



wwPDB EM Validation Summary Report ⓘ

Oct 8, 2024 – 01:42 AM EDT

PDB ID : 3J7Q
EMDB ID : EMD-2650
Title : Structure of the idle mammalian ribosome-Sec61 complex
Authors : Voorhees, R.M.; Fernandez, I.S.; Scheres, S.H.W.; Hegde, R.S.
Deposited on : 2014-08-01
Resolution : 3.40 Å(reported)
Based on initial models : 3J3B, 3J3F

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:

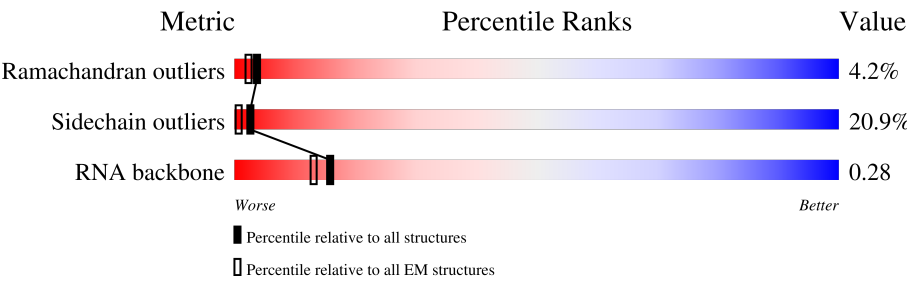
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

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 3.40 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.








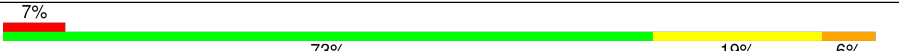

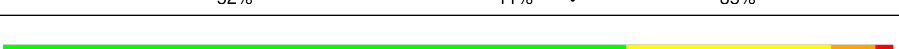
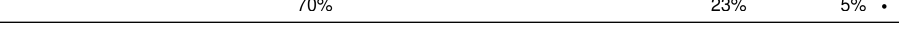
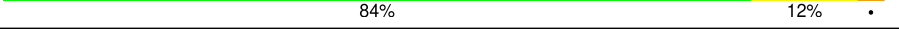





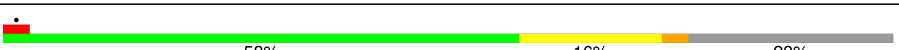


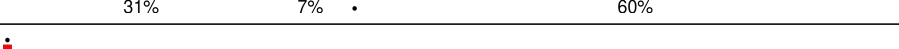






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	5	3722	<div><div>9%</div><div>47%</div><div>39%</div><div>10%</div><div>• •</div></div>
2	7	120	<div><div>•</div><div>69%</div><div>24%</div><div>6%</div><div>•</div></div>
3	8	156	<div><div>8%</div><div>53%</div><div>33%</div><div>8%</div><div>5%</div></div>
4	A	257	<div><div>71%</div><div>18%</div><div>5%</div><div>•</div><div>5%</div></div>
5	B	394	<div><div>74%</div><div>21%</div><div>•</div><div>•</div></div>
6	C	367	<div><div>•</div><div>77%</div><div>19%</div><div>•</div><div>•</div></div>
7	D	297	<div><div>•</div><div>68%</div><div>24%</div><div>5%</div><div>• •</div></div>
8	E	236	<div><div>10%</div><div>64%</div><div>25%</div><div>9%</div><div>•</div></div>

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Mol	Chain	Length	Quality of chain
9	F	225	
10	G	266	
11	H	192	
12	I	213	
13	J	178	
14	L	211	
15	M	213	
16	N	204	
17	O	201	
18	P	153	
19	Q	188	
20	R	196	
21	S	224	
22	T	160	
23	U	128	
24	V	140	
25	W	157	
26	X	156	
27	Y	145	
28	Z	136	
29	a	148	
30	b	160	
31	c	115	
32	d	125	
33	e	135	

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Mol	Chain	Length	Quality of chain
34	f	110	 78%15%5% ..
35	g	117	 77%19% ..
36	h	123	 80%12%6% ..
37	i	105	 76%17% ..
38	j	86	 73%21%6%
39	k	70	 71%27% ..
40	l	51	 76%20% ..
41	m	128	 31%8% ..59%
42	n	25	 72%20%8%
43	o	106	 69%23%6% ..
44	p	91	 82%15% ..
45	r	125	 73%23% ..
46	1	476	 65%74%8%18%
47	2	68	 71%82%6%9%
48	3	36	 100%100%

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 140540 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	5	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called Ribosomal protein uL2.

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

- Molecule 5 is a protein called Ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	394	Total	C	N	O	S	0	0
			3147	2005	591	538	13		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	85	ILE	VAL	conflict	UNP A0A480L253
B	86	VAL	ILE	conflict	UNP A0A480L253
B	140	ALA	GLU	conflict	UNP A0A480L253

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Chain	Residue	Modelled	Actual	Comment	Reference
B	141	ALA	ASP	conflict	UNP A0A480L253
B	143	ALA	LYS	conflict	UNP A0A480L253
B	144	ALA	LYS	conflict	UNP A0A480L253
B	145	ALA	GLN	conflict	UNP A0A480L253
B	147	ALA	GLU	conflict	UNP A0A480L253
B	148	ALA	ARG	conflict	UNP A0A480L253
B	155	ALA	LYS	conflict	UNP A0A480L253

- Molecule 6 is a protein called Ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	367	Total	C	N	O	S	0	0
			2919	1836	582	486	15		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	354	ALA	-	insertion	UNP A0A287AE76
C	355	ALA	-	insertion	UNP A0A287AE76
C	356	ALA	-	insertion	UNP A0A287AE76

- Molecule 7 is a protein called Ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	292	Total	C	N	O	S	0	0
			2380	1508	434	426	12		

- Molecule 8 is a protein called Ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	236	Total	C	N	O	S	0	0
			1904	1219	364	316	5		

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	62	MET	LYS	conflict	UNP Q2YGT9
E	64	MET	LEU	conflict	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9
E	?	-	SER	deletion	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9

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Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	VAL	deletion	UNP Q2YGT9
E	?	-	GLU	deletion	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9
E	?	-	VAL	deletion	UNP Q2YGT9
E	?	-	ARG	deletion	UNP Q2YGT9
E	176	VAL	SER	conflict	UNP Q2YGT9
E	206	LYS	GLU	conflict	UNP Q2YGT9

- Molecule 9 is a protein called Ribosomal protein uL30.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	31	LYS	ARG	conflict	UNP A0A480W0U3

- Molecule 10 is a protein called Ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	241	Total	C	N	O	S	0	0
			1934	1232	372	326	4		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	53	ARG	CYS	conflict	UNP A0A4X1W808
G	172	ALA	SER	conflict	UNP A0A4X1W808
G	185	LYS	ASN	conflict	UNP A0A4X1W808
G	231	ASN	ASP	conflict	UNP A0A4X1W808

- Molecule 11 is a protein called Ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called Ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	213	Total	C	N	O	S	0	0
			1713	1083	331	284	15		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	49	GLY	CYS	conflict	UNP Q29195
I	82	ARG	LYS	conflict	UNP Q29195
I	87	MET	ILE	conflict	UNP Q29195
I	145	GLU	LYS	conflict	UNP Q29195
I	187	LYS	GLU	conflict	UNP Q29195
I	189	CYS	ARG	conflict	UNP Q29195
I	200	VAL	ILE	conflict	UNP Q29195
I	203	HIS	ARG	conflict	UNP Q29195
I	211	VAL	ALA	conflict	UNP Q29195

- Molecule 13 is a protein called Ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	170	Total	C	N	O	S	0	0
			1359	856	256	241	6		

- Molecule 14 is a protein called Ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	210	Total	C	N	O	S	0	0
			1703	1064	354	280	5		

- Molecule 15 is a protein called Ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	138	Total	C	N	O	S	0	0
			1131	727	216	181	7		

- Molecule 16 is a protein called Ribosomal protein eL15.

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

- Molecule 17 is a protein called Ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	201	Total	C	N	O	S	0	0
			1651	1063	323	260	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	3	GLU	-	variant	UNP A0A481CAM4
O	4	GLY	-	variant	UNP A0A481CAM4

- Molecule 18 is a protein called Ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called Ribosomal protein eL18.

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

- Molecule 20 is a protein called Ribosomal protein eL19.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	1	TYR	-	variant	UNP A0A480VXS3

- Molecule 21 is a protein called Ribosomal protein eL20.

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

- Molecule 22 is a protein called Ribosomal protein eL21.

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

- Molecule 23 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 24 is a protein called Ribosomal protein uL14.

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

- Molecule 25 is a protein called Ribosomal protein eL24.

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

- Molecule 26 is a protein called Ribosomal protein uL23.

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

- Molecule 27 is a protein called Ribosomal protein uL24.

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

- Molecule 28 is a protein called Ribosomal protein eL27.

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

- Molecule 29 is a protein called Ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	147	Total	C	N	O	S	0	0
			1163	735	239	185	4		

- Molecule 30 is a protein called Ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 31 is a protein called Ribosomal protein eL30.

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

- Molecule 32 is a protein called Ribosomal protein eL31.

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

- Molecule 33 is a protein called Ribosomal protein eL32.

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

- Molecule 34 is a protein called Ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 35 is a protein called Ribosomal protein eL34.

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

- Molecule 36 is a protein called Ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	122	Total	C	N	O	S	0	0
			1015	642	205	167	1		

- Molecule 37 is a protein called Ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called Ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	86	Total	C	N	O	S	0	0
			706	436	155	110	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
j	82	ILE	THR	conflict	UNP A0A480UVT3

- Molecule 39 is a protein called Ribosomal protein eL38.

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

- Molecule 40 is a protein called Ribosomal protein eL39.

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

- Molecule 41 is a protein called Ribosomal protein eL40.

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

- Molecule 42 is a protein called Ribosomal protein eL41.

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

- Molecule 43 is a protein called Ribosomal protein eL42.

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

- Molecule 44 is a protein called Ribosomal protein eL43.

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

- Molecule 45 is a protein called Ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	125	Total	C	N	O	S	0	0
			1001	622	206	168	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	64	ILE	MET	conflict	UNP A0A480YX24

- Molecule 46 is a protein called Sec61 alpha subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	1	392	Total	C	N	O	S	0	0
			3051	2007	493	532	19		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	343	HIS	TYR	conflict	UNP A0A480EHF8

- Molecule 47 is a protein called Sec61 gamma subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2	62	Total	C	N	O	S	0	0
			494	326	86	79	3		

- Molecule 48 is a protein called Sec61 beta subunit.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	3	36	Total	C	N	O	0	0
			180	108	36	36		

- Molecule 49 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
49	5	119	Total	Mg	0
			119	119	
49	7	5	Total	Mg	0
			5	5	
49	8	4	Total	Mg	0
			4	4	
49	P	1	Total	Mg	0
			1	1	
49	V	1	Total	Mg	0
			1	1	

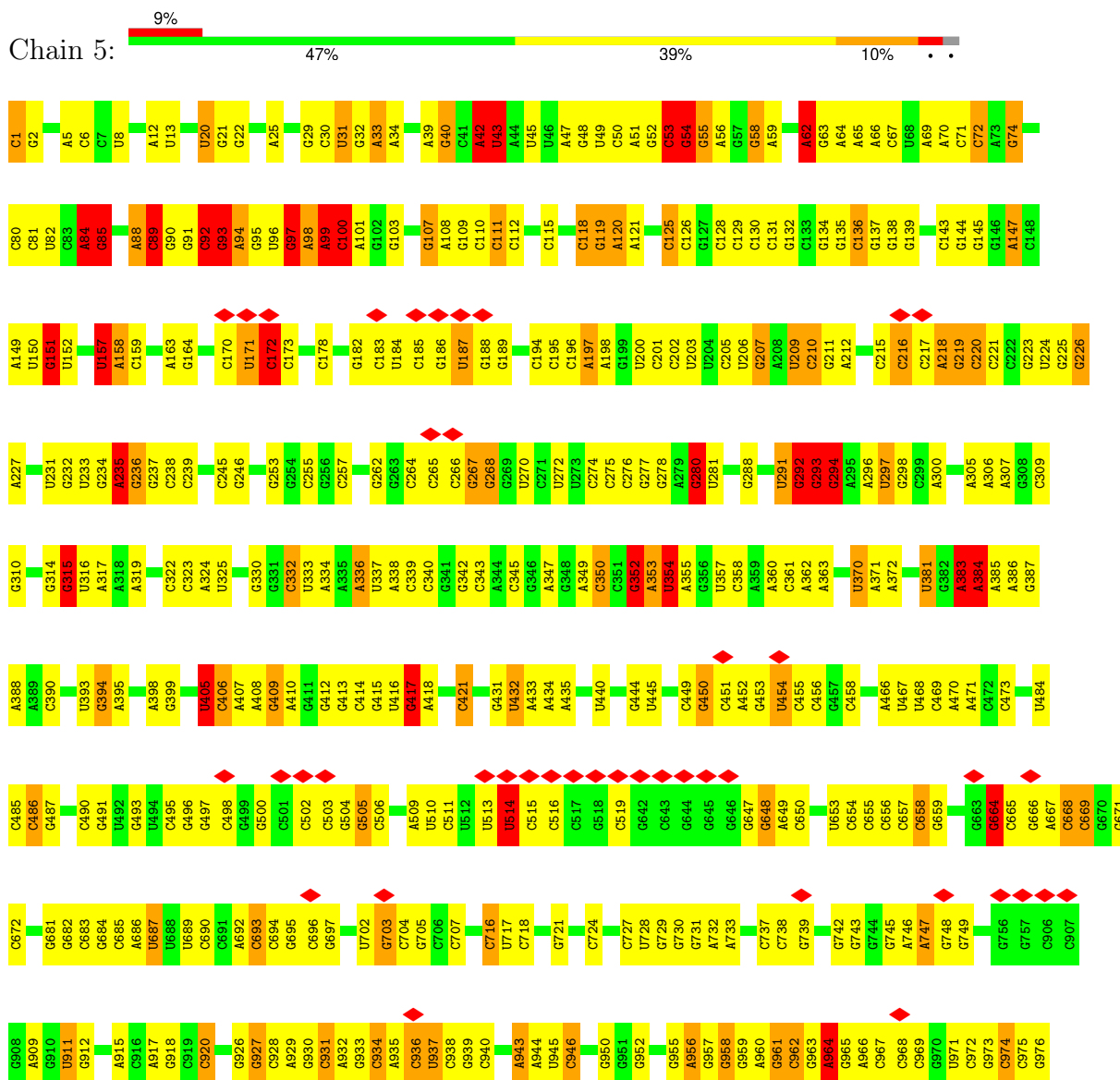
- Molecule 50 is ZINC ION (three-letter code: ZN) (formula: Zn).

