



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 02:59 PM UTC

PDB ID : 3J79 / pdb_00003j79
EMDB ID : EMD-2660
Title : Cryo-EM structure of the Plasmodium falciparum 80S ribosome bound to the anti-protozoan drug emetine, large subunit
Authors : Wong, W.; Bai, X.C.; Brown, A.; Fernandez, I.S.; Hanssen, E.; Condrón, M.; Tan, Y.H.; Baum, J.; Scheres, S.H.W.
Deposited on : 2014-06-02
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:

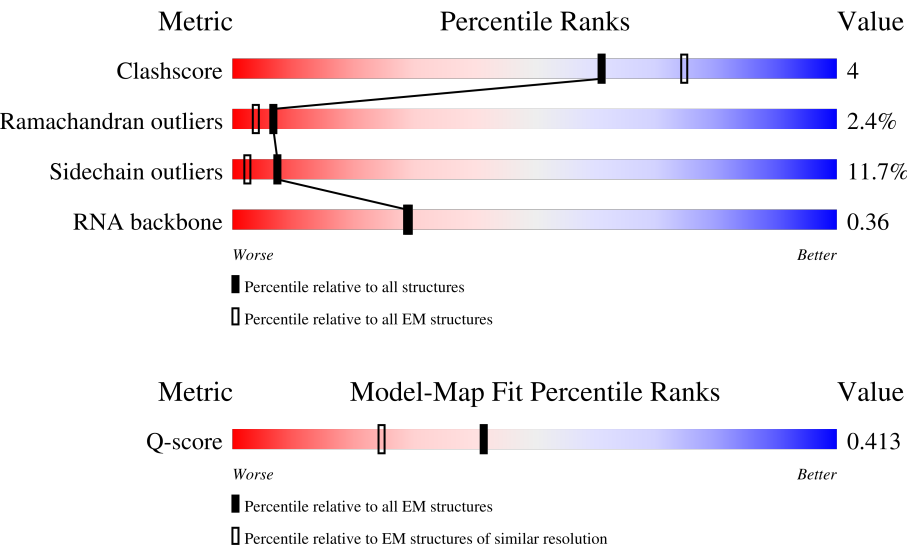
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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	A	3788	
2	B	119	
3	C	159	

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Mol	Chain	Length	Quality of chain
4	D	260	
5	E	386	
6	F	411	
7	G	173	
8	H	190	
9	I	221	
10	J	283	
11	K	202	
12	L	215	
13	M	139	
14	N	165	
15	O	148	
16	P	205	
17	Q	219	
18	R	294	
19	S	187	
20	T	182	
21	U	184	
22	V	161	
23	W	203	
24	X	139	
25	Y	190	
26	Z	126	
27	0	162	
28	1	146	

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Mol	Chain	Length	Quality of chain
29	2	127	
30	3	124	
31	4	67	
32	5	257	
33	6	108	
34	7	120	
35	8	131	
36	9	140	
37	a	150	
38	b	112	
39	c	92	
40	d	87	
41	e	51	
42	f	128	
43	g	39	
44	h	96	
45	i	104	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
47	ZN	f	100	-	-	X	-

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 124514 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3191	Total	C	N	O	P	0	0
			67935	30426	12044	22274	3191		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	118	Total	C	N	O	P	0	0
			2525	1128	461	818	118		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	151	Total	C	N	O	P	0	0
			3224	1444	589	1040	151		

- Molecule 4 is a protein called 60S ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	247	Total	C	N	O	S	0	0
			1866	1166	374	317	9		

- Molecule 5 is a protein called 60S ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	380	Total	C	N	O	S	0	0
			3061	1948	575	521	17		

- Molecule 6 is a protein called 60S ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	390	Total	C	N	O	S	0	0
			3094	1962	594	527	11		

- Molecule 7 is a protein called 60S ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	124	Total	C	N	O	S	0	0
			1010	636	197	171	6		

- Molecule 8 is a protein called 60S ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	185	Total	C	N	O	S	0	0
			1460	938	261	255	6		

- Molecule 9 is a protein called 60S ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	207	Total	C	N	O	S	0	0
			1684	1096	298	285	5		

- Molecule 10 is a protein called 60S ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	229	Total	C	N	O	S	0	0
			1873	1210	337	319	7		

- Molecule 11 is a protein called 60S ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	201	Total	C	N	O	S	0	0
			1659	1064	311	276	8		

- Molecule 12 is a protein called 60S ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	211	Total	C	N	O	S	0	0
			1761	1119	349	290	3		

- Molecule 13 is a protein called 60S ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	132	Total	C	N	O	S	0	0
			996	631	179	178	8		

- Molecule 14 is a protein called 60S ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	146	Total	C	N	O	S	0	0
			1197	779	210	202	6		

- Molecule 15 is a protein called 60S ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	147	Total	C	N	O	S	0	0
			1172	747	232	189	4		

- Molecule 16 is a protein called 60S ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	204	Total	C	N	O	S	0	0
			1697	1075	351	267	4		

- Molecule 17 is a protein called 60S ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	189	Total	C	N	O	S	0	0
			1544	984	291	261	8		

- Molecule 18 is a protein called 60S ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	252	Total	C	N	O	S	0	0
			2045	1297	384	358	6		

- Molecule 19 is a protein called 60S ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	186	Total	C	N	O	S	0	0
			1502	958	299	240	5		

- Molecule 20 is a protein called 60S ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	181	Total	C	N	O	S	0	0
			1505	949	308	244	4		

- Molecule 21 is a protein called 60S ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	180	Total	C	N	O	S	0	0
			1496	946	289	254	7		

- Molecule 22 is a protein called 60S ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	155	Total	C	N	O	S	0	0
			1275	814	241	214	6		

- Molecule 23 is a protein called 60S ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	170	Total	C	N	O	S	0	0
			1318	824	266	221	7		

- Molecule 24 is a protein called 60S ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	97	Total	C	N	O	S	0	0
			824	548	135	139	2		

- Molecule 25 is a protein called 60S ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	101	Total	C	N	O	S	0	0
			796	502	144	144	6		

- Molecule 26 is a protein called 60S ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	121	Total	C	N	O	S	0	0
			1000	626	206	165	3		

- Molecule 27 is a protein called 60S ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	0	62	Total	C	N	O	S	0	0
			521	336	97	87	1		

- Molecule 28 is a protein called 60S ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	140	Total	C	N	O	S	0	0
			1134	736	204	191	3		

- Molecule 29 is a protein called 60S ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	2	104	Total	C	N	O	S	0	0
			830	529	151	147	3		

- Molecule 30 is a protein called 60S ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	3	119	Total	C	N	O	S	0	0
			994	635	194	163	2		

- Molecule 31 is a protein called 60S ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 32 is a protein called 60S ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 33 is a protein called 60S ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	6	98	Total	C	N	O	S	0	0
			740	462	132	139	7		

- Molecule 34 is a protein called 60S ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	7	96	Total	C	N	O	S	0	0
			793	508	151	129	5		

- Molecule 35 is a protein called 60S ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	8	125	Total	C	N	O	S	0	0
			1036	660	206	163	7		

- Molecule 36 is a protein called 60S ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	9	103	Total	C	N	O	S	0	0
			844	543	163	135	3		

- Molecule 37 is a protein called 60S ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	a	106	Total	C	N	O	S	0	0
			858	530	184	138	6		

- Molecule 38 is a protein called 60S ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	b	95	Total	C	N	O		0	0
			756	477	150	129			

- Molecule 39 is a protein called 60S ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	c	89	Total	C	N	O	S	0	0
			705	439	150	111	5		

- Molecule 40 is a protein called 60S ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	d	72	Total	C	N	O	S	0	0
			603	395	107	99	2		

- Molecule 41 is a protein called 60S ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	e	43	Total	C	N	O	S	0	0
			388	243	92	52	1		

- Molecule 42 is a protein called 60S ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	f	51	Total	C	N	O	S	0	0
			413	255	87	66	5		

- Molecule 43 is a protein called 60S ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	g	37	Total	C	N	O	S	0	0
			342	210	86	44	2		

- Molecule 44 is a protein called 60S ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	h	85	Total	C	N	O	S	0	0
			658	417	127	107	7		

- Molecule 45 is a protein called 60S ribosomal protein eL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	i	95	Total	C	N	O	S	0	0
			778	490	152	127	9		

- Molecule 46 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
46	A	153	Total	Mg	0
			153	153	
46	B	3	Total	Mg	0
			3	3	
46	C	5	Total	Mg	0
			5	5	
46	M	1	Total	Mg	0
			1	1	
46	Q	1	Total	Mg	0
			1	1	

- Molecule 47 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
47	a	1	Total	Zn	0
			1	1	
47	c	1	Total	Zn	0
			1	1	

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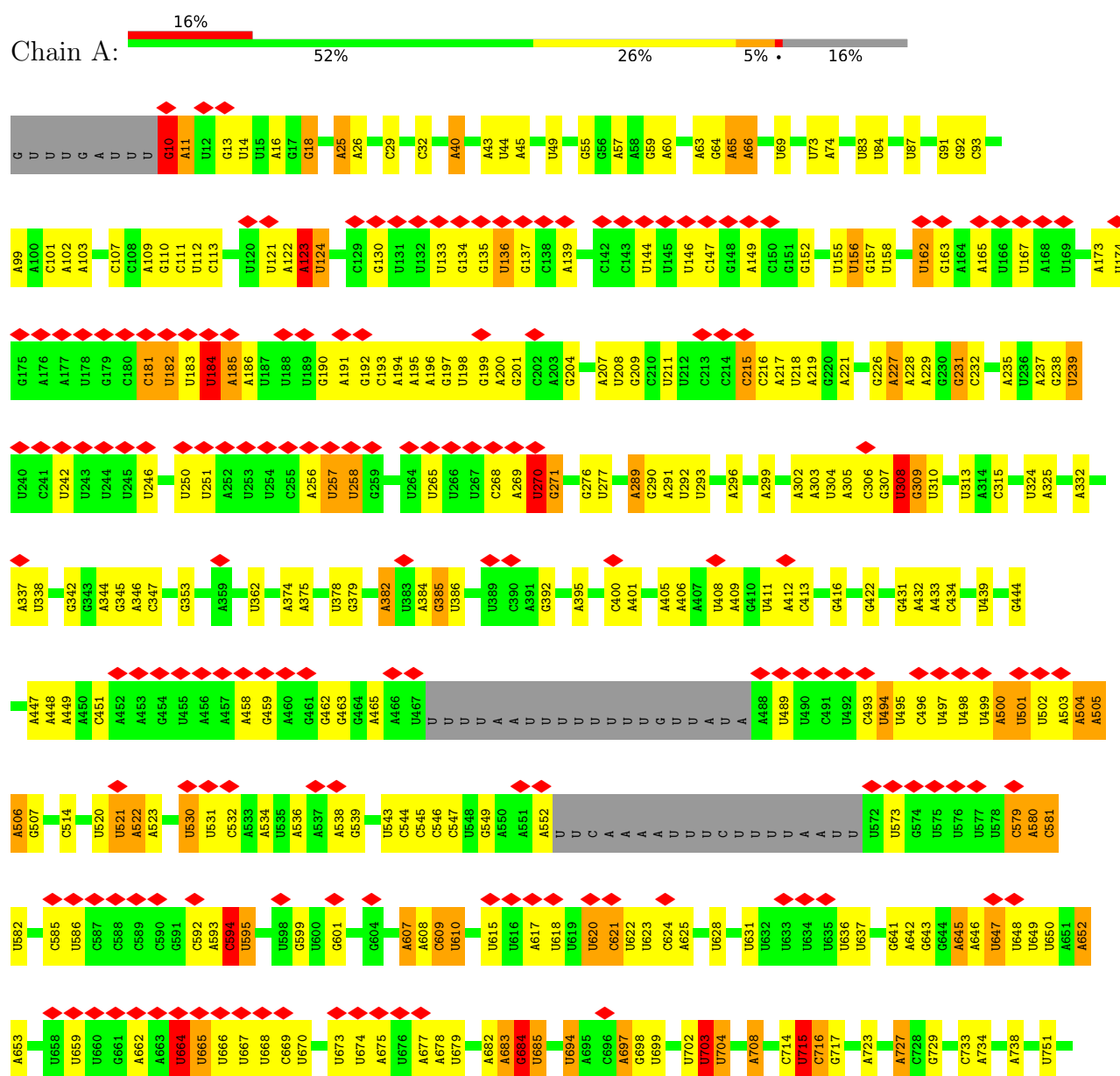
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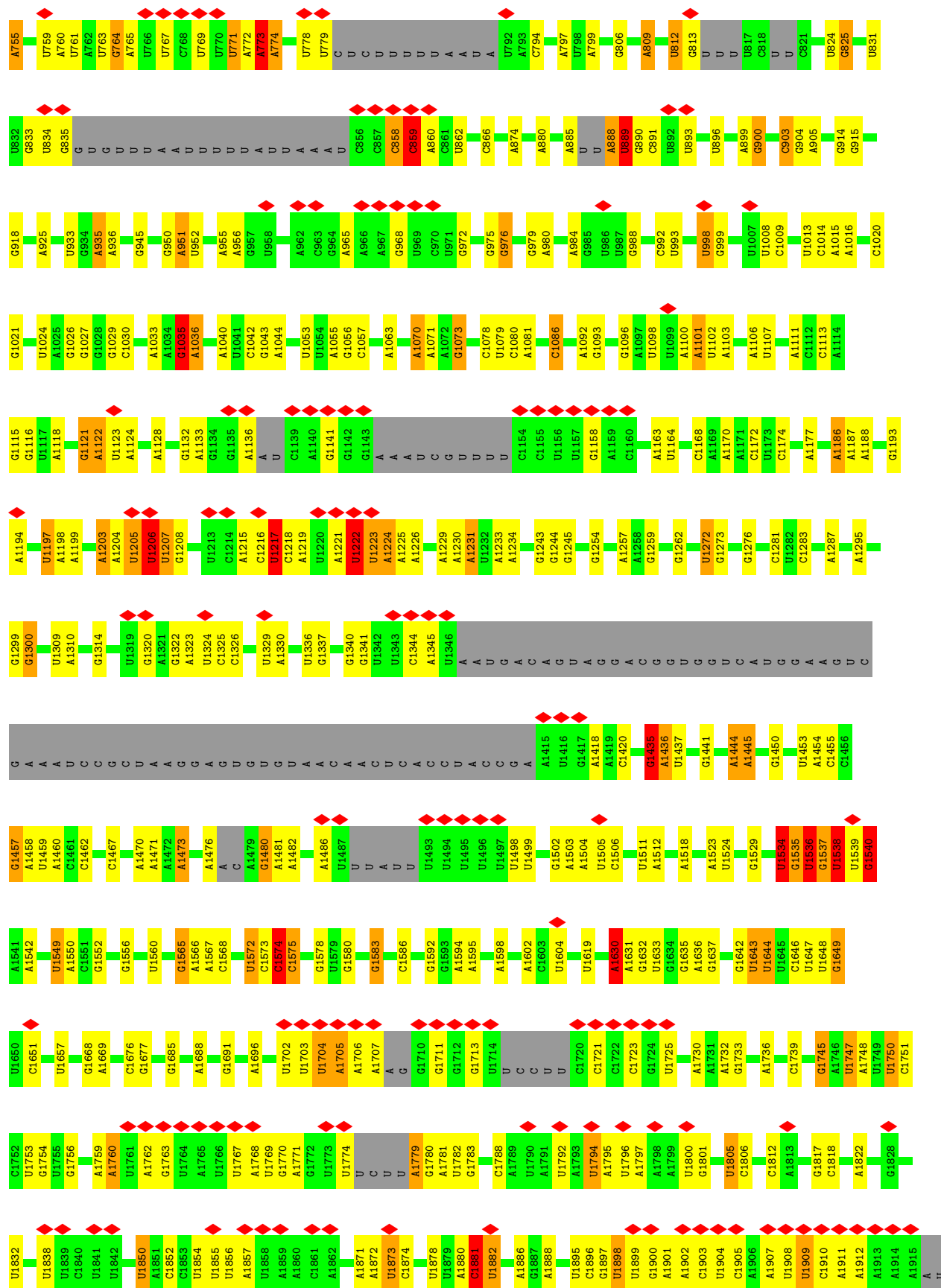
Mol	Chain	Residues	Atoms		AltConf
47	f	1	Total 1	Zn 1	0
47	h	1	Total 1	Zn 1	0
47	i	1	Total 1	Zn 1	0

