



wwPDB EM Validation Summary Report ⓘ

Nov 7, 2024 – 04:29 pm GMT

PDB ID : 8P5D
EMDB ID : EMD-17448
Title : Spraguea lophii ribosome in the closed conformation by cryo sub tomogram averaging
Authors : Gil Diez, P.; McLaren, M.; Isupov, M.N.; Daum, B.; Conners, R.; Williams, B.
Deposited on : 2023-05-23
Resolution : 10.80 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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

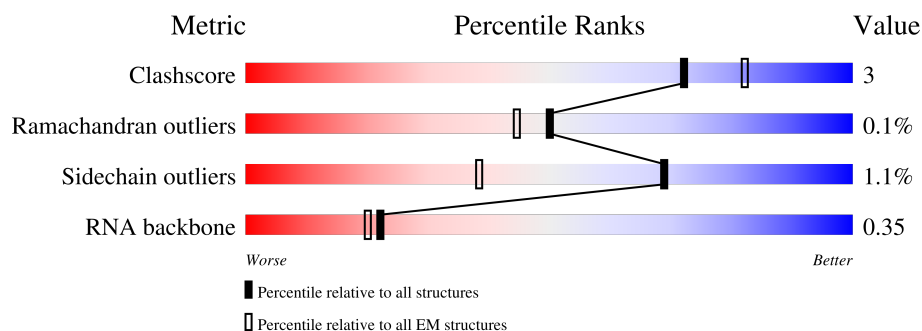
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 10.80 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)
Clashscore	210492	15764
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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	L50	2618	
2	L70	119	
3	LA0	246	
4	LAA	147	
5	LB0	392	
6	LC0	328	
7	LCC	110	

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Mol	Chain	Length	Quality of chain
8	LD0	291	
9	LDD	110	
10	LE0	171	
11	LEE	139	
12	LF0	235	
13	LFF	111	
14	LG0	206	
15	LGG	106	
16	LH0	187	
17	LHH	119	
18	LI0	218	
19	LII	98	
20	LJ0	171	
21	LJJ	92	
22	LL0	165	
23	LLL	52	
24	LM0	115	
25	LMM	127	
26	LN0	204	
27	LO0	198	
28	LOO	104	
29	LP0	167	
30	LPP	89	
31	LQ0	183	
32	LR0	168	

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Mol	Chain	Length	Quality of chain
33	LS0	171	<div> <div>43%</div> <div>96%</div> <div>..</div> </div>
34	LT0	158	<div> <div>44%</div> <div>92%</div> <div>6% ..</div> </div>
35	LU0	113	<div> <div>30%</div> <div>86%</div> <div>12%</div> </div>
36	LV0	142	<div> <div>53%</div> <div>97%</div> <div>..</div> </div>
37	LW0	131	<div> <div>50%</div> <div>67%</div> <div>10% . 22%</div> </div>
38	LX0	113	<div> <div>47%</div> <div>96%</div> <div>..</div> </div>
39	LY0	131	<div> <div>38%</div> <div>96%</div> <div>.</div> </div>
40	LZ0	153	<div> <div>47%</div> <div>76%</div> <div>. 23%</div> </div>
41	MD1	151	<div> <div>68%</div> <div>94%</div> <div>6%</div> </div>
42	S60	1368	<div> <div>44%</div> <div>37%</div> <div>15% ..</div> </div>
43	SA0	233	<div> <div>64%</div> <div>79%</div> <div>15% 6%</div> </div>
44	SAA	102	<div> <div>43%</div> <div>92%</div> <div>7% .</div> </div>
45	SB0	230	<div> <div>51%</div> <div>88%</div> <div>. 11%</div> </div>
46	SBB	82	<div> <div>48%</div> <div>94%</div> <div>..</div> </div>
47	SC0	248	<div> <div>45%</div> <div>81%</div> <div>10% 9%</div> </div>
48	SCC	65	<div> <div>82%</div> <div>82%</div> <div>14% 5%</div> </div>
49	SD0	242	<div> <div>58%</div> <div>82%</div> <div>7% 11%</div> </div>
50	SDD	65	<div> <div>40%</div> <div>86%</div> <div>14%</div> </div>
51	SE0	280	<div> <div>48%</div> <div>85%</div> <div>8% 7%</div> </div>
52	SEE	60	<div> <div>55%</div> <div>90%</div> <div>. 7%</div> </div>
53	SF0	195	<div> <div>43%</div> <div>86%</div> <div>12% ..</div> </div>
54	SFF	150	<div> <div>38%</div> <div>34%</div> <div>61%</div> </div>
55	SG0	230	<div> <div>58%</div> <div>92%</div> <div>7%</div> </div>
56	SGG	326	<div> <div>61%</div> <div>94%</div> <div>..</div> </div>
57	SH0	164	<div> <div>71%</div> <div>97%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
58	SI0	173	
59	SJ0	184	
60	SK0	107	
61	SL0	155	
62	SM0	130	
63	SN0	143	
64	SO0	135	
65	SP0	163	
66	SQ0	143	
67	SR0	120	
68	SS0	160	
69	ST0	143	
70	SU0	119	
71	SV0	67	
72	SW0	128	
73	SX0	141	
74	SY0	146	
75	SZ0	128	

2 Entry composition

There are 76 unique types of molecules in this entry. The entry contains 171817 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 RNA 28S.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L50	2499	Total	C	N	O	P	0	0
			53655	23950	9876	17330	2499		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L70	119	Total	C	N	O	P	0	0
			2542	1136	459	828	119		

- Molecule 3 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LA0	245	Total	C	N	O	S	0	0
			1889	1189	361	334	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LA0	206	ASN	THR	conflict	UNP S7W736

- Molecule 4 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LAA	147	Total	C	N	O	S	0	0
			1167	738	229	194	6		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB0	383	Total	C	N	O	S	0	0
			3039	1926	559	543	11		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC0	327	Total	C	N	O	S	0	0
			2604	1629	478	485	12		

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LCC	99	Total	C	N	O	S	0	0
			781	504	126	148	3		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LD0	281	Total	C	N	O	S	0	0
			2298	1451	410	426	11		

- Molecule 9 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LDD	109	Total	C	N	O	S	0	0
			895	575	163	154	3		

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LE0	165	Total	C	N	O	S	0	0
			1371	879	227	262	3		

- Molecule 11 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LEE	135	Total	C	N	O	S	0	0
			1090	697	205	182	6		

- Molecule 12 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LF0	231	Total	C	N	O	S	0	0
			1933	1234	342	350	7		

- Molecule 13 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LFF	111	Total	C	N	O	S	0	0
			893	567	159	162	5		

- Molecule 14 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LG0	199	Total	C	N	O	S	0	0
			1590	1015	275	290	10		

- Molecule 15 is a protein called Ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LGG	104	Total	C	N	O	S	0	0
			819	504	169	139	7		

- Molecule 16 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH0	183	Total	C	N	O	S	0	0
			1477	951	252	266	8		

- Molecule 17 is a protein called Ribosomal L29 protein (Fragment),Ribosomal L29 protein (Fragment),Ribosomal L29 protein (Fragment),Ribosomal L29 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LHH	119	Total	C	N	O	S	0	0
			992	626	188	175	3		

- Molecule 18 is a protein called S60 ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LI0	217	Total	C	N	O	S	0	0
			1750	1096	333	308	13		

- Molecule 19 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LII	97	Total	C	N	O	S	0	0
			784	496	146	136	6		

- Molecule 20 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LJ0	167	Total	C	N	O	S	0	0
			1332	847	242	236	7		

- Molecule 21 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LJJ	89	Total	C	N	O	S	0	0
			701	427	146	118	10		

- Molecule 22 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LL0	164	Total	C	N	O	S	0	0
			1353	857	252	232	12		

- Molecule 23 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LLL	51	Total	C	N	O	S	0	0
			427	272	87	65	3		

- Molecule 24 is a protein called Transposase.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LM0	115	Total	C	N	O	S	0	0
			927	588	151	183	5		

- Molecule 25 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LMM	52	Total	C	N	O	S	0	0
			427	264	89	70	4		

- Molecule 26 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LN0	203	Total	C	N	O	S	0	0
			1688	1055	346	276	11		

- Molecule 27 is a protein called Ribosomal protein L13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LO0	198	Total	C	N	O	S	0	0
			1598	1018	286	280	14		

- Molecule 28 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LOO	100	Total	C	N	O	S	0	0
			801	504	163	130	4		

- Molecule 29 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LP0	154	Total	C	N	O	S	0	0
			1238	794	225	213	6		

- Molecule 30 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LPP	87	Total	C	N	O	S	0	0
			684	427	131	116	10		

- Molecule 31 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LQ0	182	Total	C	N	O	S	0	0
			1491	950	270	266	5		

- Molecule 32 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LR0	164	Total	C	N	O	S	0	0
			1336	832	261	236	7		

- Molecule 33 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LS0	170	Total	C	N	O	S	0	0
			1400	898	241	256	5		

- Molecule 34 is a protein called 60s ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LT0	156	Total	C	N	O	S	0	0
			1270	808	233	224	5		

- Molecule 35 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LU0	100	Total	C	N	O	S	0	0
			810	526	135	147	2		

- Molecule 36 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LV0	141	Total	C	N	O	S	0	0
			1057	663	200	189	5		

- Molecule 37 is a protein called Ribosomal protein L24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LW0	102	Total	C	N	O	S	0	0
			832	539	143	147	3		

- Molecule 38 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LX0	112	Total	C	N	O	S	0	0
			874	562	156	155	1		

- Molecule 39 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LY0	131	Total	C	N	O	S	0	0
			1048	658	197	186	7		

- Molecule 40 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LZ0	118	Total	C	N	O	S	0	0
			963	618	172	169	4		

- Molecule 41 is a protein called DNL-type domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	MD1	151	Total	C	N	O	S	0	0
			1229	776	201	241	11		

- Molecule 42 is a RNA chain called RNA 16S.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	S60	1354	Total	C	N	O	P	0	0
			29181	13024	5463	9340	1354		

- Molecule 43 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SA0	220	Total	C	N	O	S	0	0
			1725	1091	292	328	14		

- Molecule 44 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SAA	101	Total	C	N	O	S	0	0
			827	513	163	145	6		

- Molecule 45 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SB0	204	Total	C	N	O	S	0	0
			1609	1018	286	298	7		

- Molecule 46 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SBB	81	Total	C	N	O	S	0	0
			627	394	108	116	9		

- Molecule 47 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SC0	226	Total	C	N	O	S	0	0
			1727	1099	300	321	7		

- Molecule 48 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SCC	62	Total	C	N	O	S	0	0
			476	295	86	91	4		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SD0	216	Total	C	N	O	S	0	0
			1700	1085	300	307	8		

- Molecule 50 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SDD	65	Total	C	N	O	S	0	0
			550	345	102	96	7		

- Molecule 51 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SE0	260	Total	C	N	O	S	0	0
			2044	1297	361	379	7		

- Molecule 52 is a protein called eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	SEE	56	Total	C	N	O	0	0
			447	284	89	74		

- Molecule 53 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SF0	192	Total	C	N	O	S	0	0
			1509	953	275	275	6		

- Molecule 54 is a protein called Ubiquitin/40s ribosomal protein S27a fusion.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SFF	58	Total	C	N	O	S	0	0
			422	261	77	79	5		

- Molecule 55 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SG0	229	Total	C	N	O	S	0	0
			1836	1179	325	328	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SG0	171	ALA	GLY	conflict	UNP S7WDE5
SG0	173	GLY	ASP	conflict	UNP S7WDE5

- Molecule 56 is a protein called Guanine nucleotide binding protein beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SGG	319	Total	C	N	O	S	0	0
			2478	1558	411	494	15		

- Molecule 57 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SH0	163	Total	C	N	O	S	0	0
			1335	855	219	255	6		

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SI0	167	Total	C	N	O	S	0	0
			1347	834	266	240	7		

- Molecule 59 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SJ0	168	Total	C	N	O	S	0	0
			1379	880	252	243	4		

- Molecule 60 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SK0	88	Total	C	N	O	S	0	0
			737	472	127	135	3		

- Molecule 61 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SL0	150	Total	C	N	O	S	0	0
			1229	790	217	216	6		

- Molecule 62 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SM0	113	Total	C	N	O	S	0	0
			876	553	156	162	5		

- Molecule 63 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SN0	142	Total	C	N	O	S	0	0
			1130	728	196	202	4		

- Molecule 64 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SO0	129	Total	C	N	O	S	0	0
			983	606	191	183	3		

- Molecule 65 is a protein called Ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SP0	117	Total	C	N	O	S	0	0
			950	598	172	173	7		

- Molecule 66 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SQ0	142	Total	C	N	O	S	0	0
			1143	726	204	207	6		

- Molecule 67 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SR0	119	Total	C	N	O	S	0	0
			974	613	172	186	3		

- Molecule 68 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SS0	144	Total	C	N	O	S	0	0
			1150	720	220	207	3		

- Molecule 69 is a protein called 40S Ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	ST0	142	Total	C	N	O	S	0	0
			1161	741	208	211	1		

- Molecule 70 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SU0	100	Total	C	N	O	S	0	0
			809	515	144	143	7		

- Molecule 71 is a protein called Ribosomal protein S21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SV0	65	Total	C	N	O	S	0	0
			521	319	96	101	5		

- Molecule 72 is a protein called 40S ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SW0	128	Total	C	N	O	S	0	0
			1022	639	195	180	8		

- Molecule 73 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SX0	140	Total	C	N	O	S	0	0
			1098	692	216	186	4		

- Molecule 74 is a protein called 40s ribosomal protein s24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SY0	136	Total	C	N	O	S	0	0
			1118	693	215	204	6		

- Molecule 75 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SZ0	76	Total	C	N	O	S	0	0
			633	403	116	113	1		

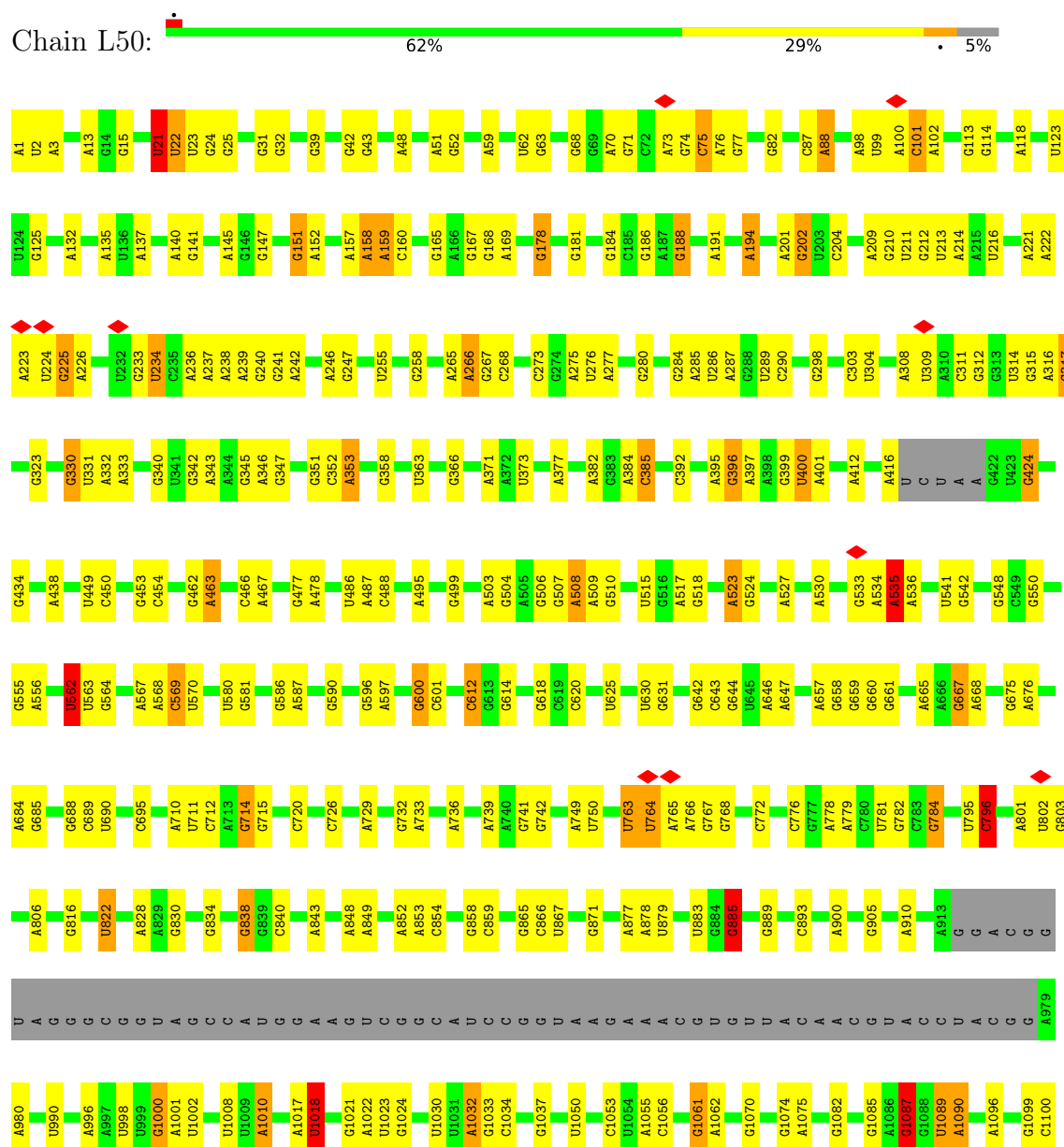
- Molecule 76 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
76	LGG	1	Total	Zn	0
			1	1	
76	LJJ	1	Total	Zn	0
			1	1	
76	LMM	1	Total	Zn	0
			1	1	
76	LOO	1	Total	Zn	0
			1	1	
76	LPP	1	Total	Zn	0
			1	1	
76	SAA	1	Total	Zn	0
			1	1	
76	SBB	1	Total	Zn	0
			1	1	
76	SDD	1	Total	Zn	0
			1	1	
76	SFF	1	Total	Zn	0
			1	1	

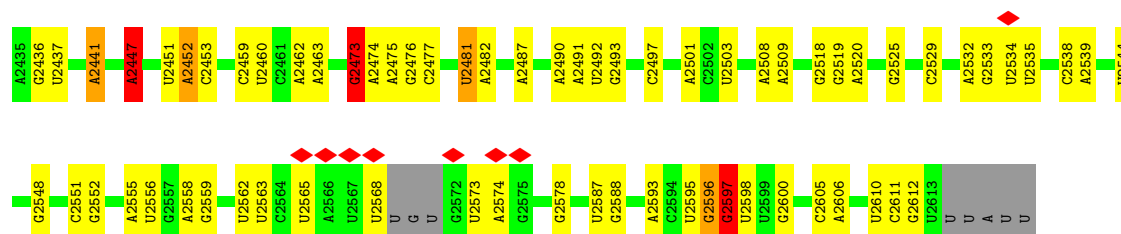
3 Residue-property plots

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.

