



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 05:40 AM UTC

PDB ID : 4V6P / pdb_00004v6p
EMDB ID : EMD-5364
Title : Structural characterization of mRNA-tRNA translocation intermediates (class 4b of the six classes)
Authors : Agirrezabala, X.; Liao, H.; Schreiner, E.; Fu, J.; Ortiz-Meoz, R.F.; Schulten, K.; Green, R.; Frank, J.
Deposited on : 2011-12-08
Resolution : 13.50 Å (reported)
Based on initial model : 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:

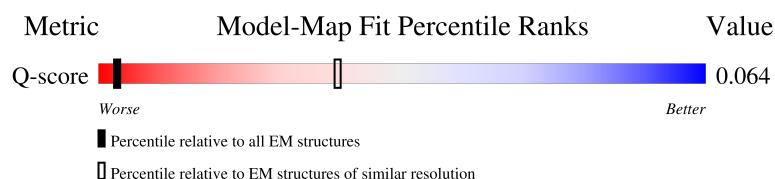
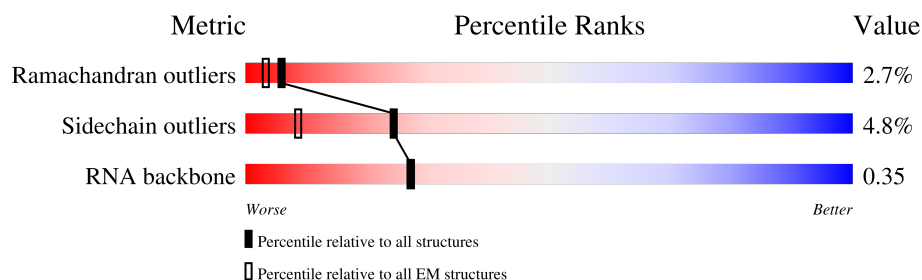
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 13.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



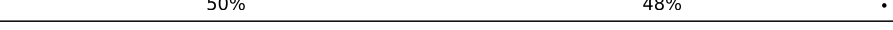
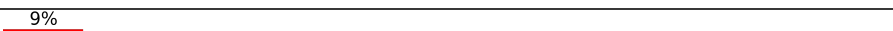
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	74 (13.00 - 14.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	
3	AC	47	
4	AD	77	

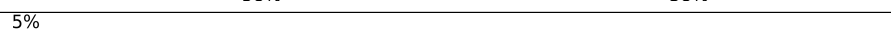
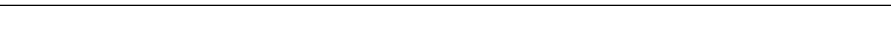
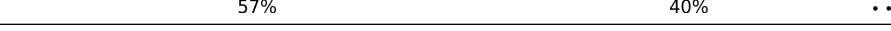
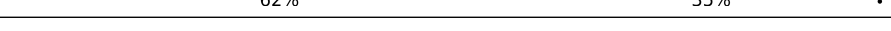
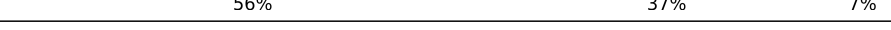
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Mol	Chain	Length	Quality of chain
5	AE	240	 61% 37% .
6	AF	232	 56% 38% 6% .
7	AG	205	 54% 42% .
8	AH	166	 60% 34% 5% .
9	AI	135	 61% 35% .
10	AJ	178	 54% 43% .
11	AK	129	 62% 37% .
12	AL	129	 64% 34% .
13	AM	103	 43% 50% 7% .
14	AN	128	 59% 40% .
15	AO	123	 52% 42% 6% .
16	AP	117	 53% 44% .
17	AQ	100	 48% 47% . .
18	AR	88	 50% 48% .
19	AS	82	 61% 37% .
20	AT	83	 64% 34% .
21	AU	74	 50% 45% . .
22	AV	91	 65% 30% 5% .
23	AW	86	 63% 35% .
24	AX	70	 54% 41% .
25	BA	120	 8% 33% 49% 9%
26	BB	2904	 7% 37% 45% 12%
27	BC	234	 9% 54% 44% .
28	BD	272	 54% 42% .
29	BE	209	 57% 40% .

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Mol	Chain	Length	Quality of chain
30	BF	201	
31	BG	178	
32	BH	176	
33	BI	149	
34	BJ	164	
35	BK	141	
36	BL	142	
37	BM	123	
38	BN	144	
39	BO	136	
40	BP	127	
41	BQ	117	
42	BR	114	
43	BS	117	
44	BT	103	
45	BU	110	
46	BV	100	
47	BW	103	
48	BX	94	
49	BY	84	
50	BZ	77	
51	B0	63	
52	B1	58	
53	B2	70	
54	B3	56	

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Mol	Chain	Length	Quality of chain
55	B4	54	61%33%6%
56	B5	46	50%46%.
57	B6	64	55%34%11%
58	B7	38	42%53%5%

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 152351 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 site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	AB	76	Total	C	N	O	P	S	0	0
			1627	731	287	532	75	2		

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	47	Total	C	N	O	P	0	0
			993	445	167	335	46		

- Molecule 4 is a RNA chain called P site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	AD	77	Total	C	N	O	P	S	0	0
			1641	734	297	533	76	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	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	AF	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	AG	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	AH	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	AI	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	AJ	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	AK	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	AL	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	AM	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	AN	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	AO	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	AP	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	AQ	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	AR	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	AS	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	AT	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	AU	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	AV	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	AW	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	AX	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

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

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 23S ribosomal RNA.

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 L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BJ	164	Total	C	N	O	S	0	0
			1233	776	220	231	6		

- Molecule 35 is a protein called 50S ribosomal protein L11.

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

- Molecule 36 is a protein called 50S ribosomal protein L13.

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

- Molecule 37 is a protein called 50S ribosomal protein L14.

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

- Molecule 38 is a protein called 50S ribosomal protein L15.

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

- Molecule 39 is a protein called 50S ribosomal protein L16.

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

- Molecule 40 is a protein called 50S ribosomal protein L17.

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

- Molecule 41 is a protein called 50S ribosomal protein L18.

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

- Molecule 42 is a protein called 50S ribosomal protein L19.

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

- Molecule 43 is a protein called 50S ribosomal protein L20.

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

- Molecule 44 is a protein called 50S ribosomal protein L21.

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

- Molecule 45 is a protein called 50S ribosomal protein L22.

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

- Molecule 46 is a protein called 50S ribosomal protein L23.

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

- Molecule 47 is a protein called 50S ribosomal protein L24.

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

- Molecule 48 is a protein called 50S ribosomal protein L25.

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

- Molecule 49 is a protein called 50S ribosomal protein L27.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B0	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 52 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B1	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 53 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	B2	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 54 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	B3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 55 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	B4	54	Total	C	N	O	0	0
			441	284	81	76		

- Molecule 56 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	B5	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

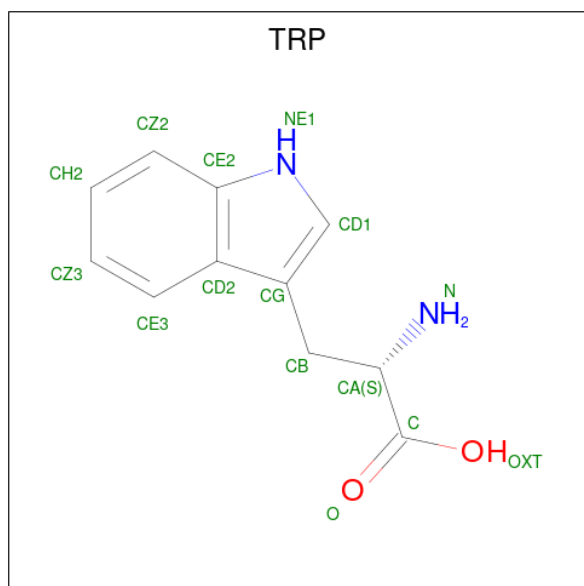
- Molecule 57 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	B6	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 58 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	B7	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 59 is TRYPTOPHAN (CCD ID: TRP) (formula: $C_{11}H_{12}N_2O_2$).



Mol	Chain	Residues	Atoms				AltConf
59	AB	1	Total	C	N	O	0
			14	11	2	1	

- Molecule 60 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: $C_6H_{11}NO_3S$).



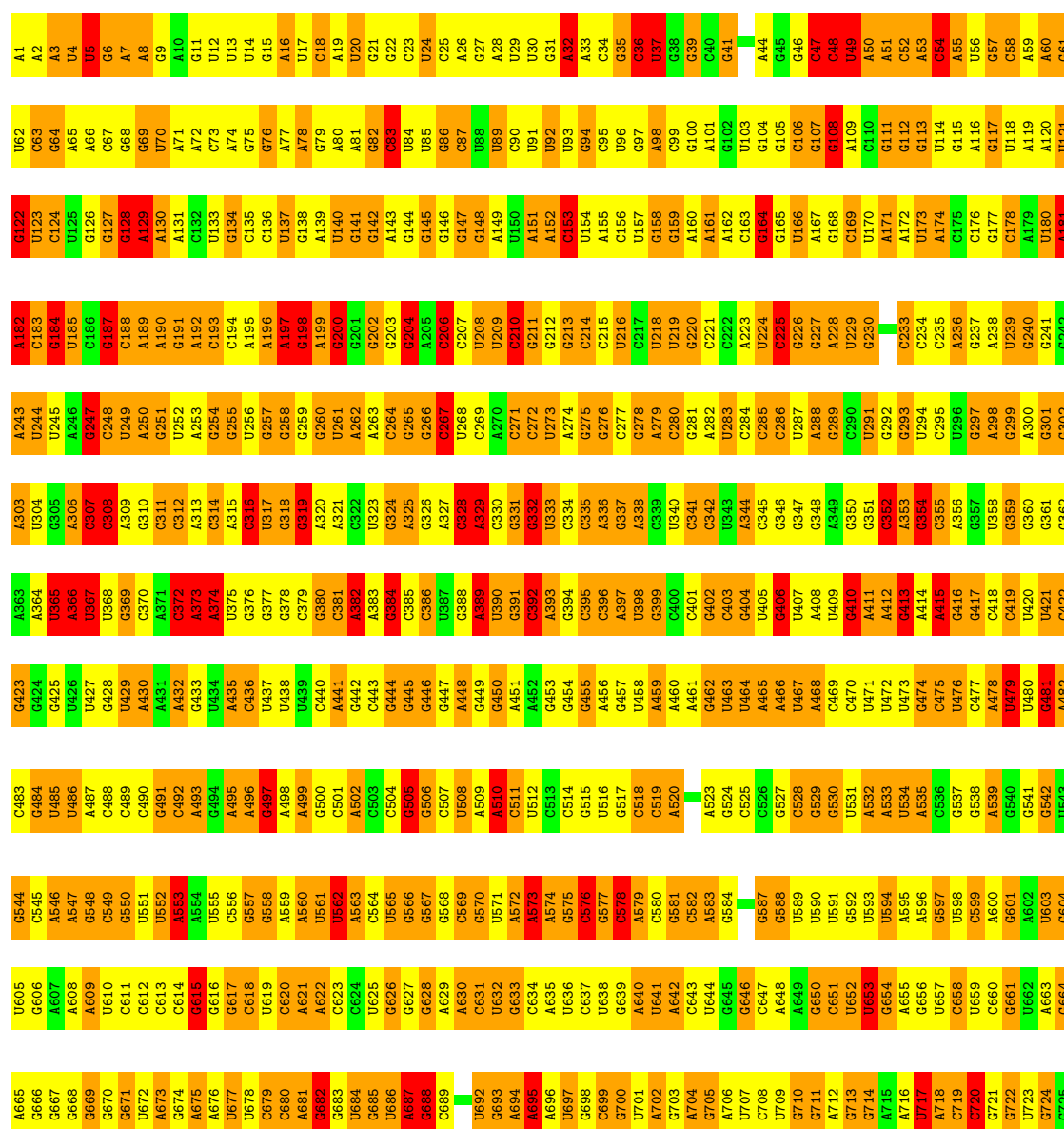
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
60	BB	1	10	6	1	2	1	0

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: 16S ribosomal RNA

Chain AA: 



A1508	G1387	C1327	G1206	A1146	U1086	G1026	G966	A906	G846
C1509	C1388	C1328	G1207	C1147	G1087	C1027	C967	A907	G847
C1510	C1389	A1329	A1208	C1148	G1088	C1028	A968	A908	C848
G1511	U1390	U1330	C1209	C1149	G1089	U1029	A969	A909	C849
U1512	U1391	G1331	A1210	A1150	U1090	U1030	C970	U911	G850
A1513	G1392	A1332	U1211	A1151	U1091	C1031	G971	U912	G851
G1452	G1393	A1333	U1212	A1152	A1092	G1032	C972	A913	G852
G1463	U1394	G1334	A1213	G1153	A1093	G1033	G973	A914	G853
G1454	A1395	U1335	C1214	G1154	G1094	G1034	A974	A915	U854
G1455	C1396	G1336	G1215	A1155	U1095	A1035	A975	U916	U855
G1456	A1397	G1337	A1216	G1156	C1096	A1036	G976	U917	C856
G1457	C1398	G1338	G1217	A1157	C1097	C1037	A977	G917	C857
G1458	A1399	G1339	G1218	C1158	U1098	G1038	A978	A918	G858
G1459	C1400	A1340	A1219	U1159	G1099	G1039	C979	A919	G859
C1460	G1401	U1341	G1220	C1160	A1100	U1040	C980	U920	A860
G1461	C1402	C1342	G1221	C1161	A1101	U1041	C981	U921	U861
C1462	U1403	G1343	G1222	C1162	A1102	A1042	U982	G922	A862
U1463	C1404	C1344	C1223	A1163	C1103	G1043	A983	A923	U863
U1464	C1405	U1345	U1224	G1164	G1104	A1044	C984	C924	U864
A1465	U1406	A1346	A1225	U1165	A1105	C1045	C985	G925	A865
C1466	C1407	G1347	C1226	G1166	G1106	A1046	U986	G926	C866
C1467	A1408	U1348	A1227	A1167	C1107	G1047	G987	G927	A867
C1468	C1409	A1349	A1228	U1168	G1108	G1048	G988	G928	C868
C1469	A1410	U1350	A1229	A1169	U1109	U1049	U989	G929	G869
U1470	G1411	A1351	G1230	A1170	A1110	G1050	C990	C930	U870
U1471	C1412	C1352	U1231	A1171	A1111	C1051	U991	C931	U871
U1472	U1413	G1353	G1232	C1172	C1112	U1052	U992	G932	A872
G1473	A1414	U1354	C1233	U1173	C1113	G1053	G993	G933	A873
G1474	G1415	G1355	G1234	G1174	C1114	A1054	A994	C934	C874
G1475	G1416	G1356	U1235	G1175	U1115	A1055	C995	A935	U875
G1476	G1417	A1357	A1236	U1176	U1116	U1056	U996	C936	A876
U1477	A1418	U1358	G1237	G1177	A1117	G1057	U997	A937	C877
U1478	G1419	C1359	A1238	G1178	U1118	U1058	C998	A938	A878
C1479	U1420	A1360	A1239	A1179	C1119	C1059	C999	G939	C879
G1482	G1421	G1361	U1240	A1180	C1120	U1060	A1000	C940	U880
A1483	G1422	A1362	G1241	G1181	U1121	G1061	C1001	G941	G881
C1484	G1423	C1363	C1242	U1182	U1122	U1062	G1002	G942	C882
U1485	U1424	U1364	G1243	U1183	U1123	C1063	G1003	U943	C883
G1486	U1425	G1365	C1244	G1184	U1124	G1064	A1004	G944	U884
G1487	G1426	G1366	A1245	G1185	U1125	U1065	A1005	G945	G885
G1488	C1427	C1367	U1247	G1186	U1126	C1066	G1006	A946	C886
U1489	A1428	U1368	A1248	G1187	G1127	A1067	U1007	G947	U887
U1490	A1429	C1369	G1249	U1188	C1128	G1068	U1008	C948	G888
G1491	A1430	G1370	A1250	U1189	C1129	C1069	U1009	A949	A889
A1492	A1431	G1371	A1251	G1190	A1130	U1070	U1010	U950	G890
A1493	G1432	U1372	A1252	A1191	G1131	C1071	C1011	G951	U891
G1494	A1433	C1373	G1253	C1192	C1132	G1072	A1012	U952	A892
U1495	A1434	A1374	A1254	G1193	G1133	U1073	G1013	G953	C893
C1496	G1435	A1375	G1255	U1194	G1134	G1074	A1014	G954	G894
G1497	U1436	U1376	A1256	C1195	U1135	U1075	G1015	U955	U895
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A1499	G1438	C1378	G1258	U1197	C1137	G1077	G1017	U957	U897
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C1501	U1440	A1380	A1260	U1199	G1139	G1079	A1019	A959	C899
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A1503	G1442	C1382	C1262	A1201	C1141	U1081	A1021	U961	C901
G1504	G1443	G1383	C1263	U1202	G1142	A1082	A1022	C962	G902
U1505	U1444	C1384	A1264	C1203	G1143	U1083	G1023	G963	G903
A1506	U1445	G1385	C1265	U1204	G1144	G1084	A1024	A964	C904
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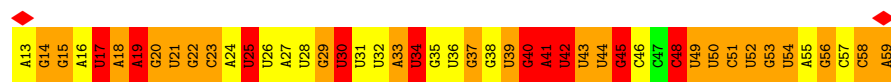
● Molecule 2: A site tRNA

