



wwPDB EM Validation Summary Report ⓘ

Jun 17, 2026 – 06:51 PM EDT

PDB ID : 9YGM / pdb_00009ygm
EMDB ID : EMD-72933
Title : Babesia divergens ribosome structure by single-particle cryo-EM (3D class3, E-site tRNA)
Authors : Gutierrez-Vargas, C.; Izhaki-Tavor, L.S.; Leger-Abraham, M.
Deposited on : 2025-09-29
Resolution : 2.70 Å (reported)
Based on initial models : ., 5XXU, 3J7A, 5XXB

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:

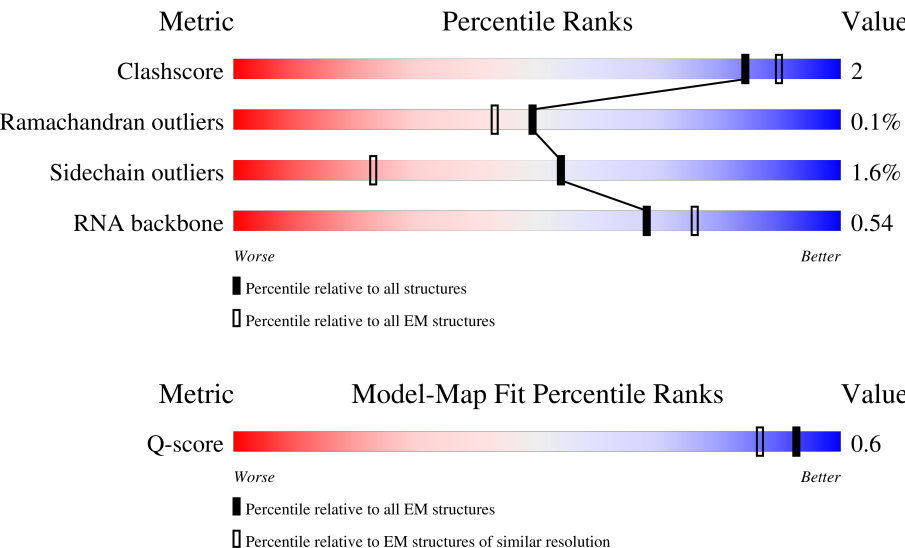
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 2.70 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.



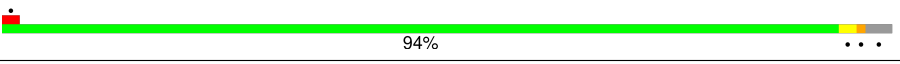
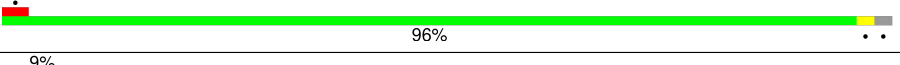

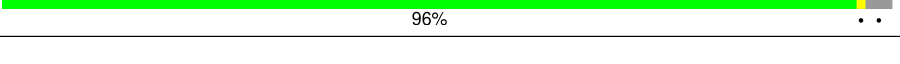

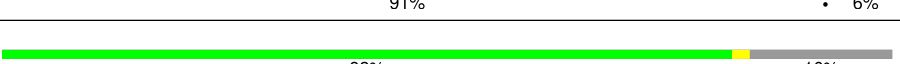
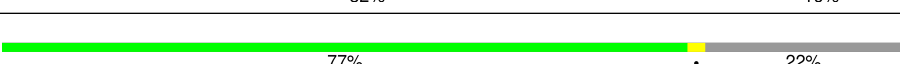
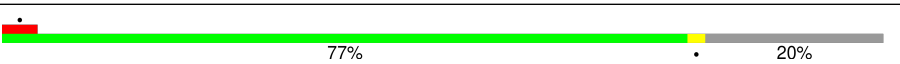

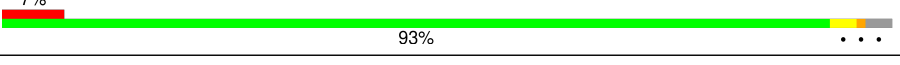
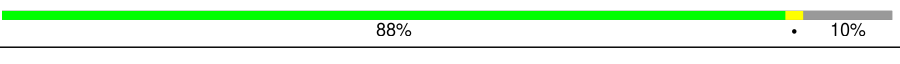
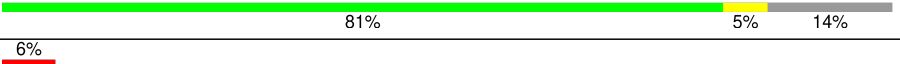

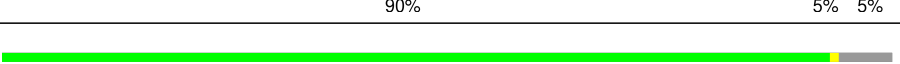
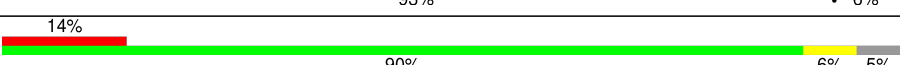
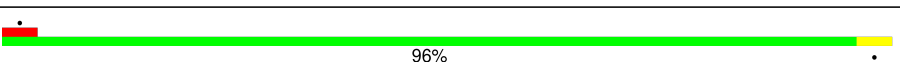

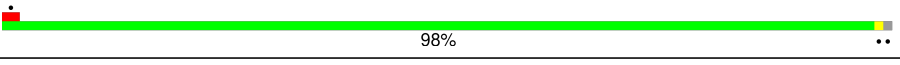
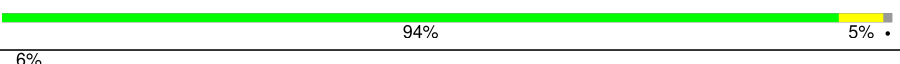


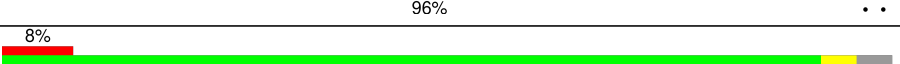
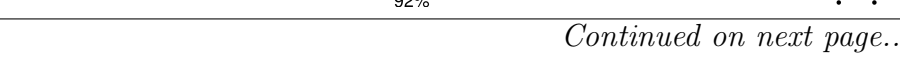


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10327 (2.20 - 3.20)

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	L3	122	<div> <div>77%</div> <div>16%</div> <div>7%</div> </div>
2	LB	257	<div> <div>92%</div> <div>.</div> <div>.</div> </div>
3	LC	395	<div> <div>91%</div> <div>5%</div> <div>.</div> </div>











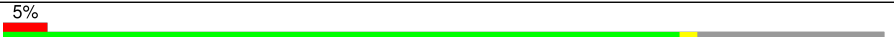


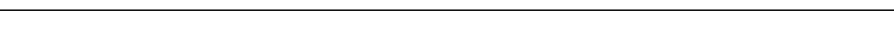
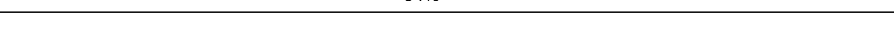
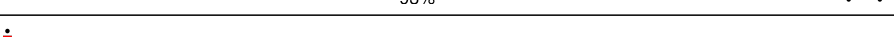



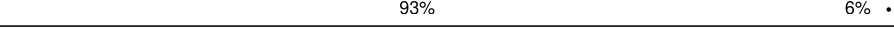


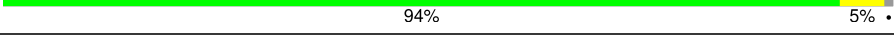

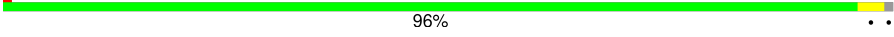
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Mol	Chain	Length	Quality of chain
4	LE	171	
5	LF	190	
6	LG	212	
7	LJ	203	
8	LK	139	
9	LP	306	
10	LQ	222	
11	LU	194	
12	LV	122	
13	LZ	146	
14	La	123	
15	Lb	59	
16	Ld	108	
17	Le	117	
18	Lf	132	
19	Lg	115	
20	LD	360	
21	LI	202	
22	LL	133	
23	LM	147	
24	LN	204	
25	LO	227	
26	LR	194	
27	LS	188	
28	LT	160	









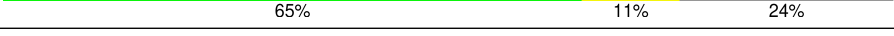

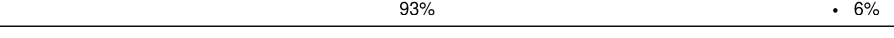
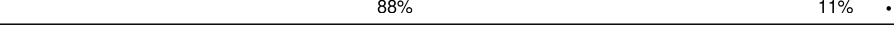

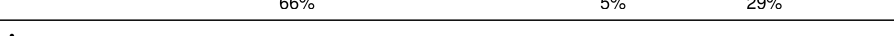


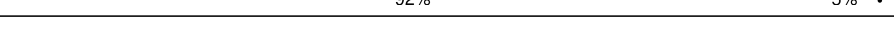

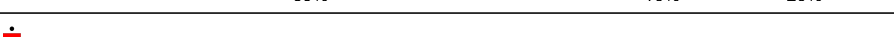






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Mol	Chain	Length	Quality of chain
29	LX	137	
30	Lc	259	
31	Lh	150	
32	Li	116	
33	Lj	98	
34	Lk	70	
35	Ll	59	
36	Lm	55	
37	Lp	94	
38	Lo	105	
39	LH	285	
40	SA	264	
41	SB	274	
42	SD	184	
43	SE	266	
44	SF	196	
45	SG	239	
46	SI	194	
47	SJ	130	
48	SK	192	
49	SP	145	
50	ST	151	
51	SU	156	
52	SY	79	
53	Sb	115	

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Mol	Chain	Length	Quality of chain
54	Sc	82	
55	Se	61	
56	SC	223	
57	SH	192	
58	SL	149	
59	SM	120	
60	SQ	135	
61	SR	154	
62	SS	66	
63	SW	149	
64	Sd	67	
65	Sg	323	
66	SN	113	
67	SZ	135	
68	Sa	104	
69	Sf	77	
70	Ln	39	
71	SV	134	
72	SO	157	
73	L4	159	
74	L5	3326	
75	S7	74	
76	S1	1728	
77	LA	217	
78	LW	153	

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Mol	Chain	Length	Quality of chain
79	LY	156	
80	SX	174	

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 189052 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 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L3	122	Total	C	N	O	P	0	0
			2610	1163	476	849	122		

- Molecule 2 is a protein called 60S ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LB	248	Total	C	N	O	S	0	0
			1892	1179	382	326	5		

- Molecule 3 is a protein called 60S ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LC	381	Total	C	N	O	S	0	0
			3036	1934	565	522	15		

- Molecule 4 is a protein called 60S ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LE	166	Total	C	N	O	S	0	0
			1345	850	250	239	6		

- Molecule 5 is a protein called 60S ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LF	186	Total	C	N	O	S	0	0
			1469	934	263	266	6		

- Molecule 6 is a protein called 60S ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LG	149	Total	C	N	O	S	0	0
			1163	753	200	205	5		

- Molecule 7 is a protein called 60S ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LJ	196	Total	C	N	O	S	0	0
			1544	970	307	256	11		

- Molecule 8 is a protein called 60S ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LK	129	Total	C	N	O	S	0	0
			973	620	179	168	6		

- Molecule 9 is a protein called 60S ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LP	289	Total	C	N	O	S	0	0
			2351	1488	436	417	10		

- Molecule 10 is a protein called 60S ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LQ	186	Total	C	N	O	S	0	0
			1449	911	285	248	5		

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LQ	?	-	VAL	deletion	UNP A0AAD9G7R0
LQ	?	-	ASP	deletion	UNP A0AAD9G7R0
LQ	?	-	PHE	deletion	UNP A0AAD9G7R0
LQ	?	-	HIS	deletion	UNP A0AAD9G7R0
LQ	?	-	GLU	deletion	UNP A0AAD9G7R0
LQ	?	-	LYS	deletion	UNP A0AAD9G7R0
LQ	?	-	ASP	deletion	UNP A0AAD9G7R0
LQ	?	-	MET	deletion	UNP A0AAD9G7R0
LQ	?	-	MET	deletion	UNP A0AAD9G7R0
LQ	?	-	MET	deletion	UNP A0AAD9G7R0
LQ	?	-	HIS	deletion	UNP A0AAD9G7R0
LQ	?	-	VAL	deletion	UNP A0AAD9G7R0
LQ	?	-	SER	deletion	UNP A0AAD9G7R0
LQ	?	-	THR	deletion	UNP A0AAD9G7R0
LQ	?	-	GLU	deletion	UNP A0AAD9G7R0
LQ	?	-	SER	deletion	UNP A0AAD9G7R0
LQ	?	-	ARG	deletion	UNP A0AAD9G7R0

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Chain	Residue	Modelled	Actual	Comment	Reference
LQ	?	-	ARG	deletion	UNP A0AAD9G7R0
LQ	?	-	SER	deletion	UNP A0AAD9G7R0
LQ	?	-	SER	deletion	UNP A0AAD9G7R0
LQ	?	-	ASP	deletion	UNP A0AAD9G7R0
LQ	?	-	SER	deletion	UNP A0AAD9G7R0
LQ	?	-	ALA	deletion	UNP A0AAD9G7R0
LQ	?	-	GLY	deletion	UNP A0AAD9G7R0
LQ	?	-	GLU	deletion	UNP A0AAD9G7R0

- Molecule 11 is a protein called 60S ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LU	152	Total	C	N	O	S	0	0
			1231	777	242	207	5		

- Molecule 12 is a protein called 60S ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LV	97	Total	C	N	O	S	0	0
			799	513	141	144	1		

- Molecule 13 is a protein called 60S ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LZ	138	Total	C	N	O	S	0	0
			1120	707	217	190	6		

- Molecule 14 is a protein called 60S ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	La	119	Total	C	N	O	S	0	0
			985	623	194	165	3		

- Molecule 15 is a protein called 60S ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Lb	53	Total	C	N	O	S	0	0
			431	267	95	66	3		

- Molecule 16 is a protein called 60S ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Ld	93	Total	C	N	O	S	0	0
			706	444	126	127	9		

- Molecule 17 is a protein called 60S ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Le	105	Total	C	N	O	S	0	0
			869	550	169	147	3		

- Molecule 18 is a protein called 60S ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Lf	125	Total	C	N	O	S	0	0
			1026	647	212	165	2		

- Molecule 19 is a protein called 60S ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Lg	108	Total	C	N	O	S	0	0
			879	563	167	144	5		

- Molecule 20 is a protein called 60S ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LD	343	Total	C	N	O	S	0	0
			2634	1657	512	453	12		

- Molecule 21 is a protein called 60S ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LI	201	Total	C	N	O	S	0	0
			1628	1038	317	264	9		

- Molecule 22 is a protein called 60S ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LL	128	Total	C	N	O	S	0	0
			1018	657	183	175	3		

- Molecule 23 is a protein called 60S ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LM	146	Total	C	N	O	S	0	0
			1159	737	230	186	6		

- Molecule 24 is a protein called 60S ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LN	202	Total	C	N	O	S	0	0
			1708	1073	360	266	9		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LN	1	MET	-	insertion	UNP A0AAD9LIN3
LN	2	GLY	-	insertion	UNP A0AAD9LIN3
LN	3	ALA	-	insertion	UNP A0AAD9LIN3
LN	4	TYR	-	insertion	UNP A0AAD9LIN3
LN	5	ARG	-	insertion	UNP A0AAD9LIN3
LN	6	TYR	-	insertion	UNP A0AAD9LIN3

- Molecule 25 is a protein called 60S ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LO	212	Total	C	N	O	S	0	0
			1706	1094	325	279	8		

- Molecule 26 is a protein called 60S ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LR	175	Total	C	N	O	S	0	0
			1433	891	300	231	11		

- Molecule 27 is a protein called 60S ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LS	184	Total	C	N	O	S	0	0
			1484	944	279	253	8		

- Molecule 28 is a protein called 60S ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LT	154	Total	C	N	O	S	0	0
			1238	784	241	207	6		

- Molecule 29 is a protein called 60S ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LX	123	Total	C	N	O	S	0	0
			1020	633	206	176	5		

- Molecule 30 is a protein called 60S ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lc	215	Total	C	N	O	S	0	0
			1759	1133	332	288	6		

- Molecule 31 is a protein called 60S ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lh	99	Total	C	N	O	S	0	0
			808	495	180	128	5		

- Molecule 32 is a protein called 60S ribosomal protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Li	108	Total	C	N	O	S	0	0
			847	530	166	146	5		

- Molecule 33 is a protein called 60S ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lj	89	Total	C	N	O	S	0	0
			703	428	155	113	7		

- Molecule 34 is a protein called 60S ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lk	65	Total	C	N	O	S	0	0
			525	333	99	92	1		

- Molecule 35 is a protein called 60S ribosomal protein eL39.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	Ll	49	Total	C	N	O	0	0
			431	275	93	63		

- Molecule 36 is a protein called 60S ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lm	50	Total	C	N	O	S	0	0
			407	252	85	63	7		