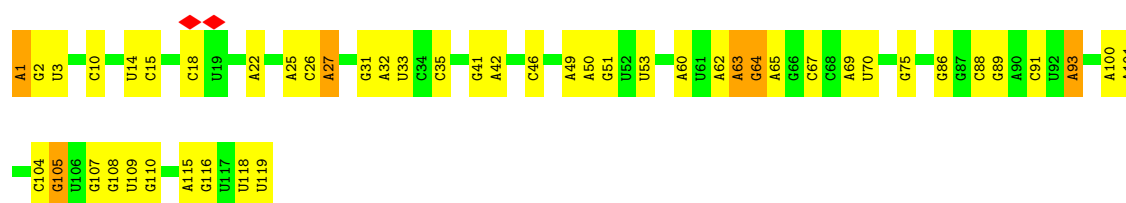
• Molecule 1: RNA 28S



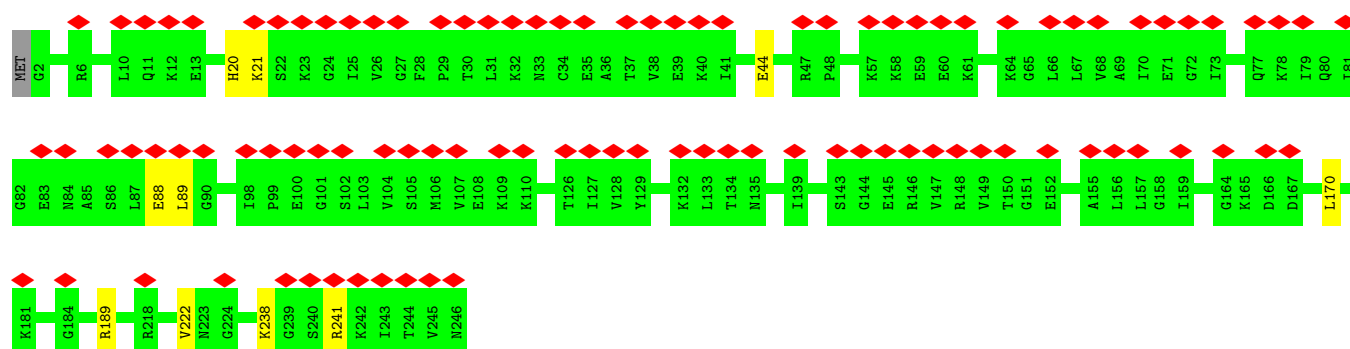
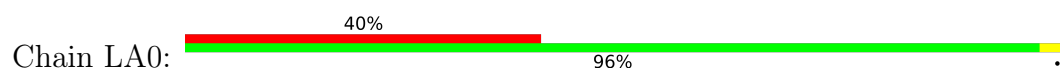
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G2212	A2213	C2217	G2221	G2224	G2225	G2226	G2227	G2228	G2229	U2234	C2235	G2239	G2240	G2241	U2243	U2244	U2245	U2246	U2247	U2253	U2254	A2255	G2256	C2257	G2260	G2261	C2262	G2266	G2267	G2272	G2275	A2279	G2286	U2291	U2292	C2293	C2296	C2303	A2304	G2305	G2306	A2309	C2310	G2313	A2314				
U2108	G2109	A2110	G2111	G2114	A2115	A2116	A2117	G2122	G2123	C2124	G2130	A2131	A2136	A2140	U2141	A2142	A2145	G2146	A2147	G2148	A2149	C2150	U2151	U2152	G2153	U2154	G2160	G2161	G2162	U2163	G2164	A2167	G2168	A2169	A2170	A2171	C2177	C2178	A2181	G2184	A2185	C2189	G2198	A2211					
U2020	C2021	G2022	A2023	G2026	A2027	G2030	U2031	A2032	A2036	C2037	G2038	G2039	A2042	G2043	A2044	G2046	A2047	G2048	A2049	G2050	C2051	A2052	C2053	U2054	U2057	G2058	U2059	A2060	C2061	A2062	G2063	A2064	G2065	U2066	A2067	U2073	A2074	A2075	A2076	G2077	A2078	G2085	A2086	G2087	G2093	C2096	U2097	A2098	C2099
U	G1930	C1931	G1932	C1933	C1934	A1935	U1936	G1937	A1938	U1939	C1940	A1941	U1942	C1943	A1944	C1945	G1946	A1949	C1950	G1955	U1956	U1957	U1958	A1959	A1960	G1961	G1962	A1963	A1966	A1967	G1968	G1973	G1977	G1978	G1985	U1991	G1995	U1996	A1997	A2007	A2008	U2009	C2010	A2011	G2012	A2013	A2014	C2015	
A1869	G1870	U1871	U1872	G1873	U1874	G1875	A1876	C1877	G1878	U1879	U1880	U1881	G1882	A1883	G1884	G1885	G1886	G1887	A1888	U	G	U	A	C	C	G	A	U	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	C				
U1734	G1735	G1738	A1739	C1742	G1743	U1746	A1749	U1750	G1751	U1755	A1760	U1770	G1771	U1772	A1783	A1797	U1798	U1799	A1800	C1801	A1808	A1809	C1810	G1811	C1820	G1821	G1822	G1828	A1832	A1833	A1834	G1835	A1836	A1837	G1838	A1839	U1846	A1854	U1868	A1869	G1860	A1868							
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A1192	A1193	G1194	G1196	A1213	A1217	A1218	A1221	A1224	U1231	A1233	A1234	U1235	A1236	U1237	G1243	G1247	C1250	U1251	G1252	U1253	C1254	G1255	U1256	A1257	G1264	G1265	U1266	G1267	U1268	U1270	C1274	U1275	U1276	G1277	U1278	C1282	A1283	C1284	C1286	A1287	A1289	A1299	G1303						
A1101	G1102	C1105	G1111	G1115	U1116	A1117	G1118	G1119	G1120	A1121	U1122	A1124	C1130	U1131	U1132	C1133	A1134	G1135	C1136	A1142	G1143	A1144	A1148	G1149	G1150	A1151	G1155	G1160	U1163	C1164	U1165	C1169	A1170	U1171	A1172	A1173	G1174	A1175	G1177	G1181	A1182	G1183	U1189	G1190	U1191				



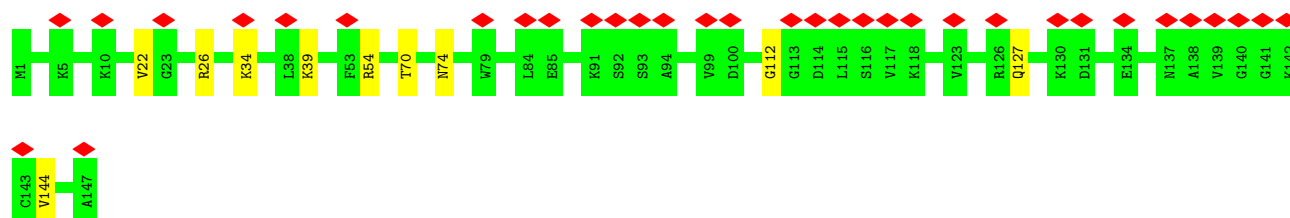
• Molecule 2: RNA 5S



• Molecule 3: 60S ribosomal protein L8

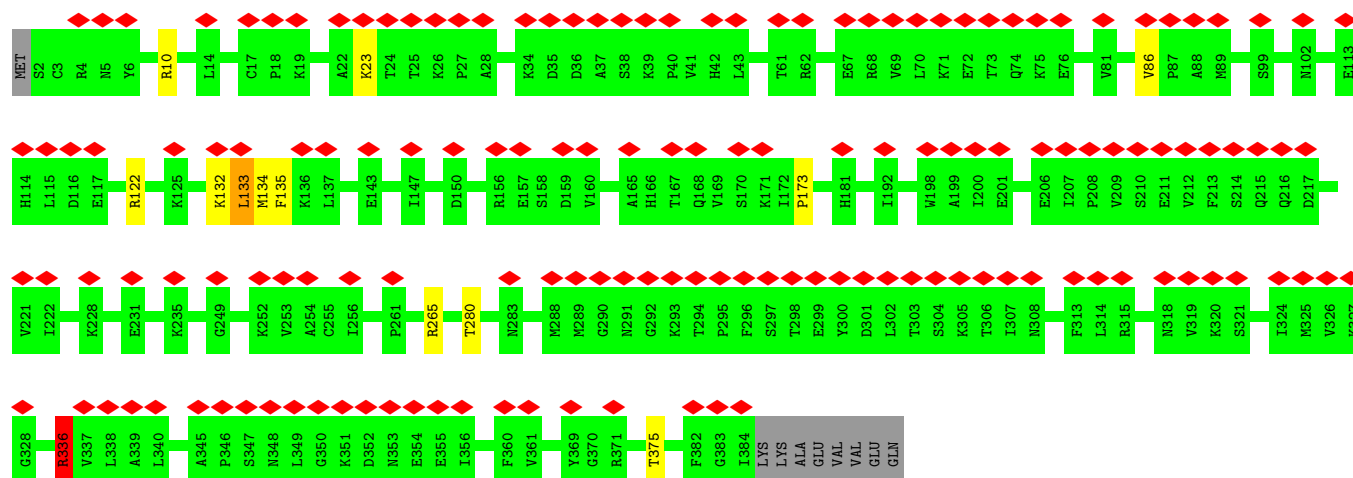


• Molecule 4: uL15

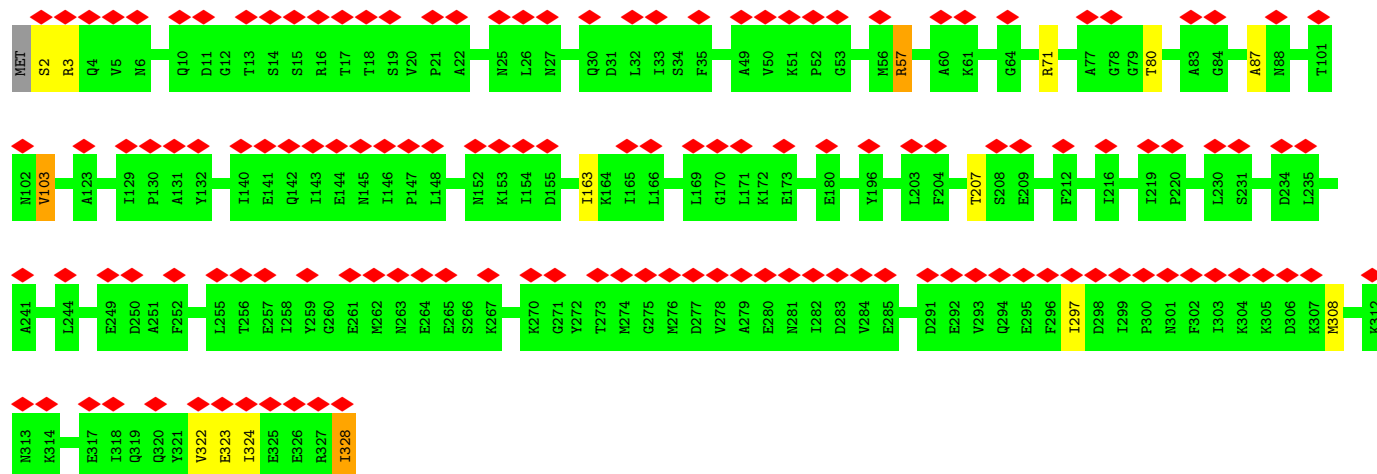
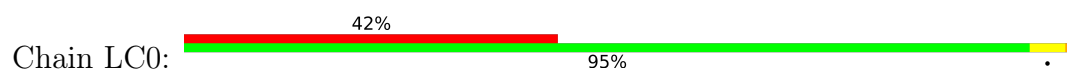


• Molecule 5: 60S ribosomal protein L3

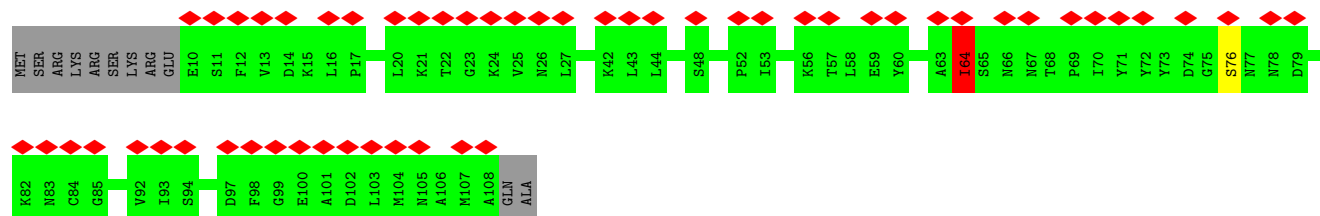
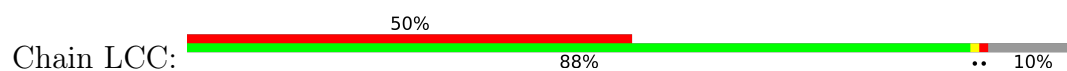




• Molecule 6: 60S ribosomal protein L4

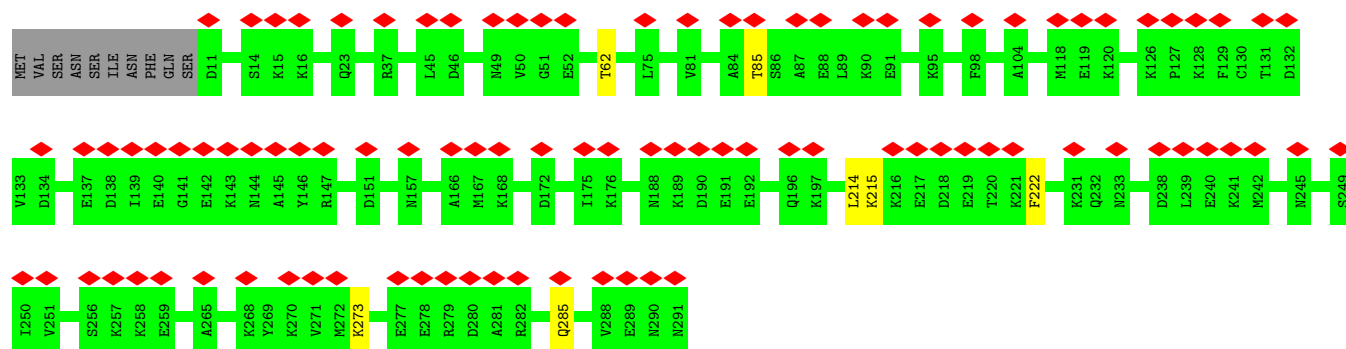


• Molecule 7: 60S ribosomal protein L3

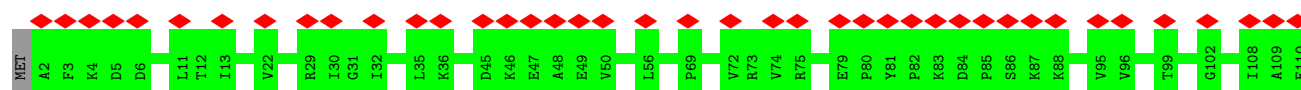


• Molecule 8: 60S ribosomal protein L5

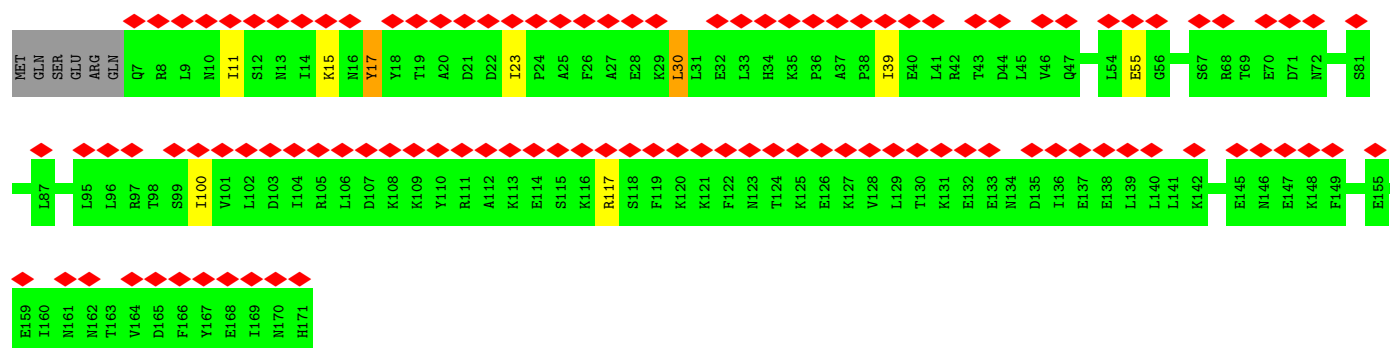




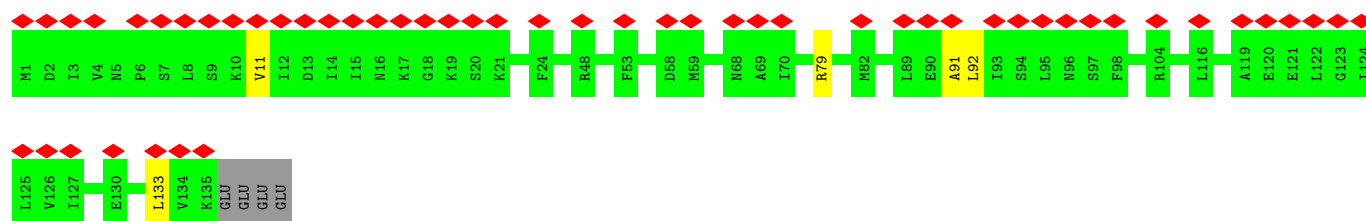
- Molecule 9: 60S ribosomal protein L31



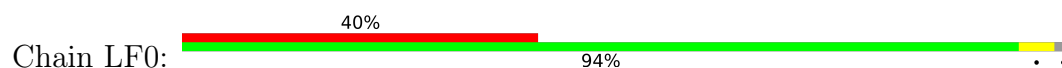
- Molecule 10: 60S ribosomal protein L6

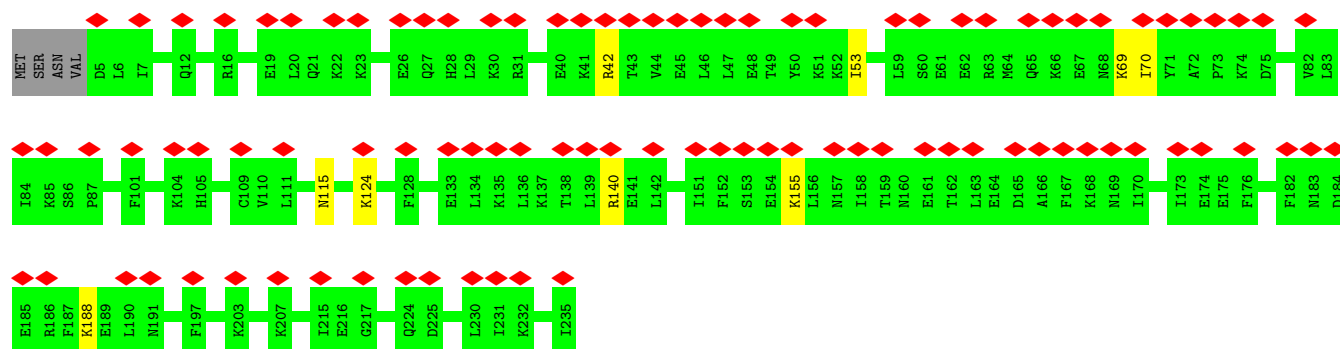


- Molecule 11: 60S ribosomal protein L32

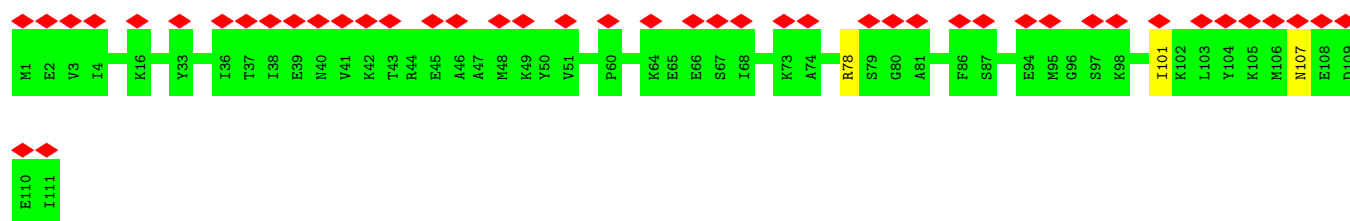
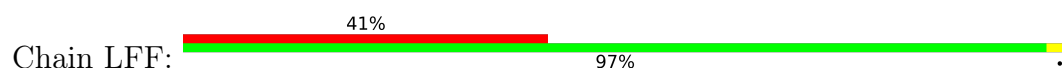


- Molecule 12: 60S ribosomal protein L7

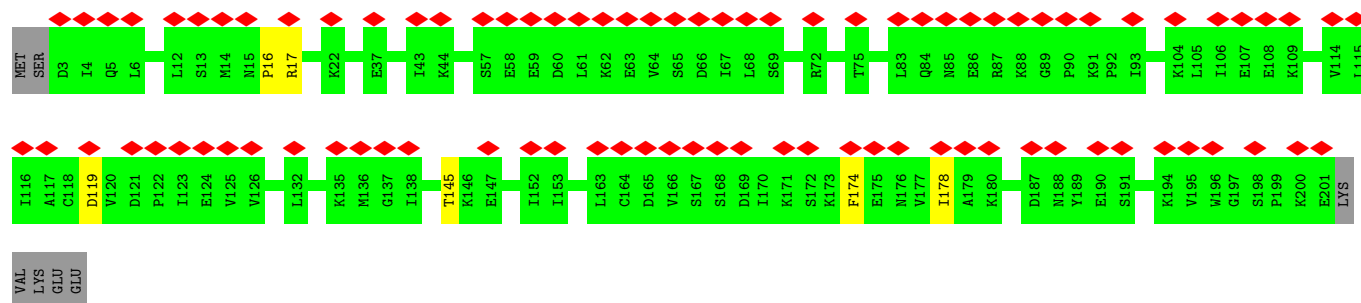




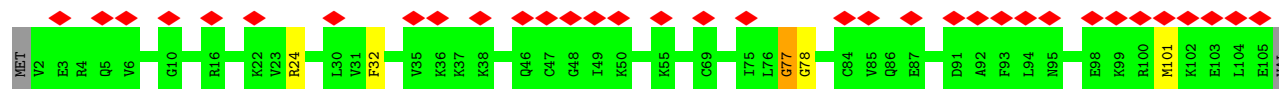
- Molecule 13: 60S ribosomal protein L35a



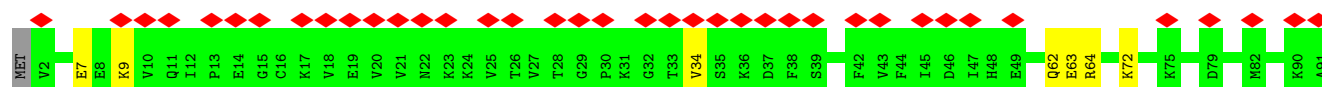
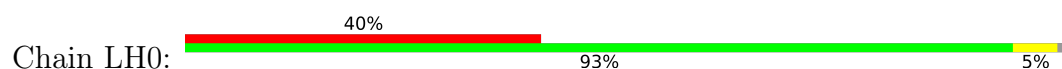
- Molecule 14: 60S ribosomal protein L8

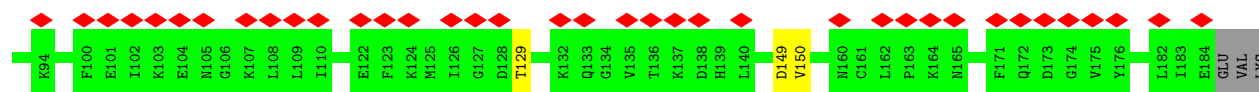


- Molecule 15: Ribosomal protein L34

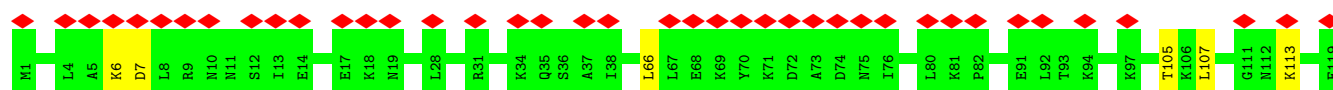


- Molecule 16: 60S ribosomal protein L9

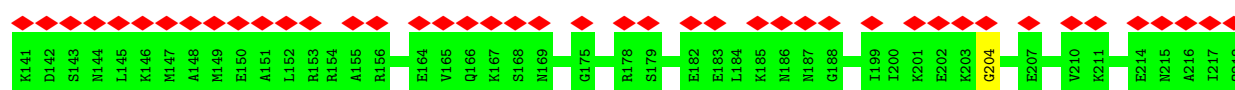
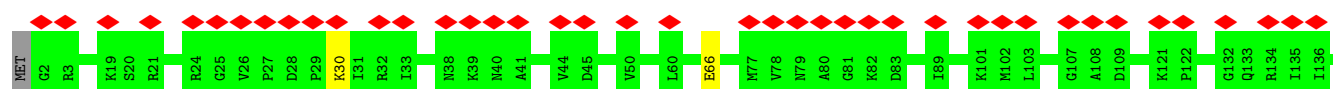




