wwPDB EM Validation Summary Report

Nov 9, 2026 – 10:53 PM JST

PDB ID	:	9XP4 / pdb_00009xp4
EMDB ID	:	EMD-66878
Title	:	Cryo-EM structure of the 70S ribosome from stationary-phase Methanolobus in complex with P/E-tRNA
Authors	:	Zhu, L.; Yi, C.; Li, W.
Deposited on	:	2025-11-15
Resolution	:	2.70 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

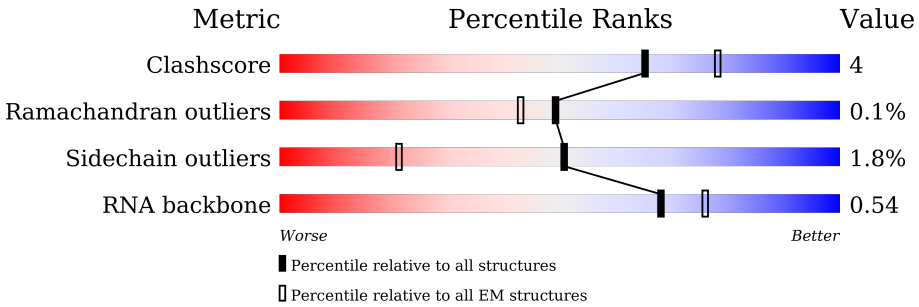
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

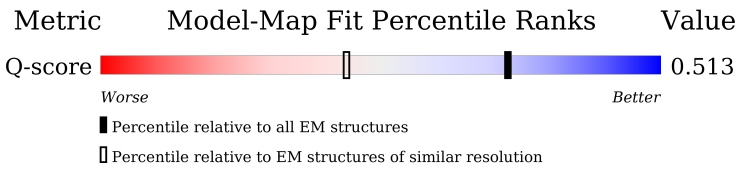
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.70 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	10327 (2.20 - 3.20)

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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	2910	15% 75% 21% ·
2	2	126	31% 75% 22% ·
3	4	1474	49% 70% 25% ·

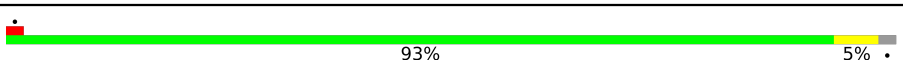
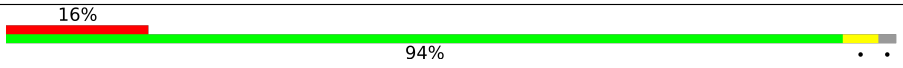
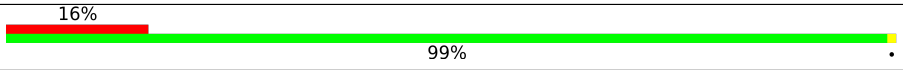
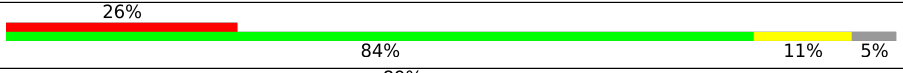
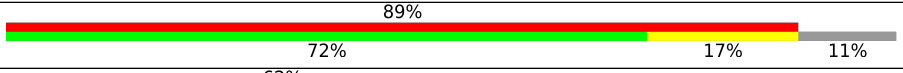
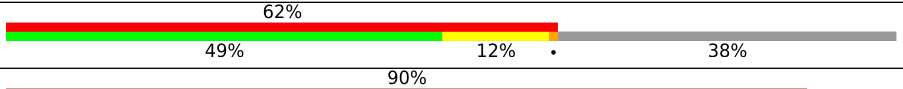
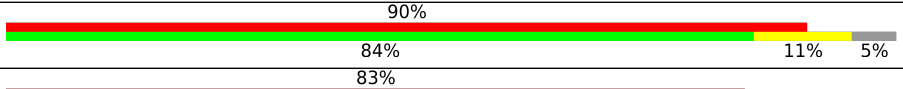
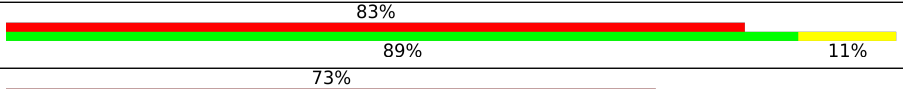
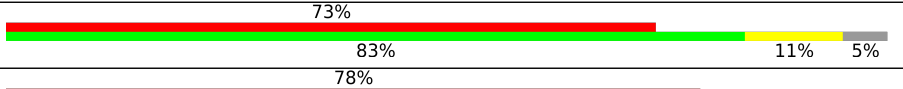
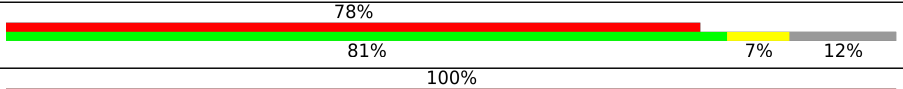
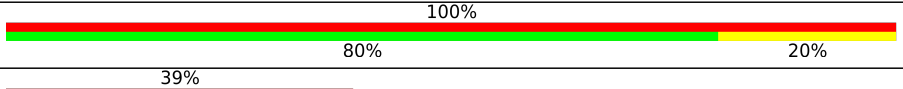
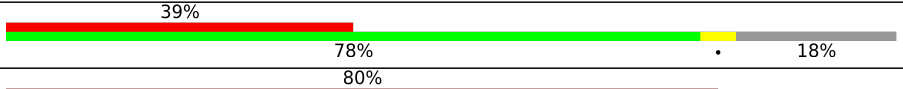
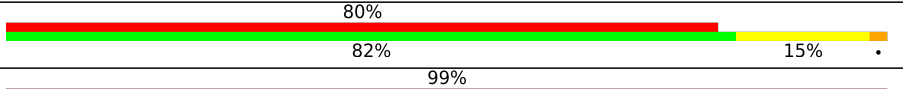
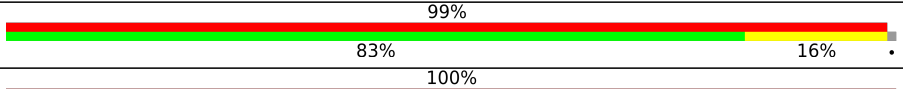
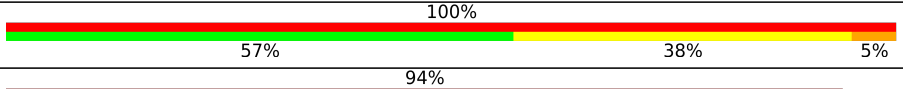
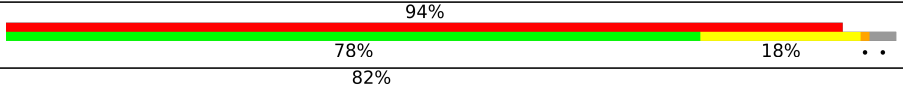
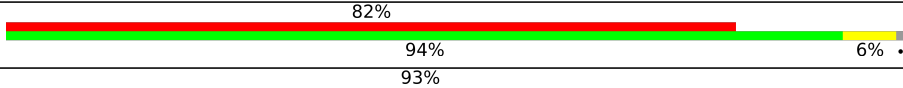
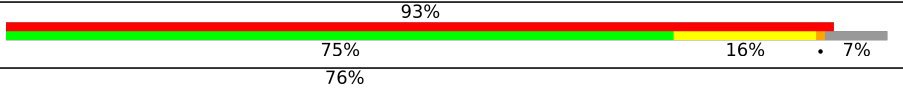
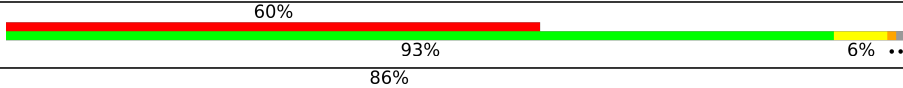
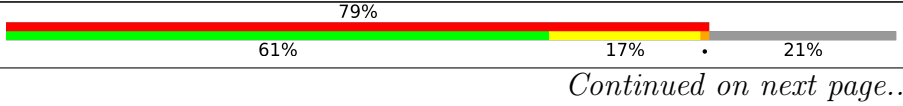
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Mol	Chain	Length	Quality of chain
4	AA	237	21% 91% 8%
5	AB	337	24% 90% 9%
6	AC	253	30% 91% 9%
7	AD	165	96% 73% 27%
8	AE	177	77% 84% 13%
9	AF	130	78% 68% 22% 10%
10	AG	142	24% 89% 8%
11	AI	132	19% 90% 9%
12	AL	147	35% 88% 11%
13	AM	196	14% 94% 5%
14	AN	172	29% 88% 6% 6%
15	AO	173	65% 88% 11%
16	AP	126	33% 92% 6%
17	AQ	152	22% 91% 7%
18	AR	58	45% 88% 10%
19	AS	97	15% 97%
20	AT	151	23% 93% 5%
21	AU	82	57% 91% 7%
22	AV	117	38% 91% 8%
23	AW	62	21% 87% 13%
24	AX	67	93% 76% 22%
25	AY	160	26% 84% 12%
26	AZ	95	79% 83% 17%
27	Aa	90	28% 82% 13%
28	Ab	129	29% 93% 5%

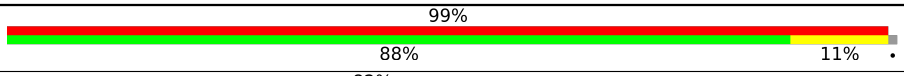
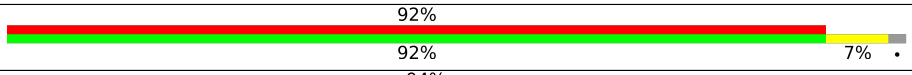
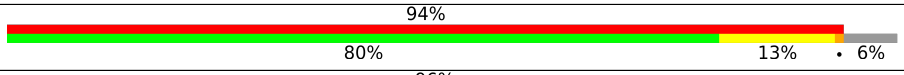
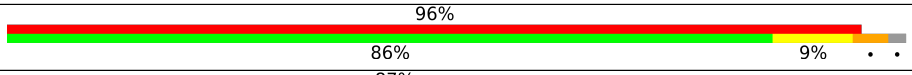
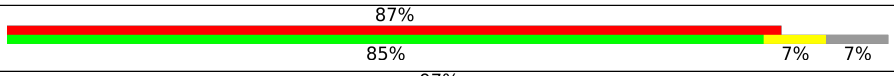
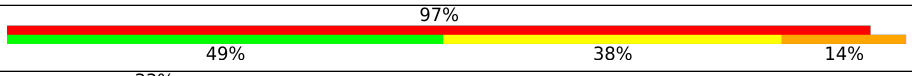
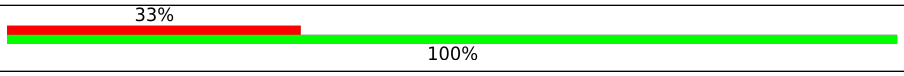
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Mol	Chain	Length	Quality of chain
29	Ad	56	
30	Af	51	
31	Ag	49	
32	Ah	92	
33	Ai	97	
34	BA	196	
35	BB	218	
36	BC	311	
37	BD	186	
38	BE	236	
39	BF	211	
40	BG	139	
41	BH	186	
42	BI	157	
43	BJ	124	
44	BK	134	
45	BL	103	
46	BM	127	
47	BN	142	
48	BO	148	
49	BP	50	
50	BQ	152	
51	BR	109	
52	BS	64	
53	BT	137	

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Mol	Chain	Length	Quality of chain
54	BU	149	
55	BV	114	
56	BY	59	
57	BZ	71	
58	Ba	57	
59	Bc	55	
60	C	72	
61	D	3	

2 Entry composition (i)

There are 62 unique types of molecules in this entry. The entry contains 154667 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 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2910	62358	27842	11402	20204	2910	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	126	2683	1199	479	879	126	0	0

- Molecule 3 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	4	1474	31571	14081	5738	10278	1474	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AA	236	1783	1114	345	317	7	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AB	335	2570	1620	460	482	8	0	0

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AC	252	1914	1183	365	359	7	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AD	165	Total	C	N	O	S	0	0
			1305	829	230	241	5		

- Molecule 8 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AE	174	Total	C	N	O	S	0	0
			1358	868	228	255	7		

- Molecule 9 is a protein called 50S ribosomal protein L17Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AF	117	Total	C	N	O	S	0	0
			858	538	143	174	3		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AG	138	Total	C	N	O	S	0	0
			1088	691	196	195	6		

- Molecule 11 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AI	132	Total	C	N	O	S	0	0
			1005	623	194	181	7		

- Molecule 12 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	146	Total	C	N	O	S	0	0
			1092	666	207	216	3		

- Molecule 13 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	195	Total	C	N	O	S	0	0
			1600	985	332	277	6		

- Molecule 14 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	161	Total	C	N	O	S	0	0
			1265	789	251	218	7		

- Molecule 15 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	172	Total	C	N	O	S	0	0
			1344	844	237	261	2		

- Molecule 16 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	125	Total	C	N	O	S	0	0
			957	604	171	179	3		

- Molecule 17 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	149	Total	C	N	O	S	0	0
			1190	733	246	206	5		

- Molecule 18 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	AR	57	Total	C	N	O	0	0
			454	290	78	86		

- Molecule 19 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	96	Total	C	N	O	S	0	0
			761	472	146	138	5		

- Molecule 20 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	150	Total	C	N	O	S	0	0
			1157	717	222	209	9		

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	81	Total	C	N	O	S	0	0
			629	404	103	114	8		

- Molecule 22 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	116	Total	C	N	O	S	0	0
			900	558	171	168	3		

- Molecule 23 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AW	62	Total	C	N	O	S	0	0
			504	319	88	92	5		

- Molecule 24 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AX	66	Total	C	N	O	S	0	0
			528	318	103	102	5		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AY	153	Total	C	N	O	S	0	0
			1199	746	228	219	6		

- Molecule 26 is a protein called Ribosomal protein L30E.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AZ	95	Total	C	N	O	S	0	0
			683	429	116	133	5		

- Molecule 27 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Aa	86	Total	C	N	O	S	0	0
			716	460	126	128	2		

- Molecule 28 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ab	126	Total	C	N	O	S	0	0
			993	626	195	171	1		

- Molecule 29 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ad	55	Total	C	N	O	S	0	0
			435	264	91	73	7		

- Molecule 30 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Af	50	Total	C	N	O	0	0
			422	261	97	64		

- Molecule 31 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ag	46	Total	C	N	O	S	0	0
			362	218	77	61	6		

- Molecule 32 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ah	92	Total	C	N	O	S	0	0
			758	472	157	123	6		

- Molecule 33 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ai	92	Total	C	N	O	S	0	0
			716	439	146	125	6		

- Molecule 34 is a protein called 30S ribosomal protein S3Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BA	188	Total	C	N	O	S	0	0
			1519	960	274	282	3		

- Molecule 35 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BB	195	Total	C	N	O	S	0	0
			1517	968	252	290	7		

- Molecule 36 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BC	192	Total	C	N	O	S	0	0
			1471	928	261	270	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BD	177	Total	C	N	O	S	0	0
			1422	893	265	262	2		

- Molecule 38 is a protein called 30S ribosomal protein S4e.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BE	236	Total	C	N	O	S	0	0
			1831	1151	333	342	5		

- Molecule 39 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BF	200	Total	C	N	O	S	0	0
			1512	941	277	287	7		

- Molecule 40 is a protein called 30S ribosomal protein S6e.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BG	123	Total	C	N	O	S	0	0
			917	578	160	175	4		

- Molecule 41 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BH	186	Total	C	N	O	S	0	0
			1468	910	281	270	7		

- Molecule 42 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BI	129	Total	C	N	O	S	0	0
			994	638	166	187	3		

- Molecule 43 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BJ	124	Total	C	N	O	S	0	0
			966	586	196	182	2		

- Molecule 44 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BK	133	Total	C	N	O	S	0	0
			1016	637	185	192	2		

- Molecule 45 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BL	103	Total	C	N	O	S	0	0
			800	499	151	145	5		

- Molecule 46 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BM	123	Total	C	N	O	S	0	0
			899	554	174	167	4		

- Molecule 47 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BN	141	Total	C	N	O	S	0	0
			1094	675	220	193	6		

- Molecule 48 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BO	137	Total	C	N	O	S	0	0
			1090	671	207	207	5		

- Molecule 49 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BP	38	Total	C	N	O	S	0	0
			318	199	62	52	5		

- Molecule 50 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BQ	151	Total	C	N	O	S	0	0
			1224	775	220	223	6		

- Molecule 51 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BR	108	Total	C	N	O	S	0	0
			851	533	152	161	5		

- Molecule 52 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BS	55	Total	C	N	O	S	0	0
			450	282	87	80	1		

- Molecule 53 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BT	108	Total	C	N	O	S	0	0
			881	555	162	161	3		

- Molecule 54 is a protein called 30S ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BU	148	Total	C	N	O	S	0	0
			1145	726	200	216	3		

- Molecule 55 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BV	93	Total	C	N	O	S	0	0
			749	473	131	140	5		

- Molecule 56 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BY	58	Total	C	N	O	S	0	0
			445	275	81	85	4		

- Molecule 57 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BZ	67	Total	C	N	O	S	0	0
			507	309	94	100	4		

- Molecule 58 is a protein called DUF5350 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Ba	56	Total	C	N	O	S	0	0
			437	270	93	73	1		

- Molecule 59 is a protein called Putative Zn-ribbon RNA-binding protein with a function in translation.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Bc	51	Total	C	N	O	S	0	0
			378	227	70	72	9		

- Molecule 60 is a RNA chain called P/E-RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	C	72	Total	C	N	O	P	0	0
			1532	684	270	506	72		

- Molecule 61 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	D	3	Total	C	N	O	P	0	0
			66	29	12	22	3		

- Molecule 62 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
62	AW	1	Total	Zn	0
			1	1	
62	Ad	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
62	Ag	1	Total Zn 1 1	0
62	Ah	1	Total Zn 1 1	0
62	Ai	1	Total Zn 1 1	0
62	BF	1	Total Zn 1 1	0
62	BP	1	Total Zn 1 1	0
62	BR	1	Total Zn 1 1	0
62	BY	1	Total Zn 1 1	0
62	Bc	1	Total Zn 1 1	0

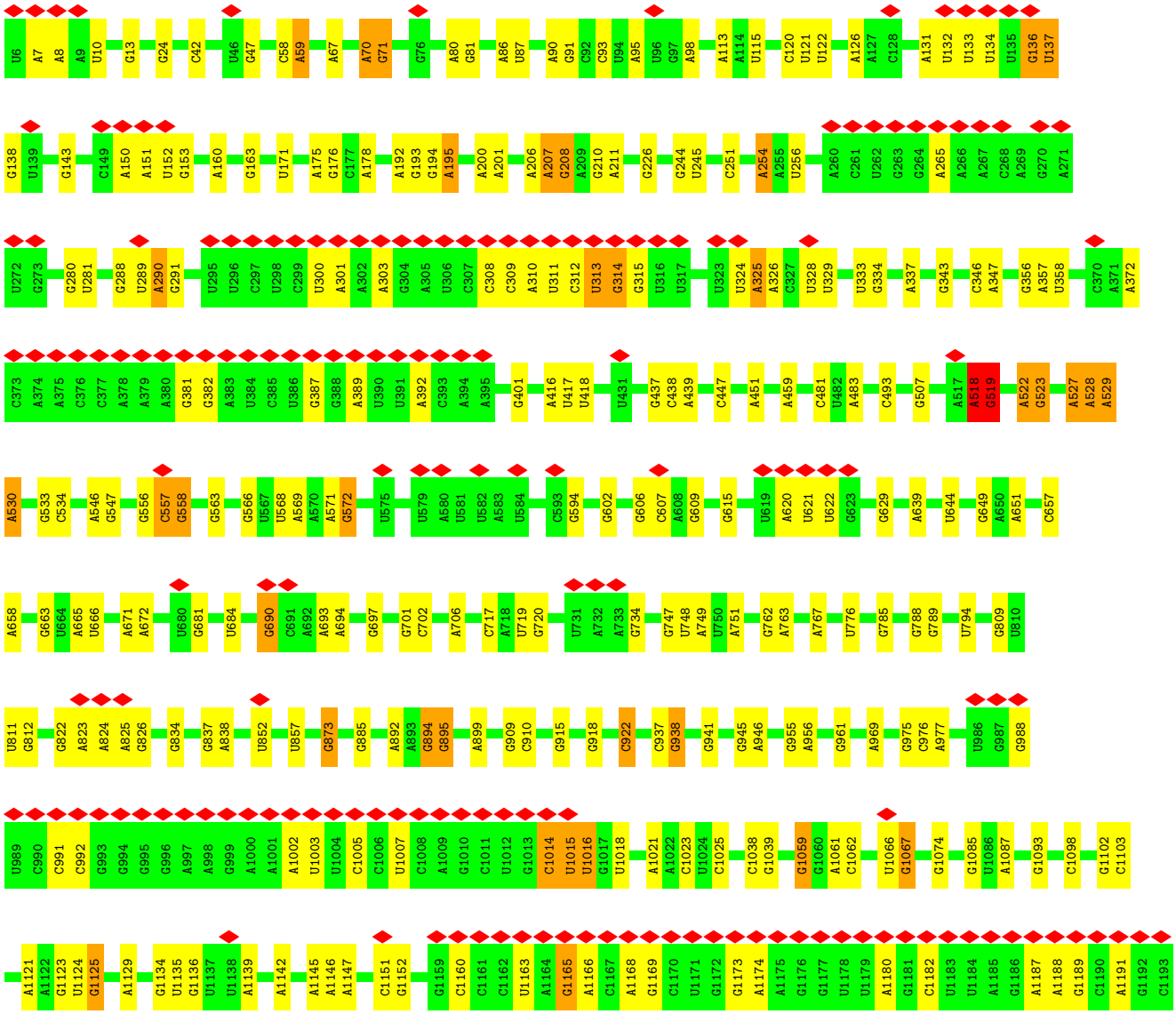
3 Residue-property plots (i)

