



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 05:19 PM UTC

PDB ID : 4V6O / pdb_00004v6o
EMDB ID : EMD-5359
Title : Structural characterization of mRNA-tRNA translocation intermediates (class 4a 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 : 2011-12-07
Resolution : 14.70 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

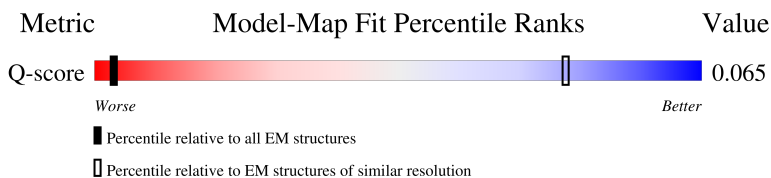
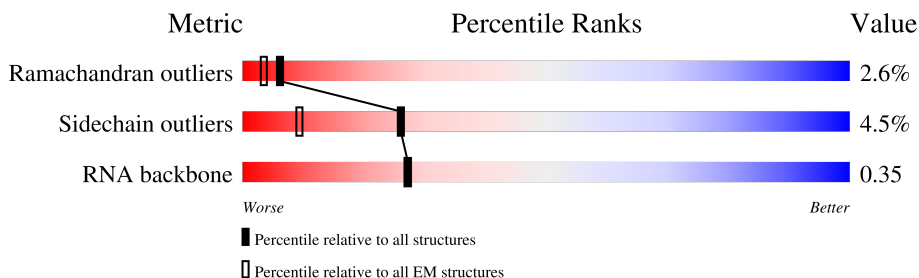
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 14.70 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.



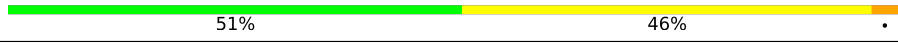
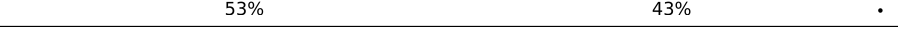
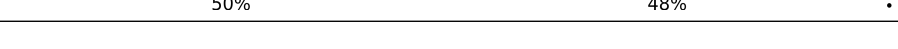
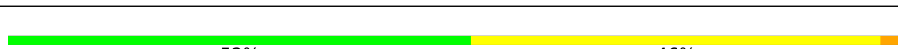
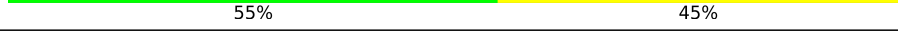
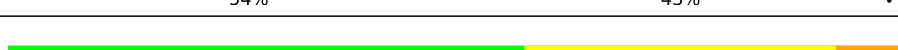
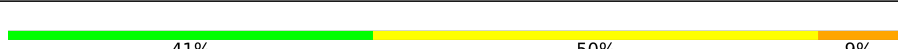
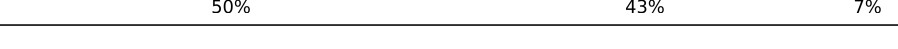
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	31 (14.20 - 15.00)

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	
6	AF	232	
7	AG	205	
8	AH	166	
9	AI	135	
10	AJ	178	
11	AK	129	
12	AL	129	
13	AM	103	
14	AN	128	
15	AO	123	
16	AP	117	
17	AQ	100	
18	AR	88	
19	AS	82	
20	AT	83	
21	AU	74	
22	AV	91	
23	AW	86	
24	AX	70	
25	BA	120	
26	BB	2904	
27	BC	234	
28	BD	272	
29	BE	209	

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Mol	Chain	Length	Quality of chain
30	BF	201	 59% 38% .
31	BG	178	 49% 43% 7% .
32	BH	176	 52% 44% .
33	BI	149	 10% 62% 34% 5%
34	BJ	164	 65% 31% .
35	BK	141	 57% 40% .
36	BL	142	 59% 37% .
37	BM	123	 61% 36% .
38	BN	144	 58% 38% 5%
39	BO	136	 60% 39% .
40	BP	127	 57% 39% .
41	BQ	117	 60% 38% .
42	BR	114	 51% 45% .
43	BS	117	 54% 38% 7% .
44	BT	103	 61% 38% .
45	BU	110	 61% 35% 5%
46	BV	100	 55% 44% .
47	BW	103	 61% 37% .
48	BX	94	 64% 33% .
49	BY	84	 51% 43% 6%
50	BZ	77	 49% 43% 8%
51	B0	63	 48% 48% 5%
52	B1	58	 60% 36% .
53	B2	70	 53% 40% 6% .
54	B3	56	 62% 32% 5%

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Mol	Chain	Length	Quality of chain
55	B4	54	 56% 41% .
56	B5	46	 46% 50% .
57	B6	64	 56% 42% .
58	B7	38	 58% 39% .

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		

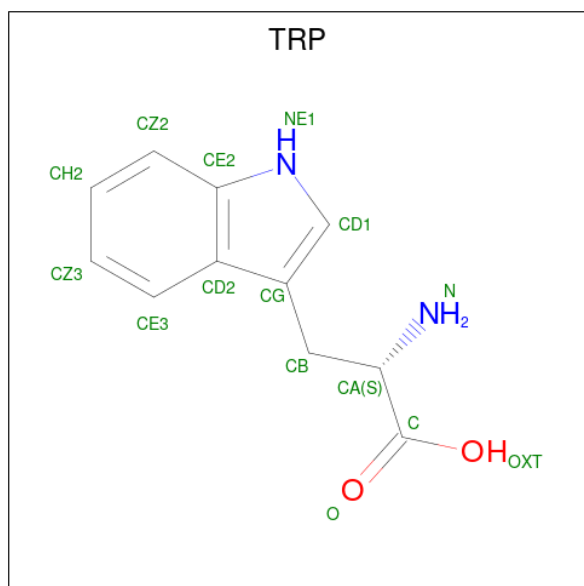
- Molecule 57 is a protein called 50S ribosomal protein L35.

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.

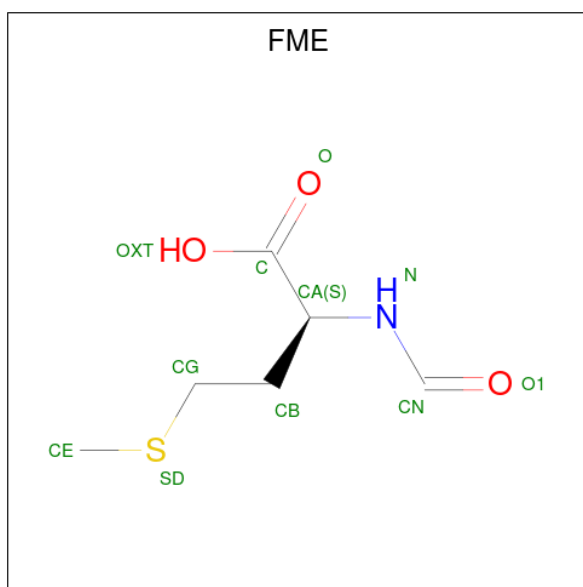
Mol	Chain	Residues	Atoms					AltConf	Trace
58	B7	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- 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: $C_6H_{11}NO_3S$).

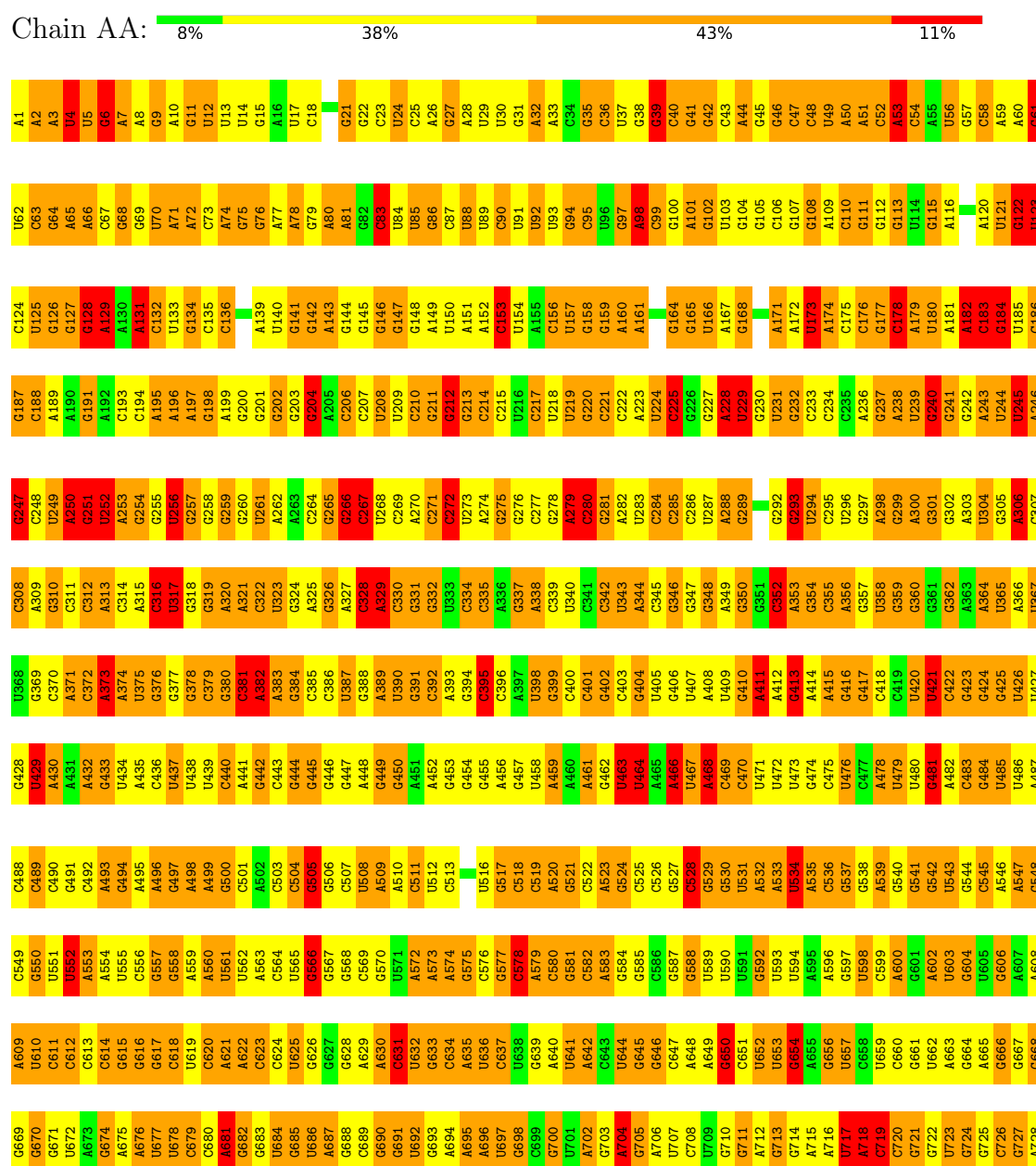


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
60	BB	1	10	6	1	2	1	0

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



G1511	U1451	U1390	U1330	A1269	C1209	G1149	G1089	U1029	A969	A909	G849	U789	A729
U1512	C1452	U1391	G1331	A1270	C1210	A1150	U1090	U1030	C970	C910	G850	U790	G730
A1513	C1453	U1392	A1332	A1271	U1211	A1151	U1091	C1031	G971	U911	G851	G791	G731
G1514	G1454	U1393	A1333	G1272	U1212	A1152	A1092	G1032	C972	C912	G852	U792	G732
G1515	G1455	U1394	A1334	G1273	A1213	G1153	A1093	G1033	G973	A913	G853	U793	G733
G1516	A1456	C1395	U1335	A1274	C1214	G1154	G1094	G1034	A974	A914	U854	A794	G734
G1517	G1457	A1396	C1336	A1275	G1215	A1155	U1095	A1035	A975	A915	U855	C795	G735
A1518	C1458	C1397	U1337	G1276	A1216	G1156	C1096	A1036	G976	U916	C856	C796	G736
A1519	G1459	A1398	C1338	G1277	C1217	A1157	C1097	C1037	A977	G917	C857	U797	G737
G1520	C1460	C1399	A1339	G1278	G1218	C1158	C1098	C1038	A978	A918	G858	U798	G738
C1521	G1461	C1400	A1340	G1279	A1219	U1159	U1099	G1039	C979	A919	G859	G799	C739
U1522	C1462	A1401	U1341	A1280	G1220	G1160	A1100	U1040	C980	U920	A860	G900	U740
G1523	A1463	C1402	C1342	C1281	G1221	C1161	A1101	U1041	U981	U921	G861	U901	G741
C1524	U1464	C1403	G1343	A1282	C1222	A1162	A1102	G1042	U982	G922	A862	A902	G742
G1525	A1465	C1404	C1344	U1283	C1223	A1163	C1103	G1043	A983	A923	U863	G903	A743
G1526	C1466	G1405	U1345	C1284	U1224	G1164	G1104	A1044	G984	C924	A864	U904	G744
U1527	C1467	U1406	A1346	A1285	A1225	U1165	A1105	U1045	C985	G925	A865	C905	G745
U1528	A1468	C1407	G1347	U1286	C1226	G1166	G1106	A1046	U986	G926	C866	C906	A746
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U1532	U1472	C1411	U1351	G1290	C1230	A1170	A1110	G1050	C990	C930	U870	C910	C750
C1533	G1473	A1412	C1352	U1291	G1231	A1171	A1111	C1051	U991	C931	U871	C911	U751
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U1537	U1477	G1416	G1356	U1295	U1235	G1175	U1115	A1055	C995	A935	U875	A915	G755
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G1486	G1426		G1365	G1304	G1244	U1184	G1124	G1064	A1004	G944	U884	G924	C764
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G1488	A1428		A1367	A1306	A1246	G1186	G1126	C1066	G1006	A946	G886	C926	A766
G1489	A1429		A1368	U1307	U1247	G1187	G1127	U1067	U1007	G947	G887	U927	A767
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C1493	A1433		U1372	A1311	A1251	A1191	G1131	C1071	C1011	G951	A891	A931	G771
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G1505	C1505		G1384	G1323	C1263	C1203	G1143	U1083	U1023	G963	G903	U943	C783
U1506	U1506		A1385	A1324	U1264	A1204	G1144	G1084	G1024	A964	U904	G944	A784
A1507	A1447		G1386	C1325	C1265	U1205	A1145	U1085	U1025	U965	A905	G945	G785
U1508	C1448		G1387		G1266	G1206	A1146	U1086	G1026	G966	A906	G946	G786
C1509	U1509		C1388	C1328	C1267	G1207	G1147	G1087	C1027	C967	A907	G947	A787
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• Molecule 2: A site tRNA

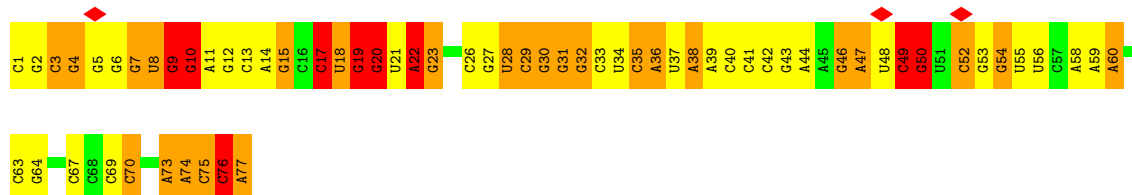
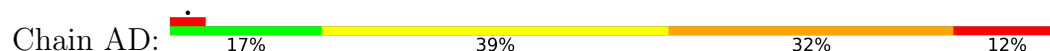
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C61	C62	C63	C64	C65	C66	C67	C68	C69	C70	C71	C72	C73	C74	C75	C76	C77	C78	C79	C80	C81	C82	C83	C84	C85	C86	C87	C88	C89	C90	C91	C92	C93	C94	C95	C96	C97	C98	C99	C100	C101	C102	C103	C104	C105	C106	C107	C108	C109	C110	C111	C112	C113	C114	C115	C116	C117	C118	C119	C120
G61	G62	G63	G64	G65	G66	G67	G68	G69	G70	G71	G72	G73	G74	G75	G76	G77	G78	G79	G80	G81	G82	G83	G84	G85	G86	G87	G88	G89	G90	G91	G92	G93	G94	G95	G96	G97	G98	G99	G100	G101	G102	G103	G104	G105	G106	G107	G108	G109	G110	G111	G112	G113	G114	G115	G116	G117	G118	G119	G120

