wwPDB EM Validation Summary Report (i)

Apr 21, 2025 – 02:18 PM EDT

PDB ID	:	9AZN / pdb_00009azn
EMDB ID	:	EMD-44017
Title	:	In situ human A/P-P/E state 80S ribosome
Authors	:	Wei, Z.; Yong, Z.
Deposited on	:	2024-03-11
Resolution	:	2.98 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

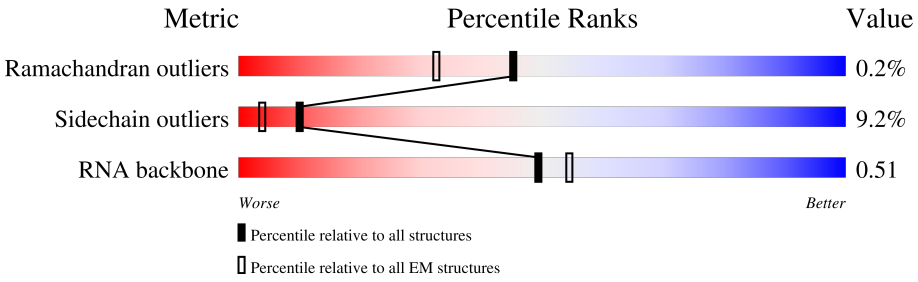
EMDB validation analysis	:	0.0.1.dev117
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.98 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	CH	132	40% 87% 13%
2	Se	47	21% 87% 13%
3	LW	118	26% 92% 8%
4	SE	262	10% 91% 9%
5	SI	206	12% 90% 10%
6	SL	153	12% 90% 10%
7	SX	141	7% 90% 10%
8	SG	237	22% 89% 10%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	SJ	185	11% 88% 12%
10	SY	131	27% 86% 13%
11	SA	221	11% 90% 10%
12	SB	214	93% 7%
13	SH	186	15% 94% 5%
14	SV	83	5% 87% 13%
15	Sa	102	6% 92% 8%
16	SC	222	90% 10%
17	SN	150	95% 5%
18	SO	140	6% 90% 10%
19	SW	129	90% 9%
20	Sb	83	11% 92% 8%
21	L5	3740	76% 23%
22	L7	120	90% 10%
23	L8	156	82% 18%
24	LA	248	93% 7%
25	LB	402	95% 5%
26	LC	368	95% 5%
27	LD	293	93% 7%
28	LE	236	7% 92% 8%
29	LF	225	96%
30	LG	241	9% 93% 7%
31	LH	190	89% 11%
32	LI	202	92% 8%
33	LJ	176	7% 91% 8%

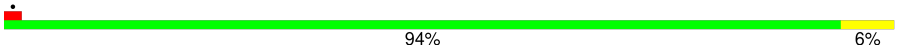
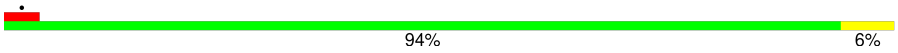
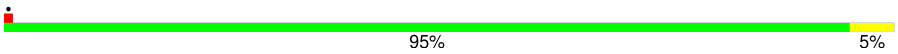
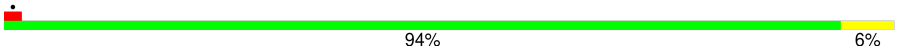
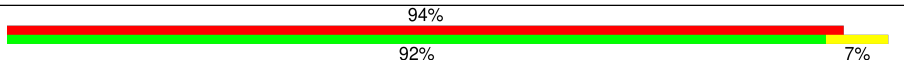
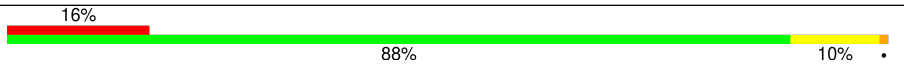
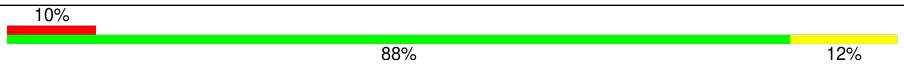
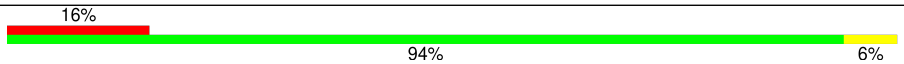
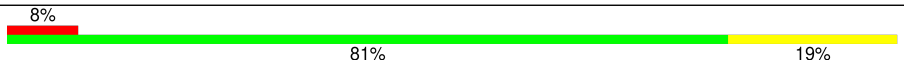
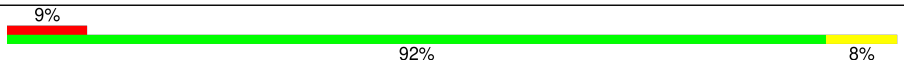
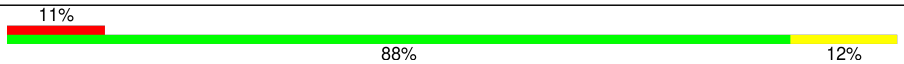
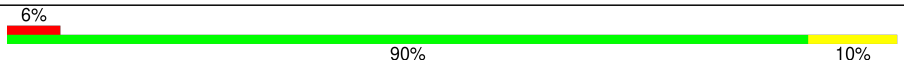
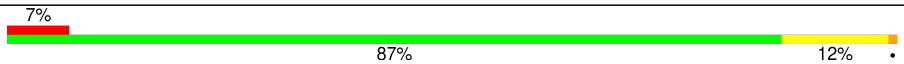
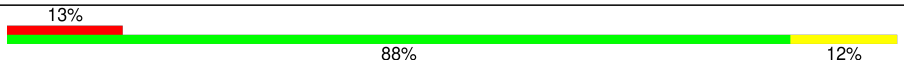
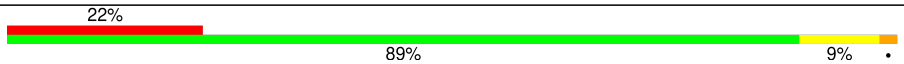
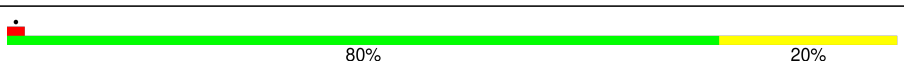
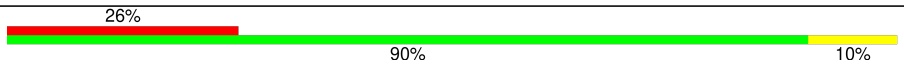
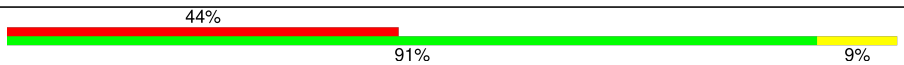
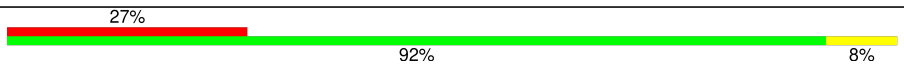
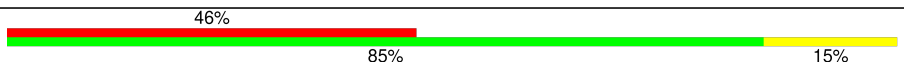
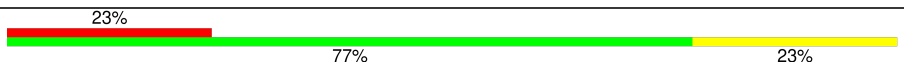
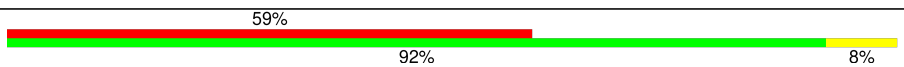
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	LL	210	93% 7%
35	LM	139	91% 8%
36	LN	203	93% 7%
37	LO	201	96%
38	LP	153	88% 12%
39	LQ	187	91% 9%
40	LR	187	5% 95% 5%
41	LS	175	94% 6%
42	LT	159	93% 7%
43	LU	101	5% 89% 11%
44	LV	131	95% 5%
45	LX	120	96%
46	LY	134	95% 5%
47	LZ	135	92% 8%
48	La	147	97%
49	Lb	109	9% 94% 6%
50	Lc	98	5% 92% 8%
51	Ld	107	90% 10%
52	Le	128	94% 6%
53	Lf	109	93% 7%
54	Lg	114	89% 11%
55	Lh	122	95% 5%
56	Li	102	94% 6%
57	Lj	86	94% 6%
58	Lk	69	87% 13%

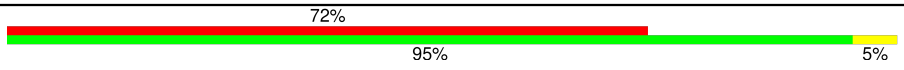
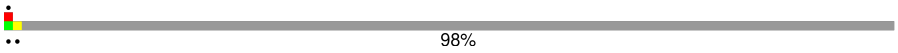
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	Ll	50	
60	Lm	52	
61	Ln	24	
62	Lo	105	
63	Lp	91	
64	Lr	125	
65	Lz	217	
66	SR	135	
67	SD	227	
68	SF	189	
69	SK	98	
70	SP	121	
71	SQ	144	
72	SS	145	
73	ST	143	
74	SU	104	
75	Sc	64	
76	Sd	55	
77	Sg	313	
78	SM	122	
79	SZ	75	
80	Sf	67	
81	AP	71	
82	PE	75	
83	Ls	196	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
84	Lt	141	
85	S2	1740	
85	S3	1740	

2 Entry composition (i)

There are 87 unique types of molecules in this entry. The entry contains 223564 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 EDF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	CH	132	1023	624	202	196	1	0	0

- Molecule 2 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	Se	47	348	210	74	64	0	0

- Molecule 3 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	LW	118	965	604	199	158	4	0	0

- Molecule 4 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	SE	262	2076	1324	386	358	8	0	0

- Molecule 5 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	SI	206	1686	1058	332	291	5	0	0

- Molecule 6 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	SL	153	1247	793	234	214	6	0	0

- Molecule 7 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 8 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 9 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 10 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 11 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 12 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 13 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

- Molecule 14 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 15 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 16 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 17 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 18 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

- Molecule 19 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 20 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 21 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	L5	3740	Total	C	N	O	P	0	0
			79860	35549	14585	25987	3739		

- Molecule 22 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 23 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 24 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 25 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 26 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 27 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 28 is a protein called 60S ribosomal protein L6 [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

- Molecule 29 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 30 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 31 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 32 is a protein called 60S ribosomal protein L10-like [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		

- Molecule 33 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 34 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 35 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 36 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 37 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 38 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 39 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 40 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 42 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 43 is a protein called Heparin-binding protein HBp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 44 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 45 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 46 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 47 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 48 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 49 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lb	109	Total 876	C 546	N 189	O 137	S 4	0	0

- Molecule 50 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lc	98	Total 764	C 485	N 135	O 138	S 6	0	0

- Molecule 51 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ld	107	Total 888	C 560	N 171	O 155	S 2	0	0

- Molecule 52 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Le	128	Total 1053	C 667	N 216	O 165	S 5	0	0

- Molecule 53 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Lf	109	Total 876	C 555	N 174	O 144	S 3	0	0

- Molecule 54 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Lg	114	Total 906	C 566	N 187	O 147	S 6	0	0

- Molecule 55 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Lh	122	Total 1015	C 641	N 205	O 168	S 1	0	0

- Molecule 56 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 57 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 58 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 59 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 60 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 61 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 62 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 63 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 64 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 65 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 66 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		

- Molecule 67 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 68 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 69 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SP	121	Total	C	N	O	S	0	0
			985	623	185	170	7		

- Molecule 71 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		

- Molecule 72 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 73 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 74 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 75 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 76 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 77 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 78 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		

- Molecule 79 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 80 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 81 is a RNA chain called A/P site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	AP	71	Total	C	N	O	P	0	0
			1514	677	275	492	70		

- Molecule 82 is a RNA chain called P/E site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	PE	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 83 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 84 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		

- Molecule 85 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	S2	32	Total	C	N	O	P	0	0
			680	304	119	225	32		
85	S3	1708	Total	C	N	O	P	0	0
			36218	16155	6480	11876	1707		

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
86	Sa	1	Total	Zn	0
			1	1	
86	Lg	1	Total	Zn	0
			1	1	
86	Lj	1	Total	Zn	0
			1	1	
86	Lm	1	Total	Zn	0
			1	1	
86	Lo	1	Total	Zn	0
			1	1	
86	Lp	1	Total	Zn	0
			1	1	

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
87	L5	211	Total	Mg	0
			211	211	
87	L7	3	Total	Mg	0
			3	3	
87	L8	5	Total	Mg	0
			5	5	
87	LA	1	Total	Mg	0
			1	1	
87	LB	1	Total	Mg	0
			1	1	

Continued on next page...

Continued from previous page...

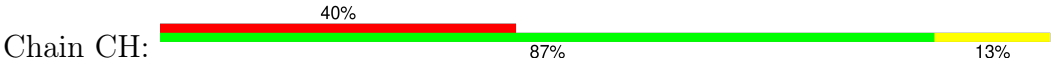
Mol	Chain	Residues	Atoms	AltConf
87	LI	1	Total Mg 1 1	0
87	LP	1	Total Mg 1 1	0
87	LV	1	Total Mg 1 1	0
87	Le	1	Total Mg 1 1	0
87	Lg	1	Total Mg 1 1	0
87	S3	29	Total Mg 29 29	0

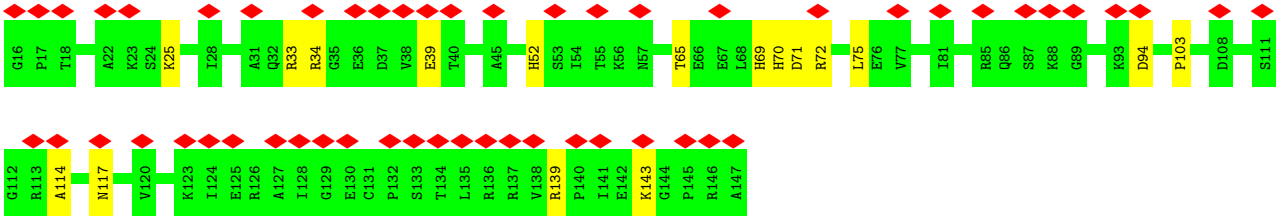
3 Residue-property plots (i)

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

• Molecule 1: EDF1

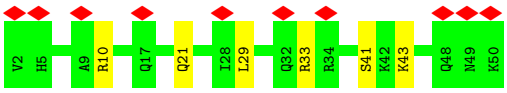
Chain CH:





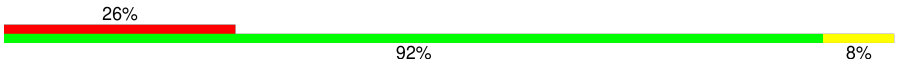
• Molecule 2: 40S ribosomal protein S30

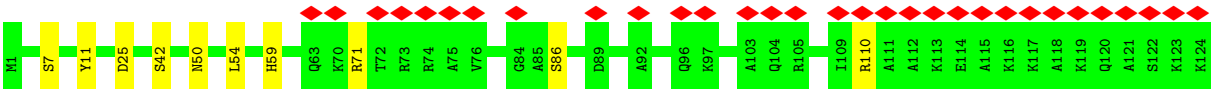
Chain Se:



• Molecule 3: 60S ribosomal protein L24

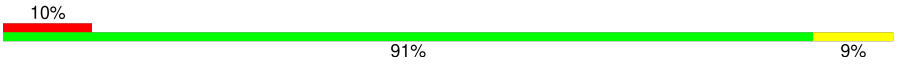
Chain LW:

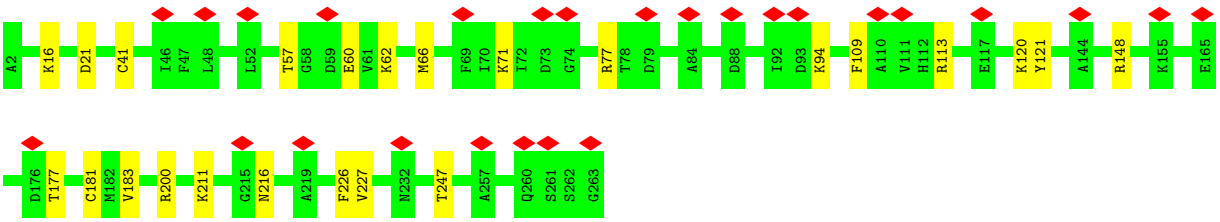




• Molecule 4: Small ribosomal subunit protein eS4, X isoform

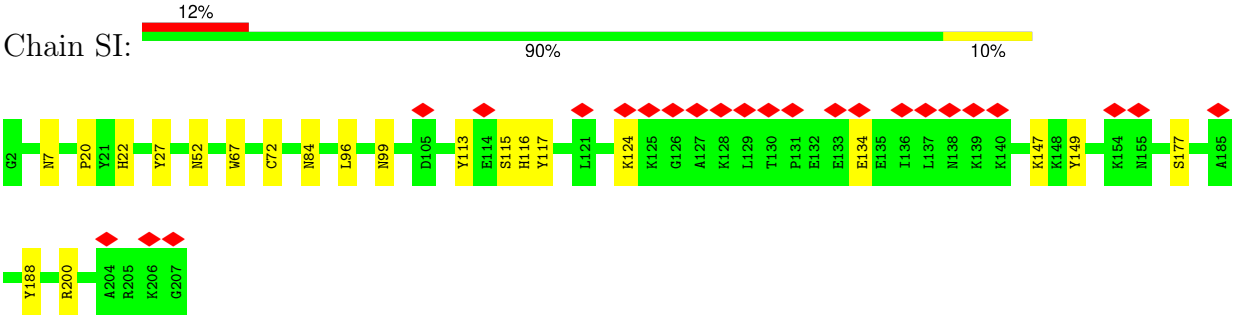
Chain SE:





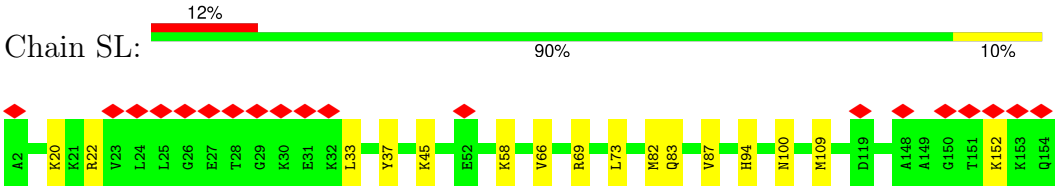
• Molecule 5: 40S ribosomal protein S8

Chain SI:



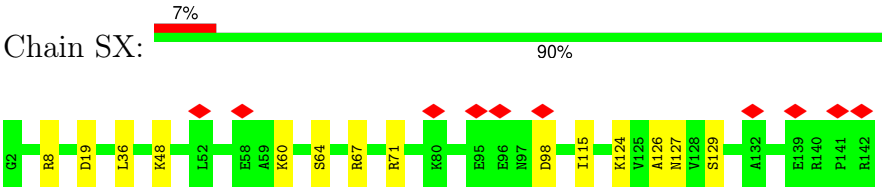
• Molecule 6: 40S ribosomal protein S11

Chain SL:



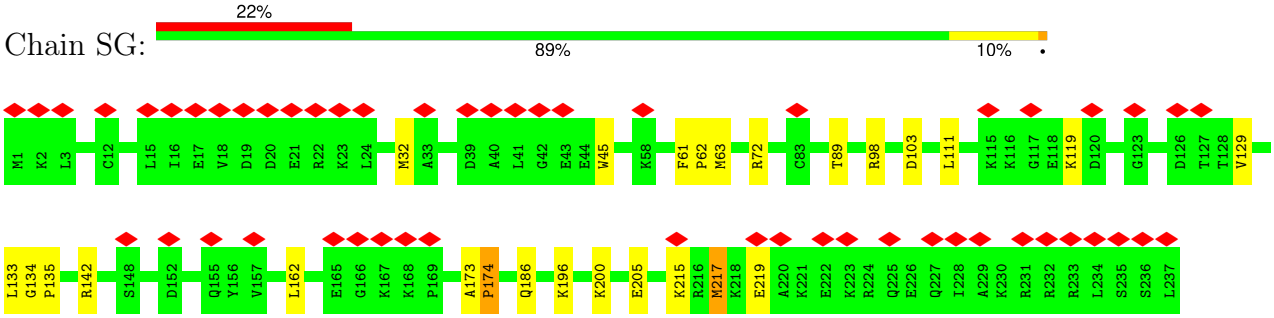
• Molecule 7: 40S ribosomal protein S23

Chain SX:



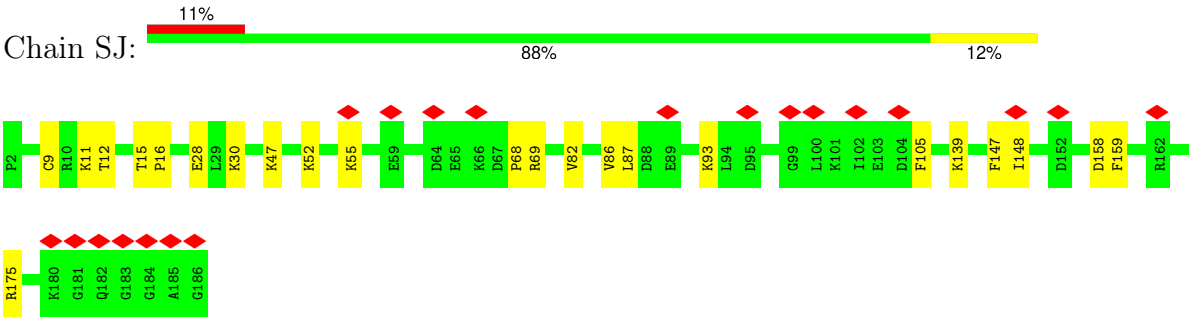
• Molecule 8: 40S ribosomal protein S6

Chain SG:



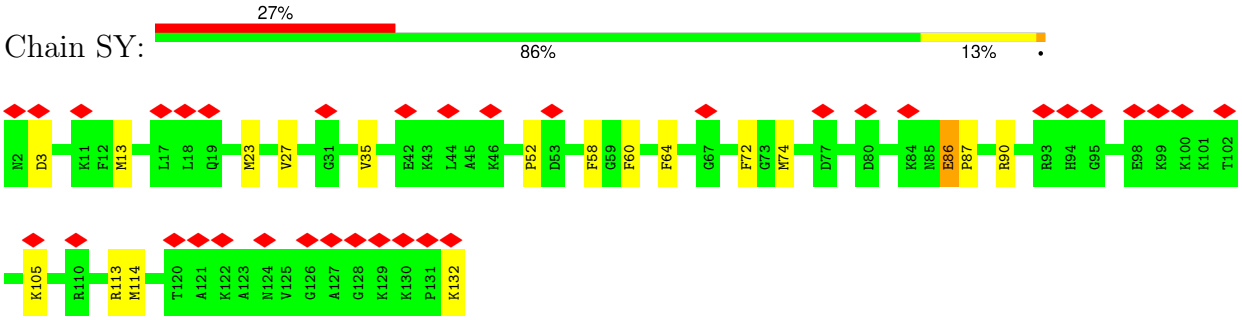
• Molecule 9: 40S ribosomal protein S9

Chain SJ:



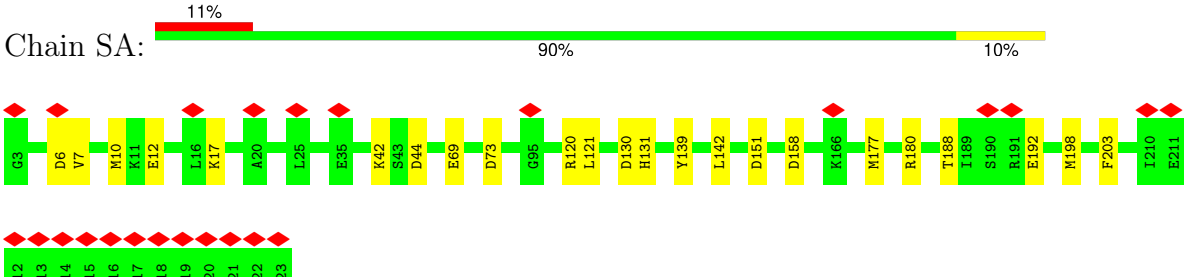
• Molecule 10: 40S ribosomal protein S24

Chain SY:



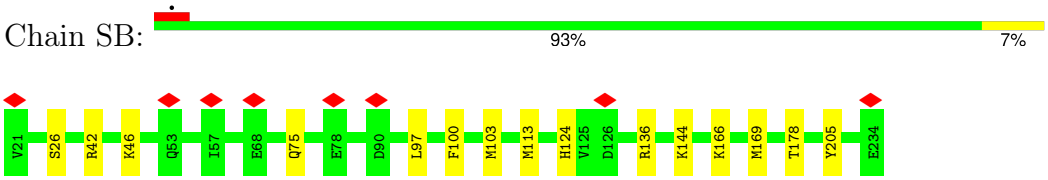
• Molecule 11: 40S ribosomal protein SA

Chain SA:



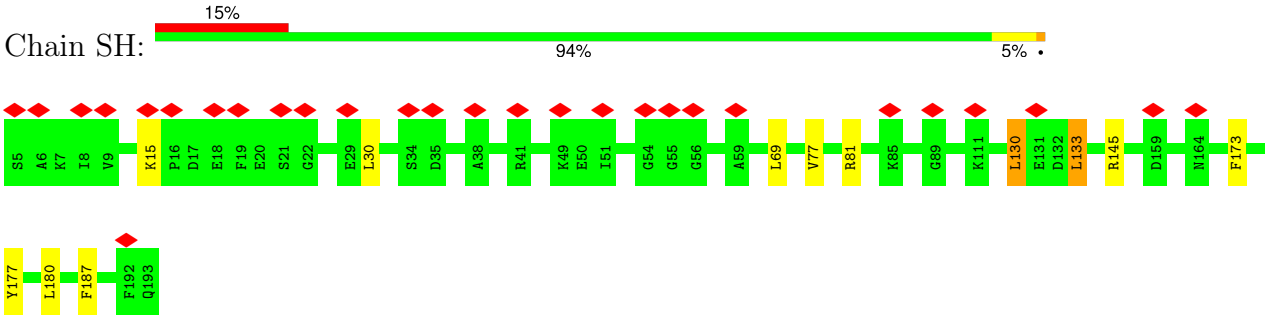
• Molecule 12: 40S ribosomal protein S3a

Chain SB:



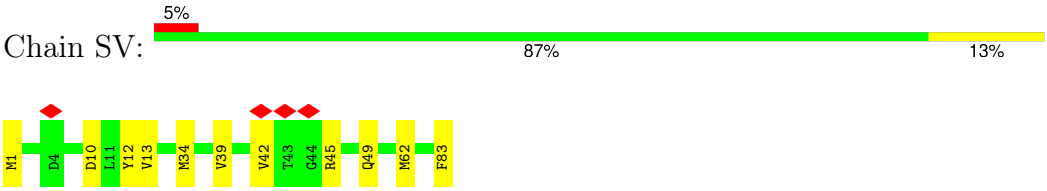
• Molecule 13: 40S ribosomal protein S7

Chain SH:



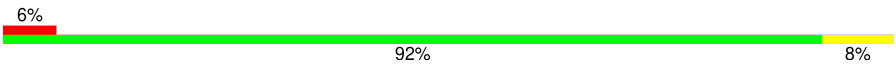
• Molecule 14: 40S ribosomal protein S21

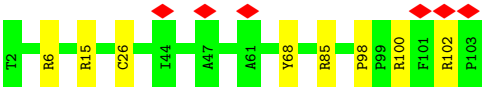
Chain SV:



• Molecule 15: 40S ribosomal protein S26

Chain Sa:



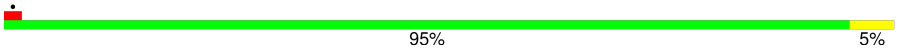


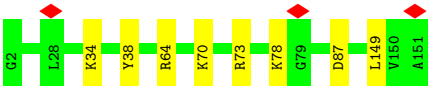
• Molecule 16: 40S ribosomal protein S2

Chain SC:

• Molecule 17: 40S ribosomal protein S13

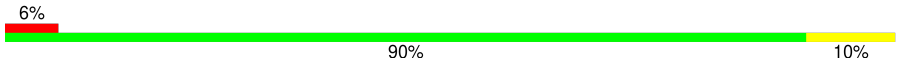
Chain SN:

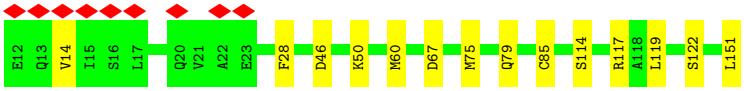




• Molecule 18: Small ribosomal subunit protein uS11

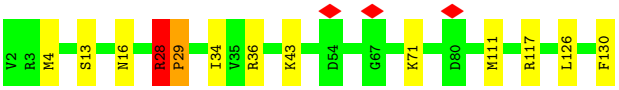
Chain SO:





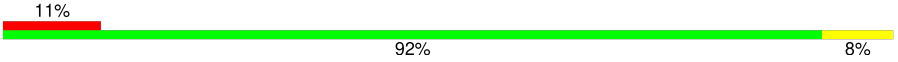
• Molecule 19: 40S ribosomal protein S15a

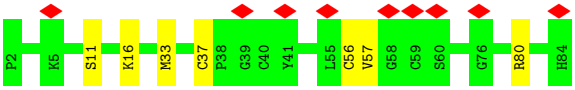
Chain SW:



• Molecule 20: Small ribosomal subunit protein eS27

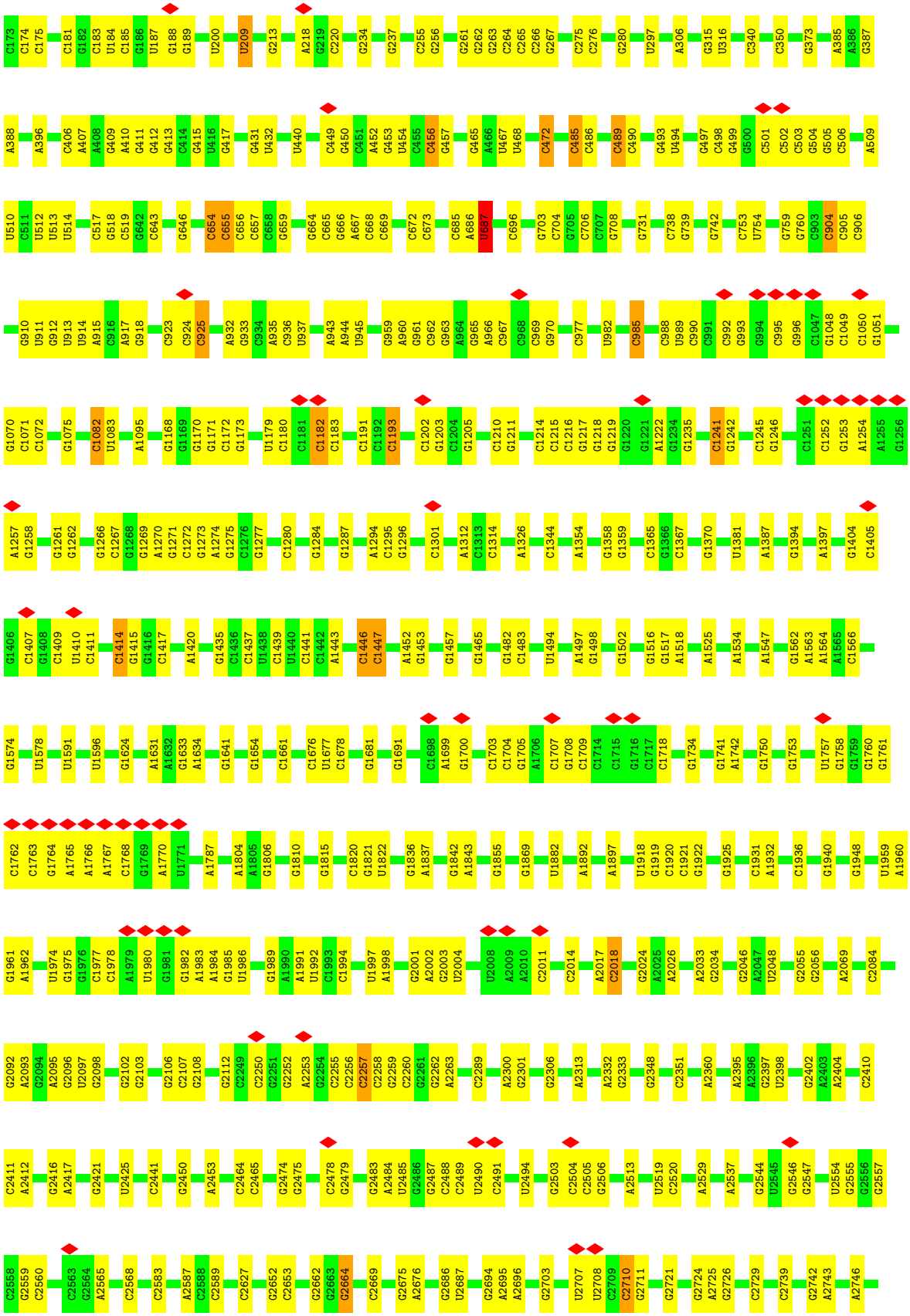
Chain Sb:

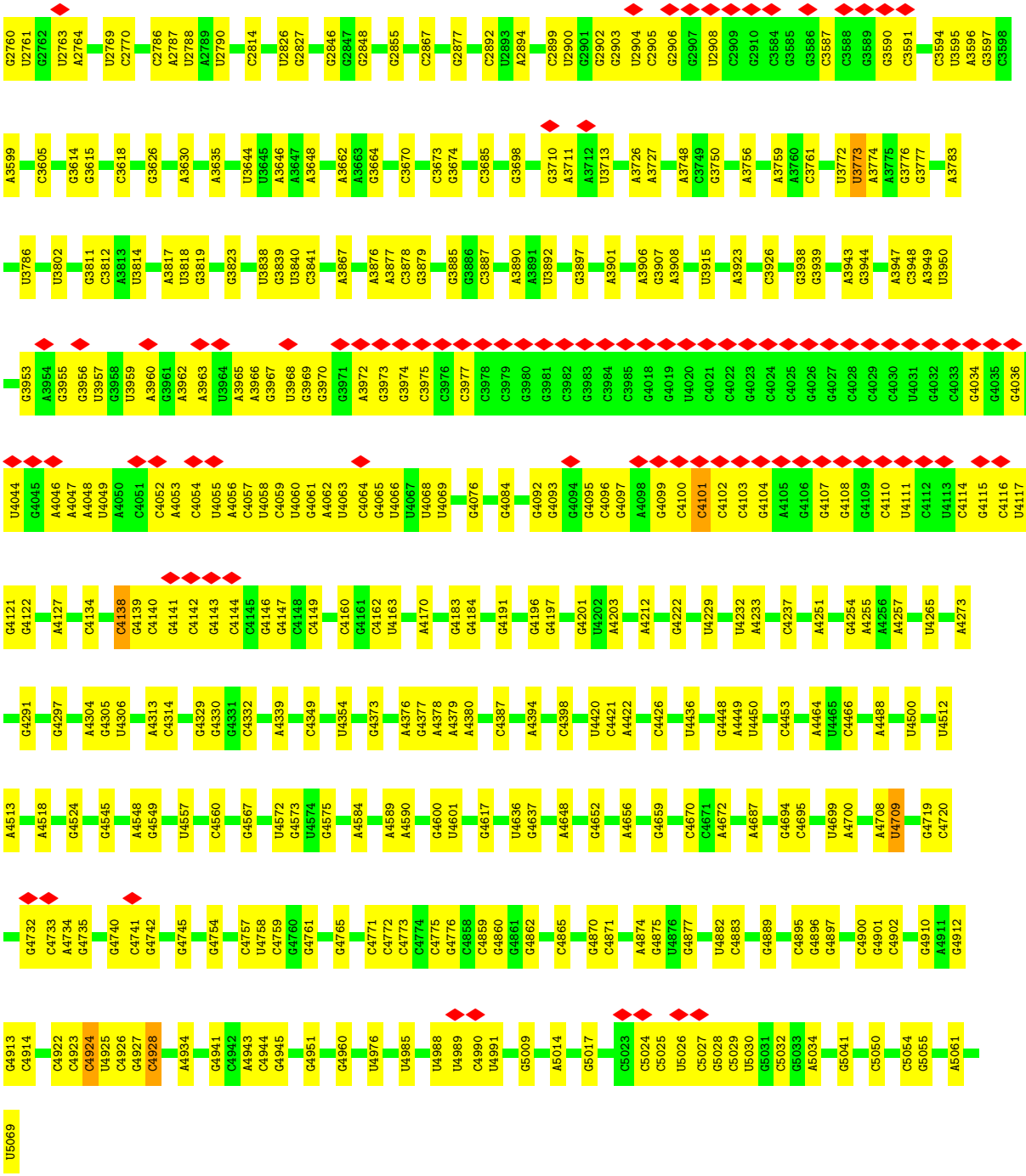




• Molecule 21: 28S rRNA

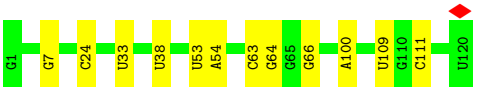
Chain L5:


C173 C174 C175 C181 G182 C183 U184 C185 G186 U187 G188 G189 U200 U209 G213 A218 G219 C220 G234 G237 C255 G256 G261 G262 G263 C264 C265 C266 G267 C275 C276 G280 U297 A306 G315 U316 C340 C350 G373 A385 A386 G387
A388 A396 C406 A407 A408 G409 A410 G411 G412 G413 C414 G415 U416 G417 C431 U432 U440 C449 G450 C451 A452 G453 U454 C455 C456 G457 G465 A466 U467 U468 C472 C485 C486 C489 C490 G493 U494 G497 C498 G499 G500 C501 C502 C503 G504 G505 C506 A509
U510 C511 U512 U513 U514 C517 G518 C519 G642 C643 G646 C654 C655 C656 C657 C658 G659 G664 C665 G666 A667 C668 C669 C672 C673 C685 A686 U687 C696 G703 C704 G705 C706 C707 G708 G731 C738 G739 G742 C753 U754 G759 G760 C903 C904 C905 C906
G910 U911 G912 U913 U914 A915 C916 A917 G918 C923 C924 C925 A932 G933 C934 A935 C936 U937 A943 A944 U945 G959 A960 G961 C962 G963 A964 G965 A966 C967 C968 C969 G970 C977 U982 C985 C988 U989 C990 C991 C992 G993 G994 C995 G996 C1047 G1048 C1049 C1050 G1051
G1070 C1071 C1072 G1075 C1082 U1083 A1095 G1168 G1169 G1170 G1171 C1172 G1173 U1179 C1180 C1181 C1182 C1183 C1191 C1192 C1193 C1202 G1203 C1204 G1205 C1210 G1211 C1214 C1215 C1216 G1217 G1218 G1219 G1220 G1221 A1222 G1234 G1235 C1241 G1242 C1245 G1246 C1251 C1252 G1253 A1254 A1255 G1256
A1257 G1258 G1261 G1262 G1266 C1267 G1268 G1269 A1270 G1271 C1272 G1273 A1274 G1275 C1276 G1277 C1280 G1284 G1287 A1294 C1295 G1296 C1301 A1312 C1313 C1314 A1326 C1344 A1354 G1358 G1359 C1365 G1366 C1367 G1370 U1381 A1387 G1394 A1397 G1404 C1405
G1406 C1407 G1408 C1409 U1410 C1411 C1414 G1415 G1416 C1417 A1420 G1435 C1436 C1437 U1438 C1439 U1440 C1441 C1442 A1443 C1446 C1447 A1452 G1453 G1457 G1465 G1482 C1483 U1494 A1497 G1498 G1502 G1516 G1517 A1518 A1525 A1534 A1547 G1562 A1563 A1564 A1565 C1566
G1574 U1578 U1591 U1596 G1624 A1631 A1632 G1633 A1634 G1641 G1654 C1661 C1676 U1677 C1678 G1681 G1691 C1698 A1699 G1700 C1703 C1704 G1705 A1706 C1707 G1708 C1709 C1714 C1715 G1716 C1717 C1718 G1734 G1741 A1742 G1750 G1753 U1757 G1758 G1759 G1760 G1761
C1762 C1763 G1764 A1765 A1766 A1767 C1768 G1769 A1770 U1771 A1787 A1804 A1805 G1806 G1810 G1815 C1820 G1821 U1822 G1836 A1837 G1842 A1843 G1855 G1869 U1882 A1892 A1897 U1918 G1919 C1920 C1921 G1922 G1925 C1931 A1932 C1936 G1940 G1948 U1959 A1960
G1961 A1962 U1974 G1975 G1976 C1977 C1978 A1979 U1980 G1981 G1982 A1983 A1984 G1985 U1986 G1989 A1990 A1991 U1992 C1993 C1994 U1997 A1998 G2001 A2002 G2003 U2004 U2008 A2009 A2010 C2011 C2014 A2017 C2018 G2024 A2025 A2026 A2033 G2034 G2046 A2047 U2048 G2055 G2056 A2069 C2084
G2092 A2093 G2094 A2095 G2096 U2097 G2098 G2102 G2103 G2106 C2107 G2108 G2112 C2249 C2250 G2251 G2252 A2253 G2254 C2255 C2256 C2257 C2258 G2259 C2260 G2261 G2262 A2263 C2289 A2300 G2301 G2306 A2313 A2332 G2333 G2348 C2351 A2360 A2395 A2396 G2397 U2398 G2402 A2403 A2404 C2410
C2411 A2412 G2416 A2417 G2421 U2425 C2441 G2450 A2453 C2464 C2465 G2474 G2475 C2478 G2479 G2483 A2484 U2485 G2486 G2487 C2488 C2489 U2490 C2491 U2494 G2503 C2504 C2505 G2506 A2513 U2519 C2520 A2529 A2537 G2544 U2545 G2546 G2547 U2554 G2555 G2556 G2557
C2558 G2559 C2560 C2563 G2564 A2565 C2568 C2583 A2587 C2588 C2589 C2627 G2652 C2653 G2662 G2663 G2664 C2669 G2675 A2676 G2686 U2687 G2694 A2695 A2696 G2703 U2707 U2708 C2709 C2710 G2711 G2721 G2724 A2725 G2726 C2729 C2739 G2742 A2743 A2746