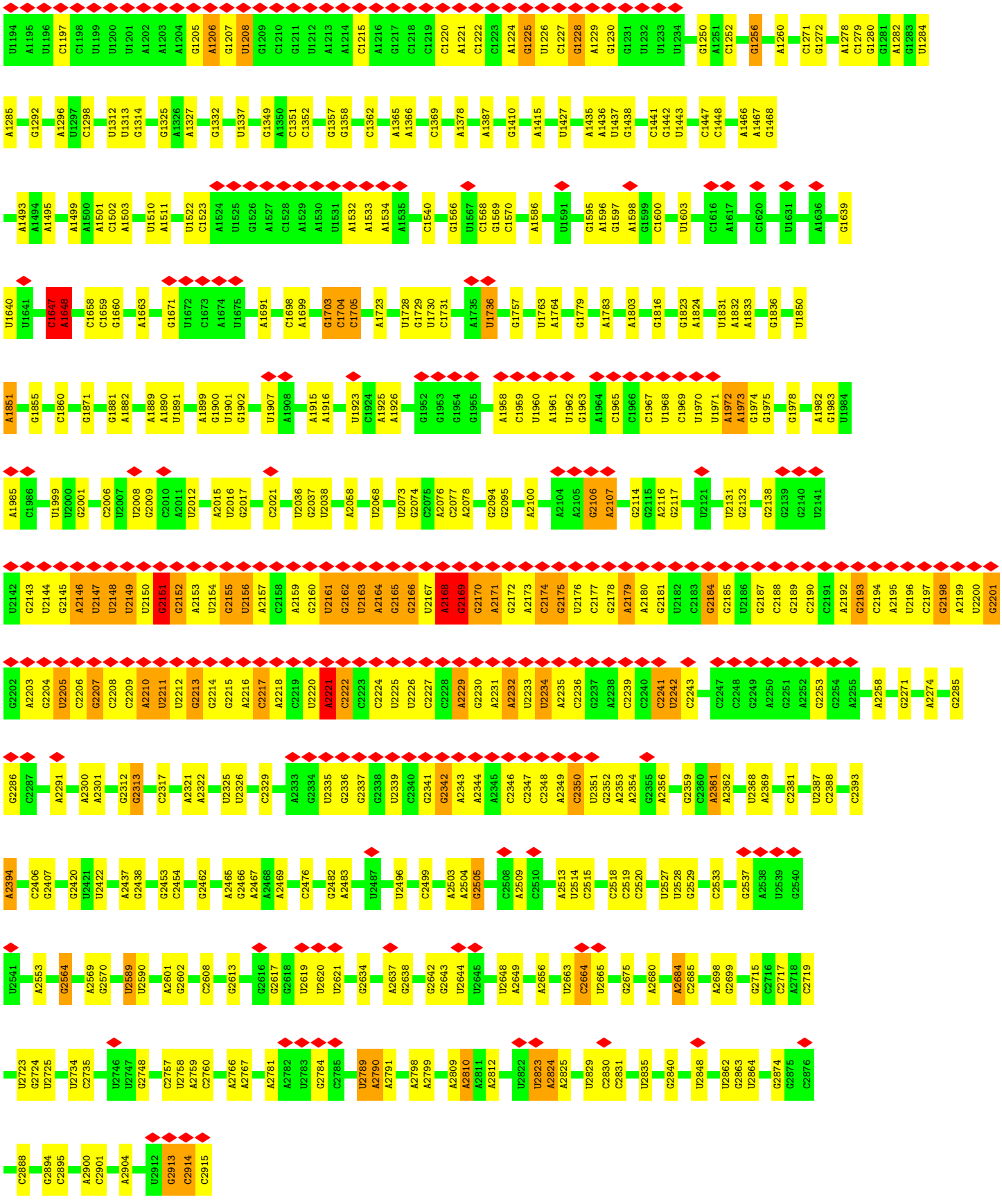
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 23S rRNA

Chain 1:



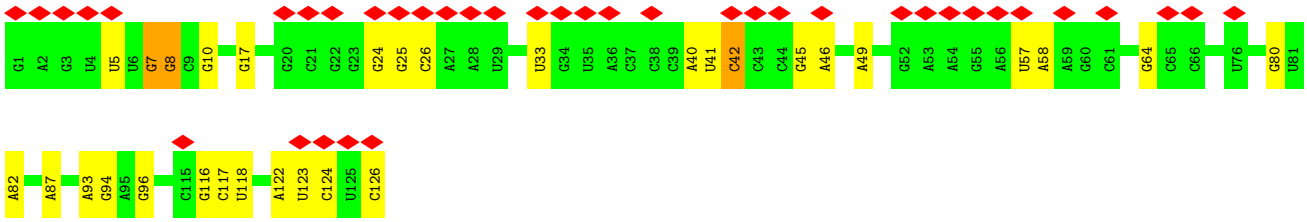



U1194 A1195 U1196 C1197 C1198 U1199 U1200 U1201 A1202 A1203 A1204 G1205 A1206 G1207 U1208 G1209 C1210 G1211 U1212 A1213 A1214 C1215 A1216 G1217 C1218 C1219 C1220 A1221 C1222 C1223 A1224 G1225 U1226 C1227 G1228 A1229 G1230 G1231 U1232 U1233 U1234 G1250 A1251 C1252 G1256 A1260 C1271 G1272 A1278 C1279 G1280 G1281 A1282 G1283 U1284
A1285 G1292 A1296 U1297 C1298 U1312 U1313 G1314 G1325 A1326 A1327 G1332 U1337 G1349 A1350 C1351 C1352 G1357 G1358 C1362 A1365 A1366 C1369 A1378 A1387 G1410 A1415 U1427 A1435 A1436 U1437 G1438 C1441 G1442 U1443 C1447 C1448 A1466 A1467 G1468
A1493 A1494 A1495 A1499 A1500 A1501 C1502 A1503 U1510 A1511 U1522 C1523 A1524 U1525 G1526 A1527 C1528 A1529 A1530 U1531 A1532 A1533 A1534 A1535 C1540 G1566 U1567 C1568 G1569 C1570 A1586 U1591 G1595 A1596 G1597 A1598 G1599 C1600 U1603 C1616 A1617 C1620 U1631 A1636 G1639
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A1985 C1986 U1999 U2000 G2001 C2006 U2007 U2008 G2009 C2010 A2011 U2012 A2015 U2016 G2017 C2021 U2036 G2037 U2038 A2058 U2068 U2073 G2074 C2075 A2076 C2077 A2078 G2094 G2095 A2100 A2104 A2105 G2106 A2107 G2114 G2115 A2116 G2117 U2121 U2131 G2132 G2138 G2139 G2140 U2141
U2142 G2143 U2144 G2145 A2146 U2147 U2148 U2149 U2150 G2151 G2152 A2153 U2154 G2155 U2156 A2157 C2158 A2159 G2160 U2161 G2162 U2163 A2164 G2165 G2166 U2167 A2168 G2169 G2170 A2171 G2172 A2173 C2174 G2175 U2176 C2177 G2178 A2179 A2180 G2181 U2182 C2183 G2184 G2185 U2186 G2187 C2188 G2189 C2190 C2191 A2192 G2193 C2194 A2195 U2196 C2197 G2198 A2199 U2200 G2201
G2202 A2203 G2204 U2205 C2206 G2207 C2208 C2209 A2210 U2211 U2212 G2213 G2214 G2215 A2216 C2217 A2218 C2219 U2220 A2221 C2222 C2223 C2224 U2225 U2226 C2227 C2228 A2229 G2230 A2231 A2232 U2233 U2234 A2235 C2236 G2237 A2238 C2239 C2240 C2241 U2242 C2243 C2247 C2248 G2249 A2250 G2251 A2252 G2253 G2254 A2255 A2258 G2271 A2274 G2285
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A2394 C2406 G2407 G2420 U2421 U2422 A2437 G2438 G2453 C2454 G2462 A2465 G2466 A2467 A2468 A2469 C2476 G2482 A2483 U2487 U2496 C2499 A2503 A2504 G2505 C2508 A2509 C2510 A2513 U2514 C2515 C2518 C2519 C2520 U2527 U2528 G2529 C2533 G2537 A2538 U2539 G2540
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U2723 G2724 U2725 U2734 C2735 U2746 U2747 G2748 C2757 U2758 A2759 C2760 A2766 A2767 A2781 A2782 U2783 G2784 C2785 U2789 A2790 A2791 A2798 A2799 A2809 A2810 A2811 A2812 U2822 U2823 A2824 A2825 U2829 C2830 C2831 U2835 G2840 U2848 U2862 G2863 U2864 G2874 C2875 C2876
C2888 G2894 C2895 A2900 C2901 A2904 U2912 G2913 C2914 C2915

- Molecule 2: 5S rRNA

Chain 2:

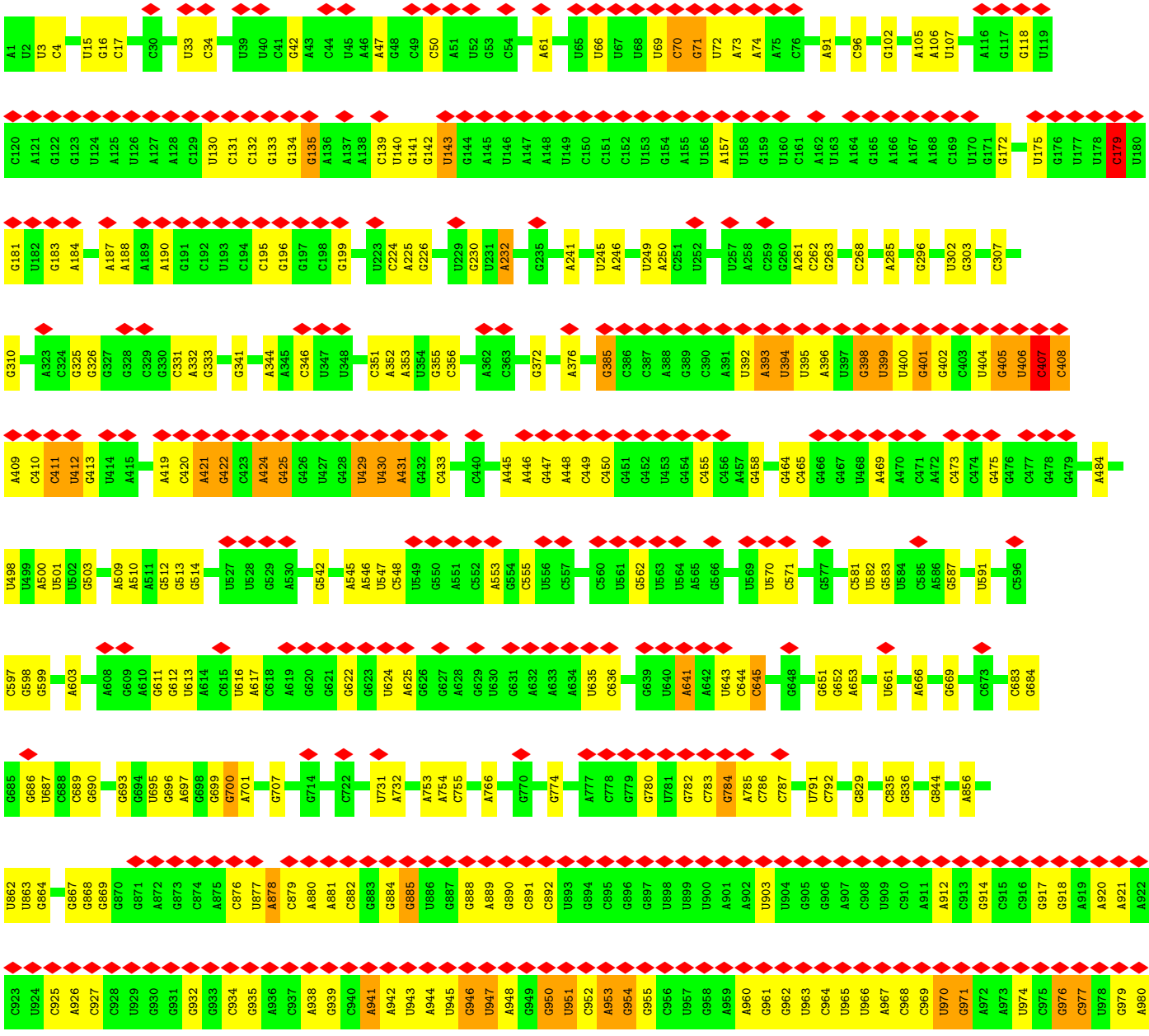


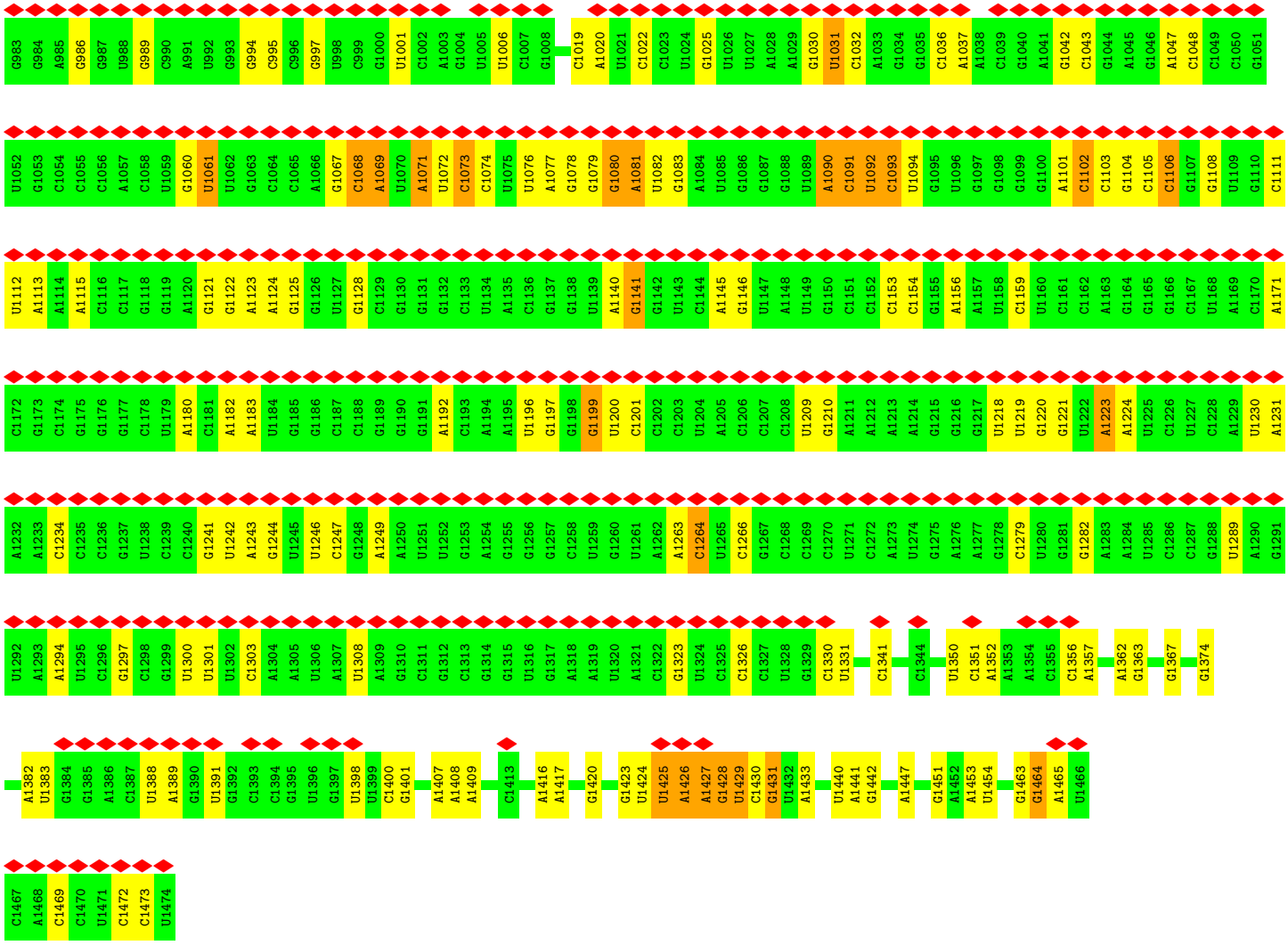


- Molecule 3: 16S rRNA

Chain 4:

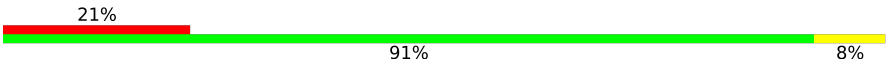


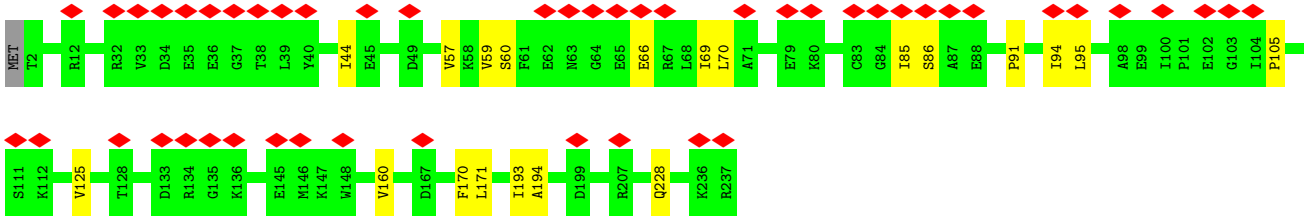




• Molecule 4: Large ribosomal subunit protein uL2

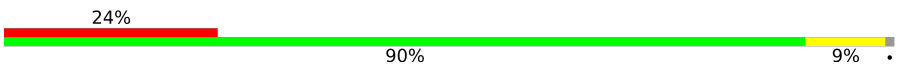
Chain AA:

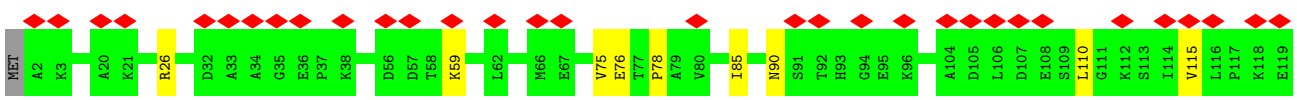


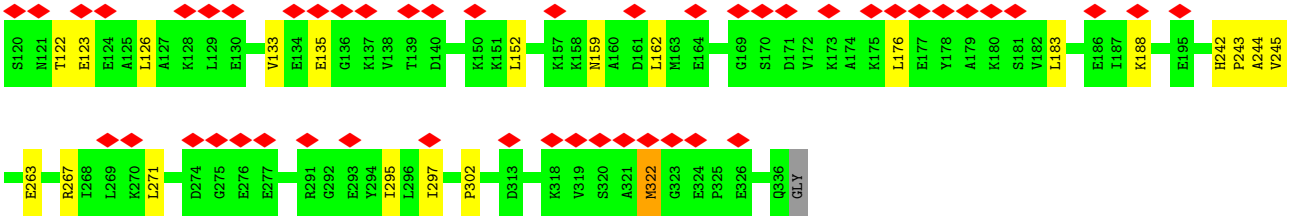


• Molecule 5: Large ribosomal subunit protein uL3

Chain AB:

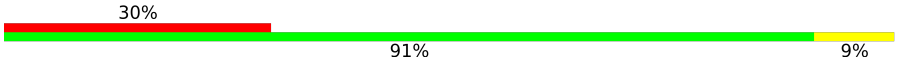


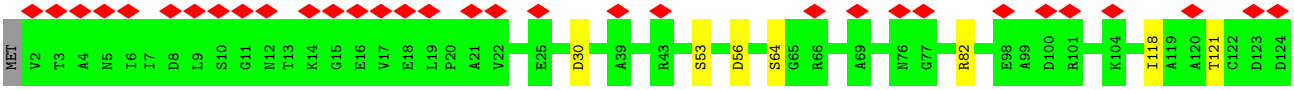


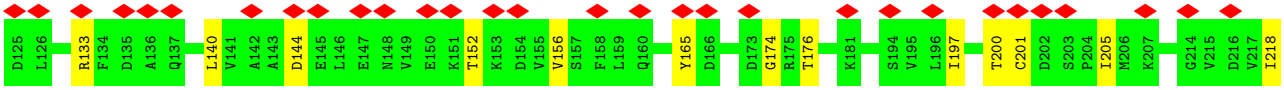


• Molecule 6: 50S ribosomal protein L4

Chain AC:

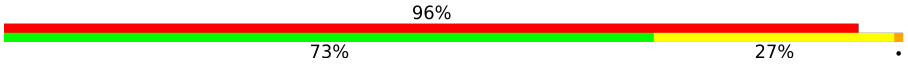


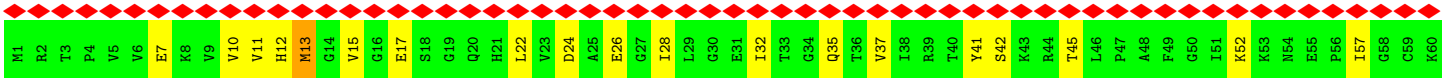


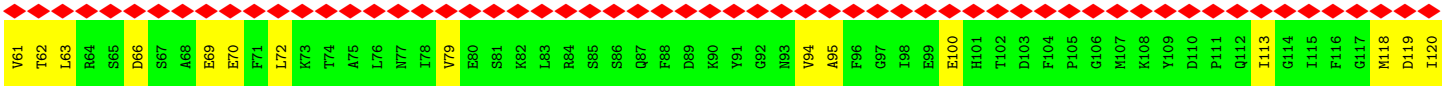


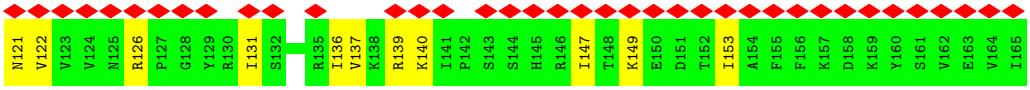
• Molecule 7: Large ribosomal subunit protein uL5

Chain AD:





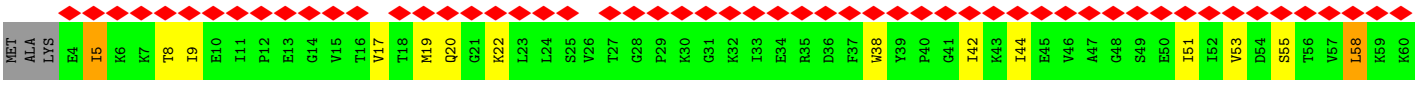


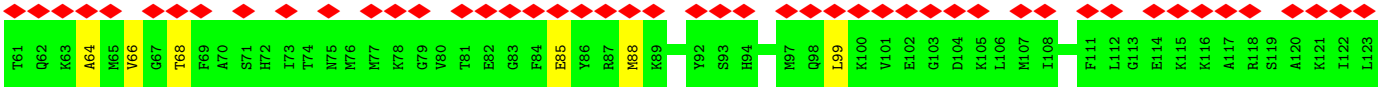


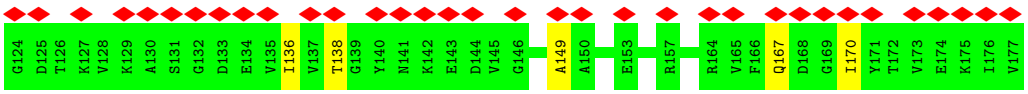
• Molecule 8: Large ribosomal subunit protein uL6

Chain AE:



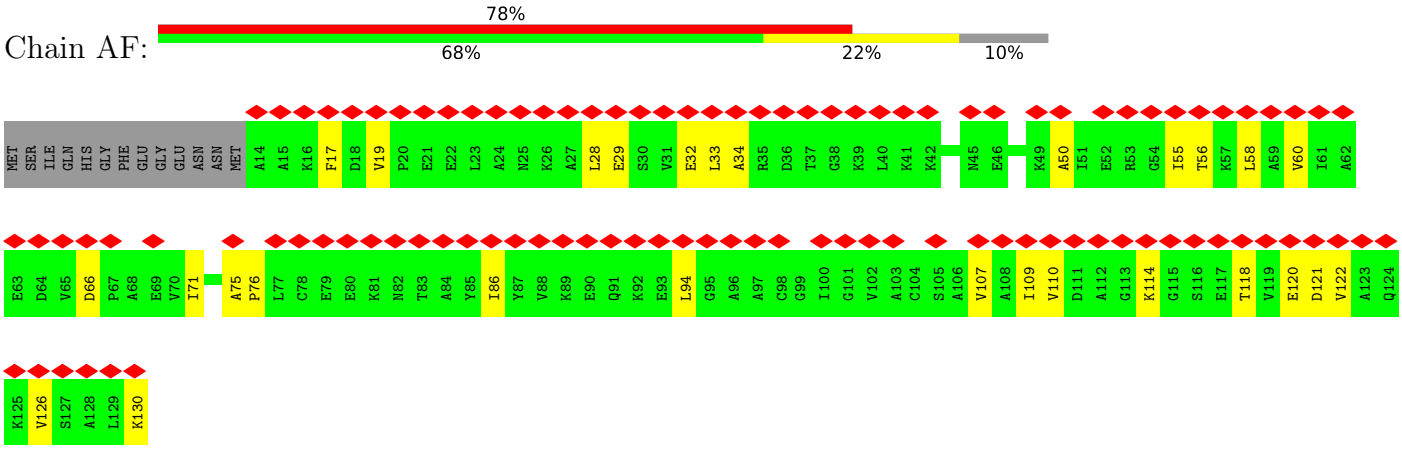






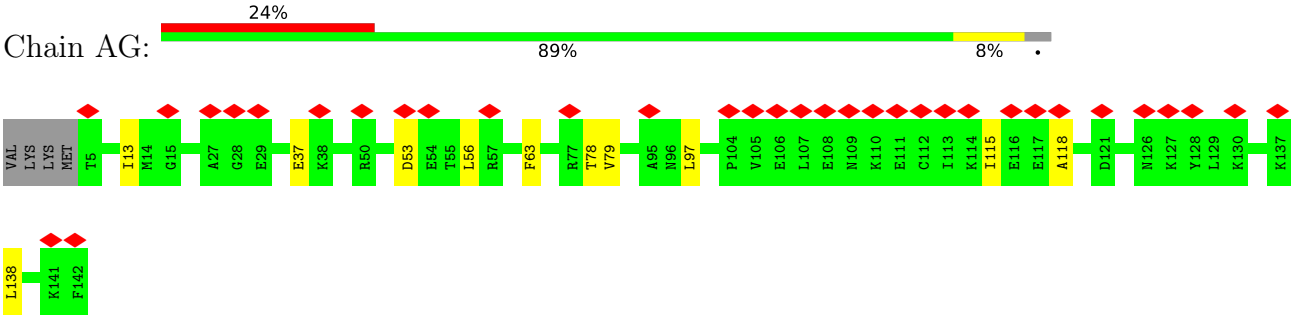
• Molecule 9: 50S ribosomal protein L17Ae

Chain AF:



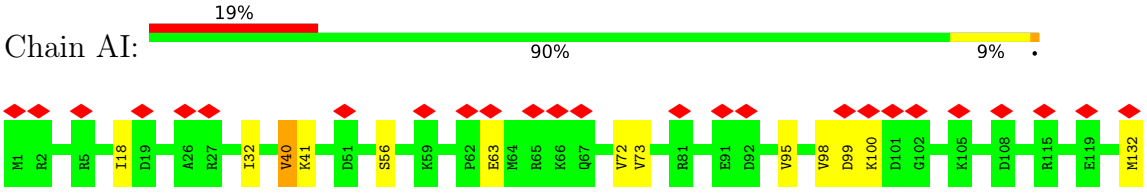
• Molecule 10: 50S ribosomal protein L13

Chain AG:



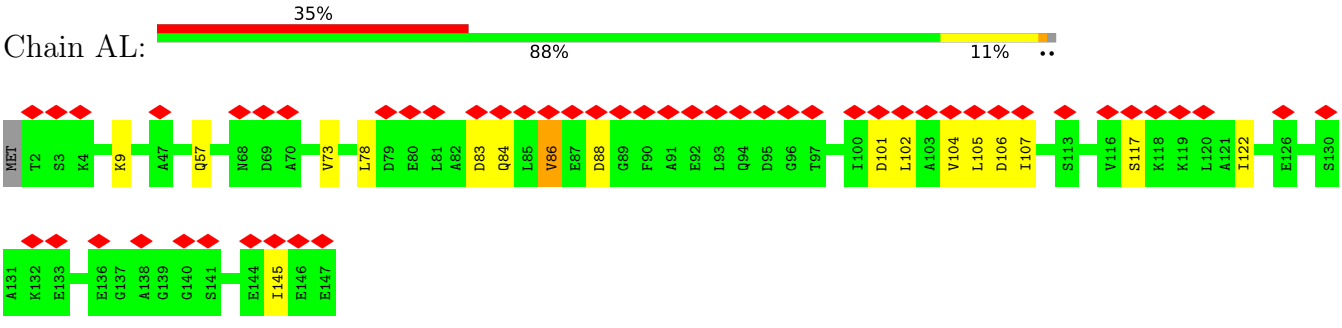
• Molecule 11: Large ribosomal subunit protein uL14

Chain AI:



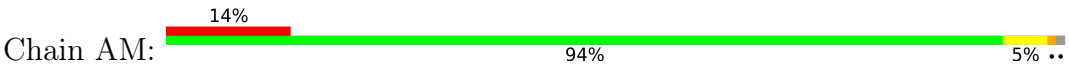
• Molecule 12: Large ribosomal subunit protein uL15

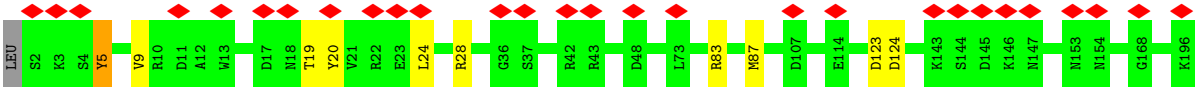
Chain AL:



• Molecule 13: 50S ribosomal protein L15e

Chain AM:

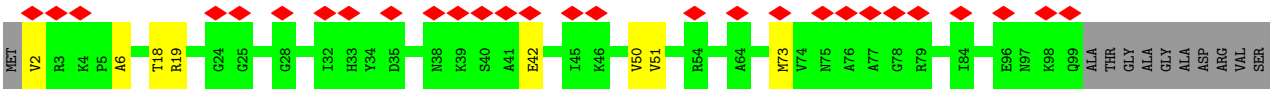


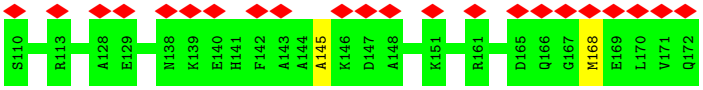


• Molecule 14: Large ribosomal subunit protein uL16

Chain AN:



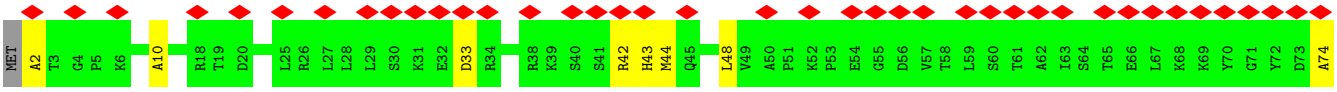


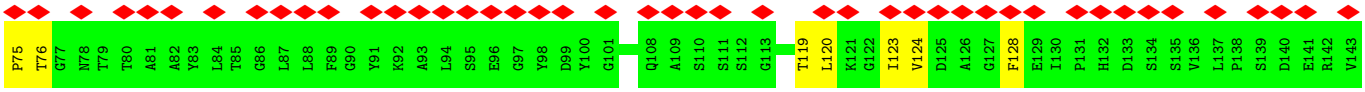


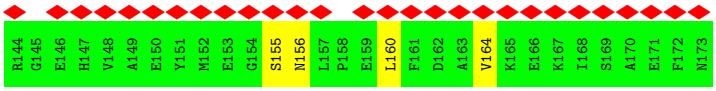
• Molecule 15: Large ribosomal subunit protein uL18

Chain AO:



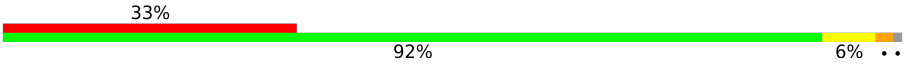


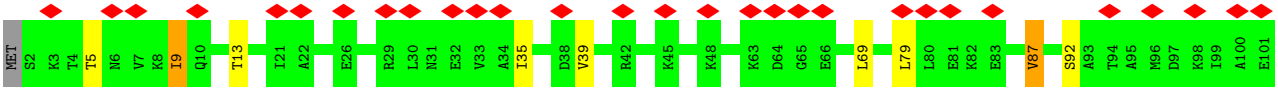


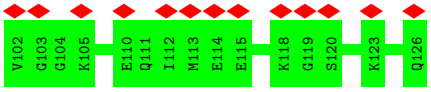


• Molecule 16: Large ribosomal subunit protein eL18

Chain AP:

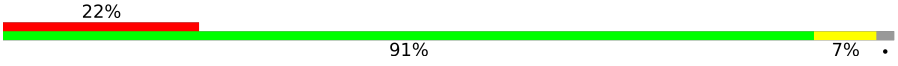


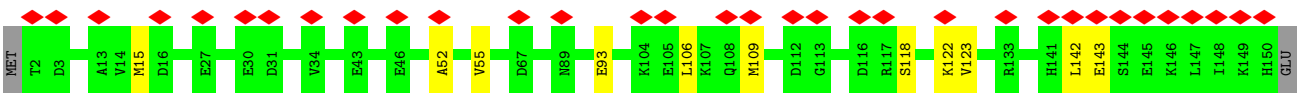




• Molecule 17: Large ribosomal subunit protein eL19

Chain AQ:

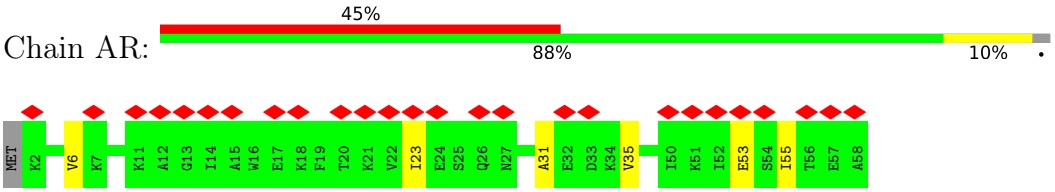






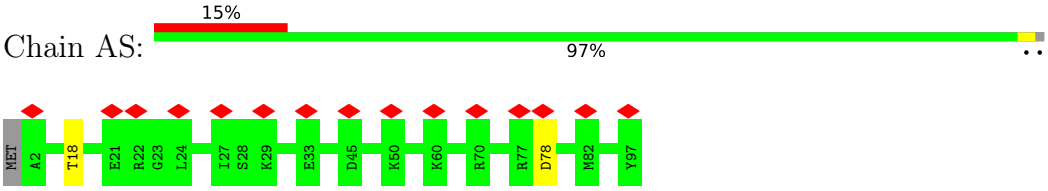
• Molecule 18: Large ribosomal subunit protein eL20

Chain AR:



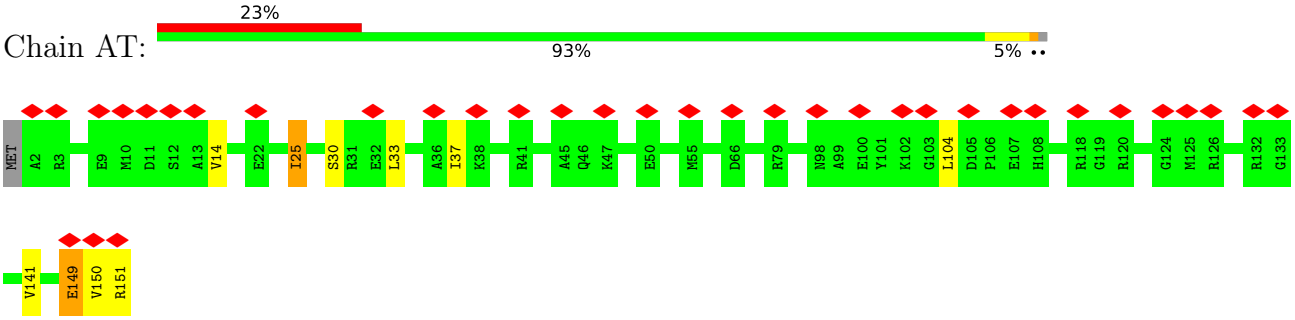
• Molecule 19: Large ribosomal subunit protein eL21

Chain AS:



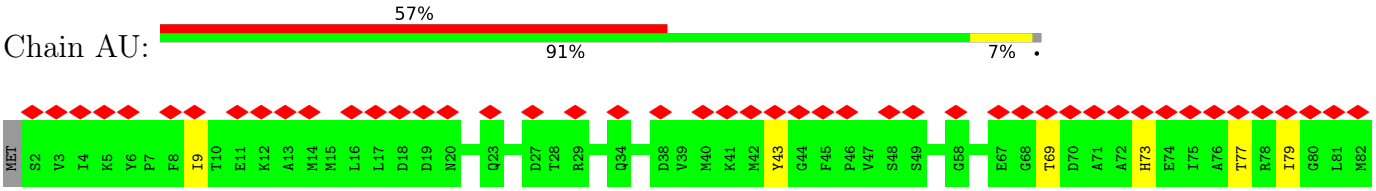
• Molecule 20: 50S ribosomal protein L22

Chain AT:



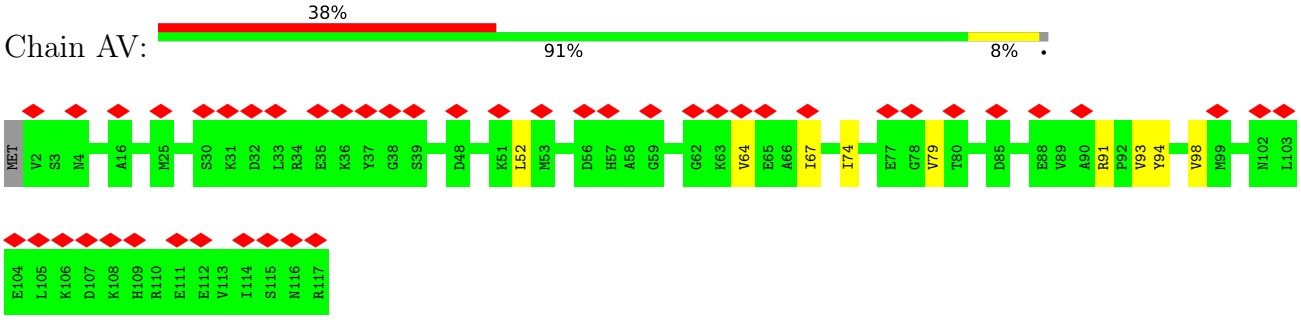
• Molecule 21: 50S ribosomal protein L23

Chain AU:



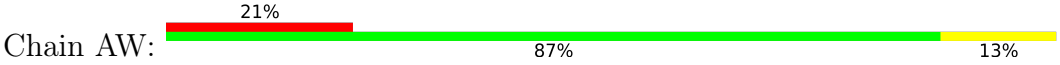
• Molecule 22: Large ribosomal subunit protein uL24

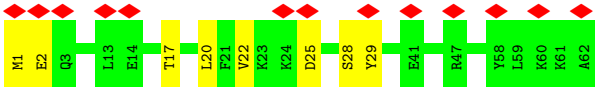
Chain AV:



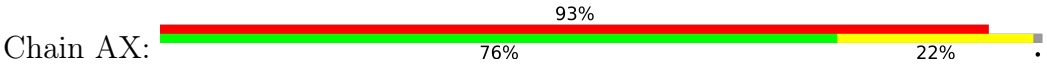
• Molecule 23: Large ribosomal subunit protein eL24

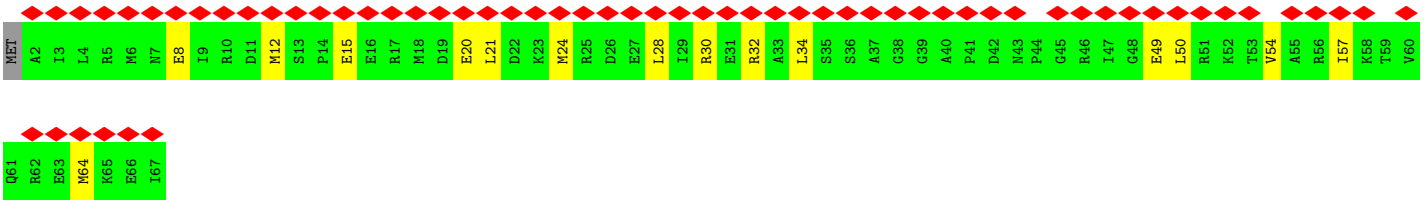
Chain AW:



