



## wwPDB EM Validation Summary Report ⓘ

Jun 9, 2025 – 09:17 PM JST

PDB ID : 8ZFI / pdb\_00008zfi  
EMDB ID : EMD-60061  
Title : Structure of E.coli ribosome in complex with an engineered arrest peptide and trigger factor  
Authors : Sriramoju, M.K.; Ko, T.P.; Draczkowski, P.; Hsu, S.T.D.  
Deposited on : 2024-05-07  
Resolution : 2.90 Å(reported)  
Based on initial model : 3JBU

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev118  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

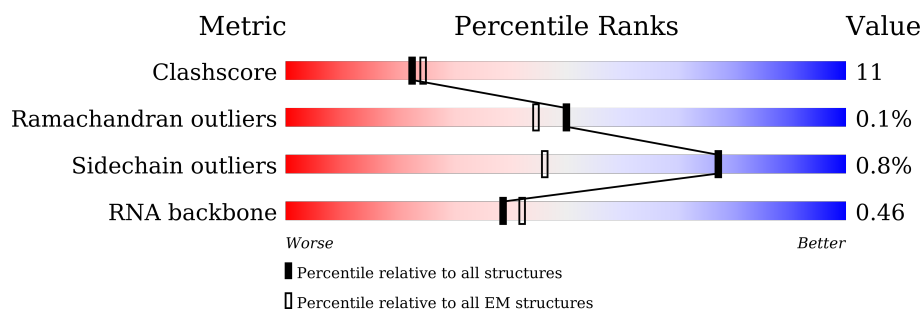
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	0	78	 76% 23% .
2	1	63	 63% 33% .
3	2	59	 81% 17% .
4	4	57	 70% 28% .
5	5	55	 80% 15% 5% .
6	6	46	 85% 15%
7	7	65	 78% 20% .










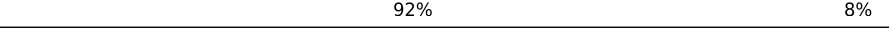

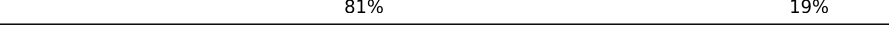







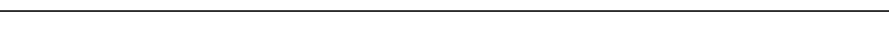

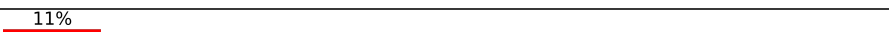
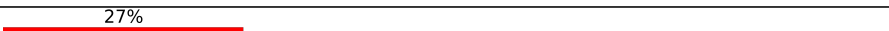


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Mol	Chain	Length	Quality of chain
8	8	38	
9	A	1533	
10	B	241	
11	C	233	
12	D	206	
13	E	167	
14	F	135	
15	G	179	
16	H	130	
17	I	130	
18	J	103	
19	K	129	
20	L	124	
21	M	118	
22	N	101	
23	O	89	
24	P	82	
25	Q	84	
26	R	75	
27	S	92	
28	T	87	
29	U	71	
30	X	76	
31	Y	77	
31	Z	77	

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Mol	Chain	Length	Quality of chain
32	a	120	
33	b	2904	
34	c	273	
35	d	209	
36	e	201	
37	f	179	
38	g	177	
39	h	149	
40	k	142	
41	l	123	
42	m	144	
43	n	136	
44	o	127	
45	p	117	
46	q	115	
47	r	118	
48	s	103	
49	t	110	
50	u	100	
51	v	104	
52	w	94	
53	x	14	
54	y	85	
55	z	49	
56	V	432	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
58	PRO	Z	163	-	-	X	-

## 2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 148019 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 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 2 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 3 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 4 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 5 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	5	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 6 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 7 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 8 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 9 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	1533	Total	C	N	O	P	0	0
			32895	14671	6036	10655	1533		

- Molecule 10 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 11 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	207	Total	C	N	O	S	0	0
			1632	1034	306	289	3		

- Molecule 12 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 13 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 14 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	106	Total	C	N	O	S	0	0
			862	545	156	154	7		

- Molecule 15 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 16 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 17 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 18 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	100	Total	C	N	O	S	0	0
			803	502	154	146	1		

- Molecule 19 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 20 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	122	Total	C	N	O	S	0	0
			949	587	195	163	4		

- Molecule 21 is a protein called 30S ribosomal protein S13.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 22 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 23 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 24 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 25 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 26 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 27 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 28 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 29 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	64	Total	C	N	O	S	0	0
			529	329	110	89	1		

- Molecule 30 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	76	Total	C	N	O	P	0	0
			1621	722	287	536	76		

- Molecule 31 is a RNA chain called P-site tRNA (Chain-Y), A-site tRNA-PRO (Chain-Z).

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Y	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		
31	Z	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		

- Molecule 32 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	120	Total	C	N	O	P	0	0
			2568	1144	468	837	119		

- Molecule 33 is a RNA chain called RNA (2903-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	2903	Total	C	N	O	P	0	0
			62321	27801	11467	20150	2903		

- Molecule 34 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 35 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 36 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 37 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	178	Total	C	N	O	S	0	0
			1419	905	251	257	6		

- Molecule 38 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 39 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 40 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 41 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 42 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 43 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 44 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 45 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	116	Total	C	N	O		0	0
			892	552	178	162			

- Molecule 46 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 47 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 48 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 49 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 50 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	u	100	Total	C	N	O	S	0	0
			786	496	146	142	2		

- Molecule 51 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	v	103	Total	C	N	O		0	0
			788	498	148	142			

- Molecule 52 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	w	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	14	Total	C	N	O	P	0	0
			299	133	55	97	14		

- Molecule 54 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	y	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 55 is a protein called eRAP-NC.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	39	Total	C	N	O	S	8	0
			398	260	72	64	2		

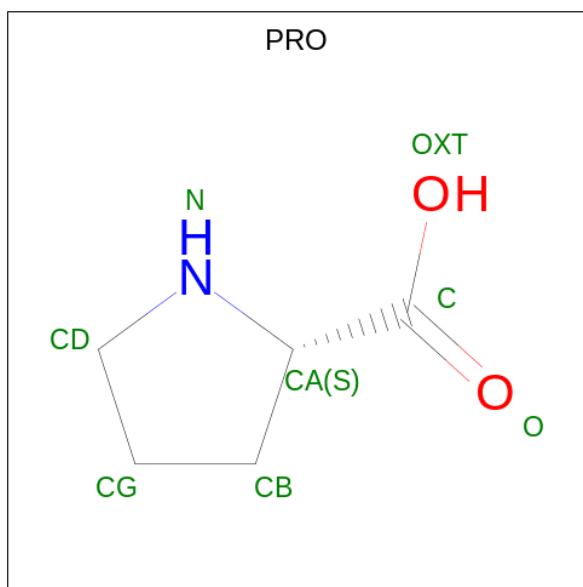
- Molecule 56 is a protein called Trigger factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	V	59	Total	C	N	O	S	0	0
			454	284	84	84	2		

- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	8	1	Total	Zn	0
			1	1	

- Molecule 58 is PROLINE (CCD ID: PRO) (formula: C<sub>5</sub>H<sub>9</sub>NO<sub>2</sub>).




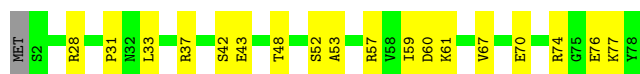
Mol	Chain	Residues	Atoms				AltConf
58	Z	1	Total	C	N	O	0
			7	5	1	1	

### 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: 50S ribosomal protein L28

Chain 0:  76% 23% .




- Molecule 2: 50S ribosomal protein L29

Chain 1:  63% 33% .



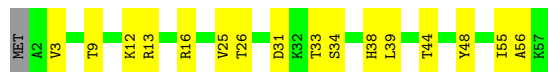
- Molecule 3: 50S ribosomal protein L30

Chain 2:  81% 17% .




- Molecule 4: 50S ribosomal protein L32

Chain 4:  70% 28% .




- Molecule 5: 50S ribosomal protein L33

Chain 5:  80% 15% 5% .




- Molecule 6: 50S ribosomal protein L34

Chain 6:  85% 15%




- Molecule 7: 50S ribosomal protein L35

Chain 7:  78% 20%



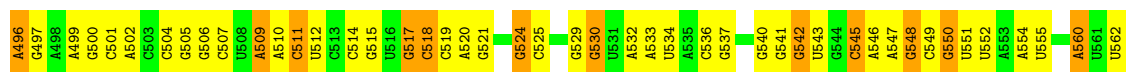
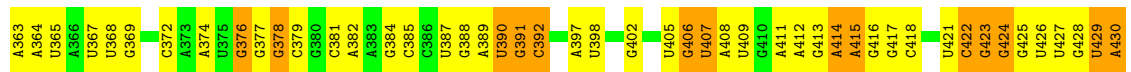
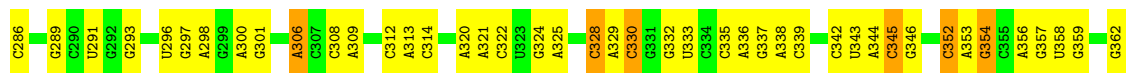
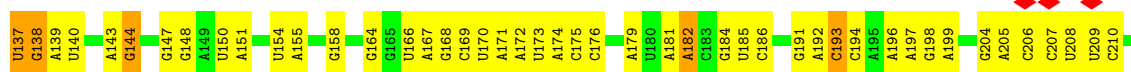
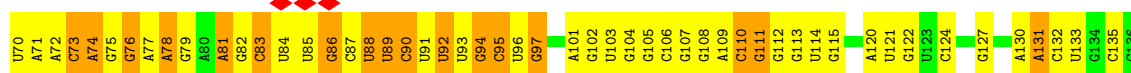
- Molecule 8: 50S ribosomal protein L36