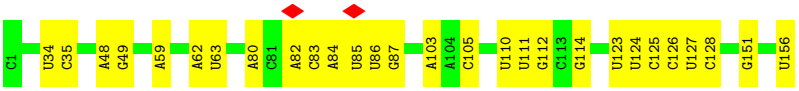
• Molecule 22: 5S rRNA

Chain L7:



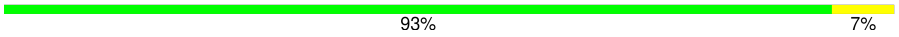
• Molecule 23: 5.8S rRNA

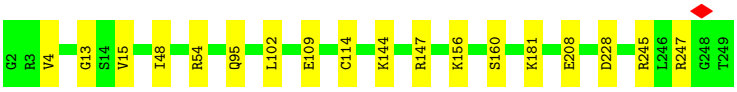
Chain L8:



• Molecule 24: 60S ribosomal protein L8

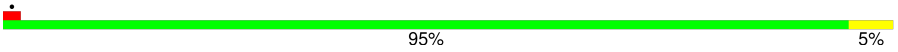
Chain LA:

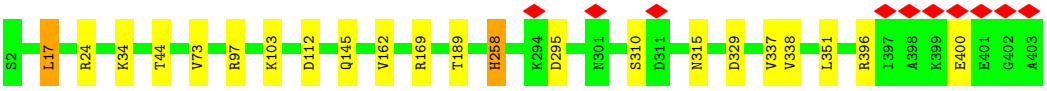




• Molecule 25: Large ribosomal subunit protein uL3

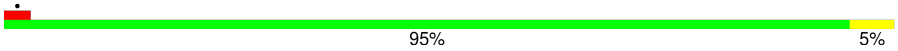
Chain LB:





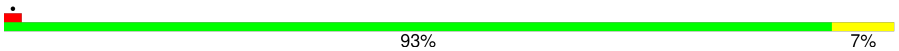
• Molecule 26: 60S ribosomal protein L4

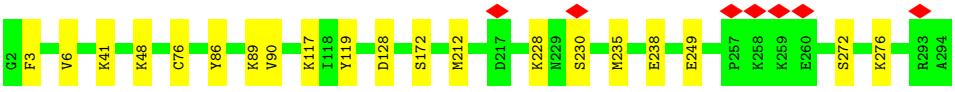
Chain LC:



• Molecule 27: Large ribosomal subunit protein uL18

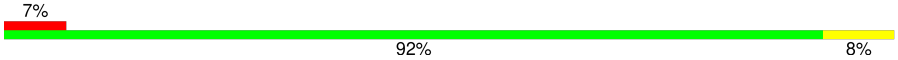
Chain LD:

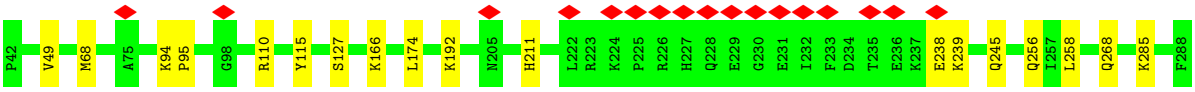




• Molecule 28: 60S ribosomal protein L6 [Homo sapiens]

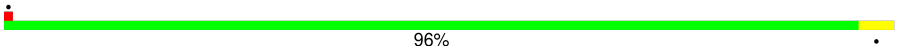
Chain LE:

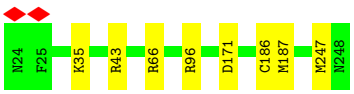




• Molecule 29: 60S ribosomal protein L7

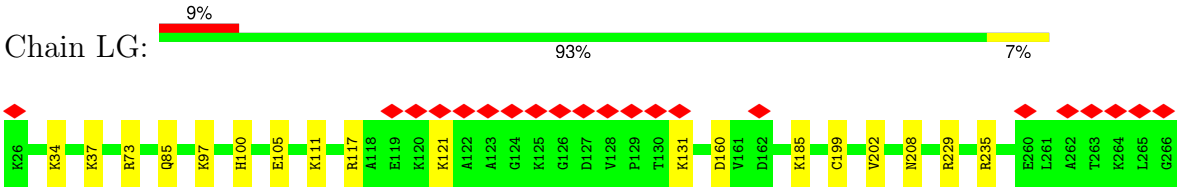
Chain LF:





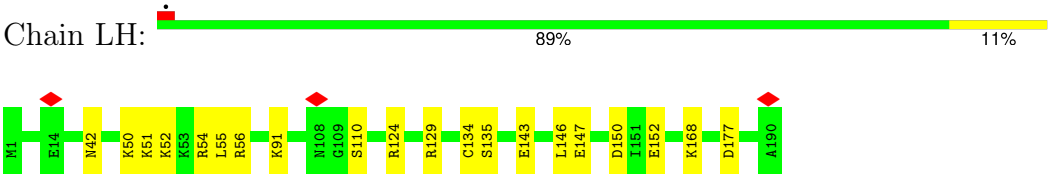
• Molecule 30: 60S ribosomal protein L7a

Chain LG:



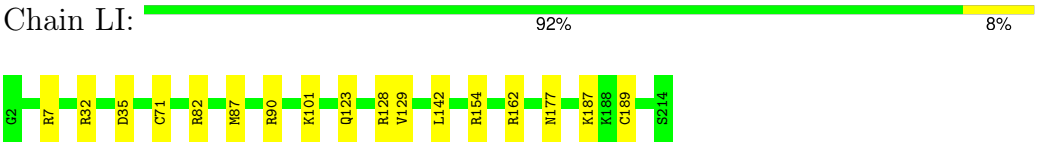
• Molecule 31: 60S ribosomal protein L9

Chain LH:



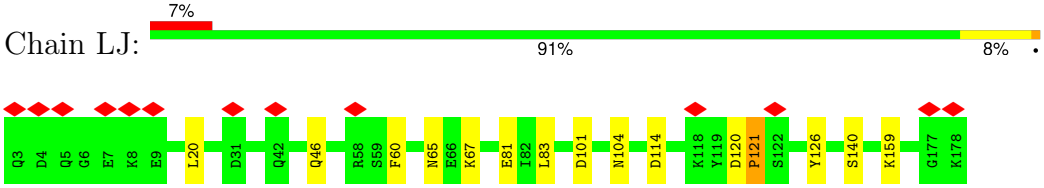
• Molecule 32: 60S ribosomal protein L10-like [Homo sapiens]

Chain LI:



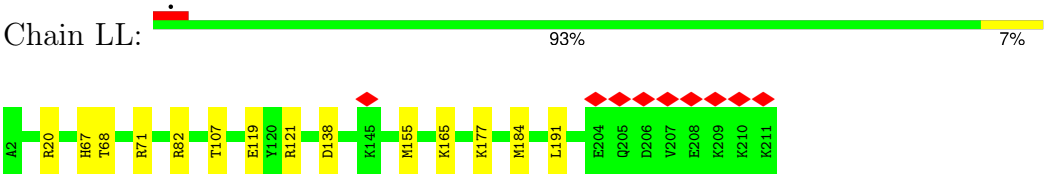
• Molecule 33: 60S ribosomal protein L11

Chain LJ:



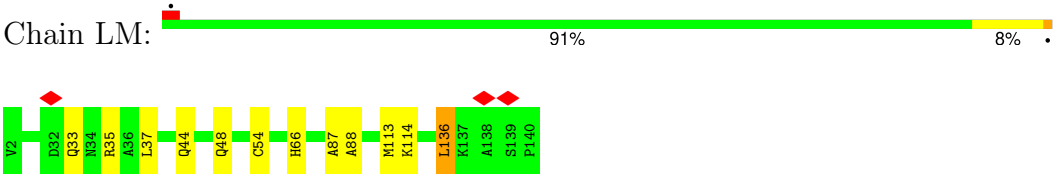
• Molecule 34: Large ribosomal subunit protein eL13

Chain LL:



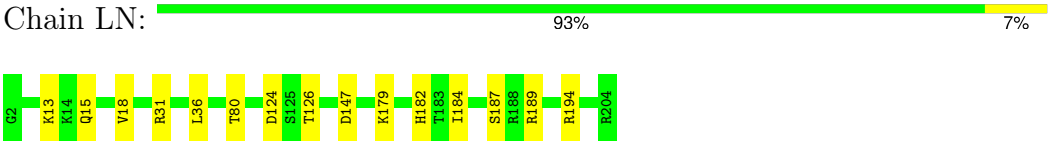
• Molecule 35: 60S ribosomal protein L14

Chain LM:



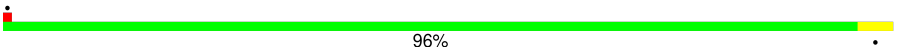
• Molecule 36: 60S ribosomal protein L15

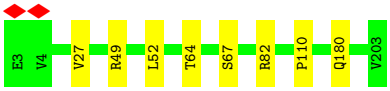
Chain LN:



• Molecule 37: 60S ribosomal protein L13a

Chain LO:





• Molecule 38: 60S ribosomal protein L17

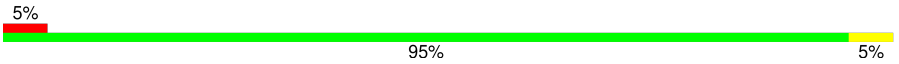
Chain LP:

• Molecule 39: 60S ribosomal protein L18

Chain LQ:

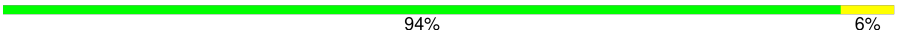
• Molecule 40: 60S ribosomal protein L19

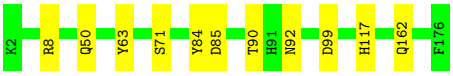
Chain LR:



• Molecule 41: 60S ribosomal protein L18a

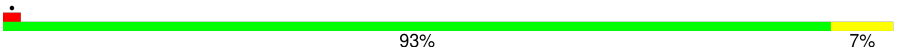
Chain LS:

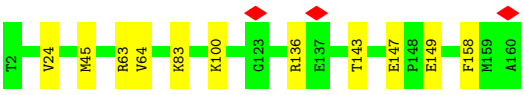




• Molecule 42: 60S ribosomal protein L21

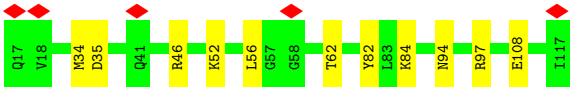
Chain LT:





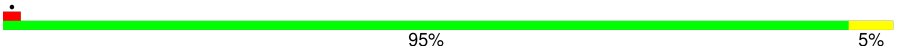
• Molecule 43: Heparin-binding protein HBp15

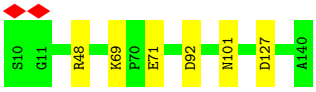
Chain LU:



• Molecule 44: 60S ribosomal protein L23

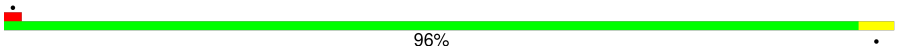
Chain LV:

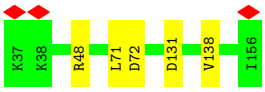




• Molecule 45: 60S ribosomal protein L23a

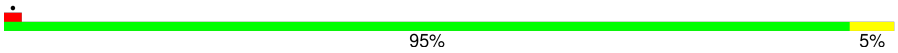
Chain LX:





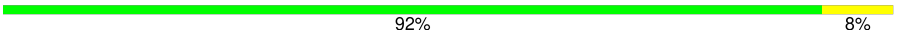
• Molecule 46: 60S ribosomal protein L26

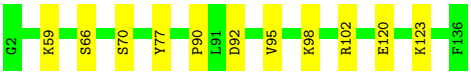
Chain LY:



• Molecule 47: 60S ribosomal protein L27

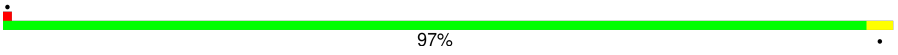
Chain LZ:

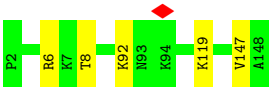




• Molecule 48: 60S ribosomal protein L27a

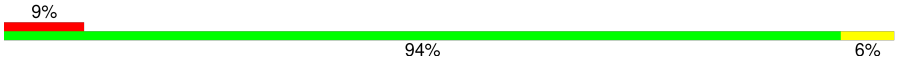
Chain La:

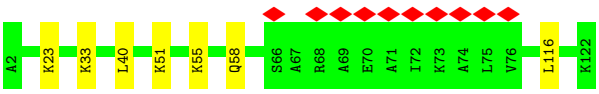




• Molecule 49: 60S ribosomal protein L29

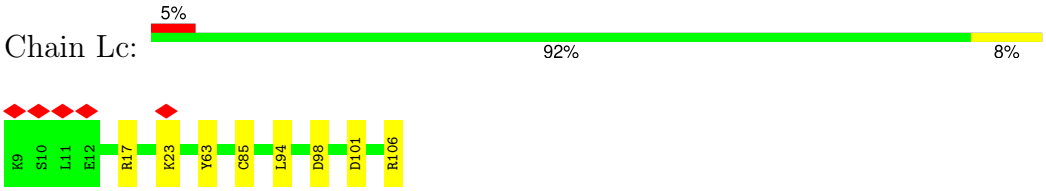
Chain Lb:





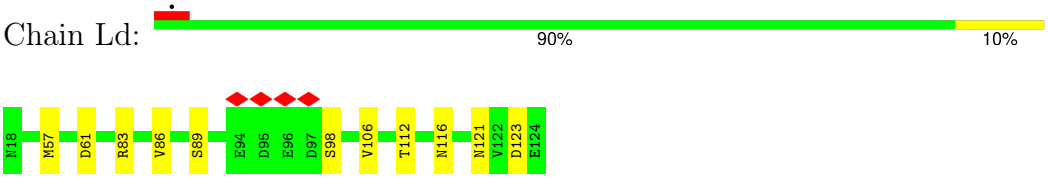
• Molecule 50: 60S ribosomal protein L30

Chain Lc:



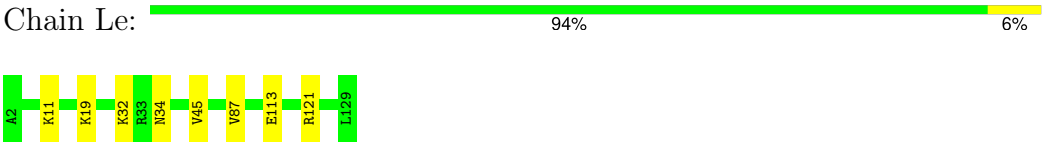
• Molecule 51: 60S ribosomal protein L31

Chain Ld:



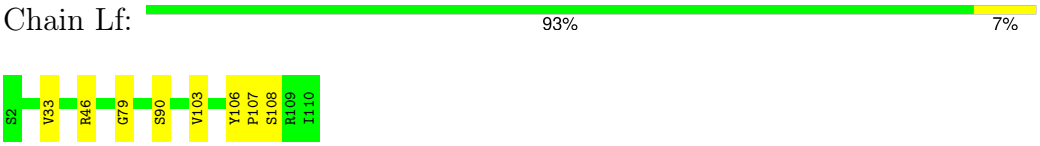
• Molecule 52: 60S ribosomal protein L32

Chain Le:



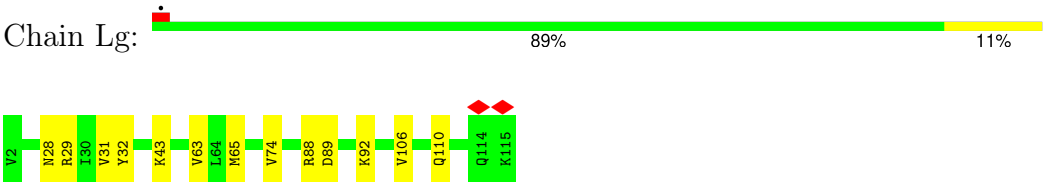
• Molecule 53: 60S ribosomal protein L35a

Chain Lf:



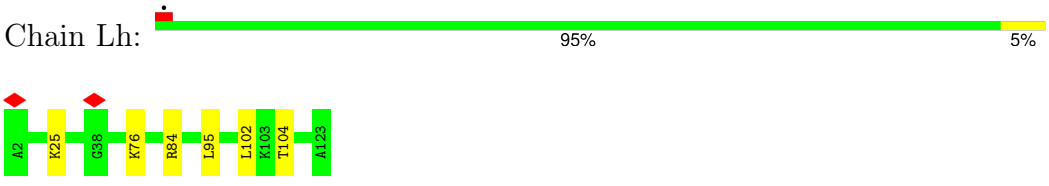
• Molecule 54: 60S ribosomal protein L34

Chain Lg:



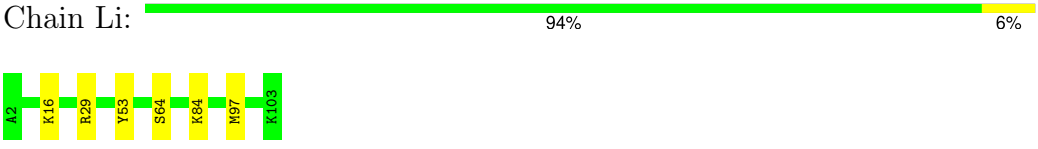
• Molecule 55: 60S ribosomal protein L35

Chain Lh:



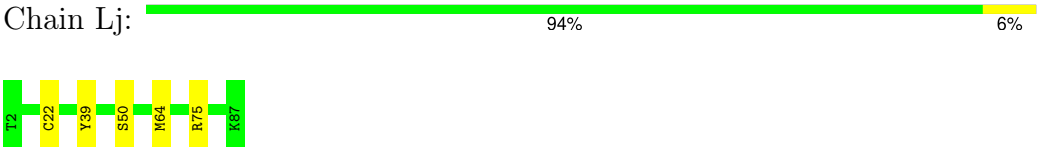
• Molecule 56: 60S ribosomal protein L36

