



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 03:05 AM UTC

PDB ID : 6T7T / pdb_00006t7t
EMDB ID : EMD-10397
Title : Structure of yeast 80S ribosome stalled on poly(A) tract.
Authors : Tesina, P.; Buschauer, R.; Cheng, J.; Berninghausen, O.; Becker, R.; Beckmann, R.
Deposited on : 2019-10-23
Resolution : 3.10 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:

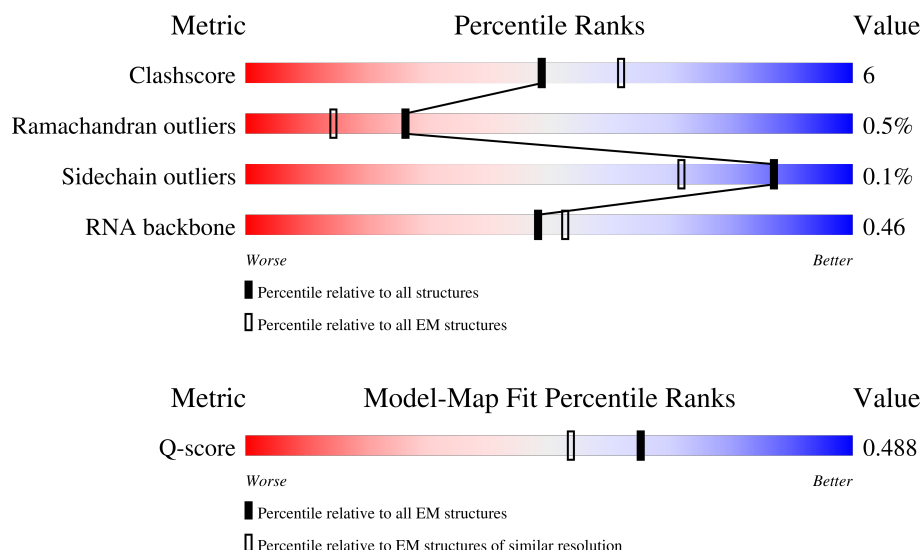
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.10 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	14724 (2.60 - 3.60)

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	LA	251	
2	SA	206	
3	LB	386	

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Mol	Chain	Length	Quality of chain
4	SB	232	
5	C2	1771	
6	SP	117	
7	SC	216	
8	SD	222	
9	SE	258	
10	SF	206	
11	SG	228	
12	SH	184	
13	SI	187	
14	SJ	184	
15	SK	92	
16	SL	144	
17	SM	121	
18	SN	150	
19	SO	127	
20	SQ	141	
21	SR	125	
22	SS	145	
23	ST	143	
24	SU	100	
25	SV	87	
26	SW	129	
27	SX	144	
28	SY	134	

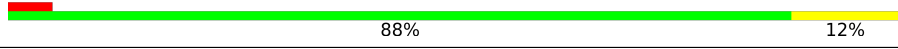
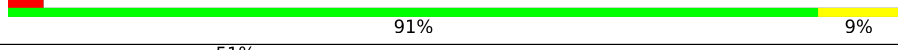
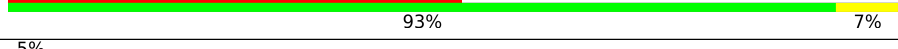
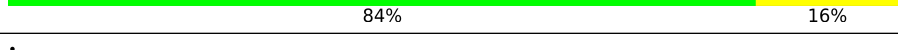
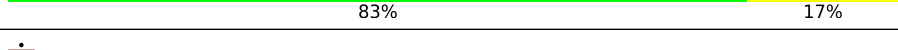
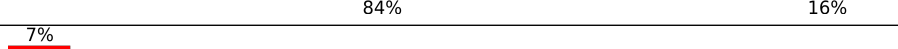
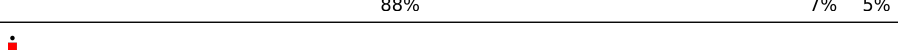
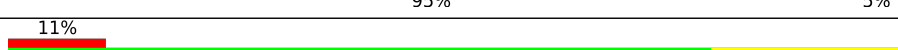
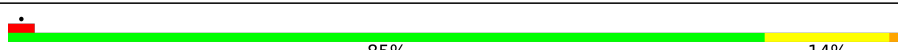
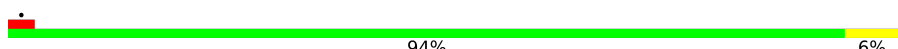
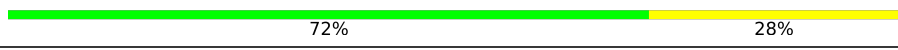
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Mol	Chain	Length	Quality of chain
29	SZ	82	
30	Sa	97	
31	Sb	81	
32	Sd	53	
33	Se	60	
34	Sf	73	
35	Sg	312	
36	Sc	63	
37	C4	121	
38	C3	158	
39	LC	361	
40	LD	294	
41	LE	175	
42	LF	222	
43	LG	233	
44	LH	191	
45	LI	218	
46	LJ	169	
47	LL	193	
48	LM	136	
49	LN	203	
50	LO	197	
51	LP	183	
52	LQ	185	
53	LR	188	

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Mol	Chain	Length	Quality of chain
54	LS	171	
55	LT	159	
56	LU	100	
57	LV	136	
58	LW	126	
59	LX	121	
60	LY	125	
61	LZ	135	
62	La	148	
63	Lb	58	
64	Lc	96	
65	Ld	109	
66	Le	127	
67	Lf	106	
68	Lg	112	
69	Lh	119	
70	Li	99	
71	Lj	85	
72	Lk	77	
73	Ll	50	
74	Lm	52	
75	Ln	25	
76	Lo	103	
77	Lp	91	
78	C1	3184	

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Mol	Chain	Length	Quality of chain
79	5	11	45% 55%
80	6	76	5% 51% 39% 9%
80	7	76	97% 61% 28% 12%
81	A	4	50% 25% 50% 25%

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 202869 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LA	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 2 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SA	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LB	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 4 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SB	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		

- Molecule 5 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C2	1771	Total	C	N	O	P	0	0
			37604	16807	6624	12402	1771		

- Molecule 6 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SP	117	Total	C	N	O	S	0	0
			916	583	171	155	7		

- Molecule 7 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SC	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 8 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SD	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 9 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SE	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 10 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SF	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 11 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SG	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 12 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	SH	184	Total	C	N	O	0	0
			1473	946	263	264		

- Molecule 13 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SI	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		

- Molecule 14 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SJ	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		

- Molecule 15 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SK	92	Total	C	N	O	S	0	0
			752	487	122	141	2		

- Molecule 16 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SL	144	Total	C	N	O	S	0	0
			1159	742	219	195	3		

- Molecule 17 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SM	121	Total	C	N	O	S	0	0
			875	551	153	169	2		

- Molecule 18 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 19 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SO	127	Total	C	N	O	S	0	0
			926	569	185	169	3		

- Molecule 20 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	SQ	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 21 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SR	121	Total	C	N	O	S	0	0
			948	596	179	171	2		

- Molecule 22 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SS	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 23 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	ST	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 24 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SU	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 25 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SV	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 26 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 27 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 28 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	SY	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 29 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	SZ	82	Total	C	N	O	0	0
			651	416	123	112		

- Molecule 30 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Sa	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 31 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Sb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 32 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Sd	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 33 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Se	60	Total	C	N	O	S	0	0
			472	298	97	76	1		

- Molecule 34 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Sf	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

- Molecule 35 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Sg	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		

- Molecule 36 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Sc	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 37 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	C4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 38 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	C3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 39 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LC	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 40 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LD	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 41 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LE	167	Total	C	N	O	S	0	0
			1305	841	234	229	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LE	146	ILE	LEU	conflict	UNP P05739
LE	173	MET	LEU	conflict	UNP P05739

- Molecule 42 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LF	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 43 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LG	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 44 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LH	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 45 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LI	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 46 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LJ	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		

- Molecule 47 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	LL	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 48 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LM	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 49 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	LN	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 50 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LO	197	Total	C	N	O	S	197	0
			1555	1003	289	262	1		

- Molecule 51 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	LP	183	Total	C	N	O		0	0
			1416	879	284	253			

- Molecule 52 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LQ	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 53 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LR	188	Total	C	N	O		0	0
			1515	932	323	260			

- Molecule 54 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LS	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 55 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	LT	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 56 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	LU	100	Total	C	N	O		0	0
			796	516	131	149			

- Molecule 57 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LV	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 58 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	LW	126	Total	C	N	O	S	0	0
			836	525	165	145	1		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	104	GLN	ASN	conflict	UNP P04449
LW	109	GLN	LEU	conflict	UNP P04449
LW	112	ASP	ASN	conflict	UNP P04449
LW	119	ALA	GLU	conflict	UNP P04449

- Molecule 59 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	LX	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	LY	125	Total	C	N	O		0	0
			984	620	191	173			

- Molecule 61 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	LZ	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 62 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	La	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 63 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	Lb	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 64 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Lc	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 65 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Ld	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 66 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Le	127	Total	C	N	O	S	0	0
			1017	644	205	167	1		

- Molecule 67 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Lf	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 68 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Lg	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 69 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Lh	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 70 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Li	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 71 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Lj	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 72 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	Lk	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 73 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Ll	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 74 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Lm	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 75 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Ln	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 76 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Lo	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 77 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Lp	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 78 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	C1	3184	Total	C	N	O	P	0	0
			68091	30415	12259	22233	3184		

- Molecule 79 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	5	11	Total	C	N	O	P	0	0
			242	110	55	66	11		

- Molecule 80 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	7	76	Total	C	N	O	P	0	0
			1616	721	281	538	76		
80	6	76	Total	C	N	O	P	0	0
			1616	721	281	538	76		

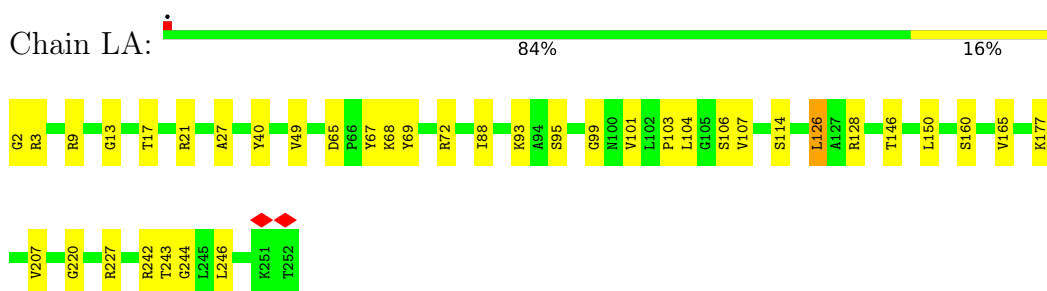
- Molecule 81 is a protein called nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
81	A	4	Total	C	N	O	1	0
			41	27	9	5		

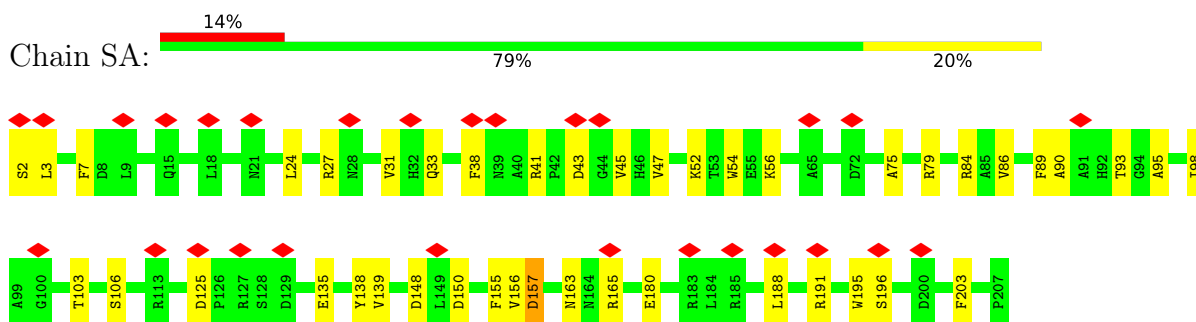
3 Residue-property plots [i](#)

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.

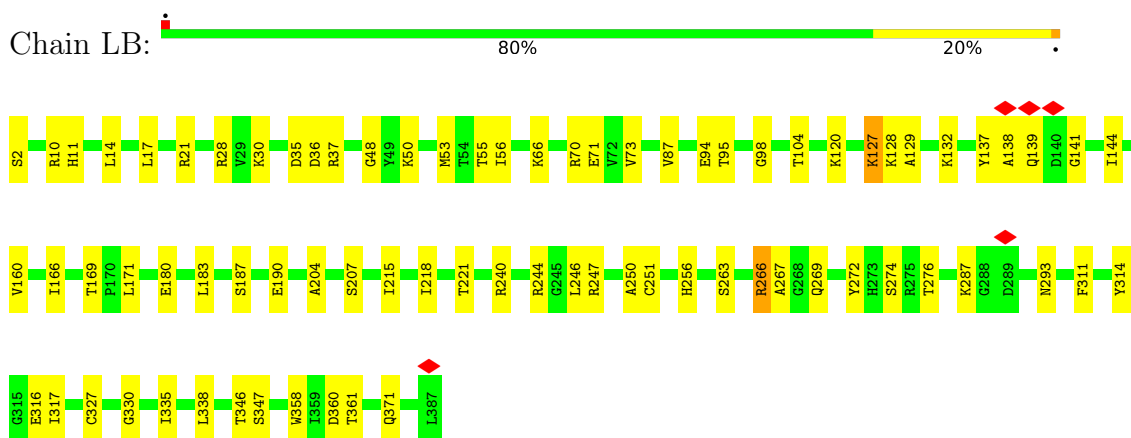
- Molecule 1: 60S ribosomal protein L2-A



- Molecule 2: 40S ribosomal protein S0-A

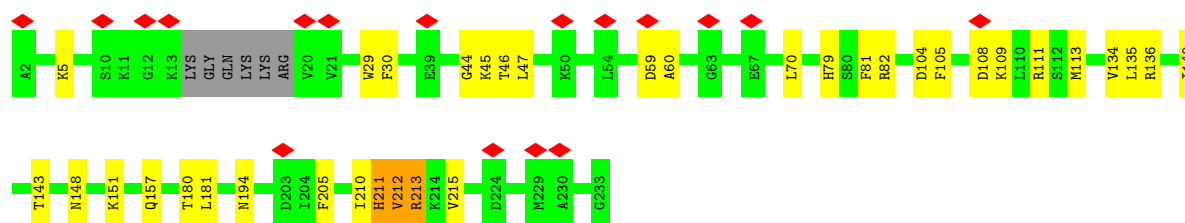


- Molecule 3: 60S ribosomal protein L3



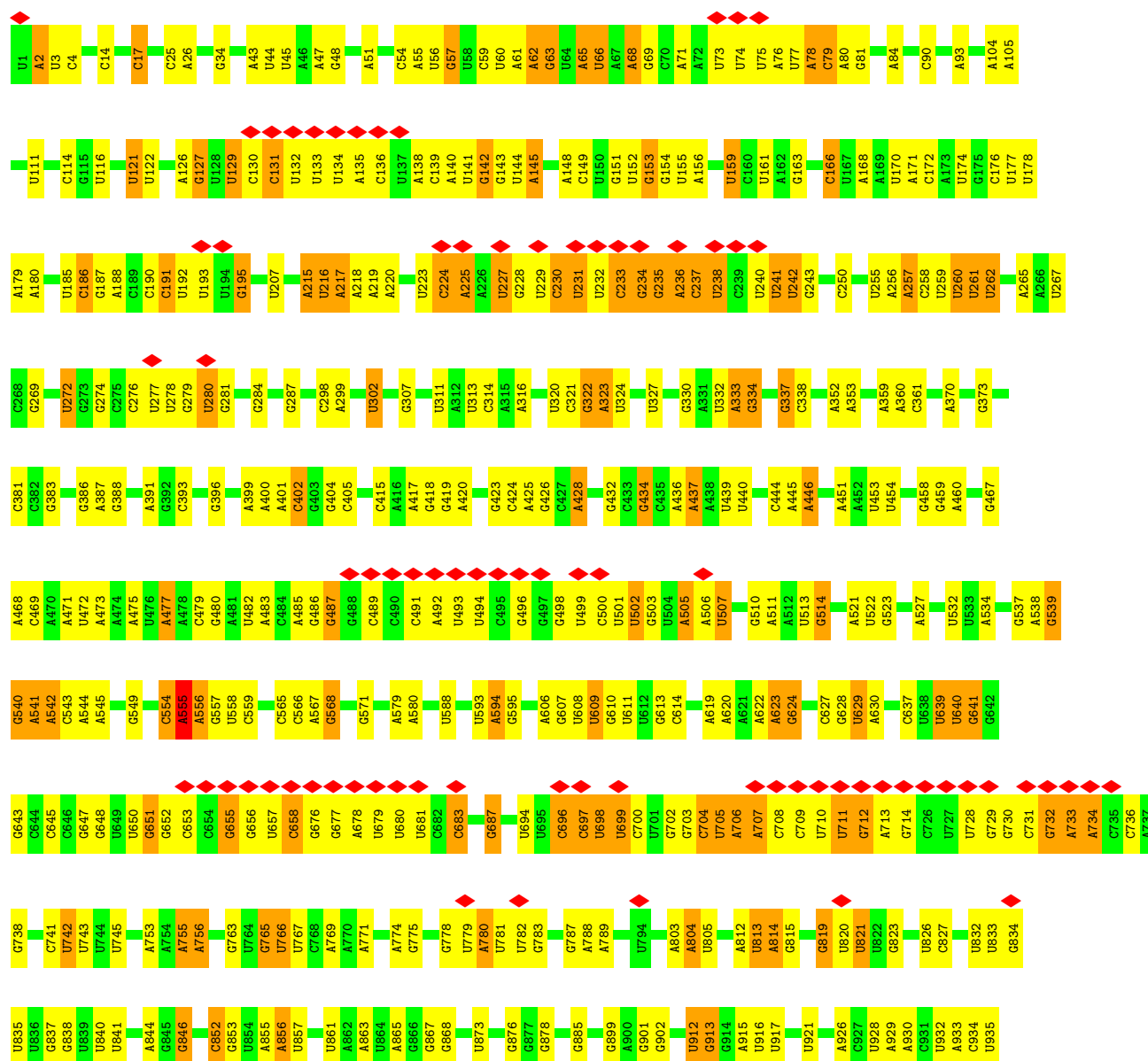
- Molecule 4: 40S ribosomal protein S1-A

