



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 12:35 AM UTC

PDB ID : 7RR5 / pdb_00007rr5
EMDB ID : EMD-24652
Title : Structure of ribosomal complex bound with Rbg1/Tma46
Authors : Zeng, F.; Li, X.; Pires-Alves, M.; Chen, X.; Hawk, C.W.; Jin, H.
Deposited on : 2021-08-09
Resolution : 3.23 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

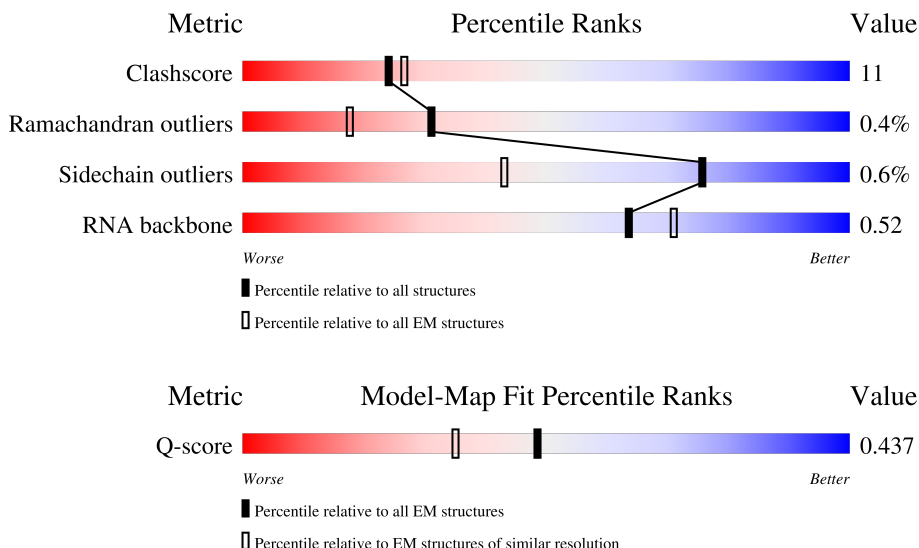
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.23 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.



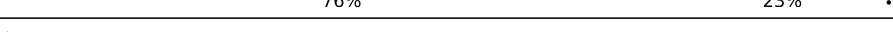
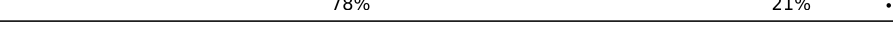
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14612 (2.73 - 3.73)

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	C1	3396	
2	C4	121	
3	C3	158	

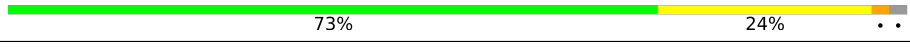
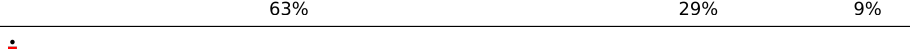
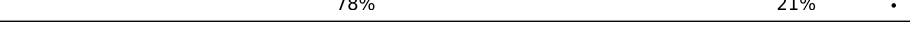
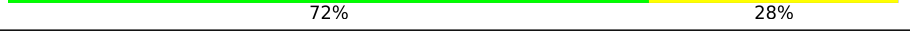
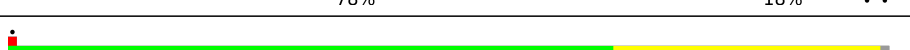
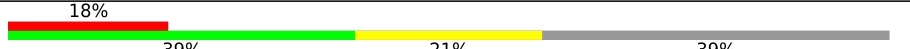
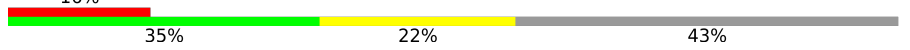
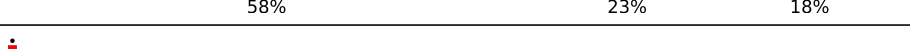
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Mol	Chain	Length	Quality of chain
4	LA	254	 74%25%.
5	LB	387	 80%20%
6	LC	362	 72%28%
7	LD	297	 75%24%.
8	LE	176	 71%24%5%.
9	LF	244	 60%31%9%
10	LG	256	 62%28%.9%
11	LH	191	 70%30%
12	LI	221	 70%29%.
13	LJ	174	 65%31%..
14	LL	199	 77%19%..
15	LM	138	 75%23%.
16	LN	204	 66%33%
17	LO	199	 77%21%..
18	LP	184	 77%22%.
19	LQ	186	 76%23%..
20	LR	189	 78%21%..
21	LS	172	 78%20%..
22	LT	160	 77%22%.
23	LU	121	 68%15%17%
24	LV	137	 74%25%.
25	LW	155	 14%74%7%19%
26	LX	142	 64%20%.15%
27	LY	127	 74%24%.
28	LZ	136	 72%27%.

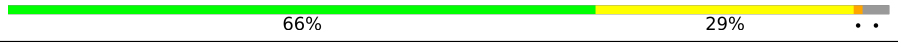
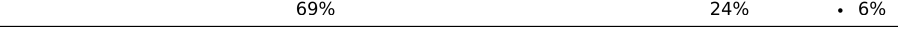
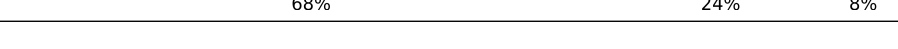
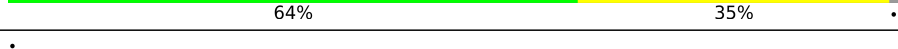
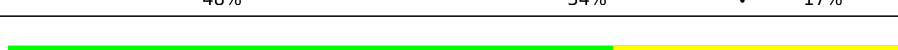
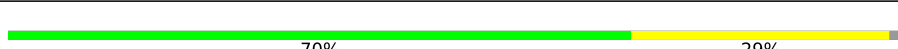
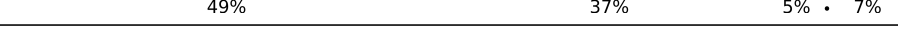
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Mol	Chain	Length	Quality of chain
29	La	149	
30	Lb	59	
31	Lc	105	
32	Ld	113	
33	Le	130	
34	Lf	107	
35	Lg	121	
36	Lh	120	
37	Li	100	
38	Lj	88	
39	Lk	78	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	P0	312	
46	P2	165	
47	C2	1800	
48	SA	252	
49	SB	255	
50	SC	254	
51	SD	240	
52	SE	261	
53	SF	225	

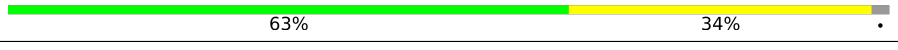
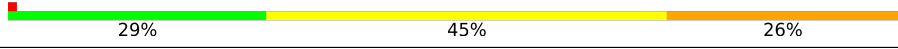
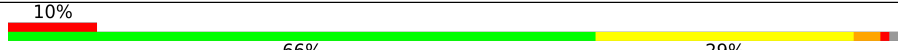
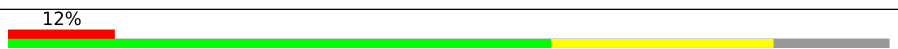
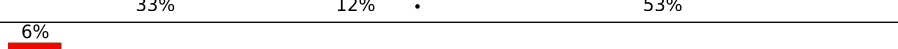
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Mol	Chain	Length	Quality of chain
54	SG	236	
55	SH	190	
56	SI	200	
57	SJ	197	
58	SK	105	
59	SL	156	
60	SM	143	
61	SN	151	
62	SO	138	
63	SP	142	
64	SQ	143	
65	SR	136	
66	SS	146	
67	ST	144	
68	SU	121	
69	SV	87	
70	SW	130	
71	SX	145	
72	SY	135	
73	SZ	108	
74	Sa	119	
75	Sb	82	
76	Sc	67	
77	Sd	56	
78	Se	63	

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Mol	Chain	Length	Quality of chain
79	Sf	152	
80	Sg	319	
81	A	76	
82	P	76	
83	m	16	
84	5	157	
85	R	410	
86	T	345	
87	L1	210	

2 Entry composition

There are 90 unique types of molecules in this entry. The entry contains 212517 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 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C1	3221	Total	C	N	O	P	0	0
			68888	30771	12409	22487	3221		

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

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

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

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

- Molecule 4 is a protein called 60S ribosomal protein L2-B.

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

- Molecule 5 is a protein called RPL3 isoform 1.

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

- Molecule 6 is a protein called RPL4A isoform 1.

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

- Molecule 7 is a protein called RPL5 isoform 1.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	167	Total	C	N	O	S	0	0
			1307	843	234	230			

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

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

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

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

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

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

- Molecule 12 is a protein called RPL10 isoform 1.

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

- Molecule 13 is a protein called RPL11B isoform 1.

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

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

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

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

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

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

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

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

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

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

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

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

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

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

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

- Molecule 21 is a protein called 60S ribosomal protein L20-A.

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

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

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

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

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

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

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

- Molecule 25 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	126	Total	C	N	O	S	0	0
			849	532	167	149	1		

- Molecule 26 is a protein called 60S ribosomal protein L25.

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

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

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

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

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

- Molecule 29 is a protein called 60S ribosomal protein L28.

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

- Molecule 30 is a protein called RPL29 isoform 1.

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

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

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

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

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

- Molecule 33 is a protein called RPL32 isoform 1.

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

- Molecule 34 is a protein called 60S ribosomal protein L33-A.

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

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

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

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

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

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

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

- Molecule 38 is a protein called Ribosomal protein L37.

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

- Molecule 39 is a protein called RPL38 isoform 1.

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

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

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

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

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

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

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

- Molecule 43 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 45 is a protein called RPP0 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	P0	189	Total	C	N	O	S	0	0
			1473	942	257	270	4		

- Molecule 46 is a protein called RPL12A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	P2	94	Total	C	N	O	S	0	0
			723	448	138	135	2		

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

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

- Molecule 48 is a protein called 40S ribosomal protein S0.

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

- Molecule 49 is a protein called RPS1A isoform 1.

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

- Molecule 50 is a protein called RPS2 isoform 1.

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

- Molecule 51 is a protein called RPS3 isoform 1.

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

- Molecule 52 is a protein called 40S ribosomal protein S4.

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

- Molecule 53 is a protein called Rps5p.

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

- Molecule 54 is a protein called 40S ribosomal protein S6.

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

- Molecule 55 is a protein called 40S ribosomal protein S7.

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

- Molecule 56 is a protein called RPS8A isoform 1.

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

- Molecule 57 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 58 is a protein called 40S ribosomal protein S10-A.

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

- Molecule 59 is a protein called 40S ribosomal protein S11-B.

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

- Molecule 60 is a protein called 40S ribosomal protein S12.

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

- Molecule 61 is a protein called 40S ribosomal protein S13.

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

- Molecule 62 is a protein called 40S ribosomal protein S14-B.

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

- Molecule 63 is a protein called RPS15 isoform 1.

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

- Molecule 64 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 65 is a protein called 40S ribosomal protein S17-A.

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

- Molecule 66 is a protein called 40S ribosomal protein S18-B.

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

- Molecule 67 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 68 is a protein called RPS20 isoform 1.

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

- Molecule 69 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 70 is a protein called RPS22A isoform 1.

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

- Molecule 71 is a protein called 40S ribosomal protein S23.

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

- Molecule 72 is a protein called 40S ribosomal protein S24.

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

- Molecule 73 is a protein called RPS25A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SZ	100	Total	C	N	O		0	0
			771	491	147	133			

- Molecule 74 is a protein called RPS26B isoform 1.

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

- Molecule 75 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 76 is a protein called RPS28A isoform 1.

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

- Molecule 77 is a protein called RPS29A isoform 1.

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

- Molecule 78 is a protein called 40S ribosomal protein S30.

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

- Molecule 79 is a protein called Ubiquitin-40S ribosomal protein S31.

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

- Molecule 80 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

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

- Molecule 81 is a RNA chain called A-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	A	76	Total	C	N	O	P	0	0
			1609	720	278	536	75		

- Molecule 82 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	P	76	Total	C	N	O	P	0	0
			1619	722	288	533	76		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	34	U	G	conflict	GB 176436

- Molecule 83 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	m	16	Total	C	N	O	P	0	0
			351	157	72	106	16		

- Molecule 84 is a protein called Eukaryotic translation initiation factor 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	5	154	Total	C	N	O	S	0	0
			1143	709	195	230	9		

- Molecule 85 is a protein called Ribosome-interacting GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	R	355	Total	C	N	O	S	0	0
			2738	1733	483	513	9		

There are 41 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	370	LYS	-	expression tag	UNP A0A6A5PWT7
R	371	ARG	-	expression tag	UNP A0A6A5PWT7
R	372	ARG	-	expression tag	UNP A0A6A5PWT7
R	373	TRP	-	expression tag	UNP A0A6A5PWT7
R	374	LYS	-	expression tag	UNP A0A6A5PWT7
R	375	LYS	-	expression tag	UNP A0A6A5PWT7
R	376	ASN	-	expression tag	UNP A0A6A5PWT7
R	377	PHE	-	expression tag	UNP A0A6A5PWT7
R	378	ILE	-	expression tag	UNP A0A6A5PWT7
R	379	ALA	-	expression tag	UNP A0A6A5PWT7
R	380	VAL	-	expression tag	UNP A0A6A5PWT7
R	381	SER	-	expression tag	UNP A0A6A5PWT7
R	382	ALA	-	expression tag	UNP A0A6A5PWT7
R	383	ALA	-	expression tag	UNP A0A6A5PWT7
R	384	ASN	-	expression tag	UNP A0A6A5PWT7
R	385	ARG	-	expression tag	UNP A0A6A5PWT7
R	386	PHE	-	expression tag	UNP A0A6A5PWT7
R	387	LYS	-	expression tag	UNP A0A6A5PWT7
R	388	LYS	-	expression tag	UNP A0A6A5PWT7
R	389	ILE	-	expression tag	UNP A0A6A5PWT7
R	390	SER	-	expression tag	UNP A0A6A5PWT7
R	391	SER	-	expression tag	UNP A0A6A5PWT7
R	392	SER	-	expression tag	UNP A0A6A5PWT7
R	393	GLY	-	expression tag	UNP A0A6A5PWT7
R	394	ALA	-	expression tag	UNP A0A6A5PWT7

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Chain	Residue	Modelled	Actual	Comment	Reference
R	395	LEU	-	expression tag	UNP A0A6A5PWT7
R	396	ASP	-	expression tag	UNP A0A6A5PWT7
R	397	TYR	-	expression tag	UNP A0A6A5PWT7
R	398	ASP	-	expression tag	UNP A0A6A5PWT7
R	399	ILE	-	expression tag	UNP A0A6A5PWT7
R	400	PRO	-	expression tag	UNP A0A6A5PWT7
R	401	THR	-	expression tag	UNP A0A6A5PWT7
R	402	THR	-	expression tag	UNP A0A6A5PWT7
R	403	ALA	-	expression tag	UNP A0A6A5PWT7
R	404	SER	-	expression tag	UNP A0A6A5PWT7
R	405	GLU	-	expression tag	UNP A0A6A5PWT7
R	406	ASN	-	expression tag	UNP A0A6A5PWT7
R	407	LEU	-	expression tag	UNP A0A6A5PWT7
R	408	TYR	-	expression tag	UNP A0A6A5PWT7
R	409	PHE	-	expression tag	UNP A0A6A5PWT7
R	410	GLN	-	expression tag	UNP A0A6A5PWT7

- Molecule 86 is a protein called Translation machinery-associated protein 46.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	T	162	Total	C	N	O	S	0	0
			1276	810	221	240	5		

- Molecule 87 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms				AltConf	Trace
87	L1	200	Total	C	N	O	0	0
			1000	600	200	200		

- Molecule 88 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

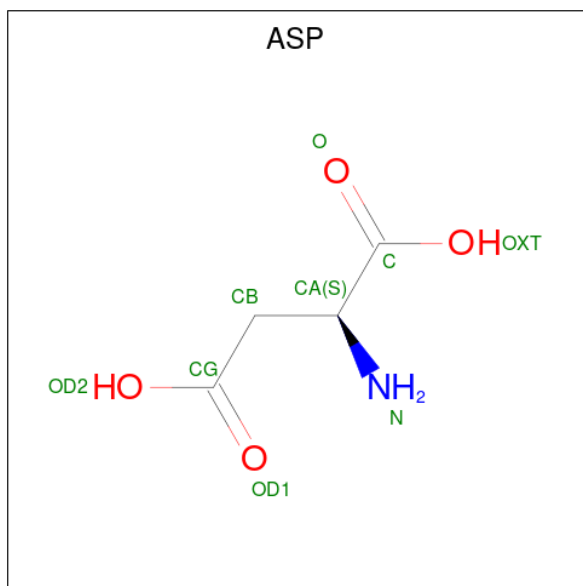
Mol	Chain	Residues	Atoms		AltConf
88	C1	192	Total	Mg	0
			192	192	
88	C4	1	Total	Mg	0
			1	1	
88	LA	2	Total	Mg	0
			2	2	
88	LB	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
88	LN	1	Total	Mg	0
			1	1	
88	LP	1	Total	Mg	0
			1	1	
88	LV	1	Total	Mg	0
			1	1	
88	Le	1	Total	Mg	0
			1	1	
88	C2	82	Total	Mg	0
			82	82	
88	SC	1	Total	Mg	0
			1	1	
88	SX	1	Total	Mg	0
			1	1	
88	Sa	1	Total	Mg	0
			1	1	
88	P	1	Total	Mg	0
			1	1	

- Molecule 89 is ASPARTIC ACID (CCD ID: ASP) (formula: $C_4H_7NO_4$).