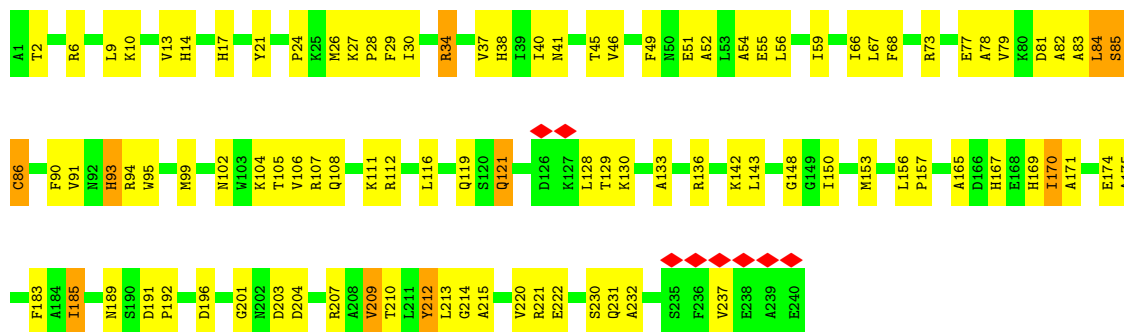
- Molecule 3: mRNA



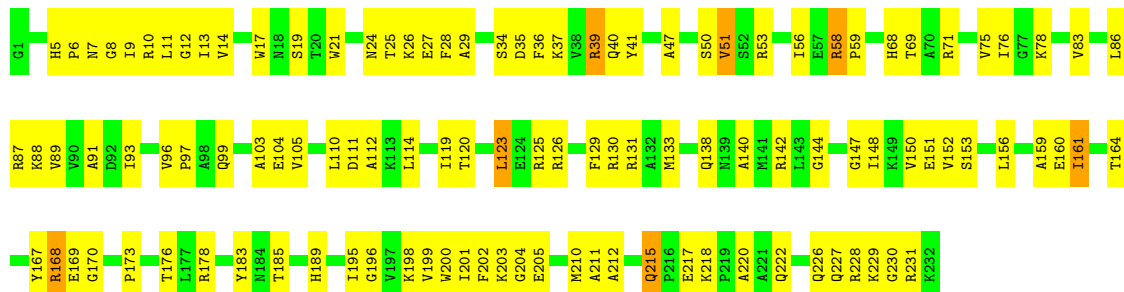
- Molecule 4: P site tRNA



- Molecule 5: 30S ribosomal protein S2

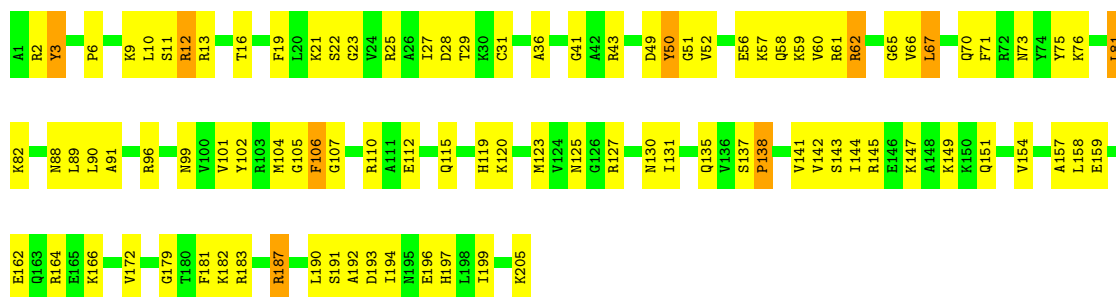


- Molecule 6: 30S ribosomal protein S3



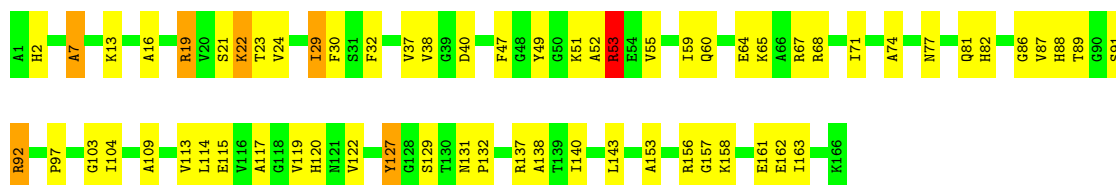
- Molecule 7: 30S ribosomal protein S4





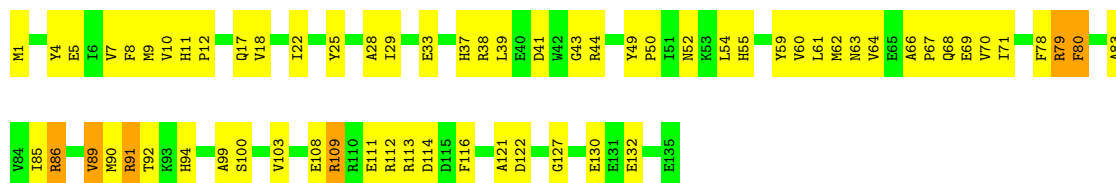
• Molecule 8: 30S ribosomal protein S5

Chain AH: 61% 34%



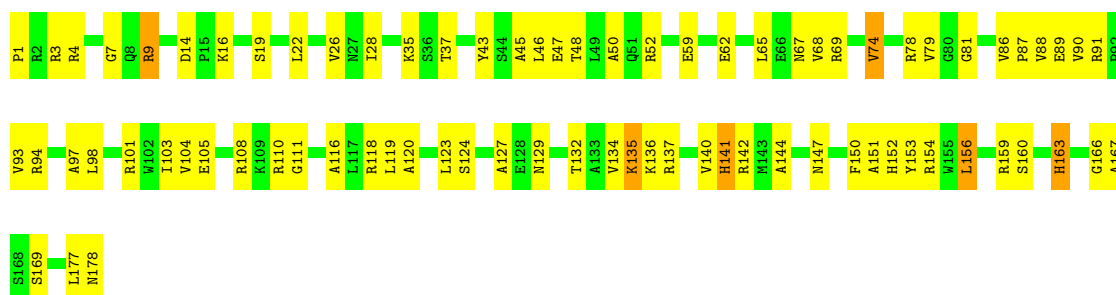
• Molecule 9: 30S ribosomal protein S6

Chain AI: 52% 44%



• Molecule 10: 30S ribosomal protein S7

Chain AJ: 56% 41%



• Molecule 11: 30S ribosomal protein S8

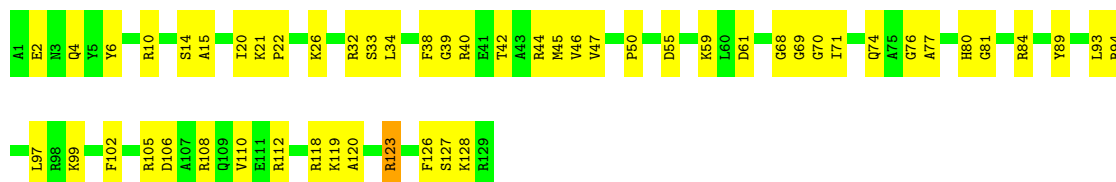
Chain AK: 54% 41% 5%





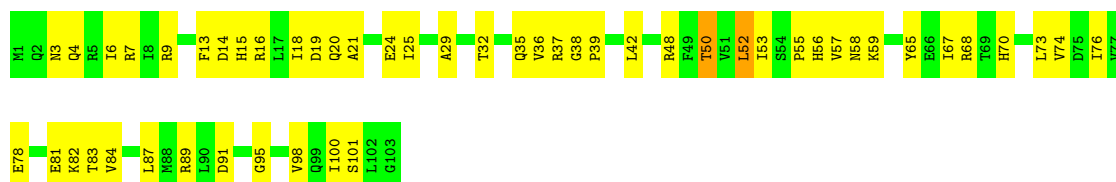
- Molecule 12: 30S ribosomal protein S9

Chain AL: 59% 40% .



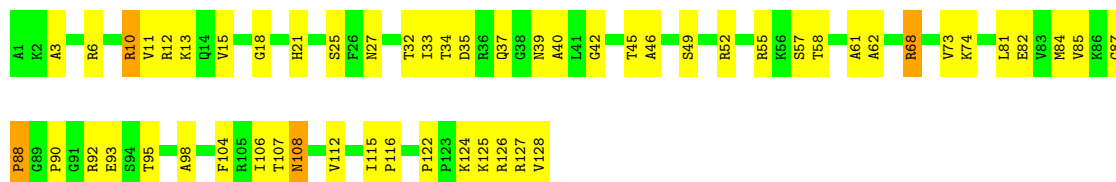
- Molecule 13: 30S ribosomal protein S10

Chain AM: 50% 48% .



- Molecule 14: 30S ribosomal protein S11

Chain AN: 57% 40% .



- Molecule 15: 30S ribosomal protein S12

Chain AO: 52% 46% .



- Molecule 16: 30S ribosomal protein S13

Chain AP: 56% 43% ..





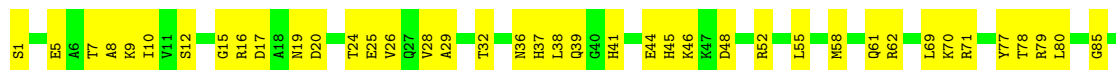
- Molecule 17: 30S ribosomal protein S14

Chain AQ: 59% 38%



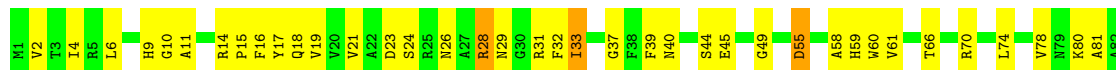
- Molecule 18: 30S ribosomal protein S15

Chain AR: 55% 45%



- Molecule 19: 30S ribosomal protein S16

Chain AS: 54% 43%



- Molecule 20: 30S ribosomal protein S17

Chain AT: 58% 35% 7%



- Molecule 21: 30S ribosomal protein S18

Chain AU: 41% 50% 9%



- Molecule 22: 30S ribosomal protein S19

Chain AV: 57% 38%



- Molecule 23: 30S ribosomal protein S20

Chain AW: 62% 34% 5%



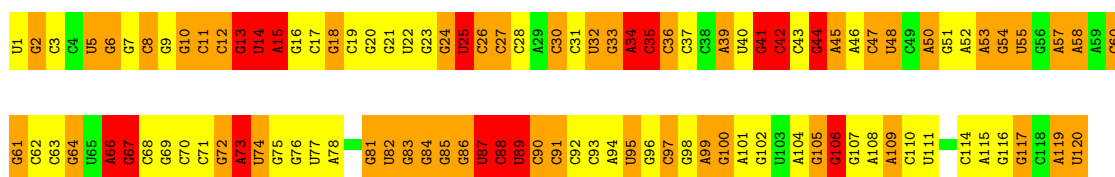
- Molecule 24: 30S ribosomal protein S21

