



wwPDB EM Validation Summary Report ⓘ

Sep 29, 2026 – 08:08 PM JST

PDB ID : 9X4I / pdb_00009x4i
EMDB ID : EMD-66550
Title : Structure of the young Killifish Ribosome
Authors : Kim, J.; Song, J.J.; Kim, Y.
Deposited on : 2025-10-10
Resolution : 2.56 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:

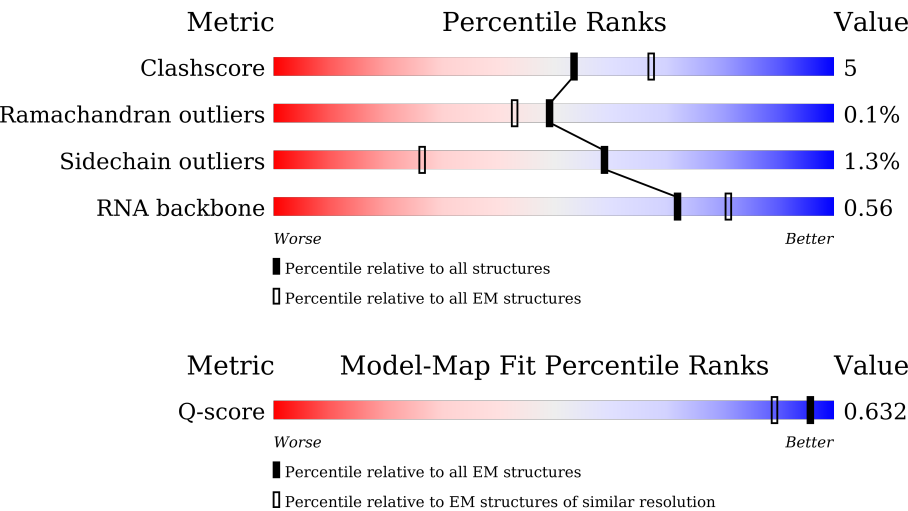
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.2
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.51

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 2.56 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	7558 (2.06 - 3.06)

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	11	51	80%18%.
2	21	128	7% 34%5%62%
3	32	84	12% 79%13%8%

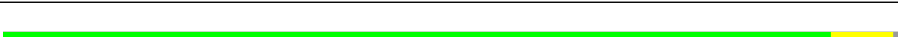
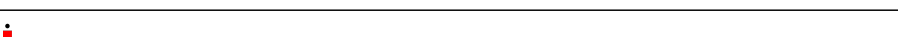
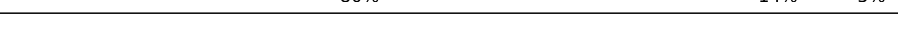
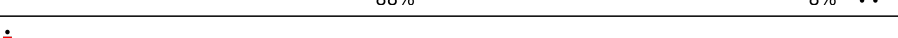
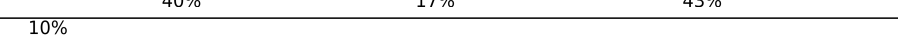
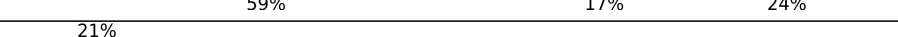
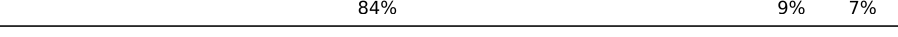
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Mol	Chain	Length	Quality of chain
4	41	137	
5	42	266	
6	51	25	
7	61	215	
8	71	178	
9	72	151	
10	81	205	
11	82	142	
12	91	116	
13	A1	4024	
14	A2	145	
15	B1	403	
16	B2	151	
17	C1	375	
18	C2	1838	
19	D1	124	
20	E1	135	
21	F1	246	
22	H1	123	
23	H2	83	
24	I1	105	
25	J1	97	
26	J2	279	
27	K1	70	
28	K2	208	

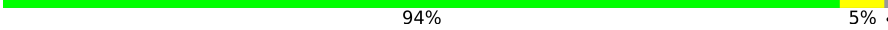
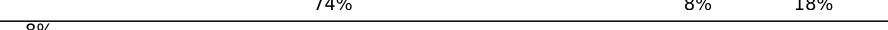
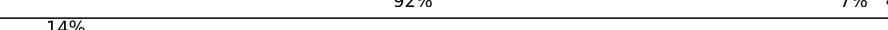
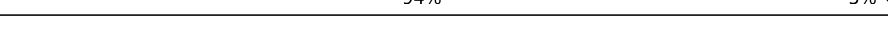
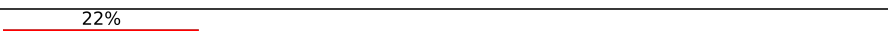
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Mol	Chain	Length	Quality of chain
29	L1	211	
30	L2	194	
31	M1	137	
32	M2	146	
33	N1	204	
34	N2	73	
35	O1	106	
36	O2	263	
37	P1	184	
38	P2	152	
39	Q1	188	
40	R1	196	
41	S1	176	
42	S2	146	
43	T1	160	
44	T2	123	
45	U1	129	
46	U2	194	
47	V1	140	
48	W1	157	
49	W2	249	
50	X1	155	
51	Y1	145	
52	Y2	161	
53	Z1	136	

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Mol	Chain	Length	Quality of chain
54	a1	257	
55	b1	64	
56	d2	69	
57	e1	117	
58	f1	110	
59	g1	92	
60	g2	313	
61	h1	297	
62	i1	120	
63	i2	134	
64	j1	161	
65	k1	192	
66	l1	259	
67	m1	266	
68	m2	132	
69	n1	148	
70	q2	119	
71	r2	130	
72	u2	203	
73	w2	247	
74	x2	133	
75	y2	143	
76	z2	166	
77	k2	317	

2 Entry composition [i](#)

There are 79 unique types of molecules in this entry. The entry contains 189912 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	11	50	Total	C	N	O	S	0	0
			443	281	98	63	1		

- Molecule 2 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	21	49	Total	C	N	O	S	0	0
			404	249	86	63	6		

- Molecule 3 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	32	77	Total	C	N	O	S	0	0
			616	387	117	107	5		

- Molecule 4 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	41	124	Total	C	N	O	S	0	0
			986	615	201	167	3		

- Molecule 5 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	42	209	Total	C	N	O	S	0	0
			1704	1081	306	303	14		

- Molecule 6 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	51	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 7 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	61	107	Total	C	N	O	S	0	0
			864	548	169	140	7		

- Molecule 8 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	71	163	Total	C	N	O	S	0	0
			1319	834	252	228	5		

- Molecule 9 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	72	127	Total	C	N	O	S	0	0
			952	581	189	176	6		

- Molecule 10 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	81	204	Total	C	N	O	S	0	0
			1660	1074	320	263	3		

- Molecule 11 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	82	95	Total	C	N	O	S	0	0
			756	468	155	127	6		

- Molecule 12 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	91	98	Total	C	N	O	S	0	0
			762	481	135	139	7		

- Molecule 13 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A1	3124	Total	C	N	O	P	0	0
			66974	29844	12241	21765	3124		

- Molecule 14 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	A2	115	Total	C	N	O	S	0	0
			947	600	176	162	9		

- Molecule 15 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	B1	394	Total	C	N	O	S	0	0
			3173	2018	597	545	13		

- Molecule 16 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	B2	149	Total	C	N	O	S	0	0
			1199	768	228	202	1		

- Molecule 17 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	C1	345	Total	C	N	O	S	0	0
			2756	1740	542	460	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	C2	1492	Total	C	N	O	P	0	0
			31864	14233	5746	10393	1492		

- Molecule 19 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	D1	104	Total	C	N	O	S	0	0
			851	536	167	144	4		

- Molecule 20 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	E1	128	Total	C	N	O	S	0	0
			1053	669	212	166	6		

- Molecule 21 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	F1	219	Total	C	N	O	S	0	0
			1813	1165	351	289	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F1	6	GLU	-	insertion	UNP A0A1A8ABD9

- Molecule 22 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	H1	121	Total	C	N	O	S	0	0
			1004	632	203	168	1		

- Molecule 23 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	H2	83	Total	C	N	O	S	0	0
			644	400	118	122	4		

- Molecule 24 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	I1	101	Total	C	N	O	S	0	0
			816	512	171	128	5		

- Molecule 25 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	J1	86	Total	C	N	O	S	0	0
			706	433	156	113	4		

- Molecule 26 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	J2	216	Total	C	N	O	S	0	0
			1671	1081	286	295	9		

- Molecule 27 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	K1	68	Total	C	N	O	S	0	0
			559	360	101	97	1		

- Molecule 28 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	K2	204	Total	C	N	O	S	0	0
			1661	1046	323	288	4		

- Molecule 29 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L1	203	Total	C	N	O	S	0	0
			1641	1020	342	274	5		

- Molecule 30 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	L2	178	Total	C	N	O	S	0	0
			1482	945	295	240	2		

- Molecule 31 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	M1	134	Total	C	N	O	S	0	0
			1093	697	206	183	7		

- Molecule 32 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	M2	141	Total	C	N	O	S	0	0
			1088	685	208	192	3		

- Molecule 33 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	N1	203	Total	C	N	O	S	0	0
			1697	1066	357	268	6		

- Molecule 34 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	N2	39	Total	C	N	O	S	0	0
			321	198	66	52	5		

- Molecule 35 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	O1	97	Total	C	N	O	S	0	0
			800	502	162	130	6		

- Molecule 36 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	O2	257	Total	C	N	O	S	0	0
			2040	1304	379	348	9		

- Molecule 37 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	P1	152	Total	C	N	O	S	0	0
			1232	770	243	210	9		

- Molecule 38 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	P2	140	Total	C	N	O	S	0	0
			1158	728	232	197	1		

- Molecule 39 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Q1	187	Total	C	N	O	S	0	0
			1509	946	315	243	5		

- Molecule 40 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	R1	175	Total	C	N	O	S	0	0
			1463	902	320	231	10		

- Molecule 41 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S1	176	Total	C	N	O	S	0	0
			1457	932	286	230	9		

- Molecule 42 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	S2	138	Total	C	N	O	S	0	0
			1090	694	203	190	3		

- Molecule 43 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	T1	156	Total	C	N	O	S	0	0
			1279	809	251	215	4		

- Molecule 44 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	T2	70	Total	C	N	O	S	0	0
			568	367	103	97	1		

- Molecule 45 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	U1	98	Total	C	N	O	S	0	0
			798	512	139	145	2		

- Molecule 46 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	U2	185	Total	C	N	O	S	0	0
			1492	950	274	267	1		

- Molecule 47 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	V1	130	Total	C	N	O	S	0	0
			973	615	183	170	5		

- Molecule 48 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	W1	61	Total	C	N	O	S	0	0
			512	329	100	81	2		

- Molecule 49 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	W2	207	Total	C	N	O	S	0	0
			1682	1056	333	286	7		

- Molecule 50 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	X1	118	Total	C	N	O	S	0	0
			968	619	182	166	1		

- Molecule 51 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Y1	130	Total	C	N	O	S	0	0
			1080	678	222	177	3		

- Molecule 52 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Y2	139	Total	C	N	O	S	0	0
			1128	714	217	192	5		

- Molecule 53 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Z1	135	Total	C	N	O	S	0	0
			1107	715	208	180	4		

- Molecule 54 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	a1	246	Total	C	N	O	S	0	0
			1890	1186	387	311	6		

- Molecule 55 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	b1	50	Total	C	N	O	S	0	0
			428	265	94	68	1		

- Molecule 56 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	d2	61	Total	C	N	O	S	0	0
			480	292	96	90	2		

- Molecule 57 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	e1	106	Total	C	N	O	S	0	0
			847	531	174	136	6		

- Molecule 58 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	f1	109	Total	C	N	O	S	0	0
			872	554	170	144	4		

- Molecule 59 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	g1	89	Total	C	N	O	S	0	0
			691	437	134	114	6		

- Molecule 60 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	g2	207	Total	C	N	O	S	0	0
			1643	1046	290	298	9		

- Molecule 61 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	h1	287	Total	C	N	O	S	0	0
			2320	1470	421	418	11		

- Molecule 62 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	i1	119	Total	C	N	O	P	0	0
			2541	1135	460	828	118		

- Molecule 63 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	i2	119	Total	C	N	O	S	0	0
			969	608	180	178	3		

- Molecule 64 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	j1	149	Total	C	N	O	P	0	0
			3177	1417	568	1043	149		

- Molecule 65 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	k1	190	Total	C	N	O	S	0	0
			1510	952	279	273	6		

- Molecule 66 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	l1	170	Total	C	N	O	S	0	0
			1367	884	257	224	2		

- Molecule 67 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	m1	219	Total	C	N	O	S	0	0
			1778	1136	339	299	4		

- Molecule 68 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	m2	122	Total	C	N	O	S	0	0
			1001	635	195	166	5		

- Molecule 69 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	n1	147	Total	C	N	O	S	0	0
			1159	736	231	187	5		

- Molecule 70 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	q2	99	Total	C	N	O	S	0	0
			785	492	149	140	4		

- Molecule 71 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	r2	129	Total	C	N	O	S	0	0
			1035	660	193	176	6		

- Molecule 72 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	u2	182	Total	C	N	O	S	0	0
			1444	905	271	261	7		

- Molecule 73 is a protein called DNA-(apurinic or apyrimidinic site) lyase.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	w2	205	Total	C	N	O	S	0	0
			1595	1018	289	281	7		

- Molecule 74 is a protein called FAU ubiquitin like and ribosomal protein S30 fusion a.