Mol	Chain	Residues	Atoms				AltConf
89	C1	1	Total	C	N	O	0
			5	3	1	1	

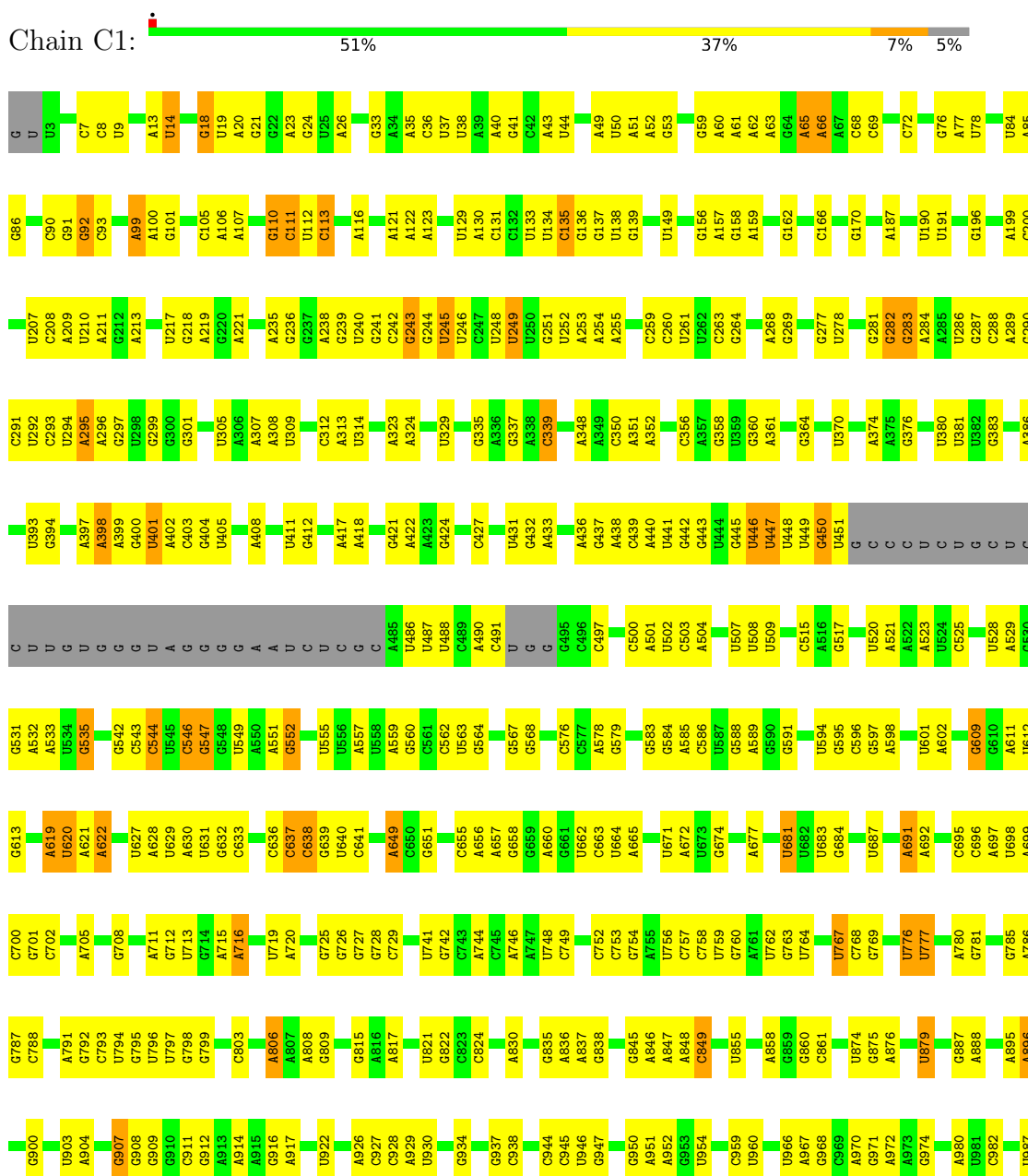
- Molecule 90 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

3 Residue-property plots

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

• Molecule 1: 25S rRNA

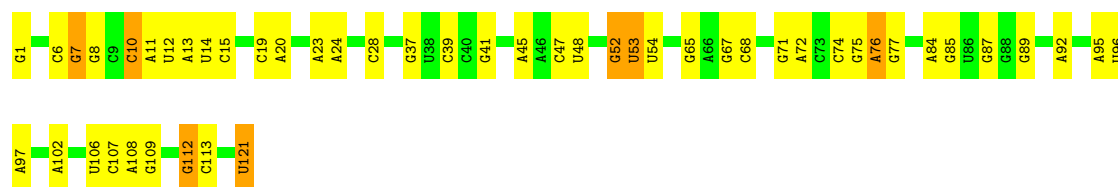




U3373	U3282	G3197	A3024	C2929	U2842	U2750	G2660	G2549	C2478	C2405	G2305	G2210
U3374	U3283	U3198	A3027	A2930	U2843	G2751	G2661	U2552	C2479	C2406	C2306	A2213
A3376	G3284	C3201	G3028	C2931	U2844	U2752	G2662	C2552	A2480	U2408	G2307	A2213
G3377	G3116	G3202	A3028	U2932	A2845	G2753	G2663	A2553	G2481	U2409	A2309	A2215
C3378	U3119	U3203	A3033	A2933	A2846	G2754	G2669	A2554	U2482	U2411	U2310	G2216
G3379	G3120	C3204	C3034	U2935	A2847	C2755	G2670	G2555	A2483	G2412	U2217	G2218
U3380	U3121	G3204	G3034	A2936	G2847	A2758	G2671	G2556	A2484	A2413	U2219	G2220
U3381	A3122	U3207	U3037	A2937	G2850	A2759	G2672	A2557	A2485	G2414	G2315	
U3382	A3123	G3208	A3040	C2942	A2851	U2763	A2673	A2561	A2486	A2419	A2320	G2221
G3386	C3126	A3209	A3041	G2947	A2852	U2767	A2674	C2568	A2488	A2424	A2321	A2222
U3389	A3129	C3212	U3042	U2948	A2853	U2768	G2677	A2569	C2489	U2428	U2328	A2223
A3296	U3130	A3213	U3043	U2949	A2854	A2769	U2681	U2570	A2491	G2429	C2329	A2224
U3304	U3131	U3214	U3047	G2950	U2855	A2770	U2682	G2573	C2492	U2430	U2334	U2226
A3307	A3132	G3215	A3048	U2954	G2856	C2772	C2682	C2574	U2493	A2431	U2335	A2229
U3313	U3133	C3217	U3050	C2960	A2857	G2773	U2683	C2575	A2494	G2432	U2336	
A3316	A3134	A3218	U3051	U2961	U2858	U2774	G2684	C2582	A2495	U2433	C2339	C2237
U3317	C3143	C3219	G3052	U2962	U2859	G2775	C2685	G2583	C2496	U2434	U2340	A2242
C3222	A3142	U3222	C3053	U2963	G2860	G2776	U2686	C2584	U2497	U2435	A2341	A2243
A3227	C3143	A3227	U3056	G2964	U2861	G2777	G2687	C2585	U2498	U2436	U2342	A2244
G3229	U3151	G3229	U3057	G2965	G2870	G2778	A2691	G2586	U2499	G2437	U2344	C2245
	C3154		G3059	G2966	G2871	U2781	U2692	U2587	A2500	U2438	A2345	
	U3155		U3064	A2967	A2872	G2786	A2694	U2588	A2501	U2439		G2249
G3232	U3156	G3232	G3065	A2971	U2875	G2794	A2695	A2593	A2502	G2440	G2250	
A3234	U3157	A3234	U3066	G2972	G2876	U2795	A2696	U2597	U2506	U2441		
C3235	U3158	C3235	G3069	G2973	G2877	G2796	A2697	U2598	U2507	A2445	A2255	A2255
G3239	C3159	G3239	A3070	U2979	G2878	C2704	G2698	U2599	U2508	U2446	A2256	A2256
A3243	U3160	A3243	G3075	U2982	C2879	G2800	A2704	C2800	U2514	A2447	C2257	C2257
A3244	C3161	A3244	U3076	C2983	U2880	A2801	C2707	A2601	A2515	U2448	U2258	U2258
A3245	A3162	A3245	U3077	C2984	U2881	A2802	C2708	G2602	U2521	G2449	A2259	
G3246	C3163	G3246	U3079	C2985	U2882	A2803	C2709	G2606	A2524	U2450	C2265	C2265
G3247	A3165	G3247	G3080	U2986	U2883	C2808	C2710	G2607	G2522	G2451	U2266	U2266
U3251	C3166	U3251	G3085	A2987	A2887	G2809	C2711	G2608	A2523	U2455	C2267	C2267
G3252	A3170	G3252	A3086	C2988	U2888	C2810	U2712	A2609	A2524	U2456	U2268	U2268
C3253	U3174	C3253	U3089	U2989	U2889	G2811	G2713	G2610	G2525	G2457	U2269	U2269
U3259	G3176	U3259	C3092	G2990	A2890	C2812	G2714	U2611	G2526	A2458	A2270	A2270
G3263	C3177	G3263	A3094	C3001	A2891	A2813	G2715	U2612	G2527	U2459	G2272	G2272
G3266	U3179	G3266	U3095	G3009	U2892	G2814	U2719	U2613	C2531	U2460	G2273	G2273
A3267	C3180	A3267	C3097	G3012	G2893	G2815	G2720	G2614	U2532	A2461	C2278	C2278
A3268	A3181	A3268	U3099	U3013	A2894	G2816	A2727	G2615	G2533	G2374	C2279	C2279
U3269	G3182	U3269	A3099	U3014	A2895	A2817	G2728	C2616	G2534		A2281	A2281
U3270	A3183	U3270	U3099	G3015	A2896	U2818	U2729	G2617	A2535	G2465	U2282	U2282
A3274	C3184	A3274	U3105	A3016	A2897	G2819	C2737	G2618	A2536	G2466	G2283	G2283
G3275	A3187	G3275	G3109	A3017	U2898	A2820		A2626	U2537	A2468	C2284	C2284
G3276	U3192	G3276	U3110	A3017	U2899	C2821	A2740	U2633	U2538	G2469	C2285	C2285
U3277	C3193	U3277	U3111	G3022	C2927	U2822	C2741	A2637	A2540	C2470	G2288	G2288
C3278	U3196	C3278	G3112	U3023	C2928	U2823	C2742	A2642	U2541	U2471	A2289	A2289
U3281		U3281				U2824	C2743	U2652	U2542	G2473	A2402	A2402
						U2825	C2744	U2653	U2543	G2474	G2403	G2403
						U2826	C2745	U2654	U2544	G2475	C2476	C2476
						U2827	C2746	U2655	C2545	C2476	A2404	A2404
						U2828	C2747	U2656	A2546	G2477		
						U2829	C2748	A2656	C2547			
						U2830	C2749					

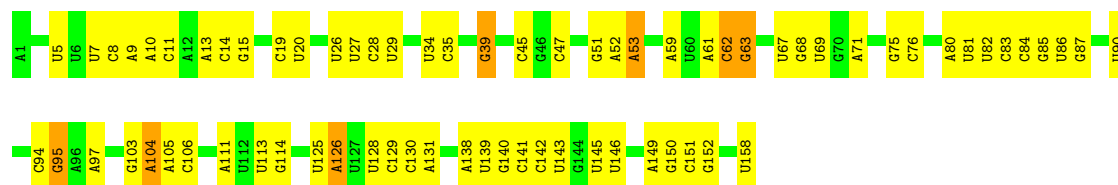
• Molecule 2: 5S rRNA

Chain C4:  60% 35% 6%



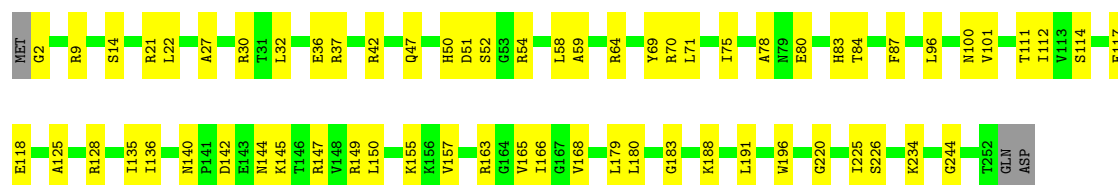
• Molecule 3: 5.8S rRNA

Chain C3:  55% 41% .



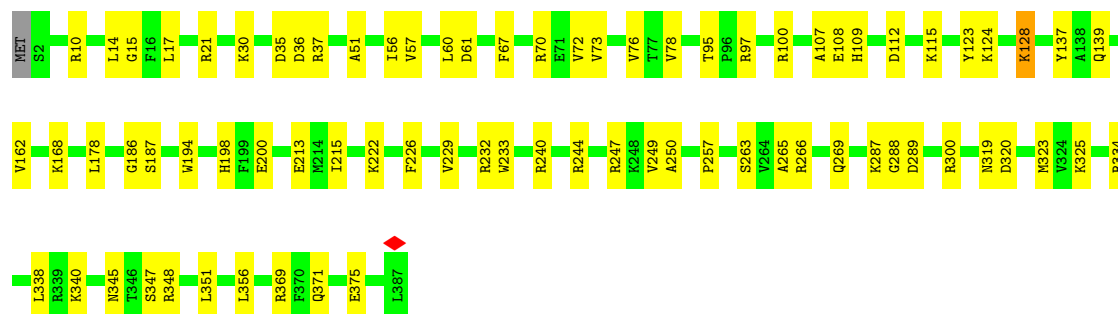
• Molecule 4: 60S ribosomal protein L2-B

Chain LA:  74% 25% .



• Molecule 5: RPL3 isoform 1

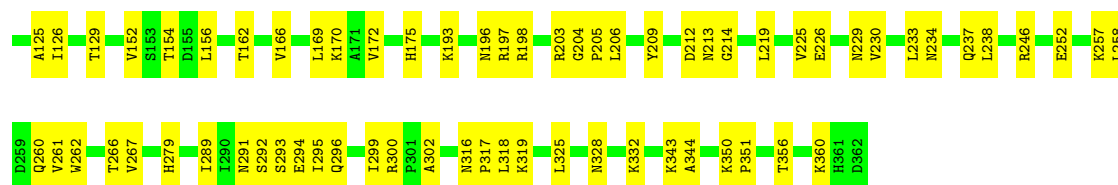
Chain LB:  80% 20%



• Molecule 6: RPL4A isoform 1

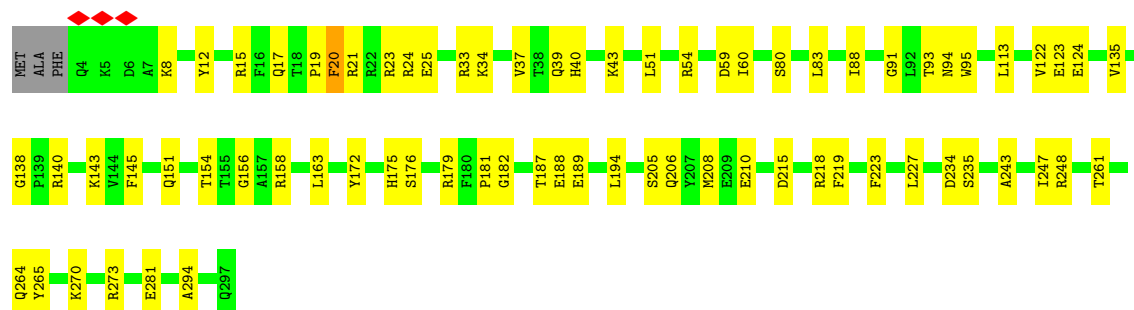
Chain LC:  72% 28%





• Molecule 7: RPL5 isoform 1

Chain LD: 75% 24%



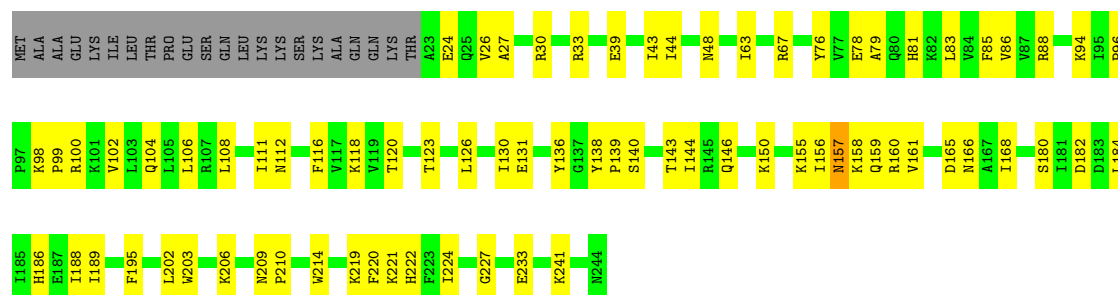
• Molecule 8: 60S ribosomal protein L6

Chain LE: 71% 24% 5%



• Molecule 9: 60S ribosomal protein L7-A

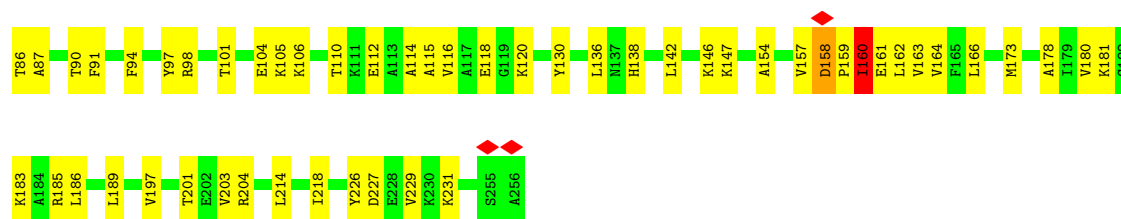
Chain LF: 60% 31% 9%



• Molecule 10: 60S ribosomal protein L8-A

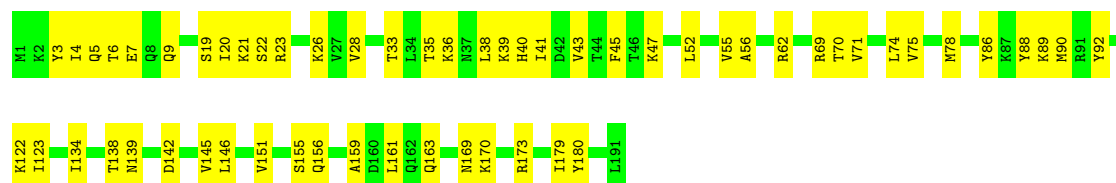
Chain LG: 62% 28% 9%





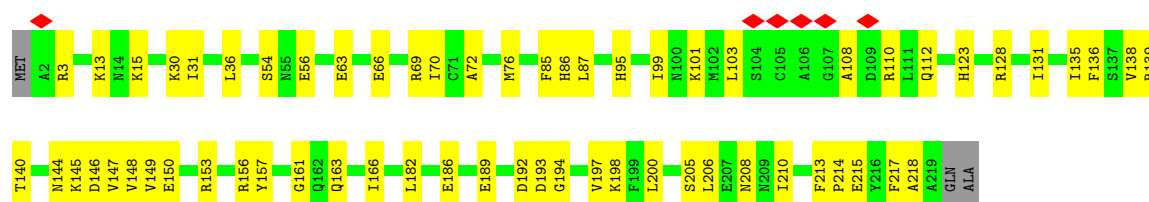
- Molecule 11: 60S ribosomal protein L9-A