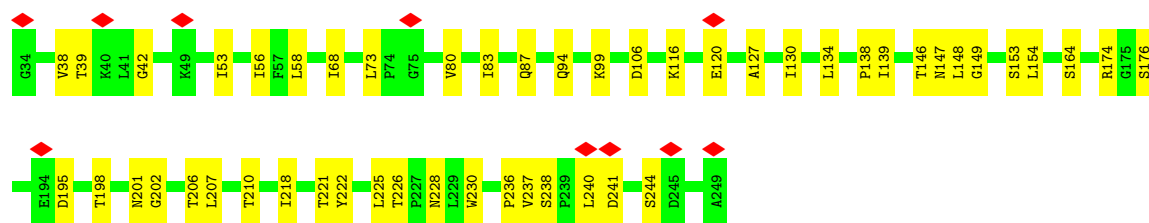
Chain SB: 



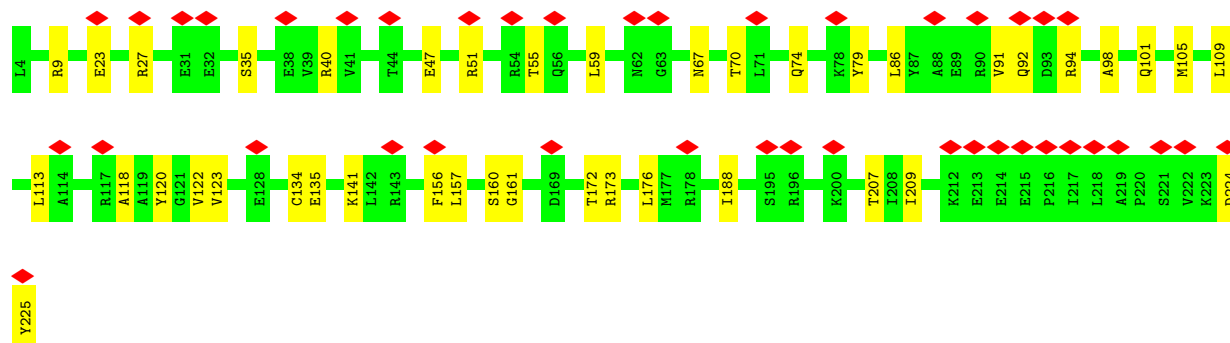
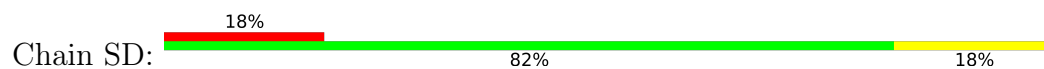
• Molecule 5: 18S rRNA

Chain C2: 

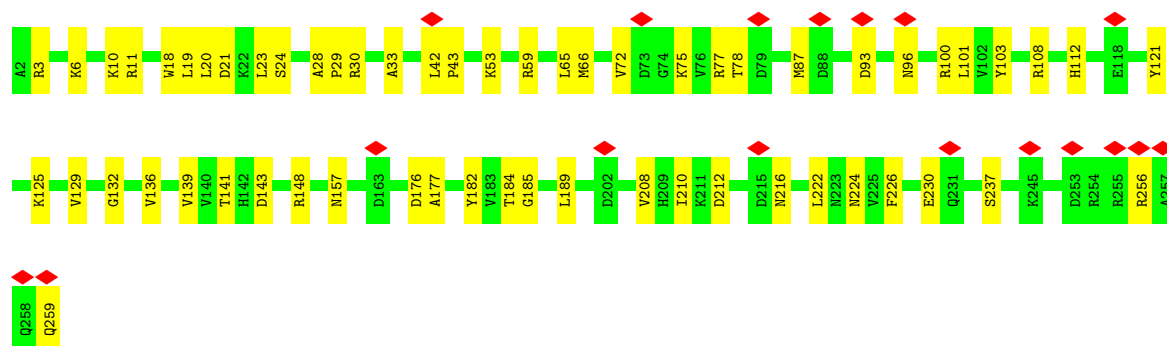
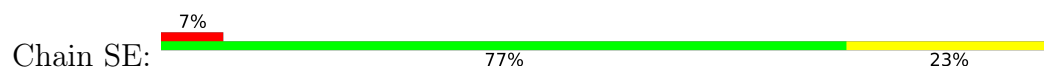




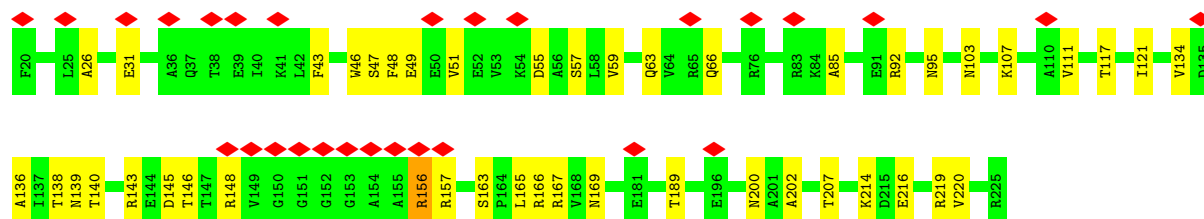
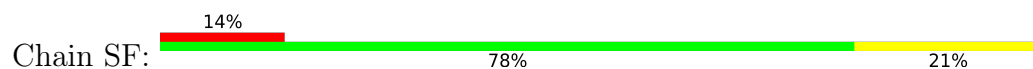
• Molecule 8: 40S ribosomal protein S3



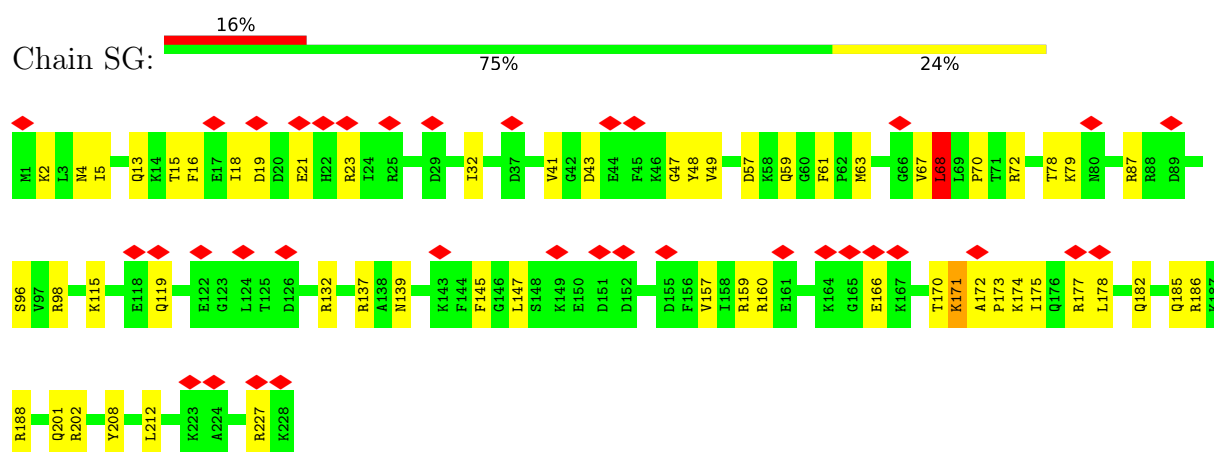
• Molecule 9: 40S ribosomal protein S4-A



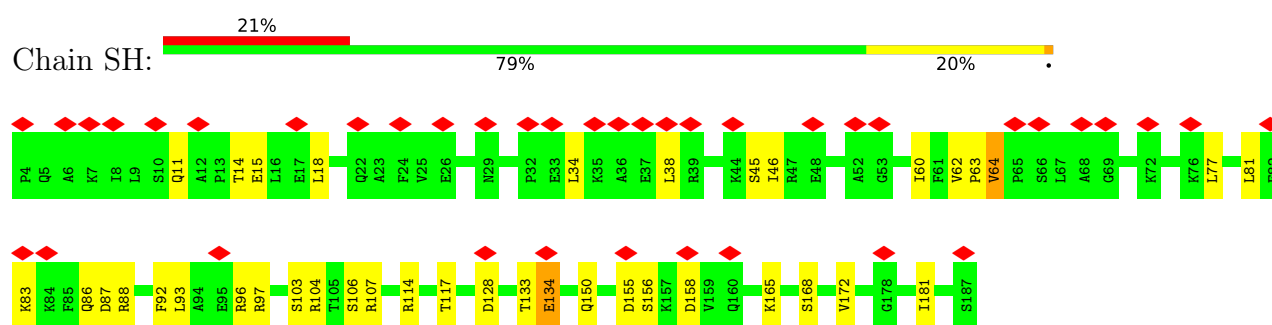
• Molecule 10: Rps5p



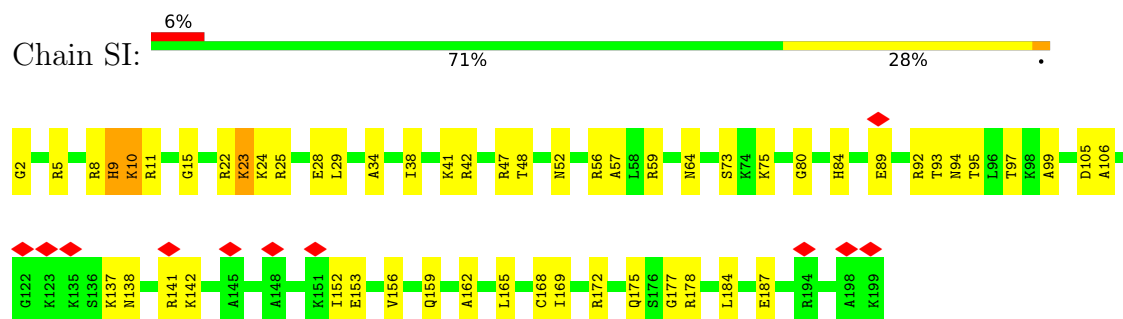
• Molecule 11: 40S ribosomal protein S6-A



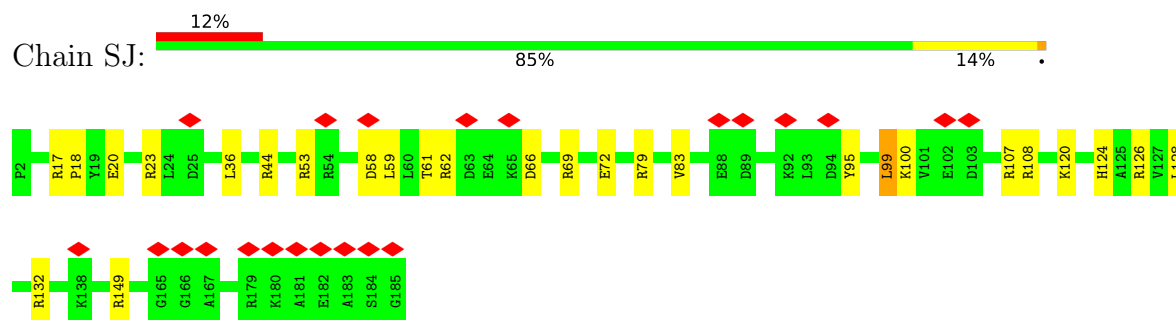
- Molecule 12: 40S ribosomal protein S7-A



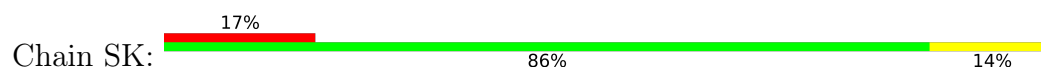
- Molecule 13: 40S ribosomal protein S8

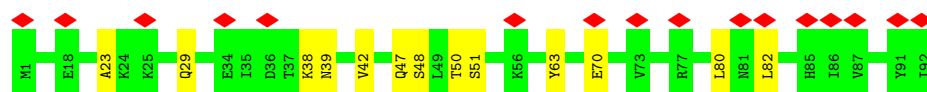


- Molecule 14: 40S ribosomal protein S9-A

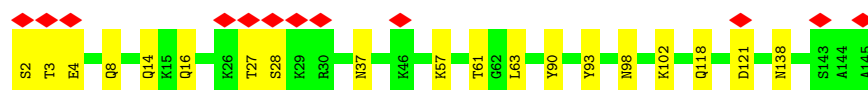
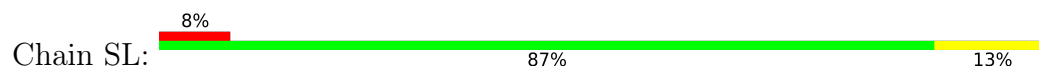


- Molecule 15: 40S ribosomal protein S10-A

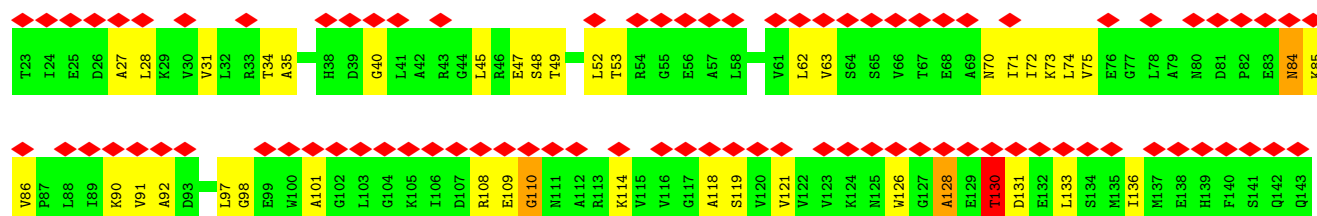
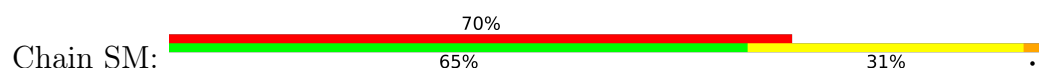




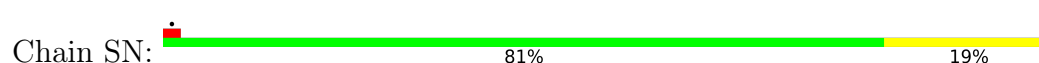
- Molecule 16: 40S ribosomal protein S11-A



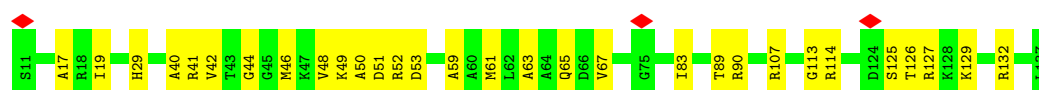
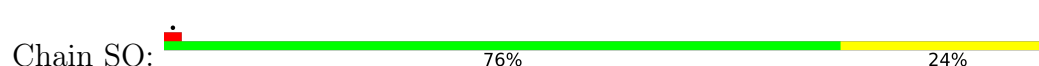
- Molecule 17: 40S ribosomal protein S12



