wwPDB EM Validation Summary Report

Oct 13, 2024 – 03:45 AM EDT

PDB ID	:	9AXV
EMDB ID	:	EMD-43976
Title	:	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 (i) 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 (i)) were used in the production of this report:

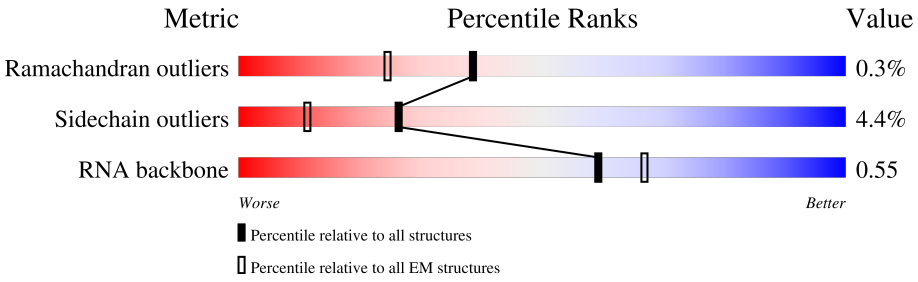
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	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	35% 70% 22% 7%
2	AD	292	20% 67% • 30%
3	AE	252	39% 80% 6% 14%
4	AF	253	10% 80% 5% 15%
5	AG	249	59% 81% 6% 13%
6	AH	262	36% 92% 8%
7	AI	203	42% 94% 6%
8	AJ	239	91% 87% 5% 8%

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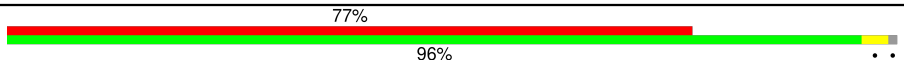
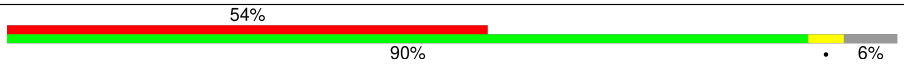
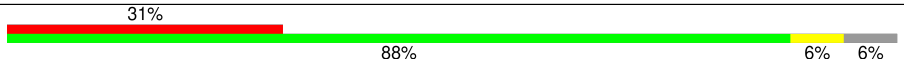
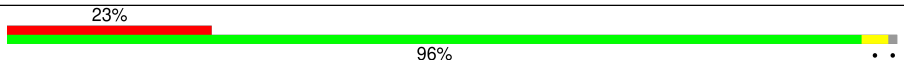
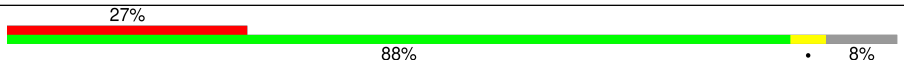
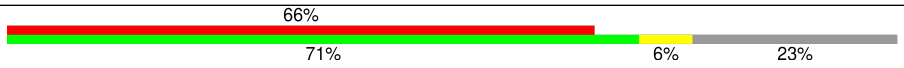
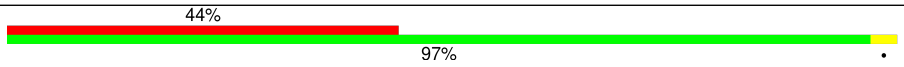
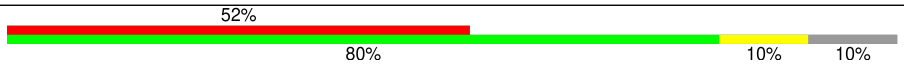
Mol	Chain	Length	Quality of chain
9	AK	195	
10	AL	200	
11	AM	192	
12	AN	147	
13	AO	152	
14	AP	145	
15	AQ	151	
16	AR	139	
17	AS	154	
18	AT	140	
19	AU	131	
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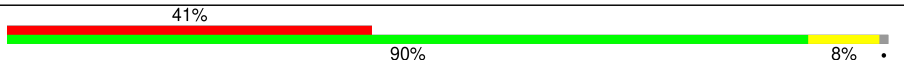
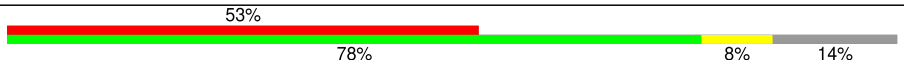
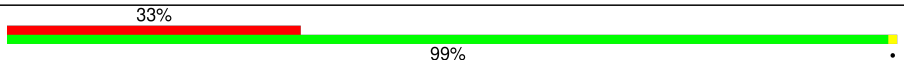
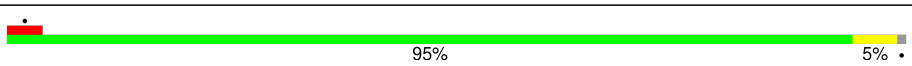
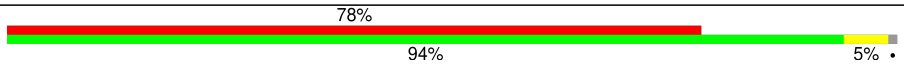
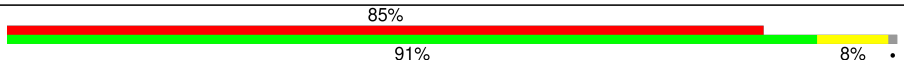
21	AW	144	
22	Aa	118	
23	Ab	87	
24	Ac	130	
25	Ad	143	
26	Ae	134	
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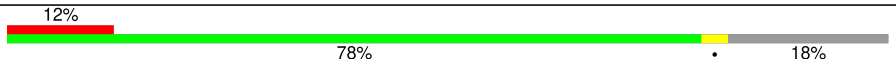
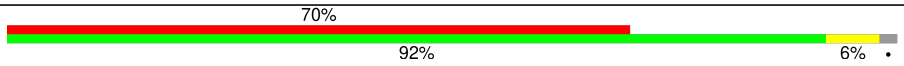
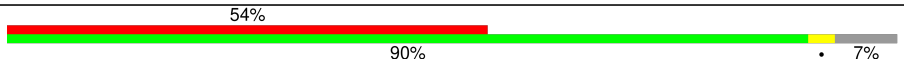
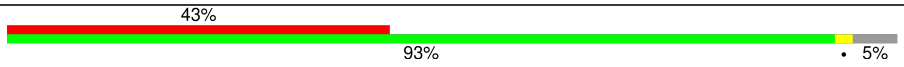
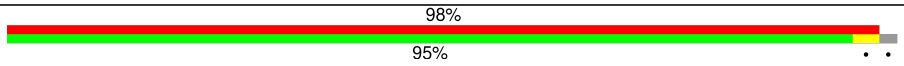
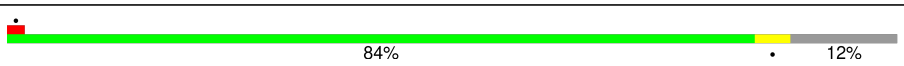
28	Ag	119	
29	Ah	83	
30	Ai	68	
31	Aj	56	
32	Ak	61	
33	B0	106	

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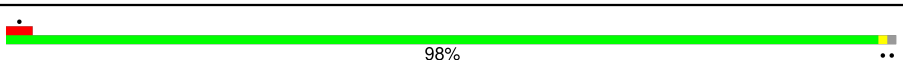
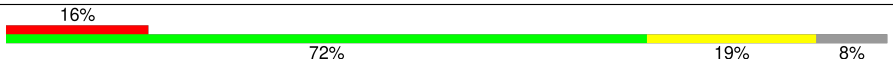
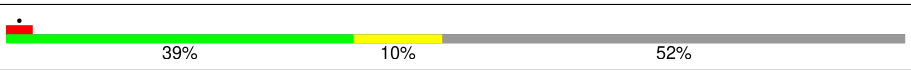
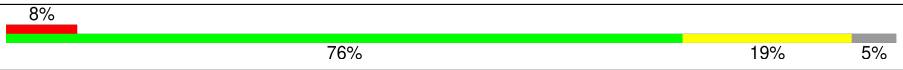
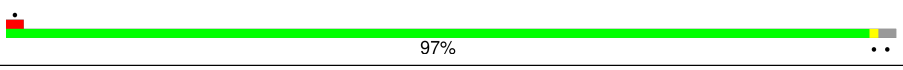
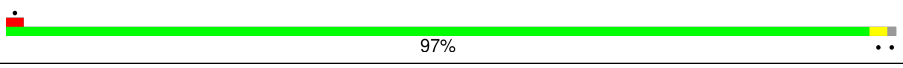
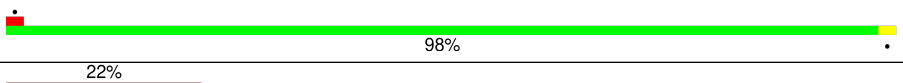
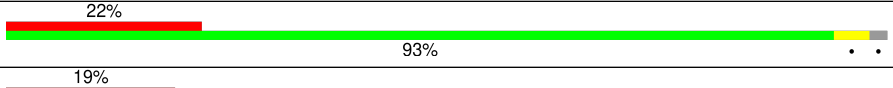
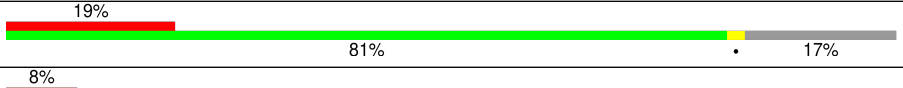
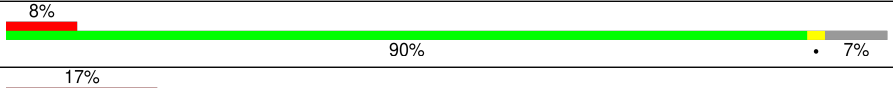
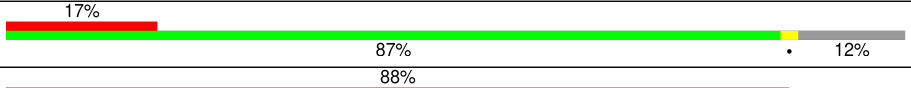
Mol	Chain	Length	Quality of chain
34	B1	94	
35	B2	3498	
36	B3	246	
37	B4	165	
38	BN	253	
39	BO	388	
40	BP	363	
41	BQ	294	
42	BR	195	
43	BS	251	
44	BT	259	
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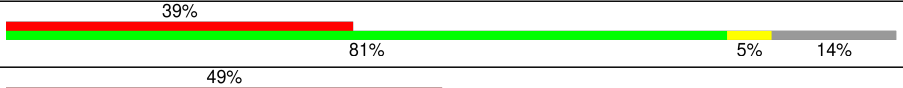
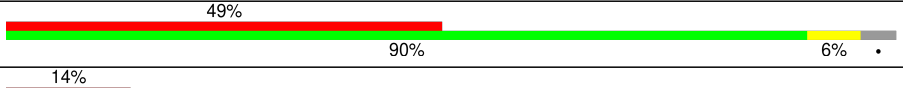
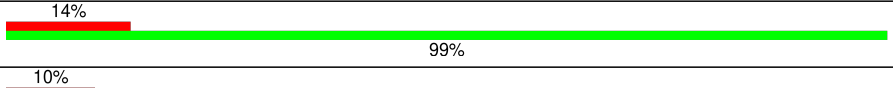
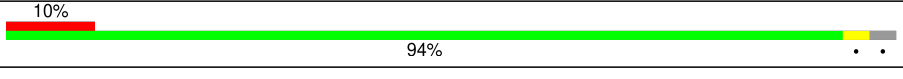
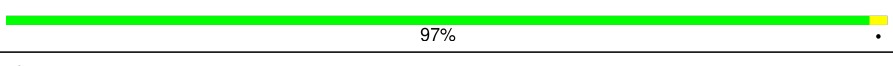
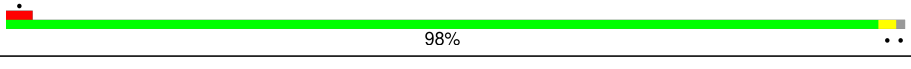
46	BV	221	
47	BW	174	
48	BX	208	
49	BY	134	
50	BZ	201	
51	Ba	197	
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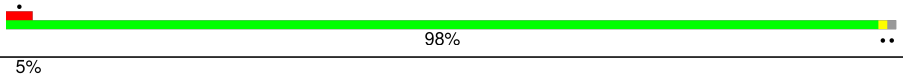
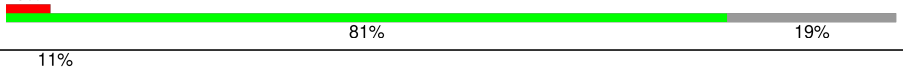
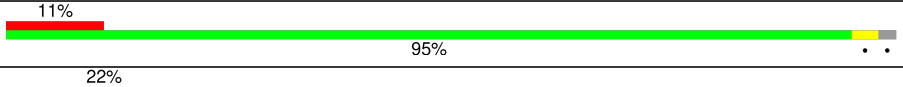
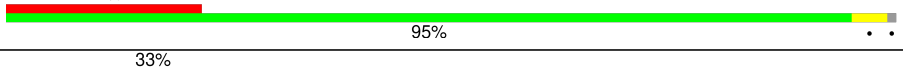
53	Bc	187	
54	Bd	193	
55	Be	176	
56	Bf	160	
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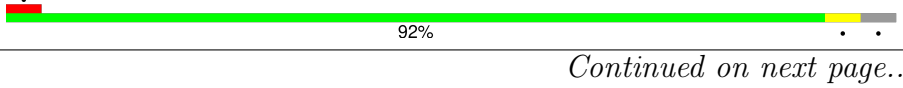
58	Bh	139	

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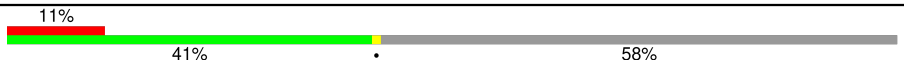
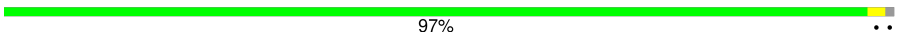
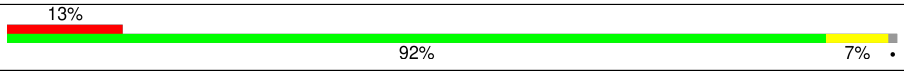
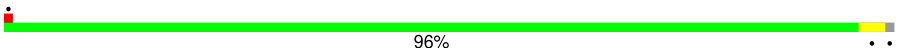
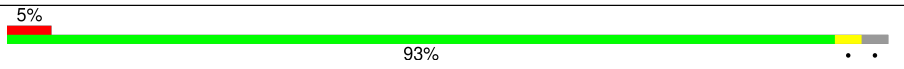
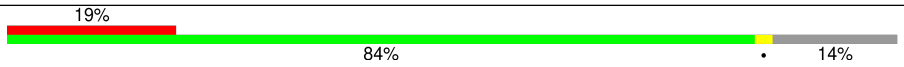
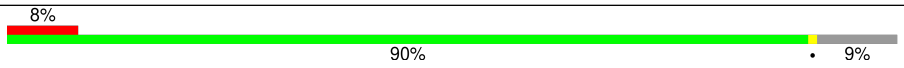
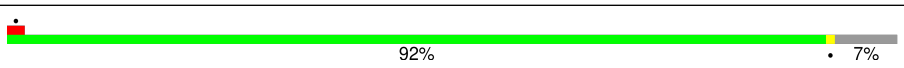
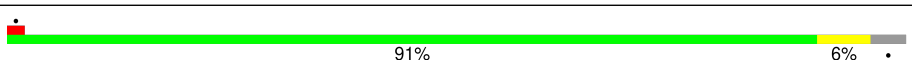
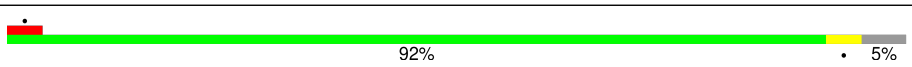
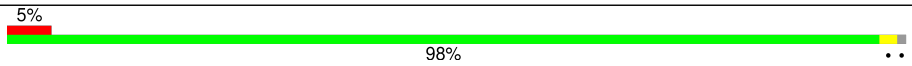
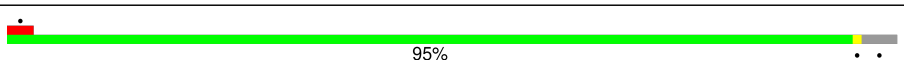
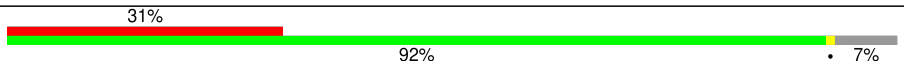
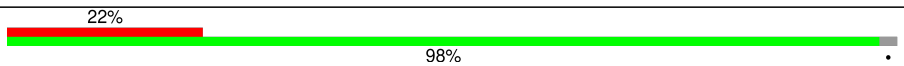
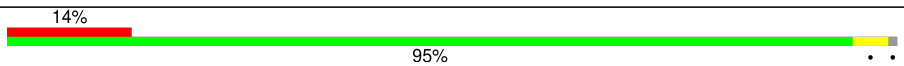
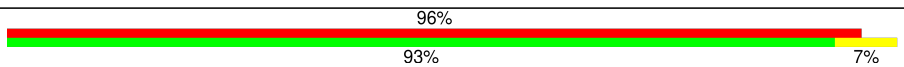
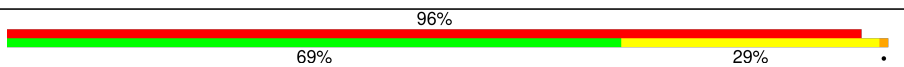
Mol	Chain	Length	Quality of chain
59	Bi	149	
60	Bj	141	
61	Bk	126	
62	Bl	136	
63	Bm	148	
64	Bn	61	
65	Bo	109	
66	Bp	113	
67	Bq	127	
68	Br	108	
69	Bs	111	
70	Bt	122	
71	Bu	99	
72	Bv	91	
73	Bw	74	
74	Bx	51	
75	By	134	
76	Am	314	
77	Sm	77	
78	Sn	75	
79	S3	10	

2 Entry composition (i)

There are 80 unique types of molecules in this entry. The entry contains 200604 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	C	N	O	S	0	0
			1286	810	247	226	3		

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

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

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

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

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

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

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

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

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

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

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

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

- 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	C	N	O	0	0
			999	629	194	176		

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
75	By	133	Total	C	N	O	S	0	0
			1031	641	203	186	1		

- Molecule 76 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Am	314	Total	C	N	O	S	0	0
			2458	1549	422	478	9		

- Molecule 77 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sm	77	Total	C	N	O	P	0	0
			1625	722	292	534	77		

- Molecule 78 is a RNA chain called A/P tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sn	75	Total	C	N	O	P	0	0
			1606	716	297	518	75		

- Molecule 79 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	S3	10	Total	C	N	O	P	0	0
			204	92	27	75	10		

- Molecule 80 is ZINC ION (three-letter code: ZN) (formula: Zn).

