



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:01 PM UTC

PDB ID : 6Z6L / pdb_00006z6l
EMDB ID : EMD-11098
Title : Cryo-EM structure of human CCDC124 bound to 80S ribosomes
Authors : Wells, J.N.; Buschauer, R.; Mackens-Kiani, T.; Best, K.; Kratzat, H.; Berninghausen, O.; Becker, T.; Cheng, J.; Beckmann, R.
Deposited on : 2020-05-28
Resolution : 3.00 Å(reported)
Based on initial model : 6EK0

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

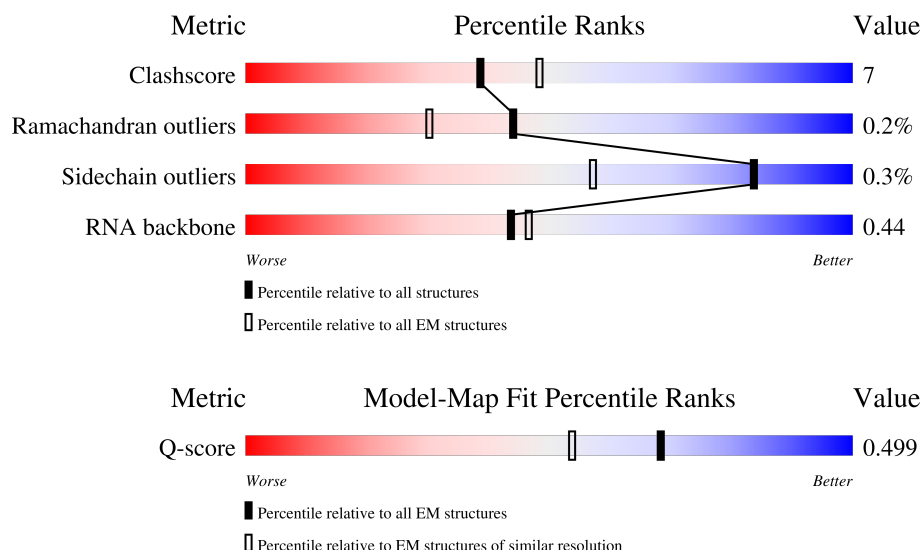
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

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



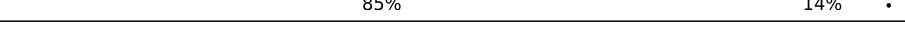
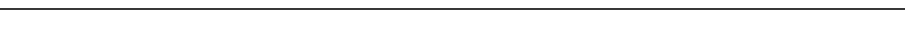
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	L5	5070	
2	L7	121	
3	L8	157	

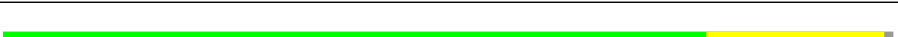
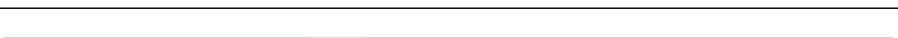
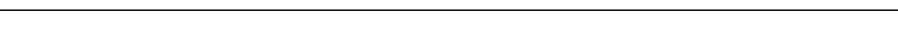
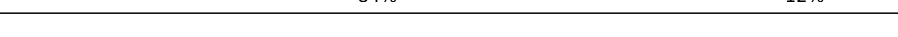
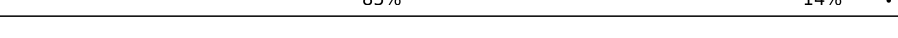
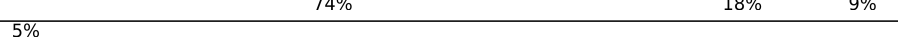
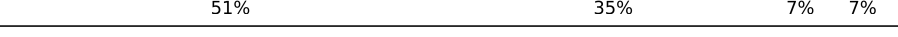
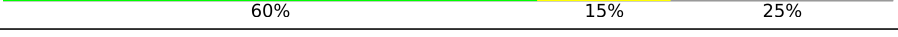
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Mol	Chain	Length	Quality of chain
4	LA	257	 77% 19% . .
5	LB	403	 80% 19% .
6	LC	427	 74% 12% 14%
7	LD	297	 81% 18% .
8	LE	288	 61% 20% 18%
9	LF	248	 77% 13% 9%
10	LG	266	 74% 17% 9%
11	LH	192	 77% 22% ..
12	LI	214	 70% 24% 6%
13	LJ	178	 75% 24% .
14	LL	211	 81% 18%
15	LM	215	 48% 15% . 35%
16	LN	204	 83% 16%
17	LO	203	 85% 14% .
18	LP	184	 72% 11% 17%
19	LQ	188	 90% 10% .
20	LR	196	 84% 11% 5%
21	LS	176	 89% 11% .
22	LT	160	 86% 14% .
23	LU	128	 64% 15% 21%
24	LV	140	 76% 17% . 6%
25	LW	157	 65% 14% 21%
26	LX	156	 65% 12% 23%
27	LY	145	 75% 17% . 8%
28	LZ	136	 72% 27% .

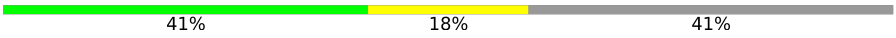
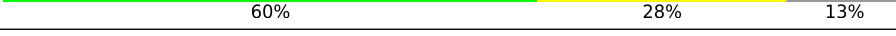
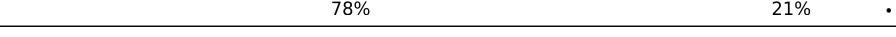
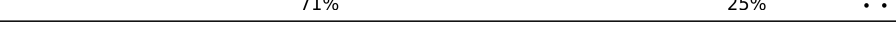
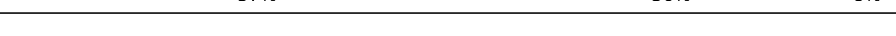
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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	104	
44	Lp	92	
45	Lr	137	
46	Lz	217	
47	S2	1869	
48	SA	295	
49	SB	264	
50	SD	243	
51	SE	263	
52	SF	204	
53	SH	194	

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Mol	Chain	Length	Quality of chain
54	SI	208	
55	SK	165	
56	SL	158	
57	SP	145	
58	SQ	146	
59	SR	135	
60	SS	152	
61	ST	145	
62	SU	119	
63	SV	83	
64	SX	143	
65	Sa	115	
66	Sc	69	
67	Sd	56	
68	Sg	317	
69	SC	293	
70	SG	249	
71	SJ	194	
72	SM	132	
73	SN	151	
74	SO	151	
75	SW	130	
76	SY	133	
77	SZ	125	
78	Sb	84	

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Mol	Chain	Length	Quality of chain
79	Se	59	
80	Sf	156	
81	CA	394	
82	CC	75	
83	CE	223	

2 Entry composition [i](#)

There are 85 unique types of molecules in this entry. The entry contains 222284 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3772	Total	C	N	O	P	0	0
			80116	35645	14585	26115	3771		

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

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

- Molecule 3 is a RNA chain called 5.8S rRNA.

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

- Molecule 4 is a protein called 60S ribosomal protein L8.

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

- Molecule 5 is a protein called 60S ribosomal protein L3.

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

- Molecule 6 is a protein called 60S ribosomal protein L4.

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

- Molecule 7 is a protein called 60S ribosomal protein L5.

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

- Molecule 8 is a protein called 60S ribosomal protein L6.

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

- Molecule 9 is a protein called 60S ribosomal protein L7.

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

- Molecule 10 is a protein called 60S ribosomal protein L7a.

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

- Molecule 11 is a protein called 60S ribosomal protein L9.

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

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

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

- Molecule 13 is a protein called 60S ribosomal protein L11.

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

- Molecule 14 is a protein called 60S ribosomal protein L13.

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

- Molecule 15 is a protein called 60S ribosomal protein L14.

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

- Molecule 16 is a protein called 60S ribosomal protein L15.

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

- Molecule 17 is a protein called 60S ribosomal protein L13a.

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

- Molecule 18 is a protein called 60S ribosomal protein L17.

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

- Molecule 19 is a protein called 60S ribosomal protein L18.

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

- Molecule 20 is a protein called 60S ribosomal protein L19.

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

- Molecule 21 is a protein called 60S ribosomal protein L18a.

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

- Molecule 22 is a protein called 60S ribosomal protein L21.

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

- Molecule 23 is a protein called 60S ribosomal protein L22.

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

- Molecule 24 is a protein called 60S ribosomal protein L23.

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

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

- Molecule 26 is a protein called 60S ribosomal protein L23a.

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

- Molecule 27 is a protein called 60S ribosomal protein L26.

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

- Molecule 28 is a protein called 60S ribosomal protein L27.

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

- Molecule 29 is a protein called 60S ribosomal protein L27a.

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

- Molecule 30 is a protein called 60S ribosomal protein L29.

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

- Molecule 31 is a protein called 60S ribosomal protein L30.

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

- Molecule 32 is a protein called 60S ribosomal protein L31.

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

- Molecule 33 is a protein called 60S ribosomal protein L32.

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

- Molecule 34 is a protein called 60S ribosomal protein L35a.

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

- Molecule 35 is a protein called 60S ribosomal protein L34.

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

- Molecule 36 is a protein called 60S ribosomal protein L35.

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

- Molecule 37 is a protein called 60S ribosomal protein L36.

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

- Molecule 38 is a protein called 60S ribosomal protein L37.

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

- Molecule 39 is a protein called 60S ribosomal protein L38.

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

- Molecule 40 is a protein called 60S ribosomal protein L39.

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

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 42 is a protein called 60S ribosomal protein L41.

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

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lo	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 44 is a protein called 60S ribosomal protein L37a.

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

- Molecule 45 is a protein called 60S ribosomal protein L28.

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

- Molecule 46 is a protein called 60S ribosomal protein L10a.

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

- Molecule 47 is a RNA chain called 18S rRNA.

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

- Molecule 48 is a protein called 40S ribosomal protein SA.

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

- Molecule 49 is a protein called 40S ribosomal protein S3a.

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

- Molecule 50 is a protein called 40S ribosomal protein S3.

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

- Molecule 51 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 52 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SF	184	Total	C	N	O	S	0	0
			1461	914	276	264	7		

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

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

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

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

- Molecule 55 is a protein called 40S ribosomal protein S10.

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

- Molecule 56 is a protein called 40S ribosomal protein S11.

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

- Molecule 57 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SP	127	Total	C	N	O	S	0	0
			1045	663	198	177	7		

- Molecule 58 is a protein called 40S ribosomal protein S16.

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

- Molecule 59 is a protein called 40S ribosomal protein S17.

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

- Molecule 60 is a protein called 40S ribosomal protein S18.

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

- Molecule 61 is a protein called 40S ribosomal protein S19.

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

- Molecule 62 is a protein called 40S ribosomal protein S20.

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

- Molecule 63 is a protein called 40S ribosomal protein S21.

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

- Molecule 64 is a protein called 40S ribosomal protein S23.

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

- Molecule 65 is a protein called 40S ribosomal protein S26.

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

- Molecule 66 is a protein called 40S ribosomal protein S28.

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

- Molecule 67 is a protein called 40S ribosomal protein S29.

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

- Molecule 68 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 69 is a protein called 40S ribosomal protein S2.

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

- Molecule 70 is a protein called 40S ribosomal protein S6.

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

- Molecule 71 is a protein called 40S ribosomal protein S9.

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

- Molecule 72 is a protein called 40S ribosomal protein S12.

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

- Molecule 73 is a protein called 40S ribosomal protein S13.

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

- Molecule 74 is a protein called 40S ribosomal protein S14.

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

- Molecule 75 is a protein called 40S ribosomal protein S15a.

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

- Molecule 76 is a protein called 40S ribosomal protein S24.

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

- Molecule 77 is a protein called 40S ribosomal protein S25.

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 40S ribosomal protein S27.

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

- Molecule 79 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	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 protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	CA	354	Total	C	N	O	S	4	0
			2764	1744	475	528	17		

- Molecule 82 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	CC	75	Total	C	N	O	P	0	0
			1589	710	279	525	75		

- Molecule 83 is a protein called Coiled-coil domain-containing protein 124.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	CE	73	Total	C	N	O	S	0	0
			613	369	122	121	1		

- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
84	L5	210	Total 210	Mg 210	0
84	L7	3	Total 3	Mg 3	0
84	L8	5	Total 5	Mg 5	0
84	LA	1	Total 1	Mg 1	0
84	LI	1	Total 1	Mg 1	0
84	LP	1	Total 1	Mg 1	0
84	LV	1	Total 1	Mg 1	0
84	Le	2	Total 2	Mg 2	0
84	Lg	1	Total 1	Mg 1	0
84	Lj	1	Total 1	Mg 1	0
84	S2	29	Total 29	Mg 29	0
84	SG	1	Total 1	Mg 1	0

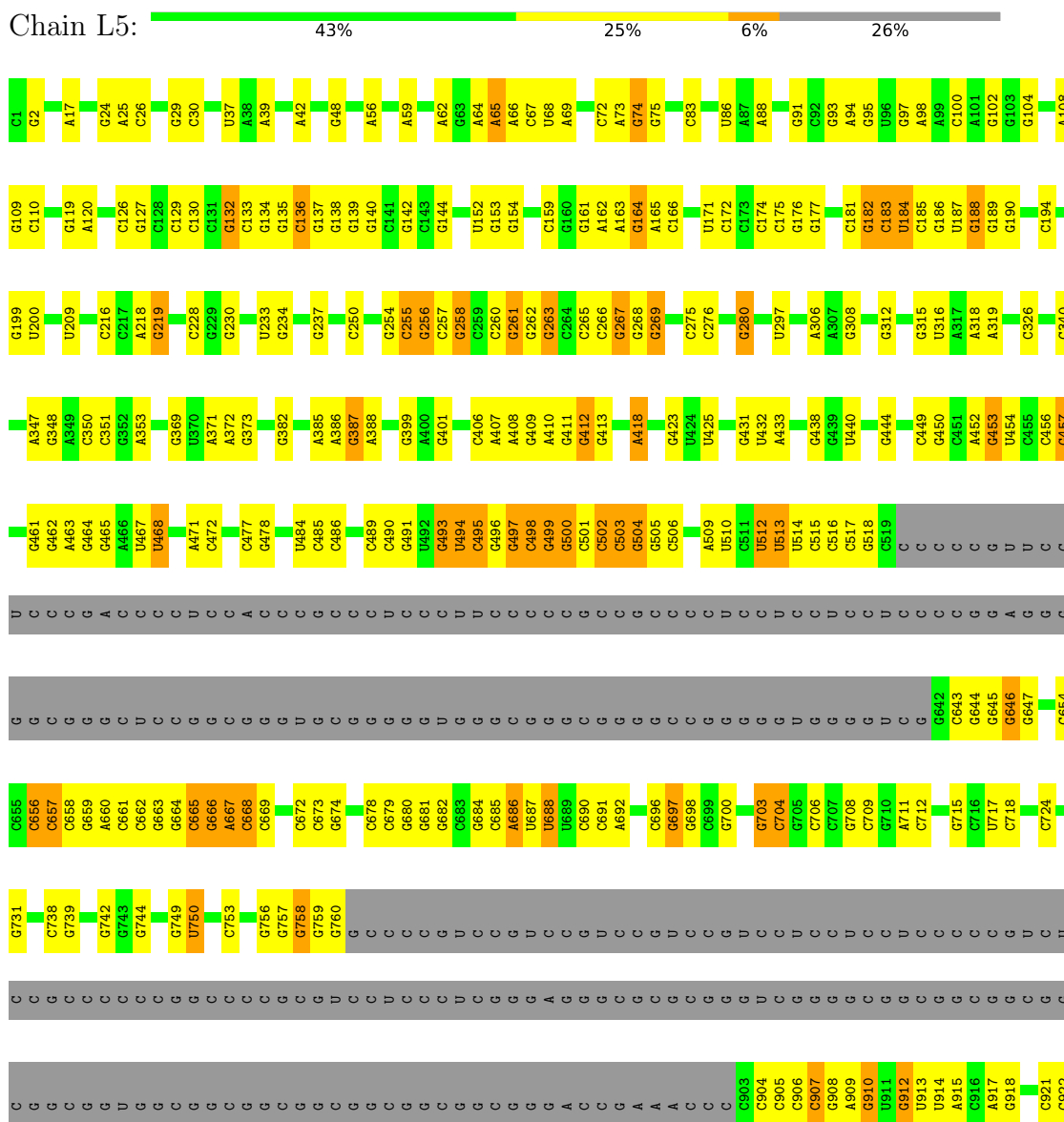
- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
85	Lg	1	Total 1	Zn 1	0
85	Lj	1	Total 1	Zn 1	0
85	Lm	1	Total 1	Zn 1	0
85	Lo	1	Total 1	Zn 1	0
85	Lp	1	Total 1	Zn 1	0
85	Sa	1	Total 1	Zn 1	0
85	Sd	1	Total 1	Zn 1	0
85	Sf	1	Total 1	Zn 1	0

