



wwPDB EM Validation Summary Report ⓘ

Jun 23, 2026 – 02:37 AM EDT

PDB ID : 4V6S / pdb_00004v6s
EMDB ID : EMD-5360
Title : Structural characterization of mRNA-tRNA translocation intermediates (class 3 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 : 2011-12-09
Resolution : 13.10 Å (reported)
Based on initial model : 2I2V

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:

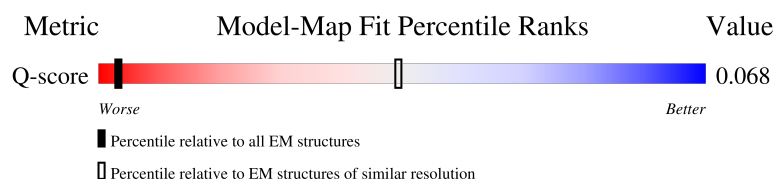
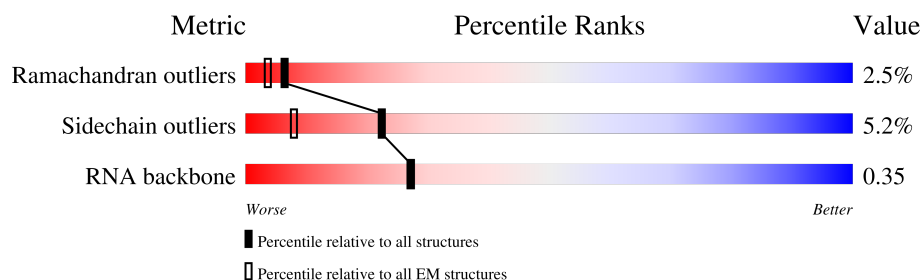
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 13.10 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	61 (12.60 - 13.60)

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	120	
2	AB	2904	
3	AC	234	
4	AD	272	

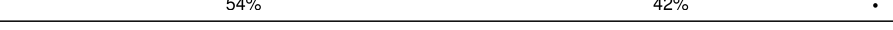
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	AE	209	
6	AF	201	
7	AG	178	
8	AH	176	
9	AI	149	
10	AJ	164	
11	AK	141	
12	AL	142	
13	AM	123	
14	AN	144	
15	AO	136	
16	AP	127	
17	AQ	117	
18	AR	114	
19	AS	117	
20	AT	103	
21	AU	110	
22	AV	100	
23	AW	103	
24	AX	94	
25	AY	84	
26	AZ	77	
27	A0	63	
28	A1	58	
29	A2	70	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
30	A3	56	
31	A4	54	
32	A5	46	
33	A6	64	
34	A7	38	
35	BA	1542	
36	BB	47	
37	BC	77	
38	BD	240	
39	BE	232	
40	BF	205	
41	BG	166	
42	BH	135	
43	BI	178	
44	BJ	129	
45	BK	129	
46	BL	103	
47	BM	128	
48	BN	123	
49	BO	117	
50	BP	100	
51	BQ	88	
52	BR	82	
53	BS	83	
54	BT	74	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
55	BU	91	57% 37% 5%
56	BV	86	56% 43%
57	BW	70	54% 40% 6%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 150700 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 5S ribosomal RNA.

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

- Molecule 2 is a RNA chain called 23S ribosomal RNA.

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

- Molecule 3 is a protein called 50S ribosomal protein L1.

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

- Molecule 4 is a protein called 50S ribosomal protein L2.

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

- Molecule 5 is a protein called 50S ribosomal protein L3.

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

- Molecule 6 is a protein called 50S ribosomal protein L4.

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

- Molecule 7 is a protein called 50S ribosomal protein L5.

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

- Molecule 8 is a protein called 50S ribosomal protein L6.

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

- Molecule 9 is a protein called 50S ribosomal protein L9.

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

- Molecule 10 is a protein called 50S ribosomal protein L10.

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

- Molecule 11 is a protein called 50S ribosomal protein L11.

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

- Molecule 12 is a protein called 50S ribosomal protein L13.

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

- Molecule 13 is a protein called 50S ribosomal protein L14.

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

- Molecule 14 is a protein called 50S ribosomal protein L15.

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

- Molecule 15 is a protein called 50S ribosomal protein L16.

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

- Molecule 16 is a protein called 50S ribosomal protein L17.

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

- Molecule 17 is a protein called 50S ribosomal protein L18.

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

- Molecule 18 is a protein called 50S ribosomal protein L19.

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

- Molecule 19 is a protein called 50S ribosomal protein L20.

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

- Molecule 20 is a protein called 50S ribosomal protein L21.

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

- Molecule 21 is a protein called 50S ribosomal protein L22.

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

- Molecule 22 is a protein called 50S ribosomal protein L23.

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

- Molecule 23 is a protein called 50S ribosomal protein L24.

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

- Molecule 24 is a protein called 50S ribosomal protein L25.

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

- Molecule 25 is a protein called 50S ribosomal protein L27.

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

- Molecule 26 is a protein called 50S ribosomal protein L28.

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

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A0	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 28 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	A1	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 29 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	A2	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	A3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 31 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	A4	54	Total	C	N	O	S	0	0
			441	284	81	76			

- Molecule 32 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	A5	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 33 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	A6	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 34 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	A7	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 35 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BA	1542	Total	C	N	O	P	0	0
			33089	14767	6064	10717	1541		

- Molecule 36 is a RNA chain called mRNA.

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

- Molecule 37 is a RNA chain called P site tRNA.

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

- Molecule 38 is a protein called 30S ribosomal protein S2.

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

- Molecule 39 is a protein called 30S ribosomal protein S3.

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

- Molecule 40 is a protein called 30S ribosomal protein S4.

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

- Molecule 41 is a protein called 30S ribosomal protein S5.

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

- Molecule 42 is a protein called 30S ribosomal protein S6.

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

- Molecule 43 is a protein called 30S ribosomal protein S7.

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

- Molecule 44 is a protein called 30S ribosomal protein S8.

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

- Molecule 45 is a protein called 30S ribosomal protein S9.

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

- Molecule 46 is a protein called 30S ribosomal protein S10.

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

- Molecule 47 is a protein called 30S ribosomal protein S11.

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

- Molecule 48 is a protein called 30S ribosomal protein S12.

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

- Molecule 49 is a protein called 30S ribosomal protein S13.

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

- Molecule 50 is a protein called 30S ribosomal protein S14.

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

- Molecule 51 is a protein called 30S ribosomal protein S15.

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

- Molecule 52 is a protein called 30S ribosomal protein S16.

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

- Molecule 53 is a protein called 30S ribosomal protein S17.

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

- Molecule 54 is a protein called 30S ribosomal protein S18.

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

- Molecule 55 is a protein called 30S ribosomal protein S19.

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

- Molecule 56 is a protein called 30S ribosomal protein S20.

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

- Molecule 57 is a protein called 30S ribosomal protein S21.

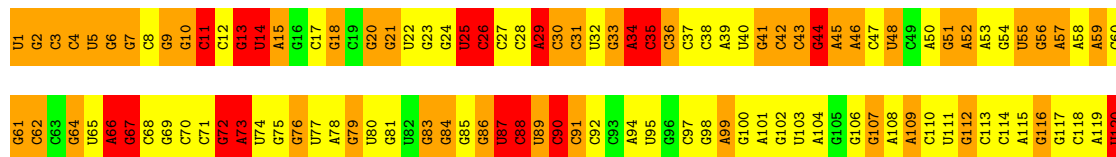
Mol	Chain	Residues	Atoms					AltConf	Trace
57	BW	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

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.

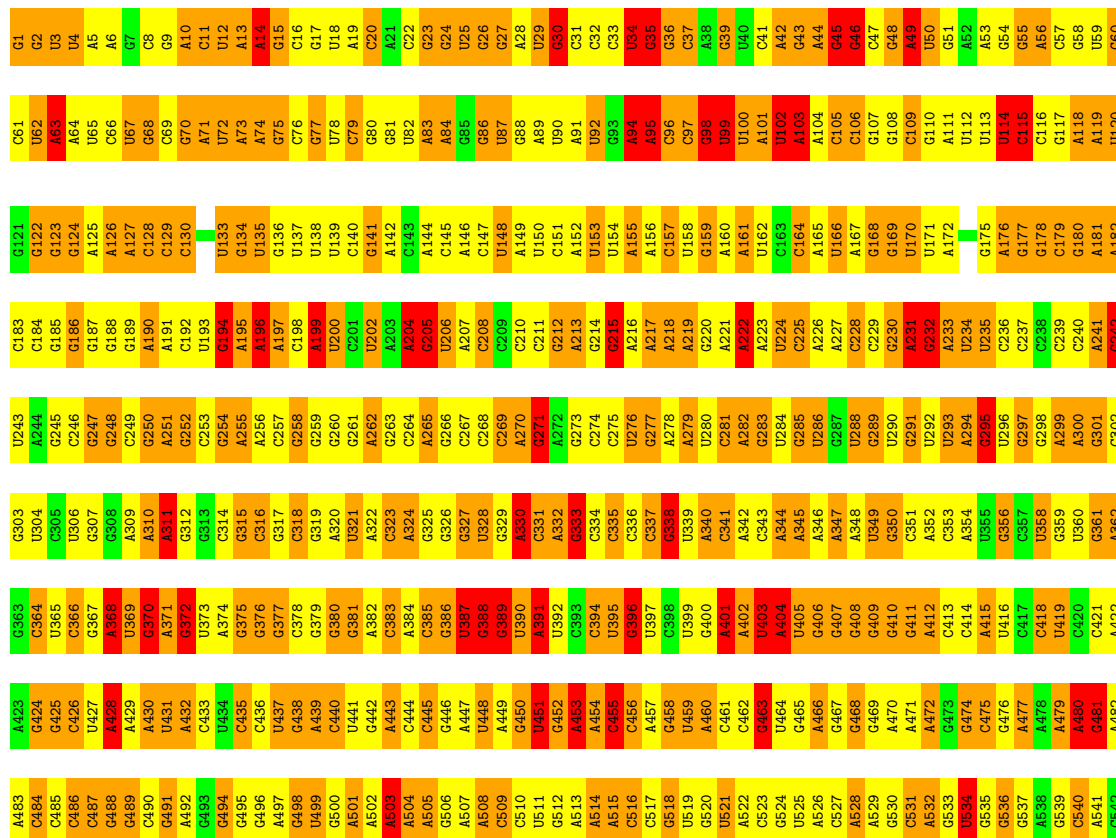
• Molecule 1: 5S ribosomal RNA

Chain AA: 



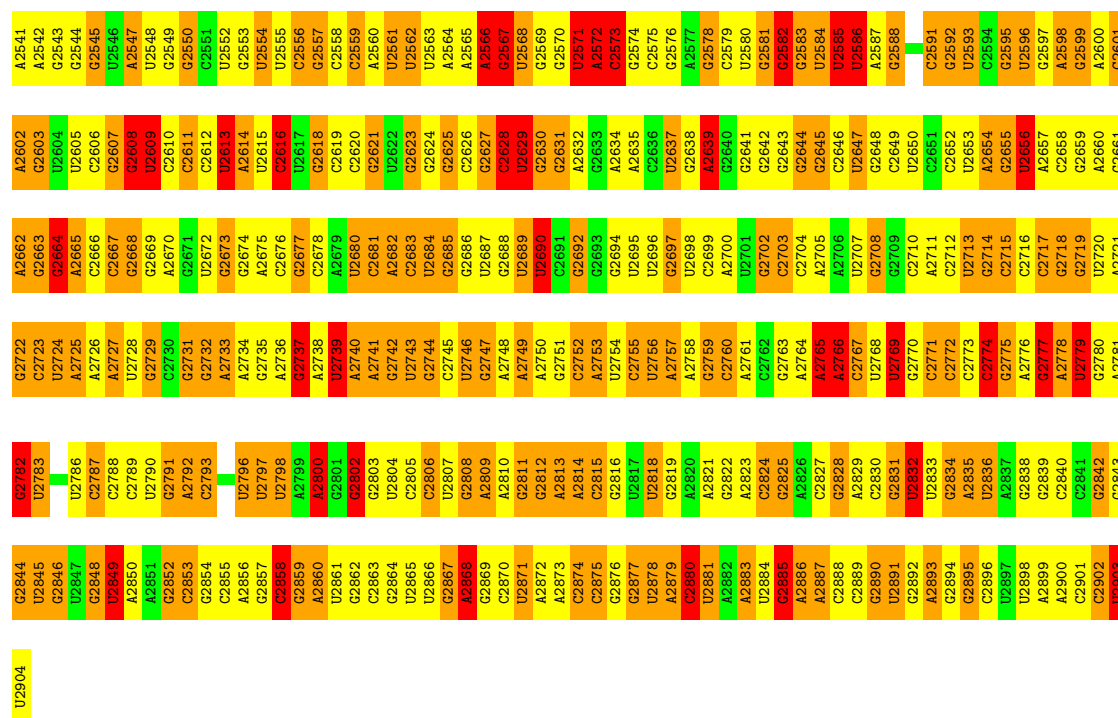
• Molecule 2: 23S ribosomal RNA

Chain AB: 



G1511	G1512	G1513	G1514	G1515	G1516	G1517	G1518	G1519	G1520	G1521	G1522	G1523	G1524	A1525	A1526	G1527	G1528	A1528	G1529	G1530	G1531	A1532	G1533	A1534	A1535	A1536	A1537	A1538	A1539	A1540	A1541	A1542	G1543	A1544	G1545	G1546	G1547	G1548	A1549	A1550	A1551	A1552	A1553	A1554	G1555	G1556	G1557	A1558	A1559	A1560	A1561	A1562	A1563	A1564	A1565	A1566	A1567	G1568	A1569	A1570	A1571	A1572
C1451	C1452	C1453	C1454	C1455	C1456	C1457	C1458	C1459	C1460	C1461	C1462	C1463	C1464	C1465	C1466	C1467	C1468	A1468	A1469	C1470	C1471	C1472	C1473	C1474	C1475	C1476	C1477	C1478	C1479	C1480	C1481	C1482	C1483	C1484	C1485	C1486	C1487	C1488	C1489	A1490	C1491	C1492	C1493	C1494	C1495	A1496	C1497	C1498	C1499	G1500	G1501	A1502	A1503	A1504	A1505	C1506	A1507	A1508	A1509	A1510	A1511	
U1391	A1392	A1393	G1394	A1395	G1396	U1397	U1398	U1399	U1400	G1401	A1402	C1403	C1404	C1405	C1406	G1407	C1408	U1409	G1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433	C1434	C1435	C1436	C1437	C1438	C1439	C1440	C1441	C1442	C1443	C1444	C1445	C1446	C1447	C1448	C1449	C1450			
G1331	G1332	G1333	G1334	G1335	A1336	G1337	G1338	G1339	U1340	G1341	A1342	C1343	U1344	A1345	C1346	G1347	C1348	C1349	C1350	C1351	C1352	C1353	A1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361	C1362	C1363	C1364	C1365	A1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1380	C1381	C1382	C1383	C1384	C1385	C1386	C1387	C1388	C1389	C1390			
G1271	A1272	G1273	A1274	C1275	A1276	G1277	C1278	G1279	G1280	G1281	U1282	G1283	A1284	A1285	A1286	A1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	A1301	A1302	C1303	A1304	C1305	C1306	A1307	A1308	C1309	G1310	G1311	U1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	A1321	A1322	C1323	G1324	G1325	G1326	U1327	A1328	C1329	C1330			
G1210	C1211	G1212	A1213	A1214	G1215	G1216	U1217	G1218	G1219	G1220		G1223	A1224	G1225	A1226	G1227	G1228	G1229	A1230	G1231	G1232	C1233	G1234	G1235	G1236	C1237	G1238	G1239	U1240	A1241	U1242	C1243	A1244	G1245	A1246	G1247	G1248	G1249	G1250	C1251	G1252	A1253	C1254	A1254	G1255	G1256	G1257	U1258	G1259	A1260	C1261	A1262	C1263	C1264	G1265	A1266	G1267	A1268	G1269	G1270		
C1150	A1151	C1152	C1153	C1154	A1155	A1156	G1157	C1158	U1159	G1160	C1161	G1162	G1163	C1164	A1165	G1166	C1167	G1168	A1169	C1170	G1171	C1172	U1173	U1174	A1175	U1176	G1177	C1178	G1179	U1180	U1181	G1182	U1183	U1184	G1185	G1186	G1187	U1188	A1189	G1190	C1191	G1192	G1193	A1194	G1195	G1196	G1197	U1198	U1199	C1200	U1201	C1202	U1203	A1204	A1205	G1206	C1207	U1208	U1209	C1210		
A1088	A1089	A1090	G1091	C1092	G1093	A1094	A1095	A1096	U1097	A1098	G1099	C1100	U1101	C1102	A1103	G1104	U1105	G1106	G1107	U1108	C1109	G1110	C1111	U1112	U1113	U1114	G1115	C1116	C1117	U1118	U1119	G1120	U1121	G1122	C1123	G1124	G1125	A1126	A1127	G1128	A1129	U1130	G1131	U1132	A1133	A1134	C1135	U1136	G1137	G1138	U1139	C1140	U1141	A1142	A1143	A1144		U1145	U1146	U1147	U1148	U1149
A1028	A1029	C1030	G1031	A1032	U1033	G1034	U1035	G1036	G1037	G1038	A1039	A1040	G1041	G1042	C1043	C1044	C1045	A1046	G1047	A1048	C1049	A1050	G1051	C1052	C1053	A1054	G1055	G1056	A1057	U1058	G1059	U1060	U1061	G1062	C1063	G1064	U1065	A1066	A1067	G1068	A1069	A1070	G1071	C1072	G1073	C1074	C1075	G1076	A1077	U1078	C1079	A1080	U1081	U1082	U1083	A1084	A1085	U1086	C1087			
C968	G969	C908	U970	G971	A972	G973	G974	C975	G976	C977	C978	A979	A980	C981	A983	A984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	A996	C997	C998	C999	G1000	G1001	G1002	C1003	U1004	C1005	C1006	C1007	A1008	A1009	A1010	G1011	G1012	G1013	A992	C983	U985	C896	C897	U958	A959	A960	C961	G962	U963	C964	C965	G966	U967		
G726	A727	C786	C787	A789	C730	C731	C732	C733	C734	C735	C736	C737	C738	A739	C740	C741	C742	C743	C744	C745	C746	C747	C748	C749	C750	C751	C752	C753	C754	C755	C756	C757	C758	C759	C760	C761	C762	C763	C764	C765	C766	C767	C768	C769	C770	C771	C772	C773	C774	C775	C776	C777	C778	C779	C780	C781	C782	C783	C784	C785		
A603	G604	C664	C665	U606	A608	C609	C610	C611	C612	C613	A614	U615	A616	C617	C618	C619	G620	A621	C622	A685	C623	C624	C625	A626	C627	C628	C629	C630	A631	A632	A633	C634	C635	C636	C637	C638	C639	C640	C641	C642	C643	C644	C645	C646	C647	C648	C649	C650	C651	C652	C653	C654	C655	C656	C657	C658	C659	C660	A661	C662	C663	
G543	C544	U545	U546	A547	A548	G549	C550	C551	U552	G553	U554	G555	A556	C557	U558	G559	C560	C561	U562	A563	C564	C565	U566	U567	U568	U569	C570	U571	A572	U573	A574	A575	U576	G577	G578	G579	U580	C581	A582	G583	C584	G585	U586	C587	U588	U589	A590	U591	U592	U593	U594	A595	C596	C597	A598	A599	G600	C601	C602			

