



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:59 PM UTC

PDB ID : 4V6R / pdb_00004v6r
EMDB ID : EMD-5362
Title : Structural characterization of mRNA-tRNA translocation intermediates (class 6 of the six classes)
Authors : Agirrezabala, X.; Liao, H.; Schreiner, E.; Fu, J.; Ortiz-Meoz, R.F.; Schulten, K.; Green, R.; Frank, J.
Deposited on : 2011-12-08
Resolution : 11.50 Å (reported)
Based on initial model : 2I2U

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

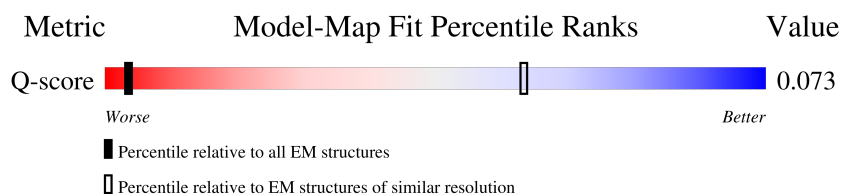
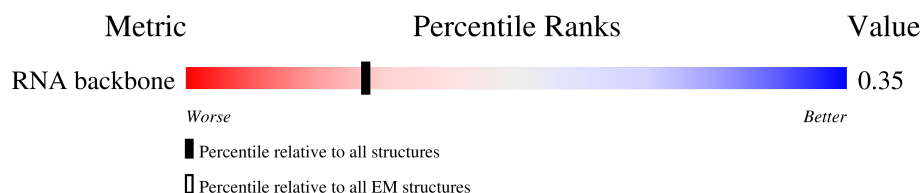
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

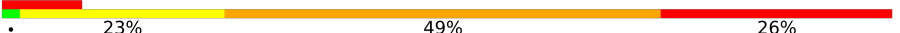
The reported resolution of this entry is 11.50 Å.

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



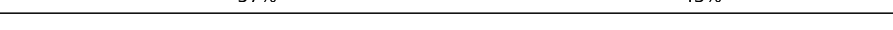
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
RNA backbone	8273	3508	-
Q-score	-	25397	117 (11.00 - 12.00)

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	 6% 37% 44% 13%
2	AB	76	 8% 28% 49% 16%
3	AC	47	 9% 23% 49% 26%
4	AD	77	 47% 43% 6%
5	AE	240	 55% 45%
6	AF	232	 59% 41%

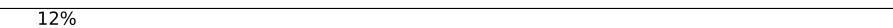
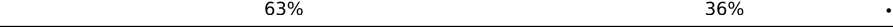
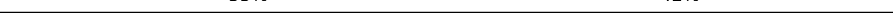
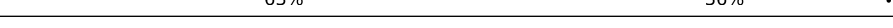
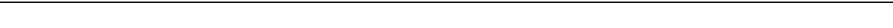
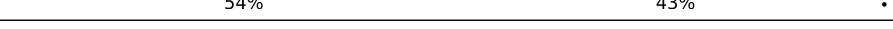
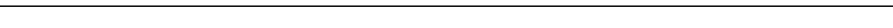
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Mol	Chain	Length	Quality of chain
7	AG	205	 61% 38%
8	AH	166	 63% 36%
9	AI	135	 56% 42%
10	AJ	178	 61% 37%
11	AK	129	 67% 32%
12	AL	129	 56% 43%
13	AM	103	 56% 43%
14	AN	128	 58% 40%
15	AO	123	 59% 39%
16	AP	117	 52% 47%
17	AQ	100	 47% 53%
18	AR	88	 52% 47%
19	AS	82	 61% 35%
20	AT	83	 57% 43%
21	AU	74	 58% 42%
22	AV	91	 51% 48%
23	AW	86	 55% 44%
24	AX	70	 54% 41%
25	BA	120	 10% 41% 41% 8%
26	BB	2904	 8% 37% 46% 10%
27	BC	234	 62% 38%
28	BD	272	 60% 39%
29	BE	209	 55% 43%
30	BF	201	 59% 39%
31	BG	178	 61% 39%

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Mol	Chain	Length	Quality of chain
32	BH	176	
33	BI	149	
34	BJ	164	
35	BK	141	
36	BL	142	
37	BM	123	
38	BN	144	
39	BO	136	
40	BP	127	
41	BQ	117	
42	BR	114	
43	BS	117	
44	BT	103	
45	BU	110	
46	BV	100	
47	BW	103	
48	BX	94	
49	BY	84	
50	BZ	77	
51	B0	63	
52	B1	58	
53	B2	70	
54	B3	56	
55	B4	54	
56	B5	46	

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Mol	Chain	Length	Quality of chain
57	B6	64	 61% 38% .
58	B7	38	 68% 32%

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		

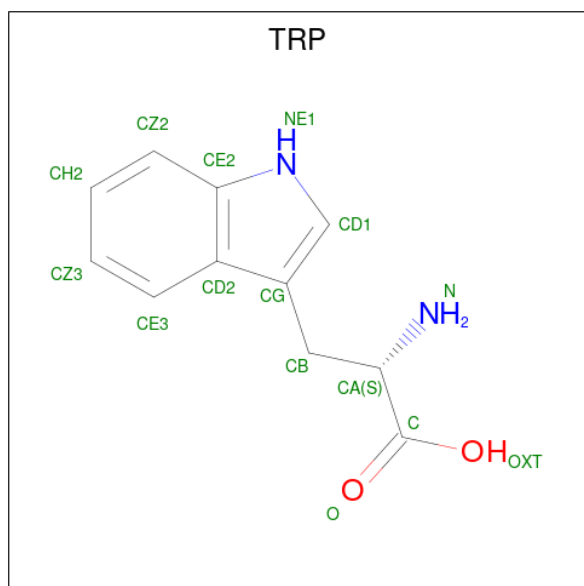
- Molecule 57 is a protein called 50S ribosomal protein L35.

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: $C_6H_{11}NO_3S$).

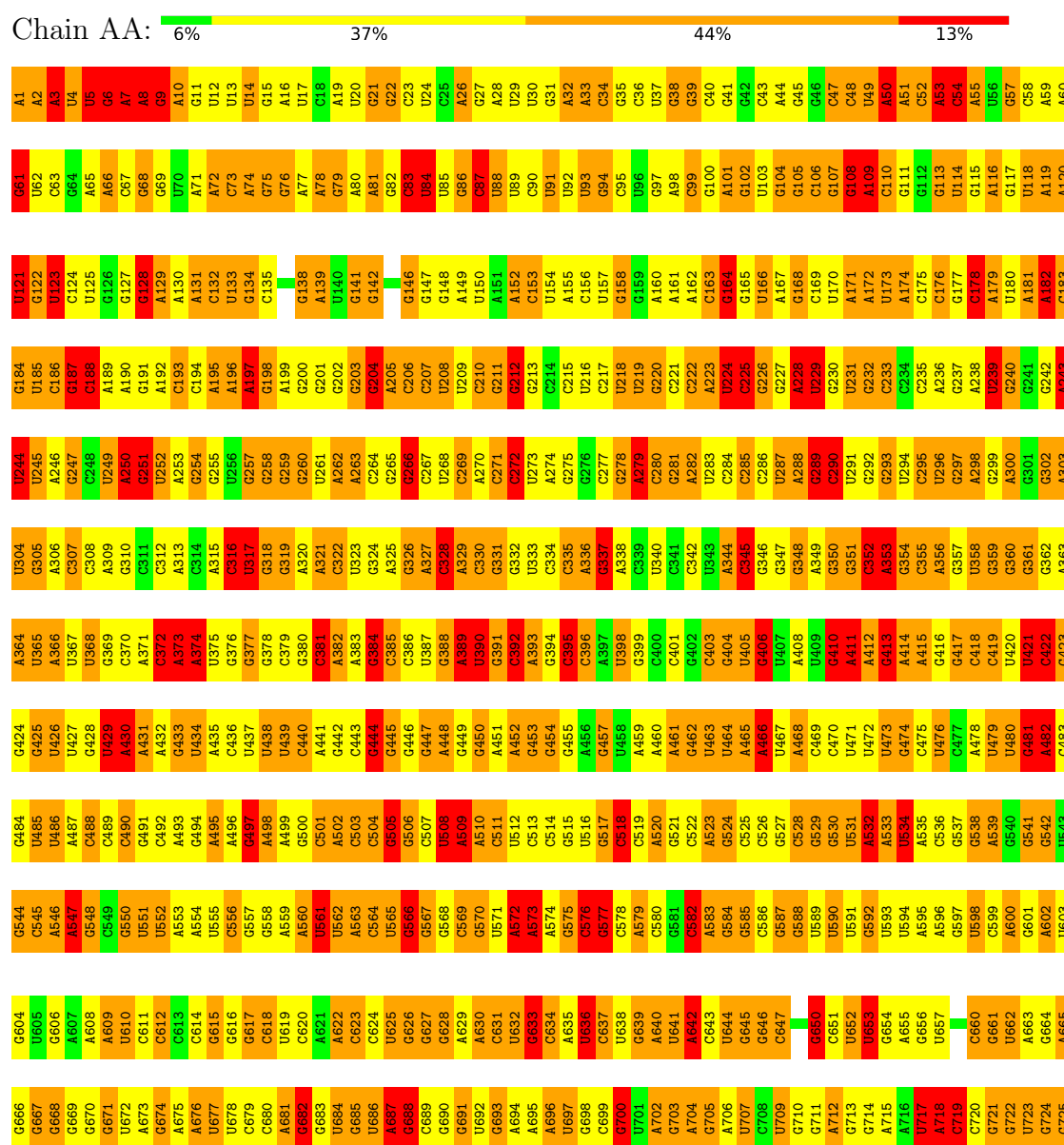


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
60	BB	1	10	6	1	2	1	0

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



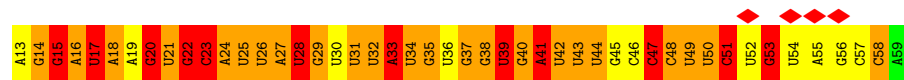
C1509	C1449	C1389	A1329	A1269	C1209	U1149	G1087	C1027	G986	A906	G846	G786	C726
C1510	U1450	U1390	U1330	G1270	C1210	C1149	G1088	C1028	C967	A907	G847	G787	C727
U1451	G1351	U1391	G1331	G1271	U1211	A1150	G1089	U1029	A968	A908	U788	A727	
C1452	C1452	C1392	A1332	C1272	U1212	A1151	U1090	U1030	A969	A909	G849	U789	
A1513	U1393	U1393	A1333	C1273	C1213	A1152	U1091	G1031	C970	C910	U850	A790	G730
C1454	U1454	A1394	G1334	A1274	C1214	G1153	A1092	G1032	G971	U911	G851	C791	G731
G1515	U1455	C1395	U1335	A1275	C1215	G1154	A1093	G1033	C972	C912	G852	A792	C732
G1516	A1396	A1396	C1336	G1276	A1216	A1155	G1094	G1034	G973	A913	G853	U793	G733
G1517	C1457	C1397	G1337	C1277	C1217	G1156	U1095	A1035	A974	A914	U854	A794	G734
A1518	G1458	A1398	G1338	G1278	C1218	A1157	C1096	A1036	A975	A915	U855	C795	G735
A1519	U1459	C1399	A1339	G1279	A1219	C1158	C1097	U1037	G976	U916	C856	C796	G736
C1520	C1460	C1400	A1340	A1280	G1220	U1159	C1098	C1038	A977	G917	C857	C797	G737
C1521	G1461	G1401	U1341	C1281	G1221	G1160	G1099	G1039	A978	A918	U858	C798	C738
U1522	C1462	C1402	C1342	C1282	G1222	C1161	C979	U1040	C979	A919	G859	G799	C739
G1523	U1463	C1403	G1343	U1283	C1223	C1162	A1101	G1041	C980	U920	A860	G900	U740
U1464	U1464	C1404	C1344	C1284	A1224	A1163	A1102	A1042	U981	U921	U861	U901	G741
G1525	G1465	G1405	U1345	A1285	A1225	G1164	C1103	G1043	U982	G922	C862	A802	G742
C1526	C1466	U1406	A1346	U1286	C1226	U1165	G1104	A1044	A983	A923	U863	G803	A743
U1527	C1467	C1407	G1347	A1287	C1227	G1166	A1105	C1045	C984	C924	A864	U904	C744
U1528	A1468	A1408	U1348	A1288	A1228	A1167	A1106	A1046	C985	G925	A865	C905	G745
C1529	C1469	C1409	A1349	A1289	A1229	U1168	C1107	G1047	U986	G926	C866	C906	A746
G1530	U1470	A1410	G1350	G1290	C1230	A1169	U1108	G1048	C987	G927	A807	U747	
A1531	U1471	C1411	U1351	U1291	G1231	A1170	C1109	U1049	G988	G928	C868	C908	G748
U1532	C1472	C1412	C1352	C1292	U1232	A1171	A1110	G1050	U989	G929	C869	C909	A749
C1533	G1473	A1413	G1353	C1293	G1233	C1172	A1111	C1051	C990	C930	U870	C910	C750
A1534	U1474	U1414	U1354	G1294	C1234	U1173	C1112	U1052	U991	C931	U871	C911	G751
C1535	G1475	G1415	G1355	U1295	U1235	G1174	C1113	G1053	U992	C932	A872	G812	G752
C1536	A1476	G1416	G1356	C1296	A1236	G1175	G993	C1054	U993	G933	A873	U813	A753
U1537	G1477	G1417	A1357	G1297	C1237	A1176	C1114	A1055	A994	C934	G874	A814	C754
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C1539	G1479	G1419	C1359	A1299	A1239	U1178	A1117	G1057	A996	C936	C876	A816	C756
U1540	A1480	U1420	A1360	G1300	U1240	A1179	U1118	G1058	U997	A937	G877	C917	U757
U1541	U1481	G1421	G1361	C1301	G1241	C1180	C1119	C1059	C998	A938	A878	G818	C758
A1542	G1482	G1422	A1362	A1302	G1242	G1181	C1120	U1060	C999	G939	C879	A819	A759
C1483	C1423	C1363	A1363	C1303	C1243	U1121	U1121	G1061	A1000	C940	C880	U820	G760
U1484	U1424	U1364	U1364	G1304	G1244	G1184	U1122	U1062	C1001	G941	C881	G821	G761
U1485	U1425	G1365	U1365	G1305	C1245	G1185	U1123	G1063	C882	G942	U822	U762	
G1486	G1426	A1306	C1366	A1306	U1246	G1186	G1124	G1064	G1003	U943	C883	C923	G763
G1487	C1427	C1367	C1367	U1307	U1247	G1187	U1025	U1065	A1004	G944	G884	G824	C764
G1488	A1428	A1368	A1368	G1308	A1248	A1188	U1126	C1066	A1005	G945	G885	A825	G765
G1489	A1429	C1369	G1369	G1309	C1249	U1189	G1127	A1067	G1006	A946	G886	C926	G766
U1490	A1430	G1370	G1370	C1310	A1250	G1190	C1128	G1068	U1007	G947	C887	U827	A767
G1491	A1431	G1371	G1371	A1311	A1251	A1191	C1129	C1069	U1008	C948	A888	U828	A768
A1492	G1432	U1372	U1372	G1312	A1252	C1192	A1130	U1070	U1009	A949	A889	G829	C769
A1493	A1433	C1373	G1373	C1313	G1253	G1193	G1131	C1071	U1010	U950	G890	G830	C770
G1494	A1434	A1374	A1254	C1314	A1254	U1194	C1132	G1072	C1011	G951	U891	A831	G771
U1495	G1435	A1375	U1375	U1315	G1255	C1195	G1133	U1073	A1012	U952	A892	G832	U772
C1496	U1436	U1376	G1376	C1316	A1256	A1196	G1134	G1074	G1013	G953	C893	G833	G773
G1497	A1437	A1377	A1377	C1317	A1257	A1197	U1135	U1075	A1014	G954	U894	U834	G774
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U1500	U1440	U1390	C1320	G1320	G1260	C1200	G1138	U1078	U1017	C897	U837	G777	
A1501	A1441	A1381	U1381	C1321	A1261	A1201	G1139	G1079		A958	G898	G778	
A1502	G1442	C1382	C1382	C1322	C1262	U1202	C1140	A1080	G1020	A959	C899	C839	C779
A1503	C1443	C1383	C1383	G1323	C1263	C1203	C1141	A1081	U1021	A960	A900	C840	A780
G1504	U1444	C1384	C1384	A1324	U1264	A1204	C1142	A1082	A1022	U961	A901	C841	A781
G1505	U1445	G1385	C1385	C1325	C1265	U1205	G1143	U1083	G1023	G902	G902	U842	C782
U1506	A1446	G1386	G1386	G1326	G1266	G1206	G1144	G1084	G1024	G903	G903	U843	C783
A1507	G1447	G1387	C1387	C1327	C1267	G1207	A1145	U1085	U1025	U904	G844	A784	
A1508	C1448	C1388	C1388	C1328	C1268	C1208	G1146	U1086	G1026	U905	A785	C785	

