



wwPDB EM Validation Summary Report ⓘ

Apr 21, 2025 – 05:35 PM EDT

PDB ID : 9B0W / pdb_00009b0w
EMDB ID : EMD-44060
Title : In situ human eEF2-A/P-P/E state 80S ribosome
Authors : Wei, Z.; Yong, Z.
Deposited on : 2024-03-12
Resolution : 2.66 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

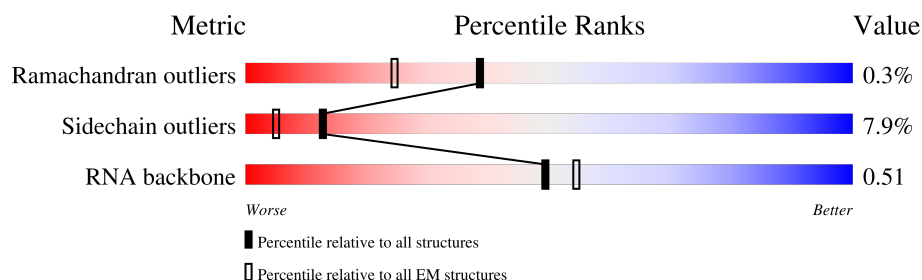
EMDB validation analysis : 0.0.1.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) :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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.66 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	Se	58	
2	CH	132	
3	LW	118	
4	SE	262	
5	SI	206	
6	SL	153	
7	SX	141	
8	SG	237	

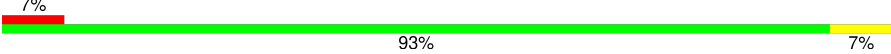
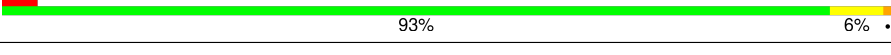
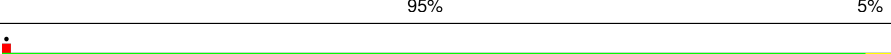

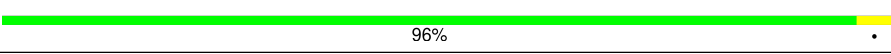
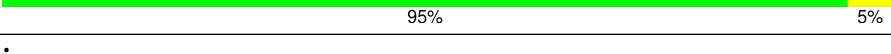
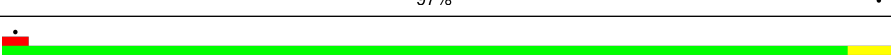

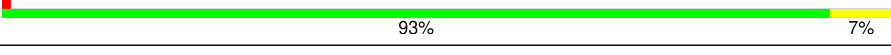
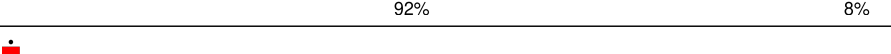
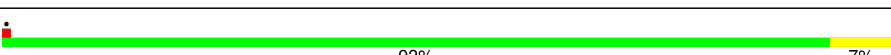
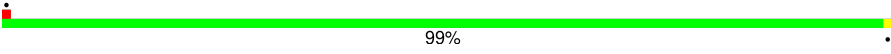
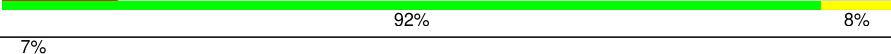
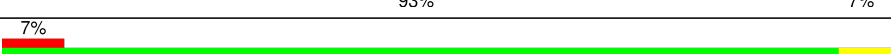
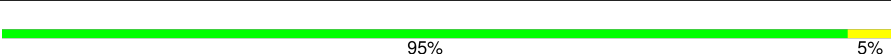
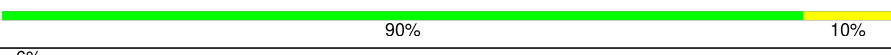
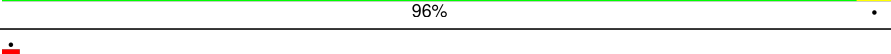
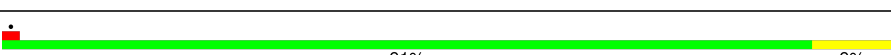

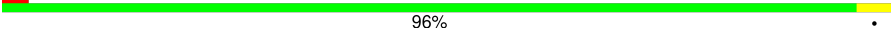



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Mol	Chain	Length	Quality of chain
9	SJ	185	
10	SY	131	
11	SA	221	
12	SB	214	
13	SH	186	
14	SV	83	
15	Sa	102	
16	SC	222	
17	SN	150	
18	SO	140	
19	SW	129	
20	Sb	83	
21	L5	3740	
22	L7	120	
23	L8	156	
24	LA	248	
25	LB	402	
26	LC	368	
27	LD	293	
28	LE	236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

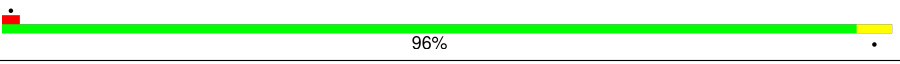
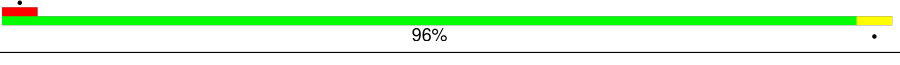

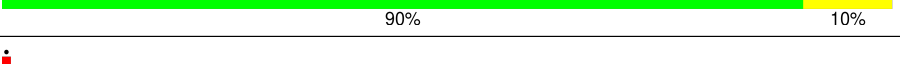
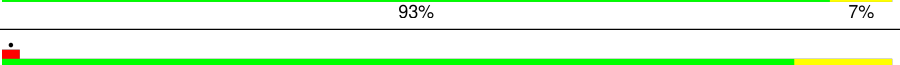
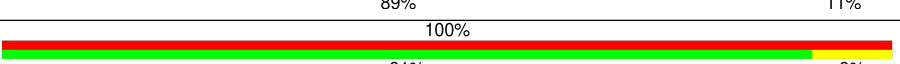
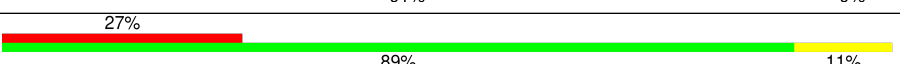
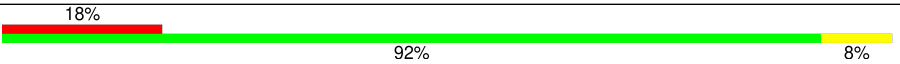
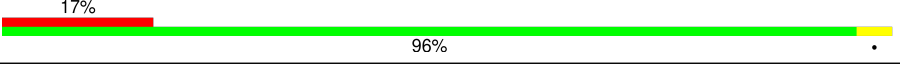

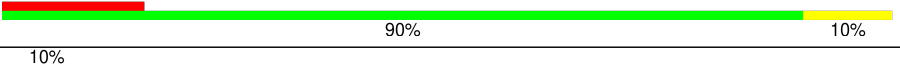
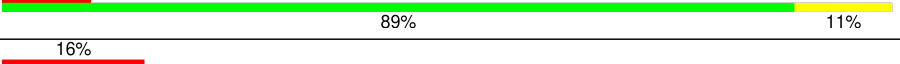
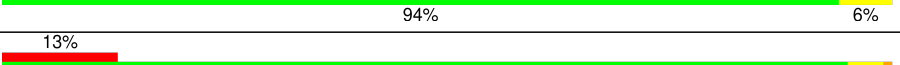
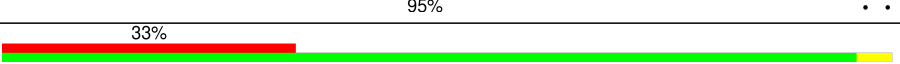
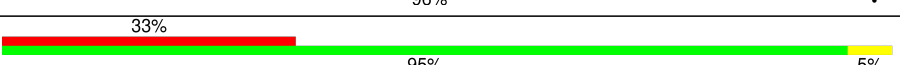


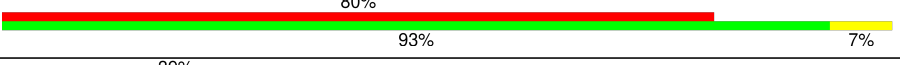
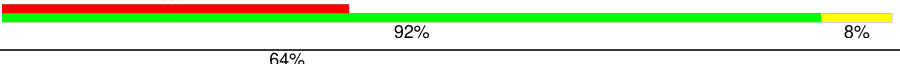
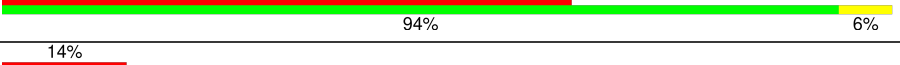


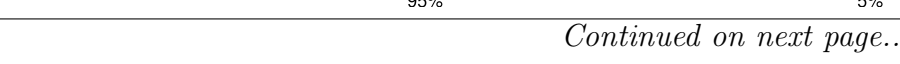


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Mol	Chain	Length	Quality of chain
34	LL	210	
35	LM	139	
36	LN	203	
37	LO	201	
38	LP	153	
39	LQ	187	
40	LR	187	
41	LS	175	
42	LT	159	
43	LU	101	
44	LV	131	
45	LX	120	
46	LY	134	
47	LZ	135	
48	La	147	
49	Lb	109	
50	Lc	98	
51	Ld	107	
52	Le	128	
53	Lf	109	
54	Lg	114	
55	Lh	122	
56	Li	102	
57	Lj	86	
58	Lk	69	

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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	

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Mol	Chain	Length	Quality of chain
84	Lt	141	<div><div></div><div>95%</div><div></div><div>94%</div><div>6%</div><div></div></div>
85	CB	846	<div><div></div><div>32%</div><div></div><div>92%</div><div>8%</div><div></div></div>
86	S2	1740	<div><div></div><div>10%</div><div></div><div>74%</div><div>25%</div><div></div></div>

2 Entry composition [i](#)

There are 88 unique types of molecules in this entry. The entry contains 230194 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 Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Se	47	Total	C	N	O	S	0	0
			378	234	84	59	1		

- Molecule 2 is a protein called Endothelial differentiation-related factor 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	CH	132	Total	C	N	O	0	0
			1018	625	199	194		

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

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

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

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

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

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

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

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

- 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.

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.

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	C	N	O	S	0	0
			876	546	189	137	4		

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

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

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

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

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

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

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

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

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

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

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

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

- 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 protein called eEF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	CB	846	Total	C	N	O	S	0	0
			6605	4193	1136	1232	44		

- Molecule 86 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	S2	1740	Total	C	N	O	P	0	0
			36898	16459	6599	12101	1739		

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 88 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
88	L5	211	Total	Mg	0
			211	211	
88	L7	3	Total	Mg	0
			3	3	
88	L8	4	Total	Mg	0
			4	4	

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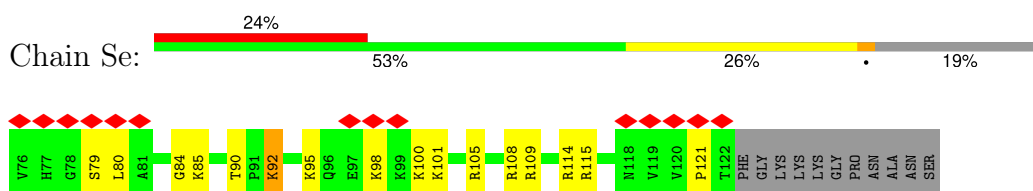
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Mol	Chain	Residues	Atoms		AltConf
88	LA	1	Total 1	Mg 1	0
88	LB	1	Total 1	Mg 1	0
88	LI	1	Total 1	Mg 1	0
88	LP	1	Total 1	Mg 1	0
88	LV	1	Total 1	Mg 1	0
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88	Lg	1	Total 1	Mg 1	0
88	S2	30	Total 30	Mg 30	0

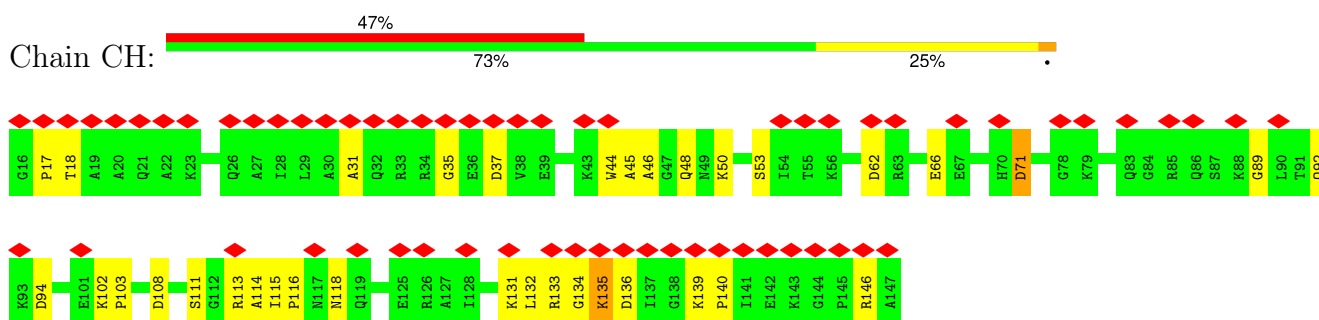
3 Residue-property plots

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

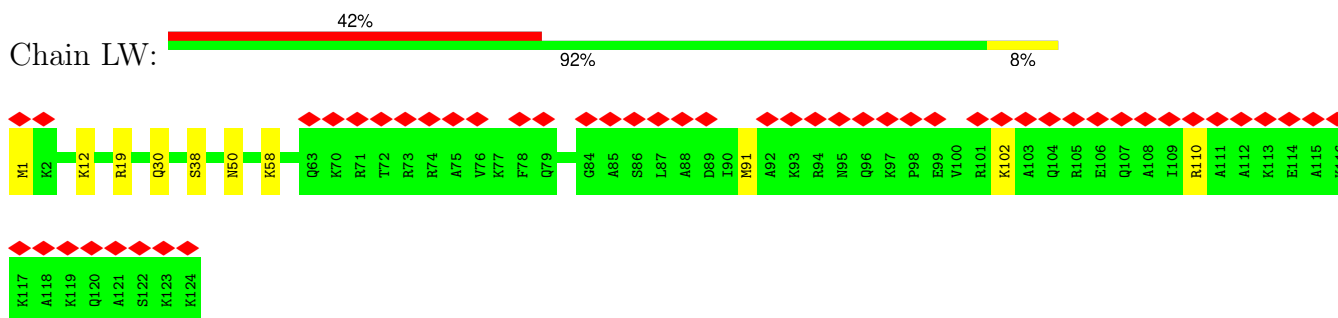
- Molecule 1: Small ribosomal subunit protein eS30



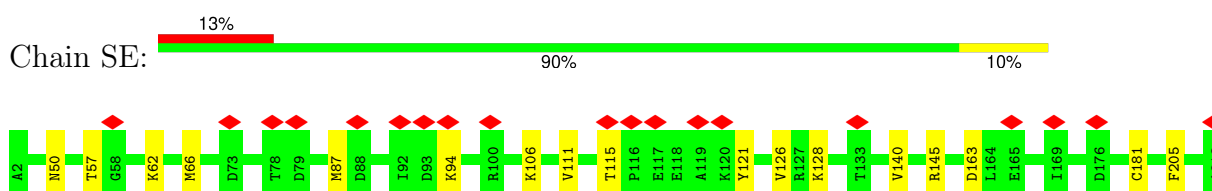
- Molecule 2: Endothelial differentiation-related factor 1

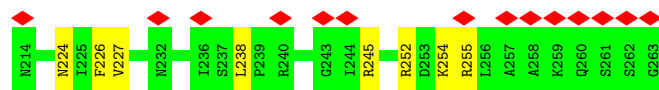


- Molecule 3: 60S ribosomal protein L24

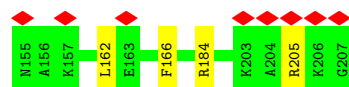
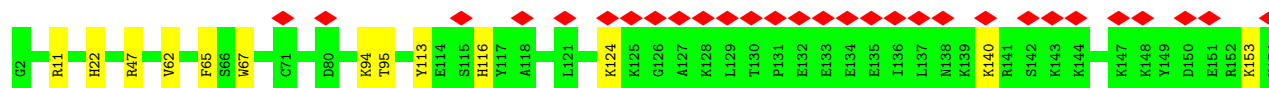
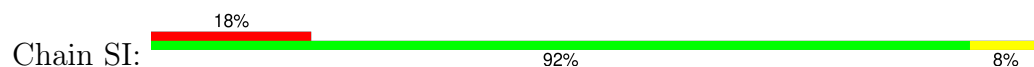