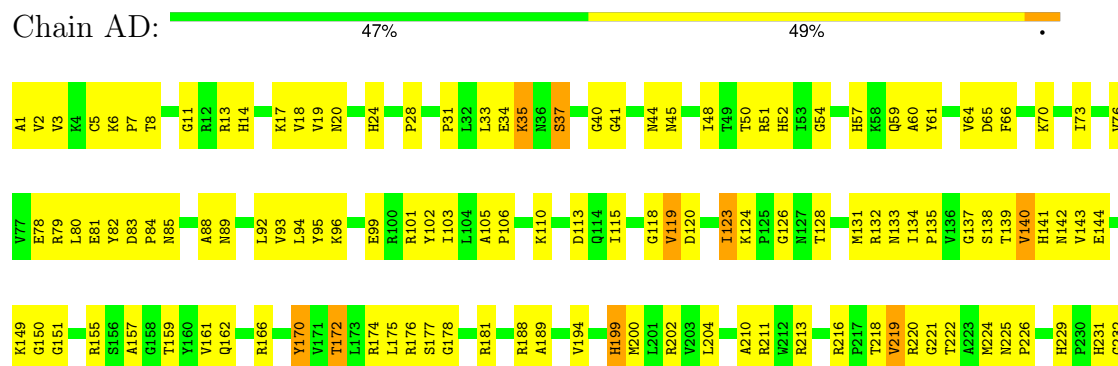
G2481	C2420	C2359	U2299	G2238	C2178	U2118	A2058	A1998	A1938	A1876	C1816	A1755	C1694	G1633	G1573
A2482	G2421	G2360	C2300	G2239	C2179	A2119	A2059	C1999	U1939	A1877	G1817	G1756	G1695	A1634	C1574
G2483	C2422	G2361	C2301	U2240	U2180	G2120	A2060	C2001	U1940	A1878	U1818	U1757	G1696	A1635	C1575
G2484	C2423	G2362	U2302	A2241	U2181	G2121	G2061	G2002	U1941	A1879	A1819	U1758	G1697	A1636	C1576
G2485	C2424	G2363	G2303	G2242	U2182	U2122	A2062	G2003	U1942	U1880	U1820	A1759	A1698	C1577	C1577
G2486	G2425	G2364	G2304	U2243	A2183	G2123	C2063	A2003	U1943	C1881	A1821	C1760	G1699	A1637	U1578
G2487	A2426	G2365	U2305	U2244	A2184	G2124	C2064	G2004	U1944	U1882	C1822	G1761	A1700	C1639	A1579
G2488	C2427	A2366	C2306	U2245	U2185	G2125	C2065	A2005	U1945	U1883	G1823	A1762	A1701	A1640	A1580
U2489	G2428	G2367	G2307	G2246	G2186	A2126	C2066	C2006	U1946		G1824	G1763	G1702	A1641	G1581
G2490	A2429	A2368	G2308	A2247	U2187	G2127	G2067	U2007	U1947	U1886	U1825	G1764	G1703	G1642	A1582
U2491	A2430	A2369	A2309	C2248	U2188	G2128	U2068	C2008	G1948	C1887	G1826	U1765	C1704	G1643	A1583
U2492	U2431	G2370	U2310	U2249	U2189	G2129	G2069	A2009	G1949	U1888	U1827	G1766	A1705	G1644	U1584
A2493	A2432	G2371	A2311	G2250	U2190	U2130	A2070	G2010	A1889	A1889	G1828	G1767	C1706	C1645	C1585
A2494	A2433	U2372	U2312	G2251	A2191	U2131	A2071	U2011	U1951	A1890	A1829	C1768	G1707	A1586	A1586
G2495	A2434	G2373	C2313	G2252	U2192	U2132	C2072	A2012	A1952	G1891	C1830	U1769	C1708	G1647	G1587
A2496	A2435	G2374	A2314	G2253	G2193	G2133	C2073	A2013	A1953	G1892	G1770	G1770	U1709	U1648	G1588
A2497	G2436	G2375	G2315	C2254	U2194	A2134	U2074	A2014	A1954	C1893	G1832	A1771	G1711	G1649	U1589
G2498	G2437	G2376	G2316	G2255	U2195	A2135	U2075	A2015	U1955	C1894	G1833	A1772	A1711	A1650	A1590
G2499		A2377	A2317	G2256	C2196	G2136	U2076	U2016	U1956	C1895	U1834	A1773	U1712	G1651	A1591
		G2378	G2318	U2257	U2197	U2137	A2077	U2017	C1957	G1896	G1835	C1774	U1713	A1652	C1592
A2440		C2380	G2319	C2258	A2198	G2138	A2078	G2018	C1958	U1897	G1836	U1775	A1714	G1653	A1593
U2441	U2441	G2381	G2320	C2259	A2199	U2139	U2079	A2019	G1959	U1898	C1837	G1776	U1715	A1654	U1594
C2442	C2442	G2382	U2321	C2260	A2200	A2140	A2080	A2020	A1960	U1899	C1838	U1777	U1716	A1655	C1595
A2504	G2444	G2383	A2322	C2261	G2201	G2141	U2081	C2021	C1961	A1900	G1839	A1778	A1717	C1656	A1596
G2445	G2445	U2384	G2323	U2262	U2202	A2142	A2082	U2022	C1962	A1901	G1840	U1779	G1718	U1657	A1597
G2446	G2446	C2385	U2324	C2263	U2203	G2143	G2083	C2023	U1963	C1902	U1841	A1780	G1719	A1598	A1598
G2447	G2447	A2386	G2325	C2264	G2204	G2144	C2084	G2024	G1964	G1903	G1842	U1781	U1720	C1660	
A2448	A2448	U2387	C2326	U2265	A2205	G2145	U2085	C2025	C1965	G1904	C1843	U1782	G1721	G1661	G1600
U2449	U2449	A2388	A2327	A2266	C2206	G2146	U2086	U2026	A1966	C1905	G1845	A1783	A1722	U1662	G1601
A2450	A2450	G2389	A2328	A2267	G2207	G2147	G2087	G2027	C1967	G1906	G1846	A1784	G1723	G1663	U1602
U2511	U2511	U2390	U2329	A2268	C2208	G2148	A2088	U2028	A1968	G1907	G1847	A1785	G1724	A1664	A1603
C2512	C2512	C2391	G2330	C2269	G2209	U2149	C2089	G2029	U1969	C1908	A1847	A1786	U1725	A1665	C1604
A2513	A2513	A2392	A2331	A2270	U2210	U2150	A2090	A2030	A1970	C1909	A1848	A1787	C1726	A1666	C1605
U2514	U2514	U2393	C2332	G2271	C2211	U2151	C2091	A2031	U1971	G1910	G1849	C1788	C1727	G1667	C1606
C2515	G2455	G2394	A2333	U2272	A2212	G2152	U2092	C2032	G1972	U1911	G1850	A1789	C1728	A1668	C1607
A2516	C2456	C2395	U2334	A2273	U2213	C2153	G2093	U2039	G1973	U1912	U1851	C1790	U1729	A1669	A1608
C2517	U2457	A2396	A2335	A2274	C2214	A2154	A2094	U2034	C1974	A1913	U1852	A1791	C1730	C1670	A1609
	G2458	G2397	A2336	C2275	C2215	U2155	A2095	G2035	G1975	C1914	A1853	G1792		U1671	A1610
U2519	U2459	U2398	G2337	G2276	G2216	U2156	C2096	C2036	U1976	3D1915	A1854	C1793	G1733	A1672	C1611
C2520	A2460	G2399	C2338	G2277	G2217	G2157	A2097	A2037	A1977	A1916	U1855	A1794	G1734	G1673	C1612
C2521	A2461	G2400	C2339	G2278	G2218	A2158	U2098	G2038	A1978	U1917	U1856	U1795	A1735	G1674	C1613
U2522	C2462	U2401	A2340	A2279	U2219	G2159	U2099	U2039	U1979	A1918	G1857	U1796	U1736	C1675	A1614
G2523	C2463	U2402	G2341	A2281	U2220	C2160	G2100	G2040	G1980	A1919	A1858	G1797	G1737	C1615	C1615
C2524	G2464	C2403	G2342	G2282	G2221	G2162	A2101	U2041	A1981	C1920	U1859	U1798	G1738	A1676	A1616
G2525	C2465	U2404	U2343	C2283	C2222	G2163	G2102	A2042	U1982	G1921	G1860	G1799	A1739	A1677	C1617
G2526	C2466	G2405	U2344	A2284	G2223	A2164	C2103	C2043	G1983	U1922	G1861	C1800	G1740	A1678	A1618
C2527	A2467	A2406	G2345	C2285	G2224	C2165	C2104	C2044	G1984	U1923	G1862	A1801	G1741	U1680	G1619
U2528	A2468	A2407	A2346	G2286	A2225	C2166	U2105	C1985	C1986	A1802	U1863	A1802	U1742	G1681	G1620
G2529	A2469	U2408	C2347	A2287	C2226	U2167	U2106	G2046	C1986	U1864	U1864	A1803	G1743	G1682	U1621
A2530	G2470	G2409	U2348	A2288	G2227	U2167	G2107	C2047	A1987	A1927	U1865	C1804	A1744	U1683	G1622
G2531	A2471	G2410	U2349	G2289	G2228	G2168	A2108	G2048	G1988	A1928	A1866	A1805	A1745	G1684	G1623
C2532	G2472	A2411	C2350	G2290	U2229	A2169	U2109	G2049	G1989	G1929	G1867	C1806	A1746	C1685	U1624
U2533	U2473	A2412	G2351	U2291	G2230	A2170	G2110	C2050	G1989	U1930	C1868	G1807	U1747	G1686	C1625
A2534	U2474	G2413	A2352	U2292	G2231	A2171	U2111	A2051	C1990	U1931	G1869	A1808	C1748	A1696	A1626
G2535	G2475	G2414	G2353	G2293	C2232	U2172	G2112	A2052	G1992	A1932	C1870	A1809	A1749	U1688	G1627
G2536	A2476	G2415	C2354	G2294	U2233	A2173	U2113	G2053	U1993	G1933	A1871	A1810	G1750	A1689	G1628
U2537	U2477	C2416	G2355	C2295	G2234	C2174	A2114	A2054	C1994	C1934	A1872		U1751	A1690	U1629
C2538	U2478	A2417	U2356	U2296	G2235	C2175	G2115	C2055	U1995	G1935	G1873		C1752	G1691	A1630
C2539	U2479	A2418	U2357	U2297	G2236	A2176	G2116	G2056	A1996	A1936	C1874	G1813	C1753	G1692	G1631
C2540	C2480	U2419	A2358	A2298	G2237	C2177	A2117	G2057	C1997	A1937	G1875	A1815		U1693	A1632