- Molecule 37 is a protein called 60S ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lp	93	Total	C	N	O	S	0	0
			733	455	145	128	5		

- Molecule 38 is a protein called 60S ribosomal protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lo	97	Total	C	N	O	S	0	0
			782	492	155	129	6		

- Molecule 39 is a protein called 60S ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LH	224	Total	C	N	O	S	0	0
			1817	1164	337	308	8		

- Molecule 40 is a protein called 40S ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	SA	215	Total	C	N	O	S	0	0
			1742	1107	313	309	13		

- Molecule 41 is a protein called 40S ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	SB	196	Total	C	N	O	S	0	0
			1553	997	269	277	10		

- Molecule 42 is a protein called 40S ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	SD	178	Total	C	N	O	S	0	0
			1474	934	287	246	7		

- Molecule 43 is a protein called 40S ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SE	258	Total	C	N	O	S	0	0
			2060	1306	383	363	8		

- Molecule 44 is a protein called 40S ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SF	180	Total	C	N	O	S	0	0
			1361	873	241	240	7		

- Molecule 45 is a protein called 40S ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SG	216	Total	C	N	O	S	0	0
			1760	1100	343	307	10		

- Molecule 46 is a protein called 40S ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SI	178	Total	C	N	O	S	0	0
			1430	916	260	251	3		

- Molecule 47 is a protein called 40S ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SJ	129	Total	C	N	O	S	0	0
			1033	661	190	176	6		

- Molecule 48 is a protein called 40S ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SK	181	Total	C	N	O	S	0	0
			1462	914	289	252	7		

- Molecule 49 is a protein called 40S ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SP	143	Total	C	N	O	S	0	0
			1124	709	224	189	2		

- Molecule 50 is a protein called 40S ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	ST	149	Total	C	N	O	S	0	0
			1213	777	228	203	5		

- Molecule 51 is a protein called 40S ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SU	151	Total	C	N	O	S	0	0
			1237	794	230	203	10		

- Molecule 52 is a protein called 40S ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SY	78	Total	C	N	O	S	0	0
			600	368	107	121	4		

- Molecule 53 is a protein called 40S ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Sb	97	Total	C	N	O	S	0	0
			777	477	165	129	6		

- Molecule 54 is a protein called 40S ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Sc	69	Total	C	N	O	S	0	0
			540	341	100	93	6		

- Molecule 55 is a protein called 40S ribosomal protein eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	Se	40	Total	C	N	O	0	0
			324	199	73	52		

- Molecule 56 is a protein called 40S ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SC	209	Total	C	N	O	S	0	0
			1627	1027	305	289	6		

- Molecule 57 is a protein called 40S ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SH	187	Total	C	N	O	S	0	0
			1474	922	281	261	10		

- Molecule 58 is a protein called 40S ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SL	134	Total	C	N	O	S	0	0
			1055	666	207	179	3		

- Molecule 59 is a protein called 40S ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SM	98	Total	C	N	O	S	0	0
			778	484	143	145	6		

- Molecule 60 is a protein called 40S ribosomal protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SQ	115	Total	C	N	O	S	0	0
			875	550	149	170	6		

- Molecule 61 is a protein called 40S ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SR	144	Total	C	N	O	S	0	0
			1147	710	226	204	7		

- Molecule 62 is a protein called 40S ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SS	50	Total	C	N	O	S	0	0
			412	260	84	64	4		

- Molecule 63 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SW	115	Total	C	N	O	S	0	0
			942	612	166	159	5		

- Molecule 64 is a protein called 40S ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Sd	63	Total	C	N	O	S	0	0
			488	301	99	87	1		

- Molecule 65 is a protein called Receptor for activated C kinase 1, RACK1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Sg	322	Total	C	N	O	S	0	0
			2489	1570	428	477	14		

- Molecule 66 is a protein called 40S ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SN	96	Total	C	N	O	S	0	0
			801	528	135	133	5		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SN	?	-	GLY	deletion	UNP A0AAD9G6F1
SN	?	-	GLU	deletion	UNP A0AAD9G6F1
SN	?	-	LEU	deletion	UNP A0AAD9G6F1
SN	?	-	ARG	deletion	UNP A0AAD9G6F1
SN	?	-	PHE	deletion	UNP A0AAD9G6F1
SN	?	-	MET	deletion	UNP A0AAD9G6F1
SN	?	-	THR	deletion	UNP A0AAD9G6F1
SN	?	-	VAL	deletion	UNP A0AAD9G6F1
SN	?	-	LEU	deletion	UNP A0AAD9G6F1
SN	?	-	THR	deletion	UNP A0AAD9G6F1
SN	?	-	TYR	deletion	UNP A0AAD9G6F1
SN	?	-	TYR	deletion	UNP A0AAD9G6F1
SN	?	-	PHE	deletion	UNP A0AAD9G6F1
SN	?	-	VAL	deletion	UNP A0AAD9G6F1
SN	?	-	GLY	deletion	UNP A0AAD9G6F1
SN	?	-	SER	deletion	UNP A0AAD9G6F1
SN	?	-	LEU	deletion	UNP A0AAD9G6F1
SN	?	-	HIS	deletion	UNP A0AAD9G6F1
SN	?	-	GLY	deletion	UNP A0AAD9G6F1
SN	?	-	ARG	deletion	UNP A0AAD9G6F1
SN	?	-	ALA	deletion	UNP A0AAD9G6F1

- Molecule 67 is a protein called 40S ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SZ	96	Total	C	N	O	S	0	0
			790	508	147	132	3		

- Molecule 68 is a protein called 40S ribosomal protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Sa	75	Total	C	N	O	S	0	0
			601	382	106	109	4		

- Molecule 69 is a protein called 40S ribosomal protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sf	64	Total	C	N	O	S	0	0
			509	325	95	83	6		

- Molecule 70 is a protein called 60S ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Ln	38	Total	C	N	O	S	0	0
			349	213	89	45	2		

- Molecule 71 is a protein called 40S ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SV	79	Total	C	N	O	S	0	0
			644	407	128	107	2		

- Molecule 72 is a protein called 40S ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SO	126	Total	C	N	O	S	0	0
			950	585	188	173	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SO	144	IAS	ASP	conflict	UNP A0AAD9GIK0

- Molecule 73 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	L4	151	Total	C	N	O	P	0	0
			3209	1437	573	1048	151		

- Molecule 74 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	L5	2871	Total	C	N	O	P	0	0
			61299	27392	10965	20071	2871		

- Molecule 75 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	S7	68	Total	C	N	O	P	0	0
			1446	646	255	478	67		

- Molecule 76 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	S1	1550	Total	C	N	O	P	0	0
			33088	14798	5892	10848	1550		

- Molecule 77 is a protein called 60S ribosomal protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	LA	217	Total	C	N	O	S	0	0
			1716	1089	308	311	8		

- Molecule 78 is a protein called 60S ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	LW	118	Total	C	N	O	S	0	0
			963	612	181	167	3		

- Molecule 79 is a protein called 60S ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	LY	59	Total	C	N	O	S	0	0
			491	319	91	80	1		

There are 43 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LY	?	-	VAL	deletion	UNP A0AAD9LE14
LY	?	-	CYS	deletion	UNP A0AAD9LE14
LY	?	-	PRO	deletion	UNP A0AAD9LE14
LY	?	-	LYS	deletion	UNP A0AAD9LE14
LY	?	-	VAL	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	CYS	deletion	UNP A0AAD9LE14
LY	?	-	ASN	deletion	UNP A0AAD9LE14
LY	?	-	ASN	deletion	UNP A0AAD9LE14
LY	?	-	PHE	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	GLN	deletion	UNP A0AAD9LE14
LY	?	-	TRP	deletion	UNP A0AAD9LE14
LY	?	-	PRO	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	HIS	deletion	UNP A0AAD9LE14
LY	?	-	ASN	deletion	UNP A0AAD9LE14
LY	?	-	ASN	deletion	UNP A0AAD9LE14
LY	?	-	CYS	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	ALA	deletion	UNP A0AAD9LE14
LY	?	-	LEU	deletion	UNP A0AAD9LE14
LY	?	-	PHE	deletion	UNP A0AAD9LE14
LY	?	-	VAL	deletion	UNP A0AAD9LE14
LY	?	-	THR	deletion	UNP A0AAD9LE14
LY	?	-	MET	deletion	UNP A0AAD9LE14
LY	?	-	VAL	deletion	UNP A0AAD9LE14
LY	?	-	THR	deletion	UNP A0AAD9LE14
LY	?	-	LEU	deletion	UNP A0AAD9LE14
LY	?	-	THR	deletion	UNP A0AAD9LE14
LY	?	-	LYS	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	ASP	deletion	UNP A0AAD9LE14
LY	?	-	ILE	deletion	UNP A0AAD9LE14
LY	?	-	PHE	deletion	UNP A0AAD9LE14
LY	?	-	ILE	deletion	UNP A0AAD9LE14
LY	?	-	ILE	deletion	UNP A0AAD9LE14
LY	?	-	LEU	deletion	UNP A0AAD9LE14
LY	?	-	ALA	deletion	UNP A0AAD9LE14
LY	?	-	PHE	deletion	UNP A0AAD9LE14
LY	?	-	LEU	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14
LY	?	-	SER	deletion	UNP A0AAD9LE14

- Molecule 80 is a protein called 40S ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	SX	159	Total	C	N	O	S	0	0
			1300	818	251	226	5		

- Molecule 81 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
81	L3	1	Total	Mg	0
			1	1	
81	L4	1	Total	Mg	0
			1	1	
81	L5	133	Total	Mg	0
			133	133	
81	S1	1	Total	Mg	0
			1	1	

- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
82	Lh	1	Total	Zn	0
			1	1	
82	Lj	1	Total	Zn	0
			1	1	
82	Lm	1	Total	Zn	0
			1	1	
82	Lp	1	Total	Zn	0
			1	1	
82	Lo	1	Total	Zn	0
			1	1	

- Molecule 83 is POTASSIUM ION (CCD ID: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
83	L5	25	Total	K	0
			25	25	
83	S1	1	Total	K	0
			1	1	

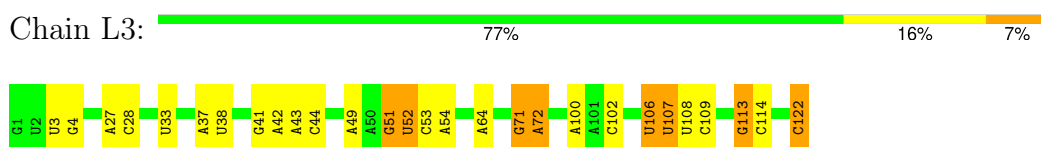
- Molecule 84 is water.

Mol	Chain	Residues	Atoms		AltConf
84	SA	2	Total 2	O 2	0
84	L5	25	Total 25	O 25	0
84	S1	7	Total 7	O 7	0

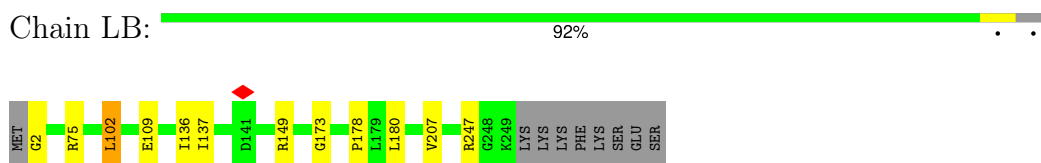
3 Residue-property plots [i](#)

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

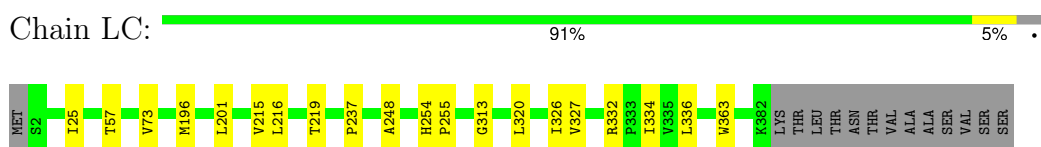
- Molecule 1: 5S ribosomal RNA



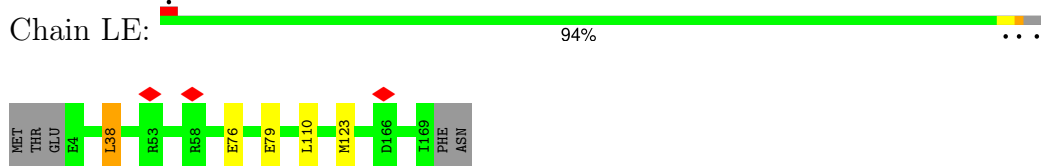
- Molecule 2: 60S ribosomal protein uL2



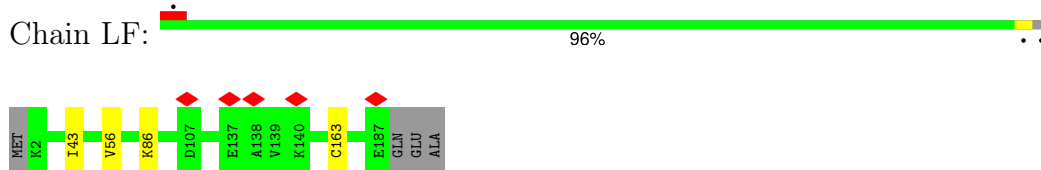
- Molecule 3: 60S ribosomal protein uL3



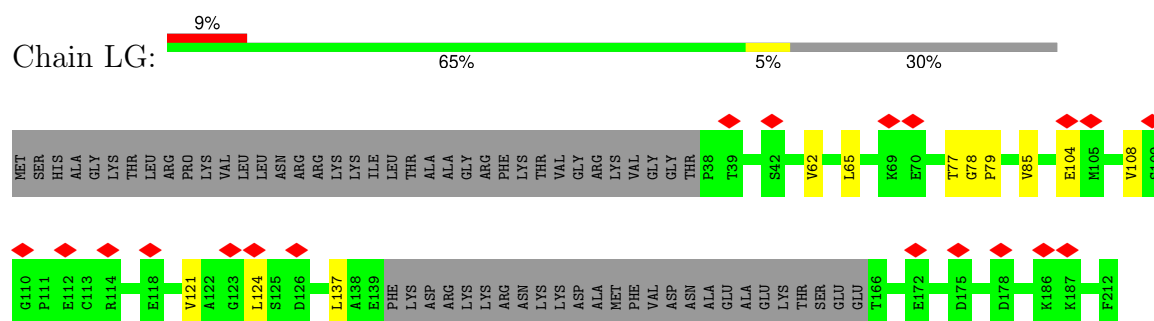
- Molecule 4: 60S ribosomal protein uL5



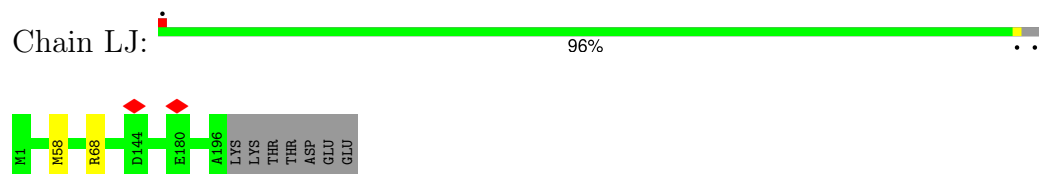
- Molecule 5: 60S ribosomal protein uL6



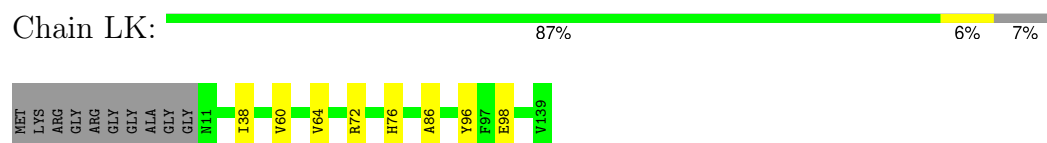
- Molecule 6: 60S ribosomal protein eL6



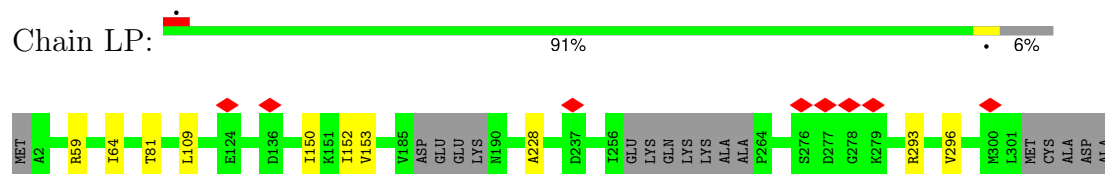
- Molecule 7: 60S ribosomal protein eL13



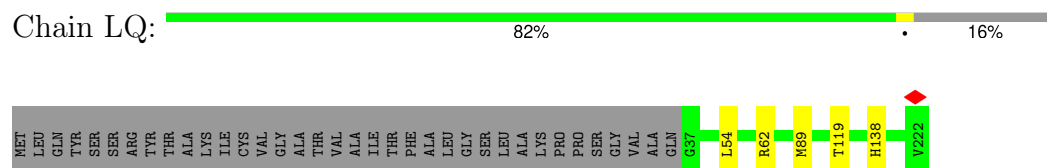
- Molecule 8: 60S ribosomal protein uL14