Chain AX: 50% 43% 7%



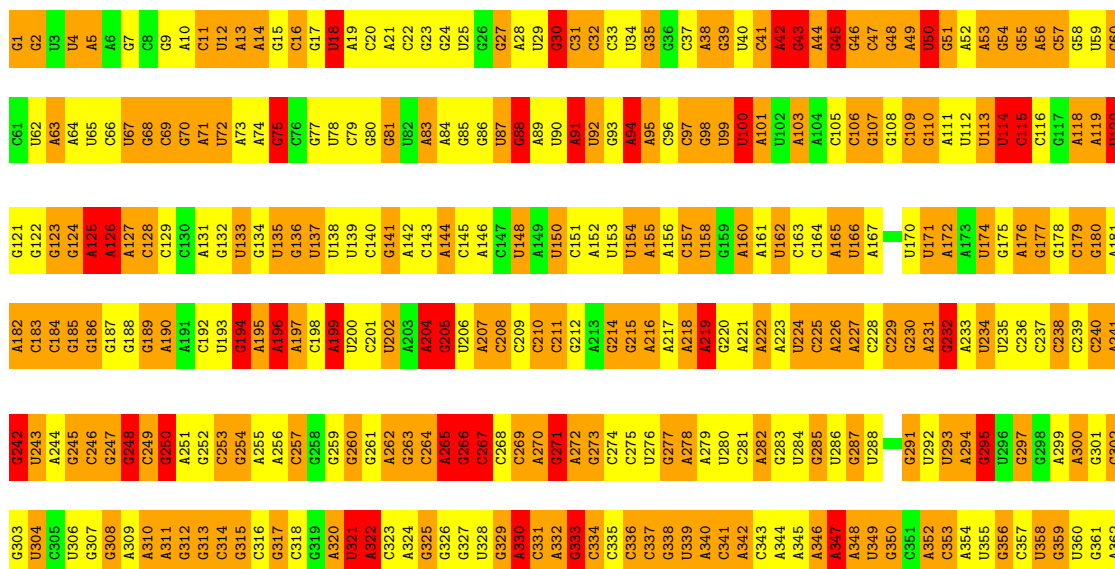
- Molecule 25: 5S ribosomal RNA

Chain BA: 11% 37% 39% 13%



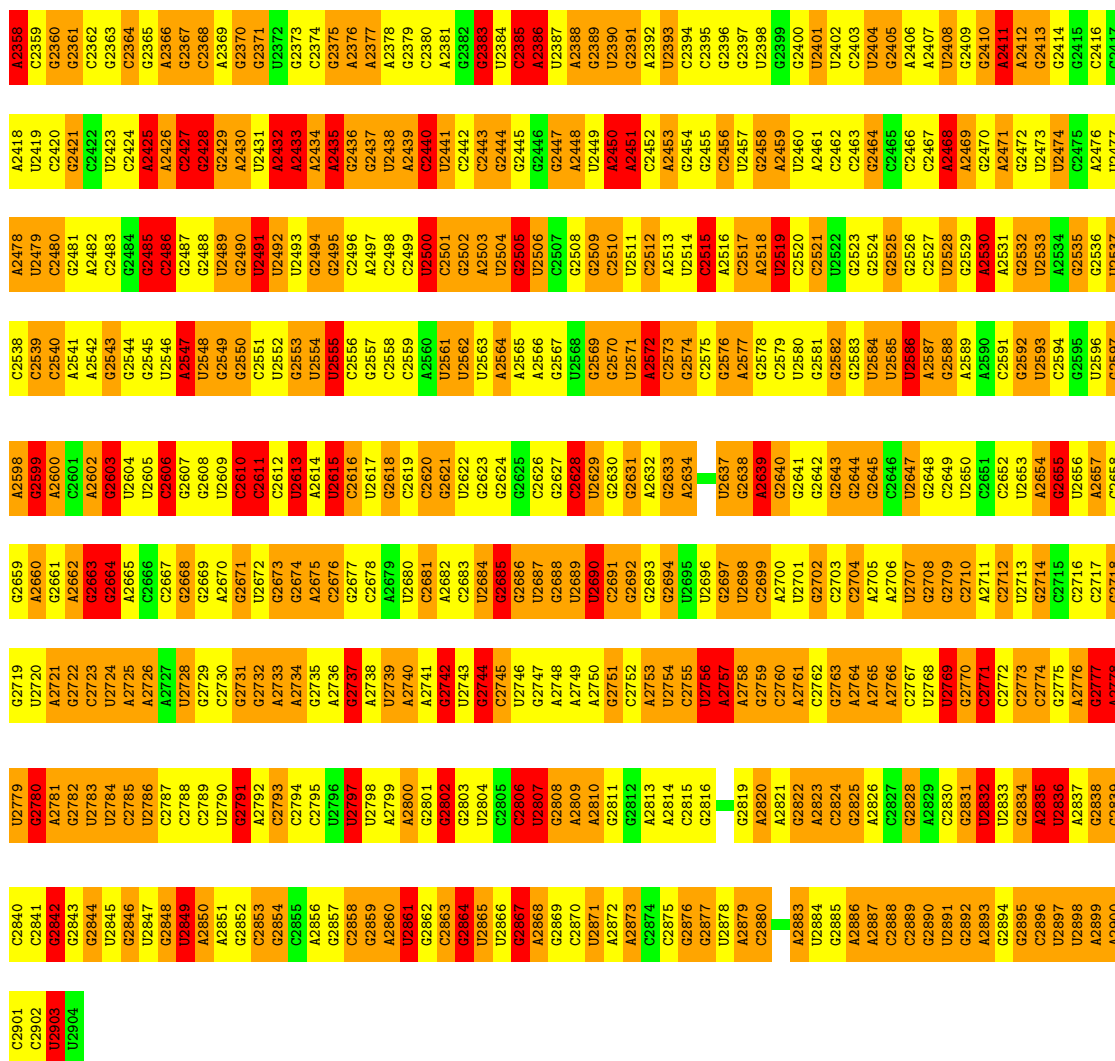
- Molecule 26: 23S ribosomal RNA

Chain BB: 8% 38% 44% 11%

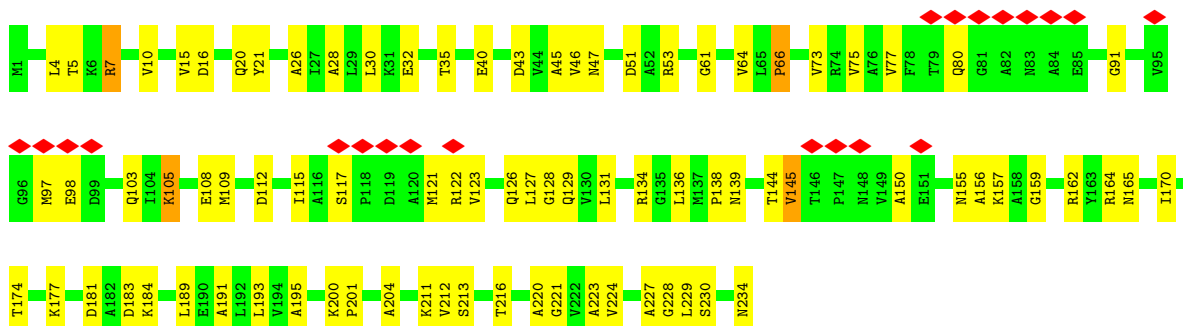


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G1332	A1272	G1212	C1152	G1091	C1030	U970	A909	A849	A789	G729	U687	U607	A547	C487	C426	C364
G1333	A1273	A1213	C1153	G1092	G1031	G971	A910	U850	C790	A730	A668	A608	G548	C488	U427	U365
G1334	A1274	A1214	G1154	G1093	A1032	A972	A911	C851	C791	C731	G669	A609	G549	G489	A428	C366
G1335	A1275	G1215	A1155	U1094	G1033	A973	C912	U852	A792	C732	A670	C610	C550	C490	A429	A367
A1336	A1276	G1216	A1156	A1095	U1034	A974	C913	C853	A793	G733	C671	C611	C551	G491	A430	A368
G1337	G1277	U1217	G1157	A1096	U1035	A975	C914	C854	A794	A734	C672	G612	U552	A492	U431	U369
G1338	G1278	G1218	C1158	U1097	G1036	G976	C915	G855	C795	A735	C673	A613	G553	G493	A432	G370
G1339	U1219	U1219	U1159	A1098	G1037	G977	G916	G856	C796	C736	G674	A614	U554	C494	A433	A371
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A1342	U1282	G1222	G1162	U1101	A1040	A980	A919	C859	G799	A739	A677	G617	C557	A497	A436	A374
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G1345	A1285	G1225	A1165	C1104	C1043	A983	C922	G862	A802	A742	C680	G620	C560	G500	A439	G377
G1346	A1286	A1226	G1166	U1105	C1044	A984	C923	A863	U803	A743	G681	A621	G561	A501	C440	C378
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C1386	U1326	G1266	G1206	C1145	A1085	U1023	C964	C903	C843	A783	U721	A661	C601	A541	G481	C418
A1387	U1327	U1267	C1207	C1146	A1086	G1025	C965	C904	A844	G784	U722	C662	A602	C542	A482	U419
G1388	A1328	A1268	G1208	C1147	G1087	G1026	G966	A905	A845	G785	G726	G663	A603	G543	A483	C420
G1389	U1329	U1269	A1088	U1149	G1088	A1027	U967	U906	U846	G786	G727	G664	C604	C544	C484	G421
U1390	C1330	C1270	G1210	C1150	A1089	A1028	C968	G907	U847	C787	A727	U665	G605	U545	G485	G424

A2298	G2287	G2116	G2056	U1995	G1933	G1873	G1813	G1753	U1693	G1633	A1572	C1512	G1451	U1391
U2299	G2288	A2117	G2057	C1996	C1934	C1874	G1814	A1754	C1694	A1634	G1573	U1513	G1452	A1392
C2300	G2289	U2118	A2058	C1997	G1935	G1875	A1815	A1755	G1695	A1635	G1574	A1515	A1453	A1393
C2301	C2178	A2119	A2059	A1998	A1936	A1876	C1816	A1756	G1696	A1636	C1575	A1516	C1454	U1394
U2302	G2242	G2120	A2060	C1999	A1937	A1877	G1817	A1757	G1697	C1637	U1576	G1517	G1455	U1395
G2303	U2243	G2121	G2061	C2000	A1938	G1878	U1818	A1758	A1698	C1638	U1577	G1518	G1456	A1396
G2304	U2244	U2122	A2062	C2001	A1939	C1879	A1819	A1759	G1699	C1639	U1578	C1519	U1457	U1397
U2305	G2245	G2123	C2063	G2002	U1940	U1880	U1820	C1760	A1700	A1640	A1579	G1520	U1458	C1398
G2306	U2246	G2124	C2064	A2003	C1941	C1881	A1821	C1761	A1701	A1641	A1580	U1521	G1459	C1399
G2307	A2247	G2125	C2065	G2004	C1942	U1882	C1822	A1762	G1702	G1642	G1581	G1522	U1460	U1400
G2308	C2248	A2126	C2066	A2005	U1943	U1883	G1823	G1763	G1703	G1643	C1582	C1461	G1401	G1401
A2309	U2249	G2127	G2067	C2006	U1944	G1884	G1824	C1764	C1704	G1644	U1583	U1523	G1462	U1402
C2310	G2250	U2128	U2068	U2007	G1945	A1885	G1825	U1765	A1705	G1645	U1584	G1524	C1463	A1403
A2311	G2251	C2129	C2069	C2008	U1946	U1886	G1826	G1766	C1706	G1646	C1585	A1525	G1464	C1404
U2312	G2252	U2130	A2070	A2009	C1947	C1887	U1827	G1767	G1707	U1647	A1586	G1526	G1465	U1405
C2313	G2253	U2131	A2071	G2010	G1948	G1888	G1828	U1768	C1708	U1648	G1587	C1527	U1466	U1406
G2314	C2254	U2132	C2072	U2011	G1949	A1889	A1830	U1769	U1709	A1649	G1588	A1528	U1467	G1407
G2315	G2255	G2133	C2073	G2012	C1950	A1890	C1830	G1770	G1710	A1650	U1589	G1529	U1468	G1408
G2316	G2256	A2134	U2074	A2013	U1951	G1891	G1831	C1771	A1711	G1651	A1590	G1530	A1469	U1409
A2317	U2257	A2135	U2075	A2014	A1952	C1892	C1832	C1772	U1712	A1652	A1591	C1531	G1470	G1410
G2318	C2258	G2136	U2076	A2015	A1953	C1893	C1833	A1773	A1713	G1653	C1592	A1532	G1471	U1411
G2319	U2259	U2137	A2077	U2016	G1954	C1894	U1834	C1774	U1714	A1654	A1593	C1533	C1472	U1412
G2320	C2260	G2138	C2078	U2017	U1955	C1895	G1835	U1775	G1715	A1655	U1594	U1534	G1473	A1413
G2321	C2261	U2139	U2079	G2018	U1956	G1896	C1836	G1776	U1716	C1656	C1595	A1535	U1474	C1414
G2322	U2262	G2140	A2080	A2019	C1957	G1897	C1837	U1777	A1717	U1657	A1596	C1536	G1475	U1415
G2323	C2263	G2141	U2081	A2020	C1958	U1898	C1838	U1778	G1718	C1658	A1597	G1537	U1476	G1416
U2324	C2264	A2142	A2082	C2021	G1959	A1899	G1839	U1779	G1719	C1659	A1598	G1538	A1477	C1417
G2325	U2265	G2143	G2083	U2022	A1960	A1900	U1840	U1780	U1720	G1660	U1599	U1539	G1478	G1418
C2326	A2266	U2137	C2084	C2023	C1961	A1901	U1841	U1781	G1721	G1661	C1600	G1540	G1479	A1419
A2327	A2267	G2144	U2085	G2024	C1962	C1902	G1842	U1782	A1722	U1662	G1601	C1541	C1480	A1420
A2328	C2268	C2145	U2086	C2025	U1963	G1903	C1843	A1783	G1723	G1663	G1602	U1542	U1481	G1421
U2329	G2269	A2146	C2087	U2026	G1964	G1904	C1844	A1784	G1724	A1664	A1603	G1543	G1482	G1422
G2330	A2270	G2148	A2088	G2027	C1965	C1905	G1845	A1785	U1725	A1665	C1604	A1544	G1483	G1423
G2331	C2271	U2149	C2089	U2028	A1966	G1906	G1846	A1786	C1726	G1666	G1605	A1545	U1484	G1424
C2332	A2272	C2150	A2090	G2029	C1967	G1907	A1847	A1787	C1727	G1667	C1606	G1546	U1485	G1425
A2333	C2273	U2151	C2091	A2030	G1968	C1908	A1848	C1788	C1728	A1668	G1607	C1547	U1486	G1426
U2334	A2274	G2152	U2092	A2031	A1969	C1909	G1849	A1789	U1729	A1669	A1608	A1548	U1487	A1427
A2335	C2275	C2153	C2093	G2032	C1970	G1910	G1850	C1790	C1730	C1670	A1609	A1549	C1488	C1428
A2336	G2276	A2154	A2094	A2033	U1971	U1911	U1851	G1791	G1731	U1671	A1610	C1550	C1489	G1429
G2337	G2277	U2155	A2095	U2034	G1972	A1912	U1852	G1792	C1732	A1672	C1611	G1551	A1490	G1430
C2338	A2278	G2156	C2096	G2035	G1973	A1913	A1853	C1793	G1733	G1673	C1612	A1552	G1491	A1431
G2339	U2279	G2157	A2097	C2036	C1974	C1914	A1854	A1794	G1734	G1674	G1613	A1553	G1492	G1432
A2340	C2280	A2158	U2098	A2037	G1975	3TD1915	U1855	G1795	A1735	C1675	A1614	U1554	C1493	A1433
G2341	A2281	G2159	U2099	A2037	U1976	A1916	U1856	U1796	U1736	A1676	C1615	G1555	A1494	A1434
C2342	G2282	C2160	G2100	G2040		U1917	G1857	G1797	G1737	A1677	A1616	C1556	A1495	G1435
U2343	C2283	C2161	A2101	U2041	G1980	A1918	A1858	U1798	G1738	A1678	C1617	C1557	G1496	G1436
U2344	A2284	G2162	G2102	A2042	A1981	A1919	U1859	G1799	A1739	A1679	A1618	C1558	U1497	C1437
G2345	C2285	C2163	C2103	C2043	U1982	C1920	G1860	C1800	G1740	G1680	G1619	U1559	C1498	U1438
A2346	G2286	A2164	G1983	C2044	G1983	G1921	G1861	A1801	C1741	G1681	G1620	G1560	A1499	A1439
C2347	A2287	C2165	U2105	C2045	G1984	G1922	G1862	A1802	U1742	G1682	U1621	C1561	G1500	U1440
U2348	U2288	U2166	U2106	G2046	C1985	U1923	G1863	A1803	G1743	G1683	G1622	U1562	G1501	G1441
G2349	G2289	G2167	G2107	C2047	C1986	C1924	U1864	C1804	A1744	G1684	G1623	U1563	A1502	U1442
C2350	U2290	A2168	A2108	G2048	A1987	C1925	U1865	A1805	A1745	C1685	U1624	C1564		
G2351	U2291	G2169	G1988	G2049	G1988	U1926	A1866	C1806	A1746	C1686	C1625	C1565	U1505	U1443
A2352	G2292	G2170	G1989	C2050	G1989	A1927	G1867	A1807	U1747	G1687	G1626	G1566	G1506	G1444
G2353	C2293	A2171	C2060	A2051	C1990	A1928	C1868	A1808	C1748	G1688	G1627	G1567	U1507	G1445
C2354	G2294	U2172	G2112	A2052	U1991	G1929	G1869	A1809	A1749	A1689	G1628	G1568	A1508	C1447
G2355	C2295	A2173	U2113	G2053	G1992	G1930	C1870	A1810	G1750	A1690			G1509	G1448
U2356	G2296	C2174	A2114	A2054	U1993	U1931	A1871	G1811	U1751	C1691	G1631		G1510	G1449
G2357	A2297	C2175	G2115	C2055	C1994	A1932	A1872	U1812	C1752	U1692	A1632		G1511	G1450

