



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 10:05 AM EST

PDB ID : 4V6L
EMDB ID : EMD-1850
Title : Structural insights into cognate vs. near-cognate discrimination during decoding.
Authors : Agirrezabala, X.; Schreiner, E.; Trabuco, L.G.; Lei, J.; Ortiz-Meoz, R.F.; Schulten, K.; Green, R.; Frank, J.
Deposited on : 2011-01-07
Resolution : 13.20 Å (reported)
Based on initial models : 3FIH, 2I2U

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

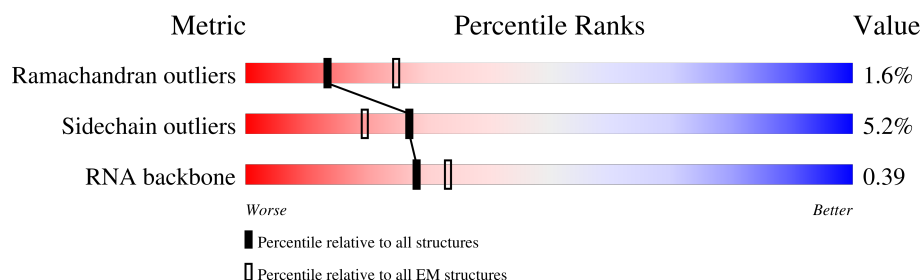
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (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 13.20 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)
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 ≥ 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	1542	
2	AB	76	
2	AE	76	
3	AC	393	
4	AD	24	
5	AF	241	
6	AG	233	
7	AH	206	

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Mol	Chain	Length	Quality of chain
8	AI	167	
9	AJ	135	
10	AK	179	
11	AL	130	
12	AM	130	
13	AN	103	
14	AO	129	
15	AP	124	
16	AQ	118	
17	AR	101	
18	AS	89	
19	AT	82	
20	AU	84	
21	AV	75	
22	AW	92	
23	AX	87	
24	AY	71	
25	BA	120	
26	BB	2904	
27	BC	234	
28	BD	273	
29	BE	209	
30	BF	201	
31	BG	179	
32	BH	177	

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Mol	Chain	Length	Quality of chain
33	BI	149	
34	BJ	142	
35	BK	142	
36	BL	123	
37	BM	144	
38	BN	136	
39	BO	127	
40	BP	117	
41	BQ	115	
42	BR	118	
43	BS	103	
44	BT	110	
45	BU	100	
46	BV	104	
47	BW	94	
48	BX	85	
49	BY	78	
50	BZ	63	
51	Ba	59	
52	Bb	70	
53	Bc	57	
54	Bd	55	
55	Be	46	
56	Bf	65	
57	Bg	38	

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 153634 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
1	AA	1542	Total	C	N	O	P	0	0
			33089	14767	6064	10717	1541		

- Molecule 2 is a RNA chain called A/T-site tRNA Phe.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	AB	76	Total	C	N	O	P	S	0	0
			1635	735	291	532	75	2		
2	AE	76	Total	C	N	O	P	S	0	0
			1635	735	291	532	75	2		

- Molecule 3 is a protein called Elongation factor Tu 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	393	Total	C	N	O	S	0	0
			3036	1918	523	582	13		

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	24	Total	C	N	O	P	0	0
			495	222	68	181	24		

- Molecule 5 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AF	240	Total	C	N	O	S	0	0
			1872	1180	332	352	8		

- Molecule 6 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AG	232	Total	C	N	O	S	0	0
			1822	1149	346	323	4		

- Molecule 7 is a protein called 30S ribosomal protein S4.

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

- Molecule 8 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AI	166	Total	C	N	O	S	0	0
			1225	761	232	226	6		

- Molecule 9 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AJ	135	Total	C	N	O	S	0	0
			1101	677	198	219	7		

- Molecule 10 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AK	178	Total	C	N	O	S	0	0
			1400	874	269	253	4		

- Molecule 11 is a protein called 30S ribosomal protein S8.

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

- Molecule 12 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AM	129	Total	C	N	O	S	0	0
			1036	642	208	183	3		

- Molecule 13 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AN	103	Total	C	N	O	S	0	0
			825	514	158	151	2		

- Molecule 14 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AO	128	Total	C	N	O	S	0	0
			965	595	196	171	3		

- Molecule 15 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AP	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 16 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AQ	117	Total	C	N	O	S	0	0
			910	564	183	160	3		

- Molecule 17 is a protein called 30S ribosomal protein S14.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AS	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 19 is a protein called 30S ribosomal protein S16.

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

- Molecule 20 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AU	83	Total	C	N	O	S	0	0
			672	425	124	120	3		

- Molecule 21 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AV	74	Total	C	N	O	S	0	0
			626	395	123	107	1		

- Molecule 22 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AW	91	Total	C	N	O	S	0	0
			727	464	139	122	2		

- Molecule 23 is a protein called 30S ribosomal protein S20.

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

- Molecule 24 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AY	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 25 is a RNA chain called 50S ribosomal RNA 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BA	120	Total	C	N	O	P	0	0
			2566	1144	468	835	119		

- Molecule 26 is a RNA chain called 50S ribosomal RNA 23S.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BB	2904	Total	C	N	O	P	0	0
			62351	27824	11469	20155	2903		

- Molecule 27 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BC	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

- Molecule 28 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BD	272	Total	C	N	O	S	0	0
			2092	1294	425	366	7		

- Molecule 29 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BE	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 30 is a protein called 50S ribosomal protein L4.

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

- Molecule 31 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BG	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 32 is a protein called 50S ribosomal protein L6.

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

- Molecule 33 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BI	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 34 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BJ	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 35 is a protein called 50S ribosomal protein L13.

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

- Molecule 36 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BL	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 37 is a protein called 50S ribosomal protein L15.

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

- Molecule 38 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BN	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 39 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BO	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

- Molecule 40 is a protein called 50S ribosomal protein L18.

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

- Molecule 41 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BQ	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 42 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BR	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 43 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BS	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 44 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BT	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 45 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BU	100	Total	C	N	O	S	0	0
			787	496	146	143	2		

- Molecule 46 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BV	103	Total	C	N	O		0	0
			789	498	148	143			

- Molecule 47 is a protein called 50S ribosomal protein L25.

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

- Molecule 48 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BX	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 49 is a protein called 50S ribosomal protein L28.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BZ	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 51 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ba	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 52 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Bb	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 53 is a protein called 50S ribosomal protein L32.

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

- Molecule 54 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	Bd	54	Total	C	N	O	0	0
			441	284	81	76		

- Molecule 55 is a protein called 50S ribosomal protein L34.

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

- Molecule 56 is a protein called 50S ribosomal protein L35.

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

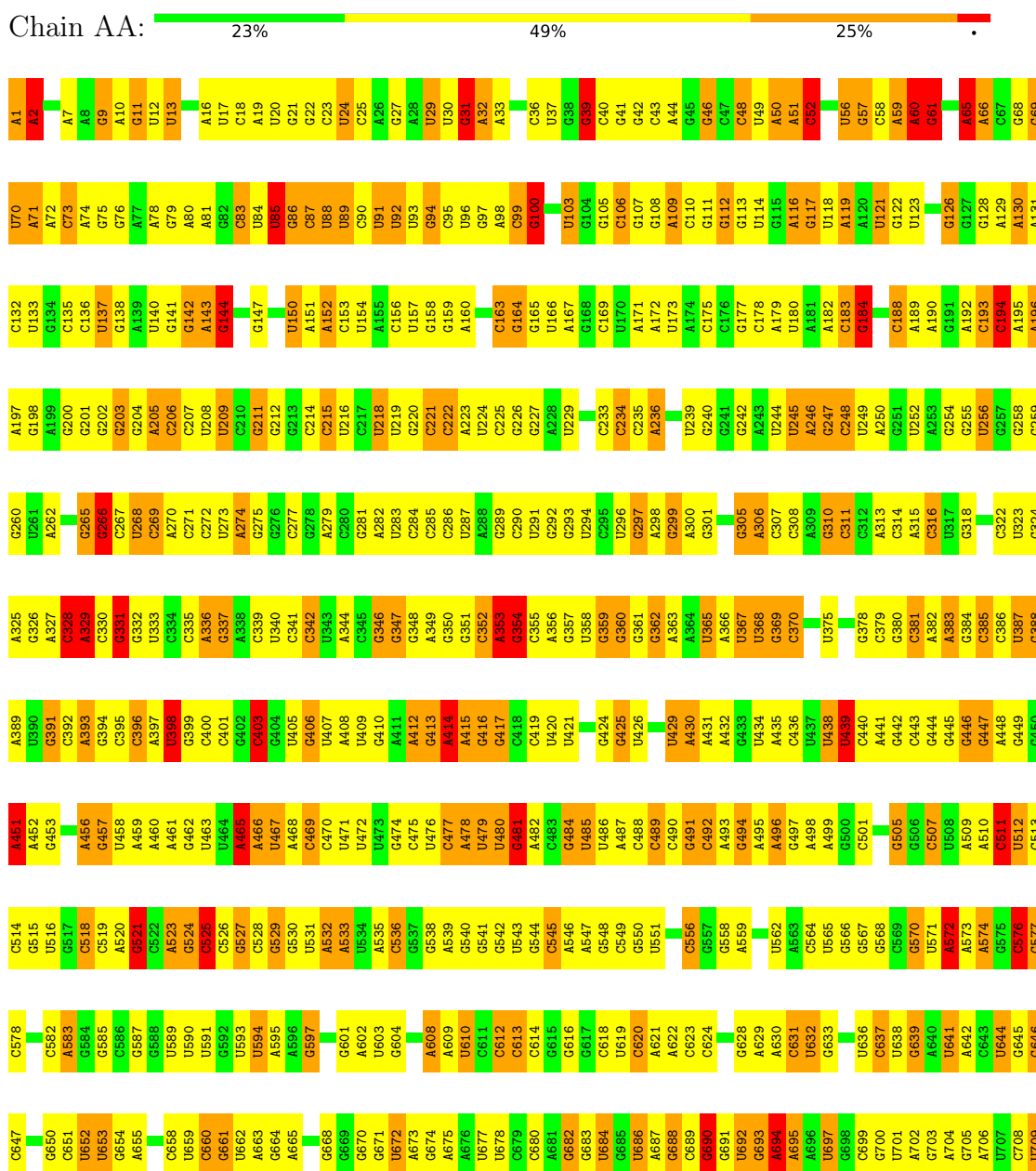
- Molecule 57 is a protein called 50S ribosomal protein L36.

