



wwPDB EM Validation Summary Report ⓘ

Apr 2, 2025 – 02:46 am BST

PDB ID : 5LKS / pdb_00005lks
EMDB ID : EMD-4070
Title : Structure-function insights reveal the human ribosome as a cancer target for antibiotics
Authors : Myasnikov, A.G.; Natchiar, S.K.; Nebout, M.; Hazemann, I.; Imbert, V.; Khat-ter, H.; Peyron, J.-F.; Klaholz, B.P.
Deposited on : 2016-07-23
Resolution : 3.60 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:

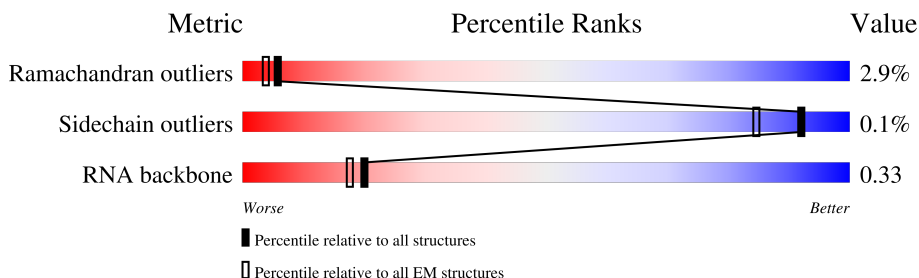
EMDB validation analysis : 0.0.1.dev117
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : 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 3.60 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.





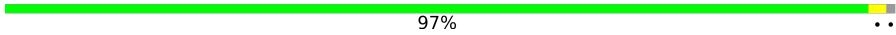
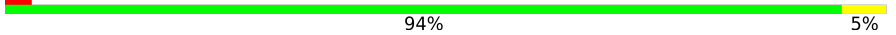
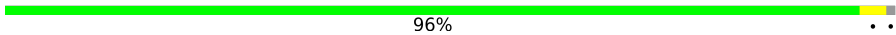
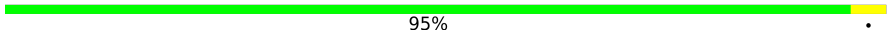

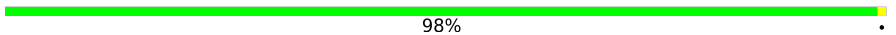
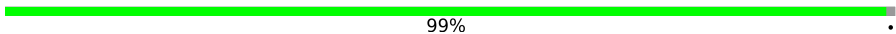

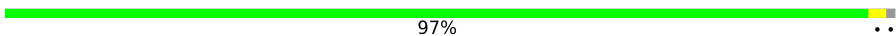
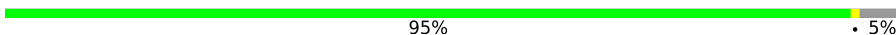

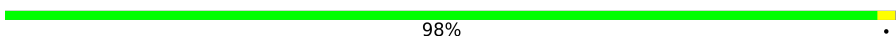





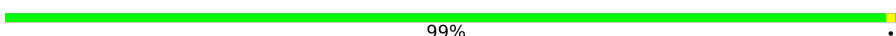
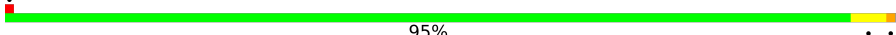




Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	L5	5070	
2	L7	121	
3	L8	157	
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	

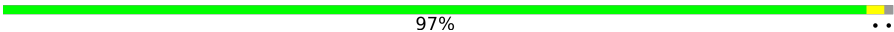
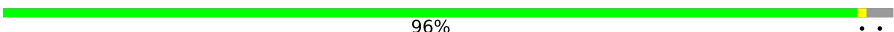
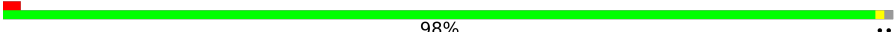
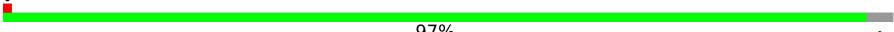








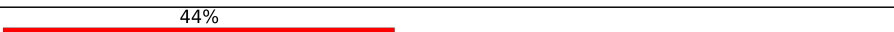

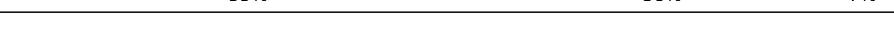

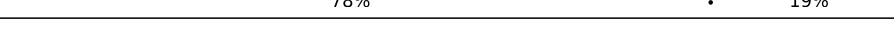

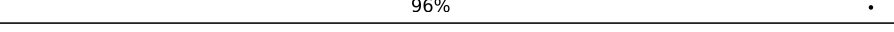

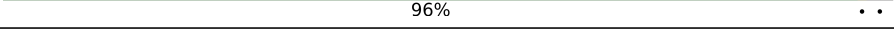
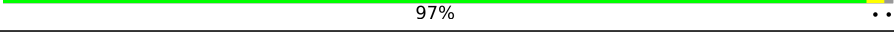

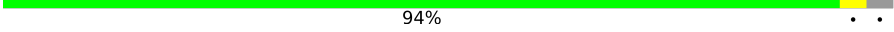

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Mol	Chain	Length	Quality of chain
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
24	LV	140	
25	LW	157	
26	LX	156	
27	LY	145	
28	LZ	136	
29	La	148	
30	Lb	157	
31	Lc	115	
32	Ld	125	
33	Le	135	

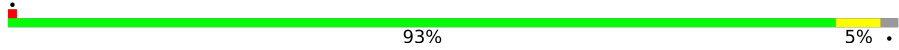
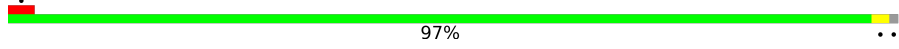
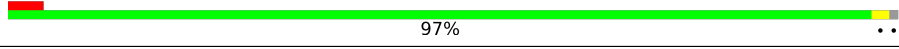

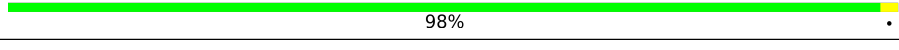
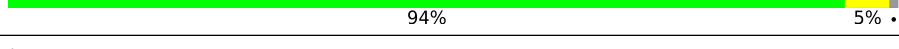
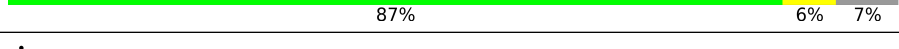
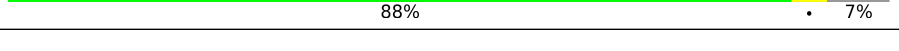
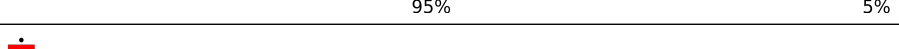
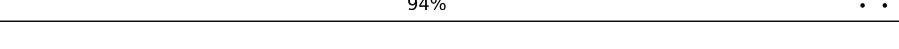
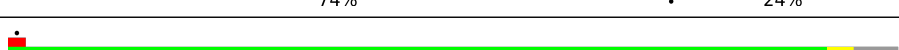
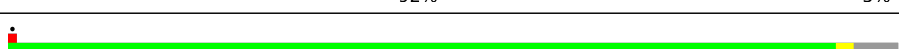
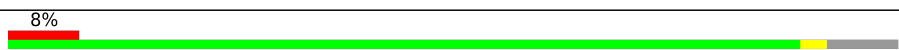
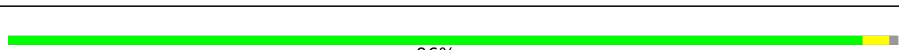
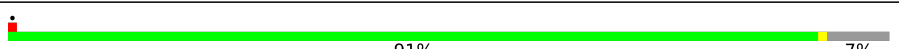

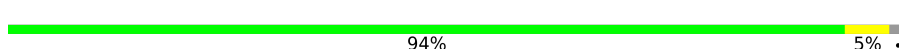

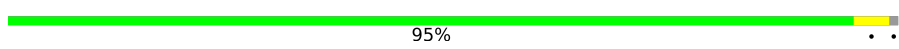



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Mol	Chain	Length	Quality of chain
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	Lz	217	
47	S2	1869	
48	SA	295	
49	SB	264	
50	SD	243	
51	SE	263	
52	SF	204	
53	SH	194	
54	SI	208	
55	SK	165	
56	SL	158	
57	SP	145	
58	SQ	146	

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Mol	Chain	Length	Quality of chain
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	
79	Se	133	
80	Sf	156	

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 217138 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3776	Total	C	N	O	P	0	0
			80184	35672	14597	26140	3775		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L5	4941	G	C	conflict	GB 86475748
L5	4942	C	A	conflict	GB 86475748

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

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

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	243	Total	C	N	O	S	0	0
			1967	1263	374	326	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	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

- 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	119	Total	C	N	O	S	0	0
			976	625	184	166	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 Ribosomal protein L29, isoform CRA_a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- 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	113	Total	C	N	O	S	0	0
			895	560	183	146	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	105	Total	C	N	O	S	0	0
			862	542	175	139	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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S2	1742	Total	C	N	O	P	0	0
			36900	16458	6595	12106	1741		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S2	582	C	U	conflict	GB 36162
S2	583	C	A	conflict	GB 36162
S2	584	G	A	conflict	GB 36162
S2	798	A	G	conflict	GB 36162
S2	1095	U	C	conflict	GB 36162

- 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	187	Total	C	N	O	S	0	0
			1479	924	282	266	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SH	189	Total	C	N	O	S	0	0
			1521	969	280	271	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	97	Total	C	N	O	S	0	0
			804	505	155	138	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SQ	146	Total	C	N	O	S	0	0
			1158	736	218	200	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SR	132	Total	C	N	O	S	0	0
			1072	673	199	195	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SS	150	Total	C	N	O	S	0	0
			1235	776	250	208	1		

- 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	107	Total	C	N	O	S	0	0
			847	528	176	138	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	53	Total	C	N	O	S	0	0
			445	278	90	72	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
			952	596	169	179	8		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SM	52	GLN	LEU	conflict	UNP P25398
SM	69	LEU	CYS	conflict	UNP P25398
SM	99	ASN	LYS	conflict	UNP P25398

- 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		

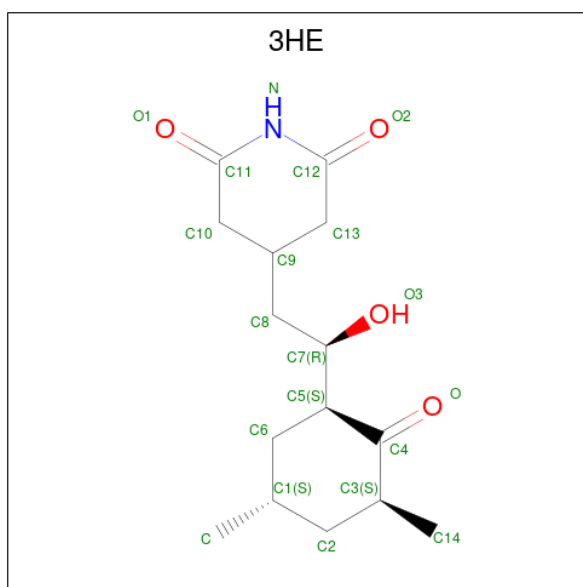
- Molecule 79 is a protein called Ribosomal protein S30.

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 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (CCD ID: 3HE) (formula: C₁₅H₂₃NO₄).



Mol	Chain	Residues	Atoms				AltConf
81	L5	1	Total	C	N	O	0
			20	15	1	4	

- Molecule 82 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
82	L5	160	Total	Mg	0
			160	160	
82	L7	3	Total	Mg	0
			3	3	
82	L8	4	Total	Mg	0
			4	4	
82	LC	1	Total	Mg	0
			1	1	
82	LD	1	Total	Mg	0
			1	1	
82	LL	1	Total	Mg	0
			1	1	
82	LP	1	Total	Mg	0
			1	1	
82	LS	2	Total	Mg	0
			2	2	
82	LV	1	Total	Mg	0
			1	1	
82	Le	1	Total	Mg	0
			1	1	
82	S2	48	Total	Mg	0
			48	48	

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Mol	Chain	Residues	Atoms		AltConf
82	Sa	1	Total 1	Mg 1	0

- Molecule 83 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 84 is water.

