wwPDB EM Validation Summary Report

Oct 13, 2024 – 01:20 AM EDT

PDB ID	:	9AXT
EMDB ID	:	EMD-43972
Title	:	Non-translating S. pombe ribosome
Authors	:	Gluc, M.; Gemin, O.; Purdy, M.; Mattei, S.; Jomaa, A.
Deposited on	:	2024-03-06
Resolution	:	2.40 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:

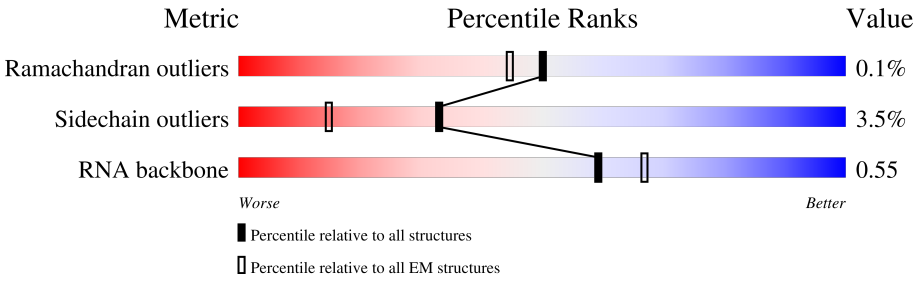
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	: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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	1842	52% 69% 23% 7%
2	AD	292	27% 67% · 30%
3	AE	252	54% 81% 5% 14%
4	AF	253	24% 81% · 15%
5	AG	249	87% 82% 5% 13%
6	AH	262	24% 94% 5%
7	AI	203	99% 97% ·
8	AJ	239	90% 89% · 8%

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Mol	Chain	Length	Quality of chain
9	AK	195	79% 93% 6%
10	AL	200	46% 92% 6%
11	AM	192	49% 89% 7%
12	AN	147	63% 62% 37%
13	AO	152	27% 90% 6%
14	AP	145	83% 78% 6% 17%
15	AQ	151	44% 97%
16	AR	139	53% 88% 8%
17	AS	154	77% 75% 23%
18	AT	140	99% 99%
19	AU	131	87% 85% 5% 10%
20	AV	152	93% 91% 7%
21	AW	144	99% 95%
22	Aa	118	85% 84% 14%
23	Ab	87	32% 94% 6%
24	Ac	130	98%
25	Ad	143	82% 96%
26	Ae	134	82% 96%
27	Af	89	78% 74% 22%
28	Ag	119	27% 77% 18%
29	Ah	83	67% 94%
30	Ai	68	88% 88% 7%
31	Aj	56	93% 93% 5%
32	Ak	61	98% 92% 7%
33	B0	106	8% 86% 12%

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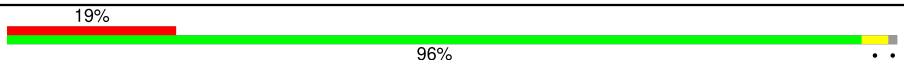
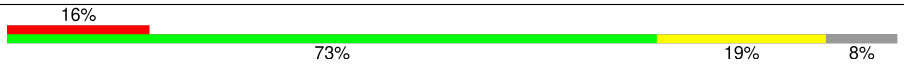
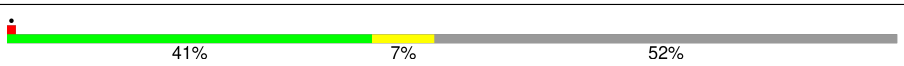
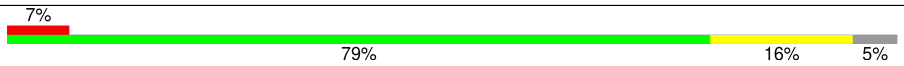
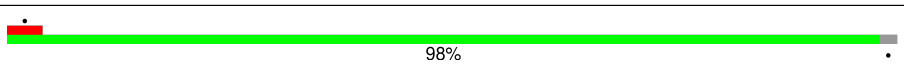
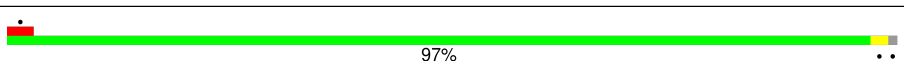
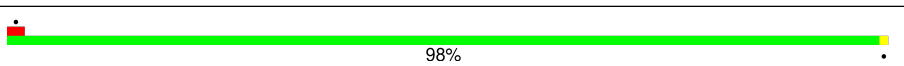
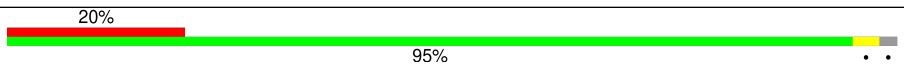
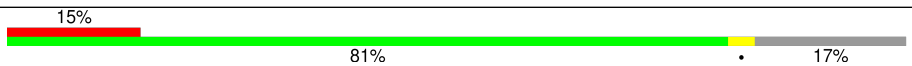
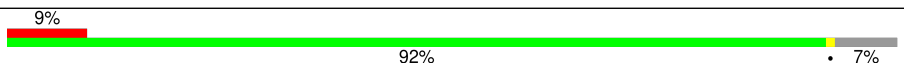
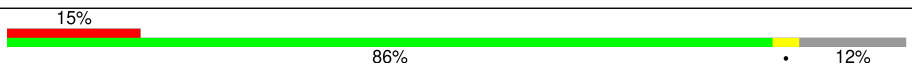
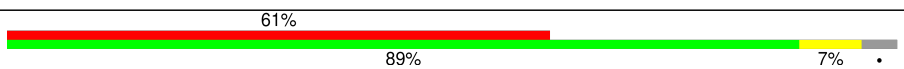
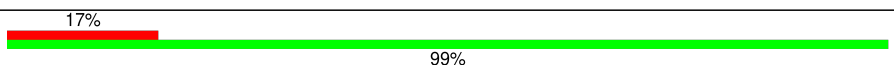
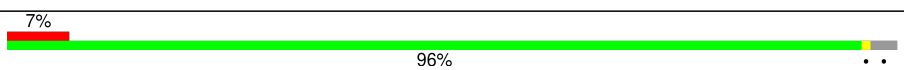
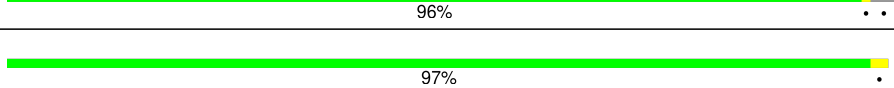
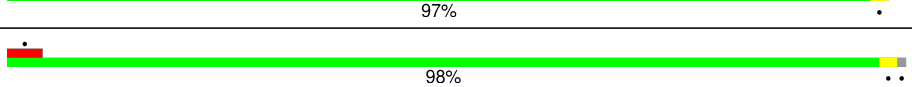
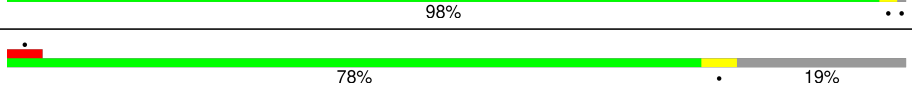
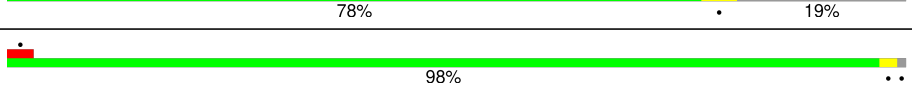
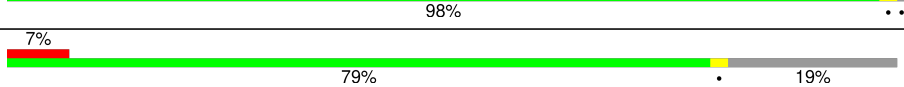
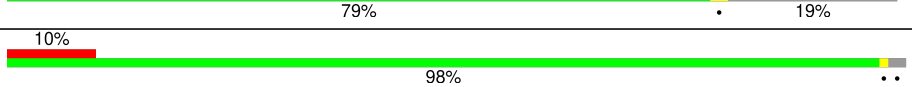
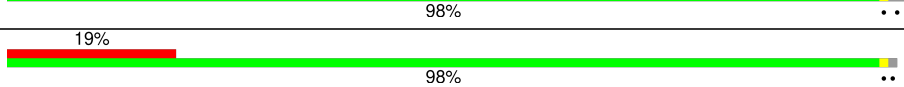
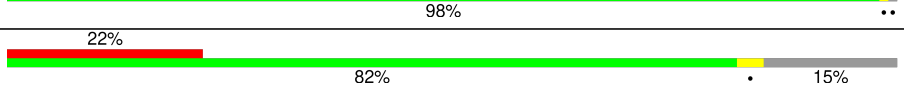
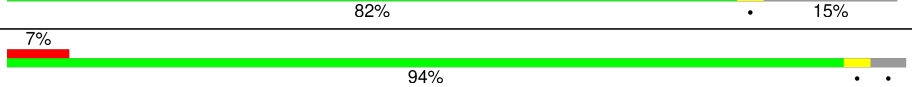
Mol	Chain	Length	Quality of chain
34	B1	94	
35	B2	3498	
36	B3	246	
37	B4	165	
38	BN	253	
39	BO	388	
40	BP	363	
41	BQ	294	
42	BR	195	
43	BS	251	
44	BT	259	
45	BU	189	
46	BV	221	
47	BW	174	
48	BX	208	
49	BY	134	
50	BZ	201	
51	Ba	197	
52	Bb	187	
53	Bc	187	
54	Bd	193	
55	Be	176	
56	Bf	160	
57	Bg	117	
58	Bh	139	

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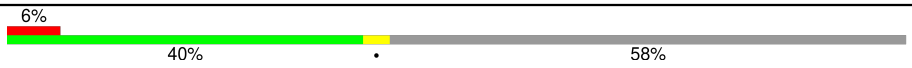
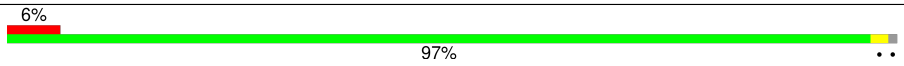
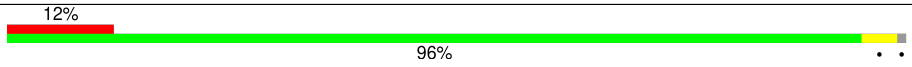
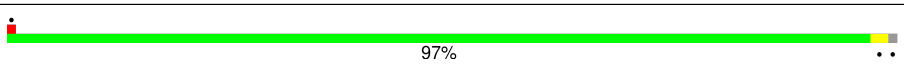
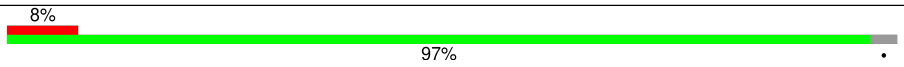
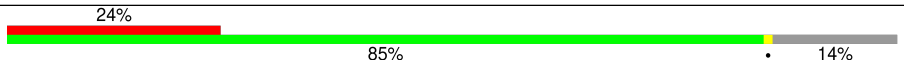
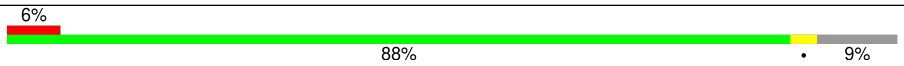
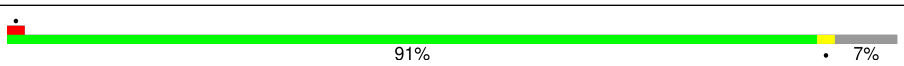
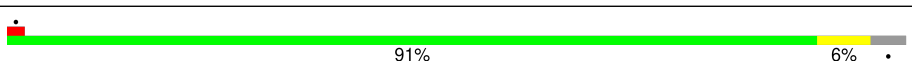
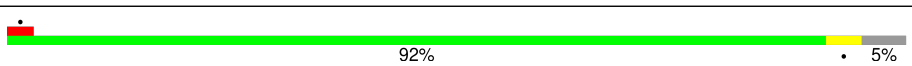
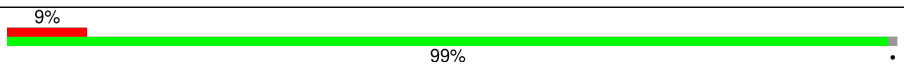
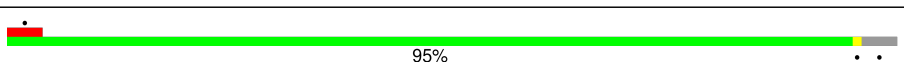
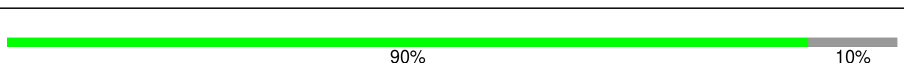
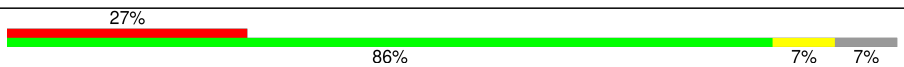
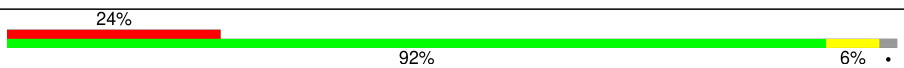
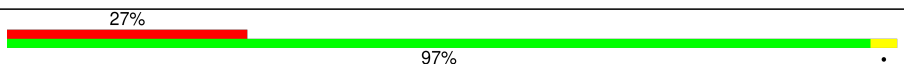
Mol	Chain	Length	Quality of chain
59	Bi	149	
60	Bj	141	
61	Bk	126	
62	Bl	136	
63	Bm	148	
64	Bn	61	
65	Bo	109	
66	Bp	113	
67	Bq	127	
68	Br	108	
69	Bs	111	
70	Bt	122	
71	Bu	99	
72	Bv	91	
73	Bw	74	
74	Bx	51	
75	By	134	

2 Entry composition (i)

There are 76 unique types of molecules in this entry. The entry contains 194719 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	AA	1705	36359	16255	6470	11929	1705	0	0

- Molecule 2 is a protein called Small ribosomal subunit protein uS2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	AD	205	1602	1016	294	287	5	0	0

- Molecule 3 is a protein called Small ribosomal subunit protein eS1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	AE	216	1733	1093	319	316	5	0	0

- Molecule 4 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AF	216	1660	1072	289	292	7	0	0

- Molecule 5 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AG	216	1701	1080	308	305	8	0	0

- Molecule 6 is a protein called Small ribosomal subunit protein eS4C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AH	261	2083	1330	391	356	6	0	0

- Molecule 7 is a protein called Small ribosomal subunit protein uS7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AI	203	Total	C	N	O	S	0	0
			1559	972	291	290	6		

- Molecule 8 is a protein called Small ribosomal subunit protein eS6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AJ	221	Total	C	N	O	S	0	0
			1784	1123	352	302	7		

- Molecule 9 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AK	193	Total	C	N	O	S	0	0
			1530	967	284	276	3		

- Molecule 10 is a protein called Small ribosomal subunit protein eS8B.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AL	188	Total	C	N	O	S	0	0
			1506	936	303	264	3		

- Molecule 11 is a protein called Small ribosomal subunit protein uS4B.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AM	178	Total	C	N	O	S	0	0
			1462	928	291	241	2		

- Molecule 12 is a protein called Small ribosomal subunit protein eS10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AN	92	Total	C	N	O	S	0	0
			748	484	132	130	2		

- Molecule 13 is a protein called Small ribosomal subunit protein uS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AO	143	Total	C	N	O	S	0	0
			1164	743	222	196	3		

- Molecule 14 is a protein called Small ribosomal subunit protein eS12A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AP	121	Total 884	C 549	N 151	O 177	S 7	0	0

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AQ	150	Total 1184	C 754	N 222	O 204	S 4	0	0

- Molecule 16 is a protein called Small ribosomal subunit protein uS11B.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AR	128	Total 949	C 587	N 184	O 174	S 4	0	0

- Molecule 17 is a protein called Small ribosomal subunit protein uS19B.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AS	119	Total 954	C 608	N 179	O 163	S 4	0	0

- Molecule 18 is a protein called Small ribosomal subunit protein uS9A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AT	140	Total 1082	C 688	N 203	O 186	S 5	0	0

- Molecule 19 is a protein called Small ribosomal subunit protein eS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AU	118	Total 972	C 606	N 185	O 179	S 2	0	0

- Molecule 20 is a protein called Small ribosomal subunit protein uS13B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AV	141	Total 1144	C 714	N 222	O 204	S 4	0	0

- Molecule 21 is a protein called Small ribosomal subunit protein eS19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AW	142	Total	C	N	O	S	0	0
			1119	699	212	205	3		

- Molecule 22 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Aa	101	Total	C	N	O	S	0	0
			815	511	156	146	2		

- Molecule 23 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Ab	87	Total	C	N	O	S	0	0
			672	411	122	135	4		

- Molecule 24 is a protein called Small ribosomal subunit protein uS8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Ac	129	Total	C	N	O	S	0	0
			1028	649	196	179	4		

- Molecule 25 is a protein called Small ribosomal subunit protein uS12A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Ad	142	Total	C	N	O	S	0	0
			1095	692	214	187	2		

- Molecule 26 is a protein called Small ribosomal subunit protein eS24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Ae	133	Total	C	N	O	S	0	0
			1078	672	217	185	4		

- Molecule 27 is a protein called Small ribosomal subunit protein eS25A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Af	69	Total	C	N	O	S	0	0
			551	350	103	97	1		

- Molecule 28 is a protein called Small ribosomal subunit protein eS26B.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ag	97	Total 795	C 491	N 167	O 132	S 5	0	0

- Molecule 29 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ah	81	Total 619	C 388	N 114	O 108	S 9	0	0

- Molecule 30 is a protein called Small ribosomal subunit protein eS28A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ai	63	Total 498	C 308	N 99	O 90	S 1	0	0

- Molecule 31 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Aj	53	Total 447	C 282	N 91	O 73	S 1	0	0

- Molecule 32 is a protein called Small ribosomal subunit protein eS30B.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ak	60	Total 475	C 296	N 99	O 78	S 2	0	0

- Molecule 33 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B0	93	Total 758	C 479	N 152	O 122	S 5	0	0

- Molecule 34 is a protein called Large ribosomal subunit protein eL43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B1	93	Total 718	C 442	N 147	O 123	S 6	0	0

- Molecule 35 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	B2	3212	Total	C	N	O	P	0	0
			68676	30687	12377	22400	3212		

- Molecule 36 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B3	119	Total	C	N	O	P	0	0
			2539	1133	454	833	119		

- Molecule 37 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	B4	157	Total	C	N	O	P	0	0
			3332	1491	583	1101	157		

- Molecule 38 is a protein called Large ribosomal subunit protein uL2C.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BN	248	Total	C	N	O	S	0	0
			1872	1166	377	324	5		

- Molecule 39 is a protein called Large ribosomal subunit protein uL3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BO	384	Total	C	N	O	S	0	0
			3050	1929	576	535	10		

- Molecule 40 is a protein called Large ribosomal subunit protein uL4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BP	362	Total	C	N	O	S	0	0
			2799	1768	538	490	3		

- Molecule 41 is a protein called Large ribosomal subunit protein uL18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BQ	287	Total	C	N	O	S	0	0
			2312	1461	410	437	4		

- Molecule 42 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BR	162	Total	C	N	O	S	0	0
			1251	802	231	215	3		

- Molecule 43 is a protein called Large ribosomal subunit protein uL30C.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BS	233	Total	C	N	O	S	0	0
			1897	1211	349	334	3		

- Molecule 44 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BT	229	Total	C	N	O	S	0	0
			1772	1135	325	309	3		

- Molecule 45 is a protein called Large ribosomal subunit protein uL6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BU	168	Total	C	N	O	S	0	0
			1319	828	244	242	5		

- Molecule 46 is a protein called Large ribosomal subunit protein uL16A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BV	191	Total	C	N	O	S	0	0
			1549	982	291	270	6		

- Molecule 47 is a protein called Large ribosomal subunit protein uL5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BW	167	Total	C	N	O	S	0	0
			1346	854	252	235	5		

- Molecule 48 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BX	207	Total	C	N	O	S	0	0
			1654	1034	329	290	1		

- Molecule 49 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BY	130	Total	C	N	O	S	0	0
			1038	662	198	174	4		

- Molecule 50 is a protein called Large ribosomal subunit protein eL15B.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BZ	200	Total	C	N	O	S	0	0
			1676	1050	348	275	3		

- Molecule 51 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ba	196	Total	C	N	O	S	0	0
			1545	991	294	256	4		

- Molecule 52 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Bb	152	Total	C	N	O	S	0	0
			1212	770	229	210	3		

- Molecule 53 is a protein called Large ribosomal subunit protein eL18B.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	Bc	186	Total	C	N	O	0	0
			1487	937	300	250		

- Molecule 54 is a protein called Large ribosomal subunit protein eL19B.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Bd	157	Total	C	N	O	S	0	0
			1301	809	275	212	5		

- Molecule 55 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Be	173	Total	C	N	O	S	0	0
			1423	916	268	234	5		

- Molecule 56 is a protein called Large ribosomal subunit protein eL21B.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Bf	159	Total 1286	C 810	N 247	O 226	S 3	0	0

- Molecule 57 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	Bg	99	Total 798	C 518	N 138	O 142	0	0

- Molecule 58 is a protein called Large ribosomal subunit protein uL14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Bh	134	Total 999	C 630	N 184	O 177	S 8	0	0

- Molecule 59 is a protein called Large ribosomal subunit protein eL24B.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Bi	63	Total 523	C 336	N 102	O 82	S 3	0	0

- Molecule 60 is a protein called Large ribosomal subunit protein uL23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Bj	118	Total 947	C 605	N 175	O 166	S 1	0	0

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

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

- Molecule 62 is a protein called Large ribosomal subunit protein eL27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Bl	135	Total 1078	C 698	N 200	O 178	S 2	0	0

- Molecule 63 is a protein called Large ribosomal subunit protein uL15B.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Bm	147	Total	C	N	O	S	0	0
			1171	740	235	194	2		

- Molecule 64 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	Bn	59	Total	C	N	O	0	0
			495	299	112	84		

- Molecule 65 is a protein called Large ribosomal subunit protein eL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Bo	94	Total	C	N	O	S	0	0
			705	450	121	130	4		

- Molecule 66 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Bp	103	Total	C	N	O	S	0	0
			857	538	167	149	3		

- Molecule 67 is a protein called Large ribosomal subunit protein eL32A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Bq	118	Total	C	N	O	S	0	0
			944	591	191	157	5		

- Molecule 68 is a protein called Large ribosomal subunit protein eL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Br	104	Total	C	N	O	S	0	0
			831	531	160	137	3		

- Molecule 69 is a protein called Large ribosomal subunit protein eL34B.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Bs	106	Total	C	N	O	S	0	0
			858	538	176	142	2		

- Molecule 70 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 71 is a protein called Large ribosomal subunit protein eL36B.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Bu	95	Total 759	C 472	N 159	O 127	S 1	0	0

