



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 07:31 PM UTC

PDB ID : 6RM3 / pdb_00006rm3
EMDB ID : EMD-4935
Title : Evolutionary compaction and adaptation visualized by the structure of the dormant microsporidian ribosome
Authors : Barandun, J.; Hunziker, M.; Vossbrinck, C.R.; Klinge, S.
Deposited on : 2019-05-05
Resolution : 3.40 Å(reported)
Based on initial model : 4V88

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:

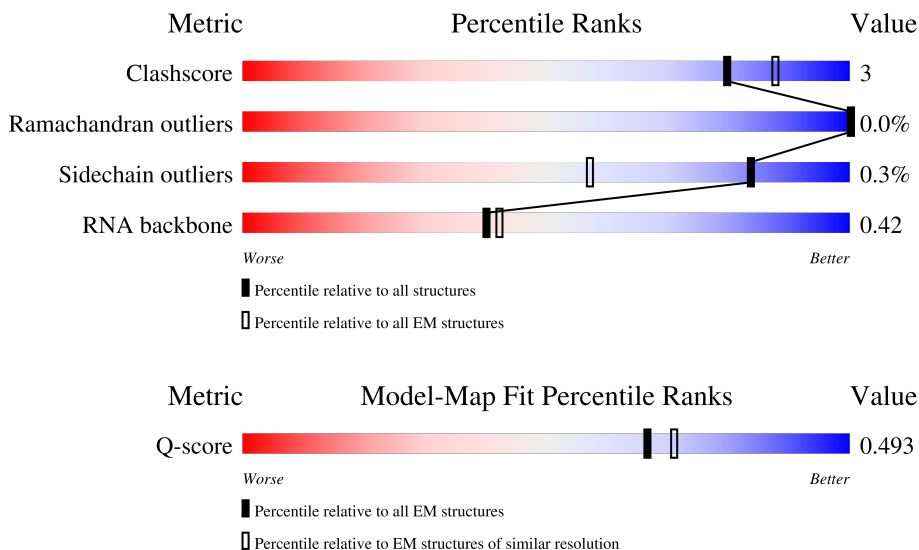
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	14717 (2.90 - 3.90)

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	S60	1244	
2	L70	119	
3	LA0	237	

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Mol	Chain	Length	Quality of chain
4	SA0	264	46% 67% 7% 25%
5	LAA	148	95% 5%
6	SAA	104	22% 85% 9% 7%
7	LB0	384	9% 88% 8%
8	SB0	237	49% 76% 13% 11%
9	LBB	55	5% 87% 5% 7%
10	SBB	94	51% 82% 5% 13%
11	LC0	334	8% 90% 9%
12	SC0	237	24% 79% 12% 8%
13	LCC	108	25% 93%
14	SCC	67	82% 82% 12% 6%
15	LD0	295	12% 90% 6%
16	SD0	215	79% 91% 7%
17	LDD	111	9% 84% 8% 8%
18	SDD	68	62% 88% 10%
19	LE0	172	78% 91% 8%
20	SE0	262	46% 91% 6%
21	LEE	139	85% 12%
22	SEE	60	53% 87% 7% 7%
23	LF0	239	5% 88% 8%
24	SF0	189	77% 92% 8%
25	LFF	98	5% 91% 7%
26	SFF	151	45% 55%
27	LG0	200	31% 92% 6%
28	SG0	217	52% 76% 17% 7%

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Mol	Chain	Length	Quality of chain
29	LGG	106	6% 83% 11% 6%
30	SGG	337	96% 81% 17%
31	LH0	186	15% 90% 9%
32	SH0	161	64% 76% 20%
33	LHH	122	7% 93% 5%
34	LI0	217	8% 91% 8%
35	SI0	166	13% 83% 12% 5%
36	LII	95	6% 91% 7%
37	LJ0	171	33% 88% 10%
38	SJ0	189	32% 81% 9% 10%
39	LJJ	93	96% ..
40	LL0	162	6% 91% 9%
41	SL0	158	27% 85% 15%
42	LLL	52	6% 94% ..
43	LM0	105	29% 82% 5% 13%
44	LMM	127	7% 35% 5% 61%
45	SM0	131	91% 83% 8% 9%
46	LN0	204	92% 8%
47	SN0	149	30% 87% 11%
48	LNN	160	35% 47% 50%
49	SNN	168	82% 88% 11%
50	LO0	192	9% 85% 5% 10%
51	SO0	135	28% 78% 19%
52	LOO	103	9% 87% 8% 5%
53	LP0	169	85% 7% 9%

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Mol	Chain	Length	Quality of chain
54	SP0	143	69% 67% 15% 17%
55	LPP	89	87% 7% 7%
56	LQ0	193	5% 89% 6% 5%
57	SQ0	155	77% 90% 8%
58	LR0	175	14% 85% 9% 6%
59	SR0	119	86% 81% 18%
60	LS0	180	6% 93% 7%
61	SS0	160	82% 84% 11% 6%
62	LT0	160	9% 92% 8%
63	ST0	133	92% 86% 13%
64	LU0	107	32% 84% 7% 9%
65	SU0	101	77% 80% 15% 5%
66	LV0	146	8% 90% 8%
67	SV0	67	36% 85% 9% 6%
68	LW0	91	34% 86% 12%
69	SW0	127	13% 93% 7%
70	LX0	102	5% 88% 9%
71	SX0	140	15% 96%
72	LXX	73	14% 68% 7% 25%
73	LY0	139	19% 88% 8%
74	SY0	133	55% 80% 14% 6%
75	LZ0	126	42% 87% 11%
76	SZ0	123	70% 66% 8% 26%
77	SK0	99	79% 77% 9% 14%
78	L50	2484	69% 22% 7%

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 164223 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 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	S60	1231	26291	11769	4701	8590	1231	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	L70	118	2523	1128	460	817	118	0	0

- Molecule 3 is a protein called uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	LA0	232	1789	1124	336	321	8	0	0

- Molecule 4 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	SA0	197	1558	1002	262	285	9	0	0

- Molecule 5 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	LAA	148	1219	778	240	196	5	0	0

- Molecule 6 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	SAA	97	776	481	157	130	8	0	0

- Molecule 7 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	LB0	368	2912	1851	537	515	9	0	0

- Molecule 8 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	SB0	210	1664	1050	297	306	11	0	0

- Molecule 9 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	LBB	51	416	262	84	68	2	0	0

- Molecule 10 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	SBB	82	637	404	107	118	8	0	0

- Molecule 11 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	LC0	329	2624	1656	482	474	12	0	0

- Molecule 12 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	SC0	217	1642	1042	287	308	5	0	0

- Molecule 13 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	LCC	104	797	510	137	146	4	0	0

- Molecule 14 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SCC	63	Total	C	N	O	S	0	0
			495	305	97	90	3		

- Molecule 15 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LD0	282	Total	C	N	O	S	0	0
			2320	1466	422	425	7		

- Molecule 16 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SD0	210	Total	C	N	O	S	0	0
			1624	1052	279	286	7		

- Molecule 17 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LDD	102	Total	C	N	O	S	0	0
			821	526	150	140	5		

- Molecule 18 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SDD	67	Total	C	N	O	S	0	0
			541	343	96	97	5		

- Molecule 19 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LE0	172	Total	C	N	O	S	0	0
			1410	899	229	274	8		

- Molecule 20 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SE0	256	Total	C	N	O	S	0	0
			2056	1320	343	386	7		

- Molecule 21 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LEE	123	Total	C	N	O	S	0	0
			1010	643	200	164	3		

- Molecule 22 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SEE	56	Total	C	N	O	S	0	0
			454	281	92	77	4		

- Molecule 23 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LF0	230	Total	C	N	O	S	0	0
			1884	1209	327	342	6		

- Molecule 24 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SF0	188	Total	C	N	O	S	0	0
			1457	897	277	277	6		

- Molecule 25 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LFF	96	Total	C	N	O	S	0	0
			771	486	154	129	2		

- Molecule 26 is a protein called eS31.

Mol	Chain	Residues	Atoms			AltConf	Trace
26	SFF	68	Total	C	N	0	0
			266	198	68		

- Molecule 27 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LG0	195	Total	C	N	O	S	0	0
			1573	1010	272	283	8		

- Molecule 28 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SG0	201	Total	C	N	O	S	0	0
			1587	990	305	286	6		

- Molecule 29 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LGG	100	Total	C	N	O	S	0	0
			814	506	170	133	5		

- Molecule 30 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SGG	330	Total	C	N	O	S	0	0
			2499	1575	414	497	13		

- Molecule 31 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LH0	184	Total	C	N	O	S	0	0
			1452	930	253	258	11		

- Molecule 32 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	SH0	155	Total	C	N	O	S	0	0
			1265	812	208	239	6		

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LHH	120	Total	C	N	O	S	0	0
			1017	640	194	179	4		

- Molecule 34 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LI0	216	Total	C	N	O	S	0	0
			1743	1102	332	298	11		

- Molecule 35 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	SI0	158	1259	784	238	234	3	0	0

- Molecule 36 is a protein called eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	LII	93	765	489	148	126	2	0	0

- Molecule 37 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	LJ0	168	1348	854	246	241	7	0	0

- Molecule 38 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	SJ0	171	1382	877	245	258	2	0	0

- Molecule 39 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	LJJ	90	719	450	152	110	7	0	0

- Molecule 40 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	LL0	162	1328	831	265	225	7	0	0

- Molecule 41 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	SL0	157	1269	805	227	231	6	0	0

- Molecule 42 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LLL	51	Total	C	N	O	S	0	0
			445	283	93	68	1		

- Molecule 43 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LM0	91	Total	C	N	O	S	0	0
			731	471	122	137	1		

- Molecule 44 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LMM	50	Total	C	N	O	S	0	0
			402	241	87	70	4		

- Molecule 45 is a protein called eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SM0	119	Total	C	N	O	S	0	0
			929	582	168	174	5		

- Molecule 46 is a protein called eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LN0	203	Total	C	N	O	S	0	0
			1677	1046	342	280	9		

- Molecule 47 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SN0	147	Total	C	N	O	S	0	0
			1177	748	212	211	6		

- Molecule 48 is a protein called MDF2.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	LNN	80	Total	C	N	O	0	0
			577	345	125	107		

- Molecule 49 is a protein called MDF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	SNN	167	1336	844	221	261	10	0	0

- Molecule 50 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	LO0	173	1371	885	249	226	11	0	0

- Molecule 51 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	SO0	131	977	602	191	177	7	0	0

- Molecule 52 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	LO0	98	792	497	162	126	7	0	0

- Molecule 53 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	LP0	154	1235	778	242	210	5	0	0

- Molecule 54 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	SP0	118	942	601	174	160	7	0	0

- Molecule 55 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	LPP	83	642	403	122	111	6	0	0

- Molecule 56 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	LQ0	184	Total	C	N	O	S	0	0
			1460	920	273	260	7		

- Molecule 57 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SQ0	152	Total	C	N	O	S	0	0
			1205	773	208	215	9		

- Molecule 58 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	LR0	165	Total	C	N	O	S	0	0
			1342	840	263	232	7		

- Molecule 59 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SR0	117	Total	C	N	O	S	0	0
			958	604	173	176	5		

- Molecule 60 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	LS0	179	Total	C	N	O	S	0	0
			1472	952	251	265	4		

- Molecule 61 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SS0	151	Total	C	N	O	S	0	0
			1186	731	237	209	9		

- Molecule 62 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	LT0	159	Total	C	N	O	S	0	0
			1310	844	242	223	1		

- Molecule 63 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	ST0	131	Total	C	N	O	S	0	0
			1048	663	173	204	8		

- Molecule 64 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	LU0	97	Total	C	N	O	S	0	0
			790	502	138	148	2		

- Molecule 65 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SU0	96	Total	C	N	O	S	0	0
			764	495	126	141	2		

- Molecule 66 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	LV0	135	Total	C	N	O	S	0	0
			1040	650	203	180	7		

- Molecule 67 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SV0	63	Total	C	N	O	S	0	0
			491	304	88	97	2		

- Molecule 68 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	LW0	90	Total	C	N	O	S	0	0
			667	415	131	120	1		

- Molecule 69 is a protein called uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SW0	127	Total	C	N	O	S	0	0
			1018	645	188	179	6		

- Molecule 70 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	LX0	93	Total	C	N	O	S	0	0
			734	466	137	127	4		

- Molecule 71 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SX0	138	Total	C	N	O	S	0	0
			1069	687	193	187	2		

- Molecule 72 is a protein called msL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	LXX	55	Total	C	N	O	S	0	0
			462	297	84	80	1		

- Molecule 73 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	LY0	134	Total	C	N	O	S	0	0
			1088	682	203	198	5		

- Molecule 74 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SY0	125	Total	C	N	O	S	0	0
			1025	637	198	186	4		

- Molecule 75 is a protein called eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	LZ0	125	Total	C	N	O	S	0	0
			1006	647	178	176	5		

- Molecule 76 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SZ0	91	Total	C	N	O	S	0	0
			724	462	128	131	3		

- Molecule 77 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SK0	85	Total	C	N	O	S	0	0
			712	456	118	135	3		

- Molecule 78 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	L50	2313	Total	C	N	O	P	0	0
			49259	22082	8715	16149	2313		

- Molecule 79 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
79	S60	49	Total	Mg	0
			49	49	
79	L70	1	Total	Mg	0
			1	1	
79	LJJ	1	Total	Mg	0
			1	1	
79	LV0	1	Total	Mg	0
			1	1	
79	L50	122	Total	Mg	0
			122	122	

- Molecule 80 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
80	SAA	1	Total	Zn	0
			1	1	
80	SBB	1	Total	Zn	0
			1	1	
80	SDD	1	Total	Zn	0
			1	1	
80	LGG	1	Total	Zn	0
			1	1	
80	LJJ	1	Total	Zn	0
			1	1	
80	LMM	1	Total	Zn	0
			1	1	
80	SNN	1	Total	Zn	0
			1	1	
80	LOO	1	Total	Zn	0
			1	1	

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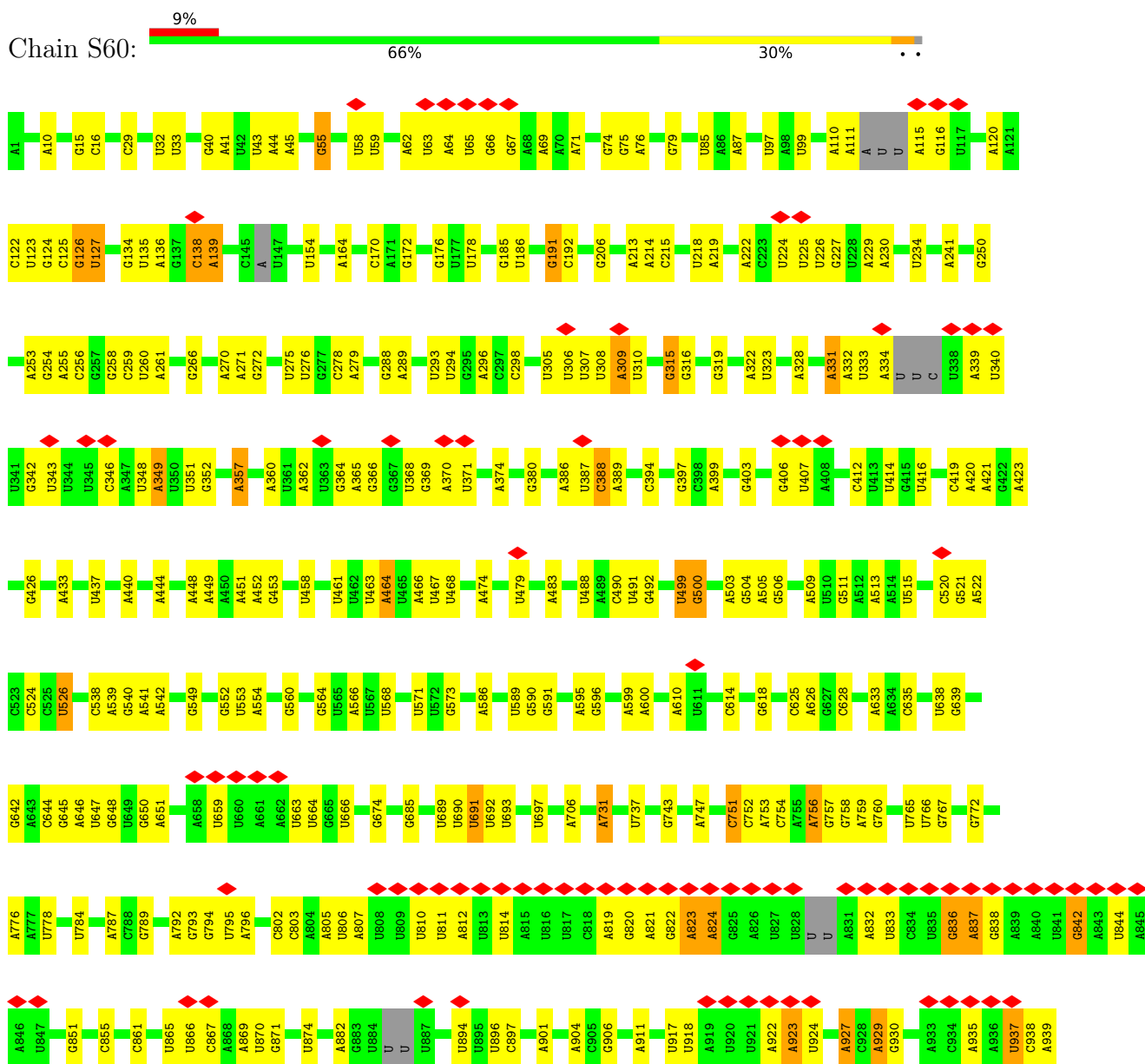
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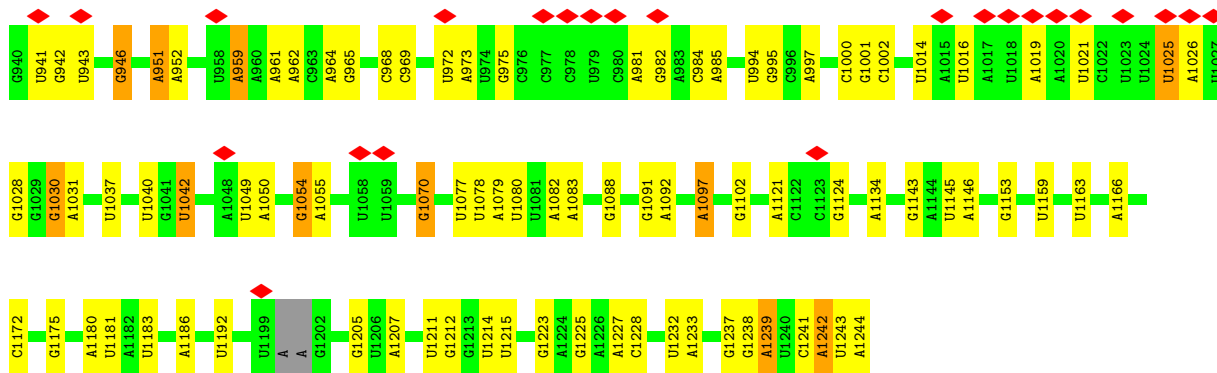
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
80	LPP	1	1	1	0

3 Residue-property plots

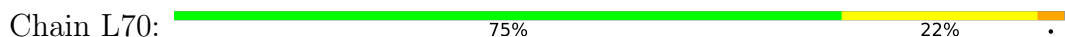
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S rRNA

