



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 10:13 PM UTC

PDB ID : 8AGW / pdb_00008agw
EMDB ID : EMD-15426
Title : Yeast RQC complex in state D
Authors : Tesina, P.; Buschauer, R.; Beckmann, R.
Deposited on : 2022-07-20
Resolution : 2.60 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

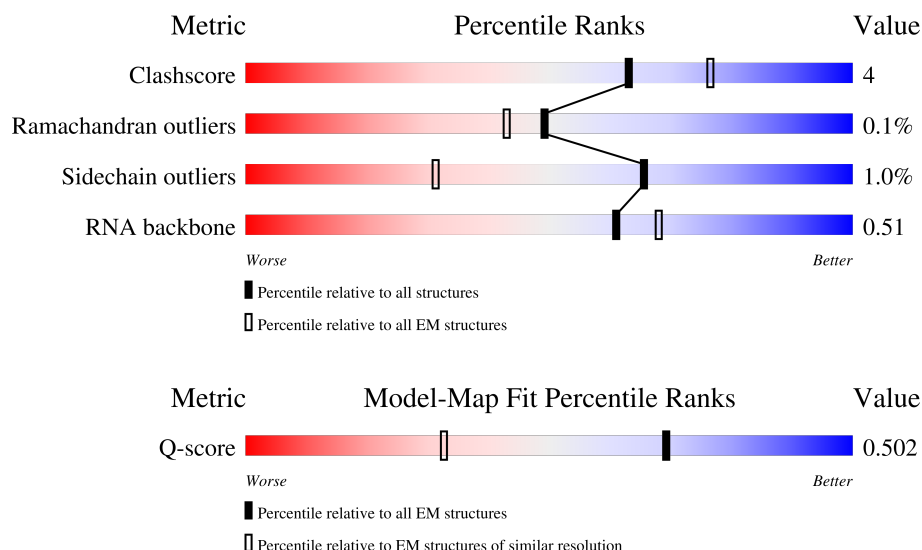
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.60 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.



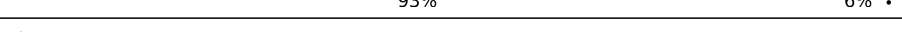
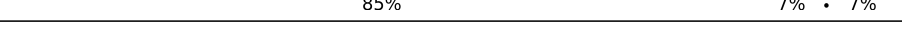
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8728 (2.10 - 3.10)

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	A	204	
2	B	199	
3	C	184	

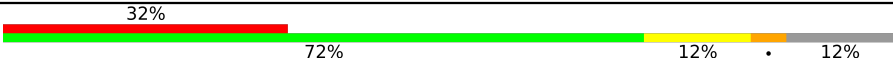
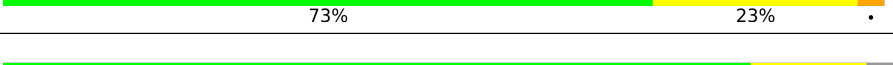
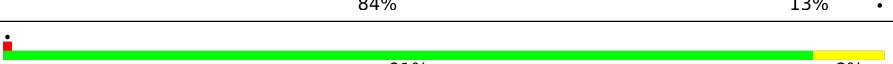
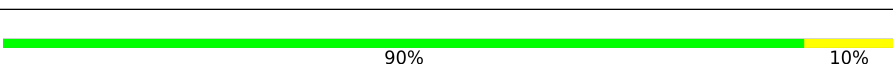
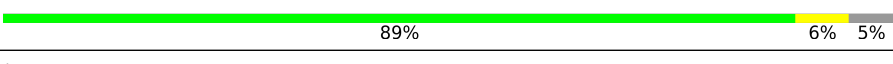
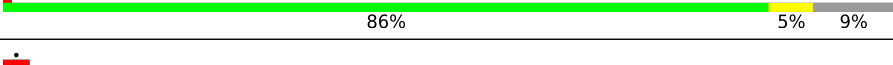
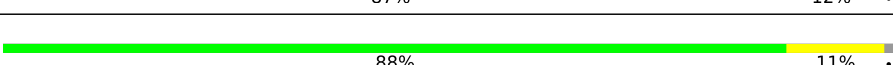
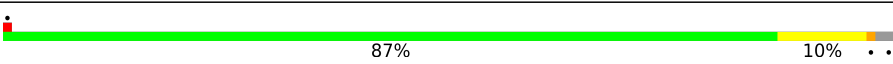
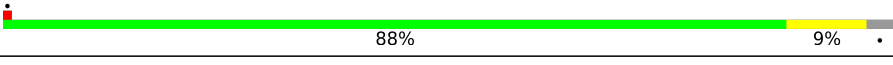
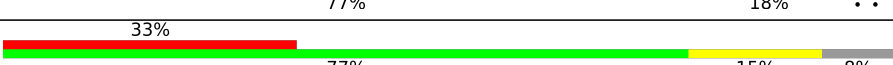
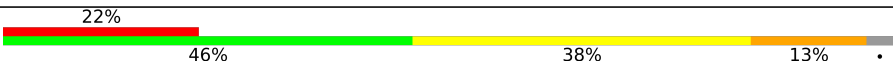
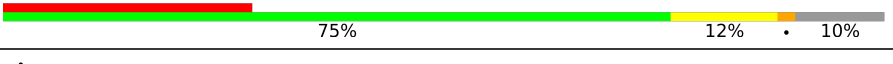
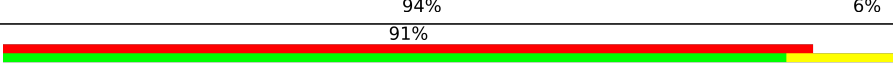
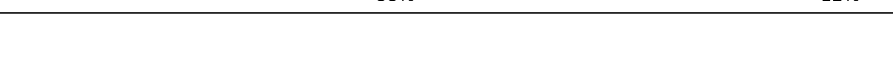
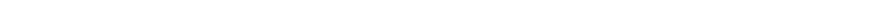
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Mol	Chain	Length	Quality of chain
4	D	186	
5	E	189	
6	F	172	
7	G	160	
8	H	121	
9	I	137	
10	J	155	
11	K	142	
12	L	127	
13	M	136	
14	N	149	
15	O	59	
16	P	105	
17	Q	113	
18	R	130	
19	S	107	
20	T	121	
21	U	120	
22	V	100	
23	W	88	
24	X	78	
25	Y	51	
26	Z	128	
27	b	106	
28	c	92	

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Mol	Chain	Length	Quality of chain
29	d	25	
30	f	3395	
31	h	121	
32	i	158	
33	j	254	
34	k	387	
35	l	362	
36	m	297	
37	n	176	
38	o	244	
39	p	256	
40	q	191	
41	r	221	
42	s	174	
43	t	199	
44	u	138	
45	a	1038	
46	e	1562	
47	g	245	
48	x	76	
48	y	76	
49	z	165	
50	0	312	
51	1	17	
52	w	217	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 150269 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 60S ribosomal protein L15-A.

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

- Molecule 2 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 3 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 4 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 5 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	156	Total	C	N	O		0	0
			1258	781	265	212			

- Molecule 6 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 7 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	159	Total	C	N	O	S	0	0
			1272	802	245	221	4		

- Molecule 8 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 9 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 10 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	63	Total	C	N	O	S	0	0
			518	333	102	82	1		

- Molecule 11 is a protein called 60S ribosomal protein L25.

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

- Molecule 12 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 13 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	135	Total	C	N	O	S	0	0
			1080	701	199	180			

- Molecule 14 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	148	Total	C	N	O	S	0	0
			1169	747	231	188	3		

- Molecule 15 is a protein called 60S ribosomal protein L29.

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

- Molecule 16 is a protein called 60S ribosomal protein L30.

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

- Molecule 17 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	127	Total	C	N	O	S	0	0
			1013	642	205	165	1		

- Molecule 19 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 21 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

- Molecule 24 is a protein called 60S ribosomal protein L38.

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

- Molecule 25 is a protein called 60S ribosomal protein L39.

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

- Molecule 26 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 27 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 28 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 29 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	22	Total	C	N	O	S	0	0
			207	127	56	23	1		

- Molecule 30 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	3216	Total	C	N	O	P	1	0
			68802	30732	12391	22462	3217		

- Molecule 31 is a RNA chain called 5S rRNA.

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

- Molecule 32 is a RNA chain called 5.8S rRNA.

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

- Molecule 33 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	j	246	Total	C	N	O	S	0	0
			1874	1168	380	325	1		

- Molecule 34 is a protein called 60S ribosomal protein L3.

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

- Molecule 35 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L5.

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

- Molecule 37 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	n	167	Total	C	N	O		0	0
			1307	843	234	230			

- Molecule 38 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 39 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 41 is a protein called 60S ribosomal protein L10.

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

- Molecule 42 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	s	169	Total	C	N	O	S	0	0
			1346	843	252	247	4		

- Molecule 43 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 45 is a protein called RQC2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	a	848	Total	C	N	O	S	0	0
			6573	4191	1139	1226	17		

- Molecule 46 is a protein called E3 ubiquitin-protein ligase listerin.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	e	1527	Total	C	N	O	S	0	0
			11512	7356	1937	2181	38		

- Molecule 47 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	g	225	Total	C	N	O	S	0	0
			1651	1030	282	332	7		

- Molecule 48 is a RNA chain called Ala tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	x	74	Total	C	N	O	P	0	0
			1579	702	278	525	74		
48	y	73	Total	C	N	O	P	0	0
			1556	692	273	518	73		

- Molecule 49 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	z	148	Total	C	N	O	0	0
			728	432	148	148		

- Molecule 50 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	0	121	Total	C	N	O	S	0	0
			961	618	167	173	3		

- Molecule 51 is a protein called CAT-tailed nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	1	17	Total	C	N	O	0	0
			85	51	17	17		

- Molecule 52 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	w	216	Total	C	N	O	S	0	0
			1709	1092	298	310	9		

- Molecule 53 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
53	A	1	Total	Mg	0
			1	1	
53	C	1	Total	Mg	0
			1	1	
53	E	1	Total	Mg	0
			1	1	
53	I	1	Total	Mg	0
			1	1	
53	R	1	Total	Mg	0
			1	1	
53	T	1	Total	Mg	0
			1	1	
53	f	3	Total	Mg	0
			3	3	
53	h	1	Total	Mg	0
			1	1	
53	j	2	Total	Mg	0
			2	2	

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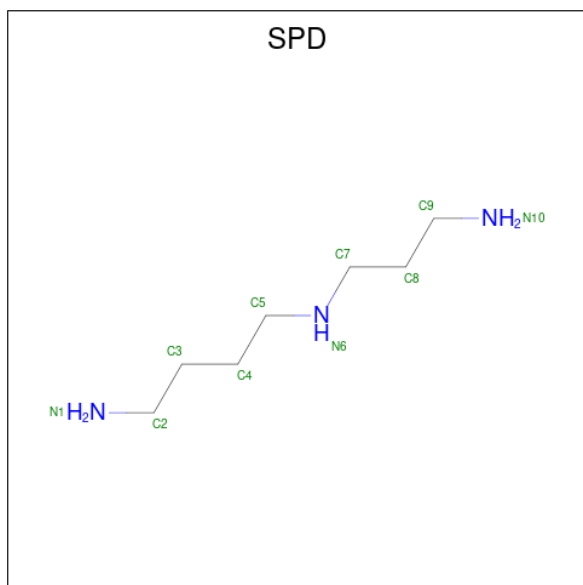
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Mol	Chain	Residues	Atoms		AltConf
53	k	1	Total	Mg	0
			1	1	

- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
54	T	1	Total	Zn	0
			1	1	
54	W	1	Total	Zn	0
			1	1	
54	Z	1	Total	Zn	0
			1	1	
54	b	1	Total	Zn	0
			1	1	
54	c	1	Total	Zn	0
			1	1	
54	e	2	Total	Zn	0
			2	2	

- Molecule 55 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



Mol	Chain	Residues	Atoms			AltConf
55	f	1	Total	C	N	0
			10	7	3	

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: 60S ribosomal protein L15-A

Chain A: 



- Molecule 2: 60S ribosomal protein L16-A

Chain B: 



- Molecule 3: 60S ribosomal protein L17-A

Chain C: 