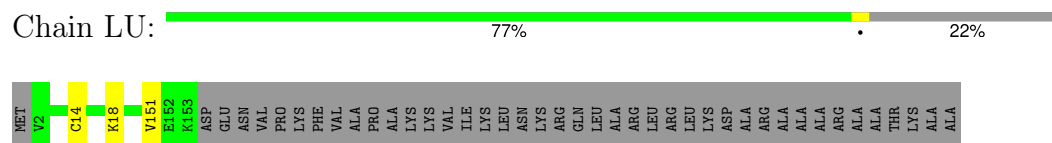
- Molecule 9: 60S ribosomal protein uL18



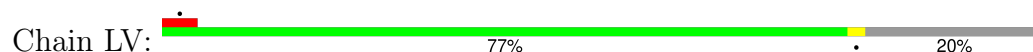
- Molecule 10: 60S ribosomal protein eL18

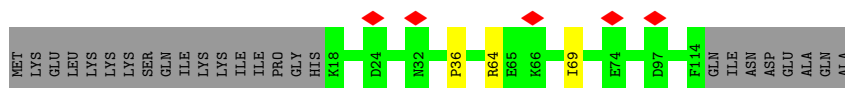


- Molecule 11: 60S ribosomal protein uL22



- Molecule 12: 60S ribosomal protein eL22

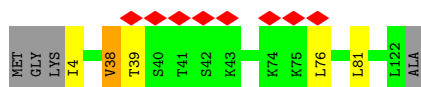




- Molecule 13: 60S ribosomal protein eL27



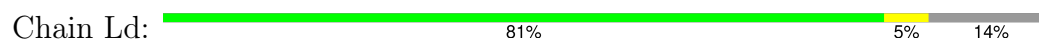
- Molecule 14: 60S ribosomal protein uL29



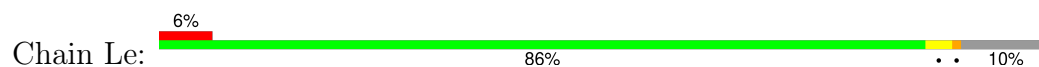
- Molecule 15: 60S ribosomal protein eL29



- Molecule 16: 60S ribosomal protein eL30



- Molecule 17: 60S ribosomal protein eL31

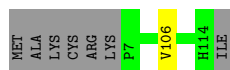


- Molecule 18: 60S ribosomal protein eL32




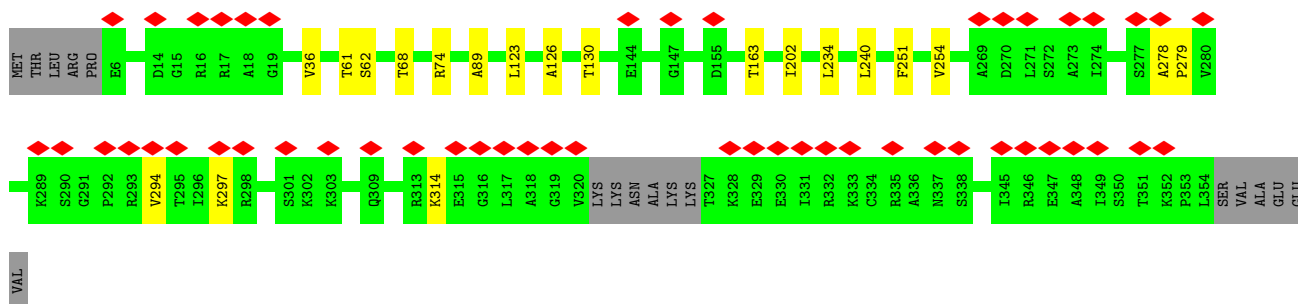
- Molecule 19: 60S ribosomal protein eL33

Chain Lg:  93% • 6%



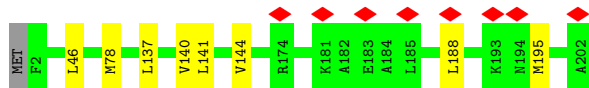
- Molecule 20: 60S ribosomal protein uL4

Chain LD:  14% 90% 6% 5%



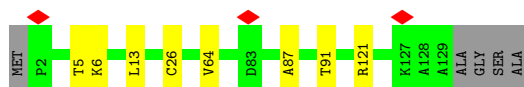
- Molecule 21: 60S ribosomal protein uL13

Chain LI:  96% •



- Molecule 22: 60S ribosomal protein eL14

Chain LL:  90% 6% •



- Molecule 23: 60S ribosomal protein uL15

Chain LM:  98% ••

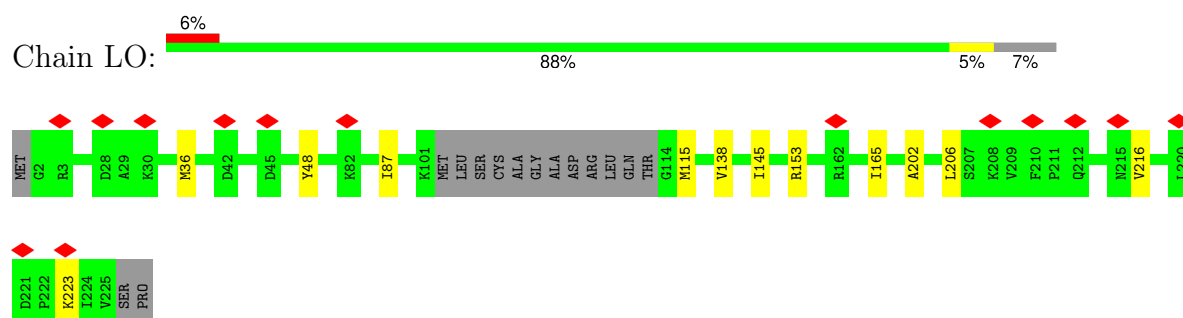


- Molecule 24: 60S ribosomal protein eL15

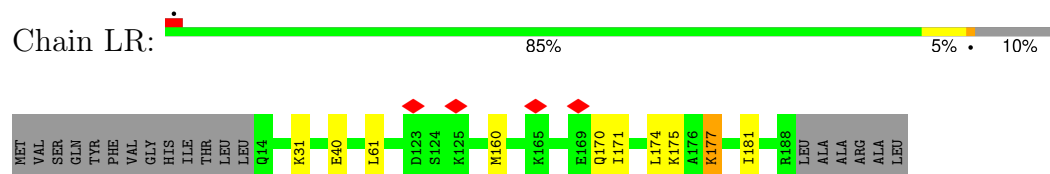
Chain LN:  94% 5% •



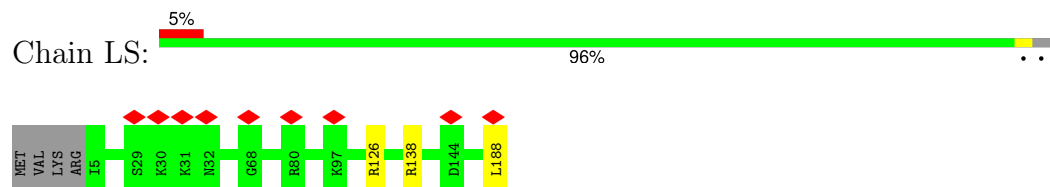
- Molecule 25: 60S ribosomal protein uL16



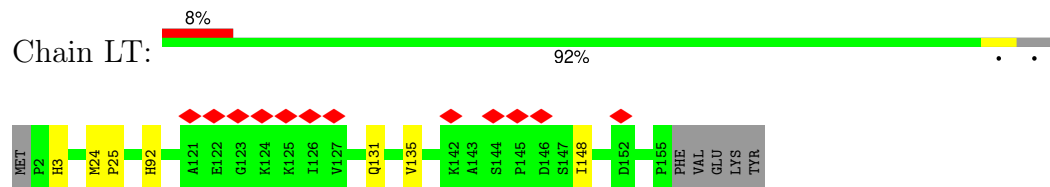
- Molecule 26: 60S ribosomal protein eL19



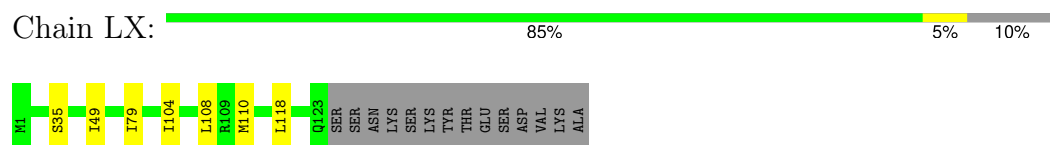
- Molecule 27: 60S ribosomal protein eL20



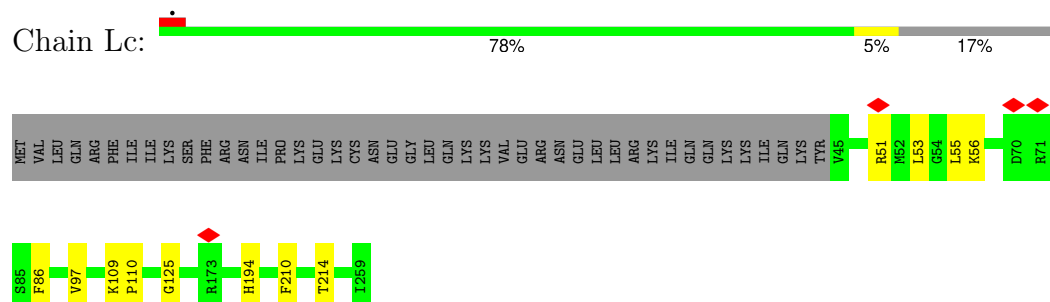
- Molecule 28: 60S ribosomal protein eL21



- Molecule 29: 60S ribosomal protein uL24

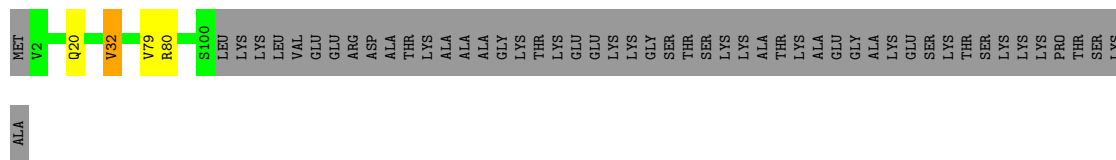


- Molecule 30: 60S ribosomal protein uL30




- Molecule 31: 60S ribosomal protein eL34

Chain Lh:  63% 34%




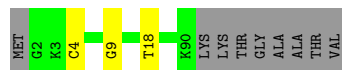
- Molecule 32: 60S ribosomal protein eL36

Chain Li:  88% 5% 7%




- Molecule 33: 60S ribosomal protein eL37

Chain Lj:  88% 9%



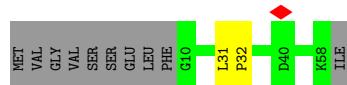
- Molecule 34: 60S ribosomal protein eL38

Chain Lk:  83% 10% 7%



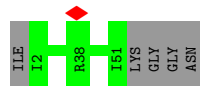
- Molecule 35: 60S ribosomal protein eL39

Chain Ll:  80% 17%




- Molecule 36: 60S ribosomal protein eL40

Chain Lm:  91% 9%

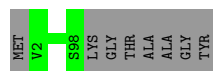


- Molecule 37: 60S ribosomal protein eL43

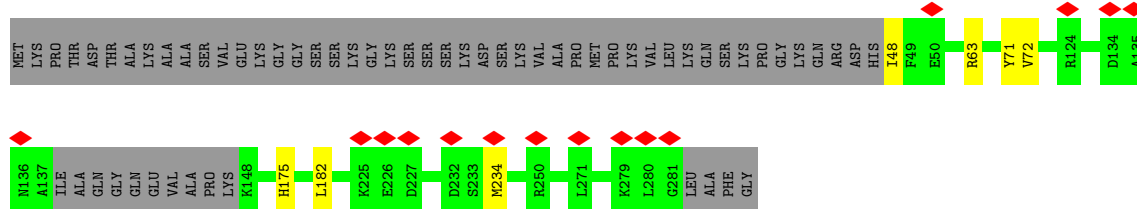
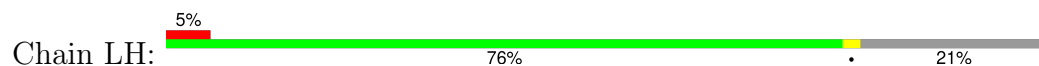
Chain Lp:  90% 7%



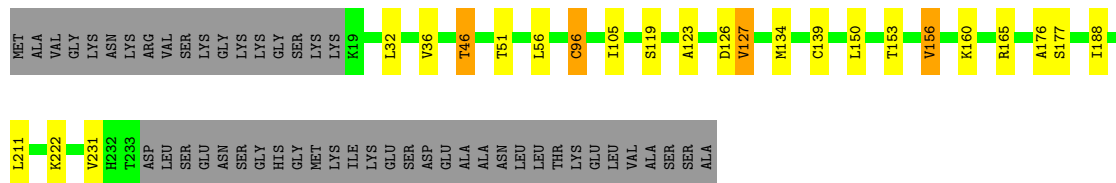
- Molecule 38: 60S ribosomal protein eL42



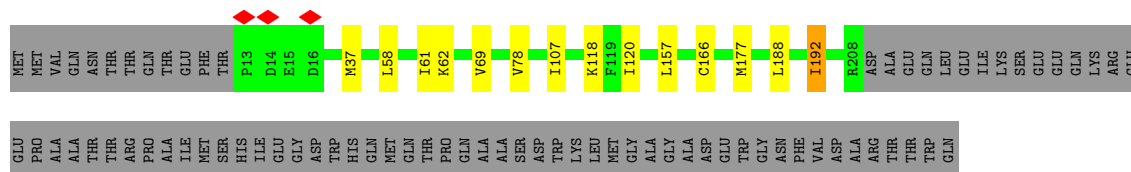
- Molecule 39: 60S ribosomal protein eL8



- Molecule 40: 40S ribosomal protein eS1



- Molecule 41: 40S ribosomal protein uS2

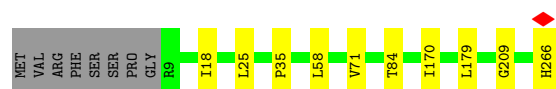


- Molecule 42: 40S ribosomal protein uS4



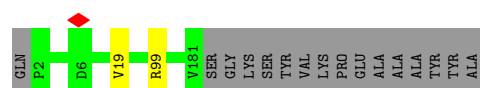
- Molecule 43: 40S ribosomal protein eS4

Chain SE:  93%




- Molecule 44: 40S ribosomal protein uS5

Chain SF:  91%




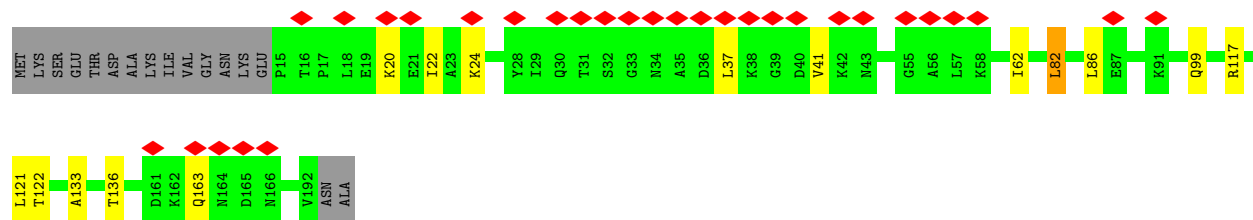
- Molecule 45: 40S ribosomal protein eS6

Chain SG:  85%



- Molecule 46: 40S ribosomal protein eS7

Chain SI:  84%




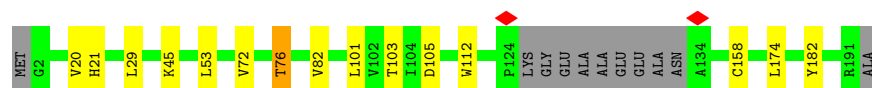
- Molecule 47: 40S ribosomal protein uS8

Chain SJ:  93%




- Molecule 48: 40S ribosomal protein eS8

Chain SK:  86%



- Molecule 49: 40S ribosomal protein uS12

Chain SP:  86%



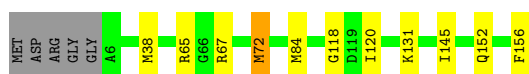
- Molecule 50: 40S ribosomal protein uS15

Chain ST: 94% 5%



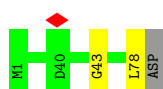
- Molecule 51: 40S ribosomal protein uS17

Chain SU: 90% 6%



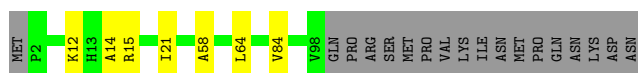
- Molecule 52: 40S ribosomal protein eS21

Chain SY: 96%



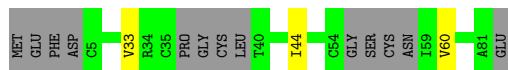
- Molecule 53: 40S ribosomal protein eS26