- Molecule 72 is a protein called Large ribosomal subunit protein eL37B.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bv	82	Total 652	C 399	N 140	O 106	S 7	0	0

- Molecule 73 is a protein called Large ribosomal subunit protein eL38A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bw	69	Total 560	C 355	N 103	O 101	S 1	0	0

- Molecule 74 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Bx	50	Total 436	C 273	N 98	O 64	S 1	0	0

- Molecule 75 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	By	134	Total 1039	C 646	N 204	O 187	S 2	0	0

- Molecule 76 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
76	Ag	1	Total 1	Zn 1	0
76	Ah	1	Total 1	Zn 1	0
76	Aj	1	Total 1	Zn 1	0

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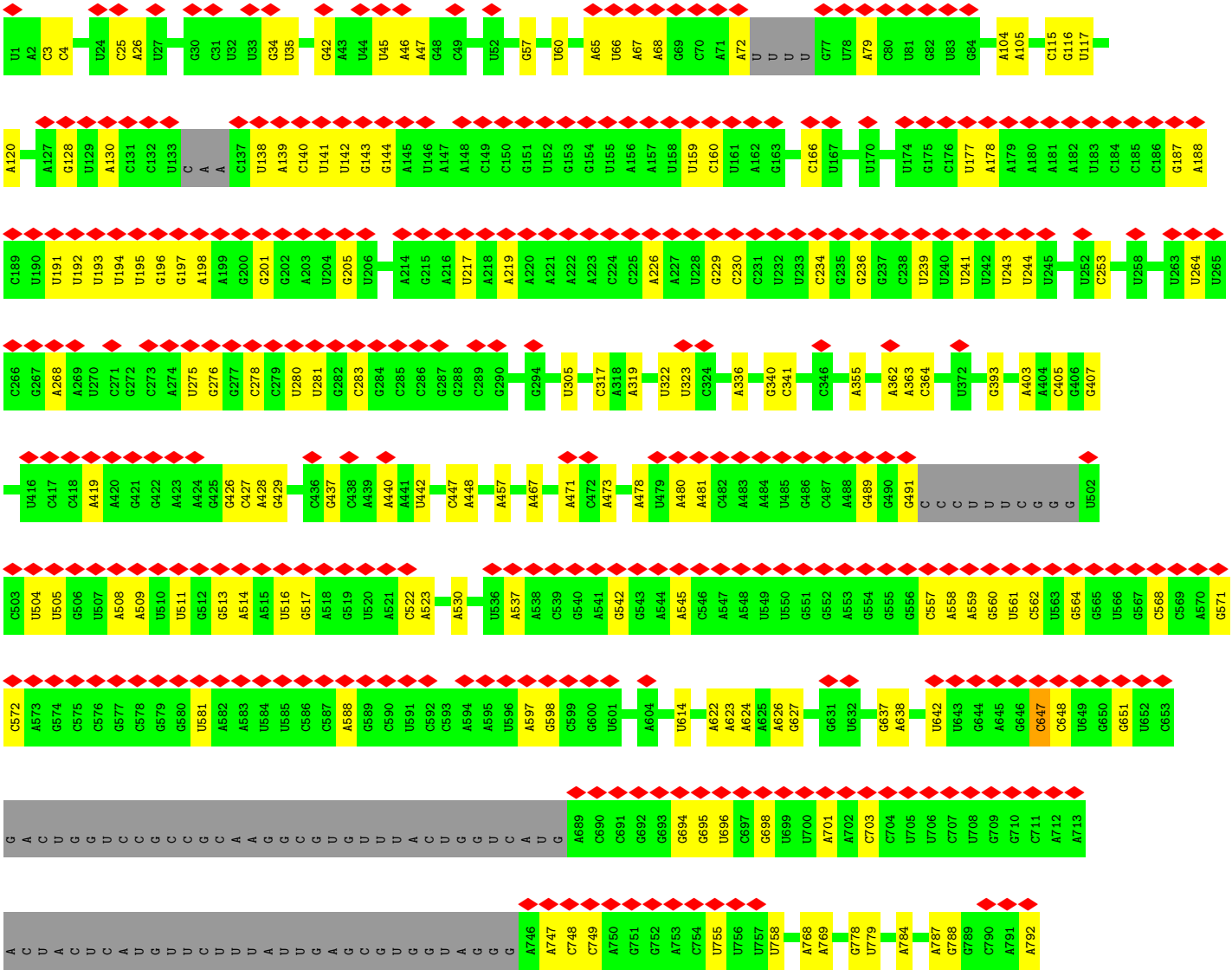
Mol	Chain	Residues	Atoms	AltConf
76	B0	1	Total Zn 1 1	0
76	B1	1	Total Zn 1 1	0
76	Bv	1	Total Zn 1 1	0

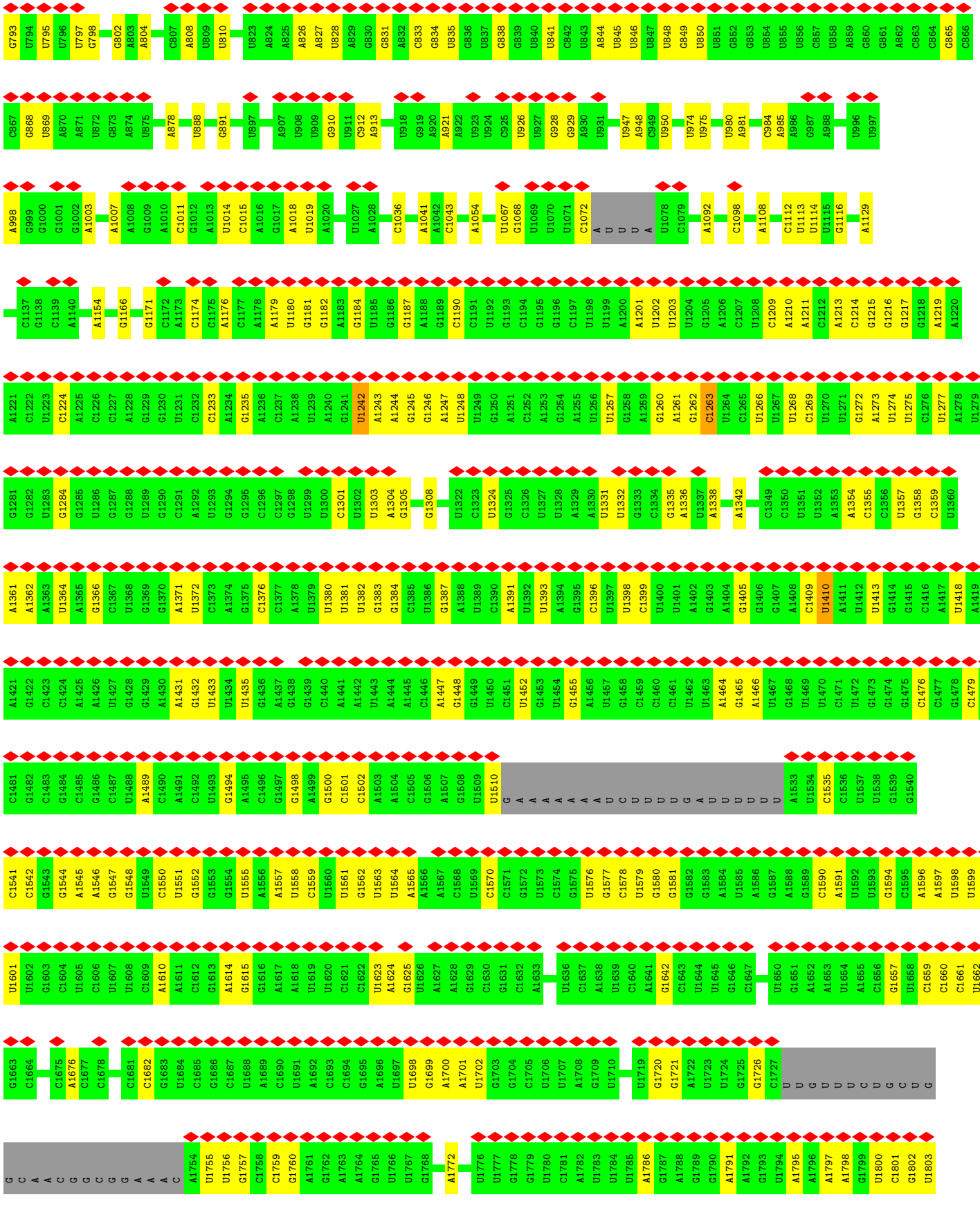
3 Residue-property plots (i)

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: 18S ribosomal RNA

Chain AA:

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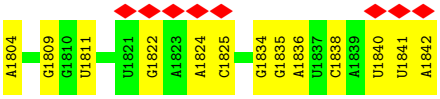
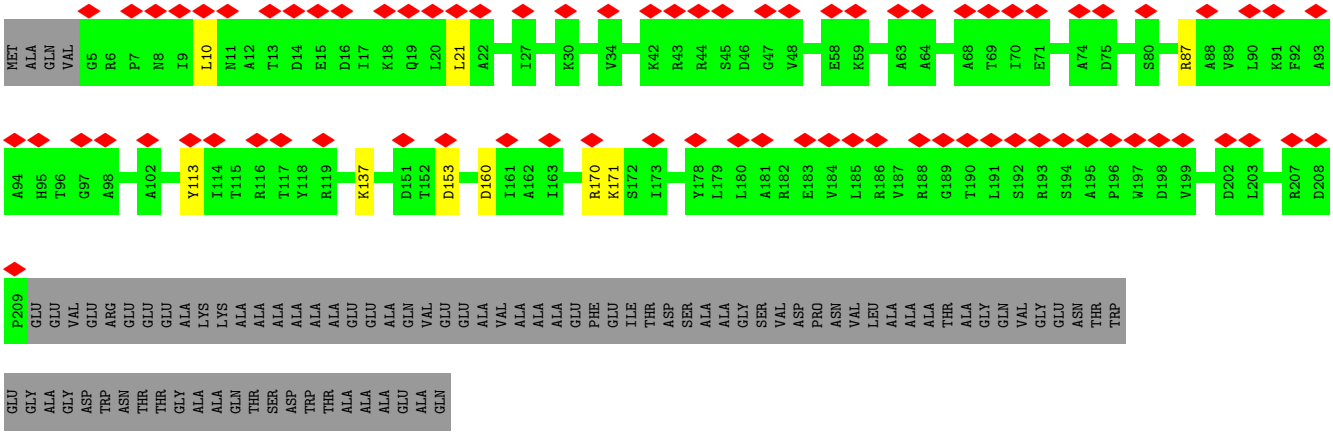
C867 G868 U869 A870 A871 U872 G873 A874 U875 A878 U888 G891 U897 A907 U908 U909 G910 U911 C912 A913 U918 G919 A920 A921 A922 U923 U924 C925 U926 U927 G928 G929 A930 U931 U947 A948 C949 U950 U974 U975 U980 A981 C984 A985 A986 G987 A988 U996 U997
A998 G999 G1000 G1001 G1002 A1003 A1007 A1008 G1009 A1010 C1011 G1012 A1013 U1014 C1015 A1016 G1017 A1018 U1019 A1020 U1027 A1028 C1036 A1041 A1042 C1043 A1054 U1067 G1068 U1069 U1070 U1071 C1072 A U U U A U1078 C1079 A1092 C1098 A1108 C1112 U1113 U1114 U1115 G1116 A1129
C1137 G1138 C1139 A1140 A1154 G1166 G1171 C1172 A1173 C1174 C1175 A1176 C1177 A1178 A1179 U1180 G1181 G1182 A1183 G1184 U1185 G1186 G1187 A1188 G1189 C1190 C1191 U1192 G1193 C1194 G1195 G1196 C1197 U1198 U1199 A1200 A1201 U1202 U1203 U1204 G1205 A1206 C1207 U1208 C1209 A1210 A1211 C1212 A1213 C1214 G1215 G1216 G1217 G1218 A1219 A1220
A1221 C1222 U1223 C1224 A1225 C1226 C1227 A1228 G1229 G1230 U1231 C1232 C1233 A1234 G1235 A1236 C1237 A1238 U1239 A1240 G1241 U1242 A1243 A1244 G1245 G1246 A1247 U1248 U1249 G1250 A1251 C1252 A1253 G1254 A1255 U1256 U1257 G1258 A1259 G1260 A1261 G1262 C1263 U1264 C1265 U1266 U1267 U1268 C1269 U1270 U1271 G1272 A1273 U1274 U1275 C1276 U1277 A1278 U1279 G1280
G1281 G1282 U1283 G1284 G1285 U1286 G1287 G1288 U1289 G1290 C1291 A1292 U1293 G1294 G1295 C1296 C1297 G1298 U1299 U1300 C1301 U1302 U1303 A1304 G1305 G1308 U1322 C1323 U1324 G1325 C1326 U1327 U1328 A1329 A1330 U1331 U1332 G1333 C1334 G1335 A1336 U1337 A1338 A1342 C1349 C1350 U1351 U1352 A1353 A1354 C1355 C1356 U1357 G1358 C1359 U1360
A1361 A1362 A1363 U1364 A1365 G1366 C1367 U1368 G1369 G1370 A1371 U1372 C1373 A1374 G1375 C1376 C1377 A1378 U1379 U1380 U1381 U1382 G1383 G1384 C1385 U1386 G1387 A1388 U1389 C1390 A1391 U1392 U1393 A1394 G1395 C1396 U1397 U1398 C1399 U1400 U1401 A1402 G1403 A1404 G1405 G1406 G1407 A1408 C1409 U1410 A1411 U1412 U1413 G1414 G1415 C1416 A1417 U1418 A1419 A1420
A1421 G1422 C1423 C1424 A1425 A1426 U1427 G1428 G1429 A1430 A1431 G1432 U1433 U1434 U1435 G1436 A1437 G1438 G1439 C1440 A1441 A1442 U1443 A1444 A1445 C1446 A1447 G1448 G1449 U1450 C1451 U1452 G1453 U1454 G1455 A1456 U1457 G1458 C1459 C1460 C1461 U1462 U1463 A1464 G1465 A1466 U1467 G1468 U1469 U1470 C1471 U1472 G1473 G1474 G1475 C1476 C1477 G1478 C1479 A1480
C1481 G1482 C1483 G1484 C1485 G1486 C1487 U1488 A1489 C1490 A1491 C1492 U1493 G1494 A1495 C1496 G1497 G1498 A1499 G1500 C1501 C1502 A1503 A1504 C1505 G1506 A1507 G1508 U1509 U1510 G A A A A A A U C U U U U U G A U U U U U U A1533 U1534 C1535 C1536 U1537 U1538 G1539 G1540
C1541 C1542 G1543 G1544 A1545 A1546 G1547 G1548 U1549 C1550 U1551 G1552 G1553 G1554 U1555 A1556 A1557 U1558 C1559 U1560 U1561 G1562 U1563 U1564 A1565 A1566 A1567 C1568 U1569 C1570 C1571 G1572 U1573 C1574 G1575 U1576 G1577 C1578 U1579 G1580 G1581 G1582 G1583 A1584 U1585 A1586 G1587 A1588 G1589 C1590 A1591 U1592 U1593 G1594 C1595 A1596 A1597 U1598 U1599 A1600
U1601 U1602 G1603 C1604 U1605 C1606 U1607 U1608 C1609 A1610 A1611 C1612 G1613 A1614 G1615 G1616 A1617 A1618 U1619 U1620 C1621 C1622 U1623 A1624 G1625 U1626 A1627 A1628 G1629 C1630 G1631 C1632 A1633 U1636 C1637 A1638 U1639 C1640 A1641 G1642 C1643 U1644 U1645 G1646 C1647 U1650 G1651 A1652 A1653 U1654 A1655 C1656 G1657 U1658 C1659 C1660 C1661 U1662
G1663 C1664 C1675 A1676 C1677 C1678 C1681 C1682 G1683 U1684 C1685 G1686 C1687 U1688 A1689 C1690 U1691 A1692 C1693 C1694 G1695 A1696 U1697 U1698 G1699 A1700 A1701 U1702 G1703 G1704 C1705 U1706 U1707 A1708 G1709 U1710 U1719 G1720 G1721 A1722 U1723 U1724 G1725 G1726 C1727 U U G U U C U G C U G
G C A A C G G C G G A A A C A1754 U1755 U1756 G1757 C1758 C1759 G1760 A1761 G1762 A1763 A1764 G1765 U1766 U1767 G1768 A1772 U1776 U1777 G1778 G1779 U1780 C1781 A1782 U1783 U1784 U1785 A1786 G1787 A1788 G1789 C1790 A1791 A1792 G1793 U1794 A1795 A1796 A1797 A1798 G1799 U1800 C1801 G1802 U1803



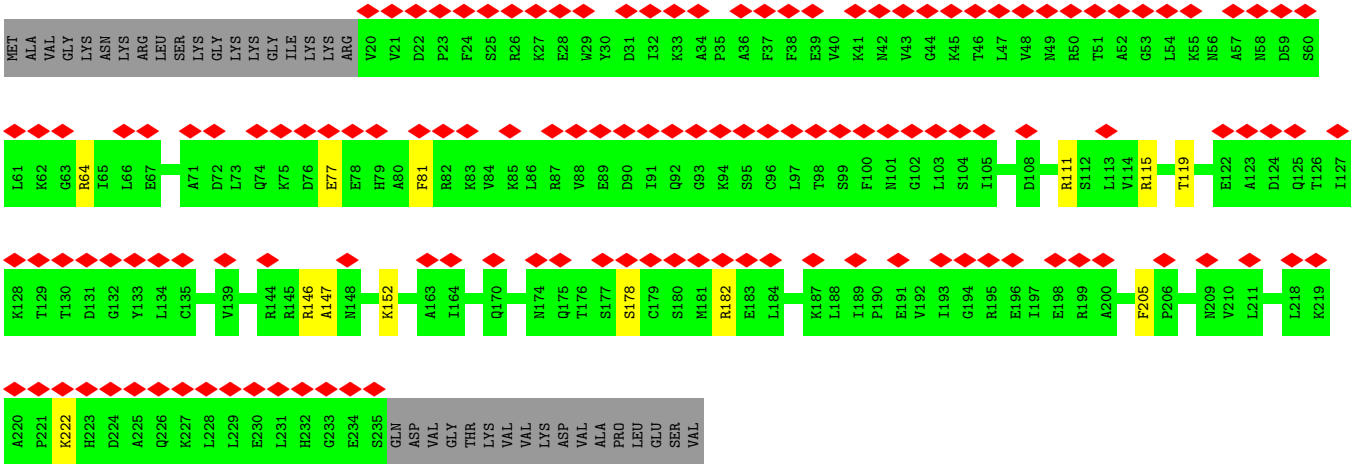
• Molecule 2: Small ribosomal subunit protein uS2A

Chain AD:



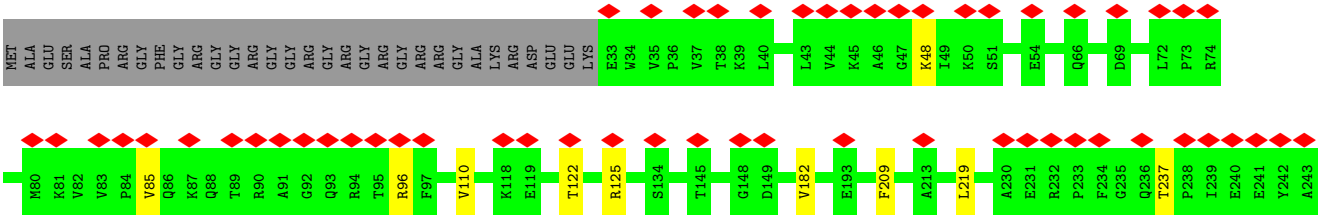
• Molecule 3: Small ribosomal subunit protein eS1B

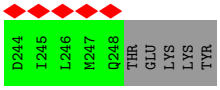
Chain AE:



• Molecule 4: Small ribosomal subunit protein uS5

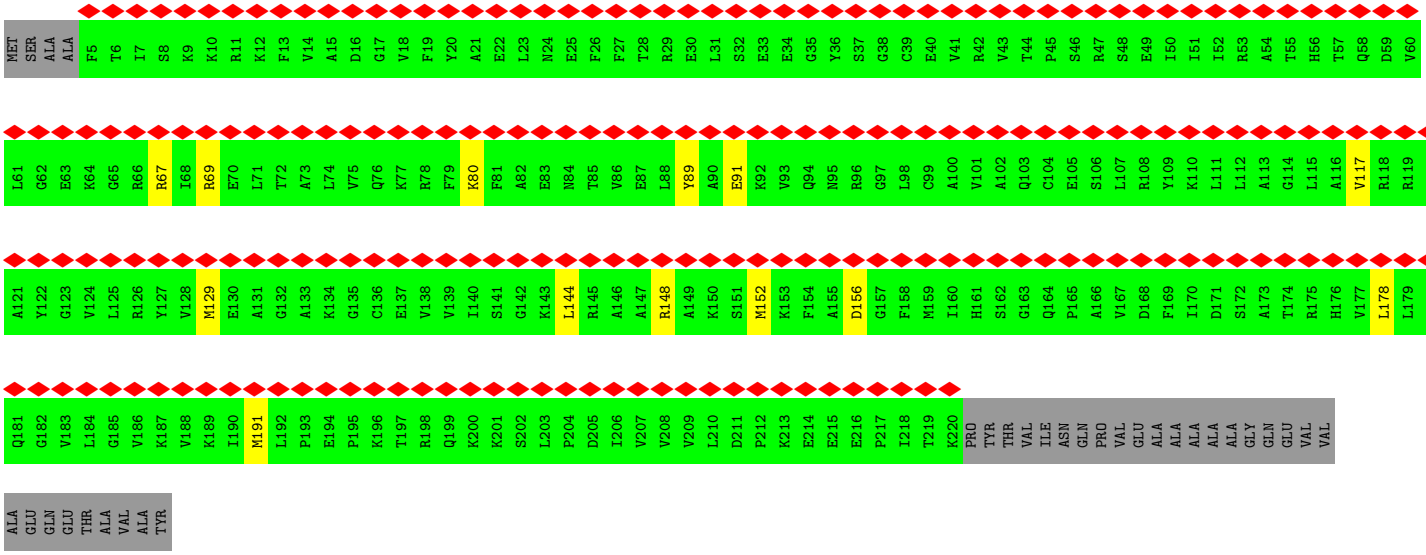
Chain AF:





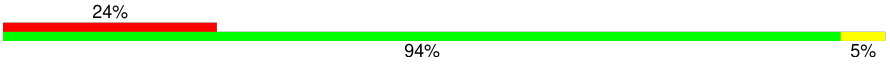
• Molecule 5: Small ribosomal subunit protein uS3