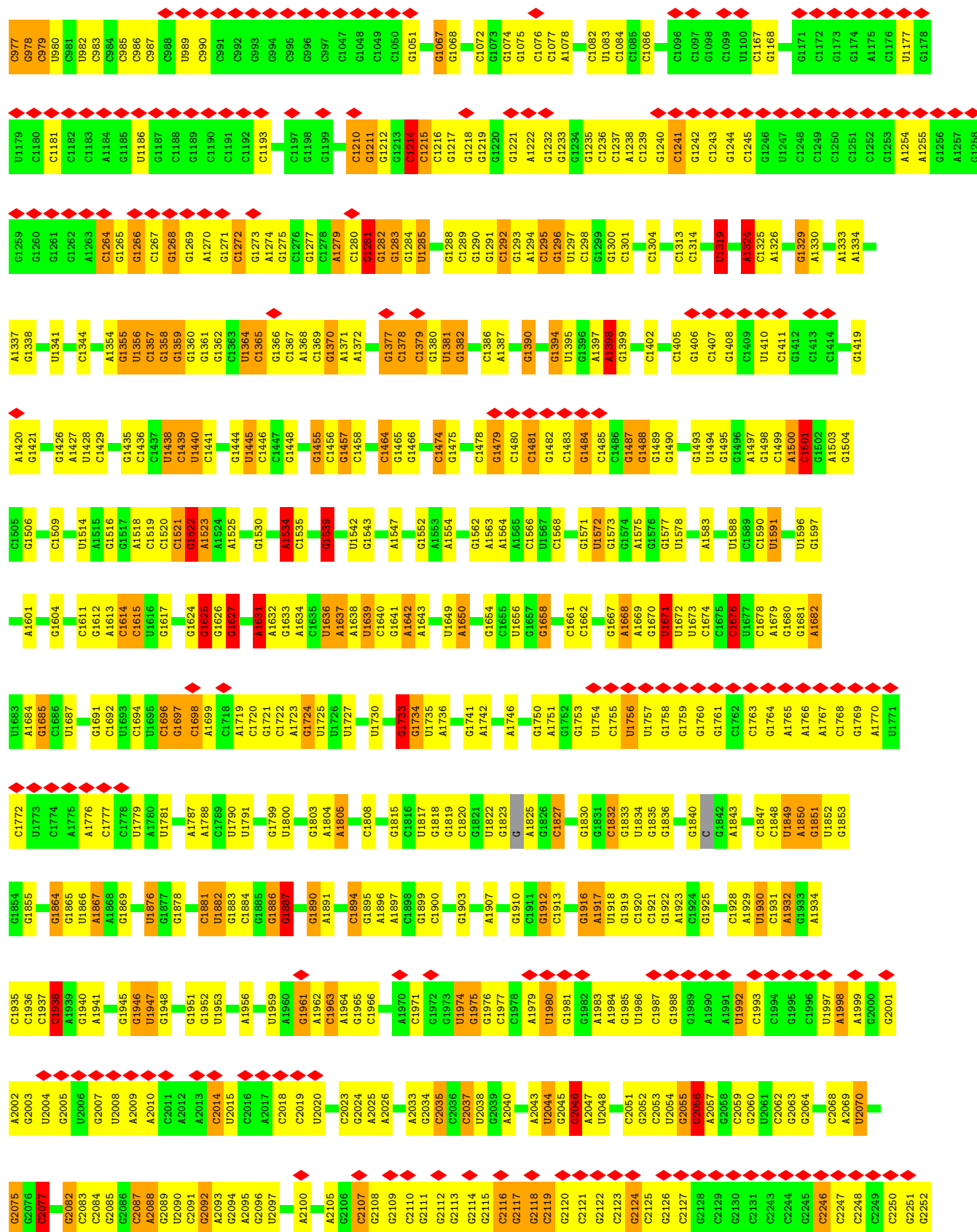
Mol	Chain	Residues	Atoms		AltConf
50	j	1	Total	Zn	0
			1	1	
50	m	1	Total	Zn	0
			1	1	
50	o	1	Total	Zn	0
			1	1	

3 Residue-property plots [i](#)

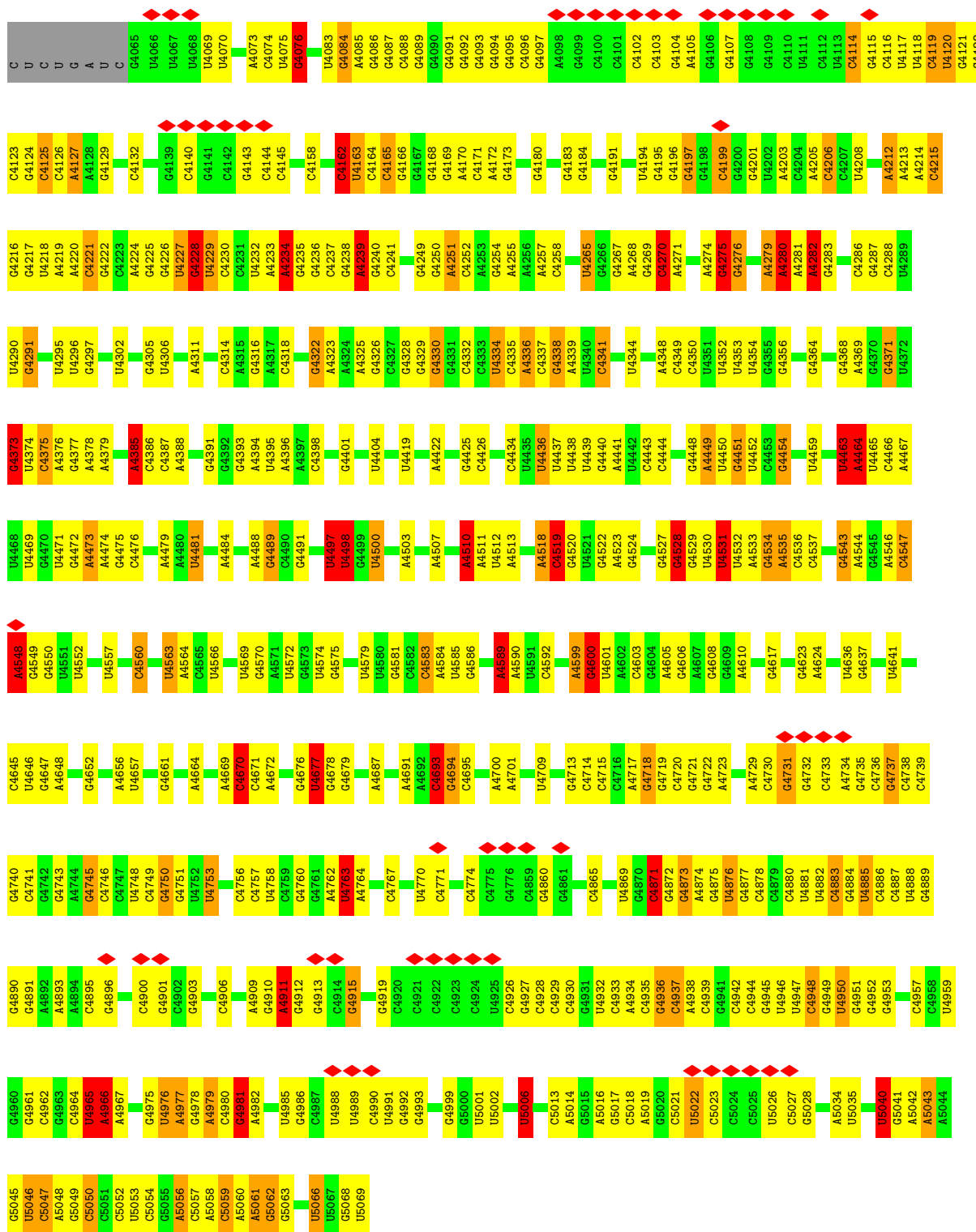
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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