3 Residue-property plots

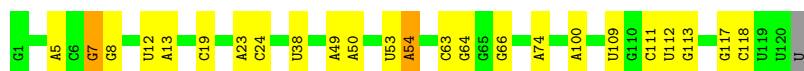
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 28S rRNA



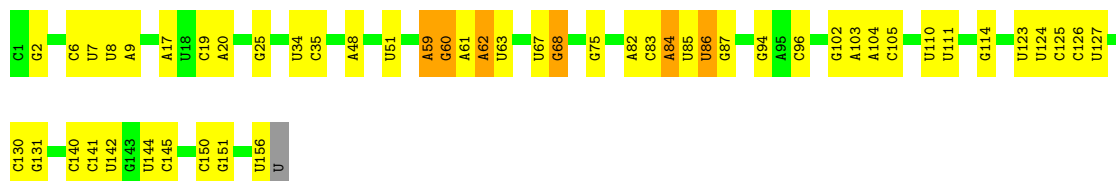






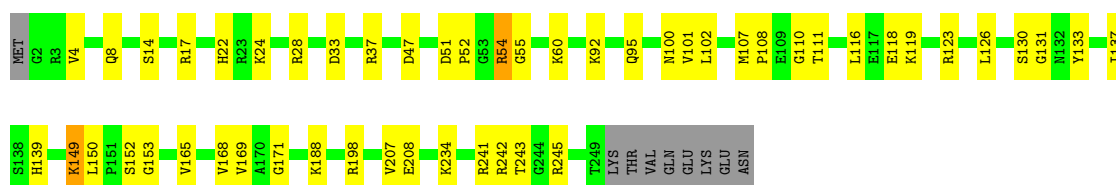
• Molecule 3: 5.8S rRNA

Chain L8: 67% 29%



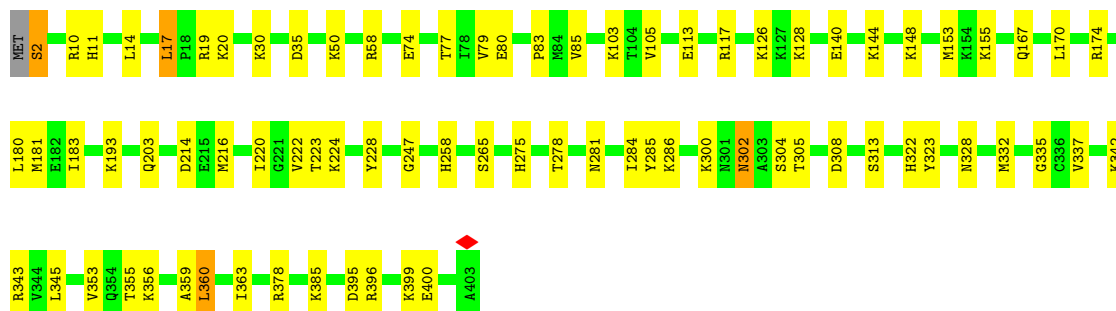
• Molecule 4: 60S ribosomal protein L8

Chain LA: 77% 19%



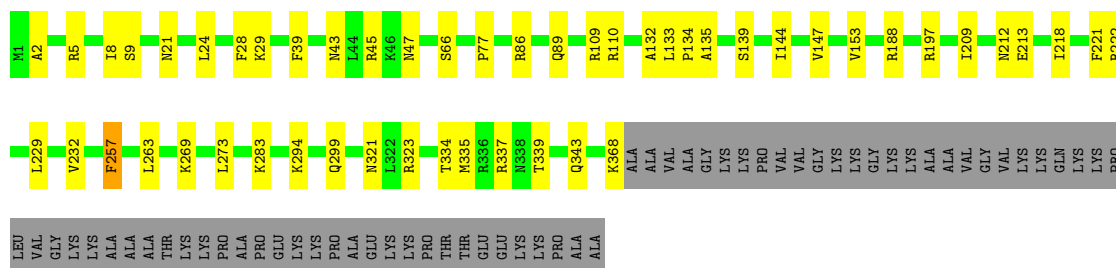
• Molecule 5: 60S ribosomal protein L3

Chain LB: 80% 19%



• Molecule 6: 60S ribosomal protein L4

Chain LC: 74% 12% 14%



- | | | | | | | | | | | | | |
|----|----|------|------|------|------|------|------|------|------|------|------|------|
| K1 | K2 | I12 | V16 | D17 | I18 | G29 | P30 | R31 | I41 | E44 | L48 | K52 | K53 | R54 | L55 | R56 | V57 | D58 | K59 | D69 | T69 | V70 | N79 | R89 | I90 | K91 | M92 | R93 | S94 | V95 | Q106 | E107 | L112 | V111 | E113 | E120 | R124 | R125 | R129 | D142 | E143 |
|----|----|------|------|------|------|------|------|------|------|------|------|------|



- Molecule 12: 60S ribosomal protein L10-like

Chain LI: 70% 24% 6%



- Molecule 13: 60S ribosomal protein L11

Chain LJ: 75% 24% .



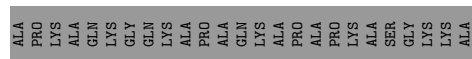
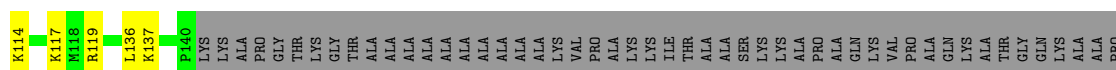
- Molecule 14: 60S ribosomal protein L13

Chain LL: 81% 18%



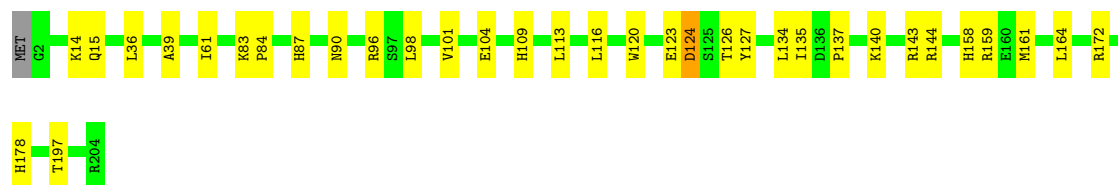
- Molecule 15: 60S ribosomal protein L14

Chain LM: 48% 15% 35%



- Molecule 16: 60S ribosomal protein L15

Chain LN: 83% 16%



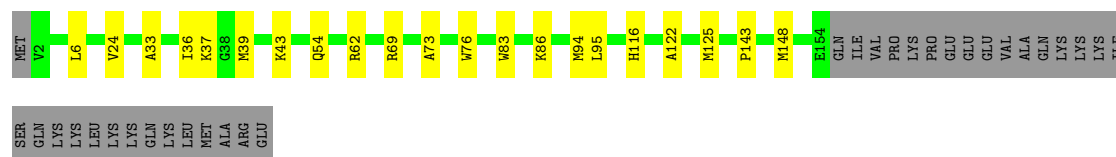
- Molecule 17: 60S ribosomal protein L13a

Chain LO: 85% 14%



- Molecule 18: 60S ribosomal protein L17

Chain LP: 72% 11% 17%



- Molecule 19: 60S ribosomal protein L18

Chain LQ: 90% 10%



- Molecule 20: 60S ribosomal protein L19

Chain LR: 84% 11% 5%



- Molecule 21: 60S ribosomal protein L18a

Chain LS: 89% 11%

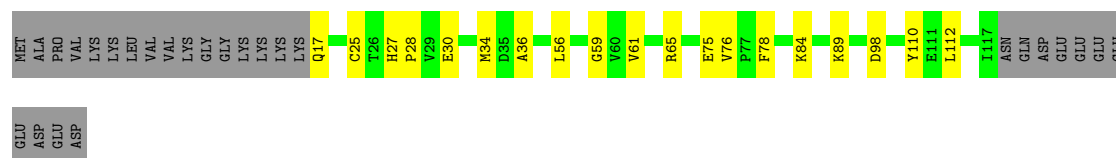


- Molecule 22: 60S ribosomal protein L21

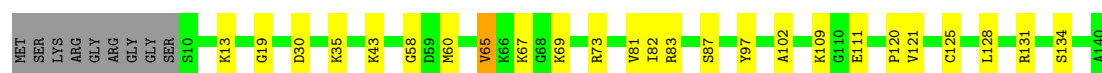
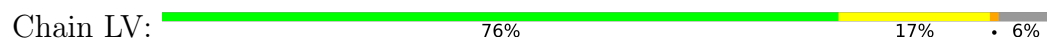
Chain LT: 86% 14%



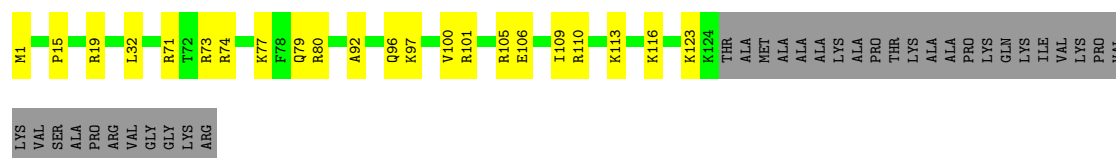
- Molecule 23: 60S ribosomal protein L22



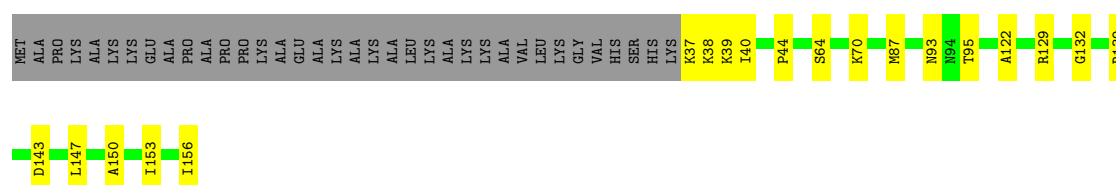
- Molecule 24: 60S ribosomal protein L23



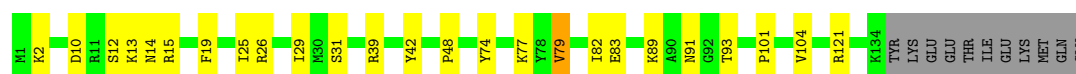
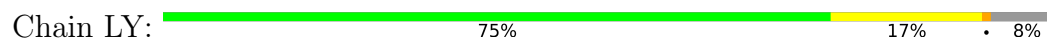
- Molecule 25: 60S ribosomal protein L24



- Molecule 26: 60S ribosomal protein L23a

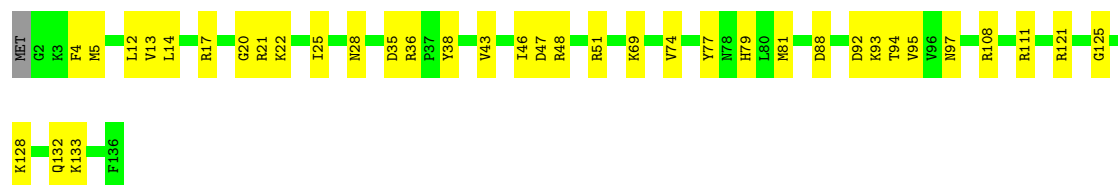


- Molecule 27: 60S ribosomal protein L26



- Molecule 28: 60S ribosomal protein L27





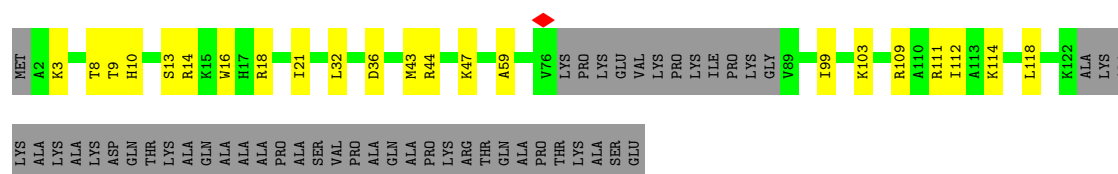
- Molecule 29: 60S ribosomal protein L27a

Chain La: 84% 15% ..



- Molecule 30: 60S ribosomal protein L29

Chain Lb: 55% 14% 31%



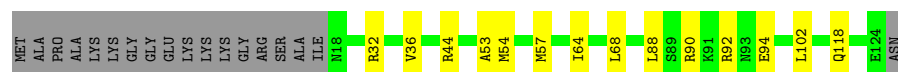
- Molecule 31: 60S ribosomal protein L30

Chain Lc: 71% 14% 15%



- Molecule 32: 60S ribosomal protein L31

Chain Ld: 74% 11% 14%



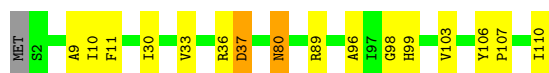
- Molecule 33: 60S ribosomal protein L32

Chain Le: 81% 13% 5%



- Molecule 34: 60S ribosomal protein L35a

Chain Lf: 85% 13% ..



