



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 07:02 PM UTC

PDB ID : 8Y0U / pdb_00008y0u
EMDB ID : EMD-37995
Title : dormant ribosome with STM1
Authors : Du, M.; Zeng, F.
Deposited on : 2024-01-23
Resolution : 3.59 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:

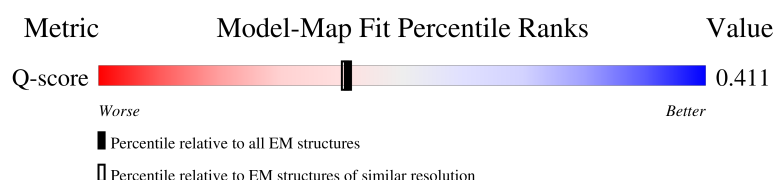
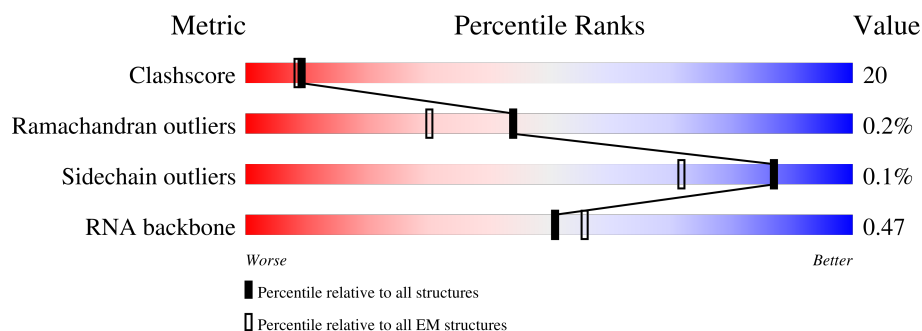
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.59 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	12565 (3.09 - 4.09)

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	LA	254	 66% 33%
2	SA	252	 42% 39% 18%
3	LB	387	 61% 39%

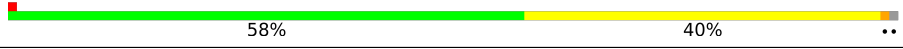
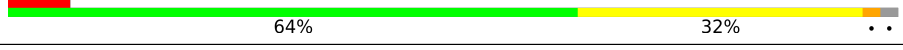
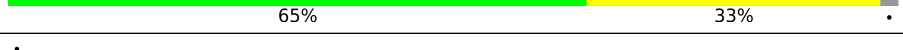
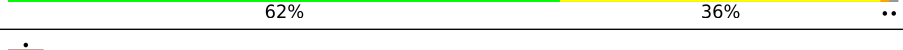
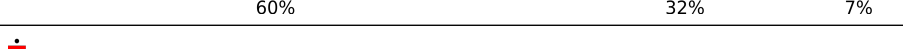
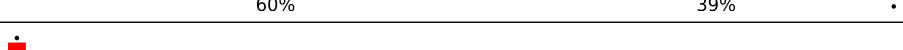
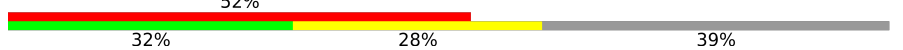
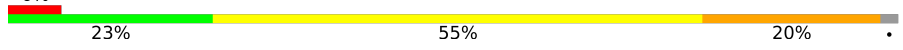
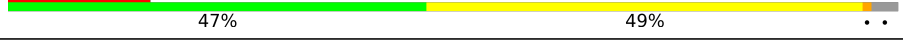
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	SB	255	
5	C1	3396	
6	C4	121	
7	C3	158	
8	LC	362	
9	LD	297	
10	LE	176	
11	LF	244	
12	LG	256	
13	LH	191	
14	LI	221	
15	LJ	174	
16	LL	199	
17	LM	138	
18	LN	204	
19	LO	199	
20	LP	184	
21	LQ	186	
22	LR	189	
23	LS	172	
24	LT	160	
25	LU	121	
26	LV	137	
27	LW	155	
28	LX	142	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	LY	127	
30	LZ	136	
31	La	149	
32	Lb	59	
33	Lc	105	
34	Ld	113	
35	Le	130	
36	Lf	107	
37	Lg	121	
38	Lh	120	
39	Li	100	
40	Lj	88	
41	Lk	78	
42	Ll	50	
43	Lm	128	
44	Ln	25	
45	Lo	106	
46	Lp	92	
47	P0	312	
48	P2	165	
49	C2	1800	
50	SC	254	
51	SE	261	
52	SG	236	
53	SH	190	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	SI	200	
55	SJ	197	
56	SK	105	
57	SL	156	
58	SM	143	
59	SN	151	
60	SO	138	
61	SV	87	
62	SW	130	
63	SX	145	
64	SY	135	
65	Sa	119	
66	Sb	82	
67	Se	63	
68	5	157	
69	Sf	152	
70	SP	142	
71	SZ	108	
72	ST	144	
73	SQ	143	
74	Sd	56	
75	SU	121	
76	Sc	67	
77	s	273	

2 Entry composition

There are 79 unique types of molecules in this entry. The entry contains 196269 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 protein called Large ribosomal subunit protein uL2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LA	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SA	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		

- Molecule 3 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LB	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 4 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SB	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		

- Molecule 5 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C1	3221	Total	C	N	O	P	0	0
			68888	30771	12409	22487	3221		

- Molecule 6 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 7 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 8 is a protein called Large ribosomal subunit protein uL4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LC	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 9 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LD	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 10 is a protein called Large ribosomal subunit protein eL6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LE	167	Total	C	N	O		0	0
			1307	843	234	230			

- Molecule 11 is a protein called Large ribosomal subunit protein uL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LF	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 12 is a protein called Large ribosomal subunit protein eL8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LG	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 13 is a protein called Large ribosomal subunit protein uL6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LH	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 14 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LI	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 15 is a protein called Large ribosomal subunit protein uL5B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LJ	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		

- Molecule 16 is a protein called Large ribosomal subunit protein eL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LL	193	Total	C	N	O	S	0	0
			1543	962	315	266			

- Molecule 17 is a protein called Large ribosomal subunit protein eL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LM	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 18 is a protein called Large ribosomal subunit protein eL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LN	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 19 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LO	197	Total	C	N	O	S	197	0
			1555	1003	289	262	1		

- Molecule 20 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LP	183	Total	C	N	O	S	0	0
			1416	879	284	253			

- Molecule 21 is a protein called Large ribosomal subunit protein eL18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LQ	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 22 is a protein called Large ribosomal subunit protein eL19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LR	188	Total	C	N	O		0	0
			1515	932	323	260			

- Molecule 23 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LS	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 24 is a protein called Large ribosomal subunit protein eL21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LT	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 25 is a protein called Large ribosomal subunit protein eL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LU	100	Total	C	N	O		0	0
			796	516	131	149			

- Molecule 26 is a protein called Large ribosomal subunit protein uL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LV	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 27 is a protein called Large ribosomal subunit protein eL24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LW	126	Total	C	N	O	S	0	0
			849	532	167	149	1		

- Molecule 28 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LX	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 29 is a protein called Large ribosomal subunit protein uL24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LY	125	Total	C	N	O		0	0
			984	620	191	173			

- Molecule 30 is a protein called Large ribosomal subunit protein eL27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LZ	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 31 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	La	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 32 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lb	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 33 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lc	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 34 is a protein called Large ribosomal subunit protein eL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ld	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 35 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Le	127	Total	C	N	O	S	0	0
			1017	644	205	167	1		

- Molecule 36 is a protein called Large ribosomal subunit protein eL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lf	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 37 is a protein called Large ribosomal subunit protein eL34A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lg	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 38 is a protein called Large ribosomal subunit protein uL29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lh	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 39 is a protein called Large ribosomal subunit protein eL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Li	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 40 is a protein called Large ribosomal subunit protein eL37A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lj	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 41 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Lk	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 42 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ll	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 43 is a protein called Ubiquitin-ribosomal protein eL40A fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lm	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 44 is a protein called Large ribosomal subunit protein eL41A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ln	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 45 is a protein called Large ribosomal subunit protein eL42A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lo	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 46 is a protein called Large ribosomal subunit protein eL43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lp	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 47 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	P0	189	Total	C	N	O	S	0	0
			1473	942	257	270	4		

- Molecule 48 is a protein called Large ribosomal subunit protein uL11A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	P2	94	Total	C	N	O	S	0	0
			723	448	138	135	2		

- Molecule 49 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	C2	1771	Total	C	N	O	P	0	0
			37604	16807	6624	12402	1771		

- Molecule 50 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SC	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SE	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 52 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SG	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 53 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	SH	184	Total	C	N	O	0	0
			1473	946	263	264		

- Molecule 54 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SI	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		

- Molecule 55 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SJ	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		

- Molecule 56 is a protein called Small ribosomal subunit protein eS10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SK	92	Total	C	N	O	S	0	0
			752	487	122	141	2		

- Molecule 57 is a protein called Small ribosomal subunit protein uS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SL	144	Total	C	N	O	S	0	0
			1159	742	219	195	3		

- Molecule 58 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SM	121	Total	C	N	O	S	0	0
			875	551	153	169	2		

- Molecule 59 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 60 is a protein called Small ribosomal subunit protein uS11B.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SO	127	Total	C	N	O	S	0	0
			926	569	185	169	3		

- Molecule 61 is a protein called Small ribosomal subunit protein eS21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SV	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 62 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 63 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 64 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SY	134	Total	C	N	O	S	0	0
			1073	676	208	189			

- Molecule 65 is a protein called Small ribosomal subunit protein eS26B.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Sa	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 66 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Sb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 67 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Se	60	Total	C	N	O	S	0	0
			472	298	97	76	1		

- Molecule 68 is a protein called Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	5	152	Total	C	N	O	S	0	0
			1118	693	189	227	9		

- Molecule 69 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sf	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

- Molecule 70 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SP	117	Total	C	N	O	S	0	0
			916	583	171	155	7		

- Molecule 71 is a protein called Small ribosomal subunit protein eS25A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SZ	100	Total	C	N	O	S	0	0
			771	491	147	133			

- Molecule 72 is a protein called Small ribosomal subunit protein eS19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	ST	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 73 is a protein called Small ribosomal subunit protein uS9A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SQ	139	Total	C	N	O	S	0	0
			1082	693	198	191			

- Molecule 74 is a protein called Small ribosomal subunit protein uS14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sd	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 75 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SU	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 76 is a protein called Small ribosomal subunit protein eS28A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sc	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 77 is a protein called Suppressor protein STM1.

Mol	Chain	Residues	Atoms				AltConf	Trace
77	s	42	Total	C	N	O	0	0
			261	153	58	50		

- Molecule 78 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
78	LA	2	Total	Mg	0
			2	2	
78	C1	187	Total	Mg	0
			187	187	
78	C4	1	Total	Mg	0
			1	1	
78	C3	1	Total	Mg	0
			1	1	
78	LN	2	Total	Mg	0
			2	2	
78	LP	1	Total	Mg	0
			1	1	
78	LV	1	Total	Mg	0
			1	1	
78	Le	1	Total	Mg	0
			1	1	
78	C2	78	Total	Mg	0
			78	78	
78	SC	1	Total	Mg	0
			1	1	
78	SE	1	Total	Mg	0
			1	1	
78	Sa	1	Total	Mg	0
			1	1	
78	ST	2	Total	Mg	0
			2	2	
78	SQ	2	Total	Mg	0
			2	2	

- Molecule 79 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
79	Lg	1	Total	Zn	0
			1	1	
79	Lj	1	Total	Zn	0
			1	1	

Continued on next page...

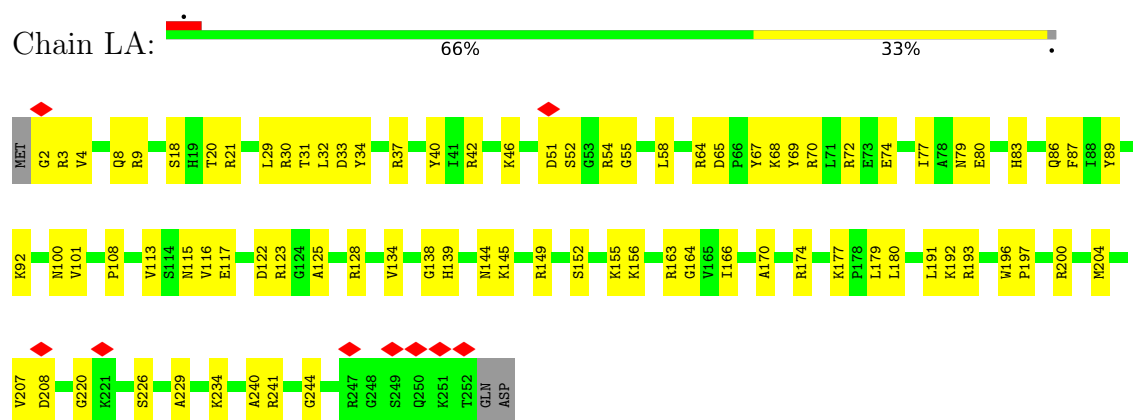
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
79	Lm	1	Total 1	Zn 1	0
79	Lo	1	Total 1	Zn 1	0
79	Lp	1	Total 1	Zn 1	0
79	Sf	1	Total 1	Zn 1	0
79	Sd	1	Total 1	Zn 1	0

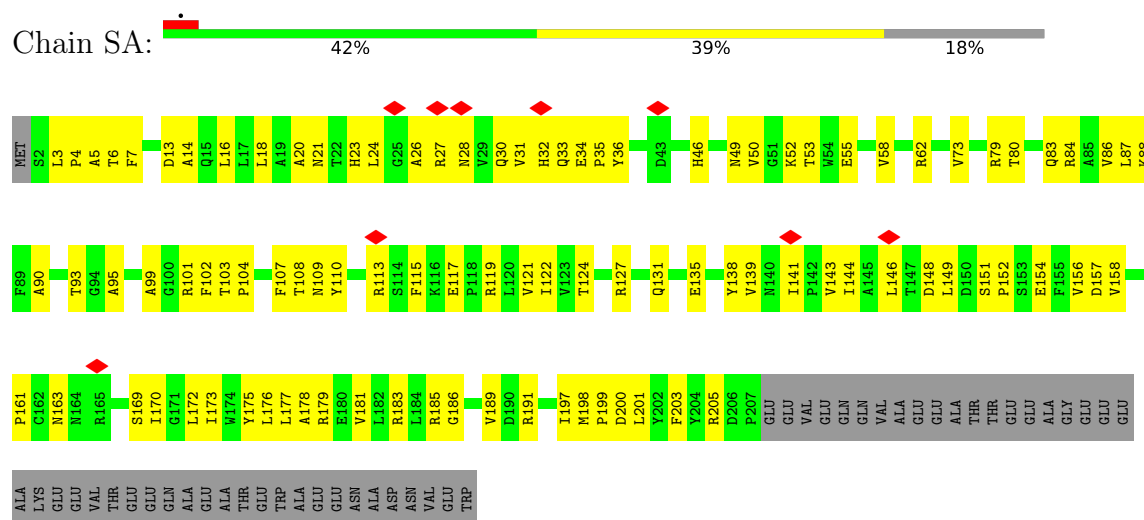
3 Residue-property plots

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: Large ribosomal subunit protein uL2A