3 Residue-property plots

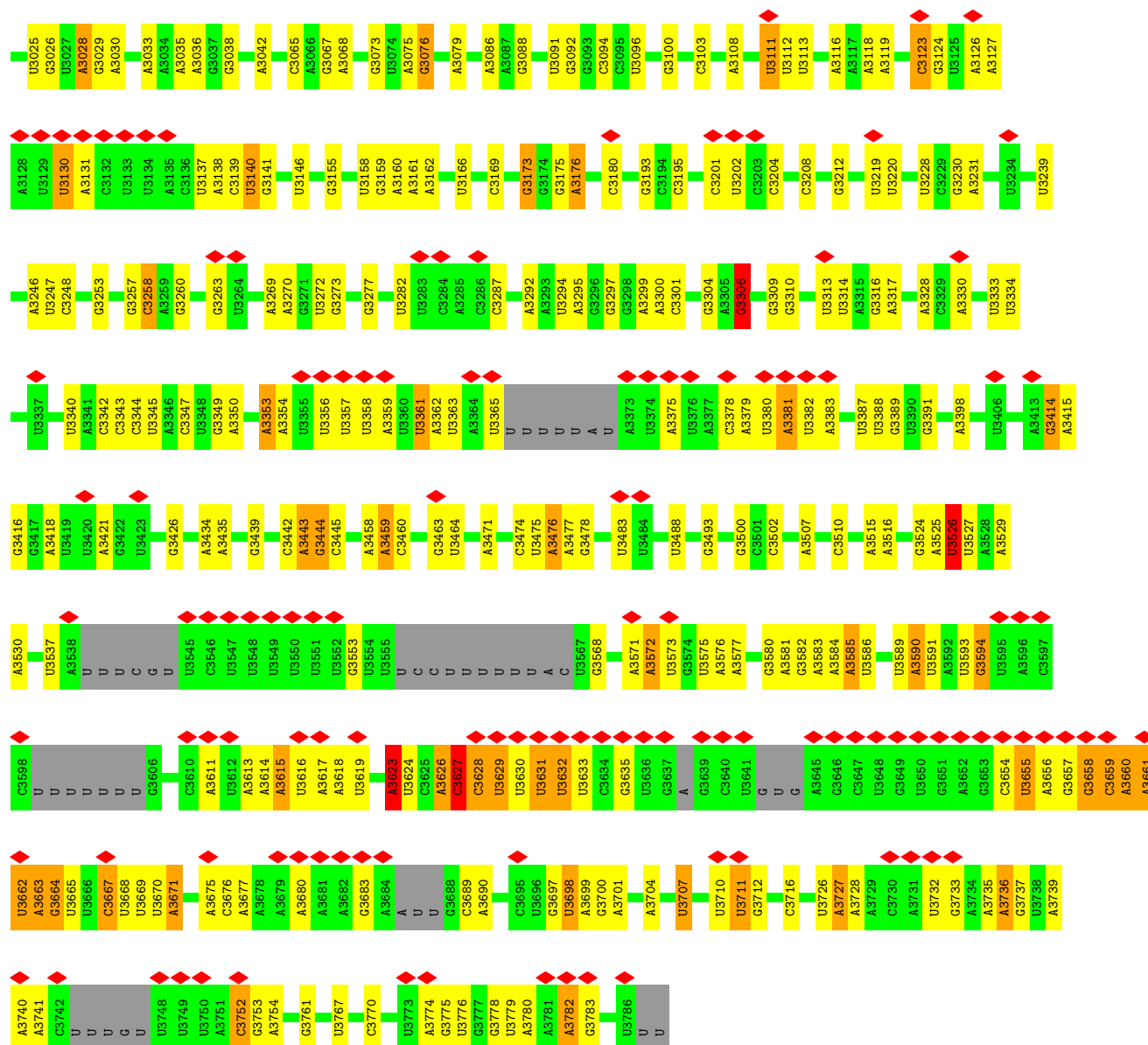
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 28S ribosomal RNA

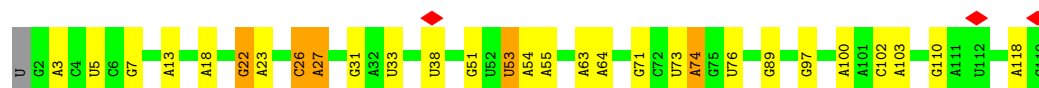
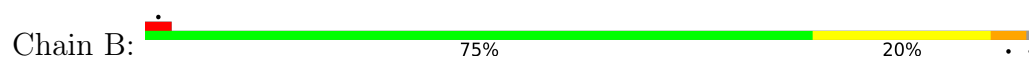




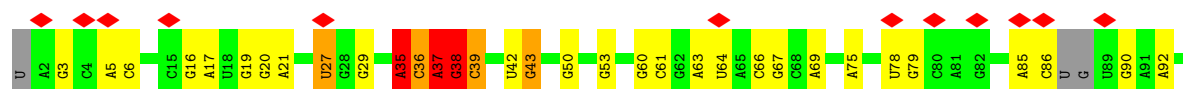


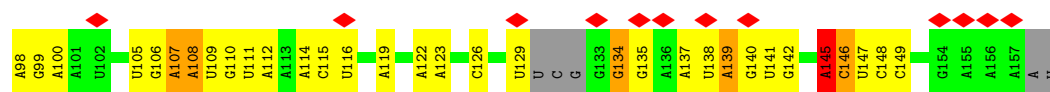


• Molecule 2: 5S ribosomal RNA

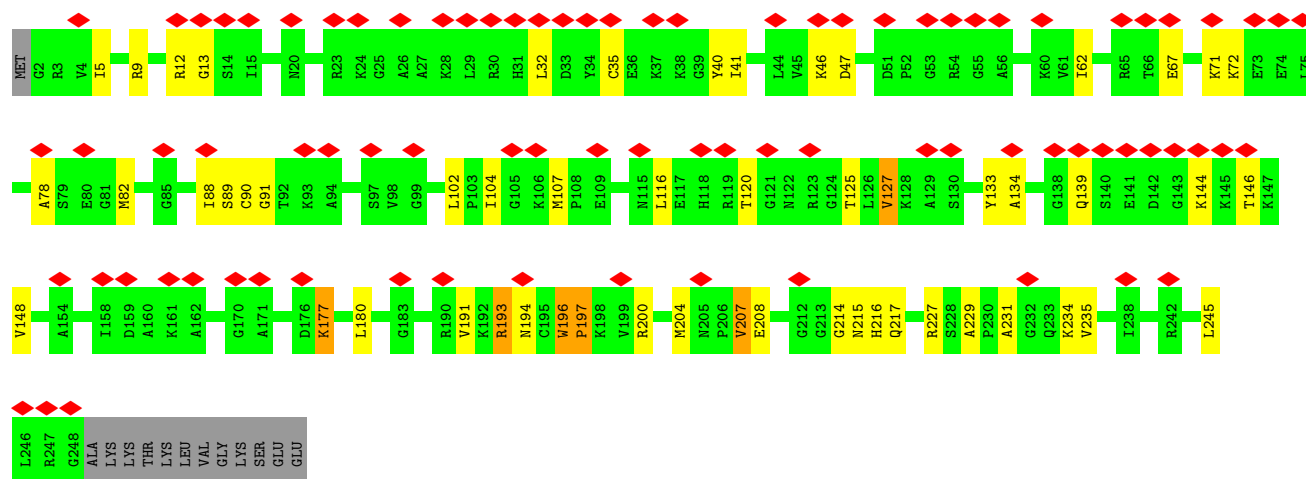
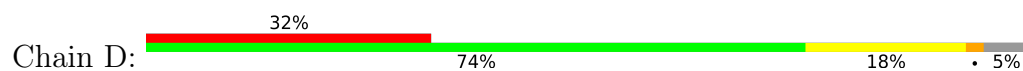


• Molecule 3: 5.8S ribosomal RNA

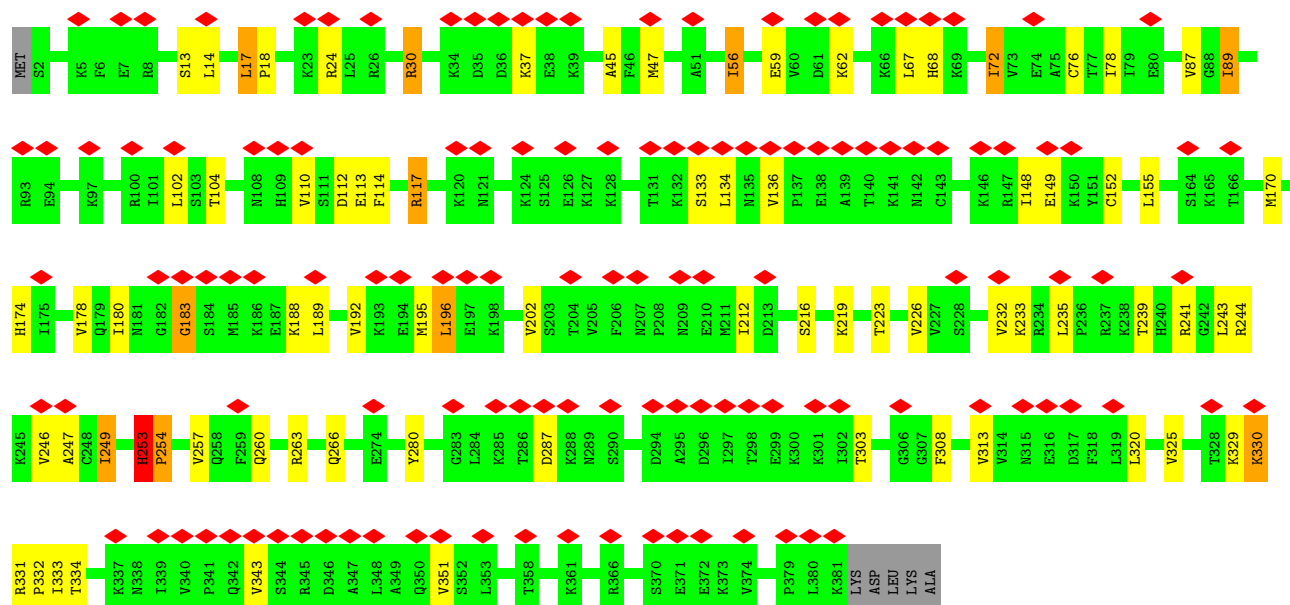
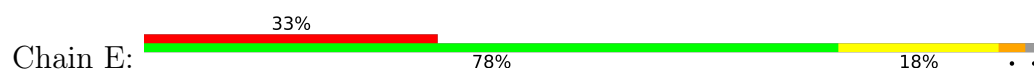