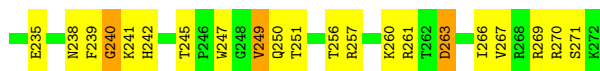


• Molecule 3: 50S ribosomal protein L1

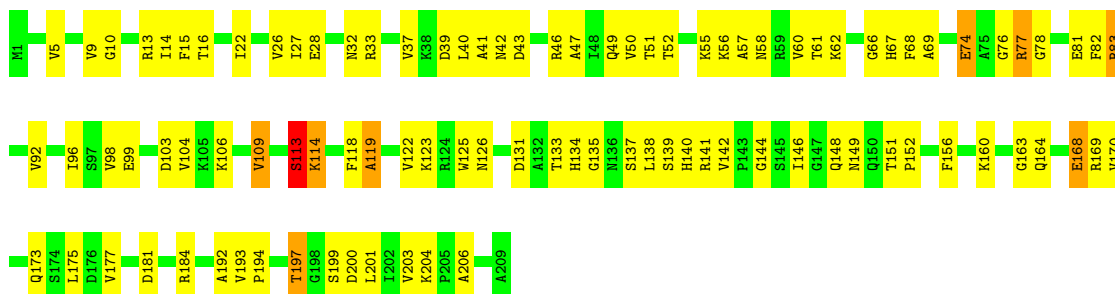


• Molecule 4: 50S ribosomal protein L2

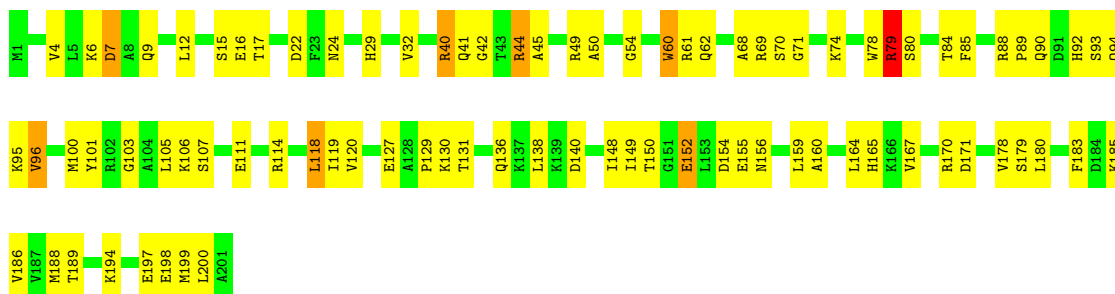




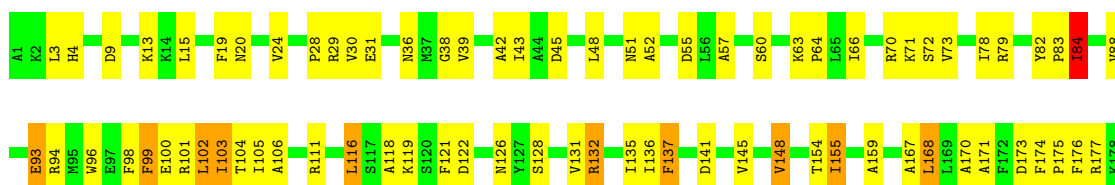
• Molecule 5: 50S ribosomal protein L3



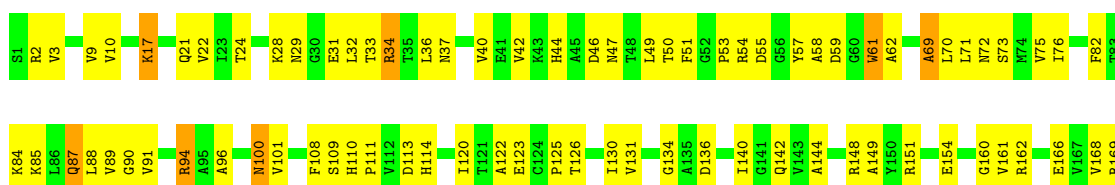
• Molecule 6: 50S ribosomal protein L4



• Molecule 7: 50S ribosomal protein L5



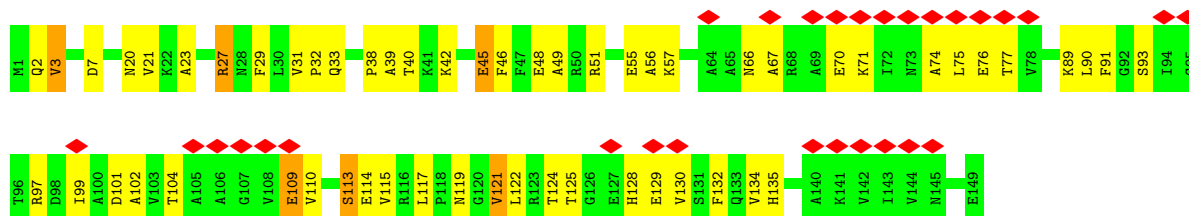
• Molecule 8: 50S ribosomal protein L6





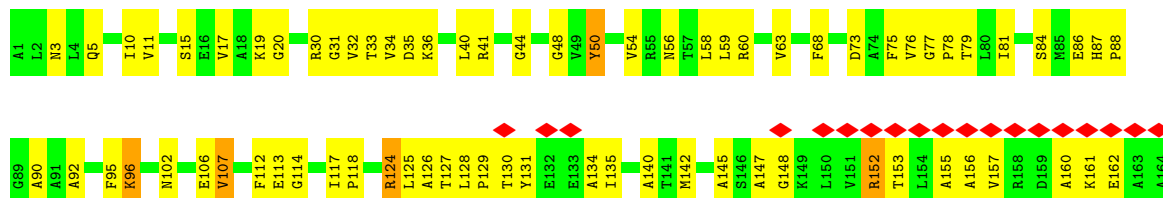
- Molecule 9: 50S ribosomal protein L9

Chain AI: 19% 62% 34%



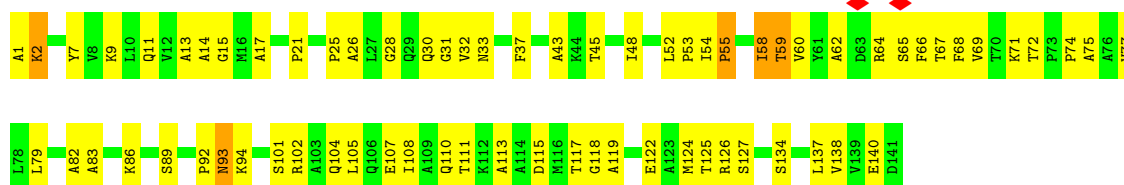
- Molecule 10: 50S ribosomal protein L10

Chain AJ: 12% 55% 41%



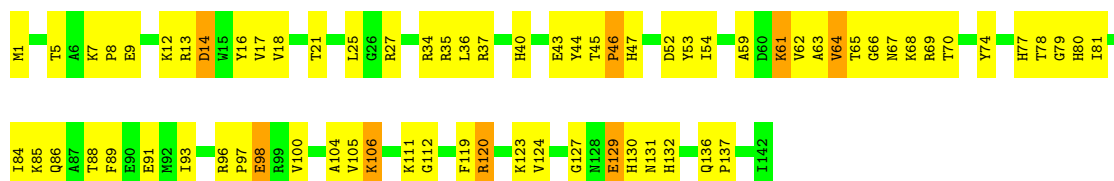
- Molecule 11: 50S ribosomal protein L11

Chain AK: 50% 46%



- Molecule 12: 50S ribosomal protein L13

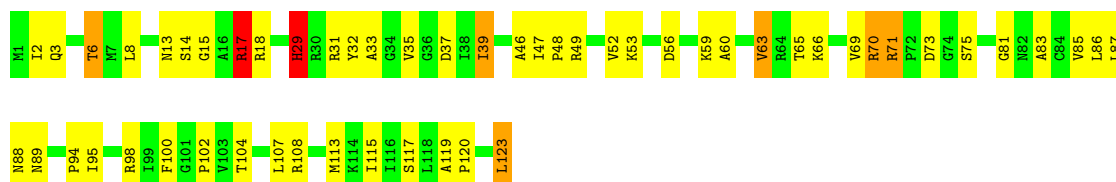
Chain AL: 50% 44% 6%



- Molecule 13: 50S ribosomal protein L14

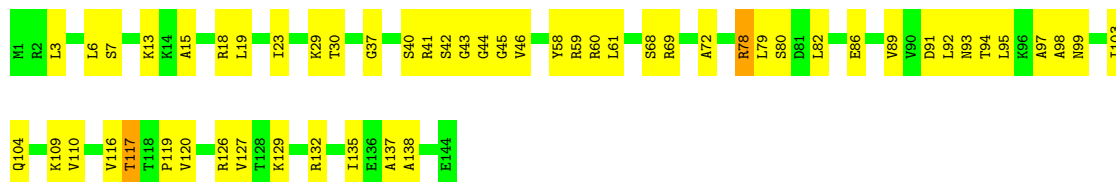
Chain AM: 56% 37% 5%





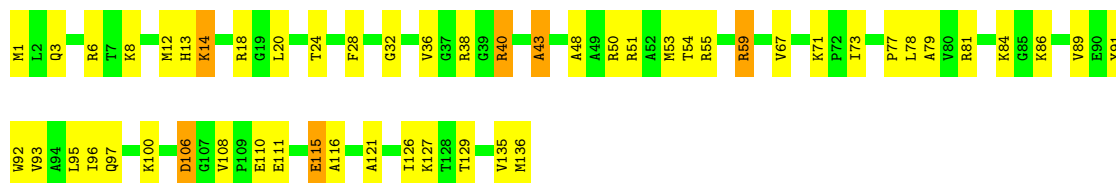
- Molecule 14: 50S ribosomal protein L15

Chain AN: 62% 36% .



- Molecule 15: 50S ribosomal protein L16

Chain AO: 62% 34% .



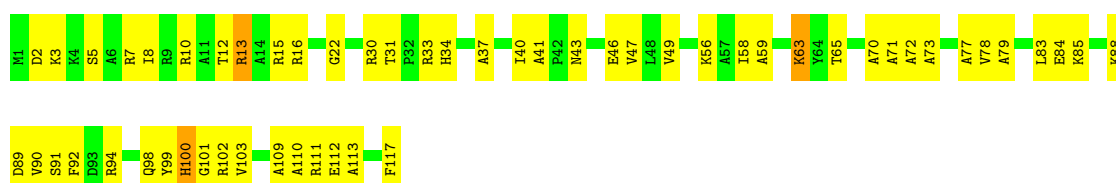
- Molecule 16: 50S ribosomal protein L17

Chain AP: 61% 35% .



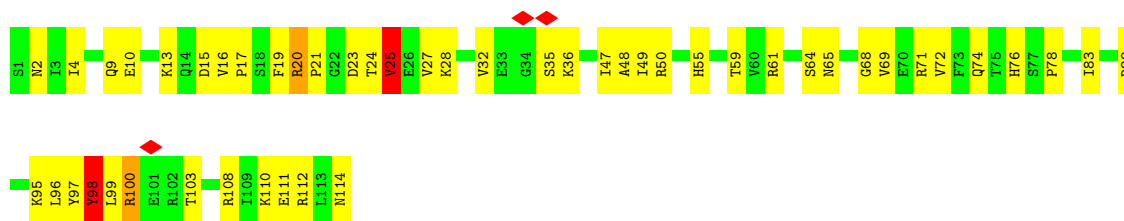
- Molecule 17: 50S ribosomal protein L18

Chain AQ: 53% 44% .



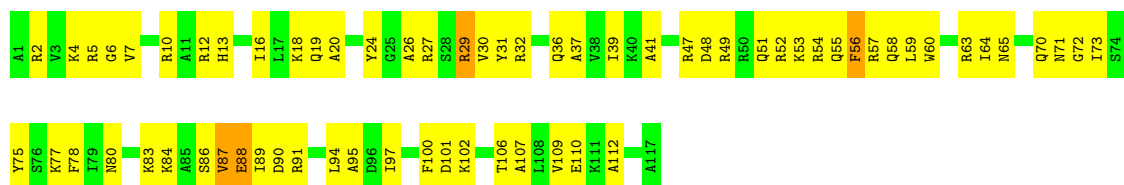
- Molecule 18: 50S ribosomal protein L19

Chain AR: 57% 39% . .



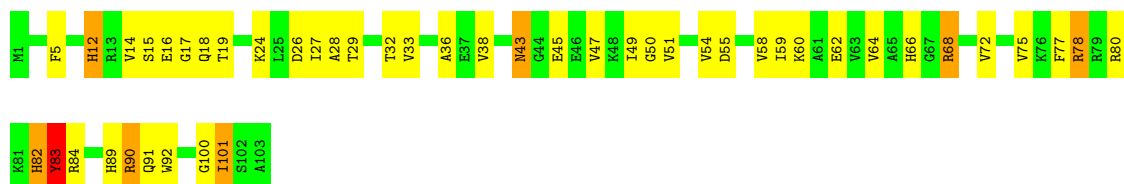
• Molecule 19: 50S ribosomal protein L20

Chain AS: 44% 53% .



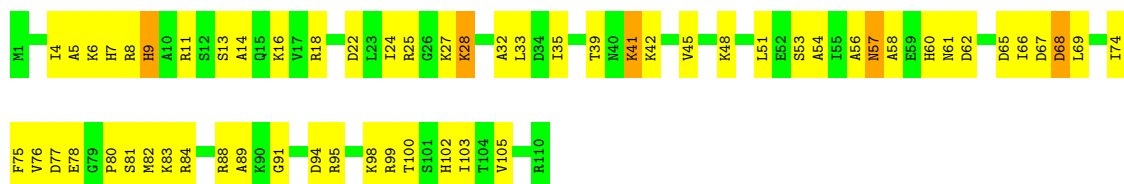
• Molecule 20: 50S ribosomal protein L21

Chain AT: 55% 37% 7% .



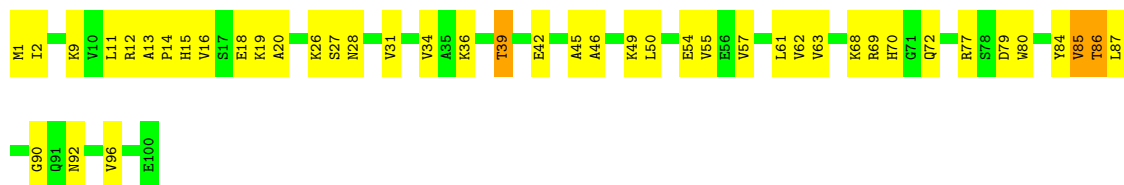
• Molecule 21: 50S ribosomal protein L22

Chain AU: 46% 49% 5% .



• Molecule 22: 50S ribosomal protein L23

Chain AV: 56% 41% .



• Molecule 23: 50S ribosomal protein L24

I102	A1	R6	V12	K25	V41	F72	A79	E87	T101
K103	A2	D7	L13	N26	K42	N73	D80	D88	
		D8	G15	V35	H44	A74	R81	G89	
			K16	I38	Q45	A75	V82	K90	
			D17		Q46	T76	G83	K91	
				R21	P54			V92	
					I64			R93	
				K25	V41	F72	A79	F94	
				N26	K42	N73	D80	F95	
				V35	H44	A74	R81	K96	
				I38	Q45	A75	V82	S97	
					Q46	T76	G83	N98	
				R21	P54				
					I64				
				K25	V41	F72	A79	E87	
				N26	K42	N73	D80	D88	
				V35	H44	A74	R81	G89	
				I38	Q45	A75	V82	K90	
					Q46	T76	G83	K91	
				R21	P54			V92	
					I64			R93	
				K25	V41	F72	A79	F94	
				N26	K42	N73	D80	F95	
				V35	H44	A74	R81	K96	
				I38	Q45	A75	V82	S97	
					Q46	T76	G83	N98	
				R21	P54				
					I64				
				K25	V41	F72	A79	E87	
				N26	K42	N73	D80	D88	
				V35	H44	A74	R81	G89	
				I38	Q45	A75	V82	K90	
					Q46	T76	G83	K91	
				R21	P54			V92	
					I64			R93	
				K25	V41	F72	A79	F94	
				N26	K42	N73	D80	F95	
				V35	H44	A74	R81	K96	
				I38	Q45	A75	V82	S97	
					Q46	T76	G83	N98	
				R21	P54				
					I64				
				K25	V41	F72	A79	E87	
				N26	K42	N73	D80	D88	
				V35	H44	A74	R81	G89	
				I38	Q45	A75	V82	K90	
					Q46	T76	G83	K91	
				R21	P54			V92	
					I64			R93	
				K25	V41	F72	A79	F94	
				N26	K42	N73	D80	F95	
				V35	H44	A74	R81	K96	
				I38	Q45	A75	V82	S97	
					Q46	T76	G83	N98	
				R21	P54				
					I64				
				K25	V41	F72	A79	E87	
				N26	K42	N73	D80	D88	
				V35	H44	A74	R81	G89	
				I38	Q45	A75	V82	K90	
					Q46	T76	G83	K91	
				R21	P54			V92	
					I64			R93	
				K25	V41	F72	A79	F94	
				N26	K42	N73	D80	F95	
				V35	H44	A74	R81	K96	
				I38	Q45	A75	V82	S97	
					Q46	T76	G83	N98	
				R21	P54				

- [illegible]

- [illegible]

- | | | | | | |
|----|----|----|----|----|-----|
| S1 | R2 | Q5 | V6 | T7 | R10 | G14 | N15 | N16 | R17 | S18 | H19 | A20 | L21 | K25 | R26 | R27 | F28 | L29 | P30 | N31 | L32 | H33 | S34 | H35 | R36 | F37 | V38 | V39 | R49 | K53 | G54 | M55 | R56 | V57 | S58 | D59 | K60 | K61 | G62 | I63 | D64 | T65 | V66 | L67 | R71 | A72 | R73 | G74 | G75 | E76 | K77 |
|----|----|----|----|----|-----|

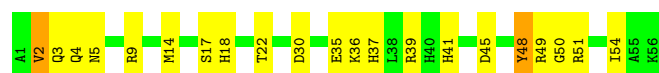
- | | | | | | |
|----|----|----|----|----|-----|
| M1 | L6 | R7 | F8 | K9 | E12 | N15 | N20 | R23 | E24 | Q25 | F26 | N27 | L28 | R29 | A33 | Q38 | Q39 | S40 | H41 | L42 | L43 | L44 | Q45 | V46 | R47 | R48 | D49 | V50 | A51 | R52 | V53 | K54 | T55 | L56 | L57 | N58 | E59 | K60 | A63 |
|----|----|----|----|----|-----|

- [illegible]

- 
- WORLDWIDE
PDB
PROTEIN DATA BANK



- Molecule 30: 50S ribosomal protein L32



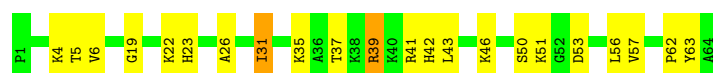
- Molecule 31: 50S ribosomal protein L33



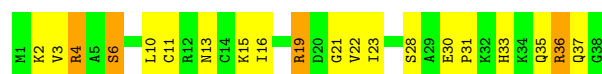
- Molecule 32: 50S ribosomal protein L34