• Molecule 2: A site tRNA

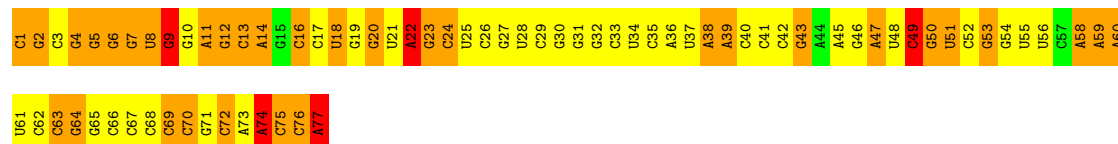
Chain AB:  8% 28% 49% 16%

A1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15	G16	G17	G18	G19	G20	G21	G22	G23	G24	G25	G26	G27	G28	G29	G30	G31	G32	G33	G34	G35	G36	G37	G38	G39	G40	G41	G42	G43	G44	G45	G46	G47	G48	G49	G50	G51	G52	G53	G54	G55	G56	G57	G58	G59	G60
C61	U62	C63	U64	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

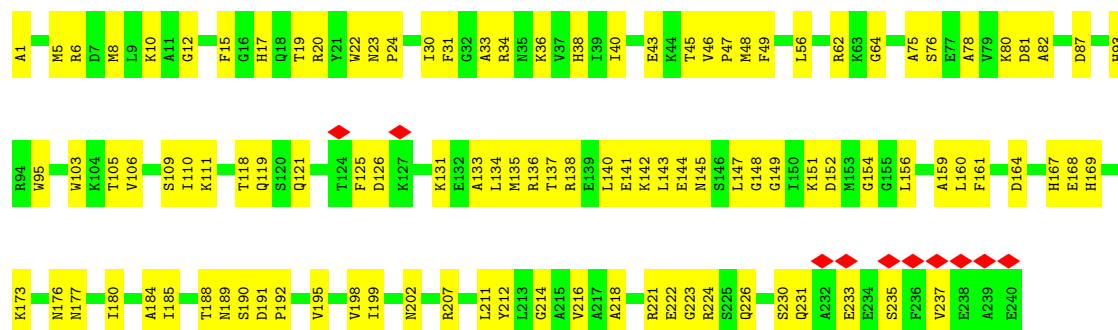
- Molecule 3: mRNA



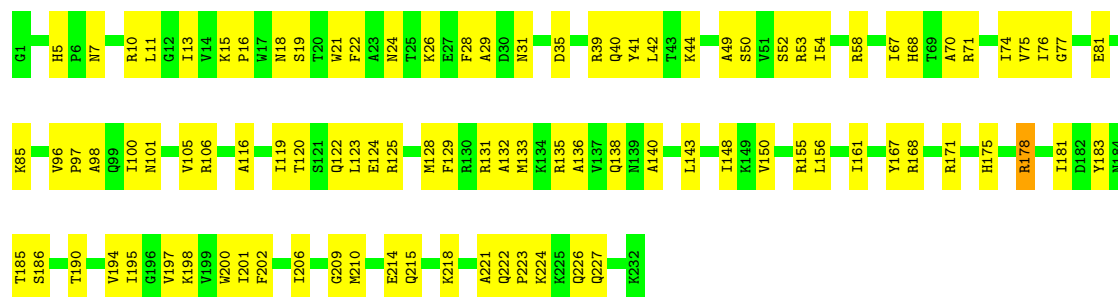
- Molecule 4: P site tRNA



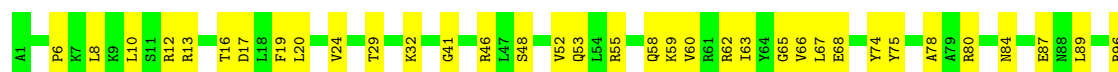
- Molecule 5: 30S ribosomal protein S2

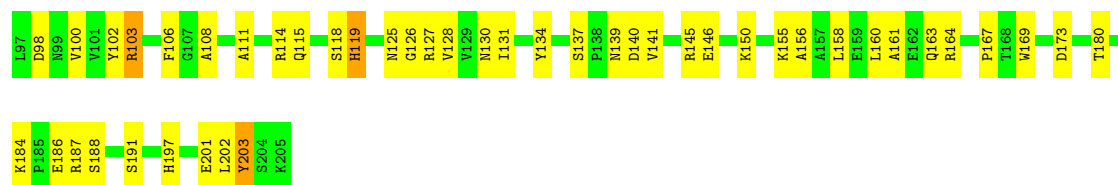


- Molecule 6: 30S ribosomal protein S3

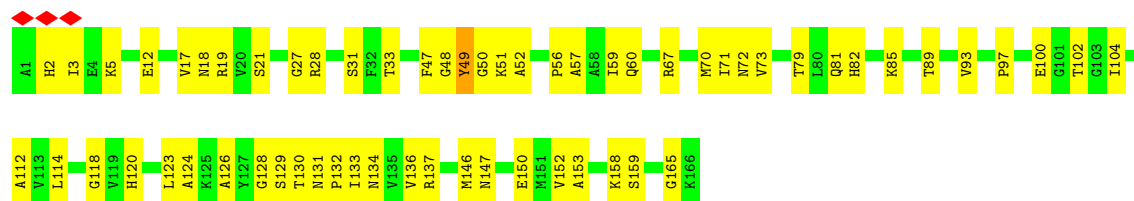


- Molecule 7: 30S ribosomal protein S4

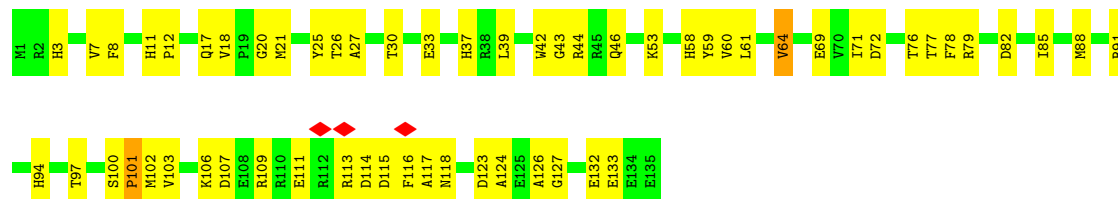




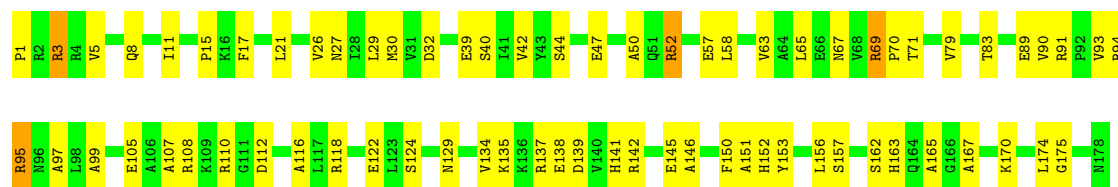
• Molecule 8: 30S ribosomal protein S5



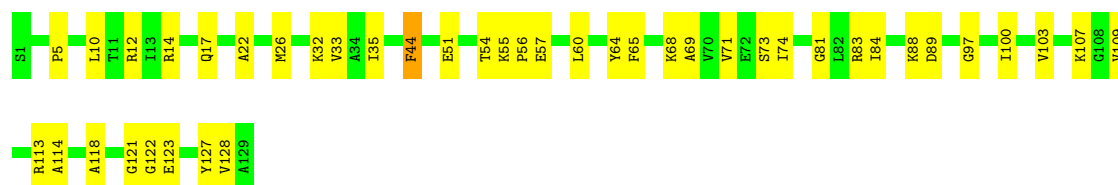
• Molecule 9: 30S ribosomal protein S6



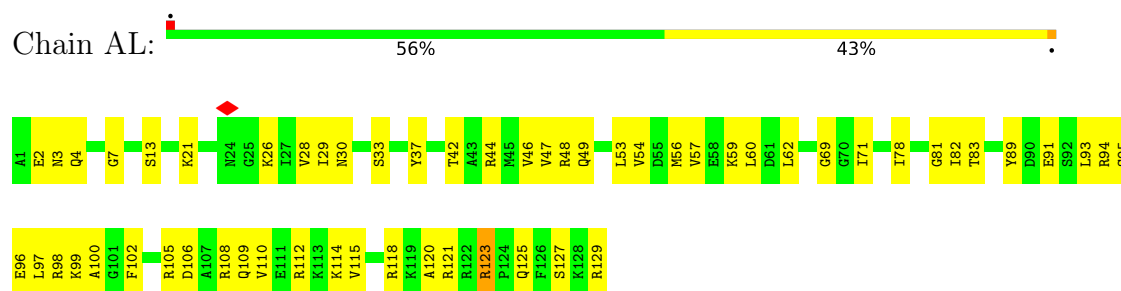
• Molecule 10: 30S ribosomal protein S7



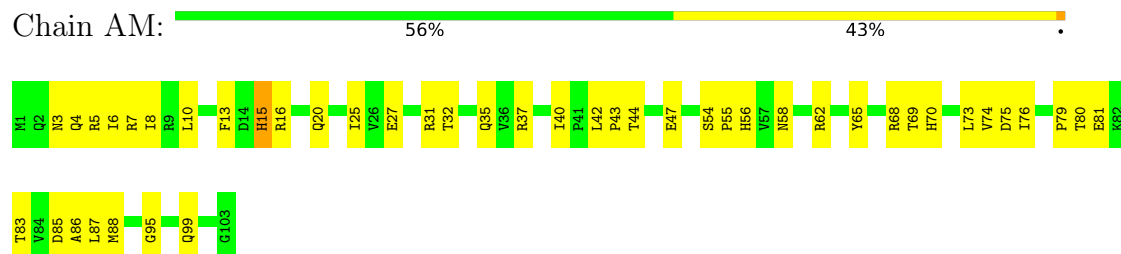
• Molecule 11: 30S ribosomal protein S8



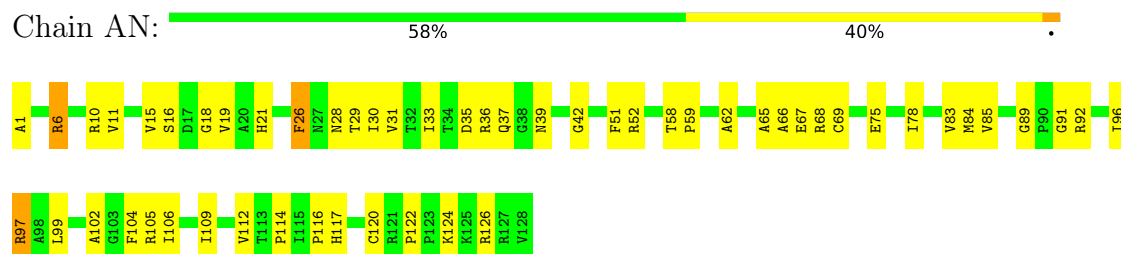
• Molecule 12: 30S ribosomal protein S9



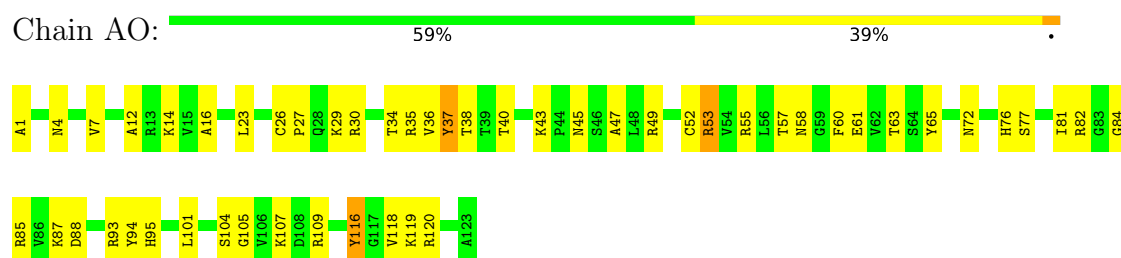
- Molecule 13: 30S ribosomal protein S10