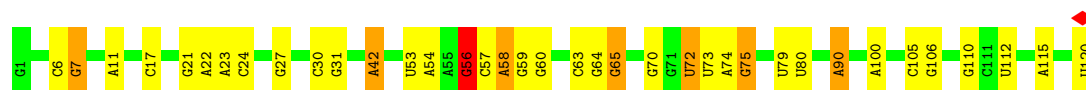


G3939	A3856	A3756	C3668	G2910	G2827	A2745	G2683	C2571	G2488	G2407	C3935	G2253
G3943	G3859	A3759	G3670	U3583	U2828	U2747	G2684	C2572	C2489	U2408	G2328	G2254
G3944	G3860	A3760	G3671	C3584	U2829	G2751	U2685	G2577	U2490	U2409	U2329	C2255
G3945	A3861	G3761	G3672	G3585	A2832	G2752	C2686	C2576	C2491	A2417	G2330	C2256
G3946	A3862	G3764	G3674	G3586	C2834	G2754	C2687	G2577	C2492	C2422	A2332	C2257
G3947	C3863	G3675	G3675	C3587	A2835	G2755	C2670	A2581	G2493	U2425	G2333	C2258
G3948	G3864	G3676	G3677	G3588	U2836	G2756	G2673	A2582	G2494	U2426	G2334	G2259
G3949	A3865	U3770	U3677	G3589	U2837	G2757	G2675	C2583	G2502	G2427	C2337	G2260
G3950	G3866	U3772	G3678	C3590	G2838	G2760	G2676	C2584	G2503	A2428	G2338	G2261
G	A3867	U3773	U3679	C3591	G2841	U2761	G2677	A2587	C2504	A2429	G2339	G2262
A	G3868	U3774	U3680	G3592	G2842	U2762	A2678	C2588	C2505	U2432	C2263	C2264
G	G3869	A3775	U3681	C3593	U2843	U2763	A2679	C2589	G2506	U2433	G2342	G2265
A	C3870	G3776	G3682	C3594	U2844	U2764	C2683	G2590	U2507	G2434	U2347	U2267
G	A3871	G3777	C3683	C3595	G2848	U2765	C2684	A2591	U2508	G2435	A2347	A2268
G	G3875	A3784	G3686	U3595	A2849	U2766	G2685	G2597	G2509	U2436	G2348	C2269
G	A3876	A3785	A3887	A3596	A2850	U2767	G2686	G2597	G2510	U2437	A2349	C2270
U	A3877	U3786	U3687	C3597	G2851	U2768	U2687	A2600	G2511	C2437	U2350	C2271
U	G3878	G3776	U3688	G3597	U2852	U2769	C2689	G2602	A2512	U2438	C2351	C2272
A	G3880	C3791	G3691	C3605	G2853	C2770	U2692	C2614	A2513	U2439	G2357	G2273
G	G3881	G3792	A3692	U3606	G2854	U2782	G2693	C2615	A2514	U2440	A2360	G2274
A	G3882	U3793	U3693	A3611	G2855	U2783	G2694	C2616	A2515	C2441	U2362	G2275
U	U3883	U3794	G3694	G3615	G2856	C2784	G2695	C2617	A2516	C2442	A2366	C2276
A	G3886	A3800	G3695	U3616	A2857	C2785	A2696	G2618	A2517	G2443	A2367	C2277
U	C3887	U3802	G3895	G3617	A2858	C2786	A2697	G2619	C2520	C2446	U2369	C2278
G	G3888	A3803	G3896	G3617	G2859	U2787	A2698	G2620	C2521	U2447	A2367	C2279
U	G3889	G3804	U3709	G3620	C2860	U2788	G2703	G2621	A2522	U2448	A2368	C2280
G	G3890	A3807	G3710	A3621	C2861	U2790	G2704	G2622	A2523	U2449	A2369	U2281
G	G3891	C3808	A3711	C3622	C2862	C2791	G2705	G2623	A2524	U2450	U2370	A2282
G	C3892	U3809	U3712	C3623	U2873	C2792	G2706	A2627	A2525	U2451	C2373	G2283
A	G3893	G3810	G3713	A3624	U2874	A2795	U2707	C2627	A2526	U2452	G2288	C2289
G	C3894	G3811	U3714	G3625	G2875	G2796	U2708	C2627	A2527	U2453	A2371	C2290
G	G3895	G3812	C3715	G3626	C2876	C2797	U2709	C2627	A2528	U2454	U2372	C2291
C	G3896	A3813	A3717	G3627	G2877	A2798	C2710	C2627	A2529	U2455	U2373	C2292
C	A3901	U3814	A3718	G3627	G2878	U2799	G2711	U2631	A2530	U2456	C2373	C2293
G	A3902	A3817	A3726	G3634	U2879	C2799	G2712	U2632	A2531	G2459	G2376	U2297
G	A3903	U3818	A3727	A3635	U2880	U2803	G2713	U2633	A2532	C2464	A2382	U2298
C	A3904	G3819	C3728	C3636	G2881	A2806	G2714	U2634	A2533	C2465	A2383	A2300
C	G3907	U3729	U3730	A3643	G2882	A2807	G2715	G2641	A2534	U2467	C2384	G2301
C	A3908	U3822	U3730	U3644	C2883	G2808	C2716	A2642	A2535	U2468	U2385	C2302
C	G3827	G3827	A3733	A3648	A2885	G2811	G2722	A2643	A2536	C2469	A2389	G2303
G	U3831	U3831	U3734	A3649	G2886	A2812	A2725	G2644	A2537	C2470	G2390	A2307
G	U3832	U3832	G3735	C3650	G2887	A2813	A2726	G2645	U2538	A2472	G2391	A2308
G	U3833	U3833	A3736	A3651	G2888	C2814	G2726	G2646	A2539	A2473	G2392	A2309
U	U3834	U3834	A3737	A3652	G2889	A2815	G2727	G2647	A2540	G2474	C2310	C2311
G	U3835	U3835	C3738	A3653	U2900	G2816	G2728	G2648	A2541	G2475	A2395	U2312
A	U3836	U3836	G3739	A3654	G2901	G2817	G2729	G2649	A2542	G2476	A2396	G2313
A	G3843	G3843	G3743	G3658	G2902	U2818	G2730	G2650	A2543	A2477	A2397	G2314
U	U3844	U3844	G3744	G3659	G2903	U2819	G2731	G2651	U2544	C2478	U2398	G2315
A	A3845	A3845	U3745	C3660	U2904	C2820	C2732	G2652	G2555	G2479	G2399	G2316
C	G3846	G3846	G3746	G3661	C2905	U2821	C2733	G2653	C2560	A2484	A2403	C2319
C	A3847	A3847	A3747	A3662	G2906	A2824	U2740	G2654	C2561	U2485	A2404	G2320
A	G3848	G3848	A3748	A3663	U2907	A2825	A2741	G2655	G2562	U2486	G2405	G2321
U	U3850	U3850	U3749	A3664	G2908	U2826	A2742	G2656	C2563	C2487	C2322	C2323
C	G3851	G3851	G3753	G3665	C2909	U2827	A2743	G2657	A2564	G2488	C2323	C2324