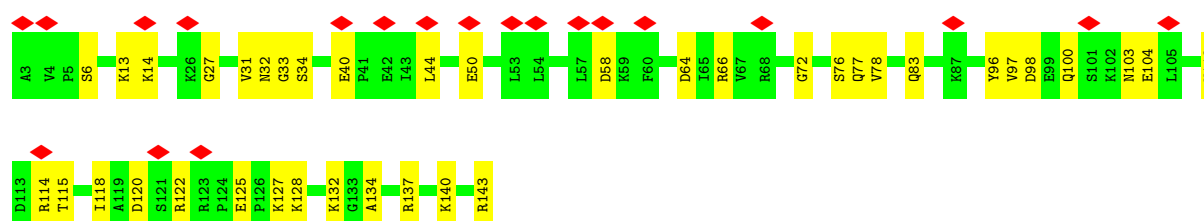
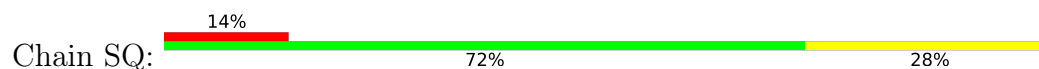
- Molecule 18: 40S ribosomal protein S13



- Molecule 19: 40S ribosomal protein S14-B

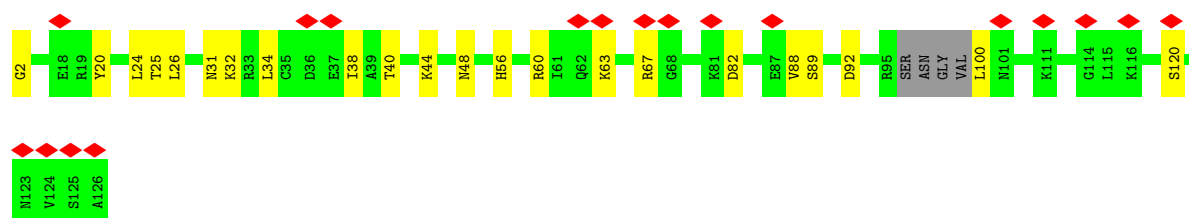


- Molecule 20: 40S ribosomal protein S16-A



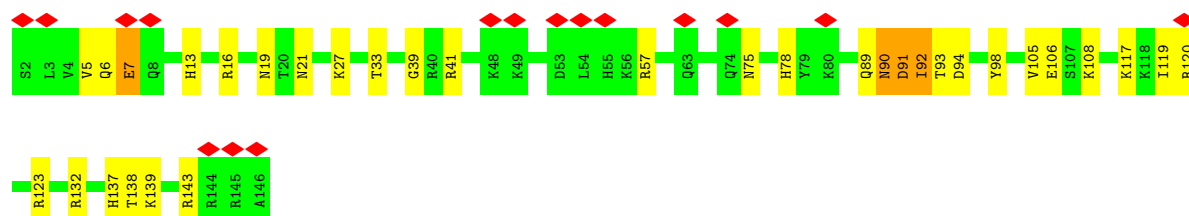
- Molecule 21: 40S ribosomal protein S17-B

Chain SR: 



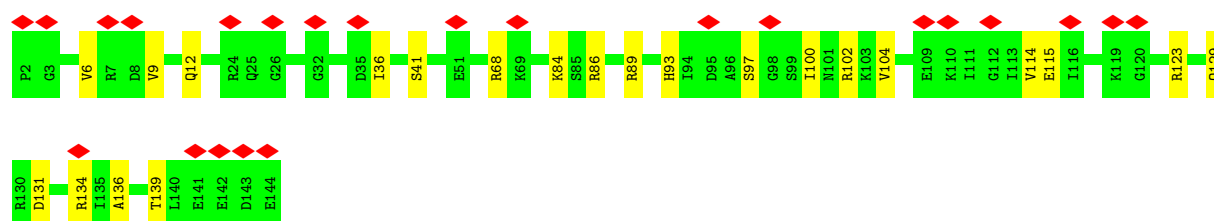
- Molecule 22: 40S ribosomal protein S18-A

Chain SS: 



- Molecule 23: 40S ribosomal protein S19-A

Chain ST: 



- Molecule 24: 40S ribosomal protein S20

Chain SU: 



- Molecule 25: 40S ribosomal protein S21-A

Chain SV: 

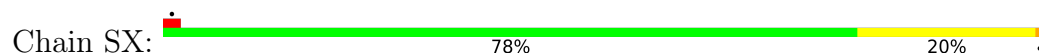


- Molecule 26: 40S ribosomal protein S22-A

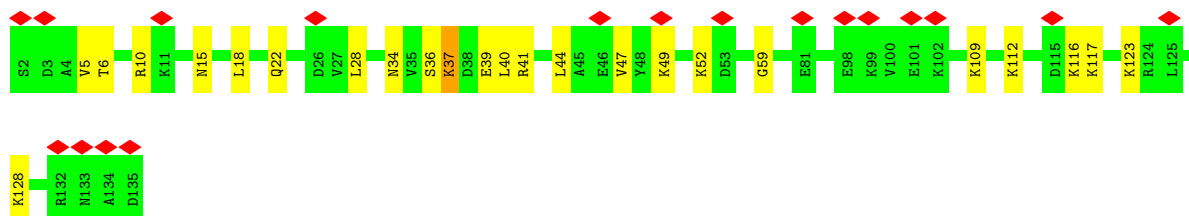
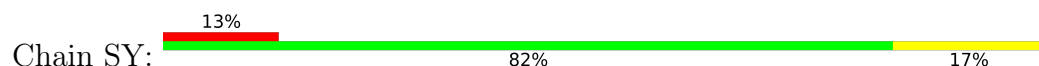
Chain SW: 



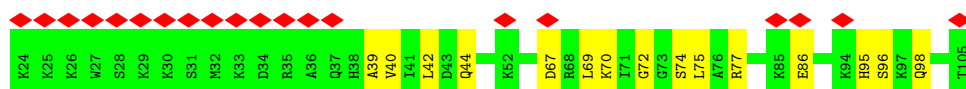
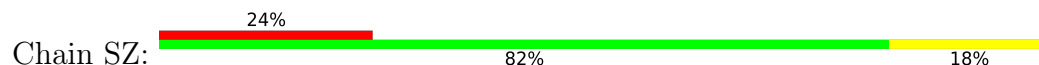
- Molecule 27: 40S ribosomal protein S23-A



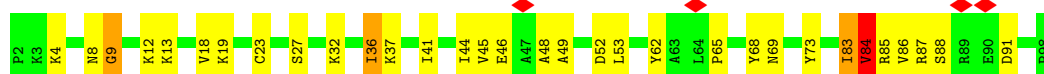
- Molecule 28: 40S ribosomal protein S24-A



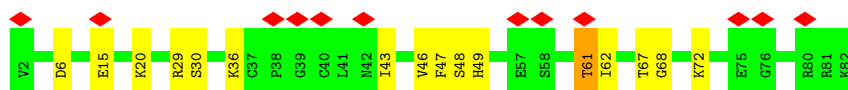
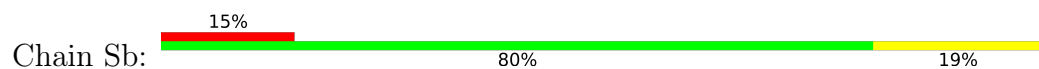
- Molecule 29: 40S ribosomal protein S25-A



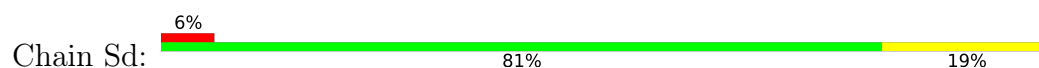
- Molecule 30: 40S ribosomal protein S26-B



- Molecule 31: 40S ribosomal protein S27-A

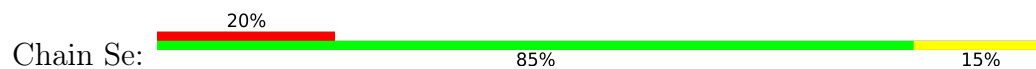


- Molecule 32: 40S ribosomal protein S29-A

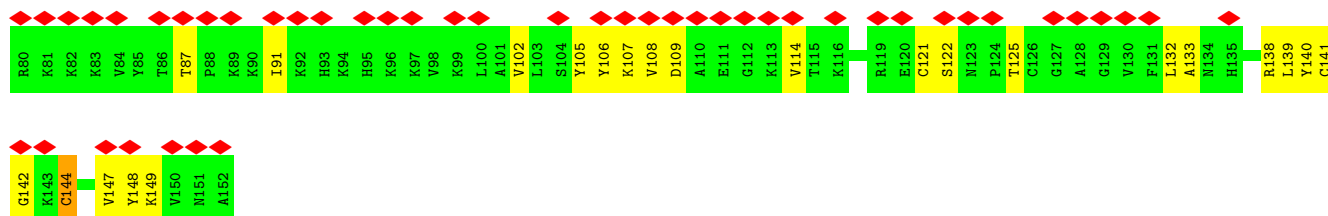




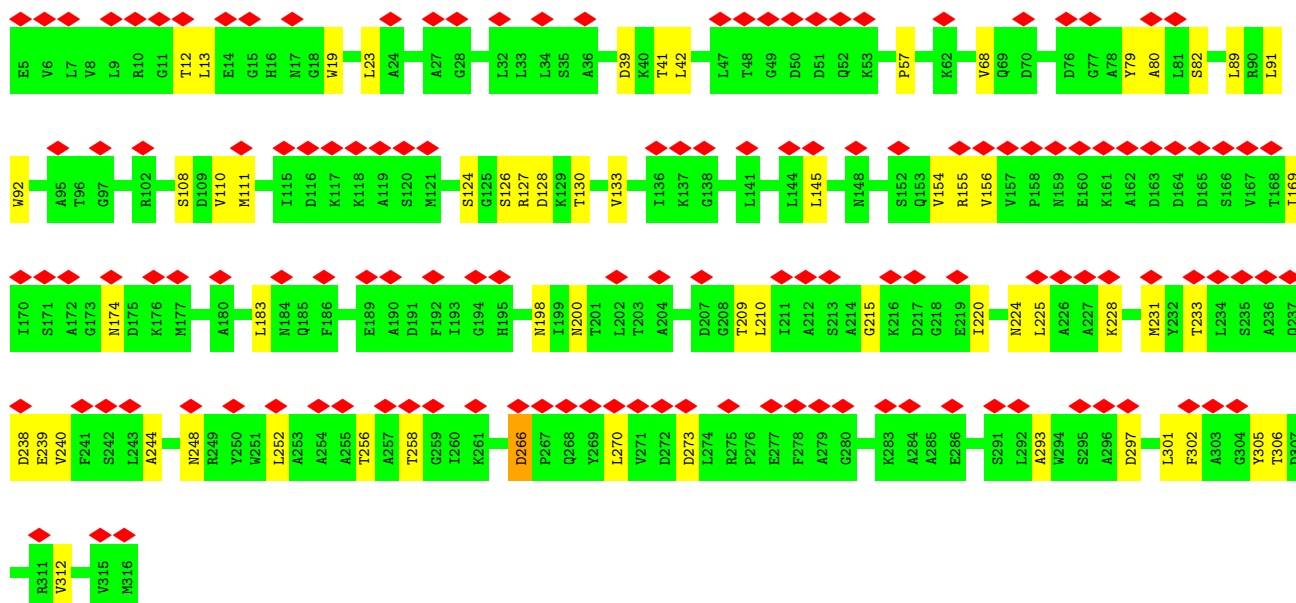
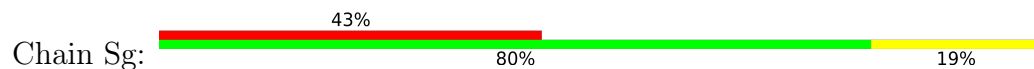
- Molecule 33: 40S ribosomal protein S30-A



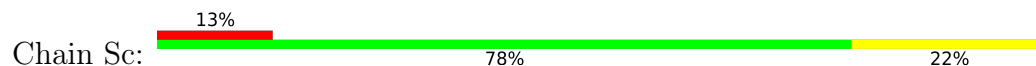
- Molecule 34: Ubiquitin-40S ribosomal protein S31

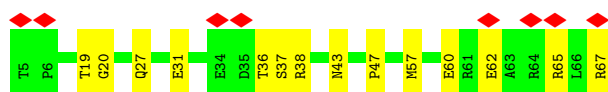


- Molecule 35: Guanine nucleotide-binding protein subunit beta-like protein



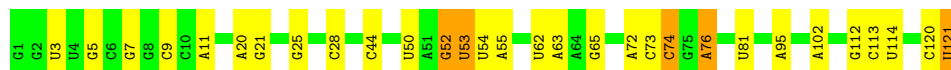
- Molecule 36: 40S ribosomal protein S28-A





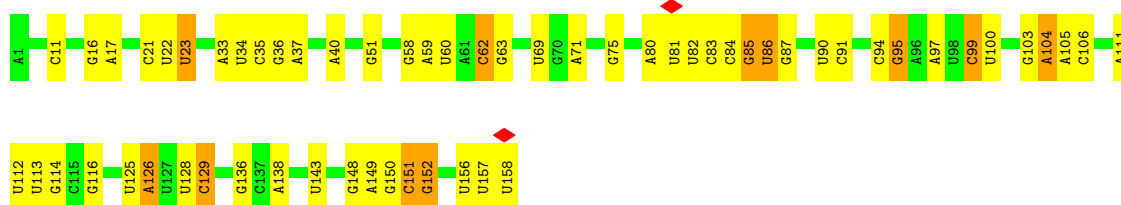
• Molecule 37: 5S rRNA

Chain C4: 75% 21% .



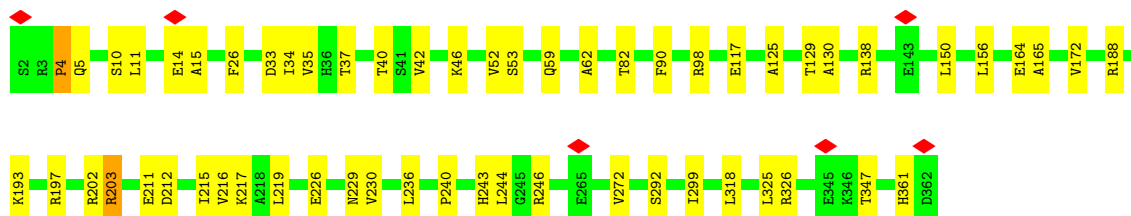
• Molecule 38: 5.8S rRNA

Chain C3: 62% 31% 7% .



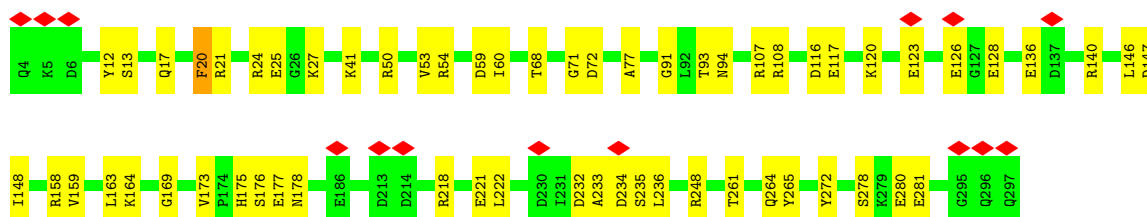
• Molecule 39: 60S ribosomal protein L4-A

Chain LC: 84% 16% .



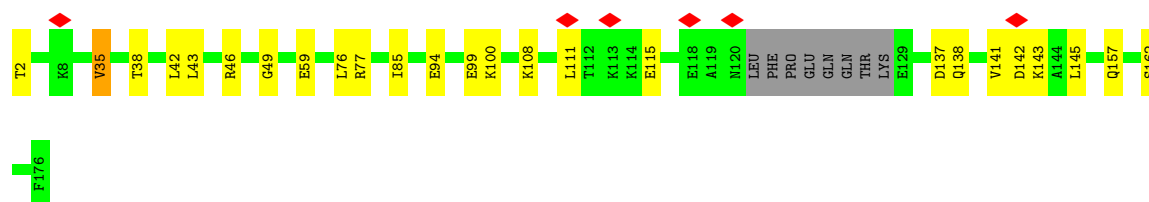
• Molecule 40: 60S ribosomal protein L5

Chain LD: 5% 80% 20% .