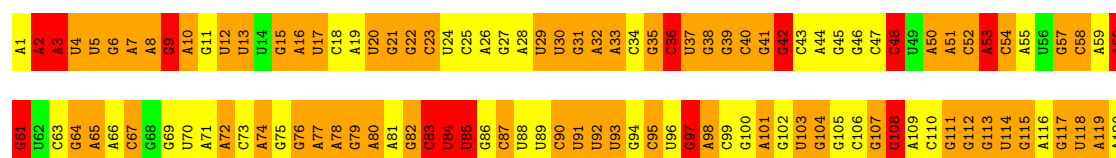
- Molecule 33: 50S ribosomal protein L35



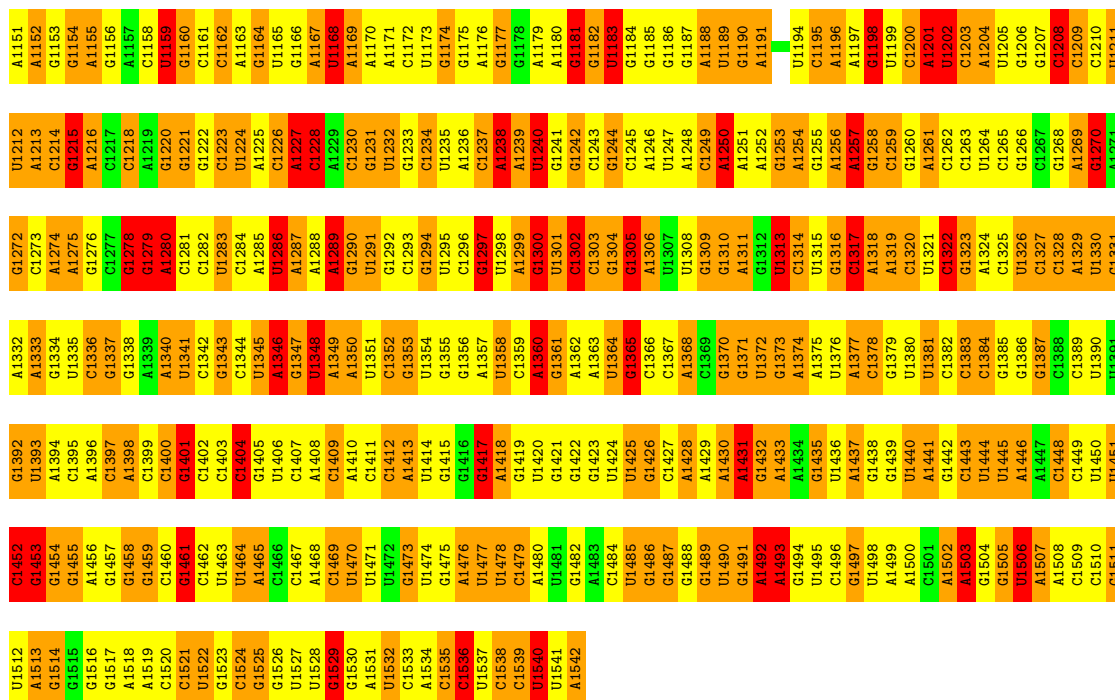
- Molecule 34: 50S ribosomal protein L36



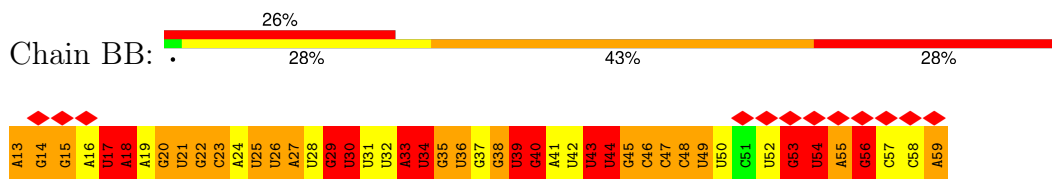
- Molecule 35: 16S ribosomal RNA



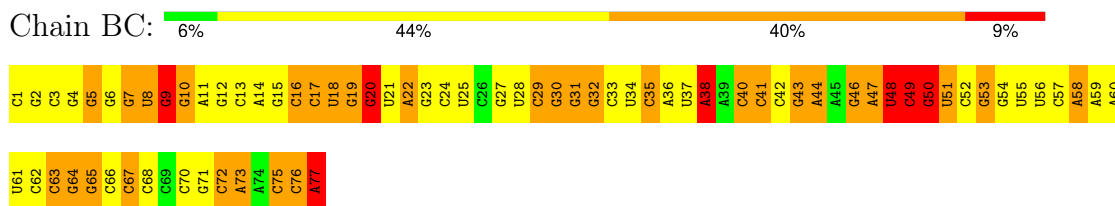
U1091	U1030	C970	A908	C848	U788	A728	C668	A608	C545	U485	G425	A364	A303	G242	A181	U121
A1092	C1031	G971	A909	G849	U789	A729	G669	A609	A546	U486	U426	U365	U304	A242	A182	G122
A1093	G1032	C972	C910	U850	U790	G730	G670	U610	A547	A487	U427	U366	G305	U244	G183	C123
G1094	G1033	G973	U911	G851	G791	G731	G671	C611	G548	C488	U428	U367	A306	U245	G184	C124
U1095	G1034	A974	C912	G852	U792	G732	U672	C612	C549	C489	U429	U368	C307	A246	U125	G126
C1096	A1035	A975	A913	G853	U793	G733	A673	C613	G550	C490	A430	G369	C308	G247	G186	G127
C1097	A1036	G976	A914	U854	A794	G734	G674	C614	U551	C491	A431	C370	A309	C248	G187	A128
C1098	C1037	A977	A915	U855	C795	C735	A675	G615	U552	C492	A432	A371	G310	U249	C188	A129
G1099	U1038	A978	U916	C856	C796	G736	A676	G616	A553	C493	G433	C372	C311	U250	A130	A130
C1100	G1039	C979	G917	C857	C797	C737	U677	G617	A554	C494	U434	A373	A312	U251	A190	G131
A1101	U1040	C980	C918	G858	U798	C738	U678	C618	U555	C495	U435	A374	A313	G252	A191	G132
C1102	G1041	U981	U920	G859	G799	C739	C679	U619	C556	A496	U436	U375	C314	G253	A192	C133
C1103	A1042	U982	U921	A860	G800	U740	C680	C620	G557	C497	U437	G376	A315	G254	G193	U134
G1104	G1043	A983	G922	G861	U801	G741	A681	A621	G558	A488	U438	G377	C316	G255	C194	G135
A1105	A1044	C984	A923	C862	A802	G742	G682	C622	A559	A499	U439	G378	U317	—	A195	C136
G1106	C1045	C985	C924	U863	G803	A743	G683	C623	A560	G500	C440	C379	A318	G258	A196	G137
C1107	A1046	U986	G925	A864	U804	C744	U684	C624	U561	C501	A441	G380	A319	G259	A197	U137
G1108	G1047	G987	G926	A865	C805	G745	G685	U625	U562	A502	G442	C381	A320	G260	G198	G138
C1109	U1048	G988	G927	C866	C806	A746	U686	G626	A563	C503	C443	A392	A321	U261	A139	A139
C1110	U1049	U989	G928	G867	A807	A747	A687	G627	C564	C504	G444	A383	C322	A262	U140	U140
A1111	G1050	C990	G929	C868	C808	G748	G688	G628	G565	G505	G445	A263	U323	A263	G202	G141
C1112	C1051	U991	C930	G869	G809	A749	C689	A629	G566	G506	G446	C385	G324	C264	G203	G142
C1113	U1052	U992	C931	U870	C810	C750	G690	A630	G567	C507	G447	C386	A325	G265	G204	A143
C1114	G1053	G993	C932	U871	C811	U751	G691	C631	G568	U508	A448	U387	A326	G266	A205	G144
U1115	C1054	A994	G933	A872	G812	G752	U692	U632	C569	A509	G449	A327	A327	C267	C206	G145
U1116	A1055	C995	C934	A873	U813	A753	C693	G633	G570	A510	G450	A389	C328	U268	C207	G146
A1117	—	A996	A935	G874	A814	G754	G700	A640	U571	C511	A451	U390	A329	C269	U208	G147
U1118	G1058	U997	C936	U875	A815	C755	A695	A635	A572	C512	A452	G391	C330	C270	G209	G148
C1119	C1059	C998	A937	C876	A816	C756	A696	U636	A573	C513	G453	C392	G331	C271	C210	A149
C1120	U1060	C999	A938	G877	C817	U757	U697	C637	A574	C514	G454	—	G332	C272	G211	U150
U1121	G1061	A1000	G939	A878	C818	C758	G698	U638	G575	G515	G455	C395	U333	U273	G212	A151
U1122	U1062	C1001	C940	C879	A819	A759	G699	G639	C576	U516	A456	C396	C334	A274	G213	A152
C1123	C1063	G1002	G941	C880	U820	G760	G700	A640	G577	C517	A457	C397	C335	G275	C214	C153
G1124	G1064	G881	—	C881	G821	G761	U701	U641	C578	C518	U458	U398	A336	G276	C215	U154
U1125	U1065	A1003	G944	C882	U822	A762	A702	A642	A579	C519	A459	G399	U216	C277	U216	A155
U1126	C1066	C1004	G945	C883	C823	G763	G703	C643	C580	A520	A460	C400	C400	G278	C217	C156
G1127	A1067	G1006	A946	U884	G824	C764	A704	U644	G581	G521	A461	C401	A338	—	U157	G157
C1128	G1068	U1007	G947	G885	A825	G765	G705	G645	C582	C522	G462	G402	—	A279	U218	C158
A1129	C1069	U1008	C948	C886	C826	A766	A706	G646	A583	A523	U463	C403	C341	C280	U219	G159
C1130	U1070	U1009	A949	G887	U827	A767	U707	C647	G584	G524	U464	G404	C342	G281	G220	A160
G1131	C1071	U1010	U950	G888	U828	A768	C708	A648	—	C525	A465	U405	U343	A282	C221	A161
C1132	G1072	G1011	G951	A889	G829	G769	U709	A649	G587	C526	A466	G406	A344	U283	C222	A162
G1133	U1073	C1012	U952	G890	G830	C770	G710	G650	U588	C527	U467	U407	G346	C285	U224	G163
C1134	G1074	G1013	G953	U891	A831	C771	G711	C651	U589	G528	A468	A408	G347	C286	C225	G164
U1135	U1075	A1014	G954	A892	G832	U772	A712	U652	U590	G529	G469	U409	G348	U287	G226	G165
C1136	C1076	G1015	U955	C893	G833	G773	G713	U653	U591	G530	C470	A410	A349	A288	G227	U166
C1137	U1077	U1016	U956	G894	U834	G774	G714	G654	G592	U531	U471	A411	G350	G289	A228	A167
G1138	G1078	U1017	U957	G895	U835	G775	A715	A655	U593	A532	U472	A412	G351	C290	U229	G168
A1139	U1079	C1018	A958	C896	G836	G776	A716	G656	—	A533	U473	G413	C352	U291	G230	C169
C1140	A1080	A1019	A959	C897	U837	A777	U717	U657	U596	U534	G474	A414	A353	G292	U231	U170
C1141	A1081	G1020	U960	G898	G838	G778	A718	G658	G597	A535	C475	A415	C354	G293	G232	A171
G1142	U1082	C1021	U961	C899	C839	C779	C719	U659	U598	C536	U476	A416	C355	U294	A172	A172
A1143	G1083	A1022	C962	A900	C840	A780	C720	C660	C599	G537	C477	G417	A356	C295	U173	U173
C1144	U1084	U1023	G963	A901	C841	A781	G721	C661	A600	C538	A478	C418	G357	U296	C235	A174
A1145	A1085	G1024	A964	G902	U842	A782	G722	U662	—	A539	U479	C419	U358	G297	A236	C175
U1146	U1086	U1025	U965	G903	U843	C783	U723	A663	U603	G540	U480	G359	U359	A298	G237	G176
G1147	G1087	G1026	G966	U904	G844	A784	G724	G664	G604	G541	C481	U421	C360	G299	A238	G177
C1148	U1088	C1027	C967	U905	A845	A785	G725	A665	G605	G542	A482	C422	G361	A300	U239	C178
U1149	G1089	U1028	A968	A906	G846	G786	C726	G666	G606	U543	C483	G423	G362	G301	G240	A179
A1150	U1090	U1029	A969	A907	G847	A787	G727	G667	A607	G544	G484	G424	A363	G302	G241	U180



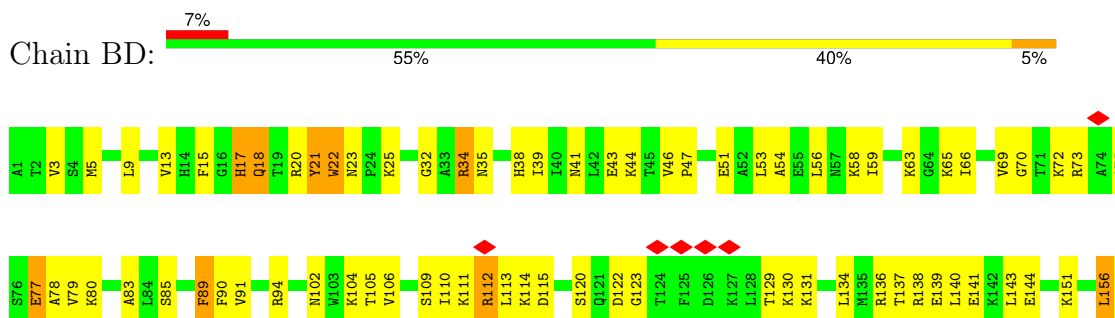
- Molecule 36: mRNA

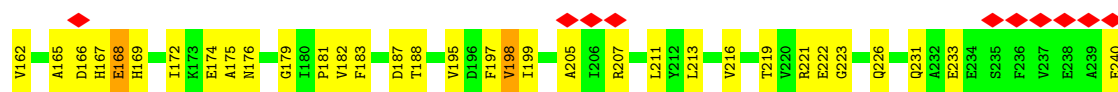


- Molecule 37: P site tRNA



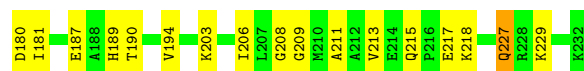
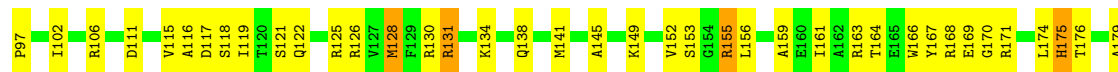
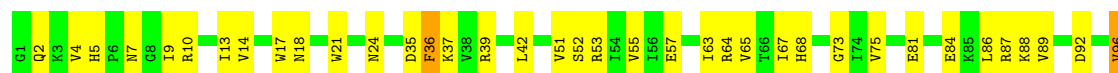
- Molecule 38: 30S ribosomal protein S2