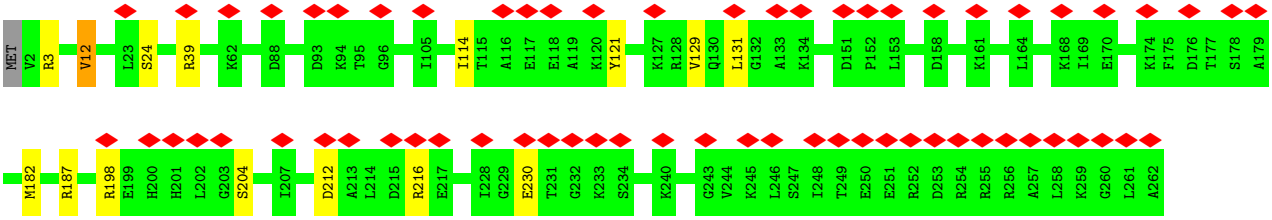
Chain AG:



• Molecule 6: Small ribosomal subunit protein eS4C

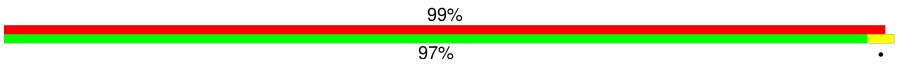
Chain AH:

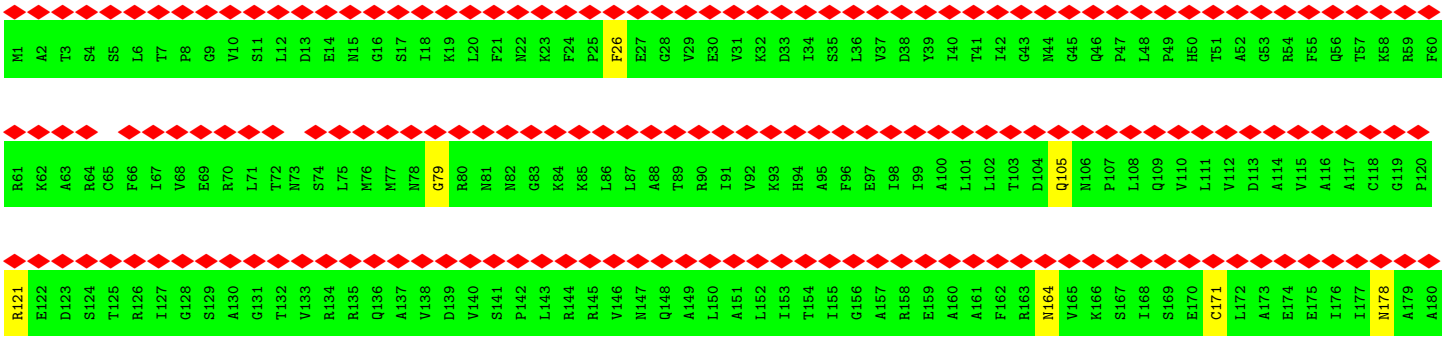


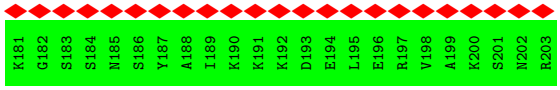


• Molecule 7: Small ribosomal subunit protein uS7A

Chain AI:

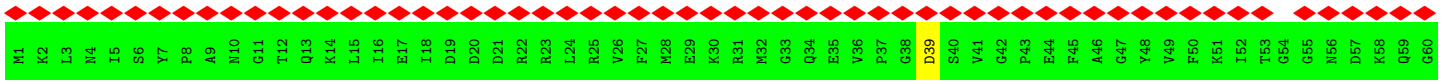


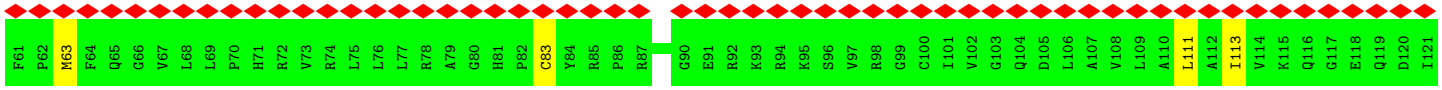


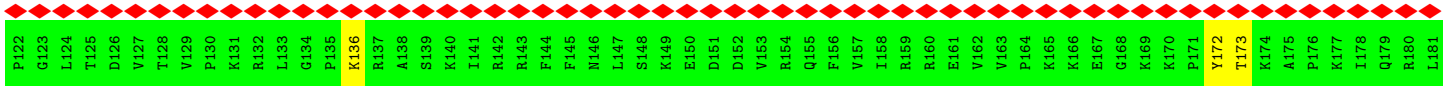


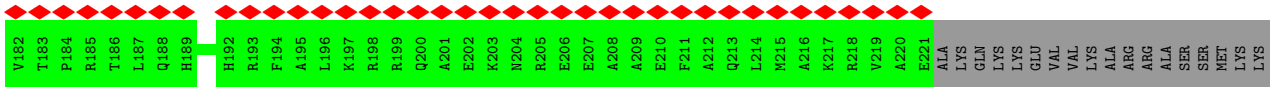
• Molecule 8: Small ribosomal subunit protein eS6B

Chain AJ:



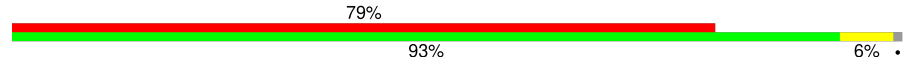


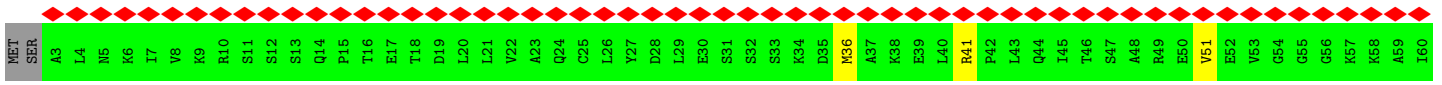


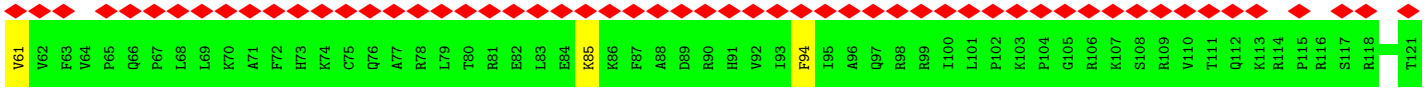


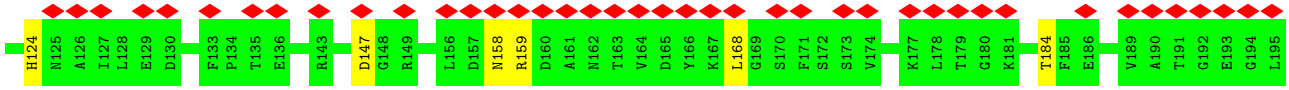
• Molecule 9: Small ribosomal subunit protein eS7

Chain AK:



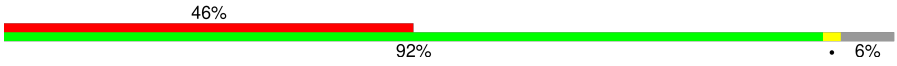


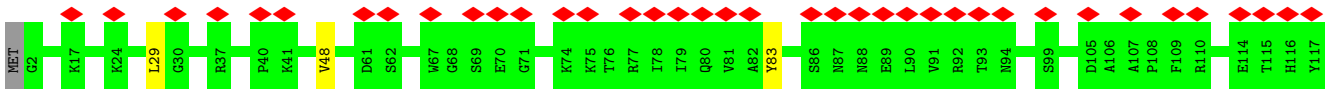


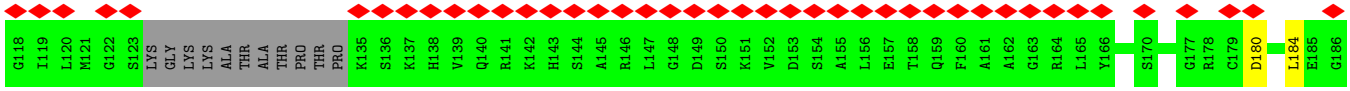


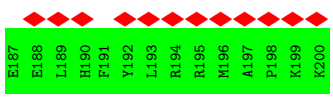
• Molecule 10: Small ribosomal subunit protein eS8B

Chain AL:



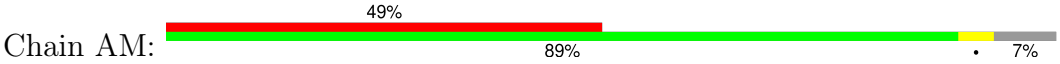


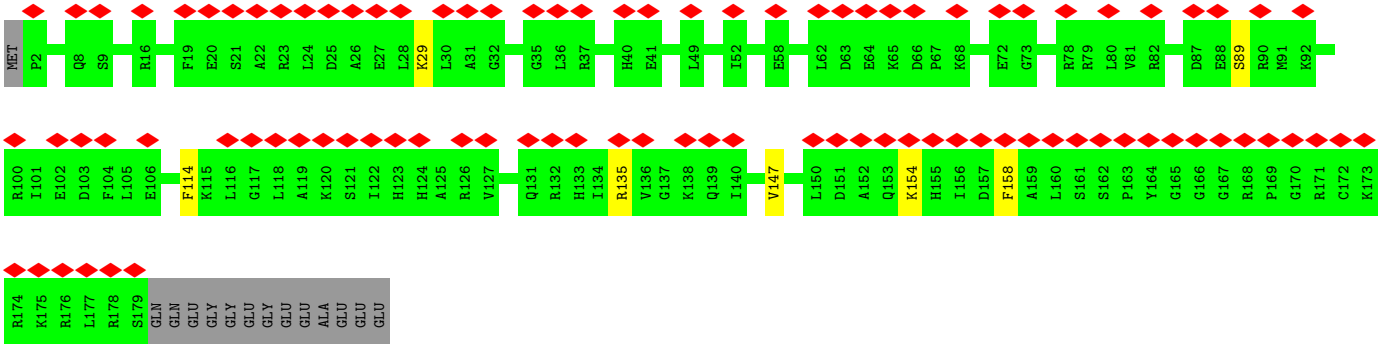




• Molecule 11: Small ribosomal subunit protein uS4B

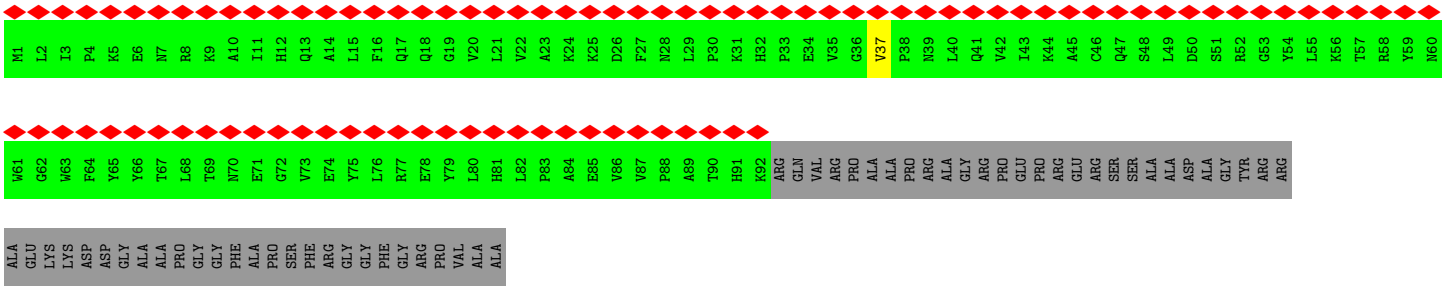
Chain AM:





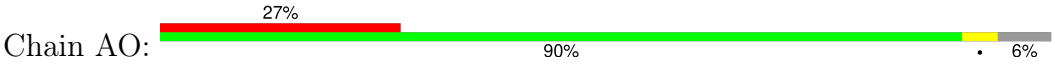
• Molecule 12: Small ribosomal subunit protein eS10B

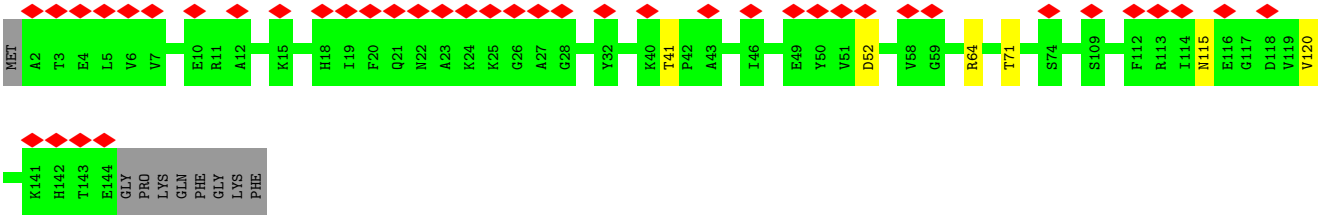
Chain AN:



• Molecule 13: Small ribosomal subunit protein uS17A

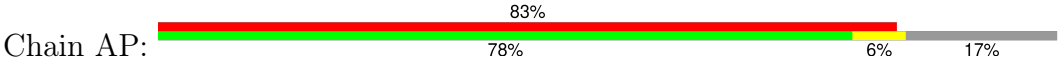
Chain AO:

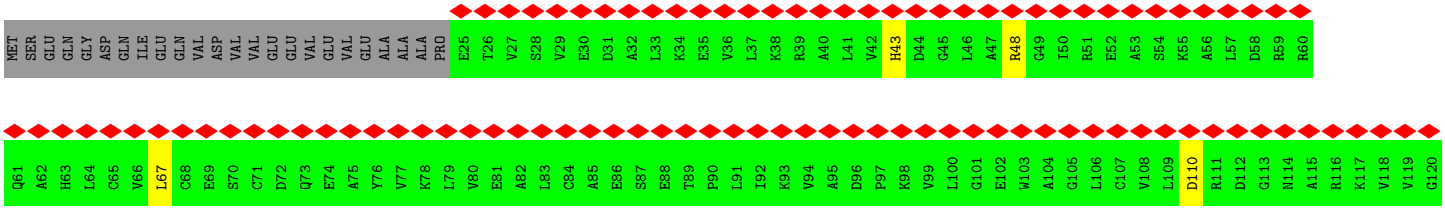


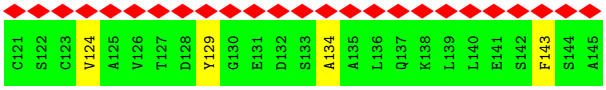


• Molecule 14: Small ribosomal subunit protein eS12A

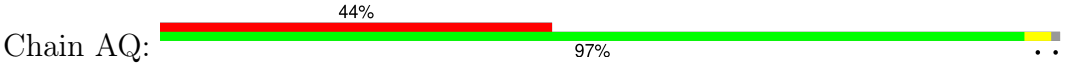
Chain AP:

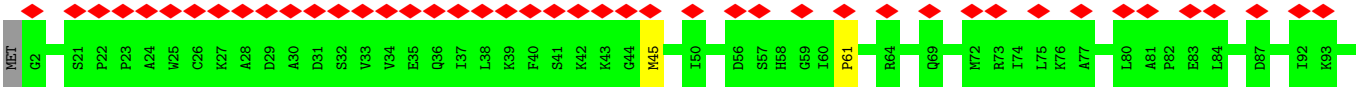


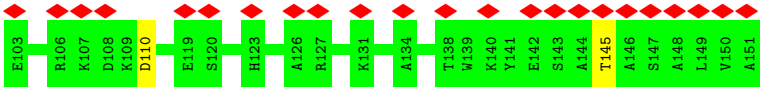




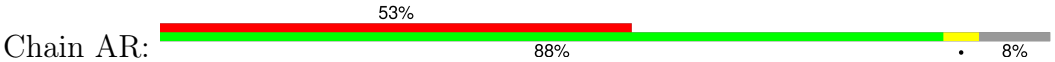
• Molecule 15: Small ribosomal subunit protein uS15

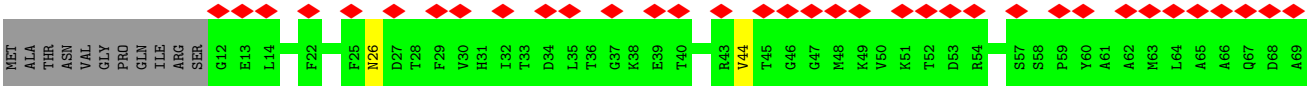


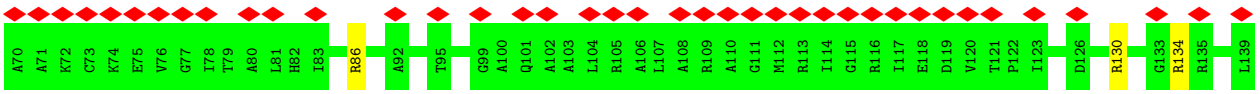




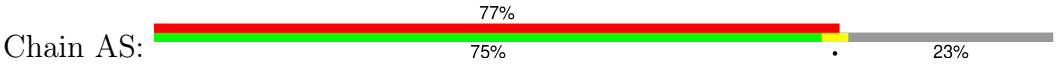
• Molecule 16: Small ribosomal subunit protein uS11B

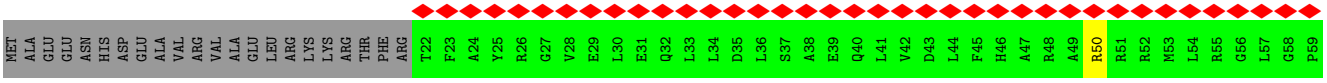


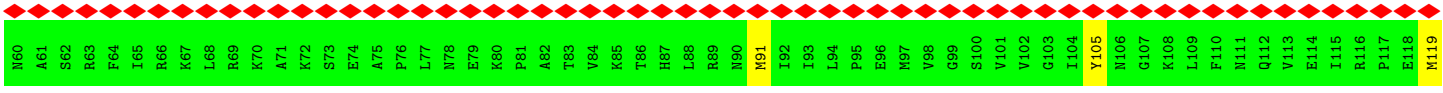


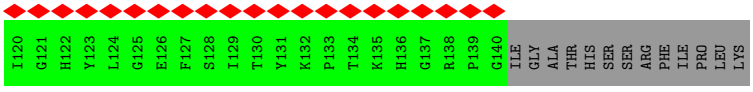


• Molecule 17: Small ribosomal subunit protein uS19B

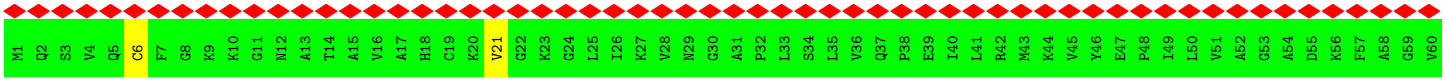








• Molecule 18: Small ribosomal subunit protein uS9A



D61 I62 R63 V64 R65 V66 S67 G68 G69 G70 H71 V72 S73 Q74 I75 Y76 A77 I78 R79 Q80 A81 I82 S83 K84 A85 I86 V87 A88 Y89 Y90 Q91 K92 F93 V94 D95 E96 H97 S98 K99 A100 A100 E101 L102 K103 K104 A105 L106 I107 T108 Y109 D110 R111 T112 L113 L114 V115 A116 D117 P118 R119 R120

M121 E122 P123 K124 K125 F126 G127 G128 H129 G130 A131 R132 A133 R134 Q135 Q136 K137 S138 Y139 R140

- Molecule 19: Small ribosomal subunit protein eS17A

Chain AU:

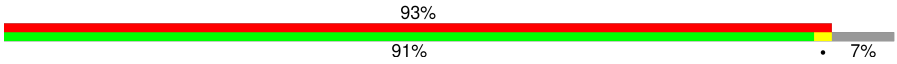
MET G2 R3 V4 R5 T6 K7 T8 R11 A12 S13 R14 V15 V16 I17 E18 K19 Y20 Y21 P22 R23 L24 T25 L26 D27 F28 Q29 T30 N31 K32 R33 I34 V35 D36 E37 V38 A39 I40 I41 A42 S43 K44 R45 L46 R47 N48 K49 I50 A51 G52 Y53 T54 T55 H56 L57 M58 K59 R60 I61

Q62 R63 G64 P65 V66 R67 G68 I69 S70 F71 K72 L73 Q74 E75 E76 E77 R78 E79 R80 K81 D82 Q83 Y84 V85 P86 E87 V88 S89 E90 L91 E92 V93 D94 R95 V96 N97 V98 D99 Q100 D101 T102 K103 D104 M105 L106 K107 S108 L109 G110 Y111 D112 Q113 I114 P115 V116 R117 V118 L119 ALA PRO

ALA PRO GLN GLU ARG PHE ARG ARG ARG GLN

- Molecule 20: Small ribosomal subunit protein uS13B

Chain AV:



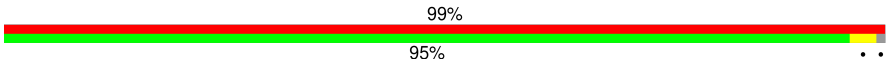
MET S2 L3 V4 V5 P6 D7 N8 F9 Q10 H11 I12 L13 R14 L15 L16 N17 T18 N19 Y20 D21 G22 K23 V24 K25 V26 M27 F28 A29 M30 T31 Q32 I33 K34 G35 V36 G37 R38 R39 Y40 A41 N42 I43 V44 C45 K46 K47 A48 D49 I50 D51 M52 S53 K54 R55 A56 G57 E58 L59 T60

T61 E62 E63 L64 E65 R66 I67 V68 T69 I70 I71 Q72 N73 P74 S75 Q76 F77 K78 I79 P80 S81 W82 F83 L84 N85 R86 Q87 K88 D89 I90 N91 D92 G93 K94 S95 F96 Q97 L98 L99 A100 N101 N102 V103 D104 S105 K106 L107 R108 E109 D110 L111 E112 R113 L114 K115 K116 I117 Q118 T119 H120

R121 G122 L123 R124 H125 A126 L127 D128 L129 R130 V131 R132 G133 Q134 H135 T136 K137 T138 T139 G140 R141 R142 GLY LYS THR VAL GLY VAL SER LYS LYS LYS

- Molecule 21: Small ribosomal subunit protein eS19A

Chain AW:



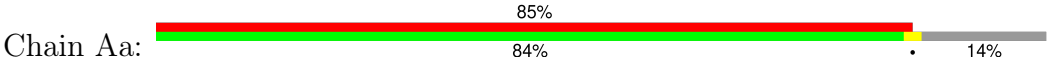
MET A2 G3 V4 S5 V6 K7 D8 V9 D10 A11 Q12 K13 F14 I15 T16 A17 Y18 A19 A20 F21 L22 K23 R24 S25 G26 K27 M28 T29 T30 P31 Q32 W33 I34 D35 I36 V37 K38 T39 G40 T41 H42 K43 E44 L45 A46 P47 Y48 D49 P50 D51 W52 Y53 Y54 V55 R56 A57 A58 A59 I60

