



wwPDB EM Validation Summary Report ⓘ

Apr 7, 2025 – 03:42 PM EDT

PDB ID : 8UJ9 / pdb_00008uj9
EMDB ID : EMD-42316
Title : In situ human P state 80S ribosome
Authors : Wei, Z.; Yong, X.
Deposited on : 2023-10-11
Resolution : 3.64 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

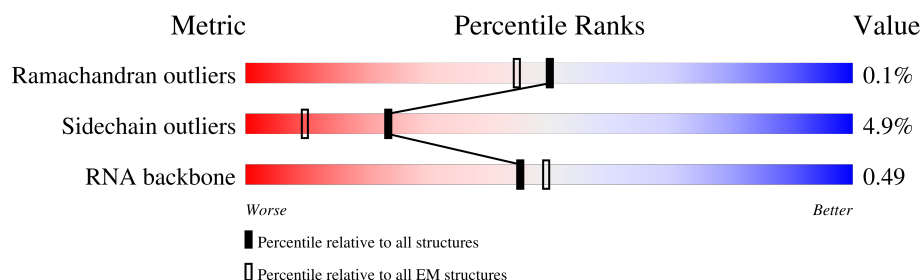
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.64 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	LW	124	
2	SE	262	
3	SI	206	
4	SL	153	
5	SX	141	
6	SG	237	
7	SJ	185	
8	SY	131	

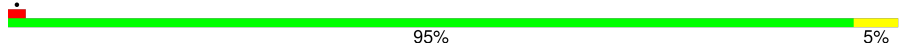
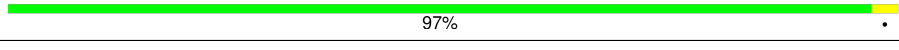
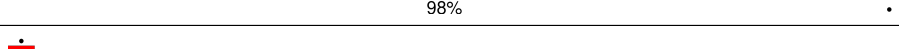
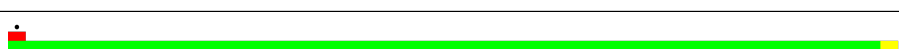

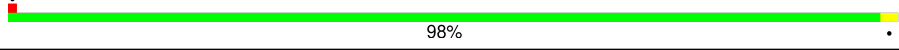
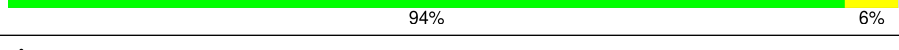
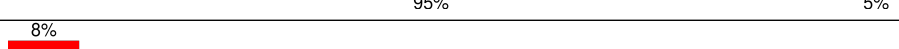

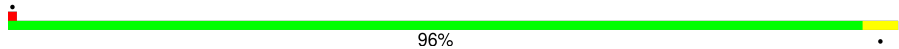
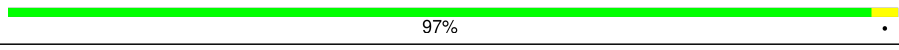
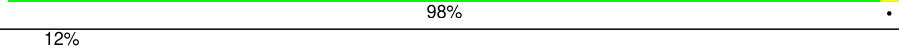

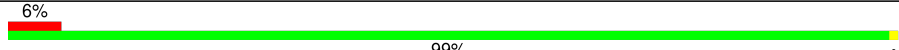
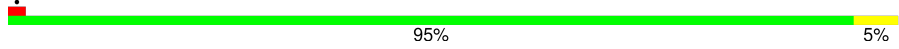
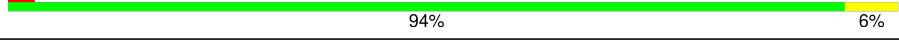
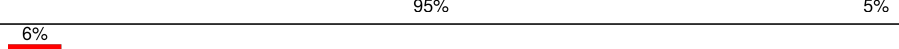


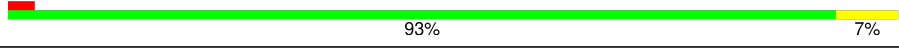
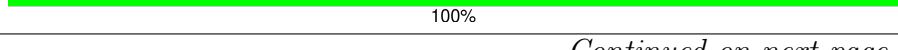



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Mol	Chain	Length	Quality of chain
9	Se	58	
10	SA	221	
11	SB	214	
12	SH	189	
13	SV	83	
14	Sa	102	
15	SC	222	
16	SN	150	
17	SO	140	
18	SW	129	
19	Sb	83	
20	L5	5070	
21	L7	120	
22	L8	156	
23	LA	248	
24	LB	402	
25	LC	368	
26	LD	293	
27	LE	247	
28	LF	225	
29	LG	241	
30	LH	190	
31	LI	213	
32	LJ	176	
33	LL	210	

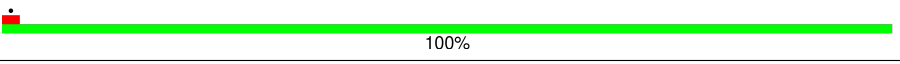
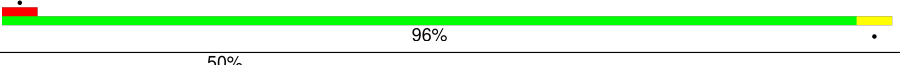
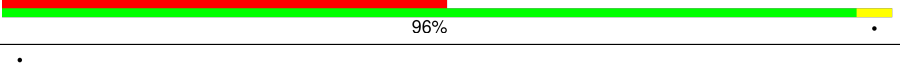
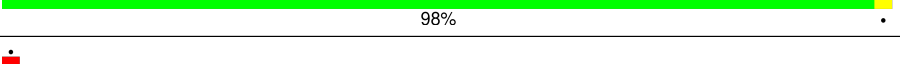
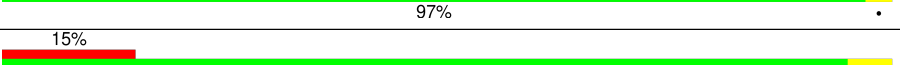
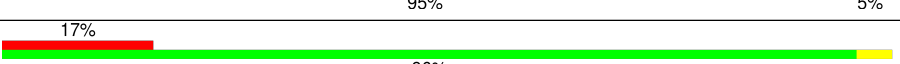
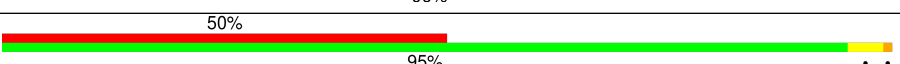
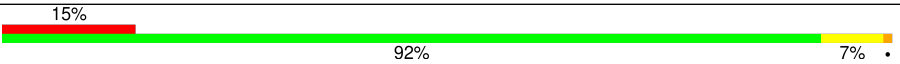
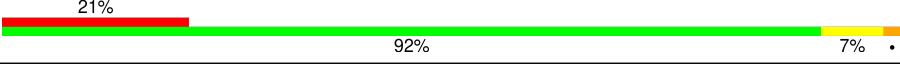
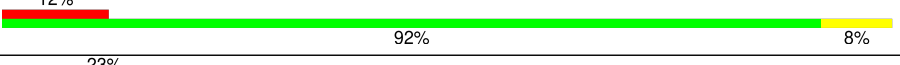
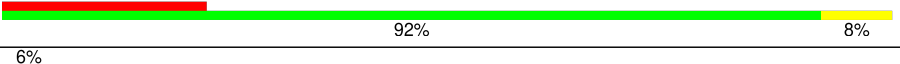
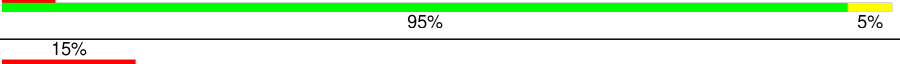
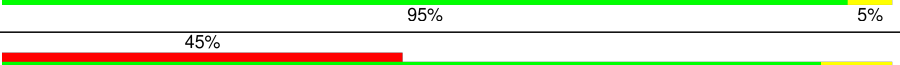
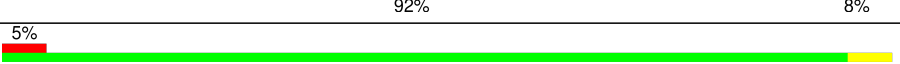
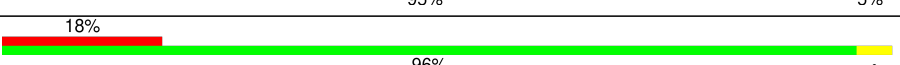
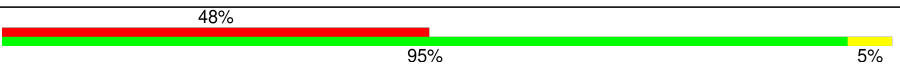
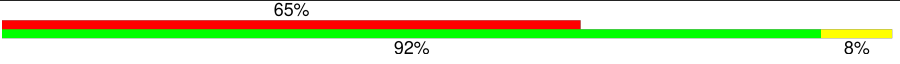
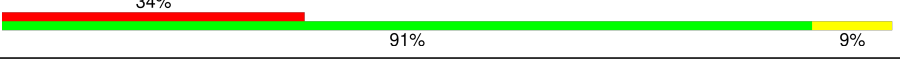

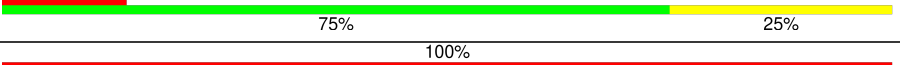
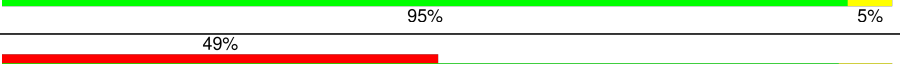
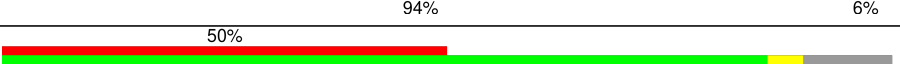



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Mol	Chain	Length	Quality of chain
34	LM	139	
35	LN	203	
36	LO	201	
37	LP	153	
38	LQ	187	
39	LR	187	
40	LS	175	
41	LT	159	
42	LU	101	
43	LV	131	
44	LX	120	
45	LY	134	
46	LZ	135	
47	La	147	
48	Lb	121	
49	Lc	98	
50	Ld	107	
51	Le	128	
52	Lf	109	
53	Lg	114	
54	Lh	122	
55	Li	102	
56	Lj	86	
57	Lk	69	
58	Ll	50	

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Mol	Chain	Length	Quality of chain
59	Lm	52	
60	Ln	24	
61	Lo	105	
62	Lp	91	
63	Lr	125	
64	SR	135	
65	SD	227	
66	SF	189	
67	SK	98	
68	SP	121	
69	SQ	144	
70	SS	145	
71	ST	143	
72	SU	104	
73	Sc	64	
74	Sd	55	
75	Sg	313	
76	SM	122	
77	SZ	75	
78	Sf	67	
79	S2	1870	
80	Pt	76	
81	Lz	217	
82	Ls	196	
83	Lt	157	

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 221165 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 Ribosomal protein L24.

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

- Molecule 2 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 3 is a protein called 40S ribosomal protein S8.

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

- Molecule 4 is a protein called 40S ribosomal protein S11.

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

- Molecule 5 is a protein called 40S ribosomal protein S23.

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

- Molecule 6 is a protein called 40S ribosomal protein S6.

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

- Molecule 7 is a protein called 40S ribosomal protein S9.

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

- Molecule 8 is a protein called 40S ribosomal protein S24.

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

- Molecule 9 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

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

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

- Molecule 11 is a protein called 40S ribosomal protein S3a.

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

- Molecule 12 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 13 is a protein called 40S ribosomal protein S21.

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

- Molecule 14 is a protein called 40S ribosomal protein S26.

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

- Molecule 15 is a protein called 40S ribosomal protein S2.

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

- Molecule 16 is a protein called 40S ribosomal protein S13.

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

- Molecule 17 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 18 is a protein called 40S ribosomal protein S15a.

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

- Molecule 19 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 20 is a RNA chain called 28S rRNA [Homo sapiens].

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

- Molecule 21 is a RNA chain called 5S rRNA [Homo sapiens].

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

- Molecule 22 is a RNA chain called 5.8S rRNA [Homo sapiens].

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

- Molecule 23 is a protein called 60S ribosomal protein L8.

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

- Molecule 24 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 25 is a protein called 60S ribosomal protein L4.

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

- Molecule 26 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 27 is a protein called Large ribosomal subunit protein eL6.

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

- Molecule 28 is a protein called 60S ribosomal protein L7.

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

- Molecule 29 is a protein called 60S ribosomal protein L7a.

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

- Molecule 30 is a protein called 60S ribosomal protein L9.

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

- Molecule 31 is a protein called Ribosomal protein uL16-like.

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

- Molecule 32 is a protein called 60S ribosomal protein L11.

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

- Molecule 33 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 34 is a protein called 60S ribosomal protein L14.

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

- Molecule 35 is a protein called 60S ribosomal protein L15.

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

- Molecule 36 is a protein called 60S ribosomal protein L13a.

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

- Molecule 37 is a protein called 60S ribosomal protein L17.

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

- Molecule 38 is a protein called 60S ribosomal protein L18.

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

- Molecule 39 is a protein called 60S ribosomal protein L19.

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

- Molecule 40 is a protein called 60S ribosomal protein L18a.

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

- Molecule 41 is a protein called 60S ribosomal protein L21.

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

- Molecule 42 is a protein called Heparin-binding protein HBp15.

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

- Molecule 43 is a protein called 60S ribosomal protein L23.

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

- Molecule 44 is a protein called 60S ribosomal protein L23a.

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

- Molecule 45 is a protein called 60S ribosomal protein L26.

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

- Molecule 46 is a protein called 60S ribosomal protein L27.

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

- Molecule 47 is a protein called 60S ribosomal protein L27a.

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

- Molecule 48 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 49 is a protein called 60S ribosomal protein L30.

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

- Molecule 50 is a protein called 60S ribosomal protein L31.

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

- Molecule 51 is a protein called 60S ribosomal protein L32.

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

- Molecule 52 is a protein called 60S ribosomal protein L35a.

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

- Molecule 53 is a protein called 60S ribosomal protein L34.

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

- Molecule 54 is a protein called 60S ribosomal protein L35.

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

- Molecule 55 is a protein called 60S ribosomal protein L36.

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

- Molecule 56 is a protein called 60S ribosomal protein L37.

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

- Molecule 57 is a protein called 60S ribosomal protein L38.

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

- Molecule 58 is a protein called 60S ribosomal protein L39.

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

- Molecule 59 is a protein called Large ribosomal subunit protein eL40.

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

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

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

- Molecule 61 is a protein called 60S ribosomal protein L36a.

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

- Molecule 62 is a protein called 60S ribosomal protein L37a.

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

- Molecule 63 is a protein called 60S ribosomal protein L28.

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

- Molecule 64 is a protein called Small ribosomal subunit protein eS17.

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

- Molecule 65 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 66 is a protein called 40S ribosomal protein S5.

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

- Molecule 67 is a protein called 40S ribosomal protein S10.

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

- Molecule 68 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 69 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 70 is a protein called 40S ribosomal protein S18.

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

- Molecule 71 is a protein called 40S ribosomal protein S19.

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

- Molecule 72 is a protein called 40S ribosomal protein S20.

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

- Molecule 73 is a protein called 40S ribosomal protein S28.

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

- Molecule 74 is a protein called 40S ribosomal protein S29.

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

- Molecule 75 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 76 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 77 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 78 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 79 is a RNA chain called 18S rRNA [Homo sapiens].

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

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S2	60	A	G	conflict	GB 1142736576
S2	140	C	U	conflict	GB 1142736576
S2	747	U	-	insertion	GB 1142736576
S2	750	C	U	conflict	GB 1142736576
S2	752	G	C	conflict	GB 1142736576

- Molecule 80 is a RNA chain called P site tRNA [Homo sapiens].

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Pt	76	Total	C	N	O	P	0	0
			1620	725	296	524	75		

- Molecule 81 is a protein called 60S ribosomal protein L10a.