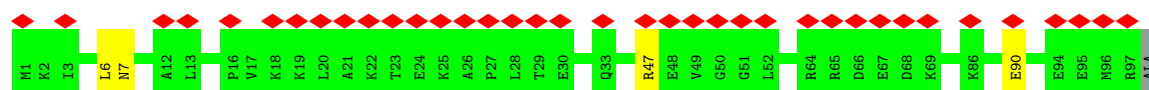
- Molecule 17: Ribosomal L29 protein (Fragment), Ribosomal L29 protein (Fragment), Ribosomal L29 protein (Fragment), Ribosomal L29 protein



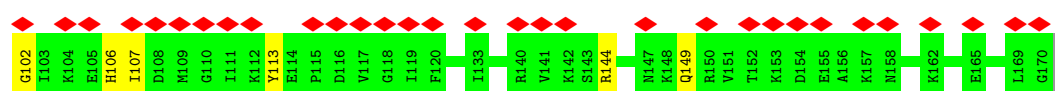
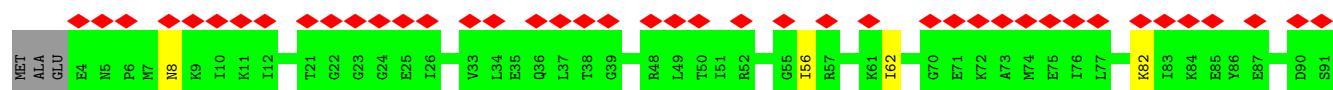
- Molecule 18: S60 ribosomal protein L10



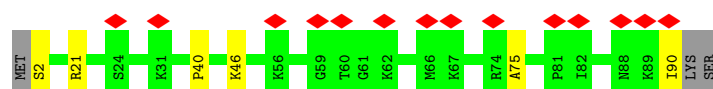
- Molecule 19: 60S ribosomal protein L36



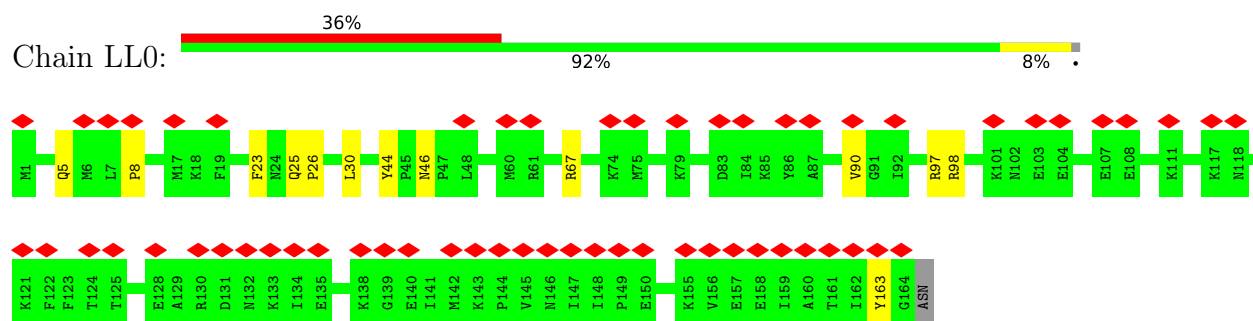
- Molecule 20: 60S ribosomal protein L11



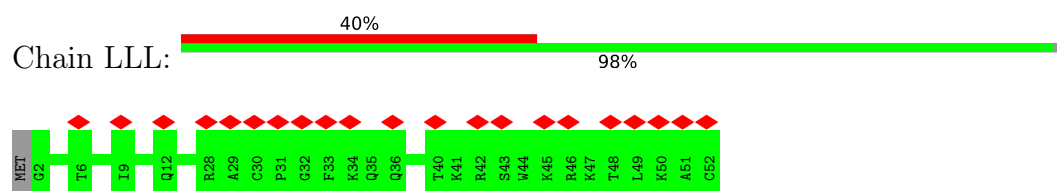
- Molecule 21: eL37



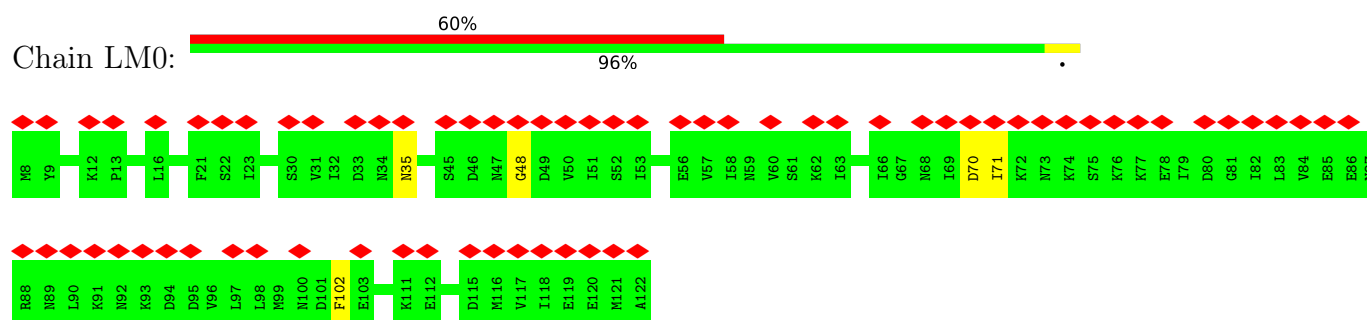
- Molecule 22: 60S ribosomal protein L13



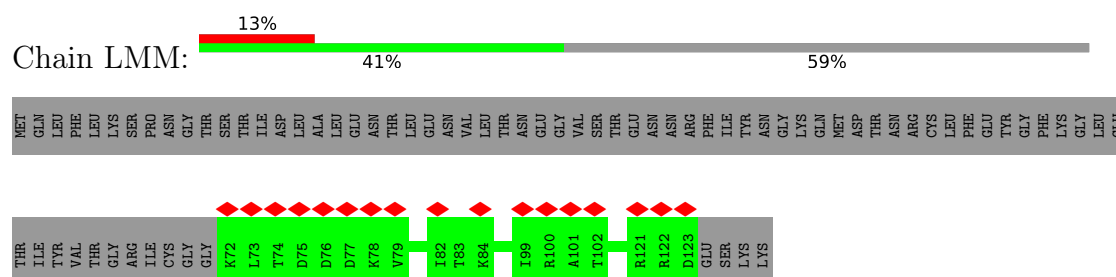
- Molecule 23: 60S ribosomal protein L39



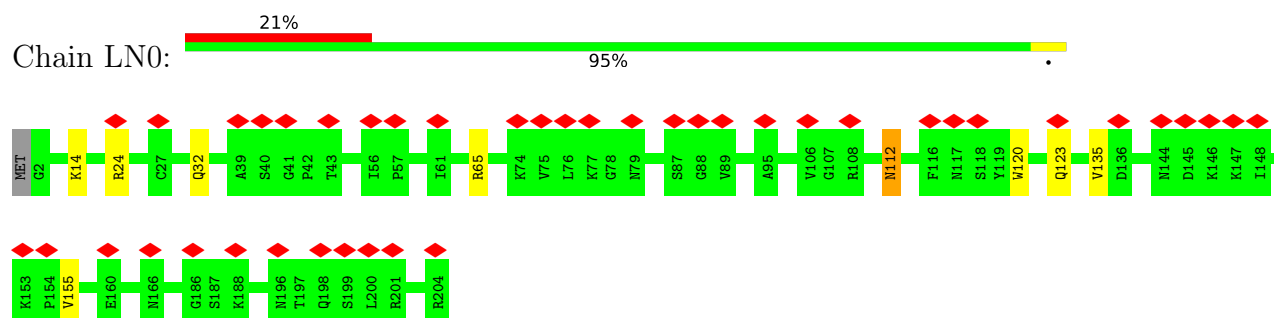
- Molecule 24: Transposase



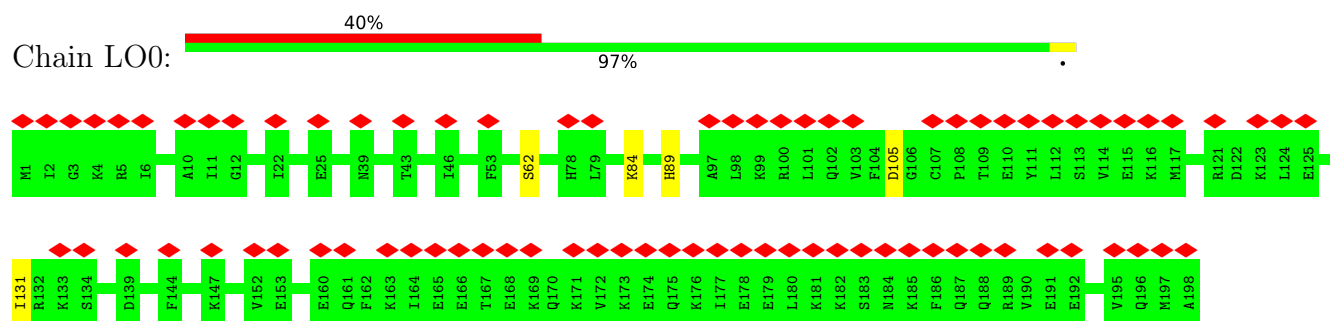
- Molecule 25: Ubiquitin



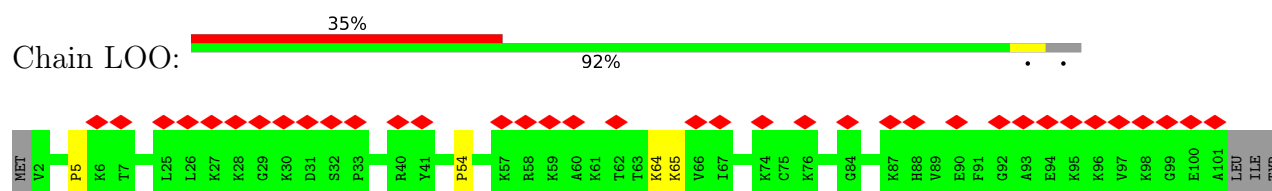
- Molecule 26: Ribosomal protein L15



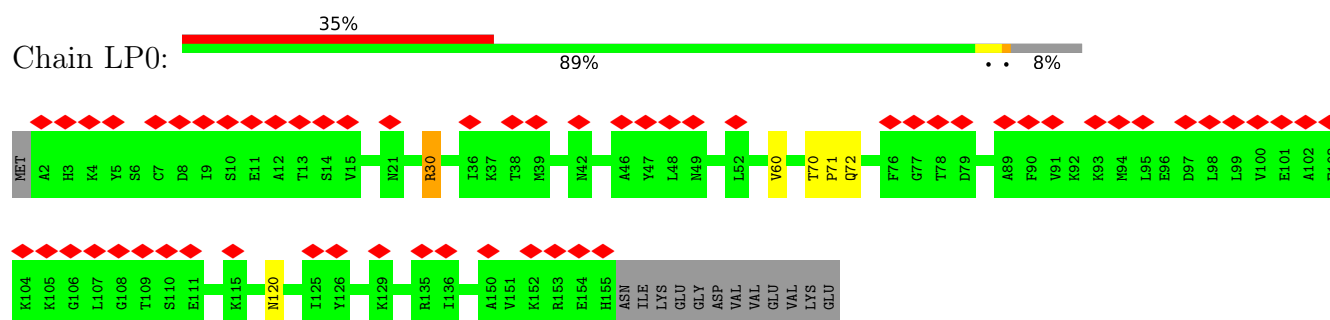
- Molecule 27: Ribosomal protein L13A



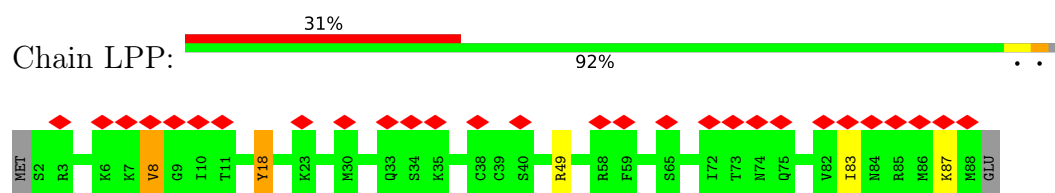
- Molecule 28: 60S ribosomal protein L44



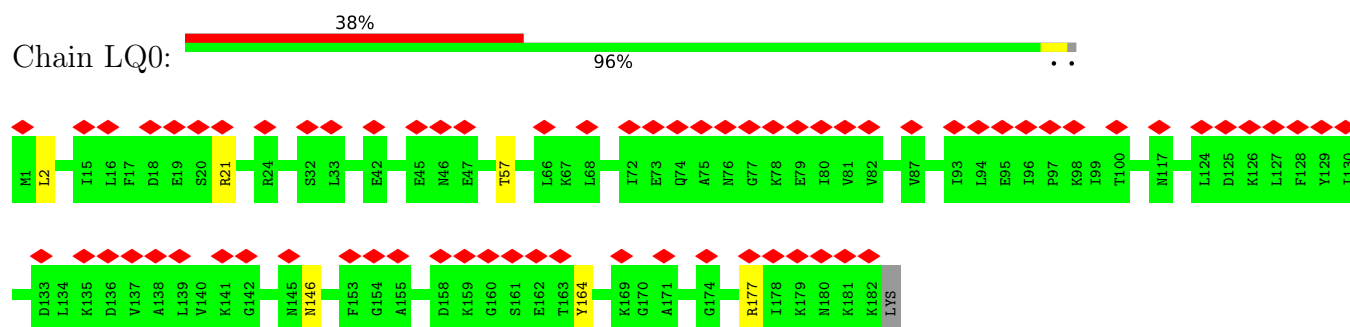
- Molecule 29: 60S ribosomal protein L17



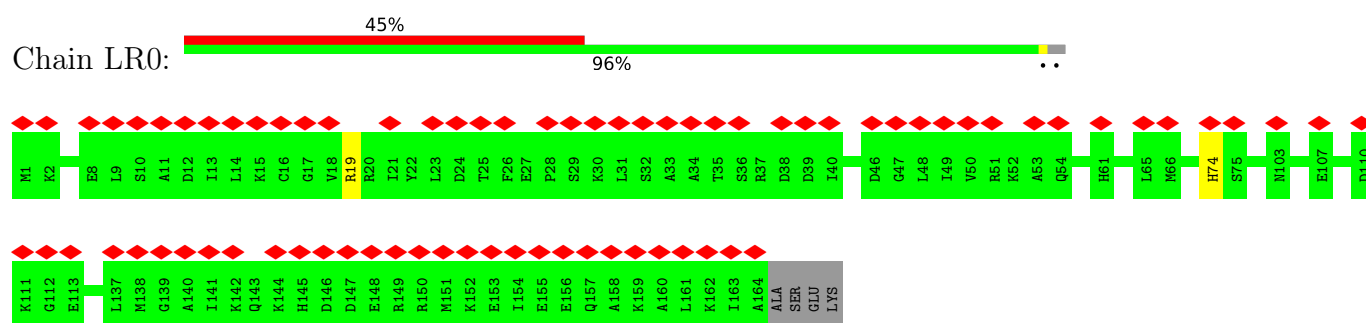
- Molecule 30: 60S ribosomal protein L37a



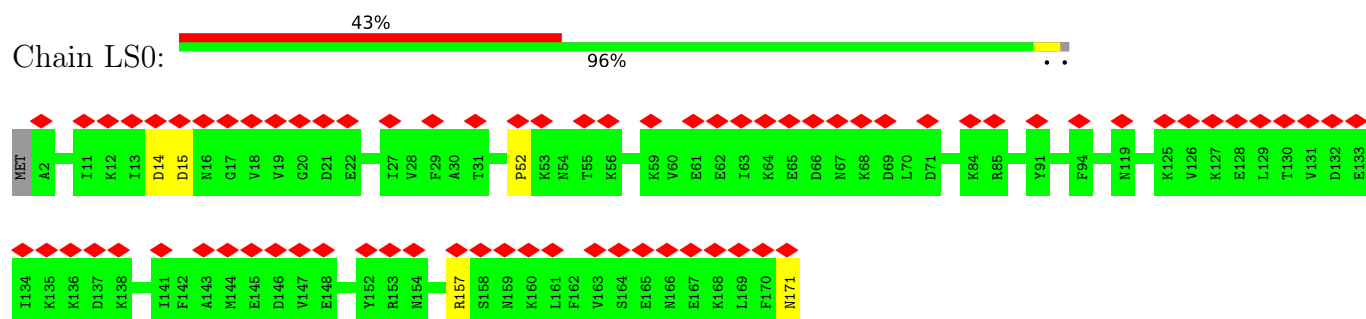
- Molecule 31: 60S ribosomal protein L18



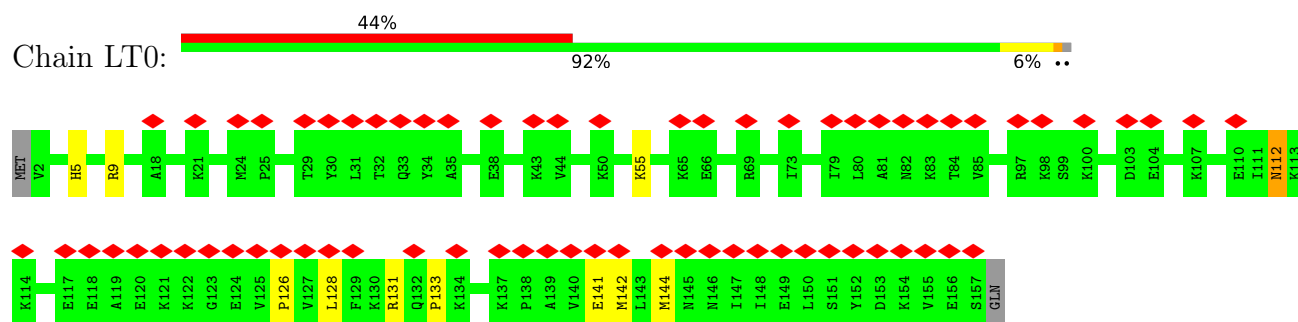
- Molecule 32: 60S ribosomal protein L19



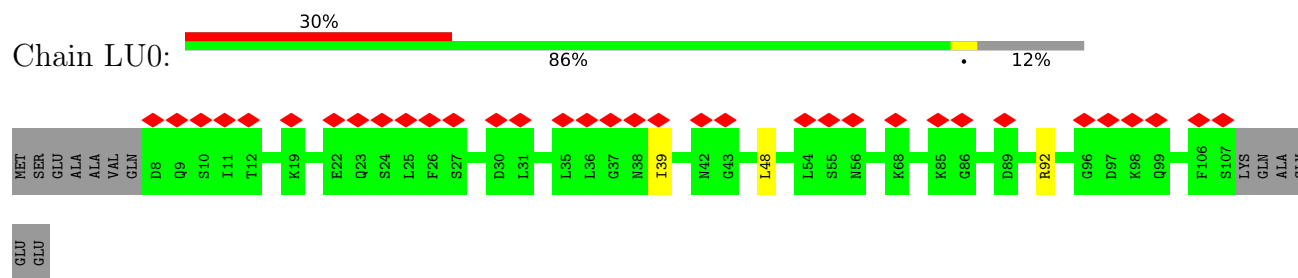
- Molecule 33: 60S ribosomal protein L20



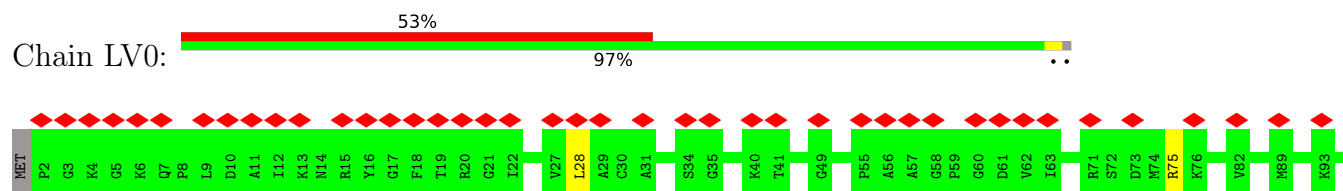
- Molecule 34: 60s ribosomal protein L21

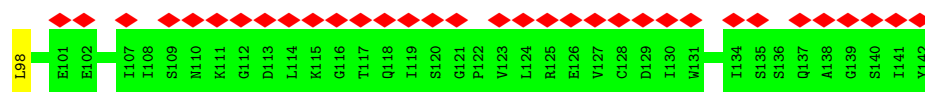


- Molecule 35: 60S ribosomal protein L22

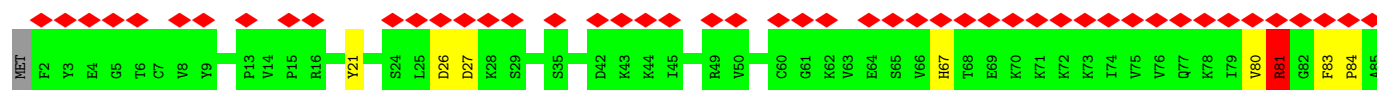
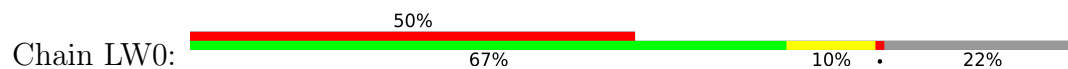


- Molecule 36: Ribosomal protein L23

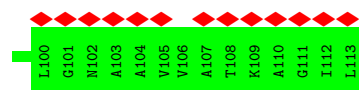
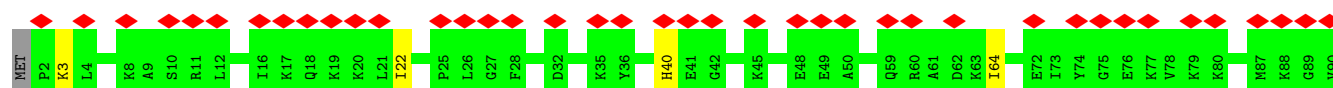