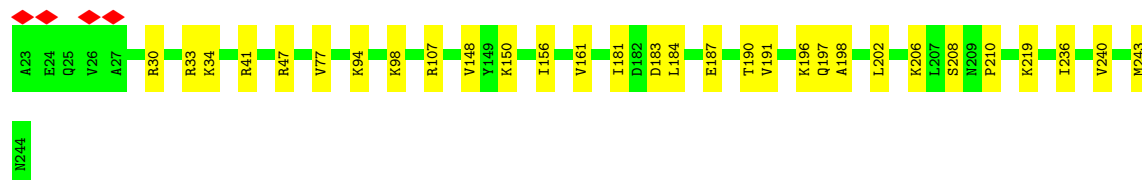


• Molecule 41: 60S ribosomal protein L6-B

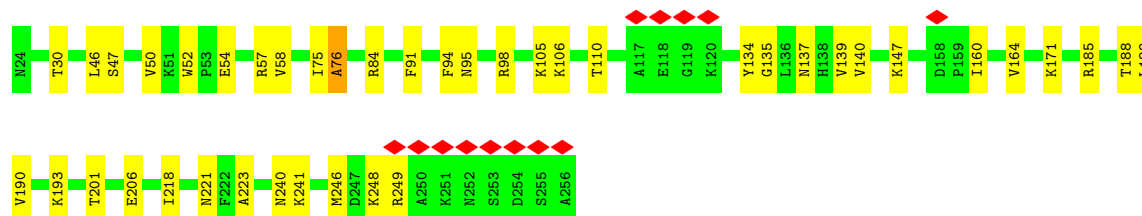
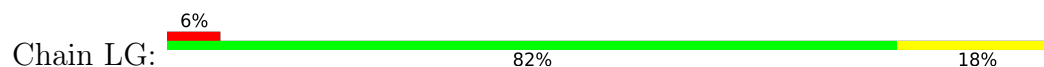
Chain LE: 81% 14% 5% .



- Molecule 42: 60S ribosomal protein L7-A



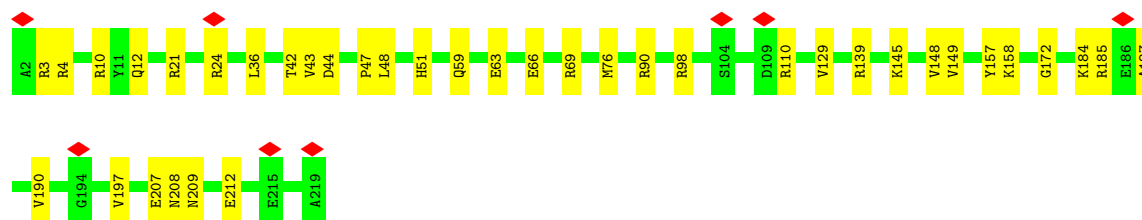
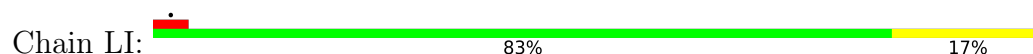
- Molecule 43: 60S ribosomal protein L8-A



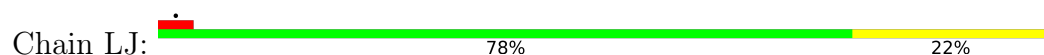
- Molecule 44: 60S ribosomal protein L9-A

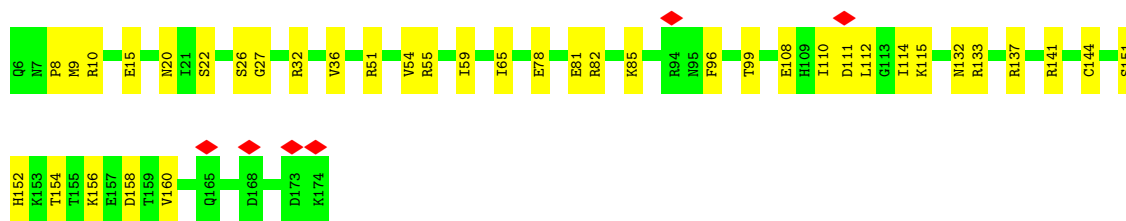


- Molecule 45: 60S ribosomal protein L10



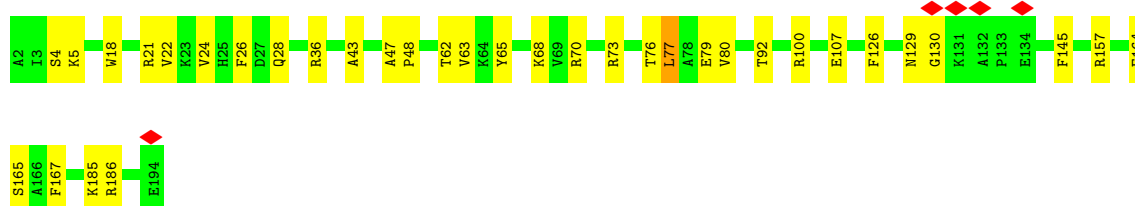
- Molecule 46: 60S ribosomal protein L11-B





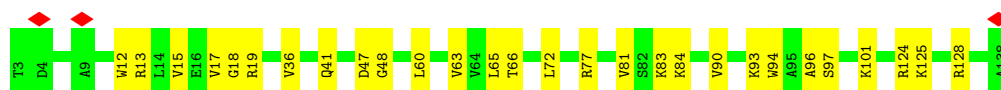
- Molecule 47: 60S ribosomal protein L13-A

Chain LL: 82% 18%



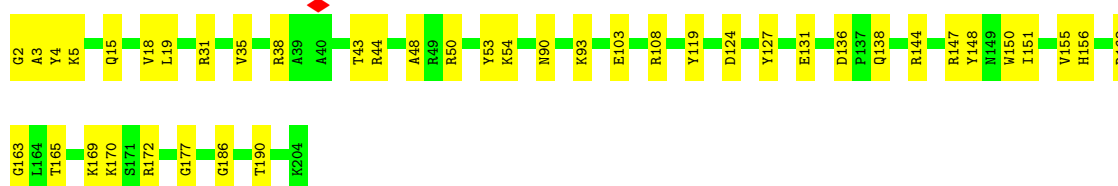
- Molecule 48: 60S ribosomal protein L14-A

Chain LM: 79% 21%



- Molecule 49: 60S ribosomal protein L15-A

Chain LN: 79% 21%



- Molecule 50: 60S ribosomal protein L16-A

Chain LO: 87% 12%

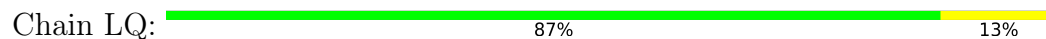


- Molecule 51: 60S ribosomal protein L17-A

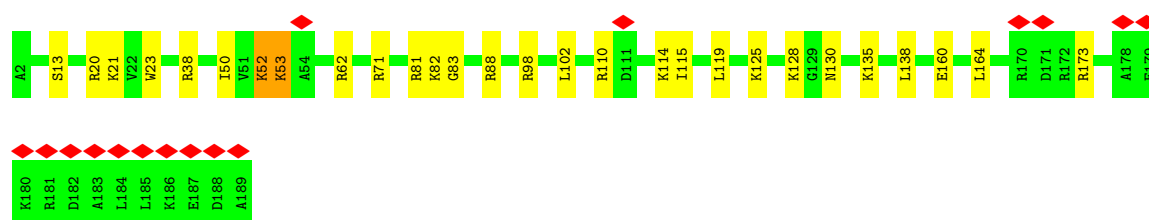
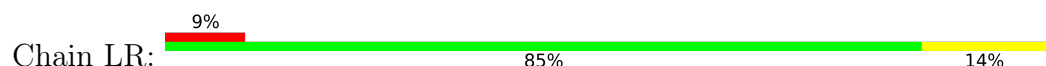
Chain LP: 7% 87% 13%



- Molecule 52: 60S ribosomal protein L18-A



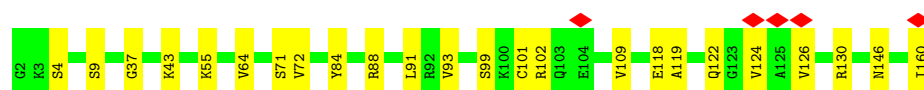
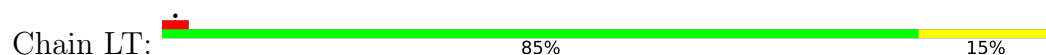
- Molecule 53: 60S ribosomal protein L19-A



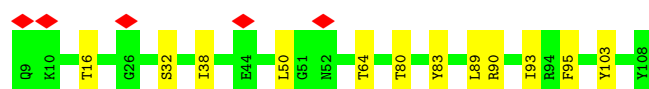
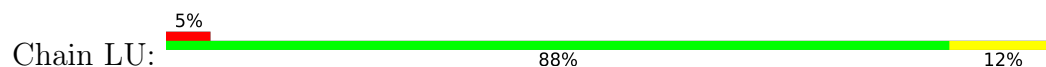
- Molecule 54: 60S ribosomal protein L20-A



- Molecule 55: 60S ribosomal protein L21-A



- Molecule 56: 60S ribosomal protein L22-A

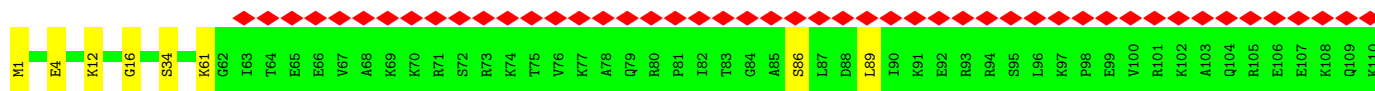


- Molecule 57: 60S ribosomal protein L23-A

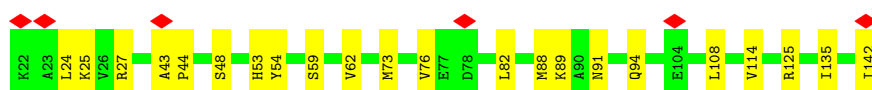
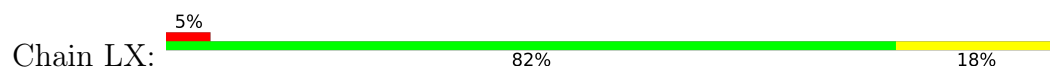




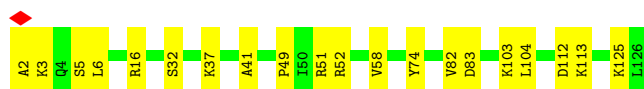
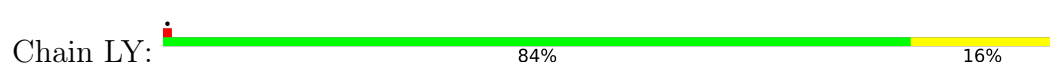
- Molecule 58: 60S ribosomal protein L24-A



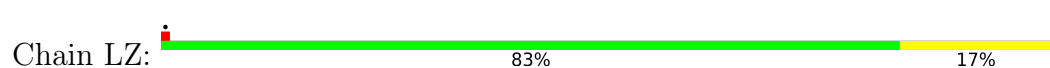
- Molecule 59: 60S ribosomal protein L25



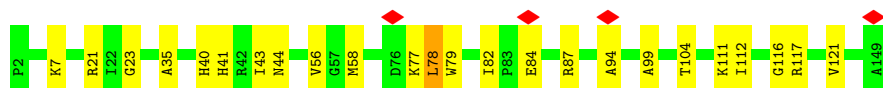
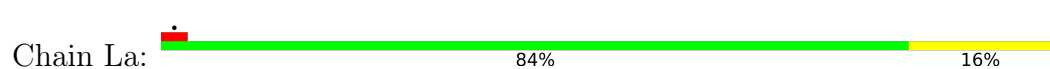
- Molecule 60: 60S ribosomal protein L26-A



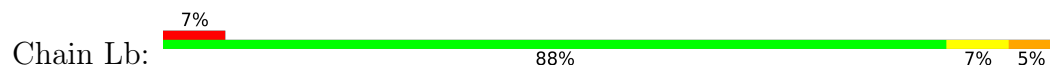
- Molecule 61: 60S ribosomal protein L27-A

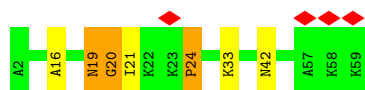


- Molecule 62: 60S ribosomal protein L28



- Molecule 63: 60S ribosomal protein L29

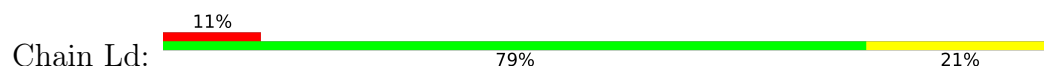




- Molecule 64: 60S ribosomal protein L30



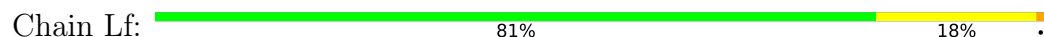
- Molecule 65: 60S ribosomal protein L31-A



- Molecule 66: 60S ribosomal protein L32



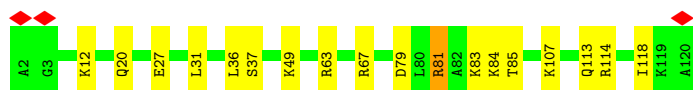
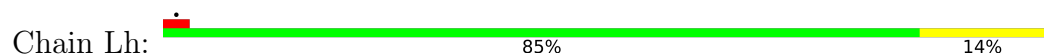
- Molecule 67: 60S ribosomal protein L33-A



- Molecule 68: 60S ribosomal protein L34-A

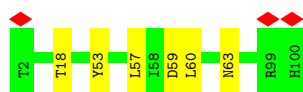


- Molecule 69: 60S ribosomal protein L35-A



- Molecule 70: 60S ribosomal protein L36-A

Chain Li:  94% 6%



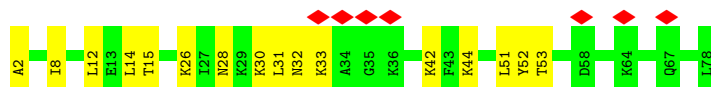
- Molecule 71: 60S ribosomal protein L37-A