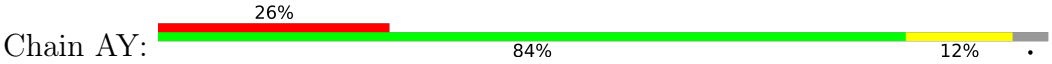


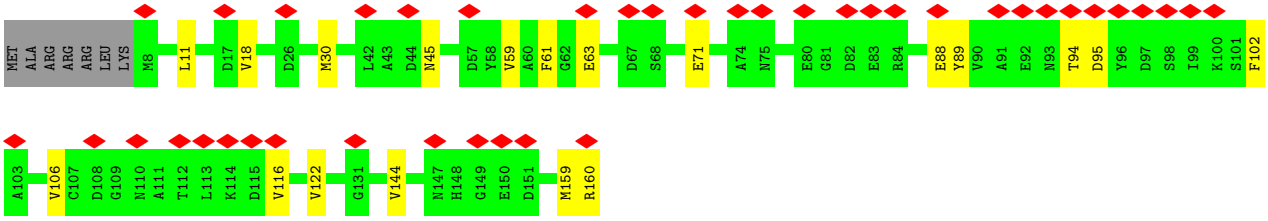
• Molecule 24: Large ribosomal subunit protein uL29



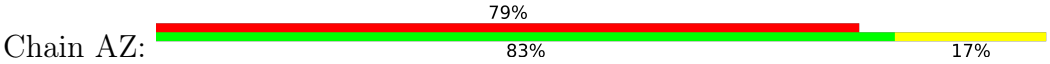


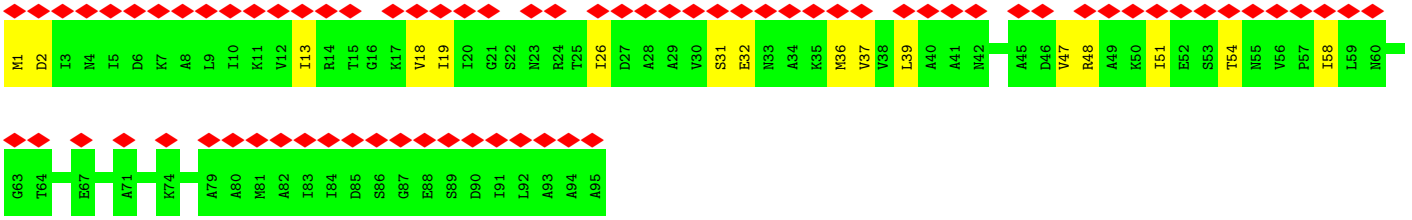
• Molecule 25: 50S ribosomal protein L30



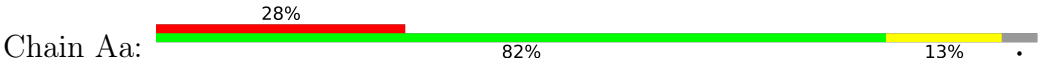


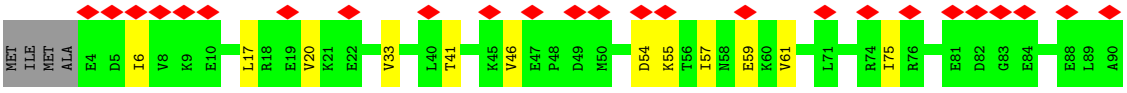
• Molecule 26: Ribosomal protein L30E



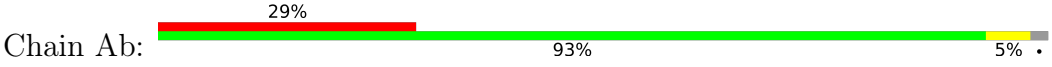


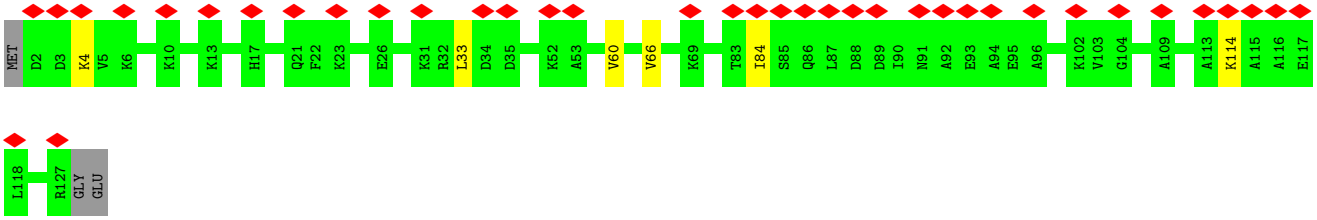
• Molecule 27: 50S ribosomal protein L31e



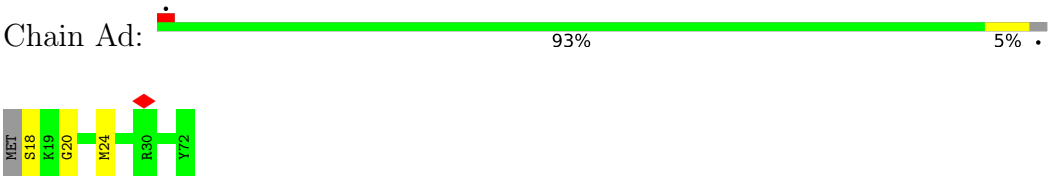


• Molecule 28: 50S ribosomal protein L32e

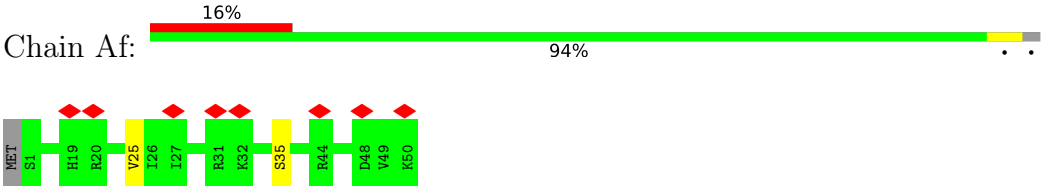




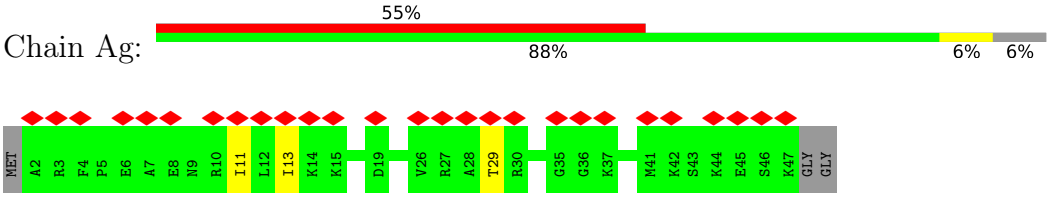
• Molecule 29: Large ribosomal subunit protein eL37



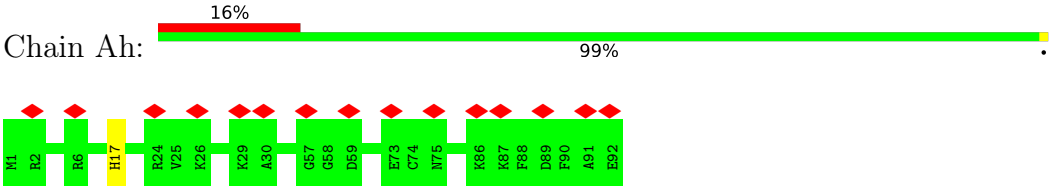
• Molecule 30: Large ribosomal subunit protein eL39



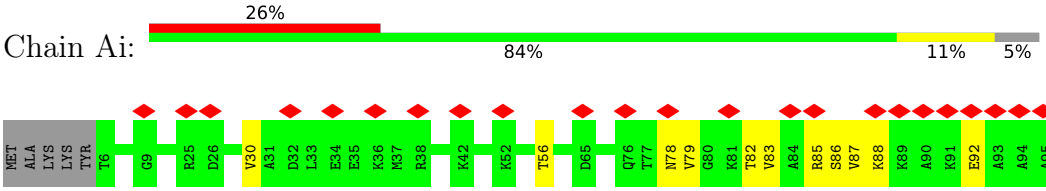
• Molecule 31: Large ribosomal subunit protein eL40



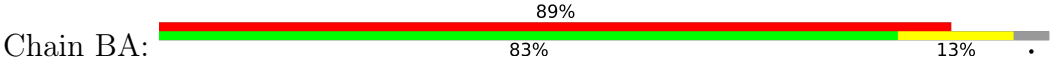
• Molecule 32: Large ribosomal subunit protein eL42

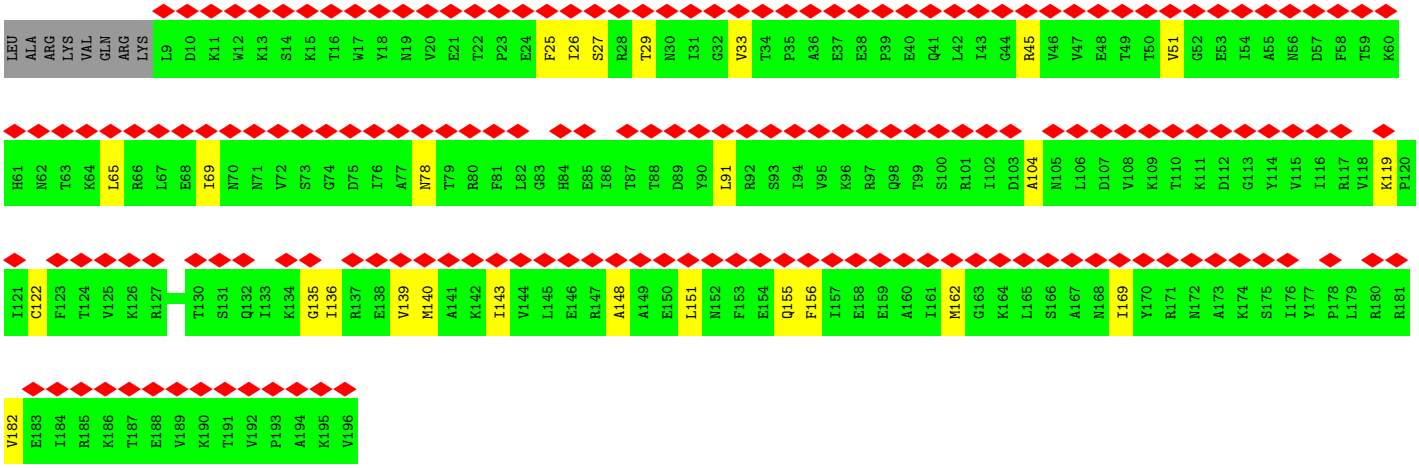


• Molecule 33: Large ribosomal subunit protein eL43



• Molecule 34: 30S ribosomal protein S3Ae

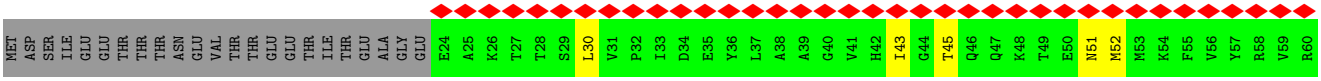


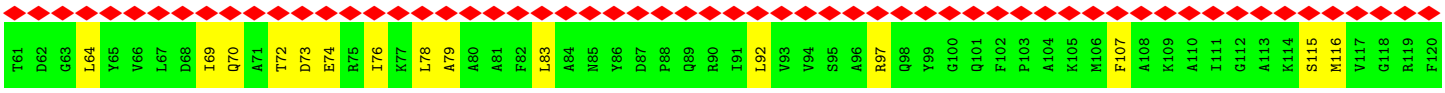


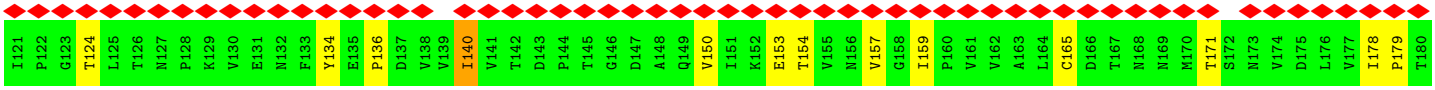
• Molecule 35: Small ribosomal subunit protein uS2

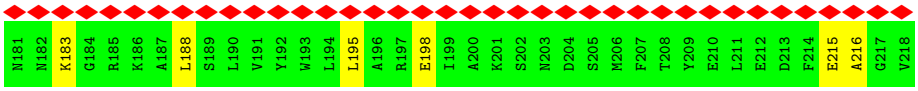
Chain BB:





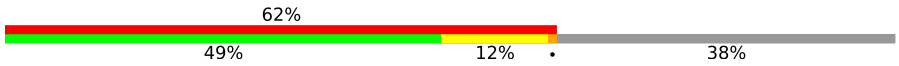


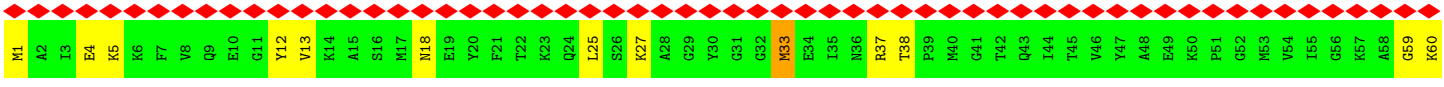


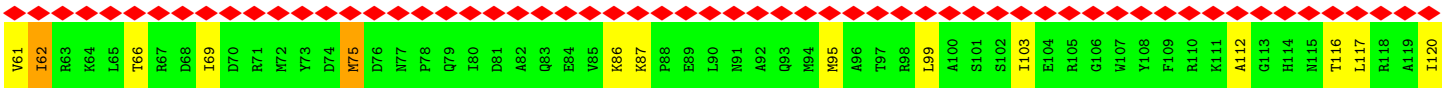


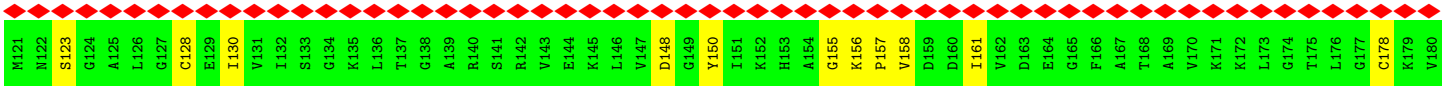
• Molecule 36: 30S ribosomal protein S3

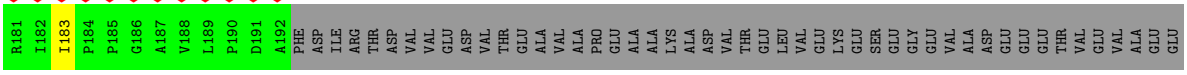
Chain BC:









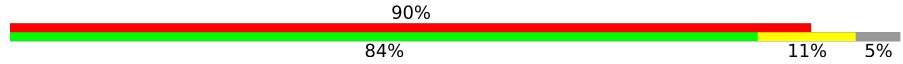


VAL ALA GLU ALA GLY VAL ALA GLU GLU ALA SER ALA GLU GLU VAL GLU GLU VAL GLU GLU GLU SER CYS ALA GLU GLU ALA ALA GLU SER ASP ASP SER ILE PRO VAL GLU ASP LEU GLY ASP GLU GLN ARG ARG LEU VAL ASP GLY VAL TRP GLN HIS LYS HIS GLU GLY TYR ASP TYR

TRP HIS PRO VAL ALA ARG VAL HIS LYS GLU GLY

• Molecule 37: Small ribosomal subunit protein uS4

Chain BD:



MET G2 K7 R8 K9 S10 Y11 D12 T13 P14 K15 H16 Q19 A20 A21 R22 M23 A24 T25 E26 V27 E28 L29 L30 K31 K32 Y33 G34 L35 R36 N37 K38 K39 E40 L41 W42 K43 A44 V45 S46 I47 L48 R49 R50 Y51 R52 A53 D54 A55 R56 R57 I58 L59 A60 E61 S62 A63 E64

T65 E66 L67 S68 G69 H70 L71 K72 T73 E74 S75 D76 Q77 I78 L79 A80 R81 L82 I83 R84 F85 S86 V87 L88 P89 S90 D91 A92 N93 I94 D95 D96 I97 L98 A99 L100 Q101 T102 E103 S104 I105 L106 E107 R108 R109 L110 Q111 T112 Q113 V114 Y115 R116 L117 G118 L119 A120 R121 T122 P123 K124

Q125 A126 R127 Q128 F129 I130 T131 H132 G133 H134 I135 A136 I137 N138 G139 Q140 K141 A142 T143 V144 P145 G146 I147 L148 I149 S150 K151 E152 E153 E154 M155 Q156 I157 D158 Y159 Y160 G161 N162 S163 P164 L165 T166 N167 E168 S169 H170 A171 E172 R173 P174 A175 Q176 I177 A178 THR SER VAL ALA GLY LYS

GLU GLU

• Molecule 38: 30S ribosomal protein S4e

Chain BE:



V1 G2 K3 P11 N12 S13 W14 Q15 I16 S17 K18 K19 S20 N21 K22 T27 R28 P31 H32 N33 K34 Q35 Q36 S37 I38 P39 L40 L44 R45 D46 M47 L48 G49 I50 V51 D52 T53 R54 A55 E56 A57 K58 R59 V60 L61 S62 E63 G64 N65 V66 L67 V68 D69 G70 V71

K74 D75 L76 R77 V80 G81 L82 L83 D84 V85 I86 T87 I88 P89 L90 E91 N92 V93 A94 Y95 R96 V97 L98 L99 D100 R101 K102 G103 R104 L105 E106 V107 H108 K109 L110 A111 D112 M113 N114 A115 N116 K117 L118 C119 R120 I121 N122 G123 K124 T125 I126 V127 K128 G129 G130 A131 V132 Q133 L134

N135 L136 N137 D138 G139 T140 N141 L142 I143 G144 S145 N146 D147 Y148 K149 P150 K151 D152 S153 L154 I155 L156 T157 M158 P159 G160 K161 E162 I163 V164 K165 H166 I167 K168 Y169 E170 V171 G172 N173 L174 A175 M176 I177 V178 G179 G180 R181 H182 T183 G184 E185 I186 I189 K190 E191 I192 N193 T194 V195

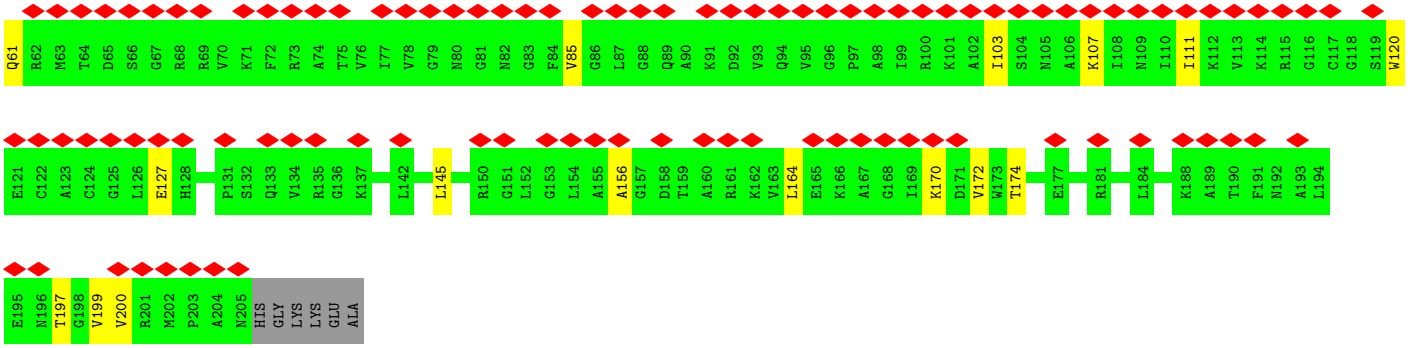
R196 R199 T202 V203 S204 I205 S206 G207 E208 Y209 D210 F211 E212 T213 I214 E215 D216 F217 V218 V219 V220 I221 G222 E223 N224 E225 P226 E227 I228 K229 L230 G231 G232 E233 V234 V235 E236

• Molecule 39: Small ribosomal subunit protein uS5

Chain BF:



MET ALA TYR GLU TYR E6 E7 E8 W9 V10 P11 Q12 T13 R14 L15 G16 K17 L18 V19 Q20 E21 G22 Q23 I24 T25 S26 M27 D28 E29 V30 I31 D32 S33 G34 L35 P36 V37 R38 E39 S40 Q41 I42 I43 D44 I45 L46 L47 P48 D49 L50 E51 D52 E53 V54 L55 D56 I57 N58 M59 V60



• Molecule 40: 30S ribosomal protein S6e

Chain BG:

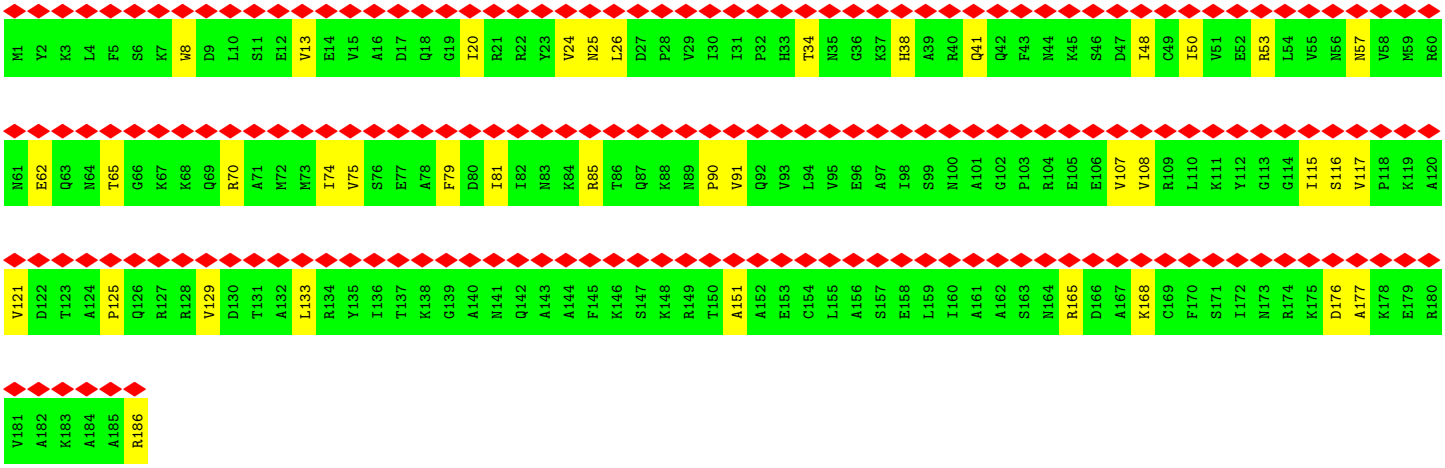




• Molecule 41: Small ribosomal subunit protein uS7

Chain BH:

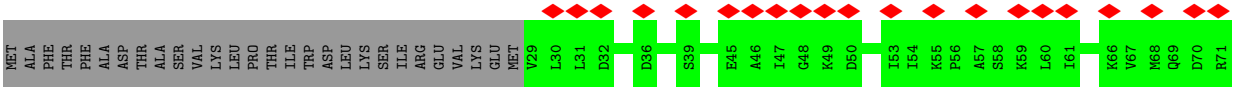


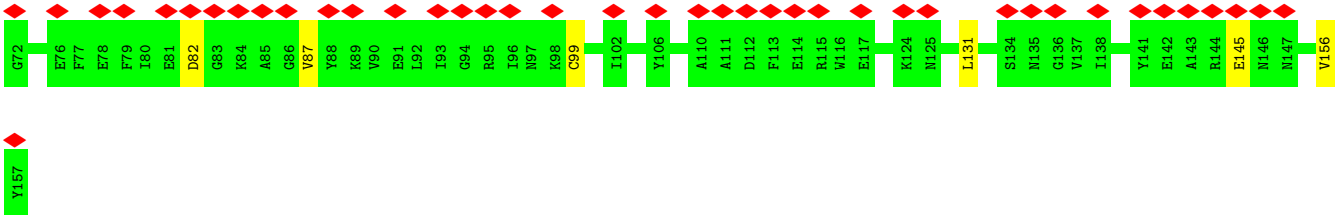


• Molecule 42: 30S ribosomal protein S8

Chain BI:



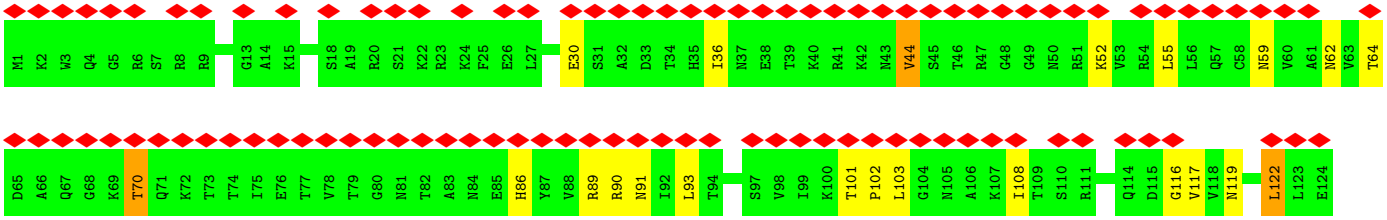




• Molecule 43: Small ribosomal subunit protein eS8

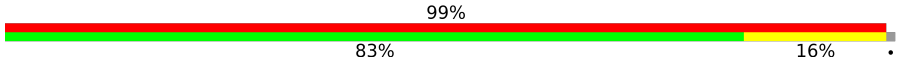
Chain BJ:

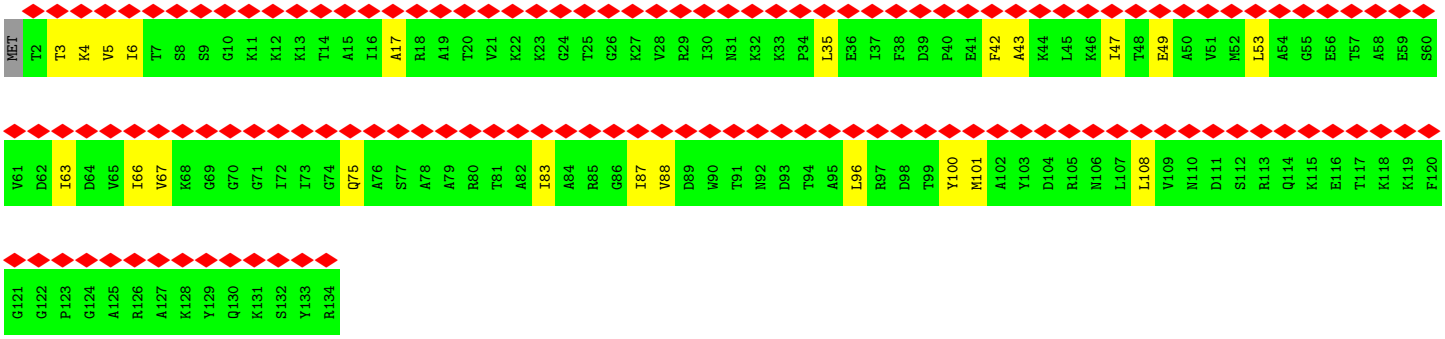




• Molecule 44: Small ribosomal subunit protein uS9

Chain BK:

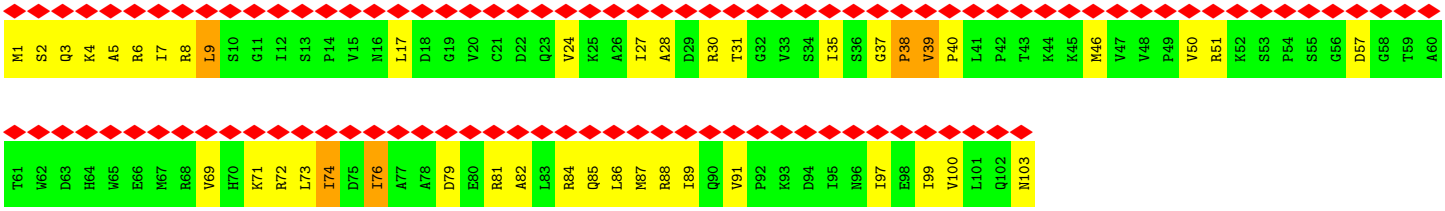




• Molecule 45: Small ribosomal subunit protein uS10

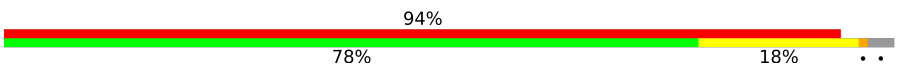
Chain BL:

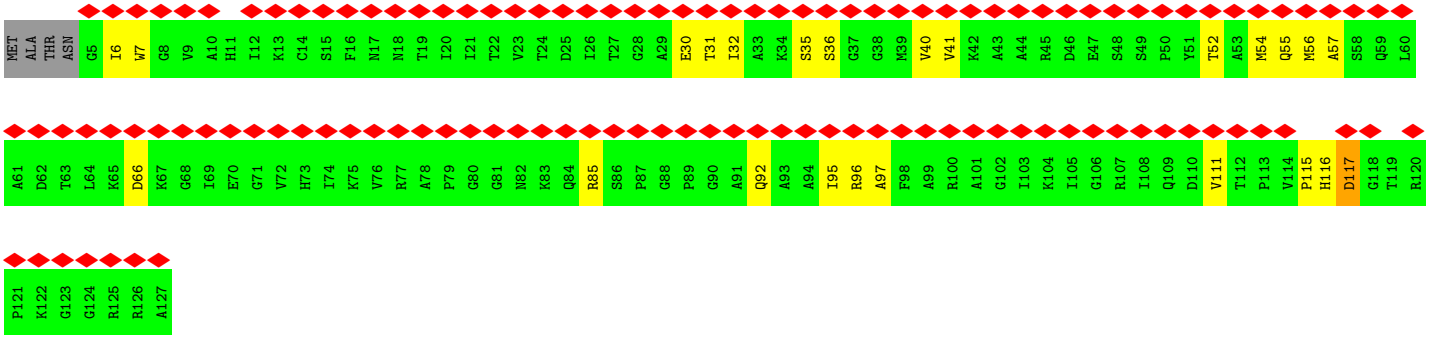




• Molecule 46: Small ribosomal subunit protein uS11

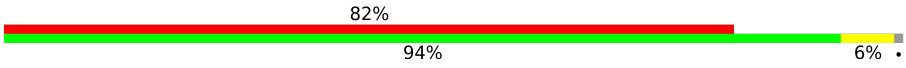
Chain BM:

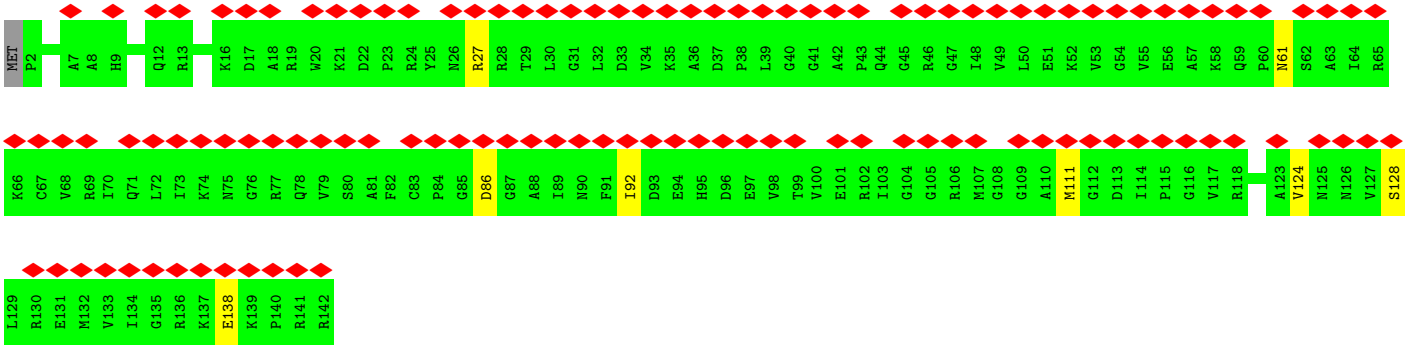




• Molecule 47: Small ribosomal subunit protein uS12

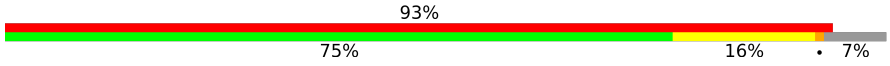
Chain BN:

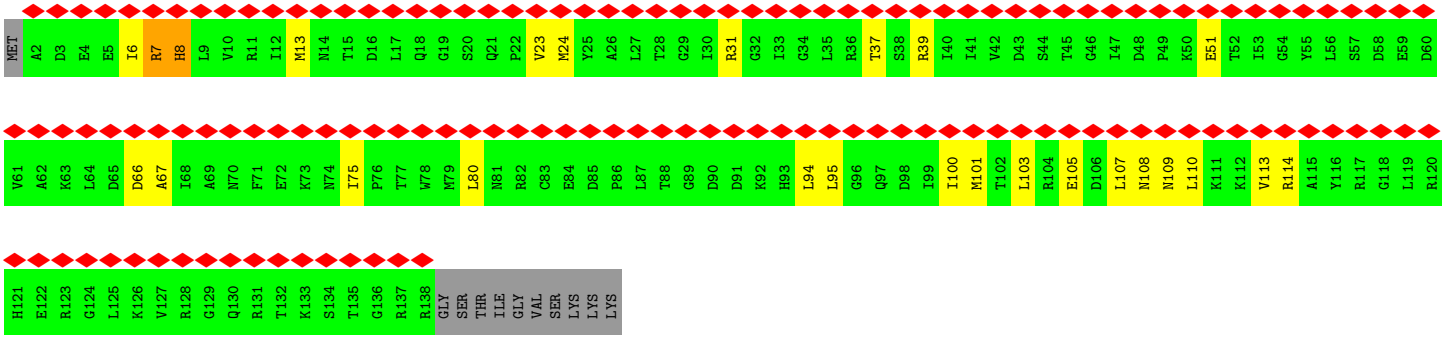




• Molecule 48: Small ribosomal subunit protein uS13

Chain BO:

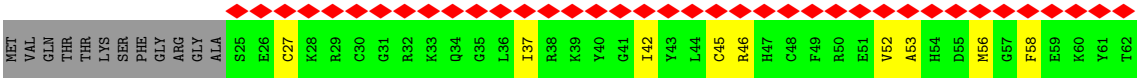




• Molecule 49: Small ribosomal subunit protein uS14

Chain BP:





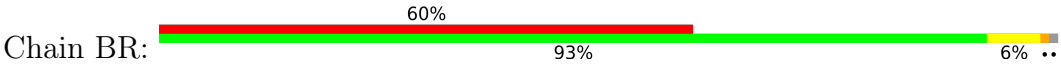
• Molecule 50: Small ribosomal subunit protein uS15

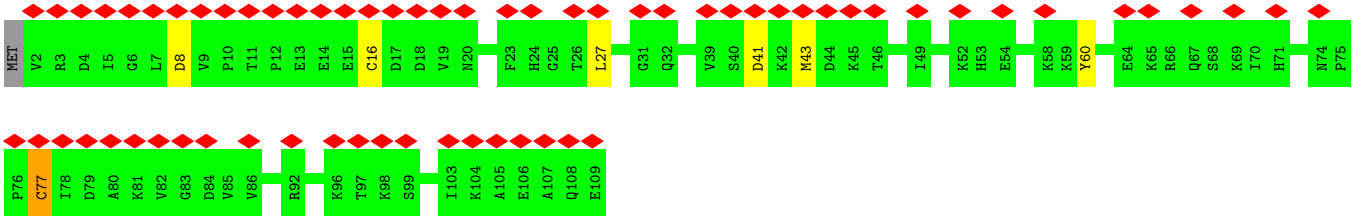
Chain BQ:



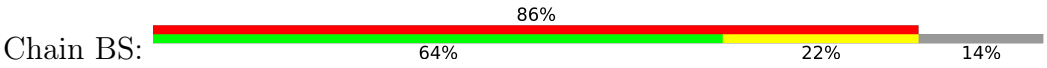


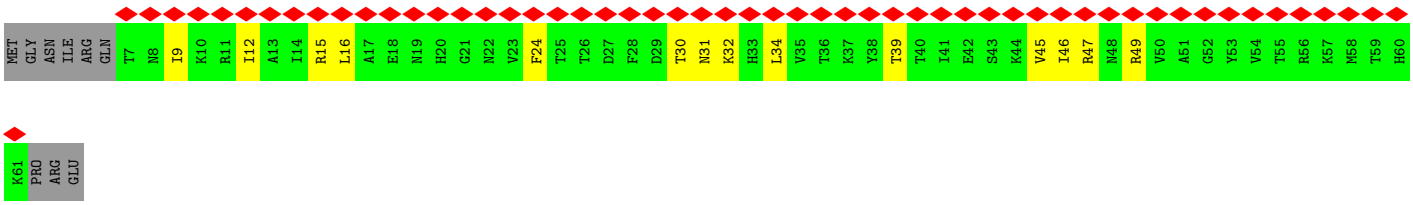
• Molecule 51: Small ribosomal subunit protein uS17



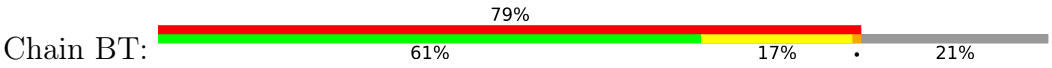


• Molecule 52: Small ribosomal subunit protein eS17



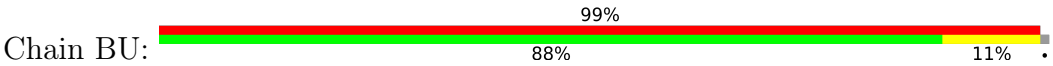


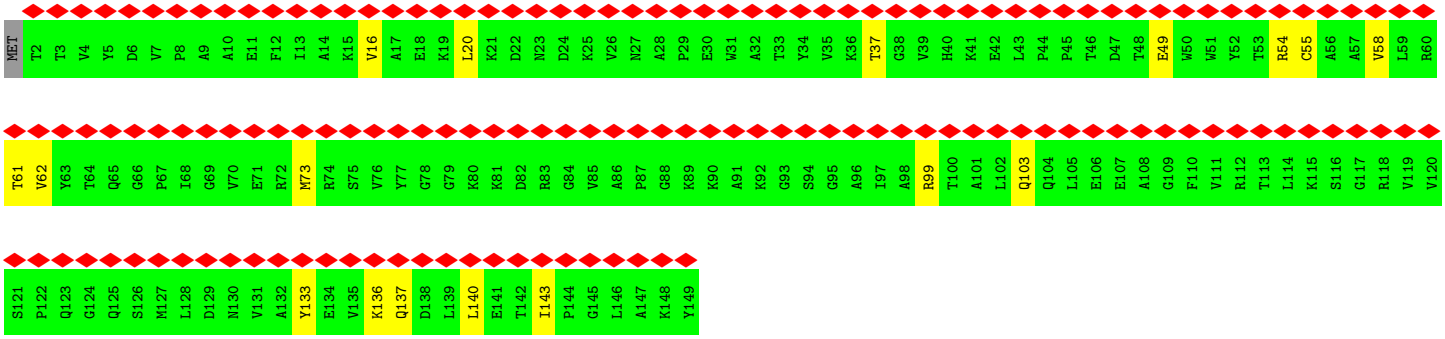
• Molecule 53: Small ribosomal subunit protein uS19





• Molecule 54: 30S ribosomal protein S19e

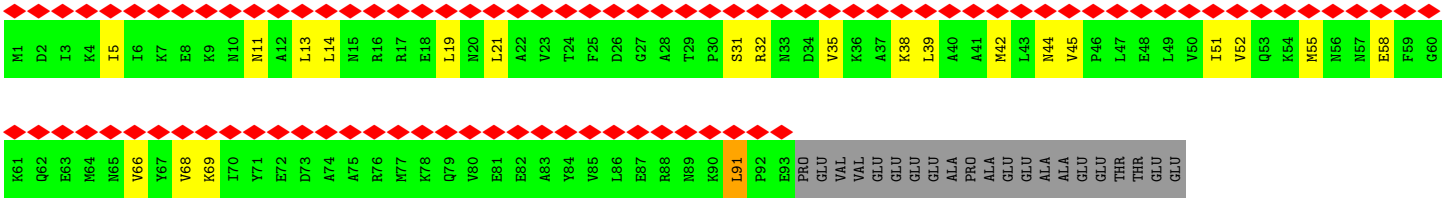




• Molecule 55: Small ribosomal subunit protein eS24

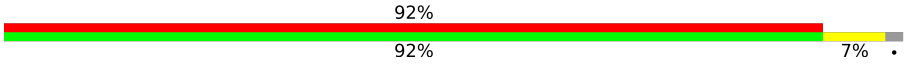
Chain BV:

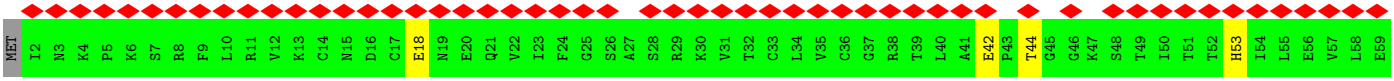




• Molecule 56: Small ribosomal subunit protein eS27

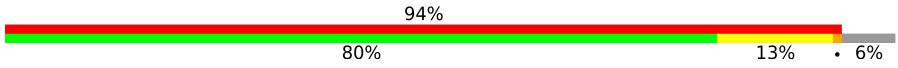
Chain BY:

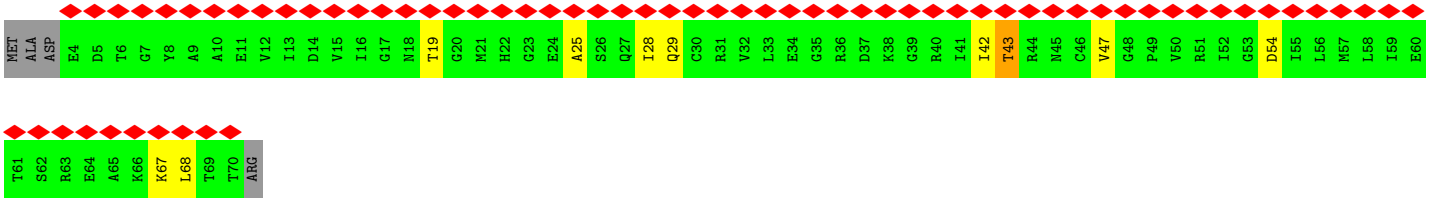




• Molecule 57: Small ribosomal subunit protein eS28

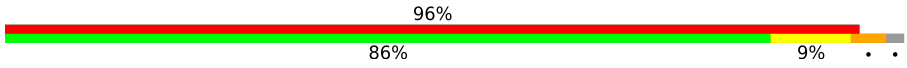
Chain BZ:

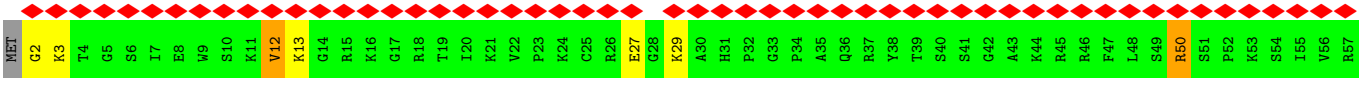




• Molecule 58: DUF5350 domain-containing protein

Chain Ba:

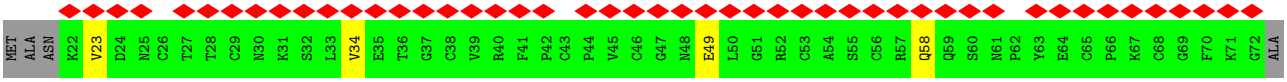




• Molecule 59: Putative Zn-ribbon RNA-binding protein with a function in translation

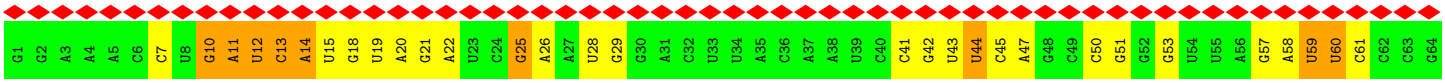
Chain Bc:

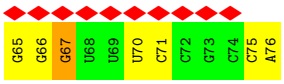




• Molecule 60: P/E-RNA







• Molecule 61: mRNA





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38077	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	1.196	Depositor
Minimum map value	-0.590	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.047	Depositor
Recommended contour level	0.33	Depositor
Map size (Å)	446.4, 446.4, 446.4	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93, 0.93, 0.93	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: ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	1	0.24	0/69829	0.67	13/108904 (0.0%)
2	2	0.21	0/2999	0.65	0/4671
3	4	0.21	0/35333	0.66	3/55109 (0.0%)
4	AA	0.14	0/1821	0.37	0/2454
5	AB	0.14	0/2620	0.35	0/3541
6	AC	0.13	0/1943	0.34	0/2620
7	AD	0.17	0/1328	0.42	0/1784
8	AE	0.16	0/1378	0.38	0/1849
9	AF	0.14	0/864	0.39	0/1165
10	AG	0.14	0/1102	0.37	0/1472
11	AI	0.15	0/1016	0.34	0/1363
12	AL	0.14	0/1102	0.37	0/1470
13	AM	0.13	0/1628	0.34	0/2173
14	AN	0.12	0/1285	0.34	0/1720
15	AO	0.14	0/1369	0.35	0/1846
16	AP	0.12	0/966	0.31	0/1299
17	AQ	0.13	0/1204	0.32	0/1598
18	AR	0.13	0/460	0.34	0/614
19	AS	0.11	0/775	0.27	0/1033
20	AT	0.14	0/1176	0.34	0/1575
21	AU	0.13	0/637	0.35	0/852
22	AV	0.13	0/911	0.33	0/1224
23	AW	0.13	0/514	0.29	0/683
24	AX	0.14	0/530	0.40	0/704
25	AY	0.15	0/1216	0.39	0/1634
26	AZ	0.20	0/689	0.48	0/934
27	Aa	0.15	0/730	0.36	0/980
28	Ab	0.15	0/1007	0.35	0/1344
29	Ad	0.11	0/442	0.32	0/582
30	Af	0.15	0/432	0.29	0/578
31	Ag	0.13	0/363	0.40	0/476
32	Ah	0.14	0/774	0.31	0/1027

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	Ai	0.18	0/727	0.40	0/968
34	BA	0.13	0/1541	0.34	0/2078
35	BB	0.14	0/1544	0.34	0/2097
36	BC	0.16	0/1493	0.43	0/2003
37	BD	0.13	0/1447	0.32	0/1951
38	BE	0.12	0/1856	0.30	0/2504
39	BF	0.13	0/1530	0.31	0/2067
40	BG	0.14	0/930	0.35	0/1251
41	BH	0.17	0/1486	0.42	0/1996
42	BI	0.14	0/1010	0.32	0/1361
43	BJ	0.15	0/974	0.36	0/1304
44	BK	0.16	0/1027	0.41	0/1376
45	BL	0.19	0/812	0.49	0/1097
46	BM	0.14	0/913	0.35	0/1229
47	BN	0.12	0/1110	0.31	0/1485
48	BO	0.25	0/1102	0.69	5/1481 (0.3%)
49	BP	0.17	0/324	0.51	0/427
50	BQ	0.13	0/1248	0.31	0/1680
51	BR	0.12	0/865	0.31	0/1170
52	BS	0.16	0/456	0.45	0/613
53	BT	0.18	0/898	0.51	0/1203
54	BU	0.16	0/1168	0.42	0/1582
55	BV	0.15	0/756	0.37	0/1015
56	BY	0.16	0/449	0.40	0/602
57	BZ	0.17	0/509	0.43	0/683
58	Ba	0.13	0/445	0.33	0/588
59	Bc	0.12	0/384	0.31	0/516
60	C	0.22	0/1711	0.74	0/2662
61	D	0.23	0/73	0.64	0/110
All	All	0.20	0/167231	0.59	21/248377 (0.0%)

There are no bond length outliers.

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	2222	C	O4'-C1'-N1	15.63	119.44	108.50
1	1	2221	A	O4'-C1'-N9	12.88	117.51	108.50
48	BO	8	HIS	N-CA-CB	11.62	127.20	110.12
1	1	2221	A	N9-C1'-C2'	10.18	123.19	112.00
1	1	2222	C	N1-C1'-C2'	9.95	122.95	112.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	62358	0	31379	270	0
2	2	2683	0	1358	10	0
3	4	31571	0	15901	154	0
4	AA	1783	0	1844	12	0
5	AB	2570	0	2632	25	0
6	AC	1914	0	1949	13	0
7	AD	1305	0	1344	33	0
8	AE	1358	0	1414	25	0
9	AF	858	0	889	16	0
10	AG	1088	0	1161	6	0
11	AI	1005	0	1067	9	0
12	AL	1092	0	1097	9	0
13	AM	1600	0	1648	6	0
14	AN	1265	0	1312	7	0
15	AO	1344	0	1337	11	0
16	AP	957	0	1022	7	0
17	AQ	1190	0	1257	9	0
18	AR	454	0	468	4	0
19	AS	761	0	778	0	0
20	AT	1157	0	1188	5	0
21	AU	629	0	666	2	0
22	AV	900	0	941	5	0
23	AW	504	0	503	5	0
24	AX	528	0	546	10	0
25	AY	1199	0	1227	14	0
26	AZ	683	0	721	15	0
27	Aa	716	0	751	7	0
28	Ab	993	0	1069	5	0
29	Ad	435	0	449	1	0
30	Af	422	0	451	1	0
31	Ag	362	0	388	2	0
32	Ah	758	0	793	0	0
33	Ai	716	0	739	8	0
34	BA	1519	0	1580	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	BB	1517	0	1532	27	0
36	BC	1471	0	1528	24	0
37	BD	1422	0	1458	14	0
38	BE	1831	0	1911	22	0
39	BF	1512	0	1558	18	0
40	BG	917	0	955	7	0
41	BH	1468	0	1519	26	0
42	BI	994	0	1016	3	0
43	BJ	966	0	1013	12	0
44	BK	1016	0	1070	19	0
45	BL	800	0	844	32	0
46	BM	899	0	924	20	0
47	BN	1094	0	1133	6	0
48	BO	1090	0	1114	24	0
49	BP	318	0	312	4	0
50	BQ	1224	0	1275	19	0
51	BR	851	0	871	7	0
52	BS	450	0	469	12	0
53	BT	881	0	876	18	0
54	BU	1145	0	1162	8	0
55	BV	749	0	784	20	0
56	BY	445	0	459	3	0
57	BZ	507	0	520	10	0
58	Ba	437	0	471	6	0
59	Bc	378	0	362	1	0
60	C	1532	0	775	14	0
61	D	66	0	33	0	0
62	AW	1	0	0	0	0
62	Ad	1	0	0	0	0
62	Ag	1	0	0	0	0
62	Ah	1	0	0	0	0
62	Ai	1	0	0	0	0
62	BF	1	0	0	0	0
62	BP	1	0	0	0	0
62	BR	1	0	0	0	0
62	BY	1	0	0	0	0
62	Bc	1	0	0	0	0
All	All	154667	0	107813	1049	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 1049 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)
53:BT:68:LEU:HD11	53:BT:86:VAL:HG12	1.50	0.94
14:AN:168:MET:HE2	14:AN:168:MET:HA	1.52	0.89
1:1:2174:C:H3'	1:1:2175:G:C8	2.15	0.82
9:AF:122:VAL:O	9:AF:126:VAL:HG23	1.83	0.79
48:BO:103:LEU:O	48:BO:107:LEU:HD13	1.83	0.78

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AA	234/237 (99%)	225 (96%)	9 (4%)	0	100	100
5	AB	333/337 (99%)	331 (99%)	1 (0%)	1 (0%)	36	60
6	AC	250/253 (99%)	243 (97%)	7 (3%)	0	100	100
7	AD	163/165 (99%)	159 (98%)	4 (2%)	0	100	100
8	AE	172/177 (97%)	168 (98%)	3 (2%)	1 (1%)	21	44
9	AF	115/130 (88%)	112 (97%)	3 (3%)	0	100	100
10	AG	136/142 (96%)	135 (99%)	1 (1%)	0	100	100
11	AI	130/132 (98%)	129 (99%)	1 (1%)	0	100	100
12	AL	144/147 (98%)	138 (96%)	6 (4%)	0	100	100
13	AM	193/196 (98%)	189 (98%)	4 (2%)	0	100	100
14	AN	157/172 (91%)	144 (92%)	13 (8%)	0	100	100
15	AO	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
16	AP	123/126 (98%)	123 (100%)	0	0	100	100
17	AQ	147/152 (97%)	147 (100%)	0	0	100	100
18	AR	55/58 (95%)	55 (100%)	0	0	100	100
19	AS	94/97 (97%)	94 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	AT	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
21	AU	79/82 (96%)	79 (100%)	0	0	100	100
22	AV	114/117 (97%)	113 (99%)	1 (1%)	0	100	100
23	AW	60/62 (97%)	60 (100%)	0	0	100	100
24	AX	64/67 (96%)	64 (100%)	0	0	100	100
25	AY	151/160 (94%)	145 (96%)	6 (4%)	0	100	100
26	AZ	93/95 (98%)	88 (95%)	4 (4%)	1 (1%)	11	29
27	Aa	84/90 (93%)	84 (100%)	0	0	100	100
28	Ab	124/129 (96%)	124 (100%)	0	0	100	100
29	Ad	53/56 (95%)	51 (96%)	2 (4%)	0	100	100
30	Af	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
31	Ag	44/49 (90%)	43 (98%)	1 (2%)	0	100	100
32	Ah	90/92 (98%)	90 (100%)	0	0	100	100
33	Ai	90/97 (93%)	86 (96%)	4 (4%)	0	100	100
34	BA	186/196 (95%)	180 (97%)	6 (3%)	0	100	100
35	BB	193/218 (88%)	189 (98%)	4 (2%)	0	100	100
36	BC	190/311 (61%)	178 (94%)	11 (6%)	1 (0%)	24	48
37	BD	175/186 (94%)	174 (99%)	1 (1%)	0	100	100
38	BE	234/236 (99%)	226 (97%)	8 (3%)	0	100	100
39	BF	198/211 (94%)	192 (97%)	6 (3%)	0	100	100
40	BG	121/139 (87%)	113 (93%)	8 (7%)	0	100	100
41	BH	184/186 (99%)	177 (96%)	7 (4%)	0	100	100
42	BI	127/157 (81%)	119 (94%)	8 (6%)	0	100	100
43	BJ	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
44	BK	131/134 (98%)	122 (93%)	9 (7%)	0	100	100
45	BL	101/103 (98%)	94 (93%)	6 (6%)	1 (1%)	12	32
46	BM	121/127 (95%)	115 (95%)	5 (4%)	1 (1%)	16	37
47	BN	139/142 (98%)	139 (100%)	0	0	100	100
48	BO	135/148 (91%)	133 (98%)	2 (2%)	0	100	100
49	BP	36/50 (72%)	31 (86%)	4 (11%)	1 (3%)	4	9
50	BQ	149/152 (98%)	146 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
51	BR	106/109 (97%)	102 (96%)	4 (4%)	0	100 100
52	BS	53/64 (83%)	50 (94%)	3 (6%)	0	100 100
53	BT	106/137 (77%)	101 (95%)	5 (5%)	0	100 100
54	BU	146/149 (98%)	143 (98%)	3 (2%)	0	100 100
55	BV	91/114 (80%)	90 (99%)	1 (1%)	0	100 100
56	BY	56/59 (95%)	53 (95%)	3 (5%)	0	100 100
57	BZ	65/71 (92%)	64 (98%)	1 (2%)	0	100 100
58	Ba	54/57 (95%)	52 (96%)	1 (2%)	1 (2%)	6 17
59	Bc	49/55 (89%)	47 (96%)	2 (4%)	0	100 100
All	All	7126/7627 (93%)	6929 (97%)	189 (3%)	8 (0%)	49 73

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
36	BC	60	LYS
45	BL	38	PRO
49	BP	53	ALA
46	BM	117	ASP
58	Ba	50	ARG

5.3.2 Protein sidechains (i)

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	AA	184/185 (100%)	182 (99%)	2 (1%)	65 85
5	AB	277/278 (100%)	275 (99%)	2 (1%)	76 90
6	AC	199/200 (100%)	195 (98%)	4 (2%)	48 76
7	AD	145/145 (100%)	142 (98%)	3 (2%)	47 75
8	AE	149/151 (99%)	148 (99%)	1 (1%)	76 90
9	AF	89/100 (89%)	85 (96%)	4 (4%)	24 52
10	AG	115/119 (97%)	113 (98%)	2 (2%)	53 79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	AI	108/108 (100%)	107 (99%)	1 (1%)	70	87
12	AL	113/114 (99%)	109 (96%)	4 (4%)	32	61
13	AM	166/167 (99%)	164 (99%)	2 (1%)	63	84
14	AN	130/136 (96%)	127 (98%)	3 (2%)	44	73
15	AO	143/144 (99%)	141 (99%)	2 (1%)	59	82
16	AP	103/104 (99%)	100 (97%)	3 (3%)	37	67
17	AQ	120/123 (98%)	119 (99%)	1 (1%)	73	88
18	AR	49/50 (98%)	48 (98%)	1 (2%)	48	76
19	AS	82/83 (99%)	80 (98%)	2 (2%)	43	72
20	AT	122/123 (99%)	119 (98%)	3 (2%)	42	71
21	AU	70/71 (99%)	68 (97%)	2 (3%)	37	67
22	AV	99/100 (99%)	98 (99%)	1 (1%)	68	86
23	AW	55/55 (100%)	53 (96%)	2 (4%)	31	60
24	AX	57/58 (98%)	57 (100%)	0	100	100
25	AY	129/135 (96%)	127 (98%)	2 (2%)	55	80
26	AZ	73/73 (100%)	73 (100%)	0	100	100
27	Aa	78/81 (96%)	78 (100%)	0	100	100
28	Ab	104/106 (98%)	104 (100%)	0	100	100
29	Ad	49/50 (98%)	48 (98%)	1 (2%)	48	76
30	Af	46/47 (98%)	45 (98%)	1 (2%)	45	74
31	Ag	39/40 (98%)	38 (97%)	1 (3%)	40	70
32	Ah	82/82 (100%)	81 (99%)	1 (1%)	63	84
33	Ai	73/77 (95%)	73 (100%)	0	100	100
34	BA	168/175 (96%)	168 (100%)	0	100	100
35	BB	165/186 (89%)	162 (98%)	3 (2%)	51	78
36	BC	154/251 (61%)	145 (94%)	9 (6%)	18	42
37	BD	150/157 (96%)	149 (99%)	1 (1%)	76	90
38	BE	205/205 (100%)	202 (98%)	3 (2%)	57	81
39	BF	163/171 (95%)	160 (98%)	3 (2%)	51	78
40	BG	100/112 (89%)	100 (100%)	0	100	100
41	BH	157/157 (100%)	153 (98%)	4 (2%)	42	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
42	BI	104/129 (81%)	103 (99%)	1 (1%)	68 86
43	BJ	105/105 (100%)	100 (95%)	5 (5%)	23 50
44	BK	105/106 (99%)	104 (99%)	1 (1%)	68 86
45	BL	90/90 (100%)	82 (91%)	8 (9%)	9 23
46	BM	91/94 (97%)	91 (100%)	0	100 100
47	BN	113/114 (99%)	112 (99%)	1 (1%)	70 87
48	BO	119/128 (93%)	119 (100%)	0	100 100
49	BP	33/42 (79%)	33 (100%)	0	100 100
50	BQ	137/138 (99%)	135 (98%)	2 (2%)	57 81
51	BR	99/100 (99%)	98 (99%)	1 (1%)	68 86
52	BS	50/58 (86%)	50 (100%)	0	100 100
53	BT	92/115 (80%)	89 (97%)	3 (3%)	33 63
54	BU	119/120 (99%)	115 (97%)	4 (3%)	32 62
55	BV	82/99 (83%)	78 (95%)	4 (5%)	22 49
56	BY	52/53 (98%)	51 (98%)	1 (2%)	50 77
57	BZ	55/58 (95%)	53 (96%)	2 (4%)	31 60
58	Ba	46/47 (98%)	45 (98%)	1 (2%)	45 74
59	Bc	45/47 (96%)	43 (96%)	2 (4%)	25 53
All	All	6047/6362 (95%)	5937 (98%)	110 (2%)	51 78

5 of 110 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	BC	38	THR
41	BH	38	HIS
59	Bc	58	GLN
54	BU	143	ILE
36	BC	75	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
41	BH	33	HIS
43	BJ	86	HIS
41	BH	35	ASN

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Mol	Chain	Res	Type
42	BI	147	ASN
46	BM	92	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2909/2910 (99%)	442 (15%)	17 (0%)
2	2	125/126 (99%)	18 (14%)	1 (0%)
3	4	1473/1474 (99%)	299 (20%)	10 (0%)
60	C	71/72 (98%)	29 (40%)	4 (5%)
61	D	2/3 (66%)	0	0
All	All	4580/4585 (99%)	788 (17%)	32 (0%)

5 of 788 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	7	A
1	1	8	A
1	1	10	U
1	1	13	G
1	1	24	G

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
60	C	11	A
60	C	14	A
1	1	2210	A
1	1	2168	A
60	C	45	C

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 10 ligands modelled in this entry, 10 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 (i)

There are no chain breaks in this entry.

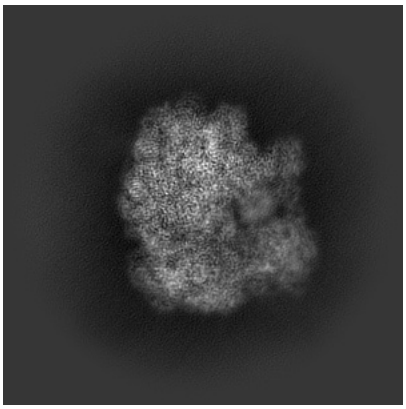
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-66878. These allow visual inspection of the internal detail of the map and identification of artifacts.

