



wwPDB EM Validation Summary Report ⓘ

Mar 4, 2026 – 11:22 PM UTC

PDB ID : 8FIZ / pdb_00008fiz
EMDB ID : EMD-29214
Title : Cryo-EM structure of E. coli 70S Ribosome containing mRNA and tRNA (in the transcription-translation complex)
Authors : Florez Ariza, A.; Wee, L.; Tong, A.; Canari, C.; Grob, P.; Nogales, E.; Bustamante, C.
Deposited on : 2022-12-18
Resolution : 3.80 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

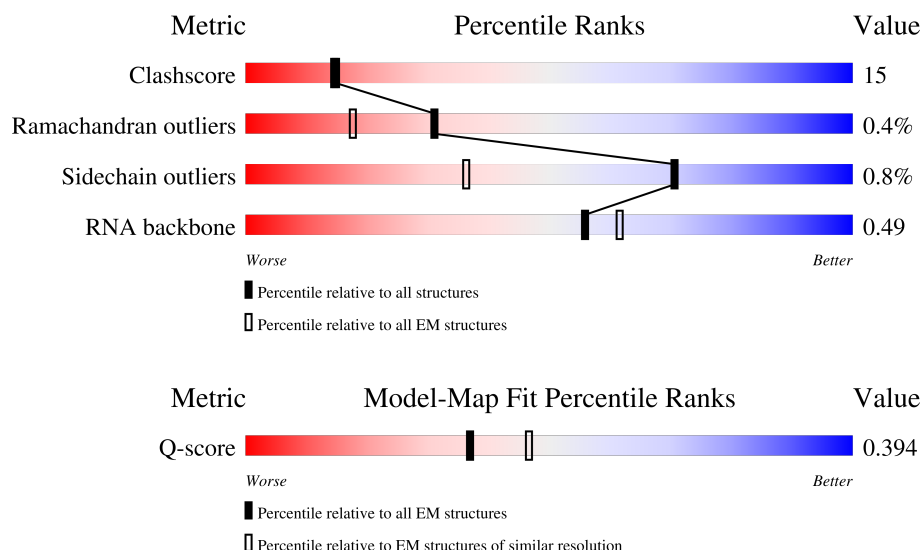
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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	AA	1534	
2	AB	87	
3	AC	124	

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Mol	Chain	Length	Quality of chain
4	AD	92	
5	AE	118	
6	AF	101	
7	AG	233	
8	AH	103	
9	AI	206	
10	AJ	241	
11	AK	130	
12	AL	179	
13	AM	129	
14	AN	135	
15	AO	82	
16	AP	167	
17	AQ	130	
18	AR	89	
19	AS	84	
20	AT	75	
21	AU	71	
22	AV	70	
23	AW	17	
24	BA	2904	
25	BB	77	
26	BC	120	
27	BD	273	
28	BE	209	

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Mol	Chain	Length	Quality of chain
29	BF	201	
30	BG	179	
31	BH	117	
32	BI	55	
33	BJ	177	
34	BK	149	
35	BL	142	
36	BM	57	
37	BN	46	
38	BO	65	
39	BP	38	
40	BQ	59	
41	BR	142	
42	BS	123	
43	BT	144	
44	BU	136	
45	BV	127	
46	BW	115	
47	BX	118	
48	BY	103	
49	BZ	110	
50	DA	100	
51	DB	104	
52	DC	94	
53	DD	85	

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Mol	Chain	Length	Quality of chain
54	DE	78	 74% 24% •
55	DF	63	 71% 27% •
56	DG	165	 16% 43% 37% •• 18%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 146125 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1534	Total	C	N	O	P	0	0
			32917	14681	6041	10661	1534		

- Molecule 2 is a protein called 30S ribosomal protein S20.

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

- Molecule 3 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	122	Total	C	N	O	S	0	0
			947	586	195	162	4		

- Molecule 4 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 5 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 6 is a protein called 30S ribosomal protein S14.

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

- Molecule 7 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 8 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	99	Total	C	N	O	S	0	0
			795	498	152	144	1		

- Molecule 9 is a protein called 30S ribosomal protein S4.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 11 is a protein called 30S ribosomal protein S9.

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

- Molecule 12 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 13 is a protein called 30S ribosomal protein S11.

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

- Molecule 14 is a protein called 30S ribosomal protein S6.

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

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 16 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	155	Total	C	N	O	S	0	0
			1144	711	216	211	6		

- Molecule 17 is a protein called 30S ribosomal protein S8.

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

- Molecule 18 is a protein called 30S ribosomal protein S15.

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

- Molecule 19 is a protein called 30S ribosomal protein S17.

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

- Molecule 20 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	AT	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	56	Total	C	N	O	S	0	0
			465	290	96	78	1		

- Molecule 22 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	69	Total	C	N	O	S	0	0
			539	333	102	98	6		

- Molecule 23 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AW	17	Total	C	N	O	P	0	0
			365	162	65	121	17		

- Molecule 24 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BA	2897	Total	C	N	O	P	2	0
			62218	27755	11451	20114	2898		

- Molecule 25 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BB	75	Total	C	N	O	P	0	0
			1598	713	290	521	74		

- Molecule 26 is a RNA chain called 5s rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BC	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 27 is a protein called 50S ribosomal protein L2.

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

- Molecule 28 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BE	208	Total	C	N	O	S	0	0
			1556	974	286	292	4		

- Molecule 29 is a protein called 50S ribosomal protein L4.

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

- Molecule 30 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BG	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 31 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BH	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 32 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	BI	51	Total	C	N	O	0	0
			414	266	76	72		

- Molecule 33 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BJ	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 34 is a protein called 50S ribosomal protein L9.

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

- Molecule 35 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BL	134	Total	C	N	O	S	0	0
			979	619	169	185	6		

- Molecule 36 is a protein called 50S ribosomal protein L32.

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

- Molecule 37 is a protein called 50S ribosomal protein L34.

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

- Molecule 38 is a protein called 50S ribosomal protein L35.

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

- Molecule 39 is a protein called 50S ribosomal protein L36.

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

- Molecule 40 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BQ	58	Total	C	N	O	S	2	0
			463	290	90	81	2		

- Molecule 41 is a protein called 50S ribosomal protein L13.

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

- Molecule 42 is a protein called 50S ribosomal protein L14.

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

- Molecule 43 is a protein called 50S ribosomal protein L15.

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

- Molecule 44 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BU	136	Total	C	N	O	S	1	0
			1082	691	208	177	6		

- Molecule 45 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BV	125	Total	C	N	O	S	0	0
			993	613	202	173	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BW	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	BX	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 48 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BY	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	BZ	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	DA	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	DB	102	Total	C	N	O	S	0	0
			779	492	146	141			

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

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

- Molecule 53 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	DD	76	Total	C	N	O	S	1	0
			591	365	121	104	1		

- Molecule 54 is a protein called 50S ribosomal protein L28.

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

- Molecule 55 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	DF	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

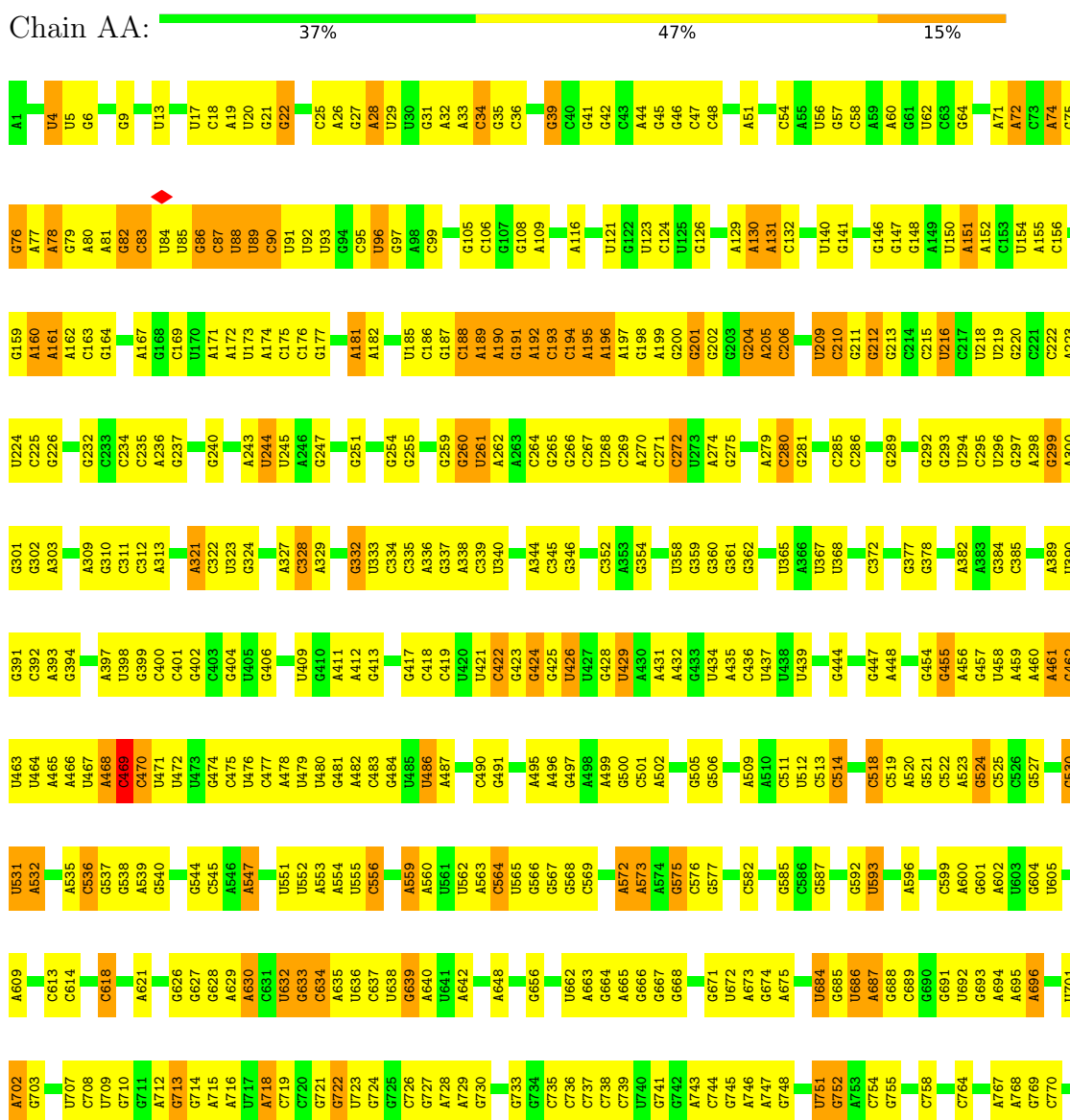
- Molecule 56 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	DG	135	Total	C	N	O	S	0	0
			1023	648	179	192	4		