- Molecule 4: Small ribosomal subunit protein eS4, X isoform

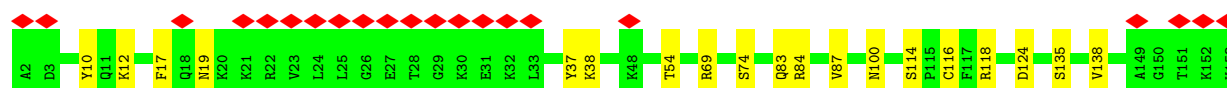
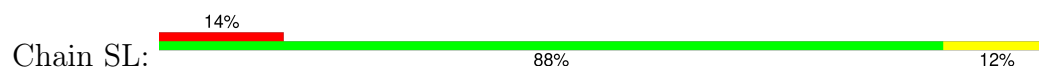




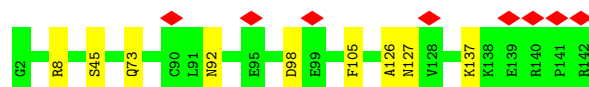
- Molecule 5: 40S ribosomal protein S8



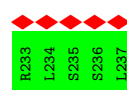
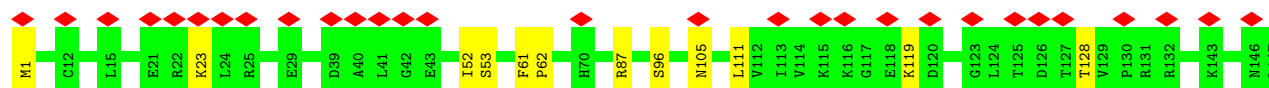
- Molecule 6: 40S ribosomal protein S11



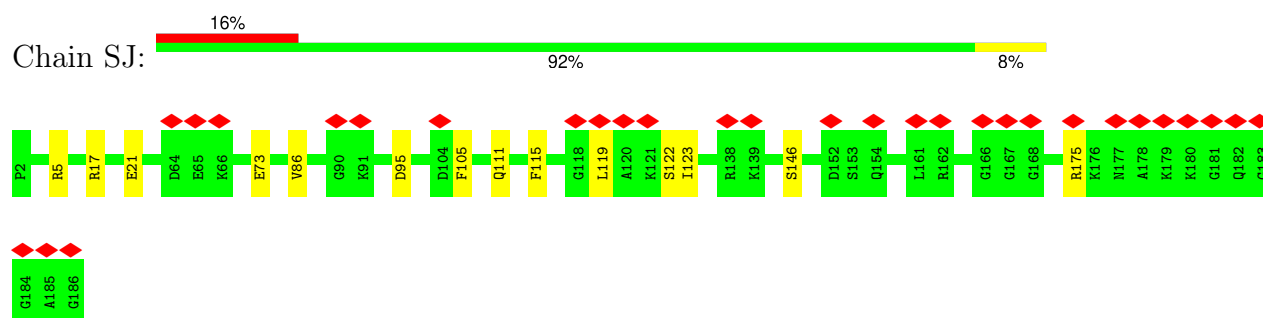
- Molecule 7: 40S ribosomal protein S23



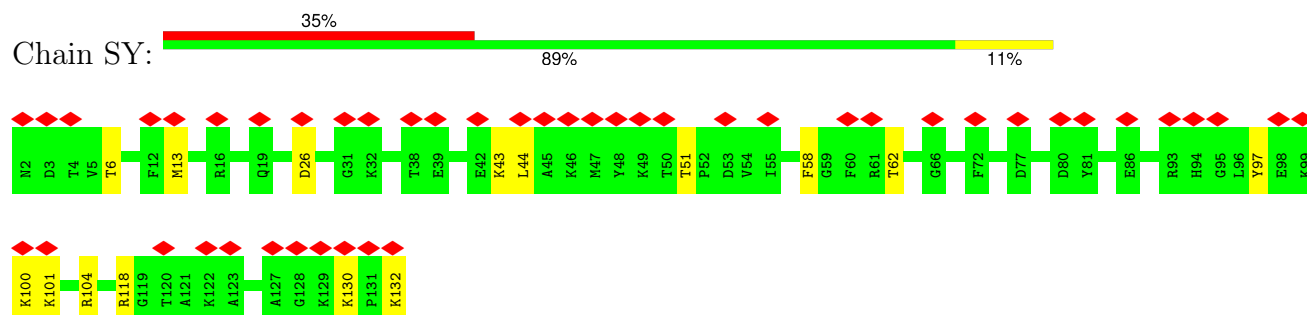
- Molecule 8: 40S ribosomal protein S6



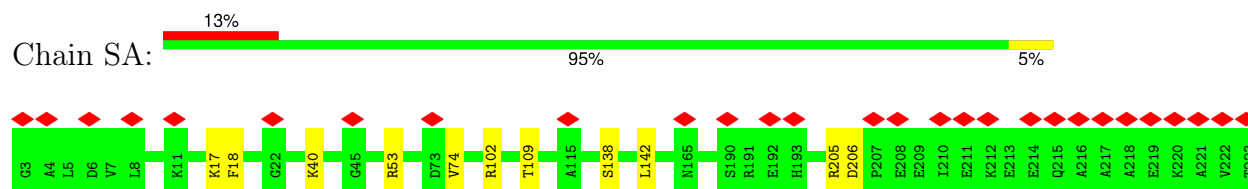
- Molecule 9: 40S ribosomal protein S9



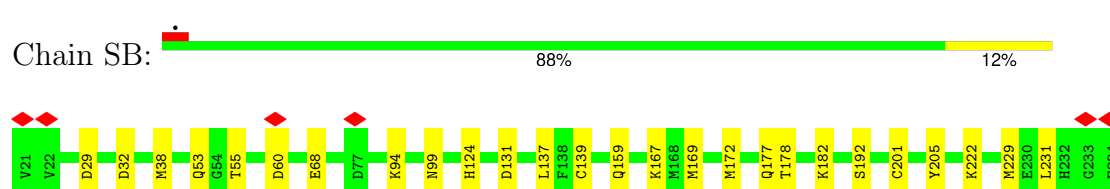
- Molecule 10: 40S ribosomal protein S24



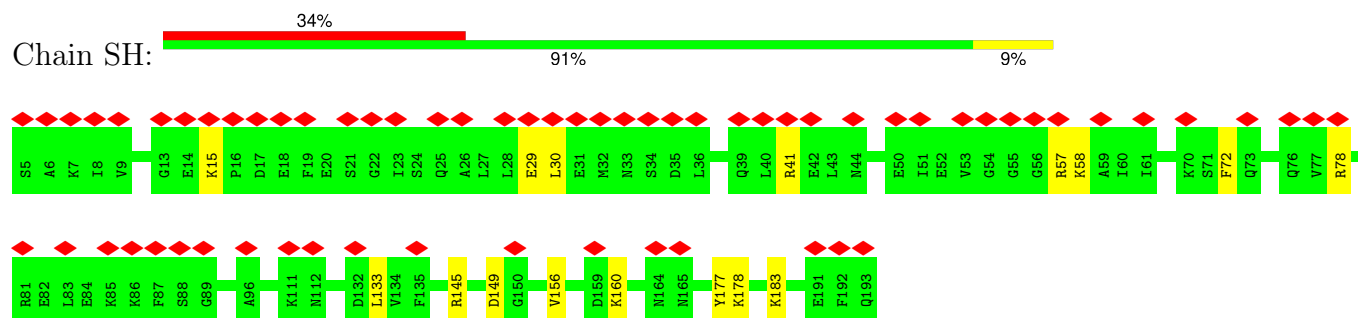
- Molecule 11: 40S ribosomal protein SA



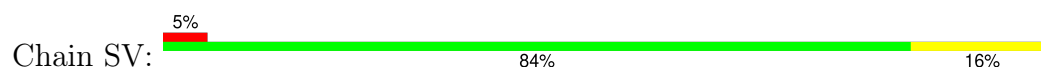
- Molecule 12: 40S ribosomal protein S3a

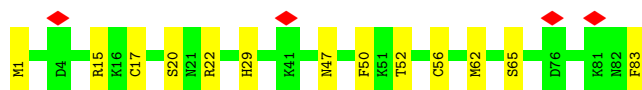


- Molecule 13: 40S ribosomal protein S7



- Molecule 14: 40S ribosomal protein S21





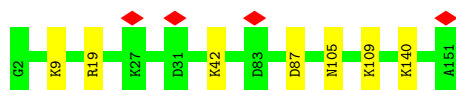
- Molecule 15: 40S ribosomal protein S26



- Molecule 16: 40S ribosomal protein S2



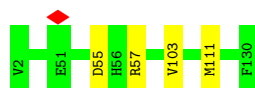
- Molecule 17: 40S ribosomal protein S13



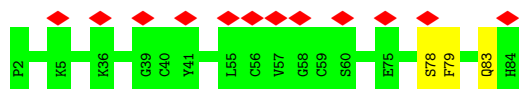
- Molecule 18: Small ribosomal subunit protein uS11



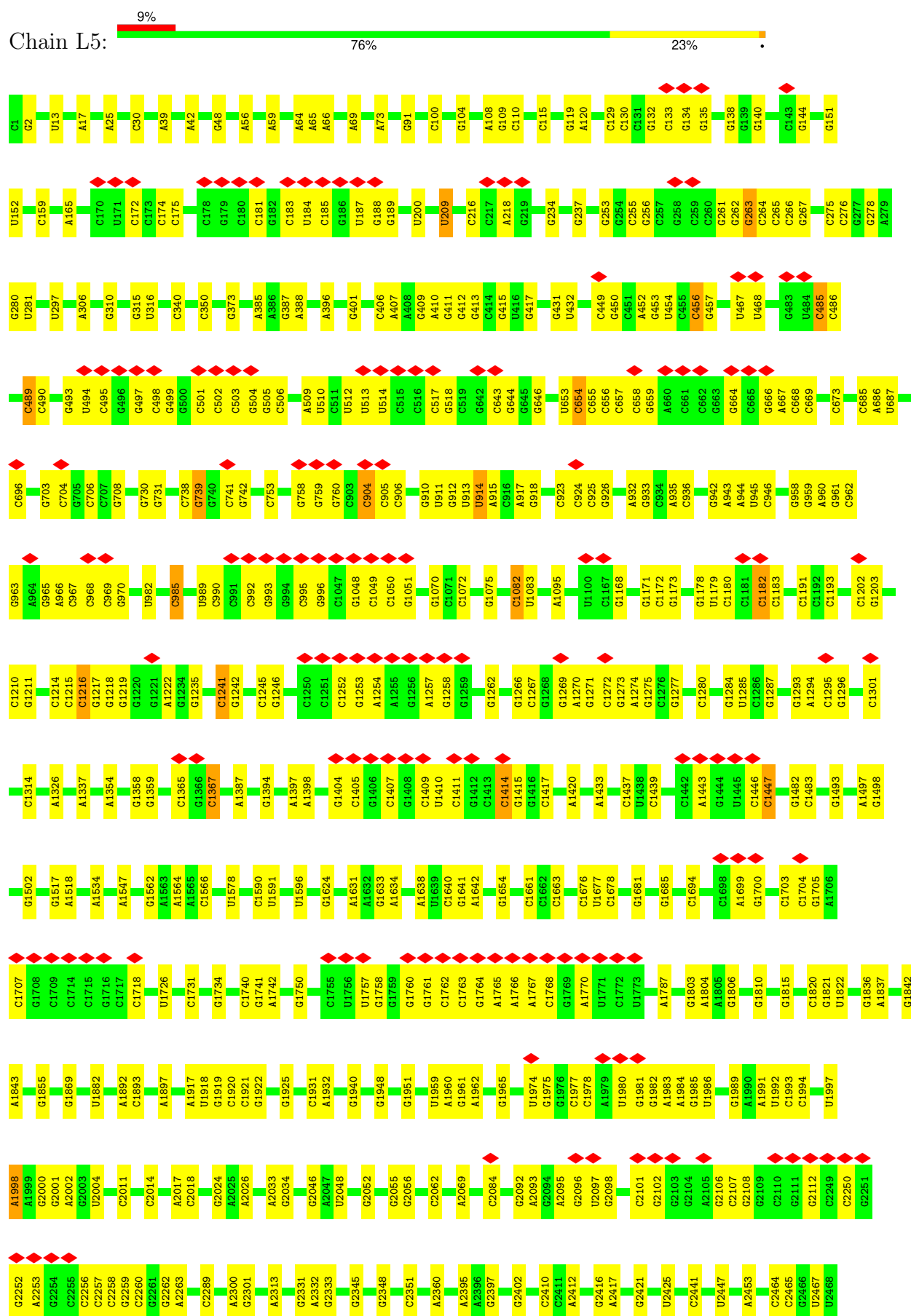
- Molecule 19: 40S ribosomal protein S15a

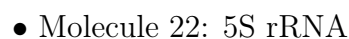


- Molecule 20: Small ribosomal subunit protein eS27



- Molecule 21: 28S rRNA

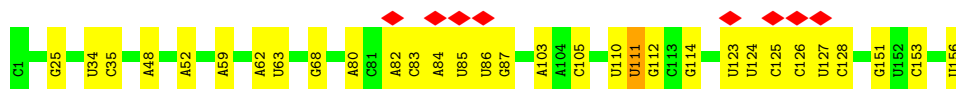
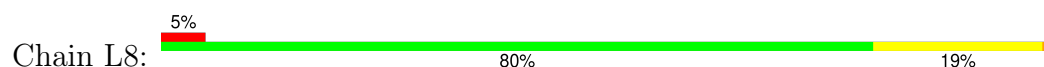




Response	Percentage
Doing a good job	91%
Not doing a good job	9%



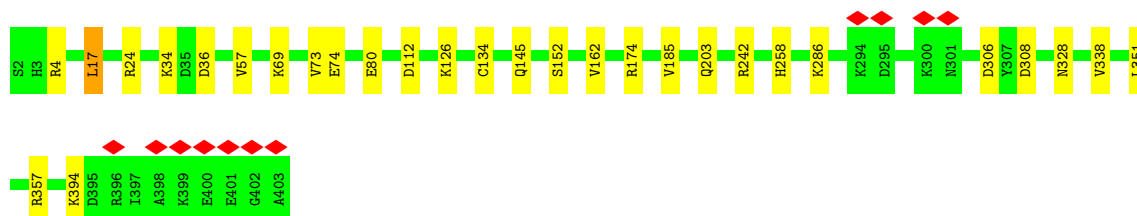
- Molecule 23: 5.8S rRNA



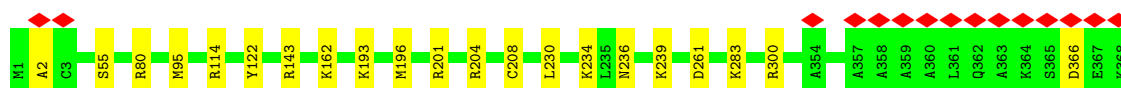
- Molecule 24: 60S ribosomal protein L8



- Molecule 25: Large ribosomal subunit protein uL3



- Molecule 26: 60S ribosomal protein L4

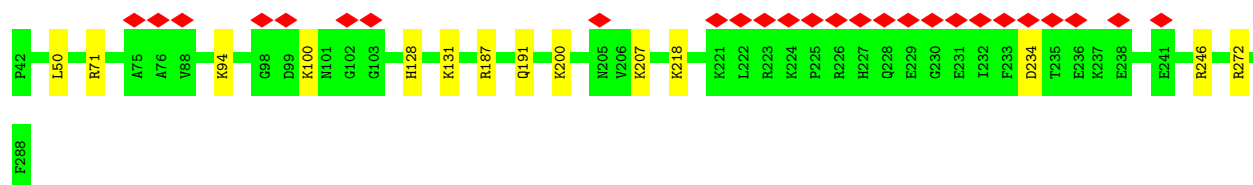


- Molecule 27: Large ribosomal subunit protein uL18



- Molecule 28: 60S ribosomal protein L6





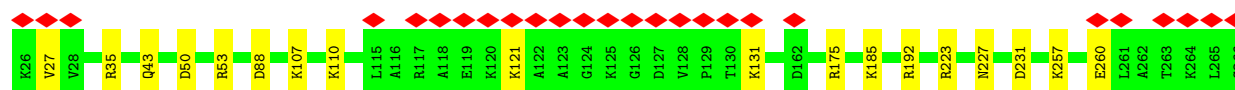
- Molecule 29: 60S ribosomal protein L7

Chain LF: 96%



- Molecule 30: 60S ribosomal protein L7a

Chain LG: 93% 7%



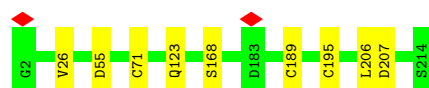
- Molecule 31: 60S ribosomal protein L9

Chain LH: 96%



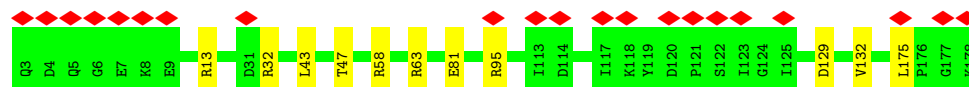
- Molecule 32: 60S ribosomal protein L10-like