Chain Lj:  73% 27%



- Molecule 72: 60S ribosomal protein L38

Chain Lk:  9% 79% 21%



- Molecule 73: 60S ribosomal protein L39

Chain Ll:  70% 30%



- Molecule 74: Ubiquitin-60S ribosomal protein L40

Chain Lm:  83% 17%



- Molecule 75: 60S ribosomal protein L41-A

Chain Ln:  72% 28%

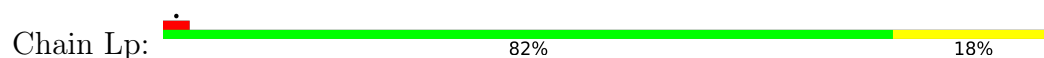


- Molecule 76: 60S ribosomal protein L42-A

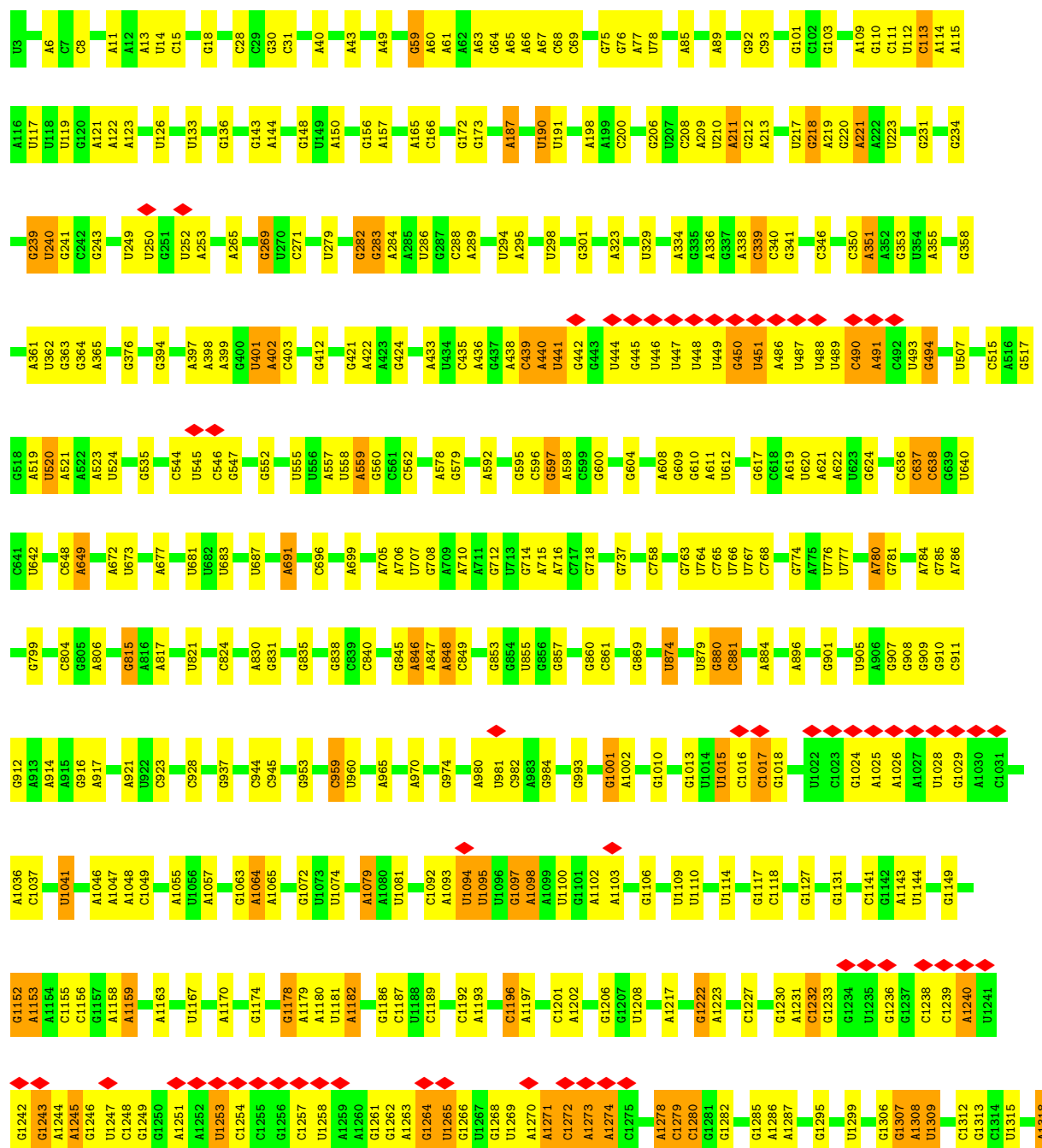
Chain Lo:  87% 13%



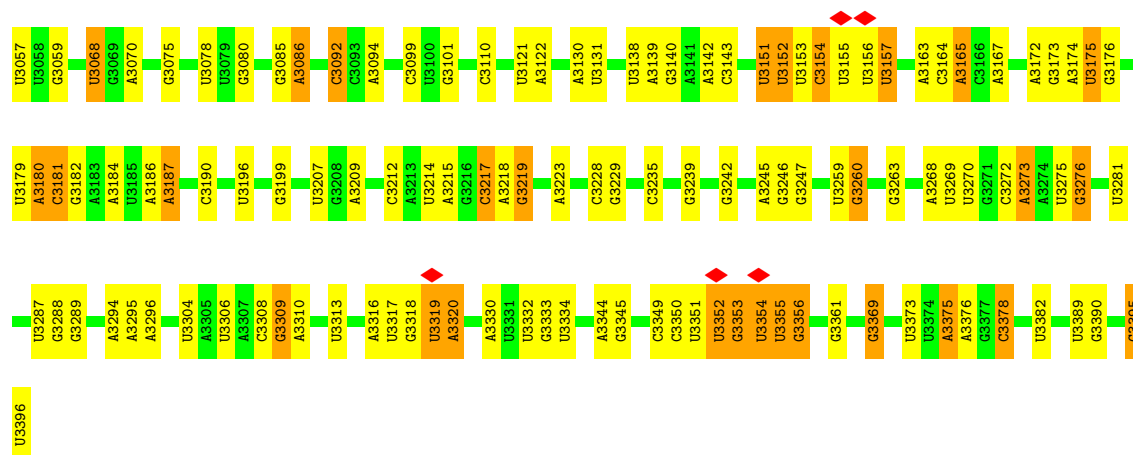
• Molecule 77: 60S ribosomal protein L43-A



• Molecule 78: 25S rRNA

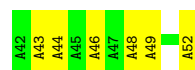


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G2912	A2801	A2673	U2551	G2435	A2312	G2185	U1935	A1816	U1694	U1568	G1444	C1320
G2913	A2802	G2674	C2552	U2436	U2313	G2186	C1943	U1817	A1695	U1569	G1445	U1321
G2914	A2803	G2675	U2553	G2437	G2314	A2188	G1949	U1818	A1696	U1570	A1446	U1322
G2918	C2810	G2676	A2554	A2438	G2315	A2189	G1949	U1819	U1702	U1571	U1323	U1323
G2918	C2810	G2677	G2555	A2439	G2323	C2192	G1952	U1820	U1703	A1572	U1324	U1325
U2923	G2814	U2681	G2556	G2442	G2324	C2192	G1952	U1821	U1704	G1573	A1452	
C2929	A2817	U2688	A2557	A2443	G2325	A2198	G1954	U1822	A1704	C1574	U1455	A1330
U2933	U2818	A2689	A2560	C2444	C2333	G2206	U1955	U1831	U1717	A1575	U1470	U1331
A2934	C2821	G2690	G2564	U2445	U2334	A2207	U1955	U1834	U1720	G1576	U1473	U1334
U2935	U2821	A2694	U2447	U2446	G2335	A2208	C2094	U1835	U1722	A1580	A1474	G1345
A2936	G2828	A2695	A2447	U2447	U2336	U2209	U2101	U1840	U1723	C1581	A1477	U1348
G2937	U2829	A2696	G2448	G2449	A2355	G2210	U2102	U1841	A1724	C1582	A1477	A1349
G2938	G2834	A2697	G2449	G2450	A2357	G2221	U2103	U1842	C1725	A1583	G1480	A1350
G2939	U2837	A2703	G2450	G2451	U2104	A2222	A2104	U1843	A1729	A1588	G1481	U1351
A2940	A2837	A2704	G2451	G2452	C2360	A2223	A2107	U1844	A1736	A1589	A1482	A1352
A2941	A2838	A2705	G2452	G2453	C2361	A2224	A2107	G1845	U1737	C1596	A1483	U1353
C2942	U2842	U2717	C2453	U2493	C2362	U2225	G2111	A1847	U1737	C1597	G1493	G1354
G2943	U2843	U2718	C2493	U2494	C2366	G2231	U2112	U1848	A1741	A1603	U1494	A1355
U2944	C2844	U2719	U2494	A2494	C2373	G2236	A2113	U1849	U1742	G1604	C1497	U1356
G2945	A2845	U2720	C2495	C2495	G2374	G2237	G2114	U1850	G1743	U1607	C1505	U1357
A2946	U2846	A2721	C2496	C2496	G2375	C2245	G2115	U1858	G1748	C1608	C1508	A1373
G2947	A2847	A2722	U2497	U2497	G2376	G2246	G2116	U1859	A1749	U1613	U1523	G1383
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G2972	U2860	C2742	A2500	U2501	G2389	A2255	G2121	A1866	A1760	U1629	C1527	A1386
G2972	U2861	C2742	U2501	U2502	U2390	C2256	G2122	A1867	U1761	U1630	U1533	G1389
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G2972	U2870	C2742	U2510	U2511	U2399	U2275	G2131	U1896	U1770	C1644	C1420	G1421
G2972	U2871	C2742	U2511	U2512	U2400	A2279	G2132	U1897	U1771	U1645	A1557	
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G2972	U2873	C2742	U2513	U2514	A2402	A2281	G2134	U1906	U1795	G1661	G1560	G1429
G2972	U2874	C2742	U2514	U2515	G2403	U2282	G2135	U1907	A1797	G1662	C1561	
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G2972	U2899	C2742	U2539	U2540	U2426	U2301	G2160	U1938				
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G2972	U2932	C2742	U2572	U2573	U2459	U2334	G2193	U1971				
G2972	U2933	C2742	U2573	U2574	U2460	U2335	G2194	U1972				
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- Molecule 79: mRNA

Chain 5: 45% 55%



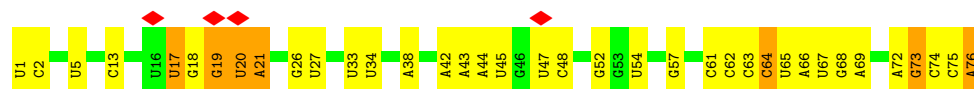
- Molecule 80: tRNA

Chain 7: 97% 61% 28% 12%



- Molecule 80: tRNA

Chain 6: 5% 51% 39% 9%



- Molecule 81: nascent chain

Chain A: 25% 50% 25%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	229084	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 ($e^-/\text{\AA}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.533	Depositor
Minimum map value	-0.254	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	433.6, 433.6, 433.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	LA	0.59	0/1933	0.67	0/2598
2	SA	0.28	0/1644	0.48	0/2249
3	LB	0.55	0/3146	0.60	0/4228
4	SB	0.36	0/1823	0.61	0/2447
5	C2	0.28	0/42053	0.40	1/65522 (0.0%)
6	SP	0.24	0/936	0.49	0/1259
7	SC	0.35	0/1656	0.52	0/2251
8	SD	0.26	0/1754	0.51	0/2361
9	SE	0.31	0/2097	0.55	0/2823
10	SF	0.28	0/1625	0.54	0/2197
11	SG	0.28	0/1839	0.54	0/2460
12	SH	0.27	0/1498	0.55	0/2019
13	SI	0.37	0/1501	0.62	1/2006 (0.0%)
14	SJ	0.29	0/1504	0.55	0/2016
15	SK	0.22	0/769	0.47	0/1039
16	SL	0.39	0/1185	0.54	0/1598
17	SM	0.25	0/883	0.69	0/1199
18	SN	0.38	0/1215	0.58	0/1638
19	SO	0.38	0/937	0.63	0/1261
20	SQ	0.28	0/1125	0.54	0/1510
21	SR	0.25	0/957	0.56	0/1283
22	SS	0.27	0/1211	0.55	0/1628
23	ST	0.26	0/1130	0.48	0/1517
24	SU	0.28	0/807	0.50	0/1091
25	SV	0.31	0/682	0.64	1/921 (0.1%)
26	SW	0.39	0/1038	0.58	1/1395 (0.1%)
27	SX	0.39	0/1139	0.57	0/1518
28	SY	0.27	0/1087	0.54	0/1449
29	SZ	0.26	0/661	0.51	0/888
30	Sa	0.43	1/782 (0.1%)	0.75	0/1047
31	Sb	0.32	0/620	0.59	0/838
32	Sd	0.28	0/452	0.48	0/600
33	Se	0.26	0/480	0.49	0/639
34	Sf	0.22	0/567	0.58	0/764

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Sg	0.22	0/2436	0.52	0/3318
36	Sc	0.29	0/493	0.55	0/663
37	C4	0.36	0/2883	0.38	0/4491
38	C3	0.40	0/3746	0.42	0/5832
39	LC	0.53	0/2800	0.58	0/3790
40	LD	0.41	0/2400	0.55	0/3239
41	LE	0.40	0/1327	0.59	1/1790 (0.1%)
42	LF	0.55	0/1821	0.60	0/2451
43	LG	0.43	0/1836	0.59	0/2481
44	LH	0.41	0/1529	0.51	0/2060
45	LI	0.49	0/1801	0.58	0/2416
46	LJ	0.39	0/1371	0.59	0/1838
47	LL	0.51	0/1568	0.61	0/2106
48	LM	0.44	0/1068	0.58	0/1438
49	LN	0.60	0/1757	0.62	1/2354 (0.0%)
50	LO	0.55	0/1585	0.58	0/2128
51	LP	0.54	0/1439	0.59	0/1938
52	LQ	0.56	1/1465 (0.1%)	0.58	0/1965
53	LR	0.47	0/1532	0.59	0/2043
54	LS	0.49	0/1473	0.57	1/1980 (0.1%)
55	LT	0.53	0/1300	0.58	0/1743
56	LU	0.34	0/812	0.50	0/1099
57	LV	0.54	0/1018	0.55	0/1369
58	LW	0.40	0/850	0.50	0/1152
59	LX	0.45	0/979	0.54	0/1321
60	LY	0.47	0/995	0.57	0/1329
61	LZ	0.41	0/1118	0.57	0/1497
62	La	0.56	0/1204	0.63	0/1612
63	Lb	0.45	0/473	0.64	0/629
64	Lc	0.43	0/745	0.54	0/1001
65	Ld	0.49	0/890	0.57	0/1196
66	Le	0.51	0/1038	0.54	0/1390
67	Lf	0.60	0/868	0.67	1/1168 (0.1%)
68	Lg	0.51	0/890	0.54	0/1189
69	Lh	0.45	0/978	0.58	0/1301
70	Li	0.41	0/772	0.58	0/1026
71	Lj	0.61	0/685	0.63	0/908
72	Lk	0.38	0/618	0.55	0/826
73	Ll	0.57	0/443	0.65	0/588
74	Lm	0.48	0/423	0.50	0/562
75	Ln	0.52	0/230	0.75	0/296
76	Lo	0.48	0/836	0.60	0/1104
77	Lp	0.51	0/701	0.58	0/934

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	C1	0.41	0/76214	0.43	0/118821
79	5	0.27	0/274	0.33	0/425
80	6	0.48	0/1804	0.41	0/2809
80	7	0.16	0/1804	0.37	0/2809
81	A	0.35	0/39	0.97	0/45
All	All	0.39	2/218067 (0.0%)	0.48	8/320729 (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
3	LB	0	3
4	SB	0	4
9	SE	0	1
11	SG	0	1
12	SH	0	1
13	SI	0	1
14	SJ	0	1
16	SL	0	1
17	SM	0	4
19	SO	0	1
20	SQ	0	2
22	SS	0	1
26	SW	0	1
27	SX	0	1
29	SZ	0	1
30	Sa	0	3
31	Sb	0	1
34	Sf	0	1
39	LC	0	1
43	LG	0	2
48	LM	0	1
50	LO	0	1
53	LR	0	1
59	LX	0	1
60	LY	0	1
61	LZ	0	1
62	La	0	1
63	Lb	0	3
69	Lh	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
81	A	0	2
All	All	0	45

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	LQ	41	ASP	C-N	5.05	1.39	1.33
30	Sa	12	LYS	CA-CB	-5.01	1.46	1.53

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	SW	28	ARG	C-N-CD	-7.70	103.67	120.60
54	LS	140	VAL	N-CA-C	-6.13	106.97	112.12
25	SV	41	GLU	N-CA-CB	-5.84	107.51	114.17
67	Lf	21	ARG	N-CA-C	5.58	119.66	112.41
13	SI	80	GLY	N-CA-C	5.47	118.56	110.63

There are no chirality outliers.

5 of 45 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	LB	127	LYS	Peptide
3	LB	139	GLN	Peptide
3	LB	141	GLY	Peptide
4	SB	44	GLY	Peptide
4	SB	81	PHE	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	LA	1899	0	1957	31	0
2	SA	1603	0	1610	27	0
3	LB	3075	0	3142	62	0
4	SB	1798	0	1890	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C2	37604	0	18919	405	0
6	SP	916	0	941	12	0
7	SC	1626	0	1715	35	0
8	SD	1729	0	1812	33	0
9	SE	2056	0	2140	39	0
10	SF	1605	0	1669	32	0
11	SG	1815	0	1894	48	0
12	SH	1473	0	1555	27	0
13	SI	1476	0	1501	44	0
14	SJ	1479	0	1556	19	0
15	SK	752	0	719	7	0
16	SL	1159	0	1225	14	0
17	SM	875	0	878	26	0
18	SN	1192	0	1255	20	0
19	SO	926	0	950	21	0
20	SQ	1105	0	1166	29	0
21	SR	948	0	990	18	0
22	SS	1192	0	1222	28	0
23	ST	1112	0	1124	18	0
24	SU	797	0	863	12	0
25	SV	673	0	662	15	0
26	SW	1021	0	1060	9	0
27	SX	1121	0	1196	24	0
28	SY	1073	0	1132	22	0
29	SZ	651	0	682	13	0
30	Sa	769	0	818	22	0
31	Sb	610	0	633	11	0
32	Sd	442	0	432	12	0
33	Se	472	0	521	6	0
34	Sf	556	0	549	19	0
35	Sg	2383	0	2332	40	0
36	Sc	491	0	524	10	0
37	C4	2579	0	1304	17	0
38	C3	3353	0	1695	36	0
39	LC	2748	0	2859	44	0
40	LD	2351	0	2294	42	0
41	LE	1305	0	1370	18	0
42	LF	1784	0	1862	25	0
43	LG	1804	0	1877	28	0
44	LH	1508	0	1572	15	0
45	LI	1764	0	1804	26	0
46	LJ	1350	0	1381	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	LL	1543	0	1608	28	0
48	LM	1053	0	1149	21	0
49	LN	1720	0	1779	33	0
50	LO	1555	0	1659	20	0
51	LP	1416	0	1433	20	0
52	LQ	1441	0	1543	20	0
53	LR	1515	0	1606	24	0
54	LS	1437	0	1475	20	0
55	LT	1276	0	1323	18	0
56	LU	796	0	812	8	0
57	LV	1003	0	1048	8	0
58	LW	836	0	709	9	0
59	LX	964	0	1025	16	0
60	LY	984	0	1075	14	0
61	LZ	1092	0	1155	16	0
62	La	1173	0	1215	18	0
63	Lb	462	0	491	8	0
64	Lc	737	0	792	5	0
65	Ld	876	0	912	15	0
66	Le	1017	0	1081	14	0
67	Lf	850	0	880	14	0
68	Lg	880	0	945	14	0
69	Lh	969	0	1078	15	0
70	Li	766	0	844	4	0
71	Lj	670	0	677	22	0
72	Lk	612	0	682	12	0
73	Ll	436	0	475	12	0
74	Lm	417	0	459	9	0
75	Ln	229	0	273	6	0
76	Lo	824	0	892	9	0
77	Lp	694	0	738	11	0
78	C1	68091	0	34216	507	0
79	5	242	0	122	1	0
80	6	1616	0	815	36	0
80	7	1616	0	816	12	0
81	A	41	0	56	18	0
All	All	202869	0	149110	1946	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 6.