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

- Molecule 82 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 83 is a protein called Large ribosomal subunit protein uL11.

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

- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

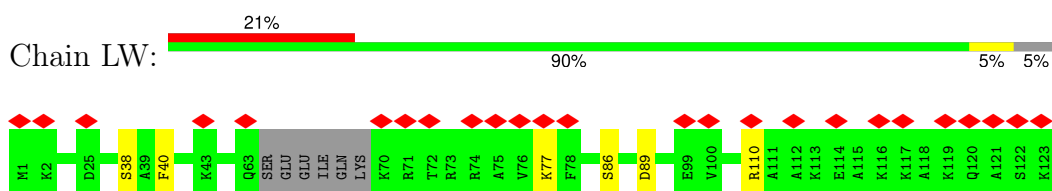
- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
85	Sa	1	Total	Mg	0
			1	1	
85	L5	214	Total	Mg	0
			214	214	
85	L7	3	Total	Mg	0
			3	3	
85	L8	6	Total	Mg	0
			6	6	
85	LA	1	Total	Mg	0
			1	1	
85	LV	1	Total	Mg	0
			1	1	
85	Le	1	Total	Mg	0
			1	1	
85	S2	28	Total	Mg	0
			28	28	

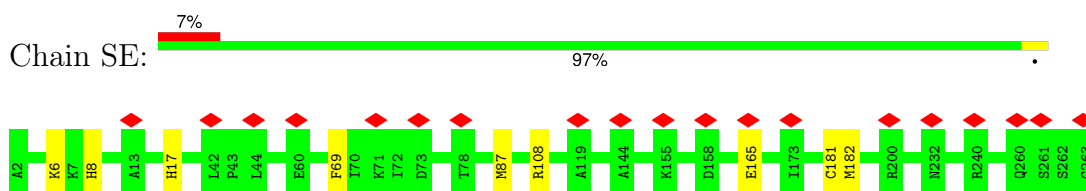
3 Residue-property plots [i](#)

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.

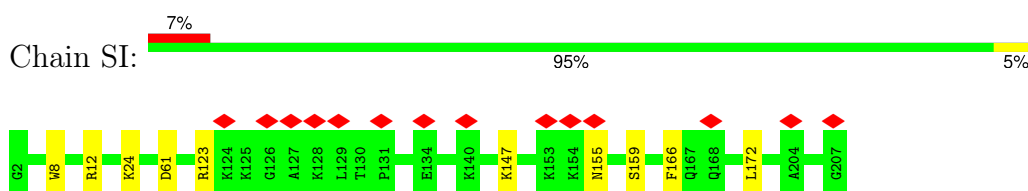
- Molecule 1: Ribosomal protein L24



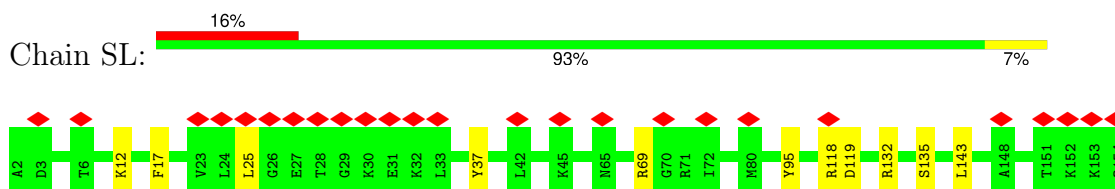
- Molecule 2: Small ribosomal subunit protein eS4, X isoform



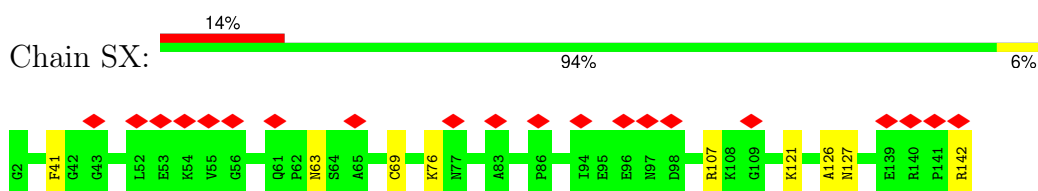
- Molecule 3: 40S ribosomal protein S8



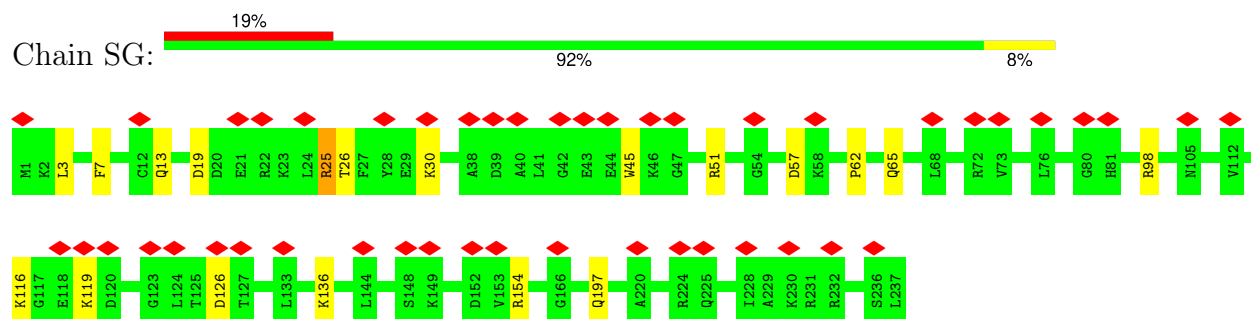
- Molecule 4: 40S ribosomal protein S11



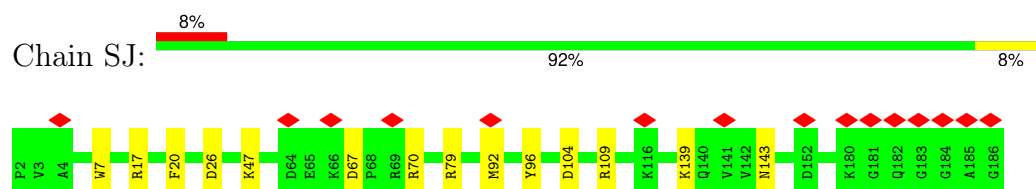
- Molecule 5: 40S ribosomal protein S23



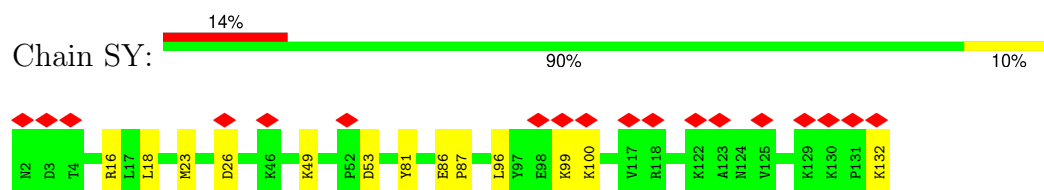
- Molecule 6: 40S ribosomal protein S6



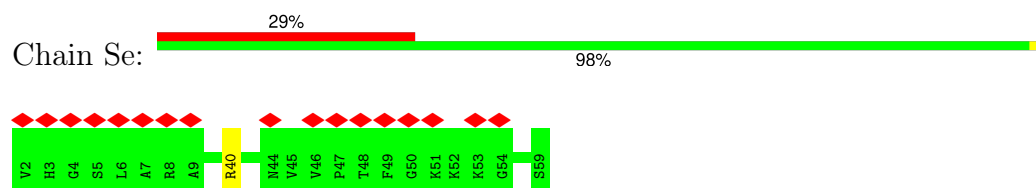
- Molecule 7: 40S ribosomal protein S9



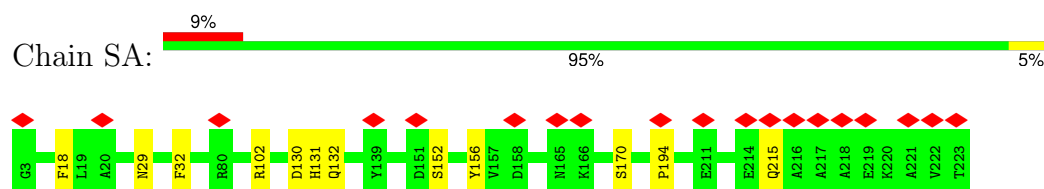
- Molecule 8: 40S ribosomal protein S24



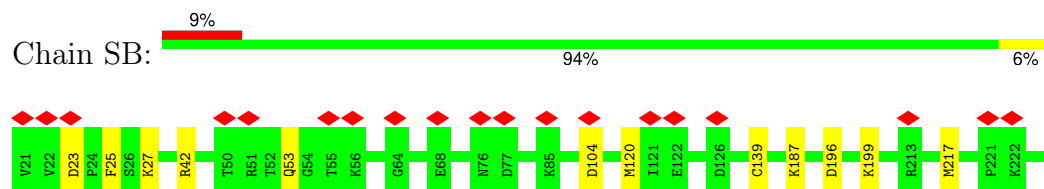
- Molecule 9: Small ribosomal subunit protein eS30



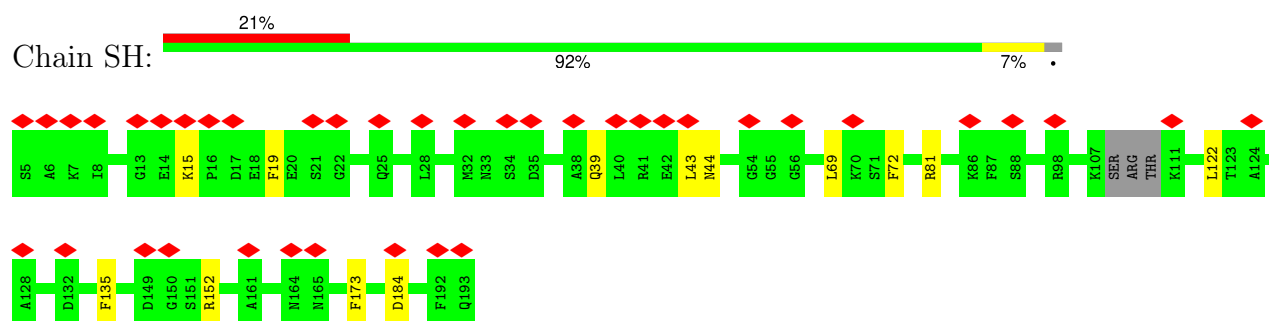
- Molecule 10: 40S ribosomal protein SA



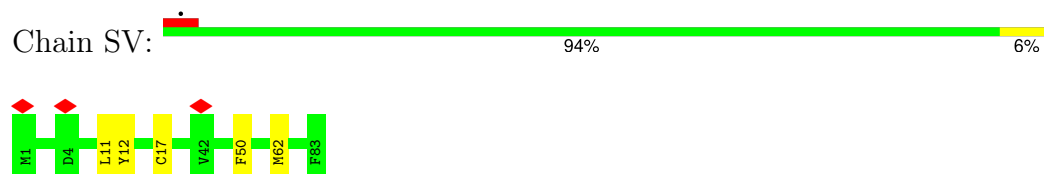
- Molecule 11: 40S ribosomal protein S3a



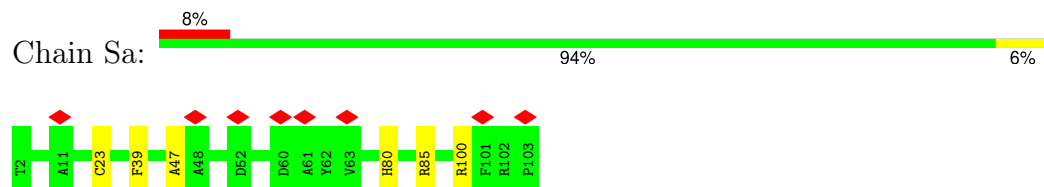
- Molecule 12: Small ribosomal subunit protein eS7



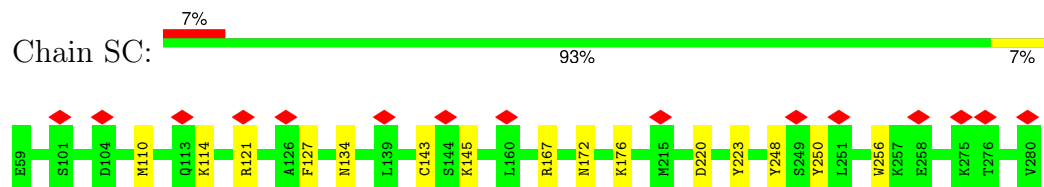
- Molecule 13: 40S ribosomal protein S21



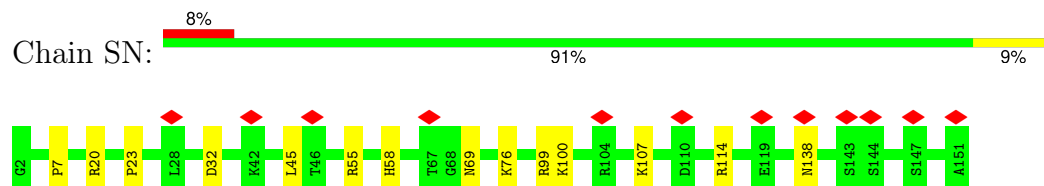
- Molecule 14: 40S ribosomal protein S26



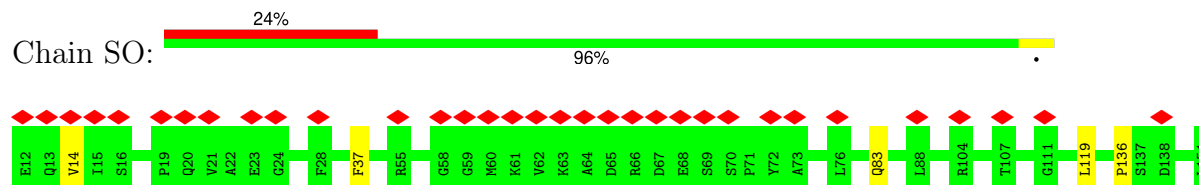
- Molecule 15: 40S ribosomal protein S2



- Molecule 16: 40S ribosomal protein S13



- Molecule 17: Small ribosomal subunit protein uS11

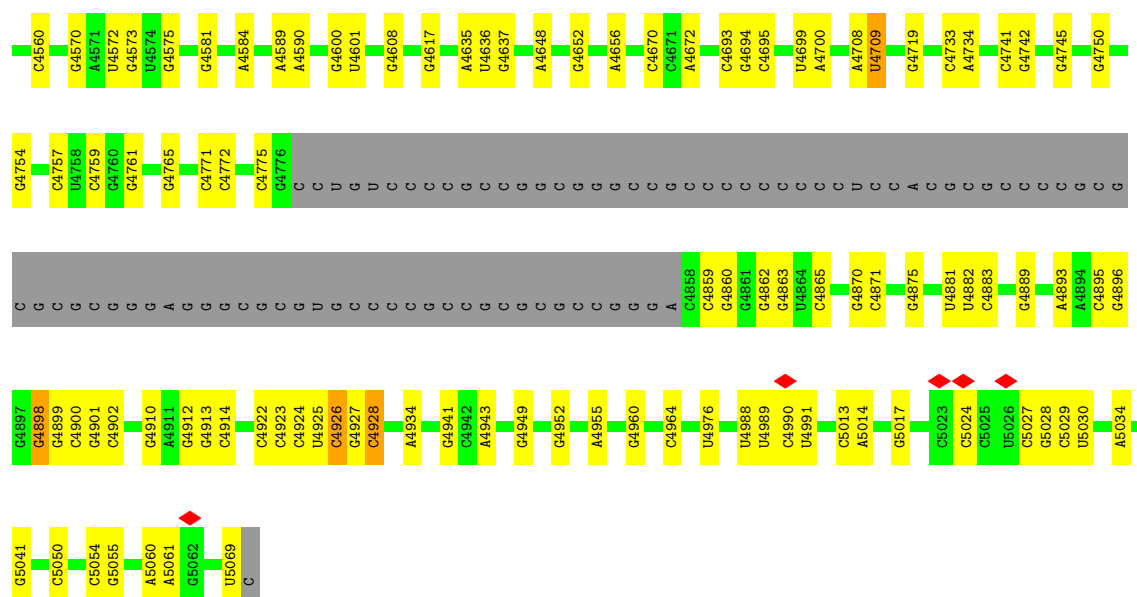


- Molecule 18: 40S ribosomal protein S15a

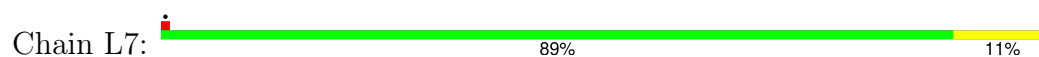




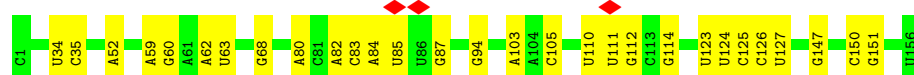
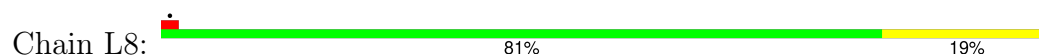