Chain Sb: 78% 6% 16%



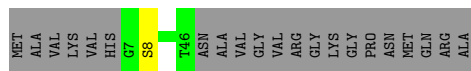
- Molecule 54: 40S ribosomal protein eS27

Chain Sc: 80% 16%



- Molecule 55: 40S ribosomal protein eS30

Chain Se: 64% 34%



- Molecule 56: 40S ribosomal protein uS3

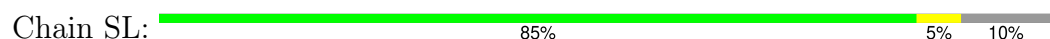
Chain SC: 86% 8% 6%



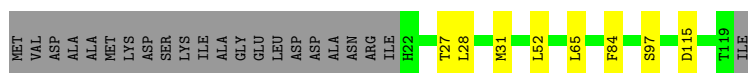
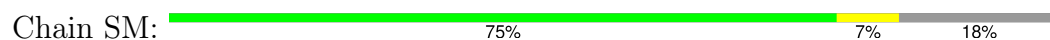
- Molecule 57: 40S ribosomal protein uS7



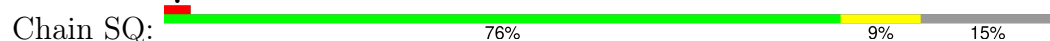
- Molecule 58: 40S ribosomal protein uS9



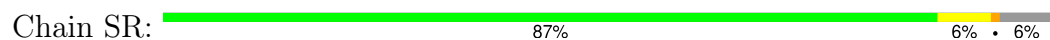
- Molecule 59: 40S ribosomal protein uS10



- Molecule 60: 40S ribosomal protein eS12



- Molecule 61: 40S ribosomal protein uS13



- Molecule 62: 40S ribosomal protein uS14

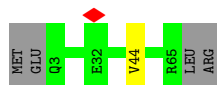


- Molecule 63: 40S ribosomal protein uS19

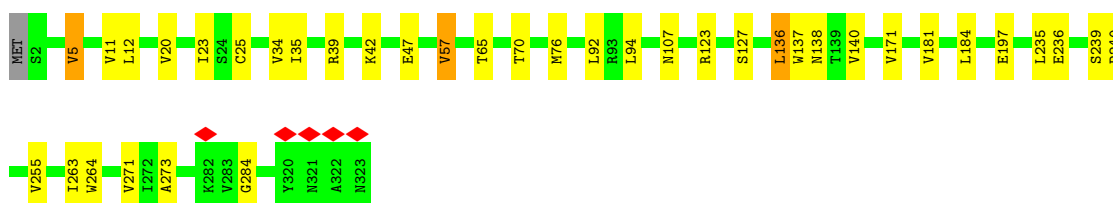
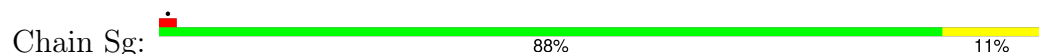




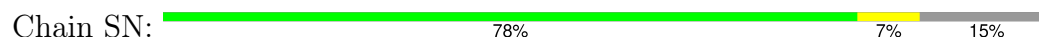
- Molecule 64: 40S ribosomal protein eS28



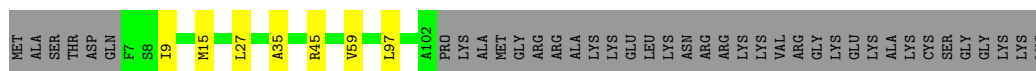
- Molecule 65: Receptor for activated C kinase 1, RACK1 protein



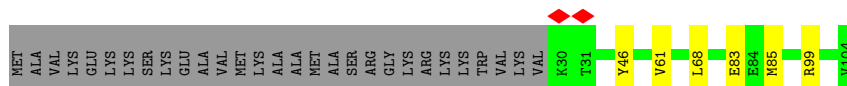
- Molecule 66: 40S ribosomal protein eS10



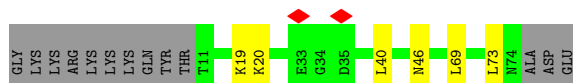
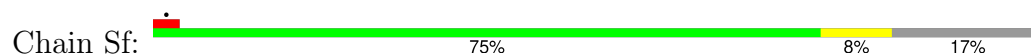
- Molecule 67: 40S ribosomal protein eS24



- Molecule 68: 40S ribosomal protein eS25



- Molecule 69: 40S ribosomal protein eS31



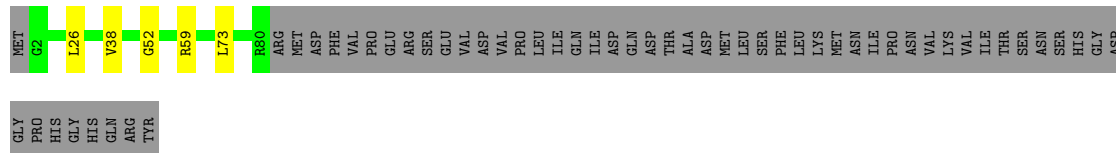
- Molecule 70: 60S ribosomal protein eL41

Chain Ln:  92% 5%



- Molecule 71: 40S ribosomal protein eS17

Chain SV:  55% 41%



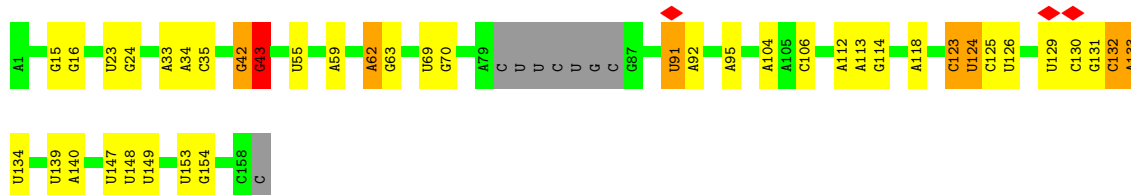
- Molecule 72: 40S ribosomal protein uS11

Chain SO:  69% 10% 20%



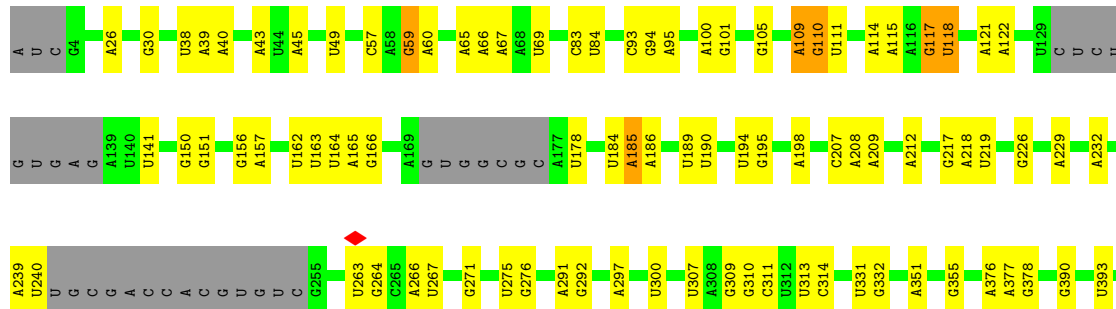
- Molecule 73: 5.8S ribosomal RNA

Chain L4:  69% 21% 5%

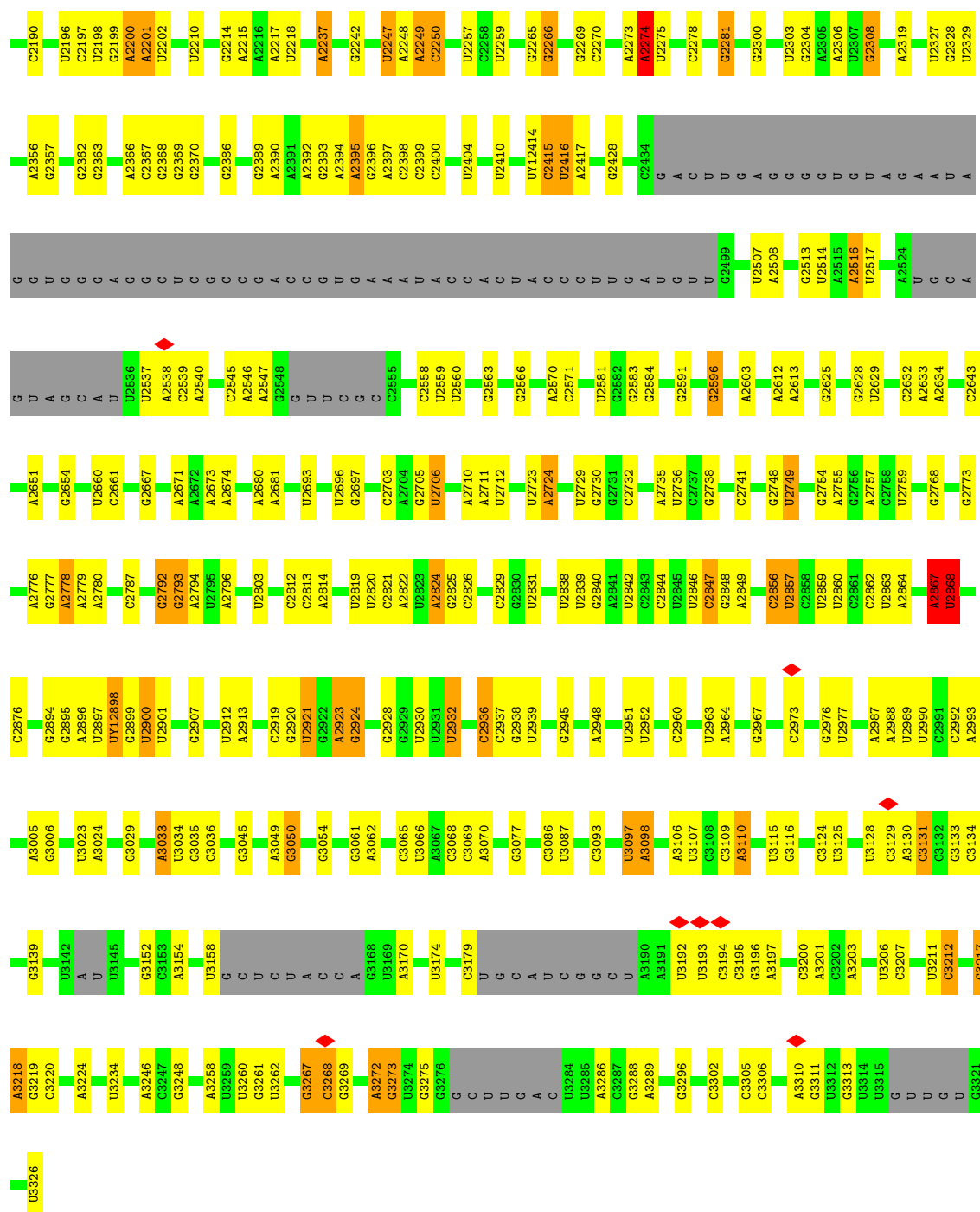


- Molecule 74: 28S ribosomal RNA

Chain L5:  63% 20% 14%

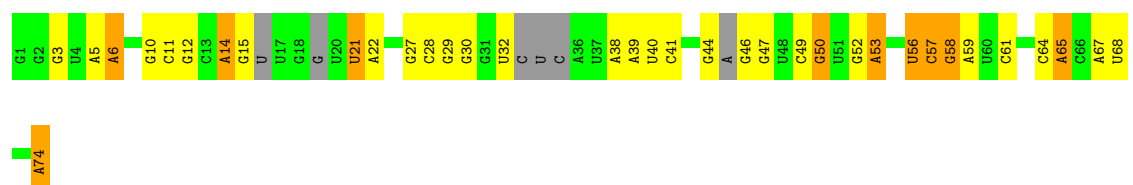






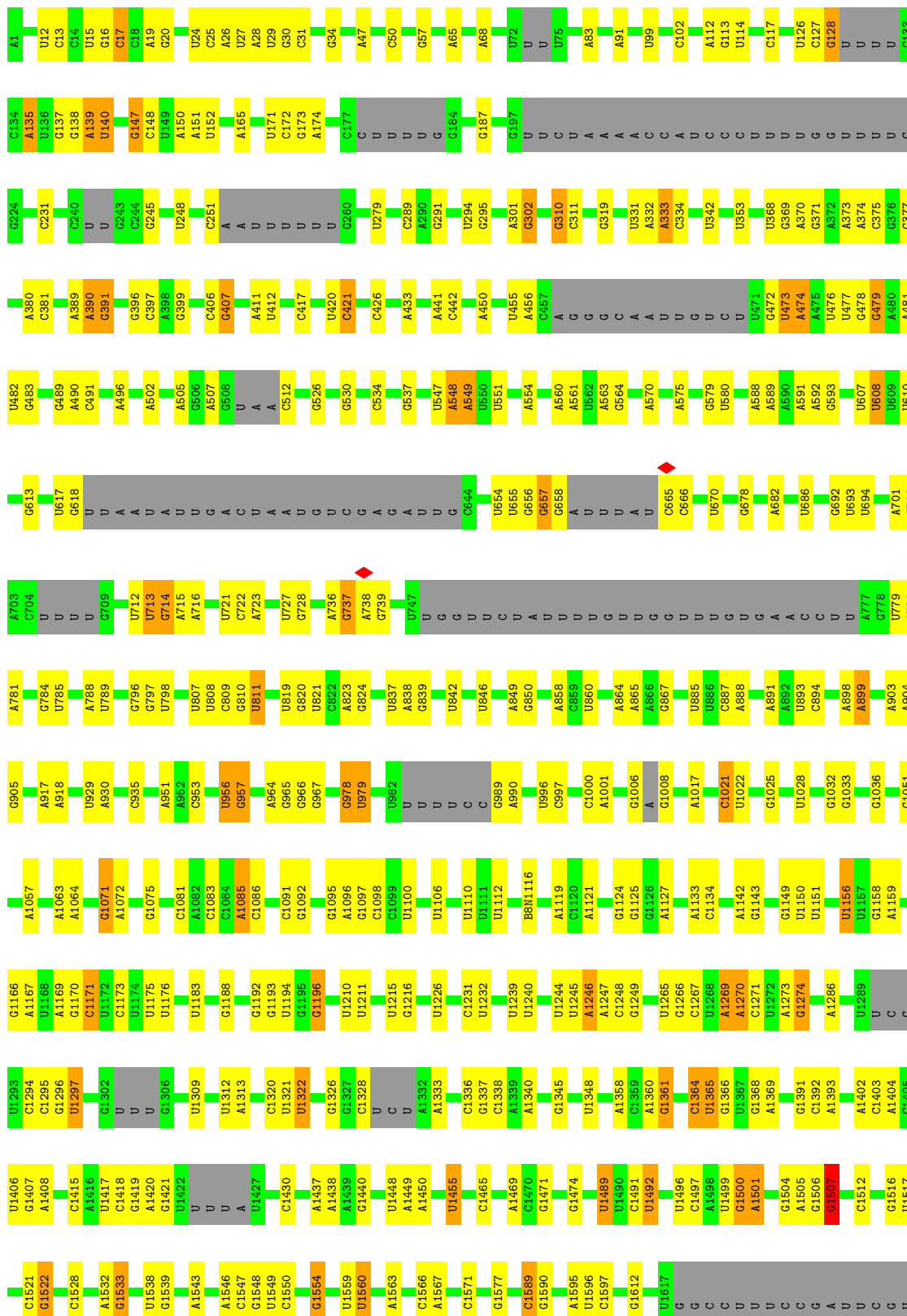
• Molecule 75: E-site tRNA

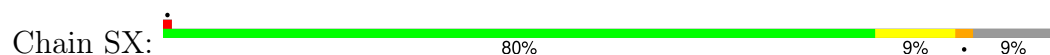
Chain S7: 43% 35% 14% 8%



• Molecule 76: 18S ribosomal RNA

Chain S1:







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	261009	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	40.365	Depositor
Minimum map value	-1.689	Depositor
Average map value	0.522	Depositor
Map value standard deviation	1.452	Depositor
Recommended contour level	4	Depositor
Map size (Å)	369.6, 369.6, 369.6	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, A2M, 5MC, K, PSU, B8N, OMU, 7MG, OMG, MA6, IAS, 1MA, UY1, 4AC, OMC, MG

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	L3	0.25	0/2918	0.28	0/4549
2	LB	0.22	0/1930	0.28	0/2589
3	LC	0.22	0/3110	0.27	0/4183
4	LE	0.17	0/1365	0.27	0/1821
5	LF	0.16	0/1488	0.24	0/2005
6	LG	0.17	0/1183	0.29	0/1588
7	LJ	0.19	0/1567	0.25	0/2092
8	LK	0.21	0/989	0.28	0/1333
9	LP	0.18	0/2394	0.23	0/3203
10	LQ	0.20	0/1470	0.26	0/1962
11	LU	0.21	0/1256	0.26	0/1685
12	LV	0.14	0/813	0.24	0/1090
13	LZ	0.17	0/1134	0.23	0/1511
14	La	0.18	0/993	0.24	0/1320
15	Lb	0.20	0/438	0.29	0/575
16	Ld	0.18	0/716	0.25	0/961
17	Le	0.19	0/885	0.24	0/1191
18	Lf	0.20	0/1043	0.24	0/1389
19	Lg	0.23	0/901	0.26	0/1203
20	LD	0.19	0/2672	0.26	0/3587
21	LI	0.21	0/1661	0.26	0/2219
22	LL	0.17	0/1033	0.24	0/1385
23	LM	0.23	0/1189	0.25	0/1586
24	LN	0.24	0/1744	0.28	0/2323
25	LO	0.17	0/1749	0.24	0/2349
26	LR	0.20	0/1451	0.26	0/1918
27	LS	0.18	0/1516	0.24	0/2039
28	LT	0.20	0/1266	0.25	0/1700
29	LX	0.19	0/1035	0.27	0/1375
30	Lc	0.20	0/1793	0.28	0/2395
31	Lh	0.21	0/818	0.24	0/1089
32	Li	0.19	0/857	0.27	0/1142