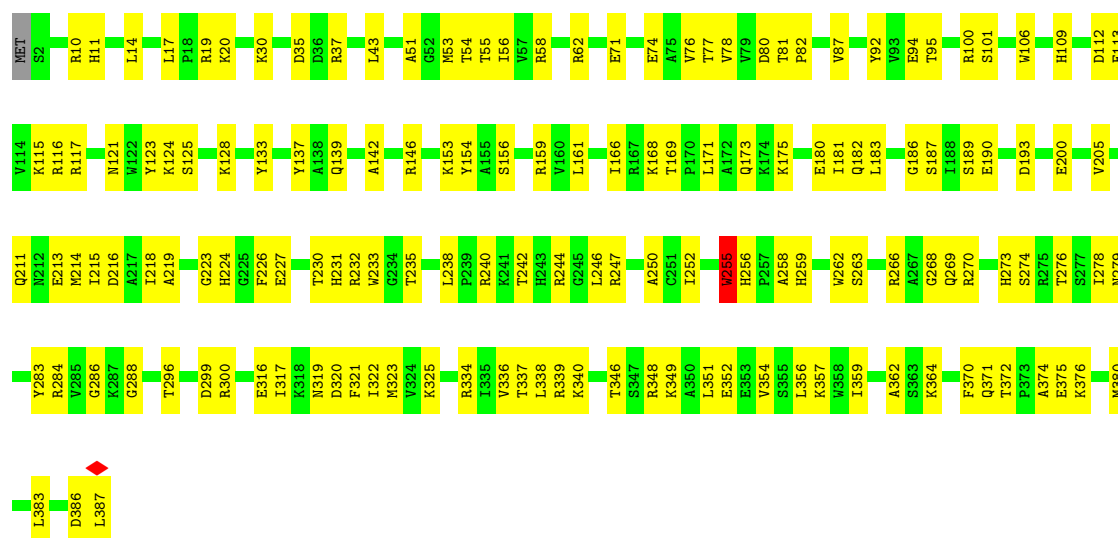


- Molecule 2: Small ribosomal subunit protein uS2A

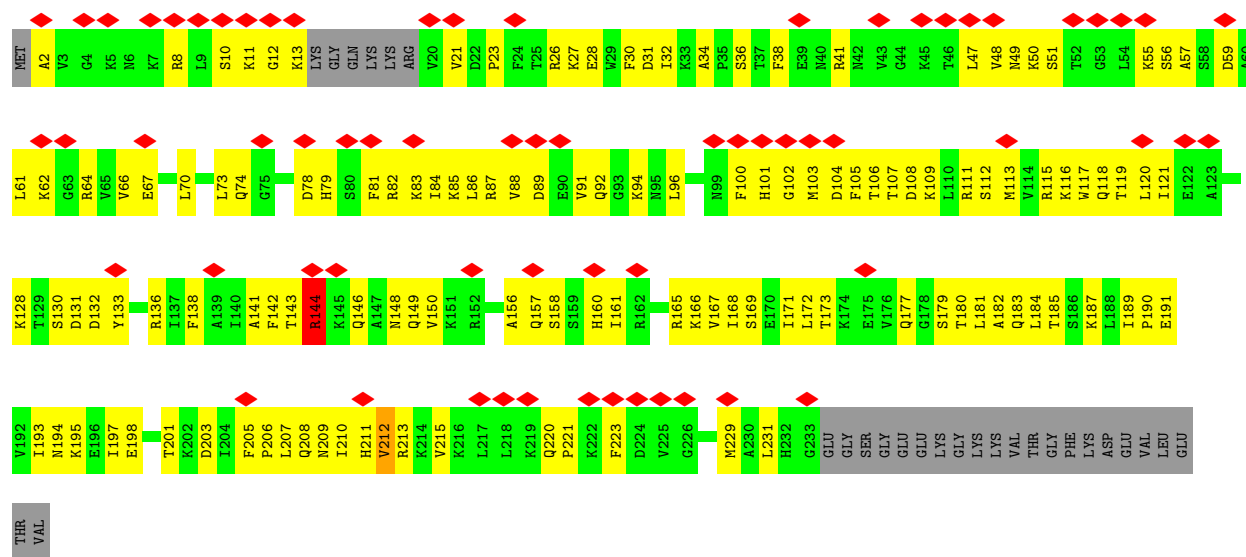


- Molecule 3: Large ribosomal subunit protein uL3

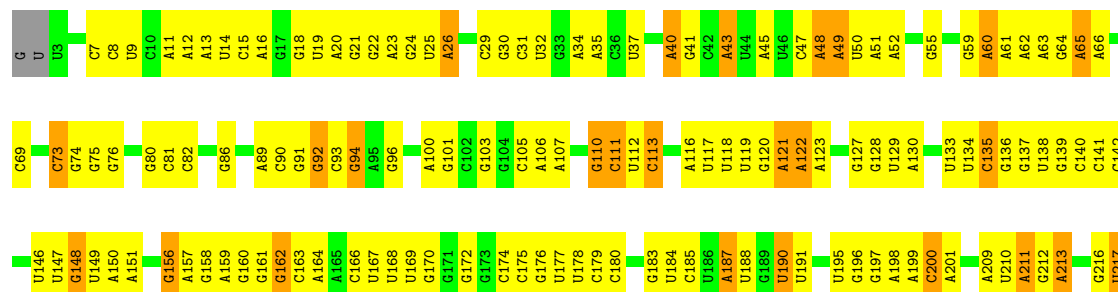




• Molecule 4: 40S ribosomal protein S1-A



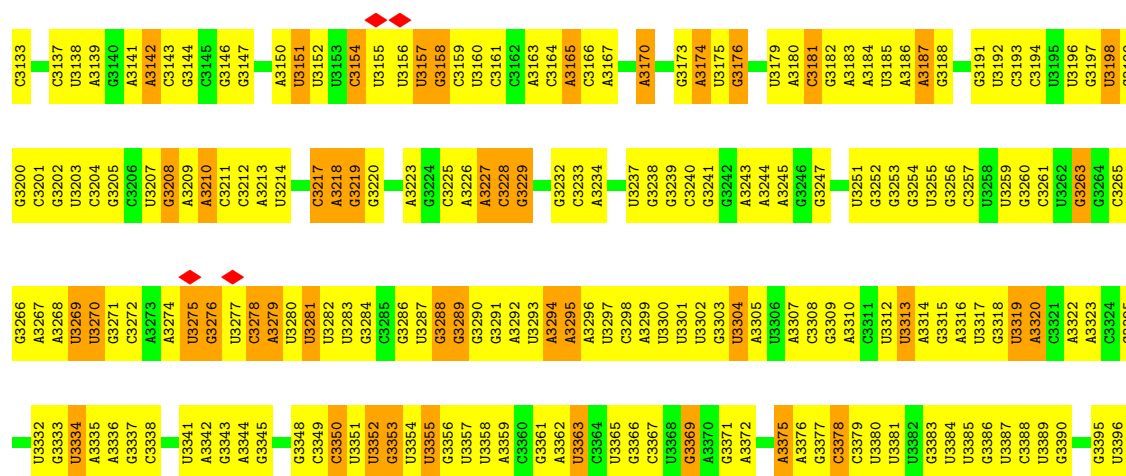
• Molecule 5: 25S rRNA



G1148	A1080	G1018	G950	G881	G812	A744	U832	C618	U553	U487	A428	A361	A285	G218
U1081	U1081	G1019	A951	A882	G813	C745	U883	A619	A584	U488	U429	U362	U286	A429
G1152	G1082	G1020	A952	A883	U814	A746	G685	U620	U555	U620	U430	G363	G287	G220
A1084	A1084	G1021	G953	A884	G815	A747	G686	A621	U556	C489	U431	G364	G288	A221
A1154	A1085	G1024	U956	U885	A316	G750	U687	A622	A557	A490	U432	A365	A289	U222
C1155	C1086	U1025	C957	G887	C818	A751	G688	U623	U558	U	A433	A366	C291	U223
C1156		A1025	C958	A888	U819	C752	U689	G624	A559	G	U434	A367	C291	C224
G1157	G1090	A1026	C959		U820	C753	U690	G625	C562		C435	G371	U292	C226
A1158	C1092	A1027	U960	G891	U821	G754	A691	U626	G495		C436		C293	G227
A1159	A1093	U1028	C961	U892	G822	A755	A692	A628	C496		A437	A374	U294	U288
A1160	U1094	G1029	A962	A895	C823	C756	U693	U629	C497		U438	A375	A295	U295
G1161	U1095	A1030	G963	A896	C824	C757	C694	A630	U498		A439	A376	A296	U230
U1162	U1096	C1031	G964	U897	U825	C758	C695	A631	G499		A440	G376	U230	U230
	U1097	U1032	A965	U897	G826	U759	C696	G632	C500		U441		G297	G231
A1165	A1098	U1033	U966		A827	G760	A697	G633	U501		U442		G303	G234
U1166		U1034	A967	G901	U828	U764	U698	C533	A502		U443	U380	A308	G235
U1167		G1035	G968	G902	A830		C700	C534	C503		U444	U381	A307	G236
U1168	G1101	A1036	C969	U903	G831	U767	C638	C637	A504		U445	U382	A308	
A1169	A1102	C1037	A970	A904	G832	C768	G639	U640	U507		U446	U383	C312	G239
A1170	A1103	G1038	A971	G907	G835	G769	A705	U641	G513		U447	A385	U314	U240
G1171	G1104	U1039	A972	G908	A836	G770	A706	C641	G514		U448	A386	C315	C242
A1172	A1105	A1040	A973	G909	A837	G771	U707	U642	C515		U449	U387	U316	G243
G1173	G1106		G974	G910	G838	G772	G708	U643	A516		U450	U388	A317	G244
U1174	C1107	U1044	U981	C911	A846	A775	A709	U644	G517		U451	U389	A318	U245
C1175	U1108	C1045	C982	G912	A847	U776	A710	A645	G518		G	U391	A319	U246
G1177	U1109	A1046	U983	G913	A848	U777	A711	A646	A519		C	G392	U324	C247
U1178	U1110	U1047	C984	A914	A849	U778	A712	A647	U520		C	U393	U249	U249
A1179	U1111	A1048	U985	G915	U850	A779	G713	C648	A521		C	A395	U250	U250
A1180	U1114	C1049	A986	A916	U851	U780	G714	A649	A522		C	A396	G251	G251
U1181	G1115	U1050	G987	A917	C851	U781	A715	A650	C525		C	A397	U327	U252
A1182	G1116	U1051	U988	G918	U852	A782	G716	A651	G526		U	A398	U328	A253
C1183	G1117	U1052	U989	A919	U853	A783	C717	A652	A527		G	A399	U329	U254
A1184	G1118	A1053	U990	A920	G854	G784	G718	A653	U528		C	G400	G330	A255
C1185	G1119	U1054	G991	A921	U855	A785	U719	C654	A529		U	U401	G331	
	U1120	A1055	A992	A926	G856	G787	A720	C655	U594		C	A402	C332	G258
U1188	U1121	U1056	A993	C927	G857	C788	G721	A656	G530		C	C403	G333	C259
C1189	U1122	A1057	G994	C928	U858	A789	G722	A657	G531		U	G404	A342	C260
U1191	U1123	U1058	A995	A929	G859	U790	G723	A658	A532		U	U405	G337	U261
C1192	G1126	G1059	A996	U930	G860	A791	G725	A659	U534		U	A406	A338	U262
A1193	G1127	U1060			C861	G792	G726	A660	G535		U	A407	C339	
G1194	U1128	A1061	G999	A833	U862	C793	G727	C661	U536		G	A408	C340	A266
A1195	A1129	G1062	C1000	G934	C863	U794	G728	U662	A537		G	A409	G341	G267
C1196	A1130	A1063	G1001	U935	C864	G795	C729	C663	A603		U	U410	A342	A268
A1197	G1131	A1064	A1002	A936	U865	U796	C730	U664	G604		G	U411		G269
	C1132	A1065	A1003	G937	G867	U797	U731	A665	U605		U	G412	G347	
C1201	A1133	G1066	U1004	C938	G868	G798	G732	G668	C606		A	U413	A348	A273
A1202	G1134	U1067	U1005	U939	G869	G799	G733	U669	A607		G	U414	A349	G274
A1203	A1135	C1068		G940	G870	G800	C734	C670	A608		G	C415	C350	U275
A1204	A1136	C1069	U1008	G941	U871	G801	A735	U671	G609		G	A416	A351	U276
	C1137	U1070	A1009	U942	C873	C802	A736	A672	A611		A	A417	A352	G277
G1207	U1138	G1072	G1010	U943	U874	C803	G737	U673	A612		A	U418	U278	U279
G1208	G1139	U1073		C945	G875	G804	A738	A674	G547		U	G419	G420	U280
U1210	G1142	U1074	G1013	U946	A876	G805	G739	G674	U548		U	G420	A357	G281
U1211	U1143	U1075	U1014	G947	C877	A806	G740	C675	G613		C	G421	G358	G282
A1212	U1144	G1076	U1015	C948	U878		U741	G676	U615		C	A422	U359	G283
G1213		U1077	C1016	G949	A879	A810	G742	A677	G616		C	G424	G360	A284
		A1078	C1017	C949	G880	U811	C743	U681	G617		A485			
		A1079						U486						

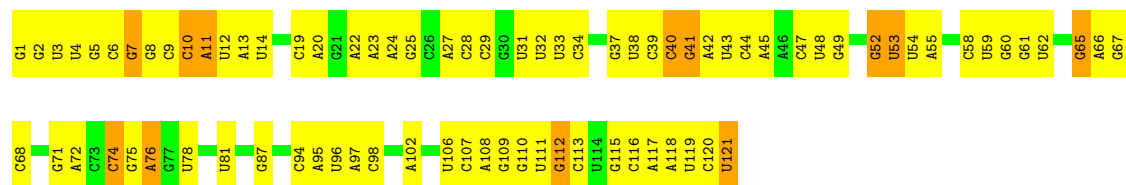


U3066	A2995	C2927	U2854	C2776	U2705	U2641	C2305	G2240	U2176
C3067	U2996	C2928	U2855	G2777	G2706	A2642	C2306	U2241	G2177
U3068	G2997	C2929	G2856	G2778	C2707	A2643	U2307	A2242	A2178
G3069	U2998	C2930	C2857	U2781	C2708	C2644	C2308	G2245	C2179
A3070	U2999	C2931	U2858	U2782	C2709	A2645	A2309	G2246	G2180
G3074	C3002	U2935	U2859	U2783	C2710	U2446	U2310	G2247	C2181
G3075	A3006	A2936	U2860	G2794	C2711	A2447	G2311	G2248	U2184
U3078	U3007	G2937	G2863	U2795	G2714	G2448	A2312	G2249	G2185
U3079	A3008	G2938	A2864	U2796	A2715	U2652	C2313	G2250	U2186
G3080	G3081	C2939	U2865	G2797	U2716	U2653	U2314	G2251	G2187
C3081	A3012	A2940	U2866	C2798	U2717	C2654	G2315	A2252	A2188
C3082	G3015	U2941	G2867	U2799	U2718	U2655	G2316	G2253	U2189
G3083	A3016	C2942	U2868	G2800	U2719	A2656	U2317	U2254	U2190
C3084	U3017	A2943	G2869	A2801	G2720	A2657	U2318	A2255	U2191
G3085	A3018	G2944	A2870	U2802	U2721	G2658	U2319	A2256	U2192
A3086	C3019	U2945	U2871	A2803	U2722	G2659	A2320	G2257	U2193
A3087	U3020	G2946	U2872	A2804	U2723	G2660	A2321	U2258	U2194
G3088	A3021	U2947	U2873	U2805	U2724	G2661	U2322	G2259	C2195
C3089	G3022	U2948	G2874	G2806	U2725	G2662	U2323	G2260	C2196
U3090	C3023	U2949	G2875	U2807	G2726	C2663	U2324	G2261	U2197
A3091	G3024	G2950	G2876	U2808	U2727	C2664	U2325	U2262	A2198
C3092	U3025	G2951	G2877	A2809	U2728	A2665	U2326	U2263	U2199
C3093	A3026	U2952	G2878	U2810	U2729	G2666	U2327	U2264	U2200
A3094	G3027	U2953	U2879	A2811	A2734	A2667	U2328	U2265	U2201
U3095	C3028	C2954	U2880	C2812	U2735	U2668	U2329	U2266	U2202
G3096	A3029	G2955	G2881	A2813	U2736	G2669	U2330	U2267	U2203
C3097	U3030	U2956	U2882	G2814	A2737	G2670	U2331	U2268	U2204
G3098	G3031	C2957	G2883	G2815	U2738	A2671	U2332	U2269	U2205
U3099	C3032	U2958	U2884	U2816	A2739	G2672	U2333	A2271	U2206
A3100	A3033	G2959	C2885	A2817	A2740	A2673	U2334	U2272	U2207
C3101	U3034	U2960	U2886	U2818	A2741	A2674	U2335	U2273	A2208
G3102	G3035	G2961	A2887	A2819	A2742	C2675	U2336	U2274	U2209
A3103	C3036	U2962	U2888	A2820	U2743	U2676	U2337	A2275	G2210
U3104	U3037	G2963	G2889	A2821	U2744	G2677	U2338	U2276	U2211
C3105	A3038	U2964	U2890	U2822	G2745	A2678	U2339	U2277	A2212
A3106	G3039	G2965	G2891	G2823	A2746	C2679	U2340	U2278	G2213
U3107	U3040	U2966	U2892	U2824	U2747	A2680	A2341	U2279	A2214
G3108	A3041	C2967	G2893	C2825	A2748	U2681	U2342	U2280	A2215
C3109	U3042	U2968	U2894	U2826	U2749	C2682	U2343	U2281	G2216
U3110	G3043	G2969	U2895	A2827	U2750	U2683	U2344	U2282	U2217
G3111	C3044	U2970	U2896	U2828	U2751	C2684	U2345	U2283	G2218
A3112	U3045	U2971	G2897	G2829	U2752	C2685	U2346	U2284	A2219
C3113	G3046	C2972	U2898	U2830	G2753	A2686	U2347	U2285	A2220
A3114	U3047	U2973	U2899	C2831	U2754	G2687	U2348	C2287	G2221
U3115	A3048	G2974	U2900	U2832	U2755	U2688	U2349	U2288	A2222
C3116	G3049	U2975	U2901	A2833	U2756	A2689	U2350	U2289	A2223
U3117	U3050	U2976	U2902	U2834	U2757	G2690	U2351	U2290	A2224
A3118	C3051	G2977	U2903	G2835	U2758	A2691	U2352	U2291	U2225
G3119	G3052	U2978	U2904	U2836	A2759	U2692	U2353	U2292	U2226
C3120	U3053	U2979	U2905	A2837	U2760	A2693	U2354	U2293	G2227
U3121	C3054	G2980	U2906	U2838	U2761	A2694	U2355	U2294	A2228
A3122	U3055	U2981	U2907	G2839	U2762	A2695	U2356	U2295	U2232
C3123	G3056	G2982	U2908	U2840	U2763	A2696	U2357	U2296	A2233
U3124	U3057	U2983	U2909	G2841	G2764	A2697	U2358	U2297	U2234
A3125	C3058	C2984	U2910	U2842	U2765	U2698	U2359	U2298	G2235
G3126	U3059	U2985	U2911	U2843	U2766	A2699	U2360	U2299	U2301
U3127	A3060	G2986	U2912	A2844	U2767	G2700	U2361	U2300	G2302
C3128	C3061	U2987	U2913	U2845	U2768	U2701	U2362	U2301	G2303
A3129	U3062	U2988	U2914	U2846	U2769	U2702	U2363	U2302	G2304
U3130	G3063	G2989	U2915	U2847	U2770	A2703	U2364	U2303	U2305
C3131	A3064	U2990	U2916	G2848	U2771	G2704	U2365	U2304	U2306
G3132	U3065	U2991	U2917	U2849	U2772	U2705	U2366	U2305	U2307
U3133	C3066	G2992	U2918	G2850	U2773	A2706	U2367	U2306	U2308
A3134	U3067	U2993	U2919	U2851	U2774	U2707	U2368	U2307	U2309
C3135	G3068	G2994	U2920	U2852	U2775	U2708	U2369	U2308	U2310
U3136	A3069	U2995	U2921	U2853	U2776	U2709	U2370	U2309	U2311
C3137	U3070	G2996	U2922	U2854	U2777	U2710	U2371	U2310	U2312
A3138	G3069	U2997	U2923	U2855	U2778	U2711	U2372	U2311	U2313
C3139	U3071	G2998	U2924	U2856	U2779	U2712	U2373	U2312	U2314
U3140	A3072	U2999	U2925	U2857	U2780	U2713	U2374	U2313	U2315
C3141	C3073	G3000	U2926	U2858	U2781	U2714	U2375	U2314	U2316
A3142	U3074	U3001	U2927	U2859	U2782	U2715	U2376	U2315	U2317
G3143	A3075	G3002	U2928	U2860	U2783	U2716	U2377	U2316	U2318
C3144	U3076	U3003	U2929	U2861	U2784	U2717	U2378	U2317	U2319
U3145	C3077	G3004	U2930	U2862	U2785	U2718	U2379	U2318	U2320
A3146	U3078	A3005	U2931	U2863	U2786	U2719	U2380	U2319	U2321
C3147	G3079	U3006	U2932	U2864	U2787	U2720	U2381	U2320	U2322
U3148	A3080	G3007	U2933	U2865	U2788	U2721	U2382	U2321	U2323
C3149	U3081	U3008	U2934	U2866	U2789	U2722	U2383	U2322	U2324
A3150	G3082	A3009	U2935	U2867	U2790	U2723	U2384	U2323	U2325
C3151	C3083	U3010	U2936	U2868	U2791	U2724	U2385	U2324	U2326
U3152	U3084	G3011	U2937	U2869	U2792	U2725	U2386	U2325	U2327
A3153	A3085	U3012	U2938	U2870	U2793	U2726	U2387	U2326	U2328
C3154	G3086	A3013	U2939	U2871	U2794	U2727	U2388	U2327	U2329
U3155	U3087	U3014	U2940	U2872	U2795	U2728	U2389	U2328	U2330
A3156	C3088	G3015	U2941	U2873	U2796	U2729	U2390	U2329	U2331
C3157	U3089	U3016	U2942	U2874	U2797	U2730	U2391	U2330	U2332
U3158	A3090	A3017	U2943	U2875	U2798	U2731	U2392	U2331	U2333
C3159	G3091	U3018	U2944	U2876	U2799	U2732	U2393	U2332	U2334
A3160	C3092	G3019	U2945	U2877	U2800	U2733	U2394	U2333	U2335
U3161	U3093	U3020	U2946	U2878	U2801	U2734	U2395	U2334	U2336
C3162	A3094	A3021	U2947	U2879	U2802	U2735	U2396	U2335	U2337
U3163	G3095	G3022	U2948	U2880	U2803	U2736	U2397	U2336	U2338
A3164	C3096	U3023	U2949	U2881	U2804	U2737	U2398	U2337	U2339
C3165	U3097	A3024	U2950	U2882	U2805	U2738	U2399	U2338	U2340
U3166	G3098	G3025	U2951	U2883	U2806	U2739	U2400	U2339	U2341
A3167	C3099	C3026	U2952	U2884	U2807	U2740	U2401	U2340	U2342
C3168	U3100	A3027	U2953	U2885	U2808	U2741	U2402	U2341	U2343
U3169	A3101	G3028	U2954	U2886	U2809	U2742	U2403	U2342	U2344
C3170	G3102	U3029	U2955	U2887	U2810	U2743	U2404	U2343	U2345
A3171	C3103	A3030	U2956	U2888	U2811	U2744	U2405	U2344	U2346
U3172	U3104	G3031	U2957	U2889	U2812	U2745	U2406	U2345	U2347
C3173	A3105	C3032	U2958	U2890	U2813	U2746	U2407	U2346	U2348
U3174	G3106	U3033	U2959	U2891	U2814	U2747	U2408	U2347	U2349
A3175	C3107	A3034	U2960	U2892	U2815	U2748	U2409	U2348	U2350
C3176	U3108	G3035	U2961	U2893	U2816	U2749	U2410	U2349	U2351
U3177	A3109	U3036	U2962	U2894	U2817	U2750	U2411	U2350	U2352
C3178	G3109	C3037	U2963	U2895	U2818	U2751	U2412	U2351	U2353
U3179	U3110	A3038	U2964	U2896	U2819	U2752	U2413	U2352	U2354
A3180	C3111	G3039	U2965	U2897	U2820	U2753	U2414	U2353	U2355
C3181	G3112	U3040	U2966	U2898	U2821	U2754	U2415	U2354	U2356
U3182	A3113	A3041	U2967	U2899	U2822	U2755	U2416	U2355	U2357
C3183	C3114	U3042	U2968	U2900	U2823	U2756	U2417	U2356	U2358
U3184	U3115	G3043	U2969	U2901	U2824	U2757	U2418	U2357	U2359
A3185	A3116	C3044	U2970	U2902	U2825	U2758	U2419	U2358	U2360
C3186	G3117	U3045	U2971	U2903	U2826	U2759	U2420	U2359	U2361
U3187	C3118	A3046	U2972	U2904	U2827	U2760	U2421	U2360	U2362
C3188	U3119	G3047	U2973	U2905	U2828	U2761	U2422	U2361	U2363
A3189	C3120	U3048	U2974	U2906	U2829	U2762	U2423	U2362	U2364
U3190	U3121	A3049	U2975	U2907	U2830	U2763	U2424	U2363	U2365
C3191	G3122	U3050	U2976	U2908	U2831	U2764	U2425	U2364	U2366
A3192	A3123	C3051	U2977	U2909	U2832	U2765	U2426	U2365	



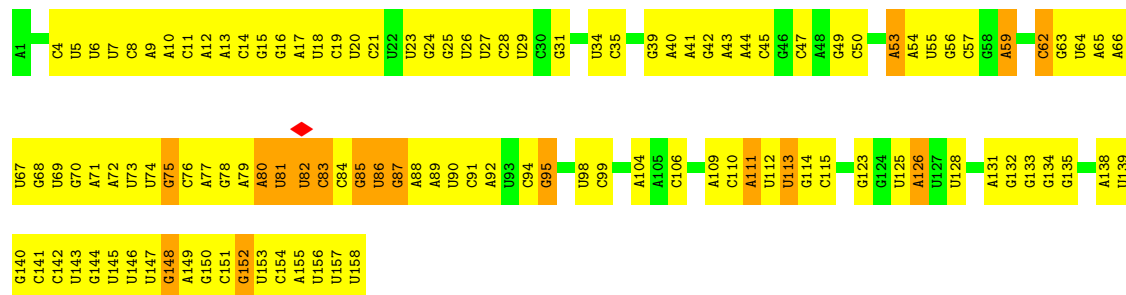
• Molecule 6: 5S rRNA

Chain C4: 33% 57% 10%



• Molecule 7: 5.8S rRNA

Chain C3: 25% 64% 11%



• Molecule 8: Large ribosomal subunit protein uL4A

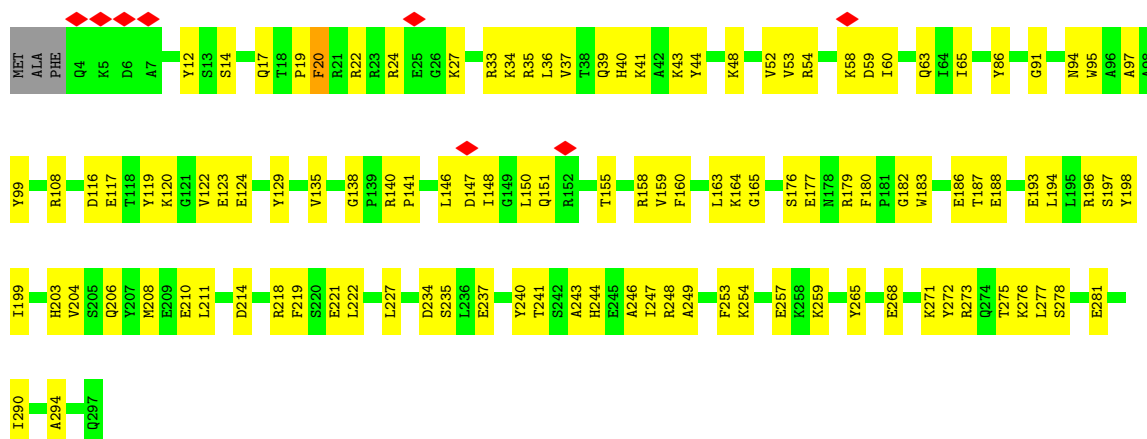
Chain LC: 66% 33% .