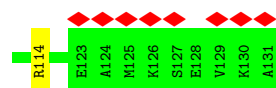
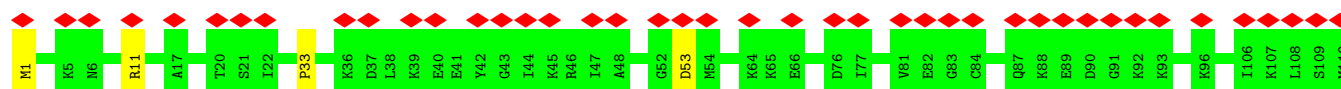
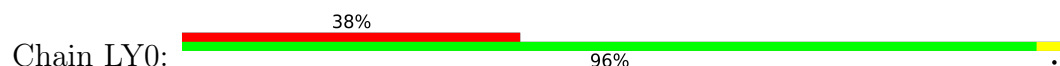
• Molecule 37: Ribosomal protein L24E



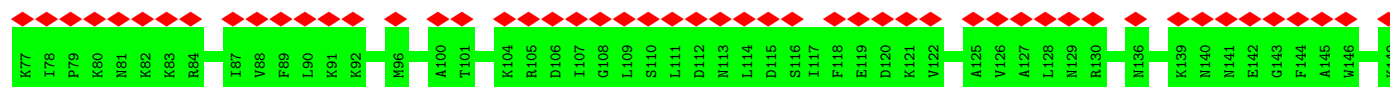
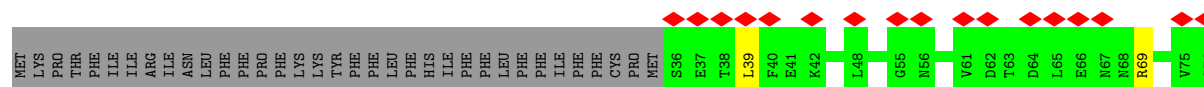
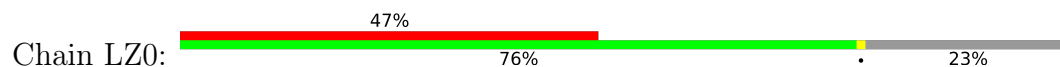
• Molecule 38: 60S ribosomal protein L23a

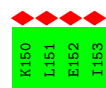


• Molecule 39: 60S ribosomal protein L26

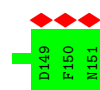
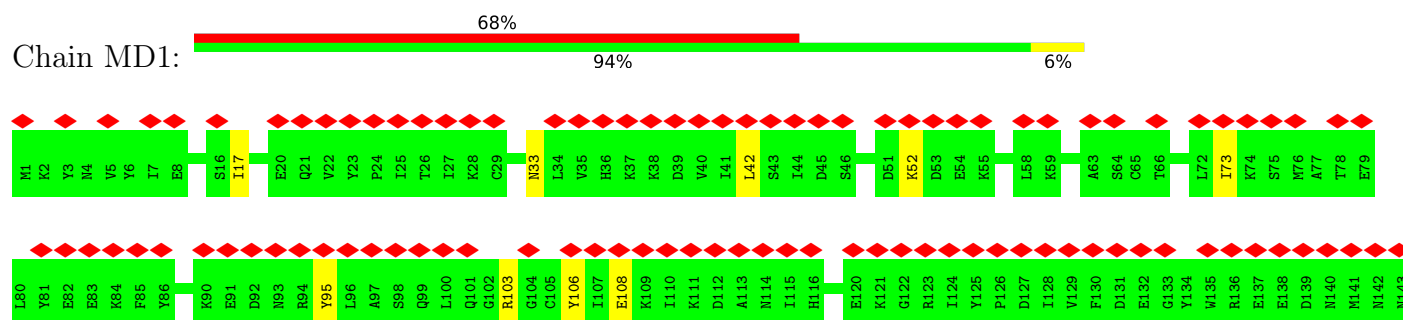


• Molecule 40: 60S ribosomal protein L27



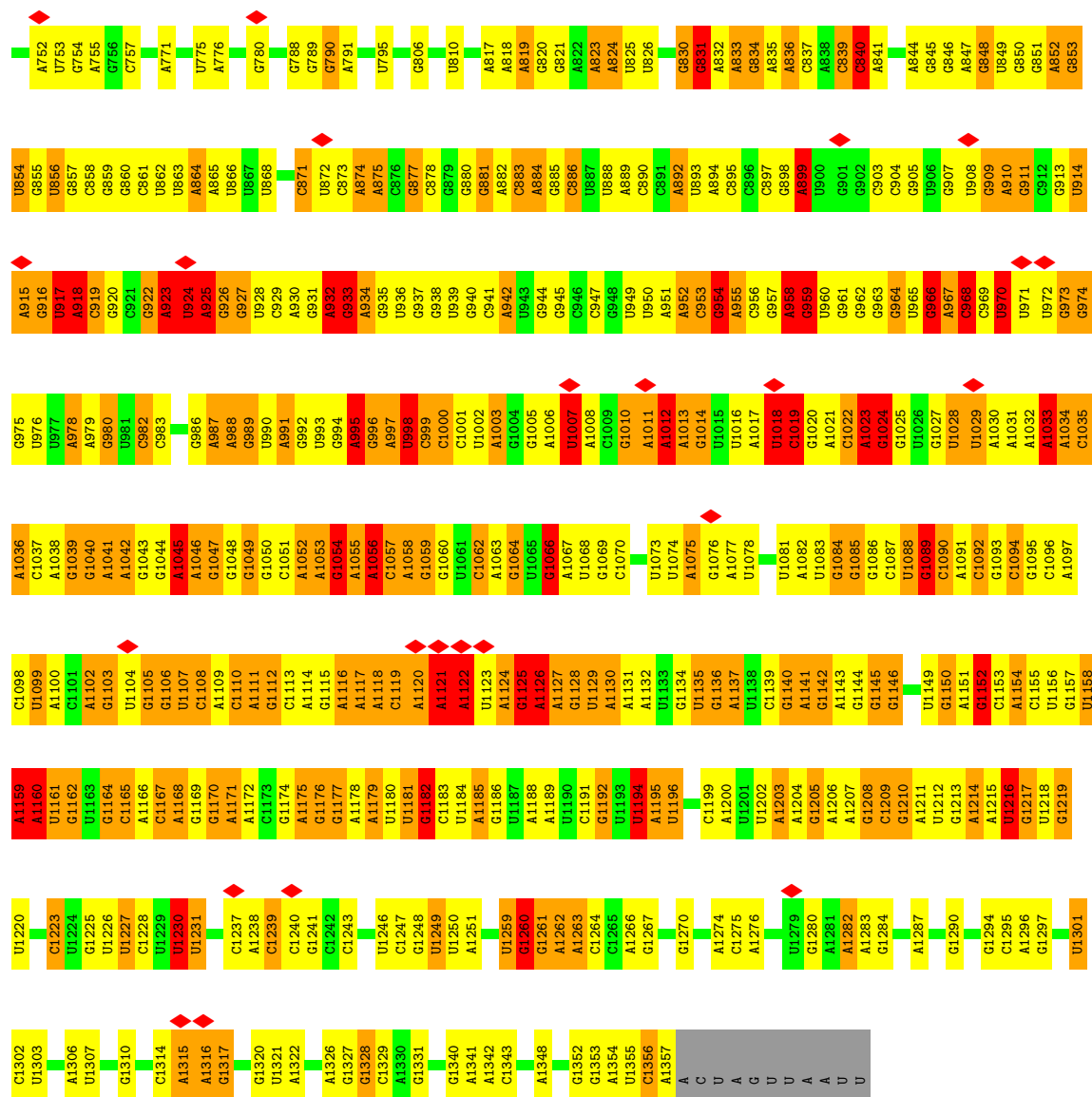


- Molecule 41: DNL-type domain-containing protein

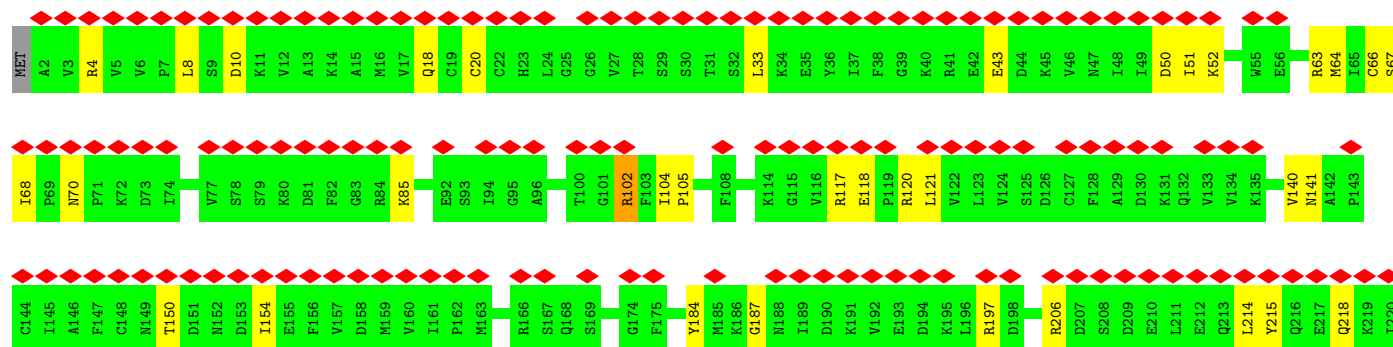
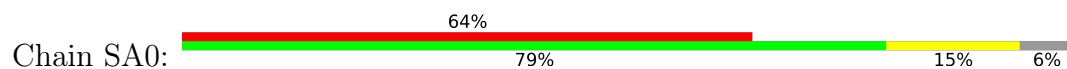


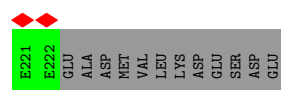
- Molecule 42: RNA 16S



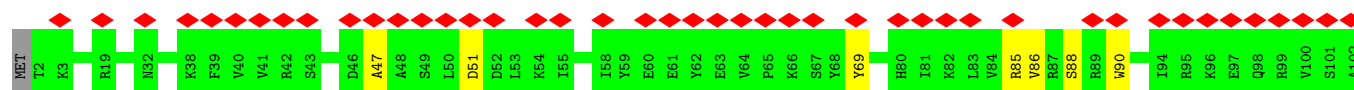


• Molecule 43: 40S ribosomal protein S0

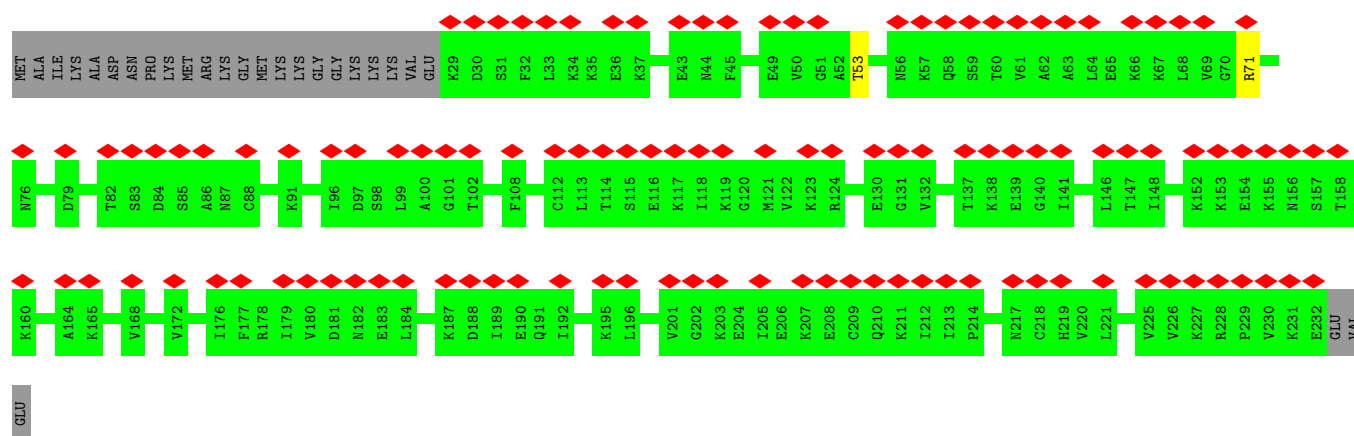




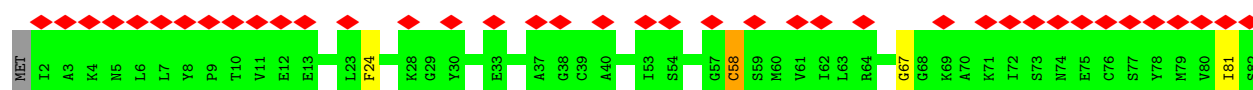
- Molecule 44: 40S ribosomal protein S26



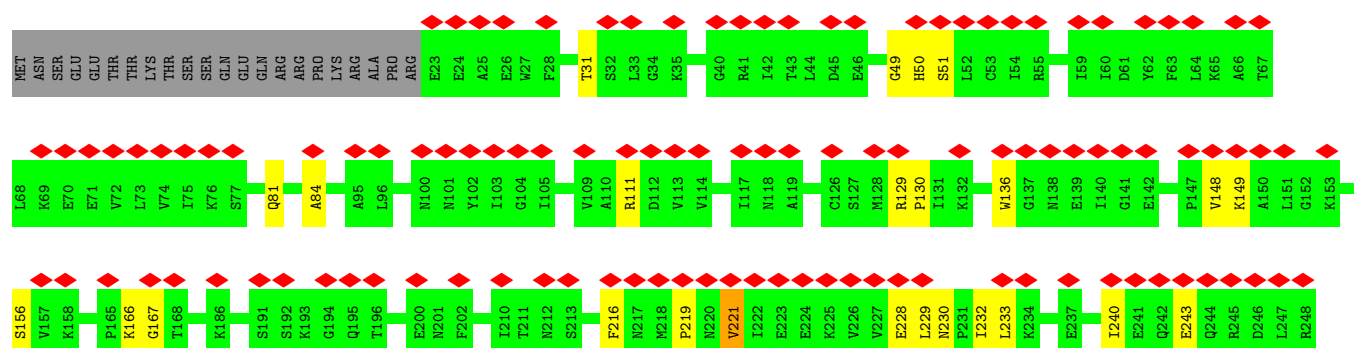
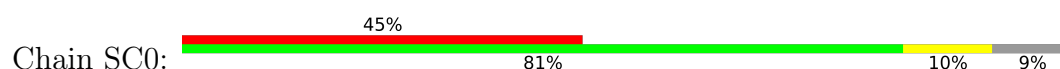
- Molecule 45: eS1



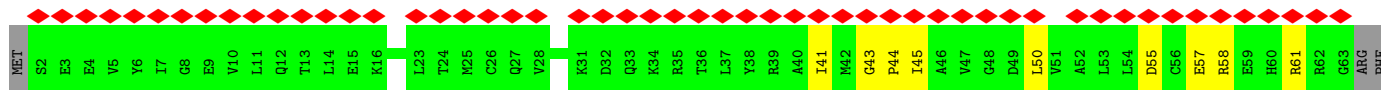
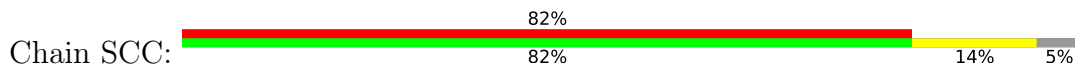
- Molecule 46: eS27



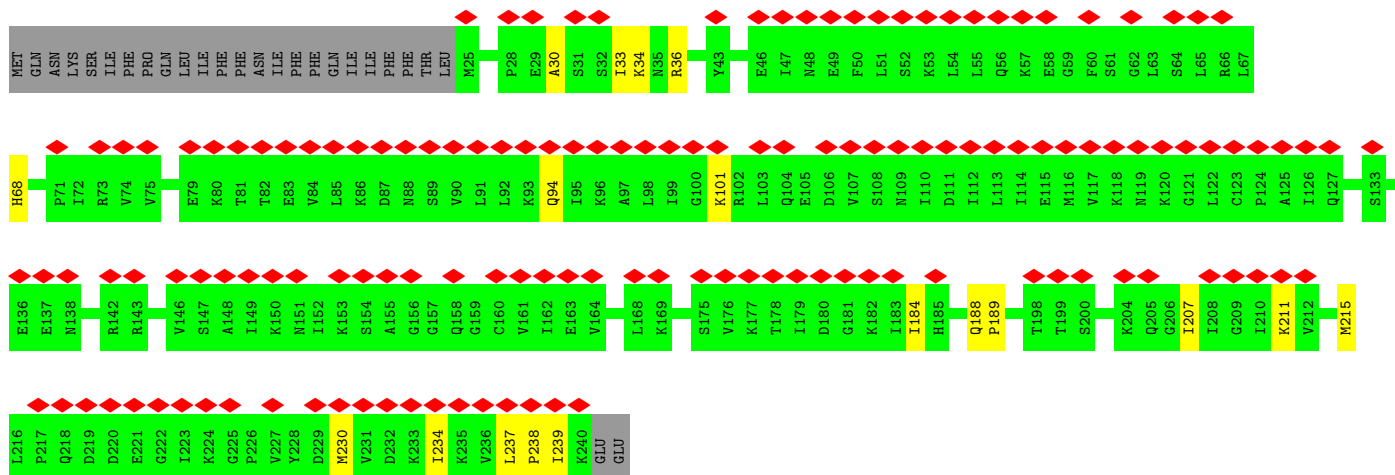
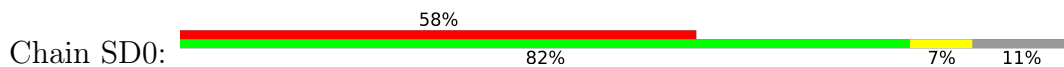
- Molecule 47: 40S ribosomal protein S2



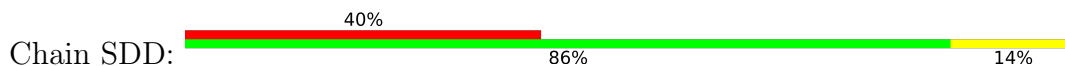
- Molecule 48: eS28



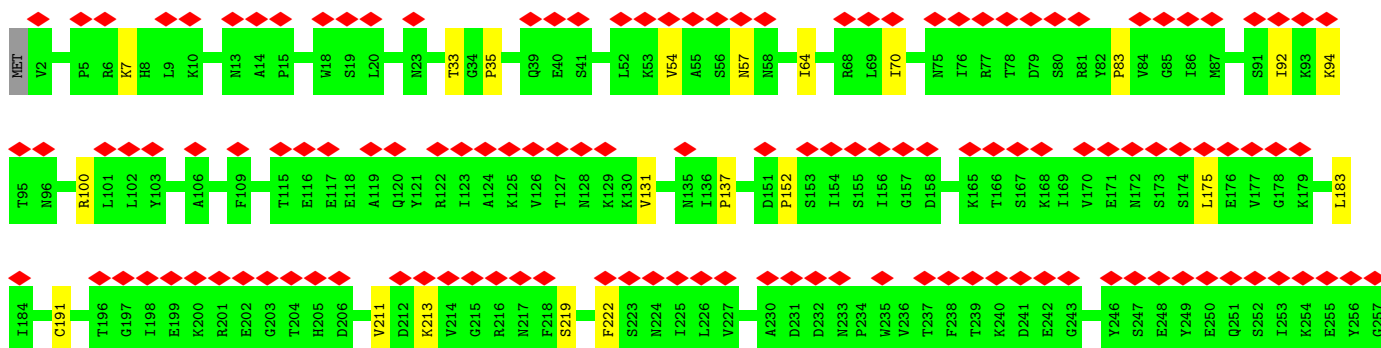
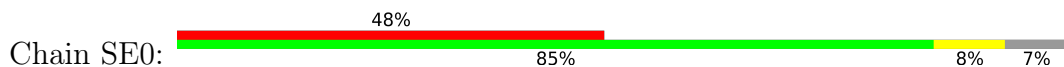
- Molecule 49: 40S ribosomal protein S3

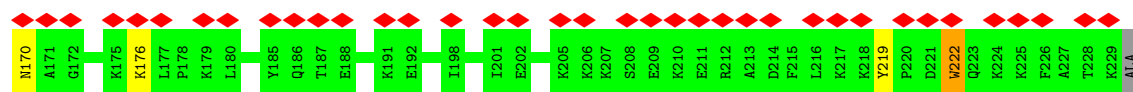


- Molecule 50: 40S ribosomal protein S29



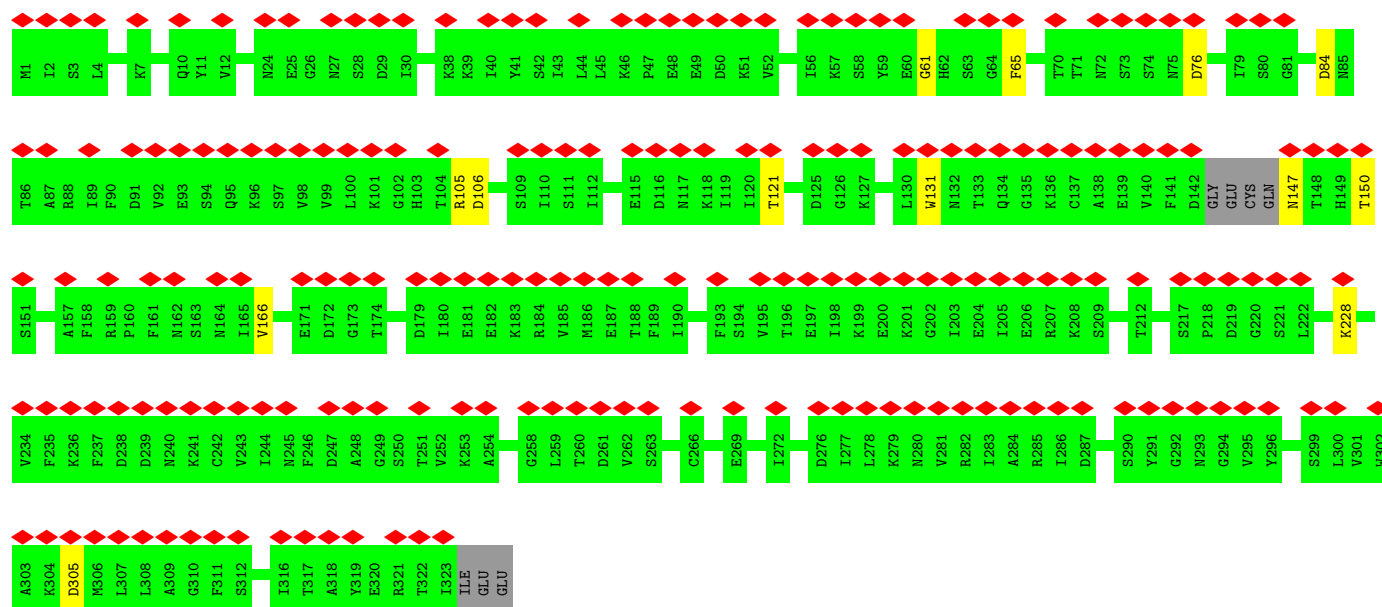
- Molecule 51: 40S ribosomal protein S4





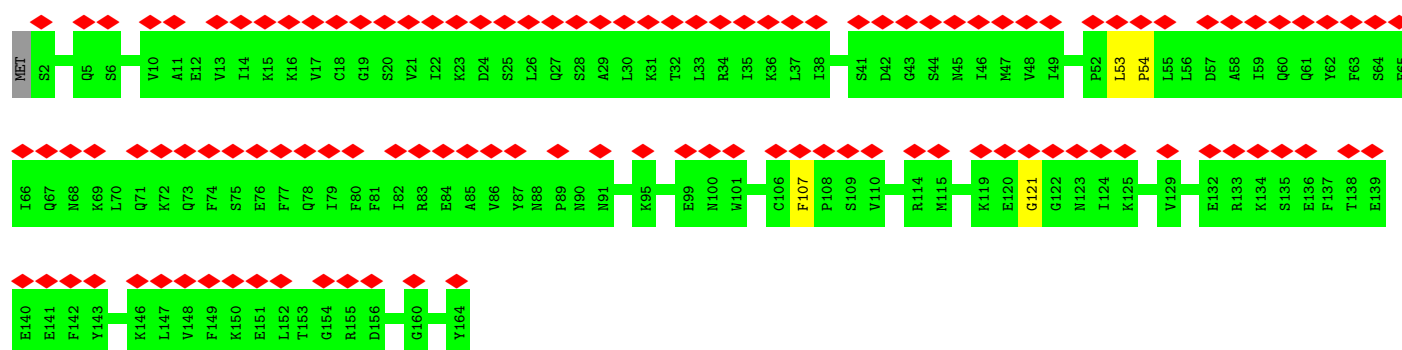
- Molecule 56: Guanine nucleotide binding protein beta subunit

