



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:31 PM UTC

PDB ID : 7NRC / pdb_00007nrc
EMDB ID : EMD-12534
Title : Structure of the yeast Gcn1 bound to a leading stalled 80S ribosome with Rbg2, Gir2, A- and P-tRNA and eIF5A
Authors : Pochopien, A.A.; Beckert, B.; Wilson, D.N.
Deposited on : 2021-03-03
Resolution : 3.90 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:

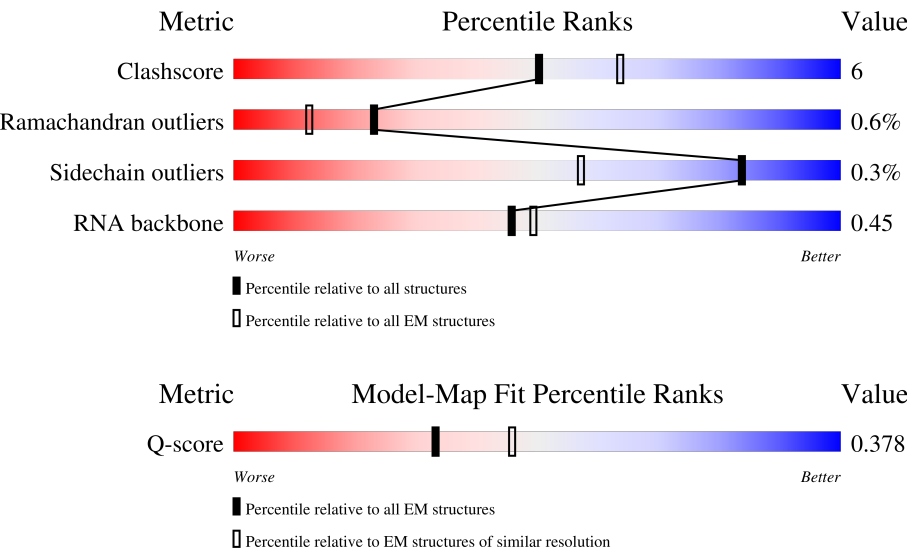
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 i

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

The reported resolution of this entry is 3.90 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	8855 (3.40 - 4.40)

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	S2	1800	54% 36% 8%
2	Sl	6	83% 17%
3	SP	206	6% 86% 14%

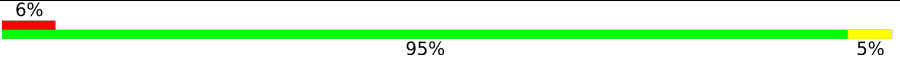
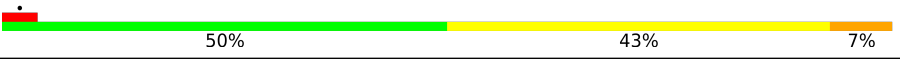
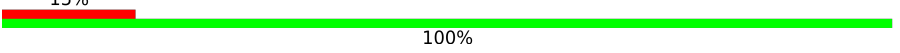
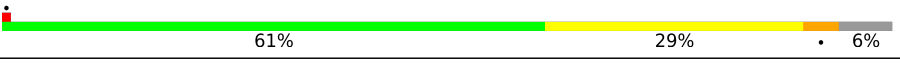
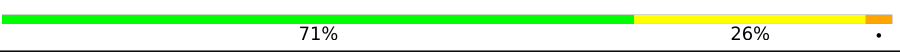
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Mol	Chain	Length	Quality of chain
4	SQ	232	
5	SE	117	
6	SR	216	
7	SA	222	
8	SS	258	
9	SB	206	
10	ST	228	
11	SU	184	
12	SV	198	
13	SW	184	
14	SC	92	
15	SX	142	
16	SD	121	
17	SY	150	
18	SZ	127	
19	SF	141	
20	SG	125	
21	SH	145	
22	SI	143	
23	SJ	100	
24	Sa	87	
25	Sb	129	
26	Sc	144	
27	Sd	134	
28	SK	82	

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Mol	Chain	Length	Quality of chain
29	Se	97	
30	Sf	81	
31	SM	53	
32	Sg	57	
33	SN	73	
34	SO	312	
35	SL	63	
36	Sm	76	
37	Sn	75	
38	So	366	
39	Sp	48	
40	LA	3394	
41	LB	121	
42	LC	158	
43	LD	251	
44	LE	386	
45	LF	361	
46	LG	294	
47	LH	175	
48	LI	222	
49	LJ	233	
50	LK	191	
51	LL	218	
52	LM	169	
53	LN	193	

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Mol	Chain	Length	Quality of chain
54	LO	136	
55	LP	203	
56	LQ	197	
57	LR	183	
58	LS	185	
59	LT	188	
60	LU	171	
61	LV	159	
62	LW	100	
63	LX	136	
64	LY	65	
65	LZ	121	
66	La	125	
67	Lb	135	
68	Lc	148	
69	Ld	58	
70	Le	96	
71	Lf	109	
72	Lg	127	
73	Lh	106	
74	Li	112	
75	Lj	119	
76	Lk	99	
77	Ll	81	
78	Lm	77	

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Mol	Chain	Length	Quality of chain
79	Ln	50	
80	Lo	52	
81	Lp	25	
82	Lq	103	
83	Lr	91	
84	Ls	154	
85	Lt	210	
86	A	1209	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
84	5CT	Ls	51	X	-	-	-

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 213576 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 18S rRNA (1771-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	S2	1771	Total	C	N	O	P	0	0
			37739	16872	6683	12413	1771		

- Molecule 2 is a RNA chain called RNA (5'-R(P*AP*UP*GP*AP*AP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Sl	6	Total	C	N	O	P	0	0
			131	59	27	39	6		

- Molecule 3 is a protein called 40S ribosomal protein S0-A.

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

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

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

- Molecule 5 is a protein called 40S ribosomal protein S15.

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

- Molecule 6 is a protein called 40S ribosomal protein S2.

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

- Molecule 7 is a protein called 40S ribosomal protein S3.

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

- Molecule 8 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 9 is a protein called 40S ribosomal protein S5.

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

- Molecule 10 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 11 is a protein called 40S ribosomal protein S7-A.

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

- Molecule 12 is a protein called 40S ribosomal protein S8-A.

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

- Molecule 13 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 14 is a protein called 40S ribosomal protein S10-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SX	142	Total	C	N	O	S	0	0
			1142	733	217	189	3		

- Molecule 16 is a protein called 40S ribosomal protein S12.

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

- Molecule 17 is a protein called 40S ribosomal protein S13.

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

- Molecule 18 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SZ	127	Total	C	N	O	S	0	0
			923	568	185	167	3		

- Molecule 19 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 20 is a protein called 40S ribosomal protein S17-B.

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

- Molecule 21 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SH	145	Total	C	N	O	S	0	0
			1188	741	237	208	2		

- Molecule 22 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 23 is a protein called 40S ribosomal protein S20.

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

- Molecule 24 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 25 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 26 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 27 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	Sd	134	Total	C	N	O	0	0
			1032	651	195	186		

- Molecule 28 is a protein called 40S ribosomal protein S25-A.

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

- Molecule 29 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Se	97	Total	C	N	O	S		
			765	473	160	127	5	0	0

- Molecule 30 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 31 is a protein called 40S ribosomal protein S29-A.

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

- Molecule 32 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Sg	57	Total	C	N	O	S		
			451	284	93	73	1	0	0

- Molecule 33 is a protein called 40S ribosomal protein S31.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SN	97	ALA	LYS	variant	UNP P05759

- Molecule 34 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

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

- Molecule 35 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 36 is a RNA chain called tRNA (76-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Sm	76	Total	C	N	O	P	0	0
			1611	721	281	534	75		

- Molecule 37 is a RNA chain called tRNA (75-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Sn	75	Total	C	N	O	P	0	0
			1606	716	297	518	75		

- Molecule 38 is a protein called Ribosome-interacting GTPase 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	So	347	Total	C	N	O	S	0	0
			2729	1723	478	518	10		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
So	62	ALA	LYS	variant	UNP P53295
So	92	ALA	ILE	variant	UNP P53295
So	94	GLU	HIS	variant	UNP P53295
So	96	GLU	ALA	variant	UNP P53295
So	134	LYS	ARG	variant	UNP P53295
So	271	ALA	THR	variant	UNP P53295
So	299	ALA	TYR	variant	UNP P53295
So	303	ALA	ARG	variant	UNP P53295
So	318	ASP	ASN	variant	UNP P53295
So	361	GLU	ASP	variant	UNP P53295

- Molecule 39 is a protein called GIR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	Sp	48	Total	C	N	O	0	0
			240	144	48	48		

- Molecule 40 is a RNA chain called 25S rRNA (3184-MER).

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

- Molecule 41 is a RNA chain called 5S rRNA (121-MER).

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

- Molecule 42 is a RNA chain called 5.8S rRNA (158-MER).

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

- Molecule 43 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L3.

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

- Molecule 45 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L5.

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

- Molecule 47 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LH	167	Total	C	N	O		0	0
			1307	843	234	230			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LH	120	LYS	ASN	variant	UNP P05739

- Molecule 48 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L10.

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

- Molecule 52 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LM	169	Total	C	N	O	S	0	0
			1346	843	252	247	4		

- Molecule 53 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LN	193	Total	C	N	O	S	0	0
			1543	962	315	266			

- Molecule 54 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 56 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LR	183	Total	C	N	O	S	0	0
			1416	879	284	253			

- Molecule 58 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 59 is a protein called 60S ribosomal protein L19-A.

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

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

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

- Molecule 61 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	LV	159	Total	C	N	O	S		
			1272	802	245	221	4	0	0

- Molecule 62 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 63 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 64 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	LY	65	Total	C	N	O	S		
			528	339	104	84	1	0	0

- Molecule 65 is a protein called 60S ribosomal protein L25.

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

- Molecule 66 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 67 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
67	Lb	135	Total	C	N	O	0	0
			1080	701	199	180		

- Molecule 68 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Lc	148	Total	C	N	O	S	0	0
			1169	747	231	188	3		

- Molecule 69 is a protein called 60S ribosomal protein L29.

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

- Molecule 70 is a protein called 60S ribosomal protein L30.

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

- Molecule 71 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L32.

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

- Molecule 73 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 74 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 75 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 76 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 77 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Ll	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

- Molecule 78 is a protein called 60S ribosomal protein L38.

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

- Molecule 79 is a protein called 60S ribosomal protein L39.

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

- Molecule 80 is a protein called 60S ribosomal protein L40-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Lo	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 81 is a protein called 60S ribosomal protein L41-A.

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

- Molecule 82 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 83 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 84 is a protein called eiF5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Ls	154	Total	C	N	O	S	0	0
			1143	709	195	230	9		

- Molecule 85 is a protein called L1 60S ribosomal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
85	Lt	210	Total	C	N	O	0	0
			1050	630	210	210		

- Molecule 86 is a protein called GCN1.

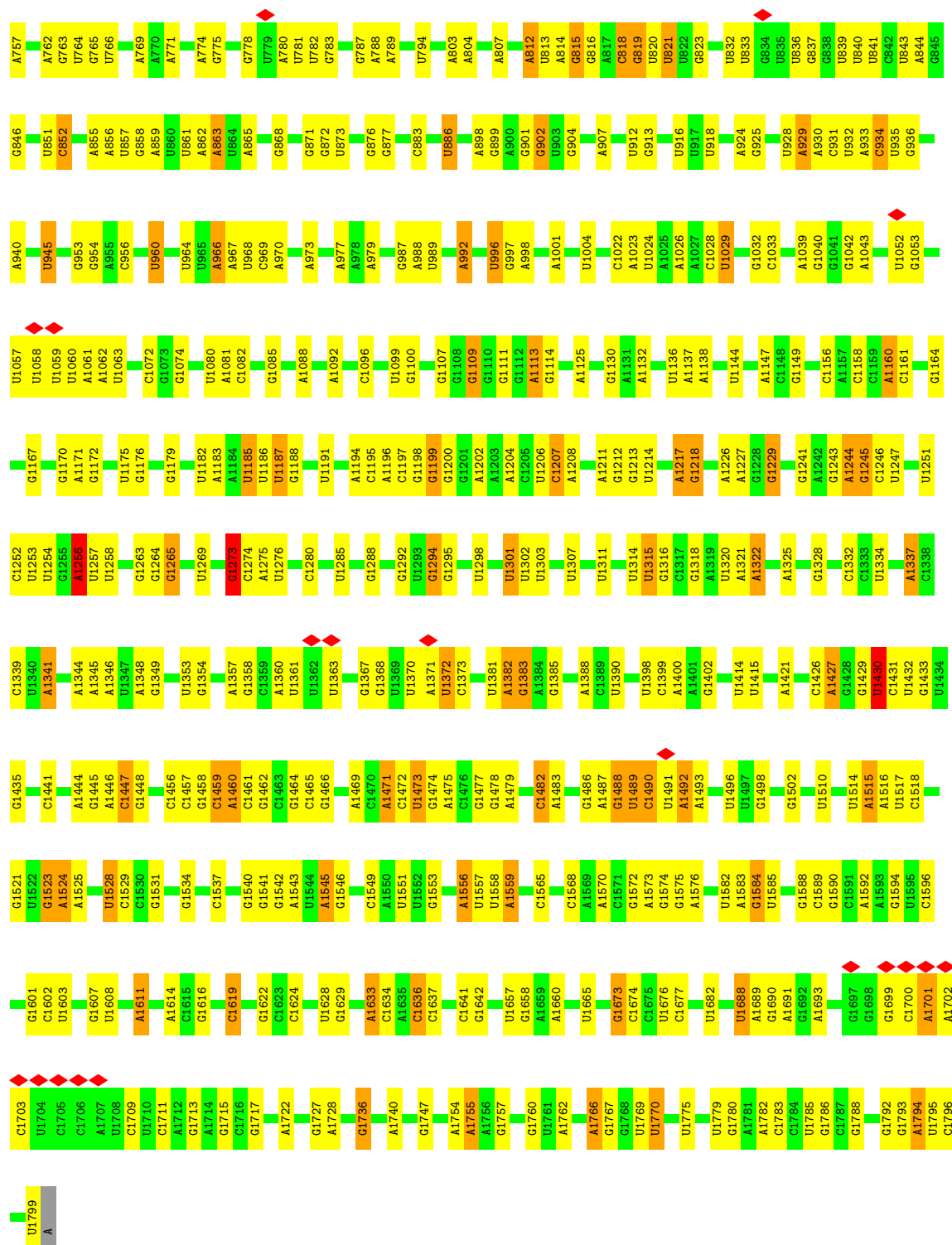
Mol	Chain	Residues	Atoms				AltConf	Trace
86	A	1209	Total	C	N	O	1	0
			6029	3609	1210	1210		

3 Residue-property plots

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

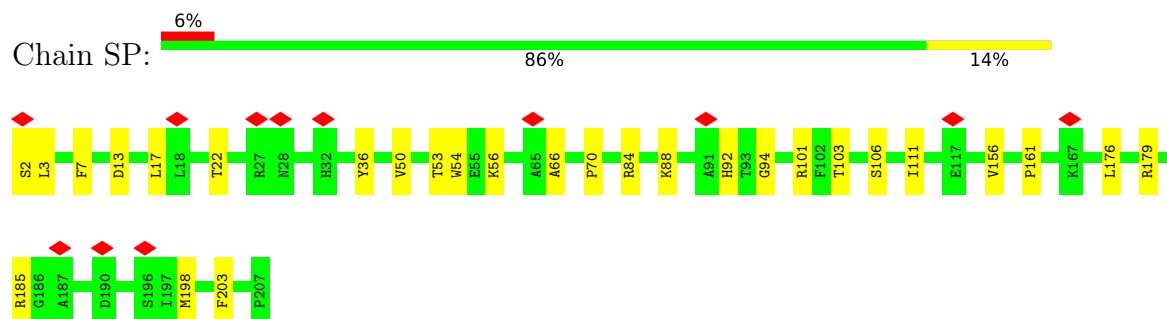
• Molecule 1: 18S rRNA (1771-MER)