Chain LH: 70% 30%



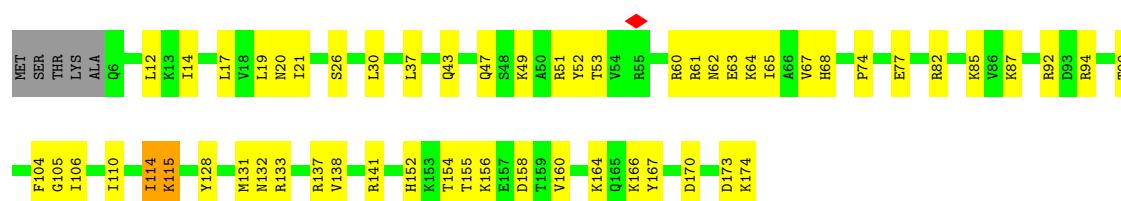
- Molecule 12: RPL10 isoform 1

Chain LI: 70% 29%



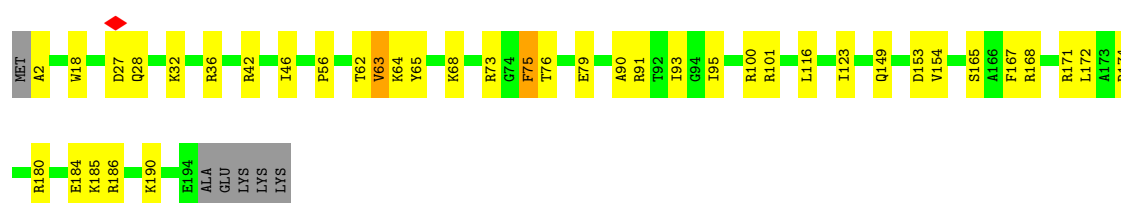
- Molecule 13: RPL11B isoform 1

Chain LJ: 65% 31%



- Molecule 14: 60S ribosomal protein L13

Chain LL: 77% 19%



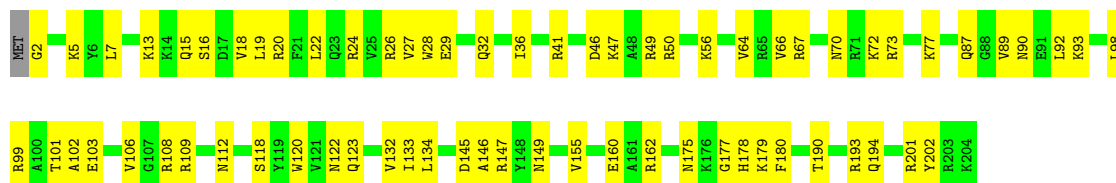
- Molecule 15: 60S ribosomal protein L14-A

Chain LM:  75% 23%



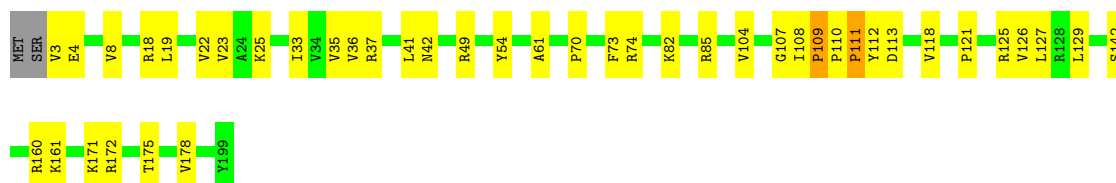
- Molecule 16: 60S ribosomal protein L15-A

Chain LN:  66% 33%



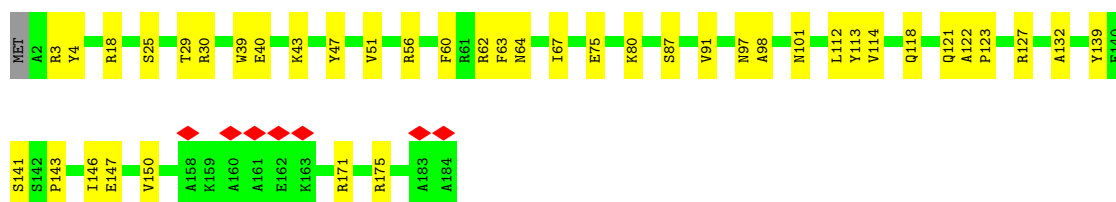
- Molecule 17: 60S ribosomal protein L16-A

Chain LO:  77% 21%



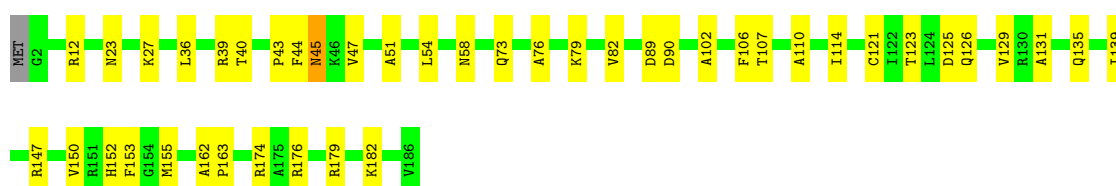
- Molecule 18: 60S ribosomal protein L17-A

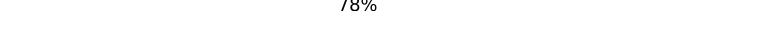
Chain LP:  77% 22%



- Molecule 19: 60S ribosomal protein L18-B

Chain LQ:  76% 23%

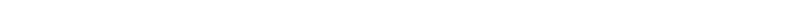


- Chain LR: 
- 

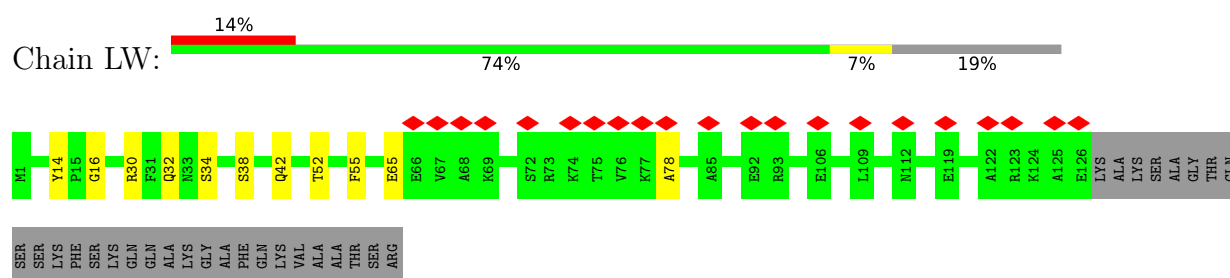
- Chain LS:  78% 20% ..
- Residues: MET, A2, E6, Y7, Q8, V9, I10, G11, R12, T16, V19, P20, E21, P22, R26, R27, R28, I36, Y43, K47, K50, V51, K52, L64, K71, V72, V77, D96, V97, L106, R115, R119, V126, V135, K136, K141, Q142, P151, S164, P168, F171, Y172.

- Chain LT:  77% 22%

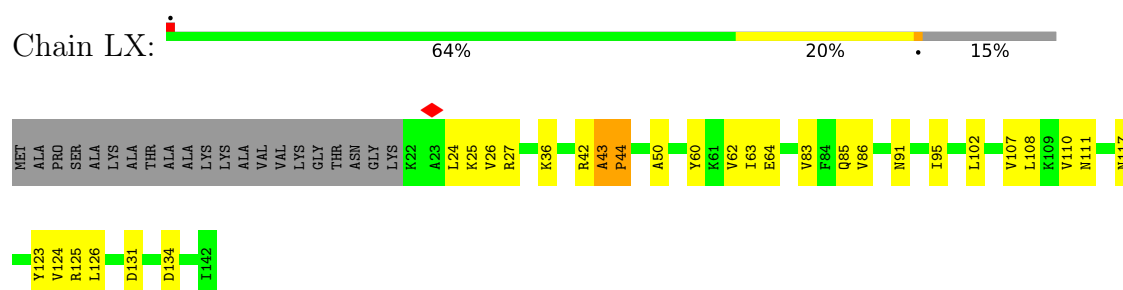
- Chain LU:  68% 15% 17%

- Chain LV: 
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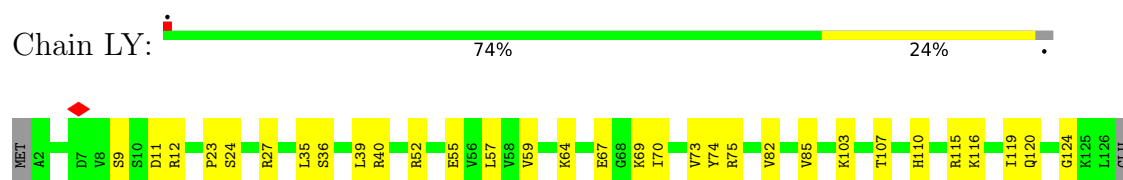
- 



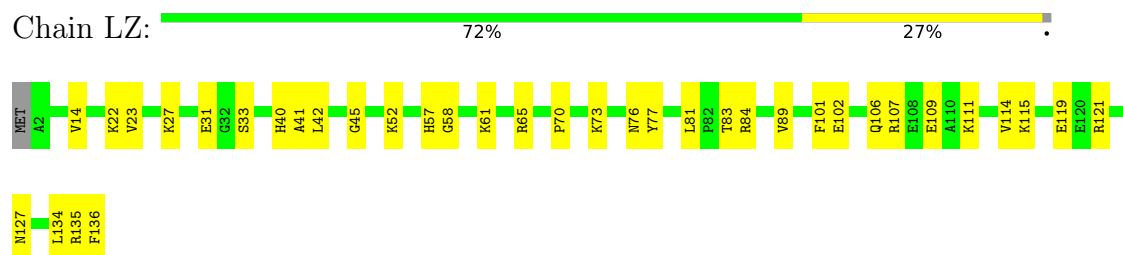
- Molecule 26: 60S ribosomal protein L25



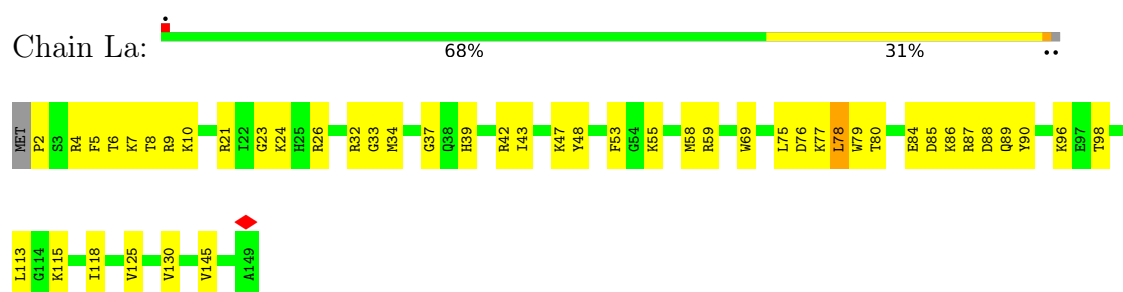
- Molecule 27: 60S ribosomal protein L26-A



- Molecule 28: 60S ribosomal protein L27

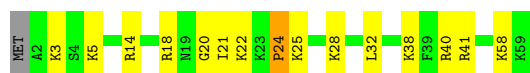


- Molecule 29: 60S ribosomal protein L28



- Molecule 30: RPL29 isoform 1

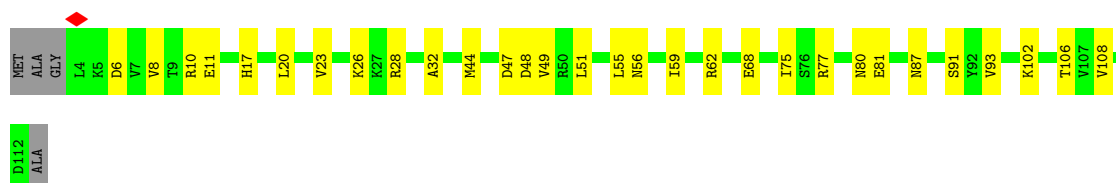




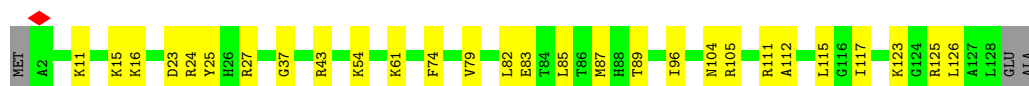
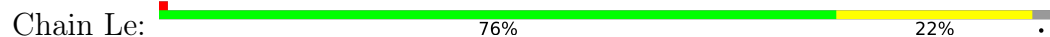
- Molecule 31: 60S ribosomal protein L30



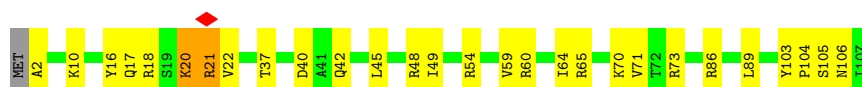
- Molecule 32: 60S ribosomal protein L31-A



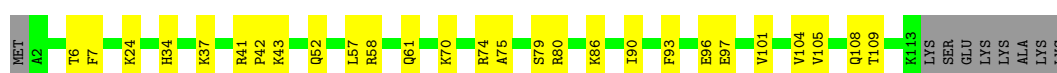
- Molecule 33: RPL32 isoform 1



- Molecule 34: 60S ribosomal protein L33-A



- Molecule 35: 60S ribosomal protein L34-A



- Molecule 36: 60S ribosomal protein L35-A





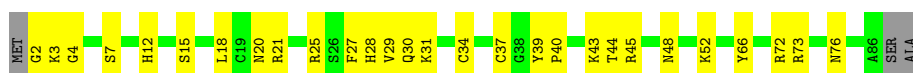
- Molecule 37: 60S ribosomal protein L36-A

Chain Li: 78% 21%



- Molecule 38: Ribosomal protein L37

Chain Lj: 65% 32%



- Molecule 39: RPL38 isoform 1

Chain Lk: 79% 19%



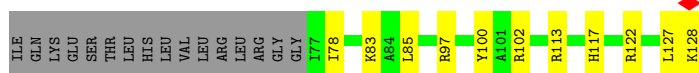
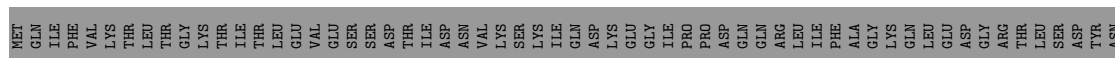
- Molecule 40: 60S ribosomal protein L39

Chain Ll: 63% 35%



- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Lm: 32% 9% 59%



- Molecule 42: 60S ribosomal protein L41-A

Chain Ln: 72% 28%

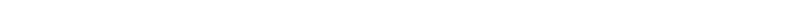


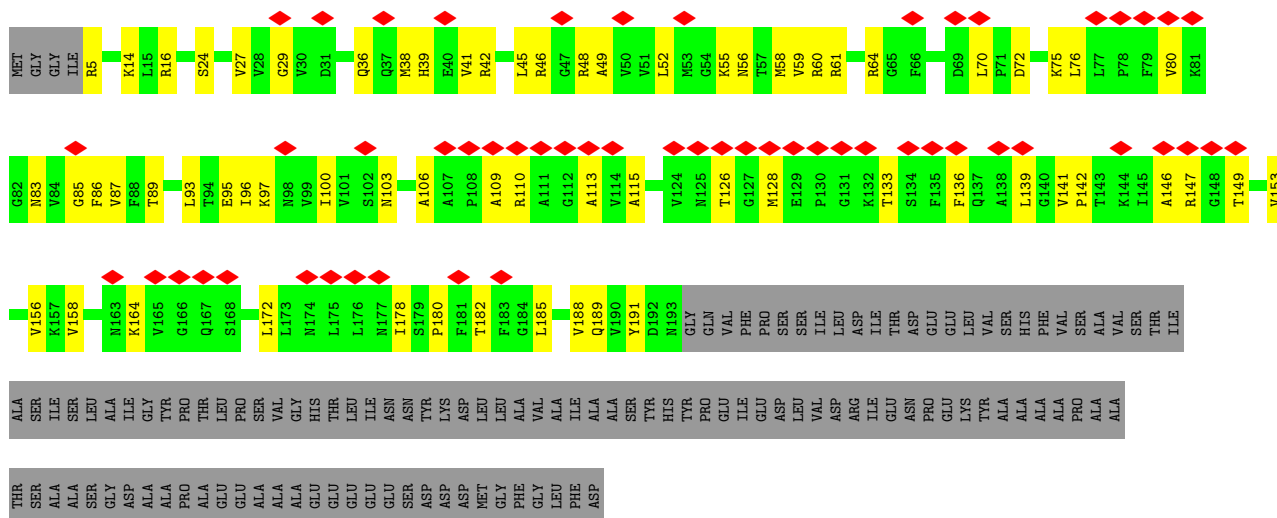
- Molecule 43: 60S ribosomal protein L42-A

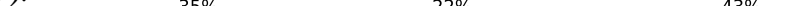
NET	V2	R8	C12	K15	R18	H23	Q27	A30	R41	R42	Y43	K46	Q47	Q53	T54	K55	K61	A62	K63	H90	F91	K97	L104	GLN	PHE
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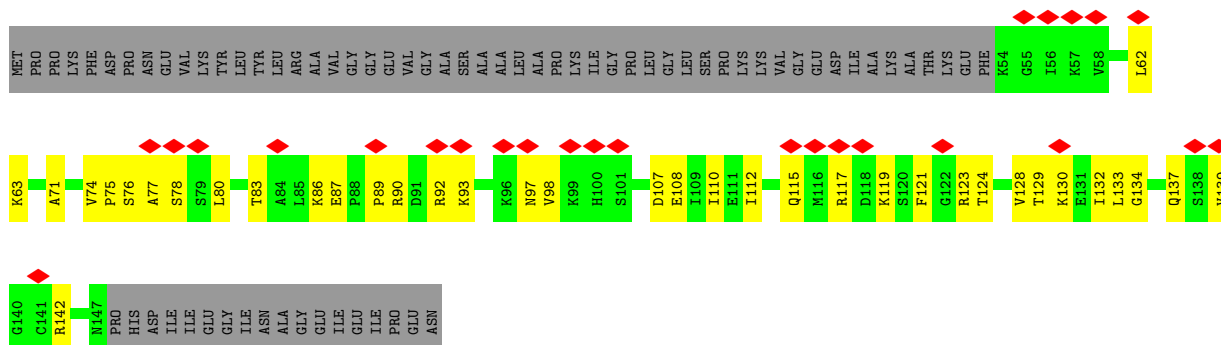
- Chain Lp: 68% 30%



