



# wwPDB EM Validation Summary Report ⓘ

Mar 22, 2026 – 07:03 PM UTC

PDB ID : 8AAF / pdb\_00008aaf  
EMDB ID : EMD-15296  
Title : Yeast RQC complex in state G  
Authors : Tesina, P.; Buschauer, R.; Beckmann, R.  
Deposited on : 2022-07-01  
Resolution : 2.50 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

---

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

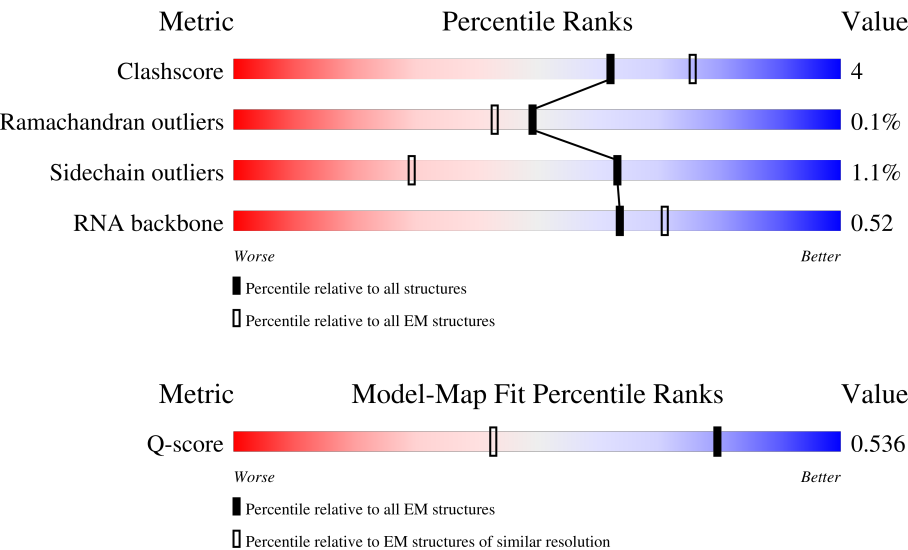
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 2.50 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.













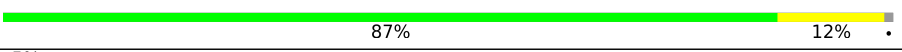




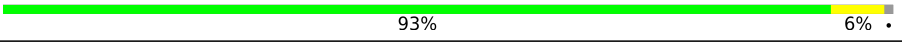

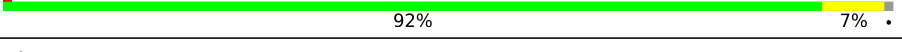


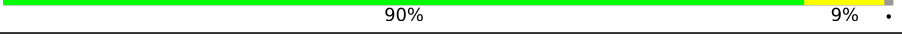
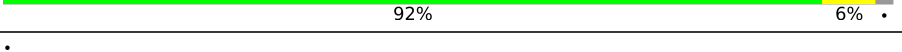

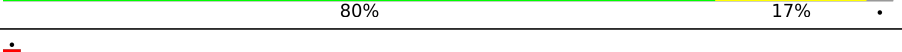
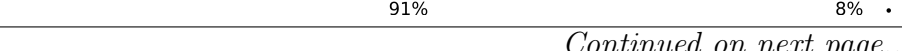
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7115 ( 2.00 - 3.00 )

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	204	
2	B	199	
3	C	184	

Continued on next page...

Continued from previous page...

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	

Continued on next page...

Continued from previous page...

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	v	157	
49	w	217	
50	x	76	
50	y	76	
51	z	165	
52	0	312	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
53	1	18	<div><div></div><div>17%</div><div>83%</div><div>17%</div></div>

## 2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 151377 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	S	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 Ribosome quality control complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	a	848	Total	C	N	O	S	0	0
			6582	4195	1142	1228	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
			11509	7355	1936	2180	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 protein called Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	v	142	Total	C	N	O	S	0	0
			1085	676	183	217	9		

- Molecule 49 is a protein called 60S ribosomal protein L1-A.

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

- Molecule 50 is a RNA chain called Ala tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	x	74	Total	C	N	O	P	0	0
			1579	702	277	526	74		
50	y	73	Total	C	N	O	P	0	0
			1556	692	272	519	73		

- Molecule 51 is a protein called 60S ribosomal protein L12-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	z	148	Total	C	N	O	0	0
			734	438	148	148		

- Molecule 52 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	0	121	Total	C	N	O	S	0	0
			967	621	170	173	3		

- Molecule 53 is a protein called CAT-tailed nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	1	18	Total	C	N	O	0	0
			90	54	18	18		

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	A	1	Total	Mg	0
			1	1	
54	C	1	Total	Mg	0
			1	1	
54	E	1	Total	Mg	0
			1	1	
54	I	1	Total	Mg	0
			1	1	
54	R	1	Total	Mg	0
			1	1	

*Continued on next page...*

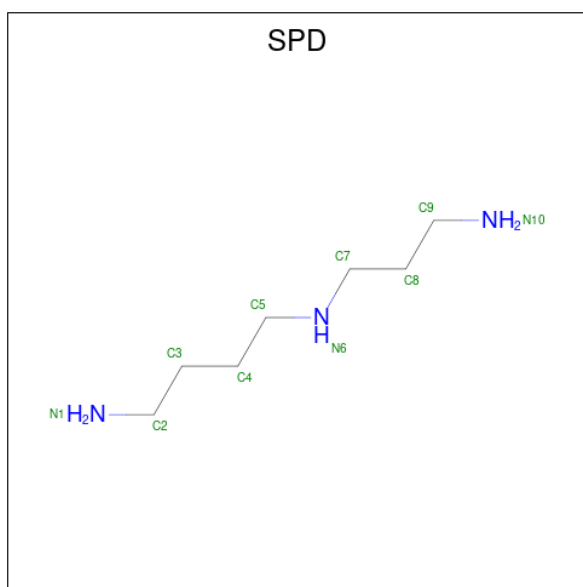
*Continued from previous page...*

Mol	Chain	Residues	Atoms		AltConf
54	T	1	Total 1	Mg 1	0
54	f	3	Total 3	Mg 3	0
54	h	1	Total 1	Mg 1	0
54	j	2	Total 2	Mg 2	0
54	k	1	Total 1	Mg 1	0

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 56 is SPERMIDINE (CCD ID: SPD) (formula: C<sub>7</sub>H<sub>19</sub>N<sub>3</sub>).

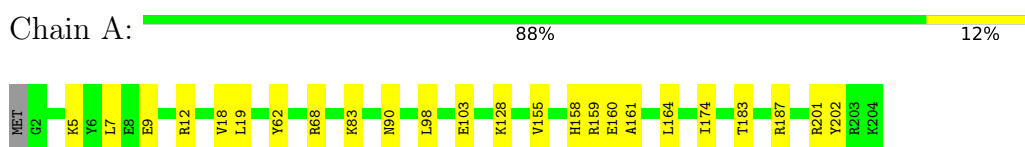


Mol	Chain	Residues	Atoms			AltConf
56	f	1	Total	C	N	0
			10	7	3	

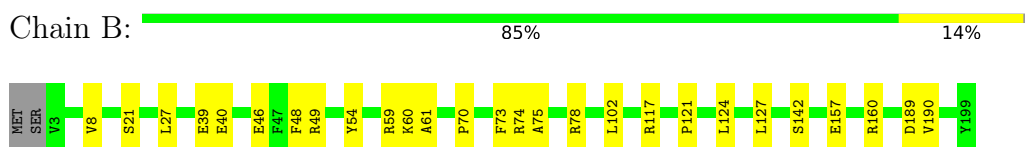
### 3 Residue-property plots [i](#)

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.

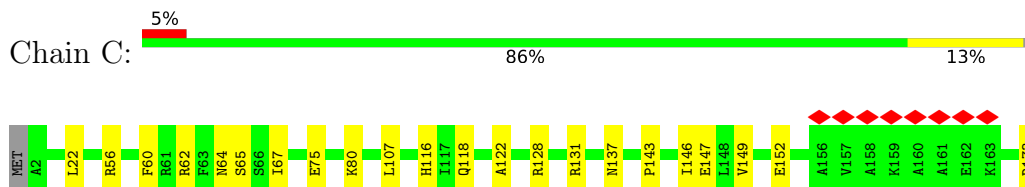
- Molecule 1: 60S ribosomal protein L15-A



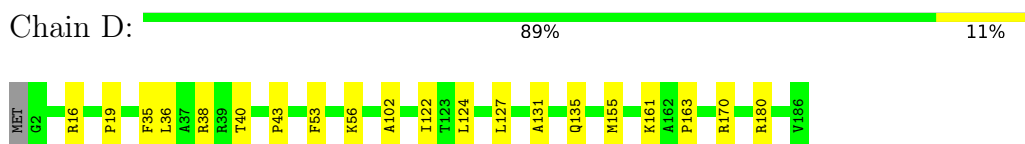
- Molecule 2: 60S ribosomal protein L16-A



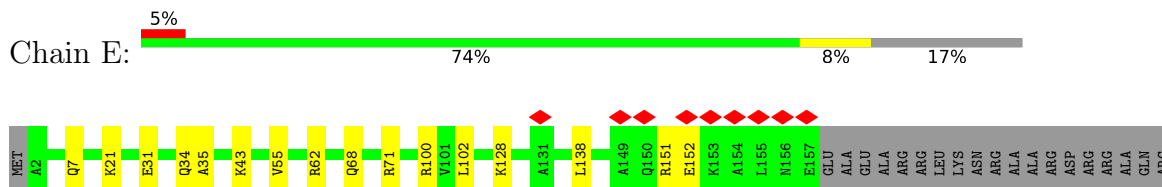
- Molecule 3: 60S ribosomal protein L17-A



- Molecule 4: 60S ribosomal protein L18-A




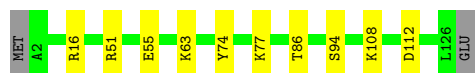
- Molecule 5: 60S ribosomal protein L19-A







Chain L:  91% 8% .




- Molecule 13: 60S ribosomal protein L27-A

Chain M:  91% 8% .




- Molecule 14: 60S ribosomal protein L28

Chain N:  87% 12% .




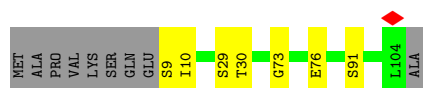
- Molecule 15: 60S ribosomal protein L29

Chain O:  5% 83% 14% . .