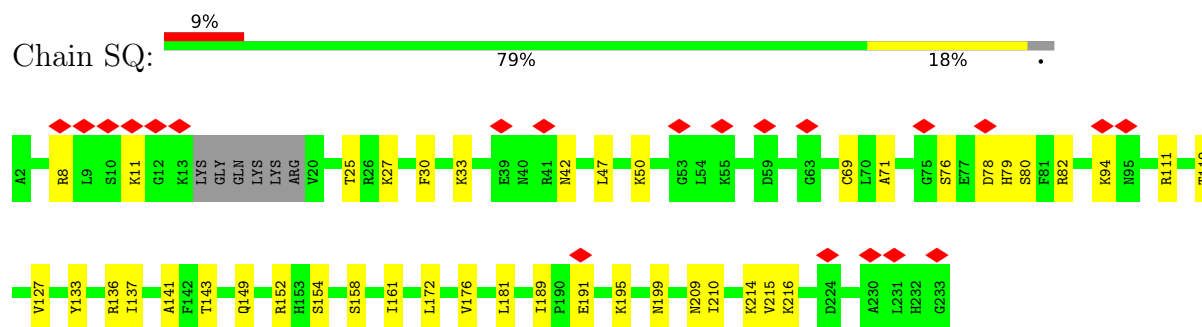


• Molecule 2: RNA (5'-R(P*AP*UP*GP*AP*AP*A)-3')

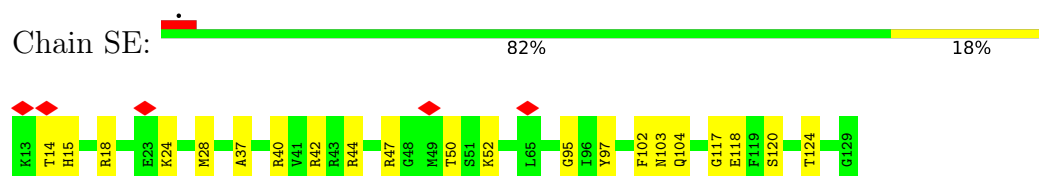
- Molecule 3: 40S ribosomal protein S0-A



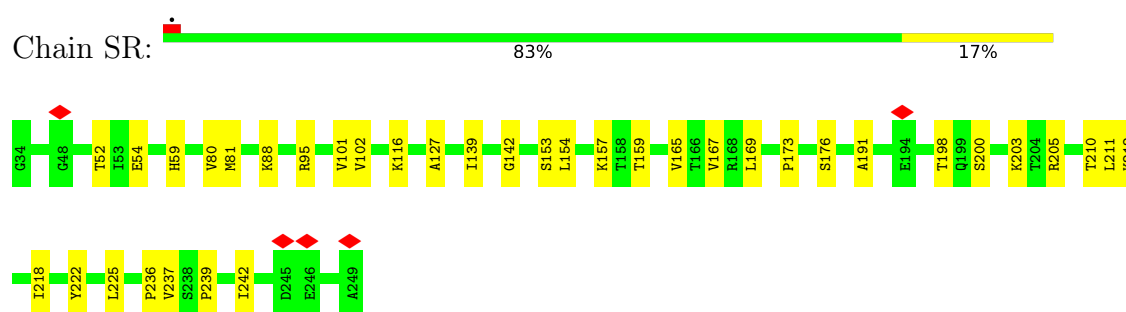
- Molecule 4: 40S ribosomal protein S1-A



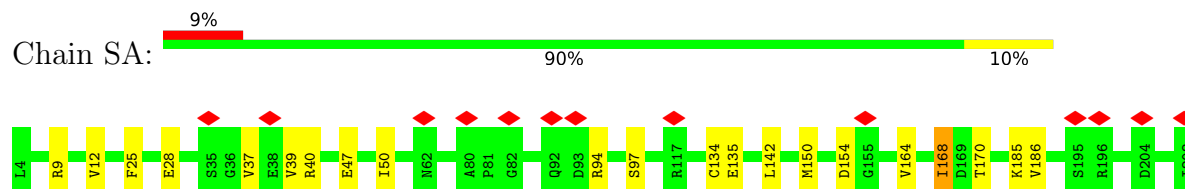
- Molecule 5: 40S ribosomal protein S15

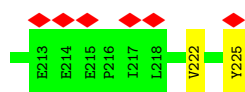


- Molecule 6: 40S ribosomal protein S2



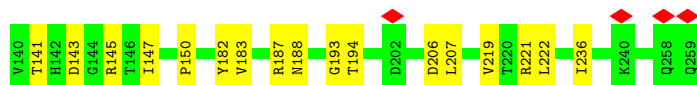
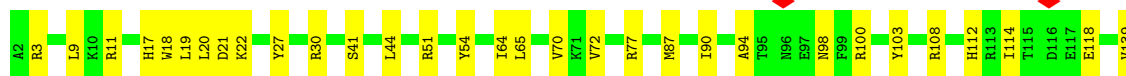
- Molecule 7: 40S ribosomal protein S3





- Molecule 8: 40S ribosomal protein S4-A

Chain SS: 81% 19%



- Molecule 9: 40S ribosomal protein S5

Chain SB: 9% 84% 16%



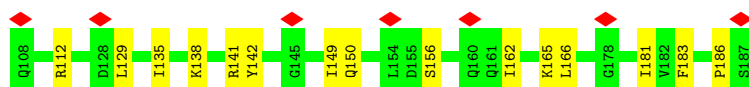
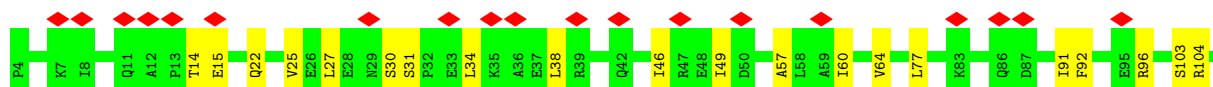
- Molecule 10: 40S ribosomal protein S6-A

Chain ST: 86% 14%



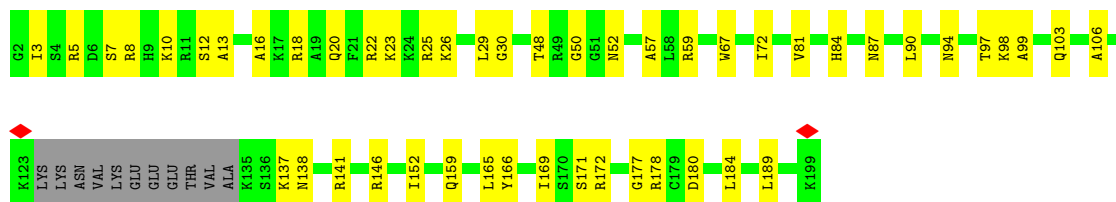
- Molecule 11: 40S ribosomal protein S7-A

Chain SU: 14% 81% 19%



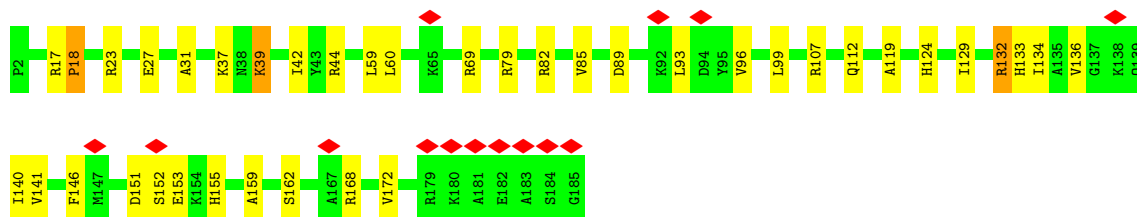
- Molecule 12: 40S ribosomal protein S8-A

Chain SV:  70% 25% 6%



- Molecule 13: 40S ribosomal protein S9-A

Chain SW:  8% 79% 20%



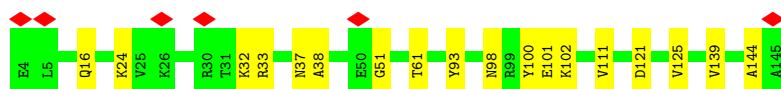
- Molecule 14: 40S ribosomal protein S10-A

Chain SC:  10% 85% 14%



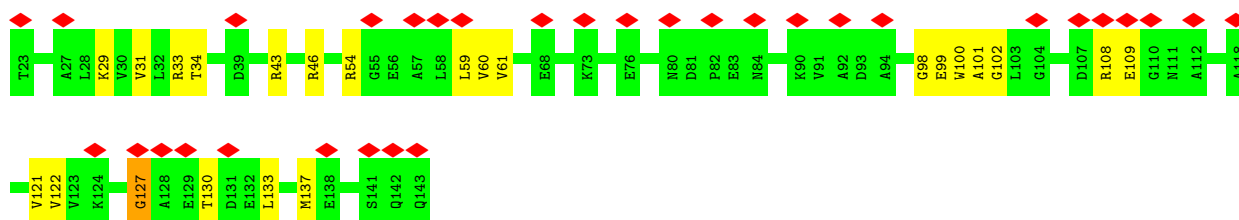
- Molecule 15: 40S ribosomal protein S11-A

Chain SX:  87% 13%



- Molecule 16: 40S ribosomal protein S12

Chain SD:  26% 81% 18%

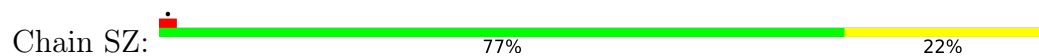


- Molecule 17: 40S ribosomal protein S13

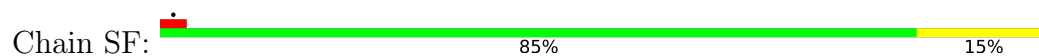
Chain SY:  5% 87% 13%



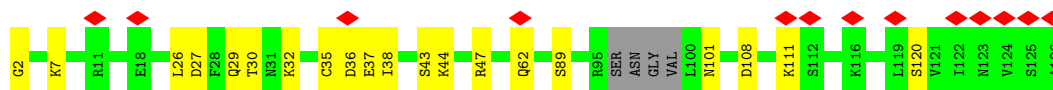
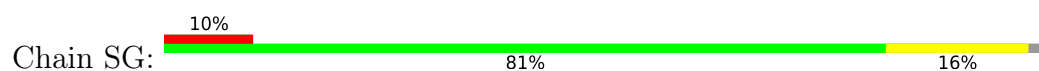
- Molecule 18: 40S ribosomal protein S14-B



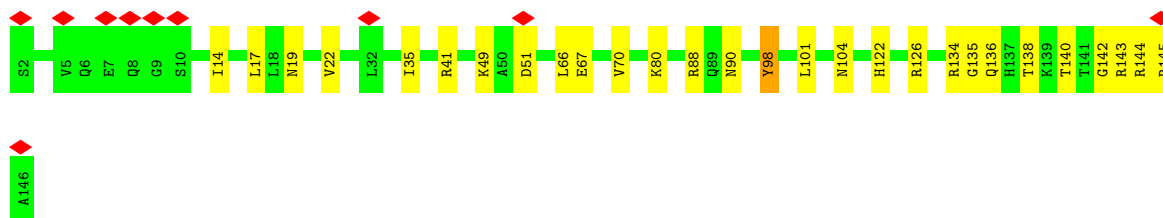
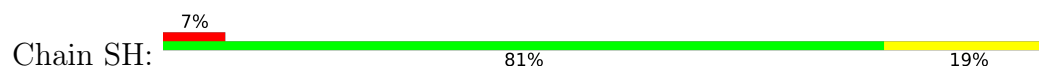
- Molecule 19: 40S ribosomal protein S16-A



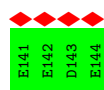
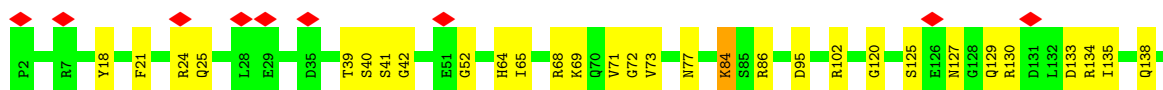
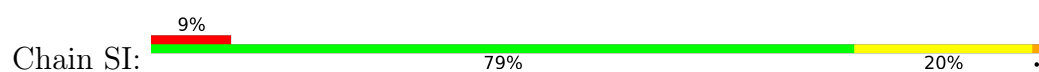
- Molecule 20: 40S ribosomal protein S17-B



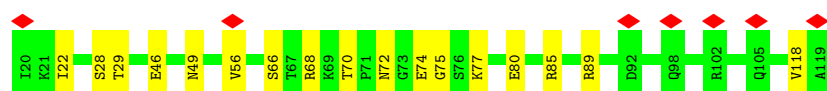
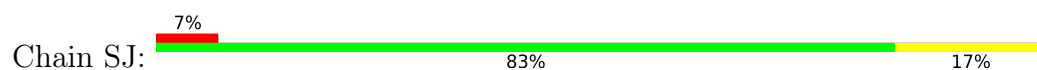
- Molecule 21: 40S ribosomal protein S18-A



- Molecule 22: 40S ribosomal protein S19-A



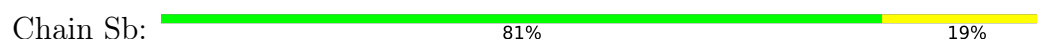
- Molecule 23: 40S ribosomal protein S20



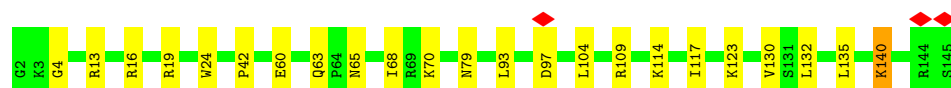
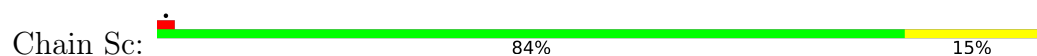
- Molecule 24: 40S ribosomal protein S21-A



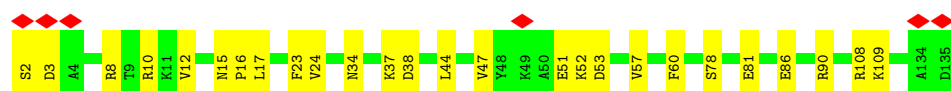
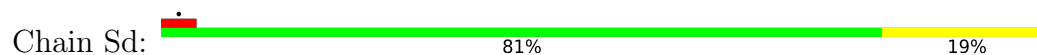
- Molecule 25: 40S ribosomal protein S22-A



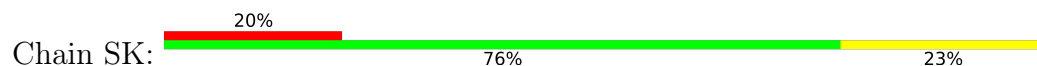
- Molecule 26: 40S ribosomal protein S23-A



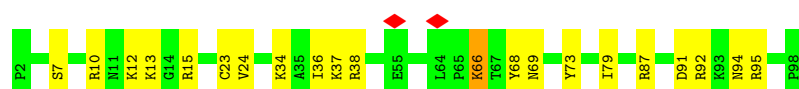
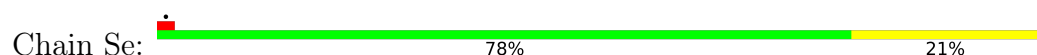
- Molecule 27: 40S ribosomal protein S24-A



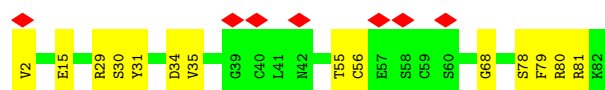
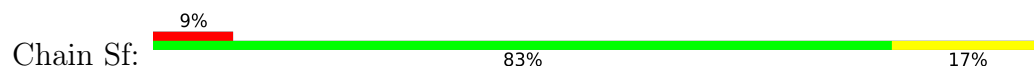
- Molecule 28: 40S ribosomal protein S25-A



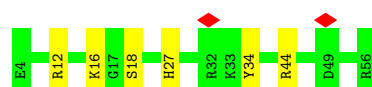
- Molecule 29: 40S ribosomal protein S26-B



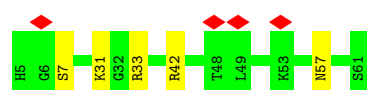
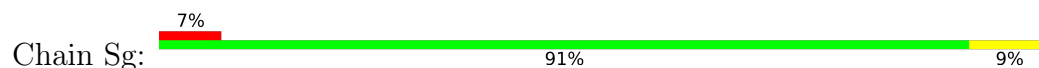
- Molecule 30: 40S ribosomal protein S27-A