Chain LI: 96%



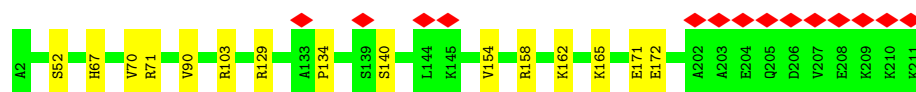
- Molecule 33: 60S ribosomal protein L11

Chain LJ: 94% 6%

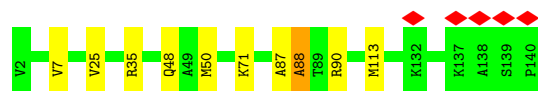


- Molecule 34: Large ribosomal subunit protein eL13

Chain LL: 93% 7%



- Molecule 35: 60S ribosomal protein L14



- Molecule 36: 60S ribosomal protein L15



- Molecule 37: 60S ribosomal protein L13a



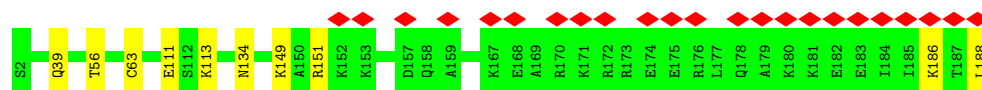
- Molecule 38: 60S ribosomal protein L17



- Molecule 39: 60S ribosomal protein L18



- Molecule 40: 60S ribosomal protein L19



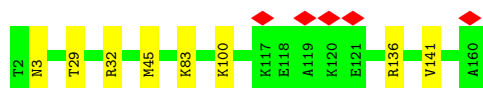
- Molecule 41: 60S ribosomal protein L18a

Chain LS:  97%




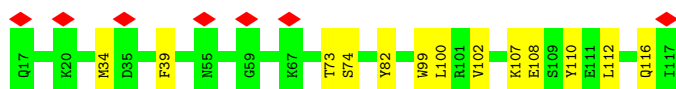
- Molecule 42: 60S ribosomal protein L21

Chain LT:  95%



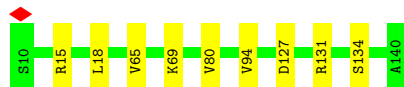
- Molecule 43: Heparin-binding protein HBp15

Chain LU:  87%



- Molecule 44: 60S ribosomal protein L23

Chain LV:  93%



- Molecule 45: 60S ribosomal protein L23a

Chain LX:  92%



- Molecule 46: 60S ribosomal protein L26

Chain LY:  96%



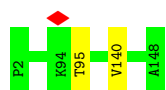
- Molecule 47: 60S ribosomal protein L27

Chain LZ:  93%



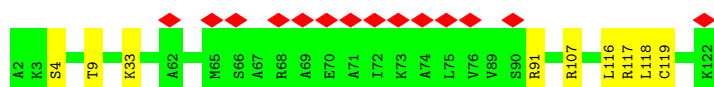
- Molecule 48: 60S ribosomal protein L27a

Chain La:  99%



- Molecule 49: 60S ribosomal protein L29

Chain Lb:  13% 92% 8%



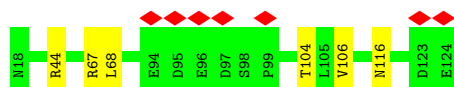
- Molecule 50: 60S ribosomal protein L30

Chain Lc:  7% 93% 7%



- Molecule 51: 60S ribosomal protein L31

Chain Ld:  7% 94% 6%



- Molecule 52: 60S ribosomal protein L32

Chain Le:  95% 5%



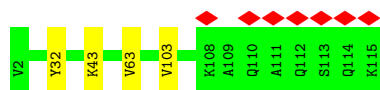
- Molecule 53: 60S ribosomal protein L35a

Chain Lf:  90% 10%



- Molecule 54: 60S ribosomal protein L34

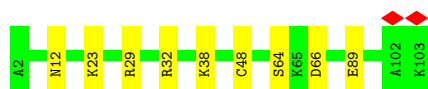
Chain Lg:  6% 96%



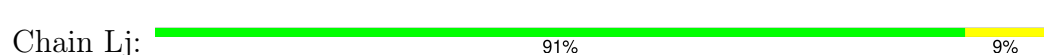
- Molecule 55: 60S ribosomal protein L35



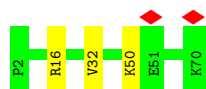
- Molecule 56: 60S ribosomal protein L36



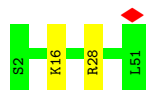
- Molecule 57: 60S ribosomal protein L37



- Molecule 58: 60S ribosomal protein L38




- Molecule 59: 60S ribosomal protein L39



- Molecule 60: Large ribosomal subunit protein eL40




- Molecule 61: 60S ribosomal protein L41

Chain Ln:  83% 17%



- Molecule 62: 60S ribosomal protein L36a

Chain Lo:  90% 10%




- Molecule 63: 60S ribosomal protein L37a

Chain Lp:  93% 7%



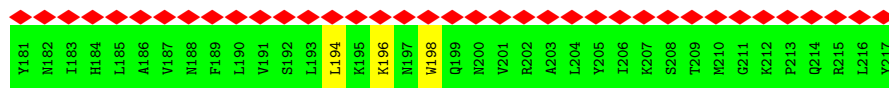
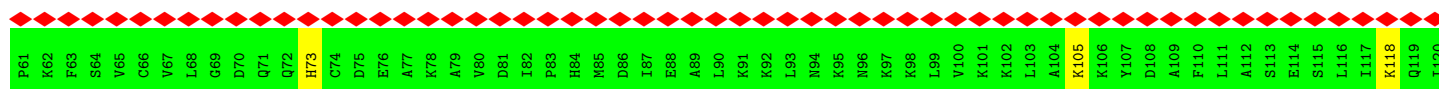
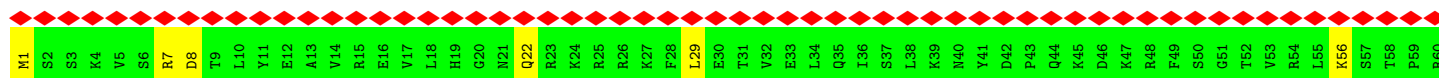
- Molecule 64: 60S ribosomal protein L28

Chain Lr:  89% 11%



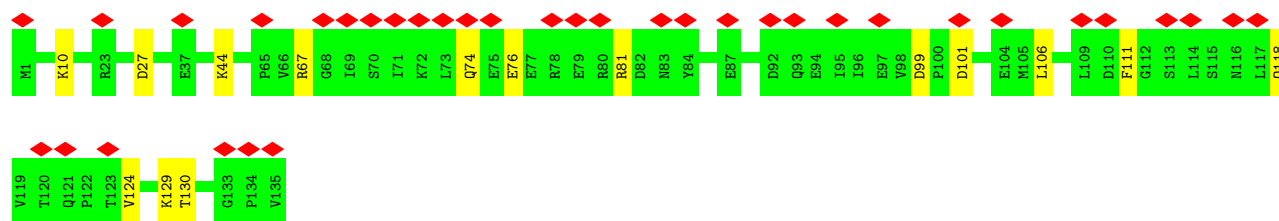
- Molecule 65: 60S ribosomal protein L10a

Chain Lz:  91% 9% 100%

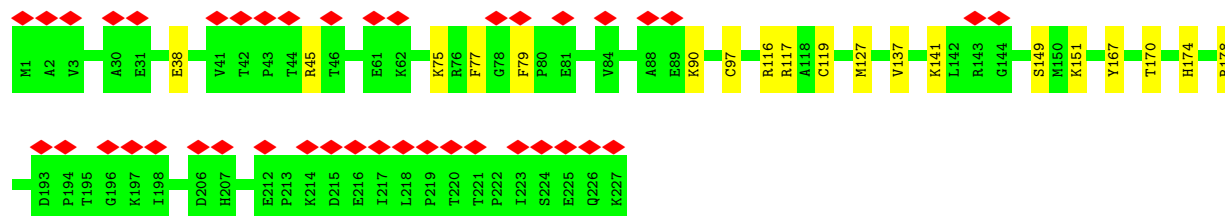


- Molecule 66: 40S ribosomal protein S17

Chain SR:  27% 89% 11%



- Molecule 67: Small ribosomal subunit protein uS3



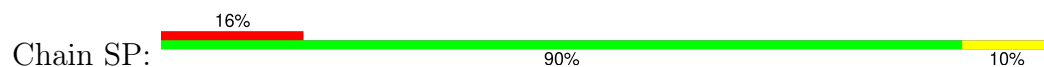
- Molecule 68: 40S ribosomal protein S5



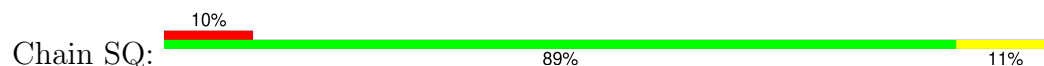
- Molecule 69: 40S ribosomal protein S10



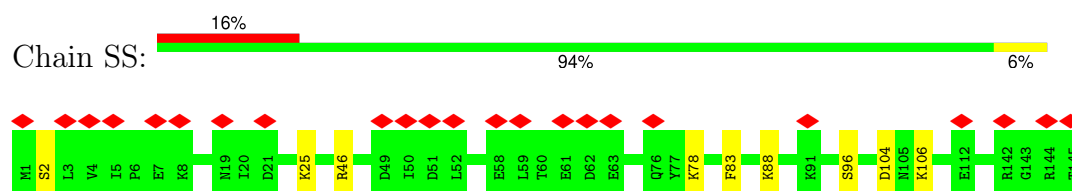
- Molecule 70: Small ribosomal subunit protein uS19



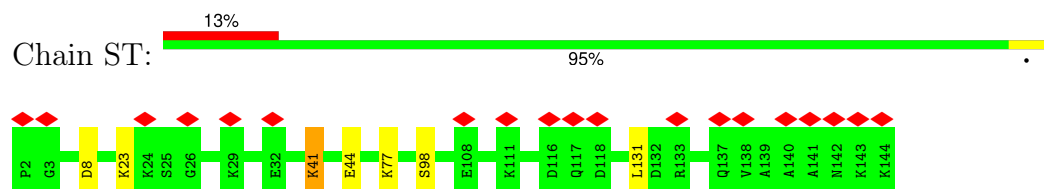
- Molecule 71: Small ribosomal subunit protein uS9



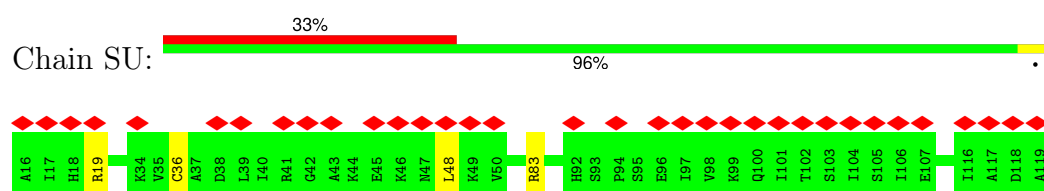
- Molecule 72: 40S ribosomal protein S18



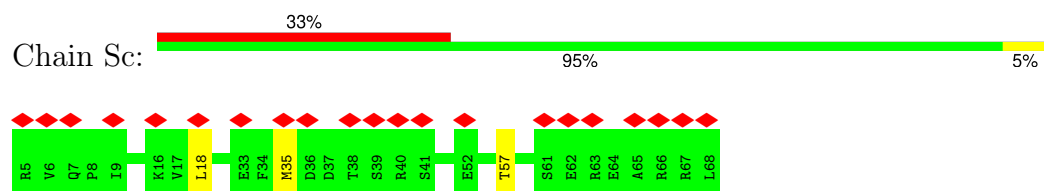
• Molecule 73: 40S ribosomal protein S19



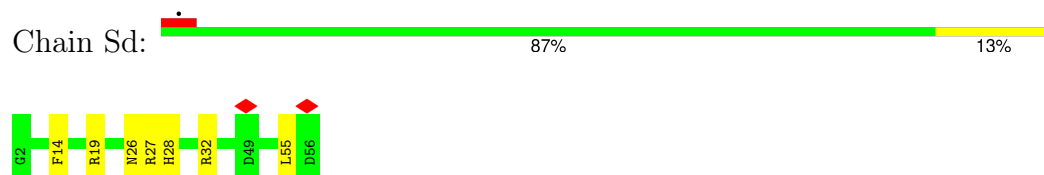
• Molecule 74: 40S ribosomal protein S20



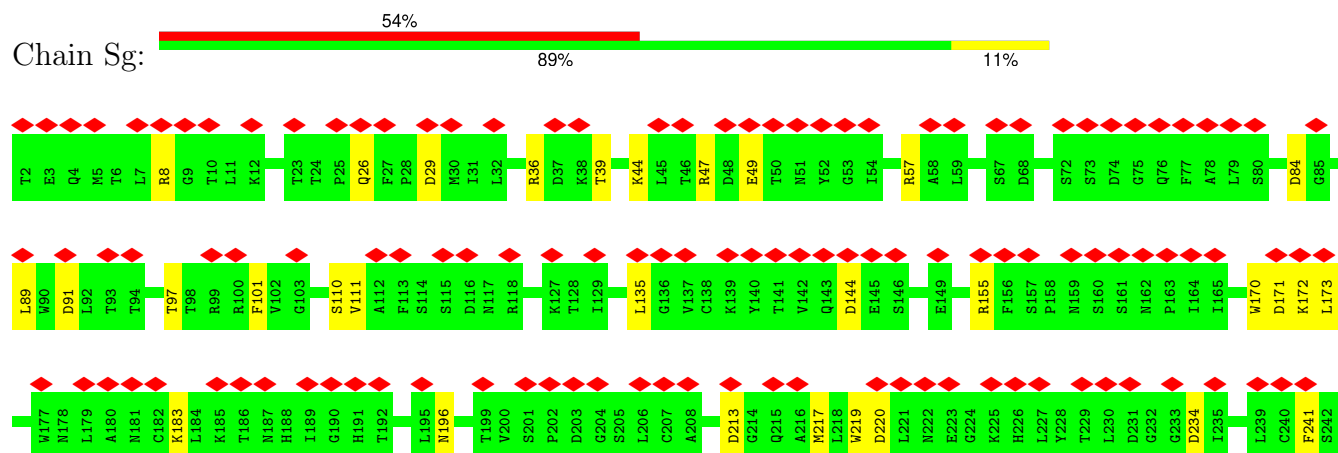
• Molecule 75: 40S ribosomal protein S28

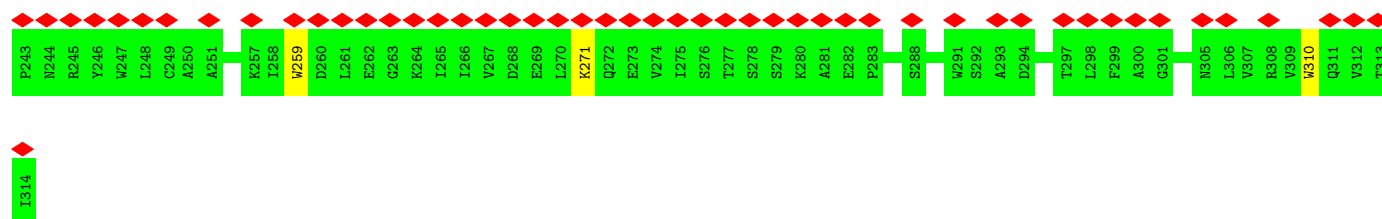


• Molecule 76: 40S ribosomal protein S29

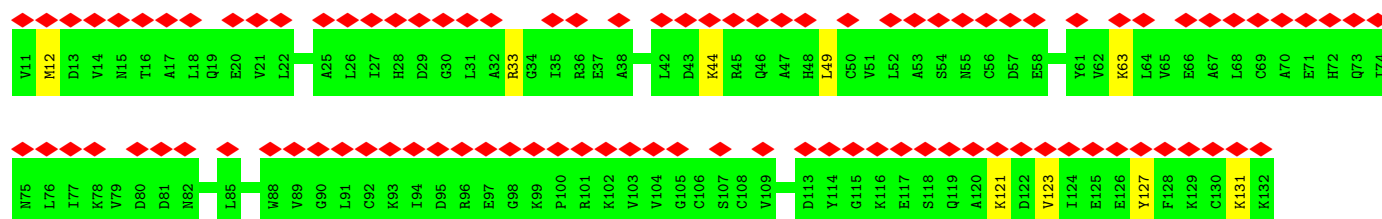
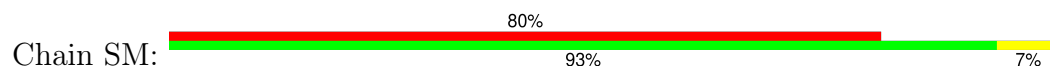