- Molecule 16: 60S ribosomal protein L30

Chain P:  85% 7% 9%




- Molecule 17: 60S ribosomal protein L31-A

Chain Q:  8% 80% 17% .



- Molecule 18: 60S ribosomal protein L32

Chain R:  89% 8% .




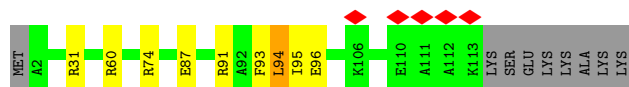
- Molecule 19: 60S ribosomal protein L33-A

Chain S:  93% 6%



- Molecule 20: 60S ribosomal protein L34-A

Chain T:  85% 7% 7%

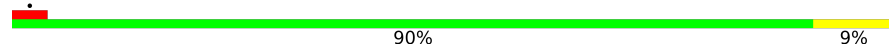


- Molecule 21: 60S ribosomal protein L35-A

Chain U:  92% 7%




- Molecule 22: 60S ribosomal protein L36-A

Chain V:  90% 9%



- Molecule 23: 60S ribosomal protein L37-A

Chain W:  76% 16% 8%



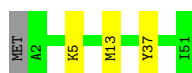
- Molecule 24: 60S ribosomal protein L38

Chain X:  90% 9%

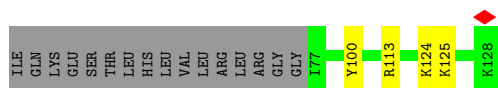
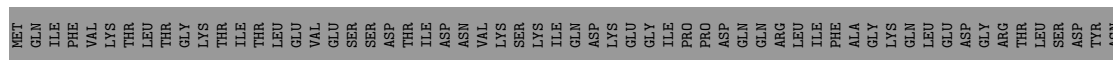


- Molecule 25: 60S ribosomal protein L39

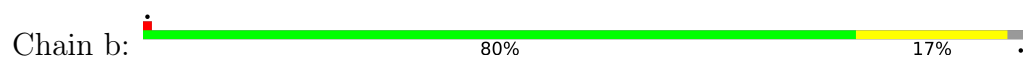
Chain Y:  92% 6%



- Molecule 26: Ubiquitin-60S ribosomal protein L40



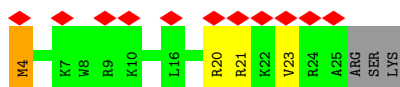
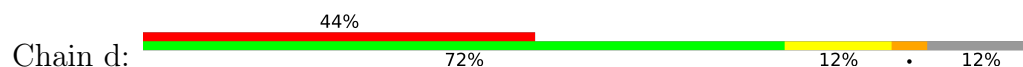
- Molecule 27: 60S ribosomal protein L42-A



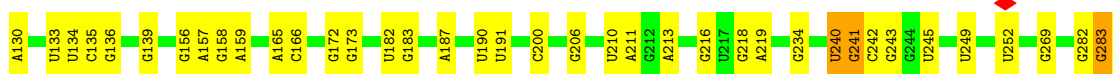
- Molecule 28: 60S ribosomal protein L43-A



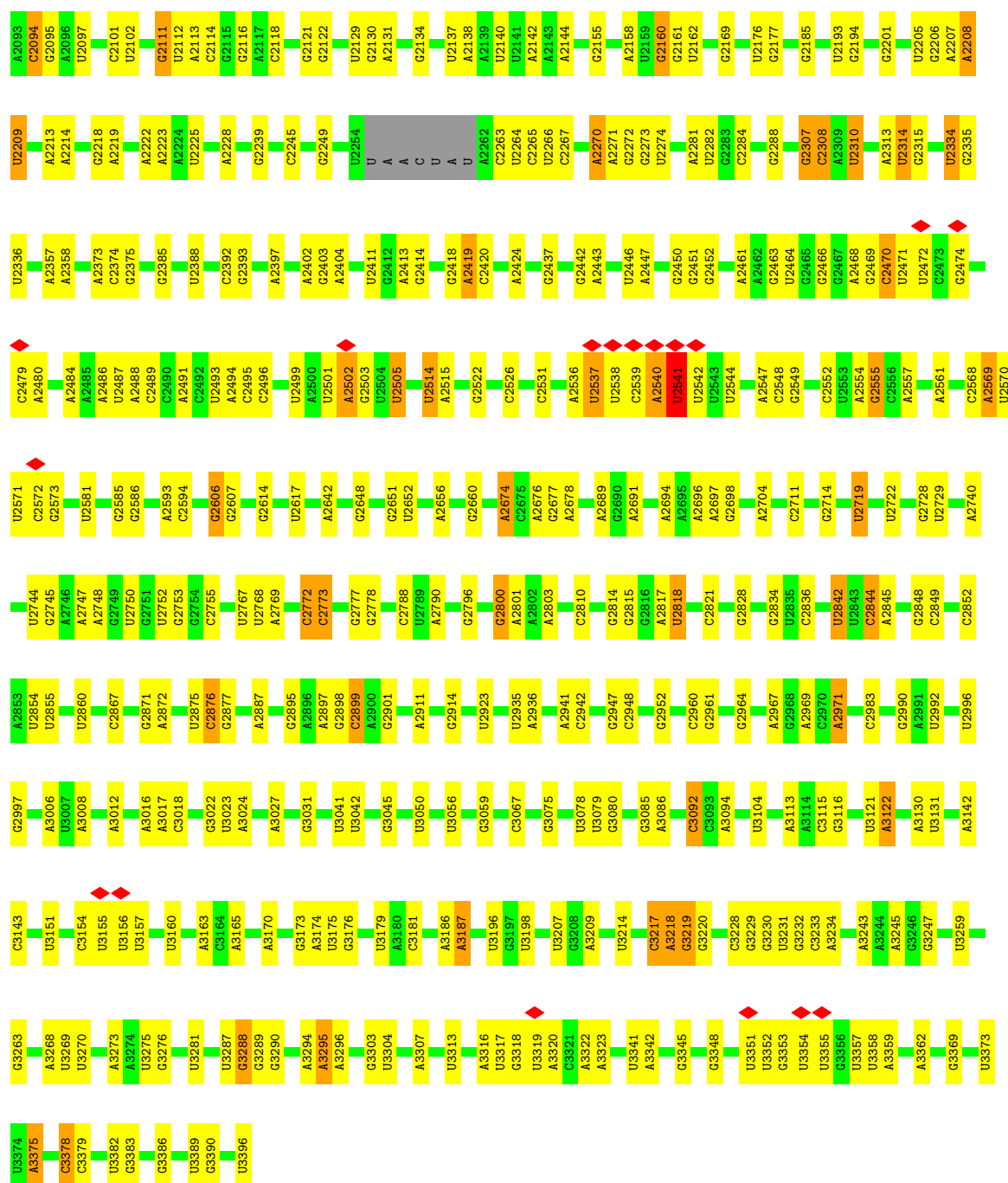
- Molecule 29: 60S ribosomal protein L41-A



- Molecule 30: 25S rRNA

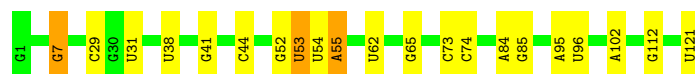


U	A	A1828	C1725	A1580	A1419	A1263	A1190	U1041	C911	U759	U627	A523	G	U451	U450	U449	U448	U447	U446	U445	U444	G443	G442
G	C	A1835	G1726	C1581	C1420	G1264	U1191	A1047	G912	G760	A628	U528	C	C	C	C	C	C	C	C	C	C	C
C	A	A1839	G1730	C1582	G1421	U1285	A1192	A1048	A914	G763	C637	A529	U	U	U	U	U	U	U	U	U	U	U
G	C	U1840	G1736	A1589	G1434	U1268	A1193	C1049	A915	U764	C638	G531	C	C	C	C	C	C	C	C	C	C	C
C	A	A1841	C	G1590	C1437	U1269	A1195	G1063	G916	U765	G639	A532	U	U	U	U	U	U	U	U	U	U	U
C	C	A1842	C	C	C	C	C1196	G1064	A917	U766	U640	G535	U	U	U	U	U	U	U	U	U	U	U
U	C	C1846	A1741	A1593	C1437	C1272	A1197	A1065	A920	G770	A649	U536	U	U	U	U	U	U	U	U	U	U	U
G	G	C	G1747	C1596	A1446	C1277	C1201	G1072	A921	U776	C655	U543	U	U	U	U	U	U	U	U	U	U	U
U	C	C1849	C	C1597	G1447	A1278	A1202	U1081	G924	U777	A656	G542	U	U	U	U	U	U	U	U	U	U	U
U	C	A1850	A1750	G1598	G1450	C1280	A1203	U1082	A925	U778	C656	C544	U	U	U	U	U	U	U	U	U	U	U
G	C	G1751	C	A1605	A1477	G1281	A1204	A1084	C937	A780	A660	C545	U	U	U	U	U	U	U	U	U	U	U
U	U	U1606	A1760	U1607	G1480	U1282	U1208	G1083	G937	U781	U660	C546	U	U	U	U	U	U	U	U	U	U	U
A	C	U1607	C1761	U1607	A1481	A1286	U1213	A1084	C938	G785	U664	C547	U	U	U	U	U	U	U	U	U	U	U
U	C	A1613	U1763	A1613	A1482	A1287	U1217	G1087	C944	A786	U673	C548	U	U	U	U	U	U	U	U	U	U	U
C	U	U1620	U1763	U1620	A1483	A1288	U1218	U1093	C945	G799	G674	A551	U	U	U	U	U	U	U	U	U	U	U
G	U	U1629	U1765	U1629	G1487	U1289	C1219	U1094	U946	G799	G675	A552	U	U	U	U	U	U	U	U	U	U	U
C	C	U1629	G1766	U1629	G1488	G1295	U1221	U1095	G947	C804	G676	G552	U	U	U	U	U	U	U	U	U	U	U
U	A	U1634	C	G1634	C1497	G1295	A1221	U1096	C959	A806	A677	U555	U	U	U	U	U	U	U	U	U	U	U
U	C	C	G1770	G1634	A1498	G1307	A1222	G1097	U960	A806	U679	U556	U	U	U	U	U	U	U	U	U	U	U
U	U	C1639	C1771	C1639	A1498	A1308	G1225	A1098	G974	G815	U680	U557	U	U	U	U	U	U	U	U	U	U	U
G	U	U1772	U1772	U1772	C1502	U1309	G1226	U1103	U981	A816	U681	U558	U	U	U	U	U	U	U	U	U	U	U
C	U	G1775	C	A1642	C1508	G1313	C1227	G1104	C982	A817	G684	U559	U	U	U	U	U	U	U	U	U	U	U
G	U	A1643	C	A1643	C1508	G1313	G1228	A1105	U829	U871	U687	A572	U	U	U	U	U	U	U	U	U	U	U
U	U	U1645	U1778	C1644	G1536	A1330	G1229	G1106	G991	A830	G688	A578	U	U	U	U	U	U	U	U	U	U	U
C	U	U1645	C1779	U1645	C1536	A1330	A1231	C1107	G994	G835	U689	G579	U	U	U	U	U	U	U	U	U	U	U
U	U	C1657	G1780	U1657	A1557	U1353	G1232	U1109	G994	G835	A692	A585	U	U	U	U	U	U	U	U	U	U	U
C	C	C	G1786	G1666	G1560	U1353	G1233	G1117	G1001	A836	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	A1667	A1787	A1667	G1560	A1350	U1234	G1118	G1001	A836	A705	G591	U	U	U	U	U	U	U	U	U	U	U
A	U	C1667	C	C1667	G1560	A1350	U1235	C1119	A1002	A837	A710	G596	U	U	U	U	U	U	U	U	U	U	U
A	C	G1661	C	G1661	U1554	U1351	U1236	G1119	A1002	A837	A711	C596	U	U	U	U	U	U	U	U	U	U	U
U	U	G1662	C	G1662	U1555	U1351	G1237	U1108	A1002	A837	A712	C597	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C1793	C	C1566	U1352	G1237	U1108	A1002	A837	A712	C597	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U	U	U	U	U	U	U	U
U	C	C	C	C	C1567	U1353	G1238	A1120	G1010	A846	C696	A589	U	U	U	U							