Chain AB: 5% 34% 45% 16%

A1	G61
G2	U62
G3	C63
G4	U64
G5	C65
G6	C66
G7	G67
U8	C68
A9	C69
G10	C70
U11	C71
U12	U72
C13	G73
A14	C74
U15	C75
U16	A76

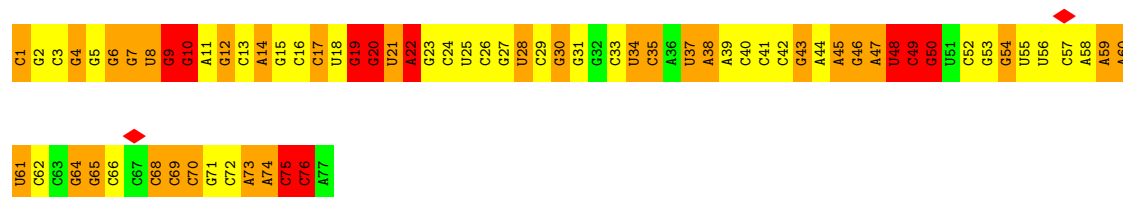
- Molecule 3: mRNA

Chain AC: 



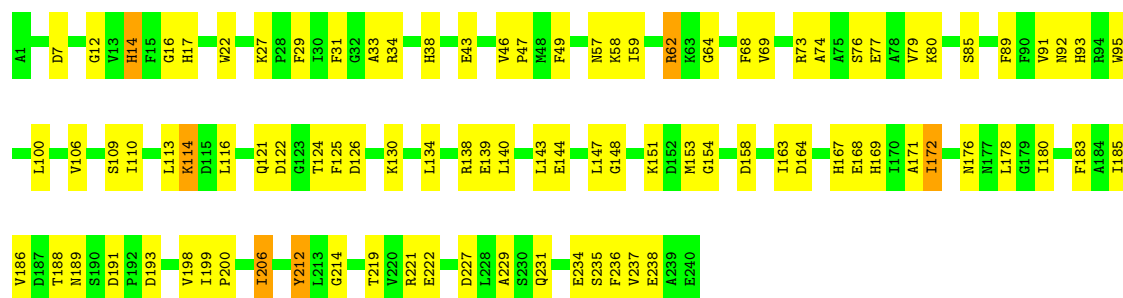
- Molecule 4: P site tRNA

Chain AD: 



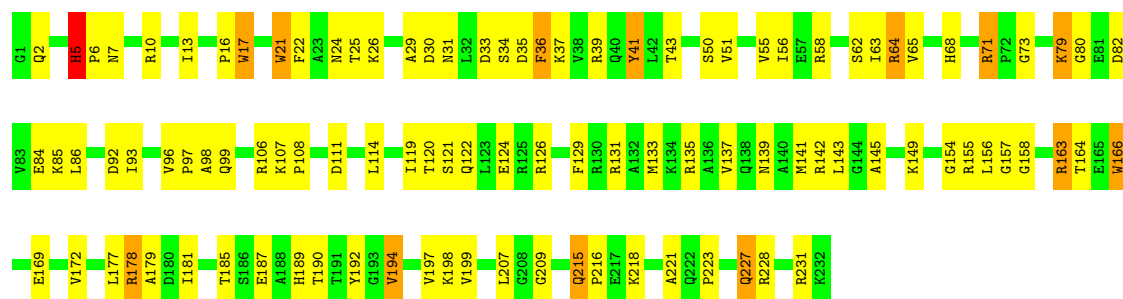
- Molecule 5: 30S ribosomal protein S2

Chain AE: 



- Molecule 6: 30S ribosomal protein S3

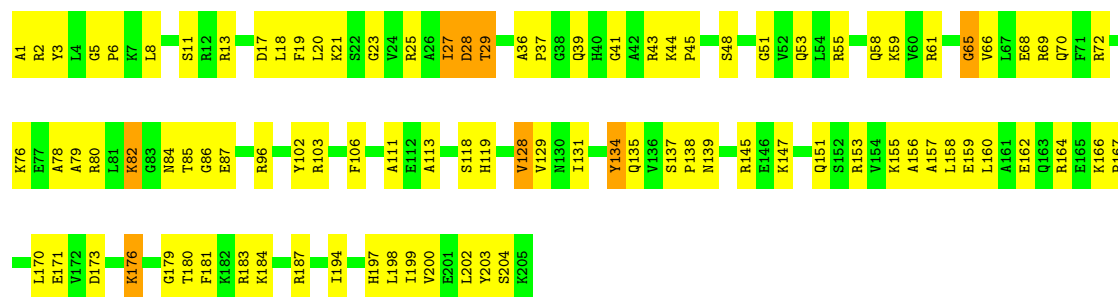
Chain AF: 



- Molecule 7: 30S ribosomal protein S4

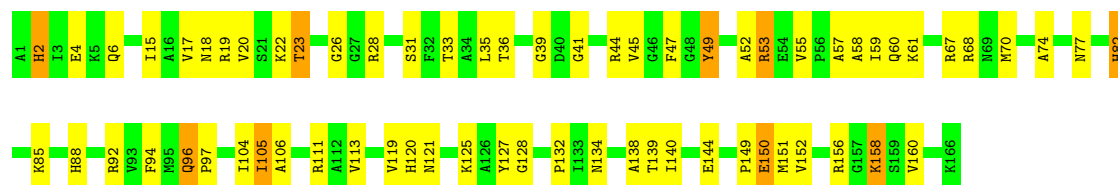
Chain AG: 





• Molecule 8: 30S ribosomal protein S5

Chain AH: 60% 34% 5%



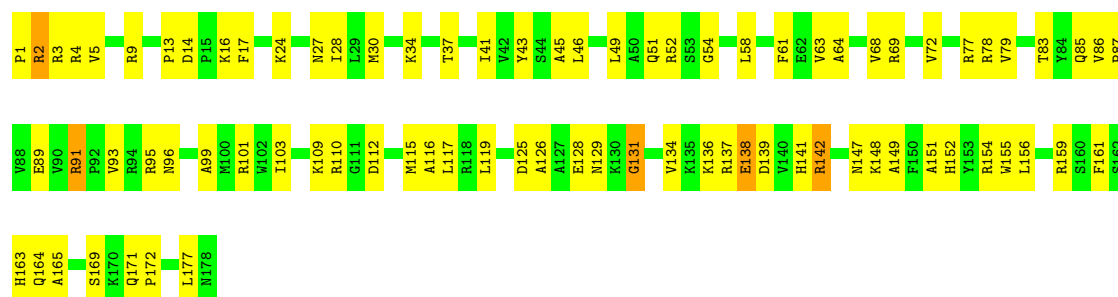
• Molecule 9: 30S ribosomal protein S6

Chain AI: 61% 35%



• Molecule 10: 30S ribosomal protein S7

Chain AJ: 54% 43%



• Molecule 11: 30S ribosomal protein S8

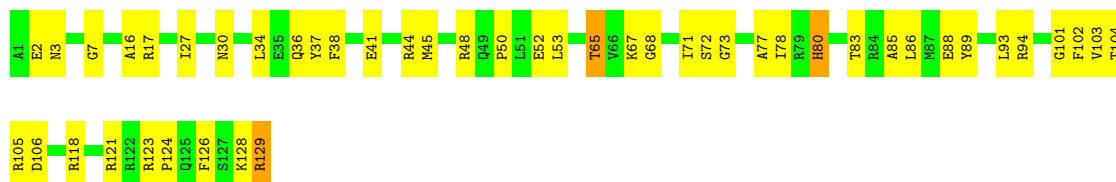
Chain AK: 62% 37%





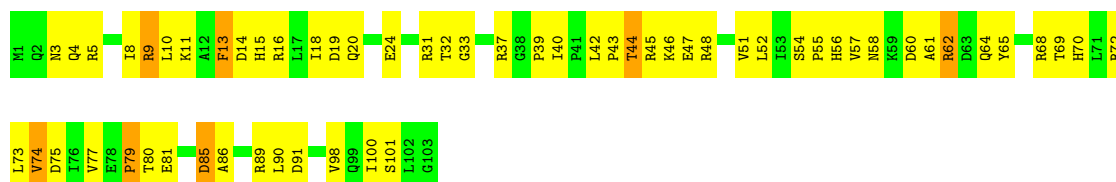
- Molecule 12: 30S ribosomal protein S9

Chain AL: 64% 34% .



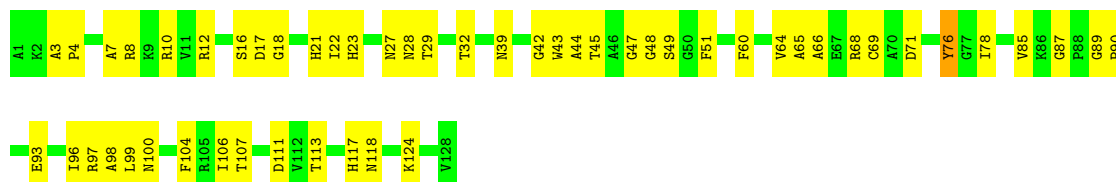
- Molecule 13: 30S ribosomal protein S10

Chain AM: 43% 50% 7% .



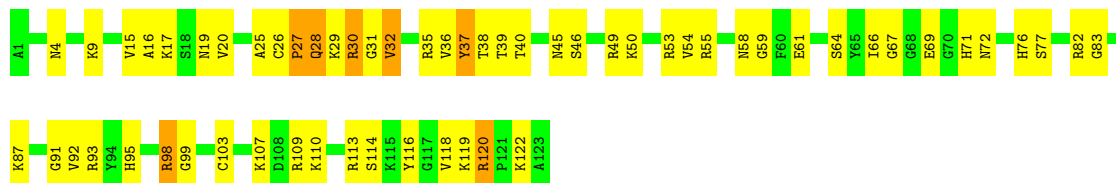
- Molecule 14: 30S ribosomal protein S11

Chain AN: 59% 40% .



- Molecule 15: 30S ribosomal protein S12

Chain AO: 52% 42% 6% .



- Molecule 16: 30S ribosomal protein S13

Chain AP: 53% 44% .





- Molecule 17: 30S ribosomal protein S14



- Molecule 18: 30S ribosomal protein S15



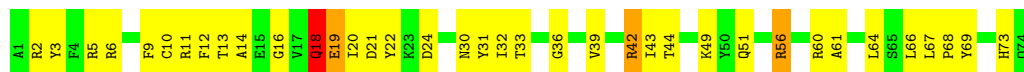
- Molecule 19: 30S ribosomal protein S16



- Molecule 20: 30S ribosomal protein S17



- Molecule 21: 30S ribosomal protein S18



- Molecule 22: 30S ribosomal protein S19





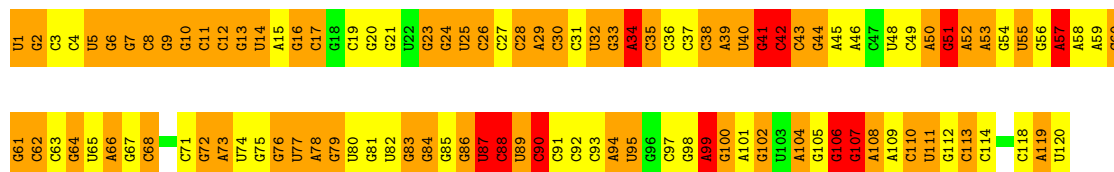
- Molecule 23: 30S ribosomal protein S20



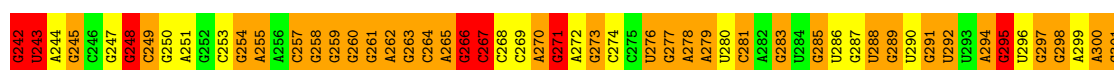
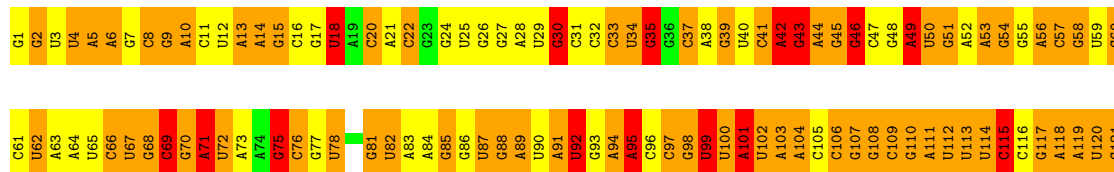
- Molecule 24: 30S ribosomal protein S21