Chain 8:  82% 18%

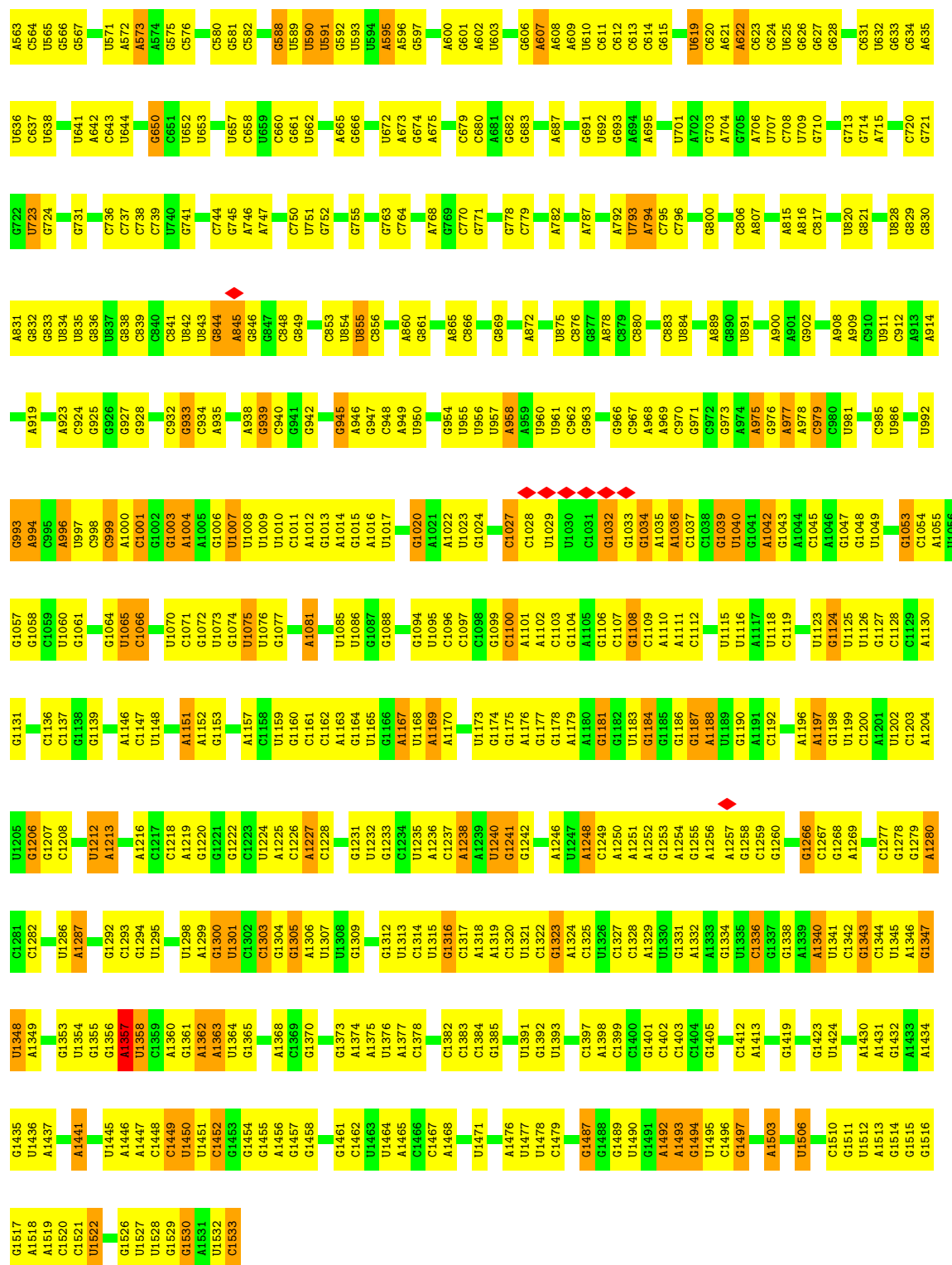


- Molecule 9: 16S rRNA

Chain A:  39% 49% 12%

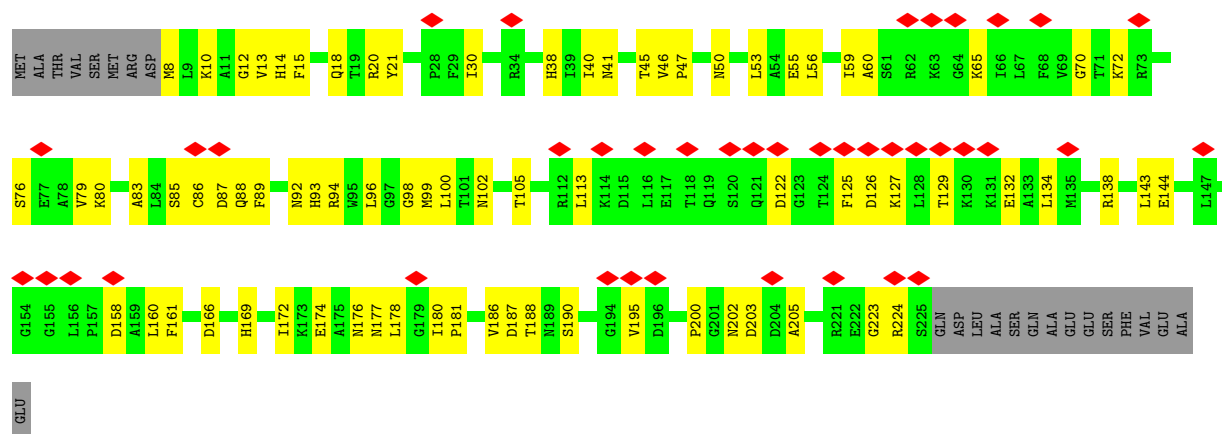






- Molecule 10: 30S ribosomal protein S2





• Molecule 11: 30S ribosomal protein S3

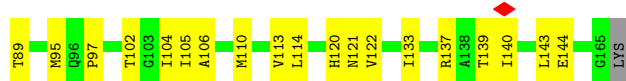


• Molecule 12: 30S ribosomal protein S4

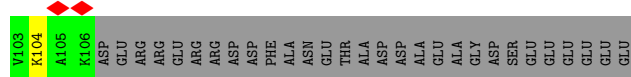
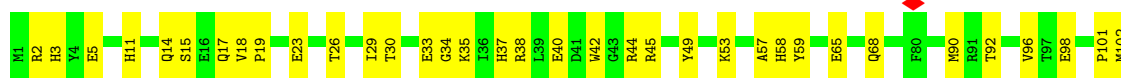


• Molecule 13: 30S ribosomal protein S5





- Molecule 14: 30S ribosomal protein S6, fully modified isoform



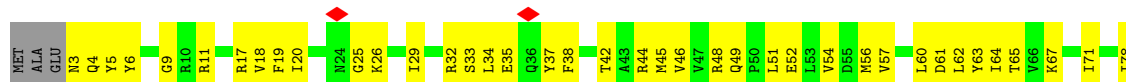
- Molecule 15: 30S ribosomal protein S7



- Molecule 16: 30S ribosomal protein S8

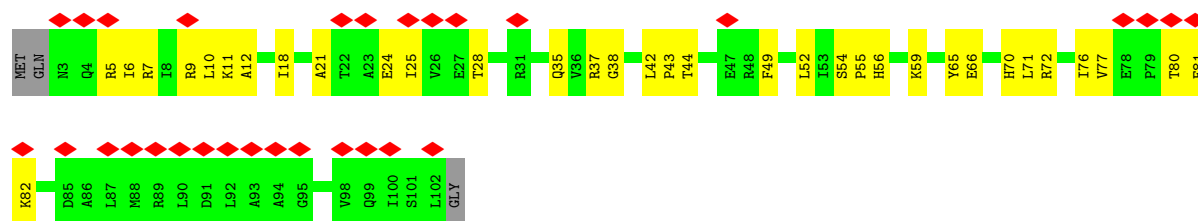


- Molecule 17: 30S ribosomal protein S9



- Molecule 18: 30S ribosomal protein S10

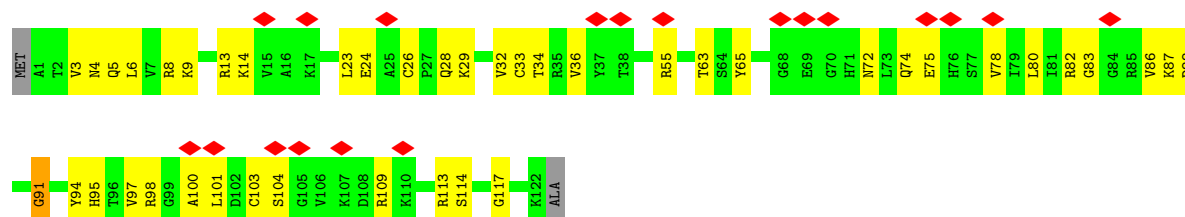




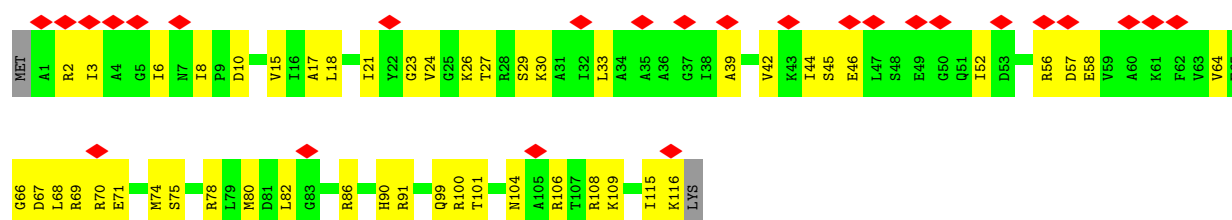
- Molecule 19: Small ribosomal subunit protein uS11



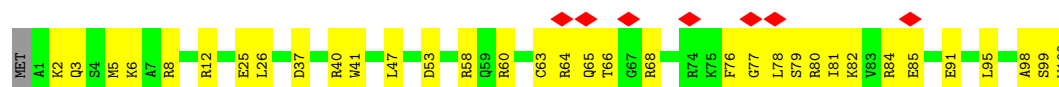
- Molecule 20: Small ribosomal subunit protein uS12



- Molecule 21: 30S ribosomal protein S13



- Molecule 22: 30S ribosomal protein S14



- Molecule 23: 30S ribosomal protein S15

Chain O:  64% 35%



- Molecule 24: 30S ribosomal protein S16

Chain P:  16% 63% 35%



- Molecule 25: 30S ribosomal protein S17

Chain Q:  68% 27% 5%



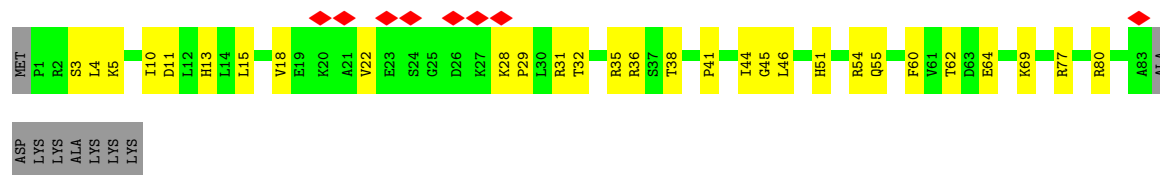
- Molecule 26: 30S ribosomal protein S18

Chain R:  15% 63% 25% 12%



- Molecule 27: 30S ribosomal protein S19

Chain S:  9% 59% 32% 10%

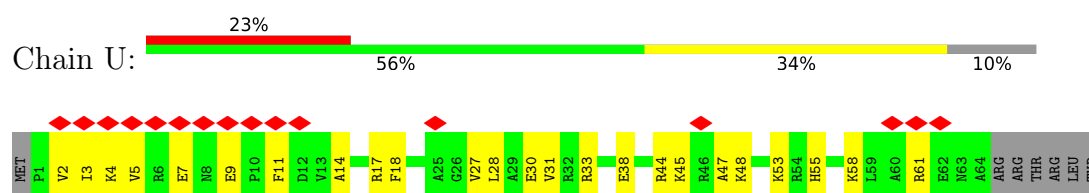


- Molecule 28: 30S ribosomal protein S20

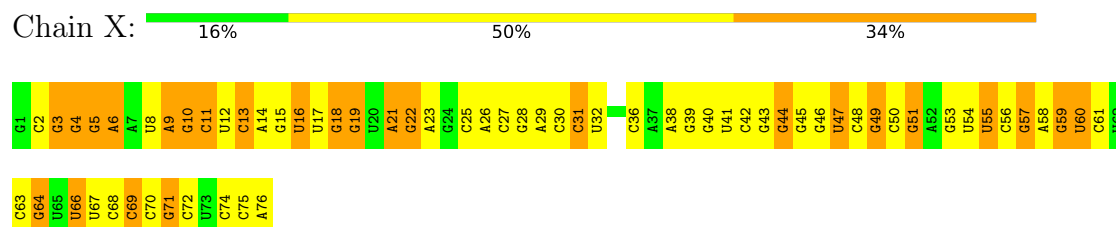
Chain T:  47% 52%



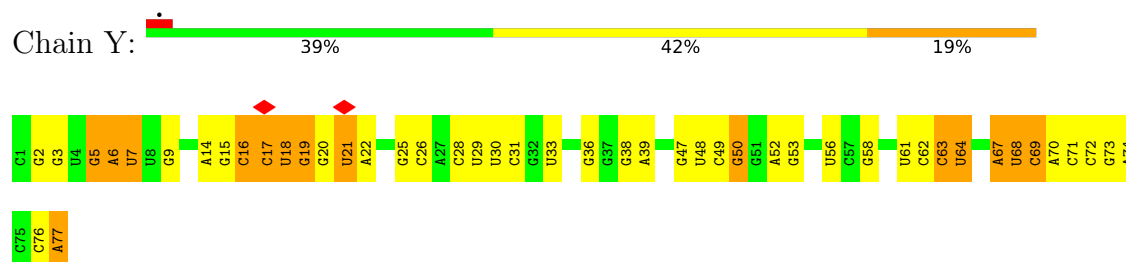
- Molecule 29: 30S ribosomal protein S21



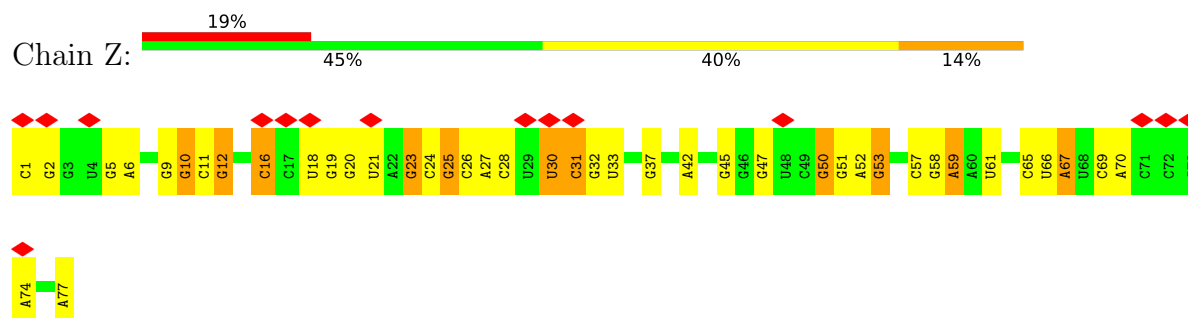
- Molecule 30: E-site tRNA



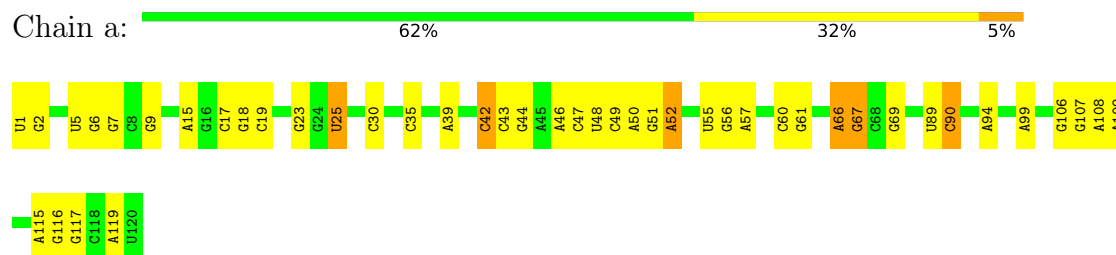
- Molecule 31: P-site tRNA (Chain-Y), A-site tRNA-PRO (Chain-Z)



- Molecule 31: P-site tRNA (Chain-Y), A-site tRNA-PRO (Chain-Z)