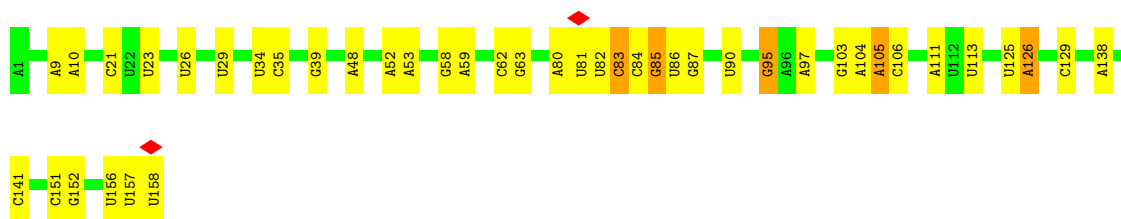
• Molecule 31: 5S rRNA

Chain h: 83% 15% .



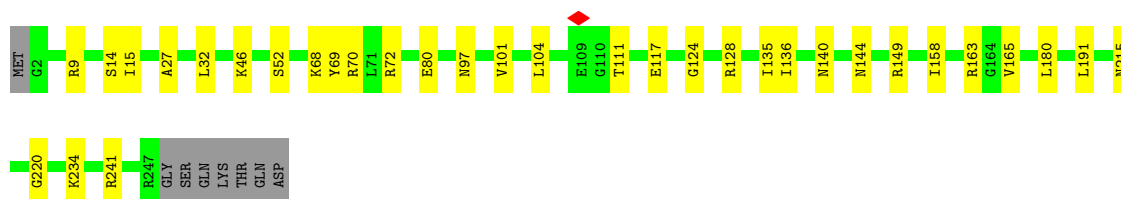
• Molecule 32: 5.8S rRNA

Chain i: 73% 24% .



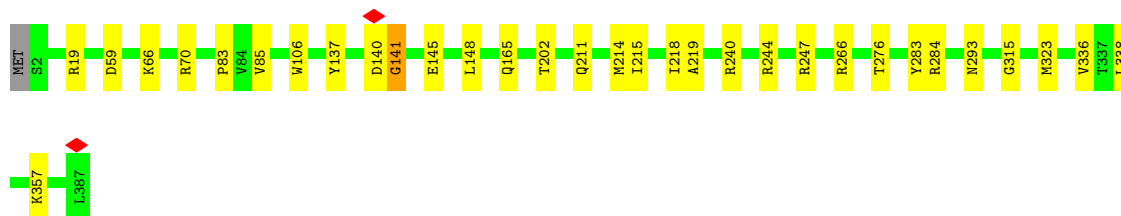
- Molecule 33: 60S ribosomal protein L2-A

Chain j: 84% 13% .



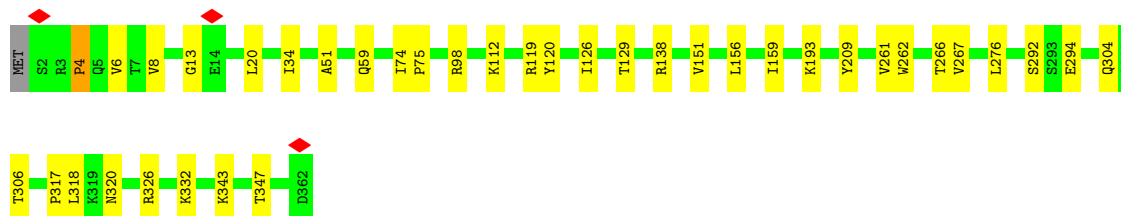
- Molecule 34: 60S ribosomal protein L3

Chain k: 91% 8%



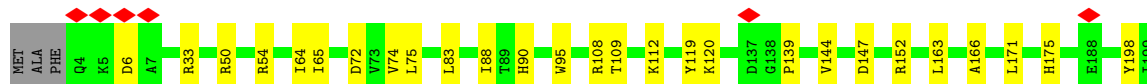
- Molecule 35: 60S ribosomal protein L4-A

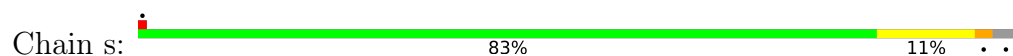
Chain l: 89% 10%



- Molecule 36: 60S ribosomal protein L5

Chain m: 82% 16% .

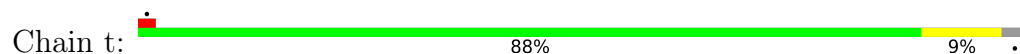








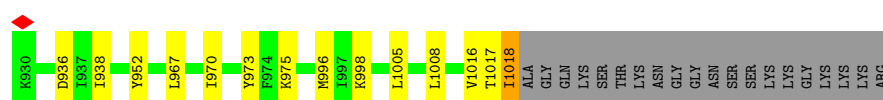
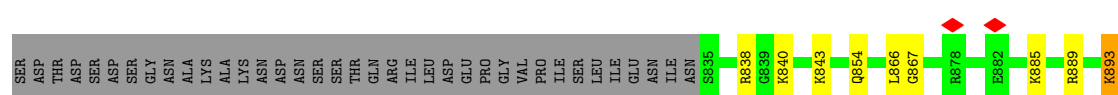
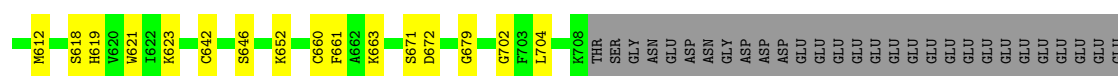
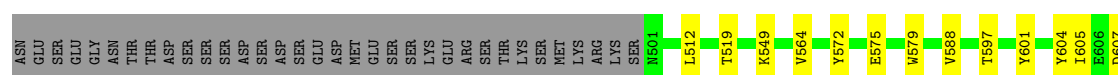
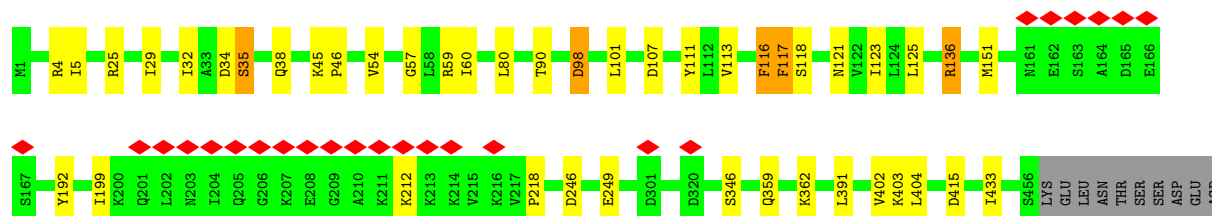
- Molecule 43: 60S ribosomal protein L13-A



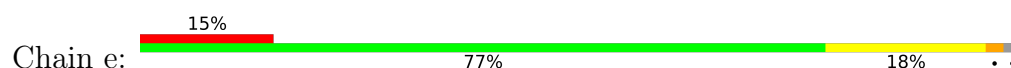
- Molecule 44: 60S ribosomal protein L14-A

