



## wwPDB EM Validation Summary Report ⓘ

Dec 10, 2022 – 10:01 am GMT

PDB ID : 5FL8  
EMDB ID : EMD-3199  
Title : CRYO-EM STRUCTURE OF THE RIX1-REA1 PRE-60S PARTICLE  
Authors : Barrio-Garcia, C.; Thoms, M.; Flemming, D.; Kater, L.; Berninghausen, O.;  
Bassler, J.; Beckmann, R.; Hurt, E.  
Deposited on : 2015-10-22  
Resolution : 9.50 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>.

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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) : 2.31.3

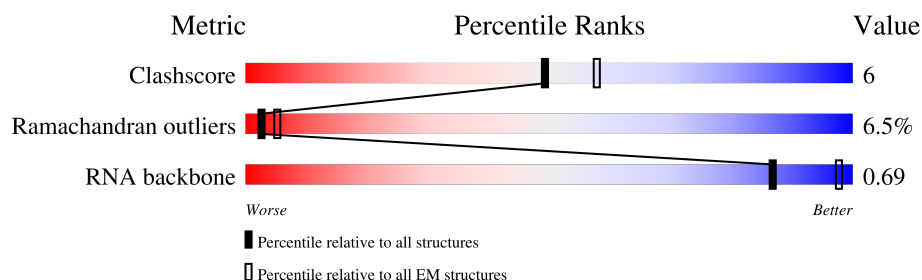
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 9.50 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
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	A	254	<div> <div>39%</div> <div>85%</div> <div>13%</div> <div>..</div> </div>
2	B	387	<div> <div>18%</div> <div>92%</div> <div>7%</div> <div>.</div> </div>
3	C	362	<div> <div>25%</div> <div>90%</div> <div>9%</div> <div>.</div> </div>
4	D	297	<div> <div>13%</div> <div>95%</div> <div>.</div> </div>
5	E	176	<div> <div>12%</div> <div>84%</div> <div>5%</div> <div>11%</div> </div>
6	F	244	<div> <div>6%</div> <div>85%</div> <div>6%</div> <div>9%</div> </div>
7	G	256	<div> <div>16%</div> <div>87%</div> <div>.</div> <div>9%</div> </div>
8	H	191	<div> <div>9%</div> <div>95%</div> <div>5%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
9	I	217	<div>84%</div> <div>94%</div> <div>6%</div>
10	J	174	<div>75%</div> <div>20%</div> <div>• •</div>
11	K	165	<div>15%</div> <div>67%</div> <div>10%</div> <div>23%</div> <div>•</div>
12	L	199	<div>14%</div> <div>88%</div> <div>8%</div> <div>• •</div>
13	M	138	<div>9%</div> <div>93%</div> <div>6%</div> <div>•</div>
14	N	204	<div>22%</div> <div>92%</div> <div>8%</div>
15	O	199	<div>23%</div> <div>87%</div> <div>11%</div> <div>• •</div>
16	P	184	<div>24%</div> <div>92%</div> <div>7%</div> <div>•</div>
17	Q	186	<div>33%</div> <div>93%</div> <div>6%</div> <div>•</div>
18	R	189	<div>49%</div> <div>88%</div> <div>12%</div> <div>•</div>
19	S	172	<div>10%</div> <div>95%</div> <div>5%</div> <div>•</div>
20	T	160	<div>62%</div> <div>79%</div> <div>18%</div> <div>• • •</div>
21	U	121	<div>76%</div> <div>7%</div> <div>17%</div>
22	V	137	<div>21%</div> <div>95%</div> <div>• •</div>
23	X	142	<div>22%</div> <div>80%</div> <div>5%</div> <div>15%</div>
24	Y	127	<div>16%</div> <div>92%</div> <div>7%</div> <div>•</div>
25	Z	136	<div>10%</div> <div>93%</div> <div>6%</div> <div>•</div>
26	a	149	<div>39%</div> <div>88%</div> <div>9%</div> <div>• •</div>
27	c	105	<div>12%</div> <div>91%</div> <div>8%</div> <div>•</div>
28	d	113	<div>14%</div> <div>93%</div> <div>• •</div>
29	e	130	<div>22%</div> <div>96%</div> <div>• •</div>
30	f	107	<div>15%</div> <div>92%</div> <div>6%</div> <div>• •</div>
31	g	121	<div>41%</div> <div>88%</div> <div>7%</div> <div>•</div>
32	h	120	<div>8%</div> <div>96%</div> <div>• •</div>
33	i	100	<div>19%</div> <div>93%</div> <div>6%</div> <div>•</div>

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Mol	Chain	Length	Quality of chain
34	j	88	
35	k	78	
36	l	51	
37	m	245	
38	n	236	
39	o	647	
40	p	92	
41	q	515	
42	r	767	
43	s	4914	
44	t	199	
45	u	380	
46	x	2779	
47	y	158	
48	z	121	

## 2 Entry composition

There are 48 unique types of molecules in this entry. The entry contains 105808 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 L2-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	252	Total	C	N	O	0	0
			1007	504	252	251		

- Molecule 2 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	386	Total	C	N	O	0	0
			1543	772	386	385		

- Molecule 3 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	361	Total	C	N	O	0	0
			1443	722	361	360		

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	296	Total	C	N	O	0	0
			1183	592	296	295		

- Molecule 5 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	E	156	Total	C	N	O	0	0
			622	312	156	154		

- Molecule 6 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	F	222	Total	C	N	O	0	0
			887	444	222	221		

- Molecule 7 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	G	233	Total	C	N	O	0	0
			931	466	233	232		

- Molecule 8 is a protein called Rpl9ap.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	H	191	Total	C	N	O	0	0
			763	382	191	190		

- Molecule 9 is a protein called 60S ribosomal protein L1-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	217	Total	C	N	O	0	0
			867	434	217	216		

- Molecule 10 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	J	169	Total	C	N	O	0	0
			675	338	169	168		

- Molecule 11 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	K	127	Total	C	N	O	0	0
			507	254	127	126		

- Molecule 12 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	L	193	Total	C	N	O	0	0
			771	386	193	192		

- Molecule 13 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	M	136	Total	C	N	O	0	0
			543	272	136	135		

- Molecule 14 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	203	Total	C	N	O	0	0
			811	406	203	202		

- Molecule 15 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	O	197	Total	C	N	O	0	0
			787	394	197	196		

- Molecule 16 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	183	Total	C	N	O	0	0
			731	366	183	182		

- Molecule 17 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	185	Total	C	N	O	0	0
			739	370	185	184		

- Molecule 18 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	188	Total	C	N	O	0	0
			751	376	188	187		

- Molecule 19 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	S	172	Total	C	N	O	0	0
			687	344	172	171		

- Molecule 20 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	T	159	Total	C	N	O	0	0
			635	318	159	158		

- Molecule 21 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	100	Total	C	N	O	0	0
			399	200	100	99		

- Molecule 22 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	V	136	Total	C	N	O	0	0
			543	272	136	135		

- Molecule 23 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	X	121	Total	C	N	O	0	0
			483	242	121	120		

- Molecule 24 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Y	126	Total	C	N	O	0	0
			503	252	126	125		

- Molecule 25 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Z	135	Total	C	N	O	0	0
			539	270	135	134		

- Molecule 26 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	a	148	Total	C	N	O	0	0
			591	296	148	147		

- Molecule 27 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	c	97	Total	C	N	O	0	0
			387	194	97	96		

- Molecule 28 is a protein called 60S ribosomal protein L31-A.



Mol	Chain	Residues	Atoms				AltConf	Trace
28	d	109	Total	C	N	O	0	0
			435	218	109	108		

- Molecule 29 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	e	127	Total	C	N	O	0	0
			507	254	127	126		

- Molecule 30 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	f	106	Total	C	N	O	0	0
			423	212	106	105		

- Molecule 31 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	g	112	Total	C	N	O	0	0
			447	224	112	111		

- Molecule 32 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	h	119	Total	C	N	O	0	0
			475	238	119	118		

- Molecule 33 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	i	99	Total	C	N	O	0	0
			395	198	99	98		

- Molecule 34 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	j	87	Total	C	N	O	0	0
			347	174	87	86		

- Molecule 35 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	k	77	Total	C	N	O	0	0
			307	154	77	76		

- Molecule 36 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	l	50	Total	C	N	O	0	0
			199	100	50	49		

- Molecule 37 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	m	224	Total	C	N	O	0	0
			895	448	224	223		

- Molecule 38 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	n	212	Total	C	N	O	0	0
			847	424	212	211		

- Molecule 39 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	o	347	Total	C	N	O	0	0
			1387	694	347	346		

- Molecule 40 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	p	91	Total	C	N	O	0	0
			363	182	91	90		

- Molecule 41 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	q	488	Total	C	N	O	0	0
			1951	976	488	487		

- Molecule 42 is a protein called Protein SDA1.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	r	333	Total	C	N	O	0	0
			1304	666	333	305		

- Molecule 43 is a protein called Midasin.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	s	2008	Total	C	N	O	0	0
			8027	4016	2008	2003		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
s	804	ASN	-	insertion	UNP Q12019
s	805	SER	-	insertion	UNP Q12019
s	999	LYS	-	insertion	UNP Q12019
s	1643	ALA	-	insertion	UNP Q12019

- Molecule 44 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	t	63	Total	C	N	O	0	0
			251	126	63	62		

- Molecule 45 is a protein called ARX1.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	u	380	Total	C	N	O	0	0
			1519	760	380	379		

- Molecule 46 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	x	2779	Total	C	N	O	P	0	0
			59475	26560	10747	19390	2778		

- Molecule 47 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	y	158	Total	C	N	O	P	0	0
			3350	1500	586	1107	157		

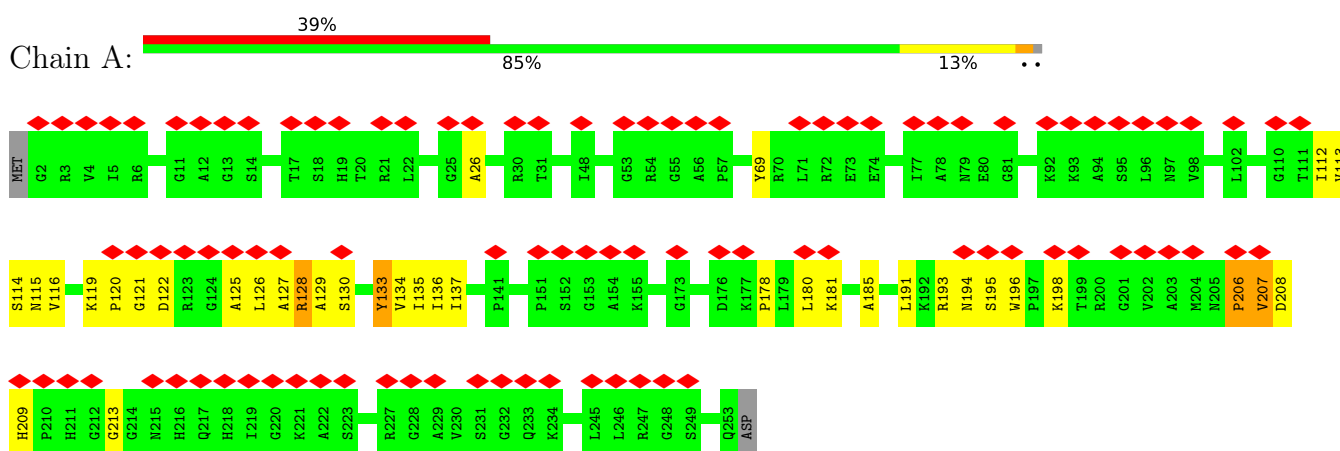
- Molecule 48 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
48	z	121	2576	1152	461	843	120	0	0

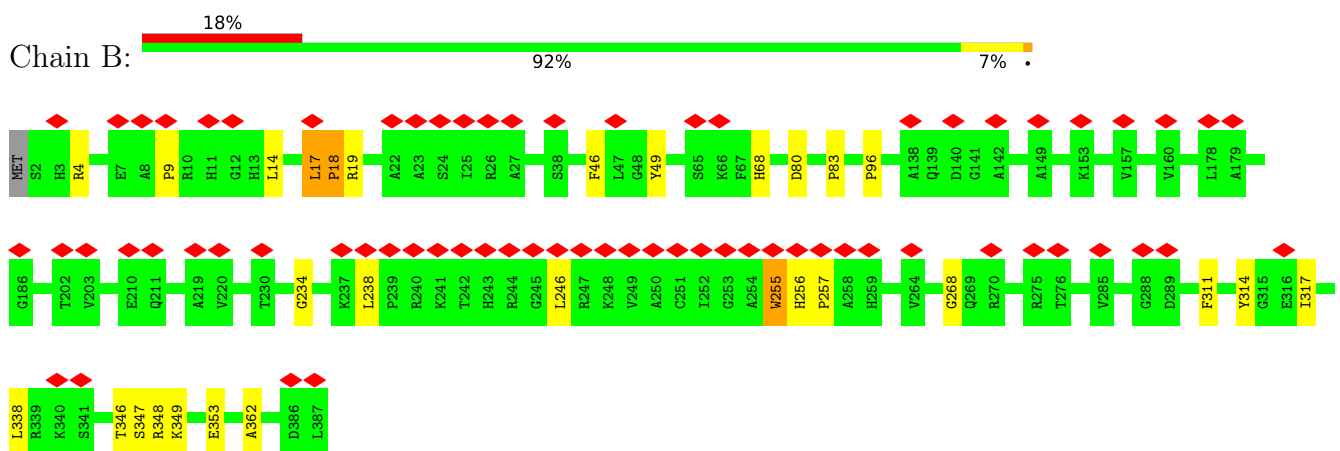
### 3 Residue-property plots

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

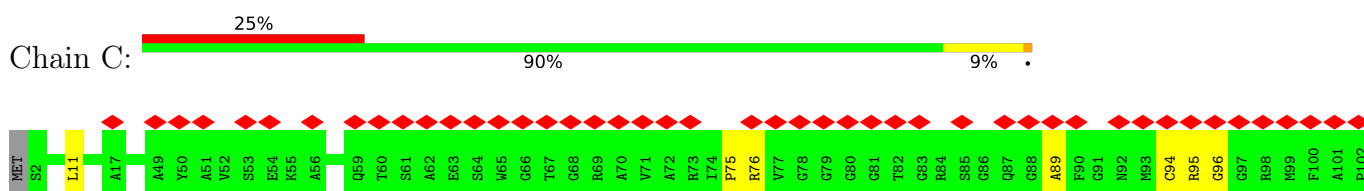
#### • Molecule 1: 60S ribosomal protein L2-A