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lj	0.23	0/718	0.31	0/951
34	Lk	0.18	0/532	0.24	0/716
35	Ll	0.20	0/441	0.22	0/585
36	Lm	0.17	0/412	0.26	0/547
37	Lp	0.24	0/744	0.31	0/991
38	Lo	0.20	0/792	0.26	0/1042
39	LH	0.17	0/1850	0.24	0/2484
40	SA	0.30	0/1767	0.29	0/2368
41	SB	0.25	0/1587	0.28	0/2155
42	SD	0.32	0/1499	0.29	0/1997
43	SE	0.33	0/2101	0.32	0/2830
44	SF	0.33	0/1390	0.31	0/1880
45	SG	0.26	0/1783	0.27	0/2373
46	SI	0.22	0/1450	0.26	0/1949
47	SJ	0.36	0/1053	0.35	0/1414
48	SK	0.35	0/1487	0.32	0/1985
49	SP	0.35	0/1143	0.37	0/1527
50	ST	0.32	0/1239	0.28	0/1662
51	SU	0.38	0/1263	0.30	0/1689
52	SY	0.28	0/607	0.28	0/818
53	Sb	0.33	0/788	0.32	0/1052
54	Sc	0.29	0/547	0.30	0/729
55	Se	0.27	0/329	0.28	0/437
56	SC	0.33	0/1648	0.29	0/2211
57	SH	0.44	0/1494	0.36	0/2006
58	SL	0.45	0/1069	0.36	0/1428
59	SM	0.34	0/790	0.31	0/1065
60	SQ	0.21	0/883	0.31	0/1192
61	SR	0.39	0/1162	0.30	0/1562
62	SS	0.44	0/423	0.39	0/566
63	SW	0.37	0/961	0.31	0/1289
64	Sd	0.36	0/492	0.29	0/657
65	Sg	0.33	0/2546	0.35	0/3461
66	SN	0.33	0/827	0.37	0/1127
67	SZ	0.32	0/805	0.30	0/1074
68	Sa	0.39	0/608	0.38	0/815
69	Sf	0.23	0/518	0.32	0/689
70	Ln	0.37	0/354	0.34	0/458
71	SV	0.37	0/652	0.31	0/865
72	SO	0.31	0/953	0.36	0/1278
73	L4	0.27	0/3559	0.35	2/5538 (0.0%)
74	L5	0.29	1/67551 (0.0%)	0.31	15/105251 (0.0%)
75	S7	0.19	0/1611	0.27	0/2500

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	S1	0.50	0/36450	0.34	2/56755 (0.0%)
77	LA	0.20	0/1740	0.47	0/2340
78	LW	0.24	0/977	0.46	0/1311
79	LY	0.32	0/505	0.57	0/676
80	SX	0.48	0/1328	0.58	0/1786
All	All	0.33	1/200805 (0.0%)	0.31	19/293438 (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
66	SN	0	1
79	LY	0	1
80	SX	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
74	L5	1472	A2M	O3'-P	5.17	1.61	1.56

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
74	L5	2868	U	OP1-P-OP2	-13.83	78.10	119.60
74	L5	1874	U	OP1-P-OP2	-12.82	81.15	119.60
74	L5	2867	A	OP2-P-O3'	-12.57	70.29	108.00
74	L5	1873	G	OP2-P-O3'	-12.43	70.70	108.00
76	S1	411	A	OP1-P-O3'	-10.98	75.05	108.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
79	LY	50	ARG	Sidechain
66	SN	53	THR	Peptide
80	SX	14	ARG	Sidechain

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	L3	2610	0	1323	14	0
2	LB	1892	0	1951	8	0
3	LC	3036	0	3146	16	0
4	LE	1345	0	1395	3	0
5	LF	1469	0	1561	2	0
6	LG	1163	0	1249	7	0
7	LJ	1544	0	1669	1	0
8	LK	973	0	1030	4	0
9	LP	2351	0	2400	8	0
10	LQ	1449	0	1576	2	0
11	LU	1231	0	1273	2	0
12	LV	799	0	836	2	0
13	LZ	1120	0	1216	4	0
14	La	985	0	1110	2	0
15	Lb	431	0	469	0	0
16	Ld	706	0	726	2	0
17	Le	869	0	914	2	0
18	Lf	1026	0	1108	3	0
19	Lg	879	0	915	0	0
20	LD	2634	0	2814	13	0
21	LI	1628	0	1736	5	0
22	LL	1018	0	1102	5	0
23	LM	1159	0	1193	2	0
24	LN	1708	0	1803	5	0
25	LO	1706	0	1756	7	0
26	LR	1433	0	1546	5	0
27	LS	1484	0	1552	3	0
28	LT	1238	0	1297	2	0
29	LX	1020	0	1086	4	0
30	Lc	1759	0	1876	8	0
31	Lh	808	0	860	2	0
32	Li	847	0	923	3	0
33	Lj	703	0	716	2	0
34	Lk	525	0	568	5	0
35	Ll	431	0	471	1	0
36	Lm	407	0	445	0	0
37	Lp	733	0	759	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	Lo	782	0	855	0	0
39	LH	1817	0	1929	4	0
40	SA	1742	0	1850	10	0
41	SB	1553	0	1605	8	0
42	SD	1474	0	1553	2	0
43	SE	2060	0	2139	7	0
44	SF	1361	0	1420	0	0
45	SG	1760	0	1881	6	0
46	SI	1430	0	1539	7	0
47	SJ	1033	0	1070	4	0
48	SK	1462	0	1512	9	0
49	SP	1124	0	1198	15	0
50	ST	1213	0	1288	3	0
51	SU	1237	0	1306	6	0
52	SY	600	0	590	1	0
53	Sb	777	0	821	4	0
54	Sc	540	0	567	1	0
55	Se	324	0	350	0	0
56	SC	1627	0	1728	8	0
57	SH	1474	0	1532	8	0
58	SL	1055	0	1125	3	0
59	SM	778	0	798	5	0
60	SQ	875	0	909	6	0
61	SR	1147	0	1188	8	0
62	SS	412	0	407	4	0
63	SW	942	0	1010	3	0
64	Sd	488	0	513	1	0
65	Sg	2489	0	2448	18	0
66	SN	801	0	812	3	0
67	SZ	790	0	823	6	0
68	Sa	601	0	638	3	0
69	Sf	509	0	544	4	0
70	Ln	349	0	393	0	0
71	SV	644	0	693	5	0
72	SO	950	0	988	8	0
73	L4	3209	0	1631	13	0
74	L5	61299	0	30924	246	0
75	S7	1446	0	737	23	0
76	S1	33088	0	16684	164	0
77	LA	1716	0	1811	33	0
78	LW	963	0	1033	13	0
79	LY	491	0	505	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	SX	1300	0	1317	11	0
81	L3	1	0	0	0	0
81	L4	1	0	0	0	0
81	L5	133	0	0	0	0
81	S1	1	0	0	0	0
82	Lh	1	0	0	0	0
82	Lj	1	0	0	0	0
82	Lm	1	0	0	0	0
82	Lo	1	0	0	0	0
82	Lp	1	0	0	0	0
83	L5	25	0	0	0	0
83	S1	1	0	0	0	0
84	L5	25	0	0	0	0
84	S1	7	0	0	0	0
84	SA	2	0	0	0	0
All	All	189052	0	143034	772	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 2.

The worst 5 of 772 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)
56:SC:27:LEU:HD12	56:SC:39:VAL:HG21	1.77	0.67
76:S1:472:G:HO2'	76:S1:473:U:H6	1.44	0.65
77:LA:35:ILE:HG22	77:LA:37:LEU:HD21	1.78	0.65
76:S1:482:U:H2'	76:S1:483:G:C8	2.31	0.65
74:L5:2793:G:O4'	74:L5:2847:5MC:HM53	1.97	0.65

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	
2	LB	246/257 (96%)	239 (97%)	7 (3%)	0	100	100
3	LC	379/395 (96%)	370 (98%)	9 (2%)	0	100	100
4	LE	164/171 (96%)	161 (98%)	3 (2%)	0	100	100
5	LF	184/190 (97%)	181 (98%)	3 (2%)	0	100	100
6	LG	145/212 (68%)	142 (98%)	3 (2%)	0	100	100
7	LJ	194/203 (96%)	191 (98%)	3 (2%)	0	100	100
8	LK	127/139 (91%)	125 (98%)	2 (2%)	0	100	100
9	LP	283/306 (92%)	279 (99%)	4 (1%)	0	100	100
10	LQ	184/222 (83%)	181 (98%)	3 (2%)	0	100	100
11	LU	150/194 (77%)	146 (97%)	4 (3%)	0	100	100
12	LV	95/122 (78%)	92 (97%)	3 (3%)	0	100	100
13	LZ	134/146 (92%)	132 (98%)	2 (2%)	0	100	100
14	La	117/123 (95%)	114 (97%)	3 (3%)	0	100	100
15	Lb	51/59 (86%)	48 (94%)	3 (6%)	0	100	100
16	Ld	91/108 (84%)	89 (98%)	2 (2%)	0	100	100
17	Le	103/117 (88%)	102 (99%)	1 (1%)	0	100	100
18	Lf	123/132 (93%)	122 (99%)	1 (1%)	0	100	100
19	Lg	106/115 (92%)	103 (97%)	3 (3%)	0	100	100
20	LD	339/360 (94%)	333 (98%)	6 (2%)	0	100	100
21	LI	199/202 (98%)	196 (98%)	3 (2%)	0	100	100
22	LL	126/133 (95%)	123 (98%)	3 (2%)	0	100	100
23	LM	144/147 (98%)	141 (98%)	3 (2%)	0	100	100
24	LN	200/204 (98%)	198 (99%)	2 (1%)	0	100	100
25	LO	208/227 (92%)	201 (97%)	7 (3%)	0	100	100
26	LR	173/194 (89%)	168 (97%)	5 (3%)	0	100	100
27	LS	182/188 (97%)	178 (98%)	4 (2%)	0	100	100
28	LT	152/160 (95%)	149 (98%)	3 (2%)	0	100	100
29	LX	121/137 (88%)	118 (98%)	3 (2%)	0	100	100
30	Lc	213/259 (82%)	205 (96%)	8 (4%)	0	100	100
31	Lh	97/150 (65%)	93 (96%)	4 (4%)	0	100	100
32	Li	106/116 (91%)	103 (97%)	3 (3%)	0	100	100
33	Lj	87/98 (89%)	84 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	Lk	63/70 (90%)	61 (97%)	1 (2%)	1 (2%)	7	20
35	Ll	47/59 (80%)	46 (98%)	1 (2%)	0	100	100
36	Lm	48/55 (87%)	48 (100%)	0	0	100	100
37	Lp	91/94 (97%)	88 (97%)	3 (3%)	0	100	100
38	Lo	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
39	LH	220/285 (77%)	218 (99%)	2 (1%)	0	100	100
40	SA	213/264 (81%)	211 (99%)	2 (1%)	0	100	100
41	SB	194/274 (71%)	184 (95%)	9 (5%)	1 (0%)	24	48
42	SD	176/184 (96%)	174 (99%)	2 (1%)	0	100	100
43	SE	256/266 (96%)	248 (97%)	8 (3%)	0	100	100
44	SF	178/196 (91%)	174 (98%)	4 (2%)	0	100	100
45	SG	212/239 (89%)	209 (99%)	3 (1%)	0	100	100
46	SI	176/194 (91%)	171 (97%)	5 (3%)	0	100	100
47	SJ	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
48	SK	177/192 (92%)	175 (99%)	2 (1%)	0	100	100
49	SP	141/145 (97%)	131 (93%)	10 (7%)	0	100	100
50	ST	147/151 (97%)	144 (98%)	3 (2%)	0	100	100
51	SU	149/156 (96%)	143 (96%)	6 (4%)	0	100	100
52	SY	76/79 (96%)	73 (96%)	3 (4%)	0	100	100
53	Sb	95/115 (83%)	85 (90%)	10 (10%)	0	100	100
54	Sc	63/82 (77%)	62 (98%)	1 (2%)	0	100	100
55	Se	38/61 (62%)	37 (97%)	1 (3%)	0	100	100
56	SC	207/223 (93%)	204 (99%)	3 (1%)	0	100	100
57	SH	183/192 (95%)	176 (96%)	7 (4%)	0	100	100
58	SL	130/149 (87%)	125 (96%)	5 (4%)	0	100	100
59	SM	96/120 (80%)	92 (96%)	4 (4%)	0	100	100
60	SQ	113/135 (84%)	110 (97%)	3 (3%)	0	100	100
61	SR	142/154 (92%)	138 (97%)	4 (3%)	0	100	100
62	SS	48/66 (73%)	46 (96%)	2 (4%)	0	100	100
63	SW	113/149 (76%)	111 (98%)	2 (2%)	0	100	100
64	Sd	61/67 (91%)	59 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
65	Sg	320/323 (99%)	302 (94%)	18 (6%)	0	100	100
66	SN	94/113 (83%)	88 (94%)	6 (6%)	0	100	100
67	SZ	94/135 (70%)	91 (97%)	3 (3%)	0	100	100
68	Sa	73/104 (70%)	64 (88%)	9 (12%)	0	100	100
69	Sf	62/77 (80%)	55 (89%)	7 (11%)	0	100	100
70	Ln	36/39 (92%)	34 (94%)	1 (3%)	1 (3%)	4	9
71	SV	77/134 (58%)	77 (100%)	0	0	100	100
72	SO	123/157 (78%)	119 (97%)	4 (3%)	0	100	100
77	LA	215/217 (99%)	188 (87%)	20 (9%)	7 (3%)	3	7
78	LW	116/153 (76%)	105 (90%)	9 (8%)	2 (2%)	7	19
79	LY	57/156 (36%)	52 (91%)	2 (4%)	3 (5%)	1	3
80	SX	157/174 (90%)	153 (98%)	4 (2%)	0	100	100
All	All	10722/12219 (88%)	10394 (97%)	313 (3%)	15 (0%)	49	73

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
77	LA	44	ARG
79	LY	32	ASP
79	LY	50	ARG
70	Ln	16	ARG
77	LA	13	ILE