- Molecule 32: 5S rRNA



- Molecule 33: RNA (2903-MER)




U1506	U1412	G1300	U1173	U1081	C1007	U895	A793	C678	U573	A480	U365	G248	G110	G1
C1507	A1413	A1301	U1174	U1082	A1008	A896	A794	C679	A574	G481	U366	C249	A118	G2
A1508	G1416	U1175	U1083	U1083	A1009	C897	C795	C679	A575	A482	G367	G250	A119	U3
A1509	C1417	A1084	U1176	A1084	U1012	C898	G801	G682	U580	A483	A368	A251	U120	U4
G1510	C1418	A1085	G1177	A1085	C1013	A899	G801	G682	C581	C487	U369	A255	A125	A5
G1511	A1419	U1315	G1178	A1086	A1014	C901	G805	U686	A582	G491	G370	G263	G9	G9
G1514	A1420	U1317	U1180	A1088	A1014	C902	G809	G690	A586	G491	A371	C264	A10	A10
G1519	G1421	U1318	U1181	A1089	U1019	A910	G809	G690	A587	G491	G372	C265	C128	G11
U1520	G1422	C1320	G1186	A1090	A1020	A911	C812	G701	U588	G495	G376	A266	A19	U18
G1523	G1425	C1321	G1187	A1091	A1021	C912	U813	G701	U589	G495	G377	G267	A131	U19
G1524	A1427	A1322	G1195	C1092	U1023	U913	C814	G704	A590	U499	C385	C268	G133	G27
A1525	C1428	G1332	G1196	U1094	G1024	G914	A819	A705	U593	G500	G386	G271	G134	A28
G1530	G1433	G1337	U1197	A1095	G1025	C915	U826	A706	U594	A503	U387	A272	U135	G35
C1531	A1434	U1338	U1198	A1096	G1026	G916	U827	U709	C595	A505	G388	G276	G140	G39
A1532	G1435	U1339	U1199	A1097	U1033	A927	U828	G713	U596	A508	U389	G277	A142	U40
C1533	G1436	U1340	A1204	A1098	G1034	G930	A845	U714	A603	C509	U391	A278	A152	C41
U1534	C1437	U1341	A1205	A1103	U1035	U931	U846	U715	G604	C510	G392	A279	A153	A42
A1535	U1438	U1342	G1206	C1104	A1039	U932	U847	A716	U604	C511	C393	U280	U154	G45
C1536	A1439	U1352	G1210	U1105	A1040	A933	A849	A717	A608	U511	C394	C281	A155	G46
G1537	U1443	U1357	G1223	U1106	G1041	G938	U850	A718	A609	G512	U395	A282	A156	C47
U1538	G1444	G1358	U1224	G1107	G1042	A941	C851	C719	A609	A513	G396	U284	G48	G48
G1540	G1445	G1361	U1234	U1108	G1047	A942	U852	U720	A613	U521	A404	G285	C163	G51
C1541	C1461	C1362	G1235	A1110	A1048	C946	G856	A722	A614	A522	G406	U286	A165	A52
G1543	G1469	A1365	G1236	A1111	C1053	A947	G857	C723	U615	C523	G407	U287	A172	A53
A1548	A1470	A1366	G1237	U1112	G1054	C948	G858	G726	A621	A529	G411	G289	A173	G61
A1549	G1471	C1370	G1238	U1113	C1055	G952	G859	G729	G622	C530	A412	U290	A178	U62
A1552	G1475	G1371	A1241	C1115	A1056	U955	A866	A730	C624	A532	C413	G295	G178	A63
A1553	U1476	G1260	G1250	G1116	G1057	G956	G874	U747	A627	U534	C414	G296	G180	A64
C1558	U1481	A1253	A1253	G1125	A1058	A859	U870	G748	U639	U545	U416	G297	A181	U65
G1560	G1482	A1254	A1254	A1126	U1059	A960	U871	G748	C640	U546	C417	G298	A182	A71
C1561	G1483	G1255	U1255	U1132	U1060	C961	U872	G757	C635	A538	U418	C305	C183	G74
U1562	U1484	A1384	G1256	A1133	U1061	A972	G880	C765	U642	G548	U419	U306	C208	U82
A1566	U1485	A1385	U1263	A1134	G1062	C964	G881	C765	A643	G549	C420	G307	C209	A83
G1567	U1486	A1386	U1263	C1135	G1063	G974	G882	G774	A644	C550	A430	A347	G215	A84
A1569	U1487	A1387	G1266	G1136	U1064	G969	U884	G775	C645	G555	C445	U349	A216	G88
C1575	G1492	U1394	U1267	U1141	U1065	U970	C885	G776	U646	A566	U451	C353	A221	G89
U1576	C1493	A1395	A1268	A1142	U1066	G971	A886	G776	U647	C557	U451	A354	A222	A91
C1577	A1494	U1396	G1270	G1150	A1067	A972	U887	G780	U653	C557	U457	U355	A223	G98
U1578	A1495	U1397	G1271	C1150	G1068	G974	C888	A782	A655	C560	A457	G356	C228	U99
G1584	U1496	A1403	U1273	C1153	G1070	A881	C889	A783	G656	A563	G473	C357	C229	U100
C1585	A1497	U1406	A1276	A1156	C1071	A984	C890	G784	U657	U568	G474	U358	A233	A101
A1586	C1498	G1407	G1281	G1158	C1075	A984	C891	G785	U658	A572	C475	G359	A233	U102
G1587	G1501	G1408	U1282	A1159	A1077	A996	C892	G785	U658	A572	C475	G361	G247	A103
U1588	A1502	U1409	G1292	G1170	U1078	U999	C893	G785	U658	A572	C475	G361	G247	A103
A1590	A1505	U1411	C1293	C1172	A1080	C1006	U894	A792	A670	A572	A479	G361	G247	A103

U1591	U1742	C1843	G1954	G2069	G2143	A2212	U2320	C2440	U2562	G2686	G2801
U1743	G1743	C1844	U1955	A2070	A2142	A2212	U2321	U2441	U2563	U2687	G2802
A1596	A1744	A1847	C1957	C2072	G2143	C2214	A2322	G2444	A2564	G2688	G2803
A1597	A1745	A1848	C1958	U2076	C2145	C2214	U2324	G2447	A2566	U2689	U2807
U1598	U1746	U1851	C1959	U2077	C2146	G2221	C2326	A2448	G2567	U2690	G2808
U1599	U1747	U1852	A1960	A2077	A2147	C2222	A2327	A2449	G2570	U2698	
C1600	A1754	U1853	U1963	C2078	G2148	A2225	A2328	A2450	U2571	A2711	A2813
C1607	U1758	A1854	C1964	C2079	U2149	A2233	U2329	G2455	A2572	C2712	A2814
A1608	U1759	G1857	C1965	A2088	U2150	U2233	A2332	G2456	G2576	U2713	A2820
A1609	U1762	A1858	A1966	C2089	U2151	G2234	A2333	A2459	G2581	G2714	A2823
A1610	A1763	U1862	C1967	G2093	C2152	G2238	U2334	G2467	G2582	C2723	
U1629	C1764	A1969	G1968	C2096	A2154	G2239	A2335	A2468	G2583	U2724	U2833
A1630	U1769	A1870	A1970	C2097	U2155	U2244	A2336	A2469	U2584	A2726	G2834
U1636	G1770	A1871	U1971	U2098	G2156	U2245	G2345	A2476	G2585	A2727	A2835
A1637	C1771	A1872	G1972	U2099	A2157	G2246	A2346	G2481	G2586	A2728	U2836
U1646	A1772	G1873	A1977	G2100	C2159	A2247	C2347	G2484	G2587	U2731	A2837
U1647	A1773	C1874	U1991	G2101	G2160	G2248	U2348	G2497	A2598	G2732	G2838
U1648	G1776	A1875	G1992	C2102	C2161	G2249	G2349	G2502	A2602	A2733	C2840
U1649	U1779	A1876	U1993	C2103	A2162	G2250	C2350	G2504	U2609	A2737	G2846
C1656	U1783	U1880	C1996	U2104	C2163	G2251	G2357	G2498	A2613	A2738	G2847
U1657	A1784	U1883	C1997	U2106	G2166	G2255	G2361	A2497	A2615	U2739	G2848
G1667	U1789	A1884	U2014	G2107	G2167	A2267	G2373	G2502	U2616	A2740	U2849
G1674	A1790	A1885	A2015	U2108	A2169	A2272	G2374	G2504	G2617	G2741	G2854
C1675	A1791	U1888	A2020	U2109	A2171	A2273	A2377	G2505	U2617	G2744	C2858
G1703	U1796	A1901	A2023	U2110	U2111	C2279	A2381	U2513	U2618	C2745	C2859
C1704	G1797	G1906	C2023	U2112	U2112	C2283	G2382	U2514	U2619	U2746	A2860
A1705	U1798	G1907	C2025	A2113	A2114	A2284	U2383	G2515	U2629	G2747	U2861
U1712	G1799	G1907	U2026	G2115	G2115	A2285	U2384	A2516	U2630	A2748	G2867
A1713	C1800	A1913	U2026	G2116	A2116	G2286	G2385	G2517	G2635	C2752	A2868
U1716	A1801	C1914	A2031	U2117	U2118	A2287	C2386	G2518	A2635	C2755	A2873
U1721	A1802	U1915	G2032	U2118	A2119	A2288	A2387	G2519	U2638	A2758	C2880
G1722	A1803	A1916	A2033	U2119	G2120	G2289	G2388	C2520	G2638	C2771	A2882
G1723	A1804	U1917	A2036	U1917	G2121	U2290	U2402	C2521	U2647	C2772	A2883
G1724	A1805	A1918	A2037	A1918	G2122	U2291	G2405	U2522	U2650	C2773	U2884
U1725	A1808	A1919	C2043	A1919	A2183	U2292	A2406	G2529	C2651	A2776	G2885
C1726	A1809	C1924	G2055	U2125	A2186	G2293	A2407	G2535	G2655	G2777	A2886
C1727	U1810	C1925	G2056	G2126	U2187	U2302	A2412	G2545	U2656	A2778	U2891
C1728	G1811	U1926	A2060	G2127	U2188	G2303	G2413	U2546	U2657	U2779	G2892
U1729	U1816	A1927	A2062	G2128	U2189	G2304	A2422	A2547	G2668	U2790	A2893
C1730	U1816	A1928	G2065	G2129	U2190	G2305	U2423	U2548	G2671	G2791	C2896
G1733	U1820	G1929	G2066	U2130	A2191	U2306	C2424	U2549	U2672	C2795	U2897
G1734	G1826	U1930	A2066	U2131	U2192	G2307	A2425	U2555	U2673	U2796	U2898
U1827	U1827	U1931	C2067	U2132	G2193	G2308	A2426	C2556	A2682	U2797	A2900
G1828	G1828	A1936	C2068	A2133	U2194	G2309	A2427	G2557	U2683	U2798	C2901
A1735	A1829	A1937	C2069	G2135	U2195	U2312	C2428	C2558	U2684	A2799	U2903
U1736	A1937	A1938	C2066	U2136	C2200	C2313	G2429	G2561	G2685		
G1737	G1830	A1938	C2067	U2137	U2203	C2314	A2430				
G1738	G1832	U1943	U2068	U2138	U2204	C2315					

U

• Molecule 34: 50S ribosomal protein L2

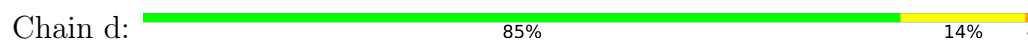
Chain c:  79% 20%

NET	M128	U2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
A2	U129	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
C6	U130	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
K7	P131	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
R13	M132	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
V20	U141	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
E23	H142	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
K28	M143	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
P29	U144	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
F30	H145	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
A31	M146	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
P32	U147	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
L33	H148	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
L34	M149	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
M45	U149	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
K71	H150	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
P75	M151	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
A89	U152	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
L93	H153	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
K97	M154	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
R101	U155	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
L110	H156	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
D114	M157	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
Q117	U156	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
S118	H157	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
A122	M158	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
M128	U157	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
T129	H158	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
L130	M159	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
P131	U158	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
M132	H159	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
I135	M160	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
V141	U159	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
M143	H160	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
M146	M161	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
G152	U160	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
C2902	H161	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900
S157	M162	G2891	G2892	A2893	U2894	G2895	U2896	A2897	U2898	G2899	U2900