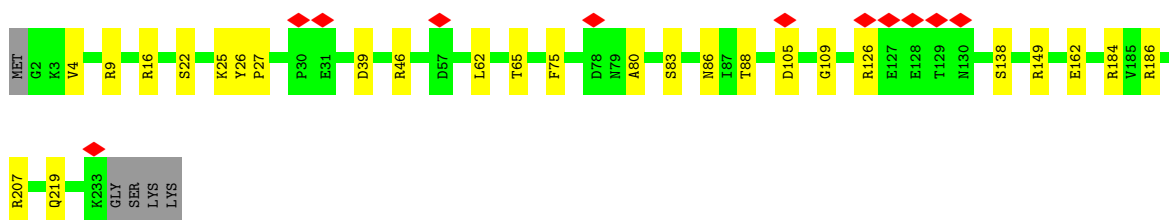




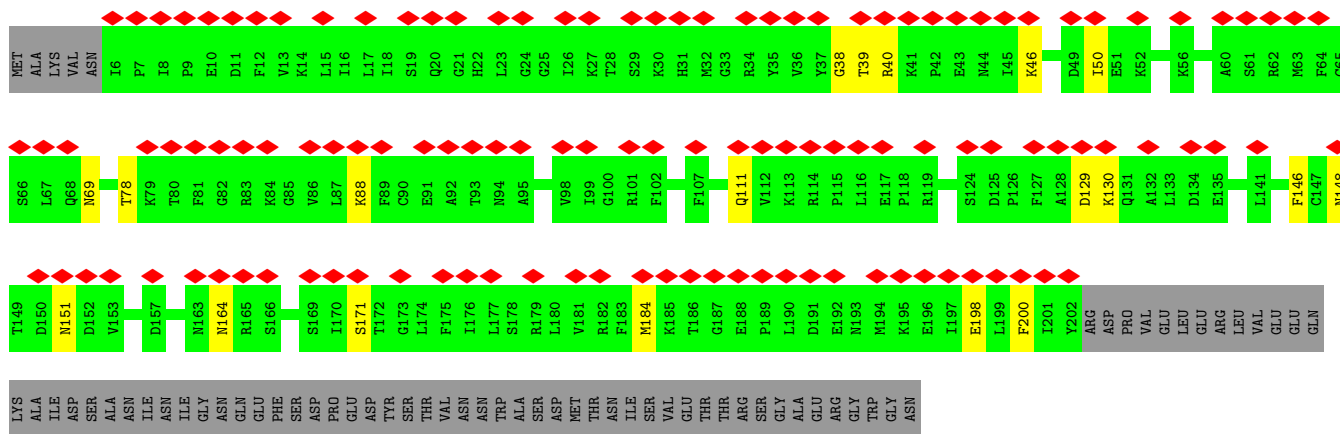
• Molecule 2: 5S rRNA



• Molecule 3: uL2



• Molecule 4: uS2

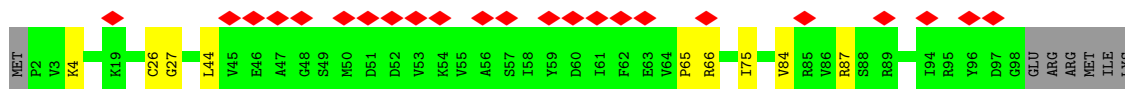
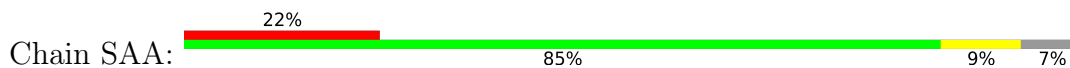


• Molecule 5: uL15

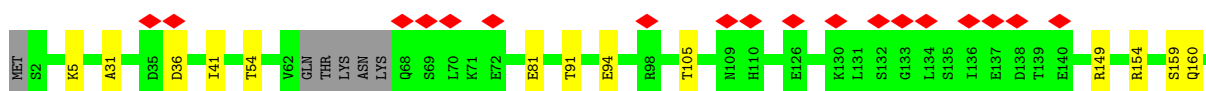




• Molecule 6: eS26

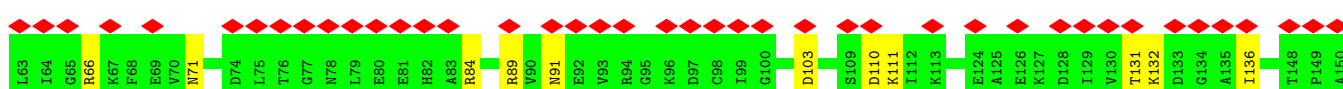
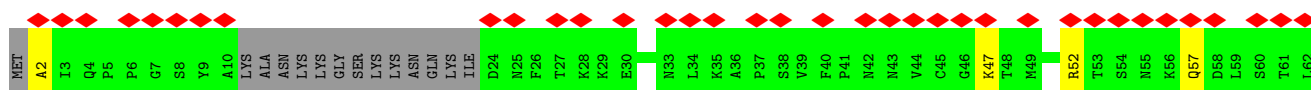
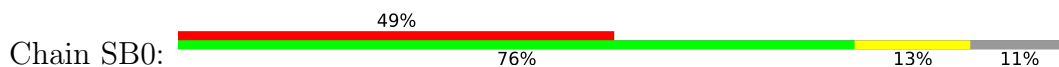


• Molecule 7: uL3



ASP

• Molecule 8: eS1

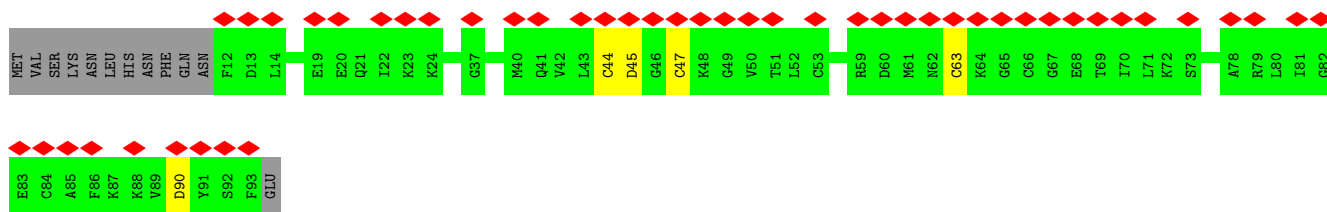
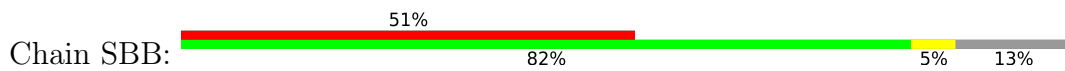


HIS, PRO, MET, THR, VAL, GLU, ALA, GLU, THR, TYR

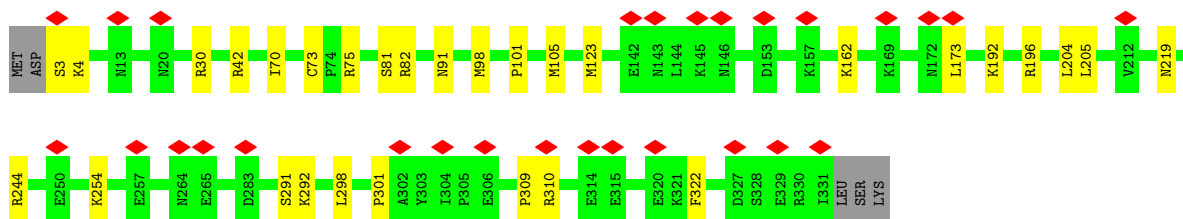
• Molecule 9: eL29



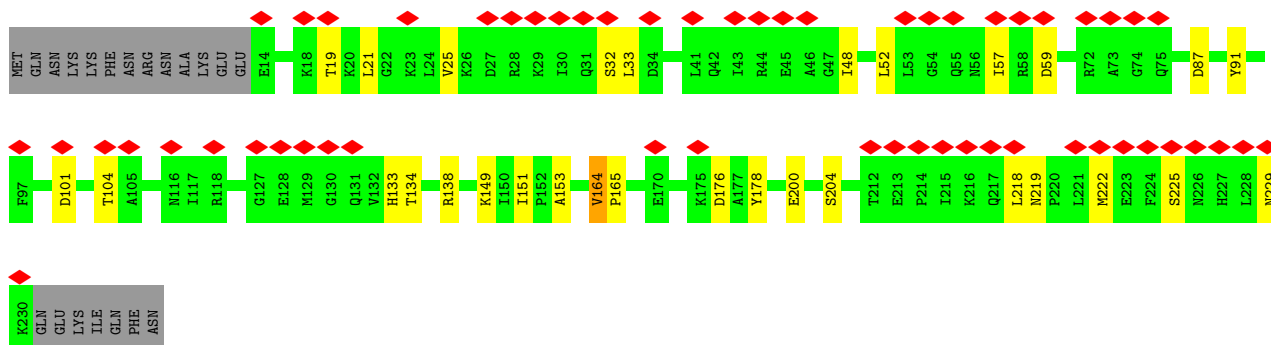
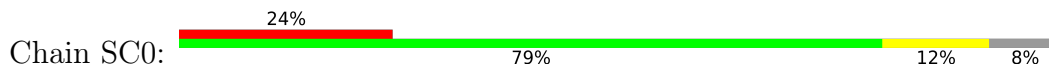
• Molecule 10: eS27



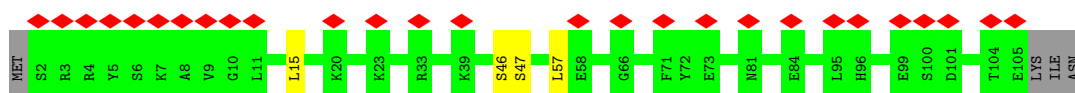
• Molecule 11: uL4



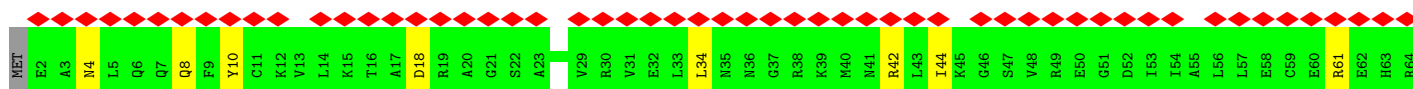
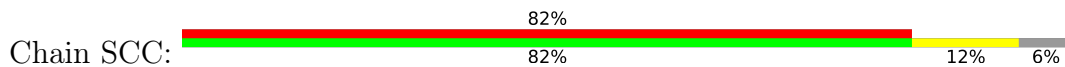
• Molecule 12: uS5



• Molecule 13: eL30

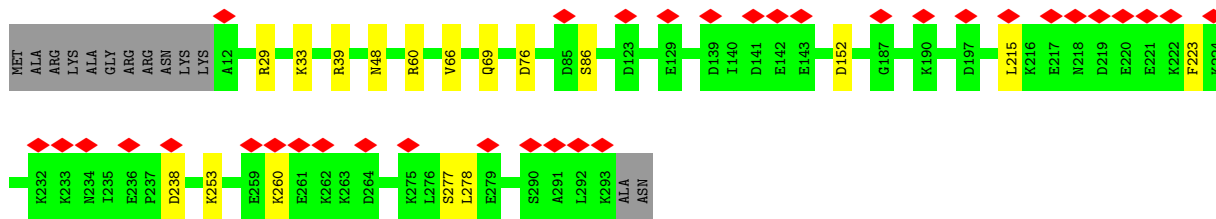


• Molecule 14: eS28

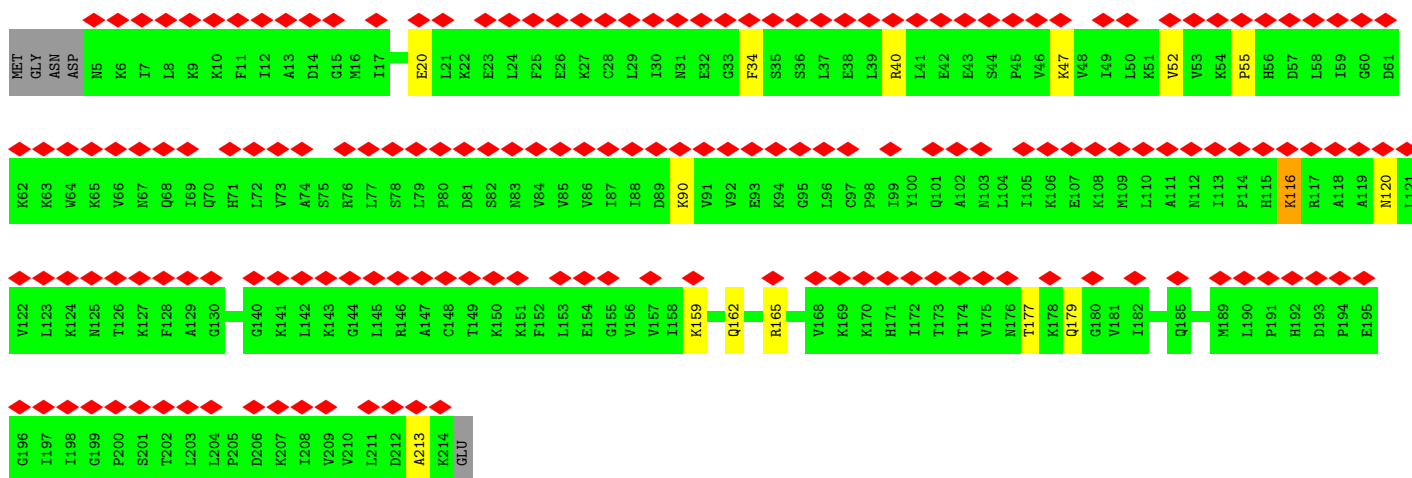
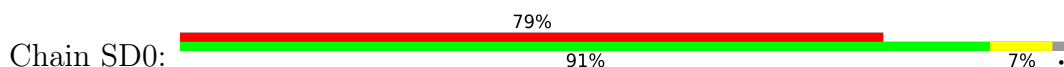


ARG
SER
ARG

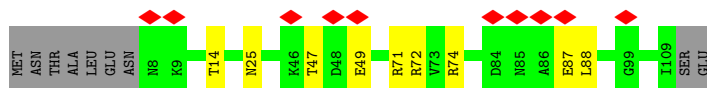
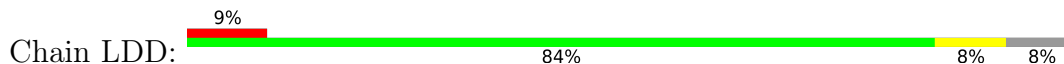
- Molecule 15: uL18



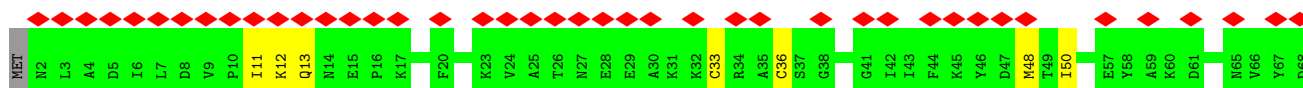
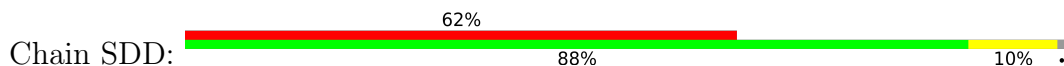
- Molecule 16: uS3



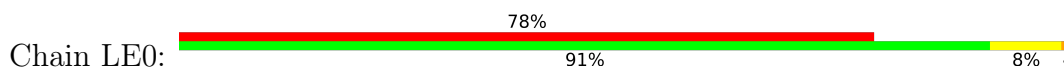
- Molecule 17: eL31

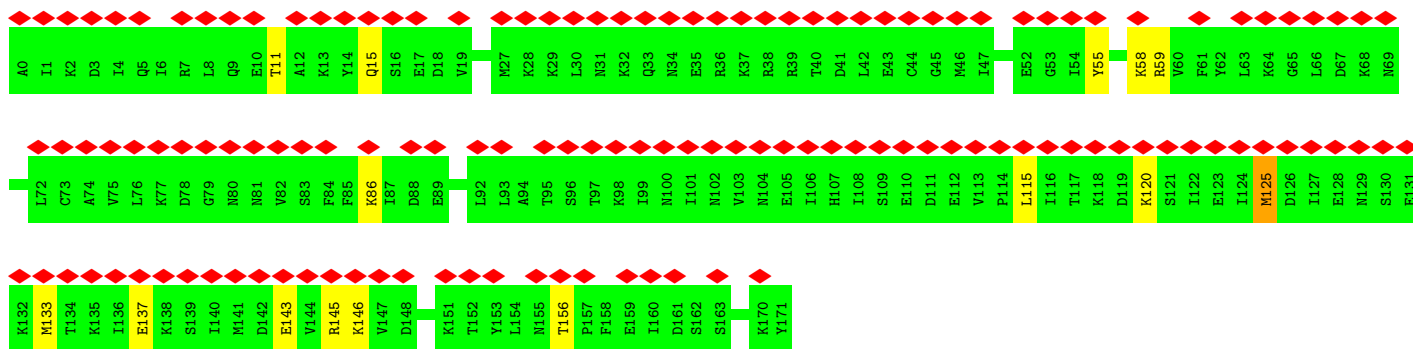


- Molecule 18: uS14

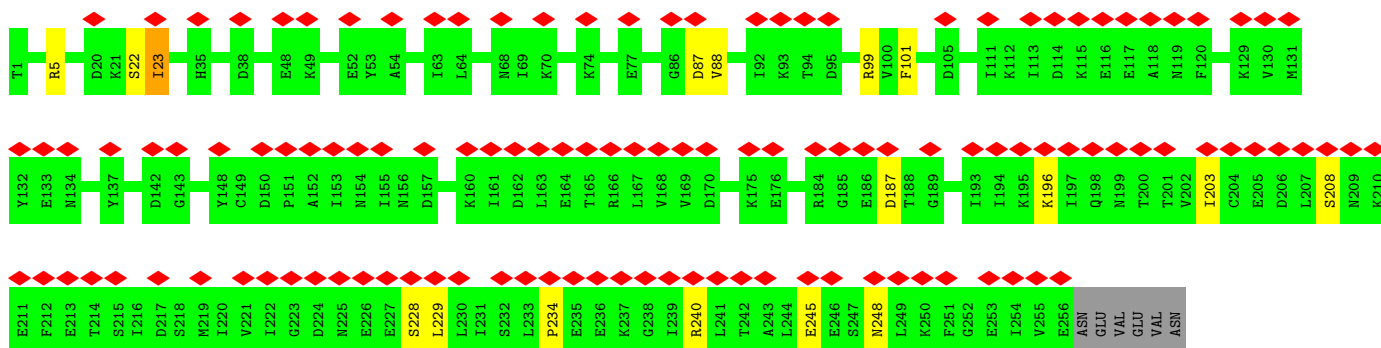


- Molecule 19: eL6

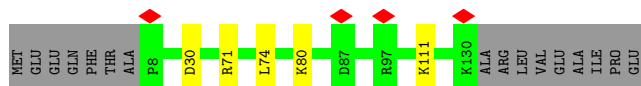
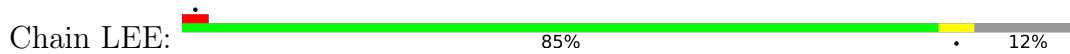




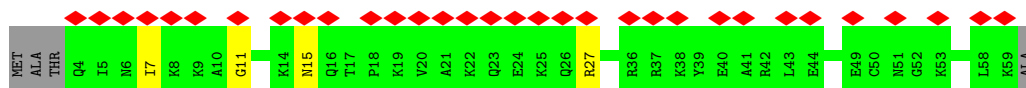
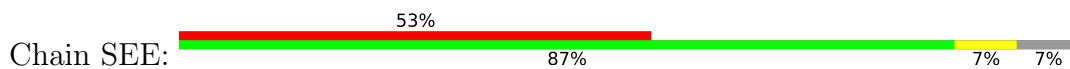
• Molecule 20: eS4