Mol	Chain	Residues	Atoms		AltConf
84	L5	13	Total 13	O 13	0
84	L8	1	Total 1	O 1	0
84	LA	1	Total 1	O 1	0
84	LD	1	Total 1	O 1	0
84	LN	1	Total 1	O 1	0
84	LT	1	Total 1	O 1	0
84	Le	1	Total 1	O 1	0
84	Lp	1	Total 1	O 1	0

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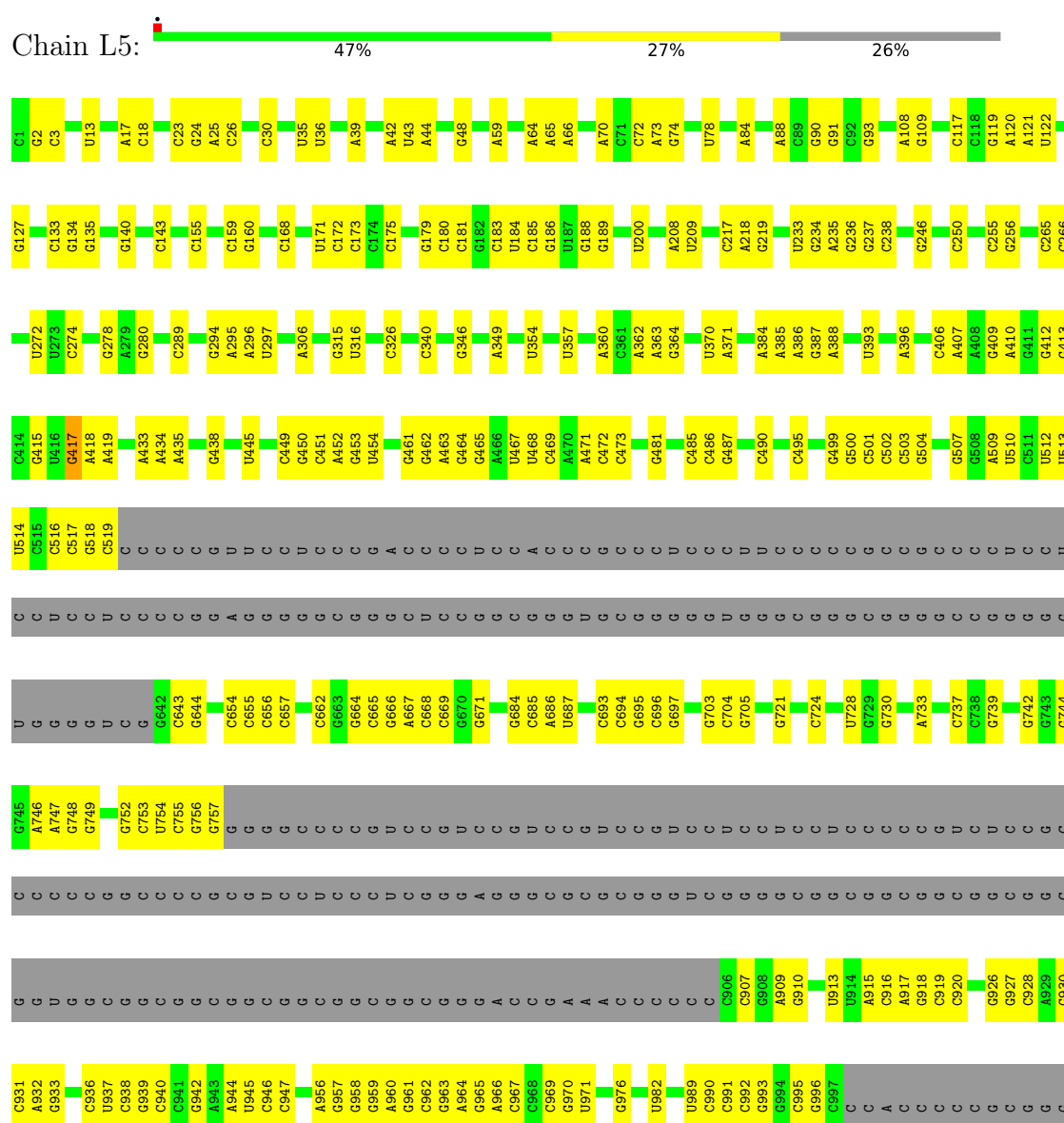
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Mol	Chain	Residues	Atoms		AltConf
84	S2	6	Total 6	O 6	0
84	SV	1	Total 1	O 1	0
84	SX	1	Total 1	O 1	0
84	SN	1	Total 1	O 1	0
84	SW	2	Total 2	O 2	0

3 Residue-property plots [i](#)

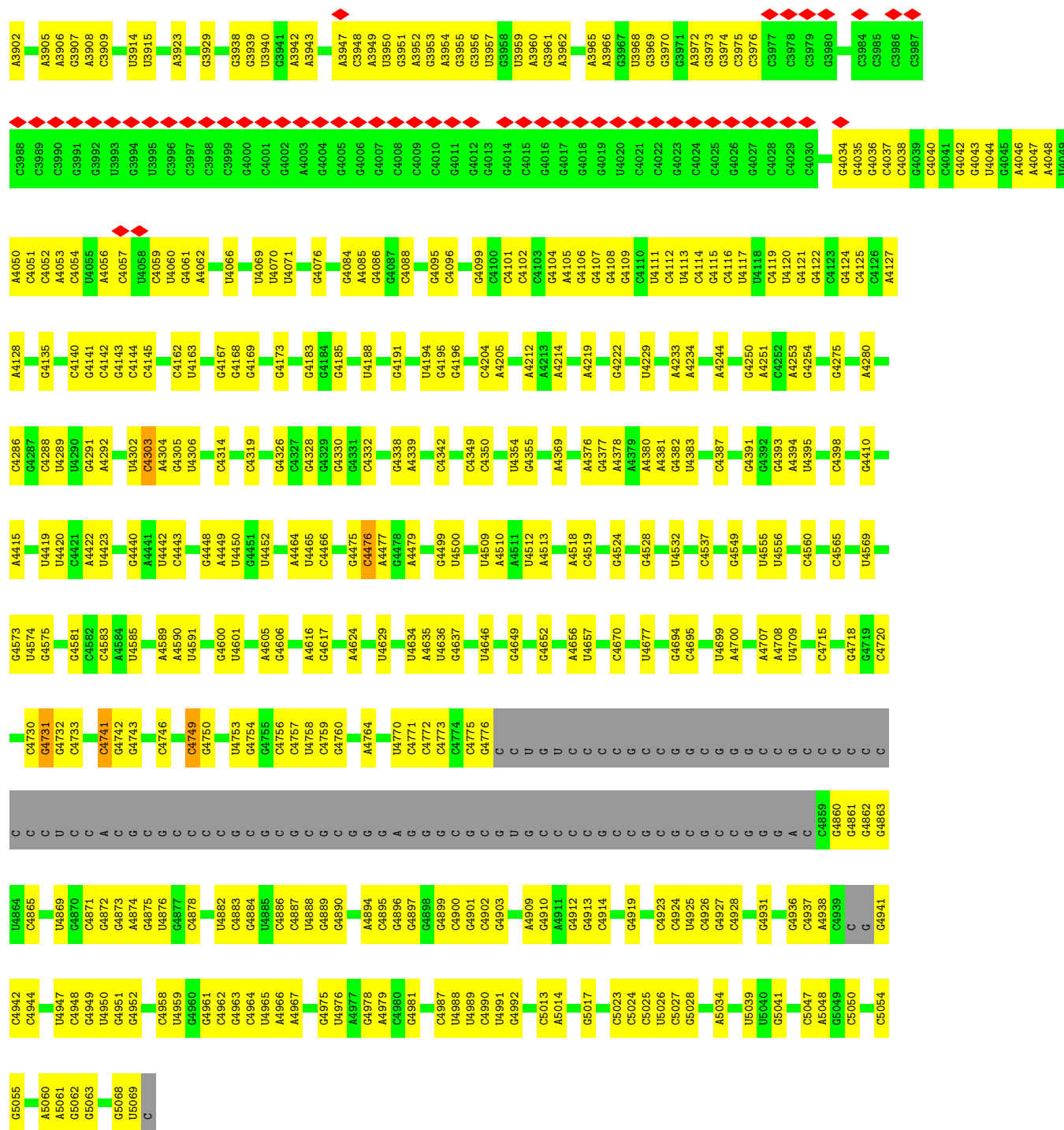
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 28S ribosomal RNA

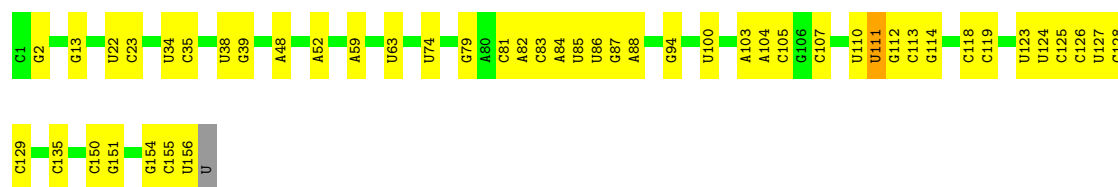








Chain L8:  69% 30% ..



- Molecule 4: 60S ribosomal protein L8

Chain LA:  93% . .



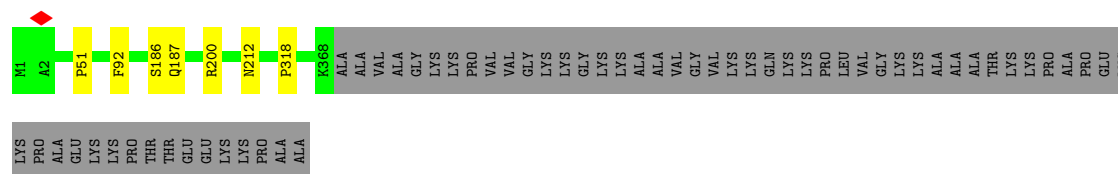
- Molecule 5: 60S ribosomal protein L3

Chain LB:  96% .



- Molecule 6: 60S ribosomal protein L4

Chain LC:  85% 14% .




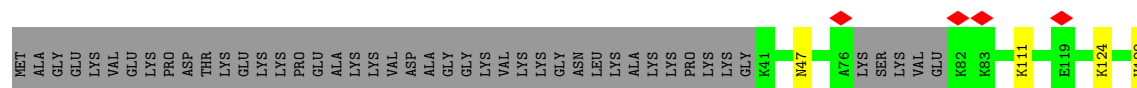
- Molecule 7: 60S ribosomal protein L5

Chain LD:  95% . .



- Molecule 8: 60S ribosomal protein L6

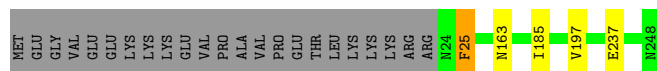
Chain LE:  81% 16% .





- Molecule 9: 60S ribosomal protein L7

Chain LF: 89% 9%



- Molecule 10: 60S ribosomal protein L7a

Chain LG: 86% 5% 9%



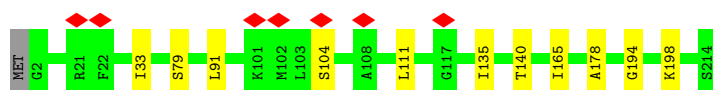
- Molecule 11: 60S ribosomal protein L9

Chain LH: 97% ..



- Molecule 12: 60S ribosomal protein L10-like

Chain LI: 94% 5%



- Molecule 13: 60S ribosomal protein L11

Chain LJ: 96% ..



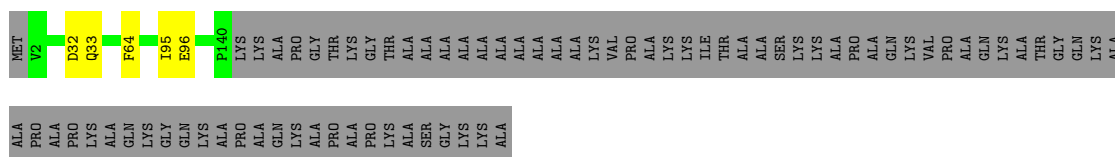
- Molecule 14: 60S ribosomal protein L13

Chain LL: 95% .



- Molecule 15: 60S ribosomal protein L14

Chain LM: 62% 35%



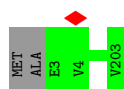
- Molecule 16: 60S ribosomal protein L15

Chain LN: 98%



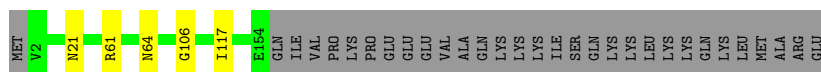
- Molecule 17: 60S ribosomal protein L13a

Chain LO: 99%



- Molecule 18: 60S ribosomal protein L17

Chain LP: 80% 17%



- Molecule 19: 60S ribosomal protein L18

Chain LQ: 97%



- Molecule 20: 60S ribosomal protein L19

Chain LR: 95% 5%



- Molecule 21: 60S ribosomal protein L18a

Chain LS: 99%



- Molecule 22: 60S ribosomal protein L21

Diagram illustrating the protein structure, showing the MET domain (grey) and the T2, H22, V126, R136, and A160 residues (yellow) connected by green lines.