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

3 Residue-property plots

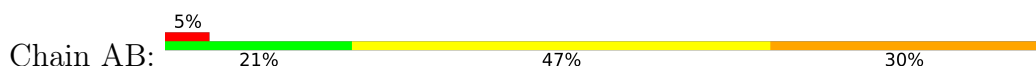
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

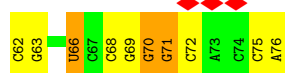
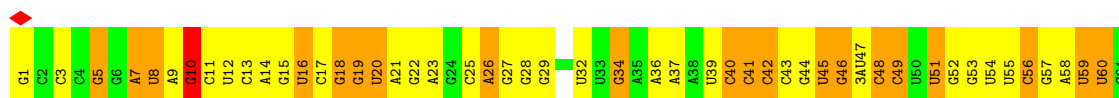
• Molecule 1: 16S ribosomal RNA



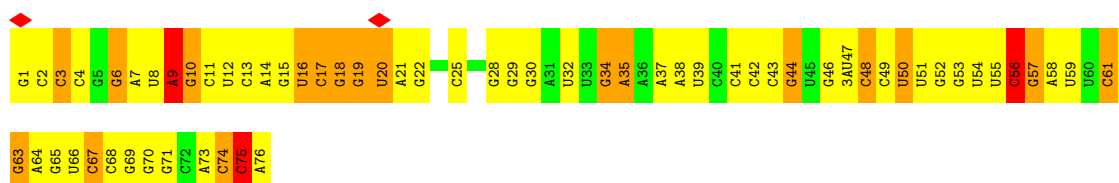
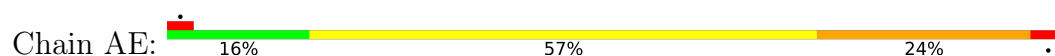
A1542	A1480	G1415	U1351	C1218	U1091	G1154	U1091	C1028	G966	C899	U837	G776	G710
	U1481	G1416	C1352	A1219	A1092	A1155	A1092	U1029	G966	A900	G838	A777	G711
	G1482	G1417	G1353	G1220	G1093	A1156	G1093	U1030	C967	A901	C839	A778	A712
	A1483	G1418	U1354	G1221	G1094	A1157	G1094	C1031	A968	G902	C840	G779	G713
	C1484	G1419	G1355	G1222	U1095	C1158	U1095	G1032	A969	G903	C841	A780	G714
	U1485		G1356	C1223	C1096	U1159	C1096	G1033	C970	G904	U842	A781	A715
	G1486	U1424	A1357	U1224	C1097	G1160	C1097	G1034	G971	U905	U843	A782	
	G1487	U1425	U1358	A1225	C1098	C1161	C1098	A1035	C972	A906	G844	C783	C719
	G1488	G1426	C1359	C1226	G1099	C1162	G1099	A1036	G973	A907	A845	C784	C720
	U1489	C1427	A1360	A1227	C1100	A1163	C1100	C1037	A974	A908	G846	G785	G721
	U1490	G1428	G1361	C1228	A1101	C1164	A1101	C1038	A975	A909	G847	G786	G722
	G1491	A1429	U1362	A1229	C1102	U1165	C1102	G1039	G976	C910	C848	A787	U723
	A1492	C1430	C1363	C1230	C1103	U1166	C1103	U1040	A977	U911	G849	U788	G724
	A1493	A1431	U1364	G1231	G1104	A1169	G1104	G1041	A978	G912	U850	G789	G725
	G1494	U1299	C1365	U1232	A1105	C1172	A1105	A1042	C979	A913	G851	A790	C726
	U1495	G1300	G1233	G1233		C1173		G1043	C980	G791			
	C1496	U1301	C1234	C1234	C1109	U1173	C1109	A1044	U981	A915	U854	A792	C732
	G1497	C1302	U1235	U1235	A1110	G1174	A1110	C1045	U982	A916	U855	U793	G733
	U1498	C1303	A1236	C1237	C1111	G1175	C1111	A1046	A983	U917	C856	A794	G734
	A1499	G1304	C1237		C1112	A1176	C1112	G1047	C984		C857	C795	C735
	U1500	U1372		G1241	C1113	G1177	C1113	G1048	C985	U920	G858	C796	C736
	C1501	G1373	A1306	G1242	C1114	G1178	C1114	U1049	U986	U921	G859	C797	C737
	A1502	U1374	U1307	G1243	U1115	A1179	U1115	G1050	G987	G922	A860	U798	C738
	G1503	U1375	U1308	C1243	U1116	A1180	U1116	C1051	G988	A923	G861	G799	C739
	U1504	U1376	G1309	C1244	C1117	G1181	C1117	U1052	U989		C862	U740	U740
	G1505	A1377	G1310	C1245	U1118	G1182	U1118	G1053	C990	G928	U863	U801	G741
	U1506	C1378	A1311	A1246	C1119	U1183	C1119	C1054	U991	G929	A864	A802	G742
	A1507	G1379	G1312	U1247	C1120	G1184	C1120	A1055	U992	C930	A865	G803	A743
	U1508	U1380	A1248	C1248	U1121	G1185	U1121	U1056	A993	C931	C866	U804	C744
	C1509	C1381	C1249	C1249	U1122	G1186	U1122	G1057	G994	C932	G867	G805	G745
		U1382	A1250		U1123	G1187	U1123	C1058	C995	G933	C868	C806	A746
	U1512	C1383		G1253	G1124	A1188	G1124	C1059	A996	C934	G869	A807	A747
	A1513	U1449	C1384	C1254	U1125	G1189	U1125	U1060	U997	A935	U870	G808	G748
	G1514	U1450	G1385	A1254	U1126	G1190	U1126	G1061	C998	C936	U871	G809	A749
	U1515	U1451		G1255	G1127	A1191	G1127	U1062	C999	A937	A872	C810	C750
	C1521	G1452	C1391	C1256	C1128	C1192	C1128	C1063	C1001	A938	A873	C811	U751
	U1522	G1453	U1392	A1256	C1129	G1193	C1129	G1064	G1002		G874	G812	G752
	G1523	G1454	C1388	A1257	U1194	U1194	A1130	U1065	G1003	G941	U875	U813	A753
		U1455	U1389	G1258	C1195	C1195	G1131	C1066	G1004	G942	C876	A814	A754
	A1518	A1456	U1391	C1259	A1196	C1196	C1132	A1067	A1005	U943	C877	A815	G755
	U1519	G1457	G1392	G1260	A1197	C1197	G1133	G1068	G1006	G944	A878	A816	C756
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	U1522	G1459	U1396	G1265	U1199	C1200	U1135	U1070	U1008	A946	C880	G818	C758
	G1526	G1460	C1397	G1266	C1201	C1201	C1136	C1071	U1009	G947	G881	A819	A759
	U1527	C1461	A1398	C1267	A1201	U1201	C1137	G1072	C948	C948	C882	U820	G760
	U1528	U1462	C1399	G1268	U1202	C1202	G1138	U1073	A949	U950	C883	G821	G761
	G1529	U1463	C1400	A1269	C1203	C1203	G1139	G1074	U951	G951	G884	U822	U762
	U1530	A1465	G1401	G1270	C1140	U1204	C1140	U1075	G952	G952	G885	G823	G763
	A1531	C1466	C1402	A1271	C1141	U1205	C1141	U1076	G953	G953	G886	G824	C764
	U1532	C1467		G1272	G1142	G1206	G1142	G1077	A1014	G954	G887	A825	G765
	C1533	G1405	G1337	C1273	G1143	G1207	G1143	U1078	G1015	G954	G888	C826	A766
	A1534	U1406	U1338	C1274	G1144	C1208	G1144	U1083	U1016	U955	A889	A767	A767
	C1535	C1407	A1339	A1275	A1145	C1209	A1145	U1017	U1016	U956	G890	U828	A768
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● Molecule 2: A-/T-site tRNA Phe

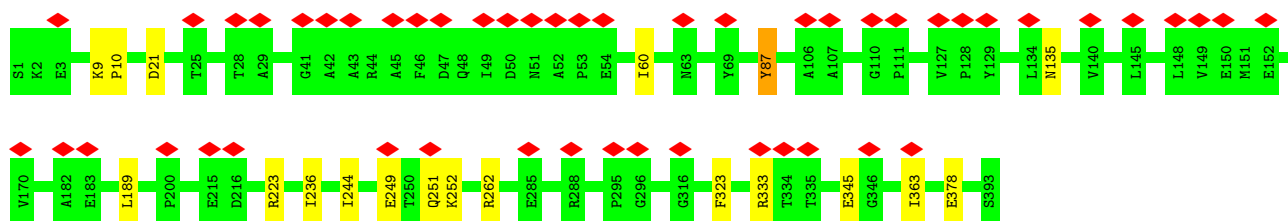




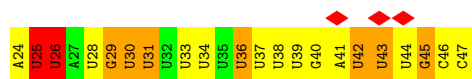
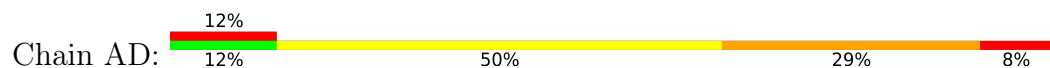
• Molecule 2: A/T-site tRNA Phe



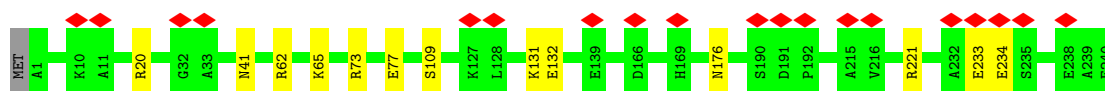
• Molecule 3: Elongation factor Tu 2



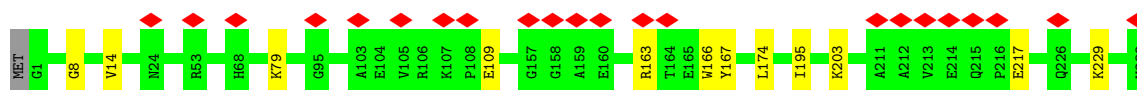
• Molecule 4: mRNA



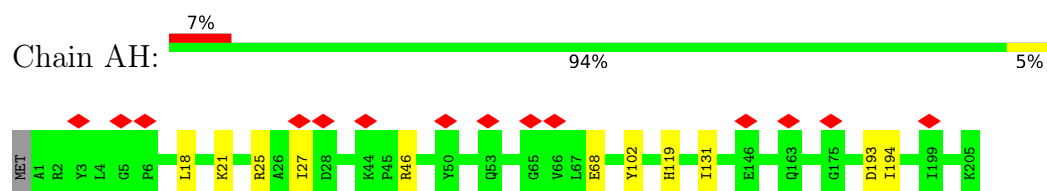
• Molecule 5: 30S ribosomal protein S2



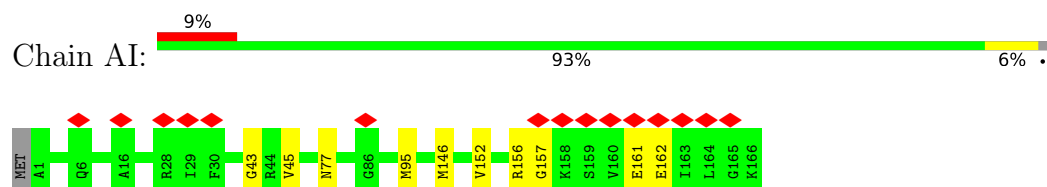
• Molecule 6: 30S ribosomal protein S3



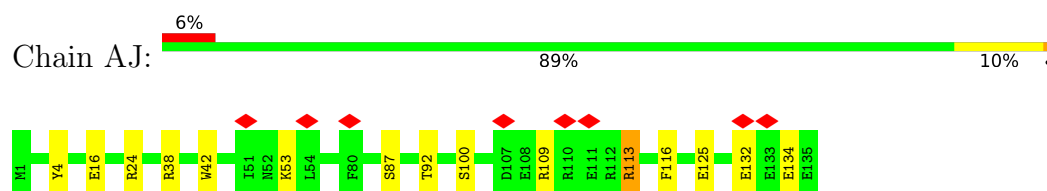
• Molecule 7: 30S ribosomal protein S4



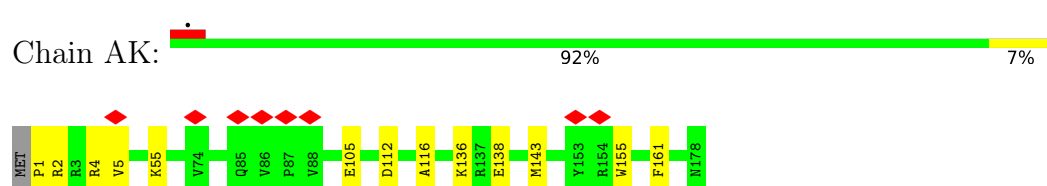
• Molecule 8: 30S ribosomal protein S5



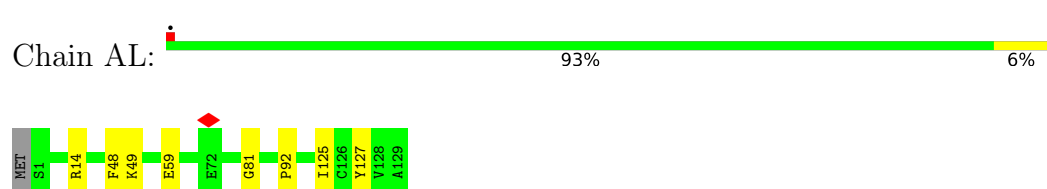
• Molecule 9: 30S ribosomal protein S6



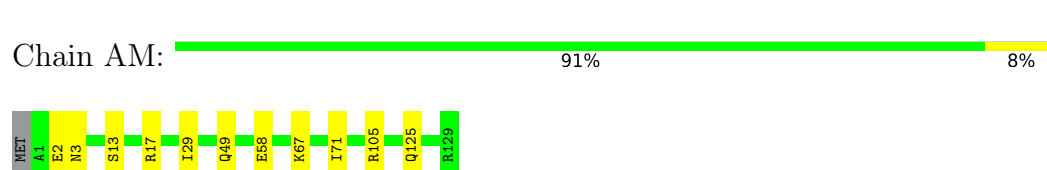
• Molecule 10: 30S ribosomal protein S7



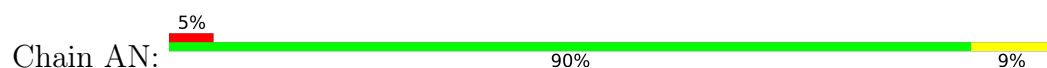
• Molecule 11: 30S ribosomal protein S8



• Molecule 12: 30S ribosomal protein S9

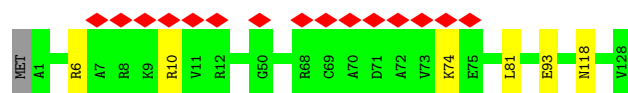


• Molecule 13: 30S ribosomal protein S10

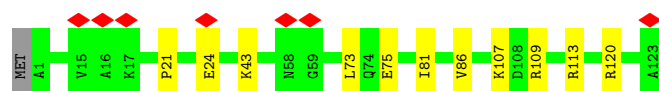
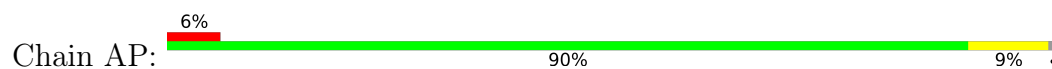