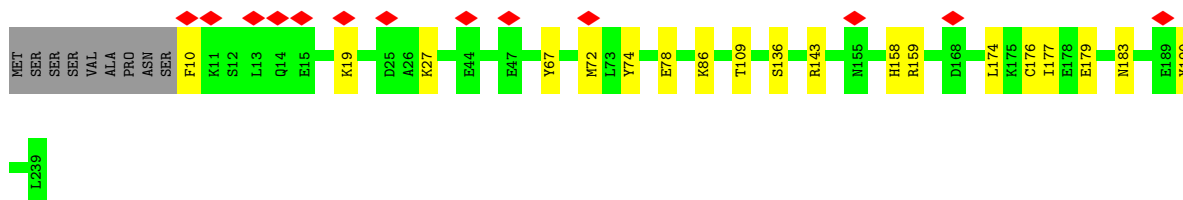
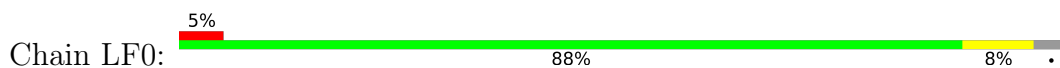
• Molecule 21: eL32



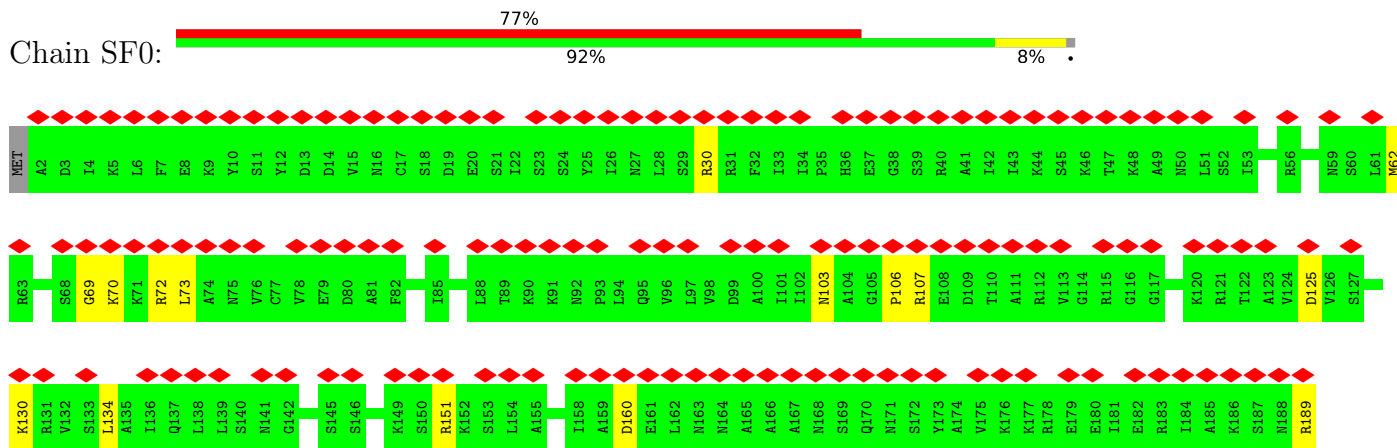
• Molecule 22: eS30



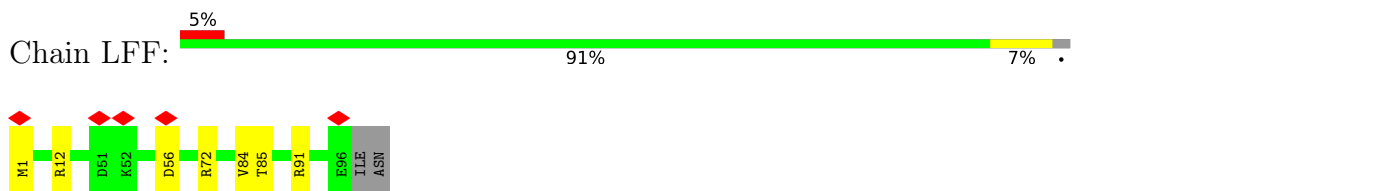
• Molecule 23: uL30



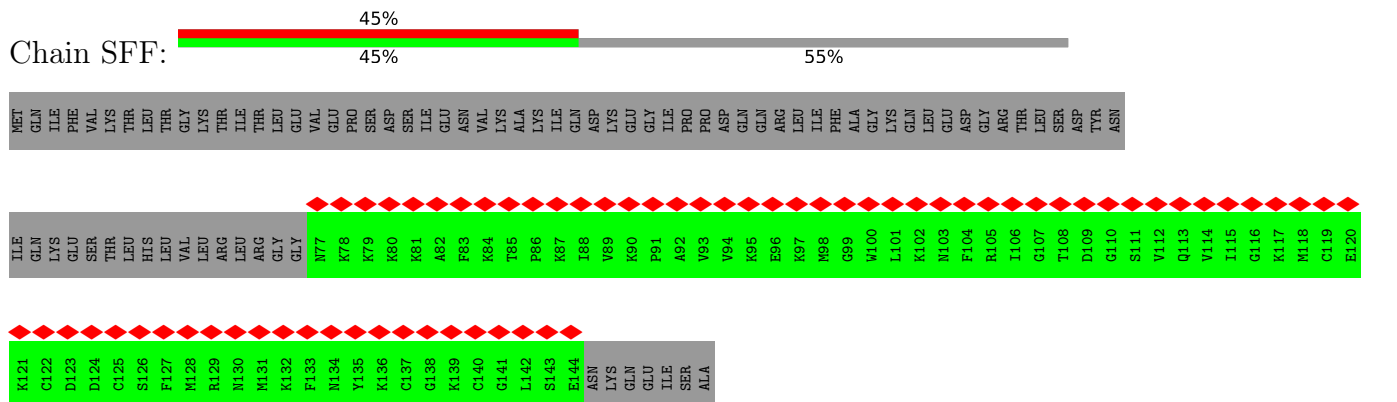
• Molecule 24: uS7



• Molecule 25: eL33



• Molecule 26: eS31



• Molecule 27: eL8

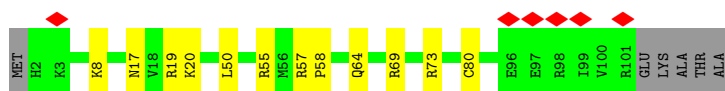
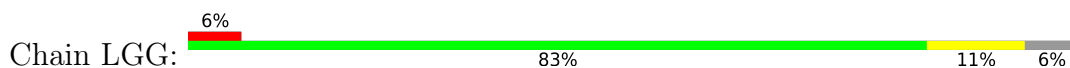


• Molecule 28: eS6

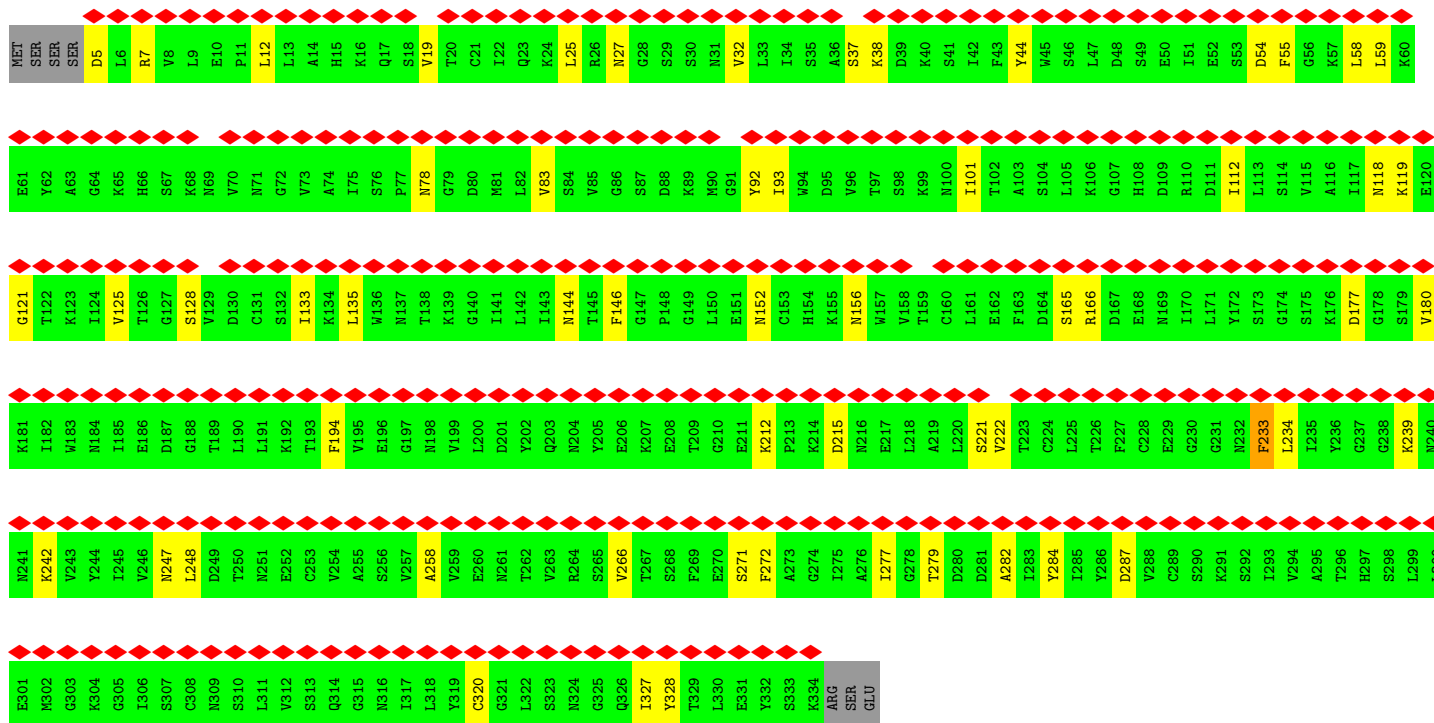
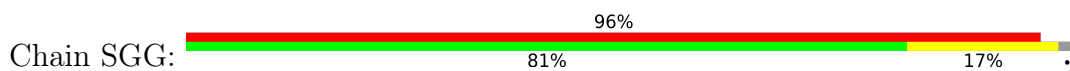




• Molecule 29: eL34



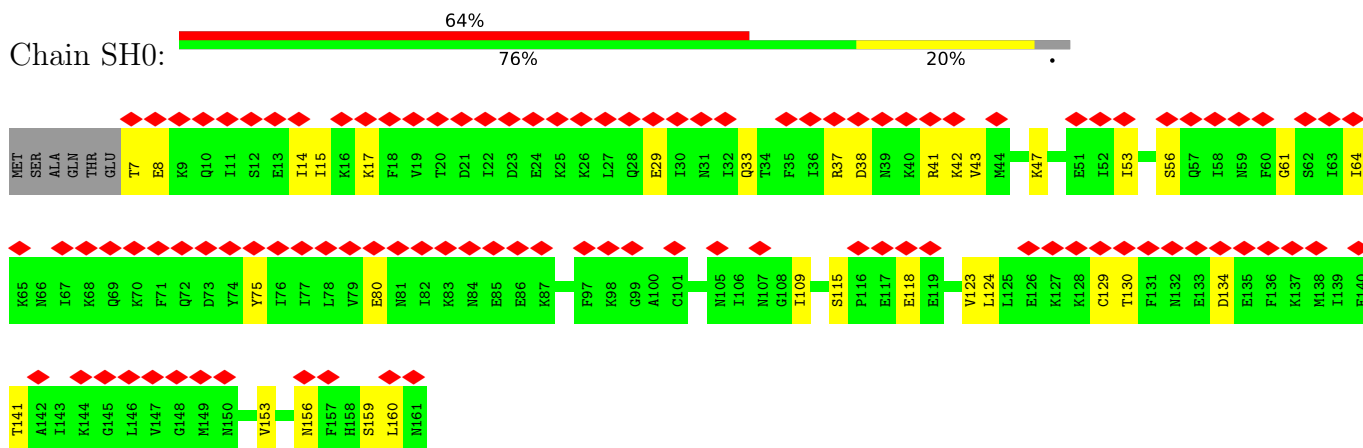
• Molecule 30: RACK1



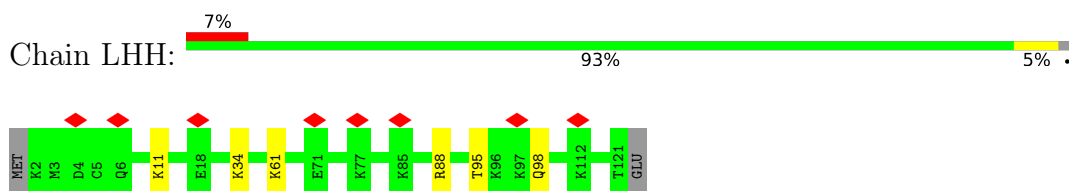
• Molecule 31: uL6



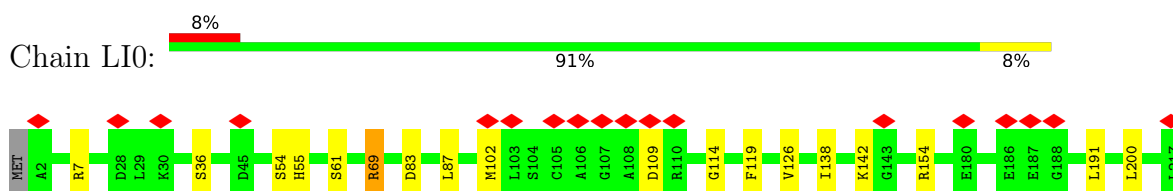
- Molecule 32: eS7



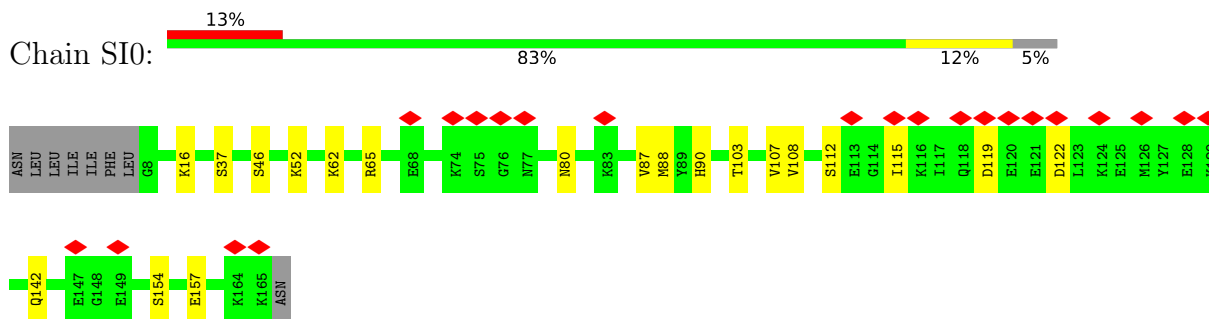
- Molecule 33: uL29



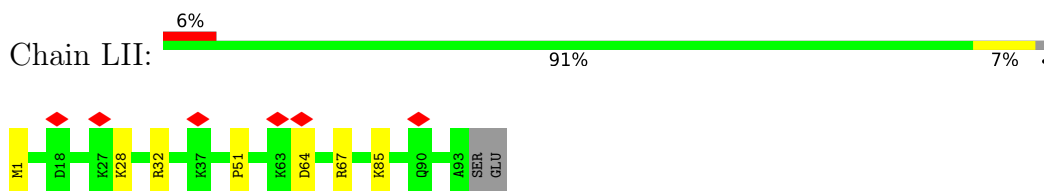
- Molecule 34: uL16



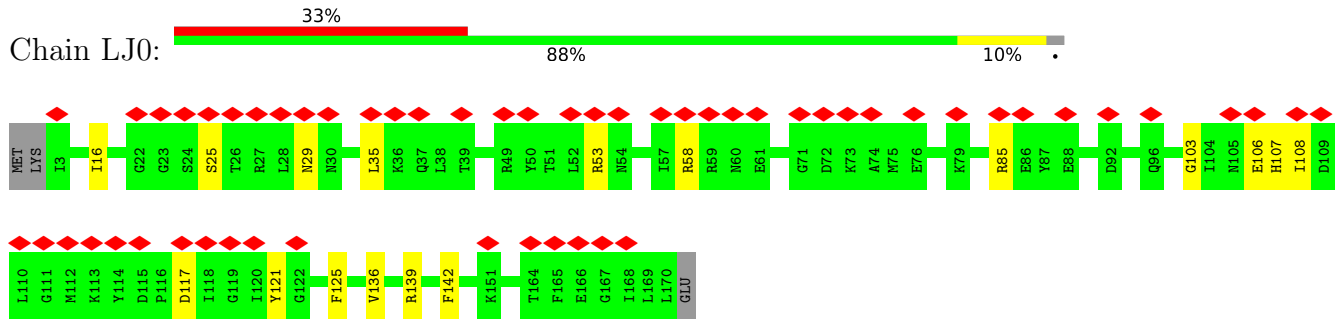
- Molecule 35: eS8



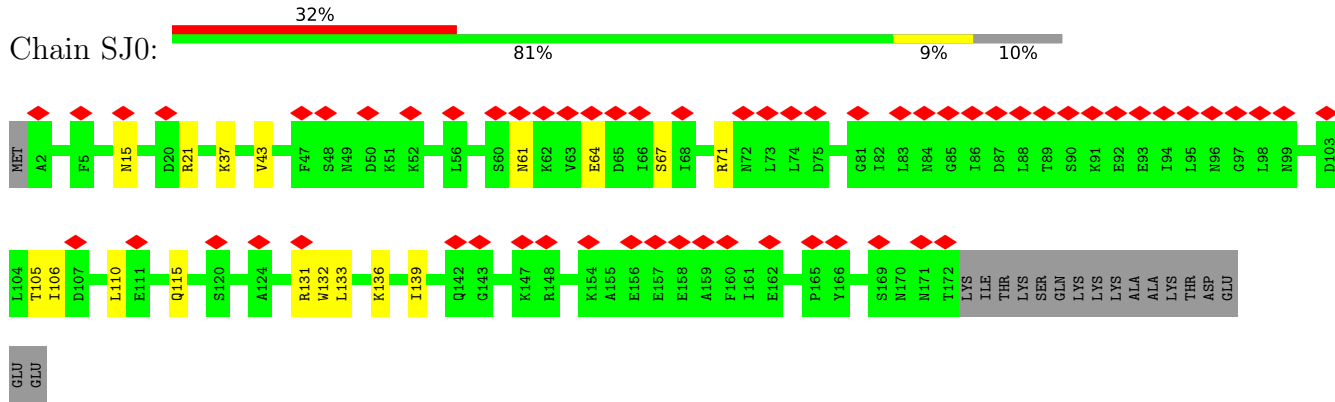
- Molecule 36: eL36



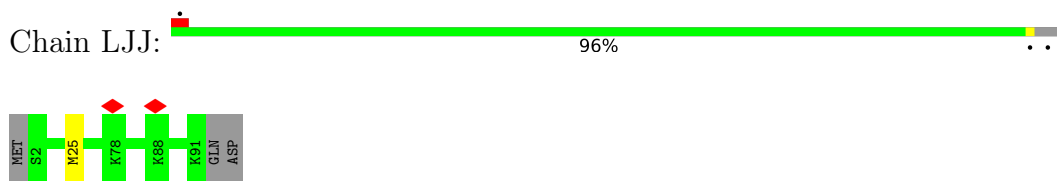
- Molecule 37: uL5



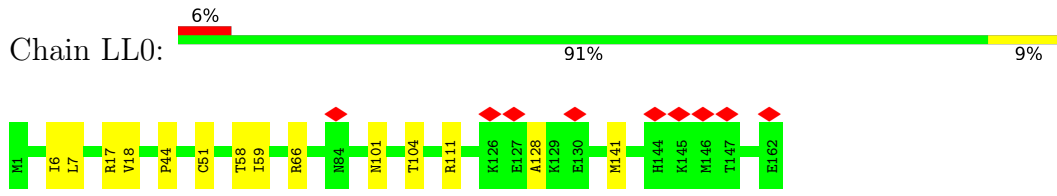
• Molecule 38: uS4



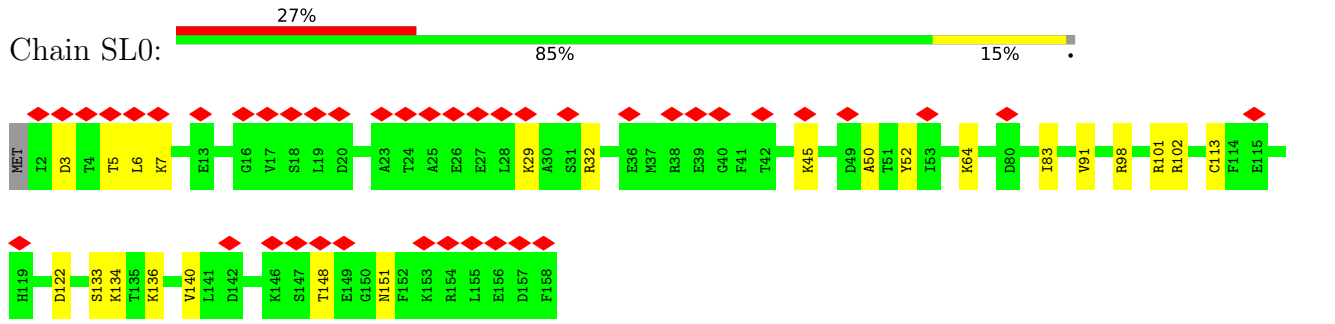
• Molecule 39: eL37



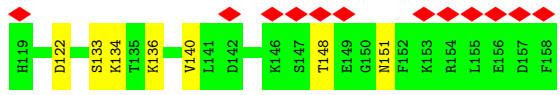
• Molecule 40: eL13

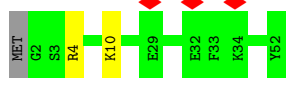


• Molecule 41: uS17

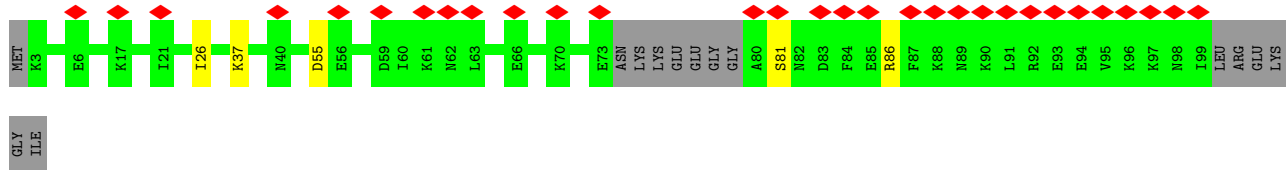
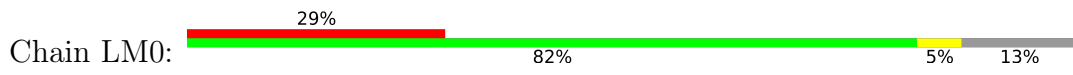