• Molecule 77: Receptor of activated protein C kinase 1

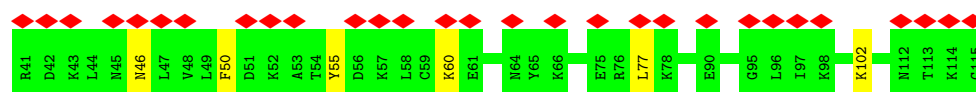
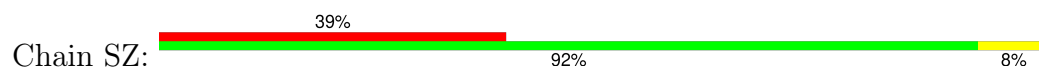




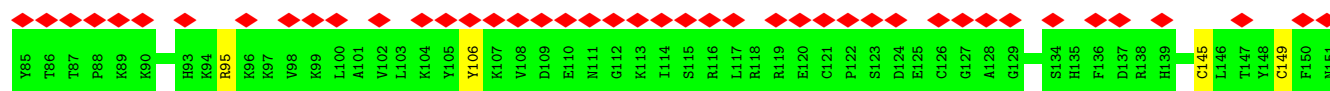
- Molecule 78: Small ribosomal subunit protein eS12



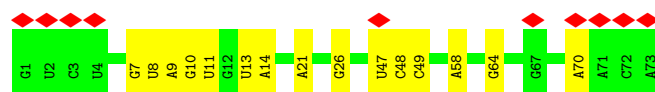
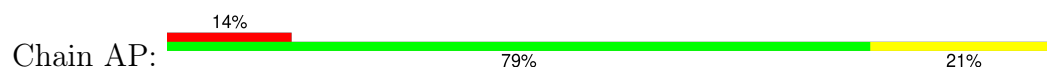
- Molecule 79: Small ribosomal subunit protein eS25



- Molecule 80: Ubiquitin-40S ribosomal protein S27a



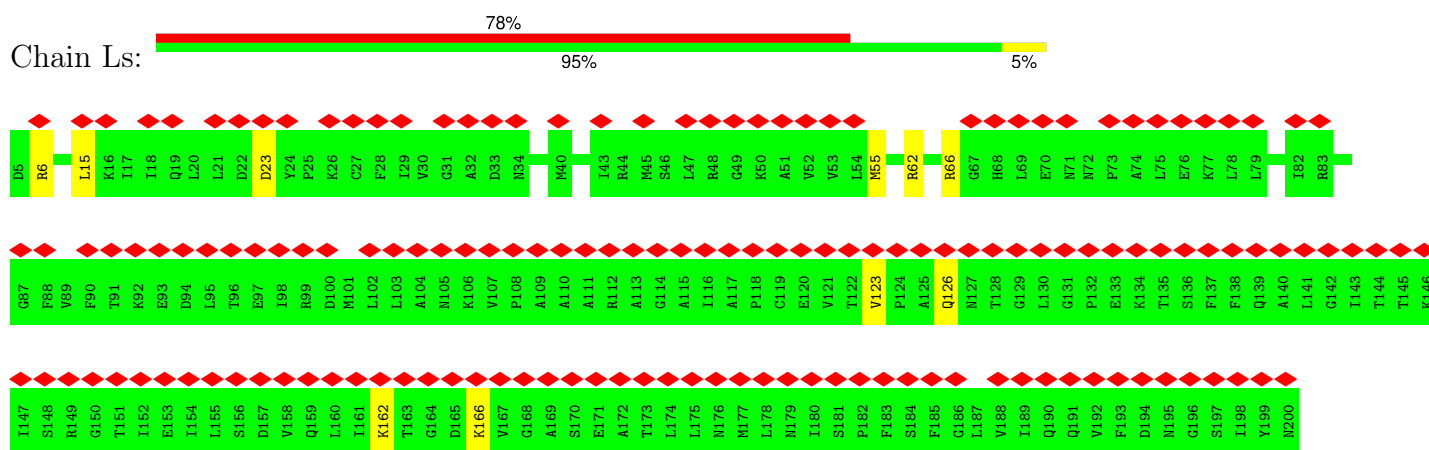
- Molecule 81: A/P site tRNA



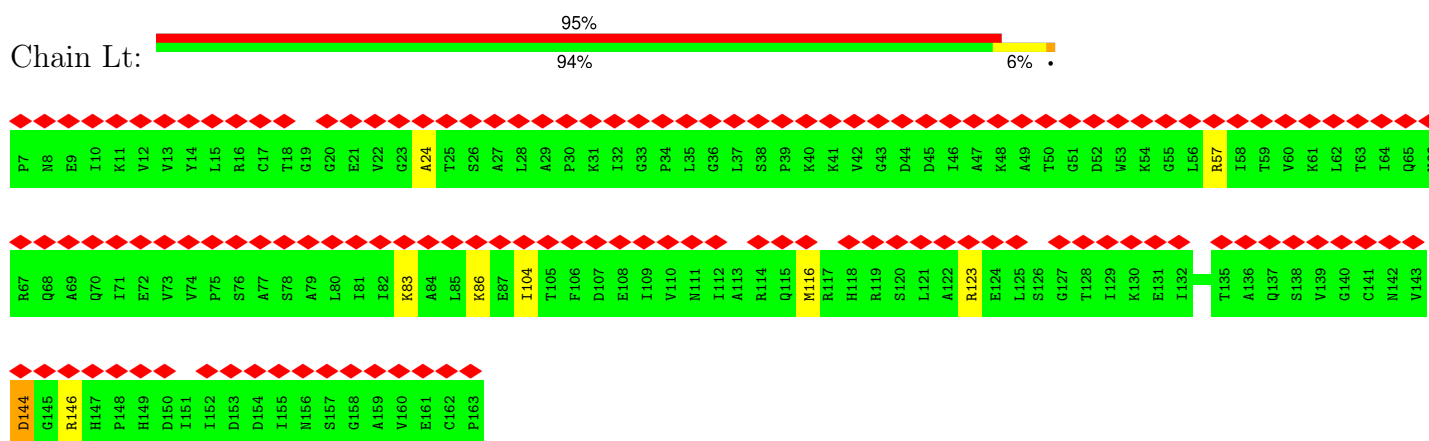
- Molecule 82: P/E site tRNA



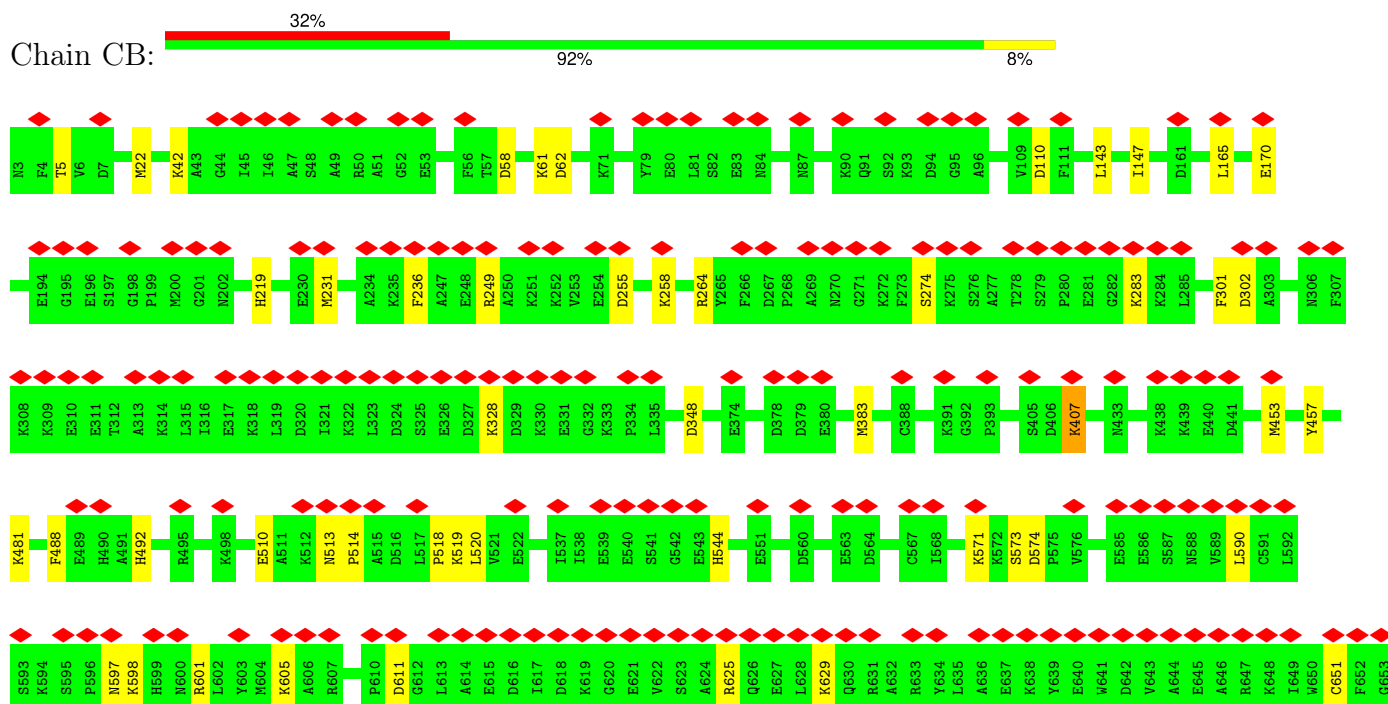
- Molecule 83: 60S acidic ribosomal protein P0

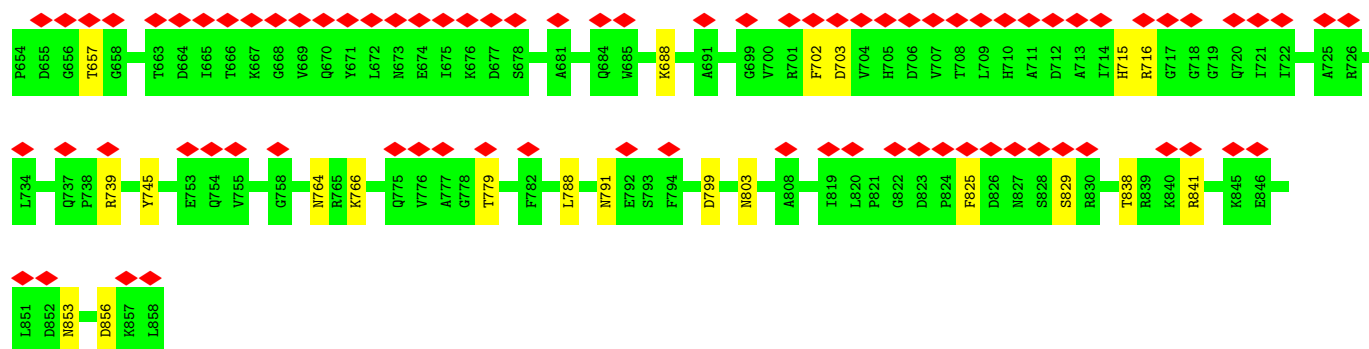


• Molecule 84: 60S ribosomal protein L12

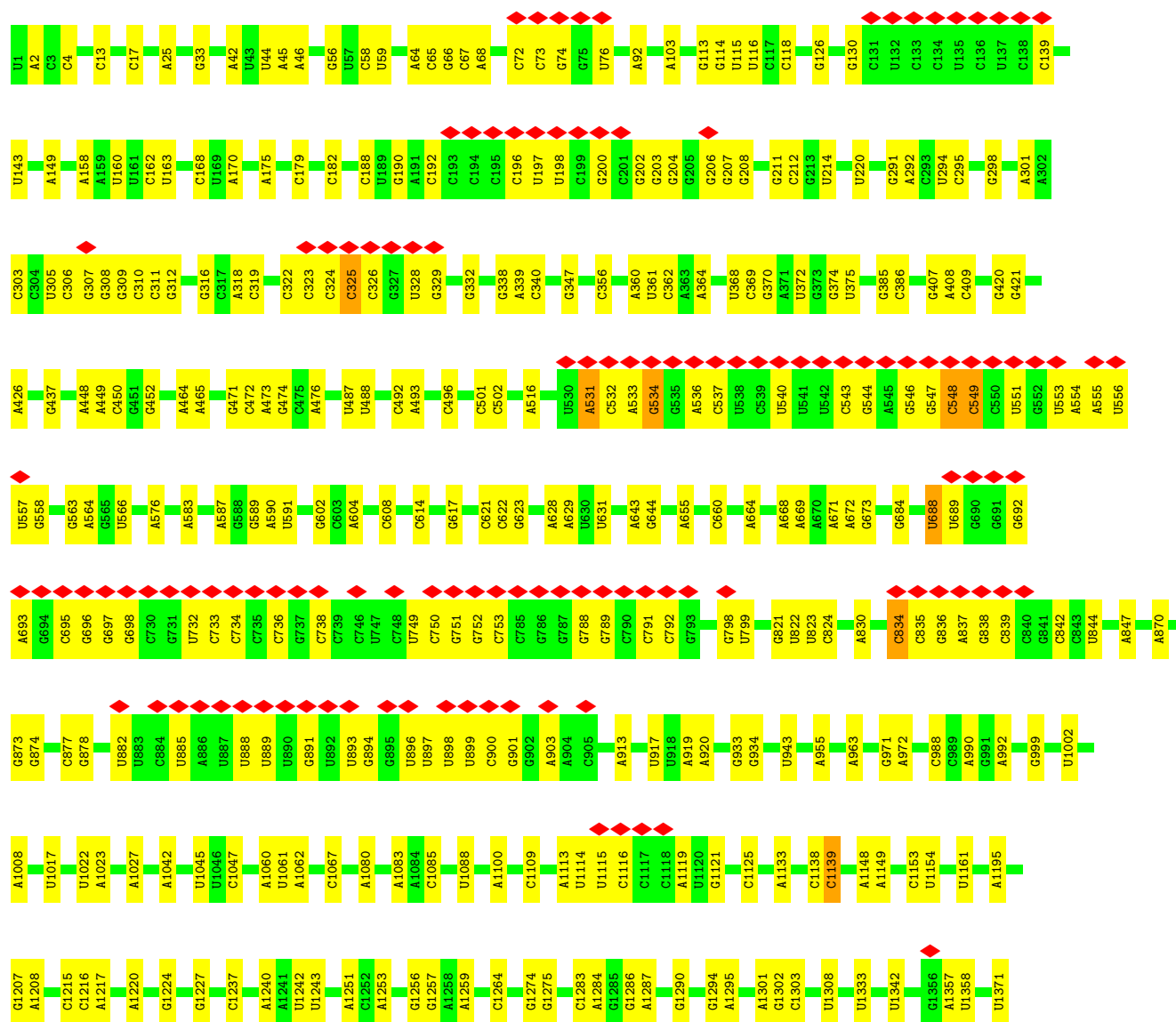
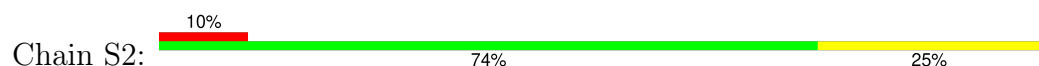


• Molecule 85: eEF2





• Molecule 86: 18S rRNA



U1372	A1522	C1683	C1798
A1376	A1533	G1693	A1809
U1377	C1534	U1694	A1810
A1378	U1535	A1695	G1811
A1401	G1536	C1696	U1812
U1404	A1537	A1699	A1813
A1405	C1544	A1712	A1822
G1406	G1552	A1715	A1823
G1411	C1553	G1722	A1824
A1414	C1554	G1726	A1825
C1415	U1555	U1729	G1826
C1416	A1556	G1743	A1831
C1417	G1570	A1744	A1835
C1418	G1571	A1745	U1838
C1419	C1572	C1752	G1849
G1420	G1573	G1753	A1850
A1421	A1579	G1754	A1851
G1422	A1580	C1755	C1852
C1423	C1581	G1756	G1861
G1424	C1582	G1757	G1862
C1433	C1583	G1758	A1863
C1434	G1584	G1759	U1864
C1435	U1585	G1760	C1865
C1436	U1586	U1761	A1869
C1437	A1587	C1762	
A1438	A1588	G1763	
U1442	A1601	G1764	
G1449	U1602	C1765	
A1452	G1603	G1766	
C1453	G1604	C1767	
A1454	G1605	A1768	
U1463	U1621	C1769	
A1474	U1622	G1770	
U1478	A1623	G1771	
A1489	A1624	C1772	
G1490	A1633	C1773	
U1494	A1634	C1774	
C1495	A1637	U1775	
U1496	G1638	G1776	
G1497	A1639	G1777	
A1498	A1640	C1778	
A1508	C1646	G1779	
G1520	A1647	G1780	
C1521	G1648	A1781	
	G1654	G1782	
	A1663	C1783	
	A1664	G1784	
	G1665	C1785	
		U1786	
		G1787	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	130154	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 ($e^-/\text{\AA}^2$)	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	0.563	Depositor
Minimum map value	-0.256	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.042	Depositor
Map size (\AA)	546.816, 546.816, 546.816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	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: ZN, MG