Chain Li:



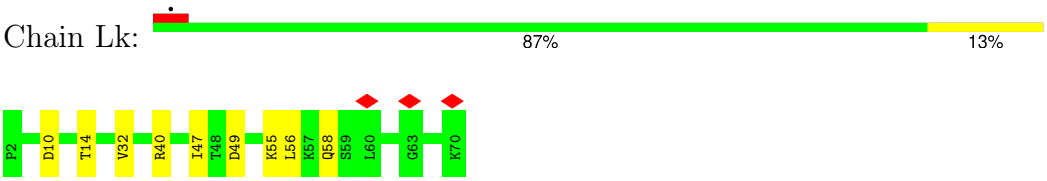
• Molecule 57: 60S ribosomal protein L37

Chain Lj:



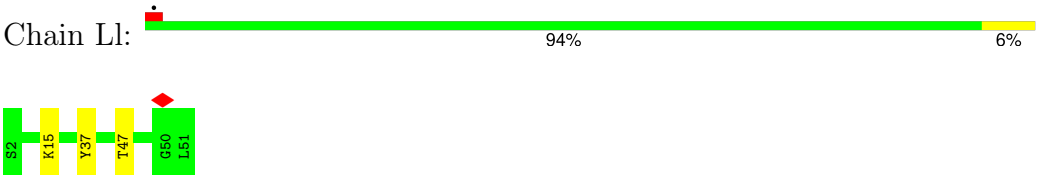
• Molecule 58: 60S ribosomal protein L38

Chain Lk:



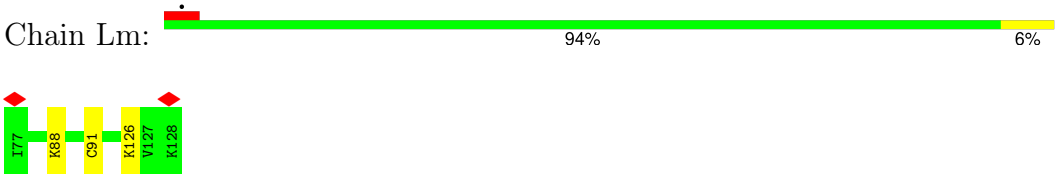
• Molecule 59: 60S ribosomal protein L39

Chain Ll:



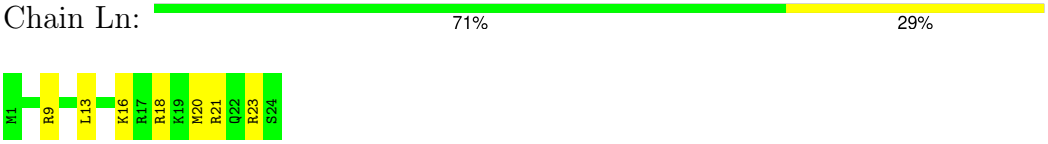
• Molecule 60: Large ribosomal subunit protein eL40

Chain Lm:



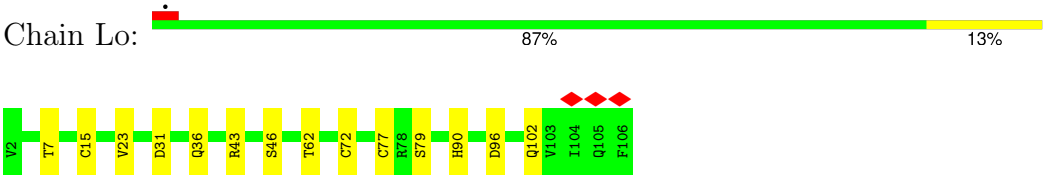
• Molecule 61: 60S ribosomal protein L41

Chain Ln:



• Molecule 62: 60S ribosomal protein L36a

Chain Lo:

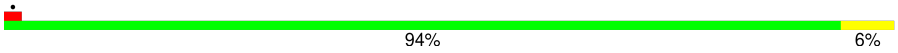


• Molecule 63: 60S ribosomal protein L37a

Chain Lp:

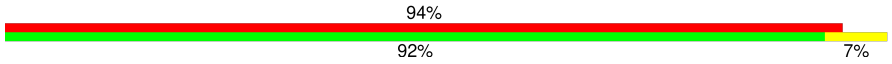
• Molecule 64: 60S ribosomal protein L28

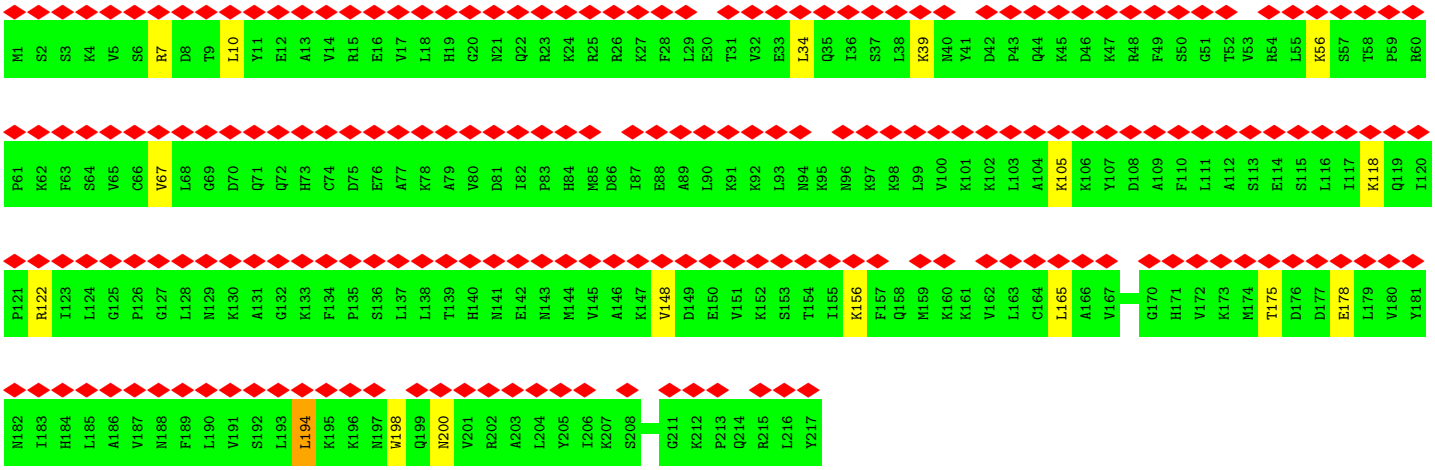
Chain Lr:



• Molecule 65: 60S ribosomal protein L10a

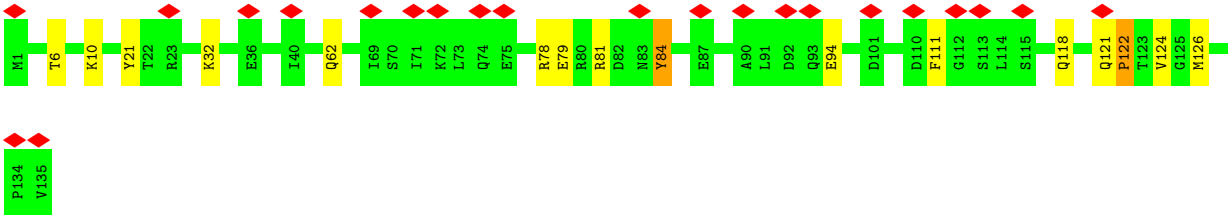
Chain Lz:





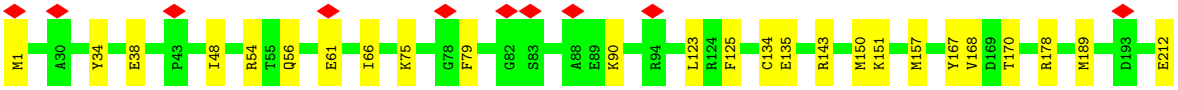
• Molecule 66: 40S ribosomal protein S17

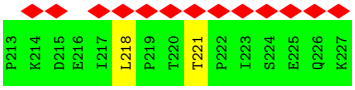
Chain SR:



• Molecule 67: Small ribosomal subunit protein uS3

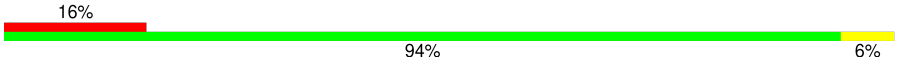
Chain SD:

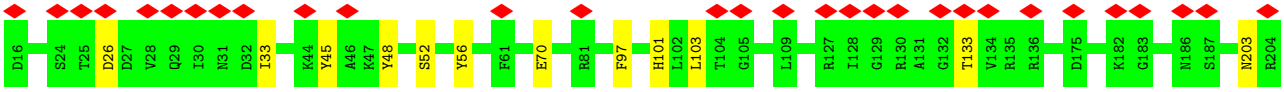




• Molecule 68: 40S ribosomal protein S5

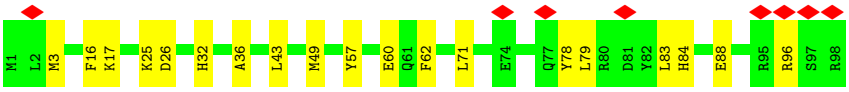
Chain SF:





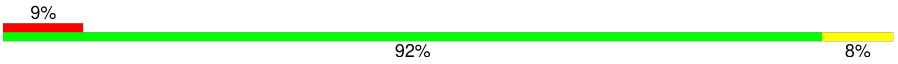
• Molecule 69: 40S ribosomal protein S10

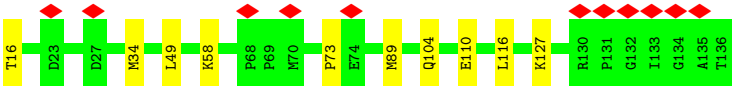
Chain SK:



• Molecule 70: Small ribosomal subunit protein uS19

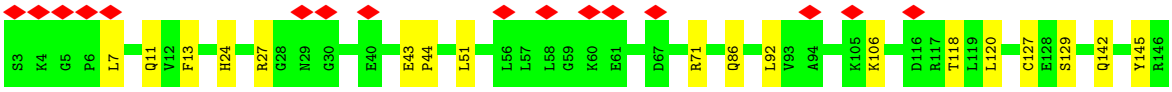
Chain SP:





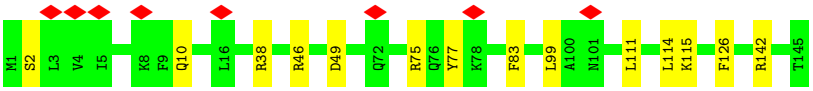
• Molecule 71: Small ribosomal subunit protein uS9

Chain SQ:



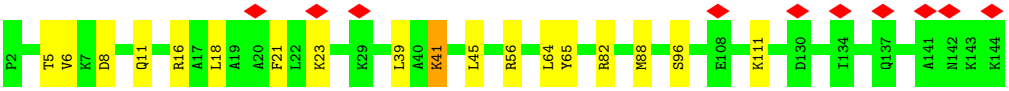
• Molecule 72: 40S ribosomal protein S18

Chain SS:



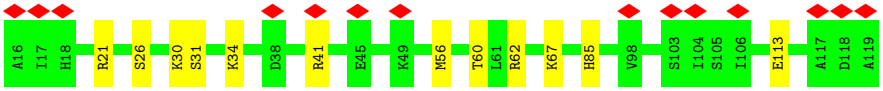
• Molecule 73: 40S ribosomal protein S19

Chain ST:



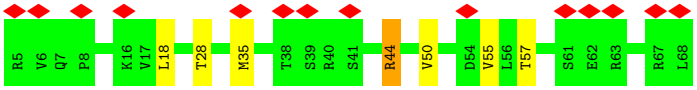
• Molecule 74: 40S ribosomal protein S20

Chain SU:



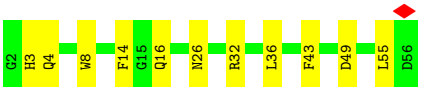
• Molecule 75: 40S ribosomal protein S28

Chain Sc:



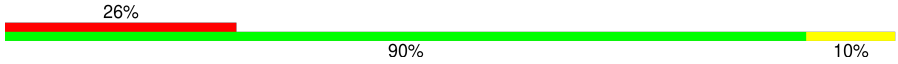
• Molecule 76: 40S ribosomal protein S29

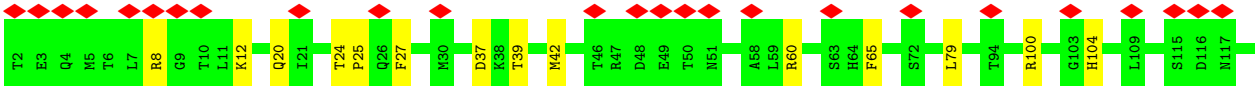
Chain Sd:

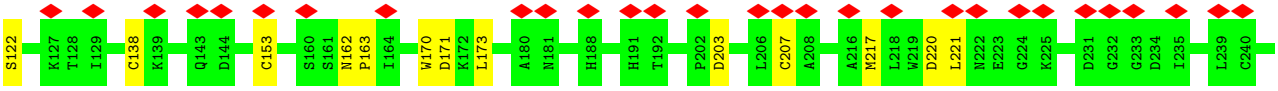


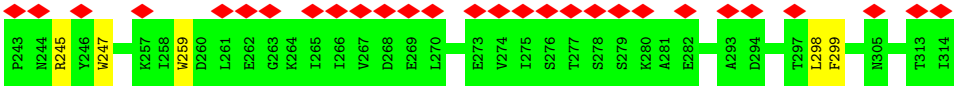
• Molecule 77: Receptor of activated protein C kinase 1

Chain Sg:



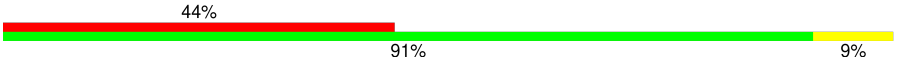


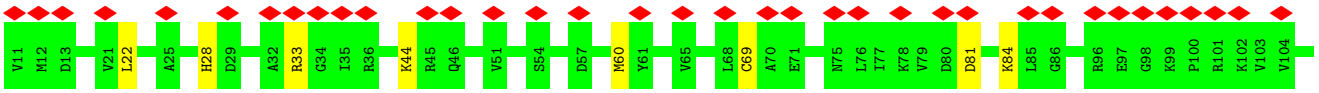


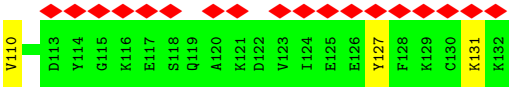


• Molecule 78: Small ribosomal subunit protein eS12

Chain SM:

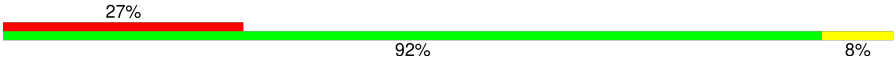


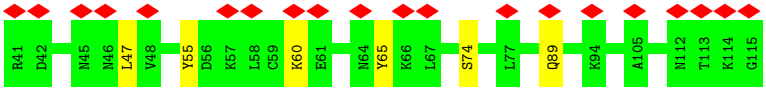




• Molecule 79: Small ribosomal subunit protein eS25

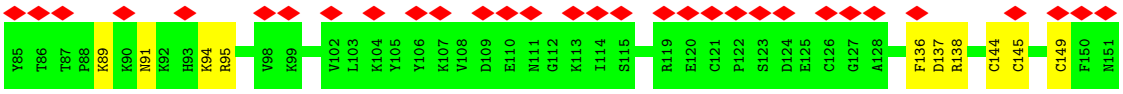
Chain SZ:





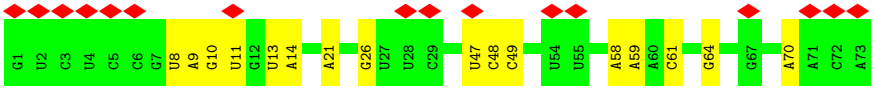
• Molecule 80: Ubiquitin-40S ribosomal protein S27a

Chain Sf:



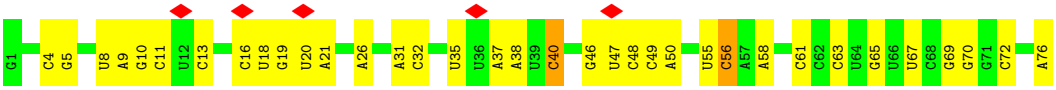
• Molecule 81: A/P site tRNA

Chain AP:



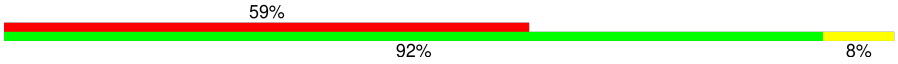
• Molecule 82: P/E site tRNA

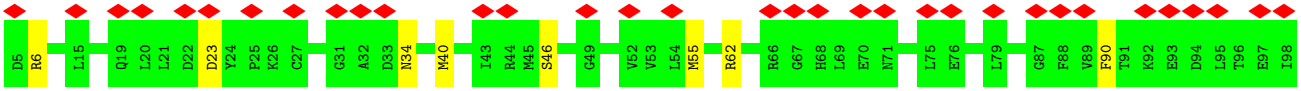
Chain PE:

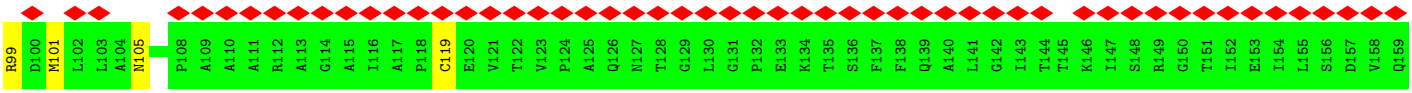


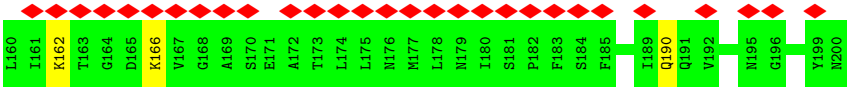
• Molecule 83: 60S acidic ribosomal protein P0

Chain Ls:



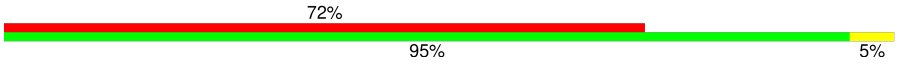


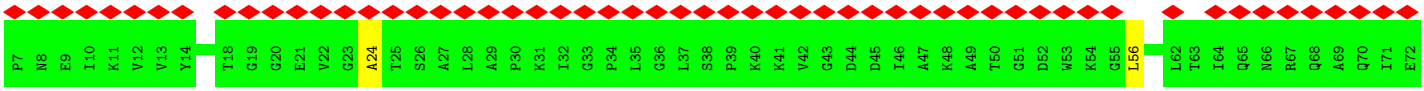


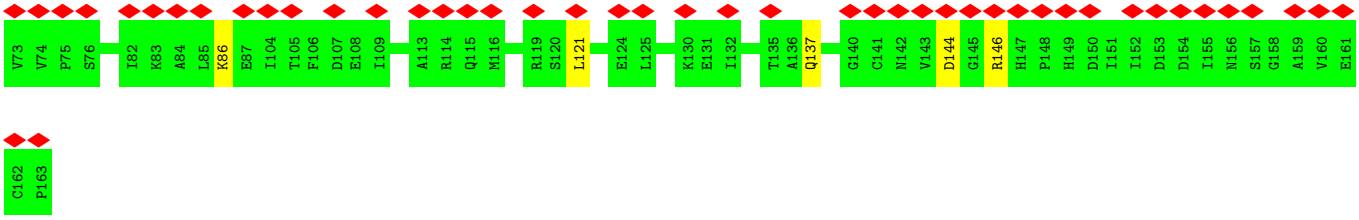


• Molecule 84: 60S ribosomal protein L12

Chain Lt:

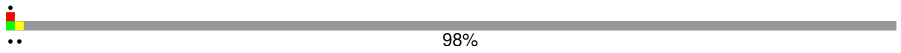


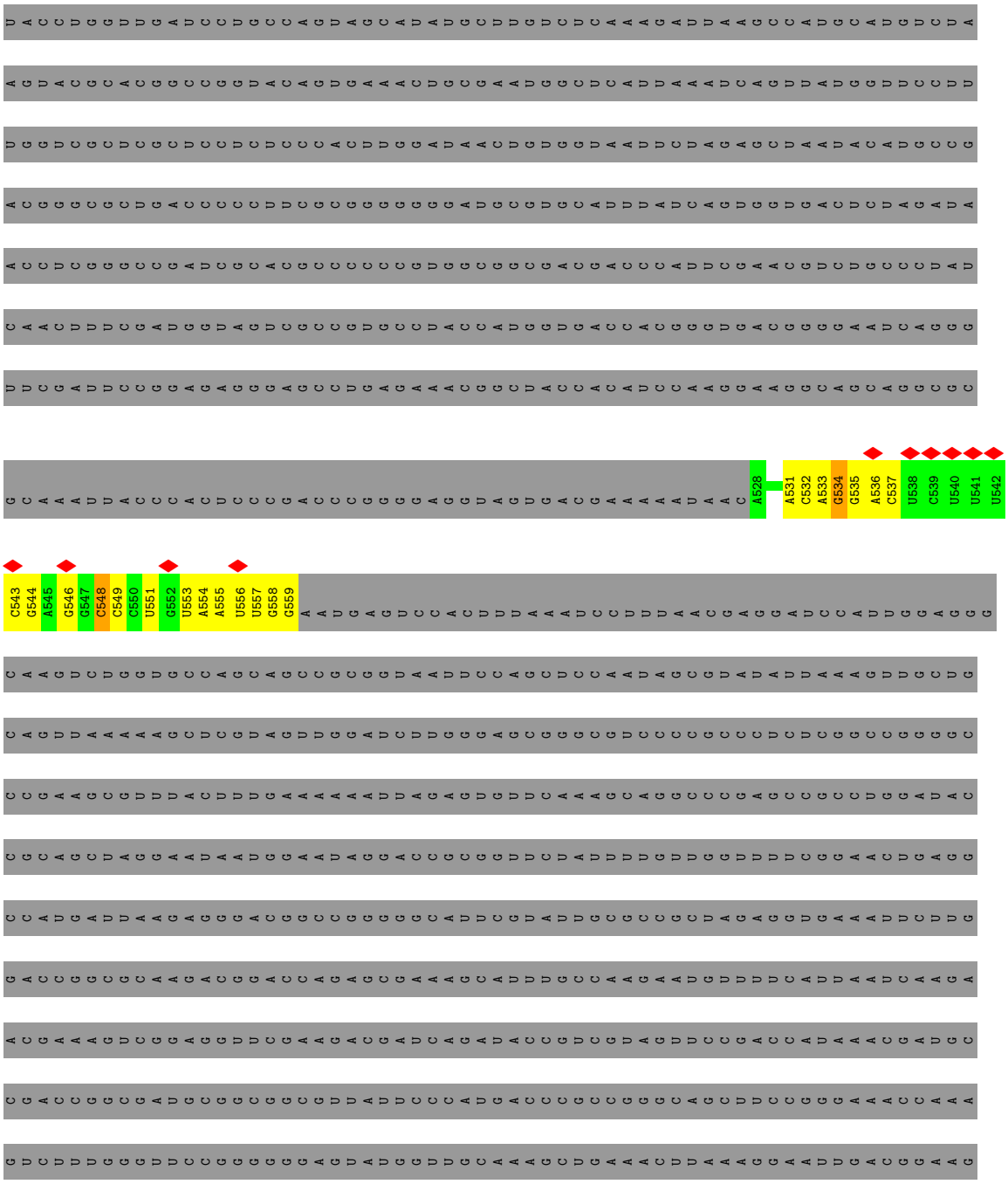


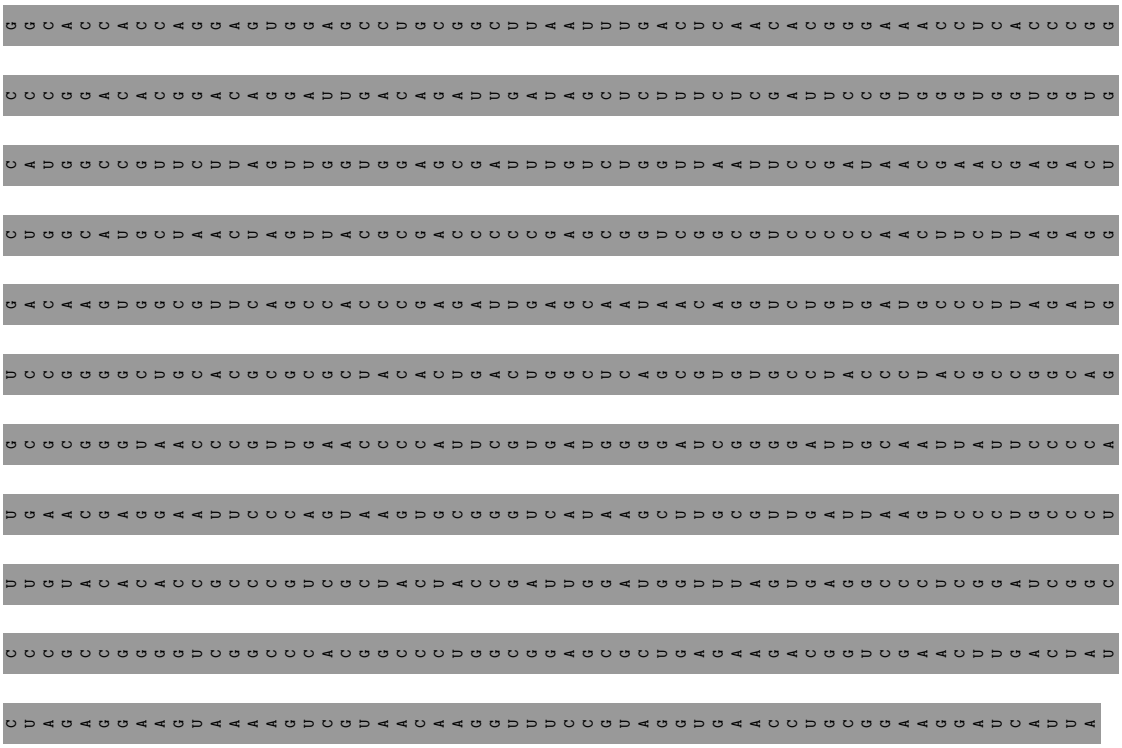


• Molecule 85: 18S rRNA

Chain S2:

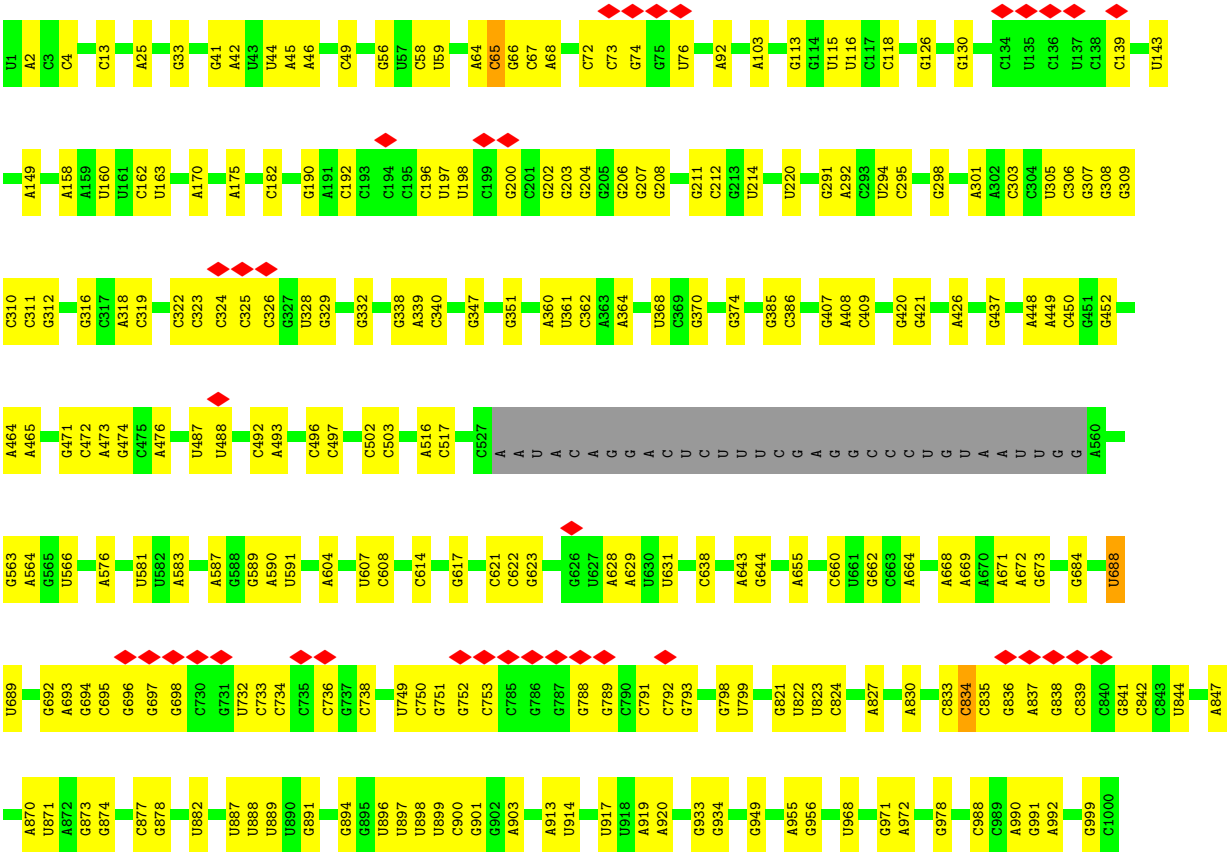


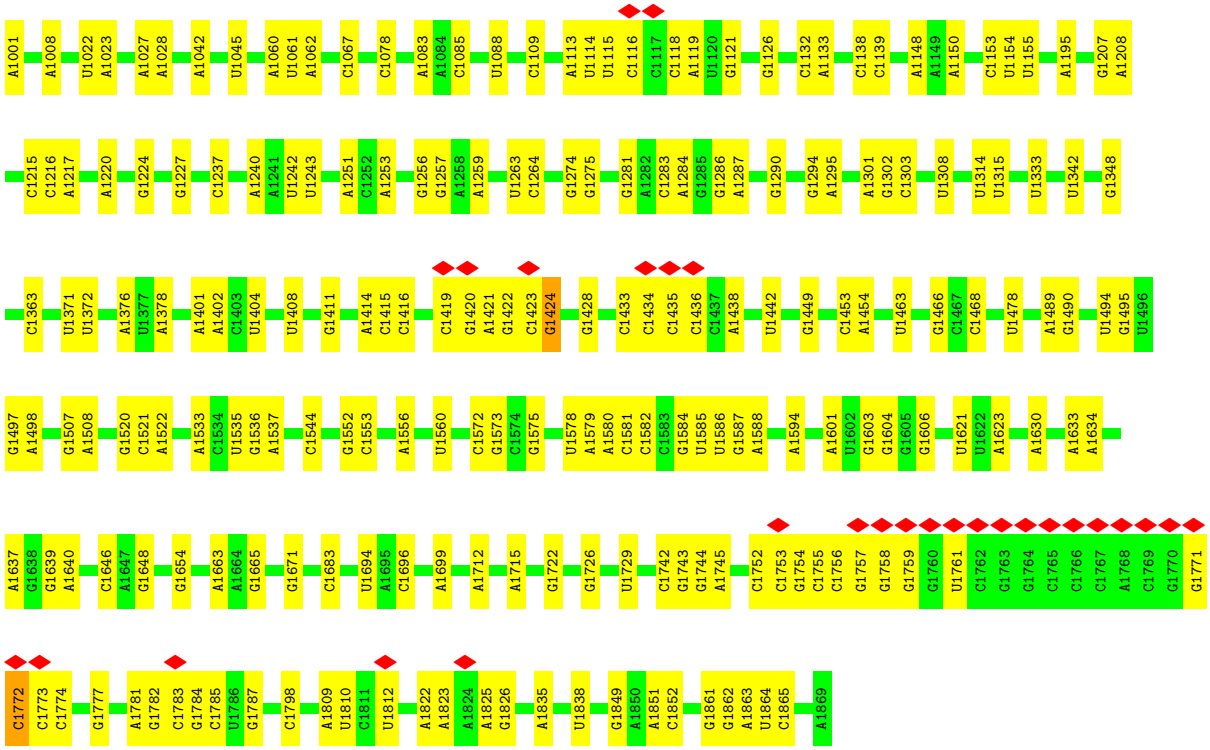




• Molecule 85: 18S rRNA

Chain S3:




A1001 A1008 U1022 A1023 A1027 A1028 A1042 U1045 A1060 U1061 A1062 C1067 C1078 A1083 A1084 C1085 U1088 C1109 A1113 U1114 U1115 C1116 C1117 C1118 A1119 U1120 G1121 G1126 C1132 A1133 C1138 C1139 A1148 A1149 A1150 C1153 U1154 U1155 A1195 G1207 A1208
C1215 C1216 A1217 A1220 G1224 G1227 C1237 A1240 A1241 U1242 U1243 A1251 C1252 A1253 G1256 G1257 A1258 A1259 U1263 C1264 G1274 G1275 G1281 A1282 C1283 A1284 G1285 G1286 A1287 G1290 G1294 A1295 A1301 G1302 C1303 U1308 U1314 U1315 U1333 U1342 G1348
C1363 U1371 U1372 A1376 U1377 A1378 A1401 A1402 C1403 U1404 U1408 G1411 A1414 C1415 C1416 C1419 G1420 A1421 G1422 C1423 G1424 G1428 C1433 C1434 C1435 C1436 C1437 A1438 U1442 G1449 C1453 A1454 U1463 G1466 C1467 C1468 U1478 A1489 G1490 U1494 G1495 U1496
G1497 A1498 G1507 A1508 G1520 C1521 A1522 A1533 C1534 U1535 G1536 A1537 C1544 G1552 C1553 A1556 U1560 C1572 G1573 C1574 G1575 U1578 A1579 A1580 C1581 C1582 C1583 G1584 U1585 U1586 G1587 A1588 A1594 A1601 U1602 G1603 G1604 G1605 G1606 U1621 U1622 A1623 A1630 A1633 A1634
A1637 G1638 G1639 A1640 C1646 A1647 G1648 G1654 A1663 A1664 G1665 G1671 C1683 U1694 A1695 C1696 A1699 A1712 A1715 G1722 G1726 U1729 C1742 G1743 G1744 A1745 C1752 C1753 G1754 C1755 C1756 G1757 G1758 G1759 G1760 U1761 C1762 G1763 C1764 C1765 C1766 C1767 A1768 C1769 G1770 G1771
C1772 C1773 C1774 G1777 A1781 G1782 C1783 G1784 C1785 U1786 G1787 C1798 A1809 U1810 C1811 U1812 A1822 A1823 A1824 A1825 G1826 A1835 U1838 G1849 A1850 A1851 C1852 G1861 G1862 A1863 U1864 C1865 A1869

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	36954	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.143	Depositor
Minimum map value	-0.062	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0182	Depositor
Map size (Å)	546.816, 546.816, 546.816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.068, 1.068, 1.068	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	CH	0.31	0/1034	0.64	1/1388 (0.1%)
2	Se	0.36	0/350	0.59	0/465
3	LW	0.33	0/979	0.58	0/1295
4	SE	0.28	0/2118	0.58	0/2849
5	SI	0.30	0/1715	0.62	1/2287 (0.0%)
6	SL	0.33	0/1268	0.62	0/1696
7	SX	0.28	0/1116	0.56	0/1490
8	SG	1.44	11/1946 (0.6%)	1.57	16/2590 (0.6%)
9	SJ	0.52	2/1550 (0.1%)	0.83	2/2069 (0.1%)
10	SY	0.75	3/1083 (0.3%)	0.93	4/1438 (0.3%)
11	SA	0.34	0/1778	0.63	0/2416
12	SB	0.31	0/1765	0.57	0/2362
13	SH	0.36	0/1519	0.64	2/2033 (0.1%)
14	SV	0.40	1/643 (0.2%)	0.68	0/860
15	Sa	0.34	0/836	0.65	1/1121 (0.1%)
16	SC	0.32	0/1762	0.60	1/2381 (0.0%)
17	SN	0.32	0/1232	0.58	0/1656
18	SO	0.29	0/1062	0.66	2/1425 (0.1%)
19	SW	0.97	3/1051 (0.3%)	0.99	5/1406 (0.4%)
20	Sb	0.30	0/665	0.58	0/891
21	L5	0.52	1/89313 (0.0%)	0.84	76/139291 (0.1%)
22	L7	0.50	0/2861	0.77	0/4459
23	L8	0.52	0/3701	0.77	0/5766
24	LA	0.40	0/1936	0.63	0/2596
25	LB	0.39	2/3306 (0.1%)	0.60	1/4424 (0.0%)
26	LC	0.33	0/2981	0.59	1/4002 (0.0%)
27	LD	0.42	2/2428 (0.1%)	0.56	0/3252
28	LE	0.44	2/1942 (0.1%)	0.60	1/2606 (0.0%)
29	LF	0.37	0/1905	0.58	0/2539
30	LG	0.34	0/1960	0.58	0/2637
31	LH	0.33	0/1537	0.61	0/2066
32	LI	0.34	0/1673	0.59	0/2233

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	LJ	0.69	2/1433 (0.1%)	0.90	3/1915 (0.2%)
34	LL	0.32	0/1732	0.59	0/2315
35	LM	0.34	0/1161	0.58	1/1554 (0.1%)
36	LN	0.35	0/1746	0.59	0/2338
37	LO	0.37	0/1682	0.58	0/2250
38	LP	0.34	0/1268	0.60	1/1701 (0.1%)
39	LQ	0.35	0/1537	0.64	1/2052 (0.0%)
40	LR	0.33	0/1582	0.62	0/2091
41	LS	0.37	0/1493	0.58	0/2003
42	LT	0.36	0/1326	0.58	0/1770
43	LU	0.36	0/839	0.65	1/1126 (0.1%)
44	LV	0.37	0/993	0.60	0/1332
45	LX	0.36	0/1002	0.62	1/1345 (0.1%)
46	LY	0.34	0/1132	0.59	0/1504
47	LZ	0.36	0/1130	0.58	0/1507
48	La	0.35	0/1191	0.57	0/1591
49	Lb	0.32	0/889	0.59	0/1175
50	Lc	0.41	1/774 (0.1%)	0.64	1/1038 (0.1%)
51	Ld	0.35	0/903	0.64	1/1216 (0.1%)
52	Le	0.35	0/1071	0.58	0/1429
53	Lf	0.39	0/895	0.63	0/1198
54	Lg	0.35	0/916	0.62	0/1220
55	Lh	0.30	0/1023	0.59	0/1351
56	Li	0.31	0/843	0.58	0/1115
57	Lj	0.35	0/720	0.62	0/952
58	Lk	0.40	0/575	0.65	0/761
59	Ll	0.30	0/454	0.59	0/599
60	Lm	0.34	0/435	0.71	0/575
61	Ln	0.25	0/231	0.74	0/294
62	Lo	0.36	0/876	0.59	0/1156
63	Lp	0.34	0/718	0.55	0/953
64	Lr	0.33	0/1017	0.60	0/1364
65	Lz	0.25	0/1769	0.56	1/2371 (0.0%)
66	SR	0.50	1/1105 (0.1%)	0.76	3/1484 (0.2%)
67	SD	0.33	0/1793	0.62	0/2414
68	SF	0.32	0/1516	0.59	0/2037
69	SK	0.37	0/851	0.68	1/1147 (0.1%)
70	SP	0.54	2/1003 (0.2%)	0.85	2/1342 (0.1%)
71	SQ	0.30	0/1160	0.66	1/1553 (0.1%)
72	SS	0.33	0/1216	0.65	0/1628
73	ST	0.28	0/1131	0.63	1/1515 (0.1%)
74	SU	0.28	0/831	0.61	0/1115
75	Sc	0.44	1/508 (0.2%)	0.76	1/680 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	Sd	0.34	0/470	0.64	0/623
77	Sg	0.88	10/2493 (0.4%)	1.08	12/3394 (0.4%)
78	SM	0.28	0/950	0.56	1/1275 (0.1%)
79	SZ	0.30	0/604	0.66	0/810
80	Sf	0.29	0/560	0.62	0/745
81	AP	0.25	0/1692	0.77	0/2634
82	PE	0.32	0/1778	0.90	2/2767 (0.1%)
83	Ls	0.29	0/1519	0.58	0/2052
84	Lt	0.27	0/1058	0.63	0/1430
85	S2	0.34	0/759	1.04	6/1180 (0.5%)
85	S3	0.35	1/40482 (0.0%)	0.82	25/63071 (0.0%)
All	All	0.46	45/239850 (0.0%)	0.78	180/352046 (0.1%)