• Molecule 42: eL39

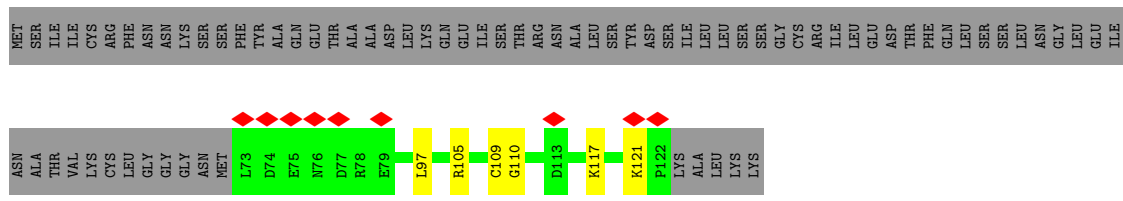
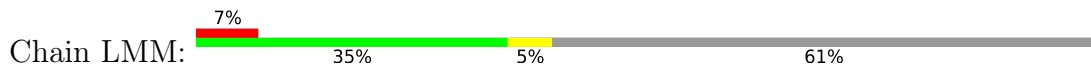




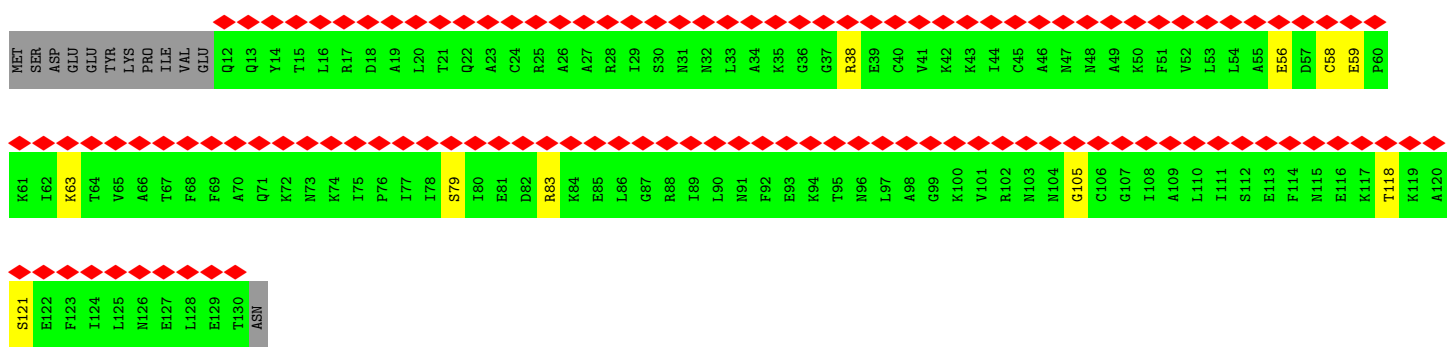
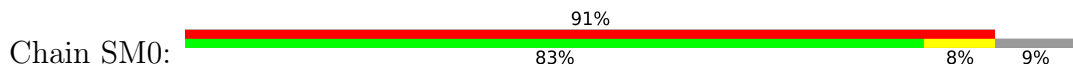
• Molecule 43: eL14



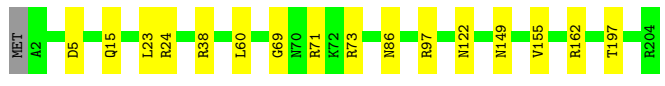
• Molecule 44: eL40



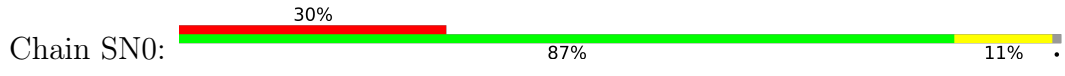
• Molecule 45: eS12

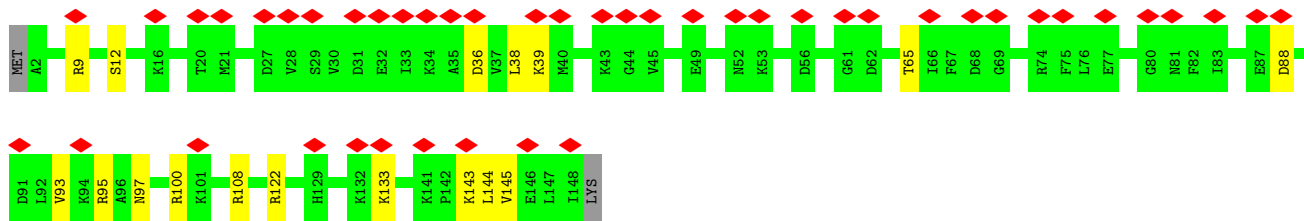


• Molecule 46: eL15

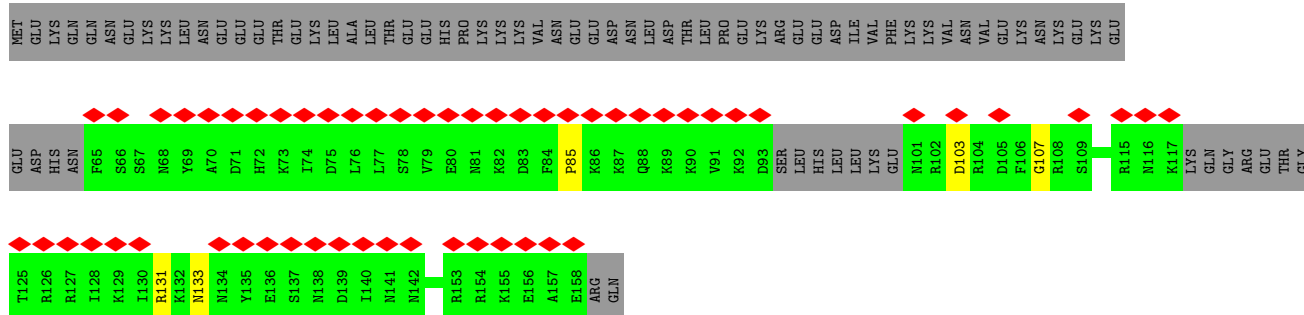


• Molecule 47: uS15

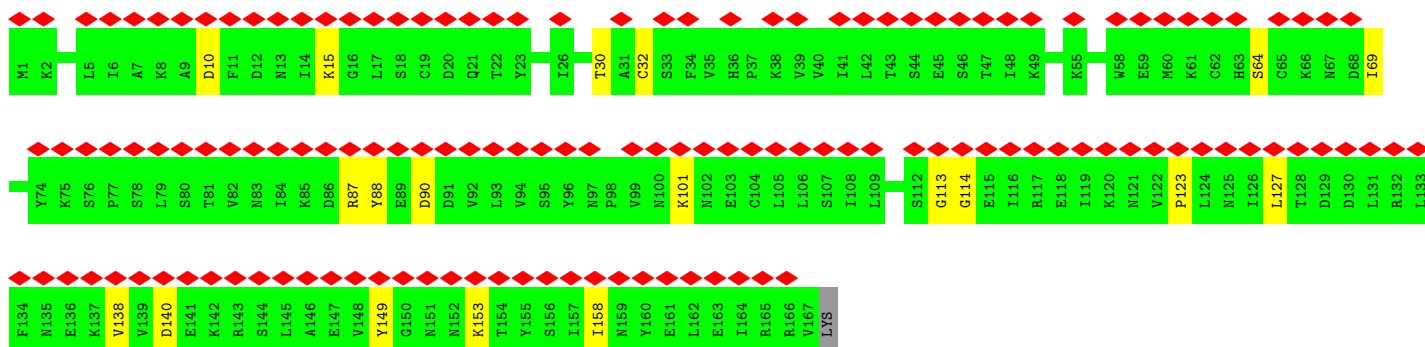
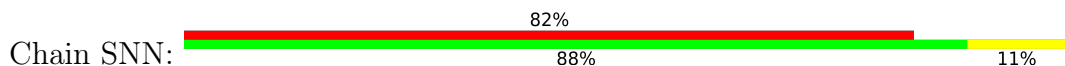




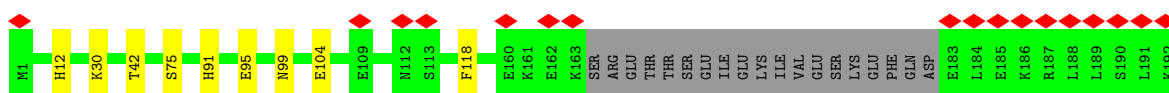
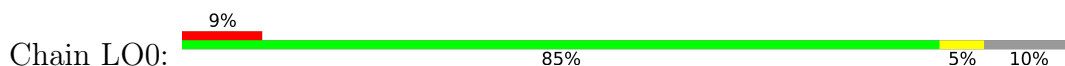
• Molecule 48: MDF2



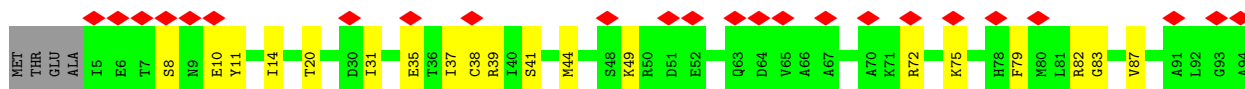
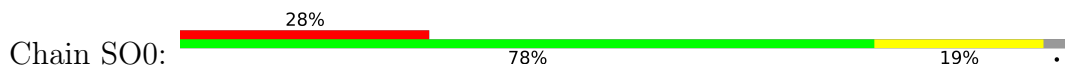
• Molecule 49: MDF1



• Molecule 50: uL13

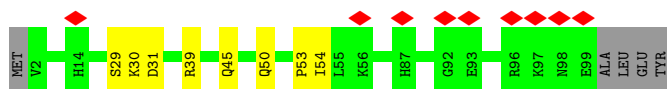
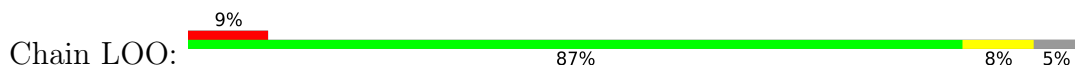


• Molecule 51: uS11

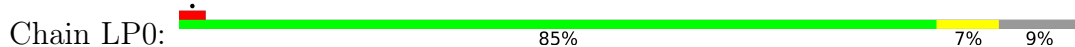




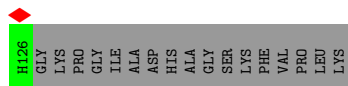
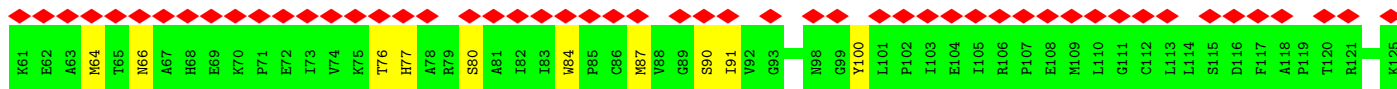
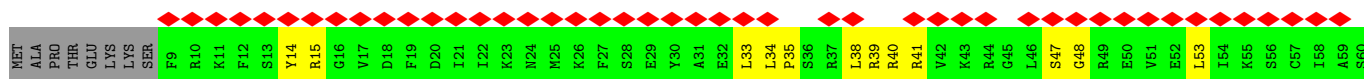
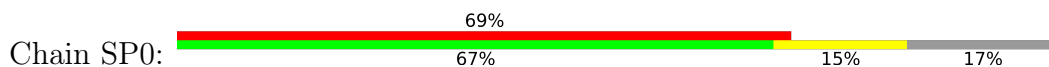
• Molecule 52: eL42



• Molecule 53: uL22



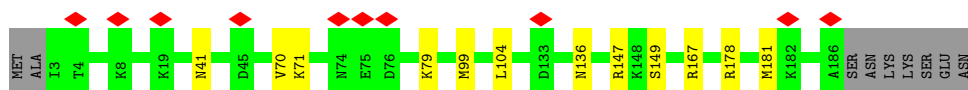
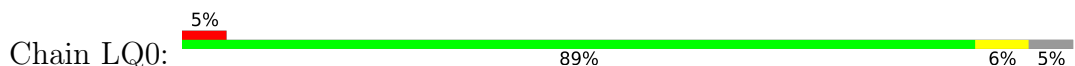
• Molecule 54: uS19



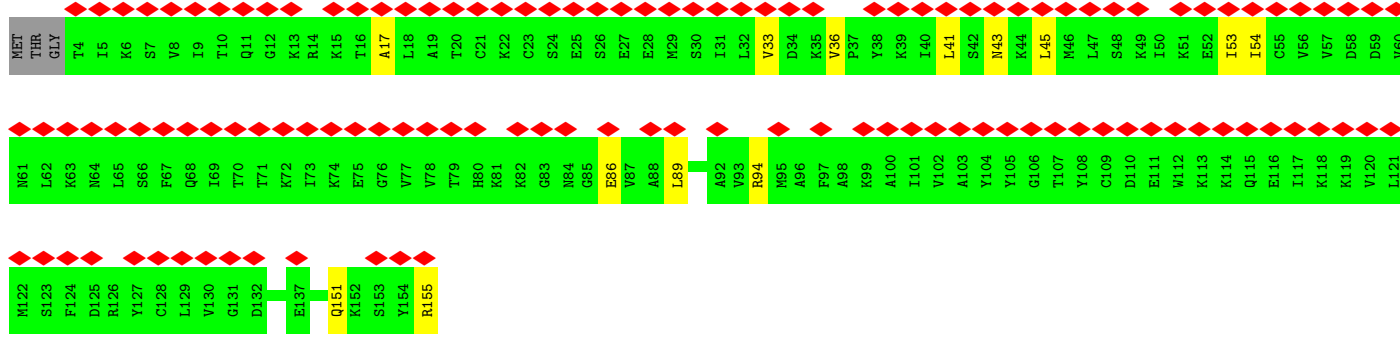
• Molecule 55: eL43



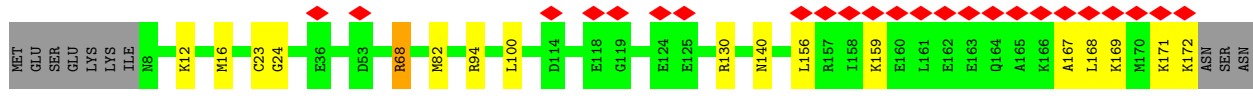
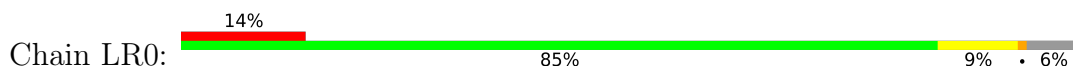
• Molecule 56: eL18



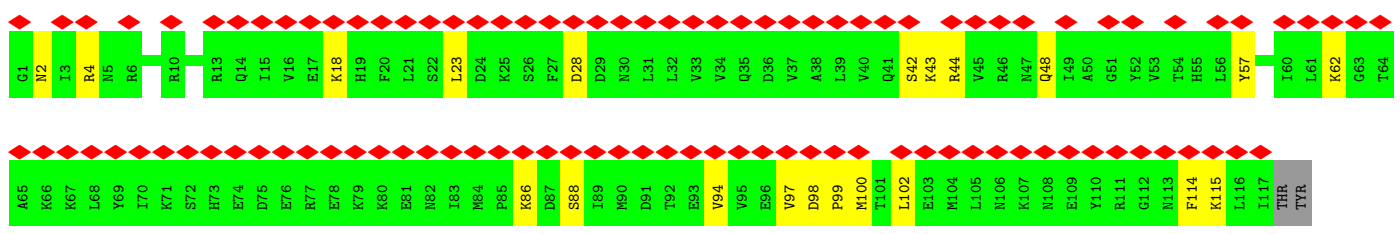
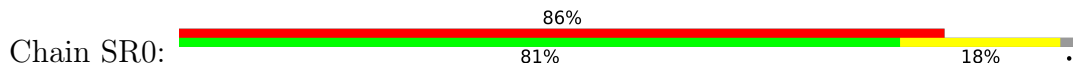
• Molecule 57: uS9



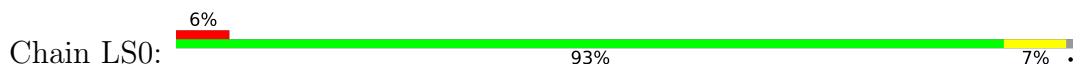
• Molecule 58: eL19



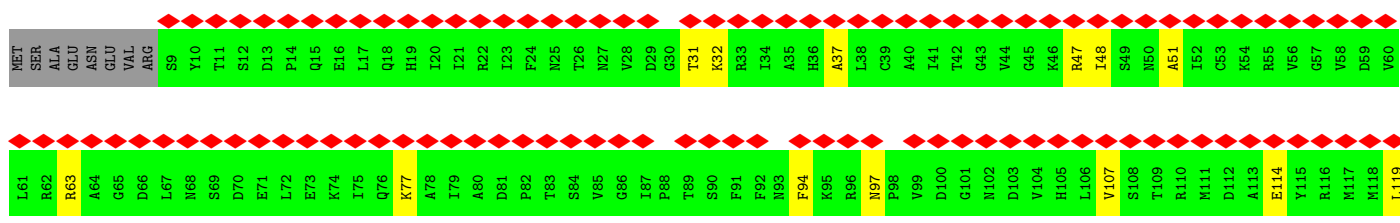
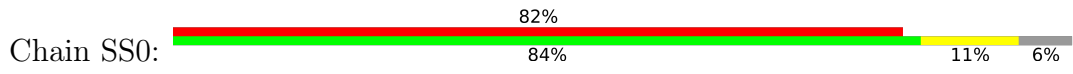
• Molecule 59: eS17