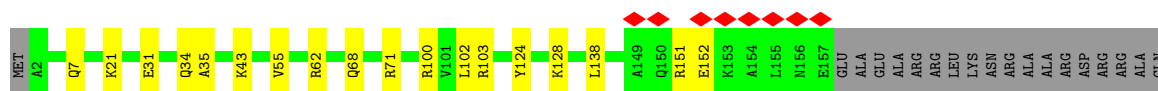
- Molecule 4: 60S ribosomal protein L18-A

Chain D: 



- Molecule 5: 60S ribosomal protein L19-A

Chain E: 



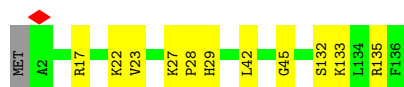
- Molecule 12: 60S ribosomal protein L26-A

Chain L:  91% 8%



- Molecule 13: 60S ribosomal protein L27-A

Chain M:  91% 8%



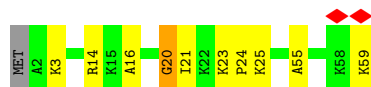
- Molecule 14: 60S ribosomal protein L28

Chain N:  87% 13%



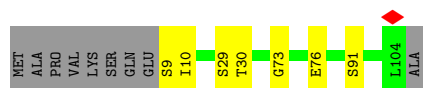
- Molecule 15: 60S ribosomal protein L29

Chain O:  81% 15%



- Molecule 16: 60S ribosomal protein L30

Chain P:  85% 7% 9%



- Molecule 17: 60S ribosomal protein L31-A

Chain Q:  5% 80% 17%



- Molecule 18: 60S ribosomal protein L32

Chain R:  89% 8%



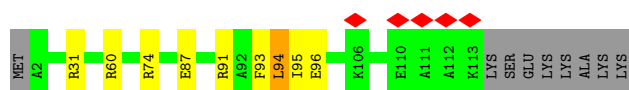
- Molecule 19: 60S ribosomal protein L33-A

Chain S: 93% 6%



- Molecule 20: 60S ribosomal protein L34-A

Chain T: 85% 7% 7%



- Molecule 21: 60S ribosomal protein L35-A

Chain U: 92% 7%



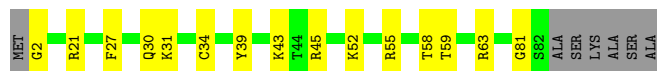
- Molecule 22: 60S ribosomal protein L36-A

Chain V: 89% 10%



- Molecule 23: 60S ribosomal protein L37-A

Chain W: 75% 17% 8%



- Molecule 24: 60S ribosomal protein L38

Chain X: 90% 9%



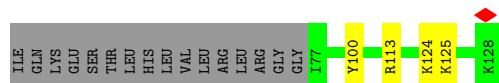
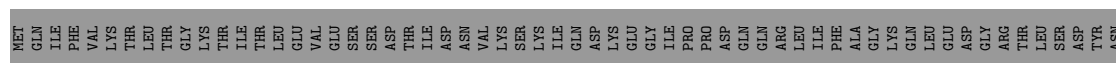
- Molecule 25: 60S ribosomal protein L39

Chain Y:  92% 6% .



- Molecule 26: Ubiquitin-60S ribosomal protein L40

Chain Z:  38% . 59%



- Molecule 27: 60S ribosomal protein L42-A

Chain b:  81% 16% .



- Molecule 28: 60S ribosomal protein L43-A

Chain c:  90% 9% .



- Molecule 29: 60S ribosomal protein L41-A

Chain d:  32% 72% 12% . 12%



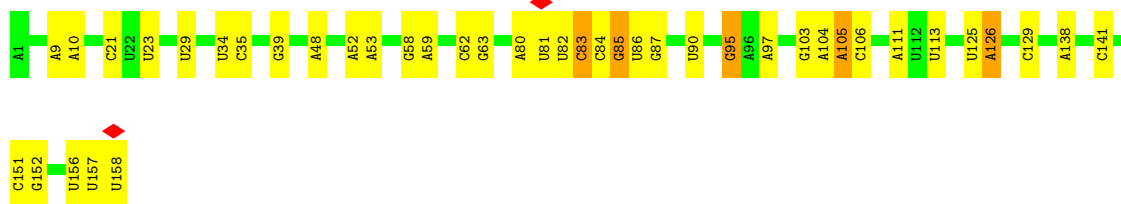
- Molecule 30: 25S rRNA

Chain f:  67% 24% . 5%



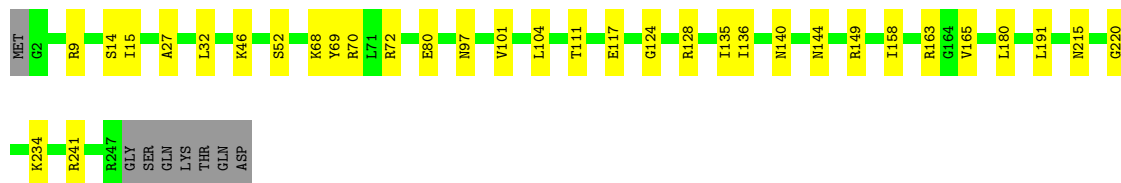


Chain i:  73% 23%

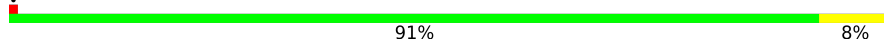


- Molecule 33: 60S ribosomal protein L2-A

Chain j:  84% 13%



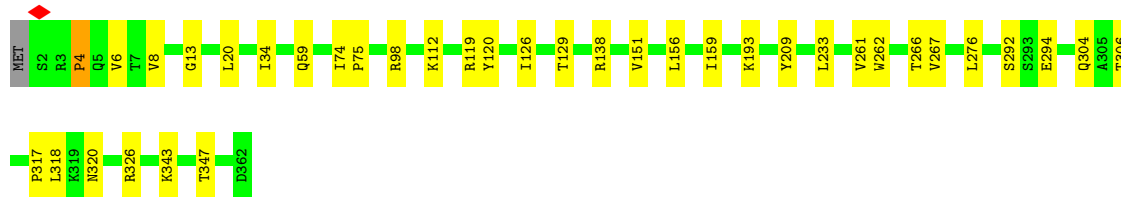
- Molecule 34: 60S ribosomal protein L3

Chain k:  91% 8%



- Molecule 35: 60S ribosomal protein L4-A

Chain l:  90% 10%



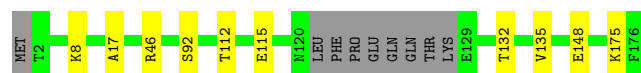
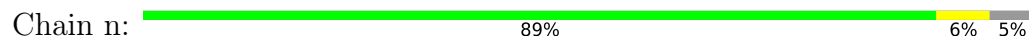
- Molecule 36: 60S ribosomal protein L5

Chain m:  82% 16%

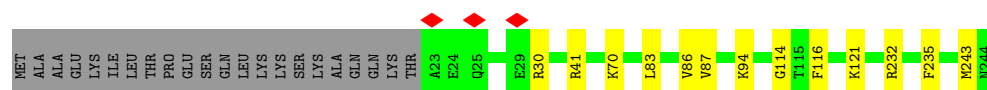
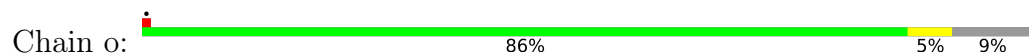




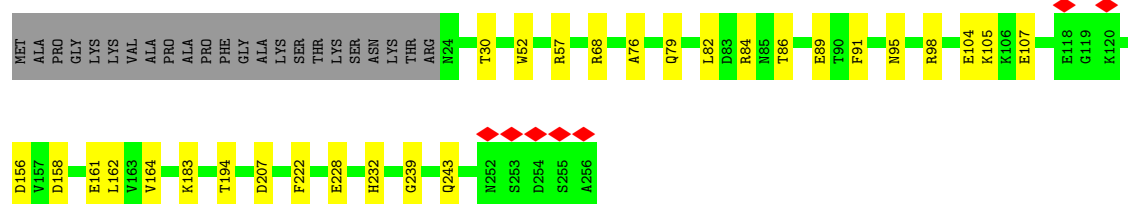
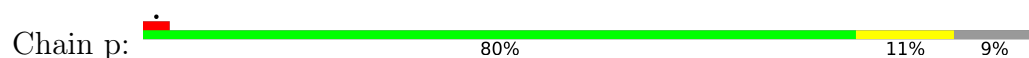
- Molecule 37: 60S ribosomal protein L6-B



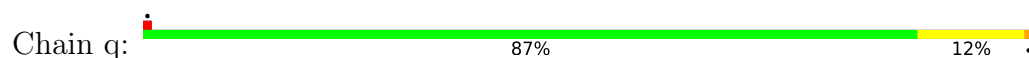
- Molecule 38: 60S ribosomal protein L7-A



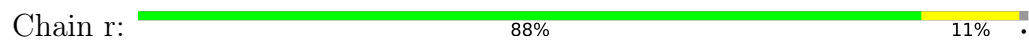
- Molecule 39: 60S ribosomal protein L8-A



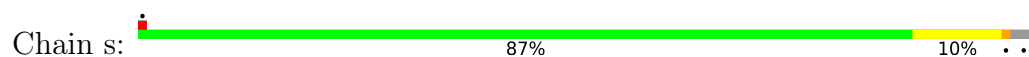
- Molecule 40: 60S ribosomal protein L9-A



- Molecule 41: 60S ribosomal protein L10

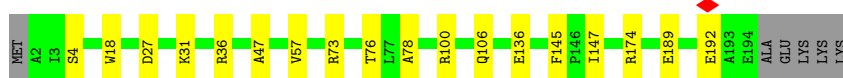
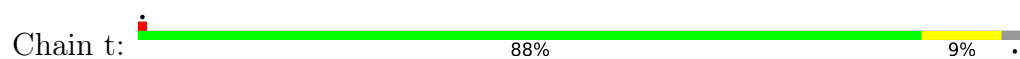


- Molecule 42: 60S ribosomal protein L11-A

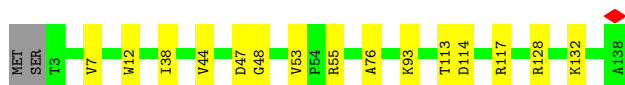
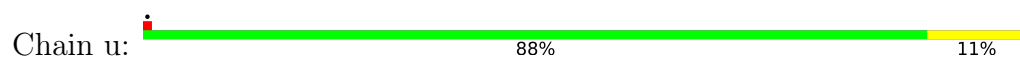




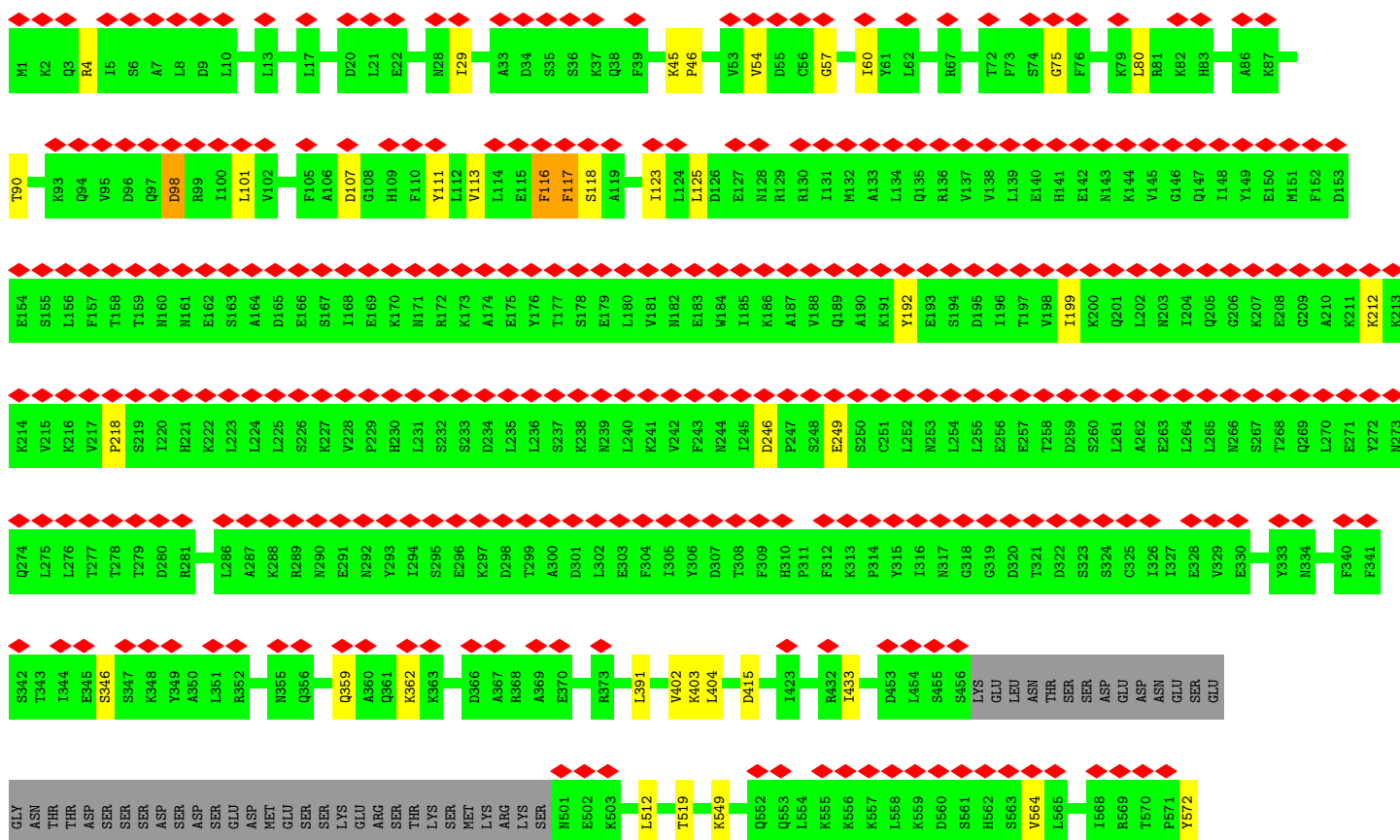
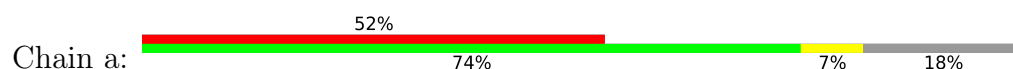
- Molecule 43: 60S ribosomal protein L13-A