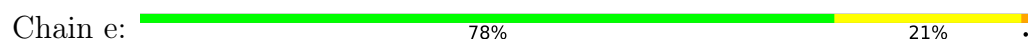




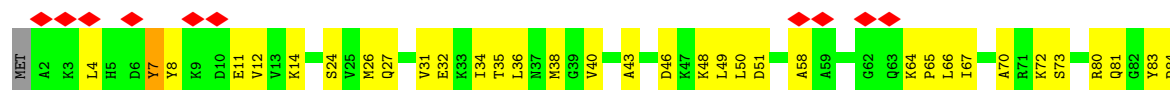
- Molecule 35: 50S ribosomal protein L3



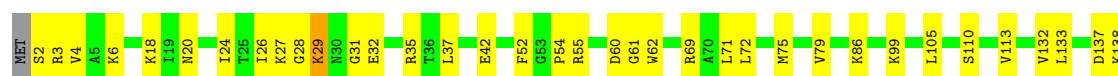
- Molecule 36: 50S ribosomal protein L4



- Molecule 37: 50S ribosomal protein L5

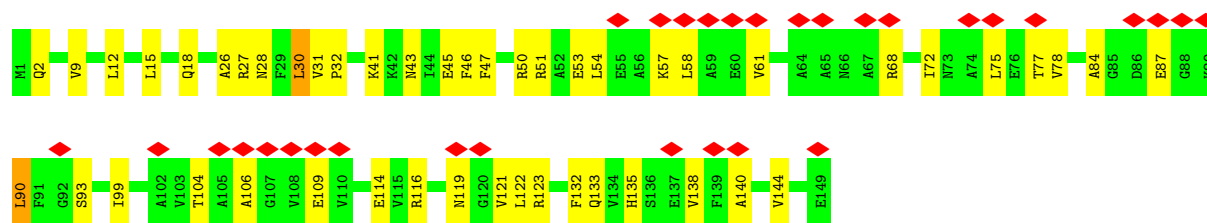


- Molecule 38: 50S ribosomal protein L6



- Molecule 39: 50S ribosomal protein L9





- Molecule 40: 50S ribosomal protein L13

Chain k: 87% 13%



- Molecule 41: 50S ribosomal protein L14

Chain l: 92% 8%



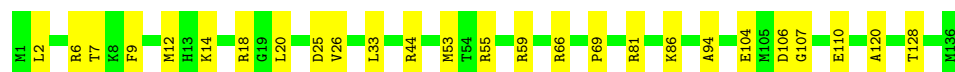
- Molecule 42: 50S ribosomal protein L15

Chain m: 81% 19%



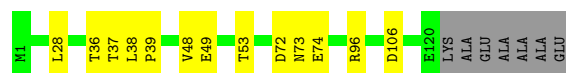
- Molecule 43: 50S ribosomal protein L16

Chain n: 81% 19%



- Molecule 44: 50S ribosomal protein L17

Chain o: 84% 10% 6%

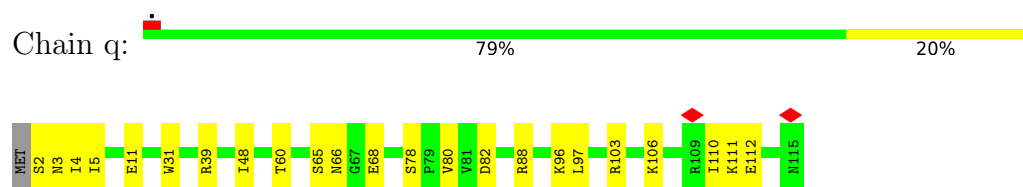


- Molecule 45: 50S ribosomal protein L18

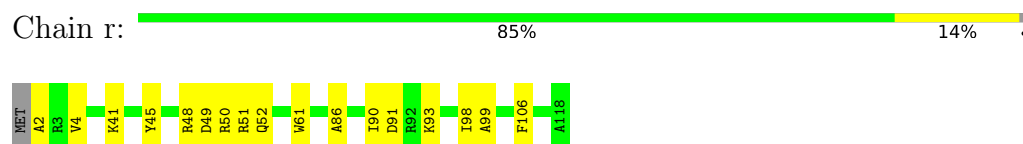
Chain p: 83% 16%



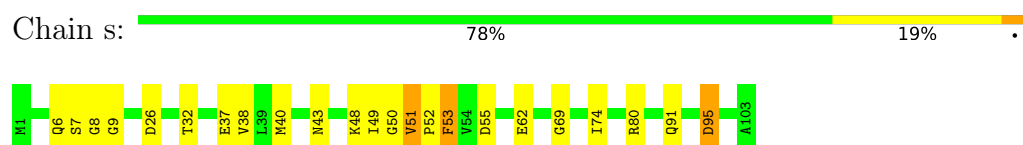
- Molecule 46: 50S ribosomal protein L19



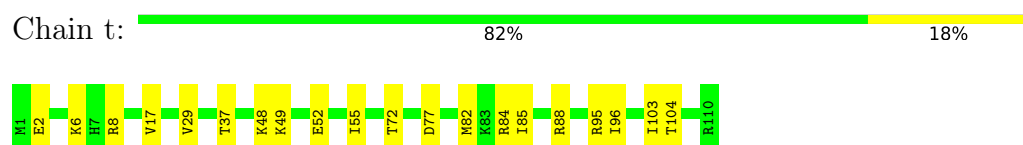
- Molecule 47: 50S ribosomal protein L20



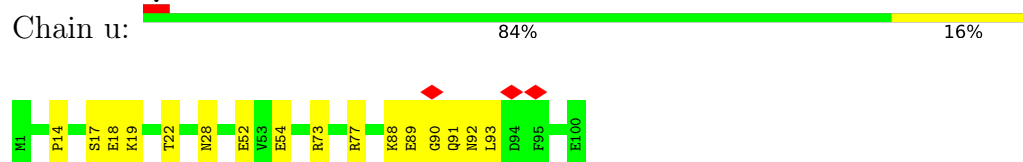
- Molecule 48: 50S ribosomal protein L21



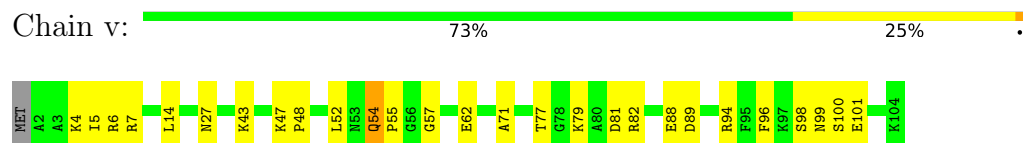
- Molecule 49: 50S ribosomal protein L22



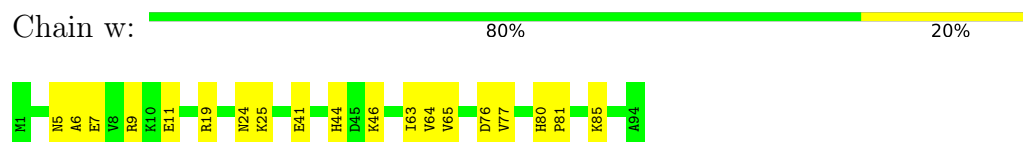
- Molecule 50: 50S ribosomal protein L23

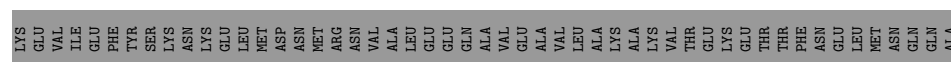
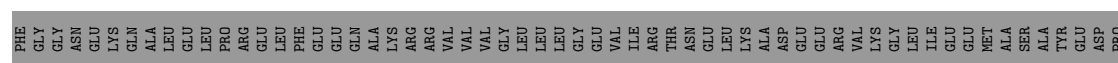
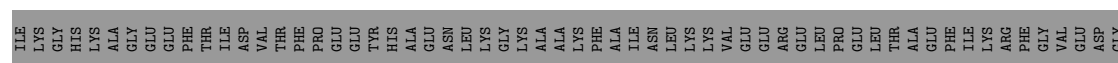
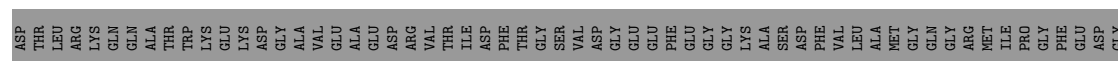
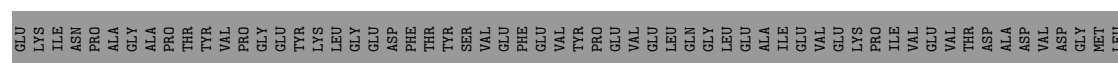
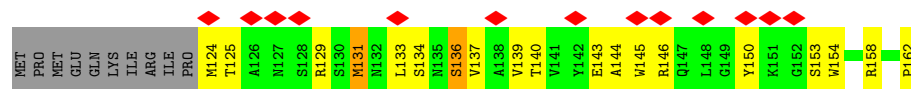
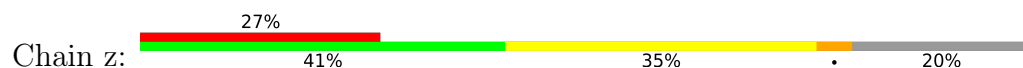
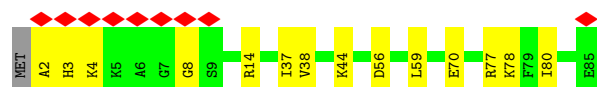
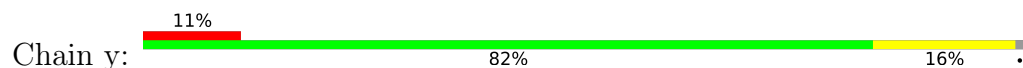


- Molecule 51: 50S ribosomal protein L24



- Molecule 52: 50S ribosomal protein L25





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	145326	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 ( $e^-/\text{\AA}^2$ )	38	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.007	Depositor
Minimum map value	-0.742	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.069	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	528.0, 528.0, 528.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:  
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	0	0.28	0/635	0.34	0/848
2	1	0.25	0/496	0.37	0/660
3	2	0.29	0/453	0.37	0/605
4	4	0.33	0/450	0.37	0/599
5	5	0.22	0/433	0.32	0/576
6	6	0.33	0/380	0.36	0/498
7	7	0.31	0/513	0.31	0/676
8	8	0.32	0/303	0.29	0/397
9	A	0.16	0/36834	0.28	1/57462 (0.0%)
10	B	0.12	0/1735	0.31	0/2338
11	C	0.12	0/1659	0.29	0/2236
12	D	0.13	0/1665	0.30	0/2227
13	E	0.15	0/1169	0.34	0/1573
14	F	0.14	0/881	0.30	0/1189
15	G	0.11	0/1219	0.25	0/1635
16	H	0.17	0/989	0.34	0/1326
17	I	0.19	0/1034	0.35	0/1375
18	J	0.14	0/813	0.37	0/1100
19	K	0.16	0/893	0.31	0/1205
20	L	0.19	0/963	0.39	0/1293
21	M	0.13	0/909	0.30	0/1215
22	N	0.12	0/817	0.26	0/1088
23	O	0.14	0/722	0.28	0/964
24	P	0.11	0/653	0.27	0/877
25	Q	0.13	0/657	0.34	0/881
26	R	0.12	0/553	0.28	0/742
27	S	0.12	0/680	0.34	0/915
28	T	0.17	0/676	0.30	0/895
29	U	0.15	0/536	0.39	0/711
30	X	0.22	0/1810	0.32	0/2820
31	Y	0.15	0/1840	0.29	0/2866
31	Z	0.18	0/1840	0.28	0/2866

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	a	0.27	0/2869	0.28	0/4474
33	b	0.34	0/69800	0.32	1/108892 (0.0%)
34	c	0.32	0/2121	0.38	0/2852
35	d	0.37	1/1586 (0.1%)	0.45	2/2134 (0.1%)
36	e	0.32	0/1571	0.33	0/2113
37	f	0.25	0/1443	0.52	2/1937 (0.1%)
38	g	0.22	0/1333	0.29	0/1805
39	h	0.30	0/1121	0.42	0/1515
40	k	0.33	0/1152	0.32	0/1551
41	l	0.28	0/955	0.39	0/1279
42	m	0.29	0/1062	0.37	0/1413
43	n	0.28	0/1093	0.34	0/1460
44	o	0.30	0/973	0.33	0/1301
45	p	0.21	0/902	0.29	0/1209
46	q	0.27	0/929	0.30	0/1242
47	r	0.35	0/960	0.32	0/1278
48	s	0.31	0/829	0.43	0/1107
49	t	0.33	0/864	0.31	0/1156
50	u	0.27	0/793	0.35	0/1060
51	v	0.56	2/796 (0.3%)	0.40	0/1062
52	w	0.25	0/766	0.33	0/1025
53	x	0.13	0/333	0.28	0/517
54	y	0.31	0/642	0.33	0/848
55	z	0.36	0/416	0.61	1/569 (0.2%)
56	V	0.40	0/457	0.70	0/612
All	All	0.28	3/160976 (0.0%)	0.32	7/241069 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	v	54	GLN	C-O	-12.92	1.17	1.23
35	d	152	PRO	CG-CD	-7.24	1.26	1.50
51	v	54	GLN	CA-C	5.31	1.57	1.53

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	d	152	PRO	N-CD-CG	10.27	118.60	103.20
35	d	152	PRO	CA-N-CD	-7.25	101.85	112.00
9	A	1357	A	C2'-C3'-O3'	6.34	123.21	113.70
33	b	2571	U	C3'-C2'-O2'	5.13	118.39	110.70
37	f	4	LEU	CA-C-N	-5.11	110.76	121.64

There are no chirality outliers.

There are no planarity outliers.

