



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 02:45 PM UTC

PDB ID : 4V6Q / pdb_00004v6q
EMDB ID : EMD-5363
Title : Structural characterization of mRNA-tRNA translocation intermediates (class 5 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:

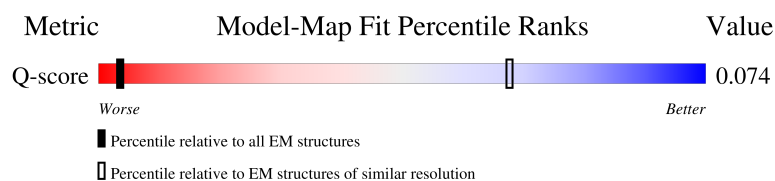
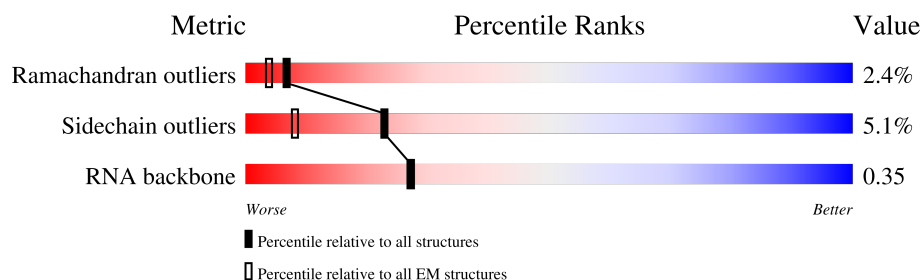
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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))
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
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	
2	AB	76	
3	AC	47	
4	AD	77	

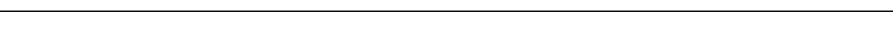
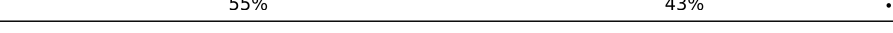
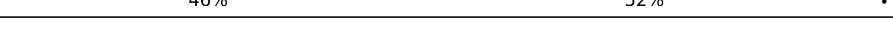
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Mol	Chain	Length	Quality of chain
5	AE	240	
6	AF	232	
7	AG	205	
8	AH	166	
9	AI	135	
10	AJ	178	
11	AK	129	
12	AL	129	
13	AM	103	
14	AN	128	
15	AO	123	
16	AP	117	
17	AQ	100	
18	AR	88	
19	AS	82	
20	AT	83	
21	AU	74	
22	AV	91	
23	AW	86	
24	AX	70	
25	BA	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	
31	BG	178	
32	BH	176	
33	BI	149	
34	BJ	164	
35	BK	141	
36	BL	142	
37	BM	123	
38	BN	144	
39	BO	136	
40	BP	127	
41	BQ	117	
42	BR	114	
43	BS	117	
44	BT	103	
45	BU	110	
46	BV	100	
47	BW	103	
48	BX	94	
49	BY	84	
50	BZ	77	
51	B0	63	
52	B1	58	
53	B2	70	
54	B3	56	

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Mol	Chain	Length	Quality of chain
55	B4	54	63% 33% .
56	B5	46	54% 39% . .
57	B6	64	56% 41% .
58	B7	38	55% 39% 5%

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 152351 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

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

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

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

- Molecule 3 is a RNA chain called mRNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 34 is a protein called 50S ribosomal protein L10.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

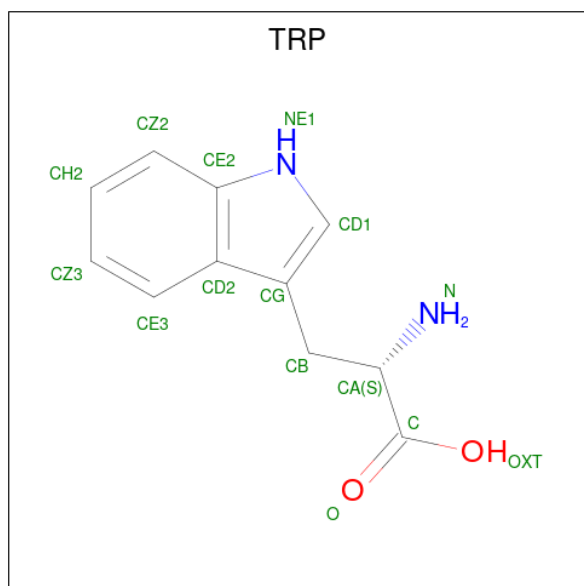
- Molecule 57 is a protein called 50S ribosomal protein L35.

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

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

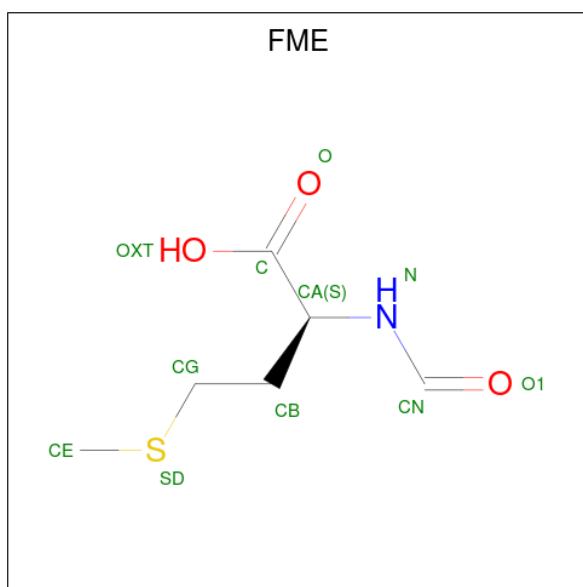
Mol	Chain	Residues	Atoms					AltConf	Trace
58	B7	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