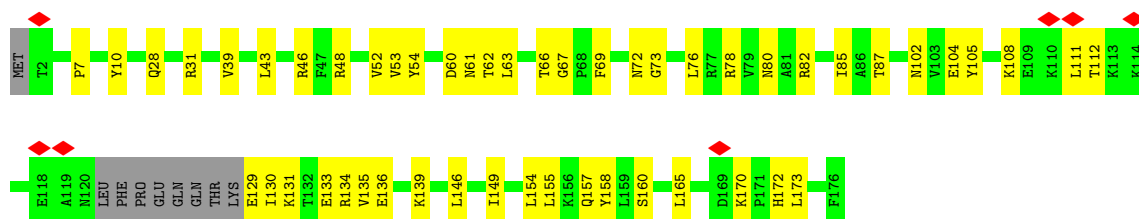
• Molecule 9: Large ribosomal subunit protein uL18

Chain LD: 61% 37%



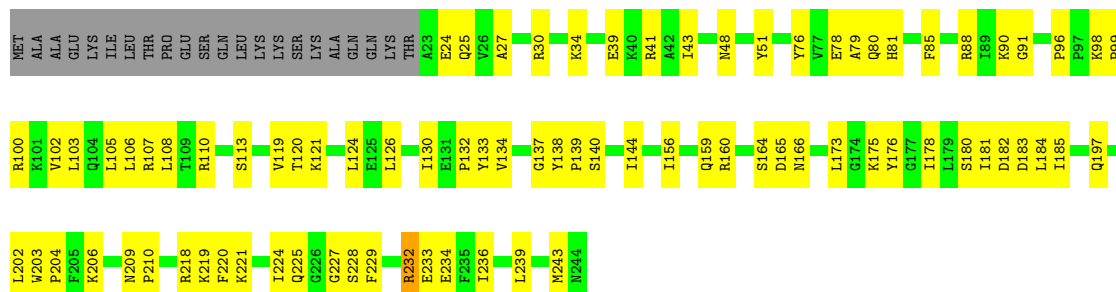
• Molecule 10: Large ribosomal subunit protein eL6B

Chain LE: 66% 29% 5%



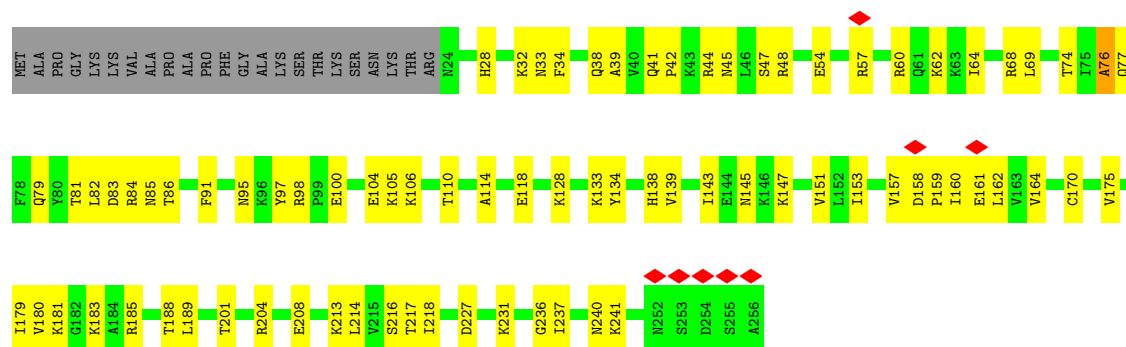
• Molecule 11: Large ribosomal subunit protein uL30A

Chain LF: 57% 34% 9%



• Molecule 12: Large ribosomal subunit protein eL8A

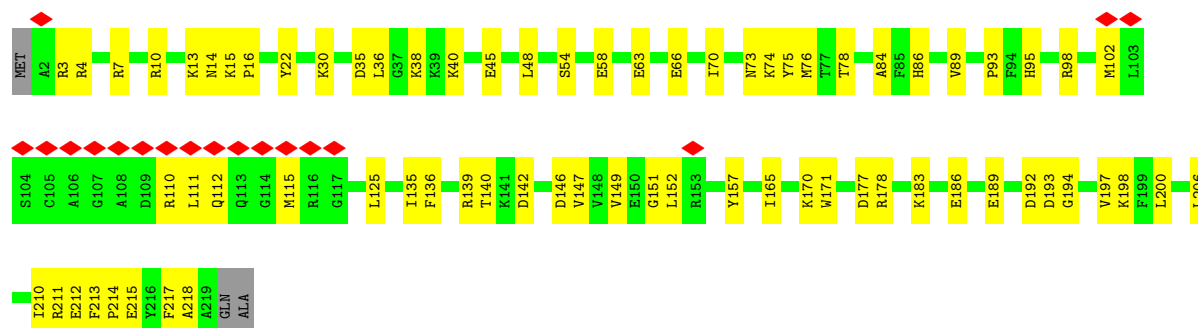
Chain LG: 60% 31% 9%



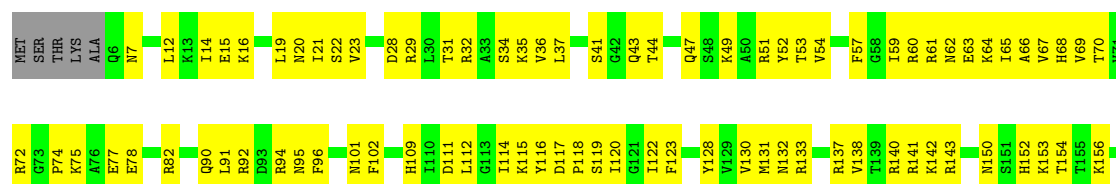
• Molecule 13: Large ribosomal subunit protein uL6A

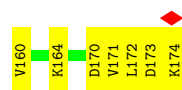


• Molecule 14: Large ribosomal subunit protein uL16

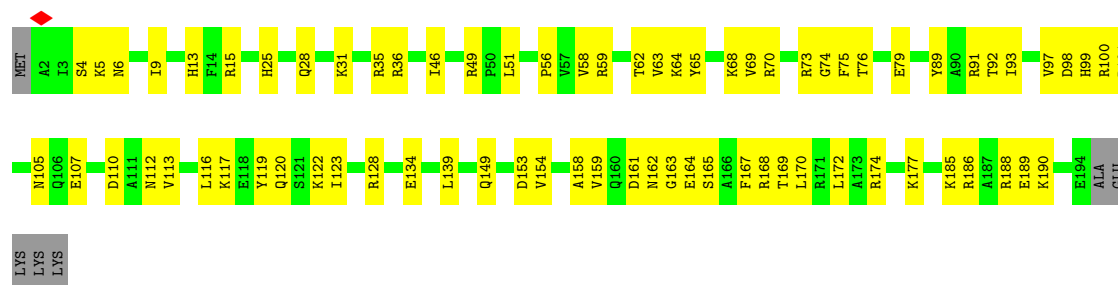


• Molecule 15: Large ribosomal subunit protein uL5B

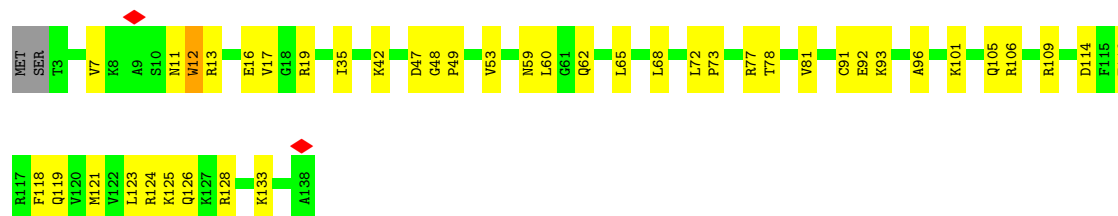




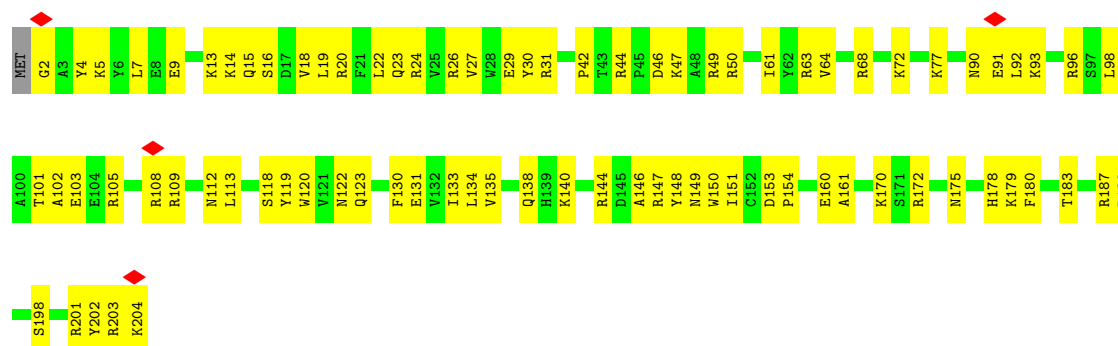
- Molecule 16: Large ribosomal subunit protein eL13A



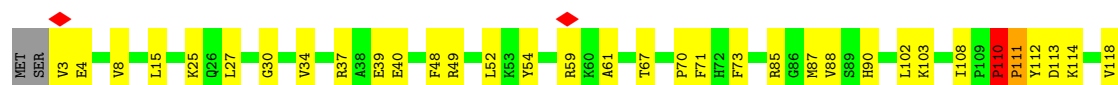
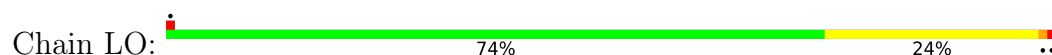
- Molecule 17: Large ribosomal subunit protein eL14A



- Molecule 18: Large ribosomal subunit protein eL15A

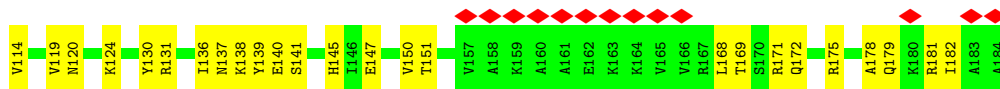


- Molecule 19: Large ribosomal subunit protein uL13A





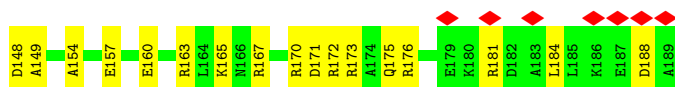
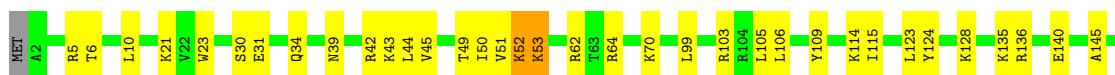
- Molecule 20: Large ribosomal subunit protein uL22A



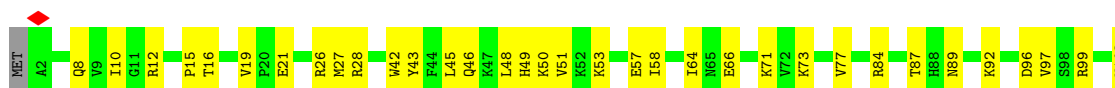
- Molecule 21: Large ribosomal subunit protein eL18A



- Molecule 22: Large ribosomal subunit protein eL19A

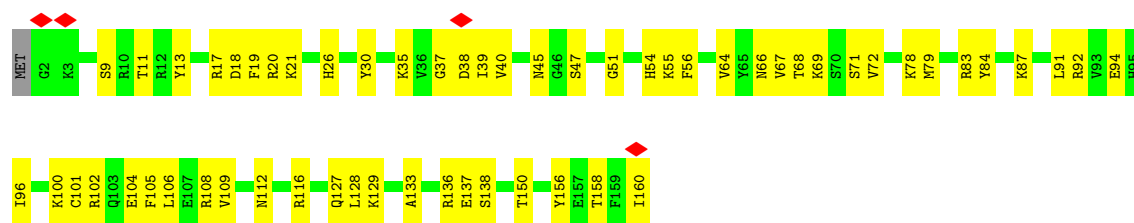


- Molecule 23: Large ribosomal subunit protein eL20A

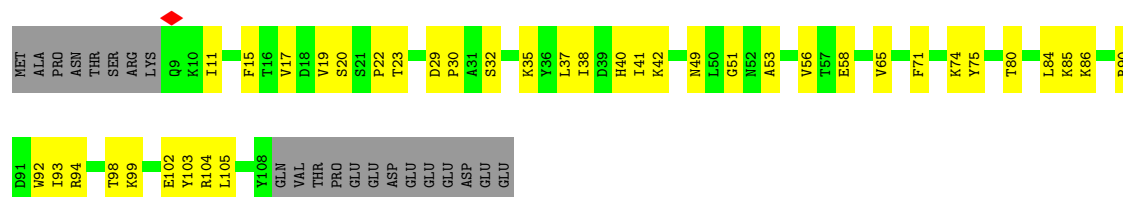


- Molecule 24: Large ribosomal subunit protein eL21A





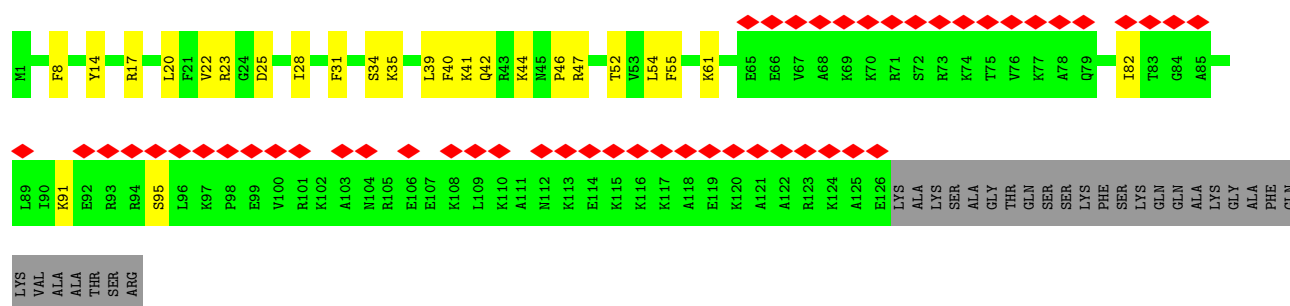
- Molecule 25: Large ribosomal subunit protein eL22A



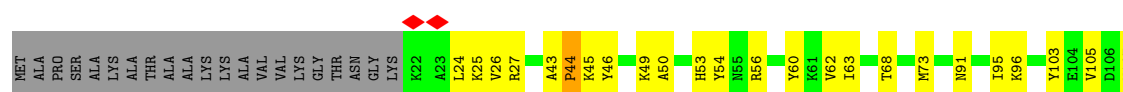
- Molecule 26: Large ribosomal subunit protein uL14A

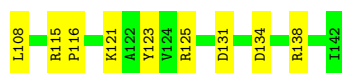


- Molecule 27: Large ribosomal subunit protein eL24A

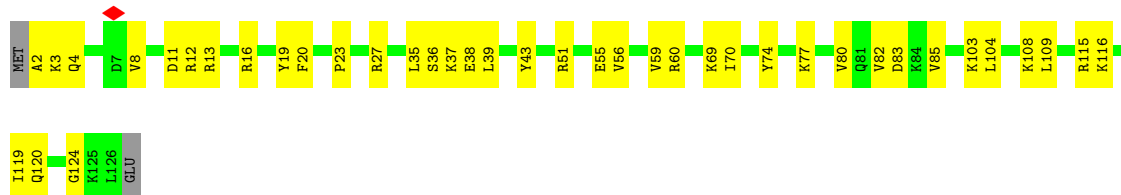


- Molecule 28: Large ribosomal subunit protein uL23

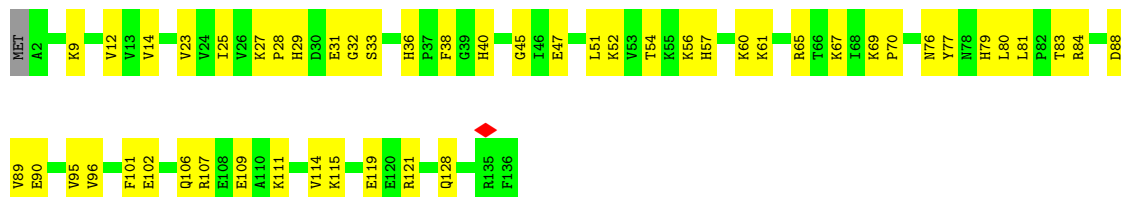




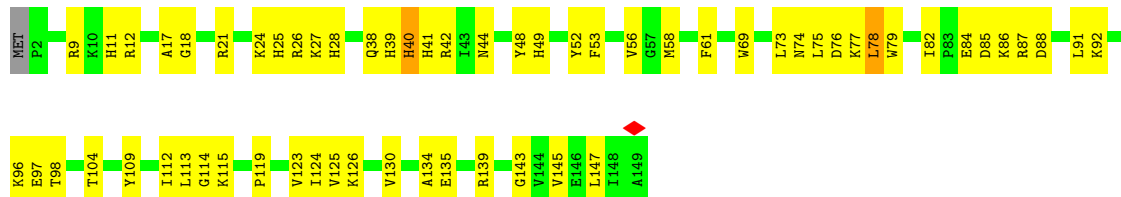
- Molecule 29: Large ribosomal subunit protein uL24A



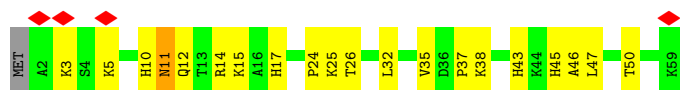
- Molecule 30: Large ribosomal subunit protein eL27A



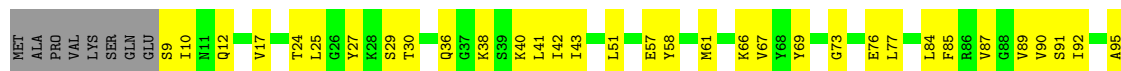
- Molecule 31: Large ribosomal subunit protein uL15



- Molecule 32: Large ribosomal subunit protein eL29



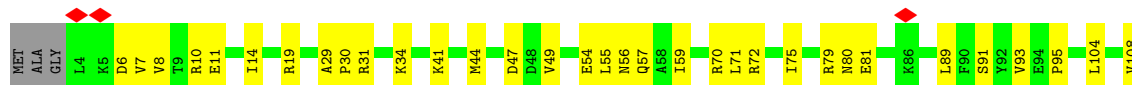
- Molecule 33: Large ribosomal subunit protein eL30





- Molecule 34: Large ribosomal subunit protein eL31A

Chain Ld: 67% 29%



- Molecule 35: Large ribosomal subunit protein eL32

Chain Le: 65% 33%



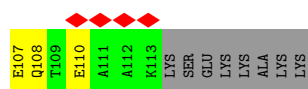
- Molecule 36: Large ribosomal subunit protein eL33A

Chain Lf: 62% 36%

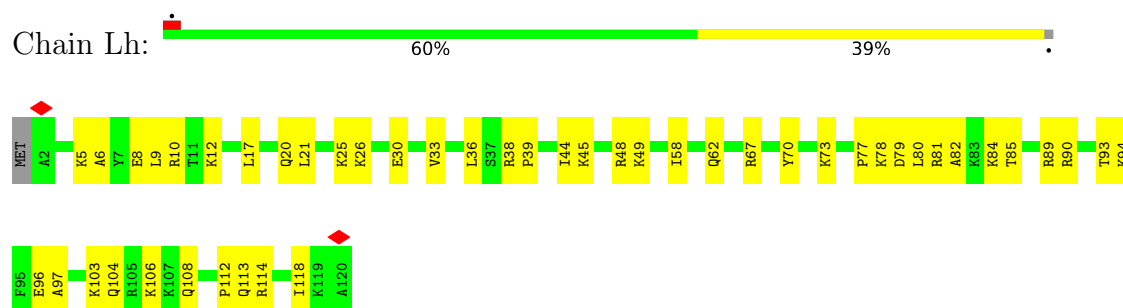


- Molecule 37: Large ribosomal subunit protein eL34A

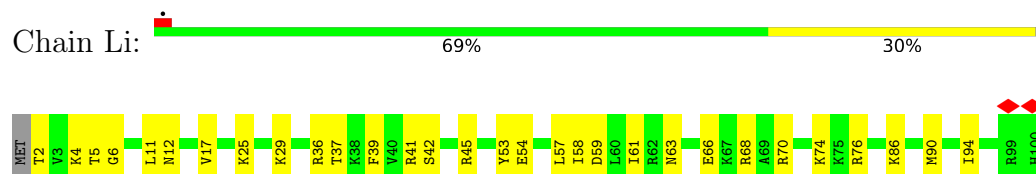
Chain Lg: 60% 32% 7%



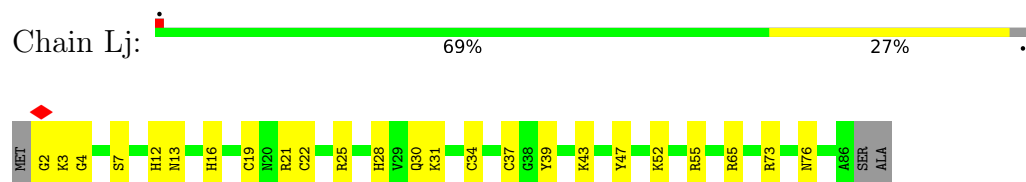
- Molecule 38: Large ribosomal subunit protein uL29A