## 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	0	625	0	652	14	0
2	1	495	0	526	14	0
3	2	449	0	488	7	0
4	4	444	0	458	14	0
5	5	426	0	464	6	0
6	6	377	0	418	5	0
7	7	504	0	572	7	0
8	8	302	0	341	4	0
9	A	32895	0	16553	715	0
10	B	1704	0	1732	58	0
11	C	1632	0	1710	59	0
12	D	1643	0	1710	80	0
13	E	1156	0	1199	33	0
14	F	862	0	864	33	0
15	G	1203	0	1256	39	0
16	H	979	0	1034	49	0
17	I	1022	0	1070	79	0
18	J	803	0	842	38	0
19	K	877	0	887	34	0
20	L	949	0	1014	43	0
21	M	900	0	968	38	0
22	N	805	0	847	37	0
23	O	714	0	737	27	0
24	P	643	0	661	22	0
25	Q	648	0	691	19	0
26	R	544	0	565	15	0
27	S	663	0	690	28	0
28	T	670	0	722	39	0
29	U	529	0	565	20	0
30	X	1621	0	820	63	0
31	Y	1647	0	832	43	0
31	Z	1647	0	832	32	0
32	a	2568	0	1302	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	b	62321	0	31344	686	0
34	c	2082	0	2154	43	0
35	d	1565	0	1616	27	0
36	e	1552	0	1619	57	0
37	f	1419	0	1457	73	0
38	g	1313	0	1358	34	0
39	h	1110	0	1148	44	0
40	k	1129	0	1162	14	0
41	l	946	0	1023	9	0
42	m	1053	0	1129	19	0
43	n	1074	0	1157	22	0
44	o	960	0	1000	9	0
45	p	892	0	923	15	0
46	q	917	0	962	19	0
47	r	947	0	1019	14	0
48	s	816	0	839	33	0
49	t	857	0	922	21	0
50	u	786	0	846	16	0
51	v	788	0	844	18	0
52	w	753	0	780	14	0
53	x	299	0	154	6	0
54	y	634	0	653	16	0
55	z	398	0	372	35	0
56	V	454	0	476	30	0
57	8	1	0	0	0	0
58	Z	7	0	7	4	0
All	All	148019	0	98986	2676	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 2676 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)
36:e:5:LEU:CD2	36:e:8:ALA:HB3	1.60	1.29
48:s:51:VAL:HB	48:s:52:PRO:CD	1.60	1.29
56:V:19:ILE:HG22	56:V:23:SER:CB	1.68	1.23
31:Y:77:A:O3'	55:z:162:PRO:C	1.88	1.15
31:Z:77:A:HO3'	58:Z:163:PRO:C	1.52	1.15

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
2	1	59/63 (94%)	57 (97%)	2 (3%)	0	100	100
3	2	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
4	4	54/57 (95%)	45 (83%)	9 (17%)	0	100	100
5	5	50/55 (91%)	48 (96%)	2 (4%)	0	100	100
6	6	44/46 (96%)	39 (89%)	5 (11%)	0	100	100
7	7	62/65 (95%)	58 (94%)	4 (6%)	0	100	100
8	8	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
10	B	216/241 (90%)	198 (92%)	18 (8%)	0	100	100
11	C	205/233 (88%)	192 (94%)	13 (6%)	0	100	100
12	D	203/206 (98%)	183 (90%)	20 (10%)	0	100	100
13	E	155/167 (93%)	142 (92%)	13 (8%)	0	100	100
14	F	104/135 (77%)	98 (94%)	6 (6%)	0	100	100
15	G	151/179 (84%)	144 (95%)	7 (5%)	0	100	100
16	H	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
17	I	125/130 (96%)	111 (89%)	14 (11%)	0	100	100
18	J	98/103 (95%)	84 (86%)	14 (14%)	0	100	100
19	K	115/129 (89%)	107 (93%)	8 (7%)	0	100	100
20	L	120/124 (97%)	105 (88%)	14 (12%)	1 (1%)	16	45
21	M	114/118 (97%)	104 (91%)	10 (9%)	0	100	100
22	N	98/101 (97%)	92 (94%)	6 (6%)	0	100	100
23	O	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
24	P	79/82 (96%)	67 (85%)	12 (15%)	0	100	100
25	Q	78/84 (93%)	72 (92%)	6 (8%)	0	100	100
26	R	64/75 (85%)	63 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	S	81/92 (88%)	72 (89%)	9 (11%)	0	100	100
28	T	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
29	U	62/71 (87%)	53 (86%)	9 (14%)	0	100	100
34	c	269/273 (98%)	248 (92%)	21 (8%)	0	100	100
35	d	207/209 (99%)	190 (92%)	17 (8%)	0	100	100
36	e	199/201 (99%)	192 (96%)	7 (4%)	0	100	100
37	f	176/179 (98%)	156 (89%)	20 (11%)	0	100	100
38	g	173/177 (98%)	162 (94%)	11 (6%)	0	100	100
39	h	147/149 (99%)	135 (92%)	12 (8%)	0	100	100
40	k	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
41	l	121/123 (98%)	106 (88%)	15 (12%)	0	100	100
42	m	142/144 (99%)	125 (88%)	17 (12%)	0	100	100
43	n	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
44	o	118/127 (93%)	110 (93%)	8 (7%)	0	100	100
45	p	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
46	q	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
47	r	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
48	s	101/103 (98%)	89 (88%)	10 (10%)	2 (2%)	6	23
49	t	108/110 (98%)	102 (94%)	6 (6%)	0	100	100
50	u	98/100 (98%)	89 (91%)	9 (9%)	0	100	100
51	v	101/104 (97%)	88 (87%)	13 (13%)	0	100	100
52	w	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
54	y	82/85 (96%)	80 (98%)	2 (2%)	0	100	100
55	z	45/49 (92%)	32 (71%)	13 (29%)	0	100	100
56	V	57/432 (13%)	52 (91%)	5 (9%)	0	100	100
All	All	5652/6324 (89%)	5216 (92%)	433 (8%)	3 (0%)	50	77

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
48	s	51	VAL
20	L	91	GLY
48	s	53	PHE

### 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	0	67/68 (98%)	67 (100%)	0	100	100
2	1	54/55 (98%)	54 (100%)	0	100	100
3	2	48/49 (98%)	48 (100%)	0	100	100
4	4	47/48 (98%)	47 (100%)	0	100	100
5	5	47/49 (96%)	47 (100%)	0	100	100
6	6	38/38 (100%)	38 (100%)	0	100	100
7	7	51/52 (98%)	51 (100%)	0	100	100
8	8	34/34 (100%)	34 (100%)	0	100	100
10	B	180/199 (90%)	180 (100%)	0	100	100
11	C	171/190 (90%)	170 (99%)	1 (1%)	84	95
12	D	172/173 (99%)	171 (99%)	1 (1%)	84	95
13	E	119/126 (94%)	119 (100%)	0	100	100
14	F	92/116 (79%)	92 (100%)	0	100	100
15	G	126/147 (86%)	126 (100%)	0	100	100
16	H	104/105 (99%)	103 (99%)	1 (1%)	73	91
17	I	105/107 (98%)	105 (100%)	0	100	100
18	J	88/90 (98%)	88 (100%)	0	100	100
19	K	90/99 (91%)	90 (100%)	0	100	100
20	L	103/104 (99%)	103 (100%)	0	100	100
21	M	94/96 (98%)	94 (100%)	0	100	100
22	N	83/84 (99%)	83 (100%)	0	100	100
23	O	76/77 (99%)	76 (100%)	0	100	100
24	P	65/65 (100%)	65 (100%)	0	100	100
25	Q	74/78 (95%)	74 (100%)	0	100	100
26	R	57/65 (88%)	57 (100%)	0	100	100
27	S	72/79 (91%)	72 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	T	65/66 (98%)	65 (100%)	0	100	100
29	U	54/61 (88%)	54 (100%)	0	100	100
34	c	216/218 (99%)	216 (100%)	0	100	100
35	d	164/164 (100%)	162 (99%)	2 (1%)	67	89
36	e	165/165 (100%)	162 (98%)	3 (2%)	54	82
37	f	149/150 (99%)	146 (98%)	3 (2%)	50	79
38	g	136/138 (99%)	134 (98%)	2 (2%)	60	85
39	h	114/114 (100%)	112 (98%)	2 (2%)	54	82
40	k	116/116 (100%)	116 (100%)	0	100	100
41	l	104/104 (100%)	104 (100%)	0	100	100
42	m	103/103 (100%)	103 (100%)	0	100	100
43	n	109/109 (100%)	109 (100%)	0	100	100
44	o	100/103 (97%)	100 (100%)	0	100	100
45	p	86/87 (99%)	84 (98%)	2 (2%)	45	77
46	q	99/100 (99%)	99 (100%)	0	100	100
47	r	89/90 (99%)	89 (100%)	0	100	100
48	s	84/84 (100%)	82 (98%)	2 (2%)	44	76
49	t	93/93 (100%)	92 (99%)	1 (1%)	70	90
50	u	84/84 (100%)	84 (100%)	0	100	100
51	v	84/85 (99%)	82 (98%)	2 (2%)	44	76
52	w	78/78 (100%)	77 (99%)	1 (1%)	65	88
54	y	62/63 (98%)	61 (98%)	1 (2%)	58	84
55	z	39/43 (91%)	34 (87%)	5 (13%)	3	11
56	V	49/359 (14%)	40 (82%)	9 (18%)	1	4
All	All	4699/5170 (91%)	4661 (99%)	38 (1%)	77	93

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
55	z	146	ARG
56	V	67	LEU
56	V	19	ILE
56	V	25	GLU
56	V	76	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
28	T	81	GLN
45	p	116	GLN
35	d	49	GLN
39	h	145	ASN
52	w	87	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	X	75/76 (98%)	40 (53%)	1 (1%)
31	Y	76/77 (98%)	20 (26%)	2 (2%)
31	Z	76/77 (98%)	19 (25%)	0
32	a	119/120 (99%)	17 (14%)	0
33	b	2902/2904 (99%)	603 (20%)	0
53	x	13/14 (92%)	5 (38%)	0
9	A	1532/1533 (99%)	371 (24%)	9 (0%)
All	All	4793/4801 (99%)	1075 (22%)	12 (0%)

5 of 1075 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	2	A
9	A	4	U
9	A	6	G
9	A	9	G
9	A	16	A

5 of 12 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	1357	A
9	A	1493	A
31	Y	16	C
30	X	21	A
9	A	429	U

## 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

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
58	PRO	Z	163	-	5,7,8	0.56	0	7,8,10	1.31	1 (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
58	PRO	Z	163	-	-	0/0/9/11	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	Z	163	PRO	O-C-CA	-2.38	118.55	124.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	Z	163	PRO	4	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



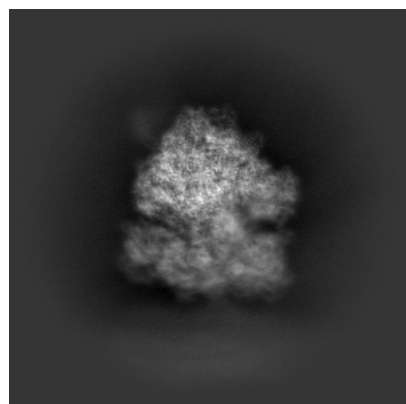
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60061. These allow visual inspection of the internal detail of the map and identification of artifacts.

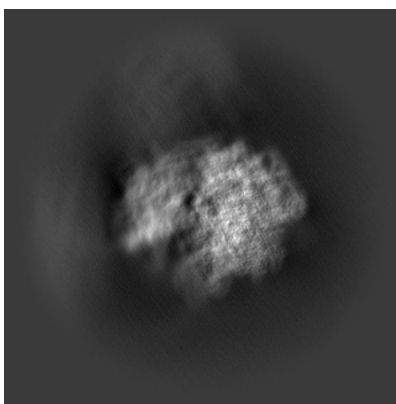
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

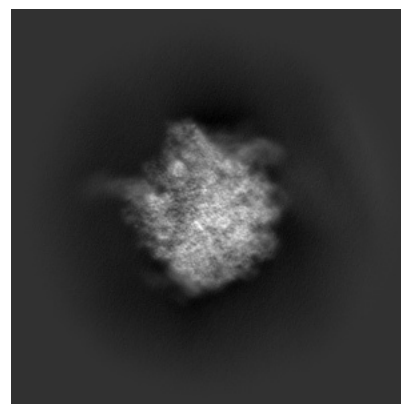
#### 6.1.1 Primary map



X

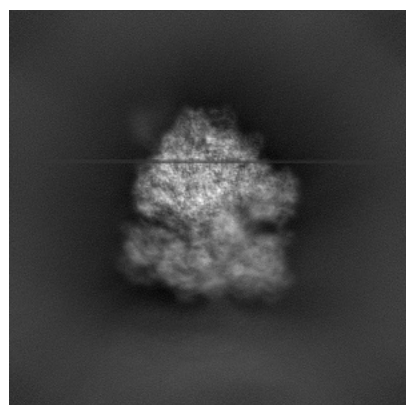


Y

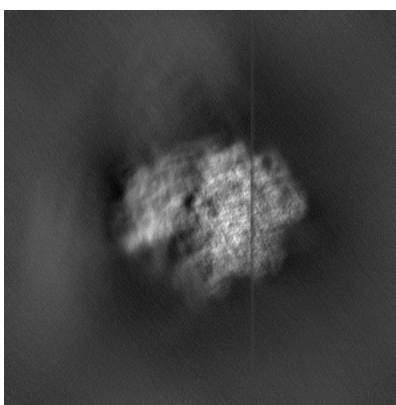


Z

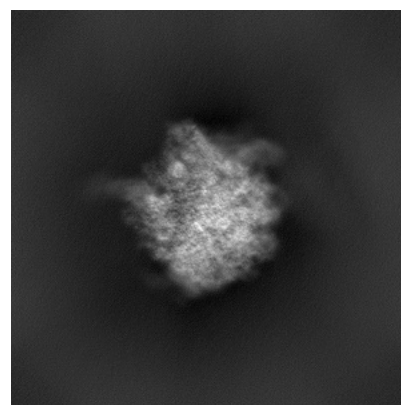
#### 6.1.2 Raw map



X



Y

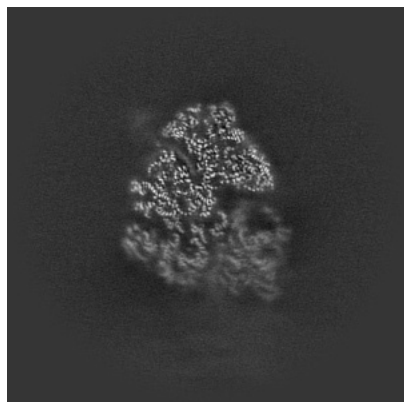


Z

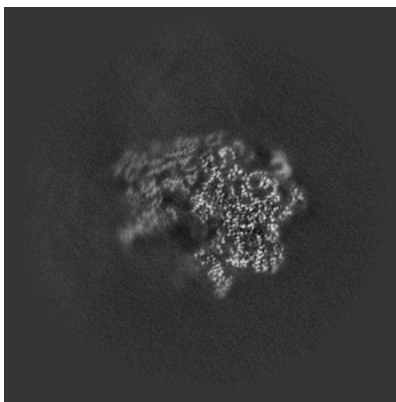
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