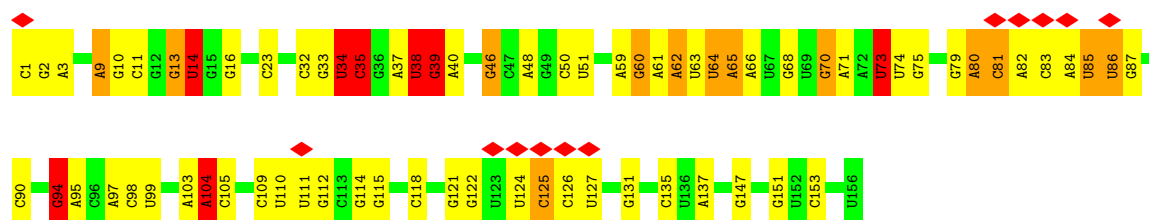


• Molecule 2: 5S ribosomal RNA

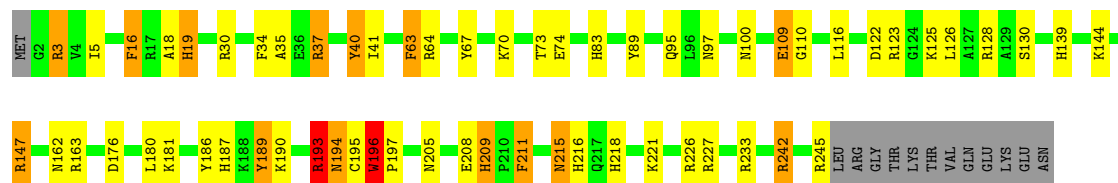
Chain 7: 69% 24% 6%



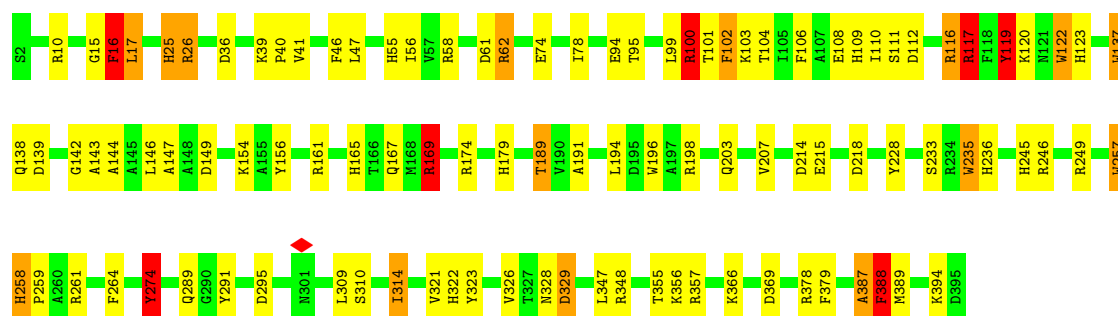
• Molecule 3: 5.8S ribosomal RNA



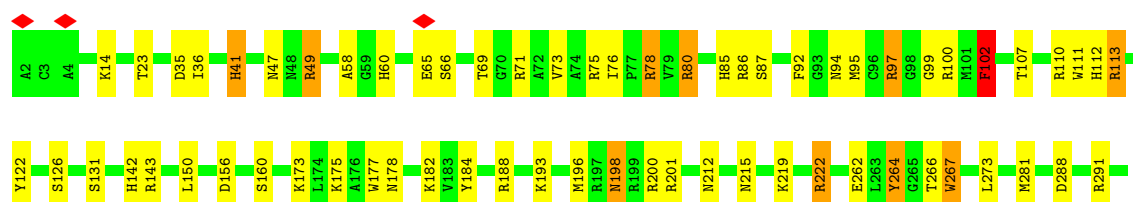
• Molecule 4: Ribosomal protein uL2

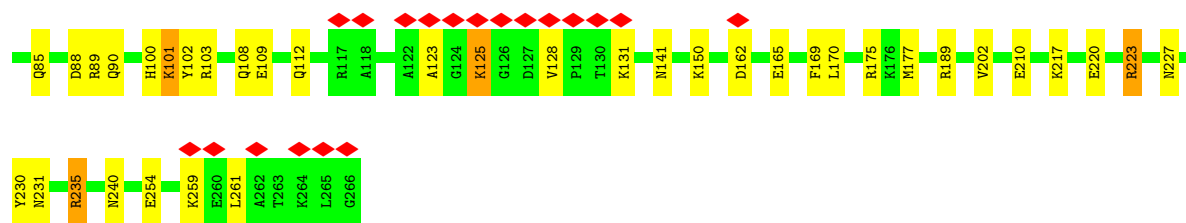


• Molecule 5: Ribosomal protein uL3



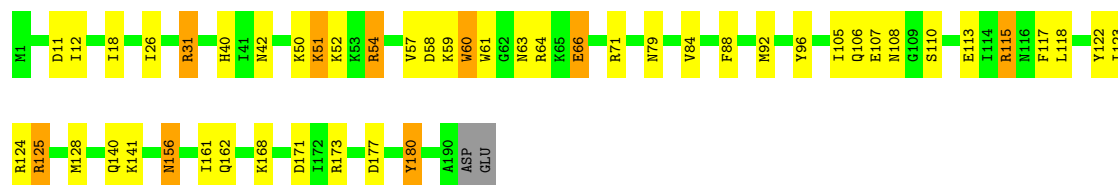
• Molecule 6: Ribosomal protein uL4





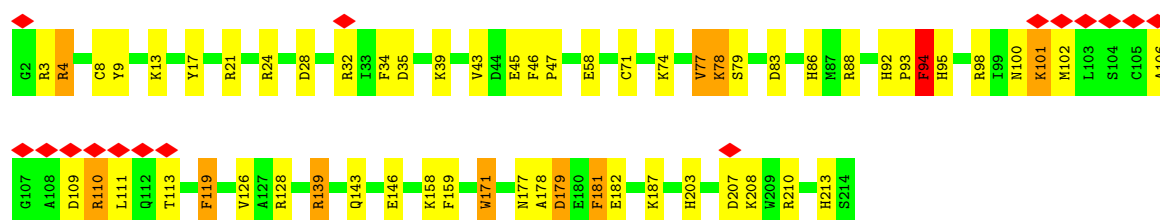
• Molecule 11: Ribosomal protein uL6

Chain H: 73% 21% 5%



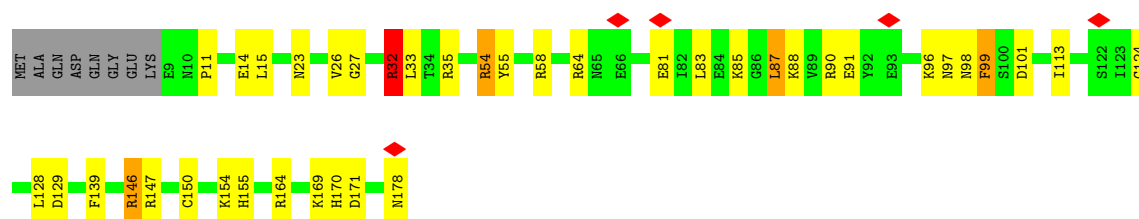
• Molecule 12: Ribosomal protein uL16

Chain I: 8% 72% 23% 5%



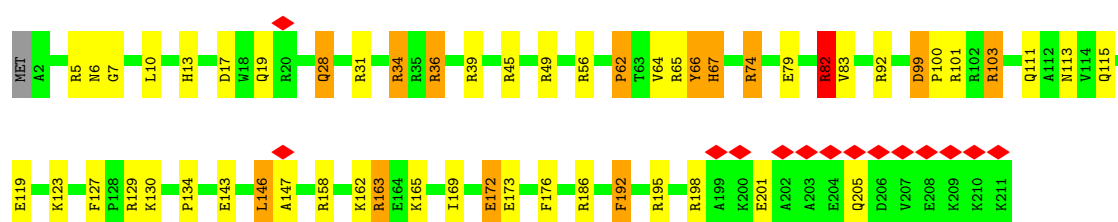
• Molecule 13: Ribosomal protein uL5

Chain J: 73% 20% 7%

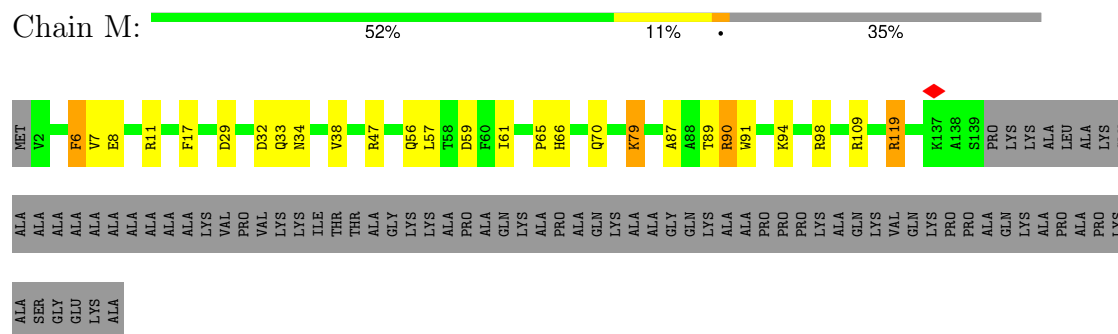


• Molecule 14: Ribosomal protein eL13

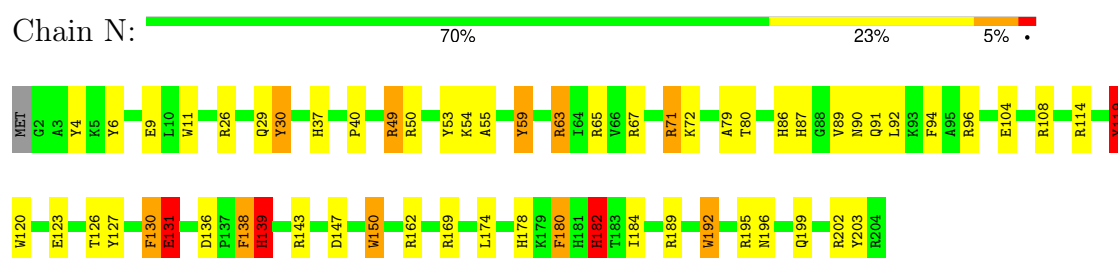
Chain L: 7% 73% 19% 6%



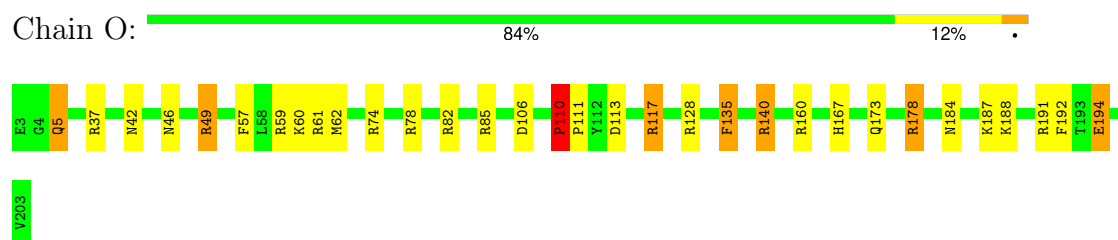
• Molecule 15: Ribosomal protein eL14



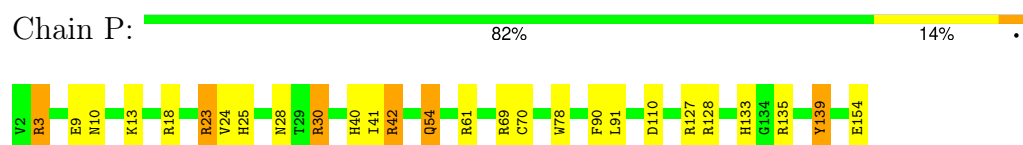
• Molecule 16: Ribosomal protein eL15



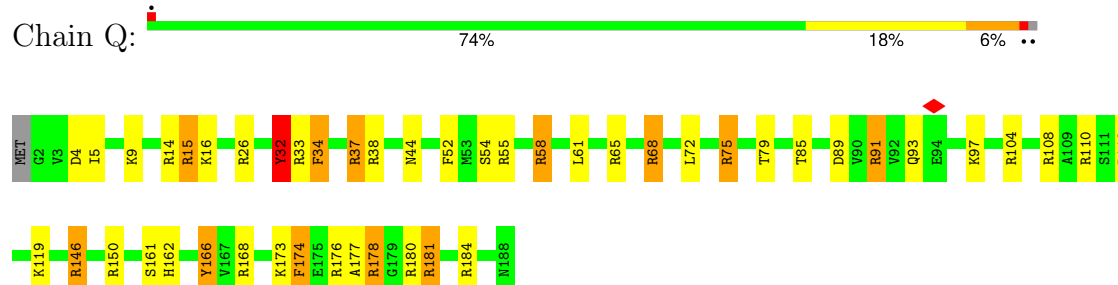
• Molecule 17: Ribosomal protein uL13



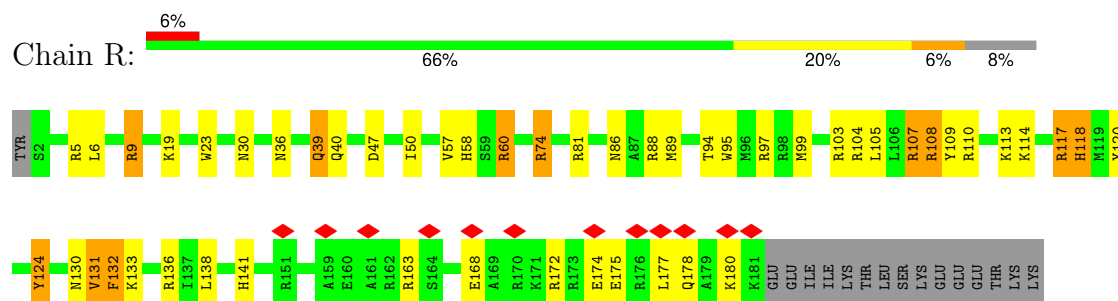
• Molecule 18: Ribosomal protein uL22



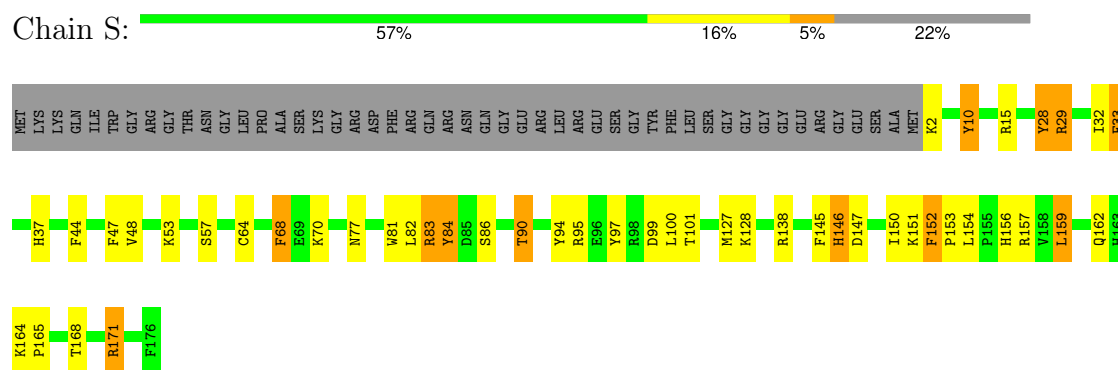
• Molecule 19: Ribosomal protein eL18



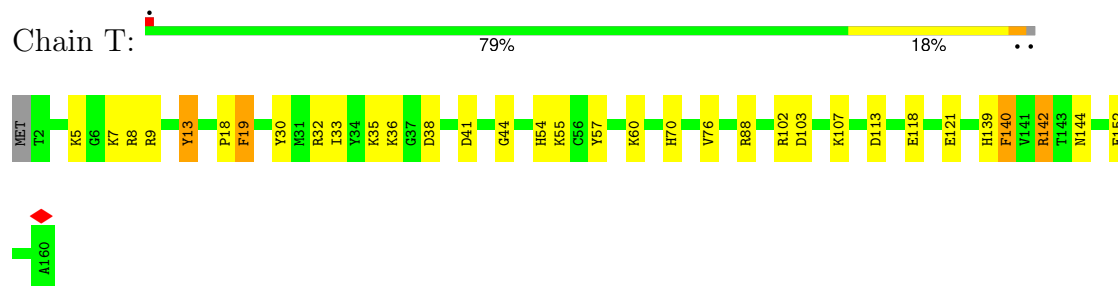
- Molecule 20: Ribosomal protein eL19



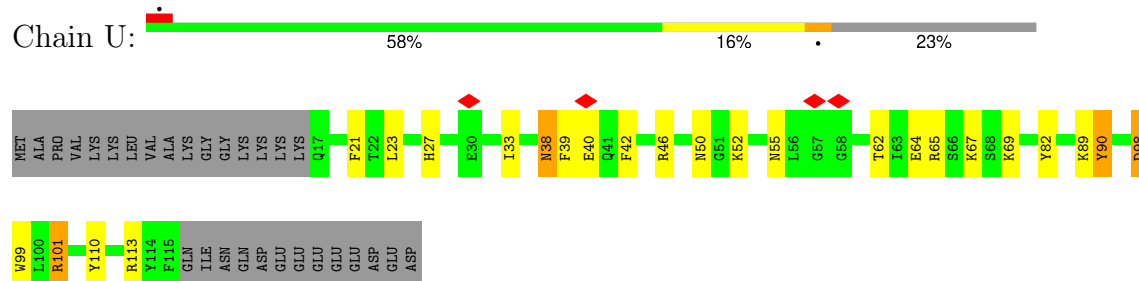
- Molecule 21: Ribosomal protein eL20



- Molecule 22: Ribosomal protein eL21



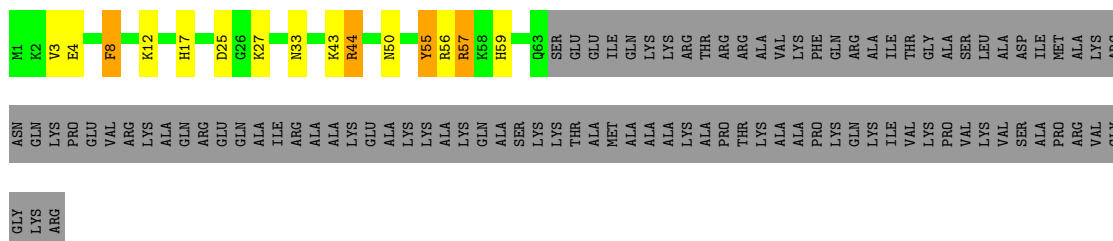
- Molecule 23: Ribosomal protein eL22



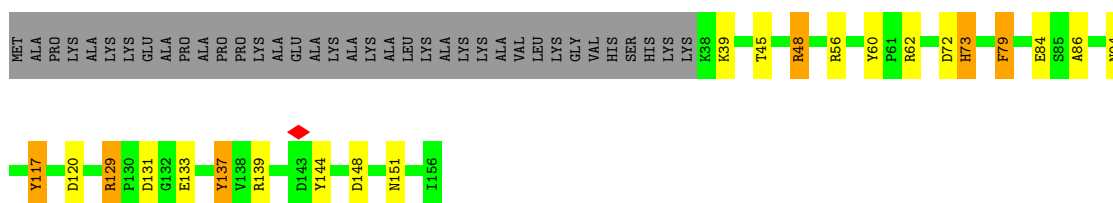
- Molecule 24: Ribosomal protein uL14



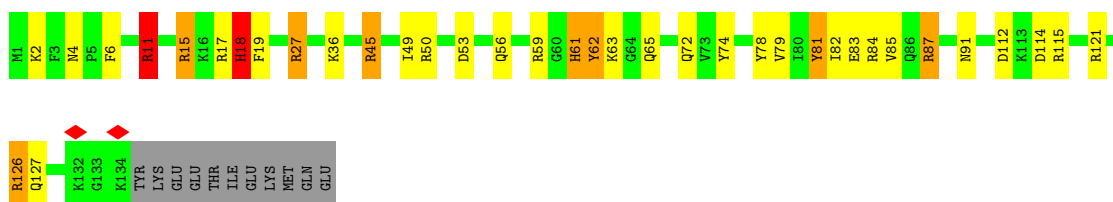
- Molecule 25: Ribosomal protein eL24



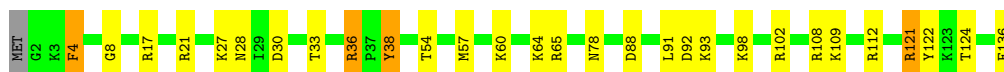
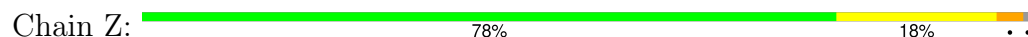
- Molecule 26: Ribosomal protein uL23



- Molecule 27: Ribosomal protein uL24




- Molecule 28: Ribosomal protein eL27



- Molecule 29: Ribosomal protein uL15




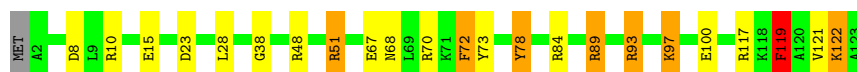
- Molecule 35: Ribosomal protein eL34

Chain g:  77% 19% ..



- Molecule 36: Ribosomal protein uL29

Chain h:  80% 12% 6% ..



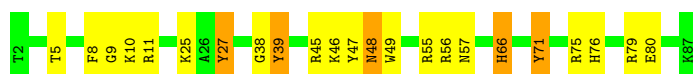
- Molecule 37: Ribosomal protein eL36

Chain i:  76% 17% ..



- Molecule 38: Ribosomal protein eL37

Chain j:  73% 21% 6% ..



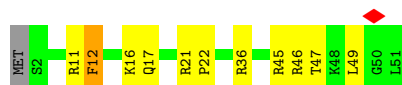
- Molecule 39: Ribosomal protein eL38

Chain k:  71% 27% ..



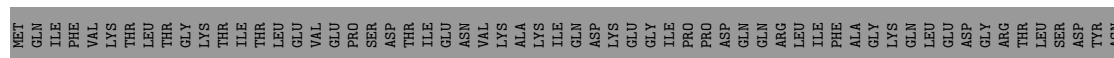
- Molecule 40: Ribosomal protein eL39

Chain l:  76% 20% ..