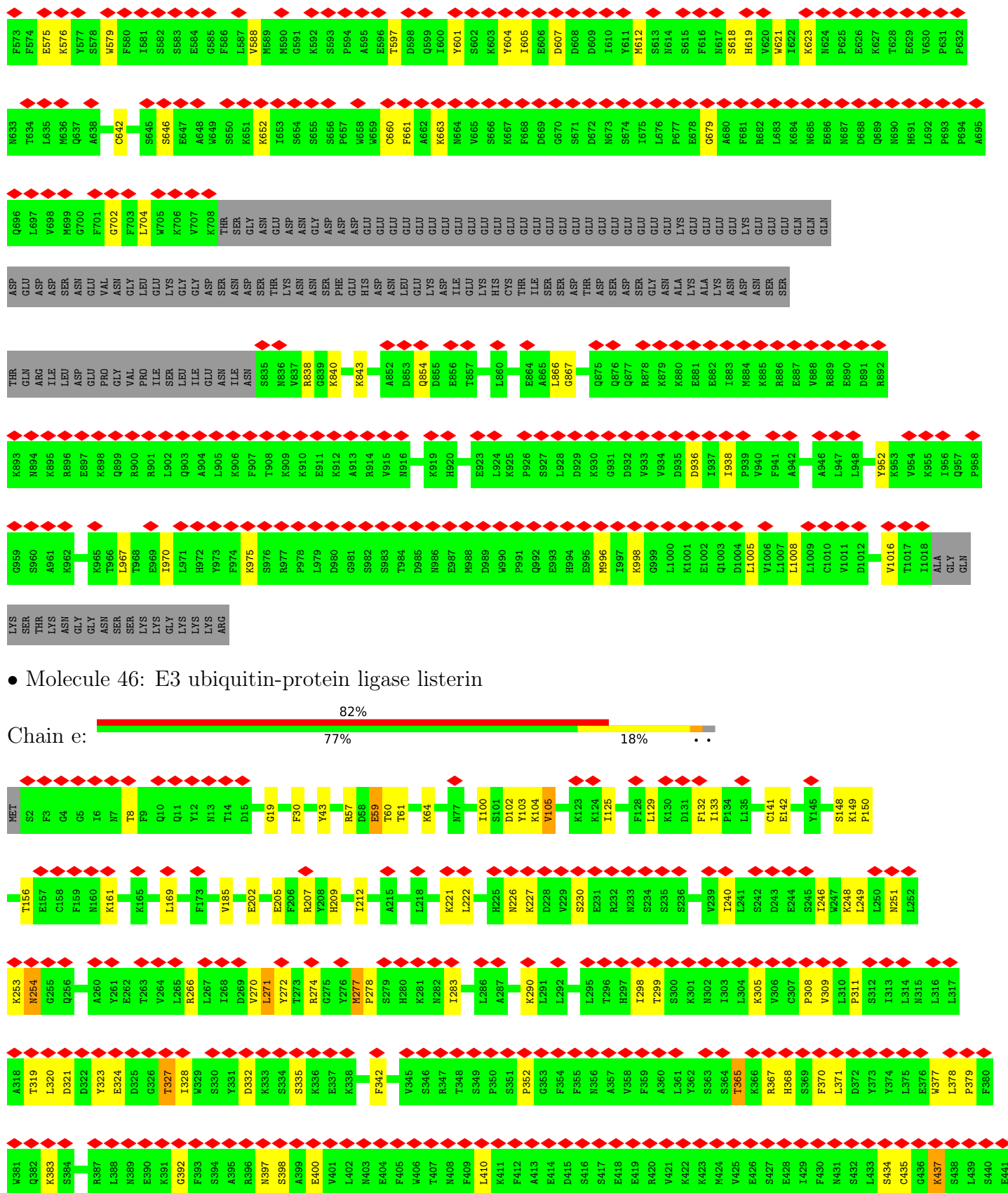


- Molecule 44: 60S ribosomal protein L14-A

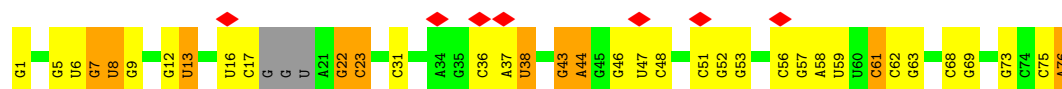


- Molecule 45: RQC2 isoform 1

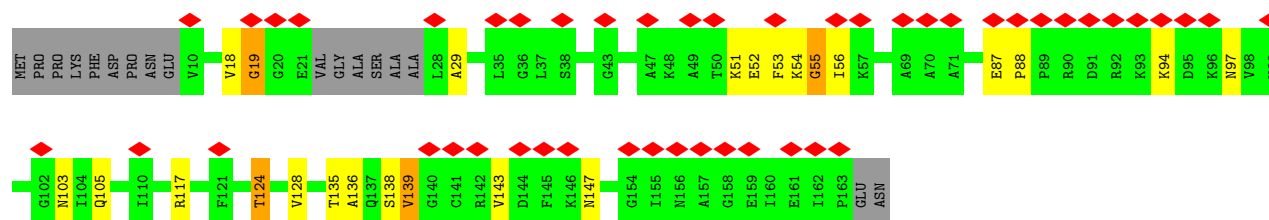
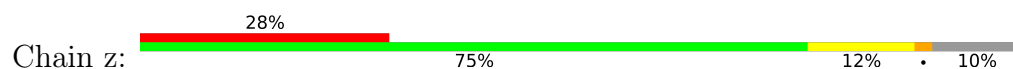




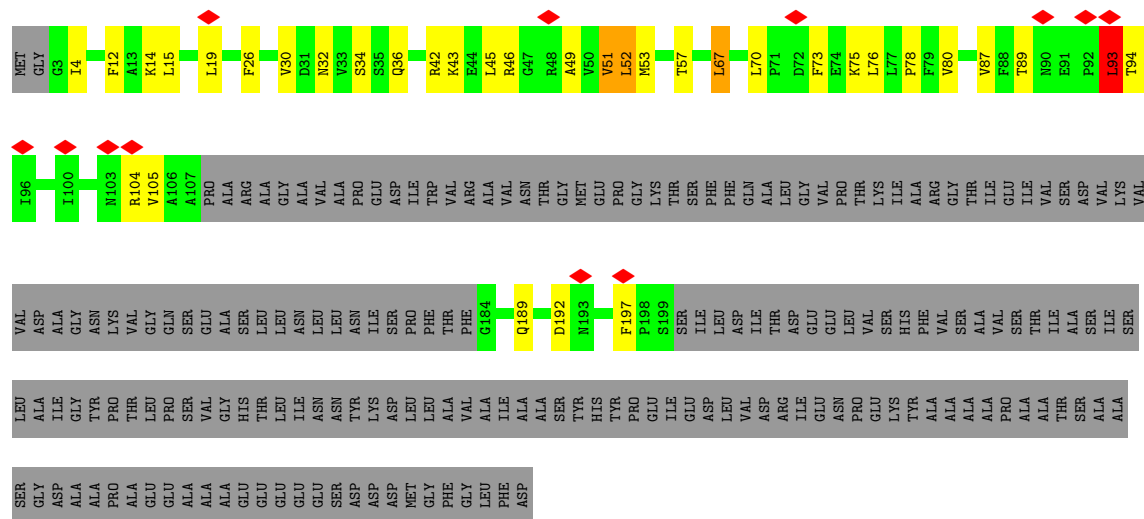
M162	E163	L164	K165	K166	L167	E168	S169	Q170	I171	K172	R173	I174	F175	E176	V177	L178	L179	M180	D181	K182	D183	I184	G185	S186	E187	I188	M189	Q190	S191	R192	L193	L194	T195	T196	L197	L198	G199	S200	D201	I202	V203	K204	T205	Q206	D208	I209	I210	E212	Y213	E214	L215	R216	I217	GLN	LYS	GLN	THR							
C1102	L1103	N1104	L1105	Y1106	E1107	T1108	L1109	S1110	Q1111	GLY	VAL	SER	LYS	ASN	GLY	GLU	ILE	SER	E1122	Y1123	G1124	D1125	E1126	I1127	Q1128	E1129	N1130	L1131	I1132	E1133	L1134	M1135	F1136	L1137	N1138	F1139	N1140	Q1141	E1142	R1143	N1144	N1145	Q1146	V1147	S1148	T1149	L1150	F1151	Y1152	Q1153	K1154	Y1155	Y1156	K1157	V1158	I1159	S1160	S1161						
E1042	P1043	S1044	F1045	T1046	T1047	V1048	R1049	L1050	L1051	L1052	L1053	D1054	F1055	F1056	T1057	K1058	L1059	M1060	R1061	F1062	E1063	G1064	V1065	L1066	D1067	M1068	G1069	I1070	T1071	A1072	F1073	E1074	L1075	S1076	E1077	R1078	L1079	L1080	A1081	D1082	S1083	L1084	S1085	M1086	C1087	Q1088	I1089	D1090	I1091	T1092	L1093	Y1094	L1095	L1096	E1097	L1098	R1099	S1100	S1101					
D922	T923	Y924	S925	S926	T927	T928	L929	N930	G931	L932	L933	A934	S935	V936	E937	S938	F939	Y940	T941	K942	T943	Y944	R945	D946	Q947	K948	S949	T950	D951	K952	D953	Y954	L955	L956	C957	A958	P959	L960	L961	L962	N963	F964	N965	R966	N968	S969	K970	D971	E972	L973	W1034	L1035	D1036	S1037	D1038	L1039	A1040	Y1041						
F962	G963	H964	T965	F966	F967	K968	H969	G970	K971	V972	N973	L974	N975	F976	S977	D978	L979	V980	G981	N982	V983	L984	Q985	P986	A987	N988	G989	G990	D991	A992	N993	L994	T995	F996	D997	E998	S900	S901	N902	S903	Y904	Y905	F906	F907	Y908	Y909	S910	R911	V912	L913	Y914	K915	V916	L917	L918	Y919	S920	T921						
K802	P803	T804	N805	L806	K807	N808	M809	Q810	K811	L812	L813	R814	Y815	A816	L817	F818	L819	D820	A821	L822	L823	D824	A825	L826	E828	R829	V830	N831	N832	H833	L834	V835	A836	F837	L838	T839	V840	V841	S842	E843	L844	V845	T846	Y848	N849	C850	L851	S852	E853	E854	P855	N856	D857	L858	Y859	Y860	D861							
A742	K743	E744	K745	Y746	V747	T748	H749	A750	V751	E752	L753	T754	N755	G756	C757	M758	D759	T760	S761	Q762	T763	F764	F765	F766	N767	N768	A769	T770	E771	V772	F773	A774	R775	Y776	M777	F778	A779	T780	D781	Y782	R783	S784	S785	L786	S788	S789	L790	S791	T792	N793	T794	H795	L796	L797	L798	T799	D800	D801						
E522	L523	E524	L525	A526	Q526	L527	D528	M529	F530	M531	K532	N533	K534	M535	F536	D537	S538	G539	G540	E541	F542	L543	K544	D545	N546	F547	V548	L549	N550	K551	Q552	F553	L554	I555	T556	L557	S558	S559	S560	S561	S562	S563	S564	S565	S566	S567	S568	S569	S570	S571	S572	S573	S574	S575	S576	S577	S578	S579	S580	T581				
D502	F503	F504	V505	Q506	L507	I508	E509	S510	D511	P512	S513	N514	V515	F516	N517	K518	Y519	D520	G521	V522	Y523	D524	A525	D526	F527	N528	Y529	F530	L531	S532	D533	M534	I535	F536	L537	N538	G539	K540	I541	G542	K543	F544	I545	N546	E547	S548	P549	T550	L551	V552	Q553	E554	S555	T556	Y557	Q558	R559	F560	A561					
G562	I563	M564	A565	Q566	Y567	S568	M569	S570	K571	F572	F573	K574	M575	N576	T577	D578	E579	I580	T581	S582	L583	E584	D585	F586	F587	N588	V589	L590	D591	S592	F593	N594	I595	P596	K597	T598	I599	I600	L601	A602	L603	M604	N605	E606	L607	D608	N609	D610	I611	Y612	Q613	Q614	L615	M616	K617	S618	D619	S620	L621					
Y442	T443	K444	L445	N446	Q447	T448	L449	S450	G451	V452	F453	P454	P455	D456	K457	W458	E459	R460	E461	I462	E463	D464	Y465	F466	N467	S468	D469	E470	D471	I472	R473	K474	I475	K476	V477	S478	F479	E480	K481	N482	L483	F484	A485	L486	L487	V488	T489	S490	P491	N492	N493	E494	S495	A496	I497	S498	R499	L500	F501					