- Molecule 25: 5S ribosomal RNA

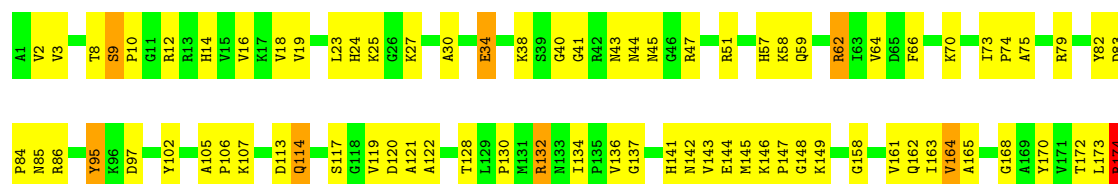


- Molecule 26: 23S ribosomal RNA



G1332	G1333	G1334	G1335	G1336	G1337	G1338	G1339	G1340	G1341	G1342	G1343	G1344	G1345	G1346	G1347	G1348	G1349	G1350	G1351	G1352	G1353	G1354	G1355	G1356	G1357	G1358	G1359	G1360	G1361	G1362	G1363	G1364	G1365	G1366	G1367	G1368	G1369	G1370	G1371	G1372	G1373	G1374	G1375	G1376	G1377	G1378	G1379	G1380	G1381	G1382	G1383	G1384	G1385	G1386	G1387	G1388	G1389	G1390	G1391			
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G1332	G1333	G1334	G1335	G1336	G1337	G1338	G1339	G1340	A1341	G1342	G1343	U1344	C1345	G1346	A1347	G1348	C1349	G1350	C1351	U1352	C1293	U1294	G1295	G1296	C1297	G1298	A1299	G1300	A1301	A1302	G1303	A1304	A1305	A1306	A1307	A1308	G1309	G1370	G1310	G1311	U1312	U1313	G1314	G1315	U1																	

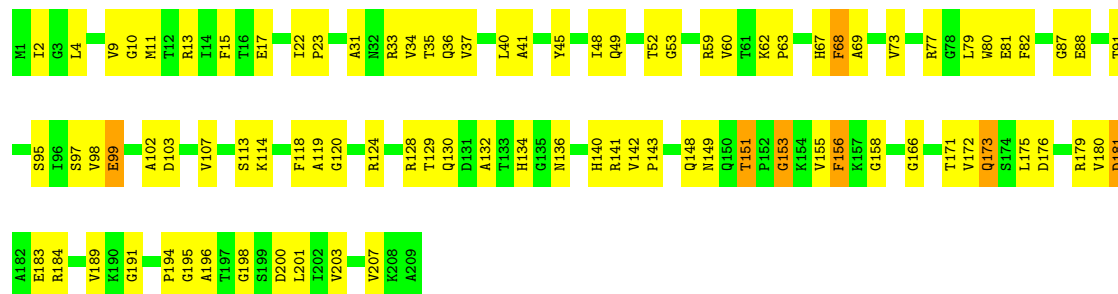
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C2355	C2295	G2235	C2175	G2115	G2055	U1995	G1935	A1875	A1815	A1754	C1694	A1634	C1574	C1513	A1452	A1393
C2356	C2296	G2236	A2176	G2116	G2056	C1996	A1936	A1876	A1816	A1755	C1695	A1635	C1575	C1514	A1453	A1394
C2357	C2297	G2237	C2177	G2117	G2057	C1997	A1937	A1877	A1817	A1756	G1696	U1637	C1576	A1515	G1455	A1395
C2358	A2298	G2238	C2178	G2118	A2058	C1998	A1938	A1878	C1818	A1757	G1697	A1637	C1577	G1516	G1456	A1396
C2359	U2299	G2239	C2179	A2119	A2059	C1999	U1939	C1879	A1819	U1758	A1698	C1638	U1578	C1517	U1457	U1397
C2360	C2300	U2240	U2180	G2120	A2060	C2000	U1940	C1880	U1820	C1759	G1699	C1639	U1579	C1518	U1458	C1398
C2361	C2301	A2241	U2181	G2121	G2061	C2001	C1941	C1881	A1821	C1760	A1700	A1640	A1579	C1519	U1459	C1399
C2362	G2302	G2242	U2182	G2122	A2062	G2002	C1942	U1882	C1822	C1761	A1701	A1641	C1581	U1520	U1460	U1400
C2363	C2303	G2243	A2183	G2123	C2063	A2003	U1943	U1883	C1823	A1762	G1702	G1642	C1582	U1521	C1461	G1401
C2364	G2304	U2244	A2184	G2124	C2064	G2004	U1944	C1884	G1824	C1763	G1703	G1643	A1522	C1462	U1402	
C2365	U2305	U2245	U2185	G2125	C2065	A2005	G1945	A1885	U1825	C1764	C1704	C1644	U1584	C1463	A1403	
A2366	C2306	G2246	G2186	A2126	C2066	C2006	U1946	U1886	G1826	U1765	A1705	G1645	C1585	G1524	G1464	C1404
C2367	G2307	A2247	U2187	G2127	G2067	U2007	C1947	C1887	U1827	C1766	C1706	C1646	A1586	C1525	U1465	U1405
C2368	G2308	C2248	U2188	G2128	U2068	C2008	G1948	C1888	G1828	C1767	G1707	U1647	C1587	C1526	U1466	
C2369	A2309	U2249	U2189	C2129	G2069	A2009	G1949	A1889	A1829	C1768	C1708	U1648	C1588	C1527	U1467	G1407
G2370	C2310	G2250	G2190	U2130	A2070	G2010	G1950	A1890	C1830	U1769	U1709	G1649	U1589	A1528	U1468	
C2371	A2311	G2251	A2191	U2131	A2071	U2011	U1951	C1891	G1831	C1770	G1710	A1650	A1590	G1529	A1469	U1409
C2372	U2312	C2252	U2192	U2132	C2072	G2012	A1952	C1892	C1832	C1771	A1591	G1651	A1591	C1530	A1470	G1410
C2373	G2313	G2253	G2193	G2133	C2073	A2013	A1953	C1893	C1833	A1772	U1712	A1652	C1592	C1531	G1471	G1411
C2374	G2314	C2254	U2194	A2134	U2074	A2014	G1954	C1894	U1834	C1773	U1713	G1653	A1593	C1532	A1472	U1412
C2375	A2315	G2255	U2195	A2135	U2075	A2015	U1955	C1895	C1835	C1774	U1714	A1654	U1594	C1533	G1473	A1413
G2376	G2316	G2256	C2196	G2136	U2076	U2016	U1956	G1896	C1836	U1775	G1715	C1655	C1595	C1534	U1474	
C2377	A2317	U2257	U2197	G2137	A2077	U2017	C1957	C1897	C1837	C1776	U1716	C1656	A1596	C1535	U1475	U1415
G2378	G2318	C2258	A2198	G2138	C2078	G2018	C1958	U1898	C1838	U1777	A1717	U1657	A1597	C1536	U1476	G1416
G2379	U2259	A2259	A2199	U2139	U2079	A2019	G1959	A1899	G1839	U1778	G1718	C1658	A1598	C1537	A1477	C1417
C2380	U2320	C2260	C2200	G2140	A2080	A2020	A1960	A1900	A1840	U1779	G1719	G1659	U1599	G1538	G1478	U1418
A2381	C2321	G2261	G2201	G2141	U2081	C2021	C1961	A1901	U1841	A1780	U1720	G1660	C1600	G1539	G1479	A1419
C2382	U2322	U2262	U2202	A2142	A2082	U2022	C1962	C1902	G1842	U1781	G1721	G1661	C1601	G1540	C1480	A1420
C2383	C2323	C2263	U2203	C2143	G2083	C2023	U1963	C1903	C1843	U1782	A1722	U1662	C1602	C1541	U1481	G1421
C2384	G2324	C2264	G2204	G2144	C2084	G2024	G1964	G1904	C1844	A1783	G1723	G1663	A1603	C1542	G1482	G1422
C2385	G2325	U2265	A2205	C2145	U2085	C2025	C1965	C1905	G1845	A1784	G1724	C1664	C1604	C1543	G1483	G1423
C2386	C2326	A2266	C2206	C2146	U2086	U2026	A1966	G1906	C1846	A1785	U1725	A1665	C1605	A1544	U1484	G1424
C2387	A2327	G2267	C2207	A2147	G2087	G2027	C1967	G1907	C1847	A1786	C1726	C1666	C1606	C1545	U1485	G1425
A2388	U2328	G2268	C2208	G2148	A2088	U2028	G1968	C1908	A1848	A1787	G1727	G1667	C1607	G1546	U1486	G1426
C2389	U2329	G2269	G2209	U2149	C2089	G2029	A1969	C1909	C1849	C1788	C1728	A1668	C1608	C1547	U1487	A1427
C2390	G2330	A2270	U2210	C2150	A2090	A2030	A1970	G1910	C1850	A1789	U1729	A1669	A1609	C1548	C1488	C1428
C2391	C2331	G2271	A2211	U2151	C2091	G2031	U1971	U1911	U1851	C1790	C1730	C1670	C1610	C1549	C1489	G1429
A2392	C2332	U2272	A2212	G2152	U2092	G2032	G1972	A1912	U1852	A1791	G1731	U1671	C1611	C1550	A1490	G1430
C2393	U2333	C2273	U2213	C2153	G2093	A2033	C1973	A1913	A1853	C1792	C1732	C1672	C1612	A1551	G1491	A1431
C2394	U2334	A2274	C2214	A2154	A2094	U2034	C1974	C1914	A1854	C1793	G1733	C1673	C1613	C1552	G1492	G1432
C2395	G2335	C2275	C2215	U2155	A2095	G2035	C1975	3T01915	U1855	A1794	G1734	C1674	A1614	A1553	C1493	A1433
A2396	C2336	G2276	G2216	G2156	C2096	C2036	C1976	A1916	U1856	C1795	C1735	C1675	C1615	U1554	A1494	A1434
C2397	G2337	G2277	G2217	C2157	A2097	A2037	A1977	U1917	C1857	U1796	U1736	A1676	C1616	C1555	A1495	G1435
C2398	U2338	A2278	G2218	A2158	U2098	G2038	A1978	A1918	C1858	C1797	G1737	A1677	C1617	C1556	A1496	G1436
C2399	C2339	G2279	U2219	G2159	U2099	U2039	U1979	A1919	U1859	U1798	G1738	A1678	C1618	C1557	U1497	C1437
G2400	A2340	G2280	U2220	C2160	G2100	G2040	G1980	C1920	G1860	C1799	A1739	A1679	G1619	C1558	C1498	U1438
U2401	G2341	A2281	G2221	C2161	A2101	U2041	A1981	C1921	G1861	C1800	G1740	U1680	G1620	C1499	U1439	
C2402	C2342	G2282	C2222	G2162	C2102	A2042	U1982	C1922	G1862	A1801	C1741	G1681	U1621	U1560	G1500	U1440
C2403	U2343	C2283	G2223	C2163	C2103	C2043	C2043	C1923	G1863	A1802	U1742	G1682	G1622	U1561	G1501	G1441
U2404	U2344	A2284	G2224	C2164	C2104	C2044	G1984	C1924	U1864	A1803	G1743	U1683	G1623	C1564	A1502	U1442
G2405	G2345	C2285	A2225	C2165	U2105	G2045	C1985	C1925	U1865	A1804	A1744	G1684	U1624	C1565	A1503	G1443
A2406	A2346	G2286	C2226	U2166	U2106	C2046	C1986	U1926	U1866	A1805	A1745	C1685	C1625	G1565	A1504	G1444
A2407	C2347	A2287	A2227	U2167	C2107	C2047	A1987	A1927	G1867	C1806	A1746	C1686	A1626	A1566	A1505	G1445
U2408	U2348	A2288	G2228	G2168	U2108	G2048	G1988	A1928	C1868	G1807	U1747	C1687	G1627	U1567	A1506	G1446
G2409	G2349	C2289	U2229	A2169	U2109	G2049	G1989	C1929	C1869	A1808	C1748	U1688	U1628	C1568	C1507	C1447
G2410	C2350	G2290	G2230	A2170	C2110	C2050	G1990	G1930	A1870	A1809	A1749	A1689	U1629	A1569	A1508	G1448
C2411	G2351	U2291	U2231	A2171	U2111	A2051	U1991	U1931	A1871	A1810	G1750	A1690	A1630	G1449	A1509	G1449
A2412	C2352	U2292	C2232	U2172	C2112	C2052	A1992	A1932	U1872	G1811	U1751	C1691	A1631	A1571	G1450	G1450
C2413	C2353	C2293	U2233	G2173	U2113	C2053	U1993	C1933	C1873		C1752	U1692	C1632	C1572	G1451	G1451