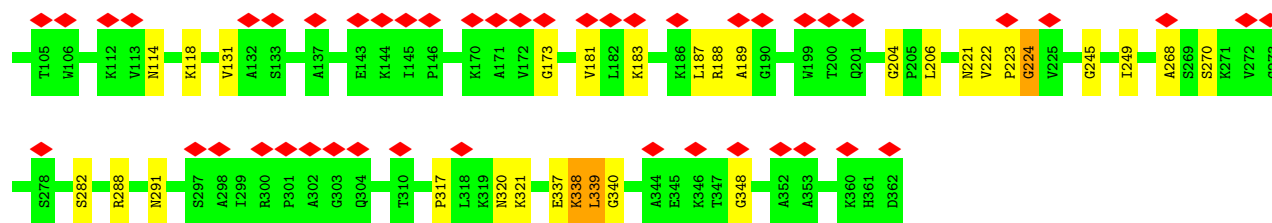


#### • Molecule 2: 60S ribosomal protein L3

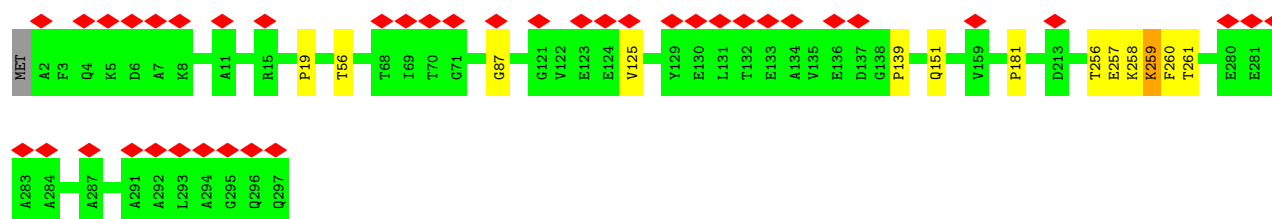


#### • Molecule 3: 60S ribosomal protein L4-A

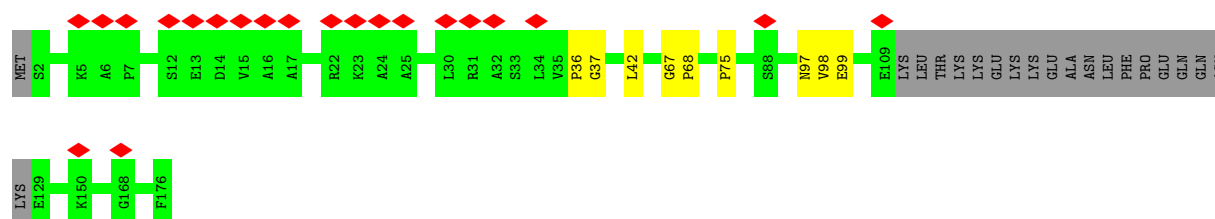
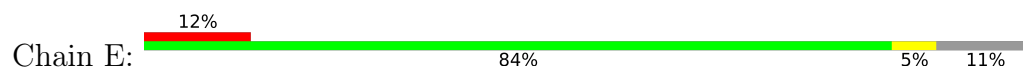




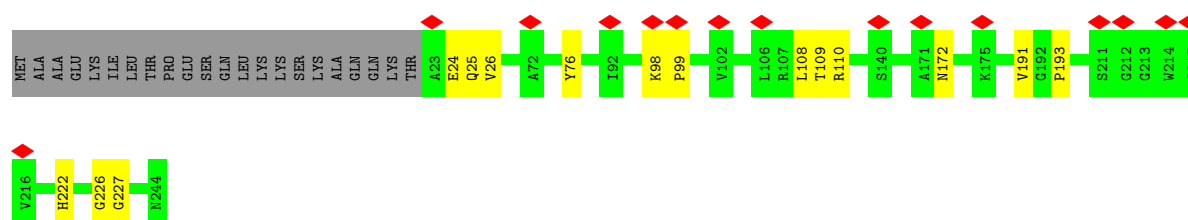
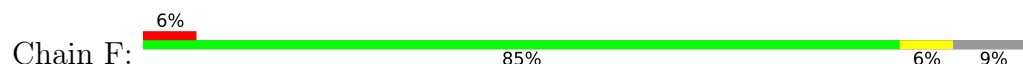
• Molecule 4: 60S ribosomal protein L5



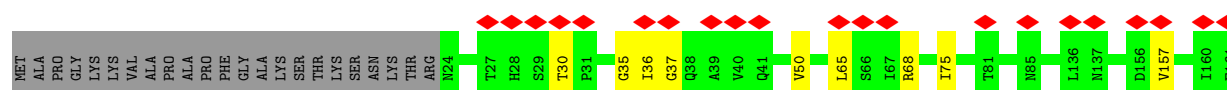
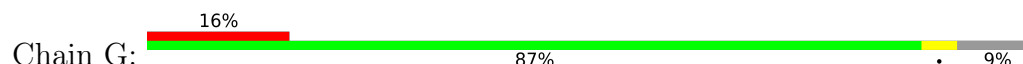
• Molecule 5: 60S ribosomal protein L6-A

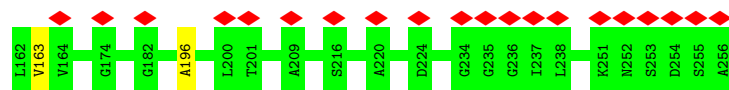


• Molecule 6: 60S ribosomal protein L7-A

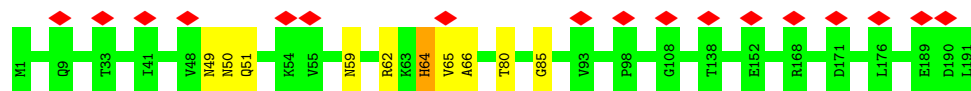


• Molecule 7: 60S ribosomal protein L8-A

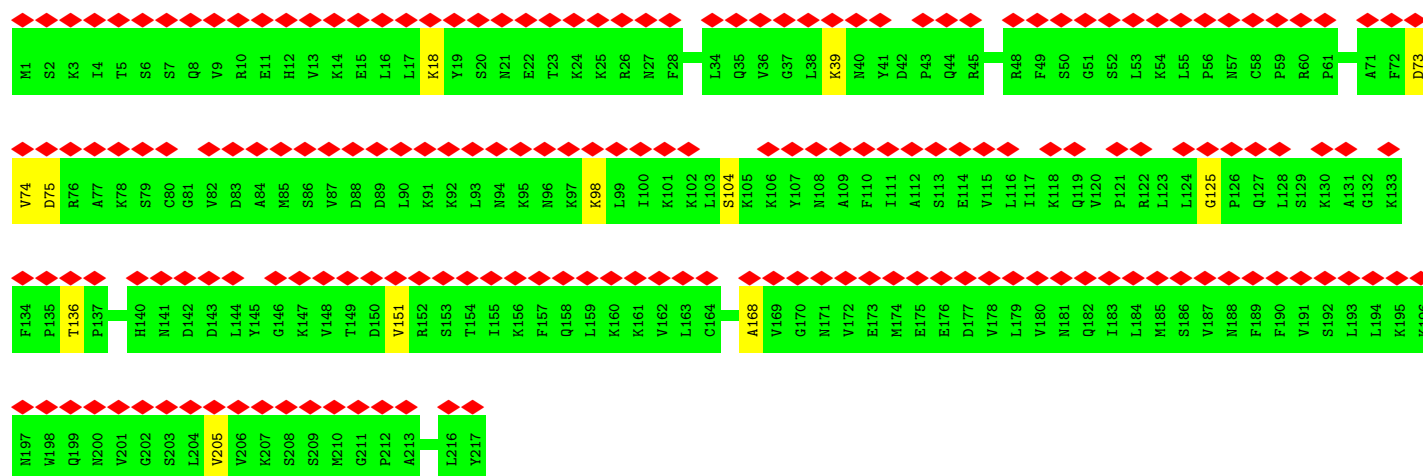
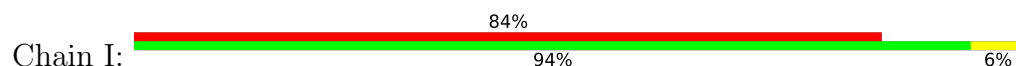




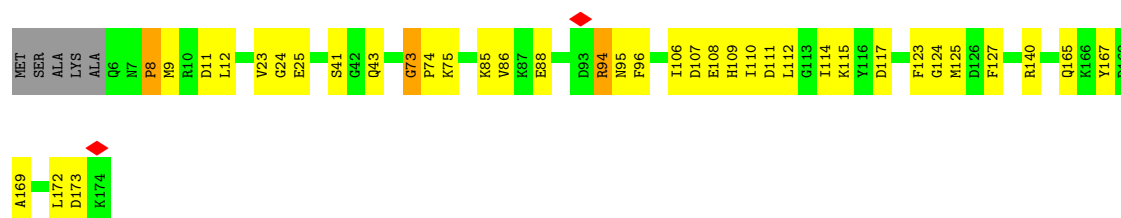
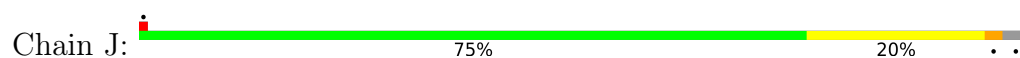
• Molecule 8: Rpl9ap



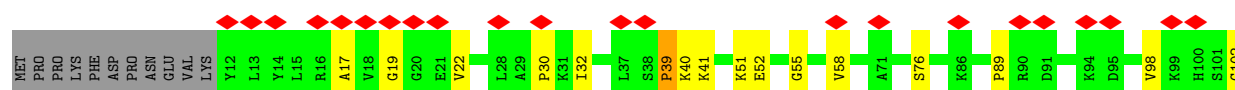
• Molecule 9: 60S ribosomal protein L1-B

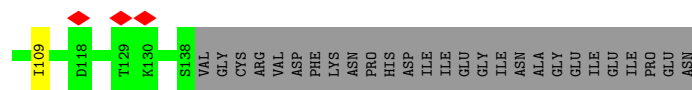


• Molecule 10: 60S ribosomal protein L11-A

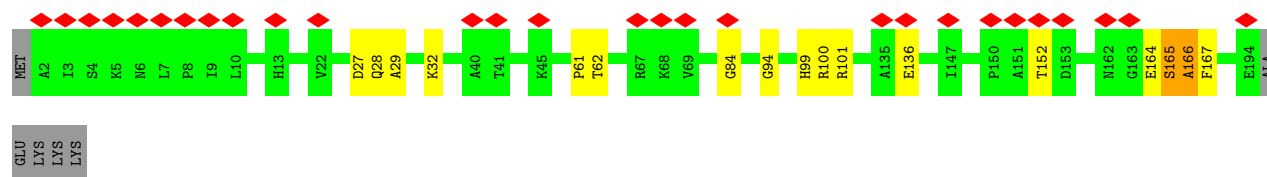
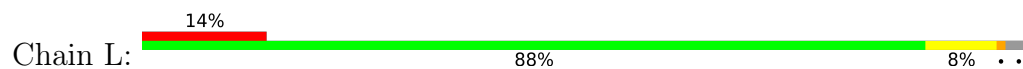


• Molecule 11: 60S ribosomal protein L12-A

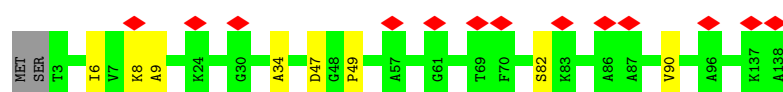
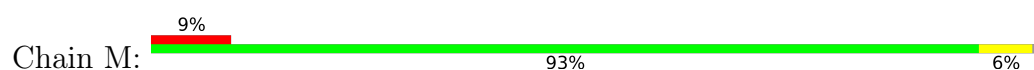




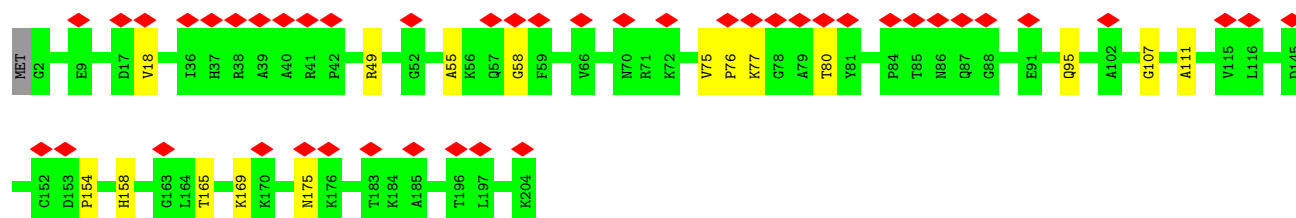
• Molecule 12: 60S ribosomal protein L13-A



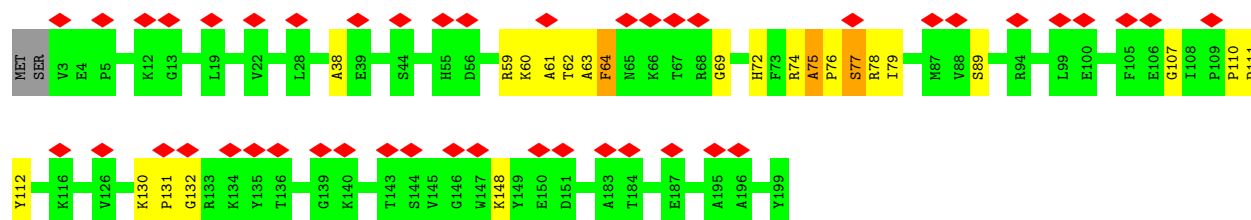
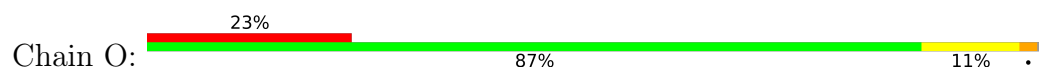
• Molecule 13: 60S ribosomal protein L14-A



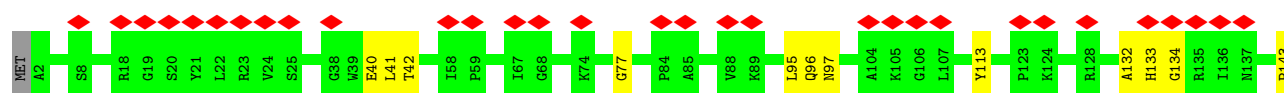
• Molecule 14: 60S ribosomal protein L15-A