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	Se	0.77	0/382	0.79	1/504 (0.2%)
2	CH	0.53	1/1028 (0.1%)	0.86	11/1376 (0.8%)
3	LW	0.26	0/979	0.57	0/1295
4	SE	0.28	0/2118	0.57	0/2849
5	SI	0.26	0/1715	0.56	0/2287
6	SL	0.26	0/1268	0.57	0/1696
7	SX	0.25	0/1116	0.53	0/1490
8	SG	0.40	2/1946 (0.1%)	0.75	5/2590 (0.2%)
9	SJ	0.28	0/1550	0.64	0/2069
10	SY	0.28	0/1083	0.61	1/1438 (0.1%)
11	SA	0.26	0/1778	0.56	0/2416
12	SB	0.27	0/1765	0.53	0/2362
13	SH	0.28	0/1519	0.57	1/2033 (0.0%)
14	SV	0.25	0/643	0.58	0/860
15	Sa	0.29	0/836	0.62	0/1121
16	SC	0.29	0/1762	0.54	0/2381
17	SN	0.26	0/1232	0.52	0/1656
18	SO	0.25	0/1062	0.64	2/1425 (0.1%)
19	SW	0.28	0/1051	0.56	0/1406
20	Sb	0.24	0/665	0.54	0/891
21	L5	0.33	0/89313	0.86	82/139291 (0.1%)
22	L7	0.30	0/2861	0.80	0/4459
23	L8	0.32	0/3701	0.79	1/5766 (0.0%)
24	LA	0.28	0/1936	0.61	1/2596 (0.0%)
25	LB	0.27	0/3306	0.56	1/4424 (0.0%)
26	LC	0.26	0/2981	0.56	1/4002 (0.0%)
27	LD	0.28	0/2428	0.53	0/3252
28	LE	0.26	0/1942	0.56	0/2606
29	LF	0.28	0/1905	0.54	0/2539
30	LG	0.26	0/1960	0.54	0/2637
31	LH	0.27	0/1537	0.57	0/2066
32	LI	0.30	0/1673	0.56	0/2233

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LJ	0.28	0/1433	0.61	0/1915
34	LL	0.26	0/1732	0.58	0/2315
35	LM	0.27	0/1161	0.56	0/1554
36	LN	0.26	0/1746	0.57	0/2338
37	LO	0.27	0/1682	0.53	0/2250
38	LP	0.26	0/1268	0.52	0/1701
39	LQ	0.31	0/1537	0.64	0/2052
40	LR	0.25	0/1582	0.58	0/2091
41	LS	0.26	0/1493	0.55	0/2003
42	LT	0.27	0/1326	0.54	0/1770
43	LU	0.27	0/839	0.61	1/1126 (0.1%)
44	LV	0.28	0/993	0.54	0/1332
45	LX	0.26	0/1002	0.56	0/1345
46	LY	0.27	0/1132	0.56	0/1504
47	LZ	0.28	0/1130	0.57	0/1507
48	La	0.27	0/1191	0.54	0/1591
49	Lb	0.24	0/889	0.62	1/1175 (0.1%)
50	Lc	0.26	0/774	0.55	0/1038
51	Ld	0.26	0/903	0.59	0/1216
52	Le	0.26	0/1071	0.55	0/1429
53	Lf	0.27	0/895	0.59	0/1198
54	Lg	0.28	0/916	0.59	0/1220
55	Lh	0.25	0/1023	0.54	0/1351
56	Li	0.25	0/843	0.58	0/1115
57	Lj	0.26	0/720	0.60	0/952
58	Lk	0.26	0/575	0.54	0/761
59	Ll	0.24	0/454	0.57	0/599
60	Lm	0.25	0/435	0.55	0/575
61	Ln	0.24	0/231	0.70	0/294
62	Lo	0.30	0/876	0.59	0/1156
63	Lp	0.34	0/718	0.53	0/953
64	Lr	0.42	1/1017 (0.1%)	0.78	2/1364 (0.1%)
65	Lz	0.25	0/1769	0.53	1/2371 (0.0%)
66	SR	0.26	0/1105	0.64	1/1484 (0.1%)
67	SD	0.26	0/1793	0.56	0/2414
68	SF	0.26	0/1516	0.53	0/2037
69	SK	0.64	4/851 (0.5%)	0.92	6/1147 (0.5%)
70	SP	0.25	0/1003	0.55	0/1342
71	SQ	0.27	0/1160	0.61	0/1553
72	SS	0.25	0/1216	0.58	0/1628
73	ST	0.26	0/1131	0.56	0/1515
74	SU	0.25	0/831	0.61	0/1115
75	Sc	0.25	0/508	0.65	0/680

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sd	0.25	0/470	0.60	0/623
77	Sg	0.32	1/2493 (0.0%)	0.59	1/3394 (0.0%)
78	SM	0.24	0/950	0.53	0/1275
79	SZ	0.27	0/604	0.63	0/810
80	Sf	0.26	0/560	0.56	0/745
81	AP	0.19	0/1692	0.78	0/2634
82	PE	0.26	0/1778	0.89	2/2767 (0.1%)
83	Ls	0.27	0/1519	0.54	1/2052 (0.0%)
84	Lt	0.28	0/1058	0.58	0/1430
85	CB	0.40	3/6734 (0.0%)	0.64	6/9094 (0.1%)
86	S2	0.25	0/41241	0.82	40/64251 (0.1%)
All	All	0.30	12/246610 (0.0%)	0.75	169/361167 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
7	SX	0	1
13	SH	0	1
24	LA	0	1
25	LB	0	2
34	LL	0	1
35	LM	0	2
37	LO	0	1
42	LT	0	1
53	Lf	0	3
57	Lj	0	1
70	SP	0	1
71	SQ	0	1
All	All	0	16

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	CB	514	PRO	CG-CD	-20.58	0.82	1.50
69	SK	33	PRO	CG-CD	-10.86	1.14	1.50
8	SG	62	PRO	CG-CD	-10.65	1.15	1.50
85	CB	513	ASN	C-N	7.86	1.49	1.34
85	CB	513	ASN	C-O	7.84	1.38	1.23

The worst 5 of 169 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	CB	514	PRO	N-CD-CG	-21.13	71.50	103.20
85	CB	514	PRO	CB-CG-CD	18.81	179.86	106.50
8	SG	62	PRO	N-CD-CG	-16.20	78.89	103.20
69	SK	33	PRO	N-CD-CG	-14.78	81.03	103.20
64	Lr	123	PRO	CA-N-CD	-14.04	91.84	111.50

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
24	LA	13	GLY	Peptide
25	LB	17	LEU	Peptide
25	LB	258	HIS	Peptide
13	SH	15	LYS	Peptide
7	SX	126	ALA	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	Se	45/58 (78%)	29 (64%)	12 (27%)	4 (9%)	0	0
2	CH	130/132 (98%)	53 (41%)	57 (44%)	20 (15%)	0	0
3	LW	114/118 (97%)	111 (97%)	3 (3%)	0	100	100
4	SE	260/262 (99%)	250 (96%)	10 (4%)	0	100	100
5	SI	204/206 (99%)	198 (97%)	6 (3%)	0	100	100
6	SL	151/153 (99%)	139 (92%)	12 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	SX	139/141 (99%)	124 (89%)	14 (10%)	1 (1%)	19	31
8	SG	235/237 (99%)	221 (94%)	14 (6%)	0	100	100
9	SJ	183/185 (99%)	175 (96%)	7 (4%)	1 (0%)	25	40
10	SY	129/131 (98%)	121 (94%)	8 (6%)	0	100	100
11	SA	219/221 (99%)	201 (92%)	18 (8%)	0	100	100
12	SB	212/214 (99%)	205 (97%)	7 (3%)	0	100	100
13	SH	182/186 (98%)	163 (90%)	19 (10%)	0	100	100
14	SV	81/83 (98%)	74 (91%)	7 (9%)	0	100	100
15	Sa	100/102 (98%)	89 (89%)	11 (11%)	0	100	100
16	SC	220/222 (99%)	207 (94%)	13 (6%)	0	100	100
17	SN	148/150 (99%)	144 (97%)	4 (3%)	0	100	100
18	SO	138/140 (99%)	127 (92%)	11 (8%)	0	100	100
19	SW	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
20	Sb	81/83 (98%)	72 (89%)	9 (11%)	0	100	100
24	LA	246/248 (99%)	226 (92%)	19 (8%)	1 (0%)	30	46
25	LB	400/402 (100%)	377 (94%)	22 (6%)	1 (0%)	37	53
26	LC	366/368 (100%)	346 (94%)	20 (6%)	0	100	100
27	LD	291/293 (99%)	275 (94%)	16 (6%)	0	100	100
28	LE	232/236 (98%)	209 (90%)	23 (10%)	0	100	100
29	LF	223/225 (99%)	215 (96%)	8 (4%)	0	100	100
30	LG	239/241 (99%)	225 (94%)	14 (6%)	0	100	100
31	LH	188/190 (99%)	177 (94%)	11 (6%)	0	100	100
32	LI	198/202 (98%)	191 (96%)	7 (4%)	0	100	100
33	LJ	174/176 (99%)	156 (90%)	18 (10%)	0	100	100
34	LL	208/210 (99%)	191 (92%)	17 (8%)	0	100	100
35	LM	137/139 (99%)	128 (93%)	8 (6%)	1 (1%)	19	31
36	LN	201/203 (99%)	193 (96%)	7 (4%)	1 (0%)	25	40
37	LO	199/201 (99%)	193 (97%)	6 (3%)	0	100	100
38	LP	151/153 (99%)	143 (95%)	8 (5%)	0	100	100
39	LQ	185/187 (99%)	179 (97%)	6 (3%)	0	100	100
40	LR	185/187 (99%)	181 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	LS	173/175 (99%)	164 (95%)	9 (5%)	0	100	100
42	LT	157/159 (99%)	146 (93%)	11 (7%)	0	100	100
43	LU	99/101 (98%)	82 (83%)	17 (17%)	0	100	100
44	LV	129/131 (98%)	126 (98%)	3 (2%)	0	100	100
45	LX	118/120 (98%)	117 (99%)	1 (1%)	0	100	100
46	LY	132/134 (98%)	129 (98%)	3 (2%)	0	100	100
47	LZ	133/135 (98%)	124 (93%)	9 (7%)	0	100	100
48	La	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
49	Lb	105/109 (96%)	98 (93%)	7 (7%)	0	100	100
50	Lc	96/98 (98%)	91 (95%)	5 (5%)	0	100	100
51	Ld	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
52	Le	126/128 (98%)	120 (95%)	6 (5%)	0	100	100
53	Lf	107/109 (98%)	100 (94%)	6 (6%)	1 (1%)	14	25
54	Lg	112/114 (98%)	112 (100%)	0	0	100	100
55	Lh	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
56	Li	100/102 (98%)	95 (95%)	5 (5%)	0	100	100
57	Lj	84/86 (98%)	79 (94%)	5 (6%)	0	100	100
58	Lk	67/69 (97%)	65 (97%)	2 (3%)	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%)	176 (82%)	39 (18%)	0	100	100
66	SR	133/135 (98%)	122 (92%)	10 (8%)	1 (1%)	16	28
67	SD	225/227 (99%)	206 (92%)	19 (8%)	0	100	100
68	SF	187/189 (99%)	166 (89%)	21 (11%)	0	100	100
69	SK	96/98 (98%)	87 (91%)	7 (7%)	2 (2%)	5	10
70	SP	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
71	SQ	142/144 (99%)	125 (88%)	16 (11%)	1 (1%)	19	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	SS	143/145 (99%)	136 (95%)	7 (5%)	0	100	100
73	ST	141/143 (99%)	131 (93%)	9 (6%)	1 (1%)	19	31
74	SU	102/104 (98%)	97 (95%)	5 (5%)	0	100	100
75	Sc	62/64 (97%)	51 (82%)	11 (18%)	0	100	100
76	Sd	53/55 (96%)	51 (96%)	1 (2%)	1 (2%)	6	11
77	Sg	311/313 (99%)	275 (88%)	36 (12%)	0	100	100
78	SM	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
79	SZ	73/75 (97%)	57 (78%)	16 (22%)	0	100	100
80	Sf	65/67 (97%)	59 (91%)	6 (9%)	0	100	100
83	Ls	194/196 (99%)	186 (96%)	8 (4%)	0	100	100
84	Lt	137/141 (97%)	111 (81%)	24 (18%)	2 (2%)	8	14
85	CB	842/846 (100%)	792 (94%)	47 (6%)	3 (0%)	30	46
All	All	12824/13009 (99%)	11907 (93%)	875 (7%)	42 (0%)	38	53

5 of 42 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	CH	48	GLN
2	CH	66	GLU
85	CB	779	THR
1	Se	85	LYS
2	CH	50	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Se	39/47 (83%)	27 (69%)	12 (31%)	0	0
2	CH	106/106 (100%)	100 (94%)	6 (6%)	17	29
3	LW	97/97 (100%)	87 (90%)	10 (10%)	6	9
4	SE	224/224 (100%)	199 (89%)	25 (11%)	5	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	SI	178/178 (100%)	161 (90%)	17 (10%)	7	10
6	SL	137/137 (100%)	118 (86%)	19 (14%)	3	4
7	SX	113/113 (100%)	106 (94%)	7 (6%)	15	26
8	SG	207/207 (100%)	191 (92%)	16 (8%)	10	17
9	SJ	161/161 (100%)	148 (92%)	13 (8%)	9	16
10	SY	113/113 (100%)	99 (88%)	14 (12%)	4	5
11	SA	183/183 (100%)	172 (94%)	11 (6%)	16	28
12	SB	195/195 (100%)	169 (87%)	26 (13%)	3	4
13	SH	166/166 (100%)	152 (92%)	14 (8%)	9	14
14	SV	67/67 (100%)	54 (81%)	13 (19%)	1	1
15	Sa	89/89 (100%)	81 (91%)	8 (9%)	8	12
16	SC	188/188 (100%)	172 (92%)	16 (8%)	8	13
17	SN	130/130 (100%)	123 (95%)	7 (5%)	18	32
18	SO	110/110 (100%)	100 (91%)	10 (9%)	7	12
19	SW	112/112 (100%)	108 (96%)	4 (4%)	30	48
20	Sb	75/75 (100%)	72 (96%)	3 (4%)	27	44
24	LA	190/190 (100%)	176 (93%)	14 (7%)	11	19
25	LB	348/348 (100%)	322 (92%)	26 (8%)	11	19
26	LC	306/306 (100%)	286 (94%)	20 (6%)	14	24
27	LD	246/247 (100%)	227 (92%)	19 (8%)	10	17
28	LE	209/209 (100%)	195 (93%)	14 (7%)	13	22
29	LF	194/194 (100%)	185 (95%)	9 (5%)	23	38
30	LG	203/205 (99%)	185 (91%)	18 (9%)	8	12
31	LH	169/169 (100%)	162 (96%)	7 (4%)	26	43
32	LI	172/172 (100%)	163 (95%)	9 (5%)	19	33
33	LJ	148/148 (100%)	137 (93%)	11 (7%)	11	19
34	LL	176/176 (100%)	162 (92%)	14 (8%)	10	16
35	LM	118/118 (100%)	110 (93%)	8 (7%)	13	22
36	LN	171/171 (100%)	162 (95%)	9 (5%)	19	33
37	LO	173/173 (100%)	168 (97%)	5 (3%)	37	58
38	LP	134/134 (100%)	123 (92%)	11 (8%)	9	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	LQ	164/164 (100%)	156 (95%)	8 (5%)	21	36
40	LR	166/166 (100%)	156 (94%)	10 (6%)	16	28
41	LS	156/156 (100%)	150 (96%)	6 (4%)	28	47
42	LT	139/139 (100%)	132 (95%)	7 (5%)	20	35
43	LU	91/91 (100%)	79 (87%)	12 (13%)	3	4
44	LV	101/101 (100%)	92 (91%)	9 (9%)	8	12
45	LX	108/108 (100%)	99 (92%)	9 (8%)	9	15
46	LY	124/124 (100%)	118 (95%)	6 (5%)	21	36
47	LZ	117/117 (100%)	107 (92%)	10 (8%)	8	13
48	La	120/120 (100%)	118 (98%)	2 (2%)	56	75
49	Lb	88/90 (98%)	80 (91%)	8 (9%)	7	12
50	Lc	83/83 (100%)	76 (92%)	7 (8%)	9	14
51	Ld	98/98 (100%)	92 (94%)	6 (6%)	15	27
52	Le	114/114 (100%)	107 (94%)	7 (6%)	15	27
53	Lf	88/88 (100%)	81 (92%)	7 (8%)	10	16
54	Lg	98/98 (100%)	94 (96%)	4 (4%)	26	43
55	Lh	109/109 (100%)	100 (92%)	9 (8%)	9	15
56	Li	86/86 (100%)	77 (90%)	9 (10%)	5	9
57	Lj	73/73 (100%)	66 (90%)	7 (10%)	7	10
58	Lk	64/64 (100%)	61 (95%)	3 (5%)	22	37
59	Ll	47/47 (100%)	45 (96%)	2 (4%)	25	41
60	Lm	48/48 (100%)	46 (96%)	2 (4%)	25	42
61	Ln	23/23 (100%)	19 (83%)	4 (17%)	1	2
62	Lo	93/93 (100%)	83 (89%)	10 (11%)	5	8
63	Lp	74/74 (100%)	68 (92%)	6 (8%)	9	16
64	Lr	109/109 (100%)	97 (89%)	12 (11%)	5	8
65	Lz	195/196 (100%)	176 (90%)	19 (10%)	6	10
66	SR	122/122 (100%)	109 (89%)	13 (11%)	5	8
67	SD	190/190 (100%)	171 (90%)	19 (10%)	6	10
68	SF	159/159 (100%)	151 (95%)	8 (5%)	20	35
69	SK	89/89 (100%)	81 (91%)	8 (9%)	8	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	SP	107/107 (100%)	96 (90%)	11 (10%)	6	9
71	SQ	119/119 (100%)	105 (88%)	14 (12%)	4	6
72	SS	126/126 (100%)	117 (93%)	9 (7%)	12	20
73	ST	113/113 (100%)	106 (94%)	7 (6%)	15	26
74	SU	94/94 (100%)	90 (96%)	4 (4%)	25	41
75	Sc	57/57 (100%)	54 (95%)	3 (5%)	19	33
76	Sd	48/48 (100%)	42 (88%)	6 (12%)	3	5
77	Sg	272/272 (100%)	240 (88%)	32 (12%)	4	6
78	SM	102/104 (98%)	93 (91%)	9 (9%)	8	12
79	SZ	66/66 (100%)	60 (91%)	6 (9%)	7	12
80	Sf	60/60 (100%)	56 (93%)	4 (7%)	13	22
83	Ls	162/164 (99%)	153 (94%)	9 (6%)	17	30
84	Lt	112/115 (97%)	104 (93%)	8 (7%)	12	20
85	CB	722/723 (100%)	656 (91%)	66 (9%)	7	12
All	All	11143/11165 (100%)	10261 (92%)	882 (8%)	13	17