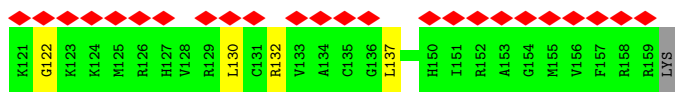


• Molecule 60: eL20

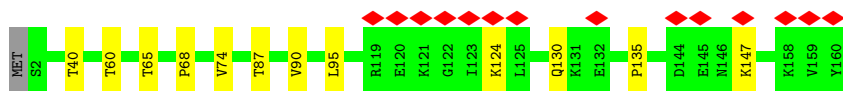
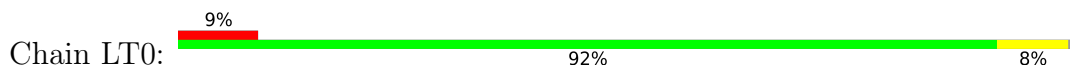


• Molecule 61: uS13

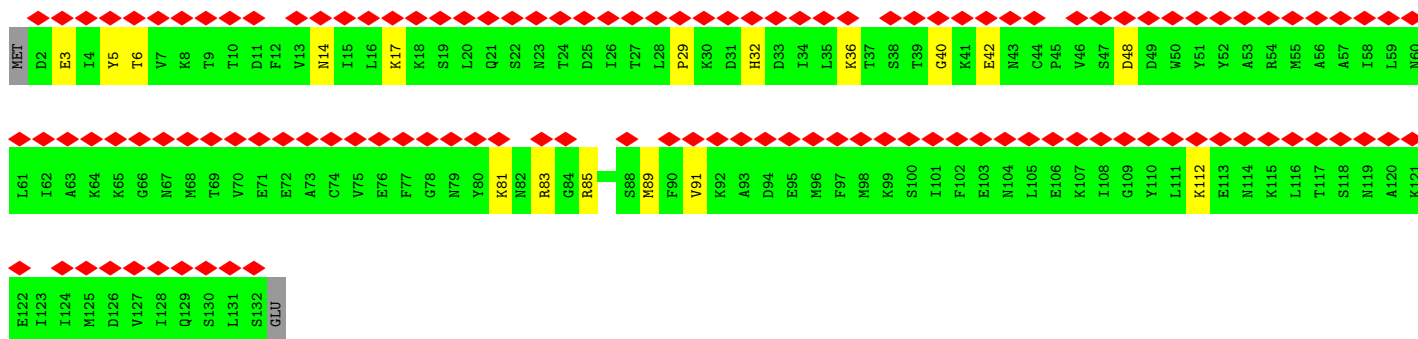
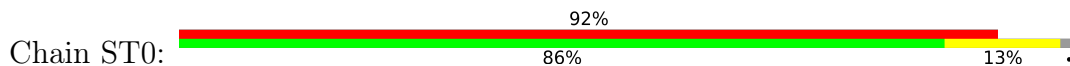




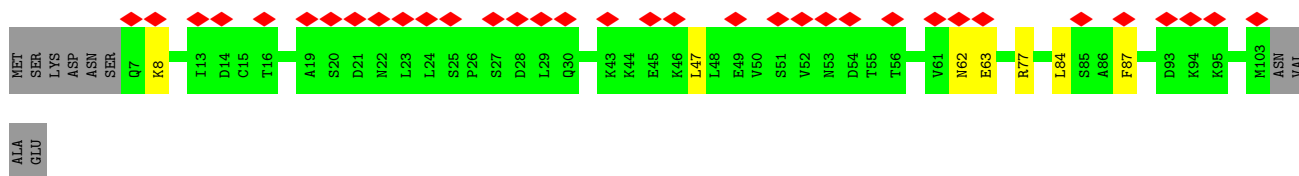
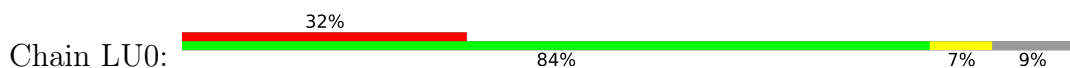
• Molecule 62: eL21



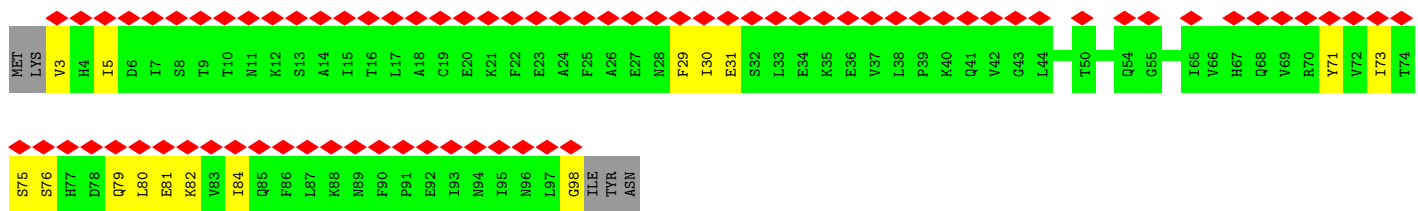
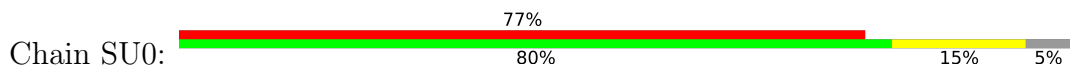
• Molecule 63: eS19



• Molecule 64: eL22

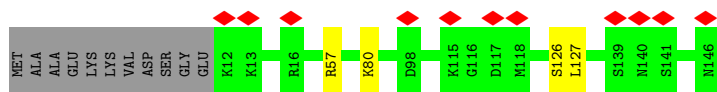


• Molecule 65: uS10

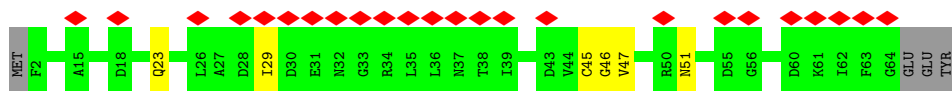
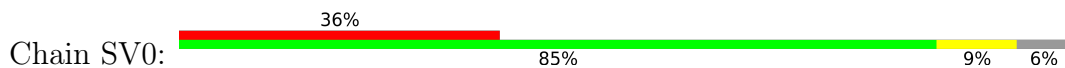


• Molecule 66: uL14

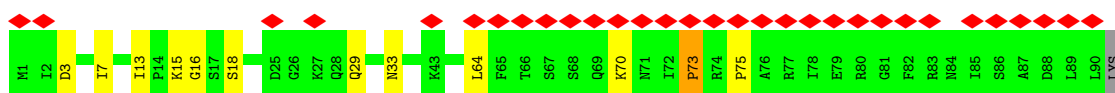
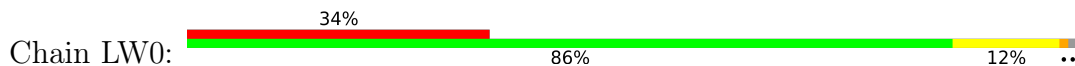




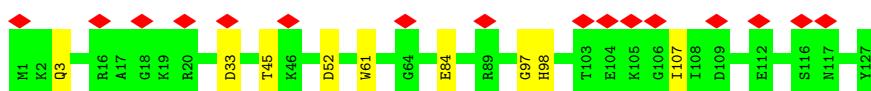
• Molecule 67: eS21



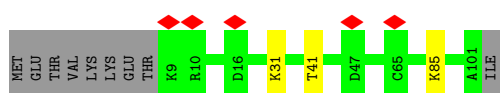
• Molecule 68: eL24



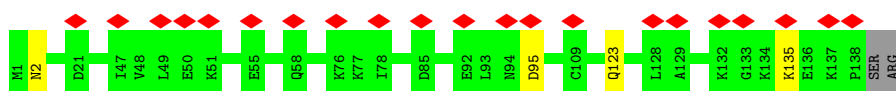
• Molecule 69: uS8



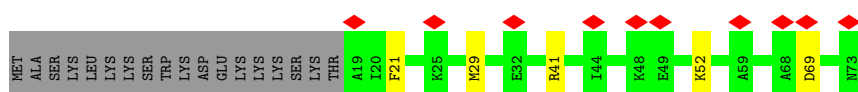
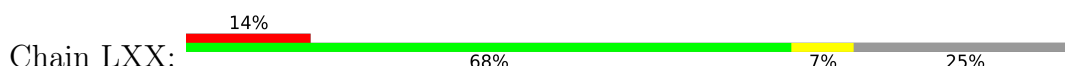
• Molecule 70: uL23



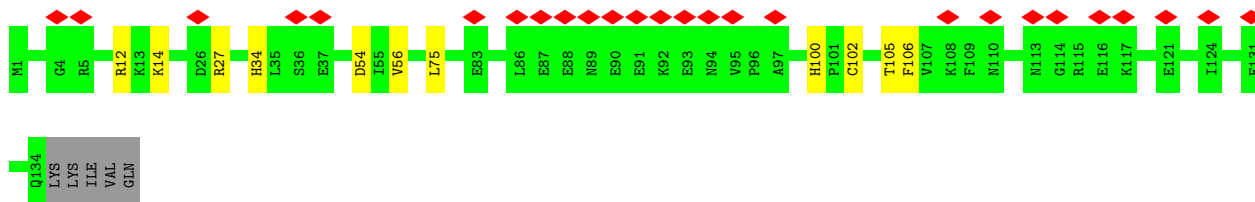
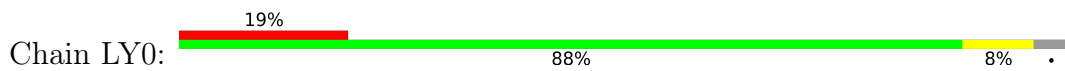
• Molecule 71: uS12



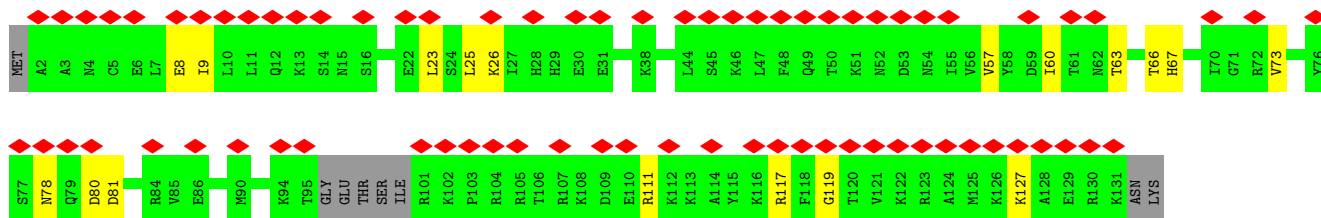
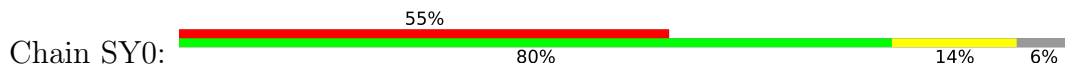
• Molecule 72: msL1



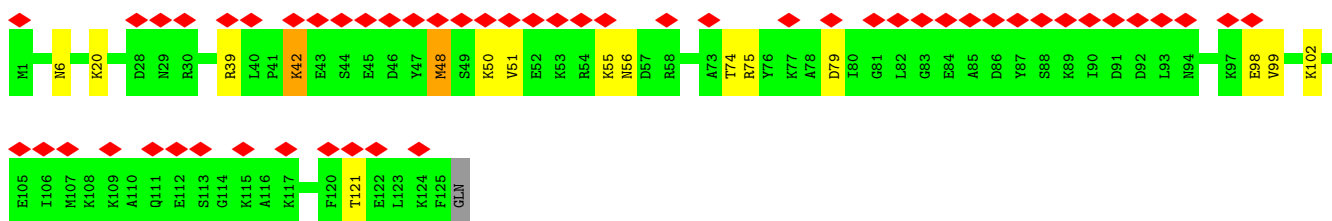
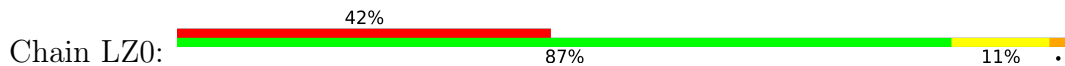
• Molecule 73: uL24



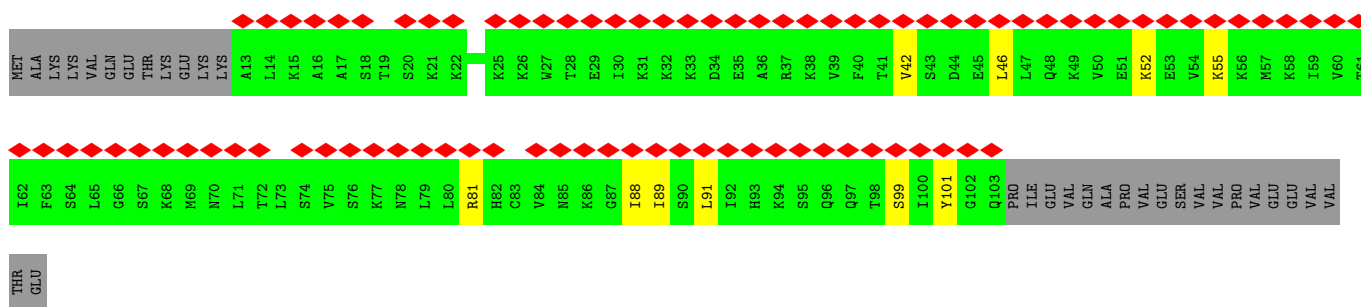
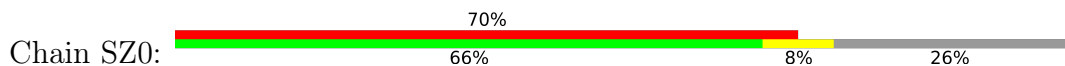
• Molecule 74: eS24



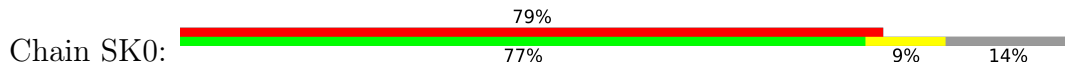
• Molecule 75: eL27

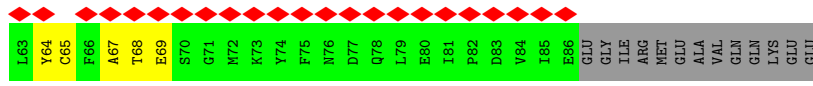
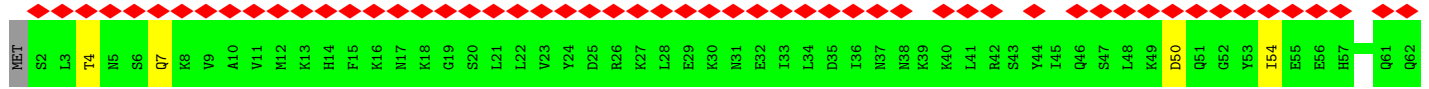


• Molecule 76: eS25

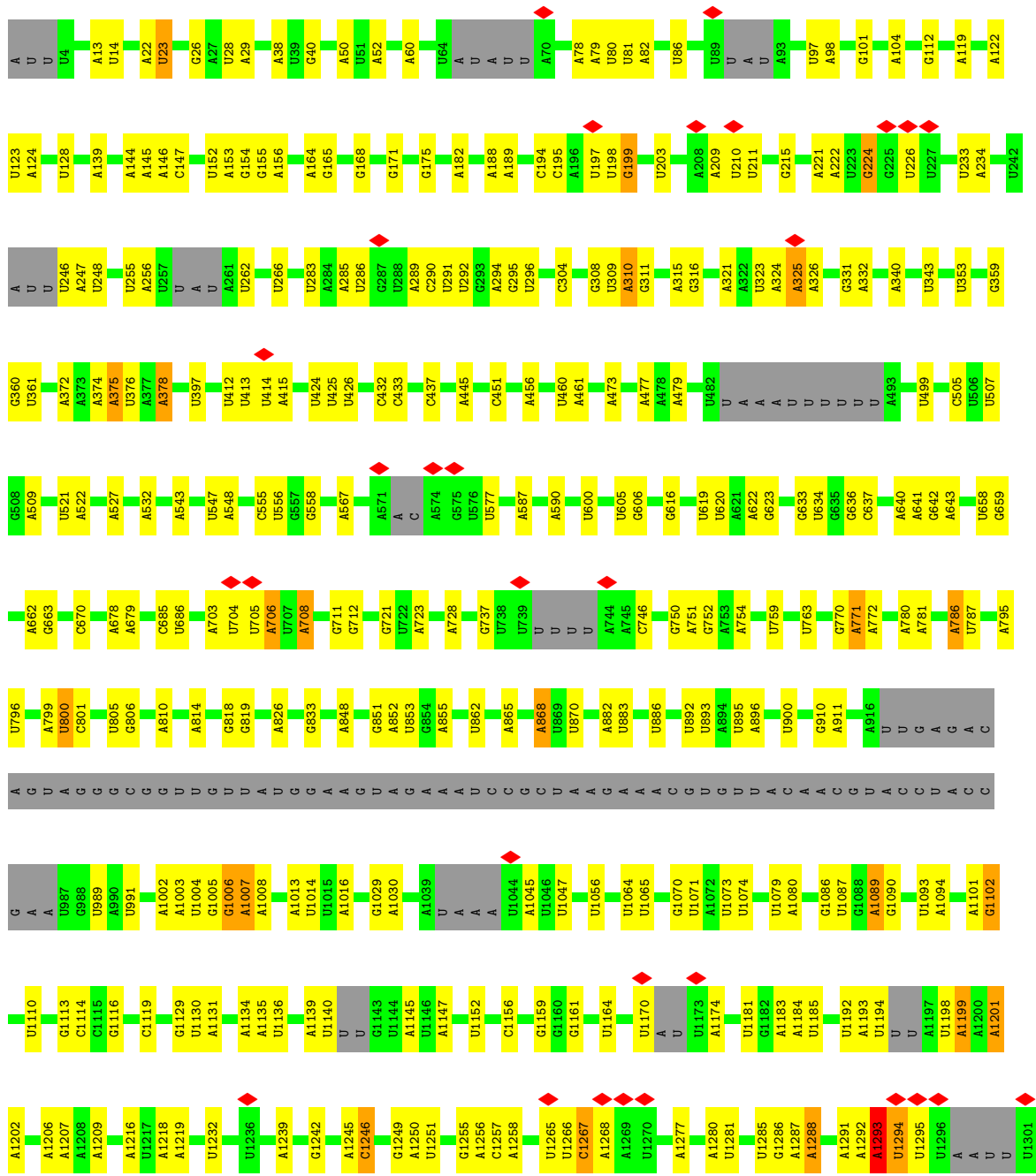
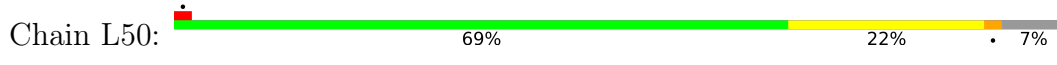