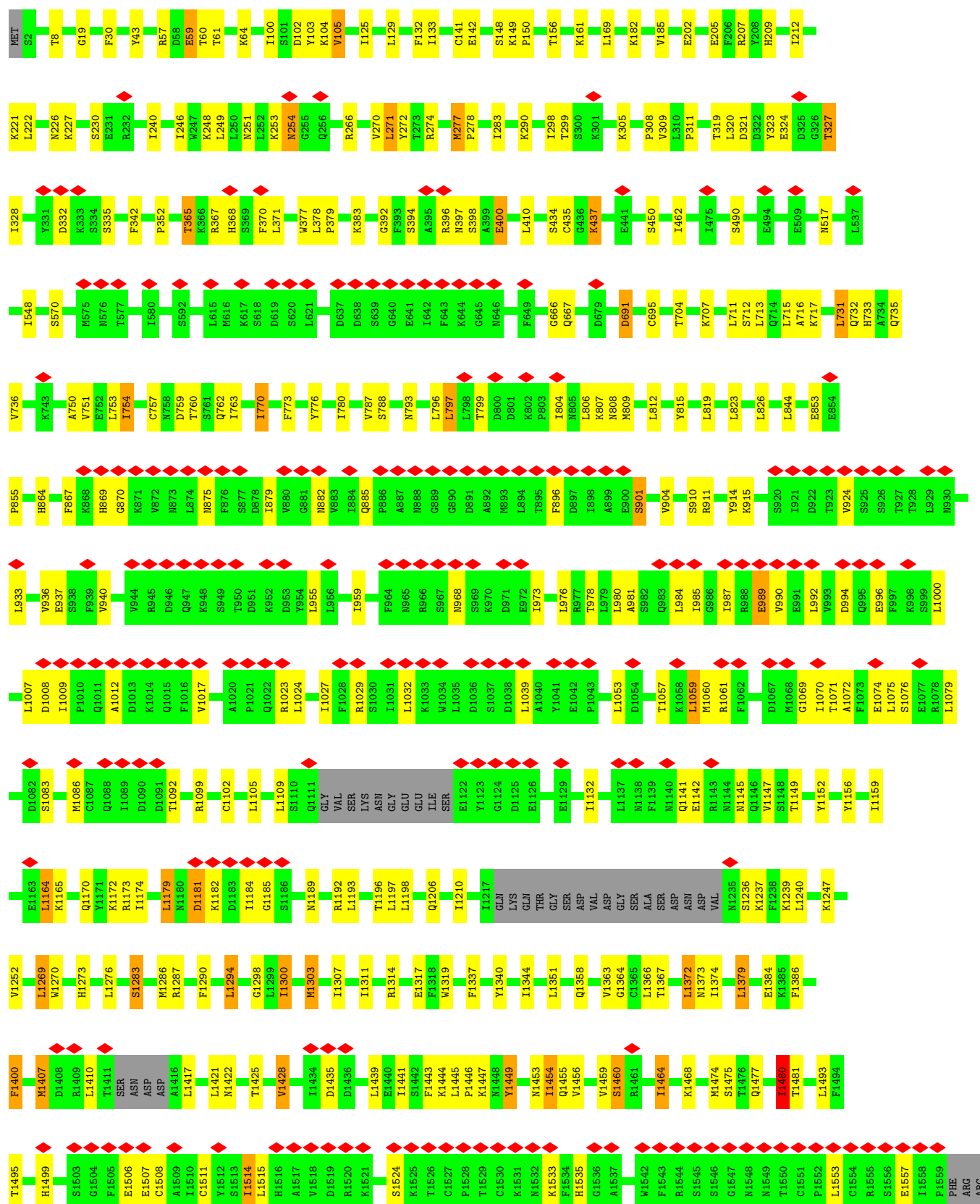



- Molecule 45: Ribosome quality control complex subunit 2

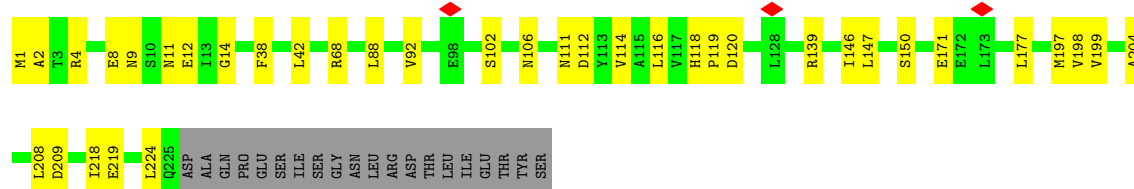


- Molecule 46: E3 ubiquitin-protein ligase listerin




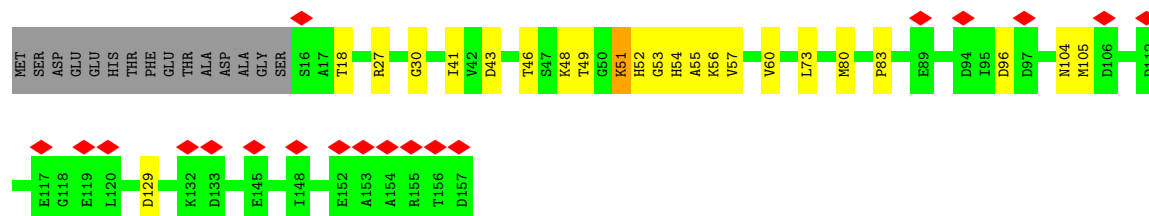


Chain g: 




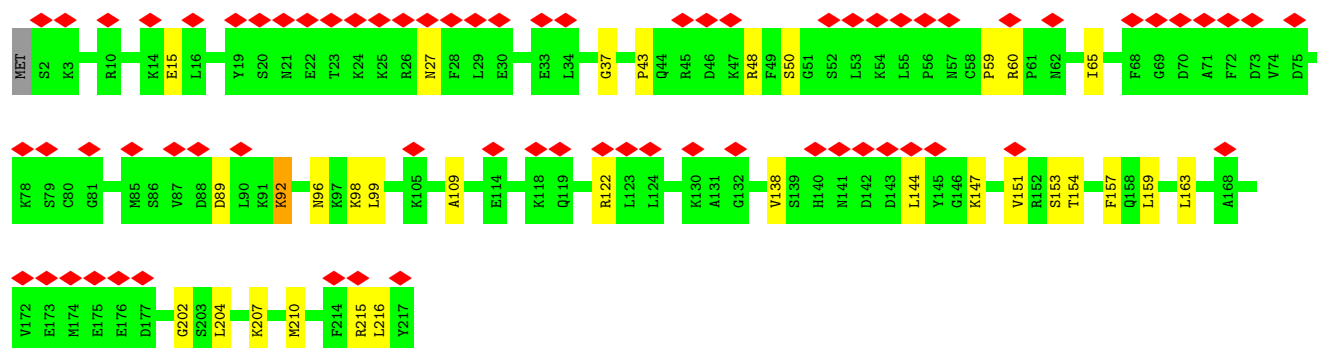
- Molecule 48: Eukaryotic translation initiation factor 5A-1

Chain v: 



- Molecule 49: 60S ribosomal protein L1-A

Chain w: 



- Molecule 50: Ala tRNA

Chain x: 

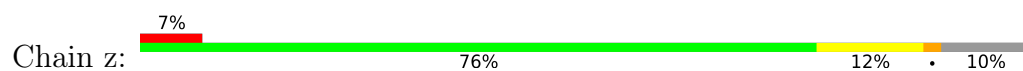


- Molecule 50: Ala tRNA

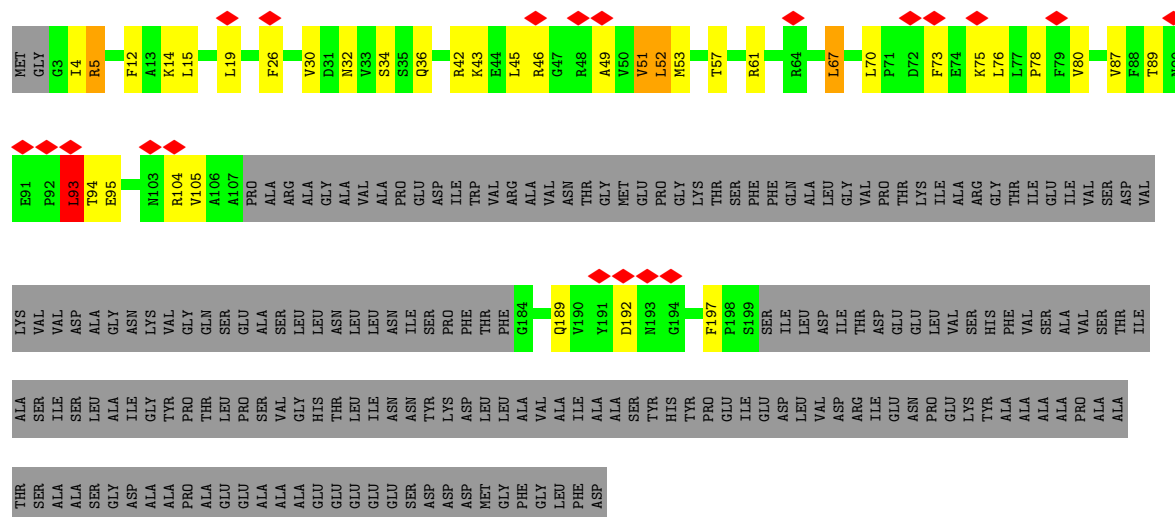
Chain y: 



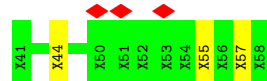
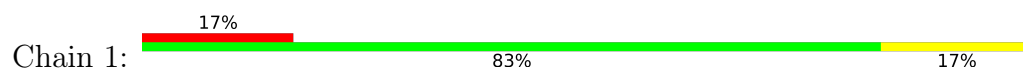
- Molecule 51: 60S ribosomal protein L12-B



- Molecule 52: 60S acidic ribosomal protein P0



- Molecule 53: CAT-tailed nascent peptide



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	56884	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	2.510	Depositor
Minimum map value	-1.743	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	476.55002, 476.55002, 476.55002	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: ZN, SPD, 5CT, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	A	0.31	0/1757	0.54	0/2354
2	B	0.31	0/1585	0.54	0/2128
3	C	0.31	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	0.28	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	0.31	0/1200	0.56	1/1607 (0.1%)
15	O	0.28	0/473	0.61	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	0.26	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	0.28	0/618	0.65	1/826 (0.1%)
25	Y	0.28	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	0.30	0/77011	0.39	5/120065 (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	0.56	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	0.33	0/1367	0.72	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	0.27	0/6692	0.56	2/9027 (0.0%)
46	e	0.62	0/11708	0.92	57/15899 (0.4%)
47	g	0.24	0/1672	0.59	1/2281 (0.0%)
48	v	0.25	0/1084	0.61	1/1456 (0.1%)
49	w	0.29	0/1736	0.62	1/2332 (0.0%)
50	x	0.56	3/1760 (0.2%)	0.74	6/2738 (0.2%)
50	y	0.31	1/1734 (0.1%)	0.44	0/2697
51	z	0.67	0/733	1.24	13/1015 (1.3%)
52	0	0.49	0/982	0.94	3/1320 (0.2%)
All	All	0.34	4/161776 (0.0%)	0.52	111/236315 (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
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	11

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	x	34	I	P-OP1	18.99	1.86	1.48
50	x	34	I	C6-O6	7.65	1.38	1.23
50	y	34	I	O3'-P	7.20	1.63	1.56
50	x	76	A	C3'-O3'	5.42	1.50	1.42

The worst 5 of 111 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	x	34	I	O5'-P-OP2	28.59	145.01	110.70
46	e	1364	GLY	N-CA-C	12.25	127.31	112.49
46	e	1460	SER	N-CA-C	10.04	122.31	111.36
46	e	1181	ASP	N-CA-C	8.83	120.91	111.28
46	e	1141	GLN	N-CA-C	8.74	120.81	111.28

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	U	83	LYS	Peptide
34	k	141	GLY	Peptide
35	l	13	GLY	Peptide
35	l	318	LEU	Peptide
39	p	30	THR	Peptide