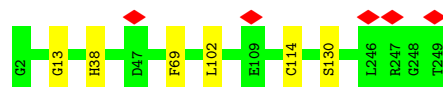
• Molecule 21: 5S rRNA [Homo sapiens]



• Molecule 22: 5.8S rRNA [Homo sapiens]



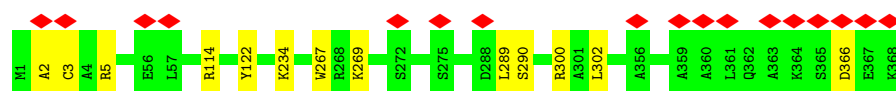
• Molecule 23: 60S ribosomal protein L8



• Molecule 24: Large ribosomal subunit protein uL3



• Molecule 25: 60S ribosomal protein L4



- Molecule 26: Large ribosomal subunit protein uL18



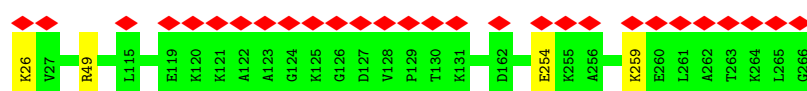
- Molecule 27: Large ribosomal subunit protein eL6



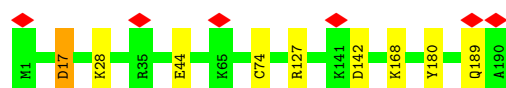
- Molecule 28: 60S ribosomal protein L7



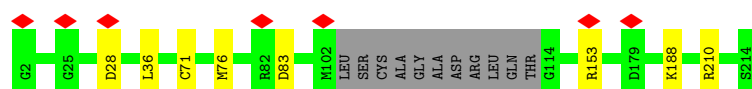
- Molecule 29: 60S ribosomal protein L7a



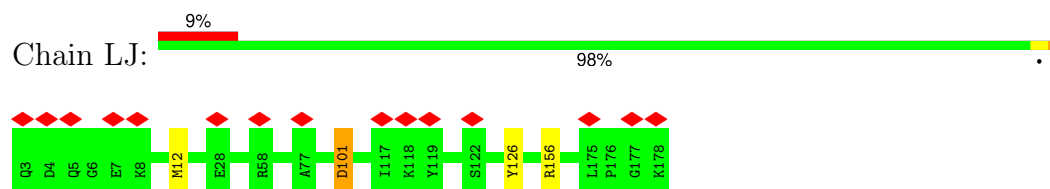
- Molecule 30: 60S ribosomal protein L9



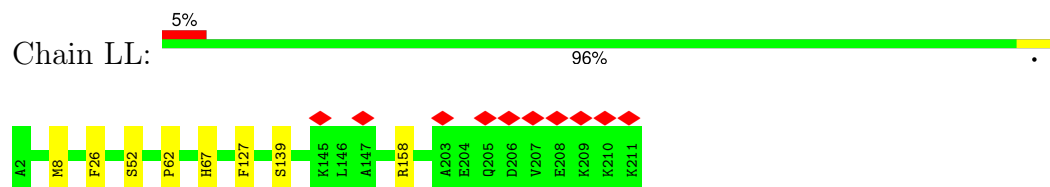
- Molecule 31: Ribosomal protein uL16-like



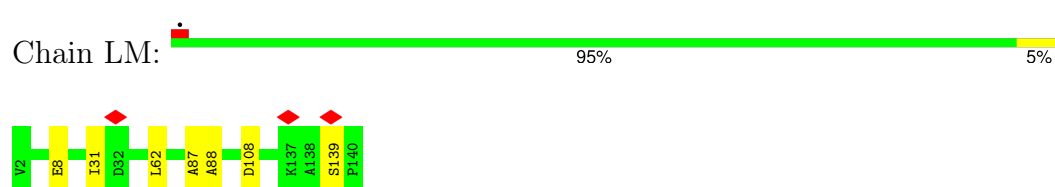
• Molecule 32: 60S ribosomal protein L11



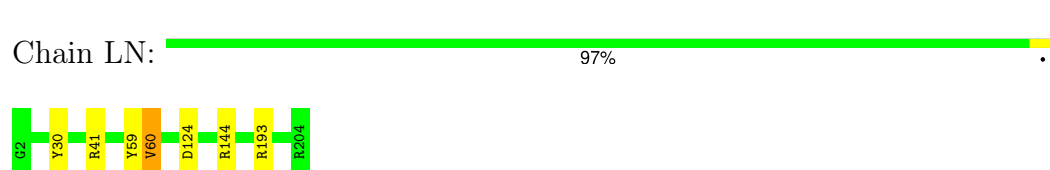
• Molecule 33: Large ribosomal subunit protein eL13



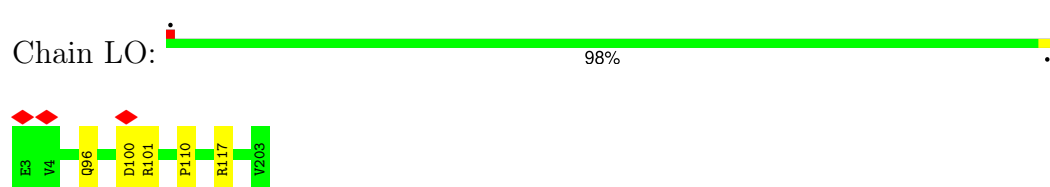
• Molecule 34: 60S ribosomal protein L14



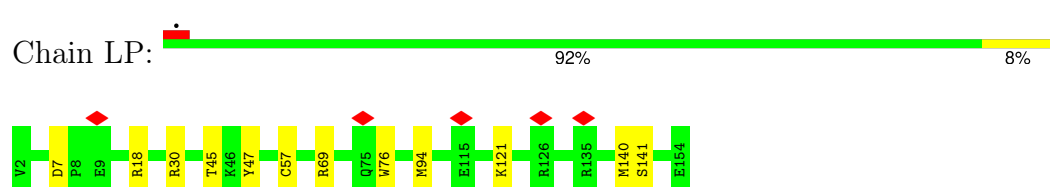
• Molecule 35: 60S ribosomal protein L15



• Molecule 36: 60S ribosomal protein L13a



• Molecule 37: 60S ribosomal protein L17

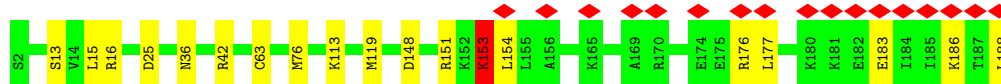
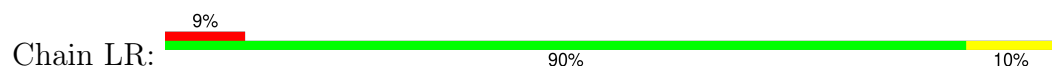


• Molecule 38: 60S ribosomal protein L18

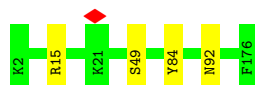




- Molecule 39: 60S ribosomal protein L19



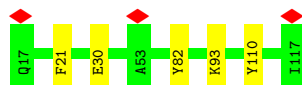
- Molecule 40: 60S ribosomal protein L18a



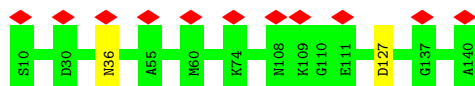
- Molecule 41: 60S ribosomal protein L21



- Molecule 42: Heparin-binding protein HBp15



- Molecule 43: 60S ribosomal protein L23



- Molecule 44: 60S ribosomal protein L23a



- Molecule 45: 60S ribosomal protein L26

Chain LY:  96%



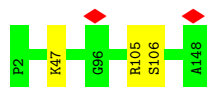
- Molecule 46: 60S ribosomal protein L27

Chain LZ:  97%




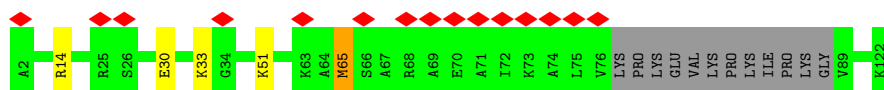
- Molecule 47: 60S ribosomal protein L27a

Chain La:  98%



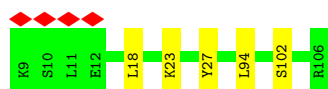
- Molecule 48: Large ribosomal subunit protein eL29

Chain Lb:  12% 86% 10%



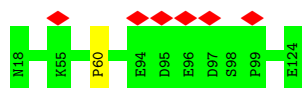
- Molecule 49: 60S ribosomal protein L30

Chain Lc:  95% 5%



- Molecule 50: 60S ribosomal protein L31

Chain Ld:  6% 99%



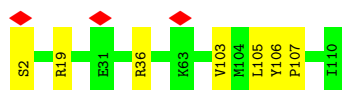
- Molecule 51: 60S ribosomal protein L32

Chain Le:  95% 5%



- Molecule 52: 60S ribosomal protein L35a

Chain Lf:  94% 6%



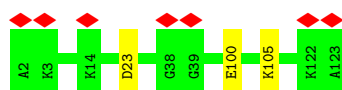
- Molecule 53: 60S ribosomal protein L34

Chain Lg:  95% 5%



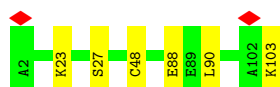
- Molecule 54: 60S ribosomal protein L35

Chain Lh:  98% 6%



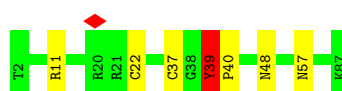
- Molecule 55: 60S ribosomal protein L36

Chain Li:  94% 6%



- Molecule 56: 60S ribosomal protein L37

Chain Lj:  92% 7%



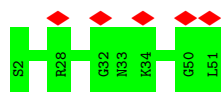
- Molecule 57: 60S ribosomal protein L38

Chain Lk:  93% 7%



- Molecule 58: 60S ribosomal protein L39

Chain Ll:  100% 10%



- Molecule 59: Large ribosomal subunit protein eL40

Chain Lm: 100%



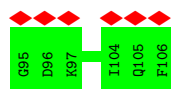
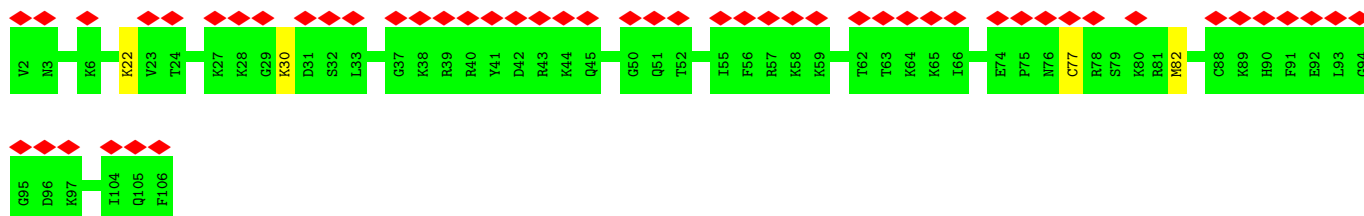
- Molecule 60: 60S ribosomal protein L41

Chain Ln: 96%



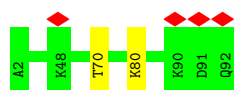
- Molecule 61: 60S ribosomal protein L36a

Chain Lo: 50% 96%



- Molecule 62: 60S ribosomal protein L37a

Chain Lp: 98%



- Molecule 63: 60S ribosomal protein L28

Chain Lr: 97%



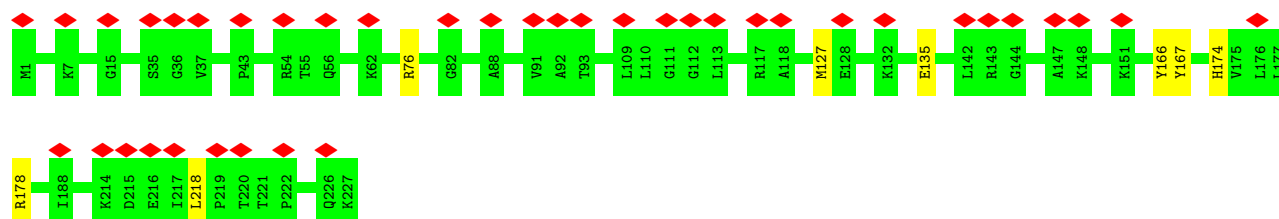
- Molecule 64: Small ribosomal subunit protein eS17

Chain SR: 15% 95% 5%



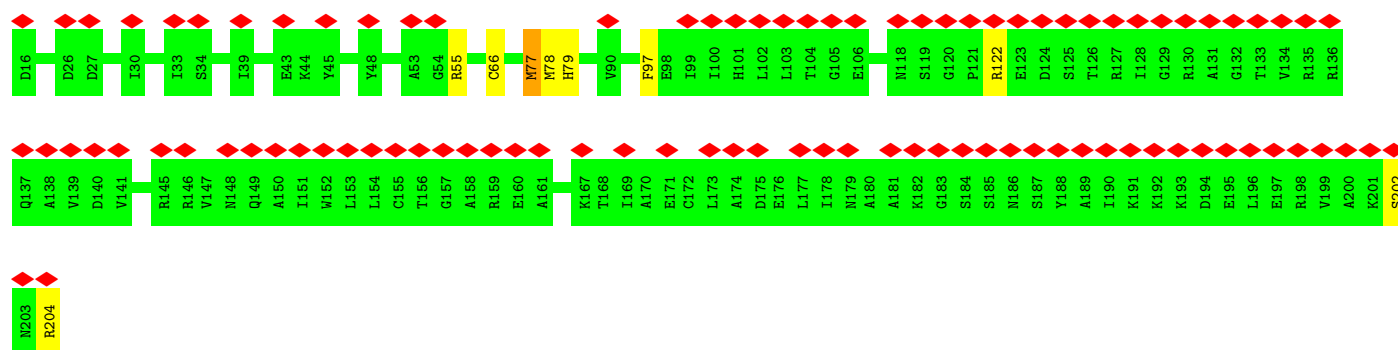
- Molecule 65: Small ribosomal subunit protein uS3

Chain SD: 17% 96%



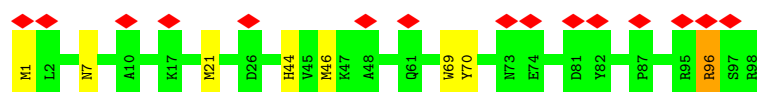
- Molecule 66: 40S ribosomal protein S5

Chain SF: 50% 95%



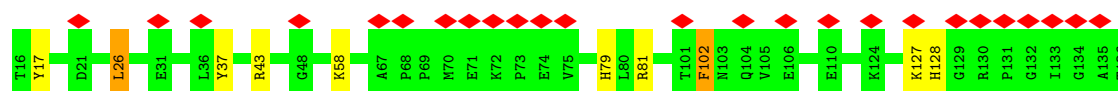
- Molecule 67: 40S ribosomal protein S10