The worst 5 of 1946 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)
80:6:76:A:H4'	81:A:177[A]:LYS:HG3	1.16	1.10
78:C1:2258:U:O2'	78:C1:2259:A:O5'	1.69	1.10
46:LJ:55:ARG:NH1	80:6:20:U:OP1	1.87	1.06
44:LH:41:ILE:HD11	44:LH:67:ALA:HB1	1.35	1.05
80:6:76:A:C4'	81:A:177[A]:LYS:HG3	1.86	1.05

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	
1	LA	249/251 (99%)	231 (93%)	17 (7%)	1 (0%)	30	61
2	SA	204/206 (99%)	182 (89%)	20 (10%)	2 (1%)	12	41
3	LB	384/386 (100%)	347 (90%)	36 (9%)	1 (0%)	36	67
4	SB	222/232 (96%)	192 (86%)	27 (12%)	3 (1%)	9	34
6	SP	115/117 (98%)	101 (88%)	14 (12%)	0	100	100
7	SC	214/216 (99%)	197 (92%)	16 (8%)	1 (0%)	24	57
8	SD	220/222 (99%)	211 (96%)	9 (4%)	0	100	100
9	SE	256/258 (99%)	233 (91%)	22 (9%)	1 (0%)	30	61
10	SF	204/206 (99%)	183 (90%)	21 (10%)	0	100	100
11	SG	226/228 (99%)	204 (90%)	18 (8%)	4 (2%)	6	28
12	SH	182/184 (99%)	161 (88%)	19 (10%)	2 (1%)	11	39
13	SI	183/187 (98%)	165 (90%)	15 (8%)	3 (2%)	7	30
14	SJ	182/184 (99%)	165 (91%)	15 (8%)	2 (1%)	11	39
15	SK	90/92 (98%)	77 (86%)	13 (14%)	0	100	100
16	SL	142/144 (99%)	128 (90%)	14 (10%)	0	100	100
17	SM	119/121 (98%)	79 (66%)	35 (29%)	5 (4%)	2	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	SN	148/150 (99%)	134 (90%)	13 (9%)	1 (1%)	18	49
19	SO	125/127 (98%)	111 (89%)	14 (11%)	0	100	100
20	SQ	139/141 (99%)	122 (88%)	17 (12%)	0	100	100
21	SR	117/125 (94%)	107 (92%)	9 (8%)	1 (1%)	14	44
22	SS	143/145 (99%)	129 (90%)	10 (7%)	4 (3%)	4	20
23	ST	141/143 (99%)	126 (89%)	15 (11%)	0	100	100
24	SU	98/100 (98%)	90 (92%)	8 (8%)	0	100	100
25	SV	85/87 (98%)	72 (85%)	12 (14%)	1 (1%)	10	37
26	SW	127/129 (98%)	116 (91%)	11 (9%)	0	100	100
27	SX	142/144 (99%)	119 (84%)	22 (16%)	1 (1%)	18	49
28	SY	132/134 (98%)	120 (91%)	11 (8%)	1 (1%)	16	47
29	SZ	80/82 (98%)	67 (84%)	12 (15%)	1 (1%)	9	35
30	Sa	95/97 (98%)	72 (76%)	19 (20%)	4 (4%)	2	13
31	Sb	79/81 (98%)	71 (90%)	8 (10%)	0	100	100
32	Sd	51/53 (96%)	49 (96%)	2 (4%)	0	100	100
33	Se	58/60 (97%)	50 (86%)	8 (14%)	0	100	100
34	Sf	71/73 (97%)	47 (66%)	24 (34%)	0	100	100
35	Sg	310/312 (99%)	281 (91%)	29 (9%)	0	100	100
36	Sc	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
39	LC	359/361 (99%)	332 (92%)	25 (7%)	2 (1%)	21	52
40	LD	292/294 (99%)	273 (94%)	18 (6%)	1 (0%)	36	67
41	LE	163/175 (93%)	147 (90%)	16 (10%)	0	100	100
42	LF	220/222 (99%)	209 (95%)	11 (5%)	0	100	100
43	LG	231/233 (99%)	209 (90%)	22 (10%)	0	100	100
44	LH	189/191 (99%)	172 (91%)	17 (9%)	0	100	100
45	LI	216/218 (99%)	205 (95%)	11 (5%)	0	100	100
46	LJ	167/169 (99%)	146 (87%)	20 (12%)	1 (1%)	21	52
47	LL	191/193 (99%)	164 (86%)	24 (13%)	3 (2%)	7	30
48	LM	134/136 (98%)	121 (90%)	13 (10%)	0	100	100
49	LN	201/203 (99%)	185 (92%)	16 (8%)	0	100	100
50	LO	195/197 (99%)	185 (95%)	8 (4%)	2 (1%)	12	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	LP	181/183 (99%)	166 (92%)	15 (8%)	0	100	100
52	LQ	183/185 (99%)	169 (92%)	14 (8%)	0	100	100
53	LR	186/188 (99%)	179 (96%)	5 (3%)	2 (1%)	11	39
54	LS	169/171 (99%)	162 (96%)	7 (4%)	0	100	100
55	LT	157/159 (99%)	143 (91%)	14 (9%)	0	100	100
56	LU	98/100 (98%)	90 (92%)	8 (8%)	0	100	100
57	LV	134/136 (98%)	124 (92%)	10 (8%)	0	100	100
58	LW	124/126 (98%)	109 (88%)	15 (12%)	0	100	100
59	LX	119/121 (98%)	109 (92%)	9 (8%)	1 (1%)	16	47
60	LY	123/125 (98%)	117 (95%)	6 (5%)	0	100	100
61	LZ	133/135 (98%)	118 (89%)	15 (11%)	0	100	100
62	La	146/148 (99%)	121 (83%)	23 (16%)	2 (1%)	9	34
63	Lb	56/58 (97%)	48 (86%)	7 (12%)	1 (2%)	6	28
64	Lc	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
65	Ld	107/109 (98%)	95 (89%)	12 (11%)	0	100	100
66	Le	125/127 (98%)	117 (94%)	8 (6%)	0	100	100
67	Lf	104/106 (98%)	102 (98%)	2 (2%)	0	100	100
68	Lg	110/112 (98%)	107 (97%)	3 (3%)	0	100	100
69	Lh	117/119 (98%)	108 (92%)	9 (8%)	0	100	100
70	Li	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
71	Lj	83/85 (98%)	78 (94%)	5 (6%)	0	100	100
72	Lk	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
73	Ll	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
74	Lm	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
75	Ln	23/25 (92%)	23 (100%)	0	0	100	100
76	Lo	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
77	Lp	89/91 (98%)	83 (93%)	6 (7%)	0	100	100
81	A	2/4 (50%)	1 (50%)	1 (50%)	0	100	100
All	All	10986/11162 (98%)	9950 (91%)	982 (9%)	54 (0%)	26	57

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	SG	68	LEU
13	SI	10	LYS
30	Sa	84	VAL
50	LO	111[A]	PRO
62	La	78	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	LA	190/193 (98%)	190 (100%)	0	100	100
2	SA	170/173 (98%)	170 (100%)	0	100	100
3	LB	320/322 (99%)	318 (99%)	2 (1%)	78	83
4	SB	200/205 (98%)	200 (100%)	0	100	100
6	SP	95/98 (97%)	95 (100%)	0	100	100
7	SC	175/175 (100%)	175 (100%)	0	100	100
8	SD	182/182 (100%)	182 (100%)	0	100	100
9	SE	220/220 (100%)	220 (100%)	0	100	100
10	SF	172/173 (99%)	171 (99%)	1 (1%)	78	83
11	SG	189/195 (97%)	189 (100%)	0	100	100
12	SH	163/165 (99%)	163 (100%)	0	100	100
13	SI	148/149 (99%)	148 (100%)	0	100	100
14	SJ	156/157 (99%)	156 (100%)	0	100	100
15	SK	77/85 (91%)	77 (100%)	0	100	100
16	SL	129/129 (100%)	129 (100%)	0	100	100
17	SM	88/98 (90%)	88 (100%)	0	100	100
18	SN	127/127 (100%)	127 (100%)	0	100	100
19	SO	91/96 (95%)	91 (100%)	0	100	100
20	SQ	117/117 (100%)	117 (100%)	0	100	100
21	SR	101/113 (89%)	101 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	SS	128/128 (100%)	128 (100%)	0	100	100
23	ST	115/115 (100%)	115 (100%)	0	100	100
24	SU	93/93 (100%)	93 (100%)	0	100	100
25	SV	71/74 (96%)	71 (100%)	0	100	100
26	SW	110/110 (100%)	110 (100%)	0	100	100
27	SX	119/119 (100%)	119 (100%)	0	100	100
28	SY	112/112 (100%)	112 (100%)	0	100	100
29	SZ	67/73 (92%)	66 (98%)	1 (2%)	57	75
30	Sa	83/83 (100%)	83 (100%)	0	100	100
31	Sb	70/70 (100%)	70 (100%)	0	100	100
32	Sd	47/47 (100%)	47 (100%)	0	100	100
33	Se	50/51 (98%)	50 (100%)	0	100	100
34	Sf	56/64 (88%)	56 (100%)	0	100	100
35	Sg	250/257 (97%)	249 (100%)	1 (0%)	84	86
36	Sc	55/56 (98%)	55 (100%)	0	100	100
39	LC	288/288 (100%)	287 (100%)	1 (0%)	86	87
40	LD	241/243 (99%)	241 (100%)	0	100	100
41	LE	138/154 (90%)	138 (100%)	0	100	100
42	LF	186/186 (100%)	186 (100%)	0	100	100
43	LG	187/191 (98%)	187 (100%)	0	100	100
44	LH	168/171 (98%)	168 (100%)	0	100	100
45	LI	185/185 (100%)	184 (100%)	1 (0%)	81	85
46	LJ	146/147 (99%)	146 (100%)	0	100	100
47	LL	154/154 (100%)	154 (100%)	0	100	100
48	LM	107/107 (100%)	107 (100%)	0	100	100
49	LN	175/175 (100%)	175 (100%)	0	100	100
50	LO	160/160 (100%)	159 (99%)	1 (1%)	78	83
51	LP	138/145 (95%)	138 (100%)	0	100	100
52	LQ	150/150 (100%)	150 (100%)	0	100	100
53	LR	152/153 (99%)	152 (100%)	0	100	100
54	LS	155/155 (100%)	155 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	LT	136/136 (100%)	136 (100%)	0	100	100
56	LU	87/87 (100%)	87 (100%)	0	100	100
57	LV	104/104 (100%)	104 (100%)	0	100	100
58	LW	56/107 (52%)	56 (100%)	0	100	100
59	LX	104/105 (99%)	104 (100%)	0	100	100
60	LY	108/108 (100%)	108 (100%)	0	100	100
61	LZ	115/115 (100%)	115 (100%)	0	100	100
62	La	118/118 (100%)	118 (100%)	0	100	100
63	Lb	46/46 (100%)	46 (100%)	0	100	100
64	Lc	81/81 (100%)	81 (100%)	0	100	100
65	Ld	92/96 (96%)	92 (100%)	0	100	100
66	Le	108/109 (99%)	108 (100%)	0	100	100
67	Lf	90/90 (100%)	89 (99%)	1 (1%)	65	78
68	Lg	95/95 (100%)	95 (100%)	0	100	100
69	Lh	104/104 (100%)	103 (99%)	1 (1%)	68	79
70	Li	80/81 (99%)	80 (100%)	0	100	100
71	Lj	69/69 (100%)	69 (100%)	0	100	100
72	Lk	68/68 (100%)	68 (100%)	0	100	100
73	Ll	45/45 (100%)	45 (100%)	0	100	100
74	Lm	47/47 (100%)	47 (100%)	0	100	100
75	Ln	22/23 (96%)	22 (100%)	0	100	100
76	Lo	87/88 (99%)	87 (100%)	0	100	100
77	Lp	71/71 (100%)	71 (100%)	0	100	100
81	A	4/3 (133%)	0	4 (100%)	0	0
All	All	9203/9384 (98%)	9189 (100%)	14 (0%)	87	89

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	LO	34[A]	VAL
67	Lf	20	LYS
81	A	177[B]	LYS
81	A	176	LYS
81	A	177[A]	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 90 such sidechains are listed below:

Mol	Chain	Res	Type
45	LI	73	ASN
55	LT	22	HIS
47	LL	114	GLN
52	LQ	5	HIS
60	LY	120	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
37	C4	120/121 (99%)	14 (11%)	1 (0%)
38	C3	157/158 (99%)	35 (22%)	2 (1%)
5	C2	1768/1771 (99%)	525 (29%)	54 (3%)
78	C1	3180/3184 (99%)	669 (21%)	44 (1%)
79	5	10/11 (90%)	5 (50%)	0
80	6	75/76 (98%)	12 (16%)	0
80	7	75/76 (98%)	22 (29%)	4 (5%)
All	All	5385/5397 (99%)	1282 (23%)	105 (1%)

5 of 1282 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	C2	2	A
5	C2	4	C
5	C2	17	C
5	C2	25	C
5	C2	26	A

5 of 105 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
78	C1	13	A
78	C1	1273	A
78	C1	3350	C
78	C1	239	G
78	C1	846	A

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
78	C1	3
5	C2	2
13	SI	1

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C1	1955:U	O3'	2093:A	P	26.47
1	SI	123:LYS	C	135:LYS	N	20.93
1	C1	2452:G	O3'	2492:C	P	17.29
1	C2	658:C	O3'	676:G	P	16.25
1	C2	714:G	O3'	726:C	P	10.98

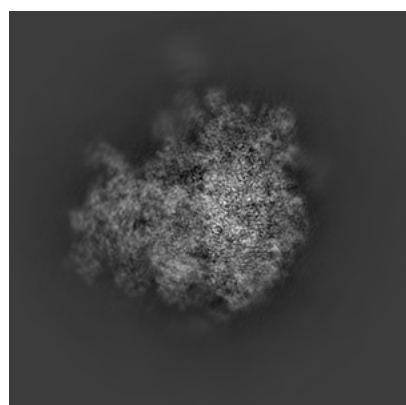
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10397. These allow visual inspection of the internal detail of the map and identification of artifacts.