- Molecule 14: 30S ribosomal protein S11



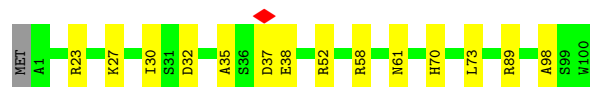
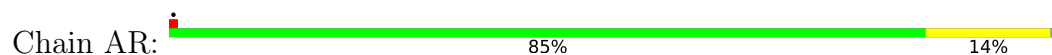
- Molecule 15: 30S ribosomal protein S12



- Molecule 16: 30S ribosomal protein S13



- Molecule 17: 30S ribosomal protein S14



- Molecule 18: 30S ribosomal protein S15



- Molecule 19: 30S ribosomal protein S16



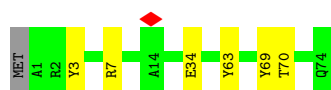
- Molecule 20: 30S ribosomal protein S17

Chain AU:  96% ..



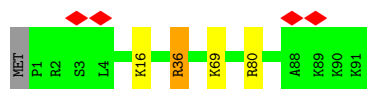
- Molecule 21: 30S ribosomal protein S18

Chain AV:  91% 8% .



- Molecule 22: 30S ribosomal protein S19

Chain AW:  95% ..




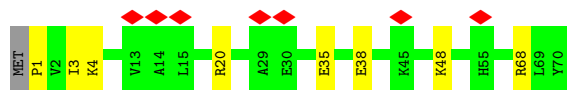
- Molecule 23: 30S ribosomal protein S20

Chain AX:  94% 5% .



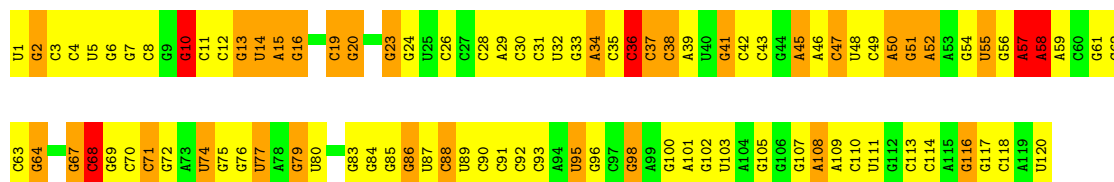
- Molecule 24: 30S ribosomal protein S21

Chain AY:  10% 87% 11% .



- Molecule 25: 50S ribosomal RNA 5S

Chain BA:  21% 50% 25% .



- Molecule 26: 50S ribosomal RNA 23S

Chain BB:  21% 49% 26% .

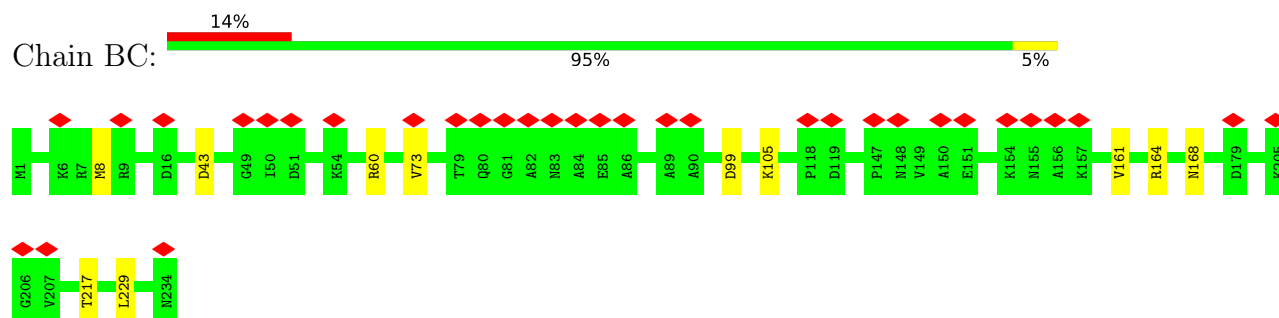
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C937	C874	U813	A752	G500	A439	G378	C318	C257	C192	C130	C66	U3
G938	C875	C814	A753	A501	C440	G379	G319	G258	U193	A131	U67	U4
G939	C876	C815	A754	A502	U441	G380	A320	G259	G194	G132	C68	A5
G940	A877	C816	A755	A503	G442	G381	U321	G260	A195	U133	C69	A6
A941	C878	C817	G757	A504	A443	A382	A322	G261	A196	G134	G70	G7
G942	C879	G818	G758	A505	C444	C383	C323	A262	C201	U135	A71	C8
A943	G880	A819	G759	A506	C445	A384	A324	G263	U202	G136	U72	C9
C944	C881	A820	A760	C509	C446	C385	G325	C264	A203	U137	A73	A10
A945	C882	A821	G761	C510	A447	C386	G326	A265	A204	U138	A74	C11
C946	G883	G822	U762	C511	U448	U387	G327	G266	G205	U139	G75	U12
G947	G884	C823	G763	U511	A449	C388	U328	C267	A206	C140	C76	U13
C948	C885	U824	A764	C512	G450	G389	G329	C268	U206	G141		A14
A949	G886	A825	G765	A513	U451	U390	A330	C269	A207	A142	G80	G15
G950	C887	U826	U766	A514	C452	A391	A331	C270	C208	A143	G81	C16
C951	C888	U827	U767	A515		U392	A332	G271	C209	A144	U82	G17
G952	G889	U828	G768	C516	C455	C393	G333	A272	C210	A145	A83	U18
C953	C890	A829	U769	C517	C456	C394	C334	G273	C211	A146	A84	A19
G954	G891	G830	G770	C518	A457	U395	C335	C274	G212	C147	G85	C20
U955	C892	G831	G771	U519	C458	G396	C336	C275	A213	U148	G86	A21
G956	C893	U832	C772	C520	U459	U397	G337	U276	G214	A149	U87	C22
C957	U894	A833	U773	U521	A460	C398	G338	G277	G215	U150	G88	C23
U958	C895	G834	G774	C522	C461	U399	U339	A278	A216	C151	A89	G24
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C960	C897	G836	G776	G524	C463	A401	C341	U280	A219	U153	A91	G26
U961	C898	C837	G777	U525	U464	A402	A342	C281	G220	U154	U92	G27
G962	A899	A838	A778	A526	G465	U403	A343	A282	A221	A155	G93	A28
U963	C899	U839	U779	C527	A466	A404	A344	U283	A222	A156	A94	U29
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G965	C903	G841	A781	A529	C468	G406	A346	G285	U224	U158	C96	C31
U966	G904	U842	A782	C530	C469	G407	A347	U286	C225	G159	C97	C32
A967	A905	G843	A783	C531	A470	G408	A348	G287	A226	A160	G98	C33
C968	U906	A844	G784	A532	A471	G409	U349	U288	A227		U99	U34
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A973	A911	U850	A789	U538	G476	C414	A354	U293		A167	A104	U39
G974	C912	C851	U790	A538	A477	A415	U355	A294	U234	G168	C105	U40
A975	U913	U852	C791	C539	C478	U416	G356	G295	U235	G169		C41
C976	G914	C853	A792	C540	A479	C417	C357	U296	C236	U170	G108	A42
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C1924	G1862	G1797	C1732	A1671	C1611	A1548	U1486	G1418	G1356	G1292	A1103	C1167	G1042	G1042
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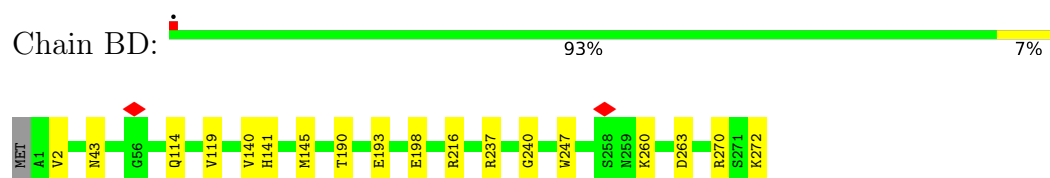
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U2903
U2904

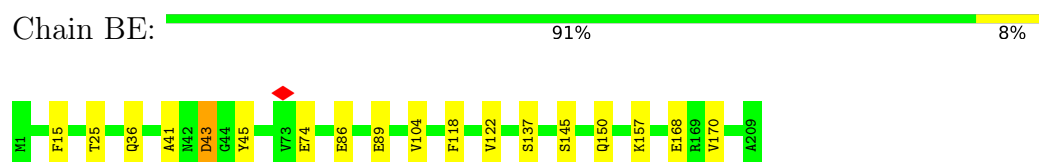
- Molecule 27: 50S ribosomal protein L1



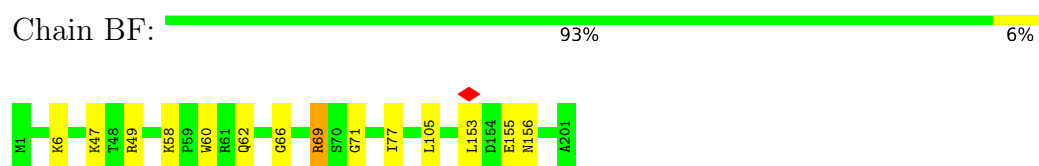
- Molecule 28: 50S ribosomal protein L2



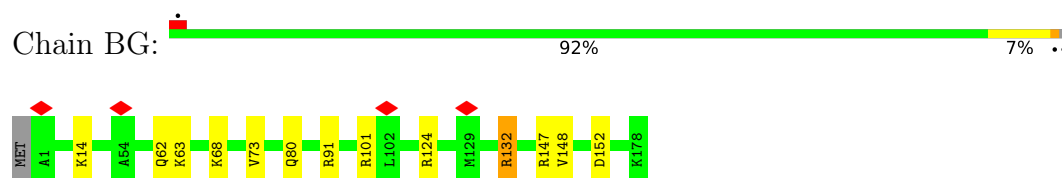
- Molecule 29: 50S ribosomal protein L3



- Molecule 30: 50S ribosomal protein L4



- Molecule 31: 50S ribosomal protein L5

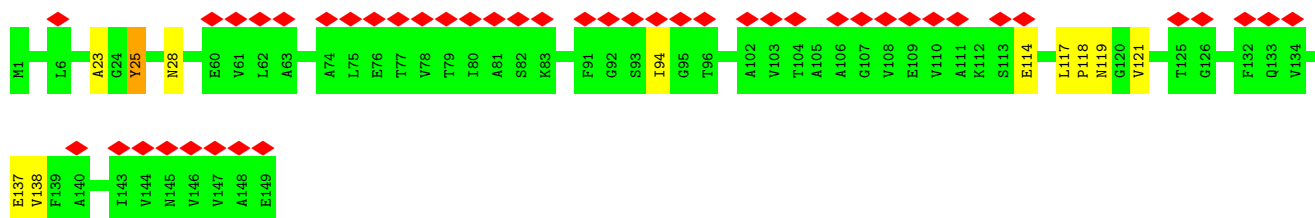


- Molecule 32: 50S ribosomal protein L6





- Molecule 33: 50S ribosomal protein L9



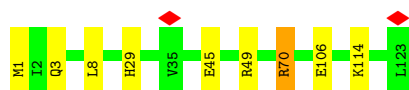
- Molecule 34: 50S ribosomal protein L11