A61 R62 H63 I64 Y65 L66 R67 K68 Q69 V70 G71 V72 G73 R74 L75 C76 K77 V78 Y79 G80 G81 S82 V83 N84 R85 G86 M87 R88 P89 S90 H91 H92 R93 D94 G95 S96 G97 S98 V99 Q100 R101 K102 V103 V104 Q105 S106 L107 E108 K109 I110 G111 V112 L113 E114 K115 S116 D117 N118 G119 G120

R121 R122 I123 S124 Q125 Q126 G127 Q128 R129 D130 L131 D132 R133 I134 A135 Y136 S137 L138 L139 E140 E141 E142 S143 GLU

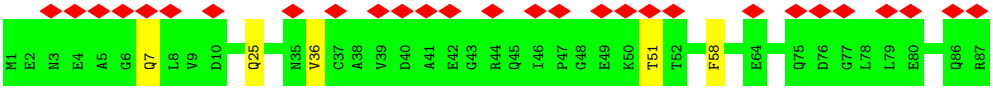
• Molecule 22: Small ribosomal subunit protein uS10

Chain Aa:



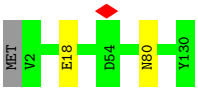
• Molecule 23: Small ribosomal subunit protein eS21

Chain Ab:



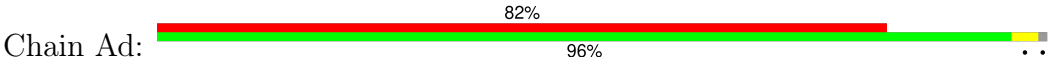
• Molecule 24: Small ribosomal subunit protein uS8A

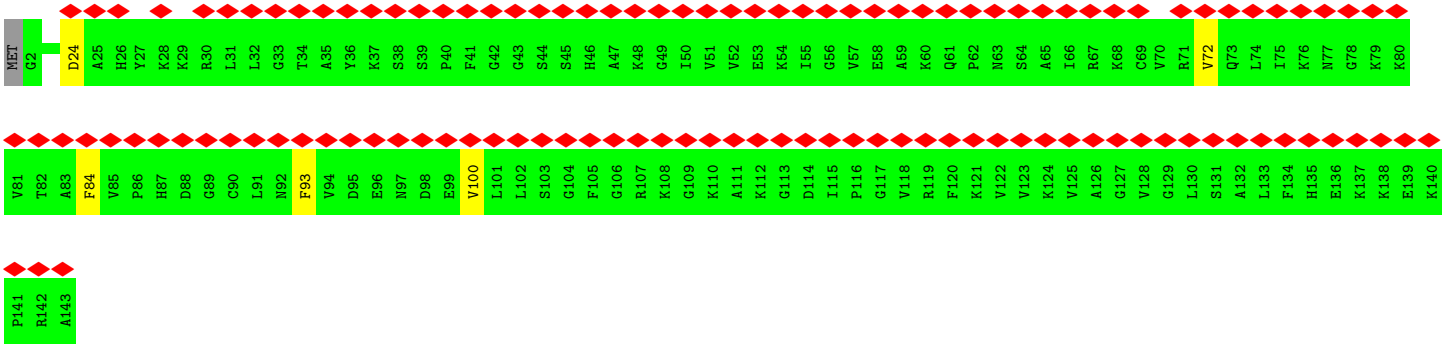
Chain Ac:



• Molecule 25: Small ribosomal subunit protein uS12A

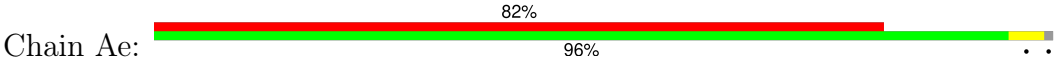
Chain Ad:

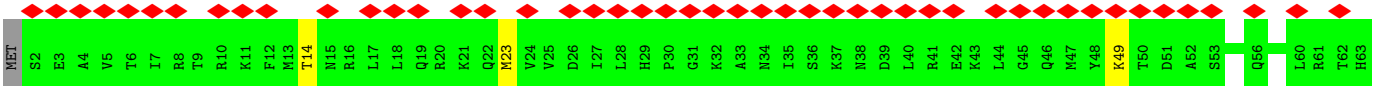


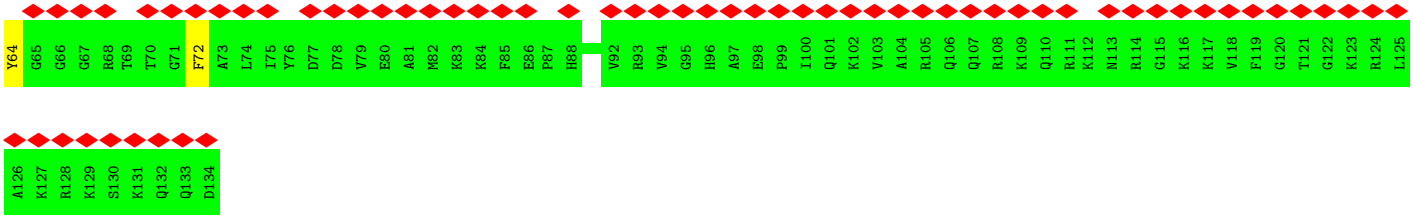


• Molecule 26: Small ribosomal subunit protein eS24A

Chain Ae:

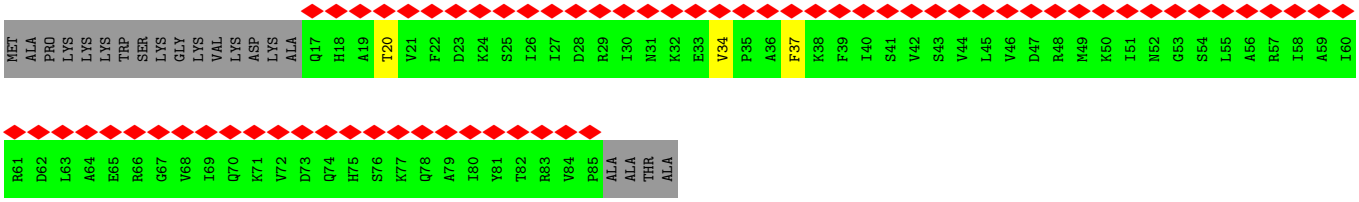






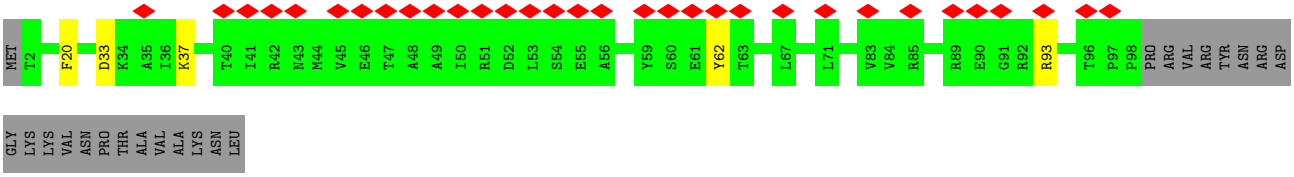
• Molecule 27: Small ribosomal subunit protein eS25A

Chain Af:



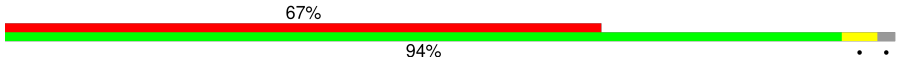
• Molecule 28: Small ribosomal subunit protein eS26B

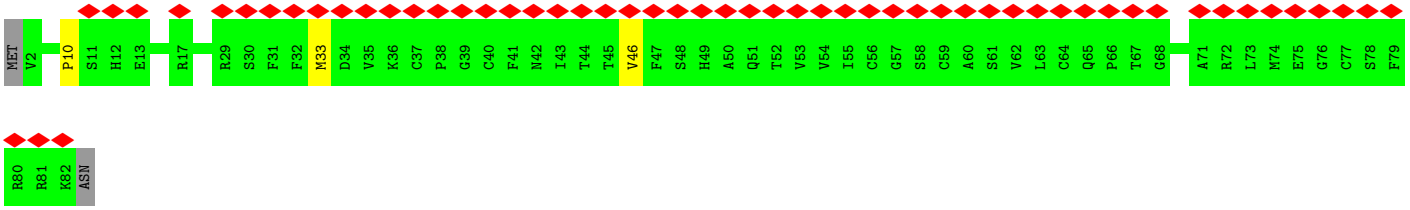
Chain Ag:



• Molecule 29: Small ribosomal subunit protein eS27

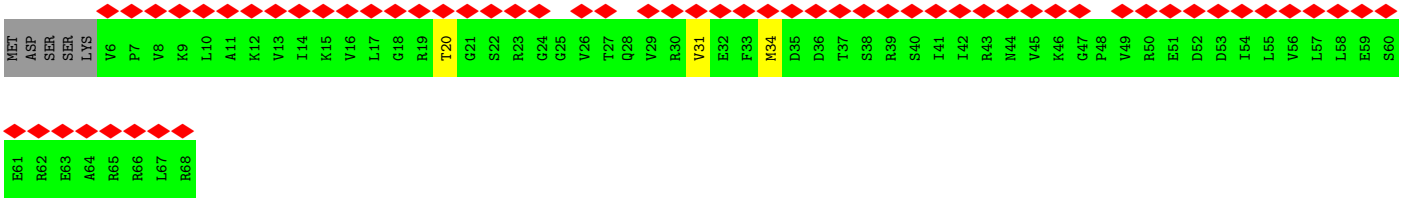
Chain Ah:





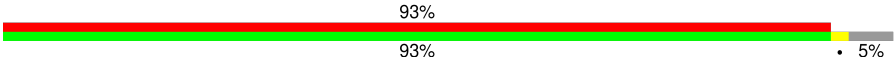
• Molecule 30: Small ribosomal subunit protein eS28A

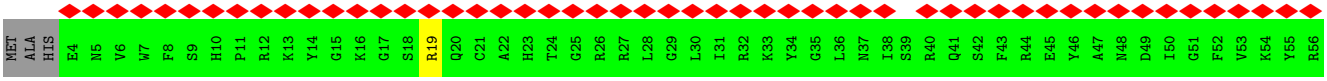
Chain Ai:



• Molecule 31: Small ribosomal subunit protein uS14

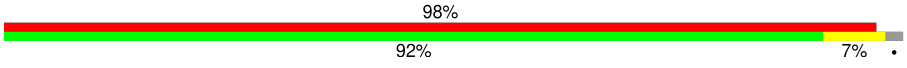
Chain Aj:

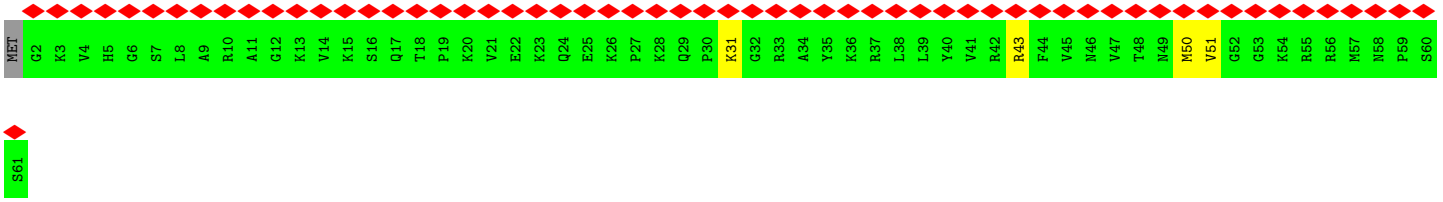




• Molecule 32: Small ribosomal subunit protein eS30B

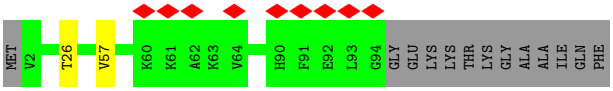
Chain Ak:





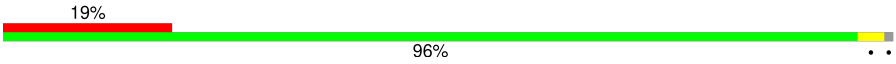
• Molecule 33: Large ribosomal subunit protein eL42

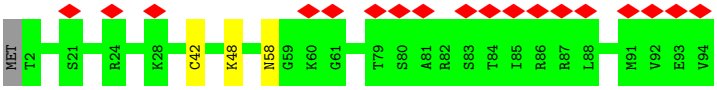
Chain B0:



• Molecule 34: Large ribosomal subunit protein eL43A

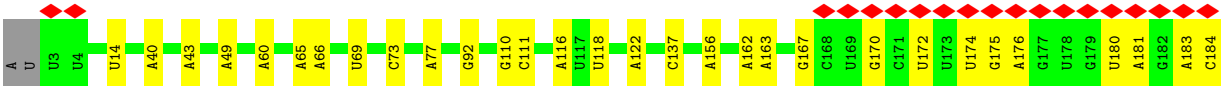
Chain B1:

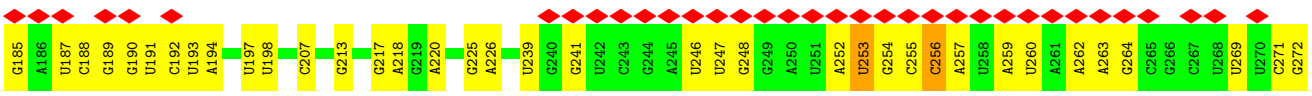


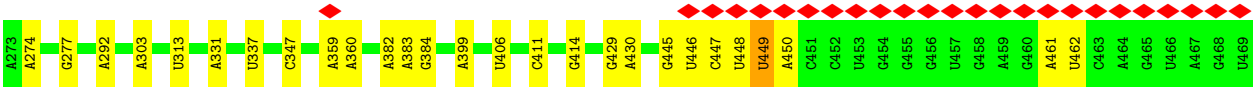


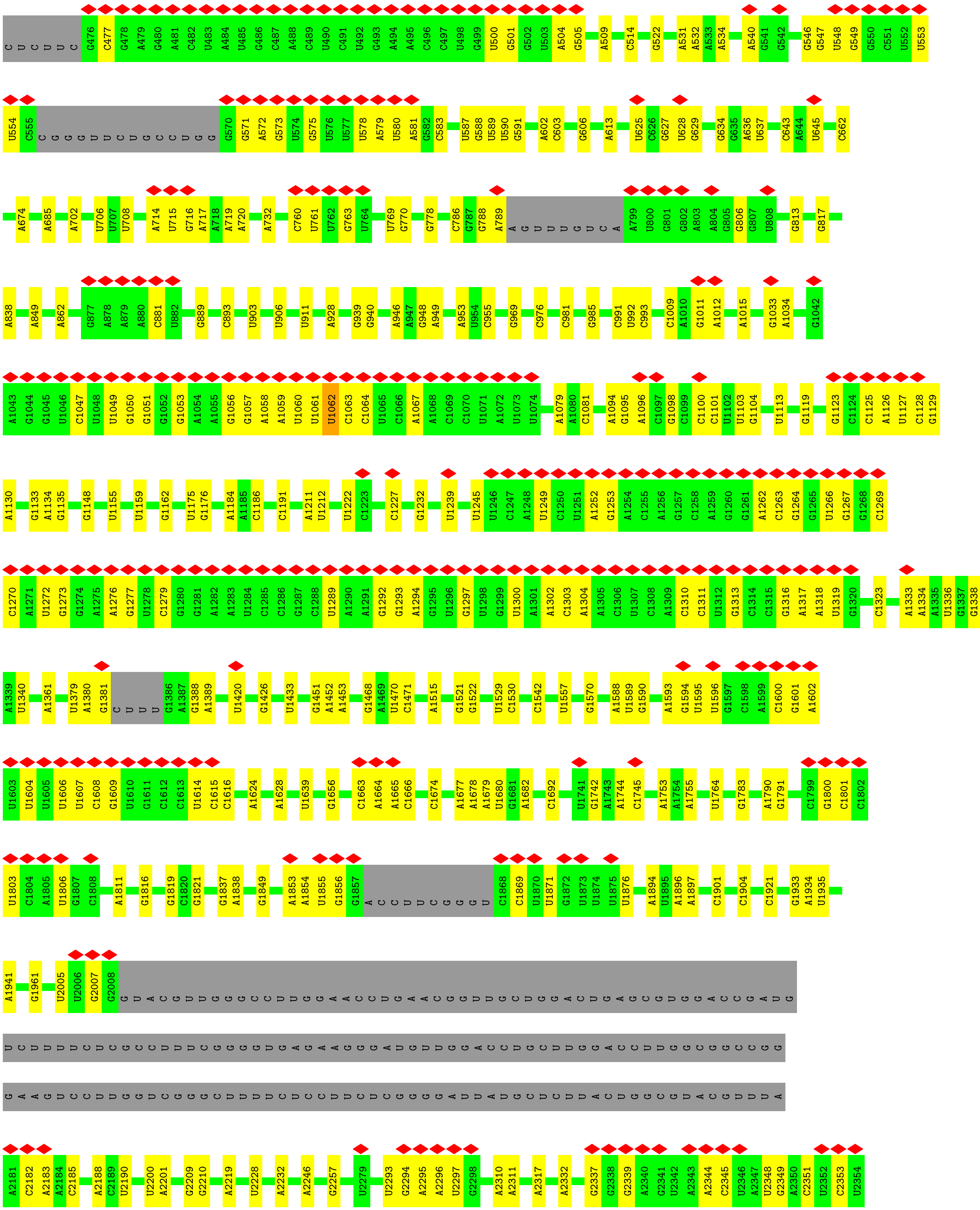
• Molecule 35: 28S ribosomal RNA

Chain B2:








C U C U U C G476 C477 G478 A479 G480 A481 C482 U483 A484 U485 G486 C487 A488 C489 U490 C491 U492 G493 A494 A495 C496 C497 U498 G499 U500 G501 G502 U503 A504 G505 A509 C514 G522 A531 A532 A533 A534 A540 G541 G542 G546 G547 U548 G549 G550 C551 U552 U553
U554 C555 C G G G U U C U G C C U G G G570 G571 A572 G573 U574 G575 U576 U577 U578 A579 U580 A581 G582 C583 U587 G588 U589 U590 G591 A602 C603 G606 A613 U625 C626 G627 U628 G629 G634 G635 A636 U637 C643 A644 U645 C662
A674 A685 A702 U706 U707 U708 A714 U715 G716 A717 A718 A719 A720 A732 C760 U761 U762 G763 U764 U769 G770 G778 C786 G787 G788 A789 A G U U U G U C A A799 U800 G801 G802 A803 A804 G805 G806 G807 U808 G813 G817
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A1043 G1044 G1045 U1046 C1047 U1048 U1049 G1050 G1051 G1052 G1053 A1054 A1055 G1056 G1057 A1058 A1059 U1060 U1061 U1062 C1063 C1064 U1065 C1066 A1067 A1068 C1069 C1070 U1071 A1072 U1073 U1074 A1079 A1080 C1081 A1094 G1095 A1096 C1097 G1098 C1099 C1100 C1101 U1102 U1103 G1104 U1113 G1119 G1123 C1124 C1125 A1126 U1127 C1128 G1129
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C1270 A1271 U1272 G1273 G1274 A1275 A1276 G1277 U1278 C1279 G1280 G1281 A1282 A1283 U1284 C1285 C1286 G1287 C1288 U1289 A1290 A1291 G1292 G1293 A1294 G1295 U1296 G1297 U1298 G1299 U1300 A1301 A1302 C1303 A1304 A1305 C1306 U1307 C1308 A1309 C1310 C1311 U1312 G1313 C1314 C1315 G1316 A1317 A1318 U1319 G1320 C1323 A1333 A1334 A1335 U1336 G1337 G1338
A1339 U1340 A1361 U1379 A1380 G1381 C U U U G1386 A1387 G1388 A1389 U1420 G1426 U1433 G1451 A1452 A1453 G1468 A1469 U1470 C1471 A1515 G1521 G1522 U1529 C1530 C1542 U1557 G1570 A1588 U1589 G1590 A1593 G1594 U1595 U1596 G1597 C1598 A1599 C1600 G1601 A1602
U1603 U1604 U1605 U1606 U1607 C1608 G1609 U1610 G1611 C1612 C1613 U1614 C1615 C1616 A1624 A1628 U1639 G1656 C1663 A1664 A1665 C1666 C1674 A1677 A1678 A1679 U1680 G1681 A1682 C1692 U1741 G1742 A1743 A1744 C1745 A1753 A1754 A1755 U1764 G1783 A1790 G1791 C1799 G1800 C1801 C1802
U1803 C1804 A1805 U1806 G1807 C1808 A1811 G1816 G1819 C1820 G1821 G1837 A1838 G1849 A1853 A1854 U1855 G1856 G1857 A C C U U C G G G U C1868 C1869 U1870 U1871 G1872 U1873 U1874 U1875 U1876 A1894 U1895 A1896 A1897 C1901 C1904 C1921 G1933 A1934 U1935
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U C U U U U C U C G C C U U U C G G G G U G A G A A G G G A U G U U G G A C C U G C U U G G A C C U U G G C G G C C G G
G A A G U C C U U G G U C G G G G C U U U U C U C C U U C U C G G G G A U U A U G G C U C U U A C U G G C G G U A C G U U U A
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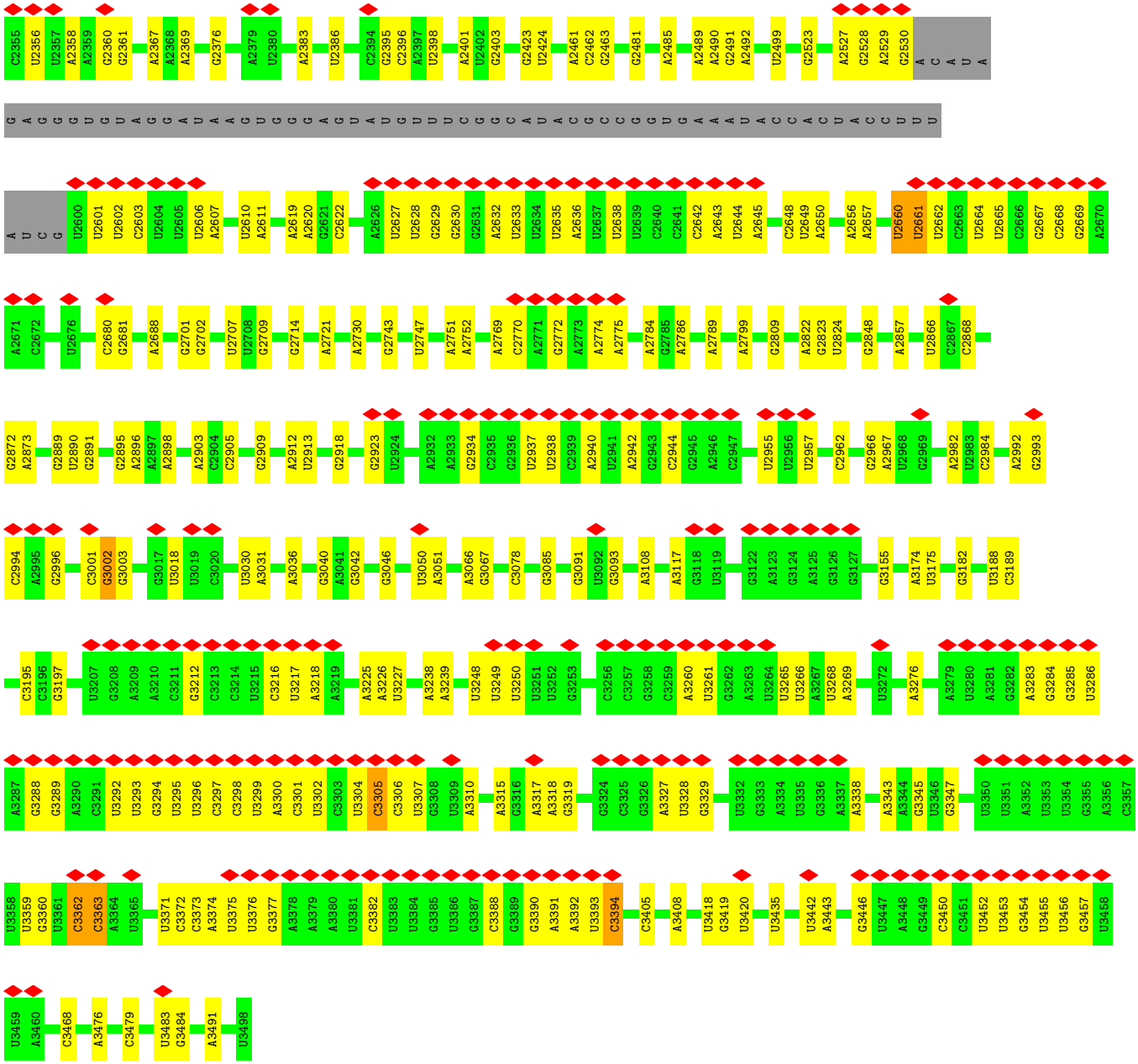
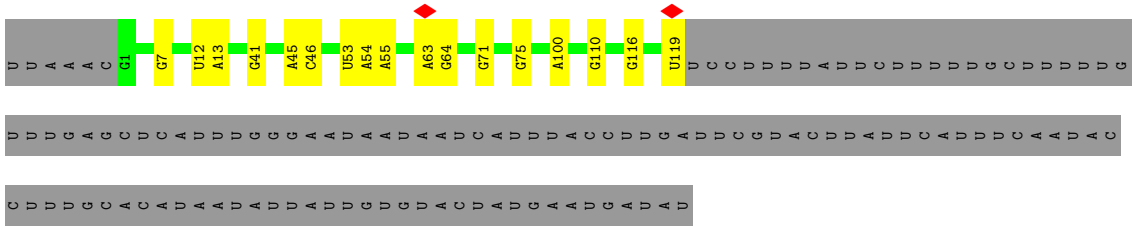