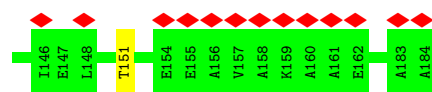
• Molecule 15: 60S ribosomal protein L16-A



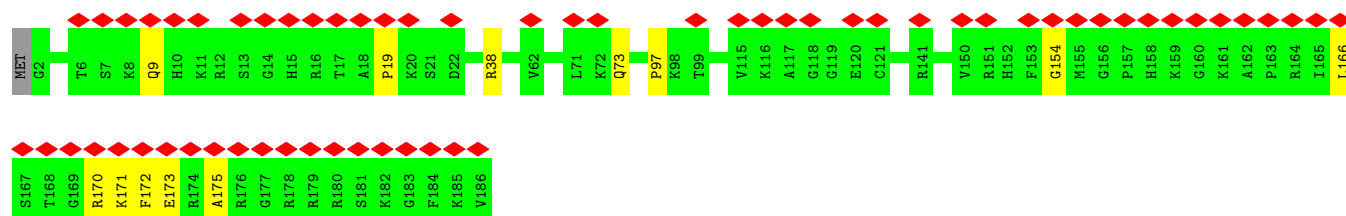
• Molecule 16: 60S ribosomal protein L17-A



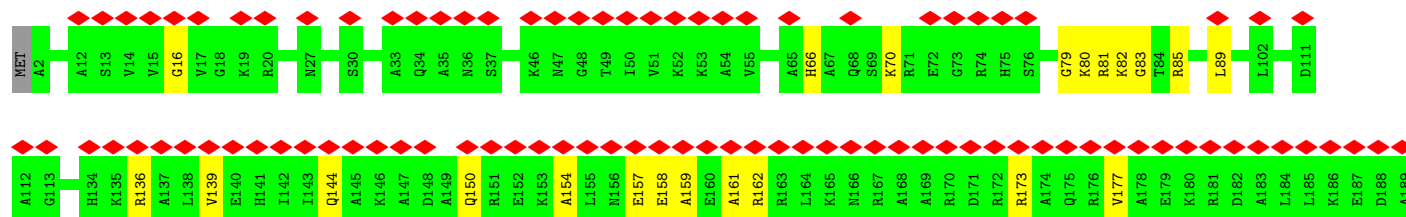
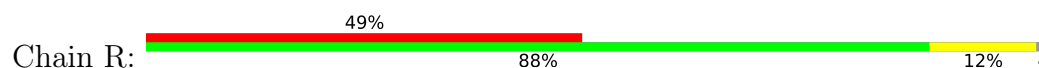




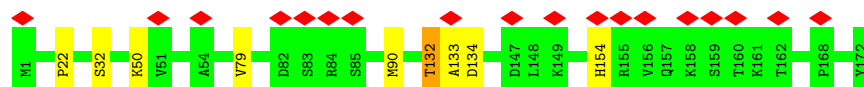
• Molecule 17: 60S ribosomal protein L18-A



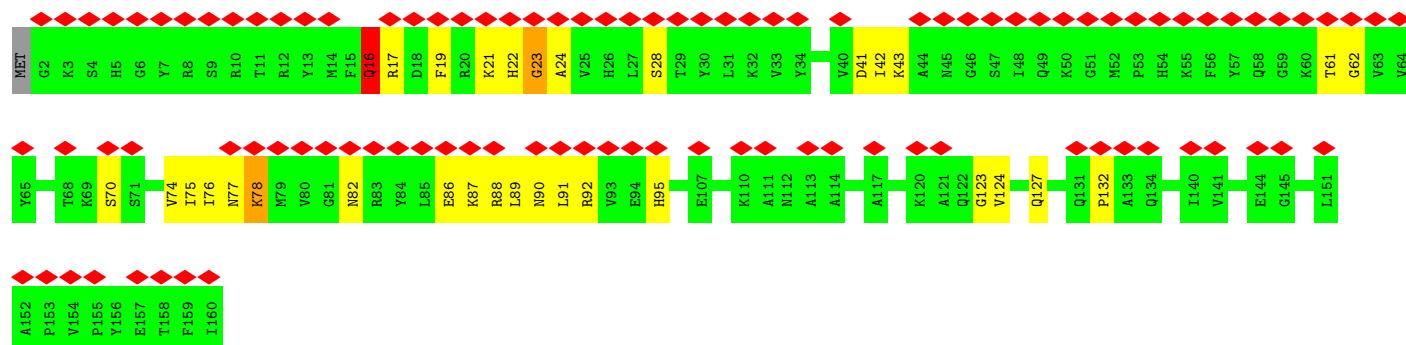
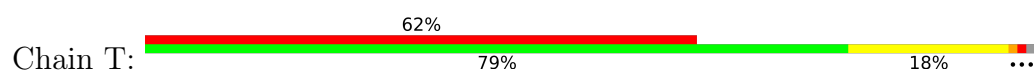
• Molecule 18: 60S ribosomal protein L19-A



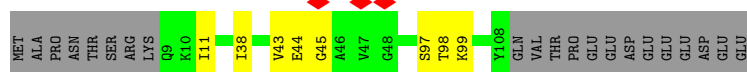
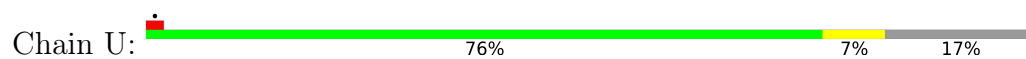
• Molecule 19: 60S ribosomal protein L20-A



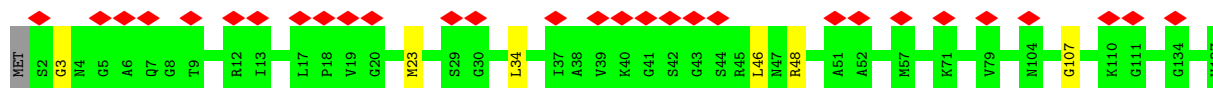
• Molecule 20: 60S ribosomal protein L21-A



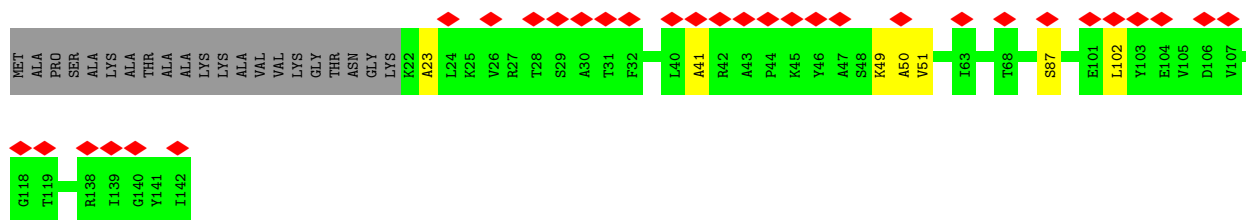
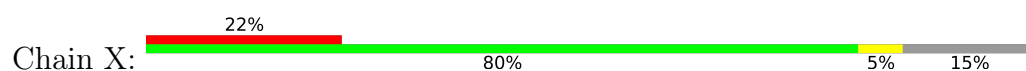
• Molecule 21: 60S ribosomal protein L22-A



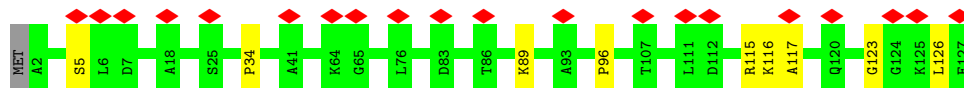
- Molecule 22: 60S ribosomal protein L23-A



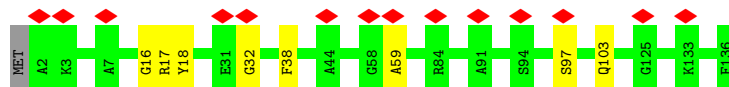
- Molecule 23: 60S ribosomal protein L25



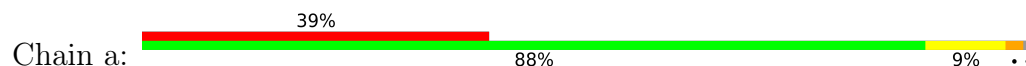
- Molecule 24: 60S ribosomal protein L26-A



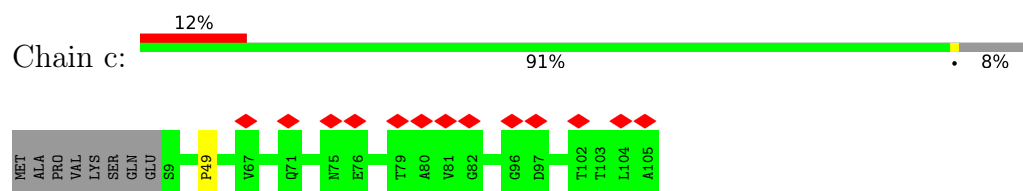
- Molecule 25: 60S ribosomal protein L27-A



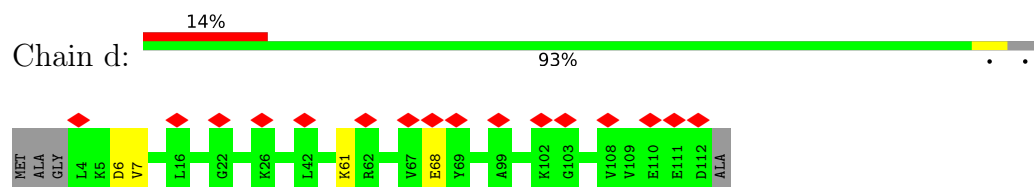
- Molecule 26: 60S ribosomal protein L28



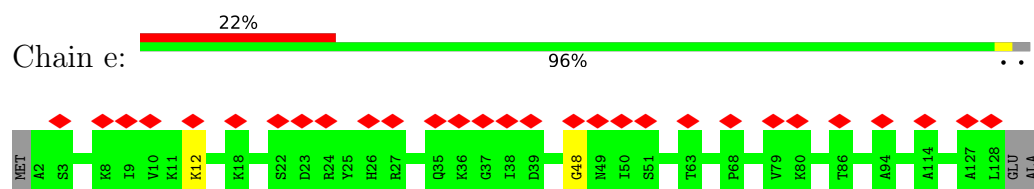
- Molecule 27: 60S ribosomal protein L30



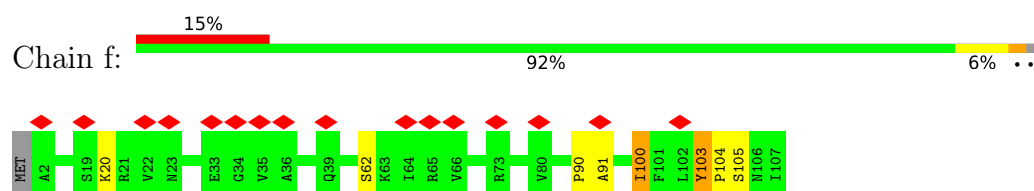
- Molecule 28: 60S ribosomal protein L31-A



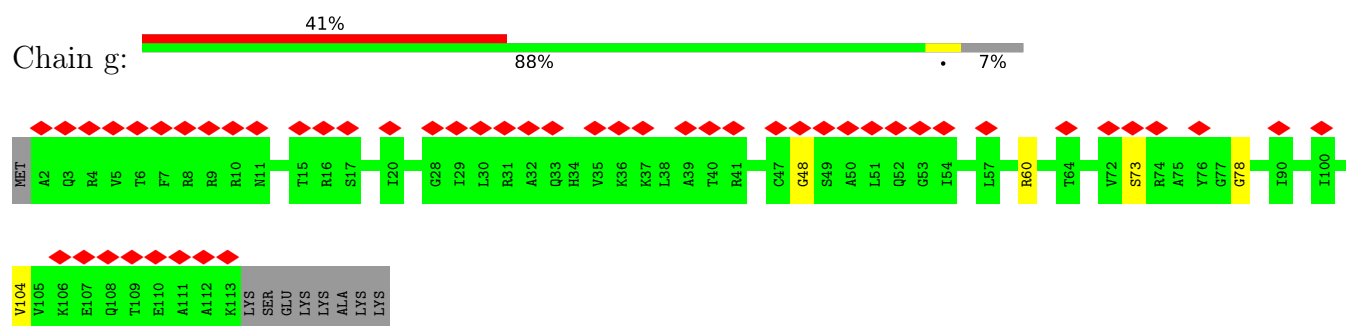
- Molecule 29: 60S ribosomal protein L32



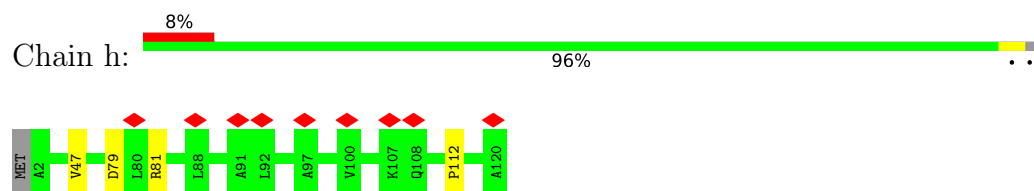
- Molecule 30: 60S ribosomal protein L33-A



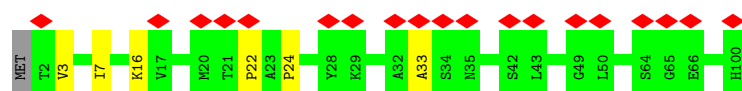
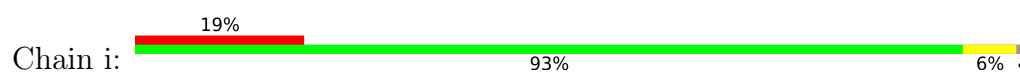
- Molecule 31: 60S ribosomal protein L34-A



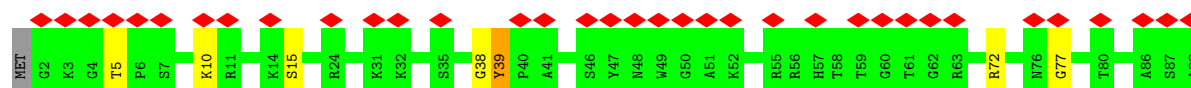
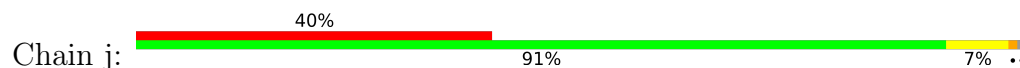
- Molecule 32: 60S ribosomal protein L35-A