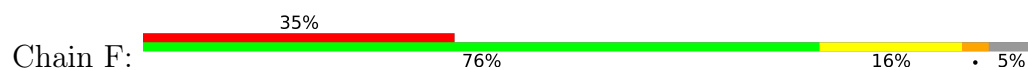
• Molecule 4: 60S ribosomal protein uL2

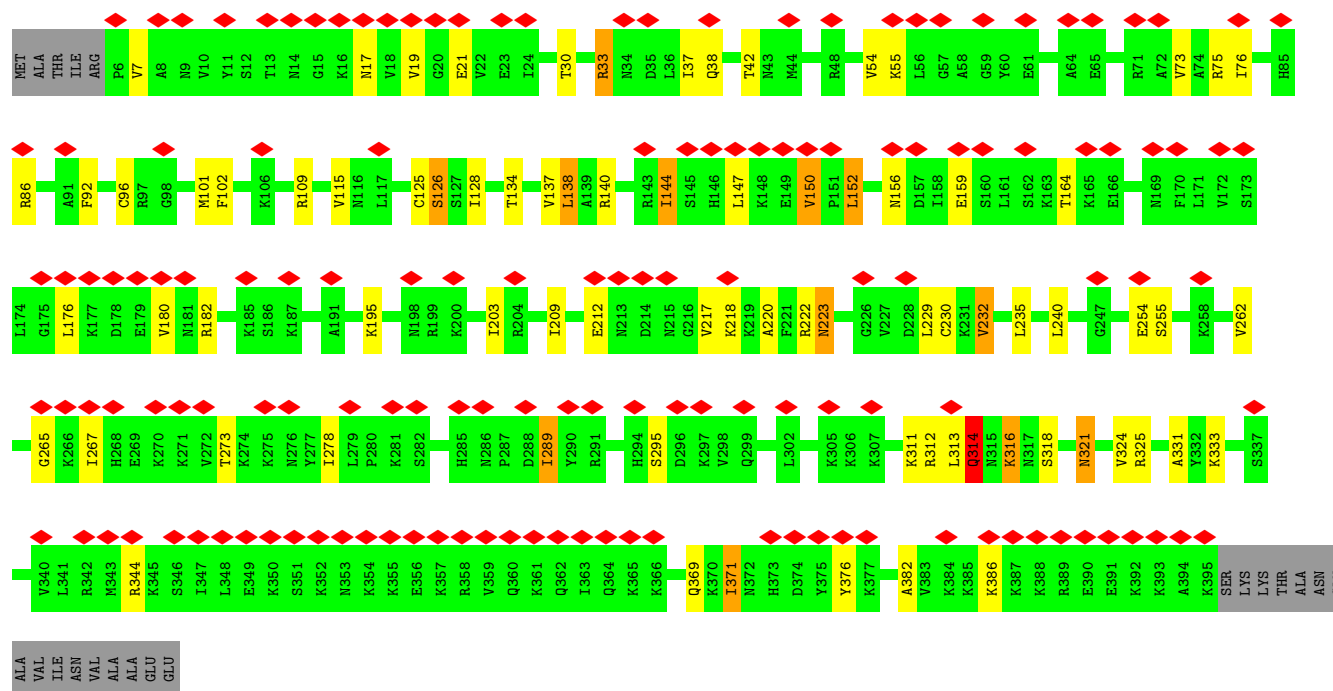


• Molecule 5: 60S ribosomal protein uL3



• Molecule 6: 60S ribosomal protein uL4





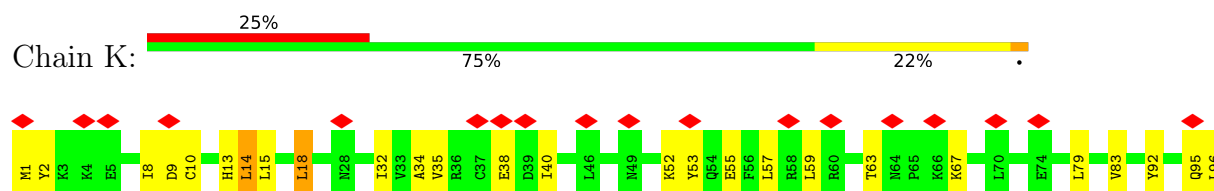
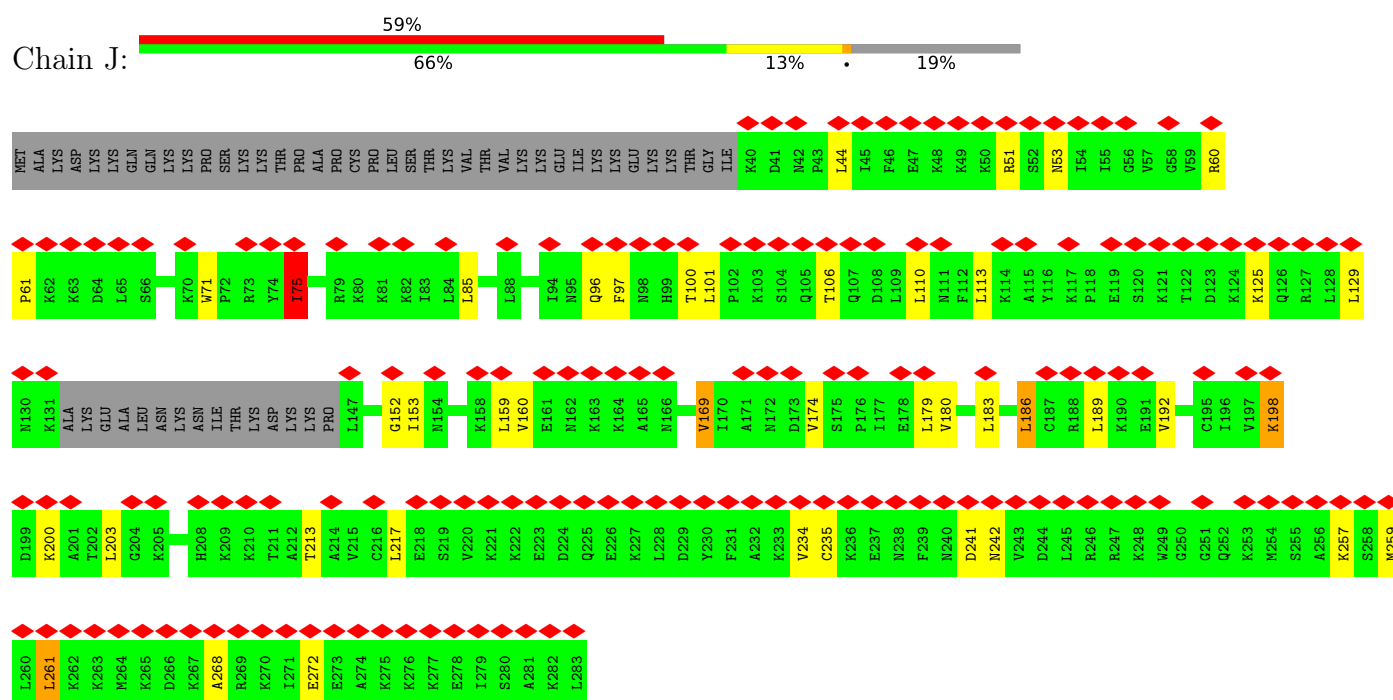
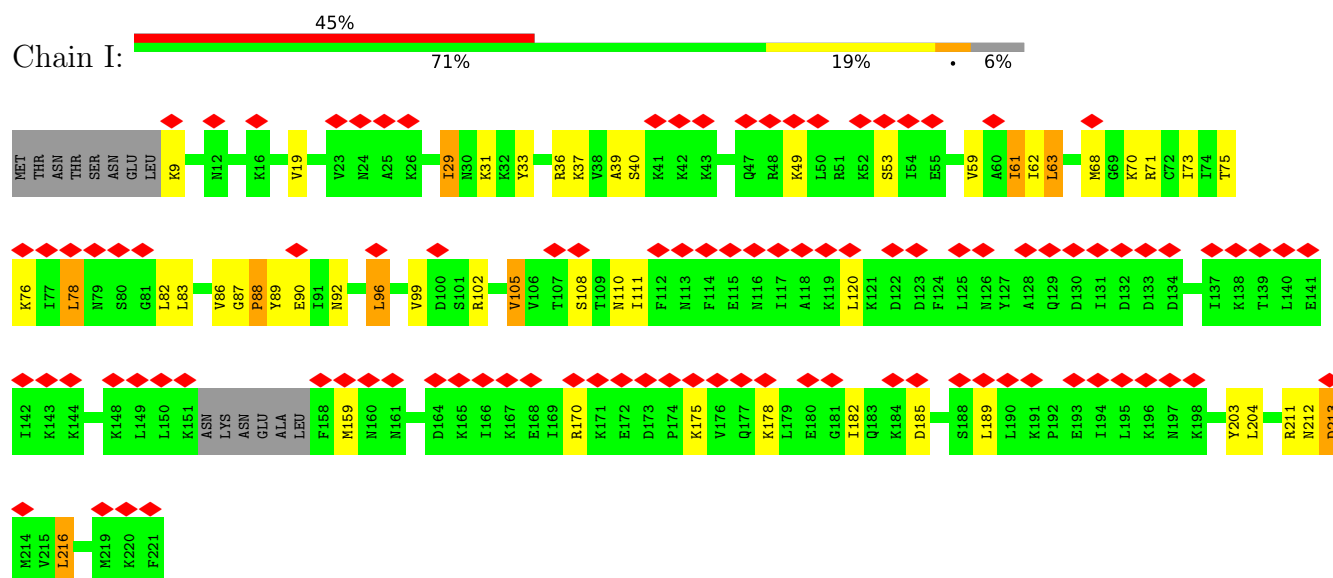
• Molecule 7: 60S ribosomal protein uL5

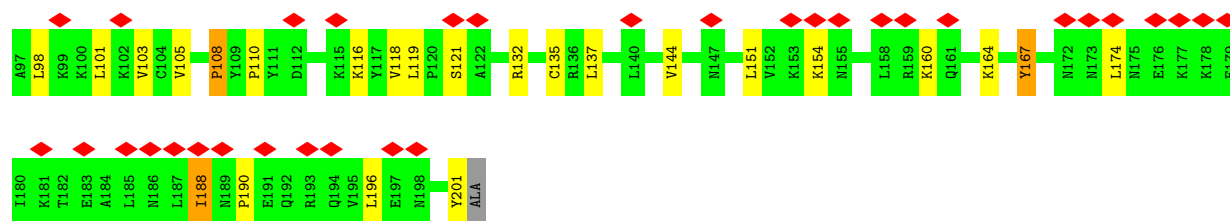


• Molecule 8: 60S ribosomal protein uL6

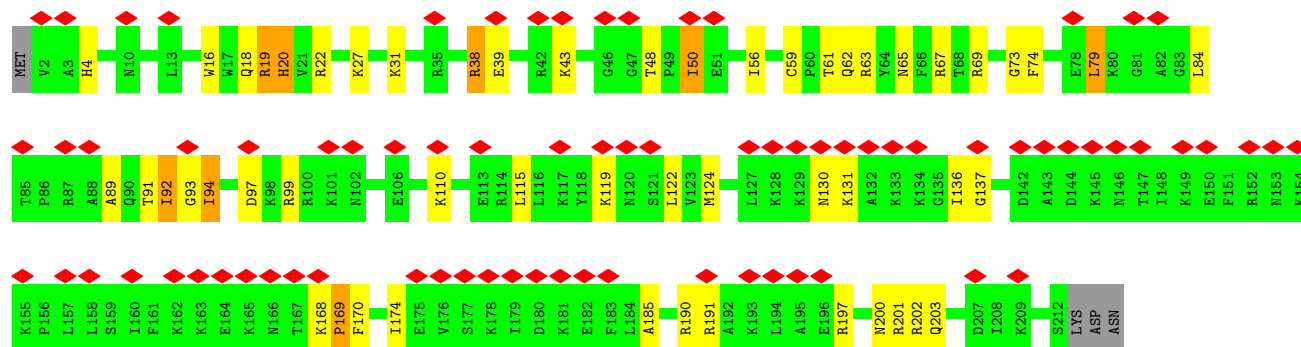
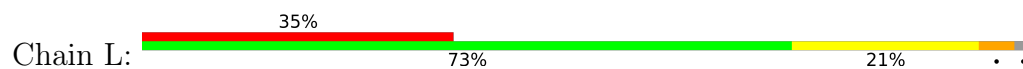


- Molecule 9: 60S ribosomal protein eL6

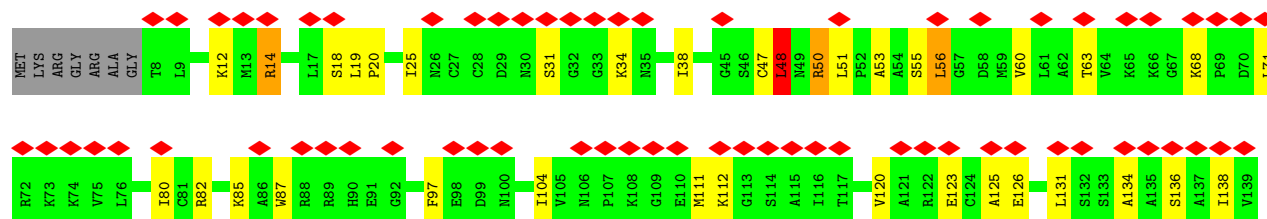




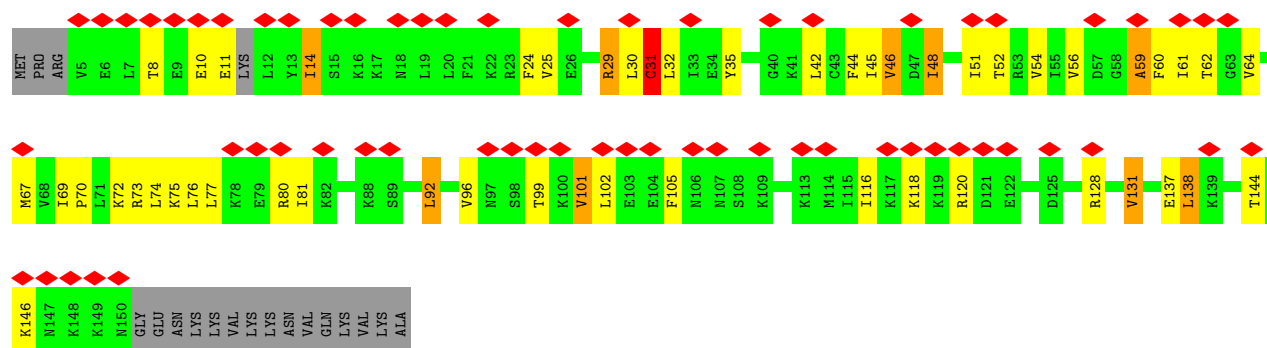
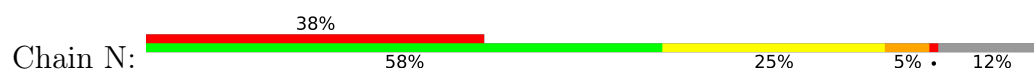
• Molecule 12: 60S ribosomal protein eL13



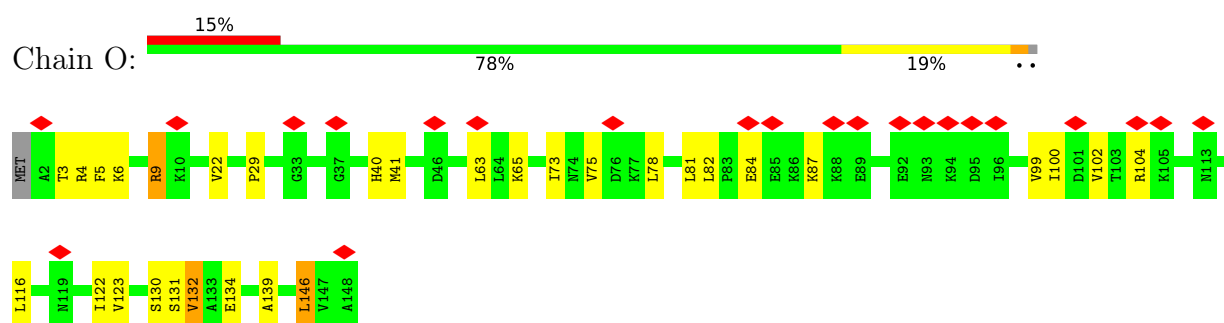
• Molecule 13: 60S ribosomal protein uL14



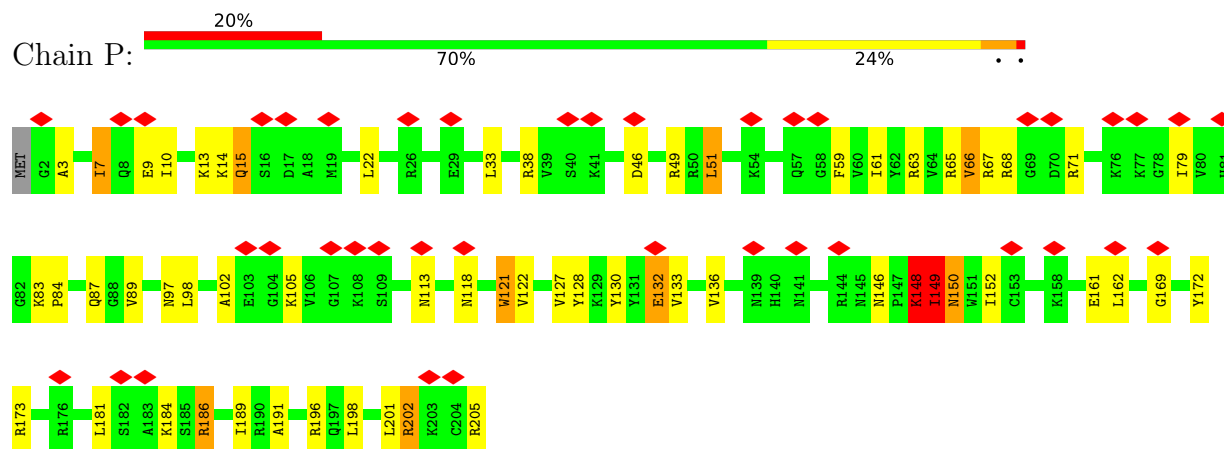
• Molecule 14: 60S ribosomal protein eL14