- Molecule 35: 60S ribosomal protein L34

Chain Lg: 86% 11%



- Molecule 36: 60S ribosomal protein L35

Chain Lh: 81% 17%



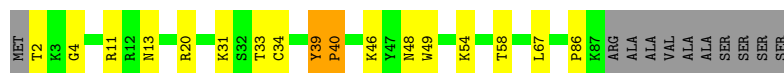
- Molecule 37: 60S ribosomal protein L36

Chain Li: 91% 6%



- Molecule 38: 60S ribosomal protein L37

Chain Lj: 71% 15% 11%



- Molecule 39: 60S ribosomal protein L38

Chain Lk: 79% 20%



- Molecule 40: 60S ribosomal protein L39

Chain Ll: 86% 12%



- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Lm: 34% 7% 59%

MET GLN ILE PHE VAL THR LEU THR GLY LYS THR ILE THR LEU GLY VAL PRO SER ASP THR ILE GLU ASN VAL LYS LYS ILE GLN ASP LYS GLY ILE PRO PRO ASP GLN ARG LEU THR PHE ALA GLY LYS GLN LEU GLU ASP GLY ARG THR LEU SER ASP TYR ASN

ILE GLN LYS SER THR LEU HIS LEU VAL LEU ARG LEU ARG GLY I77 L82 M94 R95 C96 R97 R98 C99 Y100 A101 P105 T118 K128

- Molecule 42: 60S ribosomal protein L41

Chain Ln:  84% 12%

M1 M10 R15 S24 LYS

- Molecule 43: 60S ribosomal protein L36a

Chain Lo:  85% 14%

MET V2 K6 H13 L33 Q36 Q37 K38 Q45 T52 K61 K65 R87 H90 G94 R99 Q102 Y103 I104

- Molecule 44: 60S ribosomal protein L37a

Chain Lp:  87% 12%

MET A2 K3 R4 R23 E30 Q33 T38 T45 K48 H56 T63 E88 D91 Q92

- Molecule 45: 60S ribosomal protein L28

Chain Lr:  74% 18% 9%

MET S2 M7 R11 Q23 E28 N31 L32 K33 F38 R45 R46 K47 Q50 V51 V62 G69 S76 K96 R97 R98 Y102 D105 M108 R112 R119 K122 V126 LYS ARG LYS ARG THR ARG PRO THR LYS SER SER

- Molecule 46: 60S ribosomal protein L10a

Chain Lz:  5% 69% 30%

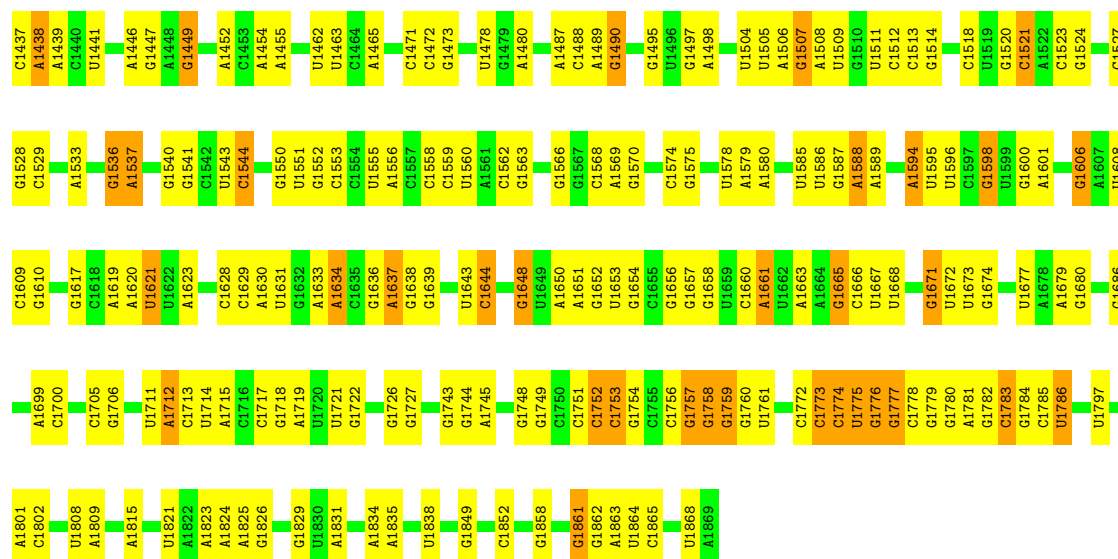
M1 T9 L10 E16 V17 L18 H19 G20 R23 R26 L29 Q35 M40 Y41 F49 S50 P59 R60 P61 K62 F63 S64 V65 C66 V67 L68 G69 D70 Q71 Q72 I82 K91 K92 K95 K98 L99 V100 L103 A104 I123 L128 K133

L137 L138 T139 N141 E142 N143 H144 V145 A146 E150 M159 K160 K161 V162 L163 A166 H171 V172 K173 M174 T175 D176 E178 L179 V180 Y181 N182 I183 H184 L185 F189 S192 L193 L194 W198 Q199 N200 V201 R202 I206 K207 S208 T209 M210 G211 K212 P213 Q214 Y217

- Molecule 47: 18S rRNA

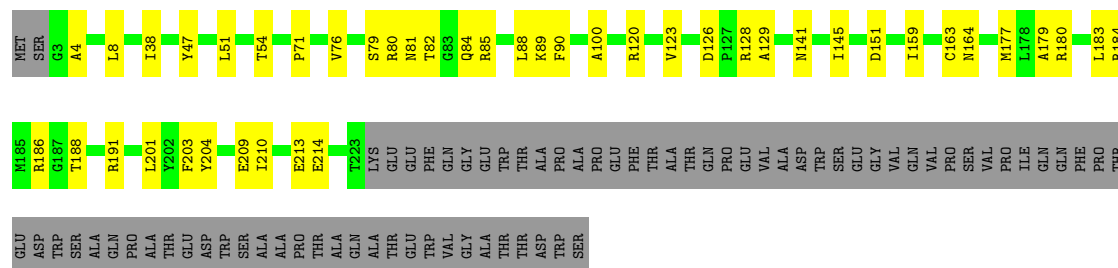
Chain S2:  51% 35% 7% 7%

A1332	G1257	U1161	A1027	G928	U857	C	G	G623	U540	G436	C321	C186	U1
U1333	A1258	G1171	A1028	G929	A858	U	G	U627	U541	A445	C322	G187	A2
C1341	A1259	U1172	C930	C931	G	A	A	G446	U542	A446	C323	G190	C3
U1342	C1261	G1033	A1034	G932	U	G	G	C639	C543	A447	C324	A191	C4
U1343	A1265	A1183	G1184	G933	G	U	C	A640	G546	A448	C325	A192	U5
G1346	U1061	G1187	U1062	G934	A859	G	G	A641	G547	A449	C326	G108	G6
G1351	A1188	A1188	A1062	U940	A870	U	A	G450	G548	C451	C327	U109	
G1351	C1271	U871	C941	G942	U871	U	A	G451	G549	G452	U328	U110	U12
G1354	C1273	A1190	A1084	U943	A872	C	C	C643	C549	G453	G329	C195	C13
G1354	C1274	C1191	C1085	A944	A873	C	C	C644	C550	A455	C331	U197	C14
A1357	G1275	U1192	U1088	A944	G874	G	A	U652	U551	A456	G332	U198	C17
U1371	A1276	U1193	U1088	C948	A875	G	C	U653	G552	A464	G338	C199	C18
U1372	C1277	A1194	A1194	G949	C877	G	G	A655	A555	A465	A339	G200	A25
C1373	A1278	A1195	C1091	C950	G878	G	G	G656	U556	A466	C117	G201	
C1374	U1281	A1199	C1094	C951	C791	C	G730	G659	U557	G466	C118	G202	U28
A1378	A1282	U1200	C1096	A955	C792	G731	U732	C660	G558	G467	G355	G204	G29
A1382	A1284	U1201	C1098	A962	A794	U733	C734	U661	A560	C471	C356	G206	C30
G1391	G1285	G1203	C1099	A963	U882	C735	C735	G662	A561	C472	A360	G207	G33
G1391	A1286	A1204	G1099	A963	U883	C736	C736	C663	U562	A473	U361	G208	A39
U1392	A1287	U1011	A1100	U969	U884	C737	C737	A664	A563	G474	C362	U210	A40
G1393	U1288	G1207	U1101	C970	U885	G738	C738	A668	U566	G477	A363	G211	G41
G1394	U1289	A1208	G1102	G971	U886	C739	C739	A671	A576	G478	A364	U212	A46
C1395	G1290	U1209	C1109	A972	U887	U804	U746	A672	A577	U487	U367	U213	C49
A1396	A1291	G1210	C1113	C975	U888	U805	C747	C673	A583	U488	U368	G214	G145
A1401	C1292	C1215	U1114	A981	U889	U806	U748	U678	U587	U488	G370	U218	U51
A1402	A1293	C1216	U1115	G982	U890	U807	C749	U689	A588	C492	U371	C223	G52
G1405	G1294	A1217	C1116	G983	U891	U808	C750	G690	G589	C493	U372	G225	C53
G1406	U1299	C1218	C1117	G984	U892	U809	C751	G691	C592	C494	G377	U154	A54
U1407	U1300	U1225	C1118	G985	U893	A810	C752	G692	C593	U495	G380	A158	G56
U1408	A1301	U1226	C1119	G986	U894	A811	C753	G693	C594	C496	C381	A159	U67
C1412	G1302	G1227	C1120	G987	U895	A812	C754	G694	C595	C502	G385	A160	C58
G1413	U1304	G1228	C1121	G988	U896	A813	C755	G695	C596	C503	C386	U161	G62
G1414	C1305	U1229	A1120	C988	U897	A814	C756	G696	C597	C504	C387	U162	U63
G1415	U1306	G1230	U1121	C989	U898	A815	C757	G697	C598	C505	U388	A164	A64
C1416	U1307	U1231	A1133	A996	U899	A816	C758	G698	C599	C506	A389	G165	C65
C1417	U1308	C1232	C1138	A997	U900	A817	C759	G699	C600	A520	U396	A166	G66
C1418	C1309	U1233	A1143	A998	U901	A818	C760	G700	G601	A521	C306	G167	C67
G1419	U1310	U1234	A1144	C1000	U902	A819	C761	G701	G602	A522	C307	C168	A68
G1420	C1311	U1235	A1145	A1001	U903	A820	C762	G702	G603	A523	G407	U169	C69
A1421	U1312	U1236	A1146	U1002	U904	A821	C763	G703	G604	A524	A408	C170	G71
G1422	A1313	U1237	C1146	G1010	U905	A822	C764	G704	G605	A525	G309	G	
C1423	U1314	U1238	C1147	A1011	U906	A823	C765	G705	G606	A526	C310	U	C72
G1424	C1317	U1239	A1148	A1012	U907	A824	C766	G706	G607	A527	C311	C	C73
C1430	U1318	U1240	A1149	U1013	U908	A825	C767	G707	G608	A528	G312	A	G74
G1431	C1319	G1241	U1152	U1014	U909	A826	C768	G708	G609	A529	A313	G	G75
U1432	U1320	U1242	C1153	U1015	U910	A827	C769	G709	G610	A530	G316	C	U76
C1433	G1324	U1243	U1154	U1016	U911	A828	C770	G710	G611	A531	C317	C	A77
C1434	U1325	U1244	U1155	U1017	U912	A829	C771	G711	G612	A532	A318	C	
C1435	U1326	U1245	U1156	A1023	U913	A830	C772	G712	G613	A533	C319	U	A92
C1436	U1327	U1246	U1157	A1024	U914	A831	C773	G713	G614	A534	G320	C	G94



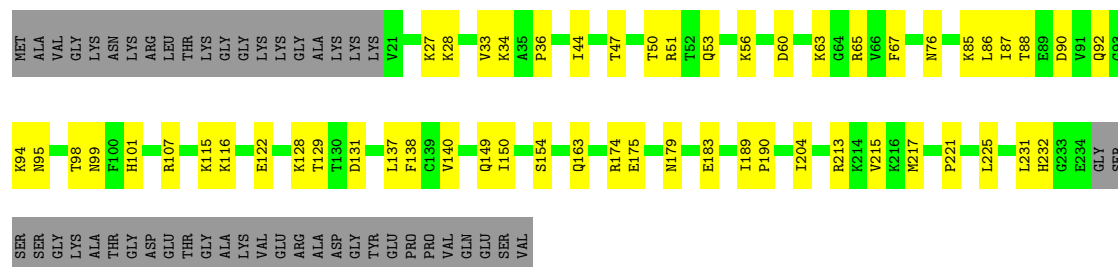
• Molecule 48: 40S ribosomal protein SA

Chain SA: 60% 15% 25%



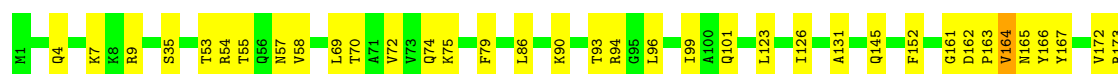
• Molecule 49: 40S ribosomal protein S3a

Chain SB: 60% 21% 19%



• Molecule 50: 40S ribosomal protein S3

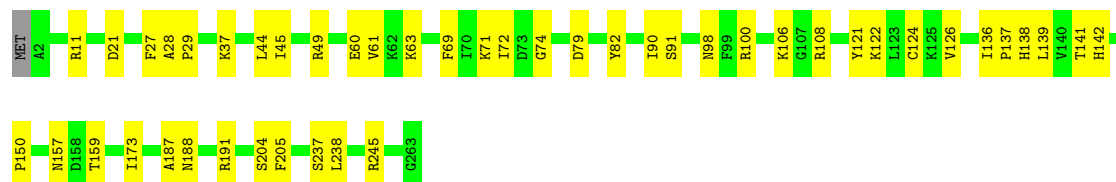
Chain SD: 75% 18% 7%





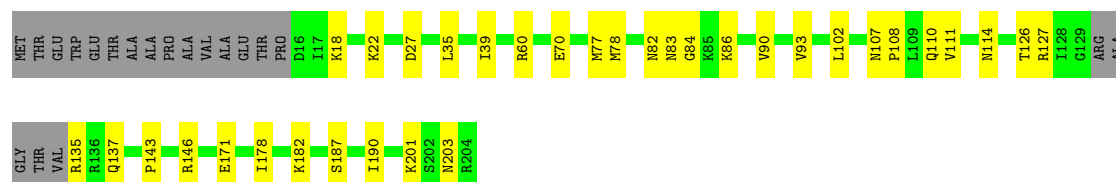
- Molecule 51: 40S ribosomal protein S4, X isoform

Chain SE: 82% 17%



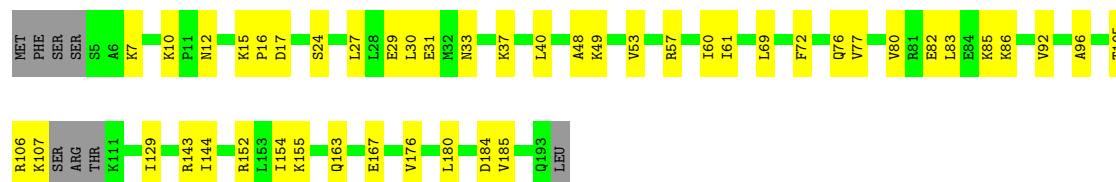
- Molecule 52: 40S ribosomal protein S5

Chain SF: 74% 17% 10%



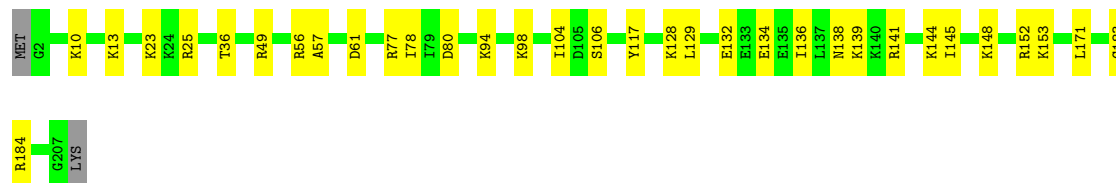
- Molecule 53: 40S ribosomal protein S7

Chain SH: 72% 24% .