- Molecule 33: 60S ribosomal protein L36-A



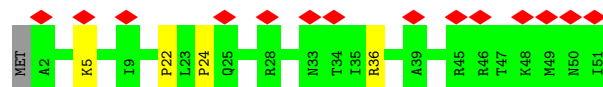
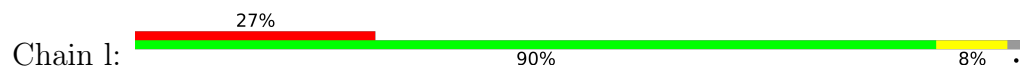
- Molecule 34: 60S ribosomal protein L37-A



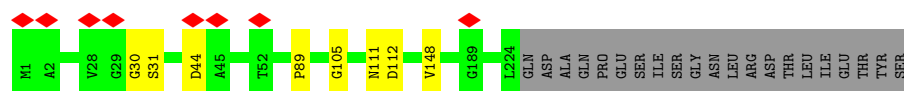
- Molecule 35: 60S ribosomal protein L38



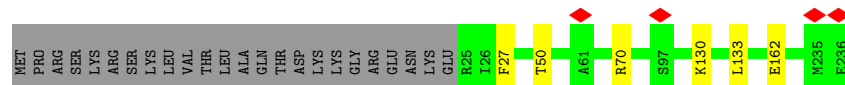
- Molecule 36: 60S ribosomal protein L39



- Molecule 37: Eukaryotic translation initiation factor 6

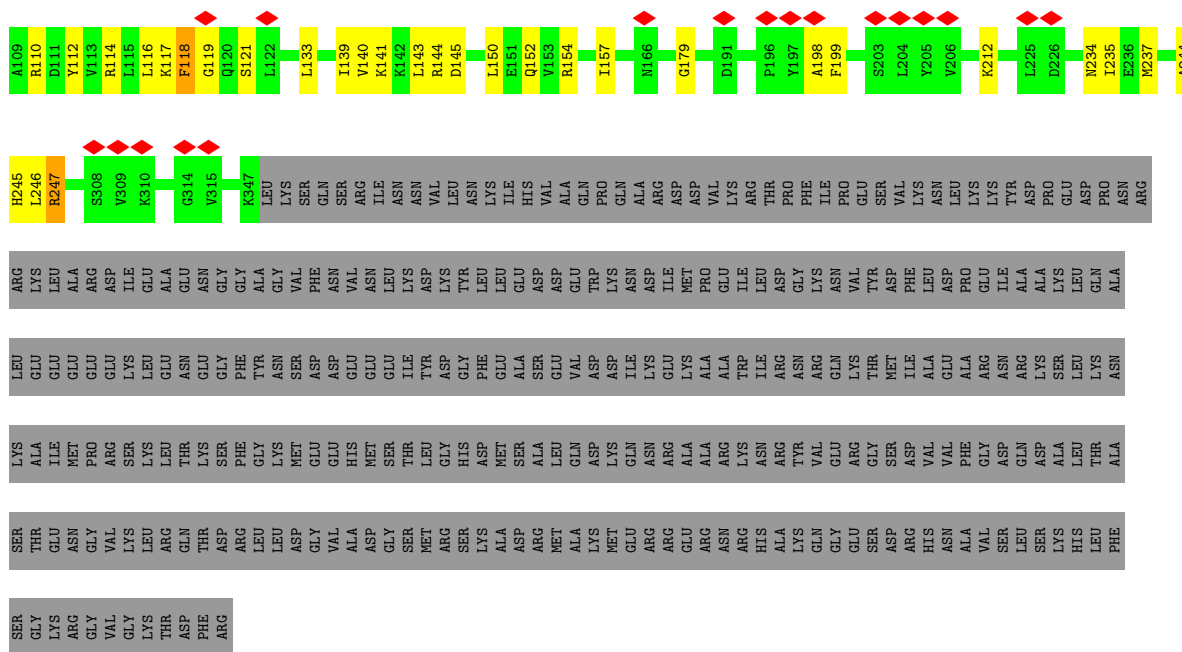


- Molecule 38: Ribosome assembly factor MRT4

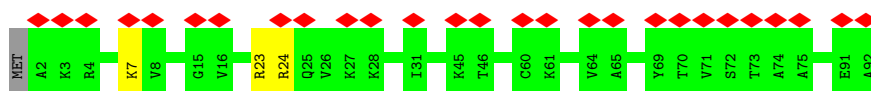


- Molecule 39: Nucleolar GTP-binding protein 1

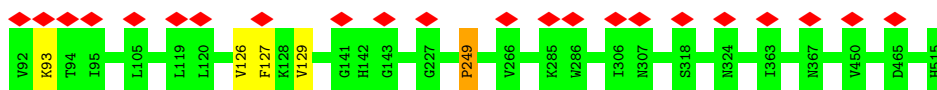
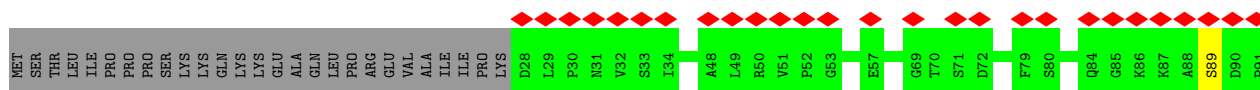
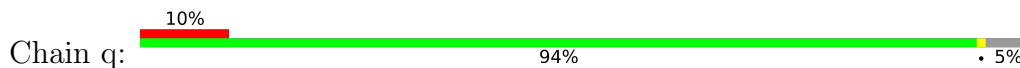




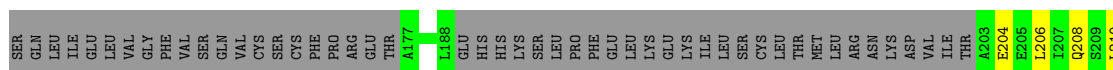
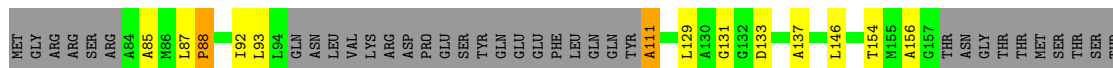
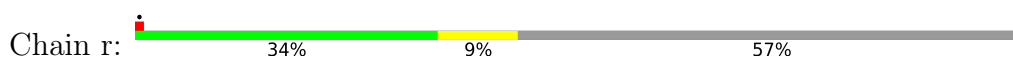
- Molecule 40: 60S ribosomal protein L43-A