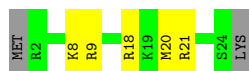
- Molecule 41: Ribosomal protein eL40

Chain m:  31% 8% 59%





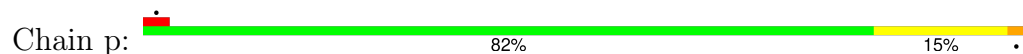
- Molecule 42: Ribosomal protein eL41



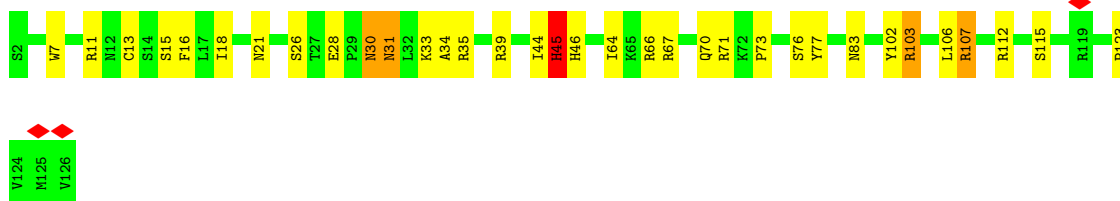
- Molecule 43: Ribosomal protein eL42



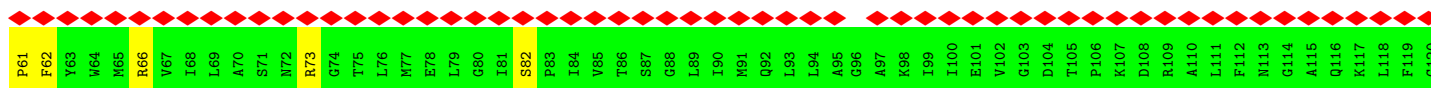
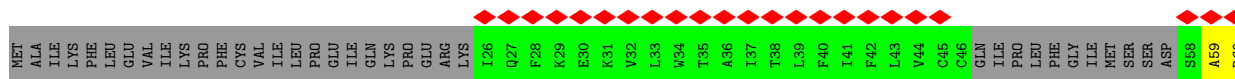
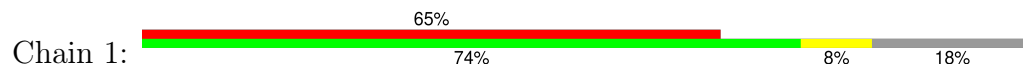
- Molecule 44: Ribosomal protein eL43

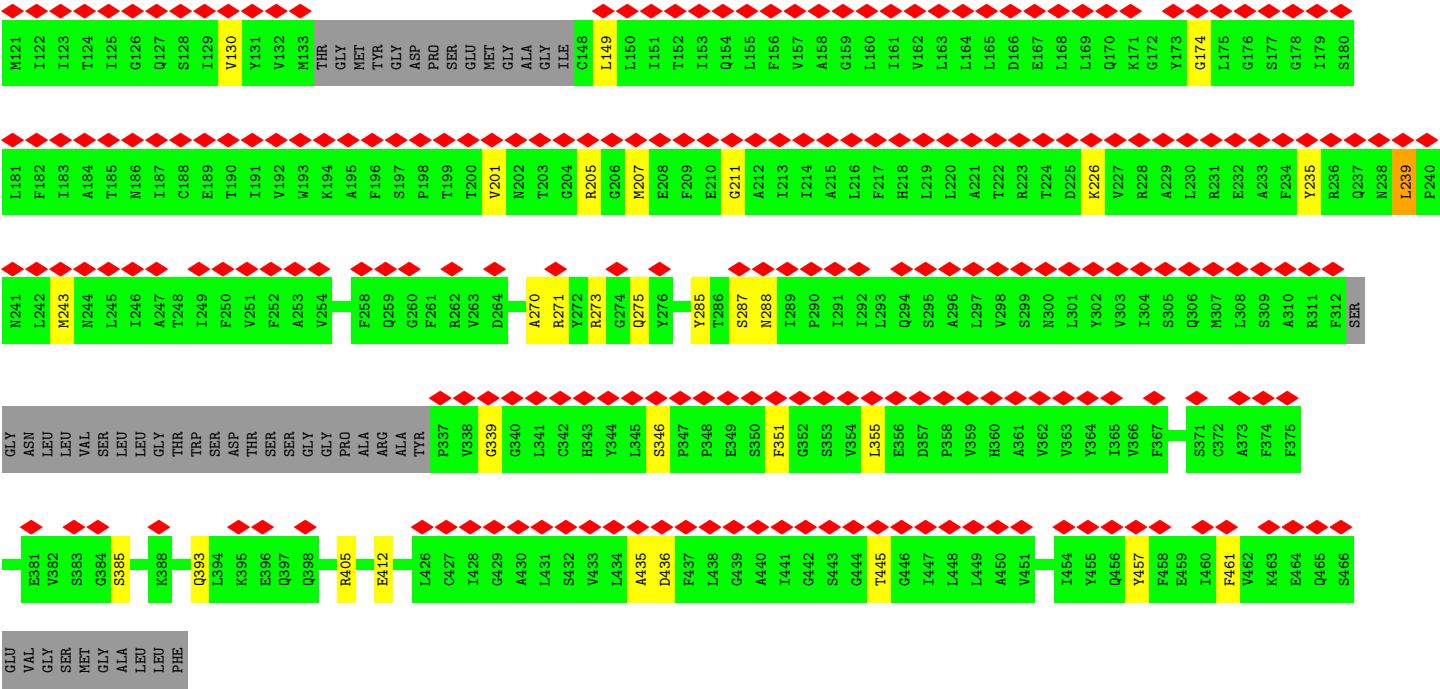


- Molecule 45: Ribosomal protein eL28

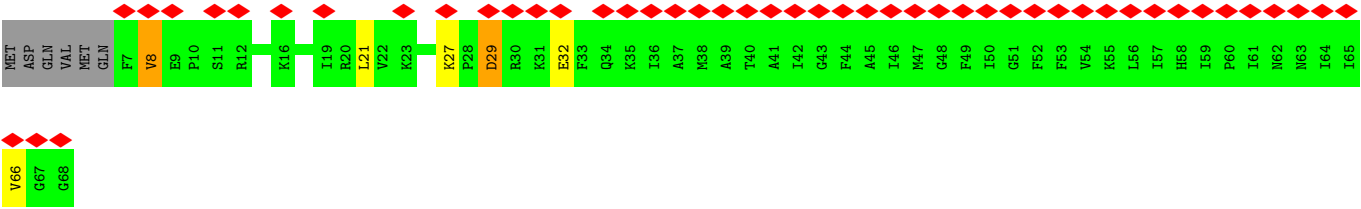
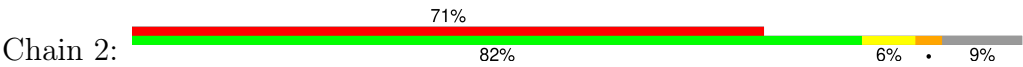


- Molecule 46: Sec61 alpha subunit

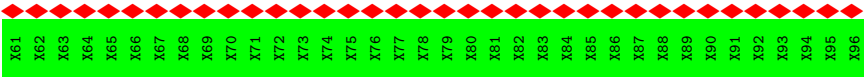




● Molecule 47: Sec61 gamma subunit



● Molecule 48: Sec61 beta subunit



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	80019	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	27	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.043	Depositor
Minimum map value	-0.599	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.09	Depositor
Map size (\AA)	562.8, 562.8, 562.8	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.3399999, 1.3399999, 1.3399999	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	5	0.64	80/87792 (0.1%)	1.13	742/136945 (0.5%)
2	7	0.54	1/2858 (0.0%)	0.96	9/4455 (0.2%)
3	8	0.68	3/3701 (0.1%)	1.20	42/5766 (0.7%)
4	A	0.80	3/1906 (0.2%)	1.26	21/2556 (0.8%)
5	B	0.81	8/3214 (0.2%)	1.16	26/4308 (0.6%)
6	C	0.73	4/2973 (0.1%)	1.12	18/3990 (0.5%)
7	D	0.73	2/2426 (0.1%)	1.23	27/3252 (0.8%)
8	E	0.73	5/1941 (0.3%)	1.21	20/2601 (0.8%)
9	F	0.80	2/1905 (0.1%)	1.27	26/2539 (1.0%)
10	G	0.76	4/1966 (0.2%)	1.09	14/2645 (0.5%)
11	H	0.77	3/1537 (0.2%)	1.17	10/2066 (0.5%)
12	I	0.66	1/1753 (0.1%)	1.11	12/2343 (0.5%)
13	J	0.63	1/1382 (0.1%)	1.04	11/1849 (0.6%)
14	L	0.71	2/1734 (0.1%)	1.12	15/2318 (0.6%)
15	M	0.76	2/1152 (0.2%)	1.11	5/1539 (0.3%)
16	N	0.84	4/1746 (0.2%)	1.33	23/2338 (1.0%)
17	O	0.72	3/1684 (0.2%)	1.11	12/2251 (0.5%)
18	P	0.74	2/1268 (0.2%)	1.10	9/1701 (0.5%)
19	Q	0.69	0/1530	1.35	31/2041 (1.5%)
20	R	0.79	3/1524 (0.2%)	1.27	21/2013 (1.0%)
21	S	0.95	8/1493 (0.5%)	1.30	19/2002 (0.9%)
22	T	0.67	1/1326 (0.1%)	1.04	7/1770 (0.4%)
23	U	0.63	1/822 (0.1%)	1.03	2/1103 (0.2%)
24	V	0.89	4/993 (0.4%)	1.11	7/1332 (0.5%)
25	W	0.71	0/541	1.23	5/720 (0.7%)
26	X	0.64	0/993	1.09	10/1334 (0.7%)
27	Y	0.72	0/1132	1.24	19/1504 (1.3%)
28	Z	0.63	0/1130	1.11	8/1507 (0.5%)
29	a	0.93	6/1192 (0.5%)	1.37	17/1591 (1.1%)
30	b	0.88	2/620 (0.3%)	1.17	5/819 (0.6%)
31	c	0.70	0/742	1.14	5/996 (0.5%)
32	d	0.84	3/903 (0.3%)	1.37	16/1216 (1.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.90	3/1071 (0.3%)	1.23	15/1429 (1.0%)
34	f	1.02	2/895 (0.2%)	1.34	17/1198 (1.4%)
35	g	0.65	0/916	1.08	5/1220 (0.4%)
36	h	0.63	0/1023	1.21	13/1350 (1.0%)
37	i	0.63	0/843	1.19	8/1115 (0.7%)
38	j	0.97	1/721 (0.1%)	1.43	11/953 (1.2%)
39	k	0.59	0/575	0.97	1/761 (0.1%)
40	l	0.68	0/454	1.07	3/599 (0.5%)
41	m	0.57	0/435	1.02	3/575 (0.5%)
42	n	0.48	0/223	1.02	0/284
43	o	0.64	0/864	1.27	9/1140 (0.8%)
44	p	0.64	1/718 (0.1%)	1.00	3/953 (0.3%)
45	r	0.68	0/1017	1.12	8/1365 (0.6%)
46	1	0.45	0/3114	0.63	0/4218
47	2	0.47	0/504	0.71	1/673 (0.1%)
All	All	0.68	165/151252 (0.1%)	1.14	1311/223243 (0.6%)

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
1	5	1	158
2	7	0	2
3	8	0	11
4	A	0	6
5	B	0	13
6	C	0	5
7	D	0	8
8	E	0	12
9	F	0	5
10	G	0	3
11	H	0	3
12	I	0	5
13	J	0	2
14	L	0	5
15	M	0	4
16	N	0	11
17	O	0	3
18	P	0	1
19	Q	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
20	R	0	6
21	S	0	11
22	T	0	2
23	U	0	2
24	V	0	3
25	W	0	1
26	X	0	1
27	Y	0	4
29	a	0	9
30	b	0	1
31	c	0	2
32	d	0	4
33	e	0	4
34	f	0	2
35	g	0	1
36	h	0	3
37	i	0	3
38	j	0	4
39	k	0	1
43	o	0	6
44	p	0	1
45	r	0	5
46	1	0	1
47	2	0	1
All	All	1	340

The worst 5 of 165 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	1823	G	O3'-P	41.48	2.10	1.61
10	G	109	GLU	CD-OE2	16.17	1.43	1.25
11	H	66	GLU	CD-OE1	15.86	1.43	1.25
34	f	6	TRP	CB-CG	-15.77	1.21	1.50
30	b	16	TRP	CB-CG	-13.52	1.25	1.50

The worst 5 of 1311 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	8	60	G	N9-C1'-C2'	16.16	135.01	114.00
38	j	11	ARG	NE-CZ-NH2	-13.83	113.38	120.30
19	Q	37	ARG	NE-CZ-NH2	12.90	126.75	120.30
1	5	92	C	N1-C1'-C2'	-12.62	97.59	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	I	139	ARG	CG-CD-NE	12.29	137.61	111.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	5	1992	U	C1'

5 of 340 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	5	22	G	Sidechain
1	5	31	U	Sidechain
1	5	42	A	Sidechain
1	5	43	U	Sidechain
1	5	53	C	Sidechain

