



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 04:46 AM UTC

PDB ID : 9CAI / pdb_00009cai
EMDB ID : EMD-45392
Title : High-resolution C. elegans 80S ribosome structure - class 1
Authors : Sehgal, E.; Serrao, V.H.B.; Arribere, J.
Deposited on : 2024-06-17
Resolution : 2.59 Å (reported)
Based on initial model : .

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:

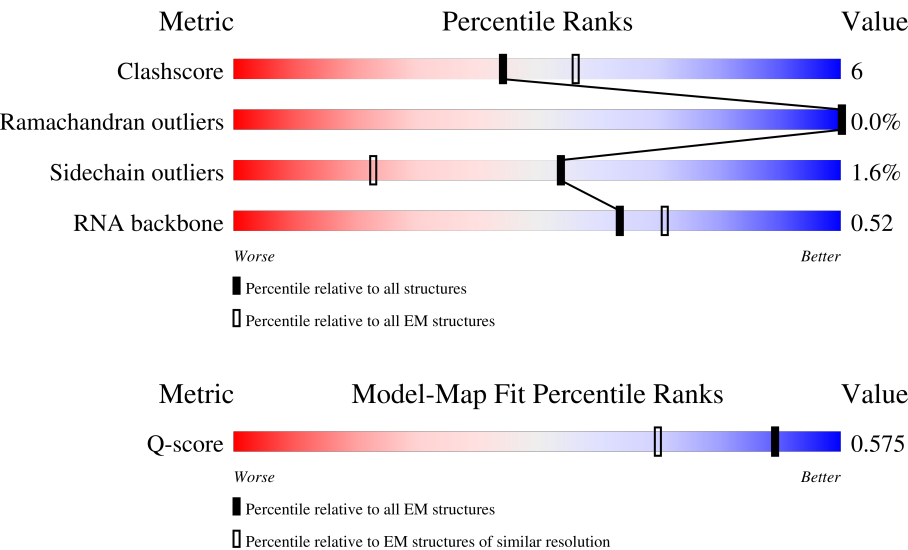
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.59 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	7741 (2.09 - 3.09)

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	AA	276	
2	CA	260	
3	DA	76	

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Mol	Chain	Length	Quality of chain
4	AB	257	
5	CB	401	
6	AC	272	
7	AD	247	
8	AE	259	
9	A7	119	
10	A8	153	
11	B2	1754	
12	A5	3510	
13	AR	130	
14	AK	149	
15	AW	130	
16	AS	154	
17	AT	146	
18	Aa	117	
19	Af	163	
20	AO	152	
21	AI	208	
22	AF	210	
23	AM	140	
24	AV	88	
25	AN	151	
26	AZ	117	
27	Ad	56	
28	AY	131	

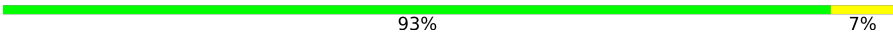
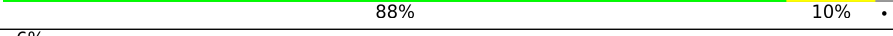
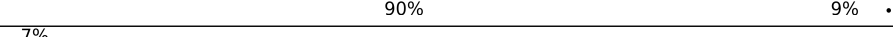
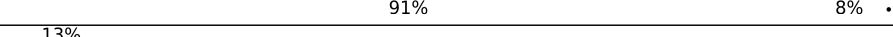
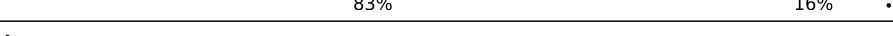
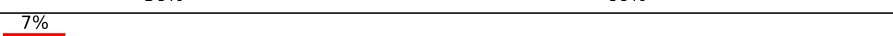
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Mol	Chain	Length	Quality of chain
29	AU	117	
30	AG	246	
31	Ab	83	
32	AP	151	
33	Ac	65	
34	Ae	130	
35	AX	143	
36	AL	155	
37	AJ	189	
38	AQ	144	
39	AH	194	
40	CF	244	
41	CS	180	
42	CV	140	
43	CU	130	
44	CL	207	
45	CG	265	
46	CI	214	
47	CO	202	
48	CC	345	
49	Ch	123	
50	CE	217	
51	Co	105	
52	Cf	124	
53	Ci	104	

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Mol	Chain	Length	Quality of chain
54	Cl	51	
55	CN	204	
56	Ca	145	
57	Cp	91	
58	CM	135	
59	Cc	115	
60	CH	189	
61	CY	142	
62	CR	198	
63	Cb	62	
64	CQ	188	
65	CT	161	
66	CD	293	
67	CZ	136	
68	CP	187	
69	Cn	22	
70	Cg	110	
71	Ck	70	
72	Cm	128	
73	Cd	122	
74	Ce	134	
75	CW	159	
76	Cj	92	
77	CJ	196	
78	CX	146	

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Mol	Chain	Length	Quality of chain
79	DC	10	

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 330203 atoms, of which 141530 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	AA	207	Total	C	H	N	O	S	0	0
			3264	1035	1652	281	289	7		

- Molecule 2 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	CA	249	Total	C	H	N	O	S	0	0
			3875	1178	1980	391	321	5		

- Molecule 3 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	DA	76	Total	C	H	N	O	P	0	0
			2448	725	821	294	532	76		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DA	74	C	U	conflict	GB 351064414
DA	75	C	G	conflict	GB 351064414
DA	76	A	U	conflict	GB 351064414

- Molecule 4 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	AB	210	Total	C	H	N	O	S	0	0
			3453	1071	1769	298	307	8		

- Molecule 5 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	CB	395	Total	C	H	N	O	S	0	0
			6478	2016	3300	605	547	10		

- Molecule 6 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	AC	215	Total	C	H	N	O	S	0	0
			3389	1062	1735	293	292	7		

- Molecule 7 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	AD	211	Total	C	H	N	O	S	0	0
			3343	1029	1706	308	291	9		

- Molecule 8 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	AE	255	Total	C	H	N	O	S	0	0
			4120	1277	2107	382	347	7		

- Molecule 9 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	A7	119	Total	C	H	N	O	P	0	0
			3810	1131	1281	447	833	118		

- Molecule 10 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	A8	146	Total	C	H	N	O	P	0	0
			4679	1390	1568	551	1025	145		

- Molecule 11 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	B2	1476	Total	C	H	N	O	P	0	0
			47369	14078	15858	5637	10320	1476		

- Molecule 12 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	A5	3022	Total	C	H	N	O	P	0	0
			96979	28814	32467	11522	21154	3022		

- Molecule 13 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AR	121	Total	C	H	N	O	S	0	0
			1985	604	1009	183	184	5		

- Molecule 14 is a protein called Plectin/S10 N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AK	93	Total	C	H	N	O	S	0	0
			1555	509	786	124	135	1		

- Molecule 15 is a protein called Ribosomal Protein, Small subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	AW	129	Total	C	H	N	O	S	0	0
			2110	654	1082	193	177	4		

- Molecule 16 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	AS	148	Total	C	H	N	O	S	0	0
			2453	754	1248	237	209	5		

- Molecule 17 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	AT	140	Total	C	H	N	O	S	0	0
			2260	704	1149	213	193	1		

- Molecule 18 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	Aa	99	Total	C	H	N	O	S	0	0
			1631	496	828	172	129	6		

- Molecule 19 is a protein called Ubiquitin-like protein 1-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	Af	50	Total	C	H	N	O	S	0	0
			789	246	392	77	69	5		

- Molecule 20 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	AO	135	Total	C	H	N	O	S	0	0
			2063	624	1049	200	185	5		

- Molecule 21 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	AI	207	Total	C	H	N	O	S	0	0
			3391	1044	1723	326	296	2		

- Molecule 22 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	AF	185	Total	C	H	N	O	S	0	0
			2969	914	1515	275	259	6		

- Molecule 23 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	AM	117	Total	C	H	N	O	S	0	0
			1808	565	904	162	170	7		

- Molecule 24 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	AV	81	Total	C	H	N	O	S	0	0
			1239	378	622	114	120	5		

- Molecule 25 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	AN	151	Total	C	H	N	O	S	0	0
			2514	769	1297	236	206	6		

- Molecule 26 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	AZ	71	Total	C	H	N	O	S	0	0
			1165	363	601	100	99	2		

- Molecule 27 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	Ad	55	Total	C	H	N	O	S	0	0
			895	284	443	93	71	4		

- Molecule 28 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	AY	123	Total	C	H	N	O	S	0	0
			2085	637	1093	188	165	2		

- Molecule 29 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	AU	100	Total	C	H	N	O	S	0	0
			1650	500	854	154	138	4		

- Molecule 30 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	AG	228	Total	C	H	N	O	S	0	0
			3791	1159	1954	350	321	7		

- Molecule 31 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	Ab	82	Total	C	H	N	O	S	0	0
			1305	404	663	119	111	8		

- Molecule 32 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	AP	128	Total	C	H	N	O	S	0	0
			2112	658	1090	189	169	6		

- Molecule 33 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	Ac	65	Total	C	H	N	O	S	0	0
			1069	314	549	106	98	2		

- Molecule 34 is a protein called Ubiquitin-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ae	45	Total	C	H	N	O	0	0
			752	219	388	84	61		

- Molecule 35 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace	
35	AX	140	Total	C	H	N	O	S	0	0
			2242	691	1150	212	186	3		

- Molecule 36 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace	
36	AL	143	Total	C	H	N	O	S	0	0
			2380	736	1222	223	194	5		

- Molecule 37 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace	
37	AJ	177	Total	C	H	N	O	S	0	0
			3060	936	1592	288	243	1		

- Molecule 38 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace	
38	AQ	140	Total	C	H	N	O	S	0	0
			2305	715	1181	215	193	1		

- Molecule 39 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	AH	192	Total	C	H	N	O	0	0
			3187	993	1643	280	271		

- Molecule 40 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	CF	213	Total	C	H	N	O	S	0	0
			3534	1119	1791	320	302	2		

- Molecule 41 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	CS	179	Total	C	H	N	O	S	0	0
			2976	936	1506	278	250	6		

- Molecule 42 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	CV	128	Total	C	H	N	O	S	0	0
			1991	614	1020	182	169	6		

- Molecule 43 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	CU	100	Total	C	H	N	O	S	0	0
			1692	532	868	147	144	1		

- Molecule 44 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	CL	204	Total	C	H	N	O	S	0	0
			3388	1025	1740	338	283	2		

- Molecule 45 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	CG	221	Total	C	H	N	O	S	0	0
			3680	1123	1892	354	309	2		

- Molecule 46 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	CI	213	Total	C	H	N	O	S	0	0
			3485	1083	1756	343	290	13		

- Molecule 47 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	CO	201	Total	C	H	N	O	S	0	0
			3328	1031	1714	314	264	5		

- Molecule 48 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	CC	335	Total	C	H	N	O	S	0	0
			5420	1675	2769	521	449	6		

- Molecule 49 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	Ch	122	Total	C	H	N	O	S	0	0
			2094	618	1105	201	169	1		

- Molecule 50 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	CE	139	Total	C	H	N	O	S	0	0
			2311	727	1195	203	185	1		

- Molecule 51 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	Co	102	Total	C	H	N	O	S	0	0
			1739	522	902	174	135	6		

- Molecule 52 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	Cf	117	Total	C	H	N	O		0	0
			1901	594	971	183	153			

- Molecule 53 is a protein called Large ribosomal subunit protein eL36.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	Ci	104	Total	C	H	N	O	S	0	0
			1754	521	918	176	137	2		

- Molecule 54 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	Cl	50	Total	C	H	N	O	S	0	0
			922	276	487	93	63	3		

- Molecule 55 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	CN	203	Total	C	H	N	O	S	0	0
			3463	1068	1763	358	272	2		

- Molecule 56 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	Ca	144	Total	C	H	N	O	S	0	0
			2299	717	1163	232	183	4		

- Molecule 57 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	Cp	88	Total	C	H	N	O	S	0	0
			1404	425	726	134	113	6		

- Molecule 58 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	CM	132	Total	C	H	N	O	S	0	0
			2204	668	1151	205	178	2		

- Molecule 59 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	Cc	96	Total	C	H	N	O	S	0	0
			1497	464	762	129	137	5		

- Molecule 60 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	CH	188	Total	C	H	N	O	S	0	0
			3081	954	1577	278	266	6		

- Molecule 61 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	CY	132	Total	C	H	N	O	S	0	0
			2181	651	1131	219	176	4		

- Molecule 62 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	CR	194	Total	C	H	N	O	S	0	0
			3384	1012	1746	349	274	3		

- Molecule 63 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	Cb	52	Total	C	H	N	O	S	0	0
			892	268	460	94	69	1		

- Molecule 64 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	CQ	187	Total	C	H	N	O	S	0	0
			3023	918	1550	299	255	1		

- Molecule 65 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	CT	160	Total	C	H	N	O	S	0	0
			2621	806	1338	256	218	3		

- Molecule 66 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
66	CD	289	Total	C	H	N	O	S	0	0
			4701	1468	2373	430	428	2		

- Molecule 67 is a protein called Large ribosomal subunit protein eL27.

Mol	Chain	Residues	Atoms						AltConf	Trace
67	CZ	135	Total	C	H	N	O	S	0	0
			2301	716	1199	200	184	2		

- Molecule 68 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	CP	154	Total	C	H	N	O	S	0	0
			2506	780	1257	249	215	5		

- Molecule 69 is a protein called eL41.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	Cn	22	Total	C	H	N	O	S	0	0
			461	128	252	54	25	2		

- Molecule 70 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	Cg	104	Total	C	H	N	O	S	0	0
			1759	526	922	170	139	2		

- Molecule 71 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms						AltConf	Trace
71	Ck	69	Total	C	H	N	O	S	0	0
			1181	359	622	100	99	1		

- Molecule 72 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	Cm	51	Total	C	H	N	O	S	0	0
			874	258	456	86	69	5		

- Molecule 73 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms						AltConf	Trace
73	Cd	105	Total	C	H	N	O	S	0	0
			1770	544	903	169	151	3		

- Molecule 74 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	Ce	128	Total	C	H	N	O	S	0	0
			2160	652	1119	216	169	4		

- Molecule 75 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
75	CW	88	Total	C	H	N	O	S	0	0
			1447	442	745	140	118	2		

- Molecule 76 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	Cj	88	Total	C	H	N	O	S	0	0
			1433	431	727	154	117	4		

- Molecule 77 is a protein called Large ribosomal subunit protein uL5B.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	CJ	186	Total	C	H	N	O	S	0	0
			3062	952	1555	281	269	5		

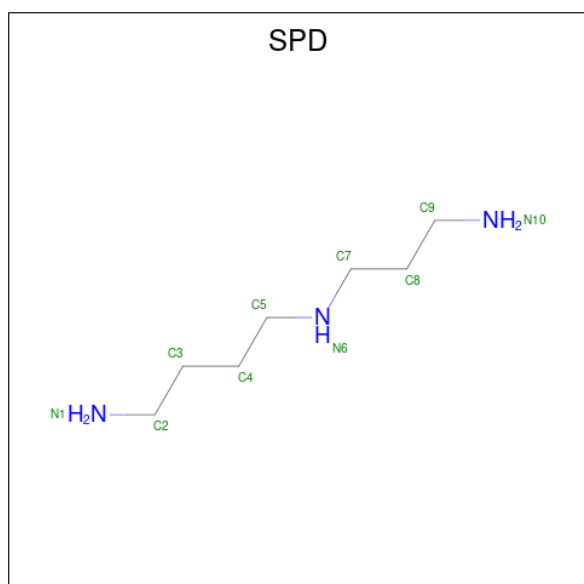
- Molecule 78 is a protein called Large ribosomal subunit protein uL23B.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	CX	119	Total	C	H	N	O	S	0	0
			1958	606	1004	181	166	1		

- Molecule 79 is a RNA chain called mRNA.

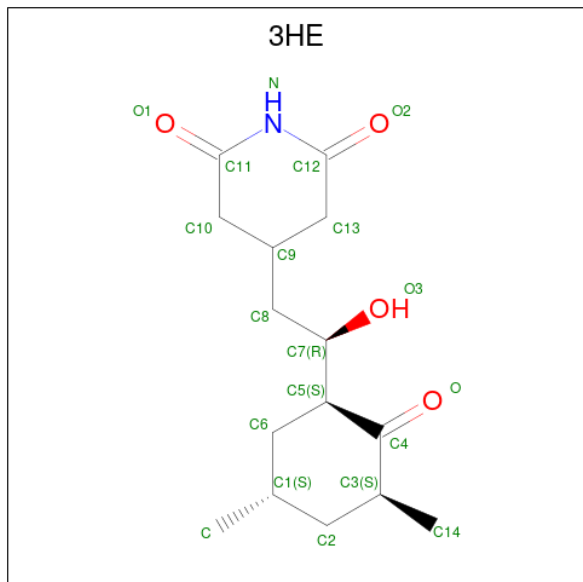
Mol	Chain	Residues	Atoms						AltConf	Trace
79	DC	10	Total	C	H	N	O	P	0	0
			301	90	101	20	80	10		

- Molecule 80 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



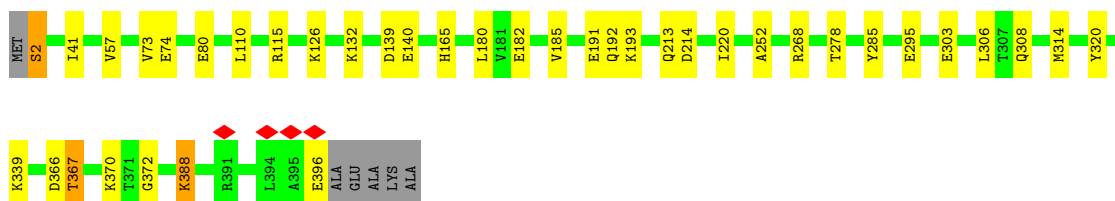
Mol	Chain	Residues	Atoms			AltConf
80	A5	1	Total	C	N	0
			10	7	3	

- Molecule 81 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (CCD ID: 3HE) (formula: C₁₅H₂₃NO₄).