Chain SGG:



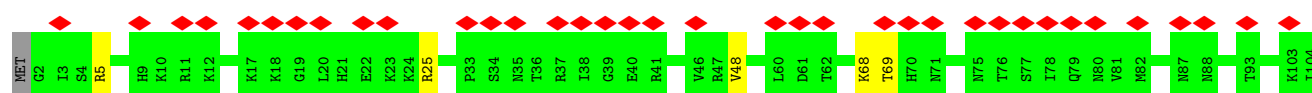
- Molecule 57: 40S ribosomal protein S7

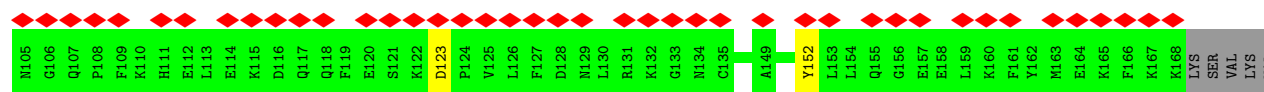
Chain SH0:



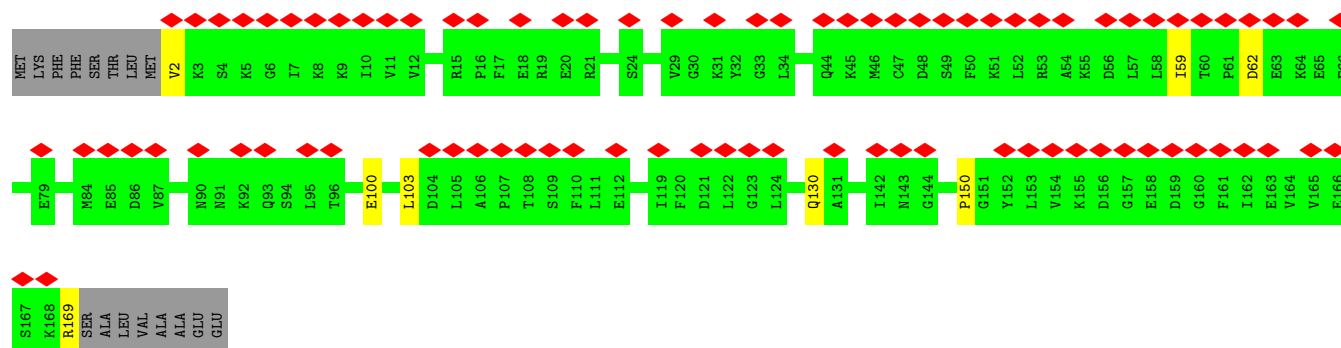
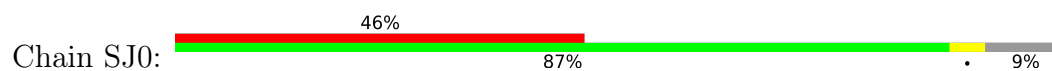
- Molecule 58: 40S ribosomal protein S8

Chain SI0:

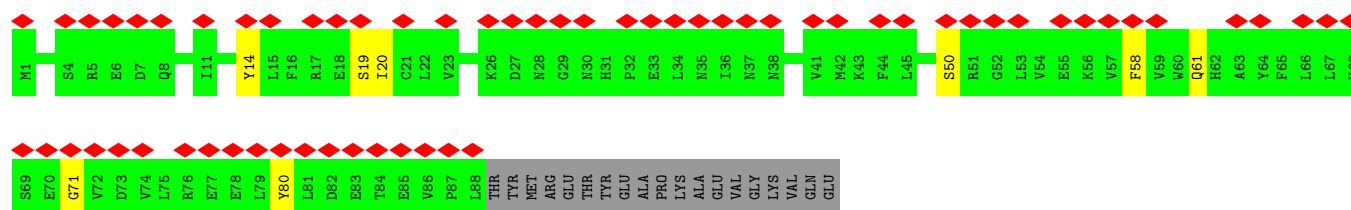
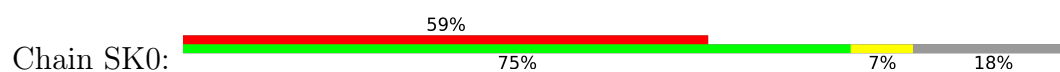




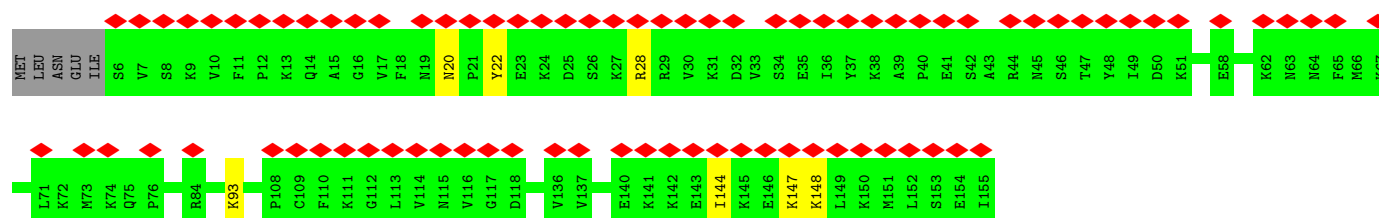
- Molecule 59: 40S ribosomal protein S9



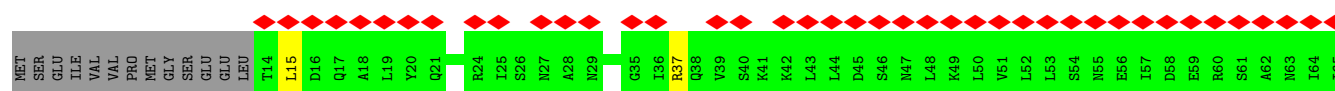
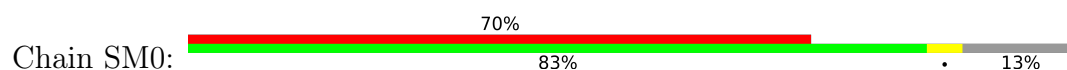
- Molecule 60: 40S ribosomal protein S10

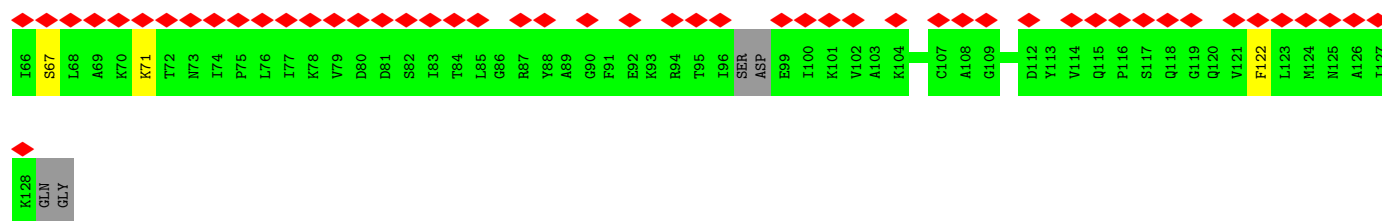


- Molecule 61: 40S ribosomal protein S11



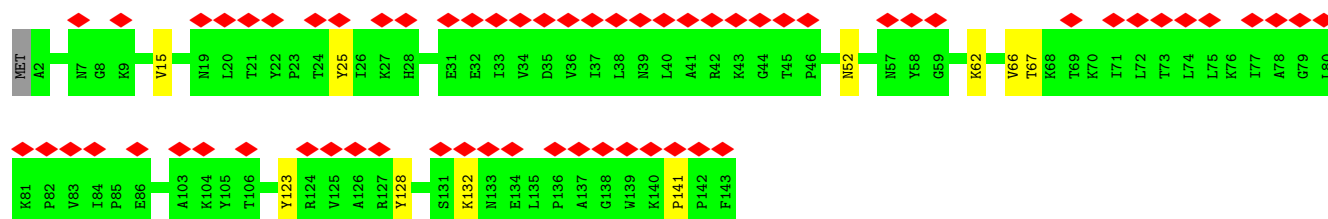
- Molecule 62: 40S ribosomal protein S12





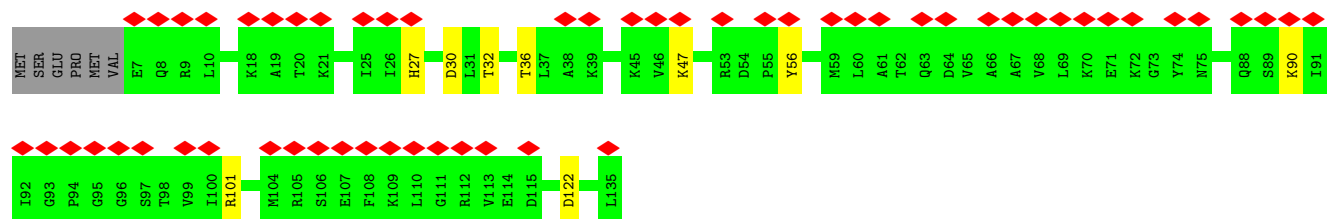
• Molecule 63: 40S ribosomal protein S13

Chain SN0: 44% 92% 7%



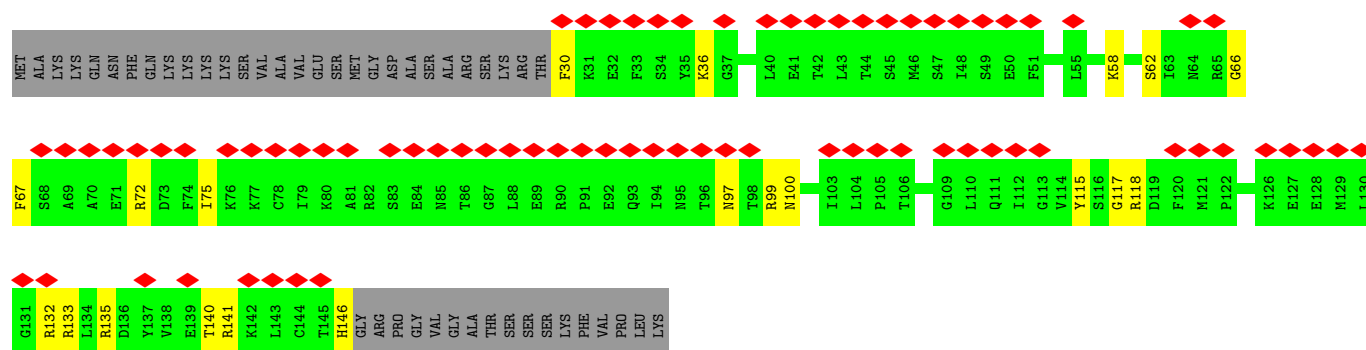
• Molecule 64: 40S ribosomal protein S14

Chain SO0: 42% 89% 7%



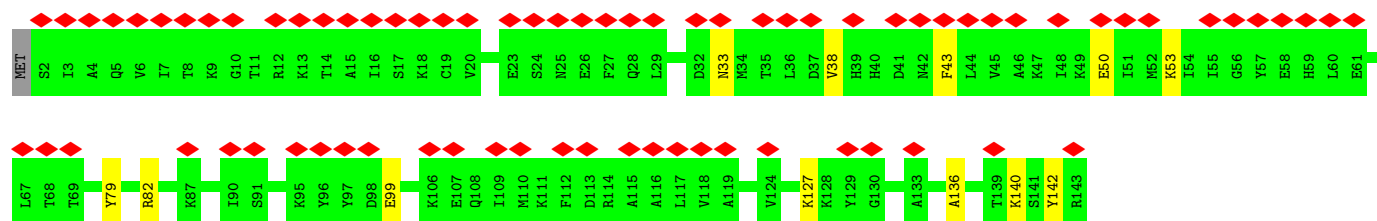
• Molecule 65: Ribosomal protein S19

Chain SP0: 47% 60% 12% 28%

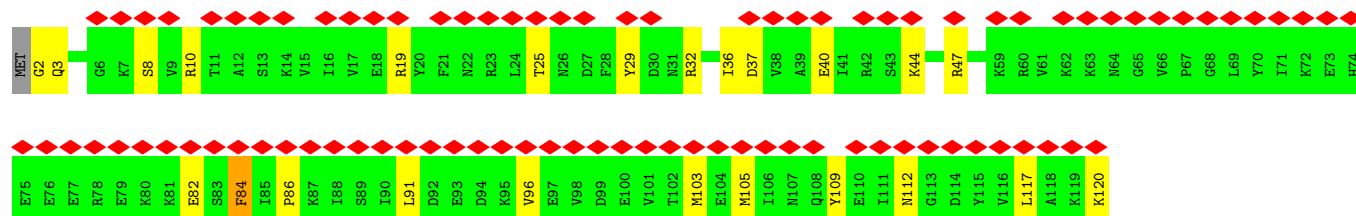
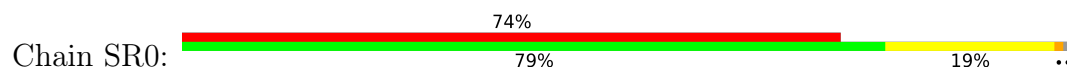


• Molecule 66: 40S ribosomal protein S16

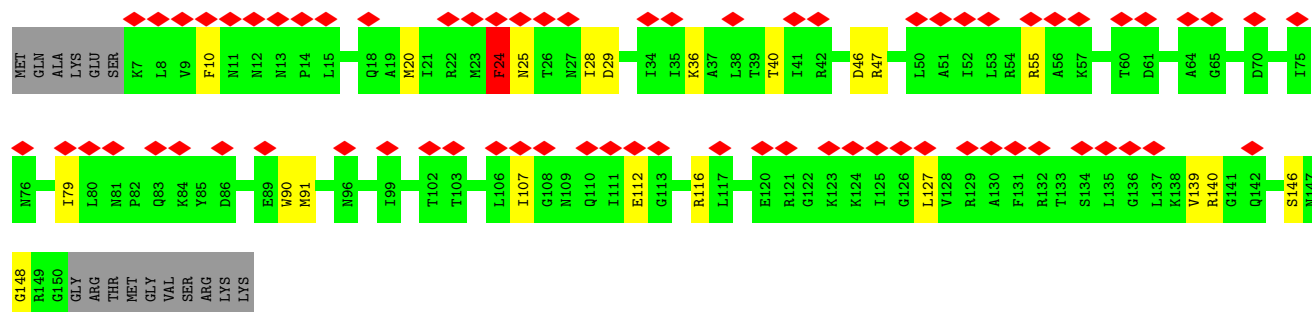
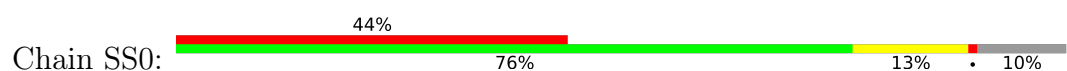
Chain SQ0: 52% 91% 8%



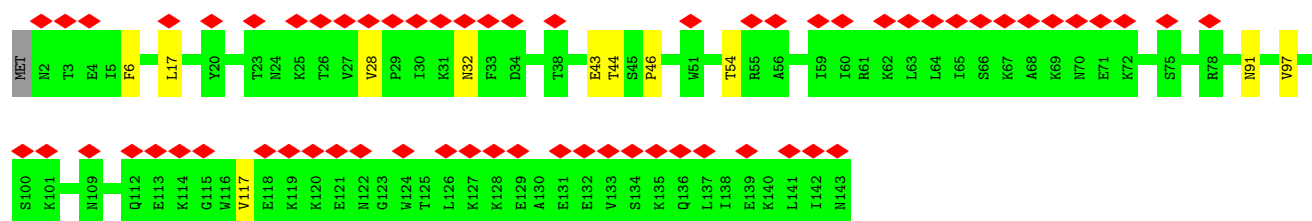
• Molecule 67: eS17



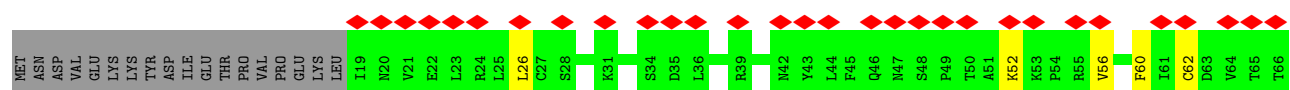
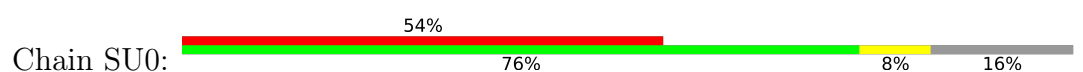
• Molecule 68: 40S ribosomal protein S18

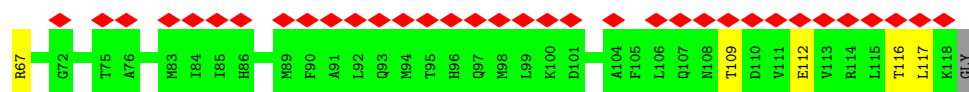


• Molecule 69: 40S Ribosomal protein S19

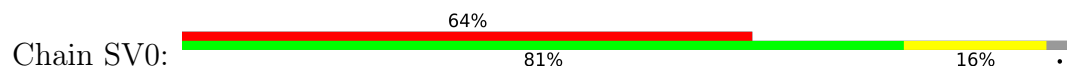


• Molecule 70: 40S ribosomal protein S20

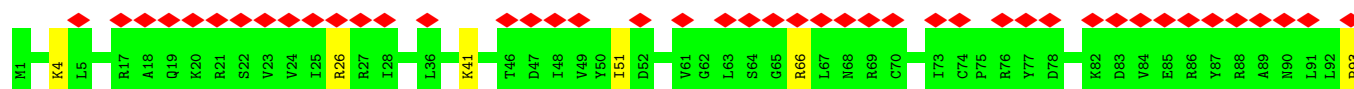




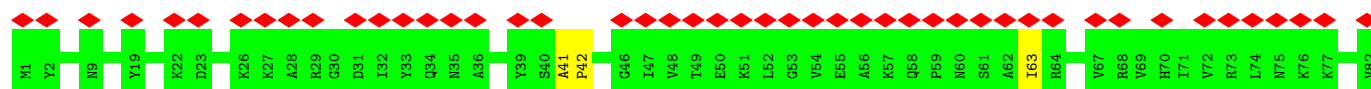
- Molecule 71: Ribosomal protein S21E



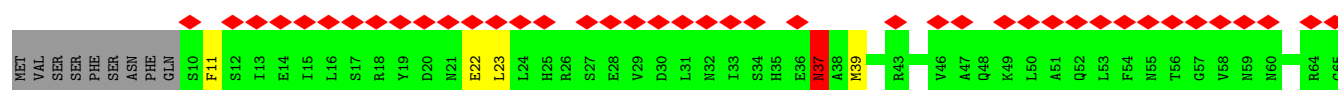
- Molecule 72: 40S ribosomal protein S15A