5 of 882 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	LS	90	THR
56	Li	23	LYS
85	CB	829	SER
83	Ls	6	ARG
43	LU	34	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
63	Lp	92	GLN
77	Sg	26	GLN
66	SR	118	GLN
69	SK	44	HIS
77	Sg	222	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
21	L5	3705/3740 (99%)	855 (23%)	21 (0%)
22	L7	119/120 (99%)	11 (9%)	0
23	L8	155/156 (99%)	31 (20%)	0
81	AP	69/71 (97%)	15 (21%)	0
82	PE	74/75 (98%)	27 (36%)	1 (1%)
86	S2	1714/1740 (98%)	436 (25%)	8 (0%)
All	All	5836/5902 (98%)	1375 (23%)	30 (0%)

5 of 1375 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
21	L5	2	G
21	L5	13	U
21	L5	17	A
21	L5	25	A
21	L5	30	C

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
21	L5	3614	G
86	S2	688	U
21	L5	4061	G
86	S2	1781	A
86	S2	531	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
21	L5	11
86	S2	7
49	Lb	1
28	LE	1
3	LW	1
85	CB	1
13	SH	1
81	AP	1
84	Lt	1
32	LI	1
82	PE	1

The worst 5 of 27 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	34.34
1	S2	753:C	O3'	785:C	P	28.13
1	LE	76:ALA	C	88:VAL	N	24.39
1	L5	2910:G	O3'	3584:C	P	20.70
1	L5	760:G	O3'	903:C	P	17.25

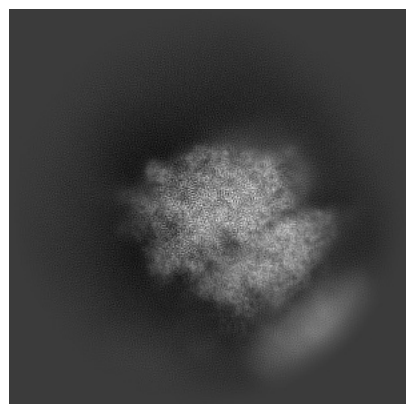
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44060. These allow visual inspection of the internal detail of the map and identification of artifacts.

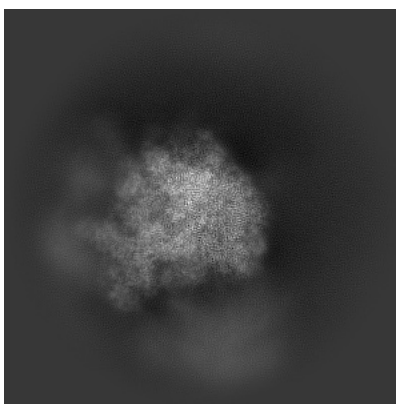
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

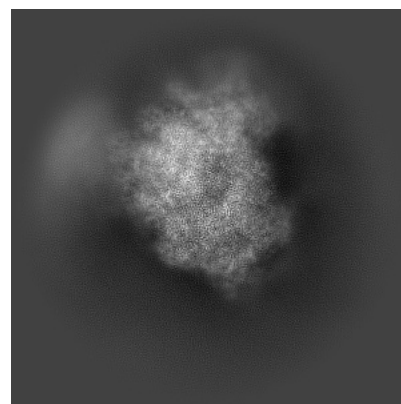
6.1.1 Primary map



X

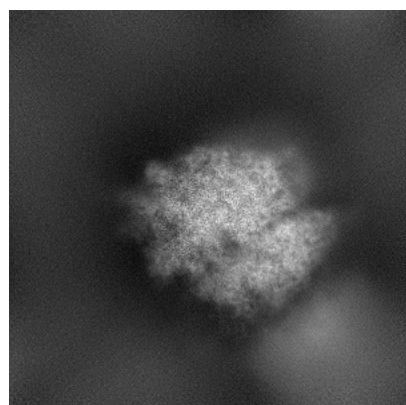


Y

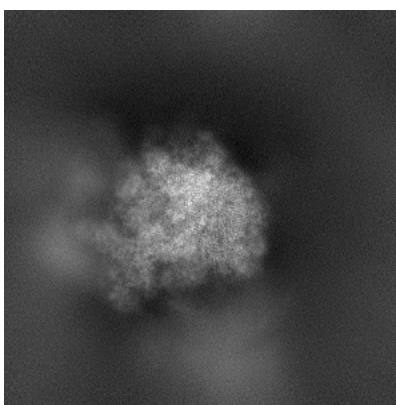


Z

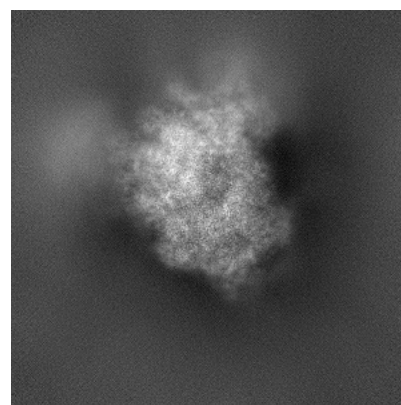
6.1.2 Raw map



X



Y

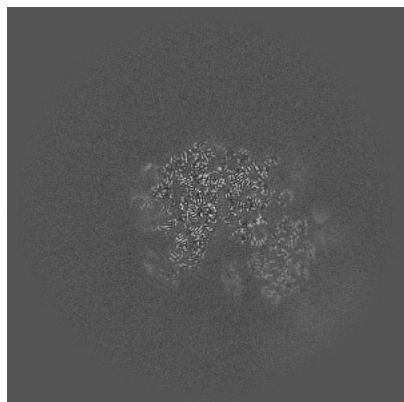


Z

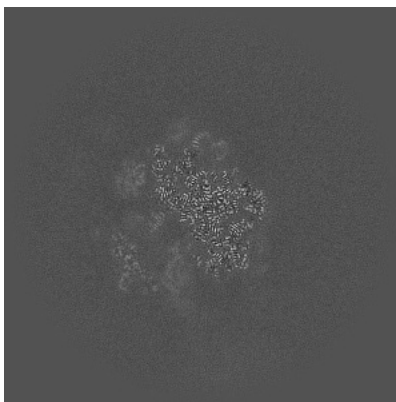
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

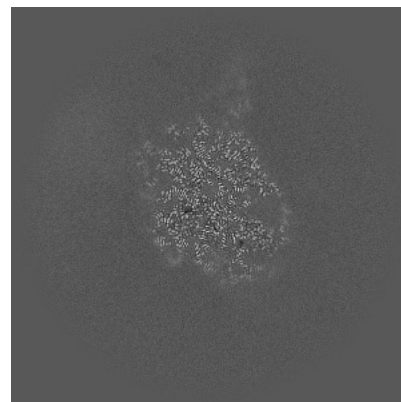
6.2.1 Primary map



X Index: 256

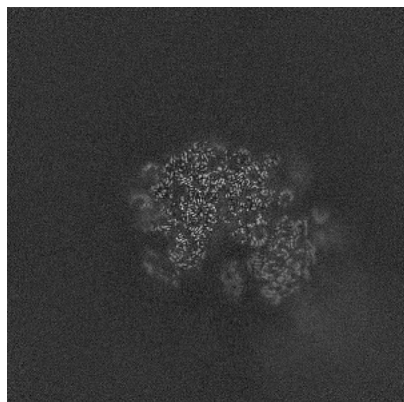


Y Index: 256

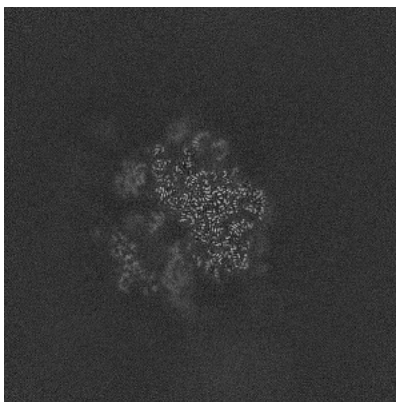


Z Index: 256

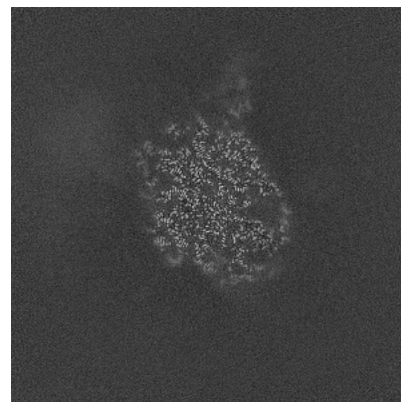
6.2.2 Raw map



X Index: 256



Y Index: 256

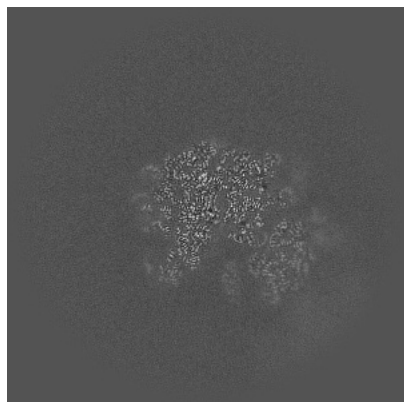


Z Index: 256

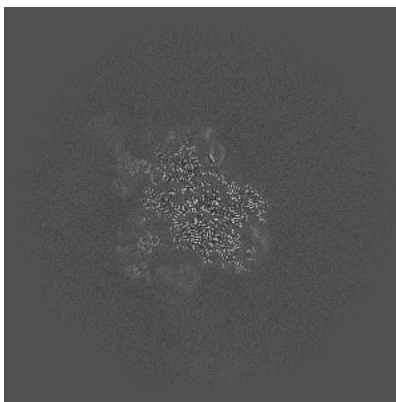
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

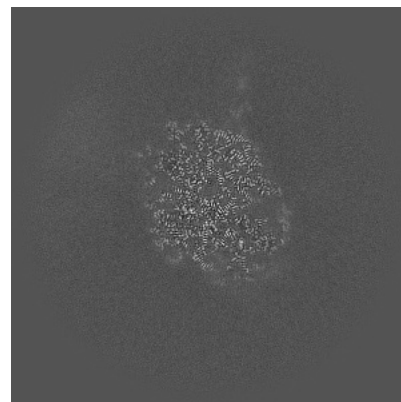
6.3.1 Primary map



X Index: 253

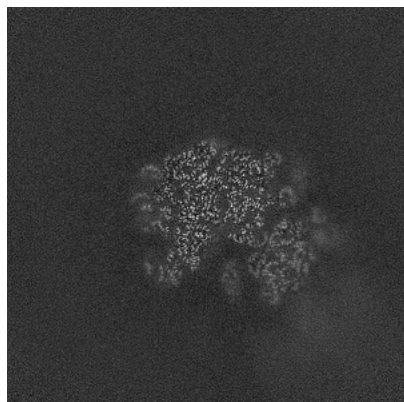


Y Index: 243

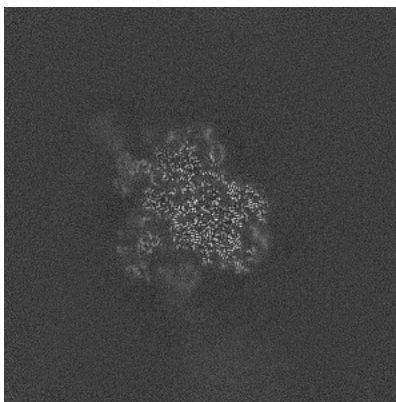


Z Index: 258

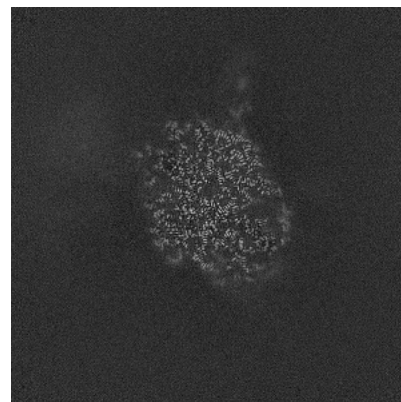
6.3.2 Raw map



X Index: 253



Y Index: 243

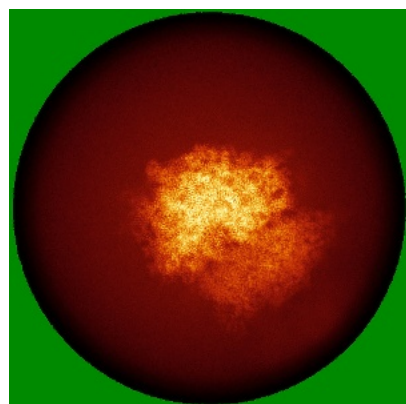


Z Index: 258

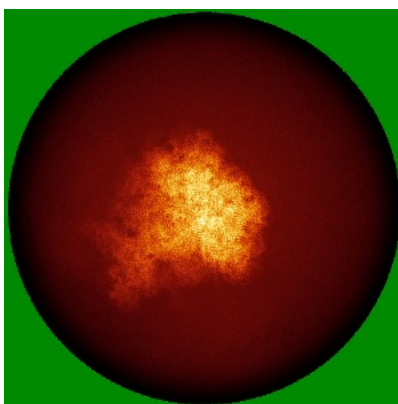
The images above show the largest variance slices of the map in three orthogonal directions.