## 5.2 Too-close contacts [i](#)

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	18	0
2	B	1555	0	1659	17	0
3	C	1416	0	1433	14	0
4	D	1441	0	1543	16	0
5	E	1258	0	1342	11	0
6	F	1437	0	1475	20	0
7	G	1272	0	1312	12	0
8	H	796	0	812	7	0
9	I	1003	0	1048	10	0
10	J	518	0	542	7	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	13	0
15	O	462	0	491	7	0
16	P	737	0	792	4	0
17	Q	876	0	912	10	0
18	R	1013	0	1077	8	0
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	844	7	0
23	W	645	0	645	12	0
24	X	612	0	682	6	0
25	Y	436	0	475	2	0
26	Z	410	0	442	5	0
27	b	824	0	888	13	0
28	c	694	0	734	8	0
29	d	207	0	250	3	0
30	f	68802	0	34573	352	0
31	h	2579	0	1304	9	0
32	i	3353	0	1695	14	0
33	j	1874	0	1943	25	0
34	k	3075	0	3142	20	0
35	l	2748	0	2859	25	0
36	m	2351	0	2294	31	0
37	n	1307	0	1377	8	0
38	o	1784	0	1862	10	0
39	p	1804	0	1877	17	0
40	q	1508	0	1572	16	0
41	r	1764	0	1804	18	0
42	s	1346	0	1370	17	0
43	t	1543	0	1608	14	0
44	u	1053	0	1149	11	0
45	a	6582	0	6484	77	0
46	e	11509	0	10768	279	0
47	g	1651	0	1613	22	0
48	v	1085	0	1087	19	0
49	w	1709	0	1799	21	0
50	x	1579	0	798	23	0
50	y	1556	0	788	18	0
51	z	734	0	344	18	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	0	967	0	990	47	0
53	1	90	0	20	7	0
54	A	1	0	0	0	0
54	C	1	0	0	0	0
54	E	1	0	0	0	0
54	I	1	0	0	0	0
54	R	1	0	0	0	0
54	T	1	0	0	0	0
54	f	3	0	0	0	0
54	h	1	0	0	0	0
54	j	2	0	0	0	0
54	k	1	0	0	0	0
55	T	1	0	0	0	0
55	W	1	0	0	0	0
55	Z	1	0	0	0	0
55	b	1	0	0	0	0
55	c	1	0	0	0	0
55	e	2	0	0	0	0
56	f	10	0	19	1	0
All	All	151377	0	113649	1110	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 1110 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	1.66
46:e:277:MET:SD	46:e:278:PRO:HD3	1.34	1.62
46:e:751:VAL:HA	46:e:754:ILE:CD1	1.30	1.59
46:e:272:TYR:HD1	46:e:277:MET:CE	1.13	1.55
46:e:272:TYR:CD1	46:e:277:MET:HE1	1.39	1.54

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
2	B	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
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%)	60 (98%)	1 (2%)	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%)	51 (91%)	4 (7%)	1 (2%)	6	12
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

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	364 (95%)	20 (5%)	0	100	100
35	l	359/362 (99%)	329 (92%)	29 (8%)	1 (0%)	36	55
36	m	292/297 (98%)	277 (95%)	15 (5%)	0	100	100
37	n	163/176 (93%)	154 (94%)	9 (6%)	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	43
41	r	216/221 (98%)	206 (95%)	10 (5%)	0	100	100
42	s	167/174 (96%)	161 (96%)	5 (3%)	1 (1%)	21	38
43	t	191/199 (96%)	174 (91%)	16 (8%)	1 (0%)	24	43
44	u	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
45	a	842/1038 (81%)	825 (98%)	16 (2%)	1 (0%)	48	68
46	e	1519/1562 (97%)	1496 (98%)	21 (1%)	2 (0%)	48	68
47	g	223/245 (91%)	215 (96%)	8 (4%)	0	100	100
48	v	139/157 (88%)	139 (100%)	0	0	100	100
49	w	214/217 (99%)	211 (99%)	3 (1%)	0	100	100
51	z	144/165 (87%)	135 (94%)	8 (6%)	1 (1%)	18	34
52	0	117/312 (38%)	116 (99%)	0	1 (1%)	14	27
All	All	9314/10279 (91%)	8951 (96%)	353 (4%)	10 (0%)	49	68

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
51	z	88	PRO
46	e	437	LYS
15	O	22	LYS
45	a	35	SER
46	e	855	PRO

### 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
3	C	138/146 (94%)	137 (99%)	1 (1%)	76	89
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%)	53 (98%)	1 (2%)	50	76
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

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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%)	142 (98%)	3 (2%)	47	74
43	t	154/159 (97%)	154 (100%)	0	100	100
44	u	107/109 (98%)	107 (100%)	0	100	100
45	a	679/949 (72%)	674 (99%)	5 (1%)	76	89
46	e	1150/1451 (79%)	1088 (95%)	62 (5%)	20	41
47	g	180/211 (85%)	180 (100%)	0	100	100
48	v	119/132 (90%)	118 (99%)	1 (1%)	73	88
49	w	197/198 (100%)	196 (100%)	1 (0%)	81	92
51	z	1/136 (1%)	1 (100%)	0	100	100
52	0	105/254 (41%)	94 (90%)	11 (10%)	6	14
All	All	7566/8826 (86%)	7480 (99%)	86 (1%)	63	84

5 of 86 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	e	1303	MET
46	e	1514	ILE
46	e	1367	THR
46	e	1421	LEU
52	0	5	ARG

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

Mol	Chain	Res	Type
46	e	79	ASN
46	e	1455	GLN
46	e	174	GLN
46	e	408	ASN
46	e	1499	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	f	3211/3395 (94%)	591 (18%)	0
31	h	120/121 (99%)	12 (10%)	0
32	i	157/158 (99%)	32 (20%)	0
50	x	70/76 (92%)	18 (25%)	0
50	y	69/76 (90%)	18 (26%)	0
All	All	3627/3826 (94%)	671 (18%)	0

5 of 671 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 ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
48	5CT	v	51	48	13,14,15	0.78	0	8,15,17	1.29	1 (12%)

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
48	5CT	v	51	48	-	9/13/14/16	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	v	51	5CT	C4-C3-C2	-2.20	108.84	113.47

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
48	v	51	5CT	NZ-C1-C2-C3
48	v	51	5CT	O1-C2-C3-C4
48	v	51	5CT	C2-C3-C4-N1
48	v	51	5CT	C-CA-CB-CG
48	v	51	5CT	N-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
48	v	51	5CT	1	0

## 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	$\# Z  > 2$
56	SPD	f	3401	-	9,9,9	0.32	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
56	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
56	f	3401	SPD	C3-C4-C5-N6
56	f	3401	SPD	N6-C7-C8-C9
56	f	3401	SPD	C2-C3-C4-C5
56	f	3401	SPD	C4-C5-N6-C7
56	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
56	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.

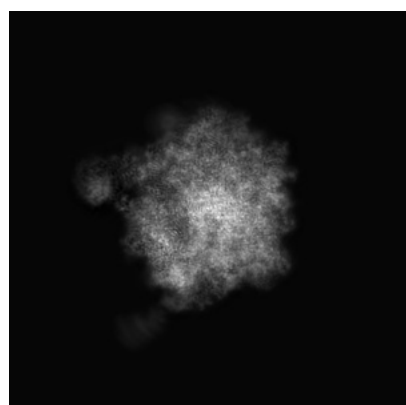
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15296. These allow visual inspection of the internal detail of the map and identification of artifacts.

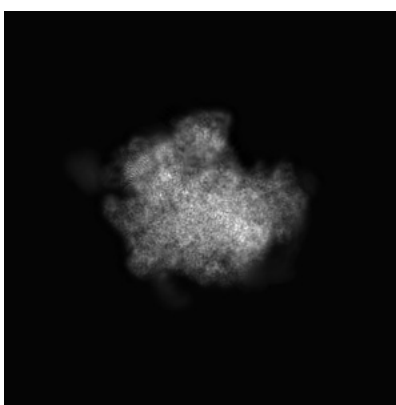
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

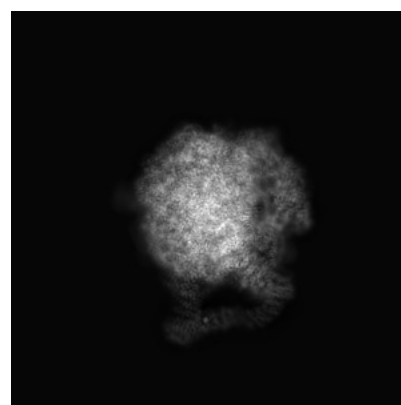
#### 6.1.1 Primary map



X



Y

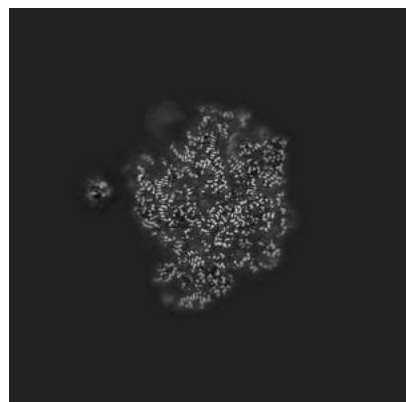


Z

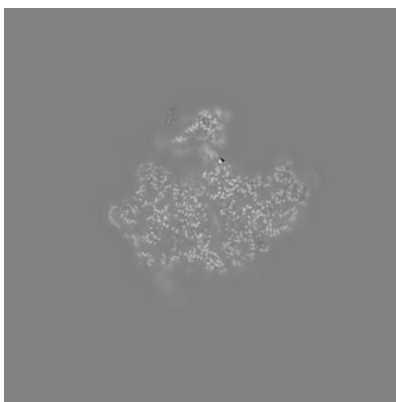
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

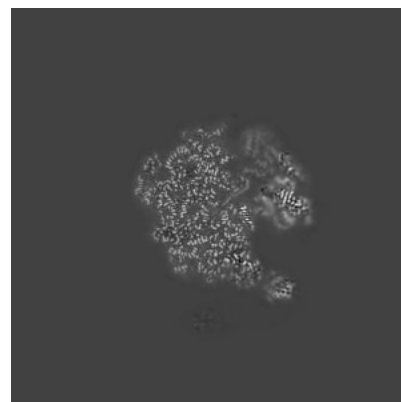
#### 6.2.1 Primary map



X Index: 225



Y Index: 225

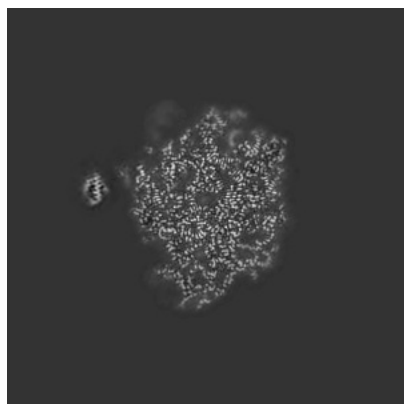


Z Index: 225

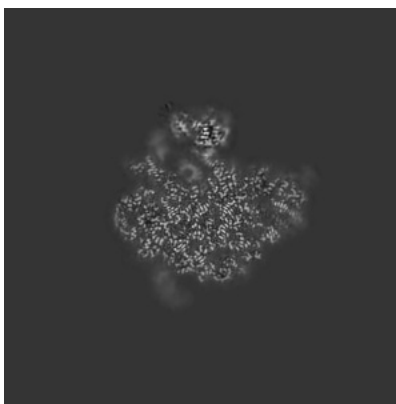
The images above show central slices of the map in three orthogonal directions.