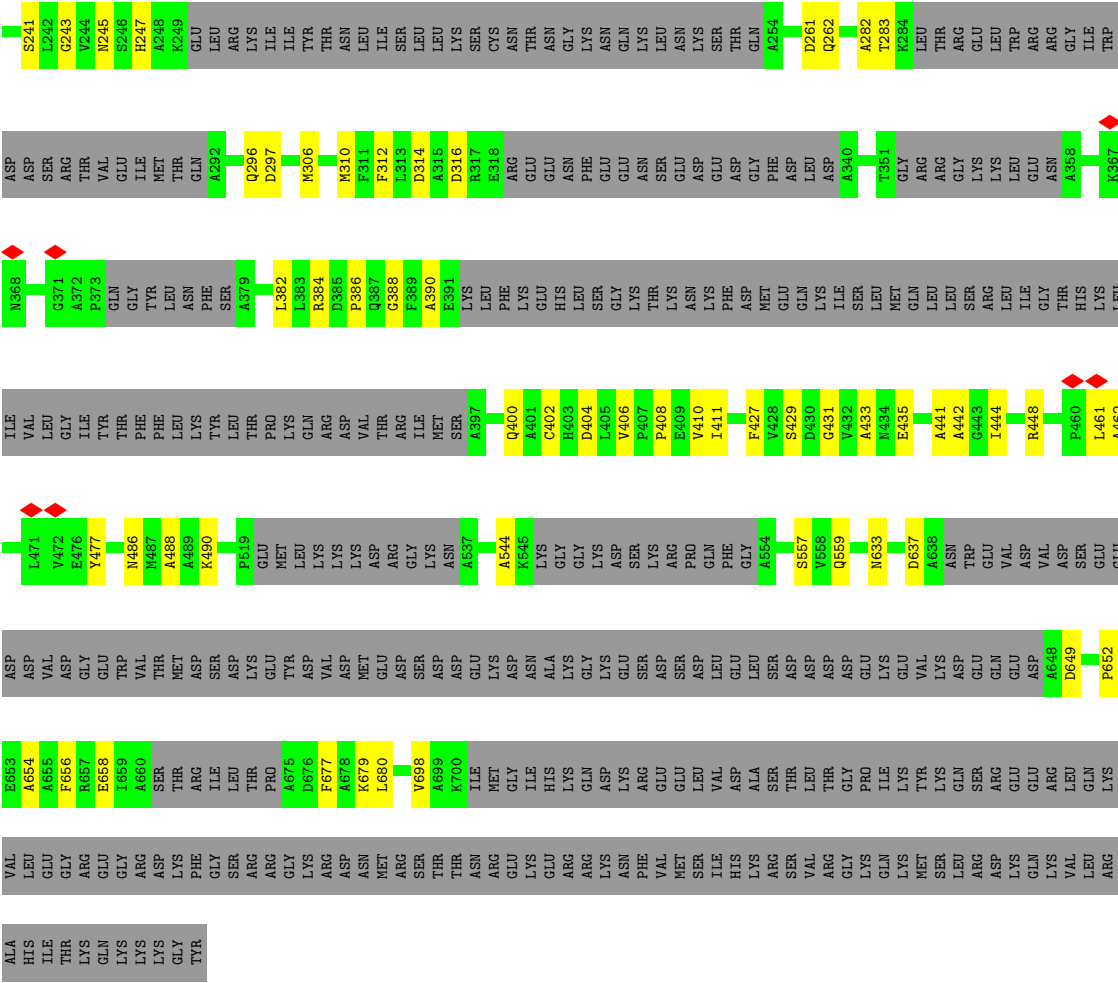


- Molecule 41: Ribosome assembly protein 4

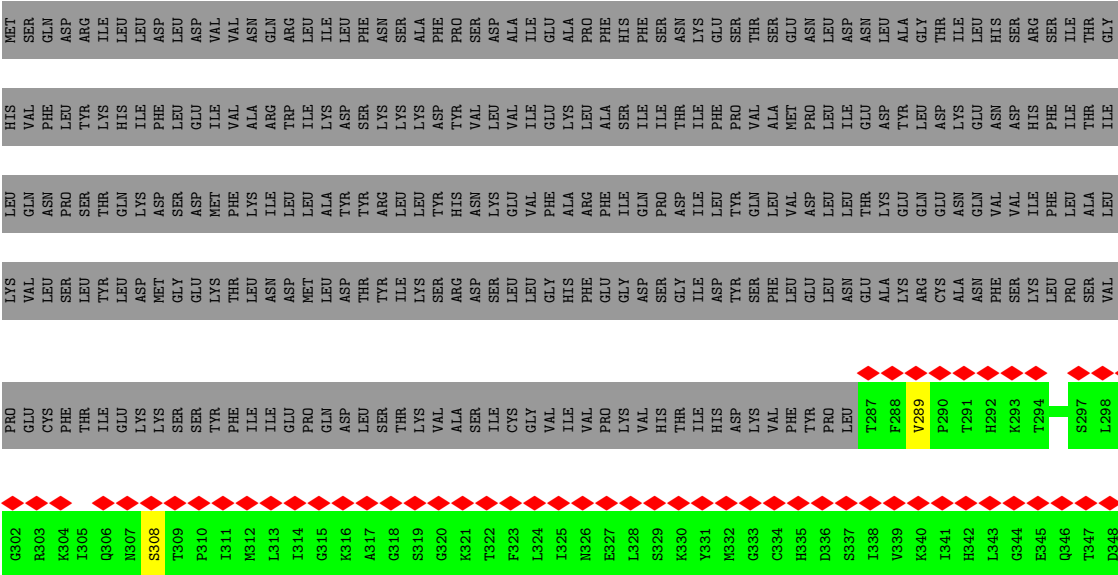


- Molecule 42: Protein SDA1





• Molecule 43: Midasin



P1185	H1186	P1187	D1188	F1189	L1190	L1191	Q1195	N1196	P1197	P1198	G1199	I1200	Y1201	G1202	G1203	R1204	K1205	I1206	L1207	S1208	R1209	A1210	R1214	I1223	D1226	E1234	R1235	C1236	A1239	Y1242	V1249	Y1250	L1253	S1254	I1255	E1256	R1257	S1258	A1259	R1261	L1262	F1263	E1264	Q1265	K1266	N1267	S1268	F1269	A1270										
E1118	Y1119	L1120	G1121	T1122	Y1123	V1124	T1125	D1126	D1127	T1128	G1129	K1130	L1131	S1132	F1133	K1134	E1135	G1136	V1137	L1138	V1139	E1140	A1141	L1142	R1143	K1144	D1151	L1155	A1156	P1157	T1158	D1159	V1160	L1161	E1162	A1163	L1164	N1165	R1166	L1167	L1168	D1169	D1170	N1171	R1172	E1173	L1174	F1175	I1176	P1177	E1178	T1179	Q1180	E1181	V1182	V1183	H1184		
PRO	SER	PRO	GLY	ASP	TYR	VAL	GLN	PHE	LYS	HIS	TRP	MET	LYS	LYS	GLY	PRO	ASN	THR	ILE	GLN	GLU	ALA	HIS	Y1056	I1057	I1058	K1064	R1071	A1072	T1073	S1074	G1075	K1076	R1077	F1078	T1086	S1087	S1088	G1089	K1090	T1091	S1092	M1093	G1102	R1107	T1108	E1112	L1116	Q1117										
E927	W928	V929	G930	N931	D932	I933	A934	K942	S953	K956	P957	S960	T965	L969	Y970	V971	T972	D973	I974	I977	Y978	S991	F992	L995	K999	K1000	I1004	L1005	K1006	P1007	S903	P904	L1014	G1015	R1016	L1017	K1018	N1019	V1020	K1021	S1022	I1023	M1024	S1025	GLN	THR	PRO												
E863	P864	I865	K866	A867	H868	P869	D870	F871	R872	I873	F874	A875	C876	N877	H878	P879	A880	T881	D882	V883	G884	K885	R886	D887	L888	P889	N890	G891	T892	R893	S894	R895	F896	T897	E898	I899	Y900	V901	H902	S903	P904	E905	R906	D907	I908	T909	D910	L911	L912	S913	K917	K921	Y922	S923	V924	S925	D926		
N803	N804	S805	S806	F807	V808	F809	N810	F811	V812	E813	G814	S815	L816	V817	K818	T819	R820	R821	A822	G823	E824	N825	L826	L827	L828	D829	E830	R831	N832	L833	A834	T835	A836	D837	T838	L839	E840	S841	T842	S843	D844	L845	L846	T847	E848	P849	D850	S851	R852	S853	T854	L855	L856	S857	E858	K859	G860	D861	A862
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T685	G686	D687	L688	L689	G690	G691	Y692	K693	P694	V695	ASN	K696	T697	V698	A699	V700	P701	I702	Q703	E704	N705	F706	E707	T708	L709	F710	N711	A712	T713	F714	S715	L716	K717	K718	N719	E720	K721	F722	H723	K724	M725	L726	H727	R728	C729	F730	N731	K732	N733	Q734	W735	K736	N737	V738	V739	K740	L741	W742	
Q617	K618	S620	M621	N622	S623	T624	L625	F626	A627	F628	T629	N630	H631	S632	L633	R634	L635	Q638	I639	T646	E647	L650	G653	E654	T655	G656	T657	G658	K659	T660	T661	V662	V663	Q664	Q665	A667	K668	M669	L670	A671	K672	K673	L674	T675	V676	I677	N678	V679	S680	Q681	Q682	T683	E684						
S487	Y488	K489	M490	V491	K492	S493	M496	M497	T498	K499	F500	I501	S502	L503	N504	K505	G506	A507	H508	T509	R510	V511	V512	S513	V514	R515	D516	L517	I518	K519	L520	C521	E522	R523	L524	D525	I526	L527	F528	K529	N530	N531	G532	I533	N534	K535	P536	D537	Q538	L539	I540	Q541	S542	S543	V544	Y545	D546	S547	
F422	Q423	L424	I425	T426	T427	V428	R429	I430	M431	E432	D433	H434	Q435	K436	D437	S438	S439	M440	K441	I442	Y443	M444	L445	M446	M447	I448	G449	M450	R451	I452	W453	M454	V455	S396	E459	D465	L466	T467	H468	I469	L470	A471	Q472	K473	F474	P475	I476	L477	T478	M479	L480	P482	K483	I485	A486				
P362	G363	T364	F365	E366	W367	R368	A369	G370	V371	L372	A373	T374	A375	V376	K377	E378	G379	R380	W381	V382	L383	I384	E385	D386	I387	D388	K389	A390	P391	T392	D393	V394	L395	S396	I397	L398	L399	S400	L401	L402	E403	K404	R405	E406	L407	T408	I409	P410	S411	R412	G413	E414	T415	V416	K417	A418	A419	N420	G421

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S2164	S2164	L2104	A2037	F1974	A1763	G1929	L1901	L1901	A1763	LEU	G1606	V1529	E1461	T1401	L1296
L2165	L2165	S2105	V2038	R1975	N1765	C1833	S1904	S1904	N1765	GLN	N1607	A1530	Q1462	D1402	L1297
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E2167	E2167	I2107	E2040	E1906	A1763	C1833	E1906	E1906	A1763	THR	T1609	A1530	Q1464	I1404	E1299
G2168	G2168	T2108	S2041	N1981	I1766	C1833	E1906	E1906	I1766	ASN	T1609	A1530	L1465	L1405	R1300
R2169	R2169	E2109	V2042	K1982	T1766	C1833	D1908	D1908	T1766	GLU	T1609	A1530	Q1466	G1406	C1301
P2170	P2170	E2110	L2043	A1983	G1767	C1833	I1909	I1909	G1767	ILE	T1609	A1530	D1467	A1407	T1302
L2171	L2171	L2111	K2044	Q1984	N1768	C1833	E1909	E1909	N1768	ILE	T1609	A1530	Q1468	Q1408	T1303
L2172	L2172	T2112	A2045	L1985	K1769	C1833	I1910	I1910	K1769	VAL	T1609	A1530	S1468	R1409	E1306
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K2181	K2181	M2121	G2056	THR	Q1779	C1833	V1924	V1924	Q1779	LEU	T1609	A1530	S1476	I1417	L1323
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E2189	E2189	A2129	E2064	ASP	G1786	C1833	G1931	G1931	G1786	SER	T1609	A1530	L1491	L1425	ASP
A2190	A2190	T2130	T2065	TYR	A1787	C1833	K1932	K1932	A1787	SER	T1609	A1530	V1502	L1426	LYS
S2191	S2191	A2131	T2066	VAL	D1788	C1833	N1932	N1932	D1788	PHE	T1609	A1530	E1494	T1427	SER
V2192	V2192	L2132	L2066	GLN	A1789	C1833	S1935	S1935	A1789	N1722	T1609	A1530	I1495	T1428	GLU
F2193	F2193	M2133	T2067	ILE	P1790	C1833	P1936	P1936	P1790	L1723	T1609	A1530	S1496	L1429	ALA
T2194	T2194	E2134	F2068	ASN	G1791	C1833	Q1936	Q1936	G1791	T1724	T1609	A1530	A1498	N1430	ILE
E2195	E2195	L2135	L2069	GLU	E1792	C1833	Q1937	Q1937	E1792	A1725	T1609	A1530	D1499	I1431	GLY
W2196	W2196	G2136	L2072	VAL	R1793	C1833	L1945	L1945	R1793	T1728	T1609	A1530	D1500	A1432	VAL
F2197	F2197	N2137	D2078	LEU	G1795	C1833	G1945	G1945	G1795	V1736	T1609	A1530	V1501	D1434	THR
D2198	D2198	L2138	V2079	ARG	E1796	C1833	L1948	L1948	E1796	R1737	T1609	A1530	E1501	N1435	TRP
G2199	G2199	T2139	F2080	ASN	F1797	C1833	K1949	K1949	F1797	R1737	T1609	A1530	E1502	Q1436	L1345
N2200	N2200	K2140	S2081	HIS	Q1799	C1833	L1950	L1950	Q1799	R1737	T1609	A1530	E1503	D1436	K1362
L2201	L2201	Y2141	N2082	TYR	P1874	C1833	L1951	L1951	P1874	R1737	T1609	A1530	E1504	V1437	E1363
V2202	V2202	L2142	M2082	ARG	S1875	C1833	N1952	N1952	S1875	R1737	T1609	A1530	E1505	D1438	L1362
K2203	K2203	T2143	N2083	TYR	S1876	C1833	Q1953	Q1953	S1876	H1742	T1609	A1530	E1506	L1439	G1372
A2204	A2204	N2144	S2084	PRO	N1879	C1833	Y1954	Y1954	N1879	I1745	T1609	A1530	E1507	K1440	R1368
V2205	V2205	D2145	D2085	ILE	P1885	C1833	S1955	S1955	P1885	I1745	T1609	A1530	E1508	E1441	R1369
E2206	E2206	L2146	T2086	THR	F1885	C1833	I1956	I1956	F1885	I1745	T1609	A1530	E1509	L1442	L1390
K2207	K2207	T2147	S2087	GLN	I1886	C1833	C1957	C1957	I1886	S1750	T1609	A1530	E1510	L1443	I1391
G2208	G2208	Y2148	N2088	ASN	E1958	C1833	E1958	E1958	E1958	S1750	T1609	A1530	E1511	Q1444	T1392
H2209	H2209	P2149	M2089	LEU	D1959	C1833	V1959	V1959	D1959	S1750	T1609	A1530	E1512	L1445	L1393
W2210	W2210	E2150	D2090	LEU	V1960	C1833	I1960	I1960	V1960	S1750	T1609	A1530	E1513	L1446	L1393
L2211	L2211	K2151	T2091	LEU	N1961	C1833	S1961	S1961	N1961	S1750	T1609	A1530	E1514	S1447	L1393
T2212	T2212	F2152	L2092	LEU	D1962	C1833	V1962	V1962	D1962	S1750	T1609	A1530	E1515	K1448	L1393
L2213	L2213	Q2153	G2093	LEU	F1963	C1833	L1963	L1963	F1963	S1750	T1609	A1530	E1516	S1449	L1393
D2214	D2214	D2154	G2094	LEU	D1964	C1833	F1964	F1964	D1964	S1750	T1609	A1530	E1517	L1450	L1393
F2215	F2215	R2155	Y2095	LEU	F1965	C1833	F1965	F1965	F1965	S1750	T1609	A1530	E1518	N1451	L1393
K2216	K2216	T2156	E2096	LEU	F1966	C1833	F1966	F1966	F1966	S1750	T1609	A1530	E1519	K1452	L1393

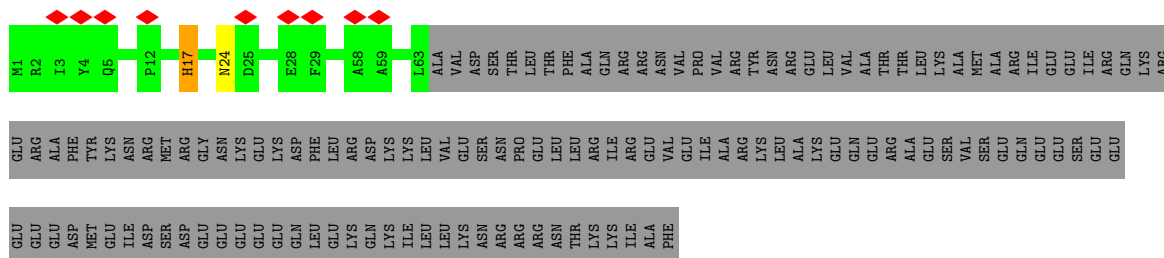




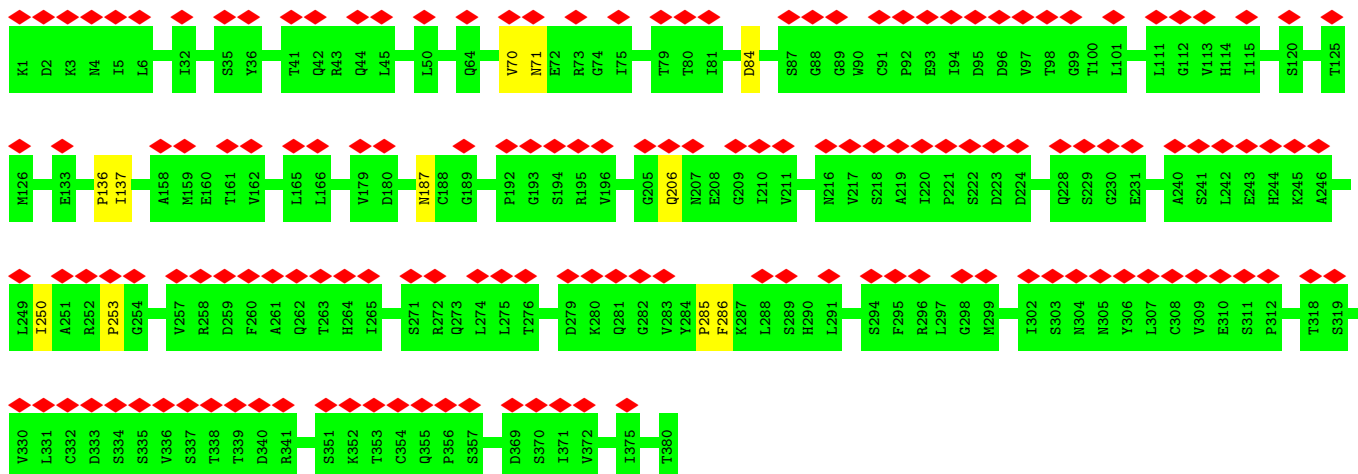
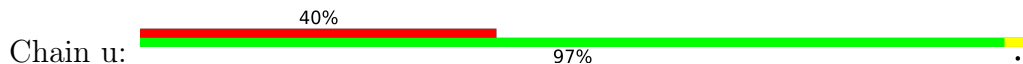


[illegible]

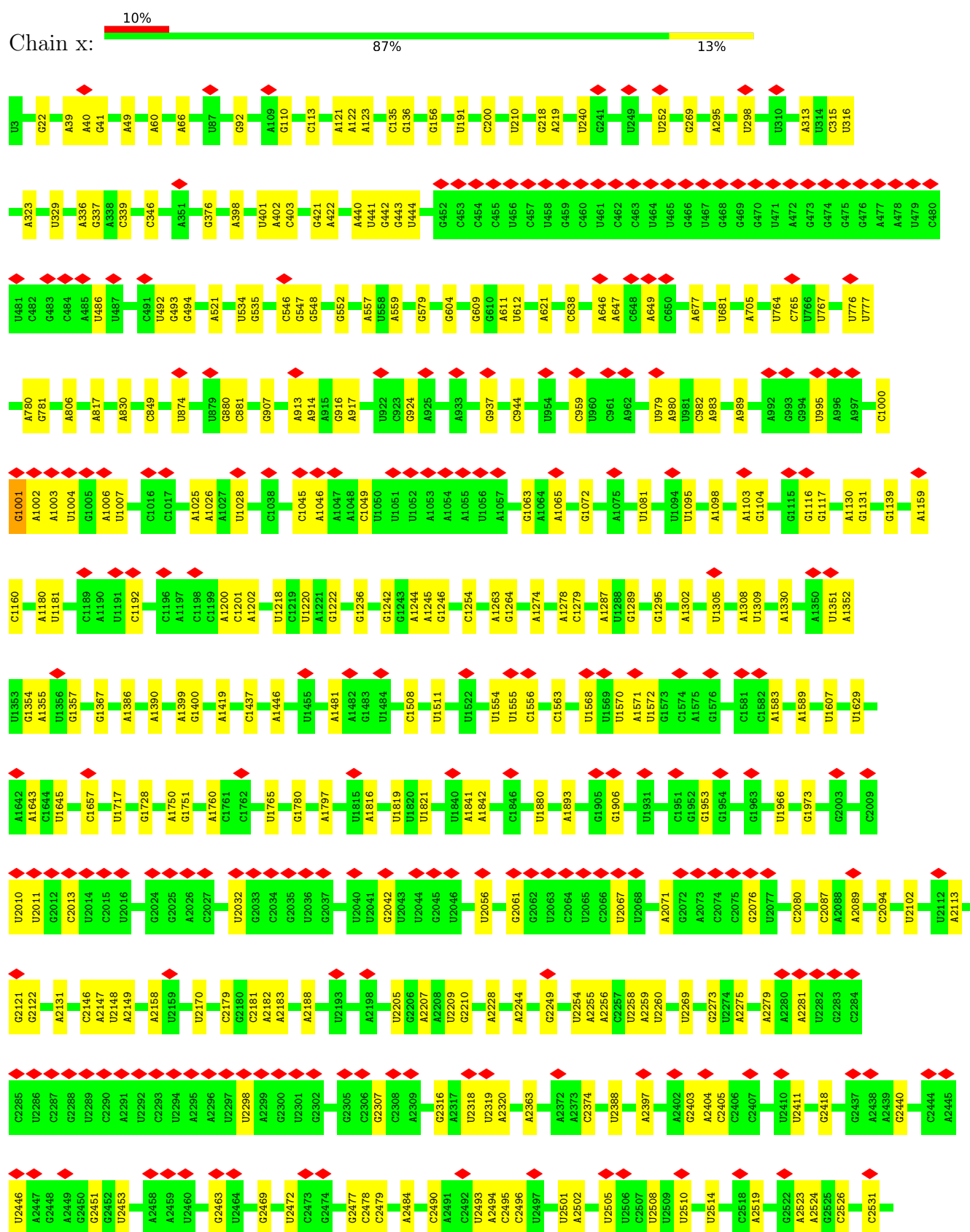
- Molecule 44: Ribosome biogenesis protein RLP24