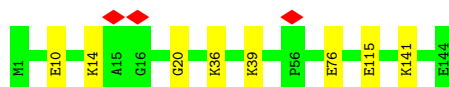
- Molecule 35: 50S ribosomal protein L13



- Molecule 36: 50S ribosomal protein L14



- Molecule 37: 50S ribosomal protein L15



- Molecule 38: 50S ribosomal protein L16





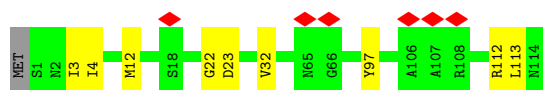
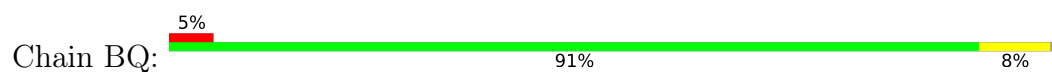
- Molecule 39: 50S ribosomal protein L17



- Molecule 40: 50S ribosomal protein L18



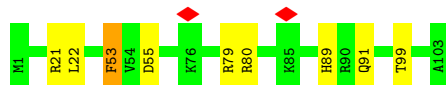
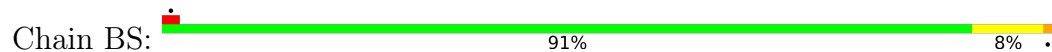
- Molecule 41: 50S ribosomal protein L19



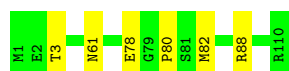
- Molecule 42: 50S ribosomal protein L20



- Molecule 43: 50S ribosomal protein L21

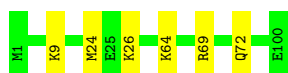


- Molecule 44: 50S ribosomal protein L22

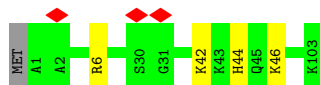


- Molecule 45: 50S ribosomal protein L23

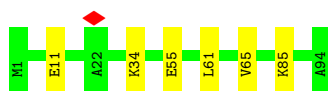




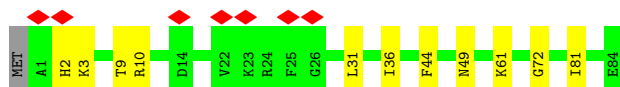
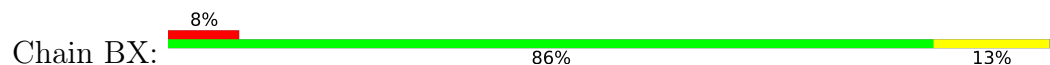
- Molecule 46: 50S ribosomal protein L24



- Molecule 47: 50S ribosomal protein L25



- Molecule 48: 50S ribosomal protein L27



- Molecule 49: 50S ribosomal protein L28



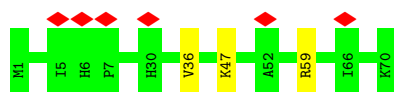
- Molecule 50: 50S ribosomal protein L29



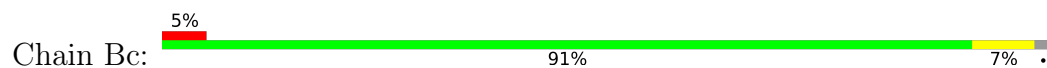
- Molecule 51: 50S ribosomal protein L30



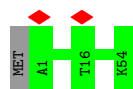
- Molecule 52: 50S ribosomal protein L31



- Molecule 53: 50S ribosomal protein L32



- Molecule 54: 50S ribosomal protein L33



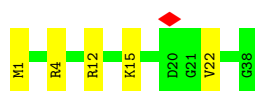
- Molecule 55: 50S ribosomal protein L34



- Molecule 56: 50S ribosomal protein L35



- Molecule 57: 50S ribosomal protein L36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	26873	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	59000	Depositor
Image detector	TVIPS TEMCAM-F415 (4k x 4k)	Depositor
Maximum map value	267.364	Depositor
Minimum map value	-80.270	Depositor
Average map value	5.966	Depositor
Map value standard deviation	25.669	Depositor
Recommended contour level	32.5	Depositor
Map size (\AA)	375, 375, 375	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing (\AA)	1.5, 1.5, 1.5	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 3AU, 5MU, H2U, PSU, 3TD, CH, 5MC, OMC, 2MG, 2MA, 1MG, 7MG, 4SU, 4OC, OMU, UR3, 6MZ, OMG, MIA, MA6

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	1.22	1/36769 (0.0%)	2.00	1273/57354 (2.2%)
2	AB	1.25	0/1580	2.01	56/2459 (2.3%)
2	AE	1.26	0/1580	2.04	66/2459 (2.7%)
3	AC	0.61	0/3092	0.97	1/4183 (0.0%)
4	AD	1.37	0/548	1.98	20/848 (2.4%)
5	AF	0.60	0/1904	1.00	1/2565 (0.0%)
6	AG	0.61	0/1852	1.04	0/2490
7	AH	0.64	0/1665	0.99	0/2227
8	AI	0.59	0/1239	1.07	1/1664 (0.1%)
9	AJ	0.62	0/1121	1.05	2/1509 (0.1%)
10	AK	0.63	0/1422	1.07	1/1908 (0.1%)
11	AL	0.59	0/989	1.01	0/1326
12	AM	0.65	0/1048	1.05	1/1394 (0.1%)
13	AN	0.57	0/835	1.08	1/1127 (0.1%)
14	AO	0.61	0/982	1.04	0/1323
15	AP	0.62	0/969	1.12	0/1300
16	AQ	0.58	0/919	1.02	0/1226
17	AR	0.63	0/817	1.15	2/1088 (0.2%)
18	AS	0.59	0/724	0.96	1/966 (0.1%)
19	AT	0.63	0/659	1.08	1/884 (0.1%)
20	AU	0.58	0/681	0.97	0/913
21	AV	0.73	0/637	1.08	0/851
22	AW	0.60	0/744	1.00	1/995 (0.1%)
23	AX	0.58	0/676	0.98	0/895
24	AY	0.69	0/598	1.18	1/792 (0.1%)
25	BA	1.24	0/2869	2.16	127/4474 (2.8%)
26	BB	1.22	0/69257	2.02	2547/108040 (2.4%)
27	BC	0.55	0/1748	0.98	0/2355
28	BD	0.62	0/2131	1.09	0/2863
29	BE	0.59	0/1586	1.04	0/2134
30	BF	0.58	0/1571	1.01	1/2113 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	BG	0.66	0/1444	1.10	0/1937
32	BH	0.59	0/1343	1.05	2/1816 (0.1%)
33	BI	0.58	0/1122	1.01	1/1515 (0.1%)
34	BJ	0.57	0/1046	0.93	0/1410
35	BK	0.64	0/1152	1.00	0/1551
36	BL	0.58	0/956	1.03	0/1279
37	BM	0.62	0/1062	1.07	0/1413
38	BN	0.63	0/1093	1.04	0/1460
39	BO	0.62	0/1021	1.06	0/1364
40	BP	0.60	0/910	1.01	0/1219
41	BQ	0.63	0/929	1.05	0/1242
42	BR	0.67	0/960	1.03	1/1278 (0.1%)
43	BS	0.63	0/829	1.06	0/1107
44	BT	0.54	0/864	0.98	0/1156
45	BU	0.57	0/794	1.02	0/1060
46	BV	0.58	0/797	1.02	0/1062
47	BW	0.61	0/766	0.98	0/1025
48	BX	0.64	0/642	1.10	0/848
49	BY	0.64	0/635	1.10	1/848 (0.1%)
50	BZ	0.56	0/510	1.05	0/677
51	Ba	0.55	0/453	0.97	0/605
52	Bb	0.62	0/559	1.10	0/745
53	Bc	0.62	0/450	1.12	0/599
54	Bd	0.60	0/448	0.96	0/594
55	Be	0.64	0/380	1.04	0/498
56	Bf	0.60	0/513	1.02	0/676
57	Bg	0.55	0/303	1.09	0/397
All	All	1.07	1/165193 (0.0%)	1.79	4109/246106 (1.7%)

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	AA	0	502
2	AB	0	19
2	AE	0	15
3	AC	0	1
4	AD	0	9
6	AG	0	1
7	AH	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
8	AI	0	3
9	AJ	0	1
11	AL	0	1
13	AN	0	1
14	AO	0	1
15	AP	0	1
17	AR	0	2
21	AV	0	1
24	AY	0	1
25	BA	0	37
26	BB	0	952
27	BC	0	3
28	BD	0	2
29	BE	0	2
30	BF	0	2
32	BH	0	2
33	BI	0	1
41	BQ	0	1
42	BR	0	1
43	BS	0	1
48	BX	0	1
49	BY	0	1
53	Bc	0	1
All	All	0	1567

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	439	U	C2-N3	5.10	1.41	1.37

The worst 5 of 4109 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BB	2092	U	O4'-C1'-N1	16.66	121.53	108.20
25	BA	49	C	O4'-C1'-N1	15.19	120.35	108.20
1	AA	465	A	O4'-C1'-N9	14.84	120.07	108.20
26	BB	736	C	O4'-C1'-N1	12.90	118.52	108.20
26	BB	1535	A	O4'-C1'-N9	12.89	118.51	108.20

There are no chirality outliers.

5 of 1567 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	10	A	Sidechain
1	AA	11	G	Sidechain
1	AA	13	U	Sidechain
1	AA	2	A	Sidechain
1	AA	7	A	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	33089	0	16678	0	0
2	AB	1635	0	849	0	0
2	AE	1635	0	849	0	0
3	AC	3036	0	3052	0	0
4	AD	495	0	249	0	0
5	AF	1872	0	1885	0	0
6	AG	1822	0	1913	0	0
7	AH	1643	0	1710	0	0
8	AI	1225	0	1273	0	0
9	AJ	1101	0	1050	0	0
10	AK	1400	0	1449	0	0
11	AL	979	0	1034	0	0
12	AM	1036	0	1084	0	0
13	AN	825	0	865	0	0
14	AO	965	0	997	0	0
15	AP	955	0	1019	0	0
16	AQ	910	0	981	0	0
17	AR	805	0	847	0	0
18	AS	716	0	742	0	0
19	AT	649	0	666	0	0
20	AU	672	0	716	0	0
21	AV	626	0	651	0	0
22	AW	727	0	769	0	0
23	AX	670	0	722	0	0
24	AY	590	0	631	0	0
25	BA	2566	0	1302	0	0
26	BB	62351	0	31387	0	0
27	BC	1733	0	1824	0	0
28	BD	2092	0	2170	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	BE	1565	0	1616	0	0
30	BF	1552	0	1619	0	0
31	BG	1420	0	1460	0	0
32	BH	1323	0	1374	0	0
33	BI	1111	0	1148	0	0
34	BJ	1032	0	1088	0	0
35	BK	1129	0	1162	0	0
36	BL	947	0	1023	0	0
37	BM	1053	0	1129	0	0
38	BN	1074	0	1157	0	0
39	BO	1008	0	1045	0	0
40	BP	900	0	935	0	0
41	BQ	917	0	965	0	0
42	BR	947	0	1022	0	0
43	BS	816	0	839	0	0
44	BT	857	0	922	0	0
45	BU	787	0	846	0	0
46	BV	789	0	847	0	0
47	BW	753	0	780	0	0
48	BX	634	0	656	0	0
49	BY	625	0	655	0	0
50	BZ	509	0	543	0	0
51	Ba	449	0	491	0	0
52	Bb	549	0	552	0	0
53	Bc	444	0	461	0	0
54	Bd	441	0	485	0	0
55	Be	377	0	418	0	0
56	Bf	504	0	574	0	0
57	Bg	302	0	343	0	0
All	All	153634	0	105519	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

