



## wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 03:55 pm GMT

PDB ID : 5MYJ  
EMDB ID : EMD-3581  
Title : Structure of 70S ribosome from *Lactococcus lactis*  
Authors : Franken, L.E.; Oostergetel, G.T.; Pijning, T.; Puri, P.; Boekema, E.J.; Poolman, B.; Guskov, A.  
Deposited on : 2017-01-26  
Resolution : 5.60 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

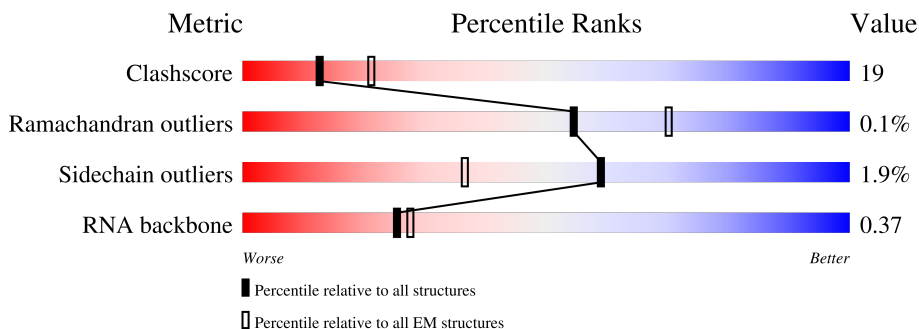
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 5.60 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.



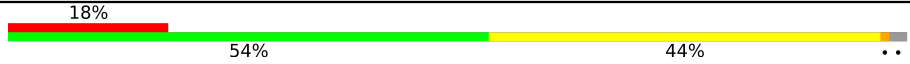
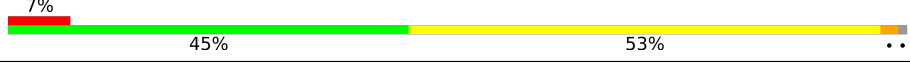




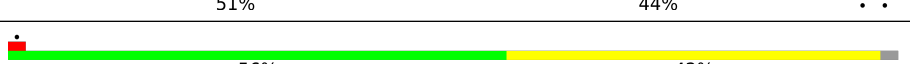
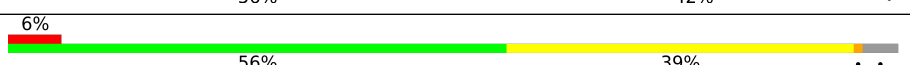
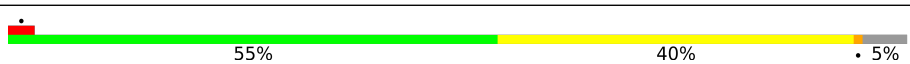


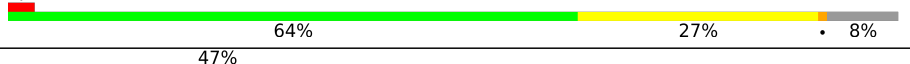

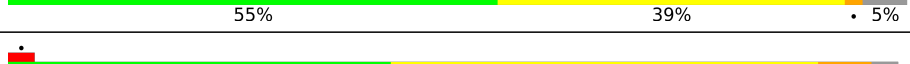
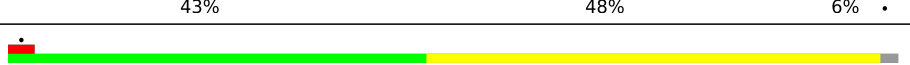



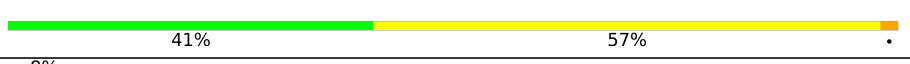


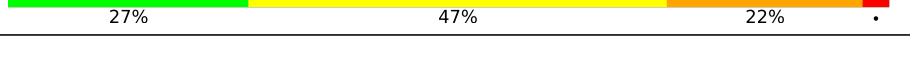
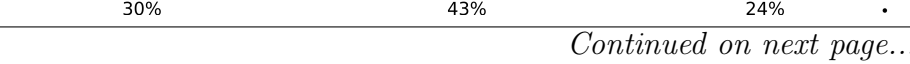


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	AA	1535	23% (red), 46% (yellow), 27% (orange), . (grey)
2	AB	255	36% (red), 59% (green), 28% (yellow), 12% (grey)
3	AC	217	17% (red), 50% (green), 47% (yellow), . (grey)
4	AD	203	9% (red), 44% (green), 53% (yellow), .. (grey)
5	AE	168	25% (red), 56% (green), 36% (yellow), . 7% (grey)
6	AF	97	16% (red), 49% (green), 51% (yellow)
7	AG	155	8% (red), 52% (green), 45% (yellow), .. (grey)

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Mol	Chain	Length	Quality of chain
8	AH	132	
9	AI	130	
10	AJ	102	
11	AK	127	
12	AL	137	
13	AM	121	
14	AN	61	
15	AO	89	
16	AP	90	
17	AQ	86	
18	AR	81	
19	AS	92	
20	AT	77	
21	AU	58	
22	B0	64	
23	B1	69	
24	B2	59	
25	B3	81	
26	B4	57	
27	B5	49	
28	B6	44	
29	B7	66	
30	B8	38	
31	BA	2897	
32	BB	115	

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Mol	Chain	Length	Quality of chain
33	BD	276	 5% 55% 41% ..
34	BE	207	 57% 38% ..
35	BF	208	 56% 41% ..
36	BG	180	 56% 39% ...
37	BH	178	 58% 38% ..
38	BM	148	 49% 47% ...
39	BN	122	 12% 66% 31% ..
40	BO	147	 56% 43% ..
41	BP	137	 54% 42% ..
42	BQ	126	 56% 41% ..
43	BR	115	 51% 44% .
44	BS	114	 9% 56% 41% .
45	BT	119	 59% 36% ..
46	BU	104	 61% 32% ...
47	BV	115	 41% 53% ..
48	BW	97	 47% 43% 9%
49	BX	101	 55% 43% .
50	BZ	94	 48% 31% 20%
51	A	185	 25% 49% 35% 14%

## 2 Entry composition [i](#)

There are 51 unique types of molecules in this entry. The entry contains 140480 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	AA	1535	32911	14689	6018	10669	1535	0	0

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	AB	224	1774	1129	311	326	8	0	0

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	AC	211	1648	1042	302	301	3	0	0

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AD	200	1610	1014	298	294	4	0	0

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AE	156	1133	711	212	209	1	0	0

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AF	97	797	507	132	156	2	0	0

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	AG	152	1207	748	236	217	6	0	0

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	AH	130	1009	641	178	188	2	0	0

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	AI	129	983	606	199	176	2	0	0

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	AJ	98	794	501	145	146	2	0	0

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	AK	118	857	530	165	160	2	0	0

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	AL	136	1054	656	215	180	3	0	0

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	AM	111	873	535	174	162	2	0	0

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	59	Total	C	N	O	S	0	0
			471	296	94	76	5		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	87	Total	C	N	O	S	0	0
			708	442	140	125	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	86	Total	C	N	O	S	0	0
			688	433	127	126	2		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	82	Total	C	N	O	S	0	0
			675	423	126	124	2		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AR	68	Total	C	N	O	S	0	0
			549	349	105	94	1		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	82	Total	C	N	O	S	0	0
			660	419	121	118	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	71	Total	C	N	O	S	0	0
			542	333	107	101	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
21	AU	56	Total	C	N	O	0	0
			440	269	95	76		

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	B0	61	Total	C	N	O	S	0	0
			477	299	91	86	1		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	B1	67	Total	C	N	O	0	0
			533	334	95	104		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B2	58	Total	C	N	O	S	0	0
			424	269	77	77	1		

- Molecule 25 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B3	79	Total	C	N	O	S	0	0
			642	408	110	122	2		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	B4	53	Total	C	N	O	0	0
			437	270	92	75		

- Molecule 27 is a protein called 50S ribosomal protein L33 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B5	47	Total	C	N	O	S	0	0
			365	225	72	64	4		

- Molecule 28 is a protein called 50S ribosomal protein L34.



Mol	Chain	Residues	Atoms					AltConf	Trace
28	B6	44	Total	C	N	O	S	0	0
			362	219	86	55	2		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	B7	64	Total	C	N	O	S	0	0
			530	327	120	80	3		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B8	36	Total	C	N	O	S	0	0
			292	182	62	44	4		

- Molecule 31 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BA	2897	Total	C	N	O	P	0	0
			62143	27749	11409	20088	2897		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BA	135	U	C	conflict	GB 124491690
BA	376	A	G	conflict	GB 124491690
BA	1239	A	G	conflict	GB 124491690
BA	1489	C	U	conflict	GB 124491690

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BB	115	Total	C	N	O	P	0	0
			2455	1097	439	804	115		

- Molecule 33 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BD	272	Total	C	N	O	S	0	0
			2041	1264	397	371	9		

- Molecule 34 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	BE	205	1522	957	282	279	4	0	0

- Molecule 35 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	BF	206	1563	980	284	299		0	0

- Molecule 36 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	BG	176	1367	867	238	256	6	0	0

- Molecule 37 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	BH	174	1303	811	237	251	4	0	0

- Molecule 38 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	BM	147	1127	714	203	205	5	0	0

- Molecule 39 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	BN	121	895	563	165	166	1	0	0

- Molecule 40 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	BO	146	1066	650	210	205	1	0	0

- Molecule 41 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BP	134	Total	C	N	O	S	0	0
			1061	675	206	174	6		

- Molecule 42 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BQ	125	Total	C	N	O	S	0	0
			990	613	188	186	3		

- Molecule 43 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BR	115	Total	C	N	O	S	0	0
			872	542	164	165	1		

- Molecule 44 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BS	114	Total	C	N	O	S	0	0
			923	578	186	158	1		

- Molecule 45 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BT	117	Total	C	N	O	S	0	0
			945	601	186	154	4		

- Molecule 46 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	BU	101	Total	C	N	O	0	0
			783	501	138	144		

- Molecule 47 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BV	112	Total	C	N	O	S	0	0
			853	536	160	156	1		

- Molecule 48 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	BW	88	689	441	116	130	2	0	0

- Molecule 49 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	BX	99	747	474	136	136	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	BZ	75	562	345	110	106	1	0	0

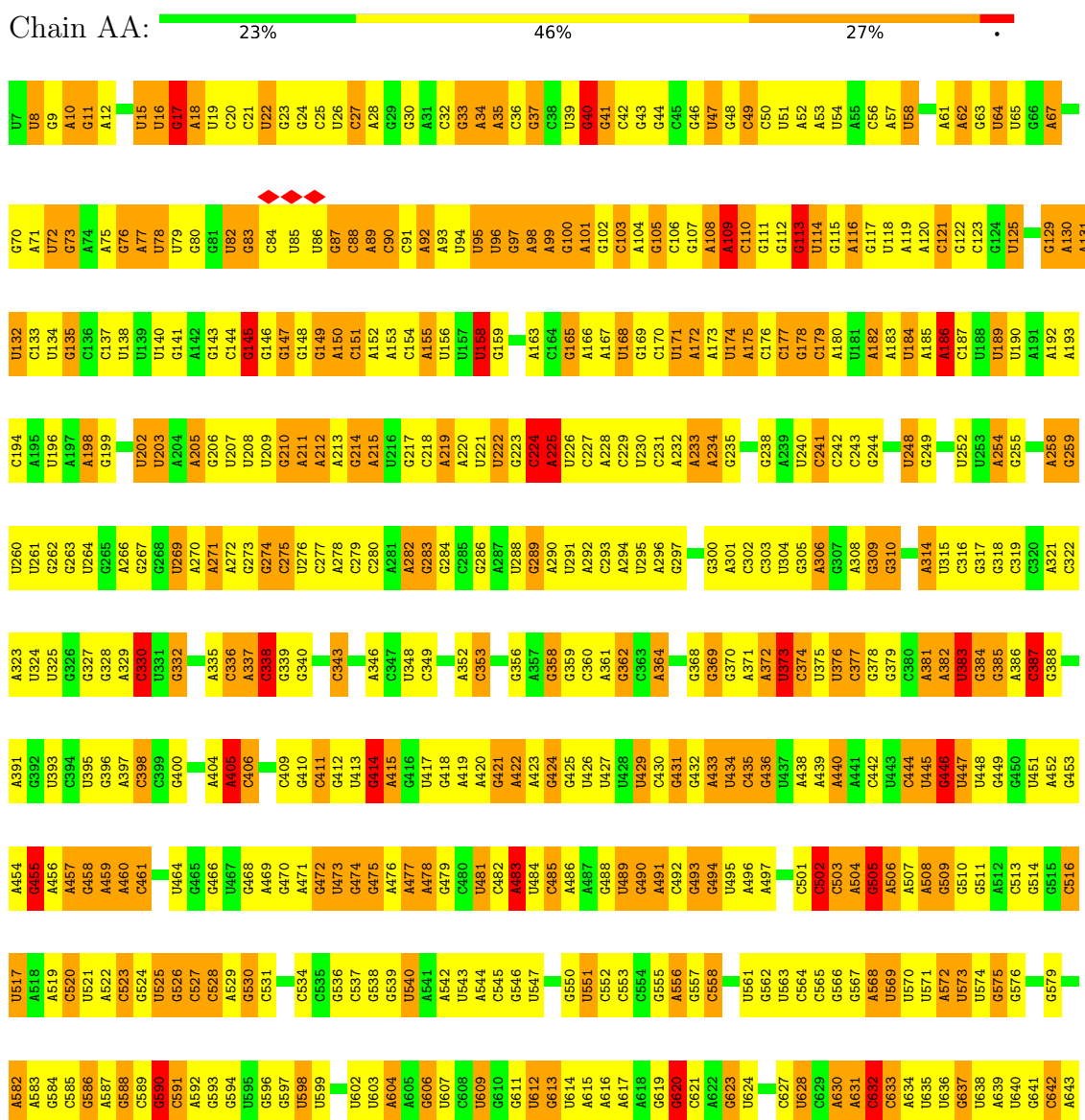
- Molecule 51 is a protein called Ribosome hibernation promotion factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	A	159	1128	698	209	218	3	0	0

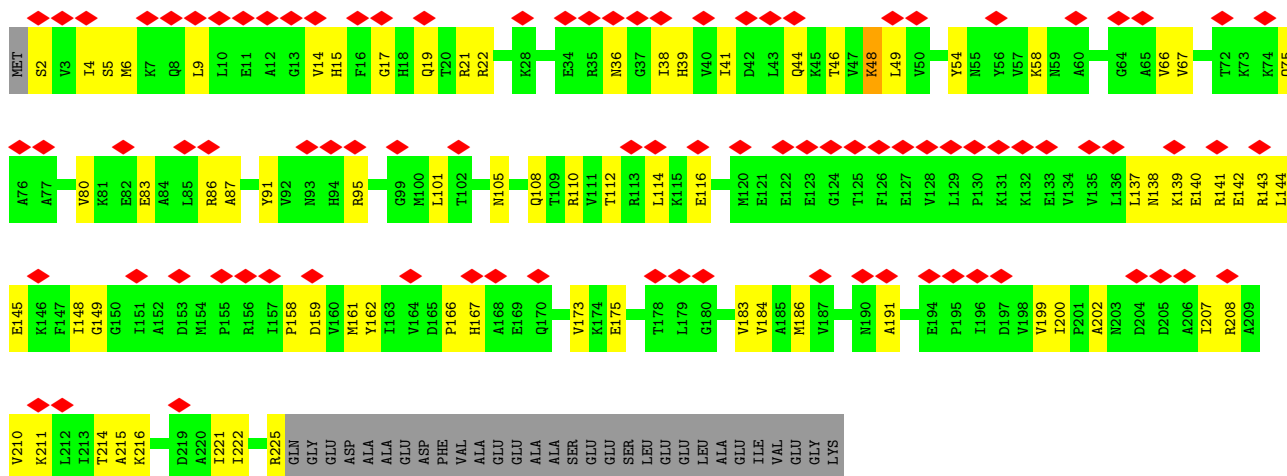
### 3 Residue-property plots [i](#)

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.