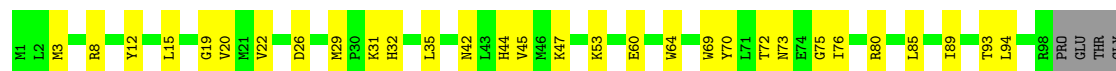
- Molecule 54: 40S ribosomal protein S8

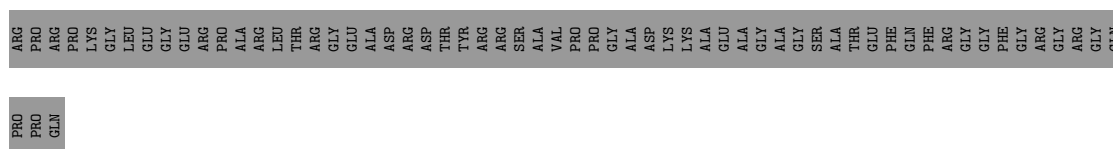
Chain SI: 83% 16% .



- Molecule 55: 40S ribosomal protein S10

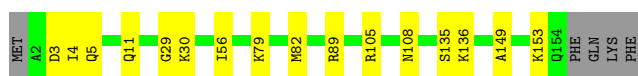
Chain SK: 41% 18% 41%





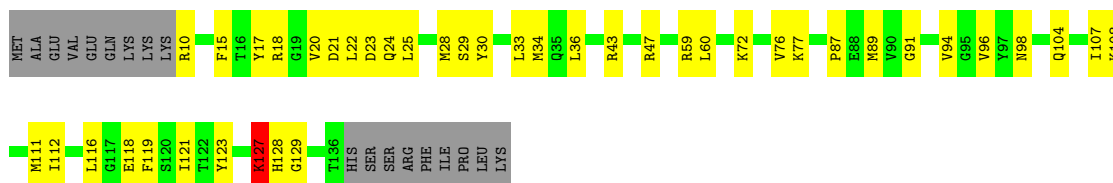
• Molecule 56: 40S ribosomal protein S11

Chain SL: 87% 10%



• Molecule 57: 40S ribosomal protein S15

Chain SP: 59% 28% 12%



• Molecule 58: 40S ribosomal protein S16

Chain SQ: 74% 24%



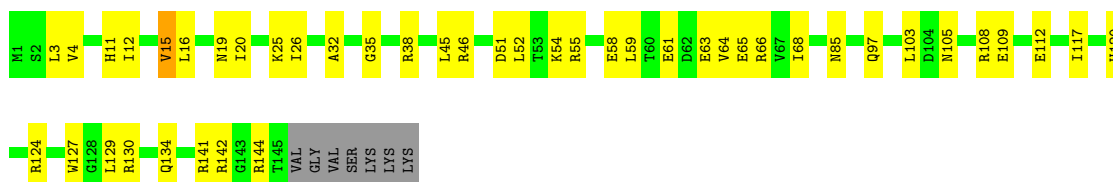
• Molecule 59: 40S ribosomal protein S17

Chain SR: 83% 17%



• Molecule 60: 40S ribosomal protein S18

Chain SS: 66% 28% 5%



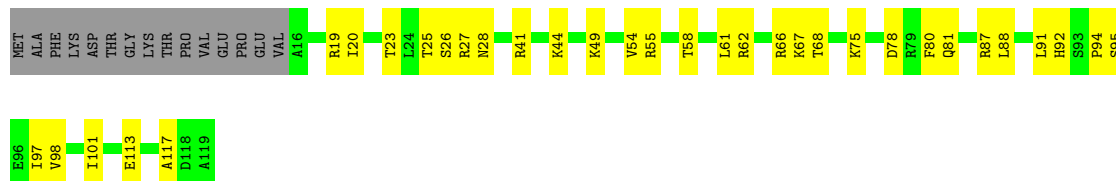
- Molecule 61: 40S ribosomal protein S19

Chain ST:  76% 23%



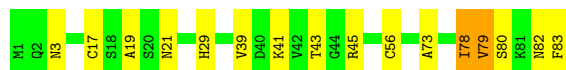
- Molecule 62: 40S ribosomal protein S20

Chain SU:  60% 28% 13%



- Molecule 63: 40S ribosomal protein S21

Chain SV:  81% 17%



- Molecule 64: 40S ribosomal protein S23

Chain SX:  78% 21%



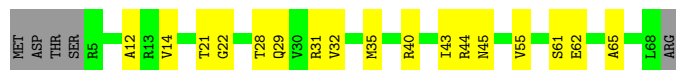
- Molecule 65: 40S ribosomal protein S26

Chain Sa:  75% 12% 11%



- Molecule 66: 40S ribosomal protein S28

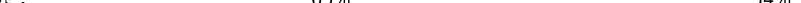
Chain Sc:  68% 25% 7%

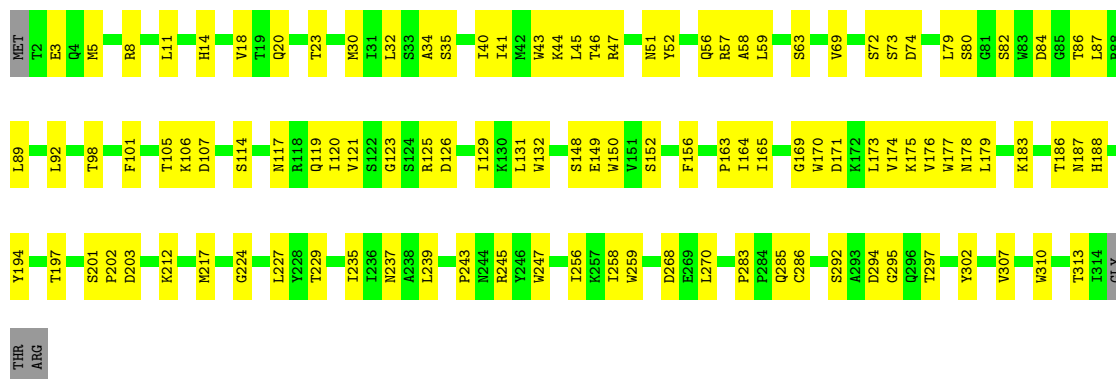


- Molecule 67: 40S ribosomal protein S29

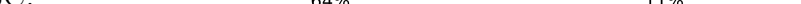
Chain Sd:  71% 25%

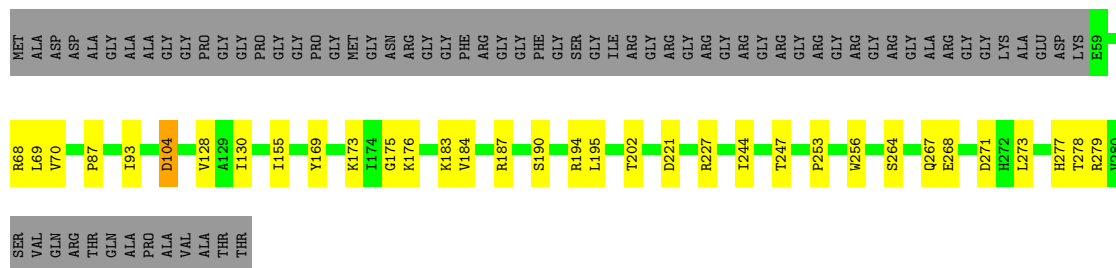
- Molecule 68: Receptor of activated protein C kinase 1

Chain Sg: 

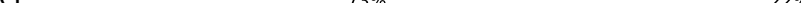


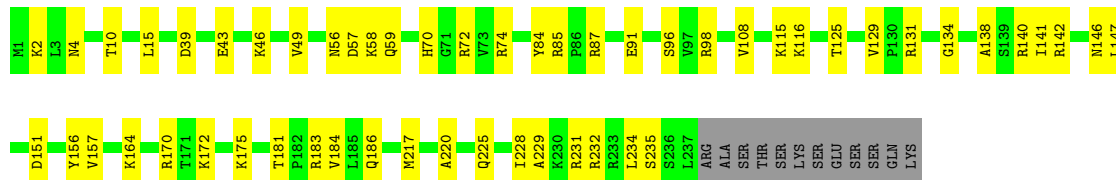
- Molecule 69: 40S ribosomal protein S2

Chain SC:  64% 11% 24%

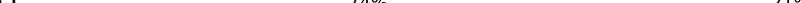


- Molecule 70: 40S ribosomal protein S6

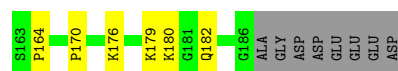
Chain SG:  73% 22% 5%



- Molecule 71: 40S ribosomal protein S9

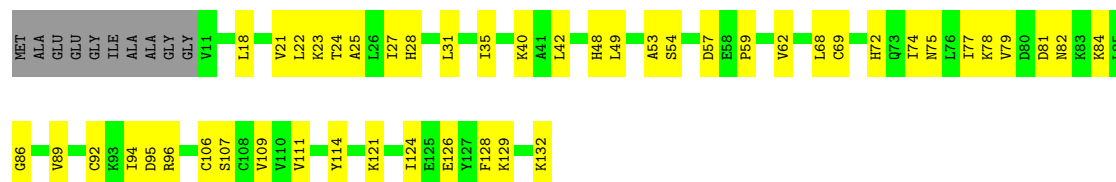
Chain SJ:  74% 21% 5%





- Molecule 72: 40S ribosomal protein S12

Chain SM: 57% 36% 8%



- Molecule 73: 40S ribosomal protein S13

Chain SN: 81% 19%



- Molecule 74: 40S ribosomal protein S14

Chain SO: 76% 17% 7%



- Molecule 75: 40S ribosomal protein S15a

Chain SW: 86% 13%



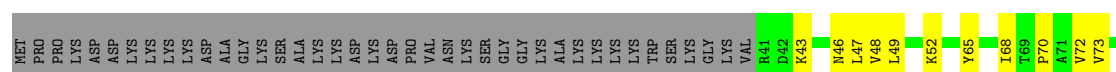
- Molecule 76: 40S ribosomal protein S24

Chain SY: 80% 18%



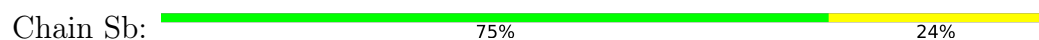
- Molecule 77: 40S ribosomal protein S25

Chain SZ: 41% 18% 40%

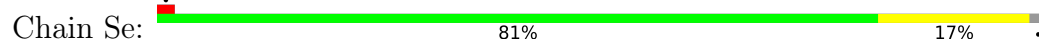




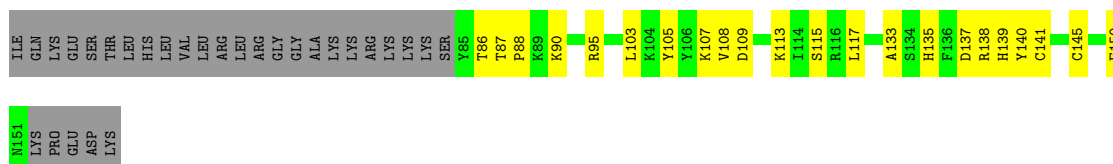
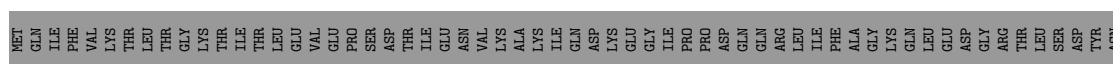
- Molecule 78: 40S ribosomal protein S27



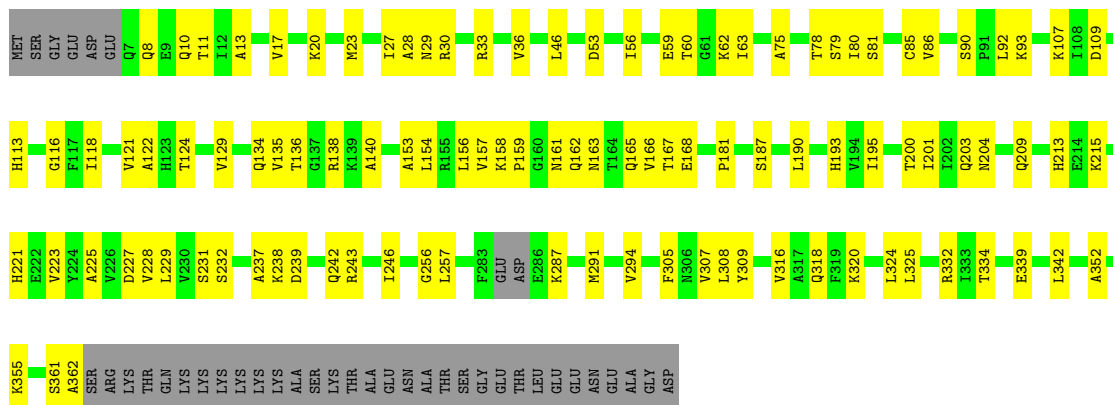
- Molecule 79: 40S ribosomal protein S30



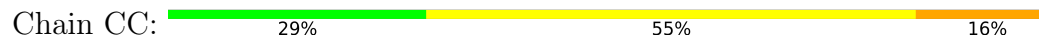
- Molecule 80: Ubiquitin-40S ribosomal protein S27a