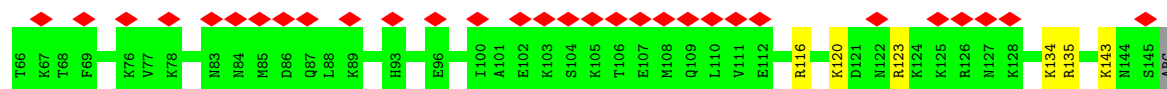
- Molecule 73: uS12

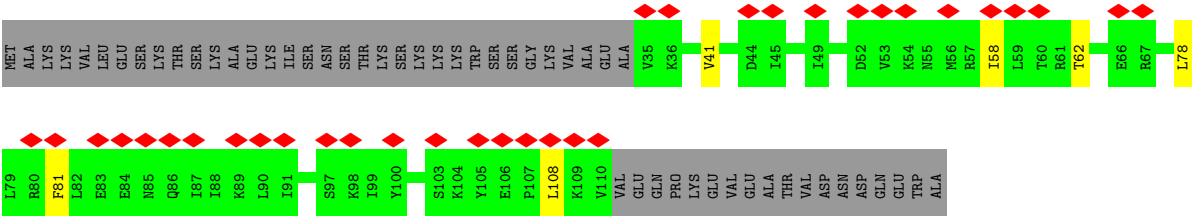


- Molecule 74: 40s ribosomal protein s24



- Molecule 75: 40S ribosomal protein S25





4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, Not provided	
Number of subtomograms used	1344	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 ($e^-/\text{\AA}^2$)	120, 120	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	6000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k), GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.622	Depositor
Minimum map value	-0.859	Depositor
Average map value	0.012	Depositor
Map value standard deviation	0.131	Depositor
Recommended contour level	0.39	Depositor
Map size (\AA)	453.00003, 453.00003, 453.00003	wwPDB
Map dimensions	100, 100, 100	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	4.53, 4.53, 4.53	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	L50	0.75	1/60107 (0.0%)	1.19	161/93753 (0.2%)
2	L70	0.75	1/2844 (0.0%)	1.11	6/4429 (0.1%)
3	LA0	0.32	0/1926	0.74	0/2590
4	LAA	0.34	0/1191	0.66	0/1586
5	LB0	0.32	0/3092	0.70	1/4144 (0.0%)
6	LC0	0.33	0/2646	0.75	1/3555 (0.0%)
7	LCC	0.32	0/794	0.62	0/1067
8	LD0	0.29	0/2328	0.67	0/3098
9	LDD	0.30	0/913	0.66	0/1223
10	LE0	0.28	0/1394	0.65	0/1875
11	LEE	0.32	0/1108	0.69	0/1477
12	LF0	0.30	0/1963	0.68	0/2618
13	LFF	0.33	0/906	0.70	0/1207
14	LG0	0.28	0/1612	0.63	0/2163
15	LGG	0.34	0/825	0.78	1/1090 (0.1%)
16	LH0	0.30	0/1503	0.66	0/2018
17	LHH	0.28	0/999	0.66	0/1324
18	LI0	0.32	0/1781	0.69	0/2382
19	LII	0.30	0/790	0.59	0/1041
20	LJ0	0.30	0/1350	0.66	0/1797
21	LJJ	0.40	0/710	0.83	2/932 (0.2%)
22	LL0	0.30	0/1374	0.76	1/1827 (0.1%)
23	LLL	0.34	0/435	0.72	0/576
24	LM0	0.32	0/935	0.65	0/1251
25	LMM	0.41	0/431	0.68	0/568
26	LN0	0.35	0/1722	0.74	1/2297 (0.0%)
27	LO0	0.30	0/1626	0.65	0/2168
28	LOO	0.34	0/811	0.70	0/1071
29	LP0	0.32	0/1262	0.77	0/1689
30	LPP	0.40	0/693	0.78	2/918 (0.2%)
31	LQ0	0.30	0/1512	0.64	0/2014
32	LR0	0.31	0/1352	0.65	1/1790 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LS0	0.30	0/1422	0.67	0/1898
34	LT0	0.31	0/1294	0.68	0/1736
35	LU0	0.30	0/826	0.67	0/1104
36	LV0	0.31	0/1068	0.70	0/1429
37	LW0	0.43	0/849	0.72	0/1129
38	LX0	0.28	0/883	0.67	0/1175
39	LY0	0.29	0/1058	0.69	1/1399 (0.1%)
40	LZ0	0.29	0/976	0.73	1/1302 (0.1%)
41	MD1	0.66	0/1249	0.87	1/1677 (0.1%)
42	S60	1.41	352/32725 (1.1%)	1.41	375/51066 (0.7%)
43	SA0	0.36	1/1751 (0.1%)	0.64	0/2358
44	SAA	0.38	0/839	0.73	0/1120
45	SB0	0.29	0/1623	0.67	0/2169
46	SBB	0.47	1/634 (0.2%)	0.65	0/844
47	SC0	0.31	0/1751	0.69	2/2359 (0.1%)
48	SCC	0.33	0/480	0.73	0/644
49	SD0	0.30	0/1721	0.66	0/2304
50	SDD	0.40	0/559	0.75	1/742 (0.1%)
51	SE0	0.32	0/2080	0.72	2/2804 (0.1%)
52	SEE	0.36	0/453	0.74	1/596 (0.2%)
53	SF0	0.31	0/1527	0.68	0/2045
54	SFF	0.43	0/427	0.68	0/573
55	SG0	0.29	0/1864	0.68	0/2485
56	SGG	0.34	0/2517	0.71	1/3397 (0.0%)
57	SH0	0.31	0/1356	0.66	0/1820
58	SI0	0.33	0/1369	0.68	0/1825
59	SJ0	0.33	0/1403	0.68	0/1880
60	SK0	0.29	0/750	0.71	0/1009
61	SL0	0.32	0/1252	0.72	2/1672 (0.1%)
62	SM0	0.32	0/881	0.71	0/1182
63	SN0	0.38	0/1154	0.78	0/1557
64	SO0	0.33	0/993	0.72	0/1326
65	SP0	0.33	0/964	0.71	0/1289
66	SQ0	0.33	0/1163	0.74	3/1556 (0.2%)
67	SR0	0.64	0/985	0.96	2/1315 (0.2%)
68	SS0	0.34	0/1165	0.74	0/1566
69	ST0	0.34	0/1181	0.75	1/1585 (0.1%)
70	SU0	0.33	0/824	0.74	2/1110 (0.2%)
71	SV0	0.33	0/525	0.66	0/700
72	SW0	0.32	0/1037	0.71	0/1389
73	SX0	0.31	0/1113	0.70	0/1486
74	SY0	0.30	0/1131	0.72	1/1503 (0.1%)
75	SZ0	0.33	0/640	0.75	0/855

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.78	356/183397 (0.2%)	1.06	573/266518 (0.2%)

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
6	LC0	0	1
13	LFF	0	1
15	LGG	0	1
All	All	0	3

The worst 5 of 356 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S60	934	A	P-O5'	10.34	1.70	1.59
42	S60	988	A	N9-C4	-8.57	1.32	1.37
43	SA0	20	CYS	C-N	8.40	1.53	1.34
1	L50	1	A	OP3-P	-8.36	1.51	1.61
42	S60	1049	G	N7-C5	-8.34	1.34	1.39

The worst 5 of 573 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	S60	1356	C	O5'-P-OP1	-18.09	89.00	110.70
42	S60	910	A	P-O3'-C3'	-11.68	105.69	119.70
42	S60	850	G	C5-N7-C8	-11.31	98.65	104.30
42	S60	1034	A	P-O3'-C3'	-11.29	106.16	119.70
42	S60	904	C	P-O3'-C3'	-10.87	106.66	119.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	LC0	87	ALA	Peptide
13	LFF	101	ILE	Peptide
15	LGG	77	GLY	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L50	53655	0	26955	118	0
2	L70	2542	0	1282	8	0
3	LA0	1889	0	1985	12	0
4	LAA	1167	0	1214	5	0
5	LB0	3039	0	3183	6	0
6	LC0	2604	0	2638	12	0
7	LCC	781	0	803	2	0
8	LD0	2298	0	2384	6	0
9	LDD	895	0	948	0	0
10	LE0	1371	0	1389	13	0
11	LEE	1090	0	1173	10	0
12	LF0	1933	0	2011	11	0
13	LFF	893	0	945	2	0
14	LG0	1590	0	1709	4	0
15	LGG	819	0	882	1	0
16	LH0	1477	0	1528	4	0
17	LHH	992	0	1097	5	0
18	LI0	1750	0	1797	2	0
19	LII	784	0	874	2	0
20	LJ0	1332	0	1411	12	0
21	LJJ	701	0	753	4	0
22	LL0	1353	0	1433	4	0
23	LLL	427	0	468	0	0
24	LM0	927	0	961	5	0
25	LMM	427	0	461	0	0
26	LN0	1688	0	1752	5	0
27	LO0	1598	0	1681	3	0
28	LOO	801	0	886	4	0
29	LP0	1238	0	1304	3	0
30	LPP	684	0	720	2	0
31	LQ0	1491	0	1587	6	0
32	LR0	1336	0	1430	0	0
33	LS0	1400	0	1450	1	0
34	LT0	1270	0	1321	15	0
35	LU0	810	0	834	1	0
36	LV0	1057	0	1139	2	0
37	LW0	832	0	873	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	LX0	874	0	956	5	0
39	LY0	1048	0	1135	2	0
40	LZ0	963	0	1022	2	0
41	MD1	1229	0	1216	10	0
42	S60	29181	0	14605	315	0
43	SA0	1725	0	1750	137	0
44	SAA	827	0	859	18	0
45	SB0	1609	0	1728	6	0
46	SBB	627	0	651	3	0
47	SC0	1727	0	1802	90	0
48	SCC	476	0	488	18	0
49	SD0	1700	0	1815	33	0
50	SDD	550	0	542	29	0
51	SE0	2044	0	2116	26	0
52	SEE	447	0	483	1	0
53	SF0	1509	0	1604	39	0
54	SFF	422	0	412	6	0
55	SG0	1836	0	1972	38	0
56	SGG	2478	0	2458	22	0
57	SH0	1335	0	1356	2	0
58	SI0	1347	0	1379	9	0
59	SJ0	1379	0	1436	15	0
60	SK0	737	0	746	17	0
61	SL0	1229	0	1302	5	0
62	SM0	876	0	937	6	0
63	SN0	1130	0	1189	10	0
64	SO0	983	0	1028	14	0
65	SP0	950	0	984	58	0
66	SQ0	1143	0	1171	19	0
67	SR0	974	0	1003	99	0
68	SS0	1150	0	1207	32	0
69	ST0	1161	0	1219	9	0
70	SU0	809	0	838	14	0
71	SV0	521	0	525	72	0
72	SW0	1022	0	1052	18	0
73	SX0	1098	0	1183	4	0
74	SY0	1118	0	1166	12	0
75	SZ0	633	0	678	13	0
76	LGG	1	0	0	0	0
76	LJJ	1	0	0	0	0
76	LMM	1	0	0	0	0
76	LOO	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
76	LPP	1	0	0	0	0
76	SAA	1	0	0	0	0
76	SBB	1	0	0	0	0
76	SDD	1	0	0	0	0
76	SFF	1	0	0	0	0
All	All	171817	0	133274	959	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 3.

The worst 5 of 959 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)
43:SA0:70:ASN:HB2	47:SC0:240:ILE:CD1	1.35	1.56
47:SC0:51:SER:HB2	71:SV0:6:ARG:NH2	1.30	1.44
49:SD0:238:PRO:C	67:SR0:19:ARG:HH12	1.27	1.36
43:SA0:70:ASN:HB2	47:SC0:240:ILE:CG1	1.56	1.35
20:LJ0:82:LYS:HB3	65:SP0:30:PHE:CE2	1.62	1.34

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	
3	LA0	243/246 (99%)	236 (97%)	7 (3%)	0	100	100
4	LAA	145/147 (99%)	142 (98%)	3 (2%)	0	100	100
5	LB0	381/392 (97%)	372 (98%)	9 (2%)	0	100	100
6	LC0	325/328 (99%)	313 (96%)	11 (3%)	1 (0%)	37	73
7	LCC	97/110 (88%)	94 (97%)	2 (2%)	1 (1%)	13	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	LD0	279/291 (96%)	274 (98%)	5 (2%)	0	100	100
9	LDD	107/110 (97%)	104 (97%)	3 (3%)	0	100	100
10	LE0	163/171 (95%)	154 (94%)	9 (6%)	0	100	100
11	LEE	133/139 (96%)	127 (96%)	6 (4%)	0	100	100
12	LF0	229/235 (97%)	224 (98%)	5 (2%)	0	100	100
13	LFF	109/111 (98%)	106 (97%)	3 (3%)	0	100	100
14	LG0	197/206 (96%)	194 (98%)	3 (2%)	0	100	100
15	LGG	102/106 (96%)	96 (94%)	5 (5%)	1 (1%)	13	49
16	LH0	181/187 (97%)	177 (98%)	4 (2%)	0	100	100
17	LHH	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
18	LI0	215/218 (99%)	214 (100%)	1 (0%)	0	100	100
19	LII	95/98 (97%)	91 (96%)	4 (4%)	0	100	100
20	LJ0	165/171 (96%)	155 (94%)	10 (6%)	0	100	100
21	LJJ	87/92 (95%)	86 (99%)	1 (1%)	0	100	100
22	LL0	162/165 (98%)	155 (96%)	6 (4%)	1 (1%)	22	60
23	LLL	49/52 (94%)	48 (98%)	1 (2%)	0	100	100
24	LM0	113/115 (98%)	106 (94%)	6 (5%)	1 (1%)	14	52
25	LMM	50/127 (39%)	50 (100%)	0	0	100	100
26	LN0	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
27	LO0	196/198 (99%)	193 (98%)	3 (2%)	0	100	100
28	LOO	98/104 (94%)	96 (98%)	2 (2%)	0	100	100
29	LP0	152/167 (91%)	145 (95%)	7 (5%)	0	100	100
30	LPP	85/89 (96%)	80 (94%)	4 (5%)	1 (1%)	11	44
31	LQ0	180/183 (98%)	175 (97%)	5 (3%)	0	100	100
32	LR0	162/168 (96%)	160 (99%)	2 (1%)	0	100	100
33	LS0	168/171 (98%)	159 (95%)	9 (5%)	0	100	100
34	LT0	154/158 (98%)	145 (94%)	9 (6%)	0	100	100
35	LU0	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
36	LV0	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
37	LW0	100/131 (76%)	93 (93%)	6 (6%)	1 (1%)	13	49
38	LX0	110/113 (97%)	106 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	LY0	129/131 (98%)	123 (95%)	6 (5%)	0	100	100
40	LZ0	116/153 (76%)	116 (100%)	0	0	100	100
41	MD1	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
43	SA0	218/233 (94%)	206 (94%)	12 (6%)	0	100	100
44	SAA	99/102 (97%)	98 (99%)	1 (1%)	0	100	100
45	SB0	202/230 (88%)	197 (98%)	5 (2%)	0	100	100
46	SBB	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
47	SC0	224/248 (90%)	220 (98%)	4 (2%)	0	100	100
48	SCC	60/65 (92%)	57 (95%)	3 (5%)	0	100	100
49	SD0	214/242 (88%)	212 (99%)	2 (1%)	0	100	100
50	SDD	63/65 (97%)	58 (92%)	5 (8%)	0	100	100
51	SE0	258/280 (92%)	247 (96%)	11 (4%)	0	100	100
52	SEE	54/60 (90%)	53 (98%)	1 (2%)	0	100	100
53	SF0	190/195 (97%)	180 (95%)	10 (5%)	0	100	100
54	SFF	56/150 (37%)	52 (93%)	4 (7%)	0	100	100
55	SG0	227/230 (99%)	214 (94%)	13 (6%)	0	100	100
56	SGG	315/326 (97%)	295 (94%)	19 (6%)	1 (0%)	37	73
57	SH0	161/164 (98%)	156 (97%)	4 (2%)	1 (1%)	22	60
58	SI0	165/173 (95%)	161 (98%)	4 (2%)	0	100	100
59	SJ0	166/184 (90%)	165 (99%)	1 (1%)	0	100	100
60	SK0	86/107 (80%)	81 (94%)	4 (5%)	1 (1%)	11	44
61	SL0	148/155 (96%)	141 (95%)	7 (5%)	0	100	100
62	SM0	109/130 (84%)	106 (97%)	3 (3%)	0	100	100
63	SN0	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
64	SO0	127/135 (94%)	120 (94%)	7 (6%)	0	100	100
65	SP0	115/163 (71%)	113 (98%)	2 (2%)	0	100	100
66	SQ0	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
67	SR0	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
68	SS0	142/160 (89%)	137 (96%)	4 (3%)	1 (1%)	19	57
69	ST0	140/143 (98%)	140 (100%)	0	0	100	100
70	SU0	98/119 (82%)	94 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
71	SV0	63/67 (94%)	62 (98%)	1 (2%)	0	100	100
72	SW0	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
73	SX0	138/141 (98%)	136 (99%)	2 (1%)	0	100	100
74	SY0	134/146 (92%)	122 (91%)	10 (8%)	2 (2%)	8	40
75	SZ0	74/128 (58%)	69 (93%)	5 (7%)	0	100	100
All	All	10629/11469 (93%)	10261 (96%)	355 (3%)	13 (0%)	50	83

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	LGG	78	GLY
74	SY0	134	LYS
30	LPP	18	TYR
37	LW0	81	ARG
68	SS0	24	PHE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	LA0	202/203 (100%)	199 (98%)	3 (2%)	60	75
4	LAA	123/123 (100%)	119 (97%)	4 (3%)	33	52
5	LB0	328/336 (98%)	319 (97%)	9 (3%)	40	58
6	LC0	277/278 (100%)	274 (99%)	3 (1%)	70	80
7	LCC	87/97 (90%)	85 (98%)	2 (2%)	45	64
8	LD0	251/261 (96%)	249 (99%)	2 (1%)	79	85
9	LDD	99/100 (99%)	99 (100%)	0	100	100
10	LE0	153/159 (96%)	150 (98%)	3 (2%)	50	68
11	LEE	118/122 (97%)	118 (100%)	0	100	100
12	LF0	212/216 (98%)	211 (100%)	1 (0%)	86	89
13	LFF	98/98 (100%)	98 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	LG0	183/190 (96%)	183 (100%)	0	100	100
15	LGG	88/90 (98%)	86 (98%)	2 (2%)	45	64
16	LH0	165/169 (98%)	161 (98%)	4 (2%)	44	62
17	LHH	110/110 (100%)	109 (99%)	1 (1%)	75	83
18	LI0	188/189 (100%)	188 (100%)	0	100	100
19	LII	84/84 (100%)	82 (98%)	2 (2%)	44	62
20	LJ0	146/149 (98%)	144 (99%)	2 (1%)	62	75
21	LJJ	78/81 (96%)	77 (99%)	1 (1%)	65	77
22	LL0	148/149 (99%)	142 (96%)	6 (4%)	26	47
23	LLL	46/47 (98%)	46 (100%)	0	100	100
24	LM0	110/110 (100%)	110 (100%)	0	100	100
25	LMM	46/112 (41%)	46 (100%)	0	100	100
26	LN0	175/176 (99%)	171 (98%)	4 (2%)	45	64
27	LO0	178/178 (100%)	177 (99%)	1 (1%)	84	88
28	LOO	85/89 (96%)	85 (100%)	0	100	100
29	LP0	135/147 (92%)	132 (98%)	3 (2%)	47	65
30	LPP	75/77 (97%)	73 (97%)	2 (3%)	40	58
31	LQ0	165/166 (99%)	165 (100%)	0	100	100
32	LR0	142/145 (98%)	141 (99%)	1 (1%)	81	87
33	LS0	155/156 (99%)	152 (98%)	3 (2%)	52	69
34	LT0	140/142 (99%)	138 (99%)	2 (1%)	62	75
35	LU0	89/98 (91%)	88 (99%)	1 (1%)	70	80
36	LV0	113/114 (99%)	112 (99%)	1 (1%)	75	83
37	LW0	93/120 (78%)	89 (96%)	4 (4%)	25	46
38	LX0	92/93 (99%)	91 (99%)	1 (1%)	70	80
39	LY0	116/116 (100%)	114 (98%)	2 (2%)	56	72
40	LZ0	106/141 (75%)	106 (100%)	0	100	100
41	MD1	139/139 (100%)	139 (100%)	0	100	100
43	SA0	194/206 (94%)	191 (98%)	3 (2%)	60	75
44	SAA	92/93 (99%)	92 (100%)	0	100	100
45	SB0	182/203 (90%)	182 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	SBB	72/73 (99%)	71 (99%)	1 (1%)	62	75
47	SC0	187/209 (90%)	185 (99%)	2 (1%)	70	80
48	SCC	51/54 (94%)	51 (100%)	0	100	100
49	SD0	189/215 (88%)	189 (100%)	0	100	100
50	SDD	57/57 (100%)	57 (100%)	0	100	100
51	SE0	231/251 (92%)	229 (99%)	2 (1%)	75	83
52	SEE	44/47 (94%)	44 (100%)	0	100	100
53	SF0	167/170 (98%)	163 (98%)	4 (2%)	44	62
54	SFF	46/136 (34%)	45 (98%)	1 (2%)	47	65
55	SG0	199/199 (100%)	195 (98%)	4 (2%)	50	68
56	SGG	282/288 (98%)	278 (99%)	4 (1%)	62	75
57	SH0	153/154 (99%)	153 (100%)	0	100	100
58	SI0	147/153 (96%)	147 (100%)	0	100	100
59	SJ0	152/165 (92%)	150 (99%)	2 (1%)	65	77
60	SK0	83/99 (84%)	82 (99%)	1 (1%)	67	78
61	SL0	140/145 (97%)	139 (99%)	1 (1%)	81	87
62	SM0	99/114 (87%)	99 (100%)	0	100	100
63	SN0	126/127 (99%)	126 (100%)	0	100	100
64	SO0	102/108 (94%)	101 (99%)	1 (1%)	73	82
65	SP0	107/144 (74%)	106 (99%)	1 (1%)	75	83
66	SQ0	120/121 (99%)	119 (99%)	1 (1%)	79	85
67	SR0	109/111 (98%)	108 (99%)	1 (1%)	75	83
68	SS0	125/138 (91%)	124 (99%)	1 (1%)	79	85
69	ST0	129/130 (99%)	126 (98%)	3 (2%)	45	64
70	SU0	92/110 (84%)	92 (100%)	0	100	100
71	SV0	61/63 (97%)	61 (100%)	0	100	100
72	SW0	111/111 (100%)	110 (99%)	1 (1%)	75	83
73	SX0	115/116 (99%)	115 (100%)	0	100	100
74	SY0	126/136 (93%)	121 (96%)	5 (4%)	27	47
75	SZ0	73/118 (62%)	73 (100%)	0	100	100
All	All	9501/10134 (94%)	9392 (99%)	109 (1%)	69	80

5 of 109 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	LS0	157	ARG
43	SA0	102	ARG
68	SS0	24	PHE
34	LT0	55	LYS
37	LW0	91	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L50	2494/2618 (95%)	736 (29%)	103 (4%)
2	L70	118/119 (99%)	36 (30%)	4 (3%)
42	S60	1352/1368 (98%)	518 (38%)	70 (5%)
All	All	3964/4105 (96%)	1290 (32%)	177 (4%)

5 of 1290 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L50	2	U
1	L50	3	A
1	L50	13	A
1	L50	15	G
1	L50	21	U

5 of 177 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
42	S60	218	A
42	S60	819	A
42	S60	262	U
42	S60	425	G
42	S60	925	A

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

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 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

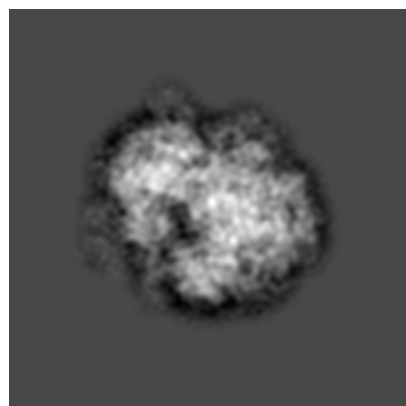
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17448. These allow visual inspection of the internal detail of the map and identification of artifacts.