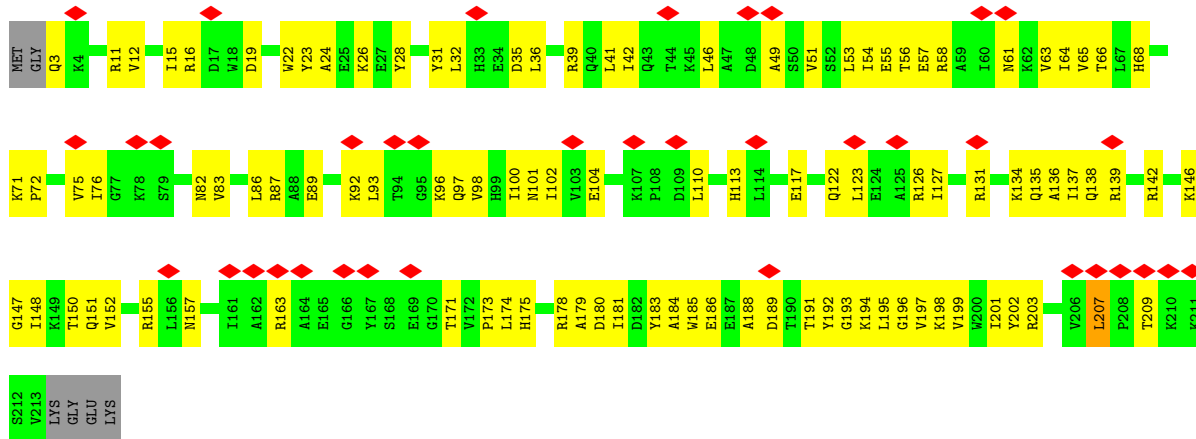
- Molecule 1: 16S ribosomal RNA



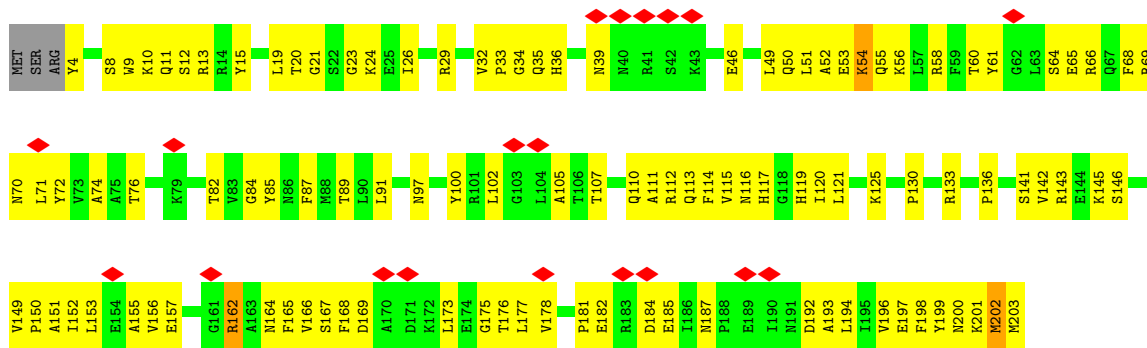
U644	C767	A776	G847	A916	G979	A1045	C1115	U1175	A1243	G1305	G1368	A1432	A1506	U665	C772	A788	G885	A916	G979	A1045	C1115	U1175	A1243	G1305	G1368	A1432	A1506
U645	G708	G777	C848	A917	C960	C1046	G1116	A1176	A1243	A1306	C1369	G1433	A1507	U666	C778	A789	G886	A917	G981	A1046	C1116	U1176	A1244	G1306	G1369	A1433	A1507
G646	G711	C778	U849	C918	G981	G1047	A1117	A1177	C1244	G1307	A1370	A1434	C1508	U667	G784	A790	G887	A918	G982	A1047	C1117	U1177	A1245	G1307	G1370	A1434	A1508
A648	U713	G784	U851	C920	A983	G1048	A1118	A1178	A1245	U1308	A1371	A1435	U1309	U668	U714	A791	G888	A919	G983	A1048	C1118	U1178	A1246	G1308	G1371	A1435	A1509
A650	A714	A785	A852	A921	G984	A1049	C1120	C1180	U1247	C1310	C1372	C1436	C1437	U669	A715	A792	G889	A920	G984	A1049	C1119	U1179	A1247	G1309	G1372	C1436	A1510
C851	U716	A786	A853	A922	A985	U1051	C1121	G1181	G1248	G1311	C1374	C1438	G1439	U670	A716	A793	G890	A921	G985	A1050	C1120	U1180	A1248	G1310	G1373	C1437	A1511
U652	A717	A787	U854	A923	C986	C1053	C1122	G1182	G1249	G1312	C1375	G1439	U1440	U671	A717	A794	G891	A922	G986	A1051	C1121	U1181	A1249	G1311	G1374	C1438	A1512
G653	U717	A788	U855	A924	C987	A1054	C1123	A1183	A1250	A1313	C1376	A1440	A1513	U672	A718	A795	G892	A923	G987	A1052	C1122	U1182	A1250	G1312	G1375	C1439	A1513
G654	U718	A789	U856	A925	C988	A1055	C1124	G1184	A1251	U1314	C1377	G1441	U1315	U673	A719	A796	G893	A924	G988	A1053	C1123	U1183	A1251	G1313	G1376	C1440	A1514
U655	U719	C791	U857	A926	U989	A1056	C1125	G1185	G1252	U1315	C1378	G1442	U1316	U674	A720	A797	G894	A925	G989	A1054	C1124	U1184	A1252	G1314	G1377	C1441	A1515
U656	A720	A792	C859	U928	U990	A1057	C1126	A1186	G1253	G1316	C1379	U1443	U1317	U675	A721	A798	G895	A926	G990	A1055	C1125	U1185	A1253	G1315	G1378	C1442	A1516
G657	G721	G794	C861	U929	C992	G1058	C1128	G1188	A1254	U1317	C1380	U1444	U1318	U676	A722	A799	G896	A927	G991	A1056	C1126	U1186	A1254	G1316	G1379	C1443	A1517
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A702	U770	U842	G911	A973	U1039	A1109	C1165	A1170	A1293	C1296	C1417	G1481	U1355	U713	A759	A836	G933	A964	G10								



• Molecule 3: 30S ribosomal protein S3

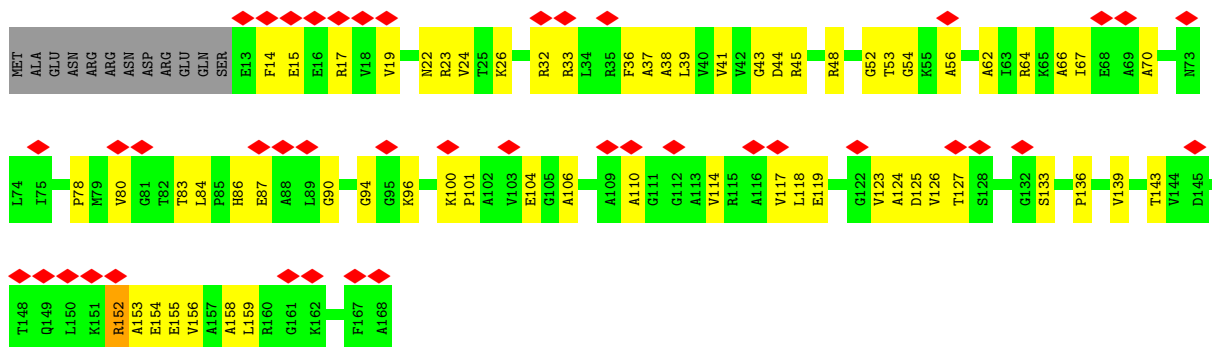


• Molecule 4: 30S ribosomal protein S4

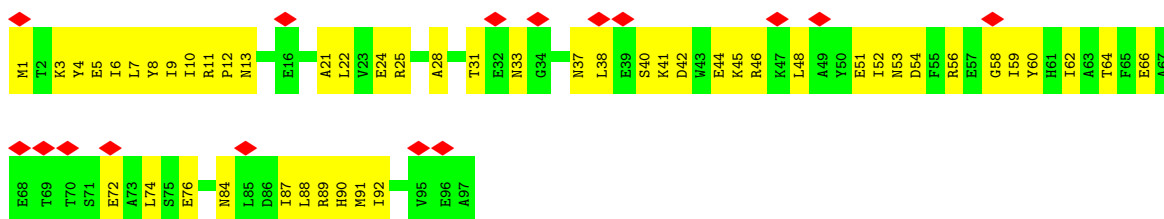


• Molecule 5: 30S ribosomal protein S5

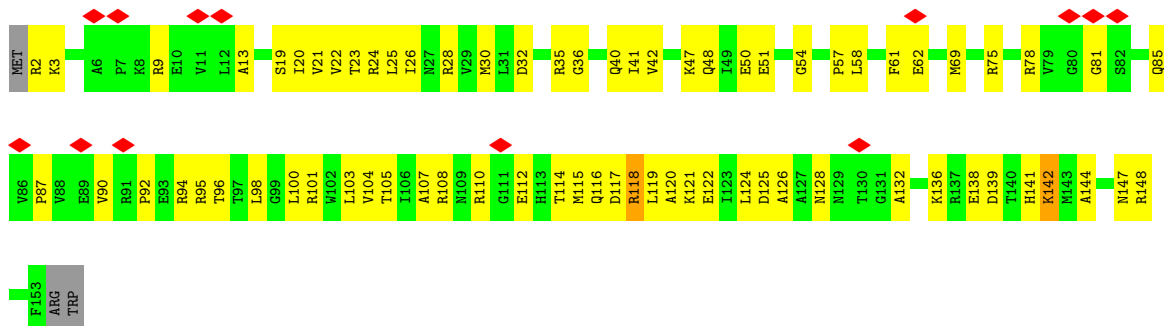




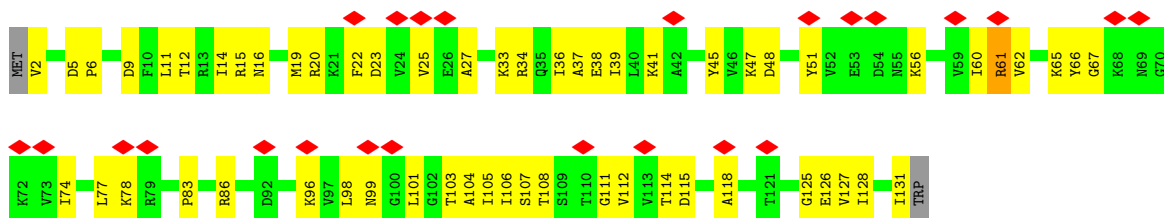
• Molecule 6: 30S ribosomal protein S6



• Molecule 7: 30S ribosomal protein S7

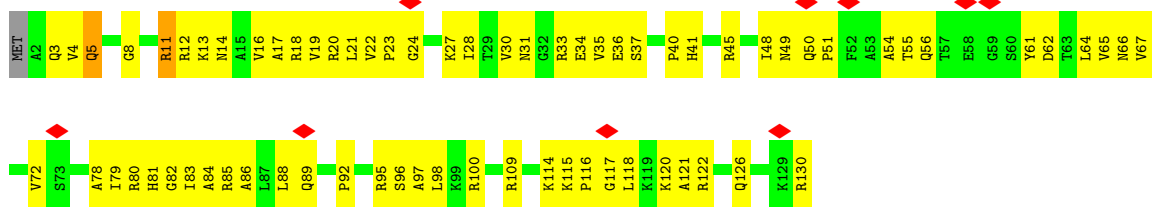


• Molecule 8: 30S ribosomal protein S8

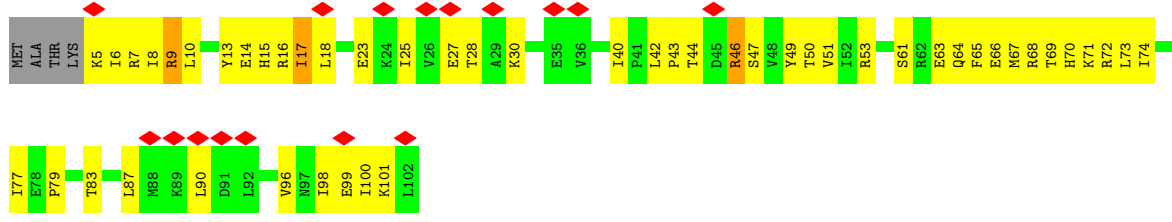


• Molecule 9: 30S ribosomal protein S9

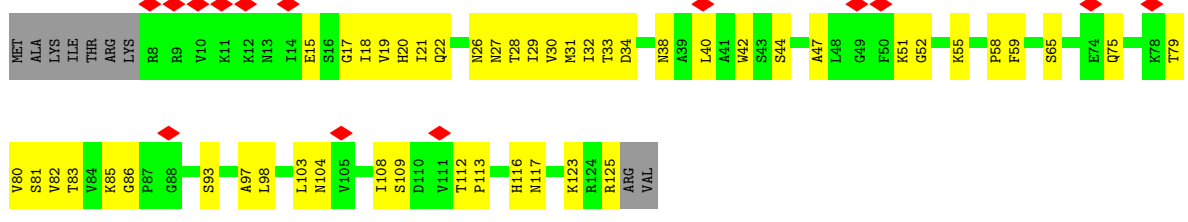




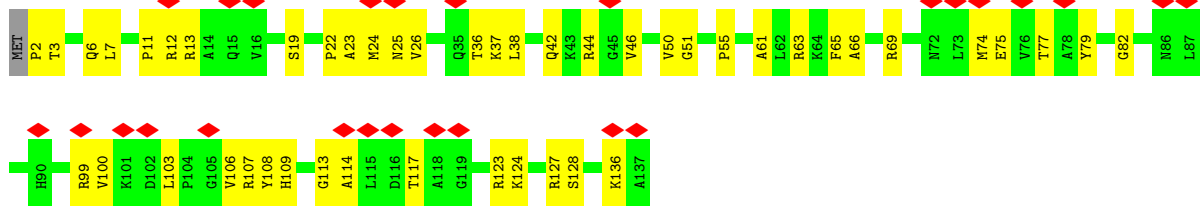
• Molecule 10: 30S ribosomal protein S10