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	A	242/257 (94%)	203 (84%)	30 (12%)	9 (4%)	2	16
5	B	392/394 (100%)	319 (81%)	40 (10%)	33 (8%)	0	4
6	C	365/367 (100%)	304 (83%)	46 (13%)	15 (4%)	2	15
7	D	290/297 (98%)	235 (81%)	33 (11%)	22 (8%)	1	5
8	E	232/236 (98%)	150 (65%)	51 (22%)	31 (13%)	0	1
9	F	223/225 (99%)	190 (85%)	23 (10%)	10 (4%)	2	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	G	239/266 (90%)	200 (84%)	32 (13%)	7 (3%)	3	19
11	H	188/192 (98%)	164 (87%)	20 (11%)	4 (2%)	5	24
12	I	211/213 (99%)	168 (80%)	30 (14%)	13 (6%)	1	8
13	J	168/178 (94%)	137 (82%)	23 (14%)	8 (5%)	2	12
14	L	208/211 (99%)	172 (83%)	25 (12%)	11 (5%)	1	10
15	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	8	30
16	N	201/204 (98%)	172 (86%)	23 (11%)	6 (3%)	3	19
17	O	199/201 (99%)	182 (92%)	14 (7%)	3 (2%)	8	30
18	P	151/153 (99%)	140 (93%)	9 (6%)	2 (1%)	10	33
19	Q	185/188 (98%)	160 (86%)	20 (11%)	5 (3%)	4	21
20	R	178/196 (91%)	153 (86%)	21 (12%)	4 (2%)	5	24
21	S	173/224 (77%)	146 (84%)	24 (14%)	3 (2%)	7	28
22	T	157/160 (98%)	128 (82%)	26 (17%)	3 (2%)	6	26
23	U	97/128 (76%)	74 (76%)	21 (22%)	2 (2%)	5	24
24	V	129/140 (92%)	112 (87%)	14 (11%)	3 (2%)	5	23
25	W	61/157 (39%)	57 (93%)	3 (5%)	1 (2%)	8	29
26	X	117/156 (75%)	108 (92%)	7 (6%)	2 (2%)	7	28
27	Y	132/145 (91%)	112 (85%)	14 (11%)	6 (4%)	2	13
28	Z	133/136 (98%)	113 (85%)	15 (11%)	5 (4%)	2	15
29	a	145/148 (98%)	111 (77%)	26 (18%)	8 (6%)	1	10
30	b	73/160 (46%)	58 (80%)	11 (15%)	4 (6%)	1	10
31	c	92/115 (80%)	78 (85%)	10 (11%)	4 (4%)	2	14
32	d	105/125 (84%)	85 (81%)	16 (15%)	4 (4%)	2	15
33	e	126/135 (93%)	110 (87%)	15 (12%)	1 (1%)	16	44
34	f	107/110 (97%)	95 (89%)	7 (6%)	5 (5%)	2	12
35	g	112/117 (96%)	103 (92%)	7 (6%)	2 (2%)	7	27
36	h	120/123 (98%)	103 (86%)	14 (12%)	3 (2%)	4	22
37	i	100/105 (95%)	91 (91%)	7 (7%)	2 (2%)	6	25
38	j	84/86 (98%)	67 (80%)	13 (16%)	4 (5%)	2	12
39	k	67/70 (96%)	55 (82%)	7 (10%)	5 (8%)	1	5
40	l	48/51 (94%)	42 (88%)	4 (8%)	2 (4%)	2	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	m	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
42	n	21/25 (84%)	21 (100%)	0	0	100	100
43	o	102/106 (96%)	85 (83%)	11 (11%)	6 (6%)	1	8
44	p	89/91 (98%)	79 (89%)	9 (10%)	1 (1%)	12	37
45	r	123/125 (98%)	97 (79%)	20 (16%)	6 (5%)	2	11
46	1	384/476 (81%)	325 (85%)	42 (11%)	17 (4%)	2	13
47	2	60/68 (88%)	51 (85%)	6 (10%)	3 (5%)	1	11
All	All	6815/7601 (90%)	5717 (84%)	811 (12%)	287 (4%)	4	14

5 of 287 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	19	HIS
4	A	197	PRO
5	B	16	PHE
5	B	40	PRO
5	B	108	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	187/199 (94%)	139 (74%)	48 (26%)	0	1
5	B	335/335 (100%)	265 (79%)	70 (21%)	1	2
6	C	305/305 (100%)	239 (78%)	66 (22%)	1	2
7	D	246/250 (98%)	178 (72%)	68 (28%)	0	1
8	E	209/209 (100%)	157 (75%)	52 (25%)	0	1
9	F	194/194 (100%)	145 (75%)	49 (25%)	0	1
10	G	206/226 (91%)	158 (77%)	48 (23%)	0	2
11	H	169/171 (99%)	125 (74%)	44 (26%)	0	1
12	I	180/180 (100%)	136 (76%)	44 (24%)	0	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
13	J	143/149 (96%)	115 (80%)	28 (20%)	1	3	
14	L	176/177 (99%)	135 (77%)	41 (23%)	0	2	
15	M	116/160 (72%)	95 (82%)	21 (18%)	1	5	
16	N	171/172 (99%)	129 (75%)	42 (25%)	0	1	
17	O	172/172 (100%)	146 (85%)	26 (15%)	2	9	
18	P	134/134 (100%)	112 (84%)	22 (16%)	2	7	
19	Q	163/164 (99%)	132 (81%)	31 (19%)	1	4	
20	R	159/175 (91%)	120 (76%)	39 (24%)	0	1	
21	S	156/192 (81%)	121 (78%)	35 (22%)	1	2	
22	T	139/140 (99%)	112 (81%)	27 (19%)	1	3	
23	U	89/114 (78%)	67 (75%)	22 (25%)	0	1	
24	V	101/107 (94%)	77 (76%)	24 (24%)	0	1	
25	W	55/126 (44%)	42 (76%)	13 (24%)	0	1	
26	X	107/133 (80%)	89 (83%)	18 (17%)	1	7	
27	Y	124/135 (92%)	96 (77%)	28 (23%)	1	2	
28	Z	117/118 (99%)	94 (80%)	23 (20%)	1	3	
29	a	119/120 (99%)	102 (86%)	17 (14%)	2	10	
30	b	63/123 (51%)	45 (71%)	18 (29%)	0	1	
31	c	79/97 (81%)	60 (76%)	19 (24%)	0	1	
32	d	98/110 (89%)	66 (67%)	32 (33%)	0	0	
33	e	114/121 (94%)	89 (78%)	25 (22%)	1	2	
34	f	88/89 (99%)	73 (83%)	15 (17%)	1	6	
35	g	98/100 (98%)	79 (81%)	19 (19%)	1	3	
36	h	109/110 (99%)	92 (84%)	17 (16%)	2	8	
37	i	86/89 (97%)	71 (83%)	15 (17%)	1	6	
38	j	73/73 (100%)	60 (82%)	13 (18%)	1	5	
39	k	64/65 (98%)	52 (81%)	12 (19%)	1	4	
40	l	47/48 (98%)	39 (83%)	8 (17%)	1	6	
41	m	48/116 (41%)	36 (75%)	12 (25%)	0	1	
42	n	22/24 (92%)	17 (77%)	5 (23%)	0	2	
43	o	92/94 (98%)	70 (76%)	22 (24%)	0	1	

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	p	74/74 (100%)	61 (82%)	13 (18%)	1	6
45	r	109/109 (100%)	85 (78%)	24 (22%)	1	2
46	1	330/398 (83%)	309 (94%)	21 (6%)	14	39
47	2	53/59 (90%)	50 (94%)	3 (6%)	17	43
All	All	5919/6456 (92%)	4680 (79%)	1239 (21%)	2	2

5 of 1239 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	Z	121	ARG
41	m	104	HIS
30	b	23	LYS
28	Z	112	ARG
34	f	4	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 188 such sidechains are listed below:

Mol	Chain	Res	Type
22	T	58	HIS
31	c	73	HIS
24	V	36	ASN
28	Z	79	HIS
33	e	126	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3647/3722 (97%)	1611 (44%)	629 (17%)
2	7	119/120 (99%)	31 (26%)	9 (7%)
3	8	155/156 (99%)	61 (39%)	22 (14%)
All	All	3921/3998 (98%)	1703 (43%)	660 (16%)

5 of 1703 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	5	A
1	5	6	C

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Mol	Chain	Res	Type
1	5	8	U
1	5	12	A

5 of 660 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	3860	A
1	5	4645	C
1	5	4084	G
1	5	3856	A
1	5	4287	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 133 ligands modelled in this entry, 133 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	12
8	E	1

The worst 5 of 13 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	72:ALA	C	84:VAL	N	23.51
1	5	4776:G	O3'	4859:C	P	17.87
1	5	757:G	O3'	906:C	P	16.89
1	5	519:C	O3'	642:G	P	16.61
1	5	2910:G	O3'	3583:U	P	16.04

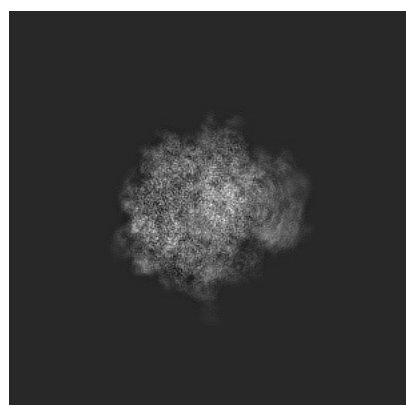
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2650. These allow visual inspection of the internal detail of the map and identification of artifacts.

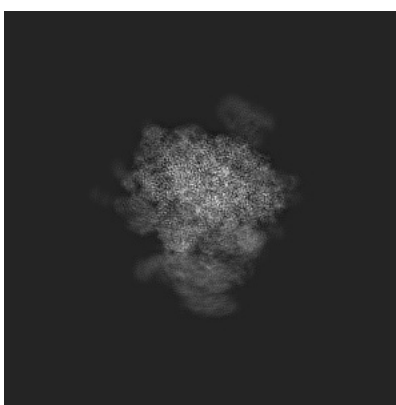
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

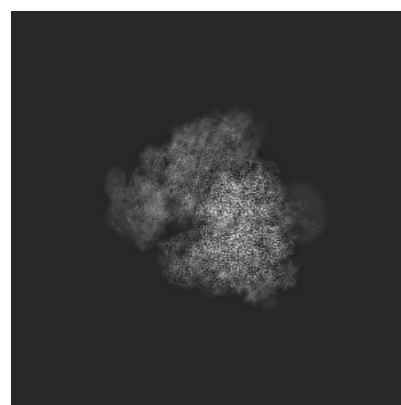
6.1.1 Primary map



X



Y

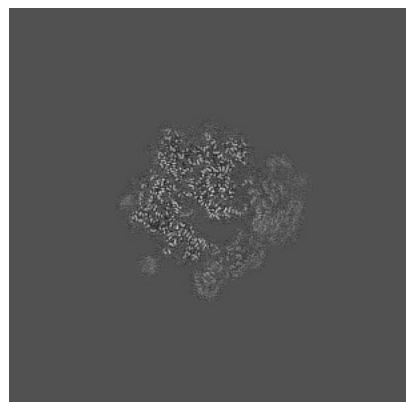


Z

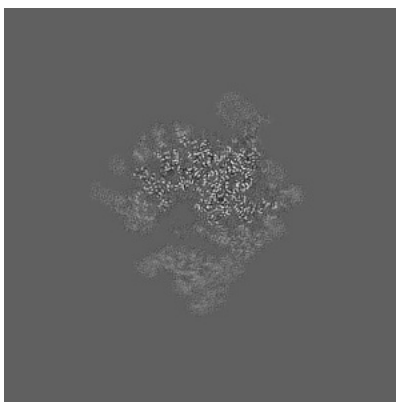
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 210



Y Index: 210

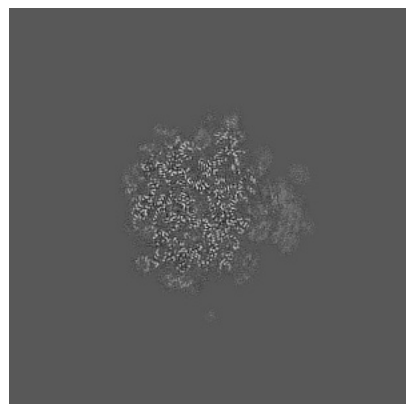


Z Index: 210

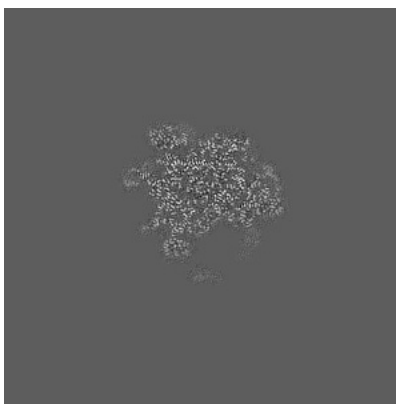
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

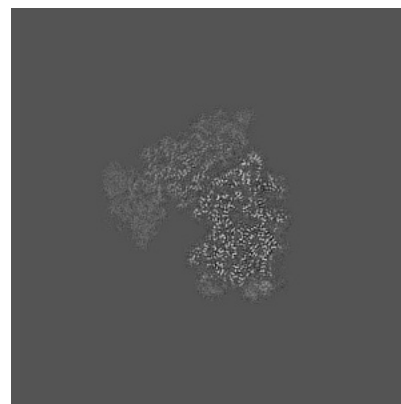
6.3.1 Primary map



X Index: 233



Y Index: 168

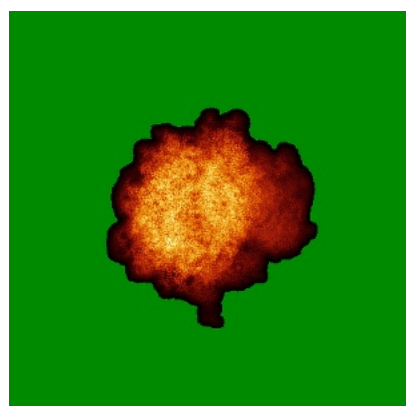


Z Index: 219

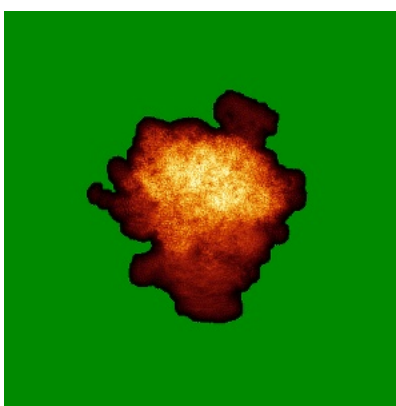
The images above show the largest variance slices of the map in three orthogonal directions.