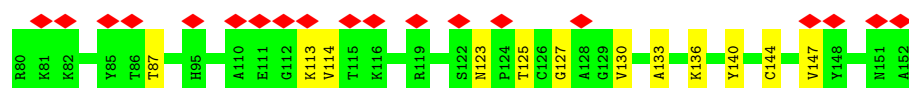
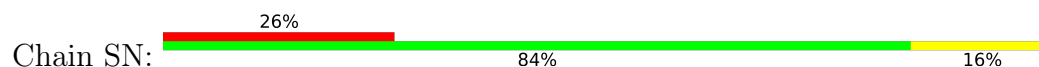
- Molecule 31: 40S ribosomal protein S29-A



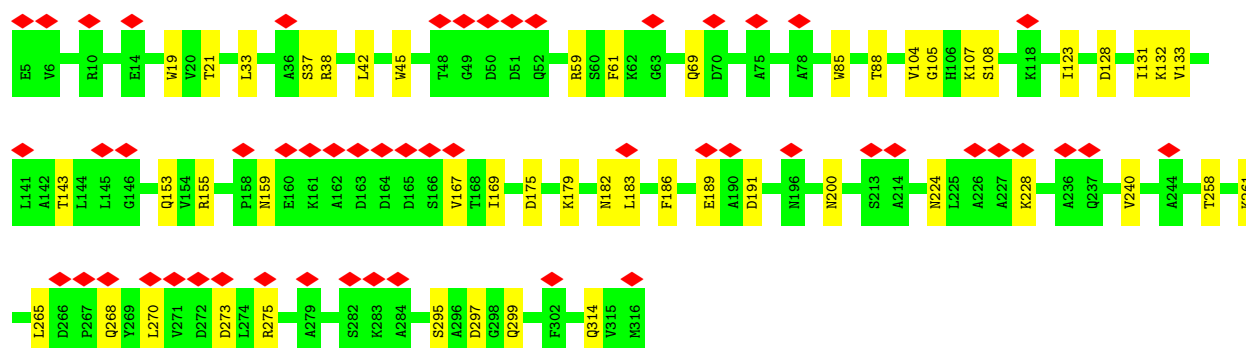
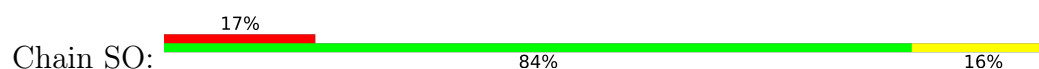
- Molecule 32: 40S ribosomal protein S30-A



- Molecule 33: 40S ribosomal protein S31

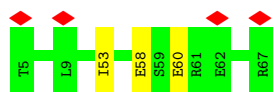


- Molecule 34: Guanine nucleotide-binding protein subunit beta-like protein

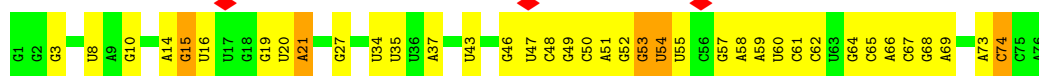


- Molecule 35: 40S ribosomal protein S28-A

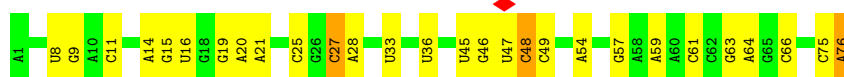




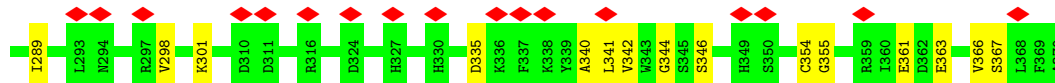
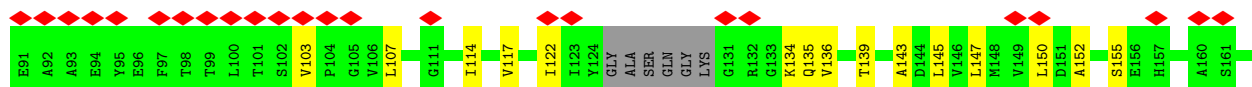
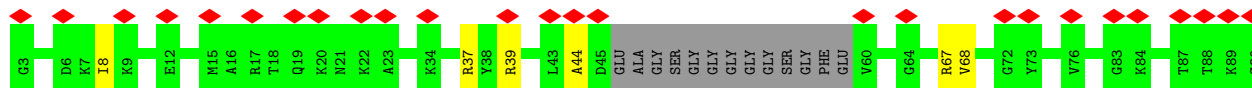
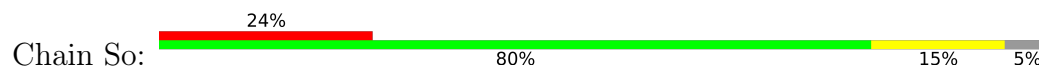
- Molecule 36: tRNA (76-MER)



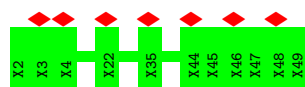
- Molecule 37: tRNA (75-MER)



- Molecule 38: Ribosome-interacting GTPase 2



- Molecule 39: GIR2

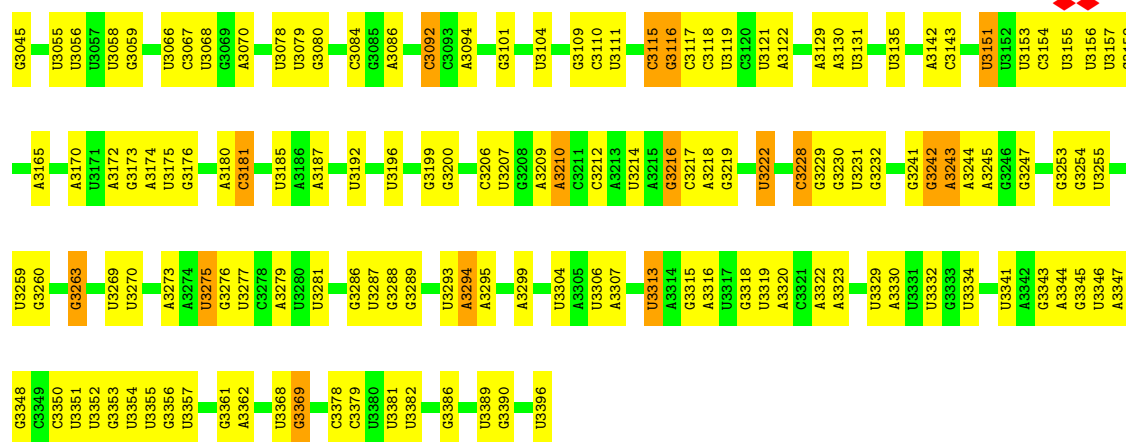


- Molecule 40: 25S rRNA (3184-MER)



A1369	U1267	U1181	A1055	G937	A836	G726	U627	A529	C	G347	G231	A109	U3
A1385	G1268	A1182	A1062	C938	A837	G727	A628	A533	C	A348	G236	G110	A6
A1386	A1270	G1186	G1063	U939	G838	G728	A630	U534	C	A349	C350	C111	A39
A1390	C1272	A1190	A1064	C944	C839	C729	C637	G635	C	A351	U240	U112	A11
G1391	A1273	U1191	A1065	A951	A848	G737	C638	G542	C	A352	G239	C113	A12
G1392	A1274	C1192	G1072	G952	C849	G738	G639	C543	U	G360	U240	A114	A13
C1275	A1275	A1193	U1078	G953	U850	G742	C841	U545	C	G364	G243	A115	U14
A1399	C1276	C1196	U1078	C959	C851	A744	C842	C546	U	G376	U249	A116	A20
G1400	A1278	A1197	U1081	U960	G860	G754	A645	G547	U	A385	U252	A121	G22
C1403	C1279	G1201	U1082	A967	C861	G758	A646	G548	C	G388	G258	A122	A26
U1410	G1280	A1202	A1084	G971	U865	C758	A649	A550	G	G389	C263	U129	G30
A1418	G1281	A1203	G1083	G974	C868	G763	U764	A551	C	G390	G264	A130	C36
A1419	A1282	A1204	A1093	G974	U871	C765	G765	G552	U	U133	A265	U133	U37
G1420	U1094	U1095	U1094	G974	U872	U766	C655	U555	A	G136	G269	A150	U38
G1421	U1096	U1096	U1096	U981	C873	C768	A656	U556	G	A395	A397	A157	A39
U1208	G1207	G1207	G1097	C982	U874	A657	G658	U557	C	A396	U270	G166	A40
G1429	U1208	A1098	U1097	U990	G875	G769	G659	U558	G	A398	C271	G156	A43
U1430	A1302	U1217	U990	C991	A876	G770	A660	A559	C	A399	G400	A157	A44
G1431	G1307	U1218	A992	G993	U879	A771	U669	G564	A	U401	U280	A164	U44
A1434	U1308	G1222	G993	G993	G894	G774	U664	G568	U	A402	G281	A164	A48
A1435	A1309	A1223	G999	G999	A895	A775	A665	A568	C	C403	G282	A165	A49
C1437	C1312	C1227	A1002	A1002	A896	U776	A666	A578	C	G408	G283	C166	U50
U1442	G1313	G1228	A1003	A1003	U899	A780	G668	G579	C	U411	A284	U169	A51
G1443	U1128	G1229	G1012	G1012	G900	G781	U669	G582	C	G412	U286	G170	G89
A1446	G1131	G1234	U1015	U1015	G901	A677	A677	G583	U	A171	C291	G171	A60
G1447	A1132	U1235	C1016	C1016	A906	G785	U681	G584	C	A417	U292	G172	A65
U1448	G1133	G1236	G1017	G1017	G907	A786	U681	A585	C	A418	A295	A187	A66
A1449	U1134	C1238	C1018	C1018	G908	G798	U689	G590	C	G421	U298	U190	A67
G1450	C1141	C1239	G1019	G1019	G909	G799	A690	G591	C	A422	G301	U191	C68
U1455	U1241	A1240	G1020	G1020	G910	A801	A691	A592	C	A423	G424	U191	C69
A1468	G1144	G1242	G1021	G1021	C911	U801	C695	C593	C	G424	C312	A198	A70
G1473	U1145	G1243	U1022	U1022	A914	C804	G695	G597	C	A436	A313	A199	C73
A1481	G1148	A1244	C1023	C1023	A915	G805	U698	G600	C	G437	U314	C200	G74
A1482	G1149	G1245	G1024	G1024	G916	A806	A699	G603	C	A438	C315	G206	G75
G1483	U1150	U1246	A1025	A1025	A917	A807	A705	G604	C	C439	A323	U210	G76
U1484	A1153	C1248	A1026	A1026	A921	U814	A706	G609	C	A440	U441	A211	A85
A1487	C1156	A1251	U1027	U1027	U922	U817	G712	G610	C	U444	U329	G212	A89
G1488	G1157	U1252	U1028	U1028	C923	A817	A715	G611	C	G445	G330	A213	C90
U1492	A1158	U1253	A1040	A1040	G924	C818	A716	U612	C	U446	A334	G216	G91
G1493	A1159	U1258	U1041	U1041	A925	A820	A717	G613	C	U447	U447	U217	G92
U1494	A1169	G1261	C1045	C1045	A929	G826	C717	A619	C	U448	A338	G218	A95
C1497	G1177	G1262	A1046	A1046	U832	A830	U719	U620	C	U449	C339	G219	A96
A1503	G1178	A1263	U1048	U1048	A833	G831	U719	A621	C	U450	C340	G220	U97
U1503	A1179	G1264	G935	G935	G934	G831	A720	U626	C	U451	G341	A221	G98
G1503	C1049	U1265	A1049	A1049	U935	G831	A720	U626	C	G	C346	A222	G99
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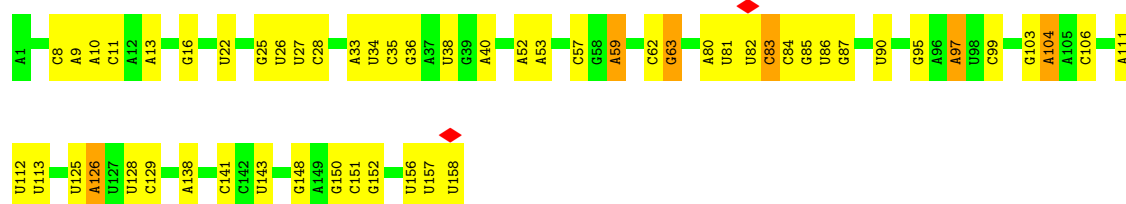




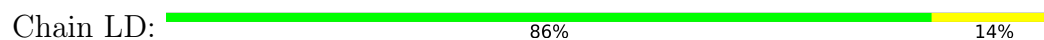
• Molecule 41: 5S rRNA (121-MER)



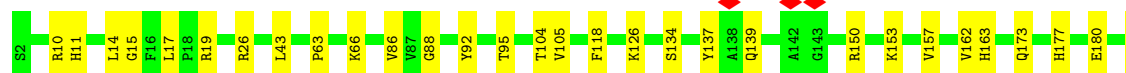
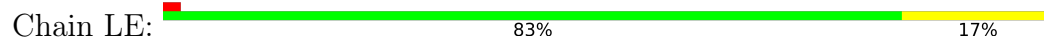
• Molecule 42: 5.8S rRNA (158-MER)

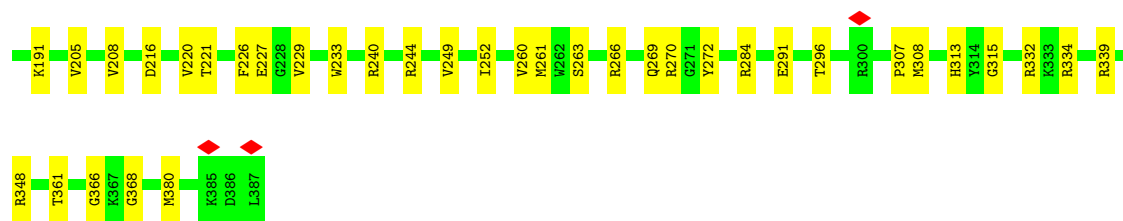


• Molecule 43: 60S ribosomal protein L2-A



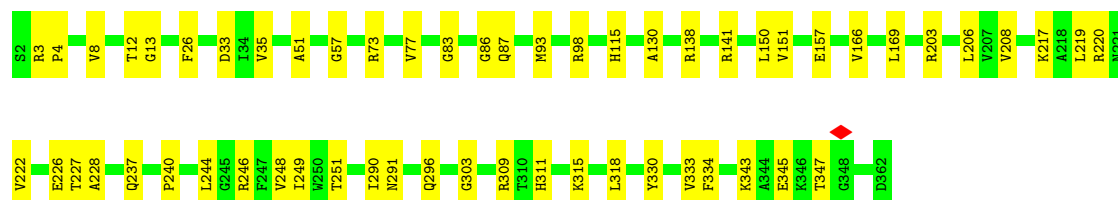
• Molecule 44: 60S ribosomal protein L3





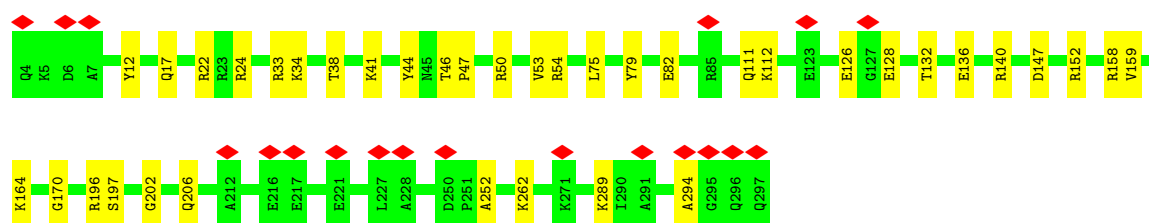
- Molecule 45: 60S ribosomal protein L4-A