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	
3	AC	391/393 (100%)	367 (94%)	21 (5%)	3 (1%)	19	60
5	AF	238/241 (99%)	215 (90%)	21 (9%)	2 (1%)	19	60
6	AG	230/233 (99%)	210 (91%)	18 (8%)	2 (1%)	17	57
7	AH	203/206 (98%)	189 (93%)	12 (6%)	2 (1%)	15	55
8	AI	164/167 (98%)	143 (87%)	18 (11%)	3 (2%)	8	40
9	AJ	133/135 (98%)	128 (96%)	3 (2%)	2 (2%)	10	46
10	AK	176/179 (98%)	159 (90%)	15 (8%)	2 (1%)	14	52
11	AL	127/130 (98%)	117 (92%)	8 (6%)	2 (2%)	9	44
12	AM	127/130 (98%)	111 (87%)	14 (11%)	2 (2%)	9	44
13	AN	101/103 (98%)	86 (85%)	11 (11%)	4 (4%)	3	23
14	AO	126/129 (98%)	113 (90%)	11 (9%)	2 (2%)	9	44
15	AP	121/124 (98%)	103 (85%)	13 (11%)	5 (4%)	3	23
16	AQ	115/118 (98%)	108 (94%)	7 (6%)	0	100	100
17	AR	98/101 (97%)	82 (84%)	9 (9%)	7 (7%)	1	14
18	AS	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
19	AT	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
20	AU	81/84 (96%)	73 (90%)	8 (10%)	0	100	100
21	AV	72/75 (96%)	65 (90%)	6 (8%)	1 (1%)	11	46
22	AW	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
23	AX	84/87 (97%)	77 (92%)	7 (8%)	0	100	100
24	AY	68/71 (96%)	62 (91%)	5 (7%)	1 (2%)	10	46
27	BC	232/234 (99%)	204 (88%)	25 (11%)	3 (1%)	12	48
28	BD	270/273 (99%)	239 (88%)	22 (8%)	9 (3%)	4	26
29	BE	207/209 (99%)	186 (90%)	15 (7%)	6 (3%)	4	29
30	BF	199/201 (99%)	182 (92%)	14 (7%)	3 (2%)	10	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	BG	176/179 (98%)	148 (84%)	25 (14%)	3 (2%)	9	42
32	BH	174/177 (98%)	162 (93%)	9 (5%)	3 (2%)	9	42
33	BI	147/149 (99%)	126 (86%)	16 (11%)	5 (3%)	3	26
34	BJ	139/142 (98%)	121 (87%)	17 (12%)	1 (1%)	22	63
35	BK	140/142 (99%)	131 (94%)	9 (6%)	0	100	100
36	BL	121/123 (98%)	107 (88%)	12 (10%)	2 (2%)	9	42
37	BM	142/144 (99%)	124 (87%)	16 (11%)	2 (1%)	11	46
38	BN	134/136 (98%)	122 (91%)	9 (7%)	3 (2%)	6	35
39	BO	125/127 (98%)	116 (93%)	8 (6%)	1 (1%)	19	60
40	BP	115/117 (98%)	106 (92%)	8 (7%)	1 (1%)	17	57
41	BQ	112/115 (97%)	99 (88%)	11 (10%)	2 (2%)	8	40
42	BR	115/118 (98%)	109 (95%)	5 (4%)	1 (1%)	17	57
43	BS	101/103 (98%)	91 (90%)	7 (7%)	3 (3%)	4	28
44	BT	108/110 (98%)	98 (91%)	9 (8%)	1 (1%)	17	57
45	BU	98/100 (98%)	86 (88%)	11 (11%)	1 (1%)	15	55
46	BV	101/104 (97%)	90 (89%)	10 (10%)	1 (1%)	15	55
47	BW	92/94 (98%)	85 (92%)	5 (5%)	2 (2%)	6	35
48	BX	82/85 (96%)	68 (83%)	11 (13%)	3 (4%)	3	24
49	BY	75/78 (96%)	64 (85%)	9 (12%)	2 (3%)	5	31
50	BZ	61/63 (97%)	49 (80%)	9 (15%)	3 (5%)	2	20
51	Ba	56/59 (95%)	53 (95%)	2 (4%)	1 (2%)	8	40
52	Bb	68/70 (97%)	57 (84%)	10 (15%)	1 (2%)	10	46
53	Bc	54/57 (95%)	46 (85%)	6 (11%)	2 (4%)	3	24
54	Bd	52/55 (94%)	45 (86%)	7 (14%)	0	100	100
55	Be	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
56	Bf	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
57	Bg	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	5	30
All	All	6548/6682 (98%)	5895 (90%)	547 (8%)	106 (2%)	13	44

5 of 106 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	AH	18	LEU

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Mol	Chain	Res	Type
12	AM	3	ASN
13	AN	74	VAL
14	AO	118	ASN
15	AP	86	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AC	326/326 (100%)	311 (95%)	15 (5%)	27	52
5	AF	198/199 (100%)	188 (95%)	10 (5%)	24	48
6	AG	189/190 (100%)	180 (95%)	9 (5%)	25	51
7	AH	172/173 (99%)	164 (95%)	8 (5%)	26	51
8	AI	125/126 (99%)	122 (98%)	3 (2%)	49	69
9	AJ	116/116 (100%)	104 (90%)	12 (10%)	7	25
10	AK	146/147 (99%)	136 (93%)	10 (7%)	16	41
11	AL	104/105 (99%)	99 (95%)	5 (5%)	25	51
12	AM	106/107 (99%)	98 (92%)	8 (8%)	13	38
13	AN	90/90 (100%)	85 (94%)	5 (6%)	21	46
14	AO	98/99 (99%)	95 (97%)	3 (3%)	40	62
15	AP	103/104 (99%)	98 (95%)	5 (5%)	25	50
16	AQ	95/96 (99%)	93 (98%)	2 (2%)	53	72
17	AR	83/84 (99%)	79 (95%)	4 (5%)	25	51
18	AS	76/77 (99%)	71 (93%)	5 (7%)	16	41
19	AT	65/65 (100%)	62 (95%)	3 (5%)	27	52
20	AU	77/78 (99%)	75 (97%)	2 (3%)	46	66
21	AV	64/65 (98%)	60 (94%)	4 (6%)	18	43
22	AW	78/79 (99%)	74 (95%)	4 (5%)	24	48
23	AX	65/66 (98%)	61 (94%)	4 (6%)	18	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	AY	60/61 (98%)	55 (92%)	5 (8%)	11	34
27	BC	181/181 (100%)	176 (97%)	5 (3%)	43	65
28	BD	217/218 (100%)	210 (97%)	7 (3%)	39	61
29	BE	164/164 (100%)	153 (93%)	11 (7%)	16	41
30	BF	165/165 (100%)	156 (94%)	9 (6%)	21	47
31	BG	149/150 (99%)	138 (93%)	11 (7%)	13	38
32	BH	137/138 (99%)	128 (93%)	9 (7%)	16	41
33	BI	114/114 (100%)	109 (96%)	5 (4%)	28	53
34	BJ	109/110 (99%)	104 (95%)	5 (5%)	27	52
35	BK	116/116 (100%)	110 (95%)	6 (5%)	23	48
36	BL	104/104 (100%)	96 (92%)	8 (8%)	13	37
37	BM	103/103 (100%)	97 (94%)	6 (6%)	20	45
38	BN	109/109 (100%)	101 (93%)	8 (7%)	14	39
39	BO	103/103 (100%)	97 (94%)	6 (6%)	20	45
40	BP	87/87 (100%)	82 (94%)	5 (6%)	20	45
41	BQ	99/100 (99%)	93 (94%)	6 (6%)	18	44
42	BR	89/90 (99%)	88 (99%)	1 (1%)	73	84
43	BS	84/84 (100%)	78 (93%)	6 (7%)	14	39
44	BT	93/93 (100%)	88 (95%)	5 (5%)	22	47
45	BU	84/84 (100%)	79 (94%)	5 (6%)	19	44
46	BV	84/85 (99%)	81 (96%)	3 (4%)	35	59
47	BW	78/78 (100%)	74 (95%)	4 (5%)	24	48
48	BX	62/63 (98%)	55 (89%)	7 (11%)	6	21
49	BY	67/68 (98%)	64 (96%)	3 (4%)	27	52
50	BZ	55/55 (100%)	54 (98%)	1 (2%)	59	77
51	Ba	48/49 (98%)	47 (98%)	1 (2%)	53	72
52	Bb	62/62 (100%)	60 (97%)	2 (3%)	39	61
53	Bc	47/48 (98%)	46 (98%)	1 (2%)	53	72
54	Bd	48/49 (98%)	48 (100%)	0	100	100
55	Be	38/38 (100%)	37 (97%)	1 (3%)	46	66
56	Bf	51/52 (98%)	49 (96%)	2 (4%)	32	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
57	Bg	34/34 (100%)	30 (88%)	4 (12%)	5 20
All	All	5417/5447 (99%)	5138 (95%)	279 (5%)	27 48

5 of 279 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	BQ	112	ARG
43	BS	79	ARG
48	BX	44	PHE
17	AR	52	ARG
16	AQ	113	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1539/1542 (99%)	193 (12%)	73 (4%)
2	AB	73/76 (96%)	12 (16%)	2 (2%)
2	AE	73/76 (96%)	13 (17%)	6 (8%)
25	BA	119/120 (99%)	15 (12%)	4 (3%)
26	BB	2898/2904 (99%)	401 (13%)	137 (4%)
4	AD	24/24 (100%)	4 (16%)	5 (20%)
All	All	4726/4742 (99%)	638 (13%)	227 (4%)

5 of 638 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	A
1	AA	9	G
1	AA	31	G
1	AA	32	A
1	AA	39	G

5 of 227 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	BB	574	A
26	BB	2791	G

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Mol	Chain	Res	Type
26	BB	1085	A
26	BB	2751	G
26	BB	2380	C