- Chain P0: 

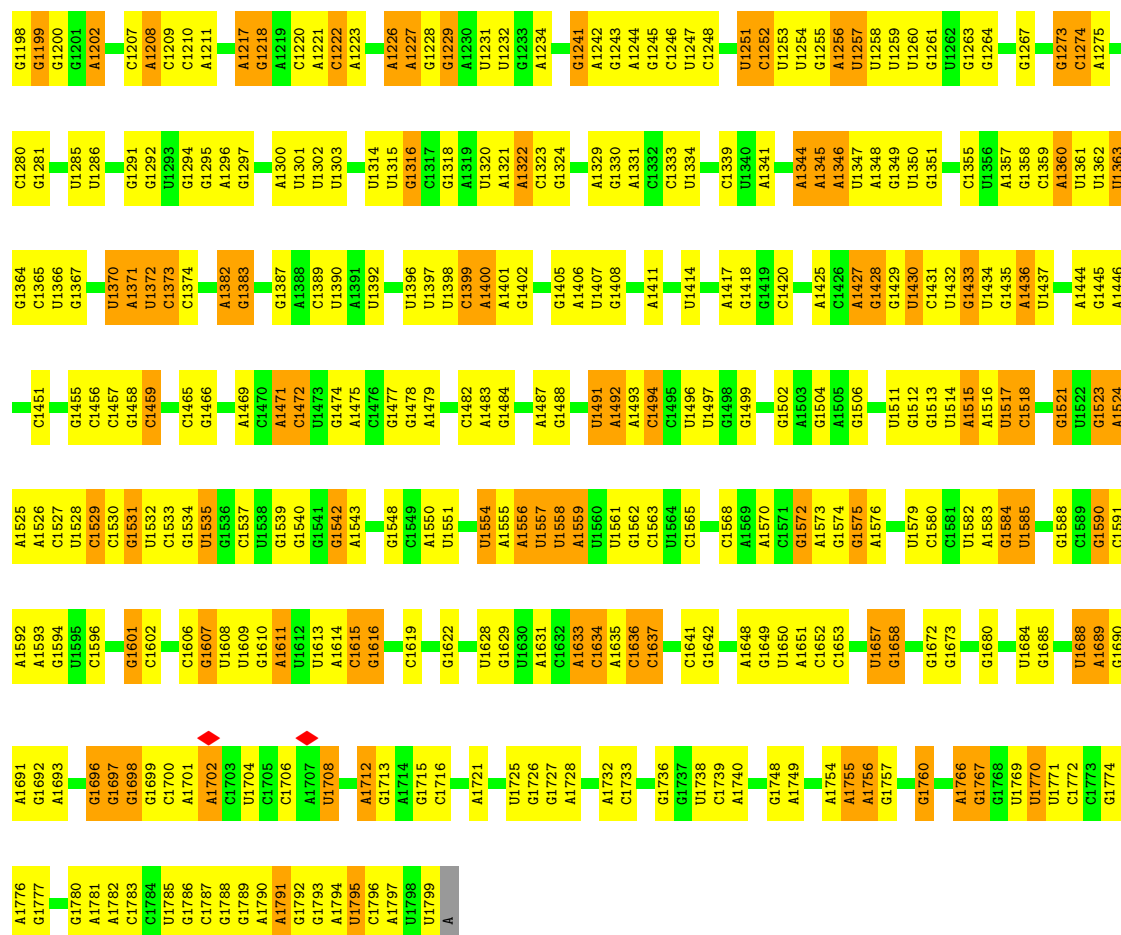


- Chain P2: 

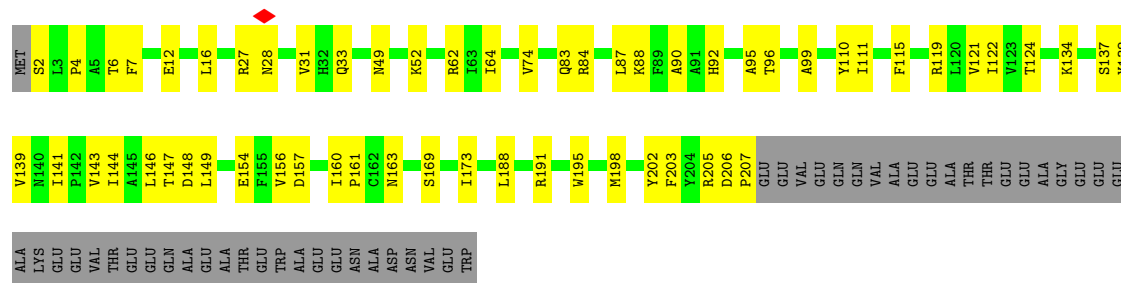


- Chain C2:

U1	A78	G163	G234	A417	U494	G566	U639	C704	G776	U854	G927	C1021	C1086
A2	C79	G166	G235	G418	C495	A567	U640	U705	C777	A855	U928	C1022	U1097
U3	A80	U167	A236	G419	G496	G568	G641	A706	G778	A856	A929	A1023	U1098
C4	G81	U168	U238	G423	G497	C569	G642	A707	U779	U857	A930	U1024	U1099
U5	U82	A168	U239	G424	A570	G570	G643	C708	U780	U861	U931	A1025	G1100
G6	G83	A171	C239	A571	U499	G571	U649	U709	U781	A862	U932	A1026	U1103
G7	A84	U240	U240	A425	C500	C572	U650	U710	U782	A863	A933	A1027	
	A85	U241	U241	G426	U501		G651	U711	C784		U935	C1028	
G10	A86	U242	U242	G430	U502	C575	G652	A712	U785	G866	G936	U1031	G1107
A11	A93	U174	G246	G431	A505	G576	C653	G713	A788	G867	A939	U1032	G1108
U12	U94	U175	A247	G432	A506	G577	G654	U714	A789	U872	U940	C1033	U1120
C13	G95	C176		G433	U507	U578	G655	C	A804	U873	U941	C1034	C1121
C14	G96	U177		G434	U508	A579	G656	C	A809	C874	G942		A1125
U15	C97	U178	C250	G435	U509	A580	U657	U	G810	G875	U945	U1037	
G16	U98	U179	A251	A436	G510	U581	C658	U	A811	G876	U946	U1038	
C17	A103	A180	A257	A437	A511	U582	C	U	A812	A804	U947	A1039	
C18	A104	A181	A257	A438	A512	A585	G	U	U813	A809	G948	U1040	A1132
C25	A105	U183	U260	U439	U513	G586	A	G	G810	G811		U1041	A1137
A26	A108	C184		C444	U514		U	C	G811	G812		U1042	A1138
U29	G109	U185	A265	A445	A515	A591	U	U	U813	A884		U1043	U1139
G30	C114	C187	A266	A446	C519	A592	U	U	U814	G885		U1044	U1144
C31	A119	C188	G269	A447	A520	U593	U	U	A815	U886		C1045	U1145
G34	A119	C189	C270	C448	A521	G595	U	U	G816	A887		U1046	G1146
C38	G123	C190	A271	C449	U522	C596	U	U	A817	U888		U1047	A1147
A39	A126	C191	U272	U450	G523	G597	G	G	C818	C890		U1050	C1148
G42	U128	C192	C274	A451	U524	U598	U	U	U820	A891		U1053	G1149
U45	U129	U193	C275	A452	A525	A599	G	G	U821	A892		U1058	G1150
A46	C131	U194	C276	U453	A526	A604	U	U	G822	G895		U1059	C1158
A47	U132	U195	U277	U454	A527	A605	A	C	G823	U896		U1060	C1159
A51	U133	G196	U283	A460	U528	A606	U	U	G824	C897		A1061	C1160
U52	U134	U197	G287	A461	C530	G607	G676	C735	U825	A898		U1062	C1161
G53	A135	C136	U278	A464	A534	U608	A677	C736	U826	U899		U1063	A1163
U56	U137	U211	U280	G465	A535	U609	U679	G738	U827	G901		C1066	G1164
G57	U138	U212	G281	A468	C536	U611	U680	A740	U828	G902		U1069	G1167
U58	C139	U213	C282	A474	G537	U612	U681	U742	U830	U903		C1070	U1168
C59	A140	A213	U293	A477	G538	A619	C682	U743	U831	G904		U1071	G1169
U60	U141	G214	U296	A478	A539	A620	C683	G751	U832	A905		U1072	G1170
A61	G142	A217	U297	A479	A540	A621	C684	A752	U833	U906		G1073	A1171
G63	U144	A218	C298	A480	A541	A622	C685	A753	U834	A907		U1074	G1172
U64	G143	A219	A300	A481	A542	A623	C686	U756	U835	U911		C1075	C1173
A65	A145	A222	A301	A482	C543	A624	G687	A757	G838	U912		U1076	G1179
U66	A148	U223	A304	U483	A544	G624	G688	U758	U840	G913		U1079	U1182
A67	U152	C224	U305	C484	G551	G627	U693	U759	U843	A915		U1080	A1183
G69	G154	A225	C306	A485	G552	U628	U694	A762	A844	U916		A1081	U1184
U73	U155	A226	G307	G486	G553	U629	U695	G763	G845	U917		C1082	U1186
U74	G154	G228	U307	U487	A555	U630	C696	U764	U846	A918		U1086	U1187
U75	U155	U229	C314	G488	A556	G631	C697	U765	U847	U919		A1087	G1188
A76	U159	U231	A315	U406	U558	U632	U698	U766	C848	U920		U1089	U1189
U77	C160	U232	A316	A407	U560	A635	U700	C768	A850	A923		U1092	A1194
			C321	A416	G561	A636	G701	A769	U851	A924		A1093	C1195
					C565	U638	G702	A774	G853	G925			C1197

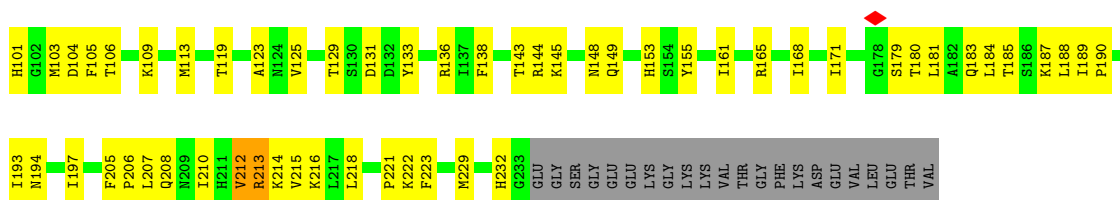


• Molecule 48: 40S ribosomal protein S0



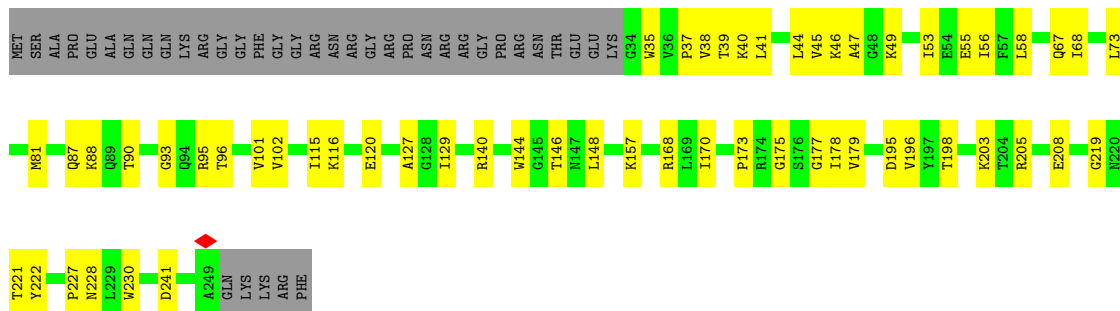
• Molecule 49: RPS1A isoform 1





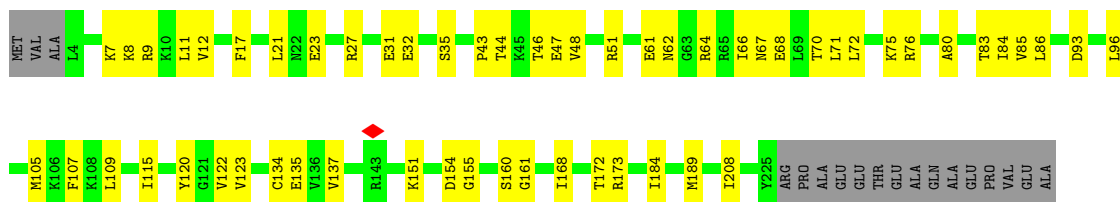
• Molecule 50: RPS2 isoform 1

Chain SC: 63% 22% 15%



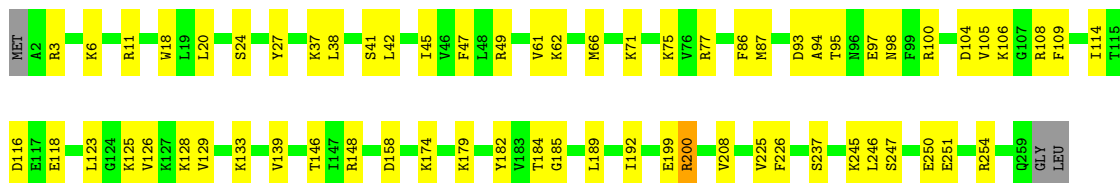
• Molecule 51: RPS3 isoform 1

Chain SD: 69% 24% 8%



• Molecule 52: 40S ribosomal protein S4

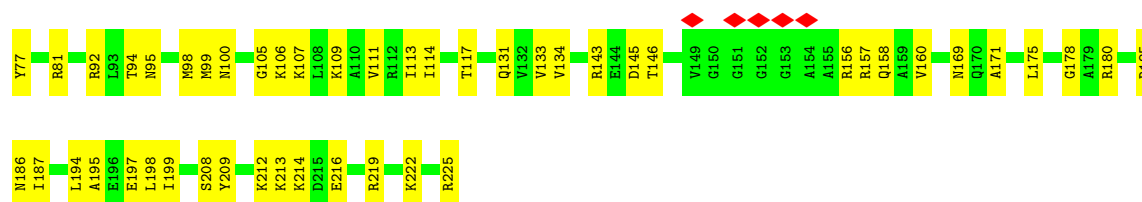
Chain SE: 74% 25%



• Molecule 53: Rps5p

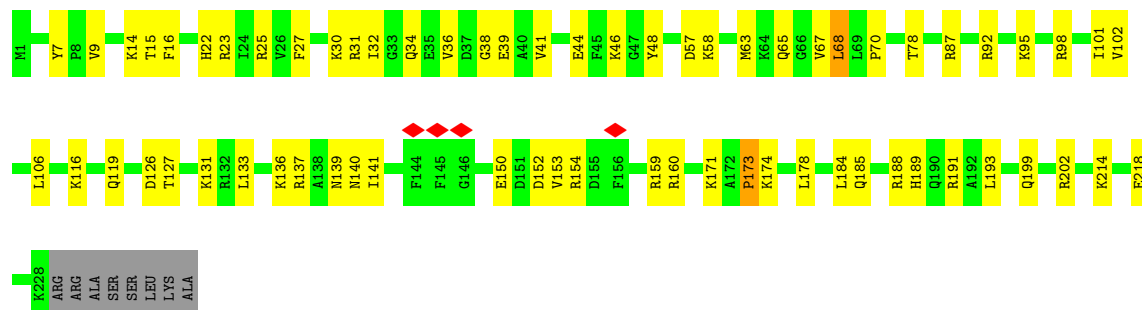
Chain SF: 58% 33% 8%





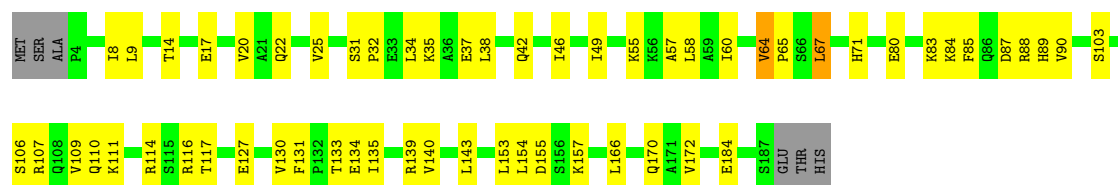
• Molecule 54: 40S ribosomal protein S6

Chain SG: 69% 27% ..



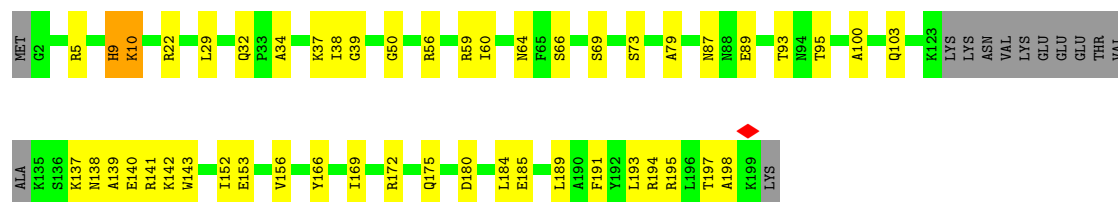
• Molecule 55: 40S ribosomal protein S7

Chain SH: 66% 29% ..