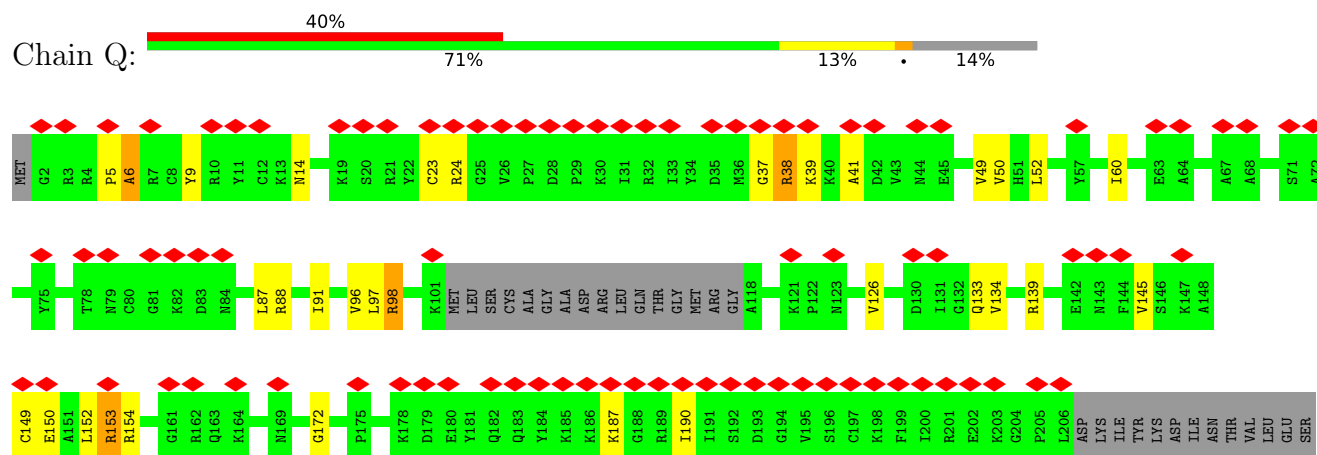
• Molecule 15: 60S ribosomal protein uL15



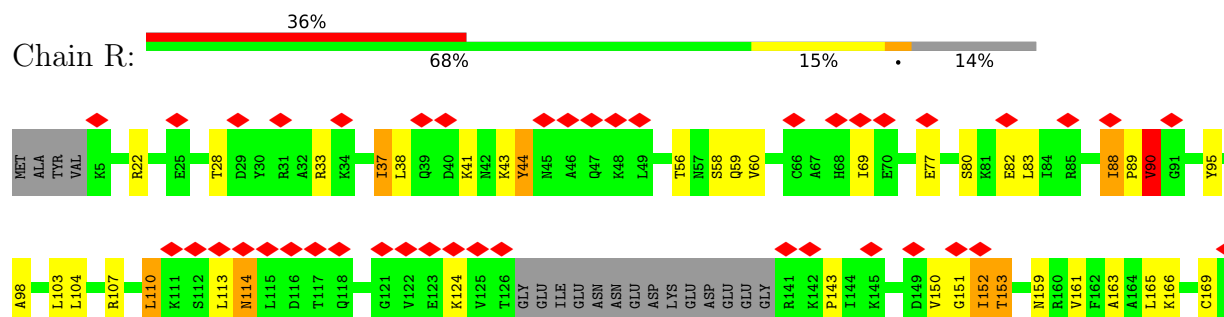
• Molecule 16: 60S ribosomal protein eL15

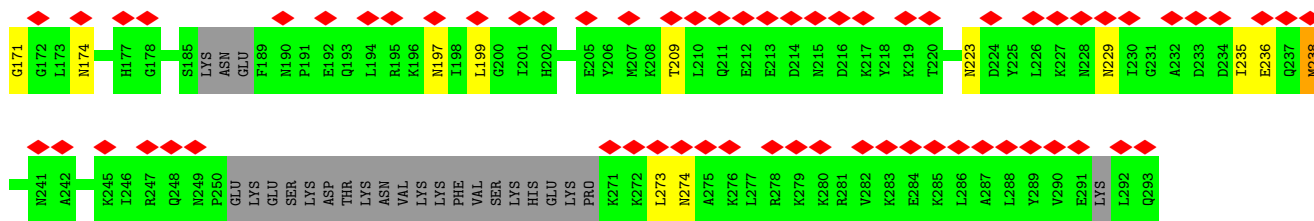


• Molecule 17: 60S ribosomal protein uL16

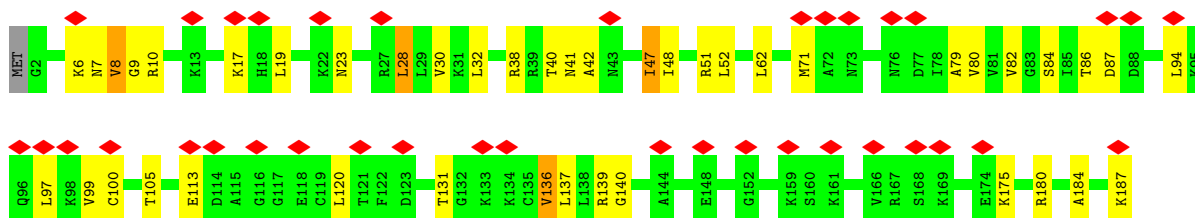
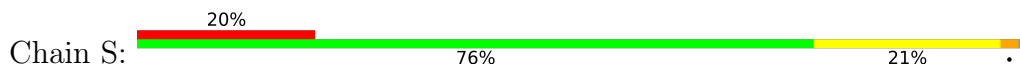


• Molecule 18: 60S ribosomal protein uL18

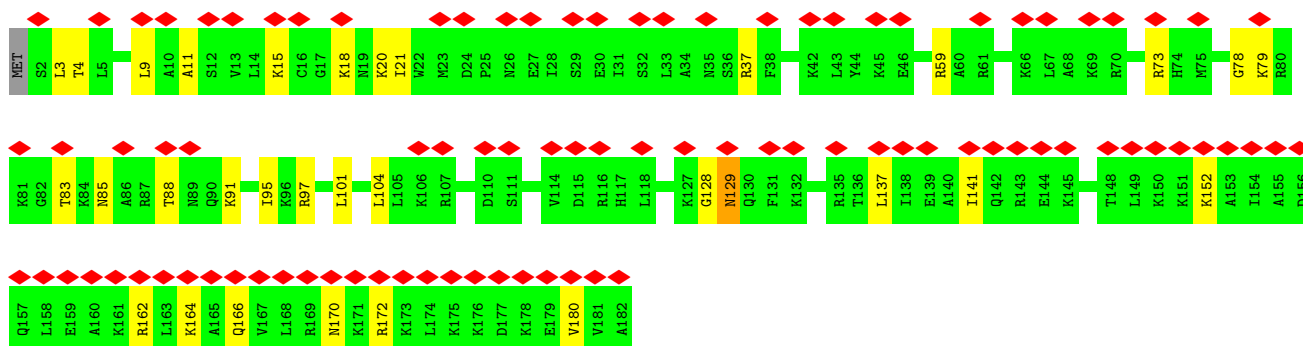
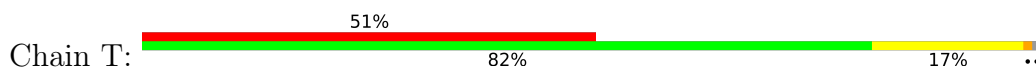




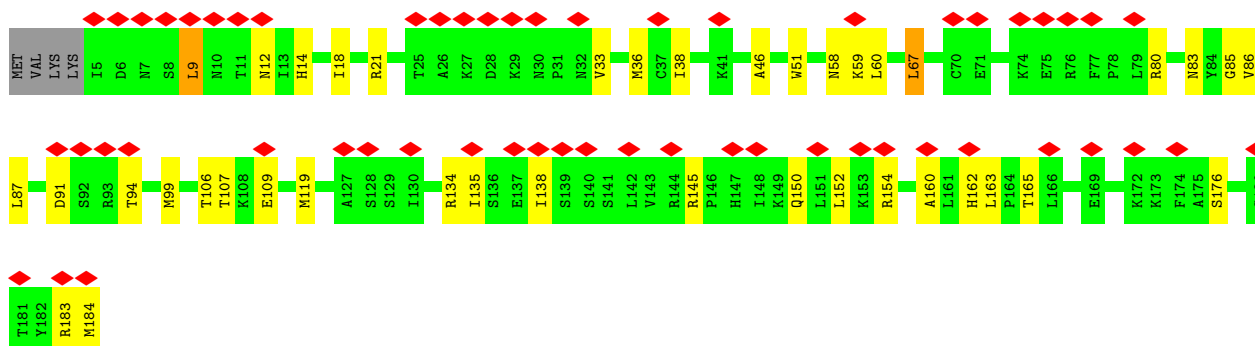
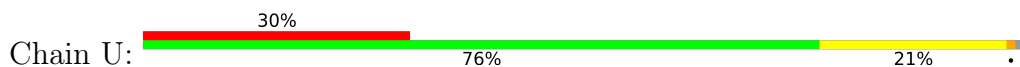
• Molecule 19: 60S ribosomal protein eL18



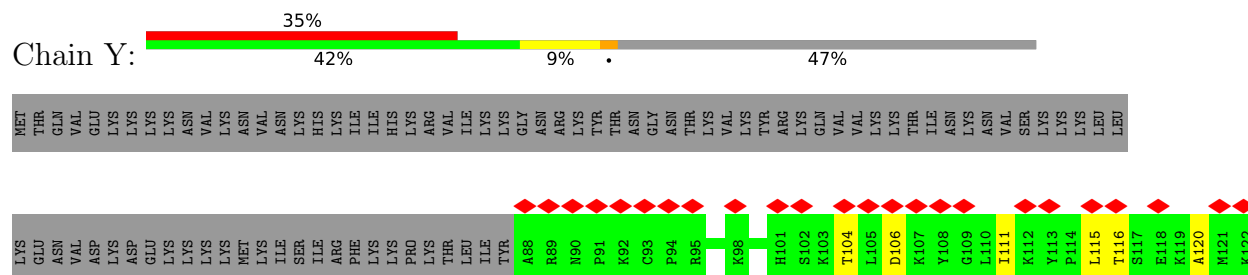
• Molecule 20: 60S ribosomal protein eL19

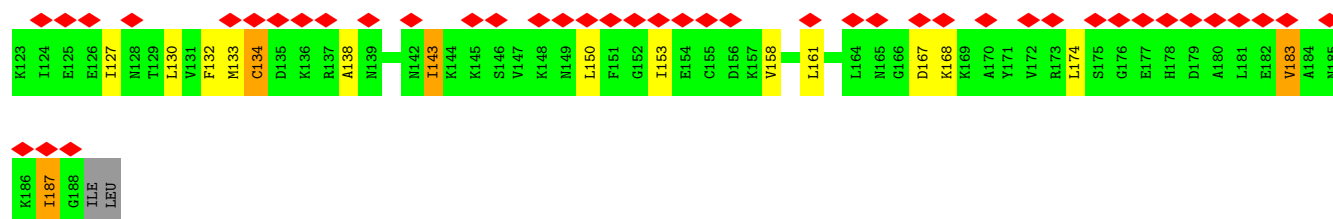


• Molecule 21: 60S ribosomal protein eL20

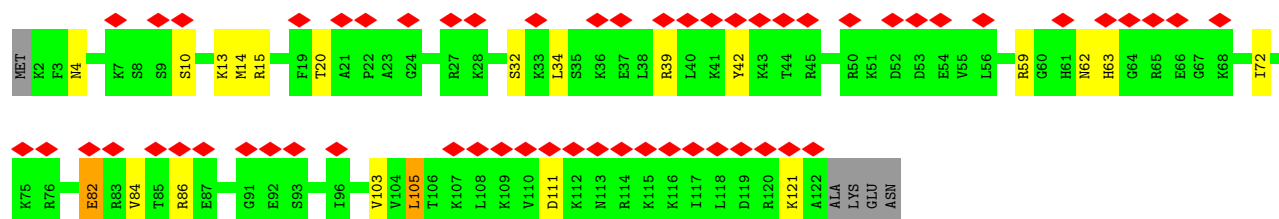
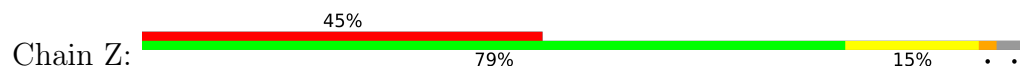


• Molecule 22: 60S ribosomal protein eL21

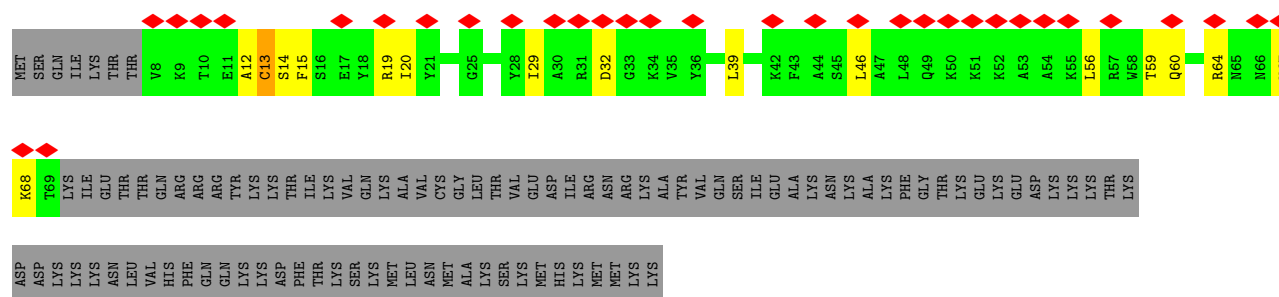




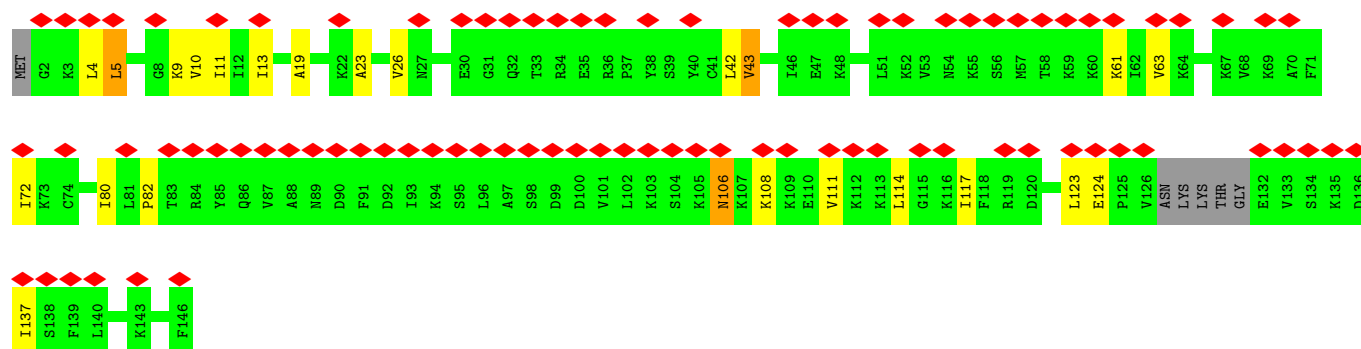
• Molecule 26: 60S ribosomal protein uL24