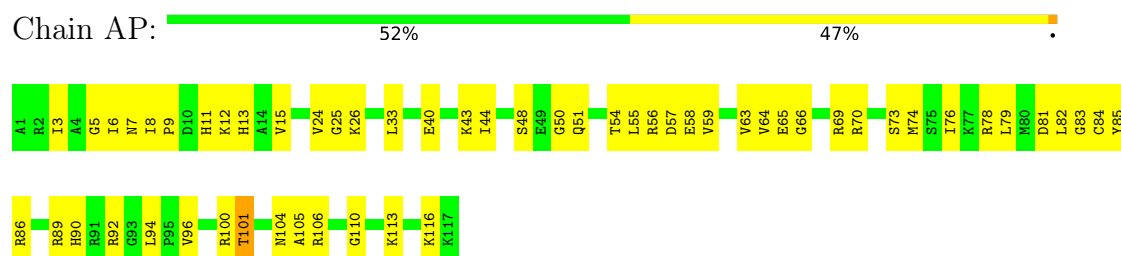
- Molecule 14: 30S ribosomal protein S11



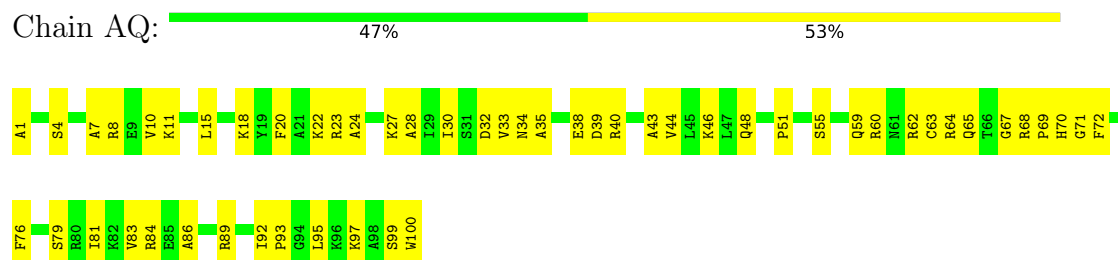
- Molecule 15: 30S ribosomal protein S12



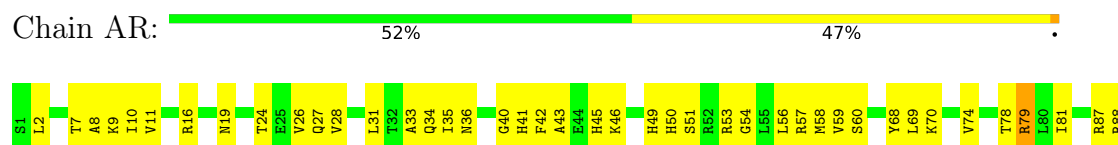
- Molecule 16: 30S ribosomal protein S13



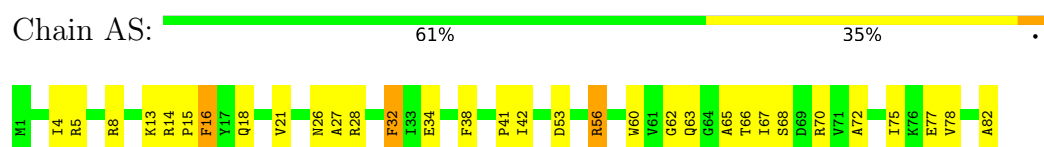
- Molecule 17: 30S ribosomal protein S14



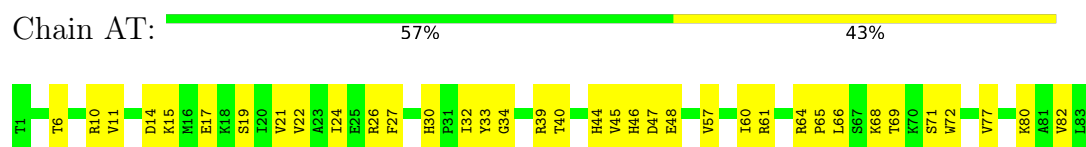
- Molecule 18: 30S ribosomal protein S15



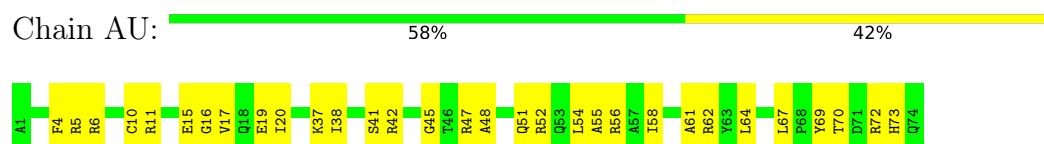
- Molecule 19: 30S ribosomal protein S16



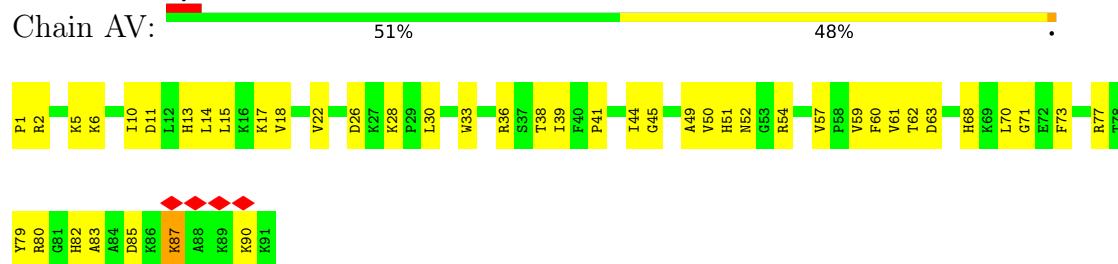
- Molecule 20: 30S ribosomal protein S17



- Molecule 21: 30S ribosomal protein S18



- Molecule 22: 30S ribosomal protein S19



- Molecule 23: 30S ribosomal protein S20

Chain AW:  55% 44%



• Molecule 24: 30S ribosomal protein S21

Chain AX:  54% 41%



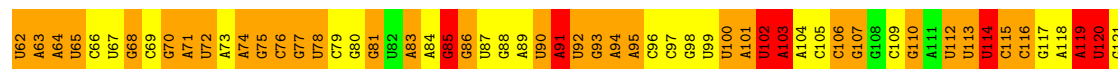
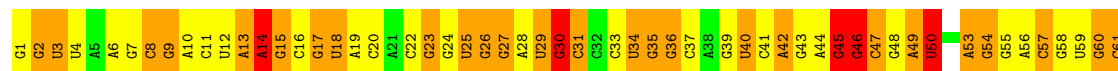
• Molecule 25: 5S ribosomal RNA

Chain BA:  10% 41% 41% 8%



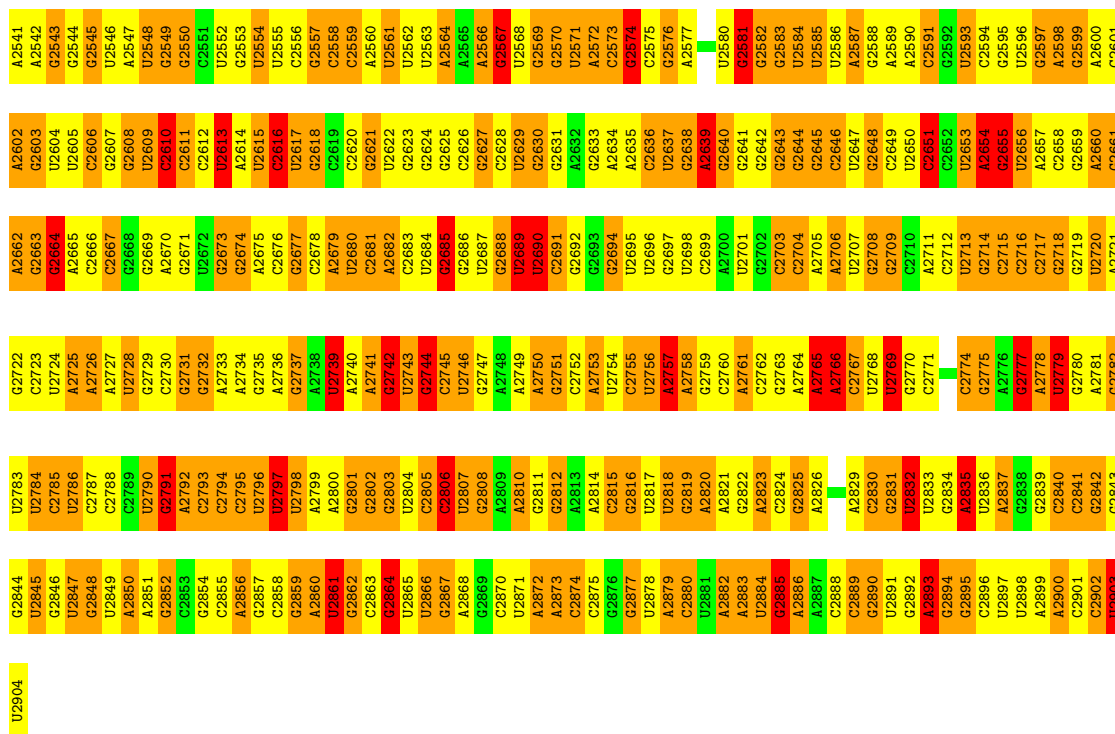
• Molecule 26: 23S ribosomal RNA

Chain BB:  8% 37% 46% 10%

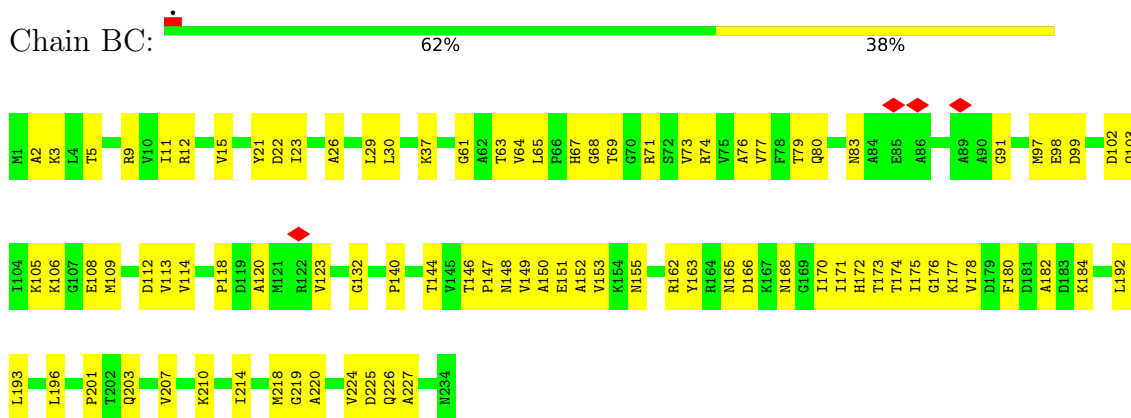


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C1512	G1450	C1330	C1270	G1210	G1149	A1086	A1027	C965	G904	A844	G784	U724	G664	G604	C544
U1513	G1451	G1331	G1271	G1211	C1150	A1089	A1028	G966	A905	G845	G785	G725	G665	G605	C545
G1514	G1452	G1332	A1272	G1212	A1151	A1090	A1029	G967	U906	U846	G786	G726	U666	U606	U546
A1515	G1453	G1333	U1273	A1213	G1152	C1091	G1030	G968	G907	U847	G787	A727	U667	U607	A547
G1516	G1454	G1334	A1274	A1214	G1153	C1092	G1031	G969	C908	C848	G788	G728	A668	A608	G548
G1517	G1455	C1335	A1275	G1215	G1154	G1093	A1032	G970	C909	A849	A789	G729	G669	A609	G549
C1518	G1456	A1336	G1276	G1216	A1155	U1094	U1033	U970	A910	U850	U790	A730	A670	C610	C550
G1519	U1457	G1337	G1277	G1217	A1156	A1095	G1034	G971	A911	C851	C791	C731	C671	G611	G551
U1458	G1458	G1338	C1278	G1218	G1157	A1096	U1035	A973	C912	U852	A792	G732	C672	G612	G552
G1459	G1459	G1339	G1279	U1219	C1158	U1097	G1036	G974	U913	C853	G793	G733	C673	A613	G553
G1521	G1460	C1340	G1280	G1220	U1159	A1098	G1037	A975	G914	G854	A794	A734	G674	A614	U554
A1522	G1461	G1341	G1281	C1221	G1160	G1099	G1038	G976	C915	G855	C795	A735	A675	U615	G555
U1523	C1462	A1342	U1282	U1222	C1161	C1100	A1039	G977	G916	G856	C796	C736	A676	A616	A556
G1524	G1463	G1343	G1283	G1223	G1162	C1101	A1040	G978	A917	G857	G797	G737	A677	G617	C557
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A1528	U1467	G1346	A1287	G1227	G1166	U1105	G1044	C982	C921	A861	G801	U741	G681	A621	G561
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U1499	G1499	G1377	G1317	C1257	G1197	G1136	G1074	U1012	G952	C891	G831	G771	G711	G651	U591
G1500	G1500	U1378	U1318	U1258	U1198	G1137	C1075	C1013	G953	A892	U832	C772	G712	U652	A592
C1501	A1501	C1379	C1319	G1259	U1199	G1138	U1078	A1014	G954	C893	A833	U773	G713	U653	U593
U1502	U1502	G1380	C1320	A1260	C1200	C1139	U1079	U1018	U955	C894	G834	U774	G714	U654	U594
A1503	G1503	A1321	A1321	C1261	U1201	C1140	C1079	U1019	G956	U895	C835	G775	A715	A655	C595
C1504	A1504	G1382	A1322	A1262	G1202	U1141	A1080	U1019	C957	A896	G836	G776	A716	G656	U596
A1505	U1505	A1383	C1323	U1263	U1203	A1142	U1081	A1021	U958	C897	C837	G777	C717	U657	G597
C1506	G1506	A1384	G1324	A1264	A1204	A1143	U1082	A1021	A959	C898	C838	G778	A718	U658	U598
U1507	C1507	A1385	U1325	A1265	A1205	A1144	U1083	G1022	A960	A899	U839	U779	C719	G659	A599
G1508	U1508	C1386	U1326	G1266	G1206	C1145	A1084	U1023	C961	A900	C840	G780	U720	C660	G600
A1509	U1509	A1387	A1327	U1267	C1207	C1146	A1085	G1043	G962	C901	G841	A781	A721	A661	C601
A1572	G1510	G1388	A1328	A1268	C1208	A1147	A1086	G1025	U963	C902	U842	A782	A722	G662	A602