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

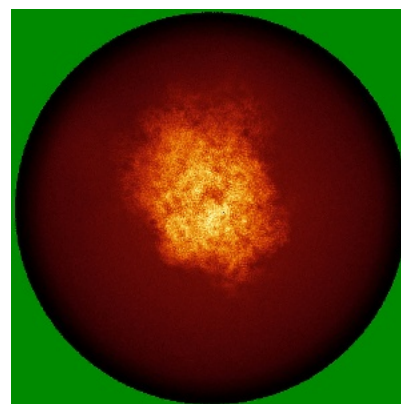
6.4.1 Primary map



X

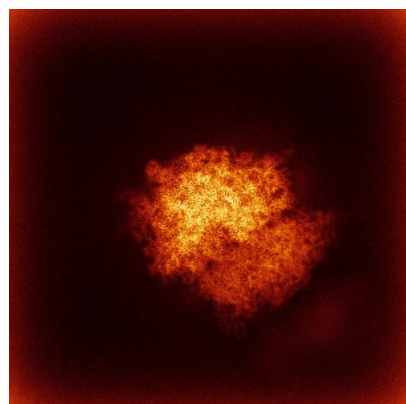


Y

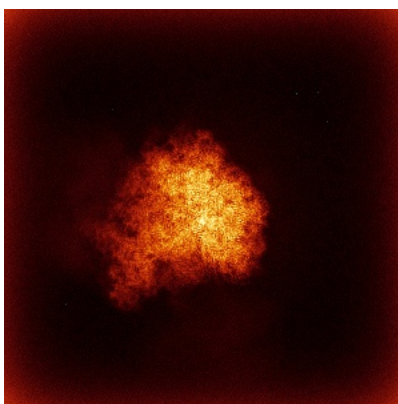


Z

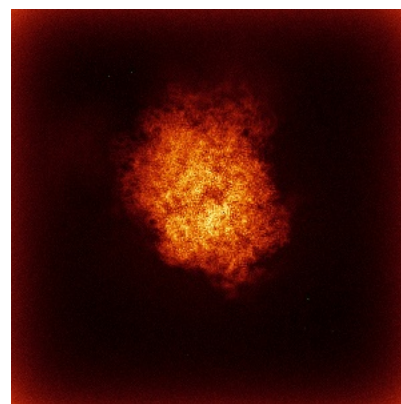
6.4.2 Raw map



X



Y

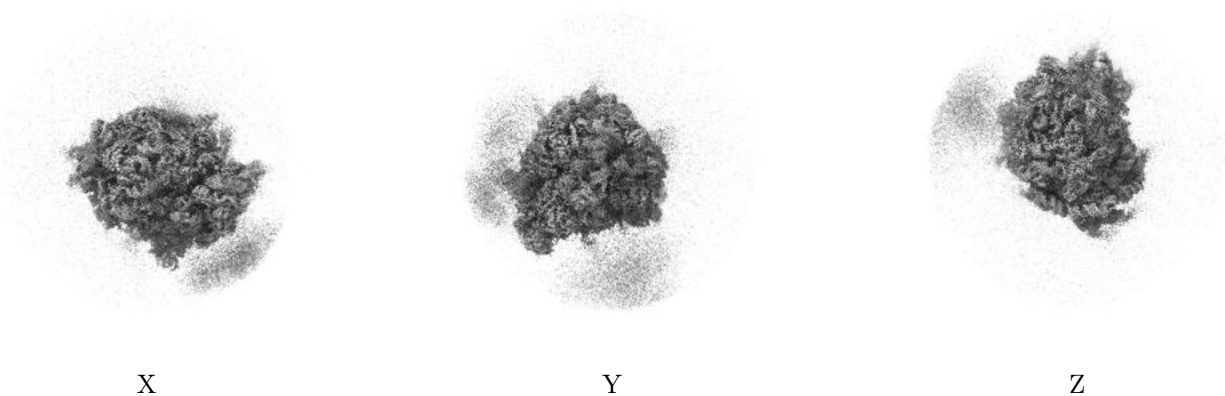


Z

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

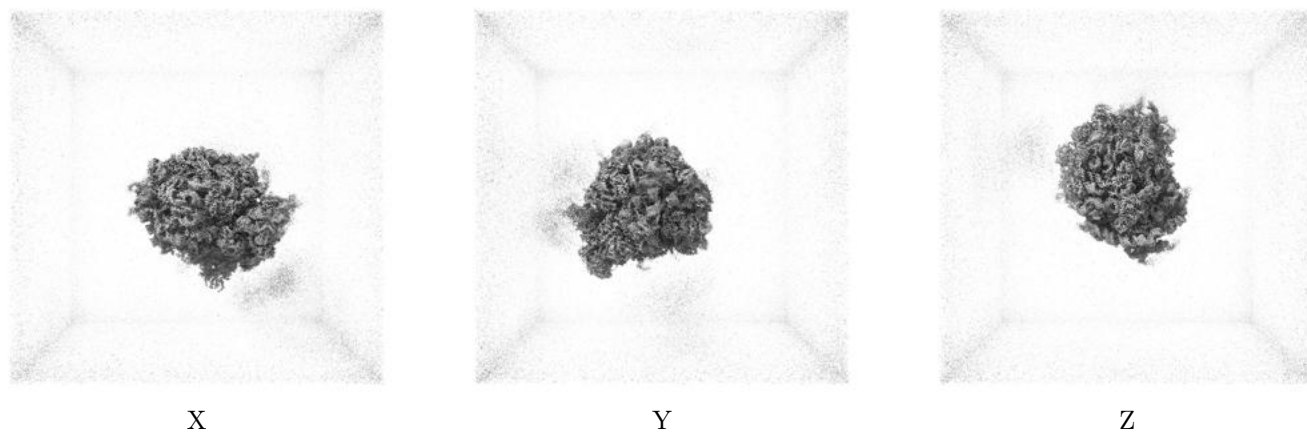
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.042. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

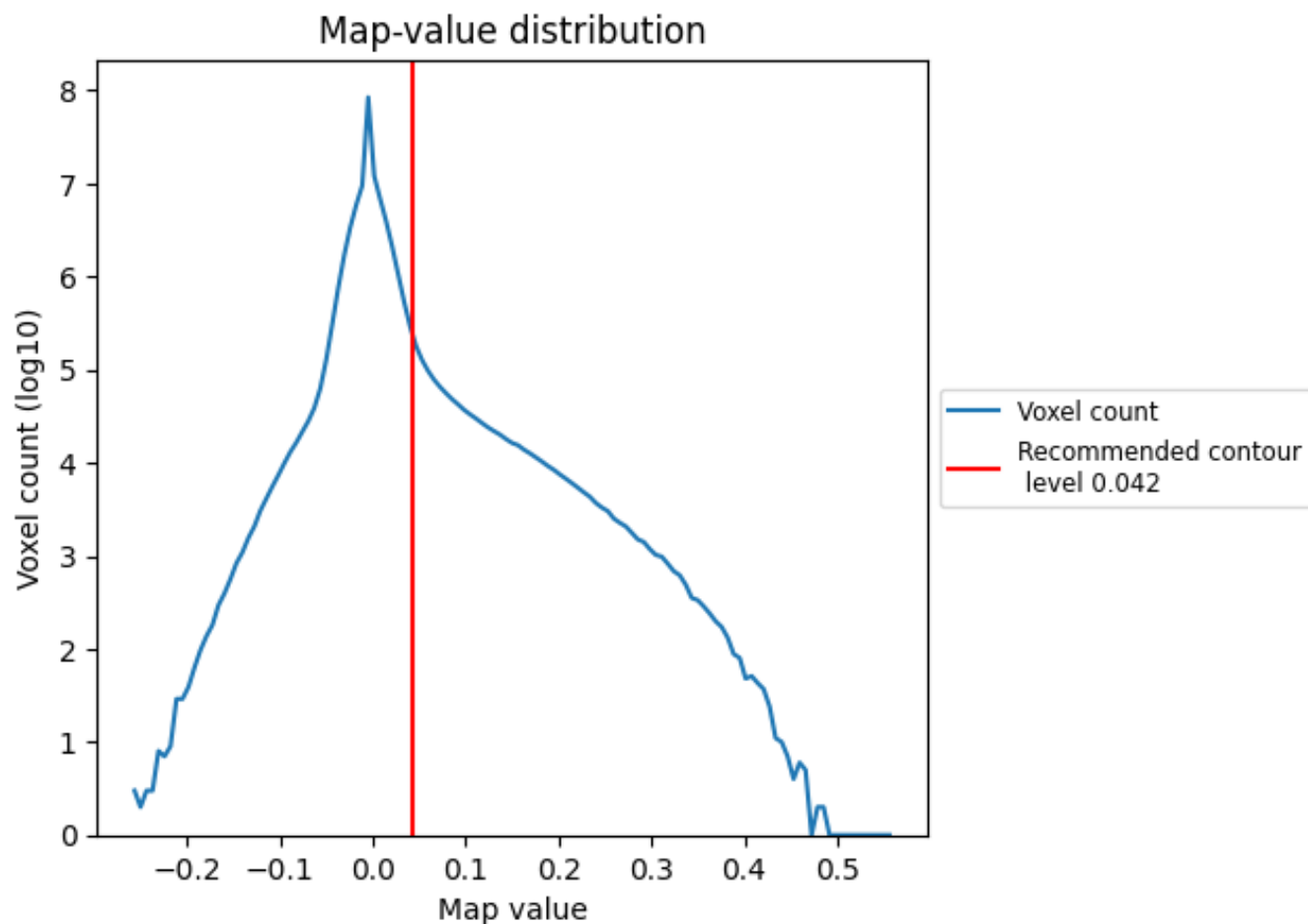
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

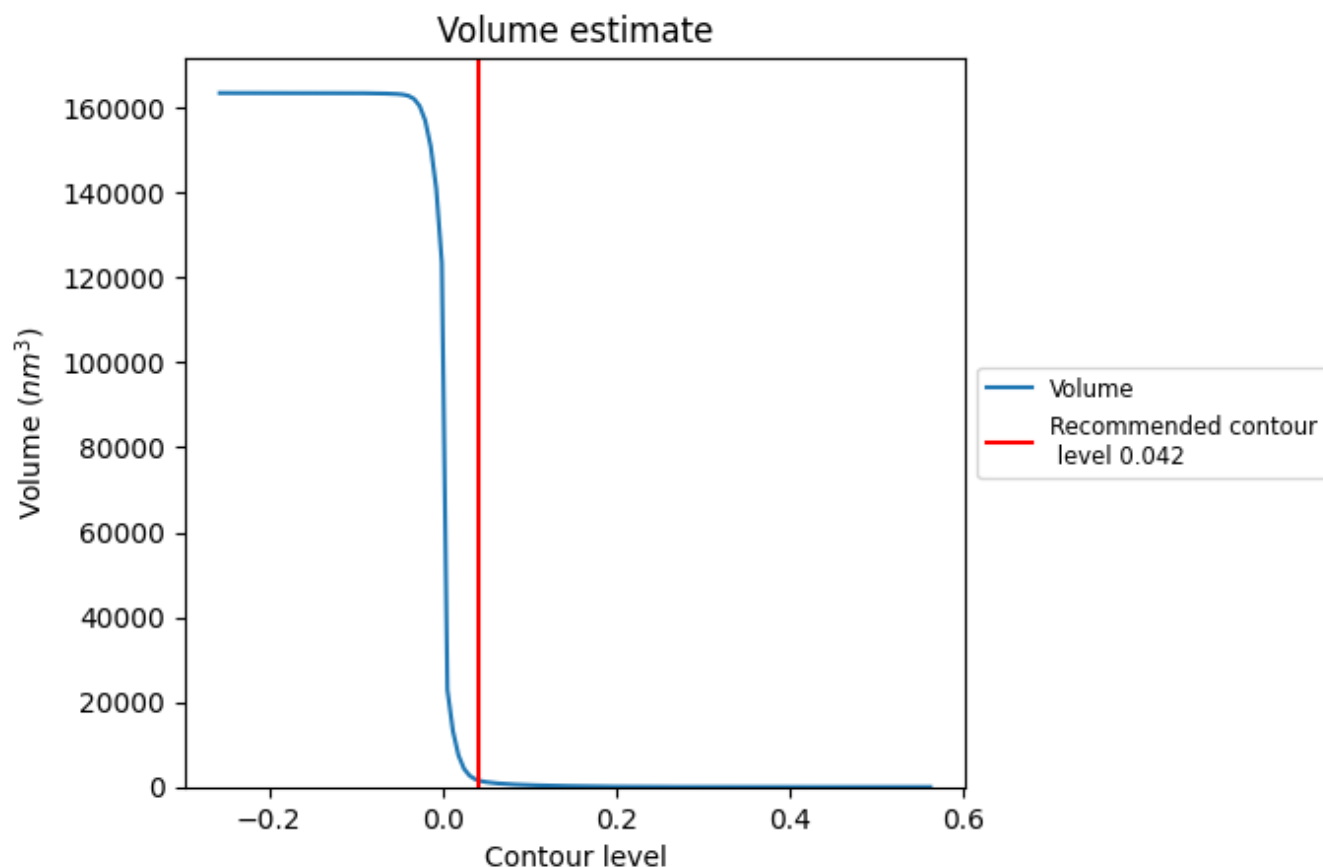
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

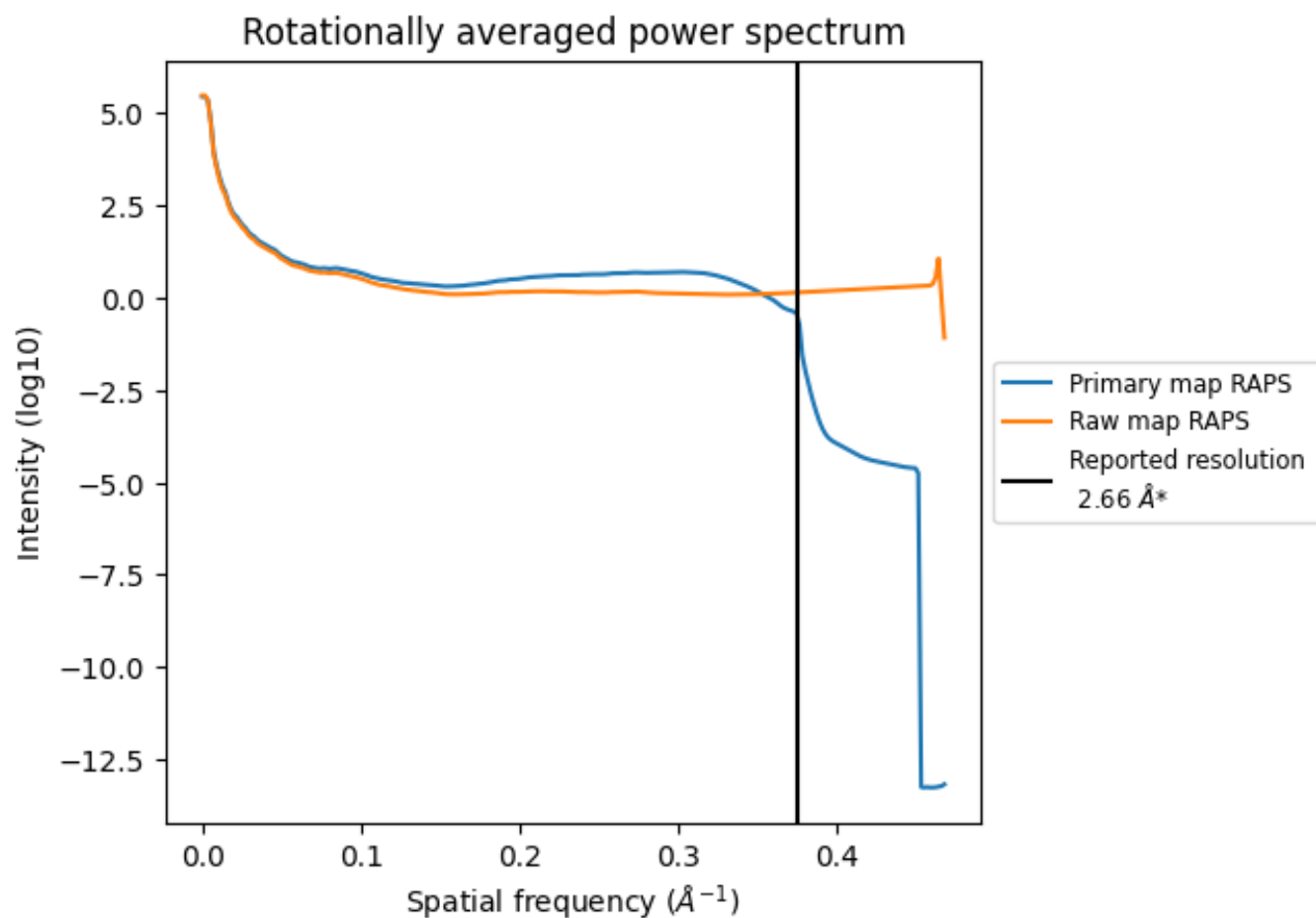
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1562 nm^3 ; this corresponds to an approximate mass of 1411 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