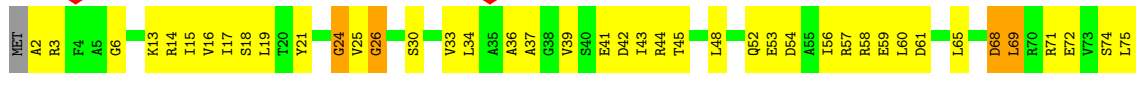
• Molecule 11: 30S ribosomal protein S11



• Molecule 12: 30S ribosomal protein S12



• Molecule 13: 30S ribosomal protein S13

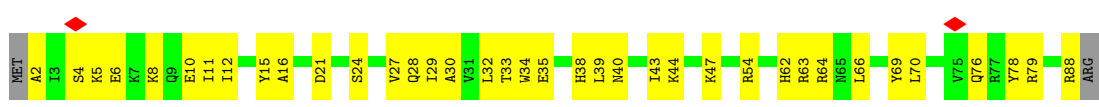




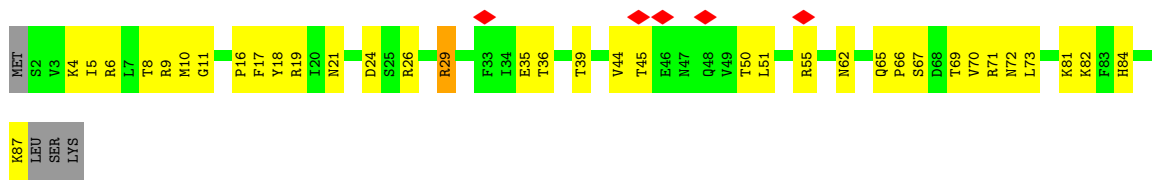
• Molecule 14: 30S ribosomal protein S14 type Z



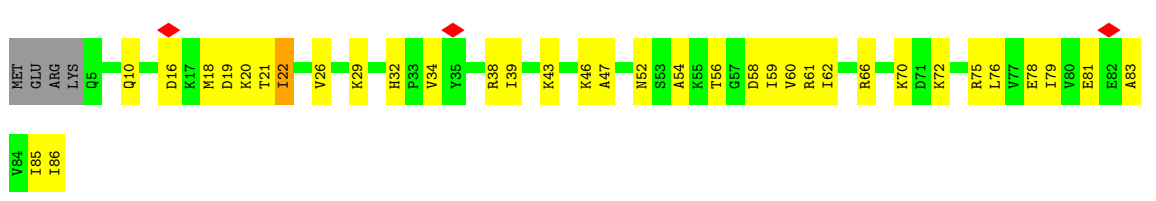
• Molecule 15: 30S ribosomal protein S15



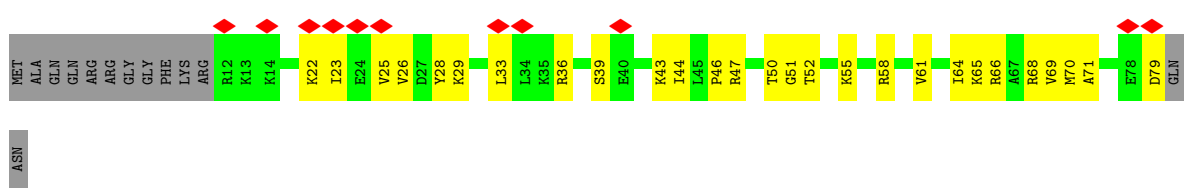
• Molecule 16: 30S ribosomal protein S16



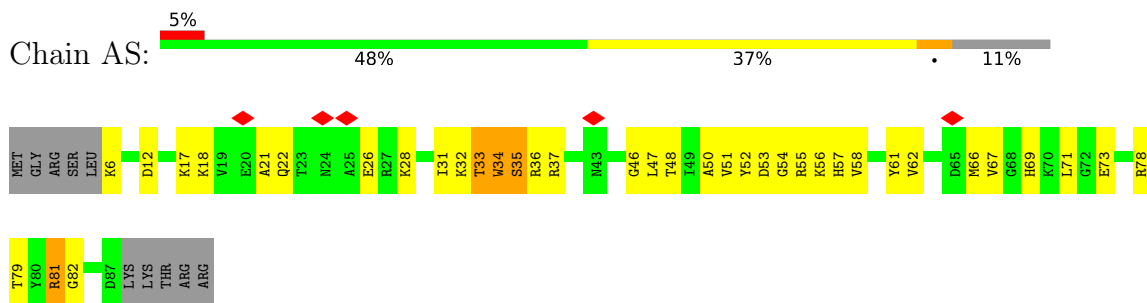
• Molecule 17: 30S ribosomal protein S17



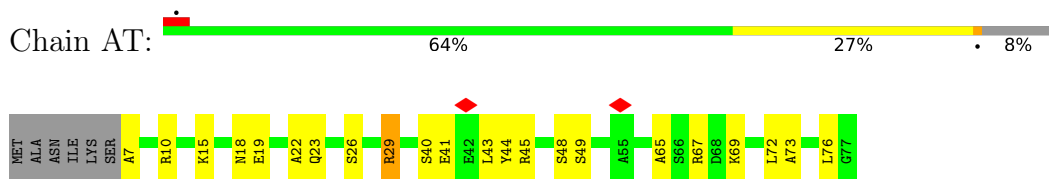
• Molecule 18: 30S ribosomal protein S18



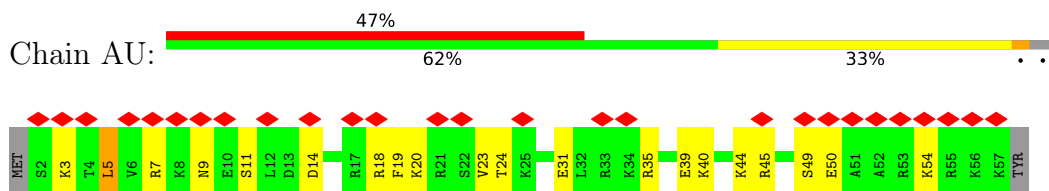
• Molecule 19: 30S ribosomal protein S19



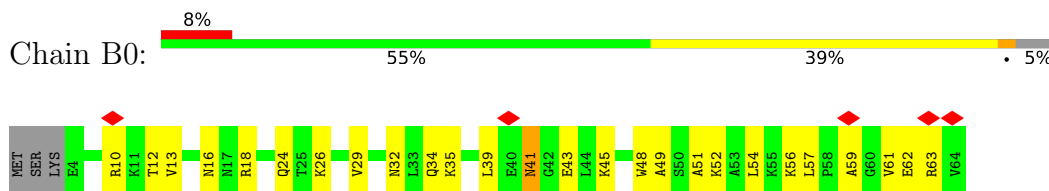
• Molecule 20: 30S ribosomal protein S20



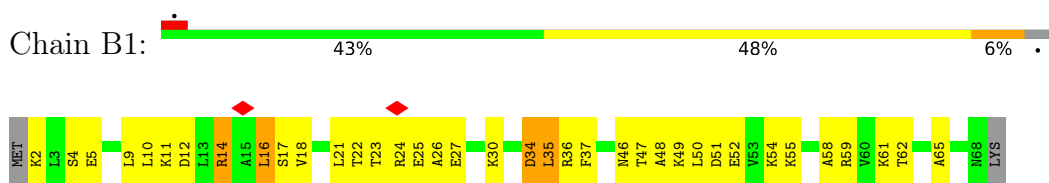
• Molecule 21: 30S ribosomal protein S21



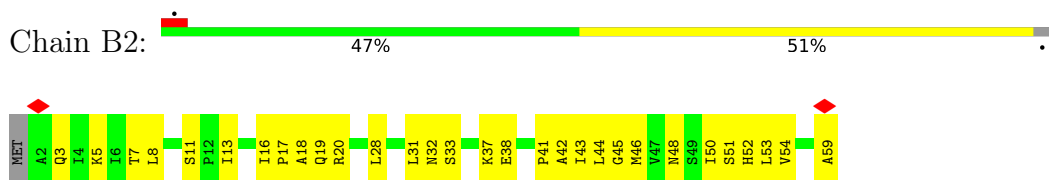
• Molecule 22: 50S ribosomal protein L28



• Molecule 23: 50S ribosomal protein L29

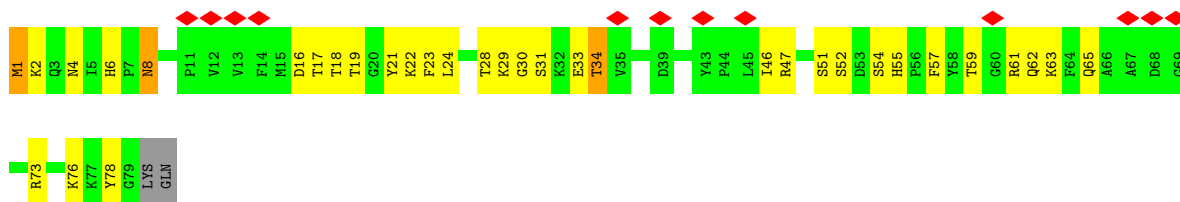


• Molecule 24: 50S ribosomal protein L30



• Molecule 25: 50S ribosomal protein L31 type B

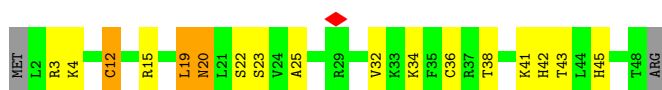




• Molecule 26: 50S ribosomal protein L32



• Molecule 27: 50S ribosomal protein L33 3



• Molecule 28: 50S ribosomal protein L34



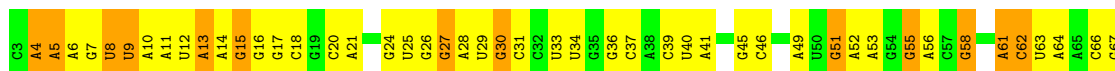
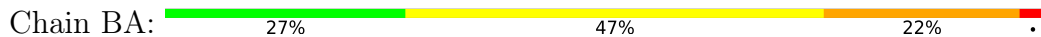
• Molecule 29: 50S ribosomal protein L35