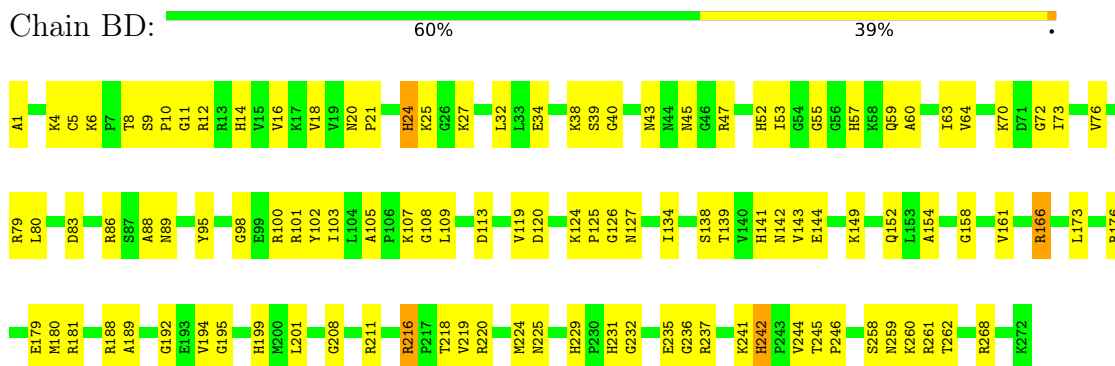
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U2419	C2420	G2421	G2422	G2423	G2424	G2425	G2426	G2427	G2428	G2429	G2430	G2431	G2432	G2433	G2434	G2435	G2436	G2437	G2438	G2439	G2440	G2441	G2442	G2443	G2444	G2445	G2446	G2447	G2448	G2449	G2450	G2451	G2452	G2453	G2454	G2455	G2456	G2457	G2458	G2459	G2460	G2461	G2462	G2463	G2464	G2465	G2466	G2467		G2470	G2471	G2472	G2473	G2474	G2475	G2476	G2477	G2478	G2479			
C2359	G2360	G2361	G2362	G2363	G2364	G2365	G2366	G2367	G2368	G2369	G2370	G2371	G2372	G2373	G2374	G2375	G2376	G2377	G2378	G2379	G2380	G2381	G2382	G2383	G2384	G2385	G2386	G2387	G2388	G2389	G2390	G2391	G2392	G2393	G2394	G2395	G2396	G2397	G2398	G2399	G2400	G2401	G2402	G2403	G2404	G2405	G2406	G2407	G2408	G2409	G2410	G2411	G2412	G2413	G2414	G2415	G2416	G2417	G2418			
U2299	C2300	C2301	C2302	G2303	G2304	U2305	C2306	G2307	G2308	G2309	G2310	G2311	U2312	G2313	G2314	G2315	G2316	G2317	G2318	G2319	U2320	G2321	U2322	G2323	G2324	G2325	G2326	G2327	G2328	G2329	G2330	G2331	G2332	G2333	G2334	G2335	G2336	G2337	G2338	G2339	G2340	G2341	G2342	U2343	U2344	G2345	G2346	G2347	G2348	G2349	G2350	G2351	G2352	G2353	G2354	G2355	G2356	G2357	G2358	G2359	G2360	
G2239	U2240	A2241	G2242	U2243	U2244	U2245	G2246	A2247	G2248	C2249	G2250	G2251	G2252	G2253	G2254	G2255	G2256	U2257	G2258	G2259	G2260	G2261	U2262	G2263	G2264	U2265	G2266	A2267	G2268	G2269	G2270	G2271	G2272	A2273	A2274	G2275	G2276	G2277	A2278	G2279	G2280	G2281	G2282	G2283	G2284	G2285	G2286	A2287	G2288	G2289	G2290	G2291	G2292	G2293	G2294	G2295	U2296	A2297	G2298	A2299		
C2179	U2180	U2181	U2182	G2183	G2184	U2185	G2186	G2187	U2188	U2189	G2190	G2191	U2192	G2193	U2194	U2195	G2196	U2197	G2198	G2199	G2200	G2201	G2202	G2203	G2204	U2205	G2206	G2207	G2208	G2209	G2210	G2211	G2212	G2213	G2214	G2215	G2216	G2217	G2218	U2219	U2220	G2221	G2222	G2223	G2224	A2225	G2226	A2227	G2228	G2229	G2230	U2231	G2232	G2233	G2234	G2235	G2236	G2237	G2238			
A2059	G2060	G2061	A2062	G2063	G2064	G2065	G2066	G2067	U2068	G2069	G2070	A2071	G2072	G2073	G2074	U2075	G2076	A2077	G2078	G2079	A2080	U2081	G2082	G2083	G2084	U2085	G2086	G2087	G2088	G2089	G2090	G2091	G2092	G2093	G2094	A2095	G2096	A2097	U2098	U2099	G2100	G2101	G2102	G2103	G2104	U2105	U2106	G2107	G2108	U2109	U2110	U2111	G2112	G2113	G2114	G2115	U2116	G2117	G2118			
A2119	G2120	G2121	U2122	G2123	G2124	G2125	G2126	G2127	G2128	G2129	U2130	U2131	U2132	G2133	G2134	G2135	G2136	U2137	G2138	G2139	G2140	G2141	G2142	G2143	G2144	G2145	G2146	G2147	G2148	U2149	G2150	U2151	G2152	G2153	G2154	U2155	G2156	G2157	A2158	G2159	G2160	G2161	G2162	A2163	G2164	G2165	U2166	G2167	G2168	A2169	G2170	G2171	U2172	G2173	G2174	G2175	A2176	G2177	G2178			
C2199	G2000	C2001	C2002	G2003	G2004	G2005	G2006	U2007	G2008	G2009	G2010	U2011	G2012	A2013	G2014	U2015	U2016	U2017	G2018	A2019	G2020	C2021	U2022	G2023	G2024	U2025	U2026	G2027	G2028	G2029	A2030	A2031	G2032	G2033	U2034	G2035	G2036	A2037	G2038	U2039	G2040	U2041	G2042	C2043	G2044	G2045	G2046	G2047	G2048	G2049	U2050	A2051	G2052	G2053	G2054	G2055	G2056	A2058				
U1939	U1940	C1941	C1942	U1943	U1944	G1945	U1946	U1947	G1948	G1949	G1950	U1951	G1952	A1953	G1954	U1955	U1956	G1957	C1958	G1959	A1960	C1961	G1962	U1963	G1964	U1965	U1966	G1967	G1968	U1969	A1970	C1971	G1972	G1973	C1974	G1975	U1976	A1977	U1978	U1979	G1980	G1981	U1982	G1983	C1984	G1985	G1986	G1987	U1988	G1989	U1990	U1991	G1992	G1993	G1994	U1995	G1996	C1997	A1998			
A1876	A1877	U1878	U1879	U1880	G1881	U1882	G1883	U1884	U1885	U1886	U1887	U1888	U1889	U1890	U1891	U1892	U1893	U1894	U1895	U1896	U1897	U1898	U1899	U1900	U1901	U1902	U1903	U1904	U1905	U1906	U1907	U1908	U1909	U1910	U1911	U1912	U1913	U1914	U1915	U1916	U1917	U1918	U1919	U1920	U1921	U1922	U1923	U1924	U1925	U1926	U1927	U1928	U1929	U1930	U1931	U1932	U1933	U1934	U1935	U1936	U1937	U1938
C1816	G1817	U1818	U1819	U1820	U1821	C1822	G1823	G1824	U1825	U1826	U1827	G1828	A1829	C1830	G1831	C1832	C1833	U1834	G1835	C1836	U1837	G1838	G1839	G1840	U1841	G1842	U1843	U1844	G1845	G1846	U1847	U1848	U1849	C1850	G1851	U1852	U1853	U1854	U1855	U1856	G1857	U1858	G1859	G1860	G1861	G1862	G1863	U1864	U1865	A1866	G1867	U1868	U1869	U1870	U1871	U1872	U1873	U1874	U1875			
A1754	A1755	G1756	A1757	U1758	U1759	C1760	C1761	A1762	G1763	G1764	U1765	G1766	G1767	U1768	U1769	U1770	U1771	A1772	U1773	C1774	U1775	U1776	U1777	U1778	U1779	U1780	U1781	U1782	U1783	U1784	U1785	U1786	U1787	U1788	U1789	C1790	U1791	U1792	C1793	U1794	U1795	U1796	U1797	U1798	U1799	U1800	A1801	A1802	A1803	U1804	U1805	G1806	G1807	U1808	U1809	U1810	U1811	U1812	U1813	U1814	U1815	
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A1634	A1635	U1636	U1637	U1638	U1639	U1640	U1641	U1642	G1643	C1644	U1645	U1646	U1647	U1648	U1649	U1650	U1651	U1652	U1653	U1654	U1655	U1656	U1657	U1658	U1659	U1660	U1661	U1662	U1663	U1664	U1665	U1666	U1667	U1668	U1669	U1670	U1671	U1672	U1673	U1674	U1675	U1676	U1677	U1678	U1679	U1680	U1681	U1682	U1683	U1684	U1685	U1686	U1687	U1688	U1689	U1690	U1691	U1692	U1693			
G1573	C1574	U1575	U1576	U1577	U1578	U1579	U1580	U1581	C1582	U1583	U1584	U1585	U1586	U1587	U1588	U1589	U1590	U1591	U1592	U1593	U1594	U1595	U1596	U1597	U1598	U1599	U1600	U1601	U1602	U1603	U1604	U1605	U1606	U1607	U1608	U1609	U1610	U1611	U1612	U1613	U1614	U1615	U1616	U1617	U1618	U1619	U1620	U1621	U1622	U1623	U1624	U1625	U1626	U1627	U1628	U1629	U1630	U1631	U1632	U1633		



• Molecule 27: 50S ribosomal protein L1

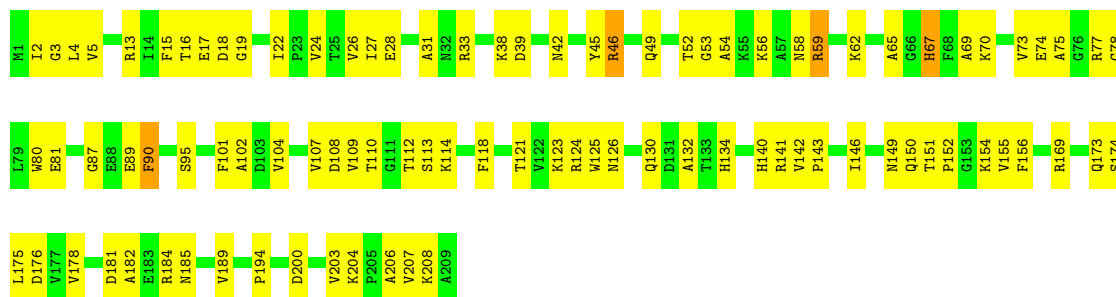


• Molecule 28: 50S ribosomal protein L2



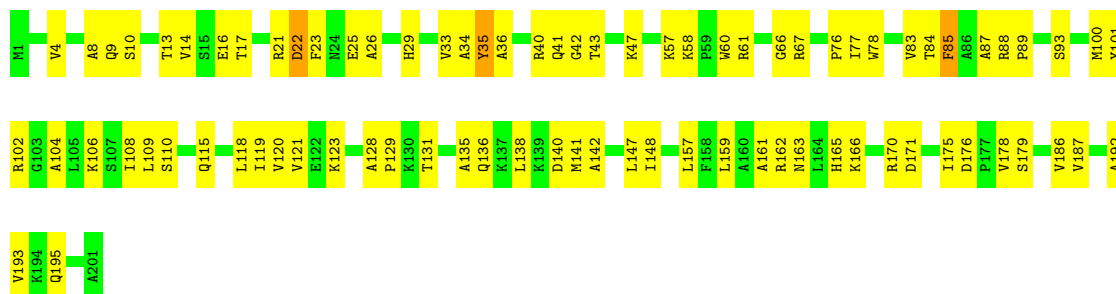
• Molecule 29: 50S ribosomal protein L3

Chain BE:  55% 43%



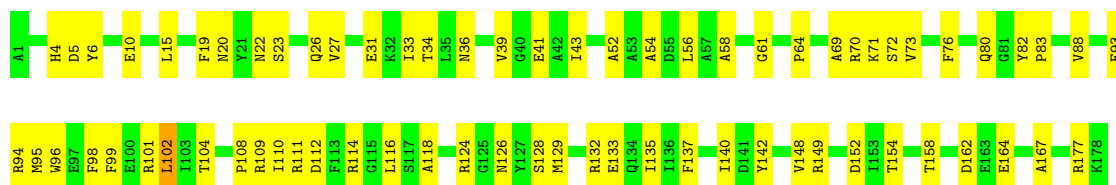
• Molecule 30: 50S ribosomal protein L4

Chain BF:  59% 39%



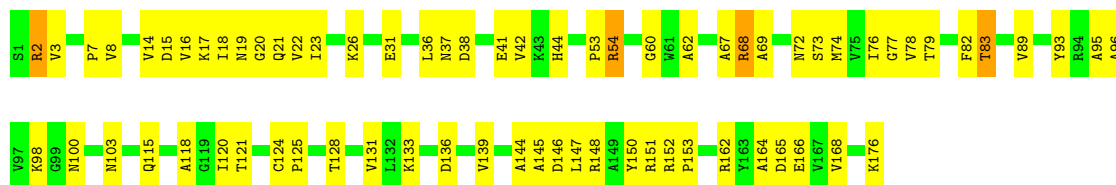
• Molecule 31: 50S ribosomal protein L5

Chain BG:  61% 39%



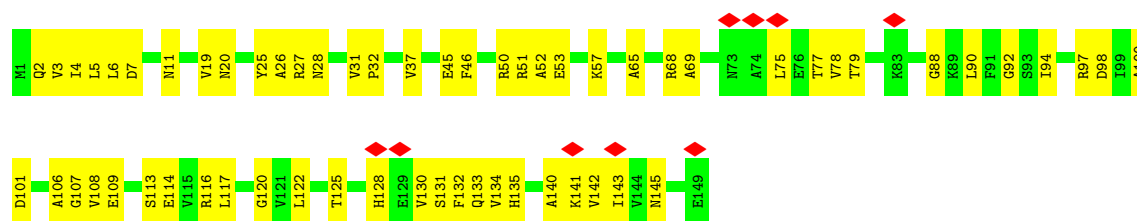
• Molecule 32: 50S ribosomal protein L6

Chain BH:  60% 38%



• Molecule 33: 50S ribosomal protein L9

Chain BI:  6% 59% 41%



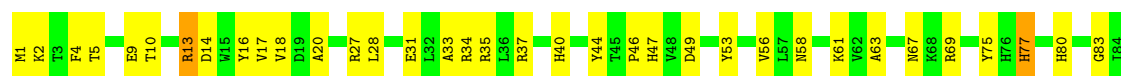
• Molecule 34: 50S ribosomal protein L10