• Molecule 49: 60S ribosomal protein L12-A



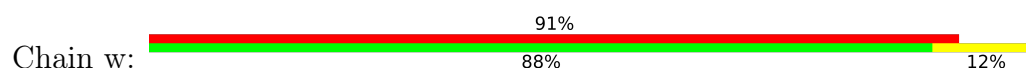
• Molecule 50: 60S acidic ribosomal protein P0



• Molecule 51: CAT-tailed nascent peptide



• Molecule 52: 60S ribosomal protein L1-A





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	58513	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	46	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.793	Depositor
Minimum map value	-0.656	Depositor
Average map value	0.021	Depositor
Map value standard deviation	0.131	Depositor
Recommended contour level	0.55	Depositor
Map size ($\text{\AA}$)	476.55002, 476.55002, 476.55002	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.059, 1.059, 1.059	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, SPD

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	A	0.31	0/1757	0.54	0/2354
2	B	0.31	0/1585	0.54	0/2128
3	C	0.29	0/1439	0.61	0/1938
4	D	0.28	0/1465	0.57	0/1965
5	E	0.29	0/1275	0.56	0/1702
6	F	0.31	0/1473	0.56	0/1980
7	G	0.27	0/1296	0.56	0/1739
8	H	0.29	0/812	0.75	2/1099 (0.2%)
9	I	0.27	0/1018	0.50	0/1369
10	J	0.27	0/530	0.52	0/703
11	K	0.31	0/979	0.57	0/1321
12	L	0.27	0/995	0.53	0/1329
13	M	0.27	0/1106	0.56	0/1485
14	N	0.32	0/1200	0.56	1/1607 (0.1%)
15	O	0.25	0/473	0.62	0/629
16	P	0.26	0/745	0.60	0/1001
17	Q	0.31	0/890	0.68	2/1196 (0.2%)
18	R	0.25	0/1034	0.47	0/1385
19	S	0.30	0/868	0.47	0/1168
20	T	0.29	0/890	0.58	2/1189 (0.2%)
21	U	0.27	0/978	0.53	0/1301
22	V	0.28	0/772	0.57	0/1026
23	W	0.32	0/660	0.60	0/875
24	X	0.29	0/618	0.65	1/826 (0.1%)
25	Y	0.29	0/443	0.46	0/588
26	Z	0.28	0/416	0.60	0/553
27	b	0.28	0/836	0.53	0/1104
28	c	0.27	0/701	0.56	0/934
29	d	0.22	0/208	0.81	2/267 (0.7%)
30	f	0.31	0/77011	0.40	4/120065 (0.0%)
31	h	0.26	0/2883	0.32	0/4491
32	i	0.30	0/3746	0.36	0/5832

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	j	0.31	0/1908	0.53	0/2564
34	k	0.29	0/3146	0.53	0/4228
35	l	0.29	0/2800	0.57	4/3790 (0.1%)
36	m	0.27	0/2400	0.57	0/3239
37	n	0.28	0/1329	0.60	0/1794
38	o	0.31	0/1821	0.58	0/2451
39	p	0.27	0/1836	0.58	1/2481 (0.0%)
40	q	0.30	0/1529	0.63	2/2060 (0.1%)
41	r	0.25	0/1801	0.49	0/2416
42	s	0.26	0/1367	0.69	4/1834 (0.2%)
43	t	0.29	0/1568	0.62	1/2106 (0.0%)
44	u	0.30	0/1068	0.53	0/1438
45	a	0.26	0/6683	0.55	2/9016 (0.0%)
46	e	0.62	0/11711	0.92	57/15903 (0.4%)
47	g	0.24	0/1672	0.58	1/2281 (0.0%)
48	x	0.35	0/1761	0.61	0/2742
48	y	0.37	0/1735	0.64	0/2701
49	z	0.67	0/726	1.24	13/1006 (1.3%)
50	0	0.49	0/976	0.94	3/1313 (0.2%)
52	w	0.27	0/1736	0.61	1/2332 (0.0%)
All	All	0.34	0/160675	0.53	103/234844 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
15	O	0	1
21	U	0	1
34	k	0	1
35	l	0	2
39	p	0	3
40	q	0	1
44	u	0	1
46	e	0	1
47	g	0	1
All	All	0	12

There are no bond length outliers.

The worst 5 of 103 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	e	1364	GLY	N-CA-C	12.28	127.34	112.49
46	e	1460	SER	N-CA-C	10.07	122.34	111.36
46	e	1181	ASP	N-CA-C	8.80	120.88	111.28
46	e	1141	GLN	N-CA-C	8.76	120.83	111.28
46	e	793	ASN	N-CA-C	-8.72	102.65	113.28

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	O	20	GLY	Peptide
21	U	83	LYS	Peptide
34	k	141	GLY	Peptide
35	l	13	GLY	Peptide
35	l	318	LEU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1720	0	1779	19	0
2	B	1555	0	1659	17	0
3	C	1416	0	1433	14	0
4	D	1441	0	1543	15	0
5	E	1258	0	1342	13	0
6	F	1437	0	1475	19	0
7	G	1272	0	1312	13	0
8	H	796	0	812	6	0
9	I	1003	0	1048	10	0
10	J	518	0	542	6	0
11	K	964	0	1025	1	0
12	L	984	0	1075	7	0
13	M	1080	0	1122	7	0
14	N	1169	0	1211	14	0
15	O	462	0	491	8	0
16	P	737	0	792	4	0
17	Q	876	0	912	10	0
18	R	1013	0	1077	8	0

Continued on next page...

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	S	850	0	880	4	0
20	T	880	0	942	8	0
21	U	969	0	1078	5	0
22	V	766	0	842	8	0
23	W	645	0	645	13	0
24	X	612	0	682	6	0
25	Y	436	0	475	2	0
26	Z	410	0	442	4	0
27	b	824	0	888	11	0
28	c	694	0	734	9	0
29	d	207	0	250	3	0
30	f	68802	0	34573	373	0
31	h	2579	0	1304	9	0
32	i	3353	0	1695	13	0
33	j	1874	0	1943	25	0
34	k	3075	0	3142	20	0
35	l	2748	0	2859	24	0
36	m	2351	0	2294	31	0
37	n	1307	0	1377	7	0
38	o	1784	0	1862	9	0
39	p	1804	0	1877	16	0
40	q	1508	0	1572	16	0
41	r	1764	0	1804	16	0
42	s	1346	0	1370	9	0
43	t	1543	0	1608	14	0
44	u	1053	0	1149	11	0
45	a	6573	0	6471	57	0
46	e	11512	0	10772	274	0
47	g	1651	0	1613	22	0
48	x	1579	0	800	25	0
48	y	1556	0	788	17	0
49	z	728	0	337	20	0
50	0	961	0	979	45	0
51	1	85	0	21	1	0
52	w	1709	0	1797	15	0
53	A	1	0	0	0	0
53	C	1	0	0	0	0
53	E	1	0	0	0	0
53	I	1	0	0	0	0
53	R	1	0	0	0	0
53	T	1	0	0	0	0
53	f	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	h	1	0	0	0	0
53	j	2	0	0	0	0
53	k	1	0	0	0	0
54	T	1	0	0	0	0
54	W	1	0	0	0	0
54	Z	1	0	0	0	0
54	b	1	0	0	0	0
54	c	1	0	0	0	0
54	e	2	0	0	0	0
55	f	10	0	19	1	0
All	All	150269	0	112534	1092	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 4.

The worst 5 of 1092 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)
46:e:272:TYR:HA	46:e:277:MET:SD	1.28	1.65
46:e:277:MET:SD	46:e:278:PRO:HD3	1.34	1.61
46:e:751:VAL:HA	46:e:754:ILE:CD1	1.30	1.60
46:e:272:TYR:HD1	46:e:277:MET:CE	1.13	1.55
46:e:371:LEU:HD12	46:e:377:TRP:CZ2	1.39	1.55

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
2	B	195/199 (98%)	192 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	181/184 (98%)	172 (95%)	9 (5%)	0	100	100
4	D	183/186 (98%)	176 (96%)	7 (4%)	0	100	100
5	E	154/189 (82%)	151 (98%)	3 (2%)	0	100	100
6	F	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
7	G	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
8	H	98/121 (81%)	93 (95%)	5 (5%)	0	100	100
9	I	134/137 (98%)	132 (98%)	2 (2%)	0	100	100
10	J	61/155 (39%)	61 (100%)	0	0	100	100
11	K	119/142 (84%)	118 (99%)	1 (1%)	0	100	100
12	L	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
13	M	133/136 (98%)	126 (95%)	7 (5%)	0	100	100
14	N	146/149 (98%)	136 (93%)	10 (7%)	0	100	100
15	O	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	6	14
16	P	94/105 (90%)	93 (99%)	1 (1%)	0	100	100
17	Q	107/113 (95%)	98 (92%)	9 (8%)	0	100	100
18	R	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
19	S	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
20	T	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
21	U	117/120 (98%)	112 (96%)	5 (4%)	0	100	100
22	V	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
23	W	79/88 (90%)	75 (95%)	4 (5%)	0	100	100
24	X	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
25	Y	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
26	Z	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
27	b	101/106 (95%)	95 (94%)	6 (6%)	0	100	100
28	c	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
29	d	20/25 (80%)	19 (95%)	1 (5%)	0	100	100
33	j	244/254 (96%)	226 (93%)	18 (7%)	0	100	100
34	k	384/387 (99%)	363 (94%)	21 (6%)	0	100	100
35	l	359/362 (99%)	329 (92%)	29 (8%)	1 (0%)	36	58
36	m	292/297 (98%)	277 (95%)	15 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	n	163/176 (93%)	155 (95%)	8 (5%)	0	100	100
38	o	220/244 (90%)	207 (94%)	13 (6%)	0	100	100
39	p	231/256 (90%)	220 (95%)	11 (5%)	0	100	100
40	q	189/191 (99%)	174 (92%)	14 (7%)	1 (0%)	24	46
41	r	216/221 (98%)	206 (95%)	10 (5%)	0	100	100
42	s	167/174 (96%)	161 (96%)	5 (3%)	1 (1%)	21	42
43	t	191/199 (96%)	174 (91%)	16 (8%)	1 (0%)	24	46
44	u	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
45	a	842/1038 (81%)	827 (98%)	15 (2%)	0	100	100
46	e	1519/1562 (97%)	1497 (99%)	20 (1%)	2 (0%)	48	70
47	g	223/245 (91%)	215 (96%)	8 (4%)	0	100	100
49	z	144/165 (87%)	135 (94%)	7 (5%)	2 (1%)	9	19
50	0	117/312 (38%)	116 (99%)	0	1 (1%)	14	30
52	w	214/217 (99%)	211 (99%)	3 (1%)	0	100	100
All	All	9175/10122 (91%)	8817 (96%)	348 (4%)	10 (0%)	49	70