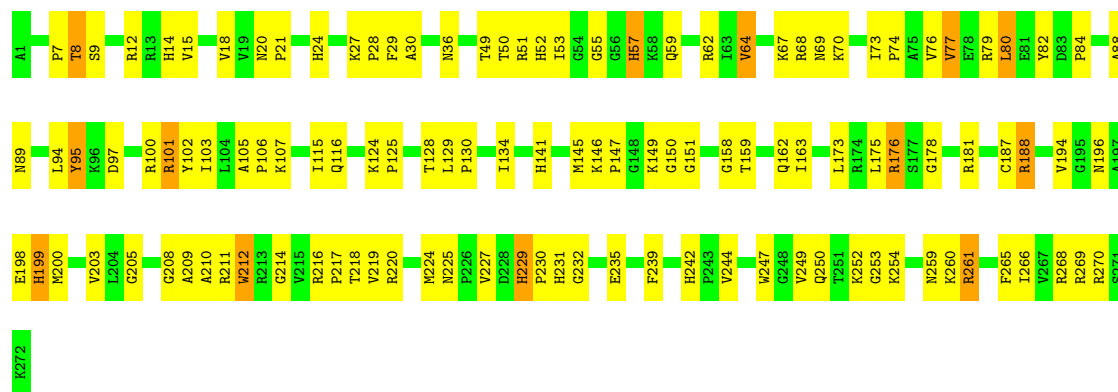


• Molecule 27: 50S ribosomal protein L1

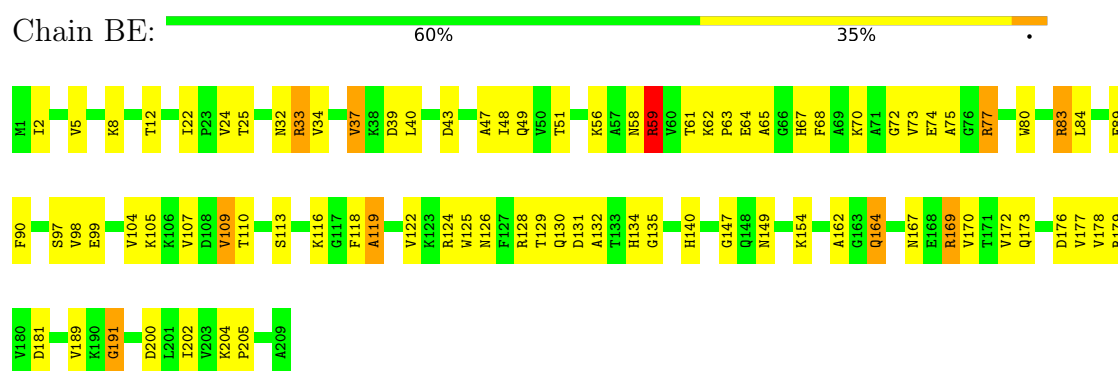


• Molecule 28: 50S ribosomal protein L2

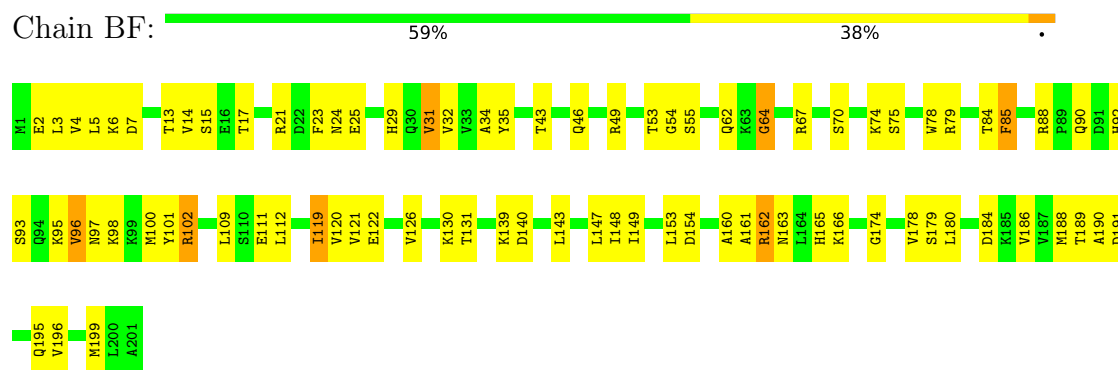




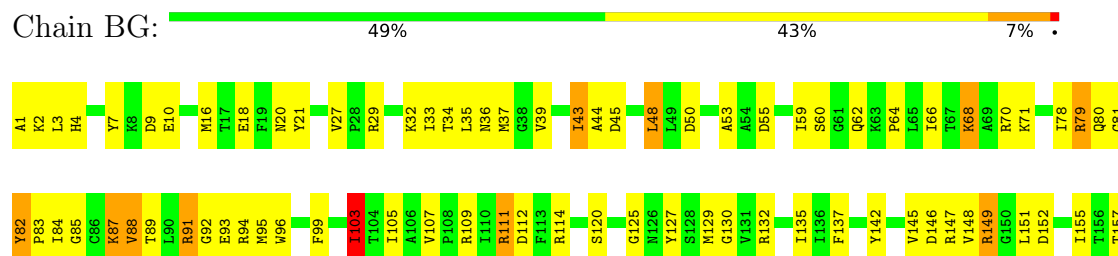
• Molecule 29: 50S ribosomal protein L3



• Molecule 30: 50S ribosomal protein L4



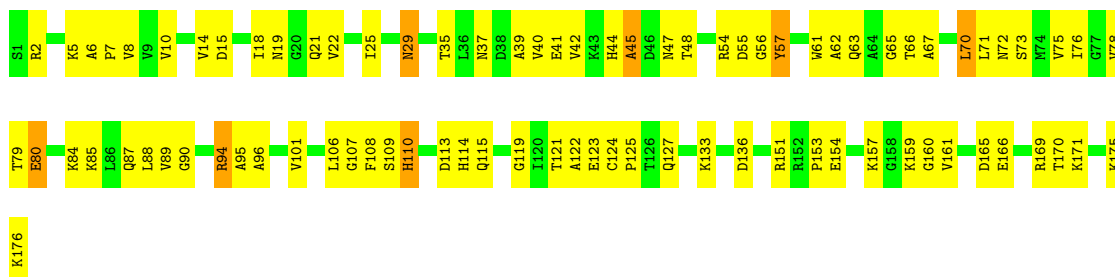
• Molecule 31: 50S ribosomal protein L5





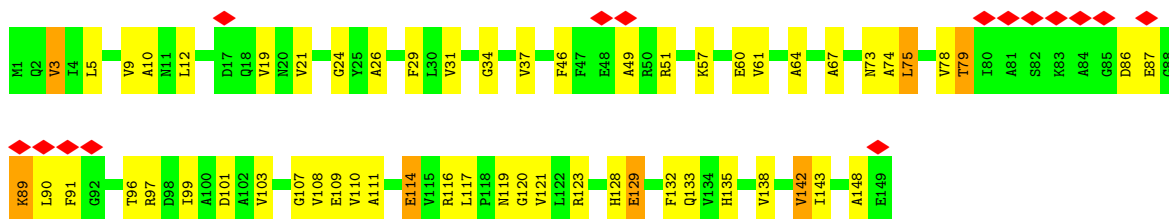
- Molecule 32: 50S ribosomal protein L6

Chain BH: 52% 44%



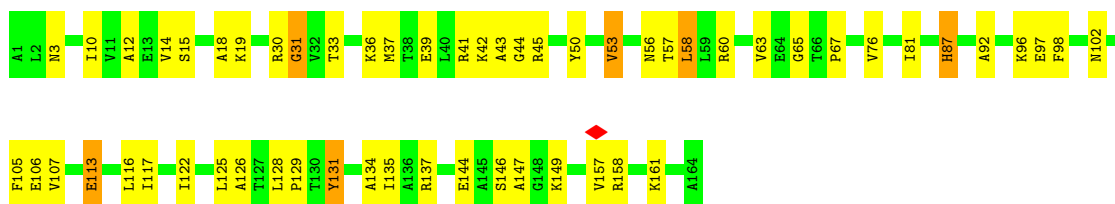
- Molecule 33: 50S ribosomal protein L9

Chain BI: 10% 62% 34% 5%



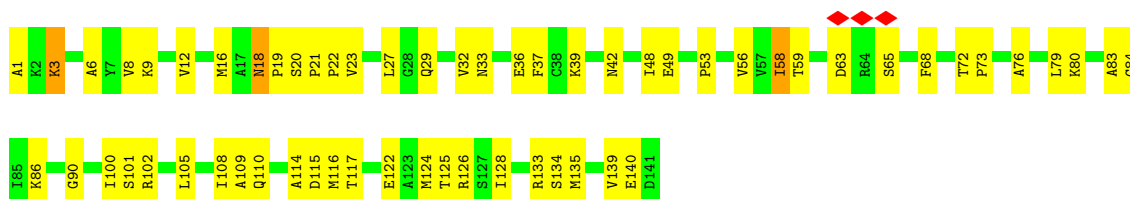
- Molecule 34: 50S ribosomal protein L10

Chain BJ: 65% 31%



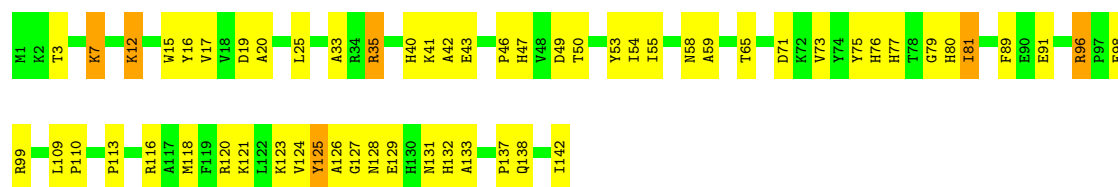
- Molecule 35: 50S ribosomal protein L11

Chain BK: 57% 40%



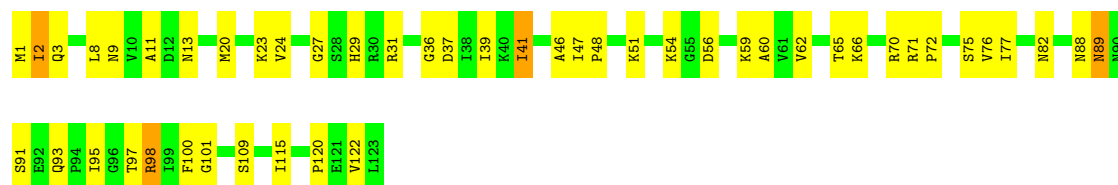
- Molecule 36: 50S ribosomal protein L13

Chain BL:  59% 37%



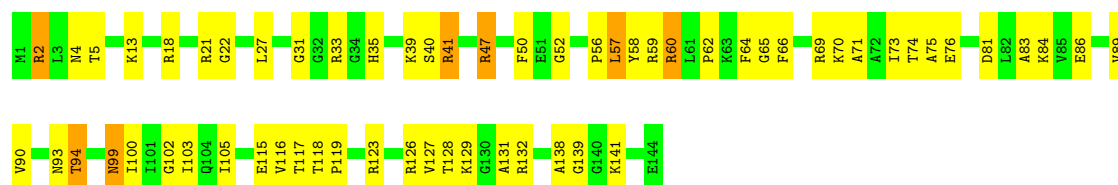
- Molecule 37: 50S ribosomal protein L14

Chain BM:  61% 36%



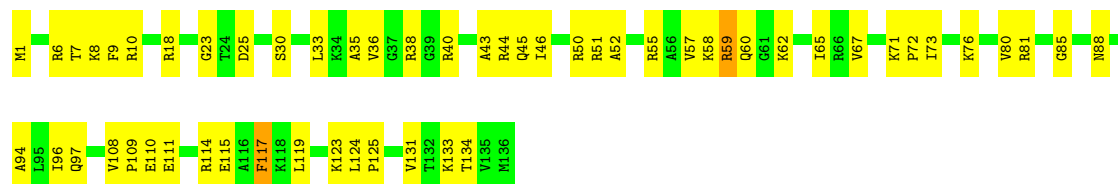
- Molecule 38: 50S ribosomal protein L15

Chain BN:  58% 38% 5%



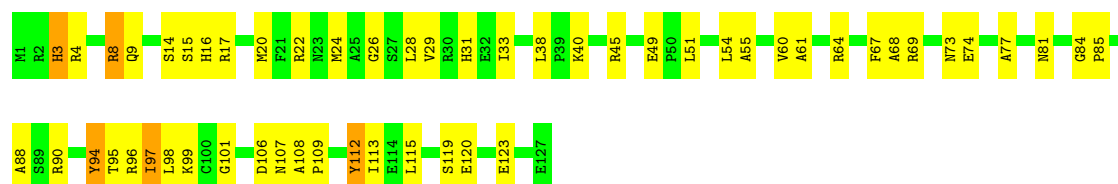
- Molecule 39: 50S ribosomal protein L16

Chain BO:  60% 39%



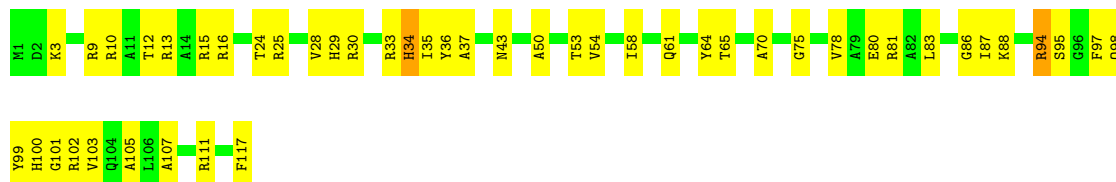
- Molecule 40: 50S ribosomal protein L17

Chain BP:  57% 39%



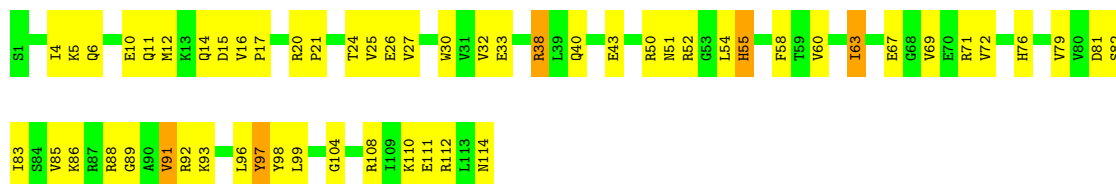
- Molecule 41: 50S ribosomal protein L18

Chain BQ:  60% 38% .



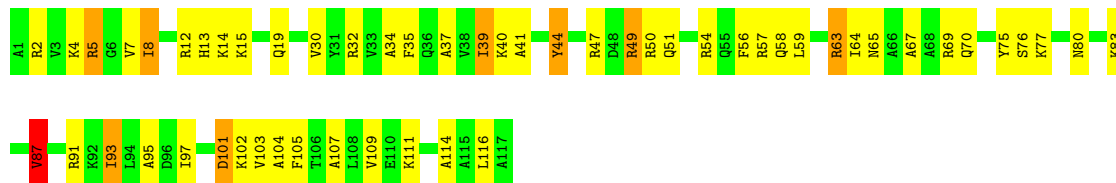
- Molecule 42: 50S ribosomal protein L19

Chain BR:  51% 45% .



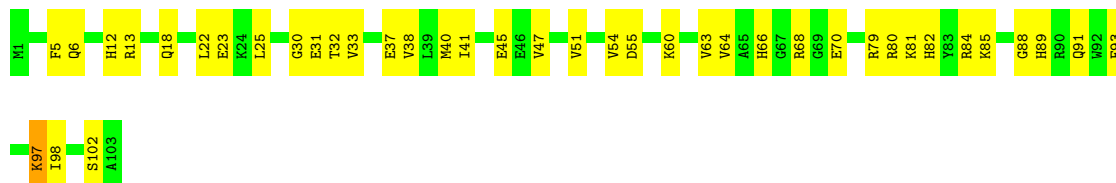
- Molecule 43: 50S ribosomal protein L20

Chain BS:  54% 38% 7% .



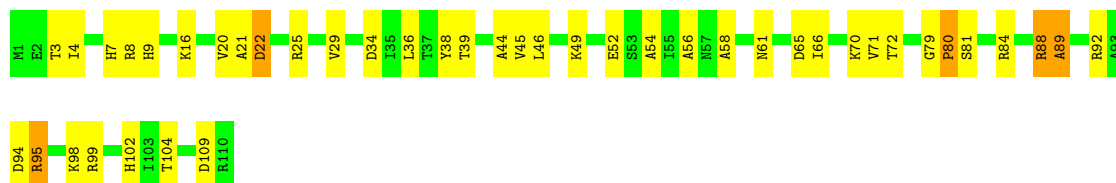
- Molecule 44: 50S ribosomal protein L21

Chain BT:  61% 38% .



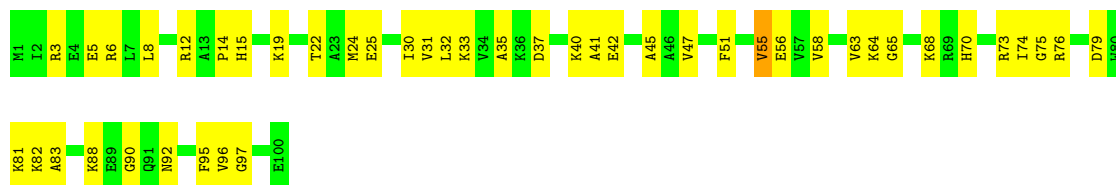
- Molecule 45: 50S ribosomal protein L22

Chain BU:  61% 35% 5% .