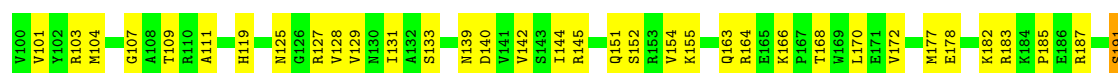
- Molecule 39: 30S ribosomal protein S3

Chain BE: 60% 37%



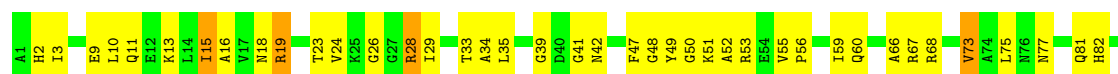
- Molecule 40: 30S ribosomal protein S4

Chain BF: 62% 35%



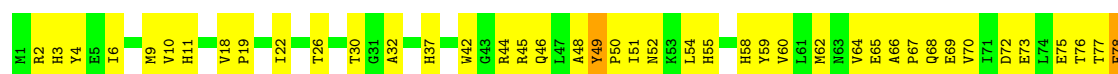
- Molecule 41: 30S ribosomal protein S5

Chain BG: 52% 44%

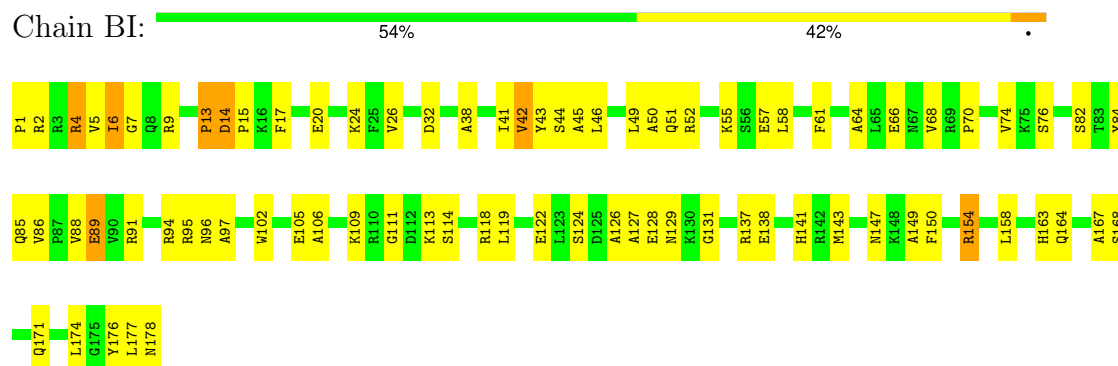


- Molecule 42: 30S ribosomal protein S6

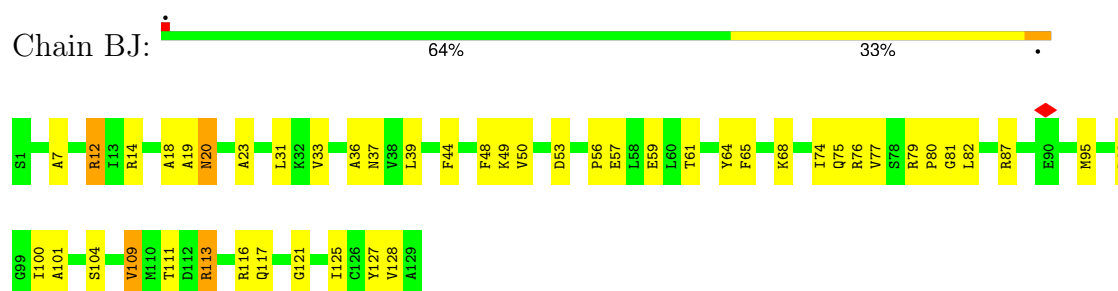
Chain BH: 44% 50% 6%



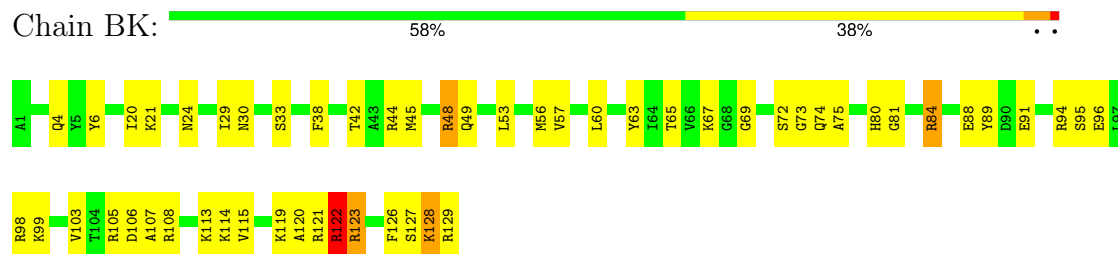
- Molecule 43: 30S ribosomal protein S7



- Molecule 44: 30S ribosomal protein S8



- Molecule 45: 30S ribosomal protein S9

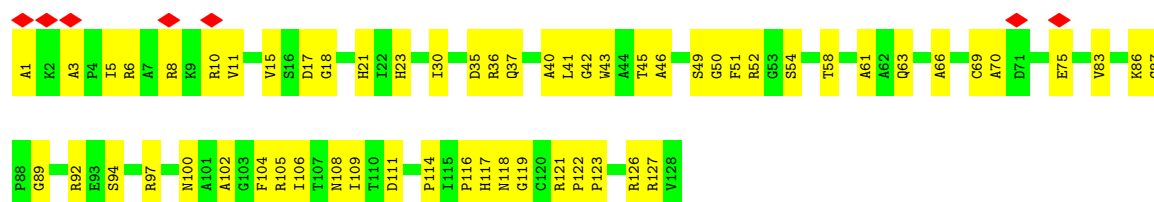


- Molecule 46: 30S ribosomal protein S10

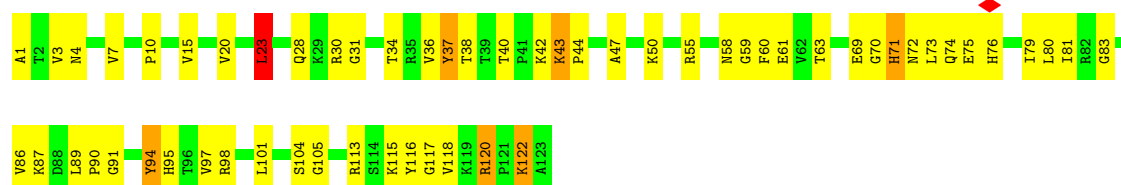


- Molecule 47: 30S ribosomal protein S11

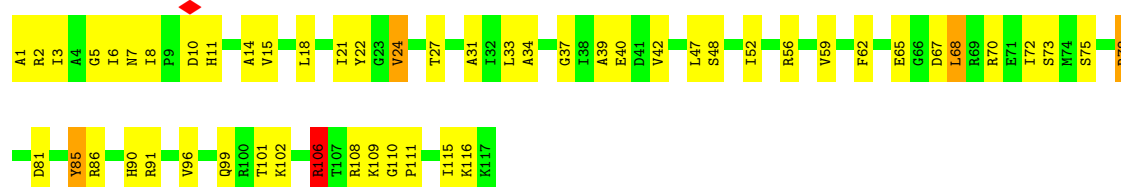




• Molecule 48: 30S ribosomal protein S12



• Molecule 49: 30S ribosomal protein S13



• Molecule 50: 30S ribosomal protein S14



• Molecule 51: 30S ribosomal protein S15



• Molecule 52: 30S ribosomal protein S16





- Molecule 53: 30S ribosomal protein S17

Chain BS: 54% 39% 7%



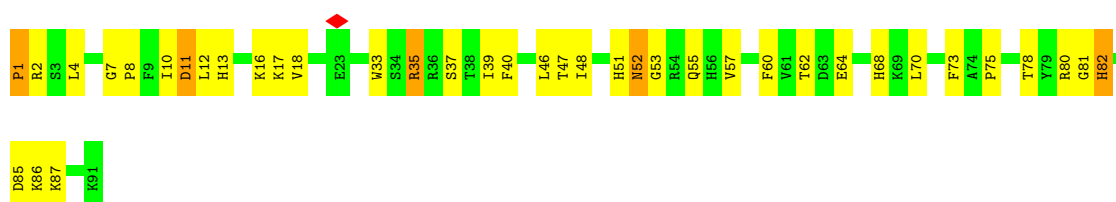
- Molecule 54: 30S ribosomal protein S18

Chain BT: 47% 50% 3%



- Molecule 55: 30S ribosomal protein S19

Chain BU: 57% 37% 5%



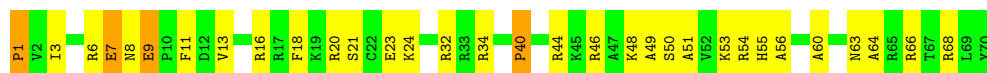
- Molecule 56: 30S ribosomal protein S20

Chain BV: 56% 43% 1%



- Molecule 57: 30S ribosomal protein S21

Chain BW: 54% 40% 6%



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	1.443	Depositor
Minimum map value	-0.456	Depositor
Average map value	0.028	Depositor
Map value standard deviation	0.182	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: 3TD, 1MG, 5MU, 5MC, 4SU, CH, H2U, 4OC, OMC, 7MG, MA6, OMU, OMG, 2MG, 2MA, PSU, UR3, 6MZ

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	1.88	46/2869 (1.6%)	1.99	159/4474 (3.6%)
2	AB	1.90	1082/69257 (1.6%)	1.98	3457/108040 (3.2%)
3	AC	1.96	33/1748 (1.9%)	2.39	106/2355 (4.5%)
4	AD	2.07	55/2131 (2.6%)	2.47	143/2863 (5.0%)
5	AE	2.00	32/1586 (2.0%)	2.41	101/2134 (4.7%)
6	AF	2.01	29/1571 (1.8%)	2.37	94/2113 (4.4%)
7	AG	1.99	24/1444 (1.7%)	2.36	73/1937 (3.8%)
8	AH	2.05	32/1343 (2.4%)	2.38	75/1816 (4.1%)
9	AI	1.96	18/1122 (1.6%)	2.42	68/1515 (4.5%)
10	AJ	2.01	23/1247 (1.8%)	2.49	84/1679 (5.0%)
11	AK	1.95	19/1046 (1.8%)	2.54	90/1410 (6.4%)
12	AL	2.03	25/1152 (2.2%)	2.51	78/1551 (5.0%)
13	AM	2.01	21/956 (2.2%)	2.41	65/1279 (5.1%)
14	AN	2.06	26/1062 (2.4%)	2.38	51/1413 (3.6%)
15	AO	1.96	14/1093 (1.3%)	2.42	66/1460 (4.5%)
16	AP	1.97	19/1021 (1.9%)	2.42	58/1364 (4.3%)
17	AQ	2.07	21/910 (2.3%)	2.41	52/1219 (4.3%)
18	AR	2.01	18/929 (1.9%)	2.32	49/1242 (3.9%)
19	AS	1.95	20/960 (2.1%)	2.59	88/1278 (6.9%)
20	AT	2.08	23/829 (2.8%)	2.38	53/1107 (4.8%)
21	AU	2.15	26/864 (3.0%)	2.39	55/1156 (4.8%)
22	AV	2.05	14/794 (1.8%)	2.44	45/1060 (4.2%)
23	AW	1.91	8/797 (1.0%)	2.35	38/1062 (3.6%)
24	AX	2.01	17/766 (2.2%)	2.35	45/1025 (4.4%)
25	AY	1.97	12/642 (1.9%)	2.44	38/848 (4.5%)
26	AZ	1.95	9/635 (1.4%)	2.58	54/848 (6.4%)
27	A0	1.93	10/510 (2.0%)	2.38	24/677 (3.5%)
28	A1	2.02	11/453 (2.4%)	2.50	28/605 (4.6%)
29	A2	2.01	8/559 (1.4%)	2.53	33/745 (4.4%)
30	A3	1.97	7/450 (1.6%)	2.39	22/599 (3.7%)
31	A4	1.91	8/448 (1.8%)	2.26	10/594 (1.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	A5	2.09	8/380 (2.1%)	2.51	23/498 (4.6%)
33	A6	2.10	11/513 (2.1%)	2.28	24/676 (3.6%)
34	A7	2.20	11/303 (3.6%)	2.31	16/397 (4.0%)
35	BA	1.89	580/36769 (1.6%)	2.01	1988/57354 (3.5%)
36	BB	1.99	24/1108 (2.2%)	2.23	81/1724 (4.7%)
37	BC	1.86	27/1721 (1.6%)	2.00	93/2683 (3.5%)
38	BD	1.94	36/1904 (1.9%)	2.39	122/2565 (4.8%)
39	BE	2.04	39/1852 (2.1%)	2.36	73/2490 (2.9%)
40	BF	1.96	29/1665 (1.7%)	2.32	80/2227 (3.6%)
41	BG	2.11	27/1239 (2.2%)	2.42	79/1664 (4.7%)
42	BH	2.01	26/1121 (2.3%)	2.47	84/1509 (5.6%)
43	BI	2.01	33/1422 (2.3%)	2.42	84/1908 (4.4%)
44	BJ	1.99	13/989 (1.3%)	2.33	54/1326 (4.1%)
45	BK	1.98	20/1048 (1.9%)	2.42	58/1394 (4.2%)
46	BL	2.05	20/835 (2.4%)	2.41	52/1127 (4.6%)
47	BM	2.05	18/982 (1.8%)	2.49	64/1323 (4.8%)
48	BN	2.03	21/969 (2.2%)	2.36	57/1300 (4.4%)
49	BO	2.03	20/919 (2.2%)	2.52	61/1226 (5.0%)
50	BP	2.01	20/817 (2.4%)	2.33	36/1088 (3.3%)
51	BQ	1.99	12/724 (1.7%)	2.44	46/966 (4.8%)
52	BR	2.05	14/659 (2.1%)	2.37	39/884 (4.4%)
53	BS	2.03	14/681 (2.1%)	2.38	43/913 (4.7%)
54	BT	1.90	9/637 (1.4%)	2.37	43/851 (5.1%)
55	BU	2.06	17/744 (2.3%)	2.36	37/995 (3.7%)
56	BV	1.96	12/676 (1.8%)	2.56	42/895 (4.7%)
57	BW	1.88	9/598 (1.5%)	2.42	35/792 (4.4%)
All	All	1.93	2780/162469 (1.7%)	2.12	8816/242243 (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	69
2	AB	0	1654
3	AC	0	3
4	AD	0	11
5	AE	0	7
6	AF	0	2
7	AG	0	1
8	AH	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
9	AI	0	3
10	AJ	0	8
11	AK	0	1
12	AL	0	3
13	AM	0	3
14	AN	0	2
15	AO	0	3
16	AP	0	5
17	AQ	0	4
18	AR	0	6
19	AS	0	3
20	AT	0	5
21	AU	0	5
22	AV	0	1
24	AX	0	5
25	AY	0	4
26	AZ	0	2
27	A0	0	4
28	A1	0	4
29	A2	0	3
30	A3	0	1
31	A4	0	2
32	A5	0	2
33	A6	0	2
34	A7	0	2
35	BA	0	882
36	BB	0	30
37	BC	0	41
38	BD	0	4
39	BE	0	9
40	BF	0	3
41	BG	0	3
42	BH	0	9
43	BI	0	3
44	BJ	0	7
45	BK	0	5
46	BL	0	2
47	BM	0	1
48	BN	0	6
49	BO	0	4
50	BP	0	1
51	BQ	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
52	BR	0	2
53	BS	0	1
54	BT	0	2
55	BU	0	4
57	BW	0	4
All	All	0	2857

The worst 5 of 2780 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	AH	134	GLY	CA-C	10.99	1.63	1.51
34	A7	30	GLU	CA-C	10.96	1.62	1.52
55	BU	57	VAL	CA-C	10.93	1.60	1.52
41	BG	55	VAL	CA-CB	10.68	1.61	1.53
2	AB	2829	A	P-O5'	10.64	1.75	1.59

The worst 5 of 8816 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	AL	120	ARG	NE-CZ-NH2	14.84	132.55	119.20
29	A2	65	ASN	CA-C-N	13.98	131.52	120.33
29	A2	65	ASN	C-N-CA	13.98	131.52	120.33
40	BF	17	ASP	CA-CB-CG	12.60	125.20	112.60
47	BM	114	PRO	N-CA-CB	12.50	114.36	103.36

There are no chirality outliers.