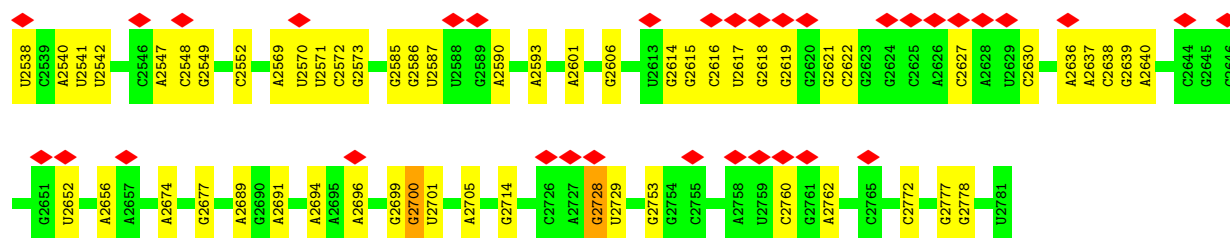


- Molecule 45: ARX1

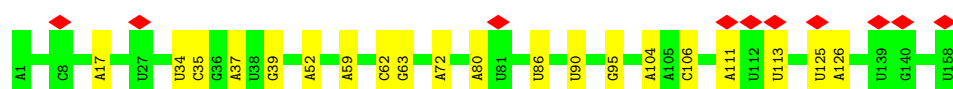
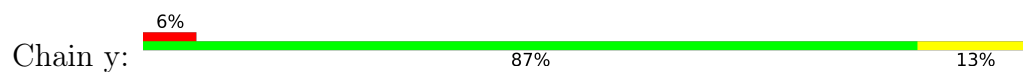


- Molecule 46: 25S ribosomal RNA

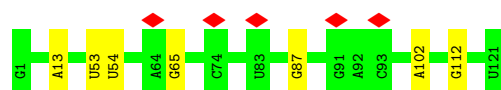




• Molecule 47: 5.8S ribosomal RNA



• Molecule 48: 5S ribosomal RNA



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	15749	Depositor
Resolution determination method	Not provided	
CTF correction method	SUBVOLUMES	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	4200	Depositor
Magnification	75000	Depositor
Image detector	GENERIC TVIPS	Depositor
Maximum map value	1.479	Depositor
Minimum map value	-0.721	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.3	Depositor
Map size ( $\text{\AA}$ )	827.6, 827.6, 827.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	2.069, 2.069, 2.069	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	A	0.35	1/1006 (0.1%)	0.47	0/1256
2	B	0.32	1/1542 (0.1%)	0.44	2/1926 (0.1%)
3	C	0.19	0/1442	0.37	1/1801 (0.1%)
4	D	0.17	0/1182	0.32	0/1476
5	E	0.55	1/620 (0.2%)	0.70	4/772 (0.5%)
6	F	0.17	0/886	0.32	0/1106
7	G	0.17	0/930	0.32	0/1161
8	H	0.17	0/762	0.30	0/951
9	I	0.17	0/866	0.31	0/1081
10	J	0.53	0/674	0.78	0/841
11	K	0.18	0/506	0.35	0/631
12	L	0.17	0/770	0.35	0/961
13	M	0.17	0/542	0.30	0/676
14	N	0.19	0/810	0.38	0/1011
15	O	0.20	0/786	0.47	1/981 (0.1%)
16	P	0.17	0/730	0.33	0/911
17	Q	0.17	0/738	0.30	0/921
18	R	0.20	0/750	0.41	0/936
19	S	0.16	0/686	0.32	0/856
20	T	0.44	1/634 (0.2%)	0.64	2/791 (0.3%)
21	U	0.17	0/398	0.31	0/496
22	V	0.22	0/542	0.34	0/676
23	X	0.17	0/482	0.29	0/601
24	Y	0.17	0/502	0.30	0/626
25	Z	0.17	0/538	0.31	0/671
26	a	0.80	3/590 (0.5%)	0.71	3/736 (0.4%)
27	c	0.17	0/386	0.27	0/481
28	d	0.17	0/434	0.31	0/541
29	e	0.17	0/506	0.32	0/631
30	f	0.49	1/422 (0.2%)	0.71	1/526 (0.2%)
31	g	0.17	0/446	0.32	0/556
32	h	0.17	0/474	0.29	0/591
33	i	0.17	0/394	0.31	0/491
34	j	0.57	1/346 (0.3%)	0.57	1/431 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	k	0.17	0/306	0.29	0/381
36	l	0.17	0/198	0.36	0/246
37	m	0.17	0/894	0.30	0/1116
38	n	0.17	0/846	0.31	0/1056
39	o	0.60	3/1386 (0.2%)	0.86	9/1731 (0.5%)
40	p	0.17	0/362	0.30	0/451
41	q	0.94	0/1950	0.91	1/2436 (0.0%)
42	r	0.56	1/1276 (0.1%)	0.92	4/1553 (0.3%)
43	s	0.43	4/8022 (0.0%)	0.50	9/10020 (0.1%)
44	t	0.34	0/250	0.52	0/311
45	u	0.92	0/1518	0.86	1/1896 (0.1%)
46	x	0.26	5/66581 (0.0%)	0.76	154/103823 (0.1%)
47	y	0.11	0/3743	0.64	0/5828
48	z	0.12	0/2880	0.64	0/4487
All	All	0.32	22/113534 (0.0%)	0.69	193/164435 (0.1%)

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
1	A	0	1
2	B	0	3
5	E	0	1
10	J	0	1
20	T	0	3
26	a	0	1
30	f	0	2
39	o	0	1
42	r	0	3
43	s	0	12
44	t	0	1
All	All	0	29

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	x	2699	G	O3'-P	41.80	2.11	1.61
43	s	825	TRP	C-N	-18.64	0.91	1.34
43	s	826	LEU	N-CA	17.84	1.82	1.46
26	a	111	LYS	N-CA	14.18	1.74	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	a	110	GLY	C-N	9.94	1.56	1.34

The worst 5 of 193 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	x	2699	G	P-O3'-C3'	-26.90	87.42	119.70
46	x	2700	G	O5'-P-OP2	26.12	142.05	110.70
46	x	2700	G	O5'-P-OP1	-25.82	79.71	110.70
43	s	858	GLU	O-C-N	-21.29	88.64	122.70
46	x	440	A	O5'-P-OP1	-19.66	87.11	110.70

There are no chirality outliers.

5 of 29 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	198	LYS	Peptide
2	B	18	PRO	Peptide
2	B	255	TRP	Peptide
2	B	256	HIS	Peptide
5	E	42	LEU	Mainchain

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1007	0	310	18	0
2	B	1543	0	433	4	0
3	C	1443	0	399	7	0
4	D	1183	0	325	1	0
5	E	622	0	160	1	0
6	F	887	0	241	3	0
7	G	931	0	242	1	0
8	H	763	0	215	3	0
9	I	867	0	230	2	0
10	J	675	0	191	11	0
11	K	507	0	140	1	0
12	L	771	0	199	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	M	543	0	145	2	0
14	N	811	0	221	3	0
15	O	787	0	214	7	0
16	P	731	0	197	4	0
17	Q	739	0	205	1	0
18	R	751	0	203	14	0
19	S	687	0	175	3	0
20	T	635	0	174	14	0
21	U	399	0	109	2	0
22	V	543	0	162	2	0
23	X	483	0	121	1	0
24	Y	503	0	134	1	0
25	Z	539	0	144	1	0
26	a	591	0	176	0	0
27	c	387	0	113	0	0
28	d	435	0	114	0	0
29	e	507	0	135	0	0
30	f	423	0	117	0	0
31	g	447	0	121	0	0
32	h	475	0	118	0	0
33	i	395	0	109	0	0
34	j	347	0	104	0	0
35	k	307	0	79	0	0
36	l	199	0	47	0	0
37	m	895	0	257	0	0
38	n	847	0	224	0	0
39	o	1387	0	358	0	0
40	p	363	0	108	0	0
41	q	1951	0	539	0	0
42	r	1304	0	336	0	0
43	s	8027	0	2141	0	0
44	t	251	0	68	0	0
45	u	1519	0	416	0	0
46	x	59475	0	29874	0	0
47	y	3350	0	1696	0	0
48	z	2576	0	1304	0	0
All	All	105808	0	43843	111	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 6.

The worst 5 of 111 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)
15:O:75:ALA:O	15:O:77:SER:N	1.85	1.10
20:T:62:GLY:N	20:T:75:ILE:H	1.51	1.08
20:T:43:LYS:O	20:T:95:HIS:CA	2.03	1.06
18:R:158:GLU:O	18:R:162:ARG:N	1.90	1.03
20:T:62:GLY:CA	20:T:75:ILE:H	1.72	1.03

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	250/254 (98%)	156 (62%)	70 (28%)	24 (10%)	0	10
2	B	384/387 (99%)	294 (77%)	71 (18%)	19 (5%)	2	20
3	C	359/362 (99%)	254 (71%)	80 (22%)	25 (7%)	1	14
4	D	294/297 (99%)	229 (78%)	53 (18%)	12 (4%)	3	23
5	E	152/176 (86%)	113 (74%)	35 (23%)	4 (3%)	5	31
6	F	220/244 (90%)	181 (82%)	30 (14%)	9 (4%)	3	23
7	G	231/256 (90%)	179 (78%)	43 (19%)	9 (4%)	3	23
8	H	189/191 (99%)	147 (78%)	37 (20%)	5 (3%)	5	31
9	I	215/217 (99%)	159 (74%)	48 (22%)	8 (4%)	3	24
10	J	167/174 (96%)	116 (70%)	29 (17%)	22 (13%)	0	5
11	K	125/165 (76%)	80 (64%)	29 (23%)	16 (13%)	0	5
12	L	191/199 (96%)	141 (74%)	39 (20%)	11 (6%)	1	18
13	M	134/138 (97%)	106 (79%)	22 (16%)	6 (4%)	2	22
14	N	201/204 (98%)	147 (73%)	44 (22%)	10 (5%)	2	20
15	O	195/199 (98%)	142 (73%)	38 (20%)	15 (8%)	1	13
16	P	181/184 (98%)	141 (78%)	35 (19%)	5 (3%)	5	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	Q	183/186 (98%)	143 (78%)	30 (16%)	10 (6%)	2	19
18	R	186/189 (98%)	136 (73%)	44 (24%)	6 (3%)	4	26
19	S	170/172 (99%)	133 (78%)	31 (18%)	6 (4%)	3	25
20	T	157/160 (98%)	90 (57%)	46 (29%)	21 (13%)	0	5
21	U	98/121 (81%)	77 (79%)	17 (17%)	4 (4%)	3	23
22	V	134/137 (98%)	95 (71%)	37 (28%)	2 (2%)	10	46
23	X	119/142 (84%)	91 (76%)	23 (19%)	5 (4%)	3	22
24	Y	124/127 (98%)	91 (73%)	26 (21%)	7 (6%)	2	19
25	Z	133/136 (98%)	97 (73%)	30 (23%)	6 (4%)	2	22
26	a	146/149 (98%)	91 (62%)	39 (27%)	16 (11%)	0	7
27	c	95/105 (90%)	84 (88%)	10 (10%)	1 (1%)	14	52
28	d	107/113 (95%)	88 (82%)	15 (14%)	4 (4%)	3	24
29	e	125/130 (96%)	99 (79%)	24 (19%)	2 (2%)	9	44
30	f	104/107 (97%)	78 (75%)	19 (18%)	7 (7%)	1	15
31	g	110/121 (91%)	78 (71%)	27 (24%)	5 (4%)	2	22
32	h	117/120 (98%)	92 (79%)	21 (18%)	4 (3%)	3	26
33	i	97/100 (97%)	78 (80%)	13 (13%)	6 (6%)	1	17
34	j	85/88 (97%)	53 (62%)	26 (31%)	6 (7%)	1	14
35	k	75/78 (96%)	66 (88%)	8 (11%)	1 (1%)	12	48
36	l	48/51 (94%)	33 (69%)	11 (23%)	4 (8%)	1	12
37	m	222/245 (91%)	170 (77%)	44 (20%)	8 (4%)	3	25
38	n	210/236 (89%)	156 (74%)	48 (23%)	6 (3%)	4	29
39	o	345/647 (53%)	218 (63%)	76 (22%)	51 (15%)	0	3
40	p	89/92 (97%)	72 (81%)	14 (16%)	3 (3%)	3	26
41	q	486/515 (94%)	459 (94%)	21 (4%)	6 (1%)	13	50
42	r	277/767 (36%)	152 (55%)	58 (21%)	67 (24%)	0	1
43	s	1998/4914 (41%)	1595 (80%)	228 (11%)	175 (9%)	1	11
44	t	61/199 (31%)	53 (87%)	6 (10%)	2 (3%)	4	26
45	u	378/380 (100%)	359 (95%)	9 (2%)	10 (3%)	5	31
All	All	9967/14174 (70%)	7612 (76%)	1704 (17%)	651 (6%)	2	16

5 of 651 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	122	ASP
1	A	128	ARG
1	A	133	TYR
1	A	135	ILE
1	A	137	ILE

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

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
46	x	2778/2779 (99%)	291 (10%)	0
47	y	157/158 (99%)	20 (12%)	0
48	z	120/121 (99%)	7 (5%)	0
All	All	3055/3058 (99%)	318 (10%)	0

5 of 318 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
46	x	22	G
46	x	49	A
46	x	60	A
46	x	66	A
46	x	92	G

There are no RNA pucker outliers to report.