Mol	Chain	Residues	Atoms				AltConf	Trace
74	x2	48	Total	C	N	O	0	0
			387	238	86	63		

- Molecule 75 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	y2	140	Total	C	N	O	S	0	0
			1090	689	216	182	3		

- Molecule 76 is a protein called Ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	z2	54	Total	C	N	O	S	0	0
			454	303	74	73	4		

- Molecule 77 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	k2	297	Total	C	N	O	S	0	0
			2303	1449	403	440	11		

- Molecule 78 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
78	21	1	Total	Zn	0
			1	1	
78	82	1	Total	Zn	0
			1	1	
78	J1	1	Total	Zn	0
			1	1	
78	N2	1	Total	Zn	0
			1	1	
78	O1	1	Total	Zn	0
			1	1	
78	e1	1	Total	Zn	0
			1	1	
78	g1	1	Total	Zn	0
			1	1	

- Molecule 79 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

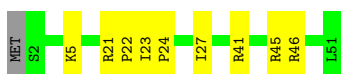
Mol	Chain	Residues	Atoms		AltConf
79	A1	62	Total	Mg	0
			62	62	
79	C2	22	Total	Mg	0
			22	22	
79	i1	1	Total	Mg	0
			1	1	

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.

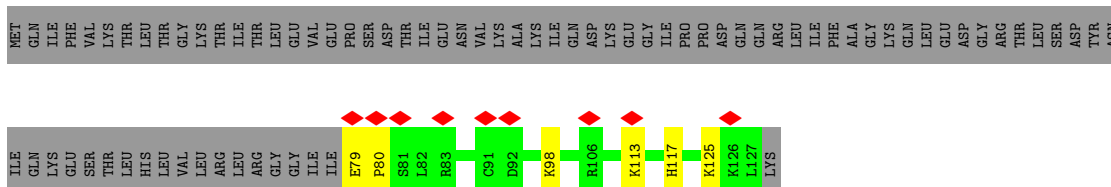
- Molecule 1: Large ribosomal subunit protein eL39

Chain 11: 



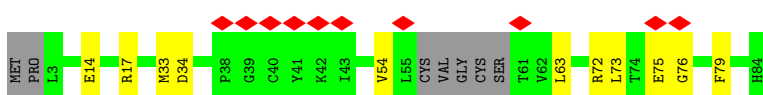
- Molecule 2: Ubiquitin-ribosomal protein eL40 fusion protein

Chain 21: 



- Molecule 3: 40S ribosomal protein S27

Chain 32: 



- Molecule 4: Large ribosomal subunit protein eL28

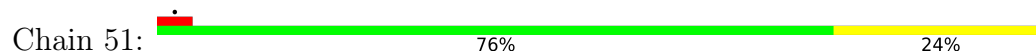
Chain 41: 



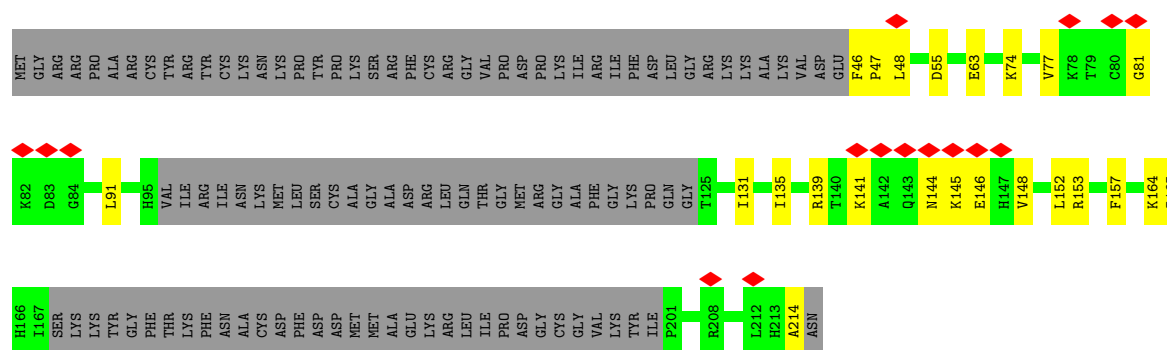
- Molecule 5: Small ribosomal subunit protein eS1

Chain 42: 

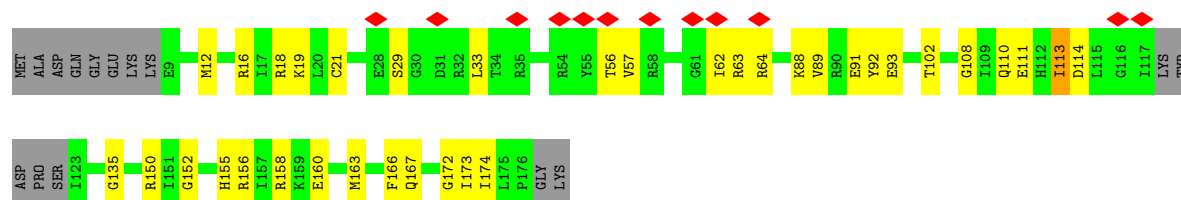
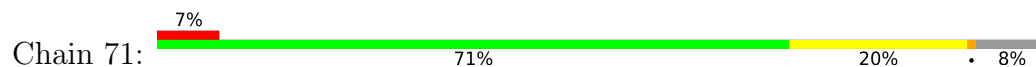
- Molecule 6: Small ribosomal subunit protein eS32



- Molecule 7: Ribosomal protein L10



- Molecule 8: Large ribosomal subunit protein uL5



- Molecule 9: Small ribosomal subunit protein uS11





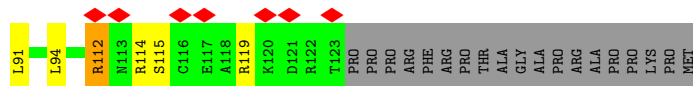
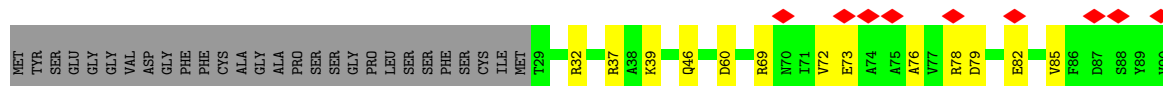
- Molecule 10: Large ribosomal subunit protein uL13

Chain 81: 92% 7%



- Molecule 11: 40S ribosomal protein S26

Chain 82: 11% 54% 13% 33%



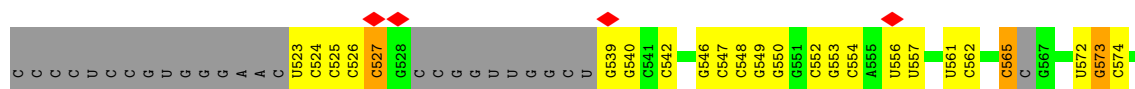
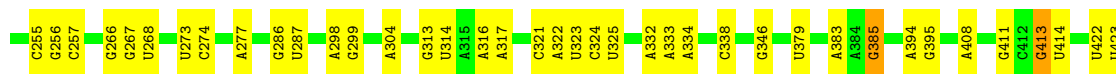
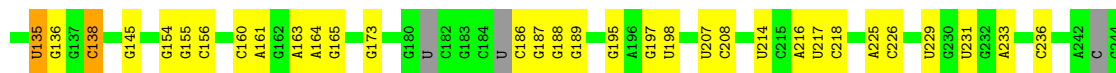
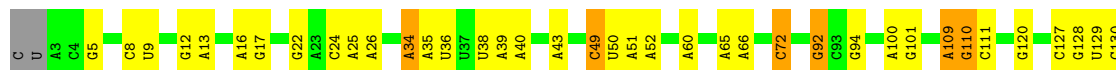
- Molecule 12: Large ribosomal subunit protein eL30

Chain 91: 74% 9% 16%



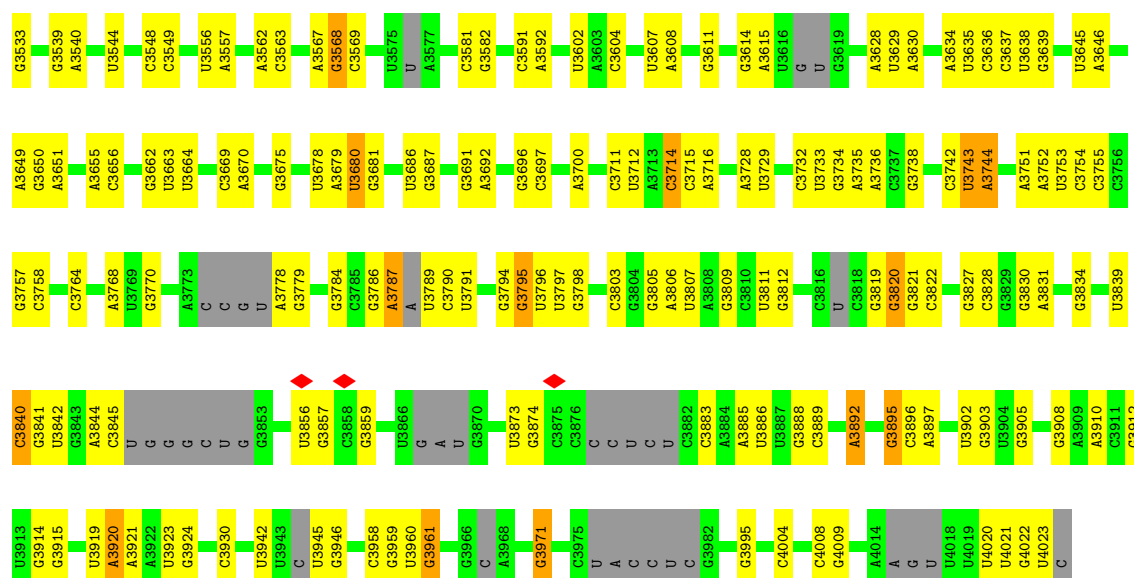
- Molecule 13: 28S rRNA

Chain A1: 53% 22% 22%

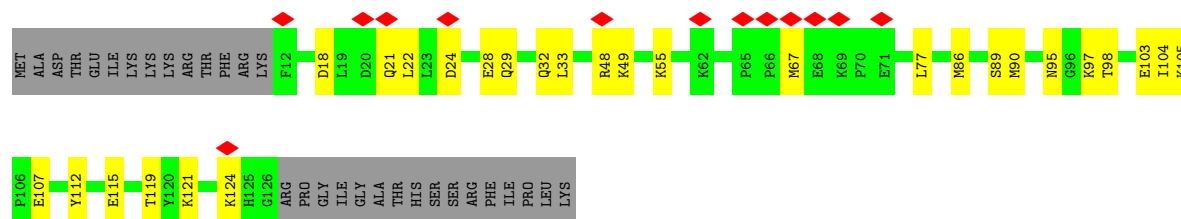




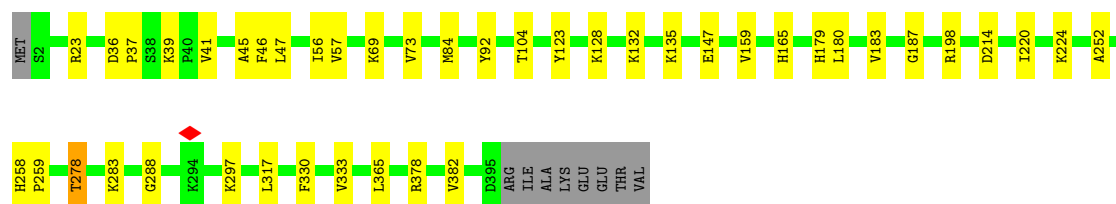
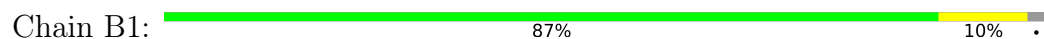




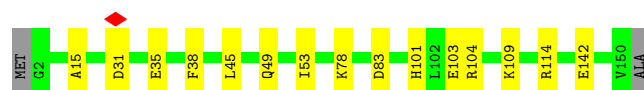
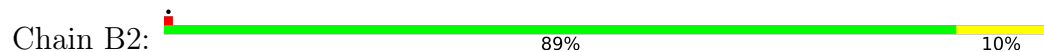
• Molecule 14: 40S ribosomal protein S15



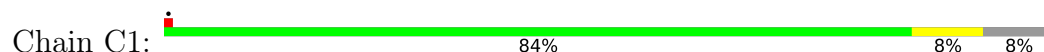
• Molecule 15: Large ribosomal subunit protein uL3