Chain LF: 84% 16%



- Molecule 46: 60S ribosomal protein L5

Chain LG: 6% 87% 13%



- Molecule 47: 60S ribosomal protein L6-B

Chain LH: 78% 18% 5%



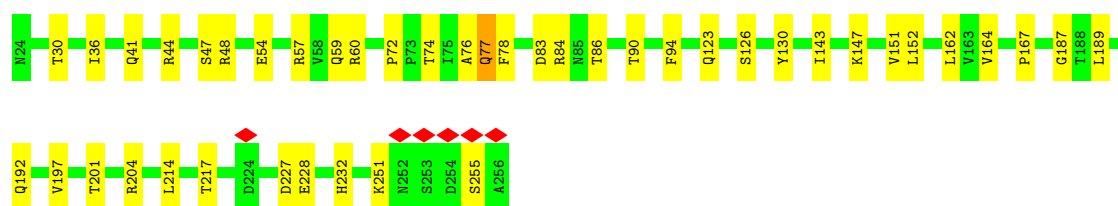
- Molecule 48: 60S ribosomal protein L7-A

Chain LI: 89% 11%



- Molecule 49: 60S ribosomal protein L8-A

Chain LJ:  82% 18%



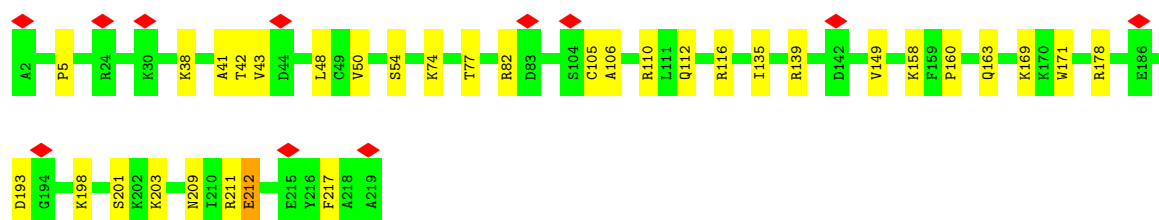
- Molecule 50: 60S ribosomal protein L9-A

Chain LK:  90% 10%



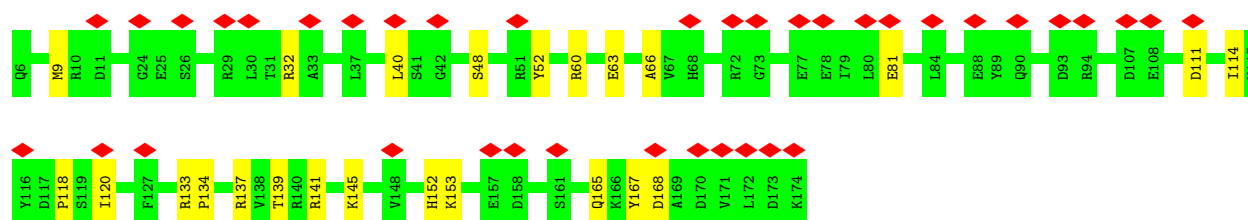
- Molecule 51: 60S ribosomal protein L10

Chain LL:  85% 15% 5%



- Molecule 52: 60S ribosomal protein L11-B

Chain LM:  86% 14% 22%



- Molecule 53: 60S ribosomal protein L13-A

Chain LN:  87% 13%



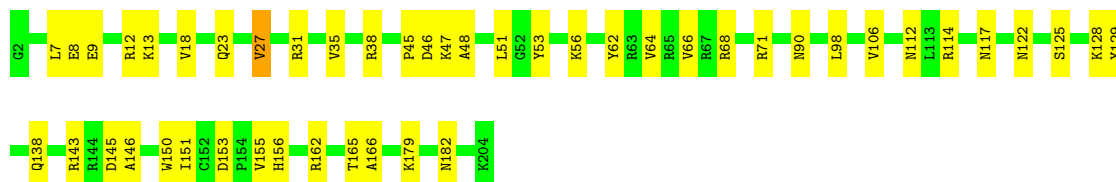
- Molecule 54: 60S ribosomal protein L14-A

Chain LO:  86% 14%



- Molecule 55: 60S ribosomal protein L15-A

Chain LP: 77% 23%



- Molecule 56: 60S ribosomal protein L16-A

Chain LQ: 90% 10%



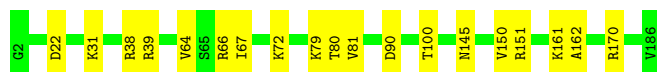
- Molecule 57: 60S ribosomal protein L17-A

Chain LR: 89% 11%



- Molecule 58: 60S ribosomal protein L18-A

Chain LS: 90% 10%



- Molecule 59: 60S ribosomal protein L19-A

Chain LT: 7% 92% 8%

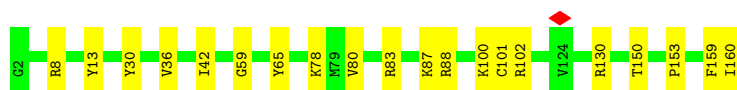


- Molecule 60: 60S ribosomal protein L20-A

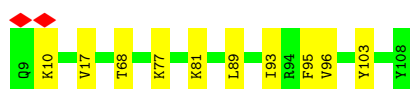
Chain LU: 7% 92% 8%



• Molecule 61: 60S ribosomal protein L21-A

Chain LV:  87% 13%

• Molecule 62: 60S ribosomal protein L22-A

Chain LW:  90% 10%

• Molecule 63: 60S ribosomal protein L23-A

Chain LX:  82% 18%

• Molecule 64: 60S ribosomal protein L24-A

Chain LY:  83% 17%

• Molecule 65: 60S ribosomal protein L25

Chain LZ:  92% 8%

• Molecule 66: 60S ribosomal protein L26-A

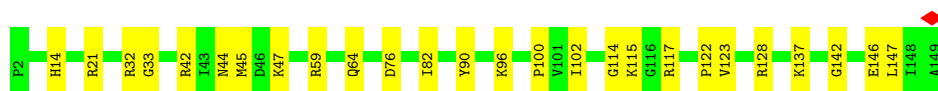
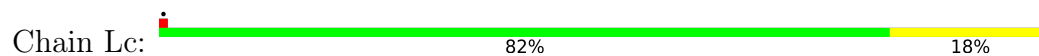
Chain La:  89% 11%

• Molecule 67: 60S ribosomal protein L27-A

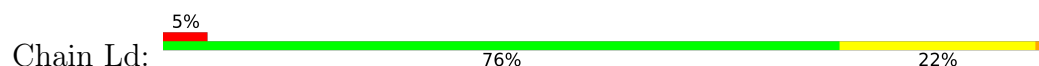
Chain Lb:  86% 14%



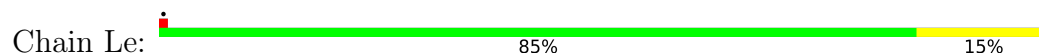
- Molecule 68: 60S ribosomal protein L28



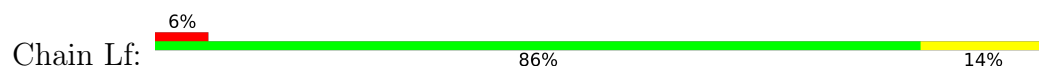
- Molecule 69: 60S ribosomal protein L29



- Molecule 70: 60S ribosomal protein L30



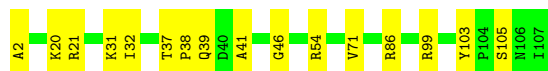
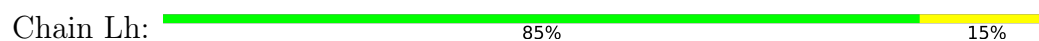
- Molecule 71: 60S ribosomal protein L31-A



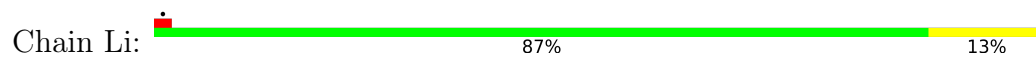
- Molecule 72: 60S ribosomal protein L32



- Molecule 73: 60S ribosomal protein L33-A



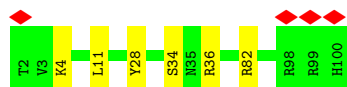
- Molecule 74: 60S ribosomal protein L34-A



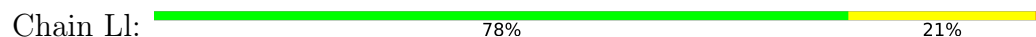
- Molecule 75: 60S ribosomal protein L35-A



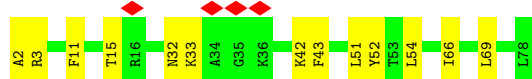
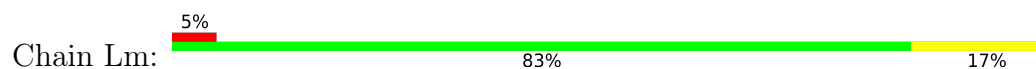
- Molecule 76: 60S ribosomal protein L36-A



- Molecule 77: 60S ribosomal protein L37-A



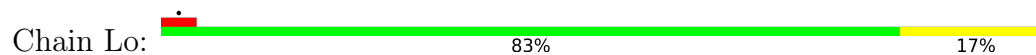
- Molecule 78: 60S ribosomal protein L38



- Molecule 79: 60S ribosomal protein L39



- Molecule 80: 60S ribosomal protein L40-A



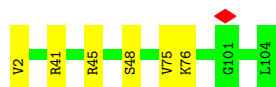
- Molecule 81: 60S ribosomal protein L41-A

Chain Lp:  92% 8%



- Molecule 82: 60S ribosomal protein L42-A

Chain Lq:  94% 6%



- Molecule 83: 60S ribosomal protein L43-A

Chain Lr:  79% 20%



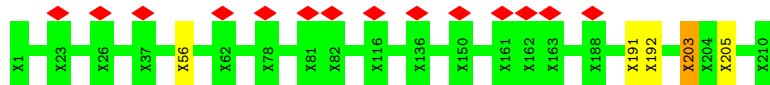
- Molecule 84: eiF5A

Chain Ls:  13% 65% 32%



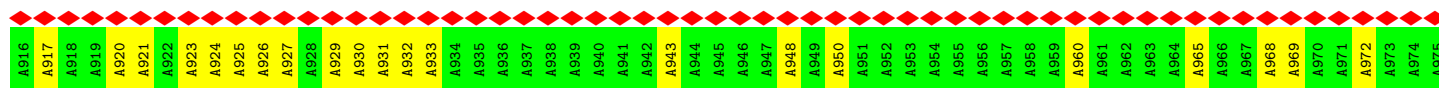
- Molecule 85: L1 60S ribosomal protein

Chain Lt:  7% 98%



- Molecule 86: GCN1

Chain A:  71% 75% 21%



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D1299	S1300	H1301	K1302	E1303	A1307	A1308	A1309	A1310	A1311	A1312	A1313	A1314	A1315	A1316	A1317	A1318	A1319	A1320	A1321	A1322	A1323	A1324	A1325	A1326	A1327	A1328	A1329	A1330	A1331	A1332	A1333	A1334	A1335	A1336	A1337	A1338	A1339	A1340	A1341	A1342	A1343	A1344	A1345	A1346	A1347	A1348	A1349	A1350	A1351	A1352	A1353	A1354	A1355	A1356	A1357	A1358	A1359	A1360	A1361	A1362	A1363	A1364	A1365	A1366	A1367	A1368	A1369	A1370	A1371	A1372	A1373	A1374	A1375	A1376	A1377	A1378	A1379																																																																																																																																																																																																																																																															
K1216	M1217	L1218	G1219	D1220	A1221	V1222	P1223	E1224	V1225	R1226	D1227	A1228	T1229	A1230	A1231	A1232	A1233	A1234	A1235	A1236	A1237	A1238	A1239	A1240	A1241	A1242	A1243	A1244	A1245	A1246	A1247	A1248	A1249	A1250	A1251	A1252	A1253	A1254	A1255	A1256	A1257	A1258	A1259	A1260	A1261	A1262	A1263	A1264	A1265	A1266	A1267	A1268	A1269	A1270	A1271	A1272	A1273	A1274	A1275	A1276	A1277	A1278	A1279	A1280	A1281	A1282	A1283	A1284	A1285	A1286	A1287	A1288	A1289	A1290	A1291	A1292	A1293	A1294	A1295	A1296	A1297	A1298	A1299	A1300																																																																																																																																																																																																																																																								
A1103	A1104	G1124	D1125	Y1126	L1127	G1128	L1129	L1130	M1131	E1132	L1133	N1134	P1135	V1136	T1137	V1138	V1139	A1140	A1141	A1142	A1143	A1144	A1145	A1146	A1147	A1148	A1149	A1150	A1151	A1152	A1153	A1154	A1155	A1156	A1157	A1158	A1159	A1160	A1161	A1162	A1163	A1164	A1165	A1166	A1167	A1168	A1169	A1170	A1171	A1172	A1173	A1174	A1175	A1176	A1177	A1178	A1179	A1180	A1181	A1182	A1183	A1184	A1185	A1186	A1187	A1188	A1189	A1190	A1191	A1192	A1193	A1194	A1195	A1196	A1197	A1198	A1199	A1200	A1201	A1202	A1203	A1204	A1205	A1206	A1207	A1208	A1209	A1210	A1211	A1212	A1213	A1214	A1215	A1216	A1217	A1218	A1219	A1220	A1221	A1222	A1223	A1224	A1225	A1226	A1227	A1228	A1229	A1230	A1231	A1232	A1233	A1234	A1235	A1236	A1237	A1238	A1239	A1240	A1241	A1242	A1243	A1244	A1245	A1246	A1247	A1248	A1249	A1250	A1251	A1252	A1253	A1254	A1255	A1256	A1257	A1258	A1259	A1260	A1261	A1262	A1263	A1264	A1265	A1266	A1267	A1268	A1269	A1270	A1271	A1272	A1273	A1274	A1275	A1276	A1277	A1278	A1279	A1280	A1281	A1282	A1283	A1284	A1285	A1286	A1287	A1288	A1289	A1290	A1291	A1292	A1293	A1294	A1295	A1296	A1297	A1298	A1299	A1300																																																																																																																																																										
A976	A977	A978	A979	A980	A981	A982	A983	A984	A985	A986	A987	A988	A989	A990	A991	A992	A993	A994	A995	A996	A997	A998	A999	A1000	A1001	A1002	A1003	A1004	A1005	A1006	A1007	A1008	A1009	A1010	A1011	A1012	A1013	A1014	A1015	A1016	A1017	A1018	A1019	A1020	A1021	A1022	A1023	A1024	A1025	A1026	A1027	A1028	A1029	A1030	A1031	A1032	A1033	A1034	A1035	A1036	A1037	A1038	A1039	A1040	A1041	A1042	A1043	A1044	A1045	A1046	A1047	A1048	A1049	A1050	A1051	A1052	A1053	A1054	A1055	A1056	A1057	A1058	A1059	A1060	A1061	A1062	A1063	A1064	A1065	A1066	A1067	A1068	A1069	A1070	A1071	A1072	A1073	A1074	A1075	A1076	A1077	A1078	A1079	A1080	A1081	A1082	A1083	A1084	A1085	A1086	A1087	A1088	A1089	A1090	A1091	A1092	A1093	A1094	A1095	A1096	A1097	A1098	A1099	A1100	A1101	A1102																																																																																																																																																																																																														

A2409	A2349	A2287	A2227
A2410	A2350	A2288	A2228
A2411	A2351	A2289	A2229
A2412	A2352	A2290	A2230
A2413	A2353	A2291	A2231
A2414	A2354	A2292	A2232
A2415	A2355	A2293	A2233
A2416	A2356	A2294	A2234
A2417	A2357	A2295	A2235
A2418	A2358	A2296	A2236
A2419	A2359	A2297	A2237
A2420	A2360	A2298	A2238
A2421	A2361	A2299	A2239
A2422	A2362	A2300	A2240
A2423	A2363	A2301	A2241
A2424	A2364	A2302	A2242
A2425	A2365	A2303	A2243
A2426	A2366	A2304	A2244
A2427	A2367	A2305	A2245
A2428	A2368	A2306	A2246
	A2369	A2307	A2247
	A2370	A2308	A2248
	A2371	A2309	A2249
	A2372	A2310	A2250
	A2373	A2311	A2251
	A2374	A2312	A2252
	A2375	A2313	A2253
	A2376	A2314	A2254
	A2377	A2315	A2255
	A2378	A2316	A2256
	A2379	A2317	A2257
	A2380	A2320	A2258
	A2381	A2321	A2259
	A2382	A2322	A2260
	A2383	A2323	A2261
	A2384	A2324	A2262
	A2385	A2325	A2263
	A2386	A2326	A2264
	A2387	A2327	A2265
	A2388	A2328	A2266
	A2389	A2329	A2267
	A2390	A2330	A2268
	A2391	A2331	A2269
	A2392	A2332	A2270
	A2393	A2333	A2271
	A2394	A2334	A2272
	A2395	A2335	A2273
	A2396	A2336	A2274
	A2397	A2337	A2275
	A2398	A2338	A2276
	A2399	A2339	A2277
	A2400	A2340	A2278
	A2401	A2341	A2279
	A2402	A2342	A2280
	A2403	A2343	A2281
	A2404	A2344	A2282
	A2405	A2345	A2283
	A2406	A2346	A2284
	A2407	A2347	A2285
	A2408	A2348	A2286