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | ALA | PRO | VAL | LYS | LYS | LEU | VAL | VAL | LYS | GLY | GLY | LYS | LYS | LYS | LYS | Q17 | P28 | K67 | T117 | ASN | GLN | ASP | ASP | GLU | GLU | GLU | GLU | GLU | ASP | GLU | ASP |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- MET SER LYS ARG GLY ARG GLY SER S10 L18 K91 S138 I139 A140

- | Gene | Protein | Length | Start | End | Score | E-value |
|------|---------|--------|-------|-----|-------|---------|
| G1 | G1 | 100 | 1 | 100 | 1.00 | 0.00 |
| G26 | G26 | 100 | 1 | 100 | 1.00 | 0.00 |
| S64 | S64 | 100 | 1 | 100 | 1.00 | 0.00 |
| I67 | I67 | 100 | 1 | 100 | 1.00 | 0.00 |
| R74 | R74 | 100 | 1 | 100 | 1.00 | 0.00 |
| I82 | I82 | 100 | 1 | 100 | 1.00 | 0.00 |
| A88 | A88 | 100 | 1 | 100 | 1.00 | 0.00 |
| D89 | D89 | 100 | 1 | 100 | 1.00 | 0.00 |
| R94 | R94 | 100 | 1 | 100 | 1.00 | 0.00 |
| N95 | N95 | 100 | 1 | 100 | 1.00 | 0.00 |
| O96 | O96 | 100 | 1 | 100 | 1.00 | 0.00 |
| K97 | K97 | 100 | 1 | 100 | 1.00 | 0.00 |
| P98 | P98 | 100 | 1 | 100 | 1.00 | 0.00 |
| E99 | E99 | 100 | 1 | 100 | 1.00 | 0.00 |
| V100 | V100 | 100 | 1 | 100 | 1.00 | 0.00 |
| K124 | K124 | 100 | 1 | 100 | 1.00 | 0.00 |
| THR | THR | 100 | 1 | 100 | 1.00 | 0.00 |
| ALA | ALA | 100 | 1 | 100 | 1.00 | 0.00 |
| MET | MET | 100 | 1 | 100 | 1.00 | 0.00 |
| ALA | ALA | 100 | 1 | 100 | 1.00 | 0.00 |
| ALA | ALA | 100 | 1 | 100 | 1.00 | 0.00 |
| ALA | ALA | 100 | 1 | 100 | 1.00 | 0.00 |
| LYS | LYS | 100 | 1 | 100 | 1.00 | 0.00 |
| PRO | PRO | 100 | 1 | 100 | 1.00 | 0.00 |
| THR | THR | 100 | 1 | 100 | 1.00 | 0.00 |
| LYS | LYS | 100 | 1 | 100 | 1.00 | 0.00 |
| ALA | ALA | 100 | 1 | 100 | 1.00 | 0.00 |
| ALA | ALA | 100 | 1 | 100 | 1.00 | 0.00 |
| PRO | PRO | 100 | 1 | 100 | 1.00 | 0.00 |
| LYS | LYS | 100 | 1 | 100 | 1.00 | 0.00 |
| GLN | GLN | 100 | 1 | 100 | 1.00 | 0.00 |
| ILE | ILE | 100 | 1 | 100 | 1.00 | 0.00 |
| VAL | VAL | 100 | 1 | 100 | 1.00 | 0.00 |
| LYS | LYS | 100 | 1 | 100 | 1.00 | 0.00 |
| PRO | PRO | 100 | 1 | 100 | 1.00 | 0.00 |
| VAL | VAL | 100 | 1 | 100 | 1.00 | 0.00 |
| LYS | LYS | 100 | 1 | 100 | 1.00 | 0.00 |
| VAL | VAL | 100 | 1 | 100 | 1.00 | 0.00 |
| SER | SER | 100 | 1 | 100 | 1.00 | 0.00 |
| ALA | ALA | 100 | 1 | 100 | 1.00 | 0.00 |
| PRO | PRO | 100 | 1 | 100 | 1.00 | 0.00 |
| ARG | ARG | 100 | 1 | 100 | 1.00 | 0.00 |
| VAL | VAL | 100 | 1 | 100 | 1.00 | 0.00 |
| GLY | GLY | 100 | 1 | 100 | 1.00 | 0.00 |
| LYS | LYS | 100 | 1 | 100 | 1.00 | 0.00 |
| ARG | ARG | 100 | 1 | 100 | 1.00 | 0.00 |

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|-----|------|------|
| MET | ALA | PRO | LYS | LYS | LYS | GLU | ALA | PRO | PRO | PRO | ALA | ALA | LYS | LYS | LEU | LYS | LYS | LYS | VAL | LEU | LYS | GLY | VAL | HIS | SER | HIS | LYS | K37 | K38 | K39 | I40 | M69 | D92 | GLI32 | GLI | K134 | T135 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|-----|------|------|

-
- | Residue | Number of Mutations |
|---------|---------------------|
| M1 | 10 |
| V58 | 10 |
| V79 | 10 |
| E83 | 10 |
| K110 | 10 |
| D114 | 10 |
| K134 | 9 |
| TVR | 0 |
| LYS | 0 |
| GLU | 0 |
| GLU | 0 |
| THR | 0 |
| ILE | 0 |
| GLU | 0 |
| GLU | 0 |
| LYS | 0 |
| MET | 0 |
| GLN | 0 |
| GLU | 0 |


- MET G2 M5 F136

- 

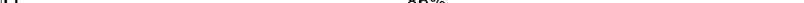
Amino Acid	Relative Abundance (approx.)
MET	1.0
P2	0.8
G20	0.6
R21	0.8
I22	0.8
G23	0.8
K24	0.6
K27	0.6
G30	0.6
D46	0.8
G115	0.8
K119	0.6
K127	0.6
A148	0.6

- Chain Lb: 

GLN	THR	LYS	ALA	GLN	ALA	ALA	PRO	PRO	SER	VAL	PRO	GLN	ALA	PRO	PRO	LYS	ARG	THR	GLN	GLN	ALA	PRO	PRO	THR	LYS	ALA	SER	GLU
MET	A2	K3	I21	V76	LYS	PRO	LYS	GLY	VAL	VAL	LYS	PRO	LYS	ILE	PRO	LYS	GLY	LYS	LEU	ARG	LEU	ALA	ALA	THR	LYS	LYS	ALA	LYS

- Chain Lc: 

MET	VAL	ALA	ALA	LYS	LYS	THR	LYS	K9	R106	SER	MET	PRO	GLU	GLN	THR	GLY	GLU	LYS
-----	-----	-----	-----	-----	-----	-----	-----	----	------	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain Ld:  86% 14%

MET	ALA	PRO	ALA	LYS	LYS	GLY	GLY	GLU	LYS	LYS	LYS	GLY	ARG	SER	ALA	ILE	N18	E124	ASN
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	-----

- Chain Le: 93% • 5%

MET
A2
Q52
A127
R128
L129
ARG
SER
GLU
GLU
ASN
GLU

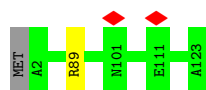
- Chain Lf: 97% ..

- Chain Lg: 96% ..

MET
V2
G51
ARG
L53
R57
K115
ALA
LYS

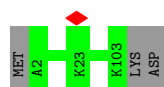
- Molecule 36: 60S ribosomal protein L35

Chain Lh:  98%




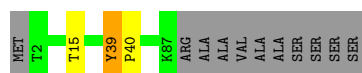
- Molecule 37: 60S ribosomal protein L36

Chain Li:  97%



- Molecule 38: 60S ribosomal protein L37

Chain Lj:  86% 11%



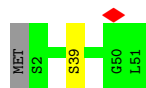
- Molecule 39: 60S ribosomal protein L38

Chain Lk:  94%



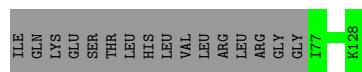
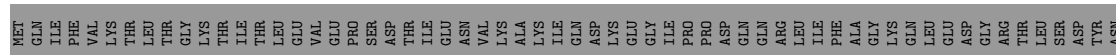
- Molecule 40: 60S ribosomal protein L39

Chain Ll:  96%



- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Lm:  41% 59%



- Molecule 42: 60S ribosomal protein L41

Chain Ln:  60% 32%



- Molecule 43: 60S ribosomal protein L36a

Chain Lo: 97%



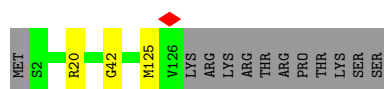
- Molecule 44: 60S ribosomal protein L37a

Chain Lp: 98%



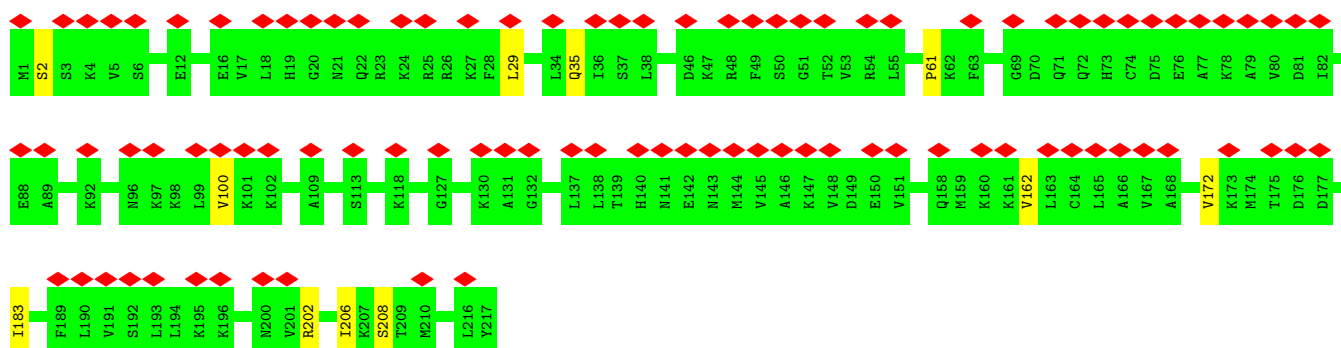
- Molecule 45: 60S ribosomal protein L28

Chain Lr: 89%



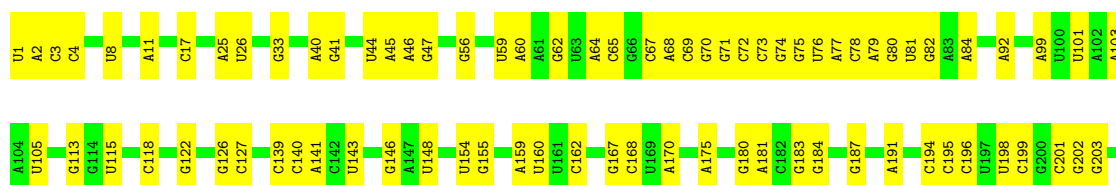
- Molecule 46: 60S ribosomal protein L10a