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

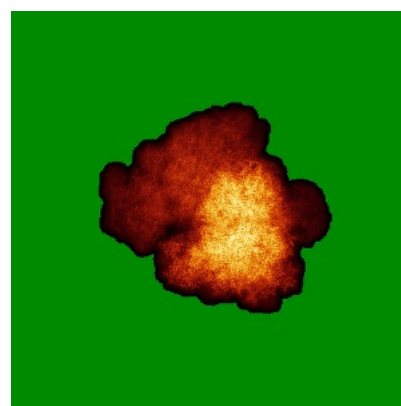
6.4.1 Primary map



X



Y

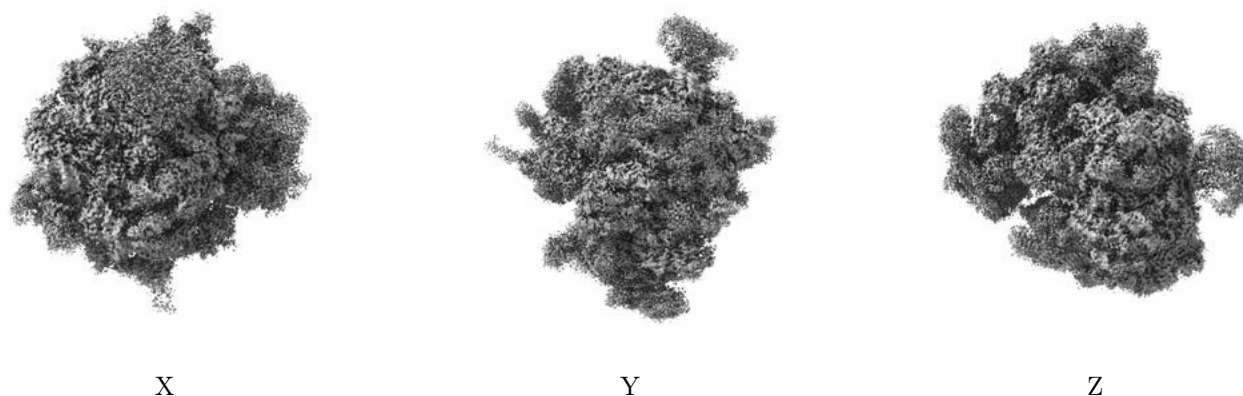


Z

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

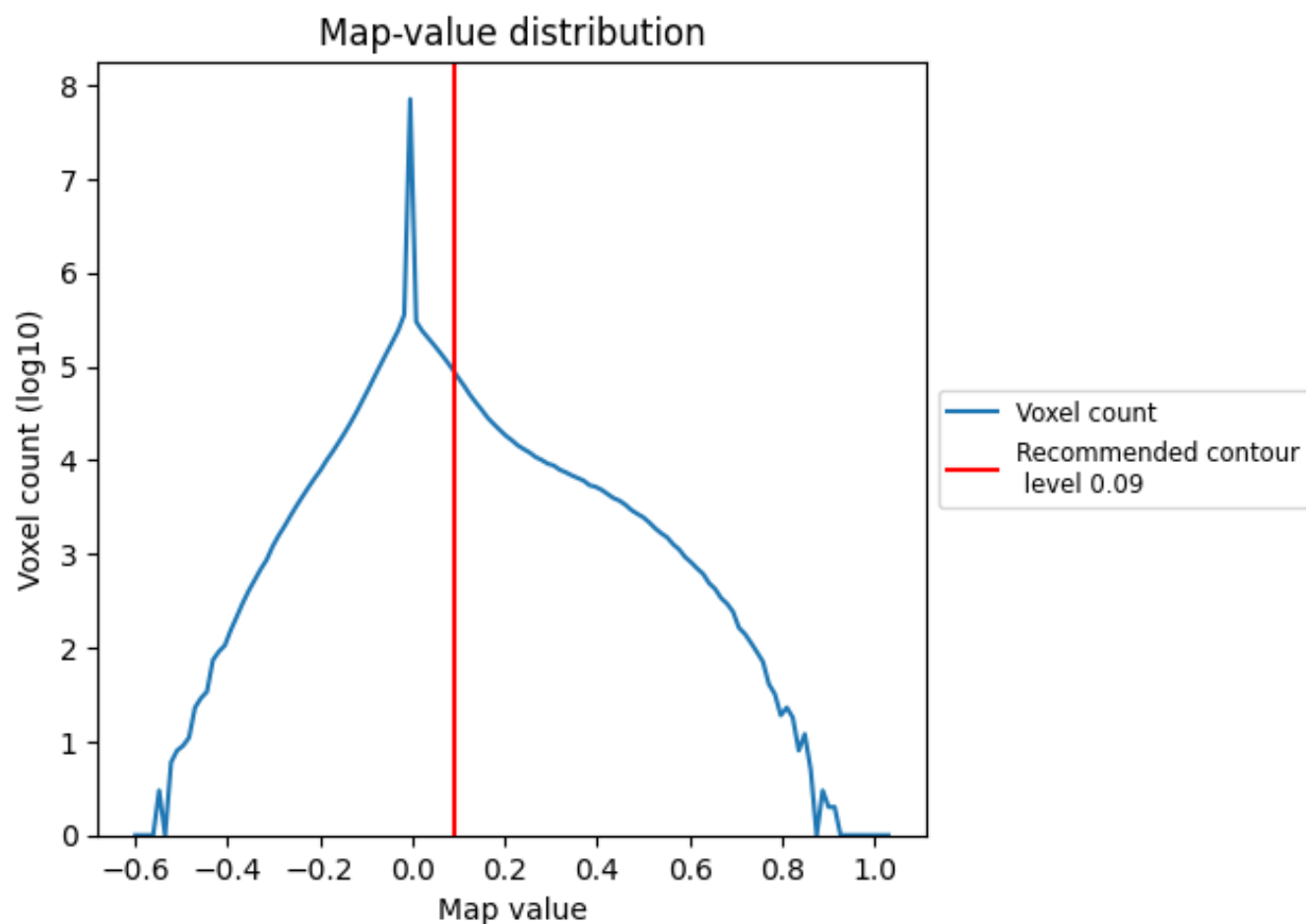
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

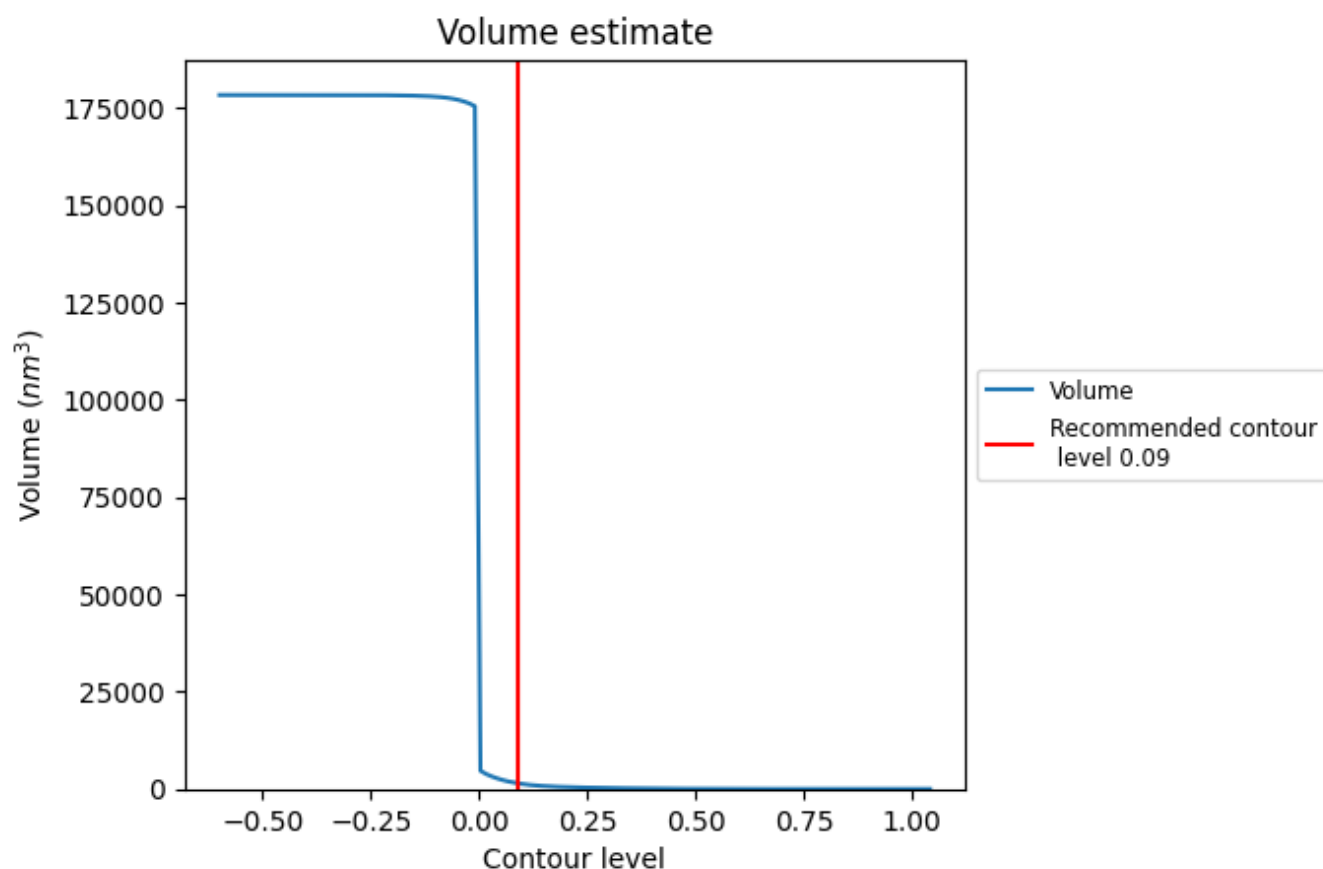
This section contains the results of statistical analysis of the map.

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.