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
49	z	88	PRO
46	e	437	LYS
46	e	855	PRO
35	l	4	PRO
40	q	107	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	175/176 (99%)	175 (100%)	0	100	100
2	B	160/162 (99%)	160 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	138/146 (94%)	138 (100%)	0	100	100
4	D	150/151 (99%)	150 (100%)	0	100	100
5	E	129/154 (84%)	129 (100%)	0	100	100
6	F	155/156 (99%)	155 (100%)	0	100	100
7	G	135/137 (98%)	135 (100%)	0	100	100
8	H	87/107 (81%)	87 (100%)	0	100	100
9	I	104/105 (99%)	104 (100%)	0	100	100
10	J	54/129 (42%)	54 (100%)	0	100	100
11	K	104/118 (88%)	104 (100%)	0	100	100
12	L	108/110 (98%)	108 (100%)	0	100	100
13	M	112/116 (97%)	112 (100%)	0	100	100
14	N	117/119 (98%)	117 (100%)	0	100	100
15	O	46/47 (98%)	46 (100%)	0	100	100
16	P	81/88 (92%)	81 (100%)	0	100	100
17	Q	92/97 (95%)	92 (100%)	0	100	100
18	R	107/111 (96%)	107 (100%)	0	100	100
19	S	90/91 (99%)	90 (100%)	0	100	100
20	T	95/103 (92%)	95 (100%)	0	100	100
21	U	104/105 (99%)	104 (100%)	0	100	100
22	V	80/82 (98%)	80 (100%)	0	100	100
23	W	67/71 (94%)	67 (100%)	0	100	100
24	X	68/69 (99%)	68 (100%)	0	100	100
25	Y	45/46 (98%)	45 (100%)	0	100	100
26	Z	45/116 (39%)	45 (100%)	0	100	100
27	b	87/91 (96%)	87 (100%)	0	100	100
28	c	71/72 (99%)	71 (100%)	0	100	100
29	d	20/23 (87%)	20 (100%)	0	100	100
33	j	189/196 (96%)	189 (100%)	0	100	100
34	k	320/323 (99%)	320 (100%)	0	100	100
35	l	288/289 (100%)	288 (100%)	0	100	100
36	m	241/245 (98%)	241 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	n	139/155 (90%)	139 (100%)	0	100	100
38	o	186/205 (91%)	186 (100%)	0	100	100
39	p	187/208 (90%)	187 (100%)	0	100	100
40	q	168/171 (98%)	168 (100%)	0	100	100
41	r	185/187 (99%)	184 (100%)	1 (0%)	81	92
42	s	145/150 (97%)	145 (100%)	0	100	100
43	t	154/159 (97%)	154 (100%)	0	100	100
44	u	107/109 (98%)	107 (100%)	0	100	100
45	a	677/949 (71%)	676 (100%)	1 (0%)	88	96
46	e	1151/1451 (79%)	1090 (95%)	61 (5%)	20	43
47	g	180/211 (85%)	180 (100%)	0	100	100
50	0	104/254 (41%)	94 (90%)	10 (10%)	8	17
52	w	197/198 (100%)	197 (100%)	0	100	100
All	All	7444/8558 (87%)	7371 (99%)	73 (1%)	65	86

5 of 73 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	e	1441	ILE
50	0	105	VAL
46	e	1464	ILE
50	0	52	LEU
46	e	799	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
45	a	438	ASN
46	e	888	ASN
45	a	599	GLN
46	e	233	ASN
46	e	1457	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	f	3211/3395 (94%)	601 (18%)	0
31	h	120/121 (99%)	12 (10%)	0
32	i	157/158 (99%)	32 (20%)	0
48	x	72/76 (94%)	26 (36%)	0
48	y	71/76 (93%)	26 (36%)	0
All	All	3631/3826 (94%)	697 (19%)	0

5 of 697 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	f	6	A
30	f	13	A
30	f	14	U
30	f	26	A
30	f	40	A

There are no RNA pucker outliers to report.

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](#)

Of 21 ligands modelled in this entry, 20 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
55	SPD	f	3401	-	9,9,9	0.31	0	8,8,8	0.85	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	SPD	f	3401	-	-	5/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	f	3401	SPD	C3-C4-C5-N6
55	f	3401	SPD	N6-C7-C8-C9
55	f	3401	SPD	C2-C3-C4-C5
55	f	3401	SPD	C4-C5-N6-C7
55	f	3401	SPD	C8-C7-N6-C5

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	f	3401	SPD	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

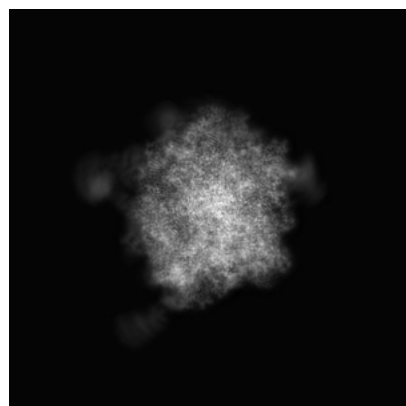
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15426. These allow visual inspection of the internal detail of the map and identification of artifacts.

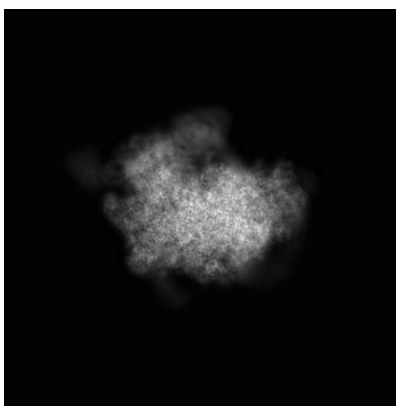
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

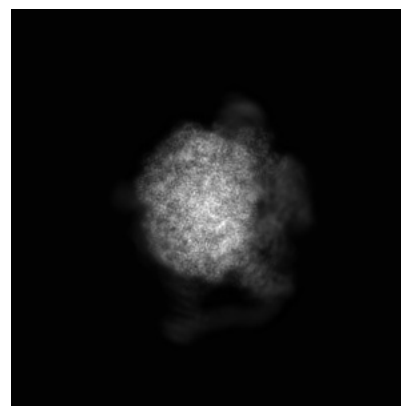
6.1.1 Primary map



X

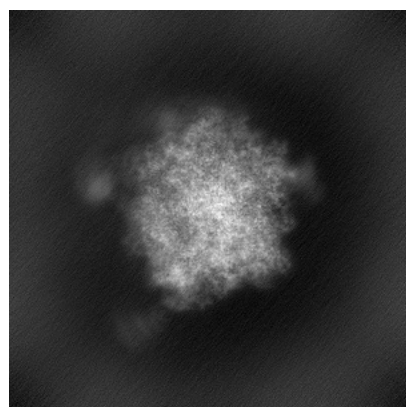


Y

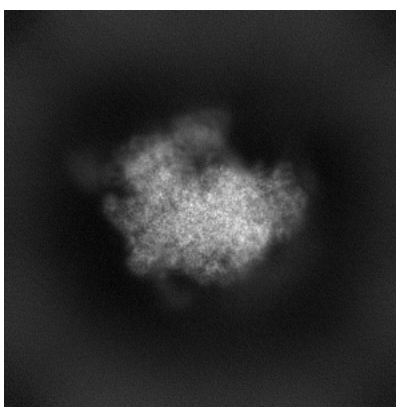


Z

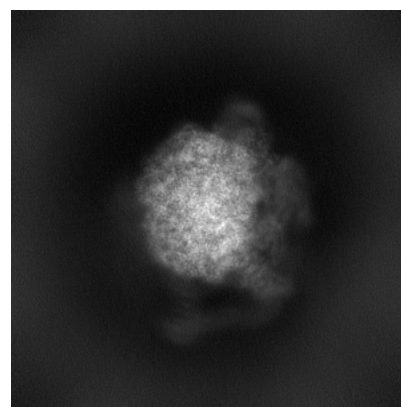
6.1.2 Raw map



X



Y

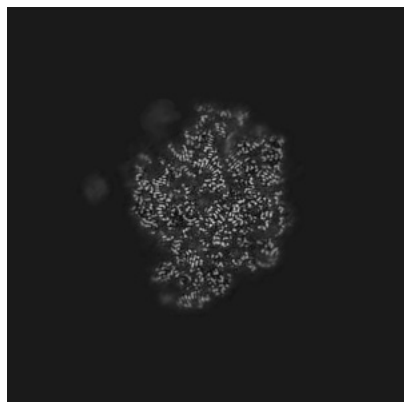


Z

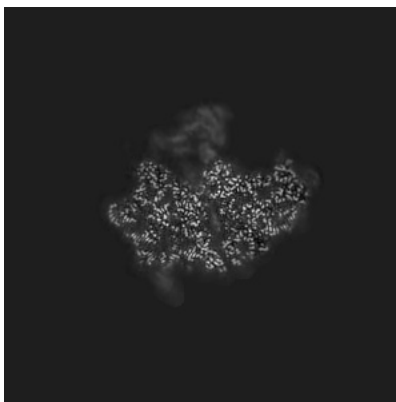
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

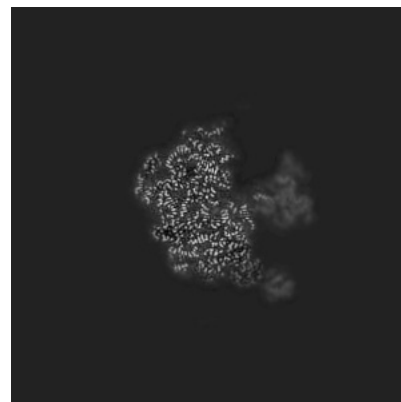
6.2.1 Primary map



X Index: 225

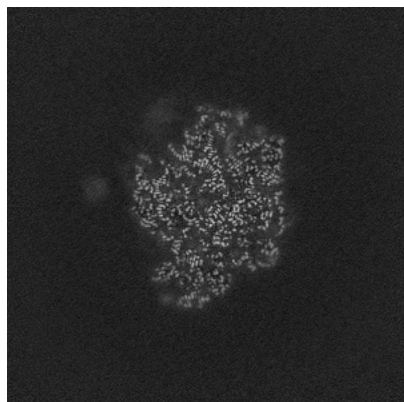


Y Index: 225

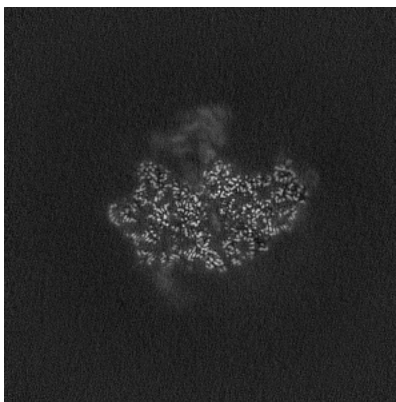


Z Index: 225

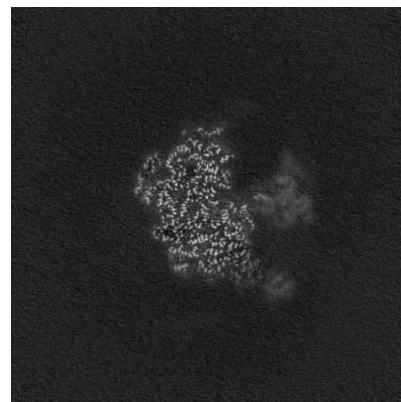
6.2.2 Raw map



X Index: 225



Y Index: 225

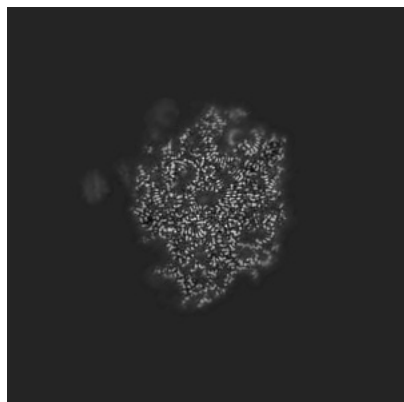


Z Index: 225

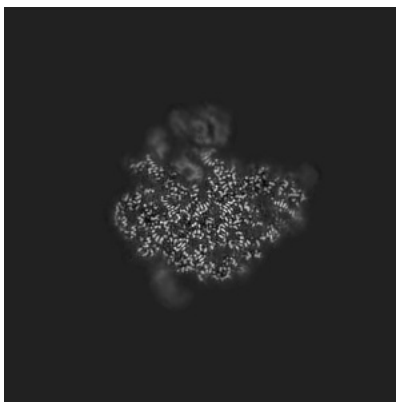
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