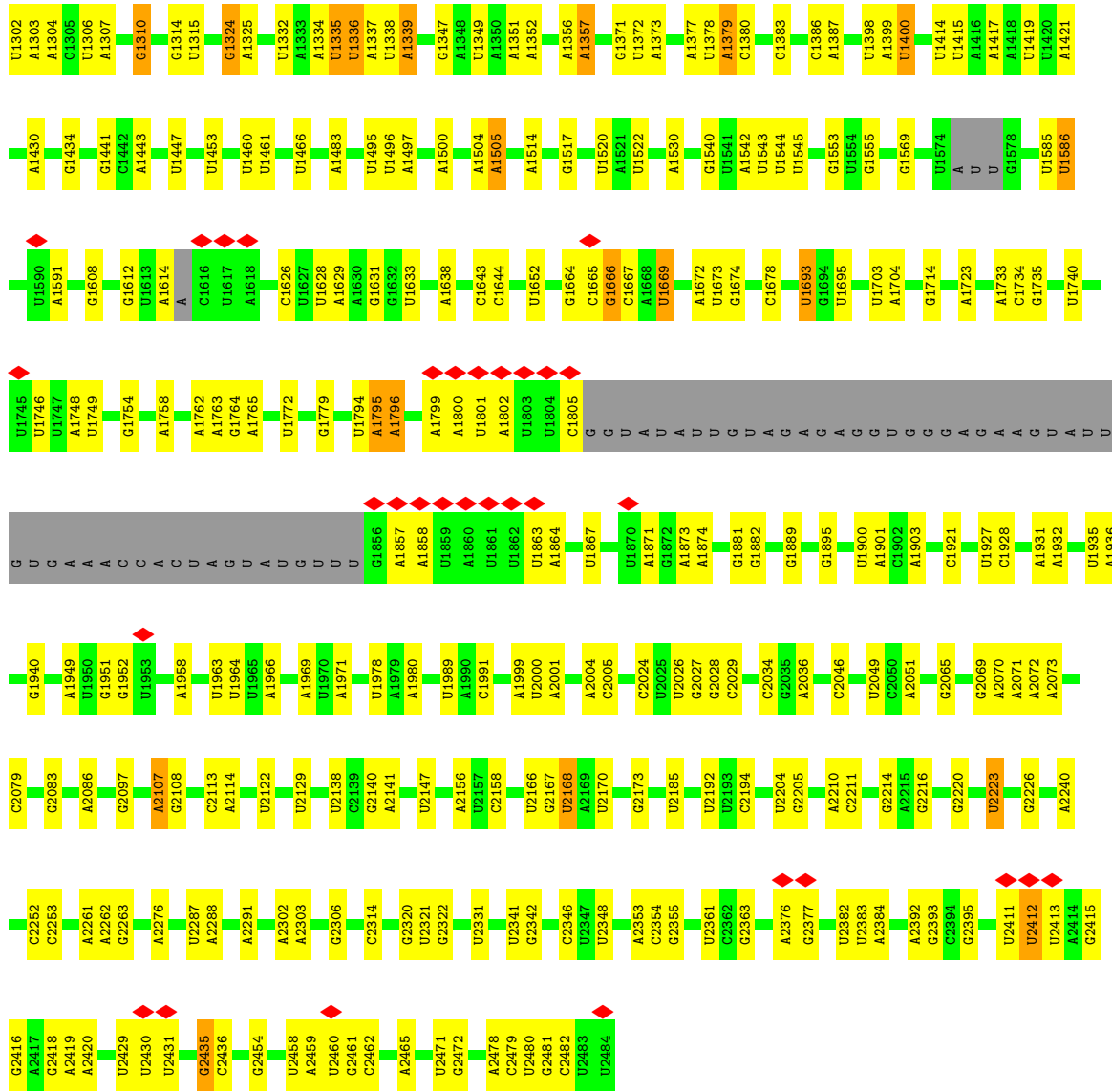
• Molecule 77: eS10





• Molecule 78: 23S rRNA





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	185445	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	5.55	Depositor
Minimum defocus (nm)	4000	Depositor
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.126	Depositor
Minimum map value	-0.072	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0199	Depositor
Map size (\AA)	408.00003, 408.00003, 408.00003	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.2, 1.2, 1.2	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	S60	0.25	0/29436	0.42	2/45858 (0.0%)
2	L70	0.29	0/2824	0.45	0/4400
3	LA0	0.30	0/1828	0.61	0/2465
4	SA0	0.24	0/1590	0.53	0/2152
5	LAA	0.28	0/1253	0.55	0/1676
6	SAA	0.25	0/788	0.56	0/1049
7	LB0	0.28	0/2966	0.51	0/3977
8	SB0	0.20	0/1687	0.49	0/2259
9	LBB	0.29	0/420	0.59	0/552
10	SBB	0.20	0/649	0.48	0/868
11	LC0	0.27	0/2669	0.53	0/3579
12	SC0	0.22	0/1668	0.54	0/2251
13	LCC	0.22	0/808	0.49	0/1087
14	SCC	0.19	0/497	0.53	0/663
15	LD0	0.24	0/2357	0.50	0/3141
16	SD0	0.20	0/1648	0.55	0/2220
17	LDD	0.27	0/829	0.51	0/1102
18	SDD	0.22	0/552	0.52	0/739
19	LE0	0.21	0/1428	0.59	0/1916
20	SE0	0.22	0/2092	0.58	0/2817
21	LEE	0.29	0/1032	0.58	0/1383
22	SEE	0.19	0/457	0.46	0/600
23	LF0	0.27	0/1914	0.51	0/2557
24	SF0	0.19	0/1470	0.53	0/1971
25	LFF	0.28	0/781	0.59	0/1048
26	SFF	0.23	0/265	0.61	0/326
27	LG0	0.21	0/1599	0.58	2/2142 (0.1%)
28	SG0	0.21	0/1611	0.51	1/2152 (0.0%)
29	LGG	0.25	0/825	0.53	0/1096
30	SGG	0.22	0/2538	0.56	0/3434
31	LH0	0.24	0/1476	0.58	0/1982
32	SH0	0.22	0/1282	0.54	0/1721

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LHH	0.24	0/1030	0.56	0/1371
34	LI0	0.28	0/1777	0.54	0/2376
35	SI0	0.24	0/1275	0.53	0/1695
36	LII	0.21	0/774	0.50	0/1025
37	LJ0	0.23	0/1367	0.54	0/1823
38	SJ0	0.22	0/1403	0.53	0/1888
39	LJJ	0.31	0/734	0.62	0/973
40	LL0	0.26	0/1350	0.56	0/1803
41	SL0	0.23	0/1291	0.50	0/1731
42	LLL	0.28	0/454	0.53	0/602
43	LM0	0.24	0/736	0.51	0/984
44	LMM	0.23	0/403	0.54	0/532
45	SM0	0.18	0/937	0.55	0/1255
46	LN0	0.29	0/1708	0.55	0/2289
47	SN0	0.22	0/1197	0.50	0/1603
48	LNN	0.21	0/578	0.57	1/770 (0.1%)
49	SNN	0.22	0/1357	0.50	0/1835
50	LO0	0.27	0/1400	0.49	0/1871
51	SO0	0.22	0/987	0.54	0/1322
52	LOO	0.24	0/801	0.52	0/1058
53	LP0	0.29	0/1255	0.55	0/1686
54	SP0	0.20	0/963	0.49	0/1294
55	LPP	0.26	0/651	0.55	0/866
56	LQ0	0.29	0/1478	0.57	0/1975
57	SQ0	0.19	0/1222	0.54	0/1633
58	LR0	0.25	0/1353	0.49	0/1787
59	SR0	0.18	0/969	0.48	0/1297
60	LS0	0.27	0/1504	0.54	2/2024 (0.1%)
61	SS0	0.21	0/1202	0.59	2/1609 (0.1%)
62	LT0	0.29	0/1339	0.56	0/1795
63	ST0	0.20	0/1063	0.57	2/1428 (0.1%)
64	LU0	0.24	0/802	0.57	0/1074
65	SU0	0.21	0/779	0.57	2/1055 (0.2%)
66	LV0	0.28	0/1056	0.56	0/1412
67	SV0	0.23	0/496	0.56	0/667
68	LW0	0.28	0/674	0.67	2/905 (0.2%)
69	SW0	0.23	0/1037	0.49	0/1389
70	LX0	0.25	0/743	0.46	0/994
71	SX0	0.24	0/1086	0.50	0/1450
72	LXX	0.20	0/464	0.48	0/609
73	LY0	0.24	0/1104	0.52	0/1470
74	SY0	0.21	0/1036	0.50	0/1379
75	LZ0	0.23	0/1019	0.60	0/1358

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SZ0	0.18	0/730	0.54	0/969
77	SK0	0.20	0/725	0.52	0/973
78	L50	0.30	0/55133	0.44	2/85837 (0.0%)
All	All	0.26	0/174681	0.48	18/252924 (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
25	LFF	0	1

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	LW0	75	PRO	N-CA-CB	7.84	110.62	103.33
68	LW0	73	PRO	N-CA-CB	7.14	110.75	103.25
48	LNN	85	PRO	N-CA-CB	6.61	110.19	103.25
28	SG0	147	PRO	N-CA-CB	6.53	110.11	103.25
61	SS0	107	VAL	CA-C-N	6.43	130.47	120.82

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
25	LFF	12	ARG	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	S60	26291	0	13176	104	0
2	L70	2523	0	1273	7	0
3	LA0	1789	0	1824	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	SA0	1558	0	1596	14	0
5	LAA	1219	0	1247	4	0
6	SAA	776	0	814	6	0
7	LB0	2912	0	3040	16	0
8	SB0	1664	0	1734	21	0
9	LBB	416	0	458	2	0
10	SBB	637	0	632	3	0
11	LC0	2624	0	2709	21	0
12	SC0	1642	0	1717	20	0
13	LCC	797	0	844	3	0
14	SCC	495	0	517	9	0
15	LD0	2320	0	2370	14	0
16	SD0	1624	0	1769	10	0
17	LDD	821	0	911	6	0
18	SDD	541	0	532	5	0
19	LE0	1410	0	1449	8	0
20	SE0	2056	0	2113	9	0
21	LEE	1010	0	1072	4	0
22	SEE	454	0	492	2	0
23	LF0	1884	0	1972	12	0
24	SF0	1457	0	1510	14	0
25	LFF	771	0	830	5	0
26	SFF	266	0	145	0	0
27	LG0	1573	0	1679	8	0
28	SG0	1587	0	1605	23	0
29	LGG	814	0	878	8	0
30	SGG	2499	0	2465	33	0
31	LH0	1452	0	1531	9	0
32	SH0	1265	0	1313	18	0
33	LHH	1017	0	1096	5	0
34	LI0	1743	0	1792	12	0
35	SI0	1259	0	1305	13	0
36	LII	765	0	860	7	0
37	LJ0	1348	0	1406	13	0
38	SJ0	1382	0	1431	10	0
39	LJJ	719	0	771	1	0
40	LL0	1328	0	1417	10	0
41	SL0	1269	0	1311	18	0
42	LLL	445	0	482	2	0
43	LM0	731	0	785	3	0
44	LMM	402	0	433	5	0
45	SM0	929	0	967	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	LN0	1677	0	1726	13	0
47	SN0	1177	0	1237	16	0
48	LNN	577	0	496	4	0
49	SNN	1336	0	1349	12	0
50	LO0	1371	0	1424	5	0
51	SO0	977	0	1032	17	0
52	LOO	792	0	889	6	0
53	LP0	1235	0	1300	6	0
54	SP0	942	0	975	14	0
55	LPP	642	0	673	4	0
56	LQ0	1460	0	1579	8	0
57	SQ0	1205	0	1285	9	0
58	LR0	1342	0	1462	12	0
59	SR0	958	0	1002	14	0
60	LS0	1472	0	1503	9	0
61	SS0	1186	0	1224	10	0
62	LT0	1310	0	1368	9	0
63	ST0	1048	0	1062	14	0
64	LU0	790	0	814	4	0
65	SU0	764	0	788	8	0
66	LV0	1040	0	1102	3	0
67	SV0	491	0	492	4	0
68	LW0	667	0	676	7	0
69	SW0	1018	0	1041	6	0
70	LX0	734	0	796	2	0
71	SX0	1069	0	1154	3	0
72	LXX	462	0	518	4	0
73	LY0	1088	0	1124	8	0
74	SY0	1025	0	1090	13	0
75	LZ0	1006	0	1080	9	0
76	SZ0	724	0	800	7	0
77	SK0	712	0	709	6	0
78	L50	49259	0	24706	111	0
79	L50	122	0	0	0	0
79	L70	1	0	0	0	0
79	LJJ	1	0	0	0	0
79	LV0	1	0	0	0	0
79	S60	49	0	0	0	0
80	LGG	1	0	0	0	0
80	LJJ	1	0	0	0	0
80	LMM	1	0	0	0	0
80	LOO	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	LPP	1	0	0	0	0
80	SAA	1	0	0	0	0
80	SBB	1	0	0	0	0
80	SDD	1	0	0	0	0
80	SNN	1	0	0	0	0
All	All	164223	0	128749	764	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 764 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)
1:S60:500:G:H1	1:S60:526:U:H3	1.11	0.98
1:S60:124:G:H22	1:S60:135:U:H3	1.40	0.69
7:LB0:283:HIS:HD2	7:LB0:314:GLU:HG3	1.61	0.65
16:SD0:40:ARG:HB2	16:SD0:47:LYS:HB2	1.78	0.65
1:S60:647:U:H3 ⁷	1:S60:648:G:H21	1.62	0.65

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	230/237 (97%)	216 (94%)	14 (6%)	0	100	100
4	SA0	195/264 (74%)	189 (97%)	6 (3%)	0	100	100
5	LAA	146/148 (99%)	135 (92%)	11 (8%)	0	100	100
6	SAA	95/104 (91%)	89 (94%)	6 (6%)	0	100	100
7	LB0	364/384 (95%)	353 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	SB0	206/237 (87%)	195 (95%)	11 (5%)	0	100	100
9	LBB	49/55 (89%)	45 (92%)	4 (8%)	0	100	100
10	SBB	80/94 (85%)	76 (95%)	4 (5%)	0	100	100
11	LC0	327/334 (98%)	312 (95%)	15 (5%)	0	100	100
12	SC0	215/237 (91%)	206 (96%)	9 (4%)	0	100	100
13	LCC	102/108 (94%)	101 (99%)	1 (1%)	0	100	100
14	SCC	61/67 (91%)	58 (95%)	3 (5%)	0	100	100
15	LD0	280/295 (95%)	273 (98%)	7 (2%)	0	100	100
16	SD0	208/215 (97%)	203 (98%)	5 (2%)	0	100	100
17	LDD	100/111 (90%)	91 (91%)	9 (9%)	0	100	100
18	SDD	65/68 (96%)	59 (91%)	6 (9%)	0	100	100
19	LE0	170/172 (99%)	163 (96%)	7 (4%)	0	100	100
20	SE0	254/262 (97%)	242 (95%)	11 (4%)	1 (0%)	30	59
21	LEE	121/139 (87%)	118 (98%)	3 (2%)	0	100	100
22	SEE	54/60 (90%)	52 (96%)	2 (4%)	0	100	100
23	LF0	228/239 (95%)	216 (95%)	12 (5%)	0	100	100
24	SF0	186/189 (98%)	182 (98%)	4 (2%)	0	100	100
25	LFF	94/98 (96%)	90 (96%)	4 (4%)	0	100	100
26	SFF	66/151 (44%)	65 (98%)	1 (2%)	0	100	100
27	LG0	193/200 (96%)	186 (96%)	7 (4%)	0	100	100
28	SG0	197/217 (91%)	188 (95%)	9 (5%)	0	100	100
29	LGG	98/106 (92%)	94 (96%)	4 (4%)	0	100	100
30	SGG	328/337 (97%)	314 (96%)	14 (4%)	0	100	100
31	LH0	182/186 (98%)	172 (94%)	10 (6%)	0	100	100
32	SH0	153/161 (95%)	145 (95%)	8 (5%)	0	100	100
33	LHH	118/122 (97%)	113 (96%)	5 (4%)	0	100	100
34	LI0	214/217 (99%)	199 (93%)	15 (7%)	0	100	100
35	SI0	156/166 (94%)	150 (96%)	6 (4%)	0	100	100
36	LII	91/95 (96%)	88 (97%)	3 (3%)	0	100	100
37	LJ0	166/171 (97%)	159 (96%)	7 (4%)	0	100	100
38	SJ0	169/189 (89%)	162 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	LJJ	88/93 (95%)	84 (96%)	4 (4%)	0	100	100
40	LL0	160/162 (99%)	150 (94%)	10 (6%)	0	100	100
41	SL0	155/158 (98%)	147 (95%)	8 (5%)	0	100	100
42	LLL	49/52 (94%)	46 (94%)	3 (6%)	0	100	100
43	LM0	87/105 (83%)	83 (95%)	4 (5%)	0	100	100
44	LMM	48/127 (38%)	45 (94%)	3 (6%)	0	100	100
45	SM0	117/131 (89%)	113 (97%)	4 (3%)	0	100	100
46	LN0	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
47	SN0	145/149 (97%)	139 (96%)	6 (4%)	0	100	100
48	LNN	74/160 (46%)	67 (90%)	7 (10%)	0	100	100
49	SNN	165/168 (98%)	152 (92%)	13 (8%)	0	100	100
50	LO0	169/192 (88%)	165 (98%)	4 (2%)	0	100	100
51	SO0	129/135 (96%)	124 (96%)	5 (4%)	0	100	100
52	LOO	96/103 (93%)	94 (98%)	2 (2%)	0	100	100
53	LP0	152/169 (90%)	147 (97%)	5 (3%)	0	100	100
54	SP0	116/143 (81%)	112 (97%)	4 (3%)	0	100	100
55	LPP	81/89 (91%)	76 (94%)	5 (6%)	0	100	100
56	LQ0	182/193 (94%)	169 (93%)	13 (7%)	0	100	100
57	SQ0	150/155 (97%)	143 (95%)	7 (5%)	0	100	100
58	LR0	163/175 (93%)	160 (98%)	3 (2%)	0	100	100
59	SR0	115/119 (97%)	112 (97%)	3 (3%)	0	100	100
60	LS0	177/180 (98%)	167 (94%)	10 (6%)	0	100	100
61	SS0	149/160 (93%)	142 (95%)	7 (5%)	0	100	100
62	LT0	157/160 (98%)	151 (96%)	6 (4%)	0	100	100
63	ST0	129/133 (97%)	124 (96%)	5 (4%)	0	100	100
64	LU0	95/107 (89%)	91 (96%)	4 (4%)	0	100	100
65	SU0	94/101 (93%)	86 (92%)	8 (8%)	0	100	100
66	LV0	133/146 (91%)	126 (95%)	7 (5%)	0	100	100
67	SV0	61/67 (91%)	56 (92%)	5 (8%)	0	100	100
68	LW0	88/91 (97%)	84 (96%)	3 (3%)	1 (1%)	11	38
69	SW0	125/127 (98%)	121 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	LX0	91/102 (89%)	84 (92%)	7 (8%)	0	100	100
71	SX0	136/140 (97%)	134 (98%)	2 (2%)	0	100	100
72	LXX	53/73 (73%)	53 (100%)	0	0	100	100
73	LY0	132/139 (95%)	126 (96%)	6 (4%)	0	100	100
74	SY0	121/133 (91%)	115 (95%)	6 (5%)	0	100	100
75	LZ0	123/126 (98%)	114 (93%)	9 (7%)	0	100	100
76	SZ0	89/123 (72%)	84 (94%)	5 (6%)	0	100	100
77	SK0	83/99 (84%)	82 (99%)	1 (1%)	0	100	100
All	All	10639/11624 (92%)	10158 (96%)	479 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
68	LW0	73	PRO
20	SE0	23	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	
3	LA0	193/197 (98%)	190 (98%)	3 (2%)	55	68
4	SA0	179/237 (76%)	179 (100%)	0	100	100
5	LAA	126/126 (100%)	125 (99%)	1 (1%)	73	77
6	SAA	86/93 (92%)	84 (98%)	2 (2%)	44	63
7	LB0	318/334 (95%)	317 (100%)	1 (0%)	86	84
8	SB0	186/210 (89%)	186 (100%)	0	100	100
9	LBB	43/47 (92%)	43 (100%)	0	100	100
10	SBB	70/82 (85%)	69 (99%)	1 (1%)	59	70
11	LC0	287/292 (98%)	286 (100%)	1 (0%)	86	84
12	SC0	179/198 (90%)	178 (99%)	1 (1%)	78	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	LCC	88/92 (96%)	88 (100%)	0	100	100
14	SCC	52/56 (93%)	52 (100%)	0	100	100
15	LD0	247/256 (96%)	247 (100%)	0	100	100
16	SD0	185/189 (98%)	183 (99%)	2 (1%)	65	74
17	LDD	93/101 (92%)	93 (100%)	0	100	100
18	SDD	58/59 (98%)	58 (100%)	0	100	100
19	LE0	162/163 (99%)	160 (99%)	2 (1%)	63	72
20	SE0	231/237 (98%)	230 (100%)	1 (0%)	84	83
21	LEE	109/122 (89%)	109 (100%)	0	100	100
22	SEE	47/49 (96%)	46 (98%)	1 (2%)	47	64
23	LF0	208/216 (96%)	208 (100%)	0	100	100
24	SF0	162/163 (99%)	162 (100%)	0	100	100
25	LFF	86/88 (98%)	86 (100%)	0	100	100
27	LG0	175/180 (97%)	175 (100%)	0	100	100
28	SG0	163/189 (86%)	163 (100%)	0	100	100
29	LGG	90/94 (96%)	89 (99%)	1 (1%)	65	74
30	SGG	280/295 (95%)	277 (99%)	3 (1%)	65	74
31	LH0	162/164 (99%)	161 (99%)	1 (1%)	78	80
32	SH0	148/153 (97%)	148 (100%)	0	100	100
33	LHH	114/116 (98%)	114 (100%)	0	100	100
34	LI0	183/184 (100%)	182 (100%)	1 (0%)	81	81
35	SI0	136/144 (94%)	135 (99%)	1 (1%)	76	78
36	LHI	83/85 (98%)	83 (100%)	0	100	100
37	LJ0	148/151 (98%)	148 (100%)	0	100	100
38	SJ0	157/173 (91%)	157 (100%)	0	100	100
39	LJJ	76/79 (96%)	76 (100%)	0	100	100
40	LL0	144/144 (100%)	144 (100%)	0	100	100
41	SL0	141/142 (99%)	141 (100%)	0	100	100
42	LLL	46/47 (98%)	46 (100%)	0	100	100
43	LM0	85/96 (88%)	85 (100%)	0	100	100
44	LMM	46/112 (41%)	46 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	SM0	100/112 (89%)	100 (100%)	0	100	100
46	LN0	176/177 (99%)	176 (100%)	0	100	100
47	SN0	134/136 (98%)	134 (100%)	0	100	100
48	LNN	46/153 (30%)	46 (100%)	0	100	100
49	SNN	158/159 (99%)	158 (100%)	0	100	100
50	LO0	148/177 (84%)	148 (100%)	0	100	100
51	SO0	102/105 (97%)	101 (99%)	1 (1%)	68	75
52	LOO	89/93 (96%)	89 (100%)	0	100	100
53	LP0	133/148 (90%)	133 (100%)	0	100	100
54	SP0	103/122 (84%)	103 (100%)	0	100	100
55	LPP	67/72 (93%)	67 (100%)	0	100	100
56	LQ0	166/174 (95%)	166 (100%)	0	100	100
57	SQ0	132/134 (98%)	132 (100%)	0	100	100
58	LR0	141/151 (93%)	140 (99%)	1 (1%)	76	78
59	SR0	108/110 (98%)	106 (98%)	2 (2%)	50	66
60	LS0	162/163 (99%)	161 (99%)	1 (1%)	78	80
61	SS0	129/137 (94%)	129 (100%)	0	100	100
62	LT0	141/142 (99%)	141 (100%)	0	100	100
63	ST0	119/121 (98%)	119 (100%)	0	100	100
64	LU0	90/99 (91%)	90 (100%)	0	100	100
65	SU0	87/92 (95%)	87 (100%)	0	100	100
66	LV0	110/118 (93%)	110 (100%)	0	100	100
67	SV0	56/60 (93%)	56 (100%)	0	100	100
68	LW0	67/82 (82%)	67 (100%)	0	100	100
69	SW0	111/111 (100%)	111 (100%)	0	100	100
70	LX0	81/90 (90%)	81 (100%)	0	100	100
71	SX0	116/119 (98%)	116 (100%)	0	100	100
72	LXX	49/66 (74%)	49 (100%)	0	100	100
73	LY0	119/124 (96%)	119 (100%)	0	100	100
74	SY0	116/123 (94%)	116 (100%)	0	100	100
75	LZ0	110/111 (99%)	108 (98%)	2 (2%)	51	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
76	SZ0	84/114 (74%)	84 (100%)	0	100	100
77	SK0	80/92 (87%)	80 (100%)	0	100	100
All	All	9402/10142 (93%)	9372 (100%)	30 (0%)	84	84