- Molecule 29: 50S ribosomal protein L3

Chain BE: 57% 40%



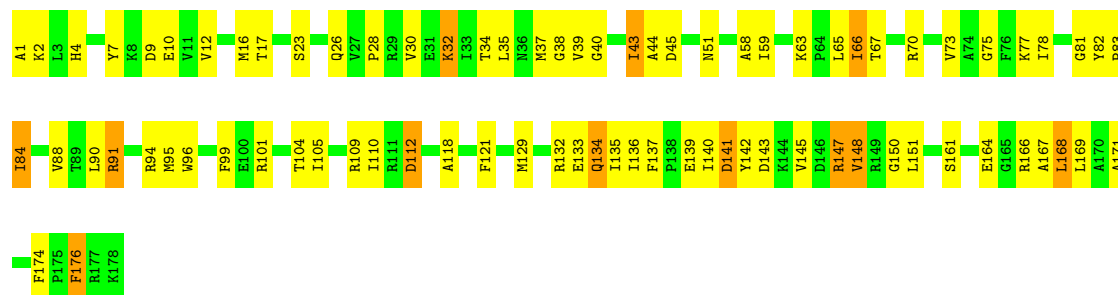
- Molecule 30: 50S ribosomal protein L4

Chain BF: 51% 45%



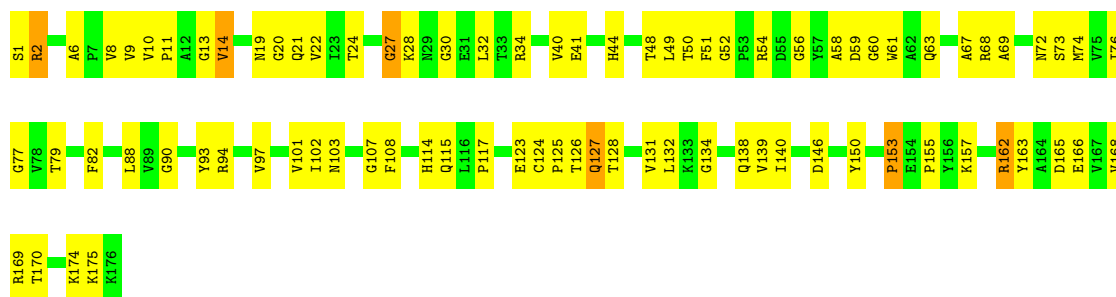
- Molecule 31: 50S ribosomal protein L5

Chain BG: 55% 38% 7%

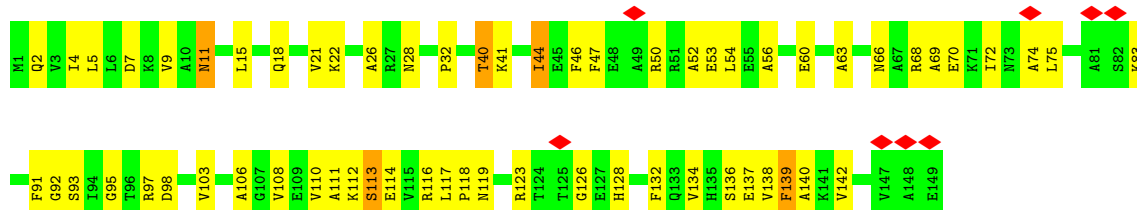


- Molecule 32: 50S ribosomal protein L6

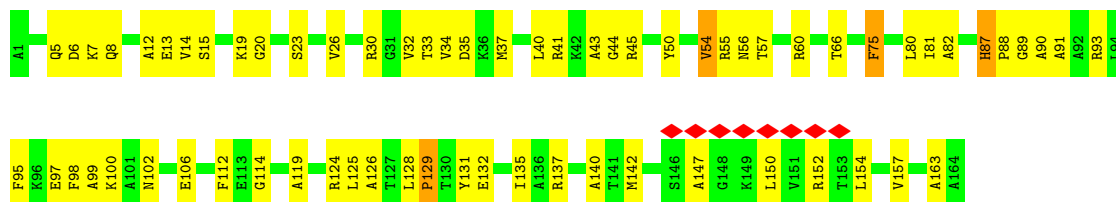
Chain BH: 53% 44%



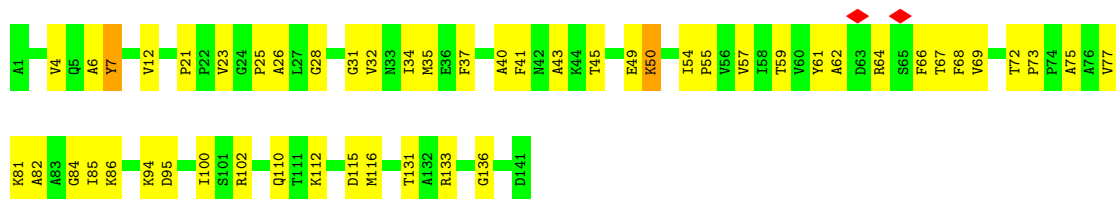
- Molecule 33: 50S ribosomal protein L9



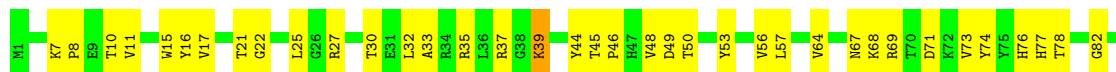
- Molecule 34: 50S ribosomal protein L10



- Molecule 35: 50S ribosomal protein L11



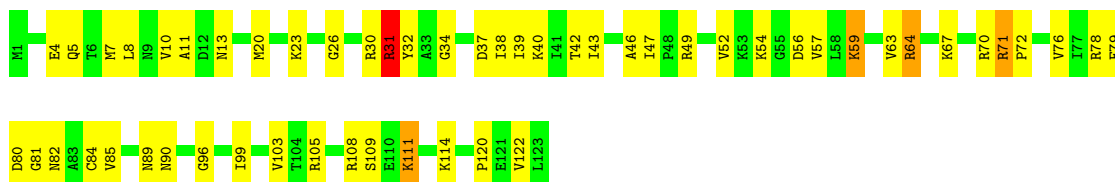
- Molecule 36: 50S ribosomal protein L13





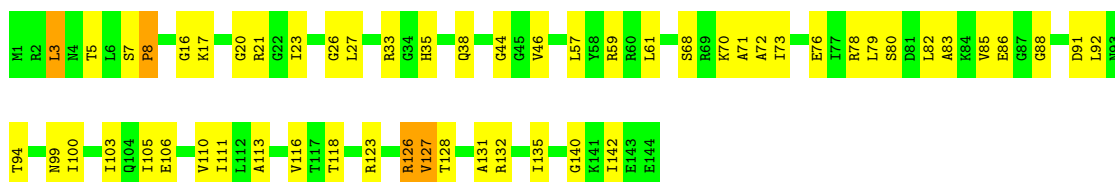
• Molecule 37: 50S ribosomal protein L14

Chain BM: 56% 40% . .



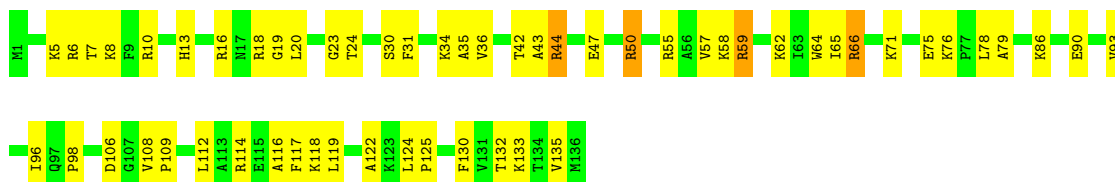
• Molecule 38: 50S ribosomal protein L15

Chain BN: 62% 35% .



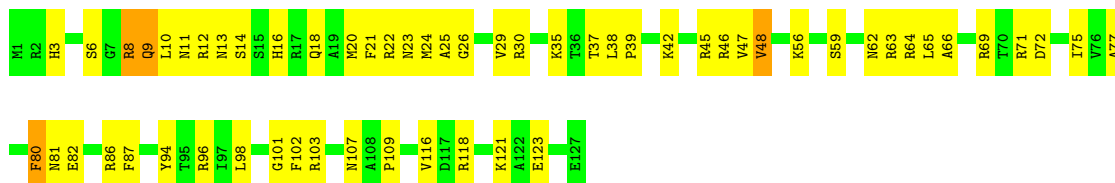
• Molecule 39: 50S ribosomal protein L16

Chain BO: 59% 38% .



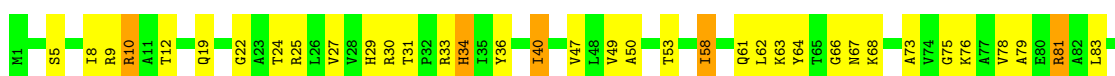
• Molecule 40: 50S ribosomal protein L17

Chain BP: 54% 43% .



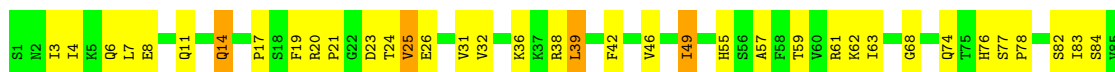
• Molecule 41: 50S ribosomal protein L18

Chain BQ: 54% 41% 5% .





- Molecule 42: 50S ribosomal protein L19



- Molecule 43: 50S ribosomal protein L20



- Molecule 44: 50S ribosomal protein L21

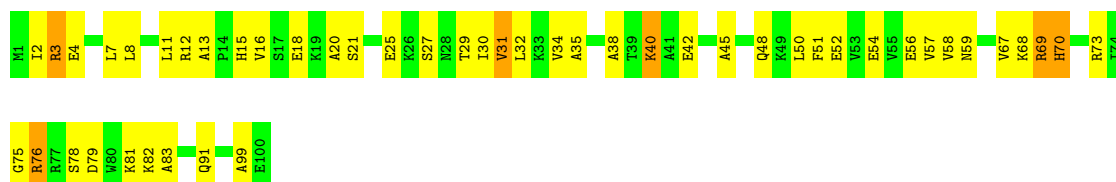


- Molecule 45: 50S ribosomal protein L22

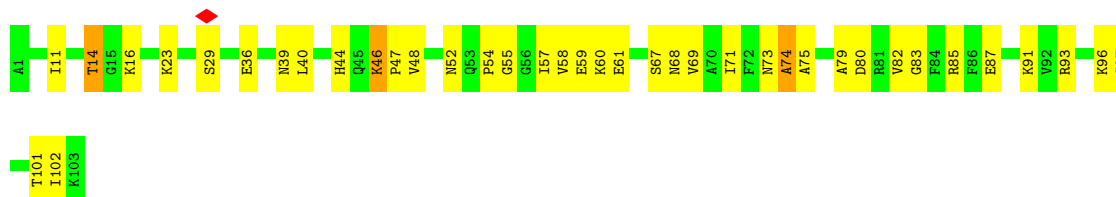


- Molecule 46: 50S ribosomal protein L23

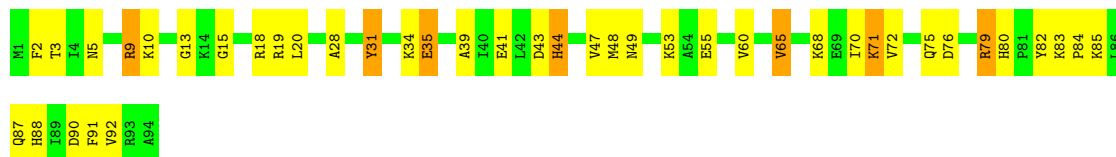




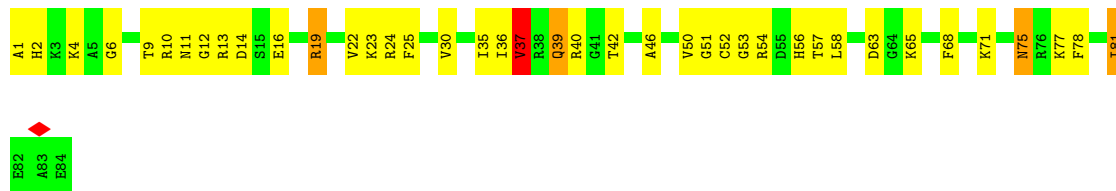
- Molecule 47: 50S ribosomal protein L24



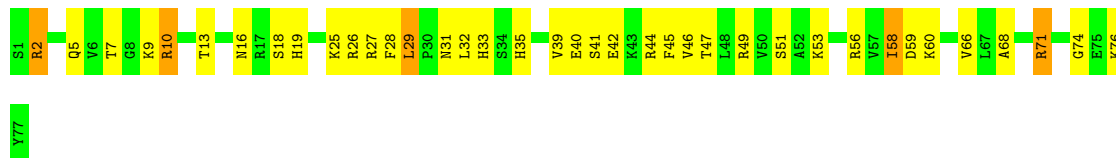
- Molecule 48: 50S ribosomal protein L25



- Molecule 49: 50S ribosomal protein L27



- Molecule 50: 50S ribosomal protein L28



- Molecule 51: 50S ribosomal protein L29





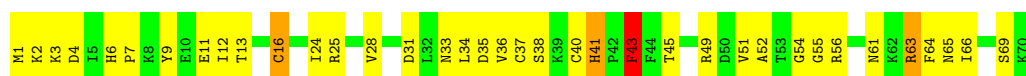
- Molecule 52: 50S ribosomal protein L30

Chain B1: 50% 45% 5%



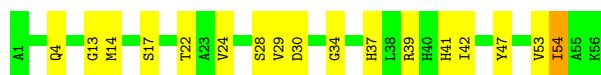
- Molecule 53: 50S ribosomal protein L31

Chain B2: 47% 47% 6%



- Molecule 54: 50S ribosomal protein L32

Chain B3: 70% 29% 1%



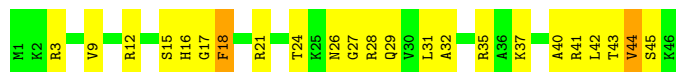
- Molecule 55: 50S ribosomal protein L33

Chain B4: 61% 33% 6%



- Molecule 56: 50S ribosomal protein L34

Chain B5: 50% 46% 4%



- Molecule 57: 50S ribosomal protein L35

Chain B6: 55% 34% 11%



- Molecule 58: 50S ribosomal protein L36

Chain B7: 42% 53% 5%

M1	K2	V3	R4	A5	S6	V7	K8	R9	L10	C11	I16	V17	K18	R19	D20	R24	V25	I26	C27	S28	A29	E30	F31	K32	H33	K34	Q35	R36	Q37	G38
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21000	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Volumes were CTF-corrected in defocus groups	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	58269	Depositor
Image detector	TVIPS TEMCAM-F415 (4k x 4k)	Depositor
Maximum map value	1.536	Depositor
Minimum map value	-0.480	Depositor
Average map value	0.031	Depositor
Map value standard deviation	0.200	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	375.0, 375.0, 375.0	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: UR3, OMC, 1MG, MA6, 2MA, PSU, FME, OMG, H2U, 4SU, 4OC, 6MZ, MIA, 2MG, OMU, 3TD, 5MC, 5MU, CH, 7MG