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

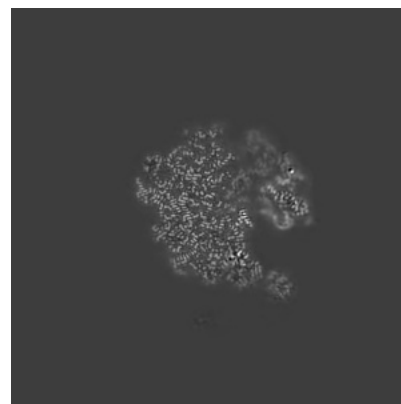
### 6.3.1 Primary map



X Index: 219



Y Index: 237

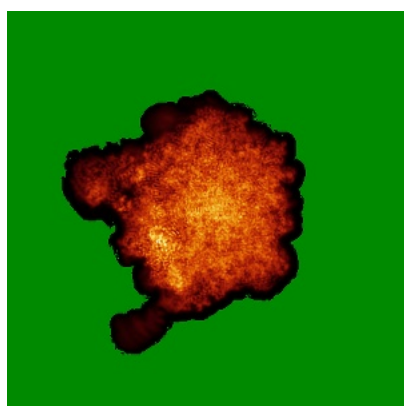


Z Index: 222

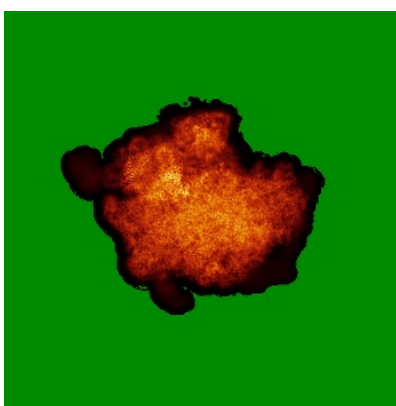
The images above show the largest variance slices of the map in three orthogonal directions.

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

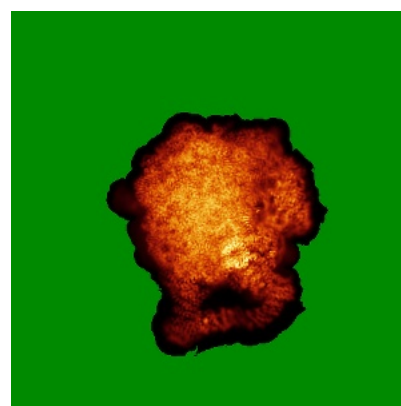
### 6.4.1 Primary map



X



Y

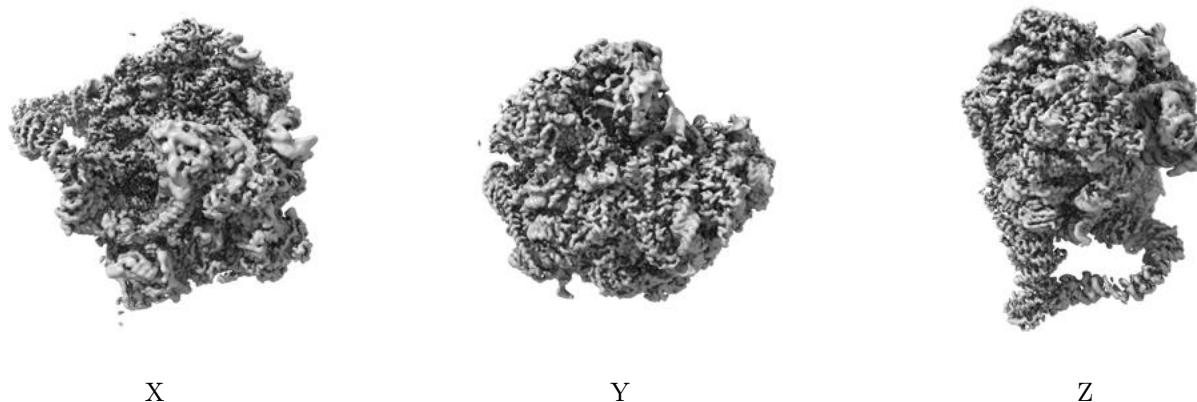


Z

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

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

### 6.5.1 Primary map



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

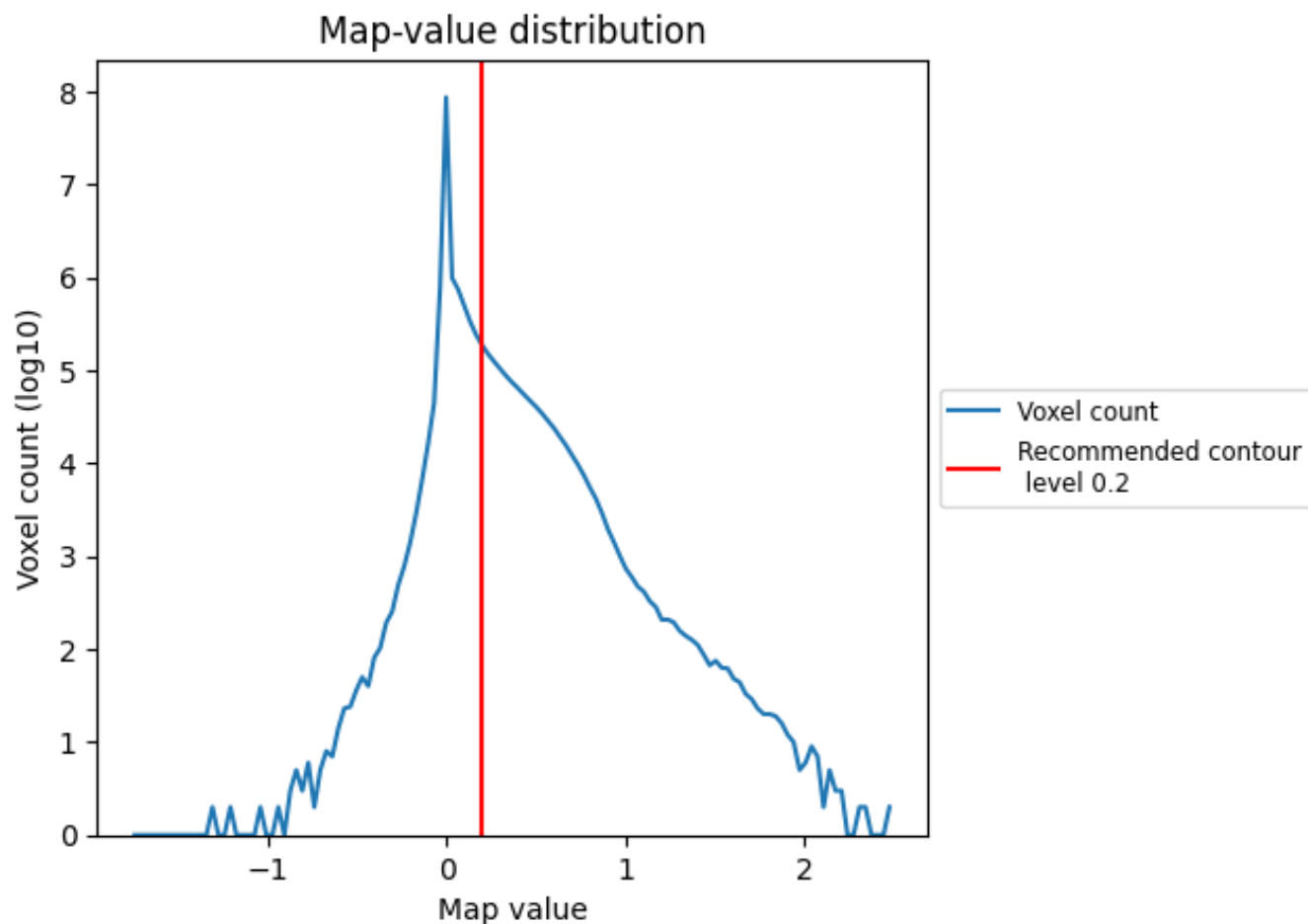
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

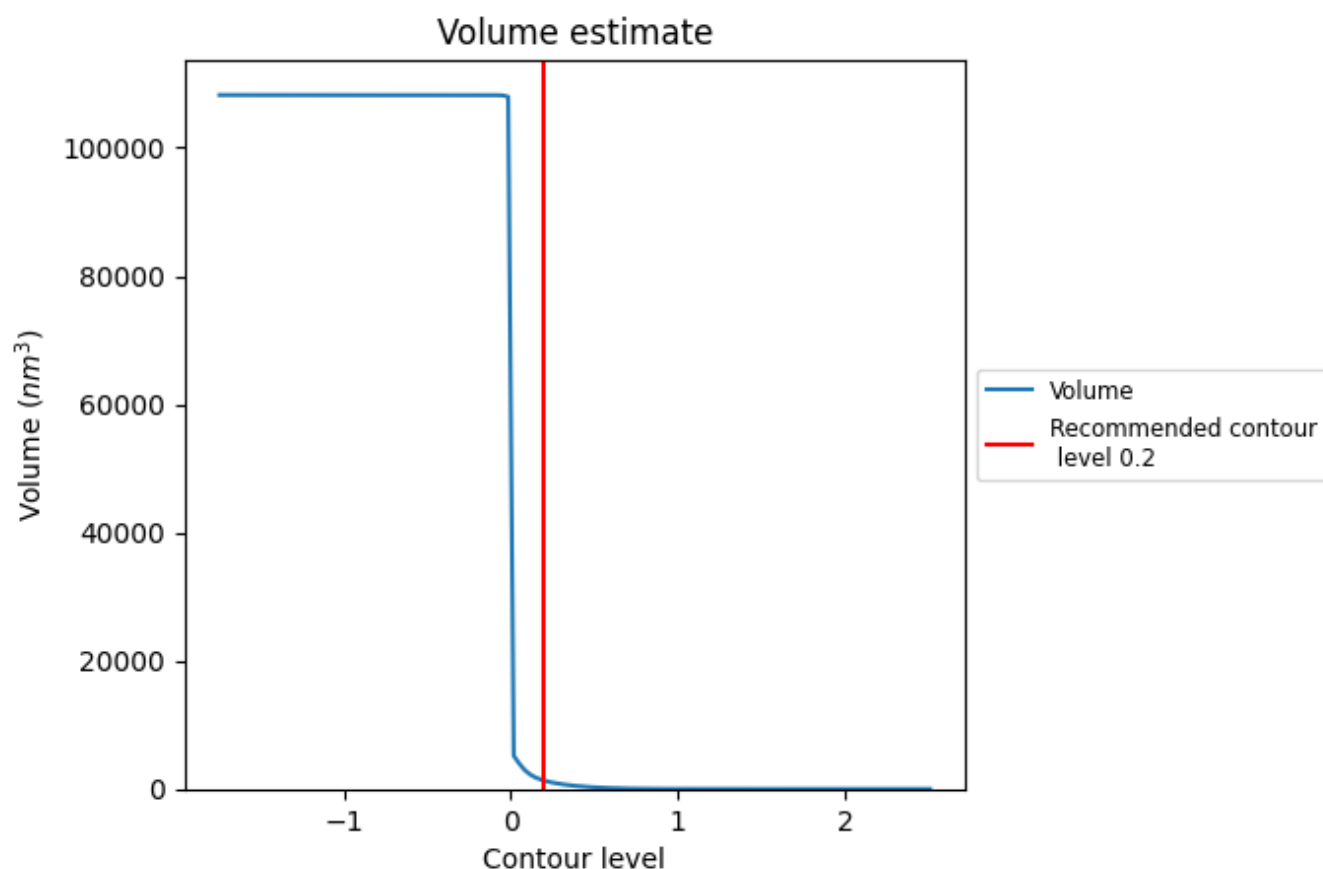
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