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
7	SX	0	1
10	SY	0	1
13	SH	0	1
19	SW	0	1
21	L5	0	1
24	LA	0	1
25	LB	0	2
35	LM	0	1
37	LO	0	1
42	LT	0	1
53	Lf	0	3
57	Lj	0	1
71	SQ	0	1
All	All	0	16

The worst 5 of 45 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	SG	62	PRO	N-CD	31.86	1.92	1.47
8	SG	62	PRO	CG-CD	-30.13	0.51	1.50
8	SG	135	PRO	N-CD	26.13	1.84	1.47
77	Sg	25	PRO	CG-CD	-21.22	0.80	1.50
8	SG	135	PRO	CG-CD	-21.10	0.81	1.50

The worst 5 of 180 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	SG	62	PRO	N-CD-CG	-45.60	34.80	103.20
8	SG	135	PRO	N-CD-CG	-31.21	56.39	103.20
77	Sg	25	PRO	N-CD-CG	-22.33	69.70	103.20
33	LJ	121	PRO	CA-N-CD	-21.99	80.71	111.50
8	SG	174	PRO	CA-N-CD	-21.29	81.69	111.50

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	L5	687	U	Sidechain
13	SH	15	LYS	Peptide
19	SW	28	ARG	Peptide
7	SX	126	ALA	Peptide
10	SY	86	GLU	Peptide

5.2 Too-close contacts (i)

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

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	CH	130/132 (98%)	103 (79%)	25 (19%)	2 (2%)	8 34
2	Se	45/47 (96%)	42 (93%)	3 (7%)	0	100 100
3	LW	114/118 (97%)	110 (96%)	4 (4%)	0	100 100
4	SE	260/262 (99%)	245 (94%)	15 (6%)	0	100 100
5	SI	204/206 (99%)	192 (94%)	12 (6%)	0	100 100
6	SL	151/153 (99%)	139 (92%)	12 (8%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
7	SX	139/141 (99%)	126 (91%)	12 (9%)	1 (1%)	19 51
8	SG	235/237 (99%)	218 (93%)	16 (7%)	1 (0%)	30 63
9	SJ	183/185 (99%)	170 (93%)	13 (7%)	0	100 100
10	SY	129/131 (98%)	118 (92%)	11 (8%)	0	100 100
11	SA	219/221 (99%)	201 (92%)	17 (8%)	1 (0%)	25 59
12	SB	212/214 (99%)	203 (96%)	9 (4%)	0	100 100
13	SH	182/186 (98%)	156 (86%)	26 (14%)	0	100 100
14	SV	81/83 (98%)	74 (91%)	7 (9%)	0	100 100
15	Sa	100/102 (98%)	92 (92%)	8 (8%)	0	100 100
16	SC	220/222 (99%)	205 (93%)	15 (7%)	0	100 100
17	SN	148/150 (99%)	144 (97%)	4 (3%)	0	100 100
18	SO	138/140 (99%)	124 (90%)	14 (10%)	0	100 100
19	SW	127/129 (98%)	121 (95%)	4 (3%)	2 (2%)	8 32
20	Sb	81/83 (98%)	73 (90%)	8 (10%)	0	100 100
24	LA	246/248 (99%)	224 (91%)	22 (9%)	0	100 100
25	LB	400/402 (100%)	370 (92%)	30 (8%)	0	100 100
26	LC	366/368 (100%)	336 (92%)	30 (8%)	0	100 100
27	LD	291/293 (99%)	276 (95%)	15 (5%)	0	100 100
28	LE	232/236 (98%)	206 (89%)	26 (11%)	0	100 100
29	LF	223/225 (99%)	211 (95%)	12 (5%)	0	100 100
30	LG	239/241 (99%)	221 (92%)	18 (8%)	0	100 100
31	LH	188/190 (99%)	173 (92%)	15 (8%)	0	100 100
32	LI	198/202 (98%)	186 (94%)	12 (6%)	0	100 100
33	LJ	174/176 (99%)	158 (91%)	15 (9%)	1 (1%)	22 55
34	LL	208/210 (99%)	188 (90%)	20 (10%)	0	100 100
35	LM	137/139 (99%)	128 (93%)	8 (6%)	1 (1%)	19 51
36	LN	201/203 (99%)	188 (94%)	12 (6%)	1 (0%)	25 59
37	LO	199/201 (99%)	191 (96%)	8 (4%)	0	100 100
38	LP	151/153 (99%)	138 (91%)	13 (9%)	0	100 100
39	LQ	185/187 (99%)	176 (95%)	9 (5%)	0	100 100
40	LR	185/187 (99%)	178 (96%)	7 (4%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	LS	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
42	LT	157/159 (99%)	147 (94%)	10 (6%)	0	100	100
43	LU	99/101 (98%)	84 (85%)	15 (15%)	0	100	100
44	LV	129/131 (98%)	122 (95%)	7 (5%)	0	100	100
45	LX	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
46	LY	132/134 (98%)	127 (96%)	5 (4%)	0	100	100
47	LZ	133/135 (98%)	122 (92%)	11 (8%)	0	100	100
48	La	145/147 (99%)	134 (92%)	11 (8%)	0	100	100
49	Lb	105/109 (96%)	96 (91%)	9 (9%)	0	100	100
50	Lc	96/98 (98%)	87 (91%)	9 (9%)	0	100	100
51	Ld	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
52	Le	126/128 (98%)	119 (94%)	7 (6%)	0	100	100
53	Lf	107/109 (98%)	99 (92%)	7 (6%)	1 (1%)	14	46
54	Lg	112/114 (98%)	109 (97%)	3 (3%)	0	100	100
55	Lh	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
56	Li	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
57	Lj	84/86 (98%)	78 (93%)	6 (7%)	0	100	100
58	Lk	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
59	Ll	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
60	Lm	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
61	Ln	22/24 (92%)	22 (100%)	0	0	100	100
62	Lo	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
63	Lp	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
64	Lr	123/125 (98%)	116 (94%)	7 (6%)	0	100	100
65	Lz	215/217 (99%)	174 (81%)	41 (19%)	0	100	100
66	SR	133/135 (98%)	113 (85%)	19 (14%)	1 (1%)	16	48
67	SD	225/227 (99%)	206 (92%)	19 (8%)	0	100	100
68	SF	187/189 (99%)	167 (89%)	20 (11%)	0	100	100
69	SK	96/98 (98%)	86 (90%)	8 (8%)	2 (2%)	5	25
70	SP	119/121 (98%)	107 (90%)	12 (10%)	0	100	100
71	SQ	142/144 (99%)	127 (89%)	14 (10%)	1 (1%)	19	51

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
72	SS	143/145 (99%)	133 (93%)	10 (7%)	0	100 100
73	ST	141/143 (99%)	129 (92%)	11 (8%)	1 (1%)	19 51
74	SU	102/104 (98%)	96 (94%)	6 (6%)	0	100 100
75	Sc	62/64 (97%)	49 (79%)	13 (21%)	0	100 100
76	Sd	53/55 (96%)	49 (92%)	3 (6%)	1 (2%)	6 28
77	Sg	311/313 (99%)	276 (89%)	35 (11%)	0	100 100
78	SM	120/122 (98%)	111 (92%)	9 (8%)	0	100 100
79	SZ	73/75 (97%)	58 (80%)	15 (20%)	0	100 100
80	Sf	65/67 (97%)	61 (94%)	4 (6%)	0	100 100
83	Ls	194/196 (99%)	184 (95%)	10 (5%)	0	100 100
84	Lt	137/141 (97%)	108 (79%)	27 (20%)	2 (2%)	8 34
All	All	11982/12152 (99%)	11036 (92%)	927 (8%)	19 (0%)	45 74

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	CH	72	ARG
8	SG	174	PRO
69	SK	96	ARG
1	CH	114	ALA
36	LN	124	ASP

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
1	CH	108/108 (100%)	94 (87%)	14 (13%)	3 14
2	Se	32/32 (100%)	26 (81%)	6 (19%)	1 6
3	LW	97/97 (100%)	87 (90%)	10 (10%)	6 22
4	SE	224/224 (100%)	200 (89%)	24 (11%)	5 21
5	SI	178/178 (100%)	158 (89%)	20 (11%)	5 19

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
6	SL	137/137 (100%)	121 (88%)	16 (12%)	4 18
7	SX	113/113 (100%)	101 (89%)	12 (11%)	5 21
8	SG	207/207 (100%)	187 (90%)	20 (10%)	6 25
9	SJ	161/161 (100%)	140 (87%)	21 (13%)	3 14
10	SY	113/113 (100%)	98 (87%)	15 (13%)	3 14
11	SA	183/183 (100%)	161 (88%)	22 (12%)	4 17
12	SB	195/195 (100%)	180 (92%)	15 (8%)	10 35
13	SH	166/166 (100%)	155 (93%)	11 (7%)	14 41
14	SV	67/67 (100%)	57 (85%)	10 (15%)	2 11
15	Sa	89/89 (100%)	82 (92%)	7 (8%)	10 33
16	SC	188/188 (100%)	167 (89%)	21 (11%)	5 19
17	SN	130/130 (100%)	122 (94%)	8 (6%)	15 43
18	SO	110/110 (100%)	98 (89%)	12 (11%)	5 20
19	SW	112/112 (100%)	101 (90%)	11 (10%)	6 25
20	Sb	75/75 (100%)	68 (91%)	7 (9%)	7 27
24	LA	190/190 (100%)	173 (91%)	17 (9%)	8 29
25	LB	348/348 (100%)	328 (94%)	20 (6%)	17 47
26	LC	306/306 (100%)	290 (95%)	16 (5%)	19 50
27	LD	246/247 (100%)	227 (92%)	19 (8%)	10 35
28	LE	209/209 (100%)	193 (92%)	16 (8%)	10 35
29	LF	194/194 (100%)	186 (96%)	8 (4%)	26 58
30	LG	203/205 (99%)	185 (91%)	18 (9%)	8 29
31	LH	169/169 (100%)	149 (88%)	20 (12%)	4 18
32	LI	172/172 (100%)	155 (90%)	17 (10%)	6 24
33	LJ	148/148 (100%)	135 (91%)	13 (9%)	8 29
34	LL	176/176 (100%)	162 (92%)	14 (8%)	10 33
35	LM	118/118 (100%)	108 (92%)	10 (8%)	8 31
36	LN	171/171 (100%)	157 (92%)	14 (8%)	9 32
37	LO	173/173 (100%)	166 (96%)	7 (4%)	27 58
38	LP	134/134 (100%)	116 (87%)	18 (13%)	3 13
39	LQ	164/164 (100%)	148 (90%)	16 (10%)	6 25

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
40	LR	166/166 (100%)	156 (94%)	10 (6%)	16 45
41	LS	156/156 (100%)	145 (93%)	11 (7%)	12 38
42	LT	139/139 (100%)	129 (93%)	10 (7%)	12 38
43	LU	91/91 (100%)	81 (89%)	10 (11%)	5 20
44	LV	101/101 (100%)	95 (94%)	6 (6%)	16 45
45	LX	108/108 (100%)	104 (96%)	4 (4%)	29 61
46	LY	124/124 (100%)	117 (94%)	7 (6%)	17 47
47	LZ	117/117 (100%)	106 (91%)	11 (9%)	7 26
48	La	120/120 (100%)	115 (96%)	5 (4%)	25 57
49	Lb	88/90 (98%)	81 (92%)	7 (8%)	10 33
50	Lc	83/83 (100%)	77 (93%)	6 (7%)	12 38
51	Ld	98/98 (100%)	88 (90%)	10 (10%)	6 23
52	Le	114/114 (100%)	106 (93%)	8 (7%)	12 39
53	Lf	88/88 (100%)	84 (96%)	4 (4%)	23 55
54	Lg	98/98 (100%)	85 (87%)	13 (13%)	3 14
55	Lh	109/109 (100%)	103 (94%)	6 (6%)	18 48
56	Li	86/86 (100%)	80 (93%)	6 (7%)	12 39
57	Lj	73/73 (100%)	69 (94%)	4 (6%)	18 48
58	Lk	64/64 (100%)	55 (86%)	9 (14%)	3 12
59	Ll	47/47 (100%)	44 (94%)	3 (6%)	14 42
60	Lm	48/48 (100%)	45 (94%)	3 (6%)	15 43
61	Ln	23/23 (100%)	16 (70%)	7 (30%)	0 1
62	Lo	93/93 (100%)	79 (85%)	14 (15%)	2 10
63	Lp	74/74 (100%)	69 (93%)	5 (7%)	13 40
64	Lr	109/109 (100%)	101 (93%)	8 (7%)	11 37
65	Lz	195/196 (100%)	178 (91%)	17 (9%)	8 30
66	SR	122/122 (100%)	108 (88%)	14 (12%)	4 19
67	SD	190/190 (100%)	163 (86%)	27 (14%)	2 12
68	SF	159/159 (100%)	147 (92%)	12 (8%)	11 36
69	SK	89/89 (100%)	73 (82%)	16 (18%)	1 7
70	SP	107/107 (100%)	98 (92%)	9 (8%)	9 31

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
71	SQ	119/119 (100%)	104 (87%)	15 (13%)	3 15
72	SS	126/126 (100%)	112 (89%)	14 (11%)	5 20
73	ST	113/113 (100%)	96 (85%)	17 (15%)	2 10
74	SU	94/94 (100%)	82 (87%)	12 (13%)	3 15
75	Sc	57/57 (100%)	50 (88%)	7 (12%)	4 16
76	Sd	48/48 (100%)	38 (79%)	10 (21%)	1 4
77	Sg	272/272 (100%)	244 (90%)	28 (10%)	6 22
78	SM	102/104 (98%)	92 (90%)	10 (10%)	6 25
79	SZ	66/66 (100%)	60 (91%)	6 (9%)	7 28
80	Sf	60/60 (100%)	50 (83%)	10 (17%)	2 8
83	Ls	162/164 (99%)	147 (91%)	15 (9%)	7 27
84	Lt	112/115 (97%)	107 (96%)	5 (4%)	23 55
All	All	10416/10429 (100%)	9460 (91%)	956 (9%)	10 27

5 of 956 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	LM	44	GLN
77	Sg	37	ASP
45	LX	72	ASP
76	Sd	32	ARG
83	Ls	105	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
57	Lj	28	HIS
68	SF	83	ASN
64	Lr	70	GLN
67	SD	57	ASN
71	SQ	24	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
21	L5	3705/3740 (99%)	860 (23%)	20 (0%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	L7	119/120 (99%)	12 (10%)	0
23	L8	155/156 (99%)	28 (18%)	1 (0%)
81	AP	69/71 (97%)	16 (23%)	0
82	PE	74/75 (98%)	34 (45%)	1 (1%)
85	S2	31/1740 (1%)	19 (61%)	1 (3%)
85	S3	1683/1740 (96%)	437 (25%)	6 (0%)
All	All	5836/7642 (76%)	1406 (24%)	29 (0%)

5 of 1406 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
21	L5	2	G
21	L5	25	A
21	L5	26	C
21	L5	30	C
21	L5	39	A

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
21	L5	3948	C
85	S3	1434	C
21	L5	4600	G
85	S3	420	G
21	L5	4420	U

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 261 ligands modelled in this entry, 261 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
21	L5	11
85	S3	5
49	Lb	1
28	LE	1
3	LW	1
81	AP	1
84	Lt	1
13	SH	1
32	LI	1
82	PE	1
19	SW	1

The worst 5 of 25 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Lb	76:VAL	C	89:VAL	N	34.29
1	S3	753:C	O3'	785:C	P	28.14
1	LE	76:ALA	C	88:VAL	N	24.31
1	L5	2910:G	O3'	3584:C	P	20.73
1	LW	63:GLN	C	70:LYS	N	17.66

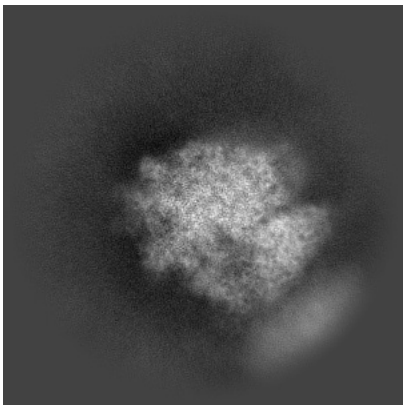
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-44017. These allow visual inspection of the internal detail of the map and identification of artifacts.

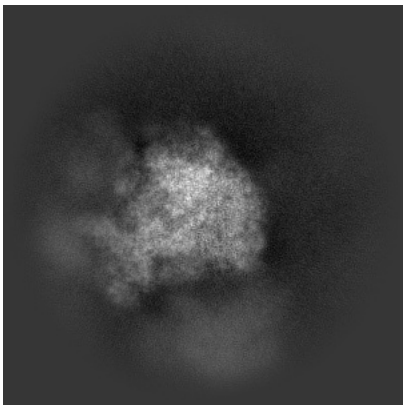
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

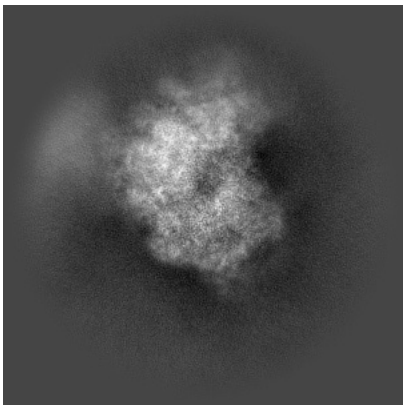
6.1.1 Primary map



X

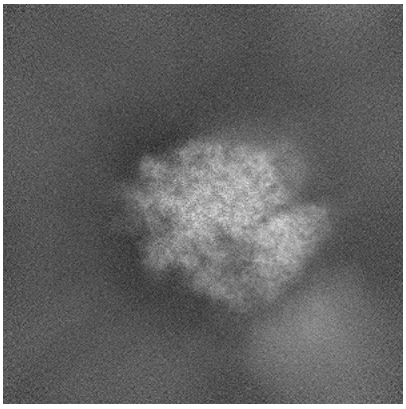


Y

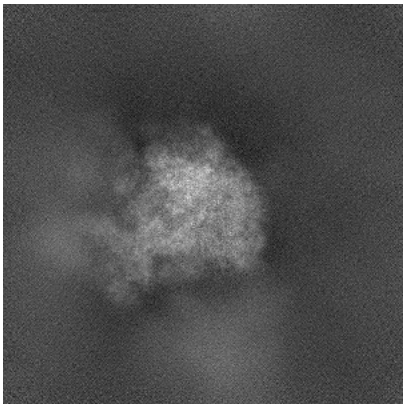


Z

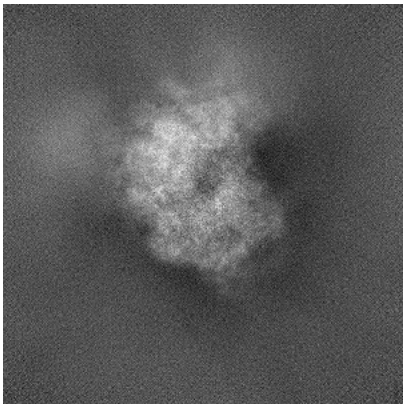
6.1.2 Raw map



X



Y

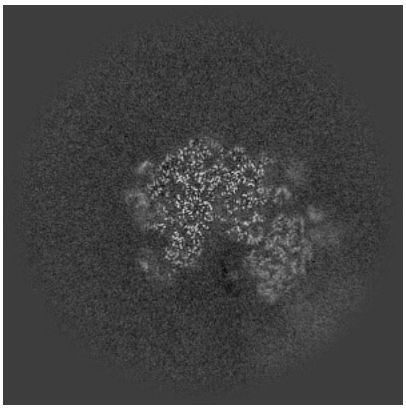


Z

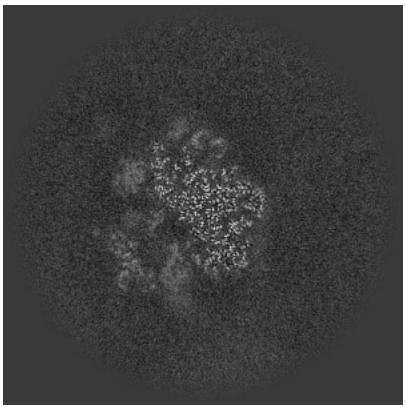
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