5 of 2857 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1	U	Sidechain
1	AA	2	G	Sidechain
1	AA	3	C	Sidechain
1	AA	4	C	Sidechain
1	AA	5	U	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	2566	0	1299	0	0
2	AB	62351	0	31248	0	0
3	AC	1733	0	1824	0	0
4	AD	2092	0	2170	0	0
5	AE	1565	0	1616	0	0
6	AF	1552	0	1619	0	0
7	AG	1420	0	1460	0	0
8	AH	1323	0	1374	0	0
9	AI	1111	0	1148	0	0
10	AJ	1233	0	1283	0	0
11	AK	1032	0	1088	0	0
12	AL	1129	0	1162	0	0
13	AM	947	0	1023	0	0
14	AN	1053	0	1129	0	0
15	AO	1074	0	1157	0	0
16	AP	1008	0	1045	0	0
17	AQ	900	0	935	0	0
18	AR	917	0	965	0	0
19	AS	947	0	1022	0	0
20	AT	816	0	839	0	0
21	AU	857	0	922	0	0
22	AV	787	0	846	0	0
23	AW	789	0	847	0	0
24	AX	753	0	780	0	0
25	AY	634	0	656	0	0
26	AZ	625	0	655	0	0
27	A0	509	0	543	0	0
28	A1	449	0	491	0	0
29	A2	549	0	552	0	0
30	A3	444	0	461	0	0
31	A4	441	0	485	0	0
32	A5	377	0	418	0	0
33	A6	504	0	574	0	0
34	A7	302	0	343	0	0
35	BA	33089	0	16599	0	0
36	BB	993	0	501	0	0
37	BC	1641	0	841	0	0
38	BD	1872	0	1885	0	0
39	BE	1822	0	1913	0	0
40	BF	1643	0	1710	0	0
41	BG	1225	0	1273	0	0
42	BH	1101	0	1050	0	0
43	BI	1400	0	1449	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BJ	979	0	1034	0	0
45	BK	1036	0	1084	0	0
46	BL	825	0	865	0	0
47	BM	965	0	997	0	0
48	BN	955	0	1019	0	0
49	BO	910	0	981	0	0
50	BP	805	0	847	0	0
51	BQ	716	0	742	0	0
52	BR	649	0	666	0	0
53	BS	672	0	716	0	0
54	BT	626	0	651	0	0
55	BU	727	0	769	0	0
56	BV	670	0	722	0	0
57	BW	590	0	631	0	0
All	All	150700	0	102924	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	
3	AC	232/234 (99%)	215 (93%)	12 (5%)	5 (2%)	5	29
4	AD	270/272 (99%)	237 (88%)	24 (9%)	9 (3%)	3	21
5	AE	207/209 (99%)	175 (84%)	24 (12%)	8 (4%)	2	19
6	AF	199/201 (99%)	173 (87%)	16 (8%)	10 (5%)	1	16
7	AG	176/178 (99%)	151 (86%)	15 (8%)	10 (6%)	1	14
8	AH	174/176 (99%)	159 (91%)	11 (6%)	4 (2%)	5	28

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	AI	147/149 (99%)	131 (89%)	12 (8%)	4 (3%)	4	25
10	AJ	162/164 (99%)	155 (96%)	6 (4%)	1 (1%)	21	59
11	AK	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	18	56
12	AL	140/142 (99%)	120 (86%)	15 (11%)	5 (4%)	2	20
13	AM	121/123 (98%)	105 (87%)	12 (10%)	4 (3%)	3	21
14	AN	142/144 (99%)	125 (88%)	14 (10%)	3 (2%)	5	30
15	AO	134/136 (98%)	124 (92%)	8 (6%)	2 (2%)	8	40
16	AP	125/127 (98%)	115 (92%)	9 (7%)	1 (1%)	16	54
17	AQ	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
18	AR	112/114 (98%)	97 (87%)	13 (12%)	2 (2%)	6	34
19	AS	115/117 (98%)	108 (94%)	3 (3%)	4 (4%)	3	20
20	AT	101/103 (98%)	89 (88%)	9 (9%)	3 (3%)	3	23
21	AU	108/110 (98%)	99 (92%)	5 (5%)	4 (4%)	2	20
22	AV	98/100 (98%)	77 (79%)	18 (18%)	3 (3%)	3	22
23	AW	101/103 (98%)	89 (88%)	9 (9%)	3 (3%)	3	23
24	AX	92/94 (98%)	84 (91%)	7 (8%)	1 (1%)	11	46
25	AY	82/84 (98%)	64 (78%)	14 (17%)	4 (5%)	1	16
26	AZ	75/77 (97%)	68 (91%)	4 (5%)	3 (4%)	2	18
27	A0	61/63 (97%)	56 (92%)	4 (7%)	1 (2%)	7	38
28	A1	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
29	A2	68/70 (97%)	64 (94%)	3 (4%)	1 (2%)	8	40
30	A3	54/56 (96%)	48 (89%)	4 (7%)	2 (4%)	2	20
31	A4	52/54 (96%)	49 (94%)	1 (2%)	2 (4%)	2	19
32	A5	44/46 (96%)	40 (91%)	2 (4%)	2 (4%)	2	17
33	A6	62/64 (97%)	58 (94%)	3 (5%)	1 (2%)	7	38
34	A7	36/38 (95%)	29 (81%)	4 (11%)	3 (8%)	0	9
38	BD	238/240 (99%)	218 (92%)	14 (6%)	6 (2%)	4	26
39	BE	230/232 (99%)	217 (94%)	9 (4%)	4 (2%)	7	36
40	BF	203/205 (99%)	186 (92%)	13 (6%)	4 (2%)	6	31
41	BG	164/166 (99%)	150 (92%)	12 (7%)	2 (1%)	10	44
42	BH	133/135 (98%)	123 (92%)	9 (7%)	1 (1%)	16	54

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	BI	176/178 (99%)	168 (96%)	5 (3%)	3 (2%)	7	36
44	BJ	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	16	54
45	BK	127/129 (98%)	114 (90%)	10 (8%)	3 (2%)	4	27
46	BL	101/103 (98%)	91 (90%)	4 (4%)	6 (6%)	1	13
47	BM	126/128 (98%)	109 (86%)	15 (12%)	2 (2%)	7	38
48	BN	121/123 (98%)	103 (85%)	16 (13%)	2 (2%)	7	36
49	BO	115/117 (98%)	109 (95%)	5 (4%)	1 (1%)	14	51
50	BP	98/100 (98%)	85 (87%)	6 (6%)	7 (7%)	1	11
51	BQ	86/88 (98%)	81 (94%)	4 (5%)	1 (1%)	10	44
52	BR	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
53	BS	81/83 (98%)	73 (90%)	7 (9%)	1 (1%)	10	44
54	BT	72/74 (97%)	62 (86%)	7 (10%)	3 (4%)	2	17
55	BU	89/91 (98%)	82 (92%)	6 (7%)	1 (1%)	11	46
56	BV	84/86 (98%)	79 (94%)	4 (5%)	1 (1%)	10	44
57	BW	68/70 (97%)	61 (90%)	4 (6%)	3 (4%)	2	17
All	All	6319/6423 (98%)	5708 (90%)	453 (7%)	158 (2%)	6	26

5 of 158 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AD	94	LEU
6	AF	62	GLN
6	AF	188	MET
7	AG	136	ILE
9	AI	3	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	181/181 (100%)	175 (97%)	6 (3%)	33	55

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AD	217/217 (100%)	206 (95%)	11 (5%)	21	42
5	AE	164/164 (100%)	153 (93%)	11 (7%)	15	36
6	AF	165/165 (100%)	160 (97%)	5 (3%)	36	57
7	AG	149/149 (100%)	140 (94%)	9 (6%)	17	39
8	AH	137/137 (100%)	124 (90%)	13 (10%)	8	25
9	AI	114/114 (100%)	106 (93%)	8 (7%)	14	35
10	AJ	122/122 (100%)	117 (96%)	5 (4%)	27	49
11	AK	109/109 (100%)	104 (95%)	5 (5%)	24	45
12	AL	116/116 (100%)	108 (93%)	8 (7%)	14	36
13	AM	104/104 (100%)	99 (95%)	5 (5%)	23	44
14	AN	103/103 (100%)	102 (99%)	1 (1%)	68	78
15	AO	109/109 (100%)	101 (93%)	8 (7%)	13	34
16	AP	103/103 (100%)	99 (96%)	4 (4%)	28	49
17	AQ	87/87 (100%)	80 (92%)	7 (8%)	11	31
18	AR	99/99 (100%)	95 (96%)	4 (4%)	28	49
19	AS	89/89 (100%)	86 (97%)	3 (3%)	32	54
20	AT	84/84 (100%)	81 (96%)	3 (4%)	31	52
21	AU	93/93 (100%)	88 (95%)	5 (5%)	20	41
22	AV	84/84 (100%)	79 (94%)	5 (6%)	17	39
23	AW	84/84 (100%)	79 (94%)	5 (6%)	17	39
24	AX	78/78 (100%)	73 (94%)	5 (6%)	16	37
25	AY	62/62 (100%)	56 (90%)	6 (10%)	8	24
26	AZ	67/67 (100%)	60 (90%)	7 (10%)	7	22
27	A0	55/55 (100%)	53 (96%)	2 (4%)	31	52
28	A1	48/48 (100%)	42 (88%)	6 (12%)	4	16
29	A2	62/62 (100%)	61 (98%)	1 (2%)	55	70
30	A3	47/47 (100%)	46 (98%)	1 (2%)	47	65
31	A4	48/48 (100%)	46 (96%)	2 (4%)	26	48
32	A5	38/38 (100%)	33 (87%)	5 (13%)	4	15
33	A6	51/51 (100%)	51 (100%)	0	100	100
34	A7	34/34 (100%)	33 (97%)	1 (3%)	37	58

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	BD	198/198 (100%)	190 (96%)	8 (4%)	28	49
39	BE	189/189 (100%)	179 (95%)	10 (5%)	20	41
40	BF	172/172 (100%)	168 (98%)	4 (2%)	44	64
41	BG	125/125 (100%)	118 (94%)	7 (6%)	19	40
42	BH	116/116 (100%)	108 (93%)	8 (7%)	14	36
43	BI	146/146 (100%)	138 (94%)	8 (6%)	19	41
44	BJ	104/104 (100%)	99 (95%)	5 (5%)	23	44
45	BK	106/106 (100%)	100 (94%)	6 (6%)	18	40
46	BL	90/90 (100%)	84 (93%)	6 (7%)	15	36
47	BM	98/98 (100%)	97 (99%)	1 (1%)	68	78
48	BN	103/103 (100%)	96 (93%)	7 (7%)	14	36
49	BO	95/95 (100%)	90 (95%)	5 (5%)	20	41
50	BP	83/83 (100%)	80 (96%)	3 (4%)	31	52
51	BQ	76/76 (100%)	75 (99%)	1 (1%)	61	74
52	BR	65/65 (100%)	59 (91%)	6 (9%)	8	27
53	BS	77/77 (100%)	70 (91%)	7 (9%)	9	27
54	BT	64/64 (100%)	61 (95%)	3 (5%)	23	45
55	BU	78/78 (100%)	71 (91%)	7 (9%)	9	27
56	BV	65/65 (100%)	65 (100%)	0	100	100
57	BW	60/60 (100%)	57 (95%)	3 (5%)	22	43
All	All	5213/5213 (100%)	4941 (95%)	272 (5%)	22	42

5 of 272 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	BN	28	GLN
49	BO	24	VAL
54	BT	18	GLN
16	AP	48	VAL
15	AO	136	MET

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	119/120 (99%)	19 (15%)	13 (10%)
2	AB	2901/2904 (99%)	552 (19%)	180 (6%)
35	BA	1541/1542 (99%)	310 (20%)	112 (7%)
36	BB	46/47 (97%)	16 (34%)	6 (13%)
37	BC	76/77 (98%)	14 (18%)	1 (1%)
All	All	4683/4690 (99%)	911 (19%)	312 (6%)

5 of 911 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	9	G
1	AA	13	G
1	AA	14	U
1	AA	25	U
1	AA	26	C

5 of 312 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	BA	552	U
35	BA	1302	C
35	BA	681	A
35	BA	944	G
35	BA	1465	A

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

40 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	1917	2	18,21,22	1.36	3 (16%)	21,30,33	1.95	5 (23%)
37	4SU	BC	8	37	18,21,22	2.00	6 (33%)	25,30,33	1.85	7 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
35	PSU	BA	516	35	18,21,22	1.69	4 (22%)	21,30,33	2.42	4 (19%)
37	PSU	BC	56	37	18,21,22	2.21	5 (27%)	21,30,33	1.26	1 (4%)
2	PSU	AB	2504	2	18,21,22	1.73	3 (16%)	21,30,33	2.30	6 (28%)
2	OMU	AB	2552	2	19,22,23	0.82	1 (5%)	25,31,34	1.42	3 (12%)
35	7MG	BA	527	35	23,26,27	2.94	6 (26%)	27,39,42	1.67	2 (7%)
2	H2U	AB	2449	2	18,21,22	1.24	1 (5%)	19,30,33	2.97	9 (47%)
2	PSU	AB	2580	2	18,21,22	1.83	4 (22%)	21,30,33	1.42	4 (19%)
2	PSU	AB	746	2	18,21,22	2.04	6 (33%)	21,30,33	2.00	6 (28%)
2	7MG	AB	2069	2	23,26,27	3.98	4 (17%)	27,39,42	1.67	5 (18%)
2	5MU	AB	747	2	19,22,23	1.51	3 (15%)	27,32,35	2.85	17 (62%)
2	2MG	AB	1835	2	23,26,27	1.08	1 (4%)	33,38,41	1.38	5 (15%)
2	2MA	AB	2503	2	22,25,26	1.21	1 (4%)	32,37,40	1.81	9 (28%)
35	2MG	BA	1207	35	23,26,27	1.21	3 (13%)	33,38,41	1.08	2 (6%)
35	MA6	BA	1518	35	23,26,27	1.03	1 (4%)	33,38,41	1.92	8 (24%)
2	OMC	AB	2498	2	19,22,23	1.28	4 (21%)	25,31,34	1.63	5 (20%)
2	1MG	AB	745	2	23,26,27	1.60	5 (21%)	33,39,42	1.50	6 (18%)
2	CH	AB	2575	2	16,21,22	1.71	2 (12%)	19,30,33	1.44	3 (15%)
2	PSU	AB	2457	2	18,21,22	1.60	3 (16%)	21,30,33	2.50	6 (28%)
2	2MG	AB	2445	2	23,26,27	1.34	3 (13%)	33,38,41	1.66	7 (21%)
2	5MU	AB	1939	2	19,22,23	1.33	1 (5%)	27,32,35	2.37	9 (33%)
35	5MC	BA	967	35	19,22,23	1.10	2 (10%)	26,32,35	1.30	4 (15%)
2	5MC	AB	1962	2	19,22,23	1.23	3 (15%)	26,32,35	1.58	7 (26%)
37	OMC	BC	33	37	19,22,23	1.25	3 (15%)	25,31,34	1.41	5 (20%)
35	UR3	BA	1498	35	19,22,23	1.27	3 (15%)	26,32,35	2.14	8 (30%)
35	4OC	BA	1402	35	20,23,24	1.18	4 (20%)	25,32,35	2.03	8 (32%)
35	MA6	BA	1519	35	23,26,27	1.15	3 (13%)	33,38,41	2.63	11 (33%)
2	3TD	AB	1915	2	19,22,23	1.31	2 (10%)	23,32,35	2.17	6 (26%)
35	2MG	BA	966	35	23,26,27	1.35	4 (17%)	33,38,41	1.46	5 (15%)
2	PSU	AB	955	2	18,21,22	1.87	3 (16%)	21,30,33	1.62	4 (19%)
37	5MU	BC	55	37	19,22,23	0.99	0	27,32,35	1.98	7 (25%)
35	2MG	BA	1516	35	23,26,27	1.25	3 (13%)	33,38,41	1.60	5 (15%)
37	H2U	BC	21	37	18,21,22	1.68	5 (27%)	19,30,33	2.08	8 (42%)
35	5MC	BA	1407	35	19,22,23	1.79	4 (21%)	26,32,35	1.53	6 (23%)
2	OMG	AB	2251	2	23,26,27	1.48	5 (21%)	32,38,41	1.59	5 (15%)
2	6MZ	AB	2030	2	22,25,26	1.83	4 (18%)	29,36,39	1.58	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PSU	AB	2605	2	18,21,22	1.83	3 (16%)	21,30,33	2.02	7 (33%)
2	6MZ	AB	1618	2	22,25,26	1.23	1 (4%)	29,36,39	1.47	6 (20%)
2	PSU	AB	1911	2	18,21,22	2.34	8 (44%)	21,30,33	1.38	4 (19%)