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	1.89	568/36769 (1.5%)	2.01	1972/57354 (3.4%)
2	AB	1.99	41/1600 (2.6%)	2.03	94/2492 (3.8%)
3	AC	1.94	22/1108 (2.0%)	2.12	74/1724 (4.3%)
4	AD	1.94	36/1721 (2.1%)	1.96	82/2683 (3.1%)
5	AE	1.92	32/1904 (1.7%)	2.41	111/2565 (4.3%)
6	AF	1.99	33/1852 (1.8%)	2.39	104/2490 (4.2%)
7	AG	2.02	34/1665 (2.0%)	2.41	101/2227 (4.5%)
8	AH	1.96	25/1239 (2.0%)	2.45	72/1664 (4.3%)
9	AI	1.93	13/1121 (1.2%)	2.37	54/1509 (3.6%)
10	AJ	1.97	28/1422 (2.0%)	2.44	90/1908 (4.7%)
11	AK	1.98	17/989 (1.7%)	2.32	48/1326 (3.6%)
12	AL	2.02	19/1048 (1.8%)	2.28	42/1394 (3.0%)
13	AM	2.04	18/835 (2.2%)	2.50	68/1127 (6.0%)
14	AN	1.99	17/982 (1.7%)	2.37	57/1323 (4.3%)
15	AO	2.05	22/969 (2.3%)	2.26	48/1300 (3.7%)
16	AP	2.10	31/919 (3.4%)	2.49	62/1226 (5.1%)
17	AQ	1.93	17/817 (2.1%)	2.33	44/1088 (4.0%)
18	AR	2.04	18/724 (2.5%)	2.50	55/966 (5.7%)
19	AS	2.04	16/659 (2.4%)	2.30	29/884 (3.3%)
20	AT	1.94	10/681 (1.5%)	2.39	34/913 (3.7%)
21	AU	2.16	18/637 (2.8%)	2.42	35/851 (4.1%)
22	AV	1.90	10/744 (1.3%)	2.31	31/995 (3.1%)
23	AW	2.00	14/676 (2.1%)	2.44	30/895 (3.4%)
24	AX	1.93	9/598 (1.5%)	2.36	33/792 (4.2%)
25	BA	1.85	36/2869 (1.3%)	2.02	149/4474 (3.3%)
26	BB	1.90	1145/69257 (1.7%)	2.00	3688/108040 (3.4%)
27	BC	1.97	35/1748 (2.0%)	2.39	105/2355 (4.5%)
28	BD	2.08	57/2131 (2.7%)	2.33	112/2863 (3.9%)
29	BE	1.95	27/1586 (1.7%)	2.38	90/2134 (4.2%)
30	BF	1.92	23/1571 (1.5%)	2.43	107/2113 (5.1%)
31	BG	1.98	18/1444 (1.2%)	2.38	74/1937 (3.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	BH	2.10	38/1343 (2.8%)	2.38	71/1816 (3.9%)
33	BI	2.07	24/1122 (2.1%)	2.32	61/1515 (4.0%)
34	BJ	1.99	18/1247 (1.4%)	2.40	76/1679 (4.5%)
35	BK	2.01	21/1046 (2.0%)	2.45	45/1410 (3.2%)
36	BL	1.95	21/1152 (1.8%)	2.48	64/1551 (4.1%)
37	BM	1.99	17/956 (1.8%)	2.36	59/1279 (4.6%)
38	BN	1.96	17/1062 (1.6%)	2.40	57/1413 (4.0%)
39	BO	1.98	22/1093 (2.0%)	2.39	48/1460 (3.3%)
40	BP	2.01	23/1021 (2.3%)	2.32	42/1364 (3.1%)
41	BQ	2.10	29/910 (3.2%)	2.35	46/1219 (3.8%)
42	BR	1.99	19/929 (2.0%)	2.26	49/1242 (3.9%)
43	BS	2.01	17/960 (1.8%)	2.55	67/1278 (5.2%)
44	BT	2.01	23/829 (2.8%)	2.22	36/1107 (3.3%)
45	BU	2.14	27/864 (3.1%)	2.40	55/1156 (4.8%)
46	BV	2.12	24/794 (3.0%)	2.39	40/1060 (3.8%)
47	BW	2.09	19/797 (2.4%)	2.21	29/1062 (2.7%)
48	BX	2.02	16/766 (2.1%)	2.31	40/1025 (3.9%)
49	BY	2.06	13/642 (2.0%)	2.43	38/848 (4.5%)
50	BZ	2.11	17/635 (2.7%)	2.38	34/848 (4.0%)
51	B0	1.87	3/510 (0.6%)	2.32	19/677 (2.8%)
52	B1	1.96	12/453 (2.6%)	2.38	26/605 (4.3%)
53	B2	2.00	14/559 (2.5%)	2.27	25/745 (3.4%)
54	B3	1.97	5/450 (1.1%)	2.31	16/599 (2.7%)
55	B4	2.00	7/448 (1.6%)	2.30	20/594 (3.4%)
56	B5	2.15	13/380 (3.4%)	2.41	23/498 (4.6%)
57	B6	2.06	12/513 (2.3%)	2.43	33/676 (4.9%)
58	B7	2.08	10/303 (3.3%)	2.34	21/397 (5.3%)
All	All	1.93	2890/164069 (1.8%)	2.11	8835/244735 (3.6%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	881
2	AB	0	40
3	AC	0	28
4	AD	0	42
5	AE	0	3
6	AF	0	11
7	AG	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
8	AH	0	2
9	AI	0	4
10	AJ	0	4
11	AK	0	2
12	AL	0	2
14	AN	0	3
15	AO	0	4
16	AP	0	1
17	AQ	0	4
18	AR	0	1
19	AS	0	2
20	AT	0	1
21	AU	0	3
22	AV	0	2
23	AW	0	1
24	AX	0	2
25	BA	0	75
26	BB	0	1720
27	BC	0	2
28	BD	0	9
29	BE	0	4
30	BF	0	3
31	BG	0	6
32	BH	0	3
33	BI	0	1
34	BJ	0	5
35	BK	0	3
36	BL	0	2
37	BM	0	5
38	BN	0	2
39	BO	0	3
40	BP	0	4
41	BQ	0	6
42	BR	0	4
43	BS	0	6
44	BT	0	4
45	BU	0	5
46	BV	0	2
48	BX	0	4
49	BY	0	5
50	BZ	0	2
51	B0	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
52	B1	0	1
53	B2	0	4
54	B3	0	1
55	B4	0	4
56	B5	0	2
57	B6	0	2
All	All	0	2949

The worst 5 of 2890 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	BB	2552	OMU	O3'-P	12.14	1.68	1.56
26	BB	2104	C	P-O5'	11.58	1.77	1.59
2	AB	8	4SU	O3'-P	11.32	1.67	1.56
1	AA	1072	G	P-O5'	10.72	1.75	1.59
13	AM	40	ILE	CA-C	10.45	1.61	1.53

The worst 5 of 8835 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	694	A	C4'-C3'-C2'	-13.67	88.93	102.60
46	BV	70	HIS	CA-CB-CG	13.47	127.27	113.80
26	BB	2903	U	O4'-C1'-C2'	-13.21	94.39	107.60
26	BB	2075	U	C4'-C3'-C2'	-13.17	89.43	102.60
4	AD	7	G	C4'-C3'-O3'	13.11	129.06	109.40

There are no chirality outliers.

5 of 2949 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	11	G	Sidechain
1	AA	3	A	Sidechain
1	AA	4	U	Sidechain
1	AA	5	U	Sidechain
1	AA	6	G	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	16619	0	0
2	AB	1627	0	844	0	0
3	AC	993	0	501	0	0
4	AD	1641	0	840	0	0
5	AE	1872	0	1885	0	0
6	AF	1822	0	1913	0	0
7	AG	1643	0	1710	0	0
8	AH	1225	0	1273	0	0
9	AI	1101	0	1050	0	0
10	AJ	1400	0	1449	0	0
11	AK	979	0	1034	0	0
12	AL	1036	0	1084	0	0
13	AM	825	0	865	0	0
14	AN	965	0	997	0	0
15	AO	955	0	1019	0	0
16	AP	910	0	981	0	0
17	AQ	805	0	847	0	0
18	AR	716	0	742	0	0
19	AS	649	0	666	0	0
20	AT	672	0	716	0	0
21	AU	626	0	651	0	0
22	AV	727	0	769	0	0
23	AW	670	0	722	0	0
24	AX	590	0	631	0	0
25	BA	2566	0	1296	0	0
26	BB	62351	0	31238	0	0
27	BC	1733	0	1824	0	0
28	BD	2092	0	2170	0	0
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	1233	0	1283	0	0
35	BK	1032	0	1088	0	0
36	BL	1129	0	1162	0	0
37	BM	947	0	1023	0	0
38	BN	1053	0	1129	0	0
39	BO	1074	0	1157	0	0
40	BP	1008	0	1045	0	0
41	BQ	900	0	935	0	0
42	BR	917	0	965	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	BS	947	0	1022	0	0
44	BT	816	0	839	0	0
45	BU	857	0	922	0	0
46	BV	787	0	846	0	0
47	BW	789	0	847	0	0
48	BX	753	0	780	0	0
49	BY	634	0	656	0	0
50	BZ	625	0	655	0	0
51	B0	509	0	543	0	0
52	B1	449	0	491	0	0
53	B2	549	0	552	0	0
54	B3	444	0	461	0	0
55	B4	441	0	485	0	0
56	B5	377	0	418	0	0
57	B6	504	0	574	0	0
58	B7	302	0	343	0	0
59	AB	14	0	9	0	0
60	BB	10	0	10	0	0
All	All	152351	0	103793	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 [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	AE	238/240 (99%)	211 (89%)	24 (10%)	3 (1%)	9	42
6	AF	230/232 (99%)	204 (89%)	20 (9%)	6 (3%)	4	25
7	AG	203/205 (99%)	182 (90%)	17 (8%)	4 (2%)	6	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	AH	164/166 (99%)	146 (89%)	15 (9%)	3 (2%)	6	34
9	AI	133/135 (98%)	118 (89%)	12 (9%)	3 (2%)	5	28
10	AJ	176/178 (99%)	163 (93%)	11 (6%)	2 (1%)	11	46
11	AK	127/129 (98%)	116 (91%)	9 (7%)	2 (2%)	7	38
12	AL	127/129 (98%)	118 (93%)	7 (6%)	2 (2%)	7	38
13	AM	101/103 (98%)	92 (91%)	5 (5%)	4 (4%)	2	18
14	AN	126/128 (98%)	111 (88%)	15 (12%)	0	100	100
15	AO	121/123 (98%)	103 (85%)	14 (12%)	4 (3%)	3	21
16	AP	115/117 (98%)	101 (88%)	11 (10%)	3 (3%)	4	25
17	AQ	98/100 (98%)	79 (81%)	13 (13%)	6 (6%)	1	13
18	AR	86/88 (98%)	82 (95%)	3 (4%)	1 (1%)	10	44
19	AS	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	9	42
20	AT	81/83 (98%)	66 (82%)	14 (17%)	1 (1%)	10	44
21	AU	72/74 (97%)	63 (88%)	6 (8%)	3 (4%)	2	17
22	AV	89/91 (98%)	79 (89%)	6 (7%)	4 (4%)	2	17
23	AW	84/86 (98%)	78 (93%)	4 (5%)	2 (2%)	4	27
24	AX	68/70 (97%)	53 (78%)	13 (19%)	2 (3%)	3	23
27	BC	232/234 (99%)	207 (89%)	20 (9%)	5 (2%)	5	29
28	BD	270/272 (99%)	232 (86%)	30 (11%)	8 (3%)	3	23
29	BE	207/209 (99%)	171 (83%)	31 (15%)	5 (2%)	4	27
30	BF	199/201 (99%)	171 (86%)	16 (8%)	12 (6%)	1	13
31	BG	176/178 (99%)	142 (81%)	24 (14%)	10 (6%)	1	14
32	BH	174/176 (99%)	149 (86%)	22 (13%)	3 (2%)	7	36
33	BI	147/149 (99%)	124 (84%)	21 (14%)	2 (1%)	9	40
34	BJ	162/164 (99%)	147 (91%)	13 (8%)	2 (1%)	10	44
35	BK	139/141 (99%)	126 (91%)	12 (9%)	1 (1%)	18	56
36	BL	140/142 (99%)	112 (80%)	21 (15%)	7 (5%)	1	16
37	BM	121/123 (98%)	104 (86%)	13 (11%)	4 (3%)	3	21
38	BN	142/144 (99%)	121 (85%)	17 (12%)	4 (3%)	4	24
39	BO	134/136 (98%)	116 (87%)	14 (10%)	4 (3%)	3	23
40	BP	125/127 (98%)	116 (93%)	8 (6%)	1 (1%)	16	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	BQ	115/117 (98%)	109 (95%)	4 (4%)	2 (2%)	7	36
42	BR	112/114 (98%)	88 (79%)	22 (20%)	2 (2%)	6	34
43	BS	115/117 (98%)	106 (92%)	7 (6%)	2 (2%)	7	36
44	BT	101/103 (98%)	90 (89%)	8 (8%)	3 (3%)	3	23
45	BU	108/110 (98%)	101 (94%)	4 (4%)	3 (3%)	4	24
46	BV	98/100 (98%)	78 (80%)	14 (14%)	6 (6%)	1	13
47	BW	101/103 (98%)	85 (84%)	13 (13%)	3 (3%)	3	23
48	BX	92/94 (98%)	82 (89%)	9 (10%)	1 (1%)	11	46
49	BY	82/84 (98%)	60 (73%)	18 (22%)	4 (5%)	1	16
50	BZ	75/77 (97%)	65 (87%)	6 (8%)	4 (5%)	1	15
51	B0	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	7	38
52	B1	56/58 (97%)	50 (89%)	5 (9%)	1 (2%)	6	34
53	B2	68/70 (97%)	45 (66%)	18 (26%)	5 (7%)	1	10
54	B3	54/56 (96%)	44 (82%)	9 (17%)	1 (2%)	6	32
55	B4	52/54 (96%)	45 (86%)	4 (8%)	3 (6%)	1	14
56	B5	44/46 (96%)	40 (91%)	2 (4%)	2 (4%)	2	17
57	B6	62/64 (97%)	54 (87%)	6 (10%)	2 (3%)	3	21
58	B7	36/38 (95%)	31 (86%)	4 (11%)	1 (3%)	4	24
All	All	6319/6423 (98%)	5506 (87%)	643 (10%)	170 (3%)	6	25

5 of 170 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	AL	86	LEU
13	AM	42	LEU
13	AM	57	VAL
16	AP	22	TYR
21	AU	11	ARG

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	
5	AE	198/198 (100%)	192 (97%)	6 (3%)	36	57
6	AF	189/189 (100%)	178 (94%)	11 (6%)	18	40
7	AG	172/172 (100%)	165 (96%)	7 (4%)	27	49
8	AH	125/125 (100%)	118 (94%)	7 (6%)	19	40
9	AI	116/116 (100%)	109 (94%)	7 (6%)	17	39
10	AJ	146/146 (100%)	142 (97%)	4 (3%)	39	61
11	AK	104/104 (100%)	103 (99%)	1 (1%)	68	78
12	AL	106/106 (100%)	104 (98%)	2 (2%)	50	67
13	AM	90/90 (100%)	82 (91%)	8 (9%)	9	28
14	AN	98/98 (100%)	97 (99%)	1 (1%)	68	78
15	AO	103/103 (100%)	93 (90%)	10 (10%)	8	24
16	AP	95/95 (100%)	90 (95%)	5 (5%)	20	41
17	AQ	83/83 (100%)	81 (98%)	2 (2%)	43	64
18	AR	76/76 (100%)	74 (97%)	2 (3%)	40	62
19	AS	65/65 (100%)	64 (98%)	1 (2%)	57	72
20	AT	77/77 (100%)	75 (97%)	2 (3%)	40	62
21	AU	64/64 (100%)	60 (94%)	4 (6%)	16	37
22	AV	78/78 (100%)	73 (94%)	5 (6%)	16	37
23	AW	65/65 (100%)	63 (97%)	2 (3%)	35	56
24	AX	60/60 (100%)	56 (93%)	4 (7%)	15	36
27	BC	181/181 (100%)	175 (97%)	6 (3%)	33	55
28	BD	217/217 (100%)	207 (95%)	10 (5%)	24	45
29	BE	164/164 (100%)	154 (94%)	10 (6%)	17	38
30	BF	165/165 (100%)	158 (96%)	7 (4%)	26	48
31	BG	149/149 (100%)	140 (94%)	9 (6%)	17	39
32	BH	137/137 (100%)	129 (94%)	8 (6%)	18	40
33	BI	114/114 (100%)	110 (96%)	4 (4%)	32	53
34	BJ	122/122 (100%)	118 (97%)	4 (3%)	33	55
35	BK	109/109 (100%)	106 (97%)	3 (3%)	38	60
36	BL	116/116 (100%)	111 (96%)	5 (4%)	26	47
37	BM	104/104 (100%)	98 (94%)	6 (6%)	18	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	BN	103/103 (100%)	97 (94%)	6 (6%)	18	40
39	BO	109/109 (100%)	105 (96%)	4 (4%)	30	51
40	BP	103/103 (100%)	93 (90%)	10 (10%)	8	24
41	BQ	87/87 (100%)	85 (98%)	2 (2%)	44	64
42	BR	99/99 (100%)	91 (92%)	8 (8%)	11	31
43	BS	89/89 (100%)	86 (97%)	3 (3%)	32	54
44	BT	84/84 (100%)	80 (95%)	4 (5%)	23	44
45	BU	93/93 (100%)	91 (98%)	2 (2%)	45	64
46	BV	84/84 (100%)	76 (90%)	8 (10%)	8	25
47	BW	84/84 (100%)	80 (95%)	4 (5%)	23	44
48	BX	78/78 (100%)	74 (95%)	4 (5%)	21	42
49	BY	62/62 (100%)	60 (97%)	2 (3%)	34	56
50	BZ	67/67 (100%)	63 (94%)	4 (6%)	17	39
51	B0	55/55 (100%)	51 (93%)	4 (7%)	13	34
52	B1	48/48 (100%)	44 (92%)	4 (8%)	10	30
53	B2	62/62 (100%)	58 (94%)	4 (6%)	15	37
54	B3	47/47 (100%)	44 (94%)	3 (6%)	16	37
55	B4	48/48 (100%)	47 (98%)	1 (2%)	47	65
56	B5	38/38 (100%)	38 (100%)	0	100	100
57	B6	51/51 (100%)	45 (88%)	6 (12%)	5	18
58	B7	34/34 (100%)	32 (94%)	2 (6%)	18	39
All	All	5213/5213 (100%)	4965 (95%)	248 (5%)	24	44