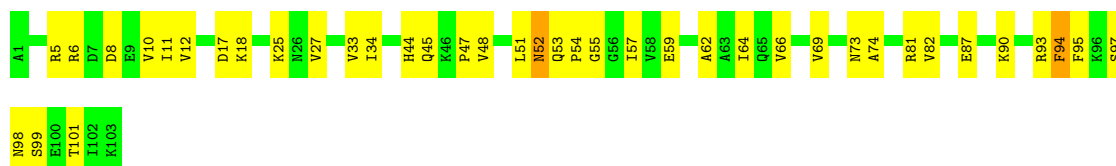
- Molecule 46: 50S ribosomal protein L23

Chain BV:  55% 44%



- Molecule 47: 50S ribosomal protein L24

Chain BW:  61% 37%



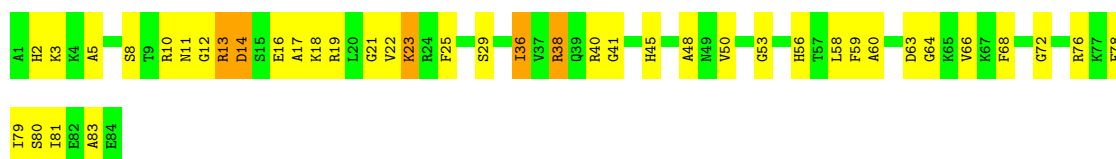
- Molecule 48: 50S ribosomal protein L25

Chain BX:  64% 33%



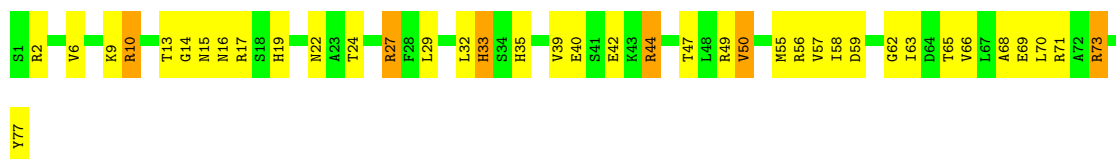
- Molecule 49: 50S ribosomal protein L27

Chain BY:  51% 43% 6%

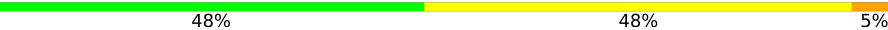


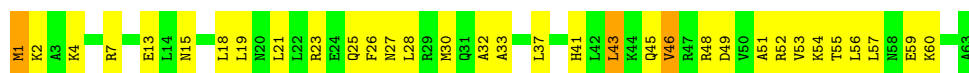
- Molecule 50: 50S ribosomal protein L28

Chain BZ:  49% 43% 8%



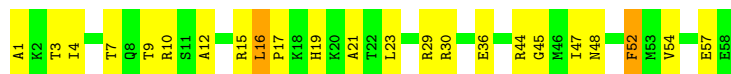
- Molecule 51: 50S ribosomal protein L29

Chain B0:  48% 48% 5%



- Molecule 52: 50S ribosomal protein L30

Chain B1:  60% 36% .



- Molecule 53: 50S ribosomal protein L31

Chain B2:  53% 40% 6% .



- Molecule 54: 50S ribosomal protein L32

Chain B3:  62% 32% 5% .



- Molecule 55: 50S ribosomal protein L33

Chain B4:  56% 41% .



- Molecule 56: 50S ribosomal protein L34

Chain B5:  46% 50% .



- Molecule 57: 50S ribosomal protein L35

Chain B6:  56% 42% .



- Molecule 58: 50S ribosomal protein L36

Chain B7:  58% 39% .



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	1.422	Depositor
Minimum map value	-0.460	Depositor
Average map value	0.029	Depositor
Map value standard deviation	0.195	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: 6MZ, 1MG, MA6, OMC, OMG, 2MA, 7MG, 4OC, OMU, FME, PSU, 5MU, H2U, MIA, 5MC, CH, 4SU, UR3, 2MG, 3TD

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	1.90	598/36769 (1.6%)	1.98	1872/57354 (3.3%)
2	AB	1.92	30/1600 (1.9%)	2.11	93/2492 (3.7%)
3	AC	1.99	26/1108 (2.3%)	2.05	65/1724 (3.8%)
4	AD	1.85	26/1721 (1.5%)	2.06	105/2683 (3.9%)
5	AE	2.00	46/1904 (2.4%)	2.37	94/2565 (3.7%)
6	AF	2.03	42/1852 (2.3%)	2.42	112/2490 (4.5%)
7	AG	1.93	30/1665 (1.8%)	2.38	102/2227 (4.6%)
8	AH	2.01	25/1239 (2.0%)	2.42	75/1664 (4.5%)
9	AI	2.03	21/1121 (1.9%)	2.44	66/1509 (4.4%)
10	AJ	1.98	30/1422 (2.1%)	2.37	77/1908 (4.0%)
11	AK	2.12	24/989 (2.4%)	2.42	63/1326 (4.8%)
12	AL	2.04	24/1048 (2.3%)	2.32	53/1394 (3.8%)
13	AM	1.97	14/835 (1.7%)	2.46	50/1127 (4.4%)
14	AN	2.03	22/982 (2.2%)	2.32	50/1323 (3.8%)
15	AO	2.06	26/969 (2.7%)	2.44	65/1300 (5.0%)
16	AP	1.98	12/919 (1.3%)	2.45	64/1226 (5.2%)
17	AQ	1.99	20/817 (2.4%)	2.43	46/1088 (4.2%)
18	AR	2.09	17/724 (2.3%)	2.40	43/966 (4.5%)
19	AS	2.05	15/659 (2.3%)	2.48	40/884 (4.5%)
20	AT	2.06	17/681 (2.5%)	2.22	31/913 (3.4%)
21	AU	2.05	12/637 (1.9%)	2.46	50/851 (5.9%)
22	AV	1.96	16/744 (2.2%)	2.34	35/995 (3.5%)
23	AW	1.99	18/676 (2.7%)	2.36	43/895 (4.8%)
24	AX	2.02	9/598 (1.5%)	2.41	41/792 (5.2%)
25	BA	1.89	48/2869 (1.7%)	2.01	150/4474 (3.4%)
26	BB	1.90	1131/69257 (1.6%)	1.98	3513/108040 (3.3%)
27	BC	2.00	36/1748 (2.1%)	2.29	61/2355 (2.6%)
28	BD	2.05	50/2131 (2.3%)	2.32	105/2863 (3.7%)
29	BE	2.02	28/1586 (1.8%)	2.32	73/2134 (3.4%)
30	BF	1.98	27/1571 (1.7%)	2.39	84/2113 (4.0%)
31	BG	2.01	35/1444 (2.4%)	2.29	69/1937 (3.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	BH	1.93	26/1343 (1.9%)	2.38	76/1816 (4.2%)
33	BI	1.99	24/1122 (2.1%)	2.42	55/1515 (3.6%)
34	BJ	2.01	28/1247 (2.2%)	2.33	49/1679 (2.9%)
35	BK	2.00	25/1046 (2.4%)	2.43	62/1410 (4.4%)
36	BL	2.01	18/1152 (1.6%)	2.35	60/1551 (3.9%)
37	BM	1.94	18/956 (1.9%)	2.33	39/1279 (3.0%)
38	BN	2.10	20/1062 (1.9%)	2.30	54/1413 (3.8%)
39	BO	2.02	21/1093 (1.9%)	2.46	62/1460 (4.2%)
40	BP	1.96	18/1021 (1.8%)	2.46	65/1364 (4.8%)
41	BQ	2.04	22/910 (2.4%)	2.33	47/1219 (3.9%)
42	BR	2.04	23/929 (2.5%)	2.34	42/1242 (3.4%)
43	BS	1.97	18/960 (1.9%)	2.49	73/1278 (5.7%)
44	BT	2.05	21/829 (2.5%)	2.21	40/1107 (3.6%)
45	BU	2.00	20/864 (2.3%)	2.33	40/1156 (3.5%)
46	BV	2.09	22/794 (2.8%)	2.34	39/1060 (3.7%)
47	BW	1.99	16/797 (2.0%)	2.28	37/1062 (3.5%)
48	BX	1.95	16/766 (2.1%)	2.23	29/1025 (2.8%)
49	BY	2.08	22/642 (3.4%)	2.39	38/848 (4.5%)
50	BZ	2.03	12/635 (1.9%)	2.44	40/848 (4.7%)
51	B0	2.00	12/510 (2.4%)	2.51	39/677 (5.8%)
52	B1	2.01	8/453 (1.8%)	2.23	19/605 (3.1%)
53	B2	2.09	21/559 (3.8%)	2.51	35/745 (4.7%)
54	B3	2.06	12/450 (2.7%)	2.42	20/599 (3.3%)
55	B4	2.01	11/448 (2.5%)	2.20	19/594 (3.2%)
56	B5	2.08	11/380 (2.9%)	2.56	33/498 (6.6%)
57	B6	2.04	9/513 (1.8%)	2.25	25/676 (3.7%)
58	B7	1.90	6/303 (2.0%)	2.29	10/397 (2.5%)
All	All	1.94	2955/164069 (1.8%)	2.10	8537/244735 (3.5%)

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	888
2	AB	0	39
3	AC	0	23
4	AD	0	34
5	AE	0	6
6	AF	0	8
7	AG	0	11

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Mol	Chain	#Chirality outliers	#Planarity outliers
8	AH	0	5
9	AI	0	11
10	AJ	0	6
11	AK	0	3
12	AL	0	5
13	AM	0	4
14	AN	0	5
15	AO	0	2
16	AP	0	3
17	AQ	0	1
19	AS	0	3
20	AT	0	1
21	AU	0	6
23	AW	0	2
24	AX	0	1
25	BA	0	71
26	BB	0	1680
27	BC	0	4
28	BD	0	11
29	BE	0	7
30	BF	0	6
31	BG	0	8
32	BH	0	3
34	BJ	0	6
36	BL	0	6
37	BM	0	3
38	BN	0	3
39	BO	0	2
40	BP	0	6
41	BQ	0	4
42	BR	0	4
43	BS	0	5
44	BT	0	1
45	BU	0	3
47	BW	0	2
48	BX	0	3
49	BY	0	5
50	BZ	0	4
51	B0	0	2
52	B1	0	2
53	B2	0	1
55	B4	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
56	B5	0	1
57	B6	0	3
58	B7	0	1
All	All	0	2927

The worst 5 of 2955 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	BB	2552	OMU	O3'-P	11.42	1.67	1.56
26	BB	757	G	P-O5'	11.28	1.76	1.59
53	B2	66	ILE	CA-CB	10.91	1.60	1.54
26	BB	2569	G	P-O5'	10.73	1.75	1.59
1	AA	1466	C	P-O5'	10.35	1.75	1.59

The worst 5 of 8537 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	AO	55	ARG	NE-CZ-NH2	-14.32	106.31	119.20
9	AI	17	GLN	CA-C-N	13.74	128.90	120.24
9	AI	17	GLN	C-N-CA	13.74	128.90	120.24
26	BB	2756	U	C2'-C3'-O3'	12.62	128.43	109.50
26	BB	1975	G	C4'-C3'-C2'	-12.49	90.11	102.60

There are no chirality outliers.

5 of 2927 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	3	A	Sidechain
1	AA	4	U	Sidechain
1	AA	6	G	Sidechain
1	AA	7	A	Sidechain
1	AA	9	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	16610	0	0
2	AB	1627	0	843	0	0
3	AC	993	0	497	0	0
4	AD	1641	0	841	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	1302	0	0
26	BB	62351	0	31246	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
43	BS	947	0	1022	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	103794	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%)	221 (93%)	13 (6%)	4 (2%)	7	36
6	AF	230/232 (99%)	200 (87%)	25 (11%)	5 (2%)	5	29
7	AG	203/205 (99%)	180 (89%)	18 (9%)	5 (2%)	4	26
8	AH	164/166 (99%)	141 (86%)	19 (12%)	4 (2%)	4	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	AI	133/135 (98%)	118 (89%)	11 (8%)	4 (3%)	3	23
10	AJ	176/178 (99%)	164 (93%)	11 (6%)	1 (1%)	21	59
11	AK	127/129 (98%)	114 (90%)	11 (9%)	2 (2%)	7	38
12	AL	127/129 (98%)	109 (86%)	17 (13%)	1 (1%)	16	54
13	AM	101/103 (98%)	90 (89%)	7 (7%)	4 (4%)	2	18
14	AN	126/128 (98%)	105 (83%)	18 (14%)	3 (2%)	4	27
15	AO	121/123 (98%)	102 (84%)	16 (13%)	3 (2%)	4	26
16	AP	115/117 (98%)	104 (90%)	10 (9%)	1 (1%)	14	51
17	AQ	98/100 (98%)	84 (86%)	10 (10%)	4 (4%)	2	18
18	AR	86/88 (98%)	80 (93%)	6 (7%)	0	100	100
19	AS	80/82 (98%)	69 (86%)	9 (11%)	2 (2%)	4	26
20	AT	81/83 (98%)	71 (88%)	10 (12%)	0	100	100
21	AU	72/74 (97%)	63 (88%)	6 (8%)	3 (4%)	2	17
22	AV	89/91 (98%)	78 (88%)	10 (11%)	1 (1%)	11	46
23	AW	84/86 (98%)	79 (94%)	4 (5%)	1 (1%)	10	44
24	AX	68/70 (97%)	55 (81%)	9 (13%)	4 (6%)	1	13
27	BC	232/234 (99%)	208 (90%)	20 (9%)	4 (2%)	7	36
28	BD	270/272 (99%)	227 (84%)	37 (14%)	6 (2%)	5	29
29	BE	207/209 (99%)	171 (83%)	25 (12%)	11 (5%)	1	15
30	BF	199/201 (99%)	167 (84%)	26 (13%)	6 (3%)	3	23
31	BG	176/178 (99%)	144 (82%)	19 (11%)	13 (7%)	1	10
32	BH	174/176 (99%)	149 (86%)	16 (9%)	9 (5%)	1	15
33	BI	147/149 (99%)	132 (90%)	12 (8%)	3 (2%)	6	31
34	BJ	162/164 (99%)	140 (86%)	16 (10%)	6 (4%)	2	20
35	BK	139/141 (99%)	128 (92%)	9 (6%)	2 (1%)	9	40
36	BL	140/142 (99%)	118 (84%)	18 (13%)	4 (3%)	3	23
37	BM	121/123 (98%)	102 (84%)	14 (12%)	5 (4%)	2	18
38	BN	142/144 (99%)	113 (80%)	25 (18%)	4 (3%)	4	24
39	BO	134/136 (98%)	120 (90%)	13 (10%)	1 (1%)	18	56
40	BP	125/127 (98%)	116 (93%)	9 (7%)	0	100	100
41	BQ	115/117 (98%)	103 (90%)	12 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	BR	112/114 (98%)	90 (80%)	16 (14%)	6 (5%)	1	15
43	BS	115/117 (98%)	105 (91%)	7 (6%)	3 (3%)	4	25
44	BT	101/103 (98%)	92 (91%)	8 (8%)	1 (1%)	12	49
45	BU	108/110 (98%)	100 (93%)	4 (4%)	4 (4%)	2	20
46	BV	98/100 (98%)	85 (87%)	12 (12%)	1 (1%)	12	49
47	BW	101/103 (98%)	84 (83%)	15 (15%)	2 (2%)	6	31
48	BX	92/94 (98%)	79 (86%)	11 (12%)	2 (2%)	5	29
49	BY	82/84 (98%)	64 (78%)	15 (18%)	3 (4%)	2	20
50	BZ	75/77 (97%)	63 (84%)	9 (12%)	3 (4%)	2	18
51	B0	61/63 (97%)	53 (87%)	6 (10%)	2 (3%)	3	21
52	B1	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
53	B2	68/70 (97%)	51 (75%)	12 (18%)	5 (7%)	1	10
54	B3	54/56 (96%)	38 (70%)	14 (26%)	2 (4%)	2	20
55	B4	52/54 (96%)	47 (90%)	4 (8%)	1 (2%)	6	32
56	B5	44/46 (96%)	39 (89%)	4 (9%)	1 (2%)	5	28
57	B6	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
58	B7	36/38 (95%)	28 (78%)	6 (17%)	2 (6%)	1	14
All	All	6319/6423 (98%)	5497 (87%)	658 (10%)	164 (3%)	6	25

5 of 164 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	AE	84	LEU
5	AE	93	HIS
7	AG	3	TYR
8	AH	77	ASN
9	AI	99	ALA