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

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

## 5.5 Carbohydrates [i](#)

There are no 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
42	r	14
46	x	1
43	s	1

The worst 5 of 16 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	r	576:GLY	C	629:GLU	N	23.87
1	r	472:VAL	C	476:GLU	N	19.67
1	r	121:MET	C	126:LEU	N	18.70
1	r	228:GLY	C	240:ASN	N	15.12
1	r	436:VAL	C	440:ALA	N	14.62

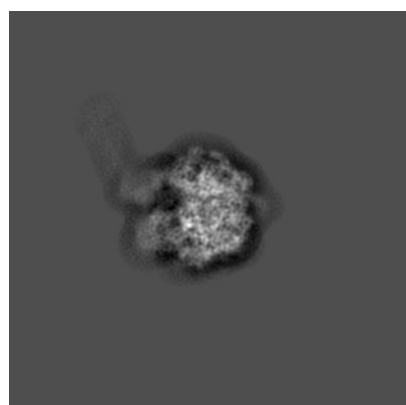
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3199. These allow visual inspection of the internal detail of the map and identification of artifacts.

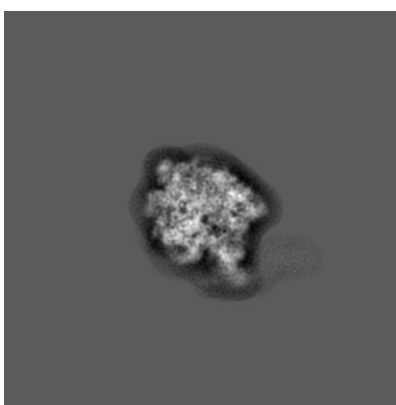
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

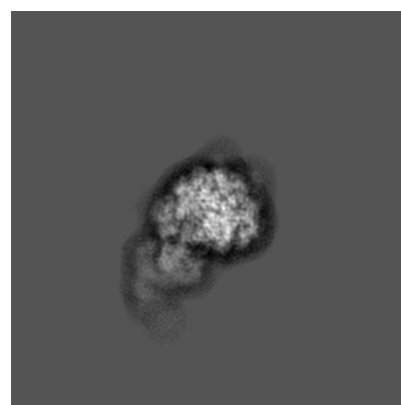
#### 6.1.1 Primary map



X



Y

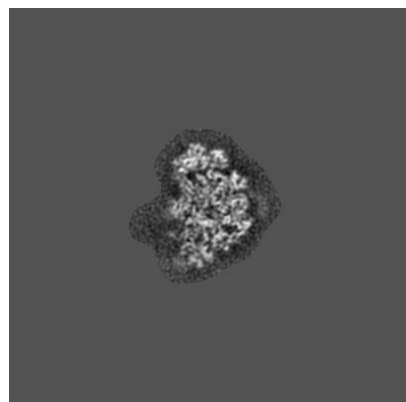


Z

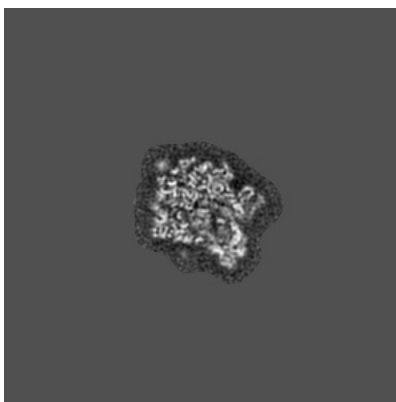
The images above show the map projected in three orthogonal directions.

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

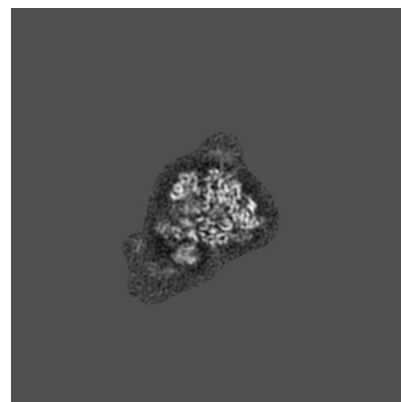
#### 6.2.1 Primary map



X Index: 200



Y Index: 200

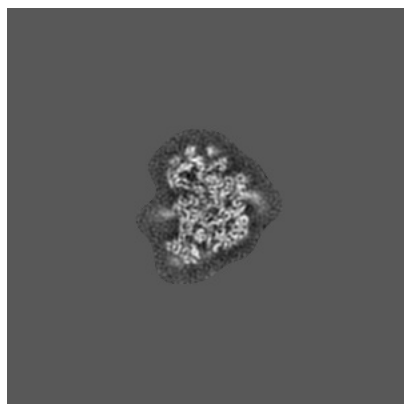


Z Index: 200

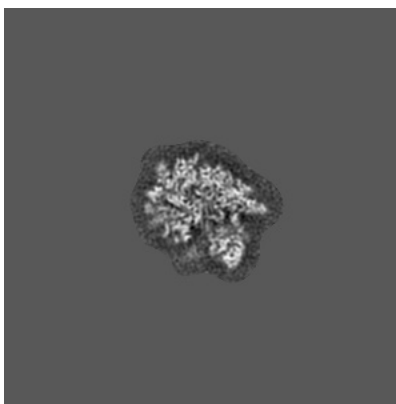
The images above show central slices of the map in three orthogonal directions.

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

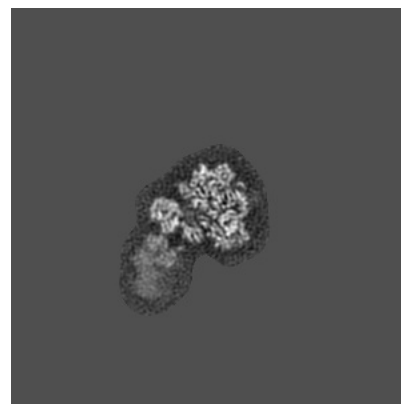
### 6.3.1 Primary map



X Index: 206



Y Index: 192



Z Index: 226

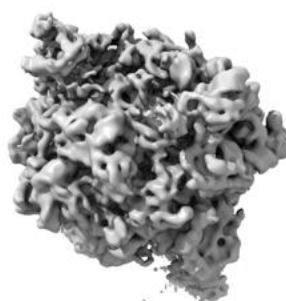
The images above show the largest variance slices of the map in three orthogonal directions.

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

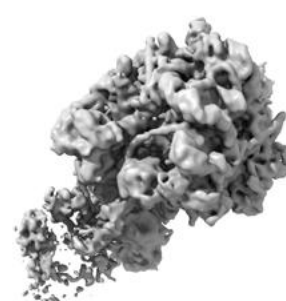
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.



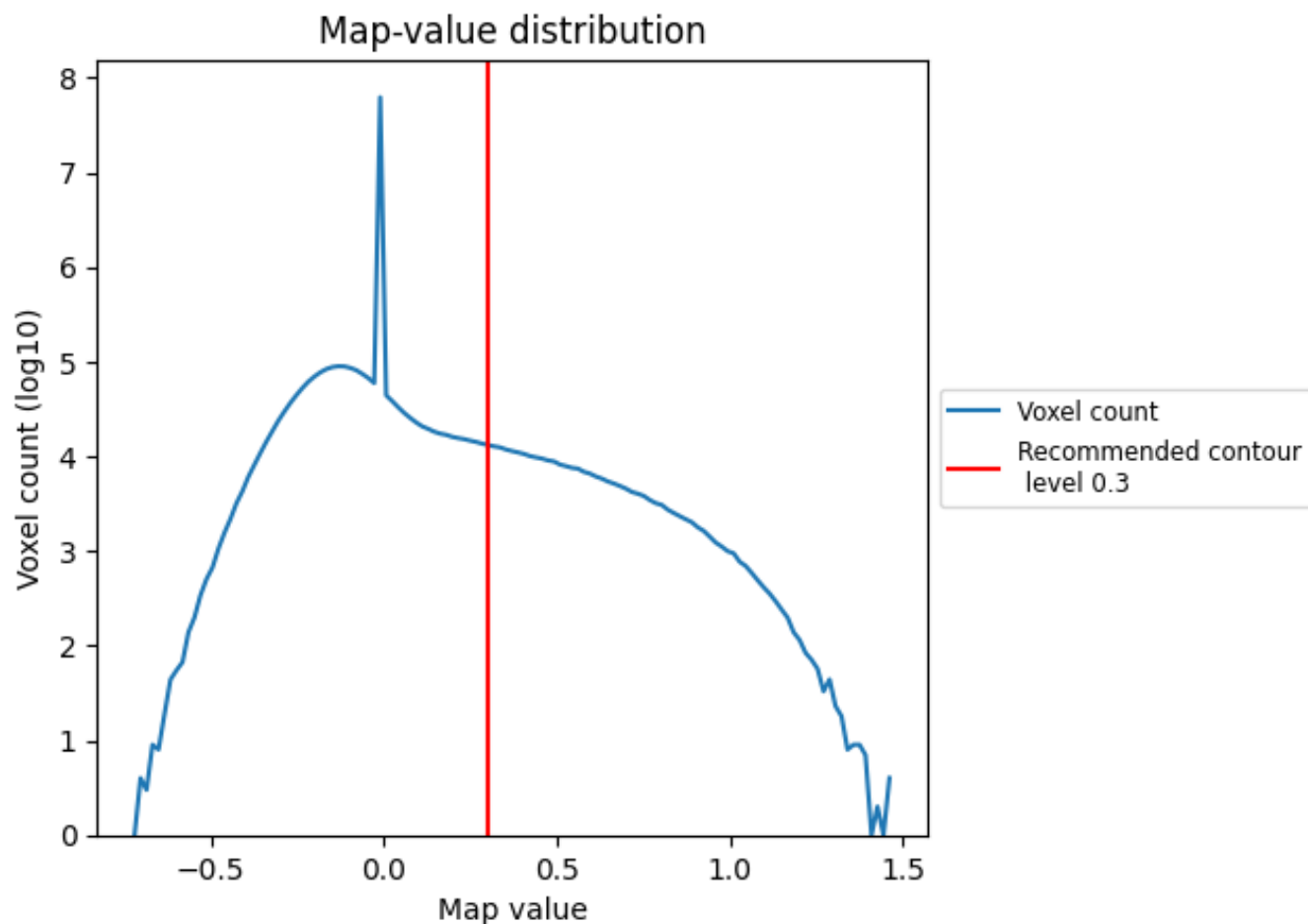
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

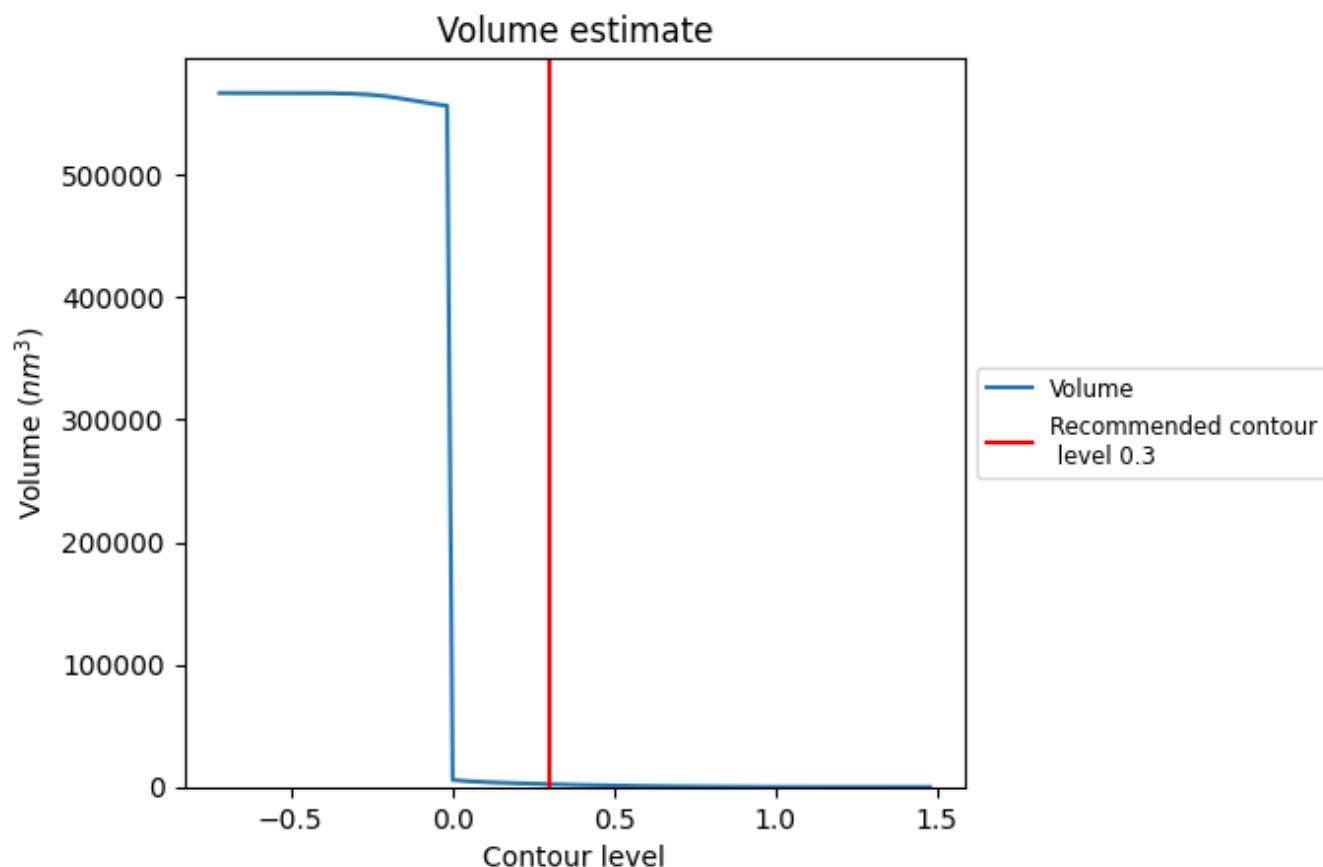
This section contains the results of statistical analysis of the map.