• Molecule 27: 60S ribosomal protein eL24

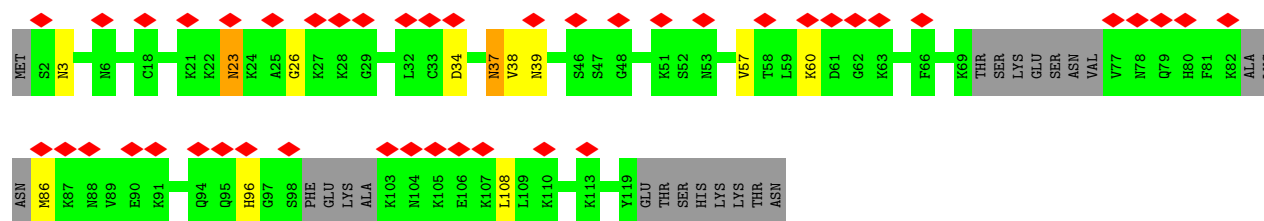


• Molecule 28: 60S ribosomal protein eL27

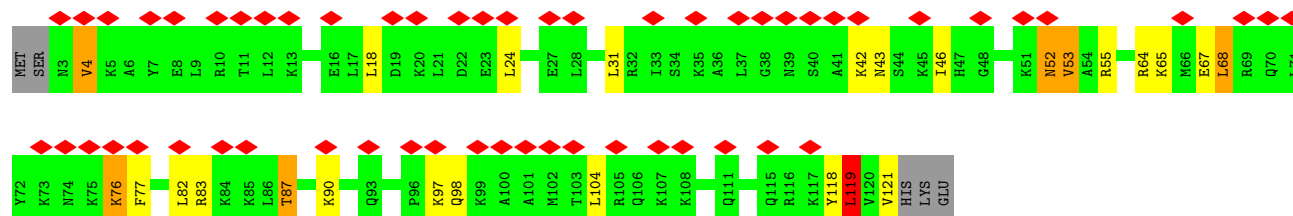
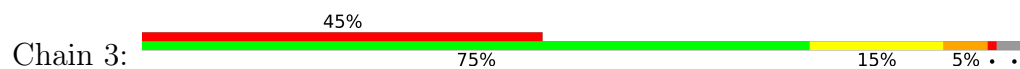


• Molecule 29: 60S ribosomal protein eL28

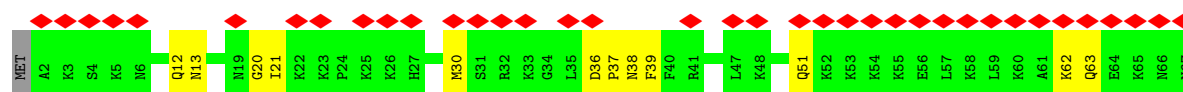
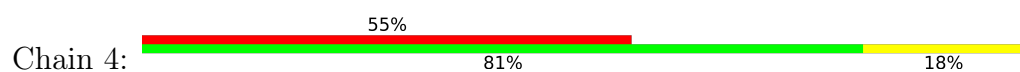




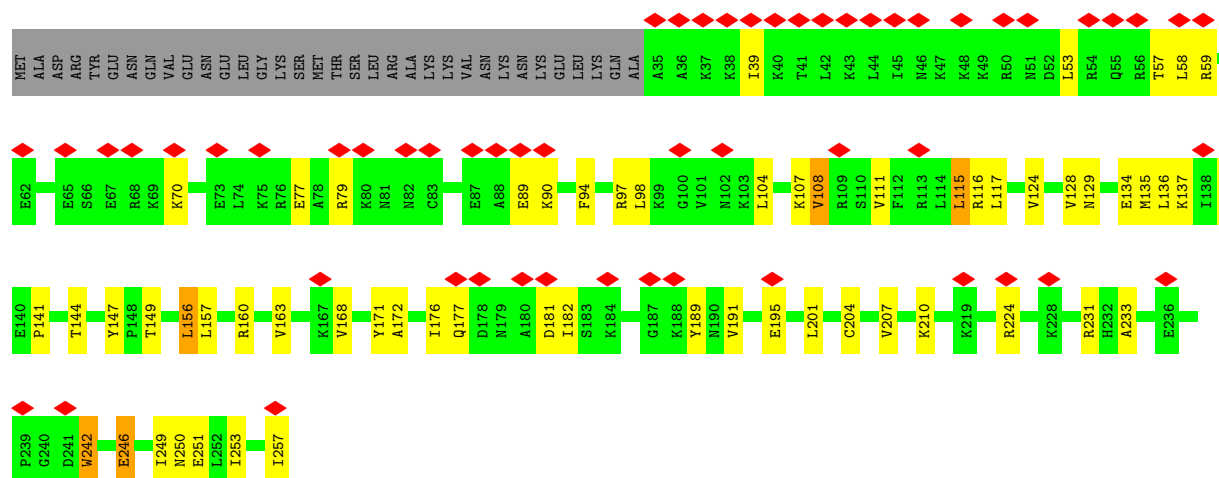
• Molecule 30: 60S ribosomal protein uL29



• Molecule 31: 60S ribosomal protein eL29



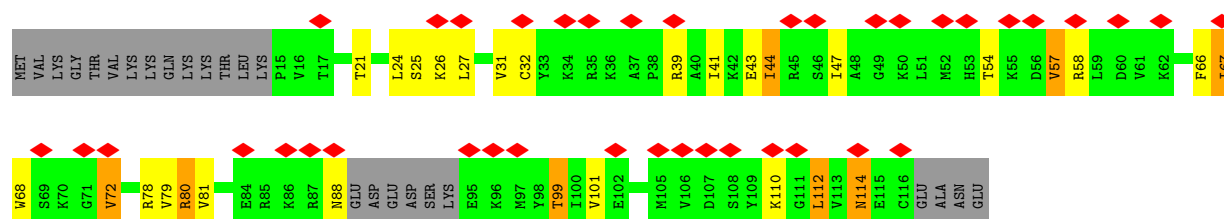
• Molecule 32: 60S ribosomal protein uL30



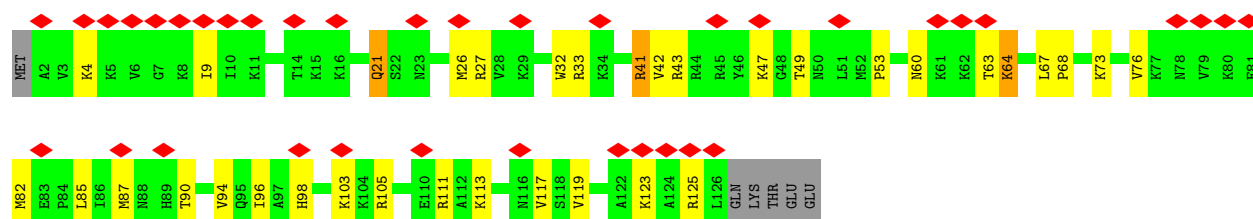
• Molecule 33: 60S ribosomal protein eL30



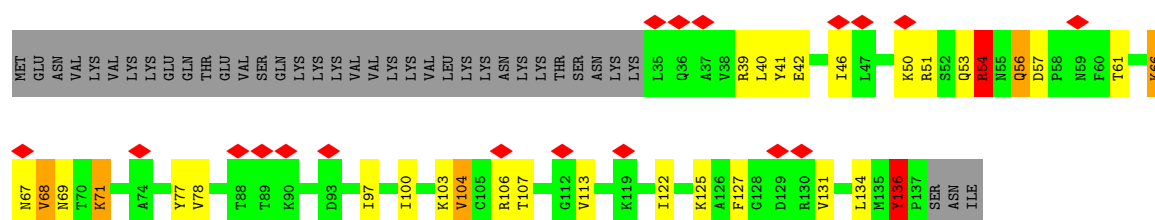
- Molecule 34: 60S ribosomal protein eL31



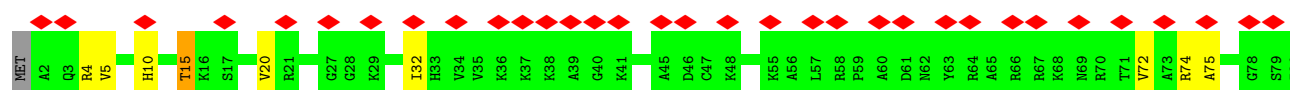
- Molecule 35: 60S ribosomal protein eL32



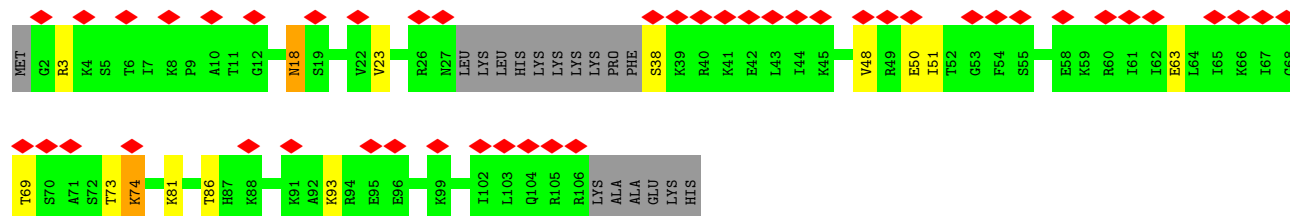
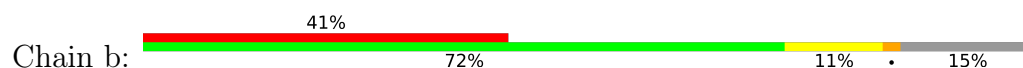
- Molecule 36: 60S ribosomal protein eL33



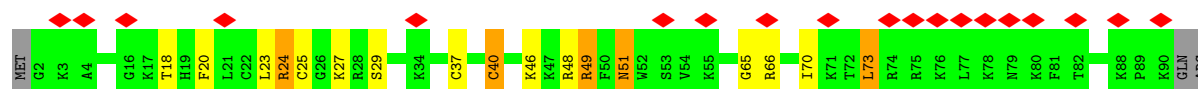
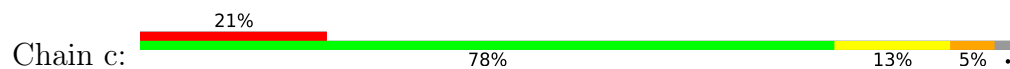
- Molecule 37: 60S ribosomal protein eL34



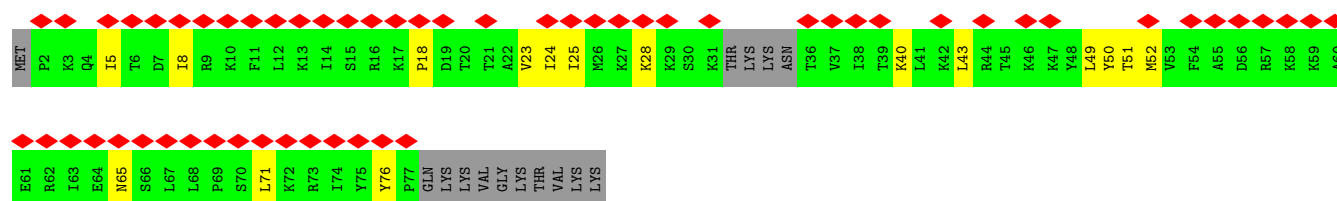
- Molecule 38: 60S ribosomal protein eL36



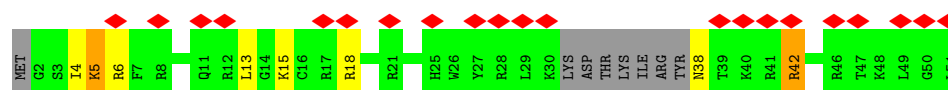
- Molecule 39: 60S ribosomal protein eL37



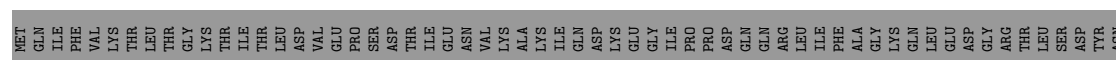
- Molecule 40: 60S ribosomal protein eL38

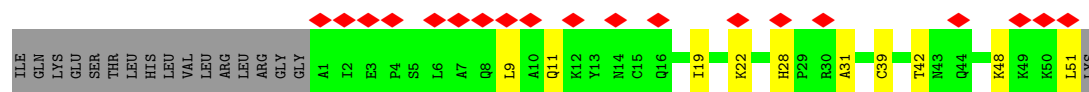


- Molecule 41: 60S ribosomal protein eL39

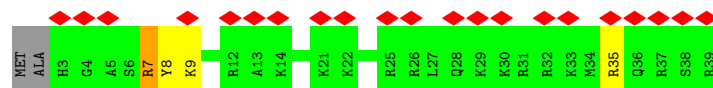
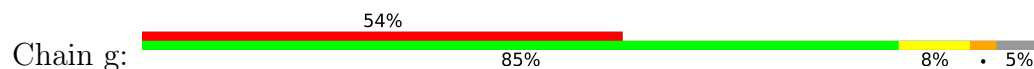


- Molecule 42: 60S ribosomal protein eL40

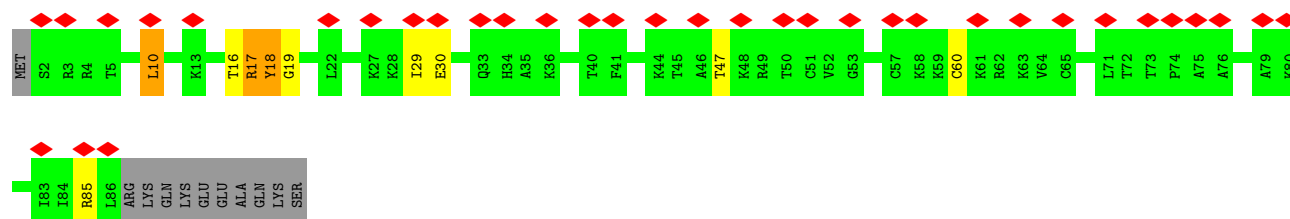
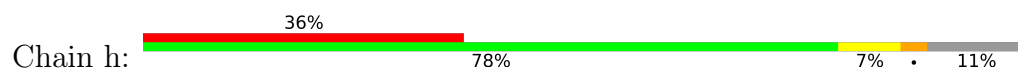




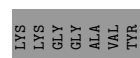
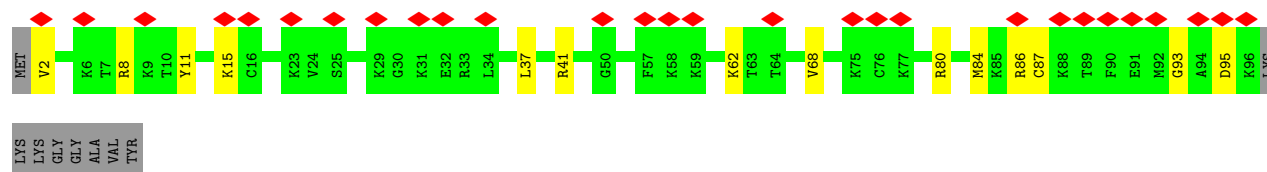
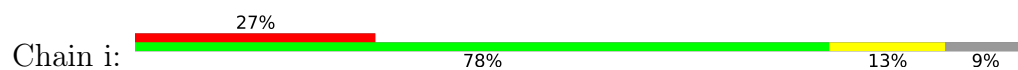
- Molecule 43: 60S ribosomal protein eL41