• Molecule 30: 50S ribosomal protein L36

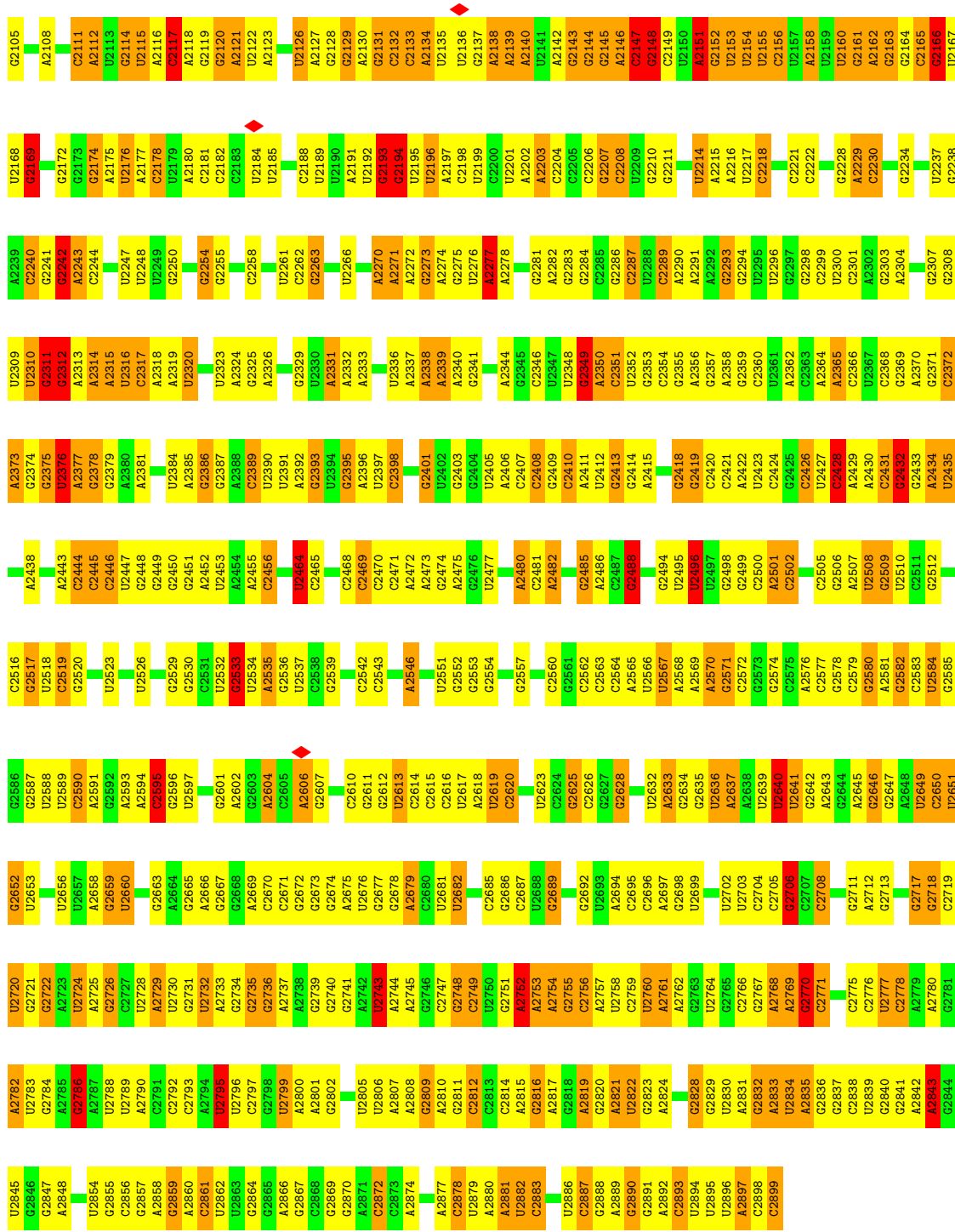


• Molecule 31: 23S ribosomal RNA

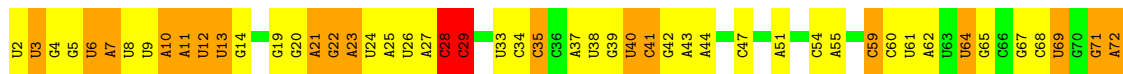


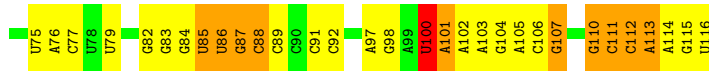
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G131	G132	U133	G134	U135	U136	A137	A138	U139	U140	G141	G142	G143	G144	U145	U146	A147	U148	U149	G153	A154	G155	A156	G157	A158	A159	U160	G161	A162	A163	A164	A165	G166	A167	A168	A169	A170	U173	A174	A175	A176	U177	U178	U179	A180	A181	C182	G183	C184	A185	G186	A187	A188	C189	U192	A195	A196	C197	A198																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
U199	C200	A203	G204	U205	U206	C207	C208	C209	C210	A212	G213	G214	A215	A216	G217	A218	G219	A220	A221	A222	G223	U224	A225	A226	A227	A228	G229	G230	G231	A232	U233	U234	U235	C236	G237	A240	G241	U242	G246	G247	C248	G249	A250	U253	G253	A254	A255	C256	A260	A261	G262	G263	A264	G265	C268																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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G410	G411	G412	G415	G416	A417	A418	A419	A420	A421	G422	G423	A424	A425	A426	A427	A428	G431	U432	U433	U434	G435	A436	A437	U438	U439	U440	U441	U442	G445	A446	A447	U448	U449	A450	U451	C452	U453	A458	A464	A465	U466	A467	A468	U469	G470	C471	U472	U473	U474	G475	U476	G477	C479																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
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G991	C992	A993	A994	A995	G996	A997	U998	A1067	U1002	A1003	C1006	G1007	A1008	C941	A1009	A1010	G1011	G1012	A1013	A1014	A1015	A1016	A1017	A1018	C1022	A1023	G1024	A1025	C1026	U1027	A1028	U1029	A1030	A1031	G1032	C1033	U1034	A1035	C1040	A1041	C1042	A1043	A1044	A1045	U1046	U1047	A1048	U1049	A1050	U1051	U1052	U1053	U1054	A1055	A1056	A1057	G1057																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
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G2036	C1966	G1901	C1832	C1787	A1705	U1564	U1503	G1376	G1314	G1253	C1188	G1122
A2037	C1967	U1902	C1835	C1788	A1706	A1565	G1504	G1377	A1315	U1294	G1189	A1123
U2038	C1968	A1903	U1836	C1789	A1707	A1566	A1505	A1378	A1316	U1295	A1190	A1124
C2040	C1969	A1904	G1837	A1770	U1708	G1567	G1506	C1379	U1317	A1256	A1191	U1125
A2041	C1970	G1908	G1838	A1771	U1709	G1568	U1507	C1380	C1318	G1257	G1192	G1126
C2042	C1971	G1909	C1839	G1772	A1710	U1569	G1508	U1381	U1319	G1258	C1193	C1127
G2043	A1973	G1910	C1840	A1773	G1711	G1570	U1510	A1382	U1320	A1259	U1194	G1128
U2044	A1974	G1911	G1841	A1774	G1712	G1571	G1511	A1383	A1321	G1260	U1195	U1129
U2045	A1975	G1912	G1842	A1775	C1713	A1573	G1512	G1384	G1322	U1261	U1196	U1130
C2046	C1976	A1916	G1844	U1776	G1714	A1574	G1513	C1385	C1324	G1262	G1197	A1132
C2047	C1977	G1917	G1845	U1777	C1715	A1575	G1514	C1386	G1325	U1263	G1198	A1133
C2048	C1978	A1918	U1846	G1778	G1716	C1576	G1515	A1387	A1326	U1264	A1199	A1134
C2049	C1979	U1919	G1847	U1779	U1717	G1577	G1516	G1388	G1327	G1265	U1200	G1135
C2050	A1985	A1920	G1848	U1780	A1718	U1578	G1517	G1389	C1327	U1266	U1201	C1136
C2051	C1986	U1921	A1849	U1781	A1719	G1579	G1518	G1452	A1325	U1267	G1202	A1137
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C2053	U1987	A1923	A1851	U1783	U1721	A1583	G1520	G1454	U1329	G1269	U1204	A1138
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A2055	G1989	G1925	G1853	A1785	G1723	U1585	A1522	C1457	G1332	U1271	U1206	U1140
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C2057	C1994	U1927	G1855	A1787	G1725	C1589	U1524	A1459	A1334	A1273	U1208	G1142
A2058	U1995	U1928	A1860	C1790	U1726	A1590	G1525	A1460	C1334	U1274	U1209	G1145
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C1998	C1998	A1831	G1863	A1793	A1730	A1593	U1528	A1463	U1340	A1277	U1212	U1148
U1999	A1999	G1932	A1864	U1794	U1731	A1594	U1529	G1464	G1339	U1278	G1216	G1149
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A2001	G1996	G1934	U1866	A1796	A1733	A1598	C1531	U1467	A1342	G1280	U1218	A1151
C2002	A2002	A1935	A1867	C1797	G1733	A1599	G1532	A1478	C1343	A1281	A1219	C1152
C2003	A1936	A1936	A1868	A1798	U1737	A1600	C1533	G1479	C1344	G1282	G1220	C1153
C2004	C1937	A1937	G1869	U1799	U1738	A1601	U1534	U1480	A1345	A1283	G1221	U1154
A2005	C1938	U1938	A1870	A1799	U1739	G1603	U1535	U1472	G1346	A1284	U1222	G1155
C2006	C2006	U1939	C1871	U1800	U1739	G1604	U1536	G1475	G1347	U1285	G1226	C1156
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A2008	C2007	A1940	U1873	C1802	U1741	G1607	A1538	C1477	A1349	C1287	U1228	C1158
C2010	C2010	A1941	A1874	U1803	G1742	U1608	C1539	A1478	A1351	G1288	U1229	C1159
U2011	U2011	U1943	G1875	A1804	U1743	A1609	A1540	G1479	A1352	G1289	U1230	G1160
C2012	C2012	U1944	C1876	A1805	A1744	G1610	U1541	U1480	G1353	G1290	U1231	A1161
G2013	C1945	C1945	U1877	A1806	A1745	C1611	U1542	U1481	C1354	A1292	U1232	A1162
G2014	C1946	C1946	C1878	C1807	A1746	G1612	A1543	A1482	C1355	U1293	A1233	A1163
U2085	A2017	U1948	G1879	C1808	G1748	A1613	A1544	A1483	C1356	G1294	A1234	A1164
U2089	A2018	U1949	A1883	G1814	G1749	A1614	G1545	U1484	G1357	A1295	C1235	U1165
U2090	U2021	C1951	U1884	G1815	C1750	A1615	G1546	G1485	U1358	G1296	C1236	G1166
C2091	U2022	G1952	A1885	G1816	A1751	A1616	U1547	A1486	G1359	U1297	U1237	U1167
A2092	U2023	G1953	U1886	U1818	G1752	G1617	G1548	A1487	C1360	A1298	C1238	A1168
U2093	A2024	G1954	G1887	G1819	C1753	U1618	U1549	U1488	G1361	G1299	A1239	C1169
A2094	G2025	U1955	A1888	U1820	C1754	A1620	A1551	C1489	C1362	G1300	A1240	C1170
U2095	U2026	A1956	A1889	A1821	G1755	U1621	U1552	U1491	C1363	G1301	U1241	G1171
U2096	A2027	A1957	U1890	U1822	C1756	A1622	G1553	G1492	C1364	C1302	G1242	G1172
C2097	C2028	G1958	U1891	U1823	U1758	U1623	G1554	C1493	G1367	A1303	A1243	G1173
A2098	C2029	U1959	G1892	G1824	U1759	C1624	G1555	U1494	U1368	A1304	A1244	G1174
U2100	U2030	A1894	A1894	G1825	G1760	U1625	A1556	C1495	G1369	G1305	G1245	C1175
U2101	G2031	C1961	A1895	G1826	A1761	A1626	U1557	U1496	U1370	A1306	G1246	U1176
U2102	U2032	C1962	C1897	U1827	U1762	G1629	A1558	A1497	C1371	U1307	U1247	A1177
C2103	C2033	A1963	C1898	G1828	U1763	G1630	U1559	U1498	G1372	A1308	A1248	A1178
A2104	U2103	A1964	C1899	U1829	A1764	U1631	U1560	G1499	U1373	U1311	U1249	U1185
U2104	A2035	C1965	A1900	G1830	G1765	A1632	A1561	A1500	C1374	G1312	A1250	A1186
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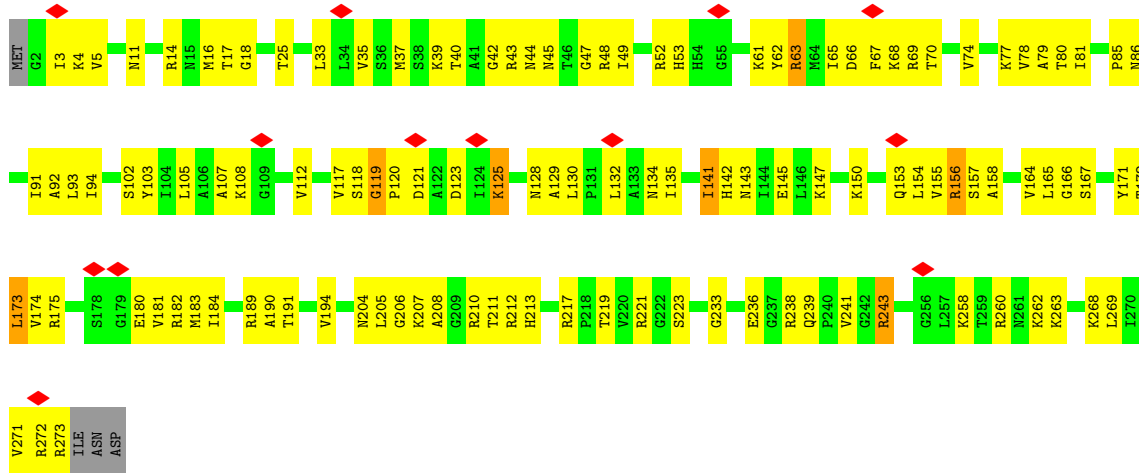