Chain Lz: 44%

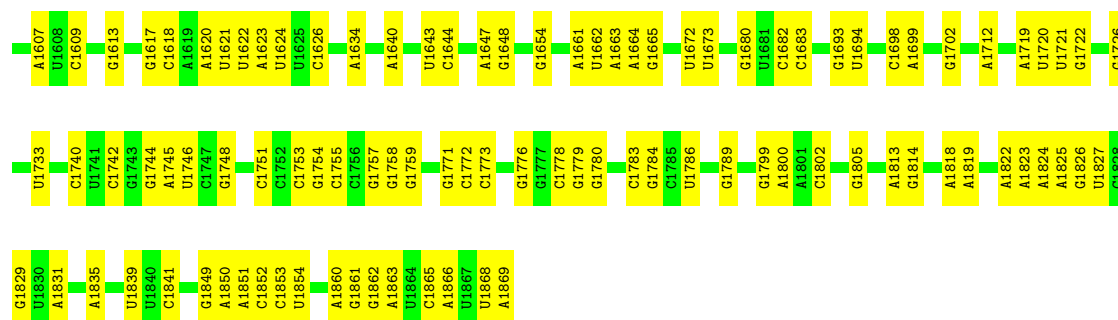


- Molecule 47: 18S ribosomal RNA

Chain S2: 55%

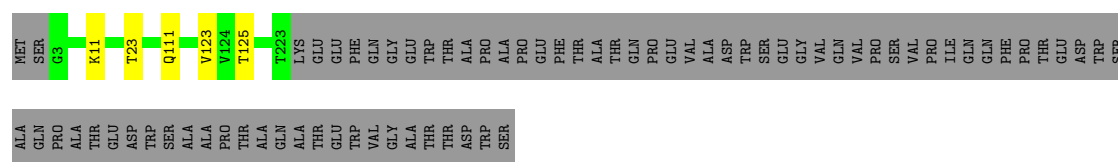


C1525	C1434	A1332	C1261	A1145	G1026	C911	A830	G750	U689	G589	C496	C369	G206
G1526	C1435	A1342	C1264	C1146	A1027	C912	C834	G751	G690	A590	G499	G370	G207
C1527	C1436	U1343	A1265	C1147	A1028	C913	C835	G752	G691	U591	G500	A371	G208
U1530	C1437	A1344	C1266	A1149	C1032	U914	C836	G753	G692	C592	C501	U384	A209
A1533	A1345	C1345	C1267	C1153	U1041	U915	C837	C	C695	C593	C502	G385	G213
				U1154	A1042	U916	C838	C	G696	C594	G386	U214	G215
G1536	C1355	G1354	G1269	U1155	A1043	U917	C839	C	G697	C595	U393	C216	
U1543	A1448	G1356	C1270	U1156	U1044	A920	C840	C	C	C596	C	G	
A1544	C1372	C1373	C1271	U1157	U1045	A921	C842	U	G	C597	C	U	U219
A1545	C1373		C1272	G1158	U1046	A922	C843	C	G	A508	C	C	
G1546	U1374		C1273	G1159	C1057		C844	C	C	A516	C	U	
C1547	U1375		C1274	U1160	A1058	G933	C845	A	C	C517	C	C	G225
U1549	A1454		C1275	U1161	G1059	G934	C846	U	G	G	U	A	
G1550	A1455		C1276	G1166	A1060	G935	C847	C	G	A604	C	U	
U1551	C1373		C1277	U1167	U1061	U943	C848	C	G	G605	C	U	
U1552	A1378		G1280	A1170	A1062	U944	C849	C	C	G606	C	U	
G1553	A1386		C1281	A1181	C1063	U945	C850	C	C				
C1554	C1389		C1282	U1188	C1064	U946	C851	C	C				
U1555	A1396		C1283	U1193	U1073	G958	C852	C	C				
A1556	U1397		C1284	A1194	G1076	A962	C853	C	C				
C1557	G1290		C1285	A1195	A1083	A963	C854	C	C				
	A1474		C1286	U1289	A1084	U954	C855	C	C				
	U1475		C1287	A1199	C1085	G970	C856	C	C				
	A1476		C1288	G1207	U1086	G971	C857	C	C				
	U1477		C1289	A1208	A1087	G972	C858	C	C				
	U1478		C1290	U1209	U1088	G973	C859	C	C				
	A1483		C1291	G1210	G1089	G974	C860	C	C				
	A1484		C1292	C1215	A1093	A983	C861	C	C				
	U1487		C1293	C1216	C1098	A990	C862	C	C				
	C1488		C1294	A1217	G1099	G991	C863	C	C				
	A1489		C1295	C1218	A1100	A992	C864	C	C				
	G1490		C1296	G1221	A1109	G995	C865	C	C				
			C1297	U1229	G1110	A996	C866	C	C				
			C1298	U1300	U1111	A997	C867	C	C				
			C1299	A1301	U1112	A998	C868	C	C				
			C1300	G1302	A1113	G999	C869	C	C				
			C1301	C1411	U1114	C1000	C870	C	C				
			C1302	C1412	U1115	A1001	C871	C	C				
			C1303	G1413	U1116	U1002	C872	C	C				
			C1304	C1414	C1117	C1006	C873	C	C				
			C1305	C1415	A1119	C1007	C874	C	C				
			C1306	C1416	U1120	A1008	C875	C	C				
			C1307	C1417	G1121	U1016	C876	C	C				
			C1308	C1418	G1122	U1017	C877	C	C				
			C1309	C1419	G1123	U1018	C878	C	C				
			C1310	G1420	G1124	U1019	C879	C	C				
			C1311	A1421	U1125	A1020	C880	C	C				
			C1312	G1422	C1118	U1021	C881	C	C				
			C1313	C1423	A1119	U1022	C882	C	C				
			C1314	C1424	U1126	A1023	C883	C	C				
			C1315	G1425	G1127	A1133	C884	C	C				
			C1316	U1426	G1128	G1256	C885	C	C				
			C1317	C1427	G1129	G1257	C886	C	C				
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			C1327	C1437	G1139	G1267	C896	C	C				
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			C1331	C1441	G1143	G1271	C900	C	C				
			C1332	G1442	G1144	G1272	C901	C	C				
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			C1334	C1444	G1146	G1274	C903	C	C				
			C1335	G1445	G1147	G1275	C904	C	C				
			C1336	U1446	G1148	G1276	C905	C	C				
			C1337	C1447	G1149	G1277	C906	C	C				
			C1338	G1448	G1150	G1278	C907	C	C				
			C1339	U1449	G1151	G1279	C908	C	C				
			C1340	C1449	G1152	G1280	C909	C	C				
			C1341	G1450	G1153	G1281	C910	C	C				
			C1342	C1451	G1154	G1282	C911	C	C				
			C1343	U1452	G1155	G1283	C912	C	C				
			C1344	G1453	G1156	G1284	C913	C	C				
			C1345	C1454	G1157	G1285	C914	C	C				
			C1346	U1455	G1158	G1286	C915	C	C				
			C1347	C1456	G1159	G1287	C916	C	C				
			C1348	G1457	G1160	G1288	C917	C	C				
			C1349	U1458	G1161	G1289	C918	C	C				
			C1350	C1459	G1162	G1290	C919	C	C				
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			C1353	C1462	G1165	G1293	C922	C	C				
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			C1357	U1466	G1169	G1297	C926	C	C				
			C1358	C1467	G1170	G1298	C927	C	C				
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			C1360	C1469	G1172	G1300	C929	C	C				
			C1361	G1470	G1173	G1301	C930	C	C				
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			C1366	U1475	G1178	G1306	C935	C	C				
			C1367	C1476	G1179	G1307	C936	C	C				
			C1368	U1477	G1180	G1308	C937	C	C				
			C1369	C1478	G1181	G1309	C938	C	C				
			C1370	U1479	G1182	G1310	C939	C	C				
			C1371	C1479	G1183	G1311	C940	C	C				
			C1372	U1480	G1184	G1312	C941	C	C				
			C1373	C1480	G1185	G1313	C942	C	C				
			C1374	U1481	G1186	G1314	C943	C	C				
			C1375	C1481	G1187	G1315	C944	C	C				
			C1376	U1482	G1188	G1316	C945	C	C				
			C1377	C1482	G1189	G1317	C946	C	C				
			C1378	U1483	G1190	G1318	C947	C	C				
			C1379	C1483	G1191	G1319	C948	C	C				
			C1380	U1484	G1192	G1320	C949	C	C				
			C1381	C1484	G1193	G1321	C950	C	C				
			C1382	U1485	G1194	G1322	C951	C	C				
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			C1384	U1486	G1196	G1324	C953	C	C				
			C1385	C1486	G1197	G1325	C954	C	C				
			C1386	U1487	G1198	G1326	C955	C	C				
			C1387	C1487	G1199	G1327	C956	C	C				
			C1388	U1488	G1200	G1328	C957	C	C				
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			C1396	C1491	G1208	G1336	C965	C	C				
			C1397	U1493	G1209	G1337	C966	C	C				
			C1398	C1492	G1210	G1338	C967	C	C				
			C1399	U1494</									



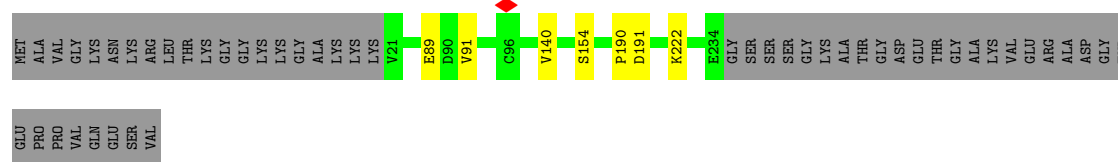
• Molecule 48: 40S ribosomal protein SA

Chain SA: 73% 25%



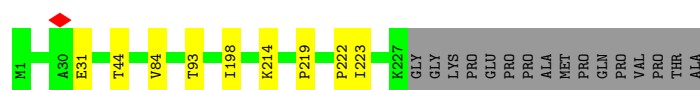
• Molecule 49: 40S ribosomal protein S3a

Chain SB: 78% 19%



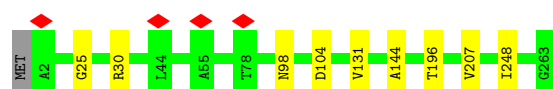
• Molecule 50: 40S ribosomal protein S3

Chain SD: 90% 7%



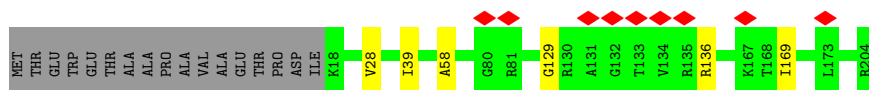
• Molecule 51: 40S ribosomal protein S4, X isoform

Chain SE: 96%

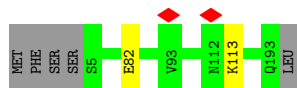


• Molecule 52: 40S ribosomal protein S5

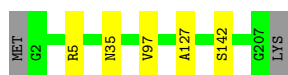
Chain SF: 89% 8%



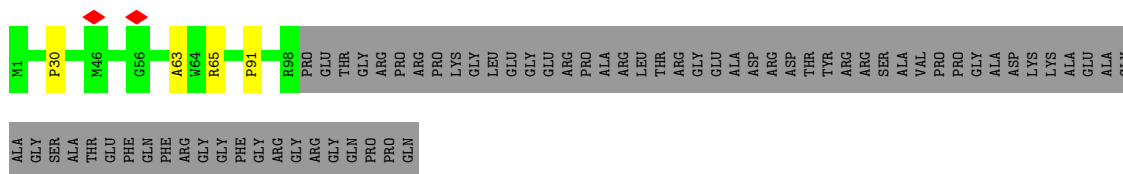
- Molecule 53: 40S ribosomal protein S7



- Molecule 54: 40S ribosomal protein S8



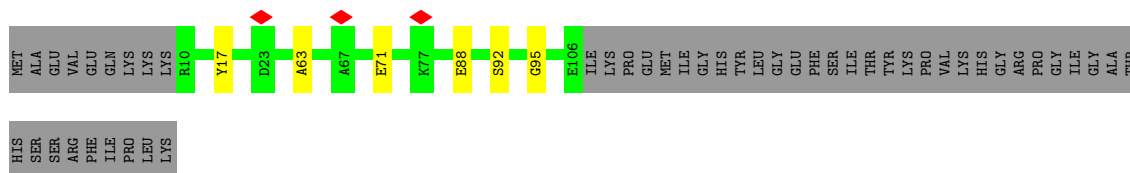
- Molecule 55: 40S ribosomal protein S10



- Molecule 56: 40S ribosomal protein S11



- Molecule 57: 40S ribosomal protein S15

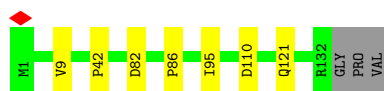


- Molecule 58: 40S ribosomal protein S16

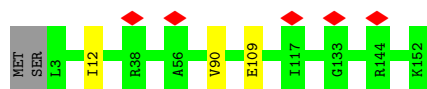




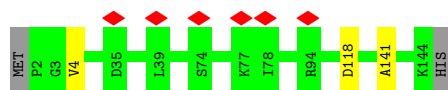
- Molecule 59: 40S ribosomal protein S17



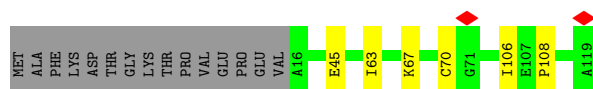
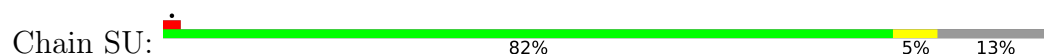
- Molecule 60: 40S ribosomal protein S18



- Molecule 61: 40S ribosomal protein S19



- Molecule 62: 40S ribosomal protein S20



- Molecule 63: 40S ribosomal protein S21



- Molecule 64: 40S ribosomal protein S23



- Molecule 65: 40S ribosomal protein S26

MET
T2
I41
E46 A47
V84
R89
R100
F101
R102
P103
A104
P108
ARG
PRO
PRO
PRO
LYS
PRO
MET

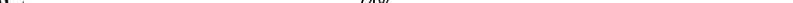
- Chain Sc:  88% 7%

Sequence logo for the R5 motif. The y-axis represents information content in bits, ranging from 0 to 1.5. The x-axis shows amino acid positions: MET, ASP, THR, SER, R5, S39, L56, E64, L68, and ARG. The R5 position has the highest information content, with a peak of approximately 1.4 bits. The L68 position also shows a significant peak, around 1.1 bits. Other positions have lower information content, generally below 0.5 bits.

- Chain Sd:  95% 5%

MET
GLY
HIS
Q4
D56

- Chain Sg:  94%

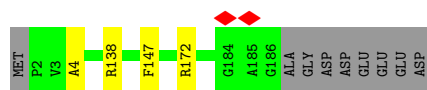
- Chain SC:  74% 24%

S77	P111	G189	G228	E279	V280	SER VAL GLN ARG THR GLN ALA PRO MET VAL ALA THR THR	MET ASP ASP ALA GLY ALA ALA GLY GLY PRO GLY GLY GLY GLY PRO GLY MET ASN ARG GLY PHE ARG GLY PHE GLY SER ILE ARG GLY ARG ARG GLY ARG ARG GLY ARG GLY ARG GLY LYS ALA GLU ASP LYS
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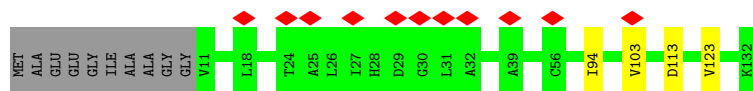
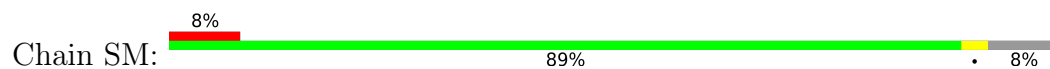
- Chain SG: 92% 5%

M1	C12	R25	E29	R87	I121	D126	L147	D152	K172	Q177	R178	L179	L234	L237	ARG	ALA	SER	THR	SER	SER	LYS	SER	GLU	SER	SER	SER	GLN	LYS
----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain SJ: 93% 5%



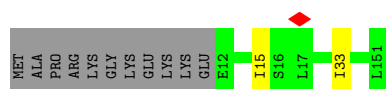
- Molecule 72: 40S ribosomal protein S12



- Molecule 73: 40S ribosomal protein S13



- Molecule 74: 40S ribosomal protein S14



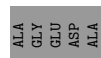
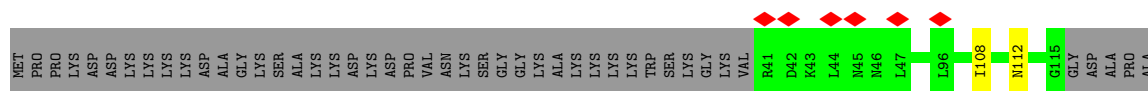
- Molecule 75: 40S ribosomal protein S15a



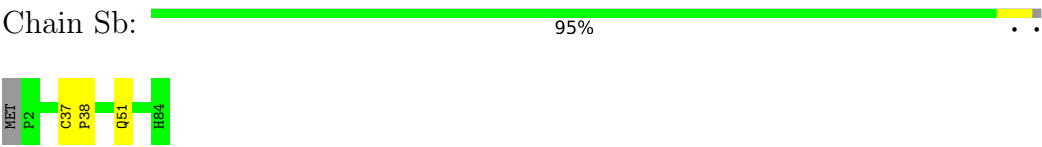
- Molecule 76: 40S ribosomal protein S24



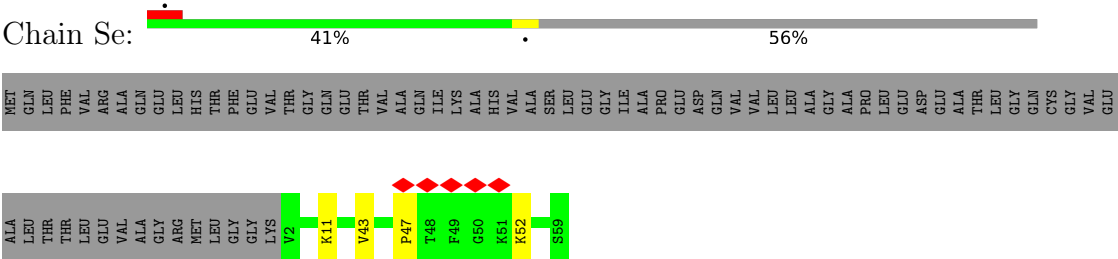
- Molecule 77: 40S ribosomal protein S25



