wwPDB EM Validation Summary Report (i)

Mar 23, 2026 – 05:28 AM UTC

PDB ID	:	9BUT / pdb_00009but
EMDB ID	:	EMD-44919
Title	:	Single particle CryoEM structure of the Pf80S ribosome in the rotated-2 PRE state (rt state with P and E-site tRNA)
Authors	:	Anton, L.; Haile, M.; Ho, C.M.
Deposited on	:	2024-05-17
Resolution	:	2.80 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:

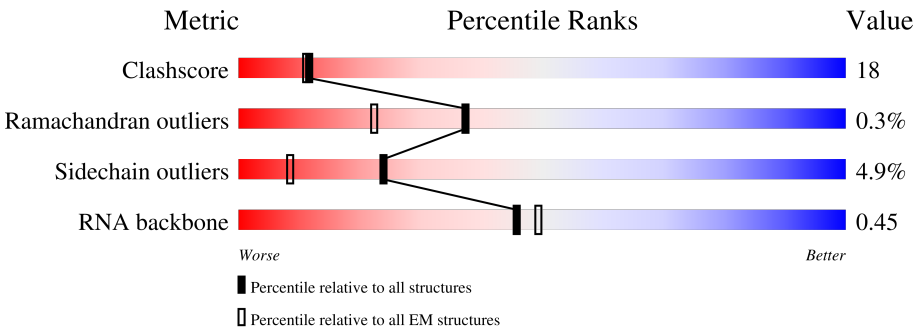
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

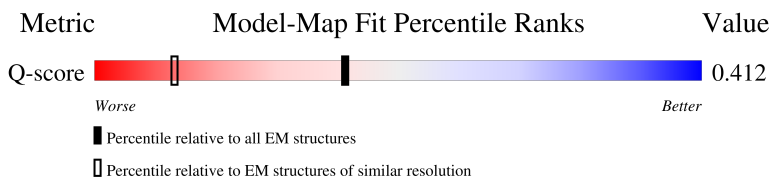
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.80 Å.

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





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	S7	76	29% 54% 17%
1	S9	76	9% 41% 45% 14%
2	AA	3788	32% 41% 11% 16%

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Mol	Chain	Length	Quality of chain
3	AC	159	36% 47% 13% 5%
4	AB	119	29% 48% 22%
5	AL	215	62% 36%
6	A1	146	16% 51% 44%
7	A2	127	54% 28% 17%
8	A4	67	70% 28%
9	A6	108	19% 41% 43% 7% 9%
10	A7	120	41% 34% 5% 20%
11	AN	165	48% 40% 11%
12	A8	131	62% 31% 5%
13	A9	140	44% 28% 26%
14	Aa	150	9% 35% 34% 29%
15	Ab	112	52% 31% 15%
16	Ad	87	7% 38% 41% 17%
17	Ae	51	49% 33% 16%
18	Af	128	8% 15% 23% 60%
19	AP	205	58% 39%
20	Ah	96	49% 36% 11%
21	Ai	104	58% 33% 9%
22	AI	221	55% 35% 6%
23	AJ	283	8% 48% 28% 22%
24	Ac	92	60% 37%
25	AK	202	56% 42%
26	AM	139	9% 53% 39% 5%
27	AS	187	70% 27%

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Mol	Chain	Length	Quality of chain
28	AO	148	66% 32%
29	AQ	219	5% 50% 36% 14%
30	AR	294	11% 43% 42% 14%
31	AW	173	66% 31%
32	AY	190	32% 21% 47%
33	AT	182	25% 58% 40%
34	AZ	126	51% 39% 6%
35	A3	124	5% 47% 45%
36	A5	257	50% 35% 13%
37	AD	260	65% 28% 5%
38	AE	386	8% 56% 39%
39	AF	411	64% 29% 5%
40	AG	173	6% 35% 34% 28%
41	AU	184	6% 55% 40%
42	AH	190	14% 47% 46%
43	AV	161	54% 40%
44	Ag	39	13% 41% 49% 5% 5%
45	AX	139	14% 36% 30% 30%
46	A0	162	14% 20% 17% 62%
47	S1	133	49% 41% 10%
48	S2	105	9% 28% 10% 61%
49	S3	107	42% 42% 5% 11%
50	S4	82	5% 60% 30% 7%
51	S5	67	6% 45% 42% 12%
52	S6	58	40% 31% 26%

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Mol	Chain	Length	Quality of chain
53	SA	2092	25% 42% 10% 23%
54	SB	262	40% 38% 20%
55	SC	263	39% 33% 26%
56	SD	221	48% 22% 29%
57	SE	189	50% 47%
58	SF	261	58% 39%
59	SG	272	50% 30% 18%
60	SH	306	39% 27% 33%
61	SI	195	50% 41% 8%
62	SJ	194	9% 52% 42%
63	SK	130	49% 44% 6%
64	SL	218	50% 28% 22%
65	SM	144	55% 39%
66	SN	118	49% 32% 17%
67	SO	137	36% 22% 42%
68	SP	151	44% 39% 16%
69	SQ	145	59% 40%
70	SR	141	6% 62% 7% 30%
71	SS	156	41% 38% 18%
72	ST	54	46% 35% 7% 11%
73	SU	151	44% 52%
74	SV	161	48% 40% 9%
75	SW	137	29% 39% 31%
76	SX	145	40% 26% 34%
77	SY	170	56% 34% 9%

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Mol	Chain	Length	Quality of chain
78	SZ	82	48% 35% 5% 12%
79	mR	9	22% 67% 11%

2 Entry composition (i)

There are 79 unique types of molecules in this entry. The entry contains 194842 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 tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	S7	76	1620	723	295	527	75	0	0
1	S9	76	1620	723	295	527	75	0	0

- Molecule 2 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	AA	3193	67884	30446	12053	22224	3161	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	AC	151	3215	1444	589	1034	148	0	0

- Molecule 4 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	AB	118	2517	1126	457	817	117	0	0

- Molecule 5 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AL	211	1761	1119	349	290	3	0	0

- Molecule 6 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	A1	140	1134	736	204	191	3	0	0

- Molecule 7 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	A2	105	837	534	152	148	3	0	0

- Molecule 8 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	A4	66	555	347	116	90	2	0	0

- Molecule 9 is a protein called 60S ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	A6	98	740	462	132	139	7	0	0

- Molecule 10 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	A7	96	793	508	151	129	5	0	0

- Molecule 11 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	AN	147	1210	787	212	205	6	0	0

- Molecule 12 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	A8	125	1036	660	206	163	7	0	0

- Molecule 13 is a protein called 60S ribosomal protein L35ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	A9	103	844	543	163	135	3	0	0

- Molecule 14 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	Aa	106	858	530	184	138	6	0	0

- Molecule 15 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	Ab	95	756	477	150	129	0	0

- Molecule 16 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	Ad	72	603	395	107	99	2	0	0

- Molecule 17 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	Ae	43	388	243	92	52	1	0	0

- Molecule 18 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	Af	51	413	255	87	66	5	0	0

- Molecule 19 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	AP	204	1697	1075	351	267	4	0	0

- Molecule 20 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	Ah	85	658	417	127	107	7	0	0

- Molecule 21 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	Ai	95	778	490	152	127	9	0	0

- Molecule 22 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	AI	207	1685	1096	298	286	5	0	0

- Molecule 23 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	AJ	222	1813	1174	323	309	7	0	0

- Molecule 24 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Ac	89	709	441	150	113	5	0	0

- Molecule 25 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	AK	201	1659	1064	311	276	8	0	0

- Molecule 26 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	AM	132	996	631	179	178	8	0	0

- Molecule 27 is a protein called 60S ribosomal protein L18-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	AS	186	1503	958	299	241	5	0	0

- Molecule 28 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	AO	147	1172	747	232	189	4	0	0

- Molecule 29 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	AQ	189	1544	984	291	261	8	0	0

- Molecule 30 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	AR	252	2049	1301	385	357	6	0	0

- Molecule 31 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	AW	170	1319	824	266	222	7	0	0

- Molecule 32 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	AY	101	796	502	144	144	6	0	0

- Molecule 33 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	AT	181	1509	952	309	244	4	0	0

- Molecule 34 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	AZ	121	1000	626	206	165	3	0	0

- Molecule 35 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	A3	119	994	635	194	163	2	0	0

- Molecule 36 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	A5	223	1879	1211	357	306	5	0	0

- Molecule 37 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	AD	247	1866	1166	374	317	9	0	0

- Molecule 38 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	AE	380	3061	1948	575	521	17	0	0

- Molecule 39 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	AF	390	3094	1962	594	527	11	0	0

- Molecule 40 is a protein called 60S ribosomal protein L11a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	AG	124	1010	636	197	171	6	0	0

- Molecule 41 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	AU	180	1497	946	289	255	7	0	0

- Molecule 42 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	AH	185	1475	950	264	255	6	0	0

- Molecule 43 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	AV	155	1275	814	241	214	6	0	0

- Molecule 44 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	Ag	37	343	210	86	45	2	0	0

- Molecule 45 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	AX	97	824	548	135	139	2	0	0

- Molecule 46 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	A0	62	521	336	97	87	1	0	0

- Molecule 47 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	S1	120	985	632	189	162	2	0	0

- Molecule 48 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
48	S2	41	320	208	56	56	0	0

- Molecule 49 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	S3	95	781	478	169	128	6	0	0

- Molecule 50 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	S4	76	586	368	102	107	9	0	0

- Molecule 51 is a protein called 40S ribosomal protein S28e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	S5	59	465	290	94	80	1	0	0

- Molecule 52 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
52	S6	43	345	213	75	57	0	0

- Molecule 53 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
53	SA	1608	34208	15346	6106	11170	1586	0	0

- Molecule 54 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	SB	210	1713	1097	301	303	12	0	0

- Molecule 55 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	SC	195	1538	990	266	273	9	0	0

- Molecule 56 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	SD	157	1228	782	225	214	7	0	0

- Molecule 57 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	SE	185	1514	962	290	260	2	0	0

- Molecule 58 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	SF	257	2061	1320	377	356	8	0	0

- Molecule 59 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	SG	224	1757	1132	307	309	9	0	0

- Molecule 60 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	SH	204	1651	1046	316	283	6	0	0

- Molecule 61 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	SI	180	1424	893	263	258	10	0	0

- Molecule 62 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	SJ	188	1528	982	264	278	4	0	0

- Molecule 63 is a protein called 40S ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	SK	129	1037	665	189	178	5	0	0

- Molecule 64 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	SL	171	1383	872	264	243	4	0	0

- Molecule 65 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	SM	138	1098	704	200	193	1	0	0

- Molecule 66 is a protein called 40S ribosomal protein S20e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	SN	98	772	484	135	148	5	0	0

- Molecule 67 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	SO	79	686	450	116	118	2	0	0

- Molecule 68 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	SP	127	954	591	184	176	3	0	0

- Molecule 69 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	SQ	144	1129	712	222	193	2	0	0

- Molecule 70 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	SR	98	746	474	123	145	4	0	0

- Molecule 71 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	SS	128	1046	657	205	180	4	0	0

- Molecule 72 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	ST	48	405	252	85	64	4	0	0

- Molecule 73 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	SU	149	1202	769	220	210	3	0	0

- Molecule 74 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	SV	146	1206	772	227	200	7	0	0

- Molecule 75 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	SW	95	785	498	149	135	3	0	0

- Molecule 76 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	SX	96	776	497	137	138	4	0	0

- Molecule 77 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	SY	154	1266	811	239	214	2	0	0

- Molecule 78 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
78	SZ	72	557	346	102	105	4	0	0

- Molecule 79 is a RNA chain called mRNA.

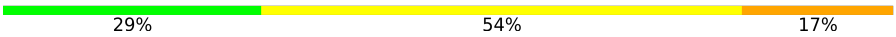
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
79	mR	9	180	81	18	72	9	0	0

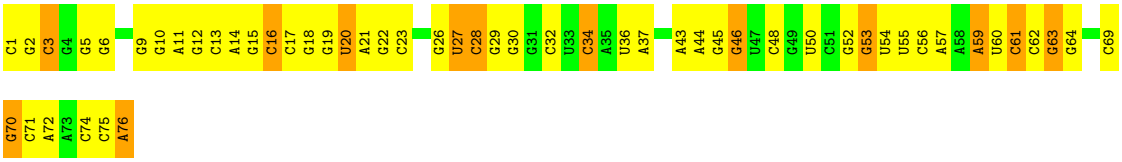
3 Residue-property plots (i)

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

- Molecule 1: tRNA

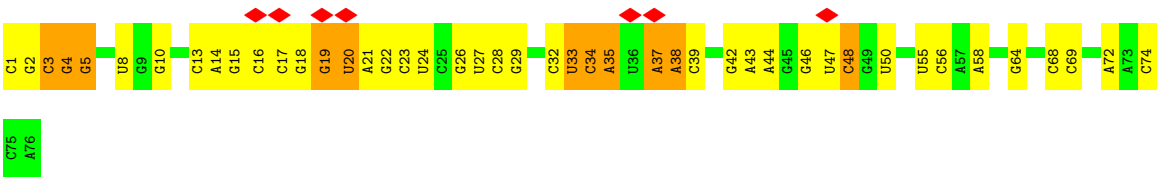
Chain S7:





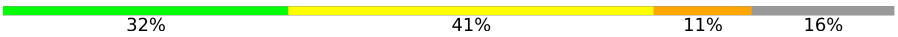
- Molecule 1: tRNA

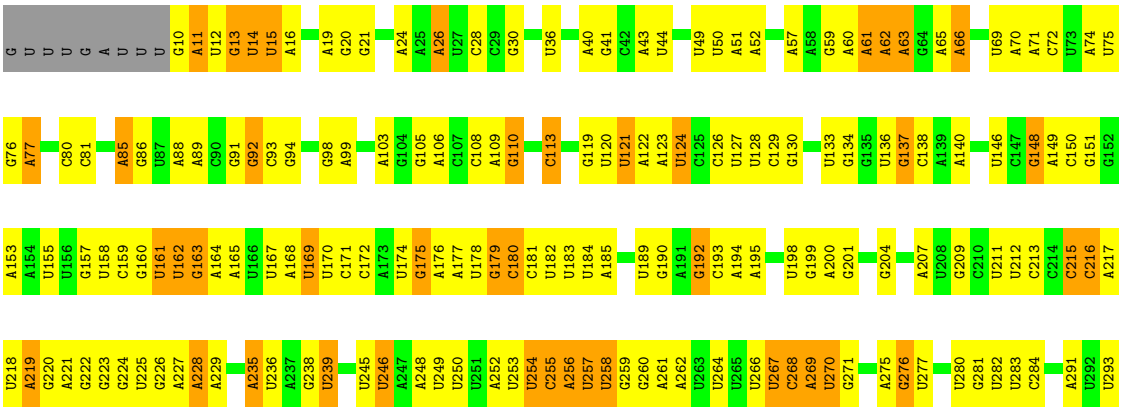
Chain S9:

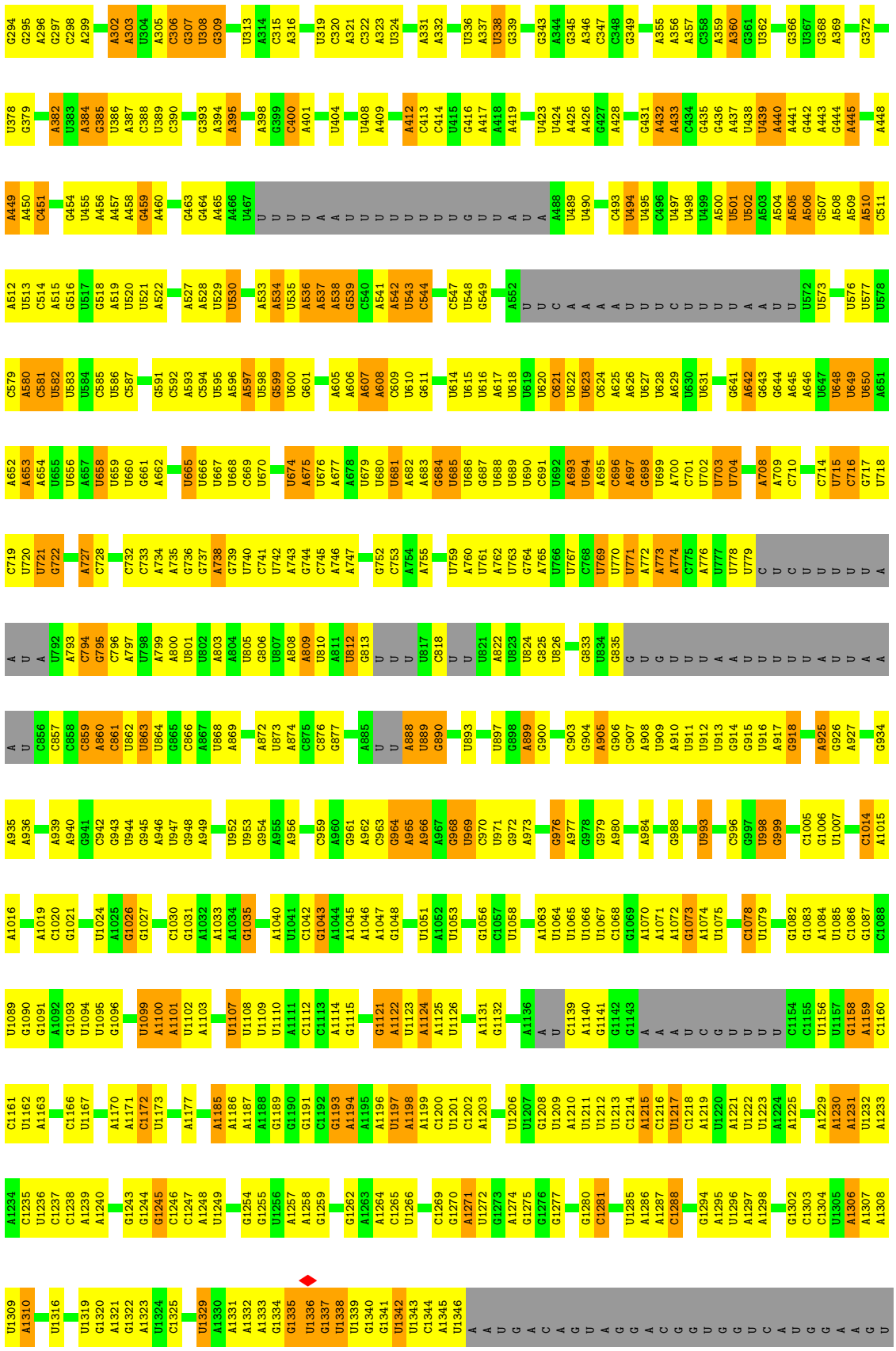


- Molecule 2: 28S ribosomal RNA

Chain AA:



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A1234 C1235 U1236 C1237 C1238 A1239 A1240 G1243 G1244 G1245 C1246 C1247 A1248 U1249 G1254 G1255 U1256 A1257 A1258 G1259 G1262 A1263 A1264 C1265 U1266 C1269 G1270 A1271 U1272 G1273 A1274 G1275 G1276 G1277 G1280 C1281 U1285 A1286 A1287 C1288 G1294 A1295 U1296 A1297 A1298 G1302 C1303 C1304 U1305 A1306 A1307 A1308
C1161 U1162 A1163 C1166 U1167 A1170 A1171 C1172 U1173 A1177 A1185 A1186 A1187 A1188 G1189 G1190 G1191 C1192 G1193 A1194 A1195 A1196 U1197 A1198 A1199 C1200 U1201 C1202 A1203 U1206 U1207 G1208 U1209 A1210 U1211 U1212 U1213 C1214 A1215 C1216 U1217 C1218 A1219 U1220 A1221 U1222 U1223 A1224 A1225 A1229 A1230 A1231 U1232 A1233
U1089 G1090 G1091 A1092 G1093 U1094 U1095 G1096 U1099 A1100 A1101 U1102 A1103 U1107 U1108 U1109 U1110 A1111 C1112 C1113 A1114 G1115 G1121 A1122 U1123 A1124 A1125 U1126 A1131 G1132 A1136 A U C1139 A1140 G1141 G1142 G1143 A A A U U C G G U U G G U U C A A A A G G A A C G G A A G G U U U C A U G A A A G U
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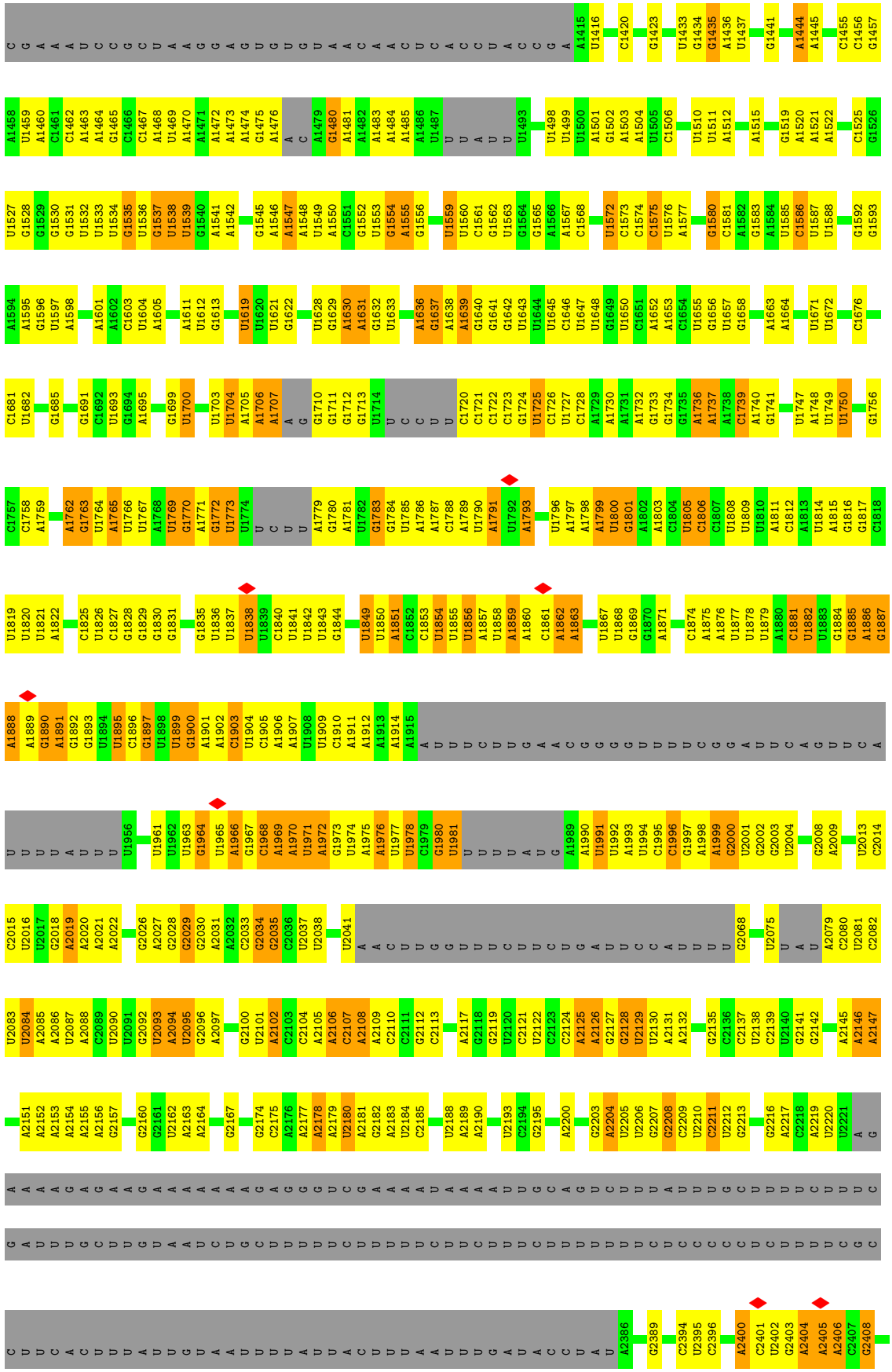
A512 U513 C514 A515 G516 U517 G518 A519 U520 U521 A522 A527 A528 U529 U530 A533 A534 U535 A536 A537 A538 G539 C540 A541 A542 U543 C544 C547 U548 G549 A552 U U U C A A A U U U U C U U U U U A A U U U U572 U573 U576 U577 U578
C579 A580 C581 U582 U583 U584 C585 U586 C587 G591 C592 A593 C594 U595 A596 A597 U598 G599 U600 G601 A605 A606 A607 A608 C609 U610 G611 U614 U615 U616 A617 U618 U619 U620 C621 U622 U623 C624 A625 A626 U627 U628 A629 U630 U631 G641 A642 G643 G644 A645 A646 U647 U648 U649 U650 A651
A652 A653 A654 U655 U656 A657 U658 U659 U660 G661 A662 U665 U666 U667 U668 C669 U670 U674 A675 U676 A677 A678 U679 U680 U681 A682 A683 G684 U685 U686 U687 U688 U689 U690 C691 U692 A693 U694 A695 C696 A697 G698 U699 A700 C701 U702 U703 U704 A708 A709 C710 C714 U715 C716 G717 U718
C719 U720 U721 G722 A727 C728 C732 C733 A734 A735 G736 G737 A738 G739 U740 C741 U742 A743 G744 C745 A746 A747 G752 C753 A754 A755 U759 A760 U761 A762 U763 G764 A765 U766 U767 C768 U769 U770 U771 A772 A773 A774 C775 A776 U777 U778 U779 C U C U U U U A
G294 G295 A296 G297 C298 A299 A302 A303 U304 A305 C306 G307 U308 G309 U313 A314 C315 A316 U319 C320 A321 C322 A323 U324 A331 A332 U336 A337 U338 G339 G343 A344 G345 A346 C347 C348 G349 A355 A356 A357 C358 A359 A360 G361 U362 G366 U367 G368 A369 G372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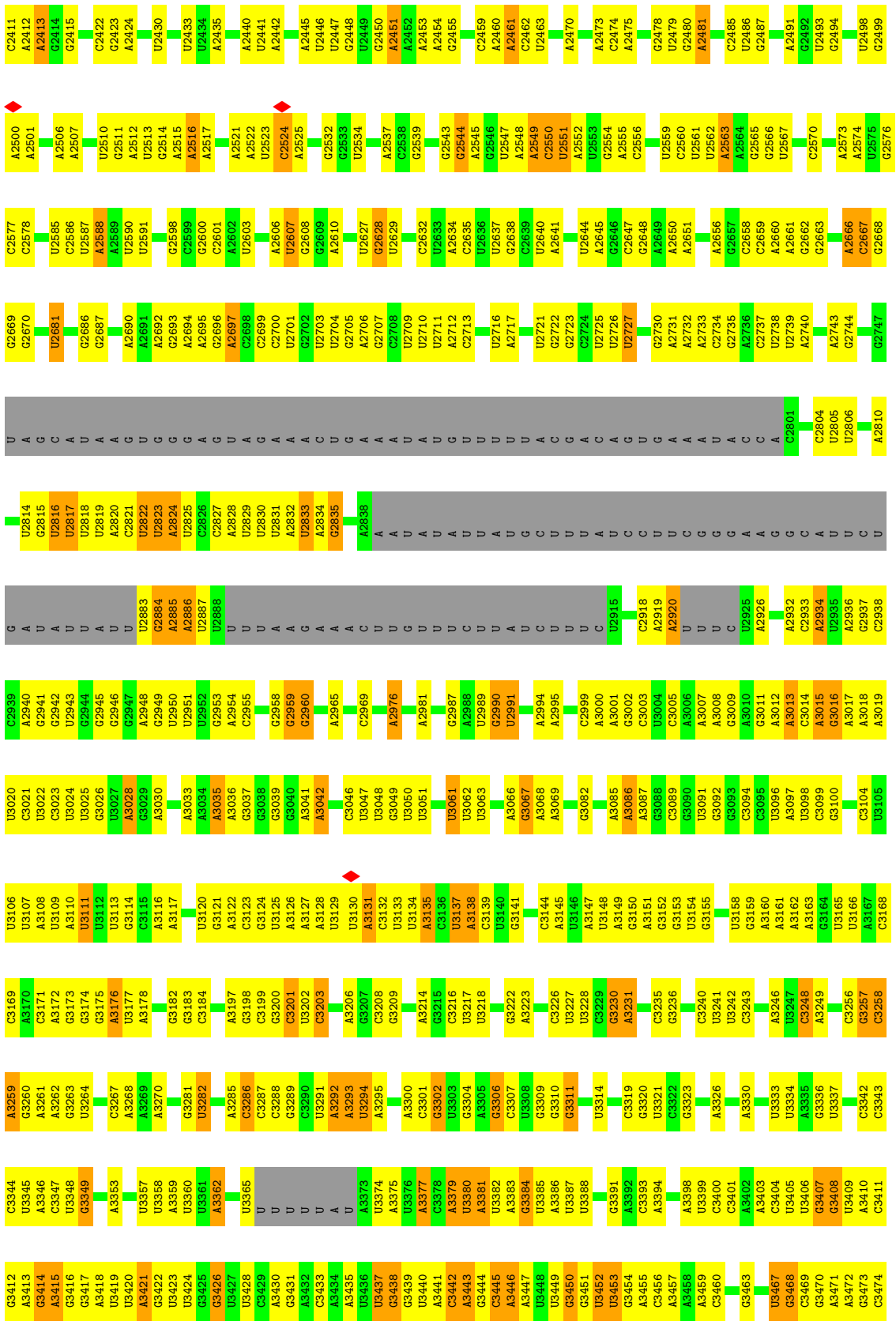
G A U U U U G C U U G A U A U G U U U C U U U U C U U U C U U U C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A2500 A2501 A2506 A2507 U2510 G2511 A2512 U2513 G2514 A2515 A2516 A2517 A2521 A2522 U2523 C2524 A2525 G2532 G2533 U2534 A2537 C2538 G2539 G2543 G2544 A2545 G2546 U2547 A2548 A2549 C2550 U2551 A2552 U2553 G2554 A2555 C2556 U2559 C2560 U2561 U2562 A2563 A2564 G2565 G2566 U2567 C2570 A2573 A2574 U2575 G2576
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U A G C A U A A G U G G G A G U A G A A A C U U G A A A U A A U G U U U U U U A C C G A C C A C2801 C2804 U2805 U2806 A2810
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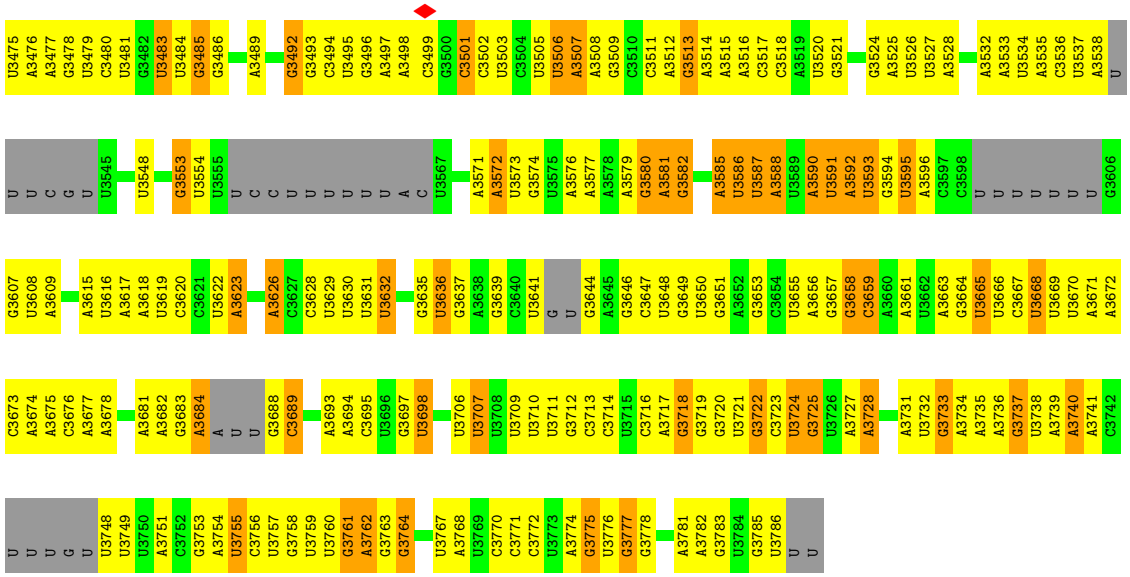
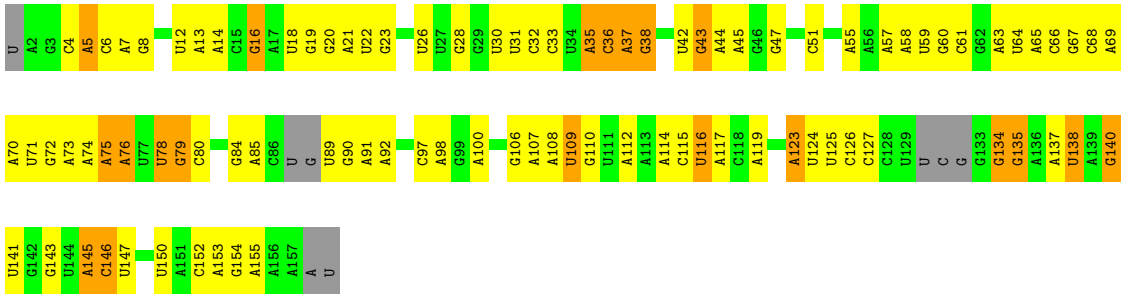


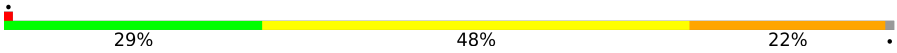
- Molecule 3: 5.8S ribosomal RNA

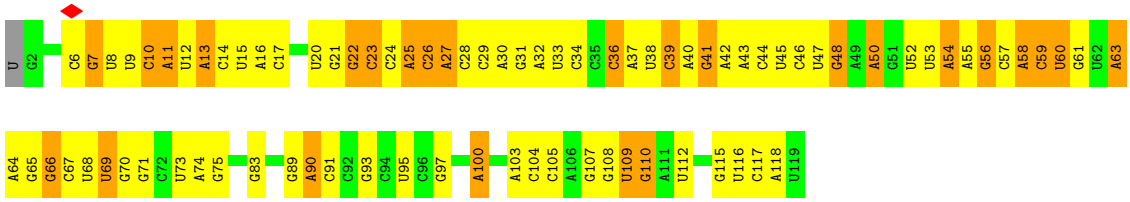
Chain AC:



- Molecule 4: 5S ribosomal RNA

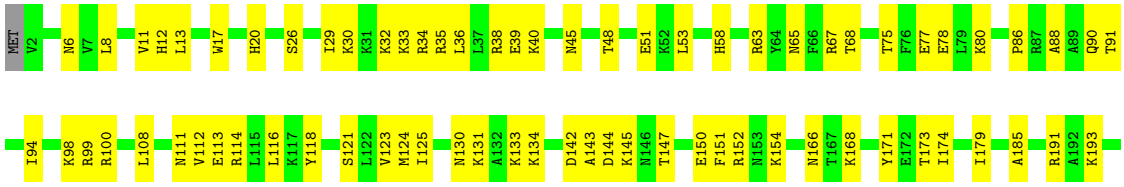
Chain AB:

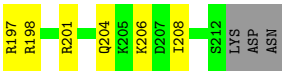




- Molecule 5: 60S ribosomal protein L13

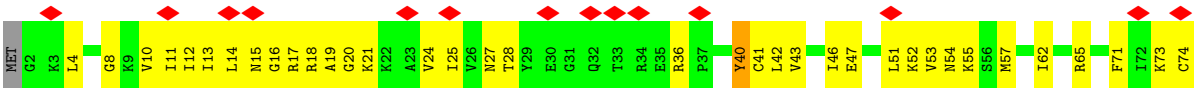
Chain AL:

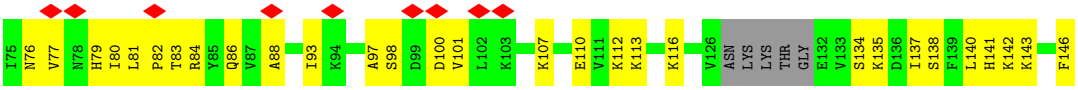




• Molecule 6: 60S ribosomal protein L27

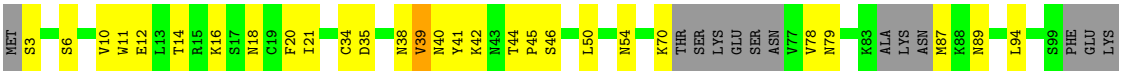
Chain A1:





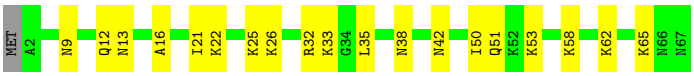
• Molecule 7: 60S ribosomal protein L28

Chain A2:



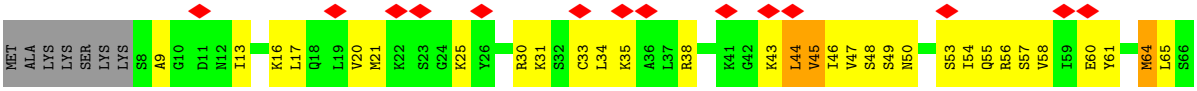
• Molecule 8: 60S ribosomal protein L29

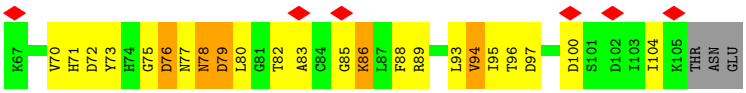
Chain A4:



• Molecule 9: 60S ribosomal protein L30e

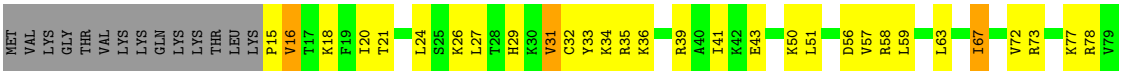
Chain A6:

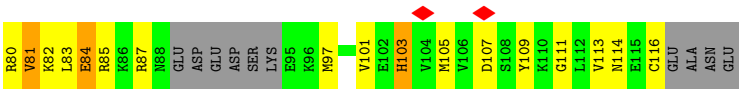




• Molecule 10: 60S ribosomal protein L31

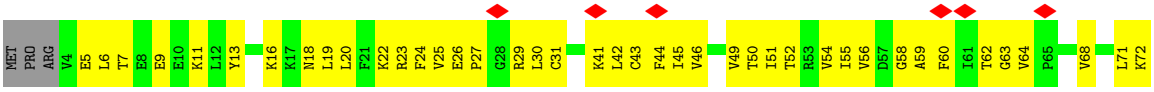
Chain A7:

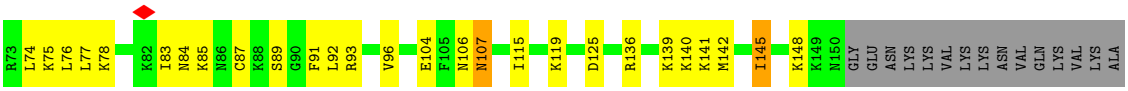




- Molecule 11: 60S ribosomal protein L14

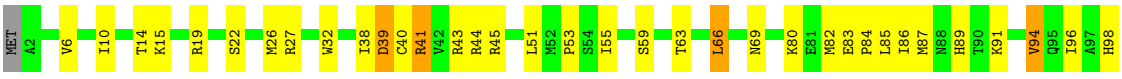
Chain AN:

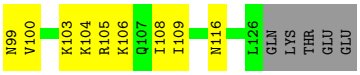




- Molecule 12: 60S ribosomal protein L32

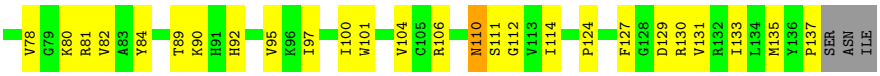
Chain A8:





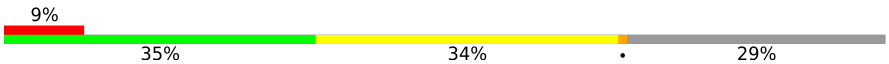
- Molecule 13: 60S ribosomal protein L35ae

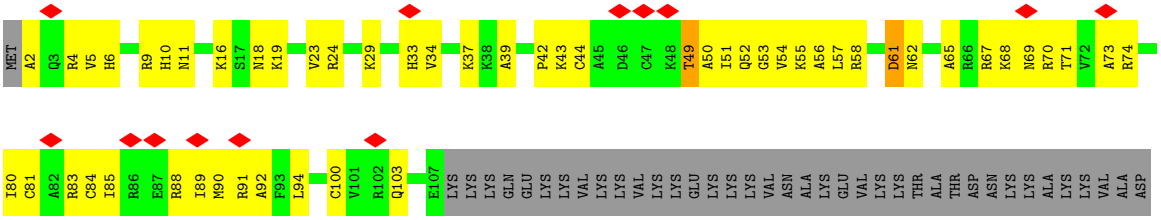
Chain A9:

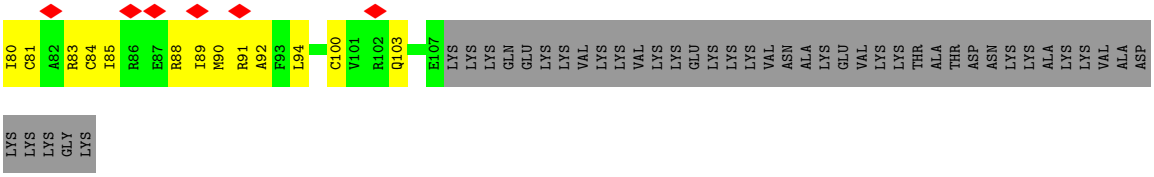


- Molecule 14: 60S ribosomal protein L34

Chain Aa:

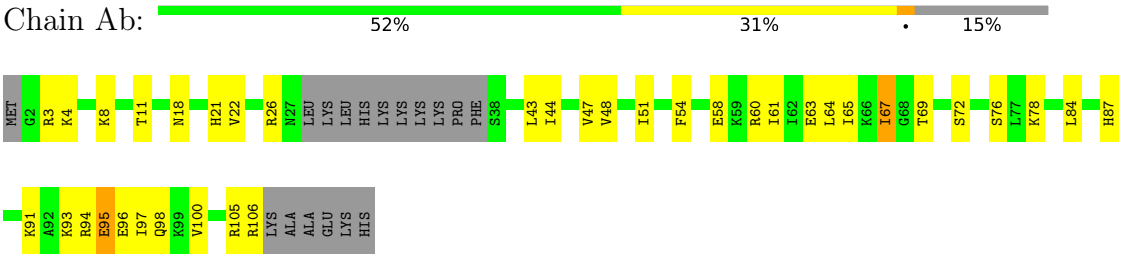






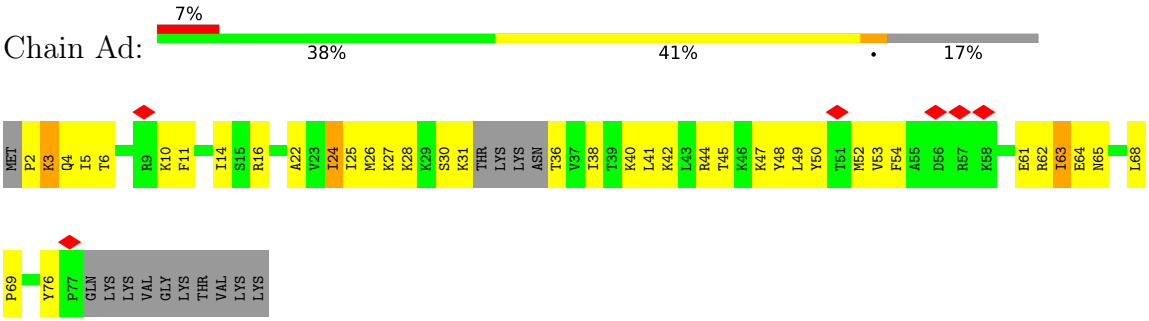
- Molecule 15: 60S ribosomal protein L36

Chain Ab:



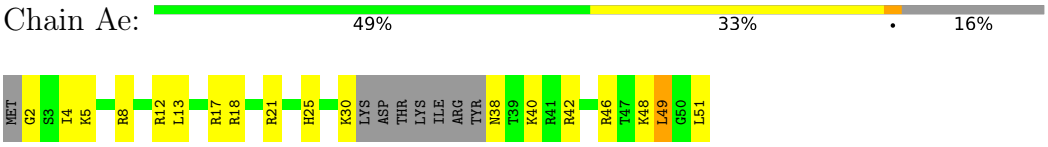
- Molecule 16: 60S ribosomal protein L38

Chain Ad:



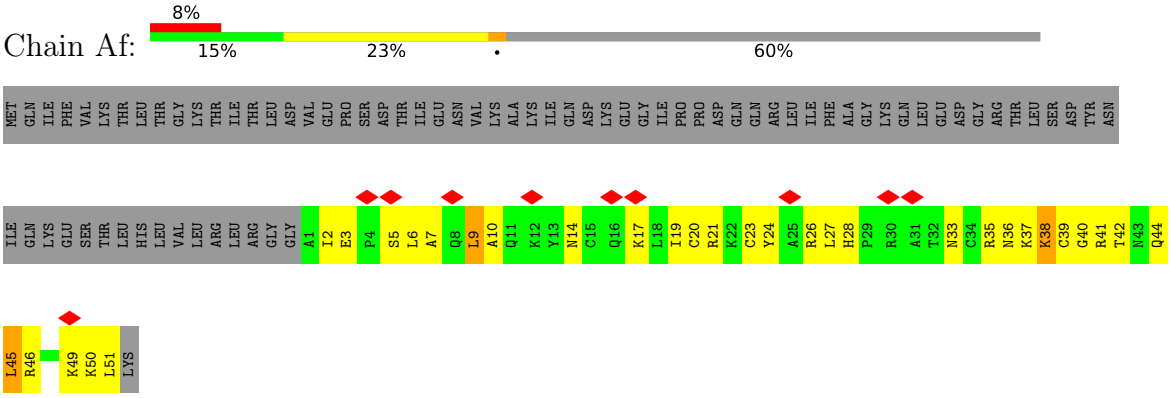
- Molecule 17: 60S ribosomal protein L39