• Molecule 35: 50S ribosomal protein L11



• Molecule 36: 50S ribosomal protein L13



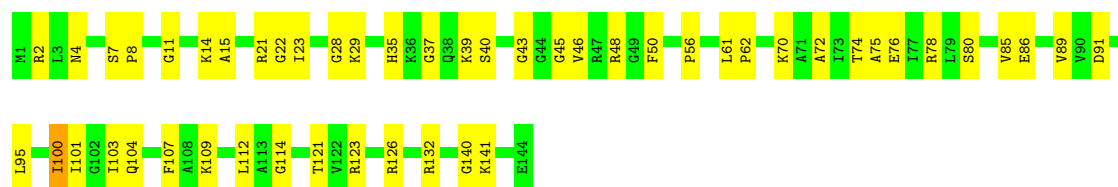
• Molecule 37: 50S ribosomal protein L14



• Molecule 38: 50S ribosomal protein L15



Chain BN:  65% 34%



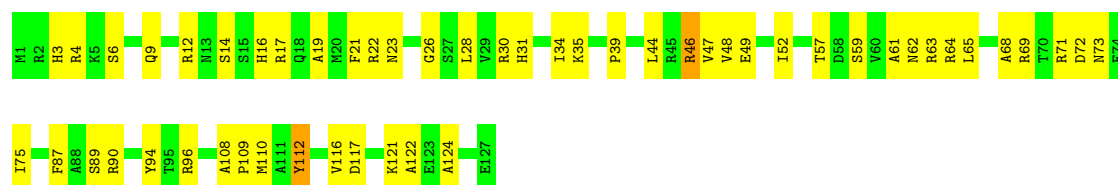
- Molecule 39: 50S ribosomal protein L16

Chain BO:  63% 36%



- Molecule 40: 50S ribosomal protein L17

Chain BP:  59% 39%



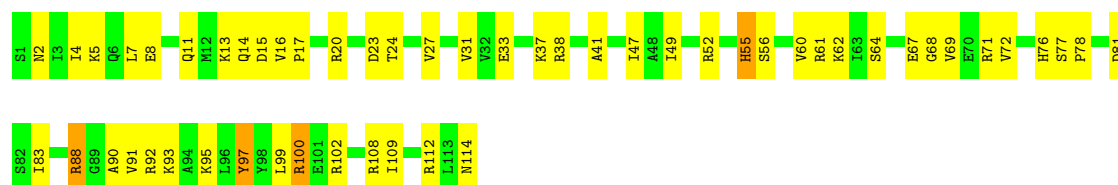
- Molecule 41: 50S ribosomal protein L18

Chain BQ:  53% 47%



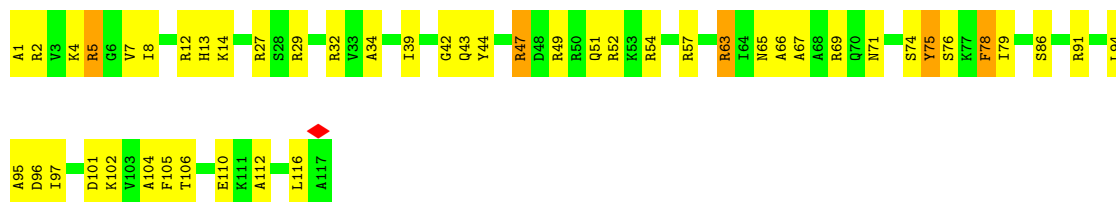
- Molecule 42: 50S ribosomal protein L19

Chain BR:  54% 43%



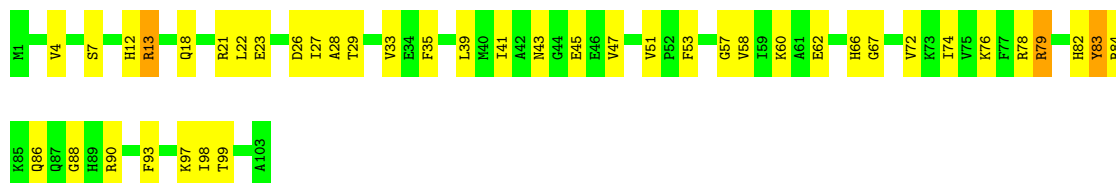
- Molecule 43: 50S ribosomal protein L20

Chain BS:  59% 37%



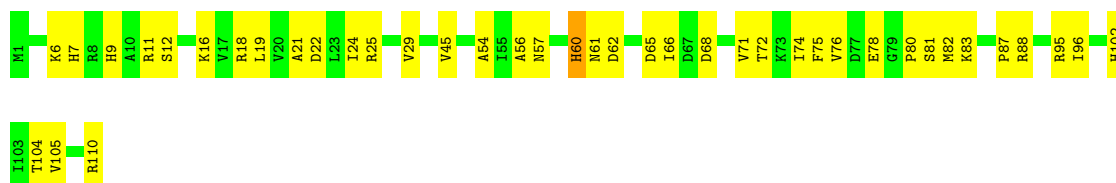
- Molecule 44: 50S ribosomal protein L21

Chain BT:  59% 38%



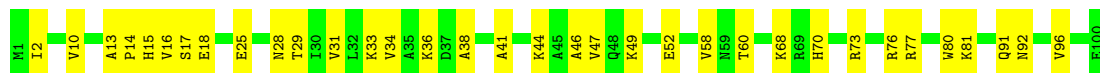
- Molecule 45: 50S ribosomal protein L22

Chain BU:  63% 36%



- Molecule 46: 50S ribosomal protein L23

Chain BV:  66% 34%



- Molecule 47: 50S ribosomal protein L24

Chain BW:  58% 42%



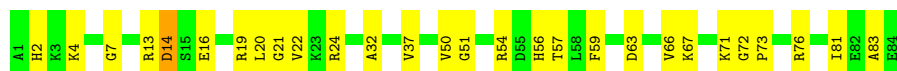
- Molecule 48: 50S ribosomal protein L25

Chain BX:  60% 39%



- Molecule 49: 50S ribosomal protein L27

Chain BY: 67% 32%



- Molecule 50: 50S ribosomal protein L28

Chain BZ: 58% 40%



- Molecule 51: 50S ribosomal protein L29

Chain B0: 60% 38%



- Molecule 52: 50S ribosomal protein L30

Chain B1: 57% 43%



- Molecule 53: 50S ribosomal protein L31

Chain B2: 59% 36% 6%



- Molecule 54: 50S ribosomal protein L32

Chain B3: 55% 41%



- Molecule 55: 50S ribosomal protein L33

Chain B4:  52% 44% .



- Molecule 56: 50S ribosomal protein L34

Chain B5:  52% 46% .



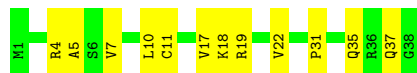
- Molecule 57: 50S ribosomal protein L35

Chain B6:  61% 38% .



- Molecule 58: 50S ribosomal protein L36

Chain B7:  68% 32% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	37000	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	1.575	Depositor
Minimum map value	-0.492	Depositor
Average map value	0.029	Depositor
Map value standard deviation	0.204	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: 2MA, 2MG, MIA, 7MG, OMC, H2U, MA6, OMG, OMU, 3TD, PSU, 5MC, 1MG, 5MU, FME, 4OC, CH, UR3, 4SU, 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	1.89	582/36769 (1.6%)	2.00	1927/57354 (3.4%)
2	AB	1.97	35/1600 (2.2%)	1.99	84/2492 (3.4%)
3	AC	1.94	18/1108 (1.6%)	2.01	59/1724 (3.4%)
4	AD	1.92	29/1721 (1.7%)	1.97	98/2683 (3.7%)
5	AE	2.03	41/1904 (2.2%)	2.46	131/2565 (5.1%)
6	AF	2.03	35/1852 (1.9%)	2.42	110/2490 (4.4%)
7	AG	1.92	27/1665 (1.6%)	2.32	82/2227 (3.7%)
8	AH	2.05	27/1239 (2.2%)	2.37	70/1664 (4.2%)
9	AI	2.01	23/1121 (2.1%)	2.44	68/1509 (4.5%)
10	AJ	1.95	25/1422 (1.8%)	2.38	83/1908 (4.4%)
11	AK	1.99	18/989 (1.8%)	2.28	41/1326 (3.1%)
12	AL	1.96	26/1048 (2.5%)	2.40	61/1394 (4.4%)
13	AM	2.04	18/835 (2.2%)	2.42	48/1127 (4.3%)
14	AN	2.10	26/982 (2.6%)	2.42	56/1323 (4.2%)
15	AO	2.01	16/969 (1.7%)	2.33	51/1300 (3.9%)
16	AP	2.10	22/919 (2.4%)	2.45	62/1226 (5.1%)
17	AQ	2.05	22/817 (2.7%)	2.37	60/1088 (5.5%)
18	AR	1.97	13/724 (1.8%)	2.50	52/966 (5.4%)
19	AS	1.97	12/659 (1.8%)	2.33	30/884 (3.4%)
20	AT	2.09	17/681 (2.5%)	2.32	35/913 (3.8%)
21	AU	2.00	12/637 (1.9%)	2.30	25/851 (2.9%)
22	AV	1.97	10/744 (1.3%)	2.51	57/995 (5.7%)
23	AW	2.08	20/676 (3.0%)	2.55	52/895 (5.8%)
24	AX	1.98	11/598 (1.8%)	2.46	45/792 (5.7%)
25	BA	1.88	50/2869 (1.7%)	1.95	142/4474 (3.2%)
26	BB	1.90	1137/69257 (1.6%)	1.98	3500/108040 (3.2%)
27	BC	2.00	35/1748 (2.0%)	2.35	95/2355 (4.0%)
28	BD	2.02	47/2131 (2.2%)	2.43	130/2863 (4.5%)
29	BE	2.09	31/1586 (2.0%)	2.44	107/2134 (5.0%)
30	BF	2.04	35/1571 (2.2%)	2.36	91/2113 (4.3%)
31	BG	1.95	25/1444 (1.7%)	2.33	76/1937 (3.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	BH	2.05	34/1343 (2.5%)	2.39	71/1816 (3.9%)
33	BI	2.03	30/1122 (2.7%)	2.34	56/1515 (3.7%)
34	BJ	2.05	28/1247 (2.2%)	2.38	66/1679 (3.9%)
35	BK	1.98	21/1046 (2.0%)	2.42	72/1410 (5.1%)
36	BL	2.03	26/1152 (2.3%)	2.33	59/1551 (3.8%)
37	BM	2.01	17/956 (1.8%)	2.43	60/1279 (4.7%)
38	BN	2.03	26/1062 (2.4%)	2.38	50/1413 (3.5%)
39	BO	1.91	17/1093 (1.6%)	2.40	58/1460 (4.0%)
40	BP	1.98	19/1021 (1.9%)	2.41	64/1364 (4.7%)
41	BQ	2.12	23/910 (2.5%)	2.42	71/1219 (5.8%)
42	BR	1.98	15/929 (1.6%)	2.47	66/1242 (5.3%)
43	BS	1.97	13/960 (1.4%)	2.52	70/1278 (5.5%)
44	BT	2.12	25/829 (3.0%)	2.29	39/1107 (3.5%)
45	BU	2.00	21/864 (2.4%)	2.42	38/1156 (3.3%)
46	BV	2.02	17/794 (2.1%)	2.38	41/1060 (3.9%)
47	BW	2.06	22/797 (2.8%)	2.36	44/1062 (4.1%)
48	BX	1.89	10/766 (1.3%)	2.36	39/1025 (3.8%)
49	BY	1.96	11/642 (1.7%)	2.32	28/848 (3.3%)
50	BZ	2.01	14/635 (2.2%)	2.37	40/848 (4.7%)
51	B0	1.94	8/510 (1.6%)	2.47	38/677 (5.6%)
52	B1	2.04	7/453 (1.5%)	2.60	37/605 (6.1%)
53	B2	2.10	15/559 (2.7%)	2.38	29/745 (3.9%)
54	B3	2.11	10/450 (2.2%)	2.42	24/599 (4.0%)
55	B4	1.91	10/448 (2.2%)	2.27	26/594 (4.4%)
56	B5	1.96	5/380 (1.3%)	2.55	25/498 (5.0%)
57	B6	1.99	10/513 (1.9%)	2.32	26/676 (3.8%)
58	B7	1.88	1/303 (0.3%)	2.33	17/397 (4.3%)
All	All	1.94	2900/164069 (1.8%)	2.11	8782/244735 (3.6%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	910
2	AB	0	43
3	AC	0	30
4	AD	0	37
5	AE	0	1
6	AF	0	3
7	AG	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
8	AH	0	2
9	AI	0	5
10	AJ	0	6
11	AK	0	2
12	AL	0	3
13	AM	0	2
14	AN	0	4
15	AO	0	9
16	AP	0	4
17	AQ	0	1
18	AR	0	3
19	AS	0	3
20	AT	0	2
21	AU	0	5
22	AV	0	3
23	AW	0	2
24	AX	0	4
25	BA	0	65
26	BB	0	1685
27	BC	0	1
28	BD	0	10
29	BE	0	8
30	BF	0	6
31	BG	0	7
32	BH	0	6
33	BI	0	3
34	BJ	0	4
35	BK	0	5
36	BL	0	8
37	BM	0	4
38	BN	0	2
39	BO	0	4
40	BP	0	2
41	BQ	0	2
42	BR	0	5
43	BS	0	6
44	BT	0	3
45	BU	0	1
46	BV	0	2
47	BW	0	1
48	BX	0	5
49	BY	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
50	BZ	0	1
51	B0	0	1
53	B2	0	5
54	B3	0	4
55	B4	0	3
56	B5	0	2
57	B6	0	1
All	All	0	2959

The worst 5 of 2900 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	BB	2552	OMU	O3'-P	14.21	1.70	1.56
1	AA	1457	G	O3'-P	10.76	1.77	1.61
52	B1	30	ARG	NE-CZ	10.56	1.44	1.33
32	BH	93	TYR	CA-C	10.32	1.66	1.53
28	BD	18	VAL	CA-C	-10.21	1.40	1.52

The worst 5 of 8782 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BB	1452	G	O4'-C4'-C3'	14.11	118.11	104.00
13	AM	95	GLY	CA-C-O	-13.30	107.05	120.75
7	AG	164	ARG	NE-CZ-NH2	-13.06	107.44	119.20
1	AA	1201	A	C2'-C3'-O3'	13.00	129.00	109.50
21	AU	62	ARG	NE-CZ-NH2	12.72	130.65	119.20

There are no chirality outliers.