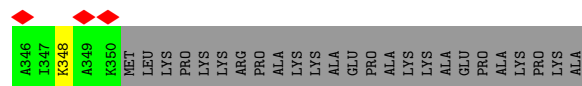


• Molecule 16: Small ribosomal subunit protein uS15



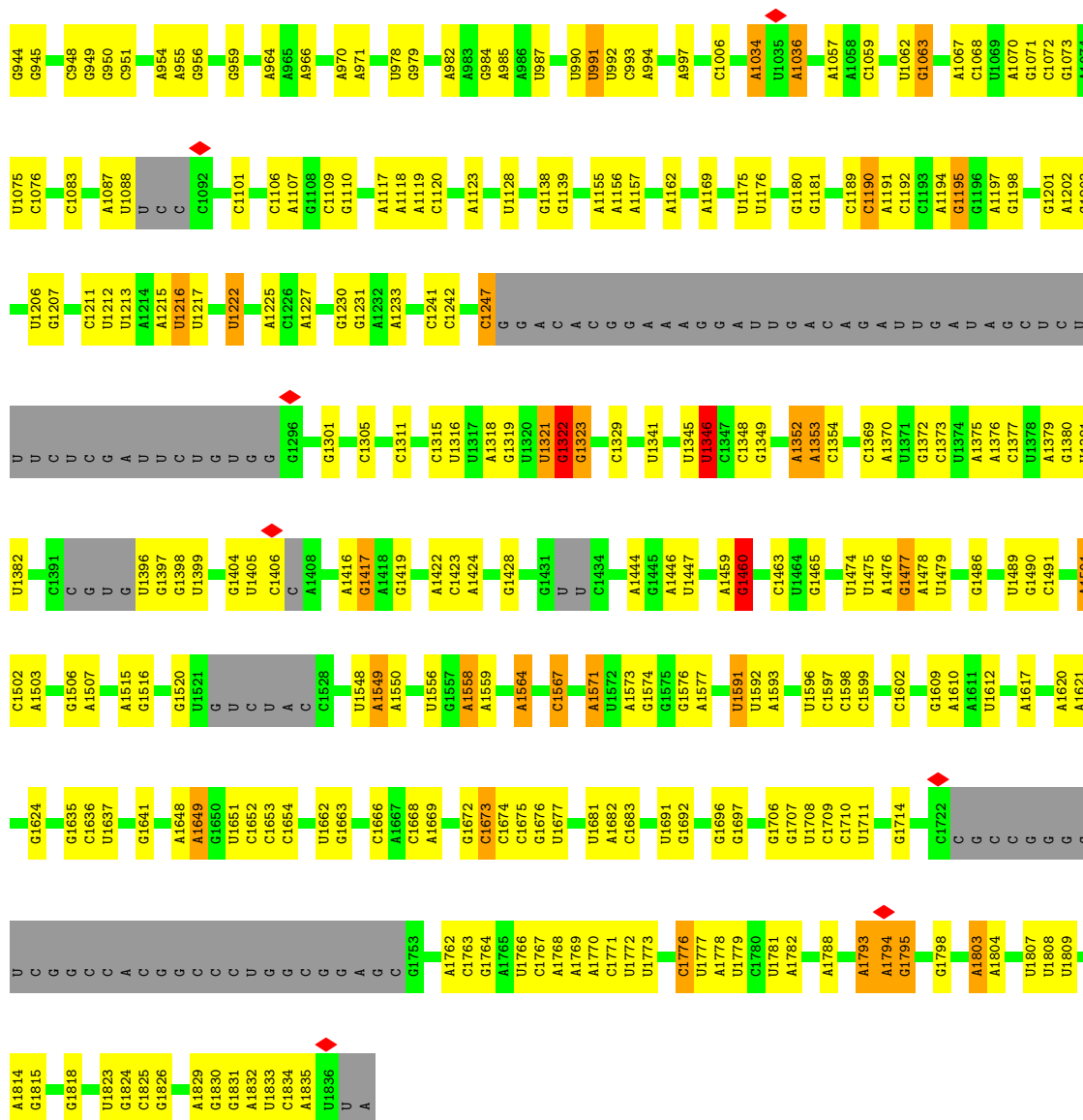
• Molecule 17: Ribosomal protein L4



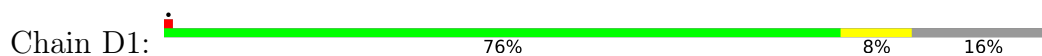


Chain C2: 52% 26% 19%





- Molecule 19: Large ribosomal subunit protein eL31

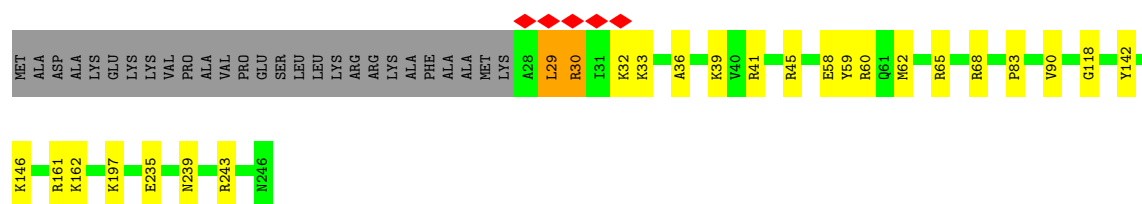


- Molecule 20: 60S ribosomal protein L32

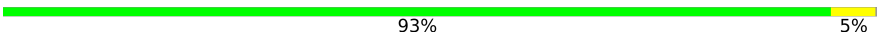


- Molecule 21: Large ribosomal subunit protein uL30

Chain F1:  79% 9% 11%



- Molecule 22: Large ribosomal subunit protein uL29

Chain H1:  93% 5%



- Molecule 23: 40S ribosomal protein S21

Chain H2:  82% 18%



- Molecule 24: 60S ribosomal protein L36

Chain I1:  88% 9%



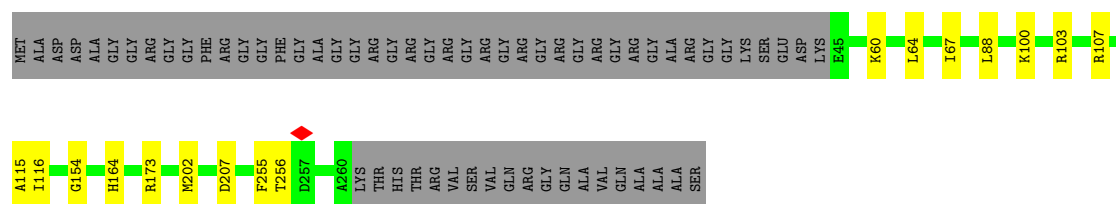
- Molecule 25: Ribosomal protein L37

Chain J1:  86% 11%



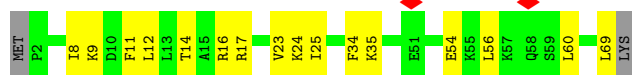
- Molecule 26: Small ribosomal subunit protein uS5

Chain J2:  72% 6% 23%



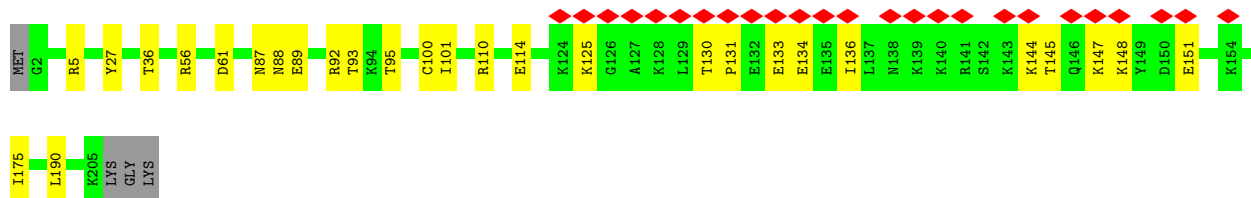
- Molecule 27: Large ribosomal subunit protein eL38

Chain K1:  74% 23% .



- Molecule 28: 40S ribosomal protein S8

Chain K2:  12% 85% 13% .



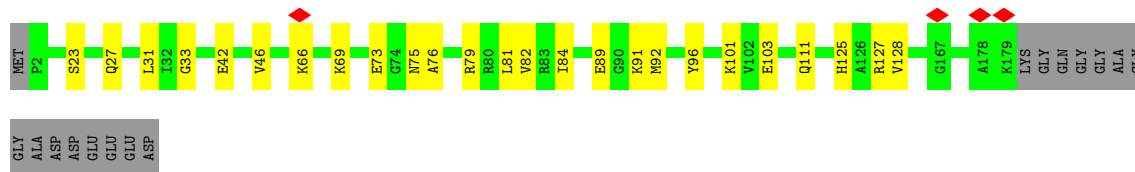
- Molecule 29: 60S ribosomal protein L13

Chain L1:  88% 9% .



- Molecule 30: Small ribosomal subunit protein uS4

Chain L2:  79% 13% 8%



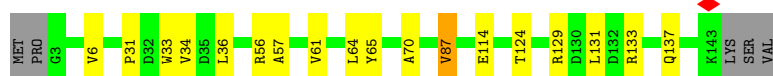
- Molecule 31: Large ribosomal subunit protein eL14

Chain M1:  88% 10% .



- Molecule 32: Small ribosomal subunit protein eS19

Chain M2:  84% 12% .

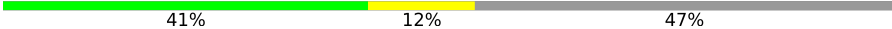


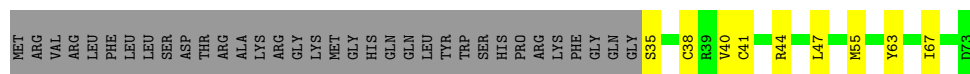
- Molecule 33: Ribosomal protein L15

Chain N1:  92% 8%



- Molecule 34: Small ribosomal subunit protein uS14

Chain N2:  41% 12% 47%



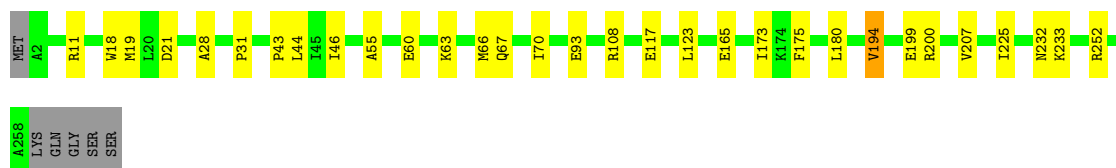
- Molecule 35: 60S ribosomal protein L36a

Chain O1:  82% 8% 8%



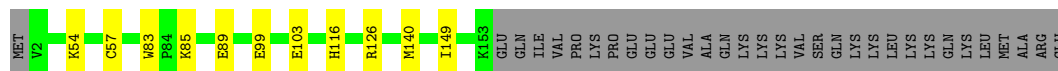
- Molecule 36: 40S ribosomal protein S4

Chain O2:  86% 11%



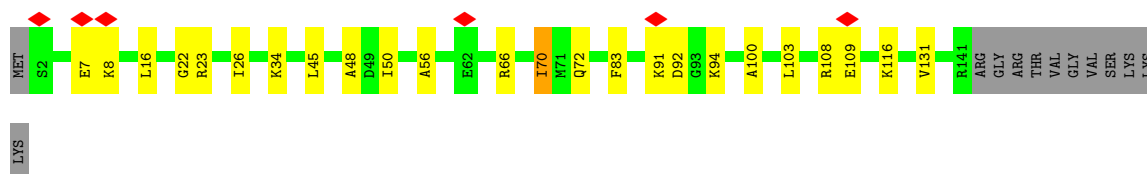
- Molecule 37: Large ribosomal subunit protein uL22

Chain P1:  77% 6% 17%

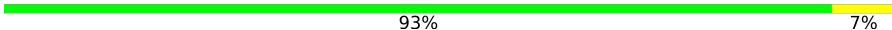


- Molecule 38: Small ribosomal subunit protein uS13

Chain P2:  76% 15% 8%

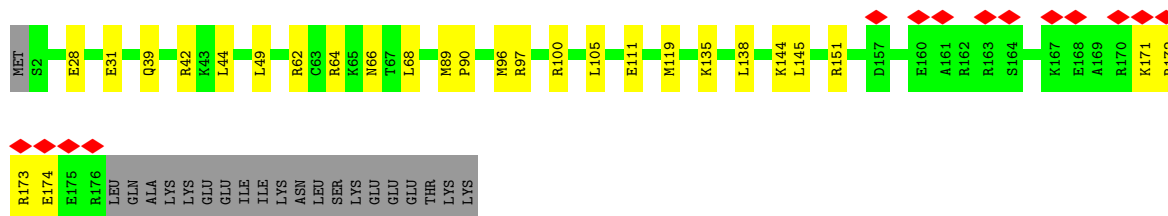
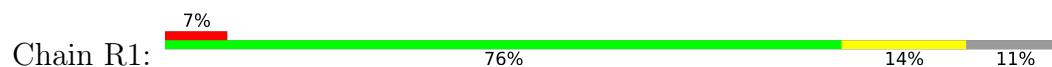


- Molecule 39: Ribosomal protein L18

Chain Q1:  93% 7%



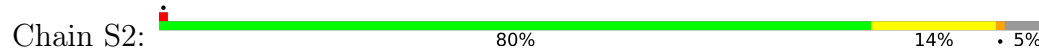
- Molecule 40: Ribosomal protein L19



- Molecule 41: 60S ribosomal protein L18a



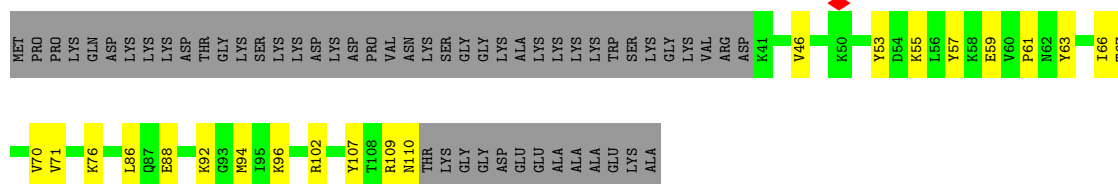
- Molecule 42: Small ribosomal subunit protein uS9