Chain SK: 15% 92% 7%



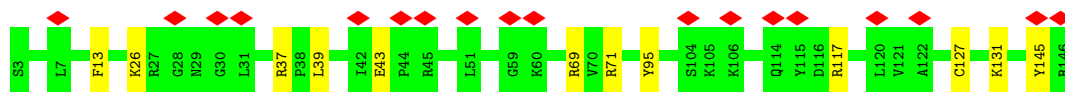
- Molecule 68: Small ribosomal subunit protein uS19

Chain SP: 21% 92% 7%

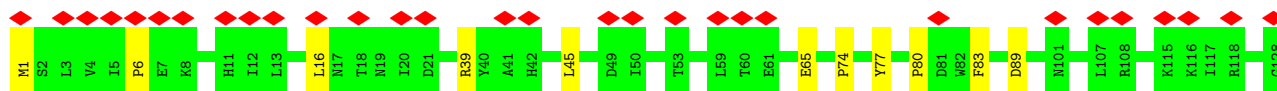


- Molecule 69: Small ribosomal subunit protein uS9

Chain SQ: 12% 92% 8%



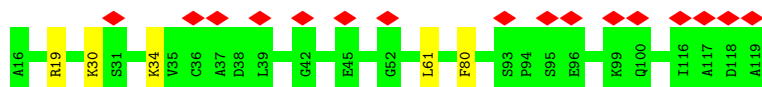
- Molecule 70: 40S ribosomal protein S18



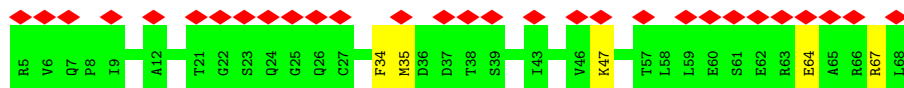
- Molecule 71: 40S ribosomal protein S19



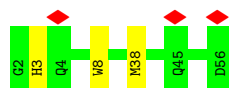
- Molecule 72: 40S ribosomal protein S20



- Molecule 73: 40S ribosomal protein S28

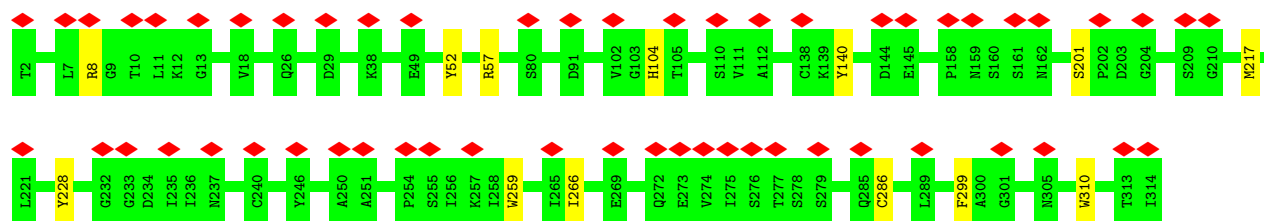


- Molecule 74: 40S ribosomal protein S29



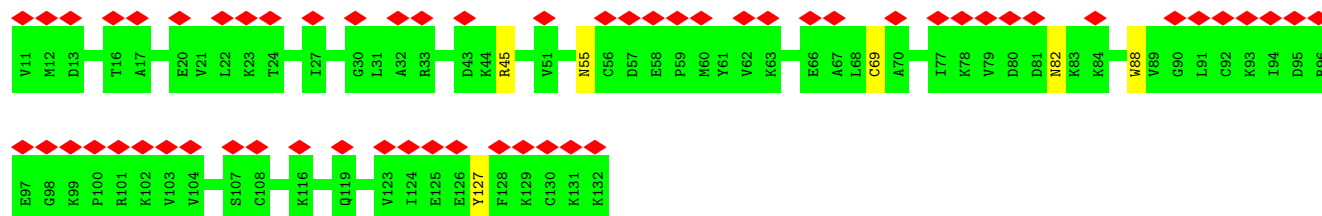
- Molecule 75: Receptor of activated protein C kinase 1





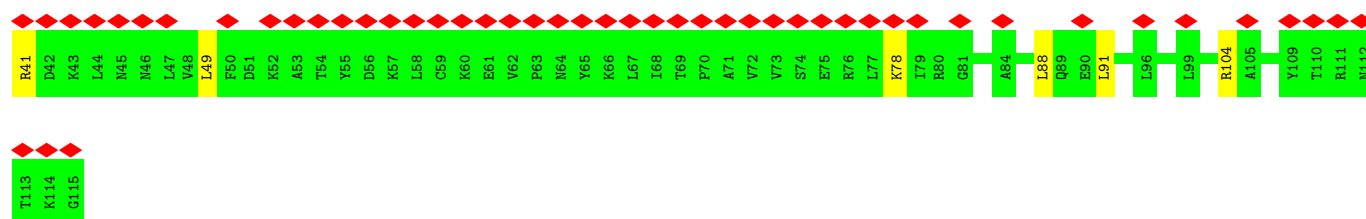
- Molecule 76: Small ribosomal subunit protein eS12

Chain SM: 48% 95% 5%



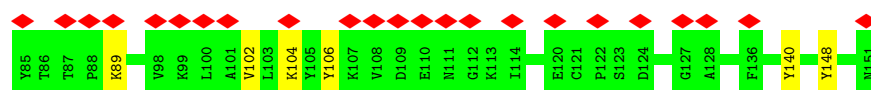
- Molecule 77: Small ribosomal subunit protein eS25

Chain SZ: 65% 92% 8%



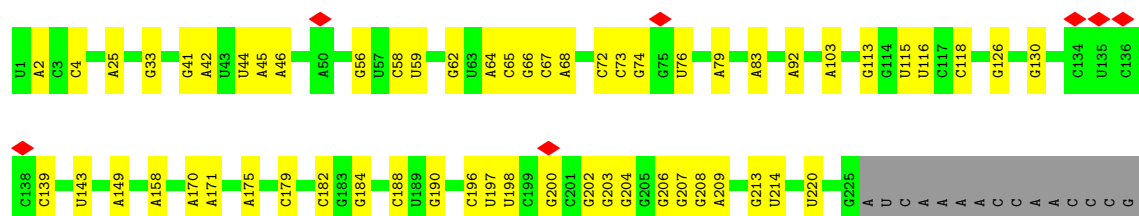
- Molecule 78: Ubiquitin-40S ribosomal protein S27a

Chain Sf: 34% 91% 9%

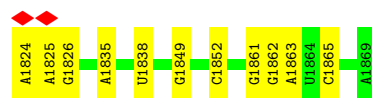


- Molecule 79: 18S rRNA [Homo sapiens]

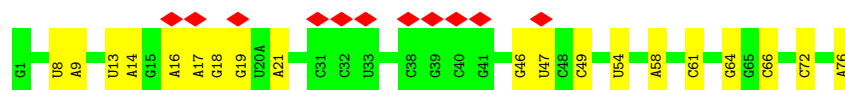
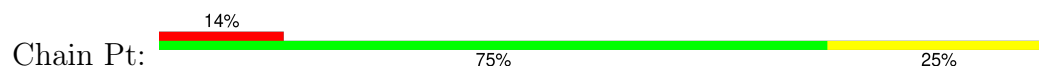
Chain S2: 68% 24% 7%



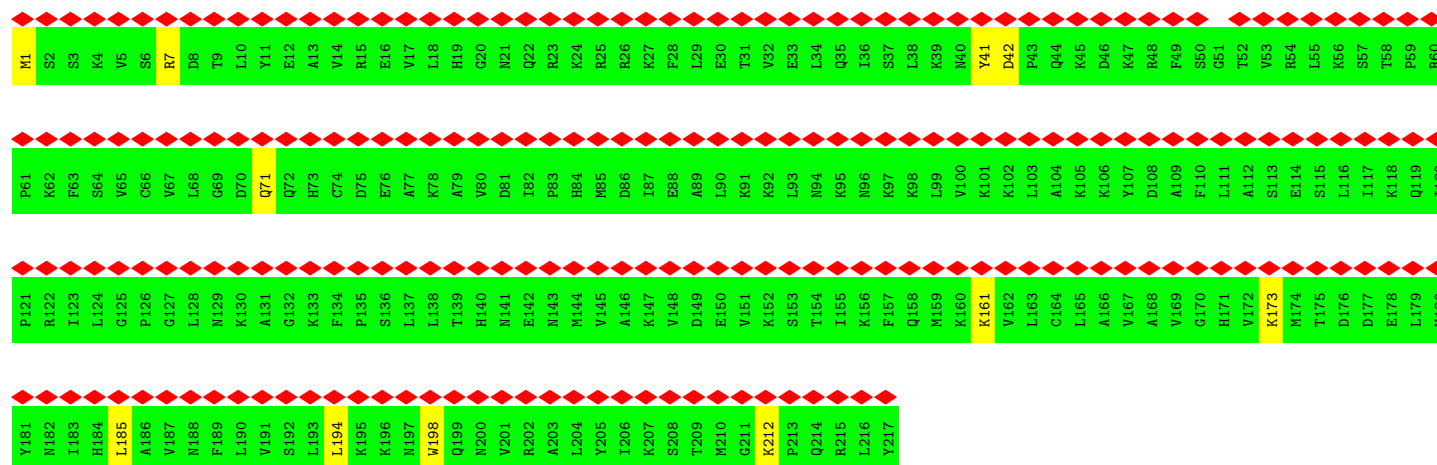




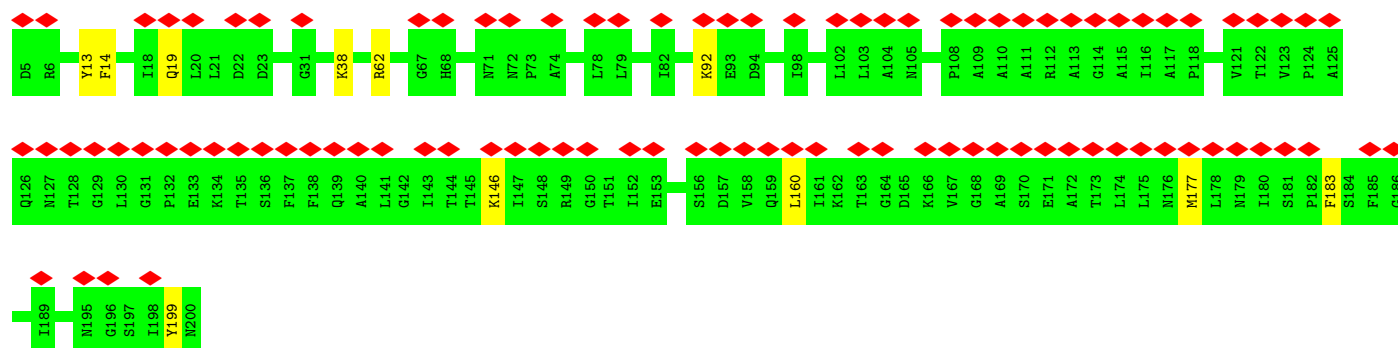
• Molecule 80: P site tRNA [Homo sapiens]



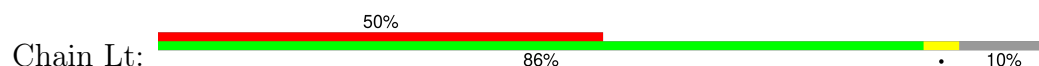
• Molecule 81: 60S ribosomal protein L10a