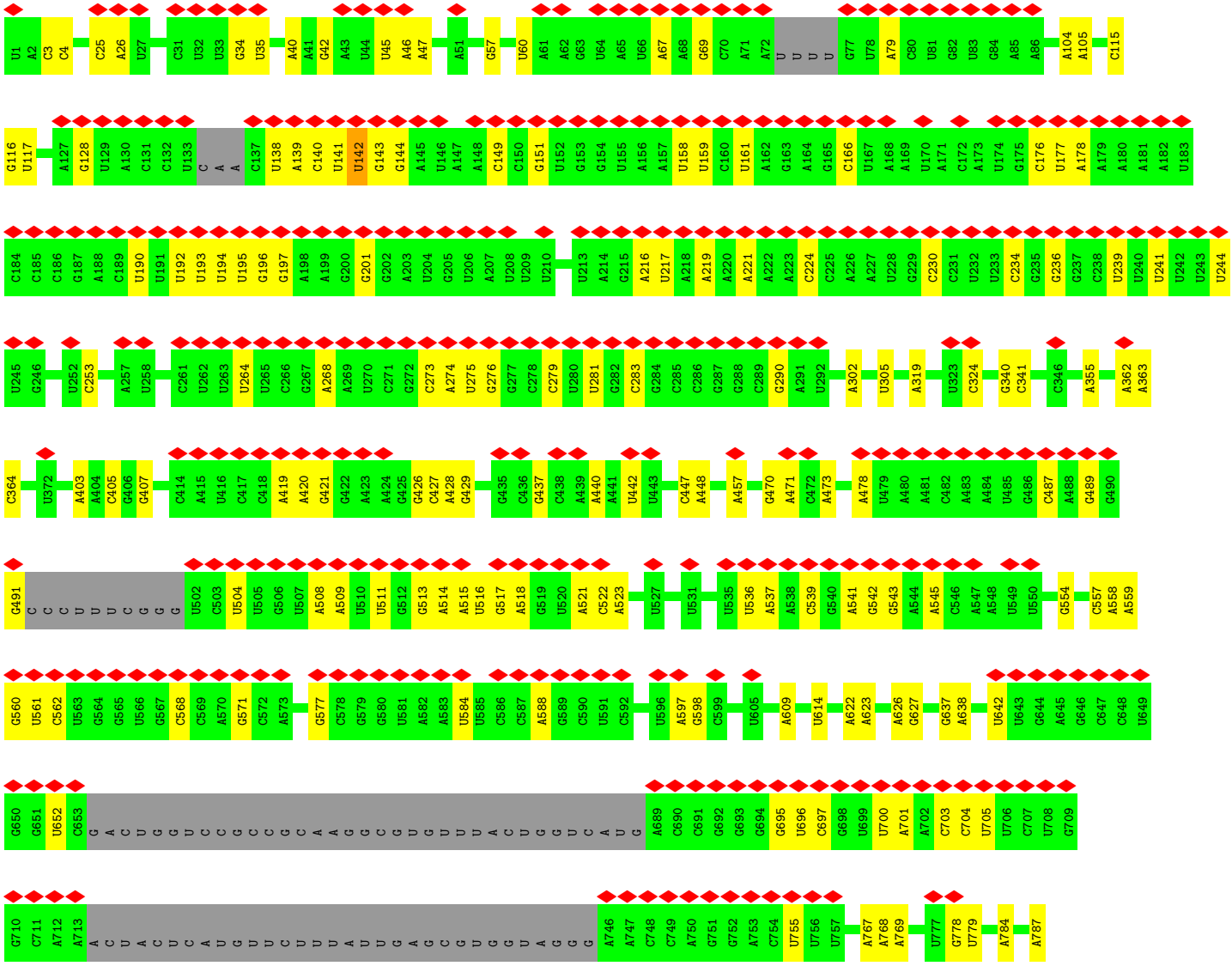
Mol	Chain	Residues	Atoms		AltConf
80	AA	1	Total	Zn	0
			1	1	
80	Ag	1	Total	Zn	0
			1	1	
80	Ah	1	Total	Zn	0
			1	1	
80	B0	1	Total	Zn	0
			1	1	
80	B1	1	Total	Zn	0
			1	1	
80	Bv	1	Total	Zn	0
			1	1	

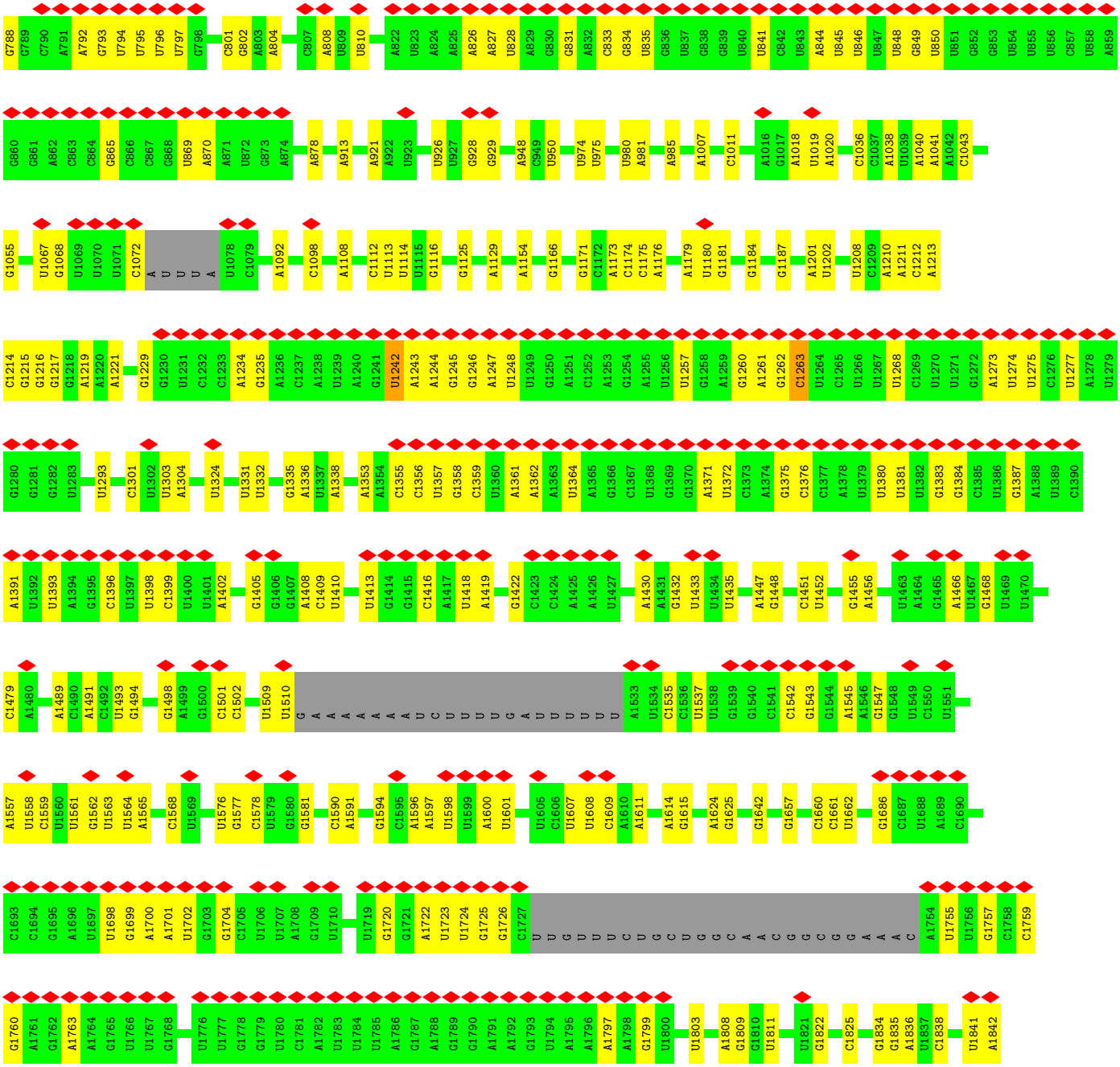
3 Residue-property plots (i)

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

- Molecule 1: 18S ribosomal RNA

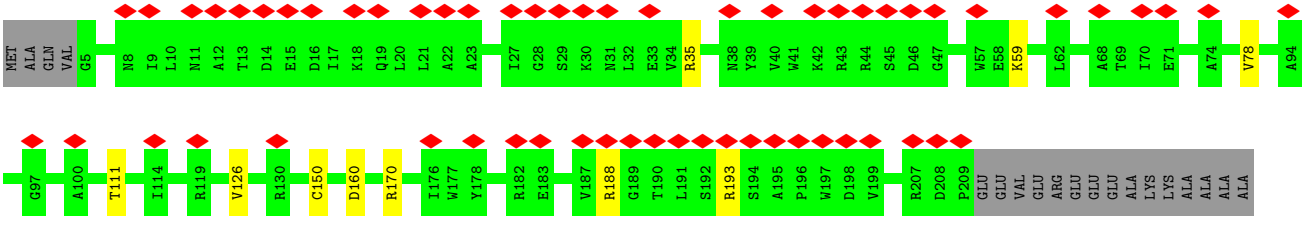
Chain AA:

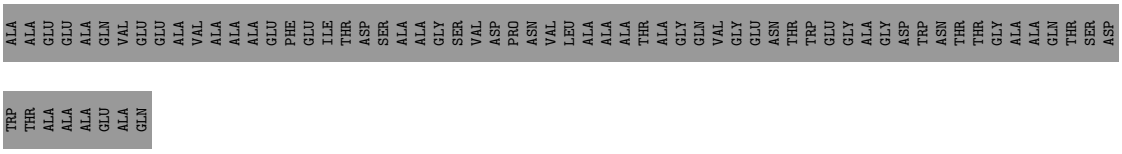




• Molecule 2: Small ribosomal subunit protein uS2A

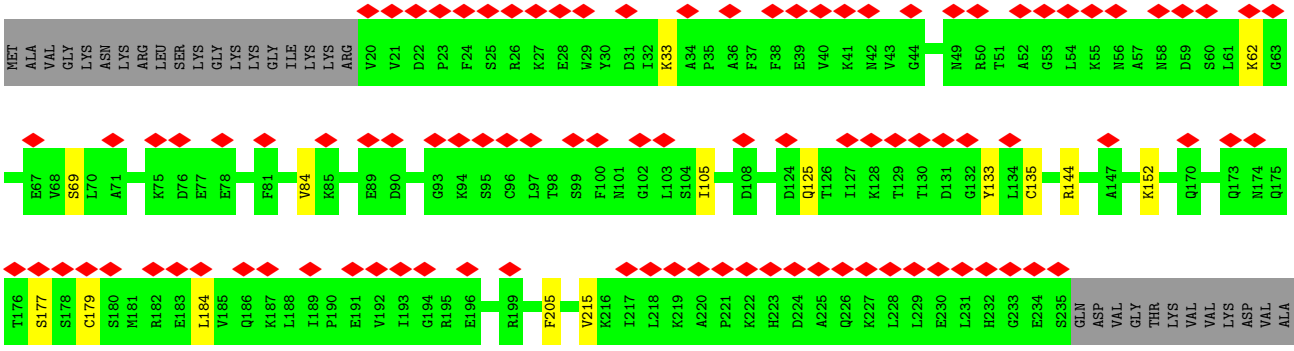
Chain AD:





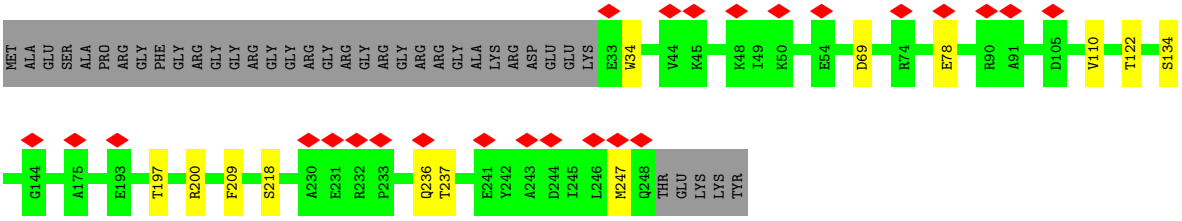
• Molecule 3: Small ribosomal subunit protein eS1B

Chain AE:



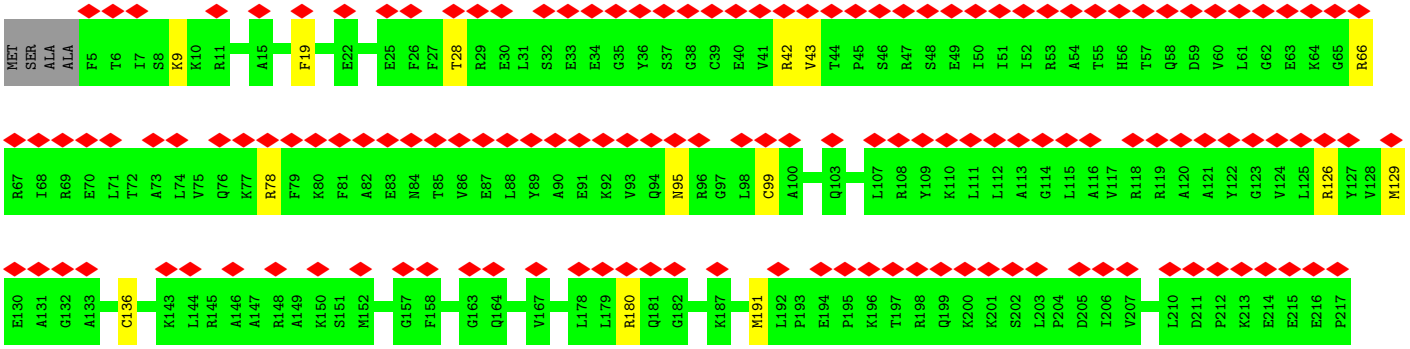
• Molecule 4: Small ribosomal subunit protein uS5

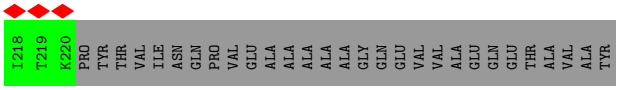
Chain AF:



• Molecule 5: Small ribosomal subunit protein uS3

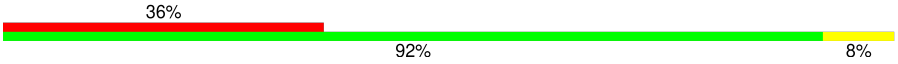
Chain AG:

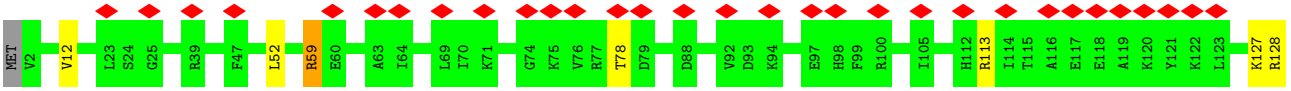


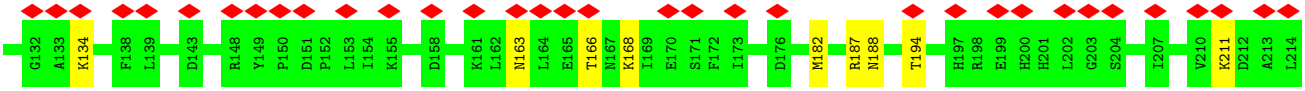


• Molecule 6: Small ribosomal subunit protein eS4C

Chain AH:

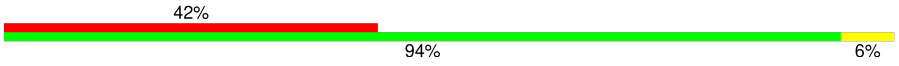


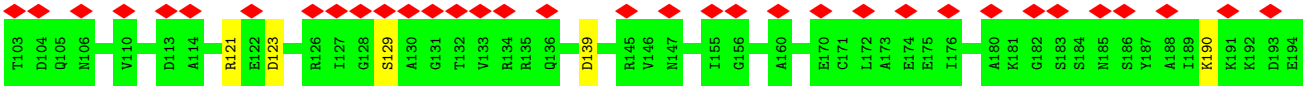


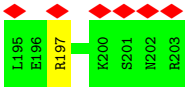


• Molecule 7: Small ribosomal subunit protein uS7A

Chain AI:

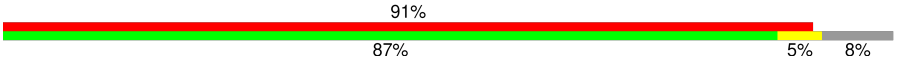


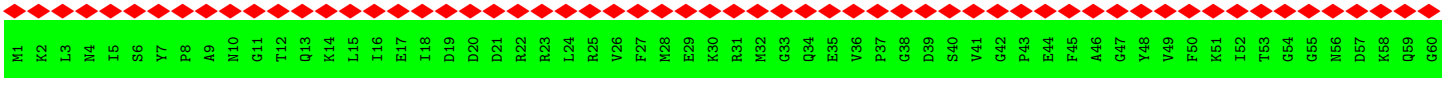


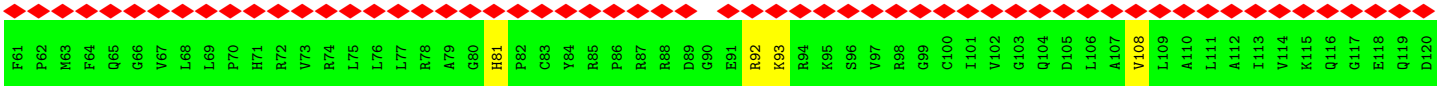


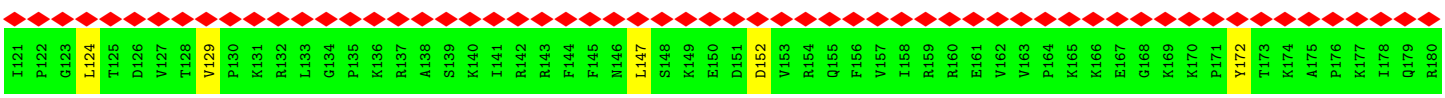
• Molecule 8: Small ribosomal subunit protein eS6B

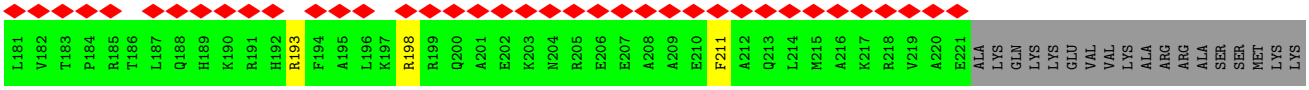
Chain AJ:



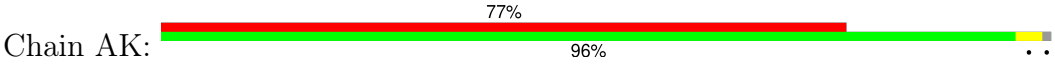


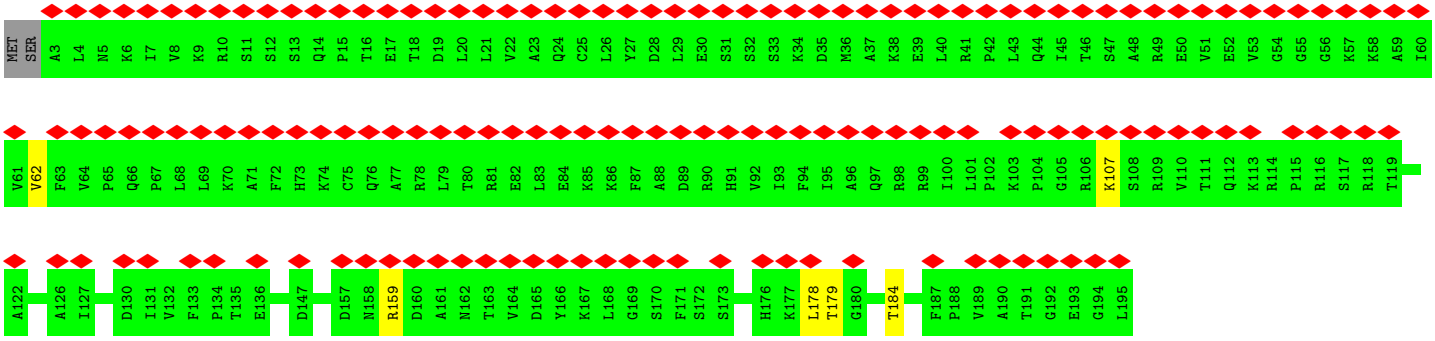




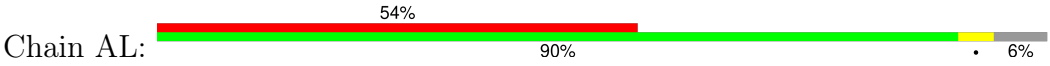


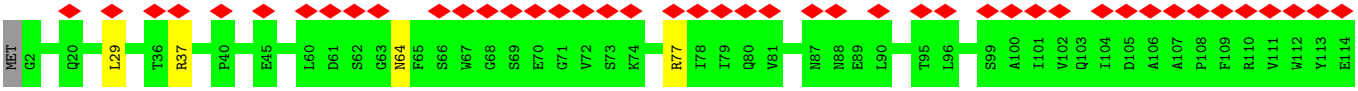
• Molecule 9: Small ribosomal subunit protein eS7



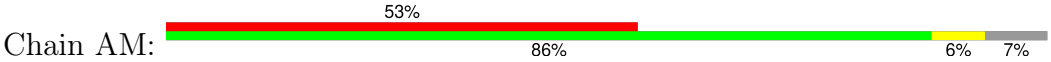


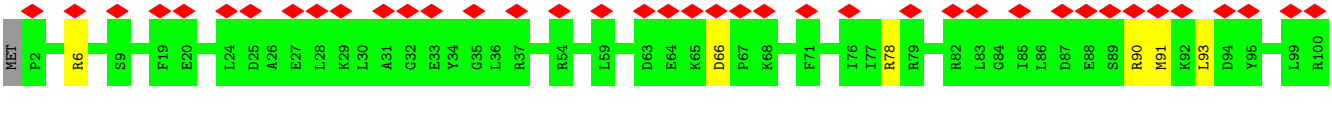
• Molecule 10: Small ribosomal subunit protein eS8B