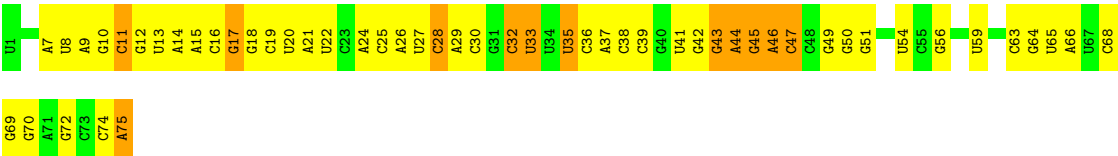


- Molecule 81: Proliferation-associated protein 2G4

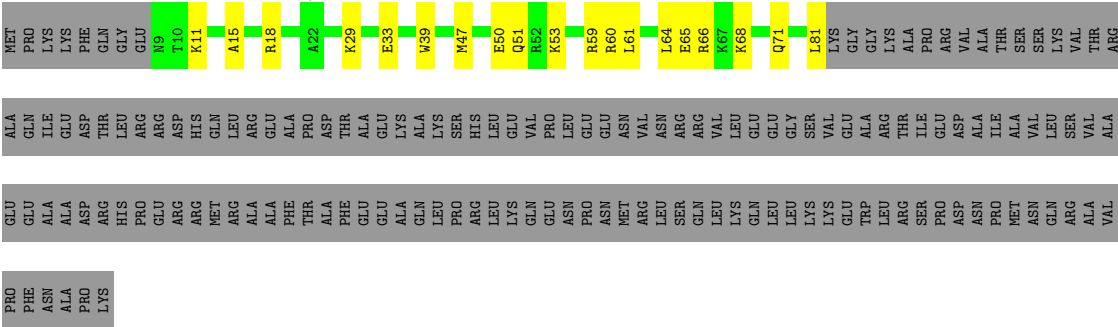


- Molecule 82: tRNA





● Molecule 83: Coiled-coil domain-containing protein 124



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	84429	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.245	Depositor
Minimum map value	-0.084	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	424.4, 424.4, 424.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.061, 1.061, 1.061	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	L5	0.35	0/89570	0.39	1/139647 (0.0%)
2	L7	0.33	0/2861	0.32	0/4459
3	L8	0.34	0/3701	0.34	0/5766
4	LA	0.38	0/1936	0.63	2/2596 (0.1%)
5	LB	0.33	0/3306	0.56	0/4424
6	LC	0.36	1/2981 (0.0%)	0.57	2/4002 (0.0%)
7	LD	0.26	0/2428	0.51	0/3252
8	LE	0.26	0/1942	0.55	0/2606
9	LF	0.35	0/1905	0.55	0/2539
10	LG	0.29	0/1960	0.54	0/2637
11	LH	0.29	0/1537	0.52	0/2066
12	LI	0.30	0/1673	0.52	0/2233
13	LJ	0.26	0/1433	0.66	0/1915
14	LL	0.29	0/1732	0.54	0/2315
15	LM	0.29	0/1161	0.57	2/1554 (0.1%)
16	LN	0.36	0/1746	0.61	0/2338
17	LO	0.32	0/1682	0.46	0/2250
18	LP	0.32	0/1268	0.50	0/1701
19	LQ	0.34	0/1537	0.54	0/2052
20	LR	0.30	0/1582	0.53	2/2091 (0.1%)
21	LS	0.32	0/1493	0.46	0/2003
22	LT	0.33	0/1326	0.56	0/1770
23	LU	0.26	0/839	0.63	0/1126
24	LV	0.34	0/993	0.53	0/1332
25	LW	0.27	0/1030	0.49	0/1364
26	LX	0.30	0/1002	0.49	0/1345
27	LY	0.30	0/1132	0.49	0/1504
28	LZ	0.29	0/1130	0.51	0/1507
29	La	0.32	0/1191	0.50	0/1591
30	Lb	0.28	0/889	0.55	0/1175
31	Lc	0.30	0/774	0.53	0/1038
32	Ld	0.33	0/903	0.54	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.36	0/1071	0.53	0/1429
34	Lf	0.34	0/895	0.56	0/1198
35	Lg	0.32	0/916	0.52	0/1220
36	Lh	0.25	0/1023	0.48	0/1351
37	Li	0.25	0/843	0.49	0/1115
38	Lj	0.36	0/720	0.59	0/952
39	Lk	0.27	0/575	0.51	0/761
40	Ll	0.34	0/454	0.54	0/599
41	Lm	0.30	0/435	0.56	0/575
42	Ln	0.32	0/231	0.53	0/294
43	Lo	0.31	0/855	0.46	0/1128
44	Lp	0.33	0/718	0.48	0/953
45	Lr	0.32	0/1017	0.52	0/1364
46	Lz	0.24	0/1769	0.60	0/2371
47	S2	0.29	0/41244	0.37	1/64263 (0.0%)
48	SA	0.27	0/1778	0.54	0/2416
49	SB	0.25	0/1765	0.51	0/2362
50	SD	0.23	0/1793	0.56	0/2414
51	SE	0.26	0/2118	0.52	0/2849
52	SF	0.23	0/1481	0.54	0/1988
53	SH	0.26	0/1519	0.60	0/2033
54	SI	0.28	0/1715	0.57	0/2287
55	SK	0.20	0/851	0.51	0/1147
56	SL	0.30	0/1268	0.50	0/1696
57	SP	0.21	0/1065	0.58	2/1423 (0.1%)
58	SQ	0.25	0/1160	0.61	0/1553
59	SR	0.22	0/1105	0.58	0/1484
60	SS	0.20	0/1216	0.52	0/1628
61	ST	0.21	0/1131	0.53	0/1515
62	SU	0.23	0/831	0.57	0/1115
63	SV	0.25	0/643	0.52	0/860
64	SX	0.31	0/1116	0.59	0/1490
65	Sa	0.31	0/836	0.61	0/1121
66	Sc	0.25	0/508	0.60	0/680
67	Sd	0.23	0/470	0.56	0/623
68	Sg	0.20	0/2493	0.57	2/3394 (0.1%)
69	SC	0.29	0/1762	0.60	0/2381
70	SG	0.22	0/1946	0.51	0/2590
71	SJ	0.26	0/1550	0.57	0/2069
72	SM	0.22	0/950	0.68	0/1275
73	SN	0.27	0/1232	0.47	0/1656
74	SO	0.28	0/1062	0.58	2/1425 (0.1%)
75	SW	0.29	0/1051	0.48	0/1406

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SY	0.23	0/1083	0.49	0/1438
77	SZ	0.26	0/604	0.68	0/810
78	Sb	0.24	0/665	0.50	0/891
79	Se	0.20	0/465	0.48	0/612
80	Sf	0.20	0/560	0.59	0/745
81	CA	0.23	0/2810	0.62	0/3780
82	CC	0.21	0/1773	0.41	0/2759
83	CE	0.21	0/616	0.53	0/812
All	All	0.31	1/238400 (0.0%)	0.45	16/349714 (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
4	LA	0	2
5	LB	0	3
11	LH	0	1
13	LJ	0	1
14	LL	0	1
15	LM	0	2
17	LO	0	2
22	LT	0	1
30	Lb	0	1
34	Lf	0	2
36	Lh	0	1
38	Lj	0	1
46	Lz	0	1
49	SB	0	1
50	SD	0	1
52	SF	0	1
53	SH	0	1
57	SP	0	1
58	SQ	0	1
61	ST	0	1
63	SV	0	1
64	SX	0	2
65	Sa	0	1
77	SZ	0	1
All	All	0	31

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	LC	47	ASN	CA-C	-6.32	1.44	1.52

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	LC	2	ALA	CA-C-N	6.29	133.03	121.70
6	LC	2	ALA	C-N-CA	6.29	133.03	121.70
74	SO	14	VAL	CA-C-N	6.01	132.52	121.70
74	SO	14	VAL	C-N-CA	6.01	132.52	121.70
15	LM	87	ALA	CA-C-N	5.93	132.86	121.54

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	LA	110	GLY	Peptide
4	LA	54	ARG	Peptide
5	LB	17	LEU	Peptide
5	LB	2	SER	Peptide
5	LB	258	HIS	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L5	80116	0	40366	842	0
2	L7	2561	0	1295	13	0
3	L8	3314	0	1683	18	0
4	LA	1898	0	1993	34	0
5	LB	3238	0	3376	54	0
6	LC	2927	0	3104	34	0
7	LD	2382	0	2410	36	0
8	LE	1904	0	2055	44	0
9	LF	1870	0	1996	24	0
10	LG	1927	0	2074	29	0
11	LH	1518	0	1601	31	0
12	LI	1634	0	1670	42	0
13	LJ	1410	0	1441	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	LL	1701	0	1818	29	0
15	LM	1138	0	1204	24	0
16	LN	1701	0	1749	21	0
17	LO	1650	0	1794	18	0
18	LP	1242	0	1269	16	0
19	LQ	1513	0	1628	16	0
20	LR	1566	0	1729	19	0
21	LS	1453	0	1490	13	0
22	LT	1298	0	1366	14	0
23	LU	825	0	850	10	0
24	LV	979	0	1039	18	0
25	LW	1015	0	1079	23	0
26	LX	985	0	1066	15	0
27	LY	1115	0	1205	18	0
28	LZ	1107	0	1182	24	0
29	La	1162	0	1213	19	0
30	Lb	876	0	948	15	0
31	Lc	764	0	804	11	0
32	Ld	888	0	930	10	0
33	Le	1053	0	1147	13	0
34	Lf	876	0	912	8	0
35	Lg	906	0	1000	10	0
36	Lh	1015	0	1148	14	0
37	Li	832	0	917	4	0
38	Lj	705	0	737	13	0
39	Lk	569	0	637	9	0
40	Ll	444	0	483	5	0
41	Lm	429	0	465	6	0
42	Ln	230	0	276	3	0
43	Lo	842	0	913	11	0
44	Lp	708	0	756	8	0
45	Lr	1002	0	1068	18	0
46	Lz	1741	0	1854	48	0
47	S2	36898	0	18603	476	0
48	SA	1741	0	1746	29	0
49	SB	1738	0	1809	39	0
50	SD	1765	0	1865	29	0
51	SE	2076	0	2177	30	0
52	SF	1461	0	1511	23	0
53	SH	1497	0	1590	32	0
54	SI	1686	0	1772	26	0
55	SK	827	0	854	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	SL	1247	0	1323	12	0
57	SP	1045	0	1095	35	0
58	SQ	1142	0	1213	28	0
59	SR	1090	0	1149	14	0
60	SS	1198	0	1261	34	0
61	ST	1112	0	1146	24	0
62	SU	821	0	883	25	0
63	SV	636	0	637	11	0
64	SX	1098	0	1167	18	0
65	Sa	821	0	870	13	0
66	Sc	506	0	536	12	0
67	Sd	459	0	450	14	0
68	Sg	2436	0	2393	71	0
69	SC	1725	0	1813	25	0
70	SG	1923	0	2089	41	0
71	SJ	1525	0	1640	31	0
72	SM	940	0	965	33	0
73	SN	1208	0	1294	20	0
74	SO	1049	0	1073	19	0
75	SW	1034	0	1080	15	0
76	SY	1065	0	1142	18	0
77	SZ	598	0	656	19	0
78	Sb	651	0	672	14	0
79	Se	459	0	503	8	0
80	Sf	548	0	550	18	0
81	CA	2764	0	2779	73	0
82	CC	1589	0	810	47	0
83	CE	613	0	625	13	0
84	L5	210	0	0	0	0
84	L7	3	0	0	0	0
84	L8	5	0	0	0	0
84	LA	1	0	0	0	0
84	LI	1	0	0	0	0
84	LP	1	0	0	0	0
84	LV	1	0	0	0	0
84	Le	2	0	0	0	0
84	Lg	1	0	0	0	0
84	Lj	1	0	0	0	0
84	S2	29	0	0	0	0
84	SG	1	0	0	0	0
85	Lg	1	0	0	0	0
85	Lj	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
85	Lm	1	0	0	0	0
85	Lo	1	0	0	0	0
85	Lp	1	0	0	0	0
85	Sa	1	0	0	0	0
85	Sd	1	0	0	0	0
85	Sf	1	0	0	0	0
All	All	222284	0	165481	2707	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 2707 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:S2:834:C:N4	47:S2:839:C:H42	1.04	1.51
1:L5:1969:G:N2	1:L5:1999:A:C2	1.91	1.38
47:S2:834:C:H42	47:S2:839:C:N4	1.22	1.35
62:SU:19:ARG:O	62:SU:117:ALA:HA	1.34	1.23
81:CA:78:THR:HA	81:CA:109:ASP:O	1.37	1.22