- Molecule 43: Large ribosomal subunit protein eL21



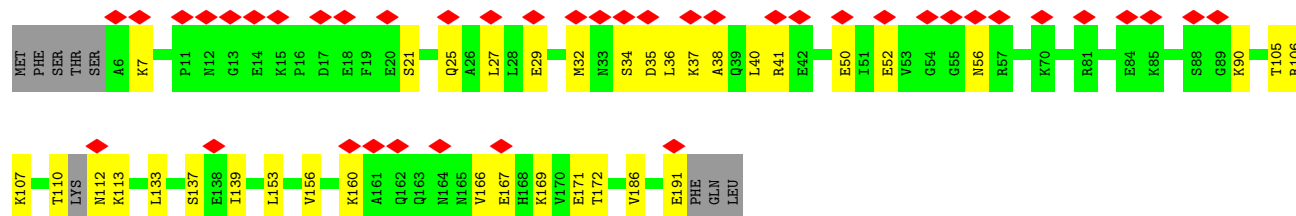
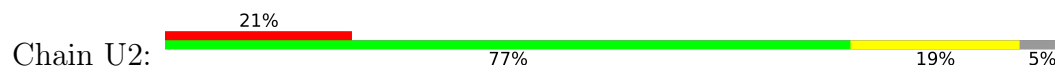
- Molecule 44: 40S ribosomal protein S25



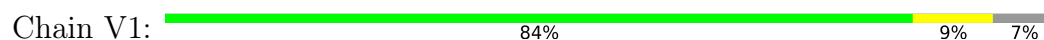
- Molecule 45: Large ribosomal subunit protein eL22



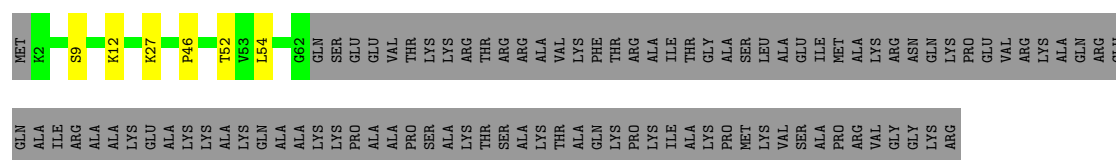
- Molecule 46: 40S ribosomal protein S7



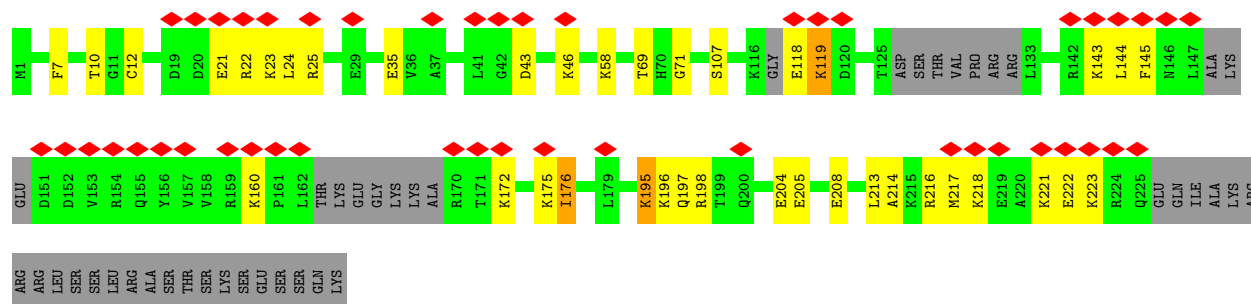
- Molecule 47: Large ribosomal subunit protein uL14



- Molecule 48: Large ribosomal subunit protein eL24

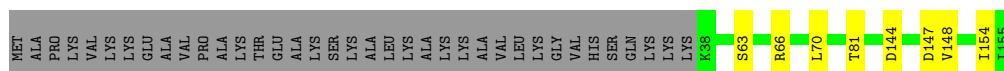


- Molecule 49: 40S ribosomal protein S6



- Molecule 50: Large ribosomal subunit protein uL23

Chain X1:  71% 5% 24%



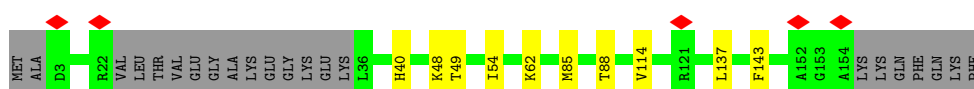
- Molecule 51: Ribosomal protein L26

Chain Y1:  78% 11% 10%



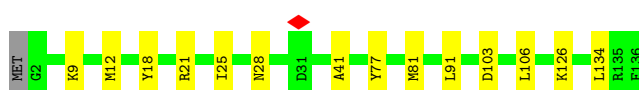
- Molecule 52: Small ribosomal subunit protein uS17

Chain Y2:  80% 6% 14%



- Molecule 53: 60S ribosomal protein L27

Chain Z1:  89% 10% 1%



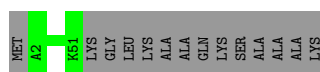
- Molecule 54: Large ribosomal subunit protein uL2

Chain a1:  86% 9% 5%



- Molecule 55: 60S ribosomal protein L29

Chain b1:  78% 22%



- Molecule 56: Small ribosomal subunit protein eS28

Chain d2:  58% 30% 12%



- Molecule 57: Large ribosomal subunit protein eL34

MET
 V2
 A84
 R88
 A94
 E98
 E99
 Q100
 V104
 L107
 LYS
 ALA
 GLN
 ALA
 GLN
 SER
 GLN
 LYS
 THR
 LYS

-

- | | | | | | | | | | | | | | | | | | | |
|-----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | A2 | T16 | L22 | V26 | S52 | T38 | C42 | T45 | S59 | C60 | K61 | T70 | V79 | R85 | L86 | K90 | ASP | GLN |
|-----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

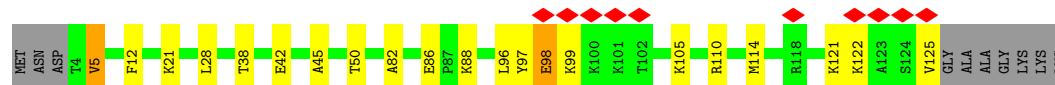
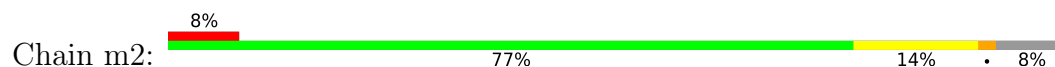
- | Protein | Category | Score | Significance |
|---------|----------|----------|--------------|
| E192 | GLN | 0.000000 | *** |
| H193 | GLN | 0.000000 | *** |
| E196 | PRO | 0.000000 | *** |
| V197 | ALA | 0.000000 | *** |
| M198 | ALA | 0.000000 | *** |
| P199 | THR | 0.000000 | *** |
| D200 | THR | 0.000000 | *** |
| P207 | ALA | 0.000000 | *** |
| E208 | ALA | 0.000000 | *** |
| GLU | ALA | 0.000000 | *** |
| I1E | ALA | 0.000000 | *** |
| GLU | ALA | 0.000000 | *** |
| LVS | ALA | 0.000000 | *** |
| GLU | PRO | 0.000000 | *** |
| VAL | VAL | 0.000000 | *** |
| GLN | THR | 0.000000 | *** |
| GLY | THR | 0.000000 | *** |
| ALA | GLY | 0.000000 | *** |
| ALA | GLU | 0.000000 | *** |
| VAL | VAL | 0.000000 | *** |
| PHE | PHE | 0.000000 | *** |
| SER | SER | 0.000000 | *** |
| ALA | GLU | 0.000000 | *** |
| VAL | ASP | 0.000000 | *** |
| LVS | THR | 0.000000 | *** |
| GLU | SER | 0.000000 | *** |
| GLN | THR | 0.000000 | *** |
| PHE | PRO | 0.000000 | *** |
| GLN | PRO | 0.000000 | *** |
| GLY | THR | 0.000000 | *** |
| GLU | THR | 0.000000 | *** |
| ASP | GLU | 0.000000 | *** |
| TRP | ASP | 0.000000 | *** |
| SER | TRP | 0.000000 | *** |
| ALA | SER | 0.000000 | *** |
| ALA | THR | 0.000000 | *** |
| PRO | PRO | 0.000000 | *** |
| THR | THR | 0.000000 | *** |
| GLU | THR | 0.000000 | *** |
| PHE | THR | 0.000000 | *** |
| ALA | ALA | 0.000000 | *** |
| GLN | GLN | 0.000000 | *** |
| H131 | GLN | 0.000000 | *** |
| Q132 | THR | 0.000000 | *** |
| P133 | SER | 0.000000 | *** |
| VAL | ASP | 0.000000 | *** |
| ALA | TRP | 0.000000 | *** |
| ASP | GLY | 0.000000 | *** |
| TRP | GLY | 0.000000 | *** |
| T142 | GLY | 0.000000 | *** |
| M177 | ALA | 0.000000 | *** |
| SER | ALA | 0.000000 | *** |
| VAL | TRP | 0.000000 | *** |
| ALA | PRO | 0.000000 | *** |
| M186 | PRO | 0.000000 | *** |
| G187 | SER | 0.000000 | *** |
| VAL | VAL | 0.000000 | *** |
| S190 | PRO | 0.000000 | *** |

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|----|----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|------|------|------|------|------|------|------|------|-----|-----|-----|-----|
| MET | GLY | PHE | V4 | K5 | R33 | R50 | C62 | Q63 | I64 | E70 | C76 | L105 | L109 | G156 | P181 | E186 | E189 | V204 | F223 | I227 | M236 | E254 | K256 | K256 | P257 | PRO | LYS | E260 | V261 | K262 | K263 | S272 | Q275 | Q291 | E292 | GLN | GLU | ASP | ALA |
|-----|-----|-----|----|----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|------|------|------|------|------|------|------|------|-----|-----|-----|-----|

- | | | | | | | | | | | | | | | | |
|----|----|----|----|----|----|----|------|------|------|------|------|------|------|------|------|
| G1 | C2 | U3 | U4 | A5 | C6 | G7 | G22 | A24 | A25 | U26 | G27 | U33 | U38 | A42 | A43 | C44 | A50 | G51 | U52 | A53 | A54 | A55 | G56 | C57 | A58 | G59 | G64 | C91 | C94 | C95 | A100 | A101 | A102 | A103 | A104 | G110 | C111 | U112 | U119 |
|----|----|----|----|----|----|----|------|------|------|------|------|------|------|------|------|



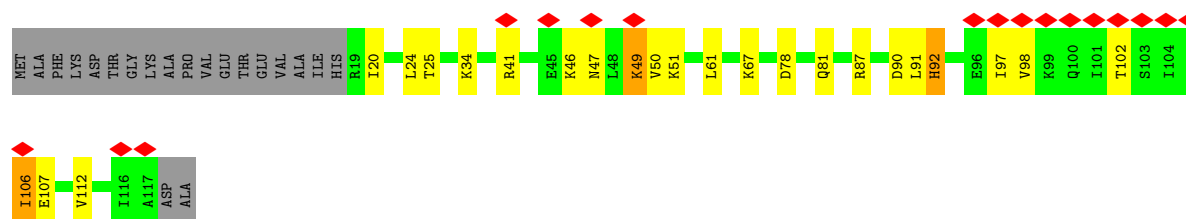
- Molecule 68: 40S ribosomal protein S24



- Molecule 69: Large ribosomal subunit protein uL15



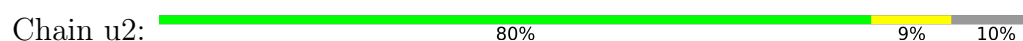
- Molecule 70: Small ribosomal subunit protein uS10



- Molecule 71: Small ribosomal subunit protein uS8



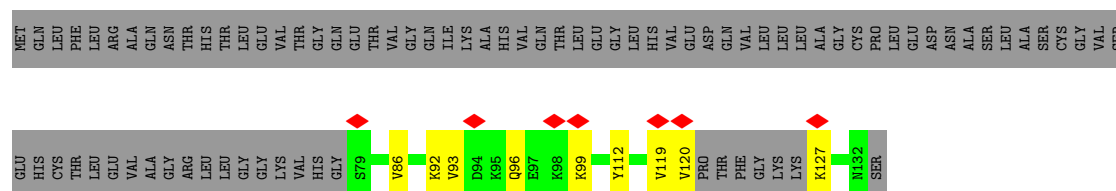
- Molecule 72: Small ribosomal subunit protein uS7



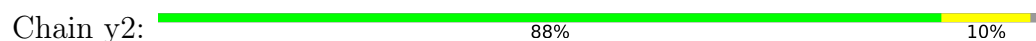
- Molecule 73: DNA-(apurinic or apyrimidinic site) lyase



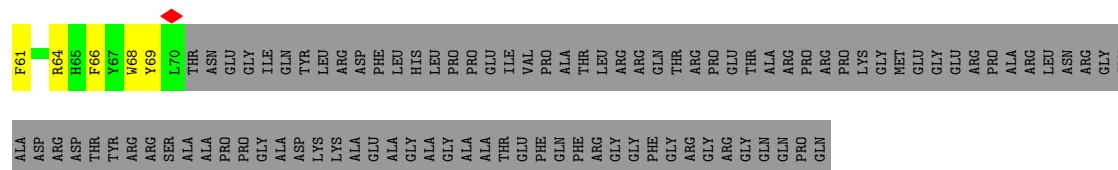
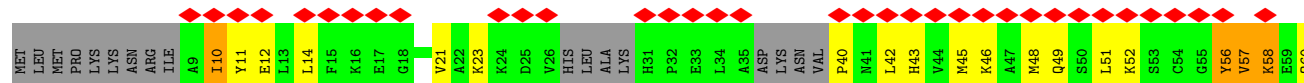
- Molecule 74: FAU ubiquitin like and ribosomal protein S30 fusion a