• Molecule 56: RPS8A isoform 1

Chain SI: 69% 24% • 6%

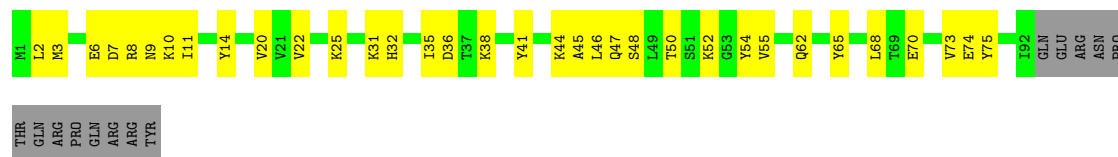


• Molecule 57: 40S ribosomal protein S9-A

Chain SJ: 62% 30% • 7%



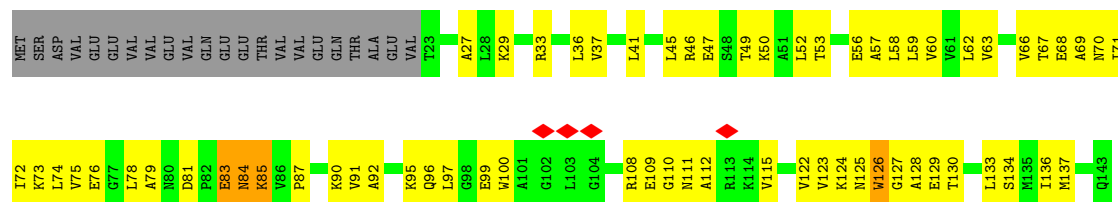
- Molecule 58: 40S ribosomal protein S10-A



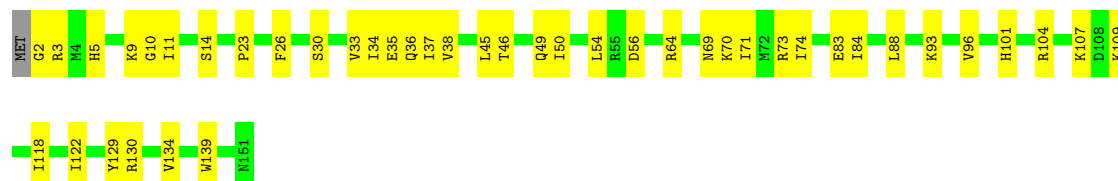
- Molecule 59: 40S ribosomal protein S11-B



- Molecule 60: 40S ribosomal protein S12

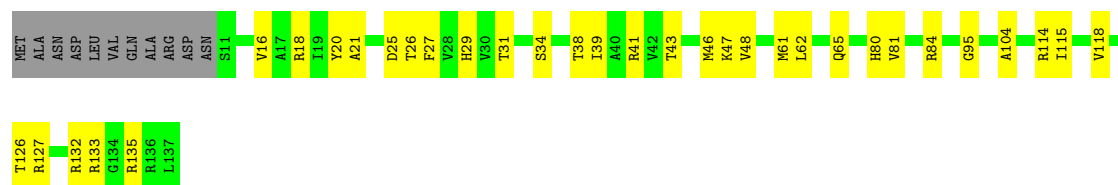


- Molecule 61: 40S ribosomal protein S13



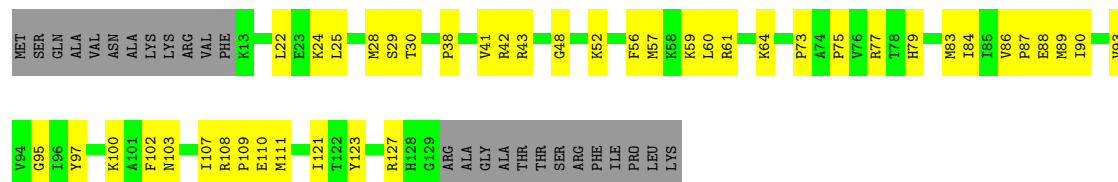
- Molecule 62: 40S ribosomal protein S14-B





- Molecule 63: RPS15 isoform 1

Chain SP: 52% 30% 18%



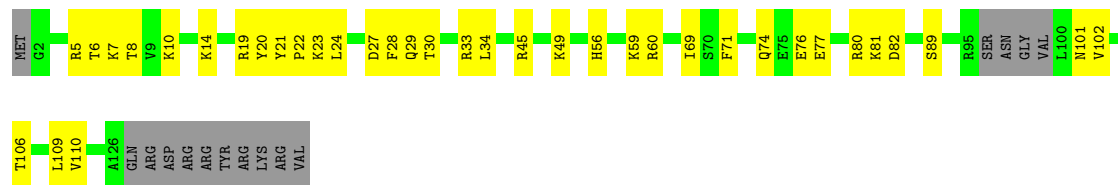
- Molecule 64: 40S ribosomal protein S16-A

Chain SQ: 64% 34% ...



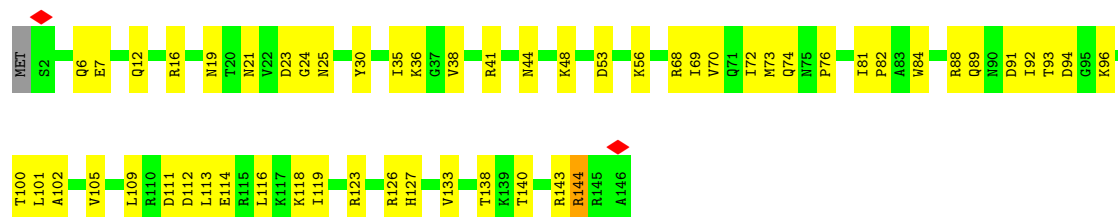
- Molecule 65: 40S ribosomal protein S17-A

Chain SR: 62% 27% 11%



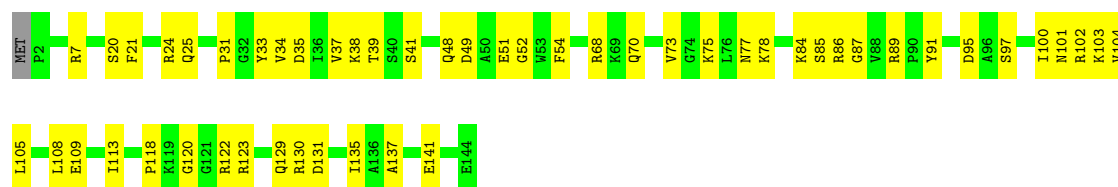
- Molecule 66: 40S ribosomal protein S18-B

Chain SS: 62% 37% ..



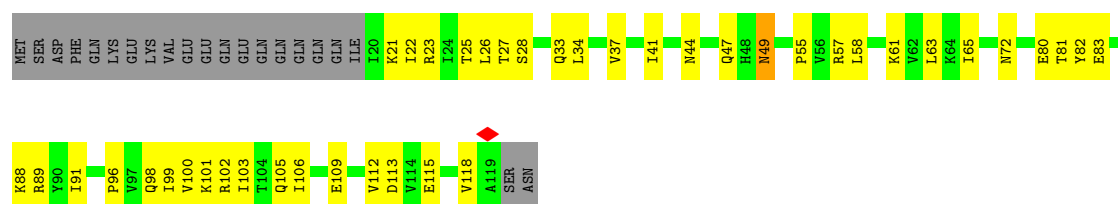
- Molecule 67: 40S ribosomal protein S19-A

Chain ST:  64% 35%



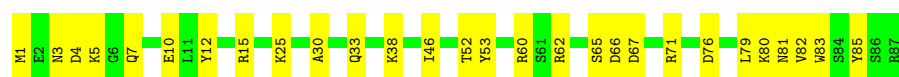
- Molecule 68: RPS20 isoform 1

Chain SU:  48% 34% 17%



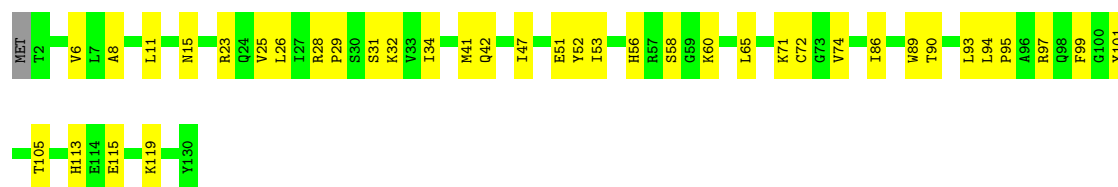
- Molecule 69: 40S ribosomal protein S21-A

Chain SV:  68% 32%



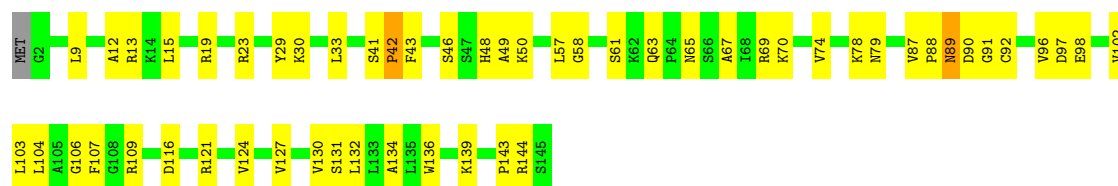
- Molecule 70: RPS22A isoform 1

Chain SW:  70% 29%



- Molecule 71: 40S ribosomal protein S23

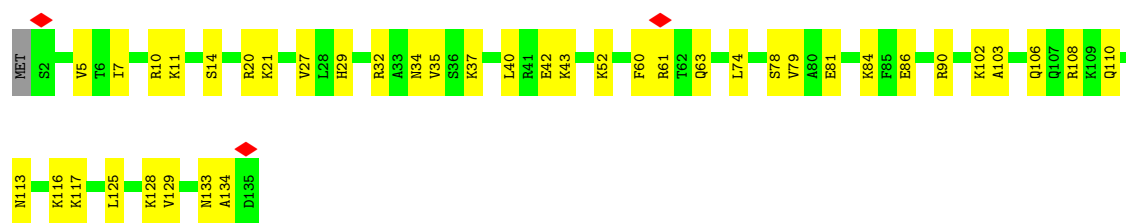
Chain SX:  62% 36%



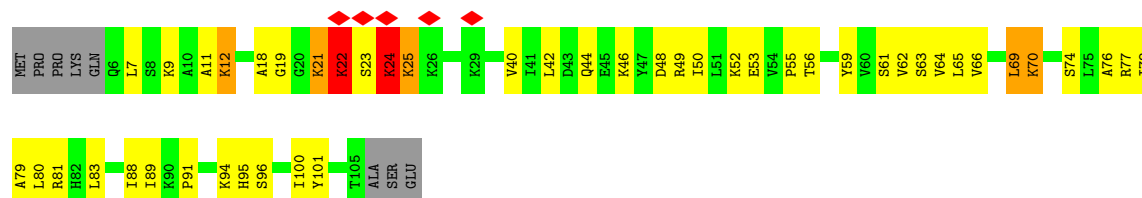
- Molecule 72: 40S ribosomal protein S24

Chain SY:  70% 30%

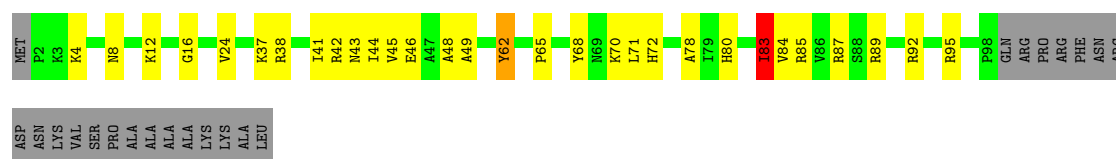




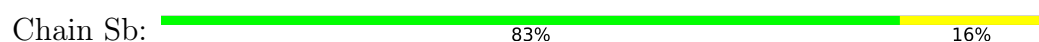
• Molecule 73: RPS25A isoform 1



• Molecule 74: RPS26B isoform 1



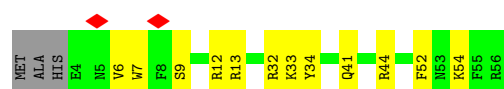
• Molecule 75: 40S ribosomal protein S27-A



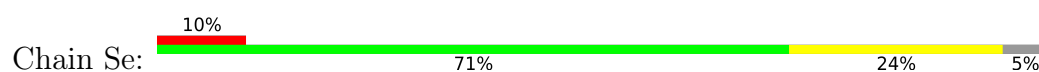
• Molecule 76: RPS28A isoform 1



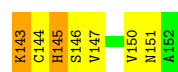
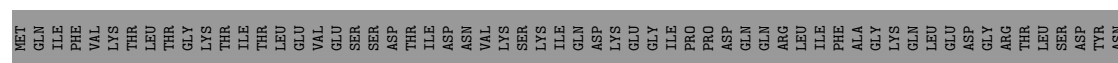
• Molecule 77: RPS29A isoform 1



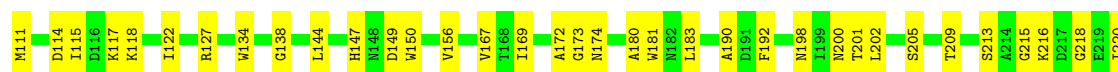
• Molecule 78: 40S ribosomal protein S30



• Molecule 79: Ubiquitin-40S ribosomal protein S31



• Molecule 80: Guanine nucleotide-binding protein subunit beta-like protein

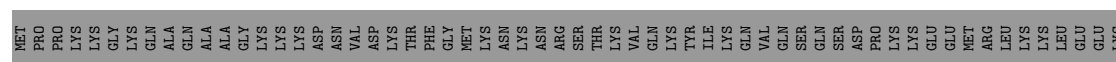


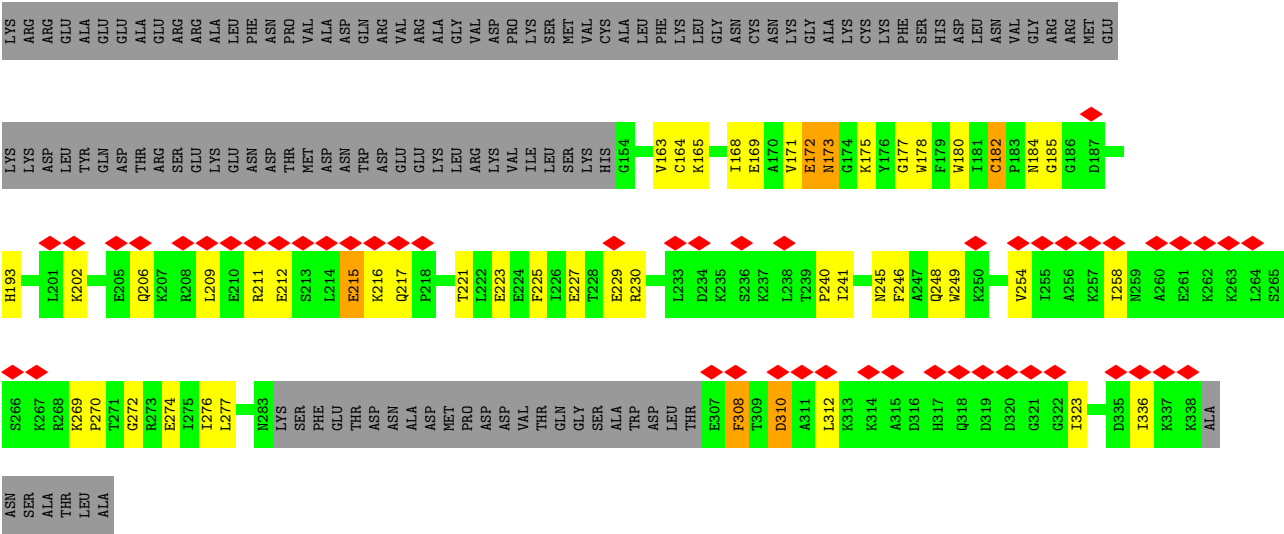
• Molecule 81: A-tRNA



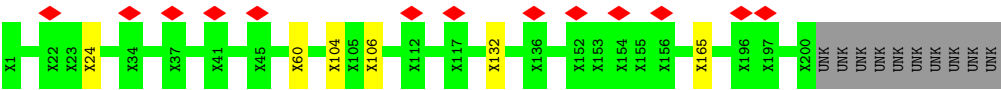
• Molecule 82: P-tRNA







● Molecule 87: 60S ribosomal protein L1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	95380	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.047	Depositor
Minimum map value	-0.029	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.003	Depositor
Map size (Å)	483.84003, 483.84003, 483.84003	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, 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	C1	0.11	0/77108	0.32	0/120216
2	C4	0.08	0/2883	0.25	0/4491
3	C3	0.10	0/3746	0.32	0/5832
4	LA	0.14	0/1933	0.44	0/2598
5	LB	0.12	0/3146	0.36	0/4228
6	LC	0.15	0/2800	0.41	0/3790
7	LD	0.15	0/2400	0.43	0/3239
8	LE	0.14	0/1329	0.43	0/1794
9	LF	0.15	0/1821	0.41	0/2451
10	LG	0.17	0/1836	0.46	0/2481
11	LH	0.16	0/1529	0.47	0/2060
12	LI	0.14	0/1801	0.41	0/2416
13	LJ	0.16	0/1371	0.51	0/1838
14	LL	0.18	0/1568	0.51	0/2106
15	LM	0.15	0/1068	0.42	0/1438
16	LN	0.14	0/1757	0.44	0/2354
17	LO	0.19	0/1585	0.48	0/2128
18	LP	0.13	0/1439	0.40	0/1938
19	LQ	0.14	0/1465	0.42	0/1965
20	LR	0.18	0/1532	0.50	0/2043
21	LS	0.15	0/1473	0.44	0/1980
22	LT	0.14	0/1300	0.39	0/1743
23	LU	0.17	0/812	0.45	0/1099
24	LV	0.12	0/1018	0.40	0/1369
25	LW	0.16	0/863	0.51	0/1169
26	LX	0.16	0/979	0.49	0/1321
27	LY	0.14	0/995	0.40	0/1329
28	LZ	0.13	0/1118	0.41	0/1497
29	La	0.13	0/1204	0.40	0/1612
30	Lb	0.14	0/473	0.45	0/629
31	Lc	0.14	0/745	0.41	0/1001
32	Ld	0.14	0/890	0.43	0/1196

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.12	0/1038	0.38	0/1390
34	Lf	0.13	0/868	0.42	0/1168
35	Lg	0.14	0/890	0.44	0/1189
36	Lh	0.17	0/978	0.47	0/1301
37	Li	0.17	0/772	0.45	0/1026
38	Lj	0.14	0/685	0.46	0/908
39	Lk	0.15	0/618	0.46	0/826
40	Ll	0.15	0/443	0.38	0/588
41	Lm	0.18	0/423	0.54	0/562
42	Ln	0.17	0/230	0.50	0/296
43	Lo	0.13	0/836	0.37	0/1104
44	Lp	0.16	0/701	0.49	0/934
45	P0	0.14	0/1498	0.46	0/2025
46	P2	0.14	0/728	0.45	0/975
47	C2	0.11	0/42053	0.34	0/65522
48	SA	0.16	0/1644	0.44	0/2249
49	SB	0.17	0/1823	0.50	0/2447
50	SC	0.16	0/1656	0.47	0/2251
51	SD	0.16	0/1754	0.45	0/2361
52	SE	0.14	0/2097	0.44	0/2823
53	SF	0.18	0/1625	0.51	0/2197
54	SG	0.16	0/1839	0.50	0/2460
55	SH	0.18	0/1498	0.52	0/2019
56	SI	0.15	0/1501	0.47	0/2006
57	SJ	0.16	0/1504	0.47	0/2016
58	SK	0.22	0/769	0.54	0/1039
59	SL	0.12	0/1185	0.41	0/1598
60	SM	0.24	0/883	0.99	6/1199 (0.5%)
61	SN	0.19	0/1215	0.52	0/1638
62	SO	0.15	0/937	0.45	0/1261
63	SP	0.16	0/936	0.48	0/1259
64	SQ	0.20	0/1125	0.55	0/1510
65	SR	0.19	0/957	0.51	0/1283
66	SS	0.17	0/1211	0.55	0/1628
67	ST	0.18	0/1130	0.53	0/1517
68	SU	0.21	0/807	0.60	0/1091
69	SV	0.15	0/682	0.50	0/921
70	SW	0.16	0/1038	0.47	0/1395
71	SX	0.18	0/1139	0.61	0/1518
72	SY	0.16	0/1087	0.52	0/1449
73	SZ	0.19	0/781	0.71	0/1045
74	Sa	0.17	0/782	0.56	0/1047
75	Sb	0.14	0/620	0.50	0/838