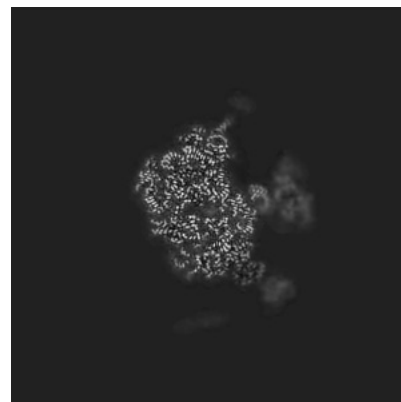
6.3.1 Primary map



X Index: 219

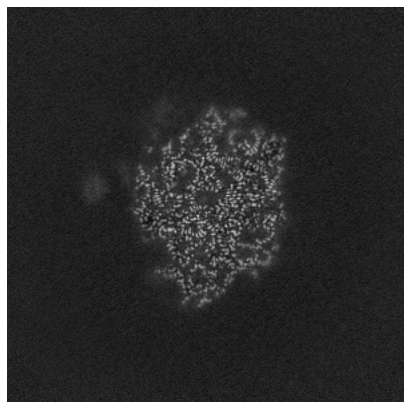


Y Index: 237

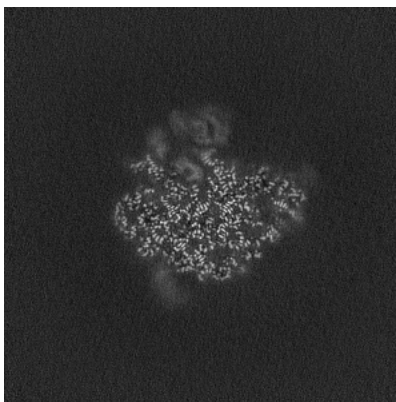


Z Index: 230

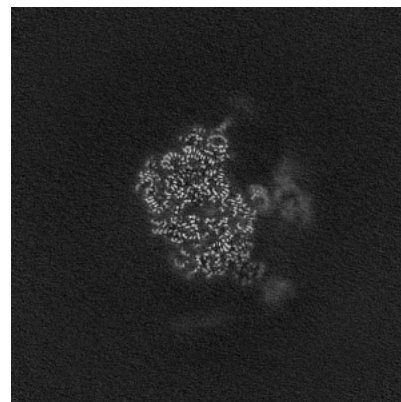
6.3.2 Raw map



X Index: 219



Y Index: 237

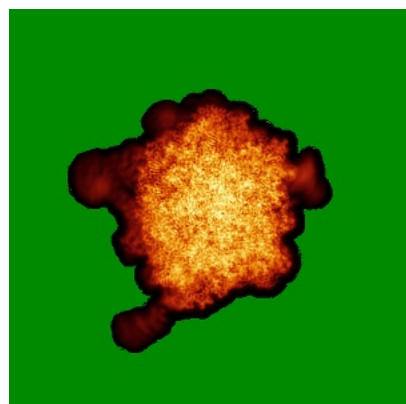


Z Index: 230

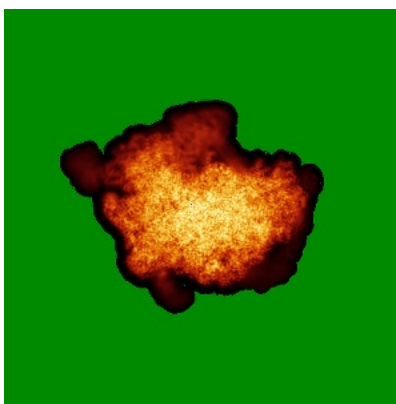
The images above show the largest variance slices of the map in three orthogonal directions.

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

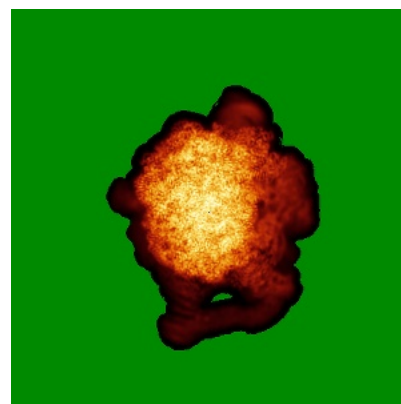
6.4.1 Primary map



X

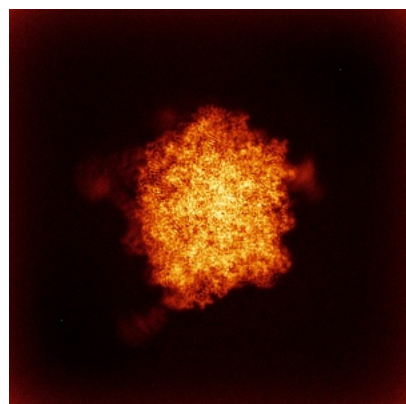


Y

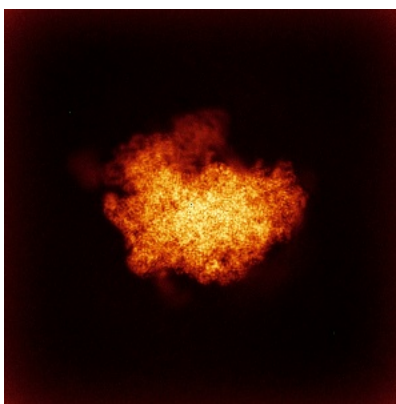


Z

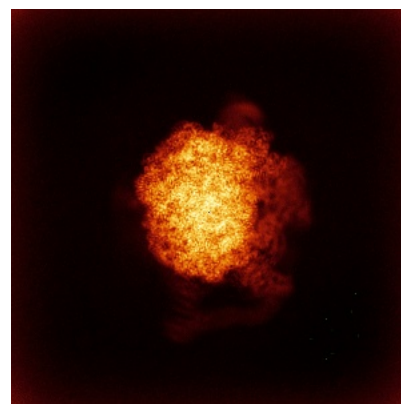
6.4.2 Raw map



X



Y

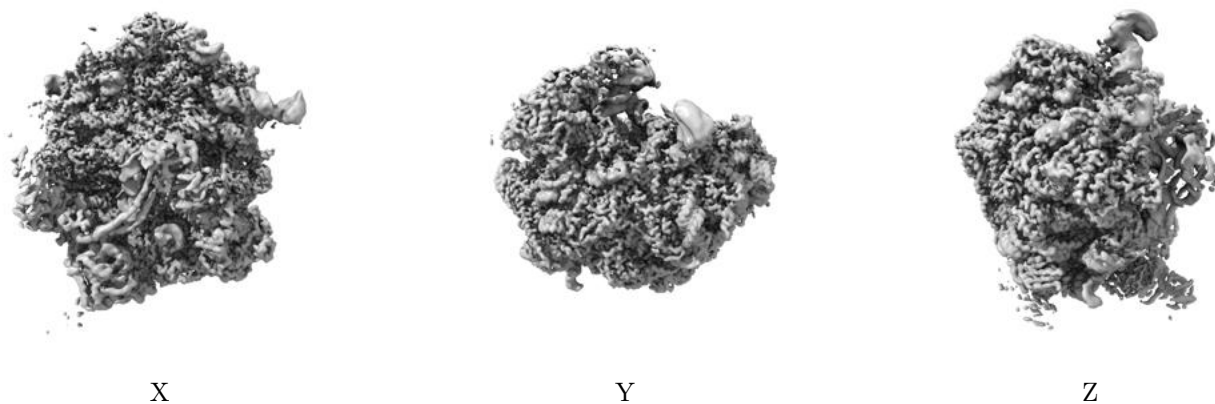


Z

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.

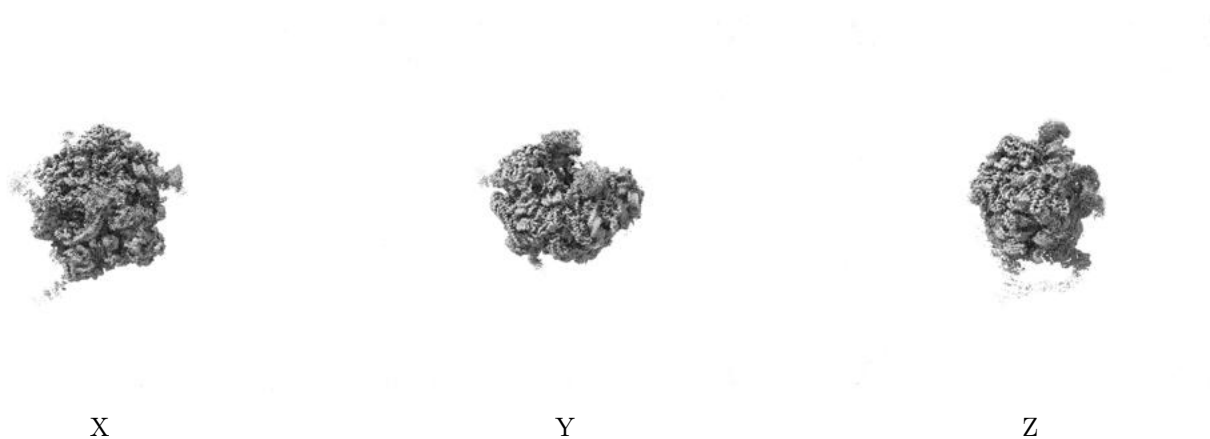
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.55. 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.

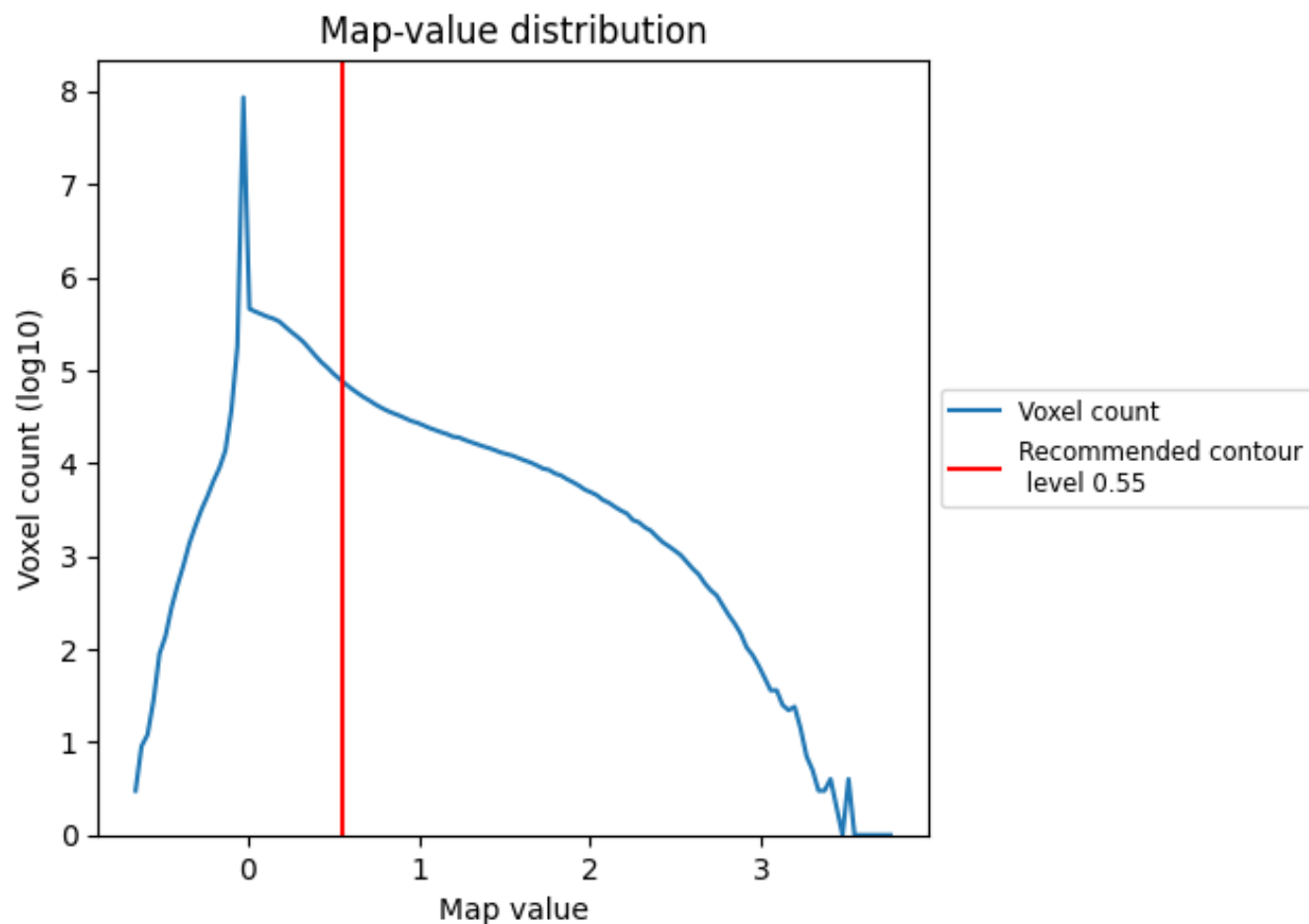
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