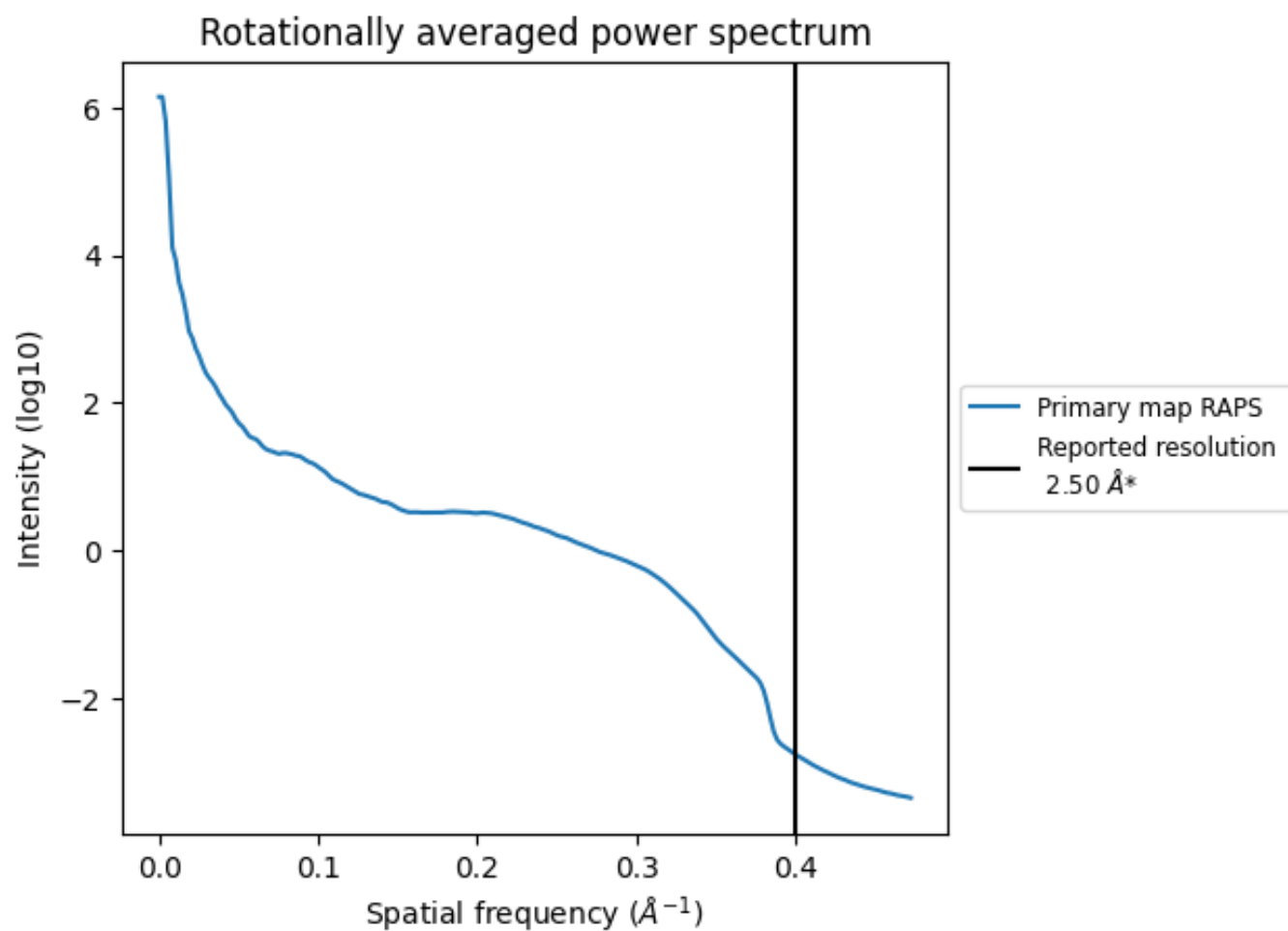
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1316 nm<sup>3</sup>; this corresponds to an approximate mass of 1189 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 ⓘ

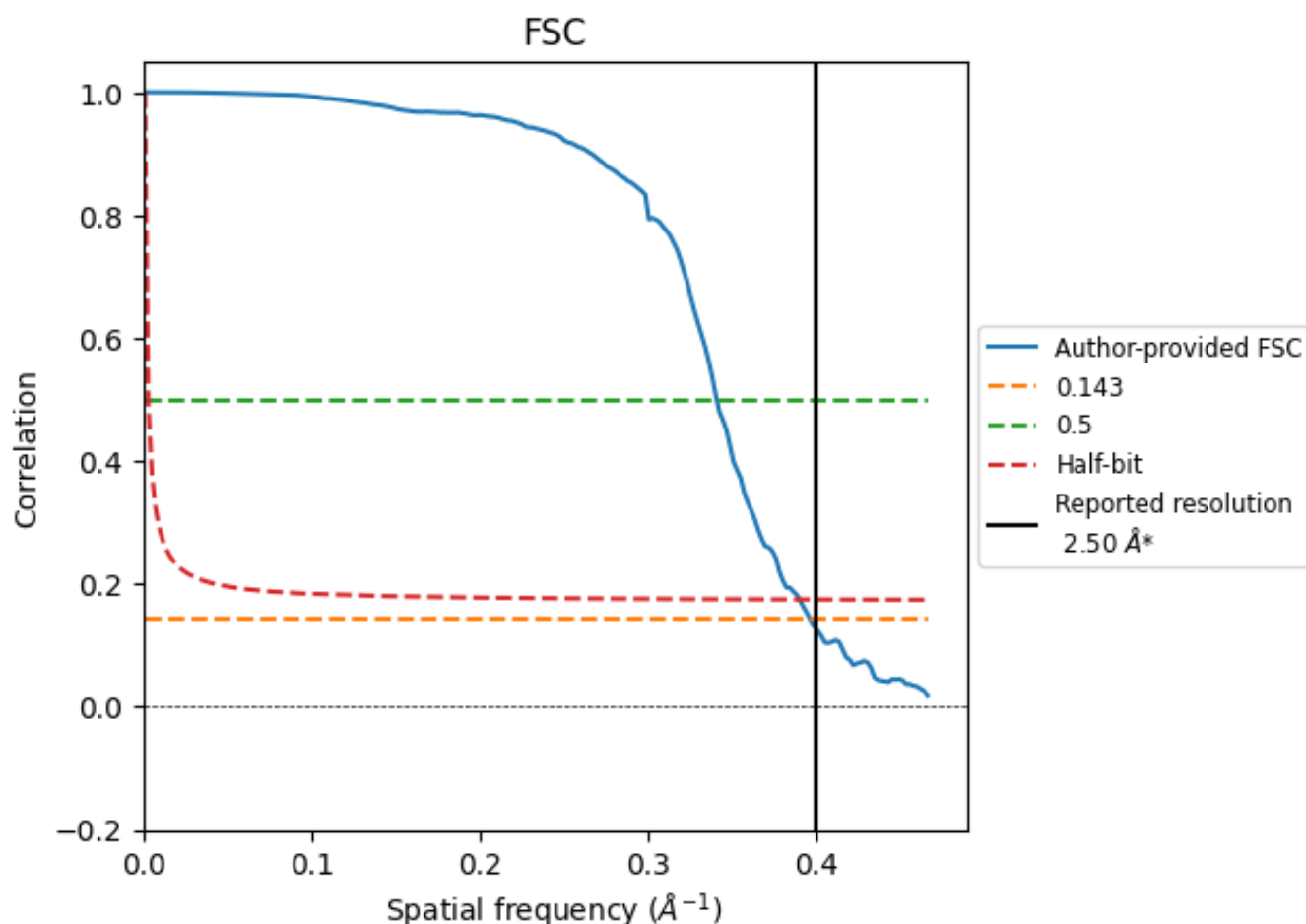


\*Reported resolution corresponds to spatial frequency of 0.400 Å<sup>-1</sup>

## 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 0.400 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

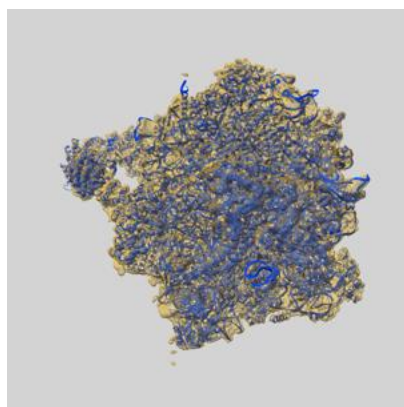
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.50	-	-
Author-provided FSC curve	2.52	2.93	2.56
Unmasked-calculated*	-	-	-

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

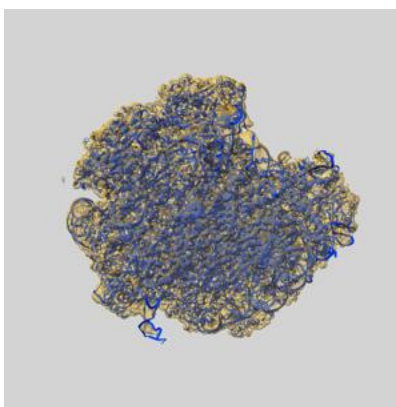
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-15296 and PDB model 8AAF. Per-residue inclusion information can be found in section 3 on page 16.