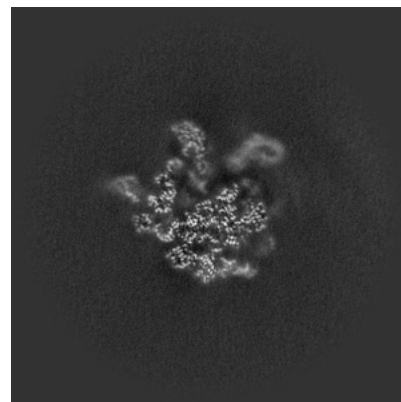
### 6.2.1 Primary map



X Index: 240

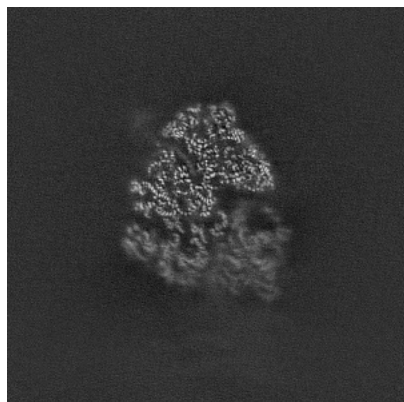


Y Index: 240

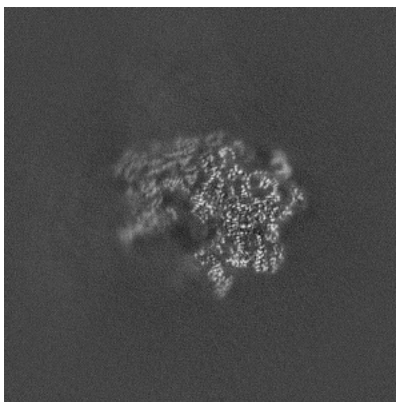


Z Index: 240

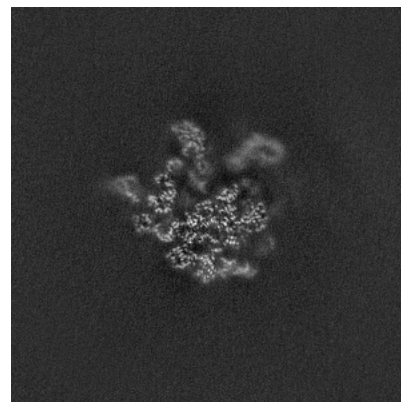
### 6.2.2 Raw map



X Index: 240



Y Index: 240

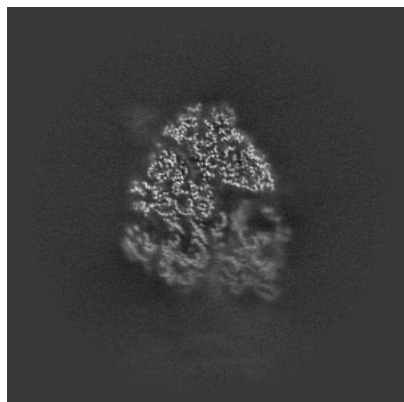


Z Index: 240

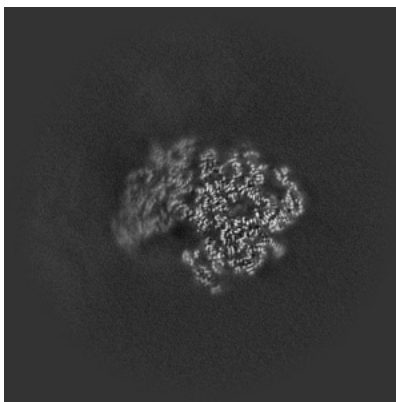
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

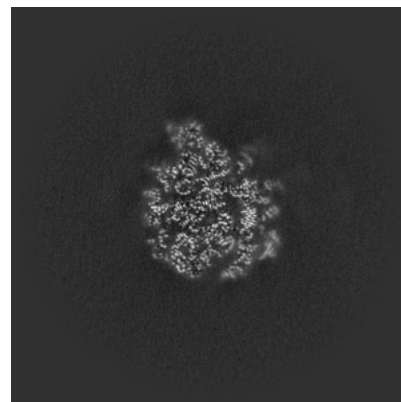
### 6.3.1 Primary map



X Index: 238

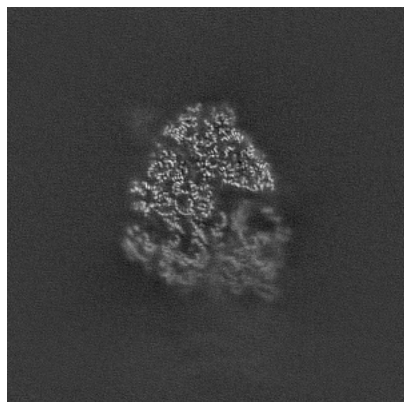


Y Index: 223

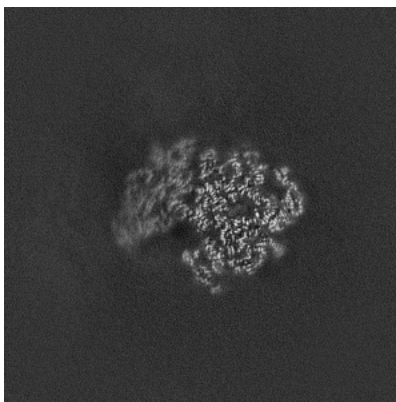


Z Index: 280

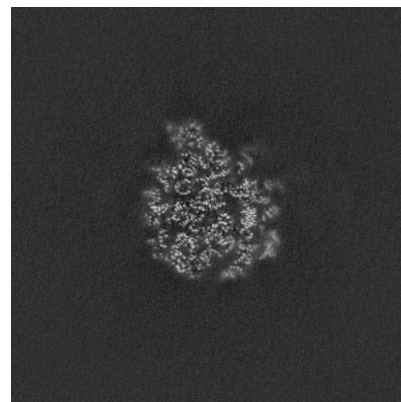
### 6.3.2 Raw map



X Index: 238



Y Index: 223

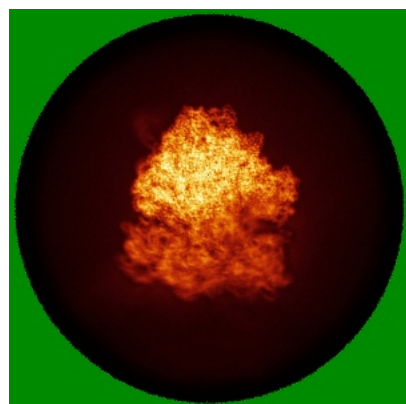


Z Index: 280

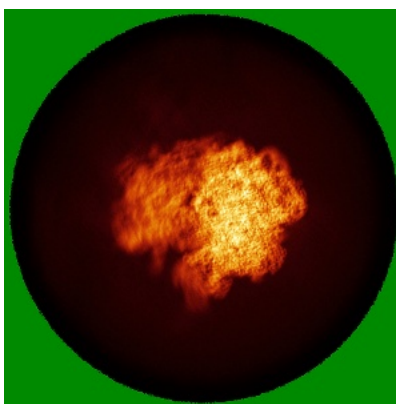
The images above show the largest variance slices of the map in three orthogonal directions.

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

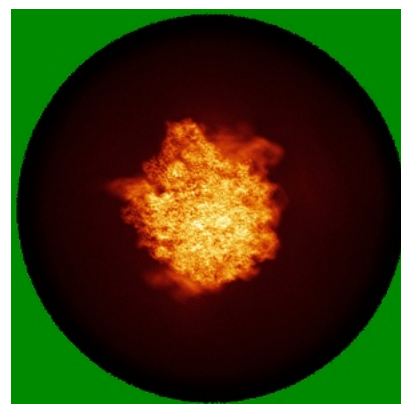
### 6.4.1 Primary map



X

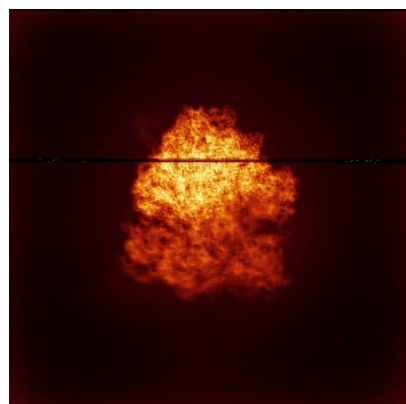


Y

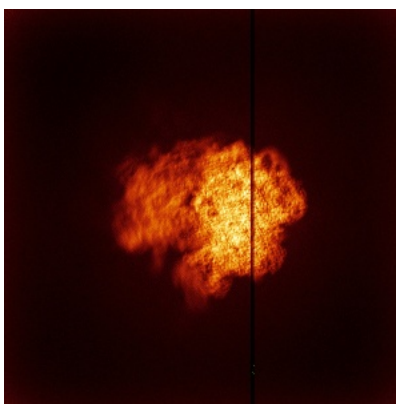


Z

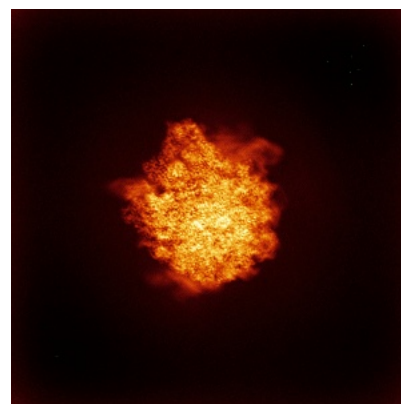
### 6.4.2 Raw map



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.

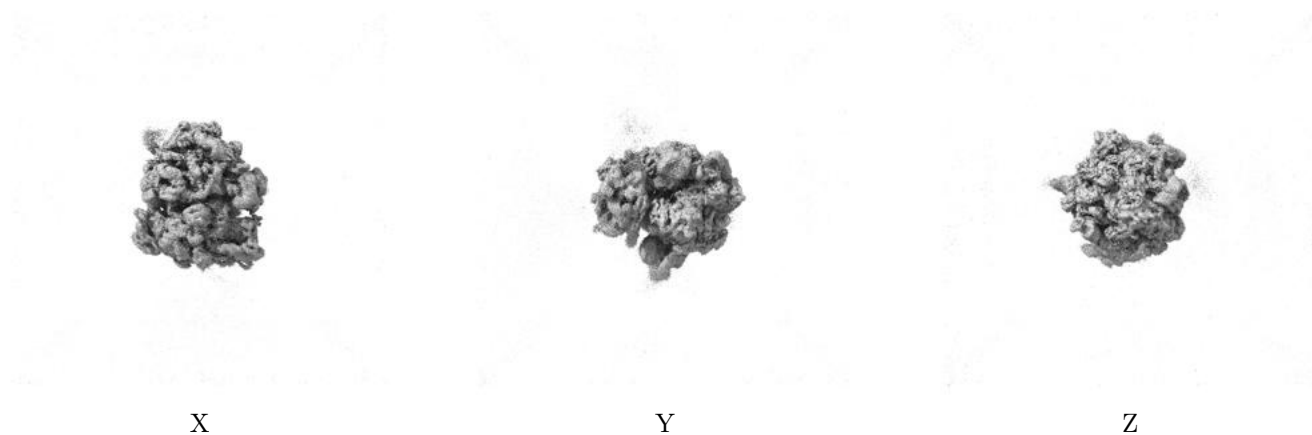
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