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	SE0	5	ARG
60	LS0	117	ARG
30	SGG	152	ASN
75	LZ0	48	MET
58	LR0	68	ARG

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

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	S60	1224/1244 (98%)	311 (25%)	11 (0%)
2	L70	117/119 (98%)	24 (20%)	2 (1%)
78	L50	2296/2484 (92%)	483 (21%)	17 (0%)
All	All	3637/3847 (94%)	818 (22%)	30 (0%)

5 of 818 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	S60	10	A
1	S60	16	C
1	S60	32	U
1	S60	33	U
1	S60	40	G

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
78	L50	308	G
78	L50	2353	A
78	L50	636	G
78	L50	2481	G

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Mol	Chain	Res	Type
78	L50	1337	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](#)

Of 183 ligands modelled in this entry, 183 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.

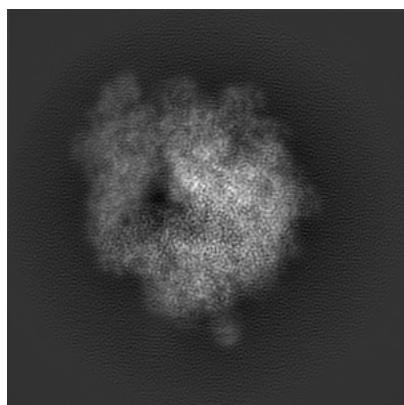
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4935. These allow visual inspection of the internal detail of the map and identification of artifacts.

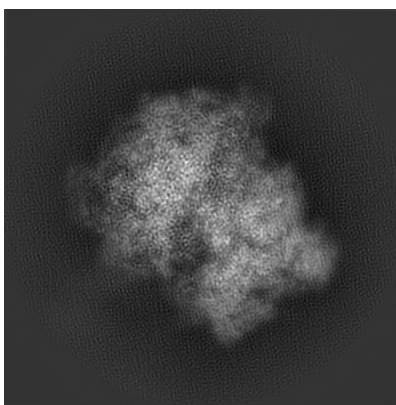
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

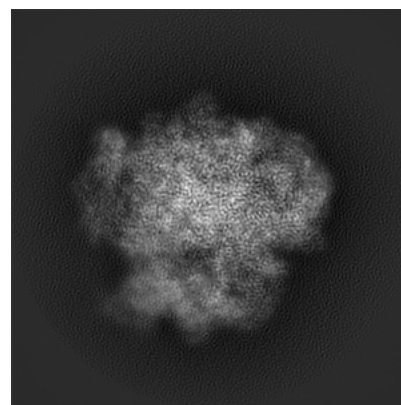
6.1.1 Primary map



X



Y

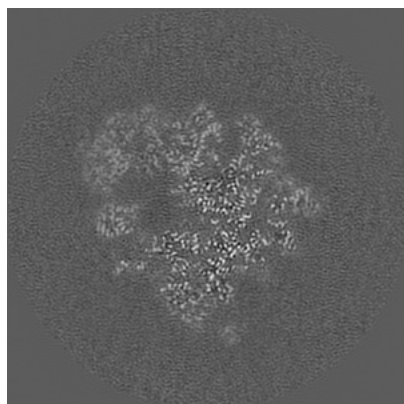


Z

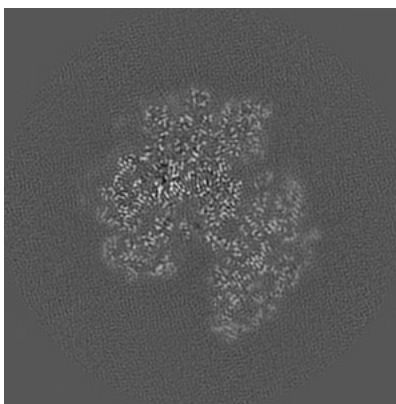
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

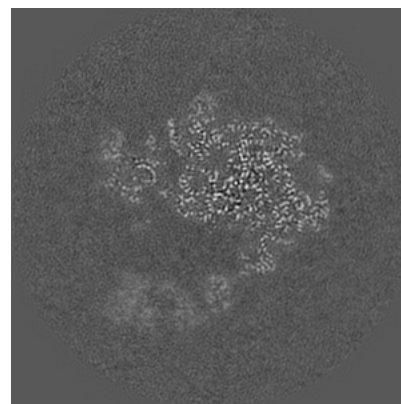
6.2.1 Primary map



X Index: 170



Y Index: 170

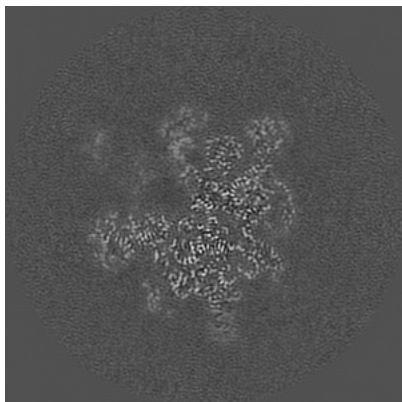


Z Index: 170

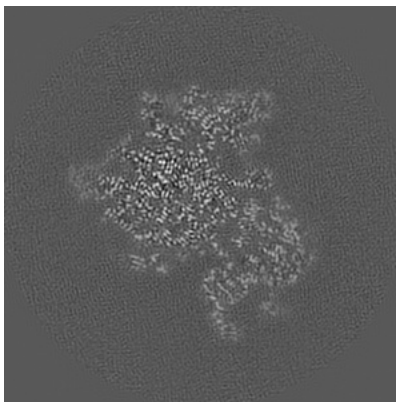
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

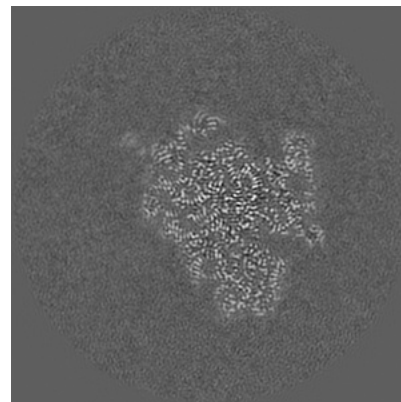
6.3.1 Primary map



X Index: 192



Y Index: 178

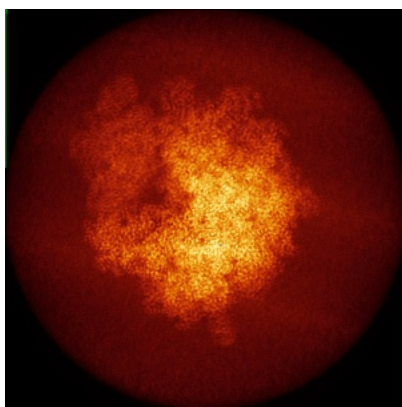


Z Index: 136

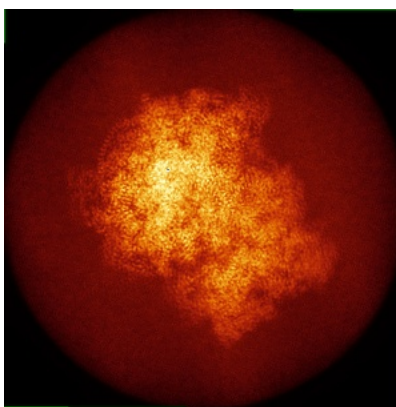
The images above show the largest variance slices of the map in three orthogonal directions.

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

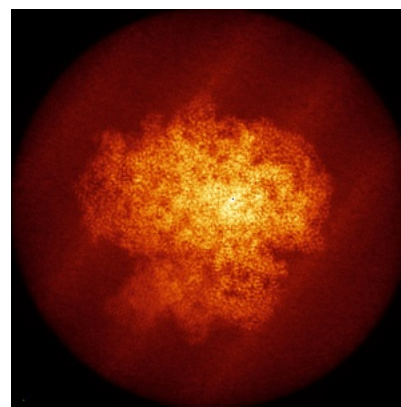
6.4.1 Primary map



X



Y



Z

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 0.0199. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

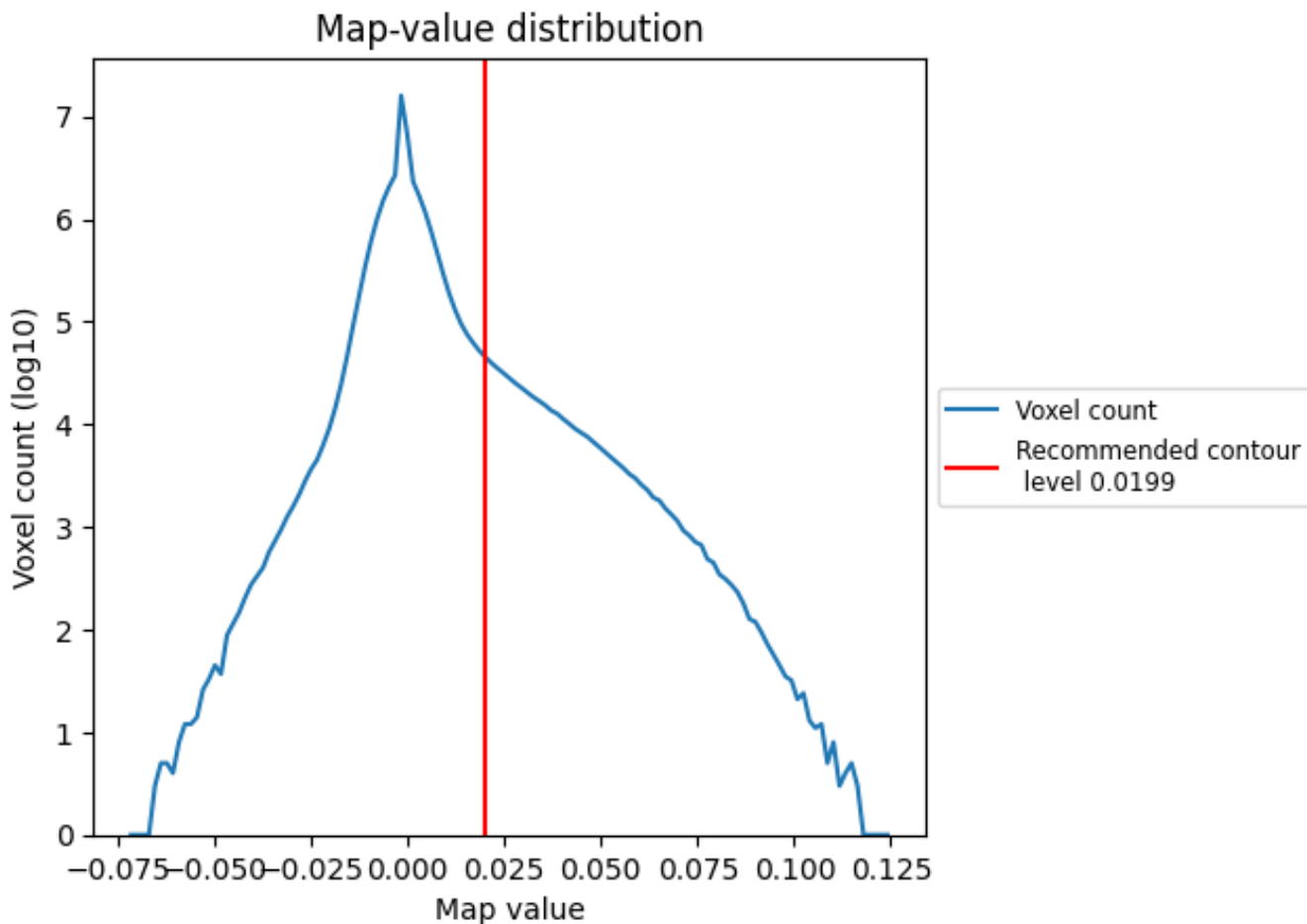
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

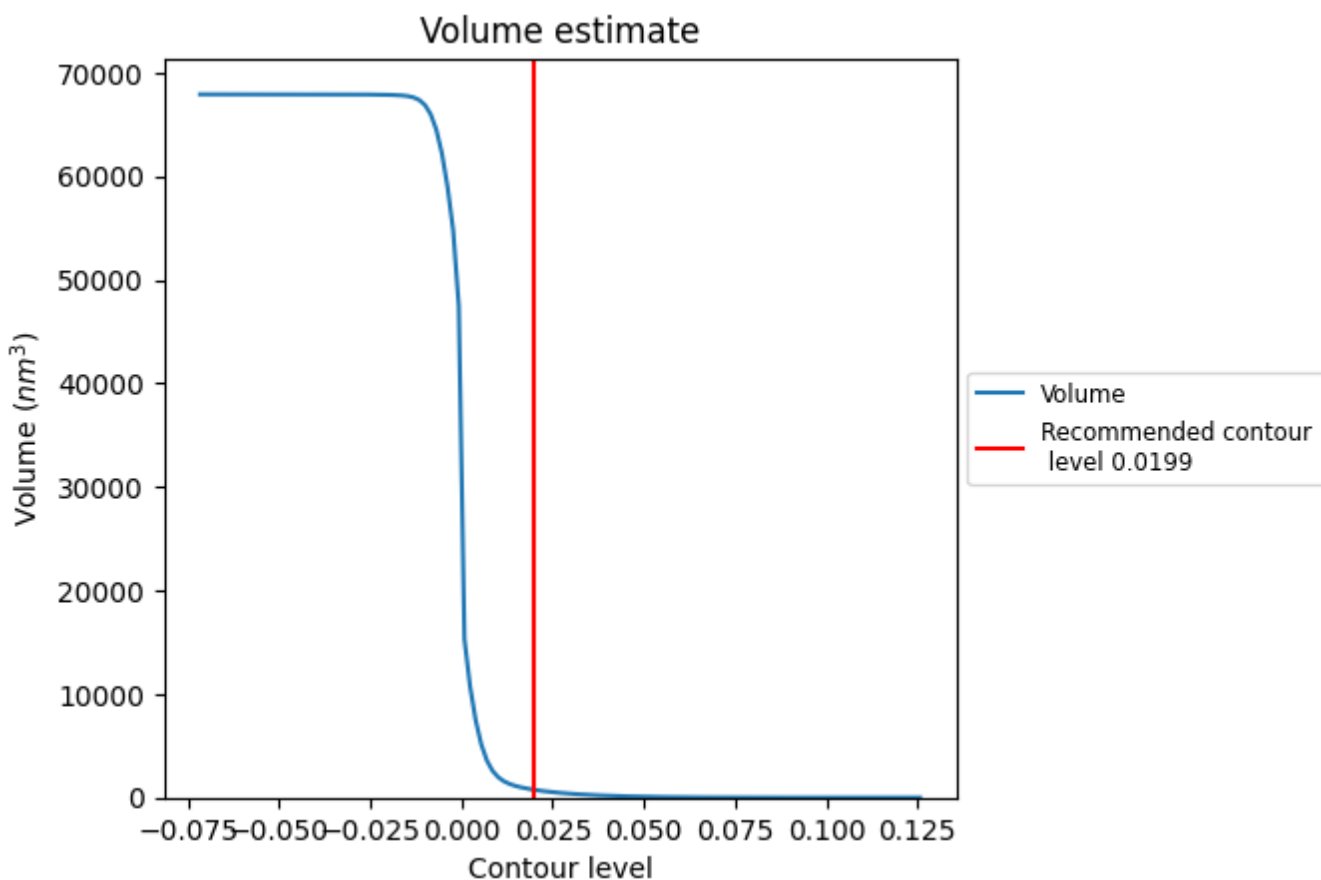
This section contains the results of statistical analysis of the map.

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.