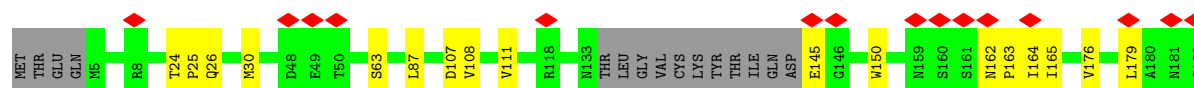
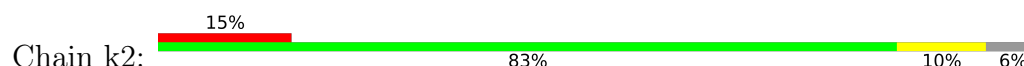
- Molecule 75: Small ribosomal subunit protein uS12

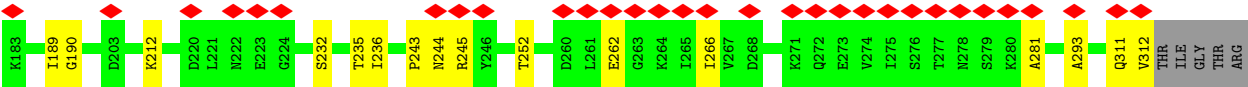


- Molecule 76: Ribosomal protein S10



- Molecule 77: Small ribosomal subunit protein RACK1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	292135	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	65.77	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	1000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.176	Depositor
Minimum map value	-0.061	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	529.92, 529.92, 529.92	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82799995, 0.82799995, 0.82799995	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

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	11	0.23	0/453	0.36	0/599
2	21	0.22	0/410	0.52	0/543
3	32	0.24	0/628	0.48	0/841
4	41	0.23	0/1001	0.33	0/1342
5	42	0.24	0/1731	0.40	0/2316
6	51	0.36	0/240	0.59	0/305
7	61	0.27	0/883	0.53	0/1181
8	71	0.24	0/1339	0.50	0/1786
9	72	0.27	0/964	0.46	0/1292
10	81	0.26	0/1692	0.41	0/2268
11	82	0.26	0/766	0.49	0/1024
12	91	0.26	0/773	0.45	0/1037
13	A1	0.49	0/74893	0.76	26/116704 (0.0%)
14	A2	0.34	0/965	0.61	0/1290
15	B1	0.23	0/3243	0.33	0/4345
16	B2	0.24	0/1222	0.38	0/1642
17	C1	0.22	0/2812	0.36	0/3778
18	C2	0.57	0/35632	0.79	32/55497 (0.1%)
19	D1	0.25	0/864	0.37	0/1161
20	E1	0.22	0/1071	0.33	0/1427
21	F1	0.24	0/1848	0.41	0/2470
22	H1	0.23	0/1011	0.37	0/1334
23	H2	0.25	0/652	0.44	0/875
24	I1	0.22	0/828	0.31	0/1099
25	J1	0.24	0/720	0.33	0/953
26	J2	0.26	0/1707	0.39	0/2308
27	K1	0.26	0/565	0.41	0/750
28	K2	0.24	0/1690	0.46	0/2254
29	L1	0.23	0/1670	0.38	0/2230
30	L2	0.24	0/1507	0.44	0/2014
31	M1	0.25	0/1113	0.37	0/1486
32	M2	0.32	0/1105	0.45	0/1483

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	N1	0.23	0/1740	0.32	0/2327
34	N2	0.37	0/325	0.45	0/429
35	O1	0.23	0/813	0.37	0/1073
36	O2	0.22	0/2081	0.39	0/2800
37	P1	0.24	0/1258	0.38	0/1687
38	P2	0.34	0/1176	0.58	0/1576
39	Q1	0.23	0/1535	0.38	0/2051
40	R1	0.24	0/1479	0.44	0/1954
41	S1	0.25	0/1497	0.37	0/2011
42	S2	0.38	0/1107	0.53	0/1484
43	T1	0.23	0/1307	0.36	0/1749
44	T2	0.36	0/575	0.58	0/772
45	U1	0.24	0/812	0.61	0/1089
46	U2	0.24	0/1513	0.50	0/2027
47	V1	0.22	0/987	0.34	0/1324
48	W1	0.24	0/525	0.32	0/699
49	W2	0.26	0/1699	0.56	0/2256
50	X1	0.24	0/986	0.35	0/1326
51	Y1	0.24	0/1096	0.39	0/1458
52	Y2	0.21	0/1148	0.31	0/1538
53	Z1	0.25	0/1130	0.33	0/1507
54	a1	0.23	0/1929	0.36	0/2584
55	b1	0.23	0/438	0.37	0/579
56	d2	0.37	0/482	0.58	0/644
57	e1	0.21	0/857	0.33	0/1143
58	f1	0.22	0/892	0.31	0/1193
59	g1	0.27	0/701	0.42	0/931
60	g2	0.29	0/1682	0.44	0/2285
61	h1	0.23	0/2364	0.37	0/3165
62	i1	0.51	0/2842	0.71	1/4430 (0.0%)
63	i2	0.41	0/980	0.73	0/1314
64	j1	0.50	0/3548	0.76	3/5524 (0.1%)
65	k1	0.26	0/1529	0.42	0/2055
66	l1	0.23	0/1391	0.38	0/1866
67	m1	0.25	0/1812	0.39	0/2438
68	m2	0.23	0/1017	0.44	0/1351
69	n1	0.21	0/1191	0.37	0/1593
70	q2	0.48	0/794	0.71	0/1066
71	r2	0.25	0/1052	0.34	0/1409
72	u2	0.37	0/1465	0.55	0/1968
73	w2	0.36	0/1619	0.64	0/2174
74	x2	0.24	0/389	0.45	0/511
75	y2	0.22	0/1108	0.40	0/1480

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	z2	0.49	0/467	0.90	0/625
77	k2	0.14	0/2358	0.38	0/3209
All	All	0.43	0/203694	0.66	62/298308 (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
42	S2	0	1

There are no bond length outliers.

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	A1	2755	A	N1-C2-N3	9.79	134.20	129.30
18	C2	1612	U	OP1-P-O3'	-9.69	78.92	108.00
18	C2	475	C	C2-N1-C1'	9.13	128.84	118.80
13	A1	1931	C	C2-N1-C1'	8.80	128.48	118.80
18	C2	475	C	N1-C2-O2	8.30	123.88	118.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
42	S2	43	GLU	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	11	443	0	483	8	0
2	21	404	0	432	5	0
3	32	616	0	636	7	0
4	41	986	0	1049	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	42	1704	0	1778	21	0
6	51	239	0	289	6	0
7	61	864	0	886	23	0
8	71	1319	0	1366	32	0
9	72	952	0	974	28	0
10	81	1660	0	1812	10	0
11	82	756	0	799	20	0
12	91	762	0	791	9	0
13	A1	66974	0	33830	531	0
14	A2	947	0	983	22	0
15	B1	3173	0	3294	28	0
16	B2	1199	0	1287	12	0
17	C1	2756	0	2914	26	0
18	C2	31864	0	16093	297	0
19	D1	851	0	905	5	0
20	E1	1053	0	1151	11	0
21	F1	1813	0	1943	16	0
22	H1	1004	0	1131	6	0
23	H2	644	0	648	12	0
24	I1	816	0	892	10	0
25	J1	706	0	734	3	0
26	J2	1671	0	1751	12	0
27	K1	559	0	624	10	0
28	K2	1661	0	1750	23	0
29	L1	1641	0	1739	13	0
30	L2	1482	0	1598	21	0
31	M1	1093	0	1149	10	0
32	M2	1088	0	1135	12	0
33	N1	1697	0	1743	14	0
34	N2	321	0	324	4	0
35	O1	800	0	866	4	0
36	O2	2040	0	2152	24	0
37	P1	1232	0	1260	5	0
38	P2	1158	0	1212	17	0
39	Q1	1509	0	1622	13	0
40	R1	1463	0	1604	21	0
41	S1	1457	0	1516	13	0
42	S2	1090	0	1151	13	0
43	T1	1279	0	1347	9	0
44	T2	568	0	621	19	0
45	U1	798	0	821	15	0
46	U2	1492	0	1588	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	V1	973	0	1034	9	0
48	W1	512	0	525	4	0
49	W2	1682	0	1822	31	0
50	X1	968	0	1039	6	0
51	Y1	1080	0	1178	10	0
52	Y2	1128	0	1183	5	0
53	Z1	1107	0	1184	8	0
54	a1	1890	0	1985	19	0
55	b1	428	0	443	0	0
56	d2	480	0	506	14	0
57	e1	847	0	934	3	0
58	f1	872	0	911	5	0
59	g1	691	0	748	15	0
60	g2	1643	0	1638	19	0
61	h1	2320	0	2349	16	0
62	i1	2541	0	1286	21	0
63	i2	969	0	1020	37	0
64	j1	3177	0	1611	37	0
65	k1	1510	0	1593	14	0
66	l1	1367	0	1491	13	0
67	m1	1778	0	1894	13	0
68	m2	1001	0	1081	15	0
69	n1	1159	0	1197	5	0
70	q2	785	0	855	18	0
71	r2	1035	0	1082	5	0
72	u2	1444	0	1492	18	0
73	w2	1595	0	1679	26	0
74	x2	387	0	427	6	0
75	y2	1090	0	1157	8	0
76	z2	454	0	452	19	0
77	k2	2303	0	2244	27	0
78	21	1	0	0	0	0
78	82	1	0	0	0	0
78	J1	1	0	0	0	0
78	N2	1	0	0	0	0
78	O1	1	0	0	0	0
78	e1	1	0	0	0	0
78	g1	1	0	0	0	0
79	A1	62	0	0	0	0
79	C2	22	0	0	0	0
79	i1	1	0	0	0	0
All	All	189912	0	142713	1737	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 5.

The worst 5 of 1737 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)
18:C2:1428:G:OP1	77:k2:281:ALA:HB2	1.62	1.00
9:72:66:ARG:HH22	72:u2:136:ARG:HD2	1.33	0.93
64:j1:120:C:H5	64:j1:136:G:H1	1.14	0.92
30:L2:79:ARG:HH12	36:O2:252:ARG:HD2	1.38	0.89
21:F1:36:ALA:HA	21:F1:39:LYS:HE3	1.56	0.88

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	11	48/51 (94%)	48 (100%)	0	0	100	100
2	21	47/128 (37%)	44 (94%)	3 (6%)	0	100	100
3	32	73/84 (87%)	72 (99%)	1 (1%)	0	100	100
4	41	122/137 (89%)	121 (99%)	1 (1%)	0	100	100
5	42	207/266 (78%)	201 (97%)	6 (3%)	0	100	100
6	51	23/25 (92%)	23 (100%)	0	0	100	100
7	61	101/215 (47%)	99 (98%)	2 (2%)	0	100	100
8	71	159/178 (89%)	155 (98%)	4 (2%)	0	100	100
9	72	125/151 (83%)	118 (94%)	7 (6%)	0	100	100
10	81	202/205 (98%)	198 (98%)	4 (2%)	0	100	100
11	82	93/142 (66%)	90 (97%)	3 (3%)	0	100	100
12	91	96/116 (83%)	93 (97%)	2 (2%)	1 (1%)	12	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	A2	113/145 (78%)	109 (96%)	4 (4%)	0	100	100
15	B1	392/403 (97%)	385 (98%)	7 (2%)	0	100	100
16	B2	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
17	C1	343/375 (92%)	337 (98%)	6 (2%)	0	100	100
19	D1	100/124 (81%)	98 (98%)	2 (2%)	0	100	100
20	E1	126/135 (93%)	124 (98%)	2 (2%)	0	100	100
21	F1	217/246 (88%)	211 (97%)	6 (3%)	0	100	100
22	H1	119/123 (97%)	117 (98%)	2 (2%)	0	100	100
23	H2	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
24	I1	99/105 (94%)	99 (100%)	0	0	100	100
25	J1	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
26	J2	214/279 (77%)	210 (98%)	4 (2%)	0	100	100
27	K1	66/70 (94%)	66 (100%)	0	0	100	100
28	K2	202/208 (97%)	195 (96%)	7 (4%)	0	100	100
29	L1	201/211 (95%)	197 (98%)	3 (2%)	1 (0%)	24	33
30	L2	176/194 (91%)	172 (98%)	4 (2%)	0	100	100
31	M1	132/137 (96%)	129 (98%)	3 (2%)	0	100	100
32	M2	139/146 (95%)	134 (96%)	5 (4%)	0	100	100
33	N1	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
34	N2	37/73 (51%)	36 (97%)	1 (3%)	0	100	100
35	O1	95/106 (90%)	88 (93%)	6 (6%)	1 (1%)	11	15
36	O2	255/263 (97%)	251 (98%)	3 (1%)	1 (0%)	30	39
37	P1	150/184 (82%)	148 (99%)	2 (1%)	0	100	100
38	P2	138/152 (91%)	134 (97%)	4 (3%)	0	100	100
39	Q1	185/188 (98%)	179 (97%)	6 (3%)	0	100	100
40	R1	173/196 (88%)	171 (99%)	2 (1%)	0	100	100
41	S1	174/176 (99%)	171 (98%)	3 (2%)	0	100	100
42	S2	136/146 (93%)	131 (96%)	4 (3%)	1 (1%)	18	25
43	T1	154/160 (96%)	150 (97%)	4 (3%)	0	100	100
44	T2	68/123 (55%)	67 (98%)	1 (2%)	0	100	100
45	U1	96/129 (74%)	92 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	U2	181/194 (93%)	170 (94%)	11 (6%)	0	100	100
47	V1	128/140 (91%)	124 (97%)	4 (3%)	0	100	100
48	W1	59/157 (38%)	58 (98%)	1 (2%)	0	100	100
49	W2	197/249 (79%)	190 (96%)	6 (3%)	1 (0%)	24	33
50	X1	116/155 (75%)	114 (98%)	2 (2%)	0	100	100
51	Y1	128/145 (88%)	125 (98%)	3 (2%)	0	100	100
52	Y2	135/161 (84%)	130 (96%)	5 (4%)	0	100	100
53	Z1	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
54	a1	244/257 (95%)	237 (97%)	7 (3%)	0	100	100
55	b1	48/64 (75%)	47 (98%)	1 (2%)	0	100	100
56	d2	59/69 (86%)	57 (97%)	2 (3%)	0	100	100
57	e1	104/117 (89%)	102 (98%)	2 (2%)	0	100	100
58	f1	107/110 (97%)	107 (100%)	0	0	100	100
59	g1	87/92 (95%)	82 (94%)	5 (6%)	0	100	100
60	g2	205/313 (66%)	191 (93%)	14 (7%)	0	100	100
61	h1	283/297 (95%)	280 (99%)	3 (1%)	0	100	100
63	i2	117/134 (87%)	112 (96%)	5 (4%)	0	100	100
65	k1	188/192 (98%)	183 (97%)	5 (3%)	0	100	100
66	l1	160/259 (62%)	156 (98%)	3 (2%)	1 (1%)	21	28
67	m1	215/266 (81%)	209 (97%)	6 (3%)	0	100	100
68	m2	120/132 (91%)	116 (97%)	3 (2%)	1 (1%)	16	22
69	n1	145/148 (98%)	136 (94%)	8 (6%)	1 (1%)	18	25
70	q2	97/119 (82%)	95 (98%)	2 (2%)	0	100	100
71	r2	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
72	u2	178/203 (88%)	172 (97%)	6 (3%)	0	100	100
73	w2	201/247 (81%)	193 (96%)	7 (4%)	1 (0%)	24	33
74	x2	44/133 (33%)	42 (96%)	2 (4%)	0	100	100
75	y2	138/143 (96%)	133 (96%)	4 (3%)	1 (1%)	18	25
76	z2	48/166 (29%)	41 (85%)	5 (10%)	2 (4%)	2	1
77	k2	293/317 (92%)	275 (94%)	17 (6%)	1 (0%)	36	44
All	All	10394/12275 (85%)	10097 (97%)	283 (3%)	14 (0%)	49	60