5 of 248 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	BE	181	ASP
50	BZ	32	LEU
33	BI	75	LEU
49	BY	39	GLN
54	B3	29	VAL

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	1541/1542 (99%)	301 (19%)	99 (6%)
2	AB	75/76 (98%)	23 (30%)	6 (8%)
25	BA	119/120 (99%)	19 (15%)	10 (8%)
26	BB	2901/2904 (99%)	572 (19%)	186 (6%)
3	AC	46/47 (97%)	18 (39%)	6 (13%)
4	AD	76/77 (98%)	17 (22%)	4 (5%)
All	All	4758/4766 (99%)	950 (19%)	311 (6%)

5 of 950 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	8	A
1	AA	32	A
1	AA	36	C
1	AA	47	C
1	AA	48	C

5 of 311 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	BB	1778	U
26	BB	2602	A
26	BB	1927	A
26	BB	2223	G
26	BB	2791	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

49 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	H2U	AB	16	2	18,21,22	1.16	1 (5%)	19,30,33	1.97	7 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	4OC	AA	1402	1	20,23,24	1.30	2 (10%)	25,32,35	1.15	2 (8%)
26	OMC	BB	2498	26	19,22,23	1.23	2 (10%)	25,31,34	1.70	5 (20%)
26	CH	BB	2575	26	16,21,22	1.80	5 (31%)	19,30,33	1.75	5 (26%)
2	5MU	AB	54	2	19,22,23	1.58	4 (21%)	27,32,35	1.98	9 (33%)
26	2MG	BB	1835	26	23,26,27	0.94	1 (4%)	33,38,41	1.77	9 (27%)
1	2MG	AA	1516	1	23,26,27	1.44	5 (21%)	33,38,41	1.30	5 (15%)
26	6MZ	BB	1618	26	22,25,26	1.11	1 (4%)	29,36,39	1.53	4 (13%)
1	PSU	AA	516	1	18,21,22	1.92	7 (38%)	21,30,33	3.16	13 (61%)
1	5MC	AA	1407	1	19,22,23	2.42	2 (10%)	26,32,35	1.63	9 (34%)
1	2MG	AA	1207	1	23,26,27	1.25	2 (8%)	33,38,41	1.48	4 (12%)
1	MA6	AA	1518	1	23,26,27	1.15	2 (8%)	33,38,41	1.98	11 (33%)
1	5MC	AA	967	1	19,22,23	1.55	4 (21%)	26,32,35	1.88	6 (23%)
2	H2U	AB	17	2	18,21,22	1.43	2 (11%)	19,30,33	2.19	4 (21%)
4	OMC	AD	33	4	19,22,23	0.91	0	25,31,34	1.87	5 (20%)
26	1MG	BB	745	26	23,26,27	1.48	5 (21%)	33,39,42	1.44	6 (18%)
26	6MZ	BB	2030	26	22,25,26	1.33	4 (18%)	29,36,39	2.02	6 (20%)
1	7MG	AA	527	1	23,26,27	4.04	4 (17%)	27,39,42	2.06	7 (25%)
26	PSU	BB	746	26	18,21,22	1.88	6 (33%)	21,30,33	1.34	3 (14%)
2	MIA	AB	37	2	28,31,32	2.27	6 (21%)	38,44,47	1.74	10 (26%)
4	PSU	AD	56	4	18,21,22	1.49	4 (22%)	21,30,33	1.38	2 (9%)
2	PSU	AB	55	2	18,21,22	1.56	3 (16%)	21,30,33	1.48	4 (19%)
2	H2U	AB	20	2	18,21,22	1.59	4 (22%)	19,30,33	1.72	6 (31%)
26	PSU	BB	1911	26	18,21,22	1.75	4 (22%)	21,30,33	1.29	2 (9%)
1	UR3	AA	1498	1	19,22,23	1.28	3 (15%)	26,32,35	1.42	4 (15%)
2	4SU	AB	8	2	18,21,22	1.37	3 (16%)	25,30,33	1.69	7 (28%)
26	PSU	BB	2605	26	18,21,22	2.01	5 (27%)	21,30,33	2.48	7 (33%)
2	OMC	AB	32	2	19,22,23	1.20	2 (10%)	25,31,34	1.34	4 (16%)
26	H2U	BB	2449	26	18,21,22	1.52	2 (11%)	19,30,33	1.95	5 (26%)
26	PSU	BB	1917	26	18,21,22	2.05	2 (11%)	21,30,33	1.82	5 (23%)
26	PSU	BB	2504	26	18,21,22	1.90	4 (22%)	21,30,33	1.73	6 (28%)
4	5MU	AD	55	4	19,22,23	1.46	2 (10%)	27,32,35	1.90	7 (25%)
26	5MU	BB	1939	26	19,22,23	1.55	5 (26%)	27,32,35	2.03	8 (29%)
4	4SU	AD	8	4	18,21,22	2.18	5 (27%)	25,30,33	1.74	7 (28%)
1	2MG	AA	966	1	23,26,27	1.21	3 (13%)	33,38,41	1.30	5 (15%)
26	PSU	BB	2457	26	18,21,22	2.14	5 (27%)	21,30,33	1.78	6 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
26	PSU	BB	955	26	18,21,22	1.80	6 (33%)	21,30,33	1.77	6 (28%)
4	H2U	AD	21	4	18,21,22	1.60	2 (11%)	19,30,33	1.67	5 (26%)
1	MA6	AA	1519	1	23,26,27	1.11	2 (8%)	33,38,41	1.42	5 (15%)
26	OMG	BB	2251	26	23,26,27	1.26	1 (4%)	32,38,41	1.32	2 (6%)
26	OMU	BB	2552	26	19,22,23	1.33	2 (10%)	25,31,34	2.37	11 (44%)
2	7MG	AB	46	2	23,26,27	4.52	6 (26%)	27,39,42	1.98	4 (14%)
26	2MA	BB	2503	26	22,25,26	1.22	2 (9%)	32,37,40	1.68	8 (25%)
26	3TD	BB	1915	26	19,22,23	1.28	2 (10%)	23,32,35	1.47	3 (13%)
26	2MG	BB	2445	26	23,26,27	1.26	3 (13%)	33,38,41	1.22	2 (6%)
26	5MU	BB	747	26	19,22,23	1.60	4 (21%)	27,32,35	2.90	8 (29%)
26	7MG	BB	2069	26	23,26,27	3.10	6 (26%)	27,39,42	1.84	3 (11%)
26	5MC	BB	1962	26	19,22,23	1.01	1 (5%)	26,32,35	1.58	3 (11%)
26	PSU	BB	2580	26	18,21,22	2.08	6 (33%)	21,30,33	2.11	6 (28%)

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	H2U	AB	16	2	-	0/7/38/39	0/2/2/2
1	4OC	AA	1402	1	-	0/9/29/30	0/2/2/2
26	OMC	BB	2498	26	-	0/9/27/28	0/2/2/2
26	CH	BB	2575	26	-	0/5/25/26	0/2/2/2
2	5MU	AB	54	2	-	1/7/25/26	0/2/2/2
26	2MG	BB	1835	26	-	0/9/27/28	0/3/3/3
1	2MG	AA	1516	1	-	0/9/27/28	0/3/3/3
26	6MZ	BB	1618	26	-	0/9/27/28	0/3/3/3
1	PSU	AA	516	1	-	2/7/25/26	0/2/2/2
1	5MC	AA	1407	1	-	0/7/25/26	0/2/2/2
1	2MG	AA	1207	1	-	0/9/27/28	0/3/3/3
1	MA6	AA	1518	1	-	0/11/29/30	0/3/3/3
1	5MC	AA	967	1	-	0/7/25/26	0/2/2/2
2	H2U	AB	17	2	-	1/7/38/39	0/2/2/2
4	OMC	AD	33	4	-	0/9/27/28	0/2/2/2
26	1MG	BB	745	26	-	0/7/25/26	0/3/3/3
26	6MZ	BB	2030	26	-	0/9/27/28	0/3/3/3
1	7MG	AA	527	1	-	1/7/37/38	0/3/3/3
26	PSU	BB	746	26	-	1/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MIA	AB	37	2	-	2/15/33/34	0/3/3/3
4	PSU	AD	56	4	-	0/7/25/26	0/2/2/2
2	PSU	AB	55	2	-	1/7/25/26	0/2/2/2
2	H2U	AB	20	2	-	2/7/38/39	0/2/2/2
26	PSU	BB	1911	26	-	1/7/25/26	0/2/2/2
1	UR3	AA	1498	1	-	1/7/25/26	0/2/2/2
2	4SU	AB	8	2	-	5/7/25/26	0/2/2/2
26	PSU	BB	2605	26	-	2/7/25/26	0/2/2/2
2	OMC	AB	32	2	-	0/9/27/28	0/2/2/2
26	H2U	BB	2449	26	-	0/7/38/39	0/2/2/2
26	PSU	BB	1917	26	-	1/7/25/26	0/2/2/2
26	PSU	BB	2504	26	-	0/7/25/26	0/2/2/2
4	5MU	AD	55	4	-	0/7/25/26	0/2/2/2
26	5MU	BB	1939	26	-	0/7/25/26	0/2/2/2
4	4SU	AD	8	4	-	0/7/25/26	0/2/2/2
1	2MG	AA	966	1	-	0/9/27/28	0/3/3/3
26	PSU	BB	2457	26	-	0/7/25/26	0/2/2/2
26	PSU	BB	955	26	-	0/7/25/26	0/2/2/2
4	H2U	AD	21	4	-	2/7/38/39	0/2/2/2
1	MA6	AA	1519	1	-	0/11/29/30	0/3/3/3
26	OMG	BB	2251	26	-	0/9/27/28	0/3/3/3
26	OMU	BB	2552	26	-	0/9/27/28	0/2/2/2
2	7MG	AB	46	2	-	1/7/37/38	0/3/3/3
26	2MA	BB	2503	26	-	2/7/25/26	0/3/3/3
26	3TD	BB	1915	26	-	0/7/25/26	0/2/2/2
26	2MG	BB	2445	26	-	0/9/27/28	0/3/3/3
26	5MU	BB	747	26	-	0/7/25/26	0/2/2/2
26	7MG	BB	2069	26	-	0/7/37/38	0/3/3/3
26	5MC	BB	1962	26	-	1/7/25/26	0/2/2/2
26	PSU	BB	2580	26	-	0/7/25/26	0/2/2/2

The worst 5 of 164 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	46	7MG	C8-N9	-20.58	1.32	1.45
1	AA	527	7MG	C8-N9	-18.50	1.33	1.45
26	BB	2069	7MG	C8-N9	-13.21	1.37	1.45
1	AA	1407	5MC	C5-C4	-8.98	1.37	1.44
2	AB	37	MIA	C2-S10	-8.41	1.68	1.75

The worst 5 of 281 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BB	747	5MU	C6-C5-C4	9.43	125.79	118.02
1	AA	516	PSU	C6-C5-C4	9.34	124.48	118.17
26	BB	2605	PSU	C6-C5-C4	8.84	124.14	118.17
26	BB	2069	7MG	N9-C8-N7	7.13	113.46	103.37
26	BB	747	5MU	C5M-C5-C6	-6.95	113.44	122.85

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	AA	516	PSU	C2'-C1'-C5-C4
2	AB	8	4SU	C2'-C1'-N1-C2
2	AB	8	4SU	C2'-C1'-N1-C6
26	BB	746	PSU	O4'-C1'-C5-C6
26	BB	2605	PSU	C2'-C1'-C5-C4

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands 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	$\# Z > 2$
60	FME	BB	3001	59	8,9,10	1.16	2 (25%)	8,9,11	1.42	1 (12%)
59	TRP	AB	101	60,2	15,15,16	2.10	4 (26%)	17,20,22	3.07	8 (47%)

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
60	FME	BB	3001	59	-	2/7/9/11	-
59	TRP	AB	101	60,2	-	0/6/6/8	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	AB	101	TRP	OXT-C	-5.04	1.21	1.42
59	AB	101	TRP	CD2-CE2	3.66	1.46	1.41
59	AB	101	TRP	C-CA	2.78	1.57	1.52
59	AB	101	TRP	CH2-CZ2	2.77	1.43	1.38
60	BB	3001	FME	CB-CG	2.13	1.60	1.51

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	AB	101	TRP	CH2-CZ3-CE3	5.63	127.18	120.24
59	AB	101	TRP	CD2-CE2-NE1	-4.96	103.39	107.52
59	AB	101	TRP	CD2-CG-CD1	-4.72	101.33	106.16
59	AB	101	TRP	CE2-CD2-CG	4.49	111.70	107.17
59	AB	101	TRP	CE3-CD2-CE2	-4.26	114.43	118.84

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	BB	3001	FME	O1-CN-N-CA
60	BB	3001	FME	CB-CA-N-CN

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
26	BB	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BB	2677:G	O3'	2678:C	P	1.76

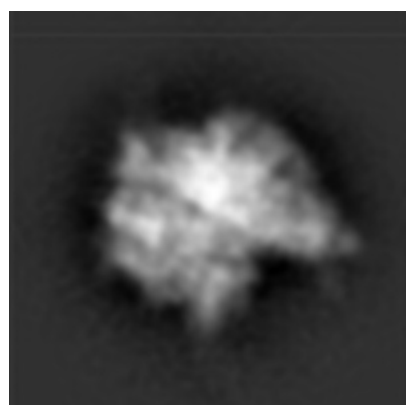
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5364. These allow visual inspection of the internal detail of the map and identification of artifacts.