3 Residue-property plots

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

• Molecule 1: 16S rRNA

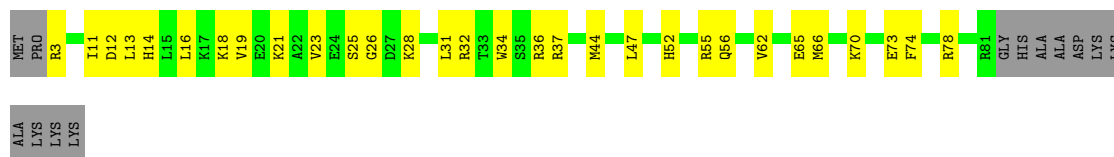






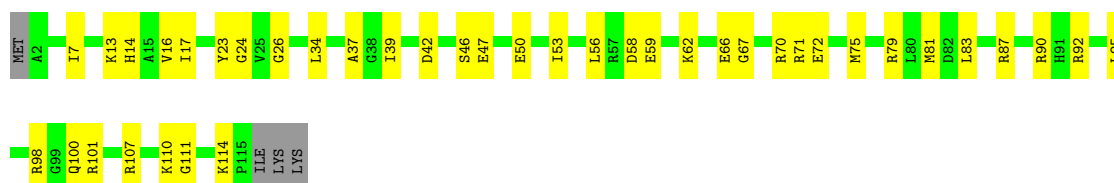
- Molecule 4: 30S ribosomal protein S19

Chain AD: 53% 33% 14%



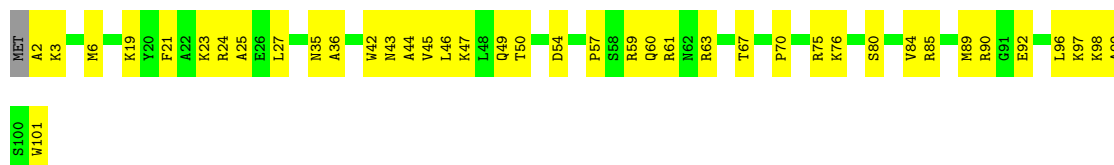
- Molecule 5: 30S ribosomal protein S13

Chain AE: 63% 34% 3%



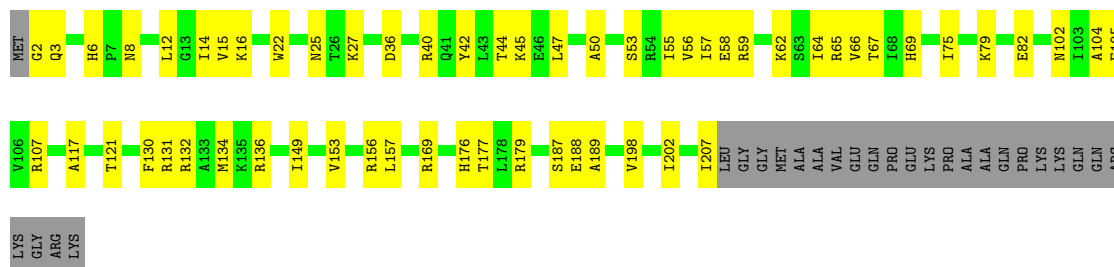
- Molecule 6: 30S ribosomal protein S14

Chain AF: 59% 40% 1%



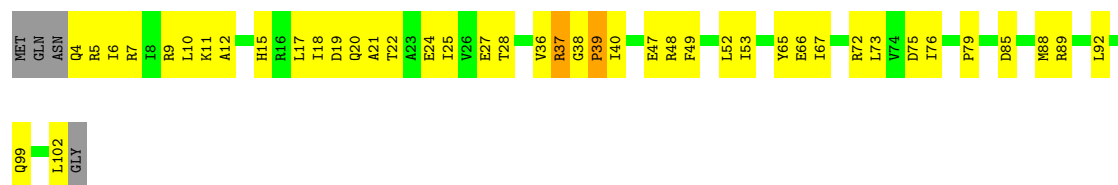
- Molecule 7: 30S ribosomal protein S3

Chain AG: 64% 25% 12%



- Molecule 8: 30S ribosomal protein S10

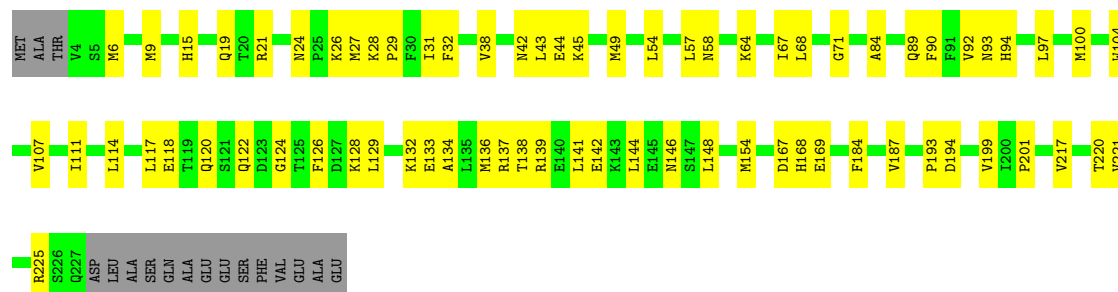
Chain AH: 54% 40% 6%



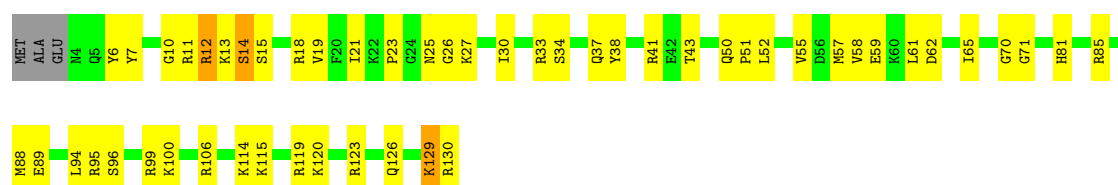
• Molecule 9: 30S ribosomal protein S4



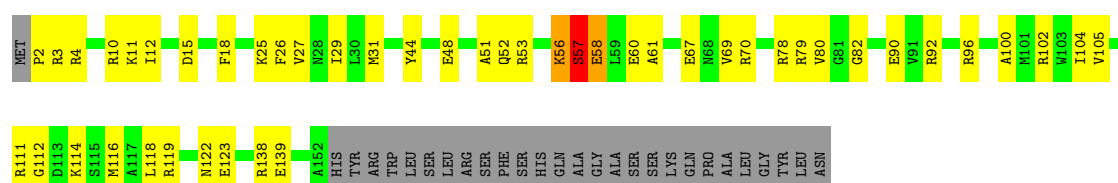
• Molecule 10: 30S ribosomal protein S2



• Molecule 11: 30S ribosomal protein S9

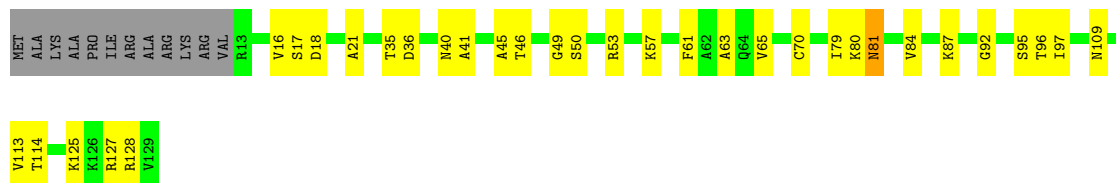


• Molecule 12: 30S ribosomal protein S7



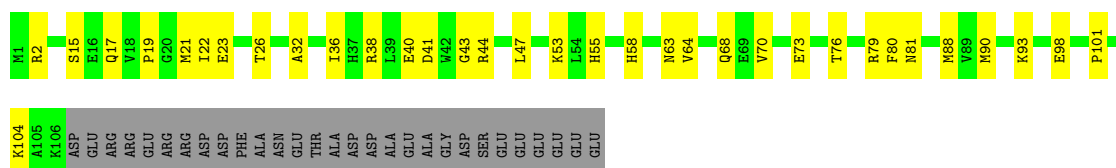
- Molecule 13: 30S ribosomal protein S11

Chain AM:  65% 25% 9%



- Molecule 14: 30S ribosomal protein S6

Chain AN:  53% 25% 21%



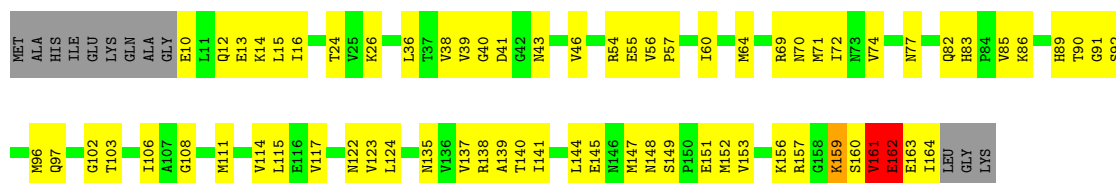
- Molecule 15: 30S ribosomal protein S16

Chain AO:  74% 26%



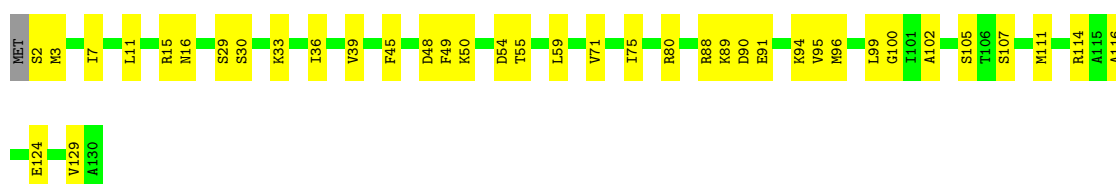
- Molecule 16: 30S ribosomal protein S5

Chain AP:  51% 40% 7%



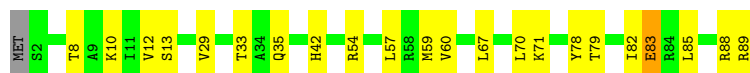
- Molecule 17: 30S ribosomal protein S8

Chain AQ:  70% 29%



- Molecule 18: 30S ribosomal protein S15

Chain AR:  74% 24% ..



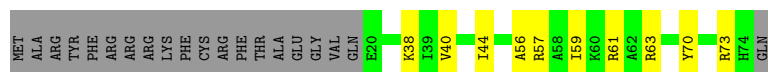
- Molecule 19: 30S ribosomal protein S17

Chain AS:  63% 32% 5%



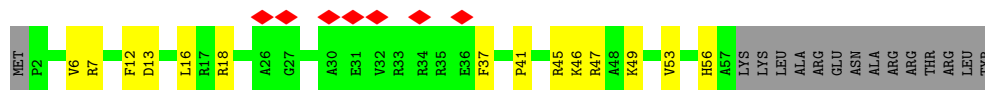
- Molecule 20: 30S ribosomal protein S18

Chain AT:  60% 13% 27%



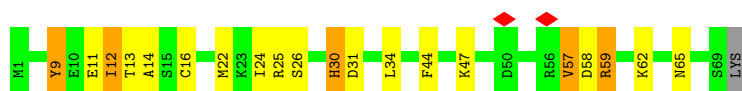
- Molecule 21: 30S ribosomal protein S21

Chain AU:  10% 59% 20% 21%



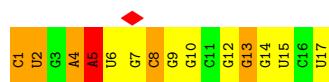
- Molecule 22: 50S ribosomal protein L31