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
29	L1	47	ALA
35	O1	90	HIS
42	S2	44	PRO
49	W2	176	ILE
66	I1	67	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	11	47/48 (98%)	47 (100%)	0	100	100
2	21	45/116 (39%)	45 (100%)	0	100	100
3	32	70/76 (92%)	70 (100%)	0	100	100
4	41	109/120 (91%)	108 (99%)	1 (1%)	70	80
5	42	191/229 (83%)	190 (100%)	1 (0%)	81	87
6	51	24/24 (100%)	22 (92%)	2 (8%)	10	15
7	61	91/181 (50%)	91 (100%)	0	100	100
8	71	137/149 (92%)	134 (98%)	3 (2%)	45	61
9	72	99/119 (83%)	98 (99%)	1 (1%)	68	78
10	81	174/175 (99%)	170 (98%)	4 (2%)	44	60
11	82	83/119 (70%)	82 (99%)	1 (1%)	63	76
12	91	83/98 (85%)	81 (98%)	2 (2%)	43	59
14	A2	104/130 (80%)	104 (100%)	0	100	100
15	B1	343/351 (98%)	341 (99%)	2 (1%)	78	85
16	B2	129/130 (99%)	129 (100%)	0	100	100
17	C1	292/314 (93%)	292 (100%)	0	100	100
19	D1	94/110 (86%)	92 (98%)	2 (2%)	47	63
20	E1	115/121 (95%)	115 (100%)	0	100	100
21	F1	190/211 (90%)	188 (99%)	2 (1%)	65	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	H1	109/110 (99%)	109 (100%)	0	100	100
23	H2	69/69 (100%)	68 (99%)	1 (1%)	59	73
24	I1	84/88 (96%)	84 (100%)	0	100	100
25	J1	73/80 (91%)	73 (100%)	0	100	100
26	J2	181/216 (84%)	181 (100%)	0	100	100
27	K1	63/65 (97%)	62 (98%)	1 (2%)	55	70
28	K2	175/178 (98%)	175 (100%)	0	100	100
29	L1	169/177 (96%)	168 (99%)	1 (1%)	78	85
30	L2	159/168 (95%)	159 (100%)	0	100	100
31	M1	115/118 (98%)	115 (100%)	0	100	100
32	M2	112/117 (96%)	111 (99%)	1 (1%)	70	80
33	N1	171/172 (99%)	170 (99%)	1 (1%)	78	85
34	N2	35/64 (55%)	32 (91%)	3 (9%)	10	14
35	O1	87/95 (92%)	83 (95%)	4 (5%)	24	35
36	O2	221/226 (98%)	220 (100%)	1 (0%)	81	87
37	P1	132/162 (82%)	131 (99%)	1 (1%)	73	82
38	P2	122/132 (92%)	115 (94%)	7 (6%)	18	28
39	Q1	159/160 (99%)	158 (99%)	1 (1%)	78	85
40	R1	153/173 (88%)	152 (99%)	1 (1%)	76	84
41	S1	155/155 (100%)	152 (98%)	3 (2%)	50	65
42	S2	113/119 (95%)	111 (98%)	2 (2%)	51	67
43	T1	139/142 (98%)	136 (98%)	3 (2%)	45	61
44	T2	62/104 (60%)	62 (100%)	0	100	100
45	U1	88/115 (76%)	86 (98%)	2 (2%)	44	60
46	U2	168/177 (95%)	167 (99%)	1 (1%)	78	85
47	V1	100/107 (94%)	99 (99%)	1 (1%)	68	78
48	W1	53/126 (42%)	52 (98%)	1 (2%)	50	65
49	W2	182/218 (84%)	176 (97%)	6 (3%)	33	48
50	X1	106/135 (78%)	106 (100%)	0	100	100
51	Y1	120/134 (90%)	116 (97%)	4 (3%)	33	48
52	Y2	124/142 (87%)	124 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	Z1	116/117 (99%)	115 (99%)	1 (1%)	70	80
54	a1	189/199 (95%)	189 (100%)	0	100	100
55	b1	46/54 (85%)	46 (100%)	0	100	100
56	d2	54/61 (88%)	51 (94%)	3 (6%)	19	28
57	e1	92/101 (91%)	92 (100%)	0	100	100
58	f1	90/91 (99%)	90 (100%)	0	100	100
59	g1	72/75 (96%)	71 (99%)	1 (1%)	59	73
60	g2	176/253 (70%)	172 (98%)	4 (2%)	44	60
61	h1	244/252 (97%)	242 (99%)	2 (1%)	73	82
63	i2	108/121 (89%)	101 (94%)	7 (6%)	15	22
65	k1	169/171 (99%)	167 (99%)	2 (1%)	63	76
66	l1	153/226 (68%)	153 (100%)	0	100	100
67	m1	190/224 (85%)	189 (100%)	1 (0%)	81	87
68	m2	108/114 (95%)	106 (98%)	2 (2%)	50	65
69	n1	118/119 (99%)	116 (98%)	2 (2%)	53	68
70	q2	91/106 (86%)	85 (93%)	6 (7%)	15	21
71	r2	112/113 (99%)	111 (99%)	1 (1%)	70	80
72	u2	155/170 (91%)	154 (99%)	1 (1%)	78	85
73	w2	169/205 (82%)	161 (95%)	8 (5%)	23	35
74	x2	40/109 (37%)	39 (98%)	1 (2%)	42	58
75	y2	112/115 (97%)	110 (98%)	2 (2%)	51	67
76	z2	47/134 (35%)	43 (92%)	4 (8%)	10	14
77	k2	255/274 (93%)	254 (100%)	1 (0%)	84	89
All	All	9125/10469 (87%)	9009 (99%)	116 (1%)	59	74

5 of 116 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
49	W2	12	CYS
75	y2	125	VAL
59	g1	60	CYS
75	y2	105	PHE
72	u2	32	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
54	a1	22	HIS
74	x2	89	GLN
55	b1	7	HIS
65	k1	163	GLN
77	k2	215	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	A1	3068/4024 (76%)	392 (12%)	8 (0%)
18	C2	1471/1838 (80%)	202 (13%)	2 (0%)
62	i1	118/120 (98%)	10 (8%)	0
64	j1	146/161 (90%)	12 (8%)	0
All	All	4803/6143 (78%)	616 (12%)	10 (0%)

5 of 616 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
13	A1	5	G
13	A1	22	G
13	A1	26	A
13	A1	34	A
13	A1	40	A

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
13	A1	3743	U
18	C2	886	C
18	C2	1556	U
13	A1	1930	C
13	A1	1934	C

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 92 ligands modelled in this entry, 92 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.

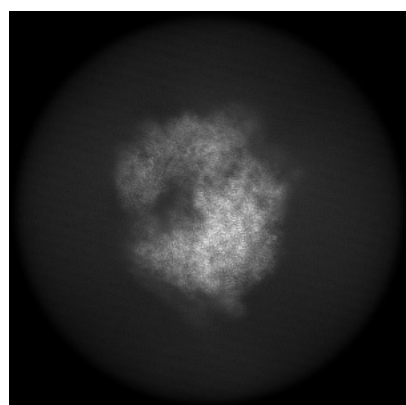
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66550. These allow visual inspection of the internal detail of the map and identification of artifacts.

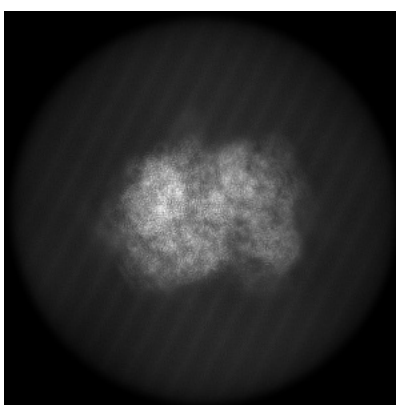
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

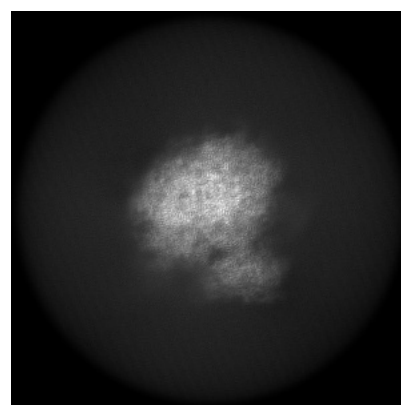
6.1.1 Primary map



X



Y

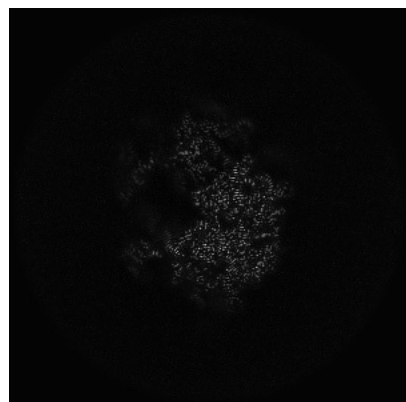


Z

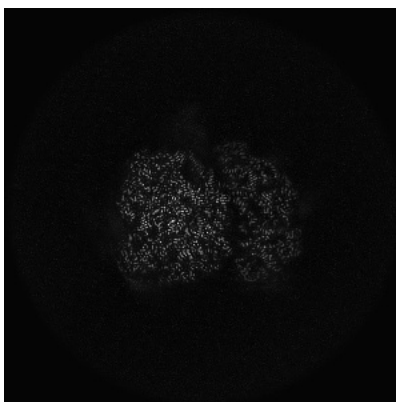
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

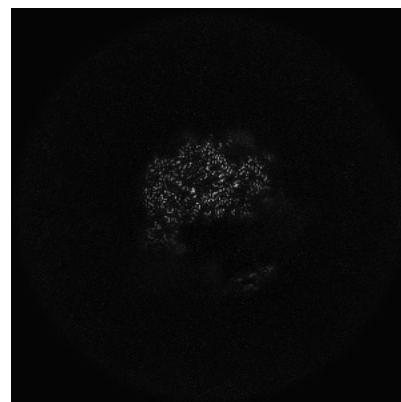
6.2.1 Primary map



X Index: 320



Y Index: 320

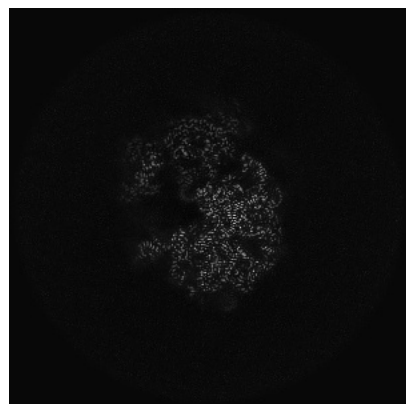


Z Index: 320

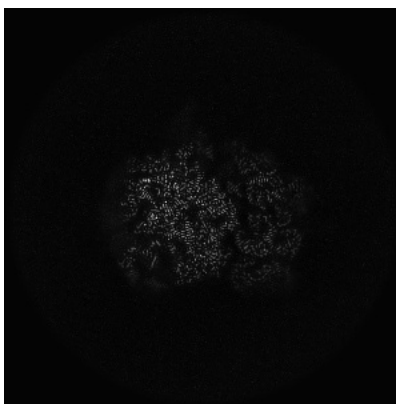
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

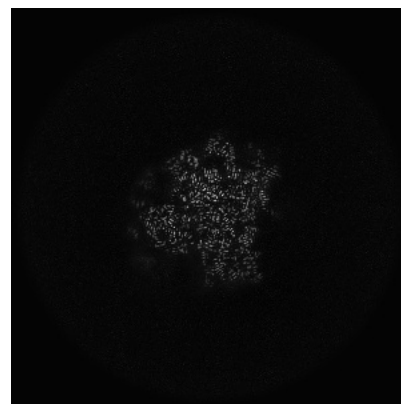
6.3.1 Primary map



X Index: 336



Y Index: 336

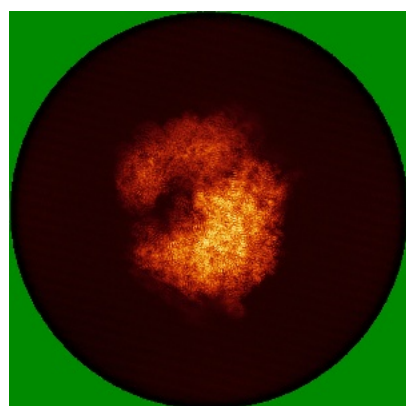


Z Index: 258

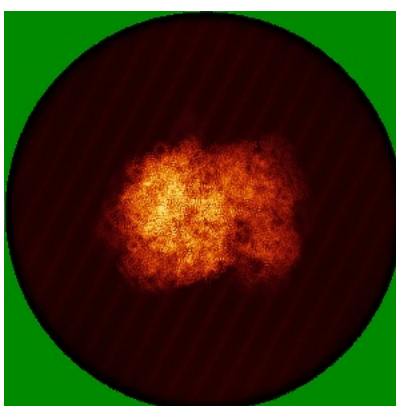
The images above show the largest variance slices of the map in three orthogonal directions.