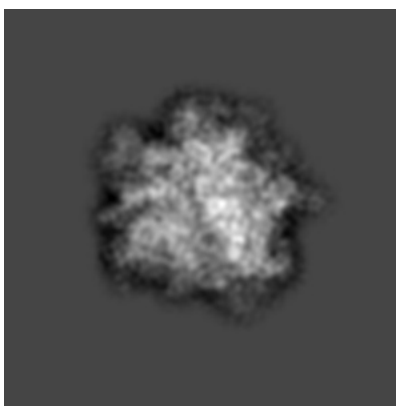
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

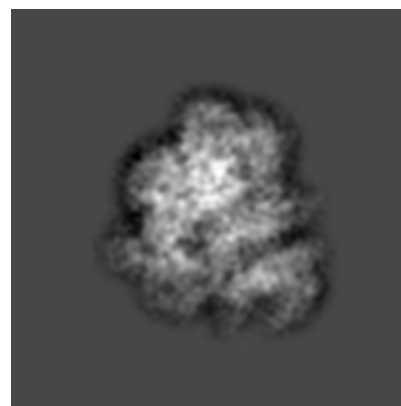
6.1.1 Primary map



X

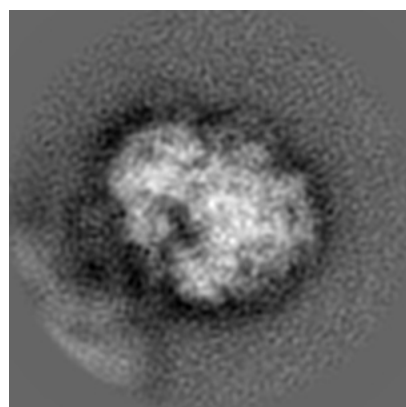


Y

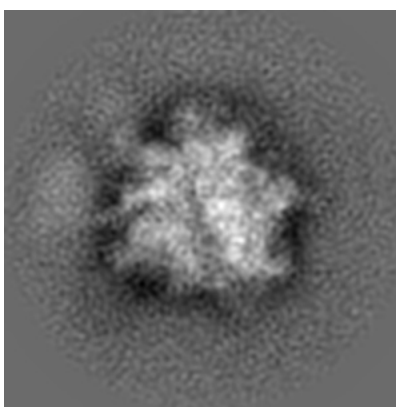


Z

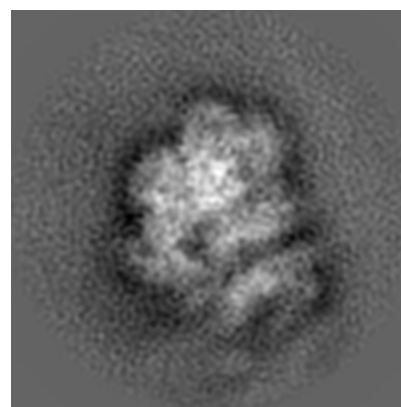
6.1.2 Raw map



X



Y

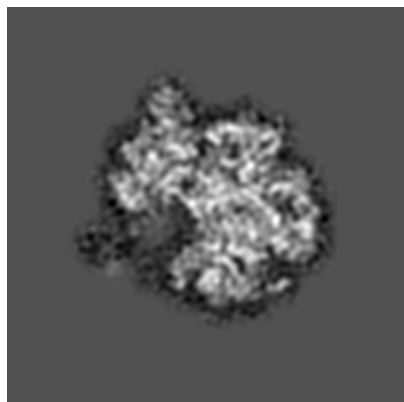


Z

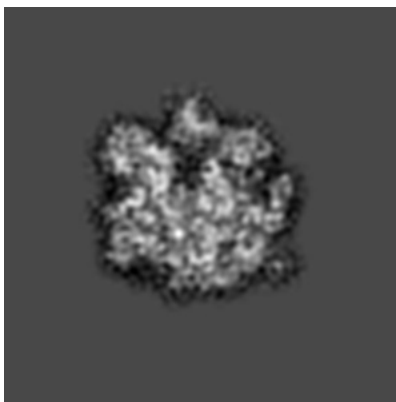
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

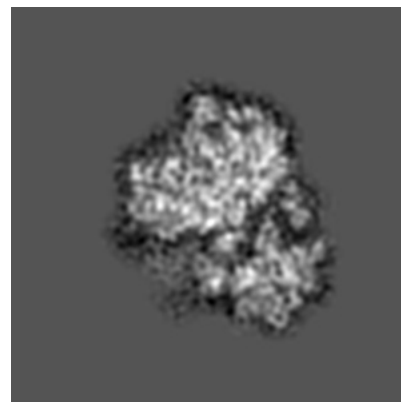
6.2.1 Primary map



X Index: 50

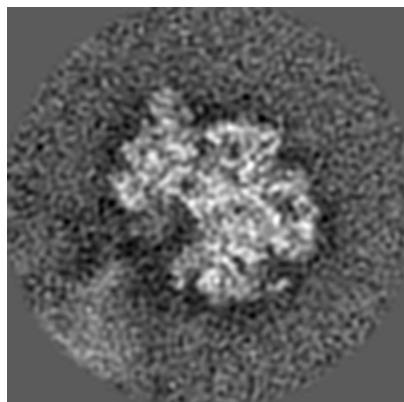


Y Index: 50

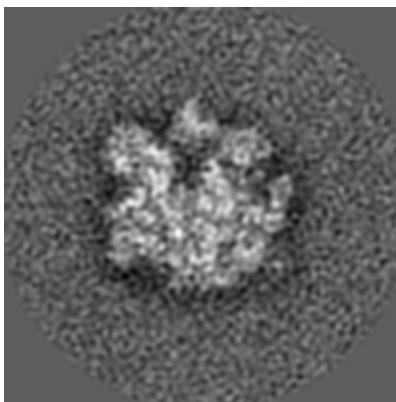


Z Index: 50

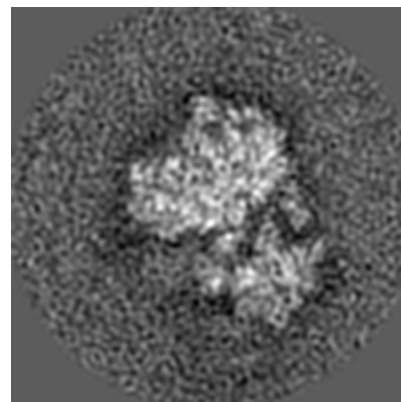
6.2.2 Raw map



X Index: 50



Y Index: 50

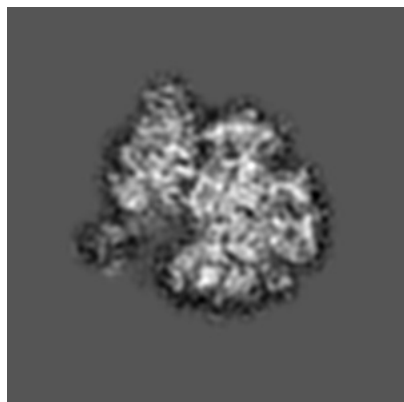


Z Index: 50

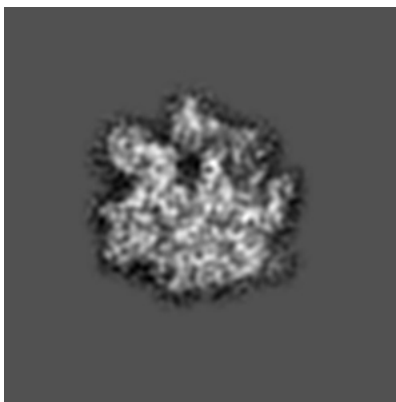
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

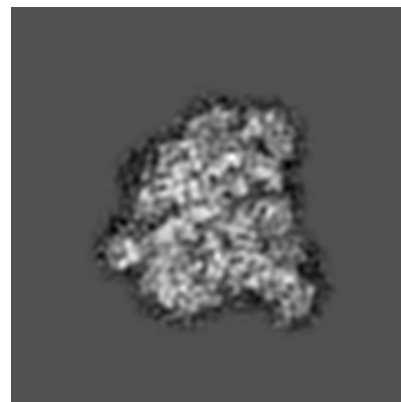
6.3.1 Primary map



X Index: 51

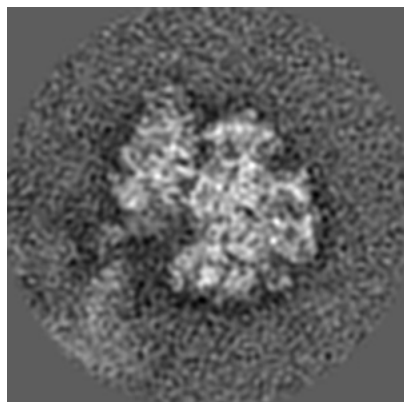


Y Index: 51

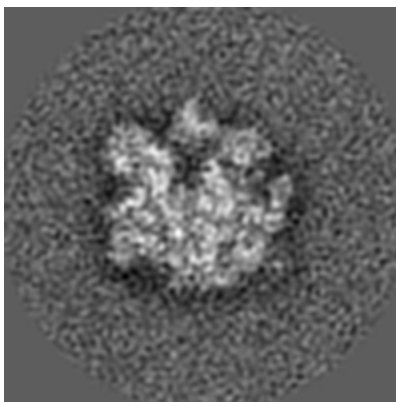


Z Index: 57

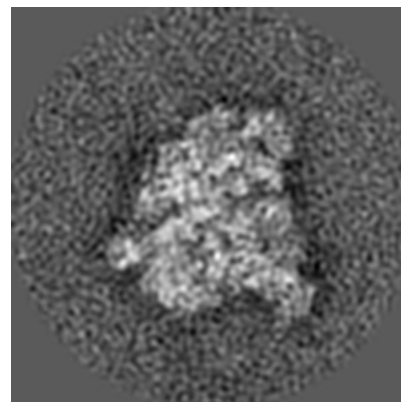
6.3.2 Raw map



X Index: 51



Y Index: 50

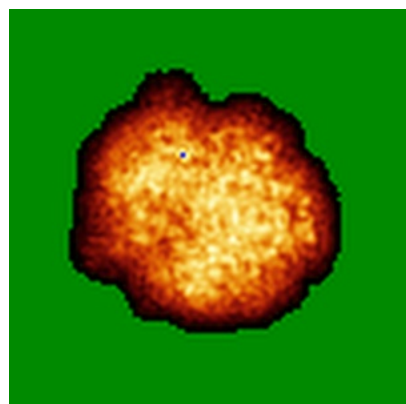


Z Index: 57

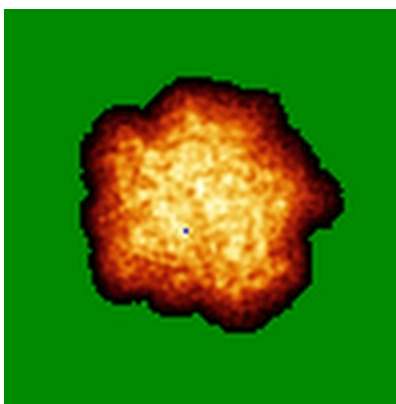
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

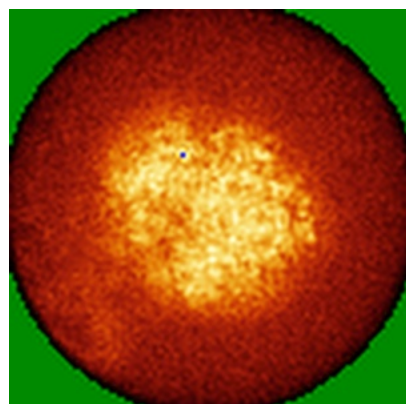


Y

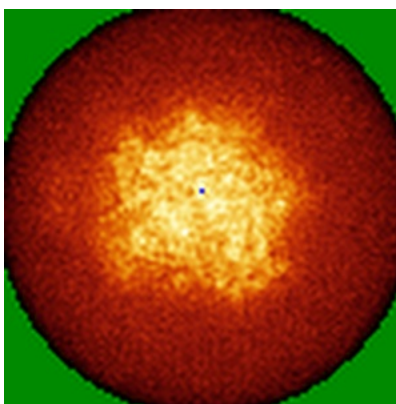


Z

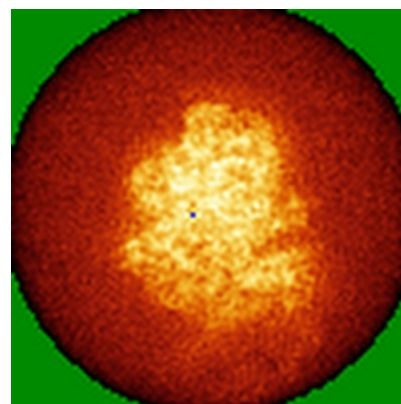
6.4.2 Raw map



X



Y

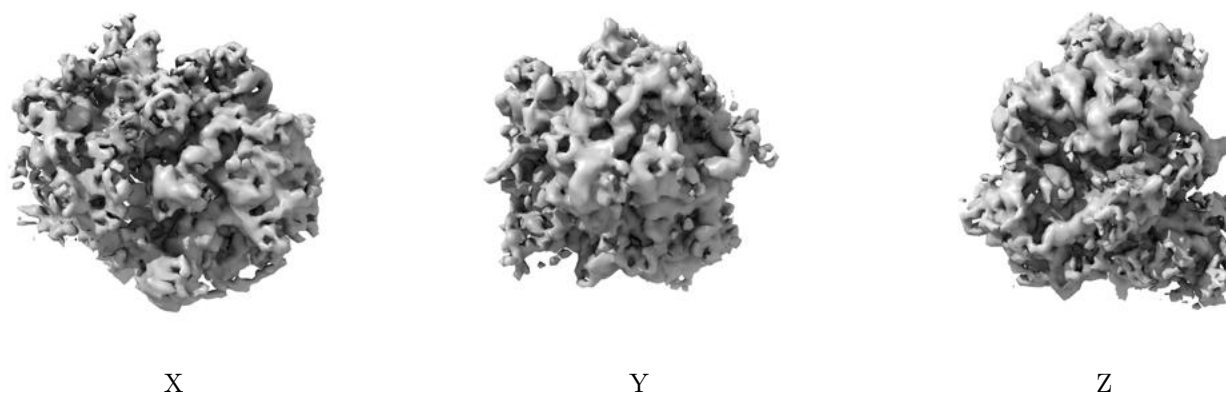


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

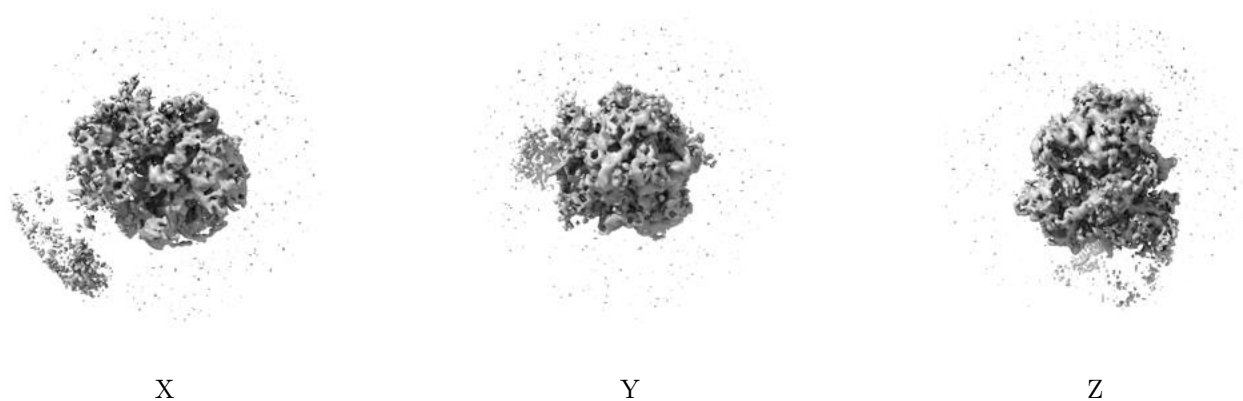
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.39. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

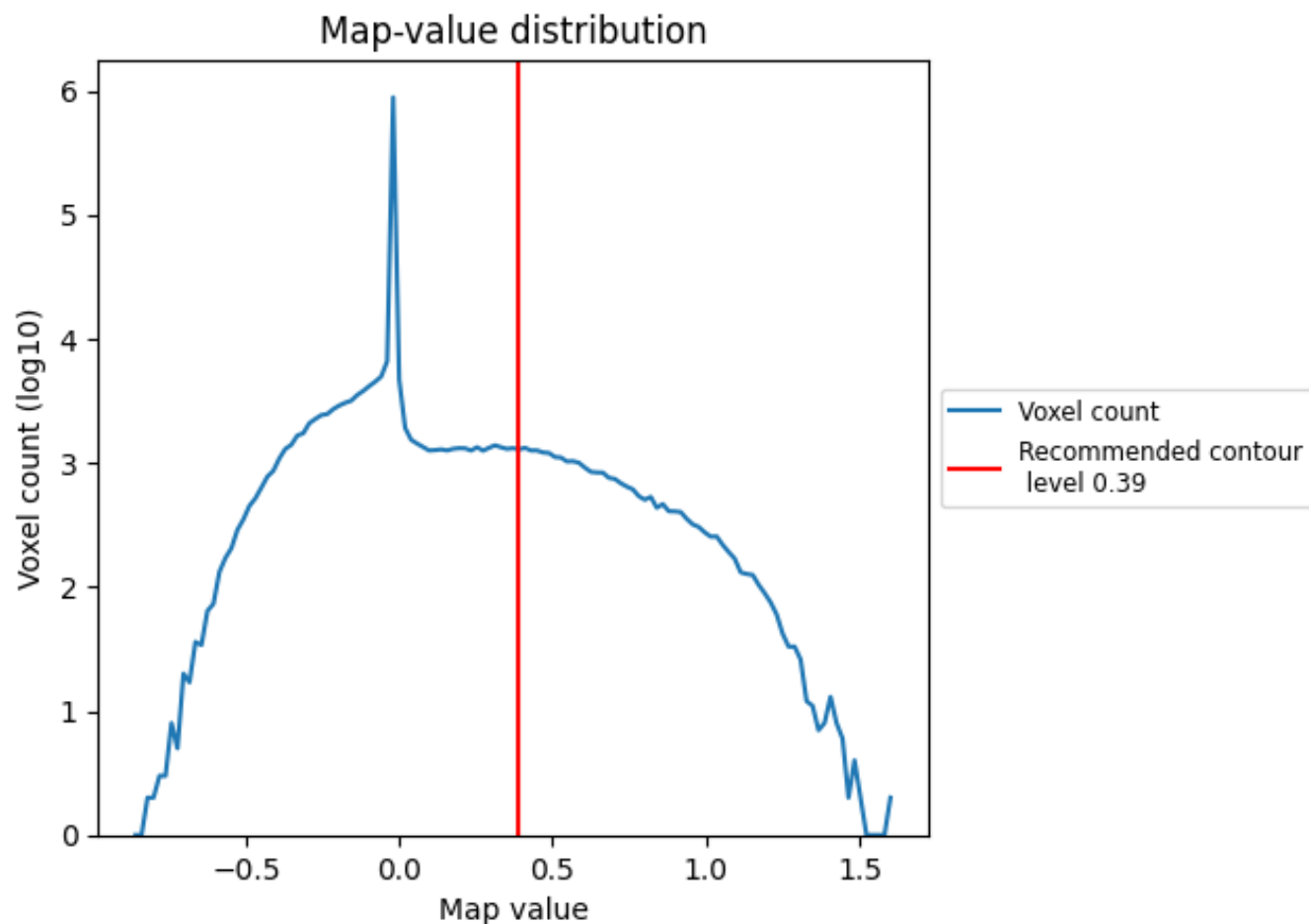
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