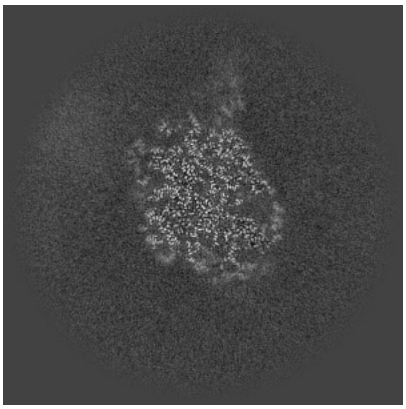
6.2.1 Primary map



X Index: 256

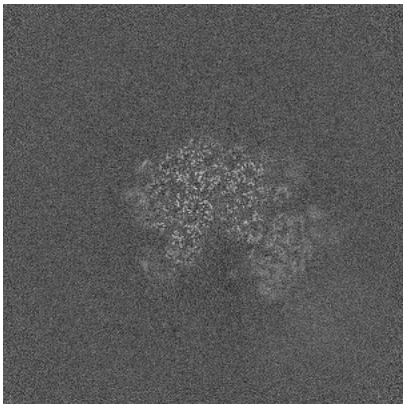


Y Index: 256

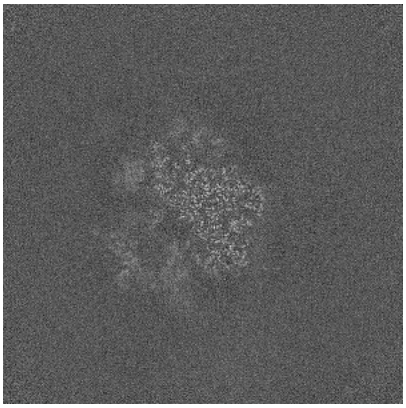


Z Index: 256

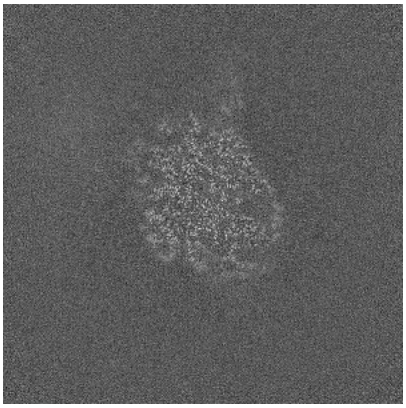
6.2.2 Raw map



X Index: 256



Y Index: 256

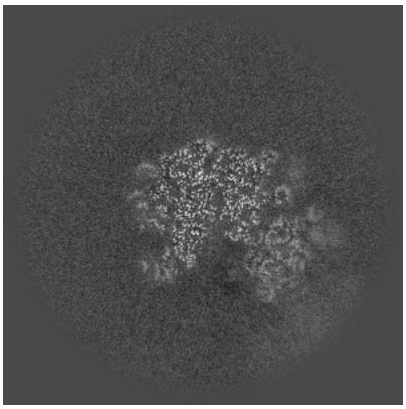


Z Index: 256

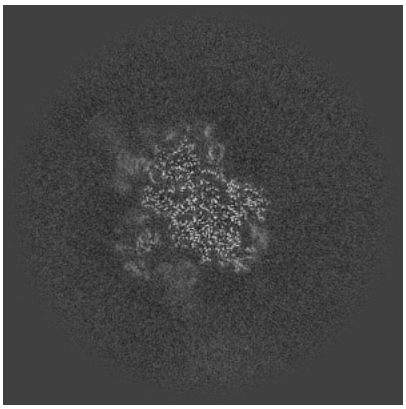
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

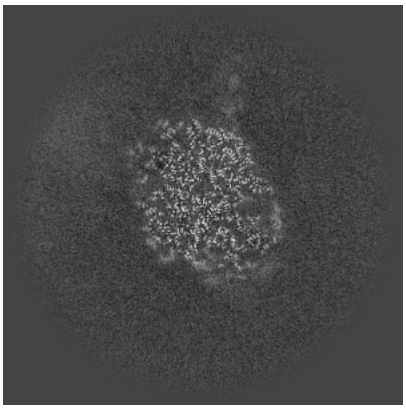
6.3.1 Primary map



X Index: 253

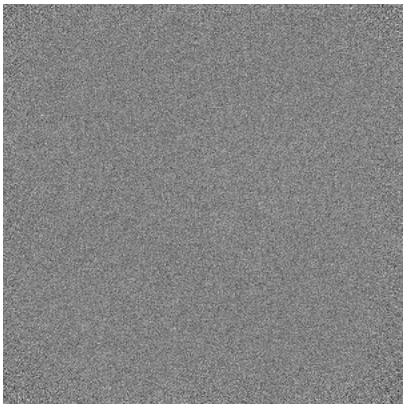


Y Index: 243

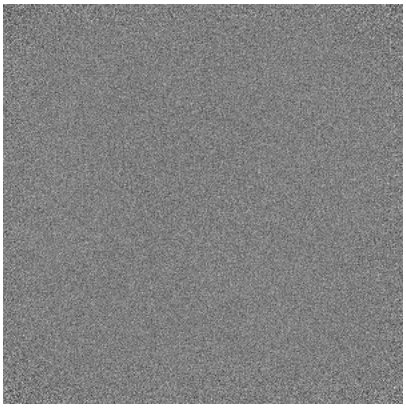


Z Index: 258

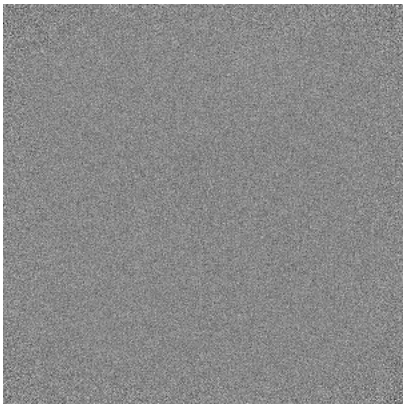
6.3.2 Raw map



X Index: 0



Y Index: 0

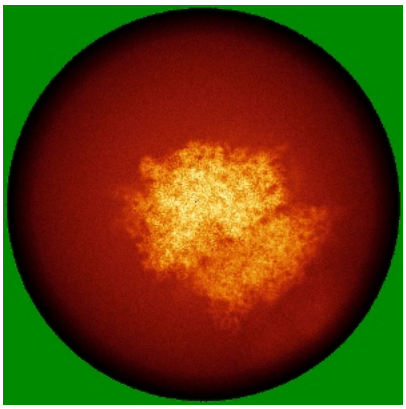


Z Index: 0

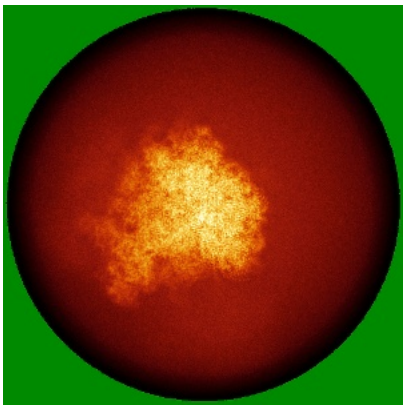
The images above show the largest variance slices of the map in three orthogonal directions.

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

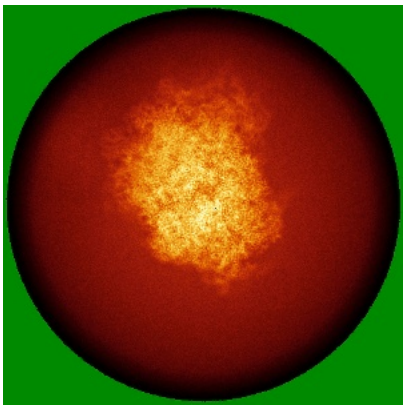
6.4.1 Primary map



X

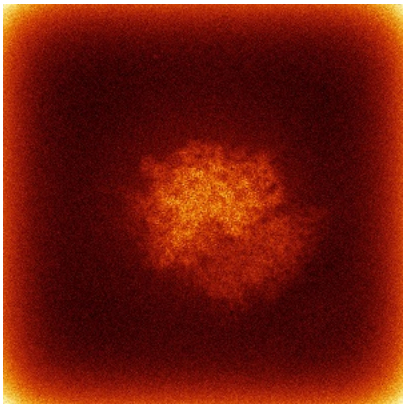


Y

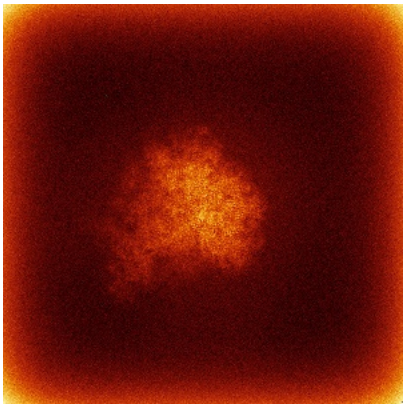


Z

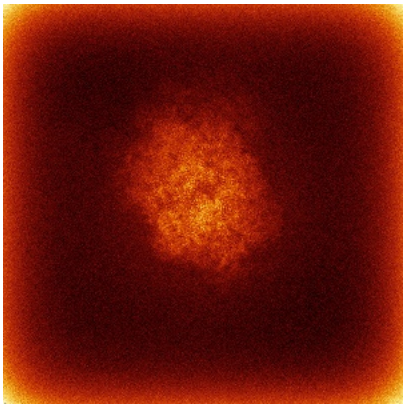
6.4.2 Raw map



X



Y

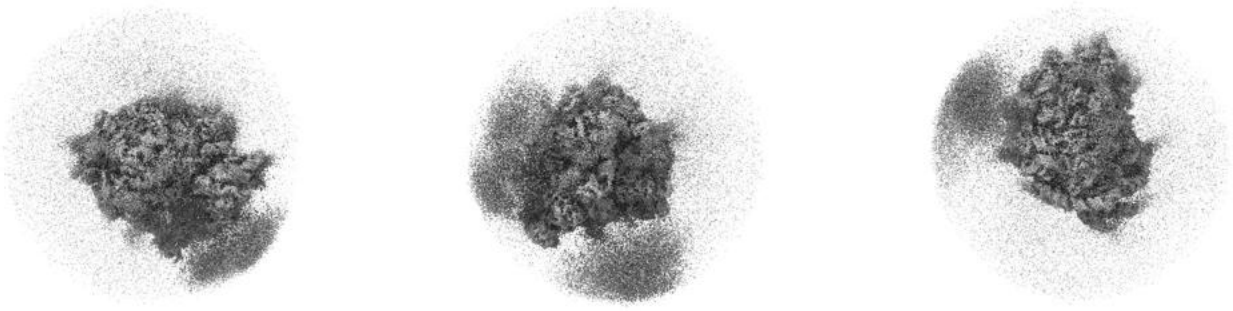


Z

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

6.5 Orthogonal surface views (i)

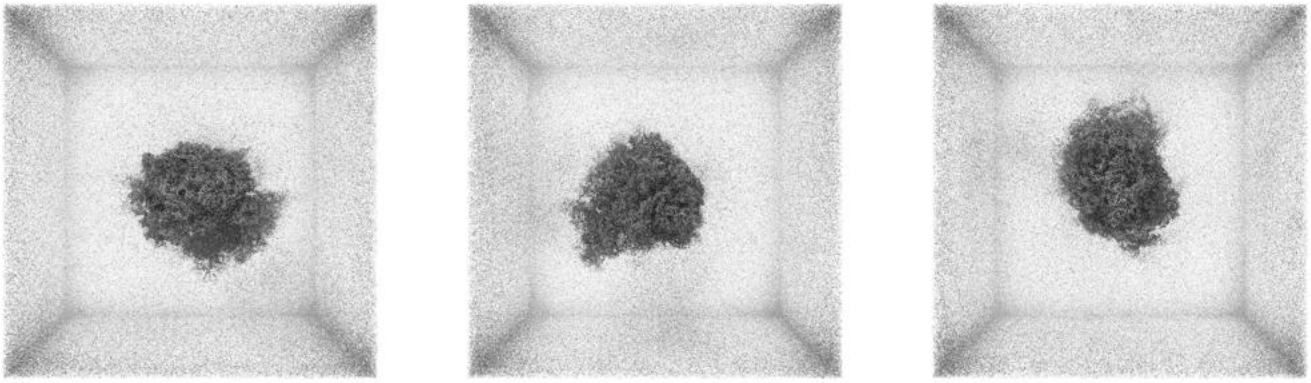
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0182. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

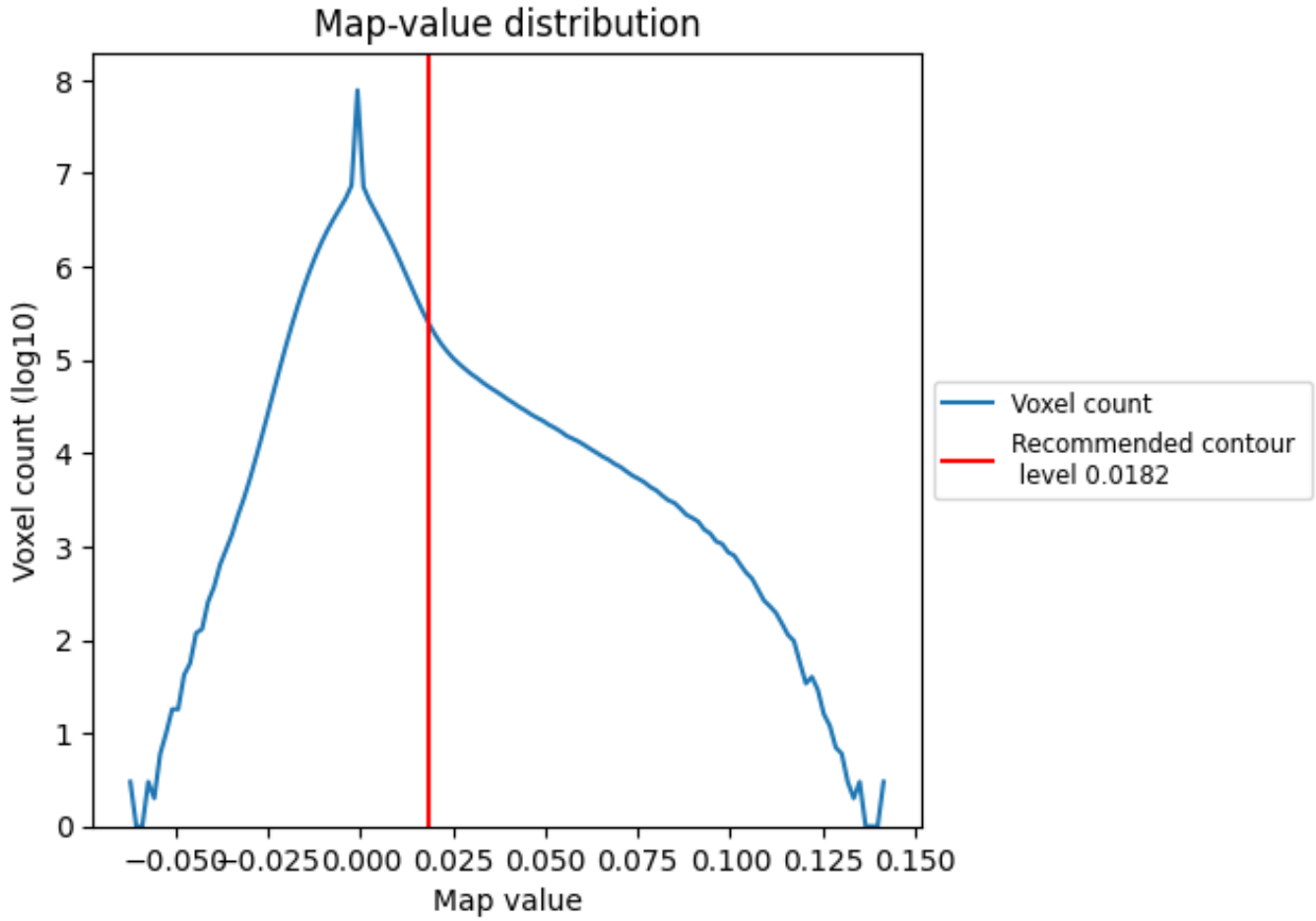
6.6 Mask visualisation (i)

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

7 Map analysis

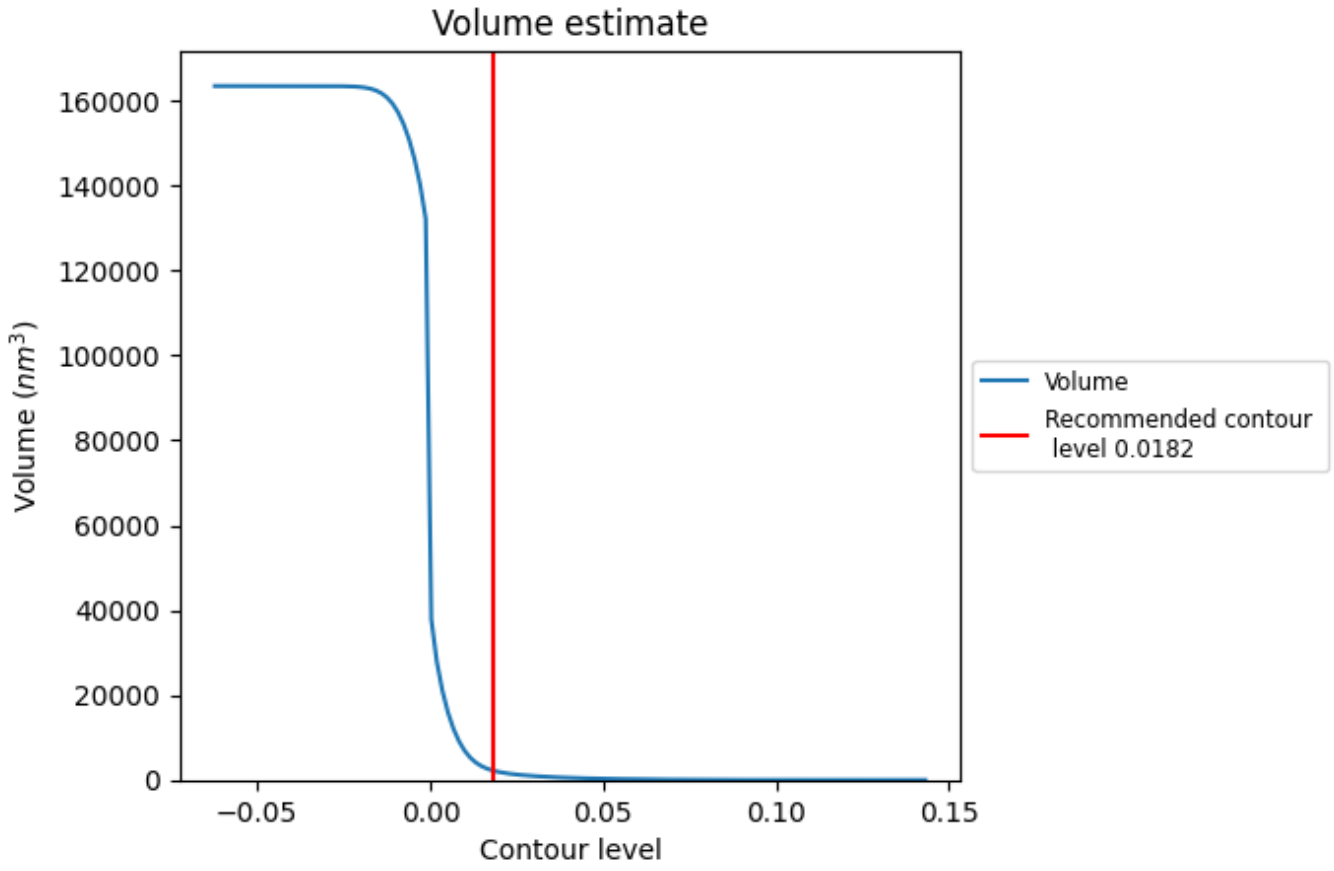
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