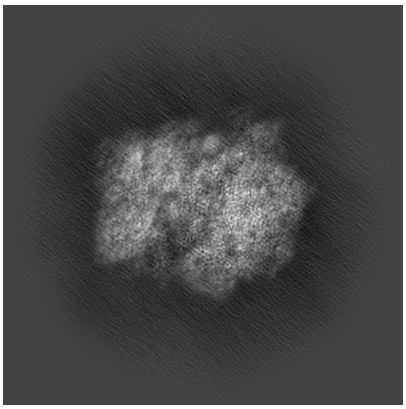
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

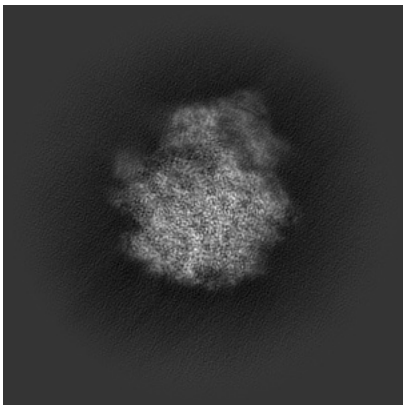
6.1.1 Primary map



X

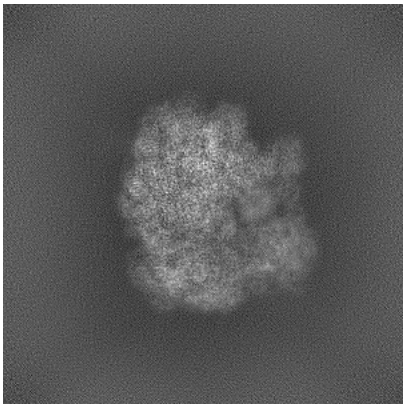


Y

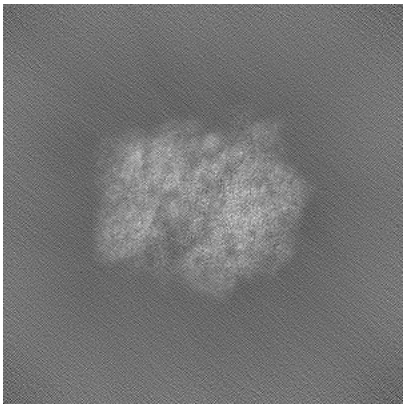


Z

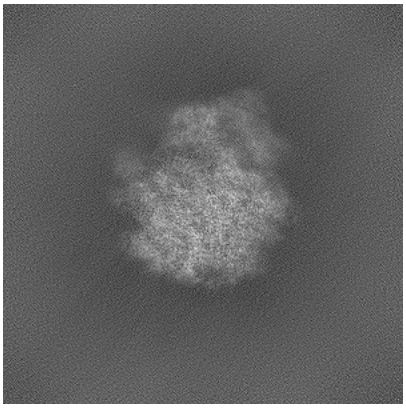
6.1.2 Raw map



X



Y

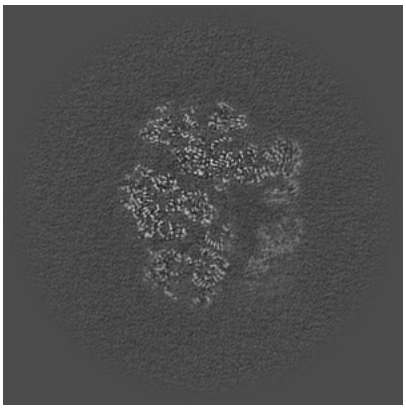


Z

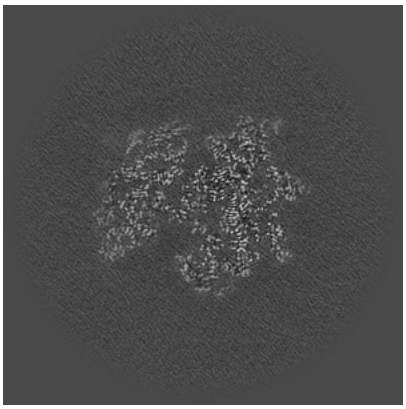
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

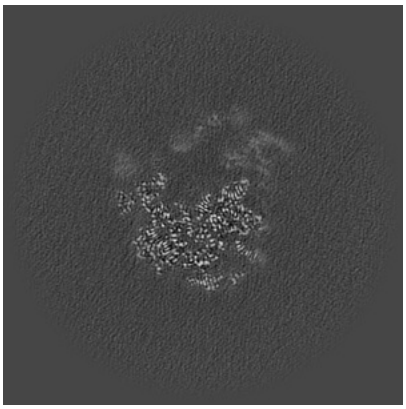
6.2.1 Primary map



X Index: 240

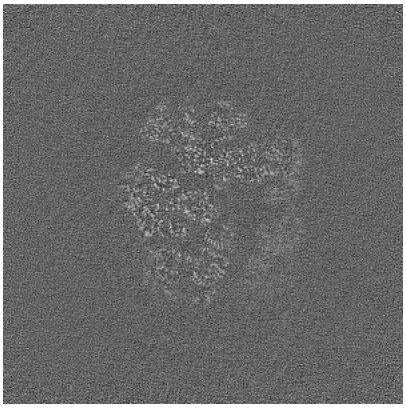


Y Index: 240

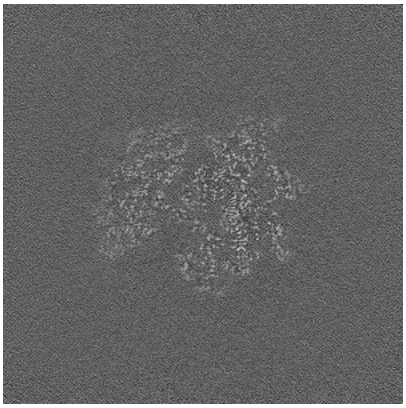


Z Index: 240

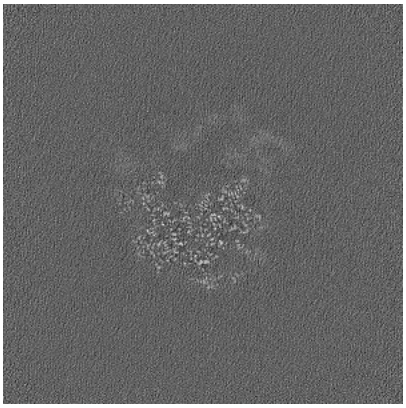
6.2.2 Raw map



X Index: 240



Y Index: 240

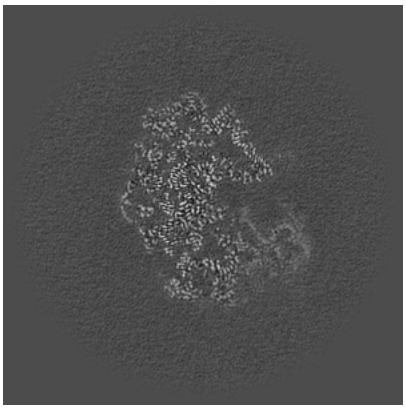


Z Index: 240

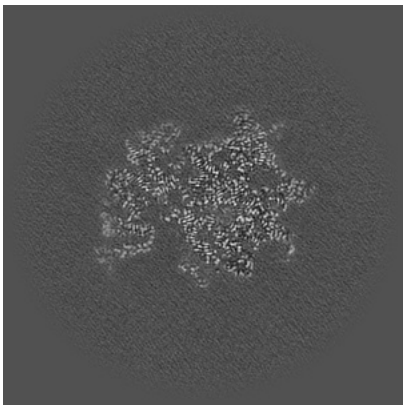
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

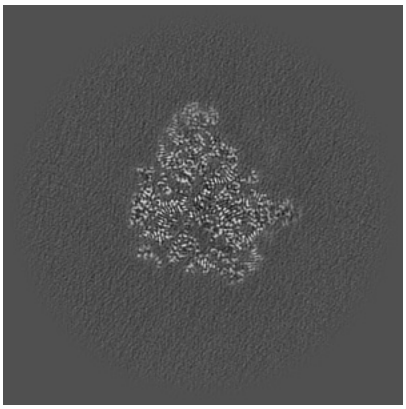
6.3.1 Primary map



X Index: 260

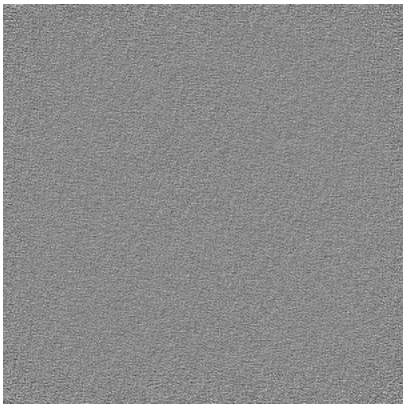


Y Index: 230

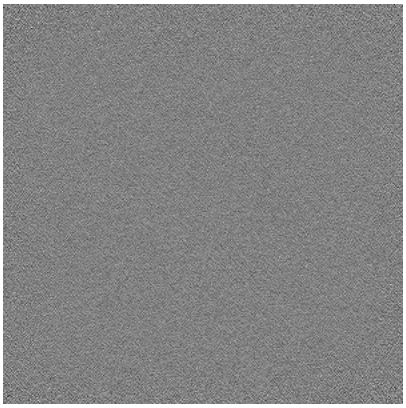


Z Index: 284

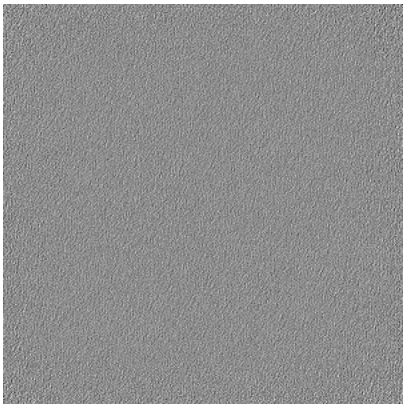
6.3.2 Raw map



X Index: 0



Y Index: 0

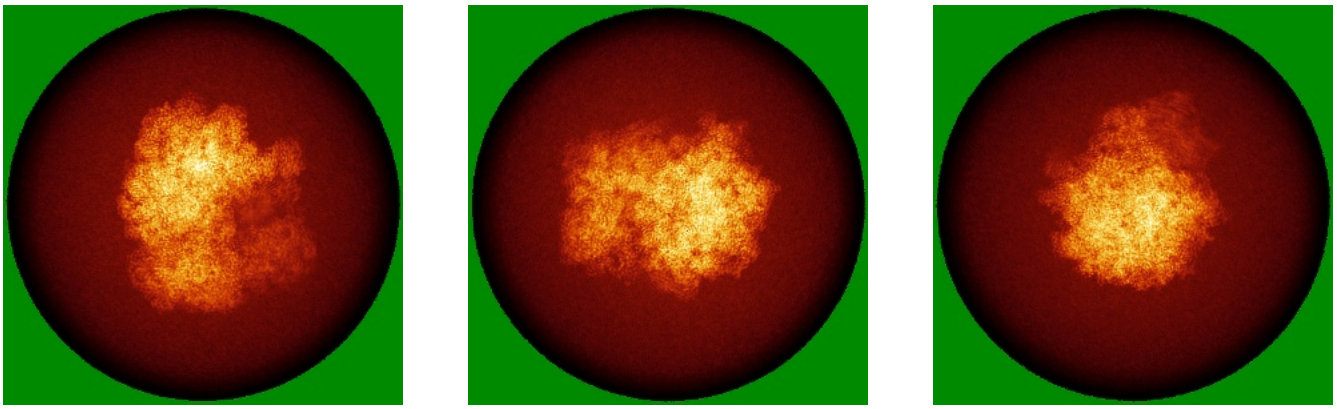


Z Index: 0

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

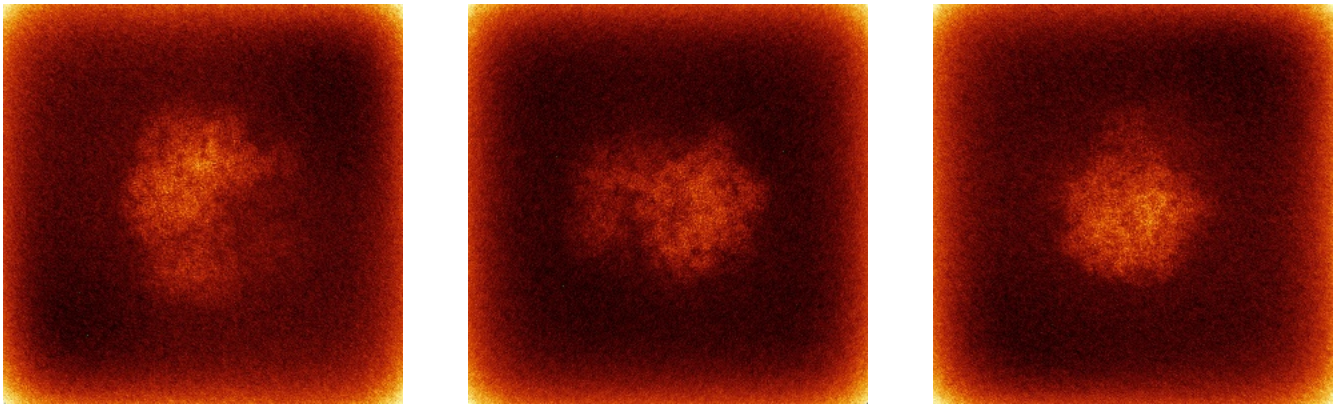
6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map



X Y Z

6.4.2 Raw map

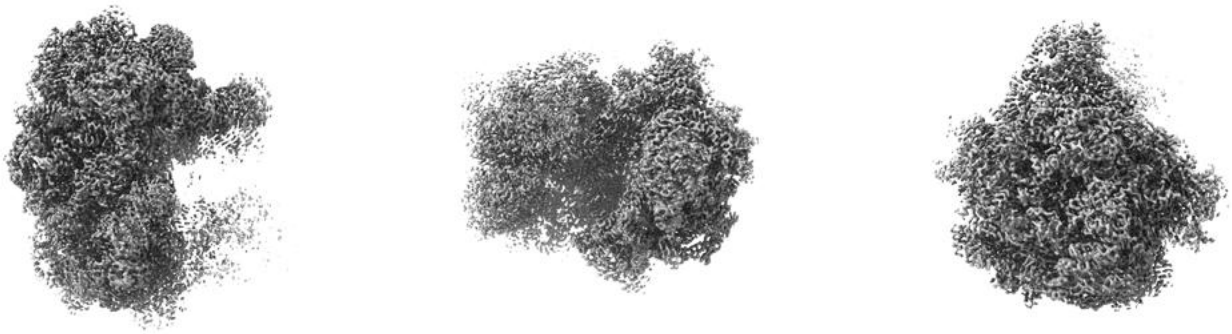


X Y Z

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)

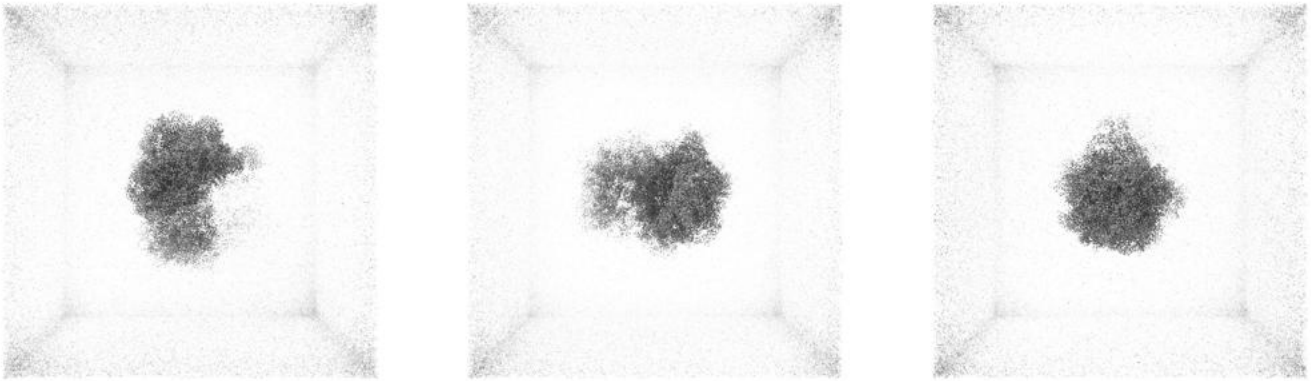
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.33. 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



X Y Z

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.

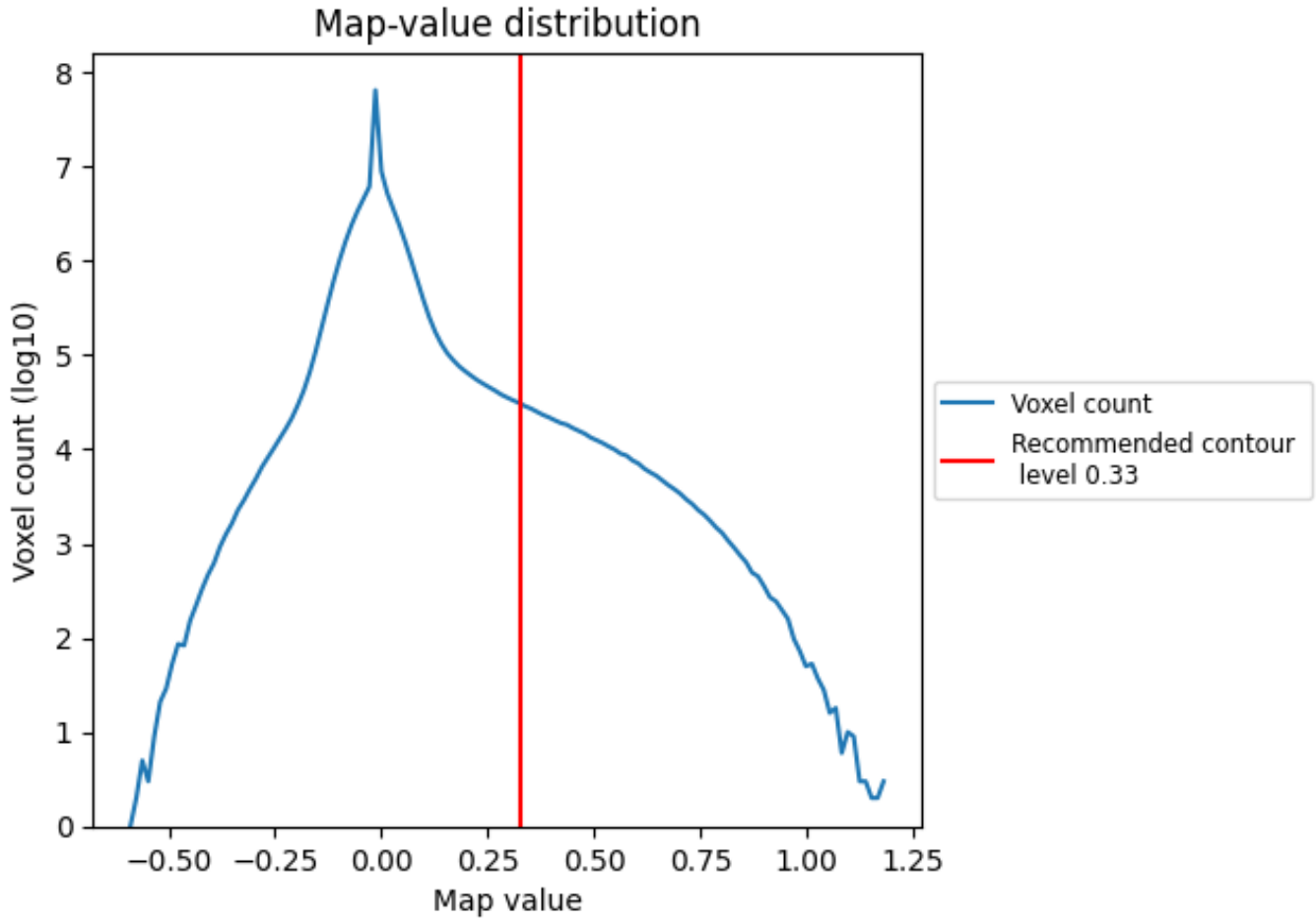
6.6 Mask visualisation (i)