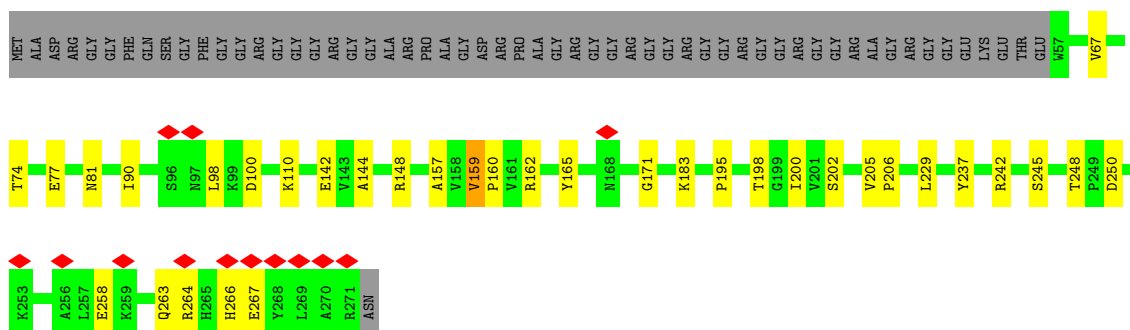


Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	N	O	
81	A5	1	43	15	23	1	4	0

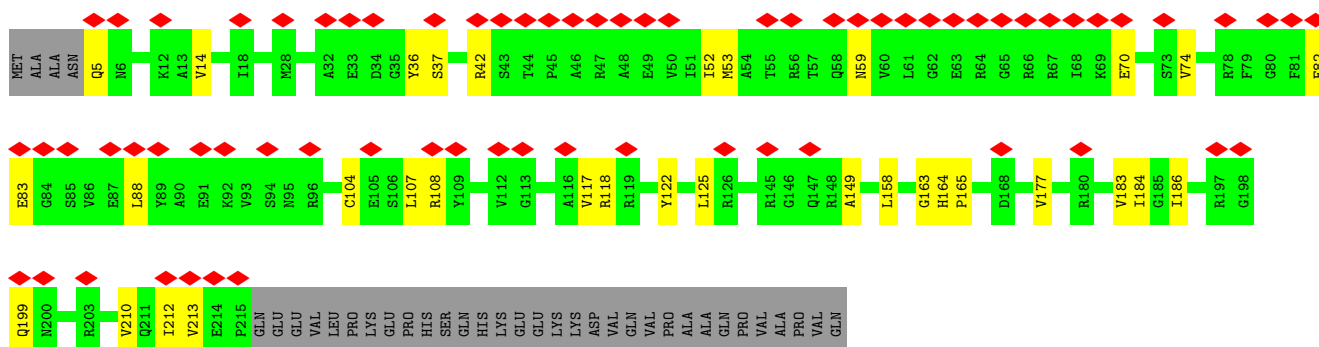
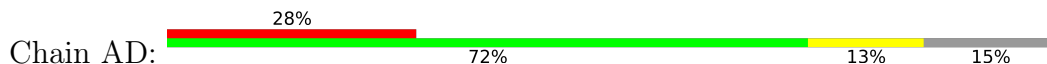
- Molecule 5: Large ribosomal subunit protein uL3



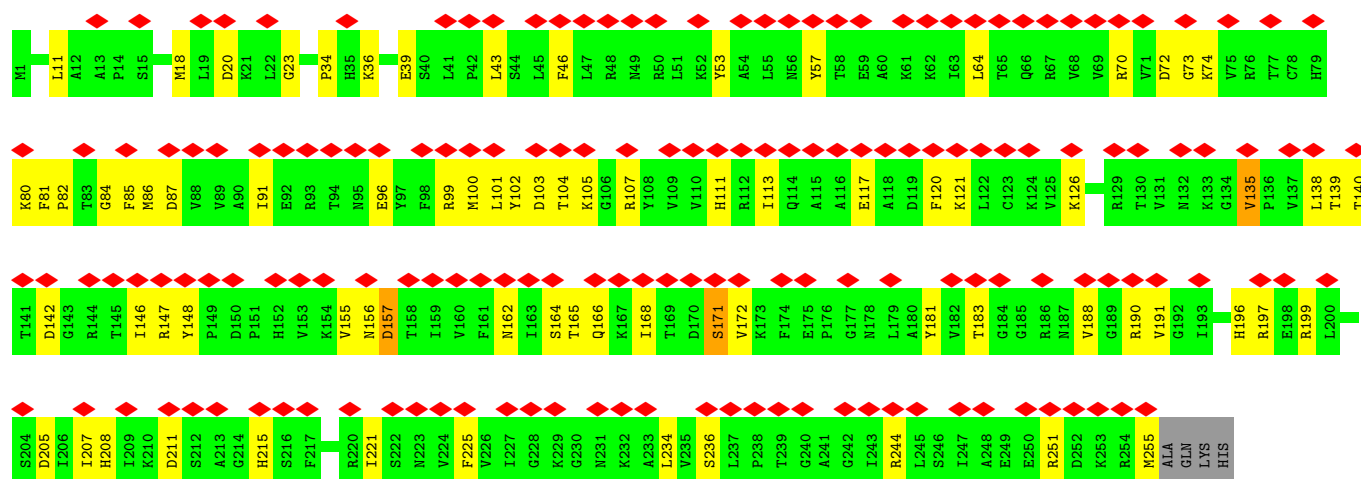
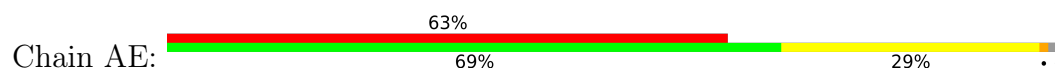
- Molecule 6: Small ribosomal subunit protein uS5



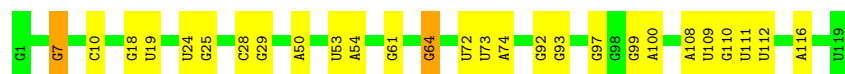
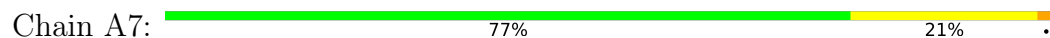
- Molecule 7: Small ribosomal subunit protein uS3



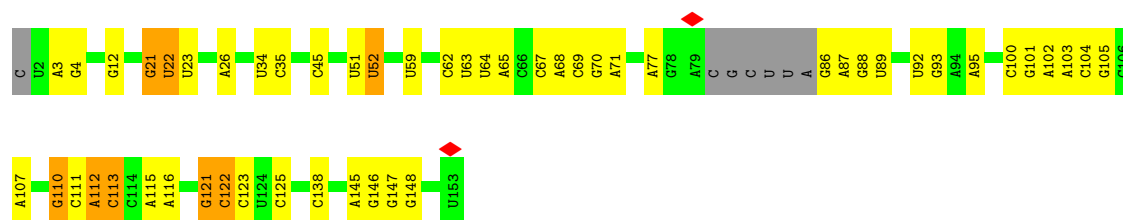
- Molecule 8: Small ribosomal subunit protein eS4



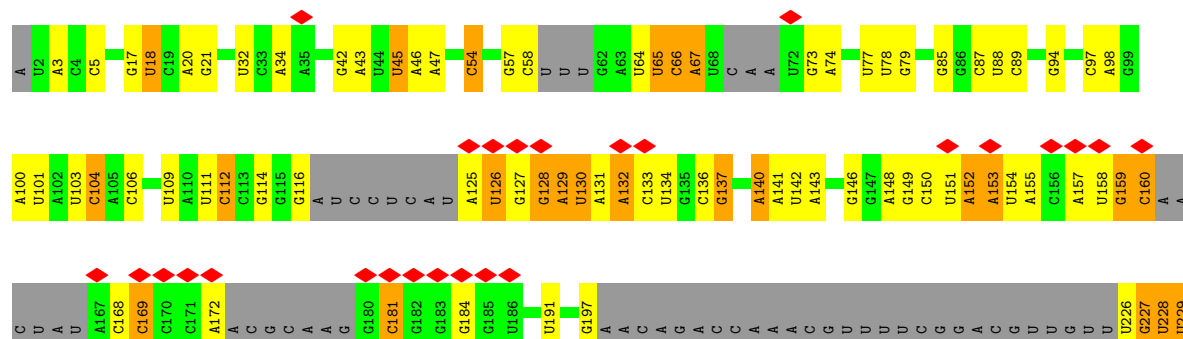
• Molecule 9: 5S rRNA

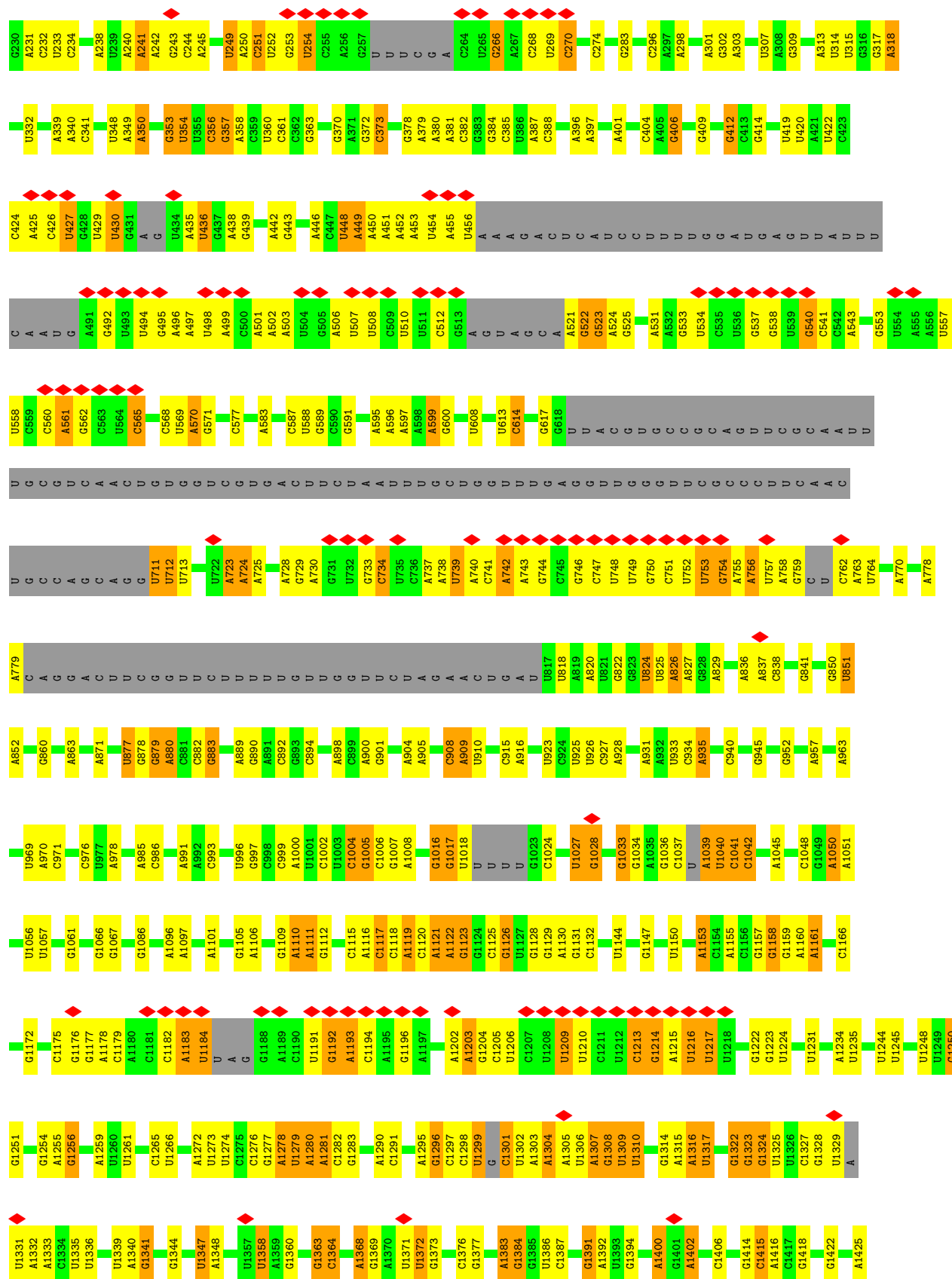


• Molecule 10: 5.8S rRNA

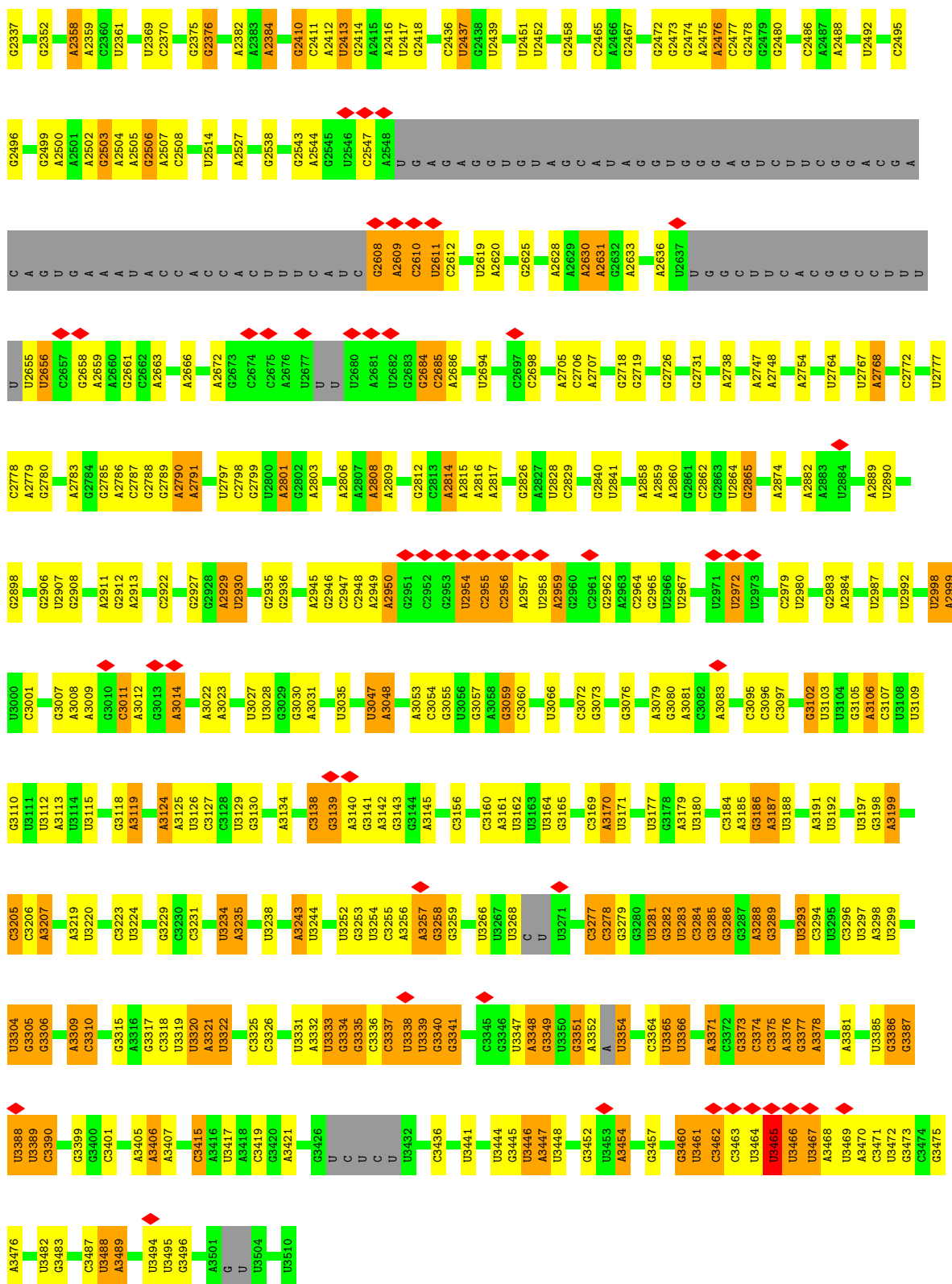


• Molecule 11: 18S rRNA

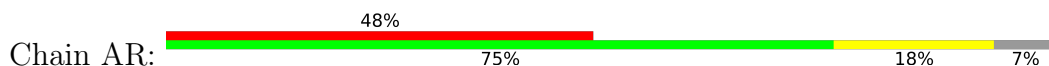


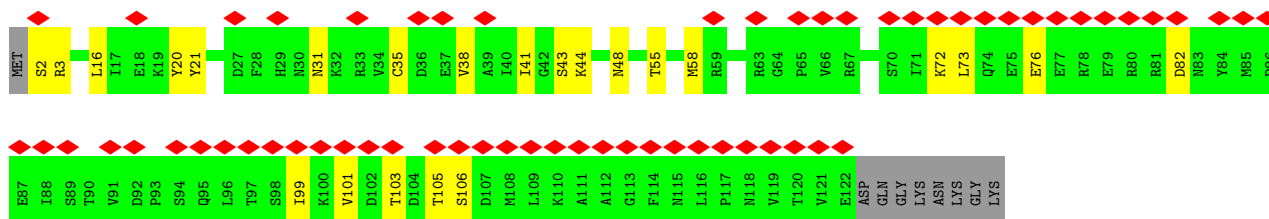




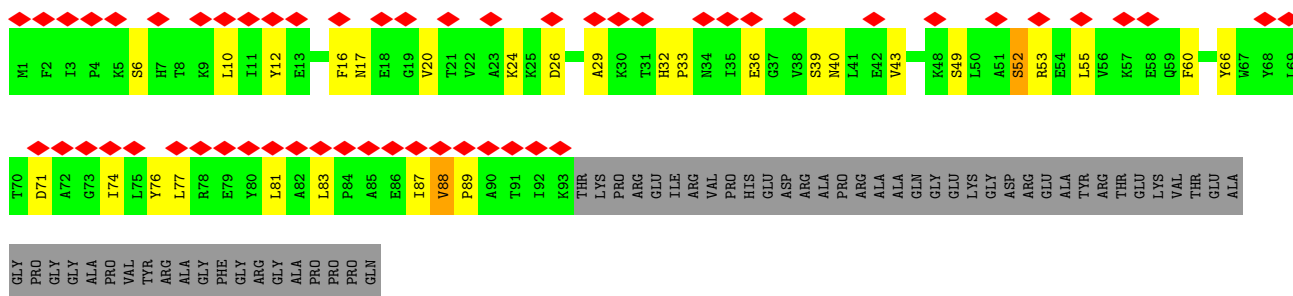
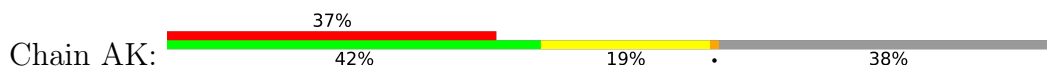