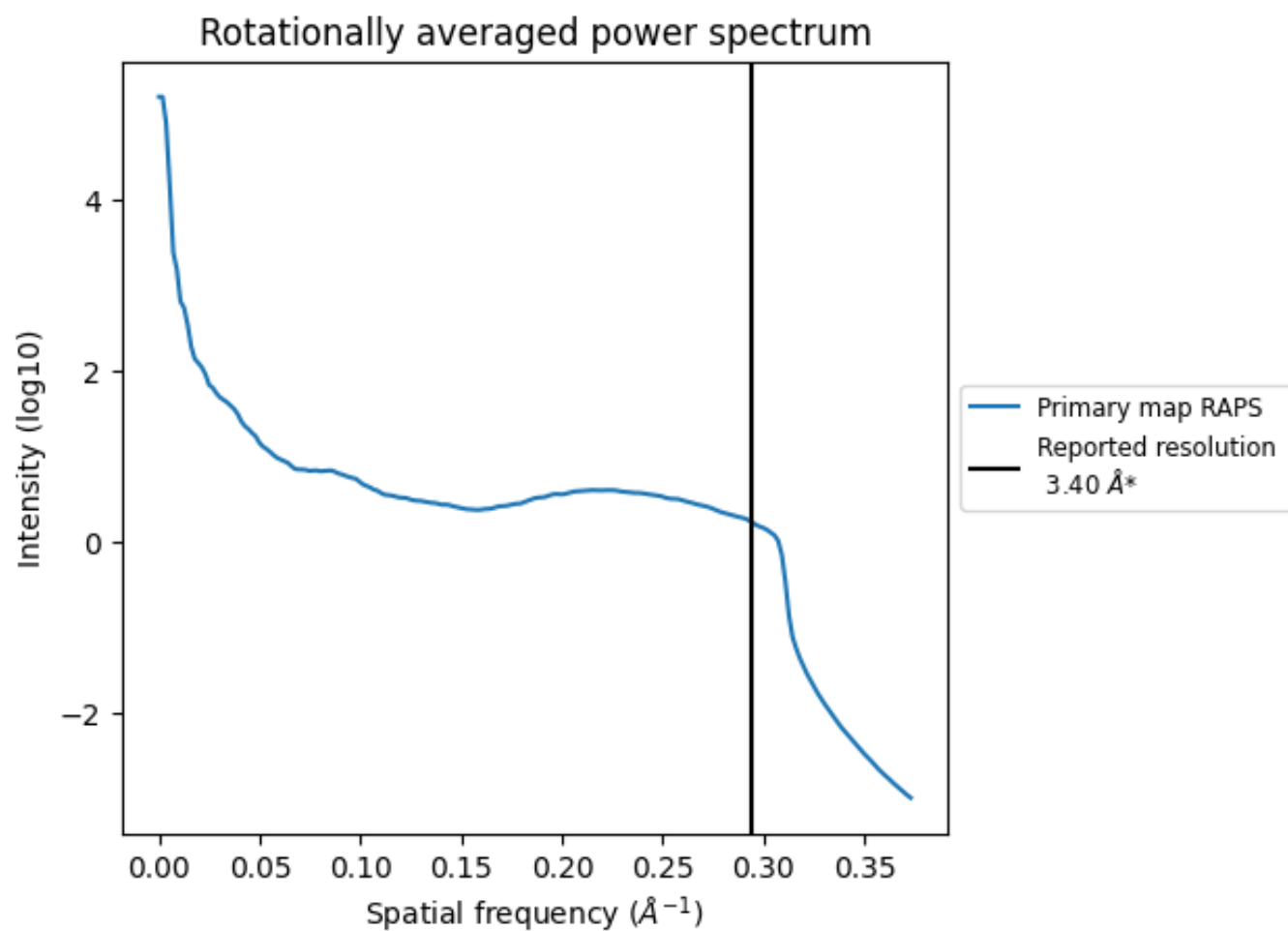
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1453 nm^3 ; this corresponds to an approximate mass of 1312 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 0.294 Å⁻¹

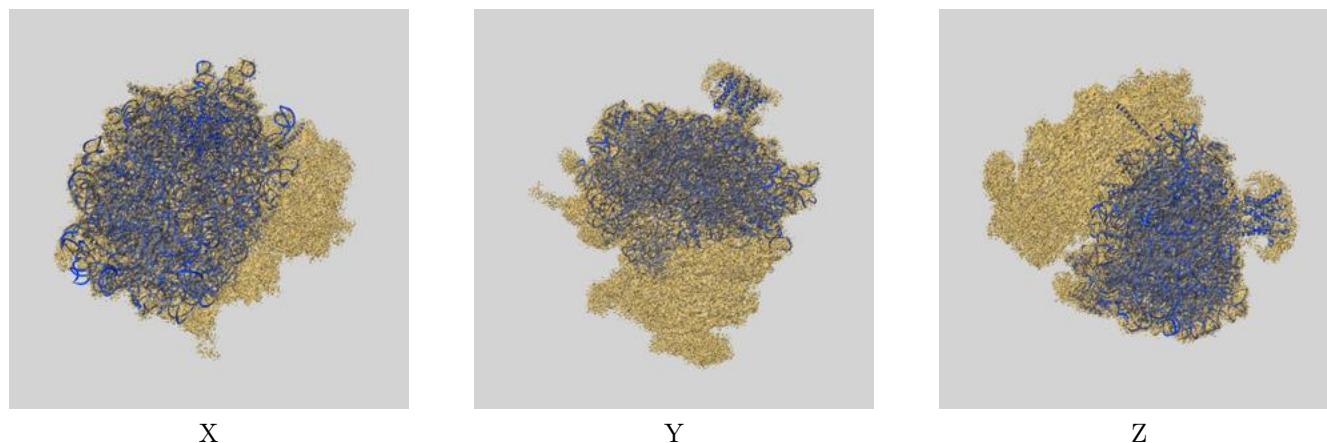
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

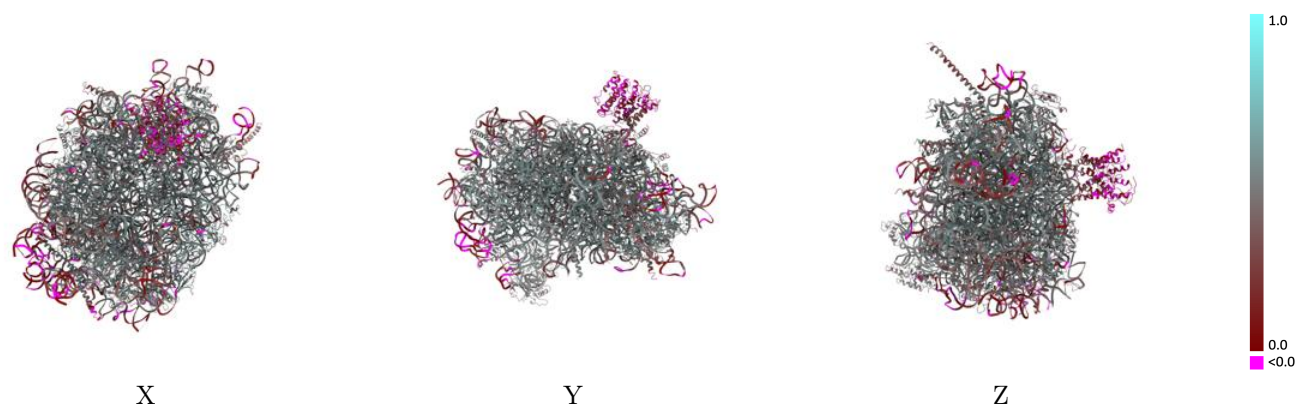
This section contains information regarding the fit between EMDB map EMD-2650 and PDB model 3J7Q. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



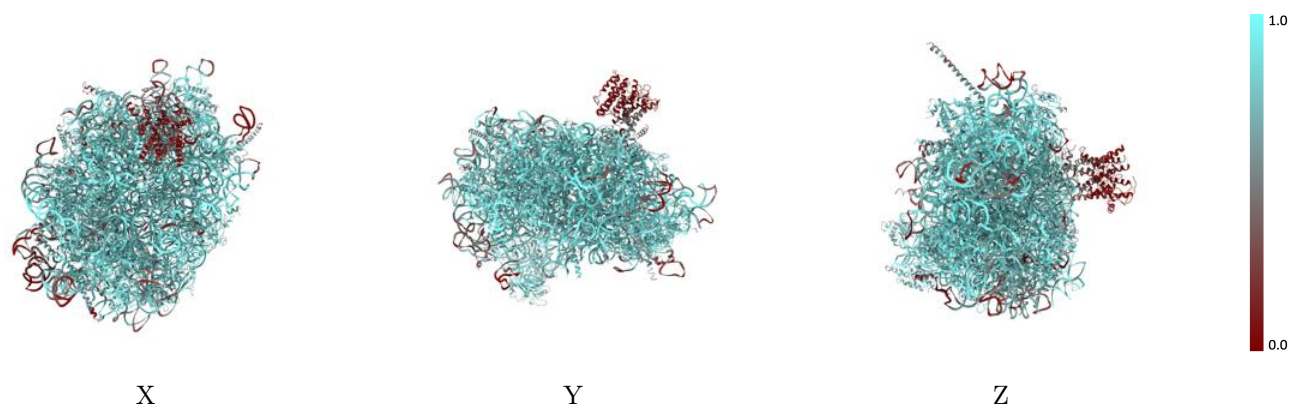
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



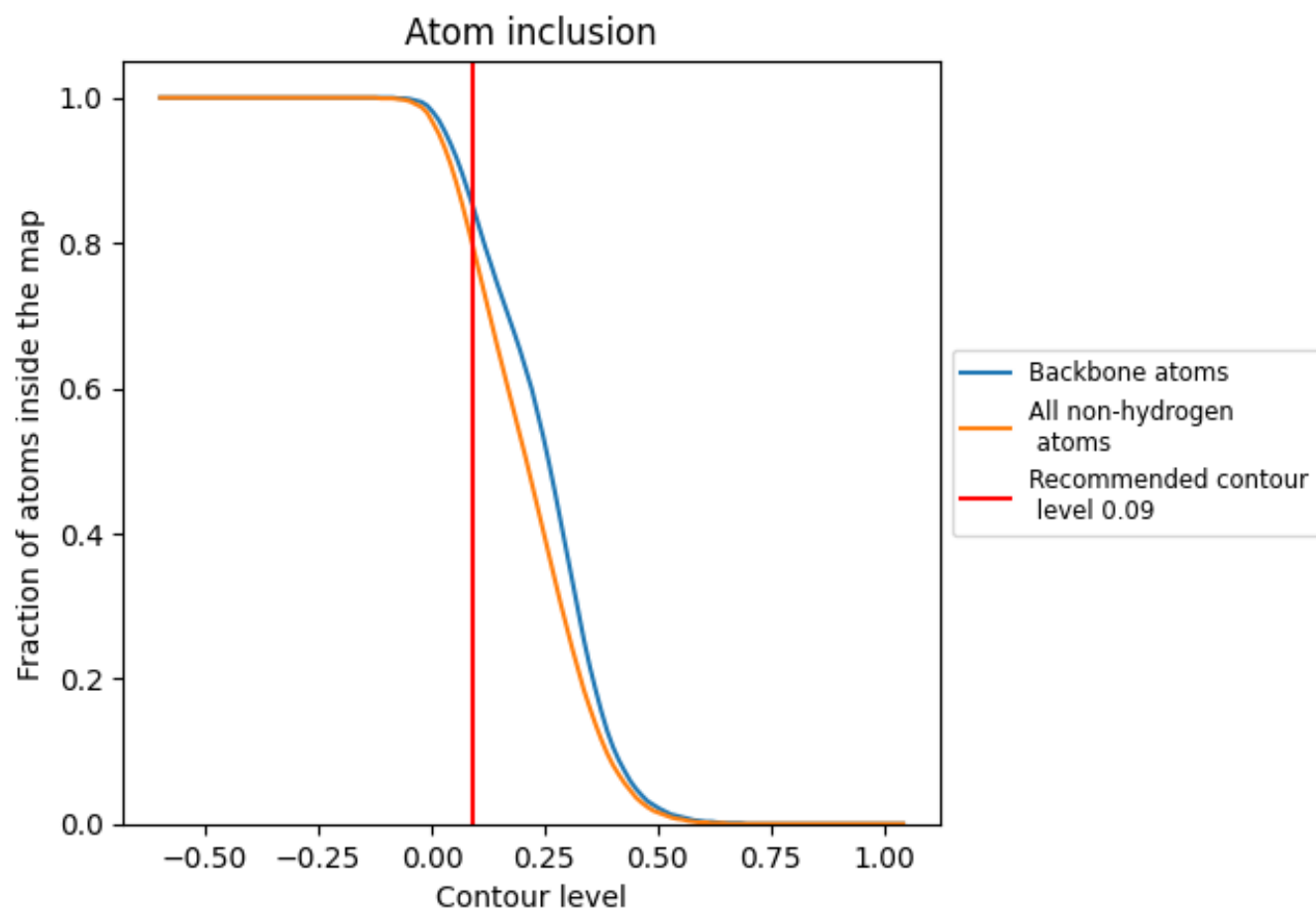
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.09).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





























The table lists the average atom inclusion at the recommended contour level (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8000	 0.4410
1	 0.2230	 0.1560
2	 0.2590	 0.1820
3	 0.0280	 0.0620
5	 0.8090	 0.4170
7	 0.9290	 0.4920
8	 0.8500	 0.4530
A	 0.8620	 0.5200
B	 0.8600	 0.5130
C	 0.8300	 0.5000
D	 0.8060	 0.4580
E	 0.7580	 0.4480
F	 0.8320	 0.5010
G	 0.7680	 0.4560
H	 0.8280	 0.5050
I	 0.8010	 0.4800
J	 0.7620	 0.4510
L	 0.7750	 0.4650
M	 0.8310	 0.5010
N	 0.8720	 0.5200
O	 0.8570	 0.5230
P	 0.8350	 0.5160
Q	 0.8610	 0.5230
R	 0.7790	 0.4670
S	 0.8610	 0.5190
T	 0.8250	 0.5020
U	 0.7200	 0.4240
V	 0.8430	 0.5190
W	 0.8210	 0.5040
X	 0.7870	 0.4910
Y	 0.8100	 0.4990
Z	 0.8310	 0.4950
a	 0.8630	 0.5160
b	 0.6780	 0.4120
c	 0.8080	 0.4850



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Chain	Atom inclusion	Q-score
d	 0.7990	 0.4790
e	 0.8470	 0.5210
f	 0.8780	 0.5260
g	 0.8150	 0.5080
h	 0.7890	 0.4880
i	 0.8040	 0.4890
j	 0.8470	 0.5010
k	 0.7540	 0.4600
l	 0.8350	 0.5180
m	 0.8490	 0.5220
n	 0.7710	 0.4760
o	 0.8010	 0.5020
p	 0.8200	 0.5160
r	 0.8390	 0.5060