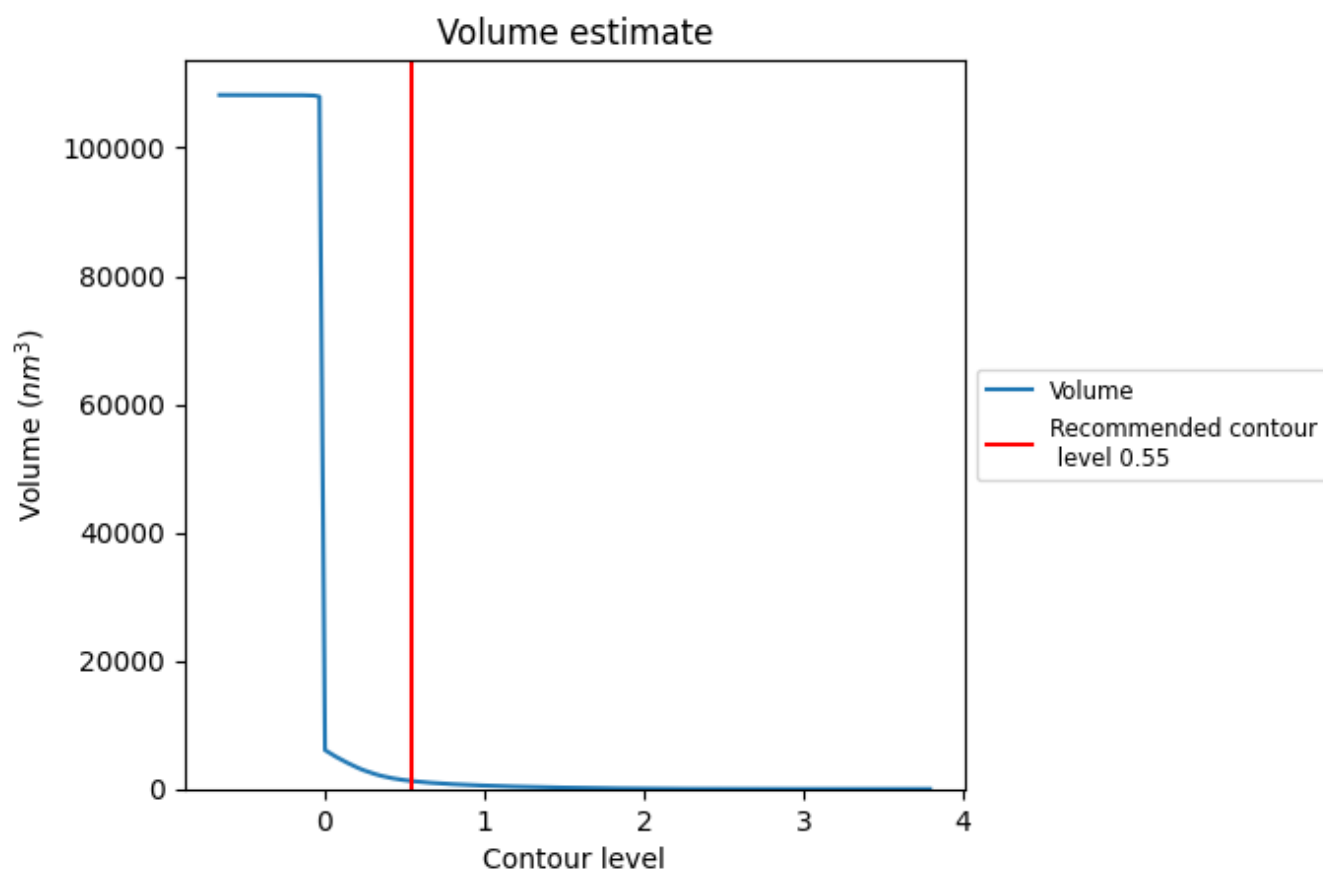
This section contains the results of statistical analysis of the map.

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.

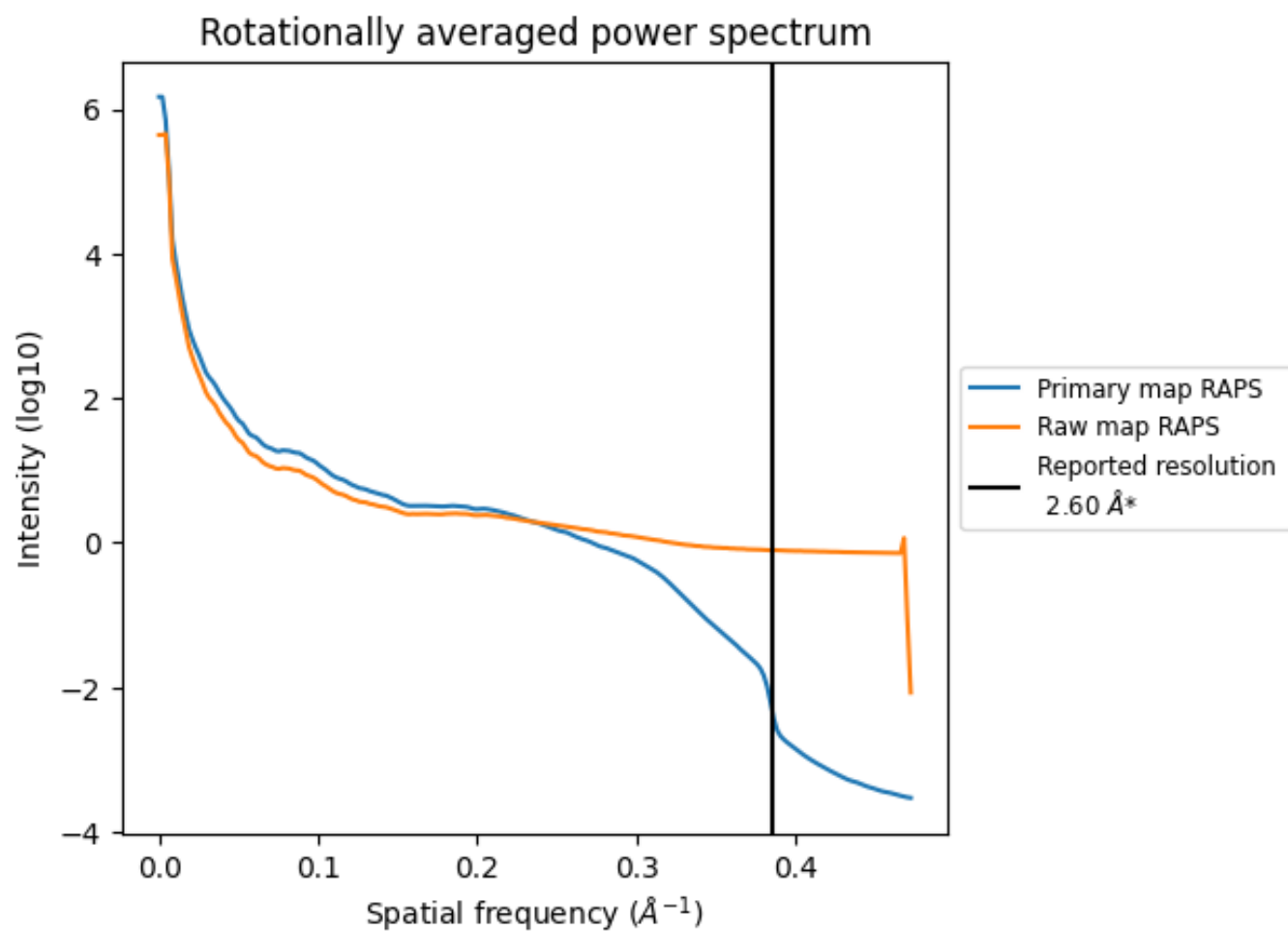
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1231 nm^3 ; this corresponds to an approximate mass of 1112 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 ⓘ

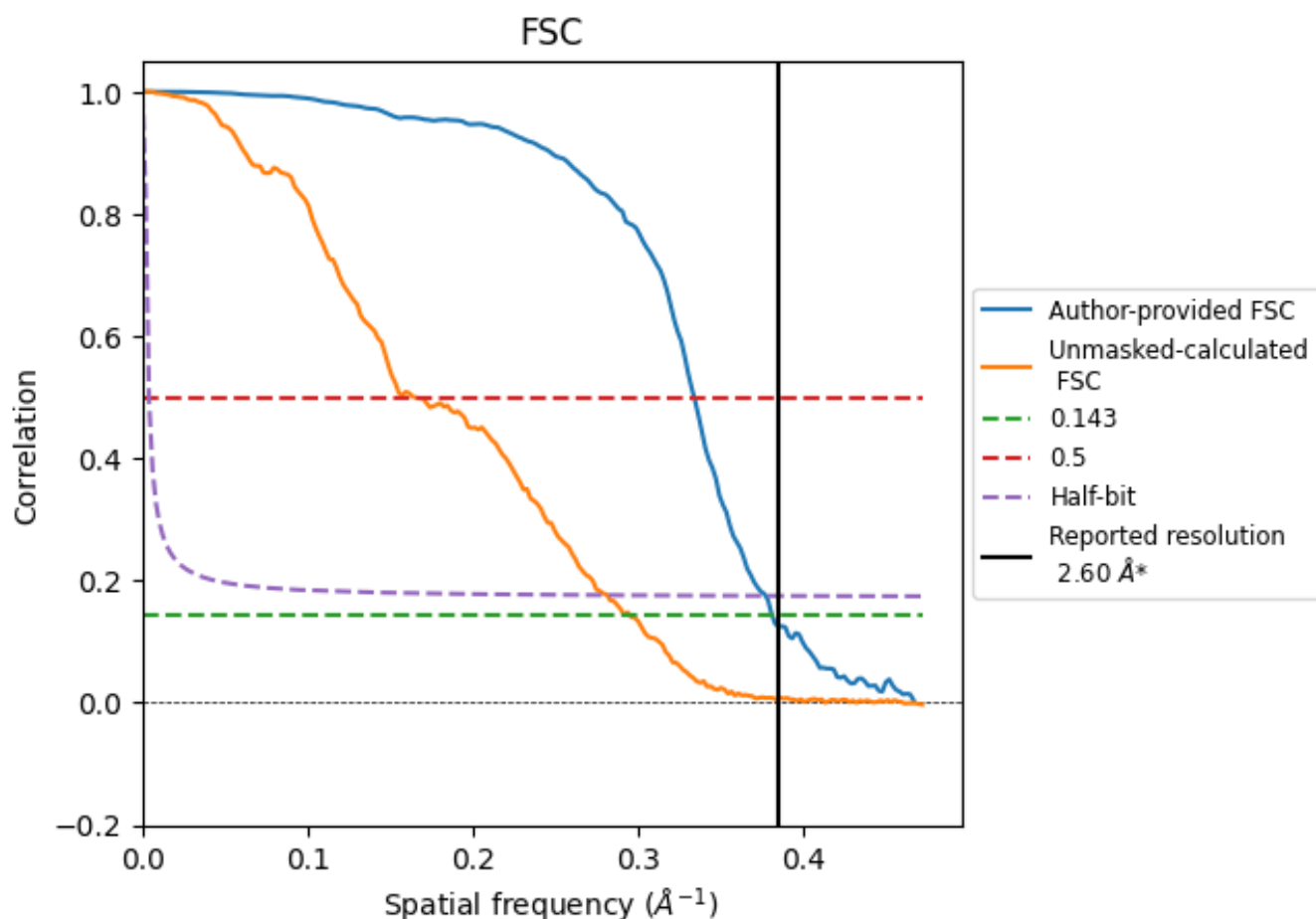


*Reported resolution corresponds to spatial frequency of $0.385 \text{ \AA}^{-1}$