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sc	0.14	0/493	0.44	0/663
77	Sd	0.14	0/452	0.36	0/600
78	Se	0.18	0/480	0.50	0/639
79	Sf	0.17	0/567	0.62	0/764
80	Sg	0.15	0/2436	0.50	0/3318
81	A	0.16	0/1796	0.43	0/2796
82	P	0.11	0/1808	0.33	0/2816
83	m	0.10	0/395	0.28	0/615
84	5	0.18	0/1142	0.68	0/1537
85	R	0.16	0/2777	0.49	1/3754 (0.0%)
86	T	0.15	0/1301	0.59	2/1745 (0.1%)
All	All	0.13	0/226620	0.39	9/332477 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	SM	110	GLY	CA-C-N	9.16	134.56	120.82
60	SM	110	GLY	C-N-CA	9.16	134.56	120.82
60	SM	111	ASN	N-CA-C	7.84	124.30	111.37
60	SM	108	ARG	CA-C-N	7.83	136.49	121.54
60	SM	108	ARG	C-N-CA	7.83	136.49	121.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	C1	68888	0	34613	1002	0
2	C4	2579	0	1304	37	0
3	C3	3353	0	1695	58	0
4	LA	1899	0	1957	53	0
5	LB	3075	0	3142	54	0
6	LC	2748	0	2859	83	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	LD	2351	0	2294	60	0
8	LE	1307	0	1377	32	0
9	LF	1784	0	1862	63	0
10	LG	1804	0	1877	48	0
11	LH	1508	0	1572	45	0
12	LI	1764	0	1804	45	0
13	LJ	1350	0	1381	47	0
14	LL	1543	0	1608	40	0
15	LM	1053	0	1149	29	0
16	LN	1720	0	1779	62	0
17	LO	1555	0	1659	36	0
18	LP	1416	0	1433	33	0
19	LQ	1441	0	1543	33	0
20	LR	1515	0	1606	31	0
21	LS	1437	0	1475	35	0
22	LT	1276	0	1323	29	0
23	LU	796	0	812	13	0
24	LV	1003	0	1048	22	0
25	LW	849	0	727	8	0
26	LX	964	0	1025	27	0
27	LY	984	0	1075	21	0
28	LZ	1092	0	1155	28	0
29	La	1173	0	1215	46	0
30	Lb	462	0	491	12	0
31	Lc	737	0	792	23	0
32	Ld	876	0	912	20	0
33	Le	1017	0	1081	23	0
34	Lf	850	0	880	23	0
35	Lg	880	0	941	22	0
36	Lh	969	0	1078	32	0
37	Li	766	0	844	15	0
38	Lj	670	0	673	26	0
39	Lk	612	0	682	12	0
40	Ll	436	0	475	20	0
41	Lm	417	0	455	11	0
42	Ln	229	0	273	7	0
43	Lo	824	0	888	17	0
44	Lp	694	0	735	26	0
45	P0	1473	0	1514	46	0
46	P2	723	0	774	29	0
47	C2	37604	0	18917	692	0
48	SA	1603	0	1610	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	SB	1798	0	1890	75	0
50	SC	1626	0	1715	50	0
51	SD	1729	0	1812	45	0
52	SE	2056	0	2140	48	0
53	SF	1605	0	1669	60	0
54	SG	1815	0	1894	58	0
55	SH	1473	0	1555	38	0
56	SI	1476	0	1501	34	0
57	SJ	1479	0	1556	58	0
58	SK	752	0	719	31	0
59	SL	1159	0	1225	33	0
60	SM	875	0	878	53	0
61	SN	1192	0	1255	34	0
62	SO	926	0	950	28	0
63	SP	916	0	941	35	0
64	SQ	1105	0	1166	49	0
65	SR	948	0	990	29	0
66	SS	1192	0	1222	45	0
67	ST	1112	0	1124	40	0
68	SU	797	0	863	35	0
69	SV	673	0	662	27	0
70	SW	1021	0	1060	31	0
71	SX	1121	0	1196	47	0
72	SY	1073	0	1132	36	0
73	SZ	771	0	826	37	0
74	Sa	769	0	818	24	0
75	Sb	610	0	633	11	0
76	Sc	491	0	524	13	0
77	Sd	442	0	428	12	0
78	Se	472	0	521	17	0
79	Sf	556	0	546	25	0
80	Sg	2383	0	2332	79	0
81	A	1609	0	816	30	0
82	P	1619	0	821	41	0
83	m	351	0	175	2	0
84	5	1143	0	1108	42	0
85	R	2738	0	2807	68	0
86	T	1276	0	1260	35	0
87	L1	1000	0	213	3	0
88	C1	192	0	0	0	0
88	C2	82	0	0	0	0
88	C4	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
88	LA	2	0	0	0	0
88	LB	1	0	0	0	0
88	LN	1	0	0	0	0
88	LP	1	0	0	0	0
88	LV	1	0	0	0	0
88	Le	1	0	0	0	0
88	P	1	0	0	0	0
88	SC	1	0	0	0	0
88	SX	1	0	0	0	0
88	Sa	1	0	0	0	0
89	C1	5	0	1	1	0
90	Lg	1	0	0	0	0
90	Lj	1	0	0	0	0
90	Lm	1	0	0	0	0
90	Lo	1	0	0	0	0
90	Lp	1	0	0	0	0
90	Sd	1	0	0	0	0
90	Sf	1	0	0	0	0
90	T	1	0	0	0	0
All	All	212517	0	157328	3926	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 11.

The worst 5 of 3926 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)
1:C1:2465:G:H21	1:C1:2491:A:N6	1.51	1.07
1:C1:1257:C:H42	1:C1:1261:G:N2	1.55	1.05
1:C1:2465:G:N2	1:C1:2491:A:H62	1.54	1.04
1:C1:1896:A:H61	1:C1:2339:C:N4	1.55	1.02
1:C1:1018:G:H1	1:C1:1034:U:H3	1.06	0.98

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	LA	249/254 (98%)	230 (92%)	19 (8%)	0	100	100
5	LB	384/387 (99%)	354 (92%)	30 (8%)	0	100	100
6	LC	359/362 (99%)	330 (92%)	27 (8%)	2 (1%)	21	53
7	LD	292/297 (98%)	274 (94%)	17 (6%)	1 (0%)	36	66
8	LE	163/176 (93%)	146 (90%)	17 (10%)	0	100	100
9	LF	220/244 (90%)	208 (94%)	12 (6%)	0	100	100
10	LG	231/256 (90%)	214 (93%)	16 (7%)	1 (0%)	30	60
11	LH	189/191 (99%)	173 (92%)	16 (8%)	0	100	100
12	LI	216/221 (98%)	205 (95%)	11 (5%)	0	100	100
13	LJ	167/174 (96%)	146 (87%)	21 (13%)	0	100	100
14	LL	191/199 (96%)	171 (90%)	19 (10%)	1 (0%)	24	56
15	LM	134/138 (97%)	124 (92%)	10 (8%)	0	100	100
16	LN	201/204 (98%)	186 (92%)	15 (8%)	0	100	100
17	LO	195/199 (98%)	189 (97%)	4 (2%)	2 (1%)	12	42
18	LP	181/184 (98%)	168 (93%)	13 (7%)	0	100	100
19	LQ	183/186 (98%)	171 (93%)	12 (7%)	0	100	100
20	LR	186/189 (98%)	179 (96%)	6 (3%)	1 (0%)	24	56
21	LS	169/172 (98%)	161 (95%)	8 (5%)	0	100	100
22	LT	157/160 (98%)	150 (96%)	7 (4%)	0	100	100
23	LU	98/121 (81%)	90 (92%)	8 (8%)	0	100	100
24	LV	134/137 (98%)	133 (99%)	1 (1%)	0	100	100
25	LW	124/155 (80%)	108 (87%)	15 (12%)	1 (1%)	16	47
26	LX	119/142 (84%)	111 (93%)	6 (5%)	2 (2%)	7	32
27	LY	123/127 (97%)	117 (95%)	6 (5%)	0	100	100
28	LZ	133/136 (98%)	124 (93%)	9 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	La	146/149 (98%)	130 (89%)	15 (10%)	1 (1%)	18	50
30	Lb	56/59 (95%)	50 (89%)	4 (7%)	2 (4%)	2	17
31	Lc	94/105 (90%)	90 (96%)	4 (4%)	0	100	100
32	Ld	107/113 (95%)	96 (90%)	11 (10%)	0	100	100
33	Le	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
34	Lf	104/107 (97%)	97 (93%)	7 (7%)	0	100	100
35	Lg	110/121 (91%)	106 (96%)	4 (4%)	0	100	100
36	Lh	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
37	Li	97/100 (97%)	92 (95%)	5 (5%)	0	100	100
38	Lj	83/88 (94%)	76 (92%)	7 (8%)	0	100	100
39	Lk	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
40	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
41	Lm	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
42	Ln	23/25 (92%)	23 (100%)	0	0	100	100
43	Lo	101/106 (95%)	94 (93%)	7 (7%)	0	100	100
44	Lp	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
45	P0	187/312 (60%)	160 (86%)	27 (14%)	0	100	100
46	P2	92/165 (56%)	74 (80%)	18 (20%)	0	100	100
48	SA	204/252 (81%)	180 (88%)	24 (12%)	0	100	100
49	SB	222/255 (87%)	192 (86%)	28 (13%)	2 (1%)	14	44
50	SC	214/254 (84%)	198 (92%)	16 (8%)	0	100	100
51	SD	220/240 (92%)	212 (96%)	8 (4%)	0	100	100
52	SE	256/261 (98%)	232 (91%)	24 (9%)	0	100	100
53	SF	204/225 (91%)	188 (92%)	16 (8%)	0	100	100
54	SG	226/236 (96%)	197 (87%)	27 (12%)	2 (1%)	14	44
55	SH	182/190 (96%)	167 (92%)	14 (8%)	1 (0%)	24	56
56	SI	183/200 (92%)	163 (89%)	18 (10%)	2 (1%)	11	40
57	SJ	182/197 (92%)	162 (89%)	19 (10%)	1 (0%)	24	56
58	SK	90/105 (86%)	76 (84%)	14 (16%)	0	100	100
59	SL	142/156 (91%)	126 (89%)	16 (11%)	0	100	100
60	SM	119/143 (83%)	81 (68%)	36 (30%)	2 (2%)	7	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	SN	148/151 (98%)	133 (90%)	15 (10%)	0	100	100
62	SO	125/138 (91%)	110 (88%)	15 (12%)	0	100	100
63	SP	115/142 (81%)	106 (92%)	9 (8%)	0	100	100
64	SQ	139/143 (97%)	128 (92%)	10 (7%)	1 (1%)	18	50
65	SR	117/136 (86%)	105 (90%)	12 (10%)	0	100	100
66	SS	143/146 (98%)	130 (91%)	12 (8%)	1 (1%)	18	50
67	ST	141/144 (98%)	124 (88%)	17 (12%)	0	100	100
68	SU	98/121 (81%)	92 (94%)	6 (6%)	0	100	100
69	SV	85/87 (98%)	74 (87%)	10 (12%)	1 (1%)	10	38
70	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
71	SX	142/145 (98%)	122 (86%)	17 (12%)	3 (2%)	5	27
72	SY	132/135 (98%)	122 (92%)	10 (8%)	0	100	100
73	SZ	98/108 (91%)	85 (87%)	10 (10%)	3 (3%)	3	19
74	Sa	95/119 (80%)	78 (82%)	14 (15%)	3 (3%)	3	19
75	Sb	79/82 (96%)	70 (89%)	9 (11%)	0	100	100
76	Sc	61/67 (91%)	55 (90%)	6 (10%)	0	100	100
77	Sd	51/56 (91%)	49 (96%)	2 (4%)	0	100	100
78	Se	58/63 (92%)	46 (79%)	12 (21%)	0	100	100
79	Sf	71/152 (47%)	44 (62%)	24 (34%)	3 (4%)	2	14
80	Sg	310/319 (97%)	280 (90%)	29 (9%)	1 (0%)	36	66
84	5	151/157 (96%)	125 (83%)	22 (15%)	4 (3%)	4	23
85	R	351/410 (86%)	330 (94%)	18 (5%)	3 (1%)	14	44
86	T	158/345 (46%)	138 (87%)	19 (12%)	1 (1%)	21	53
All	All	11941/13270 (90%)	10875 (91%)	1018 (8%)	48 (0%)	31	60

5 of 48 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	LO	111[A]	PRO
26	LX	44	PRO
56	SI	10	LYS
60	SM	109	GLU
66	SS	91	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	LA	190/196 (97%)	190 (100%)	0	100	100
5	LB	319/323 (99%)	318 (100%)	1 (0%)	86	87
6	LC	288/289 (100%)	288 (100%)	0	100	100
7	LD	241/245 (98%)	241 (100%)	0	100	100
8	LE	139/155 (90%)	138 (99%)	1 (1%)	76	81
9	LF	186/205 (91%)	185 (100%)	1 (0%)	81	84
10	LG	187/208 (90%)	184 (98%)	3 (2%)	55	72
11	LH	168/171 (98%)	168 (100%)	0	100	100
12	LI	185/187 (99%)	185 (100%)	0	100	100
13	LJ	146/151 (97%)	144 (99%)	2 (1%)	59	74
14	LL	154/159 (97%)	153 (99%)	1 (1%)	78	83
15	LM	107/109 (98%)	107 (100%)	0	100	100
16	LN	175/176 (99%)	175 (100%)	0	100	100
17	LO	160/162 (99%)	160 (100%)	0	100	100
18	LP	138/146 (94%)	138 (100%)	0	100	100
19	LQ	150/151 (99%)	149 (99%)	1 (1%)	76	81
20	LR	152/154 (99%)	151 (99%)	1 (1%)	76	81
21	LS	155/156 (99%)	154 (99%)	1 (1%)	78	83
22	LT	136/137 (99%)	136 (100%)	0	100	100
23	LU	87/107 (81%)	87 (100%)	0	100	100
24	LV	104/105 (99%)	104 (100%)	0	100	100
25	LW	60/129 (46%)	60 (100%)	0	100	100
26	LX	104/118 (88%)	104 (100%)	0	100	100
27	LY	108/110 (98%)	108 (100%)	0	100	100
28	LZ	115/116 (99%)	115 (100%)	0	100	100
29	La	118/119 (99%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	Lb	46/47 (98%)	46 (100%)	0	100	100
31	Lc	81/88 (92%)	81 (100%)	0	100	100
32	Ld	92/97 (95%)	92 (100%)	0	100	100
33	Le	108/111 (97%)	108 (100%)	0	100	100
34	Lf	90/91 (99%)	87 (97%)	3 (3%)	33	62
35	Lg	95/103 (92%)	95 (100%)	0	100	100
36	Lh	104/105 (99%)	104 (100%)	0	100	100
37	Li	80/82 (98%)	80 (100%)	0	100	100
38	Lj	69/71 (97%)	69 (100%)	0	100	100
39	Lk	68/69 (99%)	68 (100%)	0	100	100
40	Ll	45/46 (98%)	45 (100%)	0	100	100
41	Lm	47/116 (40%)	47 (100%)	0	100	100
42	Ln	22/23 (96%)	22 (100%)	0	100	100
43	Lo	87/91 (96%)	86 (99%)	1 (1%)	65	77
44	Lp	71/72 (99%)	71 (100%)	0	100	100
45	P0	160/254 (63%)	160 (100%)	0	100	100
46	P2	81/136 (60%)	81 (100%)	0	100	100
48	SA	170/210 (81%)	170 (100%)	0	100	100
49	SB	200/224 (89%)	200 (100%)	0	100	100
50	SC	175/205 (85%)	175 (100%)	0	100	100
51	SD	182/195 (93%)	182 (100%)	0	100	100
52	SE	220/222 (99%)	217 (99%)	3 (1%)	59	74
53	SF	172/191 (90%)	171 (99%)	1 (1%)	78	83
54	SG	189/201 (94%)	189 (100%)	0	100	100
55	SH	163/170 (96%)	162 (99%)	1 (1%)	78	83
56	SI	148/161 (92%)	148 (100%)	0	100	100
57	SJ	156/166 (94%)	156 (100%)	0	100	100
58	SK	77/98 (79%)	77 (100%)	0	100	100
59	SL	129/137 (94%)	128 (99%)	1 (1%)	73	80
60	SM	88/119 (74%)	85 (97%)	3 (3%)	32	61
61	SN	127/128 (99%)	127 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	SO	91/105 (87%)	91 (100%)	0	100	100
63	SP	95/118 (80%)	95 (100%)	0	100	100
64	SQ	117/119 (98%)	115 (98%)	2 (2%)	53	72
65	SR	101/124 (82%)	101 (100%)	0	100	100
66	SS	128/129 (99%)	127 (99%)	1 (1%)	73	80
67	ST	115/116 (99%)	115 (100%)	0	100	100
68	SU	93/114 (82%)	92 (99%)	1 (1%)	65	77
69	SV	71/74 (96%)	71 (100%)	0	100	100
70	SW	110/111 (99%)	110 (100%)	0	100	100
71	SX	119/120 (99%)	119 (100%)	0	100	100
72	SY	112/113 (99%)	112 (100%)	0	100	100
73	SZ	77/89 (86%)	69 (90%)	8 (10%)	7	26
74	Sa	83/100 (83%)	82 (99%)	1 (1%)	63	76
75	Sb	70/71 (99%)	70 (100%)	0	100	100
76	Sc	55/60 (92%)	55 (100%)	0	100	100
77	Sd	47/49 (96%)	47 (100%)	0	100	100
78	Se	50/54 (93%)	50 (100%)	0	100	100
79	Sf	56/135 (42%)	53 (95%)	3 (5%)	20	50
80	Sg	250/262 (95%)	249 (100%)	1 (0%)	84	85
84	5	118/132 (89%)	111 (94%)	7 (6%)	18	48
85	R	299/353 (85%)	293 (98%)	6 (2%)	48	69
86	T	134/302 (44%)	126 (94%)	8 (6%)	17	47
All	All	10005/11163 (90%)	9942 (99%)	63 (1%)	76	83

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
68	SU	49	ASN
86	T	172	GLU
73	SZ	69	LEU
85	R	348	GLN
86	T	182	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 91 such sidechains are listed below:

Mol	Chain	Res	Type
54	SG	139	ASN
66	SS	13	HIS
55	SH	22	GLN
59	SL	14	GLN
70	SW	56	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	3217/3396 (94%)	565 (17%)	36 (1%)
2	C4	120/121 (99%)	11 (9%)	1 (0%)
3	C3	157/158 (99%)	25 (15%)	1 (0%)
47	C2	1768/1800 (98%)	456 (25%)	45 (2%)
81	A	75/76 (98%)	36 (48%)	3 (4%)
82	P	75/76 (98%)	20 (26%)	0
83	m	15/16 (93%)	5 (33%)	0
All	All	5427/5643 (96%)	1118 (20%)	86 (1%)

5 of 1118 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	13	A
1	C1	14	U
1	C1	18	G
1	C1	26	A
1	C1	40	A

5 of 86 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
47	C2	765	G
47	C2	1471	A
47	C2	819	G
47	C2	1273	G
47	C2	1557	U

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

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	5	51	84	13,14,15	0.68	0	8,15,17	0.87	0

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	5	51	84	-	8/13/14/16	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
84	5	51	5CT	C2-C1-NZ-CE
84	5	51	5CT	NZ-C1-C2-C3
84	5	51	5CT	NZ-C1-C2-O1
84	5	51	5CT	C-CA-CB-CG
84	5	51	5CT	N-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	5	51	5CT	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 295 ligands modelled in this entry, 294 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
89	ASP	C1	3593	88	3,4,8	1.01	0	2,4,10	0.97	0

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
89	ASP	C1	3593	88	-	0/1/2/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
89	C1	3593	ASP	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

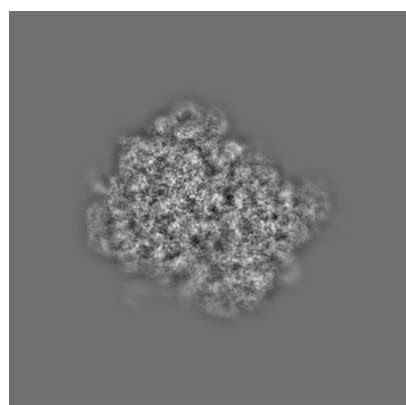
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24652. These allow visual inspection of the internal detail of the map and identification of artifacts.