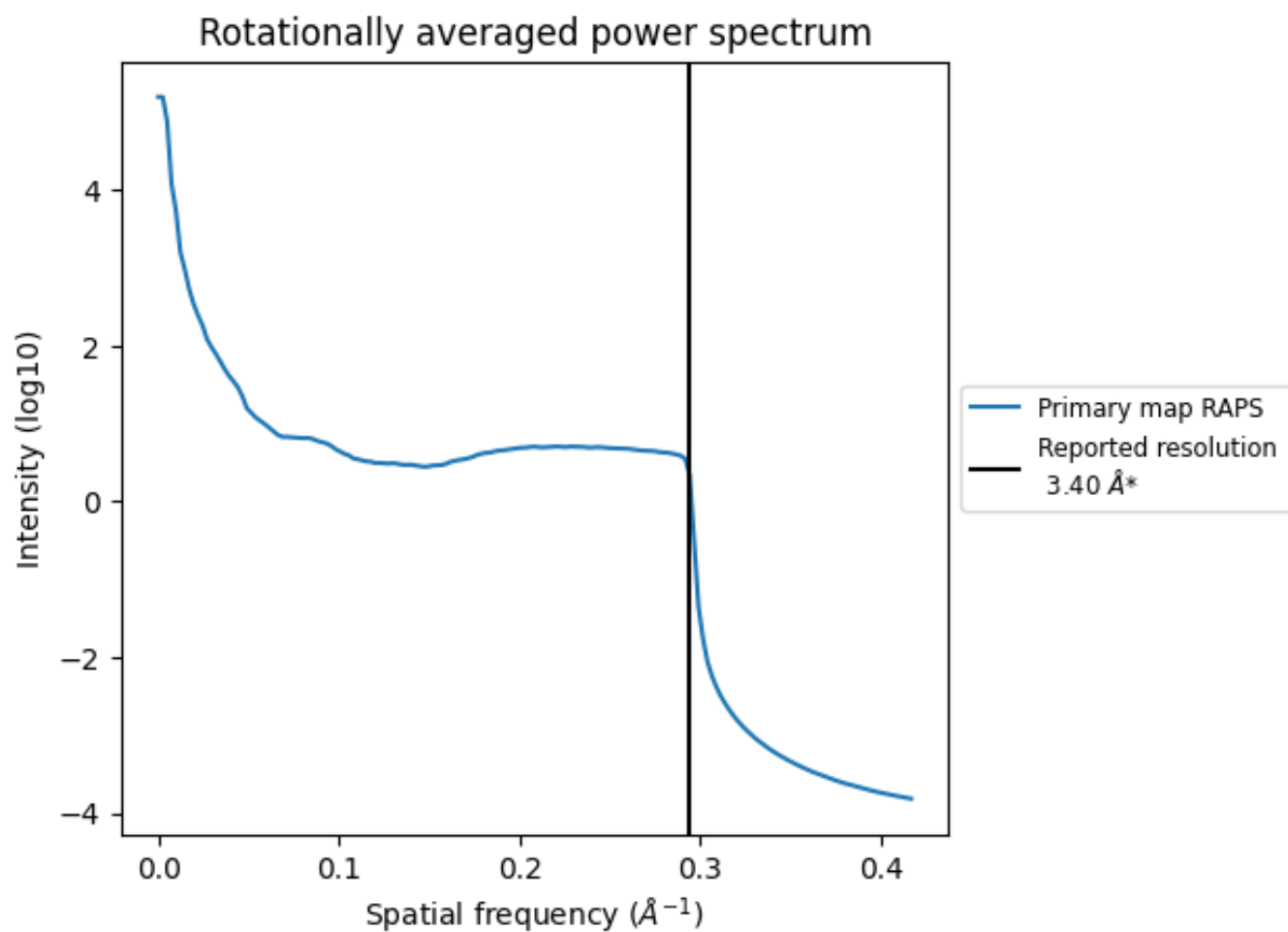
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 750 nm³; this corresponds to an approximate mass of 678 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](#)

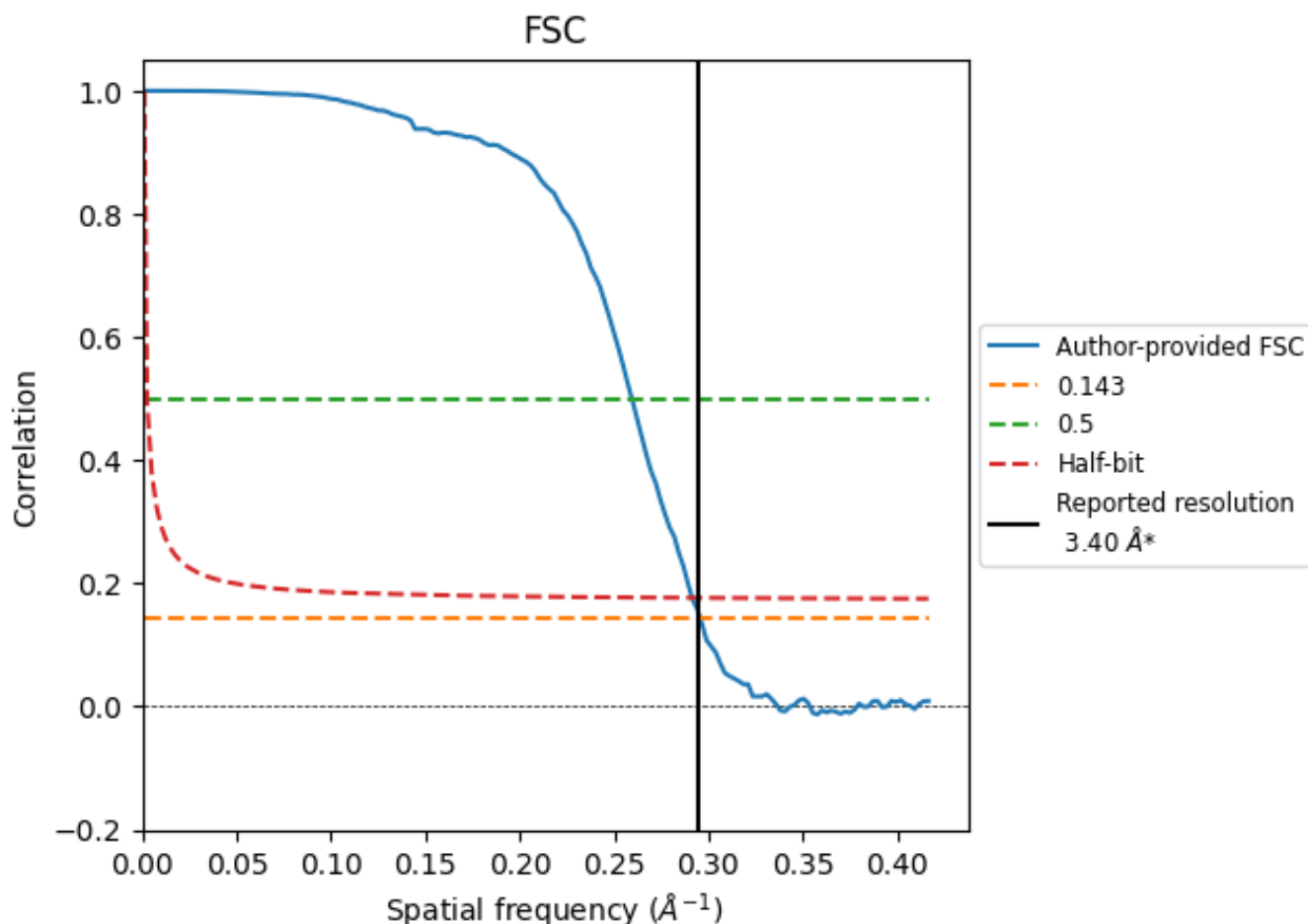


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

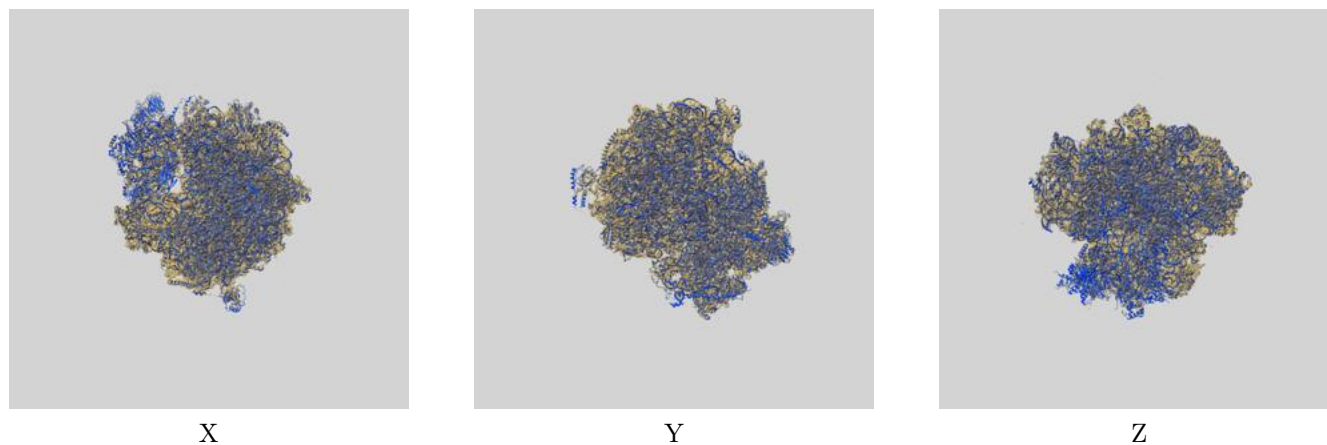
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.38	3.86	3.43
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

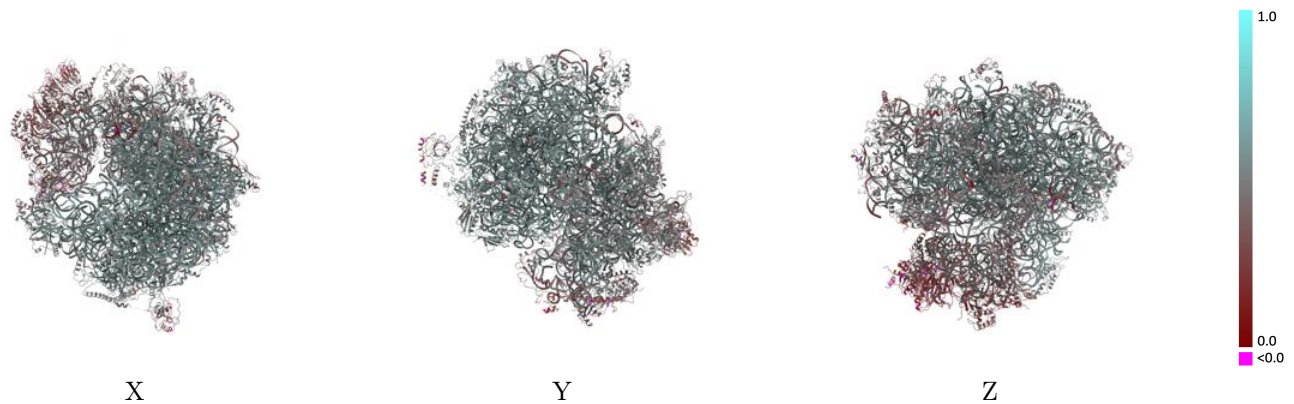
This section contains information regarding the fit between EMDB map EMD-4935 and PDB model 6RM3. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



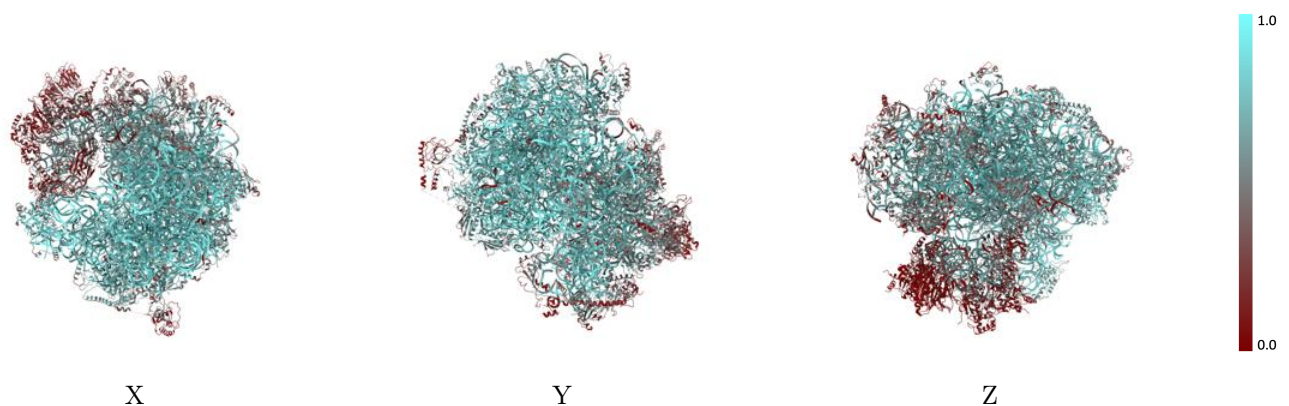
The images above show the 3D surface view of the map at the recommended contour level 0.0199 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



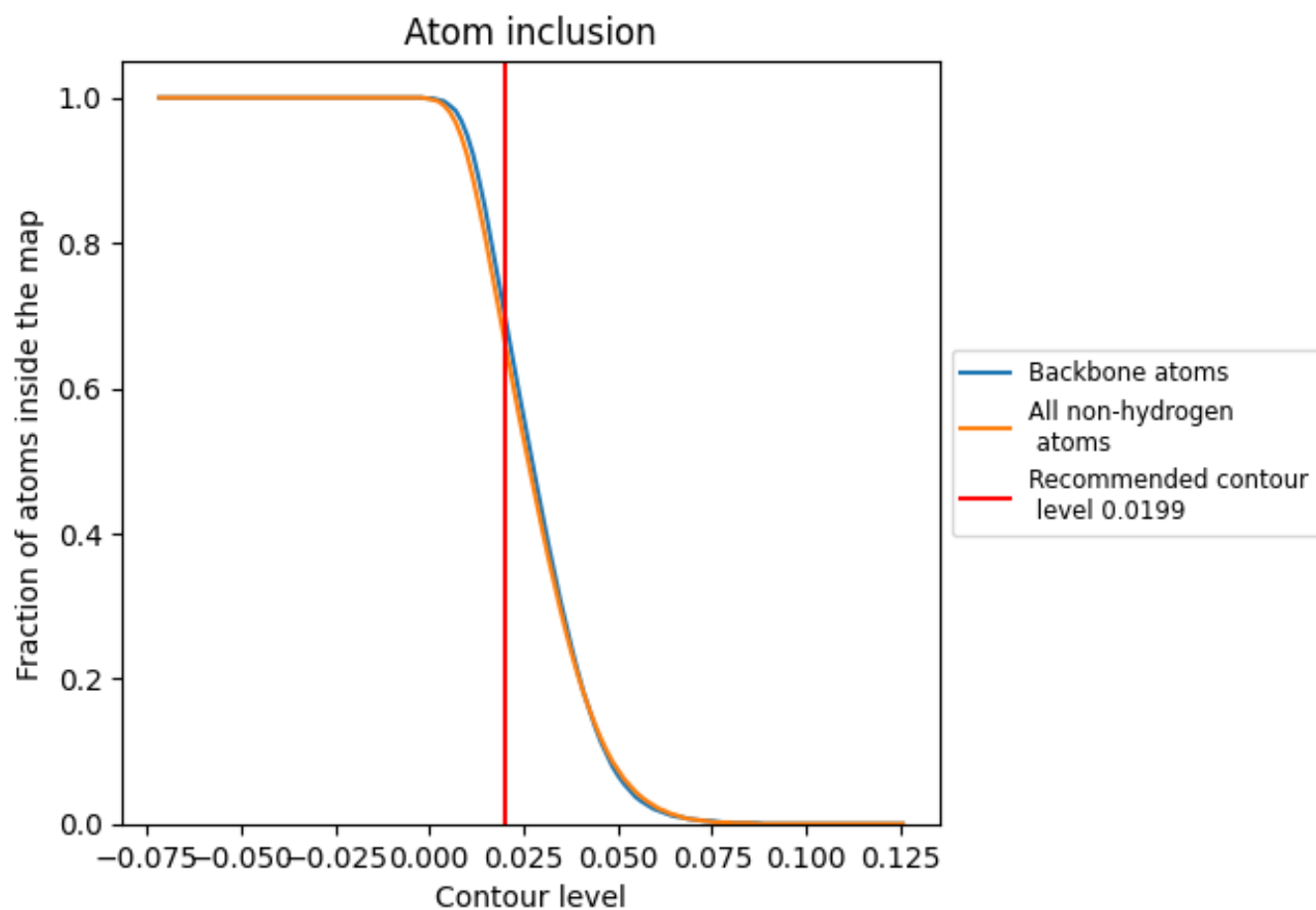
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0199).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 67% 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 (0.0199) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6670	 0.4930
L50	 0.8710	 0.5410
L70	 0.8930	 0.5290
LA0	 0.7610	 0.5440
LAA	 0.7980	 0.5560
LB0	 0.7240	 0.5410
LBB	 0.7190	 0.5300
LC0	 0.7000	 0.5260
LCC	 0.5560	 0.5070
LD0	 0.6750	 0.5050
LDD	 0.6980	 0.5330
LE0	 0.2290	 0.3880
LEE	 0.7640	 0.5400
LF0	 0.7150	 0.5270
LFF	 0.7430	 0.5390
LG0	 0.4980	 0.4720
LGG	 0.7080	 0.5330
LH0	 0.6050	 0.4990
LHH	 0.6750	 0.5190
LI0	 0.7180	 0.5340
LII	 0.6220	 0.5210
LJ0	 0.5170	 0.4740
LJJ	 0.8110	 0.5590
LL0	 0.7100	 0.5370
LLL	 0.7850	 0.5470
LM0	 0.4960	 0.4610
LMM	 0.6450	 0.5130
LN0	 0.8100	 0.5620
LNN	 0.3120	 0.4670
LO0	 0.7140	 0.5400
LOO	 0.6320	 0.5320
LP0	 0.7680	 0.5570
LPP	 0.7210	 0.5460
LQ0	 0.7310	 0.5420
LR0	 0.6390	 0.5080




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Chain	Atom inclusion	Q-score
LS0	 0.7180	 0.5300
LT0	 0.7190	 0.5320
LU0	 0.4970	 0.4350
LV0	 0.7070	 0.5410
LW0	 0.5640	 0.4960
LX0	 0.7120	 0.5350
LXX	 0.5510	 0.5010
LY0	 0.5960	 0.4940
LZ0	 0.4350	 0.4490
S60	 0.7430	 0.4810
SA0	 0.3490	 0.4270
SAA	 0.6040	 0.4950
SB0	 0.3890	 0.4220
SBB	 0.3750	 0.4460
SC0	 0.5300	 0.4890
SCC	 0.2060	 0.3790
SD0	 0.2330	 0.3800
SDD	 0.3330	 0.4170
SE0	 0.4290	 0.4410
SEE	 0.3480	 0.4500
SF0	 0.2460	 0.3870
SFF	 0.0040	 0.0910
SG0	 0.3750	 0.4010
SGG	 0.0780	 0.2750
SH0	 0.2880	 0.3830
SI0	 0.6460	 0.5110
SJ0	 0.4880	 0.4450
SK0	 0.1580	 0.3120
SL0	 0.5630	 0.4950
SM0	 0.0190	 0.1750
SN0	 0.5160	 0.4810
SNN	 0.1940	 0.4290
SO0	 0.5120	 0.4770
SP0	 0.2130	 0.3760
SQ0	 0.2450	 0.3710
SR0	 0.1810	 0.3510
SS0	 0.1700	 0.3700
ST0	 0.1520	 0.3520
SU0	 0.1750	 0.2840
SV0	 0.4260	 0.4610
SW0	 0.6140	 0.5060
SX0	 0.6080	 0.5150

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Chain	Atom inclusion	Q-score
SY0	 0.3510	 0.3950
SZ0	 0.1030	 0.3420