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 0.385 Å⁻¹

8.2 Resolution estimates [i](#)

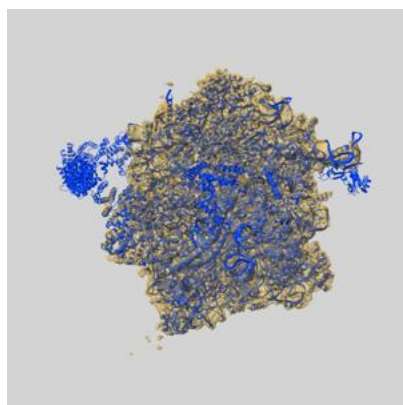
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.62	2.99	2.65
Unmasked-calculated*	3.39	6.07	3.55

*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 3.39 differs from the reported value 2.6 by more than 10 %

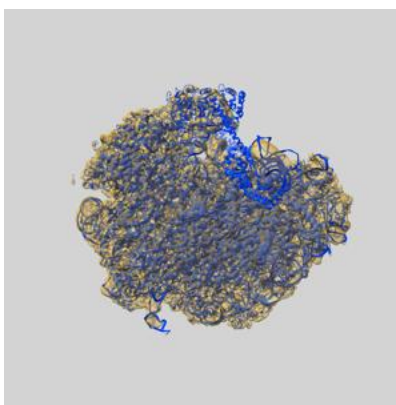
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-15426 and PDB model 8AGW. Per-residue inclusion information can be found in section [3](#) on page [14](#).

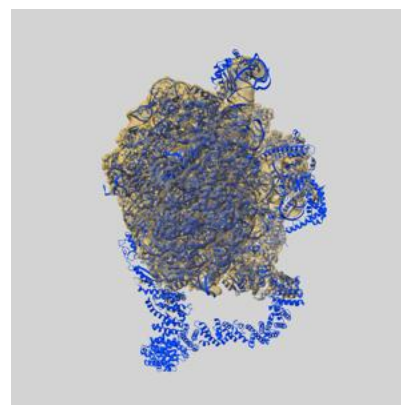
9.1 Map-model overlay [i](#)



X



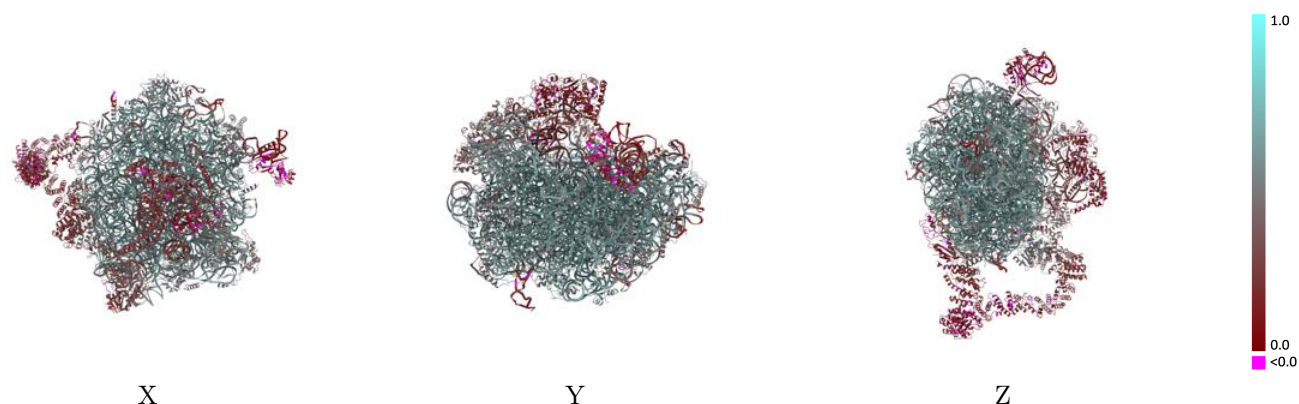
Y



Z

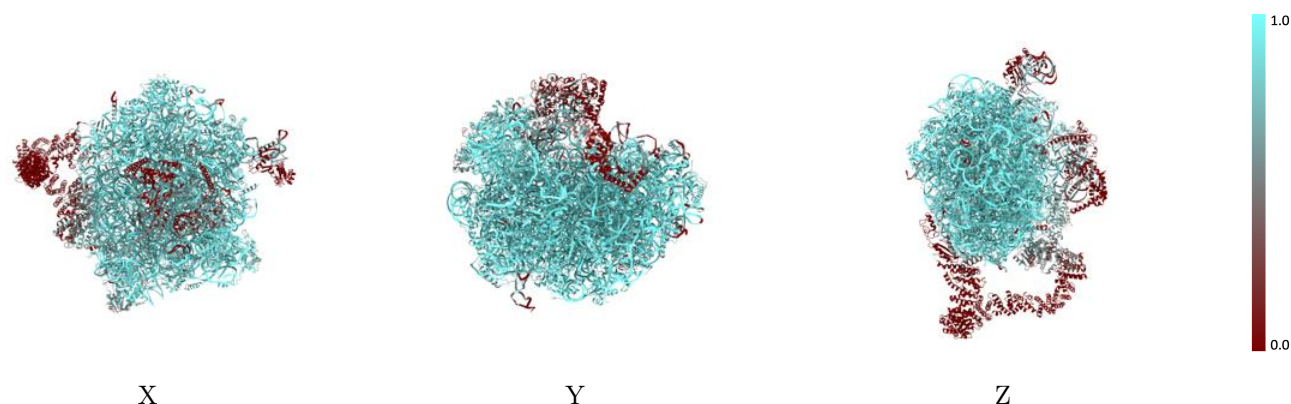
The images above show the 3D surface view of the map at the recommended contour level 0.55 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



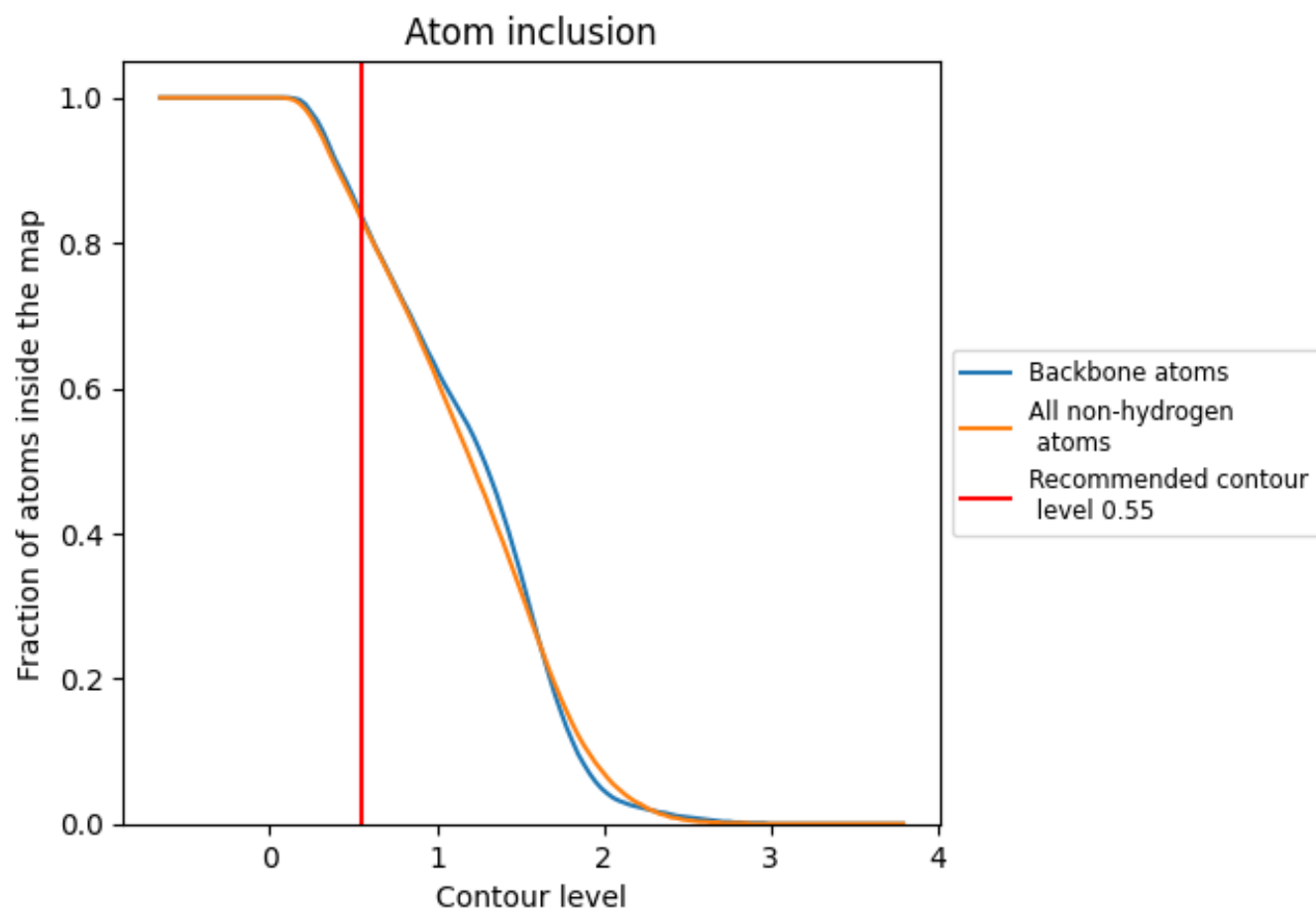
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.55).

9.4 Atom inclusion ⓘ



At the recommended contour level, 84% of all backbone atoms, 83% 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 (0.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8320	 0.5020
0	 0.6230	 0.2810
1	 0.9060	 0.4570
A	 0.9790	 0.6090
B	 0.9510	 0.5820
C	 0.9320	 0.5860
D	 0.9490	 0.5800
E	 0.8870	 0.5450
F	 0.9340	 0.5750
G	 0.9110	 0.5620
H	 0.8130	 0.4670
I	 0.9220	 0.5690
J	 0.9220	 0.5700
K	 0.9200	 0.5680
L	 0.9350	 0.5660
M	 0.8800	 0.5230
N	 0.9480	 0.5880
O	 0.9090	 0.5330
P	 0.8540	 0.5240
Q	 0.8820	 0.5500
R	 0.9510	 0.5960
S	 0.9670	 0.6090
T	 0.9210	 0.5680
U	 0.9180	 0.5520
V	 0.9030	 0.5180
W	 0.9950	 0.6250
X	 0.8130	 0.4940
Y	 0.9710	 0.5990
Z	 0.9290	 0.5650
a	 0.2800	 0.1930
b	 0.9090	 0.5700
c	 0.9160	 0.5660
d	 0.5000	 0.3930
e	 0.1380	 0.1850
f	 0.9680	 0.5670



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Chain	Atom inclusion	Q-score
g	 0.4690	 0.4560
h	 0.9930	 0.5710
i	 0.9830	 0.5960
j	 0.9590	 0.6030
k	 0.9460	 0.5800
l	 0.9370	 0.5730
m	 0.8560	 0.4820
n	 0.8820	 0.5280
o	 0.9390	 0.5660
p	 0.8780	 0.5160
q	 0.9110	 0.5430
r	 0.9040	 0.5460
s	 0.8140	 0.4390
t	 0.9210	 0.5600
u	 0.9270	 0.5460
w	 0.0770	 0.0750
x	 0.5600	 0.2560
y	 0.7970	 0.2340
z	 0.6130	 0.3040