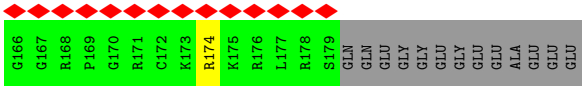




• Molecule 11: Small ribosomal subunit protein uS4B

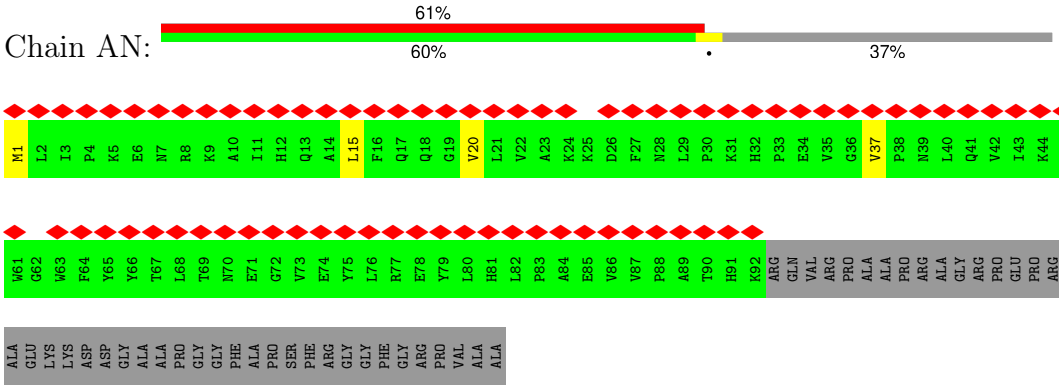






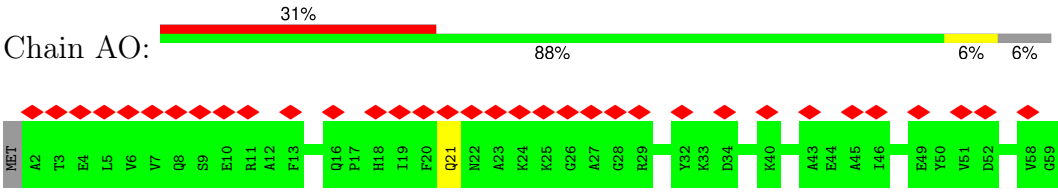
• Molecule 12: Small ribosomal subunit protein eS10B

Chain AN:



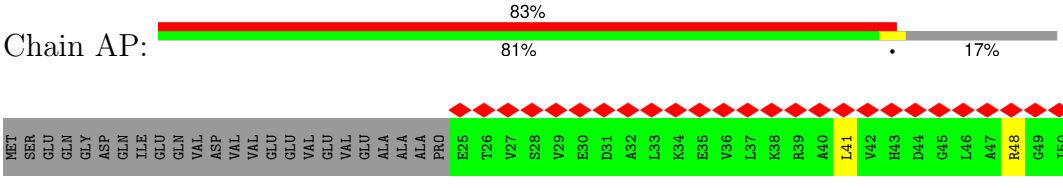
• Molecule 13: Small ribosomal subunit protein uS17A

Chain AO:



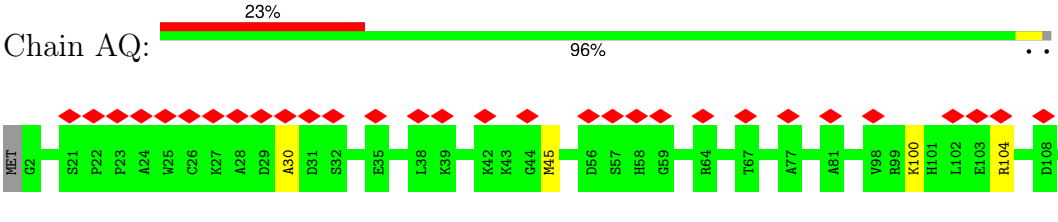
• Molecule 14: Small ribosomal subunit protein eS12A

Chain AP:



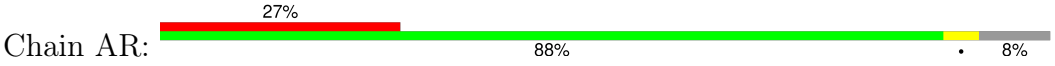
• Molecule 15: Small ribosomal subunit protein uS15

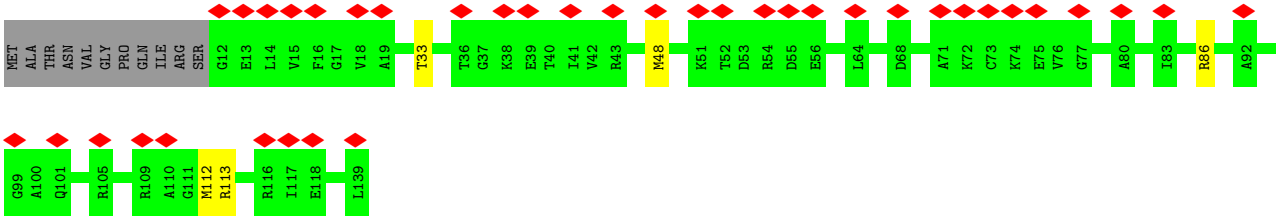
Chain AQ:



• Molecule 16: Small ribosomal subunit protein uS11B

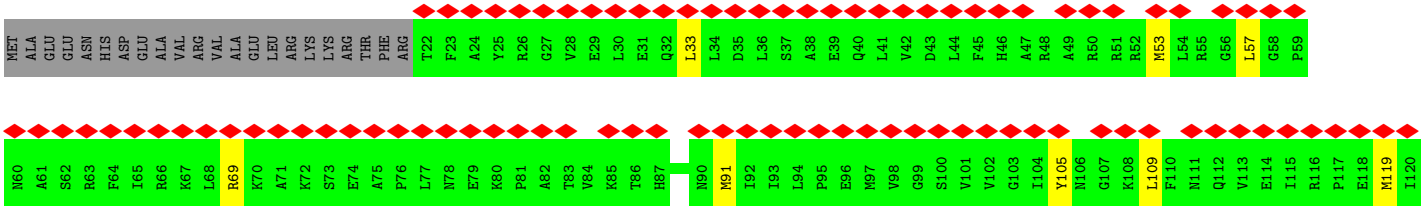
Chain AR:





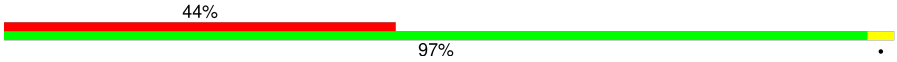
• Molecule 17: Small ribosomal subunit protein uS19B

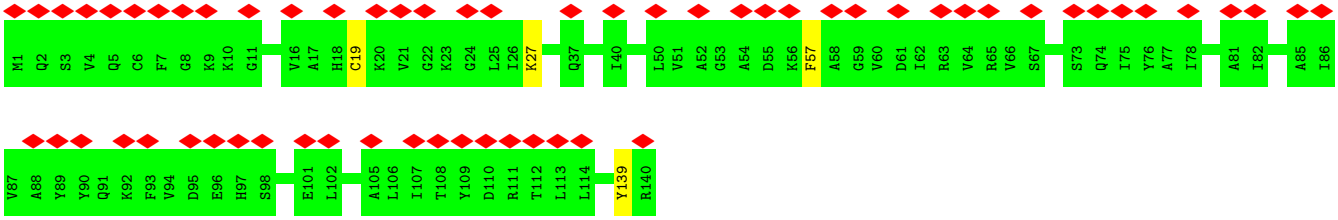
Chain AS:



• Molecule 18: Small ribosomal subunit protein uS9A

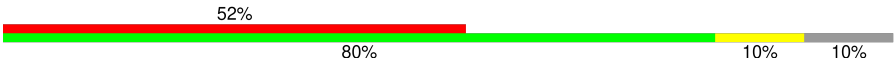
Chain AT:

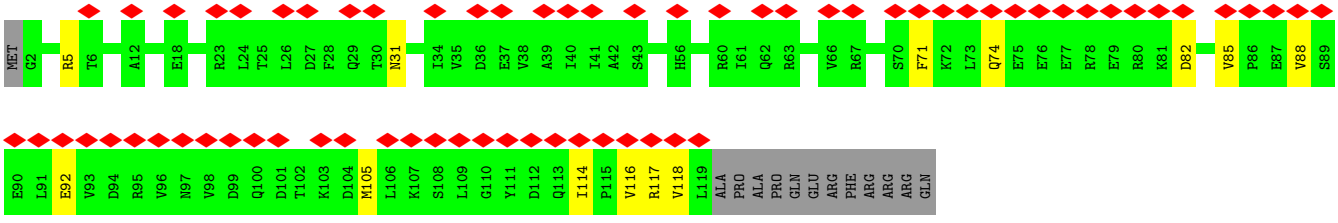




• Molecule 19: Small ribosomal subunit protein eS17A

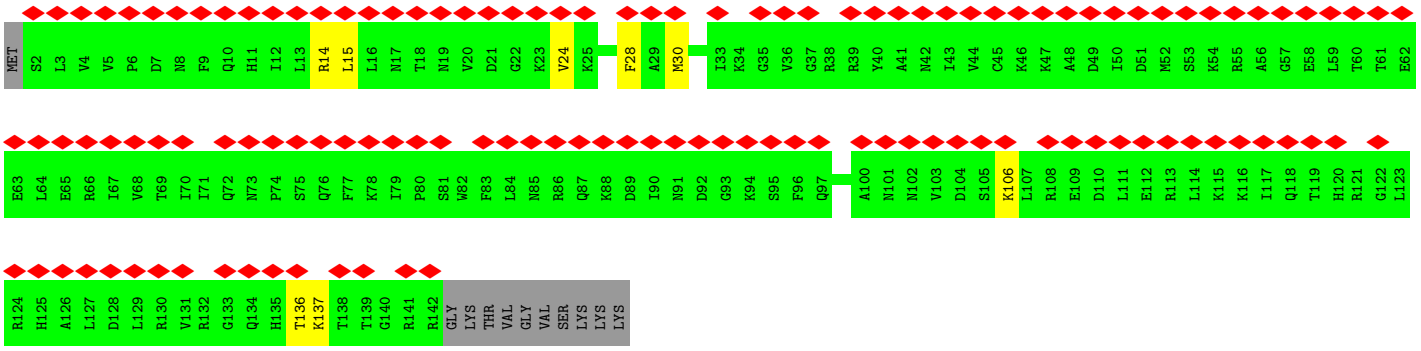
Chain AU:





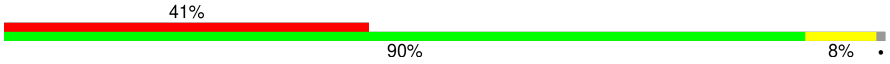
• Molecule 20: Small ribosomal subunit protein uS13B

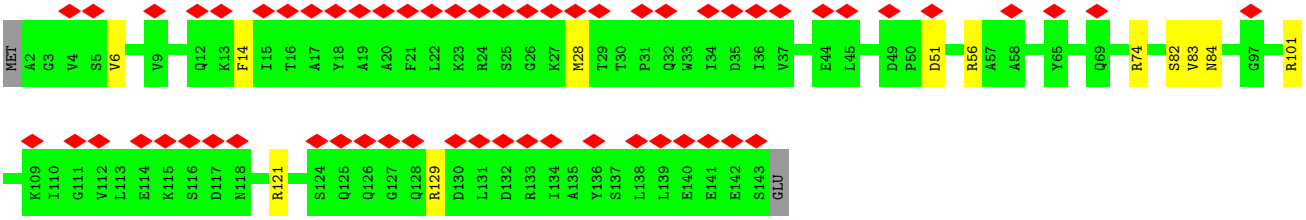
Chain AV:



• Molecule 21: Small ribosomal subunit protein eS19A

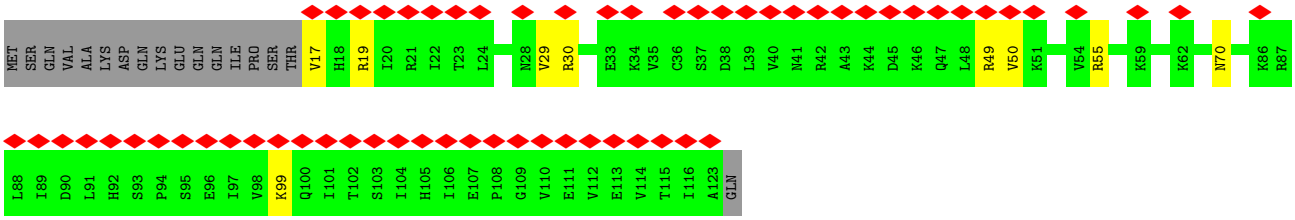
Chain AW:





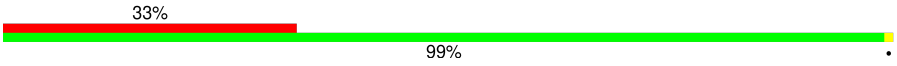
• Molecule 22: Small ribosomal subunit protein uS10

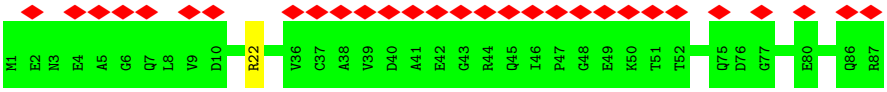
Chain Aa:



• Molecule 23: Small ribosomal subunit protein eS21

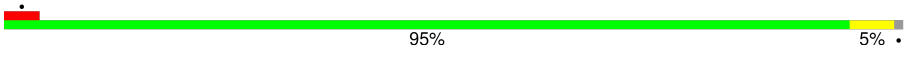
Chain Ab:

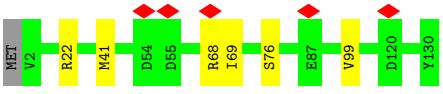




• Molecule 24: Small ribosomal subunit protein uS8A

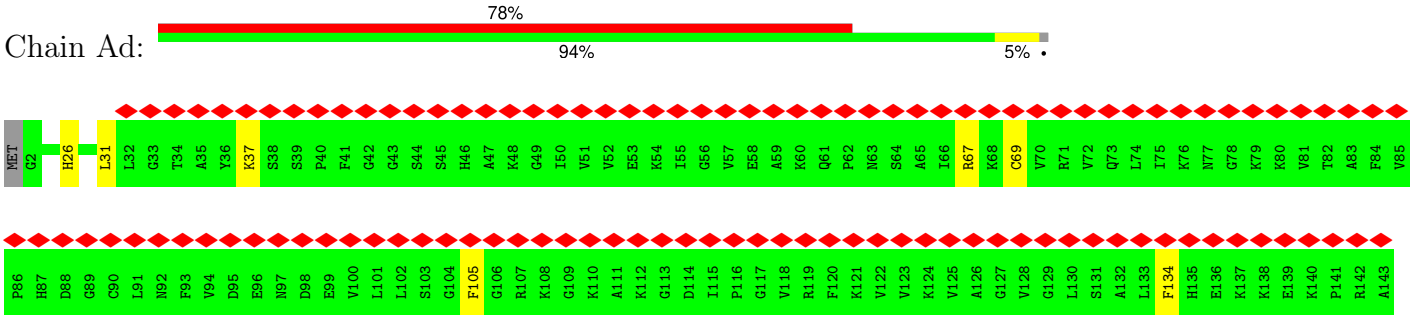
Chain Ac:





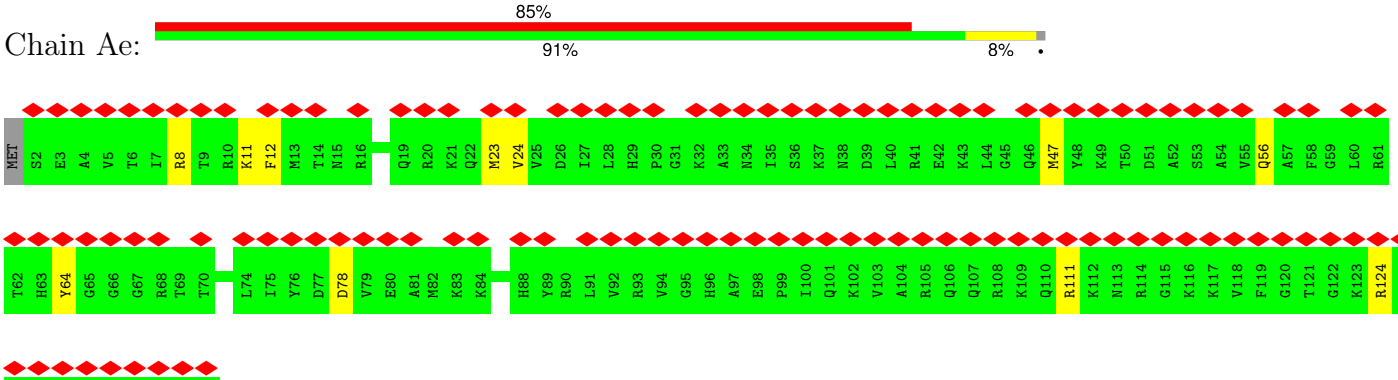
• Molecule 25: Small ribosomal subunit protein uS12A

Chain Ad:



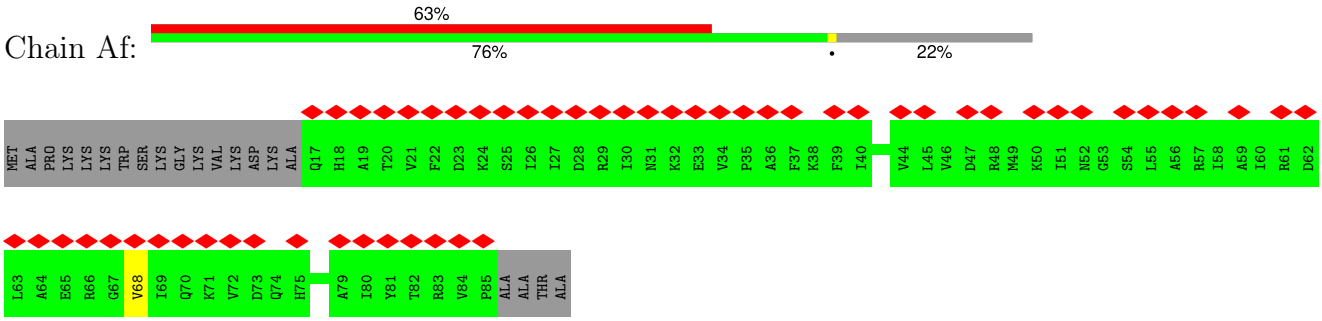
• Molecule 26: Small ribosomal subunit protein eS24A

Chain Ae:



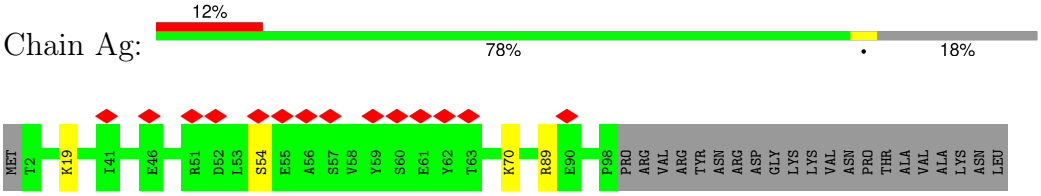
• Molecule 27: Small ribosomal subunit protein eS25A

Chain Af:



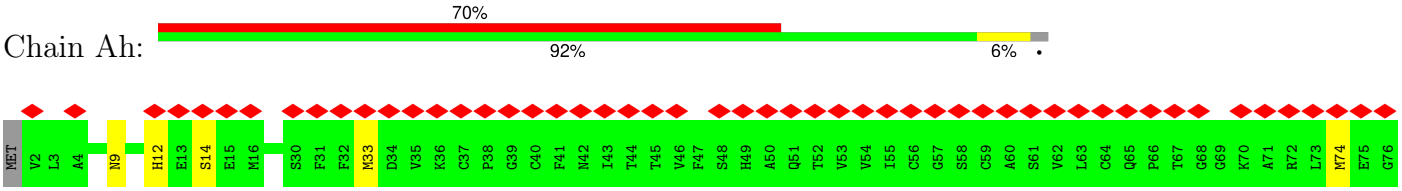
• Molecule 28: Small ribosomal subunit protein eS26B

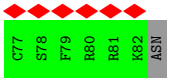
Chain Ag:



• Molecule 29: Small ribosomal subunit protein eS27

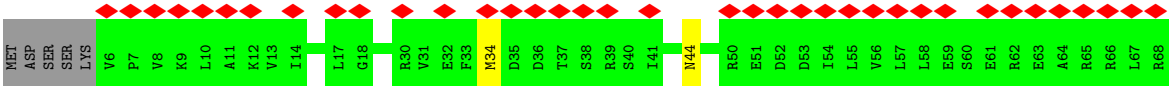
Chain Ah:





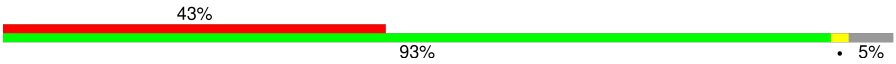
• Molecule 30: Small ribosomal subunit protein eS28A

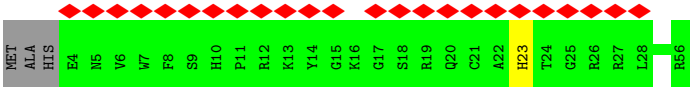
Chain Ai:



• Molecule 31: Small ribosomal subunit protein uS14

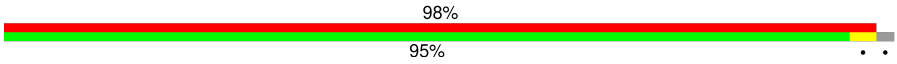
Chain Aj:





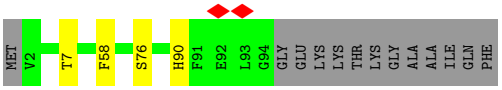
• Molecule 32: Small ribosomal subunit protein eS30B

Chain Ak:



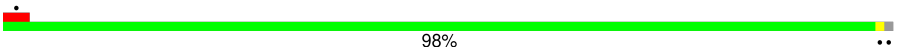
• Molecule 33: Large ribosomal subunit protein eL42

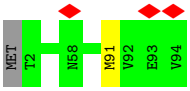
Chain B0:



• Molecule 34: Large ribosomal subunit protein eL43A

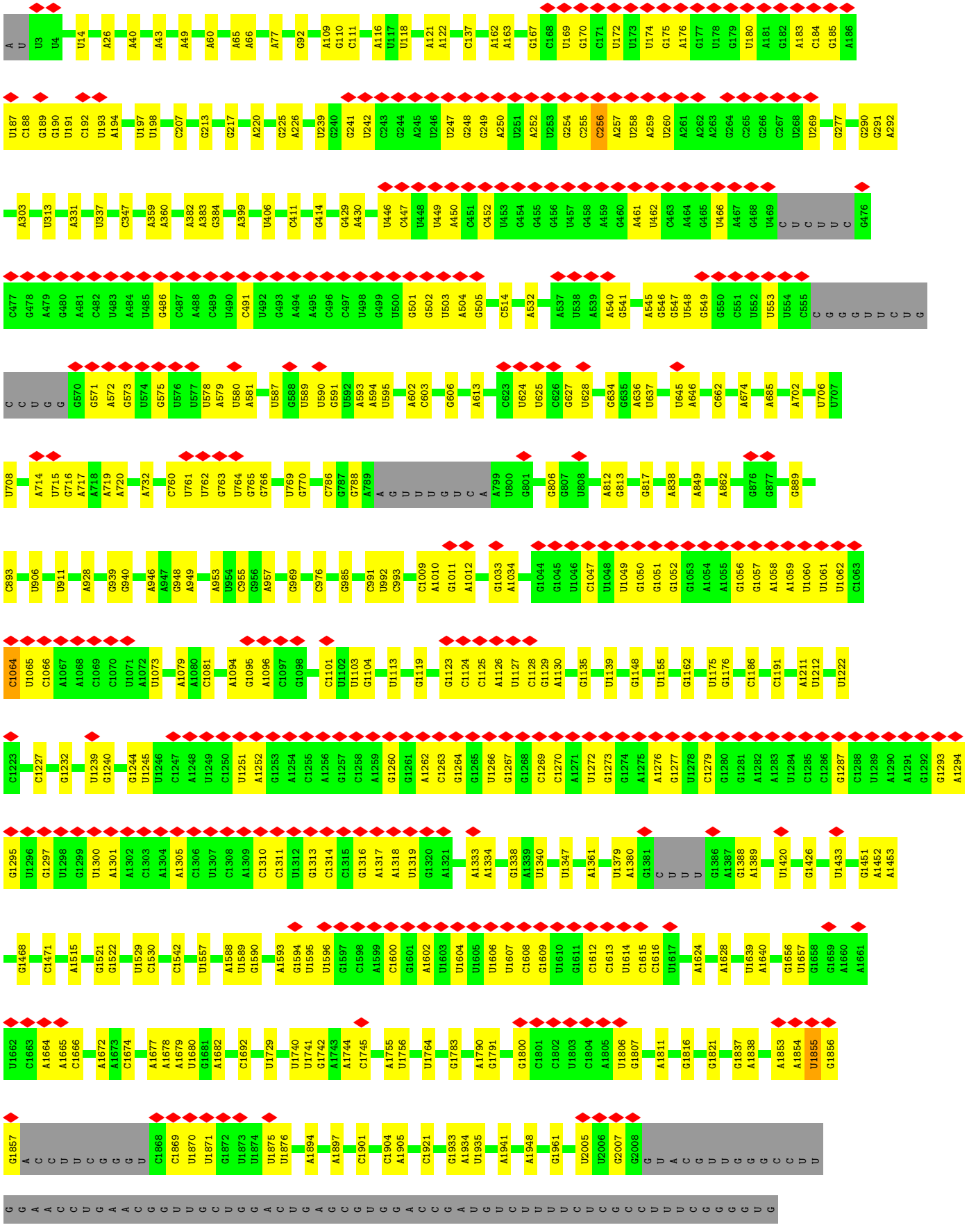
Chain B1:





• Molecule 35: 28S ribosomal RNA

Chain B2: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U187 C188 G189 G190 U191 C192 U193 A194 U197 U198 C207 G213 G217 A220 G225 A226 U239 G240 G241 U242 C243 G244 A245 U246 U247 G248 G249 A250 U251 A252 U253 G254 C255 C256 A257 U258 A259 U260 A261 A262 A263 G264 C265 C266 C267 U268 U269 G277 G290 G291 A292
A303 U313 A331 U337 C347 A359 A360 A382 A383 G384 A399 U406 C411 G414 G429 A430 U446 C447 U448 U449 A450 C451 C452 U453 G454 G455 G456 U457 G458 A459 G460 A461 U462 C463 A464 G465 U466 A467 G468 U469 C U C U U C G476
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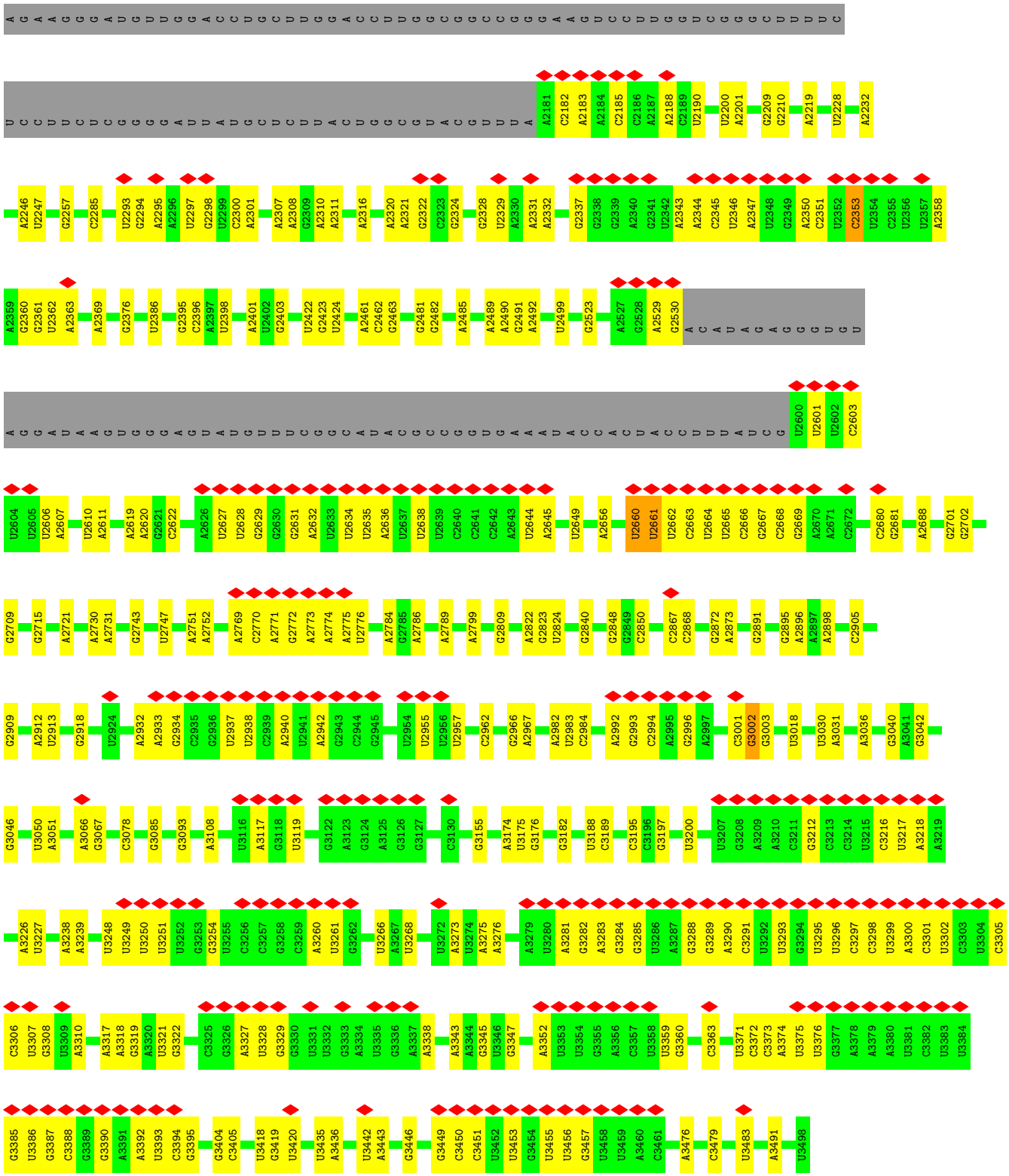
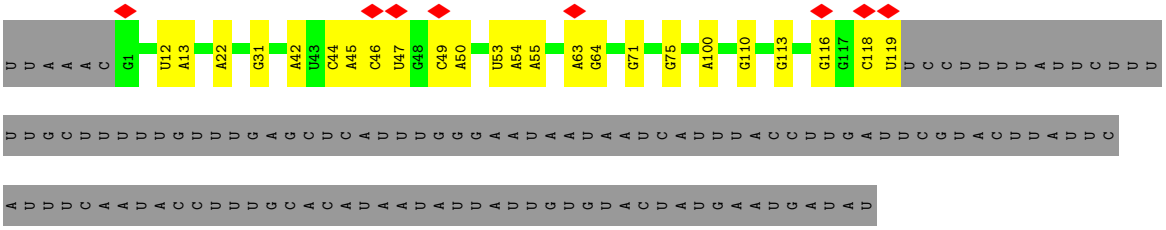


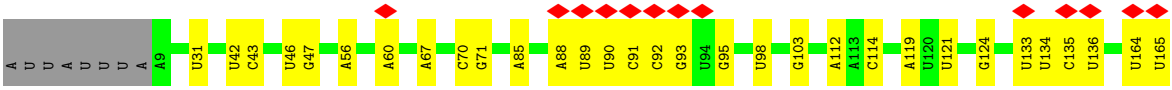
• Molecule 36: 5S ribosomal RNA

Chain B3:



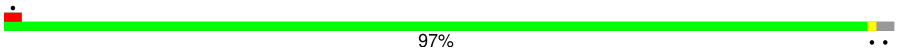
• Molecule 37: 5.8S ribosomal RNA

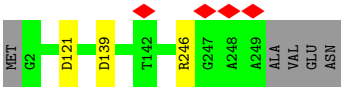
Chain B4:



• Molecule 38: Large ribosomal subunit protein uL2C

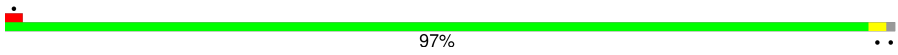
Chain BN:

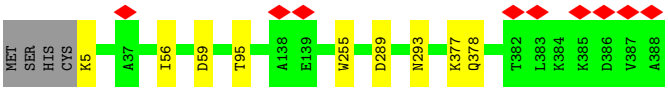




• Molecule 39: Large ribosomal subunit protein uL3A

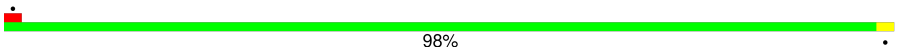
Chain BO:

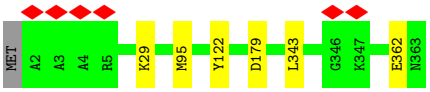




• Molecule 40: Large ribosomal subunit protein uL4A

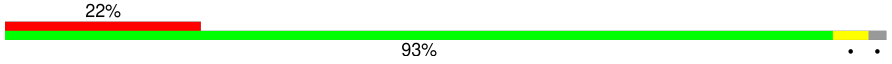
Chain BP:

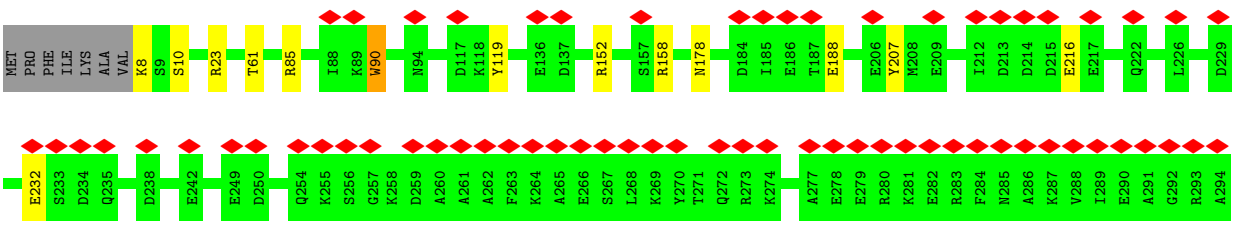




• Molecule 41: Large ribosomal subunit protein uL18B

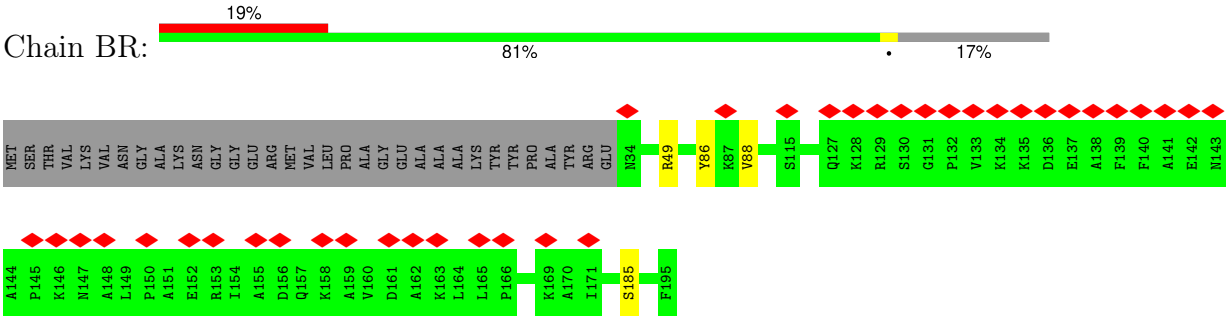
Chain BQ:





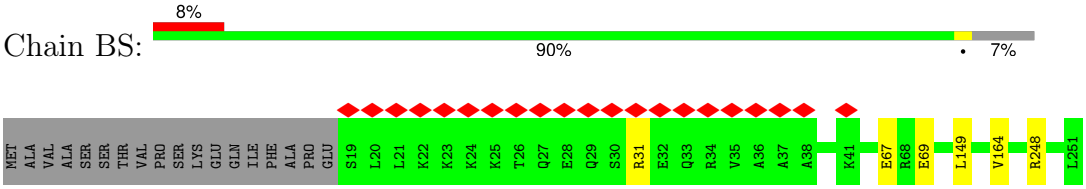
• Molecule 42: Large ribosomal subunit protein eL6

Chain BR:



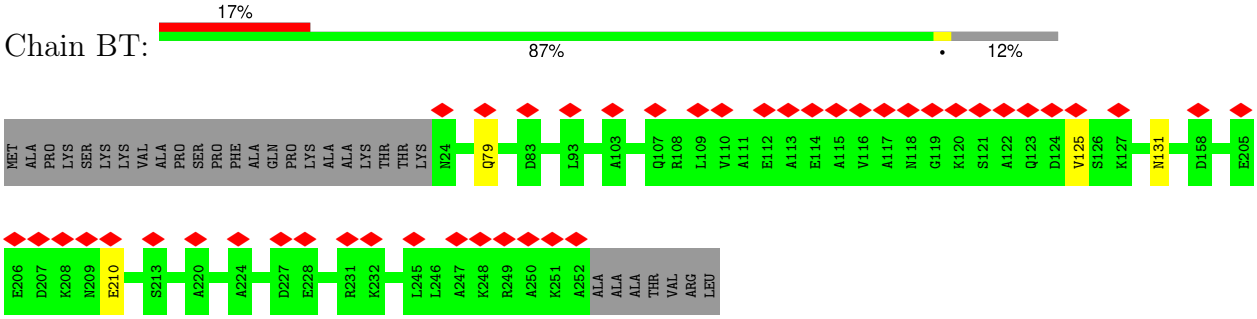
• Molecule 43: Large ribosomal subunit protein uL30C

Chain BS:



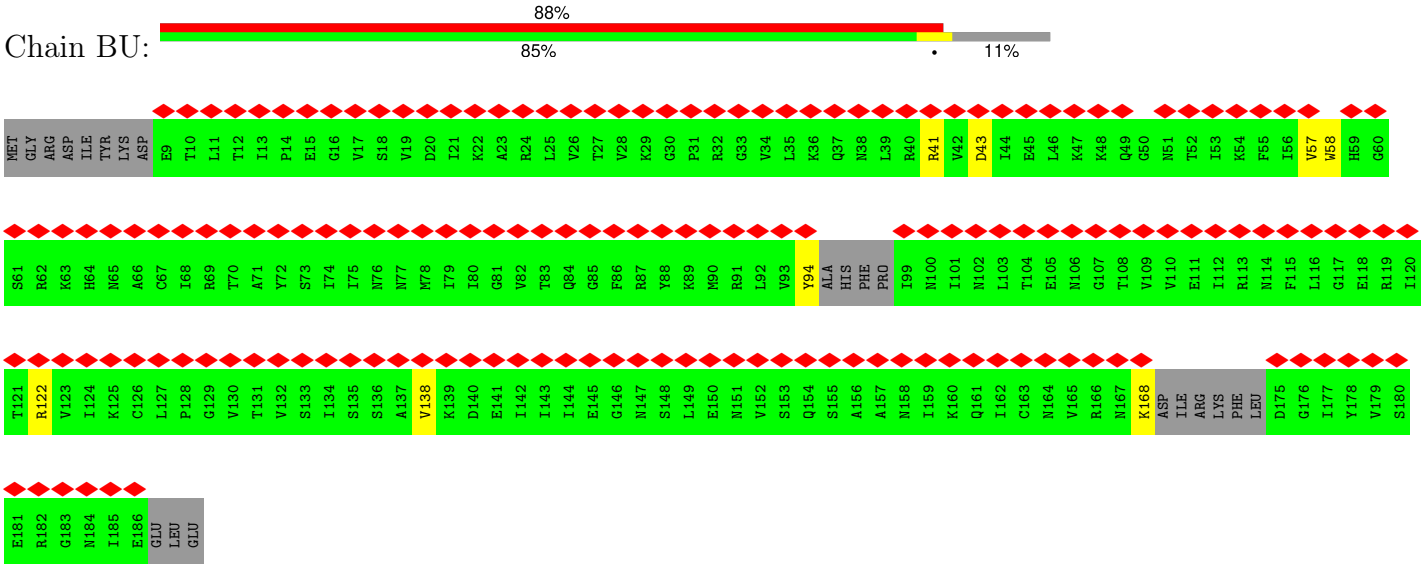
• Molecule 44: Large ribosomal subunit protein eL8

Chain BT:



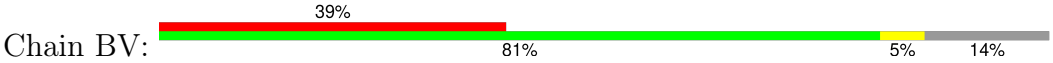
• Molecule 45: Large ribosomal subunit protein uL6B

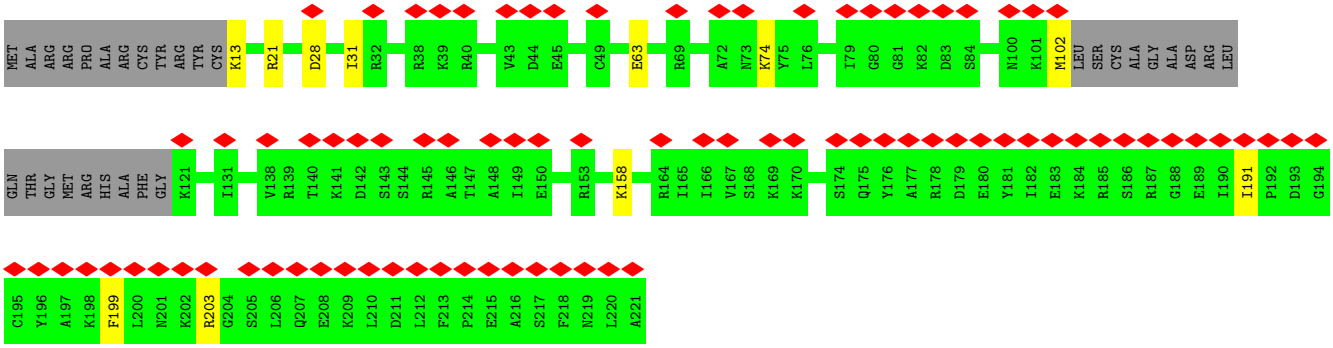
Chain BU:



• Molecule 46: Large ribosomal subunit protein uL16A

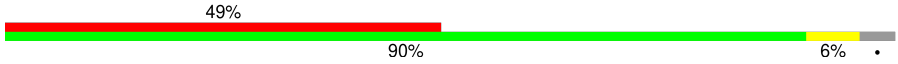
Chain BV:

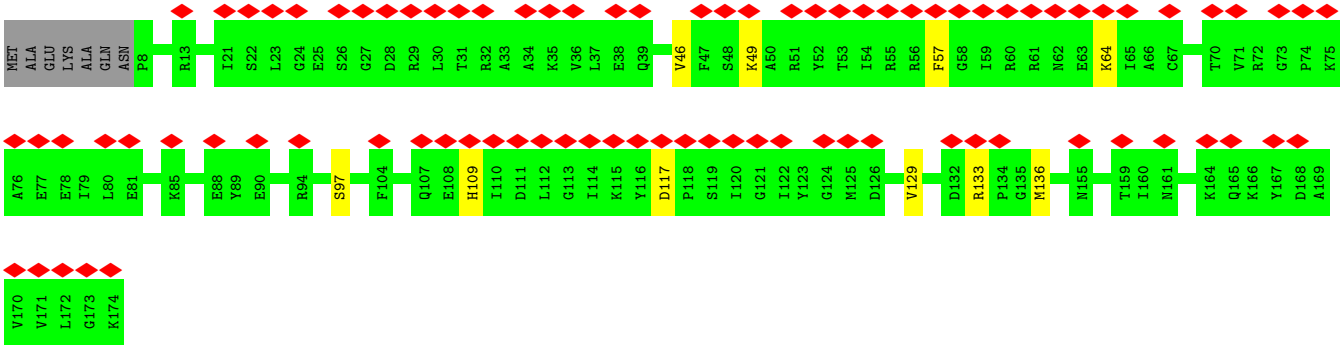




• Molecule 47: Large ribosomal subunit protein uL5A

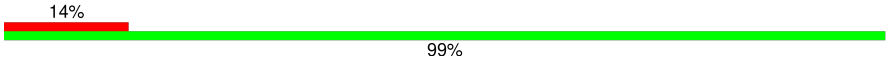
Chain BW:

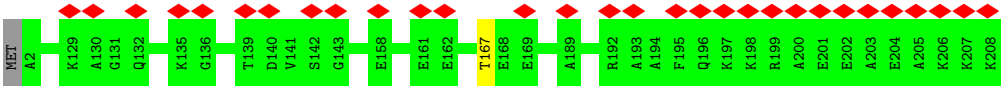




• Molecule 48: Large ribosomal subunit protein eL13

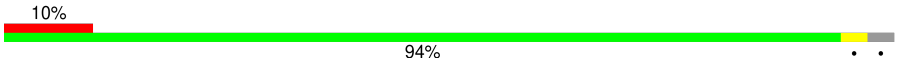
Chain BX:

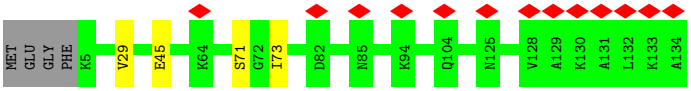




• Molecule 49: Large ribosomal subunit protein eL14

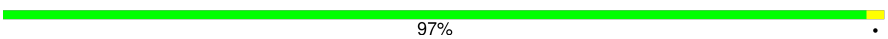
Chain BY:





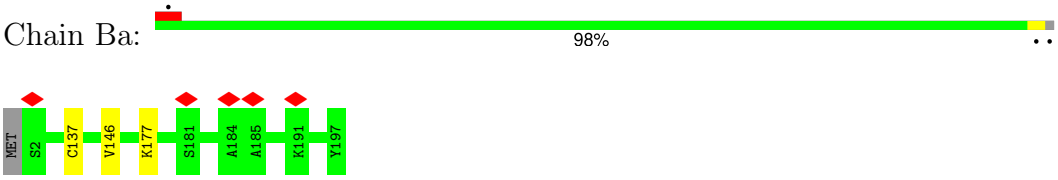
• Molecule 50: Large ribosomal subunit protein eL15B

Chain BZ:



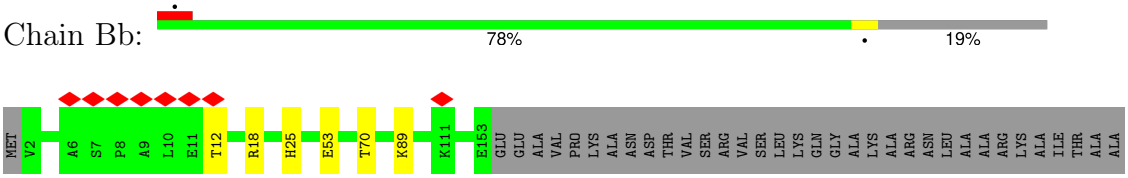
• Molecule 51: Large ribosomal subunit protein uL13A

Chain Ba:



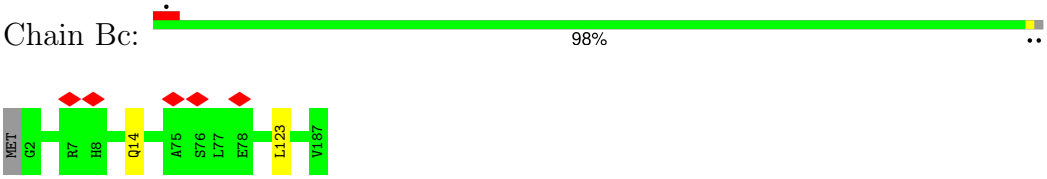
• Molecule 52: Large ribosomal subunit protein uL22A

Chain Bb:



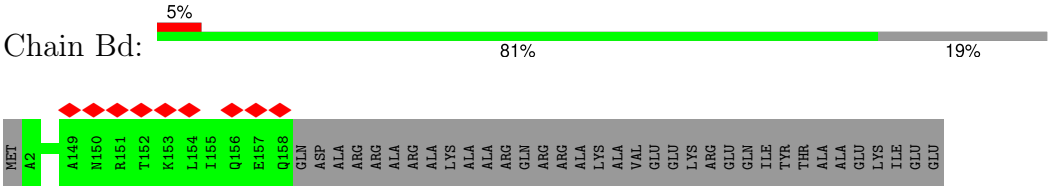
• Molecule 53: Large ribosomal subunit protein eL18B

Chain Bc:



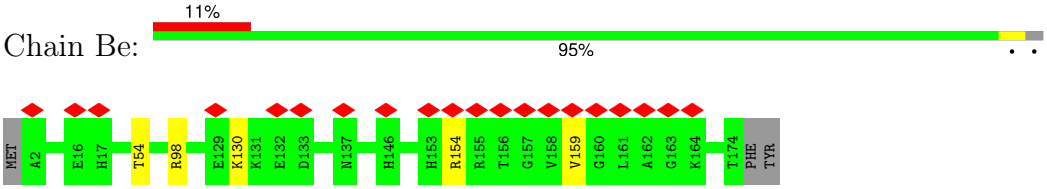
• Molecule 54: Large ribosomal subunit protein eL19B

Chain Bd:



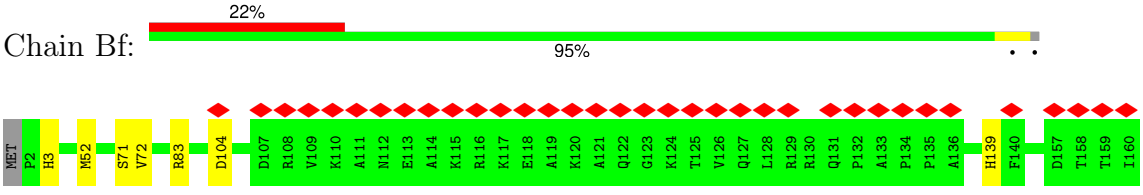
• Molecule 55: Large ribosomal subunit protein eL20A

Chain Be:



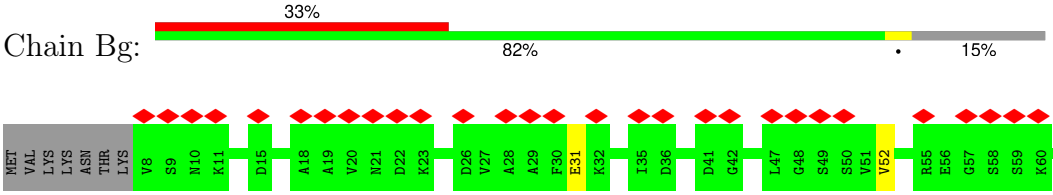
• Molecule 56: Large ribosomal subunit protein eL21B

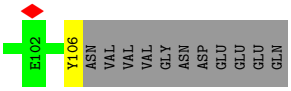
Chain Bf:



• Molecule 57: Large ribosomal subunit protein eL22

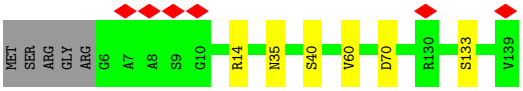
Chain Bg:





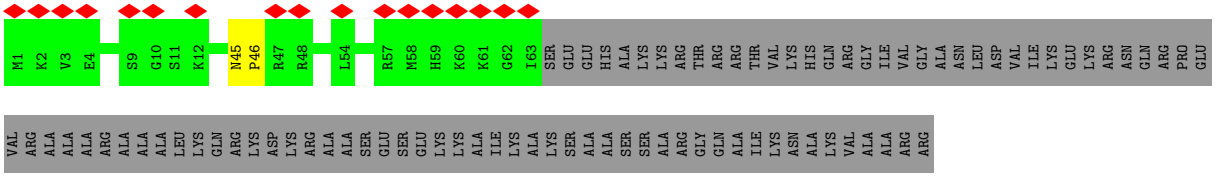
• Molecule 58: Large ribosomal subunit protein uL14B

Chain Bh:



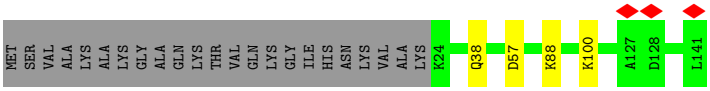
• Molecule 59: Large ribosomal subunit protein eL24B

Chain Bi:



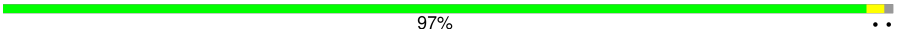
• Molecule 60: Large ribosomal subunit protein uL23A

Chain Bj:



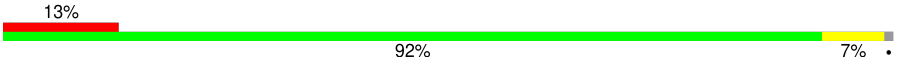
• Molecule 61: Large ribosomal subunit protein uL24

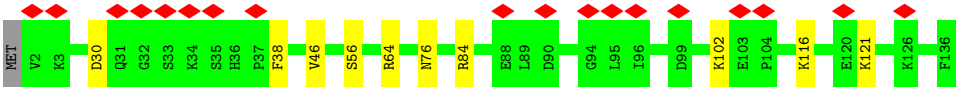
Chain Bk:



• Molecule 62: Large ribosomal subunit protein eL27A

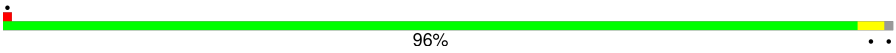
Chain Bl:

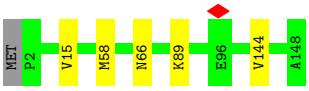




• Molecule 63: Large ribosomal subunit protein uL15B

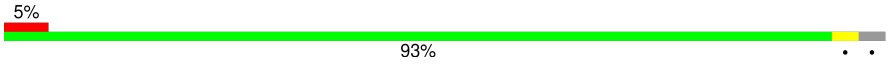
Chain Bm:

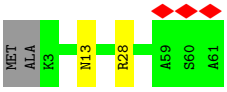




• Molecule 64: Large ribosomal subunit protein eL29

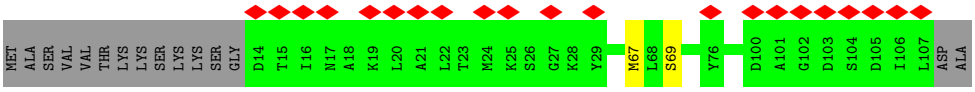
Chain Bn:





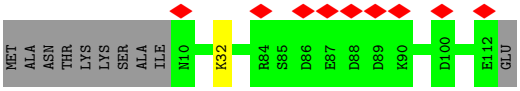
• Molecule 65: Large ribosomal subunit protein eL30A

Chain Bo:



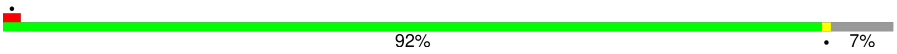
• Molecule 66: Large ribosomal subunit protein eL31

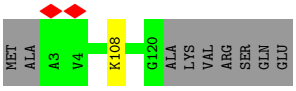
Chain Bp:



• Molecule 67: Large ribosomal subunit protein eL32A

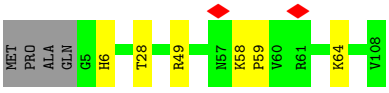
Chain Bq:





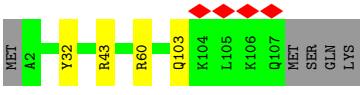
• Molecule 68: Large ribosomal subunit protein eL33A

Chain Br:



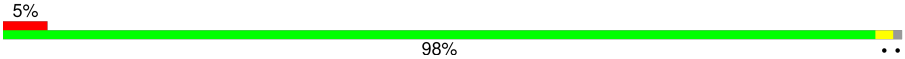
• Molecule 69: Large ribosomal subunit protein eL34B

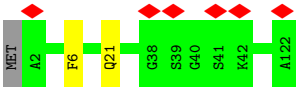
Chain Bs:



• Molecule 70: Large ribosomal subunit protein uL29

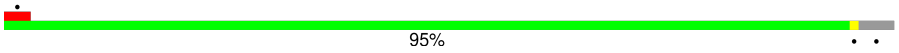
Chain Bt:

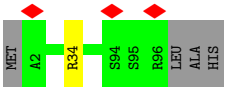




• Molecule 71: Large ribosomal subunit protein eL36B

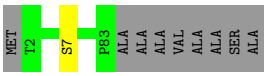
Chain Bu:





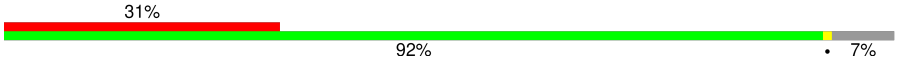
• Molecule 72: Large ribosomal subunit protein eL37B

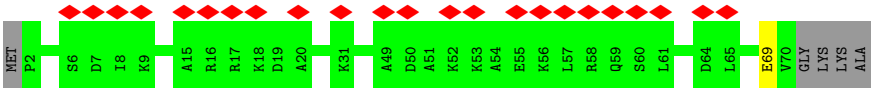
Chain Bv:



• Molecule 73: Large ribosomal subunit protein eL38A

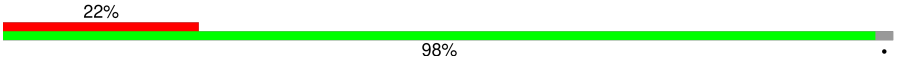
Chain Bw:

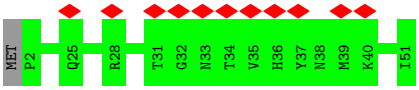




• Molecule 74: Large ribosomal subunit protein eL39

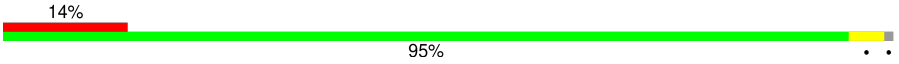
Chain Bx:

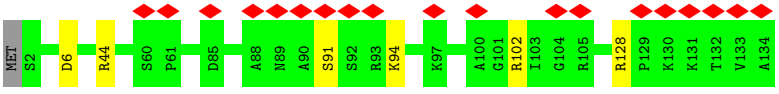




• Molecule 75: Large ribosomal subunit protein eL28

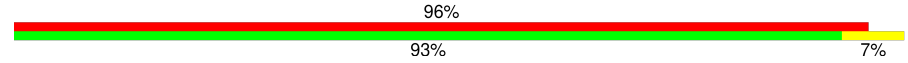
Chain By:

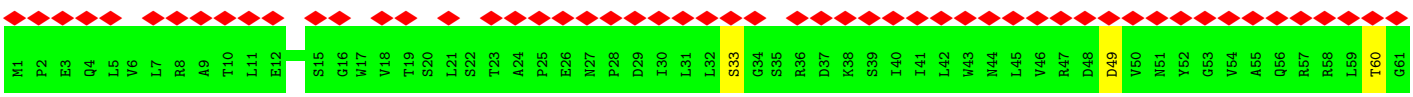


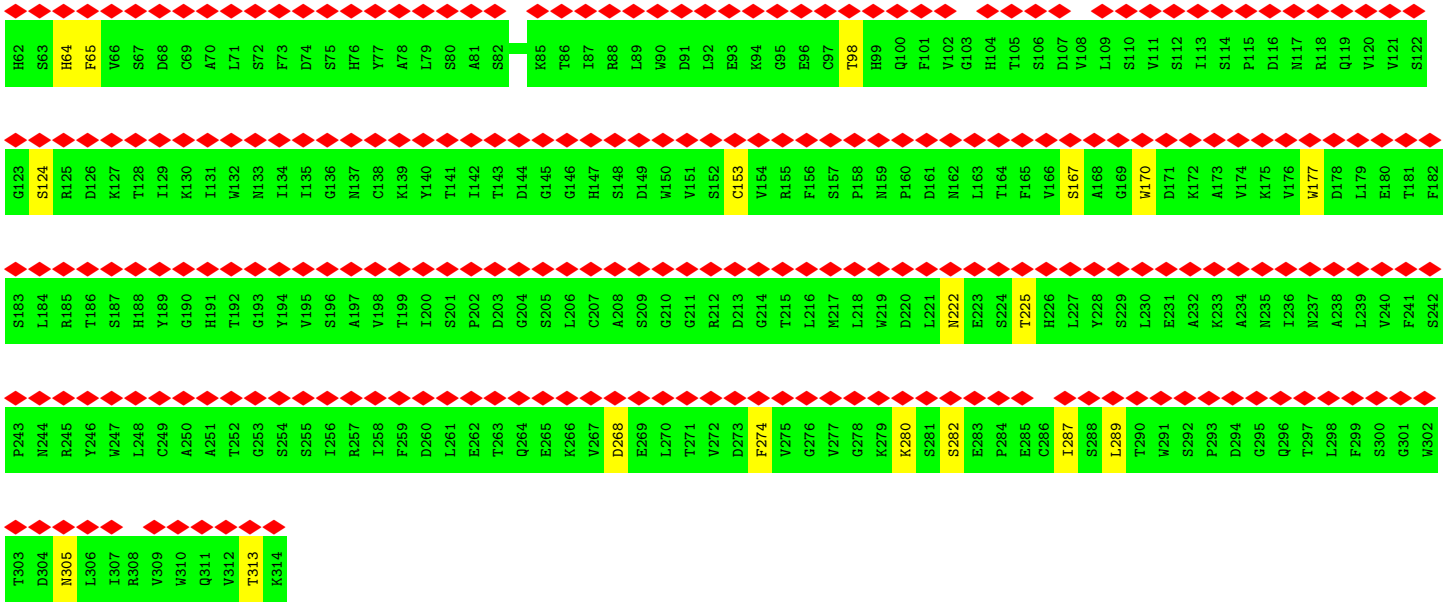


• Molecule 76: Small ribosomal subunit protein RACK1

Chain Am:

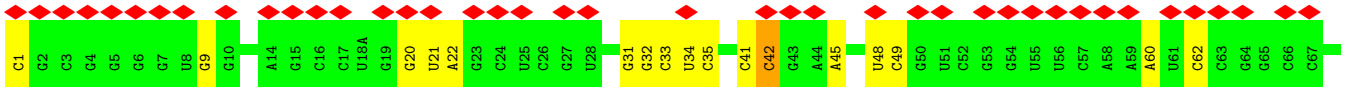






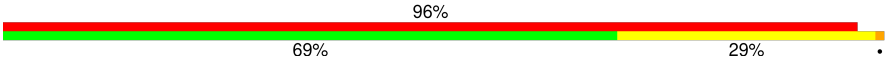
- Molecule 77: tRNA

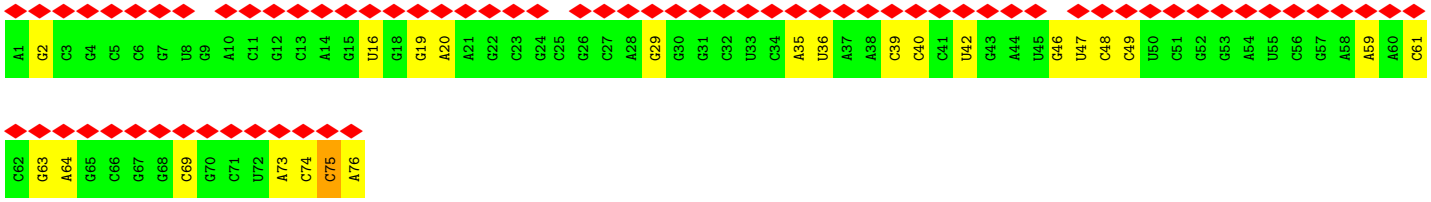
Chain Sm:



- Molecule 78: A/P tRNA

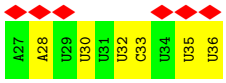
Chain Sn:





- Molecule 79: mRNA

Chain S3:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	58736	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	2.723	Depositor
Minimum map value	-1.267	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.090	Depositor
Recommended contour level	0.27	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	0/40663	0.76	12/63334 (0.0%)
2	AD	0.23	0/1635	0.52	0/2228
3	AE	0.24	0/1756	0.50	0/2358
4	AF	0.24	0/1695	0.51	1/2297 (0.0%)
5	AG	0.24	0/1726	0.53	0/2316
6	AH	0.25	0/2125	0.54	0/2858
7	AI	0.30	0/1577	0.58	2/2123 (0.1%)
8	AJ	0.26	0/1815	0.54	0/2428
9	AK	0.24	0/1554	0.52	0/2091
10	AL	0.25	0/1534	0.55	0/2050
11	AM	0.29	1/1487 (0.1%)	0.60	2/1990 (0.1%)
12	AN	0.24	0/769	0.46	0/1043
13	AO	0.25	0/1190	0.52	0/1602
14	AP	0.23	0/892	0.44	0/1208
15	AQ	0.24	0/1208	0.47	0/1624
16	AR	0.25	0/961	0.56	0/1293
17	AS	0.24	0/973	0.52	0/1307
18	AT	0.25	0/1100	0.49	0/1474
19	AU	0.23	0/983	0.54	0/1318
20	AV	0.26	0/1158	0.51	0/1552
21	AW	0.31	0/1139	0.51	0/1531
22	Aa	0.23	0/825	0.53	0/1111
23	Ab	0.23	0/680	0.51	0/918
24	Ac	0.23	0/1042	0.50	0/1399
25	Ad	0.24	0/1115	0.49	0/1489
26	Ae	0.24	0/1093	0.54	0/1453
27	Af	0.24	0/558	0.50	0/750
28	Ag	0.23	0/808	0.58	0/1083
29	Ah	0.32	0/630	0.53	0/845
30	Ai	0.22	0/500	0.59	0/669
31	Aj	0.24	0/458	0.55	0/610
32	Ak	0.23	0/482	0.52	0/639

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
33	B0	0.24	0/772	0.50	0/1025
34	B1	0.23	0/727	0.59	0/973
35	B2	0.20	0/76870	0.78	31/119823 (0.0%)
36	B3	0.18	0/2838	0.75	1/4422 (0.0%)
37	B4	0.18	0/3723	0.74	0/5796
38	BN	0.24	0/1910	0.53	0/2575
39	BO	0.24	0/3116	0.51	0/4190
40	BP	0.24	0/2852	0.49	0/3850
41	BQ	0.26	0/2361	0.51	0/3173
42	BR	0.25	0/1275	0.49	0/1719
43	BS	0.24	0/1929	0.47	0/2583
44	BT	0.24	0/1801	0.47	0/2430
45	BU	0.23	0/1330	0.50	0/1789
46	BV	0.24	0/1579	0.50	0/2115
47	BW	0.28	0/1369	0.55	0/1830
48	BX	0.24	0/1686	0.51	0/2267
49	BY	0.23	0/1054	0.49	0/1413
50	BZ	0.24	0/1717	0.53	0/2306
51	Ba	0.25	0/1575	0.48	0/2109
52	Bb	0.24	0/1237	0.48	0/1661
53	Bc	0.24	0/1511	0.54	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	0.48	0/1771
57	Bg	0.25	0/812	0.48	0/1090
58	Bh	0.25	0/1015	0.54	0/1369
59	Bi	1.23	4/534 (0.7%)	1.57	6/709 (0.8%)
60	Bj	0.24	0/963	0.51	0/1296
61	Bk	0.23	0/1008	0.54	0/1341
62	Bl	0.25	0/1101	0.50	0/1477
63	Bm	0.23	0/1200	0.52	0/1611
64	Bn	0.23	0/503	0.50	0/664
65	Bo	0.27	0/714	0.45	0/961
66	Bp	0.23	0/872	0.53	0/1172
67	Bq	0.24	0/958	0.53	0/1278
68	Br	0.71	2/853 (0.2%)	0.91	6/1146 (0.5%)
69	Bs	0.24	0/870	0.54	0/1165
70	Bt	0.23	0/1008	0.48	0/1340
71	Bu	0.23	0/766	0.54	0/1017
72	Bv	0.25	0/666	0.55	0/881
73	Bw	0.24	0/566	0.48	0/757
74	Bx	0.23	0/447	0.55	0/597
75	By	0.24	0/1045	0.51	0/1404

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	Am	0.24	0/2520	0.50	0/3434
77	Sm	0.32	1/1812 (0.1%)	0.84	2/2816 (0.1%)
78	Sn	0.20	0/1796	0.83	3/2799 (0.1%)
79	S3	0.24	0/225	0.89	0/346
All	All	0.23	8/215709 (0.0%)	0.69	66/317220 (0.0%)

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	Bi	46	PRO	CG-CD	-18.42	0.89	1.50
59	Bi	46	PRO	CB-CG	15.86	2.29	1.50
68	Br	59	PRO	N-CD	13.31	1.66	1.47
68	Br	59	PRO	CG-CD	-12.95	1.07	1.50
59	Bi	46	PRO	N-CD	10.75	1.62	1.47

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	Bi	46	PRO	CB-CG-CD	-27.30	0.02	106.50
59	Bi	46	PRO	CA-N-CD	-18.33	85.84	111.50
68	Br	59	PRO	N-CD-CG	-17.31	77.24	103.20
59	Bi	45	ASN	C-N-CD	15.58	161.12	128.40
7	AI	121	ARG	NE-CZ-NH2	-11.29	114.66	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

5.3 Torsion angles

5.3.1 Protein backbone

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%)	180 (89%)	23 (11%)	0	100	100
3	AE	214/252 (85%)	200 (94%)	14 (6%)	0	100	100
4	AF	214/253 (85%)	207 (97%)	6 (3%)	1 (0%)	25	38
5	AG	214/249 (86%)	195 (91%)	18 (8%)	1 (0%)	25	38
6	AH	259/262 (99%)	231 (89%)	23 (9%)	5 (2%)	6	8
7	AI	201/203 (99%)	176 (88%)	21 (10%)	4 (2%)	6	8
8	AJ	219/239 (92%)	212 (97%)	7 (3%)	0	100	100
9	AK	191/195 (98%)	173 (91%)	18 (9%)	0	100	100
10	AL	184/200 (92%)	175 (95%)	9 (5%)	0	100	100
11	AM	176/192 (92%)	163 (93%)	13 (7%)	0	100	100
12	AN	90/147 (61%)	79 (88%)	10 (11%)	1 (1%)	12	18
13	AO	141/152 (93%)	131 (93%)	10 (7%)	0	100	100
14	AP	119/145 (82%)	106 (89%)	12 (10%)	1 (1%)	16	26
15	AQ	148/151 (98%)	142 (96%)	5 (3%)	1 (1%)	19	29
16	AR	126/139 (91%)	114 (90%)	12 (10%)	0	100	100
17	AS	117/154 (76%)	110 (94%)	7 (6%)	0	100	100
18	AT	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
19	AU	116/131 (88%)	99 (85%)	11 (10%)	6 (5%)	1	1
20	AV	139/152 (91%)	130 (94%)	9 (6%)	0	100	100
21	AW	140/144 (97%)	133 (95%)	7 (5%)	0	100	100
22	Aa	98/118 (83%)	90 (92%)	6 (6%)	2 (2%)	6	8
23	Ab	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
24	Ac	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
25	Ad	140/143 (98%)	136 (97%)	4 (3%)	0	100	100
26	Ae	131/134 (98%)	124 (95%)	6 (5%)	1 (1%)	16	26
27	Af	67/89 (75%)	61 (91%)	6 (9%)	0	100	100
28	Ag	95/119 (80%)	89 (94%)	6 (6%)	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%)	49 (96%)	2 (4%)	0	100	100
32	Ak	58/61 (95%)	53 (91%)	4 (7%)	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%)	85 (93%)	6 (7%)	0	100	100
38	BN	246/253 (97%)	228 (93%)	18 (7%)	0	100	100
39	BO	382/388 (98%)	357 (94%)	25 (6%)	0	100	100
40	BP	360/363 (99%)	349 (97%)	11 (3%)	0	100	100
41	BQ	285/294 (97%)	257 (90%)	26 (9%)	2 (1%)	19	29
42	BR	160/195 (82%)	138 (86%)	22 (14%)	0	100	100
43	BS	231/251 (92%)	224 (97%)	7 (3%)	0	100	100
44	BT	227/259 (88%)	211 (93%)	16 (7%)	0	100	100
45	BU	162/189 (86%)	155 (96%)	7 (4%)	0	100	100
46	BV	187/221 (85%)	181 (97%)	6 (3%)	0	100	100
47	BW	165/174 (95%)	147 (89%)	16 (10%)	2 (1%)	11	16
48	BX	205/208 (99%)	201 (98%)	4 (2%)	0	100	100
49	BY	128/134 (96%)	125 (98%)	3 (2%)	0	100	100
50	BZ	198/201 (98%)	189 (96%)	9 (4%)	0	100	100
51	Ba	194/197 (98%)	191 (98%)	3 (2%)	0	100	100
52	Bb	150/187 (80%)	146 (97%)	4 (3%)	0	100	100
53	Bc	184/187 (98%)	178 (97%)	6 (3%)	0	100	100
54	Bd	155/193 (80%)	153 (99%)	2 (1%)	0	100	100
55	Be	171/176 (97%)	164 (96%)	6 (4%)	1 (1%)	22	33
56	Bf	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
57	Bg	97/117 (83%)	86 (89%)	11 (11%)	0	100	100
58	Bh	132/139 (95%)	125 (95%)	7 (5%)	0	100	100
59	Bi	61/149 (41%)	61 (100%)	0	0	100	100
60	Bj	116/141 (82%)	114 (98%)	2 (2%)	0	100	100
61	Bk	123/126 (98%)	122 (99%)	1 (1%)	0	100	100
62	Bl	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
63	Bm	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
64	Bn	57/61 (93%)	54 (95%)	3 (5%)	0	100	100
65	Bo	92/109 (84%)	92 (100%)	0	0	100	100
66	Bp	101/113 (89%)	98 (97%)	3 (3%)	0	100	100
67	Bq	116/127 (91%)	113 (97%)	3 (3%)	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%)	102 (98%)	2 (2%)	0	100	100
70	Bt	119/122 (98%)	115 (97%)	4 (3%)	0	100	100
71	Bu	93/99 (94%)	90 (97%)	3 (3%)	0	100	100
72	Bv	80/91 (88%)	75 (94%)	5 (6%)	0	100	100
73	Bw	67/74 (90%)	67 (100%)	0	0	100	100
74	Bx	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
75	By	131/134 (98%)	128 (98%)	3 (2%)	0	100	100
76	Am	312/314 (99%)	296 (95%)	16 (5%)	0	100	100
All	All	10699/11780 (91%)	10094 (94%)	576 (5%)	29 (0%)	38	51

5 of 29 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	AH	245	LYS
19	AU	88	VAL
22	Aa	50	VAL
41	BQ	216	GLU
47	BW	46	VAL

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%)	160 (94%)	10 (6%)	16	28
3	AE	193/223 (86%)	178 (92%)	15 (8%)	10	17
4	AF	175/199 (88%)	164 (94%)	11 (6%)	15	25
5	AG	181/203 (89%)	168 (93%)	13 (7%)	12	20
6	AH	226/227 (100%)	209 (92%)	17 (8%)	11	18
7	AI	169/169 (100%)	162 (96%)	7 (4%)	26	44
8	AJ	188/204 (92%)	176 (94%)	12 (6%)	14	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
9	AK	169/171 (99%)	163 (96%)	6 (4%)	30 49
10	AL	157/166 (95%)	150 (96%)	7 (4%)	23 40
11	AM	155/165 (94%)	145 (94%)	10 (6%)	14 24
12	AN	77/116 (66%)	74 (96%)	3 (4%)	27 46
13	AO	124/131 (95%)	115 (93%)	9 (7%)	11 20
14	AP	92/118 (78%)	89 (97%)	3 (3%)	33 53
15	AQ	127/128 (99%)	123 (97%)	4 (3%)	35 56
16	AR	95/104 (91%)	90 (95%)	5 (5%)	19 33
17	AS	101/131 (77%)	92 (91%)	9 (9%)	8 12
18	AT	111/111 (100%)	107 (96%)	4 (4%)	30 49
19	AU	107/120 (89%)	100 (94%)	7 (6%)	14 24
20	AV	127/136 (93%)	119 (94%)	8 (6%)	15 25
21	AW	117/119 (98%)	105 (90%)	12 (10%)	6 9
22	Aa	95/111 (86%)	88 (93%)	7 (7%)	11 19
23	Ab	73/73 (100%)	72 (99%)	1 (1%)	62 79
24	Ac	114/115 (99%)	108 (95%)	6 (5%)	19 33
25	Ad	112/113 (99%)	105 (94%)	7 (6%)	15 25
26	Ae	112/113 (99%)	102 (91%)	10 (9%)	8 12
27	Af	61/75 (81%)	60 (98%)	1 (2%)	58 76
28	Ag	87/106 (82%)	83 (95%)	4 (5%)	23 39
29	Ah	71/73 (97%)	66 (93%)	5 (7%)	12 21
30	Ai	56/61 (92%)	54 (96%)	2 (4%)	30 49
31	Aj	45/47 (96%)	44 (98%)	1 (2%)	47 67
32	Ak	51/52 (98%)	50 (98%)	1 (2%)	50 70
33	B0	84/93 (90%)	80 (95%)	4 (5%)	21 37
34	B1	74/75 (99%)	73 (99%)	1 (1%)	62 79
38	BN	188/192 (98%)	185 (98%)	3 (2%)	58 76
39	BO	318/326 (98%)	309 (97%)	9 (3%)	38 59
40	BP	293/294 (100%)	287 (98%)	6 (2%)	50 70
41	BQ	235/241 (98%)	222 (94%)	13 (6%)	18 31
42	BR	132/155 (85%)	128 (97%)	4 (3%)	36 57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	BS	198/213 (93%)	192 (97%)	6 (3%)	36	57
44	BT	182/212 (86%)	178 (98%)	4 (2%)	47	67
45	BU	149/168 (89%)	141 (95%)	8 (5%)	18	32
46	BV	165/187 (88%)	154 (93%)	11 (7%)	13	23
47	BW	141/146 (97%)	133 (94%)	8 (6%)	17	29
48	BX	166/167 (99%)	165 (99%)	1 (1%)	84	92
49	BY	110/113 (97%)	106 (96%)	4 (4%)	30	49
50	BZ	175/176 (99%)	170 (97%)	5 (3%)	37	58
51	Ba	159/160 (99%)	156 (98%)	3 (2%)	52	72
52	Bb	124/149 (83%)	118 (95%)	6 (5%)	21	37
53	Bc	157/158 (99%)	155 (99%)	2 (1%)	65	81
54	Bd	136/163 (83%)	136 (100%)	0	100	100
55	Be	151/154 (98%)	147 (97%)	4 (3%)	41	62
56	Bf	138/139 (99%)	131 (95%)	7 (5%)	20	35
57	Bg	86/103 (84%)	83 (96%)	3 (4%)	31	51
58	Bh	103/107 (96%)	97 (94%)	6 (6%)	17	29
59	Bi	57/121 (47%)	57 (100%)	0	100	100
60	Bj	105/122 (86%)	101 (96%)	4 (4%)	28	47
61	Bk	110/111 (99%)	107 (97%)	3 (3%)	40	60
62	Bl	114/115 (99%)	104 (91%)	10 (9%)	8	13
63	Bm	122/123 (99%)	117 (96%)	5 (4%)	26	44
64	Bn	50/51 (98%)	48 (96%)	2 (4%)	27	45
65	Bo	75/87 (86%)	73 (97%)	2 (3%)	40	60
66	Bp	94/102 (92%)	93 (99%)	1 (1%)	70	84
67	Bq	100/107 (94%)	99 (99%)	1 (1%)	73	86
68	Br	91/94 (97%)	87 (96%)	4 (4%)	24	41
69	Bs	91/96 (95%)	87 (96%)	4 (4%)	24	41
70	Bt	106/107 (99%)	104 (98%)	2 (2%)	52	72
71	Bu	81/84 (96%)	80 (99%)	1 (1%)	67	82
72	Bv	68/71 (96%)	67 (98%)	1 (2%)	60	77
73	Bw	63/66 (96%)	62 (98%)	1 (2%)	58	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
74	Bx	46/47 (98%)	46 (100%)	0	100 100
75	By	112/113 (99%)	106 (95%)	6 (5%)	18 32
76	Am	276/276 (100%)	255 (92%)	21 (8%)	11 18
All	All	9163/9892 (93%)	8760 (96%)	403 (4%)	26 41

5 of 403 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	BO	293	ASN
47	BW	49	LYS
76	Am	287	ILE
40	BP	343	LEU
43	BS	149	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
46	BV	162	GLN
55	Be	87	HIS
76	Am	4	GLN
49	BY	123	GLN
51	Ba	32	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1689/1842 (91%)	398 (23%)	15 (0%)
35	B2	3203/3498 (91%)	663 (20%)	26 (0%)
36	B3	118/246 (47%)	23 (19%)	1 (0%)
37	B4	156/165 (94%)	30 (19%)	1 (0%)
77	Sm	73/77 (94%)	17 (23%)	0
78	Sn	74/75 (98%)	23 (31%)	0
79	S3	9/10 (90%)	6 (66%)	1 (11%)
All	All	5322/5913 (90%)	1160 (21%)	44 (0%)

5 of 1160 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	3	C

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Mol	Chain	Res	Type
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	1665	A
35	B2	3217	U
35	B2	1854	A
35	B2	2867	C
35	B2	3298	C

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 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	7
77	Sm	2
35	B2	1
22	Aa	1

The worst 5 of 11 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B2	2363:A	O3'	2364:G	P	6.70
1	Sm	17:C	O3'	18(A):U	P	4.09
1	Sm	18(A):U	O3'	19:G	P	4.09
1	AA	1419:A	O3'	1420:A	P	3.63
1	AA	1498:G	O3'	1499:A	P	3.41

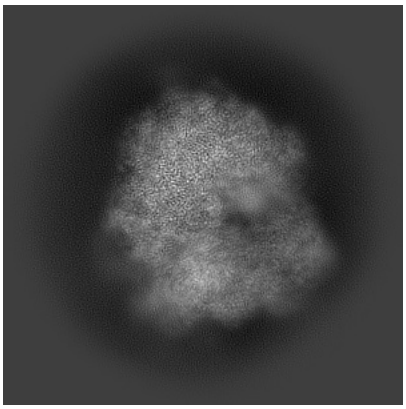
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-43976. These allow visual inspection of the internal detail of the map and identification of artifacts.