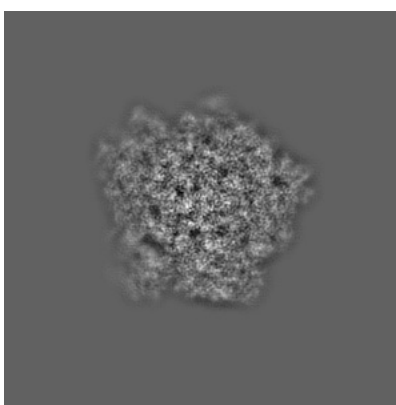
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

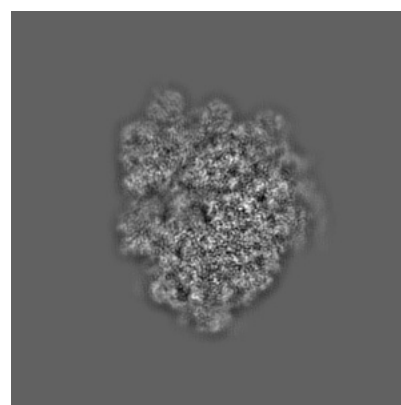
6.1.1 Primary map



X



Y

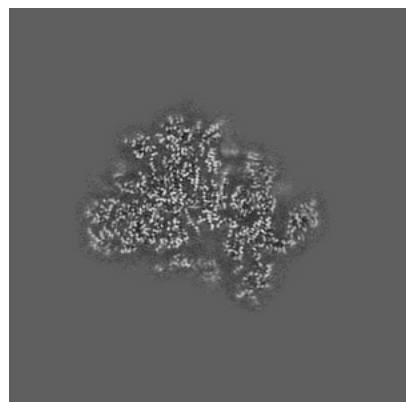


Z

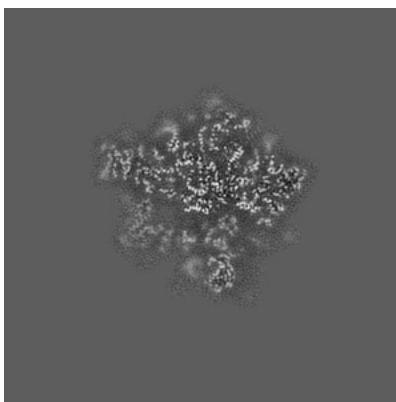
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

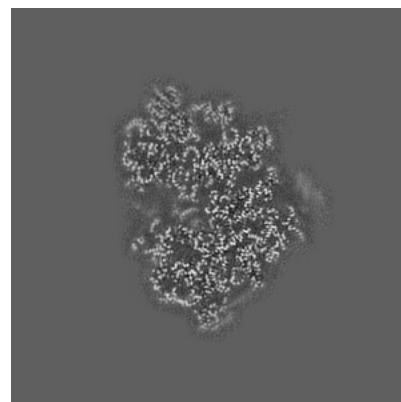
6.2.1 Primary map



X Index: 224



Y Index: 224

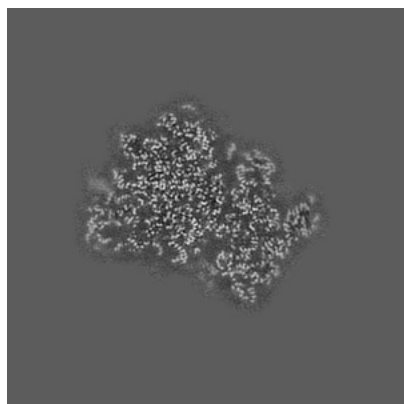


Z Index: 224

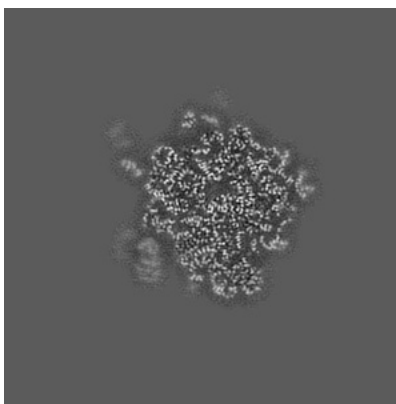
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

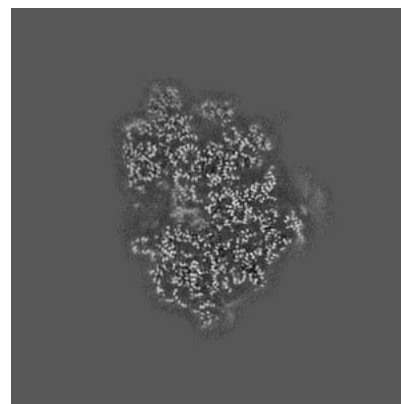
6.3.1 Primary map



X Index: 232



Y Index: 192

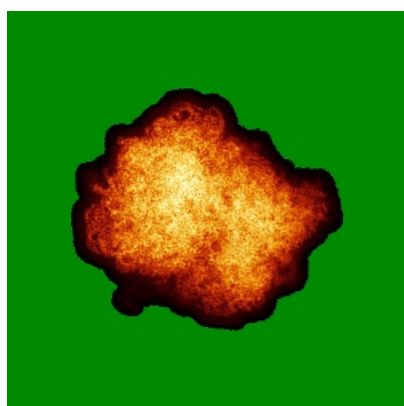


Z Index: 227

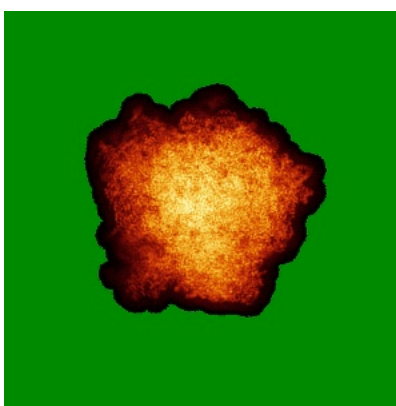
The images above show the largest variance slices of the map in three orthogonal directions.

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

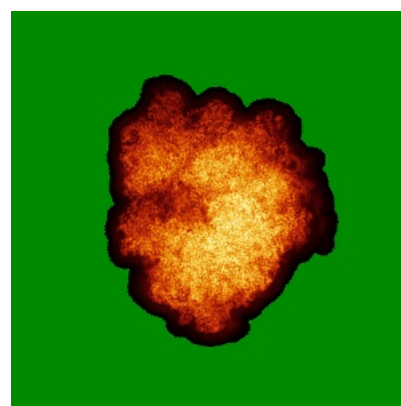
6.4.1 Primary map



X



Y

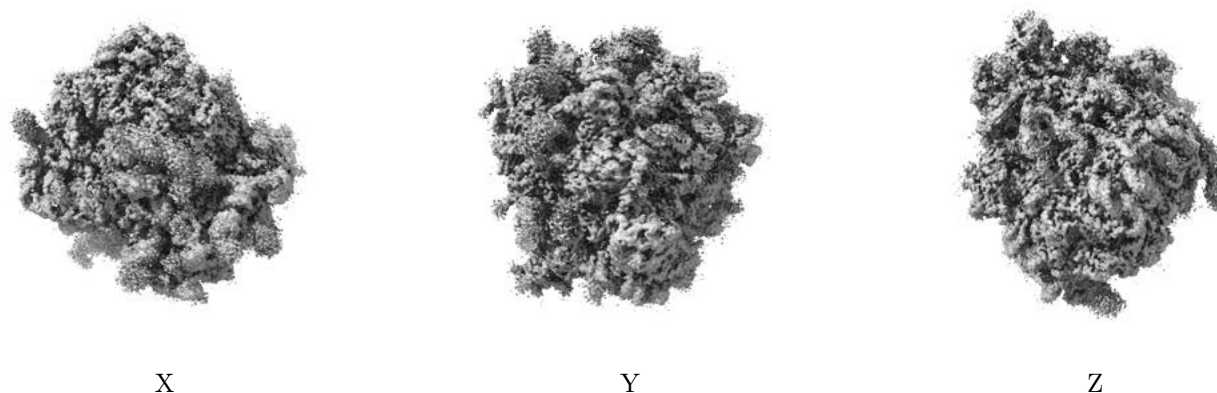


Z

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 0.003. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

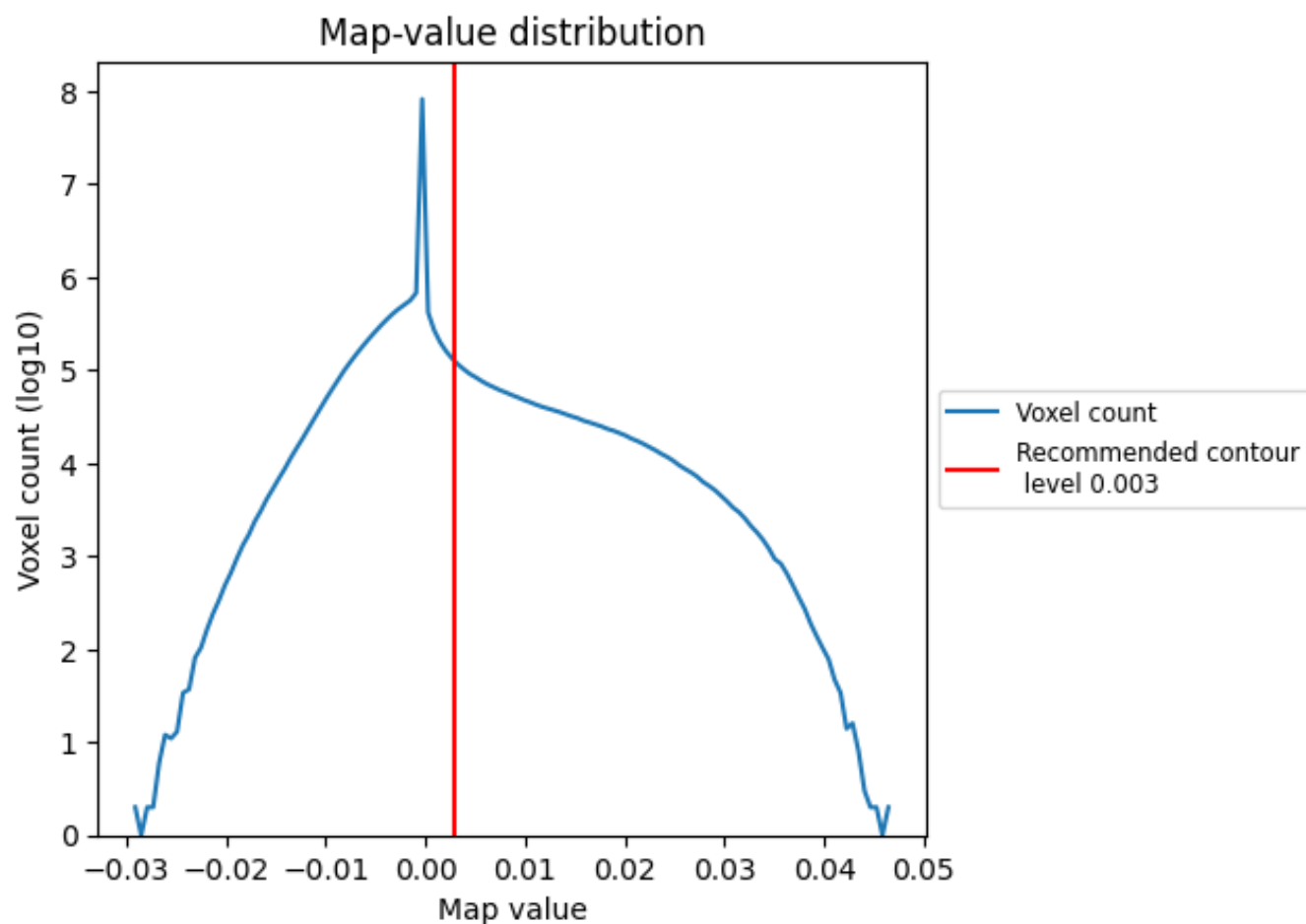
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

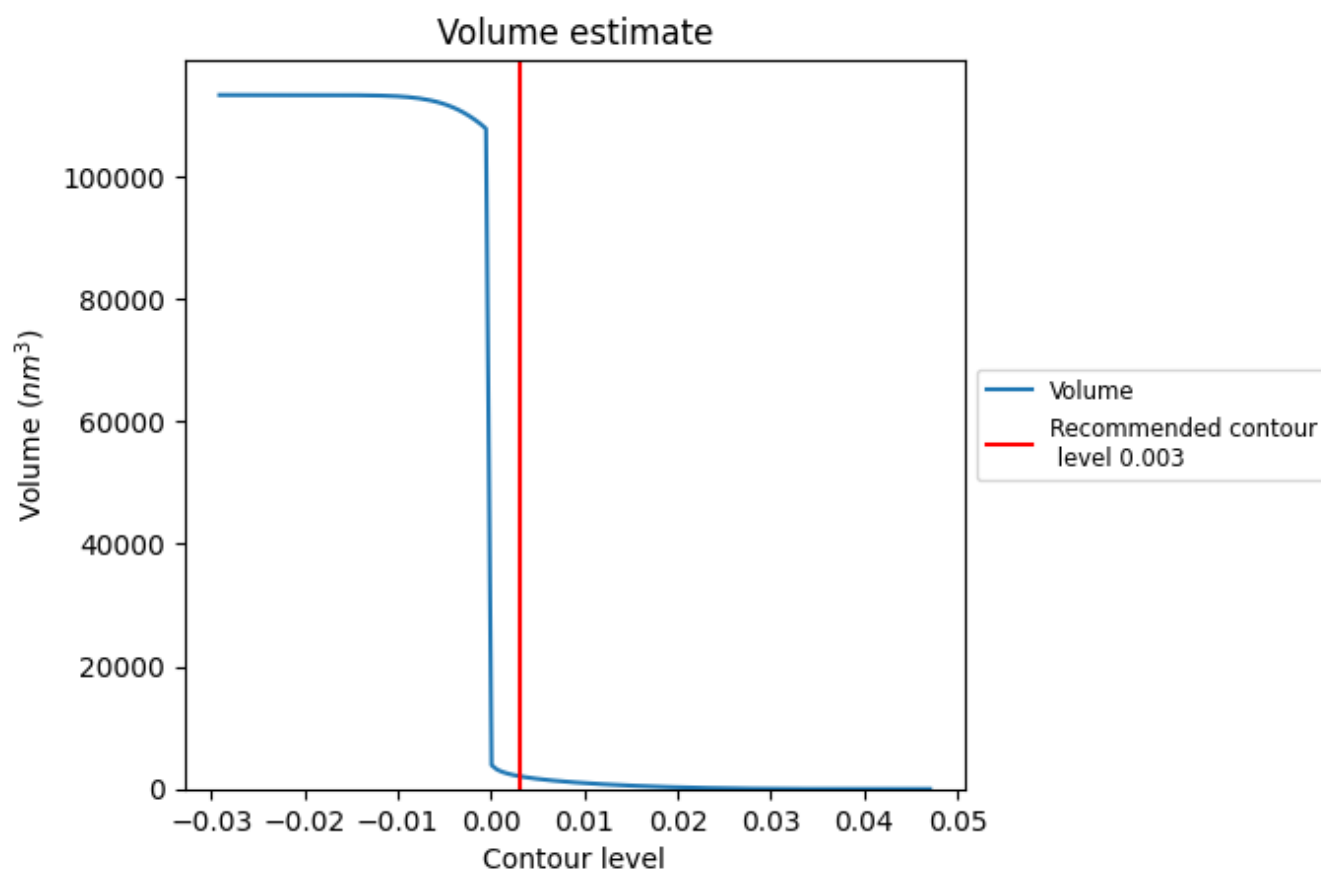
This section contains the results of statistical analysis of the map.

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.