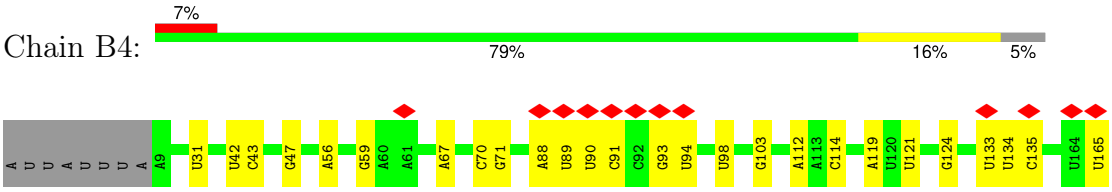
• Molecule 36: 5S ribosomal RNA

Chain B3:



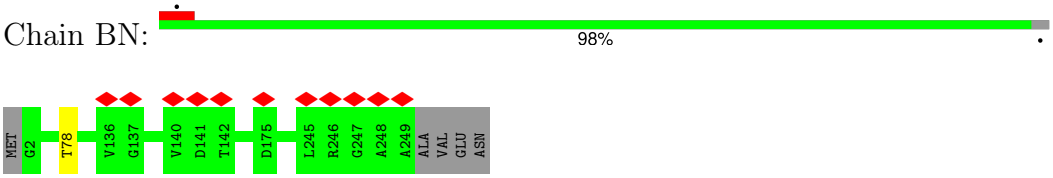
• Molecule 37: 5.8S ribosomal RNA

Chain B4:



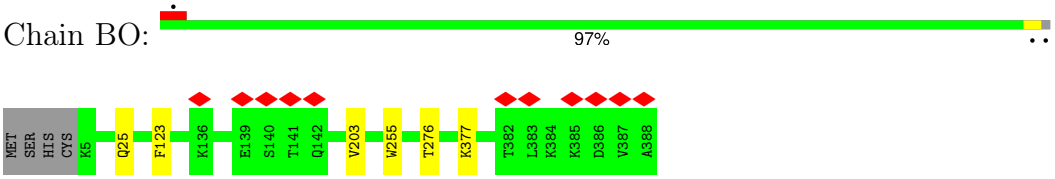
• Molecule 38: Large ribosomal subunit protein uL2C

Chain BN:



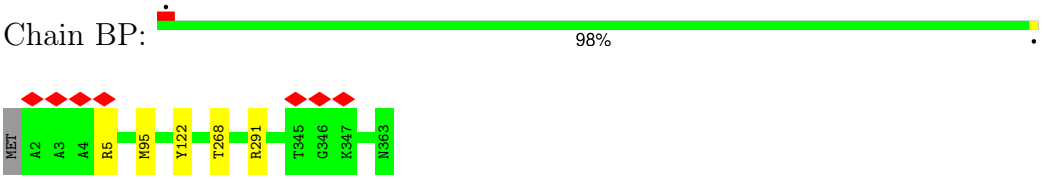
• Molecule 39: Large ribosomal subunit protein uL3A

Chain BO:



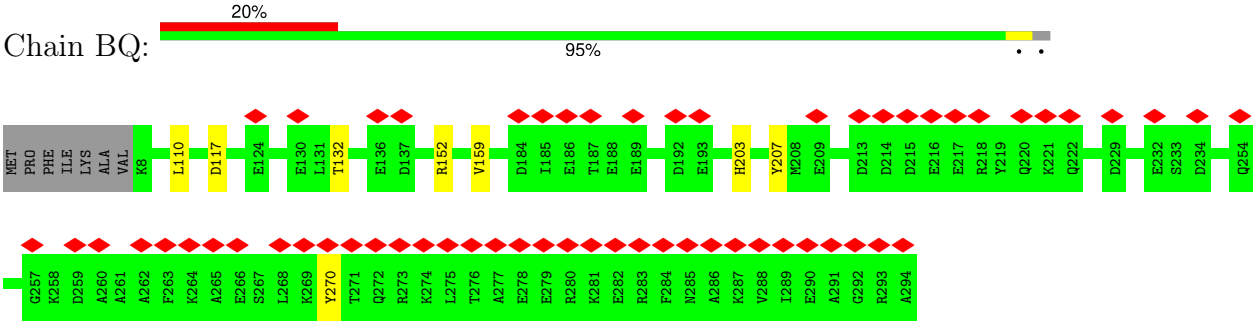
• Molecule 40: Large ribosomal subunit protein uL4A

Chain BP:



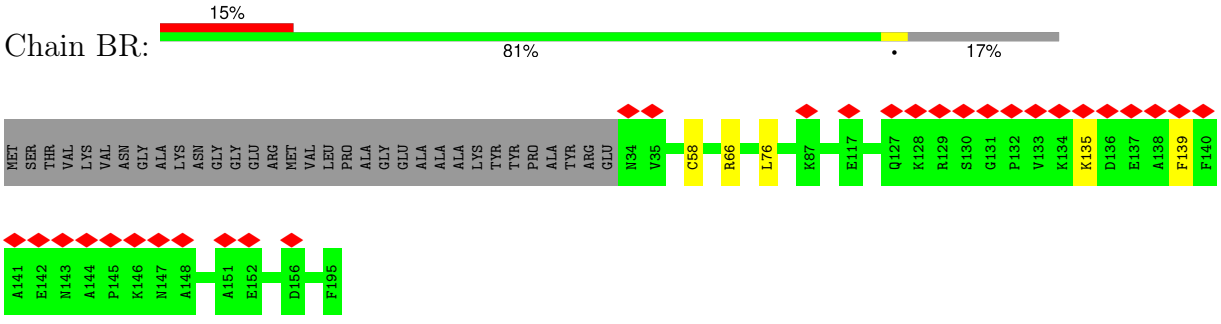
• Molecule 41: Large ribosomal subunit protein uL18B

Chain BQ:



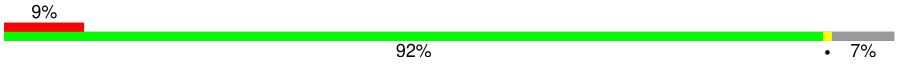
• Molecule 42: Large ribosomal subunit protein eL6

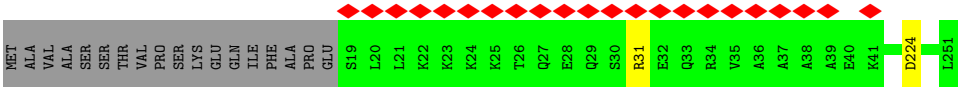
Chain BR:



• Molecule 43: Large ribosomal subunit protein uL30C

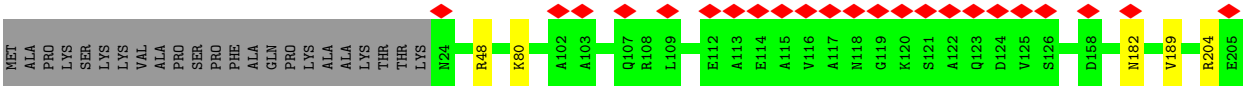
Chain BS:

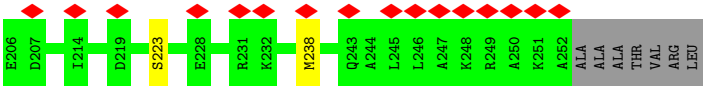




• Molecule 44: Large ribosomal subunit protein eL8

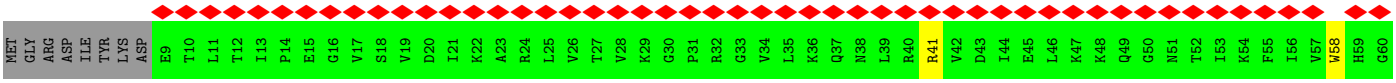
Chain BT:

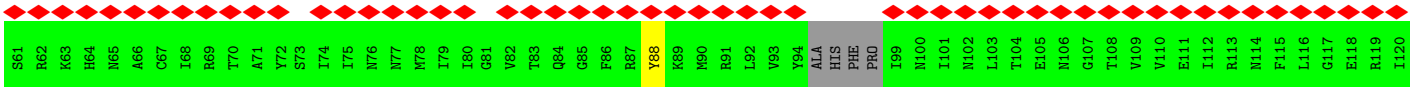


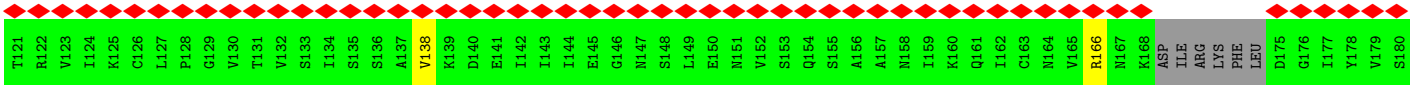


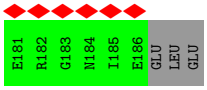
• Molecule 45: Large ribosomal subunit protein uL6B

Chain BU:



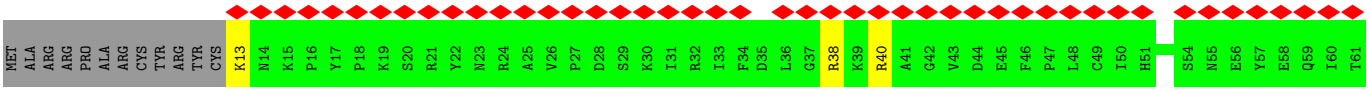


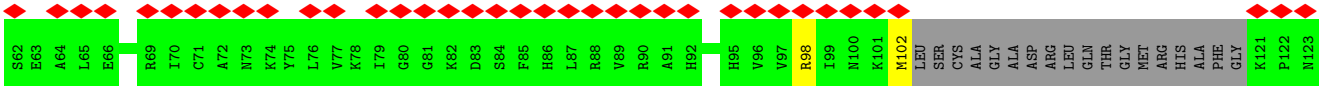


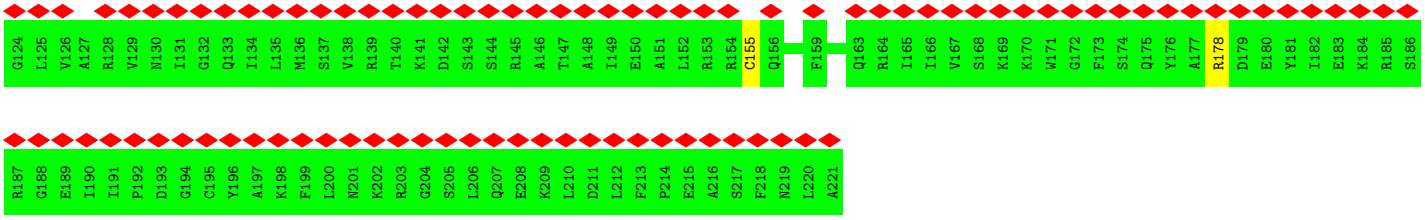


• Molecule 46: Large ribosomal subunit protein uL16A

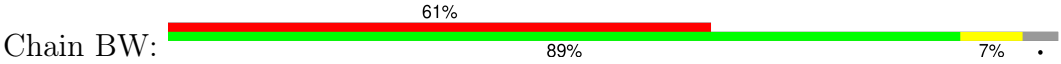
Chain BV:

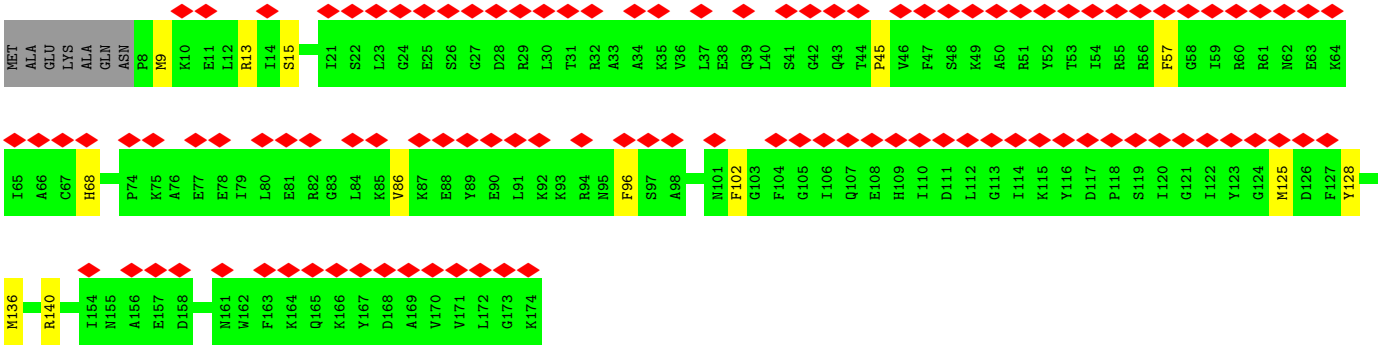




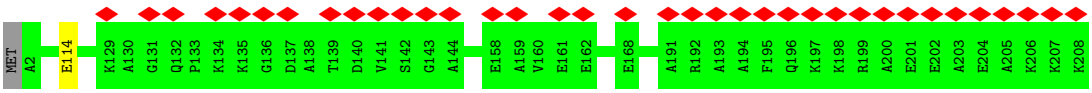


• Molecule 47: Large ribosomal subunit protein uL5A

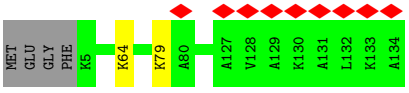




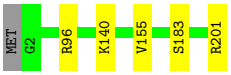
• Molecule 48: Large ribosomal subunit protein eL13



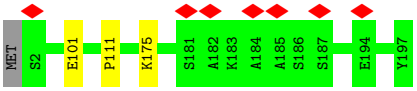
• Molecule 49: Large ribosomal subunit protein eL14



• Molecule 50: Large ribosomal subunit protein eL15B

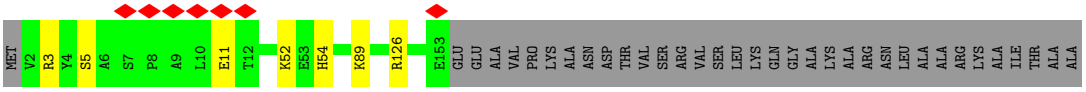


• Molecule 51: Large ribosomal subunit protein uL13A



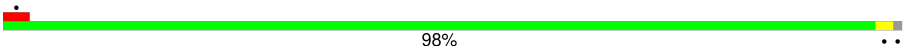
• Molecule 52: Large ribosomal subunit protein uL22A

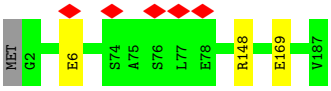
Chain Bb:



• Molecule 53: Large ribosomal subunit protein eL18B

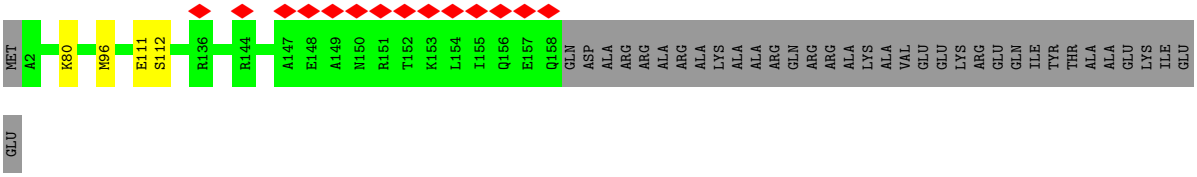
Chain Bc:





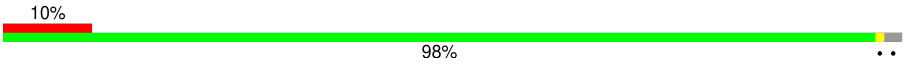
• Molecule 54: Large ribosomal subunit protein eL19B

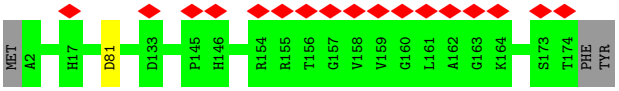
Chain Bd:



• Molecule 55: Large ribosomal subunit protein eL20A

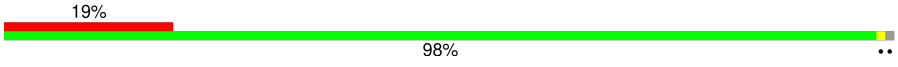
Chain Be:

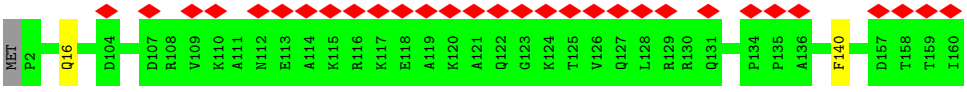




• Molecule 56: Large ribosomal subunit protein eL21B

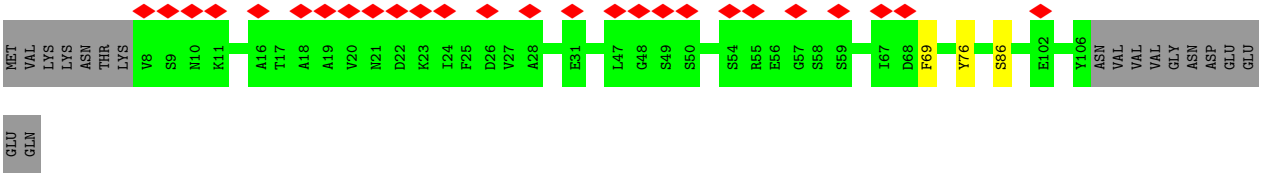
Chain Bf:





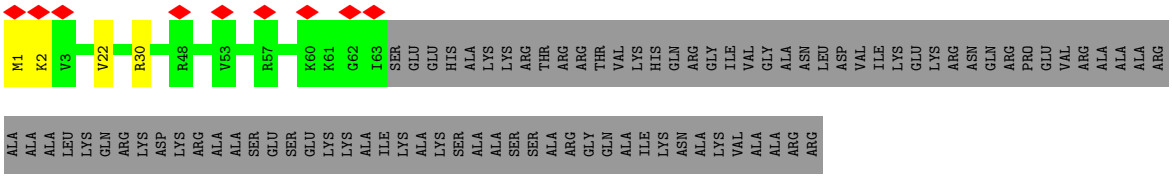
• Molecule 57: Large ribosomal subunit protein eL22

Chain Bg:

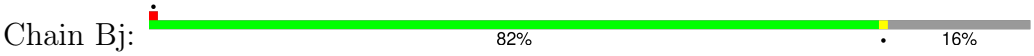


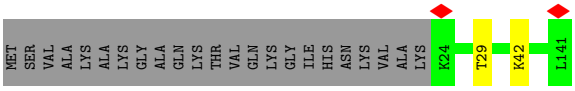
• Molecule 58: Large ribosomal subunit protein uL14B

• Molecule 59: Large ribosomal subunit protein eL24B

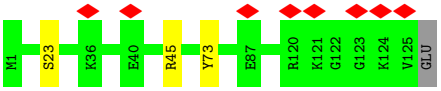


• Molecule 60: Large ribosomal subunit protein uL23A

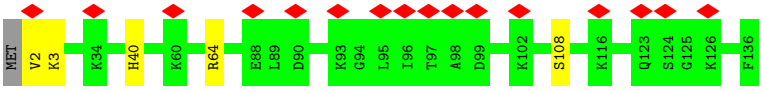




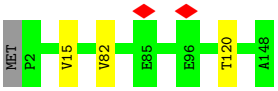
• Molecule 61: Large ribosomal subunit protein uL24



• Molecule 62: Large ribosomal subunit protein eL27A

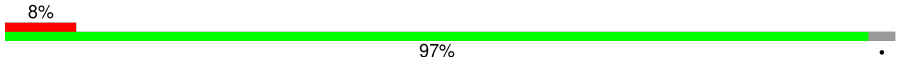


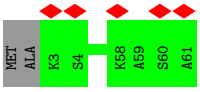
• Molecule 63: Large ribosomal subunit protein uL15B



• Molecule 64: Large ribosomal subunit protein eL29

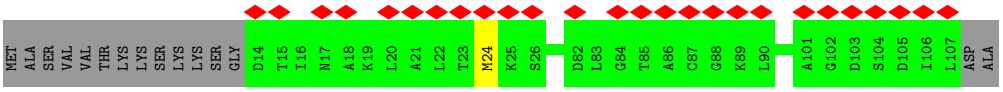
Chain Bn:





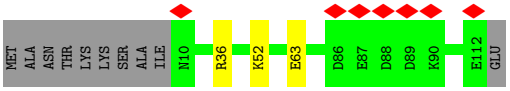
• Molecule 65: Large ribosomal subunit protein eL30A

Chain Bo:



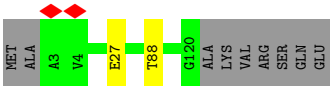
• Molecule 66: Large ribosomal subunit protein eL31

Chain Bp:



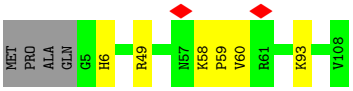
• Molecule 67: Large ribosomal subunit protein eL32A

Chain Bq:



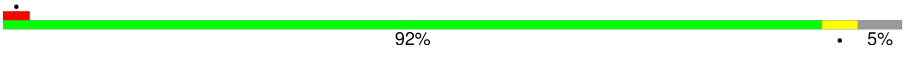
• Molecule 68: Large ribosomal subunit protein eL33A

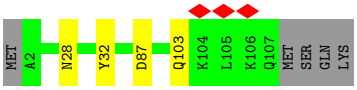
Chain Br:



• Molecule 69: Large ribosomal subunit protein eL34B

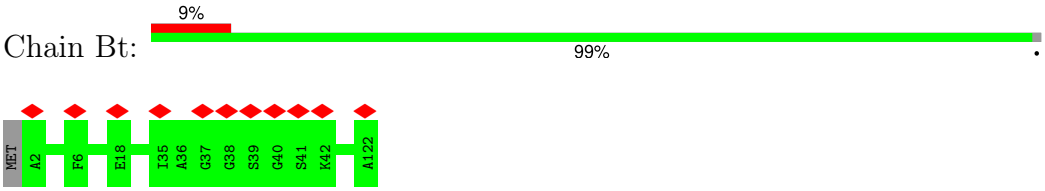
Chain Bs:





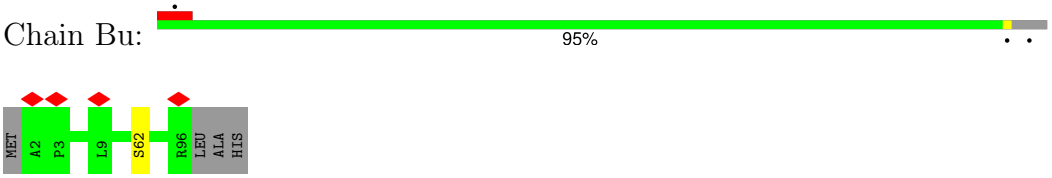
• Molecule 70: Large ribosomal subunit protein uL29

Chain Bt:



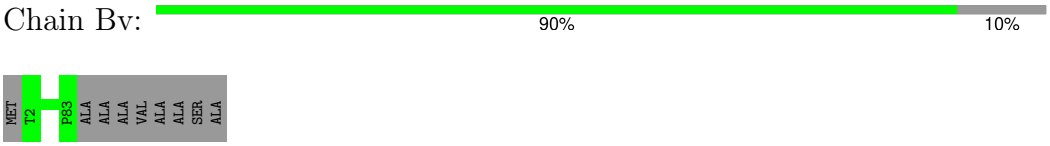
• Molecule 71: Large ribosomal subunit protein eL36B

Chain Bu:



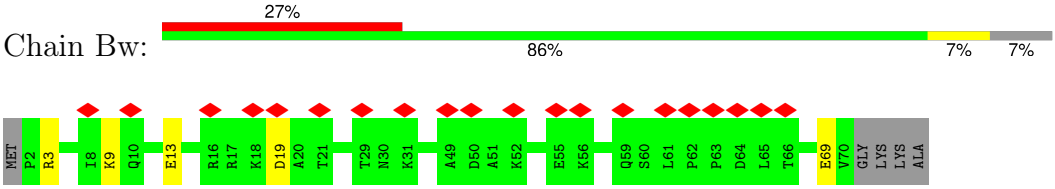
• Molecule 72: Large ribosomal subunit protein eL37B

Chain Bv:



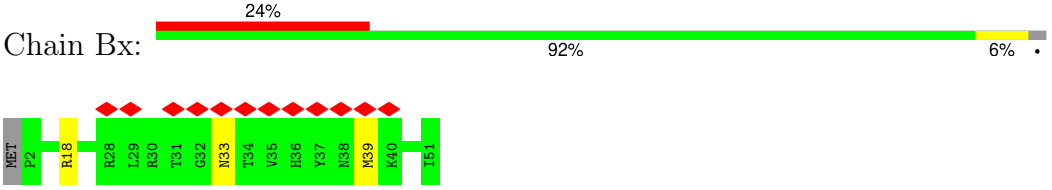
• Molecule 73: Large ribosomal subunit protein eL38A

Chain Bw:



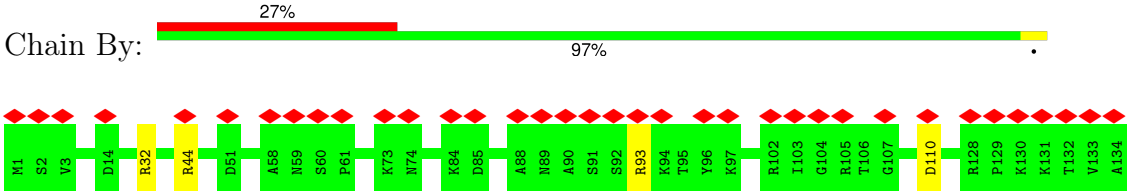
• Molecule 74: Large ribosomal subunit protein eL39

Chain Bx:



• Molecule 75: Large ribosomal subunit protein eL28

Chain By:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	73376	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.236	Depositor
Minimum map value	-1.145	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.080	Depositor
Recommended contour level	0.26	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	AA	0.17	0/40661	0.77	22/63326 (0.0%)
2	AD	0.25	0/1635	0.53	0/2228
3	AE	0.24	0/1756	0.52	0/2358
4	AF	0.26	0/1695	0.51	1/2297 (0.0%)
5	AG	0.24	0/1726	0.51	0/2316
6	AH	0.25	0/2125	0.55	0/2858
7	AI	0.24	0/1577	0.49	0/2123
8	AJ	0.25	0/1815	0.56	0/2428
9	AK	0.25	0/1554	0.54	0/2091
10	AL	0.24	0/1534	0.55	0/2050
11	AM	0.25	0/1487	0.58	0/1990
12	AN	0.24	0/769	0.48	0/1043
13	AO	0.24	0/1190	0.52	0/1602
14	AP	0.23	0/892	0.48	0/1208
15	AQ	0.83	2/1208 (0.2%)	1.04	5/1624 (0.3%)
16	AR	0.25	0/961	0.56	0/1293
17	AS	0.25	0/973	0.56	0/1307
18	AT	0.24	0/1100	0.49	0/1474
19	AU	0.23	0/983	0.55	0/1318
20	AV	0.23	0/1158	0.51	0/1552
21	AW	0.23	0/1139	0.47	0/1531
22	Aa	0.22	0/826	0.53	0/1114
23	Ab	0.23	0/680	0.49	0/918
24	Ac	0.23	0/1042	0.49	0/1399
25	Ad	0.25	0/1115	0.52	0/1489
26	Ae	0.24	0/1093	0.54	0/1453
27	Af	0.23	0/558	0.55	0/750
28	Ag	0.23	0/808	0.57	0/1083
29	Ah	0.41	1/630 (0.2%)	0.66	1/845 (0.1%)
30	Ai	0.24	0/500	0.63	0/669
31	Aj	0.24	0/458	0.56	0/610
32	Ak	0.23	0/482	0.55	0/639

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
33	B0	0.24	0/772	0.51	0/1025
34	B1	0.23	0/727	0.58	0/973
35	B2	0.19	0/76871	0.79	41/119827 (0.0%)
36	B3	0.18	0/2838	0.77	0/4422
37	B4	0.18	0/3723	0.76	0/5796
38	BN	0.24	0/1910	0.54	0/2575
39	BO	0.24	0/3116	0.51	0/4190
40	BP	0.24	0/2852	0.49	0/3850
41	BQ	0.24	0/2361	0.50	0/3173
42	BR	0.25	0/1275	0.50	0/1719
43	BS	0.24	0/1929	0.47	0/2583
44	BT	0.24	0/1801	0.45	0/2430
45	BU	0.23	0/1330	0.50	0/1789
46	BV	0.24	0/1579	0.49	0/2115
47	BW	0.58	2/1369 (0.1%)	0.74	4/1830 (0.2%)
48	BX	0.24	0/1686	0.51	0/2267
49	BY	0.23	0/1054	0.48	0/1413
50	BZ	0.23	0/1717	0.54	0/2306
51	Ba	0.25	0/1575	0.48	0/2109
52	Bb	0.25	0/1237	0.49	0/1661
53	Bc	0.24	0/1511	0.55	0/2021
54	Bd	0.23	0/1320	0.51	0/1757
55	Be	0.25	0/1458	0.51	0/1961
56	Bf	0.24	0/1314	0.49	0/1771
57	Bg	0.24	0/812	0.48	0/1090
58	Bh	0.25	0/1015	0.52	0/1369
59	Bi	0.25	0/534	0.50	0/709
60	Bj	0.24	0/963	0.49	0/1296
61	Bk	0.23	0/1008	0.54	0/1341
62	Bl	0.24	0/1101	0.49	0/1477
63	Bm	0.23	0/1200	0.52	0/1611
64	Bn	0.23	0/503	0.51	0/664
65	Bo	0.25	0/714	0.52	0/961
66	Bp	0.23	0/872	0.52	0/1172
67	Bq	0.24	0/958	0.53	0/1278
68	Br	0.53	2/853 (0.2%)	1.03	3/1146 (0.3%)
69	Bs	0.25	0/870	0.56	0/1165
70	Bt	0.23	0/1008	0.49	0/1340
71	Bu	0.23	0/766	0.53	0/1017
72	Bv	0.24	0/666	0.56	0/881
73	Bw	0.26	0/566	0.54	0/757
74	Bx	0.23	0/447	0.58	0/597
75	By	0.23	0/1053	0.51	0/1414

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
All	All	0.23	7/209364 (0.0%)	0.70	77/307834 (0.0%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	AQ	61	PRO	CG-CD	-24.71	0.69	1.50
47	BW	45	PRO	CG-CD	-18.24	0.90	1.50
68	Br	59	PRO	CB-CG	-11.28	0.93	1.50
15	AQ	61	PRO	CB-CG	11.14	2.05	1.50
29	Ah	10	PRO	CG-CD	-6.76	1.28	1.50

The worst 5 of 77 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	AQ	61	PRO	N-CD-CG	-26.75	63.07	103.20
35	B2	3363	C	O5'-P-OP1	-24.73	81.02	110.70
15	AQ	61	PRO	CA-CB-CG	-19.05	67.80	104.00
68	Br	59	PRO	CB-CG-CD	18.84	179.98	106.50
47	BW	45	PRO	N-CD-CG	-17.52	76.92	103.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AD	203/292 (70%)	183 (90%)	20 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	AE	214/252 (85%)	197 (92%)	16 (8%)	1 (0%)	25 38
4	AF	214/253 (85%)	205 (96%)	8 (4%)	1 (0%)	25 38
5	AG	214/249 (86%)	201 (94%)	13 (6%)	0	100 100
6	AH	259/262 (99%)	249 (96%)	9 (4%)	1 (0%)	30 44
7	AI	201/203 (99%)	187 (93%)	13 (6%)	1 (0%)	25 38
8	AJ	219/239 (92%)	210 (96%)	9 (4%)	0	100 100
9	AK	191/195 (98%)	181 (95%)	10 (5%)	0	100 100
10	AL	184/200 (92%)	179 (97%)	5 (3%)	0	100 100
11	AM	176/192 (92%)	166 (94%)	9 (5%)	1 (1%)	22 33
12	AN	90/147 (61%)	77 (86%)	12 (13%)	1 (1%)	12 18
13	AO	141/152 (93%)	126 (89%)	15 (11%)	0	100 100
14	AP	119/145 (82%)	103 (87%)	14 (12%)	2 (2%)	7 10
15	AQ	148/151 (98%)	143 (97%)	5 (3%)	0	100 100
16	AR	126/139 (91%)	117 (93%)	9 (7%)	0	100 100
17	AS	117/154 (76%)	102 (87%)	15 (13%)	0	100 100
18	AT	138/140 (99%)	134 (97%)	4 (3%)	0	100 100
19	AU	116/131 (88%)	107 (92%)	7 (6%)	2 (2%)	7 10
20	AV	139/152 (91%)	129 (93%)	10 (7%)	0	100 100
21	AW	140/144 (97%)	131 (94%)	9 (6%)	0	100 100
22	Aa	99/118 (84%)	97 (98%)	2 (2%)	0	100 100
23	Ab	85/87 (98%)	81 (95%)	4 (5%)	0	100 100
24	Ac	127/130 (98%)	122 (96%)	5 (4%)	0	100 100
25	Ad	140/143 (98%)	135 (96%)	5 (4%)	0	100 100
26	Ae	131/134 (98%)	126 (96%)	5 (4%)	0	100 100
27	Af	67/89 (75%)	66 (98%)	1 (2%)	0	100 100
28	Ag	95/119 (80%)	91 (96%)	4 (4%)	0	100 100
29	Ah	79/83 (95%)	75 (95%)	4 (5%)	0	100 100
30	Ai	61/68 (90%)	57 (93%)	4 (7%)	0	100 100
31	Aj	51/56 (91%)	45 (88%)	6 (12%)	0	100 100
32	Ak	58/61 (95%)	52 (90%)	5 (9%)	1 (2%)	7 10
33	B0	91/106 (86%)	88 (97%)	3 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	B1	91/94 (97%)	84 (92%)	7 (8%)	0	100	100
38	BN	246/253 (97%)	231 (94%)	15 (6%)	0	100	100
39	BO	382/388 (98%)	369 (97%)	13 (3%)	0	100	100
40	BP	360/363 (99%)	346 (96%)	14 (4%)	0	100	100
41	BQ	285/294 (97%)	279 (98%)	6 (2%)	0	100	100
42	BR	160/195 (82%)	143 (89%)	17 (11%)	0	100	100
43	BS	231/251 (92%)	226 (98%)	5 (2%)	0	100	100
44	BT	227/259 (88%)	222 (98%)	5 (2%)	0	100	100
45	BU	162/189 (86%)	157 (97%)	5 (3%)	0	100	100
46	BV	187/221 (85%)	183 (98%)	4 (2%)	0	100	100
47	BW	165/174 (95%)	157 (95%)	8 (5%)	0	100	100
48	BX	205/208 (99%)	201 (98%)	4 (2%)	0	100	100
49	BY	128/134 (96%)	126 (98%)	2 (2%)	0	100	100
50	BZ	198/201 (98%)	191 (96%)	6 (3%)	1 (0%)	25	38
51	Ba	194/197 (98%)	191 (98%)	3 (2%)	0	100	100
52	Bb	150/187 (80%)	145 (97%)	5 (3%)	0	100	100
53	Bc	184/187 (98%)	178 (97%)	6 (3%)	0	100	100
54	Bd	155/193 (80%)	151 (97%)	4 (3%)	0	100	100
55	Be	171/176 (97%)	168 (98%)	3 (2%)	0	100	100
56	Bf	157/160 (98%)	151 (96%)	6 (4%)	0	100	100
57	Bg	97/117 (83%)	87 (90%)	10 (10%)	0	100	100
58	Bh	132/139 (95%)	127 (96%)	5 (4%)	0	100	100
59	Bi	61/149 (41%)	60 (98%)	1 (2%)	0	100	100
60	Bj	116/141 (82%)	109 (94%)	7 (6%)	0	100	100
61	Bk	123/126 (98%)	121 (98%)	2 (2%)	0	100	100
62	Bl	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
63	Bm	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
64	Bn	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
65	Bo	92/109 (84%)	91 (99%)	1 (1%)	0	100	100
66	Bp	101/113 (89%)	98 (97%)	3 (3%)	0	100	100
67	Bq	116/127 (91%)	114 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	Br	102/108 (94%)	100 (98%)	2 (2%)	0	100	100
69	Bs	104/111 (94%)	101 (97%)	3 (3%)	0	100	100
70	Bt	119/122 (98%)	116 (98%)	3 (2%)	0	100	100
71	Bu	93/99 (94%)	91 (98%)	2 (2%)	0	100	100
72	Bv	80/91 (88%)	74 (92%)	6 (8%)	0	100	100
73	Bw	67/74 (90%)	65 (97%)	2 (3%)	0	100	100
74	Bx	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
75	By	132/134 (98%)	126 (96%)	6 (4%)	0	100	100
All	All	10389/11466 (91%)	9904 (95%)	473 (5%)	12 (0%)	50	65

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	AH	12	VAL
19	AU	118	VAL
3	AE	147	ALA
7	AI	79	GLY
50	BZ	183	SER

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	
2	AD	170/228 (75%)	161 (95%)	9 (5%)	19	33
3	AE	193/223 (86%)	181 (94%)	12 (6%)	15	26
4	AF	175/199 (88%)	167 (95%)	8 (5%)	23	39
5	AG	181/203 (89%)	168 (93%)	13 (7%)	12	20
6	AH	226/227 (100%)	211 (93%)	15 (7%)	14	23
7	AI	169/169 (100%)	163 (96%)	6 (4%)	30	49
8	AJ	188/204 (92%)	180 (96%)	8 (4%)	25	42
9	AK	169/171 (99%)	157 (93%)	12 (7%)	12	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	AL	157/166 (95%)	152 (97%)	5 (3%)	34	54
11	AM	155/165 (94%)	149 (96%)	6 (4%)	27	46
12	AN	77/116 (66%)	77 (100%)	0	100	100
13	AO	124/131 (95%)	118 (95%)	6 (5%)	21	37
14	AP	92/118 (78%)	86 (94%)	6 (6%)	14	24
15	AQ	127/128 (99%)	124 (98%)	3 (2%)	44	64
16	AR	95/104 (91%)	90 (95%)	5 (5%)	19	33
17	AS	101/131 (77%)	97 (96%)	4 (4%)	27	45
18	AT	111/111 (100%)	109 (98%)	2 (2%)	54	73
19	AU	107/120 (89%)	103 (96%)	4 (4%)	29	48
20	AV	127/136 (93%)	124 (98%)	3 (2%)	44	64
21	AW	117/119 (98%)	112 (96%)	5 (4%)	25	42
22	Aa	95/111 (86%)	93 (98%)	2 (2%)	48	69
23	Ab	73/73 (100%)	68 (93%)	5 (7%)	13	22
24	Ac	114/115 (99%)	112 (98%)	2 (2%)	54	73
25	Ad	112/113 (99%)	107 (96%)	5 (4%)	23	40
26	Ae	112/113 (99%)	107 (96%)	5 (4%)	23	40
27	Af	61/75 (81%)	58 (95%)	3 (5%)	21	36
28	Ag	87/106 (82%)	82 (94%)	5 (6%)	17	29
29	Ah	71/73 (97%)	69 (97%)	2 (3%)	38	59
30	Ai	56/61 (92%)	53 (95%)	3 (5%)	18	32
31	Aj	45/47 (96%)	44 (98%)	1 (2%)	47	67
32	Ak	51/52 (98%)	48 (94%)	3 (6%)	16	28
33	B0	84/93 (90%)	82 (98%)	2 (2%)	44	64
34	B1	74/75 (99%)	71 (96%)	3 (4%)	26	44
38	BN	188/192 (98%)	187 (100%)	1 (0%)	86	94
39	BO	318/326 (98%)	312 (98%)	6 (2%)	52	72
40	BP	293/294 (100%)	288 (98%)	5 (2%)	56	75
41	BQ	235/241 (98%)	227 (97%)	8 (3%)	32	52
42	BR	132/155 (85%)	127 (96%)	5 (4%)	28	47
43	BS	198/213 (93%)	196 (99%)	2 (1%)	73	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
44	BT	182/212 (86%)	175 (96%)	7 (4%)	28 47
45	BU	149/168 (89%)	144 (97%)	5 (3%)	32 52
46	BV	165/187 (88%)	158 (96%)	7 (4%)	25 43
47	BW	141/146 (97%)	129 (92%)	12 (8%)	8 14
48	BX	166/167 (99%)	165 (99%)	1 (1%)	84 92
49	BY	110/113 (97%)	108 (98%)	2 (2%)	54 73
50	BZ	175/176 (99%)	171 (98%)	4 (2%)	45 66
51	Ba	159/160 (99%)	156 (98%)	3 (2%)	52 72
52	Bb	124/149 (83%)	117 (94%)	7 (6%)	17 30
53	Bc	157/158 (99%)	154 (98%)	3 (2%)	52 72
54	Bd	136/163 (83%)	132 (97%)	4 (3%)	37 58
55	Be	151/154 (98%)	150 (99%)	1 (1%)	81 91
56	Bf	138/139 (99%)	136 (99%)	2 (1%)	62 79
57	Bg	86/103 (84%)	83 (96%)	3 (4%)	31 51
58	Bh	103/107 (96%)	99 (96%)	4 (4%)	27 46
59	Bi	57/121 (47%)	53 (93%)	4 (7%)	12 21
60	Bj	105/122 (86%)	103 (98%)	2 (2%)	52 72
61	Bk	110/111 (99%)	107 (97%)	3 (3%)	40 60
62	Bl	114/115 (99%)	109 (96%)	5 (4%)	24 41
63	Bm	122/123 (99%)	119 (98%)	3 (2%)	42 63
64	Bn	50/51 (98%)	50 (100%)	0	100 100
65	Bo	75/87 (86%)	74 (99%)	1 (1%)	65 81
66	Bp	94/102 (92%)	91 (97%)	3 (3%)	34 54
67	Bq	100/107 (94%)	98 (98%)	2 (2%)	50 70
68	Br	91/94 (97%)	86 (94%)	5 (6%)	18 31
69	Bs	91/96 (95%)	87 (96%)	4 (4%)	24 41
70	Bt	106/107 (99%)	106 (100%)	0	100 100
71	Bu	81/84 (96%)	80 (99%)	1 (1%)	67 82
72	Bv	68/71 (96%)	68 (100%)	0	100 100
73	Bw	63/66 (96%)	58 (92%)	5 (8%)	10 16
74	Bx	46/47 (98%)	43 (94%)	3 (6%)	14 24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
75	By	113/113 (100%)	109 (96%)	4 (4%)	31 51
All	All	8888/9616 (92%)	8578 (96%)	310 (4%)	33 51

5 of 310 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	BX	114	GLU
67	Bq	27	GLU
51	Ba	101	GLU
57	Bg	86	SER
73	Bw	13	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
39	BO	293	ASN
70	Bt	84	GLN
43	BS	194	HIS
70	Bt	33	GLN
75	By	41	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1687/1842 (91%)	413 (24%)	16 (0%)
35	B2	3204/3498 (91%)	644 (20%)	26 (0%)
36	B3	118/246 (47%)	17 (14%)	1 (0%)
37	B4	156/165 (94%)	26 (16%)	1 (0%)
All	All	5165/5751 (89%)	1100 (21%)	44 (0%)

5 of 1100 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	3	C
1	AA	4	C
1	AA	25	C
1	AA	26	A
1	AA	34	G

5 of 44 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	B2	1269	C
35	B2	3217	U
35	B2	1272	U
35	B2	2661	U
35	B2	3292	U

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 6 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AA	9

The worst 5 of 9 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	537:A	O3'	538:A	P	4.50
1	AA	546:C	O3'	547:A	P	4.24
1	AA	1419:A	O3'	1420:A	P	4.11
1	AA	1359:C	O3'	1360:U	P	3.79
1	AA	1483:C	O3'	1484:G	P	3.67

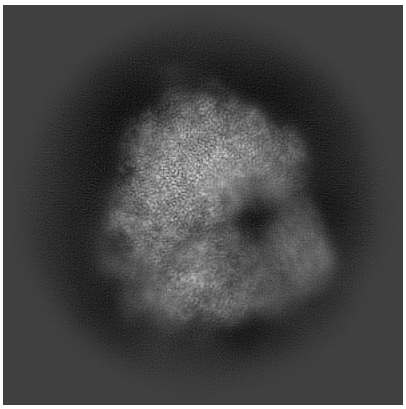
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-43972. These allow visual inspection of the internal detail of the map and identification of artifacts.