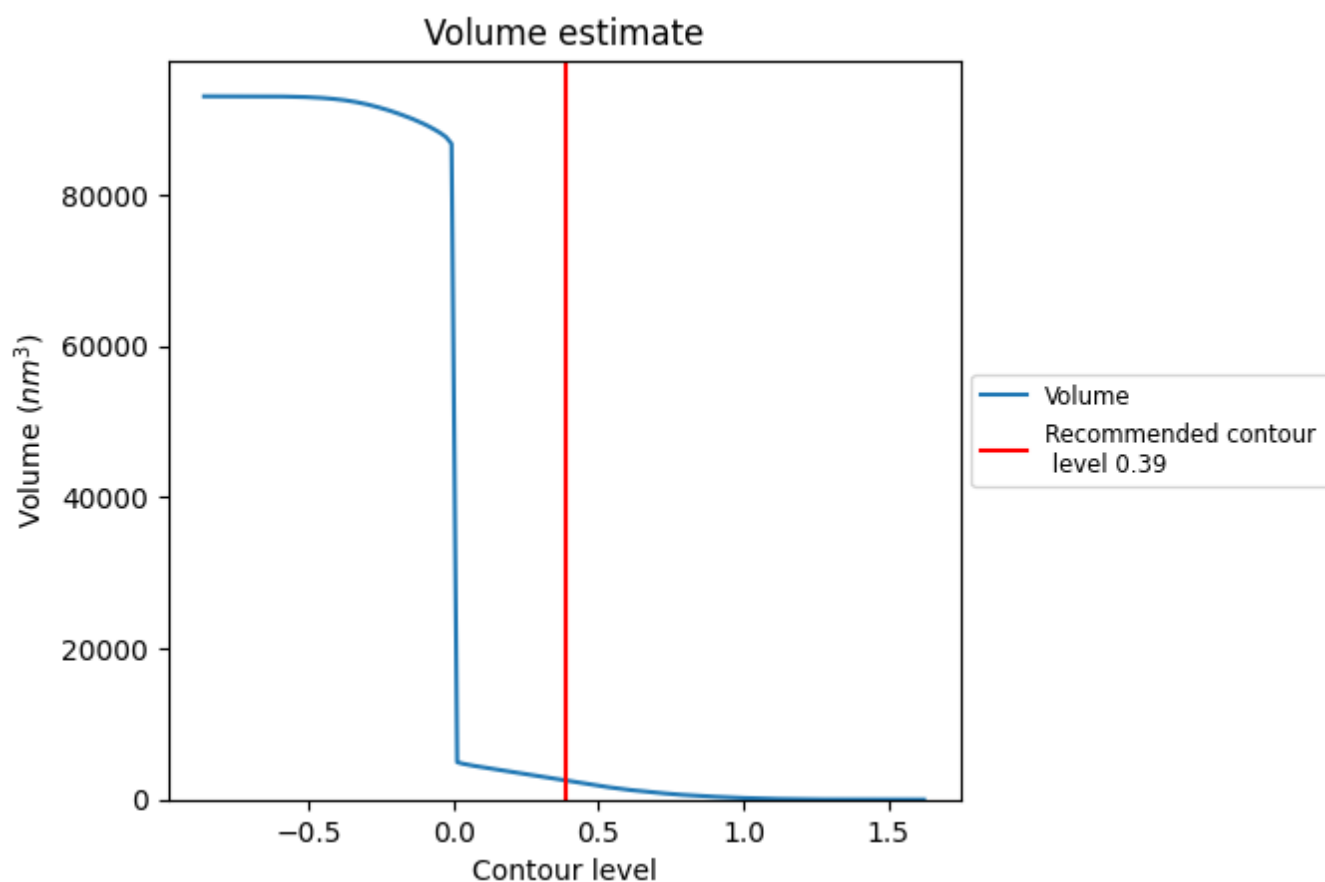
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

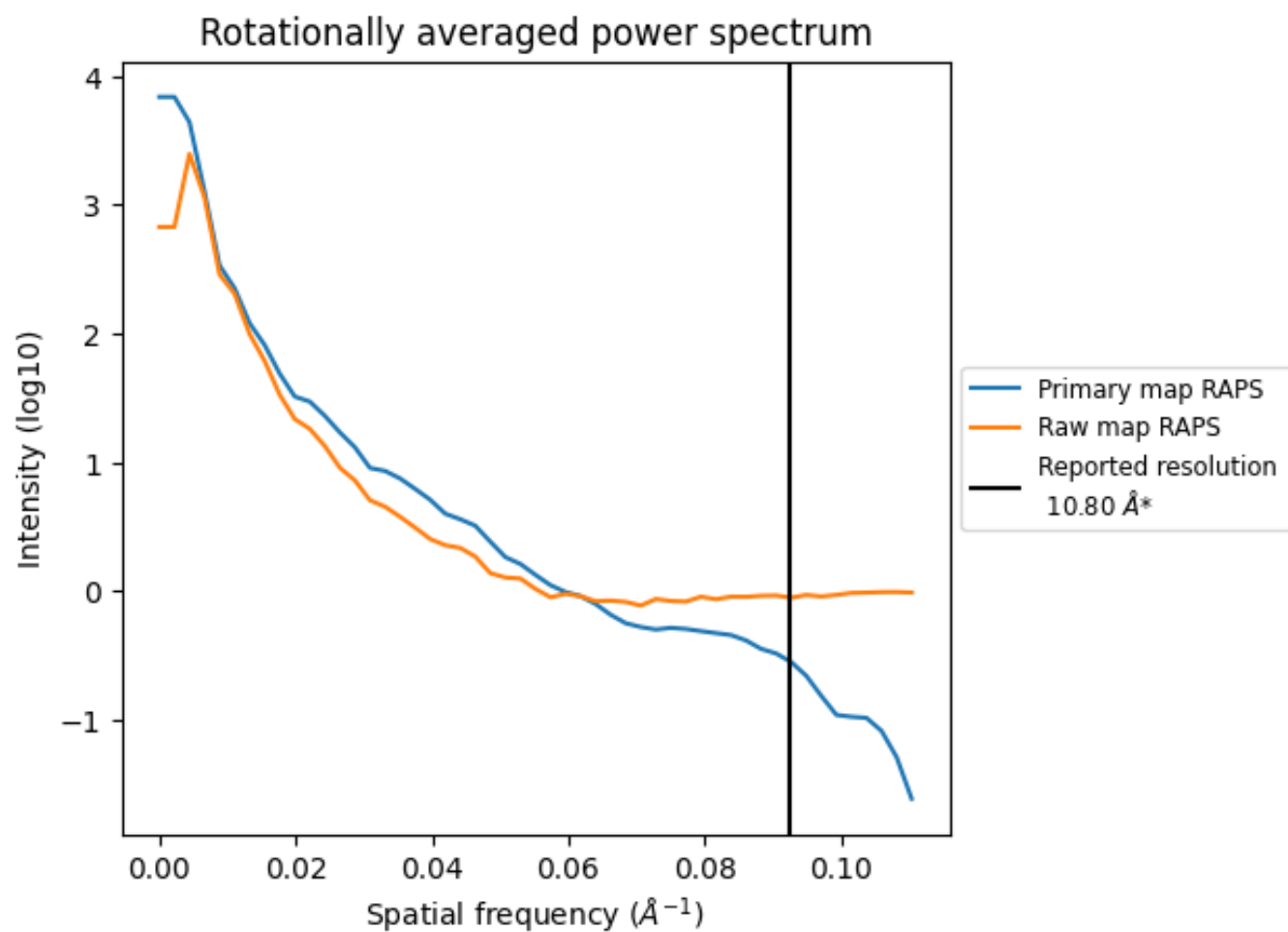
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2482 nm³; this corresponds to an approximate mass of 2242 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

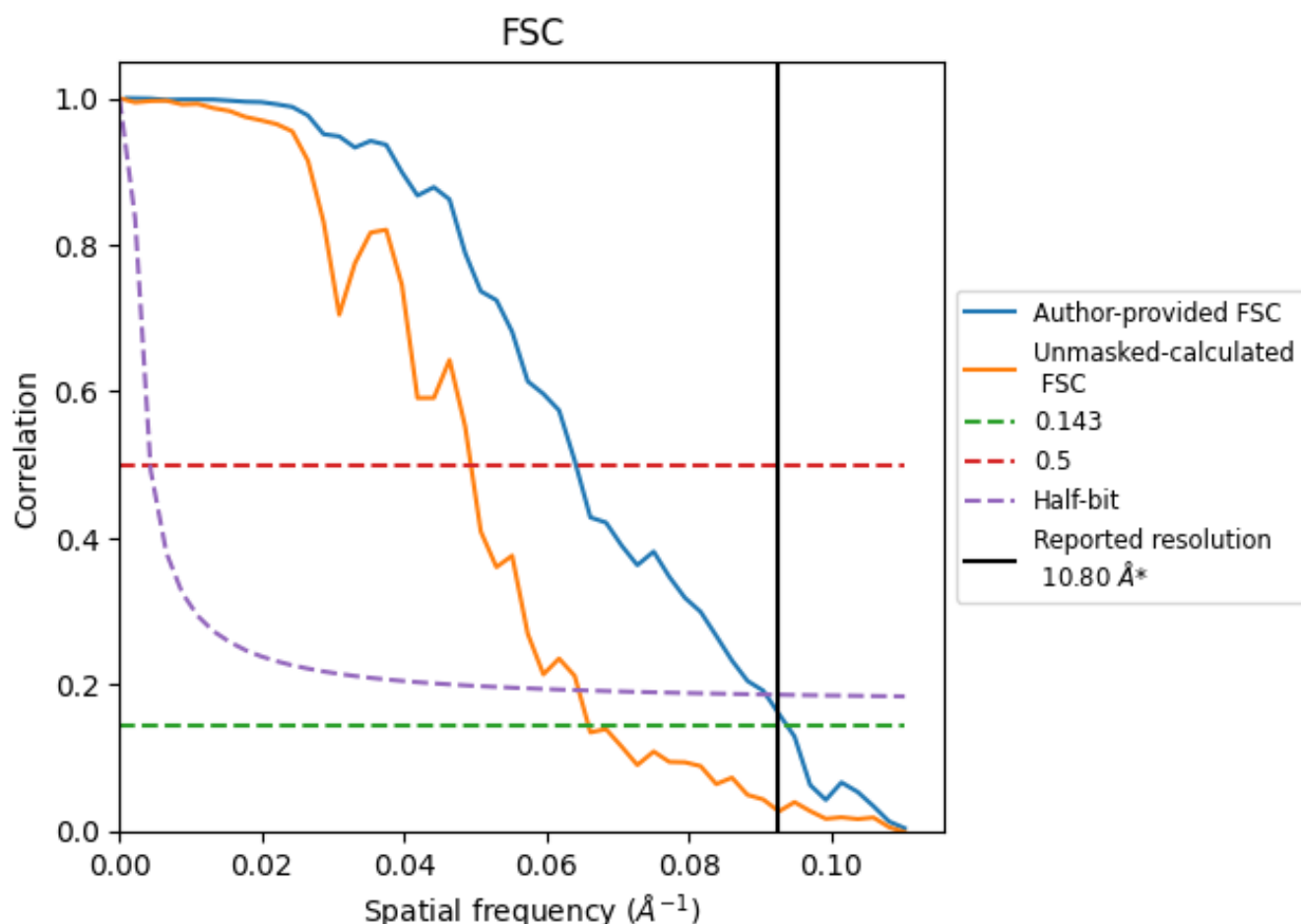


*Reported resolution corresponds to spatial frequency of 0.093 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.093 \AA^{-1}

8.2 Resolution estimates [i](#)

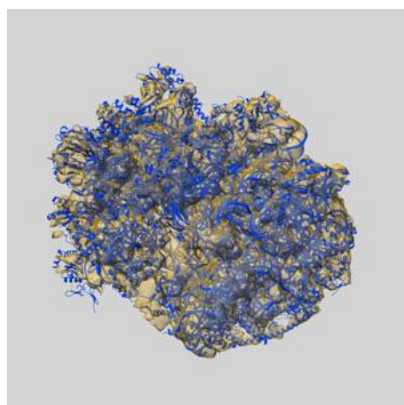
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	10.80	-	-
Author-provided FSC curve	10.65	15.58	11.00
Unmasked-calculated*	15.15	20.24	15.48

*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 15.15 differs from the reported value 10.8 by more than 10 %

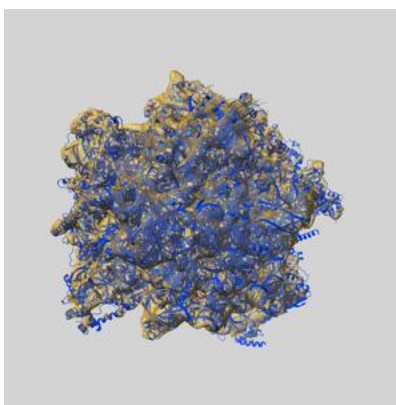
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-17448 and PDB model 8P5D. Per-residue inclusion information can be found in section [3](#) on page [18](#).

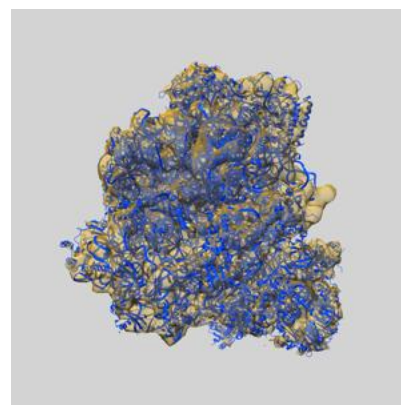
9.1 Map-model overlay [i](#)



X



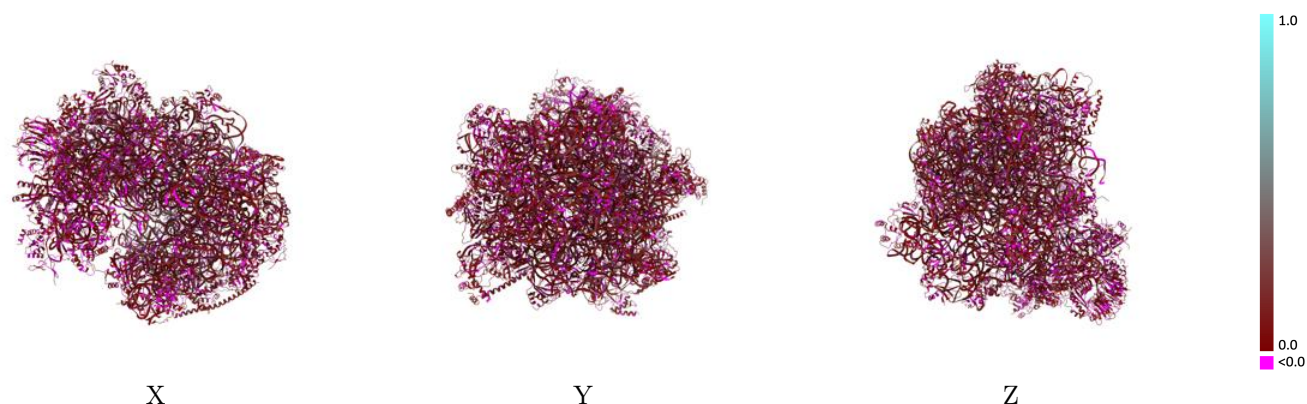
Y



Z

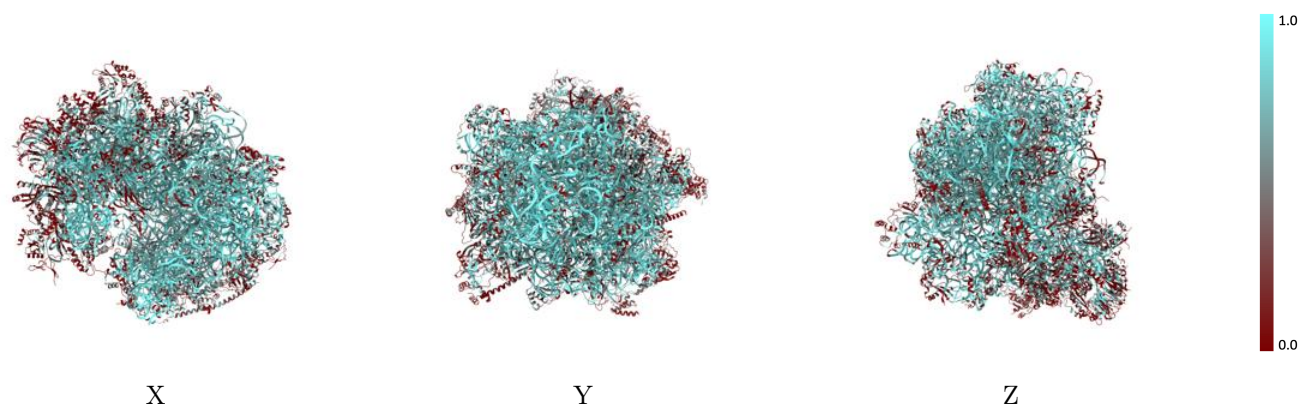
The images above show the 3D surface view of the map at the recommended contour level 0.39 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



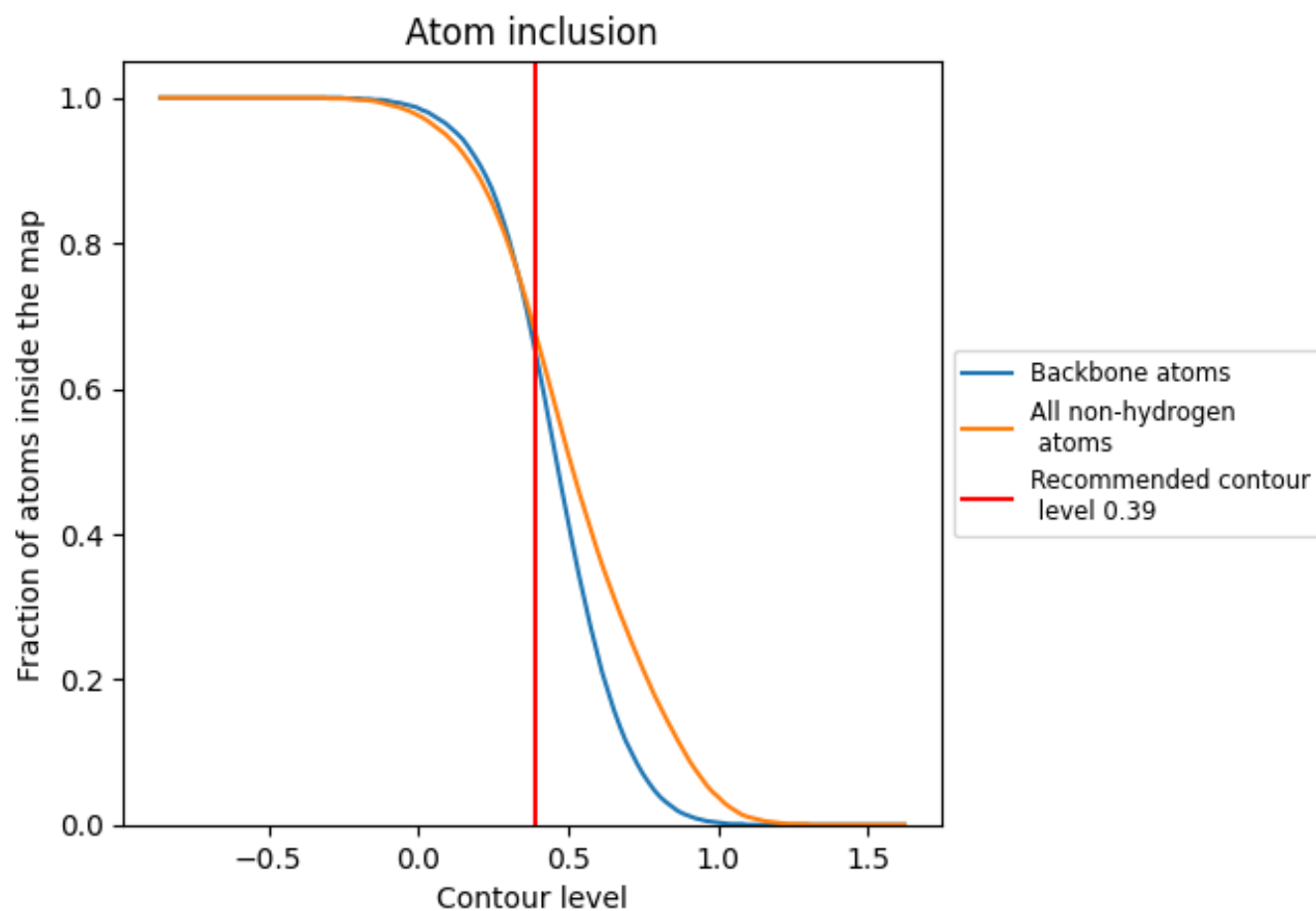
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.39).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 68% 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 (0.39) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6780	 0.0880
L50	 0.9150	 0.1100
L70	 0.9040	 0.1200
LA0	 0.5280	 0.0500
LAA	 0.7060	 0.0460
LB0	 0.5470	 0.0550
LC0	 0.5060	 0.0530
LCC	 0.4150	 0.0890
LD0	 0.5650	 0.0600
LDD	 0.5200	 0.0830
LE0	 0.3100	 0.0940
LEE	 0.5220	 0.0490
LF0	 0.4930	 0.0820
LFF	 0.5130	 0.0670
LG0	 0.4810	 0.0950
LGG	 0.5720	 0.0420
LH0	 0.4950	 0.0810
LHH	 0.5640	 0.0950
LI0	 0.5460	 0.0630
LII	 0.5210	 0.0730
LJ0	 0.5060	 0.0720
LJJ	 0.7270	 0.0670
LL0	 0.5870	 0.0660
LLL	 0.5270	 0.0420
LM0	 0.3300	 0.0970
LMM	 0.6050	 0.0700
LN0	 0.7350	 0.0210
LO0	 0.4870	 0.0860
LOO	 0.5920	 0.0590
LP0	 0.5630	 0.0720
LPP	 0.5880	 0.0790
LQ0	 0.5240	 0.0650
LR0	 0.4620	 0.0860
LS0	 0.4650	 0.0850
LT0	 0.5090	 0.0430



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Chain	Atom inclusion	Q-score
LU0	 0.5760	 0.0960
LV0	 0.3960	 0.0630
LW0	 0.2860	 0.0700
LX0	 0.4370	 0.0780
LY0	 0.5510	 0.0880
LZ0	 0.3690	 0.0760
MD1	 0.2650	 0.0630
S60	 0.8810	 0.1040
SA0	 0.2730	 0.0810
SAA	 0.4940	 0.0590
SB0	 0.3950	 0.0660
SBB	 0.4690	 0.0830
SC0	 0.4390	 0.0860
SCC	 0.1420	 0.0520
SD0	 0.2890	 0.0880
SDD	 0.5110	 0.0520
SE0	 0.4240	 0.0690
SEE	 0.3990	 0.0730
SF0	 0.4840	 0.0640
SFF	 0.0260	 0.0160
SG0	 0.3730	 0.0740
SGG	 0.3450	 0.0650
SH0	 0.2640	 0.0870
SI0	 0.4300	 0.0500
SJ0	 0.4350	 0.0830
SK0	 0.2860	 0.0660
SL0	 0.3800	 0.0780
SM0	 0.1760	 0.0430
SN0	 0.4590	 0.0740
SO0	 0.5000	 0.0440
SP0	 0.3270	 0.0440
SQ0	 0.4240	 0.0520
SR0	 0.2240	 0.0710
SS0	 0.4530	 0.0570
ST0	 0.4690	 0.0750
SU0	 0.3330	 0.0770
SV0	 0.3190	 0.0940
SW0	 0.4180	 0.0710
SX0	 0.2580	 0.0350
SY0	 0.4020	 0.0650
SZ0	 0.4930	 0.0580