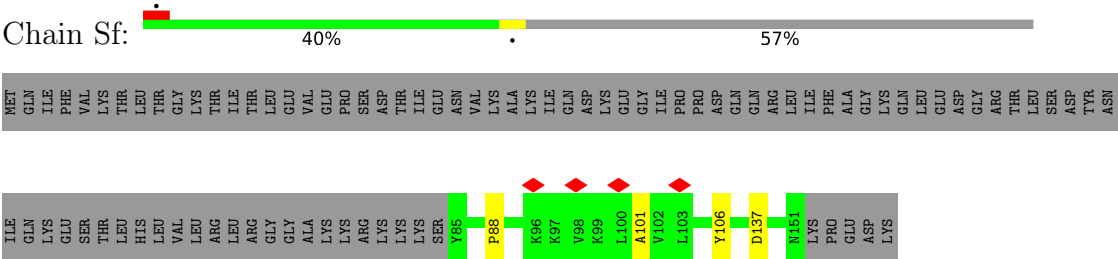
● Molecule 78: 40S ribosomal protein S27



● Molecule 79: Ribosomal protein S30



● Molecule 80: Ubiquitin-40S ribosomal protein S27a



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	79000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.206	Depositor
Minimum map value	-0.165	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.007	Depositor
Map size (Å)	506.0, 506.0, 506.0	wwPDB
Map dimensions	460, 460, 460	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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, 3HE, 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	0.71	0/89644	0.88	16/139760 (0.0%)
2	L7	0.61	0/2858	0.79	0/4455
3	L8	0.70	0/3701	0.85	2/5766 (0.0%)
4	LA	0.53	0/1936	0.58	0/2596
5	LB	0.46	0/3306	0.58	0/4424
6	LC	0.45	0/2981	0.56	0/4002
7	LD	0.39	0/2428	0.53	0/3252
8	LE	0.37	0/2005	0.57	0/2685
9	LF	0.47	0/1905	0.57	0/2539
10	LG	0.40	0/1960	0.57	0/2637
11	LH	0.40	0/1537	0.56	0/2066
12	LI	0.39	0/1751	0.51	0/2340
13	LJ	0.35	0/1433	0.57	0/1915
14	LL	0.42	0/1732	0.58	0/2315
15	LM	0.41	0/1161	0.53	0/1554
16	LN	0.51	0/1746	0.58	0/2338
17	LO	0.48	0/1682	0.57	0/2250
18	LP	0.52	0/1268	0.60	0/1701
19	LQ	0.46	0/1537	0.58	0/2052
20	LR	0.42	0/1582	0.56	0/2091
21	LS	0.47	0/1493	0.53	0/2003
22	LT	0.43	0/1326	0.59	0/1770
23	LU	0.36	0/839	0.54	0/1126
24	LV	0.49	0/993	0.59	0/1332
25	LW	0.38	0/1030	0.56	0/1364
26	LX	0.43	0/992	0.54	0/1330
27	LY	0.43	0/1132	0.55	0/1504
28	LZ	0.41	0/1130	0.53	0/1507
29	La	0.48	0/1191	0.59	0/1591
30	Lb	0.37	0/620	0.51	0/819
31	Lc	0.43	0/774	0.55	0/1038
32	Ld	0.46	0/903	0.56	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.50	0/1071	0.57	0/1429
34	Lf	0.48	0/895	0.59	0/1198
35	Lg	0.47	0/904	0.56	0/1203
36	Lh	0.40	0/1023	0.55	0/1351
37	Li	0.39	0/843	0.55	0/1115
38	Lj	0.50	0/720	0.67	1/952 (0.1%)
39	Lk	0.38	0/575	0.55	0/761
40	Ll	0.43	0/454	0.58	0/599
41	Lm	0.41	0/435	0.56	0/575
42	Ln	0.35	0/231	0.49	0/294
43	Lo	0.43	0/876	0.59	0/1156
44	Lp	0.52	0/718	0.57	0/953
45	Lr	0.44	0/1017	0.55	0/1364
46	Lz	0.24	0/1769	0.47	0/2371
47	S2	0.57	0/41243	0.84	9/64257 (0.0%)
48	SA	0.37	0/1778	0.54	0/2416
49	SB	0.39	0/1765	0.54	0/2362
50	SD	0.33	0/1793	0.55	0/2414
51	SE	0.36	0/2118	0.55	0/2849
52	SF	0.31	0/1500	0.53	0/2015
53	SH	0.34	0/1544	0.56	0/2068
54	SI	0.40	0/1715	0.57	0/2287
55	SK	0.30	0/851	0.53	0/1147
56	SL	0.44	0/1268	0.59	0/1696
57	SP	0.29	0/815	0.52	0/1087
58	SQ	0.31	0/1177	0.54	0/1575
59	SR	0.33	0/1086	0.55	0/1457
60	SS	0.31	0/1253	0.60	0/1676
61	ST	0.29	0/1131	0.51	0/1515
62	SU	0.30	0/831	0.55	0/1115
63	SV	0.37	0/643	0.53	0/860
64	SX	0.43	0/1116	0.52	0/1490
65	Sa	0.43	0/863	0.57	0/1159
66	Sc	0.31	0/508	0.58	0/680
67	Sd	0.37	0/455	0.49	0/603
68	Sg	0.27	0/2493	0.54	0/3394
69	SC	0.38	0/1762	0.55	0/2381
70	SG	0.32	0/1946	0.55	0/2590
71	SJ	0.37	0/1550	0.55	0/2069
72	SM	0.27	0/962	0.52	0/1290
73	SN	0.41	0/1232	0.55	0/1656
74	SO	0.40	0/1062	0.55	0/1425
75	SW	0.43	0/1051	0.58	0/1406

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	SY	0.33	0/1083	0.52	0/1438
77	SZ	0.31	0/604	0.58	0/810
78	Sb	0.35	0/665	0.51	0/891
79	Se	0.31	0/465	0.52	0/612
80	Sf	0.29	0/560	0.52	0/745
All	All	0.57	0/232995	0.76	28/342094 (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	1
5	LB	0	3
15	LM	0	1
38	Lj	0	1
42	Ln	0	1
58	SQ	0	1
All	All	0	8

There are no bond length outliers.

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L5	4303	C	C2-N1-C1'	7.80	127.38	118.80
38	Lj	39	TYR	C-N-CD	-7.33	104.48	120.60
47	S2	1453	C	C2-N1-C1'	6.99	126.49	118.80
1	L5	4741	C	N1-C2-O2	6.28	122.67	118.90
47	S2	356	C	N1-C2-O2	6.11	122.56	118.90

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	LA	227	ARG	Sidechain
5	LB	257	TRP	Peptide
5	LB	258	HIS	Peptide
5	LB	35	ASP	Peptide
15	LM	64	PHE	Peptide

5.2 Too-close contacts ⓘ

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

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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%)	212 (86%)	27 (11%)	7 (3%)	4	27
5	LB	400/403 (99%)	342 (86%)	44 (11%)	14 (4%)	3	24
6	LC	366/427 (86%)	333 (91%)	26 (7%)	7 (2%)	6	35
7	LD	291/297 (98%)	250 (86%)	30 (10%)	11 (4%)	2	22
8	LE	239/288 (83%)	198 (83%)	31 (13%)	10 (4%)	2	20
9	LF	223/248 (90%)	202 (91%)	16 (7%)	5 (2%)	5	32
10	LG	239/266 (90%)	210 (88%)	17 (7%)	12 (5%)	1	17
11	LH	188/192 (98%)	153 (81%)	31 (16%)	4 (2%)	5	33
12	LI	211/214 (99%)	174 (82%)	26 (12%)	11 (5%)	1	16
13	LJ	174/178 (98%)	157 (90%)	12 (7%)	5 (3%)	3	27
14	LL	208/211 (99%)	184 (88%)	15 (7%)	9 (4%)	2	19
15	LM	137/215 (64%)	122 (89%)	11 (8%)	4 (3%)	3	27
16	LN	201/204 (98%)	179 (89%)	19 (10%)	3 (2%)	8	39
17	LO	199/203 (98%)	183 (92%)	16 (8%)	0	100	100
18	LP	151/184 (82%)	132 (87%)	14 (9%)	5 (3%)	3	25
19	LQ	185/188 (98%)	168 (91%)	13 (7%)	4 (2%)	5	32
20	LR	185/196 (94%)	171 (92%)	13 (7%)	1 (0%)	25	59
21	LS	173/176 (98%)	148 (86%)	24 (14%)	1 (1%)	22	55
22	LT	157/160 (98%)	136 (87%)	18 (12%)	3 (2%)	6	35
23	LU	99/128 (77%)	81 (82%)	16 (16%)	2 (2%)	6	34
24	LV	129/140 (92%)	109 (84%)	17 (13%)	3 (2%)	5	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	LW	122/157 (78%)	104 (85%)	14 (12%)	4 (3%)	3	25
26	LX	115/156 (74%)	99 (86%)	12 (10%)	4 (4%)	3	24
27	LY	132/145 (91%)	119 (90%)	9 (7%)	4 (3%)	3	26
28	LZ	133/136 (98%)	118 (89%)	14 (10%)	1 (1%)	16	51
29	La	145/148 (98%)	119 (82%)	19 (13%)	7 (5%)	2	17
30	Lb	73/157 (46%)	66 (90%)	6 (8%)	1 (1%)	9	40
31	Lc	96/115 (84%)	87 (91%)	9 (9%)	0	100	100
32	Ld	105/125 (84%)	89 (85%)	16 (15%)	0	100	100
33	Le	126/135 (93%)	114 (90%)	10 (8%)	2 (2%)	8	38
34	Lf	107/110 (97%)	93 (87%)	12 (11%)	2 (2%)	6	35
35	Lg	109/117 (93%)	101 (93%)	7 (6%)	1 (1%)	14	48
36	Lh	120/123 (98%)	115 (96%)	4 (3%)	1 (1%)	16	51
37	Li	100/105 (95%)	94 (94%)	6 (6%)	0	100	100
38	Lj	84/97 (87%)	74 (88%)	8 (10%)	2 (2%)	5	30
39	Lk	67/70 (96%)	57 (85%)	7 (10%)	3 (4%)	2	18
40	Ll	48/51 (94%)	41 (85%)	6 (12%)	1 (2%)	5	33
41	Lm	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
42	Ln	22/25 (88%)	20 (91%)	1 (4%)	1 (4%)	2	18
43	Lo	103/106 (97%)	90 (87%)	11 (11%)	2 (2%)	6	35
44	Lp	89/92 (97%)	77 (86%)	11 (12%)	1 (1%)	12	45
45	Lr	123/137 (90%)	108 (88%)	12 (10%)	3 (2%)	5	30
46	Lz	215/217 (99%)	174 (81%)	30 (14%)	11 (5%)	1	16
48	SA	219/295 (74%)	200 (91%)	14 (6%)	5 (2%)	5	31
49	SB	212/264 (80%)	177 (84%)	28 (13%)	7 (3%)	3	25
50	SD	225/243 (93%)	190 (84%)	26 (12%)	9 (4%)	2	21
51	SE	260/263 (99%)	221 (85%)	30 (12%)	9 (4%)	3	24
52	SF	185/204 (91%)	158 (85%)	21 (11%)	6 (3%)	3	25
53	SH	187/194 (96%)	154 (82%)	31 (17%)	2 (1%)	12	45
54	SI	204/208 (98%)	173 (85%)	26 (13%)	5 (2%)	4	29
55	SK	96/165 (58%)	80 (83%)	12 (12%)	4 (4%)	2	20
56	SL	151/158 (96%)	127 (84%)	20 (13%)	4 (3%)	4	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	SP	95/145 (66%)	77 (81%)	12 (13%)	6 (6%)	1	13
58	SQ	144/146 (99%)	125 (87%)	10 (7%)	9 (6%)	1	13
59	SR	130/135 (96%)	109 (84%)	14 (11%)	7 (5%)	1	15
60	SS	148/152 (97%)	126 (85%)	19 (13%)	3 (2%)	6	34
61	ST	141/145 (97%)	124 (88%)	14 (10%)	3 (2%)	5	33
62	SU	102/119 (86%)	87 (85%)	9 (9%)	6 (6%)	1	14
63	SV	81/83 (98%)	64 (79%)	15 (18%)	2 (2%)	4	29
64	SX	139/143 (97%)	120 (86%)	12 (9%)	7 (5%)	1	17
65	Sa	105/115 (91%)	87 (83%)	11 (10%)	7 (7%)	1	12
66	Sc	62/69 (90%)	52 (84%)	7 (11%)	3 (5%)	2	17
67	Sd	51/56 (91%)	46 (90%)	5 (10%)	0	100	100
68	Sg	311/317 (98%)	253 (81%)	44 (14%)	14 (4%)	2	18
69	SC	220/293 (75%)	194 (88%)	22 (10%)	4 (2%)	7	35
70	SG	235/249 (94%)	196 (83%)	31 (13%)	8 (3%)	3	25
71	SJ	183/194 (94%)	161 (88%)	18 (10%)	4 (2%)	5	32
72	SM	120/132 (91%)	93 (78%)	23 (19%)	4 (3%)	3	25
73	SN	148/151 (98%)	133 (90%)	10 (7%)	5 (3%)	3	25
74	SO	138/151 (91%)	116 (84%)	20 (14%)	2 (1%)	9	40
75	SW	127/130 (98%)	106 (84%)	19 (15%)	2 (2%)	8	38
76	SY	129/133 (97%)	113 (88%)	10 (8%)	6 (5%)	2	18
77	SZ	73/125 (58%)	55 (75%)	16 (22%)	2 (3%)	4	28
78	Sb	81/84 (96%)	65 (80%)	13 (16%)	3 (4%)	2	22
79	Se	56/133 (42%)	47 (84%)	5 (9%)	4 (7%)	1	11
80	Sf	65/156 (42%)	51 (78%)	10 (15%)	4 (6%)	1	13
All	All	11508/12977 (89%)	9930 (86%)	1240 (11%)	338 (3%)	6	27