Chain AV:  70% 21% 7%

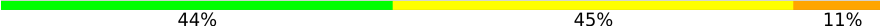


- Molecule 23: mRNA

Chain AW:  6% 18% 47% 29% 6%



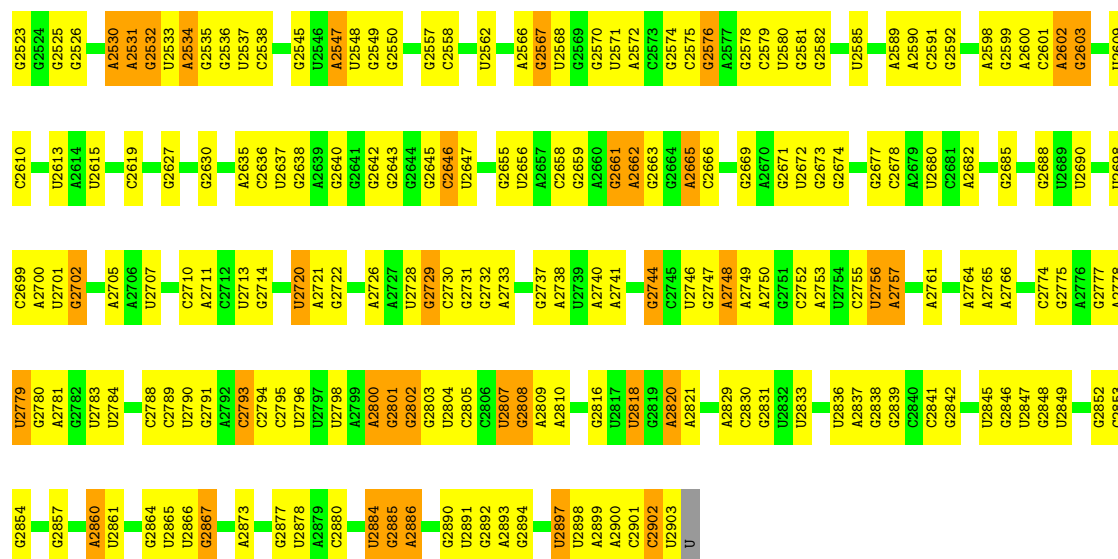
- Molecule 24: 23S rRNA

Chain BA:  44% 45% 11%



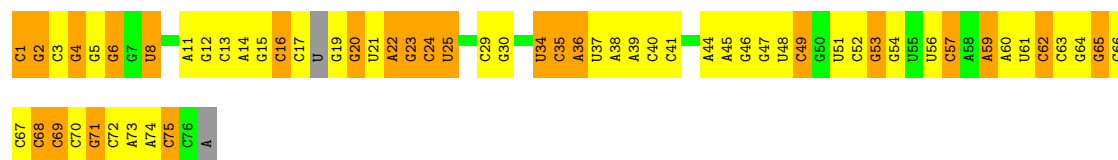
G1212	G1128	U1060	A981	C	G805	A721	G638	A572	G488	A404	C316	G230	A155	G77
G1215	U1132	U1061	C982	C	C806	A722	U639	U573	G489	U405	G317	A231	A156	U78
U1219	A1133	G1062	A983	G	U807	C723	U641	A574	G491	U406	C318	A232	U162	C79
G1220	C1135	G1063	C987	U894	C812	A727	U642	U576	G498	G411	U321	C239	C163	A84
G1223	G1136	U1064	C995	U895	U813	G728	U643	G577	U499	A412	A322	C240	C164	U87
G1224	G1137	A1067	A996	A896	C814	A730	C845	G579	U500	G413	C323	C241	A165	G88
G1225	G1138	G997	C998	C897	U819	C732	U646	U580	A501	C414	G327	U243	U170	G93
A1226	G1139	A1069	C999	C898	A820	C733	U647	C581	A502	U415	U328	G248	U171	A94
G1227	G1140	A1070	U999	A899	A819	G733	G647	A582	A503	U416	G329	C249	A95	A95
U1234	U1141	G1071	A1000	A900	U826	A734	G651	G583	A504	C417	A330	G250	A172	C96
G1235	A1142	C1072	A1001	A901	U827	U739	U652	G584	A505	U418	C331	A251	A173	C97
G1236	A1143	C1073	G1002	A910	U828	A740	U653	G585	A508	U419	A332	G252	U174	G99
G1237	U1148	C1074	U1003	A911	U829	C740	A654	A586	C509	C420	A333	G253	G175	U99
A1237	G1149	U1077	C1005	U913	U830	A742	G656	U588	C421	C421	G345	G254	A176	G177
G1238	G1149	U1078	G1006	U914	A743	A743	U657	U589	A526	A430	C352	A255	G178	U100
G1239	C1150	G1079	C1007	U919	U832	U746	U658	A590	G527	U431	C353	G271	G185	G107
G1245	A1151	A1080	A1008	U919	A833	U747	G659	U591	A528	A435	U355	A272	A181	G108
A1246	C1152	U1081	A1009	C922	A834	G748	G660	A592	A529	U436	U356	A273	A182	C109
A1247	C1153	U1082	C835	C923	A845	U749	A675	A593	A530	G438	C357	C275	A191	G110
G1248	G1154	U1083	C836	G923	U846	A676	A677	U594	C531	U439	U358	U276	U193	A111
U1249	A1155	A1084	C837	C937	A849	U762	C578	U595	A532	C440	G359	G277	G194	G117
G1252	C1158	A1085	C1013	A925	A849	A763	C579	G605	U534	U441	U360	A278	A195	A118
A1253	U1159	A1086	G1016	G926	G843	A766	G681	G612	A538	A443	A362	A282	A196	A119
G1256	C1164	G1087	G1017	A927	A844	G757	A678	A613	G539	U448	C364	G283	A197	U120
G1257	A1165	A1088	U1018	A928	A845	G758	U686	A614	C542	U449	G367	U284	U202	G128
U1258	G1166	A1090	G1022	C935	U847	A761	A689	A616	C543	C456	G370	U285	A203	C129
G1259	G1166	G1091	G1022	A936	C848	U762	U690	G618	C544	A457	A371	U286	A204	U133
G1265	A1169	C1092	G1026	C937	A849	A763	C579	G605	U545	G458	G372	U287	G205	G134
A1266	C1170	G1093	A1027	A943	G856	C765	G681	G605	U546	U454	G372	U288	U206	U135
G1267	G1171	U1094	A1028	C944	C857	U766	G682	G621	A547	G463	G377	U290	A207	G136
U1267	C1172	A1095	A1028	A945	C858	U766	G682	A621	G548	U464	G377	G291	C209	U137
A1268	U1173	U1096	U1033	C946	G859	G775	U686	A622	G549	G465	G386	G294	A213	U138
G1271	U1174	A1098	G1034	A947	C863	G776	U686	A623	C550	A466	U387	A294	G214	U139
A1272	A1175	G1099	G1037	C948	G864	G777	U686	C624	C551	G467	G387	A299	G215	C140
G1278	U1176	C1100	G1038	G949	C864	G778	U686	G625	U552	G468	G388	A300	A142	C141
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G1281	U1180	C1104	G1041	U958	U872	A782	C598	A627	G553	G469	G389	G301	A146	C147
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G1283	U1184	G1107	C1043	C962	C873	G784	U702	C623	C551	G467	G387	A294	G220	C151
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C1289	U1198	U1113	A1050	C968	C879	U790	U708	G629	U558	G474	C393	C306	A226	A151
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C1291	C1200	G1115	G1051	C970	C881	A792	U710	A631	U562	G476	U395	G307	A228	C228
G1292	G1206	G1116	G1055	G971	C882	A793	G711	A632	A563	A477	G396	A309	U229	U154
C1293	G1206	G1116	G1056	A972	C885	A794	A716	A633	U568	A478	C396	A310	A226	C229
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G2447	G2448	G2355	A2287	C2176	A2114	G1959	G1869	A1794	G1710	C1612	G1540	C1463	G1389	C1299
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G2451	G2452	G2357	A2278	C2178	G2116	C1962	A1871	C1796	U1712	A1614	G1543	G1465	U1391	A1302
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G2455	G2456	G2359	A2280	U2181	A2118	G1964	U1882	U1798	U1714	A1616	A1545	U1467	A1395	G1304
U2457	U2458	C2360	C2283	U2182	G2120	C1965	U1883	G1799	G1715	C1617	G1546	U1468	U1396	A1304
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A2461	A2462	G2362	C2285	A2184	U2122	C1967	A1889	A1801	G1723	A1632	A1548	A1470	U1400	G1310
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A2476	A2477	G2369	U2291	U2129	U2130	A1981	C1905	G1812	G1734	A1641	G1560	U1493	U1408	C1320
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C2481	C2482	G2371	A2298	U2132	U2132	G1987	U1911	C1816	G1737	U1647	U1562	A1494	U1411	G1324
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A2517	A2518	G2389	G2224	U2155	U2155	A2020	C1936	G1847	C1766	U1686	U1589	A1522	G1441	U1372
U2519	U2520	G2390	A2225	G2156	G2156	G2023	U1937	A1848	C1767	G1687	A1590	U1523	U1442	A1378
G2521	G2522	G2391	G2226	C2161	C2161	G2024	A1938	G1849	A1773	U1688	A1591	G1524	U1443	G1448
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G2527	G2528	G2394	G2229	C2164	C2164	G2027	U1941	A1854	U1779	G1695	A1594	G1527	C1448	A1384
U2529	U2530	G2395	G2230	G2165	G2165	G2028	C1942	G1857	U1780	U1696	C1595	A1528	G1449	A1385
C2531	C2532	G2396	U2231	C2166	C2166	G2029	G1943	A1858	U1781	G1697	A1596	G1529	G1452	C1386
U2533	U2534	G2397	G2232	U2167	U2167	A2031	U1944	G1859	A1784	A1700	U1597	C1534	U1457	A1387
G2535	G2536	G2398	G2233	G2168	G2168	G2032	U1945	G1860	C1787	G1703	C1604	U1535	U1458	G1459
C2537	C2538	G2399	G2234	A2169	A2169	A2033	G1946	G1861	A1788	A1705	G1605	C1536	C1387	
U2539	U2540	G2400	U2243	G2170	G2170	G2034	U1947	G1862	U1789	G1704	C1606	G1537	U1459	
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C2545	C2546	G2403	G2246	G2173	G2173	U2038	U1955	G1865						
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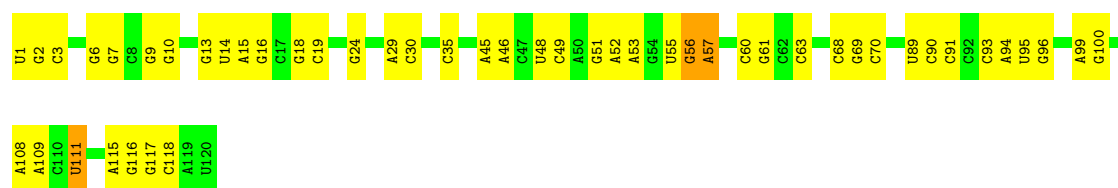
• Molecule 25: P-site tRNA

Chain BB: 19% 47% 31% .



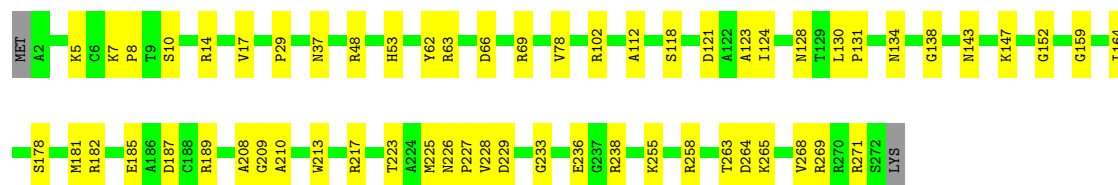
• Molecule 26: 5s rRNA

Chain BC: 59% 38% .



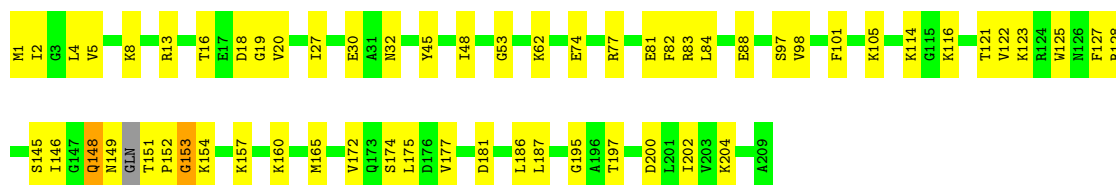
• Molecule 27: 50S ribosomal protein L2

Chain BD: 78% 22% .



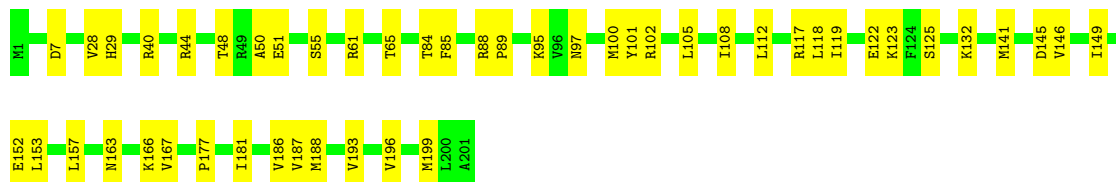
• Molecule 28: 50S ribosomal protein L3

Chain BE: 71% 27% .



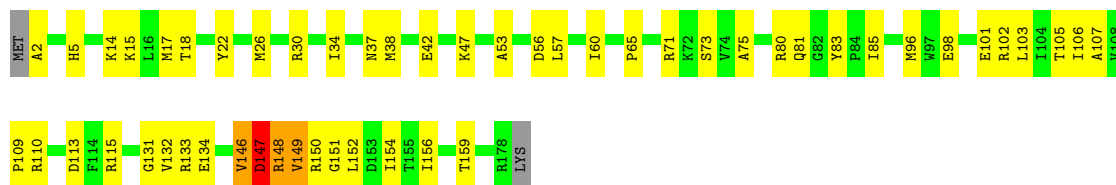
- Molecule 29: 50S ribosomal protein L4

Chain BF: 76% 24%



- Molecule 30: 50S ribosomal protein L5

Chain BG: 70% 27% ...



- Molecule 31: 50S ribosomal protein L18

Chain BH: 77% 23%



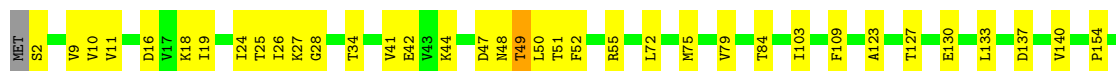
- Molecule 32: 50S ribosomal protein L33

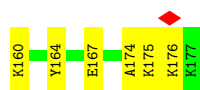
Chain BI: 65% 27% 7%



- Molecule 33: 50S ribosomal protein L6

Chain BJ: 76% 23% ..

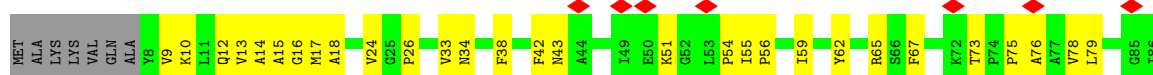




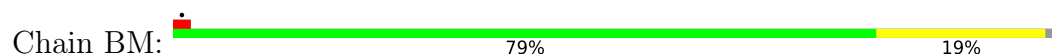
- Molecule 34: 50S ribosomal protein L9



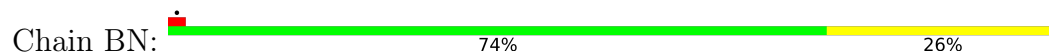
- Molecule 35: 50S ribosomal protein L11



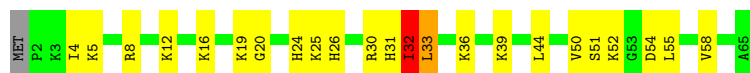
- Molecule 36: 50S ribosomal protein L32



- Molecule 37: 50S ribosomal protein L34

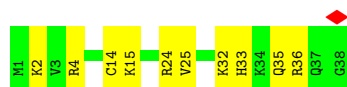


- Molecule 38: 50S ribosomal protein L35



- Molecule 39: 50S ribosomal protein L36

Chain BP:  74% 26%



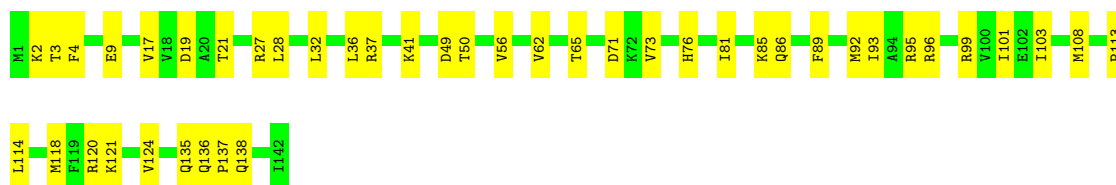
- Molecule 40: 50S ribosomal protein L30