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

55 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	PSU	AB	55	2	18,21,22	0.95	1 (5%)	22,30,33	0.93	1 (4%)
26	3TD	BB	1915	26	18,22,23	0.86	0	22,32,35	1.18	2 (9%)
1	MA6	AA	1519	1	19,26,27	1.01	1 (5%)	18,38,41	1.20	1 (5%)
2	PSU	AE	55	2	18,21,22	0.98	1 (5%)	22,30,33	1.08	1 (4%)
26	5MU	BB	1939	26	19,22,23	0.82	0	28,32,35	1.37	3 (10%)
26	OMC	BB	2498	26	19,22,23	0.61	0	26,31,34	0.87	0
2	4SU	AE	8	2	18,21,22	1.38	2 (11%)	26,30,33	1.45	3 (11%)
1	PSU	AA	516	1	18,21,22	0.85	0	22,30,33	1.31	2 (9%)
26	H2U	BB	2449	26	18,21,22	0.81	0	21,30,33	1.12	1 (4%)
2	5MU	AB	54	2	19,22,23	0.66	0	28,32,35	1.21	4 (14%)
26	6MZ	BB	1618	26	18,25,26	0.95	1 (5%)	16,36,39	1.35	2 (12%)
26	OMU	BB	2552	26	19,22,23	0.75	0	26,31,34	0.99	1 (3%)
26	CH	BB	2575	26	16,21,22	1.02	1 (6%)	20,30,33	1.06	1 (5%)
26	PSU	BB	2504	26	18,21,22	0.95	0	22,30,33	1.20	2 (9%)
1	7MG	AA	527	1	22,26,27	4.57	2 (9%)	29,39,42	1.35	1 (3%)
1	2MG	AA	966	1	18,26,27	1.18	1 (5%)	16,38,41	1.34	2 (12%)
1	4OC	AA	1402	1	20,23,24	0.72	0	26,32,35	1.11	1 (3%)
26	PSU	BB	2457	26	18,21,22	0.97	1 (5%)	22,30,33	1.31	3 (13%)
26	PSU	BB	1911	26	18,21,22	0.84	0	22,30,33	1.02	1 (4%)
26	7MG	BB	2069	26	22,26,27	4.58	1 (4%)	29,39,42	1.39	2 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	5MU	AE	54	2	19,22,23	0.64	0	28,32,35	0.98	2 (7%)
26	2MG	BB	1835	26	18,26,27	1.22	3 (16%)	16,38,41	0.73	0
26	PSU	BB	955	26	18,21,22	0.96	1 (5%)	22,30,33	1.08	1 (4%)
1	2MG	AA	1207	1	18,26,27	1.22	2 (11%)	16,38,41	0.95	0
2	7MG	AE	46	2	22,26,27	4.46	2 (9%)	29,39,42	1.50	3 (10%)
2	H2U	AB	20	2	18,21,22	0.85	0	21,30,33	1.05	1 (4%)
1	UR3	AA	1498	1	19,22,23	0.70	0	26,32,35	1.17	3 (11%)
1	5MC	AA	1407	1	18,22,23	0.62	0	26,32,35	0.81	1 (3%)
2	H2U	AE	20	2	18,21,22	0.81	0	21,30,33	1.00	1 (4%)
26	2MA	BB	2503	26	17,25,26	1.19	3 (17%)	17,37,40	1.43	3 (17%)
2	PSU	AB	32	2	18,21,22	0.93	1 (5%)	22,30,33	1.10	1 (4%)
2	4SU	AB	8	2	18,21,22	1.42	1 (5%)	26,30,33	1.01	2 (7%)
2	MIA	AB	37	2	24,31,32	1.04	3 (12%)	26,44,47	1.61	4 (15%)
1	5MC	AA	967	1	18,22,23	0.67	0	26,32,35	0.85	1 (3%)
2	3AU	AB	47	-	24,28,29	0.83	1 (4%)	33,40,43	0.80	1 (3%)
26	PSU	BB	1917	26	18,21,22	0.92	0	22,30,33	0.99	2 (9%)
2	PSU	AE	32	2	18,21,22	0.95	1 (5%)	22,30,33	1.14	2 (9%)
1	2MG	AA	1516	1	18,26,27	1.20	2 (11%)	16,38,41	0.79	0
2	PSU	AB	39	2	18,21,22	0.91	0	22,30,33	0.92	1 (4%)
2	H2U	AB	16	2	18,21,22	0.86	0	21,30,33	1.32	2 (9%)
26	PSU	BB	2580	26	18,21,22	0.95	0	22,30,33	0.94	0
2	3AU	AE	47	-	24,28,29	0.85	1 (4%)	33,40,43	1.19	2 (6%)
26	1MG	BB	745	26	18,26,27	1.13	1 (5%)	19,39,42	1.26	1 (5%)
26	OMG	BB	2251	26	18,26,27	1.11	2 (11%)	19,38,41	1.02	1 (5%)
26	5MC	BB	1962	26	18,22,23	0.56	0	26,32,35	1.22	2 (7%)
26	6MZ	BB	2030	26	18,25,26	1.01	1 (5%)	16,36,39	1.45	3 (18%)
2	PSU	AE	39	2	18,21,22	0.89	1 (5%)	22,30,33	1.20	1 (4%)
2	H2U	AE	16	2	18,21,22	0.79	0	21,30,33	1.01	1 (4%)
26	PSU	BB	2605	26	18,21,22	0.91	1 (5%)	22,30,33	0.93	1 (4%)
2	MIA	AE	37	2	24,31,32	1.08	3 (12%)	26,44,47	1.55	3 (11%)
26	2MG	BB	2445	26	18,26,27	1.24	3 (16%)	16,38,41	0.60	0
26	5MU	BB	747	26	19,22,23	0.73	0	28,32,35	1.39	3 (10%)
1	MA6	AA	1518	1	19,26,27	1.01	1 (5%)	18,38,41	1.03	0
26	PSU	BB	746	26	18,21,22	0.97	1 (5%)	22,30,33	1.10	2 (9%)
2	7MG	AB	46	2	22,26,27	4.64	2 (9%)	29,39,42	1.32	1 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PSU	AB	55	2	-	1/7/25/26	0/2/2/2
26	3TD	BB	1915	26	-	0/7/25/26	0/2/2/2
1	MA6	AA	1519	1	-	0/7/29/30	0/3/3/3
2	PSU	AE	55	2	-	1/7/25/26	0/2/2/2
26	5MU	BB	1939	26	-	0/7/25/26	0/2/2/2
26	OMC	BB	2498	26	-	1/9/27/28	0/2/2/2
2	4SU	AE	8	2	-	0/7/25/26	0/2/2/2
1	PSU	AA	516	1	-	0/7/25/26	0/2/2/2
26	H2U	BB	2449	26	-	0/7/38/39	0/2/2/2
2	5MU	AB	54	2	-	0/7/25/26	0/2/2/2
26	6MZ	BB	1618	26	-	0/5/27/28	0/3/3/3
26	OMU	BB	2552	26	-	0/9/27/28	0/2/2/2
26	CH	BB	2575	26	-	1/5/25/26	0/2/2/2
26	PSU	BB	2504	26	-	1/7/25/26	0/2/2/2
1	7MG	AA	527	1	-	1/7/37/38	0/3/3/3
1	2MG	AA	966	1	-	0/5/27/28	0/3/3/3
1	4OC	AA	1402	1	-	0/9/29/30	0/2/2/2
26	PSU	BB	2457	26	-	0/7/25/26	0/2/2/2
26	PSU	BB	1911	26	-	1/7/25/26	0/2/2/2
26	7MG	BB	2069	26	-	0/7/37/38	0/3/3/3
2	5MU	AE	54	2	-	0/7/25/26	0/2/2/2
26	2MG	BB	1835	26	-	0/5/27/28	0/3/3/3
26	PSU	BB	955	26	-	0/7/25/26	0/2/2/2
1	2MG	AA	1207	1	-	0/5/27/28	0/3/3/3
2	7MG	AE	46	2	-	0/7/37/38	0/3/3/3
2	H2U	AB	20	2	-	1/7/38/39	0/2/2/2
1	UR3	AA	1498	1	-	0/7/25/26	0/2/2/2
1	5MC	AA	1407	1	-	0/7/25/26	0/2/2/2
2	H2U	AE	20	2	-	0/7/38/39	0/2/2/2
26	2MA	BB	2503	26	-	0/3/25/26	0/3/3/3
2	PSU	AB	32	2	-	0/7/25/26	0/2/2/2
2	4SU	AB	8	2	-	0/7/25/26	0/2/2/2
2	MIA	AB	37	2	-	0/11/33/34	0/3/3/3
1	5MC	AA	967	1	-	0/7/25/26	0/2/2/2
2	3AU	AB	47	-	-	2/16/34/35	0/2/2/2
26	PSU	BB	1917	26	-	0/7/25/26	0/2/2/2
2	PSU	AE	32	2	-	0/7/25/26	0/2/2/2
1	2MG	AA	1516	1	-	0/5/27/28	0/3/3/3
2	PSU	AB	39	2	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	H2U	AB	16	2	-	1/7/38/39	0/2/2/2
26	PSU	BB	2580	26	-	2/7/25/26	0/2/2/2
2	3AU	AE	47	-	-	5/16/34/35	0/2/2/2
26	1MG	BB	745	26	-	0/3/25/26	0/3/3/3
26	OMG	BB	2251	26	-	0/5/27/28	0/3/3/3
26	5MC	BB	1962	26	-	5/7/25/26	0/2/2/2
26	6MZ	BB	2030	26	-	1/5/27/28	0/3/3/3
2	PSU	AE	39	2	-	0/7/25/26	0/2/2/2
2	H2U	AE	16	2	-	0/7/38/39	0/2/2/2
26	PSU	BB	2605	26	-	0/7/25/26	0/2/2/2
2	MIA	AE	37	2	-	0/11/33/34	0/3/3/3
26	2MG	BB	2445	26	-	0/5/27/28	0/3/3/3
26	5MU	BB	747	26	-	4/7/25/26	0/2/2/2
1	MA6	AA	1518	1	-	0/7/29/30	0/3/3/3
26	PSU	BB	746	26	-	4/7/25/26	0/2/2/2
2	7MG	AB	46	2	-	1/7/37/38	0/3/3/3

The worst 5 of 49 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	46	7MG	C8-N9	-21.46	1.34	1.46
26	BB	2069	7MG	C8-N9	-21.24	1.34	1.46
1	AA	527	7MG	C8-N9	-21.18	1.34	1.46
2	AE	46	7MG	C8-N9	-20.62	1.34	1.46
2	AB	8	4SU	C5-C4	-5.15	1.35	1.42

The worst 5 of 86 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AE	46	7MG	N9-C8-N7	6.12	112.13	103.38
26	BB	2069	7MG	N9-C8-N7	6.09	112.09	103.38
1	AA	527	7MG	N9-C8-N7	6.04	112.02	103.38
2	AB	46	7MG	N9-C8-N7	5.67	111.49	103.38
1	AA	516	PSU	C6-C5-C4	4.37	121.26	118.20

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	AA	527	7MG	C4'-C5'-O5'-P

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Mol	Chain	Res	Type	Atoms
2	AB	46	7MG	C4'-C5'-O5'-P
26	BB	746	PSU	C2'-C1'-C5-C4
26	BB	746	PSU	C2'-C1'-C5-C6
26	BB	747	5MU	C2'-C1'-N1-C2

There are no ring outliers.

No monomer is involved in short contacts.

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.

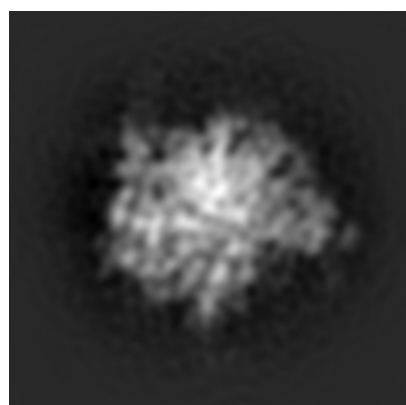
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1850. These allow visual inspection of the internal detail of the map and identification of artifacts.

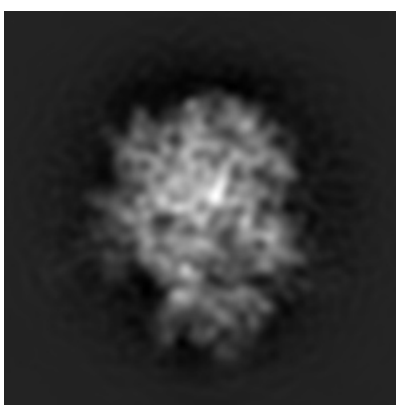
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

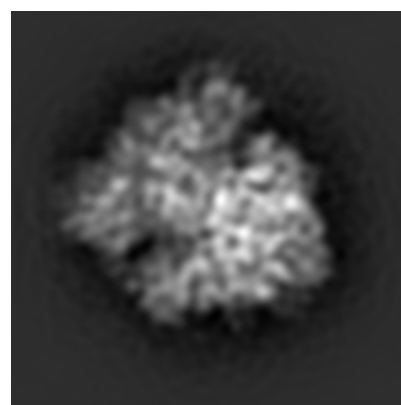
6.1.1 Primary map



X



Y

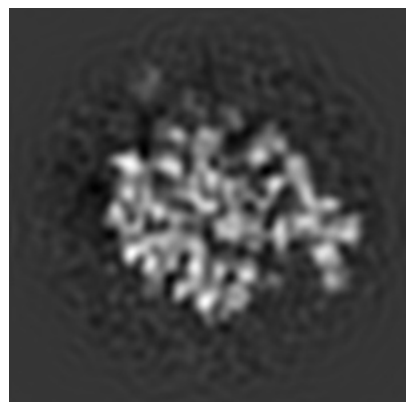


Z

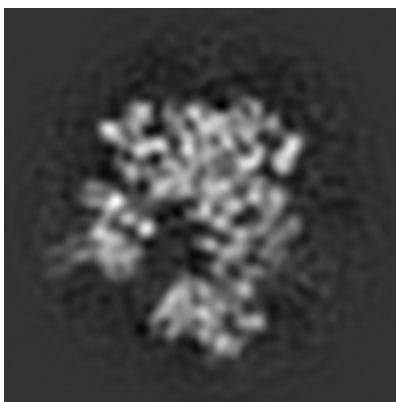
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