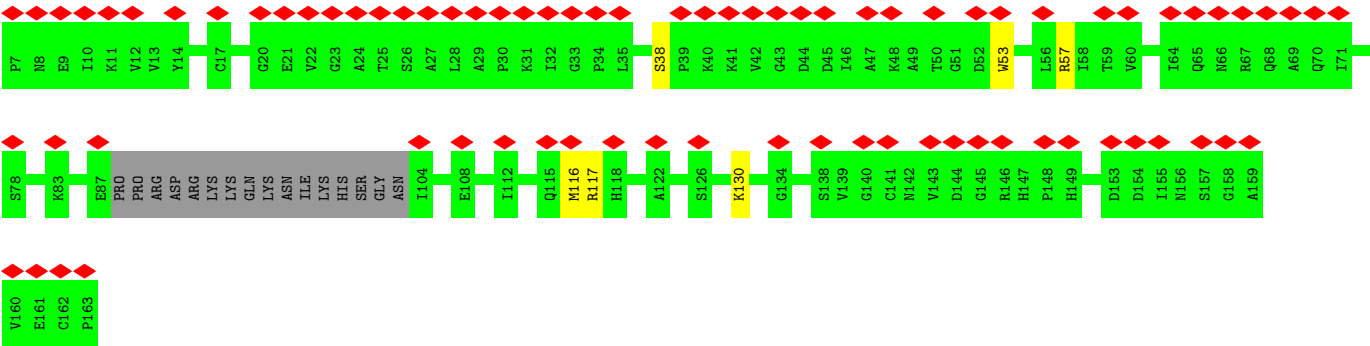


• Molecule 82: 60S acidic ribosomal protein P0



• Molecule 83: Large ribosomal subunit protein uL11





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	9662	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)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.073	Depositor
Minimum map value	-0.058	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0122	Depositor
Map size (\AA)	512.64, 512.64, 512.64	wwPDB
Map dimensions	576, 576, 576	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.89000005, 0.89000005, 0.89000005	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	LW	0.34	0/979	0.60	0/1295
2	SE	0.32	0/2118	0.58	0/2849
3	SI	0.33	0/1715	0.61	0/2287
4	SL	0.37	1/1268 (0.1%)	0.65	0/1696
5	SX	0.40	1/1116 (0.1%)	0.64	0/1490
6	SG	0.90	3/1946 (0.2%)	0.88	7/2590 (0.3%)
7	SJ	0.45	3/1550 (0.2%)	0.67	0/2069
8	SY	1.10	3/1083 (0.3%)	0.99	6/1438 (0.4%)
9	Se	0.28	0/465	0.60	0/612
10	SA	0.34	0/1778	0.67	2/2416 (0.1%)
11	SB	0.32	0/1765	0.57	0/2362
12	SH	0.35	0/1519	0.61	0/2033
13	SV	0.31	0/643	0.61	0/860
14	Sa	0.31	0/836	0.61	0/1121
15	SC	0.32	0/1762	0.60	1/2381 (0.0%)
16	SN	0.77	4/1232 (0.3%)	0.98	4/1656 (0.2%)
17	SO	0.33	0/1062	0.78	4/1425 (0.3%)
18	SW	0.36	0/1051	0.66	0/1406
19	Sb	0.34	0/665	0.63	1/891 (0.1%)
20	L5	0.60	0/89311	0.86	62/139283 (0.0%)
21	L7	0.60	0/2861	0.79	0/4459
22	L8	0.62	0/3701	0.80	0/5766
23	LA	0.38	0/1936	0.62	0/2596
24	LB	0.40	0/3306	0.59	1/4424 (0.0%)
25	LC	0.35	0/2981	0.58	1/4002 (0.0%)
26	LD	0.36	0/2428	0.57	0/3252
27	LE	0.34	0/1942	0.59	1/2606 (0.0%)
28	LF	0.44	0/1905	0.59	0/2539
29	LG	0.35	0/1960	0.61	0/2637
30	LH	0.42	0/1537	0.65	2/2066 (0.1%)
31	LI	0.38	0/1673	0.61	0/2233
32	LJ	0.36	0/1433	0.63	1/1915 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LL	0.38	0/1732	0.66	1/2315 (0.0%)
34	LM	0.48	1/1161 (0.1%)	0.63	0/1554
35	LN	0.44	1/1746 (0.1%)	0.64	0/2338
36	LO	0.38	0/1682	0.57	0/2250
37	LP	0.40	0/1268	0.67	1/1701 (0.1%)
38	LQ	0.44	1/1537 (0.1%)	0.71	2/2052 (0.1%)
39	LR	0.58	1/1582 (0.1%)	0.75	3/2091 (0.1%)
40	LS	0.46	0/1493	0.60	0/2003
41	LT	0.37	0/1326	0.63	0/1770
42	LU	0.39	0/839	0.63	0/1126
43	LV	0.40	0/993	0.60	0/1332
44	LX	0.37	0/1002	0.59	0/1345
45	LY	0.39	0/1132	0.60	0/1504
46	LZ	0.37	0/1130	0.58	0/1507
47	La	0.40	0/1191	0.57	0/1591
48	Lb	0.33	0/889	0.73	1/1175 (0.1%)
49	Lc	0.38	0/774	0.60	1/1038 (0.1%)
50	Ld	0.36	0/903	0.65	1/1216 (0.1%)
51	Le	0.36	0/1071	0.58	0/1429
52	Lf	0.41	0/895	0.65	0/1198
53	Lg	0.36	0/916	0.65	0/1220
54	Lh	0.34	0/1023	0.65	0/1351
55	Li	0.36	0/843	0.69	1/1115 (0.1%)
56	Lj	0.38	0/720	0.69	2/952 (0.2%)
57	Lk	0.34	0/575	0.64	0/761
58	Ll	0.34	0/454	0.60	0/599
59	Lm	0.35	0/435	0.62	0/575
60	Ln	0.33	0/231	0.87	0/294
61	Lo	0.35	0/876	0.59	0/1156
62	Lp	0.40	0/718	0.61	0/953
63	Lr	0.46	2/1017 (0.2%)	0.78	3/1364 (0.2%)
64	SR	0.35	0/1105	0.66	0/1484
65	SD	0.30	0/1793	0.61	1/2414 (0.0%)
66	SF	0.31	0/1516	0.69	1/2037 (0.0%)
67	SK	0.34	0/851	0.65	1/1147 (0.1%)
68	SP	0.54	3/1003 (0.3%)	0.73	1/1342 (0.1%)
69	SQ	0.30	0/1160	0.64	0/1553
70	SS	0.66	4/1216 (0.3%)	1.20	10/1628 (0.6%)
71	ST	0.27	0/1131	0.57	0/1515
72	SU	0.29	0/831	0.64	2/1115 (0.2%)
73	Sc	0.36	0/508	0.68	0/680
74	Sd	0.34	0/470	0.59	0/623
75	Sg	0.36	0/2493	0.62	2/3394 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SM	0.27	0/950	0.50	0/1275
77	SZ	0.30	0/604	0.72	1/810 (0.1%)
78	Sf	0.31	0/560	0.76	3/745 (0.4%)
79	S2	0.42	2/41242 (0.0%)	0.86	63/64255 (0.1%)
80	Pt	0.37	0/1812	0.81	0/2823
81	Lz	0.26	0/1769	0.52	0/2371
82	Ls	0.36	0/1519	0.70	1/2052 (0.0%)
83	Lt	0.29	0/1058	0.61	0/1430
All	All	0.50	30/237272 (0.0%)	0.78	195/348223 (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
5	SX	0	1
6	SG	0	1
12	SH	0	1
23	LA	0	1
24	LB	0	2
34	LM	0	1
36	LO	0	1
39	LR	0	2
52	Lf	0	2
56	Lj	0	1
66	SF	0	1
68	SP	0	1
69	SQ	0	1
77	SZ	0	1
All	All	0	17

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	SG	62	PRO	CG-CD	-33.86	0.39	1.50
8	SY	87	PRO	CG-CD	-30.70	0.49	1.50
16	SN	7	PRO	CG-CD	-20.84	0.81	1.50
39	LR	153	LYS	C-N	-17.41	0.94	1.34
6	SG	62	PRO	CB-CG	12.07	2.10	1.50

The worst 5 of 195 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	SN	7	PRO	N-CD-CG	-21.49	70.96	103.20
6	SG	62	PRO	N-CD-CG	-21.47	71.00	103.20
8	SY	87	PRO	N-CD-CG	-20.92	71.82	103.20
70	SS	74	PRO	N-CD-CG	-20.85	71.92	103.20
70	SS	74	PRO	CB-CG-CD	18.84	179.99	106.50

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
23	LA	13	GLY	Peptide
24	LB	17	LEU	Peptide
6	SG	25	ARG	Sidechain
12	SH	15	LYS	Peptide
5	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	LW	114/124 (92%)	108 (95%)	6 (5%)	0	100	100
2	SE	260/262 (99%)	239 (92%)	21 (8%)	0	100	100
3	SI	204/206 (99%)	192 (94%)	12 (6%)	0	100	100
4	SL	151/153 (99%)	141 (93%)	10 (7%)	0	100	100
5	SX	139/141 (99%)	124 (89%)	14 (10%)	1 (1%)	19	50
6	SG	235/237 (99%)	214 (91%)	21 (9%)	0	100	100
7	SJ	183/185 (99%)	169 (92%)	14 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	SY	129/131 (98%)	118 (92%)	11 (8%)	0	100	100
9	Se	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
10	SA	219/221 (99%)	199 (91%)	20 (9%)	0	100	100
11	SB	212/214 (99%)	202 (95%)	10 (5%)	0	100	100
12	SH	182/189 (96%)	158 (87%)	24 (13%)	0	100	100
13	SV	81/83 (98%)	74 (91%)	7 (9%)	0	100	100
14	Sa	100/102 (98%)	93 (93%)	6 (6%)	1 (1%)	13	43
15	SC	220/222 (99%)	206 (94%)	14 (6%)	0	100	100
16	SN	148/150 (99%)	144 (97%)	4 (3%)	0	100	100
17	SO	138/140 (99%)	123 (89%)	15 (11%)	0	100	100
18	SW	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
19	Sb	81/83 (98%)	69 (85%)	12 (15%)	0	100	100
23	LA	246/248 (99%)	222 (90%)	24 (10%)	0	100	100
24	LB	400/402 (100%)	364 (91%)	36 (9%)	0	100	100
25	LC	366/368 (100%)	338 (92%)	28 (8%)	0	100	100
26	LD	291/293 (99%)	278 (96%)	13 (4%)	0	100	100
27	LE	232/247 (94%)	209 (90%)	23 (10%)	0	100	100
28	LF	223/225 (99%)	209 (94%)	14 (6%)	0	100	100
29	LG	239/241 (99%)	219 (92%)	20 (8%)	0	100	100
30	LH	188/190 (99%)	172 (92%)	16 (8%)	0	100	100
31	LI	198/213 (93%)	183 (92%)	15 (8%)	0	100	100
32	LJ	174/176 (99%)	160 (92%)	14 (8%)	0	100	100
33	LL	208/210 (99%)	188 (90%)	20 (10%)	0	100	100
34	LM	137/139 (99%)	123 (90%)	13 (10%)	1 (1%)	19	50
35	LN	201/203 (99%)	188 (94%)	12 (6%)	1 (0%)	25	57
36	LO	199/201 (99%)	189 (95%)	10 (5%)	0	100	100
37	LP	151/153 (99%)	142 (94%)	9 (6%)	0	100	100
38	LQ	185/187 (99%)	176 (95%)	9 (5%)	0	100	100
39	LR	185/187 (99%)	175 (95%)	8 (4%)	2 (1%)	12	42
40	LS	173/175 (99%)	158 (91%)	15 (9%)	0	100	100
41	LT	157/159 (99%)	148 (94%)	9 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	LU	99/101 (98%)	84 (85%)	15 (15%)	0	100	100
43	LV	129/131 (98%)	121 (94%)	8 (6%)	0	100	100
44	LX	118/120 (98%)	116 (98%)	2 (2%)	0	100	100
45	LY	132/134 (98%)	127 (96%)	5 (4%)	0	100	100
46	LZ	133/135 (98%)	119 (90%)	14 (10%)	0	100	100
47	La	145/147 (99%)	135 (93%)	10 (7%)	0	100	100
48	Lb	105/121 (87%)	94 (90%)	11 (10%)	0	100	100
49	Lc	96/98 (98%)	86 (90%)	10 (10%)	0	100	100
50	Ld	105/107 (98%)	97 (92%)	8 (8%)	0	100	100
51	Le	126/128 (98%)	113 (90%)	13 (10%)	0	100	100
52	Lf	107/109 (98%)	98 (92%)	8 (8%)	1 (1%)	14	45
53	Lg	112/114 (98%)	108 (96%)	4 (4%)	0	100	100
54	Lh	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
55	Li	100/102 (98%)	94 (94%)	6 (6%)	0	100	100
56	Lj	84/86 (98%)	77 (92%)	7 (8%)	0	100	100
57	Lk	67/69 (97%)	63 (94%)	4 (6%)	0	100	100
58	Ll	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
59	Lm	50/52 (96%)	50 (100%)	0	0	100	100
60	Ln	22/24 (92%)	22 (100%)	0	0	100	100
61	Lo	103/105 (98%)	97 (94%)	6 (6%)	0	100	100
62	Lp	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
63	Lr	123/125 (98%)	114 (93%)	9 (7%)	0	100	100
64	SR	133/135 (98%)	114 (86%)	18 (14%)	1 (1%)	16	47
65	SD	225/227 (99%)	210 (93%)	15 (7%)	0	100	100
66	SF	187/189 (99%)	165 (88%)	21 (11%)	1 (0%)	25	57
67	SK	96/98 (98%)	84 (88%)	11 (12%)	1 (1%)	13	43
68	SP	119/121 (98%)	110 (92%)	9 (8%)	0	100	100
69	SQ	142/144 (99%)	124 (87%)	18 (13%)	0	100	100
70	SS	143/145 (99%)	135 (94%)	8 (6%)	0	100	100
71	ST	141/143 (99%)	128 (91%)	12 (8%)	1 (1%)	19	50
72	SU	102/104 (98%)	95 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	Sc	62/64 (97%)	53 (86%)	9 (14%)	0	100	100
74	Sd	53/55 (96%)	47 (89%)	6 (11%)	0	100	100
75	Sg	311/313 (99%)	273 (88%)	38 (12%)	0	100	100
76	SM	120/122 (98%)	109 (91%)	11 (9%)	0	100	100
77	SZ	73/75 (97%)	60 (82%)	13 (18%)	0	100	100
78	Sf	65/67 (97%)	56 (86%)	9 (14%)	0	100	100
81	Lz	215/217 (99%)	172 (80%)	43 (20%)	0	100	100
82	Ls	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
83	Lt	137/157 (87%)	105 (77%)	32 (23%)	0	100	100
All	All	11863/12090 (98%)	10871 (92%)	981 (8%)	11 (0%)	50	78

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
39	LR	153	LYS
39	LR	154	LEU
71	ST	39	LEU
5	SX	127	ASN
14	Sa	47	ALA

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	LW	97/103 (94%)	91 (94%)	6 (6%)	15	41
2	SE	224/224 (100%)	215 (96%)	9 (4%)	27	52
3	SI	178/178 (100%)	168 (94%)	10 (6%)	17	44
4	SL	137/137 (100%)	127 (93%)	10 (7%)	11	35
5	SX	113/113 (100%)	107 (95%)	6 (5%)	19	45
6	SG	207/207 (100%)	191 (92%)	16 (8%)	10	34
7	SJ	161/161 (100%)	148 (92%)	13 (8%)	9	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	SY	113/113 (100%)	103 (91%)	10 (9%)	8	30
9	Se	47/47 (100%)	46 (98%)	1 (2%)	48	68
10	SA	183/183 (100%)	172 (94%)	11 (6%)	16	42
11	SB	195/195 (100%)	182 (93%)	13 (7%)	13	38
12	SH	166/169 (98%)	154 (93%)	12 (7%)	12	35
13	SV	67/67 (100%)	62 (92%)	5 (8%)	11	34
14	Sa	89/89 (100%)	84 (94%)	5 (6%)	17	44
15	SC	188/188 (100%)	174 (93%)	14 (7%)	11	35
16	SN	130/130 (100%)	120 (92%)	10 (8%)	10	34
17	SO	110/110 (100%)	108 (98%)	2 (2%)	54	72
18	SW	112/112 (100%)	106 (95%)	6 (5%)	18	45
19	Sb	75/75 (100%)	72 (96%)	3 (4%)	27	52
23	LA	190/190 (100%)	185 (97%)	5 (3%)	41	61
24	LB	348/348 (100%)	335 (96%)	13 (4%)	29	54
25	LC	306/306 (100%)	294 (96%)	12 (4%)	27	53
26	LD	246/247 (100%)	228 (93%)	18 (7%)	11	35
27	LE	209/220 (95%)	205 (98%)	4 (2%)	52	70
28	LF	194/194 (100%)	187 (96%)	7 (4%)	30	55
29	LG	203/205 (99%)	199 (98%)	4 (2%)	50	69
30	LH	169/169 (100%)	161 (95%)	8 (5%)	22	47
31	LI	172/180 (96%)	164 (95%)	8 (5%)	22	47
32	LJ	148/148 (100%)	144 (97%)	4 (3%)	40	60
33	LL	176/176 (100%)	169 (96%)	7 (4%)	27	52
34	LM	118/118 (100%)	114 (97%)	4 (3%)	32	56
35	LN	171/171 (100%)	165 (96%)	6 (4%)	31	56
36	LO	173/173 (100%)	169 (98%)	4 (2%)	45	64
37	LP	134/134 (100%)	123 (92%)	11 (8%)	9	32
38	LQ	164/164 (100%)	163 (99%)	1 (1%)	84	91
39	LR	166/166 (100%)	152 (92%)	14 (8%)	9	31
40	LS	156/156 (100%)	152 (97%)	4 (3%)	41	61
41	LT	139/139 (100%)	130 (94%)	9 (6%)	14	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	LU	91/91 (100%)	86 (94%)	5 (6%)	18	44
43	LV	101/101 (100%)	99 (98%)	2 (2%)	50	69
44	LX	108/108 (100%)	106 (98%)	2 (2%)	52	70
45	LY	124/124 (100%)	118 (95%)	6 (5%)	21	47
46	LZ	117/117 (100%)	113 (97%)	4 (3%)	32	56
47	La	120/120 (100%)	117 (98%)	3 (2%)	42	62
48	Lb	88/101 (87%)	83 (94%)	5 (6%)	17	43
49	Lc	83/83 (100%)	79 (95%)	4 (5%)	21	47
50	Ld	98/98 (100%)	98 (100%)	0	100	100
51	Le	114/114 (100%)	108 (95%)	6 (5%)	19	45
52	Lf	88/88 (100%)	84 (96%)	4 (4%)	23	49
53	Lg	98/98 (100%)	92 (94%)	6 (6%)	15	41
54	Lh	109/109 (100%)	106 (97%)	3 (3%)	38	60
55	Li	86/86 (100%)	81 (94%)	5 (6%)	17	43
56	Lj	73/73 (100%)	67 (92%)	6 (8%)	9	32
57	Lk	64/64 (100%)	59 (92%)	5 (8%)	10	33
58	Ll	47/47 (100%)	47 (100%)	0	100	100
59	Lm	48/48 (100%)	48 (100%)	0	100	100
60	Ln	23/23 (100%)	22 (96%)	1 (4%)	25	50
61	Lo	93/93 (100%)	89 (96%)	4 (4%)	25	50
62	Lp	74/74 (100%)	72 (97%)	2 (3%)	40	60
63	Lr	109/109 (100%)	106 (97%)	3 (3%)	38	60
64	SR	122/122 (100%)	116 (95%)	6 (5%)	21	46
65	SD	190/190 (100%)	183 (96%)	7 (4%)	29	54
66	SF	159/159 (100%)	152 (96%)	7 (4%)	24	50
67	SK	89/89 (100%)	82 (92%)	7 (8%)	10	33
68	SP	107/107 (100%)	98 (92%)	9 (8%)	9	31
69	SQ	119/119 (100%)	108 (91%)	11 (9%)	7	28
70	SS	126/126 (100%)	118 (94%)	8 (6%)	15	40
71	ST	113/113 (100%)	107 (95%)	6 (5%)	19	45
72	SU	94/94 (100%)	90 (96%)	4 (4%)	25	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	Sc	57/57 (100%)	52 (91%)	5 (9%)	8	30
74	Sd	48/48 (100%)	45 (94%)	3 (6%)	15	40
75	Sg	272/272 (100%)	261 (96%)	11 (4%)	27	52
76	SM	102/104 (98%)	96 (94%)	6 (6%)	16	42
77	SZ	66/66 (100%)	62 (94%)	4 (6%)	15	41
78	Sf	60/60 (100%)	56 (93%)	4 (7%)	13	38
81	Lz	195/196 (100%)	184 (94%)	11 (6%)	17	44
82	Ls	162/164 (99%)	152 (94%)	10 (6%)	15	41
83	Lt	112/130 (86%)	106 (95%)	6 (5%)	18	45
All	All	10323/10390 (99%)	9817 (95%)	506 (5%)	23	46