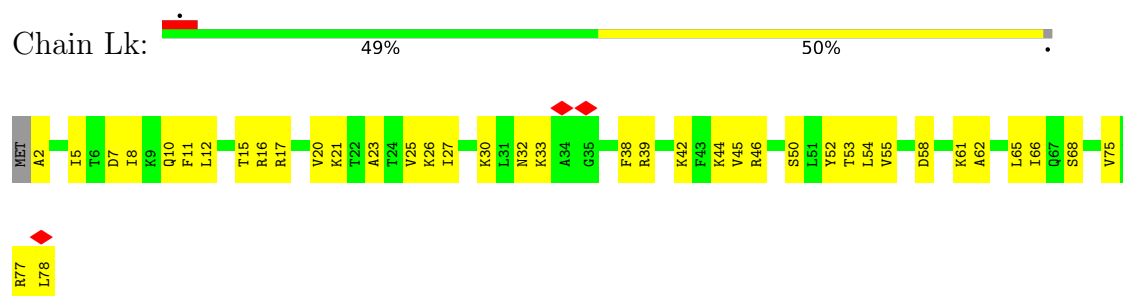
- Molecule 39: Large ribosomal subunit protein eL36A



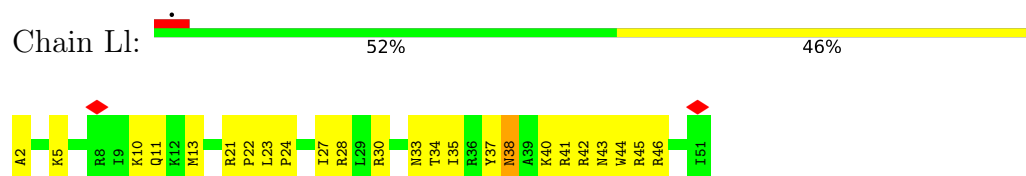
- Molecule 40: Large ribosomal subunit protein eL37A



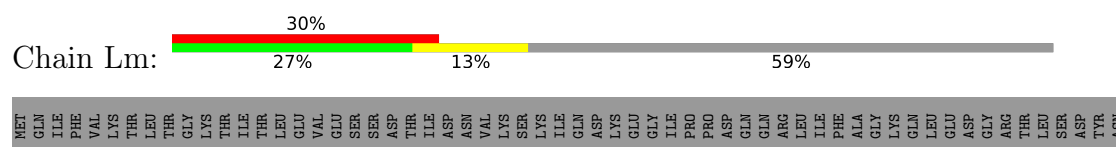
- Molecule 41: Large ribosomal subunit protein eL38



- Molecule 42: Large ribosomal subunit protein eL39

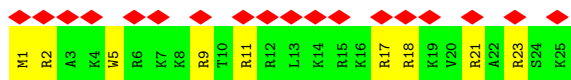
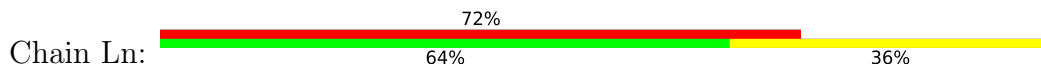


- Molecule 43: Ubiquitin-ribosomal protein eL40A fusion protein





- Molecule 44: Large ribosomal subunit protein eL41A



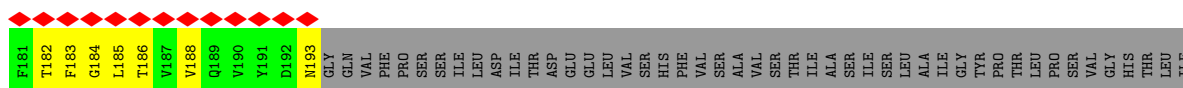
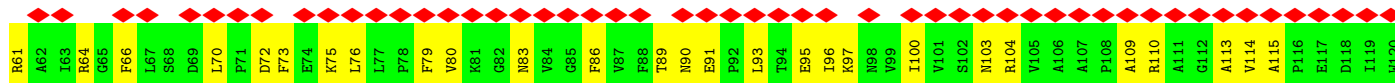
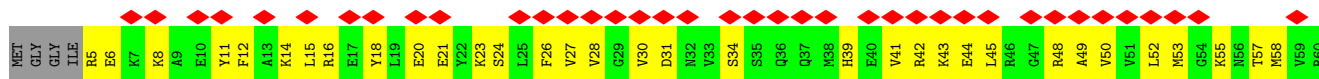
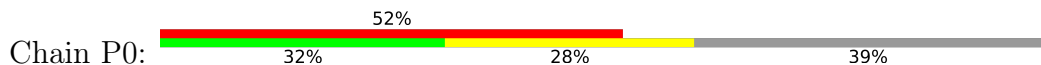
- Molecule 45: Large ribosomal subunit protein eL42A

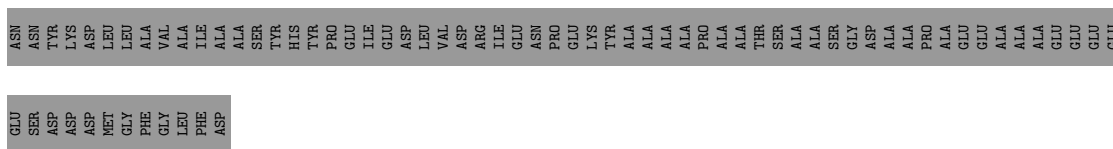


- Molecule 46: Large ribosomal subunit protein eL43A

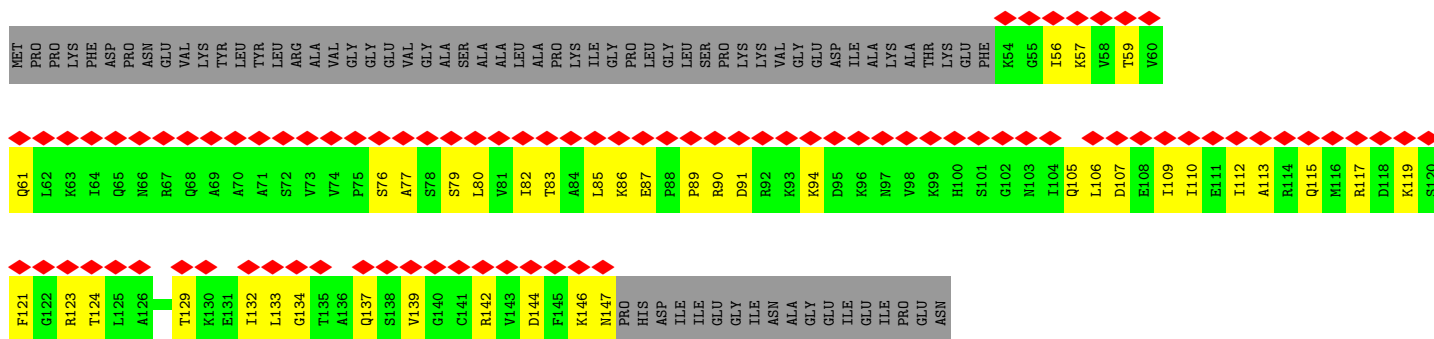
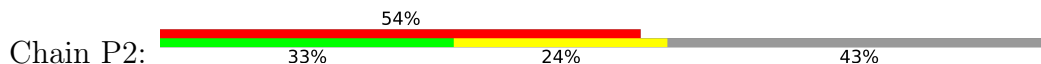


- Molecule 47: Large ribosomal subunit protein uL10

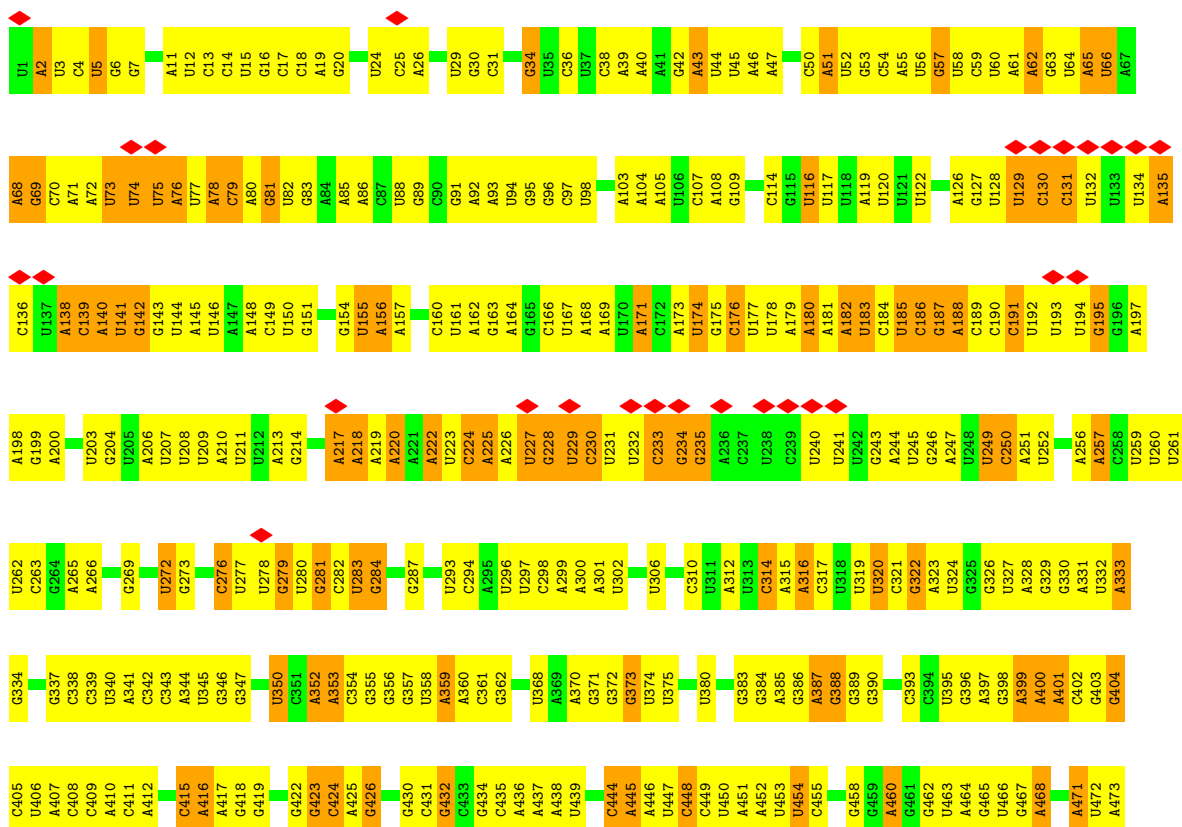




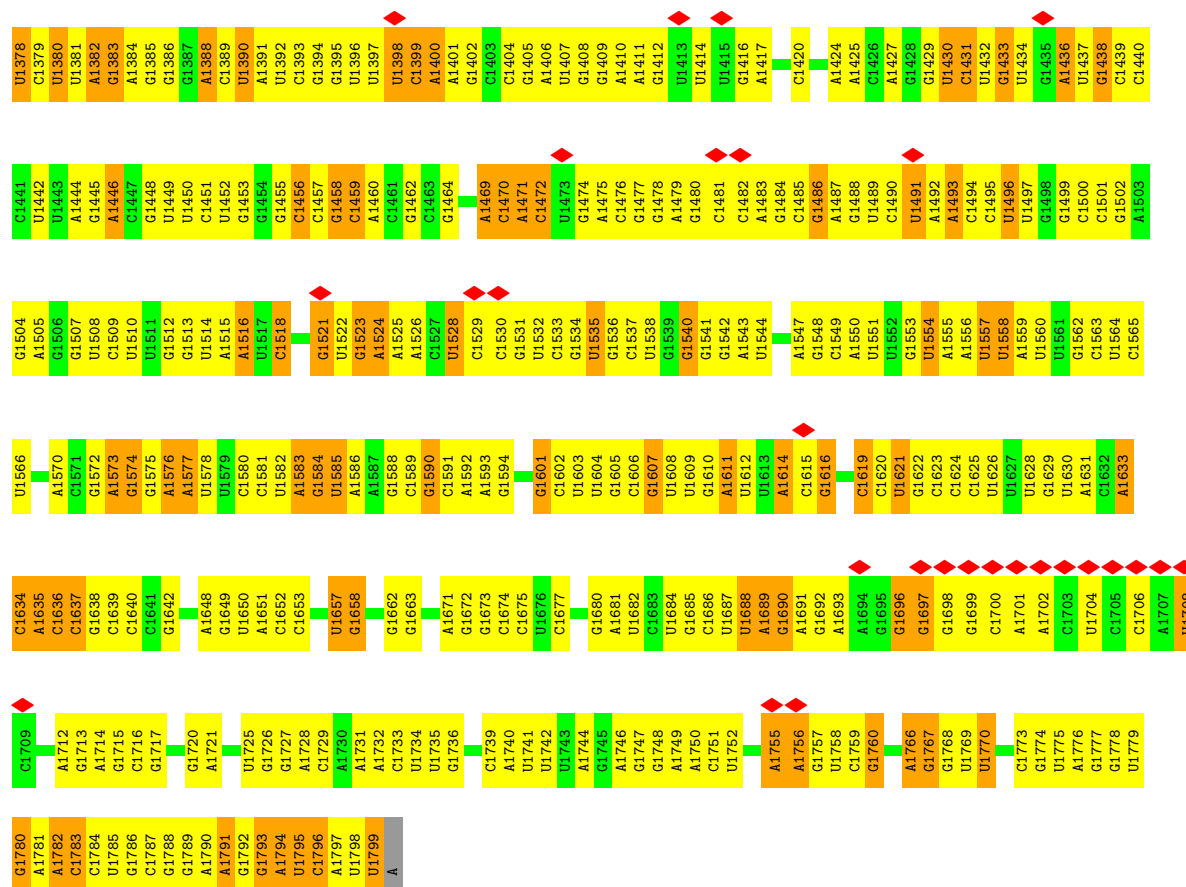
- Molecule 48: Large ribosomal subunit protein uL11A



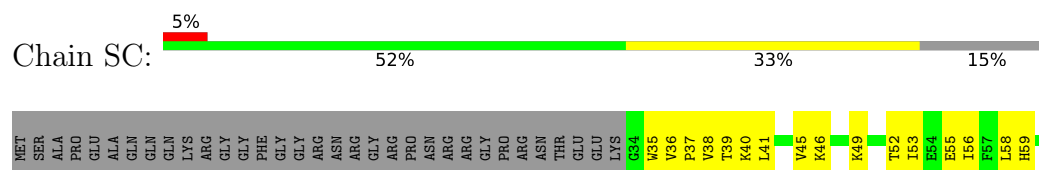
- Molecule 49: 18S rRNA



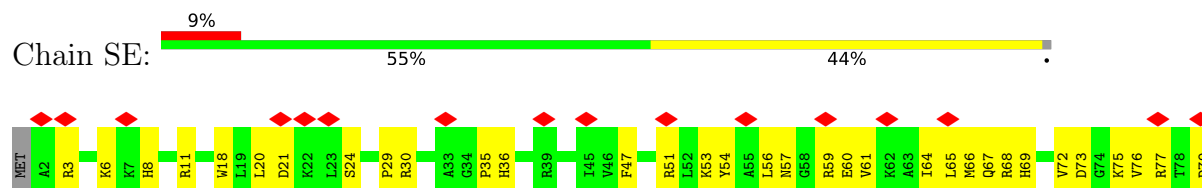


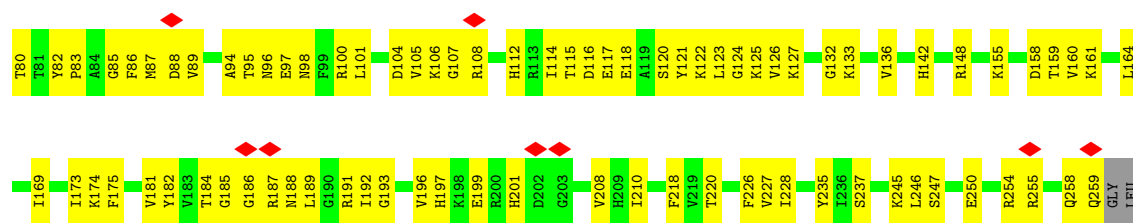


• Molecule 50: 40S ribosomal protein S2

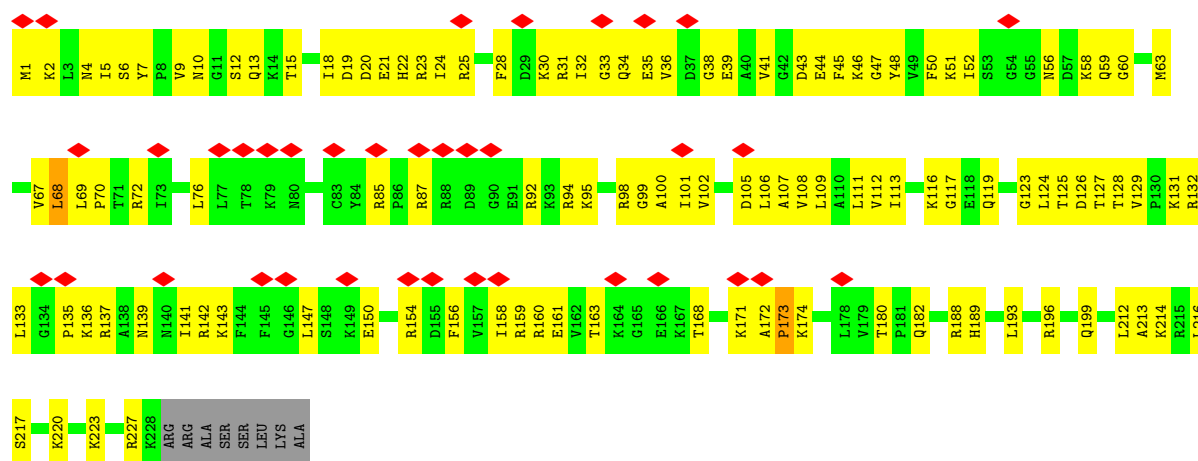


• Molecule 51: 40S ribosomal protein S4-A

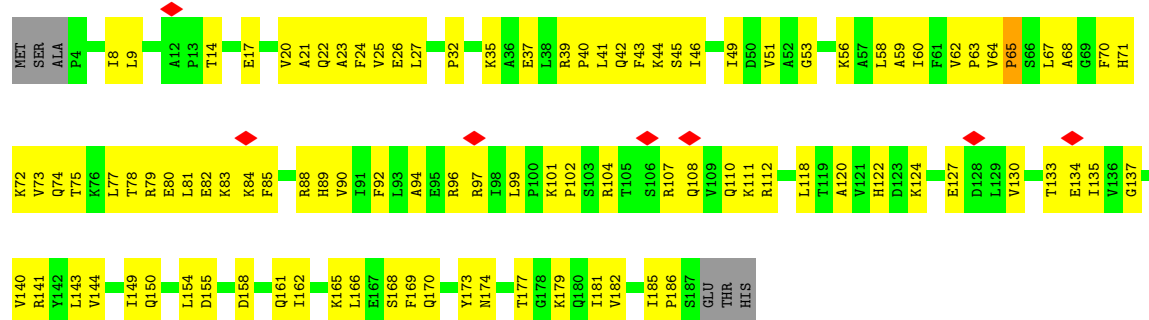




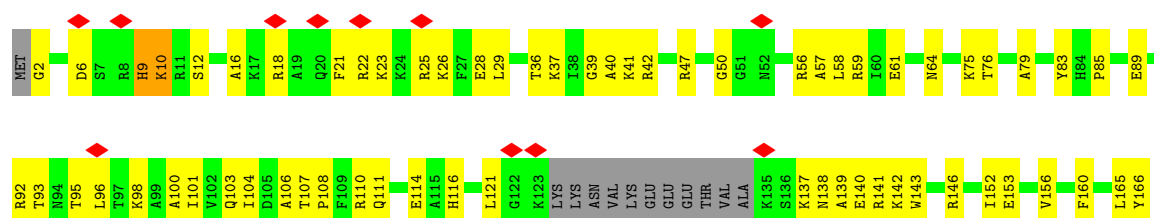
• Molecule 52: 40S ribosomal protein S6-A



• Molecule 53: 40S ribosomal protein S7-A



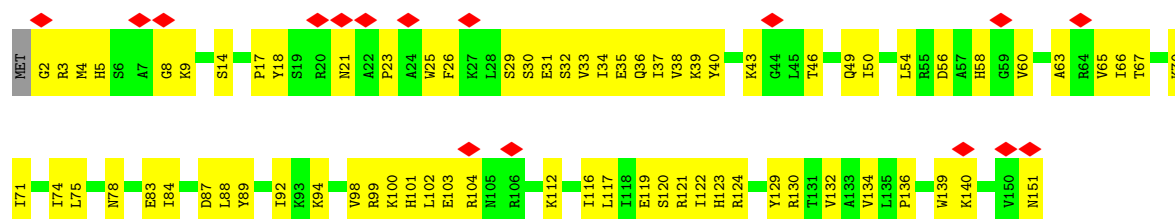
• Molecule 54: 40S ribosomal protein S8-A