5 of 338 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	LA	118	GLU
4	LA	130	SER
4	LA	239	ALA
5	LB	334	LYS
6	LC	200	ARG

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%)	190 (100%)	0	100	100
5	LB	348/349 (100%)	348 (100%)	0	100	100
6	LC	306/348 (88%)	306 (100%)	0	100	100
7	LD	246/250 (98%)	246 (100%)	0	100	100
8	LE	216/252 (86%)	216 (100%)	0	100	100
9	LF	194/215 (90%)	193 (100%)	1 (0%)	86	93
10	LG	203/223 (91%)	203 (100%)	0	100	100
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	180/181 (99%)	180 (100%)	0	100	100
13	LJ	148/149 (99%)	148 (100%)	0	100	100
14	LL	176/177 (99%)	176 (100%)	0	100	100
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%)	164 (100%)	0	100	100
20	LR	166/175 (95%)	166 (100%)	0	100	100
21	LS	156/157 (99%)	156 (100%)	0	100	100
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%)	101 (100%)	0	100	100
25	LW	103/126 (82%)	103 (100%)	0	100	100
26	LX	107/133 (80%)	107 (100%)	0	100	100
27	LY	124/135 (92%)	124 (100%)	0	100	100
28	LZ	117/118 (99%)	117 (100%)	0	100	100
29	La	120/121 (99%)	119 (99%)	1 (1%)	79	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	Lb	63/125 (50%)	63 (100%)	0	100	100
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%)	88 (100%)	0	100	100
35	Lg	97/100 (97%)	97 (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
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%)	15 (65%)	8 (35%)	0	1
43	Lo	93/94 (99%)	93 (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%)	195 (100%)	0	100	100
48	SA	183/243 (75%)	183 (100%)	0	100	100
49	SB	195/231 (84%)	195 (100%)	0	100	100
50	SD	190/202 (94%)	190 (100%)	0	100	100
51	SE	224/225 (100%)	224 (100%)	0	100	100
52	SF	157/170 (92%)	157 (100%)	0	100	100
53	SH	169/174 (97%)	169 (100%)	0	100	100
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	87/130 (67%)	87 (100%)	0	100	100
58	SQ	121/121 (100%)	121 (100%)	0	100	100
59	SR	120/122 (98%)	120 (100%)	0	100	100
60	SS	130/132 (98%)	130 (100%)	0	100	100
61	ST	113/115 (98%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	113 (100%)	0	100	100
65	Sa	90/98 (92%)	90 (100%)	0	100	100
66	Sc	57/62 (92%)	57 (100%)	0	100	100
67	Sd	47/49 (96%)	47 (100%)	0	100	100
68	Sg	272/275 (99%)	272 (100%)	0	100	100
69	SC	188/225 (84%)	188 (100%)	0	100	100
70	SG	207/218 (95%)	207 (100%)	0	100	100
71	SJ	161/168 (96%)	161 (100%)	0	100	100
72	SM	104/108 (96%)	104 (100%)	0	100	100
73	SN	130/131 (99%)	130 (100%)	0	100	100
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	47/104 (45%)	47 (100%)	0	100	100
80	Sf	60/140 (43%)	60 (100%)	0	100	100
All	All	10030/11052 (91%)	10020 (100%)	10 (0%)	92	97

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	Ln	19	LYS
42	Ln	20	MET
42	Ln	21	ARG
42	Ln	10	MET
42	Ln	11	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 124 such sidechains are listed below:

Mol	Chain	Res	Type
34	Lf	21	GLN

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Mol	Chain	Res	Type
70	SG	65	GLN
48	SA	84	GLN
70	SG	13	GLN
76	SY	22	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3707/5070 (73%)	1340 (36%)	102 (2%)
2	L7	119/121 (98%)	33 (27%)	1 (0%)
3	L8	155/157 (98%)	47 (30%)	4 (2%)
47	S2	1717/1869 (91%)	699 (40%)	41 (2%)
All	All	5698/7217 (78%)	2119 (37%)	148 (2%)

5 of 2119 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	3	C
1	L5	13	U
1	L5	17	A
1	L5	18	C

5 of 148 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
47	S2	589	G
47	S2	1664	A
47	S2	659	G
47	S2	1273	C
1	L5	2262	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 233 ligands modelled in this entry, 232 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
81	3HE	L5	5101	-	21,21,21	3.56	8 (38%)	19,30,30	2.32	8 (42%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
81	3HE	L5	5101	-	-	1/8/36/36	0/2/2/2

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	L5	5101	3HE	C13-C12	-8.46	1.35	1.50
81	L5	5101	3HE	C10-C11	-7.03	1.37	1.50
81	L5	5101	3HE	C5-C4	-6.68	1.42	1.51
81	L5	5101	3HE	C3-C4	-6.27	1.40	1.51
81	L5	5101	3HE	C13-C9	-4.14	1.46	1.53

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	L5	5101	3HE	C11-N-C12	-5.06	119.64	125.78
81	L5	5101	3HE	C-C1-C2	-3.78	104.75	111.18
81	L5	5101	3HE	C13-C12-N	3.73	120.52	115.95
81	L5	5101	3HE	C5-C6-C1	-3.60	105.80	113.14
81	L5	5101	3HE	C10-C11-N	3.08	119.72	115.95

There are no chirality outliers.

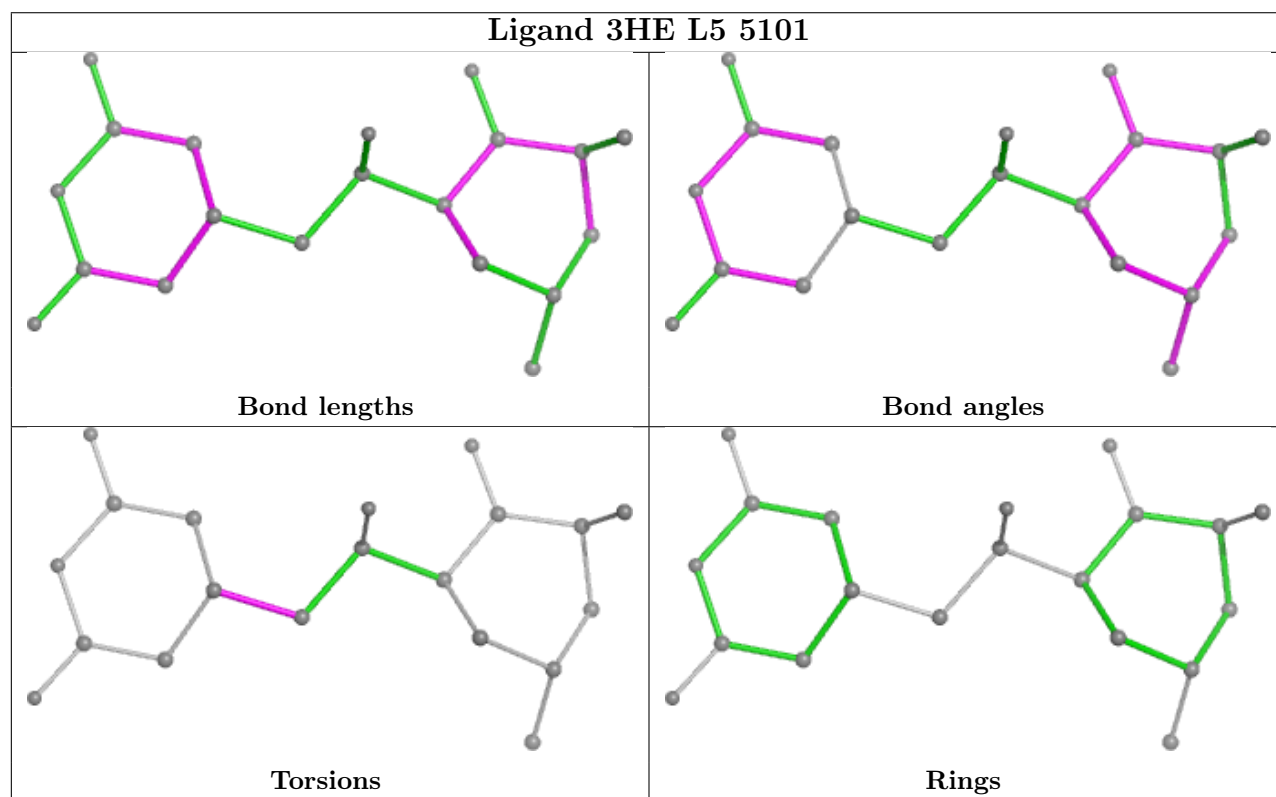
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
81	L5	5101	3HE	C7-C8-C9-C13

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	L5	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L5	3983:G	O3'	3984:C	P	10.43

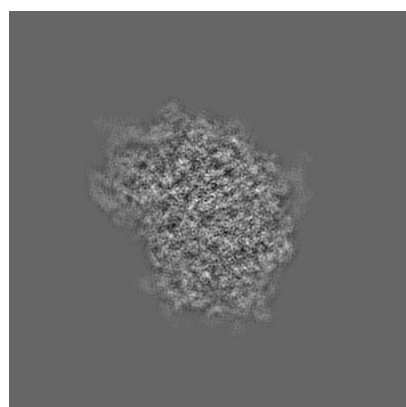
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4070. These allow visual inspection of the internal detail of the map and identification of artifacts.

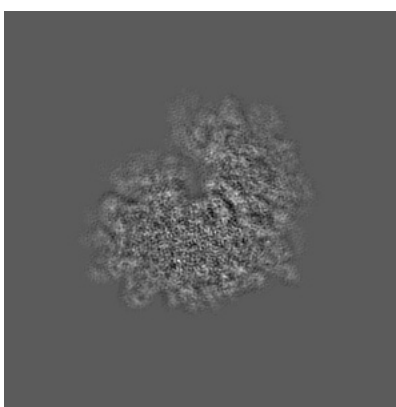
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

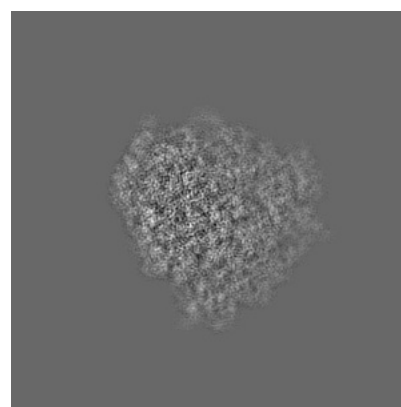
6.1.1 Primary map



X



Y

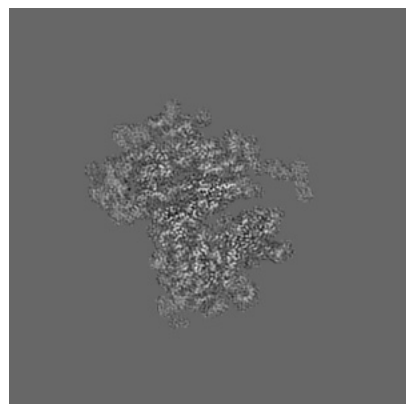


Z

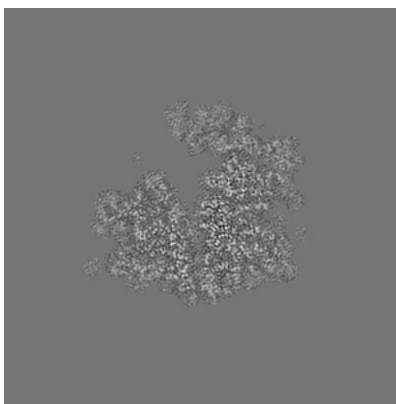
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

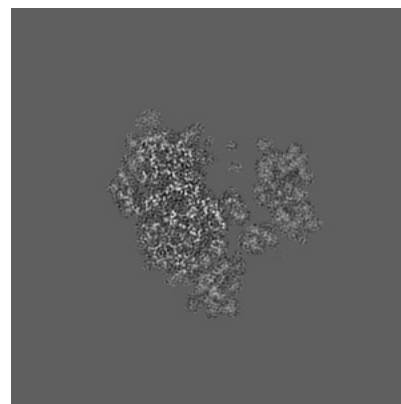
6.2.1 Primary map



X Index: 230



Y Index: 230

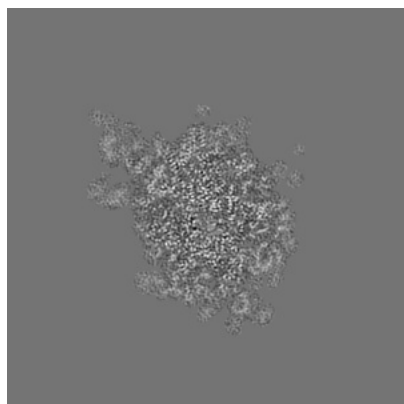


Z Index: 230

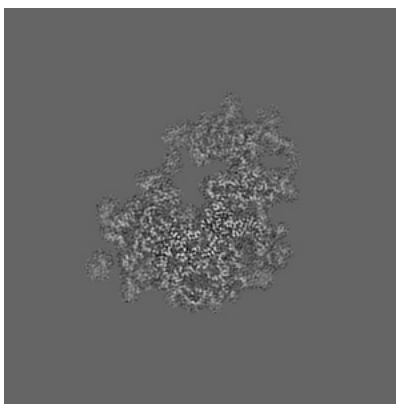
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