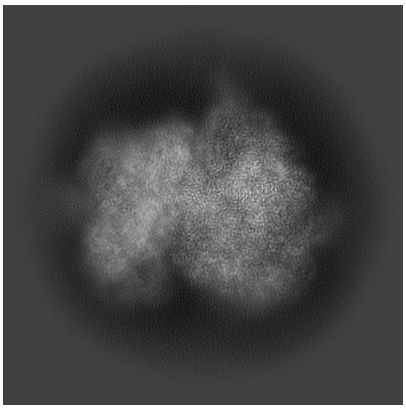
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

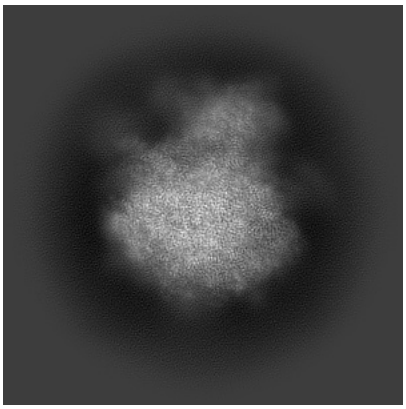
6.1.1 Primary map



X

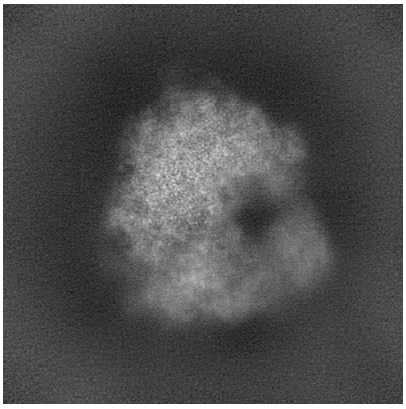


Y

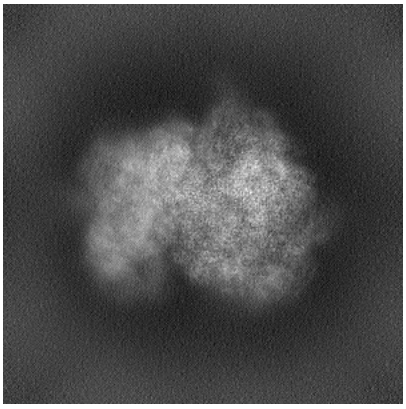


Z

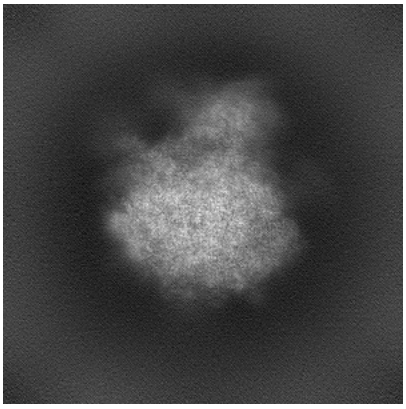
6.1.2 Raw map



X



Y

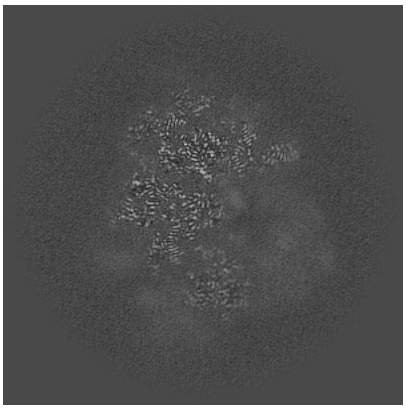


Z

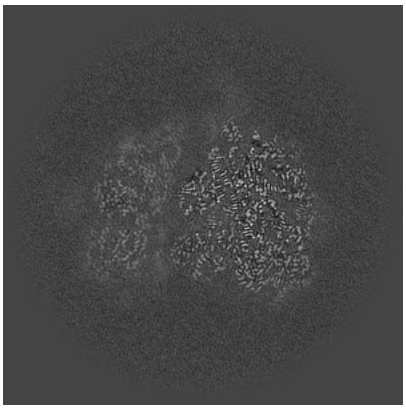
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

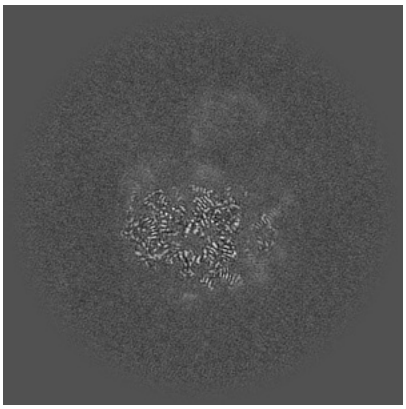
6.2.1 Primary map



X Index: 256

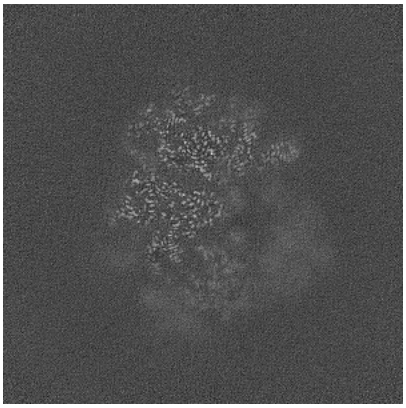


Y Index: 256

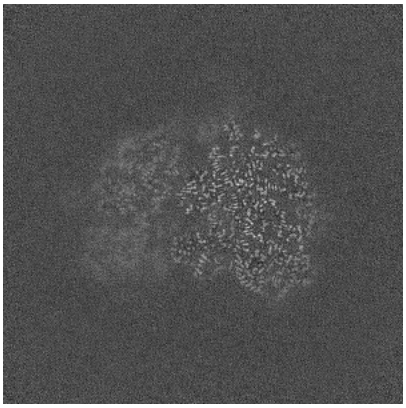


Z Index: 256

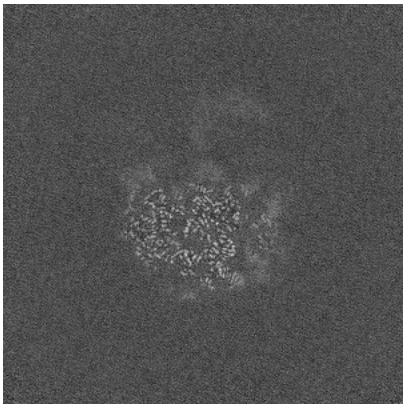
6.2.2 Raw map



X Index: 256



Y Index: 256

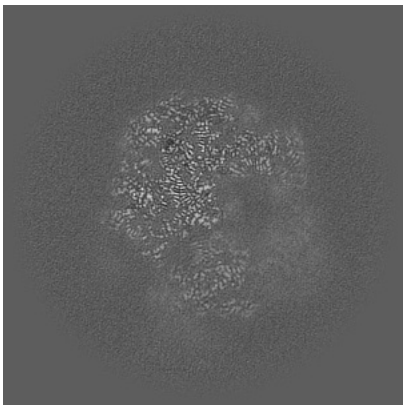


Z Index: 256

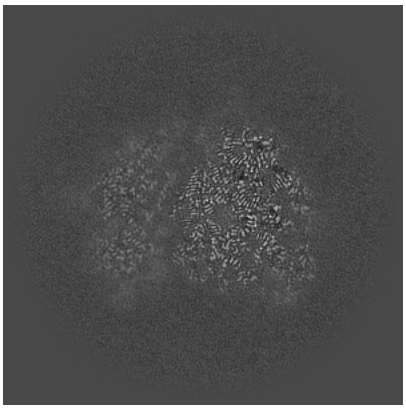
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

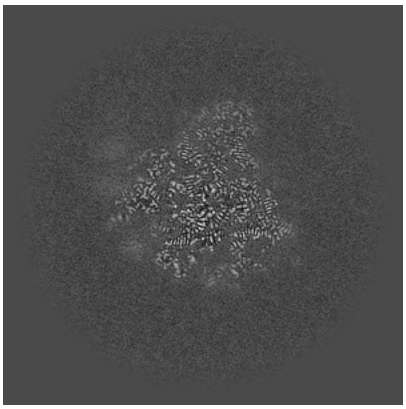
6.3.1 Primary map



X Index: 275

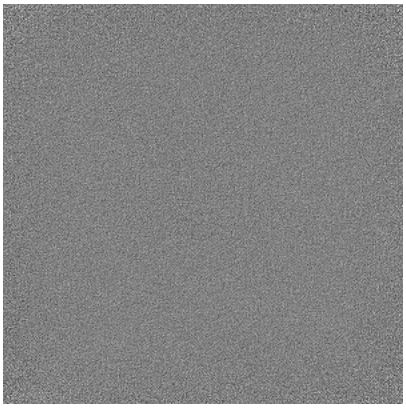


Y Index: 247

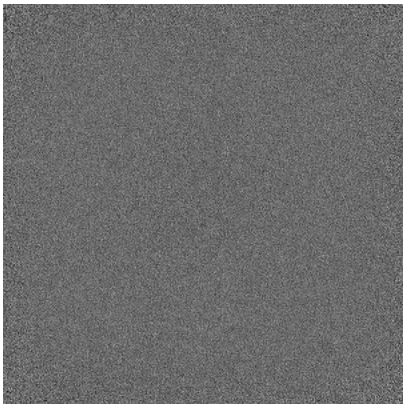


Z Index: 323

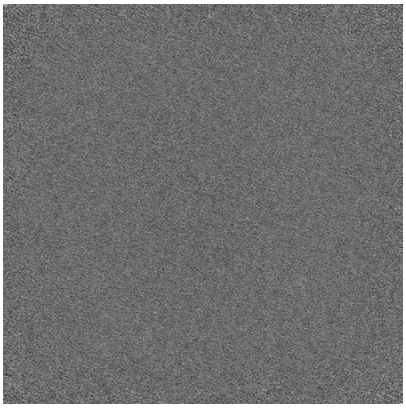
6.3.2 Raw map



X Index: 0



Y Index: 0

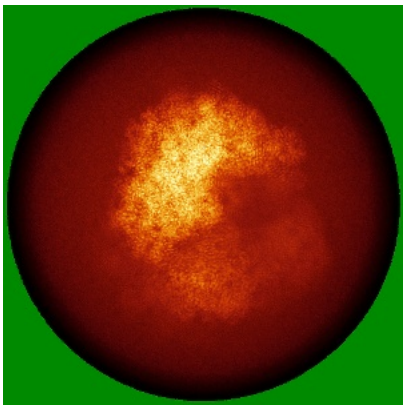


Z Index: 0

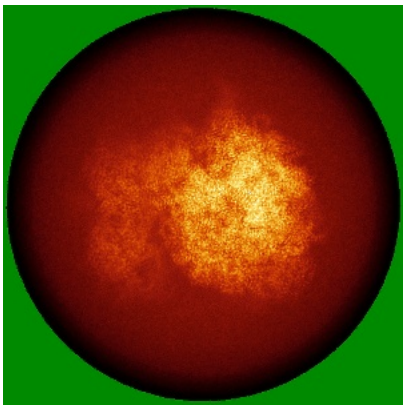
The images above show the largest variance slices of the map in three orthogonal directions.

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

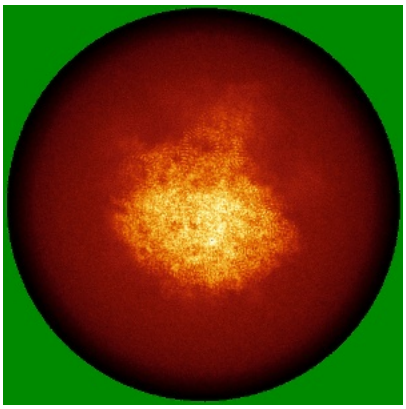
6.4.1 Primary map



X

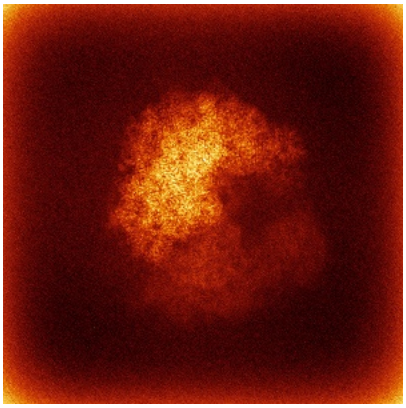


Y

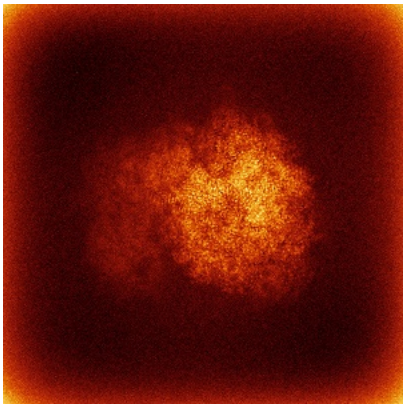


Z

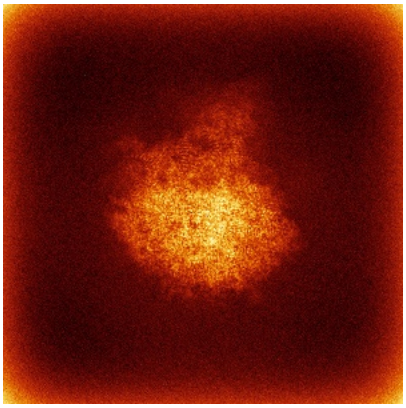
6.4.2 Raw map



X



Y

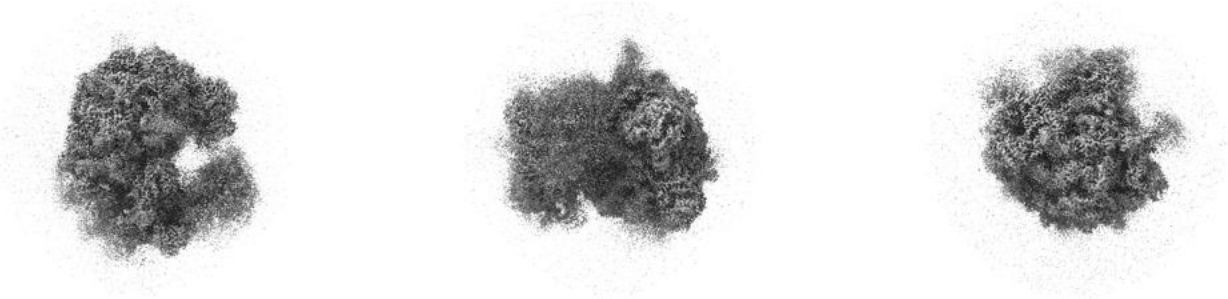


Z

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)

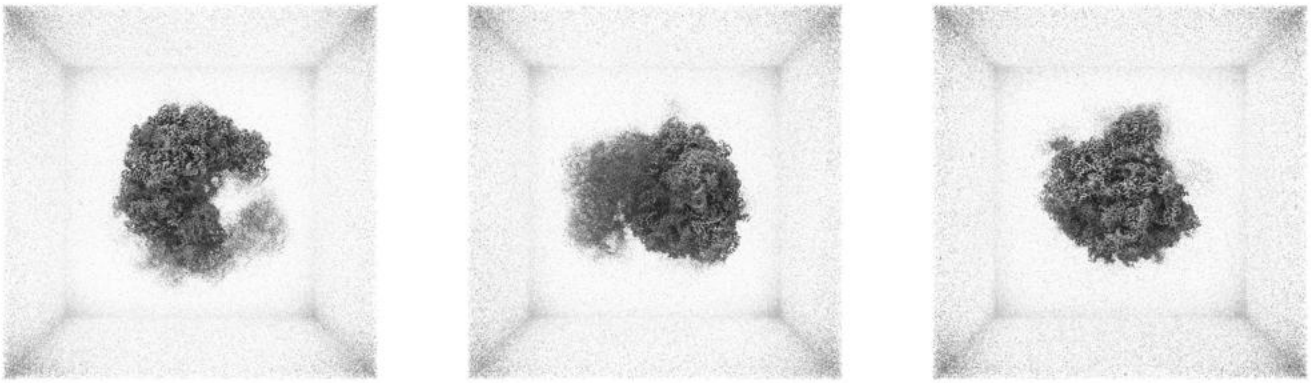
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.26. 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.

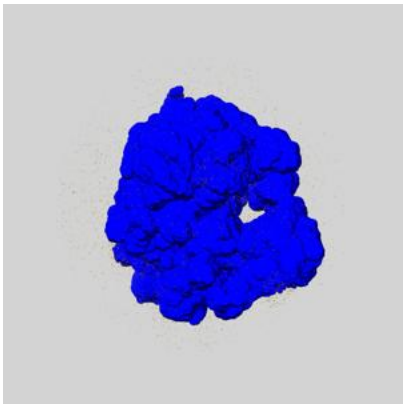
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

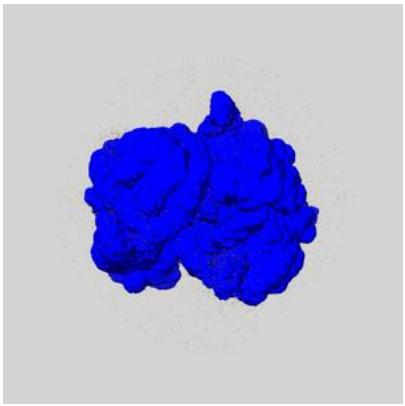
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

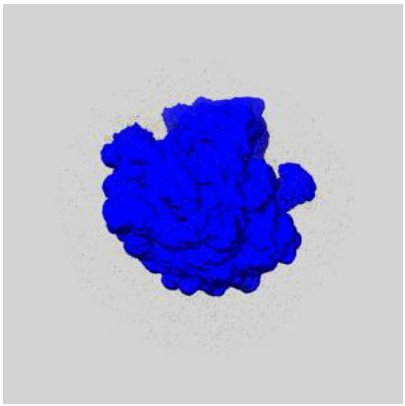
6.6.1 emd_43972_msk_1.map (i)