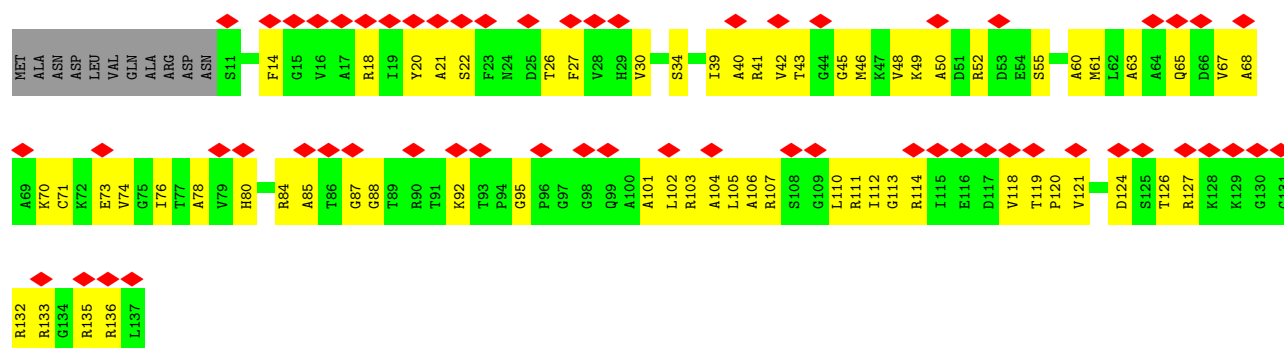




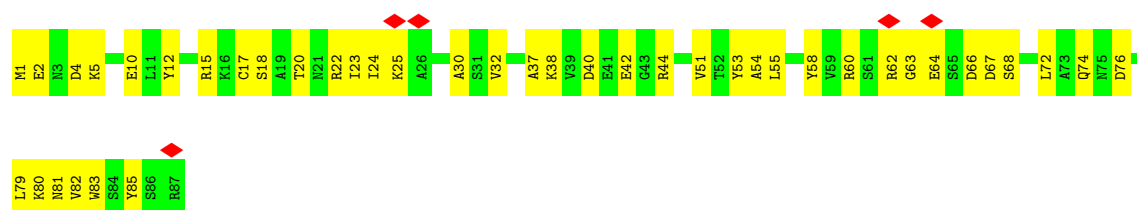
• Molecule 59: 40S ribosomal protein S13



• Molecule 60: Small ribosomal subunit protein uS11B

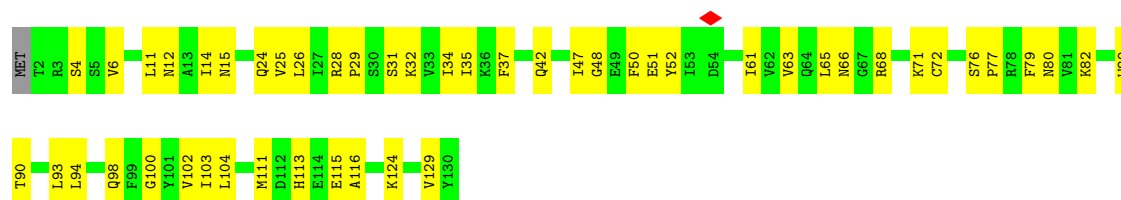


• Molecule 61: Small ribosomal subunit protein eS21A

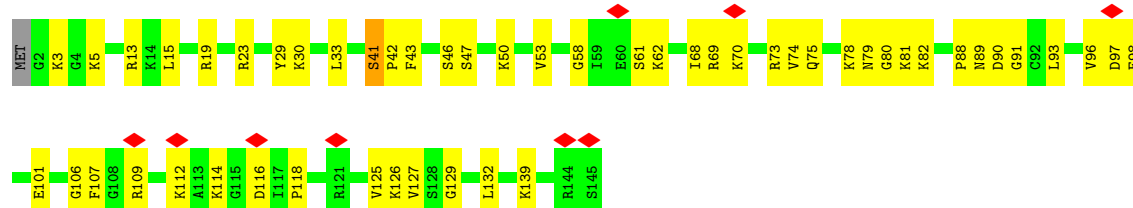


• Molecule 62: 40S ribosomal protein S22-A

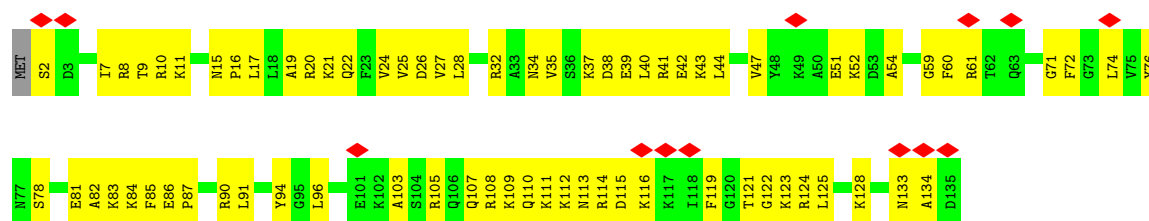




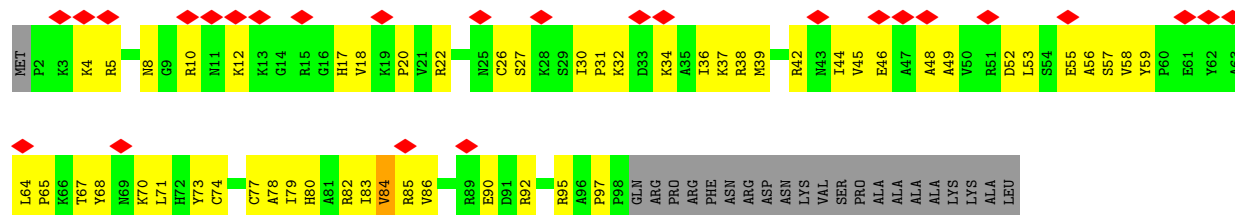
- Molecule 63: 40S ribosomal protein S23-A



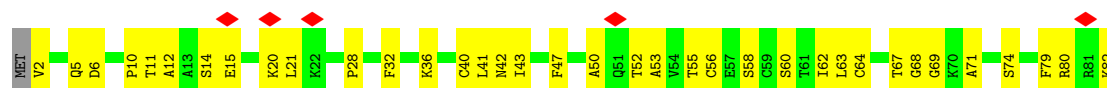
- Molecule 64: 40S ribosomal protein S24-A



- Molecule 65: Small ribosomal subunit protein eS26B

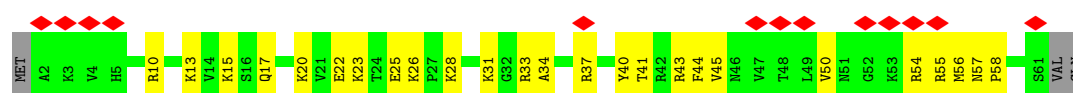


- Molecule 66: 40S ribosomal protein S27-A



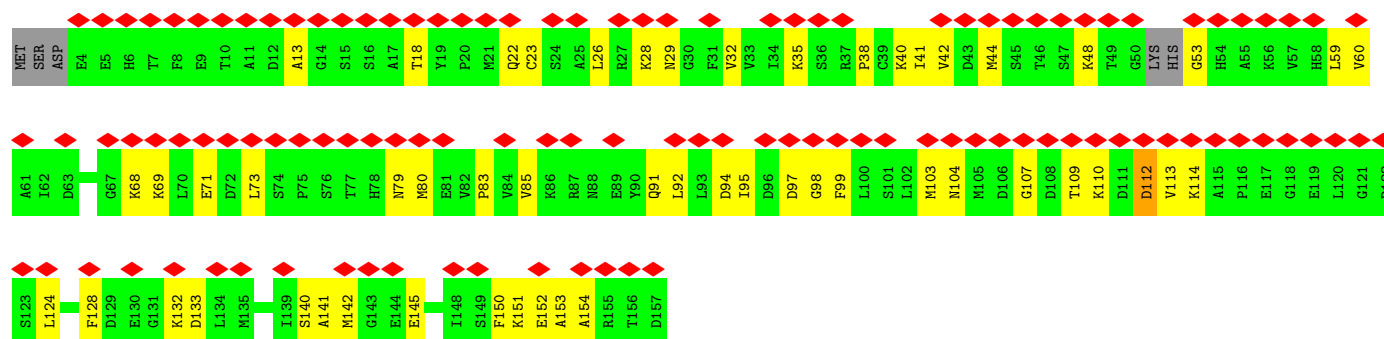
- Molecule 67: 40S ribosomal protein S30-A

Chain Se: 



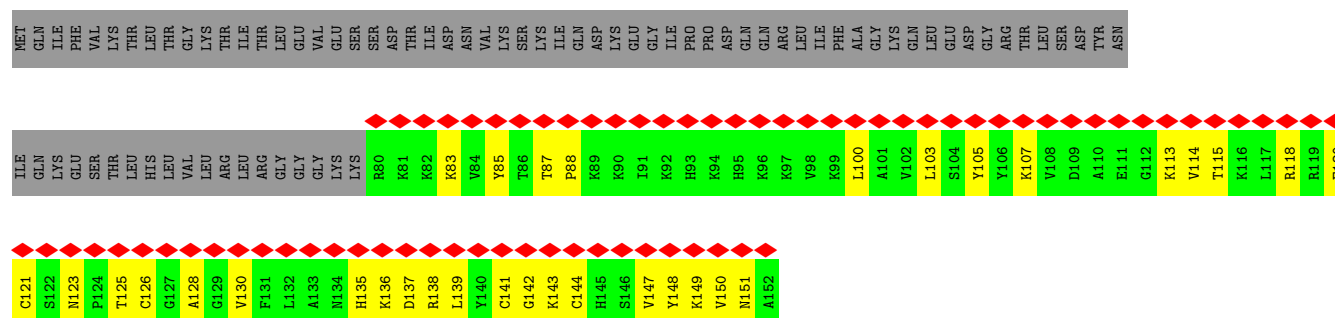
- Molecule 68: Eukaryotic translation initiation factor 5A-1

Chain 5: 



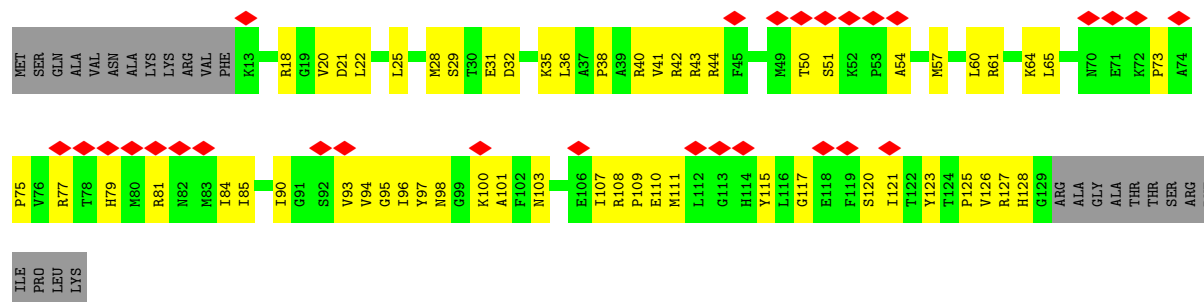
- Molecule 69: Ubiquitin-ribosomal protein eS31 fusion protein

Chain Sf: 

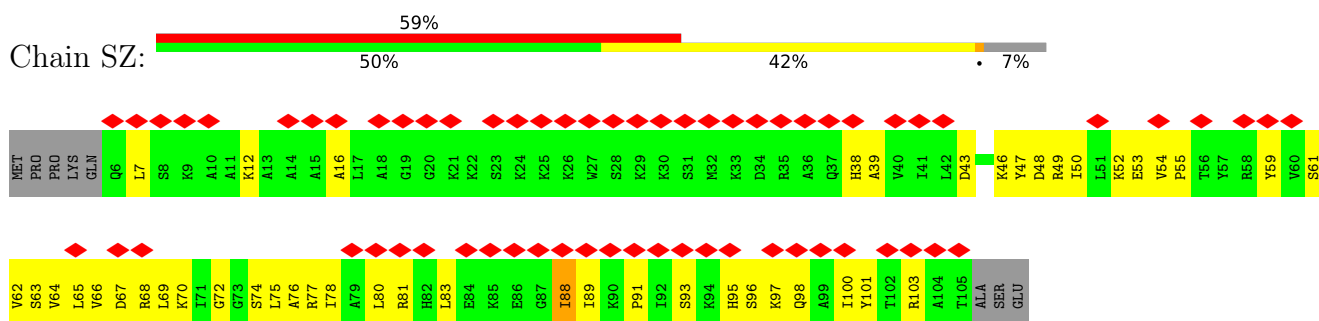


- Molecule 70: Small ribosomal subunit protein uS19

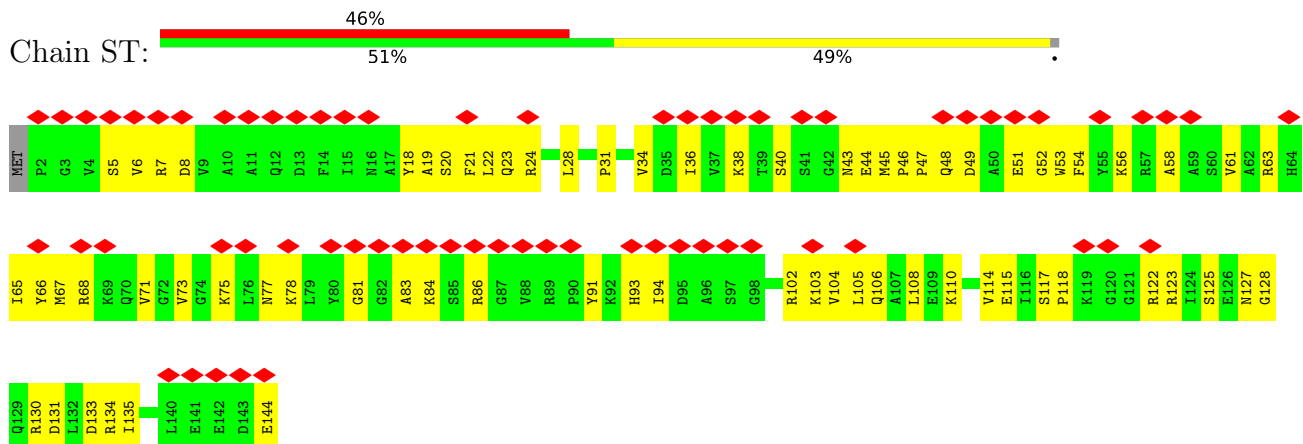
Chain SP: 



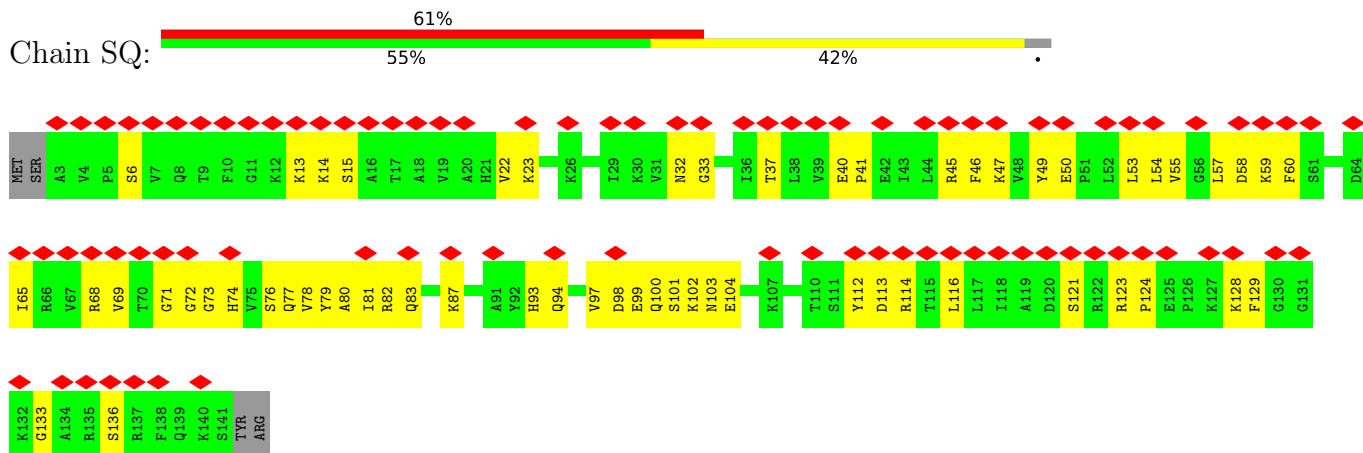
- Molecule 71: Small ribosomal subunit protein eS25A



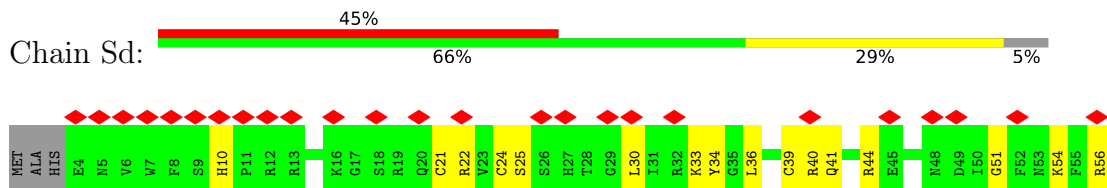
• Molecule 72: Small ribosomal subunit protein eS19A



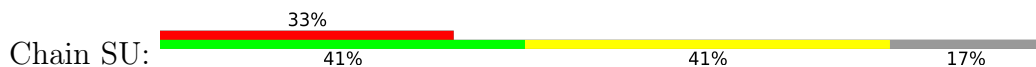
• Molecule 73: Small ribosomal subunit protein uS9A



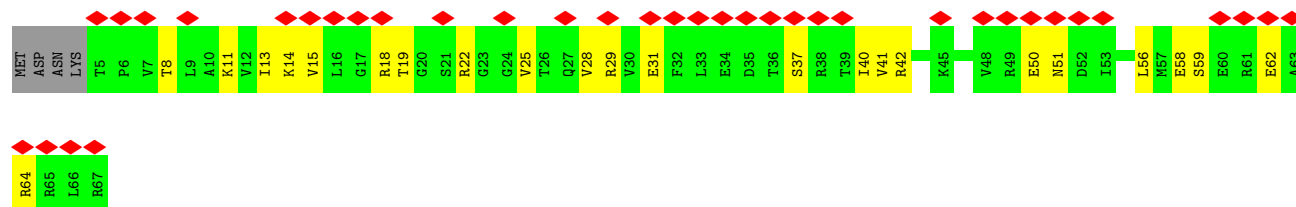
• Molecule 74: Small ribosomal subunit protein uS14A



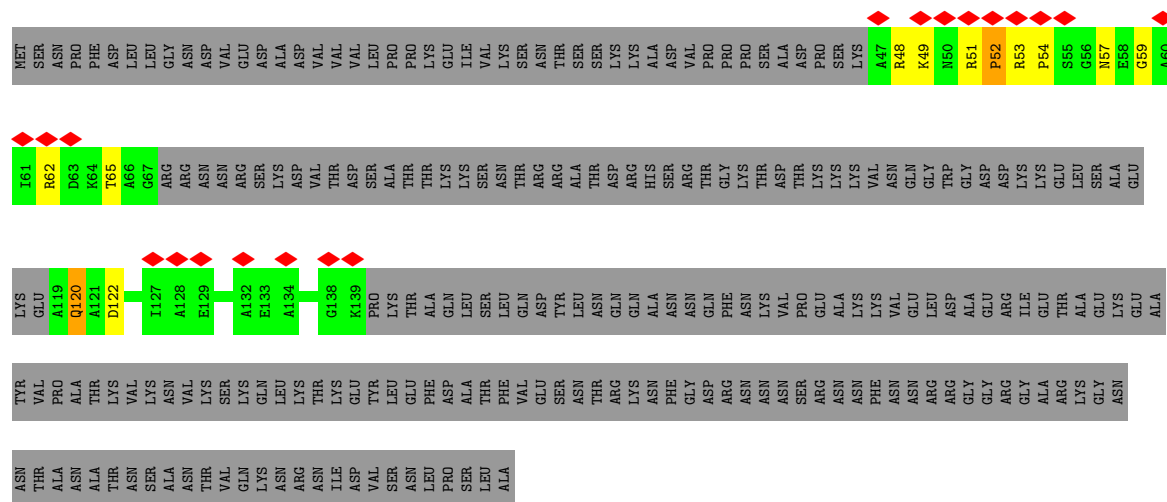
• Molecule 75: Small ribosomal subunit protein uS10



- Molecule 76: Small ribosomal subunit protein eS28A



- Molecule 77: Suppressor protein STM1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	80383	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.035	Depositor
Minimum map value	-0.021	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	484.15363, 484.15363, 484.15363	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0807, 1.0807, 1.0807	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	LA	0.46	0/1933	0.62	2/2598 (0.1%)
2	SA	0.30	0/1644	0.53	0/2249
3	LB	0.43	0/3146	0.57	1/4228 (0.0%)
4	SB	0.28	0/1823	0.65	3/2447 (0.1%)
5	C1	0.41	0/77108	0.38	0/120216
6	C4	0.38	0/2883	0.32	0/4491
7	C3	0.43	0/3746	0.38	0/5832
8	LC	0.42	0/2800	0.57	0/3790
9	LD	0.38	0/2400	0.56	2/3239 (0.1%)
10	LE	0.36	0/1329	0.54	0/1794
11	LF	0.45	0/1821	0.54	0/2451
12	LG	0.39	0/1836	0.61	0/2481
13	LH	0.37	0/1529	0.61	0/2060
14	LI	0.37	0/1801	0.54	0/2416
15	LJ	0.35	0/1371	0.66	0/1838
16	LL	0.42	0/1568	0.65	0/2106
17	LM	0.41	0/1068	0.54	0/1438
18	LN	0.47	0/1757	0.58	0/2354
19	LO	0.43	0/1585	0.54	0/2128
20	LP	0.41	0/1439	0.54	0/1938
21	LQ	0.44	0/1465	0.54	0/1965
22	LR	0.39	0/1532	0.57	0/2043
23	LS	0.42	0/1473	0.55	0/1980
24	LT	0.42	0/1300	0.54	0/1743
25	LU	0.37	0/812	0.56	0/1099
26	LV	0.42	0/1018	0.52	0/1369
27	LW	0.36	0/863	0.55	0/1169
28	LX	0.42	0/979	0.56	0/1321
29	LY	0.40	0/995	0.56	0/1329
30	LZ	0.36	0/1118	0.52	0/1497
31	La	0.43	0/1204	0.57	0/1612
32	Lb	0.36	0/473	0.61	0/629