- Molecule 13: Small ribosomal subunit protein eS17

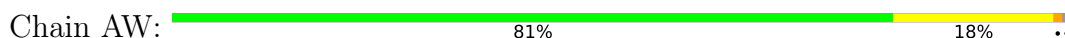




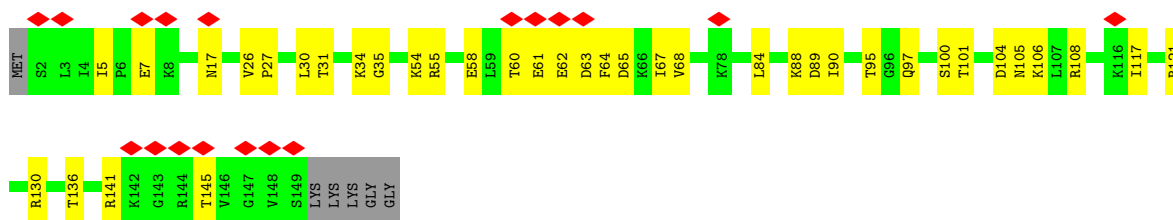
- Molecule 14: Plectin/S10 N-terminal domain-containing protein



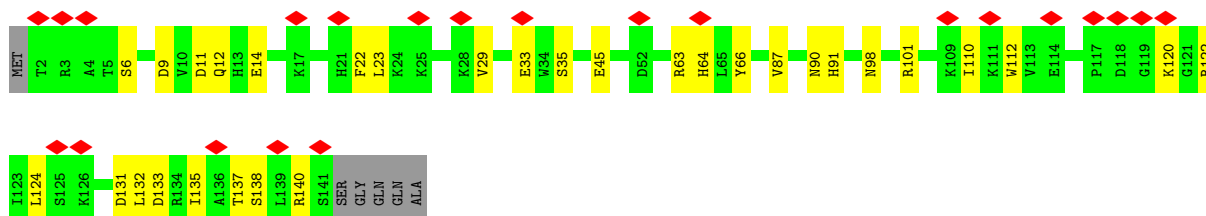
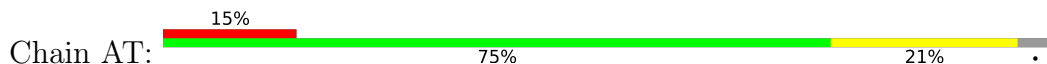
- Molecule 15: Ribosomal Protein, Small subunit

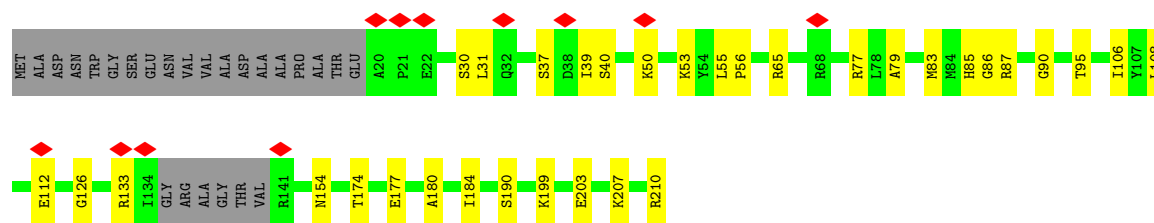


- Molecule 16: Small ribosomal subunit protein uS13

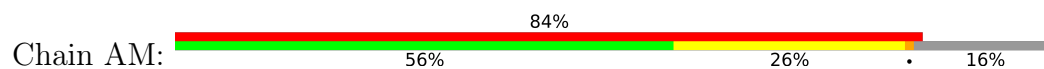


- Molecule 17: Small ribosomal subunit protein eS19

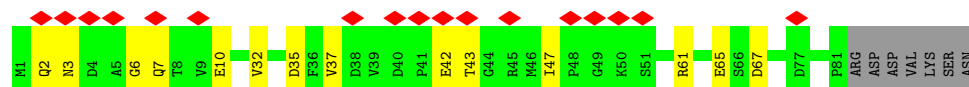
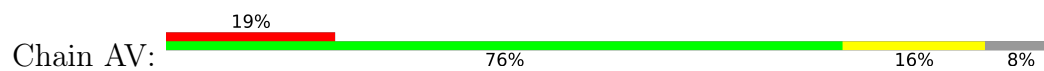




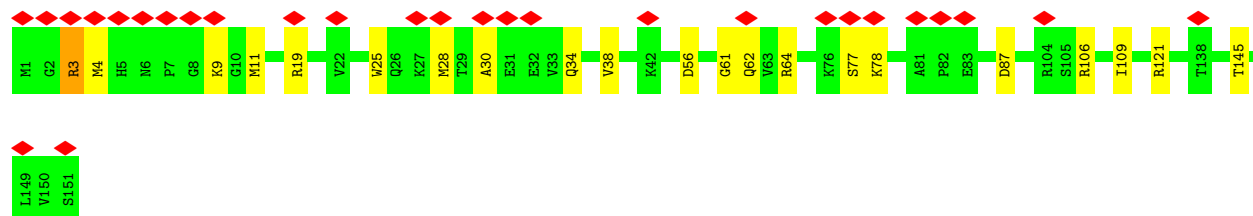
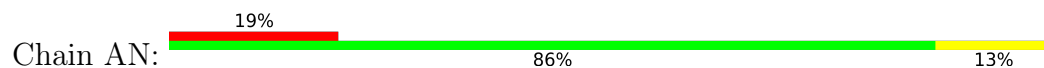
- Molecule 23: Small ribosomal subunit protein eS12



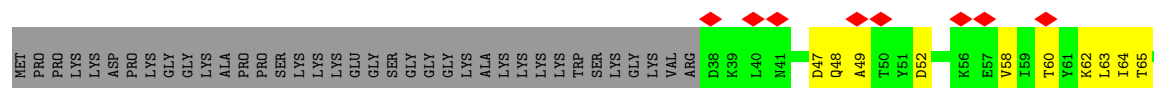
- Molecule 24: Small ribosomal subunit protein eS21

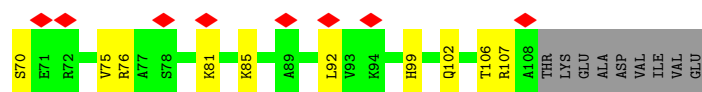


- Molecule 25: Small ribosomal subunit protein uS15

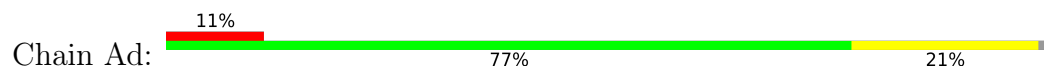


- Molecule 26: Small ribosomal subunit protein eS25

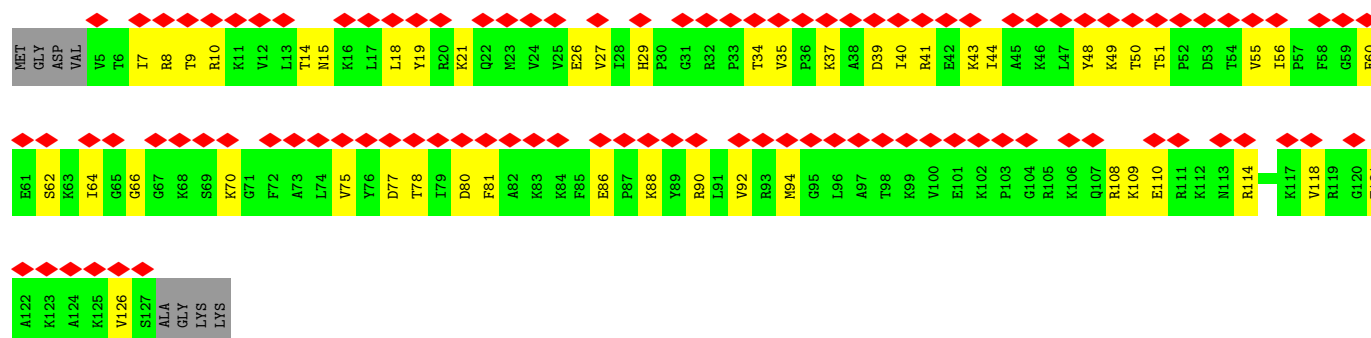
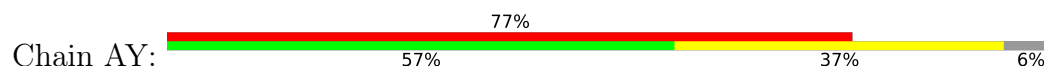




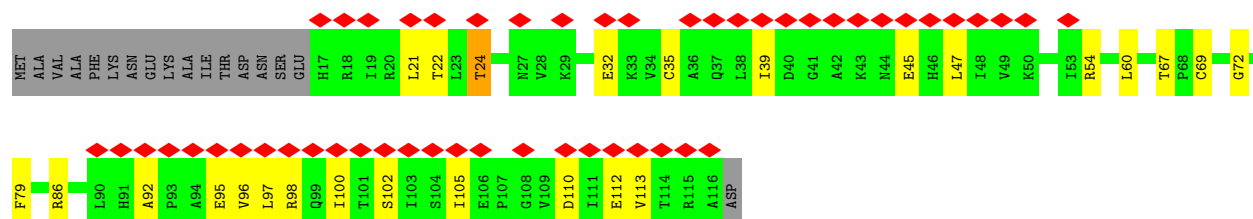
- Molecule 27: Small ribosomal subunit protein uS14



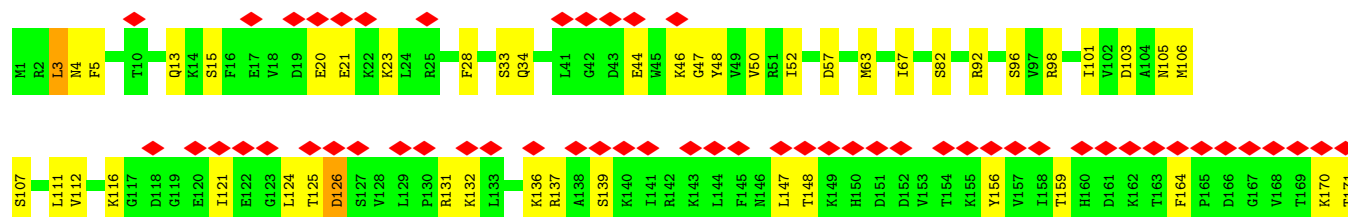
- Molecule 28: Small ribosomal subunit protein eS24

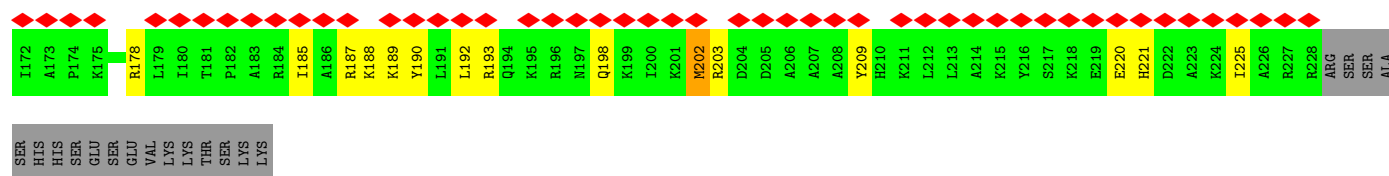


- Molecule 29: Small ribosomal subunit protein uS10

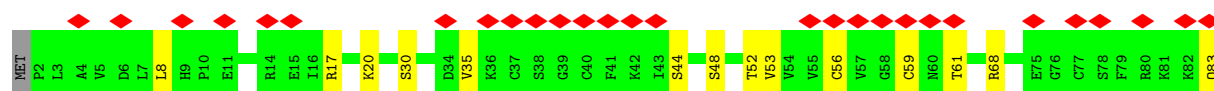
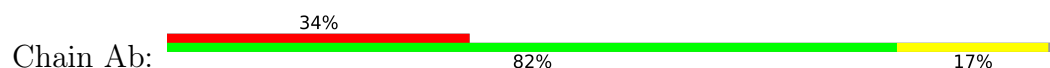


- Molecule 30: Small ribosomal subunit protein eS6

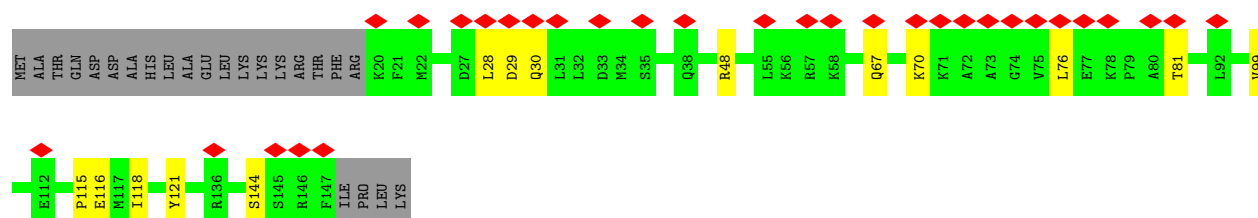
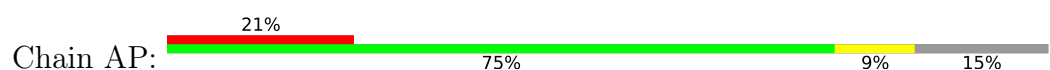




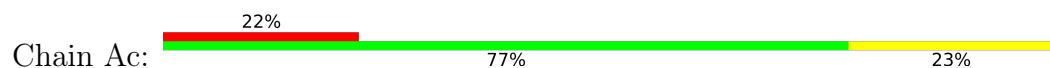
- Molecule 31: Small ribosomal subunit protein eS27



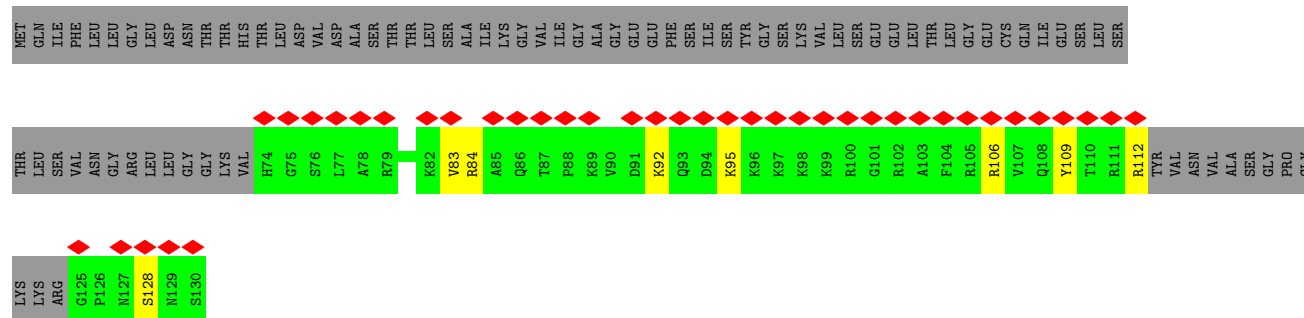
- Molecule 32: Small ribosomal subunit protein uS19



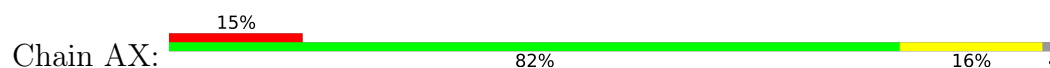
- Molecule 33: Small ribosomal subunit protein eS28

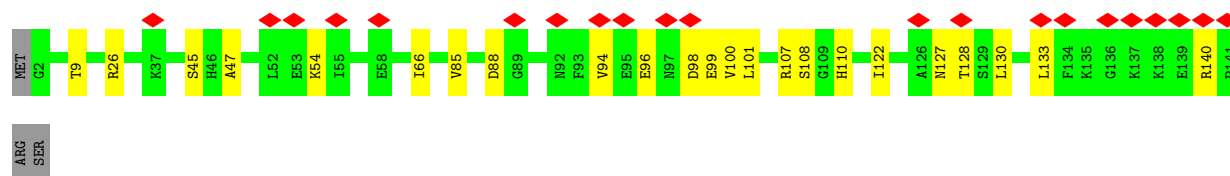


- Molecule 34: Ubiquitin-like domain-containing protein

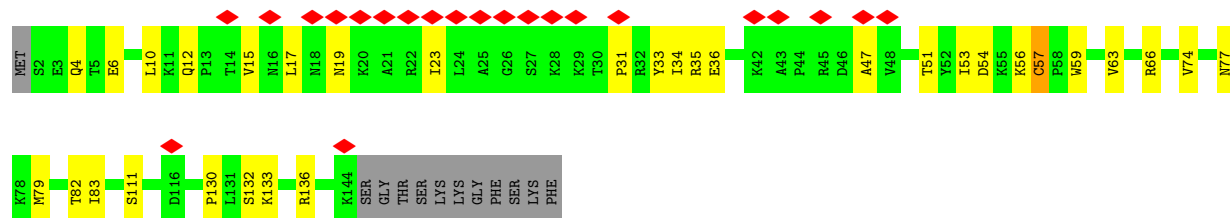
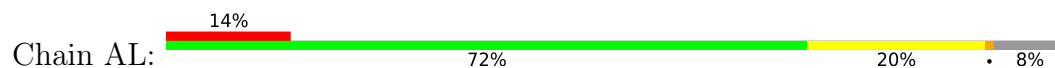


- Molecule 35: Small ribosomal subunit protein uS12

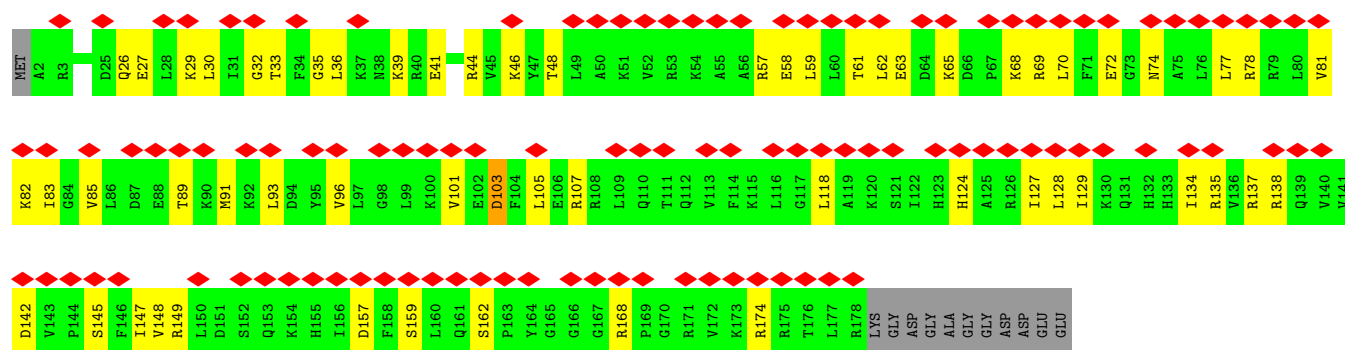




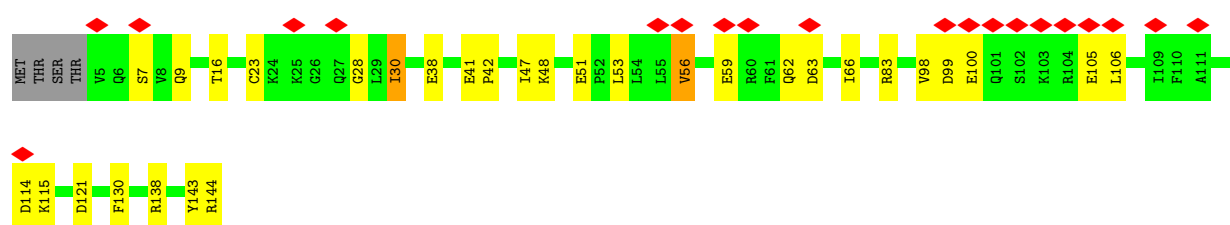
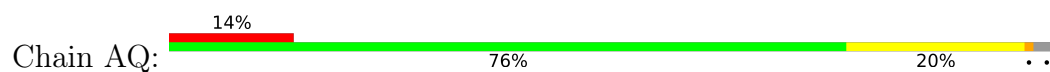
- Molecule 36: Small ribosomal subunit protein uS17