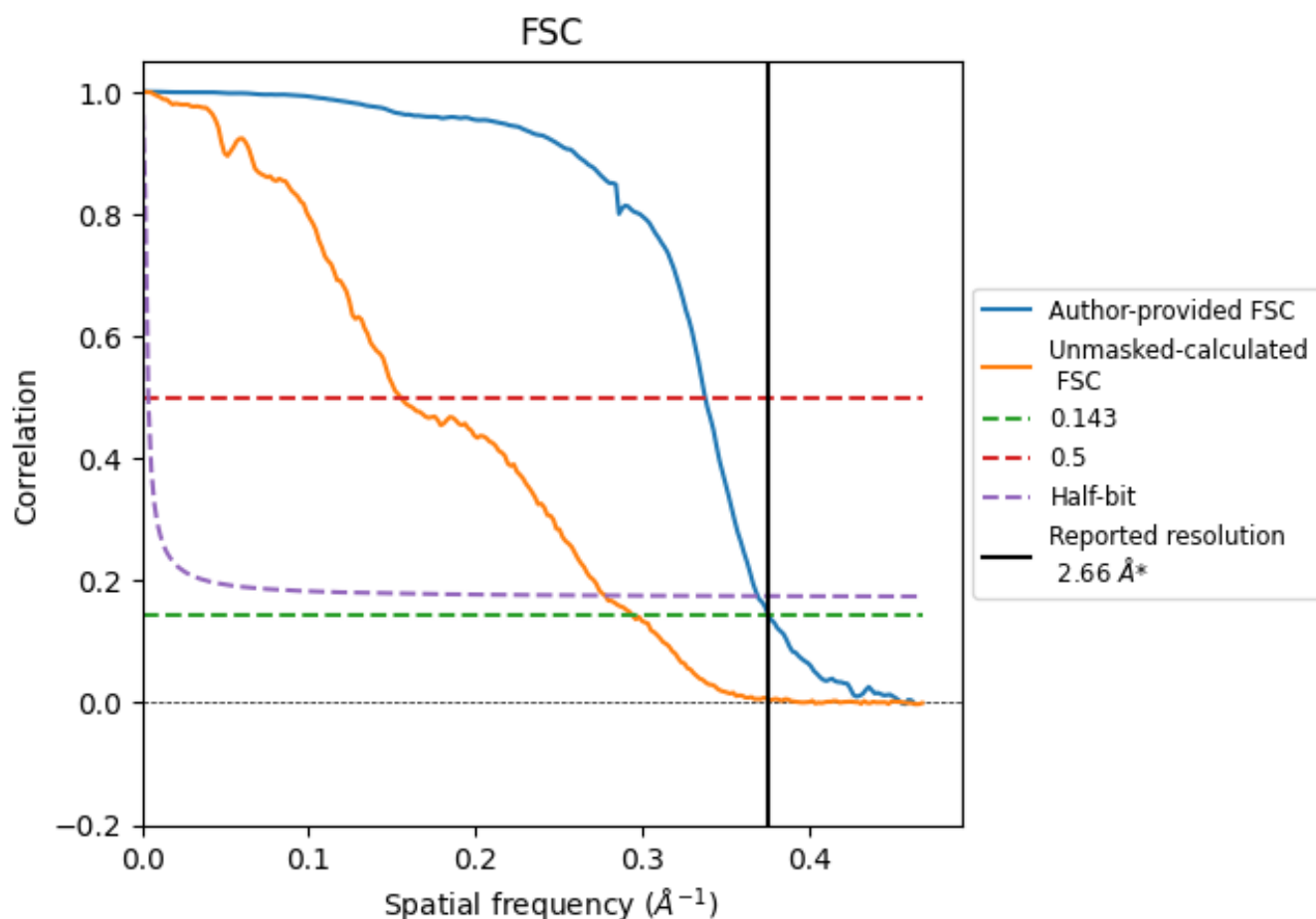


*Reported resolution corresponds to spatial frequency of 0.376 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.376 \AA^{-1}

8.2 Resolution estimates [i](#)

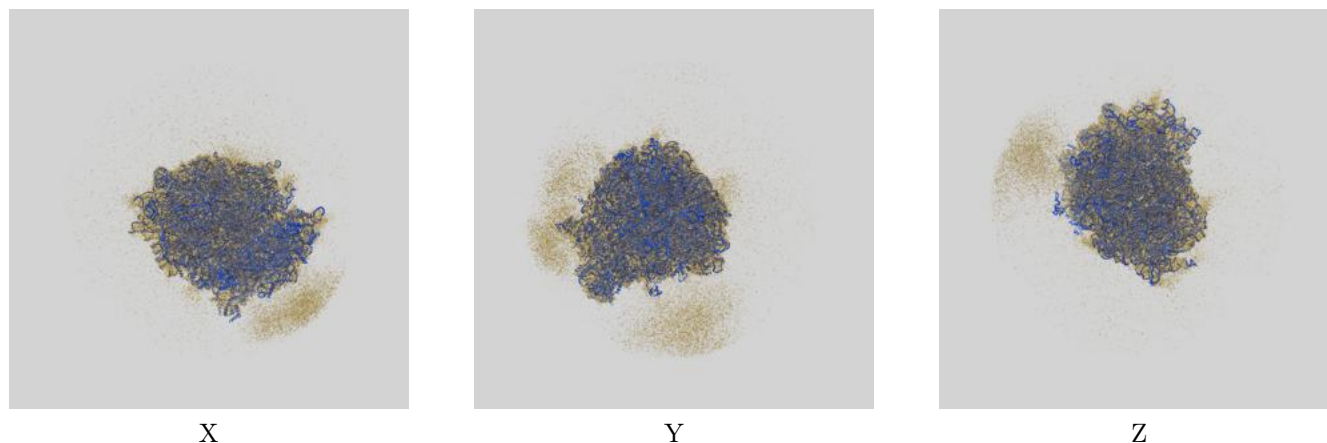
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.66	-	-
Author-provided FSC curve	2.66	2.96	2.71
Unmasked-calculated*	3.40	6.45	3.60

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.40 differs from the reported value 2.66 by more than 10 %

9 Map-model fit [i](#)

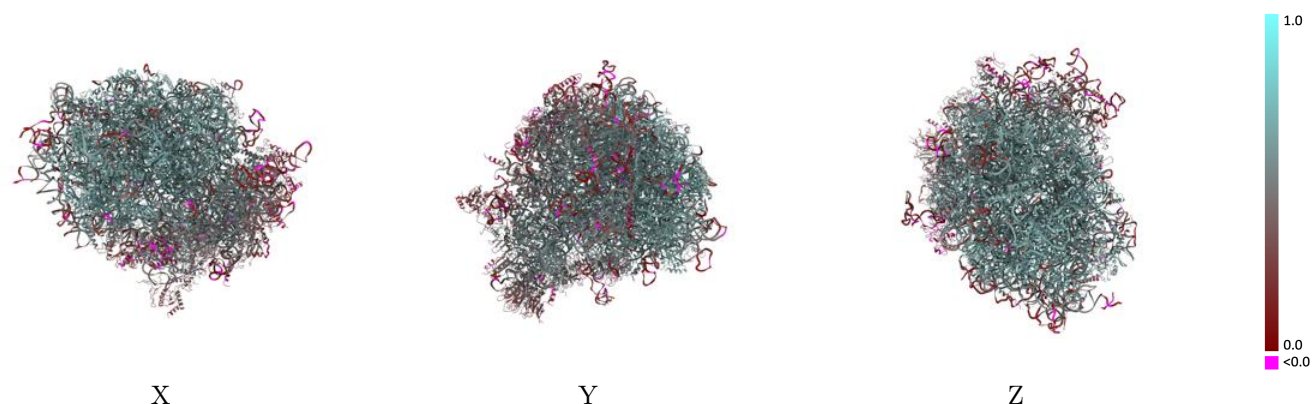
This section contains information regarding the fit between EMDB map EMD-44060 and PDB model 9B0W. Per-residue inclusion information can be found in [section 3](#) on [page 21](#).

9.1 Map-model overlay [i](#)



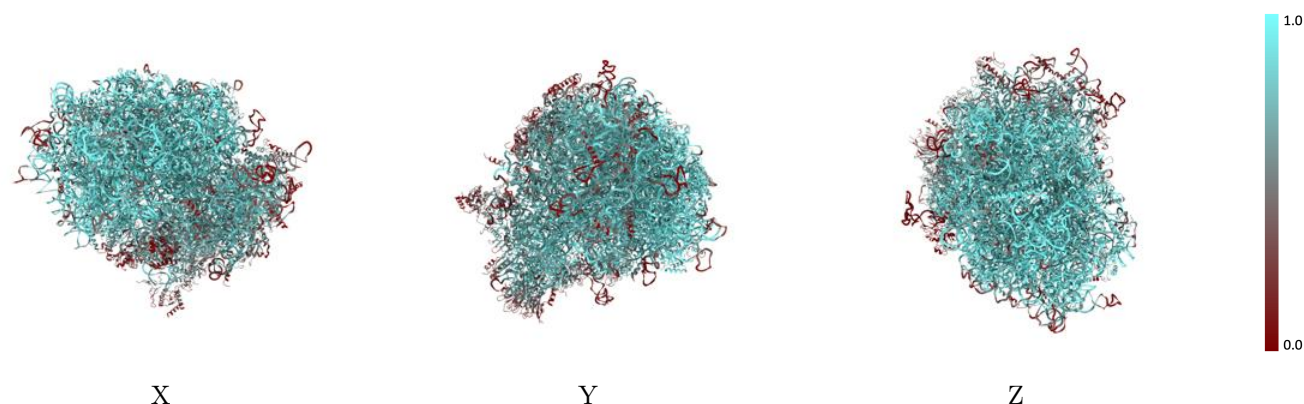
The images above show the 3D surface view of the map at the recommended contour level 0.042 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



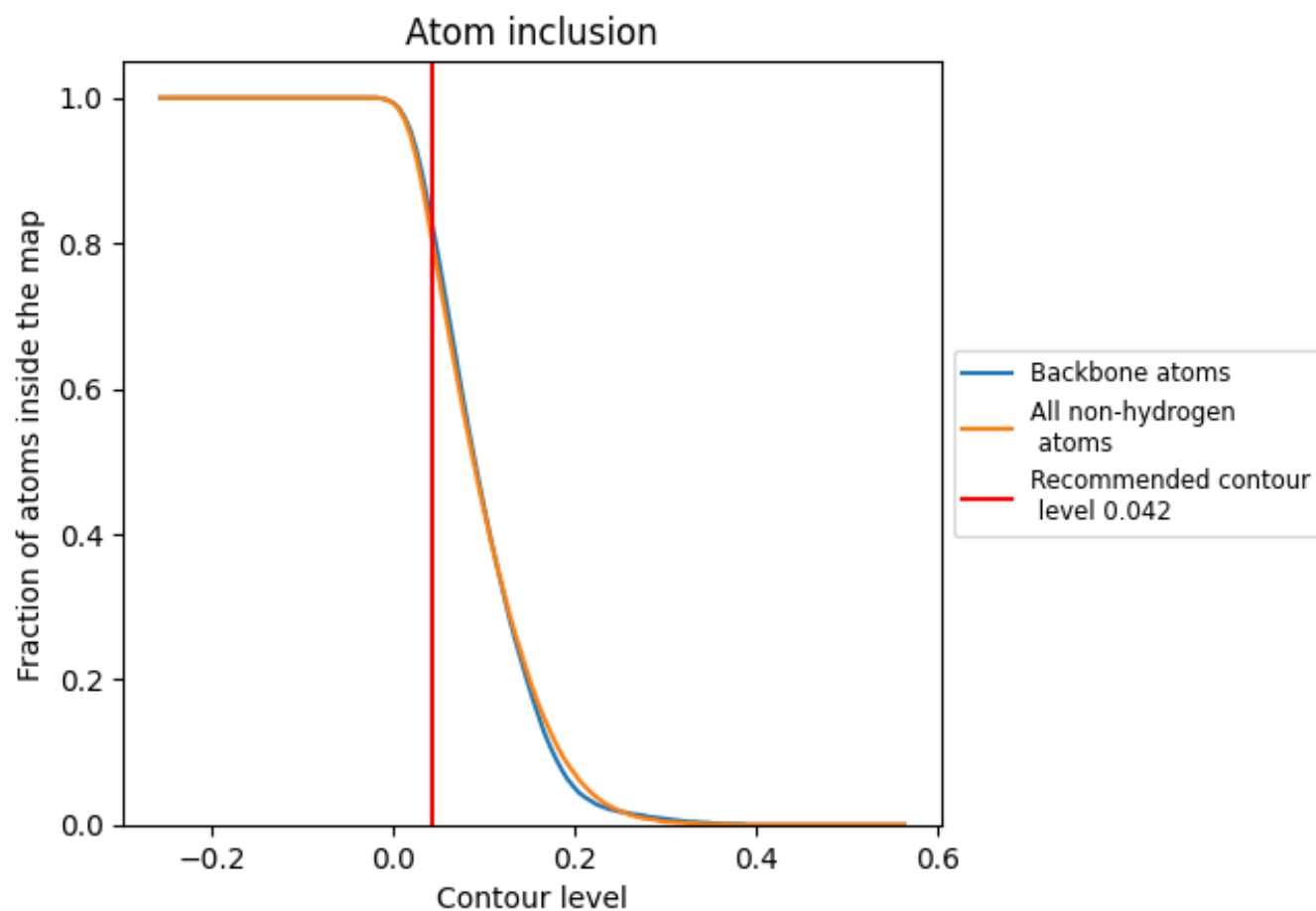
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.042).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 81% 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 (0.042) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8090	 0.5230
AP	 0.6160	 0.3940
CB	 0.5300	 0.4080
CH	 0.3920	 0.3130
L5	 0.8790	 0.5500
L7	 0.9840	 0.6250
L8	 0.9300	 0.5900
LA	 0.9580	 0.6320
LB	 0.9140	 0.6100
LC	 0.9160	 0.6150
LD	 0.8620	 0.5800
LE	 0.8050	 0.5460
LF	 0.9460	 0.6240
LG	 0.8080	 0.5640
LH	 0.8950	 0.5950
LI	 0.9240	 0.6180
LJ	 0.7530	 0.5060
LL	 0.8700	 0.5890
LM	 0.9050	 0.5930
LN	 0.9820	 0.6440
LO	 0.9440	 0.6280
LP	 0.9380	 0.6330
LQ	 0.9640	 0.6390
LR	 0.8240	 0.5420
LS	 0.9620	 0.6360
LT	 0.8890	 0.5920
LU	 0.7530	 0.4940
LV	 0.9370	 0.6190
LW	 0.5890	 0.4250
LX	 0.8960	 0.6100
LY	 0.9000	 0.6130
LZ	 0.8970	 0.5930
La	 0.9600	 0.6420
Lb	 0.8020	 0.5440
Lc	 0.8720	 0.5680






















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Chain	Atom inclusion	Q-score
Ld	 0.8690	 0.5910
Le	 0.9620	 0.6370
Lf	 0.9630	 0.6360
Lg	 0.9020	 0.6040
Lh	 0.9110	 0.6140
Li	 0.9000	 0.6080
Lj	 0.9660	 0.6340
Lk	 0.7810	 0.5560
Ll	 0.9340	 0.6250
Lm	 0.9060	 0.6120
Ln	 0.8950	 0.5960
Lo	 0.9030	 0.6100
Lp	 0.9420	 0.6220
Lr	 0.9430	 0.6290
Ls	 0.2310	 0.2220
Lt	 0.1220	 0.1540
Lz	 0.0320	 0.1050
PE	 0.6220	 0.2960
S2	 0.8420	 0.4990
SA	 0.6970	 0.4820
SB	 0.7770	 0.5480
SC	 0.8050	 0.5360
SD	 0.6380	 0.4600
SE	 0.6670	 0.4490
SF	 0.6490	 0.4600
SG	 0.5310	 0.3980
SH	 0.5340	 0.3940
SI	 0.6580	 0.4620
SJ	 0.6660	 0.4460
SK	 0.6510	 0.4220
SL	 0.7370	 0.4910
SM	 0.2310	 0.2550
SN	 0.8130	 0.5470
SO	 0.7690	 0.5210
SP	 0.6850	 0.4880
SQ	 0.6740	 0.4630
SR	 0.5830	 0.4080
SS	 0.6860	 0.4790
ST	 0.6870	 0.4680
SU	 0.5420	 0.3870
SV	 0.7120	 0.4900
SW	 0.8620	 0.5610

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Chain	Atom inclusion	Q-score
SX	 0.7710	 0.5250
SY	 0.5050	 0.3590
SZ	 0.5110	 0.3900
Sa	 0.8250	 0.5450
Sb	 0.6950	 0.4870
Sc	 0.5000	 0.3310
Sd	 0.8440	 0.5460
Se	 0.5650	 0.3570
Sf	 0.3170	 0.2480
Sg	 0.3910	 0.3370