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lc	0.39	0/745	0.51	0/1001
34	Ld	0.41	0/890	0.56	0/1196
35	Le	0.42	0/1038	0.55	0/1390
36	Lf	0.46	0/868	0.55	0/1168
37	Lg	0.41	0/890	0.55	0/1189
38	Lh	0.40	0/978	0.57	0/1301
39	Li	0.36	0/772	0.58	0/1026
40	Lj	0.42	0/685	0.51	0/908
41	Lk	0.35	0/618	0.56	0/826
42	Ll	0.45	0/443	0.60	0/588
43	Lm	0.34	0/423	0.54	0/562
44	Ln	0.25	0/230	0.52	0/296
45	Lo	0.40	0/836	0.51	0/1104
46	Lp	0.42	0/701	0.61	0/934
47	P0	0.23	0/1498	0.54	0/2025
48	P2	0.19	0/728	0.53	0/975
49	C2	0.28	0/42053	0.35	0/65522
50	SC	0.35	0/1656	0.64	0/2251
51	SE	0.30	0/2097	0.53	0/2823
52	SG	0.24	0/1839	0.58	0/2460
53	SH	0.28	0/1498	0.65	0/2019
54	SI	0.30	0/1501	0.59	0/2006
55	SJ	0.30	0/1504	0.61	1/2016 (0.0%)
56	SK	0.20	0/769	0.52	0/1039
57	SL	0.34	0/1185	0.53	0/1598
58	SM	0.20	0/883	0.63	0/1199
59	SN	0.30	0/1215	0.59	0/1638
60	SO	0.25	0/937	0.57	0/1261
61	SV	0.35	0/682	0.67	0/921
62	SW	0.40	0/1038	0.64	0/1395
63	SX	0.36	0/1139	0.61	0/1518
64	SY	0.28	0/1087	0.66	0/1449
65	Sa	0.27	0/782	0.61	0/1047
66	Sb	0.26	0/620	0.51	0/838
67	Se	0.27	0/480	0.59	0/639
68	5	0.22	0/1131	0.61	0/1522
69	Sf	0.19	0/567	0.57	0/764
70	SP	0.25	0/936	0.59	1/1259 (0.1%)
71	SZ	0.22	0/781	0.62	1/1045 (0.1%)
72	ST	0.22	0/1130	0.56	0/1517
73	SQ	0.26	0/1101	0.54	0/1478
74	Sd	0.23	0/452	0.43	0/600
75	SU	0.25	0/807	0.60	0/1091

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sc	0.23	0/493	0.51	0/663
77	s	0.25	0/261	0.67	0/351
All	All	0.37	0/210786	0.46	11/310268 (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
3	LB	0	1
4	SB	0	1
8	LC	0	1
11	LF	0	1
12	LG	0	1
17	LM	0	1
19	LO	0	1
28	LX	0	1
52	SG	0	1
54	SI	0	1
63	SX	0	1
65	Sa	0	1
68	5	0	1
77	s	0	1
All	All	0	14

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
71	SZ	88	ILE	N-CA-C	-6.10	107.00	112.12
3	LB	255	TRP	CB-CA-C	-5.99	101.87	111.39
4	SB	144	ARG	N-CA-CB	5.97	119.87	110.56
70	SP	125	PRO	CA-N-CD	-5.56	104.22	112.00
1	LA	101	VAL	CA-C-N	-5.51	113.29	123.65

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	LB	255	TRP	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
8	LC	13	GLY	Peptide
11	LF	232	ARG	Peptide
12	LG	76	ALA	Peptide
4	SB	144	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	LA	1899	0	1957	85	0
2	SA	1603	0	1610	99	0
3	LB	3075	0	3142	125	0
4	SB	1798	0	1890	128	0
5	C1	68888	0	34610	2281	0
6	C4	2579	0	1304	92	0
7	C3	3353	0	1695	136	0
8	LC	2748	0	2859	119	0
9	LD	2351	0	2294	94	0
10	LE	1307	0	1377	46	0
11	LF	1784	0	1862	77	0
12	LG	1804	0	1877	69	0
13	LH	1508	0	1572	66	0
14	LI	1764	0	1804	57	0
15	LJ	1350	0	1381	82	0
16	LL	1543	0	1608	81	0
17	LM	1053	0	1149	39	0
18	LN	1720	0	1779	89	0
19	LO	1555	0	1659	50	0
20	LP	1416	0	1433	54	0
21	LQ	1441	0	1543	50	0
22	LR	1515	0	1606	47	0
23	LS	1437	0	1475	51	0
24	LT	1276	0	1323	51	0
25	LU	796	0	812	29	0
26	LV	1003	0	1048	34	0
27	LW	849	0	727	21	0
28	LX	964	0	1025	26	0
29	LY	984	0	1075	38	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	LZ	1092	0	1155	38	0
31	La	1173	0	1215	57	0
32	Lb	462	0	491	19	0
33	Lc	737	0	792	22	0
34	Ld	876	0	912	28	0
35	Le	1017	0	1081	42	0
36	Lf	850	0	880	42	0
37	Lg	880	0	941	35	0
38	Lh	969	0	1078	44	0
39	Li	766	0	844	26	0
40	Lj	670	0	673	27	0
41	Lk	612	0	682	31	0
42	Ll	436	0	475	33	0
43	Lm	417	0	455	17	0
44	Ln	229	0	273	10	0
45	Lo	824	0	888	37	0
46	Lp	694	0	735	33	0
47	P0	1473	0	1514	74	0
48	P2	723	0	774	37	0
49	C2	37604	0	18916	1387	0
50	SC	1626	0	1715	87	0
51	SE	2056	0	2140	105	0
52	SG	1815	0	1894	131	0
53	SH	1473	0	1555	87	0
54	SI	1476	0	1501	73	0
55	SJ	1479	0	1556	92	0
56	SK	752	0	719	39	0
57	SL	1159	0	1225	56	0
58	SM	875	0	878	47	0
59	SN	1192	0	1255	62	0
60	SO	926	0	950	70	0
61	SV	673	0	662	50	0
62	SW	1021	0	1060	45	0
63	SX	1121	0	1196	57	0
64	SY	1073	0	1132	77	0
65	Sa	769	0	818	60	0
66	Sb	610	0	633	26	0
67	Se	472	0	521	31	0
68	5	1118	0	1077	40	0
69	Sf	556	0	546	29	0
70	SP	916	0	941	62	0
71	SZ	771	0	826	39	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	ST	1112	0	1124	64	0
73	SQ	1082	0	1144	52	0
74	Sd	442	0	428	20	0
75	SU	797	0	863	51	0
76	Sc	491	0	524	19	0
77	s	261	0	232	13	0
78	C1	187	0	0	0	0
78	C2	78	0	0	0	0
78	C3	1	0	0	0	0
78	C4	1	0	0	0	0
78	LA	2	0	0	0	0
78	LN	2	0	0	0	0
78	LP	1	0	0	0	0
78	LV	1	0	0	0	0
78	Le	1	0	0	0	0
78	SC	1	0	0	0	0
78	SE	1	0	0	0	0
78	SQ	2	0	0	0	0
78	ST	2	0	0	1	0
78	Sa	1	0	0	0	0
79	Lg	1	0	0	0	0
79	Lj	1	0	0	0	0
79	Lm	1	0	0	0	0
79	Lo	1	0	0	0	0
79	Lp	1	0	0	0	0
79	Sd	1	0	0	0	0
79	Sf	1	0	0	0	0
All	All	196269	0	143385	6832	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 20.

The worst 5 of 6832 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)
5:C1:1257:C:H42	5:C1:1261:G:N2	1.52	1.07
5:C1:583:G:H4'	36:Lf:106:ASN:HD21	1.23	1.04
5:C1:1257:C:N4	5:C1:1261:G:H22	1.56	1.02
5:C1:3164:C:HO2'	5:C1:3165:A:H8	1.01	1.00
69:Sf:121:CYS:HB3	69:Sf:126:CYS:SG	2.02	0.98

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	
1	LA	249/254 (98%)	221 (89%)	28 (11%)	0	100	100
2	SA	204/252 (81%)	180 (88%)	24 (12%)	0	100	100
3	LB	384/387 (99%)	339 (88%)	45 (12%)	0	100	100
4	SB	222/255 (87%)	185 (83%)	36 (16%)	1 (0%)	24	57
8	LC	359/362 (99%)	318 (89%)	39 (11%)	2 (1%)	21	54
9	LD	292/297 (98%)	266 (91%)	25 (9%)	1 (0%)	36	65
10	LE	163/176 (93%)	140 (86%)	23 (14%)	0	100	100
11	LF	220/244 (90%)	205 (93%)	15 (7%)	0	100	100
12	LG	231/256 (90%)	216 (94%)	15 (6%)	0	100	100
13	LH	189/191 (99%)	170 (90%)	19 (10%)	0	100	100
14	LI	216/221 (98%)	203 (94%)	13 (6%)	0	100	100
15	LJ	167/174 (96%)	144 (86%)	23 (14%)	0	100	100
16	LL	191/199 (96%)	168 (88%)	22 (12%)	1 (0%)	24	57
17	LM	134/138 (97%)	124 (92%)	10 (8%)	0	100	100
18	LN	201/204 (98%)	180 (90%)	21 (10%)	0	100	100
19	LO	195/199 (98%)	186 (95%)	7 (4%)	2 (1%)	12	45
20	LP	181/184 (98%)	165 (91%)	16 (9%)	0	100	100
21	LQ	183/186 (98%)	170 (93%)	13 (7%)	0	100	100
22	LR	186/189 (98%)	178 (96%)	6 (3%)	2 (1%)	11	43
23	LS	169/172 (98%)	160 (95%)	9 (5%)	0	100	100
24	LT	157/160 (98%)	147 (94%)	10 (6%)	0	100	100
25	LU	98/121 (81%)	86 (88%)	12 (12%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	LV	134/137 (98%)	127 (95%)	7 (5%)	0	100	100
27	LW	124/155 (80%)	111 (90%)	13 (10%)	0	100	100
28	LX	119/142 (84%)	111 (93%)	7 (6%)	1 (1%)	16	49
29	LY	123/127 (97%)	114 (93%)	9 (7%)	0	100	100
30	LZ	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
31	La	146/149 (98%)	126 (86%)	18 (12%)	2 (1%)	9	38
32	Lb	56/59 (95%)	50 (89%)	5 (9%)	1 (2%)	6	34
33	Lc	94/105 (90%)	88 (94%)	6 (6%)	0	100	100
34	Ld	107/113 (95%)	96 (90%)	11 (10%)	0	100	100
35	Le	125/130 (96%)	116 (93%)	9 (7%)	0	100	100
36	Lf	104/107 (97%)	95 (91%)	9 (9%)	0	100	100
37	Lg	110/121 (91%)	105 (96%)	5 (4%)	0	100	100
38	Lh	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
39	Li	97/100 (97%)	88 (91%)	9 (9%)	0	100	100
40	Lj	83/88 (94%)	78 (94%)	5 (6%)	0	100	100
41	Lk	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
42	Ll	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
43	Lm	50/128 (39%)	46 (92%)	4 (8%)	0	100	100
44	Ln	23/25 (92%)	23 (100%)	0	0	100	100
45	Lo	101/106 (95%)	94 (93%)	7 (7%)	0	100	100
46	Lp	89/92 (97%)	80 (90%)	9 (10%)	0	100	100
47	P0	187/312 (60%)	164 (88%)	23 (12%)	0	100	100
48	P2	92/165 (56%)	76 (83%)	16 (17%)	0	100	100
50	SC	214/254 (84%)	201 (94%)	13 (6%)	0	100	100
51	SE	256/261 (98%)	229 (90%)	27 (10%)	0	100	100
52	SG	226/236 (96%)	202 (89%)	23 (10%)	1 (0%)	30	61
53	SH	182/190 (96%)	159 (87%)	22 (12%)	1 (0%)	24	57
54	SI	183/200 (92%)	156 (85%)	26 (14%)	1 (0%)	24	57
55	SJ	182/197 (92%)	160 (88%)	21 (12%)	1 (0%)	24	57
56	SK	90/105 (86%)	81 (90%)	9 (10%)	0	100	100
57	SL	142/156 (91%)	122 (86%)	20 (14%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	SM	119/143 (83%)	84 (71%)	35 (29%)	0	100	100
59	SN	148/151 (98%)	131 (88%)	17 (12%)	0	100	100
60	SO	125/138 (91%)	112 (90%)	13 (10%)	0	100	100
61	SV	85/87 (98%)	67 (79%)	17 (20%)	1 (1%)	10	41
62	SW	127/130 (98%)	116 (91%)	11 (9%)	0	100	100
63	SX	142/145 (98%)	123 (87%)	18 (13%)	1 (1%)	18	51
64	SY	132/135 (98%)	121 (92%)	11 (8%)	0	100	100
65	Sa	95/119 (80%)	79 (83%)	16 (17%)	0	100	100
66	Sb	79/82 (96%)	67 (85%)	12 (15%)	0	100	100
67	Se	58/63 (92%)	51 (88%)	7 (12%)	0	100	100
68	5	148/157 (94%)	124 (84%)	22 (15%)	2 (1%)	9	38
69	Sf	71/152 (47%)	42 (59%)	29 (41%)	0	100	100
70	SP	115/142 (81%)	104 (90%)	11 (10%)	0	100	100
71	SZ	98/108 (91%)	83 (85%)	15 (15%)	0	100	100
72	ST	141/144 (98%)	130 (92%)	11 (8%)	0	100	100
73	SQ	137/143 (96%)	127 (93%)	10 (7%)	0	100	100
74	Sd	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
75	SU	98/121 (81%)	91 (93%)	7 (7%)	0	100	100
76	Sc	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
77	s	38/273 (14%)	31 (82%)	6 (16%)	1 (3%)	4	27
All	All	10471/11721 (89%)	9388 (90%)	1061 (10%)	22 (0%)	44	72

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
31	La	78	LEU
54	SI	10	LYS
68	5	113	VAL
19	LO	111[A]	PRO
28	LX	44	PRO

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	
1	LA	190/196 (97%)	190 (100%)	0	100	100
2	SA	170/210 (81%)	170 (100%)	0	100	100
3	LB	319/323 (99%)	319 (100%)	0	100	100
4	SB	200/224 (89%)	200 (100%)	0	100	100
8	LC	288/289 (100%)	288 (100%)	0	100	100
9	LD	241/245 (98%)	241 (100%)	0	100	100
10	LE	139/155 (90%)	139 (100%)	0	100	100
11	LF	186/205 (91%)	186 (100%)	0	100	100
12	LG	187/208 (90%)	187 (100%)	0	100	100
13	LH	168/171 (98%)	167 (99%)	1 (1%)	78	79
14	LI	185/187 (99%)	185 (100%)	0	100	100
15	LJ	146/151 (97%)	146 (100%)	0	100	100
16	LL	154/159 (97%)	154 (100%)	0	100	100
17	LM	107/109 (98%)	107 (100%)	0	100	100
18	LN	175/176 (99%)	175 (100%)	0	100	100
19	LO	160/162 (99%)	160 (100%)	0	100	100
20	LP	138/146 (94%)	138 (100%)	0	100	100
21	LQ	150/151 (99%)	150 (100%)	0	100	100
22	LR	152/154 (99%)	152 (100%)	0	100	100
23	LS	155/156 (99%)	155 (100%)	0	100	100
24	LT	136/137 (99%)	136 (100%)	0	100	100
25	LU	87/107 (81%)	87 (100%)	0	100	100
26	LV	104/105 (99%)	104 (100%)	0	100	100
27	LW	60/129 (46%)	60 (100%)	0	100	100
28	LX	104/118 (88%)	104 (100%)	0	100	100
29	LY	108/110 (98%)	108 (100%)	0	100	100
30	LZ	115/116 (99%)	115 (100%)	0	100	100
31	La	118/119 (99%)	118 (100%)	0	100	100
32	Lb	46/47 (98%)	45 (98%)	1 (2%)	45	65

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	Lc	81/88 (92%)	81 (100%)	0	100	100
34	Ld	92/97 (95%)	92 (100%)	0	100	100
35	Le	108/111 (97%)	108 (100%)	0	100	100
36	Lf	90/91 (99%)	89 (99%)	1 (1%)	65	74
37	Lg	95/103 (92%)	95 (100%)	0	100	100
38	Lh	104/105 (99%)	104 (100%)	0	100	100
39	Li	80/82 (98%)	80 (100%)	0	100	100
40	Lj	69/71 (97%)	69 (100%)	0	100	100
41	Lk	68/69 (99%)	68 (100%)	0	100	100
42	Ll	45/45 (100%)	44 (98%)	1 (2%)	45	65
43	Lm	47/116 (40%)	47 (100%)	0	100	100
44	Ln	22/23 (96%)	22 (100%)	0	100	100
45	Lo	87/91 (96%)	87 (100%)	0	100	100
46	Lp	71/72 (99%)	71 (100%)	0	100	100
47	P0	160/254 (63%)	160 (100%)	0	100	100
48	P2	81/136 (60%)	81 (100%)	0	100	100
50	SC	175/205 (85%)	175 (100%)	0	100	100
51	SE	220/222 (99%)	220 (100%)	0	100	100
52	SG	189/201 (94%)	189 (100%)	0	100	100
53	SH	163/170 (96%)	163 (100%)	0	100	100
54	SI	148/161 (92%)	148 (100%)	0	100	100
55	SJ	156/166 (94%)	156 (100%)	0	100	100
56	SK	77/98 (79%)	77 (100%)	0	100	100
57	SL	129/137 (94%)	128 (99%)	1 (1%)	73	77
58	SM	88/119 (74%)	88 (100%)	0	100	100
59	SN	127/128 (99%)	127 (100%)	0	100	100
60	SO	91/105 (87%)	91 (100%)	0	100	100
61	SV	71/74 (96%)	71 (100%)	0	100	100
62	SW	110/111 (99%)	110 (100%)	0	100	100
63	SX	119/120 (99%)	119 (100%)	0	100	100
64	SY	112/113 (99%)	112 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
65	Sa	83/100 (83%)	83 (100%)	0	100	100
66	Sb	70/71 (99%)	70 (100%)	0	100	100
67	Se	50/54 (93%)	50 (100%)	0	100	100
68	5	117/133 (88%)	117 (100%)	0	100	100
69	Sf	56/135 (42%)	56 (100%)	0	100	100
70	SP	95/118 (80%)	95 (100%)	0	100	100
71	SZ	77/89 (86%)	77 (100%)	0	100	100
72	ST	115/116 (99%)	115 (100%)	0	100	100
73	SQ	115/119 (97%)	115 (100%)	0	100	100
74	Sd	47/49 (96%)	47 (100%)	0	100	100
75	SU	93/114 (82%)	93 (100%)	0	100	100
76	Sc	55/60 (92%)	55 (100%)	0	100	100
77	s	15/228 (7%)	15 (100%)	0	100	100
All	All	8751/9835 (89%)	8746 (100%)	5 (0%)	87	87

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	LH	59	ASN
32	Lb	11	ASN
36	Lf	42	GLN
42	Ll	38	ASN
57	SL	21	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 89 such sidechains are listed below:

Mol	Chain	Res	Type
47	P0	56	ASN
57	SL	81	HIS
48	P2	137	GLN
54	SI	88	ASN
59	SN	58	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
49	C2	1768/1800 (98%)	501 (28%)	46 (2%)
5	C1	3217/3396 (94%)	637 (19%)	43 (1%)
6	C4	120/121 (99%)	15 (12%)	1 (0%)
7	C3	157/158 (99%)	28 (17%)	1 (0%)
All	All	5262/5475 (96%)	1181 (22%)	91 (1%)

5 of 1181 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	C1	13	A
5	C1	14	U
5	C1	15	C
5	C1	18	G
5	C1	26	A

5 of 91 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	C2	541	A
49	C2	1226	A
49	C2	609	U
49	C2	711	U
49	C2	1274	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 288 ligands modelled in this entry, 288 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

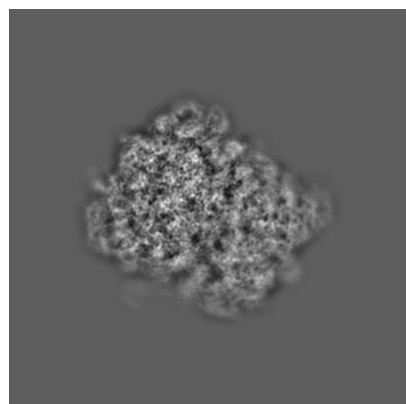
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37995. These allow visual inspection of the internal detail of the map and identification of artifacts.