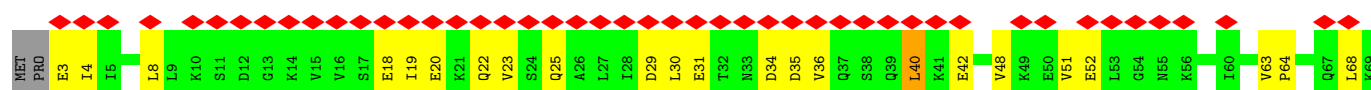
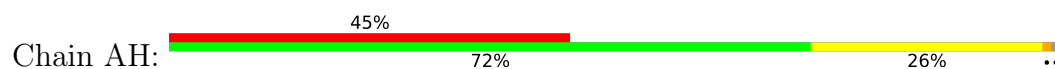
- Molecule 37: Small ribosomal subunit protein uS4

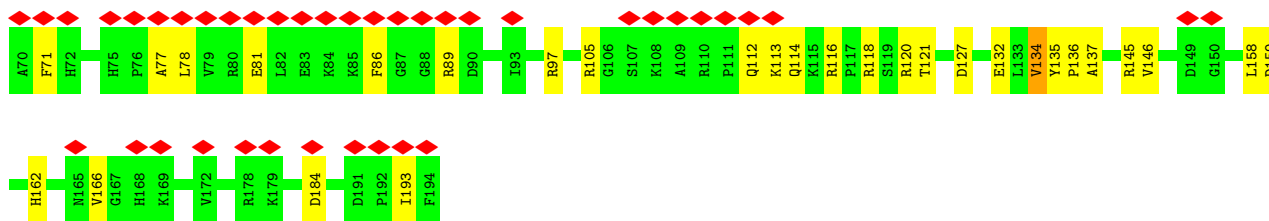


- Molecule 38: Small ribosomal subunit protein uS9

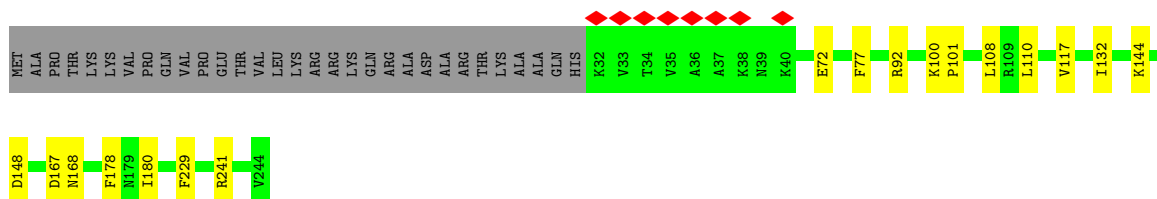
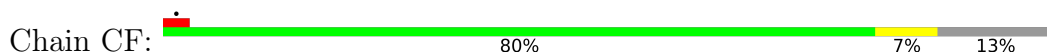


- Molecule 39: Small ribosomal subunit protein eS7

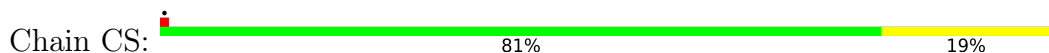




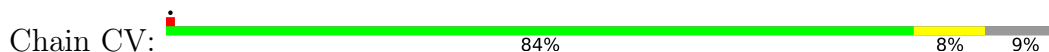
- Molecule 40: Large ribosomal subunit protein uL30



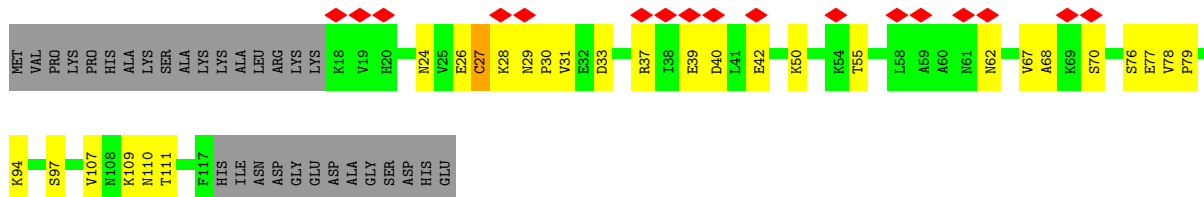
- Molecule 41: Large ribosomal subunit protein eL20



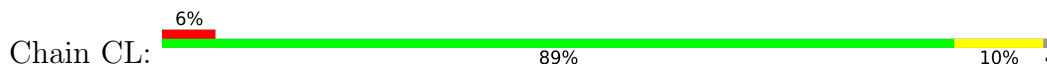
- Molecule 42: Large ribosomal subunit protein uL14

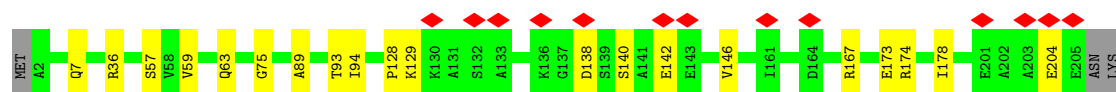


- Molecule 43: Large ribosomal subunit protein eL22

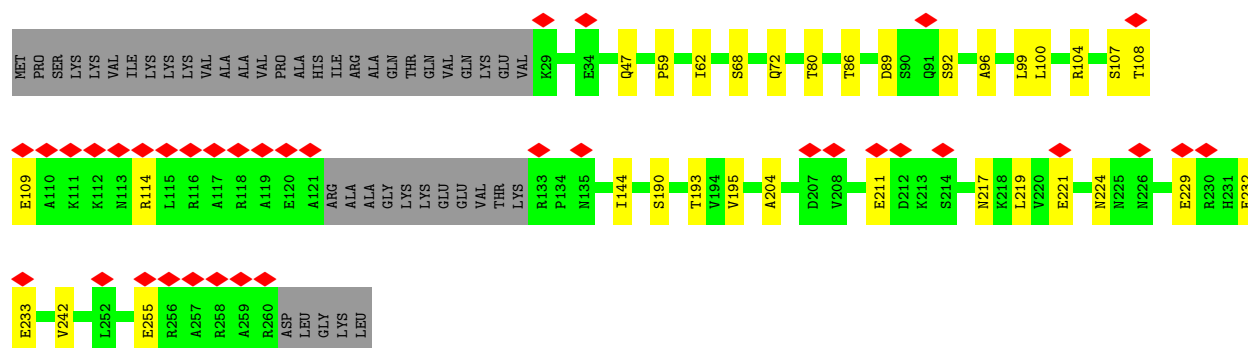
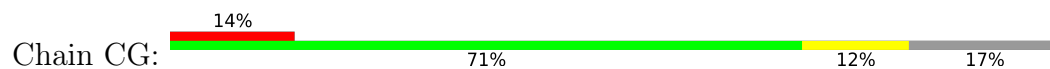


- Molecule 44: Large ribosomal subunit protein eL13

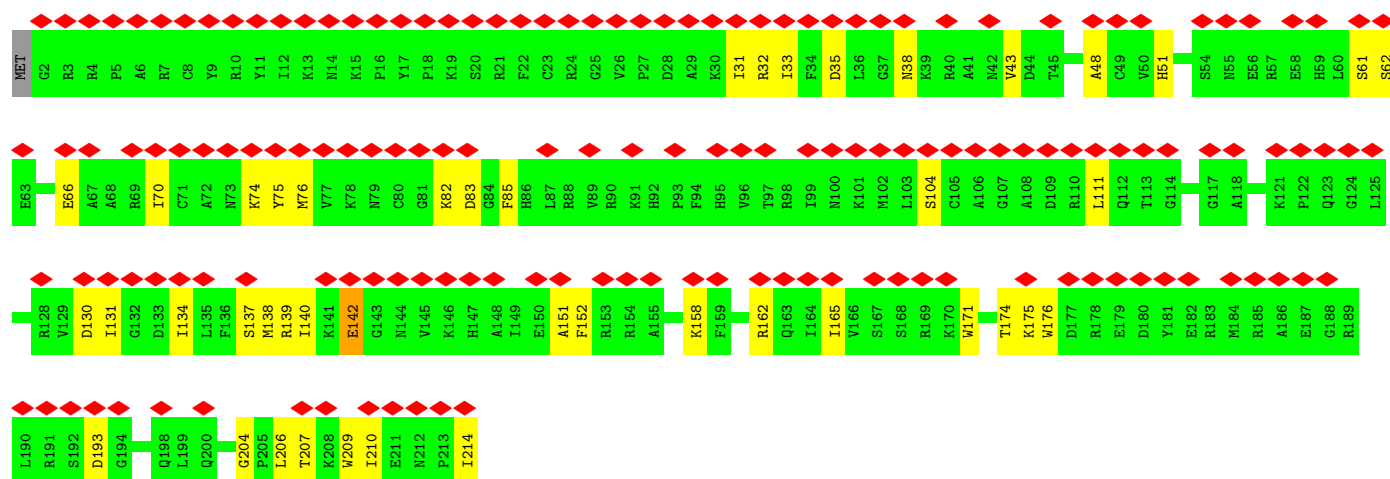
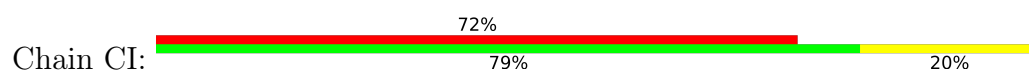




- Molecule 45: Large ribosomal subunit protein eL8



- Molecule 46: Large ribosomal subunit protein uL16

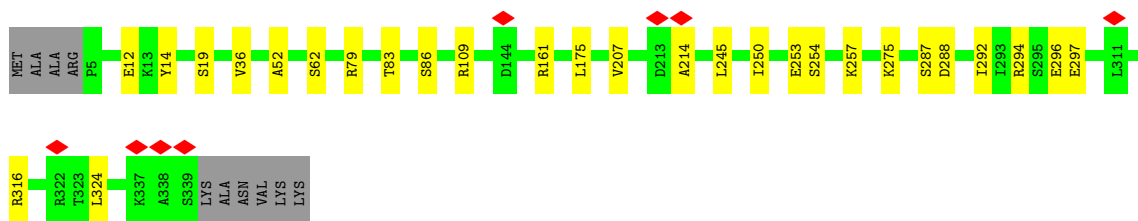


- Molecule 47: Large ribosomal subunit protein uL13

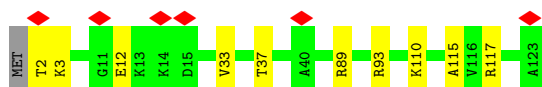


- Molecule 48: Large ribosomal subunit protein uL4

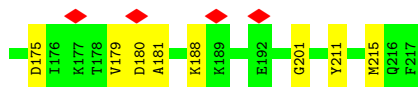
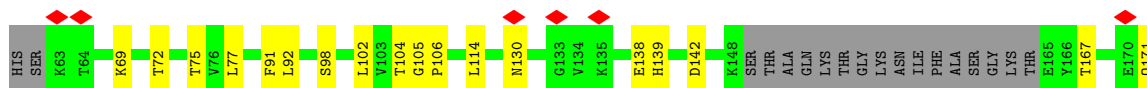
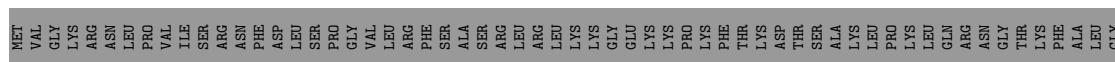




- Molecule 49: Large ribosomal subunit protein uL29



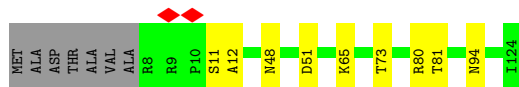
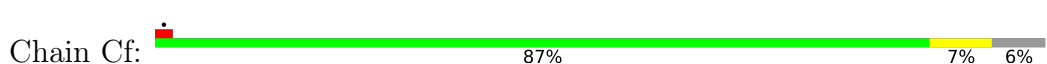
- Molecule 50: Large ribosomal subunit protein eL6



- Molecule 51: Large ribosomal subunit protein eL42



- Molecule 52: Large ribosomal subunit protein eL33

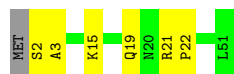


- Molecule 53: Large ribosomal subunit protein eL36

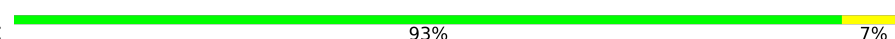


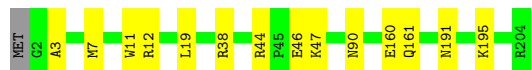
- Molecule 54: Large ribosomal subunit protein eL39

Chain Cl:  86% 12% .



- Molecule 55: Large ribosomal subunit protein eL15

Chain CN:  93% 7%



- Molecule 56: Large ribosomal subunit protein uL15

Chain Ca:  86% 12% ..



- Molecule 57: Large ribosomal subunit protein eL43

Chain Cp:  84% 12% ..



- Molecule 58: Large ribosomal subunit protein eL14

Chain CM:  79% 19% .



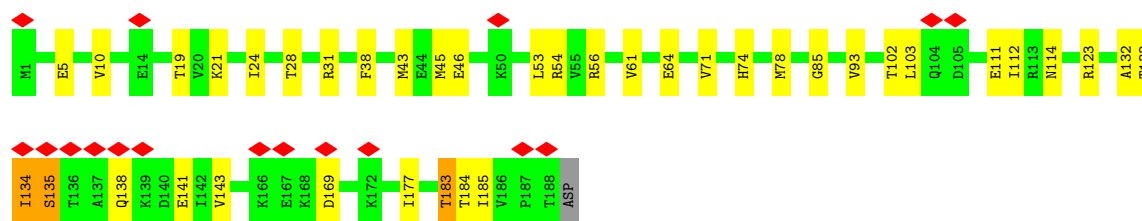
- Molecule 59: Large ribosomal subunit protein eL30

Chain Cc:  5% 66% 16% 17%



- Molecule 60: Large ribosomal subunit protein uL6

Chain CH:  9% 79% 19% ..



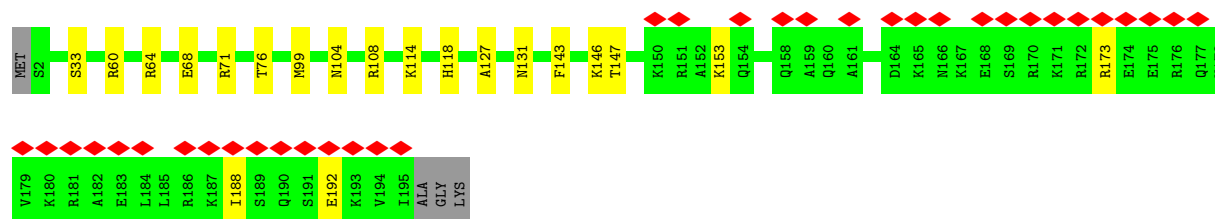
- Molecule 61: Large ribosomal subunit protein uL24

Chain CY: 82% 11% 7%



- Molecule 62: Large ribosomal subunit protein eL19

Chain CR: 18% 88% 10%



- Molecule 63: 60S ribosomal protein L29

Chain Cb: 6% 73% 11% 16%



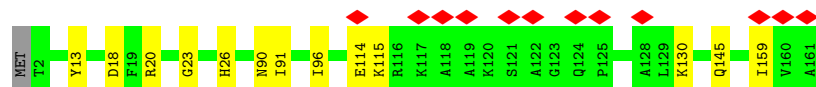
- Molecule 64: Large ribosomal subunit protein eL18

Chain CQ: 90% 9%



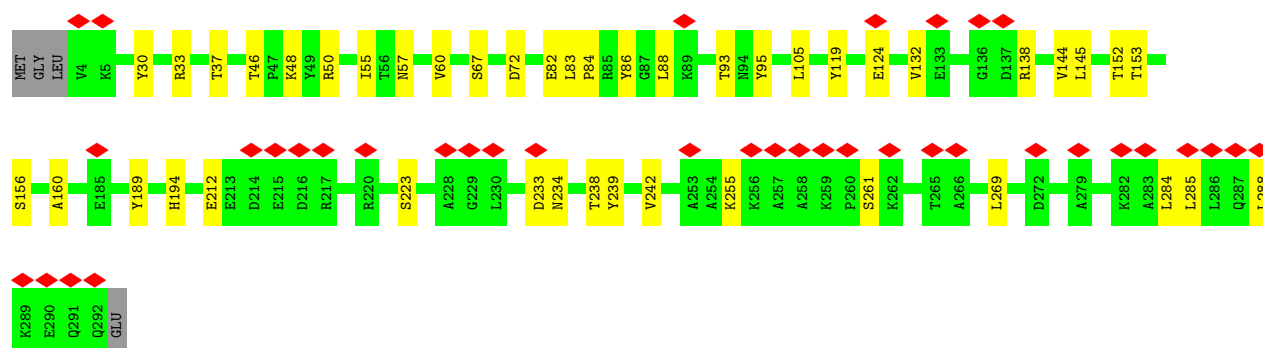
- Molecule 65: Large ribosomal subunit protein eL21

Chain CT: 7% 91% 8%



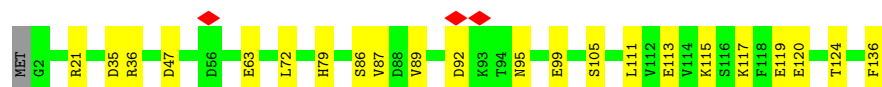
- Molecule 66: Large ribosomal subunit protein uL18

Chain CD: 