5 of 506 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	LH	180	TYR
72	SU	30	LYS
39	LR	119	MET
71	ST	41	LYS
77	SZ	88	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
40	LS	144	GLN
64	SR	31	ASN
83	Lt	142	ASN
41	LT	66	ASN
51	Le	92	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
20	L5	3703/5070 (73%)	882 (23%)	24 (0%)
21	L7	119/120 (99%)	13 (10%)	0
22	L8	155/156 (99%)	29 (18%)	0
79	S2	1715/1870 (91%)	448 (26%)	7 (0%)
80	Pt	75/76 (98%)	19 (25%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	5767/7292 (79%)	1391 (24%)	31 (0%)

5 of 1391 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
20	L5	13	U
20	L5	25	A
20	L5	26	C
20	L5	30	C
20	L5	39	A

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
20	L5	2760	G
79	S2	563	G
20	L5	3673	C
79	S2	1434	C
79	S2	291	G

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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
79	S2	3
20	L5	2
39	LR	1

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S2	739:C	O3'	746:C	P	13.79
1	S2	1693:G	O3'	1694:U	P	5.44
1	L5	3944:G	O3'	3945:A	P	4.63
1	L5	4068:U	O3'	4069:U	P	3.15
1	S2	1210:G	O3'	1211:G	P	3.09

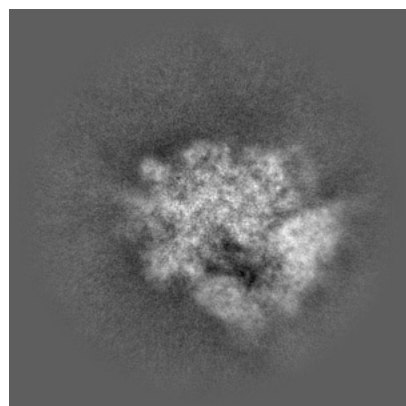
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42316. These allow visual inspection of the internal detail of the map and identification of artifacts.

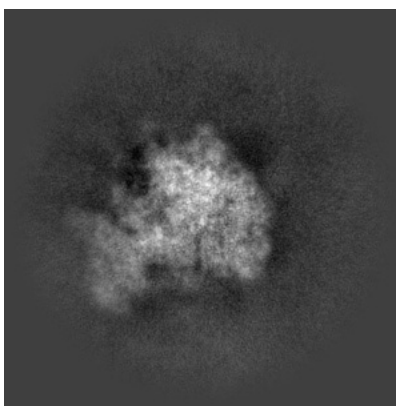
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

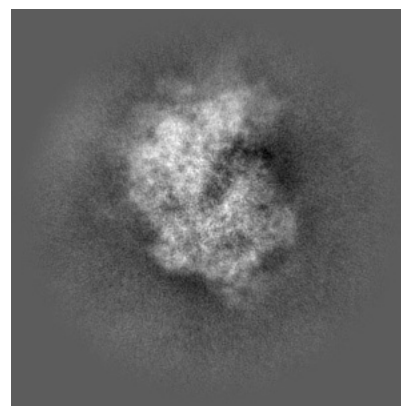
6.1.1 Primary map



X

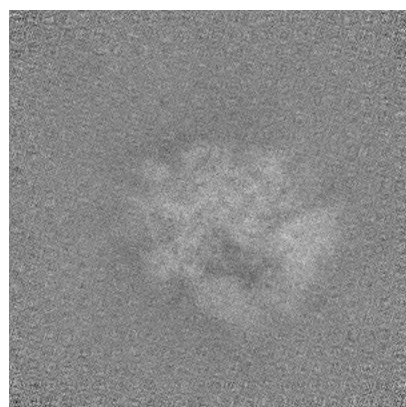


Y

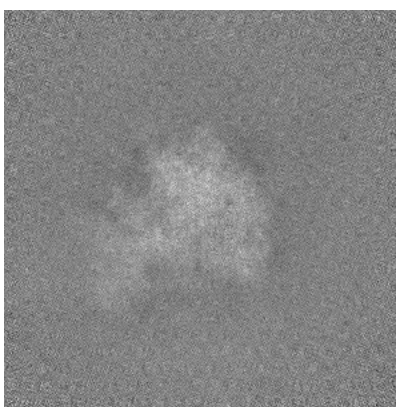


Z

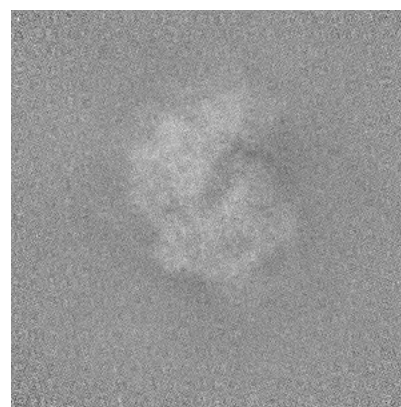
6.1.2 Raw map



X



Y

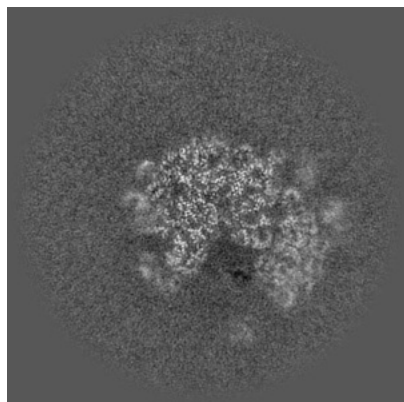


Z

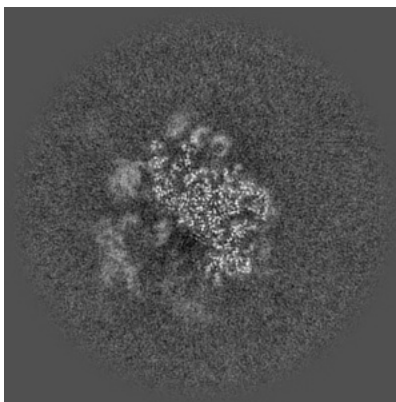
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

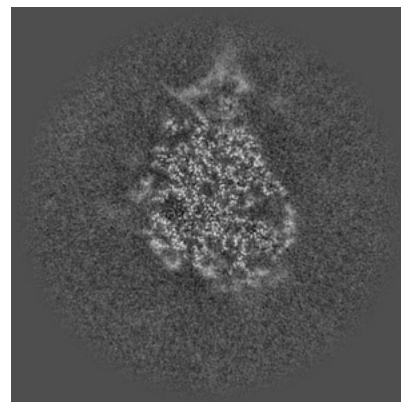
6.2.1 Primary map



X Index: 288

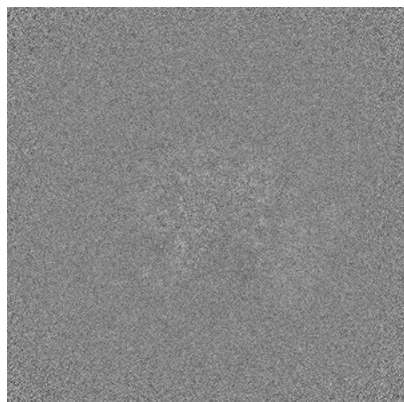


Y Index: 288

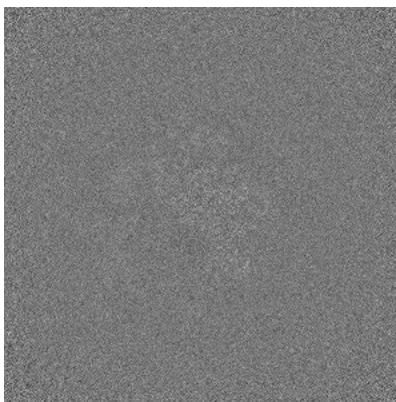


Z Index: 288

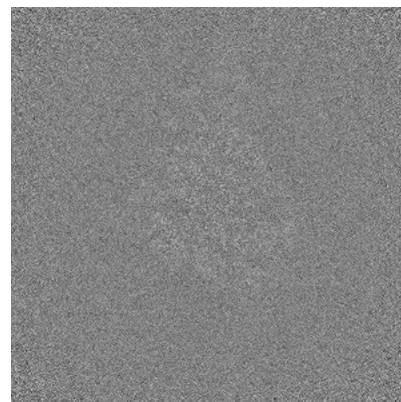
6.2.2 Raw map



X Index: 288



Y Index: 288

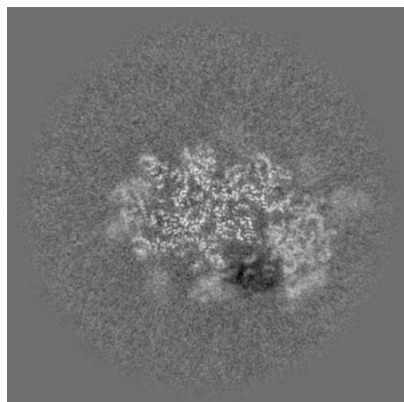


Z Index: 288

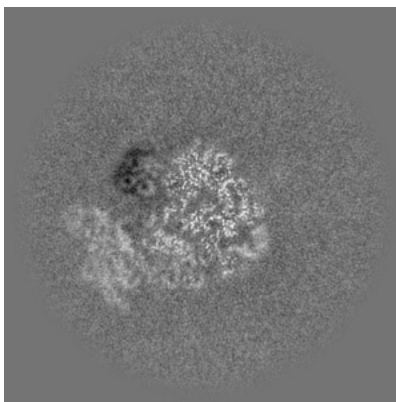
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

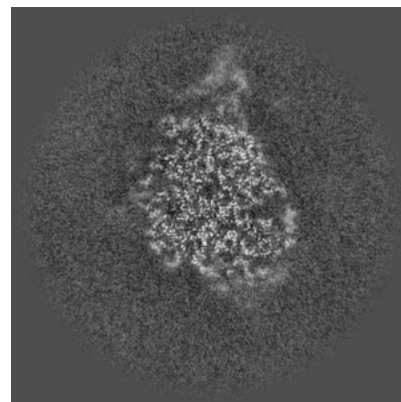
6.3.1 Primary map



X Index: 314

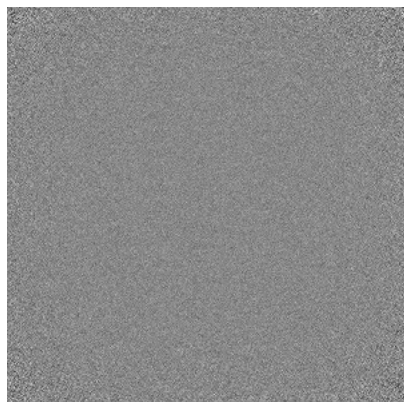


Y Index: 352

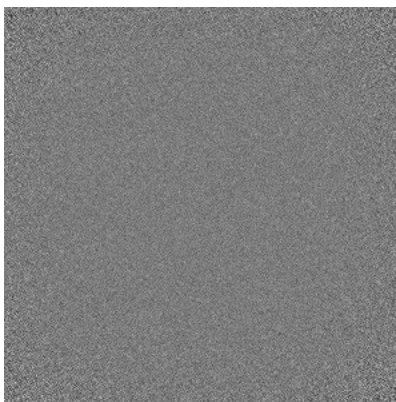


Z Index: 291

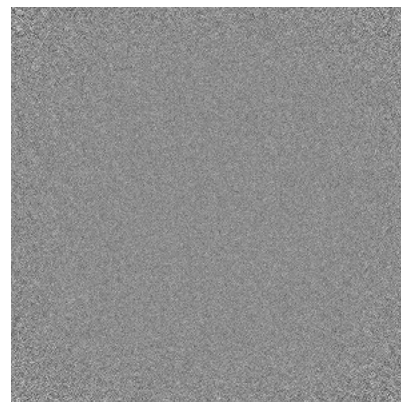
6.3.2 Raw map



X Index: 0



Y Index: 0

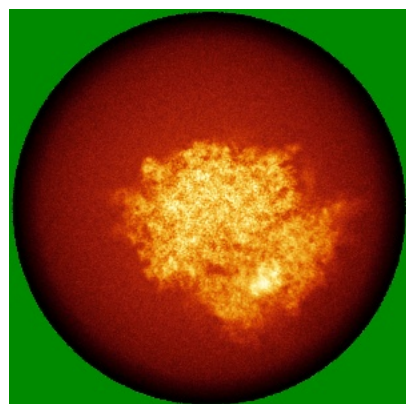


Z Index: 0

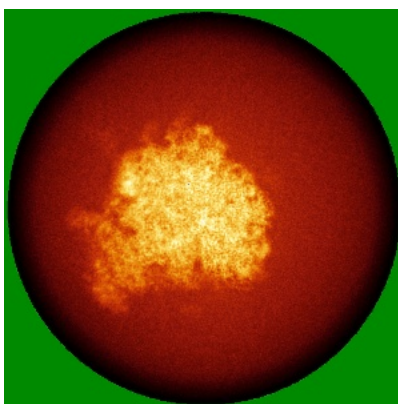
The images above show the largest variance slices of the map in three orthogonal directions.

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

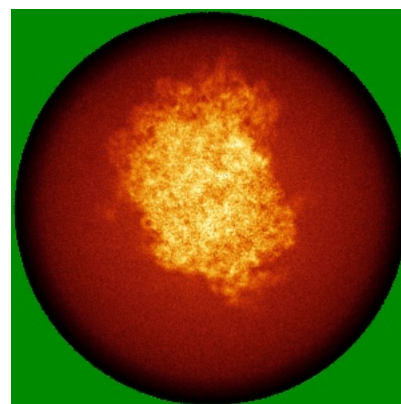
6.4.1 Primary map



X

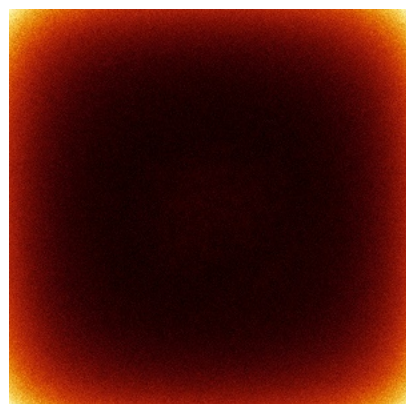


Y

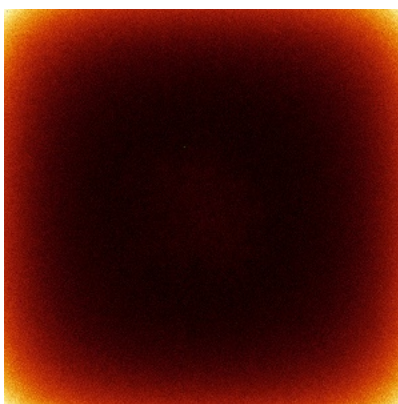


Z

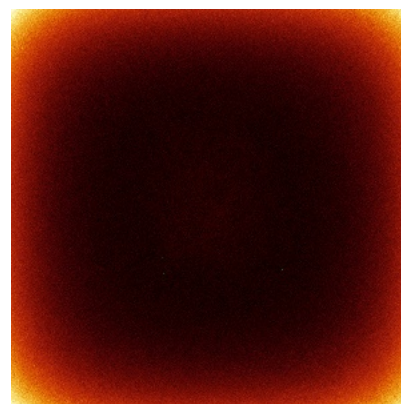
6.4.2 Raw map



X



Y

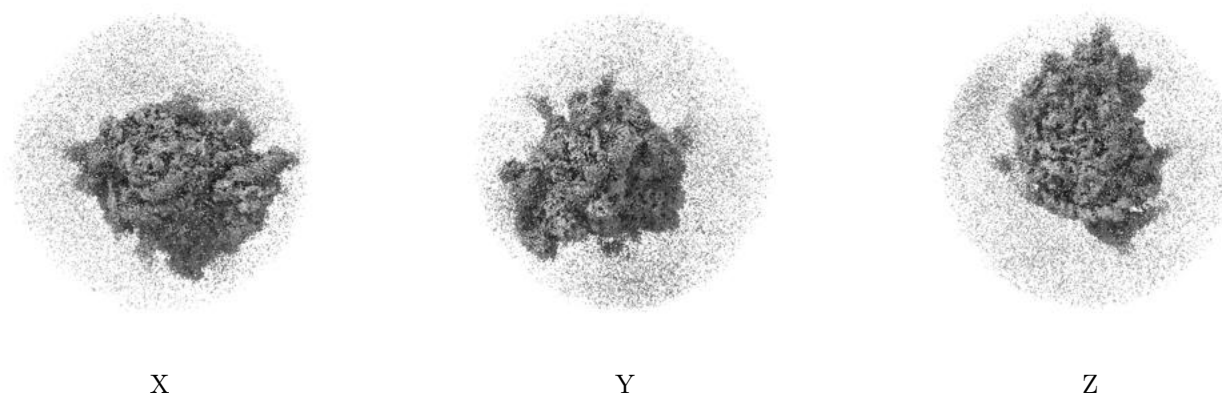


Z

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.