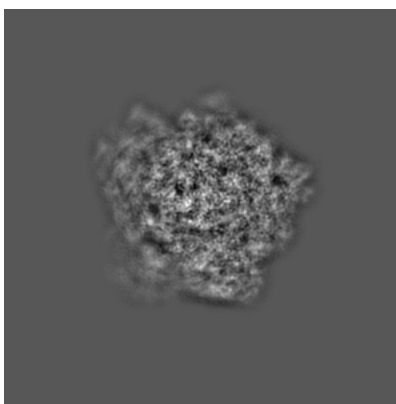
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

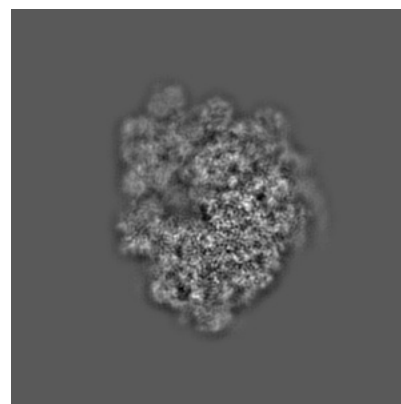
6.1.1 Primary map



X

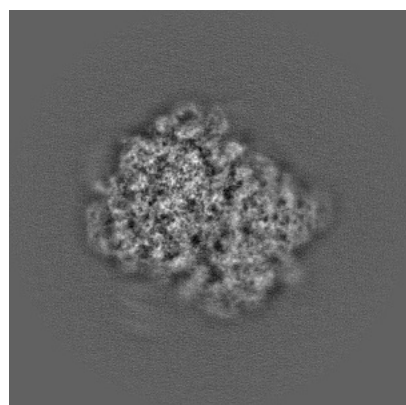


Y

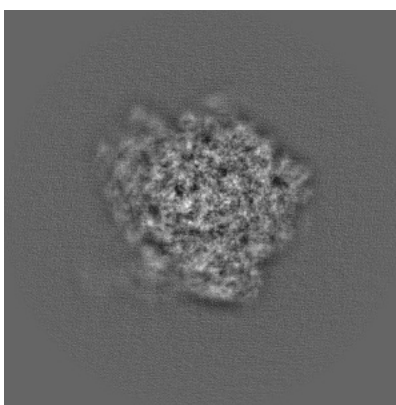


Z

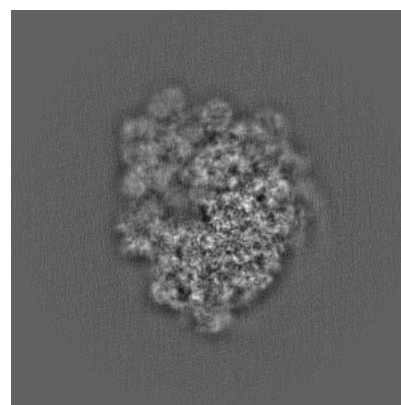
6.1.2 Raw map



X



Y

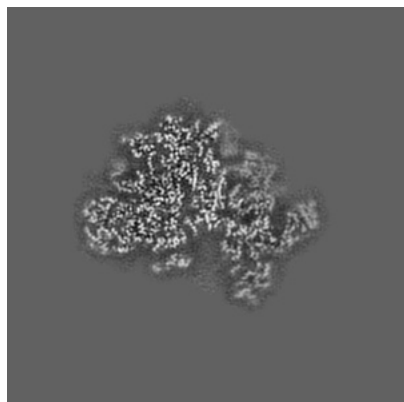


Z

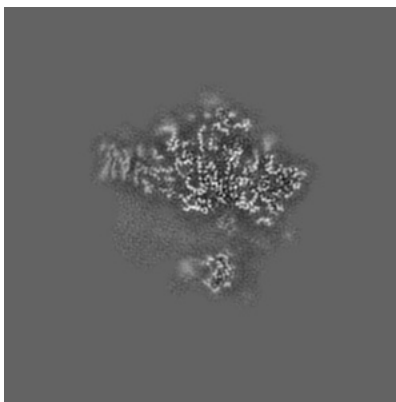
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

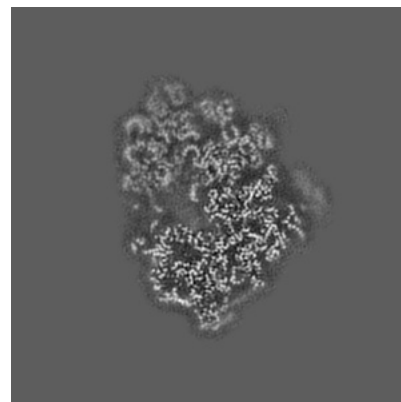
6.2.1 Primary map



X Index: 224

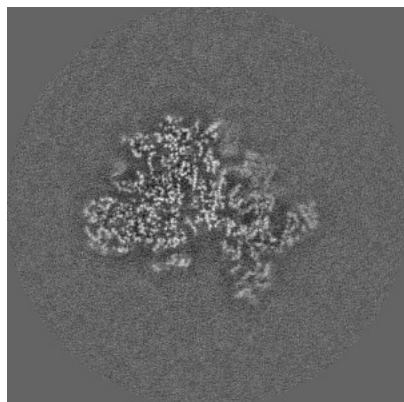


Y Index: 224

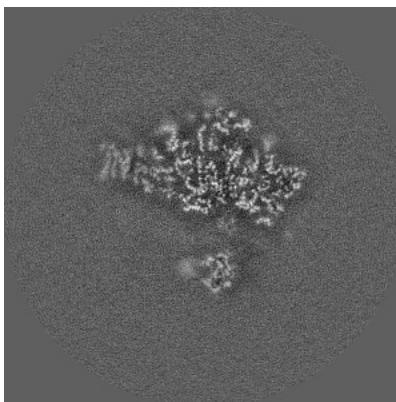


Z Index: 224

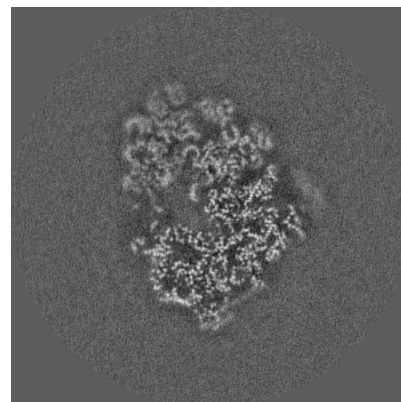
6.2.2 Raw map



X Index: 224



Y Index: 224

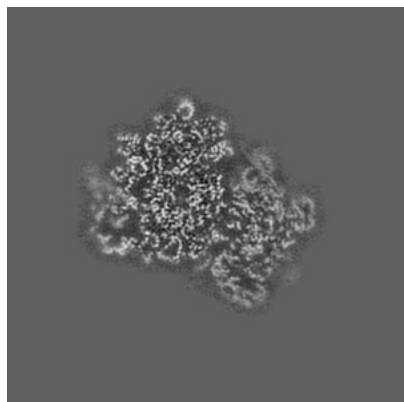


Z Index: 224

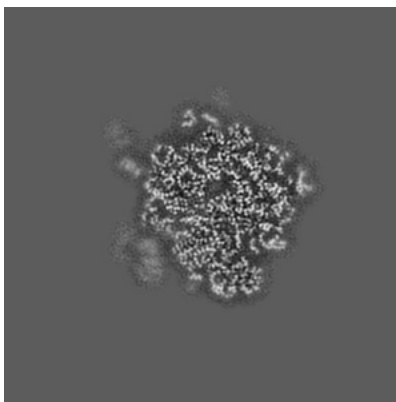
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

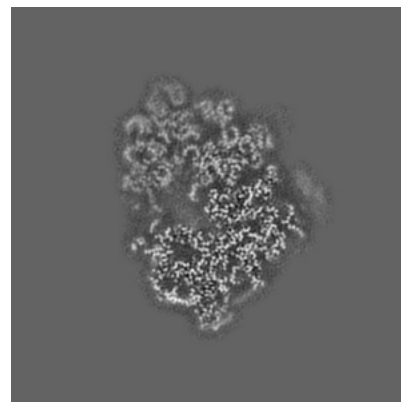
6.3.1 Primary map



X Index: 240

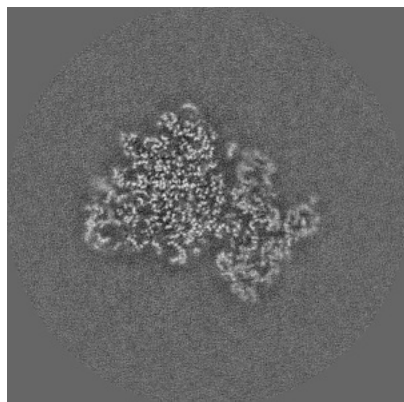


Y Index: 191

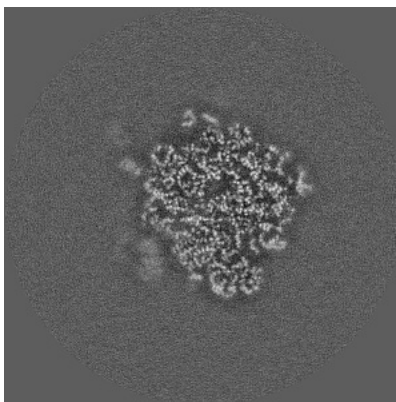


Z Index: 223

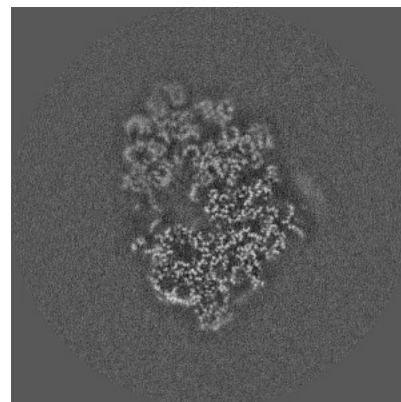
6.3.2 Raw map



X Index: 232



Y Index: 191

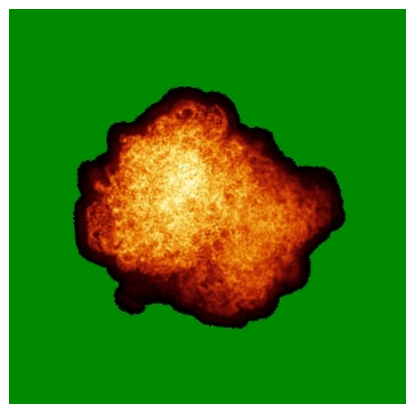


Z Index: 223

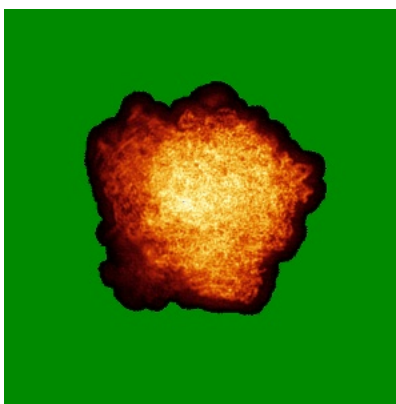
The images above show the largest variance slices of the map in three orthogonal directions.

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

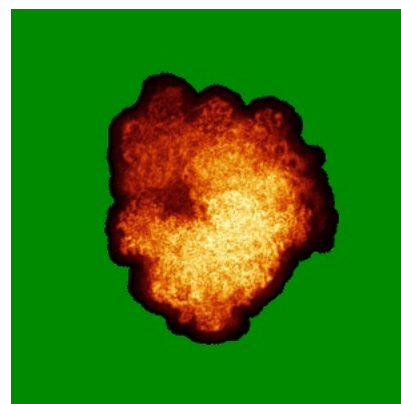
6.4.1 Primary map



X

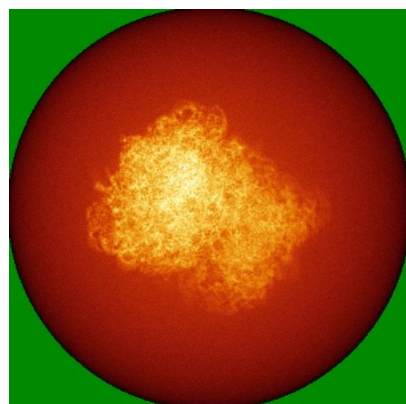


Y

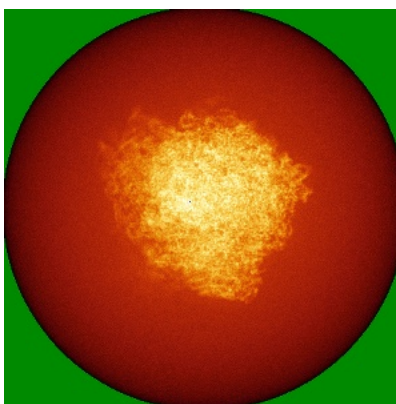


Z

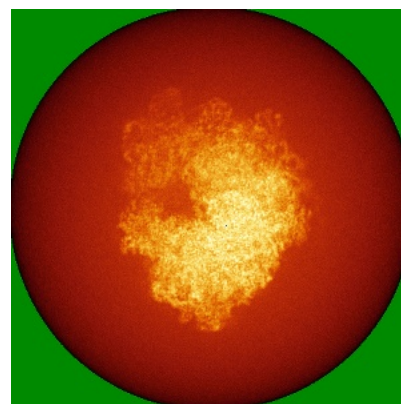
6.4.2 Raw map



X



Y

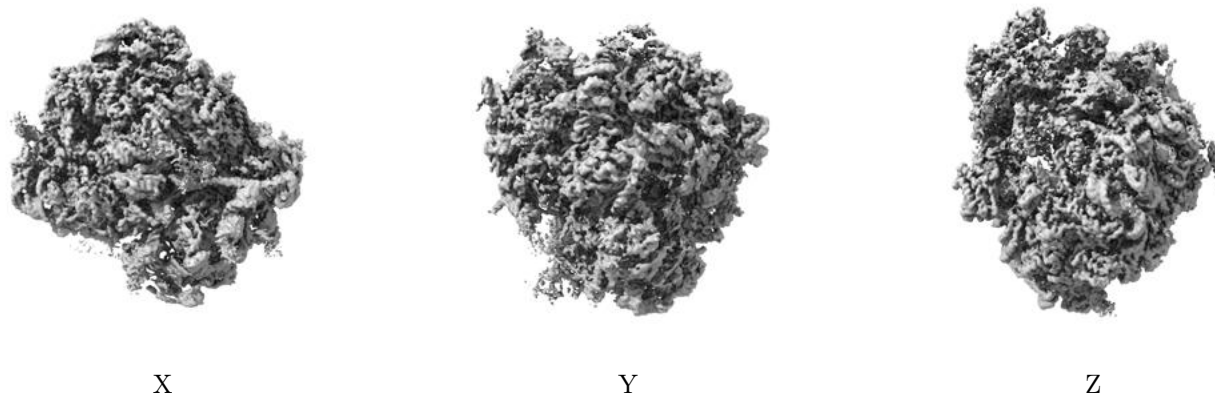


Z

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.

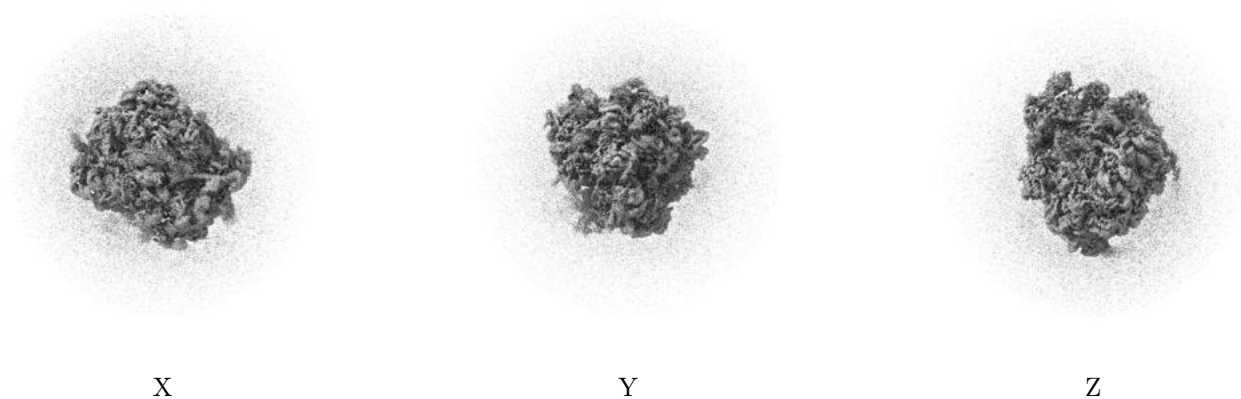
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. 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.

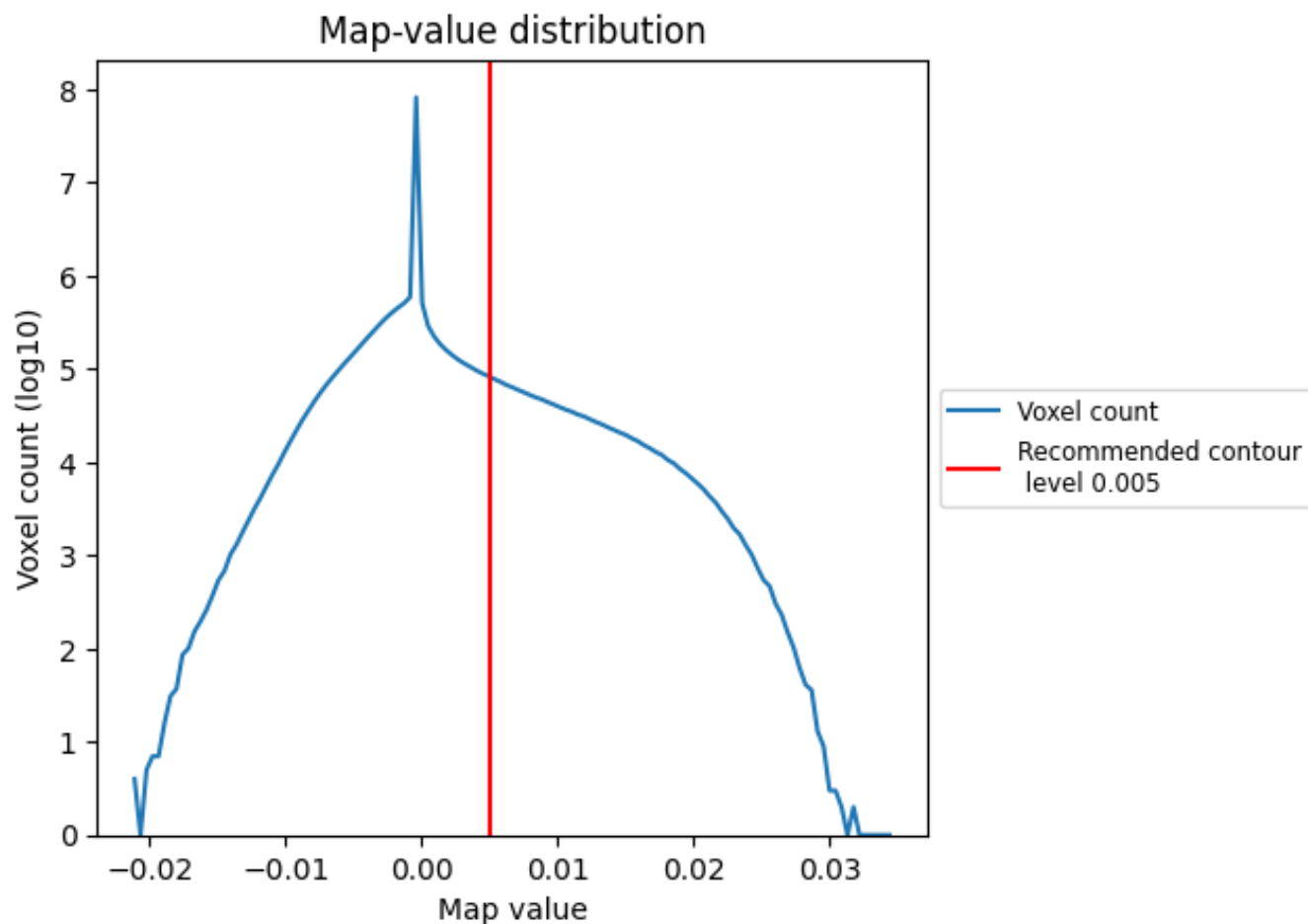
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

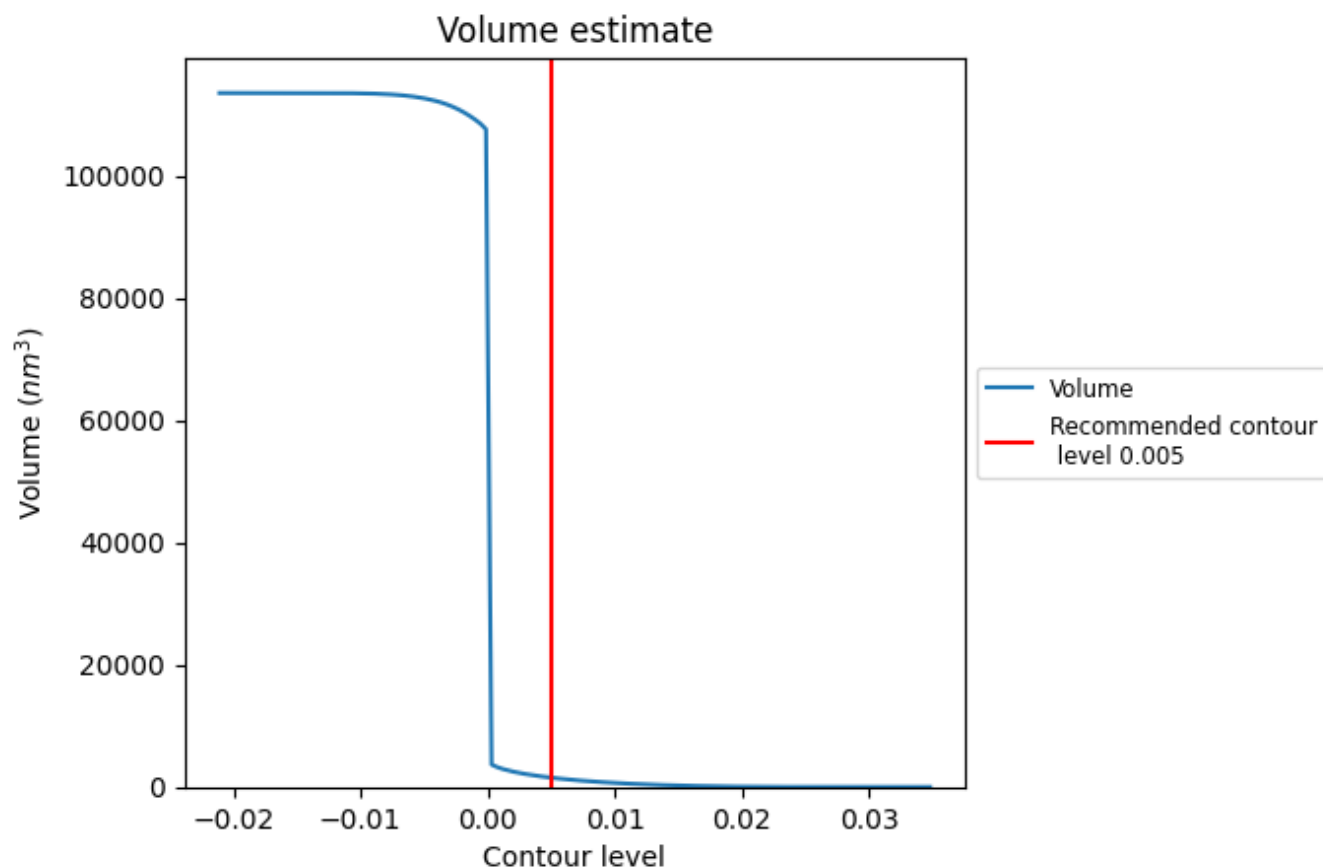
This section contains the results of statistical analysis of the map.