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

7 Map analysis

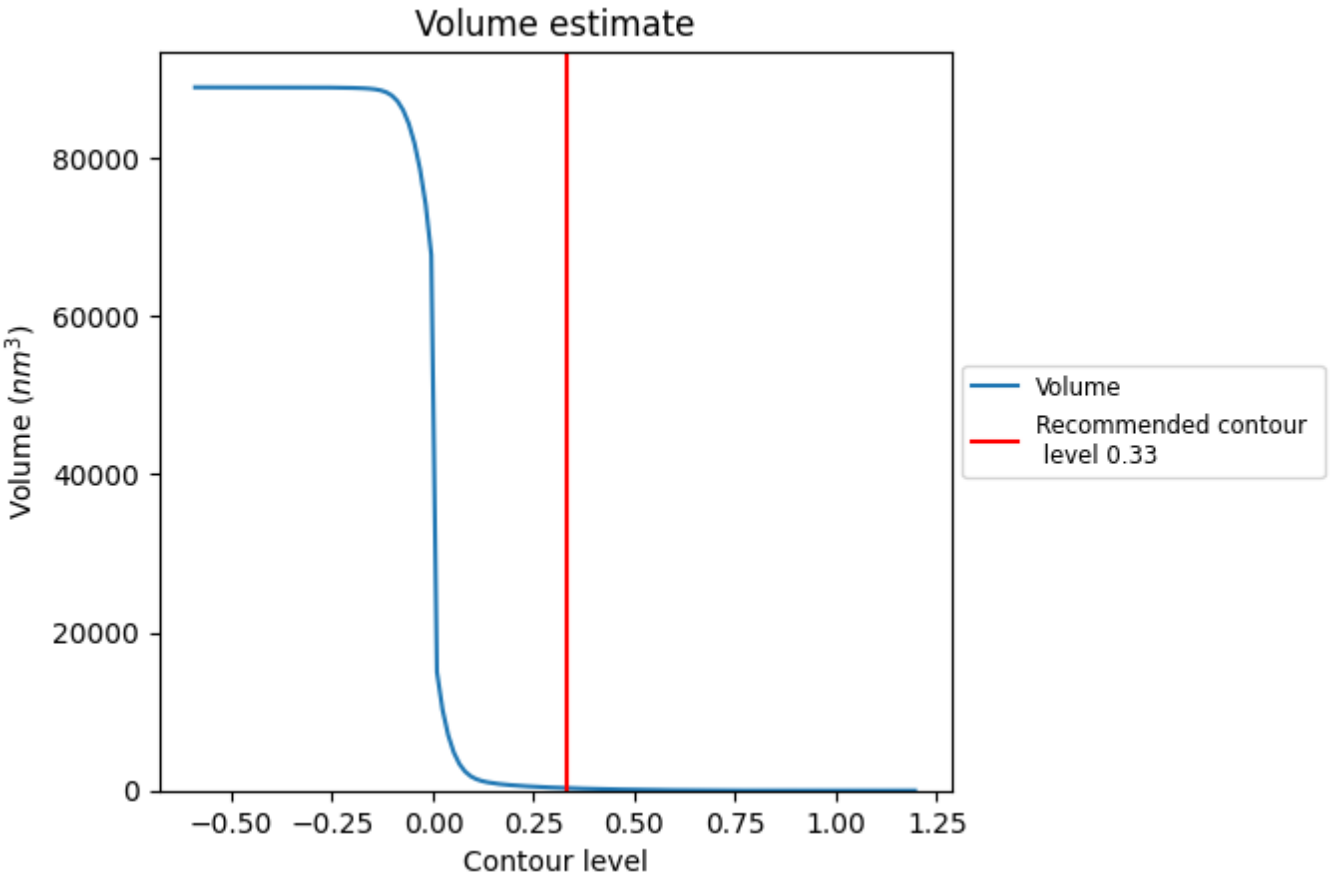
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

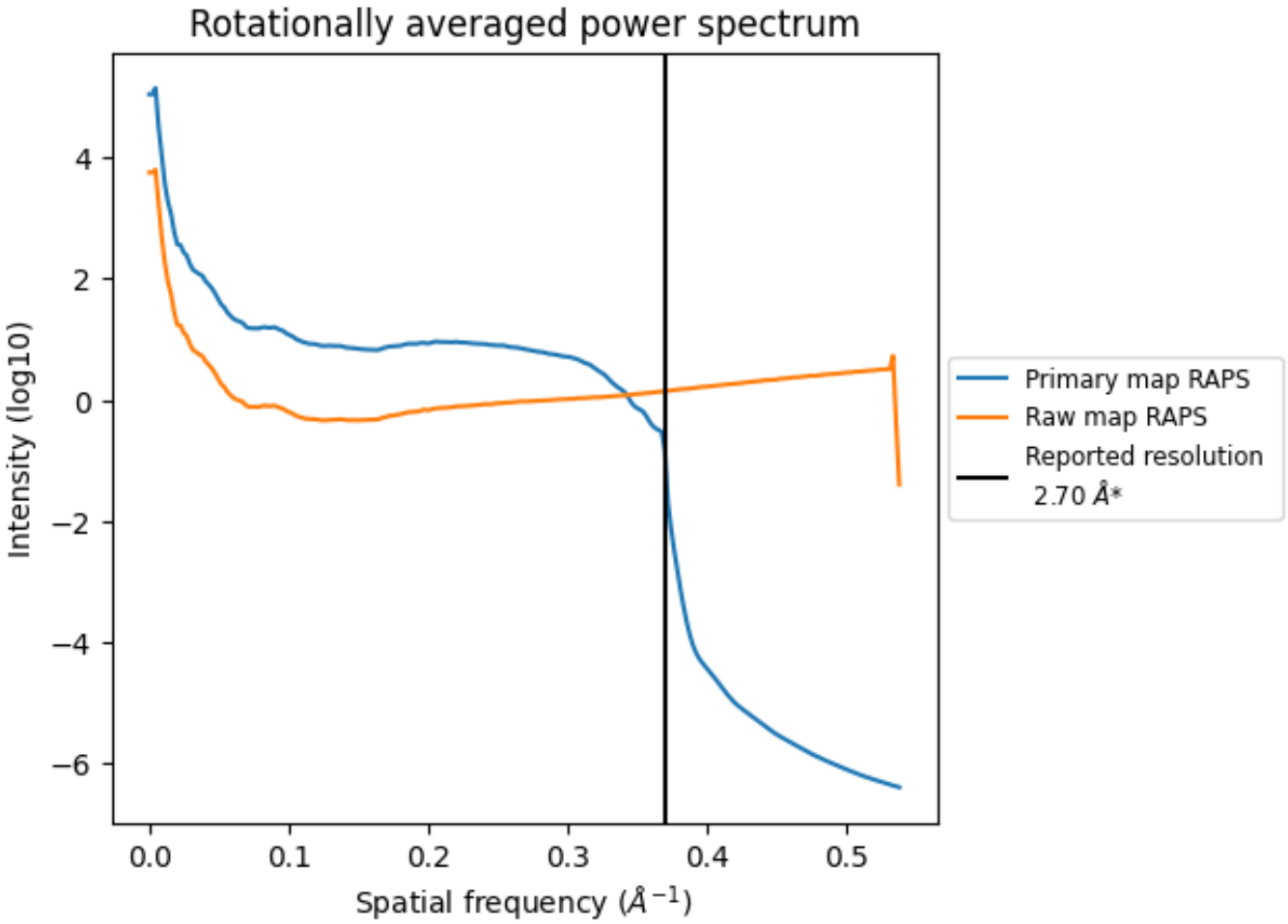
7.2 Volume estimate (i)



The volume at the recommended contour level is 316 nm^3; this corresponds to an approximate mass of 286 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 (i)

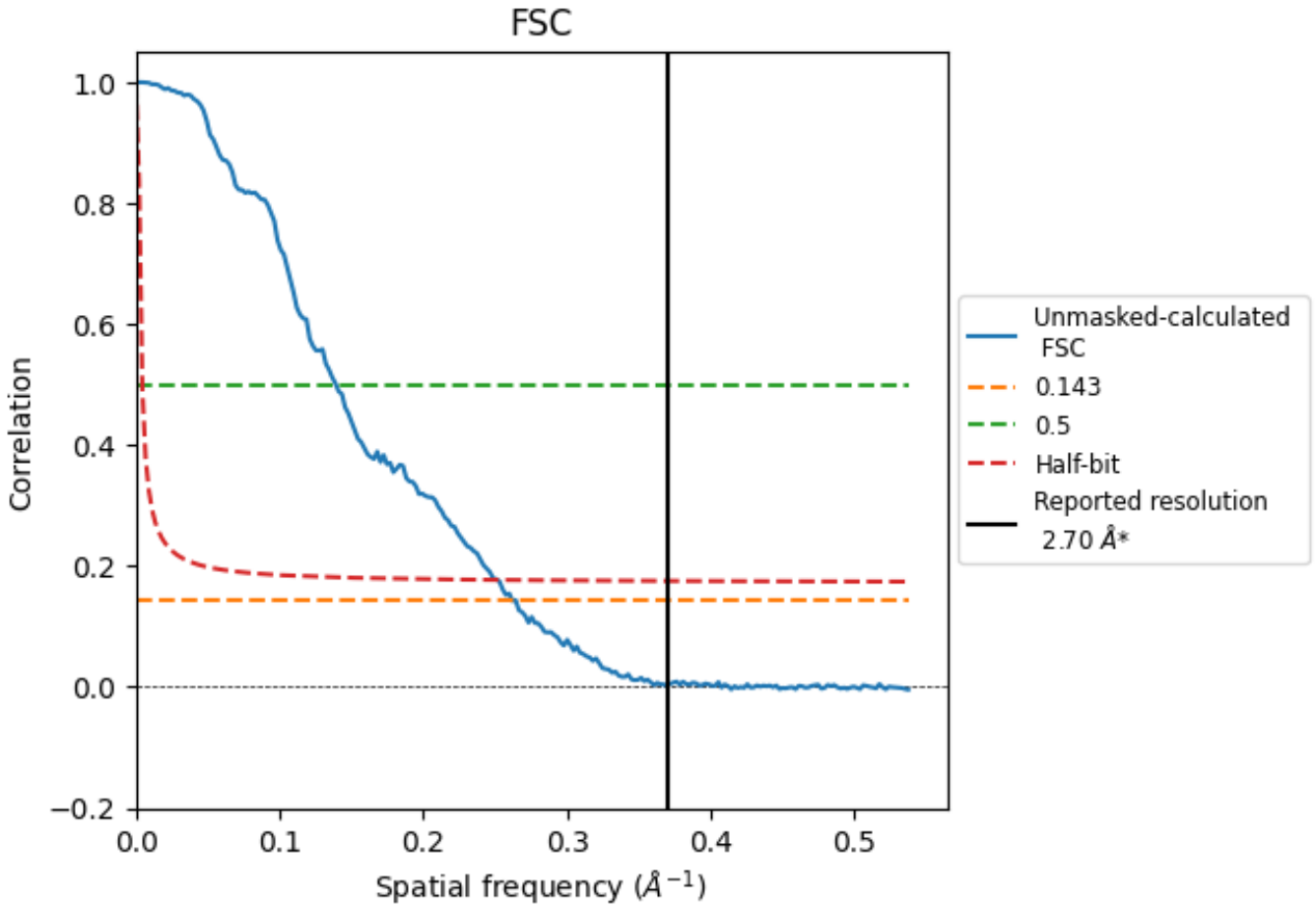


*Reported resolution corresponds to spatial frequency of 0.370 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.370 Å^{-1}

8.2 Resolution estimates (i)

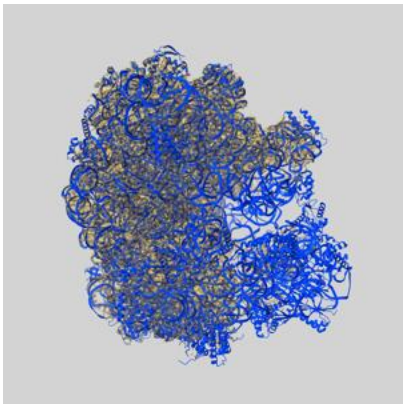
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.82	7.18	3.97

*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 3.82 differs from the reported value 2.7 by more than 10 %

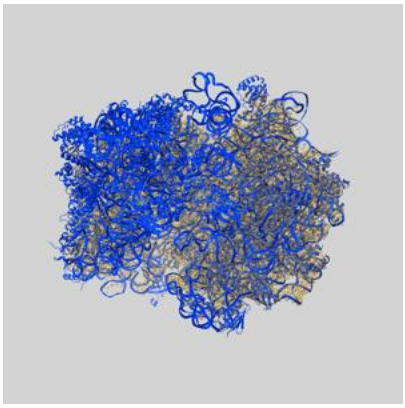
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-66878 and PDB model 9XP4. Per-residue inclusion information can be found in section 3 on page 16.

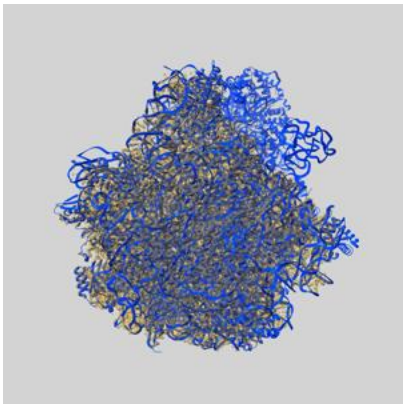
9.1 Map-model overlay



X



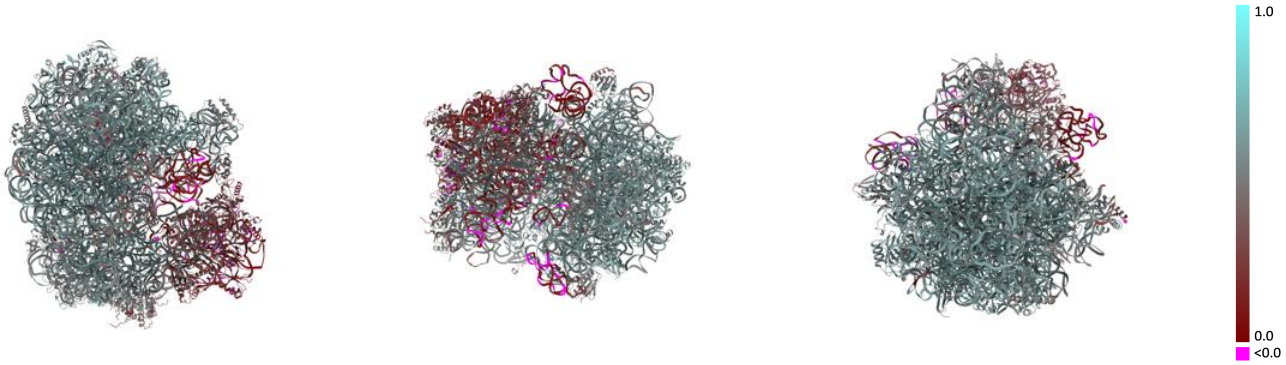
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.33 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.

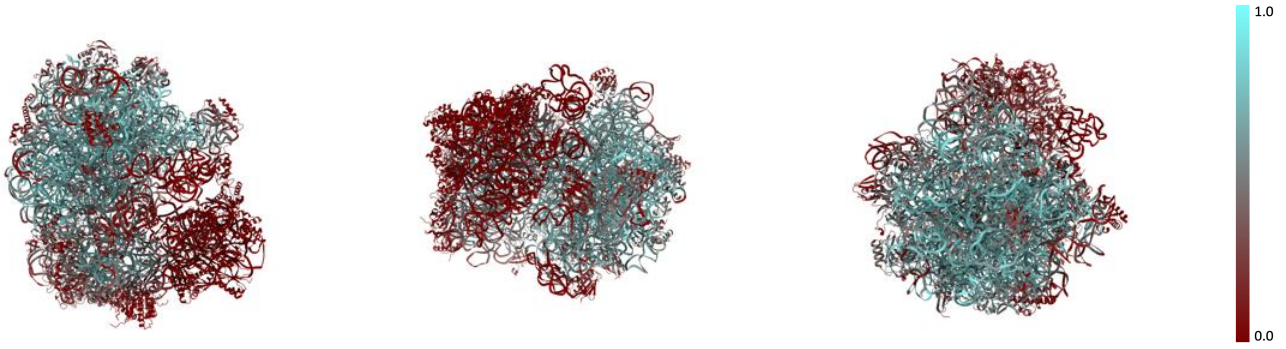
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

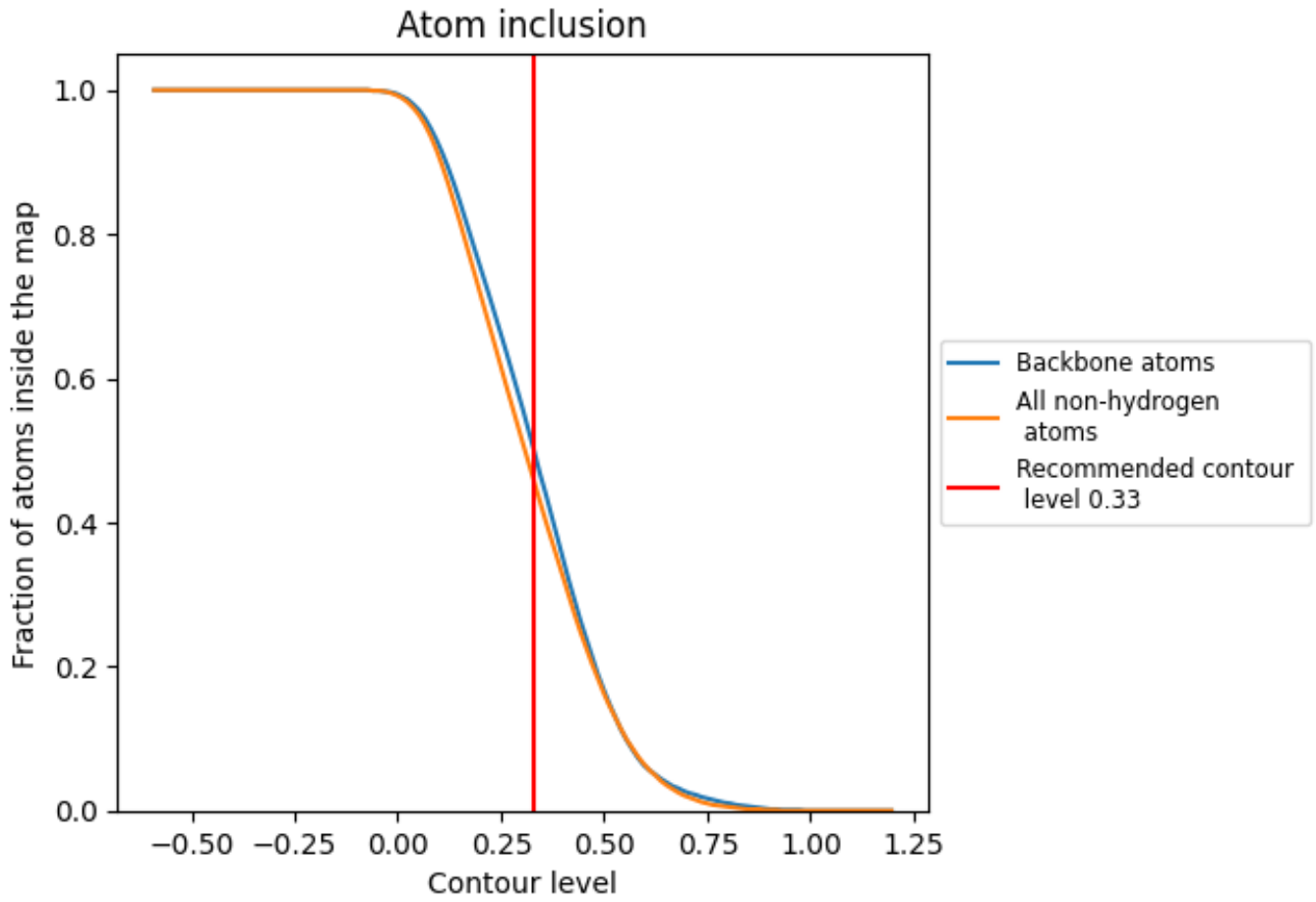
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.33).

9.4 Atom inclusion (i)



At the recommended contour level, 50% of all backbone atoms, 46% 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 (0.33) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4570	0.5130
1	0.6390	0.5500
2	0.5000	0.5440
4	0.3710	0.4740
AA	0.5630	0.5940
AB	0.5700	0.6010
AC	0.4970	0.5850
AD	0.0700	0.4160
AE	0.2440	0.5210
AF	0.1330	0.4690
AG	0.5250	0.5850
AI	0.5760	0.6070
AL	0.4800	0.5720
AM	0.6080	0.6000
AN	0.4990	0.5910
AO	0.3170	0.5380
AP	0.4850	0.5850
AQ	0.5590	0.5910
AR	0.4180	0.5700
AS	0.5940	0.6090
AT	0.5610	0.5920
AU	0.3370	0.5490
AV	0.4510	0.5710
AW	0.5740	0.6070
AX	0.1530	0.5190
AY	0.5260	0.5860
AZ	0.2090	0.4900
Aa	0.5190	0.5910
Ab	0.5330	0.5830
Ad	0.6890	0.6230
Af	0.5990	0.6020
Ag	0.3810	0.5700
Ah	0.5770	0.6100
Ai	0.5270	0.5790
BA	0.1390	0.4470



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Chain	Atom inclusion	Q-score
BB	0.0520	0.4350
BC	0.0000	0.2480
BD	0.1370	0.4680
BE	0.2090	0.5090
BF	0.2370	0.5180
BG	0.1390	0.5170
BH	0.0040	0.2780
BI	0.4020	0.5540
BJ	0.2390	0.5300
BK	0.0030	0.2560
BL	0.0030	0.2200
BM	0.1130	0.4260
BN	0.2740	0.5550
BO	0.0000	0.2630
BP	0.0000	0.3220
BQ	0.2560	0.5070
BR	0.3260	0.5340
BS	0.0000	0.2610
BT	0.0000	0.2080
BU	0.0010	0.2580
BV	0.0500	0.4360
BY	0.1050	0.4930
BZ	0.0040	0.3120
Ba	0.1100	0.4920
Bc	0.1240	0.4830
C	0.0720	0.3630
D	0.3790	0.5680