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	
2	LB	189/198 (96%)	187 (99%)	2 (1%)	65	85
3	LC	333/345 (96%)	333 (100%)	0	100	100
4	LE	146/151 (97%)	145 (99%)	1 (1%)	76	90
5	LF	167/170 (98%)	165 (99%)	2 (1%)	63	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	LG	129/181 (71%)	127 (98%)	2 (2%)	55	80
7	LJ	163/170 (96%)	163 (100%)	0	100	100
8	LK	100/104 (96%)	99 (99%)	1 (1%)	68	86
9	LP	248/261 (95%)	248 (100%)	0	100	100
10	LQ	157/184 (85%)	156 (99%)	1 (1%)	78	91
11	LU	132/163 (81%)	132 (100%)	0	100	100
12	LV	89/111 (80%)	89 (100%)	0	100	100
13	LZ	124/129 (96%)	123 (99%)	1 (1%)	73	88
14	La	109/111 (98%)	106 (97%)	3 (3%)	38	68
15	Lb	47/52 (90%)	46 (98%)	1 (2%)	47	75
16	Ld	79/94 (84%)	77 (98%)	2 (2%)	42	71
17	Le	96/105 (91%)	94 (98%)	2 (2%)	47	75
18	Lf	110/117 (94%)	109 (99%)	1 (1%)	70	87
19	Lg	93/99 (94%)	92 (99%)	1 (1%)	65	85
20	LD	273/288 (95%)	272 (100%)	1 (0%)	84	93
21	LI	171/172 (99%)	171 (100%)	0	100	100
22	LL	108/110 (98%)	107 (99%)	1 (1%)	70	87
23	LM	120/121 (99%)	120 (100%)	0	100	100
24	LN	175/176 (99%)	173 (99%)	2 (1%)	65	85
25	LO	176/188 (94%)	174 (99%)	2 (1%)	65	85
26	LR	149/164 (91%)	146 (98%)	3 (2%)	48	76
27	LS	160/164 (98%)	159 (99%)	1 (1%)	78	91
28	LT	133/139 (96%)	129 (97%)	4 (3%)	36	66
29	LX	115/128 (90%)	115 (100%)	0	100	100
30	Lc	185/228 (81%)	185 (100%)	0	100	100
31	Lh	85/125 (68%)	84 (99%)	1 (1%)	63	84
32	Li	93/100 (93%)	92 (99%)	1 (1%)	65	85
33	Lj	72/78 (92%)	72 (100%)	0	100	100
34	Lk	58/62 (94%)	58 (100%)	0	100	100
35	Ll	45/54 (83%)	45 (100%)	0	100	100
36	Lm	46/49 (94%)	46 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	Lp	75/76 (99%)	72 (96%)	3 (4%)	28	56
38	Lo	86/90 (96%)	86 (100%)	0	100	100
39	LH	195/243 (80%)	192 (98%)	3 (2%)	57	81
40	SA	198/237 (84%)	188 (95%)	10 (5%)	21	48
41	SB	173/238 (73%)	172 (99%)	1 (1%)	78	91
42	SD	158/163 (97%)	156 (99%)	2 (1%)	61	83
43	SE	228/235 (97%)	226 (99%)	2 (1%)	70	87
44	SF	146/157 (93%)	144 (99%)	2 (1%)	59	82
45	SG	193/208 (93%)	191 (99%)	2 (1%)	68	86
46	SI	160/173 (92%)	156 (98%)	4 (2%)	42	71
47	SJ	113/114 (99%)	111 (98%)	2 (2%)	51	78
48	SK	158/164 (96%)	157 (99%)	1 (1%)	78	91
49	SP	116/118 (98%)	115 (99%)	1 (1%)	70	87
50	ST	131/132 (99%)	130 (99%)	1 (1%)	73	88
51	SU	137/140 (98%)	133 (97%)	4 (3%)	37	67
52	SY	67/68 (98%)	66 (98%)	1 (2%)	57	81
53	Sb	86/104 (83%)	84 (98%)	2 (2%)	44	73
54	Sc	62/73 (85%)	61 (98%)	1 (2%)	55	80
55	Se	33/48 (69%)	32 (97%)	1 (3%)	36	66
56	SC	173/186 (93%)	165 (95%)	8 (5%)	24	51
57	SH	159/162 (98%)	157 (99%)	2 (1%)	61	83
58	SL	110/122 (90%)	105 (96%)	5 (4%)	24	52
59	SM	91/108 (84%)	89 (98%)	2 (2%)	45	74
60	SQ	99/116 (85%)	95 (96%)	4 (4%)	28	56
61	SR	123/131 (94%)	121 (98%)	2 (2%)	55	80
62	SS	44/58 (76%)	43 (98%)	1 (2%)	44	73
63	SW	103/132 (78%)	101 (98%)	2 (2%)	50	77
64	Sd	50/54 (93%)	50 (100%)	0	100	100
65	Sg	280/281 (100%)	267 (95%)	13 (5%)	24	51
66	SN	91/105 (87%)	89 (98%)	2 (2%)	45	74
67	SZ	84/115 (73%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	Sa	67/90 (74%)	66 (98%)	1 (2%)	57	81
69	Sf	57/68 (84%)	57 (100%)	0	100	100
70	Ln	34/35 (97%)	33 (97%)	1 (3%)	37	67
71	SV	67/118 (57%)	66 (98%)	1 (2%)	57	81
72	SO	98/122 (80%)	94 (96%)	4 (4%)	27	56
77	LA	192/192 (100%)	184 (96%)	8 (4%)	26	55
78	LW	108/135 (80%)	101 (94%)	7 (6%)	15	37
79	LY	52/126 (41%)	46 (88%)	6 (12%)	5	14
80	SX	139/151 (92%)	132 (95%)	7 (5%)	22	48
All	All	9411/10479 (90%)	9256 (98%)	155 (2%)	54	80

5 of 155 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
65	Sg	235	LEU
79	LY	14	SER
66	SN	79	GLN
77	LA	141	ASP
80	SX	23	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
45	SG	180	GLN
51	SU	90	HIS
46	SI	68	HIS
50	ST	49	GLN
57	SH	70	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L3	121/122 (99%)	15 (12%)	3 (2%)
73	L4	149/159 (93%)	25 (16%)	3 (2%)
74	L5	2850/3326 (85%)	462 (16%)	19 (0%)
75	S7	63/74 (85%)	17 (26%)	0
76	S1	1531/1728 (88%)	233 (15%)	9 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	4714/5409 (87%)	752 (15%)	34 (0%)

5 of 752 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L3	33	U
1	L3	38	U
1	L3	52	U
1	L3	53	C
1	L3	54	A

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
76	S1	665	C
76	S1	978	G
76	S1	1269	A
74	L5	882	C
74	L5	782	U

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

65 non-standard protein/DNA/RNA residues are 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
74	UY1	L5	2414	74	19,22,23	4.27	8 (42%)	21,31,34	2.17	6 (28%)
74	OMG	L5	814	74	23,26,27	2.37	8 (34%)	32,38,41	2.07	10 (31%)
74	UY1	L5	2898	74,81	19,22,23	4.35	8 (42%)	21,31,34	1.99	5 (23%)
76	A2M	S1	28	76	22,25,26	3.58	10 (45%)	30,36,39	2.64	10 (33%)
74	PSU	L5	2842	74	18,21,22	2.26	7 (38%)	21,30,33	2.13	5 (23%)
74	A2M	L5	1158	74	22,25,26	3.58	10 (45%)	30,36,39	2.61	10 (33%)
72	IAS	SO	144	72	6,7,8	1.23	0	4,8,10	2.22	2 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
76	OMU	S1	1309	76	19,22,23	2.68	6 (31%)	25,31,34	2.05	5 (20%)
76	PSU	S1	1560	76	18,21,22	2.53	8 (44%)	21,30,33	2.16	3 (14%)
74	PSU	L5	2831	74	18,21,22	2.24	6 (33%)	21,30,33	2.11	4 (19%)
74	OMU	L5	2706	74	19,22,23	2.83	6 (31%)	25,31,34	1.86	5 (20%)
74	OMC	L5	2856	74	19,22,23	2.91	8 (42%)	25,31,34	0.67	0
74	OMG	L5	2894	74	23,26,27	2.42	9 (39%)	32,38,41	2.05	9 (28%)
76	PSU	S1	1322	76	18,21,22	2.39	8 (44%)	21,30,33	2.15	6 (28%)
76	B8N	S1	1116	76	25,29,30	3.43	7 (28%)	28,42,45	2.01	8 (28%)
76	PSU	S1	1112	76	18,21,22	2.49	7 (38%)	21,30,33	2.14	4 (19%)
74	A2M	L5	658	74	22,25,26	3.53	9 (40%)	30,36,39	2.62	10 (33%)
74	A2M	L5	945	74	22,25,26	3.52	9 (40%)	30,36,39	2.67	13 (43%)
76	OMC	S1	1571	76	19,22,23	2.83	8 (42%)	25,31,34	0.74	0
76	MA6	S1	1710	76	23,26,27	1.49	4 (17%)	33,38,41	3.13	12 (36%)
74	PSU	L5	2857	74	18,21,22	2.30	7 (38%)	21,30,33	2.08	4 (19%)
74	PSU	L5	2921	83,74,81	18,21,22	2.27	7 (38%)	21,30,33	2.14	4 (19%)
76	PSU	S1	1106	76	18,21,22	2.51	8 (44%)	21,30,33	2.16	4 (19%)
76	MA6	S1	1709	76	23,26,27	1.47	5 (21%)	33,38,41	3.11	11 (33%)
76	A2M	S1	899	76	22,25,26	3.59	9 (40%)	30,36,39	2.63	9 (30%)
74	A2M	L5	826	74,81	22,25,26	3.54	9 (40%)	30,36,39	2.62	11 (36%)
74	OMU	L5	2410	74	19,22,23	2.83	6 (31%)	25,31,34	1.90	7 (28%)
76	PSU	S1	1727	76	18,21,22	2.43	8 (44%)	21,30,33	2.24	4 (19%)
74	A2M	L5	1472	74,81	22,25,26	3.56	9 (40%)	30,36,39	2.87	14 (46%)
74	OMG	L5	2281	74	23,26,27	2.37	8 (34%)	32,38,41	1.98	9 (28%)
74	5MC	L5	2847	83,74	19,22,23	4.03	9 (47%)	26,32,35	1.16	1 (3%)
74	PSU	L5	2259	74	18,21,22	2.19	6 (33%)	21,30,33	2.03	3 (14%)
74	PSU	L5	2581	74	18,21,22	2.28	6 (33%)	21,30,33	2.11	3 (14%)
74	OMU	L5	2712	74	19,22,23	2.85	6 (31%)	25,31,34	1.87	5 (20%)
74	A2M	L5	661	74	22,25,26	3.53	9 (40%)	30,36,39	2.66	10 (33%)
74	A2M	L5	2319	74	22,25,26	3.51	9 (40%)	30,36,39	2.64	11 (36%)
74	A2M	L5	2923	74,81	22,25,26	3.55	9 (40%)	30,36,39	2.65	11 (36%)
76	PSU	S1	1215	76	18,21,22	2.44	7 (38%)	21,30,33	2.19	5 (23%)
74	OMG	L5	1872	74	23,26,27	2.38	8 (34%)	32,38,41	1.98	9 (28%)
74	PSU	L5	2803	74	18,21,22	2.27	7 (38%)	21,30,33	2.15	5 (23%)
76	A2M	S1	83	76	22,25,26	3.54	9 (40%)	30,36,39	2.65	11 (36%)
76	PSU	S1	686	76	18,21,22	2.39	7 (38%)	21,30,33	2.16	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
76	4AC	S1	1701	76	21,24,25	3.06	10 (47%)	28,34,37	1.01	3 (10%)
74	OMG	L5	2899	74	23,26,27	2.42	9 (39%)	32,38,41	2.03	9 (28%)
74	A2M	L5	2724	74	22,25,26	3.56	9 (40%)	30,36,39	2.68	13 (43%)
74	A2M	L5	2274	74	22,25,26	3.44	9 (40%)	30,36,39	2.80	14 (46%)
74	OMG	L5	917	83,74	23,26,27	2.44	8 (34%)	32,38,41	2.06	10 (31%)
73	OMG	L4	43	73	23,26,27	2.40	9 (39%)	32,38,41	2.04	9 (28%)
76	A2M	S1	1678	76	22,25,26	3.59	10 (45%)	30,36,39	2.64	9 (30%)
74	1MA	L5	657	74,81	21,25,26	2.79	6 (28%)	30,37,40	2.68	7 (23%)
76	OMU	S1	1156	76	19,22,23	2.75	6 (31%)	25,31,34	1.89	4 (16%)
74	PSU	L5	2952	74	18,21,22	2.28	6 (33%)	21,30,33	2.13	4 (19%)
74	OMG	L5	2792	74	23,26,27	2.36	8 (34%)	32,38,41	2.05	10 (31%)
74	PSU	L5	2901	74	18,21,22	2.22	6 (33%)	21,30,33	2.07	5 (23%)
76	7MG	S1	1507	76	23,26,27	3.16	10 (43%)	27,39,42	2.24	9 (33%)
74	PSU	L5	2897	74,81	18,21,22	2.27	6 (33%)	21,30,33	2.08	4 (19%)
76	OMU	S1	547	76	19,22,23	2.89	7 (36%)	25,31,34	1.85	5 (20%)
74	PSU	L5	2900	74	18,21,22	2.21	6 (33%)	21,30,33	2.02	3 (14%)
74	OMG	L5	2596	74	23,26,27	2.43	7 (30%)	32,38,41	2.01	9 (28%)
76	OMG	S1	1361	76	23,26,27	2.34	7 (30%)	32,38,41	1.95	9 (28%)
74	OMC	L5	2936	74	19,22,23	2.93	8 (42%)	25,31,34	0.72	0
76	OMG	S1	1196	76	23,26,27	2.33	8 (34%)	32,38,41	2.02	9 (28%)
74	PSU	L5	2932	74	18,21,22	2.26	6 (33%)	21,30,33	2.12	4 (19%)
74	PSU	L5	2257	74	18,21,22	2.33	6 (33%)	21,30,33	2.03	3 (14%)
74	PSU	L5	2210	74	18,21,22	2.22	6 (33%)	21,30,33	2.10	3 (14%)

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
74	UY1	L5	2414	74	-	1/9/27/28	0/2/2/2
74	OMG	L5	814	74	-	0/9/27/28	0/3/3/3
74	UY1	L5	2898	74,81	-	4/9/27/28	0/2/2/2
76	A2M	S1	28	76	-	0/9/27/28	0/3/3/3
74	PSU	L5	2842	74	-	0/7/25/26	0/2/2/2
74	A2M	L5	1158	74	-	0/9/27/28	0/3/3/3
72	IAS	SO	144	72	-	2/5/6/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
76	OMU	S1	1309	76	-	2/9/27/28	0/2/2/2
76	PSU	S1	1560	76	-	0/7/25/26	0/2/2/2
74	PSU	L5	2831	74	-	0/7/25/26	0/2/2/2
74	OMU	L5	2706	74	-	0/9/27/28	0/2/2/2
74	OMC	L5	2856	74	-	0/9/27/28	0/2/2/2
74	OMG	L5	2894	74	-	0/9/27/28	0/3/3/3
76	PSU	S1	1322	76	-	2/7/25/26	0/2/2/2
76	B8N	S1	1116	76	-	4/16/34/35	0/2/2/2
76	PSU	S1	1112	76	-	0/7/25/26	0/2/2/2
74	A2M	L5	658	74	-	2/9/27/28	0/3/3/3
74	A2M	L5	945	74	-	0/9/27/28	0/3/3/3
76	OMC	S1	1571	76	-	0/9/27/28	0/2/2/2
76	MA6	S1	1710	76	-	2/11/29/30	0/3/3/3
74	PSU	L5	2857	74	-	0/7/25/26	0/2/2/2
74	PSU	L5	2921	83,74,81	-	0/7/25/26	0/2/2/2
76	PSU	S1	1106	76	-	0/7/25/26	0/2/2/2
76	MA6	S1	1709	76	-	0/11/29/30	0/3/3/3
76	A2M	S1	899	76	-	0/9/27/28	0/3/3/3
74	A2M	L5	826	74,81	-	1/9/27/28	0/3/3/3
74	OMU	L5	2410	74	-	2/9/27/28	0/2/2/2
76	PSU	S1	1727	76	-	2/7/25/26	0/2/2/2
74	A2M	L5	1472	74,81	-	0/9/27/28	0/3/3/3
74	OMG	L5	2281	74	-	2/9/27/28	0/3/3/3
74	5MC	L5	2847	83,74	-	3/7/25/26	0/2/2/2
74	PSU	L5	2259	74	-	0/7/25/26	0/2/2/2
74	PSU	L5	2581	74	-	0/7/25/26	0/2/2/2
74	OMU	L5	2712	74	-	0/9/27/28	0/2/2/2
74	A2M	L5	661	74	-	2/9/27/28	0/3/3/3
74	A2M	L5	2319	74	-	0/9/27/28	0/3/3/3
74	A2M	L5	2923	74,81	-	2/9/27/28	0/3/3/3
76	PSU	S1	1215	76	-	0/7/25/26	0/2/2/2
74	OMG	L5	1872	74	-	0/9/27/28	0/3/3/3
74	PSU	L5	2803	74	-	0/7/25/26	0/2/2/2
76	A2M	S1	83	76	-	2/9/27/28	0/3/3/3
76	PSU	S1	686	76	-	0/7/25/26	0/2/2/2
76	4AC	S1	1701	76	-	0/11/29/30	0/2/2/2
74	OMG	L5	2899	74	-	1/9/27/28	0/3/3/3
74	A2M	L5	2724	74	-	2/9/27/28	0/3/3/3
74	A2M	L5	2274	74	-	2/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
74	OMG	L5	917	83,74	-	1/9/27/28	0/3/3/3
73	OMG	L4	43	73	-	1/9/27/28	0/3/3/3
76	A2M	S1	1678	76	-	0/9/27/28	0/3/3/3
74	1MA	L5	657	74,81	-	2/7/25/26	0/3/3/3
76	OMU	S1	1156	76	-	2/9/27/28	0/2/2/2
74	PSU	L5	2952	74	-	0/7/25/26	0/2/2/2
74	OMG	L5	2792	74	-	0/9/27/28	0/3/3/3
74	PSU	L5	2901	74	-	0/7/25/26	0/2/2/2
76	7MG	S1	1507	76	-	0/7/37/38	0/3/3/3
74	PSU	L5	2897	74,81	-	2/7/25/26	0/2/2/2
76	OMU	S1	547	76	-	0/9/27/28	0/2/2/2
74	PSU	L5	2900	74	-	3/7/25/26	0/2/2/2
74	OMG	L5	2596	74	-	3/9/27/28	0/3/3/3
76	OMG	S1	1361	76	-	1/9/27/28	0/3/3/3
74	OMC	L5	2936	74	-	0/9/27/28	0/2/2/2
76	OMG	S1	1196	76	-	1/9/27/28	0/3/3/3
74	PSU	L5	2932	74	-	2/7/25/26	0/2/2/2
74	PSU	L5	2257	74	-	0/7/25/26	0/2/2/2
74	PSU	L5	2210	74	-	0/7/25/26	0/2/2/2

The worst 5 of 487 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
74	L5	2898	UY1	C6-C5	11.37	1.47	1.35
74	L5	2414	UY1	C6-C5	11.05	1.47	1.35
74	L5	2898	UY1	C2-N1	9.77	1.49	1.36
74	L5	2414	UY1	C2-N1	9.61	1.49	1.36
74	L5	1472	A2M	C2'-C1'	-9.48	1.29	1.53

The worst 5 of 437 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
76	S1	1709	MA6	N1-C6-N6	-11.44	102.91	116.86
76	S1	1710	MA6	N1-C6-N6	-10.99	103.47	116.86
74	L5	657	1MA	C1'-N9-C8	-8.00	103.99	126.73
76	S1	1709	MA6	C5-C6-N6	7.31	136.90	125.33
74	L5	2274	A2M	N6-C6-N1	-7.09	102.58	118.38

There are no chirality outliers.