Chain BQ:  76% 22%



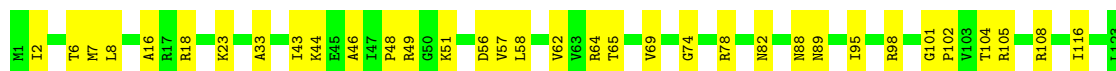
- Molecule 41: 50S ribosomal protein L13

Chain BR:  70% 30%



- Molecule 42: 50S ribosomal protein L14

Chain BS:  72% 28%



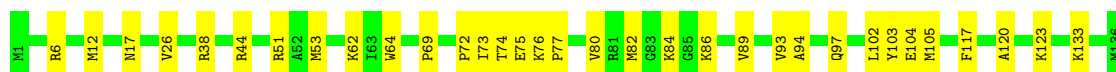
- Molecule 43: 50S ribosomal protein L15

Chain BT:  76% 24%



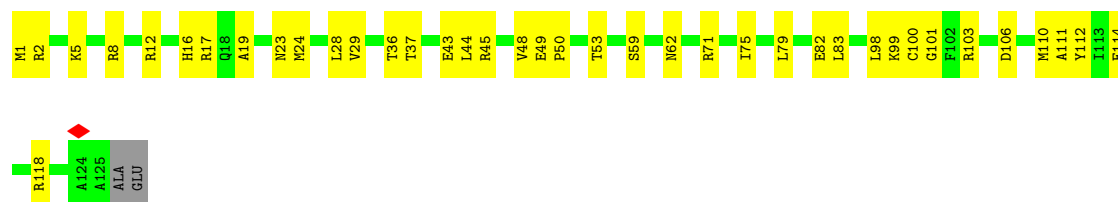
- Molecule 44: 50S ribosomal protein L16

Chain BU:  76% 24%



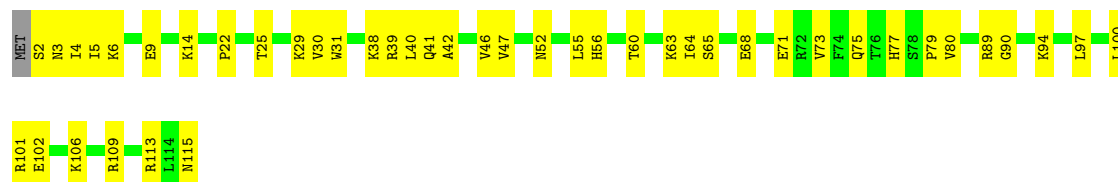
- Molecule 45: 50S ribosomal protein L17

Chain BV:  68% 31%



- Molecule 46: 50S ribosomal protein L19

Chain BW: 61% 38%



- Molecule 47: 50S ribosomal protein L20

Chain BX: 82% 17%



- Molecule 48: Ribosomal protein L21

Chain BY: 72% 24%



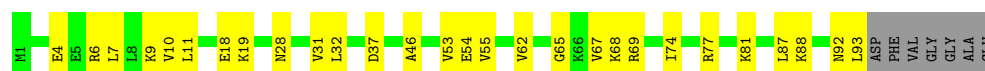
- Molecule 49: 50S ribosomal protein L22

Chain BZ: 75% 25%



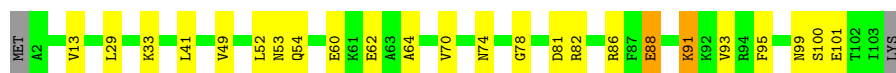
- Molecule 50: 50S ribosomal protein L23

Chain DA: 65% 28% 7%

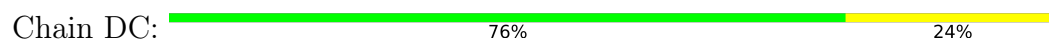


- Molecule 51: 50S ribosomal protein L24

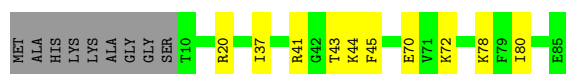
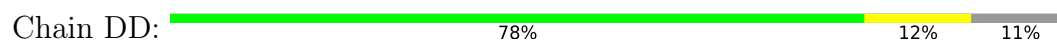
Chain DB: 75% 21%



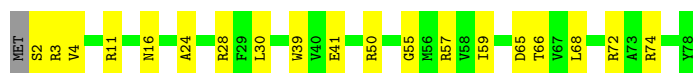
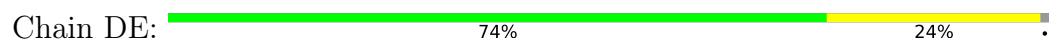
- Molecule 52: 50S ribosomal protein L25



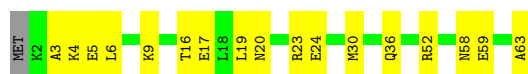
- Molecule 53: 50S ribosomal protein L27



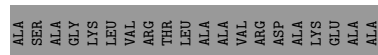
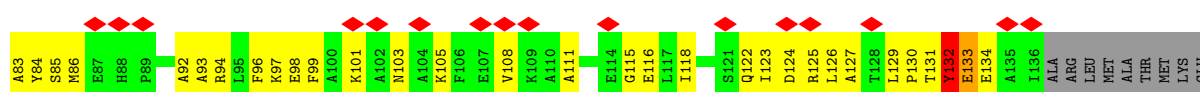
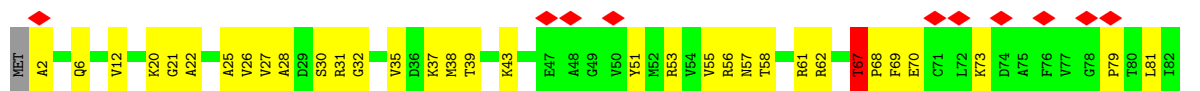
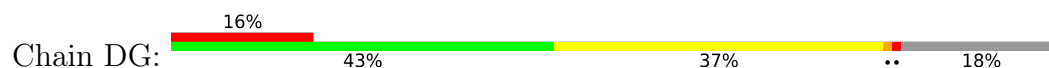
- Molecule 54: 50S ribosomal protein L28



- Molecule 55: 50S ribosomal protein L29



- Molecule 56: 50S ribosomal protein L10



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18629	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.405	Depositor
Minimum map value	-0.133	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.06	Depositor
Map size ($\text{\AA}$)	601.952, 601.952, 601.952	wwPDB
Map dimensions	416, 416, 416	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.447, 1.447, 1.447	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	AA	0.16	0/36859	0.32	5/57501 (0.0%)
2	AB	0.17	0/676	0.41	0/895
3	AC	0.27	0/960	0.57	0/1286
4	AD	0.15	0/652	0.39	0/877
5	AE	0.16	0/892	0.44	0/1193
6	AF	0.17	0/817	0.47	0/1088
7	AG	0.18	0/1651	0.45	0/2225
8	AH	0.44	1/805 (0.1%)	0.98	3/1089 (0.3%)
9	AI	0.14	0/1665	0.34	0/2227
10	AJ	0.16	0/1784	0.43	0/2403
11	AK	0.44	1/1034 (0.1%)	0.50	1/1375 (0.1%)
12	AL	0.22	0/1195	0.43	0/1602
13	AM	0.15	0/893	0.39	0/1205
14	AN	0.17	0/881	0.49	0/1189
15	AO	0.16	0/659	0.46	0/884
16	AP	0.26	0/1157	0.56	0/1557
17	AQ	0.17	0/989	0.48	2/1326 (0.2%)
18	AR	0.19	0/722	0.50	1/964 (0.1%)
19	AS	0.20	0/657	0.53	0/881
20	AT	0.18	0/462	0.41	0/621
21	AU	0.13	0/472	0.38	0/627
22	AV	0.94	0/549	1.60	7/734 (1.0%)
23	AW	0.53	2/407 (0.5%)	0.70	2/633 (0.3%)
24	BA	0.15	1/69710 (0.0%)	0.28	2/108752 (0.0%)
25	BB	0.33	1/1784 (0.1%)	0.45	0/2778
26	BC	0.12	0/2872	0.22	0/4478
27	BD	0.17	0/2121	0.40	0/2852
28	BE	0.22	0/1576	0.43	0/2119
29	BF	0.14	0/1571	0.36	0/2113
30	BG	0.31	0/1434	0.55	4/1926 (0.2%)
31	BH	0.16	0/910	0.42	0/1219
32	BI	0.15	0/421	0.39	0/561
33	BJ	0.24	0/1343	0.44	0/1816
34	BK	0.30	0/1121	0.62	2/1515 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	BL	0.19	0/993	0.53	0/1341
36	BM	0.15	0/450	0.37	0/599
37	BN	0.13	0/380	0.32	0/498
38	BO	0.29	0/513	0.53	0/676
39	BP	0.15	0/303	0.32	0/397
40	BQ	0.14	0/467	0.35	0/623
41	BR	0.16	0/1152	0.36	0/1551
42	BS	0.17	0/955	0.40	0/1279
43	BT	0.16	0/1062	0.38	0/1413
44	BU	0.22	0/1104	0.42	0/1474
45	BV	0.16	0/1006	0.42	0/1345
46	BW	0.17	0/929	0.40	0/1242
47	BX	0.16	0/960	0.36	0/1278
48	BY	0.35	0/829	0.52	0/1107
49	BZ	0.15	0/864	0.40	0/1156
50	DA	0.19	0/744	0.45	0/994
51	DB	0.21	0/787	0.42	0/1051
52	DC	0.16	0/766	0.48	0/1025
53	DD	0.14	0/598	0.37	0/790
54	DE	0.17	0/635	0.41	0/848
55	DF	0.17	0/502	0.50	0/667
56	DG	0.27	0/1037	0.53	0/1400
All	All	0.19	6/158737 (0.0%)	0.36	29/237265 (0.0%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	AK	129	LYS	C-N	12.25	1.50	1.33
24	BA	1915	U	C1'-N1	7.26	1.59	1.48
23	AW	2	U	C1'-N1	6.08	1.57	1.48
8	AH	38	GLY	N-CA	5.82	1.52	1.44
25	BB	36	A	C1'-N9	-5.36	1.40	1.48

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1310	G	O3'-P-O5'	-20.26	73.61	104.00
8	AH	38	GLY	CA-C-N	-17.07	102.32	119.56
8	AH	38	GLY	C-N-CA	-17.07	102.32	119.56
8	AH	39	PRO	CA-N-CD	-8.93	99.49	112.00
24	BA	2902	C	C2'-C3'-O3'	8.07	121.61	109.50

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	AA	32917	0	16563	855	0
2	AB	670	0	719	14	0
3	AC	947	0	1011	70	0
4	AD	637	0	665	26	0
5	AE	883	0	941	35	0
6	AF	805	0	844	31	0
7	AG	1624	0	1696	40	0
8	AH	795	0	836	47	0
9	AI	1643	0	1707	52	0
10	AJ	1753	0	1780	50	0
11	AK	1022	0	1070	52	0
12	AL	1181	0	1238	38	0
13	AM	877	0	887	28	0
14	AN	862	0	864	29	0
15	AO	649	0	666	13	0
16	AP	1144	0	1185	66	0
17	AQ	979	0	1031	35	0
18	AR	714	0	734	15	0
19	AS	648	0	691	25	0
20	AT	455	0	478	12	0
21	AU	465	0	491	9	0
22	AV	539	0	539	34	0
23	AW	365	0	184	22	0
24	BA	62218	0	31285	1369	0
25	BB	1598	0	817	97	0
26	BC	2569	0	1301	31	0
27	BD	2082	0	2154	44	0
28	BE	1556	0	1607	64	0
29	BF	1552	0	1619	43	0
30	BG	1410	0	1444	75	0
31	BH	900	0	935	21	0
32	BI	414	0	442	13	0
33	BJ	1323	0	1371	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	BK	1110	0	1148	59	0
35	BL	979	0	1028	47	0
36	BM	444	0	458	12	0
37	BN	377	0	418	9	0
38	BO	504	0	572	24	0
39	BP	302	0	343	7	0
40	BQ	463	0	504	9	0
41	BR	1129	0	1162	37	0
42	BS	946	0	1023	27	0
43	BT	1053	0	1129	30	0
44	BU	1082	0	1170	27	0
45	BV	993	0	1034	31	0
46	BW	917	0	962	31	0
47	BX	947	0	1019	21	0
48	BY	816	0	839	48	0
49	BZ	857	0	922	21	0
50	DA	738	0	807	23	0
51	DB	779	0	831	29	0
52	DC	753	0	780	17	0
53	DD	591	0	606	9	0
54	DE	625	0	652	18	0
55	DF	501	0	531	19	0
56	DG	1023	0	1050	89	0
All	All	146125	0	98783	3601	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 15.