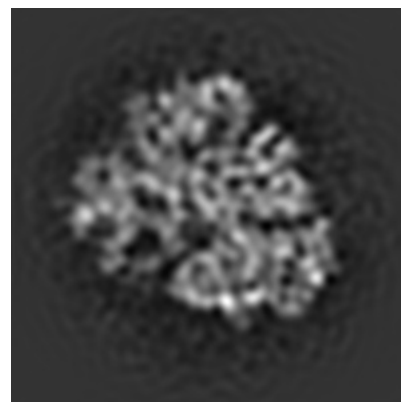
6.2.1 Primary map



X Index: 125



Y Index: 125

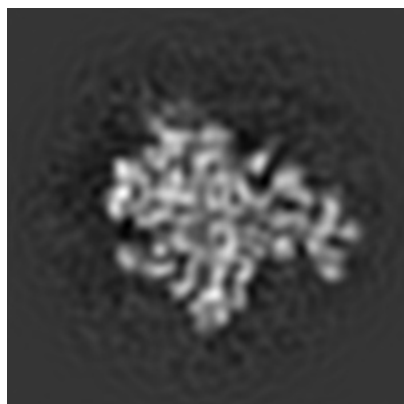


Z Index: 125

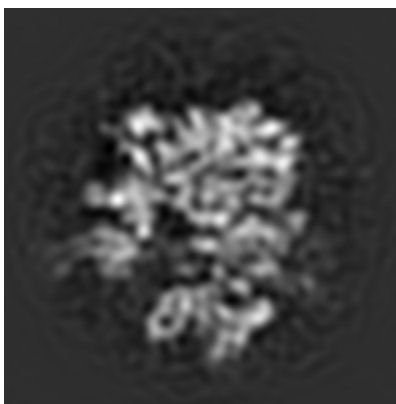
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

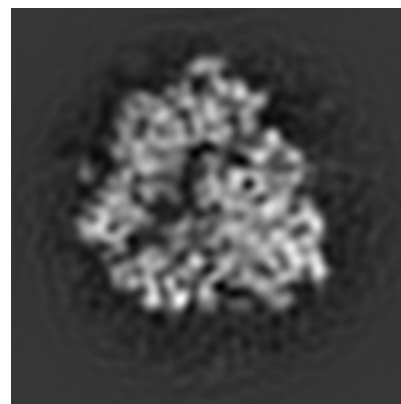
6.3.1 Primary map



X Index: 131



Y Index: 130

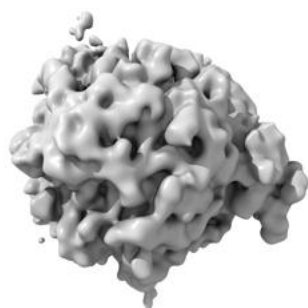


Z Index: 115

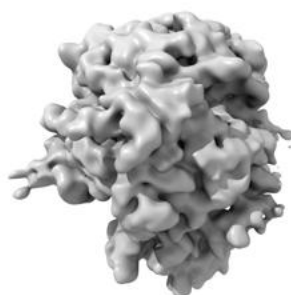
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

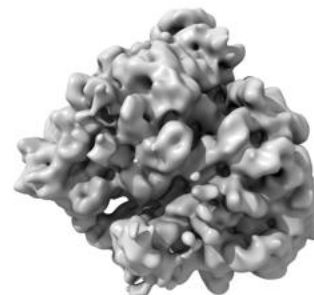
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 32.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

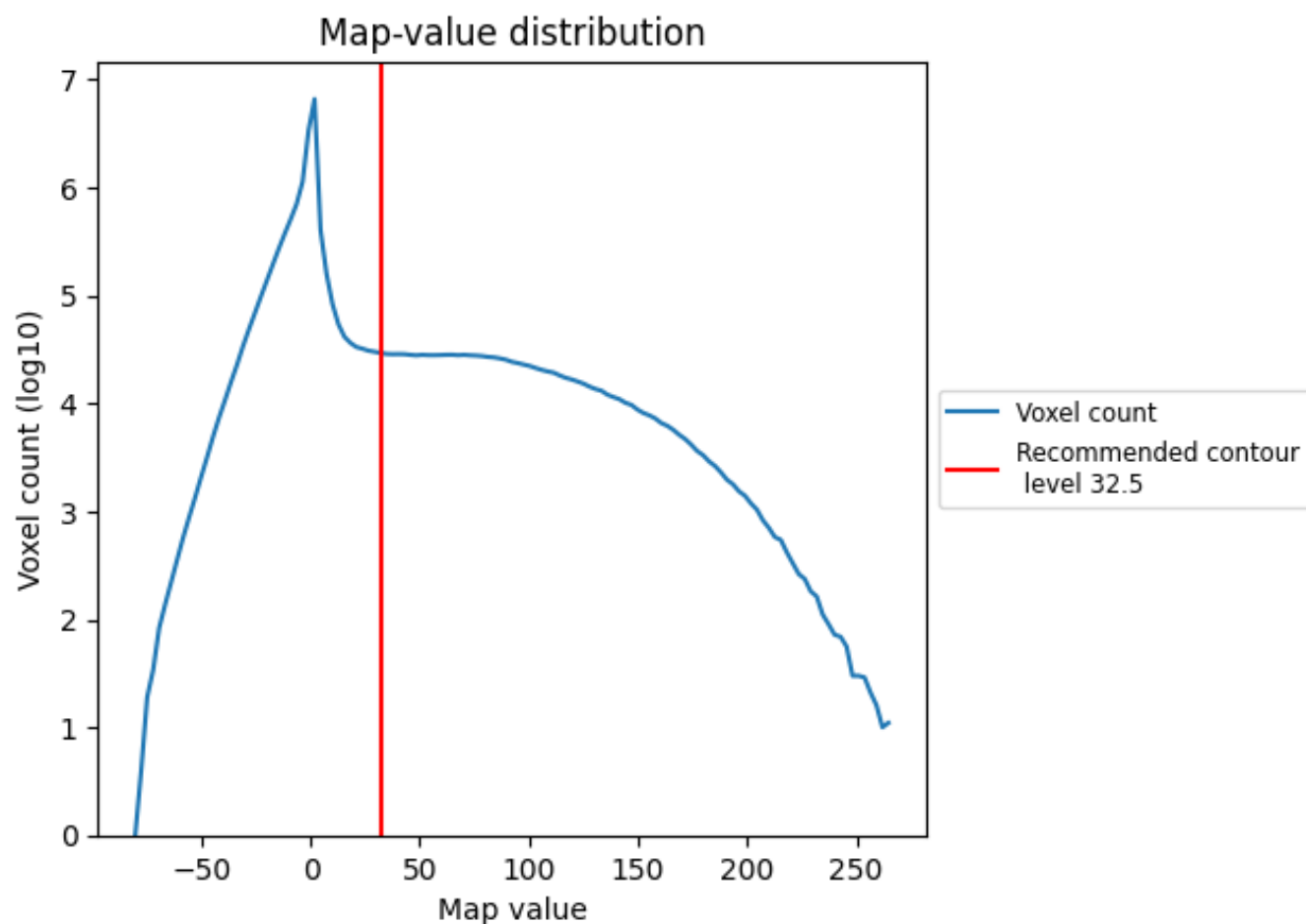
6.5 Mask visualisation

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

7 Map analysis [i](#)

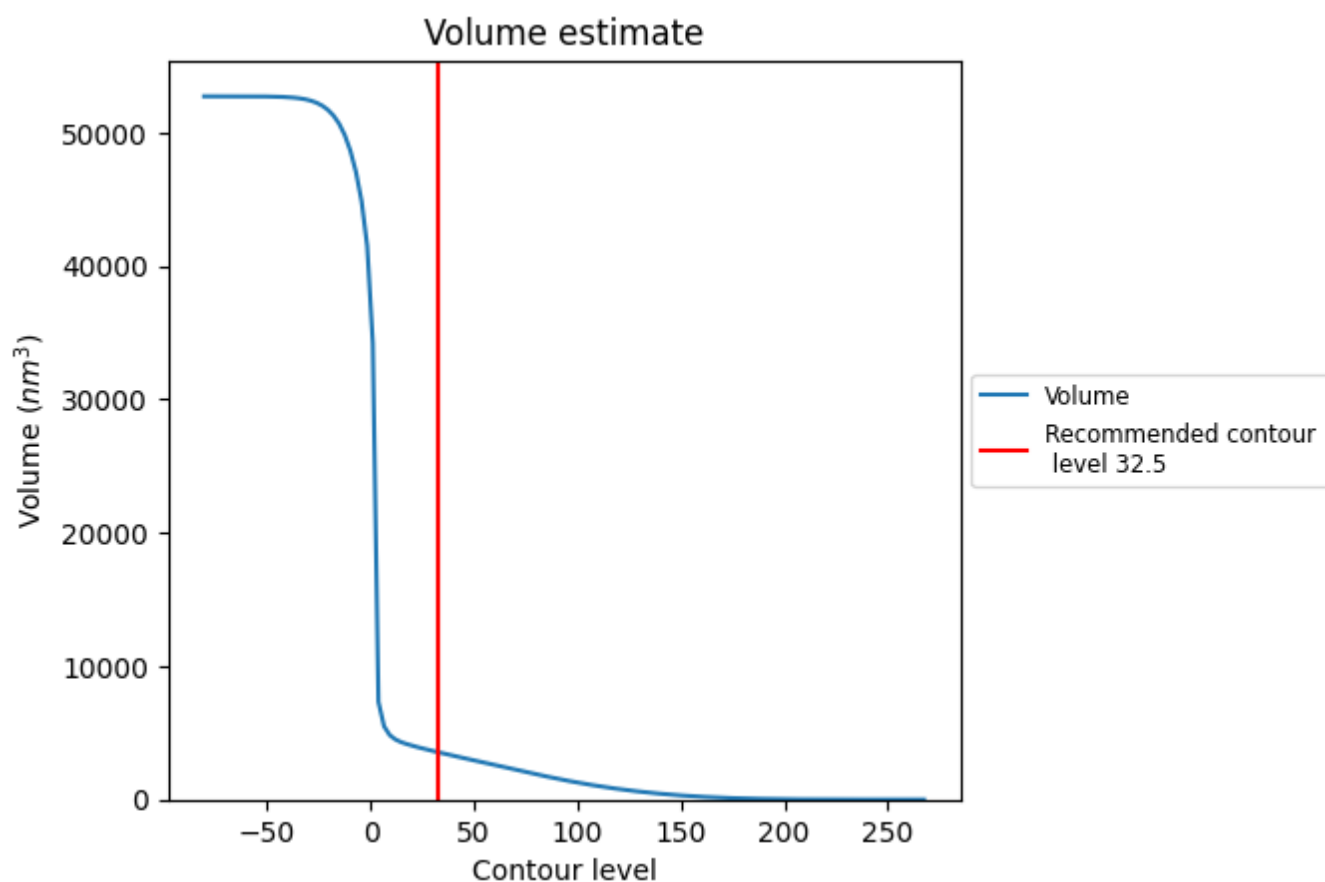
This section contains the results of statistical analysis of the map.

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.