Chain Ae:



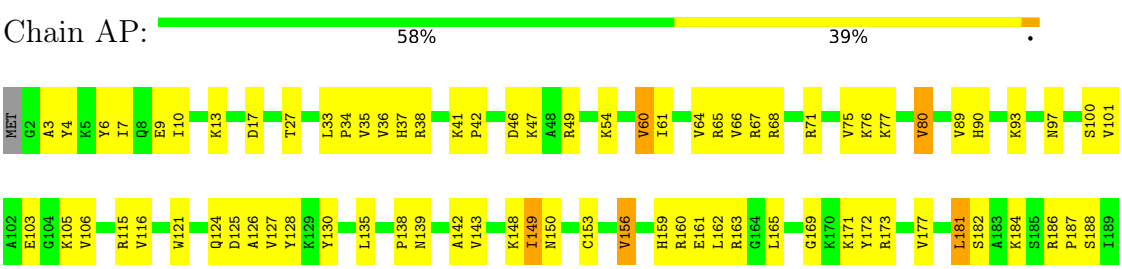
- Molecule 18: Ubiquitin-60S ribosomal protein L40

Chain Af:



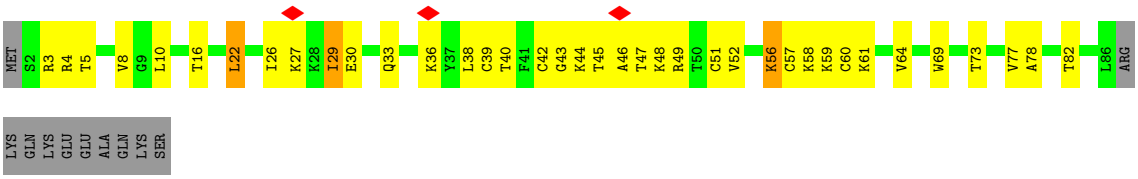
- Molecule 19: Ribosomal protein L15

Chain AP:



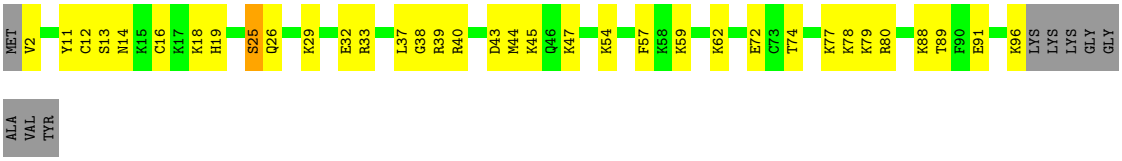
• Molecule 20: Large ribosomal subunit protein eL43

Chain Ah:



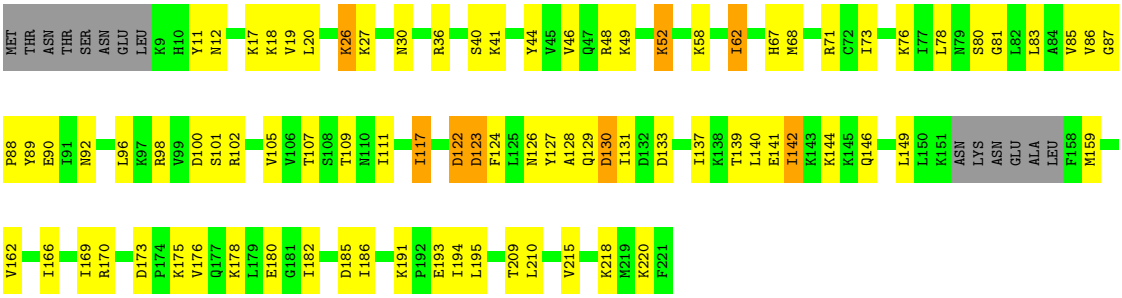
• Molecule 21: Large ribosomal subunit protein eL42

Chain Ai:



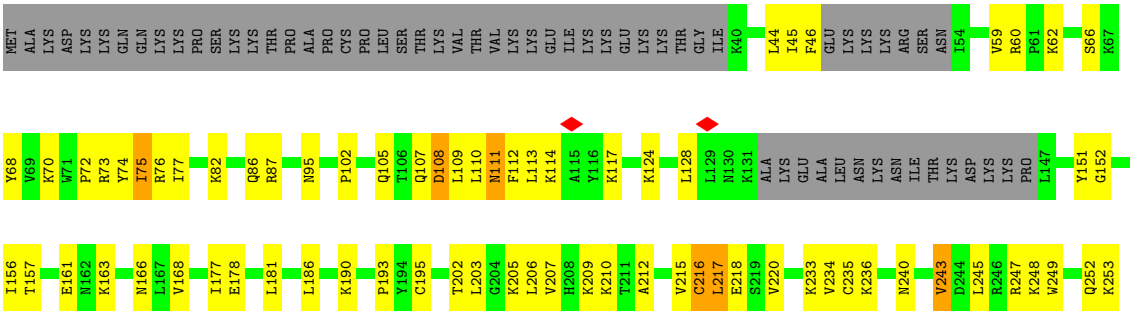
• Molecule 22: 60S ribosomal protein L6

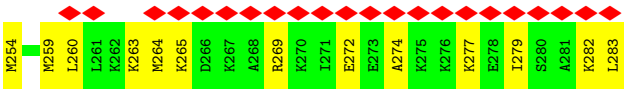
Chain AI:



• Molecule 23: 60S ribosomal protein L7a

Chain AJ:



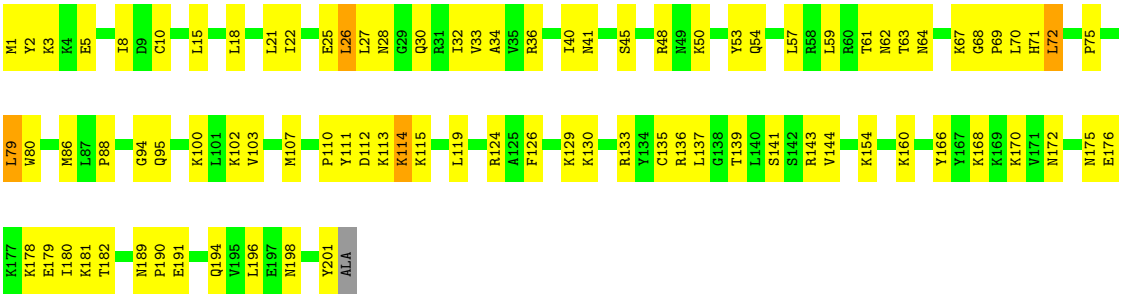


• Molecule 24: Ribosomal protein L37

Chain Ac:

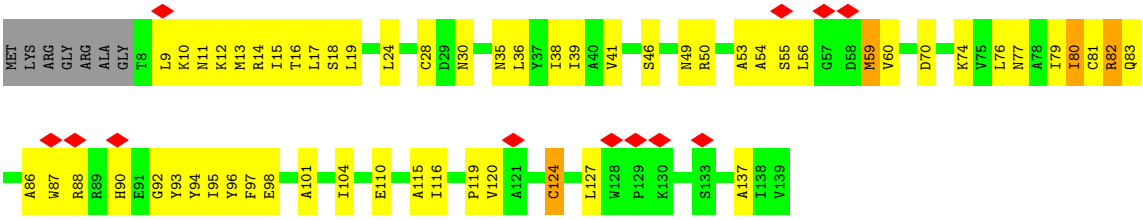
• Molecule 25: 60S ribosomal protein L13

Chain AK:



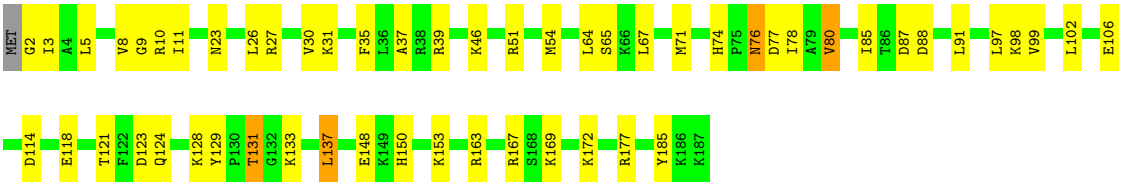
• Molecule 26: 60S ribosomal protein L23

Chain AM:



• Molecule 27: 60S ribosomal protein L18-2

Chain AS:

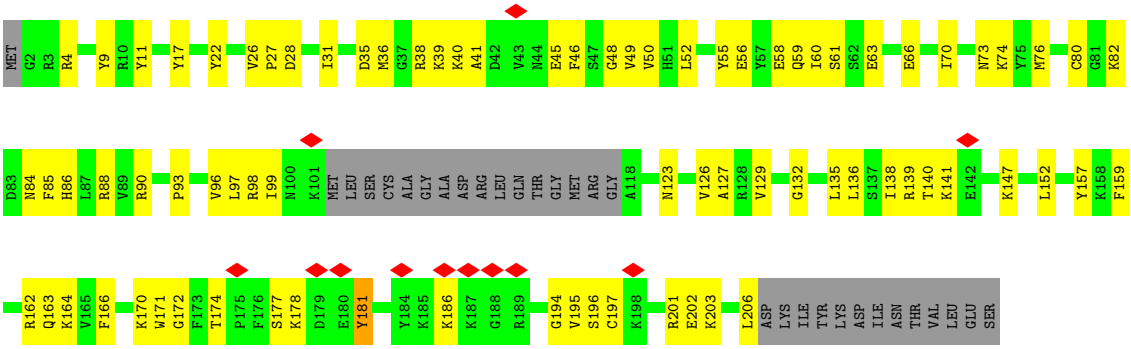


• Molecule 28: 60S ribosomal protein L27a

Chain AO:

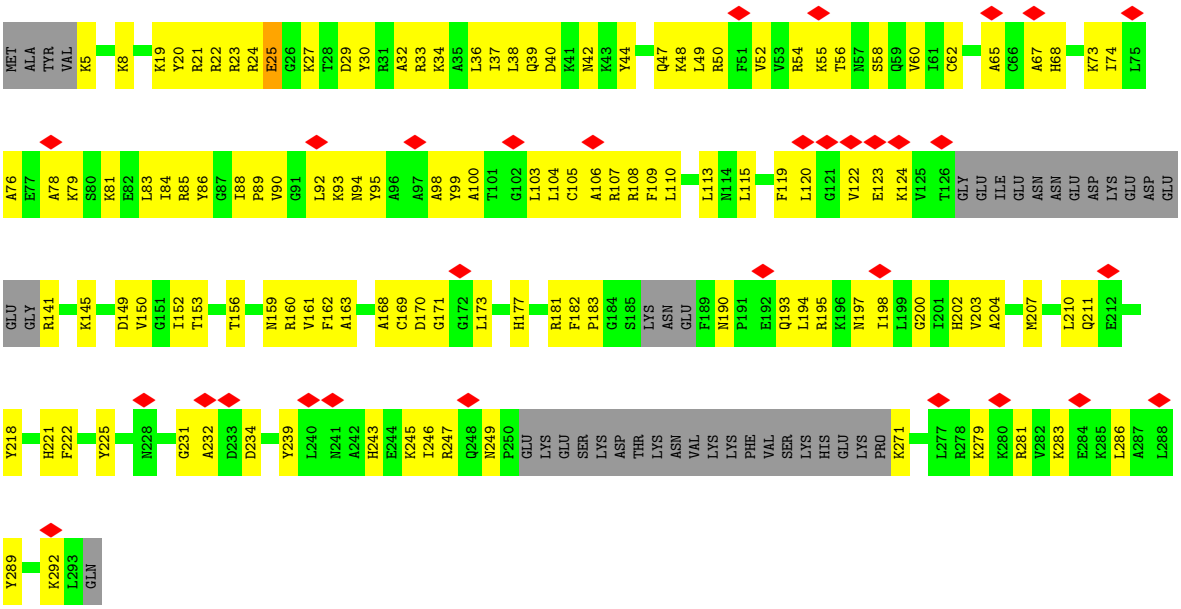
• Molecule 29: 60S ribosomal protein L10

Chain AQ:



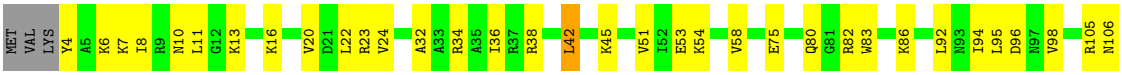
• Molecule 30: 60S ribosomal protein L5

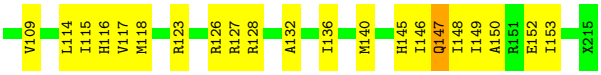
Chain AR:



• Molecule 31: 60S ribosomal protein L17

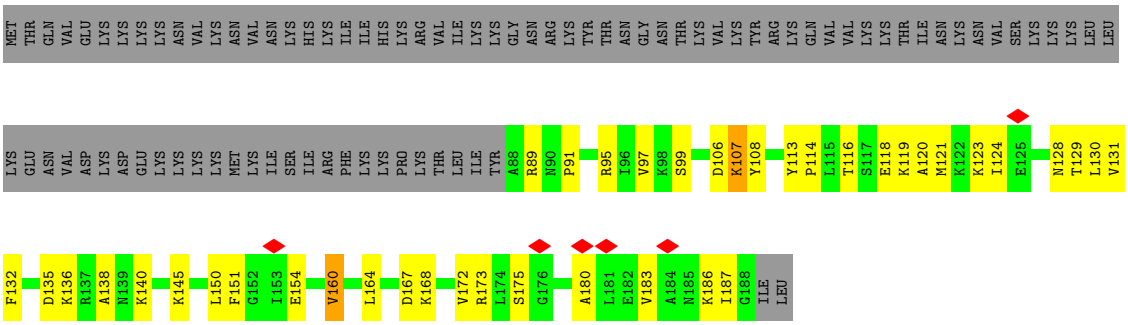
Chain AW:





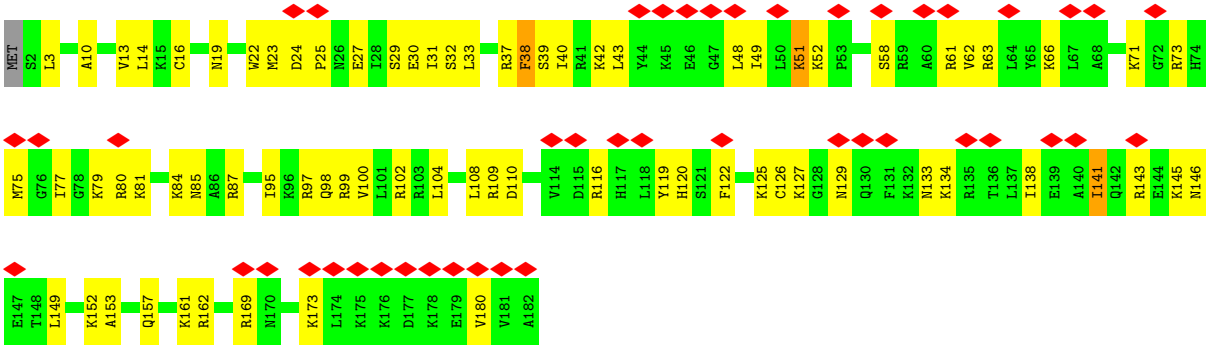
- Molecule 32: 60S ribosomal protein L23

Chain AY:



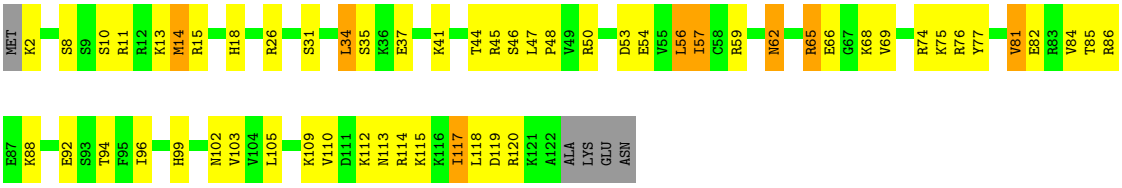
- Molecule 33: 60S ribosomal protein L19

Chain AT:



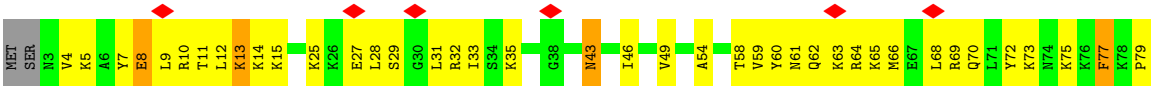
- Molecule 34: 60S ribosomal protein L26

Chain AZ:



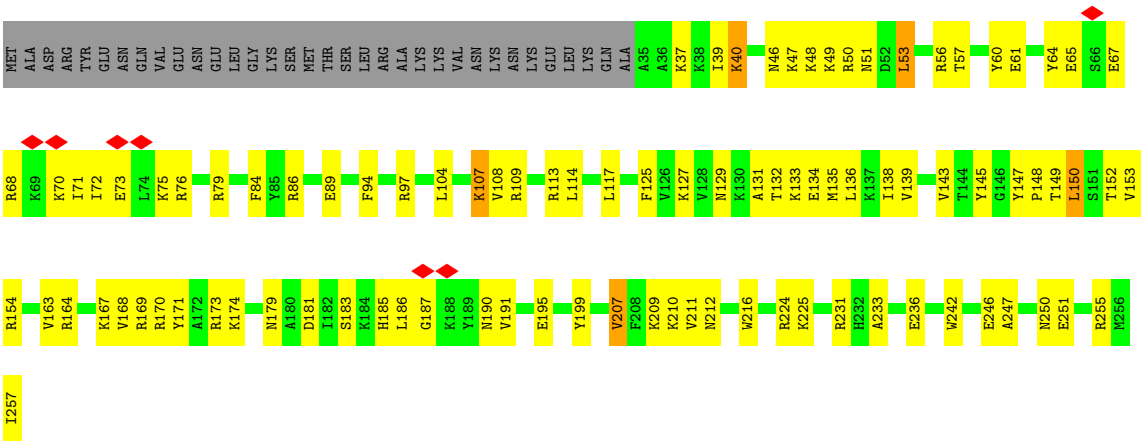
- Molecule 35: 60S ribosomal protein L35

Chain A3:



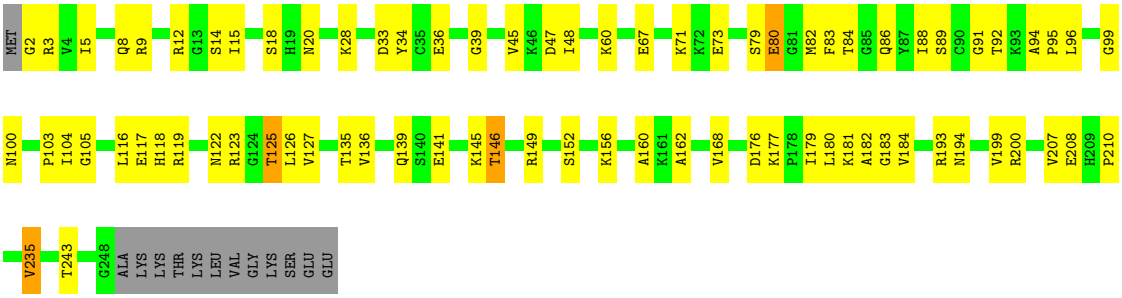
• Molecule 36: 60S ribosomal protein L7

Chain A5:



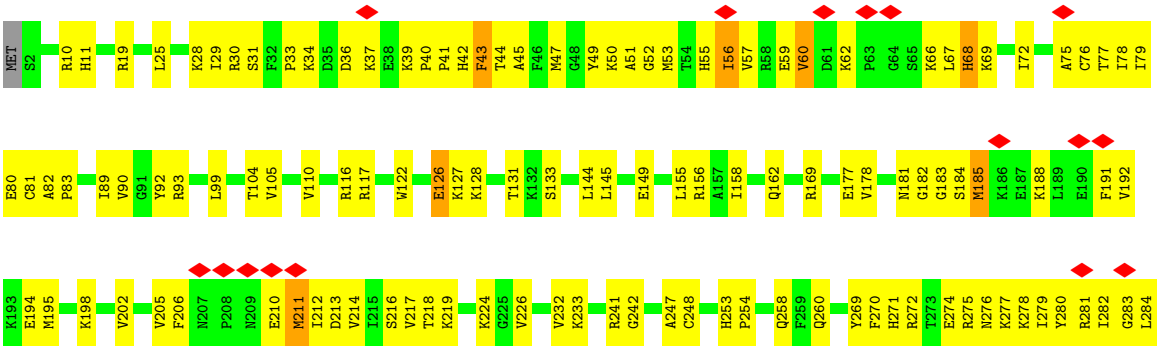
• Molecule 37: 60S ribosomal protein L2

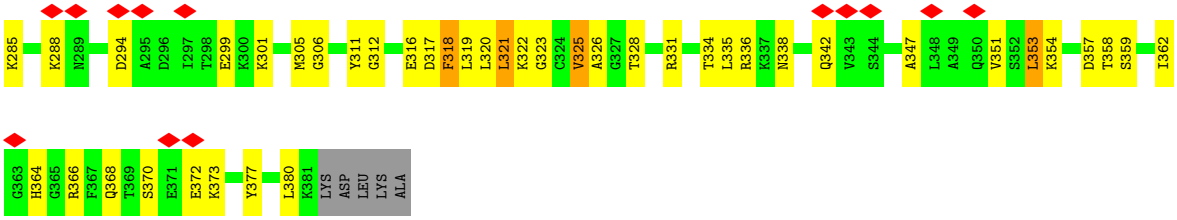
Chain AD:



• Molecule 38: 60S ribosomal protein L3

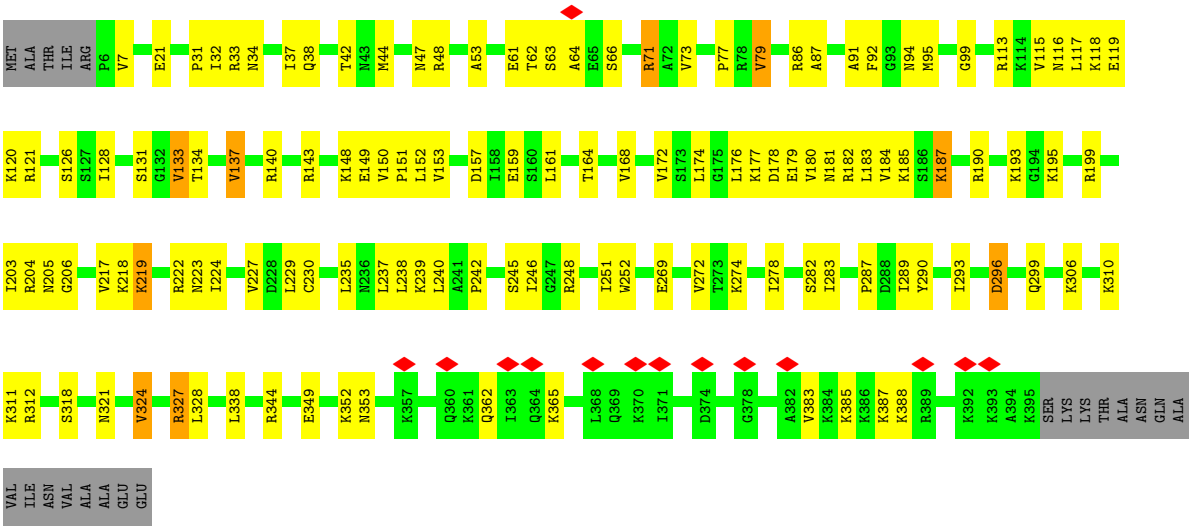
Chain AE:





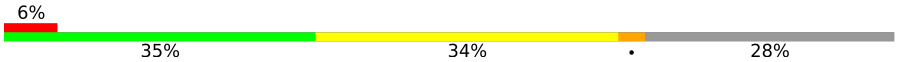
• Molecule 39: 60S ribosomal protein L4

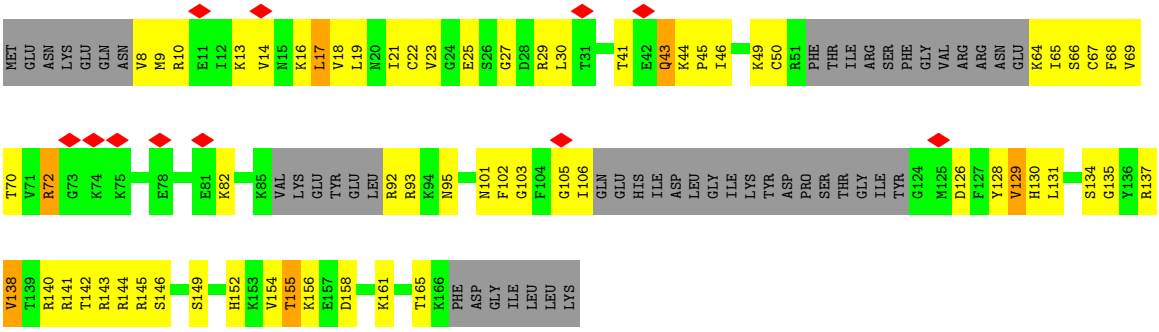
Chain AF:



• Molecule 40: 60S ribosomal protein L11a

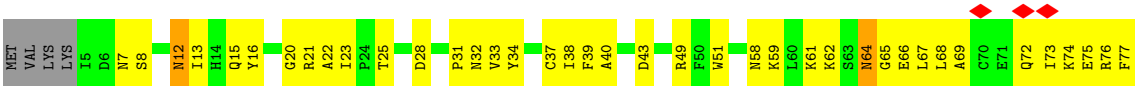
Chain AG:

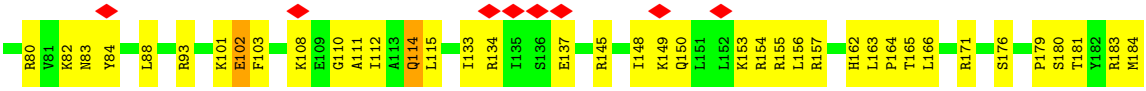




• Molecule 41: 60S ribosomal protein L18a

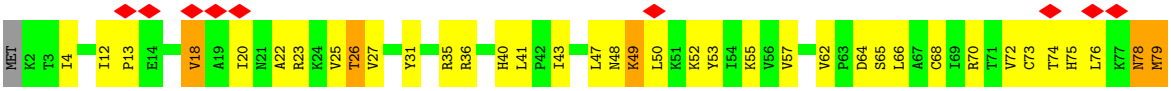
Chain AU:

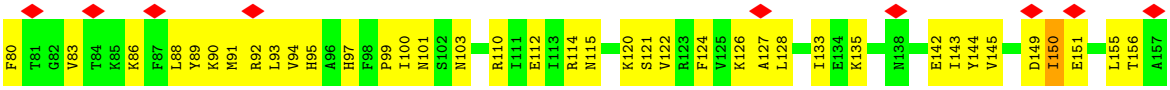




- Molecule 42: 60S ribosomal protein L6

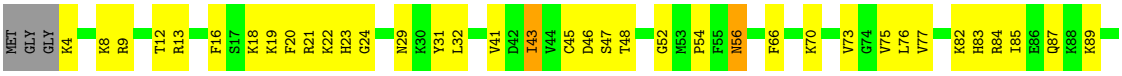
Chain AH:

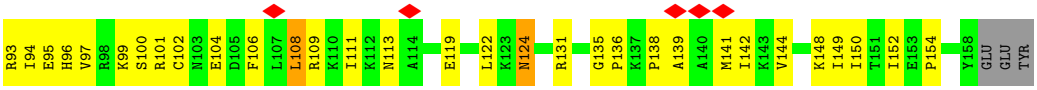




- Molecule 43: 60S ribosomal protein L21

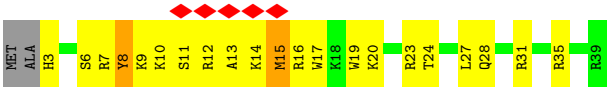
Chain AV:





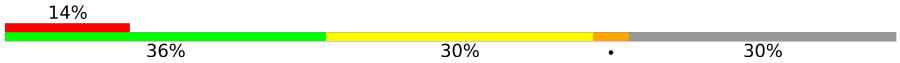
- Molecule 44: 60S ribosomal protein L41

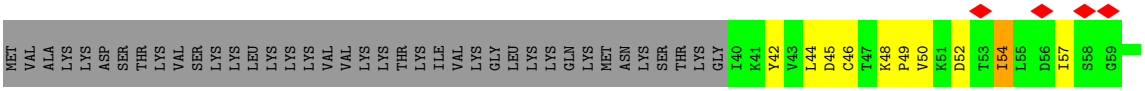
Chain Ag:

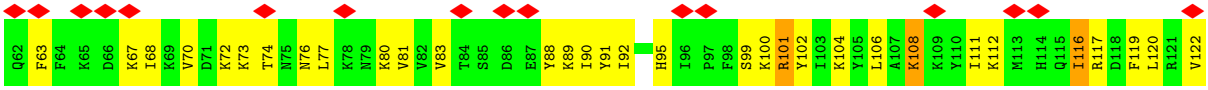


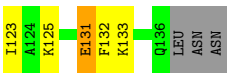
- Molecule 45: 60S ribosomal protein L22

Chain AX:



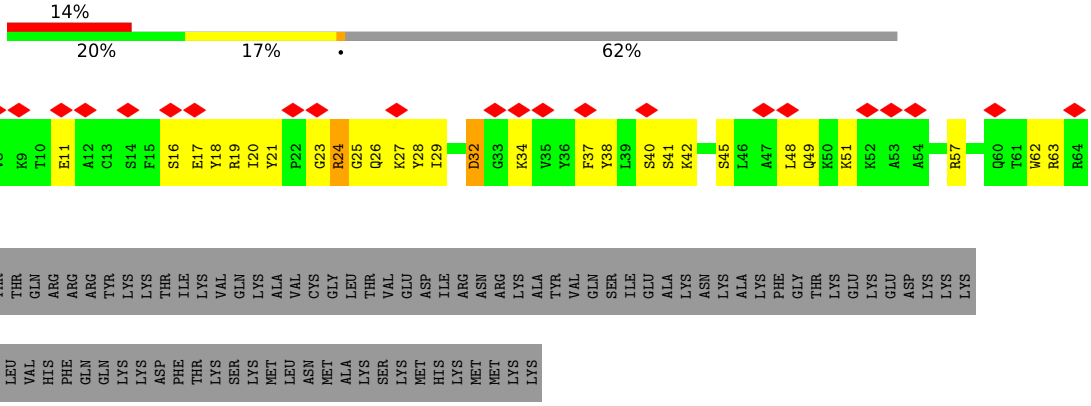






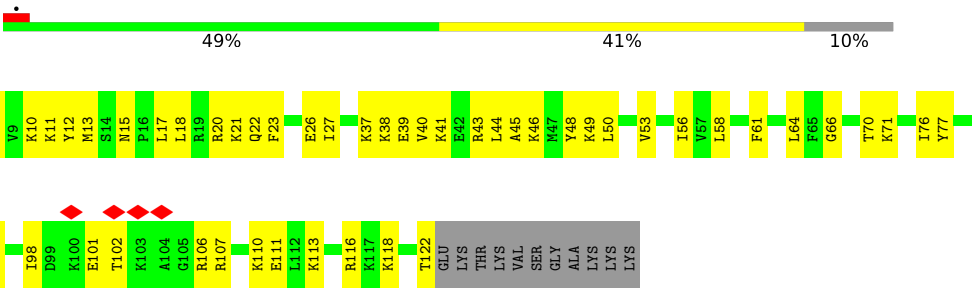
- Molecule 46: 60S ribosomal protein L24

Chain A0:



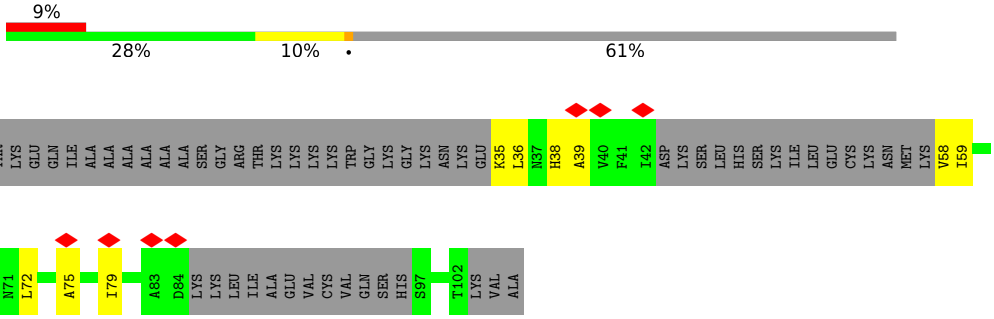
- Molecule 47: 40S ribosomal protein S24

Chain S1:



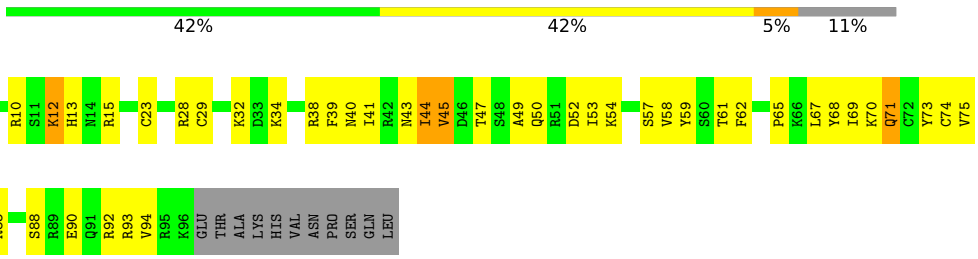
- Molecule 48: 40S ribosomal protein S25

Chain S2:



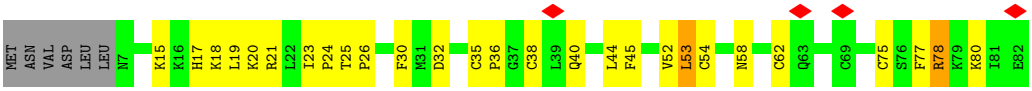
- Molecule 49: 40S ribosomal protein S26

Chain S3:



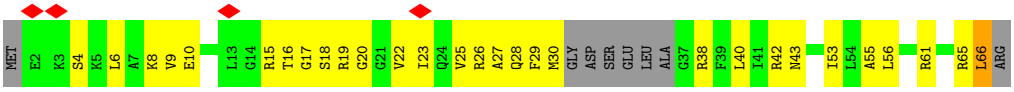
- Molecule 50: 40S ribosomal protein S27

Chain S4:



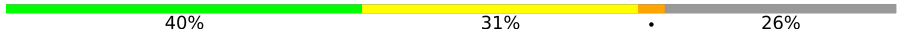
• Molecule 51: 40S ribosomal protein S28e

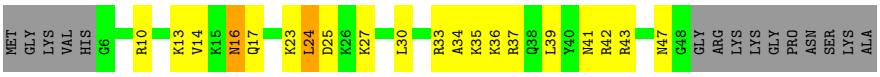
Chain S5:



• Molecule 52: 40S ribosomal protein S30

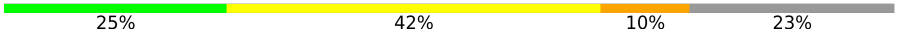
Chain S6:

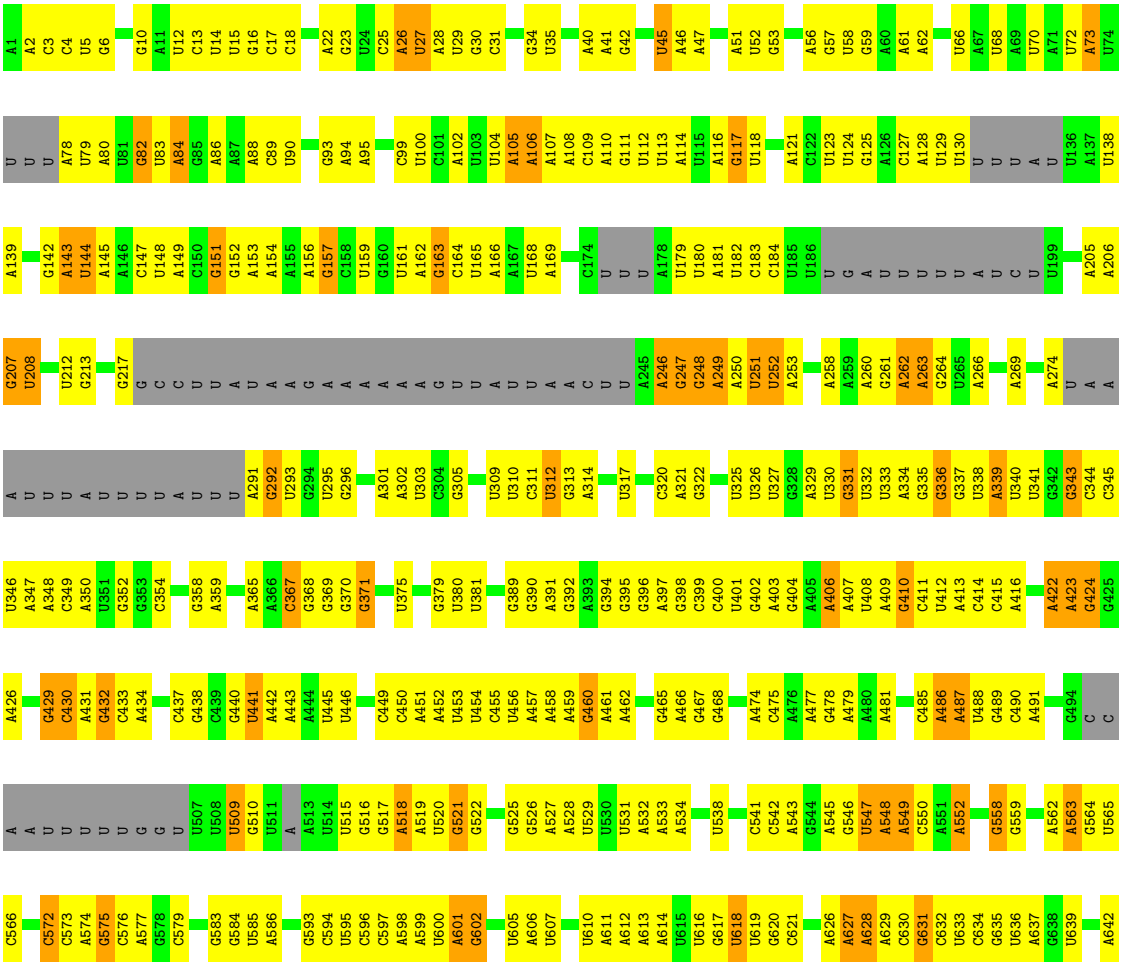


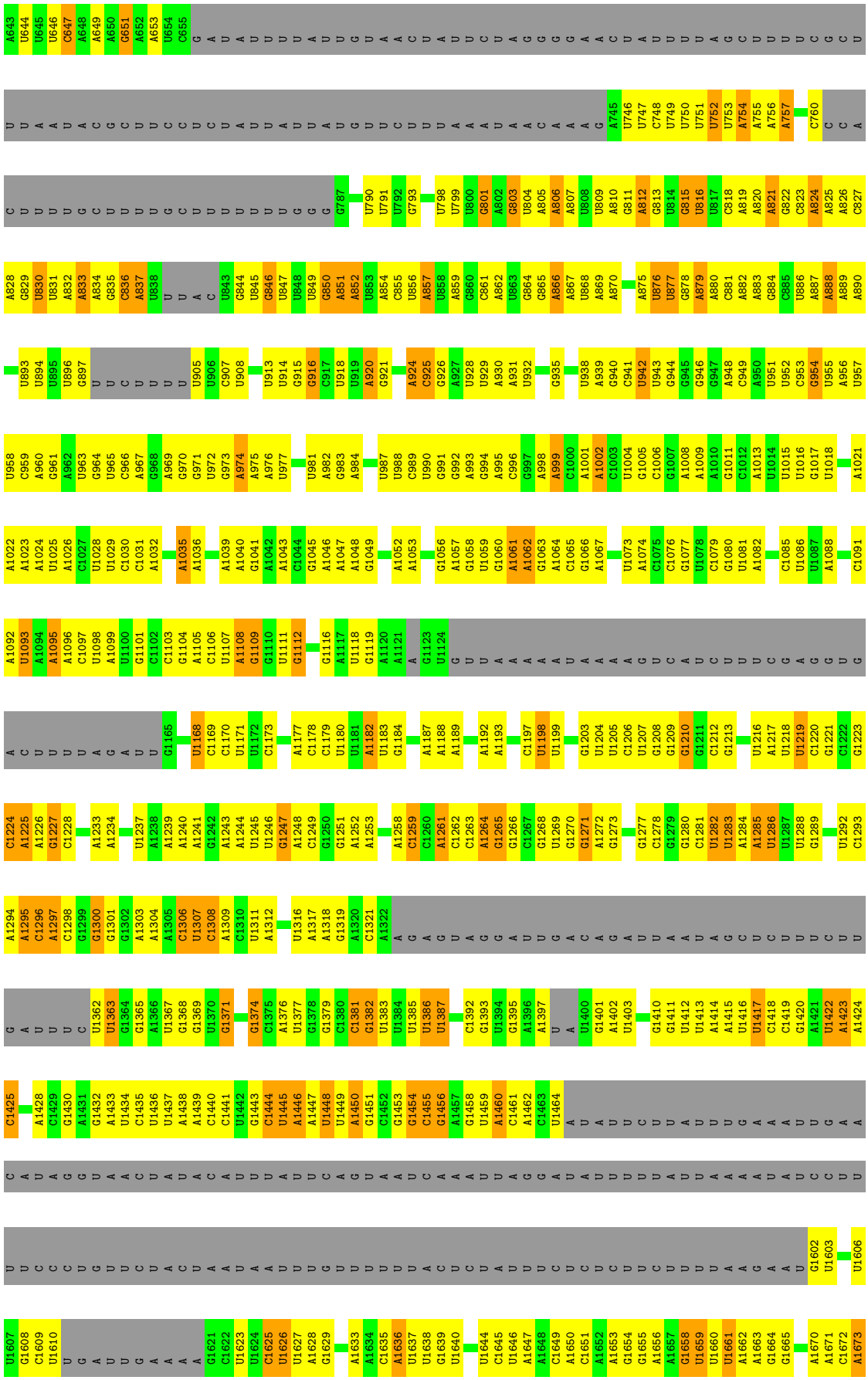


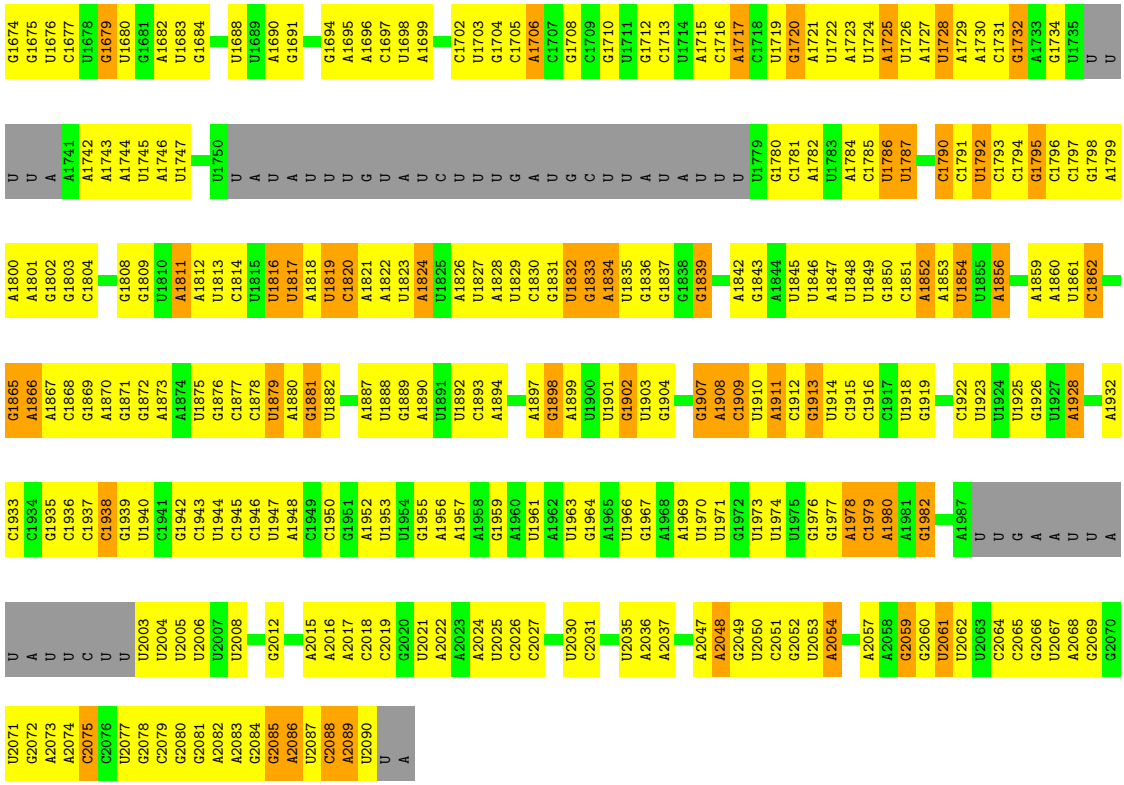
• Molecule 53: 18S ribosomal RNA

Chain SA:



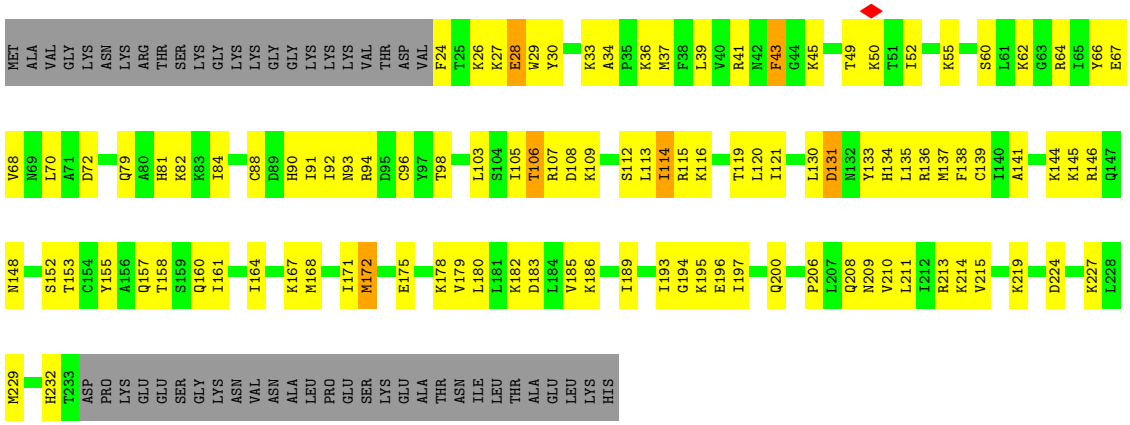



U1607 G1608 C1609 U1610 U G A U U A A G A A A G1621 C1622 U1623 U1624 C1625 U1626 U1627 A1628 G1629 A1633 A1634 C1635 A1636 U1637 U1638 G1639 U1640 U1644 C1645 U1646 A1647 A1648 C1649 A1650 C1651 A1652 A1653 G1654 G1655 A1656 A1657 G1658 U1659 U1660 U1661 A1662 A1663 G1664 G1665 A1670 A1671 C1672 A1673
U U C C C U U G G U U U C U U A A A U A A U U A A U A U U A A U U U U U U U G1602 U1603 U1606
C A U A G G U A A C U U A U U A C A A U U C A A U U A A U G G C A U U C A A U U A A U U A A U U



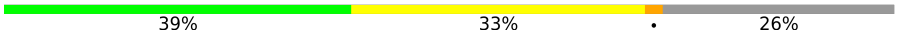
- Molecule 54: 40S ribosomal protein S3a

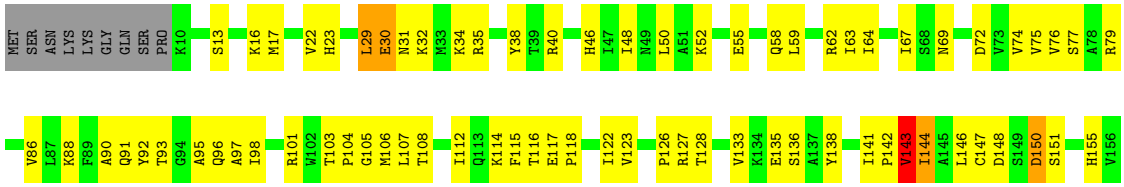
Chain SB:



- Molecule 55: 40S ribosomal protein SA

Chain SC:





D157 I158 C162 N163 K167 L172 M173 L177 A178 V181 L182 Y183 L184 V187 I188 P189 R190 M197 M200 F201 L202 W203 R204 ASP PRO GLU GLN PHE GLU LEU LYS ASN LEU ALA ASN GLU GLU ASN THR PRO THR ALA PRO HIS LEU ILE GLU ASN GLN TYR ALA ALA

GLU ALA PRO TYR ASP GLU TRP THR LYS LYS GLU GLU GLU TRP ASN ASP ASN THR ASN GLU ASP TRP LYS ASN PRO ILE ALA ALA GLU GLU GLU TRP

- Molecule 56: 40S ribosomal protein S3

Chain SD: 48% 22% 29%

MET SER ALA P4 I12 G15 V16 F17 Q18 A19 E20 E23 F24 I28 V39 ARG VAL THR PRO ILE ARG THR GLU VAL ILE ILE ARG ALA THR ARG THR ARG GLU VAL LEU GLY ASP LYS GLY ARG R65 L69 L72 F78 ASN LYS SER THR ASN SER VAL GLU

LEU PHE ALA GLU ARG VAL GLU HIS ARG GLY L97 M100 E104 S105 L106 R107 Y108 K109 L110 L111 C120 V123 L124 R125 H126 I127 M128 G134 K142 L143 R144 A145 Q146 R147 M151 K152 F153 R154 D155 G156 Y157 E163 P164 S165 K166 Q177 L178 K186 M190

T193 ALA ILE ASP THR ARG THR GLY LEU THR S207 I208 L209 P210 D211 N212 I213 L216 GLU PRO LYS THR ASP THR VAL ASP LEU

- Molecule 57: 40S ribosomal protein S9

Chain SE: 50% 47%

MET P2 K3 S4 Y5 R6 N7 Y8 T11 N14 P15 K16 R17 P18 K21 E22 R23 L24 D25 L28 K29 L30 I31 Y34 G35 L36 K37 N38 K39 R40 E41 I42 V45 Q46 Y47 L48 L49 A50 K51 I52 R53 R57 Y58 L59 L62 S66 R69 I70 F71 Q72

G73 E74 R78 R79 M80 V81 R82 L85 L86 K92 L93 L97 G98 L99 P102 K103 L104 L105 E106 R107 R108 L109 Q110 T111 K112 V113 L116 G117 L118 A119 K120 A125 L128 I129 R130 Q131 R132 H133 I134 R135 V136 G137 K138 Q139 M140 I143 F146 L147 V148

D151 A159 P163 R168 R171 R174 L177 K178 K179 Q180 K183 T184 E185 A186 GLU ALA GLU

- Molecule 58: 40S ribosomal protein S4

Chain SF: 58% 39%

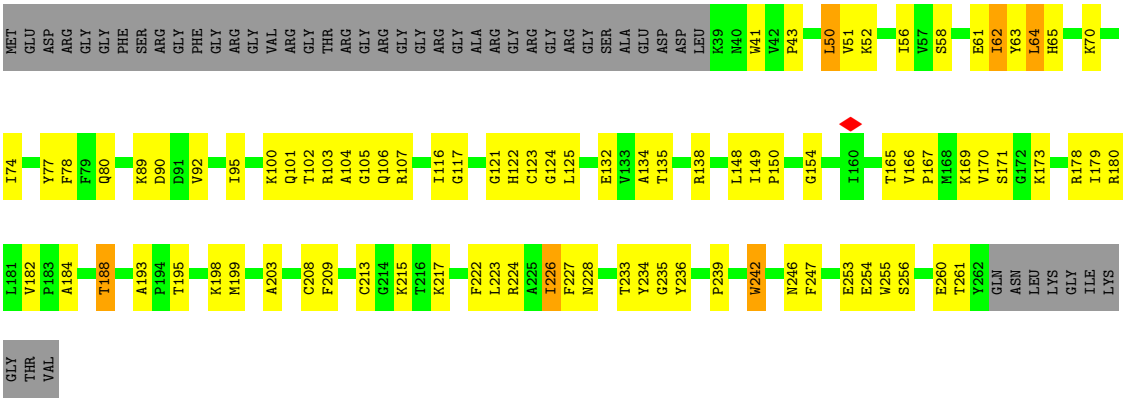
MET G2 K3 K6 K7 H8 L9 K10 R11 N21 K22 M23 G24 G25 Q26 Y27 K30 P35 H36 K37 S41 I42 I46 L47 L48 R51 L52 A55 L56 E60 V61 K62 M63 I66 Q67 K68 I69 V70 K71 V72 D73 N74 R77 T78 P83 V84 G85 L86

M87 I90 K94 S95 N96 E97 Y98 F99 R100 L101 L102 Y103 D104 I105 K106 G107 R108 F109 V110 R113 I114 E118 S119 K122 K125 V126 L131 R135 I138 A139 V140 T141 H142 D143 S146 I150 H151 V154 T159 V160 R161 L164 E165 T166 G167 K168

V169 L170 L173 K174 F175 M182 V183 T184 S188 R191 I195 I198 G203 T204 Y205 I208 H209 V210 K211 N215 F218 R221 L222 S223 N224 V225 K245 L246 D247 I248 I249 E250 E251 R252 R253 N254 K257 A258 LEU ASN ASN

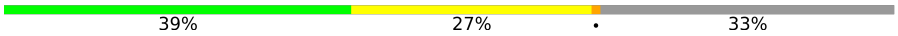
- Molecule 59: 40S ribosomal protein S5

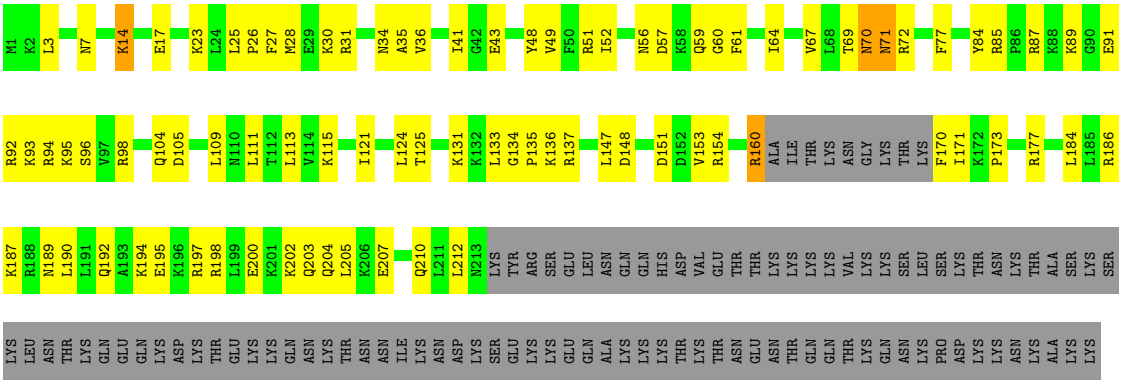
Chain SG: 50% 30% 18%



• Molecule 60: 40S ribosomal protein S6

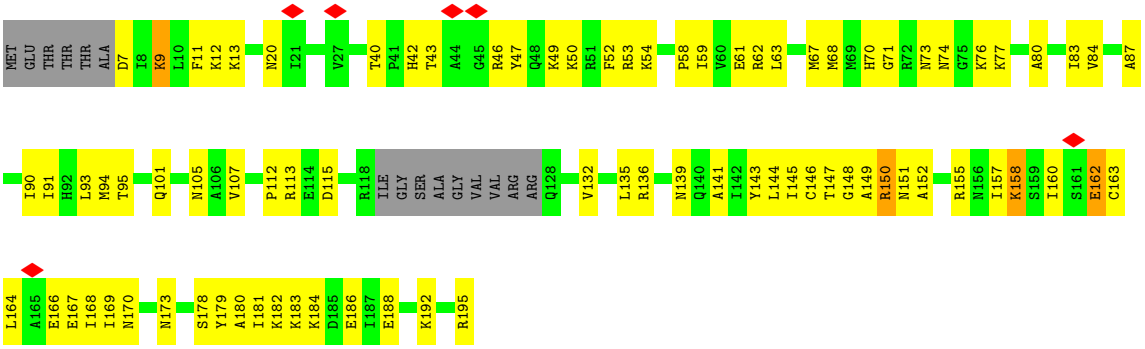
Chain SH:





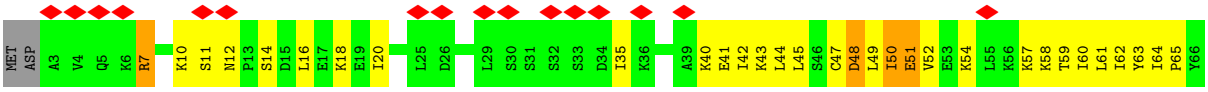
• Molecule 61: 40S ribosomal protein S5

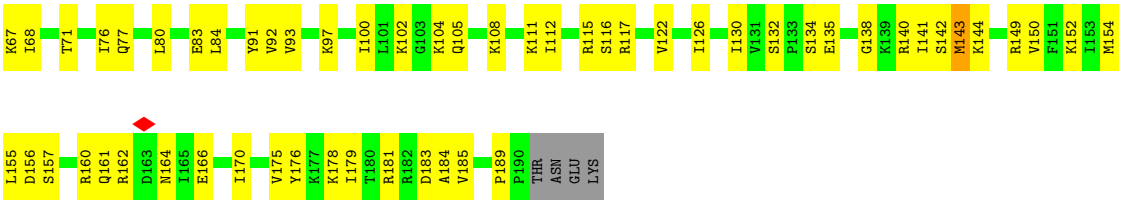
Chain SI:



• Molecule 62: 40S ribosomal protein S7

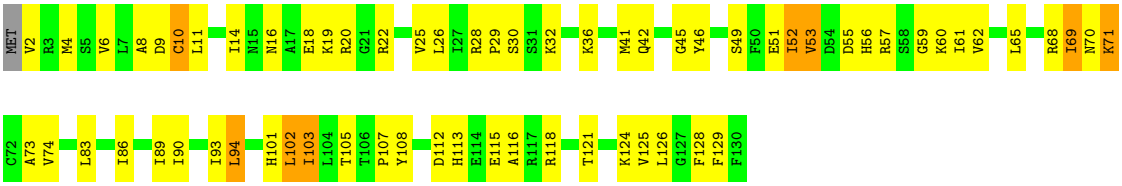
Chain SJ:





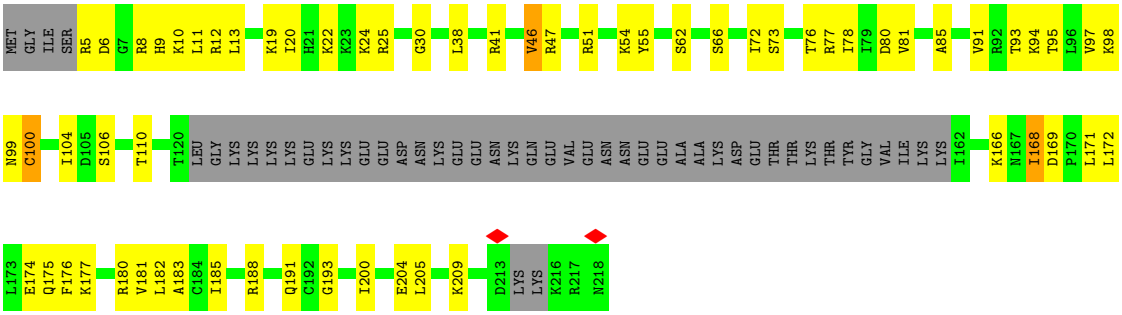
- Molecule 63: 40S ribosomal protein S15A

Chain SK:



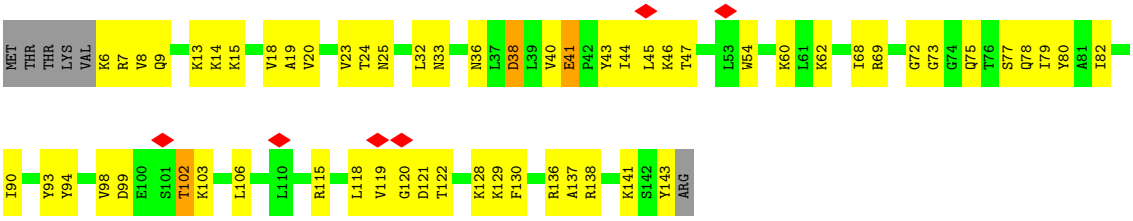
- Molecule 64: 40S ribosomal protein S8

Chain SL:



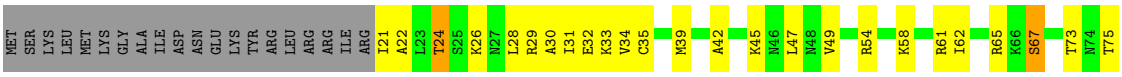
- Molecule 65: 40S ribosomal protein S16

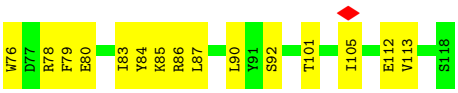
Chain SM:



- Molecule 66: 40S ribosomal protein S20e

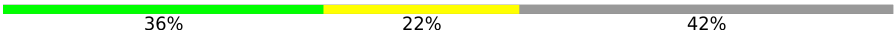
Chain SN:

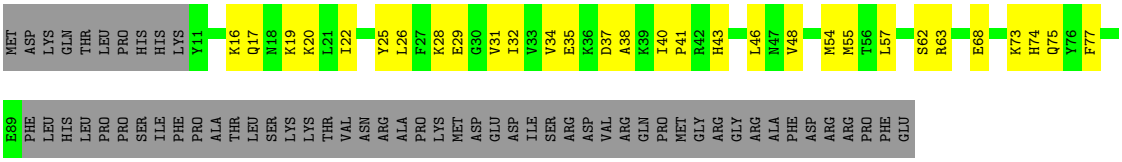




- Molecule 67: 40S ribosomal protein S10

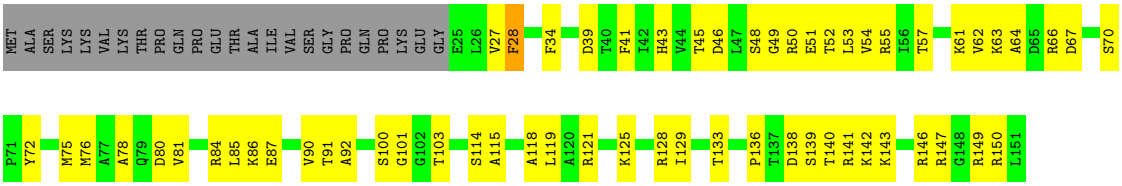
Chain SO:





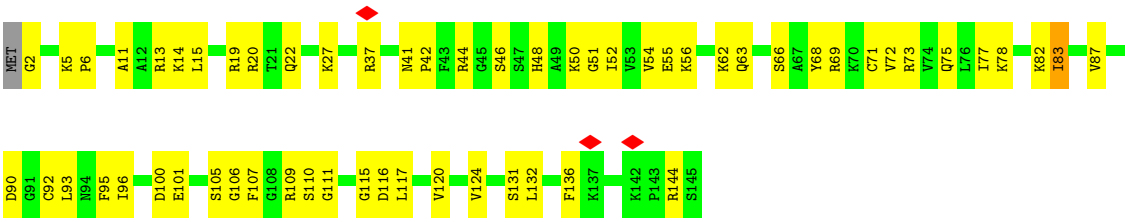
- Molecule 68: 40S ribosomal protein S11

Chain SP:



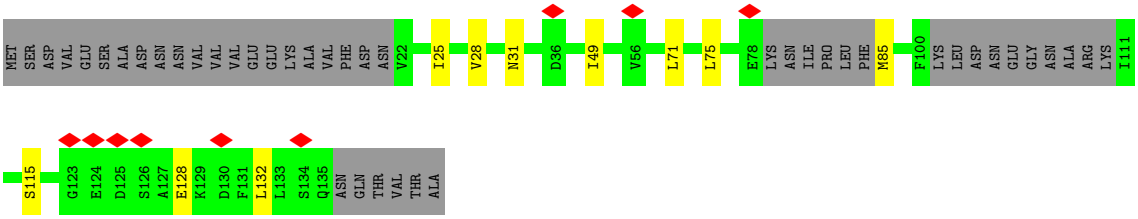
- Molecule 69: 40S ribosomal protein S23

Chain SQ:



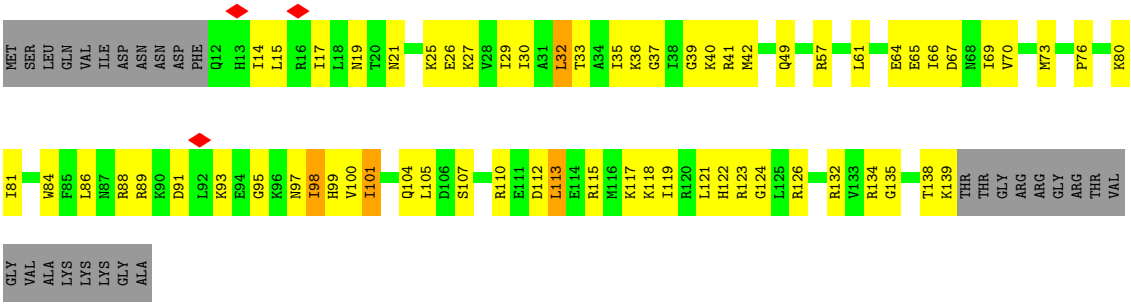
- Molecule 70: 40S ribosomal protein S12

Chain SR:



- Molecule 71: 40S ribosomal protein S18

Chain SS:

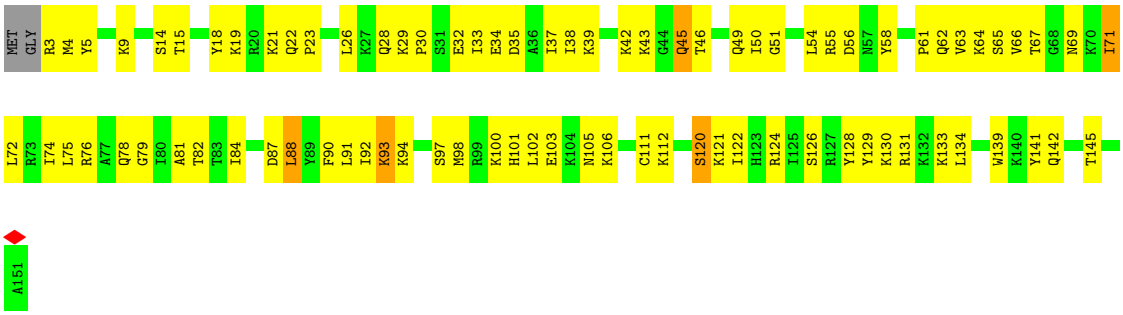


- Molecule 72: 40S ribosomal protein S29

Chain ST:

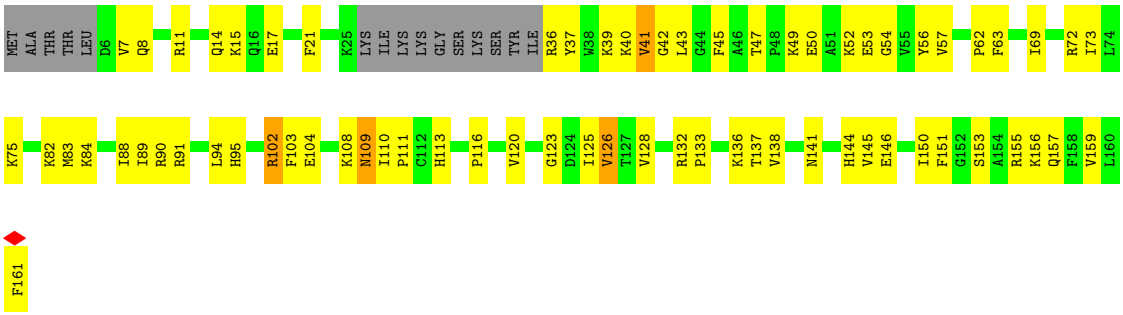
- Molecule 73: 40S ribosomal protein S15

Chain SU:



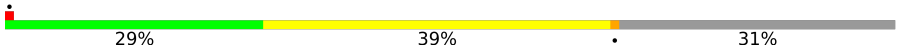
- Molecule 74: 40S ribosomal protein S11

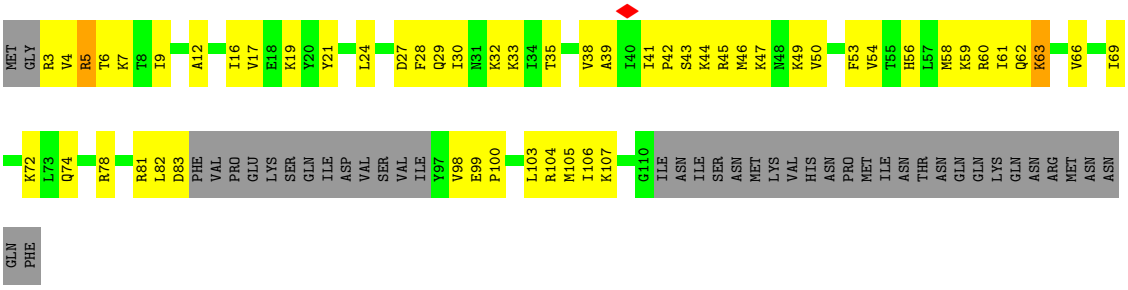
Chain SV:



- Molecule 75: 40S ribosomal protein S17

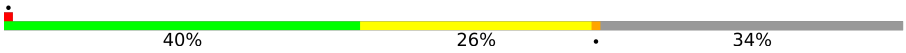
Chain SW:

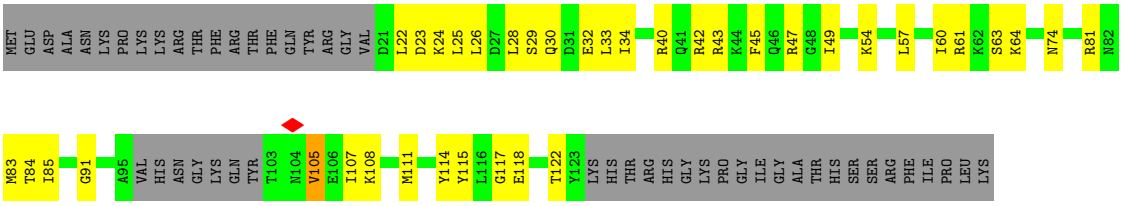




• Molecule 76: 40S ribosomal protein S19

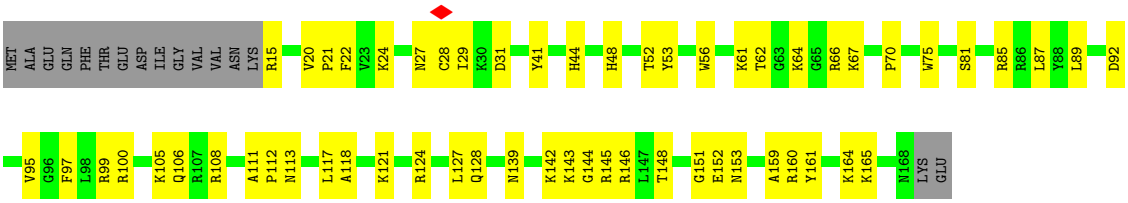
Chain SX:





• Molecule 77: 40S ribosomal protein S19

Chain SY:

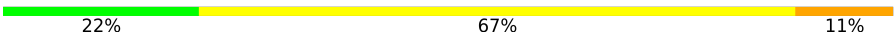


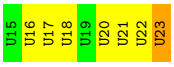
• Molecule 78: 40S ribosomal protein S21

Chain SZ:

• Molecule 79: mRNA

Chain mR:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	69147	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 ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.068	Depositor
Minimum map value	-0.027	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.00277	Depositor
Map size (Å)	415.0, 415.0, 415.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	S7	0.11	0/1810	0.28	0/2821
1	S9	0.09	0/1810	0.25	0/2821
2	AA	0.13	0/75947	0.30	0/118255
3	AC	0.12	0/3599	0.27	0/5603
4	AB	0.15	0/2816	0.34	0/4388
5	AL	0.14	0/1793	0.40	0/2387
6	A1	0.15	0/1151	0.44	0/1531
7	A2	0.14	0/846	0.39	0/1124
8	A4	0.16	0/564	0.38	0/737
9	A6	0.18	0/748	0.48	0/1001
10	A7	0.16	0/805	0.40	0/1073
11	AN	0.13	0/1226	0.38	0/1632
12	A8	0.16	0/1053	0.47	0/1399
13	A9	0.16	0/864	0.44	0/1160
14	Aa	0.18	0/871	0.52	0/1161
15	Ab	0.16	0/762	0.43	0/1008
16	Ad	0.15	0/611	0.45	0/812
17	Ae	0.12	0/396	0.30	0/521
18	Af	0.16	0/418	0.48	0/556
19	AP	0.14	0/1735	0.40	1/2320 (0.0%)
20	Ah	0.16	0/667	0.43	0/887
21	Ai	0.12	0/788	0.36	0/1032
22	AI	0.14	0/1708	0.37	0/2274
23	AJ	0.14	0/1840	0.37	0/2456
24	Ac	0.13	0/722	0.37	0/951
25	AK	0.14	0/1689	0.35	0/2260
26	AM	0.15	0/1012	0.43	0/1363
27	AS	0.13	0/1531	0.36	0/2040
28	AO	0.15	0/1199	0.38	0/1597
29	AQ	0.14	0/1579	0.41	0/2113
30	AR	0.18	0/2078	0.45	1/2776 (0.0%)
31	AW	0.14	0/1244	0.37	0/1663
32	AY	0.16	0/805	0.40	0/1074
33	AT	0.15	0/1525	0.42	0/2016

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
34	AZ	0.14	0/1012	0.41	0/1339
35	A3	0.21	0/1004	0.48	0/1329
36	A5	0.16	0/1917	0.45	0/2562
37	AD	0.14	0/1901	0.35	0/2544
38	AE	0.14	0/3129	0.38	0/4195
39	AF	0.14	0/3144	0.36	0/4205
40	AG	0.16	0/1020	0.45	1/1349 (0.1%)
41	AU	0.16	0/1527	0.41	0/2043
42	AH	0.18	0/1500	0.51	0/2025
43	AV	0.18	0/1300	0.44	0/1732
44	Ag	0.18	0/348	0.45	0/448
45	AX	0.12	0/841	0.38	0/1125
46	A0	0.13	0/533	0.36	0/711
47	S1	0.10	0/998	0.31	0/1321
48	S2	0.09	0/323	0.26	0/435
49	S3	0.16	0/793	0.45	0/1055
50	S4	0.24	0/597	0.50	0/801
51	S5	0.11	0/466	0.35	0/616
52	S6	0.16	0/348	0.54	0/458
53	SA	0.10	0/38276	0.25	0/59598
54	SB	0.15	0/1737	0.42	0/2321
55	SC	0.15	0/1569	0.41	0/2129
56	SD	0.15	0/1240	0.44	0/1652
57	SE	0.13	0/1538	0.38	0/2055
58	SF	0.12	0/2097	0.35	0/2819
59	SG	0.16	0/1799	0.40	0/2429
60	SH	0.12	0/1668	0.35	0/2214
61	SI	0.14	0/1443	0.42	0/1936
62	SJ	0.20	0/1544	0.46	1/2064 (0.0%)
63	SK	0.16	0/1054	0.43	0/1411
64	SL	0.12	0/1407	0.35	0/1879
65	SM	0.12	0/1113	0.36	0/1487
66	SN	0.15	0/780	0.38	0/1053
67	SO	0.14	0/705	0.39	0/950
68	SP	0.15	0/966	0.44	0/1295
69	SQ	0.14	0/1149	0.37	0/1532
70	SR	0.09	0/754	0.28	0/1013
71	SS	0.15	0/1062	0.46	0/1425
72	ST	0.16	0/412	0.42	0/544
73	SU	0.15	0/1223	0.43	0/1634
74	SV	0.17	0/1233	0.47	0/1645
75	SW	0.16	0/792	0.47	0/1053
76	SX	0.12	0/787	0.44	0/1050

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
77	SY	0.11	0/1294	0.32	0/1742
78	SZ	0.14	0/565	0.46	0/758
79	mR	0.10	0/197	0.29	0/302
All	All	0.13	0/209317	0.33	4/307095 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	A6	0	1
50	S4	0	1
62	SJ	0	2
All	All	0	4

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
62	SJ	51	GLU	CA-CB-CG	7.04	128.17	114.10
19	AP	156	VAL	N-CA-C	-6.40	107.25	113.53
30	AR	48	LYS	CB-CA-C	-5.11	104.64	111.89
40	AG	155	THR	CB-CA-C	-5.08	109.75	115.79

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	A6	64	MET	Peptide
50	S4	78	ARG	Sidechain
62	SJ	50	ILE	Peptide
62	SJ	51	GLU	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	S7	1620	0	827	29	0
1	S9	1620	0	827	38	0
2	AA	67884	0	34243	1768	0
3	AC	3215	0	1633	86	0
4	AB	2517	0	1275	108	0
5	AL	1761	0	1896	77	0
6	A1	1134	0	1245	58	0
7	A2	837	0	896	21	0
8	A4	555	0	599	20	0
9	A6	740	0	763	49	0
10	A7	793	0	869	51	0
11	AN	1210	0	1329	58	0
12	A8	1036	0	1139	36	0
13	A9	844	0	886	32	0
14	Aa	858	0	912	54	0
15	Ab	756	0	842	32	0
16	Ad	603	0	686	40	0
17	Ae	388	0	421	18	0
18	Af	413	0	452	35	0
19	AP	1697	0	1802	74	0
20	Ah	658	0	727	37	0
21	Ai	778	0	859	29	0
22	AI	1685	0	1849	70	0
23	AJ	1813	0	1985	73	0
24	Ac	709	0	761	30	0
25	AK	1659	0	1782	63	0
26	AM	996	0	1044	57	0
27	AS	1503	0	1636	40	0
28	AO	1172	0	1230	43	0
29	AQ	1544	0	1582	71	0
30	AR	2049	0	2145	119	0
31	AW	1319	0	1303	42	0
32	AY	796	0	850	36	0
33	AT	1509	0	1682	75	0
34	AZ	1000	0	1099	52	0
35	A3	994	0	1121	59	0
36	A5	1879	0	2005	91	0
37	AD	1866	0	1964	56	0
38	AE	3061	0	3205	135	0
39	AF	3094	0	3333	102	0
40	AG	1010	0	1073	66	0
41	AU	1497	0	1556	67	0
42	AH	1475	0	1574	94	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	AV	1275	0	1355	60	0
44	Ag	343	0	388	23	0
45	AX	824	0	882	34	0
46	A0	521	0	539	33	0
47	S1	985	0	1076	54	0
48	S2	320	0	338	10	0
49	S3	781	0	820	45	0
50	S4	586	0	604	18	0
51	S5	465	0	505	19	0
52	S6	345	0	381	21	0
53	SA	34208	0	17266	1074	0
54	SB	1713	0	1838	91	0
55	SC	1538	0	1600	66	0
56	SD	1228	0	1311	46	0
57	SE	1514	0	1605	89	0
58	SF	2061	0	2200	93	0
59	SG	1757	0	1811	76	0
60	SH	1651	0	1807	72	0
61	SI	1424	0	1471	80	0
62	SJ	1528	0	1680	70	0
63	SK	1037	0	1099	67	0
64	SL	1383	0	1434	57	0
65	SM	1098	0	1183	53	0
66	SN	772	0	813	37	0
67	SO	686	0	695	19	0
68	SP	954	0	997	52	0
69	SQ	1129	0	1196	52	0
70	SR	746	0	754	7	0
71	SS	1046	0	1101	54	0
72	ST	405	0	419	27	0
73	SU	1202	0	1299	77	0
74	SV	1206	0	1239	62	0
75	SW	785	0	858	50	0
76	SX	776	0	832	33	0
77	SY	1266	0	1316	55	0
78	SZ	557	0	558	29	0
79	mR	180	0	91	3	0
All	All	194842	0	145268	5896	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 18.

The worst 5 of 5896 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AA:1132:G:H1	2:AA:1163:A:N6	1.42	1.17
2:AA:3410:A:H62	2:AA:3417:G:N2	1.48	1.09
2:AA:3410:A:N6	2:AA:3417:G:H21	1.50	1.08
2:AA:541:A:C2	2:AA:611:G:N1	2.24	1.05
53:SA:956:A:N6	53:SA:994:G:H1	1.54	1.04

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	AL	209/215 (97%)	197 (94%)	12 (6%)	0	100	100
6	A1	136/146 (93%)	122 (90%)	14 (10%)	0	100	100
7	A2	97/127 (76%)	93 (96%)	4 (4%)	0	100	100
8	A4	64/67 (96%)	60 (94%)	4 (6%)	0	100	100
9	A6	96/108 (89%)	88 (92%)	7 (7%)	1 (1%)	12	38
10	A7	92/120 (77%)	91 (99%)	1 (1%)	0	100	100
11	AN	145/165 (88%)	132 (91%)	13 (9%)	0	100	100
12	A8	123/131 (94%)	109 (89%)	14 (11%)	0	100	100
13	A9	101/140 (72%)	95 (94%)	6 (6%)	0	100	100
14	Aa	104/150 (69%)	94 (90%)	10 (10%)	0	100	100
15	Ab	91/112 (81%)	85 (93%)	6 (7%)	0	100	100
16	Ad	68/87 (78%)	61 (90%)	7 (10%)	0	100	100
17	Ae	39/51 (76%)	38 (97%)	1 (3%)	0	100	100
18	Af	49/128 (38%)	42 (86%)	7 (14%)	0	100	100
19	AP	202/205 (98%)	185 (92%)	16 (8%)	1 (0%)	24	55
20	Ah	83/96 (86%)	77 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	Ai	93/104 (89%)	85 (91%)	8 (9%)	0	100	100
22	AI	203/221 (92%)	190 (94%)	11 (5%)	2 (1%)	12	38
23	AJ	216/283 (76%)	204 (94%)	11 (5%)	1 (0%)	24	55
24	Ac	87/92 (95%)	76 (87%)	11 (13%)	0	100	100
25	AK	199/202 (98%)	191 (96%)	7 (4%)	1 (0%)	24	55
26	AM	130/139 (94%)	124 (95%)	6 (5%)	0	100	100
27	AS	184/187 (98%)	173 (94%)	11 (6%)	0	100	100
28	AO	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
29	AQ	185/219 (84%)	163 (88%)	21 (11%)	1 (0%)	24	55
30	AR	244/294 (83%)	227 (93%)	17 (7%)	0	100	100
31	AW	149/173 (86%)	143 (96%)	6 (4%)	0	100	100
32	AY	99/190 (52%)	95 (96%)	4 (4%)	0	100	100
33	AT	179/182 (98%)	170 (95%)	9 (5%)	0	100	100
34	AZ	119/126 (94%)	112 (94%)	7 (6%)	0	100	100
35	A3	117/124 (94%)	110 (94%)	7 (6%)	0	100	100
36	A5	221/257 (86%)	203 (92%)	18 (8%)	0	100	100
37	AD	245/260 (94%)	229 (94%)	14 (6%)	2 (1%)	16	44
38	AE	378/386 (98%)	356 (94%)	22 (6%)	0	100	100
39	AF	388/411 (94%)	369 (95%)	19 (5%)	0	100	100
40	AG	116/173 (67%)	97 (84%)	19 (16%)	0	100	100
41	AU	178/184 (97%)	169 (95%)	9 (5%)	0	100	100
42	AH	183/190 (96%)	168 (92%)	14 (8%)	1 (0%)	24	55
43	AV	153/161 (95%)	147 (96%)	6 (4%)	0	100	100
44	Ag	35/39 (90%)	27 (77%)	8 (23%)	0	100	100
45	AX	95/139 (68%)	92 (97%)	3 (3%)	0	100	100
46	A0	60/162 (37%)	54 (90%)	6 (10%)	0	100	100
47	S1	118/133 (89%)	116 (98%)	2 (2%)	0	100	100
48	S2	35/105 (33%)	35 (100%)	0	0	100	100
49	S3	93/107 (87%)	84 (90%)	9 (10%)	0	100	100
50	S4	74/82 (90%)	61 (82%)	13 (18%)	0	100	100
51	S5	55/67 (82%)	53 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	S6	41/58 (71%)	35 (85%)	5 (12%)	1 (2%)	4	17
54	SB	208/262 (79%)	191 (92%)	17 (8%)	0	100	100
55	SC	193/263 (73%)	176 (91%)	15 (8%)	2 (1%)	12	38
56	SD	149/221 (67%)	144 (97%)	5 (3%)	0	100	100
57	SE	183/189 (97%)	170 (93%)	13 (7%)	0	100	100
58	SF	255/261 (98%)	244 (96%)	10 (4%)	1 (0%)	30	60
59	SG	222/272 (82%)	208 (94%)	14 (6%)	0	100	100
60	SH	200/306 (65%)	192 (96%)	7 (4%)	1 (0%)	24	55
61	SI	176/195 (90%)	160 (91%)	16 (9%)	0	100	100
62	SJ	186/194 (96%)	170 (91%)	15 (8%)	1 (0%)	24	55
63	SK	127/130 (98%)	114 (90%)	13 (10%)	0	100	100
64	SL	165/218 (76%)	151 (92%)	13 (8%)	1 (1%)	21	51
65	SM	136/144 (94%)	128 (94%)	7 (5%)	1 (1%)	18	47
66	SN	96/118 (81%)	90 (94%)	6 (6%)	0	100	100
67	SO	77/137 (56%)	72 (94%)	4 (5%)	1 (1%)	9	31
68	SP	125/151 (83%)	115 (92%)	10 (8%)	0	100	100
69	SQ	142/145 (98%)	132 (93%)	9 (6%)	1 (1%)	18	47
70	SR	92/141 (65%)	86 (94%)	6 (6%)	0	100	100
71	SS	126/156 (81%)	111 (88%)	13 (10%)	2 (2%)	7	27
72	ST	46/54 (85%)	46 (100%)	0	0	100	100
73	SU	147/151 (97%)	136 (92%)	11 (8%)	0	100	100
74	SV	142/161 (88%)	133 (94%)	8 (6%)	1 (1%)	18	47
75	SW	91/137 (66%)	86 (94%)	3 (3%)	2 (2%)	5	19
76	SX	92/145 (63%)	81 (88%)	11 (12%)	0	100	100
77	SY	152/170 (89%)	147 (97%)	5 (3%)	0	100	100
78	SZ	70/82 (85%)	65 (93%)	4 (6%)	1 (1%)	9	30
All	All	10114/12049 (84%)	9412 (93%)	676 (7%)	26 (0%)	37	66

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	AJ	75	ILE
42	AH	53	TYR

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Mol	Chain	Res	Type
62	SJ	112	ILE
65	SM	41	GLU
71	SS	101	ILE

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	
5	AL	190/194 (98%)	187 (98%)	3 (2%)	55	83
6	A1	127/132 (96%)	122 (96%)	5 (4%)	28	64
7	A2	98/118 (83%)	94 (96%)	4 (4%)	27	62
8	A4	60/61 (98%)	58 (97%)	2 (3%)	33	69
9	A6	83/92 (90%)	74 (89%)	9 (11%)	6	21
10	A7	90/112 (80%)	81 (90%)	9 (10%)	7	24
11	AN	136/152 (90%)	130 (96%)	6 (4%)	25	59
12	A8	114/120 (95%)	106 (93%)	8 (7%)	14	40
13	A9	90/127 (71%)	85 (94%)	5 (6%)	19	50
14	Aa	89/128 (70%)	86 (97%)	3 (3%)	32	68
15	Ab	82/97 (84%)	76 (93%)	6 (7%)	13	38
16	Ad	69/83 (83%)	64 (93%)	5 (7%)	13	39
17	Ae	40/48 (83%)	38 (95%)	2 (5%)	22	54
18	Af	45/114 (40%)	42 (93%)	3 (7%)	15	42
19	AP	179/180 (99%)	168 (94%)	11 (6%)	17	46
20	Ah	70/80 (88%)	65 (93%)	5 (7%)	13	39
21	Ai	87/93 (94%)	85 (98%)	2 (2%)	44	78
22	AI	189/203 (93%)	175 (93%)	14 (7%)	13	37
23	AJ	204/260 (78%)	198 (97%)	6 (3%)	37	73
24	Ac	74/77 (96%)	73 (99%)	1 (1%)	59	85
25	AK	181/182 (100%)	173 (96%)	8 (4%)	25	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	AM	106/110 (96%)	98 (92%)	8 (8%)	12	37
27	AS	158/159 (99%)	152 (96%)	6 (4%)	29	64
28	AO	121/122 (99%)	116 (96%)	5 (4%)	27	62
29	AQ	165/190 (87%)	159 (96%)	6 (4%)	31	66
30	AR	215/254 (85%)	207 (96%)	8 (4%)	30	65
31	AW	128/131 (98%)	121 (94%)	7 (6%)	19	51
32	AY	90/177 (51%)	86 (96%)	4 (4%)	25	59
33	AT	162/163 (99%)	157 (97%)	5 (3%)	35	70
34	AZ	111/115 (96%)	101 (91%)	10 (9%)	9	28
35	A3	110/115 (96%)	101 (92%)	9 (8%)	10	33
36	A5	201/231 (87%)	191 (95%)	10 (5%)	22	54
37	AD	191/202 (95%)	182 (95%)	9 (5%)	23	57
38	AE	335/340 (98%)	311 (93%)	24 (7%)	13	39
39	AF	336/352 (96%)	322 (96%)	14 (4%)	26	61
40	AG	110/155 (71%)	100 (91%)	10 (9%)	9	28
41	AU	162/166 (98%)	153 (94%)	9 (6%)	19	50
42	AH	168/173 (97%)	158 (94%)	10 (6%)	17	47
43	AV	140/144 (97%)	134 (96%)	6 (4%)	26	60
44	Ag	34/35 (97%)	31 (91%)	3 (9%)	9	29
45	AX	92/131 (70%)	84 (91%)	8 (9%)	9	30
46	A0	53/146 (36%)	50 (94%)	3 (6%)	18	49
47	S1	104/115 (90%)	103 (99%)	1 (1%)	68	88
48	S2	35/88 (40%)	33 (94%)	2 (6%)	18	49
49	S3	87/98 (89%)	79 (91%)	8 (9%)	8	27
50	S4	70/76 (92%)	68 (97%)	2 (3%)	37	73
51	S5	48/54 (89%)	47 (98%)	1 (2%)	47	79
52	S6	36/47 (77%)	34 (94%)	2 (6%)	19	50
54	SB	195/238 (82%)	182 (93%)	13 (7%)	15	42
55	SC	167/227 (74%)	157 (94%)	10 (6%)	17	47
56	SD	132/188 (70%)	129 (98%)	3 (2%)	44	78
57	SE	161/167 (96%)	156 (97%)	5 (3%)	35	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	SF	233/237 (98%)	223 (96%)	10 (4%)	26	60
59	SG	191/222 (86%)	179 (94%)	12 (6%)	16	45
60	SH	182/279 (65%)	177 (97%)	5 (3%)	39	74
61	SI	154/165 (93%)	148 (96%)	6 (4%)	28	64
62	SJ	177/183 (97%)	171 (97%)	6 (3%)	32	68
63	SK	115/116 (99%)	106 (92%)	9 (8%)	11	35
64	SL	151/193 (78%)	147 (97%)	4 (3%)	40	75
65	SM	116/122 (95%)	113 (97%)	3 (3%)	40	75
66	SN	91/109 (84%)	88 (97%)	3 (3%)	33	69
67	SO	76/129 (59%)	75 (99%)	1 (1%)	61	86
68	SP	99/119 (83%)	94 (95%)	5 (5%)	21	54
69	SQ	120/121 (99%)	114 (95%)	6 (5%)	22	54
70	SR	83/121 (69%)	82 (99%)	1 (1%)	63	87
71	SS	114/136 (84%)	109 (96%)	5 (4%)	25	59
72	ST	43/48 (90%)	38 (88%)	5 (12%)	5	18
73	SU	132/133 (99%)	125 (95%)	7 (5%)	20	52
74	SV	131/144 (91%)	126 (96%)	5 (4%)	29	64
75	SW	86/127 (68%)	83 (96%)	3 (4%)	32	67
76	SX	88/130 (68%)	85 (97%)	3 (3%)	32	68
77	SY	137/151 (91%)	136 (99%)	1 (1%)	76	91
78	SZ	60/70 (86%)	52 (87%)	8 (13%)	4	14
All	All	9099/10617 (86%)	8653 (95%)	446 (5%)	24	55