## 6.6 Mask visualisation [i](#)

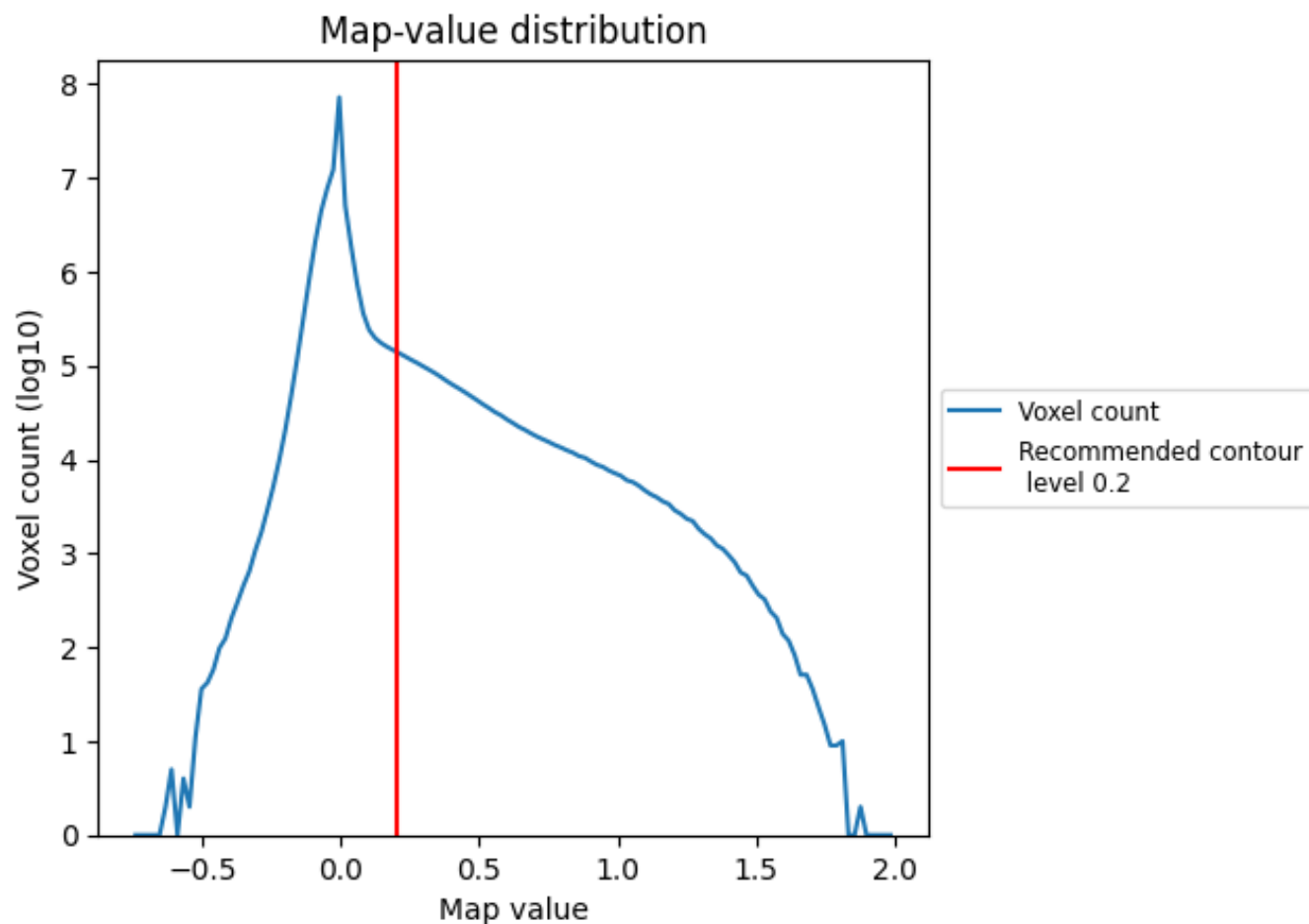
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

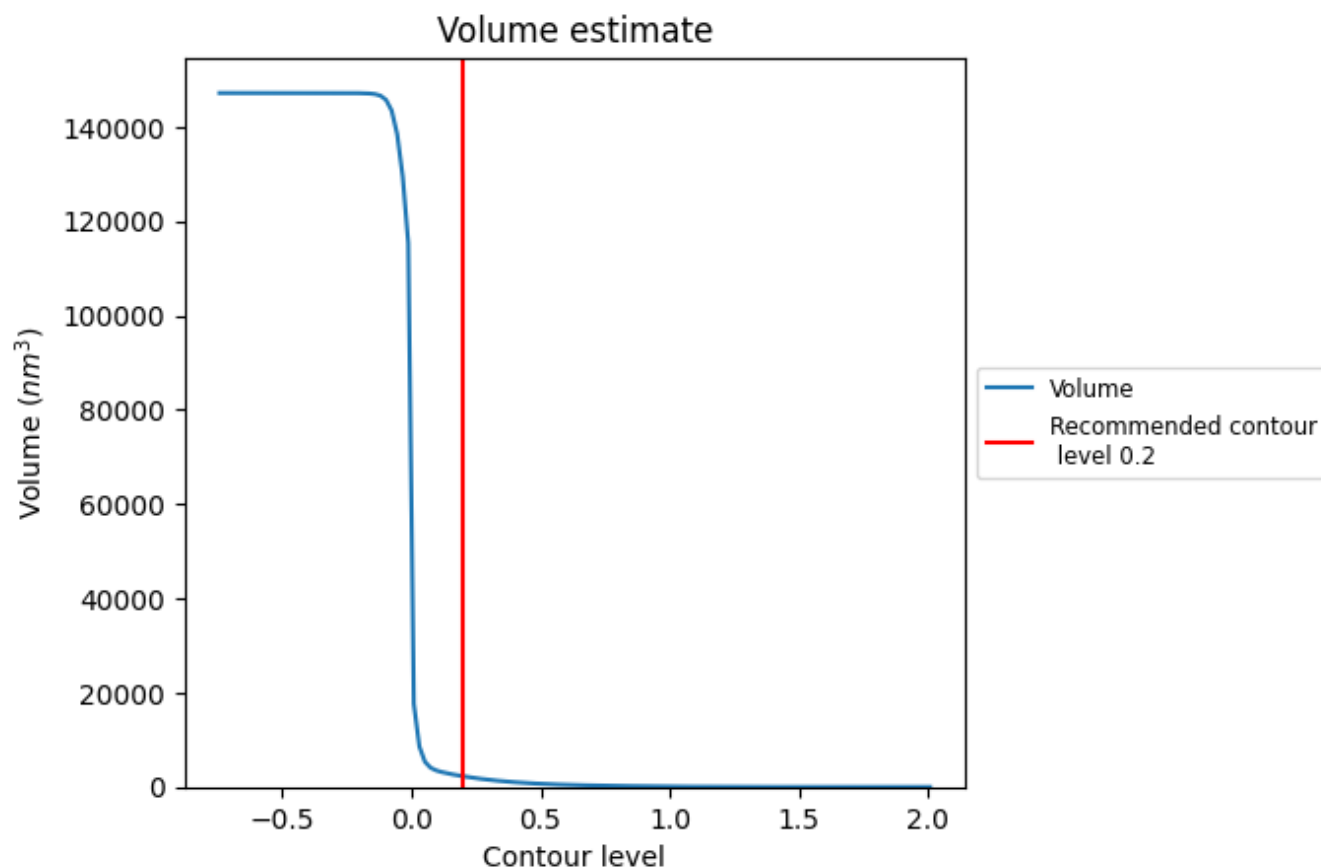
This section contains the results of statistical analysis of the map.

### 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.

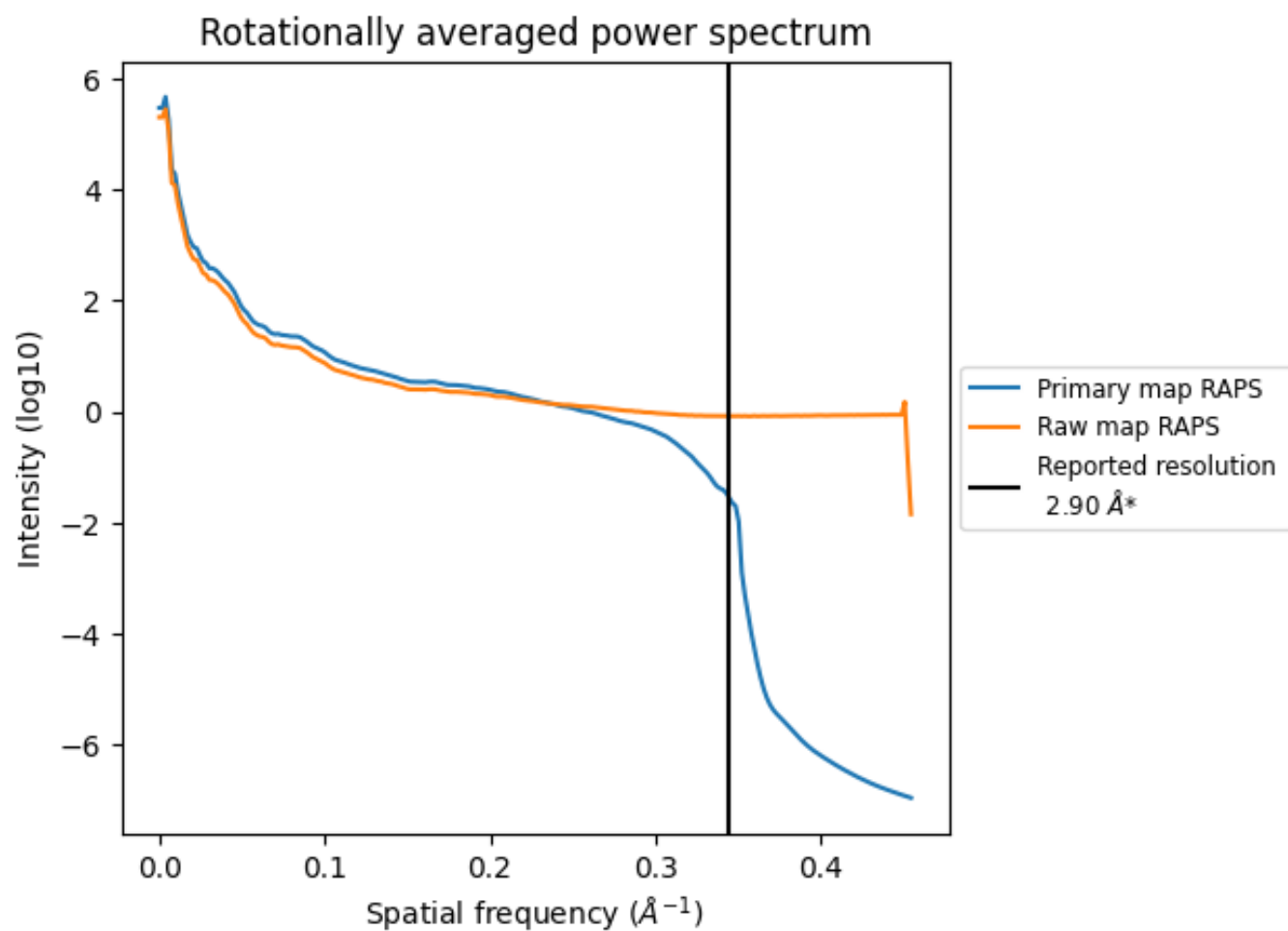
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2269  $\text{nm}^3$ ; this corresponds to an approximate mass of 2050 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 ⓘ



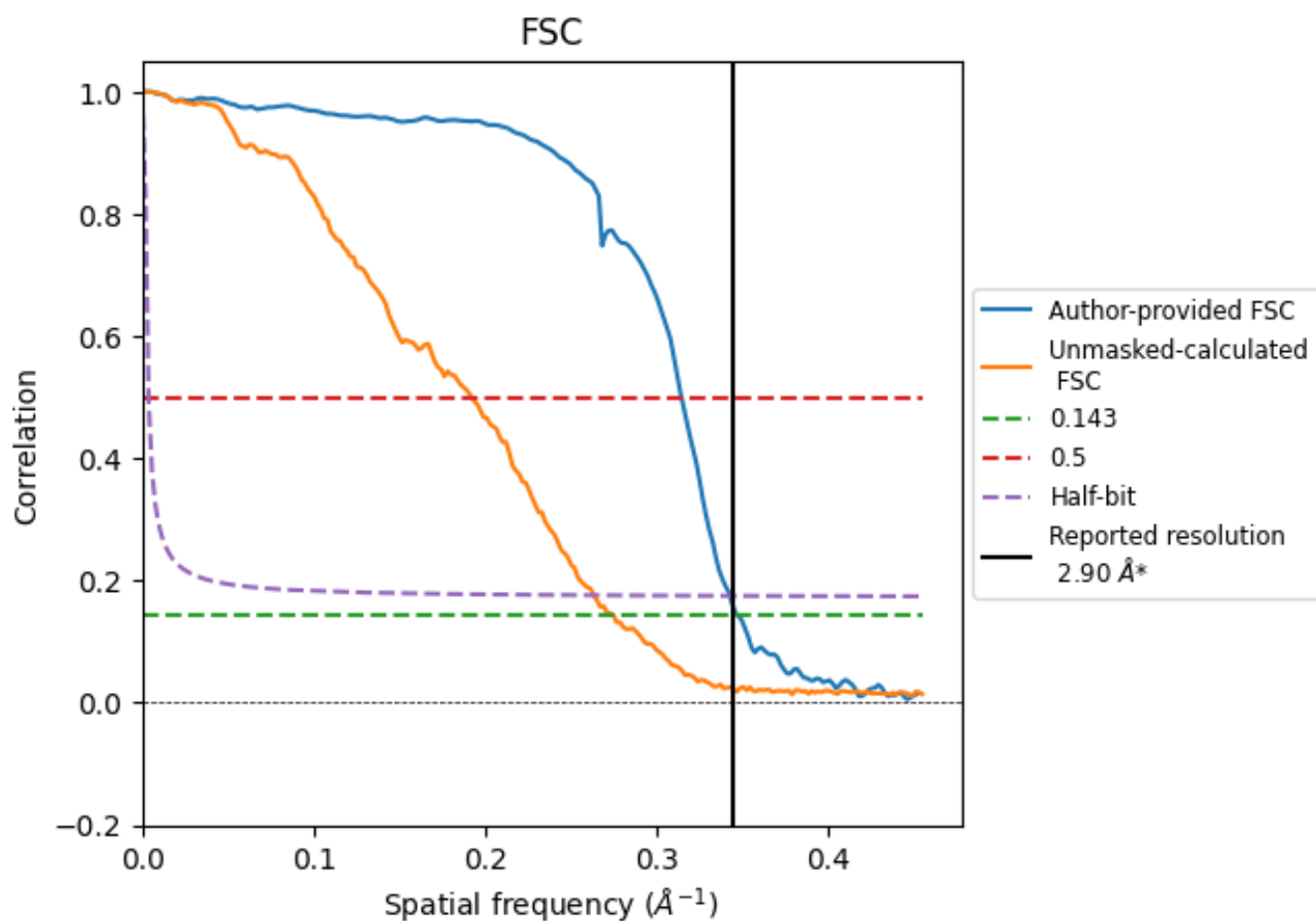
\*Reported resolution corresponds to spatial frequency of  $0.345 \text{ \AA}^{-1}$



## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.345  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

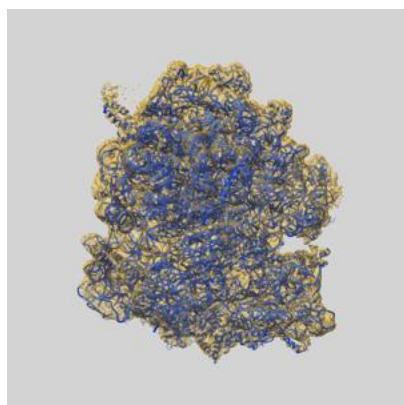
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.88	3.18	2.92
Unmasked-calculated*	3.64	5.21	3.80

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.64 differs from the reported value 2.9 by more than 10 %

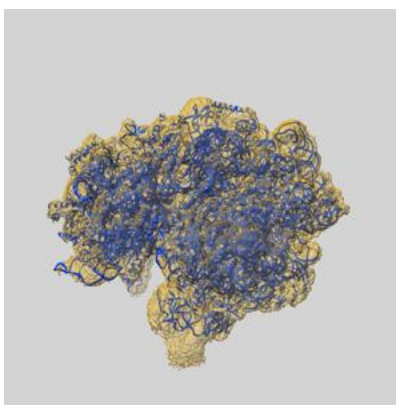
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-60061 and PDB model 8ZFI. Per-residue inclusion information can be found in section 3 on page 15.

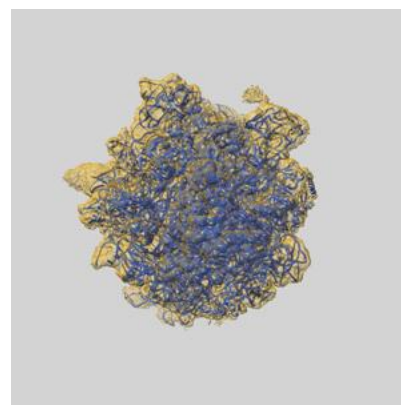
### 9.1 Map-model overlay [i](#)



X



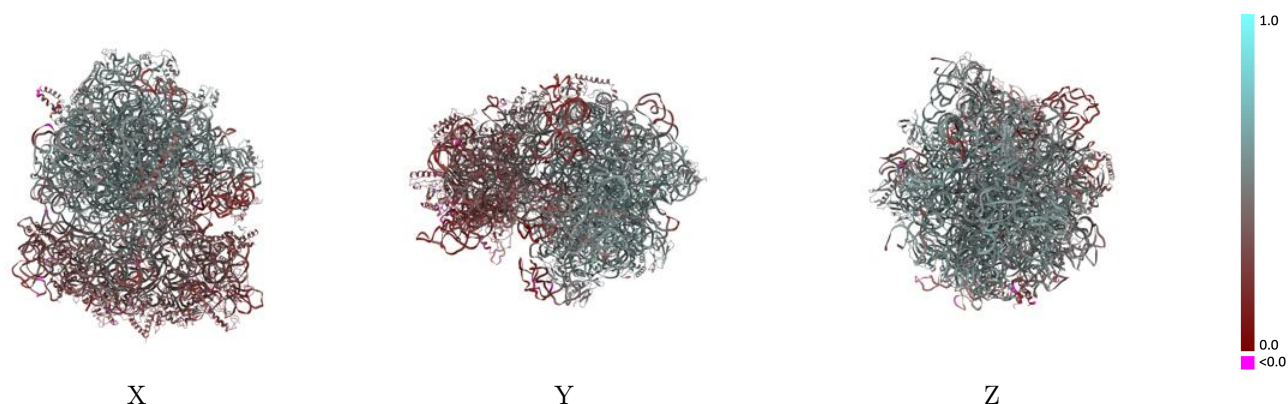
Y



Z

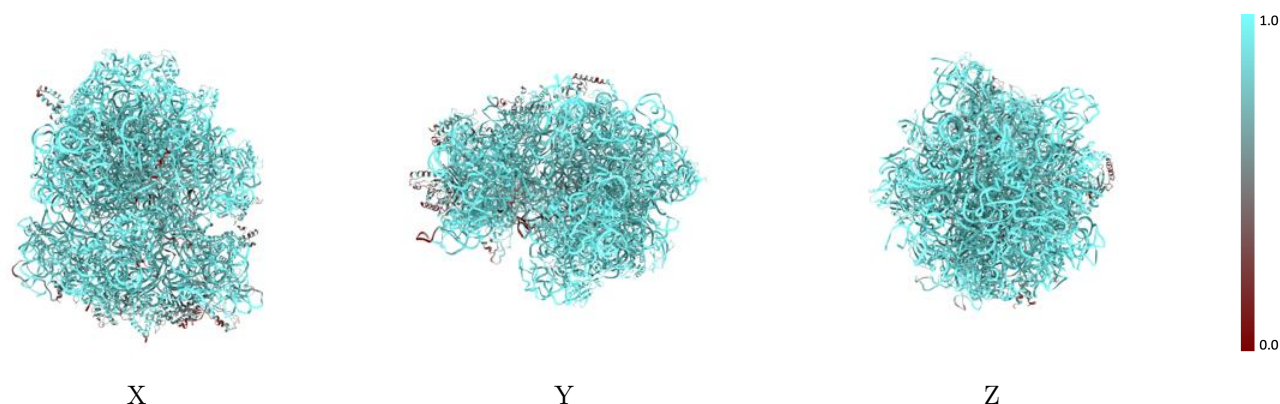
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



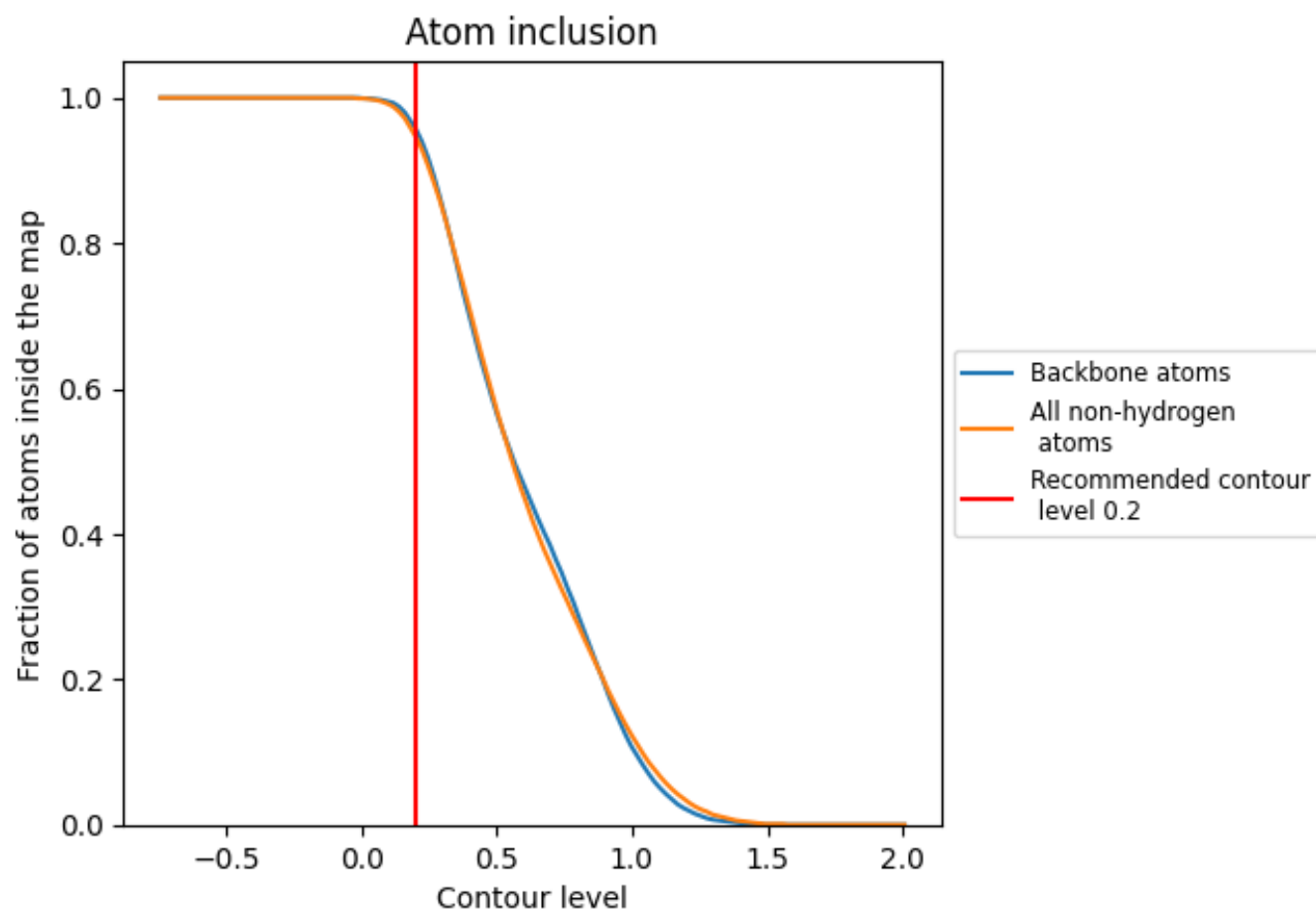
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).







































































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9470	 0.4410
0	 0.9980	 0.5010
1	 0.9900	 0.4730
2	 0.9730	 0.5430
4	 0.9700	 0.5400
5	 0.9500	 0.5100
6	 0.9970	 0.5680
7	 0.9760	 0.5700
8	 0.9900	 0.5500
A	 0.9680	 0.3400
B	 0.6660	 0.3070
C	 0.6200	 0.3200
D	 0.6430	 0.1970
E	 0.8770	 0.3710
F	 0.9330	 0.3760
G	 0.9030	 0.3000
H	 0.8860	 0.3760
I	 0.9060	 0.2590
J	 0.6270	 0.2650
K	 0.8510	 0.3980
L	 0.7120	 0.2850
M	 0.6600	 0.2880
N	 0.8590	 0.2440
O	 0.9480	 0.4050
P	 0.7870	 0.3160
Q	 0.8690	 0.3130
R	 0.7710	 0.3560
S	 0.8360	 0.2420
T	 0.8700	 0.2700
U	 0.6170	 0.3470
V	 0.6430	 0.2910
X	 0.9460	 0.2420
Y	 0.8890	 0.3530
Z	 0.6520	 0.3790
a	 0.9980	 0.5120



*Continued on next page...*

*Continued from previous page...*

Chain	Atom inclusion	Q-score
b	 0.9960	 0.5150
c	 0.9890	 0.5490
d	 0.9770	 0.5530
e	 0.9720	 0.5170
f	 0.8420	 0.3280
g	 0.9850	 0.4950
h	 0.7010	 0.3980
k	 0.9780	 0.5560
l	 0.9030	 0.5420
m	 0.9770	 0.5370
n	 0.9790	 0.5480
o	 0.9880	 0.5560
p	 0.9760	 0.4790
q	 0.9190	 0.5330
r	 0.9840	 0.5460
s	 0.9850	 0.5340
t	 0.9770	 0.5360
u	 0.9510	 0.4870
v	 0.9850	 0.4930
w	 0.9770	 0.5210
x	 0.8960	 0.3890
y	 0.8900	 0.5140
z	 0.5540	 0.3540