The worst 5 of 3601 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:523:A:C2	3:AC:88:LYS:CB	1.94	1.48
24:BA:222:A:H62	24:BA:232:G:N2	1.14	1.46
3:AC:44:LYS:CG	3:AC:45:PRO:HD2	1.44	1.45
24:BA:222:A:N6	24:BA:232:G:H21	1.15	1.45
1:AA:1347:G:N7	11:AK:13:LYS:HE2	1.14	1.43

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	
2	AB	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
3	AC	118/124 (95%)	110 (93%)	6 (5%)	2 (2%)	7	34
4	AD	77/92 (84%)	73 (95%)	4 (5%)	0	100	100
5	AE	112/118 (95%)	104 (93%)	8 (7%)	0	100	100
6	AF	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
7	AG	204/233 (88%)	198 (97%)	6 (3%)	0	100	100
8	AH	97/103 (94%)	89 (92%)	8 (8%)	0	100	100
9	AI	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
10	AJ	222/241 (92%)	208 (94%)	14 (6%)	0	100	100
11	AK	125/130 (96%)	116 (93%)	9 (7%)	0	100	100
12	AL	149/179 (83%)	142 (95%)	6 (4%)	1 (1%)	18	51
13	AM	115/129 (89%)	110 (96%)	5 (4%)	0	100	100
14	AN	104/135 (77%)	103 (99%)	1 (1%)	0	100	100
15	AO	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
16	AP	153/167 (92%)	143 (94%)	6 (4%)	4 (3%)	4	27
17	AQ	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
18	AR	86/89 (97%)	86 (100%)	0	0	100	100
19	AS	78/84 (93%)	75 (96%)	3 (4%)	0	100	100
20	AT	53/75 (71%)	53 (100%)	0	0	100	100
21	AU	54/71 (76%)	53 (98%)	1 (2%)	0	100	100
22	AV	67/70 (96%)	53 (79%)	11 (16%)	3 (4%)	2	18
27	BD	269/273 (98%)	260 (97%)	9 (3%)	0	100	100
28	BE	204/209 (98%)	197 (97%)	6 (3%)	1 (0%)	24	57
29	BF	199/201 (99%)	194 (98%)	5 (2%)	0	100	100
30	BG	175/179 (98%)	159 (91%)	15 (9%)	1 (1%)	21	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	BH	115/117 (98%)	111 (96%)	4 (4%)	0	100	100
32	BI	49/55 (89%)	48 (98%)	1 (2%)	0	100	100
33	BJ	174/177 (98%)	166 (95%)	6 (3%)	2 (1%)	11	41
34	BK	147/149 (99%)	133 (90%)	11 (8%)	3 (2%)	6	32
35	BL	132/142 (93%)	123 (93%)	9 (7%)	0	100	100
36	BM	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
37	BN	44/46 (96%)	44 (100%)	0	0	100	100
38	BO	62/65 (95%)	58 (94%)	3 (5%)	1 (2%)	7	35
39	BP	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
40	BQ	57/59 (97%)	56 (98%)	1 (2%)	0	100	100
41	BR	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
42	BS	121/123 (98%)	118 (98%)	3 (2%)	0	100	100
43	BT	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
44	BU	135/136 (99%)	130 (96%)	5 (4%)	0	100	100
45	BV	123/127 (97%)	112 (91%)	11 (9%)	0	100	100
46	BW	112/115 (97%)	112 (100%)	0	0	100	100
47	BX	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
48	BY	101/103 (98%)	94 (93%)	5 (5%)	2 (2%)	6	32
49	BZ	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
50	DA	91/100 (91%)	84 (92%)	7 (8%)	0	100	100
51	DB	100/104 (96%)	96 (96%)	4 (4%)	0	100	100
52	DC	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
53	DD	75/85 (88%)	73 (97%)	2 (3%)	0	100	100
54	DE	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
55	DF	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
56	DG	133/165 (81%)	114 (86%)	15 (11%)	4 (3%)	3	25
All	All	5846/6220 (94%)	5567 (95%)	255 (4%)	24 (0%)	31	62

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AC	44	LYS
16	AP	160	SER

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Mol	Chain	Res	Type
22	AV	31	ASP
22	AV	62	LYS
22	AV	65	ASN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	65/66 (98%)	65 (100%)	0	100	100
3	AC	102/104 (98%)	96 (94%)	6 (6%)	18	43
4	AD	70/79 (89%)	70 (100%)	0	100	100
5	AE	92/96 (96%)	92 (100%)	0	100	100
6	AF	83/84 (99%)	83 (100%)	0	100	100
7	AG	170/190 (90%)	170 (100%)	0	100	100
8	AH	87/90 (97%)	86 (99%)	1 (1%)	65	73
9	AI	172/173 (99%)	172 (100%)	0	100	100
10	AJ	186/199 (94%)	186 (100%)	0	100	100
11	AK	105/107 (98%)	103 (98%)	2 (2%)	50	66
12	AL	124/147 (84%)	121 (98%)	3 (2%)	43	62
13	AM	90/99 (91%)	89 (99%)	1 (1%)	65	73
14	AN	92/116 (79%)	92 (100%)	0	100	100
15	AO	65/65 (100%)	65 (100%)	0	100	100
16	AP	118/126 (94%)	115 (98%)	3 (2%)	42	61
17	AQ	104/105 (99%)	104 (100%)	0	100	100
18	AR	76/77 (99%)	76 (100%)	0	100	100
19	AS	74/78 (95%)	74 (100%)	0	100	100
20	AT	48/65 (74%)	48 (100%)	0	100	100
21	AU	48/61 (79%)	48 (100%)	0	100	100
22	AV	61/62 (98%)	56 (92%)	5 (8%)	10	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	BD	216/218 (99%)	216 (100%)	0	100	100
28	BE	163/164 (99%)	162 (99%)	1 (1%)	78	79
29	BF	165/165 (100%)	165 (100%)	0	100	100
30	BG	148/150 (99%)	146 (99%)	2 (1%)	59	70
31	BH	87/87 (100%)	87 (100%)	0	100	100
32	BI	45/49 (92%)	45 (100%)	0	100	100
33	BJ	137/138 (99%)	137 (100%)	0	100	100
34	BK	114/114 (100%)	111 (97%)	3 (3%)	40	60
35	BL	104/110 (94%)	104 (100%)	0	100	100
36	BM	47/48 (98%)	47 (100%)	0	100	100
37	BN	38/38 (100%)	38 (100%)	0	100	100
38	BO	51/52 (98%)	49 (96%)	2 (4%)	28	52
39	BP	34/34 (100%)	34 (100%)	0	100	100
40	BQ	49/49 (100%)	49 (100%)	0	100	100
41	BR	116/116 (100%)	116 (100%)	0	100	100
42	BS	104/104 (100%)	104 (100%)	0	100	100
43	BT	103/103 (100%)	103 (100%)	0	100	100
44	BU	110/109 (101%)	110 (100%)	0	100	100
45	BV	102/103 (99%)	102 (100%)	0	100	100
46	BW	99/100 (99%)	99 (100%)	0	100	100
47	BX	89/90 (99%)	89 (100%)	0	100	100
48	BY	84/84 (100%)	79 (94%)	5 (6%)	17	43
49	BZ	93/93 (100%)	93 (100%)	0	100	100
50	DA	80/84 (95%)	80 (100%)	0	100	100
51	DB	83/85 (98%)	81 (98%)	2 (2%)	43	62
52	DC	78/78 (100%)	78 (100%)	0	100	100
53	DD	58/63 (92%)	58 (100%)	0	100	100
54	DE	67/68 (98%)	67 (100%)	0	100	100
55	DF	54/55 (98%)	54 (100%)	0	100	100
56	DG	103/123 (84%)	100 (97%)	3 (3%)	37	58
All	All	4853/5063 (96%)	4814 (99%)	39 (1%)	70	76

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	BO	33	LEU
51	DB	91	LYS
48	BY	48	LYS
48	BY	54	VAL
56	DG	132	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
33	BJ	88	GLN
46	BW	56	HIS
33	BJ	128	GLN
35	BL	105	GLN
47	BX	81	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1533/1534 (99%)	420 (27%)	36 (2%)
23	AW	16/17 (94%)	5 (31%)	0
24	BA	2893/2904 (99%)	638 (22%)	35 (1%)
25	BB	74/77 (96%)	28 (37%)	1 (1%)
26	BC	119/120 (99%)	14 (11%)	0
All	All	4635/4652 (99%)	1105 (23%)	72 (1%)

5 of 1105 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	4	U
1	AA	5	U
1	AA	6	G
1	AA	9	G
1	AA	13	U

5 of 72 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	BA	2145	C
25	BB	1	C

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Mol	Chain	Res	Type
24	BA	2184	A
24	BA	2504	U
1	AA	1225	A

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

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

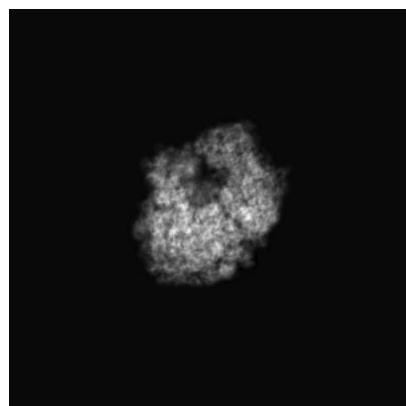
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29214. These allow visual inspection of the internal detail of the map and identification of artifacts.

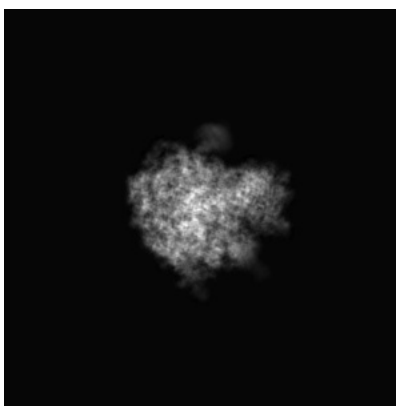
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

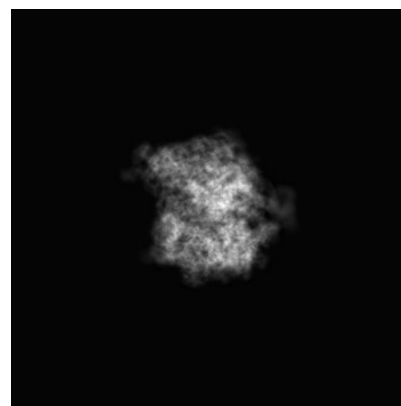
6.1.1 Primary map



X

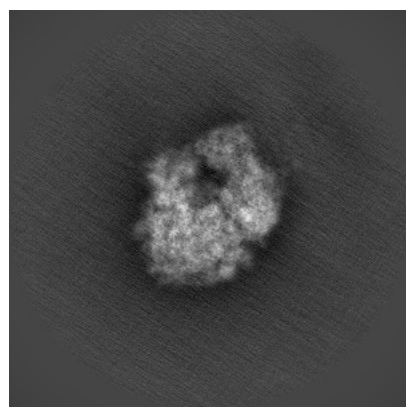


Y

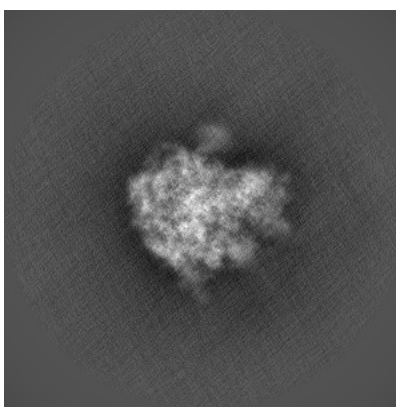


Z

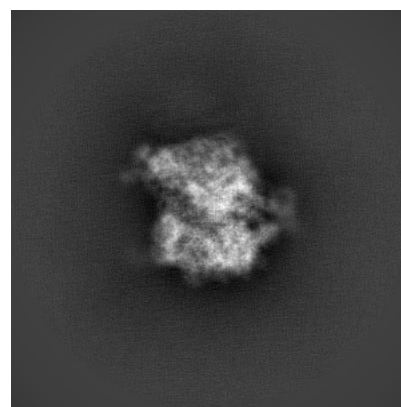
6.1.2 Raw map



X



Y

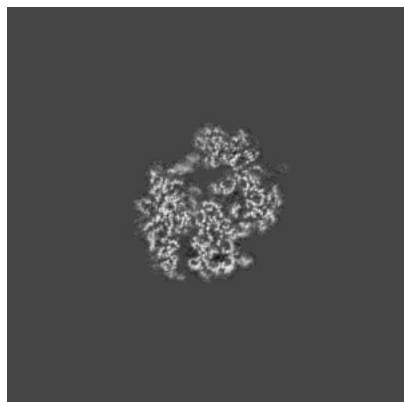


Z

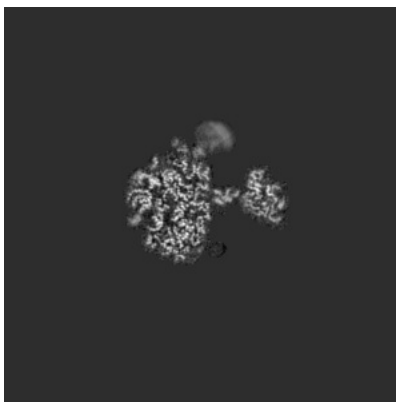
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