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LA	246/257 (96%)	224 (91%)	21 (8%)	1 (0%)	30	65
5	LB	400/403 (99%)	370 (92%)	28 (7%)	2 (0%)	24	60
6	LC	366/427 (86%)	331 (90%)	34 (9%)	1 (0%)	36	70
7	LD	291/297 (98%)	271 (93%)	20 (7%)	0	100	100
8	LE	232/288 (81%)	216 (93%)	16 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	LF	223/248 (90%)	213 (96%)	10 (4%)	0	100	100
10	LG	239/266 (90%)	223 (93%)	16 (7%)	0	100	100
11	LH	188/192 (98%)	168 (89%)	20 (11%)	0	100	100
12	LI	198/214 (92%)	183 (92%)	15 (8%)	0	100	100
13	LJ	174/178 (98%)	158 (91%)	16 (9%)	0	100	100
14	LL	208/211 (99%)	191 (92%)	17 (8%)	0	100	100
15	LM	137/215 (64%)	125 (91%)	11 (8%)	1 (1%)	18	53
16	LN	201/204 (98%)	191 (95%)	8 (4%)	2 (1%)	12	45
17	LO	199/203 (98%)	190 (96%)	9 (4%)	0	100	100
18	LP	151/184 (82%)	140 (93%)	11 (7%)	0	100	100
19	LQ	185/188 (98%)	176 (95%)	9 (5%)	0	100	100
20	LR	185/196 (94%)	180 (97%)	5 (3%)	0	100	100
21	LS	173/176 (98%)	162 (94%)	11 (6%)	0	100	100
22	LT	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
23	LU	99/128 (77%)	85 (86%)	13 (13%)	1 (1%)	12	45
24	LV	129/140 (92%)	120 (93%)	9 (7%)	0	100	100
25	LW	122/157 (78%)	115 (94%)	7 (6%)	0	100	100
26	LX	118/156 (76%)	112 (95%)	6 (5%)	0	100	100
27	LY	132/145 (91%)	120 (91%)	12 (9%)	0	100	100
28	LZ	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
29	La	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
30	Lb	105/159 (66%)	97 (92%)	8 (8%)	0	100	100
31	Lc	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
32	Ld	105/125 (84%)	100 (95%)	5 (5%)	0	100	100
33	Le	126/135 (93%)	120 (95%)	5 (4%)	1 (1%)	16	50
34	Lf	107/110 (97%)	98 (92%)	7 (6%)	2 (2%)	6	30
35	Lg	112/117 (96%)	108 (96%)	4 (4%)	0	100	100
36	Lh	120/123 (98%)	117 (98%)	3 (2%)	0	100	100
37	Li	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
38	Lj	84/97 (87%)	76 (90%)	7 (8%)	1 (1%)	10	40
39	Lk	67/70 (96%)	61 (91%)	6 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	Ll	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
41	Lm	50/128 (39%)	50 (100%)	0	0	100	100
42	Ln	22/25 (88%)	22 (100%)	0	0	100	100
43	Lo	101/104 (97%)	95 (94%)	6 (6%)	0	100	100
44	Lp	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
45	Lr	123/137 (90%)	116 (94%)	7 (6%)	0	100	100
46	Lz	215/217 (99%)	171 (80%)	44 (20%)	0	100	100
48	SA	219/295 (74%)	196 (90%)	23 (10%)	0	100	100
49	SB	212/264 (80%)	197 (93%)	15 (7%)	0	100	100
50	SD	225/243 (93%)	202 (90%)	23 (10%)	0	100	100
51	SE	260/263 (99%)	242 (93%)	18 (7%)	0	100	100
52	SF	180/204 (88%)	165 (92%)	15 (8%)	0	100	100
53	SH	182/194 (94%)	161 (88%)	21 (12%)	0	100	100
54	SI	204/208 (98%)	193 (95%)	11 (5%)	0	100	100
55	SK	96/165 (58%)	85 (88%)	11 (12%)	0	100	100
56	SL	151/158 (96%)	139 (92%)	12 (8%)	0	100	100
57	SP	125/145 (86%)	115 (92%)	10 (8%)	0	100	100
58	SQ	142/146 (97%)	128 (90%)	13 (9%)	1 (1%)	18	53
59	SR	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
60	SS	143/152 (94%)	131 (92%)	12 (8%)	0	100	100
61	ST	141/145 (97%)	129 (92%)	11 (8%)	1 (1%)	18	53
62	SU	102/119 (86%)	91 (89%)	11 (11%)	0	100	100
63	SV	81/83 (98%)	73 (90%)	7 (9%)	1 (1%)	10	40
64	SX	139/143 (97%)	124 (89%)	14 (10%)	1 (1%)	18	53
65	Sa	100/115 (87%)	90 (90%)	9 (9%)	1 (1%)	12	45
66	Sc	62/69 (90%)	50 (81%)	12 (19%)	0	100	100
67	Sd	53/56 (95%)	49 (92%)	4 (8%)	0	100	100
68	Sg	311/317 (98%)	267 (86%)	44 (14%)	0	100	100
69	SC	220/293 (75%)	206 (94%)	14 (6%)	0	100	100
70	SG	235/249 (94%)	218 (93%)	17 (7%)	0	100	100
71	SJ	183/194 (94%)	170 (93%)	13 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	SM	120/132 (91%)	109 (91%)	11 (9%)	0	100	100
73	SN	148/151 (98%)	140 (95%)	8 (5%)	0	100	100
74	SO	138/151 (91%)	126 (91%)	12 (9%)	0	100	100
75	SW	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
76	SY	129/133 (97%)	121 (94%)	8 (6%)	0	100	100
77	SZ	73/125 (58%)	59 (81%)	13 (18%)	1 (1%)	9	36
78	Sb	81/84 (96%)	70 (86%)	11 (14%)	0	100	100
79	Se	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
80	Sf	65/156 (42%)	54 (83%)	11 (17%)	0	100	100
81	CA	350/394 (89%)	332 (95%)	18 (5%)	0	100	100
83	CE	71/223 (32%)	70 (99%)	1 (1%)	0	100	100
All	All	11958/13520 (88%)	11007 (92%)	933 (8%)	18 (0%)	44	76

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LN	124	ASP
64	SX	127	ASN
15	LM	88	ALA
61	ST	41	LYS
5	LB	302	ASN

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	
4	LA	190/199 (96%)	188 (99%)	2 (1%)	65	83
5	LB	348/349 (100%)	347 (100%)	1 (0%)	86	91
6	LC	306/348 (88%)	304 (99%)	2 (1%)	76	86
7	LD	246/250 (98%)	246 (100%)	0	100	100
8	LE	209/252 (83%)	208 (100%)	1 (0%)	81	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	LF	194/215 (90%)	193 (100%)	1 (0%)	81	89
10	LG	203/223 (91%)	203 (100%)	0	100	100
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	172/181 (95%)	172 (100%)	0	100	100
13	LJ	148/149 (99%)	148 (100%)	0	100	100
14	LL	176/177 (99%)	175 (99%)	1 (1%)	78	88
15	LM	118/161 (73%)	118 (100%)	0	100	100
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	173/174 (99%)	173 (100%)	0	100	100
18	LP	134/163 (82%)	134 (100%)	0	100	100
19	LQ	164/165 (99%)	163 (99%)	1 (1%)	78	88
20	LR	166/175 (95%)	166 (100%)	0	100	100
21	LS	156/157 (99%)	155 (99%)	1 (1%)	78	88
22	LT	139/140 (99%)	139 (100%)	0	100	100
23	LU	91/115 (79%)	91 (100%)	0	100	100
24	LV	101/107 (94%)	100 (99%)	1 (1%)	68	84
25	LW	103/126 (82%)	103 (100%)	0	100	100
26	LX	108/133 (81%)	108 (100%)	0	100	100
27	LY	124/135 (92%)	123 (99%)	1 (1%)	73	86
28	LZ	117/118 (99%)	115 (98%)	2 (2%)	53	78
29	La	120/121 (99%)	118 (98%)	2 (2%)	53	78
30	Lb	88/126 (70%)	87 (99%)	1 (1%)	65	83
31	Lc	83/97 (86%)	83 (100%)	0	100	100
32	Ld	98/110 (89%)	98 (100%)	0	100	100
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	86 (98%)	2 (2%)	44	74
35	Lg	98/100 (98%)	98 (100%)	0	100	100
36	Lh	109/110 (99%)	109 (100%)	0	100	100
37	Li	86/89 (97%)	86 (100%)	0	100	100
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	64 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	Ll	47/48 (98%)	47 (100%)	0	100	100
41	Lm	48/116 (41%)	48 (100%)	0	100	100
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	91/92 (99%)	91 (100%)	0	100	100
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	109/121 (90%)	109 (100%)	0	100	100
46	Lz	195/196 (100%)	193 (99%)	2 (1%)	68	84
48	SA	183/243 (75%)	182 (100%)	1 (0%)	81	89
49	SB	195/231 (84%)	195 (100%)	0	100	100
50	SD	190/202 (94%)	189 (100%)	1 (0%)	81	89
51	SE	224/225 (100%)	223 (100%)	1 (0%)	84	90
52	SF	156/170 (92%)	156 (100%)	0	100	100
53	SH	166/174 (95%)	165 (99%)	1 (1%)	78	88
54	SI	178/180 (99%)	178 (100%)	0	100	100
55	SK	89/136 (65%)	89 (100%)	0	100	100
56	SL	137/142 (96%)	137 (100%)	0	100	100
57	SP	113/130 (87%)	113 (100%)	0	100	100
58	SQ	119/121 (98%)	118 (99%)	1 (1%)	73	86
59	SR	122/122 (100%)	121 (99%)	1 (1%)	73	86
60	SS	126/132 (96%)	124 (98%)	2 (2%)	55	79
61	ST	113/115 (98%)	113 (100%)	0	100	100
62	SU	94/107 (88%)	94 (100%)	0	100	100
63	SV	67/67 (100%)	67 (100%)	0	100	100
64	SX	113/115 (98%)	112 (99%)	1 (1%)	70	85
65	Sa	89/98 (91%)	88 (99%)	1 (1%)	65	83
66	Sc	57/62 (92%)	57 (100%)	0	100	100
67	Sd	48/49 (98%)	47 (98%)	1 (2%)	47	75
68	Sg	272/275 (99%)	272 (100%)	0	100	100
69	SC	188/225 (84%)	187 (100%)	1 (0%)	81	89
70	SG	207/218 (95%)	207 (100%)	0	100	100
71	SJ	161/168 (96%)	161 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	SM	102/108 (94%)	102 (100%)	0	100	100
73	SN	130/131 (99%)	129 (99%)	1 (1%)	73	86
74	SO	110/119 (92%)	110 (100%)	0	100	100
75	SW	112/113 (99%)	112 (100%)	0	100	100
76	SY	113/115 (98%)	113 (100%)	0	100	100
77	SZ	66/103 (64%)	66 (100%)	0	100	100
78	Sb	75/76 (99%)	75 (100%)	0	100	100
79	Se	47/48 (98%)	47 (100%)	0	100	100
80	Sf	60/140 (43%)	60 (100%)	0	100	100
81	CA	303/336 (90%)	303 (100%)	0	100	100
83	CE	62/190 (33%)	62 (100%)	0	100	100
All	All	10421/11521 (90%)	10387 (100%)	34 (0%)	84	91

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
60	SS	103	LEU
64	SX	13	LEU
69	SC	104	ASP
28	LZ	46	ILE
27	LY	79	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 161 such sidechains are listed below:

Mol	Chain	Res	Type
57	SP	24	GLN
73	SN	5	HIS
58	SQ	80	GLN
66	Sc	7	GLN
78	Sb	84	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3704/5070 (73%)	961 (25%)	19 (0%)
2	L7	119/121 (98%)	10 (8%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	L8	155/157 (98%)	31 (20%)	2 (1%)
47	S2	1715/1869 (91%)	424 (24%)	8 (0%)
82	CC	74/75 (98%)	22 (29%)	3 (4%)
All	All	5767/7292 (79%)	1448 (25%)	32 (0%)

5 of 1448 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	17	A
1	L5	25	A
1	L5	26	C
1	L5	30	C

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
47	S2	1434	C
82	CC	35	U
1	L5	2786	C
1	L5	2760	G
82	CC	37	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 264 ligands modelled in this entry, 264 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

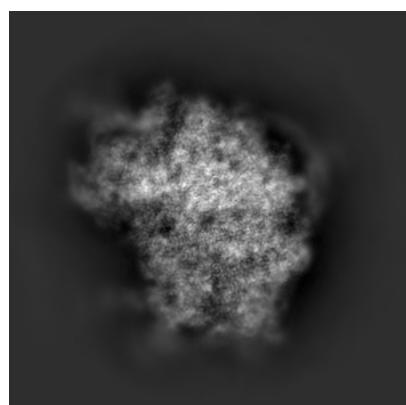
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11098. These allow visual inspection of the internal detail of the map and identification of artifacts.

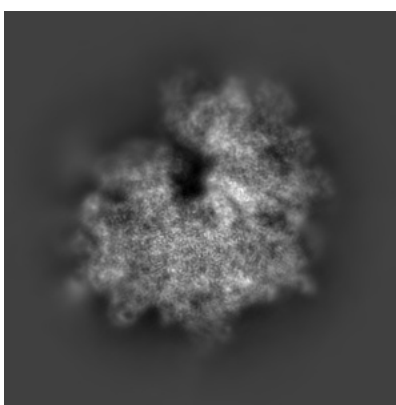
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

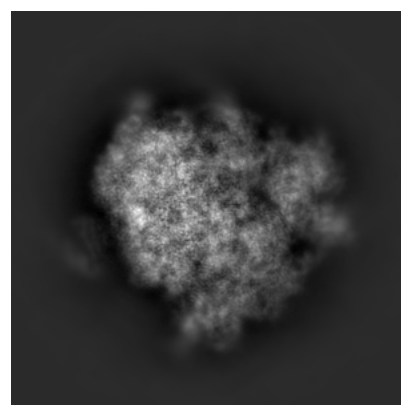
6.1.1 Primary map



X



Y

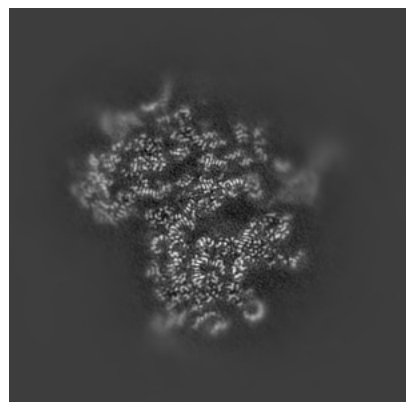


Z

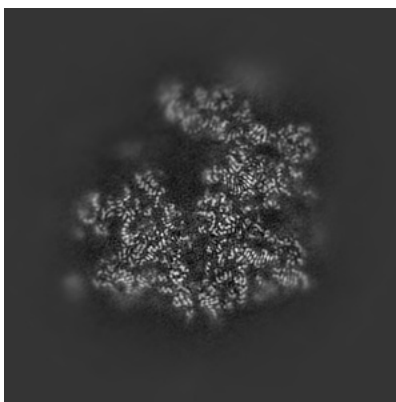
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

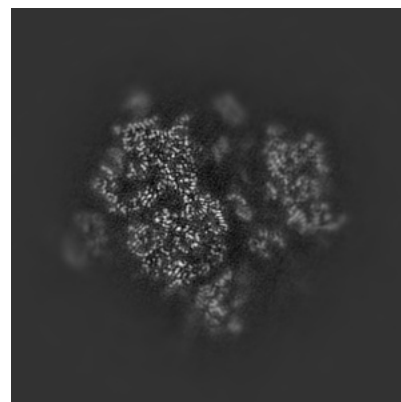
6.2.1 Primary map



X Index: 200



Y Index: 200

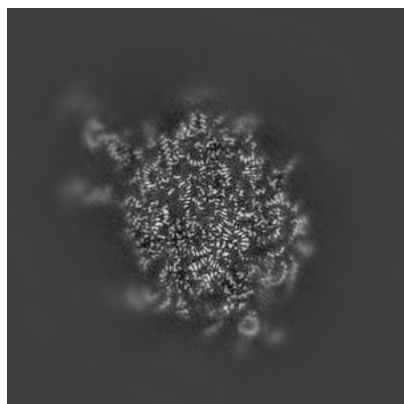


Z Index: 200

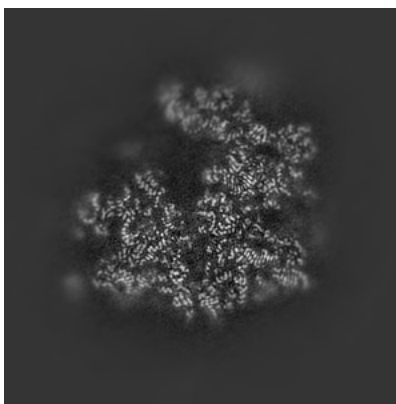
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

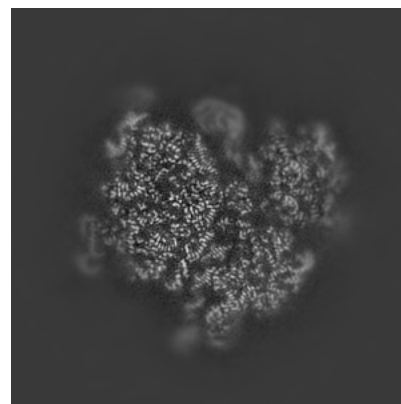
6.3.1 Primary map



X Index: 172



Y Index: 200

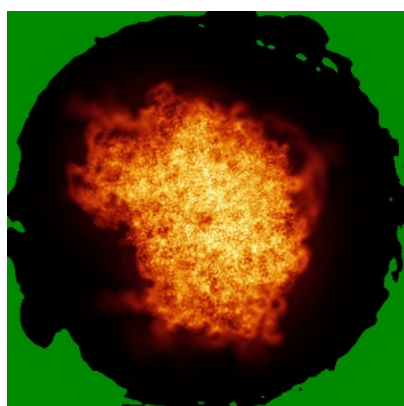


Z Index: 222

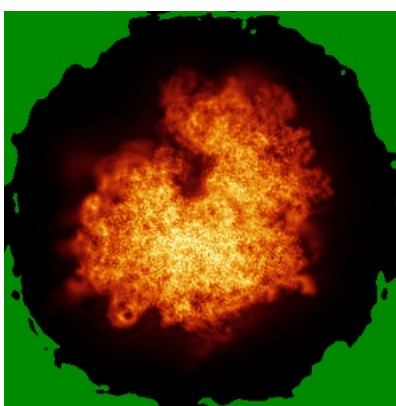
The images above show the largest variance slices of the map in three orthogonal directions.