• Molecule 32: 5S ribosomal RNA

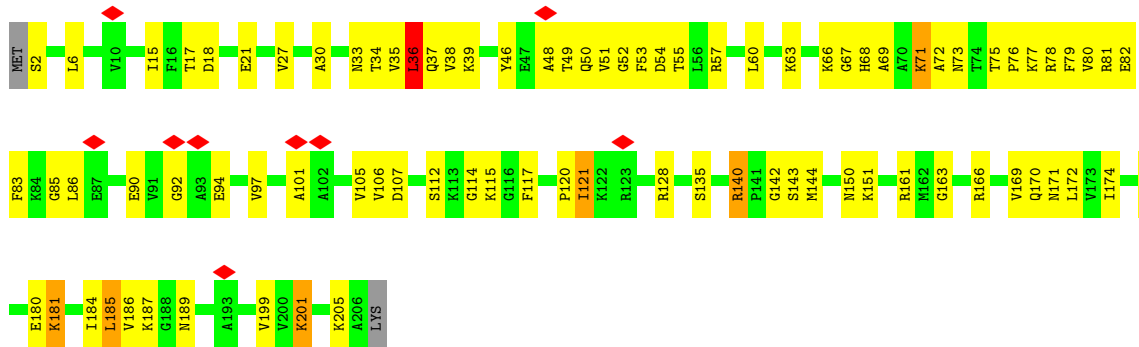




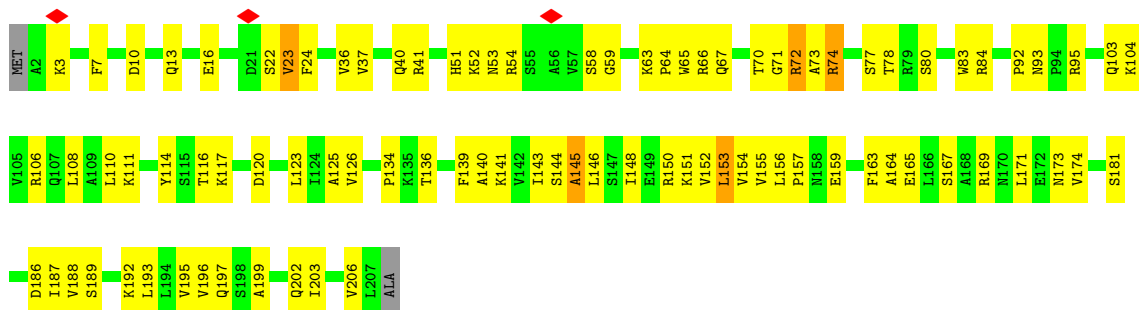
• Molecule 33: 50S ribosomal protein L2



• Molecule 34: 50S ribosomal protein L3

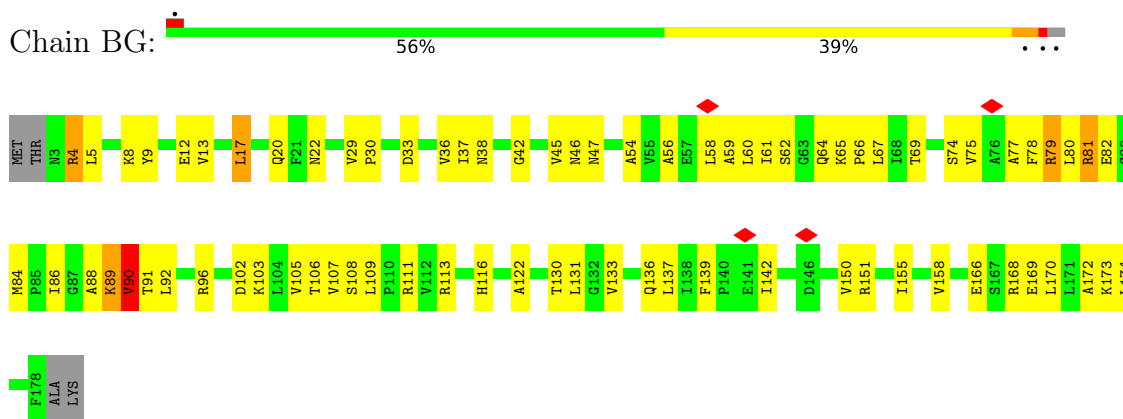


• Molecule 35: 50S ribosomal protein L4

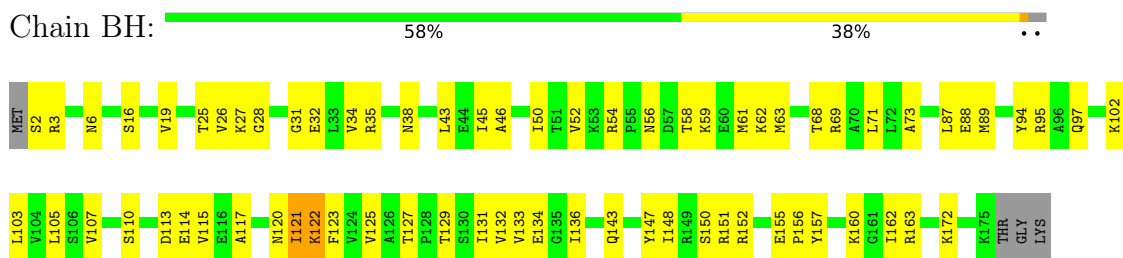




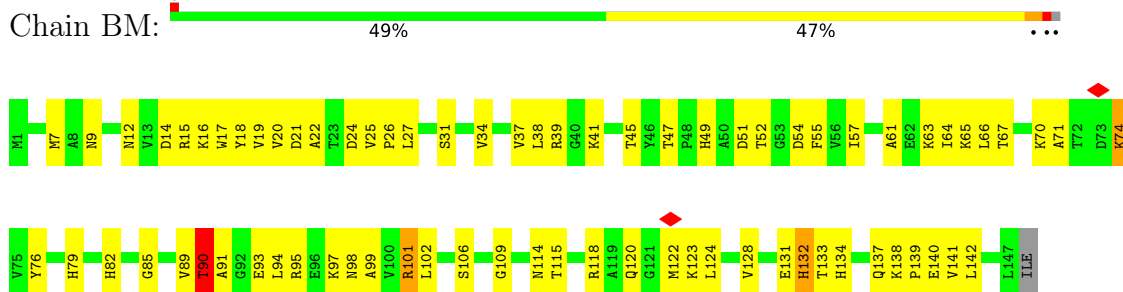
• Molecule 36: 50S ribosomal protein L5



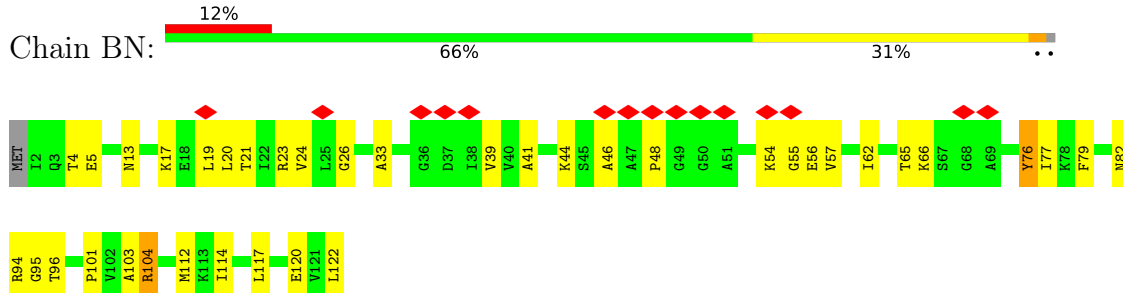
• Molecule 37: 50S ribosomal protein L6



• Molecule 38: 50S ribosomal protein L13

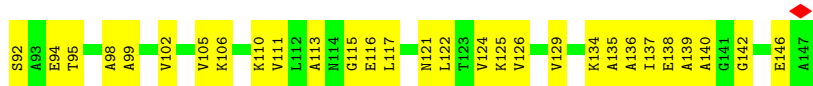
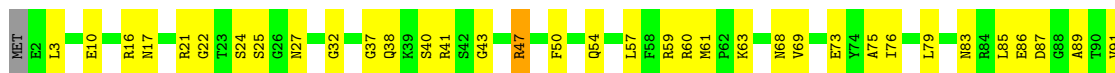


• Molecule 39: 50S ribosomal protein L14



• Molecule 40: 50S ribosomal protein L15

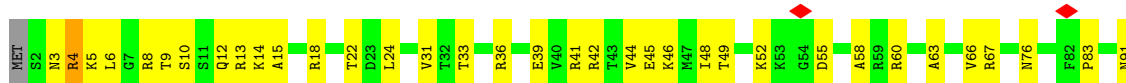




• Molecule 41: 50S ribosomal protein L16



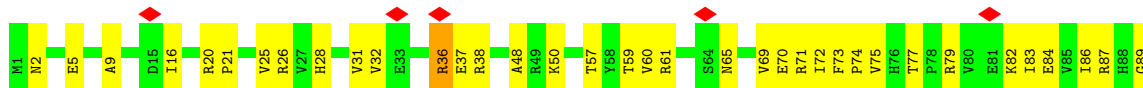
• Molecule 42: 50S ribosomal protein L17



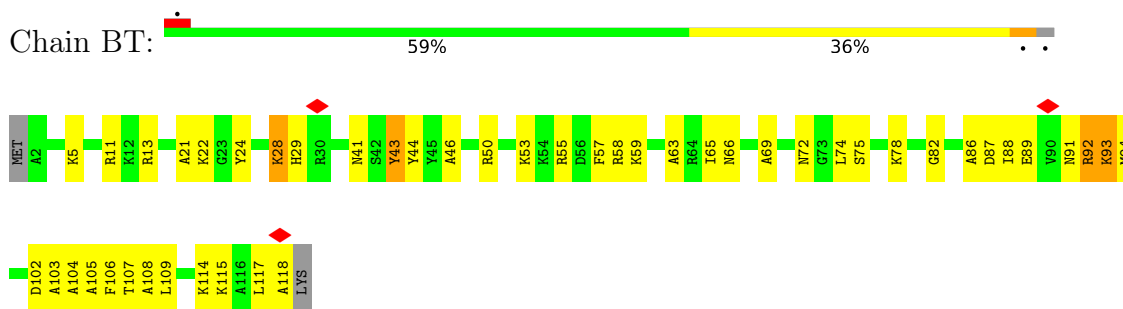
• Molecule 43: 50S ribosomal protein L18



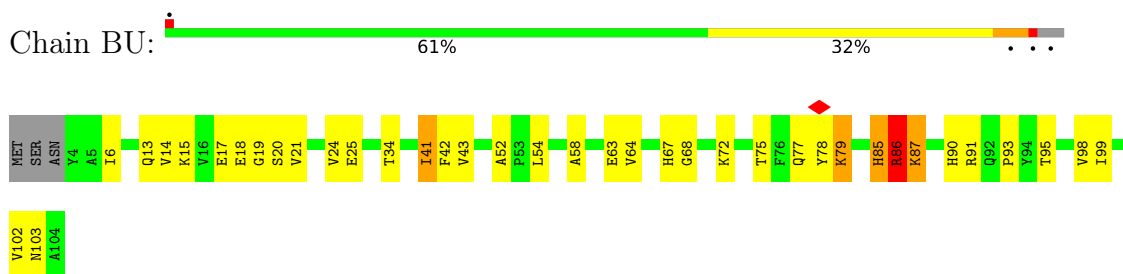
• Molecule 44: 50S ribosomal protein L19



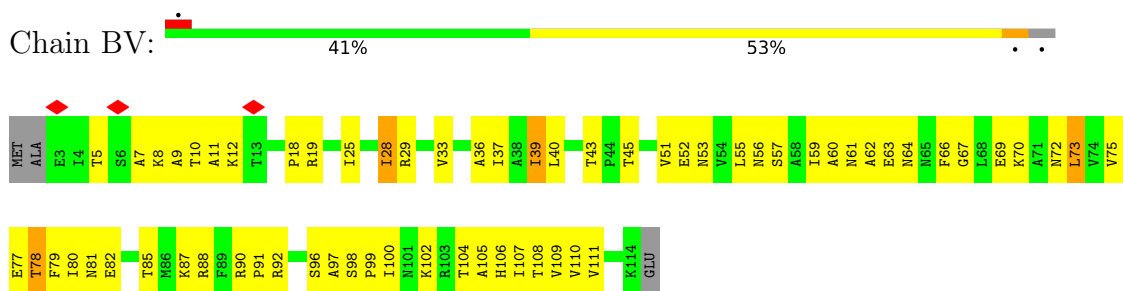
• Molecule 45: 50S ribosomal protein L20



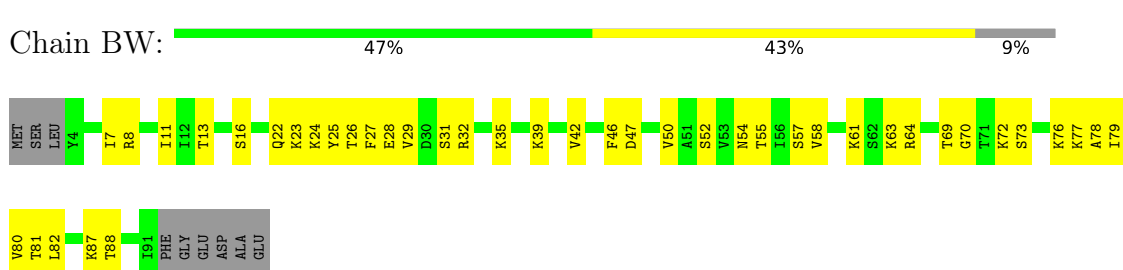
• Molecule 46: 50S ribosomal protein L21



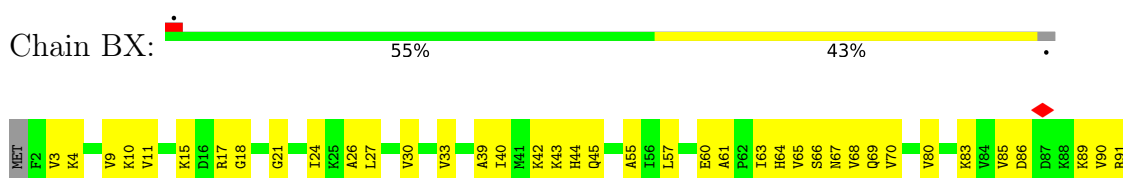
• Molecule 47: 50S ribosomal protein L22

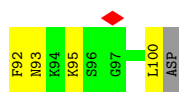


• Molecule 48: 50S ribosomal protein L23



• Molecule 49: 50S ribosomal protein L24

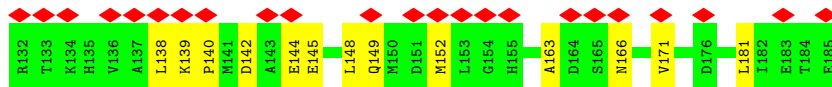
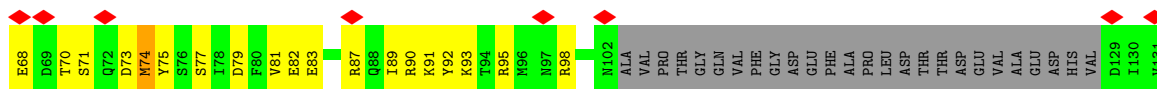
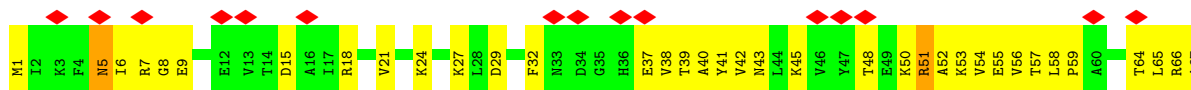




- Molecule 50: 50S ribosomal protein L27



- Molecule 51: Ribosome hibernation promotion factor



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	43530	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 ( $e^-/\text{\AA}^2$ )	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.161	Depositor
Minimum map value	-0.064	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	663.0, 663.0, 663.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.105, 1.105, 1.105	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	AA	0.68	0/36854	1.35	448/57482 (0.8%)
2	AB	0.32	0/1805	0.65	0/2442
3	AC	0.32	0/1674	0.62	0/2259
4	AD	0.34	0/1639	0.62	0/2205
5	AE	0.34	0/1143	0.63	0/1540
6	AF	0.40	0/809	0.77	2/1089 (0.2%)
7	AG	0.31	0/1224	0.61	0/1649
8	AH	0.35	0/1020	0.58	0/1374
9	AI	0.30	0/995	0.71	0/1334
10	AJ	0.30	0/805	0.69	2/1084 (0.2%)
11	AK	0.33	0/870	0.63	0/1175
12	AL	0.35	0/1070	0.72	0/1433
13	AM	0.38	0/880	0.80	2/1176 (0.2%)
14	AN	0.32	0/479	0.56	0/637
15	AO	0.31	0/718	0.62	0/958
16	AP	0.33	0/699	0.56	0/938
17	AQ	0.33	0/684	0.66	0/915
18	AR	0.36	0/554	0.75	0/740
19	AS	0.36	0/676	0.68	0/911
20	AT	0.32	0/545	0.59	0/723
21	AU	0.31	0/443	0.61	1/583 (0.2%)
22	B0	0.39	0/483	0.75	0/649
23	B1	0.40	0/534	0.96	2/713 (0.3%)
24	B2	0.36	0/427	0.72	0/575
25	B3	0.39	0/659	0.86	0/888
26	B4	0.44	0/447	0.66	0/599
27	B5	0.38	0/368	0.72	0/489
28	B6	0.38	0/366	0.71	0/481
29	B7	0.37	0/538	0.75	0/704
30	B8	0.37	0/297	0.64	0/396
31	BA	0.86	7/69612 (0.0%)	1.37	856/108576 (0.8%)
32	BB	0.75	1/2746 (0.0%)	1.29	22/4278 (0.5%)
33	BD	0.41	0/2071	0.80	2/2789 (0.1%)
34	BE	0.44	0/1544	0.79	2/2079 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	BF	0.39	0/1586	0.72	1/2145 (0.0%)
36	BG	0.40	0/1385	0.84	2/1866 (0.1%)
37	BH	0.37	0/1317	0.66	0/1776
38	BM	0.40	0/1147	0.74	0/1549
39	BN	0.41	0/904	0.75	1/1215 (0.1%)
40	BO	0.39	0/1072	0.72	0/1430
41	BP	0.43	0/1084	0.64	0/1450
42	BQ	0.39	0/998	0.79	0/1338
43	BR	0.42	0/881	0.83	3/1184 (0.3%)
44	BS	0.38	0/935	0.70	1/1255 (0.1%)
45	BT	0.47	0/958	0.70	1/1273 (0.1%)
46	BU	0.46	0/796	0.82	2/1070 (0.2%)
47	BV	0.39	0/862	0.76	1/1164 (0.1%)
48	BW	0.37	0/697	0.62	0/935
49	BX	0.40	0/755	0.75	0/1013
50	BZ	0.37	0/570	0.75	1/760 (0.1%)
51	A	0.36	0/1138	0.64	0/1538
All	All	0.71	8/152763 (0.0%)	1.23	1352/228824 (0.6%)

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
2	AB	0	1
3	AC	0	1
4	AD	0	2
6	AF	0	1
9	AI	0	1
10	AJ	0	1
11	AK	0	2
13	AM	0	4
14	AN	0	2
19	AS	0	3
22	B0	0	1
23	B1	0	3
24	B2	0	2
25	B3	0	3
26	B4	0	1
27	B5	0	1
33	BD	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
34	BE	0	4
35	BF	0	2
36	BG	0	3
37	BH	0	1
38	BM	0	4
39	BN	0	2
43	BR	0	2
44	BS	0	1
45	BT	0	1
46	BU	0	4
47	BV	0	2
48	BW	0	1
49	BX	0	1
All	All	0	61

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	BA	2480	A	N9-C4	-5.85	1.34	1.37
31	BA	1719	A	N9-C4	-5.55	1.34	1.37
31	BA	1089	A	N9-C4	-5.36	1.34	1.37
32	BB	21	A	N9-C4	-5.19	1.34	1.37
31	BA	542	A	N9-C4	5.19	1.41	1.37

The worst 5 of 1352 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	BA	1503	U	N3-C2-O2	-17.92	109.66	122.20
1	AA	1310	C	C2-N1-C1'	13.33	133.47	118.80
31	BA	2117	C	N1-C2-O2	13.13	126.78	118.90
31	BA	2117	C	C2-N1-C1'	12.12	132.14	118.80
31	BA	568	U	C5-C6-N1	12.06	128.73	122.70

There are no chirality outliers.