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	30016	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	0.512	Depositor
Minimum map value	-0.389	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	758.8, 758.8, 758.8	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5CT

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	S2	0.28	0/42211	0.59	14/65773 (0.0%)
2	SI	0.26	0/147	0.46	0/227
3	SP	0.34	0/1644	0.79	0/2249
4	SQ	0.37	0/1823	0.90	3/2447 (0.1%)
5	SE	0.37	0/936	0.87	0/1259
6	SR	0.38	0/1656	0.85	0/2251
7	SA	0.33	0/1754	0.78	0/2361
8	SS	0.38	0/2097	0.87	0/2823
9	SB	0.36	0/1625	0.83	2/2197 (0.1%)
10	ST	0.35	0/1839	0.85	0/2460
11	SU	0.39	0/1498	0.88	0/2019
12	SV	0.31	0/1501	0.78	0/2006
13	SW	0.33	0/1504	0.83	1/2016 (0.0%)
14	SC	0.37	0/769	0.85	0/1039
15	SX	0.30	0/1168	0.75	0/1575
16	SD	0.40	0/883	0.95	0/1199
17	SY	0.35	0/1215	0.83	0/1638
18	SZ	0.36	0/934	0.86	2/1257 (0.2%)
19	SF	0.33	0/1125	0.84	0/1510
20	SG	0.33	0/957	0.75	0/1283
21	SH	0.34	0/1207	0.86	0/1623
22	SI	0.36	0/1130	0.83	2/1517 (0.1%)
23	SJ	0.34	0/807	0.78	0/1091
24	Sa	0.29	0/682	0.78	1/921 (0.1%)
25	Sb	0.38	0/1038	0.87	0/1395
26	Sc	0.36	0/1139	0.86	2/1518 (0.1%)
27	Sd	0.34	0/1046	0.80	0/1401
28	SK	0.38	0/661	0.92	1/888 (0.1%)
29	Se	0.32	0/778	0.81	0/1042
30	Sf	0.29	0/620	0.82	0/838
31	SM	0.32	0/452	0.83	0/600
32	Sg	0.32	0/459	0.89	0/611

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	SN	0.33	0/567	0.89	1/764 (0.1%)
34	SO	0.32	0/2436	0.84	0/3318
35	SL	0.36	0/493	0.96	0/663
36	Sm	0.32	0/1799	0.69	0/2801
37	Sn	0.31	0/1796	0.62	0/2799
38	So	0.25	0/2769	0.67	0/3736
40	LA	0.28	0/76214	0.55	10/118821 (0.0%)
41	LB	0.25	0/2883	0.51	1/4491 (0.0%)
42	LC	0.28	0/3746	0.55	0/5832
43	LD	0.33	0/1933	0.79	0/2598
44	LE	0.33	0/3146	0.78	1/4228 (0.0%)
45	LF	0.34	0/2800	0.80	0/3790
46	LG	0.33	0/2400	0.77	2/3239 (0.1%)
47	LH	0.35	0/1329	0.81	1/1794 (0.1%)
48	LI	0.35	0/1821	0.78	0/2451
49	LJ	0.35	0/1836	0.79	0/2481
50	LK	0.32	0/1529	0.77	0/2060
51	LL	0.32	0/1801	0.80	5/2416 (0.2%)
52	LM	0.35	0/1367	0.85	0/1834
53	LN	0.32	0/1568	0.78	1/2106 (0.0%)
54	LO	0.32	0/1068	0.77	0/1438
55	LP	0.38	0/1757	0.80	0/2354
56	LQ	0.37	0/1585	0.75	0/2128
57	LR	0.32	0/1439	0.72	0/1938
58	LS	0.32	0/1465	0.79	0/1965
59	LT	0.30	0/1532	0.72	0/2043
60	LU	0.32	0/1473	0.75	0/1980
61	LV	0.32	0/1296	0.76	0/1739
62	LW	0.34	0/812	0.77	0/1099
63	LX	0.30	0/1018	0.71	0/1369
64	LY	0.23	0/540	0.66	0/717
65	LZ	0.31	0/979	0.79	0/1321
66	La	0.28	0/995	0.73	0/1329
67	Lb	0.29	0/1106	0.78	0/1485
68	Lc	0.33	0/1200	0.78	0/1607
69	Ld	0.31	0/473	0.79	0/629
70	Le	0.30	0/745	0.76	0/1001
71	Lf	0.34	0/890	0.81	0/1196
72	Lg	0.30	0/1038	0.71	0/1390
73	Lh	0.32	0/868	0.79	1/1168 (0.1%)
74	Li	0.38	0/890	0.82	0/1189
75	Lj	0.31	0/978	0.74	0/1301
76	Lk	0.31	0/772	0.77	0/1026

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
77	Ll	0.43	0/660	0.94	0/875
78	Lm	0.34	0/618	0.74	0/826
79	Ln	0.32	0/443	0.81	0/588
80	Lo	0.30	0/416	0.84	0/553
81	Lp	0.37	0/230	0.87	0/296
82	Lq	0.33	0/836	0.80	0/1104
83	Lr	0.33	0/701	0.80	1/934 (0.1%)
84	Ls	0.43	0/1142	1.26	18/1537 (1.2%)
86	A	1.43	24/6015 (0.4%)	1.76	69/8386 (0.8%)
All	All	0.38	24/227518 (0.0%)	0.72	139/333767 (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
8	SS	0	1
9	SB	0	2
11	SU	0	1
16	SD	0	1
18	SZ	0	1
19	SF	0	1
22	SI	0	1
25	Sb	0	1
33	SN	0	1
45	LF	0	3
48	LI	0	1
49	LJ	0	3
58	LS	0	1
68	Lc	0	2
69	Ld	0	2
70	Le	0	1
71	Lf	0	1
75	Lj	0	1
84	Ls	1	2
85	Lt	0	4
86	A	0	12
All	All	1	43

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	A	2351	ALA	N-CA	20.84	1.70	1.46
86	A	1840	ALA	N-CA	20.80	1.70	1.46
86	A	2040	ALA	N-CA	20.79	1.70	1.46
86	A	2240	ALA	N-CA	20.75	1.70	1.46
86	A	2300	ALA	N-CA	18.20	1.69	1.46

The worst 5 of 139 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	A	1181	GLU	CA-C-N	20.41	145.35	119.84
86	A	1181	GLU	C-N-CA	20.41	145.35	119.84
86	A	1420	VAL	CA-C-N	17.02	141.12	119.84
86	A	1420	VAL	C-N-CA	17.02	141.12	119.84
86	A	1360	GLY	CA-C-N	15.08	138.70	119.84

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
84	Ls	51	5CT	C2

5 of 43 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	SB	125	THR	Peptide
9	SB	42	LEU	Peptide
16	SD	108	ARG	Peptide
8	SS	193	GLY	Peptide
11	SU	64	VAL	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	S2	37739	0	18988	295	0
2	SI	131	0	66	0	0
3	SP	1603	0	1610	19	0
4	SQ	1798	0	1890	26	0
5	SE	916	0	941	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	SR	1626	0	1715	24	0
7	SA	1729	0	1812	17	0
8	SS	2056	0	2140	33	0
9	SB	1605	0	1669	20	0
10	ST	1815	0	1894	25	0
11	SU	1473	0	1555	20	0
12	SV	1476	0	1501	37	0
13	SW	1479	0	1556	26	0
14	SC	752	0	719	9	0
15	SX	1142	0	1209	13	0
16	SD	875	0	878	12	0
17	SY	1192	0	1255	14	0
18	SZ	923	0	948	20	0
19	SF	1105	0	1166	15	0
20	SG	948	0	990	13	0
21	SH	1188	0	1218	25	0
22	SI	1112	0	1122	67	0
23	SJ	797	0	863	13	0
24	Sa	673	0	662	10	0
25	Sb	1021	0	1060	17	0
26	Sc	1121	0	1196	17	0
27	Sd	1032	0	1044	18	0
28	SK	651	0	682	11	0
29	Se	765	0	814	16	0
30	Sf	610	0	633	10	0
31	SM	442	0	432	5	0
32	Sg	451	0	494	6	0
33	SN	556	0	552	7	0
34	SO	2383	0	2332	30	0
35	SL	491	0	524	3	0
36	Sm	1611	0	817	5	0
37	Sn	1606	0	816	8	0
38	So	2729	0	2780	33	0
39	Sp	240	0	50	0	0
40	LA	68091	0	34217	406	0
41	LB	2579	0	1304	19	0
42	LC	3353	0	1695	32	0
43	LD	1899	0	1957	29	0
44	LE	3075	0	3142	48	0
45	LF	2748	0	2859	39	0
46	LG	2351	0	2294	26	0
47	LH	1307	0	1377	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	LI	1784	0	1862	15	0
49	LJ	1804	0	1877	32	0
50	LK	1508	0	1572	12	0
51	LL	1764	0	1804	22	0
52	LM	1346	0	1370	23	0
53	LN	1543	0	1608	20	0
54	LO	1053	0	1149	14	0
55	LP	1720	0	1779	36	0
56	LQ	1555	0	1659	13	0
57	LR	1416	0	1433	15	0
58	LS	1441	0	1543	17	0
59	LT	1515	0	1606	14	0
60	LU	1437	0	1475	13	0
61	LV	1272	0	1312	17	0
62	LW	796	0	812	6	0
63	LX	1003	0	1048	16	0
64	LY	528	0	546	9	0
65	LZ	964	0	1025	7	0
66	La	984	0	1075	10	0
67	Lb	1080	0	1122	11	0
68	Lc	1169	0	1211	24	0
69	Ld	462	0	491	11	0
70	Le	737	0	792	7	0
71	Lf	876	0	912	7	0
72	Lg	1017	0	1081	12	0
73	Lh	850	0	880	10	0
74	Li	880	0	945	16	0
75	Lj	969	0	1078	7	0
76	Lk	766	0	844	5	0
77	Ll	645	0	649	14	0
78	Lm	612	0	682	8	0
79	Ln	436	0	475	15	0
80	Lo	410	0	446	7	0
81	Lp	229	0	273	2	0
82	Lq	824	0	892	6	0
83	Lr	694	0	738	17	0
84	Ls	1143	0	1104	25	0
85	Lt	1050	0	230	1	0
86	A	6029	0	5195	439	0
All	All	213576	0	158033	1993	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 1993 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)
22:SI:138:GLN:HG2	86:A:1303:GLU:CA	1.24	1.55
86:A:2240:ALA:N	86:A:2240:ALA:CA	1.70	1.54
86:A:2411:ALA:N	86:A:2411:ALA:CA	1.69	1.54
86:A:1421:PRO:N	86:A:1421:PRO:CA	1.69	1.53
86:A:2040:ALA:N	86:A:2040:ALA:CA	1.70	1.53

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	
3	SP	204/206 (99%)	183 (90%)	21 (10%)	0	100	100
4	SQ	222/232 (96%)	201 (90%)	21 (10%)	0	100	100
5	SE	115/117 (98%)	100 (87%)	15 (13%)	0	100	100
6	SR	214/216 (99%)	190 (89%)	24 (11%)	0	100	100
7	SA	220/222 (99%)	209 (95%)	11 (5%)	0	100	100
8	SS	256/258 (99%)	229 (90%)	27 (10%)	0	100	100
9	SB	204/206 (99%)	189 (93%)	15 (7%)	0	100	100
10	ST	226/228 (99%)	211 (93%)	14 (6%)	1 (0%)	30	64
11	SU	182/184 (99%)	163 (90%)	19 (10%)	0	100	100
12	SV	183/198 (92%)	167 (91%)	16 (9%)	0	100	100
13	SW	182/184 (99%)	165 (91%)	16 (9%)	1 (0%)	24	59
14	SC	90/92 (98%)	79 (88%)	11 (12%)	0	100	100
15	SX	140/142 (99%)	124 (89%)	16 (11%)	0	100	100
16	SD	119/121 (98%)	91 (76%)	26 (22%)	2 (2%)	7	35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	SY	148/150 (99%)	133 (90%)	15 (10%)	0	100	100
18	SZ	125/127 (98%)	110 (88%)	15 (12%)	0	100	100
19	SF	139/141 (99%)	125 (90%)	14 (10%)	0	100	100
20	SG	117/125 (94%)	112 (96%)	5 (4%)	0	100	100
21	SH	143/145 (99%)	131 (92%)	12 (8%)	0	100	100
22	SI	141/143 (99%)	128 (91%)	13 (9%)	0	100	100
23	SJ	98/100 (98%)	88 (90%)	10 (10%)	0	100	100
24	Sa	85/87 (98%)	73 (86%)	12 (14%)	0	100	100
25	Sb	127/129 (98%)	113 (89%)	14 (11%)	0	100	100
26	Sc	142/144 (99%)	123 (87%)	19 (13%)	0	100	100
27	Sd	132/134 (98%)	124 (94%)	8 (6%)	0	100	100
28	SK	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
29	Se	95/97 (98%)	84 (88%)	11 (12%)	0	100	100
30	Sf	79/81 (98%)	67 (85%)	12 (15%)	0	100	100
31	SM	51/53 (96%)	48 (94%)	3 (6%)	0	100	100
32	Sg	55/57 (96%)	43 (78%)	12 (22%)	0	100	100
33	SN	71/73 (97%)	48 (68%)	23 (32%)	0	100	100
34	SO	310/312 (99%)	268 (86%)	42 (14%)	0	100	100
35	SL	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
38	So	341/366 (93%)	311 (91%)	30 (9%)	0	100	100
43	LD	249/251 (99%)	223 (90%)	26 (10%)	0	100	100
44	LE	384/386 (100%)	355 (92%)	29 (8%)	0	100	100
45	LF	359/361 (99%)	323 (90%)	35 (10%)	1 (0%)	36	69
46	LG	292/294 (99%)	266 (91%)	26 (9%)	0	100	100
47	LH	163/175 (93%)	147 (90%)	16 (10%)	0	100	100
48	LI	220/222 (99%)	203 (92%)	17 (8%)	0	100	100
49	LJ	231/233 (99%)	208 (90%)	23 (10%)	0	100	100
50	LK	189/191 (99%)	174 (92%)	15 (8%)	0	100	100
51	LL	216/218 (99%)	189 (88%)	27 (12%)	0	100	100
52	LM	167/169 (99%)	153 (92%)	14 (8%)	0	100	100
53	LN	191/193 (99%)	171 (90%)	19 (10%)	1 (0%)	24	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	LO	134/136 (98%)	121 (90%)	13 (10%)	0	100	100
55	LP	201/203 (99%)	181 (90%)	19 (10%)	1 (0%)	24	59
56	LQ	195/197 (99%)	186 (95%)	9 (5%)	0	100	100
57	LR	181/183 (99%)	168 (93%)	13 (7%)	0	100	100
58	LS	183/185 (99%)	170 (93%)	13 (7%)	0	100	100
59	LT	186/188 (99%)	178 (96%)	8 (4%)	0	100	100
60	LU	169/171 (99%)	159 (94%)	10 (6%)	0	100	100
61	LV	157/159 (99%)	143 (91%)	14 (9%)	0	100	100
62	LW	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
63	LX	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
64	LY	63/65 (97%)	59 (94%)	4 (6%)	0	100	100
65	LZ	119/121 (98%)	110 (92%)	9 (8%)	0	100	100
66	La	123/125 (98%)	117 (95%)	6 (5%)	0	100	100
67	Lb	133/135 (98%)	117 (88%)	16 (12%)	0	100	100
68	Lc	146/148 (99%)	130 (89%)	16 (11%)	0	100	100
69	Ld	56/58 (97%)	47 (84%)	9 (16%)	0	100	100
70	Le	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
71	Lf	107/109 (98%)	93 (87%)	14 (13%)	0	100	100
72	Lg	125/127 (98%)	115 (92%)	10 (8%)	0	100	100
73	Lh	104/106 (98%)	98 (94%)	6 (6%)	0	100	100
74	Li	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
75	Lj	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
76	Lk	97/99 (98%)	91 (94%)	6 (6%)	0	100	100
77	Ll	79/81 (98%)	71 (90%)	8 (10%)	0	100	100
78	Lm	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
79	Ln	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
80	Lo	50/52 (96%)	44 (88%)	6 (12%)	0	100	100
81	Lp	23/25 (92%)	23 (100%)	0	0	100	100
82	Lq	101/103 (98%)	93 (92%)	8 (8%)	0	100	100
83	Lr	89/91 (98%)	87 (98%)	2 (2%)	0	100	100
84	Ls	151/154 (98%)	117 (78%)	31 (20%)	3 (2%)	6	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
86	A	1182/1209 (98%)	929 (79%)	190 (16%)	63 (5%)	1	17
All	All	12588/12828 (98%)	11260 (90%)	1255 (10%)	73 (1%)	23	55