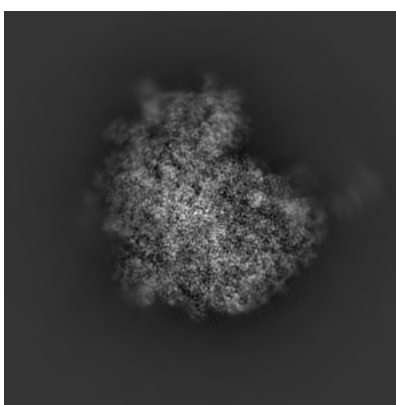
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

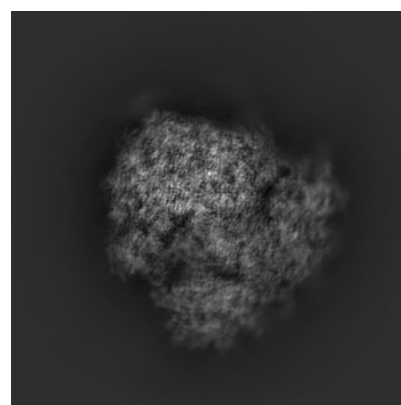
6.1.1 Primary map



X



Y

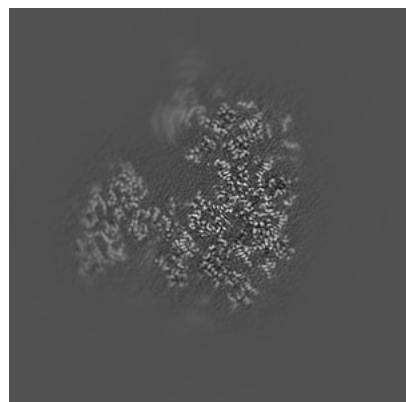


Z

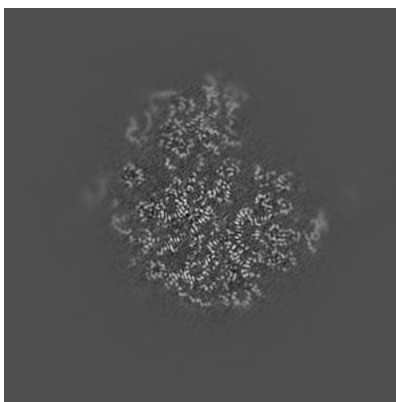
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

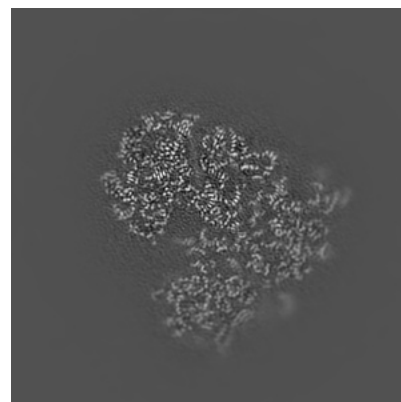
6.2.1 Primary map



X Index: 200



Y Index: 200

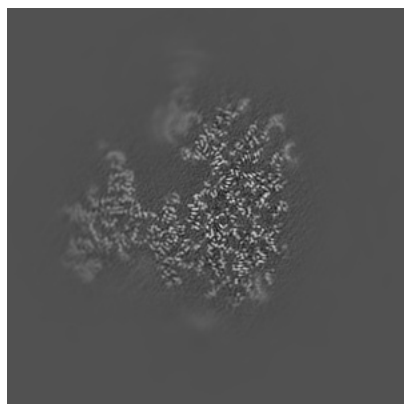


Z Index: 200

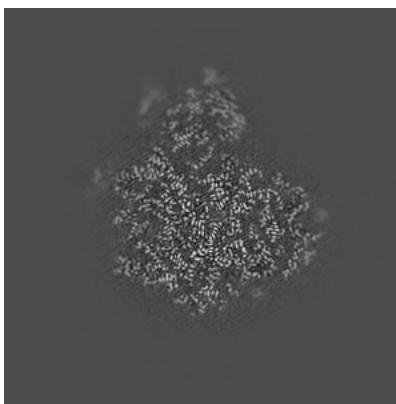
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

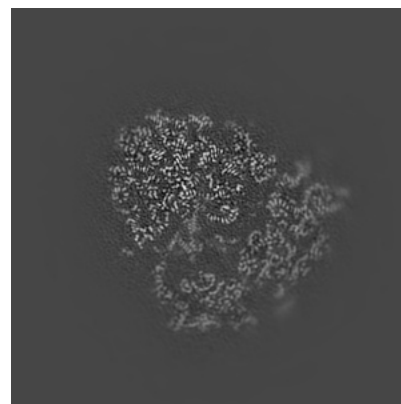
6.3.1 Primary map



X Index: 207



Y Index: 215

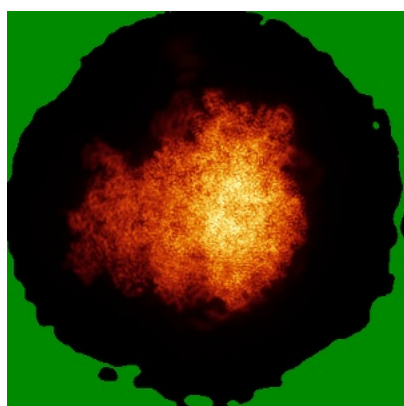


Z Index: 210

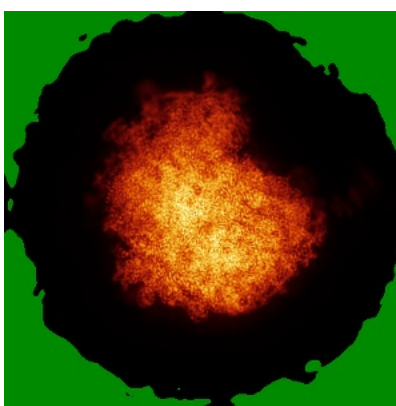
The images above show the largest variance slices of the map in three orthogonal directions.

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

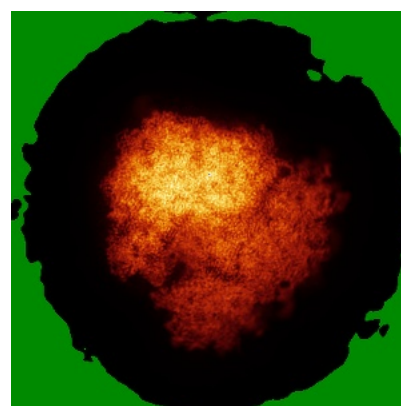
6.4.1 Primary map



X



Y

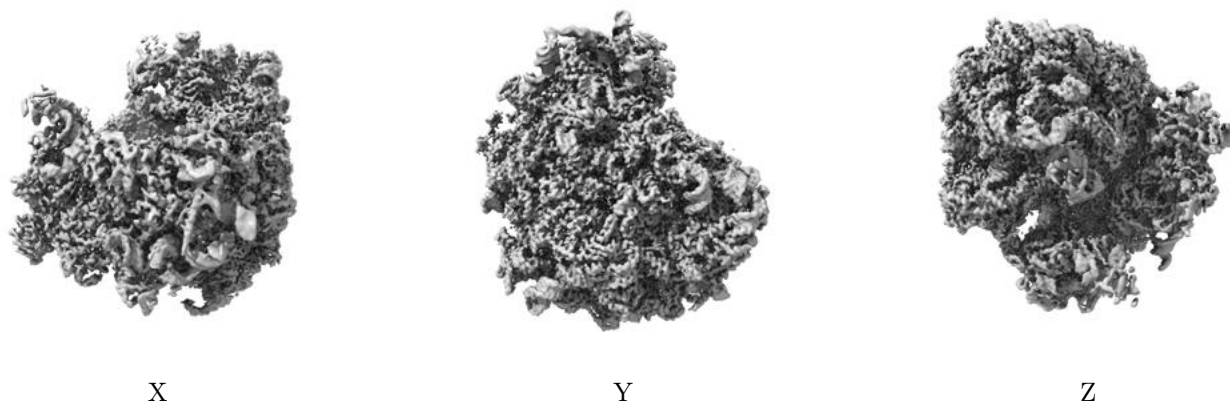


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

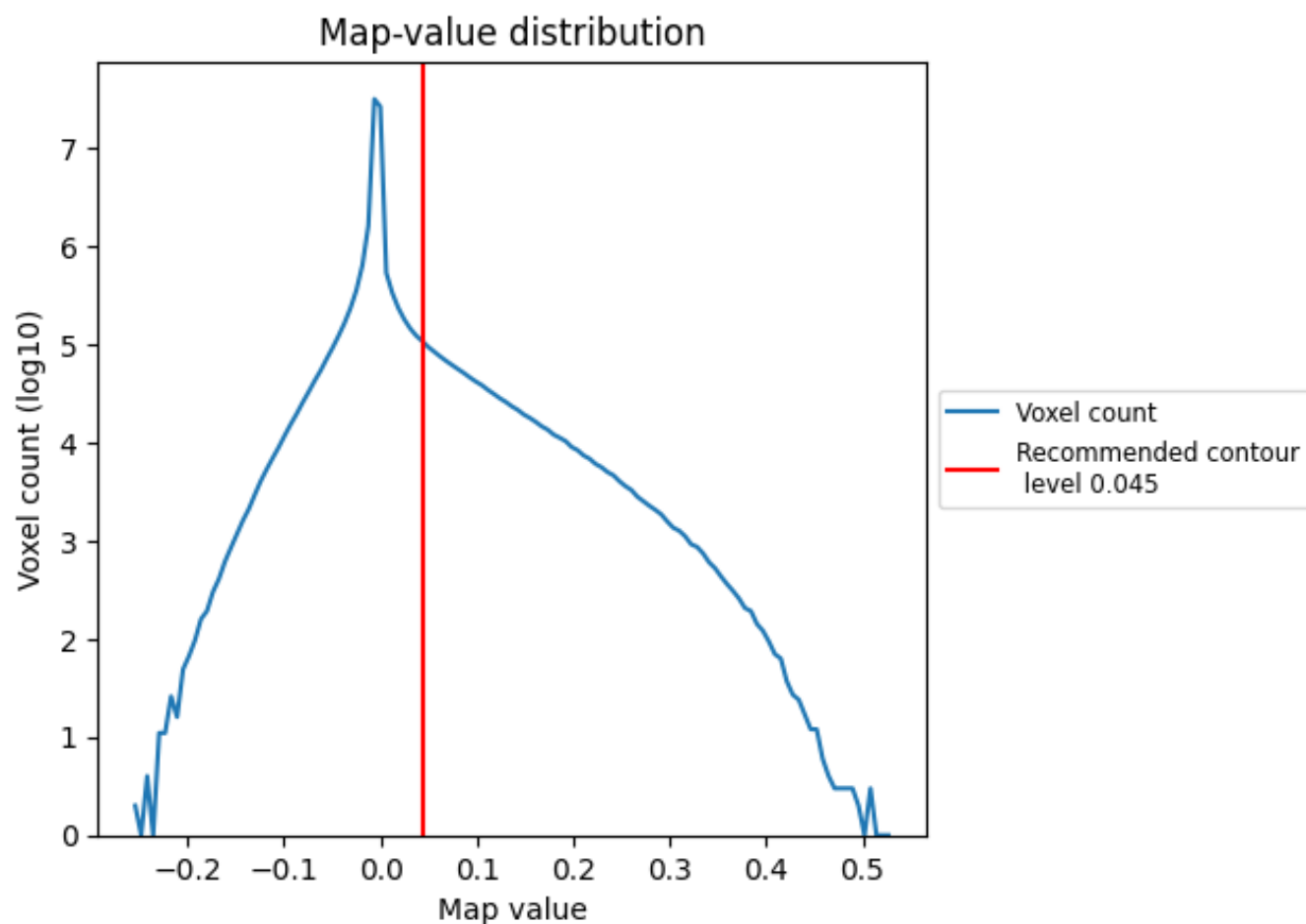
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

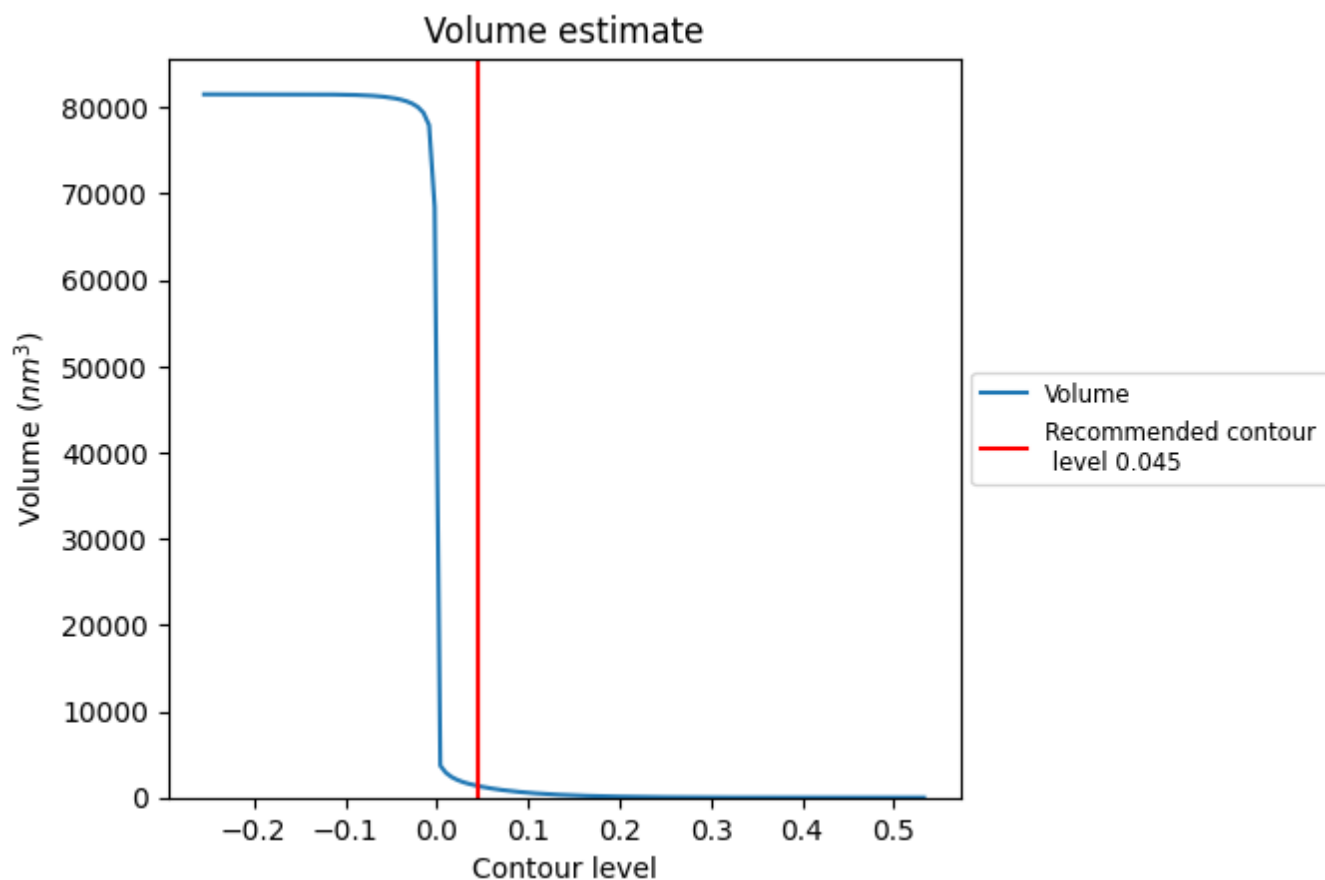
This section contains the results of statistical analysis of the map.

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.

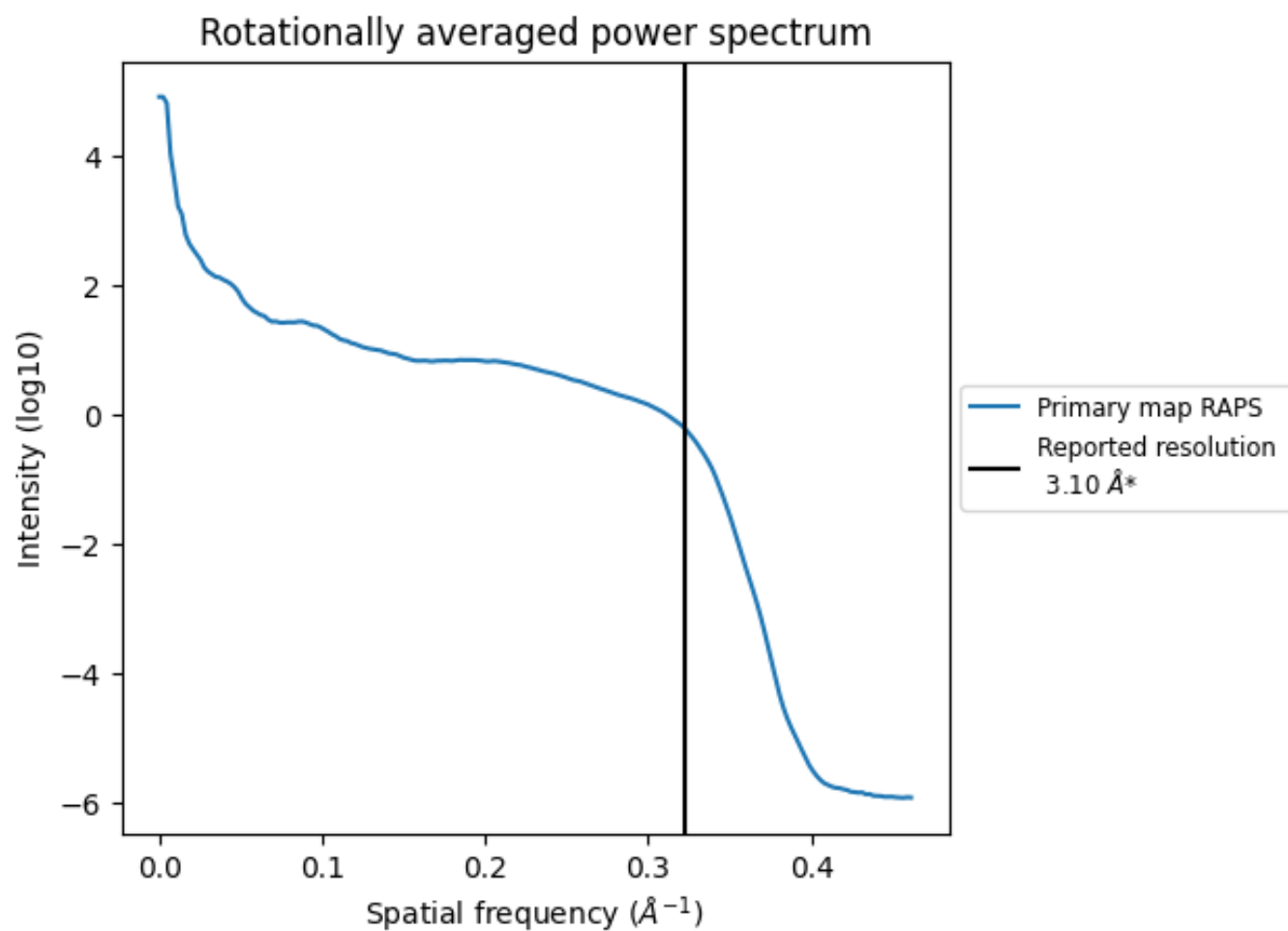
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1348 nm³; this corresponds to an approximate mass of 1218 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 ⓘ