5 of 61 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	4	ILE	Peptide
3	AC	207	LEU	Peptide
4	AD	187	ASN	Peptide
4	AD	201	LYS	Peptide

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Mol	Chain	Res	Type	Group
6	AF	51	GLU	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	AA	32911	0	16551	930	0
2	AB	1774	0	1820	83	0
3	AC	1648	0	1704	81	0
4	AD	1610	0	1632	100	0
5	AE	1133	0	1205	48	0
6	AF	797	0	795	35	0
7	AG	1207	0	1235	64	0
8	AH	1009	0	1068	46	0
9	AI	983	0	1025	59	0
10	AJ	794	0	841	48	0
11	AK	857	0	886	45	0
12	AL	1054	0	1141	40	0
13	AM	873	0	912	70	0
14	AN	471	0	499	25	0
15	AO	708	0	737	32	0
16	AP	688	0	716	34	0
17	AQ	675	0	704	28	0
18	AR	549	0	599	26	0
19	AS	660	0	658	35	0
20	AT	542	0	577	26	0
21	AU	440	0	448	14	0
22	B0	477	0	503	18	0
23	B1	533	0	572	25	0
24	B2	424	0	471	19	0
25	B3	642	0	620	31	0
26	B4	437	0	444	17	0
27	B5	365	0	389	15	0
28	B6	362	0	400	31	0
29	B7	530	0	573	28	0
30	B8	292	0	320	14	0
31	BA	62143	0	31234	1411	0
32	BB	2455	0	1236	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	BD	2041	0	2142	102	0
34	BE	1522	0	1608	69	0
35	BF	1563	0	1606	77	0
36	BG	1367	0	1417	60	0
37	BH	1303	0	1343	54	0
38	BM	1127	0	1176	50	0
39	BN	895	0	951	29	0
40	BO	1066	0	1109	58	0
41	BP	1061	0	1111	48	0
42	BQ	990	0	1037	47	0
43	BR	872	0	911	52	0
44	BS	923	0	983	41	0
45	BT	945	0	1012	40	0
46	BU	783	0	818	32	0
47	BV	853	0	915	57	0
48	BW	689	0	738	32	0
49	BX	747	0	808	32	0
50	BZ	562	0	567	29	0
51	A	1128	0	992	93	0
All	All	140480	0	93759	3990	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 19.

The worst 5 of 3990 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1439:G:N2	1:AA:1475:A:N7	1.81	1.28
31:BA:1487:A:C2	31:BA:2706:G:N1	2.06	1.23
2:AB:207:ILE:HD11	51:A:144:GLU:O	1.48	1.11
2:AB:207:ILE:CD1	51:A:145:GLU:HA	1.84	1.07
31:BA:2312:G:N1	31:BA:2315:A:C2	2.22	1.06

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	222/255 (87%)	194 (87%)	28 (13%)	0	100	100
3	AC	209/217 (96%)	177 (85%)	32 (15%)	0	100	100
4	AD	198/203 (98%)	163 (82%)	34 (17%)	1 (0%)	29	69
5	AE	154/168 (92%)	138 (90%)	16 (10%)	0	100	100
6	AF	95/97 (98%)	73 (77%)	22 (23%)	0	100	100
7	AG	150/155 (97%)	136 (91%)	14 (9%)	0	100	100
8	AH	128/132 (97%)	110 (86%)	18 (14%)	0	100	100
9	AI	127/130 (98%)	104 (82%)	23 (18%)	0	100	100
10	AJ	96/102 (94%)	82 (85%)	14 (15%)	0	100	100
11	AK	116/127 (91%)	102 (88%)	14 (12%)	0	100	100
12	AL	134/137 (98%)	110 (82%)	24 (18%)	0	100	100
13	AM	109/121 (90%)	82 (75%)	27 (25%)	0	100	100
14	AN	57/61 (93%)	44 (77%)	13 (23%)	0	100	100
15	AO	85/89 (96%)	72 (85%)	13 (15%)	0	100	100
16	AP	84/90 (93%)	74 (88%)	10 (12%)	0	100	100
17	AQ	80/86 (93%)	65 (81%)	15 (19%)	0	100	100
18	AR	66/81 (82%)	53 (80%)	13 (20%)	0	100	100
19	AS	80/92 (87%)	61 (76%)	19 (24%)	0	100	100
20	AT	69/77 (90%)	57 (83%)	12 (17%)	0	100	100
21	AU	54/58 (93%)	46 (85%)	8 (15%)	0	100	100
22	B0	59/64 (92%)	45 (76%)	14 (24%)	0	100	100
23	B1	65/69 (94%)	51 (78%)	14 (22%)	0	100	100
24	B2	56/59 (95%)	45 (80%)	11 (20%)	0	100	100
25	B3	77/81 (95%)	52 (68%)	25 (32%)	0	100	100
26	B4	51/57 (90%)	43 (84%)	8 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	B5	45/49 (92%)	32 (71%)	12 (27%)	1 (2%)	6	35
28	B6	42/44 (96%)	35 (83%)	7 (17%)	0	100	100
29	B7	62/66 (94%)	51 (82%)	11 (18%)	0	100	100
30	B8	34/38 (90%)	32 (94%)	2 (6%)	0	100	100
33	BD	270/276 (98%)	193 (72%)	77 (28%)	0	100	100
34	BE	203/207 (98%)	164 (81%)	39 (19%)	0	100	100
35	BF	204/208 (98%)	157 (77%)	46 (22%)	1 (0%)	29	69
36	BG	174/180 (97%)	137 (79%)	36 (21%)	1 (1%)	25	65
37	BH	172/178 (97%)	144 (84%)	28 (16%)	0	100	100
38	BM	145/148 (98%)	119 (82%)	25 (17%)	1 (1%)	22	62
39	BN	119/122 (98%)	99 (83%)	20 (17%)	0	100	100
40	BO	144/147 (98%)	117 (81%)	27 (19%)	0	100	100
41	BP	132/137 (96%)	120 (91%)	12 (9%)	0	100	100
42	BQ	123/126 (98%)	109 (89%)	14 (11%)	0	100	100
43	BR	113/115 (98%)	90 (80%)	22 (20%)	1 (1%)	17	56
44	BS	112/114 (98%)	95 (85%)	17 (15%)	0	100	100
45	BT	115/119 (97%)	103 (90%)	12 (10%)	0	100	100
46	BU	99/104 (95%)	67 (68%)	32 (32%)	0	100	100
47	BV	110/115 (96%)	99 (90%)	11 (10%)	0	100	100
48	BW	86/97 (89%)	78 (91%)	8 (9%)	0	100	100
49	BX	97/101 (96%)	73 (75%)	24 (25%)	0	100	100
50	BZ	73/94 (78%)	64 (88%)	9 (12%)	0	100	100
51	A	155/185 (84%)	130 (84%)	25 (16%)	0	100	100
All	All	5450/5778 (94%)	4487 (82%)	957 (18%)	6 (0%)	54	85

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	BM	132	HIS
4	AD	202	MET
27	B5	12	CYS
35	BF	23	VAL
36	BG	82	GLU

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	190/213 (89%)	187 (98%)	3 (2%)	62	79
3	AC	168/172 (98%)	166 (99%)	2 (1%)	71	84
4	AD	172/175 (98%)	170 (99%)	2 (1%)	71	84
5	AE	115/126 (91%)	113 (98%)	2 (2%)	60	78
6	AF	84/84 (100%)	81 (96%)	3 (4%)	35	59
7	AG	125/128 (98%)	122 (98%)	3 (2%)	49	69
8	AH	111/113 (98%)	109 (98%)	2 (2%)	59	77
9	AI	99/100 (99%)	98 (99%)	1 (1%)	76	86
10	AJ	89/92 (97%)	88 (99%)	1 (1%)	73	84
11	AK	89/97 (92%)	88 (99%)	1 (1%)	73	84
12	AL	113/114 (99%)	113 (100%)	0	100	100
13	AM	93/100 (93%)	92 (99%)	1 (1%)	73	84
14	AN	50/53 (94%)	49 (98%)	1 (2%)	55	73
15	AO	74/76 (97%)	74 (100%)	0	100	100
16	AP	77/81 (95%)	75 (97%)	2 (3%)	46	67
17	AQ	76/80 (95%)	75 (99%)	1 (1%)	69	82
18	AR	59/69 (86%)	59 (100%)	0	100	100
19	AS	70/79 (89%)	69 (99%)	1 (1%)	67	80
20	AT	53/58 (91%)	52 (98%)	1 (2%)	57	75
21	AU	42/53 (79%)	41 (98%)	1 (2%)	49	69
22	B0	52/56 (93%)	52 (100%)	0	100	100
23	B1	58/60 (97%)	57 (98%)	1 (2%)	60	78
24	B2	48/49 (98%)	48 (100%)	0	100	100
25	B3	69/71 (97%)	68 (99%)	1 (1%)	67	80
26	B4	46/50 (92%)	46 (100%)	0	100	100
27	B5	41/43 (95%)	39 (95%)	2 (5%)	25	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	B6	37/37 (100%)	36 (97%)	1 (3%)	44	65
29	B7	54/56 (96%)	48 (89%)	6 (11%)	6	24
30	B8	34/35 (97%)	34 (100%)	0	100	100
33	BD	219/223 (98%)	214 (98%)	5 (2%)	50	70
34	BE	162/164 (99%)	156 (96%)	6 (4%)	34	58
35	BF	170/171 (99%)	168 (99%)	2 (1%)	71	84
36	BG	150/154 (97%)	147 (98%)	3 (2%)	55	73
37	BH	140/147 (95%)	139 (99%)	1 (1%)	84	90
38	BM	122/123 (99%)	118 (97%)	4 (3%)	38	61
39	BN	93/95 (98%)	90 (97%)	3 (3%)	39	61
40	BO	107/109 (98%)	106 (99%)	1 (1%)	78	88
41	BP	106/107 (99%)	102 (96%)	4 (4%)	33	57
42	BQ	104/105 (99%)	102 (98%)	2 (2%)	57	75
43	BR	90/90 (100%)	89 (99%)	1 (1%)	73	84
44	BS	98/98 (100%)	95 (97%)	3 (3%)	40	62
45	BT	90/92 (98%)	88 (98%)	2 (2%)	52	71
46	BU	85/88 (97%)	84 (99%)	1 (1%)	71	84
47	BV	92/94 (98%)	90 (98%)	2 (2%)	52	71
48	BW	77/84 (92%)	77 (100%)	0	100	100
49	BX	83/85 (98%)	82 (99%)	1 (1%)	71	84
50	BZ	59/73 (81%)	59 (100%)	0	100	100
51	A	93/163 (57%)	89 (96%)	4 (4%)	29	54
All	All	4528/4785 (95%)	4444 (98%)	84 (2%)	59	75

5 of 84 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	BM	90	THR
44	BS	36	ARG
38	BM	138	LYS
41	BP	10	ARG
45	BT	93	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 81 such sidechains are listed below:

Mol	Chain	Res	Type
40	BO	27	ASN
46	BU	67	HIS
40	BO	78	ASN
41	BP	123	HIS
49	BX	64	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1534/1535 (99%)	663 (43%)	8 (0%)
31	BA	2896/2897 (99%)	1094 (37%)	20 (0%)
32	BB	114/115 (99%)	45 (39%)	0
All	All	4544/4547 (99%)	1802 (39%)	28 (0%)

5 of 1802 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	8	U
1	AA	9	G
1	AA	10	A
1	AA	11	G
1	AA	15	U

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
31	BA	1281	A
31	BA	2760	U
31	BA	1317	U
31	BA	2065	G
31	BA	1313	A

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.



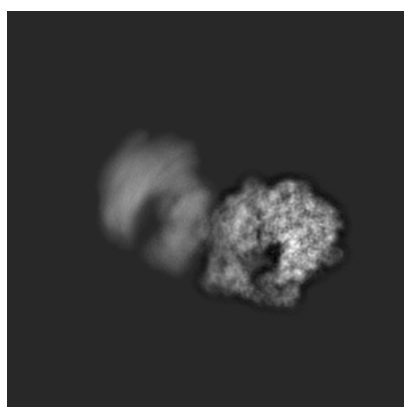
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3581. These allow visual inspection of the internal detail of the map and identification of artifacts.

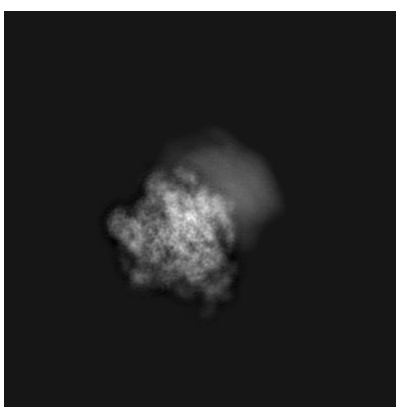
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

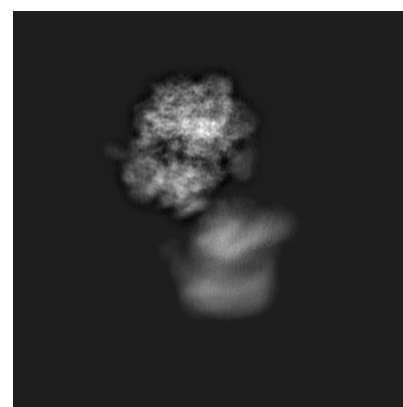
#### 6.1.1 Primary map



X



Y

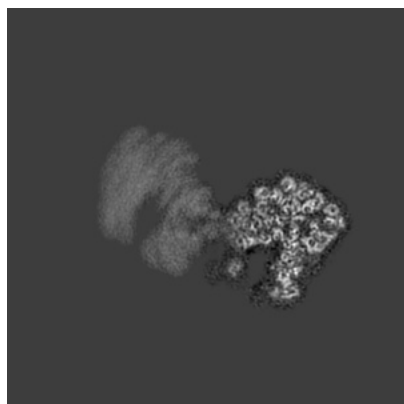


Z

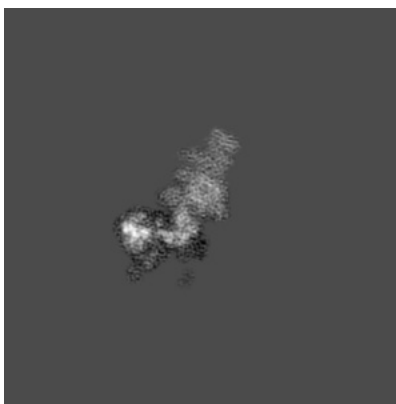
The images above show the map projected in three orthogonal directions.