5 of 2959 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1	A	Sidechain
1	AA	2	A	Sidechain
1	AA	3	A	Sidechain
1	AA	5	U	Sidechain
1	AA	6	G	Sidechain

5.2 Too-close contacts [i](#)

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	16599	0	0
2	AB	1627	0	841	0	0
3	AC	993	0	498	0	0
4	AD	1641	0	839	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	1294	0	0
26	BB	62351	0	31277	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	BR	917	0	965	0	0
43	BS	947	0	1022	0	0
44	BT	816	0	839	0	0
45	BU	857	0	922	0	0
46	BV	787	0	846	0	0
47	BW	789	0	847	0	0
48	BX	753	0	780	0	0
49	BY	634	0	656	0	0
50	BZ	625	0	655	0	0
51	B0	509	0	543	0	0
52	B1	449	0	491	0	0
53	B2	549	0	552	0	0
54	B3	444	0	461	0	0
55	B4	441	0	485	0	0
56	B5	377	0	418	0	0
57	B6	504	0	574	0	0
58	B7	302	0	343	0	0
59	AB	14	0	9	0	0
60	BB	10	0	10	0	0
All	All	152351	0	103803	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](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1541/1542 (99%)	307 (19%)	100 (6%)
2	AB	75/76 (98%)	24 (32%)	7 (9%)
25	BA	119/120 (99%)	20 (16%)	0
26	BB	2901/2904 (99%)	553 (19%)	145 (4%)
3	AC	46/47 (97%)	25 (54%)	12 (26%)
4	AD	76/77 (98%)	10 (13%)	5 (6%)
All	All	4758/4766 (99%)	939 (19%)	269 (5%)

5 of 939 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	3	A
1	AA	4	U
1	AA	5	U
1	AA	6	G
1	AA	7	A

5 of 269 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	BB	2118	U
26	BB	2282	G
26	BB	2791	G
1	AA	1491	G
1	AA	1347	G

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
26	2MG	BB	2445	26	23,26,27	1.12	3 (13%)	33,38,41	1.03	0
2	H2U	AB	17	2	18,21,22	1.38	1 (5%)	19,30,33	1.62	3 (15%)
26	1MG	BB	745	26	23,26,27	1.48	4 (17%)	33,39,42	2.11	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
26	6MZ	BB	1618	26	22,25,26	1.61	6 (27%)	29,36,39	1.70	7 (24%)
1	4OC	AA	1402	1	20,23,24	1.58	6 (30%)	25,32,35	1.86	9 (36%)
1	7MG	AA	527	1	23,26,27	5.44	6 (26%)	27,39,42	1.93	6 (22%)
26	PSU	BB	1911	26	18,21,22	1.95	5 (27%)	21,30,33	1.31	3 (14%)
26	7MG	BB	2069	26	23,26,27	3.56	4 (17%)	27,39,42	1.78	5 (18%)
1	2MG	AA	1207	1	23,26,27	1.48	5 (21%)	33,38,41	1.78	7 (21%)
1	PSU	AA	516	1	18,21,22	1.97	4 (22%)	21,30,33	1.40	4 (19%)
1	UR3	AA	1498	1	19,22,23	1.02	1 (5%)	26,32,35	1.46	5 (19%)
26	OMC	BB	2498	26	19,22,23	1.32	3 (15%)	25,31,34	1.12	2 (8%)
1	MA6	AA	1518	1	23,26,27	1.49	6 (26%)	33,38,41	2.01	8 (24%)
1	5MC	AA	967	1	19,22,23	1.53	3 (15%)	26,32,35	2.12	10 (38%)
2	5MU	AB	54	2	19,22,23	1.69	5 (26%)	27,32,35	1.86	7 (25%)
1	2MG	AA	1516	1	23,26,27	1.01	0	33,38,41	1.33	2 (6%)
2	OMC	AB	32	2	19,22,23	1.25	2 (10%)	25,31,34	1.97	7 (28%)
4	PSU	AD	56	4	18,21,22	1.92	3 (16%)	21,30,33	2.30	6 (28%)
26	5MC	BB	1962	26	19,22,23	1.54	4 (21%)	26,32,35	2.04	6 (23%)
26	CH	BB	2575	26	16,21,22	1.56	3 (18%)	19,30,33	1.53	4 (21%)
2	7MG	AB	46	2	23,26,27	4.80	7 (30%)	27,39,42	1.87	2 (7%)
2	4SU	AB	8	2	18,21,22	1.74	3 (16%)	25,30,33	1.59	5 (20%)
26	PSU	BB	1917	26	18,21,22	2.05	8 (44%)	21,30,33	2.68	9 (42%)
1	2MG	AA	966	1	23,26,27	1.30	4 (17%)	33,38,41	1.64	8 (24%)
2	PSU	AB	55	2	18,21,22	1.33	1 (5%)	21,30,33	1.84	7 (33%)
2	H2U	AB	16	2	18,21,22	1.57	4 (22%)	19,30,33	1.28	3 (15%)
2	H2U	AB	20	2	18,21,22	1.23	2 (11%)	19,30,33	1.37	3 (15%)
26	PSU	BB	746	26	18,21,22	1.80	5 (27%)	21,30,33	1.67	5 (23%)
4	H2U	AD	21	4	18,21,22	1.77	4 (22%)	19,30,33	1.90	5 (26%)
26	3TD	BB	1915	26	19,22,23	1.50	2 (10%)	23,32,35	1.95	5 (21%)
26	H2U	BB	2449	26	18,21,22	1.33	2 (11%)	19,30,33	1.61	3 (15%)
26	OMU	BB	2552	26	19,22,23	1.23	1 (5%)	25,31,34	2.14	11 (44%)
26	2MG	BB	1835	26	23,26,27	1.41	6 (26%)	33,38,41	1.42	4 (12%)
26	OMG	BB	2251	26	23,26,27	1.20	2 (8%)	32,38,41	1.51	8 (25%)
26	2MA	BB	2503	26	22,25,26	1.41	5 (22%)	32,37,40	1.33	5 (15%)
26	PSU	BB	2457	26	18,21,22	1.55	5 (27%)	21,30,33	2.18	7 (33%)
26	5MU	BB	747	26	19,22,23	1.92	6 (31%)	27,32,35	2.00	6 (22%)
26	PSU	BB	2504	26	18,21,22	1.99	6 (33%)	21,30,33	2.12	7 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MA6	AA	1519	1	23,26,27	1.82	8 (34%)	33,38,41	1.71	8 (24%)
26	PSU	BB	2580	26	18,21,22	1.46	3 (16%)	21,30,33	1.44	4 (19%)
4	5MU	AD	55	4	19,22,23	1.61	5 (26%)	27,32,35	1.50	4 (14%)
4	OMC	AD	33	4	19,22,23	1.02	0	25,31,34	1.85	9 (36%)
2	MIA	AB	37	2	28,31,32	1.98	8 (28%)	38,44,47	2.44	7 (18%)
26	5MU	BB	1939	26	19,22,23	1.74	3 (15%)	27,32,35	1.79	4 (14%)
26	PSU	BB	2605	26	18,21,22	1.57	3 (16%)	21,30,33	1.38	2 (9%)
1	5MC	AA	1407	1	19,22,23	1.36	2 (10%)	26,32,35	2.12	8 (30%)
4	4SU	AD	8	4	18,21,22	2.05	3 (16%)	25,30,33	2.40	9 (36%)
26	PSU	BB	955	26	18,21,22	1.37	2 (11%)	21,30,33	2.02	6 (28%)
26	6MZ	BB	2030	26	22,25,26	1.57	3 (13%)	29,36,39	2.03	7 (24%)

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
26	2MG	BB	2445	26	-	0/9/27/28	0/3/3/3
2	H2U	AB	17	2	-	0/7/38/39	0/2/2/2
26	1MG	BB	745	26	-	0/7/25/26	0/3/3/3
26	6MZ	BB	1618	26	-	0/9/27/28	0/3/3/3
1	4OC	AA	1402	1	-	0/9/29/30	0/2/2/2
1	7MG	AA	527	1	-	1/7/37/38	0/3/3/3
26	PSU	BB	1911	26	-	1/7/25/26	0/2/2/2
26	7MG	BB	2069	26	-	0/7/37/38	0/3/3/3
1	2MG	AA	1207	1	-	0/9/27/28	0/3/3/3
1	PSU	AA	516	1	-	0/7/25/26	0/2/2/2
1	UR3	AA	1498	1	-	0/7/25/26	0/2/2/2
26	OMC	BB	2498	26	-	0/9/27/28	0/2/2/2
1	MA6	AA	1518	1	-	0/11/29/30	0/3/3/3
1	5MC	AA	967	1	-	3/7/25/26	0/2/2/2
2	5MU	AB	54	2	-	0/7/25/26	0/2/2/2
1	2MG	AA	1516	1	-	0/9/27/28	0/3/3/3
2	OMC	AB	32	2	-	2/9/27/28	0/2/2/2
4	PSU	AD	56	4	-	1/7/25/26	0/2/2/2
26	5MC	BB	1962	26	-	2/7/25/26	0/2/2/2
26	CH	BB	2575	26	-	0/5/25/26	0/2/2/2
2	7MG	AB	46	2	-	1/7/37/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	4SU	AB	8	2	-	5/7/25/26	0/2/2/2
26	PSU	BB	1917	26	-	2/7/25/26	0/2/2/2
1	2MG	AA	966	1	-	0/9/27/28	0/3/3/3
2	PSU	AB	55	2	-	2/7/25/26	0/2/2/2
2	H2U	AB	16	2	-	0/7/38/39	0/2/2/2
2	H2U	AB	20	2	-	0/7/38/39	0/2/2/2
26	PSU	BB	746	26	-	3/7/25/26	0/2/2/2
4	H2U	AD	21	4	-	2/7/38/39	0/2/2/2
26	3TD	BB	1915	26	-	1/7/25/26	0/2/2/2
26	H2U	BB	2449	26	-	0/7/38/39	0/2/2/2
26	OMU	BB	2552	26	-	1/9/27/28	0/2/2/2
26	2MG	BB	1835	26	-	1/9/27/28	0/3/3/3
26	OMG	BB	2251	26	-	0/9/27/28	0/3/3/3
26	2MA	BB	2503	26	-	2/7/25/26	0/3/3/3
26	PSU	BB	2457	26	-	0/7/25/26	0/2/2/2
26	5MU	BB	747	26	-	0/7/25/26	0/2/2/2
26	PSU	BB	2504	26	-	0/7/25/26	0/2/2/2
1	MA6	AA	1519	1	-	0/11/29/30	0/3/3/3
26	PSU	BB	2580	26	-	1/7/25/26	0/2/2/2
4	5MU	AD	55	4	-	0/7/25/26	0/2/2/2
4	OMC	AD	33	4	-	0/9/27/28	0/2/2/2
2	MIA	AB	37	2	-	1/15/33/34	0/3/3/3
26	5MU	BB	1939	26	-	0/7/25/26	0/2/2/2
26	PSU	BB	2605	26	-	1/7/25/26	0/2/2/2
1	5MC	AA	1407	1	-	0/7/25/26	0/2/2/2
4	4SU	AD	8	4	-	0/7/25/26	0/2/2/2
26	PSU	BB	955	26	-	0/7/25/26	0/2/2/2
26	6MZ	BB	2030	26	-	0/9/27/28	0/3/3/3

The worst 5 of 187 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	527	7MG	C8-N9	-25.10	1.29	1.45
2	AB	46	7MG	C8-N9	-21.49	1.31	1.45
26	BB	2069	7MG	C8-N9	-15.89	1.35	1.45
4	AD	8	4SU	C5-C4	-7.18	1.33	1.42
2	AB	8	4SU	C5-C4	-5.85	1.35	1.42

The worst 5 of 278 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AB	37	MIA	C11-S10-C2	11.74	111.06	102.25
26	BB	745	1MG	C2-N1-C6	7.91	127.59	120.99
2	AB	46	7MG	N9-C8-N7	7.72	114.30	103.37
1	AA	527	7MG	N9-C8-N7	7.14	113.48	103.37
26	BB	1917	PSU	C6-C5-C4	7.05	122.93	118.17

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AB	8	4SU	C2'-C1'-N1-C6
2	AB	32	OMC	O4'-C1'-N1-C2
2	AB	32	OMC	O4'-C1'-N1-C6
2	AB	37	MIA	C12-C13-C14-C16
2	AB	55	PSU	C2'-C1'-C5-C4

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
60	FME	BB	3001	59	8,9,10	0.98	0	8,9,11	2.38	4 (50%)
59	TRP	AB	101	2,60	15,15,16	1.70	2 (13%)	17,20,22	2.29	6 (35%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	FME	BB	3001	59	-	2/7/9/11	-
59	TRP	AB	101	2,60	-	2/6/6/8	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	AB	101	TRP	OXT-C	-4.76	1.22	1.42
59	AB	101	TRP	CD2-CE2	2.26	1.44	1.41

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	AB	101	TRP	CE2-NE1-CD1	5.23	113.73	109.08
59	AB	101	TRP	CD2-CE2-NE1	-5.20	103.18	107.52
60	BB	3001	FME	CA-N-CN	4.83	130.26	122.82
59	AB	101	TRP	CZ2-CE2-NE1	2.75	135.15	130.74
59	AB	101	TRP	CZ3-CH2-CZ2	-2.53	117.12	120.24

There are no chirality outliers.