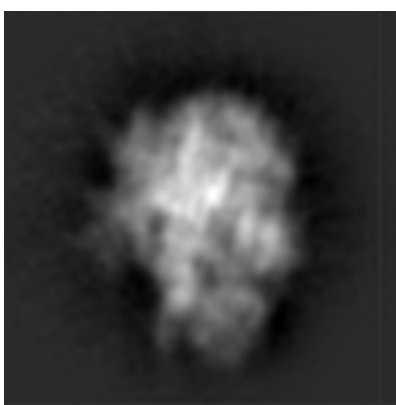
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

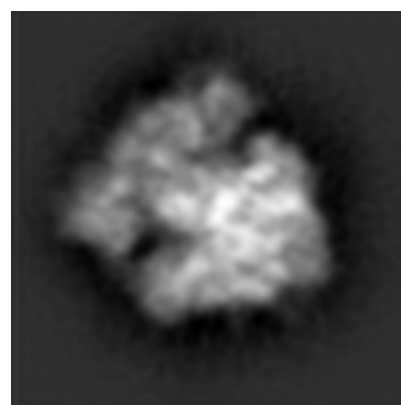
6.1.1 Primary map



X



Y

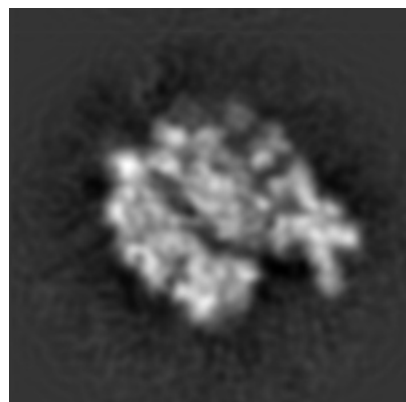


Z

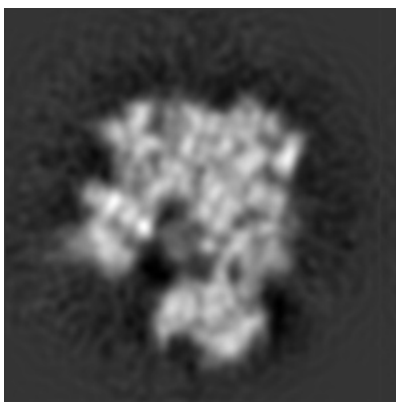
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

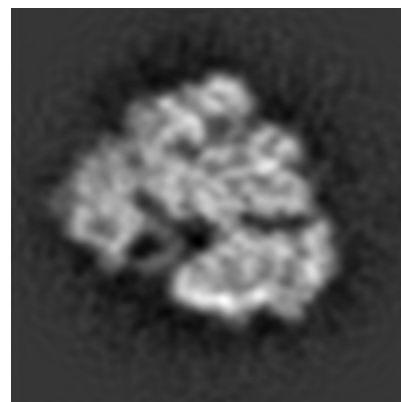
6.2.1 Primary map



X Index: 125



Y Index: 125

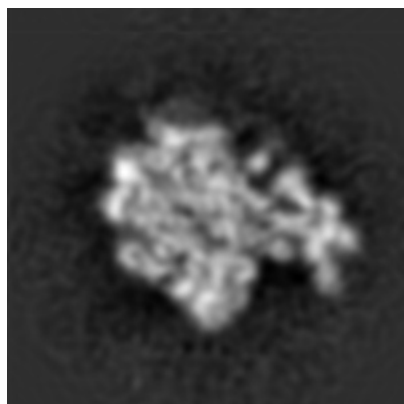


Z Index: 125

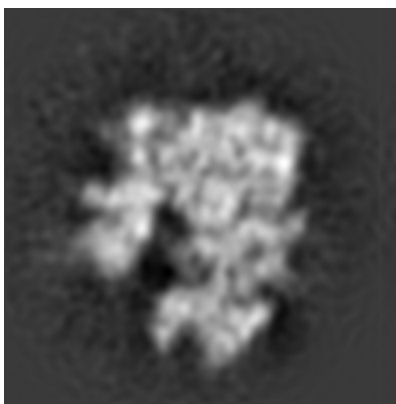
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

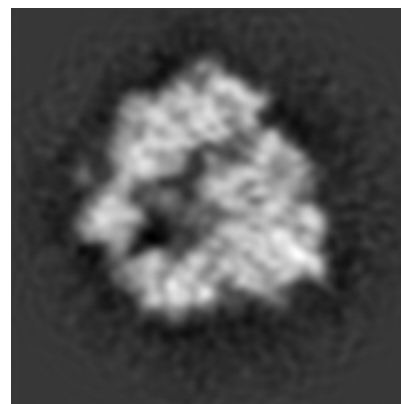
6.3.1 Primary map



X Index: 130



Y Index: 130

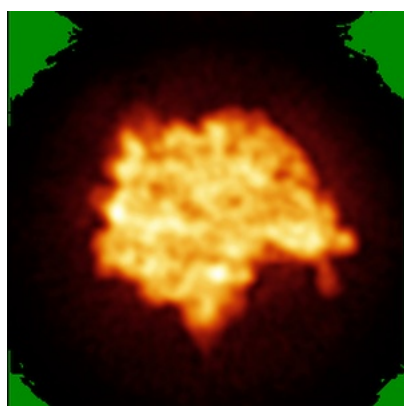


Z Index: 114

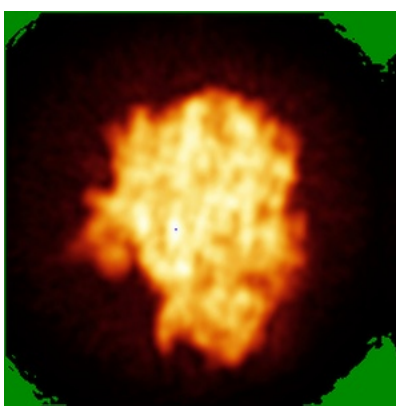
The images above show the largest variance slices of the map in three orthogonal directions.

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

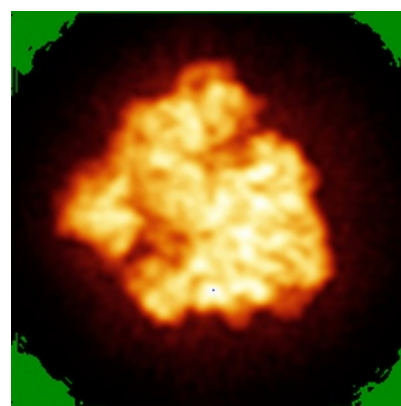
6.4.1 Primary map



X



Y

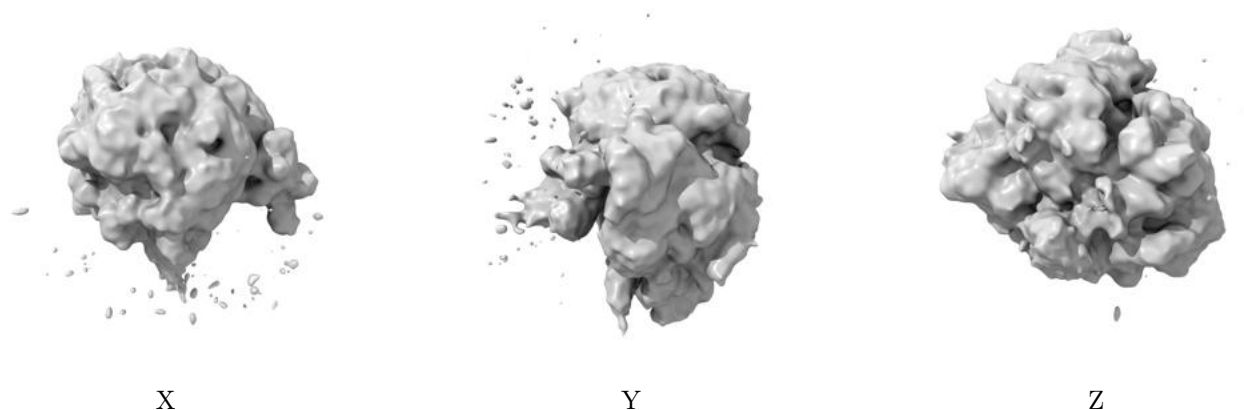


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

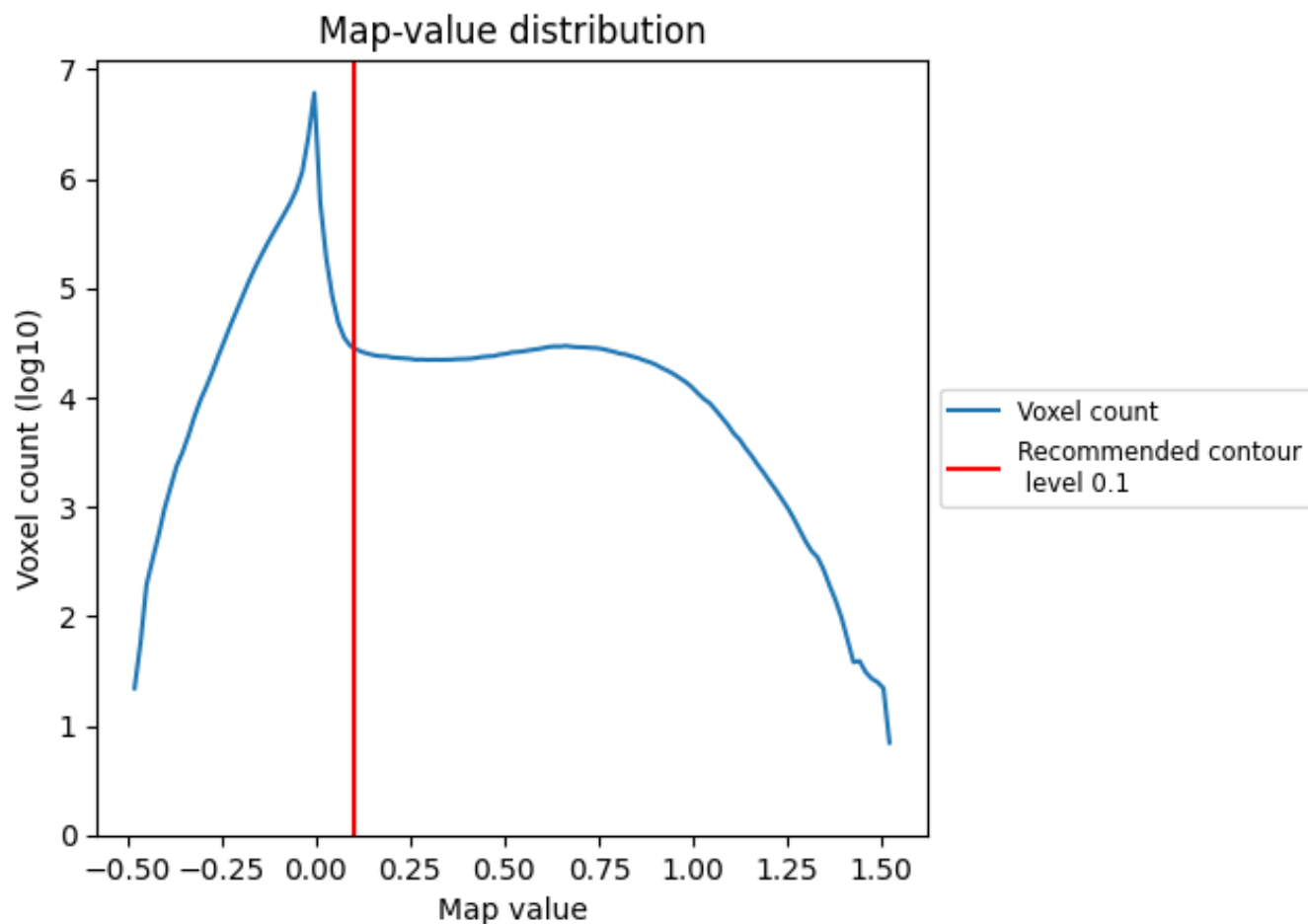
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

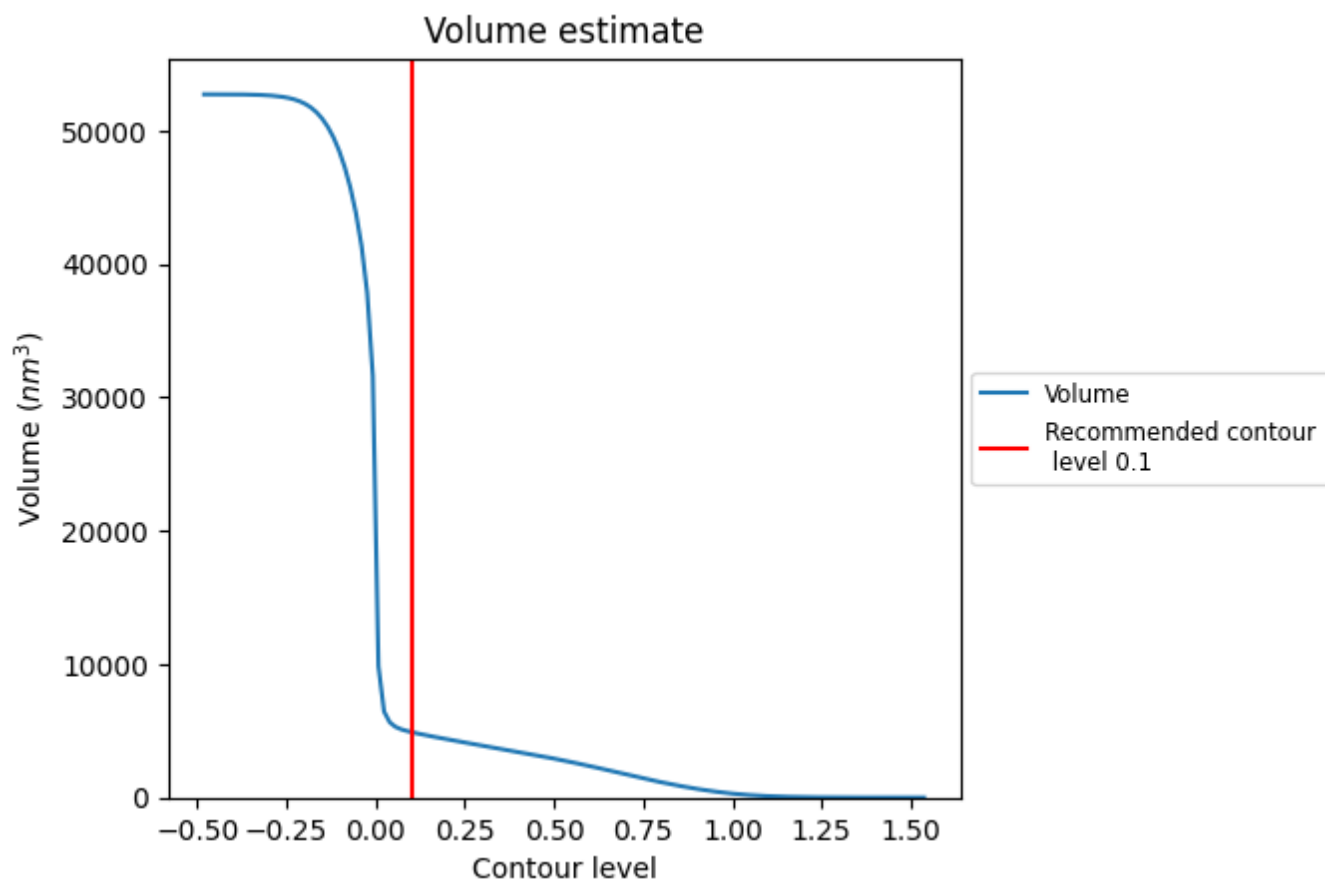
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