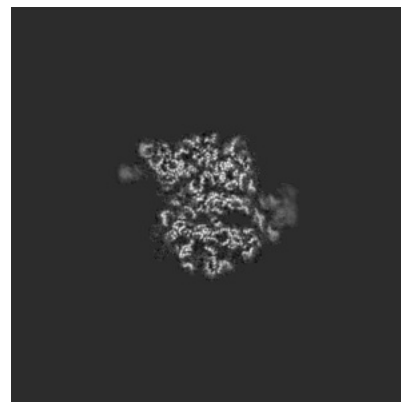
6.2.1 Primary map



X Index: 208

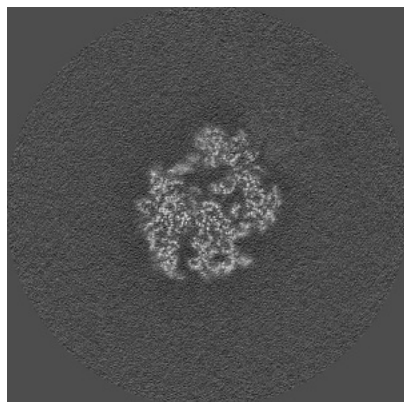


Y Index: 208

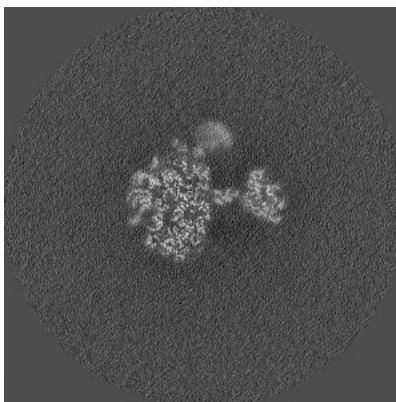


Z Index: 208

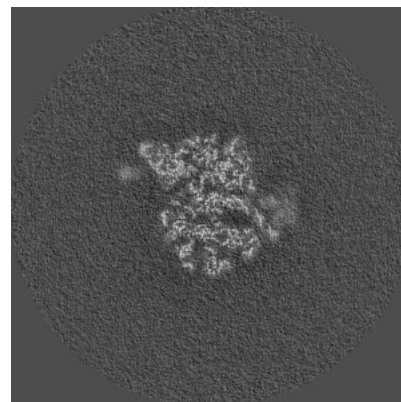
6.2.2 Raw map



X Index: 208



Y Index: 208

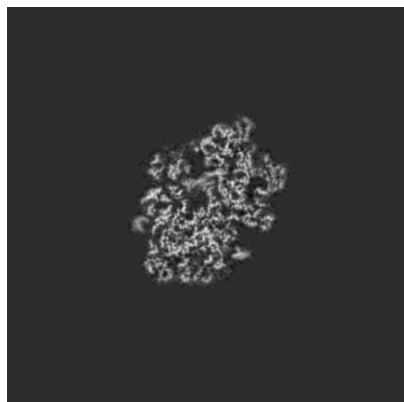


Z Index: 208

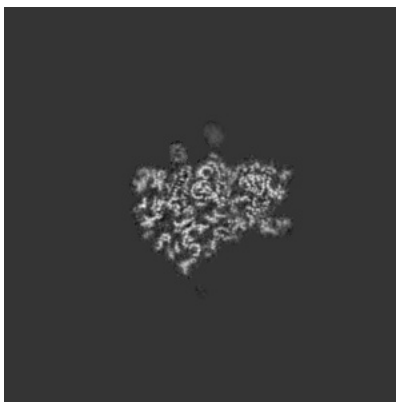
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

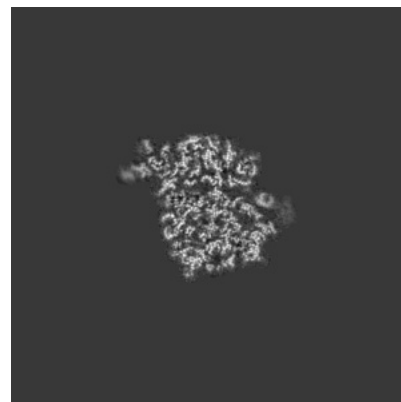
6.3.1 Primary map



X Index: 221

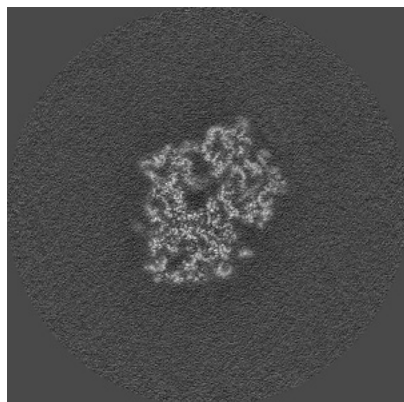


Y Index: 231

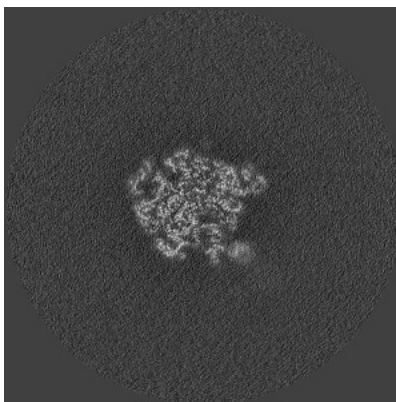


Z Index: 202

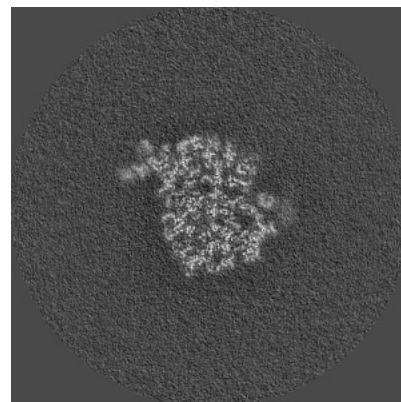
6.3.2 Raw map



X Index: 227



Y Index: 171

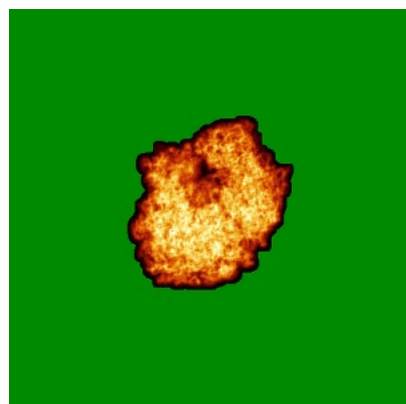


Z Index: 203

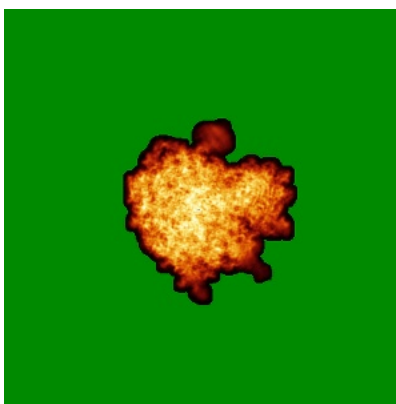
The images above show the largest variance slices of the map in three orthogonal directions.

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

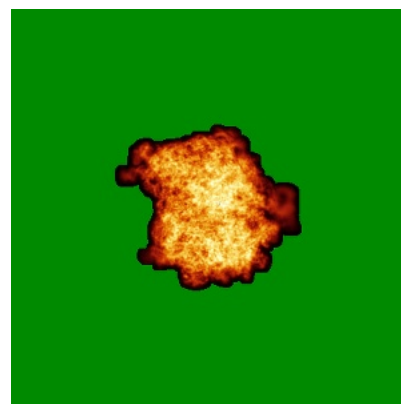
6.4.1 Primary map



X

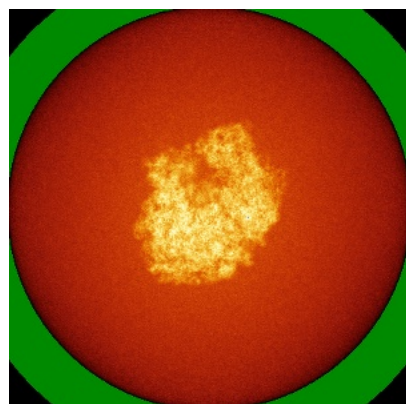


Y

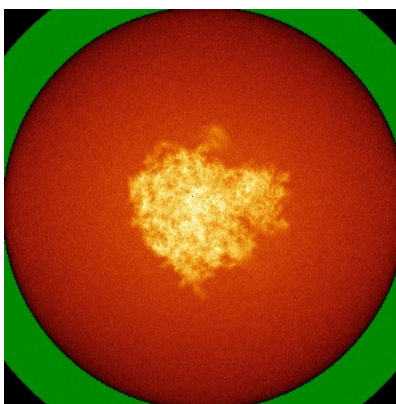


Z

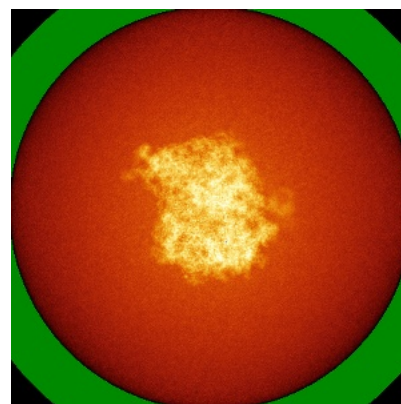
6.4.2 Raw map



X



Y



Z

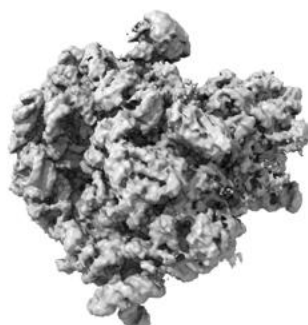
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



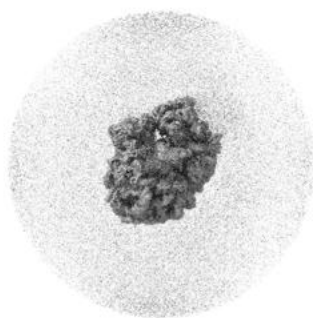
Y



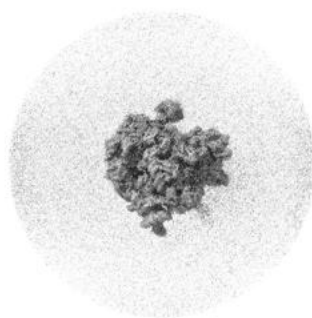
Z

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.

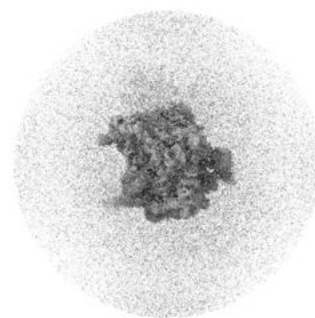
6.5.2 Raw map



X



Y



Z

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.

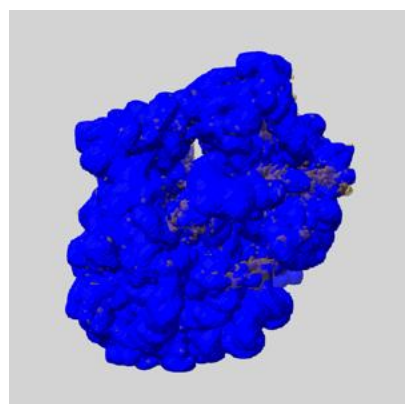
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

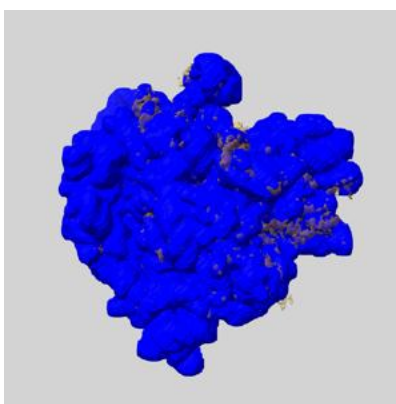
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

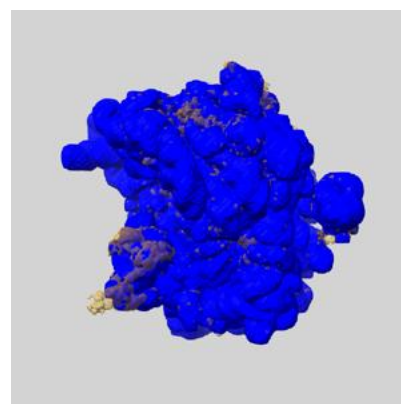
6.6.1 emd_29214_msk_1.map [i](#)