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.

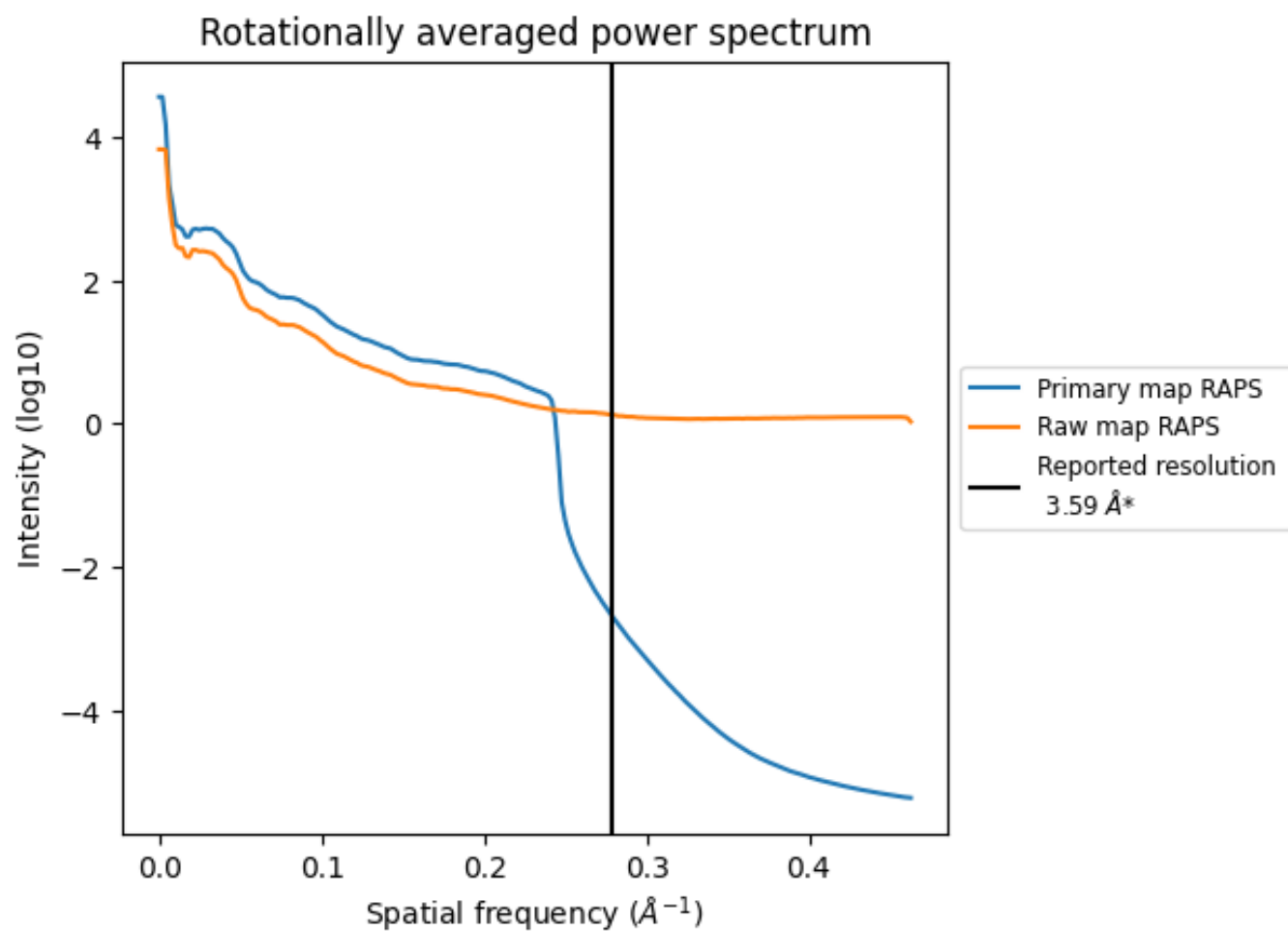
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1519 nm^3 ; this corresponds to an approximate mass of 1372 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 ⓘ

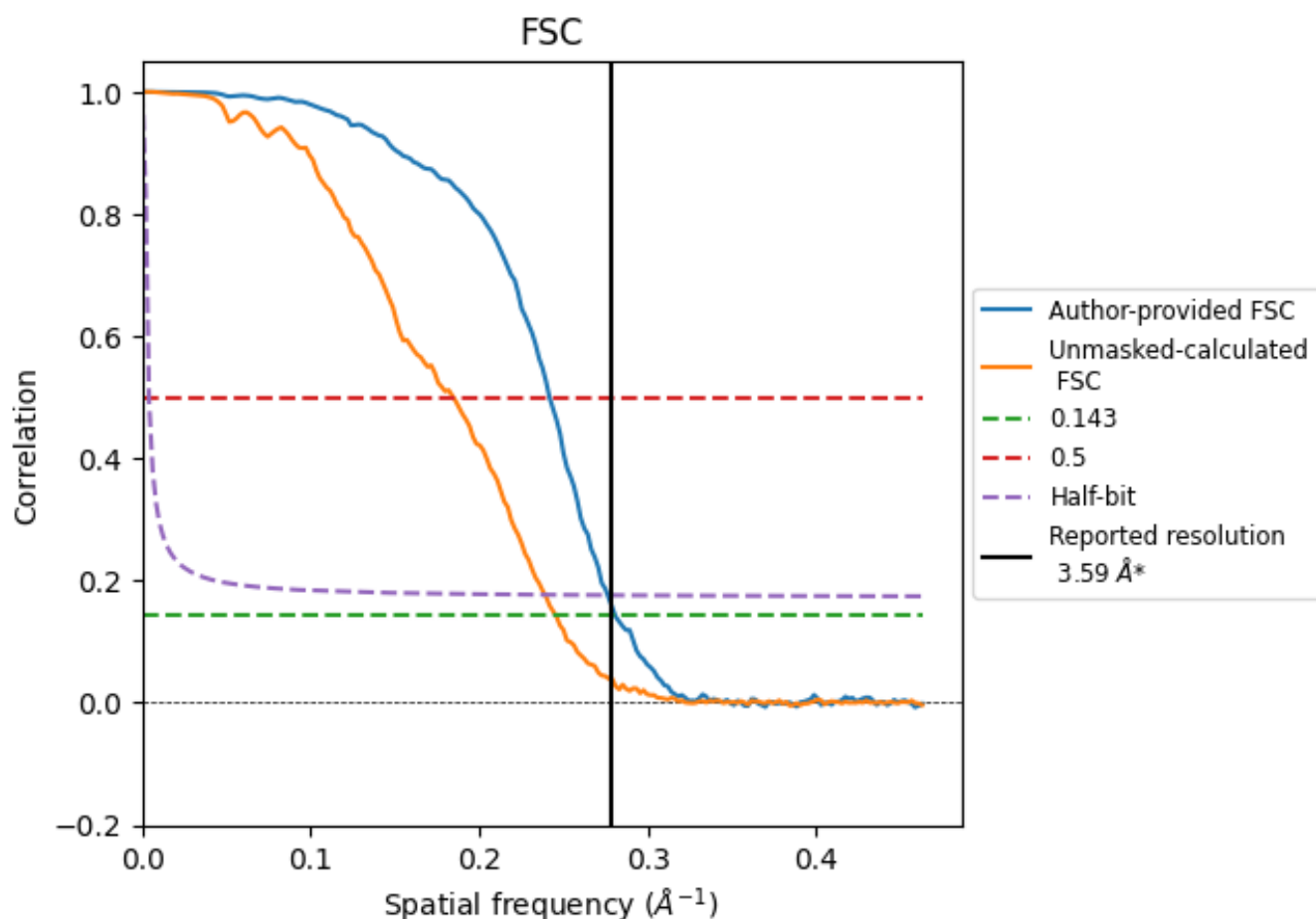


*Reported resolution corresponds to spatial frequency of 0.279 $\text{\AA}^{-1}$

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 0.279 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

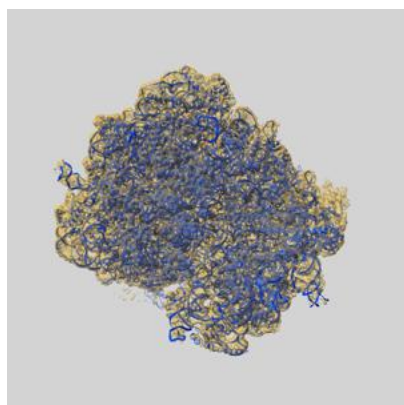
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.59	-	-
Author-provided FSC curve	3.56	4.14	3.62
Unmasked-calculated*	4.08	5.42	4.18

*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 4.08 differs from the reported value 3.59 by more than 10 %

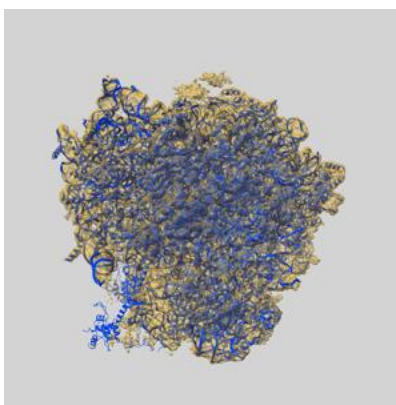
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37995 and PDB model 8Y0U. Per-residue inclusion information can be found in section [3](#) on page [19](#).

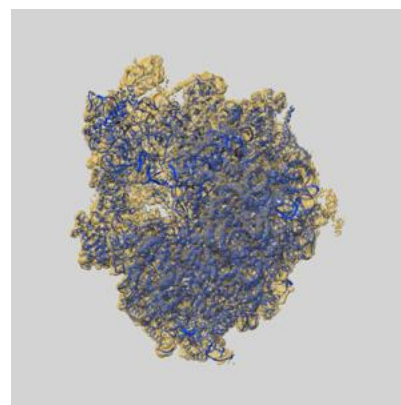
9.1 Map-model overlay [i](#)



X



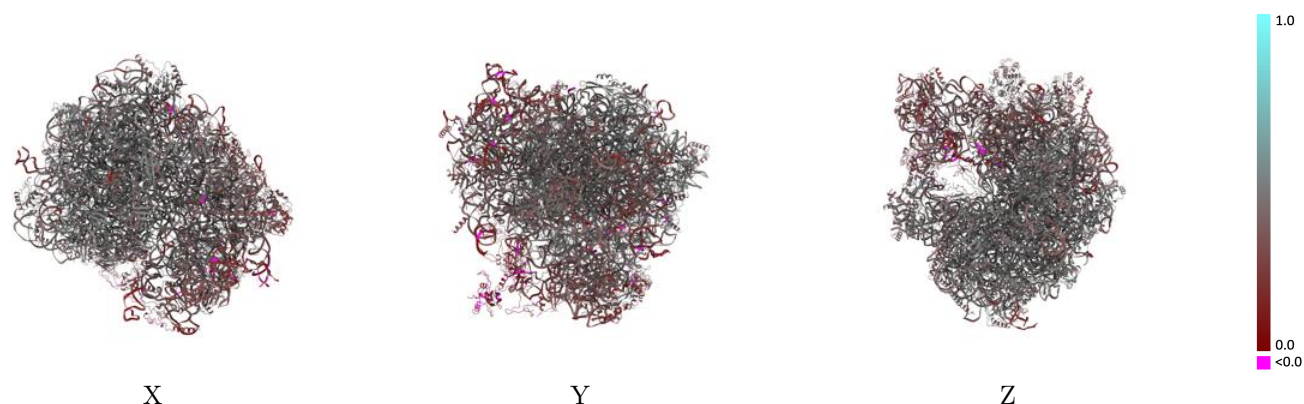
Y



Z

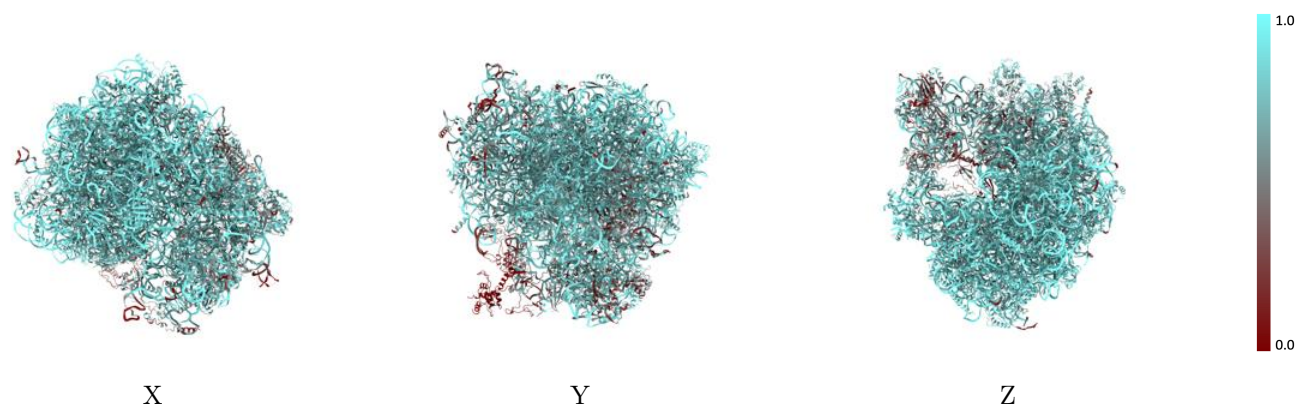
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



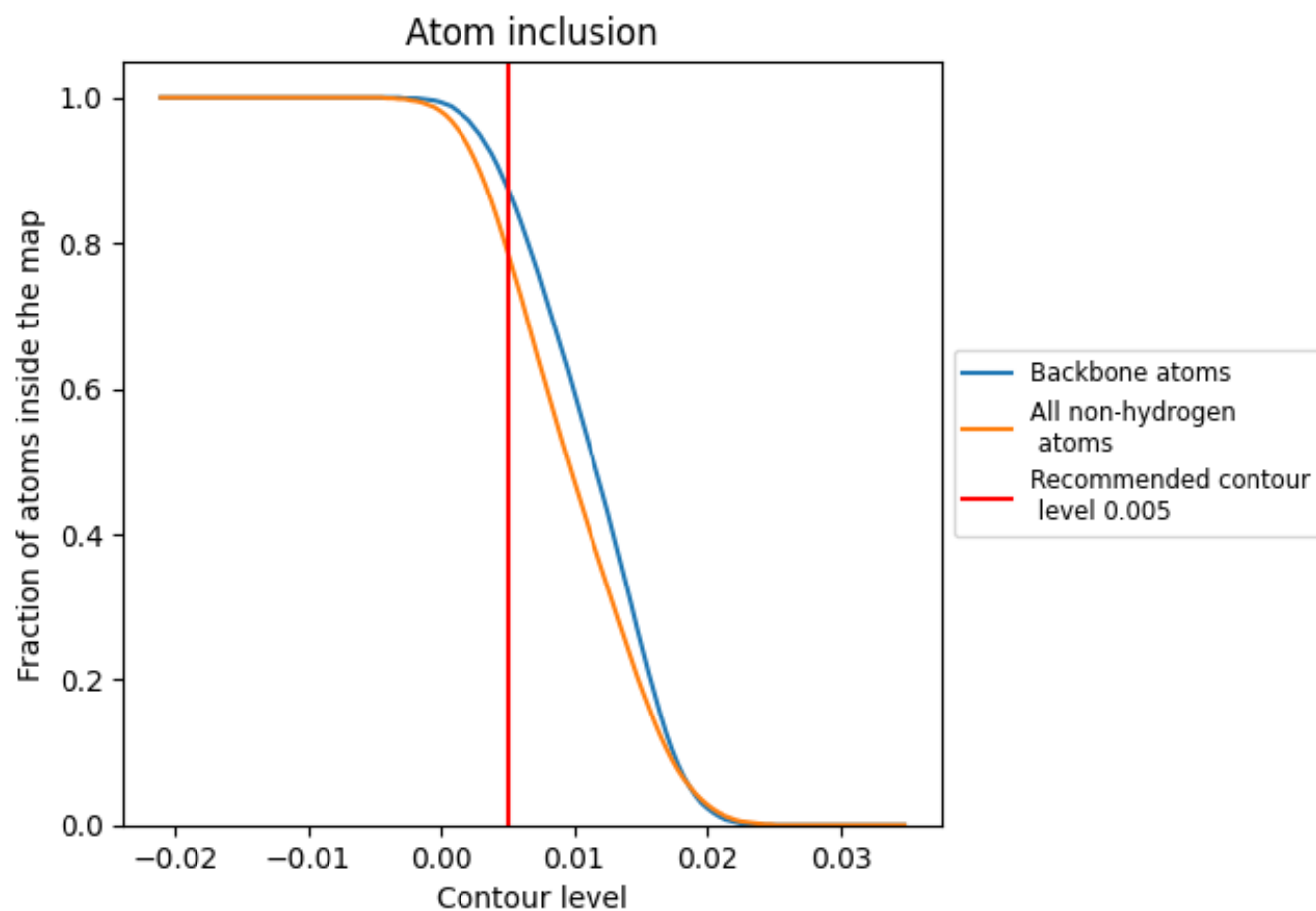
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 79% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7880	 0.4110
5	 0.2420	 0.3670
C1	 0.8980	 0.4270
C2	 0.8110	 0.3730
C3	 0.9280	 0.4480
C4	 0.9560	 0.4460
LA	 0.7400	 0.4880
LB	 0.8010	 0.4780
LC	 0.8220	 0.4760
LD	 0.7950	 0.4230
LE	 0.7670	 0.4340
LF	 0.8040	 0.4610
LG	 0.8090	 0.4440
LH	 0.7960	 0.4540
LI	 0.7460	 0.4440
LJ	 0.7760	 0.4310
LL	 0.8200	 0.4620
LM	 0.8230	 0.4560
LN	 0.7200	 0.4840
LO	 0.7940	 0.4640
LP	 0.7610	 0.4640
LQ	 0.7760	 0.4750
LR	 0.7830	 0.4320
LS	 0.7850	 0.4790
LT	 0.7790	 0.4740
LU	 0.8260	 0.4290
LV	 0.7260	 0.4890
LW	 0.5730	 0.3620
LX	 0.7740	 0.4770
LY	 0.8130	 0.4760
LZ	 0.7900	 0.4570
La	 0.7930	 0.4800
Lb	 0.7040	 0.4560
Lc	 0.8510	 0.4550
Ld	 0.7980	 0.4600



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Le	 0.7540	 0.4870
Lf	 0.7350	 0.4880
Lg	 0.6980	 0.4680
Lh	 0.8090	 0.4520
Li	 0.8000	 0.4420
Lj	 0.8060	 0.4970
Lk	 0.7810	 0.4470
Ll	 0.7210	 0.4730
Lm	 0.2750	 0.4310
Ln	 0.3560	 0.4310
Lo	 0.7820	 0.4810
Lp	 0.7920	 0.4600
P0	 0.1530	 0.1650
P2	 0.0730	 0.1360
SA	 0.7220	 0.3850
SB	 0.5460	 0.3300
SC	 0.7080	 0.4180
SE	 0.6590	 0.4180
SG	 0.6140	 0.3470
SH	 0.7180	 0.3580
SI	 0.6750	 0.4150
SJ	 0.6370	 0.3700
SK	 0.2900	 0.1880
SL	 0.6750	 0.4370
SM	 0.0170	 0.0980
SN	 0.6600	 0.3880
SO	 0.4500	 0.3290
SP	 0.5510	 0.3310
SQ	 0.3470	 0.3190
ST	 0.4380	 0.3160
SU	 0.4760	 0.3010
SV	 0.7640	 0.4060
SW	 0.6690	 0.4360
SX	 0.6590	 0.4420
SY	 0.6560	 0.3610
SZ	 0.3080	 0.2110
Sa	 0.5570	 0.3840
Sb	 0.7260	 0.3930
Sc	 0.3430	 0.2750
Sd	 0.4010	 0.3410
Se	 0.5530	 0.3700
Sf	 0.0420	 0.1600

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
s	 0.4590	 0.2750