- Molecule 67: Large ribosomal subunit protein eL27

Chain CZ: 



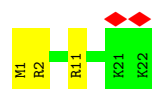
- Molecule 68: Large ribosomal subunit protein uL22

Chain CP: 



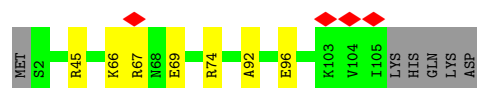
- Molecule 69: eL41

Chain Cn: 



- Molecule 70: Large ribosomal subunit protein eL34

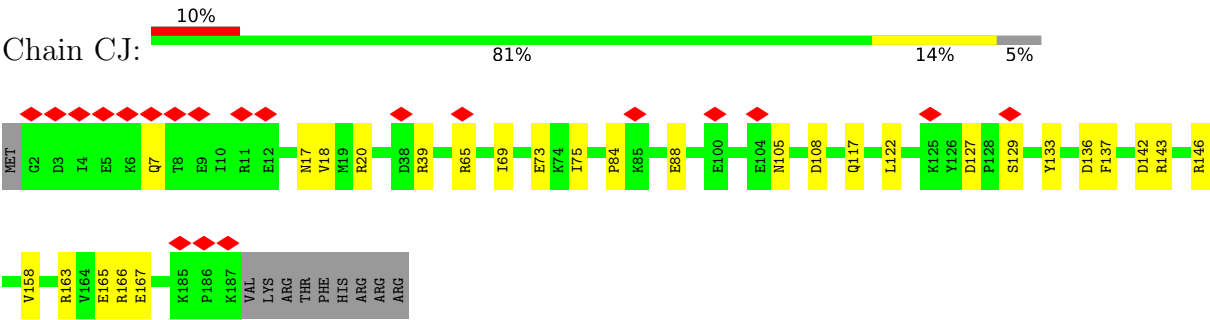
Chain Cg: 



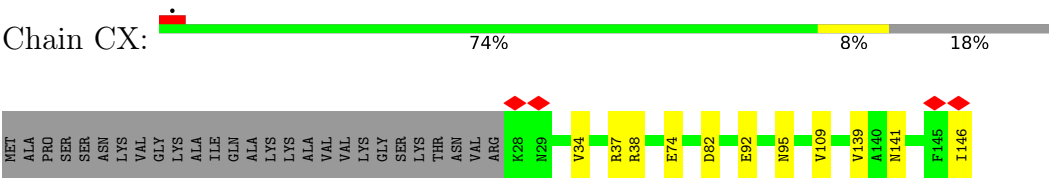
- Molecule 71: Large ribosomal subunit protein eL38

Chain Ck: 

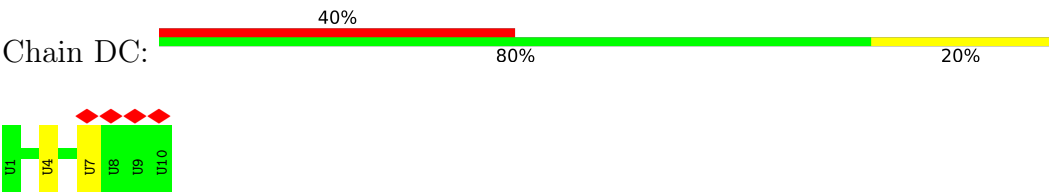
• Molecule 77: Large ribosomal subunit protein uL5B



• Molecule 78: Large ribosomal subunit protein uL23B



• Molecule 79: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	145659	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.94	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	2.035	Depositor
Minimum map value	-1.231	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.066	Depositor
Recommended contour level	0.199	Depositor
Map size (Å)	441.99997, 441.99997, 441.99997	wwPDB
Map dimensions	680, 680, 680	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.65, 0.65, 0.65	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 3HE, SPD

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	AA	0.14	0/1645	0.35	0/2230
2	CA	0.13	0/1932	0.31	0/2593
3	DA	0.09	0/1819	0.23	0/2833
4	AB	0.14	0/1710	0.33	0/2294
5	CB	0.13	0/3247	0.30	0/4355
6	AC	0.13	0/1689	0.31	0/2289
7	AD	0.12	0/1659	0.28	0/2226
8	AE	0.18	0/2053	0.42	0/2767
9	A7	0.11	0/2826	0.23	0/4402
10	A8	0.13	0/3477	0.27	0/5416
11	B2	0.12	0/35236	0.28	0/54876
12	A5	0.26	9/72151 (0.0%)	0.29	16/112424 (0.0%)
13	AR	0.16	0/988	0.33	0/1328
14	AK	0.16	0/790	0.40	0/1072
15	AW	0.14	0/1043	0.33	0/1399
16	AS	0.13	0/1225	0.33	0/1641
17	AT	0.14	0/1135	0.34	0/1524
18	Aa	0.12	0/819	0.31	0/1097
19	Af	0.11	0/404	0.33	0/540
20	AO	0.13	0/1027	0.32	0/1377
21	AI	0.16	0/1698	0.41	0/2277
22	AF	0.12	0/1475	0.31	0/1986
23	AM	0.16	0/917	0.43	0/1231
24	AV	0.16	0/625	0.35	0/842
25	AN	0.13	0/1240	0.32	0/1658
26	AZ	0.13	0/572	0.36	0/770
27	Ad	0.13	0/464	0.30	0/615
28	AY	0.14	0/1008	0.38	0/1344
29	AU	0.17	0/808	0.44	0/1090
30	AG	0.16	0/1863	0.39	0/2483
31	Ab	0.15	0/655	0.39	0/880
32	AP	0.12	0/1041	0.31	0/1391

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ac	0.13	0/521	0.31	0/695
34	Ae	0.14	0/367	0.37	0/480
35	AX	0.15	0/1112	0.35	0/1487
36	AL	0.16	0/1182	0.36	0/1591
37	AJ	0.17	0/1490	0.39	0/1991
38	AQ	0.15	0/1143	0.36	0/1529
39	AH	0.18	0/1572	0.42	0/2114
40	CF	0.13	0/1782	0.30	0/2402
41	CS	0.13	0/1505	0.31	0/2026
42	CV	0.13	0/985	0.30	0/1319
43	CU	0.16	0/838	0.38	0/1126
44	CL	0.13	0/1673	0.31	0/2235
45	CG	0.14	0/1816	0.32	0/2443
46	CI	0.13	0/1767	0.33	0/2362
47	CO	0.14	0/1645	0.32	0/2198
48	CC	0.14	0/2706	0.31	0/3649
49	Ch	0.11	0/995	0.26	0/1318
50	CE	0.15	0/1140	0.35	0/1530
51	Co	0.12	0/850	0.29	0/1118
52	Cf	0.14	0/953	0.30	0/1283
53	Ci	0.11	0/845	0.26	0/1119
54	Cl	0.12	0/443	0.32	0/582
55	CN	0.13	0/1741	0.30	0/2328
56	Ca	0.12	0/1166	0.28	0/1561
57	Cp	0.13	0/687	0.30	0/915
58	CM	0.14	0/1062	0.32	0/1418
59	Cc	0.13	0/744	0.30	0/1004
60	CH	0.14	0/1528	0.35	0/2058
61	CY	0.12	0/1065	0.32	0/1421
62	CR	0.12	0/1658	0.27	0/2201
63	Cb	0.12	0/439	0.34	0/578
64	CQ	0.12	0/1498	0.28	0/2012
65	CT	0.13	0/1308	0.29	0/1755
66	CD	0.13	0/2368	0.32	0/3179
67	CZ	0.14	0/1123	0.32	0/1497
68	CP	0.13	0/1277	0.28	0/1717
69	Cn	0.13	0/210	0.37	0/266
70	Cg	0.12	0/847	0.29	0/1136
71	Ck	0.18	0/565	0.41	0/748
72	Cm	0.12	0/423	0.30	0/557
73	Cd	0.12	0/881	0.27	0/1184
74	Ce	0.12	0/1057	0.29	0/1407
75	CW	0.12	0/712	0.30	0/949

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Cj	0.12	0/720	0.29	0/956
77	CJ	0.15	0/1533	0.34	0/2052
78	CX	0.11	0/972	0.28	0/1310
79	DC	0.11	0/219	0.30	0/336
All	All	0.19	9/202374 (0.0%)	0.30	16/296392 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
15	AW	0	1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	A5	3462	C	C1'-N1	37.03	2.04	1.48
12	A5	3465	U	N3-C4	22.25	1.82	1.38
12	A5	3465	U	C2-N3	19.80	1.77	1.37
12	A5	3465	U	N1-C2	19.14	1.76	1.38
12	A5	3465	U	N1-C6	17.31	1.72	1.38

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	A5	3462	C	C6-N1-C2	-12.65	82.26	120.20
12	A5	3462	C	N1-C1'-C2'	9.78	126.67	112.00
12	A5	600	U	OP1-P-O3'	-9.41	79.77	108.00
12	A5	588	G	OP1-P-O3'	-8.90	81.29	108.00
12	A5	3388	U	OP1-P-O3'	-8.88	81.34	108.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	AW	28	ARG	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	AA	1612	1652	1652	45	0
2	CA	1895	1980	1980	17	0
3	DA	1627	821	821	19	0
4	AB	1684	1769	1769	18	0
5	CB	3178	3300	3299	28	0
6	AC	1654	1735	1735	25	0
7	AD	1637	1706	1706	26	0
8	AE	2013	2107	2107	62	0
9	A7	2529	1281	1281	16	0
10	A8	3111	1568	1570	28	0
11	B2	31511	15858	15878	404	0
12	A5	64512	32467	32487	582	0
13	AR	976	1009	1009	21	0
14	AK	769	786	786	27	0
15	AW	1028	1082	1082	20	0
16	AS	1205	1248	1248	27	0
17	AT	1111	1149	1148	26	0
18	Aa	803	828	828	14	0
19	Af	397	392	392	6	0
20	AO	1014	1049	1049	17	0
21	AI	1668	1723	1723	46	0
22	AF	1454	1515	1515	24	0
23	AM	904	904	904	30	0
24	AV	617	622	622	14	0
25	AN	1217	1297	1297	18	0
26	AZ	564	601	601	13	0
27	Ad	452	443	443	8	0
28	AY	992	1093	1093	43	0
29	AU	796	854	854	18	0
30	AG	1837	1954	1954	50	0
31	Ab	642	663	663	12	0
32	AP	1022	1090	1090	12	0
33	Ac	520	549	549	11	0
34	Ae	364	388	388	6	0
35	AX	1092	1150	1150	20	0
36	AL	1158	1222	1222	23	0
37	AJ	1468	1592	1592	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	AQ	1124	1181	1181	28	0
39	AH	1544	1643	1643	48	0
40	CF	1743	1791	1790	11	0
41	CS	1470	1506	1506	25	0
42	CV	971	1020	1020	9	0
43	CU	824	868	868	19	0
44	CL	1648	1740	1739	17	0
45	CG	1788	1892	1892	21	0
46	CI	1729	1756	1756	38	0
47	CO	1614	1714	1713	14	0
48	CC	2651	2769	2769	20	0
49	Ch	989	1105	1105	9	0
50	CE	1116	1195	1195	19	0
51	Co	837	902	902	2	0
52	Cf	930	971	971	8	0
53	Ci	836	918	918	4	0
54	Cl	435	487	487	5	0
55	CN	1700	1763	1763	9	0
56	Ca	1136	1163	1163	16	0
57	Cp	678	726	725	9	0
58	CM	1053	1151	1151	18	0
59	Cc	735	762	762	11	0
60	CH	1504	1577	1577	28	0
61	CY	1050	1131	1131	9	0
62	CR	1638	1746	1746	12	0
63	Cb	432	460	460	5	0
64	CQ	1473	1550	1550	11	0
65	CT	1283	1338	1338	12	0
66	CD	2328	2373	2372	35	0
67	CZ	1102	1199	1199	15	0
68	CP	1249	1257	1257	12	0
69	Cn	209	252	252	4	0
70	Cg	837	922	922	5	0
71	Ck	559	622	622	8	0
72	Cm	418	456	456	4	0
73	Cd	867	903	903	4	0
74	Ce	1041	1119	1119	10	0
75	CW	702	745	745	3	0
76	Cj	706	727	727	7	0
77	CJ	1507	1555	1555	20	0
78	CX	954	1004	1004	10	0
79	DC	200	101	101	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	A5	10	0	19	2	0
81	A5	20	23	23	1	0
All	All	188673	141530	141584	2087	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 6.

The worst 5 of 2087 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)
12:A5:3465:U:C6	12:A5:3465:U:N1	1.72	1.57
12:A5:3465:U:N3	12:A5:3465:U:C2	1.77	1.52
12:A5:3465:U:N1	12:A5:3465:U:C2	1.76	1.51
12:A5:3465:U:N3	12:A5:3465:U:C4	1.82	1.47
12:A5:3462:C:N1	12:A5:3465:U:C2	1.82	1.43

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	203/276 (74%)	195 (96%)	8 (4%)	0	100	100
2	CA	247/260 (95%)	238 (96%)	9 (4%)	0	100	100
4	AB	208/257 (81%)	205 (99%)	3 (1%)	0	100	100
5	CB	393/401 (98%)	389 (99%)	4 (1%)	0	100	100
6	AC	213/272 (78%)	211 (99%)	2 (1%)	0	100	100
7	AD	209/247 (85%)	206 (99%)	3 (1%)	0	100	100
8	AE	253/259 (98%)	244 (96%)	9 (4%)	0	100	100
13	AR	119/130 (92%)	116 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	AK	91/149 (61%)	88 (97%)	3 (3%)	0	100	100
15	AW	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
16	AS	146/154 (95%)	140 (96%)	6 (4%)	0	100	100
17	AT	138/146 (94%)	132 (96%)	6 (4%)	0	100	100
18	Aa	97/117 (83%)	95 (98%)	2 (2%)	0	100	100
19	Af	48/163 (29%)	43 (90%)	5 (10%)	0	100	100
20	AO	133/152 (88%)	127 (96%)	6 (4%)	0	100	100
21	AI	205/208 (99%)	196 (96%)	9 (4%)	0	100	100
22	AF	181/210 (86%)	174 (96%)	6 (3%)	1 (1%)	21	42
23	AM	113/140 (81%)	100 (88%)	13 (12%)	0	100	100
24	AV	79/88 (90%)	75 (95%)	4 (5%)	0	100	100
25	AN	149/151 (99%)	148 (99%)	1 (1%)	0	100	100
26	AZ	69/117 (59%)	68 (99%)	1 (1%)	0	100	100
27	Ad	53/56 (95%)	53 (100%)	0	0	100	100
28	AY	121/131 (92%)	115 (95%)	6 (5%)	0	100	100
29	AU	98/117 (84%)	96 (98%)	2 (2%)	0	100	100
30	AG	226/246 (92%)	221 (98%)	5 (2%)	0	100	100
31	Ab	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
32	AP	126/151 (83%)	120 (95%)	6 (5%)	0	100	100
33	Ac	63/65 (97%)	59 (94%)	4 (6%)	0	100	100
34	Ae	41/130 (32%)	40 (98%)	1 (2%)	0	100	100
35	AX	138/143 (96%)	137 (99%)	1 (1%)	0	100	100
36	AL	141/155 (91%)	137 (97%)	4 (3%)	0	100	100
37	AJ	175/189 (93%)	165 (94%)	10 (6%)	0	100	100
38	AQ	138/144 (96%)	136 (99%)	2 (1%)	0	100	100
39	AH	190/194 (98%)	176 (93%)	14 (7%)	0	100	100
40	CF	211/244 (86%)	202 (96%)	9 (4%)	0	100	100
41	CS	177/180 (98%)	170 (96%)	7 (4%)	0	100	100
42	CV	126/140 (90%)	126 (100%)	0	0	100	100
43	CU	98/130 (75%)	95 (97%)	3 (3%)	0	100	100
44	CL	202/207 (98%)	200 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	CG	217/265 (82%)	212 (98%)	5 (2%)	0	100	100
46	CI	211/214 (99%)	209 (99%)	2 (1%)	0	100	100
47	CO	199/202 (98%)	197 (99%)	2 (1%)	0	100	100
48	CC	333/345 (96%)	327 (98%)	6 (2%)	0	100	100
49	Ch	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
50	CE	135/217 (62%)	127 (94%)	8 (6%)	0	100	100
51	Co	100/105 (95%)	97 (97%)	3 (3%)	0	100	100
52	Cf	115/124 (93%)	112 (97%)	3 (3%)	0	100	100
53	Ci	102/104 (98%)	97 (95%)	5 (5%)	0	100	100
54	Cl	48/51 (94%)	48 (100%)	0	0	100	100
55	CN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
56	Ca	142/145 (98%)	136 (96%)	6 (4%)	0	100	100
57	Cp	86/91 (94%)	82 (95%)	4 (5%)	0	100	100
58	CM	130/135 (96%)	126 (97%)	4 (3%)	0	100	100
59	Cc	94/115 (82%)	94 (100%)	0	0	100	100
60	CH	186/189 (98%)	180 (97%)	6 (3%)	0	100	100
61	CY	130/142 (92%)	125 (96%)	5 (4%)	0	100	100
62	CR	192/198 (97%)	190 (99%)	2 (1%)	0	100	100
63	Cb	50/62 (81%)	45 (90%)	5 (10%)	0	100	100
64	CQ	185/188 (98%)	181 (98%)	4 (2%)	0	100	100
65	CT	158/161 (98%)	155 (98%)	3 (2%)	0	100	100
66	CD	287/293 (98%)	278 (97%)	9 (3%)	0	100	100
67	CZ	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
68	CP	152/187 (81%)	149 (98%)	3 (2%)	0	100	100
69	Cn	20/22 (91%)	20 (100%)	0	0	100	100
70	Cg	102/110 (93%)	101 (99%)	1 (1%)	0	100	100
71	Ck	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
72	Cm	49/128 (38%)	49 (100%)	0	0	100	100
73	Cd	103/122 (84%)	99 (96%)	4 (4%)	0	100	100
74	Ce	126/134 (94%)	122 (97%)	4 (3%)	0	100	100
75	CW	84/159 (53%)	83 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
76	Cj	86/92 (94%)	84 (98%)	2 (2%)	0	100	100
77	CJ	184/196 (94%)	182 (99%)	2 (1%)	0	100	100
78	CX	117/146 (80%)	116 (99%)	1 (1%)	0	100	100
All	All	10469/11907 (88%)	10172 (97%)	296 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	AF	86	GLY