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

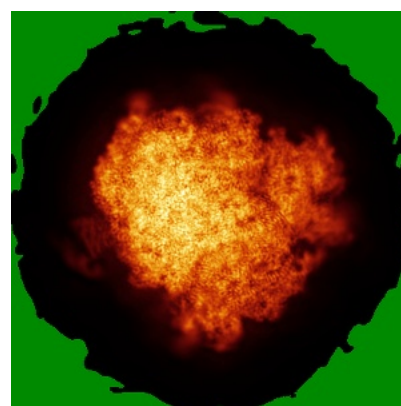
6.4.1 Primary map



X



Y



Z

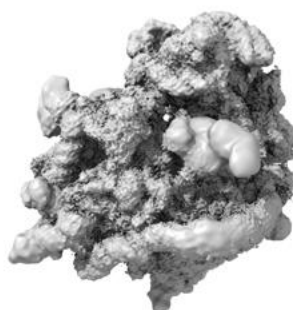
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

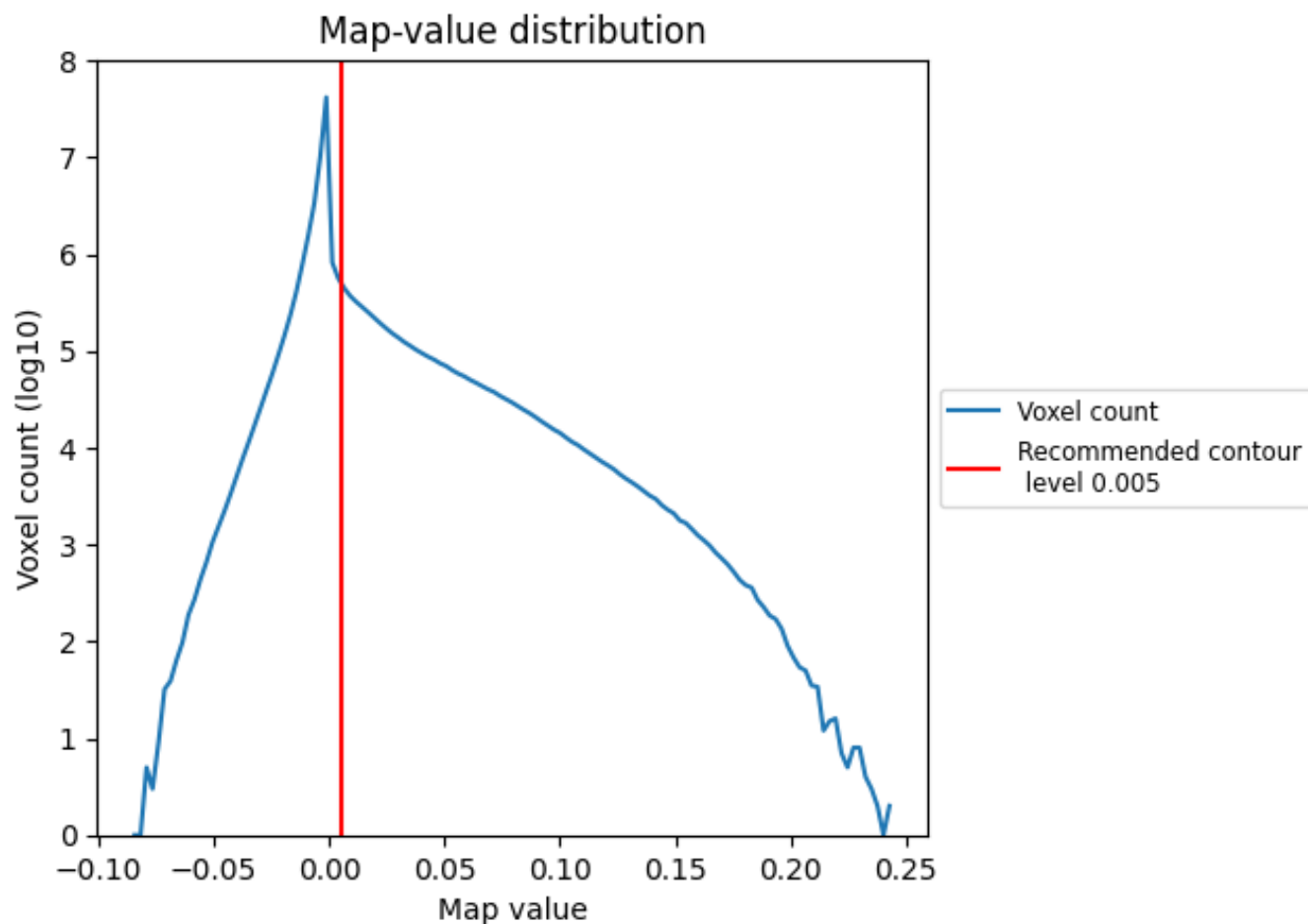
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

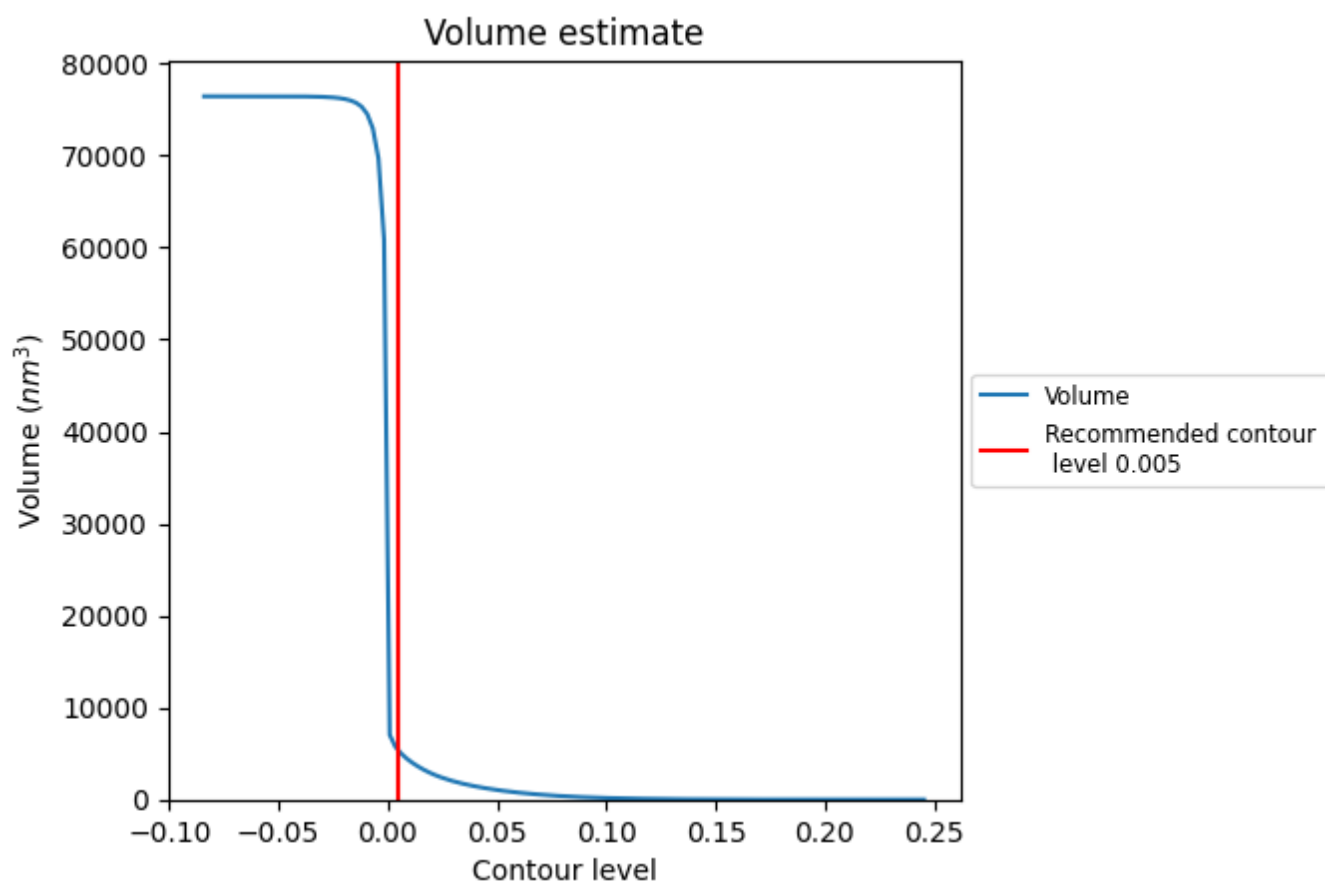
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

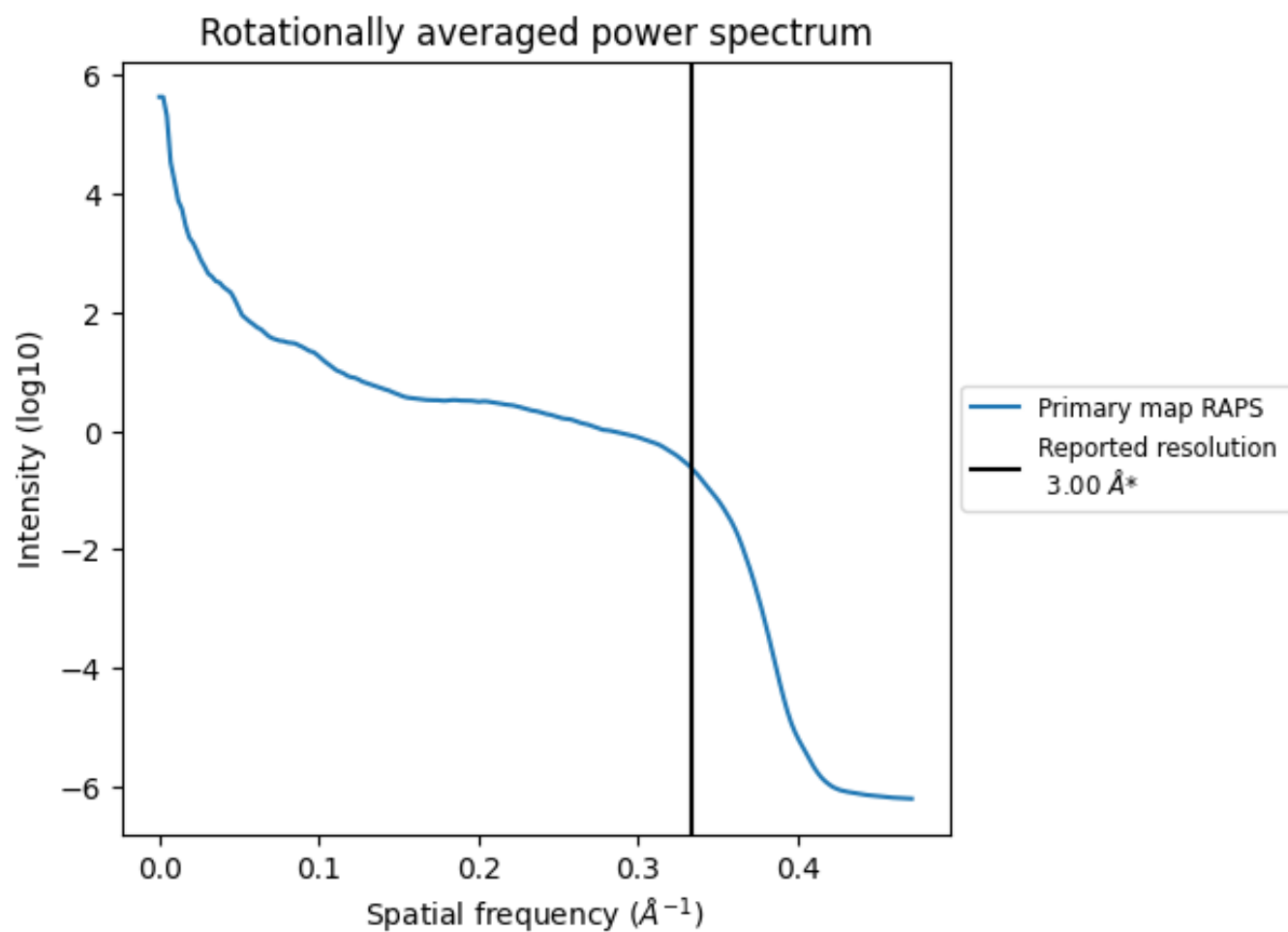
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5303 nm³; this corresponds to an approximate mass of 4790 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 ⓘ