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

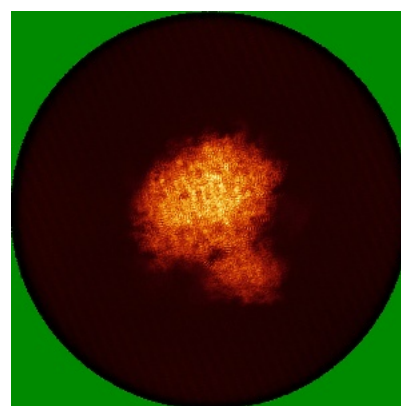
6.4.1 Primary map



X



Y

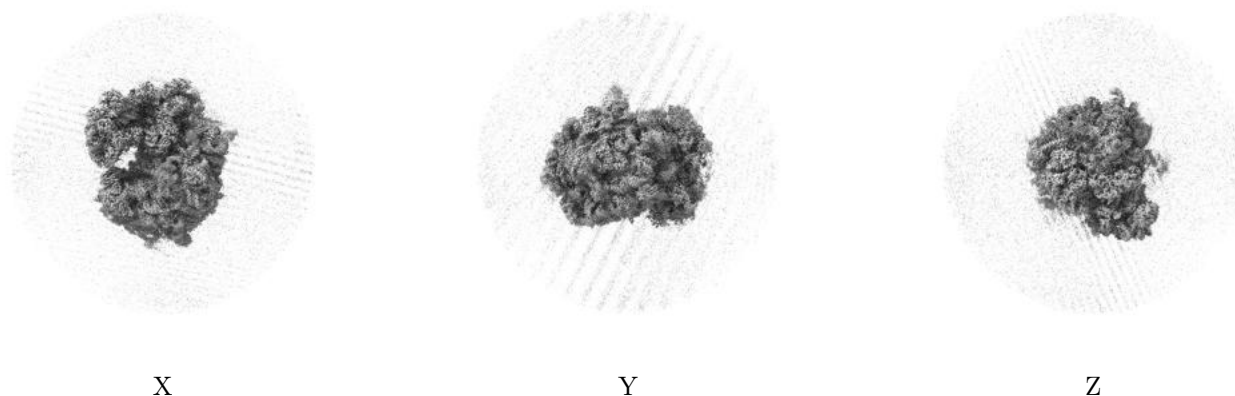


Z

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

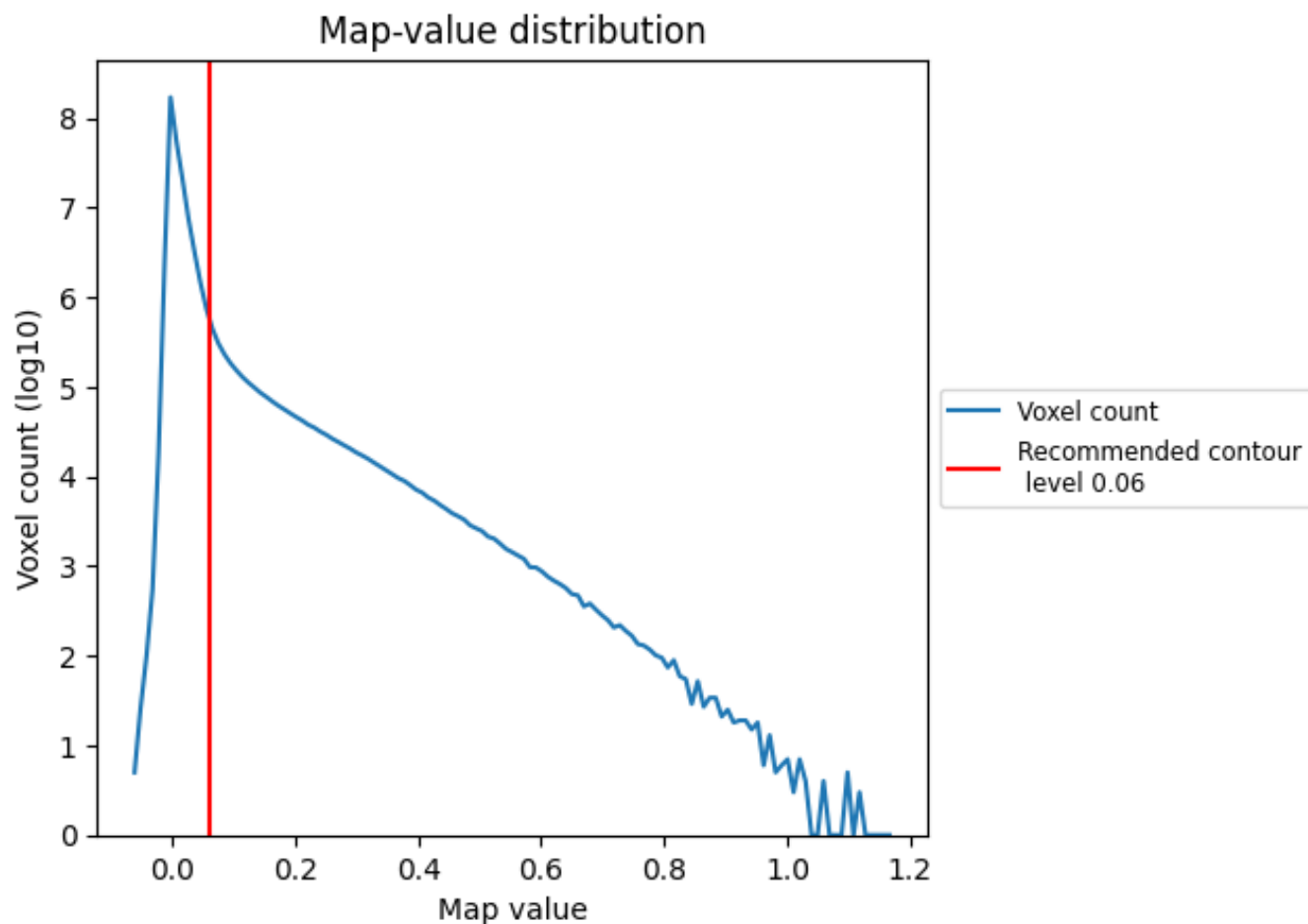
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

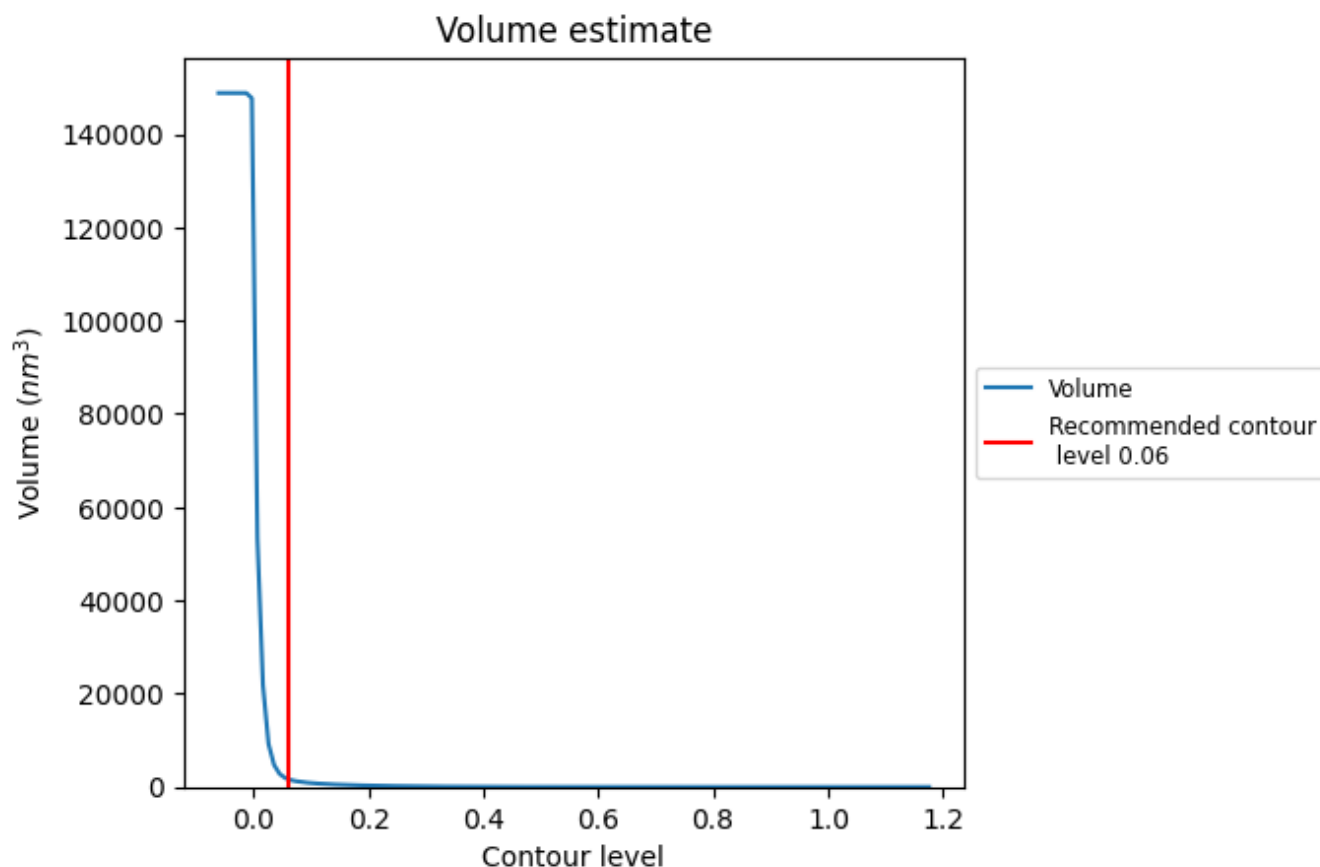
This section contains the results of statistical analysis of the map.

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.

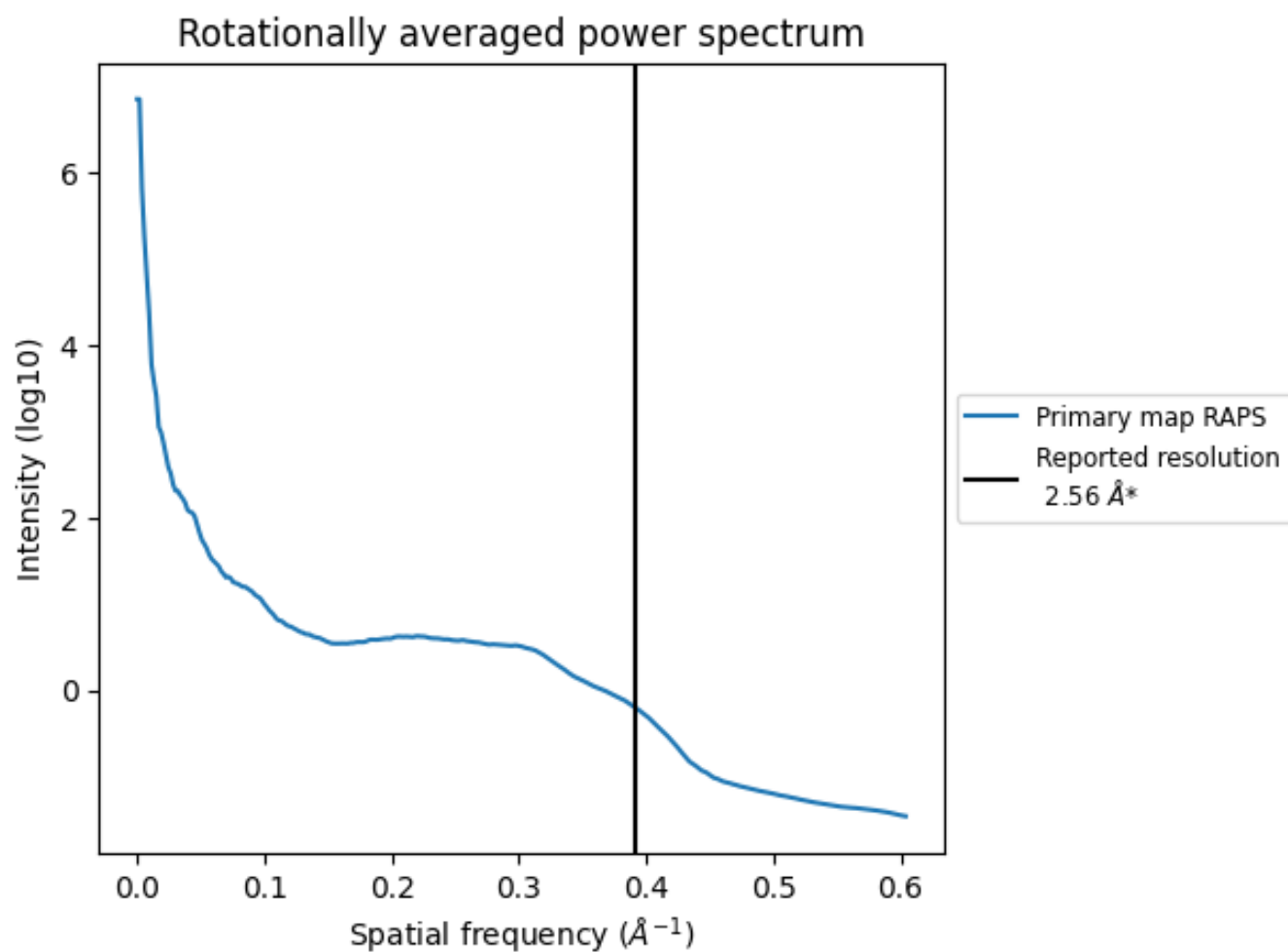
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1700 nm^3 ; this corresponds to an approximate mass of 1536 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 0.391 Å⁻¹