- Molecule 44: 60S ribosomal protein eL43



- Molecule 45: 60S ribosomal protein eL44



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	105247	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3800	Depositor
Magnification	104748	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.962	Depositor
Minimum map value	-0.545	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.044	Depositor
Recommended contour level	0.18	Depositor
Map size ($\text{\AA}$)	482.40002, 482.40002, 482.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.34, 1.34, 1.34	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.39	0/75991	0.81	121/118299 (0.1%)
2	B	0.39	0/2826	0.73	0/4404
3	C	0.39	0/3608	0.83	8/5615 (0.1%)
4	D	0.67	0/1901	1.00	4/2544 (0.2%)
5	E	0.60	0/3129	0.94	3/4195 (0.1%)
6	F	0.56	0/3144	1.10	3/4205 (0.1%)
7	G	0.57	0/1020	1.04	1/1349 (0.1%)
8	H	0.59	0/1485	0.98	1/2009 (0.0%)
9	I	0.56	0/1707	1.05	0/2274
10	J	0.58	0/1901	1.10	3/2537 (0.1%)
11	K	0.60	0/1689	1.12	2/2260 (0.1%)
12	L	0.57	0/1793	1.07	1/2387 (0.0%)
13	M	0.66	0/1012	0.92	1/1363 (0.1%)
14	N	0.59	0/1213	1.12	2/1616 (0.1%)
15	O	0.60	0/1199	0.96	0/1597
16	P	0.61	0/1735	1.07	3/2320 (0.1%)
17	Q	0.55	0/1579	0.95	0/2113
18	R	0.56	0/2074	1.07	1/2773 (0.0%)
19	S	0.58	0/1530	1.00	0/2040
20	T	0.61	0/1521	1.08	0/2012
21	U	0.60	0/1526	0.91	0/2043
22	V	0.55	0/1300	0.86	0/1732
23	W	0.60	0/1338	1.01	1/1793 (0.1%)
24	X	0.55	0/841	0.96	0/1125
25	Y	0.57	0/805	1.01	1/1074 (0.1%)
26	Z	0.53	0/1012	0.95	0/1339
27	0	0.60	0/533	0.93	1/711 (0.1%)
28	1	0.49	0/1151	0.94	0/1531
29	2	0.52	0/839	0.94	0/1114
30	3	0.58	0/1004	1.16	1/1329 (0.1%)
31	4	0.51	0/564	1.15	0/737
32	5	0.60	0/1917	1.15	6/2562 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	6	0.57	0/748	1.26	3/1001 (0.3%)
34	7	0.62	0/805	1.03	0/1073
35	8	0.63	0/1053	1.01	3/1399 (0.2%)
36	9	0.66	0/864	1.00	2/1160 (0.2%)
37	a	0.50	0/871	0.93	0/1161
38	b	0.60	0/762	1.23	1/1008 (0.1%)
39	c	0.63	0/718	0.99	0/946
40	d	0.58	0/611	1.05	1/812 (0.1%)
41	e	0.61	0/396	0.94	0/521
42	f	0.67	0/418	1.07	0/556
43	g	0.58	0/347	1.12	0/448
44	h	0.54	0/667	0.92	0/887
45	i	0.55	0/788	0.84	0/1032
All	All	0.48	0/133935	0.89	174/197006 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	D	0	1
5	E	0	3
6	F	0	1
9	I	0	1
11	K	0	1
14	N	0	1
23	W	0	1
32	5	0	1
33	6	0	1
36	9	0	1
39	c	0	1
All	All	0	13

There are no bond length outliers.

The worst 5 of 174 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	683	A	C4'-C3'-O3'	10.81	125.61	109.40
1	A	1805	U	C2'-C3'-O3'	9.95	128.62	113.70
1	A	289	A	C2'-C3'-O3'	9.52	127.98	113.70
1	A	1574	C	C4'-C3'-O3'	9.41	123.52	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	773	A	C4'-C3'-O3'	9.40	123.49	109.40

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	196	TRP	Peptide
5	E	17	LEU	Peptide
5	E	195	MET	Peptide
5	E	253	HIS	Peptide
6	F	150	VAL	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	67935	0	34190	472	0
2	B	2525	0	1274	7	0
3	C	3224	0	1630	22	0
4	D	1866	0	1964	22	0
5	E	3061	0	3205	42	0
6	F	3094	0	3333	38	0
7	G	1010	0	1073	15	0
8	H	1460	0	1532	21	0
9	I	1684	0	1849	16	0
10	J	1873	0	2055	10	0
11	K	1659	0	1782	18	0
12	L	1761	0	1895	22	0
13	M	996	0	1044	20	0
14	N	1197	0	1312	27	0
15	O	1172	0	1230	17	0
16	P	1697	0	1802	33	0
17	Q	1544	0	1582	12	0
18	R	2045	0	2129	17	0
19	S	1502	0	1636	18	0
20	T	1505	0	1671	14	0
21	U	1496	0	1556	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	V	1275	0	1355	10	0
23	W	1318	0	1319	11	0
24	X	824	0	882	5	0
25	Y	796	0	850	14	0
26	Z	1000	0	1099	4	0
27	0	521	0	539	6	0
28	1	1134	0	1245	10	0
29	2	830	0	887	3	0
30	3	994	0	1121	10	0
31	4	555	0	599	3	0
32	5	1879	0	2005	24	0
33	6	740	0	763	10	0
34	7	793	0	869	10	0
35	8	1036	0	1139	12	0
36	9	844	0	886	14	0
37	a	858	0	911	2	0
38	b	756	0	842	7	0
39	c	705	0	754	7	0
40	d	603	0	686	6	0
41	e	388	0	421	3	0
42	f	413	0	449	5	0
43	g	342	0	388	1	0
44	h	658	0	724	6	0
45	i	778	0	857	2	0
46	A	153	0	0	0	0
46	B	3	0	0	0	0
46	C	5	0	0	0	0
46	M	1	0	0	0	0
46	Q	1	0	0	0	0
47	a	1	0	0	0	0
47	c	1	0	0	0	0
47	f	1	0	0	2	0
47	h	1	0	0	1	0
47	i	1	0	0	0	0
All	All	124514	0	91334	940	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 4.

The worst 5 of 940 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3626:A:C6	1:A:3660:A:C6	2.12	1.37
1:A:3626:A:C2	1:A:3660:A:C2	2.31	1.19
1:A:3123:C:O2	12:L:202:ARG:NH2	1.80	1.14
1:A:3626:A:C5	1:A:3660:A:C6	2.38	1.12
1:A:3016:G:O6	1:A:3019:A:N6	1.87	1.07

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	D	245/260 (94%)	225 (92%)	15 (6%)	5 (2%)	6	31
5	E	378/386 (98%)	345 (91%)	26 (7%)	7 (2%)	6	33
6	F	388/411 (94%)	359 (92%)	20 (5%)	9 (2%)	5	29
7	G	116/173 (67%)	106 (91%)	7 (6%)	3 (3%)	4	26
8	H	183/190 (96%)	150 (82%)	26 (14%)	7 (4%)	2	18
9	I	203/221 (92%)	179 (88%)	15 (7%)	9 (4%)	2	15
10	J	225/283 (80%)	203 (90%)	16 (7%)	6 (3%)	4	25
11	K	199/202 (98%)	185 (93%)	10 (5%)	4 (2%)	6	31
12	L	209/215 (97%)	183 (88%)	17 (8%)	9 (4%)	2	16
13	M	130/139 (94%)	119 (92%)	8 (6%)	3 (2%)	5	29
14	N	144/165 (87%)	135 (94%)	5 (4%)	4 (3%)	4	25
15	O	145/148 (98%)	133 (92%)	12 (8%)	0	100	100
16	P	202/205 (98%)	185 (92%)	11 (5%)	6 (3%)	3	23
17	Q	185/219 (84%)	157 (85%)	22 (12%)	6 (3%)	3	21
18	R	244/294 (83%)	218 (89%)	17 (7%)	9 (4%)	2	18
19	S	184/187 (98%)	167 (91%)	12 (6%)	5 (3%)	4	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	T	179/182 (98%)	172 (96%)	4 (2%)	3 (2%)	7	35
21	U	178/184 (97%)	166 (93%)	9 (5%)	3 (2%)	7	35
22	V	153/161 (95%)	134 (88%)	13 (8%)	6 (4%)	2	18
23	W	166/203 (82%)	152 (92%)	13 (8%)	1 (1%)	21	56
24	X	95/139 (68%)	86 (90%)	6 (6%)	3 (3%)	3	21
25	Y	99/190 (52%)	93 (94%)	6 (6%)	0	100	100
26	Z	119/126 (94%)	102 (86%)	14 (12%)	3 (2%)	4	27
27	0	60/162 (37%)	55 (92%)	3 (5%)	2 (3%)	3	21
28	1	136/146 (93%)	125 (92%)	10 (7%)	1 (1%)	18	52
29	2	96/127 (76%)	85 (88%)	9 (9%)	2 (2%)	5	31
30	3	117/124 (94%)	104 (89%)	10 (8%)	3 (3%)	4	26
31	4	64/67 (96%)	56 (88%)	5 (8%)	3 (5%)	2	14
32	5	221/257 (86%)	197 (89%)	20 (9%)	4 (2%)	6	34
33	6	96/108 (89%)	92 (96%)	2 (2%)	2 (2%)	5	31
34	7	92/120 (77%)	88 (96%)	4 (4%)	0	100	100
35	8	123/131 (94%)	109 (89%)	10 (8%)	4 (3%)	3	21
36	9	101/140 (72%)	86 (85%)	12 (12%)	3 (3%)	3	23
37	a	104/150 (69%)	98 (94%)	4 (4%)	2 (2%)	6	33
38	b	91/112 (81%)	86 (94%)	3 (3%)	2 (2%)	5	29
39	c	87/92 (95%)	68 (78%)	15 (17%)	4 (5%)	2	15
40	d	68/87 (78%)	65 (96%)	3 (4%)	0	100	100
41	e	39/51 (76%)	38 (97%)	1 (3%)	0	100	100
42	f	49/128 (38%)	45 (92%)	4 (8%)	0	100	100
43	g	35/39 (90%)	31 (89%)	4 (11%)	0	100	100
44	h	83/96 (86%)	74 (89%)	8 (10%)	1 (1%)	10	42
45	i	93/104 (89%)	82 (88%)	7 (8%)	4 (4%)	2	16
All	All	6124/7124 (86%)	5538 (90%)	438 (7%)	148 (2%)	7	28

5 of 148 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	197	PRO
5	E	18	PRO

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Mol	Chain	Res	Type
6	F	102	PHE
7	G	130	HIS
7	G	143	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	
4	D	191/202 (95%)	169 (88%)	22 (12%)	5	24
5	E	335/340 (98%)	307 (92%)	28 (8%)	10	38
6	F	336/352 (96%)	304 (90%)	32 (10%)	8	32
7	G	110/155 (71%)	93 (84%)	17 (16%)	2	14
8	H	164/173 (95%)	132 (80%)	32 (20%)	1	8
9	I	189/203 (93%)	164 (87%)	25 (13%)	4	19
10	J	211/260 (81%)	188 (89%)	23 (11%)	6	26
11	K	181/182 (100%)	156 (86%)	25 (14%)	3	18
12	L	190/194 (98%)	164 (86%)	26 (14%)	3	18
13	M	106/110 (96%)	93 (88%)	13 (12%)	4	22
14	N	134/152 (88%)	112 (84%)	22 (16%)	2	12
15	O	121/122 (99%)	110 (91%)	11 (9%)	9	34
16	P	179/180 (99%)	158 (88%)	21 (12%)	5	23
17	Q	165/190 (87%)	151 (92%)	14 (8%)	10	37
18	R	214/254 (84%)	185 (86%)	29 (14%)	3	18
19	S	158/159 (99%)	140 (89%)	18 (11%)	5	24
20	T	161/163 (99%)	146 (91%)	15 (9%)	8	33
21	U	162/166 (98%)	150 (93%)	12 (7%)	13	43
22	V	140/144 (97%)	131 (94%)	9 (6%)	16	48
23	W	128/178 (72%)	110 (86%)	18 (14%)	3	17
24	X	92/131 (70%)	86 (94%)	6 (6%)	15	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	Y	90/177 (51%)	81 (90%)	9 (10%)	7	30
26	Z	111/115 (96%)	97 (87%)	14 (13%)	4	21
27	0	53/146 (36%)	47 (89%)	6 (11%)	5	24
28	1	127/132 (96%)	113 (89%)	14 (11%)	6	26
29	2	97/118 (82%)	91 (94%)	6 (6%)	16	49
30	3	110/115 (96%)	94 (86%)	16 (14%)	3	16
31	4	60/61 (98%)	55 (92%)	5 (8%)	10	38
32	5	201/231 (87%)	177 (88%)	24 (12%)	5	23
33	6	83/92 (90%)	68 (82%)	15 (18%)	2	9
34	7	90/112 (80%)	68 (76%)	22 (24%)	1	4
35	8	114/120 (95%)	96 (84%)	18 (16%)	2	13
36	9	90/127 (71%)	74 (82%)	16 (18%)	2	10
37	a	89/128 (70%)	77 (86%)	12 (14%)	4	19
38	b	82/97 (84%)	76 (93%)	6 (7%)	13	43
39	c	73/77 (95%)	66 (90%)	7 (10%)	8	32
40	d	69/83 (83%)	62 (90%)	7 (10%)	7	30
41	e	40/48 (83%)	33 (82%)	7 (18%)	2	10
42	f	45/114 (40%)	42 (93%)	3 (7%)	15	47
43	g	34/35 (97%)	31 (91%)	3 (9%)	9	35
44	h	70/80 (88%)	65 (93%)	5 (7%)	13	44
45	i	87/93 (94%)	81 (93%)	6 (7%)	14	45
All	All	5482/6311 (87%)	4843 (88%)	639 (12%)	7	23

5 of 639 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	2	34	ASP
36	9	68	VAL
30	3	76	LYS
29	2	23	ASN
33	6	54	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 137 such sidechains are listed below:

Mol	Chain	Res	Type
34	7	88	ASN
36	9	56	GLN
42	f	33	ASN
16	P	15	GLN
15	O	118	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3164/3788 (83%)	954 (30%)	167 (5%)
2	B	117/119 (98%)	23 (19%)	1 (0%)
3	C	148/159 (93%)	44 (29%)	8 (5%)
All	All	3429/4066 (84%)	1021 (29%)	176 (5%)

5 of 1021 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	A
1	A	13	G
1	A	14	U
1	A	16	A
1	A	18	G

5 of 176 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2437	A
1	A	3381	A
1	A	2523	U
1	A	2886	A
1	A	3477	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 168 ligands modelled in this entry, 168 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

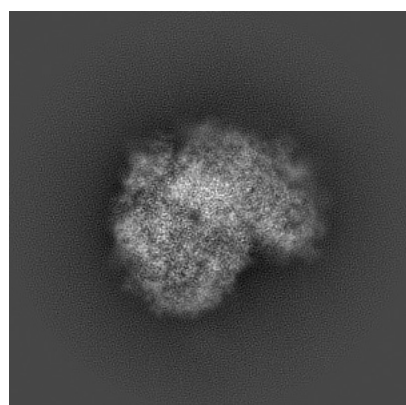
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2660. These allow visual inspection of the internal detail of the map and identification of artifacts.