5 of 446 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	AF	133	VAL
78	SZ	63	GLU
45	AX	123	ILE
78	SZ	11	ILE
68	SP	85	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
40	AG	20	ASN
58	SF	176	GLN
42	AH	168	ASN
52	S6	38	GLN
60	SH	59	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	S7	75/76 (98%)	30 (40%)	2 (2%)
1	S9	75/76 (98%)	15 (20%)	1 (1%)
2	AA	3162/3788 (83%)	768 (24%)	57 (1%)
3	AC	148/159 (93%)	34 (22%)	4 (2%)
4	AB	117/119 (98%)	41 (35%)	1 (0%)
53	SA	1587/2092 (75%)	360 (22%)	24 (1%)
79	mR	8/9 (88%)	6 (75%)	0
All	All	5172/6319 (81%)	1254 (24%)	89 (1%)

5 of 1254 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	S7	3	C
1	S7	6	G
1	S7	9	G
1	S7	10	G
1	S7	11	A

5 of 89 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	AA	3658	G
53	SA	844	G
3	AC	35	A
53	SA	246	A
53	SA	1182	A

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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
31	AW	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AW	154:ASN	C	197:UNK	N	32.90

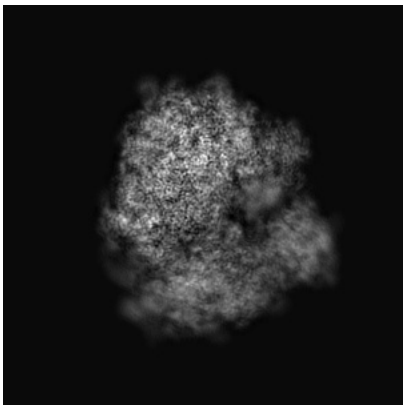
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-44919. These allow visual inspection of the internal detail of the map and identification of artifacts.

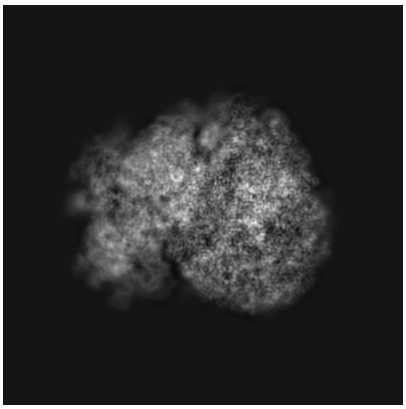
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

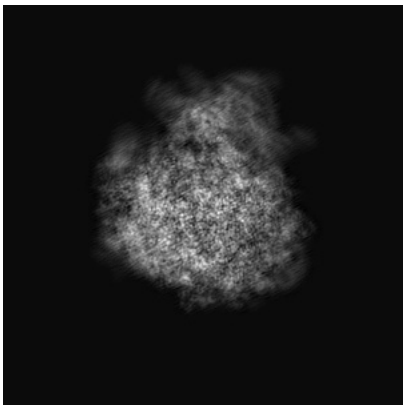
6.1.1 Primary map



X

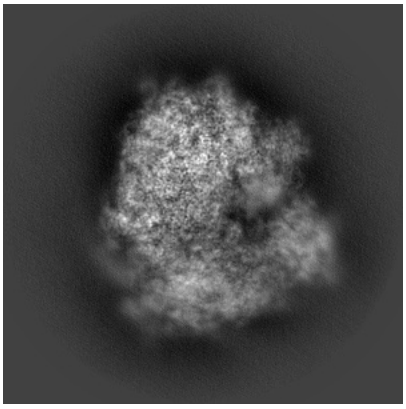


Y

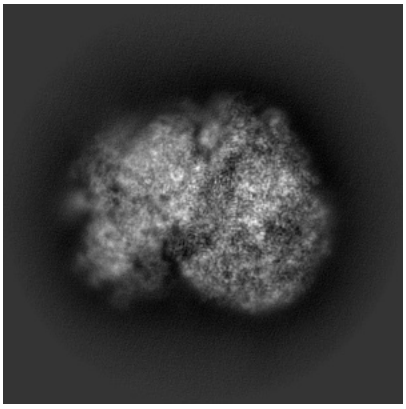


Z

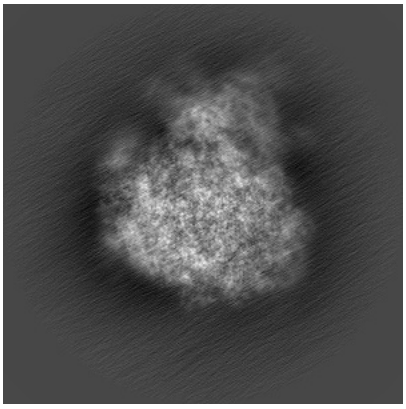
6.1.2 Raw map



X



Y

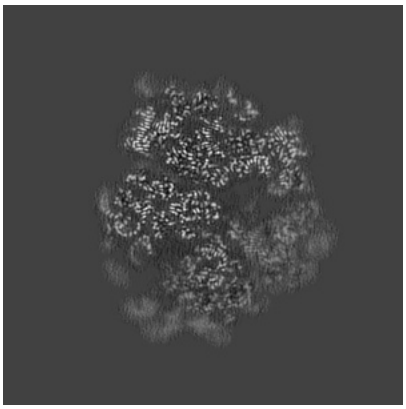


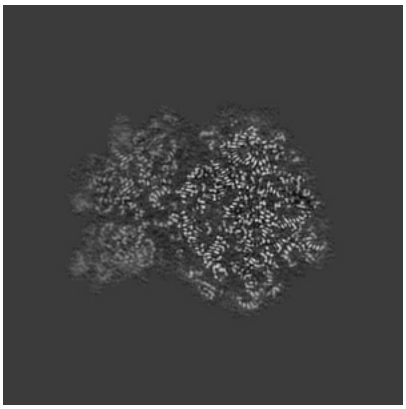
Z

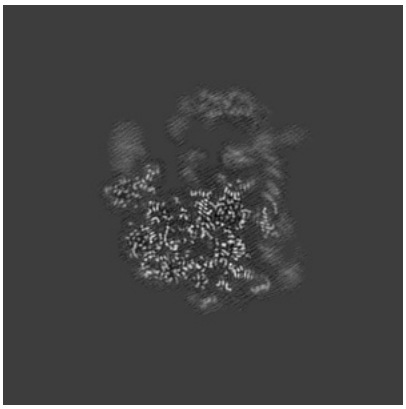
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

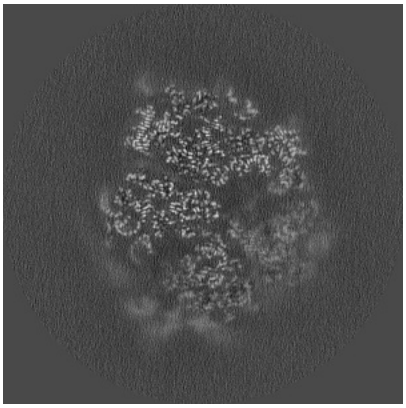
6.2.1 Primary map

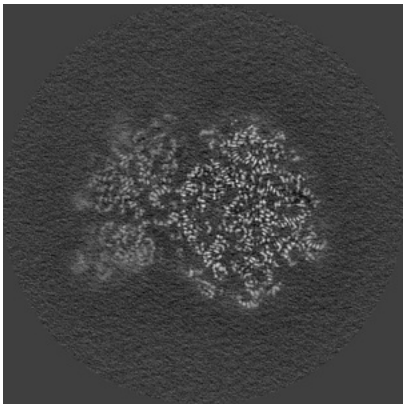

X Index: 250

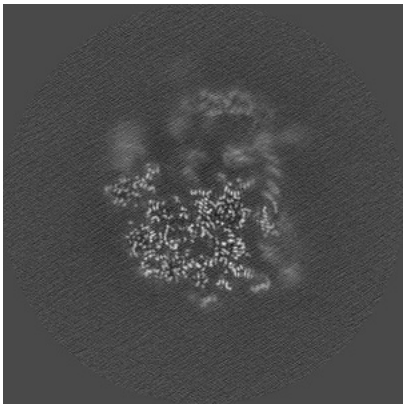

Y Index: 250


Z Index: 250

6.2.2 Raw map


X Index: 250

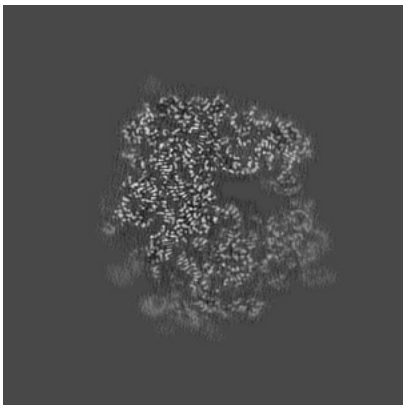

Y Index: 250


Z Index: 250

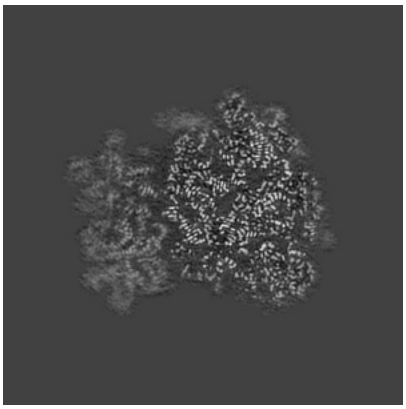
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

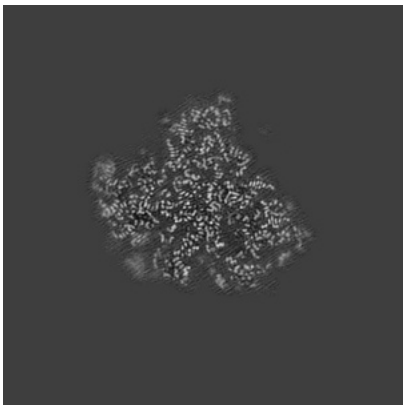
6.3.1 Primary map



X Index: 269

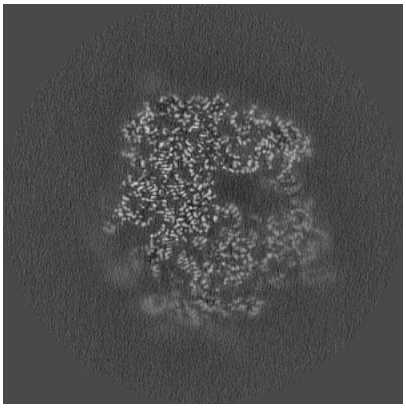


Y Index: 222

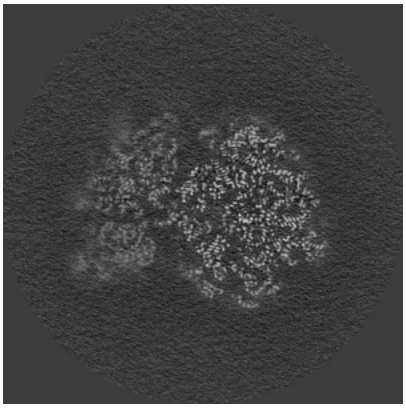


Z Index: 310

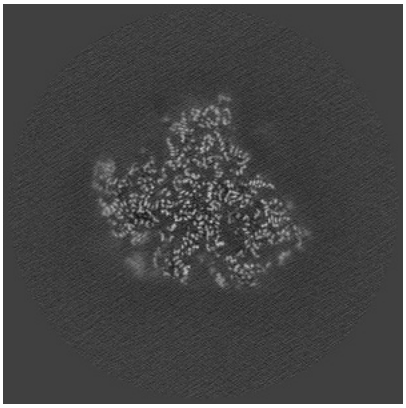
6.3.2 Raw map



X Index: 269



Y Index: 251

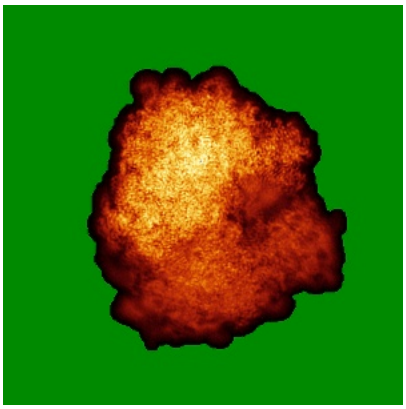


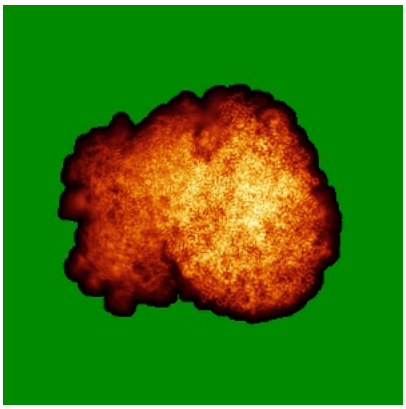
Z Index: 310

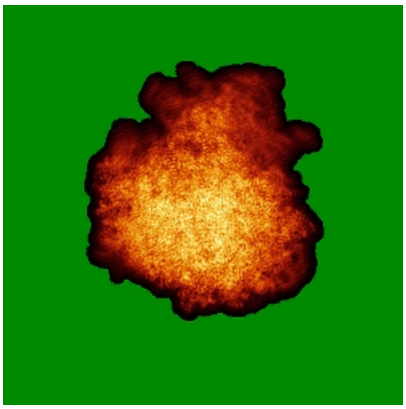
The images above show the largest variance slices of the map in three orthogonal directions.

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

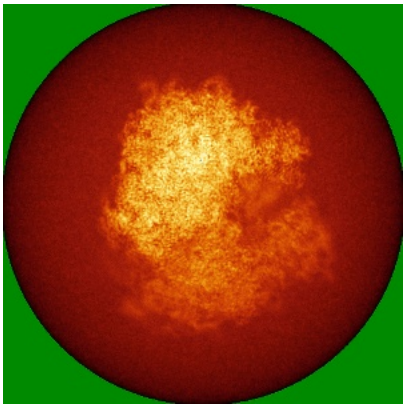
6.4.1 Primary map

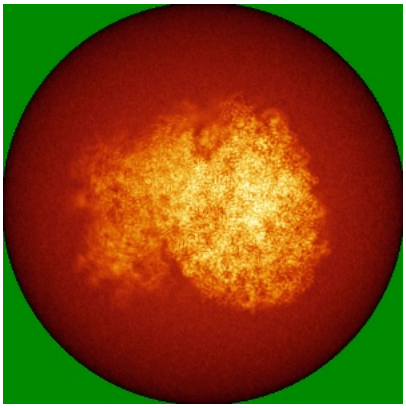

X

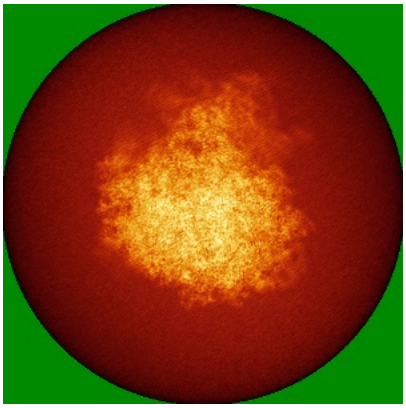

Y


Z

6.4.2 Raw map


X

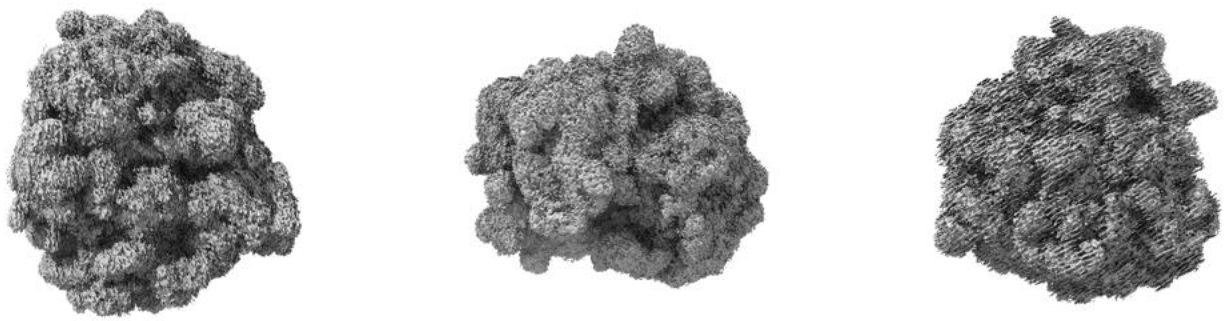

Y


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 0.00277. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X Y Z

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

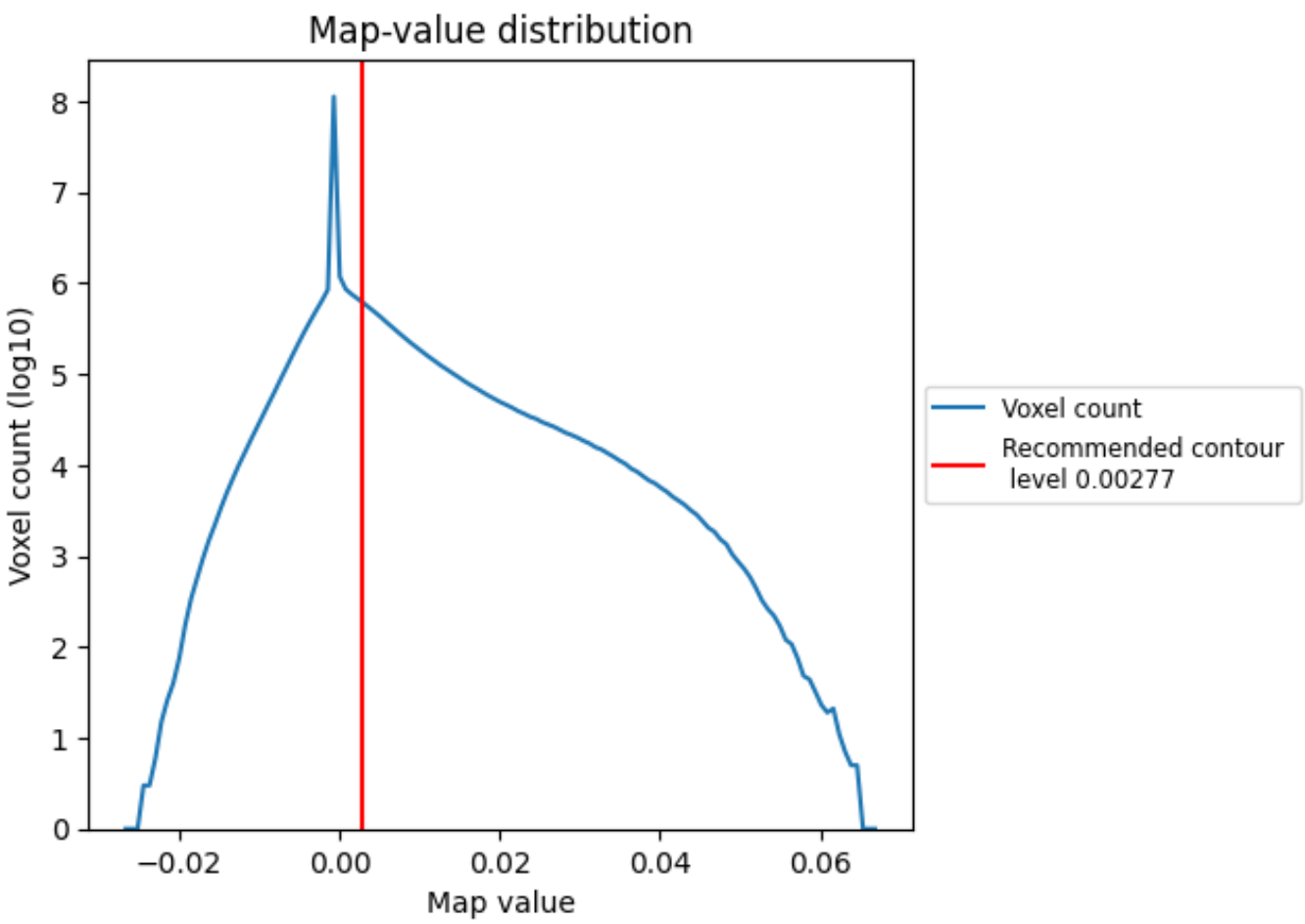
6.6 Mask visualisation (i)