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

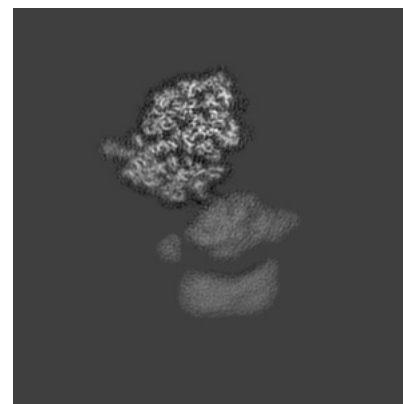
#### 6.2.1 Primary map



X Index: 300



Y Index: 300

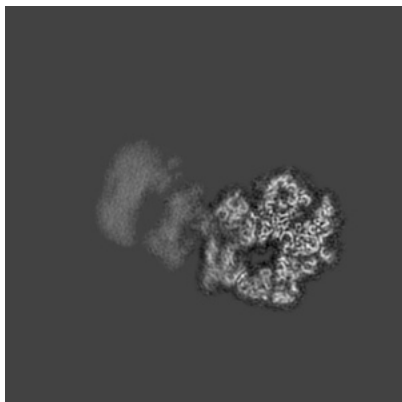


Z Index: 300

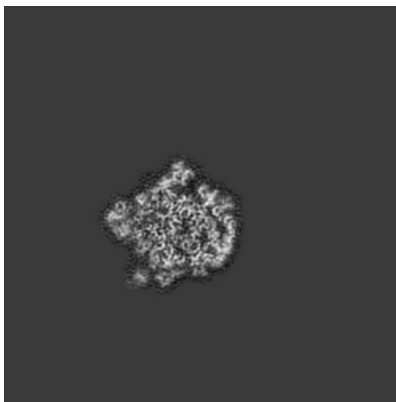
The images above show central slices of the map in three orthogonal directions.

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

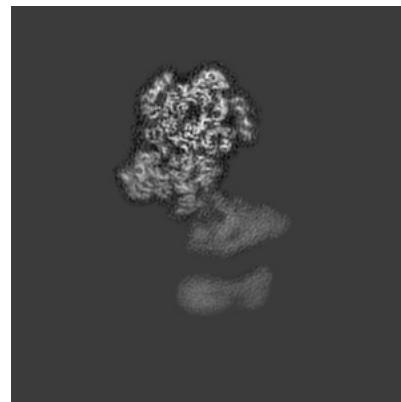
### 6.3.1 Primary map



X Index: 278



Y Index: 428

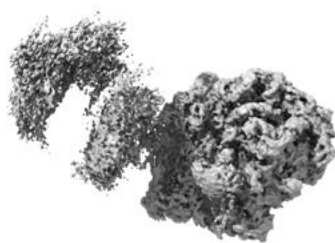


Z Index: 277

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

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

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

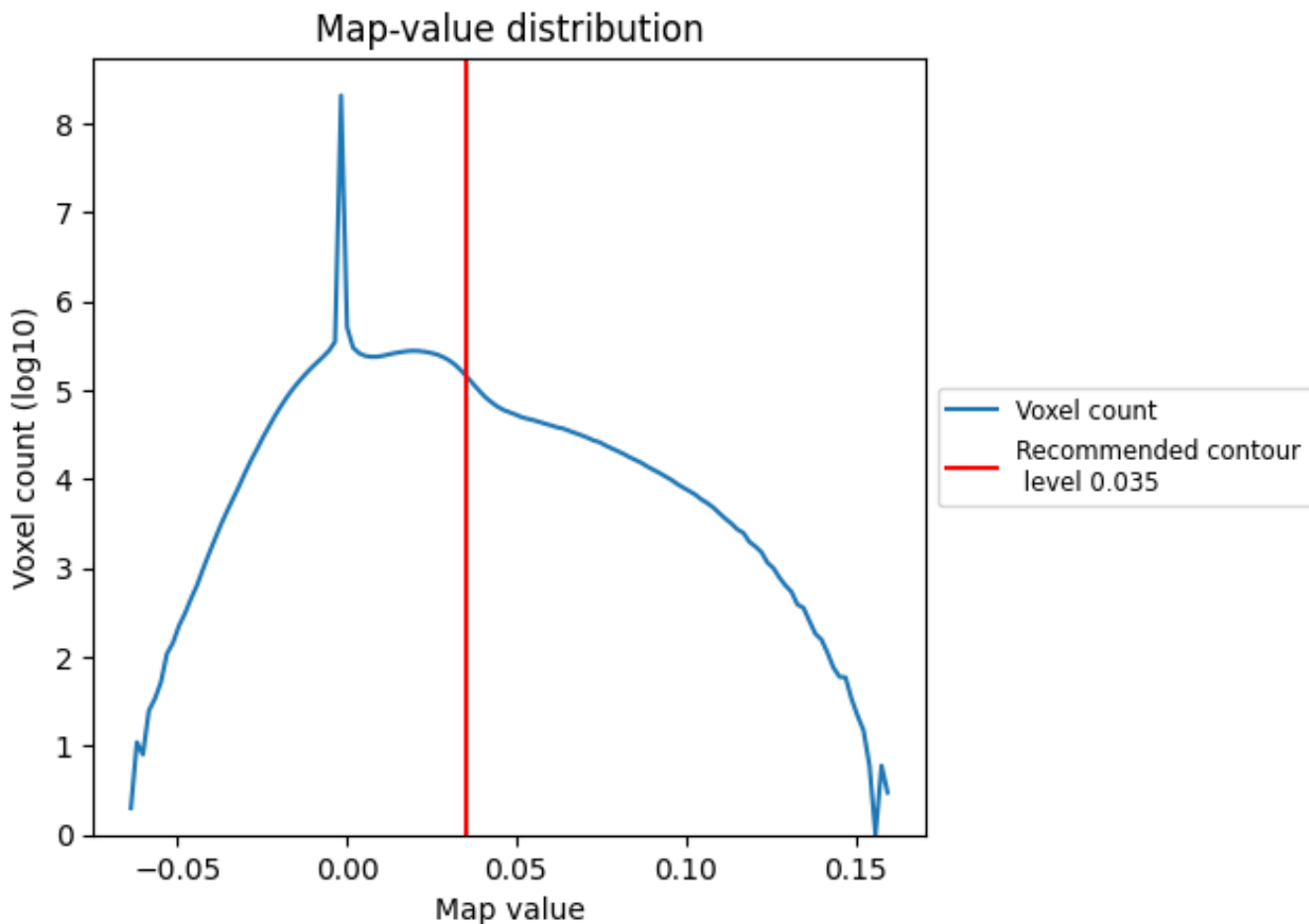
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

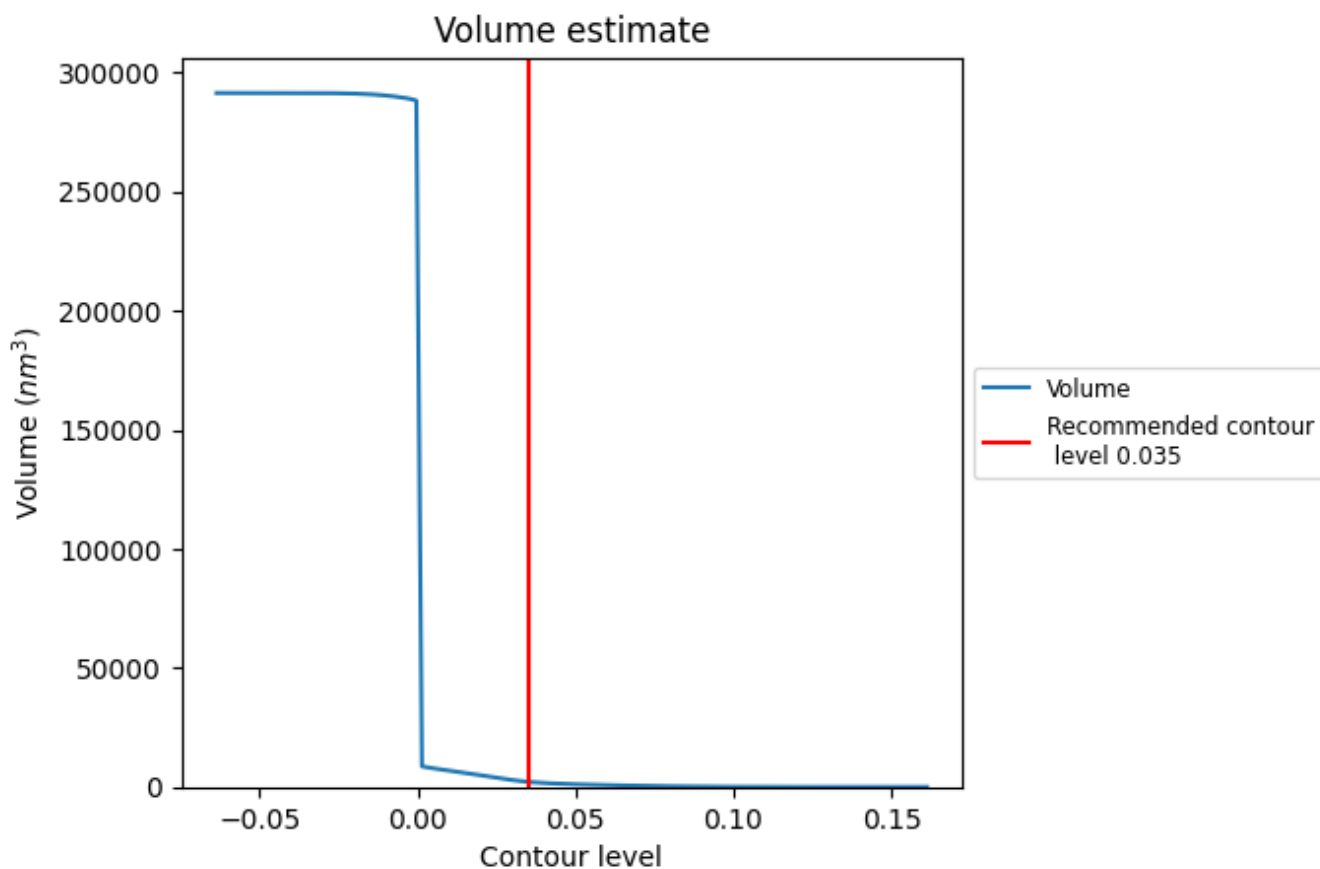
This section contains the results of statistical analysis of the map.

### 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.

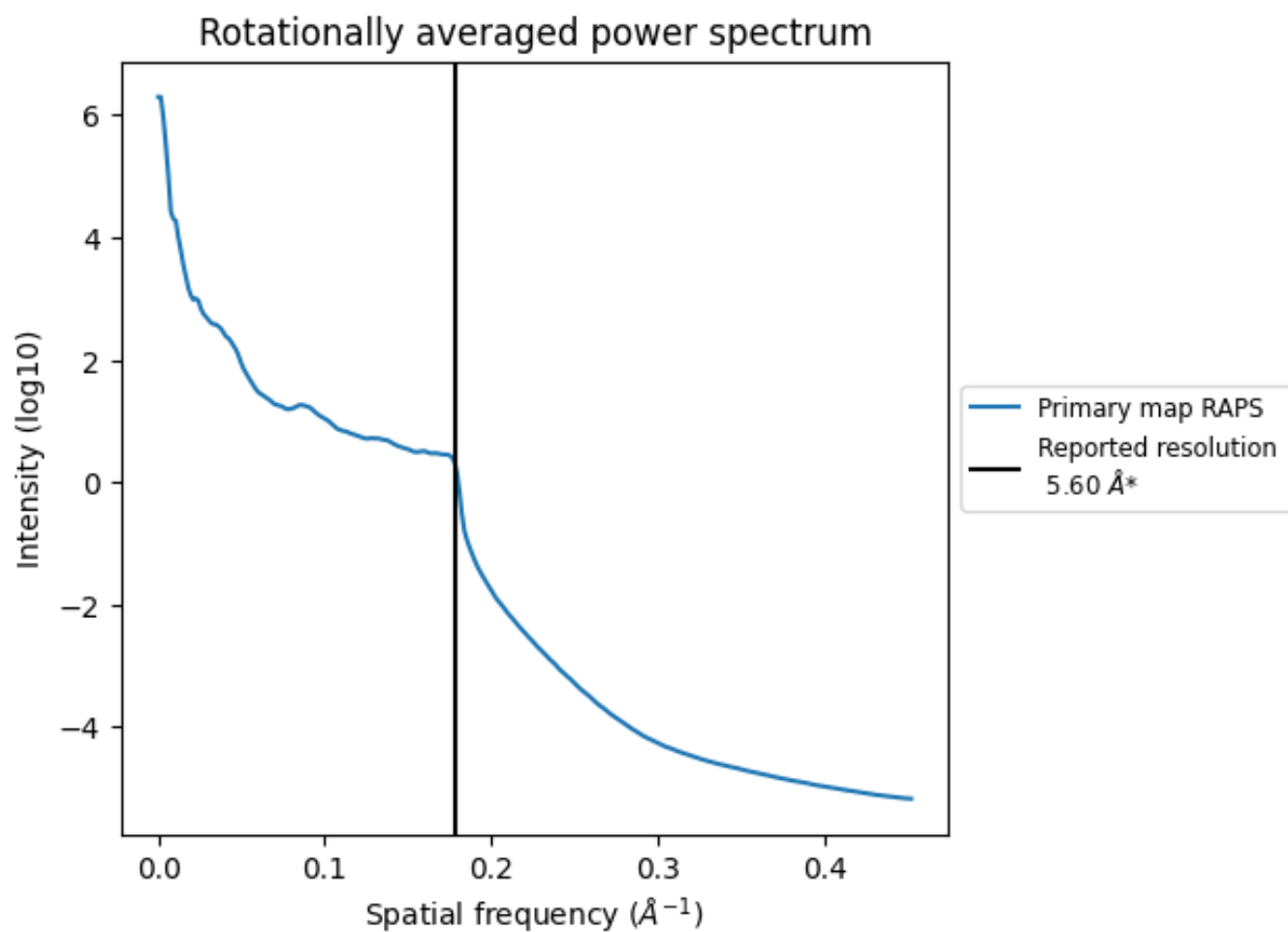
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2160 nm<sup>3</sup>; this corresponds to an approximate mass of 1951 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 [i](#)