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%)	181 (96%)	8 (4%)	26	48
7	AG	172/172 (100%)	167 (97%)	5 (3%)	37	58
8	AH	125/125 (100%)	120 (96%)	5 (4%)	28	49
9	AI	116/116 (100%)	110 (95%)	6 (5%)	21	42
10	AJ	146/146 (100%)	139 (95%)	7 (5%)	23	44
11	AK	104/104 (100%)	100 (96%)	4 (4%)	29	50
12	AL	106/106 (100%)	104 (98%)	2 (2%)	50	67
13	AM	90/90 (100%)	84 (93%)	6 (7%)	15	36
14	AN	98/98 (100%)	95 (97%)	3 (3%)	35	56
15	AO	103/103 (100%)	101 (98%)	2 (2%)	50	67
16	AP	95/95 (100%)	91 (96%)	4 (4%)	26	48
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%)	70 (91%)	7 (9%)	9	27
21	AU	64/64 (100%)	59 (92%)	5 (8%)	11	32
22	AV	78/78 (100%)	72 (92%)	6 (8%)	12	32
23	AW	65/65 (100%)	64 (98%)	1 (2%)	57	72
24	AX	60/60 (100%)	57 (95%)	3 (5%)	22	43
27	BC	181/181 (100%)	169 (93%)	12 (7%)	15	37
28	BD	217/217 (100%)	205 (94%)	12 (6%)	19	41
29	BE	164/164 (100%)	153 (93%)	11 (7%)	15	36
30	BF	165/165 (100%)	157 (95%)	8 (5%)	23	44
31	BG	149/149 (100%)	139 (93%)	10 (7%)	15	36
32	BH	137/137 (100%)	130 (95%)	7 (5%)	21	42
33	BI	114/114 (100%)	108 (95%)	6 (5%)	20	41
34	BJ	122/122 (100%)	115 (94%)	7 (6%)	18	40
35	BK	109/109 (100%)	105 (96%)	4 (4%)	30	51
36	BL	116/116 (100%)	111 (96%)	5 (4%)	26	47
37	BM	104/104 (100%)	102 (98%)	2 (2%)	50	67
38	BN	103/103 (100%)	97 (94%)	6 (6%)	18	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	BO	109/109 (100%)	107 (98%)	2 (2%)	51	68
40	BP	103/103 (100%)	99 (96%)	4 (4%)	28	49
41	BQ	87/87 (100%)	86 (99%)	1 (1%)	65	76
42	BR	99/99 (100%)	94 (95%)	5 (5%)	21	42
43	BS	89/89 (100%)	86 (97%)	3 (3%)	32	54
44	BT	84/84 (100%)	81 (96%)	3 (4%)	31	52
45	BU	93/93 (100%)	90 (97%)	3 (3%)	34	56
46	BV	84/84 (100%)	78 (93%)	6 (7%)	13	35
47	BW	84/84 (100%)	81 (96%)	3 (4%)	31	52
48	BX	78/78 (100%)	75 (96%)	3 (4%)	29	50
49	BY	62/62 (100%)	61 (98%)	1 (2%)	55	70
50	BZ	67/67 (100%)	62 (92%)	5 (8%)	12	33
51	B0	55/55 (100%)	52 (94%)	3 (6%)	19	41
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%)	46 (98%)	1 (2%)	47	65
55	B4	48/48 (100%)	46 (96%)	2 (4%)	26	48
56	B5	38/38 (100%)	36 (95%)	2 (5%)	20	41
57	B6	51/51 (100%)	48 (94%)	3 (6%)	18	39
58	B7	34/34 (100%)	32 (94%)	2 (6%)	18	39
All	All	5213/5213 (100%)	4978 (96%)	235 (4%)	26	46

5 of 235 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	BE	84	LEU
53	B2	3	LYS
32	BH	166	GLU
52	B1	29	ARG
46	BV	32	LEU

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%)	292 (18%)	93 (6%)
2	AB	75/76 (98%)	23 (30%)	7 (9%)
25	BA	119/120 (99%)	23 (19%)	13 (10%)
26	BB	2901/2904 (99%)	555 (19%)	180 (6%)
3	AC	47/47 (100%)	30 (63%)	14 (29%)
4	AD	76/77 (98%)	13 (17%)	4 (5%)
All	All	4759/4766 (99%)	936 (19%)	311 (6%)

5 of 936 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	A
1	AA	5	U
1	AA	6	G
1	AA	32	A
1	AA	36	C

5 of 311 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	BB	1697	G
26	BB	2500	U
26	BB	1786	A
26	BB	2129	C
26	BB	2756	U

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	$\# Z > 2$
1	7MG	AA	527	1	23,26,27	3.55	7 (30%)	27,39,42	2.11	7 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MIA	AB	37	2	28,31,32	1.73	4 (14%)	38,44,47	2.59	9 (23%)
4	OMC	AD	33	4	19,22,23	1.45	3 (15%)	25,31,34	1.36	5 (20%)
2	7MG	AB	46	2	23,26,27	4.09	5 (21%)	27,39,42	1.91	6 (22%)
26	PSU	BB	2457	26	18,21,22	1.12	2 (11%)	21,30,33	2.57	9 (42%)
26	OMC	BB	2498	26	19,22,23	1.19	2 (10%)	25,31,34	1.39	3 (12%)
2	PSU	AB	55	2	18,21,22	1.45	2 (11%)	21,30,33	2.46	7 (33%)
26	OMU	BB	2552	26	19,22,23	1.43	4 (21%)	25,31,34	2.16	7 (28%)
26	PSU	BB	2580	26	18,21,22	1.48	2 (11%)	21,30,33	1.85	10 (47%)
26	2MG	BB	1835	26	23,26,27	1.41	5 (21%)	33,38,41	1.47	5 (15%)
26	PSU	BB	1911	26	18,21,22	1.53	3 (16%)	21,30,33	2.31	4 (19%)
26	PSU	BB	2504	26	18,21,22	1.36	3 (16%)	21,30,33	2.02	7 (33%)
26	PSU	BB	2605	26	18,21,22	1.63	4 (22%)	21,30,33	1.91	3 (14%)
4	PSU	AD	56	4	18,21,22	1.75	5 (27%)	21,30,33	1.39	3 (14%)
1	5MC	AA	967	1	19,22,23	1.45	3 (15%)	26,32,35	1.25	1 (3%)
26	PSU	BB	955	26	18,21,22	1.76	3 (16%)	21,30,33	1.45	4 (19%)
2	H2U	AB	16	2	18,21,22	1.46	1 (5%)	19,30,33	1.96	6 (31%)
26	PSU	BB	746	26	18,21,22	2.32	6 (33%)	21,30,33	2.29	8 (38%)
26	2MA	BB	2503	26	22,25,26	1.52	3 (13%)	32,37,40	1.65	6 (18%)
1	MA6	AA	1519	1	23,26,27	1.20	3 (13%)	33,38,41	1.77	11 (33%)
1	UR3	AA	1498	1	19,22,23	1.15	1 (5%)	26,32,35	1.61	6 (23%)
4	H2U	AD	21	4	18,21,22	1.36	3 (16%)	19,30,33	2.33	5 (26%)
1	5MC	AA	1407	1	19,22,23	1.42	2 (10%)	26,32,35	1.99	6 (23%)
2	H2U	AB	17	2	18,21,22	1.34	3 (16%)	19,30,33	2.13	2 (10%)
26	5MU	BB	747	26	19,22,23	1.13	1 (5%)	27,32,35	1.65	7 (25%)
26	2MG	BB	2445	26	23,26,27	1.33	2 (8%)	33,38,41	1.71	6 (18%)
1	2MG	AA	966	1	23,26,27	1.05	2 (8%)	33,38,41	1.99	9 (27%)
1	4OC	AA	1402	-	20,23,24	1.30	2 (10%)	25,32,35	1.47	6 (24%)
26	6MZ	BB	1618	26	22,25,26	1.50	4 (18%)	29,36,39	2.00	8 (27%)
26	5MC	BB	1962	26	19,22,23	1.62	6 (31%)	26,32,35	1.67	6 (23%)
26	6MZ	BB	2030	26	22,25,26	1.00	1 (4%)	29,36,39	1.68	8 (27%)
26	OMG	BB	2251	26	23,26,27	1.23	3 (13%)	32,38,41	1.60	6 (18%)
1	PSU	AA	516	1	18,21,22	1.38	3 (16%)	21,30,33	2.99	7 (33%)
26	3TD	BB	1915	26	19,22,23	1.82	5 (26%)	23,32,35	1.34	2 (8%)
26	CH	BB	2575	26	16,21,22	1.56	3 (18%)	19,30,33	2.31	8 (42%)
4	5MU	AD	55	4	19,22,23	1.35	4 (21%)	27,32,35	2.18	6 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	2MG	AA	1516	1	23,26,27	1.72	5 (21%)	33,38,41	1.59	9 (27%)
26	PSU	BB	1917	26	18,21,22	1.43	3 (16%)	21,30,33	1.63	4 (19%)
1	2MG	AA	1207	1	23,26,27	1.46	2 (8%)	33,38,41	1.89	7 (21%)
26	5MU	BB	1939	26	19,22,23	1.46	4 (21%)	27,32,35	2.08	11 (40%)
2	5MU	AB	54	2	19,22,23	0.95	1 (5%)	27,32,35	1.51	5 (18%)
26	H2U	BB	2449	26	18,21,22	1.65	3 (16%)	19,30,33	1.65	3 (15%)
2	H2U	AB	20	2	18,21,22	1.51	3 (16%)	19,30,33	1.41	3 (15%)
2	OMC	AB	32	2	19,22,23	1.51	4 (21%)	25,31,34	1.67	5 (20%)
2	4SU	AB	8	2	18,21,22	1.77	2 (11%)	25,30,33	1.97	4 (16%)
26	1MG	BB	745	26	23,26,27	1.35	3 (13%)	33,39,42	1.94	9 (27%)
4	4SU	AD	8	4	18,21,22	1.80	5 (27%)	25,30,33	2.07	7 (28%)
26	7MG	BB	2069	26	23,26,27	3.66	5 (21%)	27,39,42	1.97	7 (25%)
1	MA6	AA	1518	1	23,26,27	1.45	3 (13%)	33,38,41	2.18	11 (33%)

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
1	7MG	AA	527	1	-	2/7/37/38	0/3/3/3
2	MIA	AB	37	2	-	0/15/33/34	0/3/3/3
4	OMC	AD	33	4	-	0/9/27/28	0/2/2/2
2	7MG	AB	46	2	-	3/7/37/38	0/3/3/3
26	PSU	BB	2457	26	-	0/7/25/26	0/2/2/2
26	OMC	BB	2498	26	-	0/9/27/28	0/2/2/2
2	PSU	AB	55	2	-	1/7/25/26	0/2/2/2
26	OMU	BB	2552	26	-	0/9/27/28	0/2/2/2
26	PSU	BB	2580	26	-	4/7/25/26	0/2/2/2
26	2MG	BB	1835	26	-	0/9/27/28	0/3/3/3
26	PSU	BB	1911	26	-	1/7/25/26	0/2/2/2
26	PSU	BB	2504	26	-	0/7/25/26	0/2/2/2
26	PSU	BB	2605	26	-	0/7/25/26	0/2/2/2
4	PSU	AD	56	4	-	0/7/25/26	0/2/2/2
1	5MC	AA	967	1	-	0/7/25/26	0/2/2/2
26	PSU	BB	955	26	-	0/7/25/26	0/2/2/2
2	H2U	AB	16	2	-	0/7/38/39	0/2/2/2
26	PSU	BB	746	26	-	0/7/25/26	0/2/2/2
26	2MA	BB	2503	26	-	2/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MA6	AA	1519	1	-	0/11/29/30	0/3/3/3
1	UR3	AA	1498	1	-	2/7/25/26	0/2/2/2
4	H2U	AD	21	4	-	0/7/38/39	0/2/2/2
1	5MC	AA	1407	1	-	0/7/25/26	0/2/2/2
2	H2U	AB	17	2	-	0/7/38/39	0/2/2/2
26	5MU	BB	747	26	-	0/7/25/26	0/2/2/2
26	2MG	BB	2445	26	-	0/9/27/28	0/3/3/3
1	2MG	AA	966	1	-	0/9/27/28	0/3/3/3
1	4OC	AA	1402	-	-	0/9/29/30	0/2/2/2
26	6MZ	BB	1618	26	-	1/9/27/28	0/3/3/3
26	5MC	BB	1962	26	-	1/7/25/26	0/2/2/2
26	6MZ	BB	2030	26	-	2/9/27/28	0/3/3/3
26	OMG	BB	2251	26	-	0/9/27/28	0/3/3/3
1	PSU	AA	516	1	-	0/7/25/26	0/2/2/2
26	3TD	BB	1915	26	-	2/7/25/26	0/2/2/2
26	CH	BB	2575	26	-	0/5/25/26	0/2/2/2
4	5MU	AD	55	4	-	0/7/25/26	0/2/2/2
1	2MG	AA	1516	1	-	0/9/27/28	0/3/3/3
26	PSU	BB	1917	26	-	3/7/25/26	0/2/2/2
1	2MG	AA	1207	1	-	1/9/27/28	0/3/3/3
26	5MU	BB	1939	26	-	0/7/25/26	0/2/2/2
2	5MU	AB	54	2	-	1/7/25/26	0/2/2/2
26	H2U	BB	2449	26	-	1/7/38/39	0/2/2/2
2	H2U	AB	20	2	-	0/7/38/39	0/2/2/2
2	OMC	AB	32	2	-	0/9/27/28	0/2/2/2
2	4SU	AB	8	2	-	5/7/25/26	0/2/2/2
26	1MG	BB	745	26	-	0/7/25/26	0/3/3/3
4	4SU	AD	8	4	-	0/7/25/26	0/2/2/2
26	7MG	BB	2069	26	-	0/7/37/38	0/3/3/3
1	MA6	AA	1518	1	-	2/11/29/30	0/3/3/3

The worst 5 of 158 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	46	7MG	C8-N9	-17.83	1.34	1.45
26	BB	2069	7MG	C8-N9	-16.09	1.35	1.45
1	AA	527	7MG	C8-N9	-15.35	1.35	1.45
26	BB	955	PSU	C2-N1	6.43	1.45	1.36
26	BB	746	PSU	C2-N1	5.40	1.43	1.36

The worst 5 of 304 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AB	37	MIA	C11-S10-C2	12.37	111.53	102.25
1	AA	516	PSU	C6-C5-C4	8.81	124.12	118.17
26	BB	1911	PSU	C6-C5-C4	8.66	124.02	118.17
2	AB	17	H2U	O4'-C1'-N1	8.59	121.00	109.30
2	AB	46	7MG	N9-C8-N7	7.00	113.28	103.37

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	AA	1207	2MG	N3-C2-N2-CM2
2	AB	8	4SU	C2'-C1'-N1-C2
2	AB	8	4SU	C2'-C1'-N1-C6
2	AB	46	7MG	C4'-C5'-O5'-P
26	BB	1915	3TD	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	$\# Z > 2$
59	TRP	AB	101	60,2	15,15,16	1.79	5 (33%)	17,20,22	2.56	7 (41%)
60	FME	BB	3001	59	8,9,10	1.64	1 (12%)	8,9,11	1.90	4 (50%)

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
59	TRP	AB	101	60,2	-	4/6/6/8	0/2/2/2
60	FME	BB	3001	59	-	2/7/9/11	-

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	-3.98	1.25	1.42
60	BB	3001	FME	CA-N	-3.81	1.41	1.46
59	AB	101	TRP	CD2-CG	2.59	1.48	1.44
59	AB	101	TRP	C-CA	2.51	1.56	1.52
59	AB	101	TRP	CE2-NE1	2.37	1.41	1.37

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	AB	101	TRP	CZ2-CE2-CD2	-5.56	116.81	122.19
59	AB	101	TRP	CZ2-CE2-NE1	5.01	138.77	130.74
59	AB	101	TRP	CD2-CE2-NE1	-3.71	104.43	107.52
60	BB	3001	FME	CG-CB-CA	3.15	122.50	112.87
59	AB	101	TRP	CZ3-CE3-CD2	3.04	125.30	119.80

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	BB	3001	FME	O1-CN-N-CA
60	BB	3001	FME	CB-CG-SD-CE
59	AB	101	TRP	N-CA-CB-CG
59	AB	101	TRP	CA-CB-CG-CD1
59	AB	101	TRP	CA-CB-CG-CD2

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	1614:A	O3'	1615:C	P	1.76

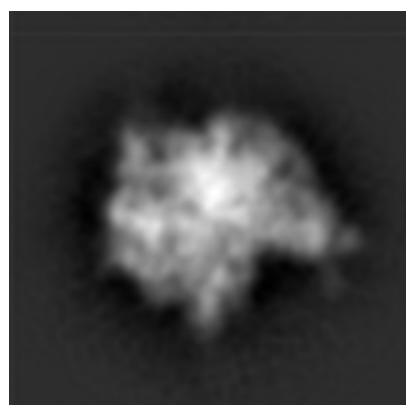
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5359. These allow visual inspection of the internal detail of the map and identification of artifacts.