5 of 73 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
84	Ls	133	ASP
86	A	1162	ALA
86	A	1163	LEU
86	A	1164	SER
86	A	1182	PRO

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	
3	SP	170/173 (98%)	170 (100%)	0	100	100
4	SQ	200/205 (98%)	200 (100%)	0	100	100
5	SE	95/98 (97%)	95 (100%)	0	100	100
6	SR	175/175 (100%)	175 (100%)	0	100	100
7	SA	182/182 (100%)	180 (99%)	2 (1%)	65	74
8	SS	220/220 (100%)	220 (100%)	0	100	100
9	SB	172/173 (99%)	172 (100%)	0	100	100
10	ST	189/195 (97%)	189 (100%)	0	100	100
11	SU	163/165 (99%)	163 (100%)	0	100	100
12	SV	148/159 (93%)	148 (100%)	0	100	100
13	SW	156/157 (99%)	155 (99%)	1 (1%)	78	80
14	SC	77/85 (91%)	76 (99%)	1 (1%)	61	71
15	SX	126/127 (99%)	125 (99%)	1 (1%)	73	77
16	SD	88/98 (90%)	88 (100%)	0	100	100
17	SY	127/127 (100%)	126 (99%)	1 (1%)	73	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	SZ	90/96 (94%)	90 (100%)	0	100	100
19	SF	117/117 (100%)	116 (99%)	1 (1%)	70	75
20	SG	101/113 (89%)	101 (100%)	0	100	100
21	SH	127/128 (99%)	126 (99%)	1 (1%)	73	77
22	SI	115/115 (100%)	114 (99%)	1 (1%)	70	75
23	SJ	93/93 (100%)	93 (100%)	0	100	100
24	Sa	71/74 (96%)	71 (100%)	0	100	100
25	Sb	110/110 (100%)	110 (100%)	0	100	100
26	Sc	119/119 (100%)	118 (99%)	1 (1%)	73	77
27	Sd	102/112 (91%)	102 (100%)	0	100	100
28	SK	67/73 (92%)	67 (100%)	0	100	100
29	Se	82/83 (99%)	81 (99%)	1 (1%)	63	72
30	Sf	70/70 (100%)	70 (100%)	0	100	100
31	SM	47/47 (100%)	47 (100%)	0	100	100
32	Sg	48/49 (98%)	48 (100%)	0	100	100
33	SN	56/63 (89%)	56 (100%)	0	100	100
34	SO	250/257 (97%)	250 (100%)	0	100	100
35	SL	55/56 (98%)	55 (100%)	0	100	100
38	So	298/308 (97%)	297 (100%)	1 (0%)	86	85
43	LD	190/193 (98%)	190 (100%)	0	100	100
44	LE	318/322 (99%)	317 (100%)	1 (0%)	86	85
45	LF	288/288 (100%)	287 (100%)	1 (0%)	86	85
46	LG	241/243 (99%)	241 (100%)	0	100	100
47	LH	139/154 (90%)	138 (99%)	1 (1%)	76	78
48	LI	186/186 (100%)	186 (100%)	0	100	100
49	LJ	187/191 (98%)	187 (100%)	0	100	100
50	LK	168/171 (98%)	168 (100%)	0	100	100
51	LL	185/185 (100%)	185 (100%)	0	100	100
52	LM	145/147 (99%)	145 (100%)	0	100	100
53	LN	154/154 (100%)	154 (100%)	0	100	100
54	LO	107/107 (100%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	LP	175/175 (100%)	174 (99%)	1 (1%)	78	80
56	LQ	160/160 (100%)	160 (100%)	0	100	100
57	LR	138/145 (95%)	138 (100%)	0	100	100
58	LS	150/150 (100%)	149 (99%)	1 (1%)	76	78
59	LT	152/153 (99%)	152 (100%)	0	100	100
60	LU	155/155 (100%)	155 (100%)	0	100	100
61	LV	135/136 (99%)	135 (100%)	0	100	100
62	LW	87/87 (100%)	87 (100%)	0	100	100
63	LX	104/104 (100%)	104 (100%)	0	100	100
64	LY	54/57 (95%)	54 (100%)	0	100	100
65	LZ	104/105 (99%)	104 (100%)	0	100	100
66	La	108/108 (100%)	107 (99%)	1 (1%)	70	75
67	Lb	112/115 (97%)	112 (100%)	0	100	100
68	Lc	117/118 (99%)	117 (100%)	0	100	100
69	Ld	46/46 (100%)	46 (100%)	0	100	100
70	Le	81/81 (100%)	81 (100%)	0	100	100
71	Lf	92/96 (96%)	92 (100%)	0	100	100
72	Lg	108/109 (99%)	108 (100%)	0	100	100
73	Lh	90/90 (100%)	89 (99%)	1 (1%)	65	74
74	Li	95/95 (100%)	95 (100%)	0	100	100
75	Lj	104/104 (100%)	103 (99%)	1 (1%)	68	75
76	Lk	80/81 (99%)	79 (99%)	1 (1%)	61	71
77	Ll	67/67 (100%)	64 (96%)	3 (4%)	24	49
78	Lm	68/68 (100%)	68 (100%)	0	100	100
79	Ln	45/45 (100%)	45 (100%)	0	100	100
80	Lo	45/47 (96%)	45 (100%)	0	100	100
81	Lp	22/23 (96%)	22 (100%)	0	100	100
82	Lq	87/88 (99%)	87 (100%)	0	100	100
83	Lr	71/71 (100%)	70 (99%)	1 (1%)	59	71
84	Ls	118/129 (92%)	117 (99%)	1 (1%)	73	77
All	All	9584/9771 (98%)	9558 (100%)	26 (0%)	84	85

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	LH	156	LYS
66	La	74	TYR
83	Lr	45	LYS
58	LS	31	LYS
73	Lh	20	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 140 such sidechains are listed below:

Mol	Chain	Res	Type
67	Lb	122	HIS
68	Lc	62	HIS
74	Li	61	GLN
25	Sb	80	ASN
25	Sb	56	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	S2	1768/1800 (98%)	533 (30%)	52 (2%)
2	Sl	5/6 (83%)	1 (20%)	0
36	Sm	75/76 (98%)	35 (46%)	0
37	Sn	74/75 (98%)	23 (31%)	0
40	LA	3180/3394 (93%)	717 (22%)	42 (1%)
41	LB	120/121 (99%)	15 (12%)	1 (0%)
42	LC	157/158 (99%)	32 (20%)	3 (1%)
All	All	5379/5630 (95%)	1356 (25%)	98 (1%)

5 of 1356 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	S2	2	A
1	S2	4	C
1	S2	14	C
1	S2	25	C
1	S2	26	A

5 of 98 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
40	LA	849	C
40	LA	1815	U
40	LA	896	A
40	LA	1307	G
40	LA	2445	A

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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
84	5CT	Ls	51	84	13,14,15	2.37	1 (7%)	8,15,17	2.18	3 (37%)

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
84	5CT	Ls	51	84	1/1/2/4	5/13/14/16	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	Ls	51	5CT	O1-C2	-8.40	1.18	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	Ls	51	5CT	O1-C2-C3	3.83	119.57	109.35
84	Ls	51	5CT	O1-C2-C1	3.52	120.84	109.29
84	Ls	51	5CT	C1-NZ-CE	-2.74	107.41	113.38

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
84	Ls	51	5CT	C2

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
84	Ls	51	5CT	C2-C1-NZ-CE
84	Ls	51	5CT	NZ-C1-C2-C3
84	Ls	51	5CT	O1-C2-C3-C4
84	Ls	51	5CT	C2-C3-C4-N1
84	Ls	51	5CT	CE-CD-CG-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	Ls	51	5CT	1	0

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
86	A	13

The worst 5 of 13 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1104:ALA	C	1124:GLY	N	40.36
1	A	997:ALA	C	1019:ALA	N	35.44
1	A	1917:ALA	C	2000:ALA	N	14.67
1	A	1044:ALA	C	1055:ALA	N	12.76
1	A	1074:ALA	C	1084:ALA	N	11.98

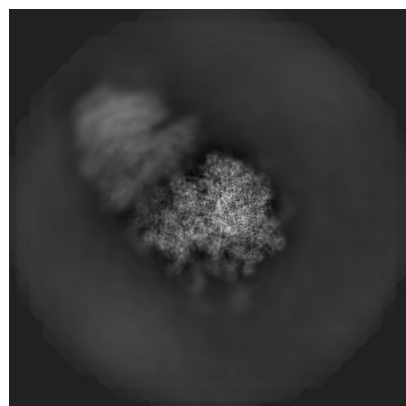
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12534. These allow visual inspection of the internal detail of the map and identification of artifacts.

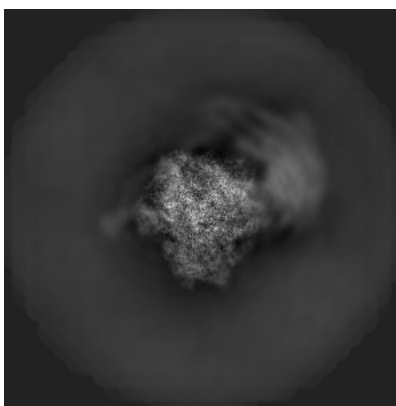
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

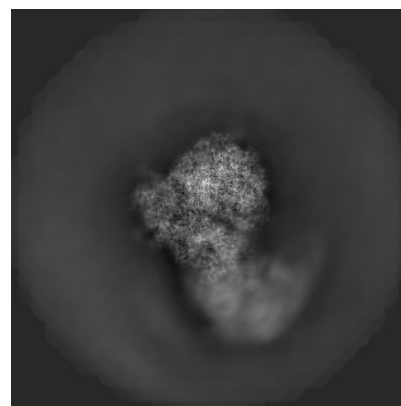
6.1.1 Primary map



X

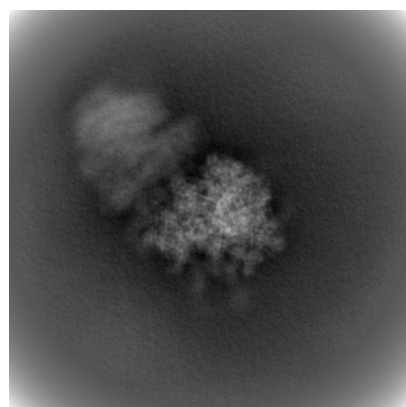


Y

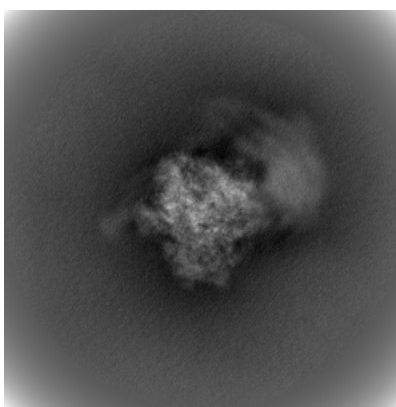


Z

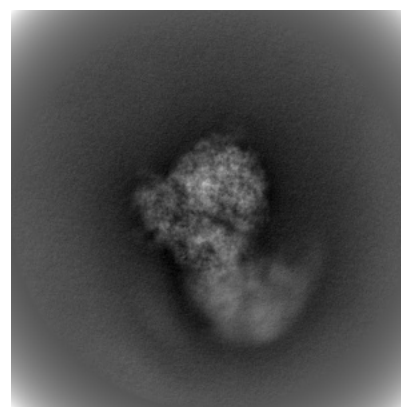
6.1.2 Raw map



X



Y

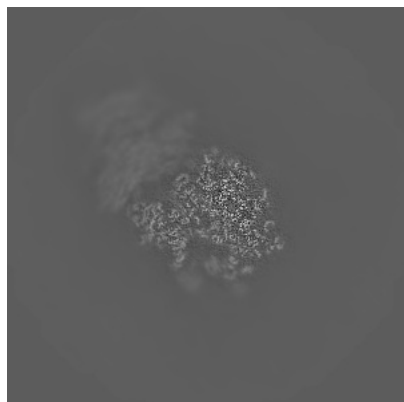


Z

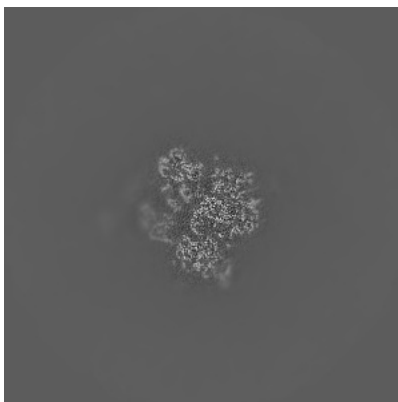
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

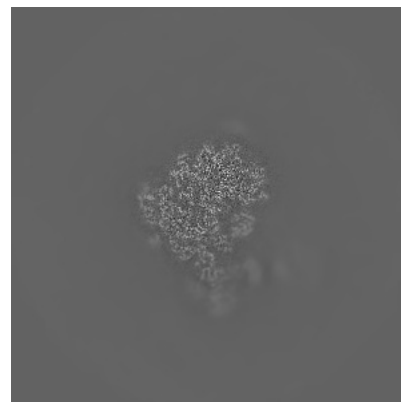
6.2.1 Primary map



X Index: 350

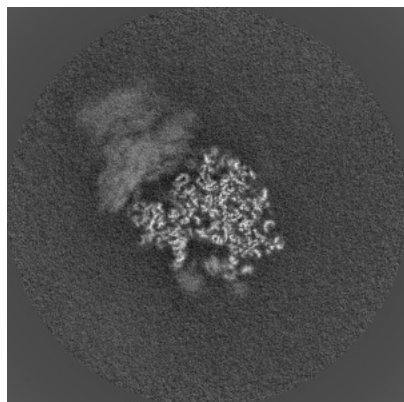


Y Index: 350

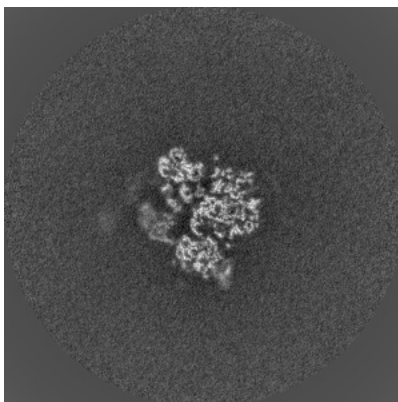


Z Index: 350

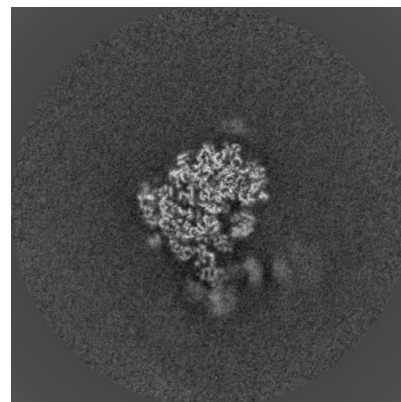
6.2.2 Raw map



X Index: 350



Y Index: 350

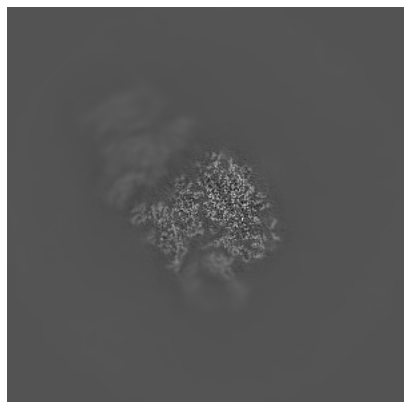


Z Index: 350

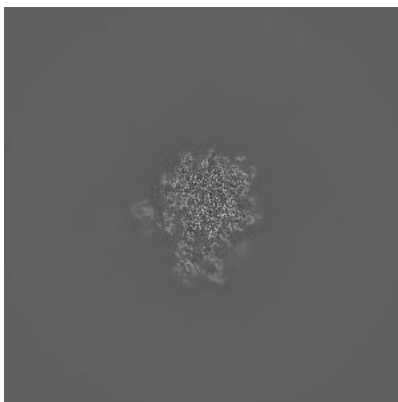
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 338