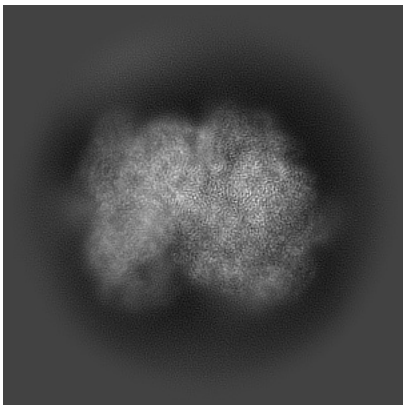
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

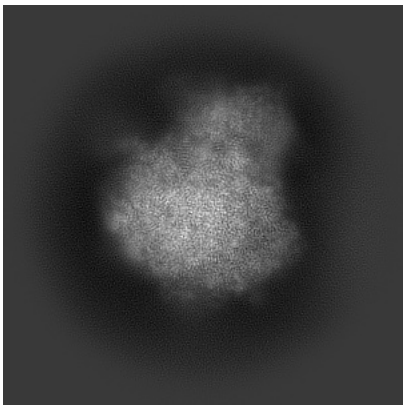
6.1.1 Primary map



X

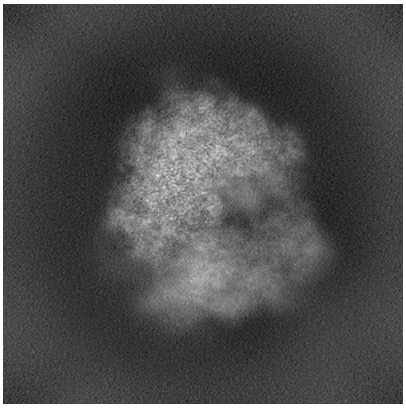


Y

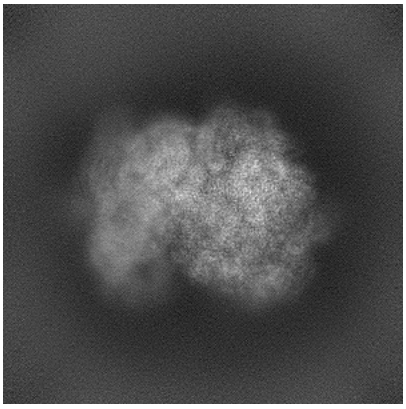


Z

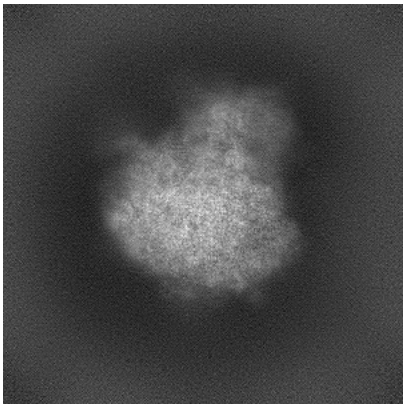
6.1.2 Raw map



X



Y

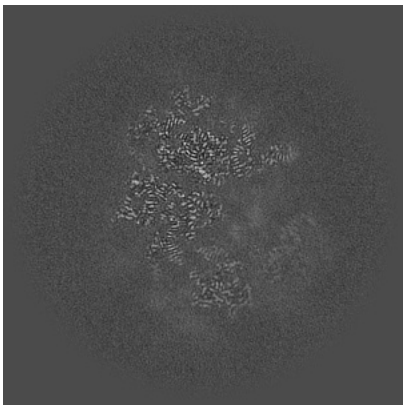


Z

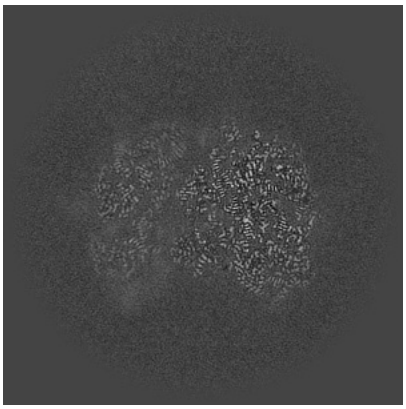
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

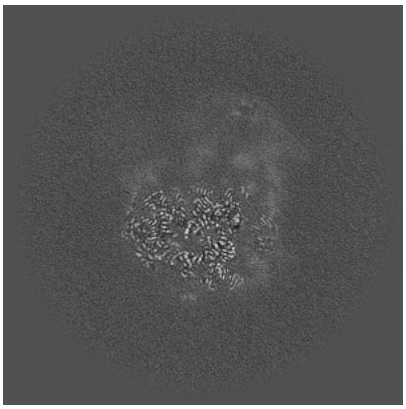
6.2.1 Primary map



X Index: 256

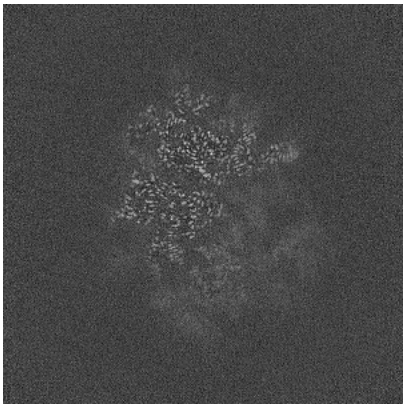


Y Index: 256

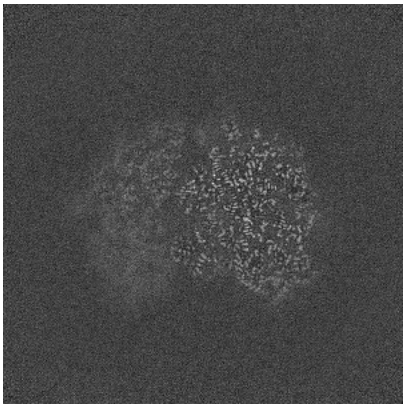


Z Index: 256

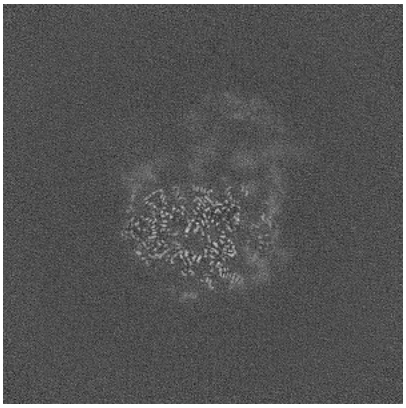
6.2.2 Raw map



X Index: 256



Y Index: 256

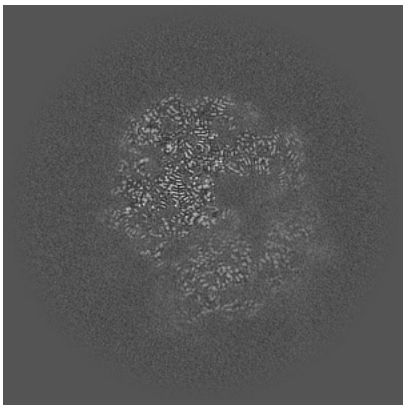


Z Index: 256

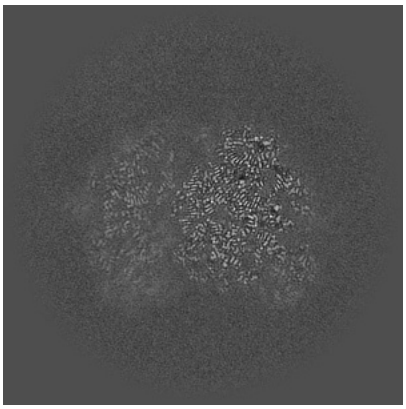
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

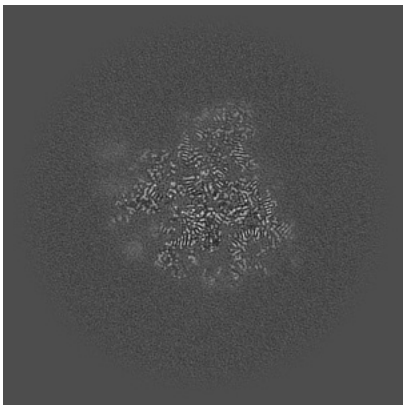
6.3.1 Primary map



X Index: 276

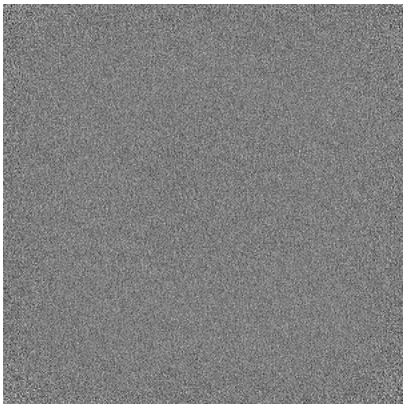


Y Index: 246

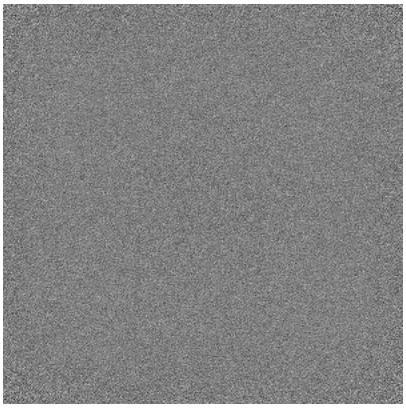


Z Index: 323

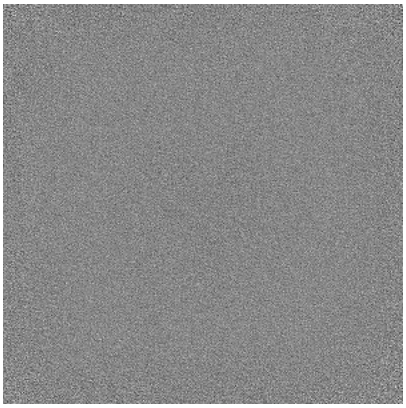
6.3.2 Raw map



X Index: 0



Y Index: 0

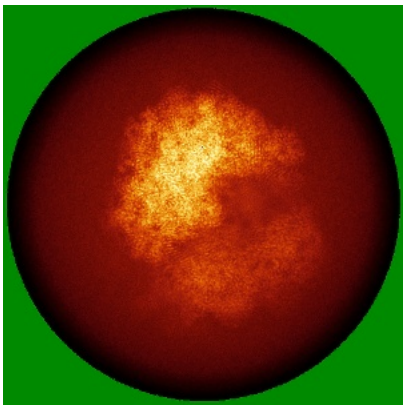


Z Index: 0

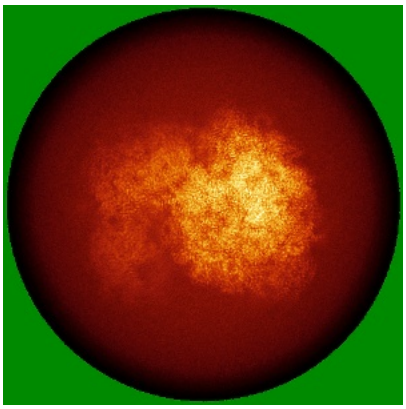
The images above show the largest variance slices of the map in three orthogonal directions.

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

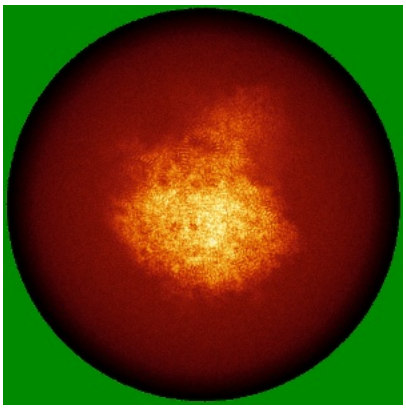
6.4.1 Primary map



X

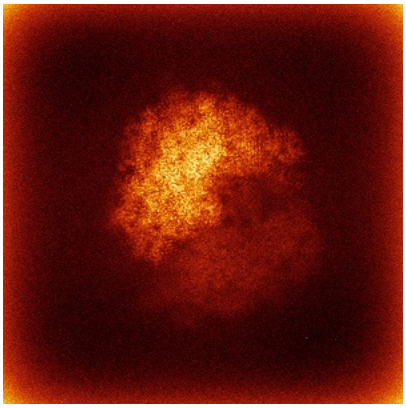


Y

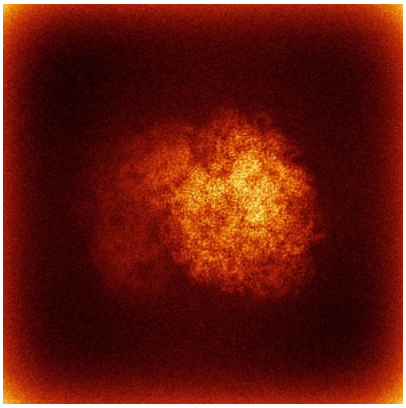


Z

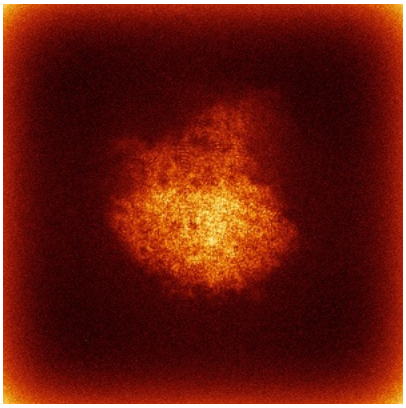
6.4.2 Raw map



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.

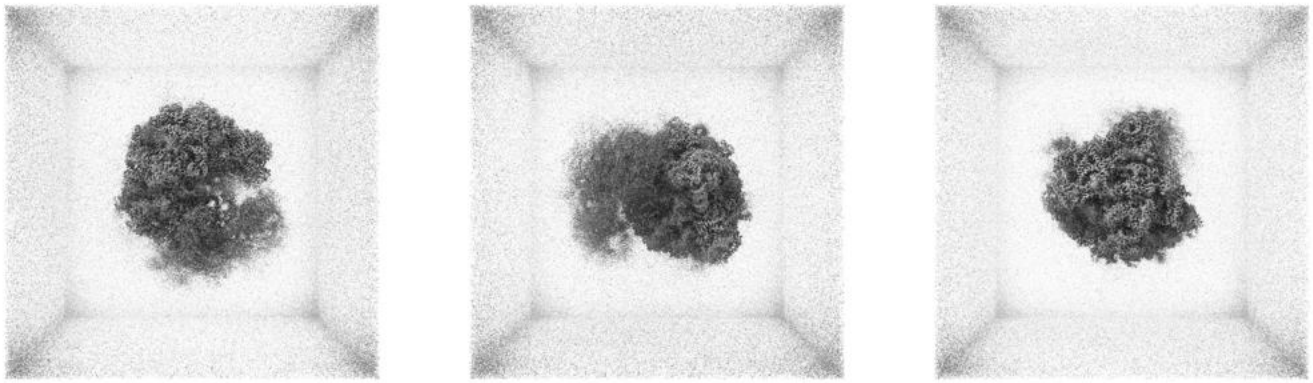
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.27. 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.

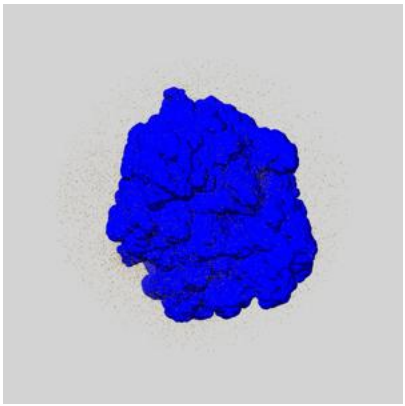
6.6 Mask visualisation (i)

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

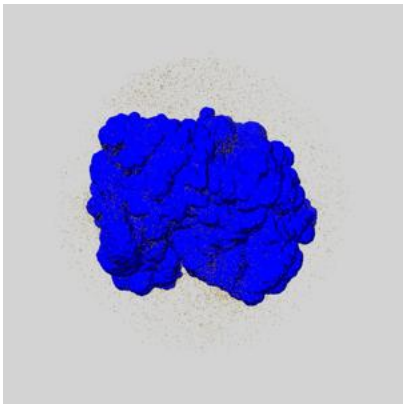
A mask typically either:

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

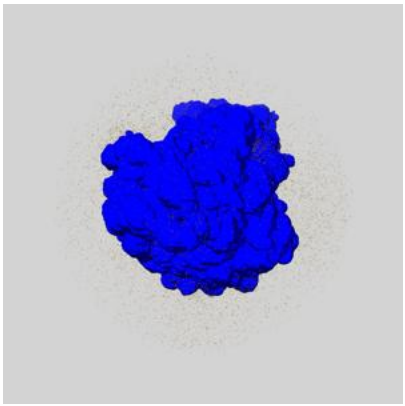
6.6.1 emd_43976_msk_1.map (i)



X



Y

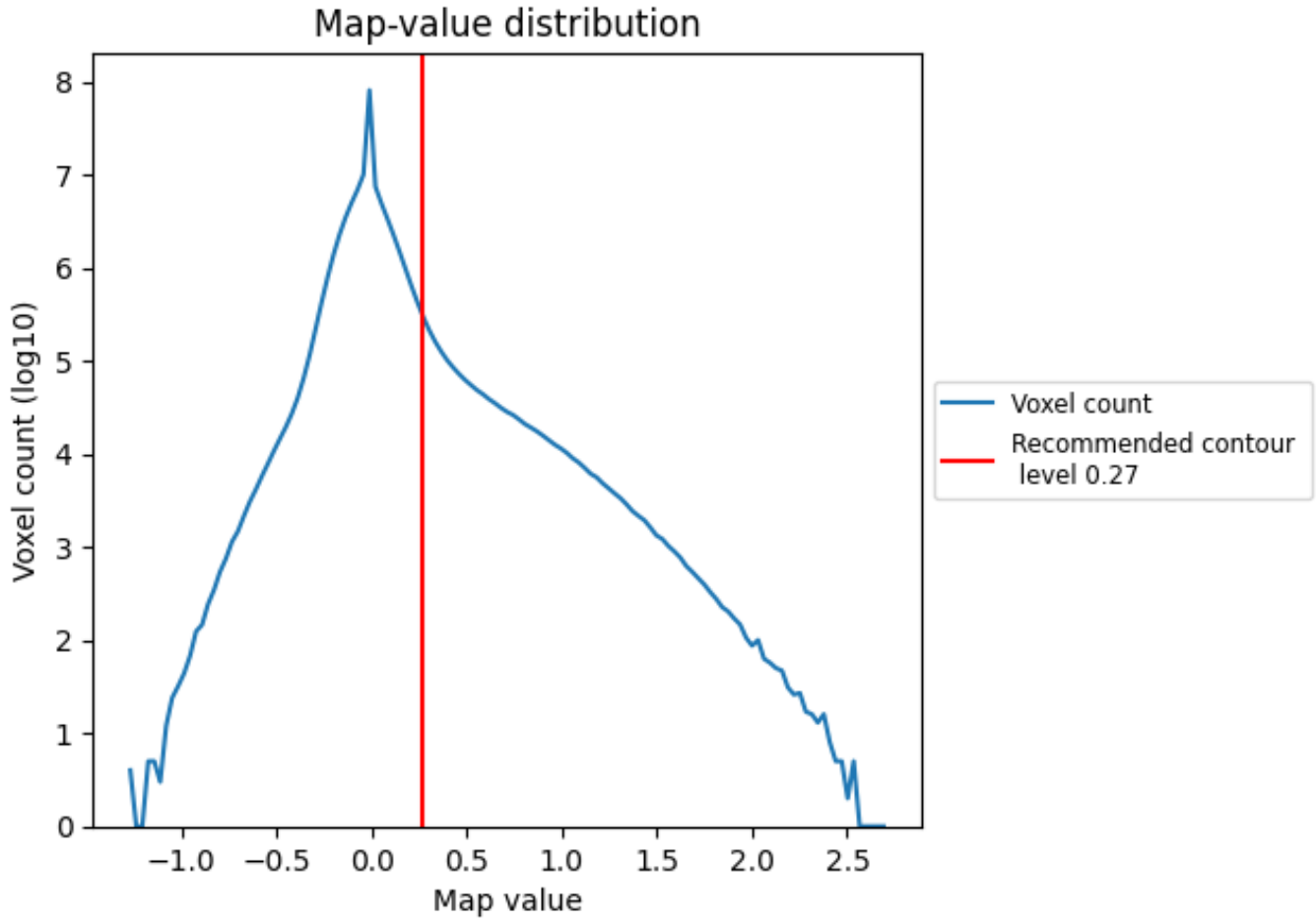


Z

7 Map analysis

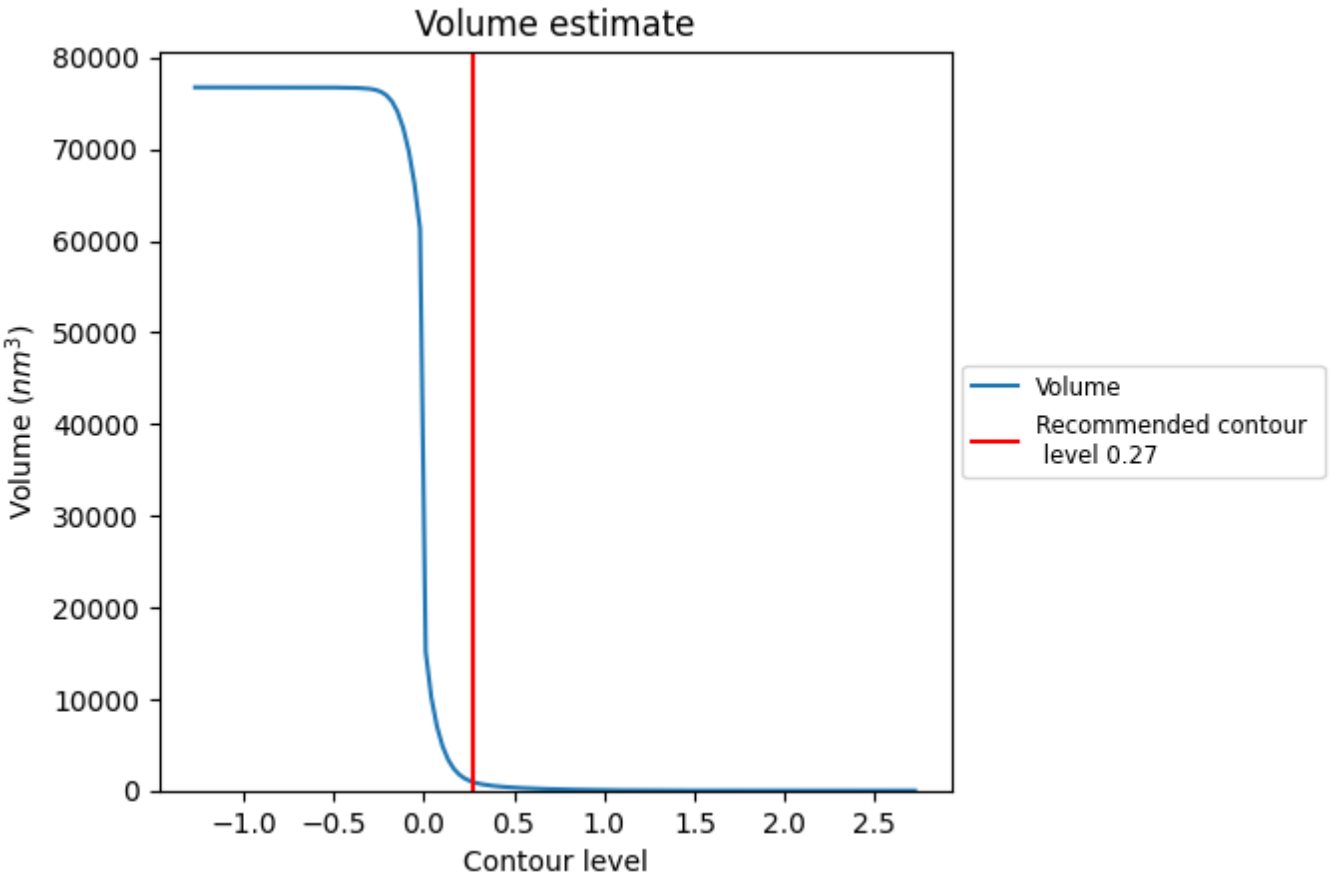
This section contains the results of statistical analysis of the map.