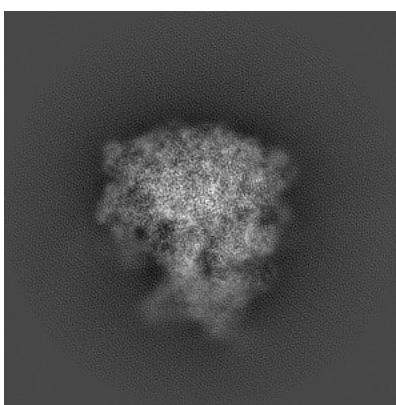
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

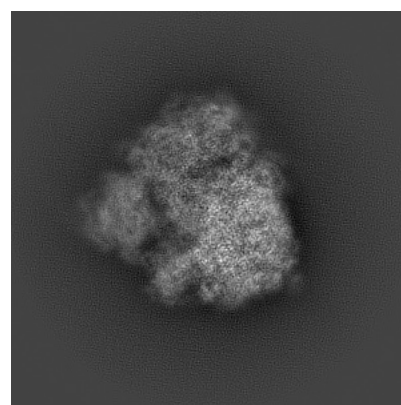
6.1.1 Primary map



X



Y

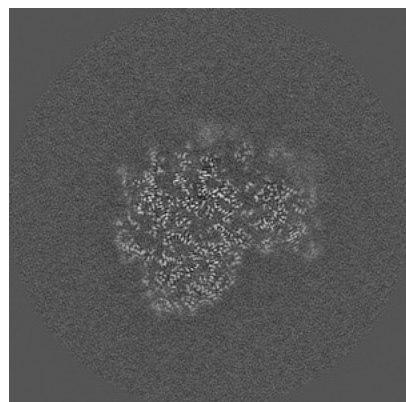


Z

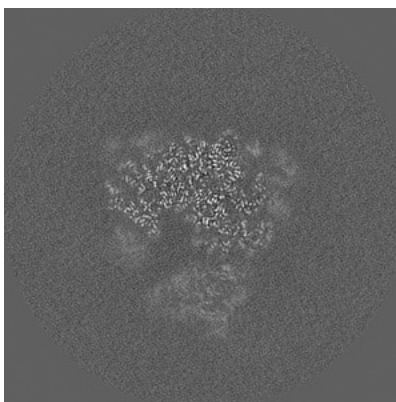
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

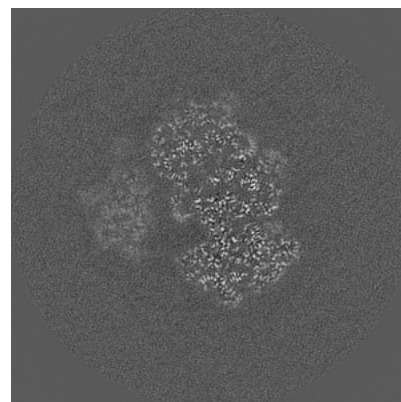
6.2.1 Primary map



X Index: 180



Y Index: 180

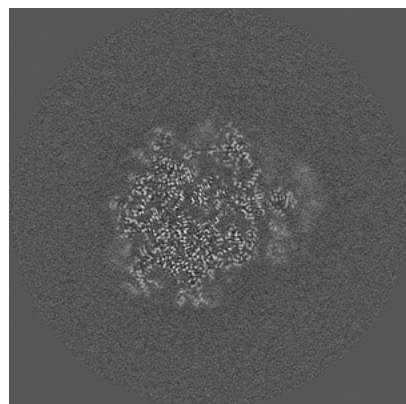


Z Index: 180

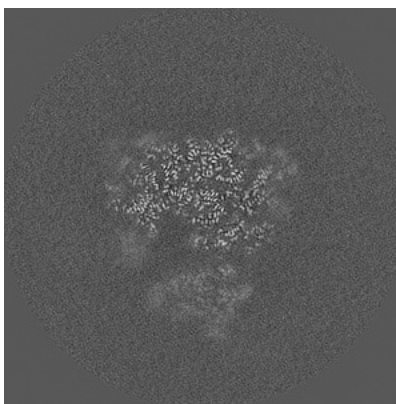
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

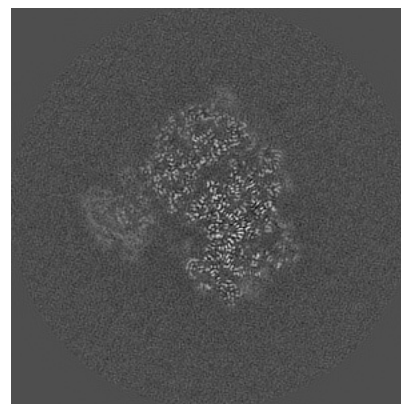
6.3.1 Primary map



X Index: 201



Y Index: 183

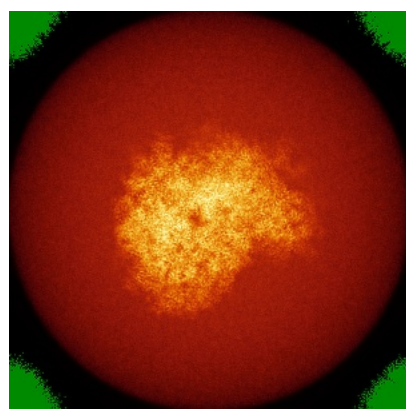


Z Index: 187

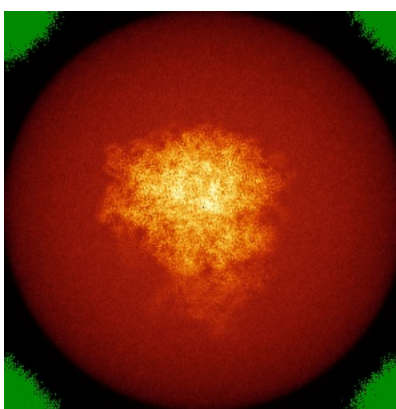
The images above show the largest variance slices of the map in three orthogonal directions.

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

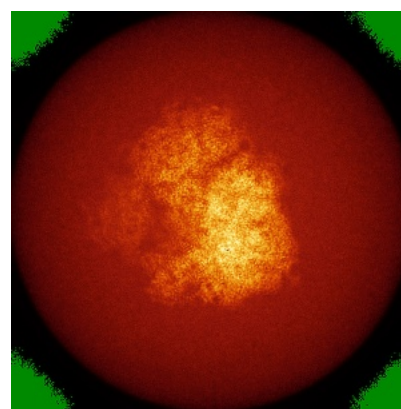
6.4.1 Primary map



X



Y

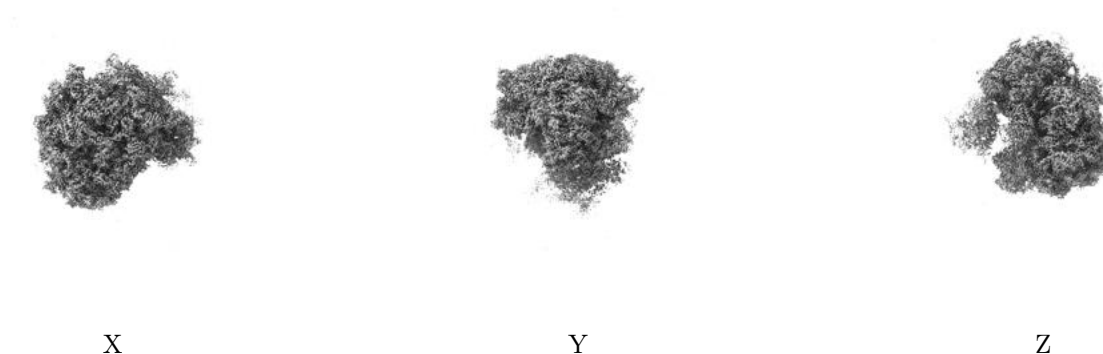


Z

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

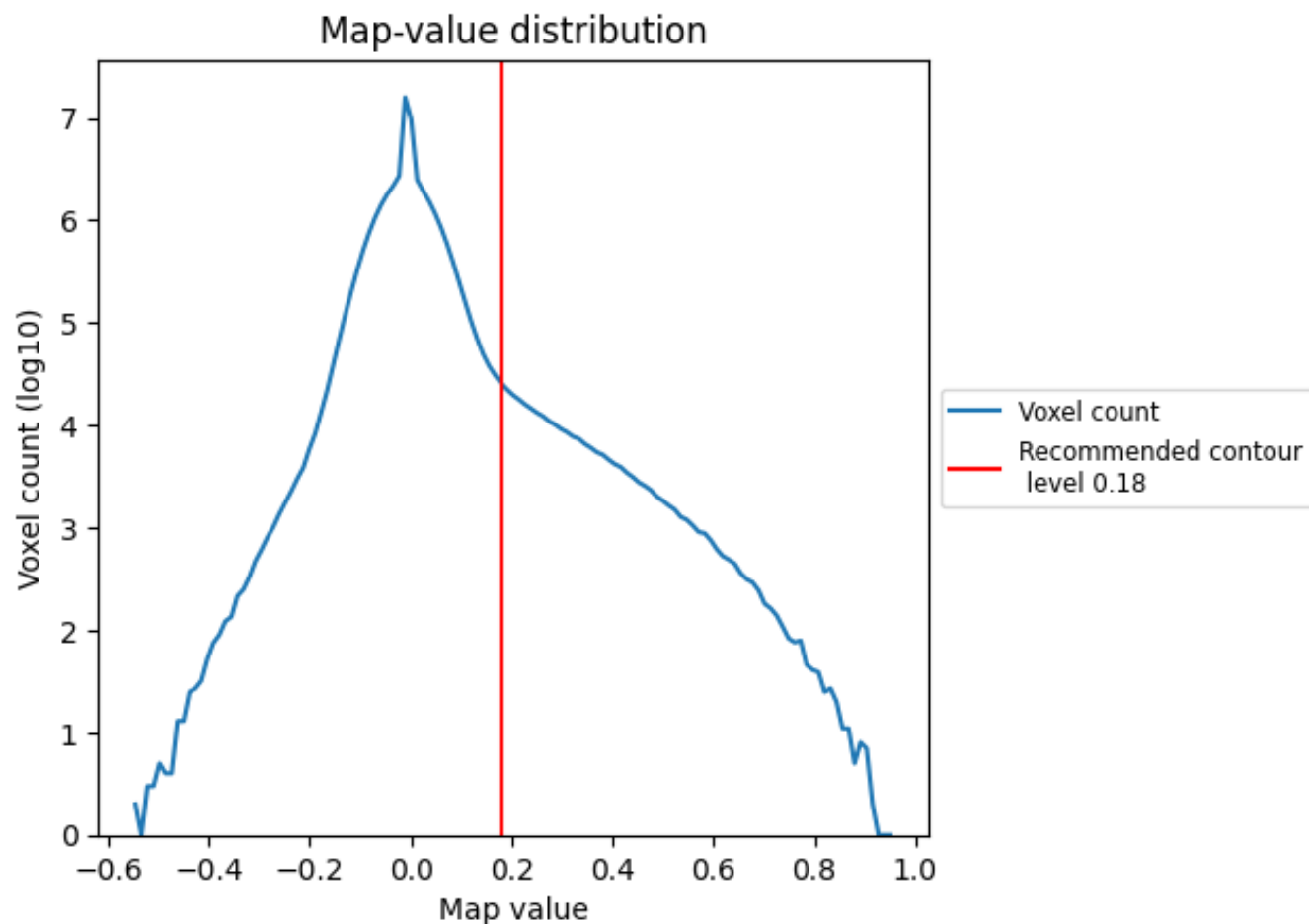
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

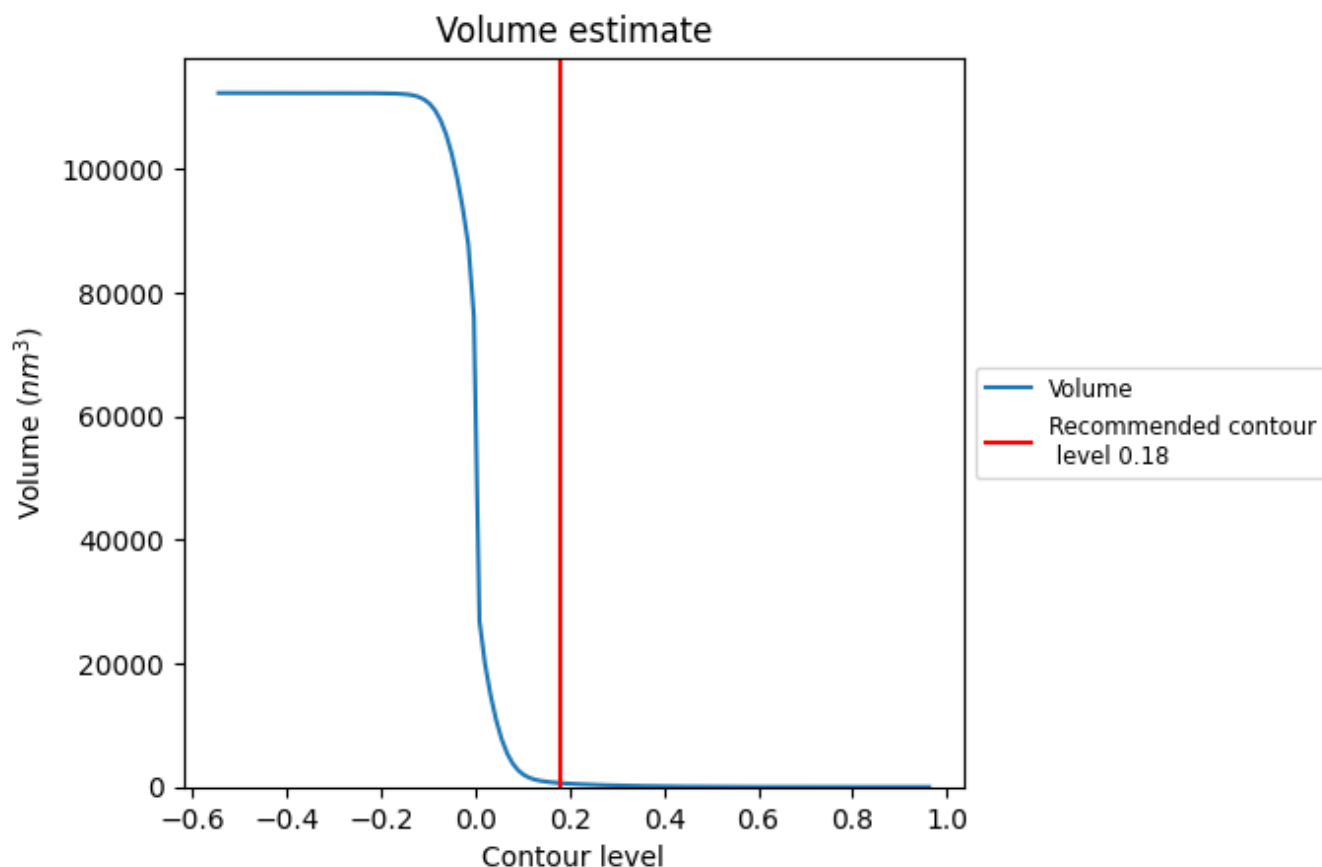
This section contains the results of statistical analysis of the map.