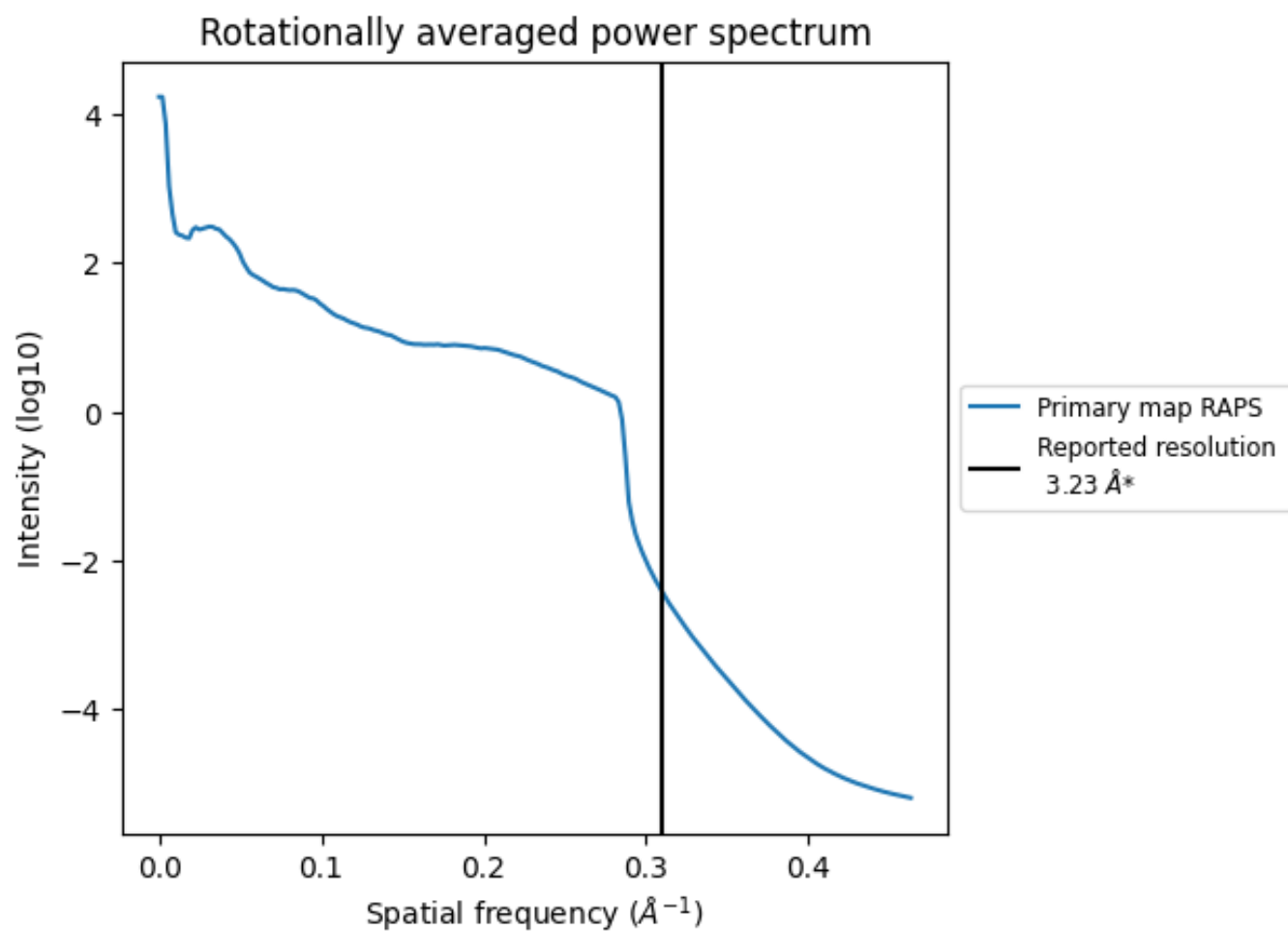
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2093 nm^3 ; this corresponds to an approximate mass of 1891 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 ⓘ

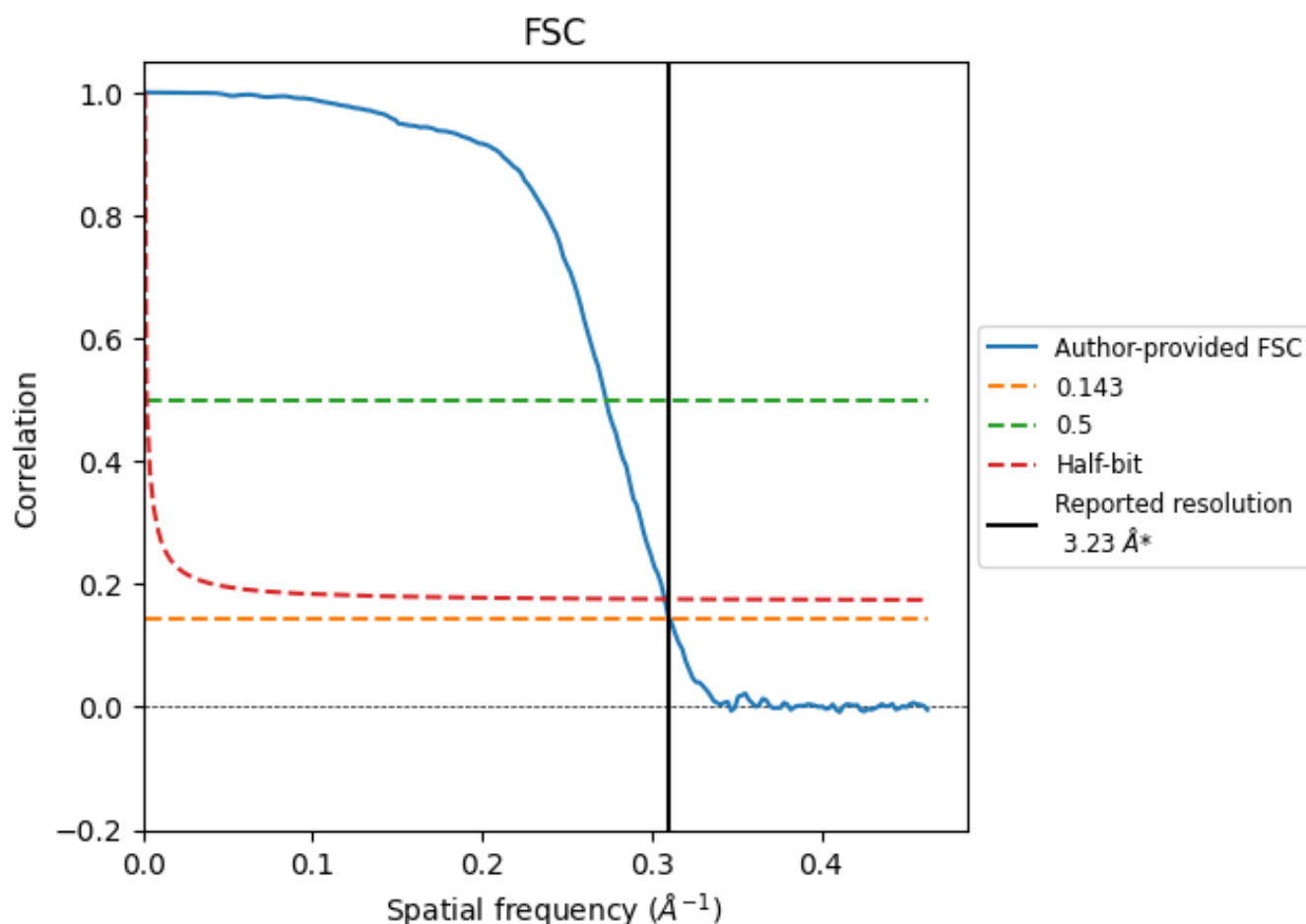


*Reported resolution corresponds to spatial frequency of 0.310 Å⁻¹

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 0.310 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.23	-	-
Author-provided FSC curve	3.22	3.66	3.25
Unmasked-calculated*	-	-	-

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

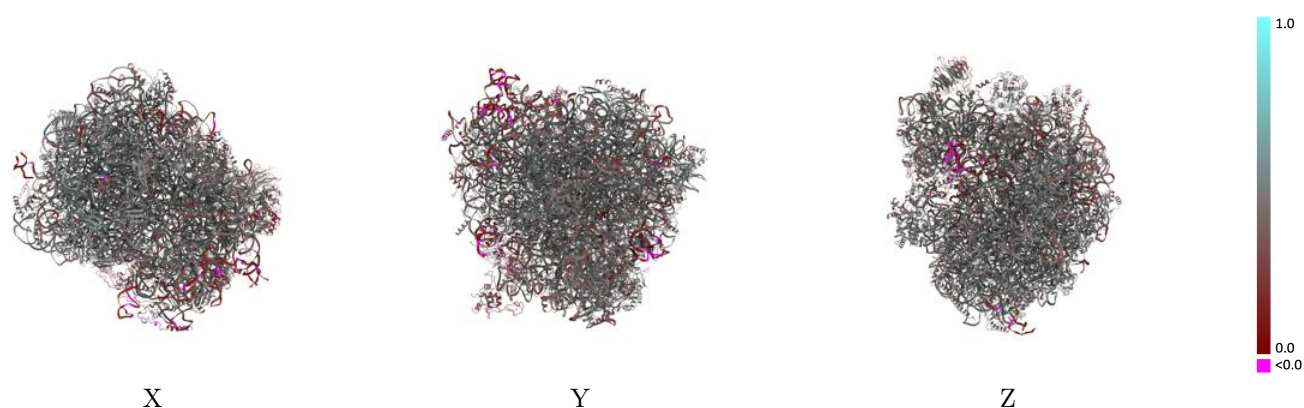
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24652 and PDB model 7RR5. Per-residue inclusion information can be found in section 3 on page 23.

9.1 Map-model overlay [i](#)

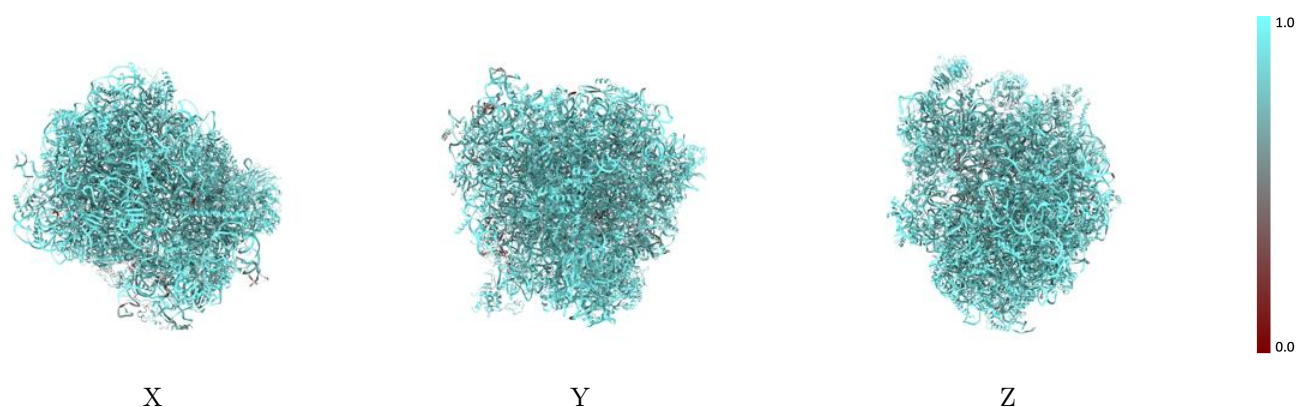
This section was not generated.

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



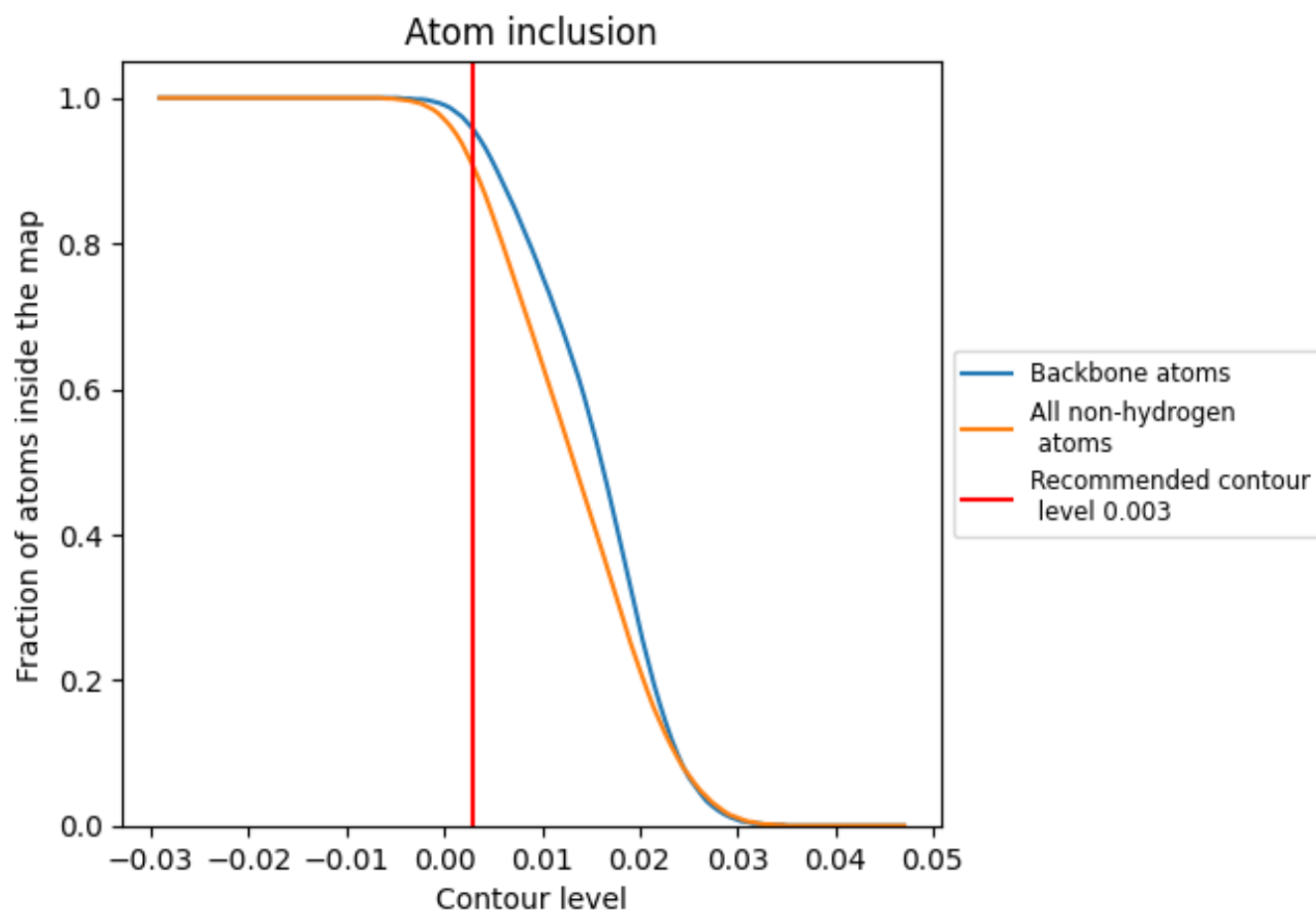
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.003).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 90% 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 (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9050	 0.4370
5	 0.7240	 0.3570
A	 0.9130	 0.3670
C1	 0.9420	 0.4440
C2	 0.9290	 0.4180
C3	 0.9570	 0.4650
C4	 0.9730	 0.4790
L1	 0.8580	 0.3200
LA	 0.8770	 0.5050
LB	 0.9190	 0.5110
LC	 0.9070	 0.4810
LD	 0.9050	 0.4590
LE	 0.8980	 0.4520
LF	 0.8880	 0.4740
LG	 0.9000	 0.4540
LH	 0.9100	 0.4720
LI	 0.8900	 0.4840
LJ	 0.8800	 0.4470
LL	 0.9020	 0.4560
LM	 0.9180	 0.4880
LN	 0.8760	 0.5060
LO	 0.8960	 0.4920
LP	 0.8770	 0.4680
LQ	 0.8810	 0.4830
LR	 0.8950	 0.4390
LS	 0.8890	 0.4880
LT	 0.8890	 0.4960
LU	 0.9390	 0.4610
LV	 0.8840	 0.5050
LW	 0.7500	 0.3550
LX	 0.8580	 0.4600
LY	 0.9230	 0.5030
LZ	 0.8860	 0.4490
La	 0.9120	 0.4960
Lb	 0.8410	 0.4450



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Chain	Atom inclusion	Q-score
Lc	 0.9320	 0.4680
Ld	 0.8930	 0.4850
Le	 0.8840	 0.5040
Lf	 0.8990	 0.5160
Lg	 0.8530	 0.4700
Lh	 0.9050	 0.4640
Li	 0.8930	 0.4550
Lj	 0.8870	 0.4940
Lk	 0.8980	 0.4450
Ll	 0.8840	 0.5020
Lm	 0.8610	 0.4730
Ln	 0.8510	 0.4700
Lo	 0.8930	 0.4940
Lp	 0.8820	 0.4820
P	 0.9070	 0.3590
P0	 0.5840	 0.1510
P2	 0.6260	 0.0780
R	 0.6920	 0.3460
SA	 0.9080	 0.4490
SB	 0.8530	 0.4130
SC	 0.8930	 0.4760
SD	 0.8540	 0.4290
SE	 0.8710	 0.4560
SF	 0.8670	 0.4290
SG	 0.8650	 0.3990
SH	 0.8590	 0.3560
SI	 0.8920	 0.4690
SJ	 0.8750	 0.4590
SK	 0.8920	 0.4210
SL	 0.8720	 0.4750
SM	 0.8050	 0.2760
SN	 0.8700	 0.4510
SO	 0.8680	 0.4580
SP	 0.9100	 0.4390
SQ	 0.8600	 0.4710
SR	 0.8880	 0.4300
SS	 0.8940	 0.4340
ST	 0.8840	 0.4500
SU	 0.8350	 0.4280
SV	 0.9160	 0.4540
SW	 0.8760	 0.4840
SX	 0.8570	 0.4800

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Chain	Atom inclusion	Q-score
SY	 0.8690	 0.4350
SZ	 0.8420	 0.3920
Sa	 0.8720	 0.4590
Sb	 0.8980	 0.4120
Sc	 0.8560	 0.4340
Sd	 0.8260	 0.4800
Se	 0.8050	 0.4260
Sf	 0.8240	 0.2690
Sg	 0.8900	 0.4080
T	 0.5870	 0.2400
m	 0.7120	 0.3330