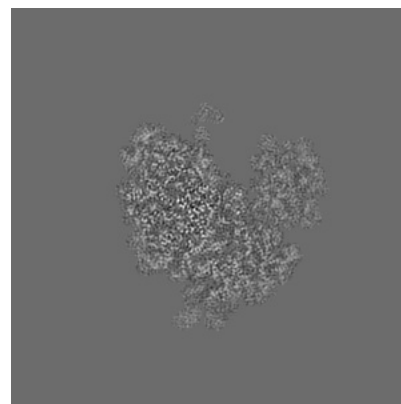
6.3.1 Primary map



X Index: 205



Y Index: 242

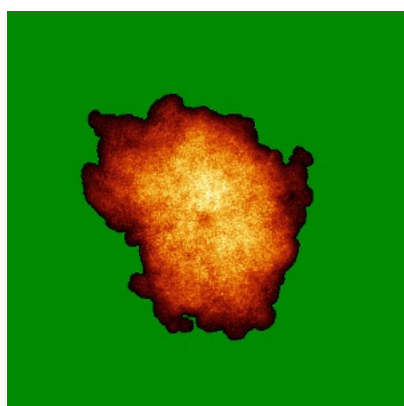


Z Index: 252

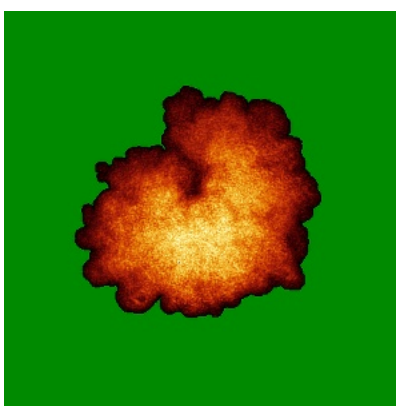
The images above show the largest variance slices of the map in three orthogonal directions.

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

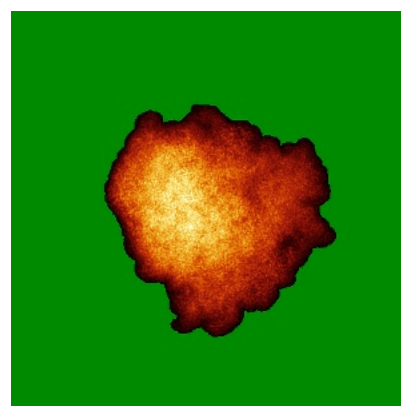
6.4.1 Primary map



X



Y

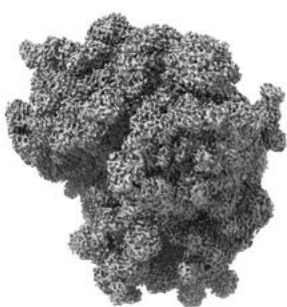


Z

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](#)

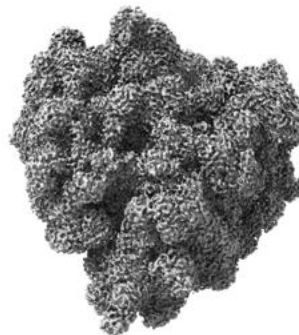
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.007. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

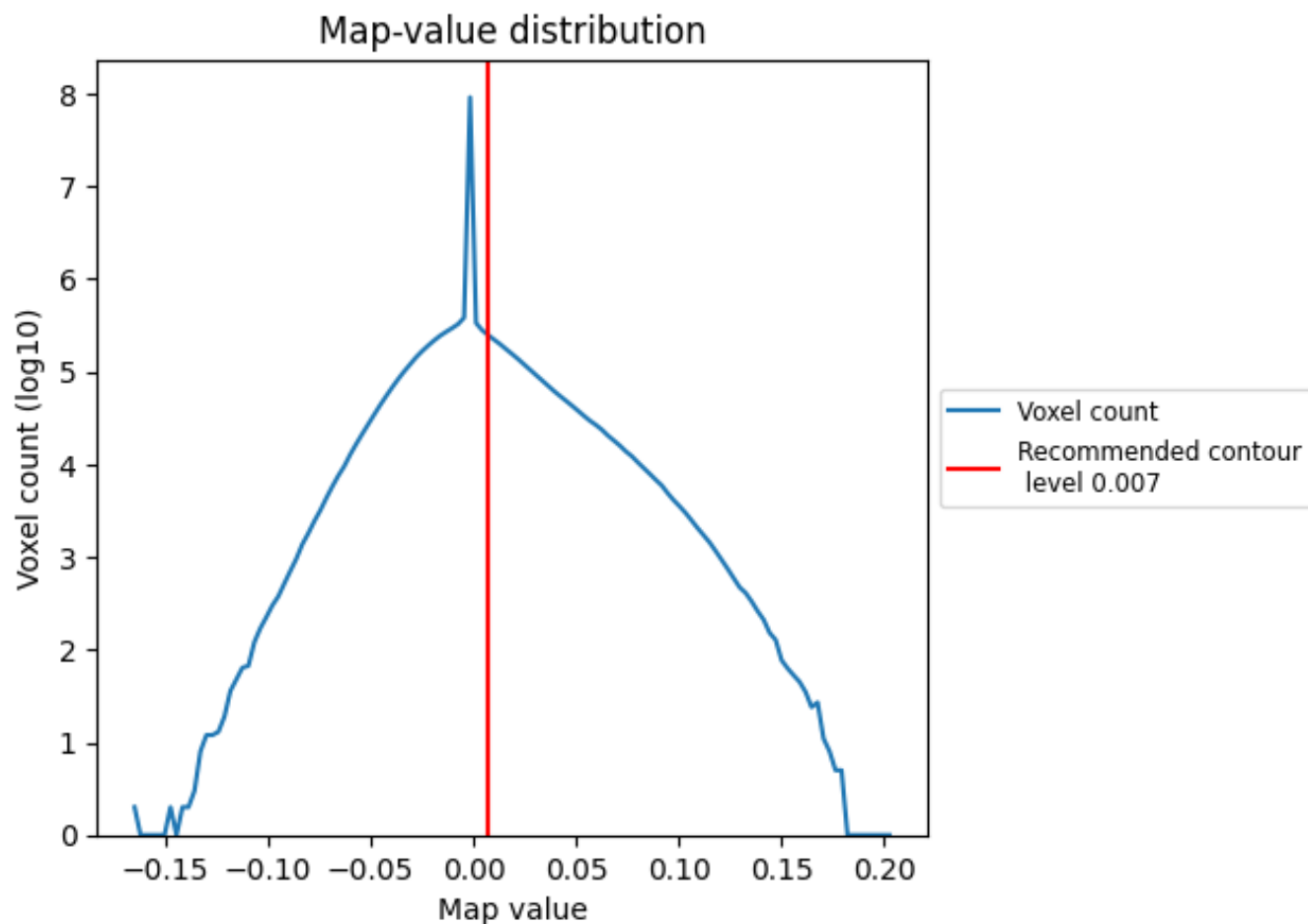
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

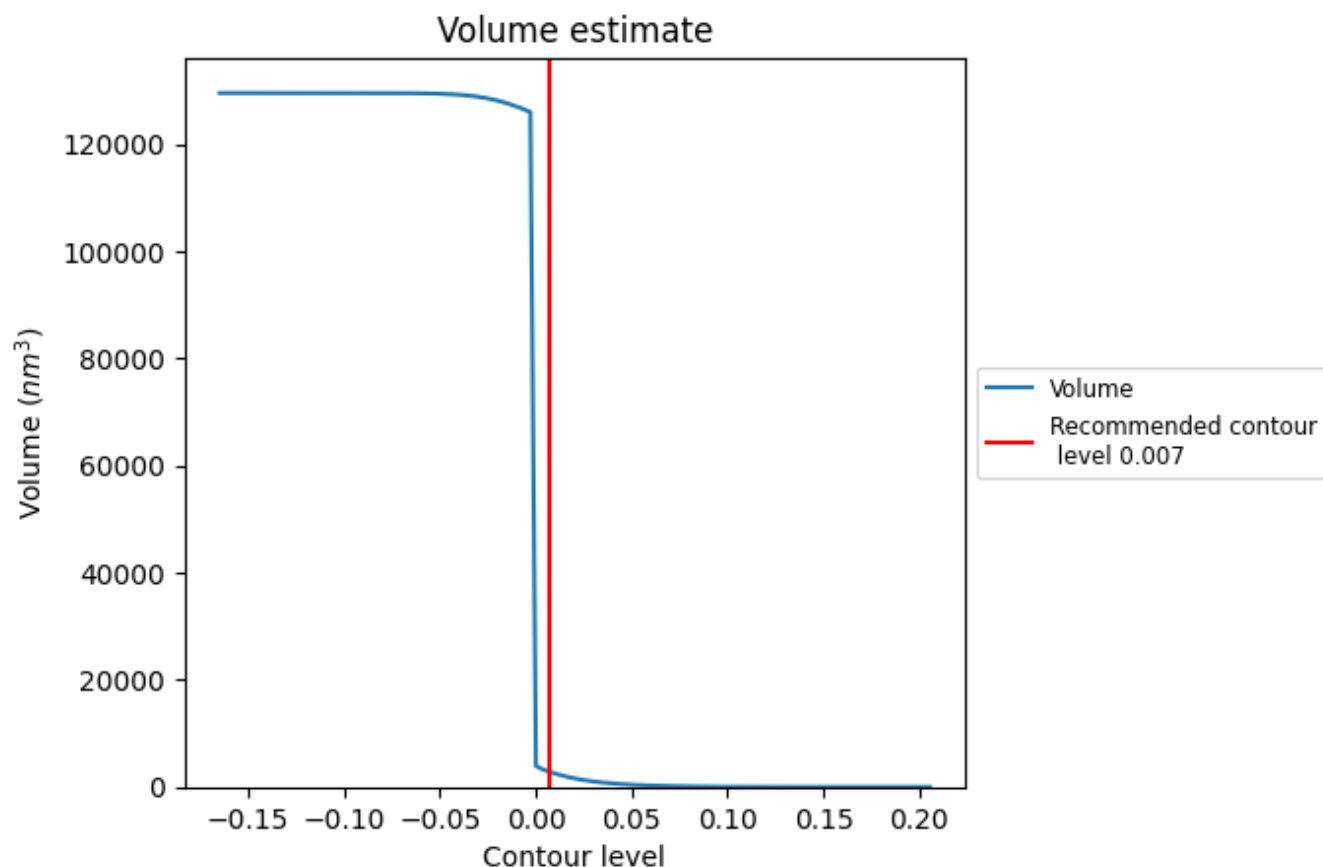
This section contains the results of statistical analysis of the map.

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.

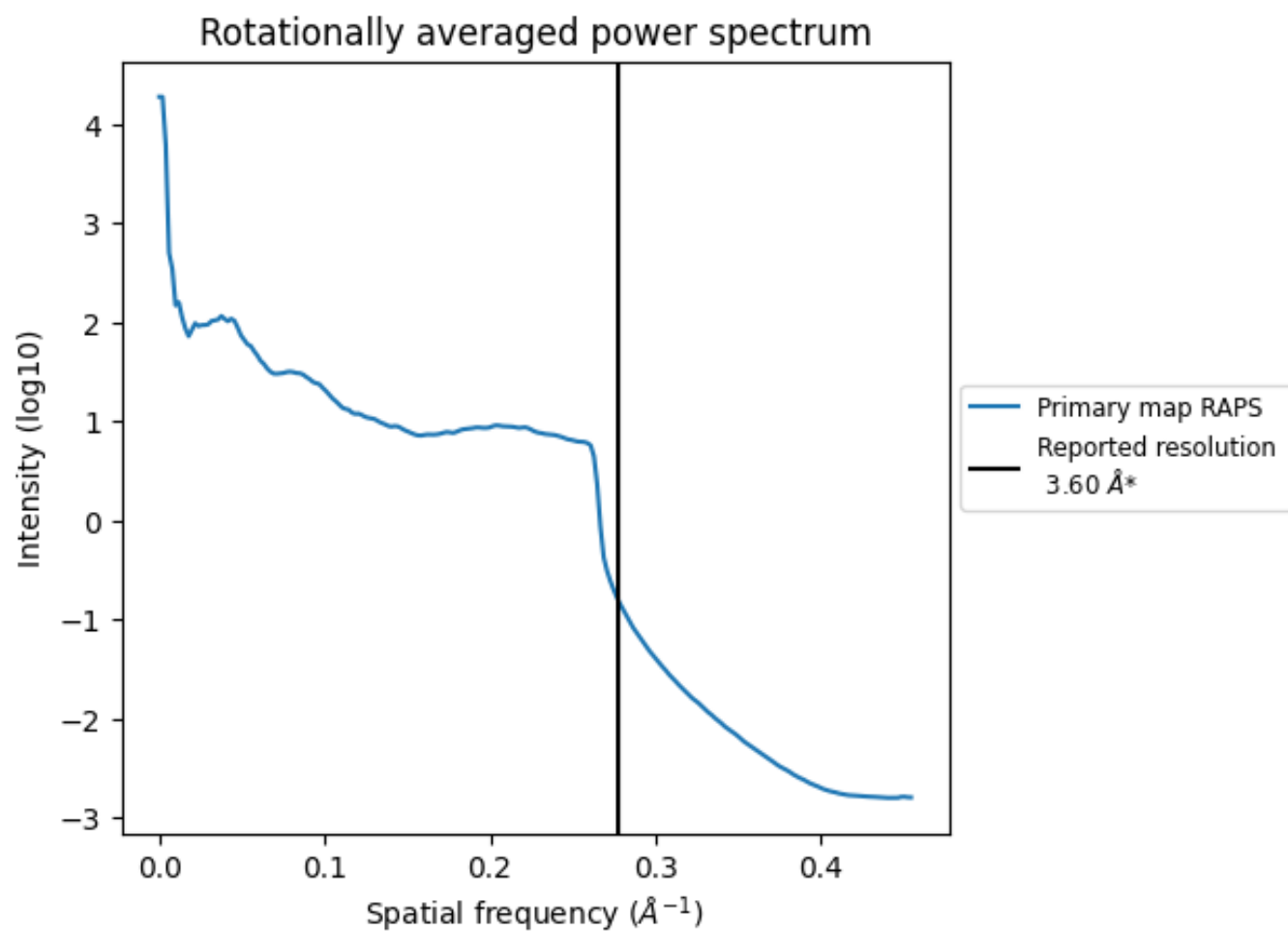
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2861 nm^3 ; this corresponds to an approximate mass of 2584 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 0.278 \AA^{-1}