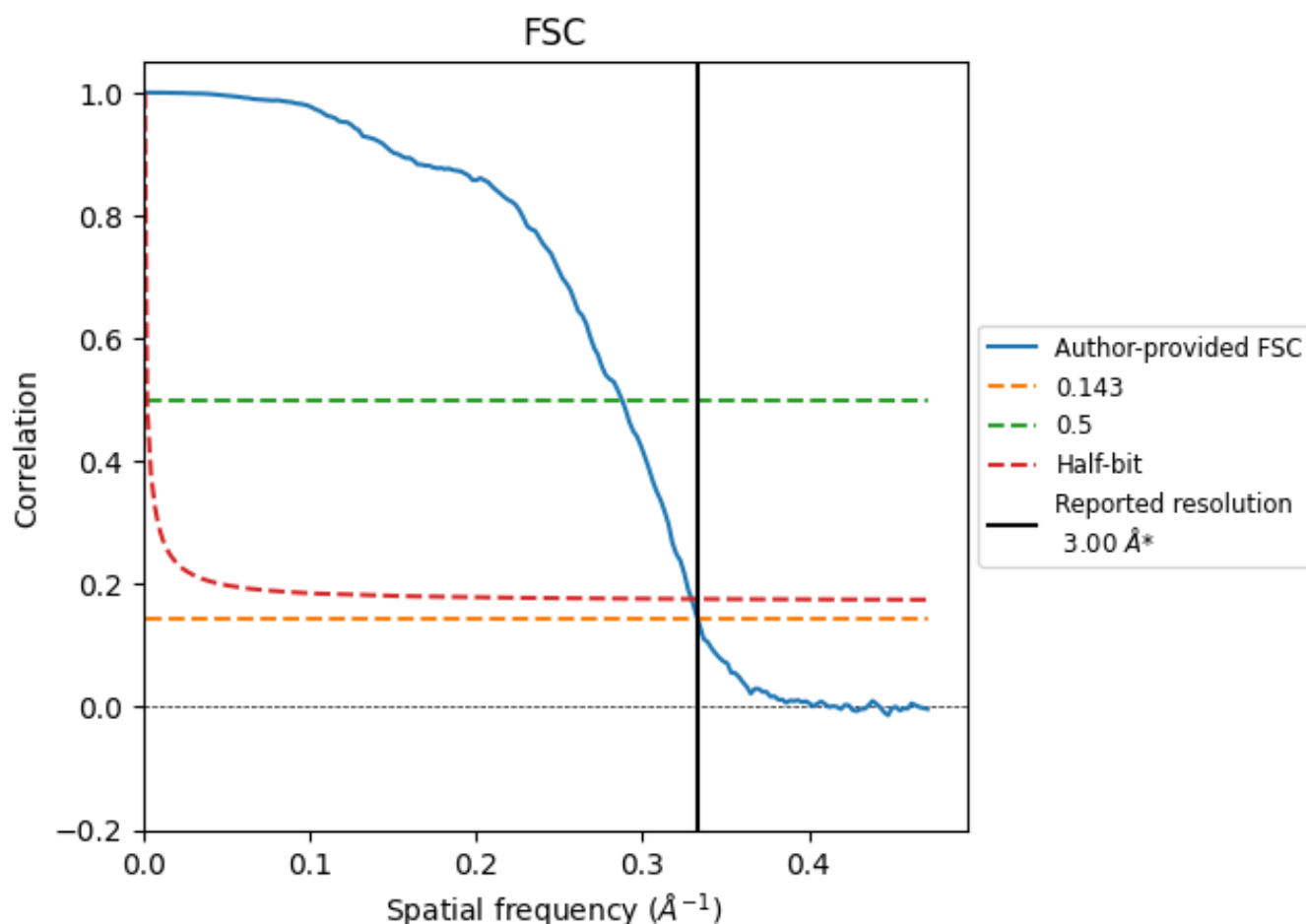


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

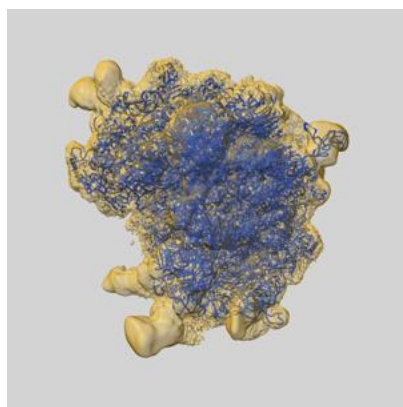
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.00	3.48	3.03
Unmasked-calculated*	-	-	-

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

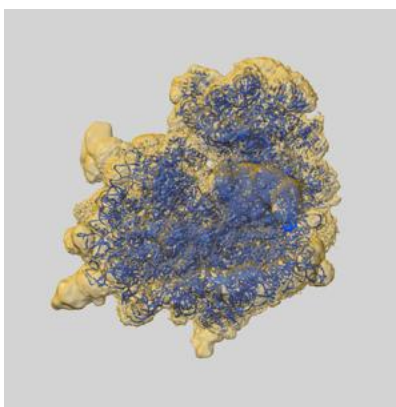
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11098 and PDB model 6Z6L. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

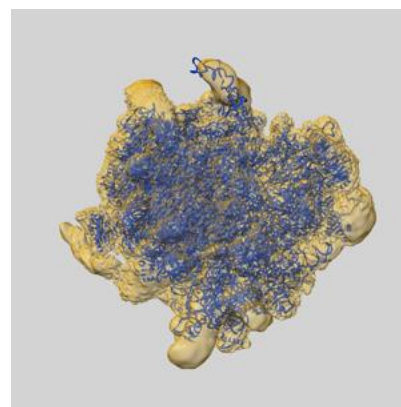
9.1 Map-model overlay [i](#)



X



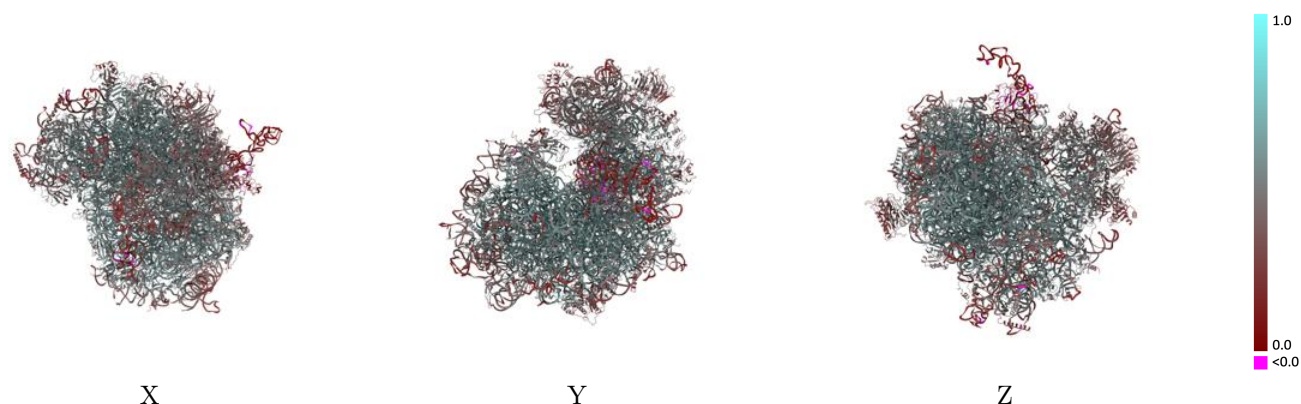
Y



Z

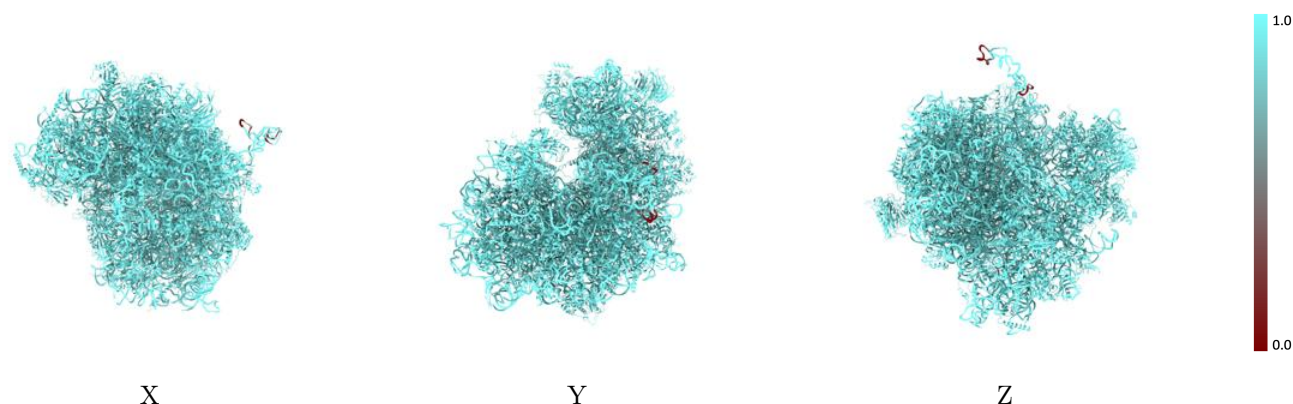
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



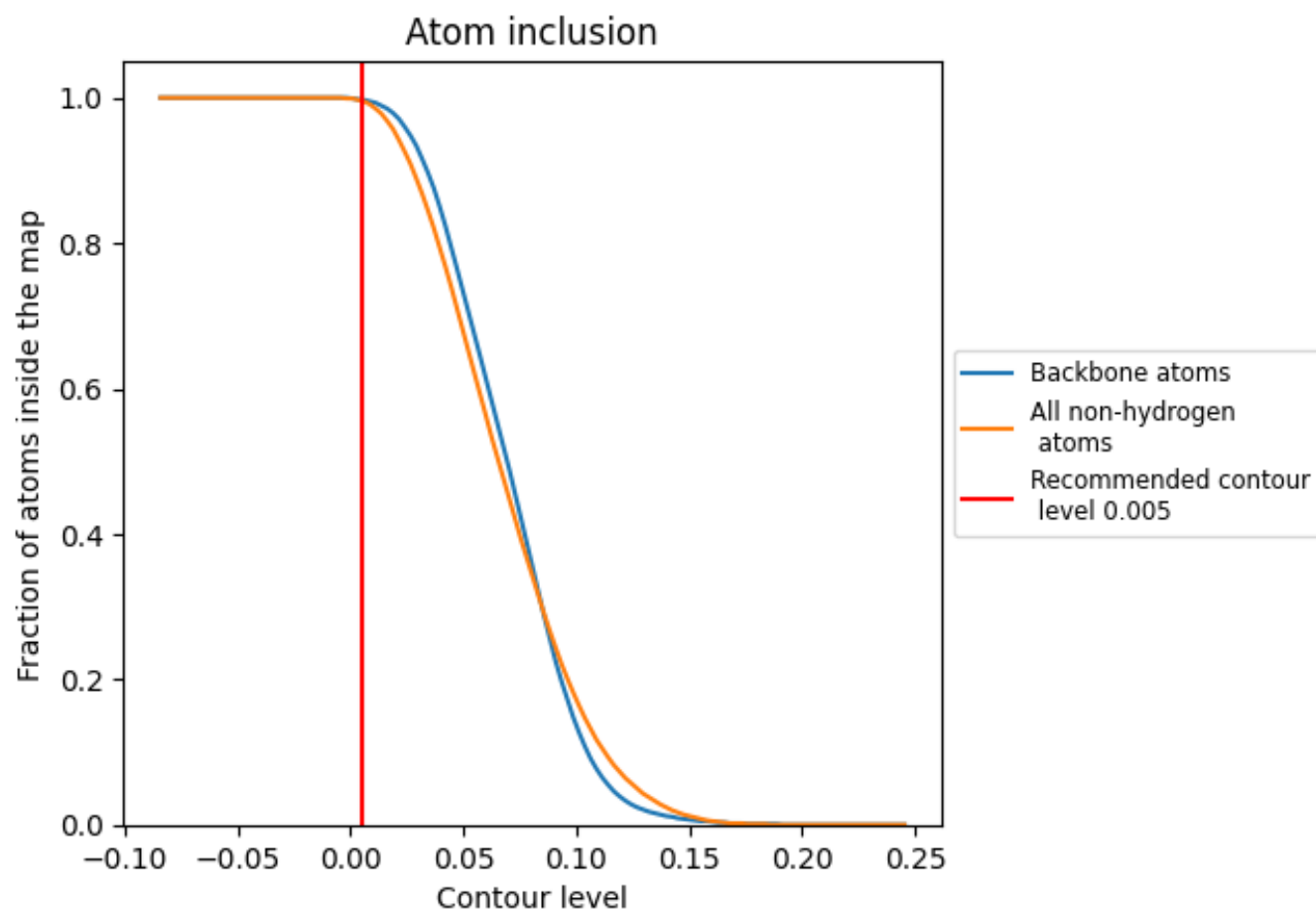
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9960	 0.4990
CA	 0.9810	 0.3130
CC	 0.9900	 0.3030
CE	 0.8550	 0.3980
L5	 0.9980	 0.5190
L7	 1.0000	 0.5610
L8	 0.9990	 0.5420
LA	 0.9940	 0.5970
LB	 0.9950	 0.5600
LC	 0.9960	 0.5540
LD	 1.0000	 0.4970
LE	 0.9970	 0.4710
LF	 0.9960	 0.5580
LG	 0.9940	 0.4750
LH	 0.9970	 0.5240
LI	 0.9920	 0.5480
LJ	 0.9890	 0.4430
LL	 0.9930	 0.5130
LM	 0.9950	 0.5090
LN	 0.9960	 0.5940
LO	 0.9930	 0.5690
LP	 0.9960	 0.5780
LQ	 0.9940	 0.5800
LR	 0.9980	 0.5240
LS	 0.9990	 0.5750
LT	 0.9910	 0.5470
LU	 0.9990	 0.4450
LV	 0.9920	 0.5750
LW	 0.9920	 0.4110
LX	 0.9920	 0.5400
LY	 0.9980	 0.5300
LZ	 1.0000	 0.5180
La	 0.9960	 0.5790
Lb	 0.9880	 0.4870
Lc	 0.9880	 0.5300



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Chain	Atom inclusion	Q-score
Ld	 0.9970	 0.5370
Le	 0.9950	 0.5880
Lf	 0.9910	 0.5860
Lg	 0.9950	 0.5650
Lh	 0.9910	 0.5190
Li	 0.9980	 0.5100
Lj	 0.9940	 0.5850
Lk	 0.9950	 0.4860
Ll	 0.9880	 0.5700
Lm	 0.9900	 0.5420
Ln	 0.9950	 0.5990
Lo	 0.9900	 0.5580
Lp	 0.9870	 0.5760
Lr	 0.9980	 0.5470
Lz	 0.9360	 0.1350
S2	 1.0000	 0.4920
SA	 0.9980	 0.4750
SB	 0.9960	 0.5010
SC	 0.9950	 0.5190
SD	 0.9950	 0.4220
SE	 0.9990	 0.5130
SF	 0.9940	 0.4390
SG	 0.9980	 0.4140
SH	 0.9950	 0.4040
SI	 0.9940	 0.4970
SJ	 0.9910	 0.4820
SK	 1.0000	 0.3350
SL	 0.9870	 0.5410
SM	 0.9970	 0.2010
SN	 0.9900	 0.5370
SO	 0.9720	 0.5010
SP	 0.9960	 0.3540
SQ	 0.9960	 0.4320
SR	 0.9950	 0.4330
SS	 0.9960	 0.3880
ST	 1.0000	 0.4070
SU	 0.9960	 0.3900
SV	 1.0000	 0.4810
SW	 0.9910	 0.5500
SX	 0.9930	 0.5450
SY	 0.9980	 0.4420
SZ	 1.0000	 0.3380

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Chain	Atom inclusion	Q-score
Sa	 0.9910	 0.5280
Sb	 1.0000	 0.4910
Sc	 0.9940	 0.4410
Sd	 0.9960	 0.4590
Se	 0.9600	 0.4460
Sf	 1.0000	 0.2130
Sg	 1.0000	 0.3530