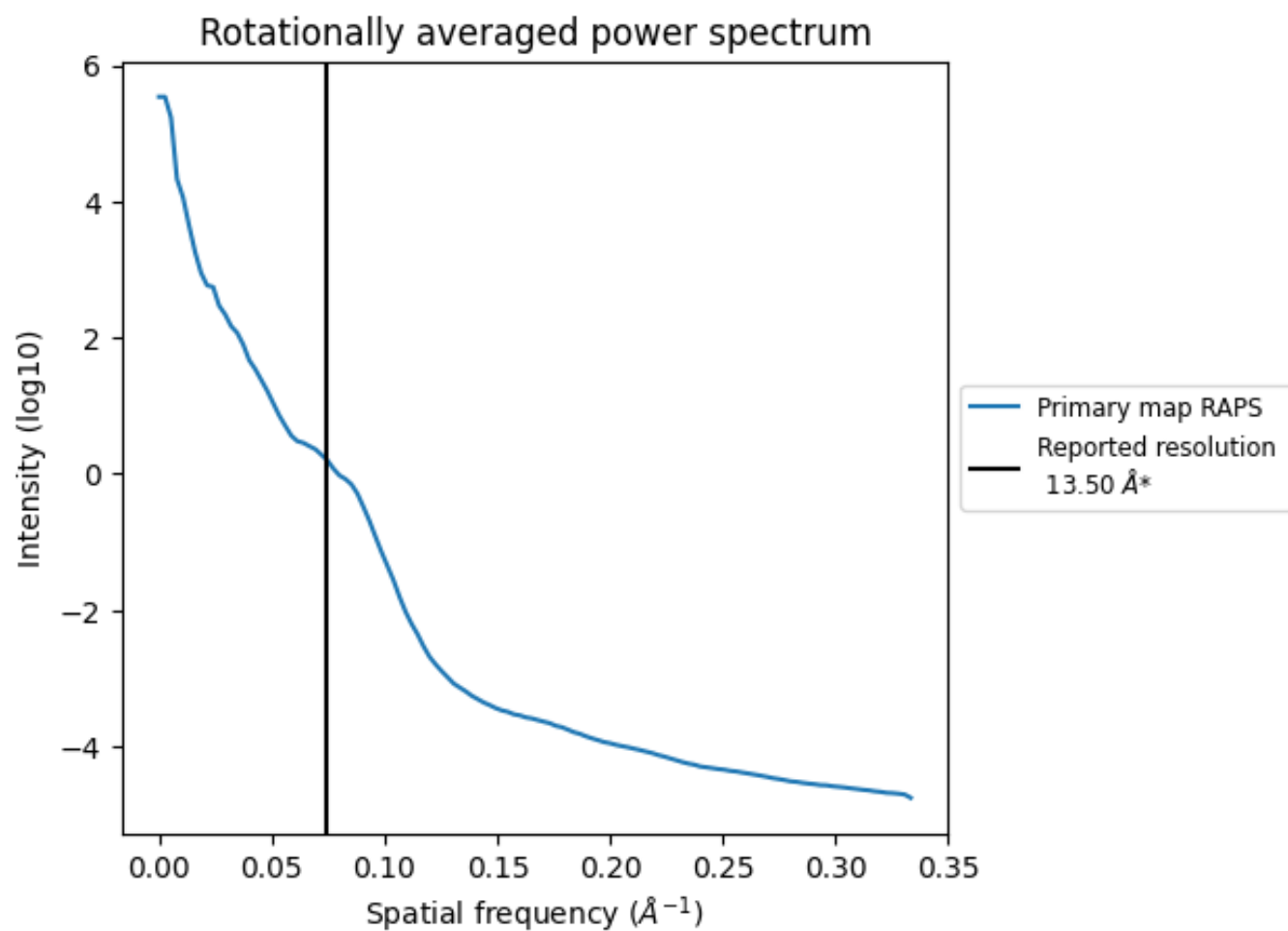
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4913 nm^3 ; this corresponds to an approximate mass of 4438 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 0.074 Å⁻¹

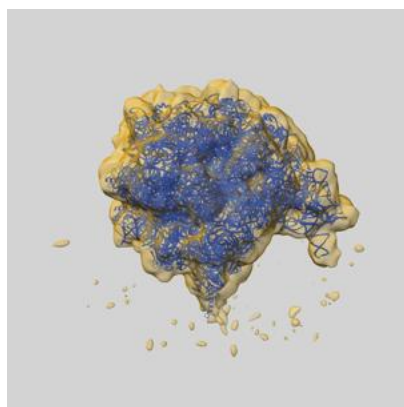
8 Fourier-Shell correlation

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

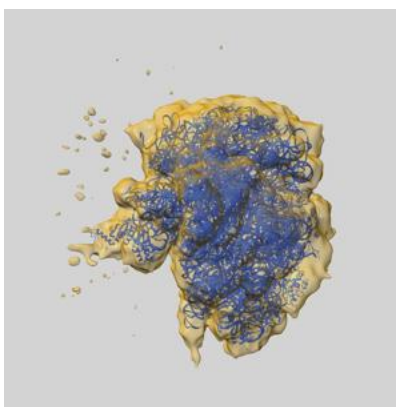
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5364 and PDB model 4V6P. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

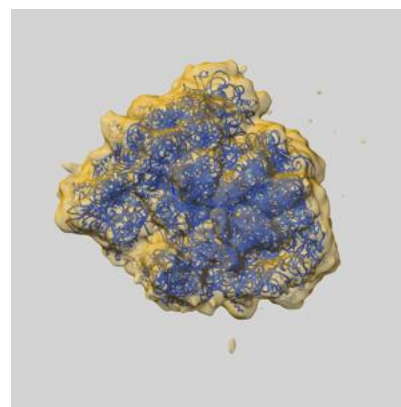
9.1 Map-model overlay [i](#)



X



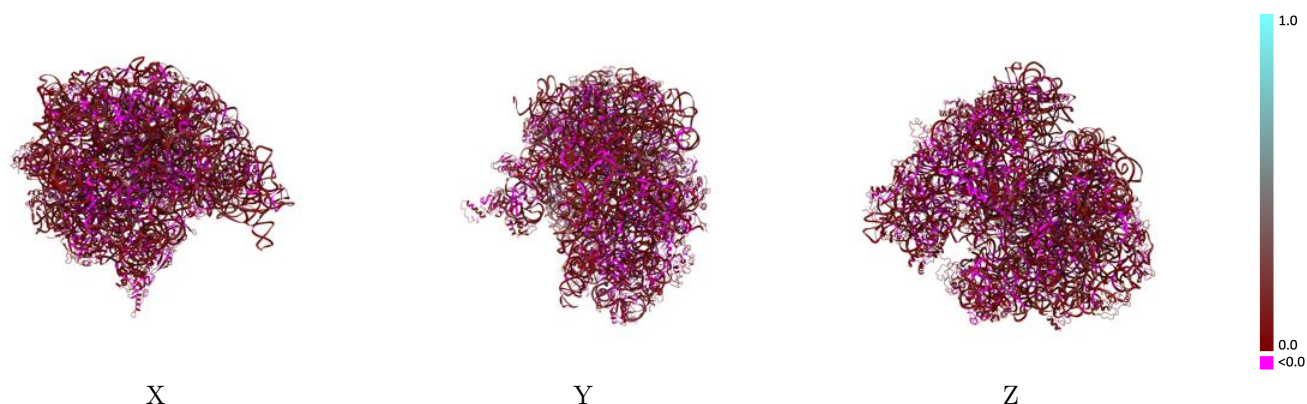
Y



Z

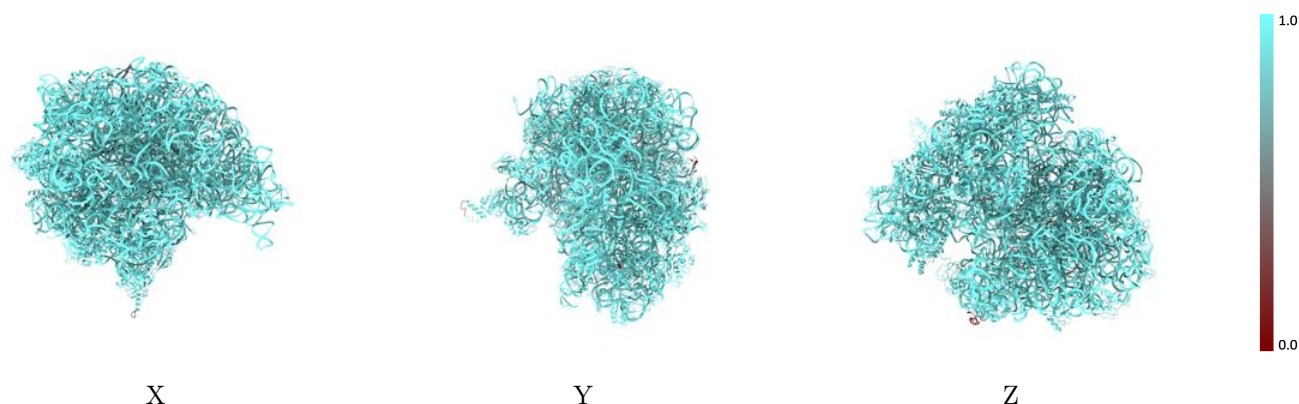
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



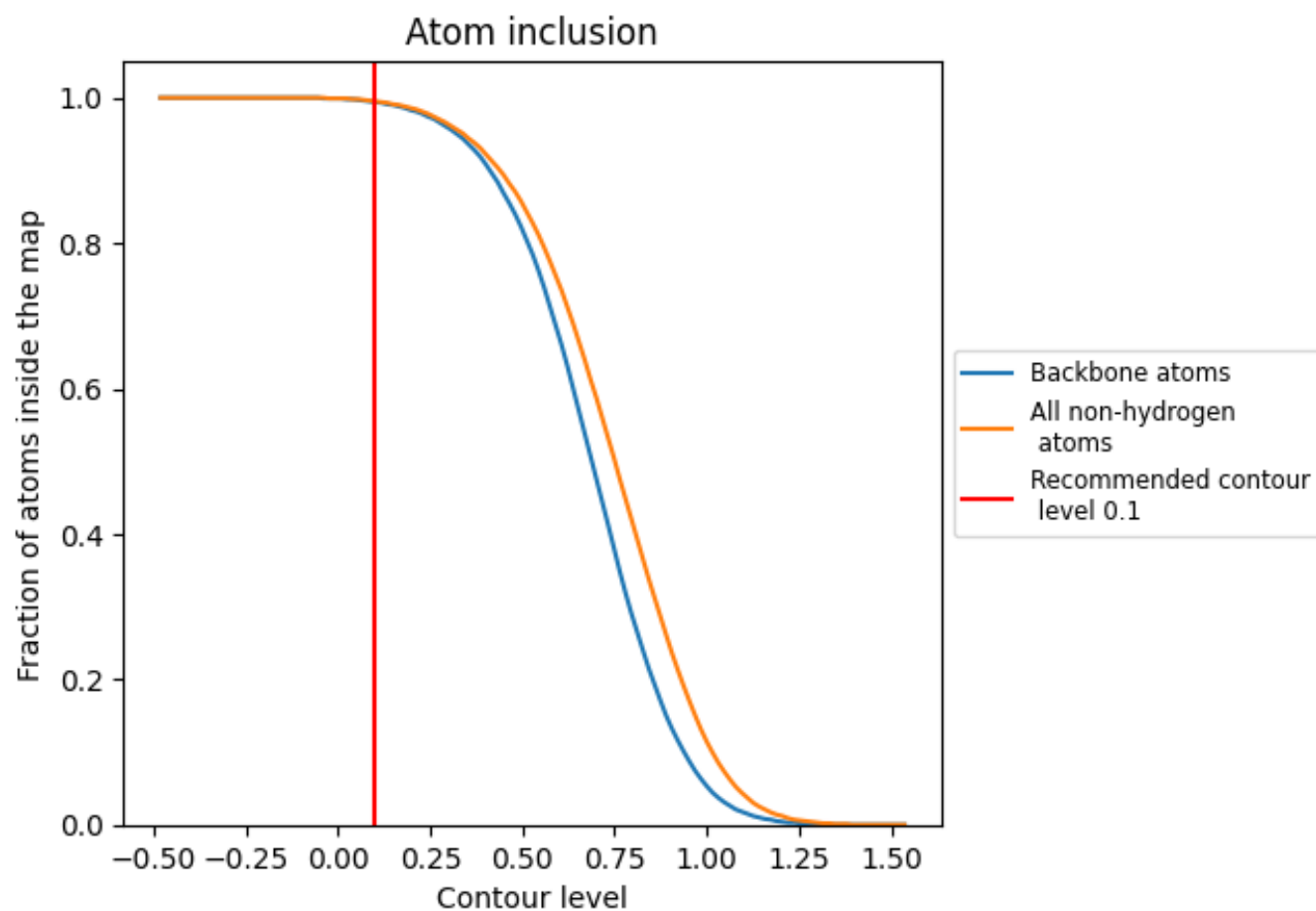
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 100% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9950	 0.0640
AA	 0.9990	 0.0780
AB	 0.9570	 0.0490
AC	 0.9190	 -0.0060
AD	 0.9460	 0.0460
AE	 0.9900	 0.0400
AF	 0.9990	 0.0530
AG	 1.0000	 0.0350
AH	 1.0000	 0.0530
AI	 0.9780	 0.0440
AJ	 1.0000	 0.0500
AK	 0.9960	 0.0360
AL	 0.9990	 0.0480
AM	 1.0000	 0.0260
AN	 1.0000	 0.0430
AO	 0.9910	 0.0130
AP	 1.0000	 0.0490
AQ	 1.0000	 0.0080
AR	 1.0000	 0.0430
AS	 1.0000	 0.0320
AT	 1.0000	 0.0420
AU	 1.0000	 0.0640
AV	 0.9560	 0.0190
AW	 1.0000	 0.0310
AX	 0.9840	 0.0110
B0	 1.0000	 0.0200
B1	 1.0000	 0.0440
B2	 0.9980	 0.0410
B3	 1.0000	 0.0340
B4	 1.0000	 0.0440
B5	 1.0000	 0.0120
B6	 1.0000	 -0.0200
B7	 1.0000	 0.0490
BA	 1.0000	 0.0900
BB	 0.9990	 0.0820



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Chain	Atom inclusion	Q-score
BC	 0.9240	 0.0270
BD	 1.0000	 0.0120
BE	 1.0000	 0.0220
BF	 1.0000	 0.0580
BG	 1.0000	 0.0490
BH	 1.0000	 0.0260
BI	 0.9260	 0.0230
BJ	 0.9490	 0.0530
BK	 0.9800	 0.0350
BL	 1.0000	 0.0110
BM	 0.9960	 0.0340
BN	 1.0000	 0.0120
BO	 1.0000	 0.0240
BP	 1.0000	 0.0150
BQ	 0.9980	 0.0620
BR	 0.9940	 0.0170
BS	 0.9920	 0.0070
BT	 1.0000	 0.0430
BU	 1.0000	 0.0100
BV	 1.0000	 0.0120
BW	 0.9940	 0.0540
BX	 1.0000	 0.0680
BY	 0.9810	 -0.0030
BZ	 1.0000	 0.0140