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

7 Map analysis (i)

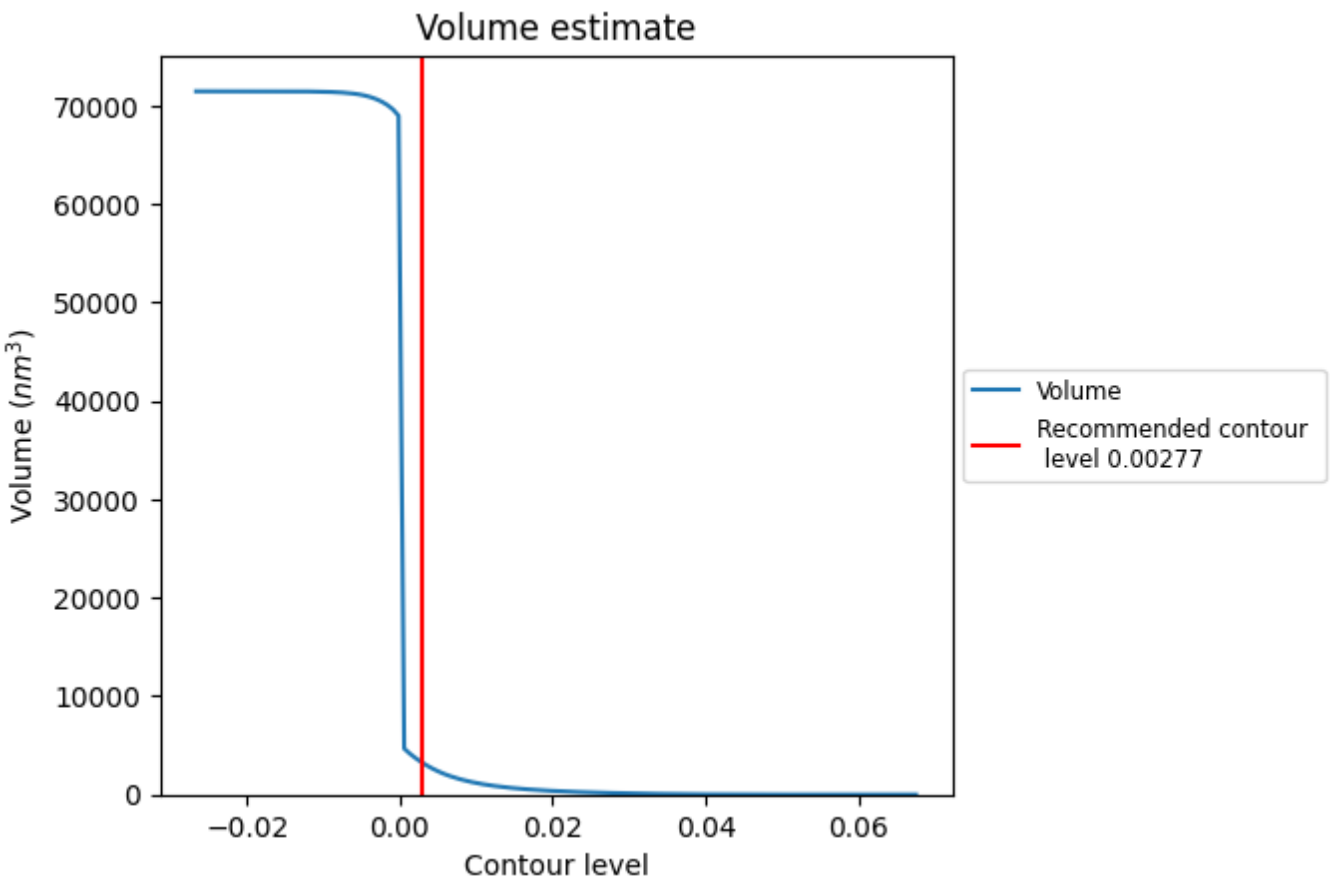
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

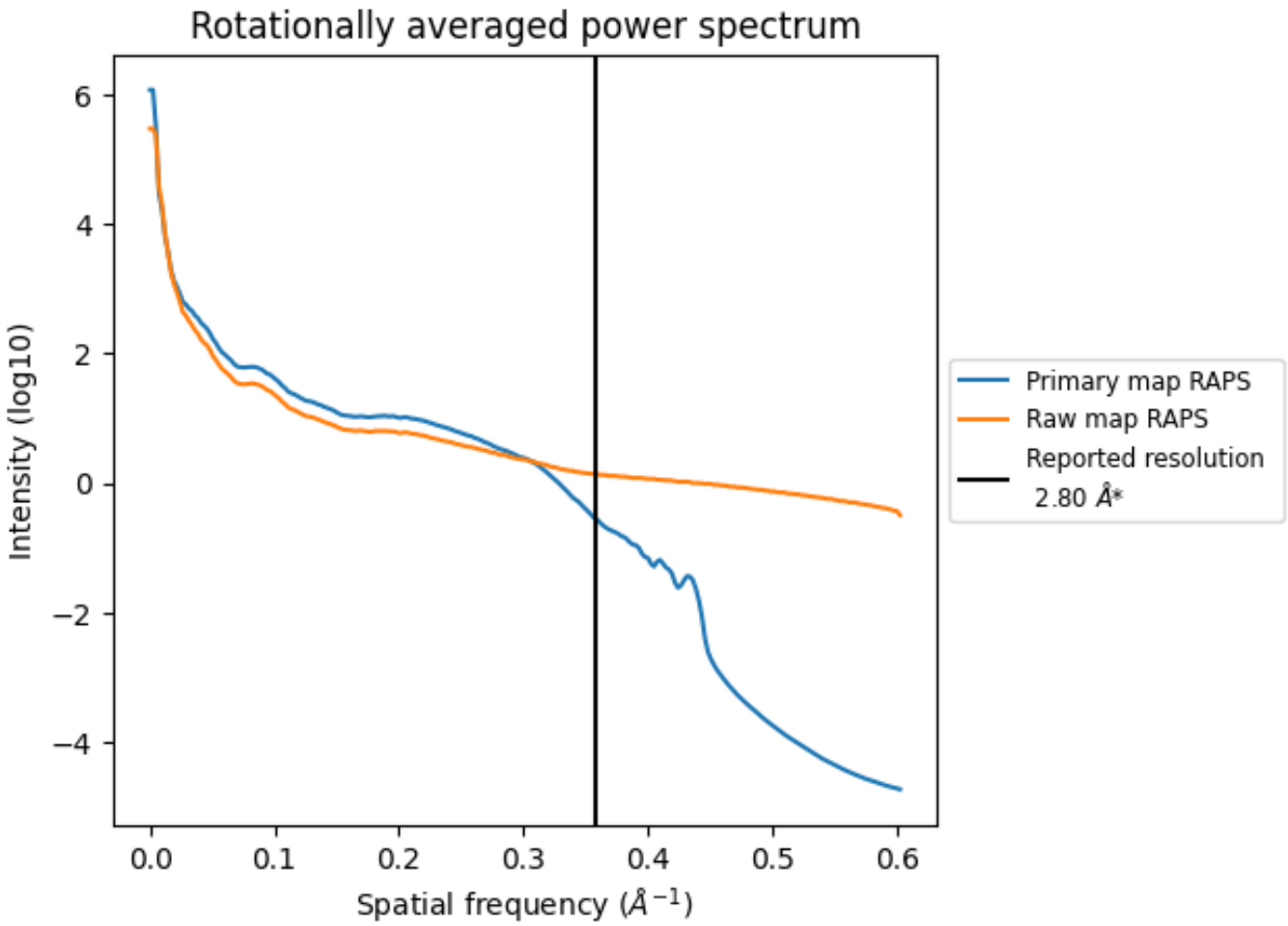
7.2 Volume estimate (i)



The volume at the recommended contour level is 3322 nm^3; this corresponds to an approximate mass of 3000 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)

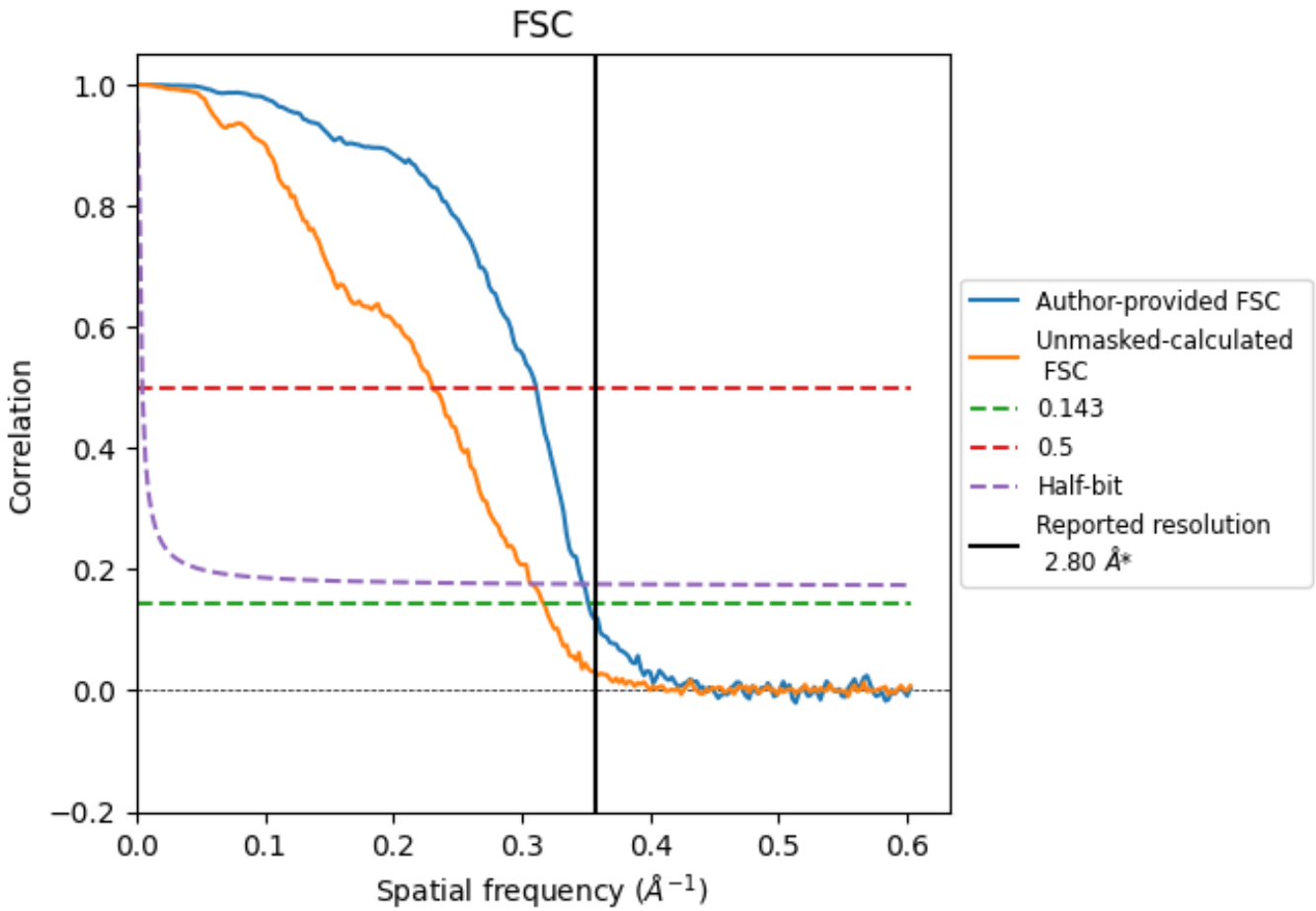


*Reported resolution corresponds to spatial frequency of 0.357 Å^{-1}

8 Fourier-Shell correlation (i)

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

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.357 Å^{-1}

8.2 Resolution estimates (i)

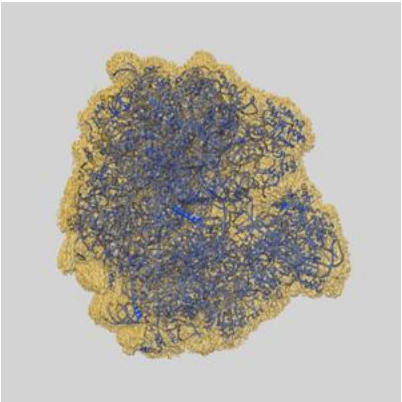
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.84	3.21	2.88
Unmasked-calculated*	3.15	4.33	3.25

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.15 differs from the reported value 2.8 by more than 10 %

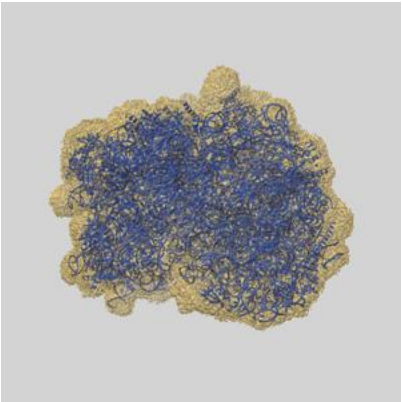
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-44919 and PDB model 9BUT. Per-residue inclusion information can be found in section 3 on page 19.

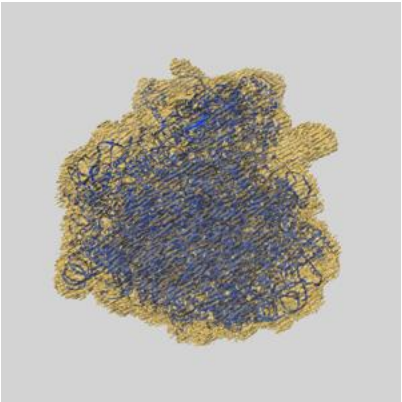
9.1 Map-model overlay (i)



X



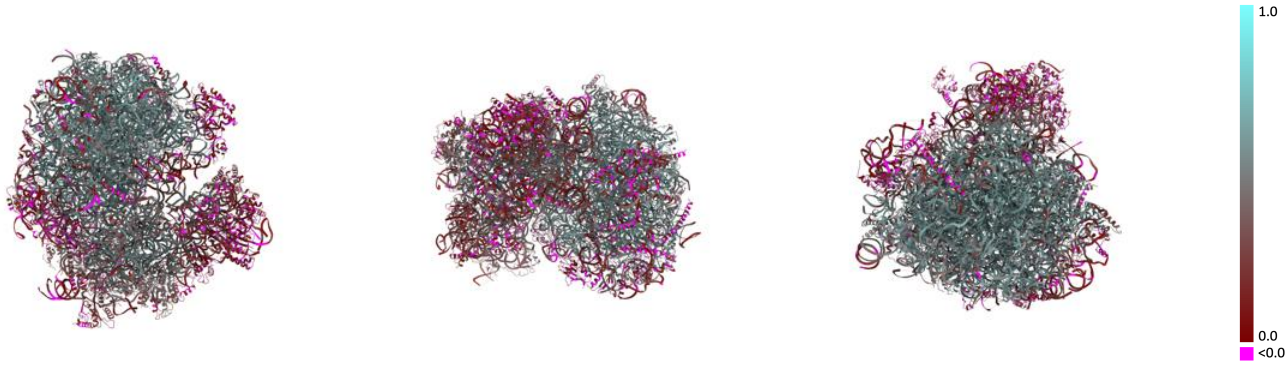
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.00277 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.

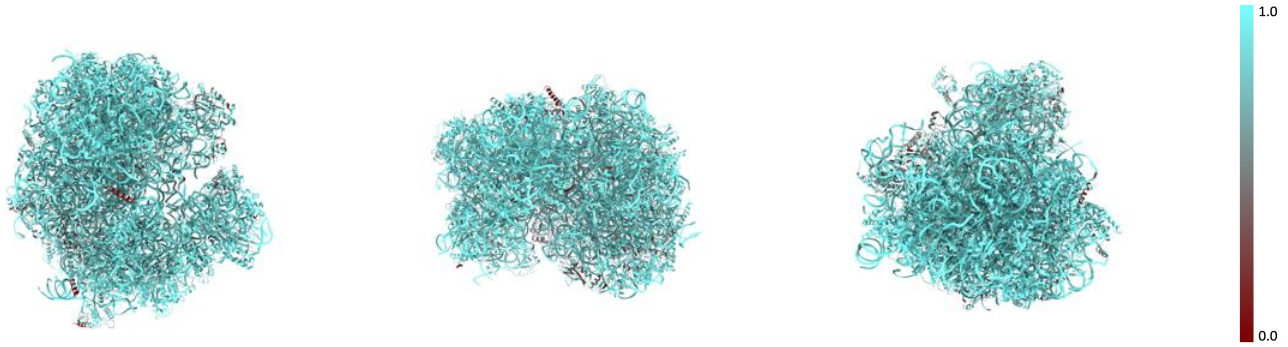
9.2 Q-score mapped to coordinate model (i)



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.

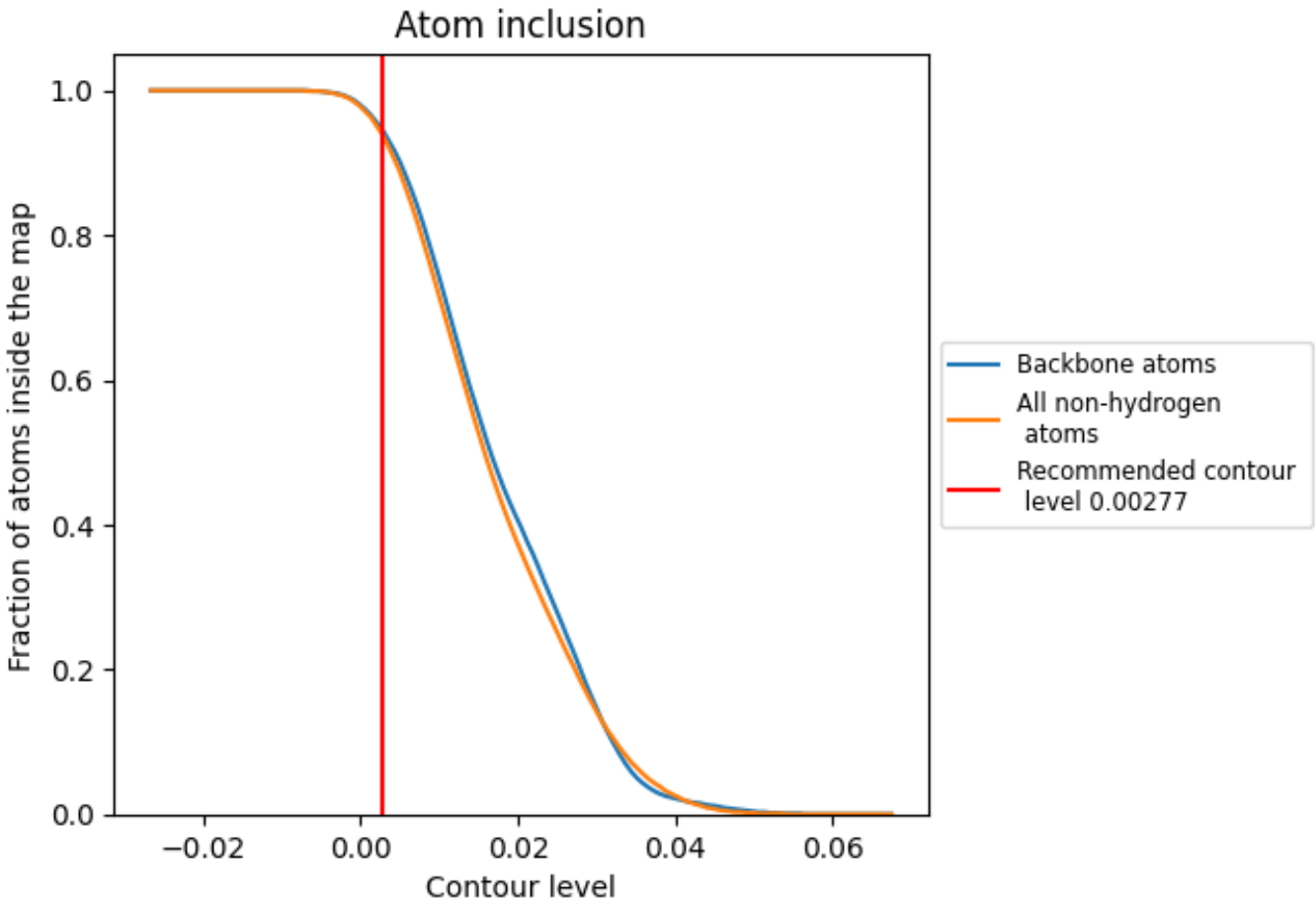
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.00277).

9.4 Atom inclusion (i)



At the recommended contour level, 95% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.00277) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9390	0.4120
A0	0.5860	0.1210
A1	0.7370	0.1510
A2	0.9630	0.5330
A3	0.8730	0.3190
A4	0.9490	0.4440
A5	0.9170	0.4390
A6	0.6920	0.1620
A7	0.9210	0.4350
A8	0.9670	0.5730
A9	0.9850	0.5930
AA	0.9690	0.4960
AB	0.9030	0.2660
AC	0.9890	0.5240
AD	0.9760	0.5890
AE	0.8760	0.4080
AF	0.9260	0.4930
AG	0.8190	0.2030
AH	0.7310	0.1770
AI	0.9840	0.5250
AJ	0.8350	0.3580
AK	0.9800	0.5670
AL	0.9640	0.5070
AM	0.8280	0.3920
AN	0.8690	0.3210
AO	0.9890	0.5910
AP	0.9870	0.5980
AQ	0.8400	0.3320
AR	0.7850	0.1750
AS	0.9840	0.5930
AT	0.6760	0.2100
AU	0.8350	0.3430
AV	0.9250	0.4680
AW	0.9870	0.5770
AX	0.6750	0.1580

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Chain	Atom inclusion	Q-score
AY	0.8690	0.3510
AZ	0.9670	0.4850
Aa	0.7860	0.3000
Ab	0.9780	0.5220
Ac	0.9800	0.5790
Ad	0.7960	0.1890
Ae	0.9810	0.5660
Af	0.7520	0.1890
Ag	0.7640	0.3090
Ah	0.8780	0.4310
Ai	0.9710	0.5700
S1	0.9320	0.1980
S2	0.5570	0.0970
S3	0.9670	0.4470
S4	0.8430	0.2350
S5	0.8100	0.1290
S6	0.8890	0.2070
S7	0.9650	0.3200
S9	0.7470	0.1840
SA	0.9860	0.3800
SB	0.9290	0.3840
SC	0.9610	0.3740
SD	0.9070	0.1930
SE	0.9190	0.2830
SF	0.9520	0.3210
SG	0.9430	0.3990
SH	0.9440	0.2720
SI	0.8600	0.1400
SJ	0.8520	0.2520
SK	0.9630	0.4680
SL	0.9370	0.3440
SM	0.8740	0.1120
SN	0.8970	0.1580
SO	0.9330	0.1380
SP	0.9600	0.4100
SQ	0.8870	0.4070
SR	0.8170	0.0640
SS	0.8890	0.2190
ST	0.8920	0.2030
SU	0.9260	0.4010
SV	0.9290	0.4170
SW	0.9010	0.1400

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Chain	Atom inclusion	Q-score
SX	0.9370	0.2260
SY	0.9230	0.1670
SZ	0.9630	0.3980
mR	0.9560	0.3810