X



Y

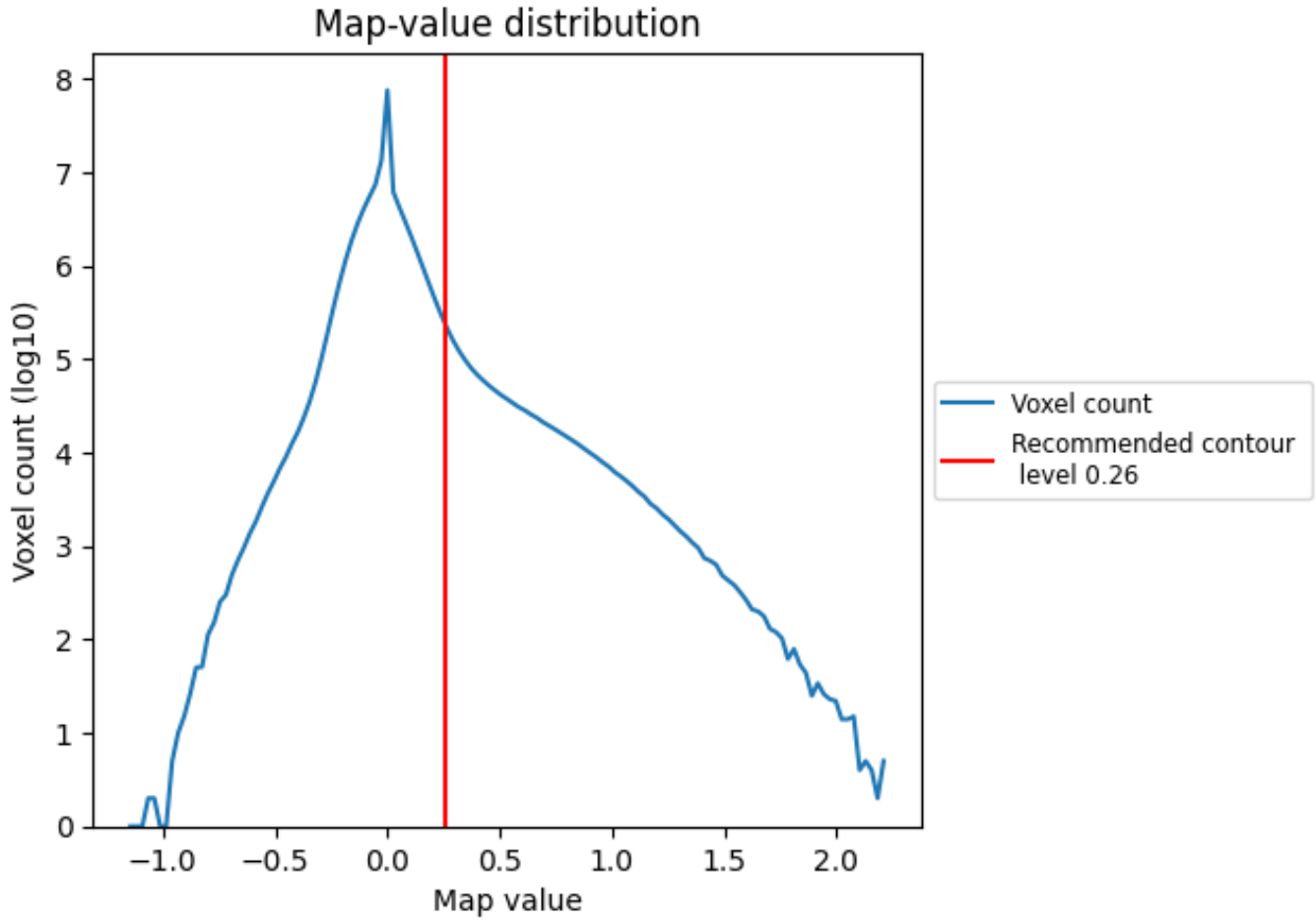


Z

7 Map analysis

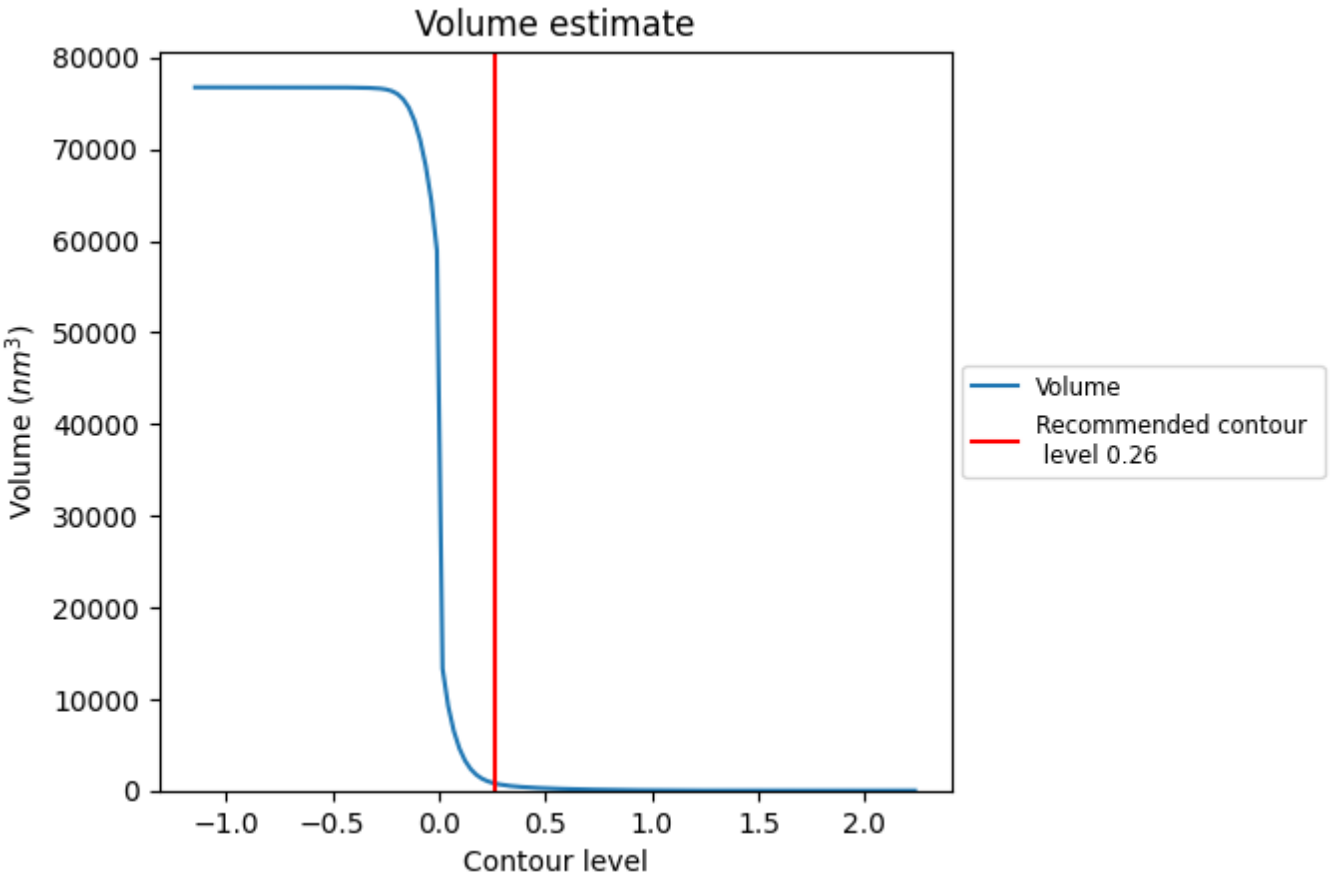
This section contains the results of statistical analysis of the map.

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.

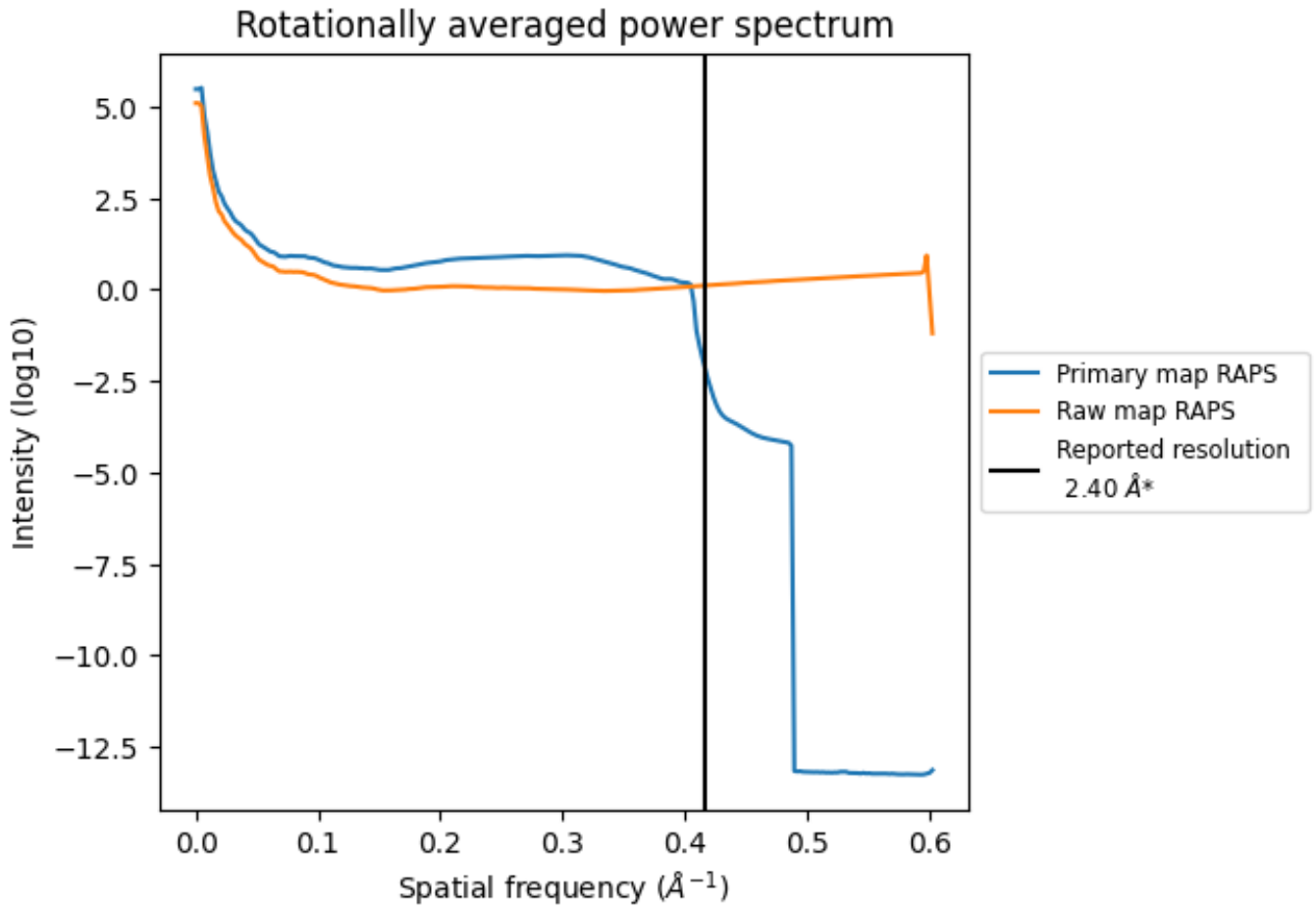
7.2 Volume estimate (i)



The volume at the recommended contour level is 798 nm^3; this corresponds to an approximate mass of 720 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)

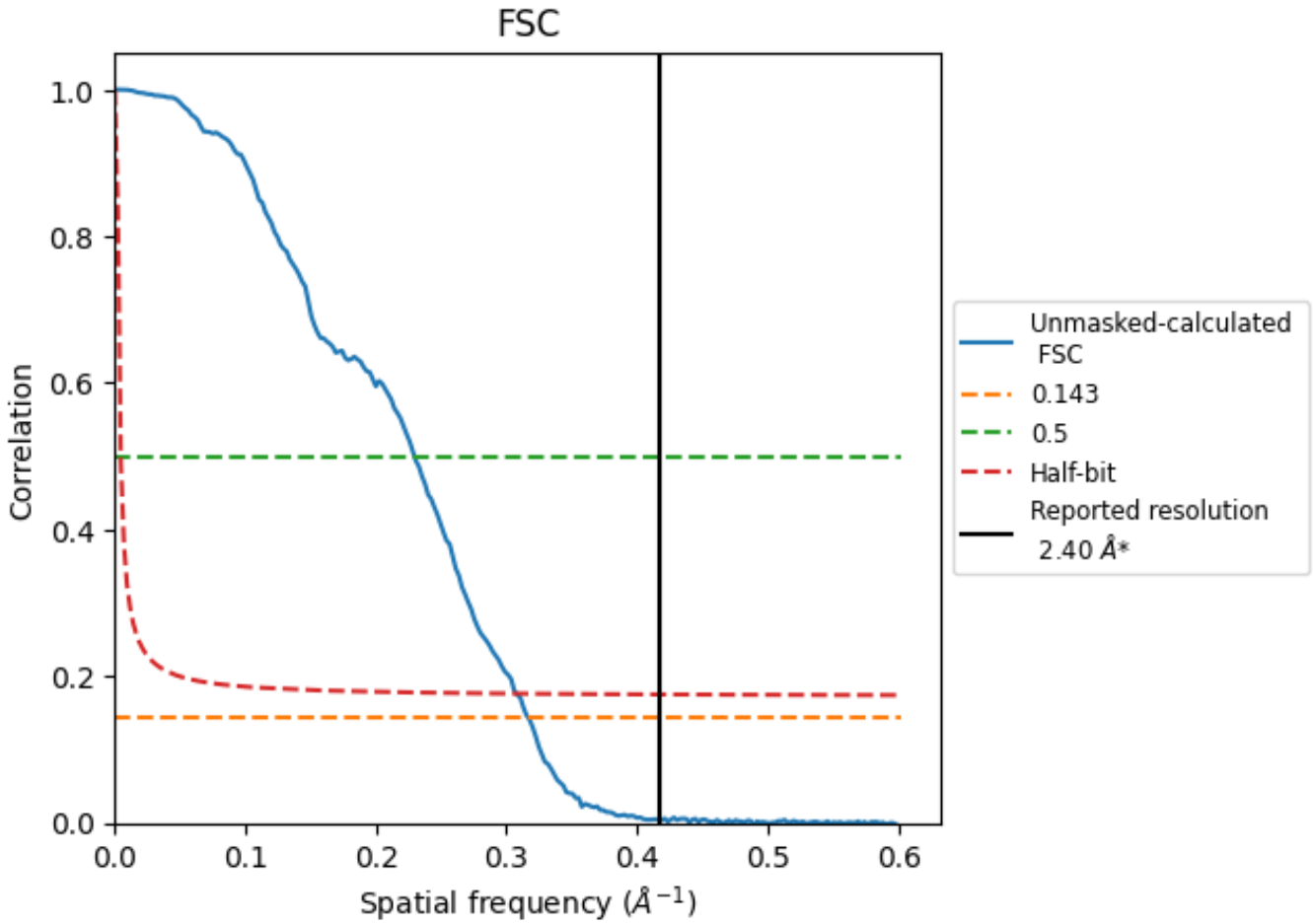


*Reported resolution corresponds to spatial frequency of 0.417 Å^{-1}

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 0.417 Å^{-1}

8.2 Resolution estimates (i)

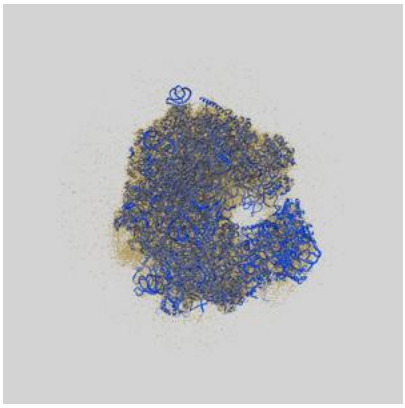
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.16	4.36	3.25

*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 3.16 differs from the reported value 2.4 by more than 10 %

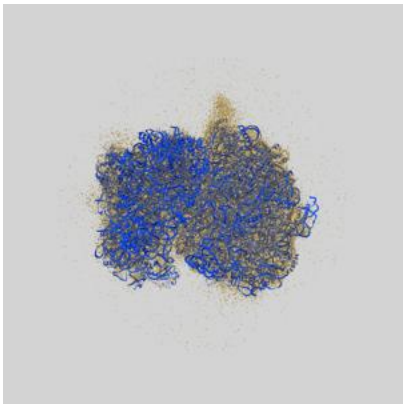
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-43972 and PDB model 9AXT. Per-residue inclusion information can be found in section 3 on page 18.

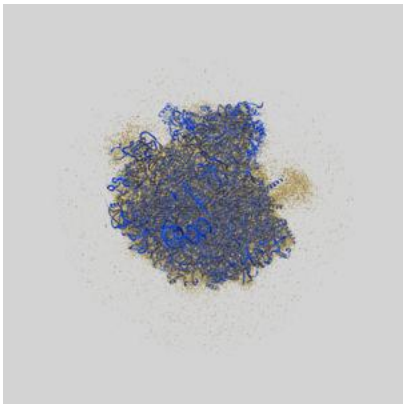
9.1 Map-model overlay



X



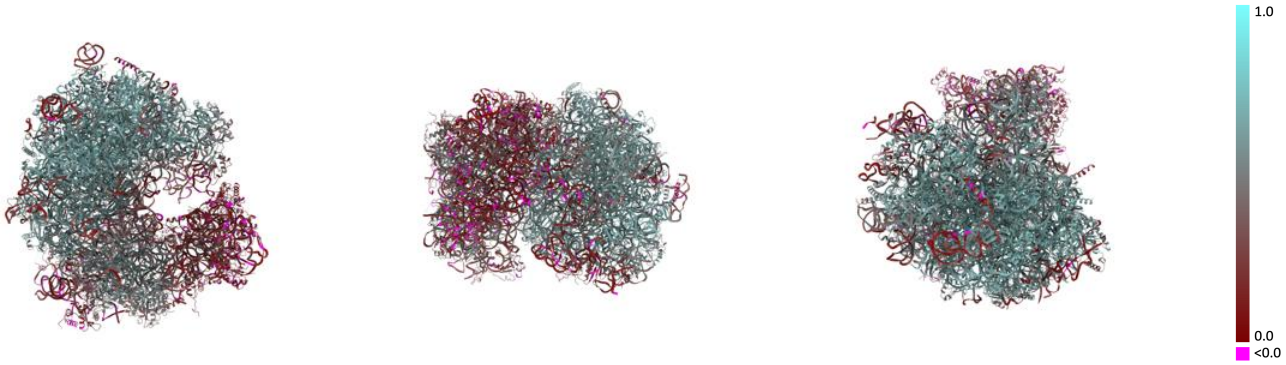
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.26 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.

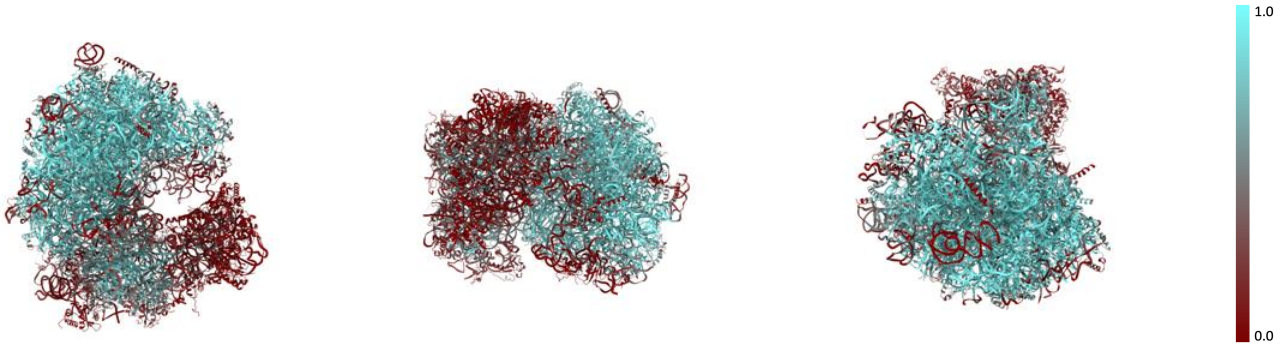
9.2 Q-score mapped to coordinate model (i)



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.

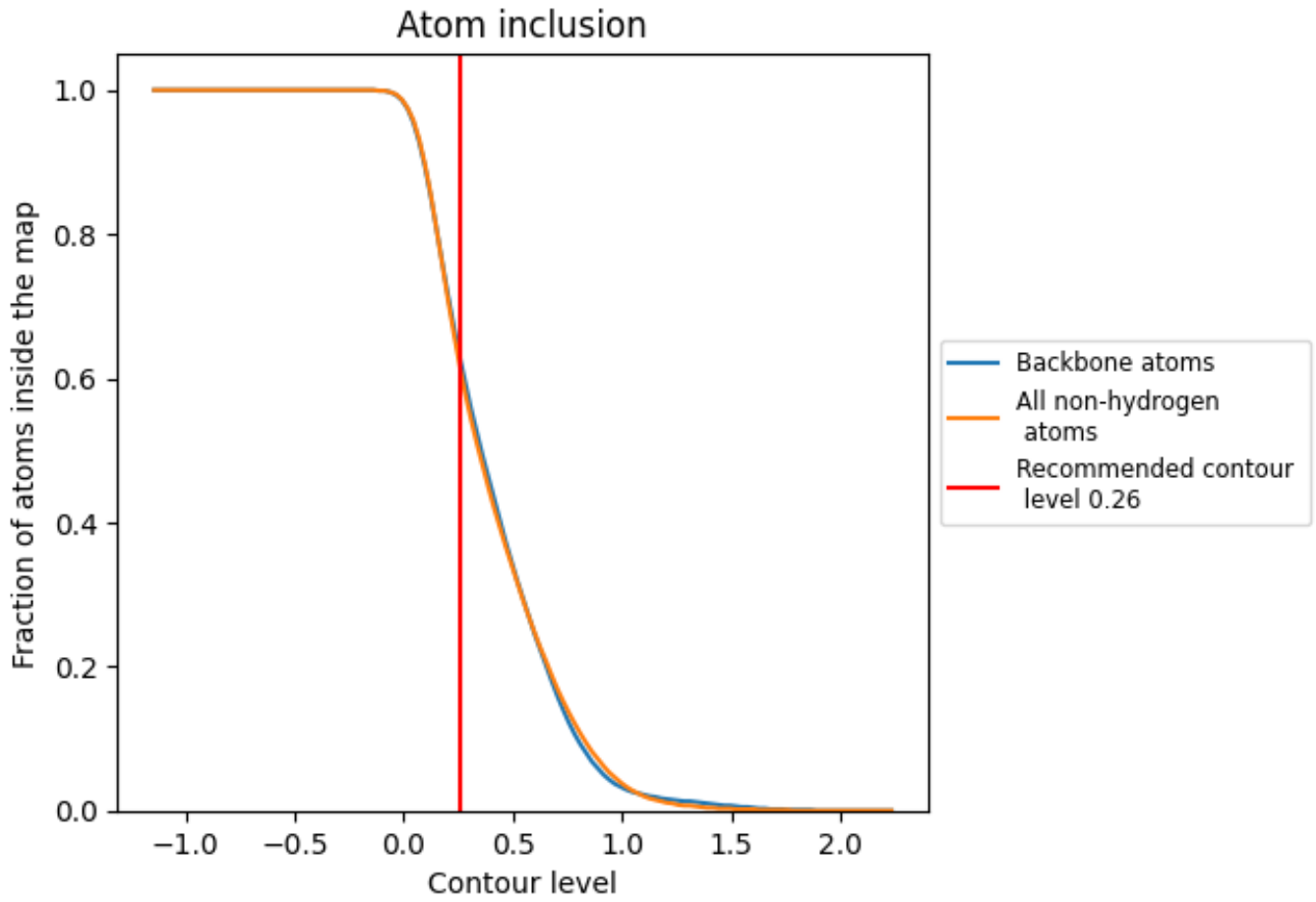
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.26).

9.4 Atom inclusion (i)



At the recommended contour level, 62% of all backbone atoms, 61% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.26) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6110	0.4710
AA	0.3830	0.3040
AD	0.4760	0.4750
AE	0.3310	0.4020
AF	0.5420	0.4860
AG	0.0350	0.1970
AH	0.5600	0.4930
AI	0.0700	0.2400
AJ	0.0850	0.2720
AK	0.1760	0.3090
AL	0.4000	0.4120
AM	0.3840	0.4250
AN	0.0180	0.1400
AO	0.5670	0.4850
AP	0.0020	0.1310
AQ	0.4300	0.4500
AR	0.3800	0.4060
AS	0.0380	0.1410
AT	0.0660	0.2240
AU	0.1050	0.2880
AV	0.0490	0.1830
AW	0.0630	0.2100
Aa	0.0760	0.2020
Ab	0.5120	0.4800
Ac	0.7430	0.5550
Ad	0.1950	0.3170
Ae	0.2370	0.3540
Af	0.0200	0.1580
Ag	0.4830	0.4510
Ah	0.2880	0.4020
Ai	0.0820	0.3060
Aj	0.0540	0.2630
Ak	0.0220	0.2230
B0	0.7550	0.5840
B1	0.7120	0.5720

Continued on next page...

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Chain	Atom inclusion	Q-score
B2	0.7780	0.5350
B3	0.8450	0.5590
B4	0.8680	0.5760
BN	0.9080	0.6490
BO	0.9010	0.6430
BP	0.8980	0.6450
BQ	0.6680	0.5380
BR	0.6630	0.5350
BS	0.8430	0.6070
BT	0.7310	0.5850
BU	0.0610	0.2580
BV	0.1460	0.3590
BW	0.3270	0.3660
BX	0.7540	0.5940
BY	0.7320	0.5710
BZ	0.9730	0.6700
Ba	0.8950	0.6410
Bb	0.9090	0.6520
Bc	0.9020	0.6490
Bd	0.8390	0.6140
Be	0.8170	0.6100
Bf	0.7600	0.5740
Bg	0.5590	0.5040
Bh	0.8420	0.6260
Bi	0.7280	0.5810
Bj	0.8640	0.6230
Bk	0.8030	0.6140
Bl	0.7320	0.5650
Bm	0.9360	0.6580
Bn	0.8620	0.6210
Bo	0.6070	0.5150
Bp	0.8550	0.6230
Bq	0.9110	0.6470
Br	0.9230	0.6500
Bs	0.8970	0.6480
Bt	0.8000	0.6100
Bu	0.8170	0.6170
Bv	0.9600	0.6670
Bw	0.5920	0.5100
Bx	0.7080	0.5240
By	0.6030	0.5620