All (4) torsion outliers are listed below:

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

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
1	AA	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	1457:G	O3'	1458:G	P	1.77

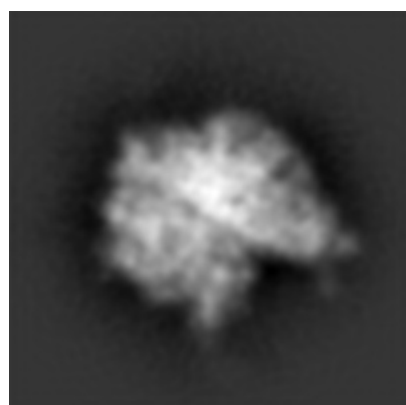
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5362. These allow visual inspection of the internal detail of the map and identification of artifacts.

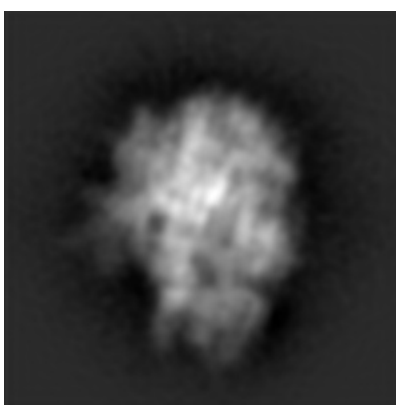
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

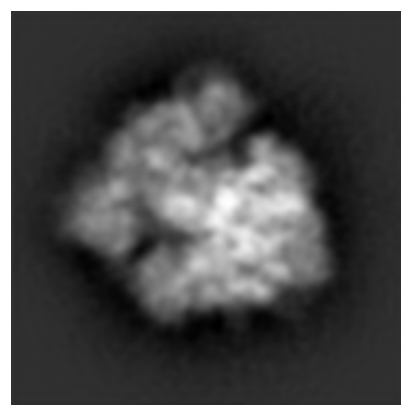
6.1.1 Primary map



X



Y

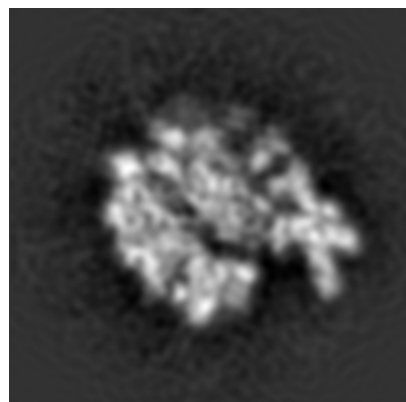


Z

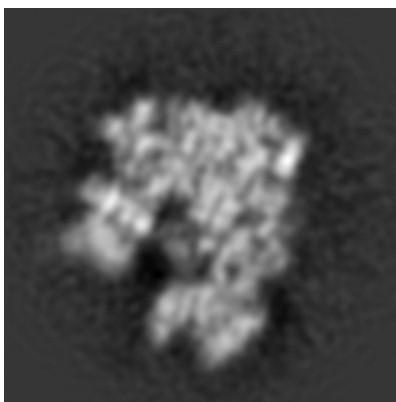
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

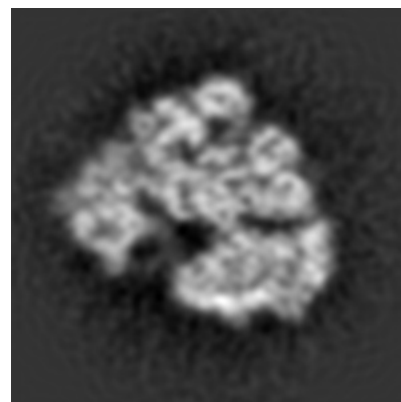
6.2.1 Primary map



X Index: 125



Y Index: 125

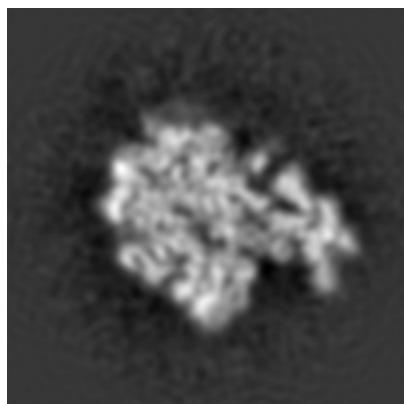


Z Index: 125

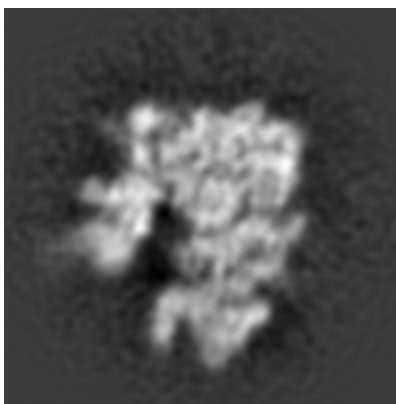
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

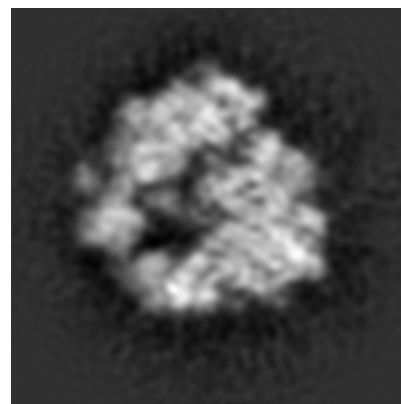
6.3.1 Primary map



X Index: 130



Y Index: 130

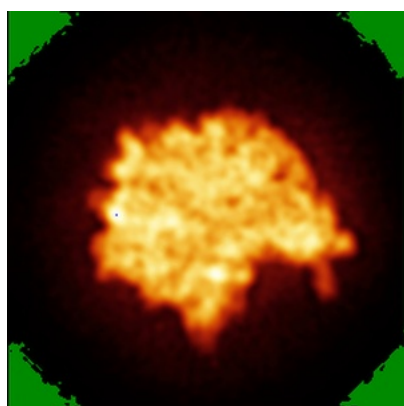


Z Index: 114

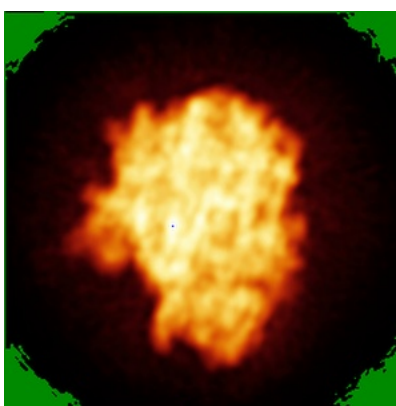
The images above show the largest variance slices of the map in three orthogonal directions.

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

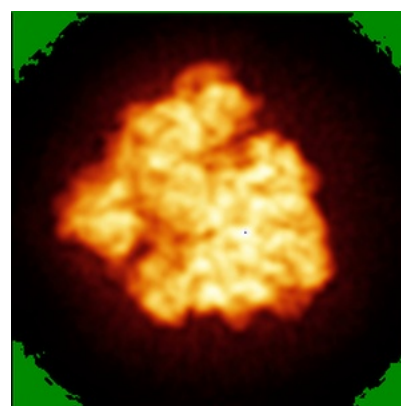
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

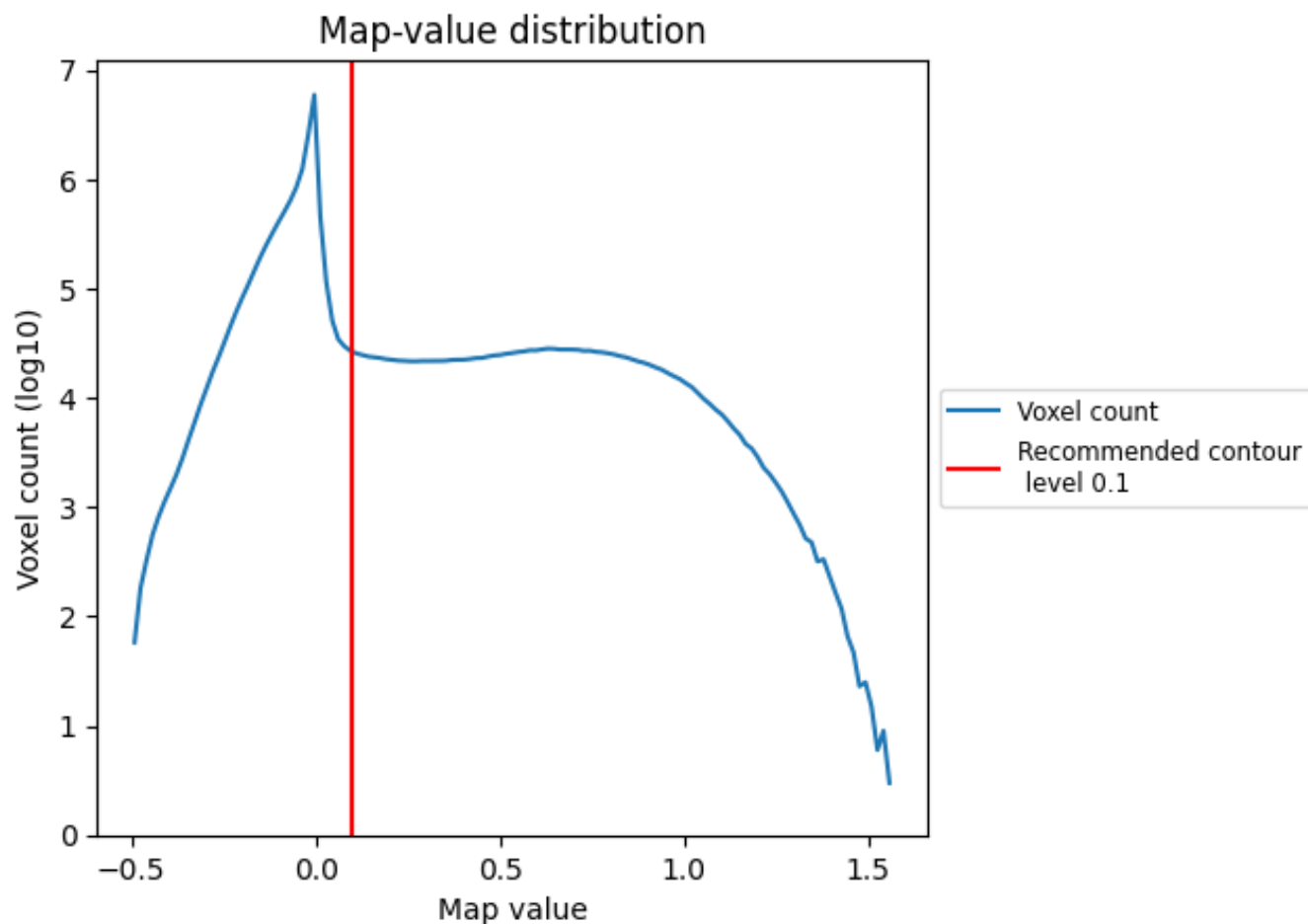
6.6 Mask visualisation

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

7 Map analysis [i](#)

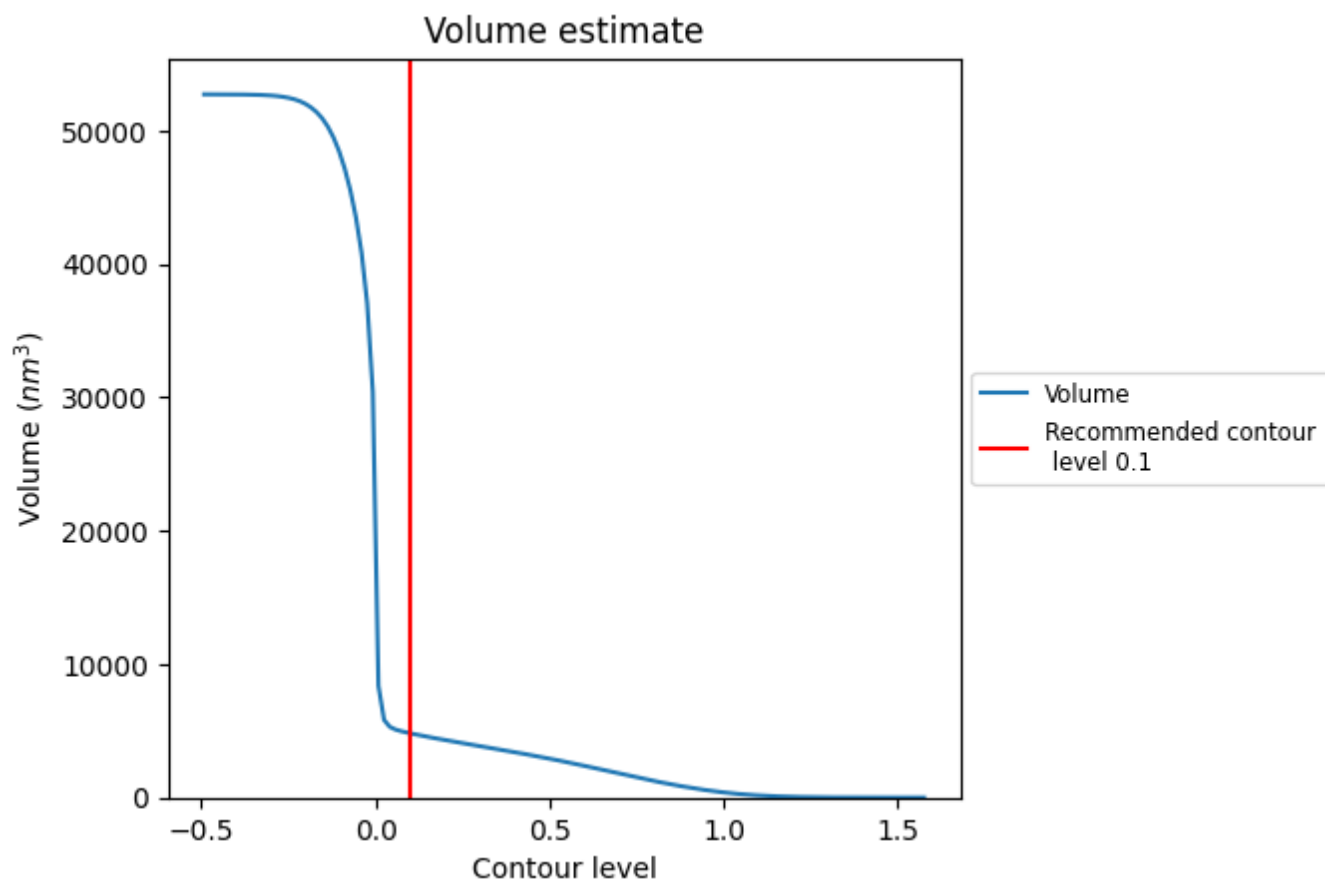
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