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	1917	2	-	3/7/25/26	0/2/2/2
37	4SU	BC	8	37	-	0/7/25/26	0/2/2/2
35	PSU	BA	516	35	-	1/7/25/26	0/2/2/2
37	PSU	BC	56	37	-	0/7/25/26	0/2/2/2
2	PSU	AB	2504	2	-	2/7/25/26	0/2/2/2
2	OMU	AB	2552	2	-	1/9/27/28	0/2/2/2
35	7MG	BA	527	35	-	1/7/37/38	0/3/3/3
2	H2U	AB	2449	2	-	0/7/38/39	0/2/2/2
2	PSU	AB	2580	2	-	3/7/25/26	0/2/2/2
2	PSU	AB	746	2	-	1/7/25/26	0/2/2/2
2	7MG	AB	2069	2	-	0/7/37/38	0/3/3/3
2	5MU	AB	747	2	-	0/7/25/26	0/2/2/2
2	2MG	AB	1835	2	-	0/9/27/28	0/3/3/3
2	2MA	AB	2503	2	-	2/7/25/26	0/3/3/3
35	2MG	BA	1207	35	-	0/9/27/28	0/3/3/3
35	MA6	BA	1518	35	-	0/11/29/30	0/3/3/3
2	OMC	AB	2498	2	-	0/9/27/28	0/2/2/2
2	1MG	AB	745	2	-	0/7/25/26	0/3/3/3
2	CH	AB	2575	2	-	0/5/25/26	0/2/2/2
2	PSU	AB	2457	2	-	0/7/25/26	0/2/2/2
2	2MG	AB	2445	2	-	0/9/27/28	0/3/3/3
2	5MU	AB	1939	2	-	0/7/25/26	0/2/2/2
35	5MC	BA	967	35	-	1/7/25/26	0/2/2/2
2	5MC	AB	1962	2	-	0/7/25/26	0/2/2/2
37	OMC	BC	33	37	-	0/9/27/28	0/2/2/2
35	UR3	BA	1498	35	-	0/7/25/26	0/2/2/2
35	4OC	BA	1402	35	-	0/9/29/30	0/2/2/2
35	MA6	BA	1519	35	-	0/11/29/30	0/3/3/3
2	3TD	AB	1915	2	-	0/7/25/26	0/2/2/2
35	2MG	BA	966	35	-	0/9/27/28	0/3/3/3
2	PSU	AB	955	2	-	0/7/25/26	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
37	5MU	BC	55	37	-	0/7/25/26	0/2/2/2
35	2MG	BA	1516	35	-	0/9/27/28	0/3/3/3
37	H2U	BC	21	37	-	0/7/38/39	0/2/2/2
35	5MC	BA	1407	35	-	0/7/25/26	0/2/2/2
2	OMG	AB	2251	2	-	0/9/27/28	0/3/3/3
2	6MZ	AB	2030	2	-	0/9/27/28	0/3/3/3
2	PSU	AB	2605	2	-	0/7/25/26	0/2/2/2
2	6MZ	AB	1618	2	-	1/9/27/28	0/3/3/3
2	PSU	AB	1911	2	-	1/7/25/26	0/2/2/2

The worst 5 of 130 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	2069	7MG	C8-N9	-17.64	1.34	1.45
35	BA	527	7MG	C8-N9	-11.88	1.38	1.45
2	AB	2575	CH	C2'-C1'	5.31	1.61	1.53
2	AB	1911	PSU	C2'-C1'	-5.12	1.46	1.53
37	BC	56	PSU	C1'-C5	5.07	1.61	1.50

The worst 5 of 239 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AB	2457	PSU	C6-C5-C4	8.06	123.62	118.17
35	BA	516	PSU	C3'-C2'-C1'	7.51	110.55	101.69
2	AB	2449	H2U	O2-C2-N1	-7.47	114.12	123.10
2	AB	2504	PSU	C6-C5-C4	6.92	122.84	118.17
2	AB	1939	5MU	C5M-C5-C4	6.89	126.14	118.78

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AB	746	PSU	C2'-C1'-C5-C4
2	AB	2503	2MA	O4'-C1'-N9-C8
2	AB	2503	2MA	O4'-C1'-N9-C4
2	AB	2552	OMU	C1'-C2'-O2'-CM2
2	AB	1917	PSU	O4'-C4'-C5'-O5'

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	AB	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AB	2831:G	O3'	2832:U	P	1.76

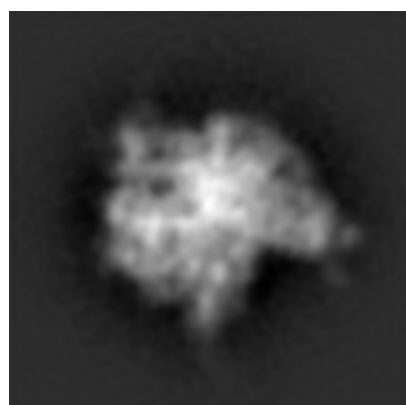
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5360. These allow visual inspection of the internal detail of the map and identification of artifacts.

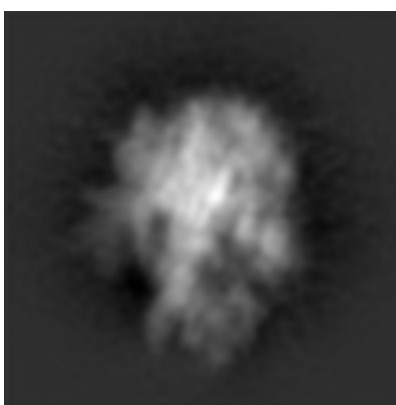
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

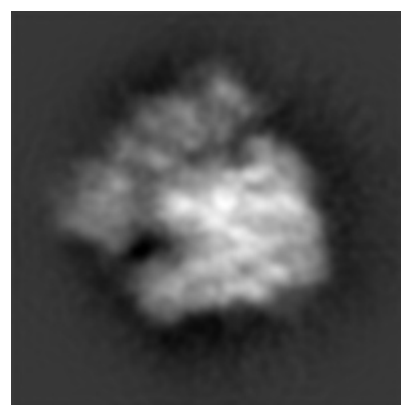
6.1.1 Primary map



X



Y

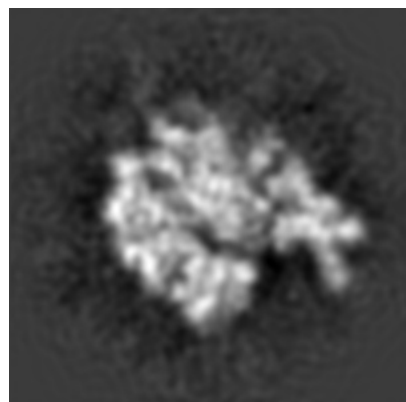


Z

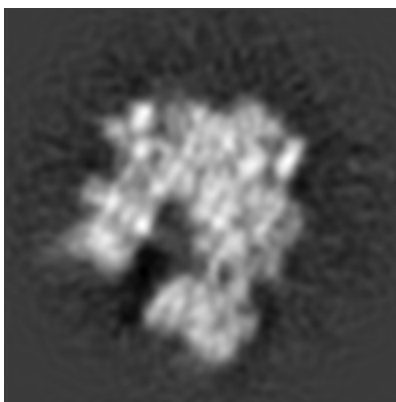
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

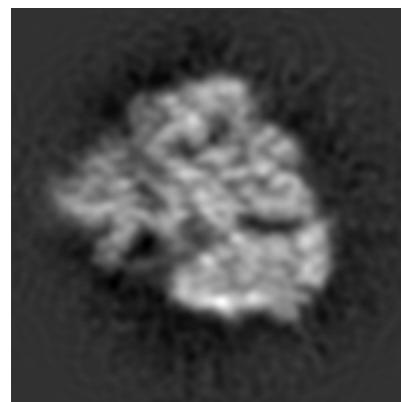
6.2.1 Primary map



X Index: 125



Y Index: 125

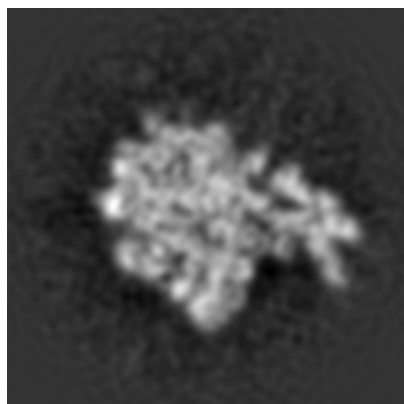


Z Index: 125

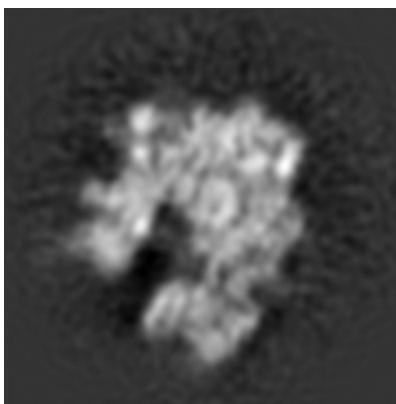
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

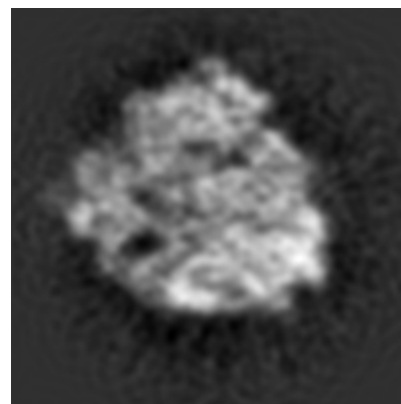
6.3.1 Primary map



X Index: 131



Y Index: 128

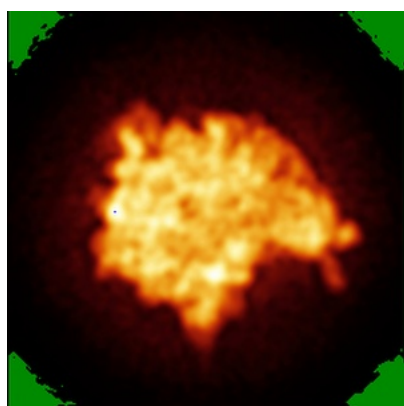


Z Index: 118

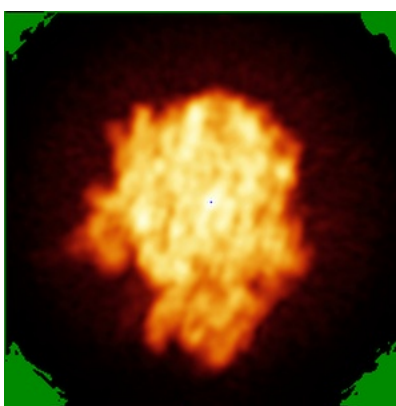
The images above show the largest variance slices of the map in three orthogonal directions.

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

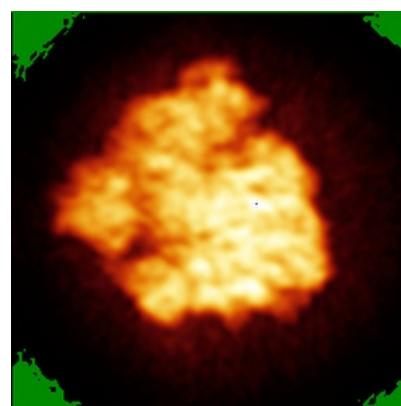
6.4.1 Primary map



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.

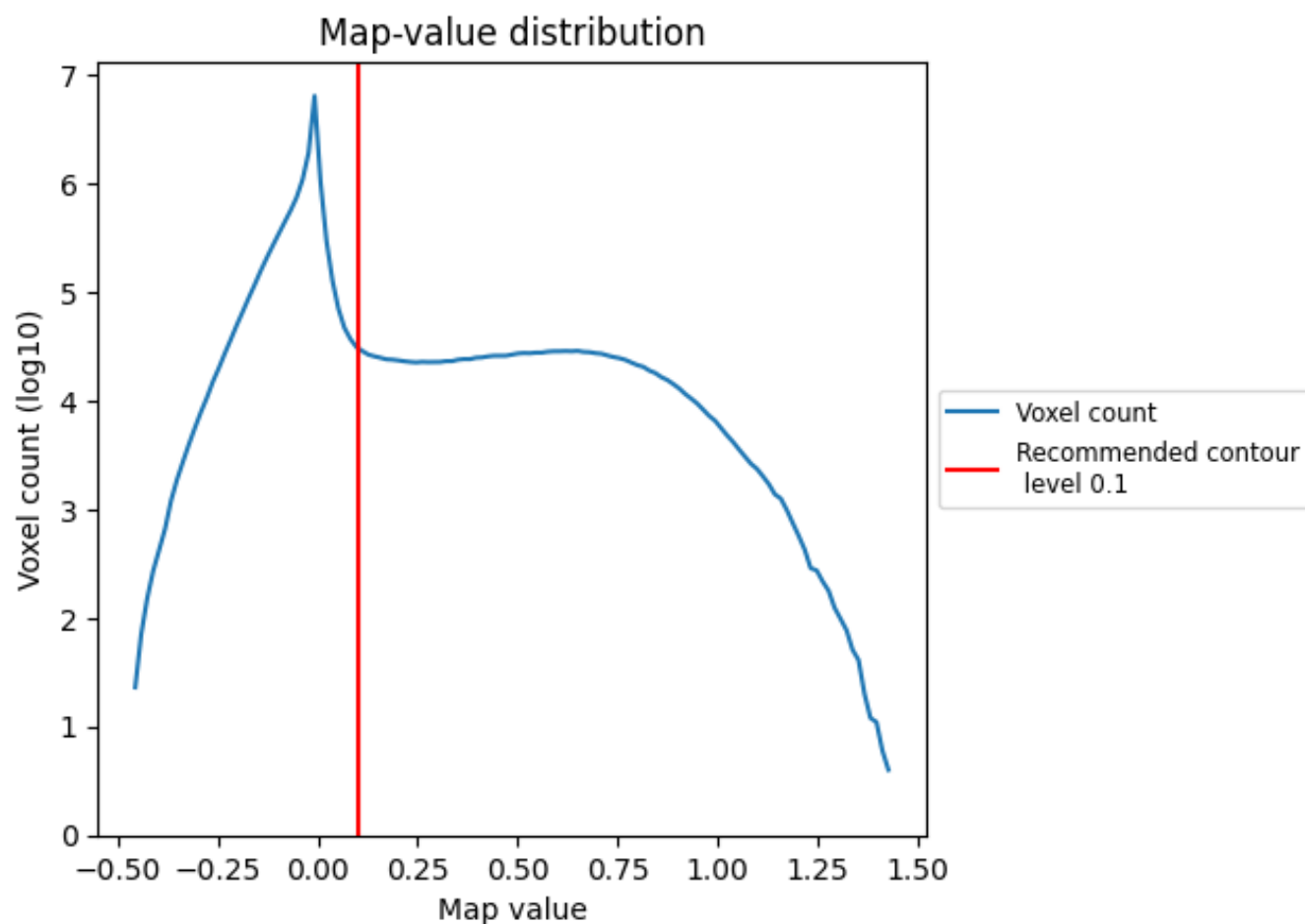
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

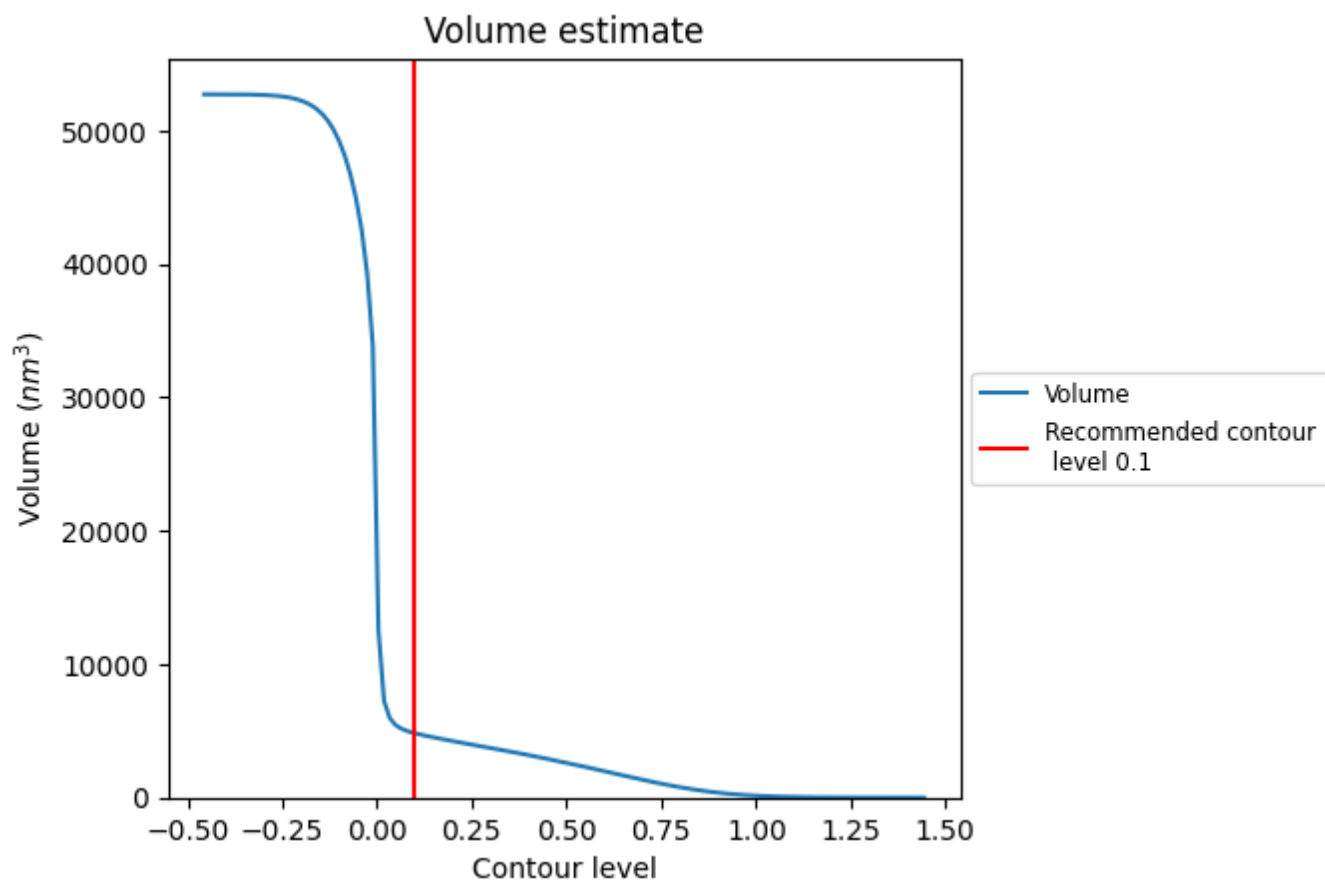
This section contains the results of statistical analysis of the map.