5 of 58 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
72	SO	144	IAS	N-CA-CB-CG
72	SO	144	IAS	C-CA-CB-CG
74	L5	2281	OMG	O4'-C4'-C5'-O5'
74	L5	2410	OMU	O4'-C4'-C5'-O5'
74	L5	2414	UY1	C1'-C2'-O2'-CM2

There are no ring outliers.

23 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
74	L5	814	OMG	1	0
74	L5	1158	A2M	1	0
72	SO	144	IAS	1	0
76	S1	1560	PSU	1	0
74	L5	2856	OMC	1	0
76	S1	1322	PSU	1	0
74	L5	2857	PSU	1	0
74	L5	2921	PSU	1	0
76	S1	1709	MA6	1	0
76	S1	899	A2M	1	0
74	L5	826	A2M	1	0
74	L5	1472	A2M	1	0
74	L5	2847	5MC	2	0
74	L5	661	A2M	1	0
76	S1	1701	4AC	1	0
74	L5	2724	A2M	2	0
74	L5	2274	A2M	3	0
73	L4	43	OMG	1	0
74	L5	657	1MA	1	0
74	L5	2792	OMG	1	0
76	S1	1507	7MG	1	0
74	L5	2936	OMC	1	0
76	S1	1196	OMG	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 167 ligands modelled in this entry, 167 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

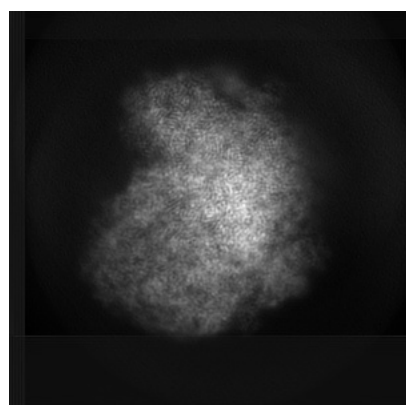
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72933. These allow visual inspection of the internal detail of the map and identification of artifacts.

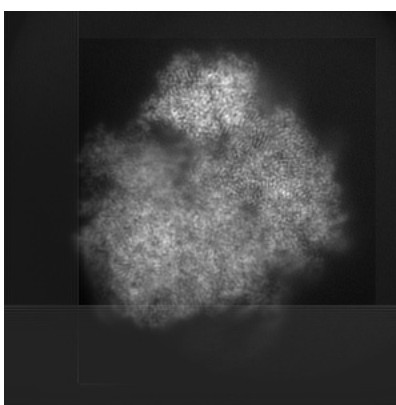
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

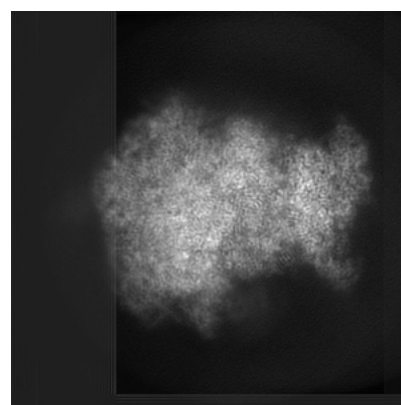
6.1.1 Primary map



X



Y

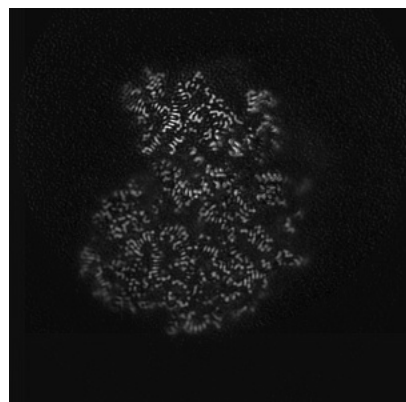


Z

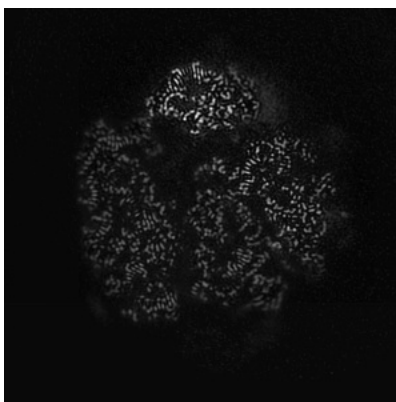
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

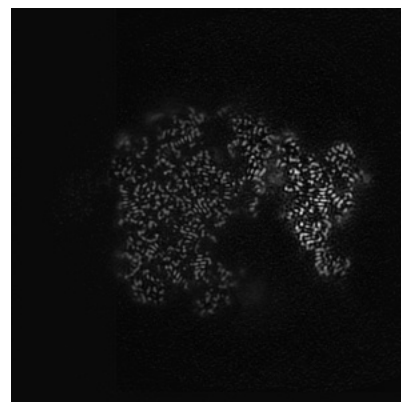
6.2.1 Primary map



X Index: 224



Y Index: 224

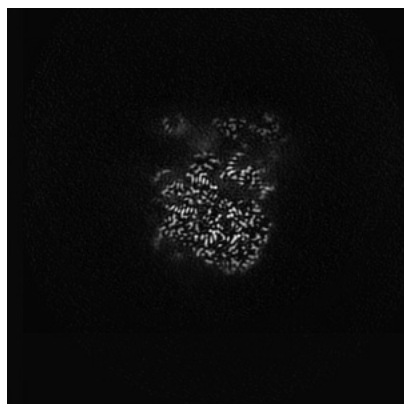


Z Index: 224

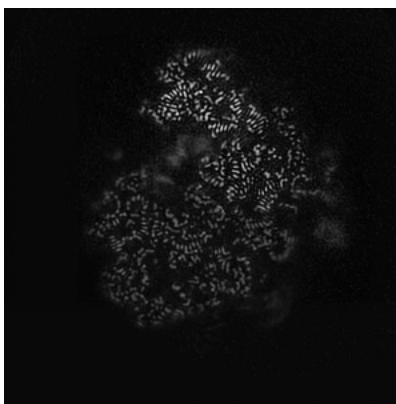
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

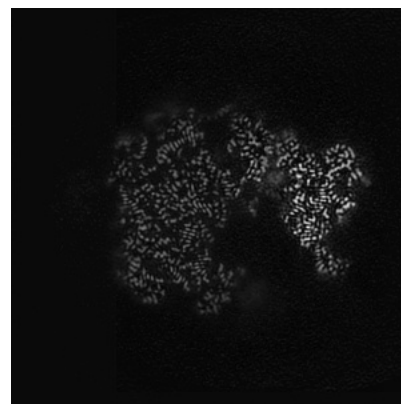
6.3.1 Primary map



X Index: 333



Y Index: 254

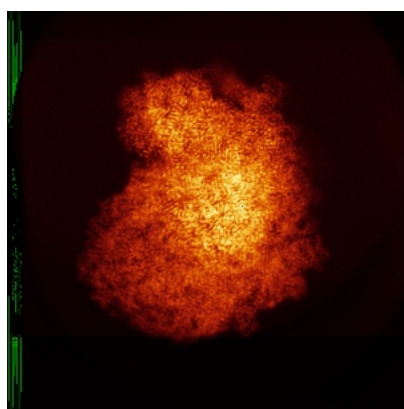


Z Index: 222

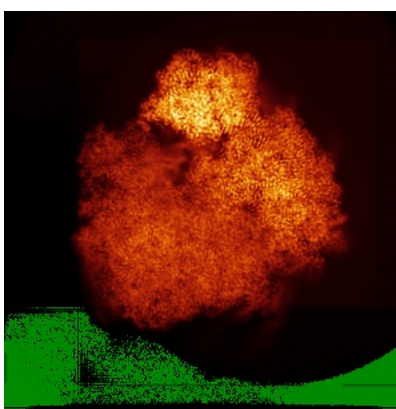
The images above show the largest variance slices of the map in three orthogonal directions.

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

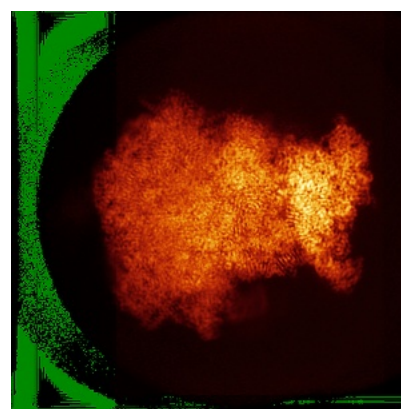
6.4.1 Primary map



X



Y

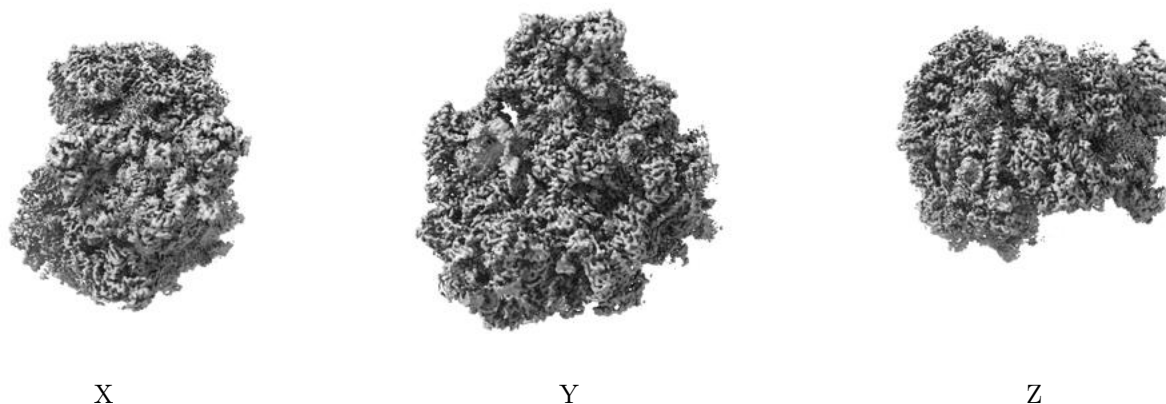


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

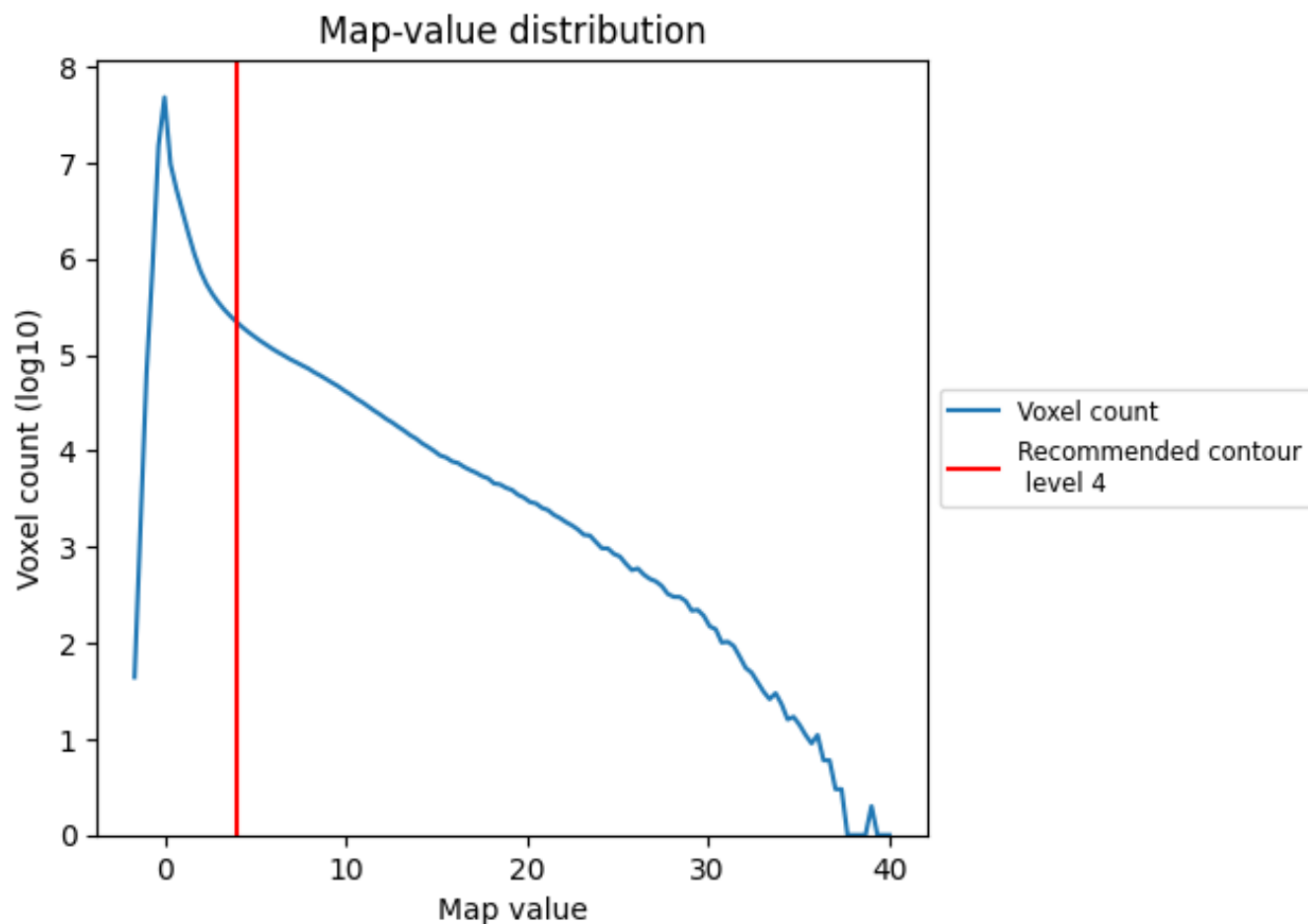
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

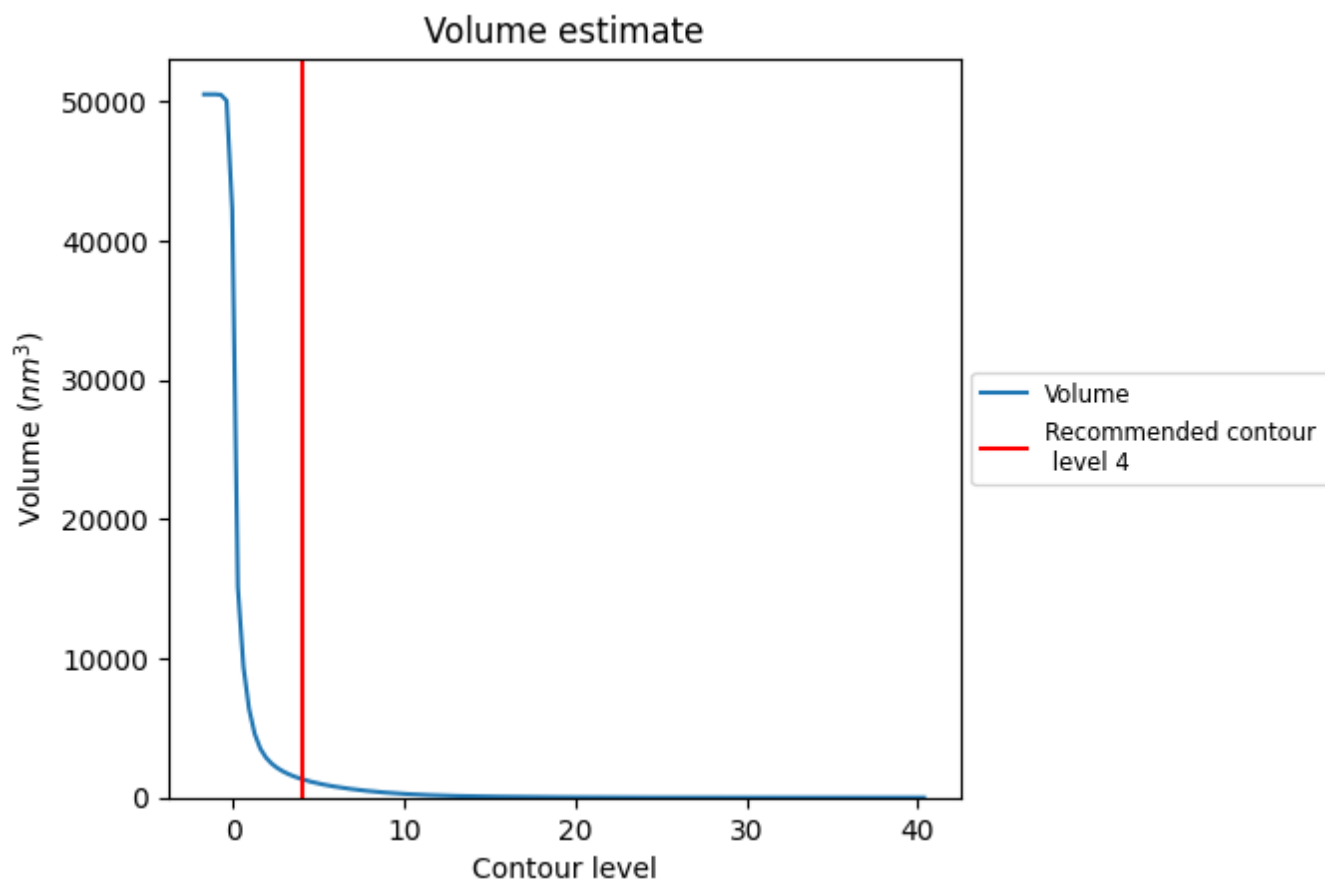
This section contains the results of statistical analysis of the map.