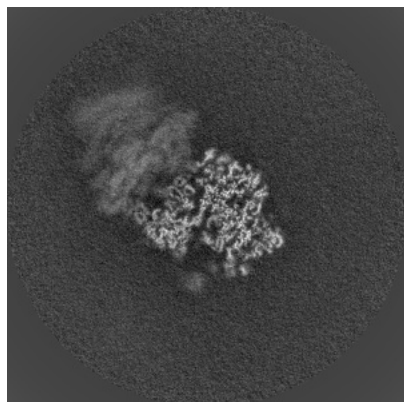


Y Index: 381

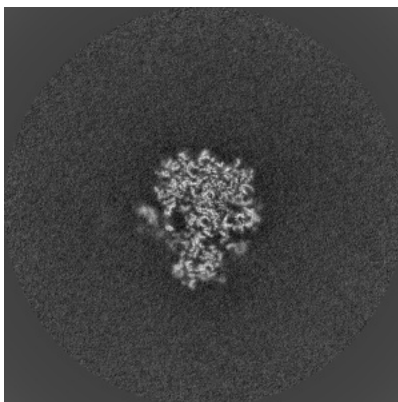


Z Index: 356

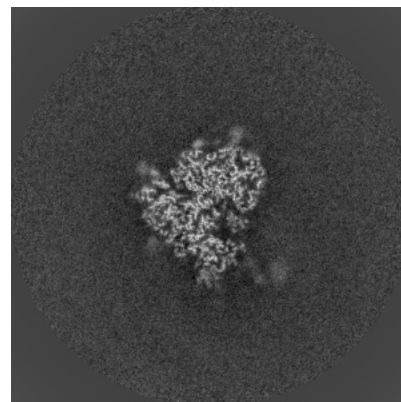
6.3.2 Raw map



X Index: 360



Y Index: 369

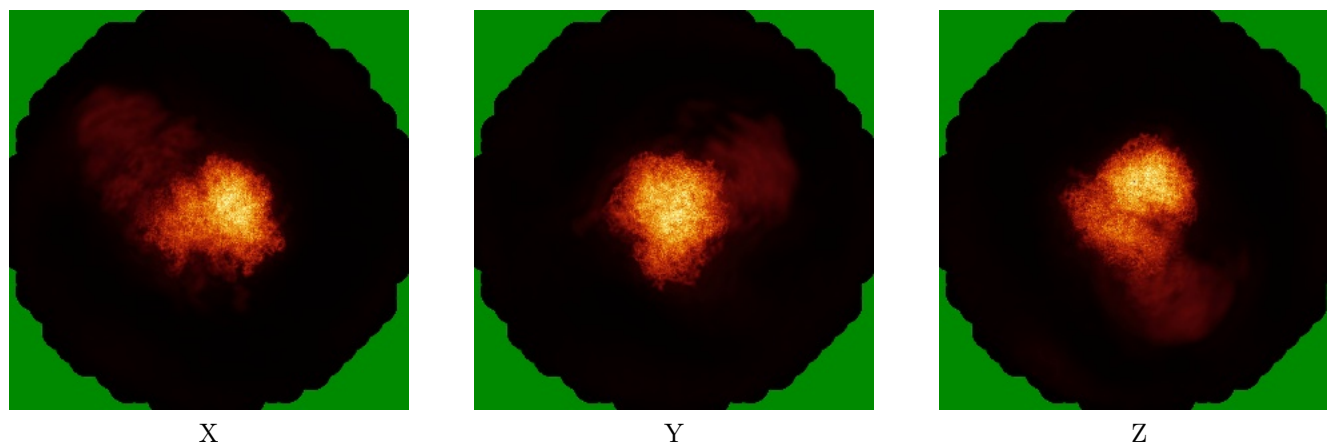


Z Index: 334

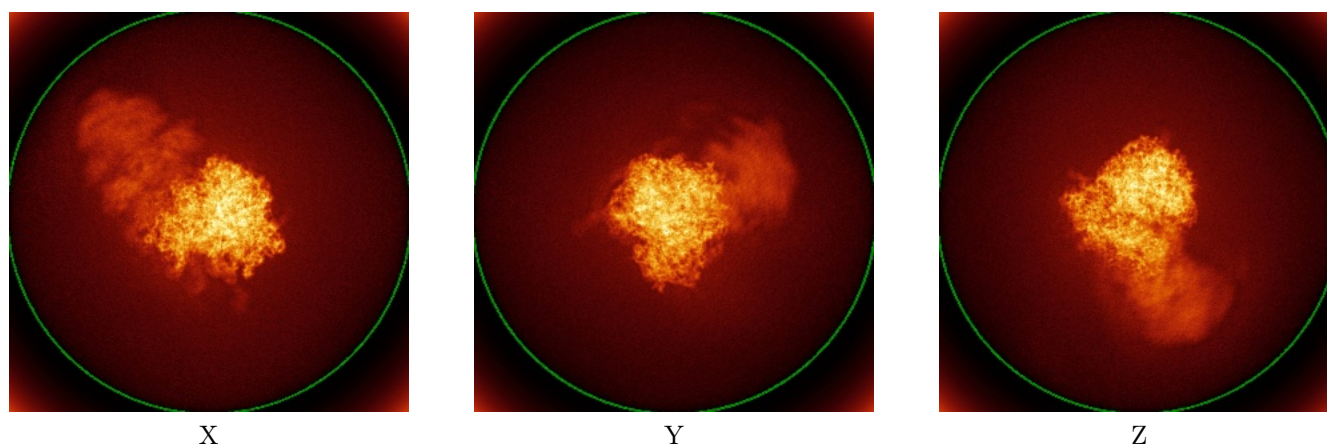
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

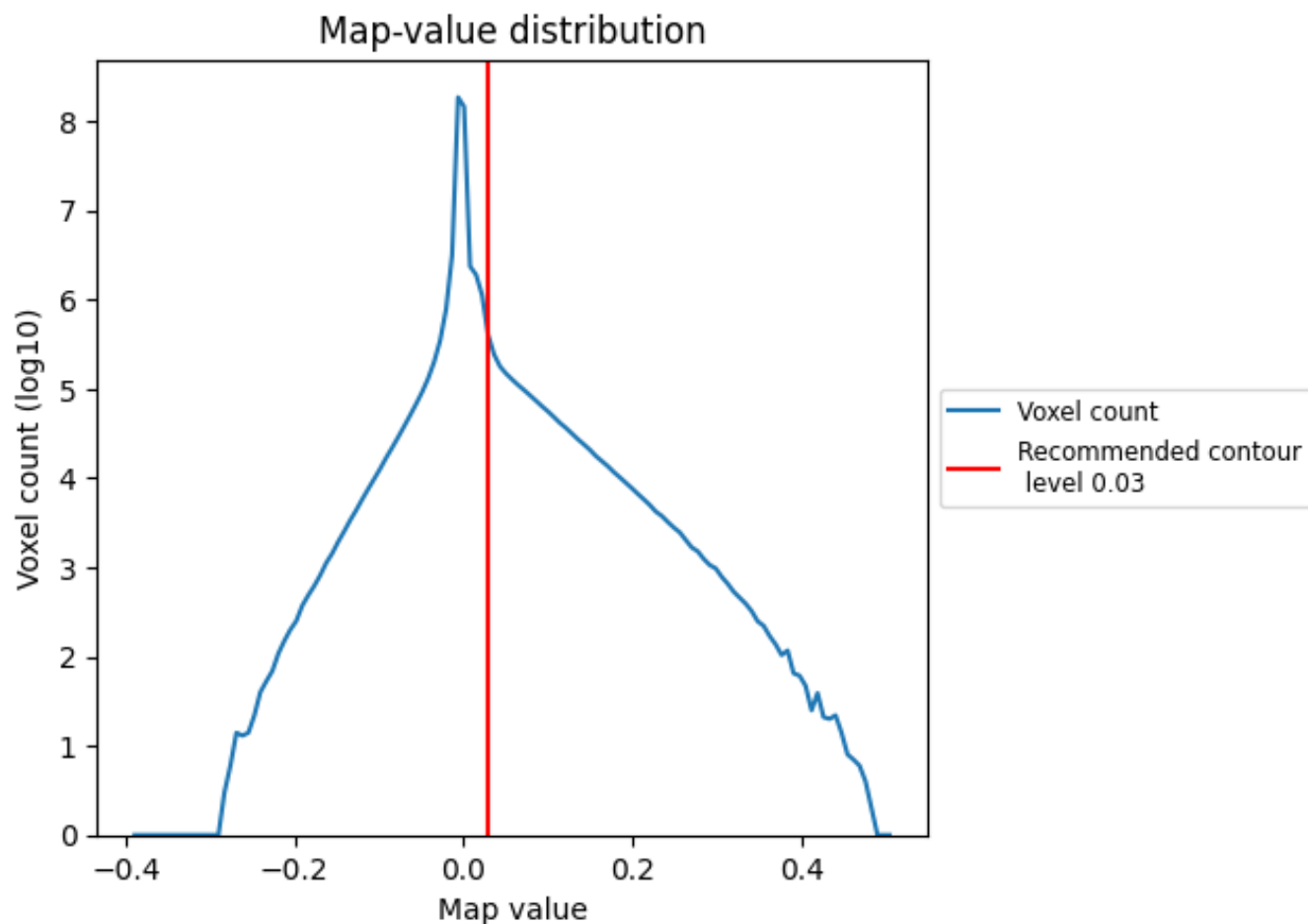
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

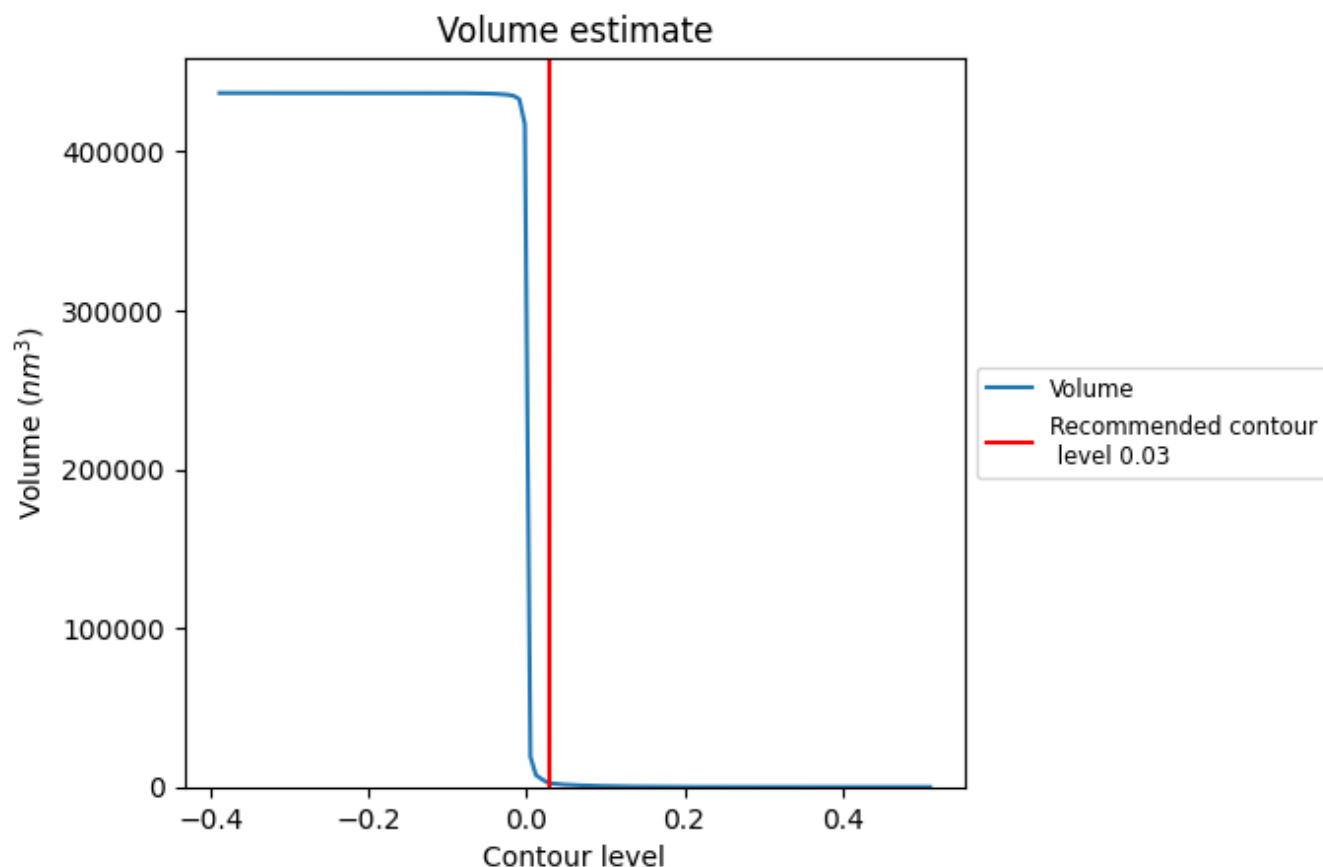
This section contains the results of statistical analysis of the map.

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.