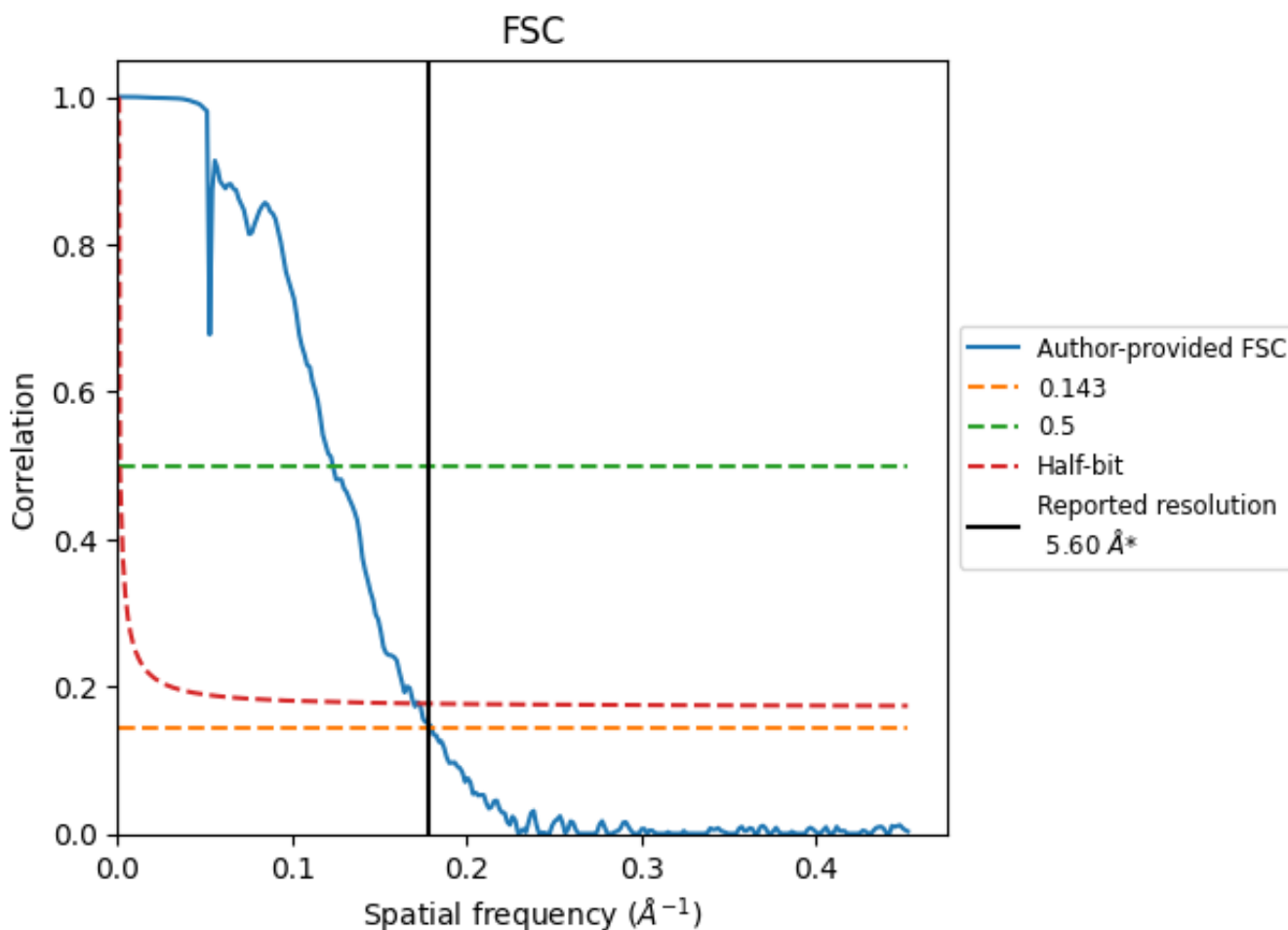


\*Reported resolution corresponds to spatial frequency of  $0.179 \text{\AA}^{-1}$

## 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 0.179 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	5.60	-	-
Author-provided FSC curve	5.56	8.11	5.89
Unmasked-calculated*	-	-	-

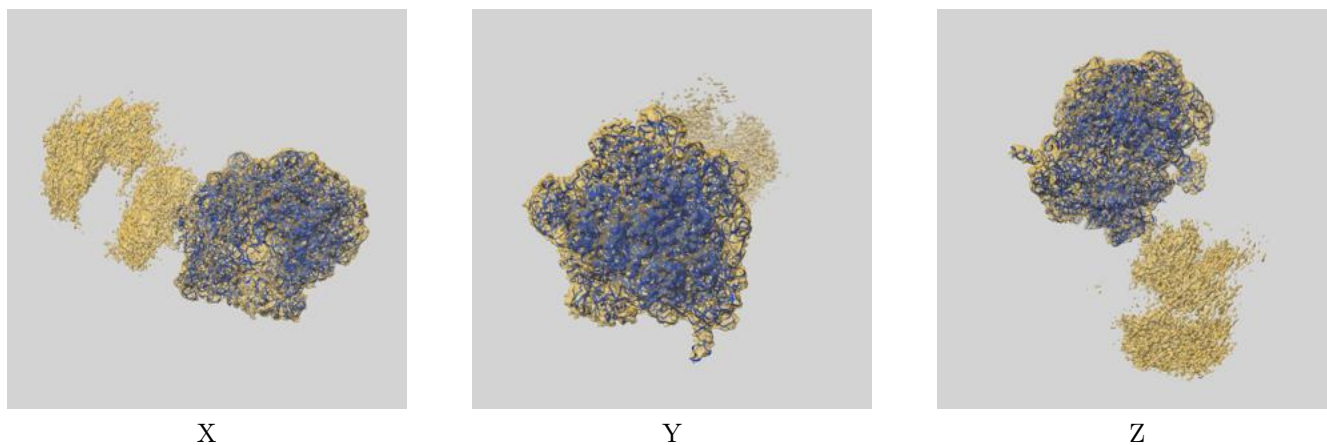
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



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

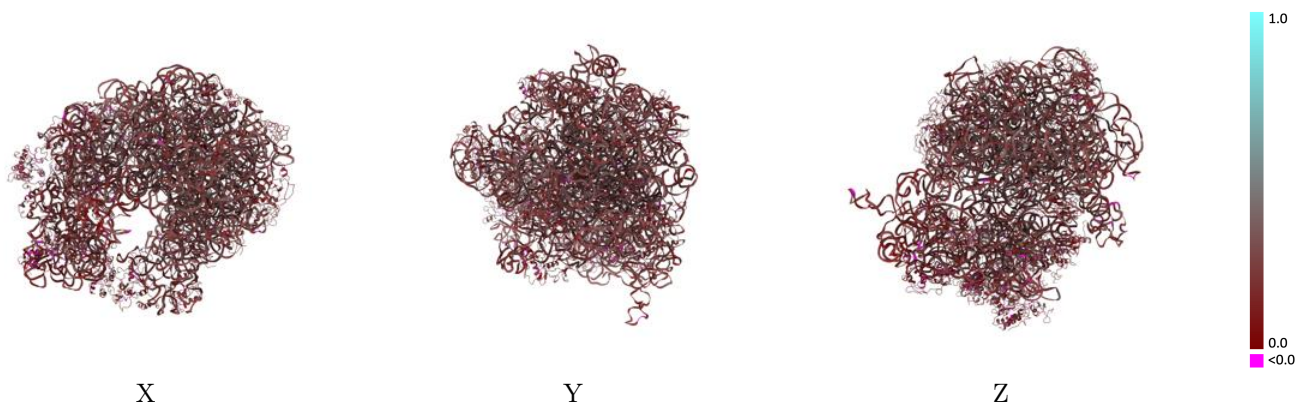
This section contains information regarding the fit between EMDB map EMD-3581 and PDB model 5MYJ. Per-residue inclusion information can be found in section 3 on page 13.

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



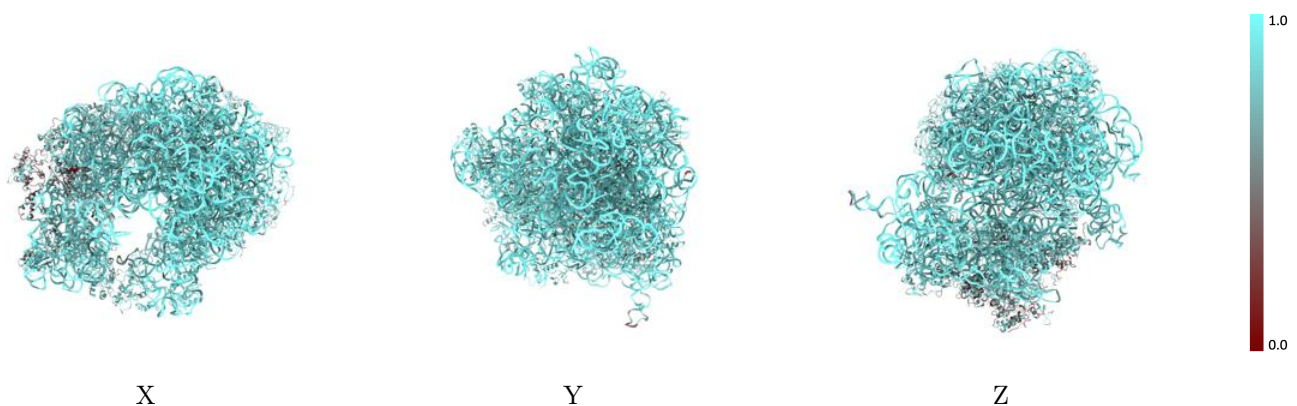
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



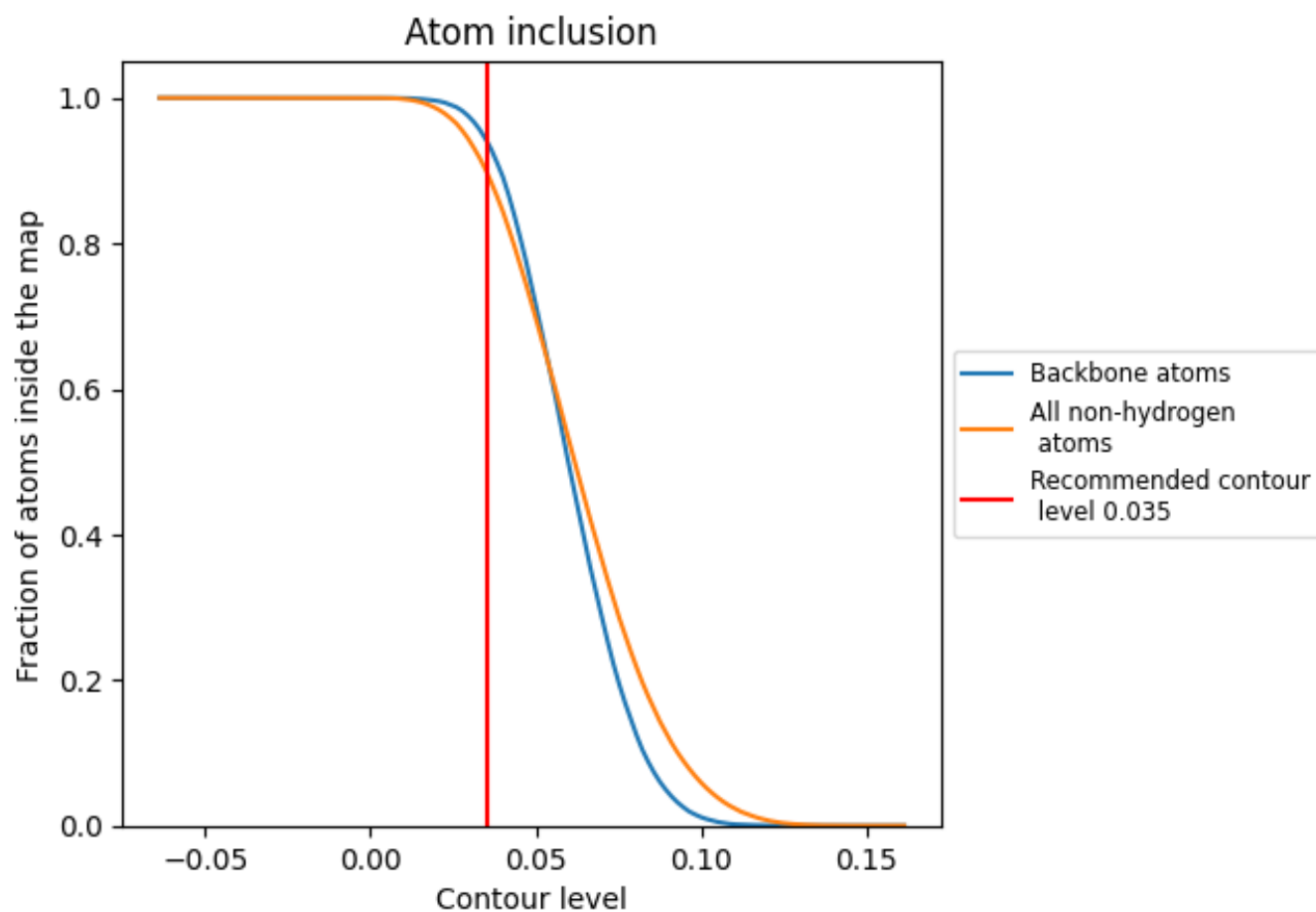
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 90% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8996	 0.2480
A	 0.5444	 0.2100
AA	 0.9501	 0.2270
AB	 0.4756	 0.2060
AC	 0.6563	 0.1880
AD	 0.7401	 0.1680
AE	 0.5600	 0.2170
AF	 0.6500	 0.2120
AG	 0.7112	 0.2150
AH	 0.6336	 0.1770
AI	 0.7758	 0.1630
AJ	 0.7063	 0.1710
AK	 0.6971	 0.2320
AL	 0.6412	 0.2190
AM	 0.8014	 0.2000
AN	 0.8502	 0.1690
AO	 0.7645	 0.2070
AP	 0.7779	 0.1640
AQ	 0.7169	 0.2110
AR	 0.6259	 0.2300
AS	 0.8075	 0.1760
AT	 0.7940	 0.1940
AU	 0.3919	 0.2390
B0	 0.7495	 0.2530
B1	 0.8069	 0.2010
B2	 0.8167	 0.2620
B3	 0.7755	 0.2060
B4	 0.8417	 0.2820
B5	 0.7949	 0.2340
B6	 0.8387	 0.2630
B7	 0.7941	 0.2500
B8	 0.8932	 0.2530
BA	 0.9725	 0.2760
BB	 0.9898	 0.2650
BD	 0.7658	 0.2590



*Continued on next page...*

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Chain	Atom inclusion	Q-score
BE	 0.8260	 0.2460
BF	 0.8279	 0.2400
BG	 0.8214	 0.2190
BH	 0.8583	 0.2290
BM	 0.8108	 0.2500
BN	 0.6976	 0.2490
BO	 0.8348	 0.2450
BP	 0.8353	 0.2580
BQ	 0.8015	 0.2240
BR	 0.9001	 0.2090
BS	 0.7348	 0.2520
BT	 0.7978	 0.1910
BU	 0.8232	 0.2520
BV	 0.7844	 0.2540
BW	 0.8233	 0.2550
BX	 0.8527	 0.2200
BZ	 0.8561	 0.2660