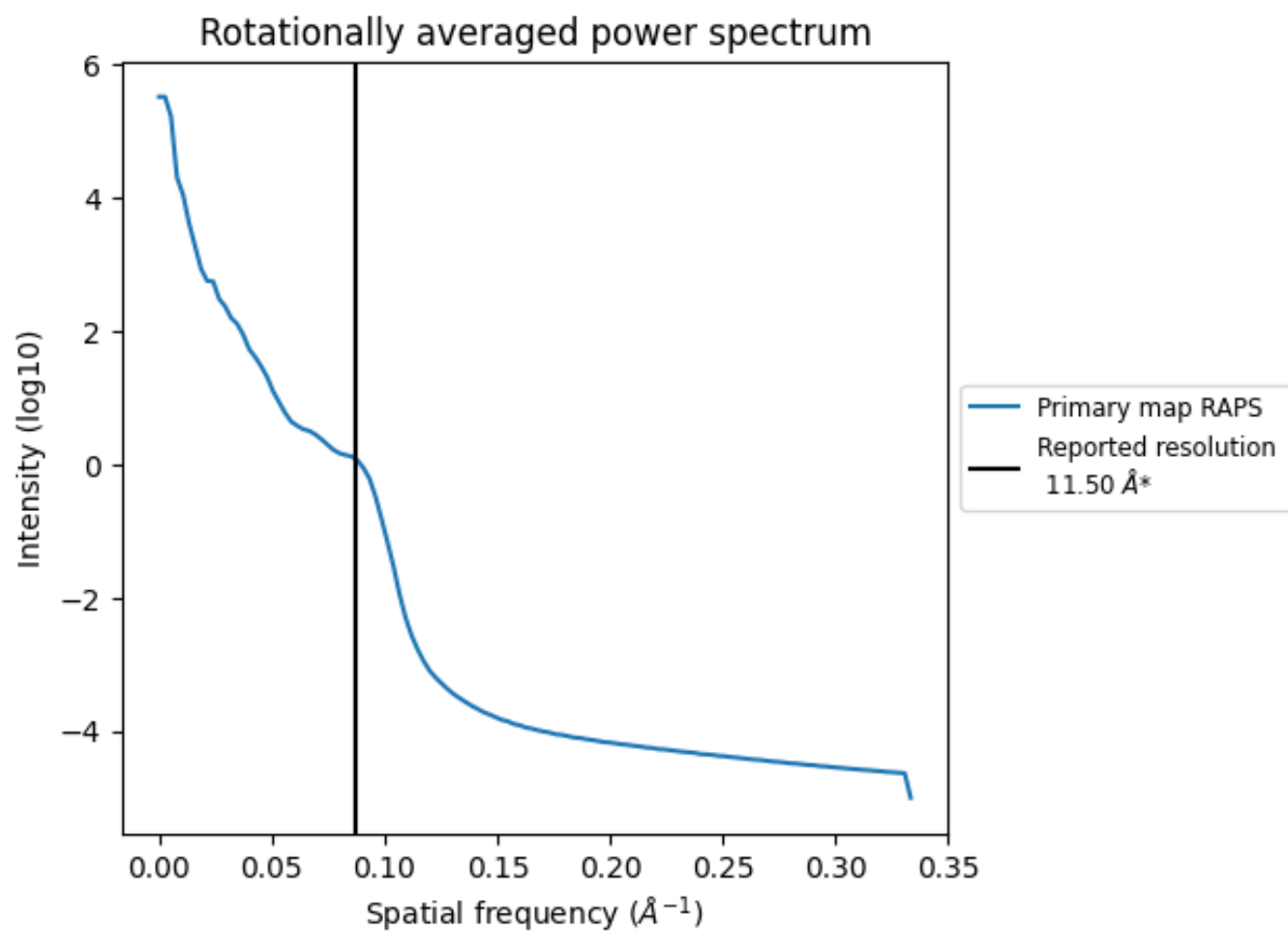
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4817 nm^3 ; this corresponds to an approximate mass of 4352 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 0.087 Å⁻¹

8 Fourier-Shell correlation

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

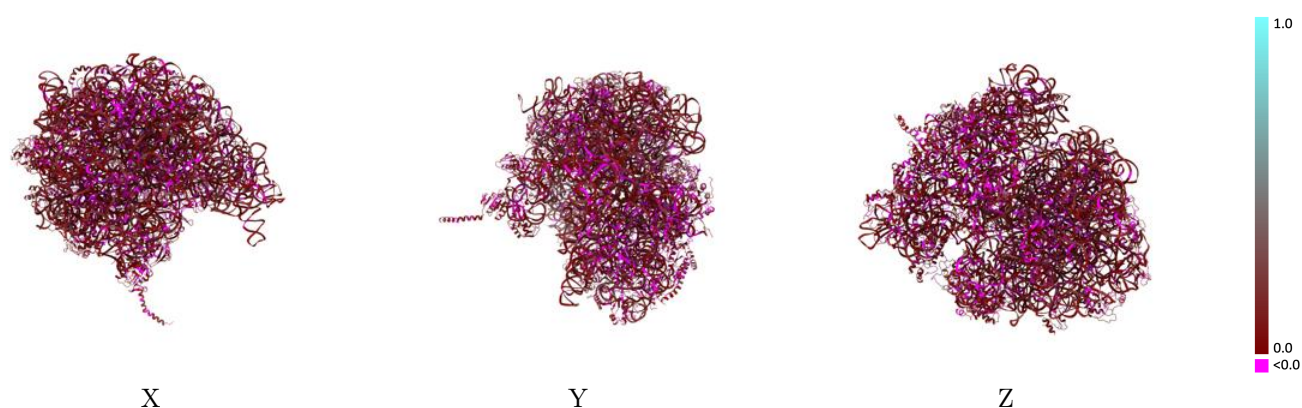
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5362 and PDB model 4V6R. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)

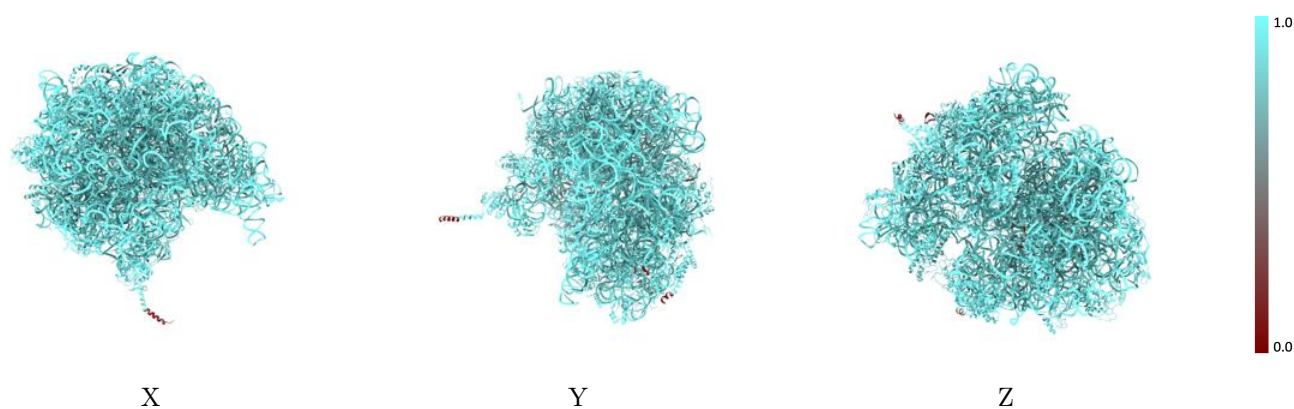
This section was not generated.

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



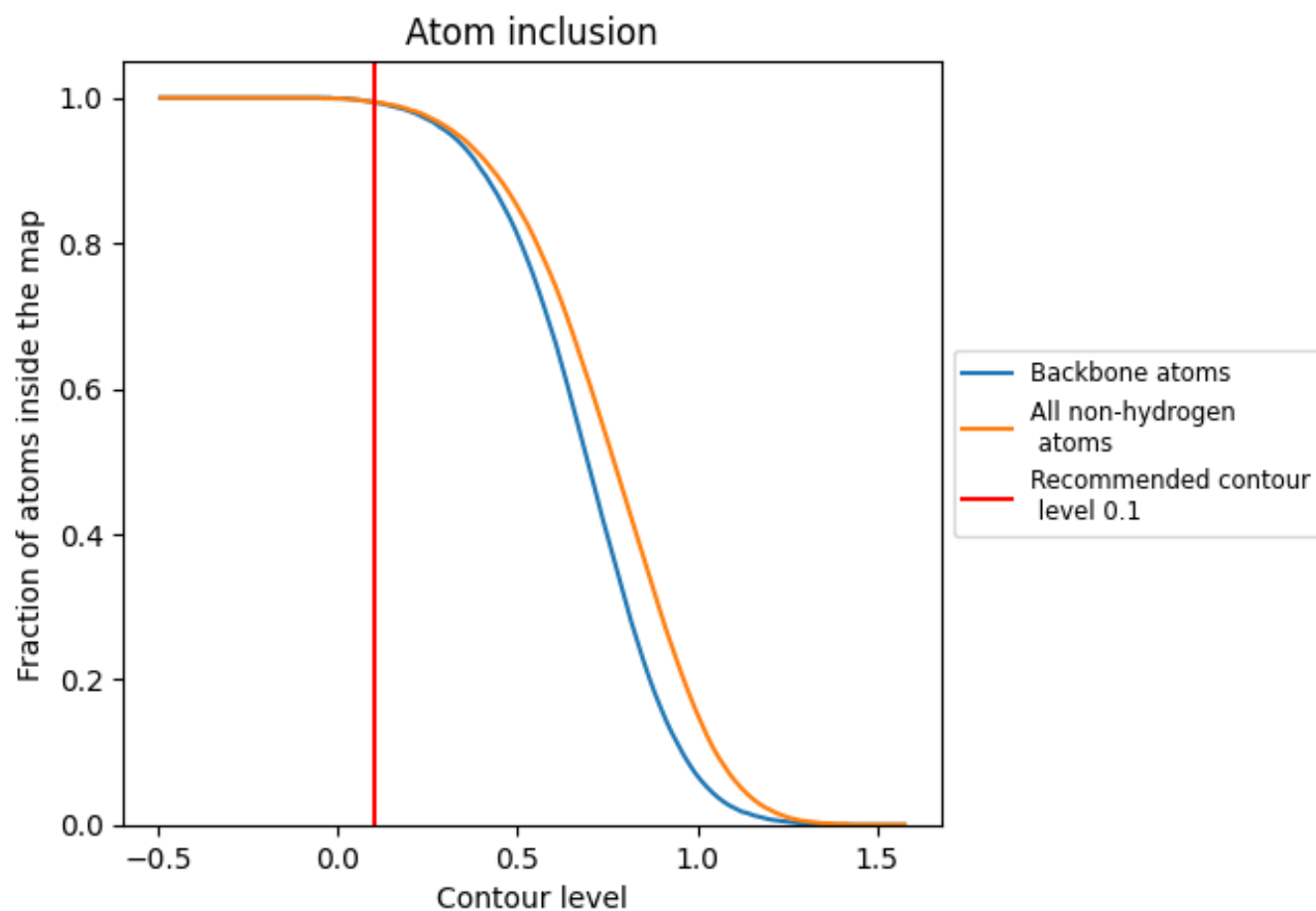
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	0.9940	0.0730
AA	0.9990	0.0890
AB	0.9640	0.0680
AC	0.8950	0.0140
AD	0.9890	0.0900
AE	0.9460	0.0440
AF	0.9980	0.0620
AG	1.0000	0.0410
AH	0.9790	0.0420
AI	0.9770	0.0440
AJ	0.9930	0.0580
AK	0.9960	0.0360
AL	0.9840	0.0480
AM	1.0000	0.0190
AN	0.9960	0.0410
AO	0.9850	0.0310
AP	0.9850	0.0460
AQ	0.9960	0.0380
AR	1.0000	0.0560
AS	1.0000	0.0230
AT	1.0000	0.0420
AU	1.0000	0.0380
AV	0.9610	0.0280
AW	1.0000	0.0430
AX	1.0000	0.0360
B0	1.0000	0.0200
B1	0.9980	0.0540
B2	0.9670	0.0250
B3	1.0000	0.0320
B4	1.0000	0.0530
B5	1.0000	-0.0070
B6	1.0000	-0.0070
B7	1.0000	0.0400
BA	1.0000	0.0990
BB	1.0000	0.0910



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Chain	Atom inclusion	Q-score
BC	 0.9690	 0.0360
BD	 1.0000	 0.0220
BE	 0.9970	 0.0200
BF	 0.9990	 0.0620
BG	 0.9950	 0.0600
BH	 0.9950	 0.0250
BI	 0.9100	 0.0260
BJ	 0.8810	 0.0570
BK	 0.9750	 0.0420
BL	 1.0000	 0.0300
BM	 0.9910	 0.0580
BN	 1.0000	 0.0250
BO	 1.0000	 0.0430
BP	 1.0000	 0.0240
BQ	 0.9930	 0.0530
BR	 0.9900	 0.0190
BS	 0.9950	 0.0210
BT	 1.0000	 0.0630
BU	 0.9990	 0.0110
BV	 0.9960	 0.0250
BW	 0.9990	 0.0530
BX	 0.9990	 0.0620
BY	 0.9950	 0.0290
BZ	 1.0000	 0.0290