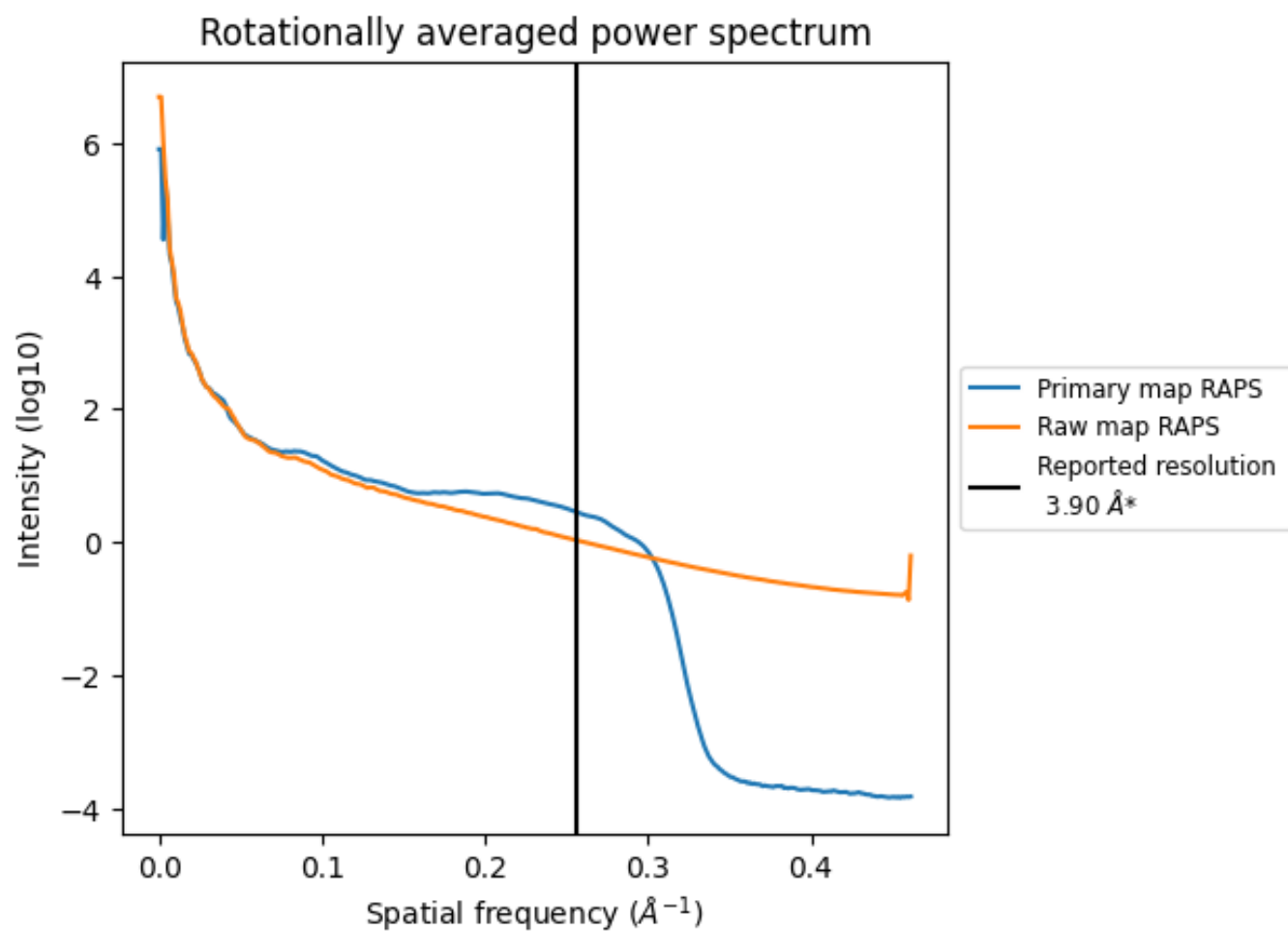
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2499 nm³; this corresponds to an approximate mass of 2257 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 ⓘ

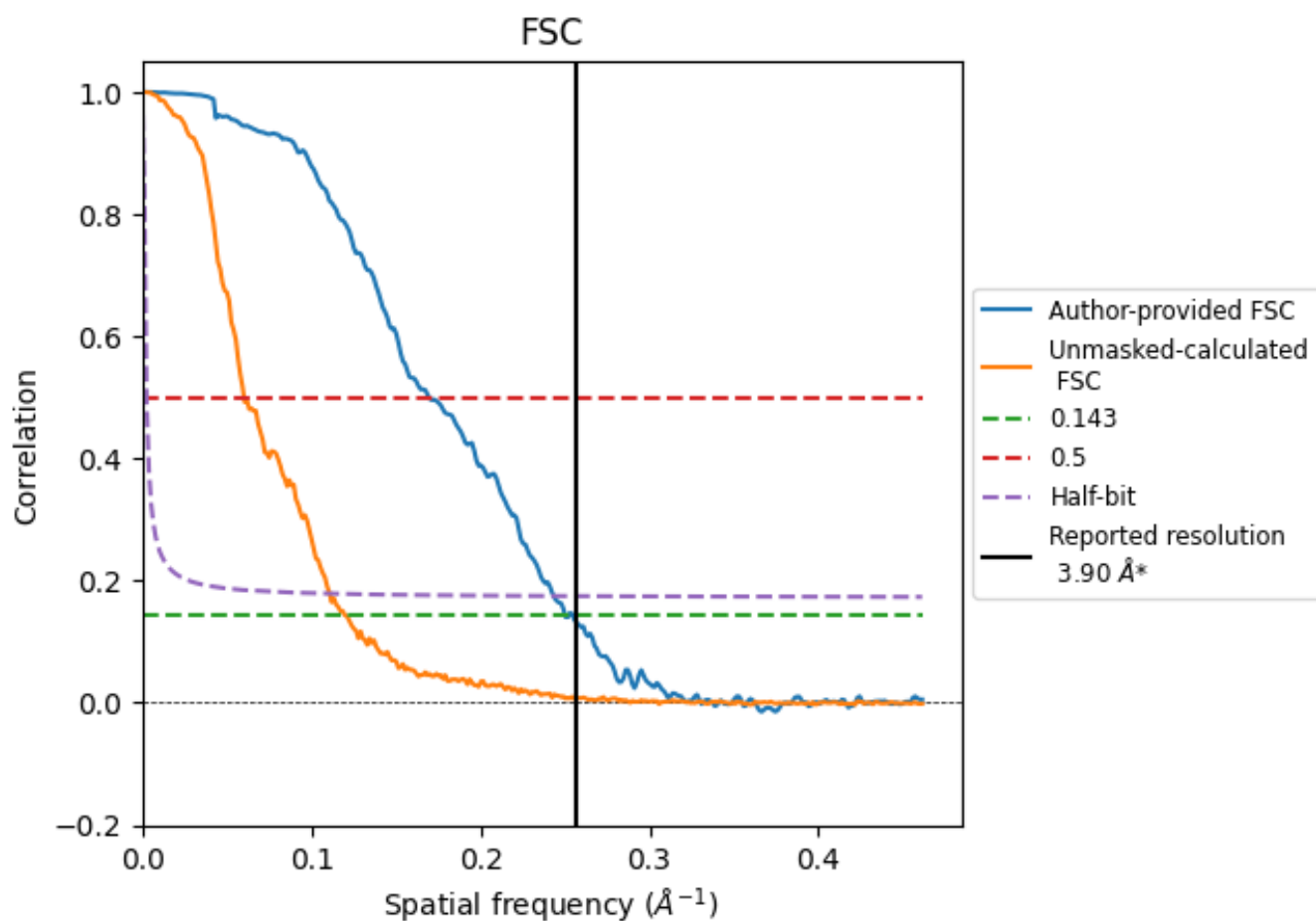


*Reported resolution corresponds to spatial frequency of $0.256 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	4.00	5.90	4.11
Unmasked-calculated*	8.33	16.61	9.03

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.33 differs from the reported value 3.9 by more than 10 %

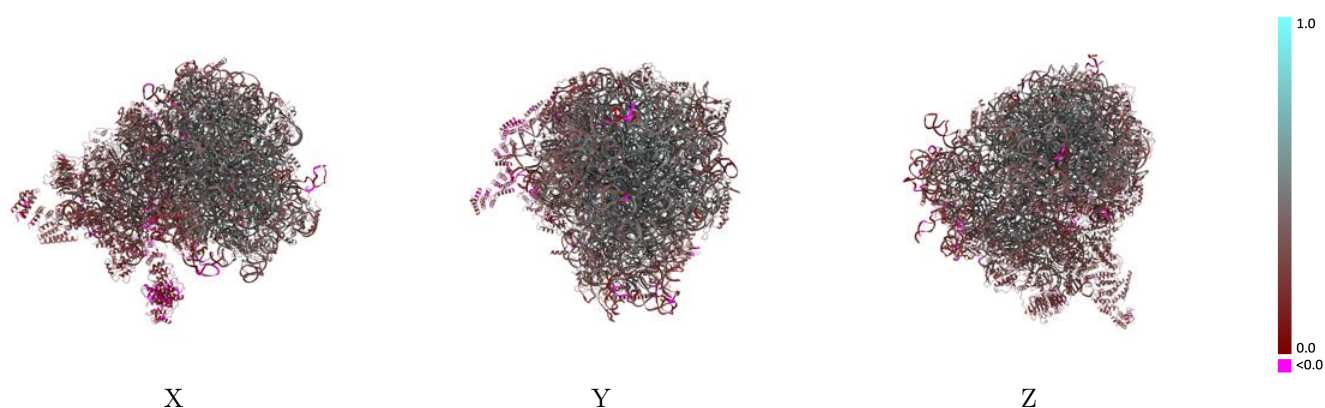
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12534 and PDB model 7NRC. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)

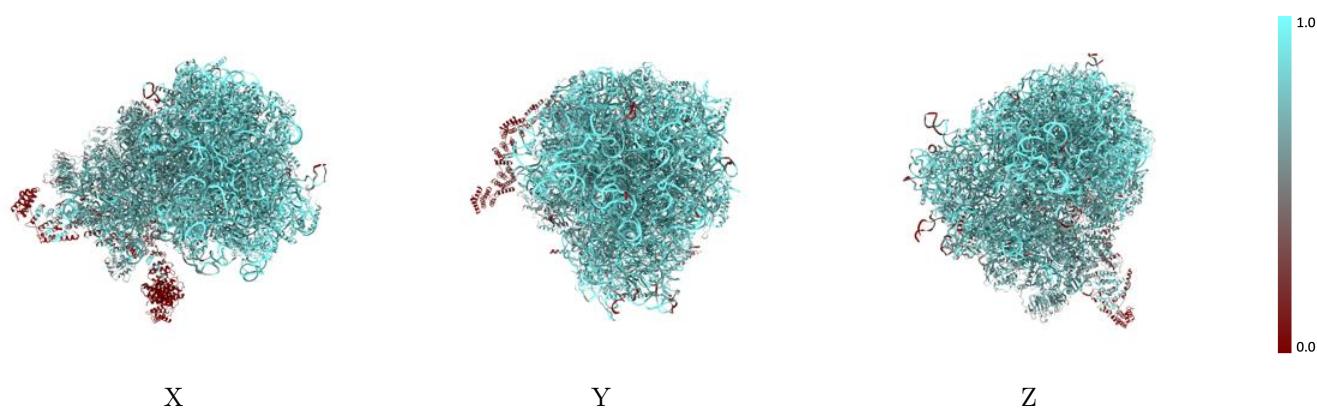
This section was not generated.

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



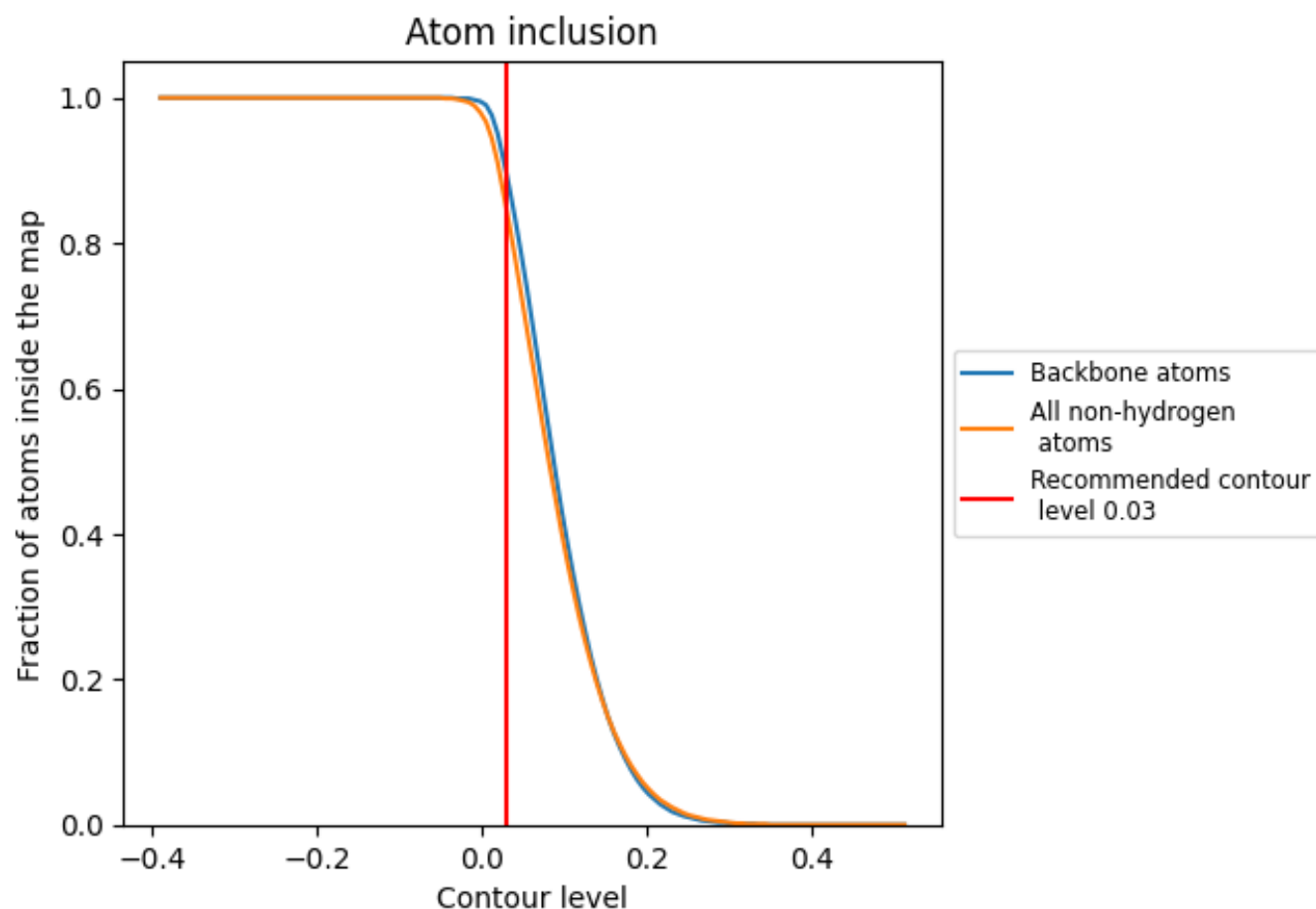
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 84% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8450	 0.3780
A	 0.2820	 0.1550
LA	 0.9450	 0.4340
LB	 0.9490	 0.3610
LC	 0.9520	 0.4520
LD	 0.8640	 0.4660
LE	 0.8640	 0.4320
LF	 0.8480	 0.4070
LG	 0.7670	 0.2890
LH	 0.8260	 0.3730
LI	 0.8670	 0.4010
LJ	 0.8090	 0.3590
LK	 0.8110	 0.3720
LL	 0.7860	 0.3500
LM	 0.6150	 0.1650
LN	 0.8410	 0.3960
LO	 0.8610	 0.3760
LP	 0.8800	 0.4560
LQ	 0.8740	 0.4510
LR	 0.8630	 0.4320
LS	 0.8550	 0.4130
LT	 0.7830	 0.3720
LU	 0.8390	 0.4170
LV	 0.8430	 0.4050
LW	 0.7860	 0.3220
LX	 0.8210	 0.4320
LY	 0.8500	 0.4500
LZ	 0.8320	 0.4090
La	 0.8350	 0.3670
Lb	 0.8310	 0.3800
Lc	 0.8660	 0.4240
Ld	 0.8520	 0.3950
Le	 0.8040	 0.3710
Lf	 0.8120	 0.4100
Lg	 0.8670	 0.4440



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Chain	Atom inclusion	Q-score
Lh	 0.8840	 0.4680
Li	 0.8060	 0.4110
Lj	 0.8220	 0.3790
Lk	 0.8090	 0.3610
Ll	 0.8950	 0.4670
Lm	 0.7860	 0.3300
Ln	 0.8750	 0.4410
Lo	 0.8260	 0.3990
Lp	 0.8030	 0.4130
Lq	 0.8350	 0.4320
Lr	 0.8280	 0.4270
Ls	 0.6430	 0.3290
Lt	 0.8380	 0.2970
S2	 0.9020	 0.3700
SA	 0.6950	 0.3000
SB	 0.6820	 0.2860
SC	 0.6760	 0.2400
SD	 0.5780	 0.1730
SE	 0.7390	 0.2740
SF	 0.7310	 0.3150
SG	 0.6800	 0.2890
SH	 0.7010	 0.2750
SI	 0.6770	 0.2650
SJ	 0.7050	 0.2900
SK	 0.6080	 0.2620
SL	 0.6960	 0.3260
SM	 0.7850	 0.3670
SN	 0.5750	 0.1420
SO	 0.6180	 0.2390
SP	 0.7100	 0.3030
SQ	 0.6700	 0.3000
SR	 0.7780	 0.3720
SS	 0.7970	 0.3580
ST	 0.7680	 0.3090
SU	 0.6480	 0.2620
SV	 0.8290	 0.3660
SW	 0.7500	 0.3100
SX	 0.7890	 0.3990
SY	 0.7630	 0.3580
SZ	 0.7420	 0.3590
Sa	 0.7410	 0.3490
Sb	 0.8140	 0.3970

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Chain	Atom inclusion	Q-score
Sc	 0.8090	 0.4200
Sd	 0.7740	 0.3140
Se	 0.8140	 0.3980
Sf	 0.7390	 0.3380
Sg	 0.7490	 0.3190
Sl	 0.9470	 0.4400
Sm	 0.8870	 0.3140
Sn	 0.8950	 0.3330
So	 0.5370	 0.2640
Sp	 0.7580	 0.2700