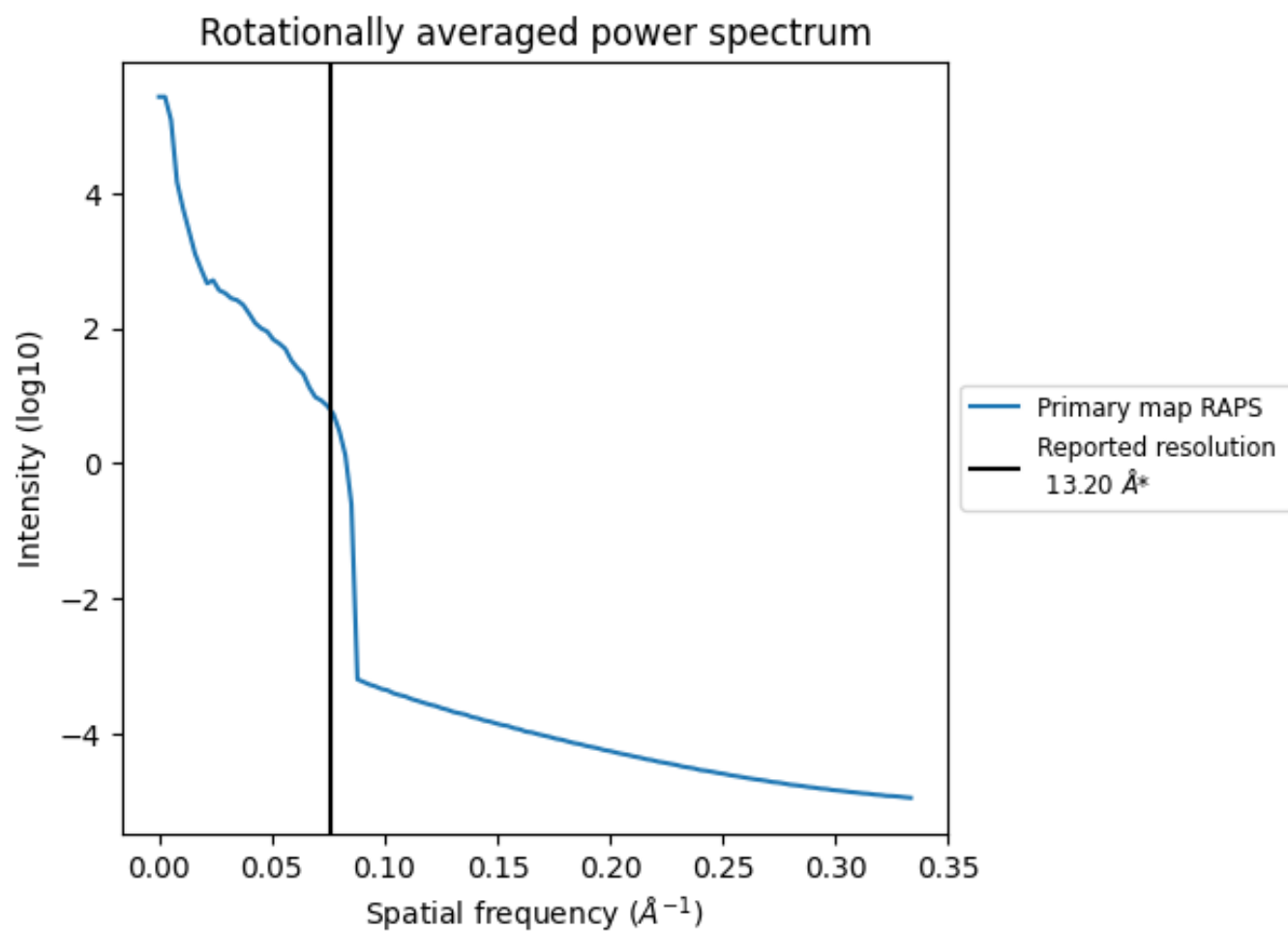
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3559 nm³; this corresponds to an approximate mass of 3215 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 0.076 Å⁻¹

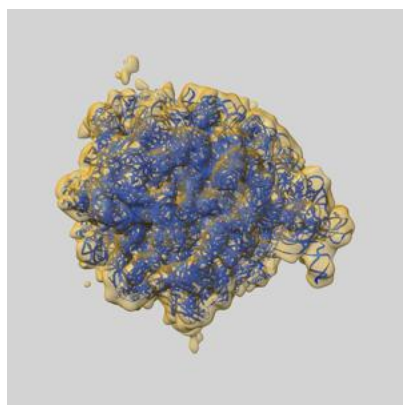
8 Fourier-Shell correlation

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

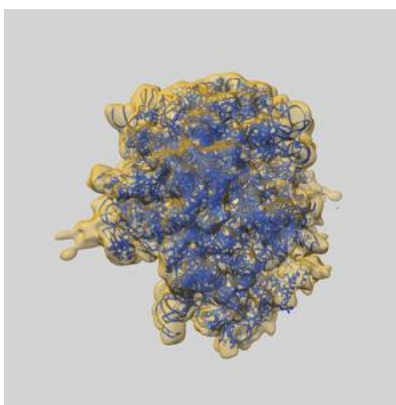
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1850 and PDB model 4V6L. Per-residue inclusion information can be found in section [3](#) on page [14](#).

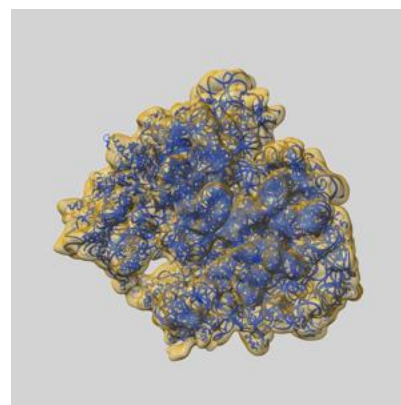
9.1 Map-model overlay [i](#)



X



Y



Z

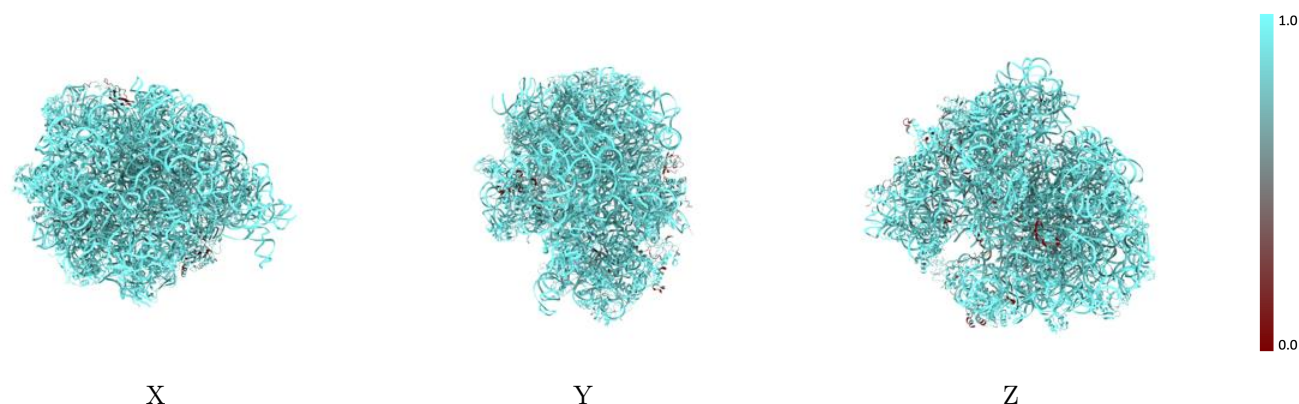
The images above show the 3D surface view of the map at the recommended contour level 32.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



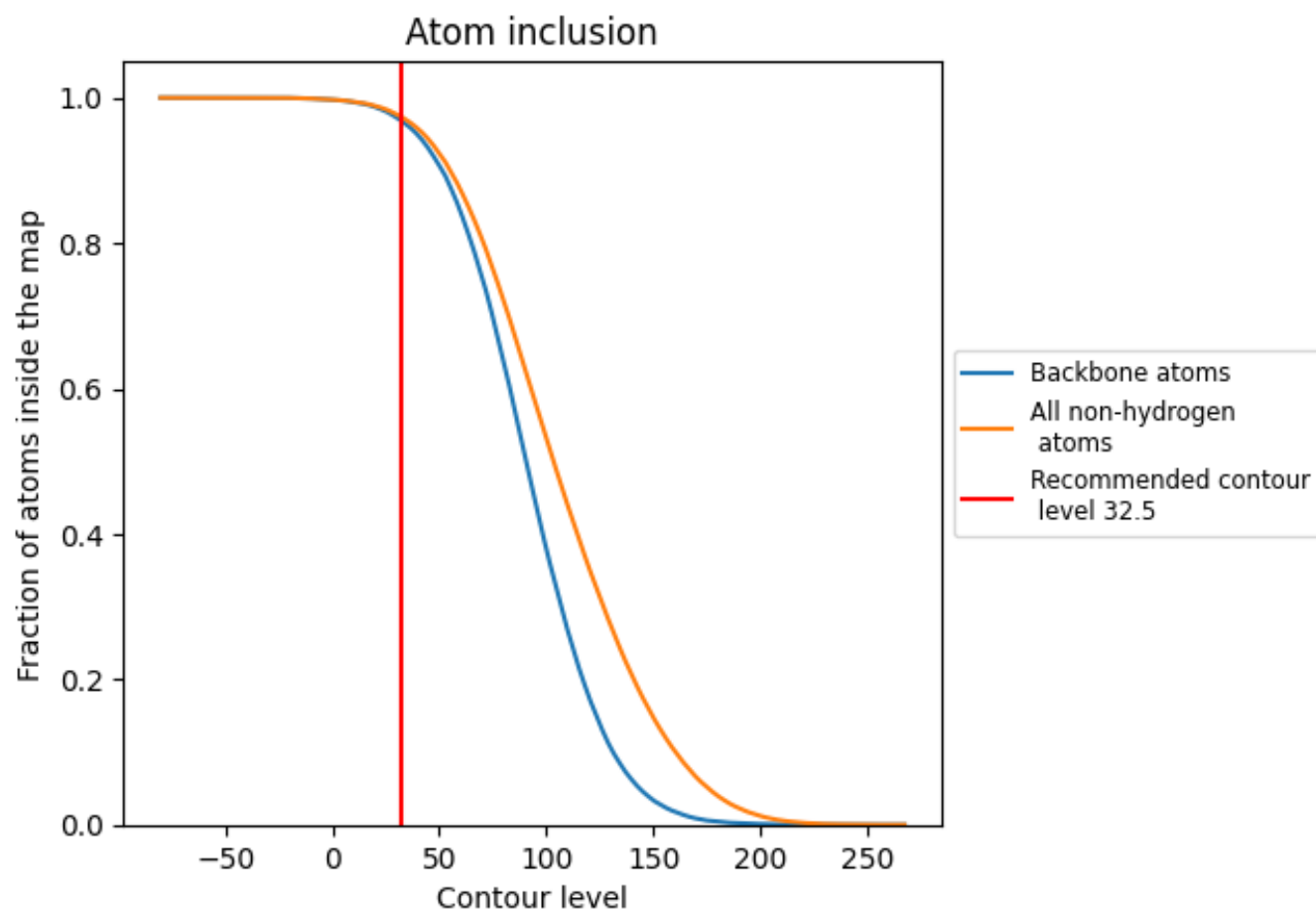
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (32.5).

9.4 Atom inclusion ⓘ



At the recommended contour level, 97% of all backbone atoms, 97% 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 (32.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9734	0.0980
AA	0.9914	0.1100
AB	0.8777	0.0990
AC	0.8429	0.0640
AD	0.8788	0.0820
AE	0.9554	0.1100
AF	0.9028	0.0860
AG	0.9007	0.0700
AH	0.9082	0.0520
AI	0.8836	0.0690
AJ	0.8843	0.0670
AK	0.9322	0.0820
AL	0.9760	0.0640
AM	0.9879	0.0900
AN	0.9313	0.0220
AO	0.8599	0.0650
AP	0.9349	0.0400
AQ	0.9818	0.0790
AR	0.9871	0.0490
AS	0.9986	0.0720
AT	0.9872	0.0420
AU	0.9863	0.0910
AV	0.9732	0.0630
AW	0.9564	0.0560
AX	0.9573	0.0440
AY	0.8982	0.0720
BA	0.9973	0.1240
BB	0.9953	0.1180
BC	0.8208	0.0410
BD	0.9886	0.0490
BE	0.9831	0.0520
BF	0.9809	0.0670
BG	0.9740	0.0790
BH	0.9892	0.0910
BI	0.6642	0.0550



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Chain	Atom inclusion	Q-score
BJ	 0.9628	 0.0800
BK	 0.9627	 0.0660
BL	 0.9729	 0.0580
BM	 0.9756	 0.0380
BN	 0.9520	 0.0600
BO	 0.9969	 0.0630
BP	 0.9885	 0.0680
BQ	 0.9448	 0.0880
BR	 0.9868	 0.0620
BS	 0.9674	 0.0750
BT	 0.9964	 0.0720
BU	 0.9896	 0.0730
BV	 0.9653	 0.0830
BW	 0.9837	 0.0860
BX	 0.8835	 0.0410
BY	 0.9784	 0.0720
BZ	 0.9779	 0.0990
Ba	 0.9840	 0.0660
Bb	 0.9033	 0.0860
Bc	 0.9486	 0.0380
Bd	 0.9538	 0.0570
Be	 0.9972	 0.0200
Bf	 0.9593	 0.0230
Bg	 0.9795	 0.0240