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	
1	AA	172/228 (75%)	169 (98%)	3 (2%)	53	78
2	CA	191/202 (95%)	189 (99%)	2 (1%)	68	86
4	AB	191/228 (84%)	186 (97%)	5 (3%)	40	68
5	CB	335/338 (99%)	332 (99%)	3 (1%)	70	87
6	AC	175/202 (87%)	173 (99%)	2 (1%)	65	84
7	AD	173/204 (85%)	168 (97%)	5 (3%)	37	65
8	AE	218/221 (99%)	213 (98%)	5 (2%)	44	71
13	AR	111/118 (94%)	110 (99%)	1 (1%)	70	87
14	AK	82/122 (67%)	80 (98%)	2 (2%)	43	70
15	AW	110/111 (99%)	108 (98%)	2 (2%)	51	76
16	AS	130/134 (97%)	129 (99%)	1 (1%)	73	88
17	AT	116/120 (97%)	114 (98%)	2 (2%)	53	78
18	Aa	84/94 (89%)	82 (98%)	2 (2%)	43	70
19	Af	42/134 (31%)	40 (95%)	2 (5%)	23	47
20	AO	103/115 (90%)	102 (99%)	1 (1%)	68	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	AI	172/173 (99%)	164 (95%)	8 (5%)	23	48
22	AF	156/172 (91%)	152 (97%)	4 (3%)	40	68
23	AM	94/108 (87%)	91 (97%)	3 (3%)	34	62
24	AV	68/75 (91%)	68 (100%)	0	100	100
25	AN	130/130 (100%)	127 (98%)	3 (2%)	44	71
26	AZ	62/98 (63%)	62 (100%)	0	100	100
27	Ad	46/47 (98%)	44 (96%)	2 (4%)	26	51
28	AY	107/112 (96%)	105 (98%)	2 (2%)	50	75
29	AU	90/104 (86%)	89 (99%)	1 (1%)	65	84
30	AG	195/212 (92%)	184 (94%)	11 (6%)	19	40
31	Ab	75/76 (99%)	75 (100%)	0	100	100
32	AP	108/128 (84%)	107 (99%)	1 (1%)	70	87
33	Ac	58/58 (100%)	57 (98%)	1 (2%)	53	78
34	Ae	37/107 (35%)	35 (95%)	2 (5%)	20	42
35	AX	115/118 (98%)	114 (99%)	1 (1%)	70	87
36	AL	126/136 (93%)	124 (98%)	2 (2%)	55	79
37	AJ	160/167 (96%)	158 (99%)	2 (1%)	61	82
38	AQ	115/119 (97%)	111 (96%)	4 (4%)	32	59
39	AH	170/172 (99%)	167 (98%)	3 (2%)	51	76
40	CF	184/210 (88%)	184 (100%)	0	100	100
41	CS	156/157 (99%)	155 (99%)	1 (1%)	78	91
42	CV	101/107 (94%)	100 (99%)	1 (1%)	68	86
43	CU	92/116 (79%)	89 (97%)	3 (3%)	33	61
44	CL	167/170 (98%)	166 (99%)	1 (1%)	78	91
45	CG	192/228 (84%)	187 (97%)	5 (3%)	40	68
46	CI	179/180 (99%)	175 (98%)	4 (2%)	45	72
47	CO	165/166 (99%)	162 (98%)	3 (2%)	51	76
48	CC	279/286 (98%)	277 (99%)	2 (1%)	76	89
49	Ch	106/107 (99%)	106 (100%)	0	100	100
50	CE	122/188 (65%)	121 (99%)	1 (1%)	73	88
51	Co	90/93 (97%)	89 (99%)	1 (1%)	65	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	Cf	95/99 (96%)	94 (99%)	1 (1%)	65	84
53	Ci	86/86 (100%)	86 (100%)	0	100	100
54	Cl	46/47 (98%)	46 (100%)	0	100	100
55	CN	172/173 (99%)	172 (100%)	0	100	100
56	Ca	116/117 (99%)	113 (97%)	3 (3%)	40	68
57	Cp	68/71 (96%)	67 (98%)	1 (2%)	57	80
58	CM	111/114 (97%)	110 (99%)	1 (1%)	70	87
59	Cc	80/95 (84%)	77 (96%)	3 (4%)	29	56
60	CH	167/168 (99%)	161 (96%)	6 (4%)	31	58
61	CY	114/123 (93%)	113 (99%)	1 (1%)	70	87
62	CR	172/174 (99%)	169 (98%)	3 (2%)	53	78
63	Cb	47/56 (84%)	45 (96%)	2 (4%)	26	51
64	CQ	152/153 (99%)	151 (99%)	1 (1%)	76	89
65	CT	135/136 (99%)	135 (100%)	0	100	100
66	CD	239/242 (99%)	236 (99%)	3 (1%)	61	82
67	CZ	119/120 (99%)	117 (98%)	2 (2%)	53	78
68	CP	130/159 (82%)	129 (99%)	1 (1%)	73	88
69	Cn	20/20 (100%)	20 (100%)	0	100	100
70	Cg	92/98 (94%)	92 (100%)	0	100	100
71	Ck	63/64 (98%)	62 (98%)	1 (2%)	55	79
72	Cm	47/115 (41%)	47 (100%)	0	100	100
73	Cd	96/112 (86%)	96 (100%)	0	100	100
74	Ce	111/117 (95%)	110 (99%)	1 (1%)	70	87
75	CW	73/128 (57%)	72 (99%)	1 (1%)	59	81
76	Cj	73/77 (95%)	72 (99%)	1 (1%)	59	81
77	CJ	160/170 (94%)	159 (99%)	1 (1%)	78	91
78	CX	103/124 (83%)	103 (100%)	0	100	100
All	All	9037/10049 (90%)	8894 (98%)	143 (2%)	54	79

5 of 143 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
58	CM	113	MET

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Mol	Chain	Res	Type
60	CH	28	THR
63	Cb	14	LYS
22	AF	37	SER
22	AF	31	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
52	Cf	104	HIS
76	Cj	12	HIS
55	CN	201	HIS
66	CD	287	GLN
78	CX	97	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A8	144/153 (94%)	26 (18%)	0
11	B2	1459/1754 (83%)	340 (23%)	31 (2%)
12	A5	3007/3510 (85%)	574 (19%)	75 (2%)
3	DA	75/76 (98%)	17 (22%)	0
79	DC	9/10 (90%)	2 (22%)	0
9	A7	118/119 (99%)	7 (5%)	0
All	All	4812/5622 (85%)	966 (20%)	106 (2%)

5 of 966 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	DA	4	U
3	DA	9	A
3	DA	16	U
3	DA	17	U
3	DA	19	G

5 of 106 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	A5	1118	A
12	A5	2608	G
12	A5	3365	U

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Mol	Chain	Res	Type
12	A5	1150	G
12	A5	1844	A

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](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
80	SPD	A5	3601	-	9,9,9	0.33	0	8,8,8	0.82	0
81	3HE	A5	3602	-	21,21,21	0.42	0	23,30,30	0.99	1 (4%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
80	SPD	A5	3601	-	-	1/7/7/7	-
81	3HE	A5	3602	-	-	2/8/36/36	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	A5	3602	3HE	C6-C5-C4	2.13	111.81	108.29

There are no chirality outliers.

All (3) torsion outliers are listed below:

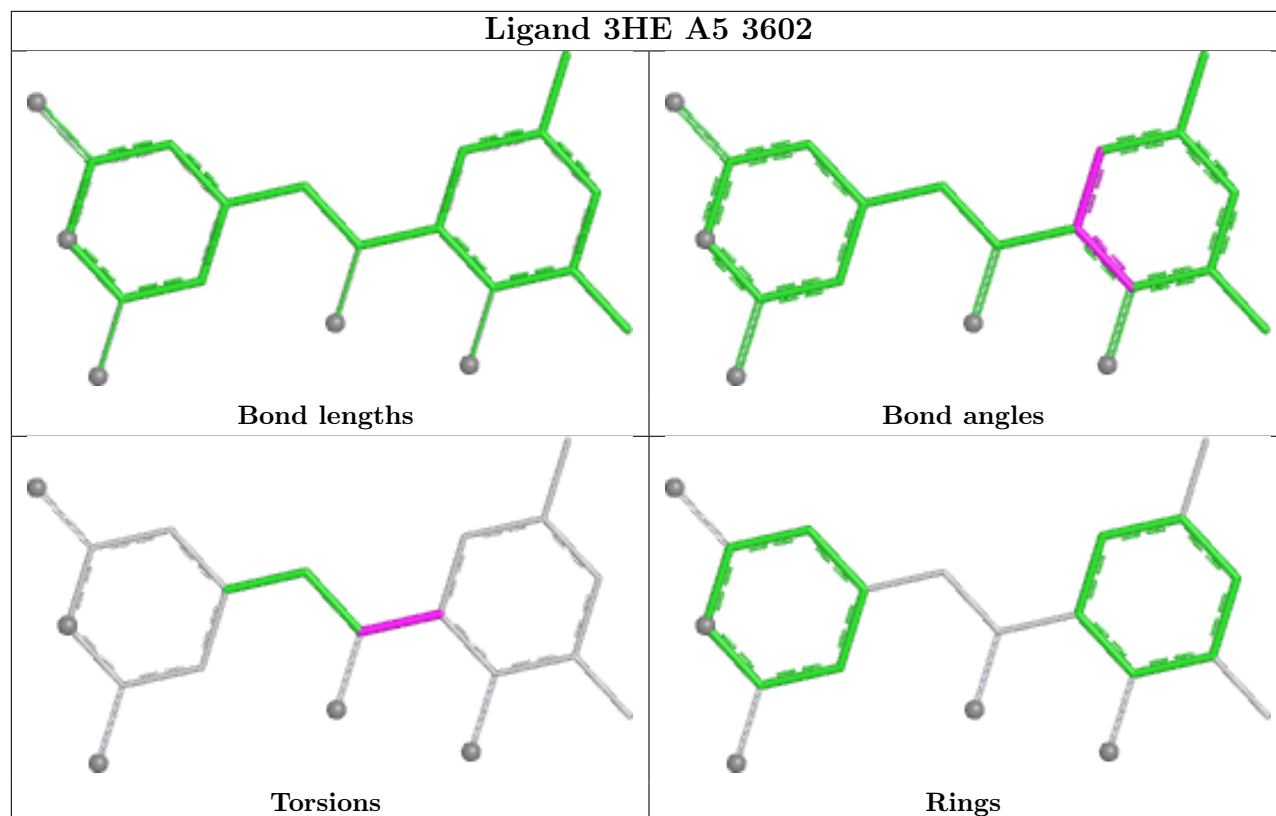
Mol	Chain	Res	Type	Atoms
81	A5	3602	3HE	C6-C5-C7-C8
81	A5	3602	3HE	C6-C5-C7-O3
80	A5	3601	SPD	C4-C5-N6-C7

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
80	A5	3601	SPD	2	0
81	A5	3602	3HE	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
12	A5	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A5	3461:U	O3'	3462:C	P	8.47

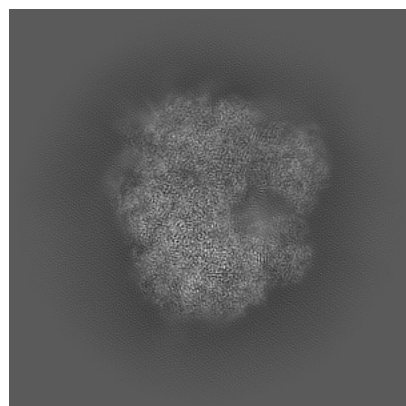
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45392. These allow visual inspection of the internal detail of the map and identification of artifacts.

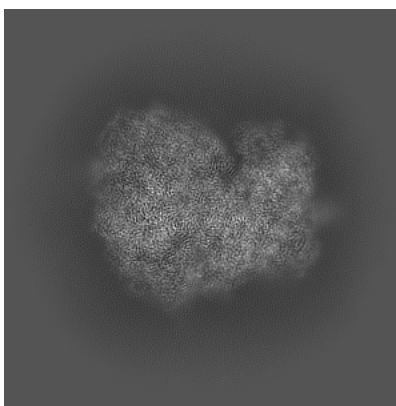
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

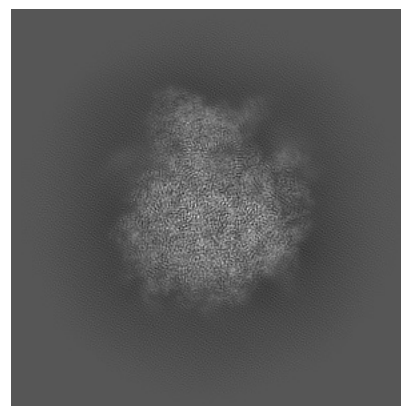
6.1.1 Primary map



X

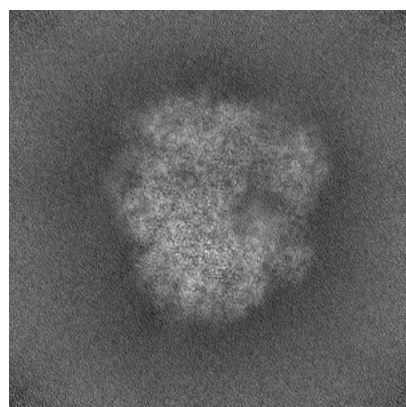


Y

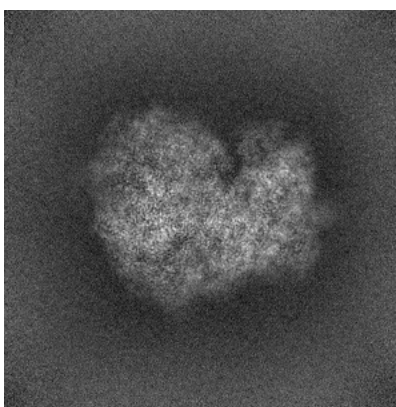


Z

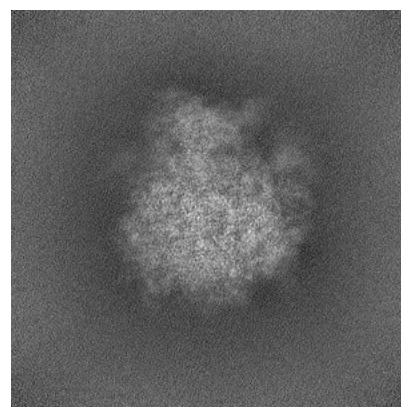
6.1.2 Raw map



X



Y

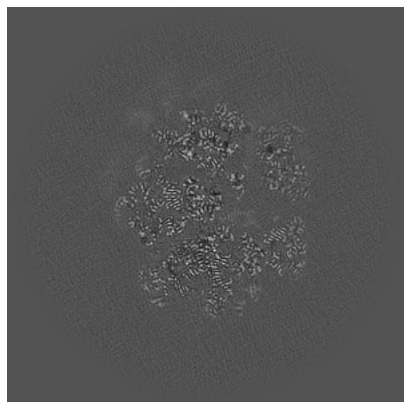


Z

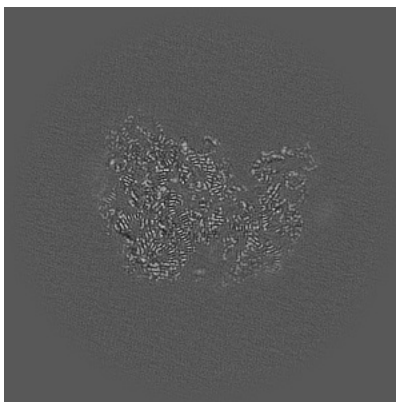
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

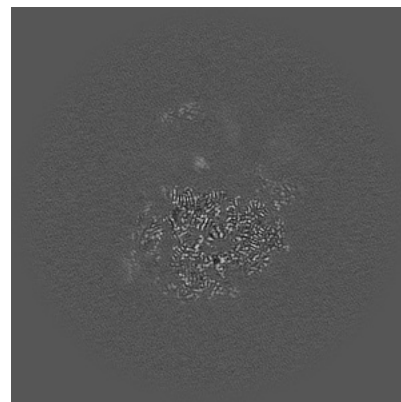
6.2.1 Primary map



X Index: 340

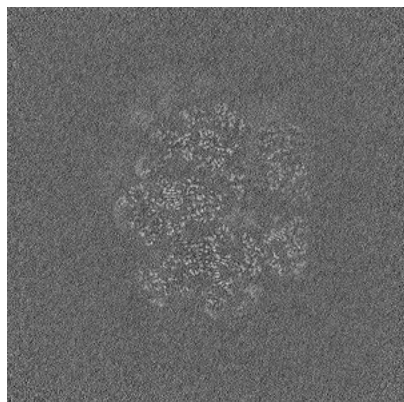


Y Index: 340

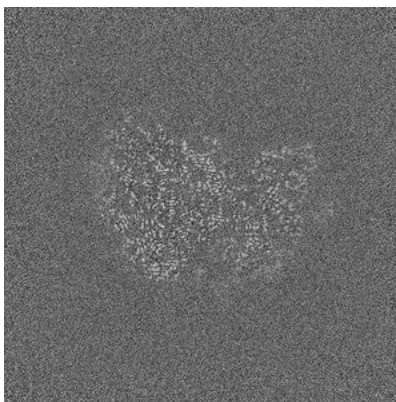


Z Index: 340

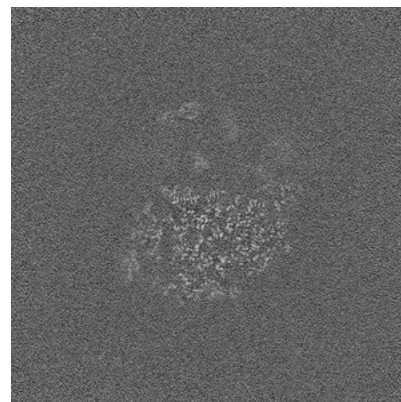
6.2.2 Raw map



X Index: 340



Y Index: 340

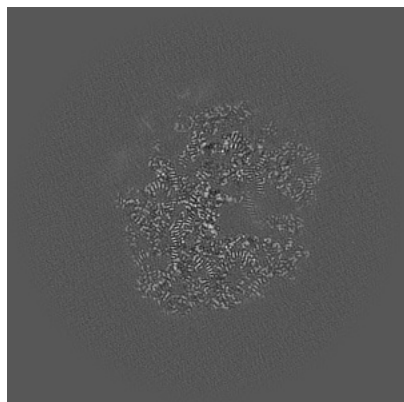


Z Index: 340

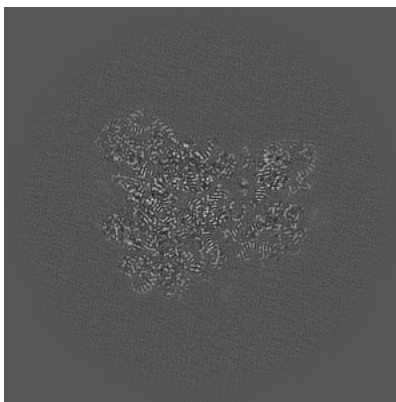
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