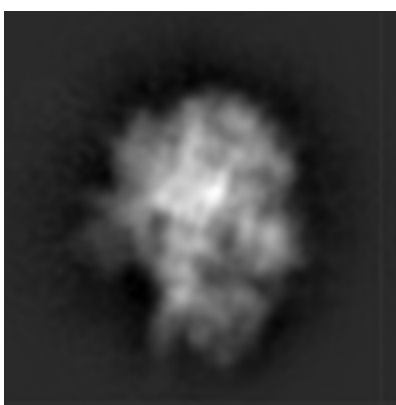
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

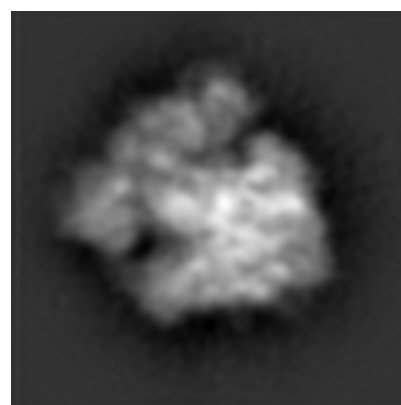
6.1.1 Primary map



X



Y

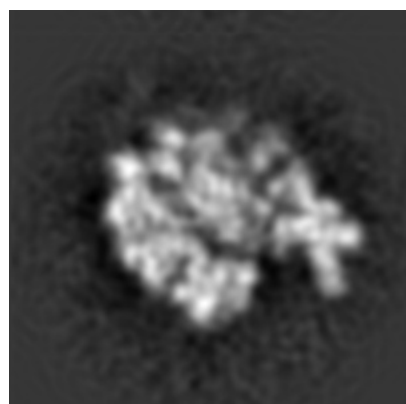


Z

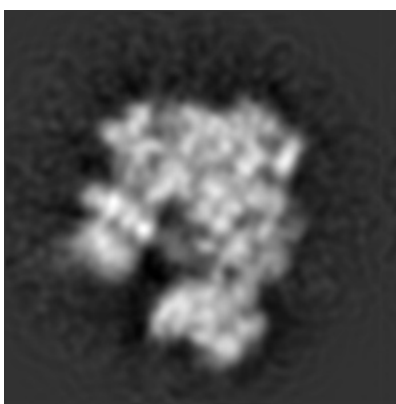
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

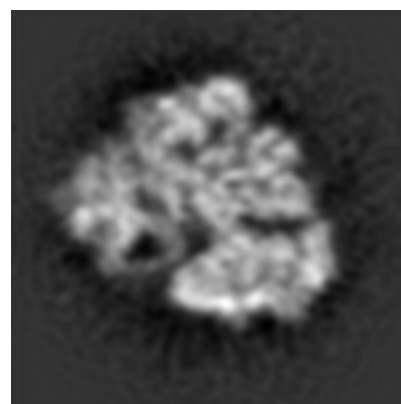
6.2.1 Primary map



X Index: 125



Y Index: 125

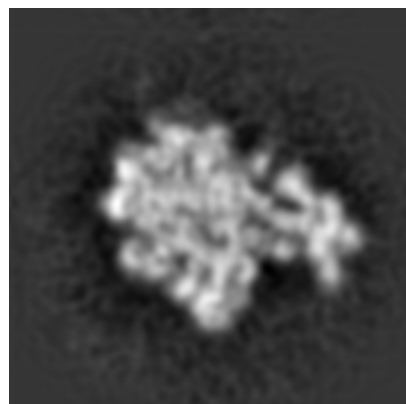


Z Index: 125

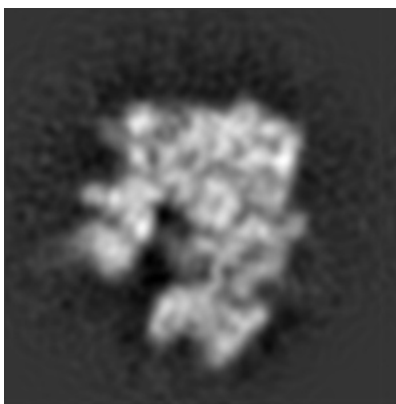
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

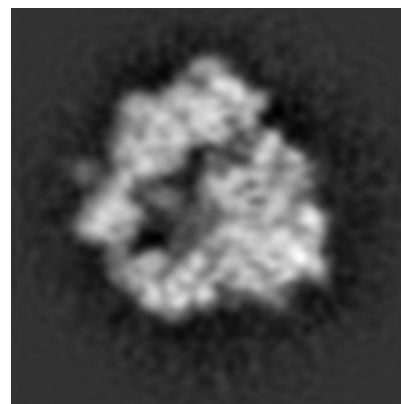
6.3.1 Primary map



X Index: 131



Y Index: 129

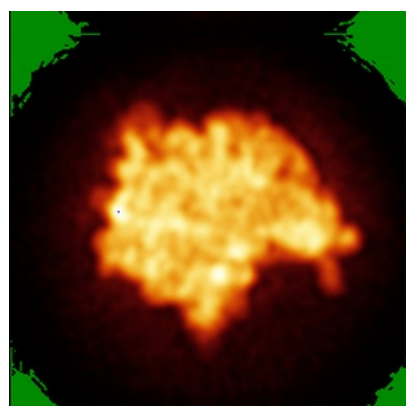


Z Index: 114

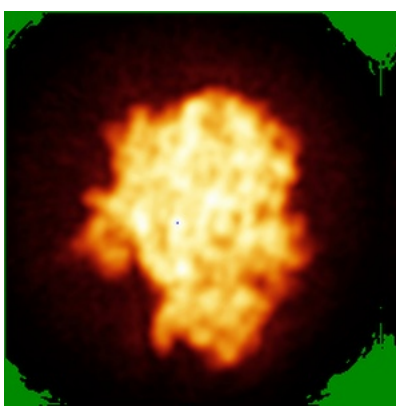
The images above show the largest variance slices of the map in three orthogonal directions.

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

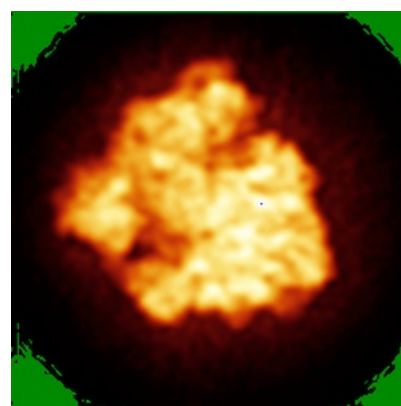
6.4.1 Primary map



X



Y

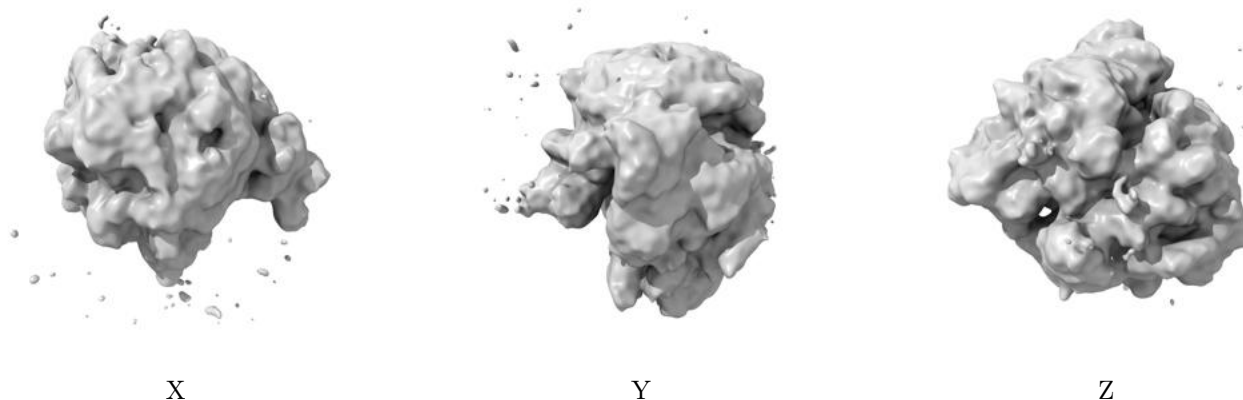


Z

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.

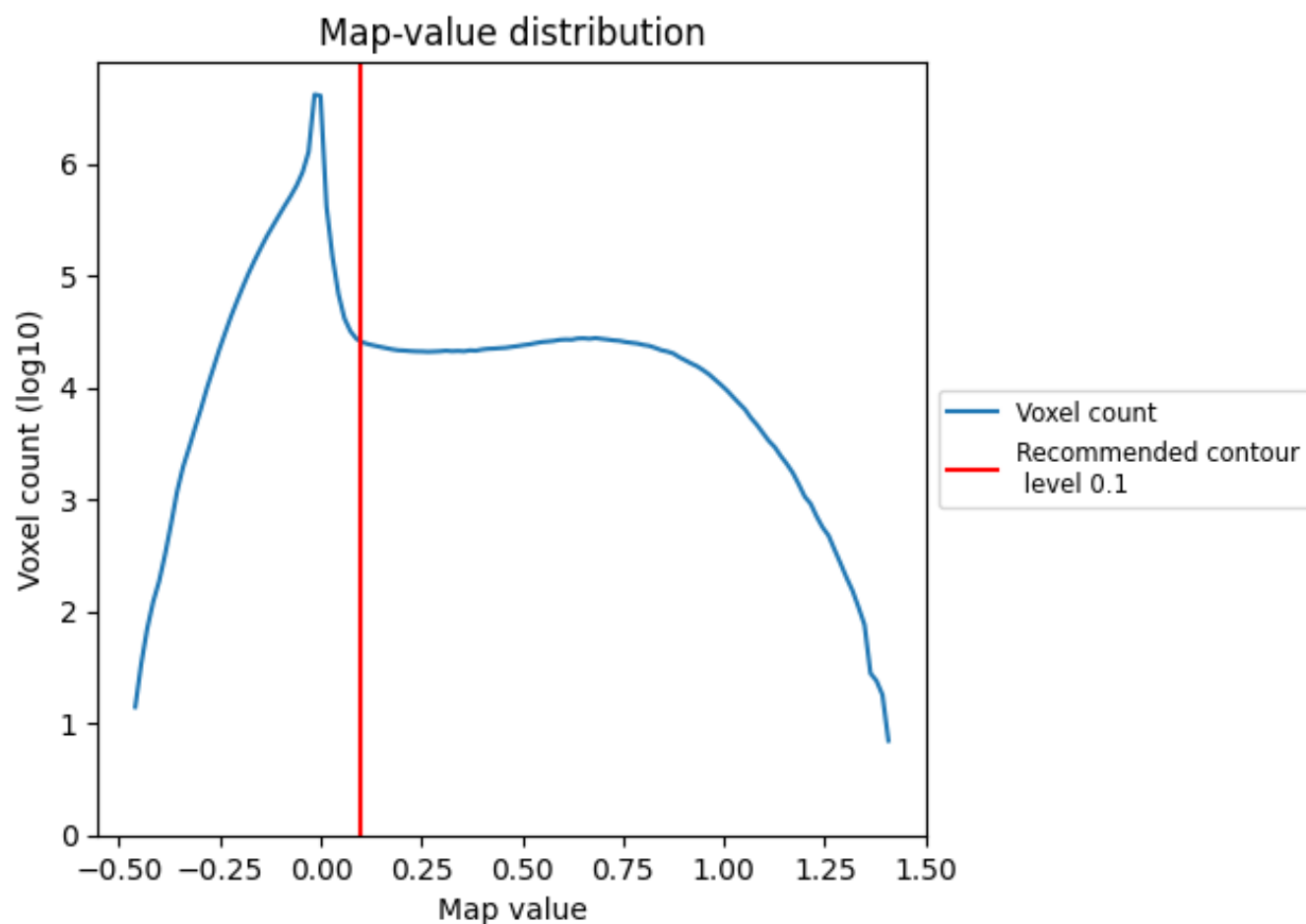
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

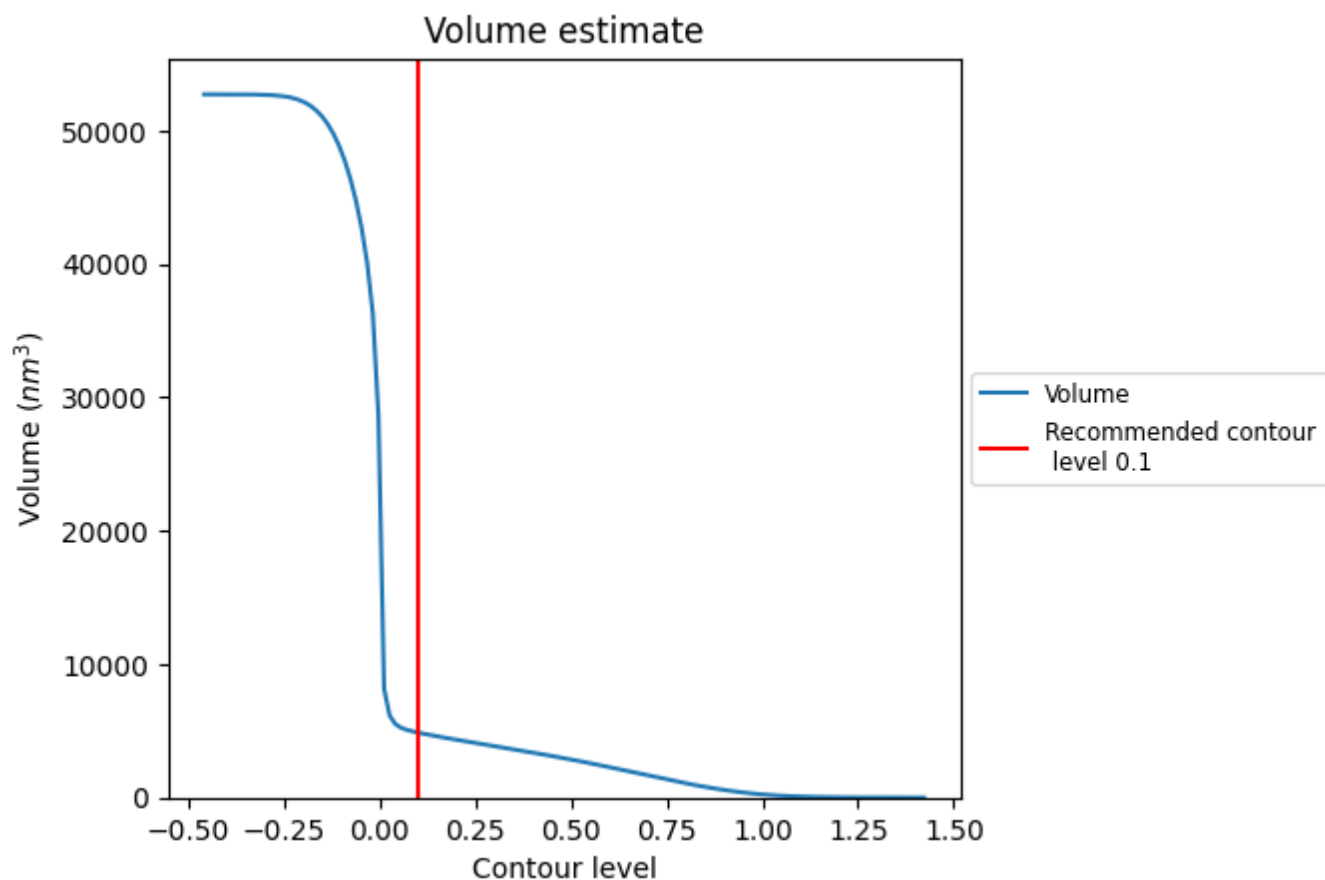
This section contains the results of statistical analysis of the map.