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.

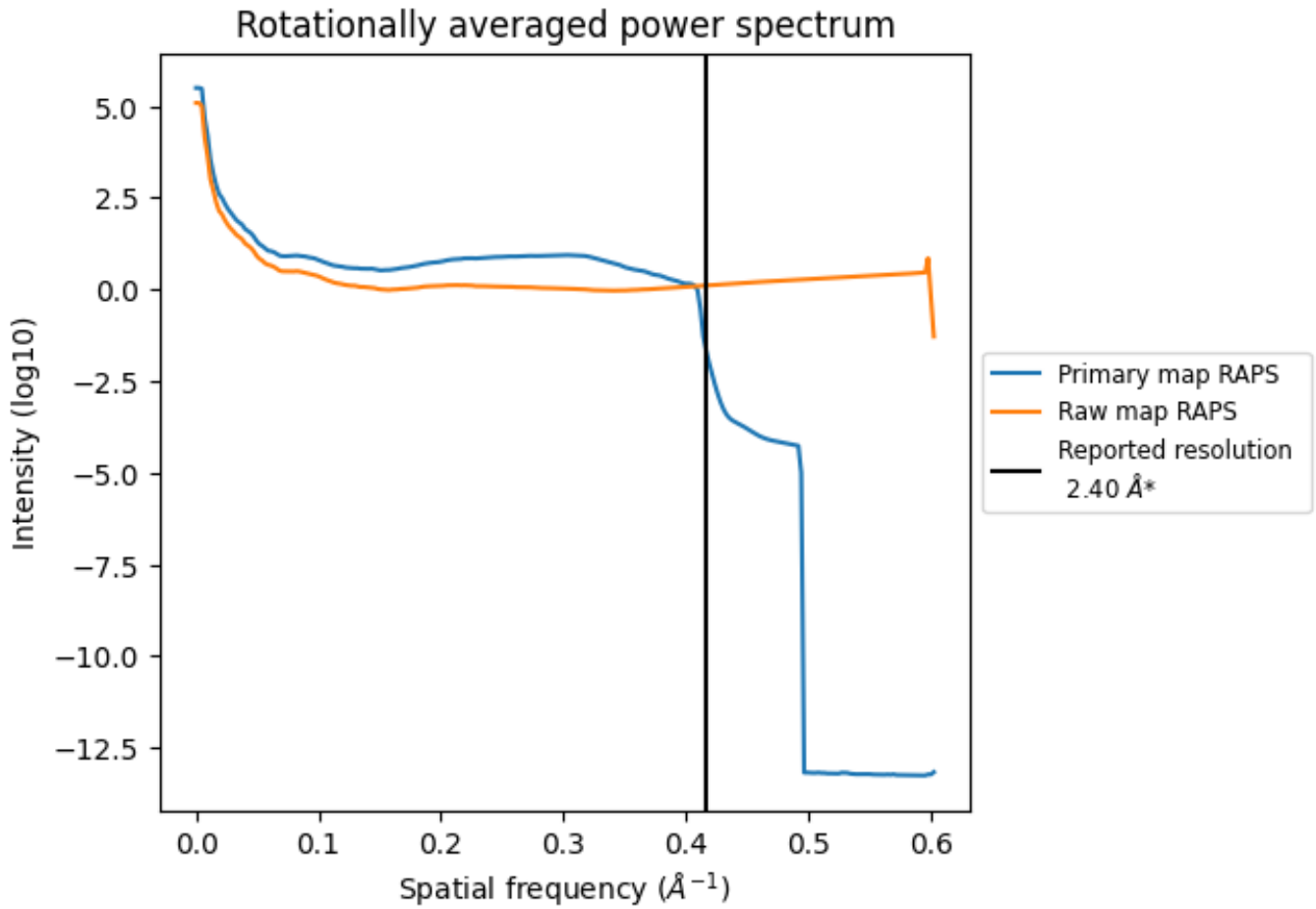
7.2 Volume estimate (i)



The volume at the recommended contour level is 958 nm^3; this corresponds to an approximate mass of 866 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)

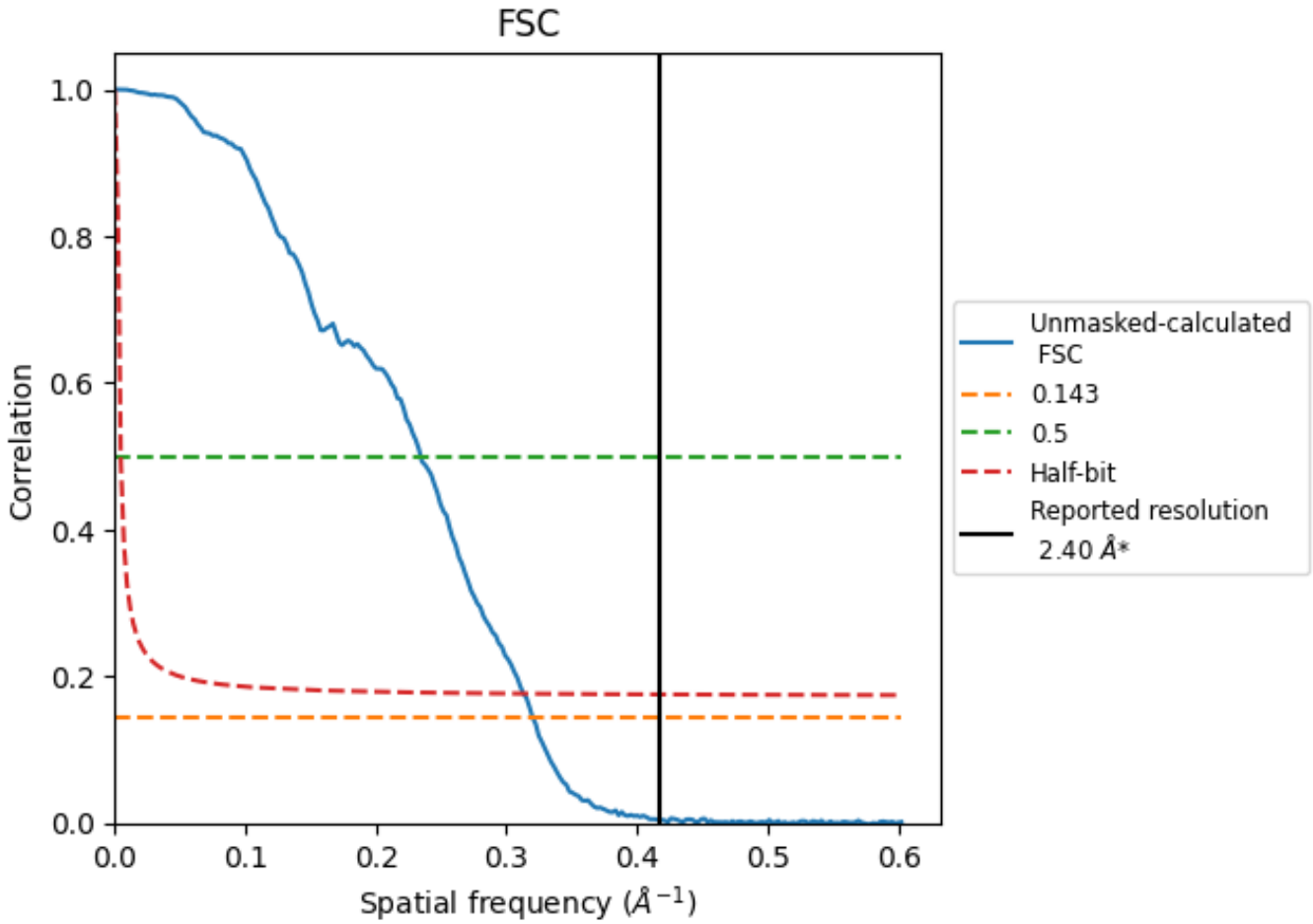


*Reported resolution corresponds to spatial frequency of 0.417 $Å^{-1}$

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)

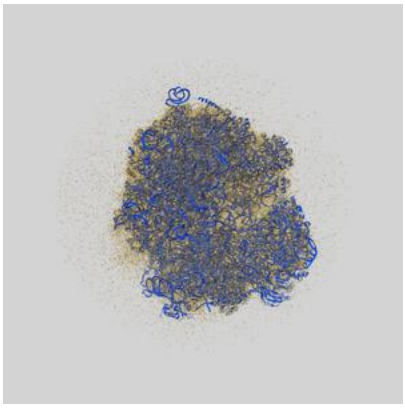
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.12	4.27	3.20

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

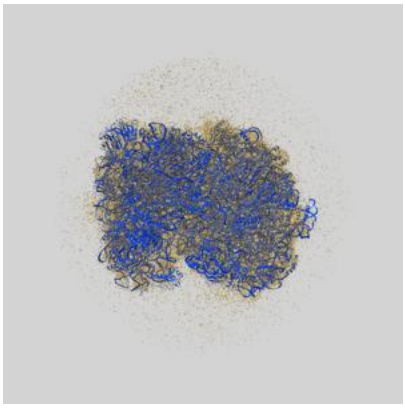
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-43976 and PDB model 9AXV. Per-residue inclusion information can be found in section 3 on page 18.

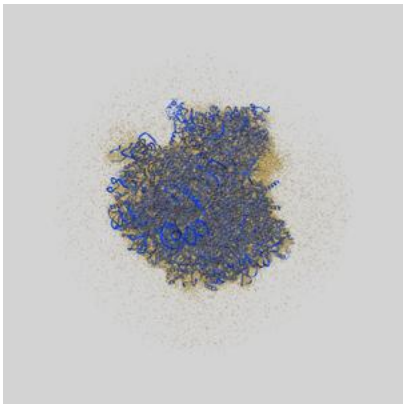
9.1 Map-model overlay



X



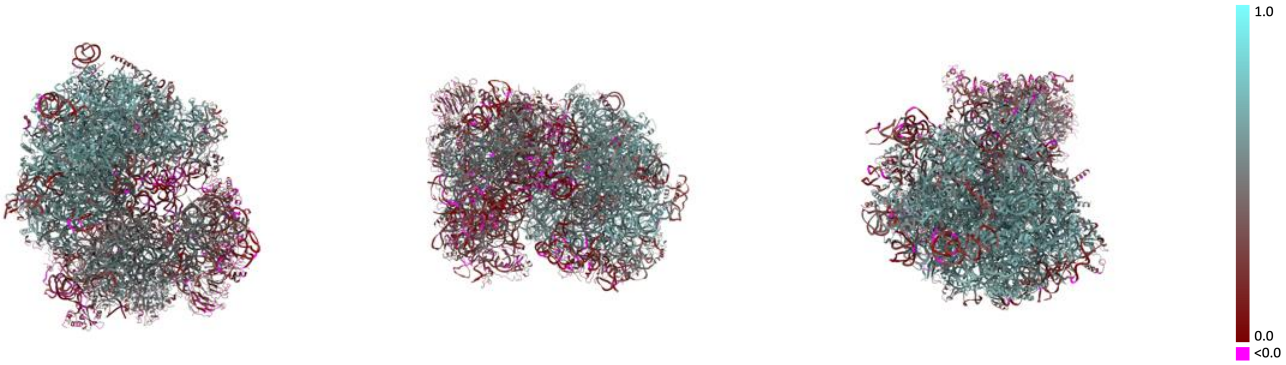
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.27 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.

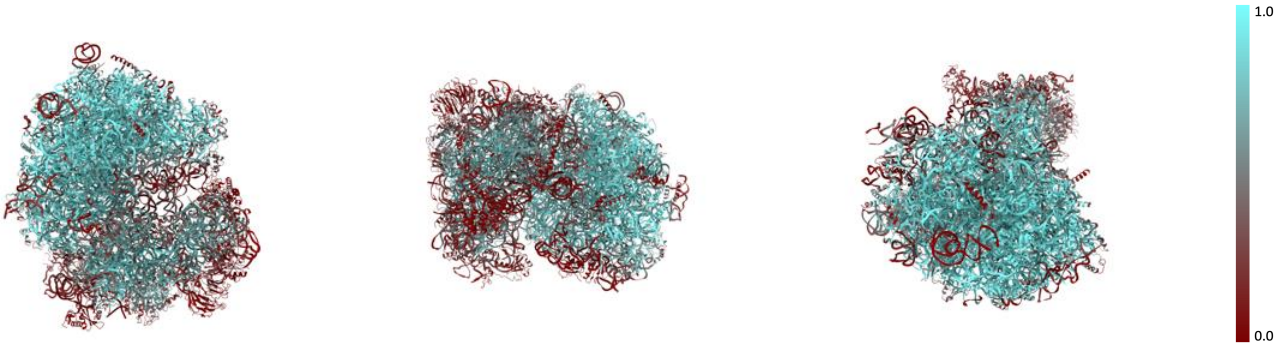
9.2 Q-score mapped to coordinate model (i)



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.

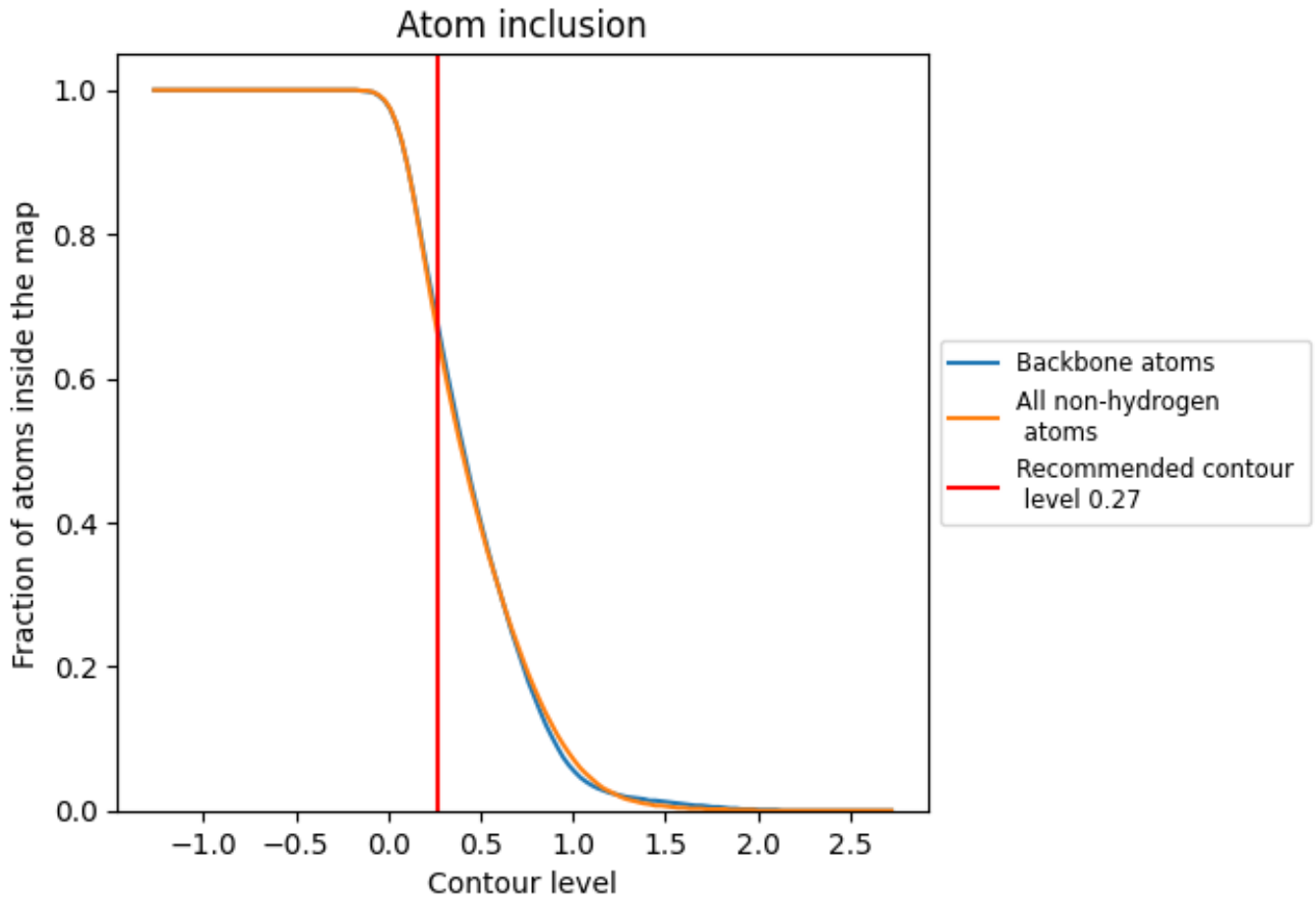
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.27).

9.4 Atom inclusion (i)



At the recommended contour level, 67% of all backbone atoms, 66% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.27) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6560	0.4730
AA	0.5230	0.3480
AD	0.5350	0.4730
AE	0.4340	0.4290
AF	0.6760	0.5340
AG	0.2910	0.3540
AH	0.4900	0.4410
AI	0.4620	0.4050
AJ	0.0630	0.1850
AK	0.1960	0.2750
AL	0.3600	0.3340
AM	0.3600	0.3370
AN	0.0850	0.1680
AO	0.5520	0.4440
AP	0.0020	0.1390
AQ	0.5880	0.4850
AR	0.5370	0.4580
AS	0.2010	0.2310
AT	0.4620	0.3620
AU	0.3630	0.3510
AV	0.1510	0.2150
AW	0.4610	0.3840
Aa	0.3570	0.3620
Ab	0.5380	0.4800
Ac	0.7930	0.5670
Ad	0.2370	0.3260
Ae	0.2100	0.3000
Af	0.2230	0.3030
Ag	0.6880	0.5230
Ah	0.3150	0.3760
Ai	0.3370	0.2930
Aj	0.4460	0.3810
Ak	0.0220	0.1540
Am	0.1060	0.2800
B0	0.8550	0.6190

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Chain	Atom inclusion	Q-score
B1	0.8480	0.6040
B2	0.7900	0.5310
B3	0.8000	0.5050
B4	0.8730	0.5780
BN	0.9410	0.6560
BO	0.9040	0.6390
BP	0.9230	0.6530
BQ	0.6850	0.5290
BR	0.6610	0.5010
BS	0.8470	0.6180
BT	0.7280	0.5570
BU	0.0540	0.2100
BV	0.4470	0.4290
BW	0.4130	0.3620
BX	0.8090	0.6050
BY	0.7600	0.5640
BZ	0.9740	0.6720
Ba	0.9030	0.6380
Bb	0.9100	0.6510
Bc	0.9340	0.6550
Bd	0.8670	0.6190
Be	0.8310	0.6060
Bf	0.7570	0.5670
Bg	0.5120	0.4480
Bh	0.8640	0.6230
Bi	0.6170	0.5400
Bj	0.8700	0.6220
Bk	0.8740	0.6350
Bl	0.7340	0.5340
Bm	0.9440	0.6670
Bn	0.8890	0.6290
Bo	0.6960	0.5020
Bp	0.8610	0.6230
Bq	0.9340	0.6610
Br	0.9360	0.6540
Bs	0.8980	0.6460
Bt	0.8380	0.6200
Bu	0.8520	0.6140
Bv	0.9710	0.6740
Bw	0.5790	0.4740
Bx	0.7370	0.5270
By	0.7680	0.5840

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Chain	Atom inclusion	Q-score
S3	0.4410	0.2470
Sm	0.3770	0.1570
Sn	0.1330	0.0590