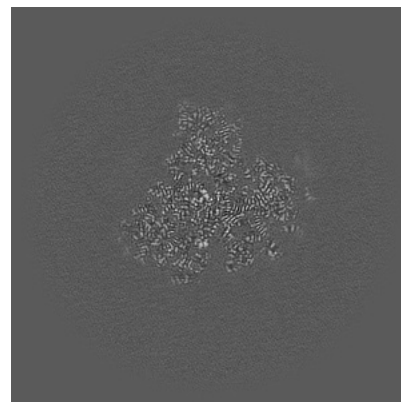
6.3.1 Primary map



X Index: 317

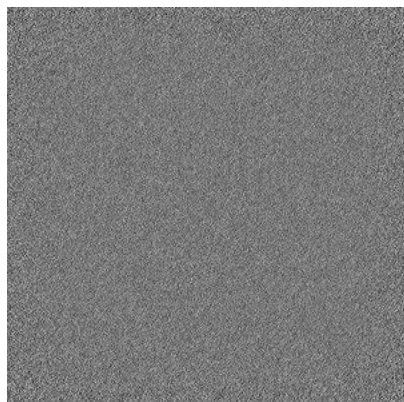


Y Index: 324

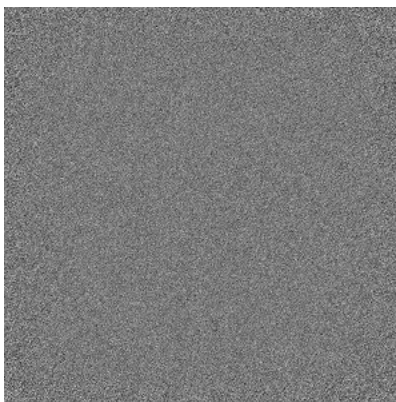


Z Index: 266

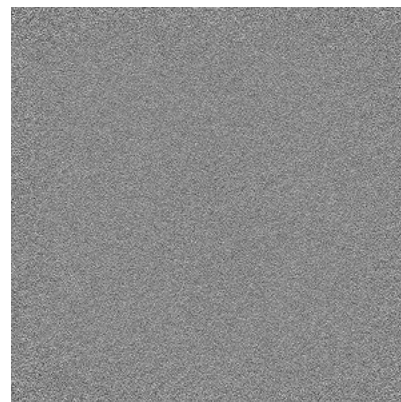
6.3.2 Raw map



X Index: 0



Y Index: 0

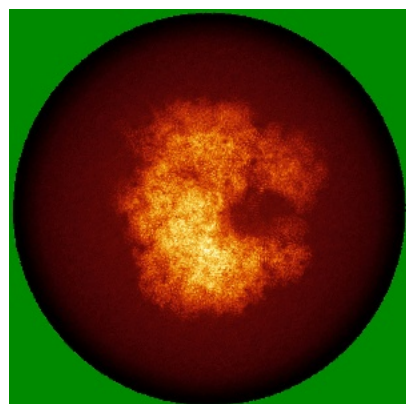


Z Index: 679

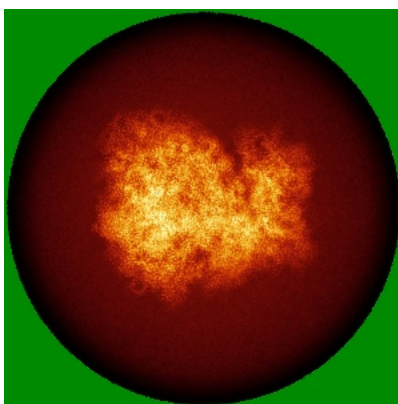
The images above show the largest variance slices of the map in three orthogonal directions.

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

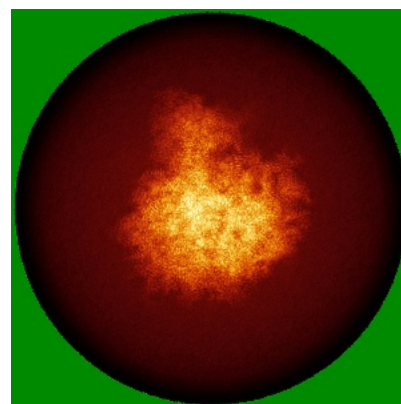
6.4.1 Primary map



X

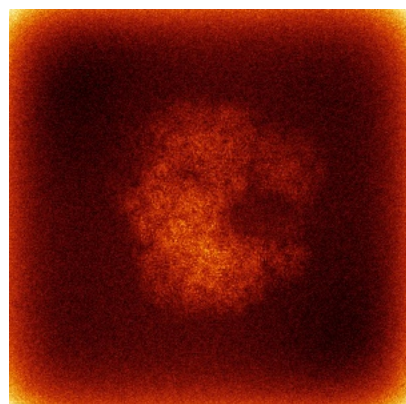


Y

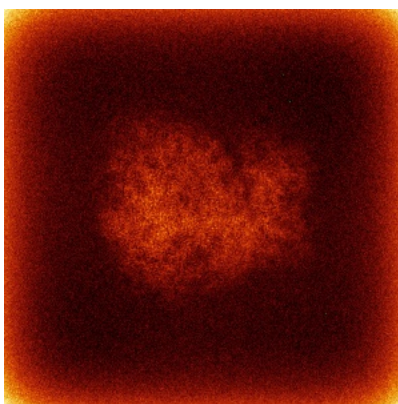


Z

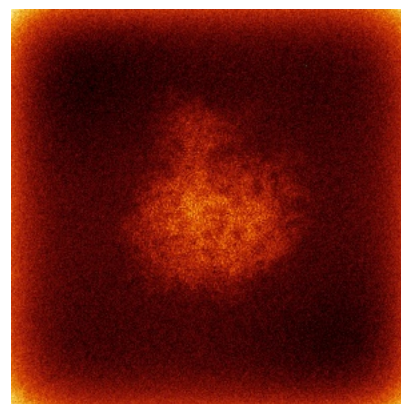
6.4.2 Raw map



X



Y

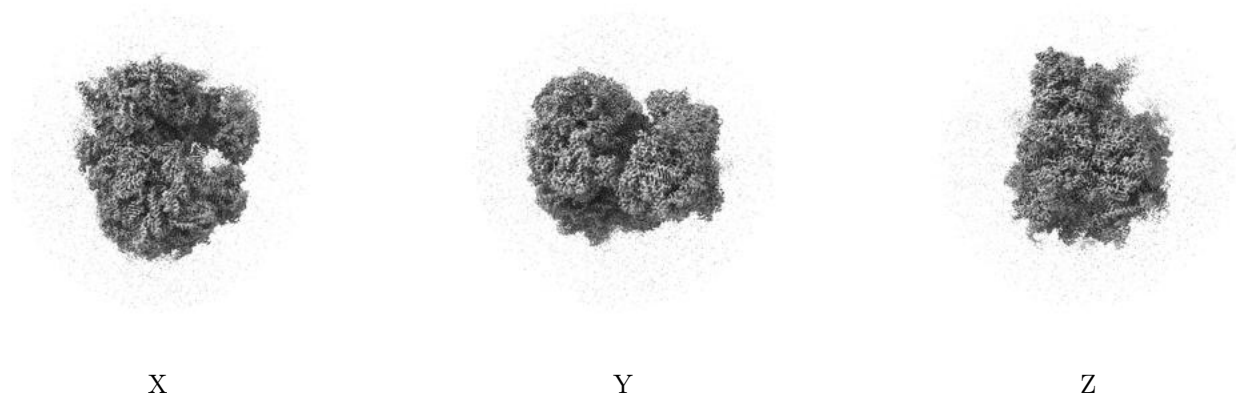


Z

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.

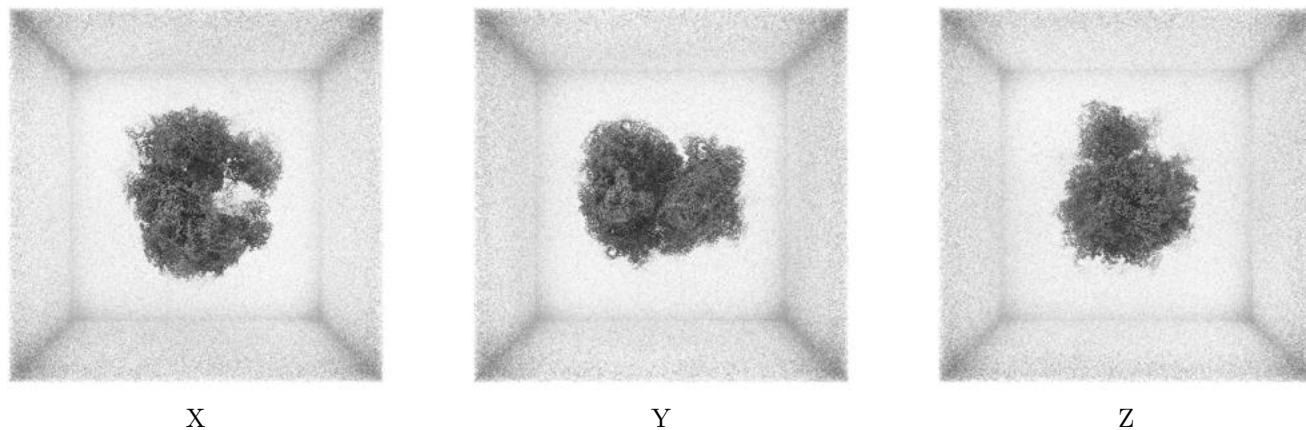
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.199. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

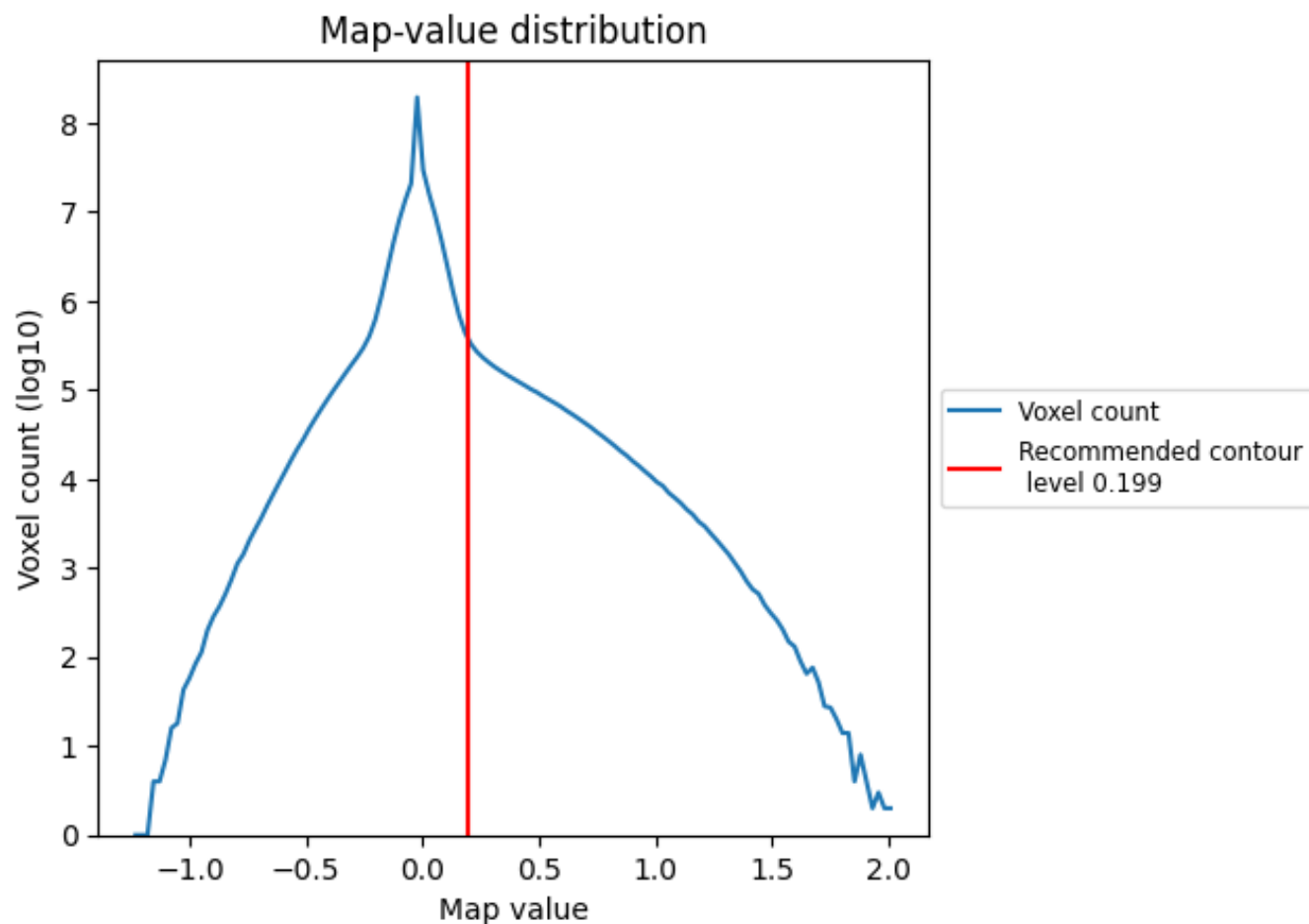
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

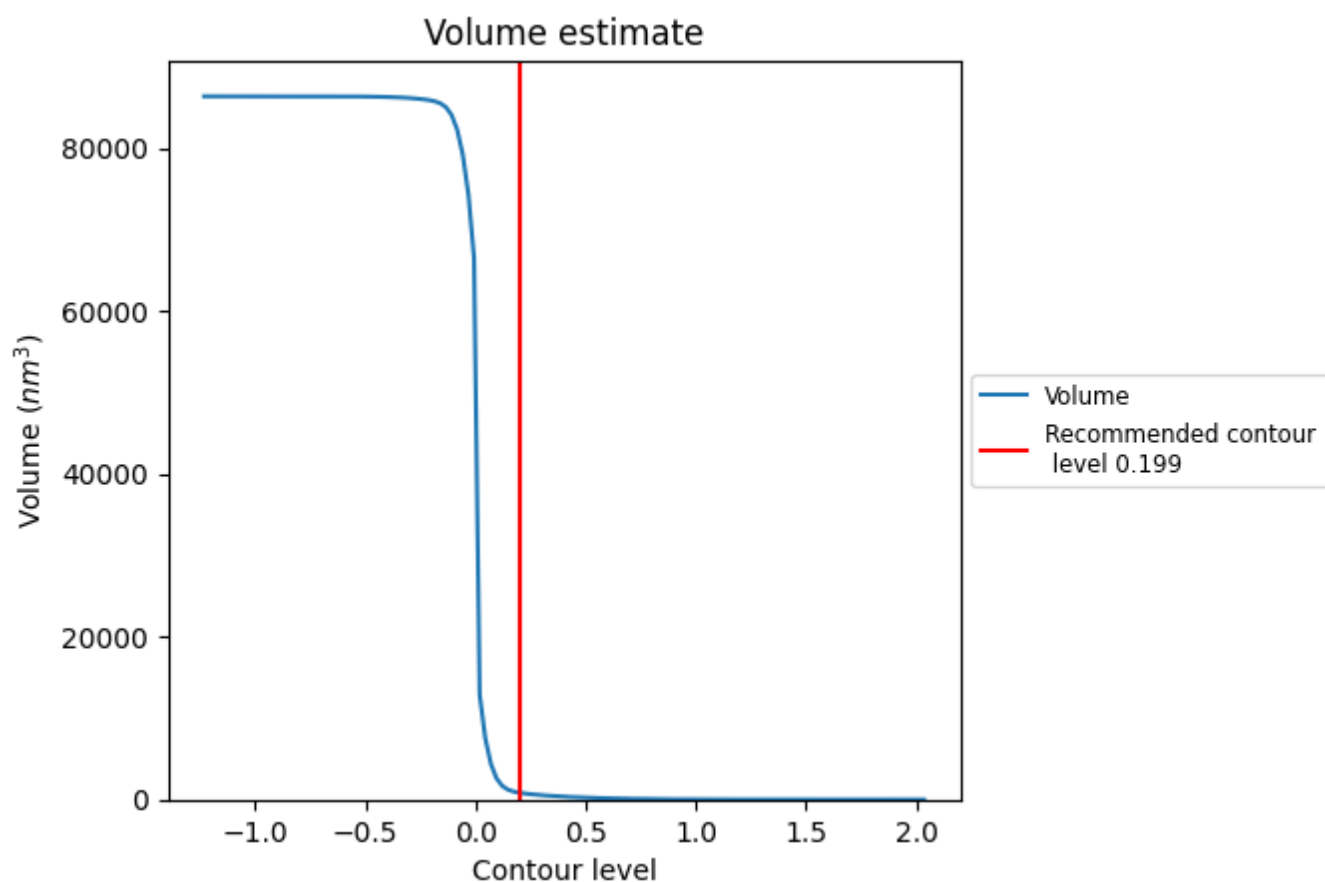
This section contains the results of statistical analysis of the map.

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.