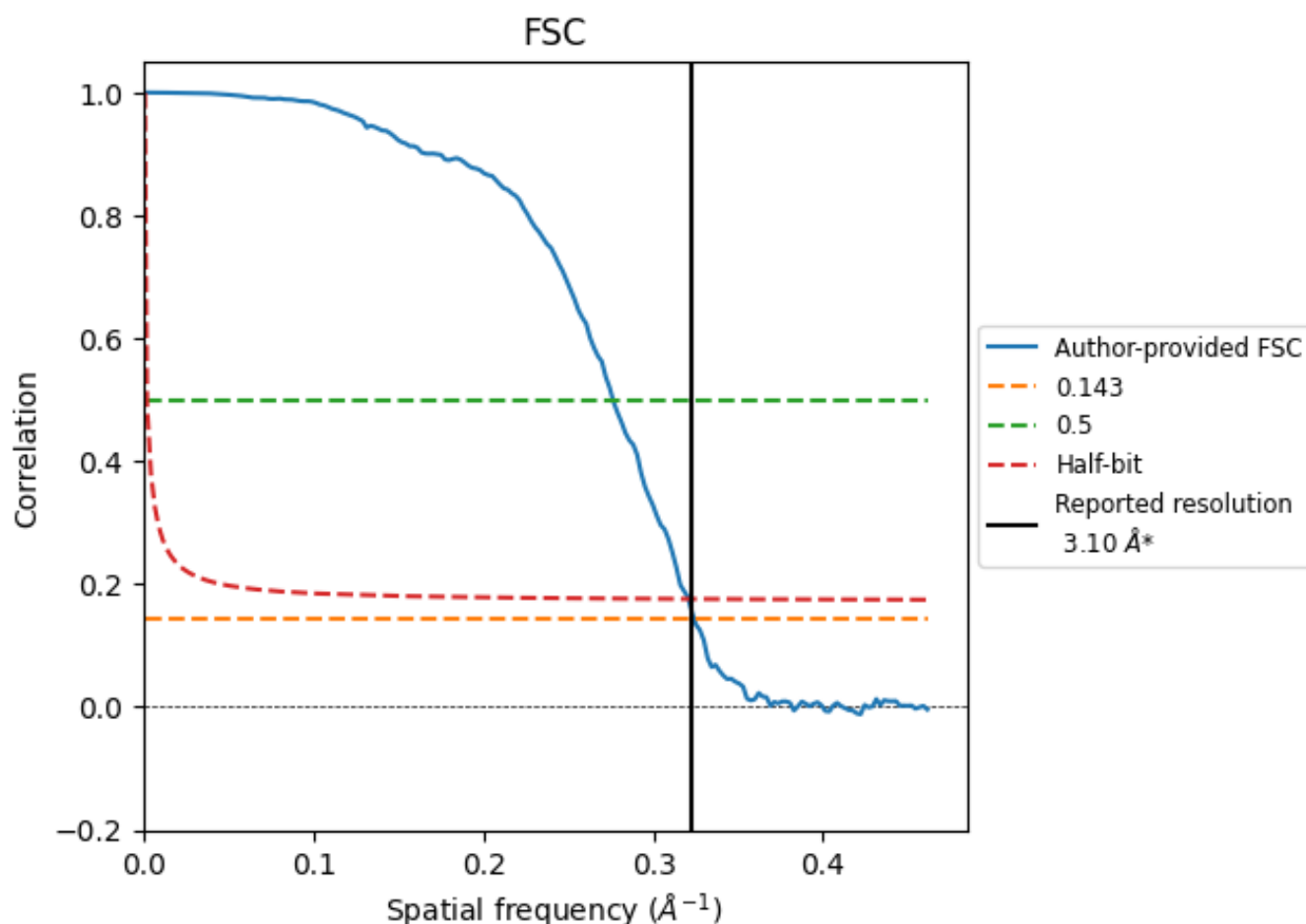


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

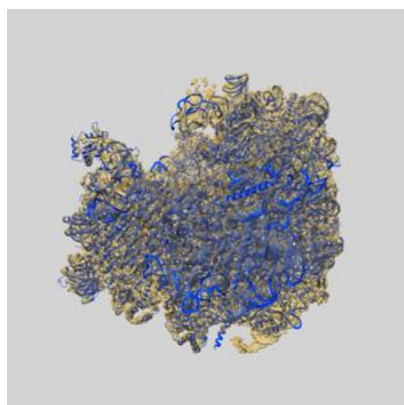
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.09	3.62	3.12
Unmasked-calculated*	-	-	-

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

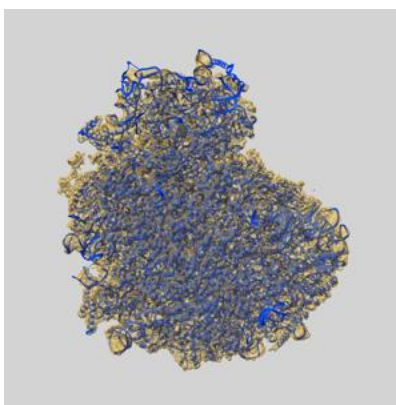
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10397 and PDB model 6T7T. Per-residue inclusion information can be found in section [3](#) on page [19](#).

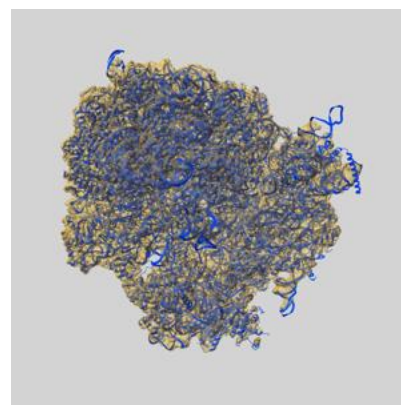
9.1 Map-model overlay [i](#)



X



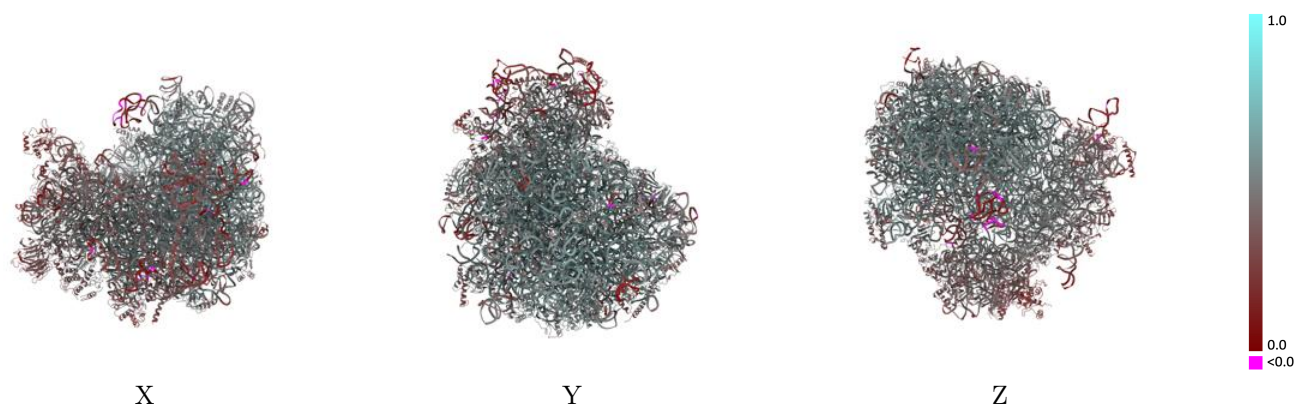
Y



Z

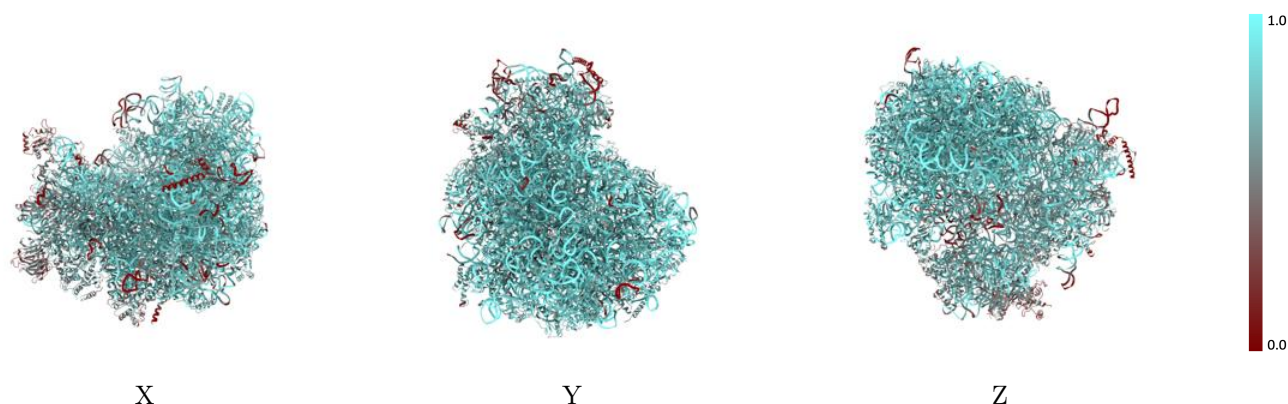
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



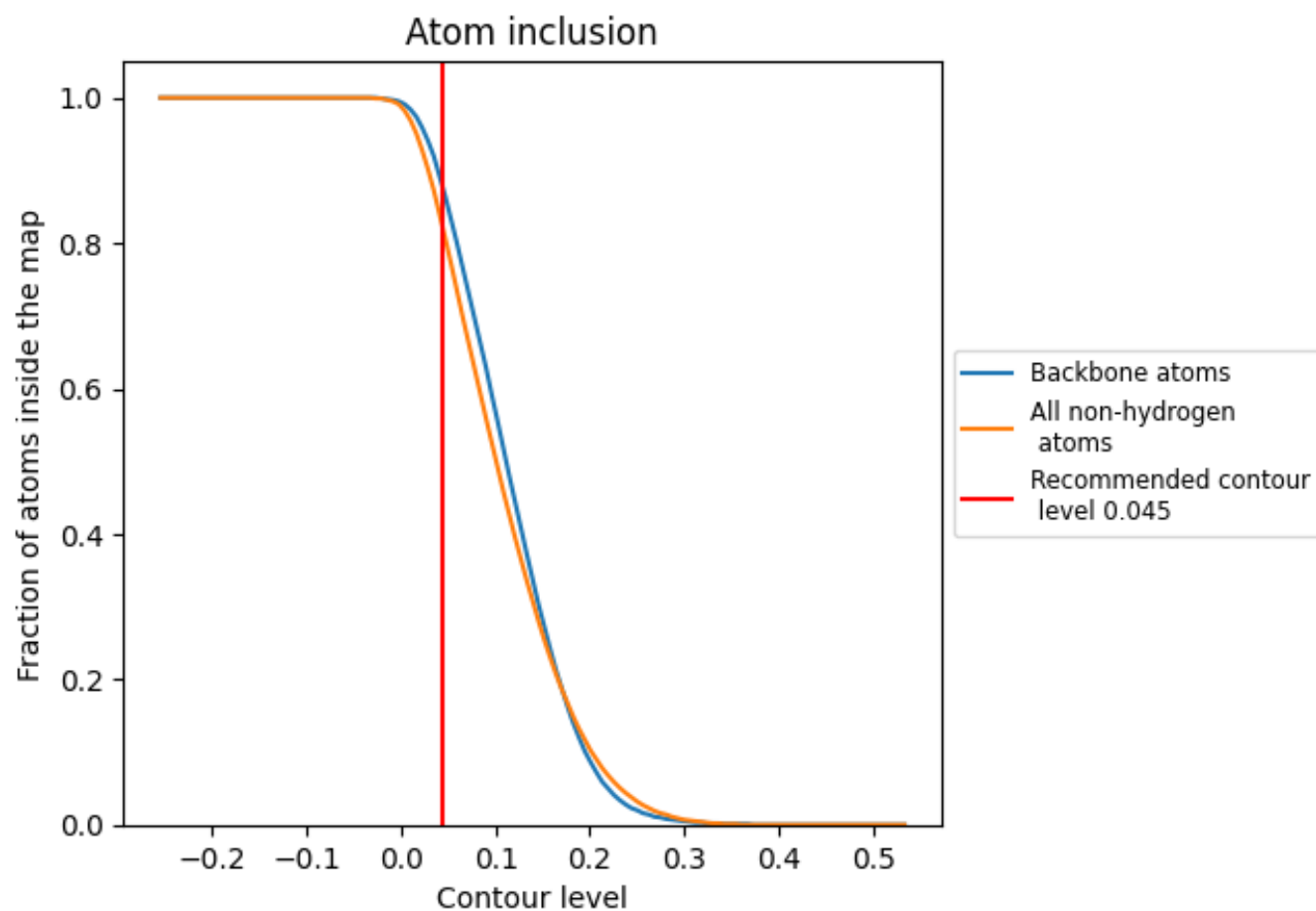
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.045).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8180	 0.4880
5	 0.8430	 0.5060
6	 0.8900	 0.4990
7	 0.0310	 0.2020
A	 0.5310	 0.5220
C1	 0.9240	 0.5340
C2	 0.8580	 0.4450
C3	 0.9440	 0.5450
C4	 0.9610	 0.5380
LA	 0.8470	 0.5610
LB	 0.8530	 0.5390
LC	 0.8250	 0.5300
LD	 0.7700	 0.4760
LE	 0.7730	 0.4820
LF	 0.8270	 0.5200
LG	 0.7430	 0.4690
LH	 0.7820	 0.5080
LI	 0.7920	 0.5190
LJ	 0.7440	 0.4700
LL	 0.8080	 0.5200
LM	 0.8110	 0.5020
LN	 0.8640	 0.5640
LO	 0.8360	 0.5370
LP	 0.8150	 0.5320
LQ	 0.8500	 0.5470
LR	 0.7380	 0.4850
LS	 0.8290	 0.5370
LT	 0.8270	 0.5460
LU	 0.7150	 0.4460
LV	 0.8110	 0.5470
LW	 0.4960	 0.4240
LX	 0.7730	 0.5030
LY	 0.7870	 0.5040
LZ	 0.7710	 0.4760
La	 0.8500	 0.5500



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Chain	Atom inclusion	Q-score
Lb	 0.7740	 0.5080
Lc	 0.7670	 0.4810
Ld	 0.7690	 0.5160
Le	 0.8300	 0.5490
Lf	 0.8770	 0.5640
Lg	 0.7870	 0.5170
Lh	 0.7760	 0.4820
Li	 0.7610	 0.4920
Lj	 0.8790	 0.5590
Lk	 0.6860	 0.4610
Ll	 0.8510	 0.5480
Lm	 0.7940	 0.5330
Ln	 0.7310	 0.5130
Lo	 0.8160	 0.5350
Lp	 0.7760	 0.5390
SA	 0.6320	 0.4080
SB	 0.6650	 0.4520
SC	 0.6860	 0.4600
SD	 0.5490	 0.3990
SE	 0.6530	 0.4390
SF	 0.6160	 0.3990
SG	 0.6210	 0.3900
SH	 0.5790	 0.3820
SI	 0.7250	 0.4780
SJ	 0.6370	 0.4120
SK	 0.5460	 0.3440
SL	 0.7350	 0.5000
SM	 0.2570	 0.2250
SN	 0.7330	 0.4700
SO	 0.7310	 0.4770
SP	 0.5700	 0.3820
SQ	 0.6130	 0.4130
SR	 0.6050	 0.3810
SS	 0.6240	 0.3970
ST	 0.5910	 0.3820
SU	 0.5520	 0.3820
SV	 0.6600	 0.4370
SW	 0.7330	 0.4850
SX	 0.7270	 0.5050
SY	 0.6160	 0.3820
SZ	 0.5140	 0.3660
Sa	 0.7670	 0.4950

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Chain	Atom inclusion	Q-score
Sb	 0.6670	 0.4460
Sc	 0.6030	 0.4290
Sd	 0.7490	 0.4550
Se	 0.6010	 0.4280
Sf	 0.3330	 0.2360
Sg	 0.4430	 0.3320