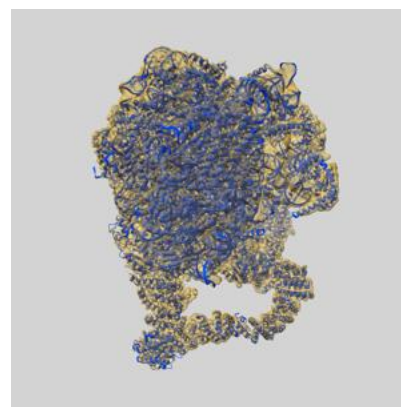
### 9.1 Map-model overlay [i](#)



X



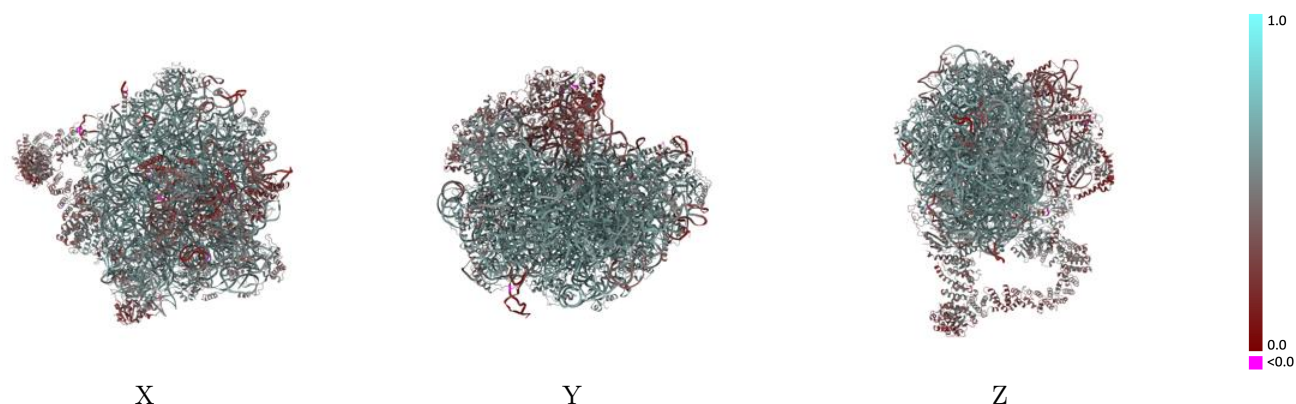
Y



Z

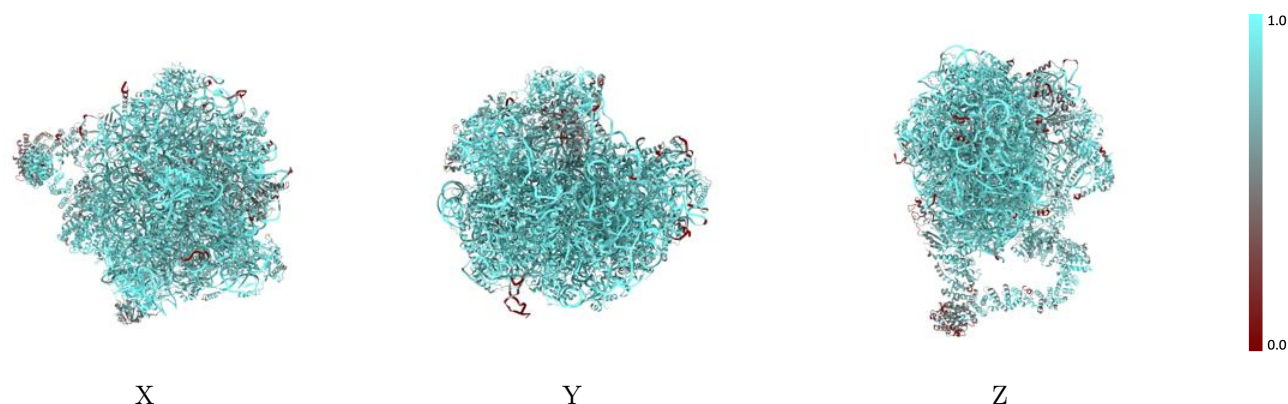
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



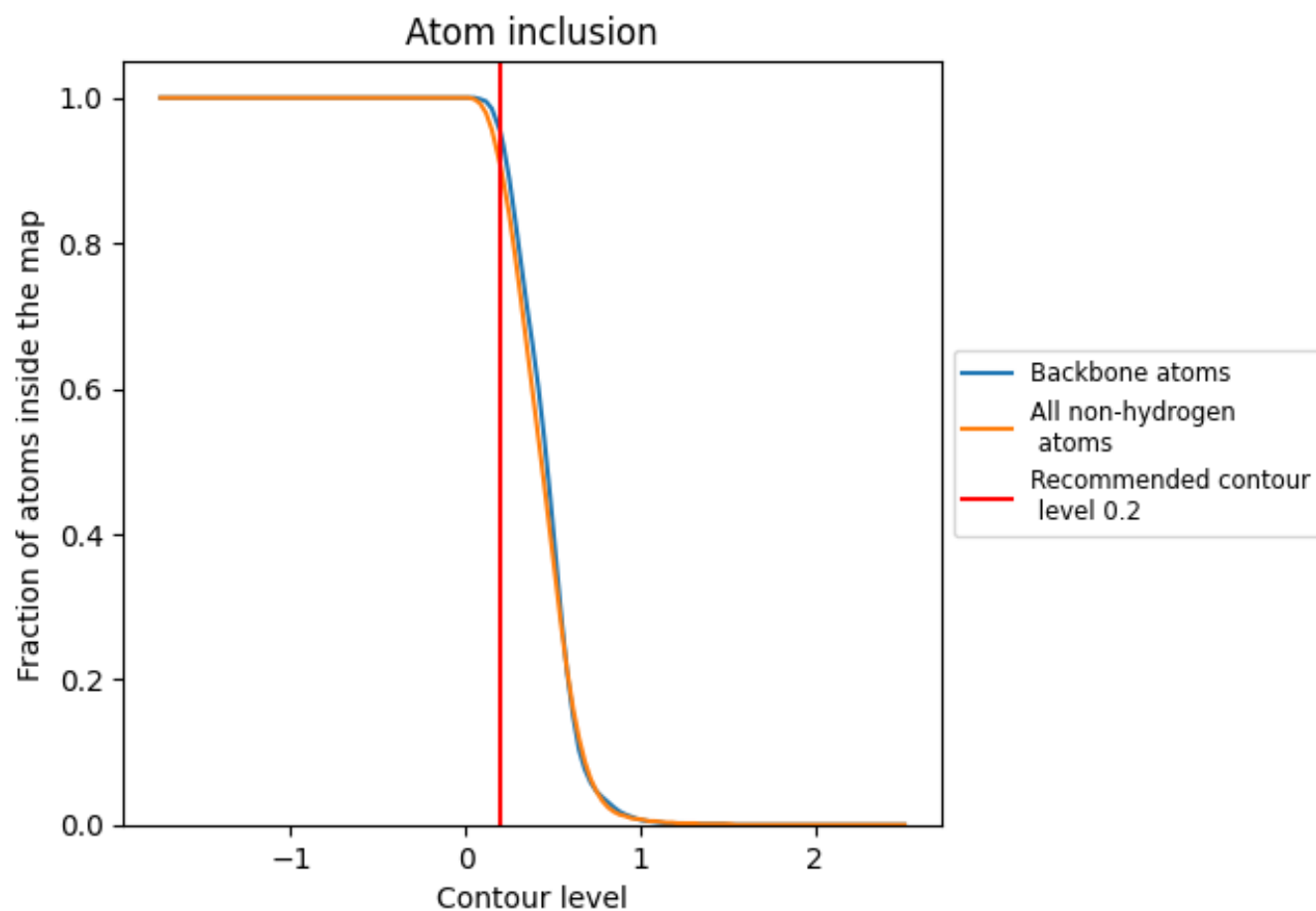
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.2).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 91% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ









































The table lists the average atom inclusion at the recommended contour level (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9070	 0.5360
0	 0.5990	 0.3310
1	 0.7000	 0.3950
A	 0.9700	 0.6130
B	 0.9410	 0.5890
C	 0.9200	 0.5910
D	 0.9420	 0.5890
E	 0.8750	 0.5540
F	 0.9200	 0.5820
G	 0.9000	 0.5640
H	 0.7980	 0.4780
I	 0.9420	 0.5450
J	 0.9220	 0.5820
K	 0.9020	 0.5750
L	 0.9030	 0.5720
M	 0.8480	 0.5270
N	 0.9360	 0.5970
O	 0.8890	 0.5430
P	 0.8330	 0.5210
Q	 0.8570	 0.5540
R	 0.9350	 0.6020
S	 0.9670	 0.6220
T	 0.9090	 0.5770
U	 0.8930	 0.5570
V	 0.8650	 0.5320
W	 0.9900	 0.6270
X	 0.7830	 0.5030
Y	 0.9490	 0.6030
Z	 0.9570	 0.5900
a	 0.8480	 0.3780
b	 0.8880	 0.5770
c	 0.9030	 0.5720
d	 0.4150	 0.4170
e	 0.6940	 0.3990
f	 0.9660	 0.5740



*Continued on next page...*

*Continued from previous page...*

Chain	Atom inclusion	Q-score
g	 0.7960	 0.4720
h	 0.9920	 0.5690
i	 0.9820	 0.5990
j	 0.9460	 0.6050
k	 0.9370	 0.5860
l	 0.9190	 0.5780
m	 0.8340	 0.4920
n	 0.8520	 0.5300
o	 0.9180	 0.5720
p	 0.8460	 0.5240
q	 0.9240	 0.5700
r	 0.8820	 0.5470
s	 0.8060	 0.4560
t	 0.9040	 0.5620
u	 0.8960	 0.5500
v	 0.6300	 0.4210
w	 0.4840	 0.2890
x	 0.9730	 0.3510
y	 0.8980	 0.2690
z	 0.8840	 0.4150