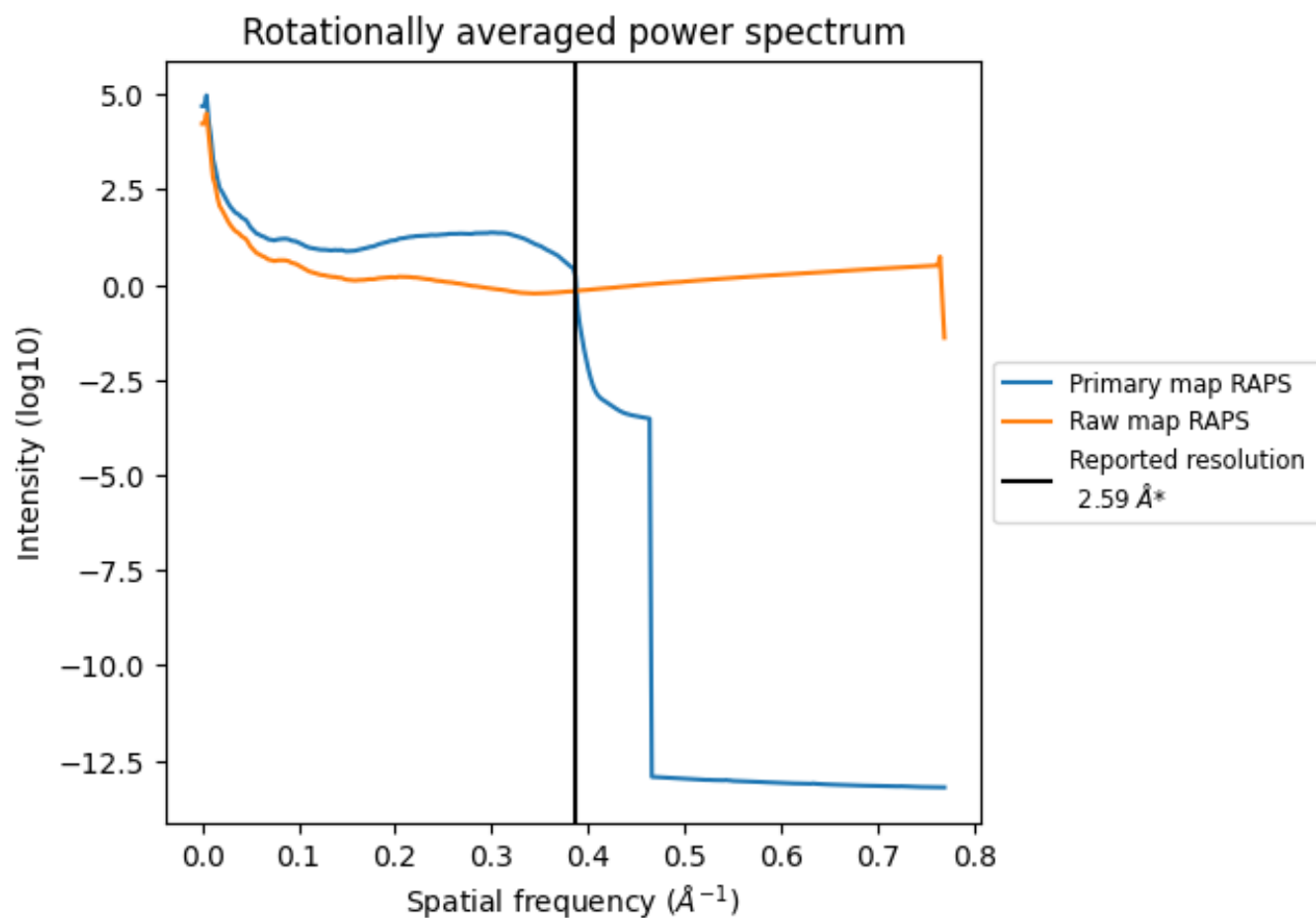
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 836 nm³; this corresponds to an approximate mass of 755 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 ⓘ

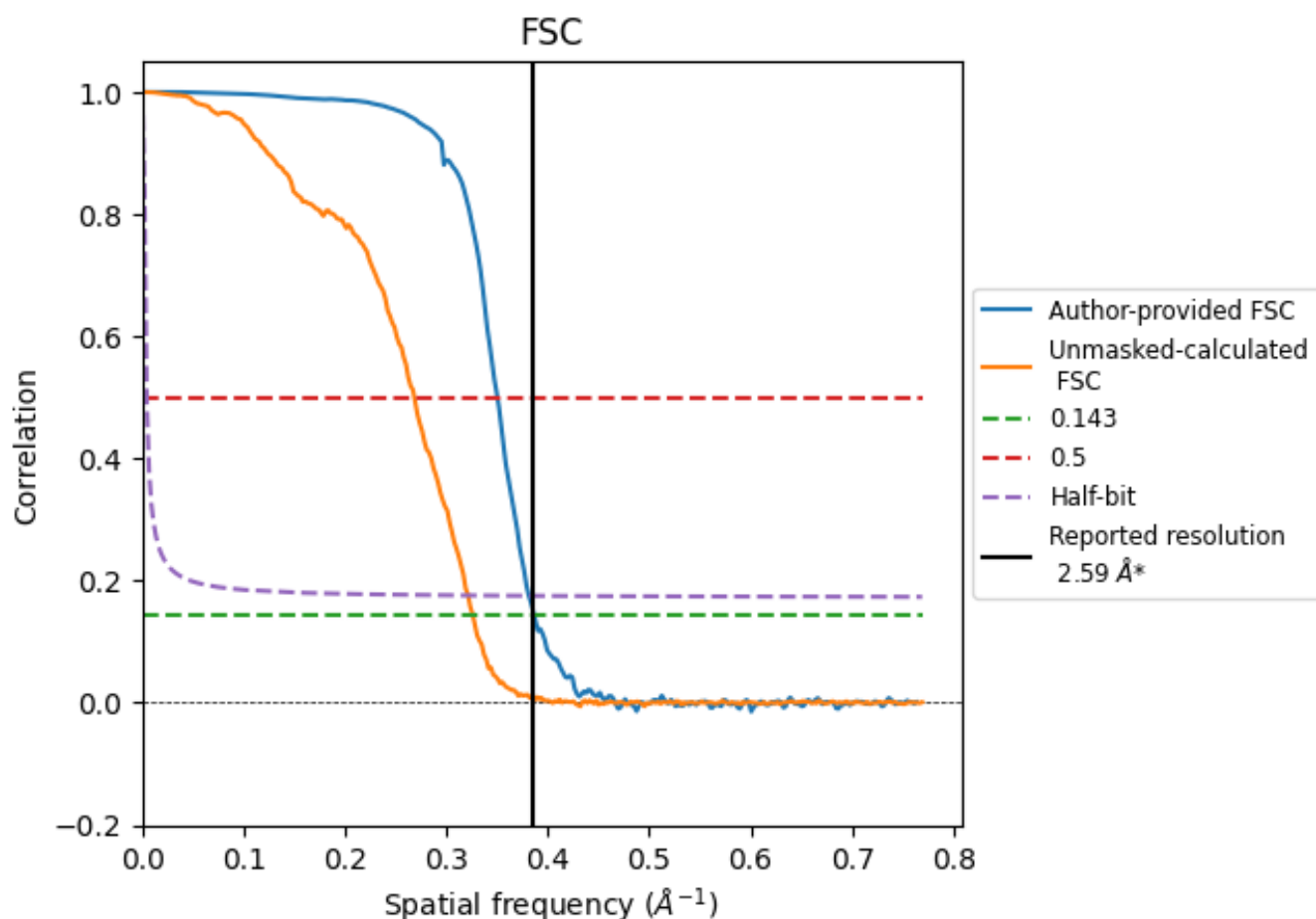


*Reported resolution corresponds to spatial frequency of 0.386 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.386 \text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

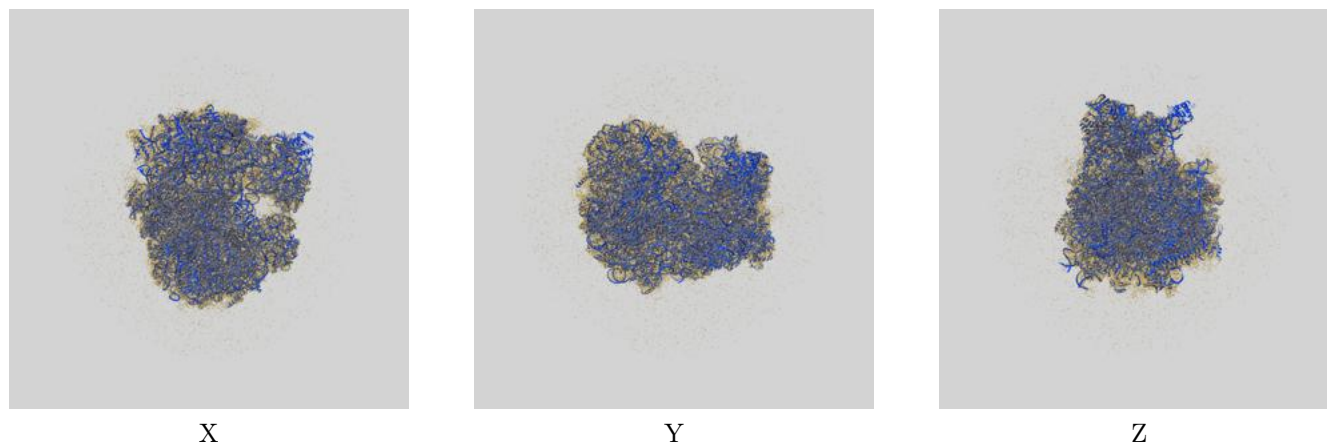
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.59	-	-
Author-provided FSC curve	2.59	2.85	2.62
Unmasked-calculated*	3.07	3.73	3.11

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.07 differs from the reported value 2.59 by more than 10 %

9 Map-model fit [i](#)

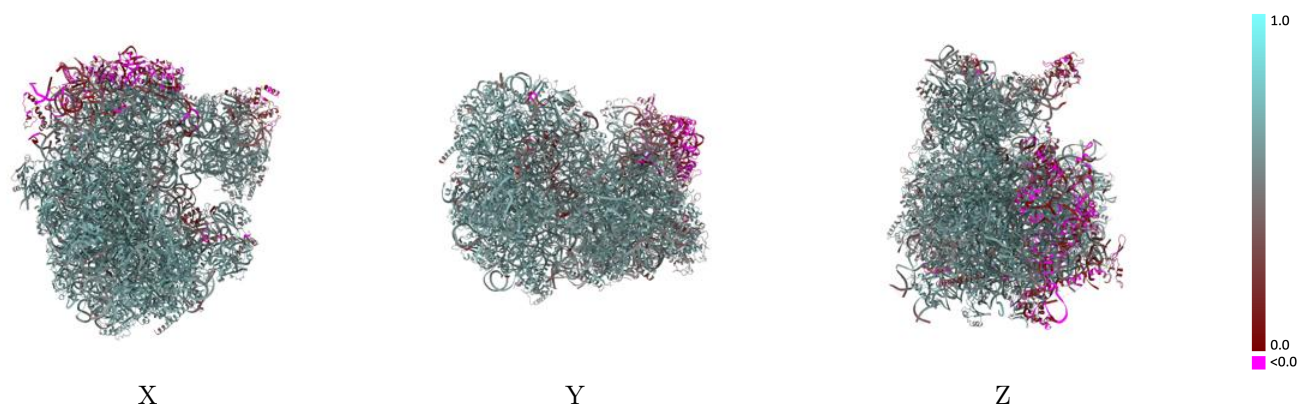
This section contains information regarding the fit between EMDB map EMD-45392 and PDB model 9CAI. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



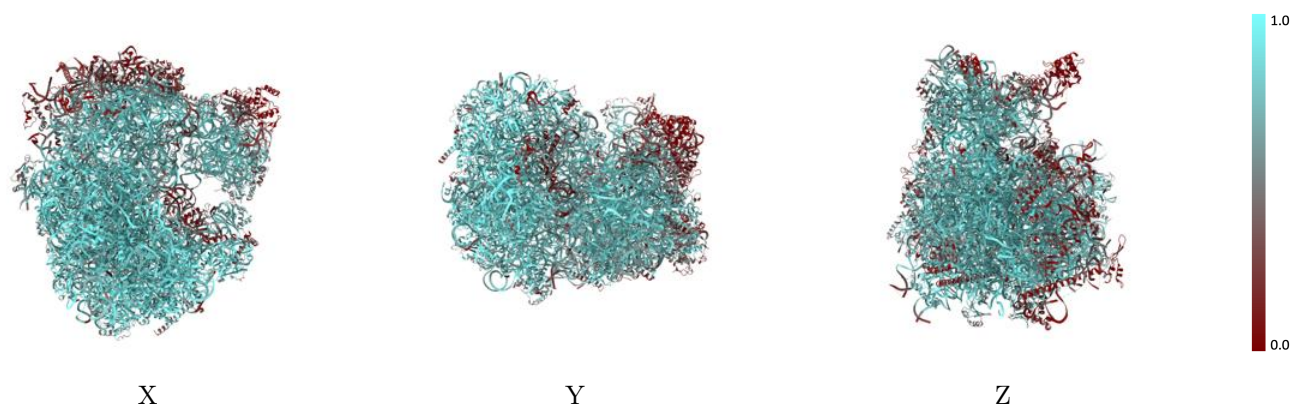
The images above show the 3D surface view of the map at the recommended contour level 0.199 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



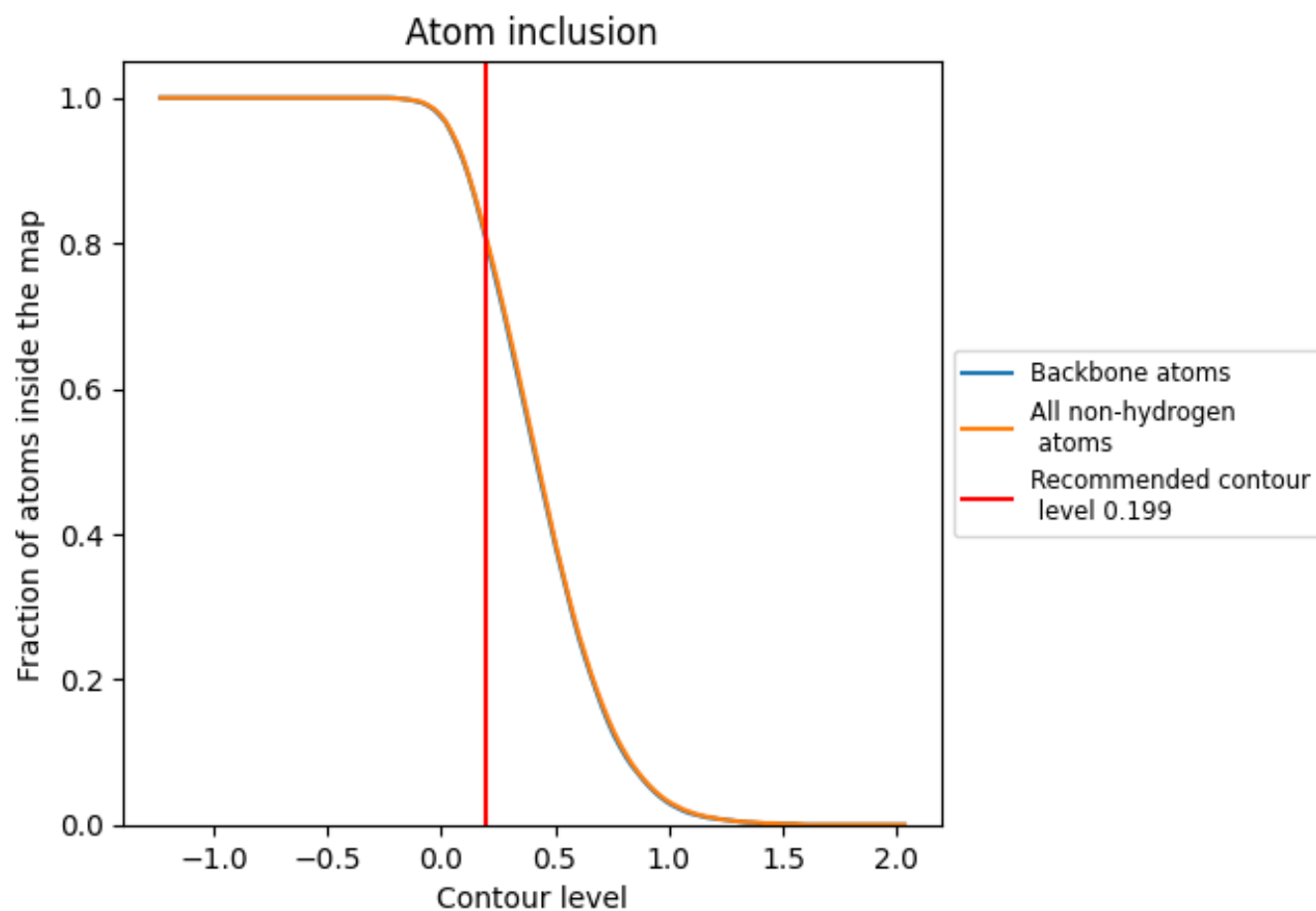
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.199).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 81% 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 (0.199) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8070	 0.5750
A5	 0.8980	 0.6140
A7	 0.9460	 0.6350
A8	 0.9330	 0.6220
AA	 0.7030	 0.5720
AB	 0.7470	 0.5860
AC	 0.8250	 0.6280
AD	 0.5490	 0.5360
AE	 0.3460	 0.1420
AF	 0.7570	 0.5840
AG	 0.4570	 0.3320
AH	 0.4720	 0.4430
AI	 0.6510	 0.4300
AJ	 0.3230	 0.1320
AK	 0.3770	 0.4860
AL	 0.7690	 0.5170
AM	 0.0190	 0.1640
AN	 0.6800	 0.5620
AO	 0.8470	 0.6110
AP	 0.5890	 0.5350
AQ	 0.6900	 0.5650
AR	 0.4810	 0.4810
AS	 0.7000	 0.5830
AT	 0.6680	 0.5650
AU	 0.4830	 0.4660
AV	 0.6740	 0.5490
AW	 0.8980	 0.6380
AX	 0.7420	 0.5140
AY	 0.2280	 0.0580
AZ	 0.5700	 0.5240
Aa	 0.8450	 0.6240
Ab	 0.5510	 0.4950
Ac	 0.6520	 0.5320
Ad	 0.7560	 0.5920
Ae	 0.1700	 0.1380



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Chain	Atom inclusion	Q-score
Af	 0.0600	 0.1980
B2	 0.8230	 0.5530
CA	 0.9500	 0.6630
CB	 0.9250	 0.6580
CC	 0.8810	 0.6380
CD	 0.7670	 0.5860
CE	 0.7810	 0.5980
CF	 0.8980	 0.6440
CG	 0.7280	 0.5740
CH	 0.7560	 0.5900
CI	 0.2900	 0.4140
CJ	 0.7130	 0.5740
CL	 0.8320	 0.6220
CM	 0.8570	 0.6300
CN	 0.9640	 0.6610
CO	 0.9150	 0.6520
CP	 0.9310	 0.6580
CQ	 0.9420	 0.6590
CR	 0.7550	 0.5630
CS	 0.9010	 0.6410
CT	 0.8480	 0.6250
CU	 0.6660	 0.5570
CV	 0.9300	 0.6580
CW	 0.6780	 0.5110
CX	 0.8380	 0.6190
CY	 0.8690	 0.6330
CZ	 0.8320	 0.6180
Ca	 0.9290	 0.6530
Cb	 0.8260	 0.6070
Cc	 0.8390	 0.6220
Cd	 0.8590	 0.6260
Ce	 0.8890	 0.6420
Cf	 0.9300	 0.6560
Cg	 0.8840	 0.6380
Ch	 0.8260	 0.6170
Ci	 0.8140	 0.6110
Cj	 0.9230	 0.6460
Ck	 0.6640	 0.5690
Cl	 0.8950	 0.6460
Cm	 0.2350	 0.4620
Cn	 0.7340	 0.5880
Co	 0.8760	 0.6500

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Chain	Atom inclusion	Q-score
Cp	 0.9020	 0.6480
DA	 0.5330	 0.4730
DC	 0.5200	 0.4420