X



Y

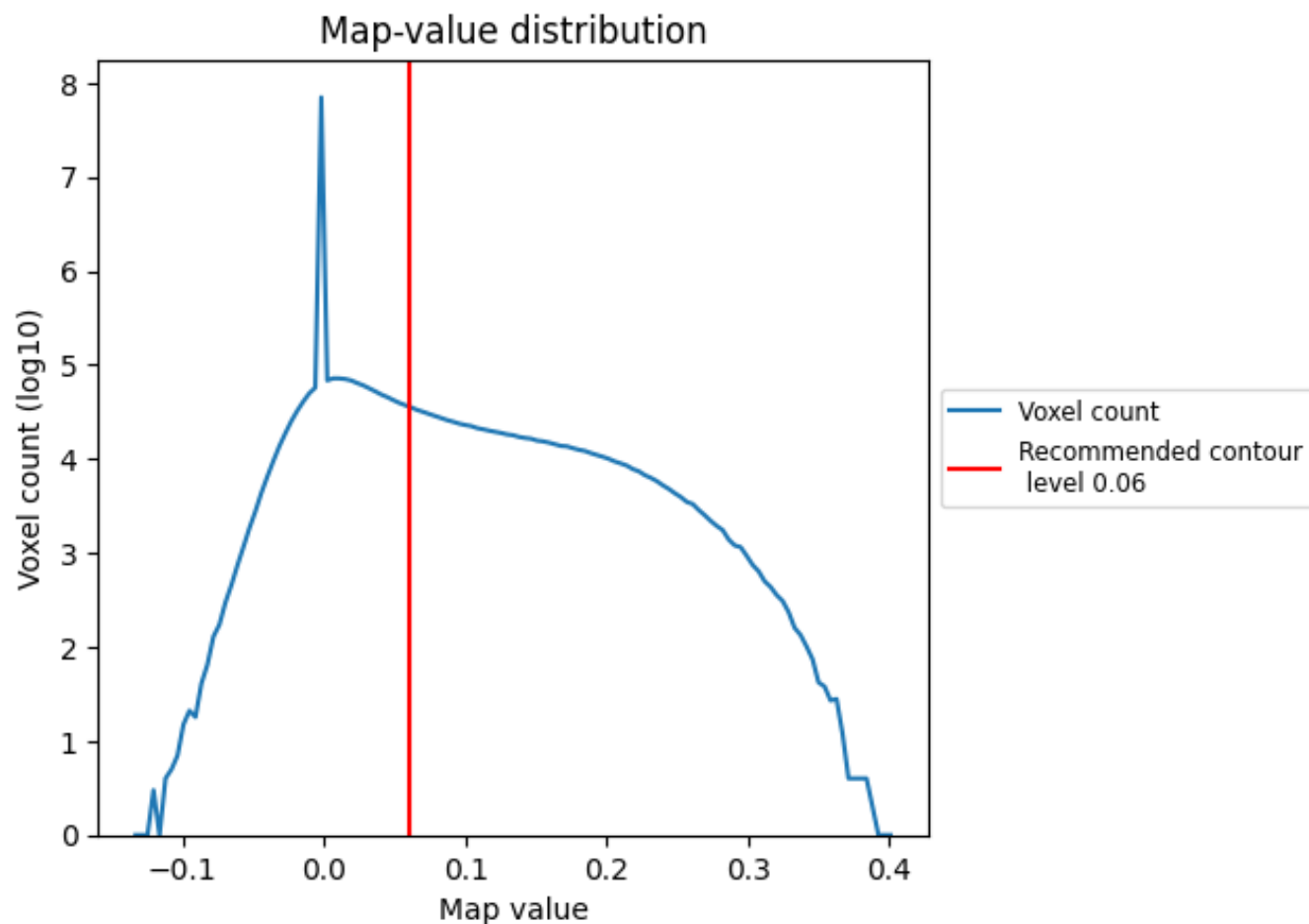


Z

7 Map analysis [i](#)

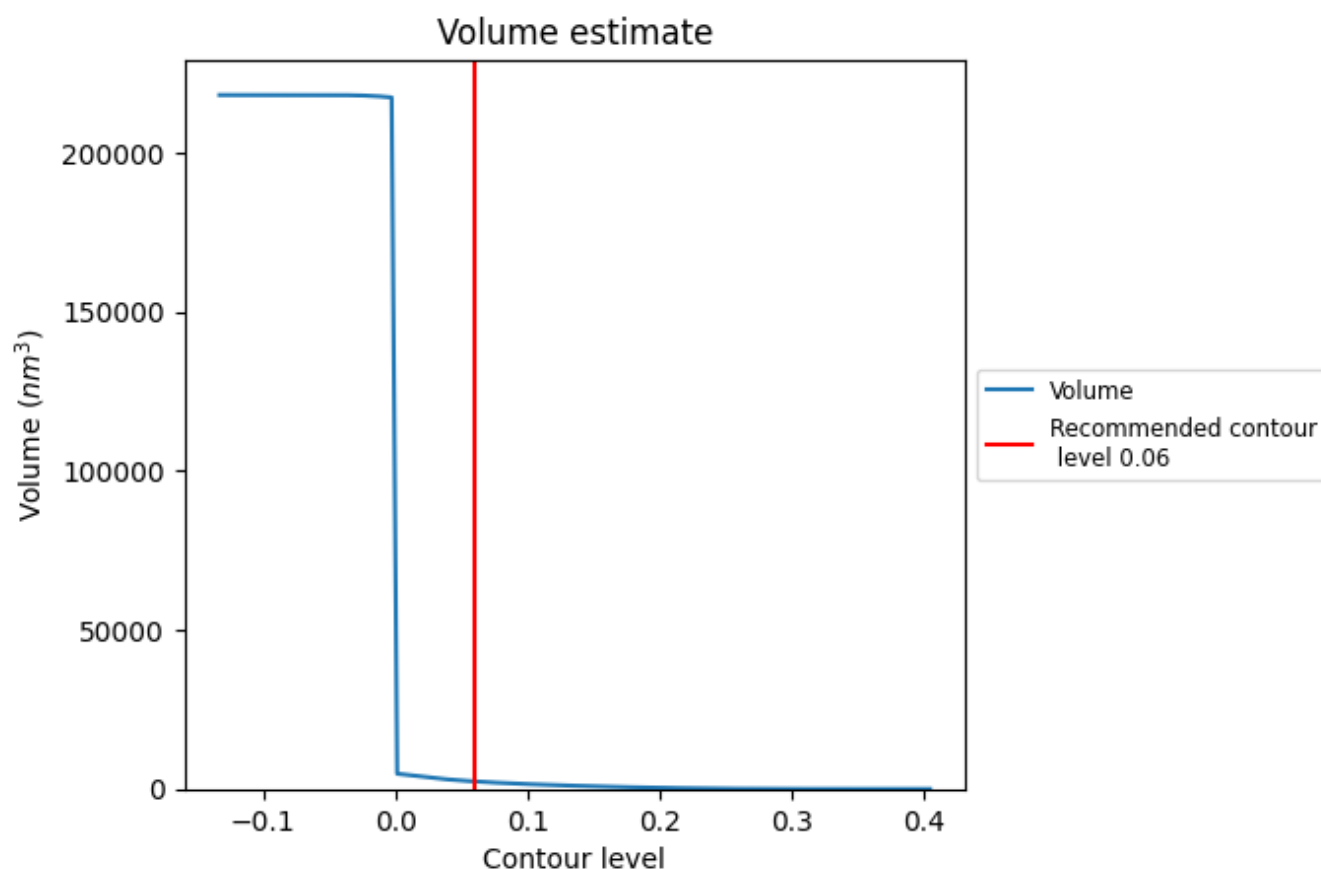
This section contains the results of statistical analysis of the map.

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.

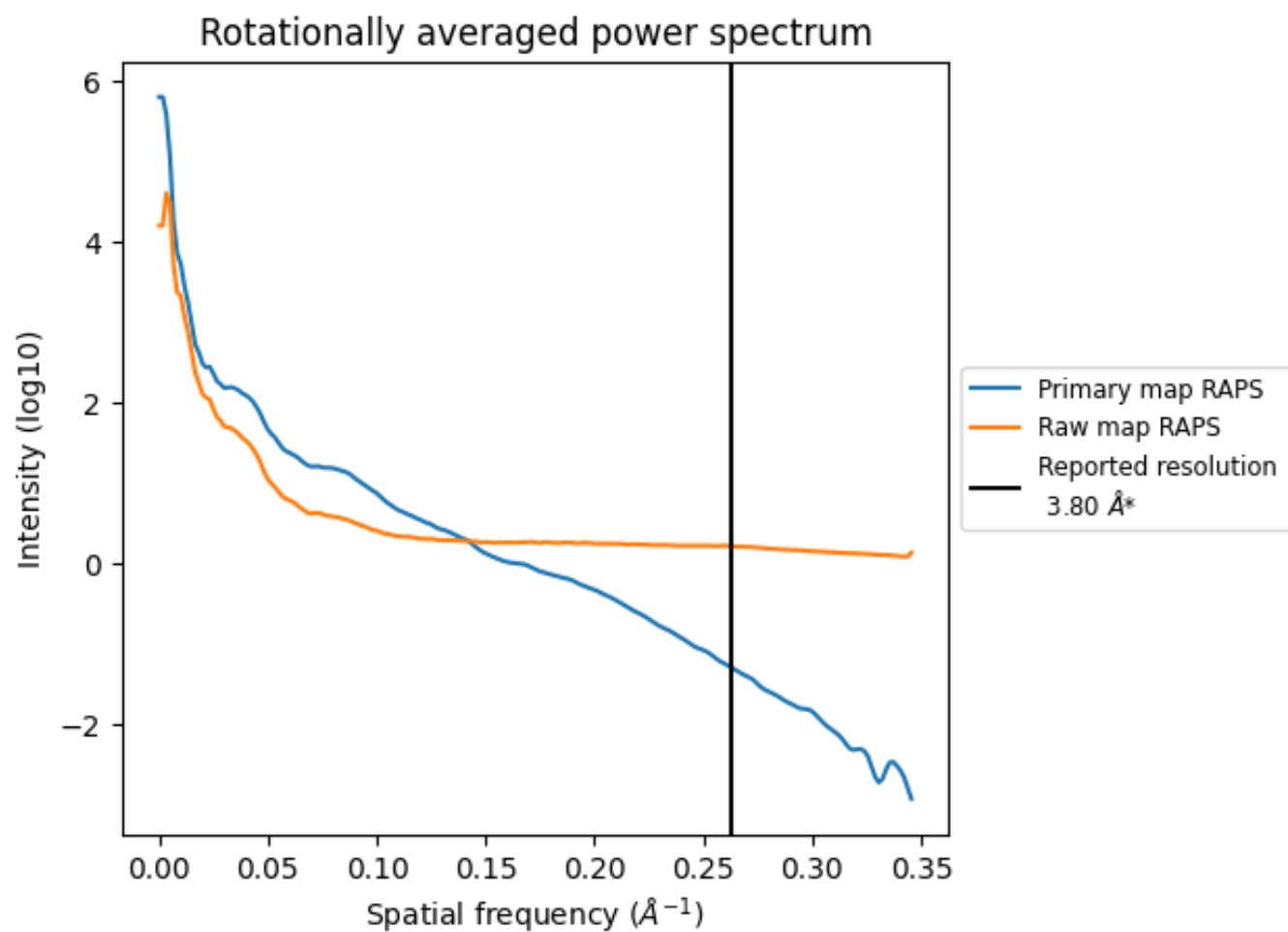
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2370 nm³; this corresponds to an approximate mass of 2141 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 ⓘ

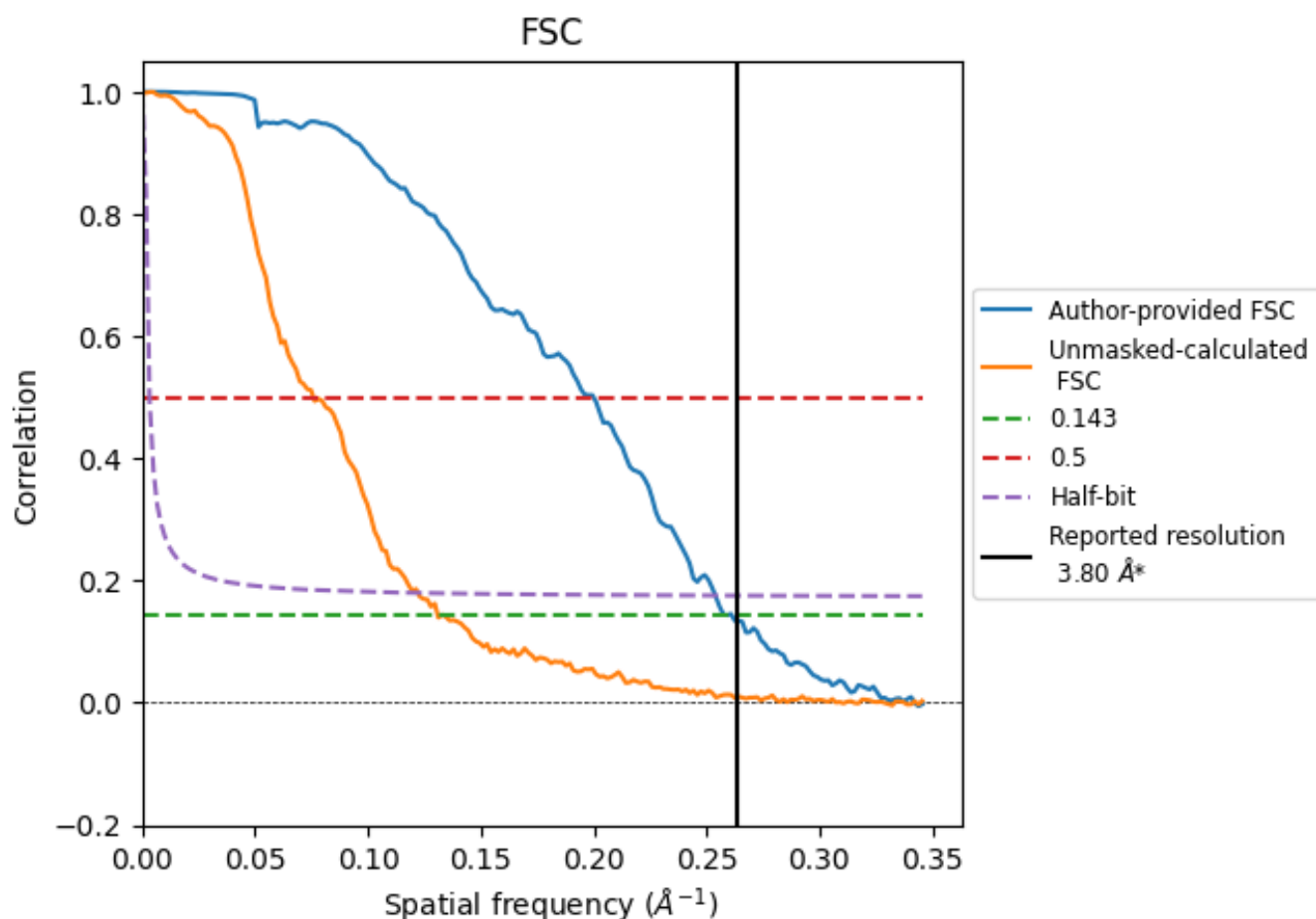


*Reported resolution corresponds to spatial frequency of 0.263 $\text{\AA}^{-1}$

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 $0.263 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