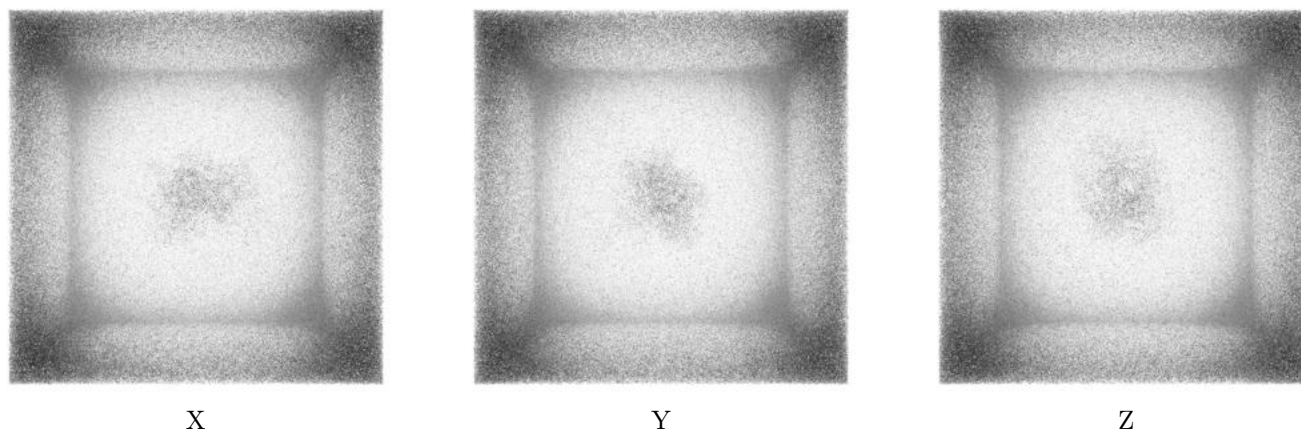
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0122. 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.

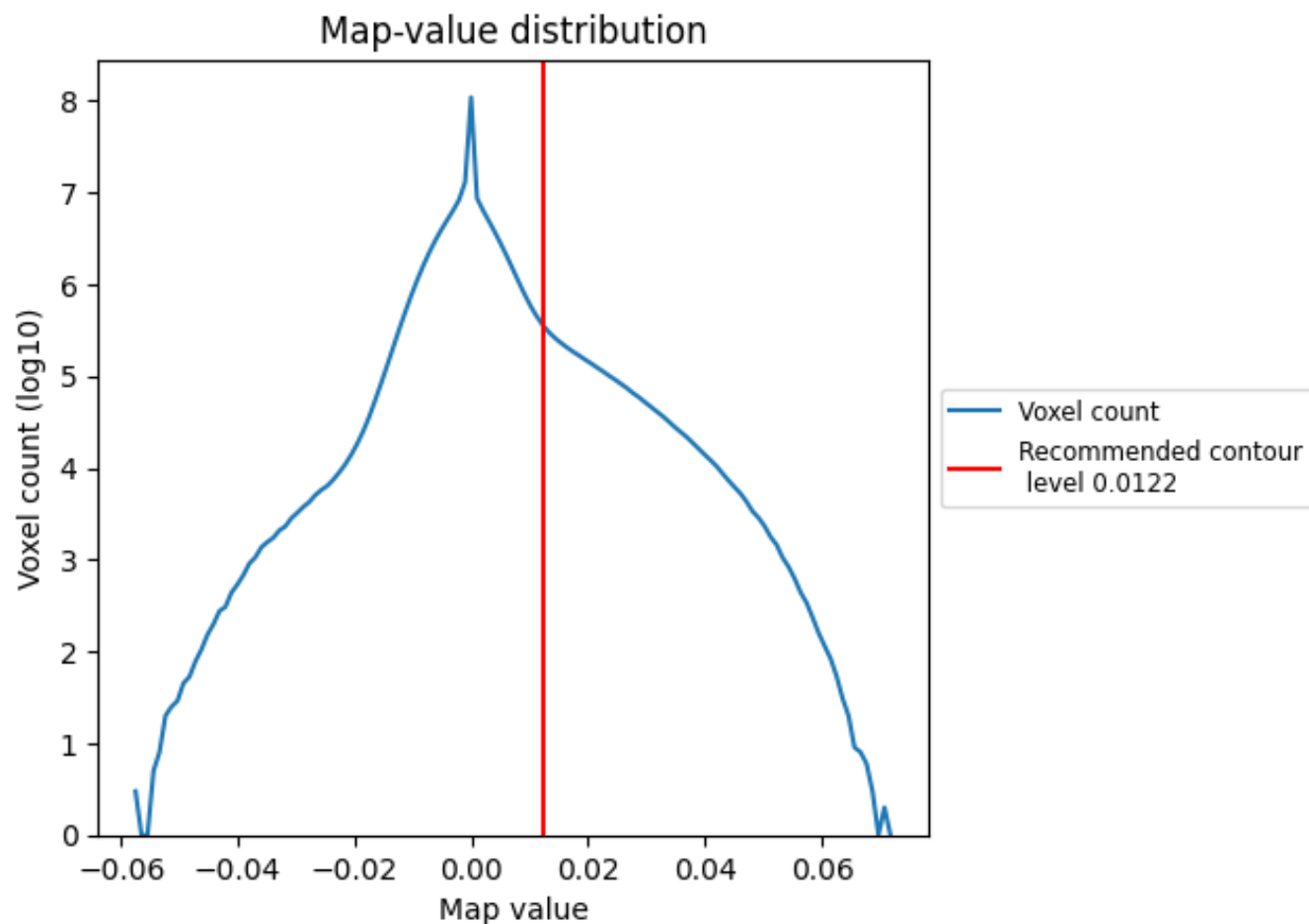
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

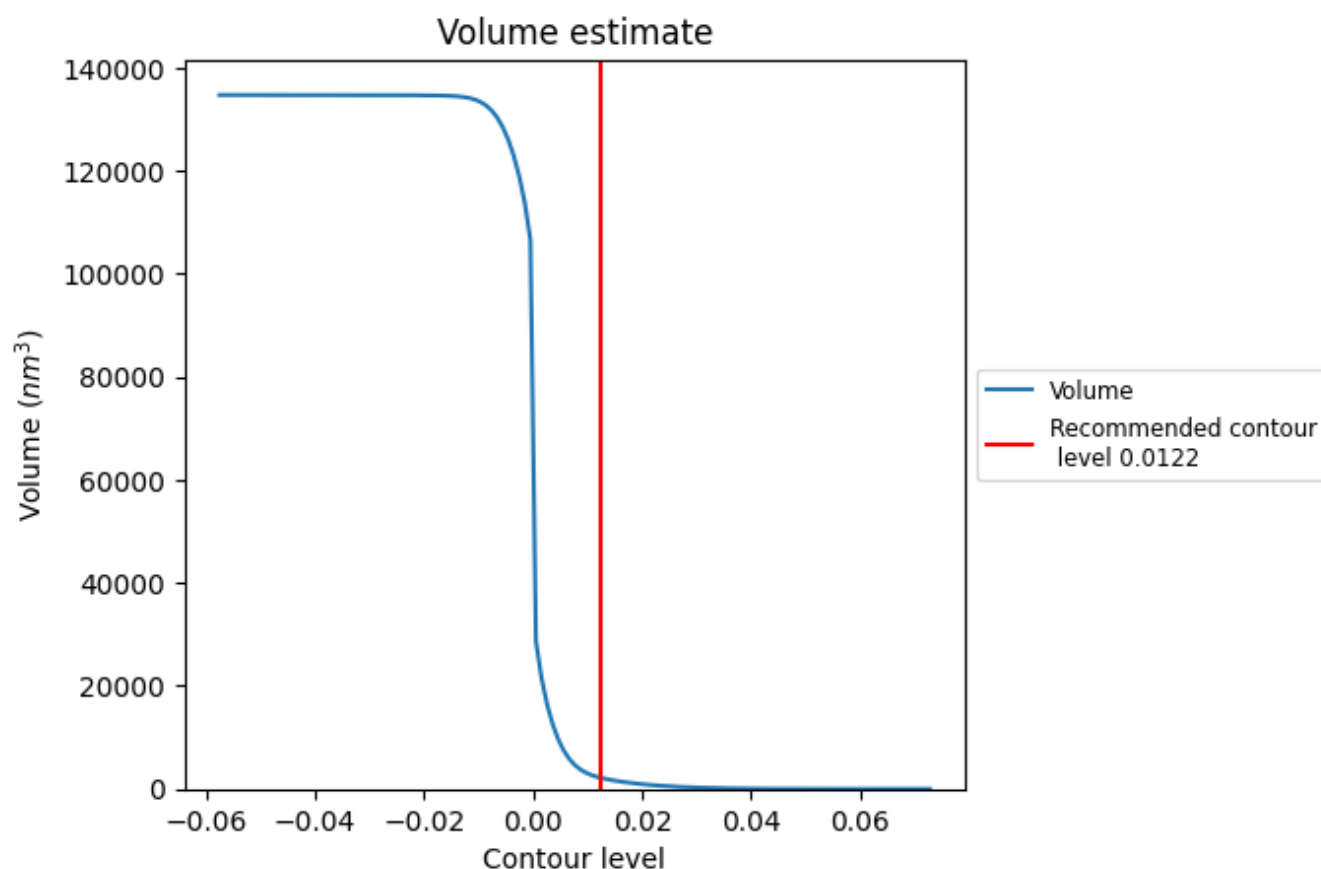
This section contains the results of statistical analysis of the map.

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.

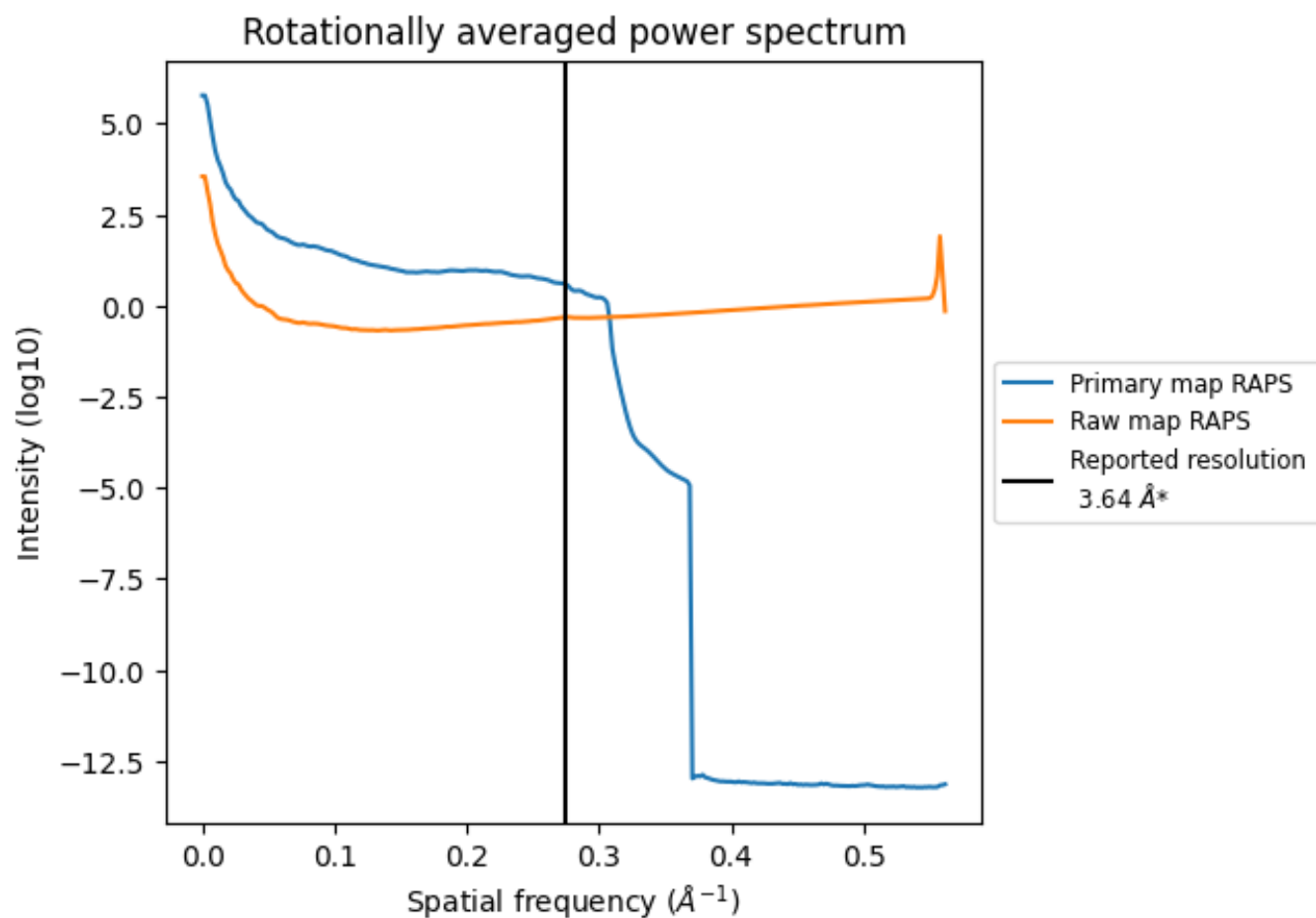
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2212 nm³; 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 ⓘ