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.

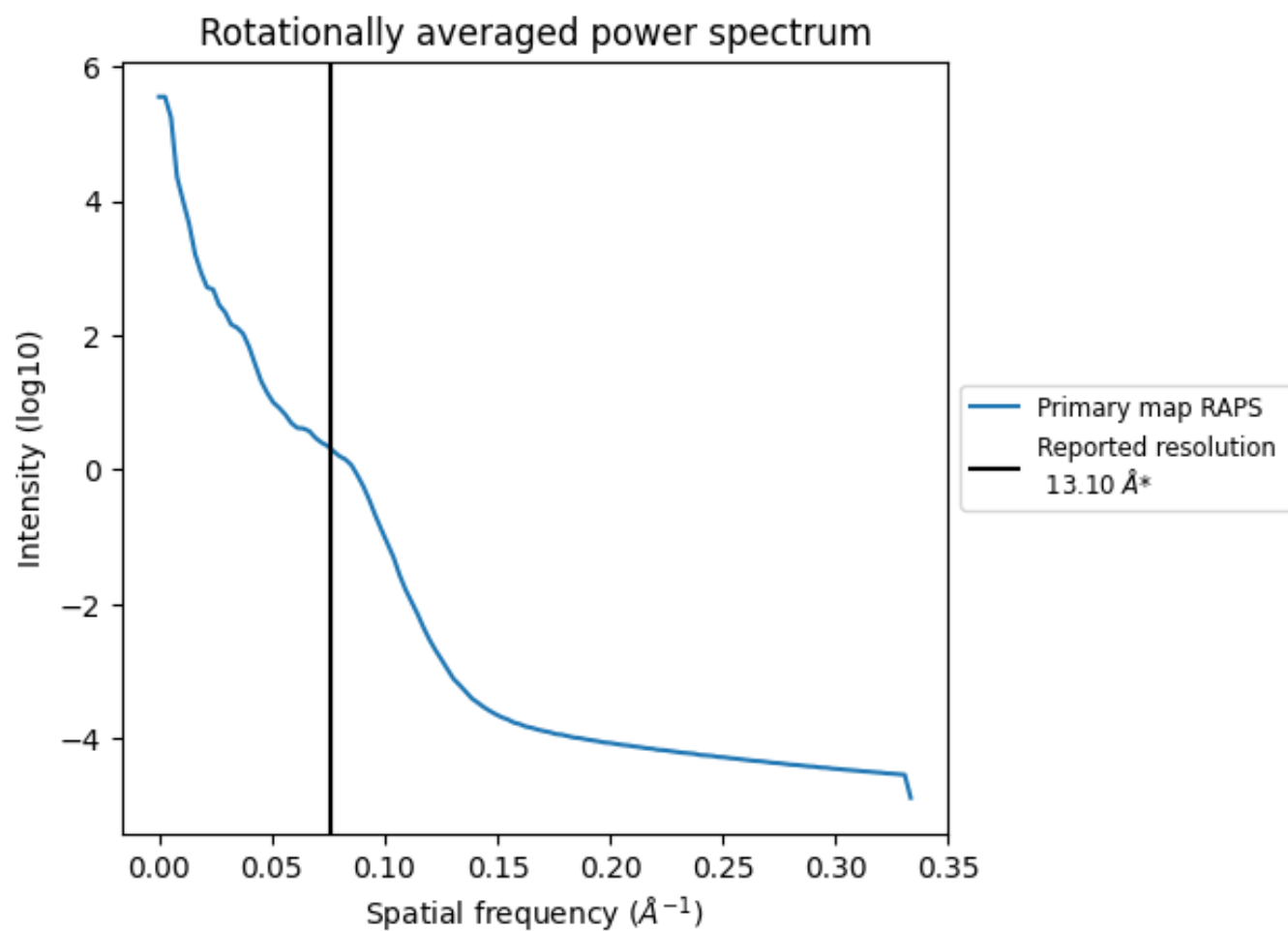
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4825 nm³; this corresponds to an approximate mass of 4359 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 $\text{\AA}^{-1}$

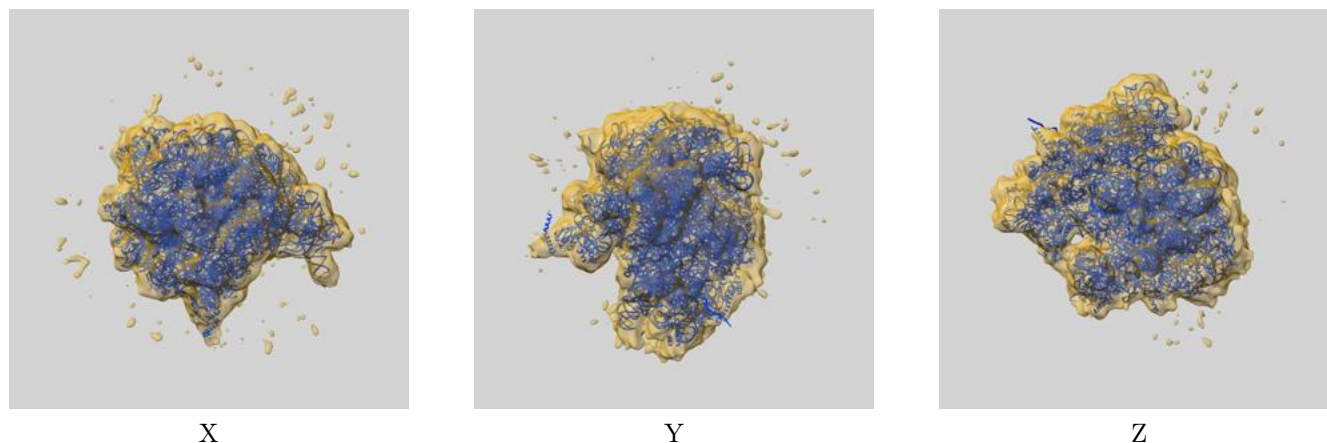
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

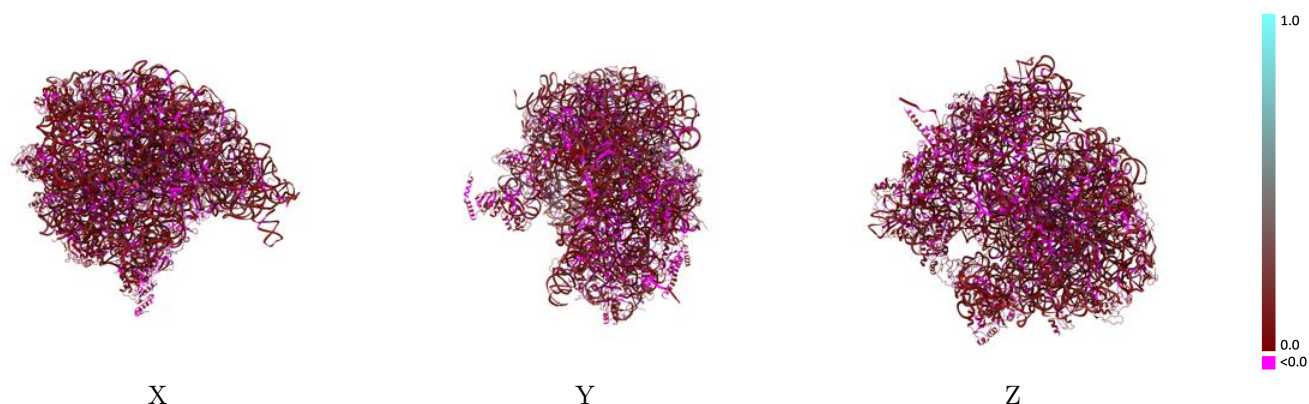
This section contains information regarding the fit between EMDB map EMD-5360 and PDB model 4V6S. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



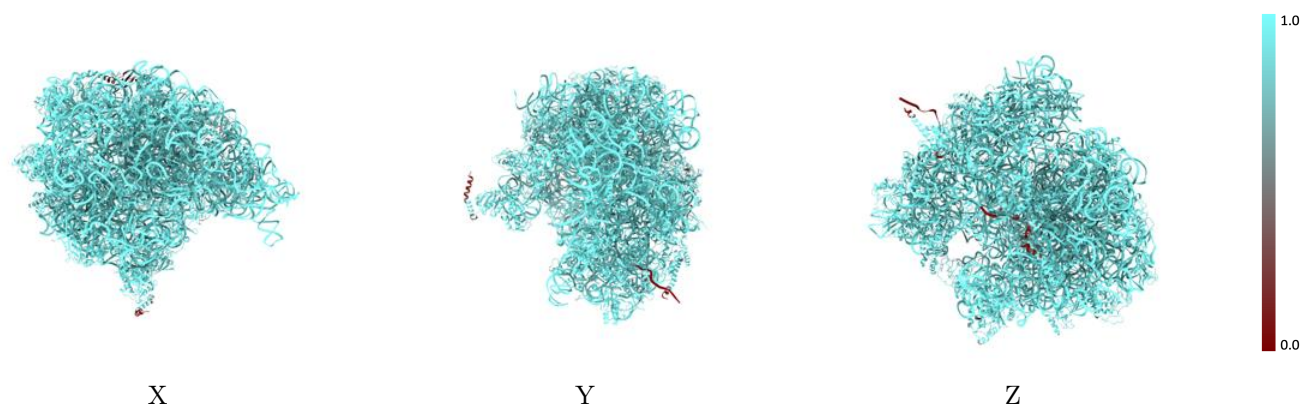
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



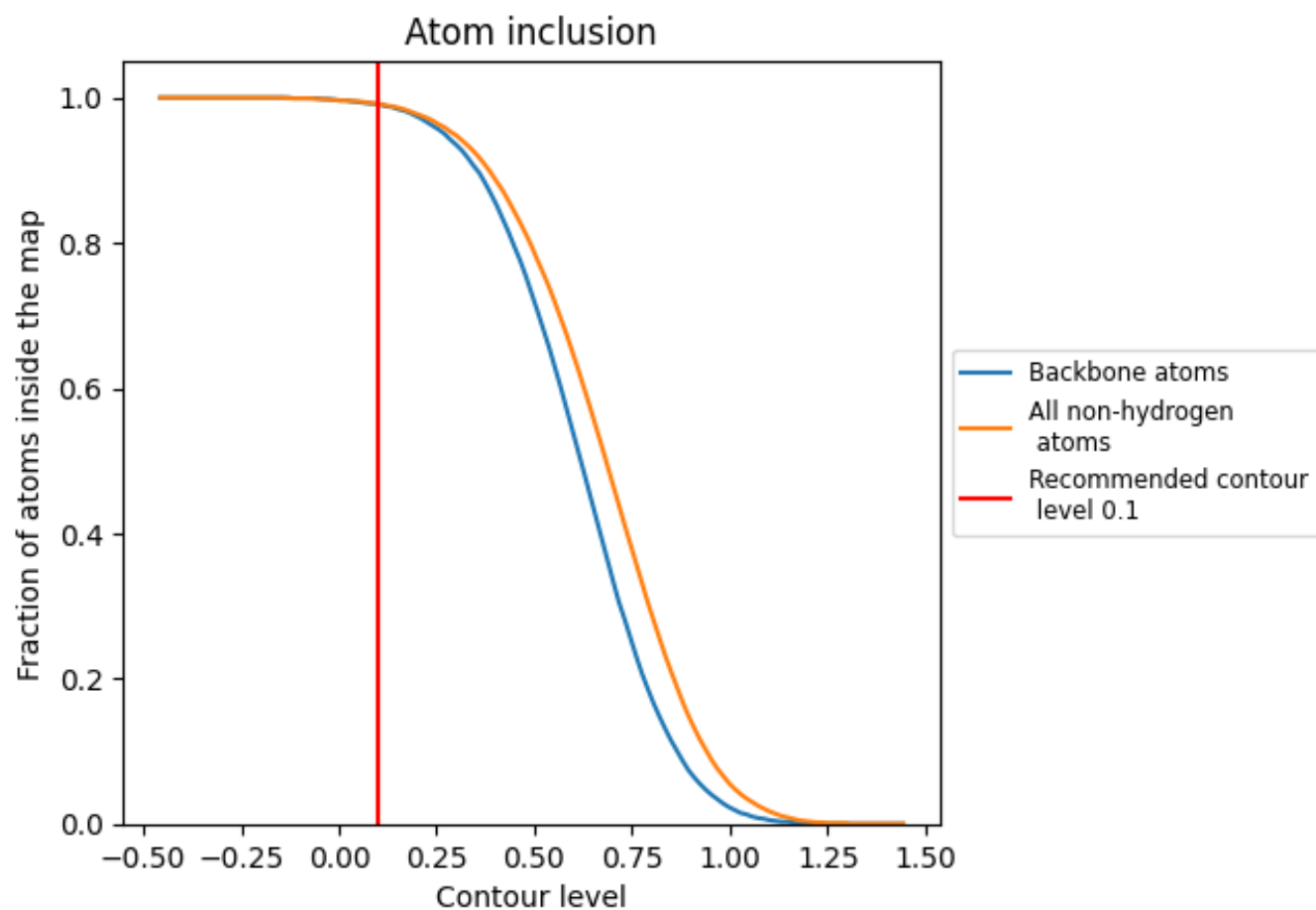
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% 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	0.9910	0.0680
A0	1.0000	0.0510
A1	0.9950	0.0290
A2	0.9110	0.0270
A3	1.0000	0.0260
A4	1.0000	0.0490
A5	1.0000	-0.0180
A6	1.0000	-0.0250
A7	1.0000	0.0160
AA	1.0000	0.0850
AB	0.9990	0.0850
AC	0.9610	0.0370
AD	1.0000	0.0210
AE	0.9960	0.0150
AF	0.9970	0.0470
AG	0.9980	0.0730
AH	0.9990	0.0210
AI	0.7900	0.0310
AJ	0.8700	0.0350
AK	0.9800	0.0440
AL	0.9990	0.0250
AM	0.9900	0.0340
AN	0.9940	0.0100
AO	1.0000	0.0310
AP	1.0000	0.0080
AQ	0.9930	0.0550
AR	0.9790	0.0230
AS	0.9980	0.0170
AT	1.0000	0.0470
AU	1.0000	0.0140
AV	1.0000	0.0310
AW	1.0000	0.0770
AX	1.0000	0.0740
AY	0.9980	0.0080
AZ	1.0000	0.0600



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
BA	 0.9990	 0.0840
BB	 0.7340	 -0.0130
BC	 1.0000	 0.0980
BD	 0.9090	 0.0220
BE	 0.9980	 0.0640
BF	 1.0000	 0.0460
BG	 0.9970	 0.0420
BH	 0.9620	 0.0290
BI	 0.9930	 0.0680
BJ	 0.9730	 0.0280
BK	 0.9880	 0.0480
BL	 1.0000	 0.0400
BM	 0.9370	 0.0550
BN	 0.9770	 0.0330
BO	 0.9720	 0.0480
BP	 1.0000	 0.0270
BQ	 1.0000	 0.0410
BR	 1.0000	 0.0480
BS	 1.0000	 0.0660
BT	 1.0000	 0.0540
BU	 0.9820	 0.0270
BV	 1.0000	 0.0460
BW	 0.9960	 0.0570