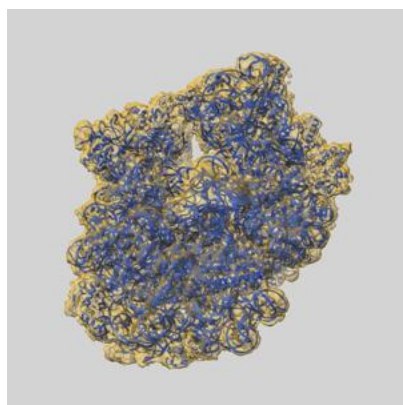
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.83	5.00	3.94
Unmasked-calculated*	7.63	13.19	8.19

*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 7.63 differs from the reported value 3.8 by more than 10 %

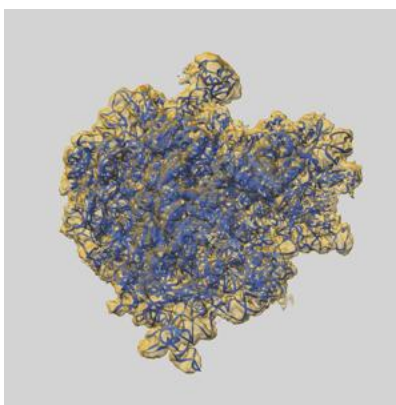
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-29214 and PDB model 8FIZ. Per-residue inclusion information can be found in section 3 on page 15.

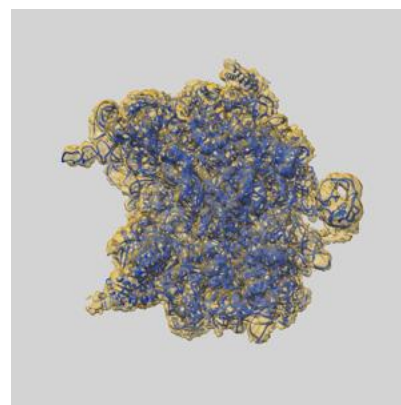
9.1 Map-model overlay [i](#)



X



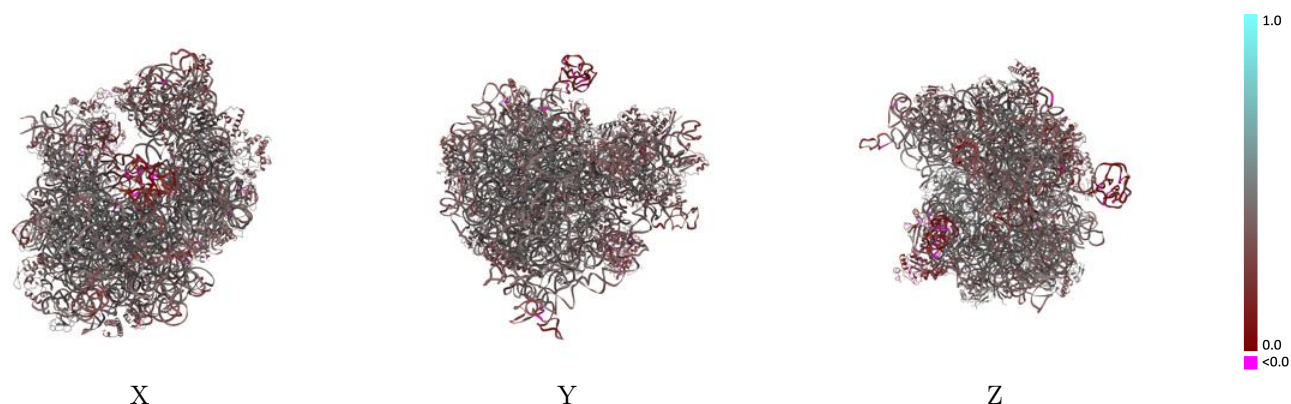
Y



Z

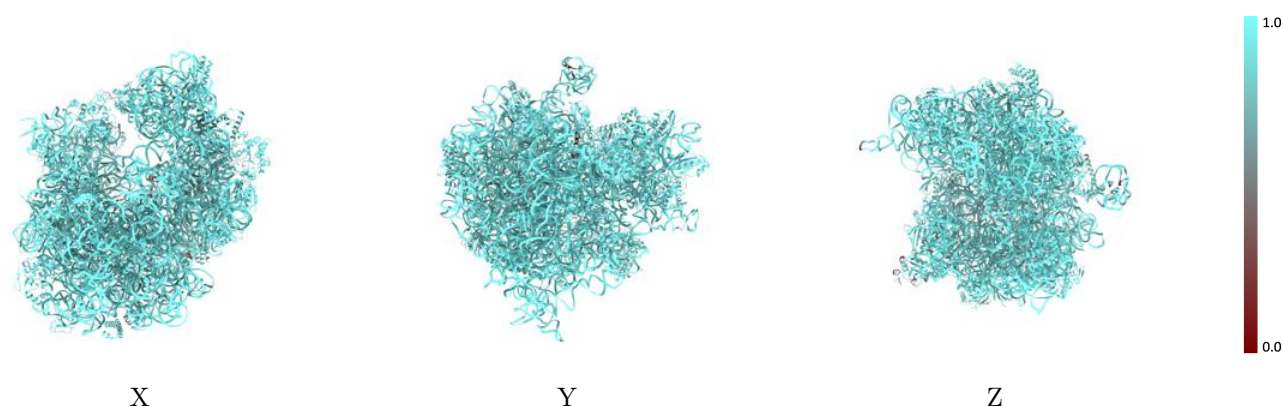
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



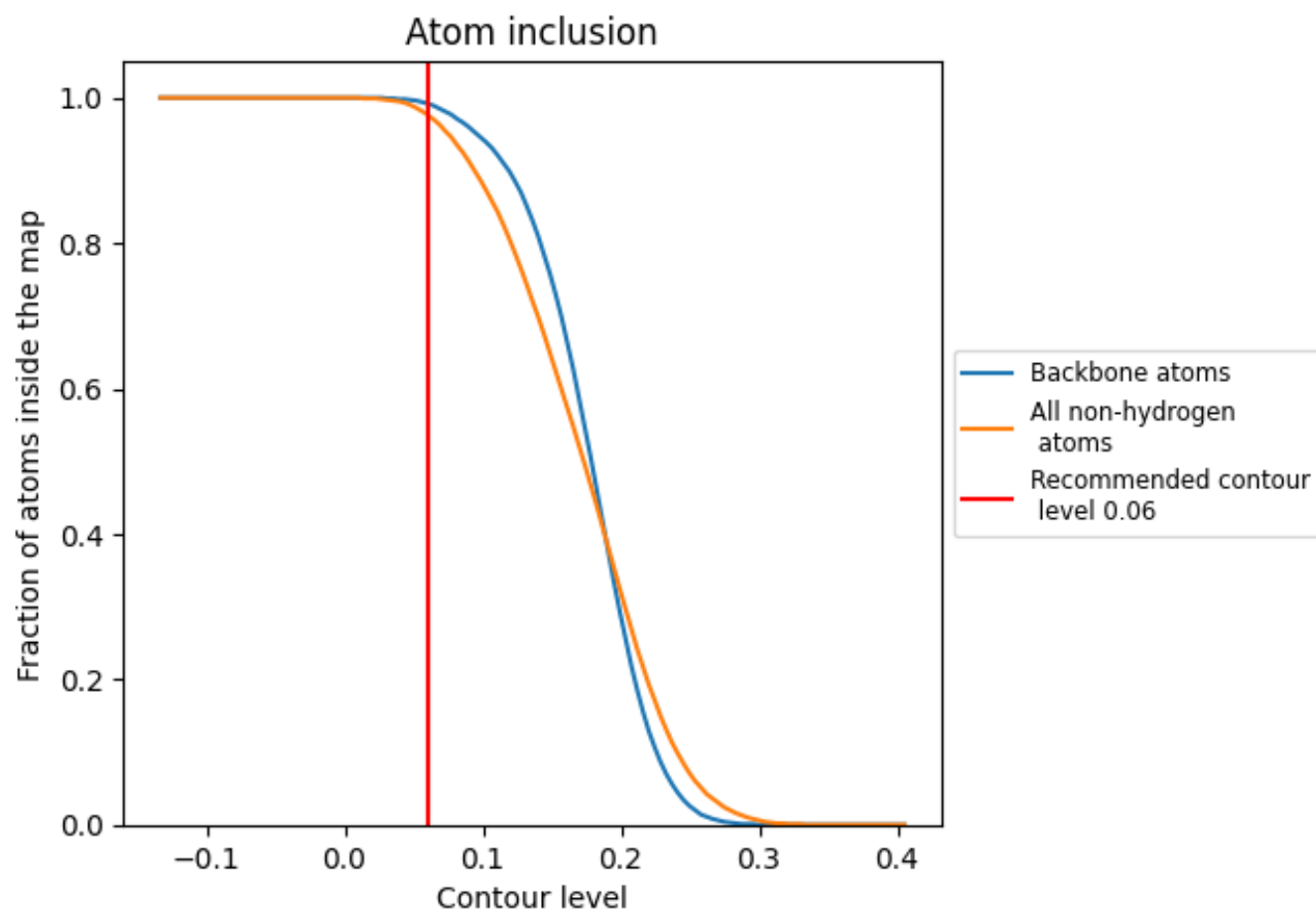
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 99% of all backbone atoms, 98% 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	 0.9770	 0.3940
AA	 0.9930	 0.3980
AB	 0.9280	 0.3370
AC	 0.9560	 0.4160
AD	 0.9530	 0.3690
AE	 0.9800	 0.3710
AF	 0.9570	 0.3720
AG	 0.9350	 0.3930
AH	 0.9550	 0.3630
AI	 0.9420	 0.3770
AJ	 0.9310	 0.3390
AK	 0.9600	 0.3680
AL	 0.9330	 0.3320
AM	 0.9730	 0.3840
AN	 0.9770	 0.3740
AO	 0.9410	 0.4140
AP	 0.9720	 0.4120
AQ	 0.9620	 0.4070
AR	 0.9730	 0.3750
AS	 0.9490	 0.3750
AT	 0.9630	 0.3780
AU	 0.7320	 0.3420
AV	 0.8750	 0.2720
AW	 0.8740	 0.2470
BA	 0.9950	 0.4060
BB	 0.9730	 0.3040
BC	 1.0000	 0.4080
BD	 0.9710	 0.4410
BE	 0.9610	 0.4240
BF	 0.9600	 0.4020
BG	 0.9530	 0.3730
BH	 0.9690	 0.3930
BI	 0.9410	 0.4180
BJ	 0.9380	 0.3760
BK	 0.8180	 0.3130



Continued on next page...

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Chain	Atom inclusion	Q-score
BL	 0.8090	 0.1180
BM	 0.9630	 0.4190
BN	 0.9440	 0.4260
BO	 0.9510	 0.4420
BP	 0.9450	 0.4480
BQ	 0.9430	 0.4190
BR	 0.9660	 0.4210
BS	 0.9390	 0.4250
BT	 0.9560	 0.4250
BU	 0.9550	 0.4250
BV	 0.9530	 0.4020
BW	 0.9600	 0.4180
BX	 0.9800	 0.4030
BY	 0.9850	 0.4140
BZ	 0.9390	 0.4170
DA	 0.9400	 0.3820
DB	 0.9470	 0.3880
DC	 0.9700	 0.4010
DD	 0.9650	 0.4420
DE	 0.9570	 0.4190
DF	 0.9320	 0.3100
DG	 0.7120	 0.1490