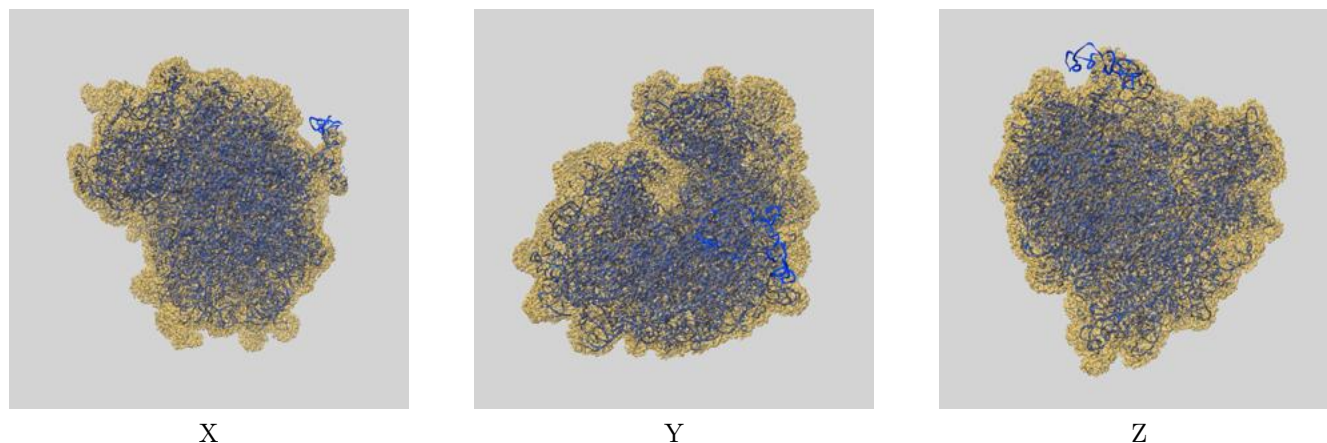
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

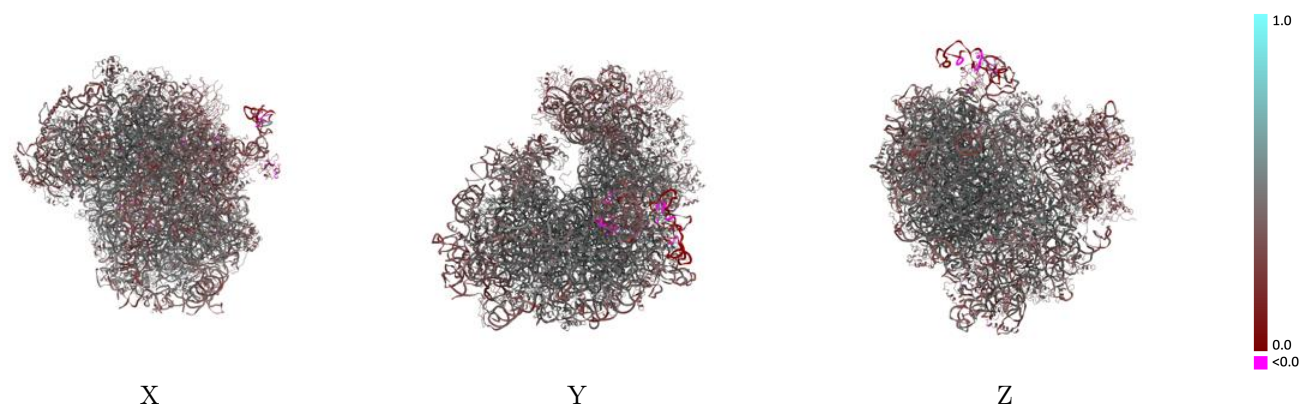
This section contains information regarding the fit between EMDB map EMD-4070 and PDB model 5LKS. Per-residue inclusion information can be found in [section 3](#) on [page 21](#).

9.1 Map-model overlay [i](#)



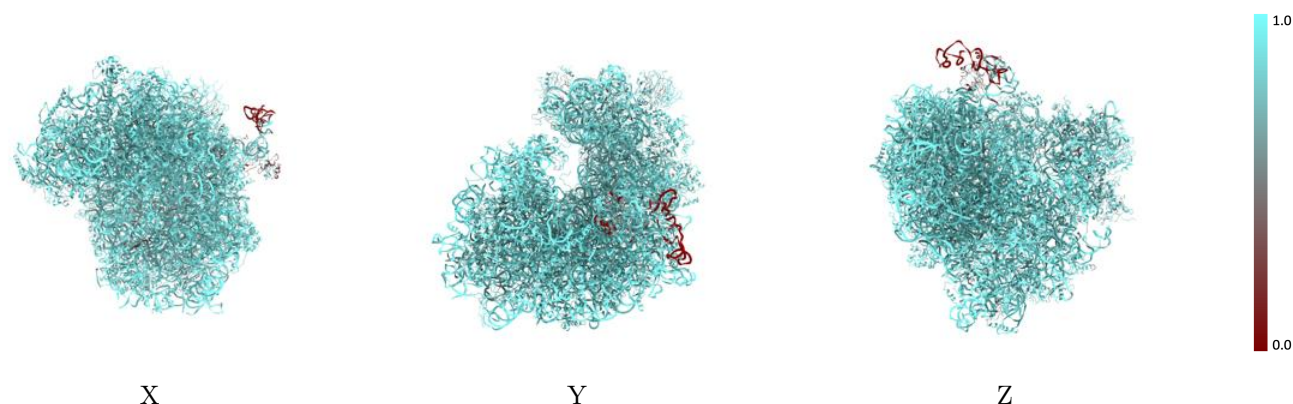
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



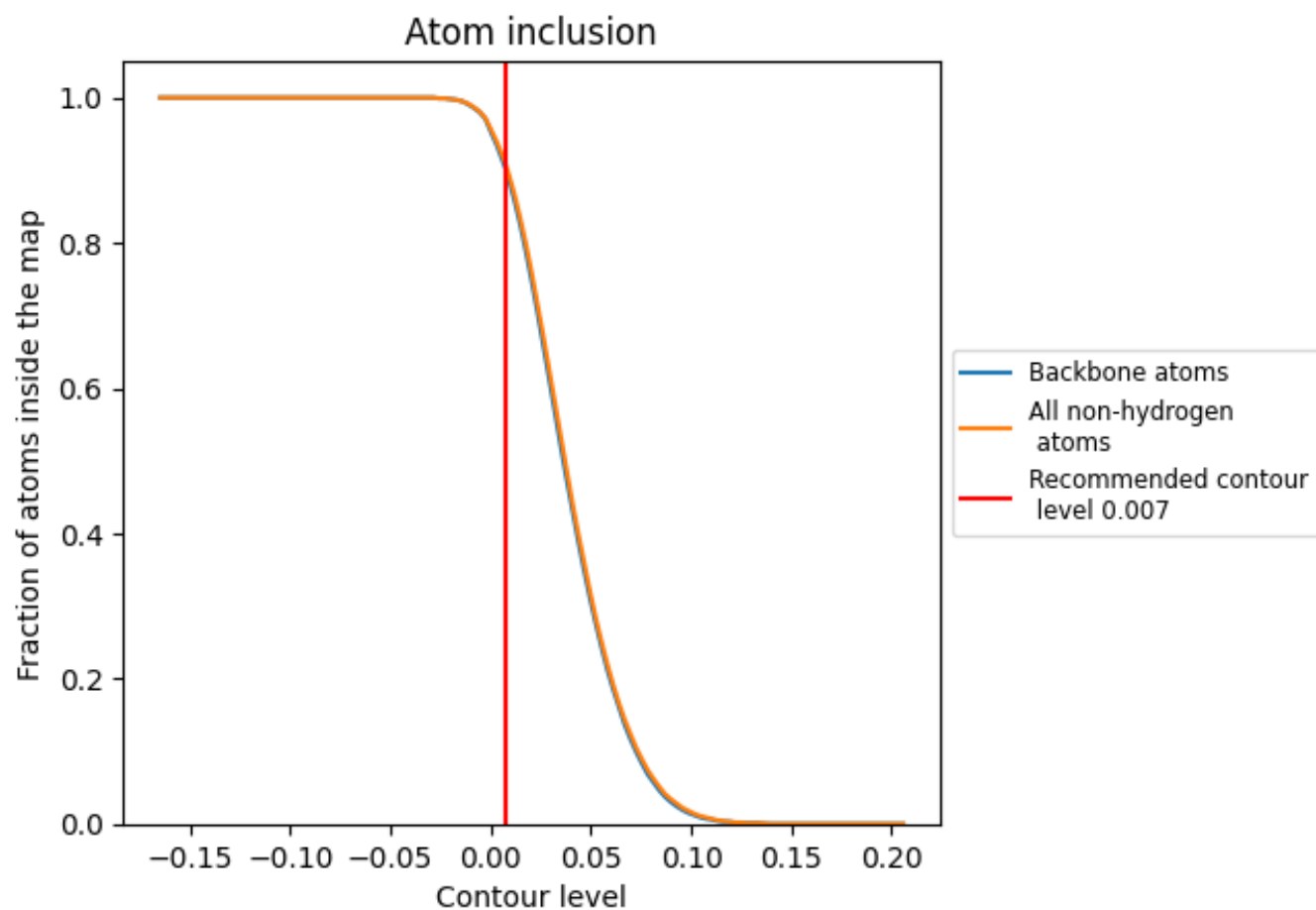
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 91% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9120	 0.4290
L5	 0.9430	 0.4380
L7	 0.9720	 0.4490
L8	 0.9570	 0.4500
LA	 0.9040	 0.4980
LB	 0.9130	 0.4700
LC	 0.9030	 0.4760
LD	 0.9080	 0.4100
LE	 0.8740	 0.4100
LF	 0.8840	 0.4640
LG	 0.8870	 0.4160
LH	 0.9180	 0.4470
LI	 0.8760	 0.4360
LJ	 0.8900	 0.3970
LL	 0.9170	 0.4500
LM	 0.9210	 0.4430
LN	 0.8860	 0.4970
LO	 0.9080	 0.4770
LP	 0.9050	 0.4850
LQ	 0.9080	 0.4850
LR	 0.9180	 0.4560
LS	 0.9320	 0.4810
LT	 0.9120	 0.4800
LU	 0.8980	 0.4010
LV	 0.8990	 0.4830
LW	 0.8160	 0.3870
LX	 0.9120	 0.4650
LY	 0.8940	 0.4530
LZ	 0.9010	 0.4340
La	 0.8990	 0.4840
Lb	 0.8670	 0.4340
Lc	 0.9290	 0.4620
Ld	 0.9190	 0.4700
Le	 0.9170	 0.4930
Lf	 0.8870	 0.4920




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Chain	Atom inclusion	Q-score
Lg	 0.8750	 0.4620
Lh	 0.8870	 0.4420
Li	 0.9170	 0.4450
Lj	 0.9240	 0.5060
Lk	 0.9050	 0.4190
Ll	 0.8860	 0.4820
Lm	 0.9180	 0.4800
Ln	 0.9140	 0.5050
Lo	 0.9150	 0.4560
Lp	 0.9100	 0.4840
Lr	 0.9300	 0.4710
Lz	 0.4760	 0.2120
S2	 0.9410	 0.4220
SA	 0.9000	 0.4180
SB	 0.8930	 0.4190
SC	 0.8930	 0.4390
SD	 0.8330	 0.3540
SE	 0.8740	 0.4240
SF	 0.8140	 0.3470
SG	 0.8790	 0.3770
SH	 0.8910	 0.4000
SI	 0.8830	 0.4340
SJ	 0.8840	 0.4110
SK	 0.8560	 0.3420
SL	 0.8790	 0.4480
SM	 0.7280	 0.2670
SN	 0.8850	 0.4460
SO	 0.8940	 0.4390
SP	 0.8360	 0.3180
SQ	 0.7760	 0.3340
SR	 0.8650	 0.3720
SS	 0.8350	 0.3260
ST	 0.7870	 0.3350
SU	 0.8490	 0.3630
SV	 0.9150	 0.4250
SW	 0.8840	 0.4520
SX	 0.9100	 0.4670
SY	 0.8730	 0.3860
SZ	 0.8040	 0.3340
Sa	 0.9010	 0.4490
Sb	 0.9200	 0.4410
Sc	 0.8440	 0.3580

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Chain	Atom inclusion	Q-score
Sd	 0.8360	 0.3910
Se	 0.8110	 0.3870
Sf	 0.7880	 0.2880
Sg	 0.7960	 0.2980