### 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.

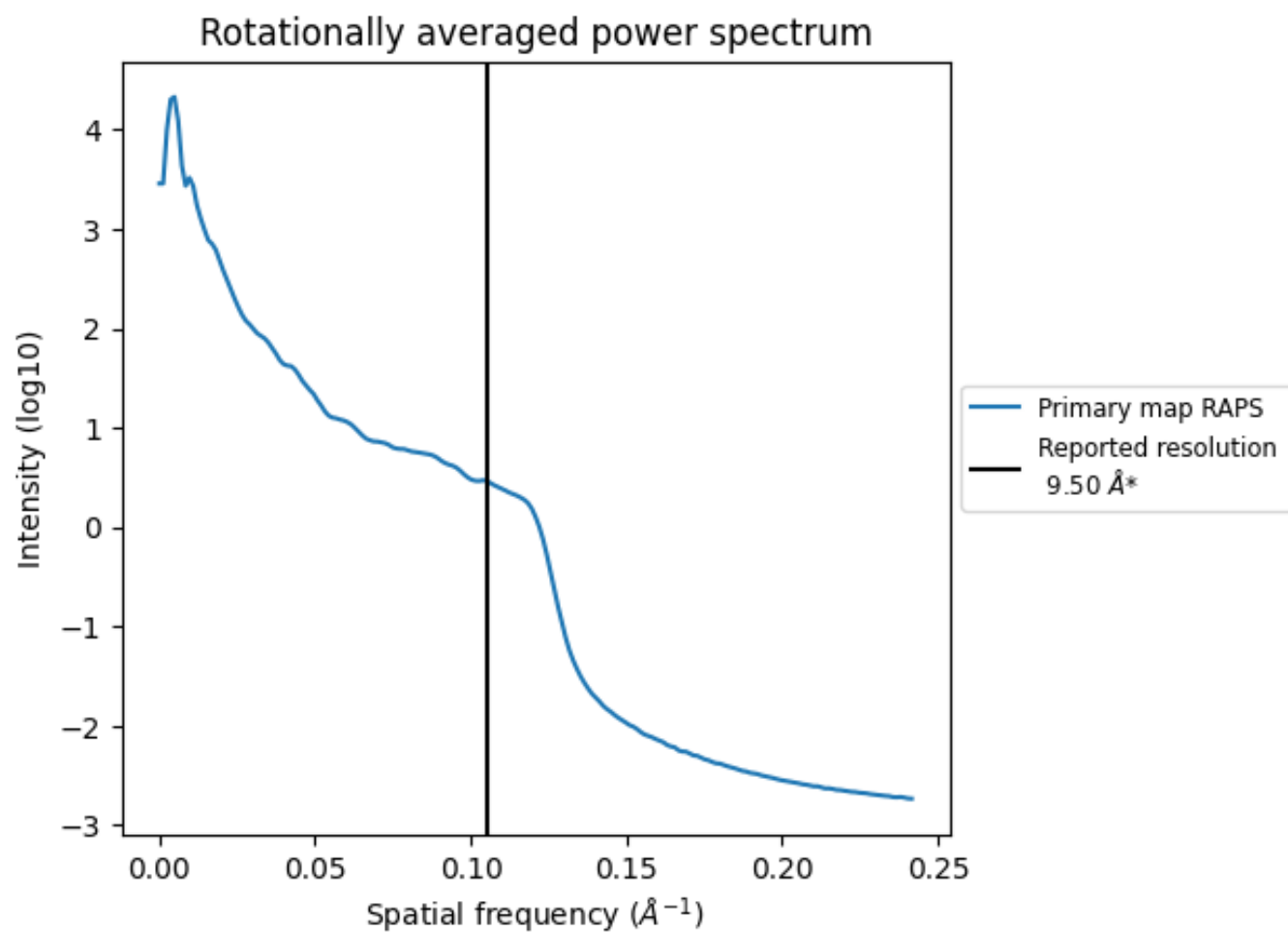
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2263 nm<sup>3</sup>; this corresponds to an approximate mass of 2044 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 0.105 Å<sup>-1</sup>

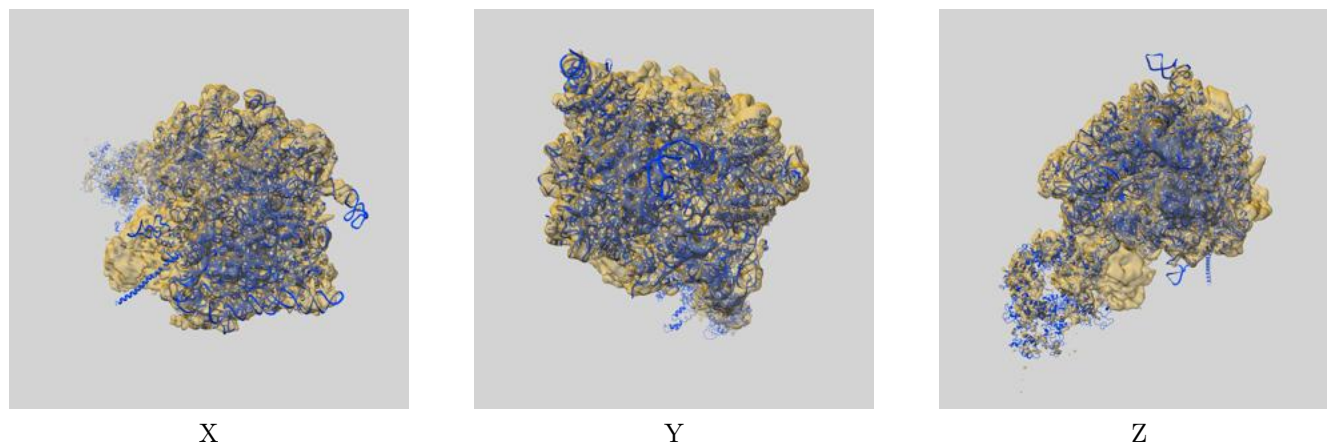
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

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

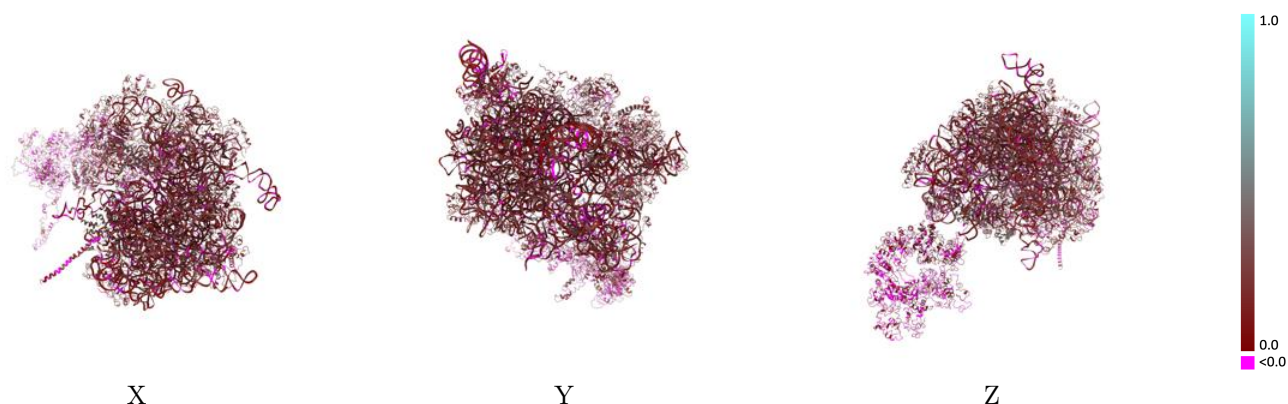
This section contains information regarding the fit between EMDB map EMD-3199 and PDB model 5FL8. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

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



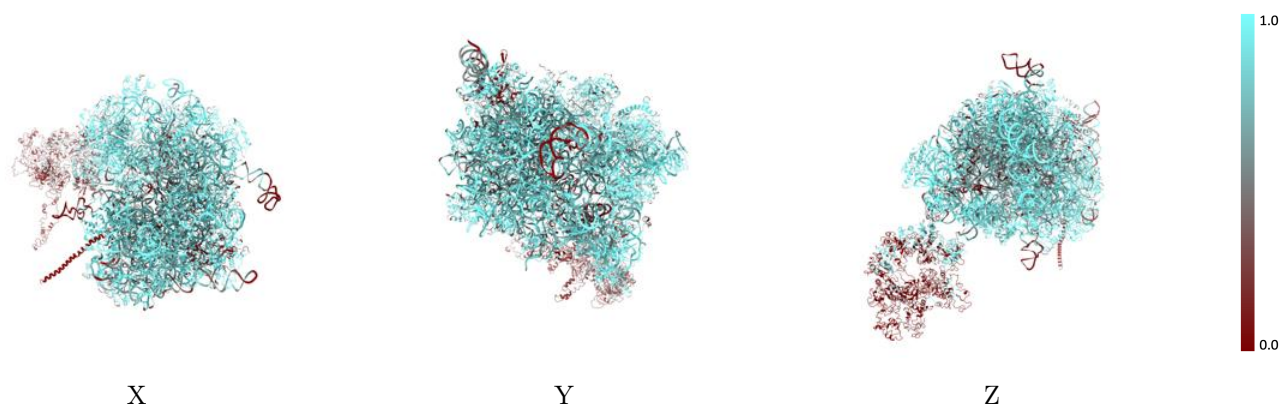
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



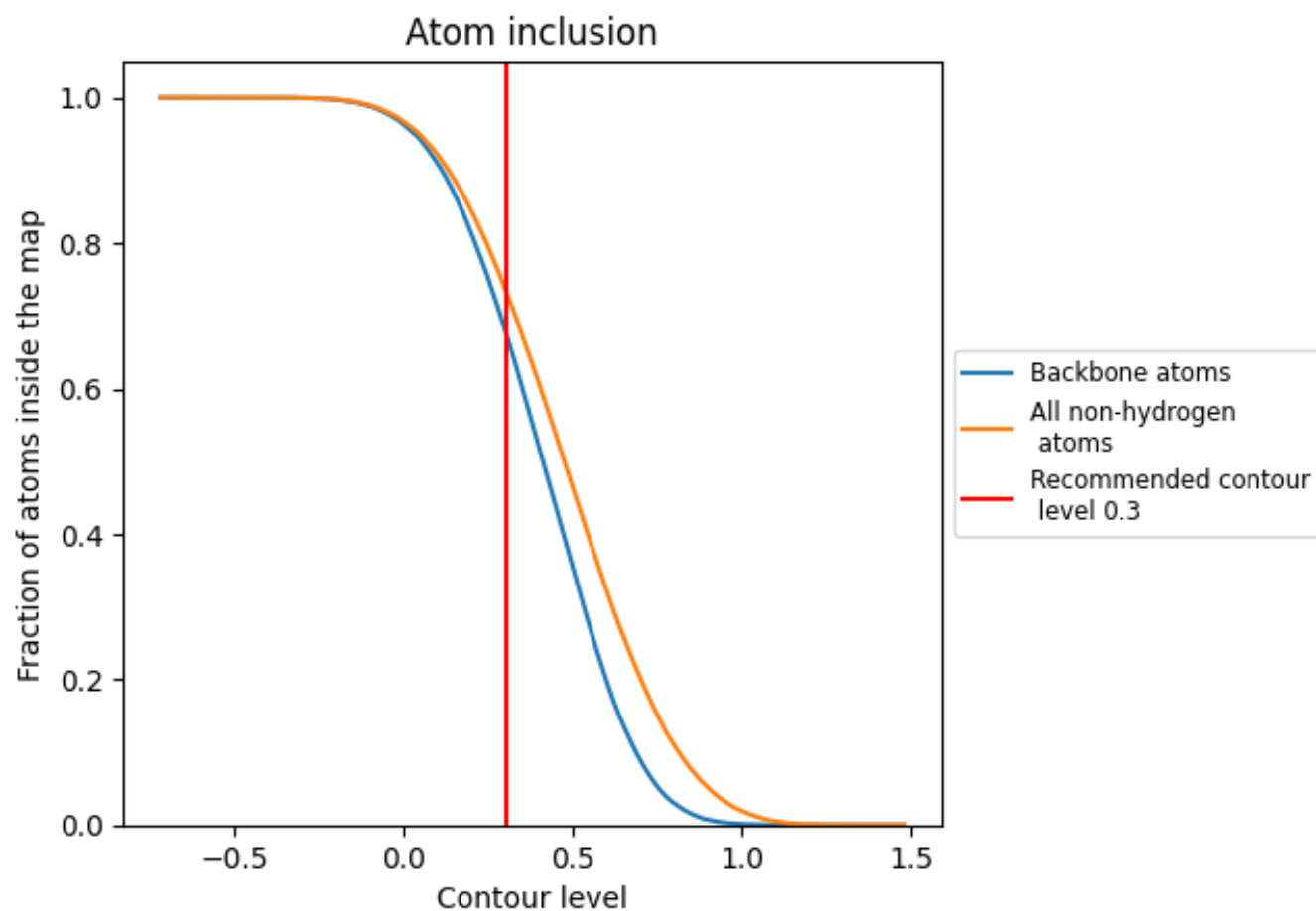
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

## 9.4 Atom inclusion [i](#)









































































At the recommended contour level, 68% of all backbone atoms, 74% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7350	 0.1470
A	 0.5511	 0.1290
B	 0.7673	 0.1550
C	 0.6972	 0.1630
D	 0.8292	 0.1870
E	 0.8119	 0.1920
F	 0.8760	 0.2180
G	 0.7905	 0.1700
H	 0.8742	 0.2110
I	 0.1442	 0.0270
J	 0.9748	 0.2210
K	 0.7712	 0.1550
L	 0.8119	 0.2240
M	 0.8545	 0.2110
N	 0.7152	 0.1600
O	 0.7548	 0.1840
P	 0.7004	 0.1780
Q	 0.6292	 0.1620
R	 0.4967	 0.1260
S	 0.8588	 0.2170
T	 0.3449	 0.0350
U	 0.9223	 0.2360
V	 0.7274	 0.1840
X	 0.6791	 0.1640
Y	 0.8032	 0.1760
Z	 0.8516	 0.1750
a	 0.5804	 0.1180
c	 0.8424	 0.2040
d	 0.7793	 0.1840
e	 0.7081	 0.1950
f	 0.7707	 0.1620
g	 0.5324	 0.1170
h	 0.8716	 0.2300
i	 0.7570	 0.1910
j	 0.5591	 0.1000



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Chain	Atom inclusion	Q-score
k	 0.8827	 0.2140
l	 0.6482	 0.1760
m	 0.9352	 0.1940
n	 0.9504	 0.2070
o	 0.8738	 0.2310
p	 0.6364	 0.1530
q	 0.8621	 0.1840
r	 0.9724	 0.3470
s	 0.2119	 0.0610
t	 0.8127	 0.1450
u	 0.5510	 0.1650
x	 0.7868	 0.1400
y	 0.8113	 0.1410
z	 0.8863	 0.1520