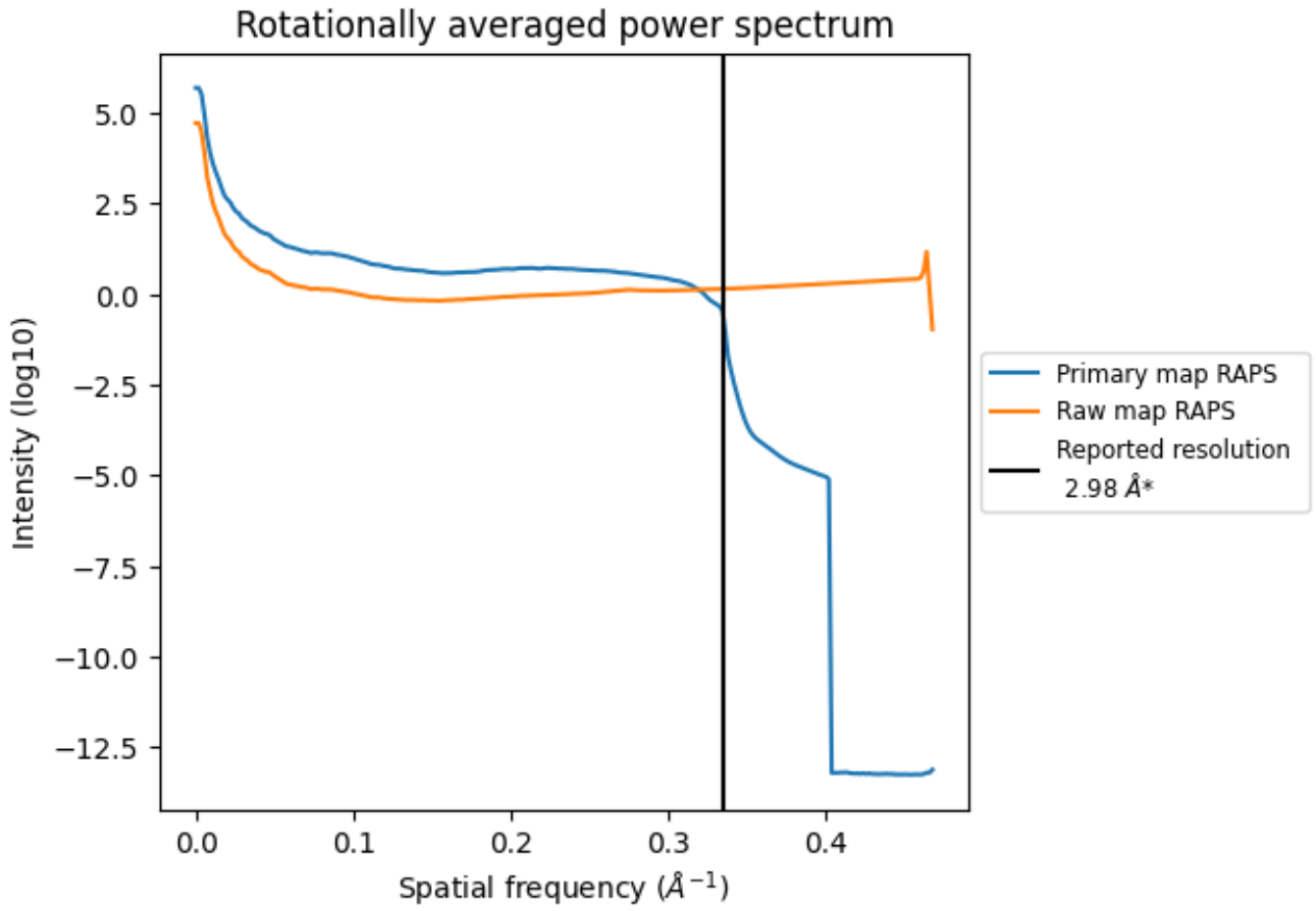
7.2 Volume estimate



The volume at the recommended contour level is 2211 nm^3; this corresponds to an approximate mass of 1998 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)

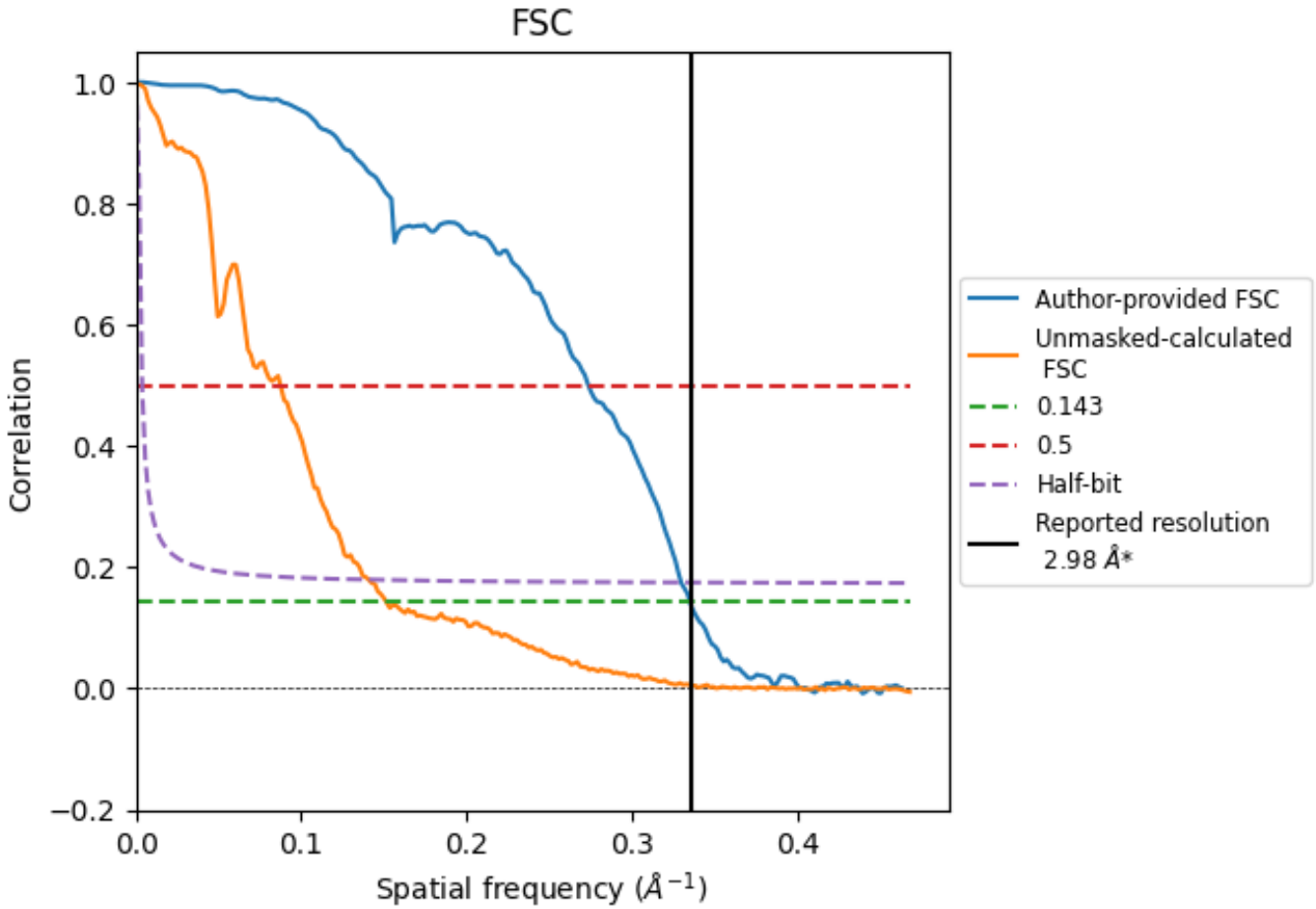


*Reported resolution corresponds to spatial frequency of 0.336 Å^{-1}

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.336 $Å^{-1}$

8.2 Resolution estimates (i)

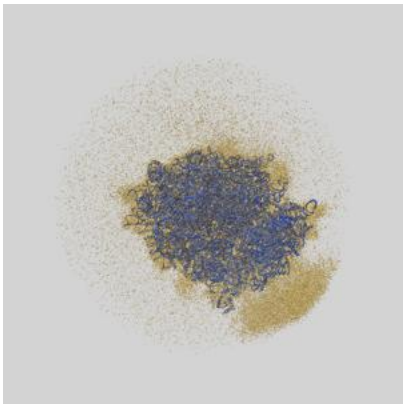
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.98	-	-
Author-provided FSC curve	2.98	3.65	3.03
Unmasked-calculated*	6.61	11.45	7.10

*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 6.61 differs from the reported value 2.98 by more than 10 %

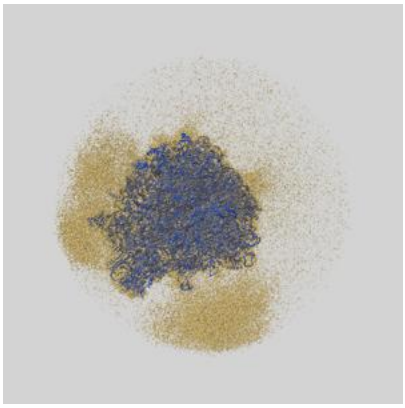
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-44017 and PDB model 9AZN. Per-residue inclusion information can be found in section 3 on page 21.

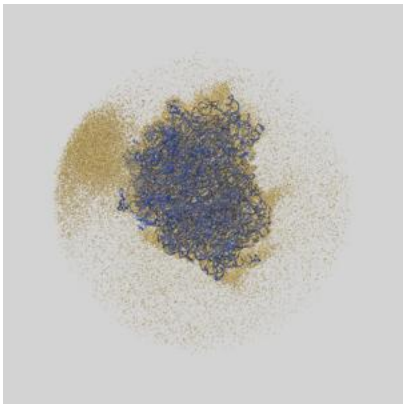
9.1 Map-model overlay



X



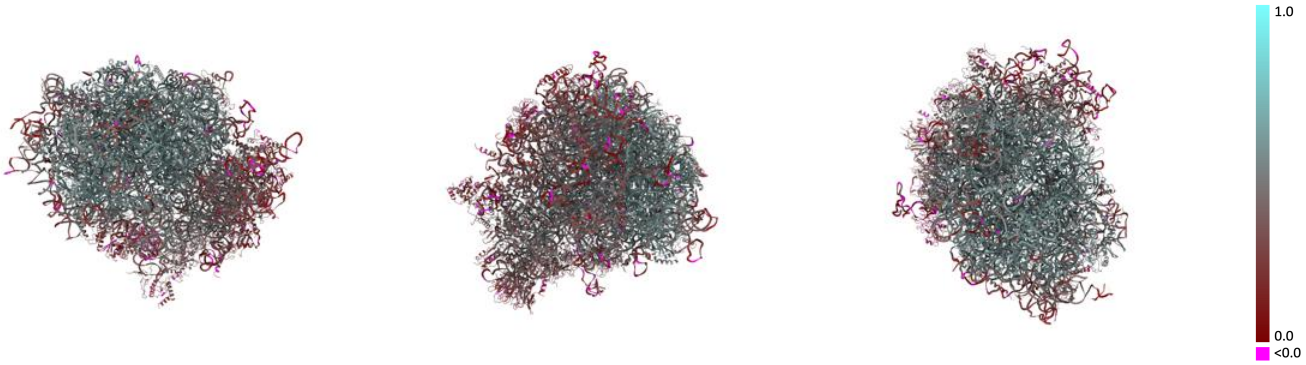
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0182 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

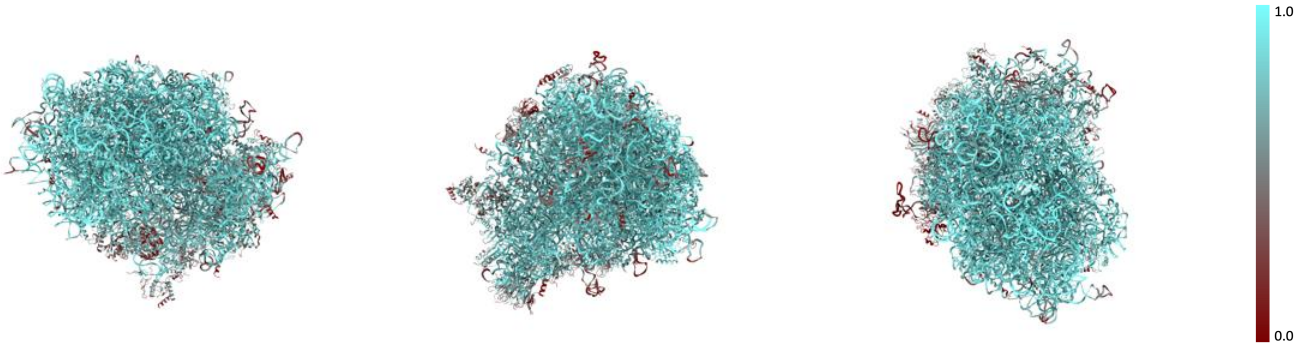
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

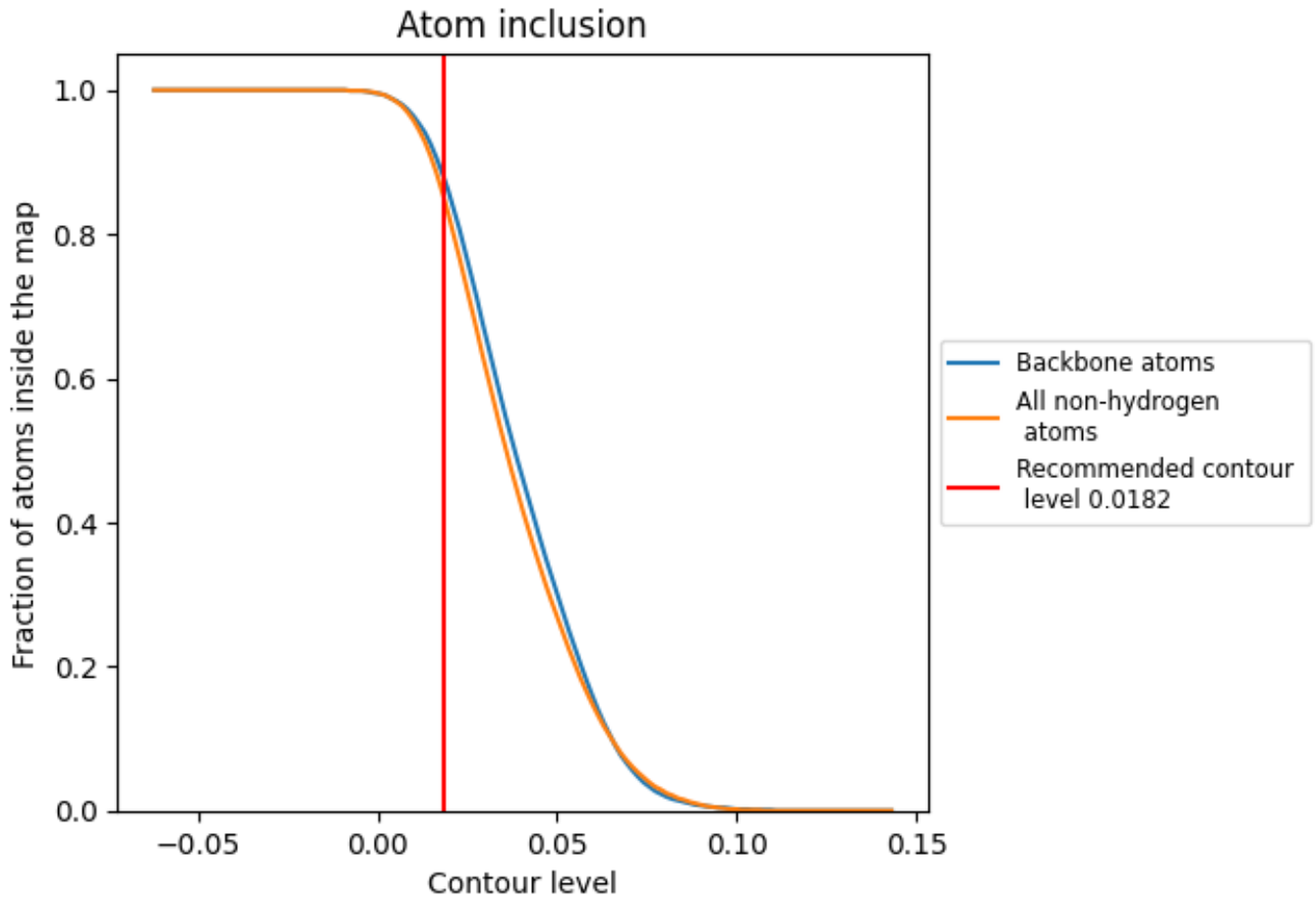
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0182).

9.4 Atom inclusion (i)



At the recommended contour level, 88% of all backbone atoms, 86% 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 (0.0182) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8550	0.4560
AP	0.5670	0.2840
CH	0.4960	0.3070
L5	0.9190	0.4920
L7	0.9810	0.5490
L8	0.9470	0.5240
LA	0.9370	0.5720
LB	0.9020	0.5460
LC	0.9050	0.5520
LD	0.8700	0.5060
LE	0.8260	0.4890
LF	0.9180	0.5560
LG	0.8290	0.4930
LH	0.8800	0.5230
LI	0.9030	0.5510
LJ	0.7830	0.4480
LL	0.8670	0.5260
LM	0.9030	0.5290
LN	0.9600	0.5840
LO	0.9240	0.5600
LP	0.9160	0.5670
LQ	0.9300	0.5750
LR	0.8570	0.5020
LS	0.9250	0.5700
LT	0.8910	0.5430
LU	0.8070	0.4470
LV	0.9050	0.5570
LW	0.6830	0.3910
LX	0.8770	0.5370
LY	0.9080	0.5490
LZ	0.9050	0.5210
La	0.9320	0.5750
Lb	0.8230	0.4690
Lc	0.8550	0.4910
Ld	0.8840	0.5360

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Le	0.9200	0.5710
Lf	0.9510	0.5810
Lg	0.9000	0.5520
Lh	0.8830	0.5420
Li	0.8910	0.5400
Lj	0.9780	0.5780
Lk	0.7950	0.4860
Ll	0.9240	0.5660
Lm	0.9160	0.5420
Ln	0.9040	0.5270
Lo	0.8820	0.5460
Lp	0.9090	0.5520
Lr	0.9170	0.5580
Ls	0.3560	0.2130
Lt	0.2810	0.1440
Lz	0.0990	0.1200
PE	0.7510	0.2590
S2	0.5370	0.1220
S3	0.9040	0.4010
SA	0.7410	0.3910
SB	0.7830	0.4540
SC	0.8080	0.4280
SD	0.7300	0.3710
SE	0.7300	0.3400
SF	0.6890	0.3600
SG	0.6210	0.3070
SH	0.6630	0.3440
SI	0.7350	0.3790
SJ	0.7100	0.3330
SK	0.7180	0.3580
SL	0.7820	0.4250
SM	0.4190	0.2230
SN	0.8390	0.4590
SO	0.7830	0.4480
SP	0.7550	0.4120
SQ	0.7150	0.3760
SR	0.6780	0.3450
SS	0.7550	0.4050
ST	0.7480	0.3800
SU	0.7290	0.3410
SV	0.7600	0.3880
SW	0.8680	0.4700

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
SX	0.7530	0.4290
SY	0.5870	0.2510
SZ	0.5850	0.3060
Sa	0.8340	0.4710
Sb	0.7530	0.4030
Sc	0.6320	0.3070
Sd	0.8800	0.4270
Se	0.6400	0.3170
Sf	0.4730	0.2350
Sg	0.5750	0.2800