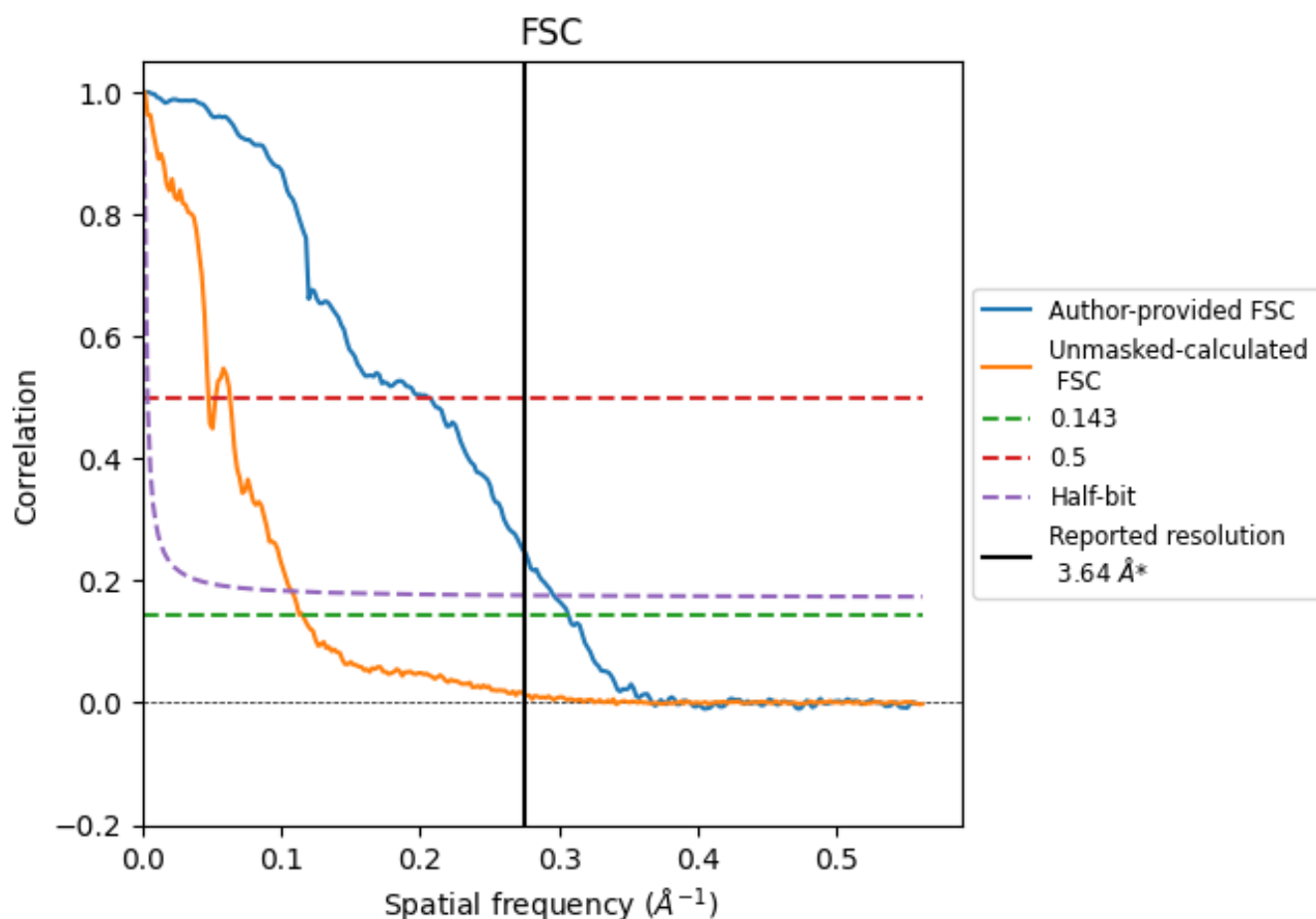


*Reported resolution corresponds to spatial frequency of 0.275 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.275 \AA^{-1}

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.64	-	-
Author-provided FSC curve	3.26	4.86	3.37
Unmasked-calculated*	8.65	20.92	9.29

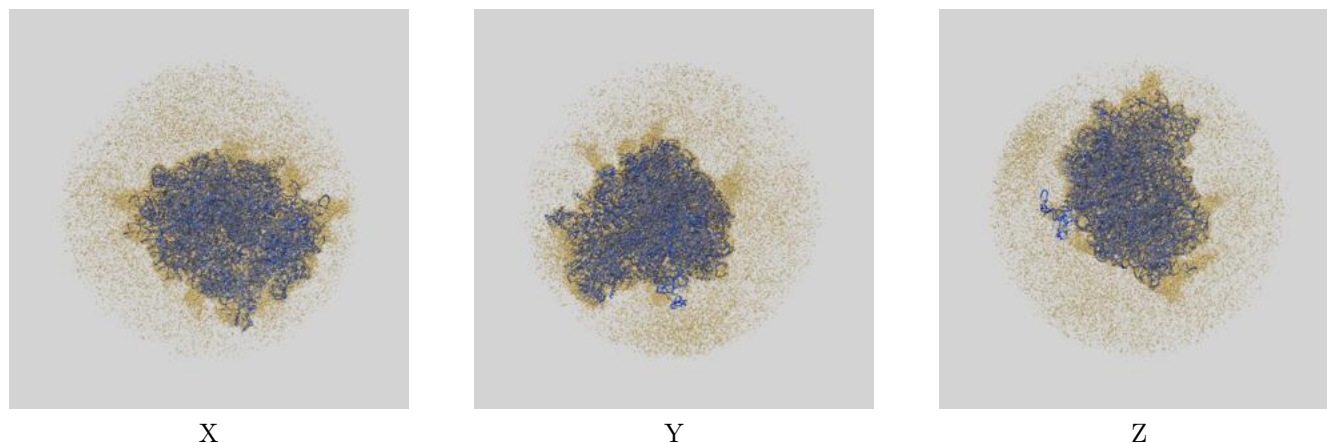
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.26 differs from the reported value 3.64 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.65 differs from the reported value 3.64 by more than 10 %

9 Map-model fit [i](#)

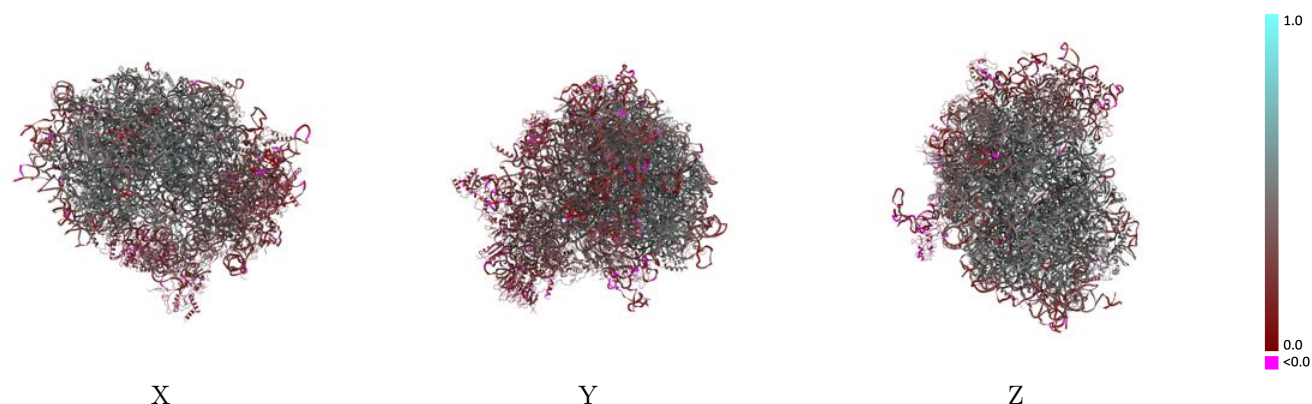
This section contains information regarding the fit between EMDB map EMD-42316 and PDB model 8UJ9. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

9.1 Map-model overlay [i](#)



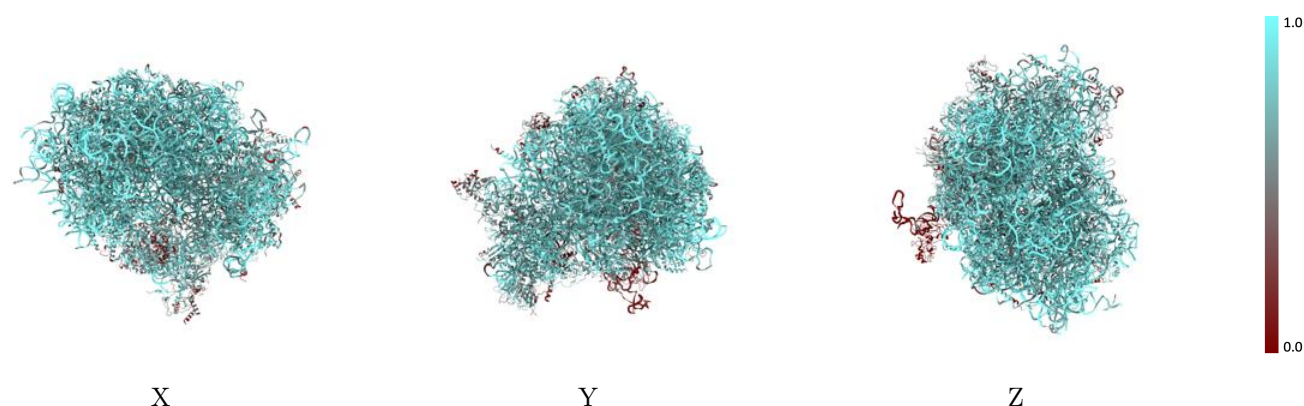
The images above show the 3D surface view of the map at the recommended contour level 0.0122 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



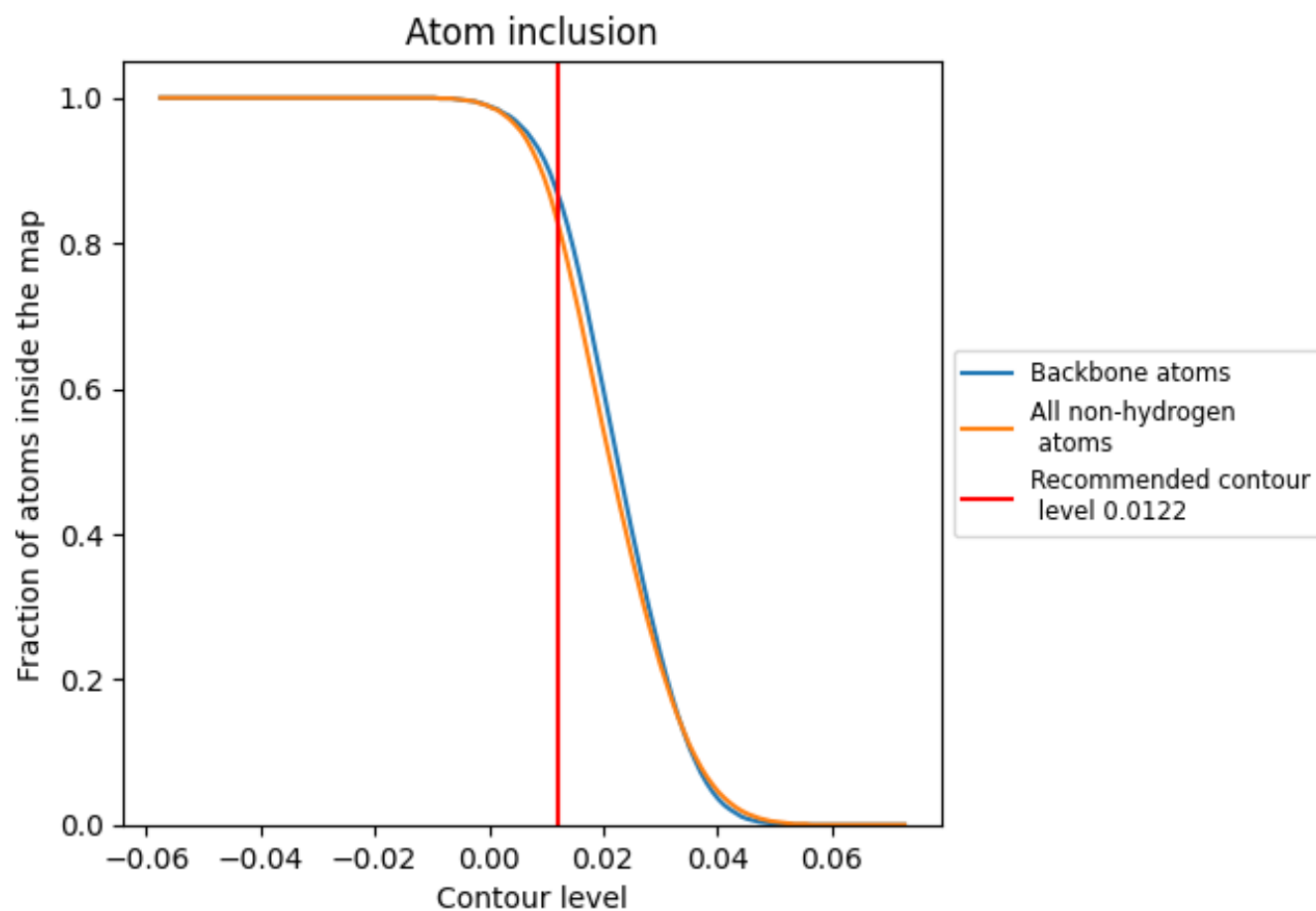
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0122).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 82% 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 (0.0122) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8240	 0.3880
L5	 0.9030	 0.4220
L7	 0.9760	 0.4580
L8	 0.9270	 0.4430
LA	 0.8120	 0.5110
LB	 0.8250	 0.4900
LC	 0.8050	 0.4920
LD	 0.8600	 0.4280
LE	 0.7900	 0.4060
LF	 0.8240	 0.4900
LG	 0.7850	 0.4240
LH	 0.7960	 0.4530
LI	 0.7830	 0.4820
LJ	 0.7590	 0.3850
LL	 0.8030	 0.4530
LM	 0.8390	 0.4590
LN	 0.8680	 0.5170
LO	 0.8120	 0.4900
LP	 0.8100	 0.5080
LQ	 0.8130	 0.5090
LR	 0.7620	 0.4230
LS	 0.8470	 0.5030
LT	 0.8140	 0.4850
LU	 0.8510	 0.3900
LV	 0.7330	 0.4930
LW	 0.6560	 0.3380
LX	 0.8070	 0.4740
LY	 0.8390	 0.4810
LZ	 0.8970	 0.4580
La	 0.8560	 0.5070
Lb	 0.7470	 0.4010
Lc	 0.8180	 0.4400
Ld	 0.7880	 0.4650
Le	 0.7850	 0.5090
Lf	 0.8180	 0.5110

















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Chain	Atom inclusion	Q-score
Lg	 0.8100	 0.4770
Lh	 0.7840	 0.4470
Li	 0.8090	 0.4640
Lj	 0.8680	 0.5170
Lk	 0.8310	 0.4210
Ll	 0.7780	 0.4970
Lm	 0.7980	 0.4900
Ln	 0.7660	 0.4650
Lo	 0.4290	 0.4730
Lp	 0.7740	 0.4850
Lr	 0.8280	 0.5010
Ls	 0.4570	 0.1890
Lt	 0.4090	 0.1560
Lz	 0.0100	 0.0880
Pt	 0.6080	 0.2950
S2	 0.8870	 0.3230
SA	 0.7540	 0.3160
SB	 0.7260	 0.3700
SC	 0.7620	 0.3490
SD	 0.6490	 0.2710
SE	 0.7730	 0.3170
SF	 0.4190	 0.2530
SG	 0.6730	 0.2660
SH	 0.6460	 0.2630
SI	 0.7440	 0.3550
SJ	 0.7740	 0.3110
SK	 0.6610	 0.2260
SL	 0.6850	 0.3810
SM	 0.4130	 0.1880
SN	 0.7350	 0.3830
SO	 0.5890	 0.3580
SP	 0.6450	 0.2610
SQ	 0.6990	 0.2770
SR	 0.6930	 0.2770
SS	 0.6340	 0.2710
ST	 0.7500	 0.2540
SU	 0.6850	 0.2360
SV	 0.7570	 0.3200
SW	 0.7750	 0.3840
SX	 0.6720	 0.3900
SY	 0.7250	 0.2400
SZ	 0.3000	 0.2070

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Chain	Atom inclusion	Q-score
Sa	 0.7890	 0.3930
Sb	 0.7320	 0.3540
Sc	 0.5020	 0.2570
Sd	 0.7710	 0.2690
Se	 0.5990	 0.2690
Sf	 0.5820	 0.1730
Sg	 0.6400	 0.2020