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.

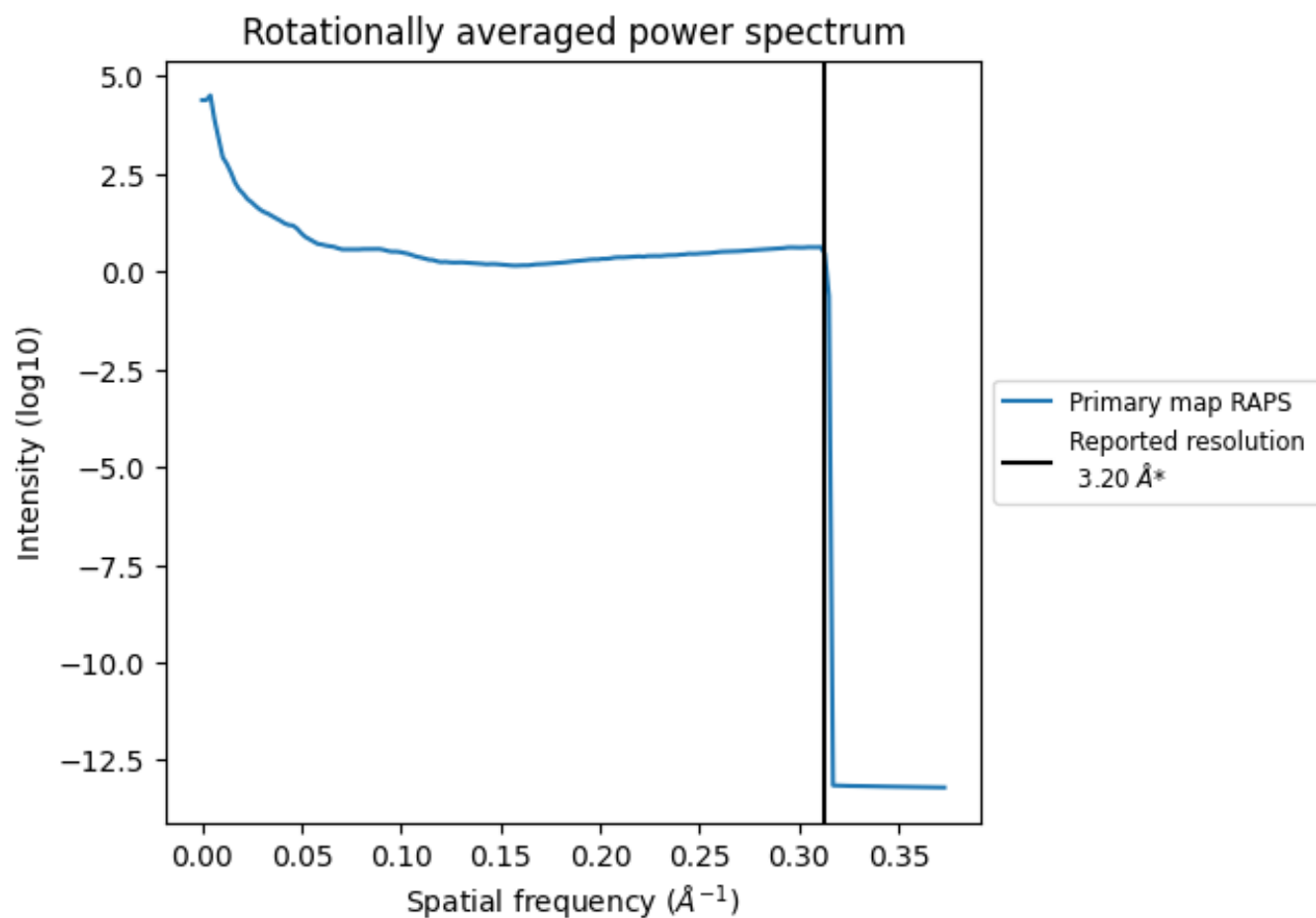
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 628 nm^3 ; this corresponds to an approximate mass of 567 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

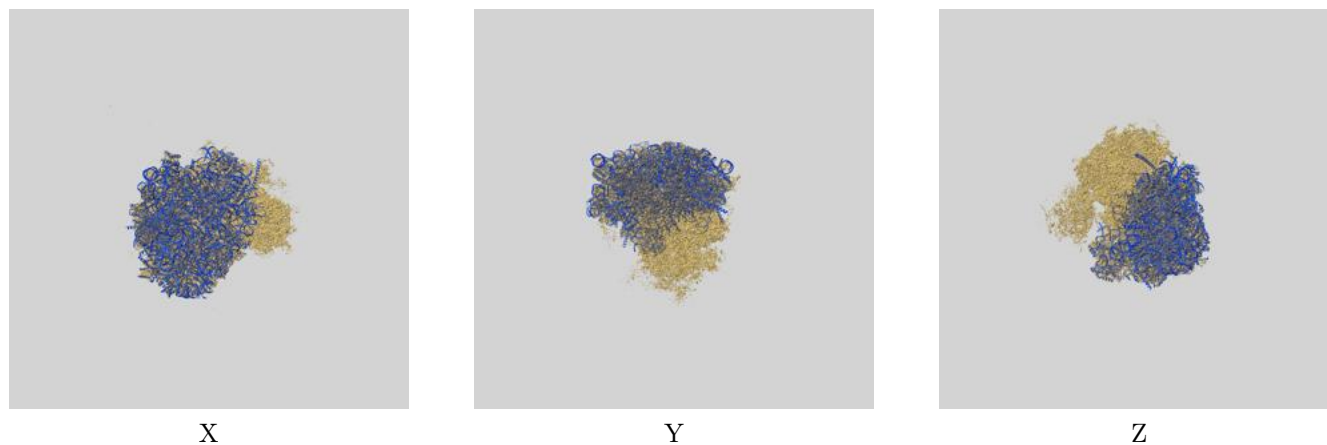
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

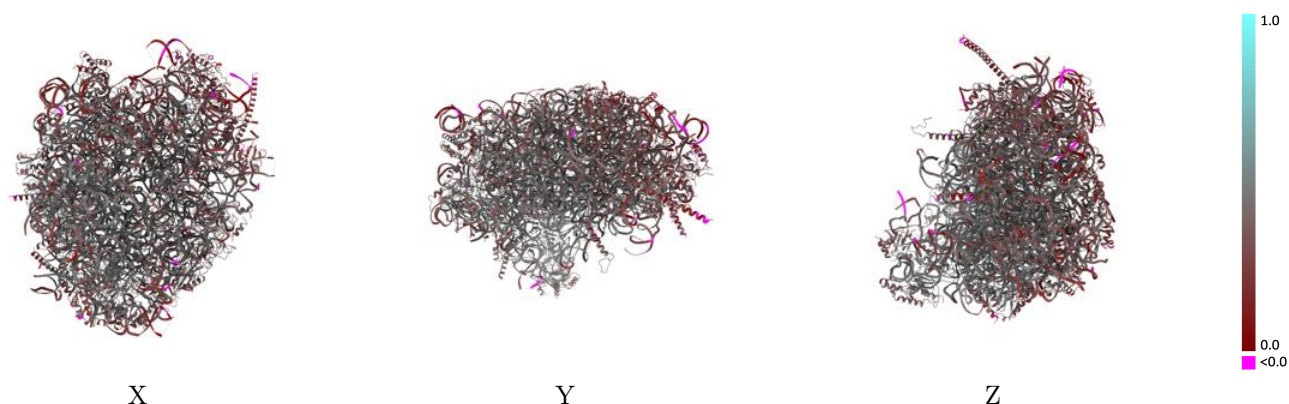
This section contains information regarding the fit between EMDB map EMD-2660 and PDB model 3J79. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



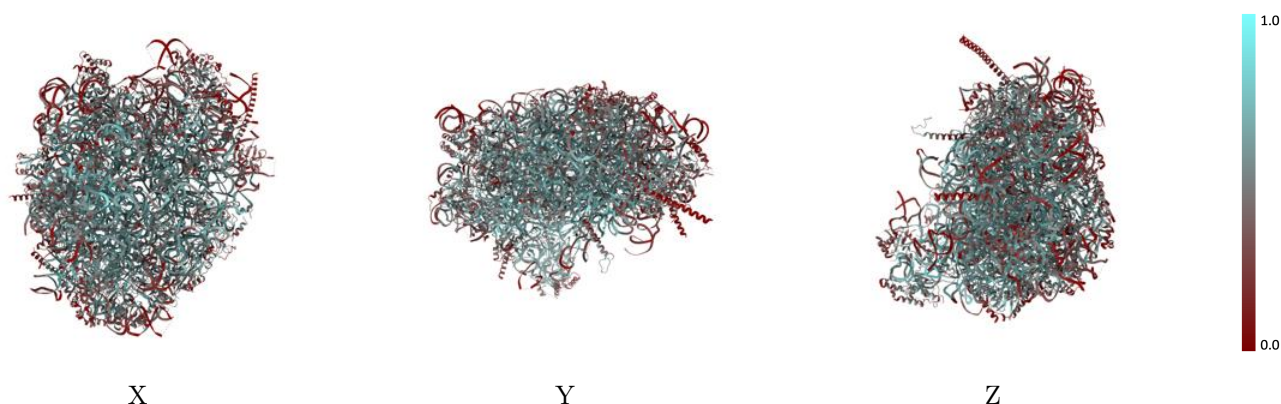
The images above show the 3D surface view of the map at the recommended contour level 0.18 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



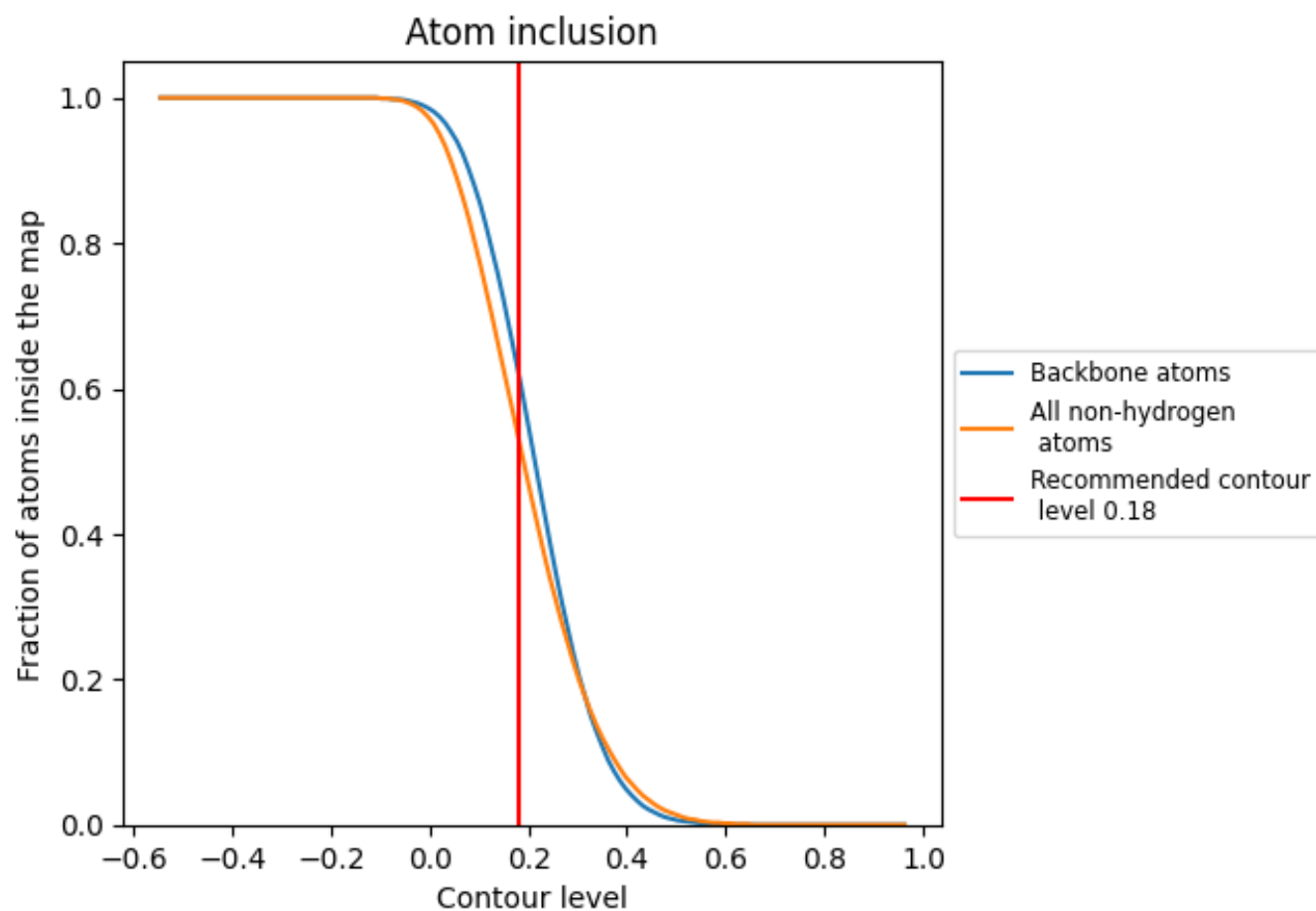
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.18).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 53% 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 (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5310	 0.4130
0	 0.4280	 0.3590
1	 0.3430	 0.3170
2	 0.4380	 0.4140
3	 0.4240	 0.3430
4	 0.3690	 0.3690
5	 0.5410	 0.4550
6	 0.3500	 0.3010
7	 0.4580	 0.3790
8	 0.5330	 0.4460
9	 0.5650	 0.4670
A	 0.5790	 0.4220
B	 0.6660	 0.4710
C	 0.5840	 0.4100
D	 0.4860	 0.4040
E	 0.4910	 0.4040
F	 0.4730	 0.4010
G	 0.3920	 0.3850
H	 0.4480	 0.4090
I	 0.4170	 0.4080
J	 0.2910	 0.3230
K	 0.5300	 0.4370
L	 0.4750	 0.4030
M	 0.4140	 0.4000
N	 0.4460	 0.4180
O	 0.5780	 0.4660
P	 0.5590	 0.4360
Q	 0.4480	 0.4290
R	 0.4300	 0.4090
S	 0.5580	 0.4590
T	 0.3720	 0.3230
U	 0.5080	 0.4560
V	 0.4810	 0.4410
W	 0.5380	 0.4150
X	 0.2250	 0.2790



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Chain	Atom inclusion	Q-score
Y	 0.3430	 0.3370
Z	 0.4150	 0.3610
a	 0.4240	 0.3640
b	 0.4100	 0.3850
c	 0.5340	 0.3980
d	 0.2450	 0.2470
e	 0.4630	 0.3890
f	 0.4870	 0.4140
g	 0.3750	 0.3220
h	 0.4390	 0.3710
i	 0.4780	 0.4550