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.

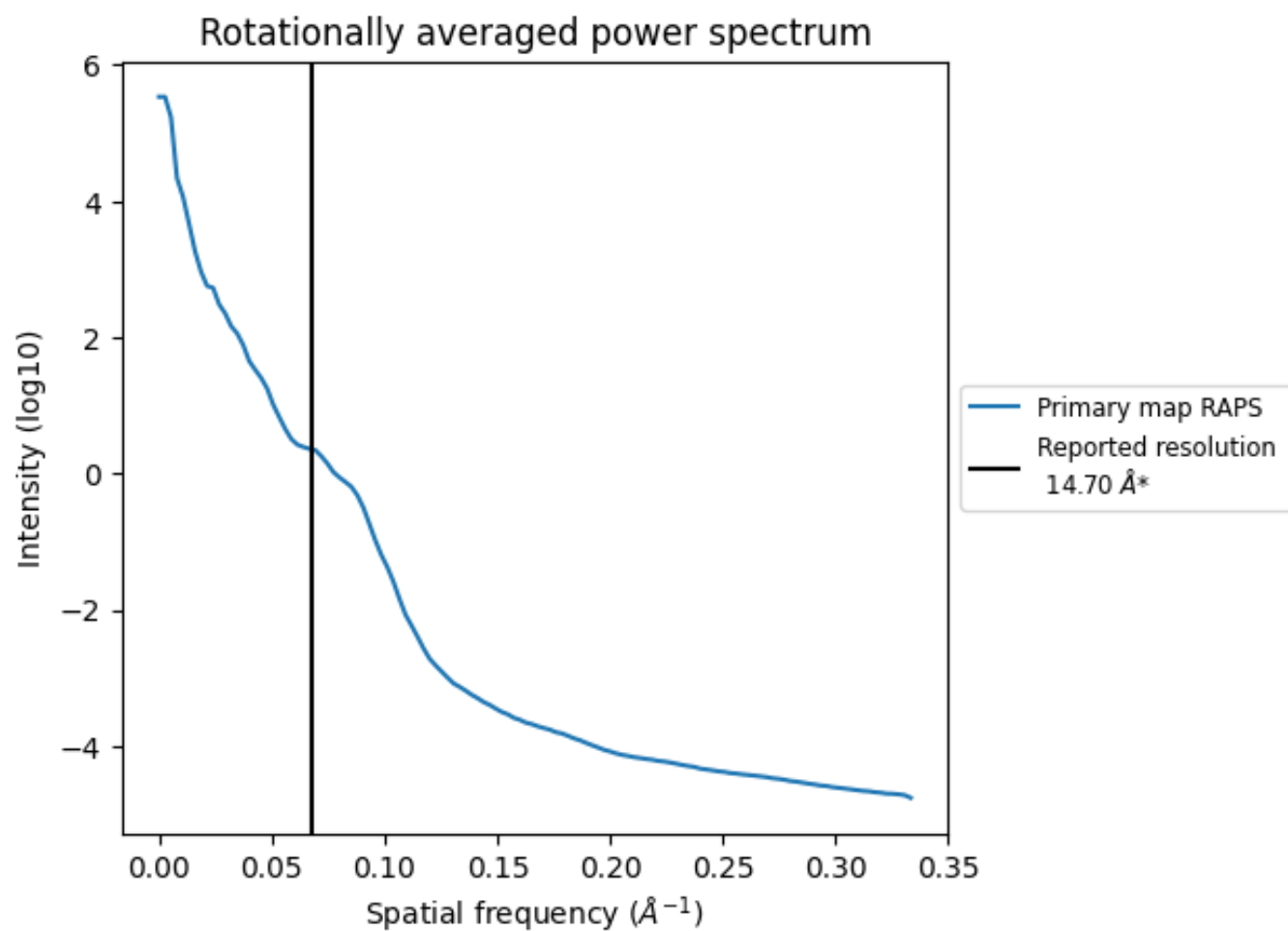
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4871 nm^3 ; this corresponds to an approximate mass of 4400 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 0.068 Å⁻¹

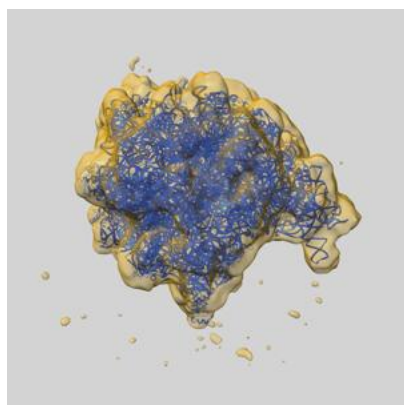
8 Fourier-Shell correlation

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

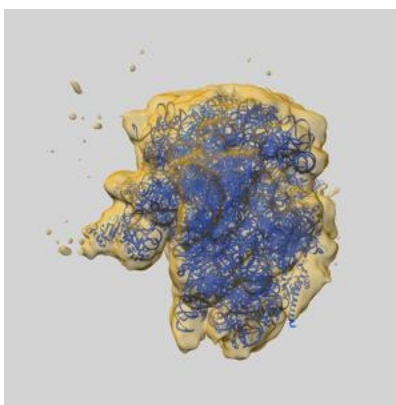
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5359 and PDB model 4V6O. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

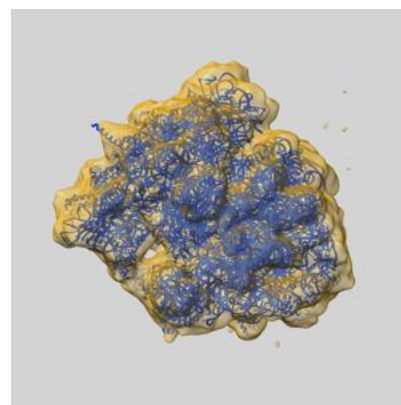
9.1 Map-model overlay [i](#)



X



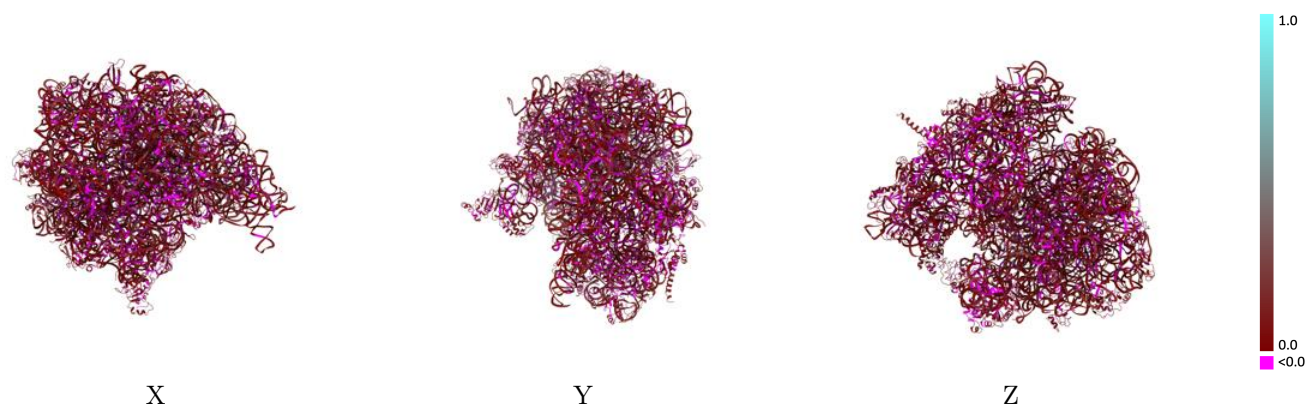
Y



Z

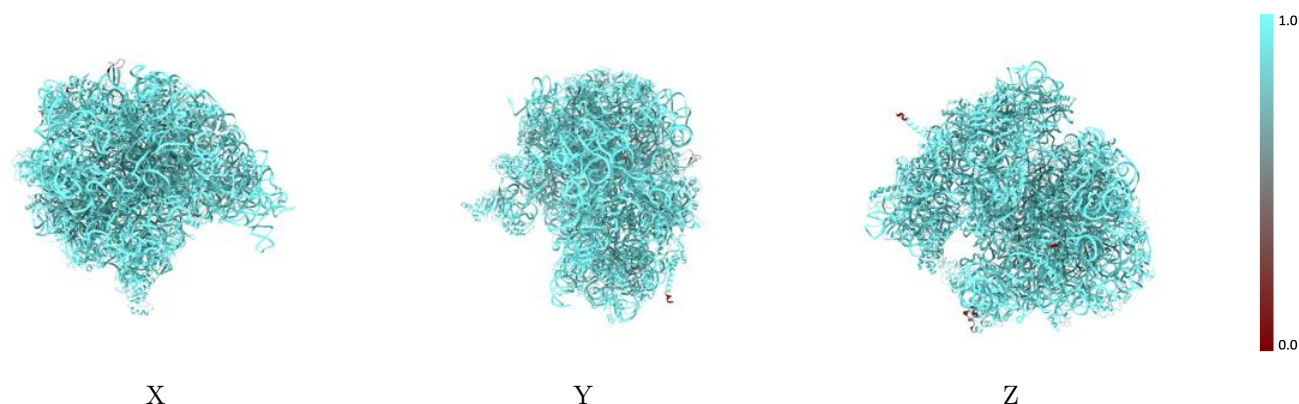
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



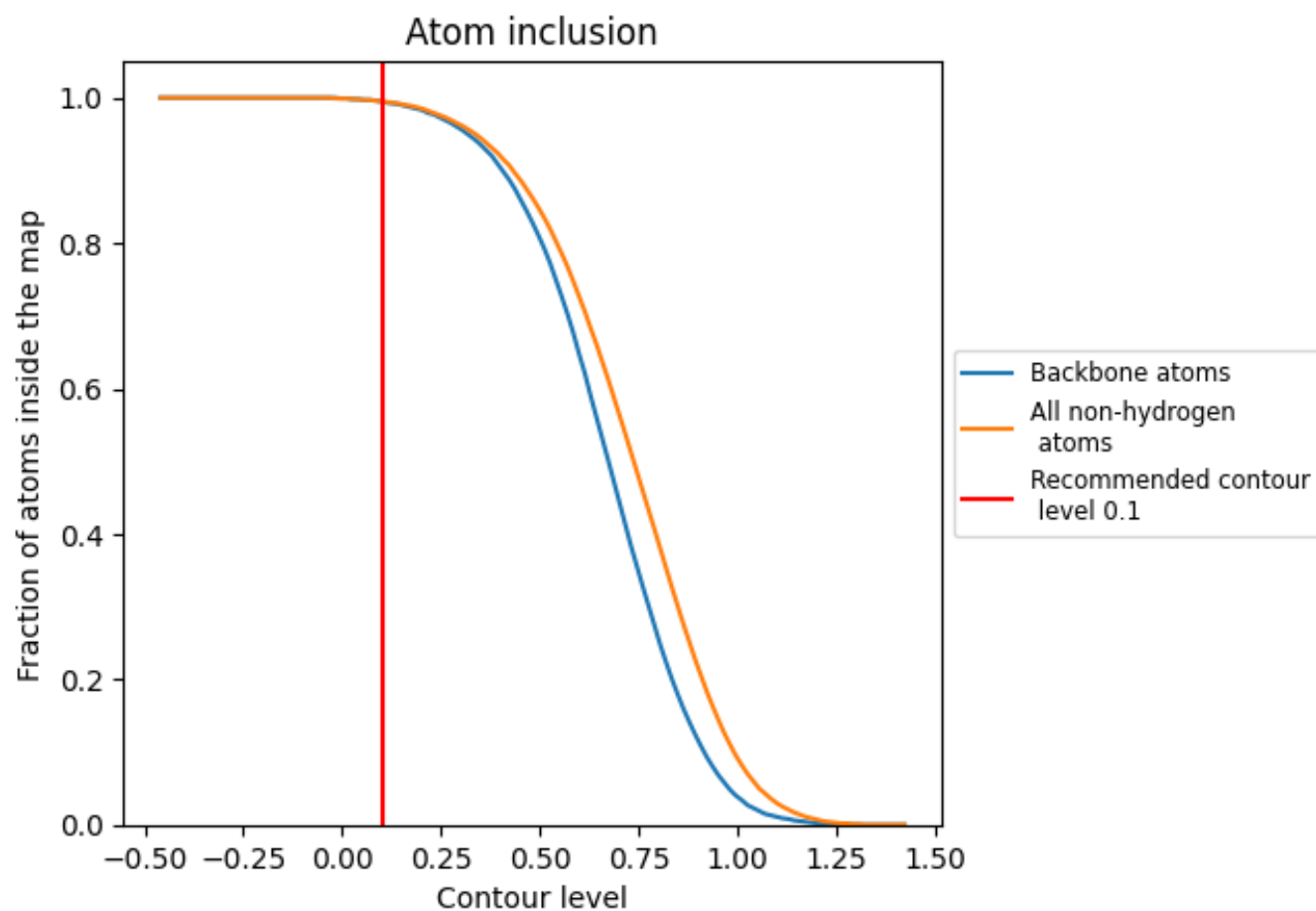
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 100% 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	 0.0650
AA	 1.0000	 0.0830
AB	 0.9690	 0.0430
AC	 0.8940	 -0.0220
AD	 0.9520	 0.0710
AE	 0.9670	 0.0380
AF	 0.9970	 0.0560
AG	 1.0000	 0.0330
AH	 0.9980	 0.0240
AI	 0.9970	 0.0450
AJ	 1.0000	 0.0640
AK	 1.0000	 0.0190
AL	 0.9890	 0.0450
AM	 1.0000	 0.0320
AN	 0.9960	 0.0540
AO	 0.9890	 0.0180
AP	 0.9980	 0.0630
AQ	 1.0000	 0.0310
AR	 1.0000	 0.0320
AS	 1.0000	 0.0250
AT	 1.0000	 0.0470
AU	 1.0000	 0.0490
AV	 1.0000	 0.0290
AW	 1.0000	 0.0250
AX	 0.9980	 0.0020
B0	 1.0000	 0.0290
B1	 0.9950	 0.0370
B2	 0.9960	 0.0110
B3	 1.0000	 0.0300
B4	 1.0000	 0.0400
B5	 1.0000	 0.0280
B6	 1.0000	 0.0010
B7	 1.0000	 0.0530
BA	 1.0000	 0.0950
BB	 1.0000	 0.0830



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Chain	Atom inclusion	Q-score
BC	 0.9100	 0.0280
BD	 1.0000	 0.0180
BE	 0.9990	 0.0270
BF	 1.0000	 0.0500
BG	 1.0000	 0.0610
BH	 0.9990	 0.0300
BI	 0.8800	 0.0350
BJ	 0.9880	 0.0510
BK	 0.9760	 0.0350
BL	 1.0000	 0.0130
BM	 0.9900	 0.0300
BN	 1.0000	 0.0050
BO	 1.0000	 0.0130
BP	 1.0000	 0.0190
BQ	 0.9950	 0.0460
BR	 0.9920	 0.0300
BS	 1.0000	 0.0050
BT	 0.9990	 0.0530
BU	 0.9990	 0.0180
BV	 1.0000	 0.0110
BW	 1.0000	 0.0510
BX	 1.0000	 0.0520
BY	 1.0000	 -0.0050
BZ	 1.0000	 0.0250