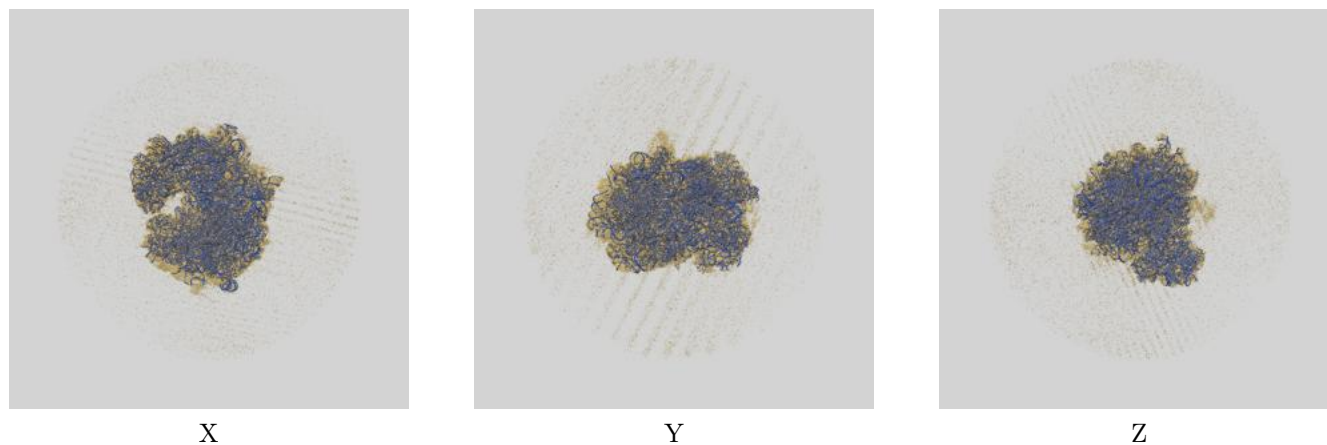
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

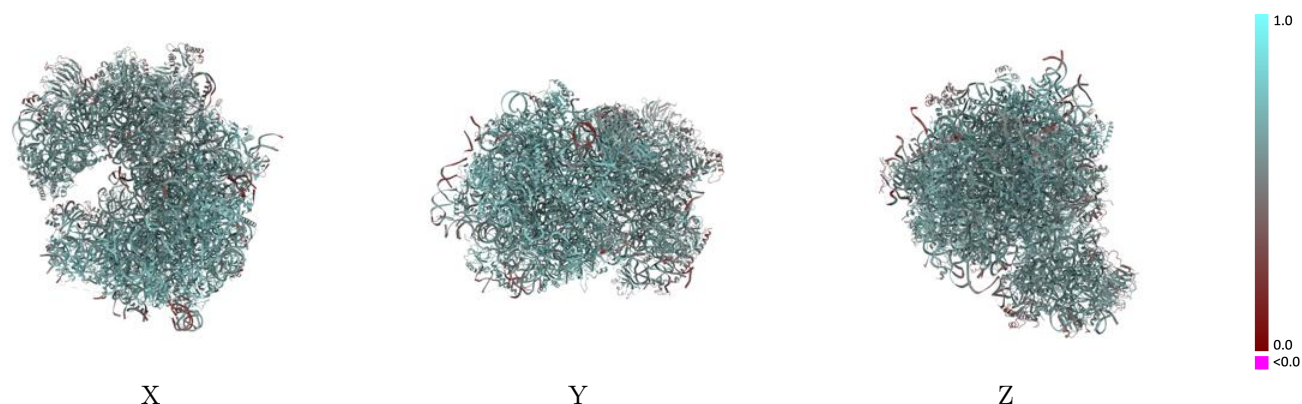
This section contains information regarding the fit between EMDB map EMD-66550 and PDB model 9X4I. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



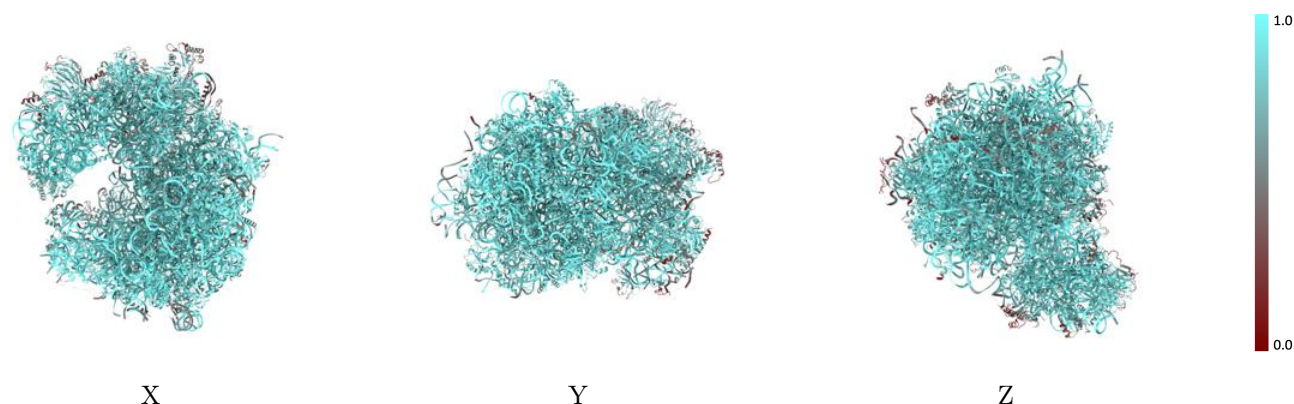
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



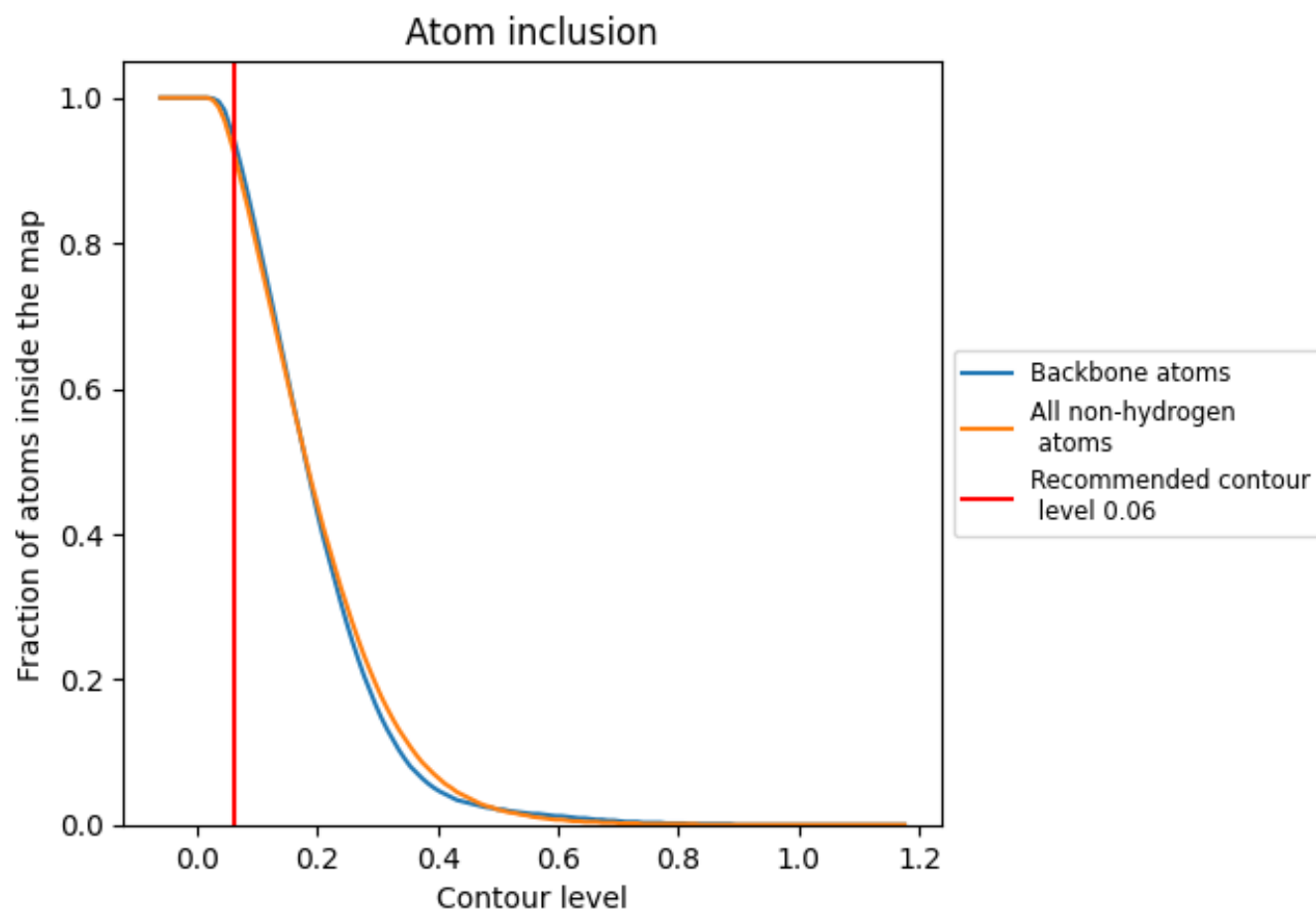
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9280	 0.6320
11	 0.9740	 0.6800
21	 0.6960	 0.5760
32	 0.7760	 0.5620
41	 0.9660	 0.6920
42	 0.7890	 0.5600
51	 0.8070	 0.5990
61	 0.6960	 0.4970
71	 0.7860	 0.5530
72	 0.8150	 0.5550
81	 0.9770	 0.7020
82	 0.6990	 0.5520
91	 0.9330	 0.6440
A1	 0.9620	 0.6440
A2	 0.7190	 0.5420
B1	 0.9690	 0.7020
B2	 0.8970	 0.6060
C1	 0.9690	 0.6980
C2	 0.9540	 0.6080
D1	 0.9560	 0.6690
E1	 0.9820	 0.7080
F1	 0.9470	 0.6900
H1	 0.9530	 0.6810
H2	 0.8480	 0.5850
I1	 0.9530	 0.6640
J1	 0.9900	 0.7120
J2	 0.9140	 0.6150
K1	 0.8480	 0.6160
K2	 0.8060	 0.5800
L1	 0.9430	 0.6750
L2	 0.8920	 0.5970
M1	 0.9670	 0.6780
M2	 0.8860	 0.5950
N1	 0.9980	 0.7280
N2	 0.9610	 0.6250



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Chain	Atom inclusion	Q-score
O1	 0.9380	 0.6730
O2	 0.9310	 0.6180
P1	 0.9820	 0.7140
P2	 0.7990	 0.5610
Q1	 0.9870	 0.7100
R1	 0.8740	 0.6350
S1	 0.9830	 0.7020
S2	 0.9520	 0.6270
T1	 0.9470	 0.6810
T2	 0.8680	 0.5710
U1	 0.6890	 0.4770
U2	 0.6450	 0.5120
V1	 0.9640	 0.6960
W1	 0.9680	 0.6960
W2	 0.6270	 0.5080
X1	 0.9590	 0.6890
Y1	 0.9630	 0.6920
Y2	 0.9100	 0.6270
Z1	 0.9450	 0.6650
a1	 0.9930	 0.7160
b1	 0.9710	 0.6720
d2	 0.8330	 0.5460
e1	 0.9640	 0.6850
f1	 0.9870	 0.7210
g1	 0.9630	 0.6670
g2	 0.8440	 0.5730
h1	 0.9110	 0.6440
i1	 0.9980	 0.6710
i2	 0.6930	 0.5170
j1	 0.9890	 0.6670
k1	 0.9210	 0.6310
k2	 0.7280	 0.5230
l1	 0.8660	 0.6250
m1	 0.9110	 0.6510
m2	 0.8110	 0.5690
n1	 0.9860	 0.7180
q2	 0.7170	 0.5260
r2	 0.9540	 0.6320
u2	 0.9220	 0.5890
w2	 0.7680	 0.5310
x2	 0.7610	 0.5570
y2	 0.9290	 0.6250

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Chain	Atom inclusion	Q-score
z2	 0.3560	 0.3820