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.

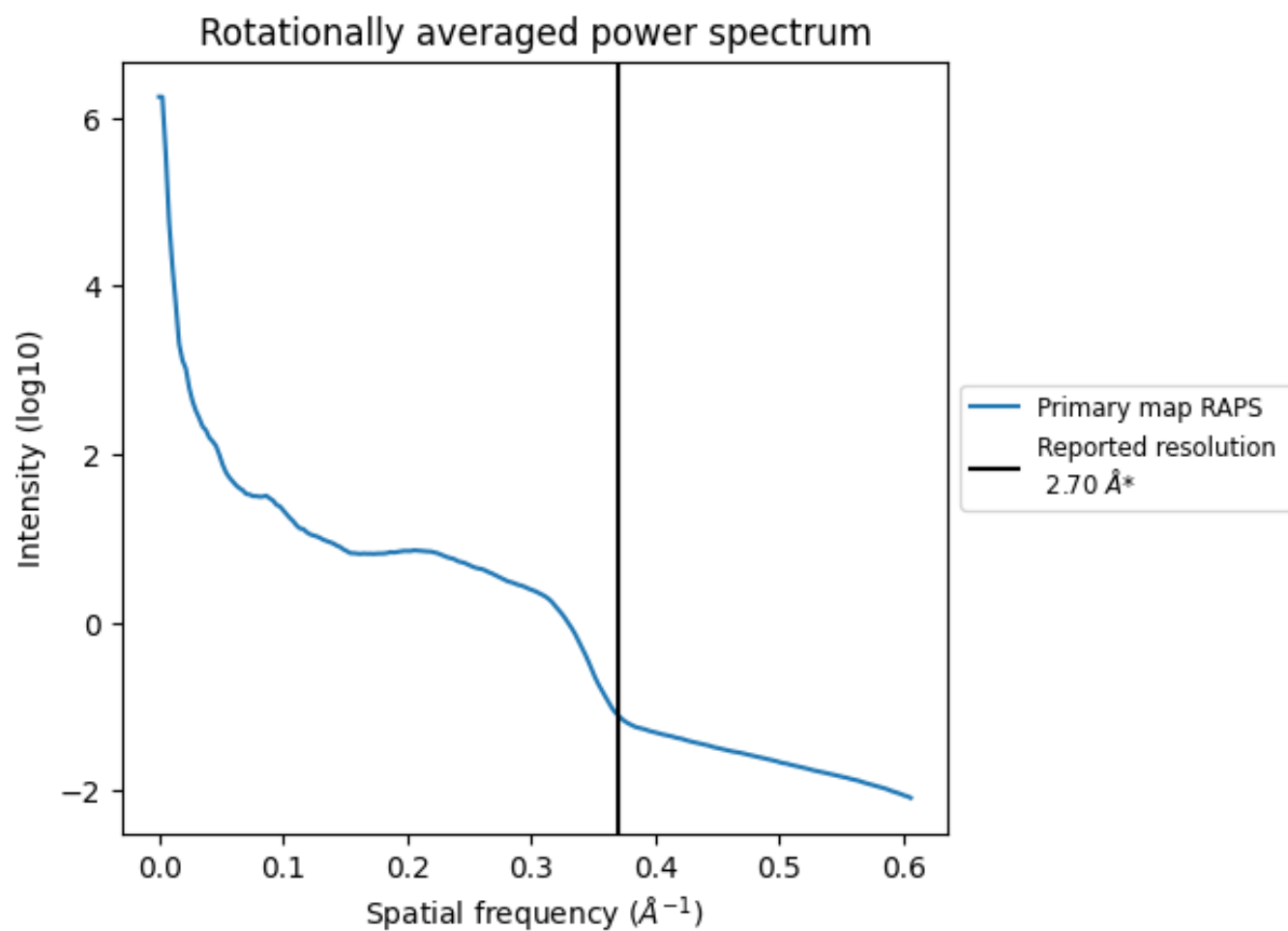
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1334 nm^3 ; this corresponds to an approximate mass of 1205 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 0.370 Å⁻¹

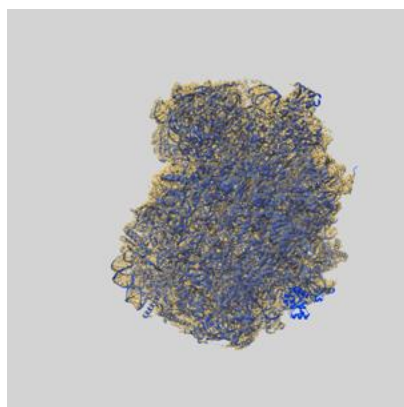
8 Fourier-Shell correlation

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

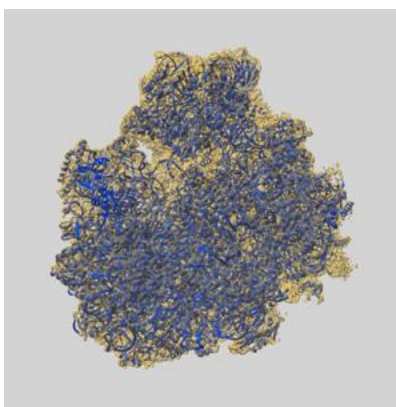
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-72933 and PDB model 9YGM. Per-residue inclusion information can be found in section [3](#) on page [23](#).

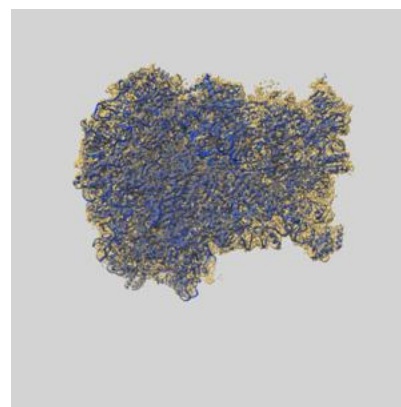
9.1 Map-model overlay [i](#)



X



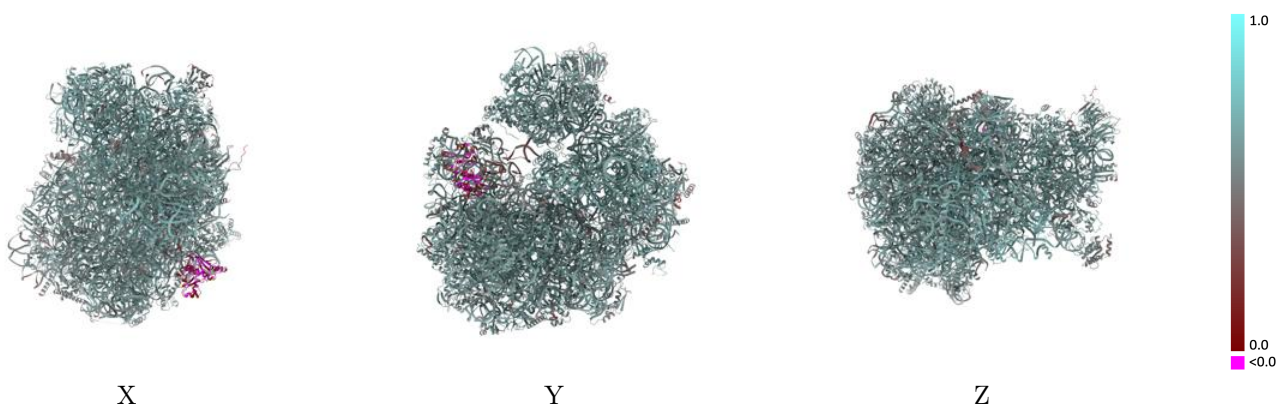
Y



Z

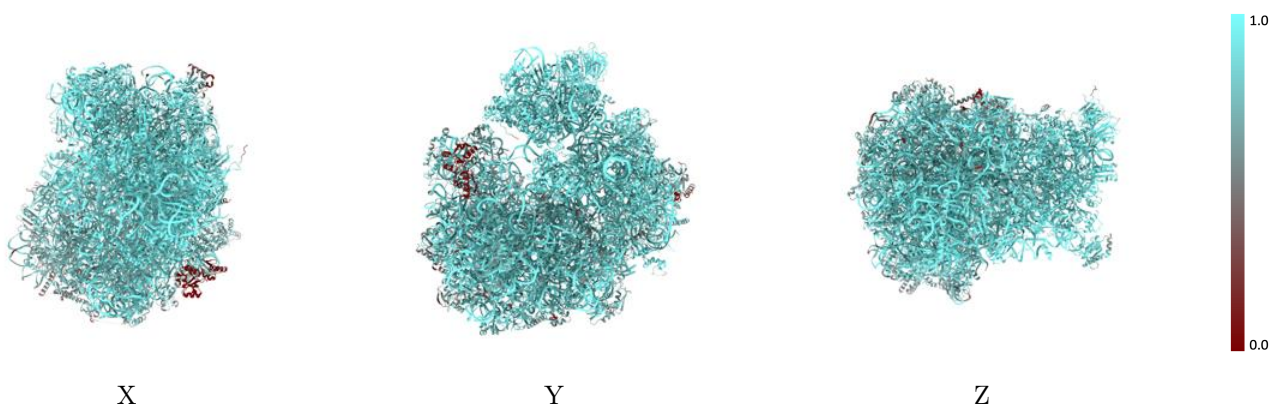
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



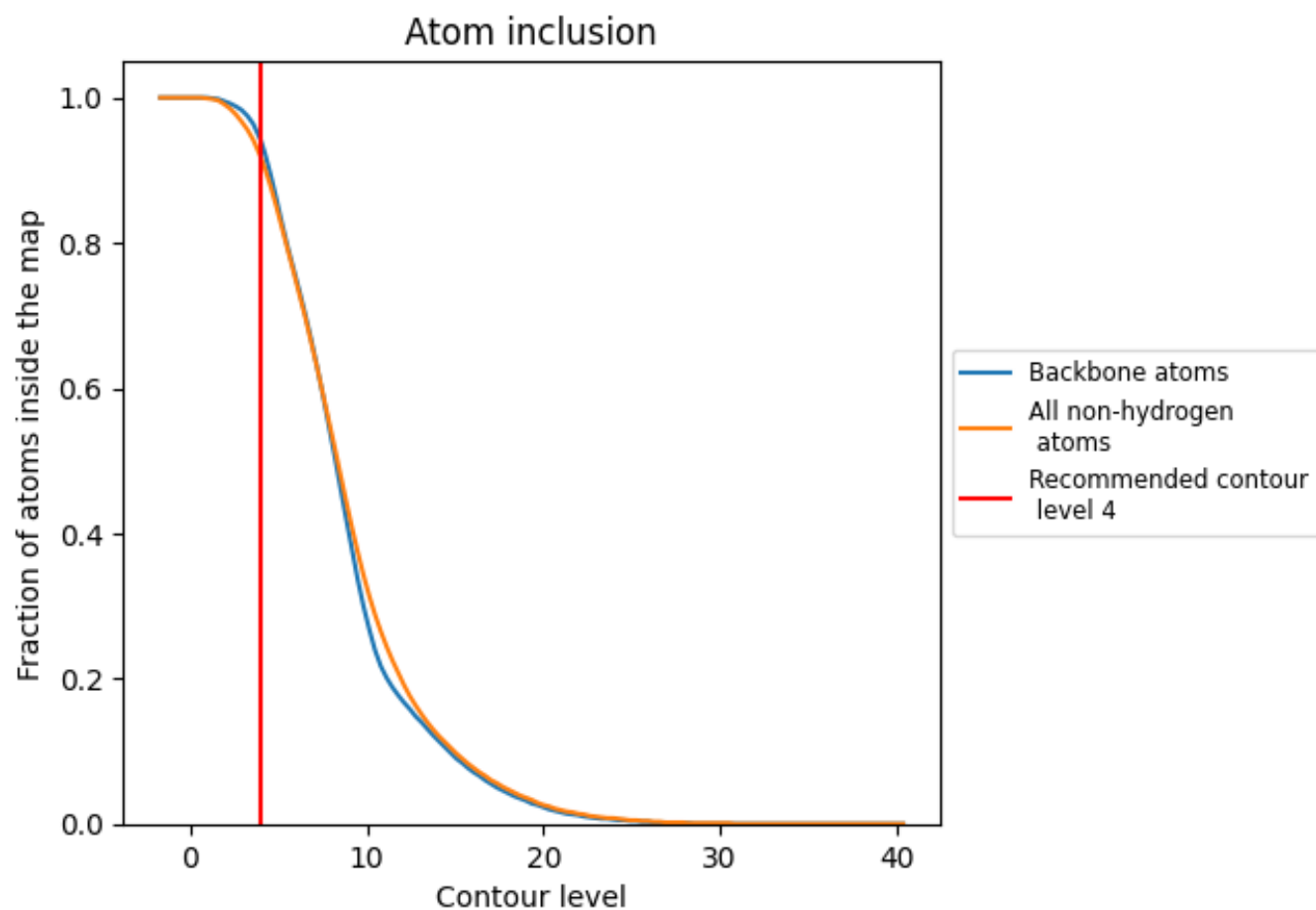
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (4).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 92% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9180	 0.6000
L3	 0.9730	 0.6000
L4	 0.9410	 0.5990
L5	 0.9620	 0.6070
LA	 0.2130	 0.0540
LB	 0.9220	 0.6230
LC	 0.9070	 0.6200
LD	 0.7160	 0.5860
LE	 0.7710	 0.5430
LF	 0.7510	 0.5740
LG	 0.6490	 0.5500
LH	 0.7570	 0.5770
LI	 0.8460	 0.6020
LJ	 0.8360	 0.6030
LK	 0.8990	 0.5960
LL	 0.7250	 0.5830
LM	 0.8820	 0.6250
LN	 0.9280	 0.6310
LO	 0.7530	 0.5810
LP	 0.7740	 0.5710
LQ	 0.8480	 0.6090
LR	 0.8550	 0.5740
LS	 0.7780	 0.5890
LT	 0.7870	 0.5950
LU	 0.8960	 0.6190
LV	 0.7250	 0.5400
LW	 0.7930	 0.5840
LX	 0.8400	 0.5910
LY	 0.8720	 0.5790
LZ	 0.7280	 0.5630
La	 0.7610	 0.5640
Lb	 0.8440	 0.5950
Lc	 0.8320	 0.5950
Ld	 0.8530	 0.5680
Le	 0.8470	 0.6010











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Chain	Atom inclusion	Q-score
Lf	 0.8560	 0.6150
Lg	 0.9140	 0.6290
Lh	 0.8970	 0.6200
Li	 0.8430	 0.5910
Lj	 0.9330	 0.6360
Lk	 0.7340	 0.5650
Ll	 0.8880	 0.6260
Lm	 0.7850	 0.5860
Ln	 0.9600	 0.6440
Lo	 0.9200	 0.6090
Lp	 0.8900	 0.5800
S1	 0.9900	 0.6280
S7	 0.9920	 0.3800
SA	 0.9290	 0.6150
SB	 0.8740	 0.5850
SC	 0.9590	 0.5690
SD	 0.9320	 0.6280
SE	 0.9430	 0.6360
SF	 0.9640	 0.6340
SG	 0.8870	 0.6000
SH	 0.9910	 0.6140
SI	 0.7150	 0.5590
SJ	 0.9680	 0.6390
SK	 0.9600	 0.6260
SL	 0.9870	 0.6280
SM	 0.9570	 0.5780
SN	 0.9860	 0.5980
SO	 0.9680	 0.6150
SP	 0.9410	 0.6330
SQ	 0.8110	 0.4850
SR	 0.9820	 0.6070
SS	 0.9950	 0.6260
ST	 0.9470	 0.6290
SU	 0.9660	 0.6520
SV	 0.9580	 0.5790
SW	 0.9720	 0.5960
SX	 0.9750	 0.6170
SY	 0.8900	 0.6150
SZ	 0.9290	 0.6260
Sa	 0.9410	 0.5890
Sb	 0.9620	 0.6280
Sc	 0.8850	 0.6220

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Chain	Atom inclusion	Q-score
Sd	 0.9660	 0.5790
Se	 0.9220	 0.6180
Sf	 0.8960	 0.5500
Sg	 0.9200	 0.5620