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



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

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

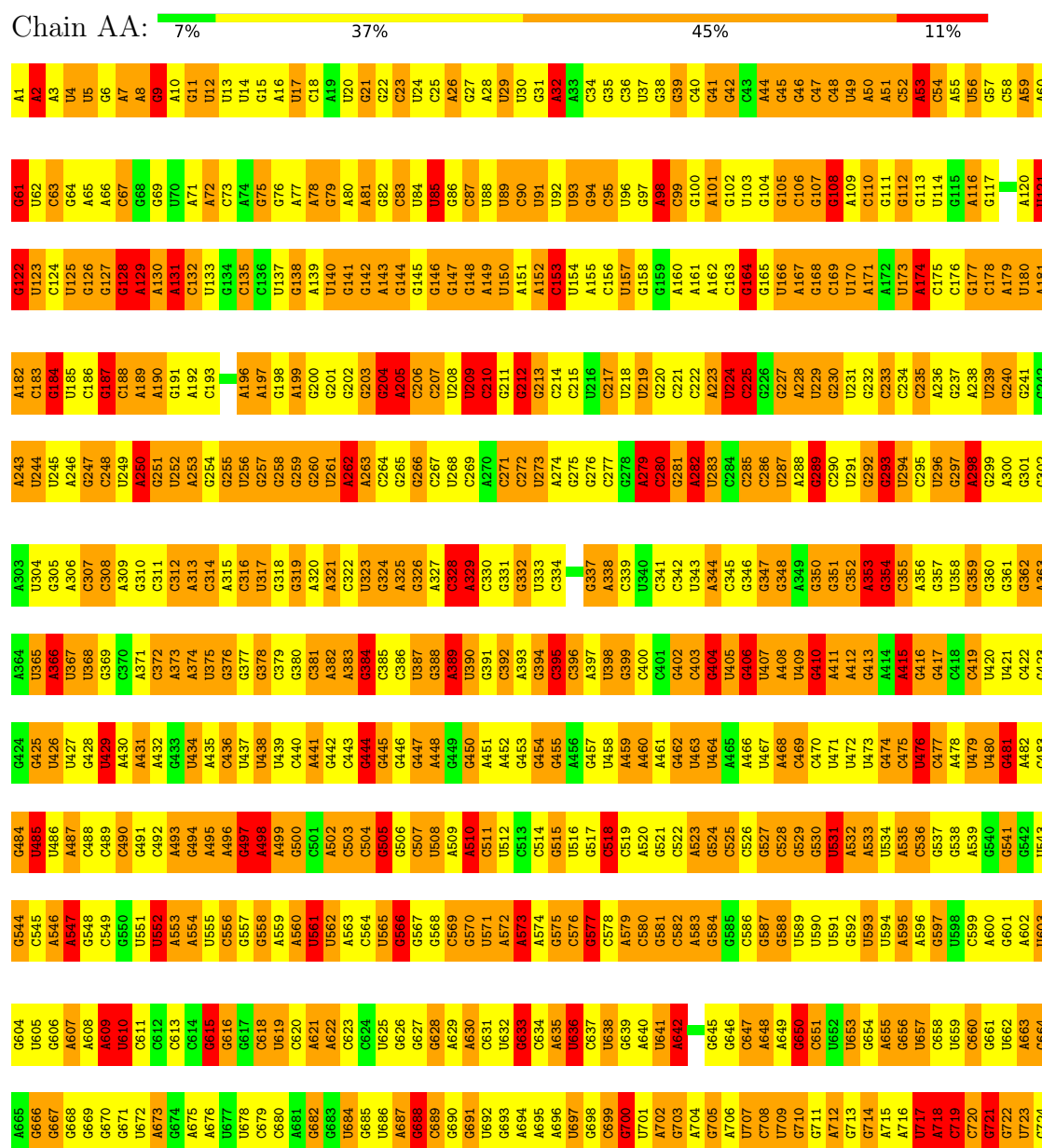


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
60	BB	1	10	6	1	2	1	0

3 Residue-property plots

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

• Molecule 1: 16S ribosomal RNA



G125	G785	A845	U905	G966	G1026	U1086	G1147	G1207	G1267	C1327	C1388	C1448	A1508
C726	G786	G846	A906	C967	C1027	G1087	U1148	C1208	G1268	C1328	C1389	C1449	C1508
G727	A787	G847	A907	A968	G1028	G1088	C1149	C1209	A1269	A1329	C1390	C1450	C1509
A728	G788	C848	A908	A969	U1029	G1089	A1150	C1210	A1270	U1330	U1391	U1451	C1510
A729	U789	G849	A909	G970	U1030	U1091	A1151	U1211	A1271	G1331	G1392	G1452	U1512
G730	U790	U850	C910	G971	C1031	U1091	A1152	U1212	G1272	A1332	G1393	G1453	A1513
G731	G791	G851	U911	C972	G1032	A1092	G1153	C1213	C1273	A1333	A1394	G1454	G1514
C732	A792	G852	C912	G973	G1033	A1093	G1154	C1214	A1274	G1334	G1395	G1455	G1515
G733	U793	C853	A913	A974	G1034	U1094	A1155	G1215	A1275	U1335	A1396	A1456	G1516
A734	A794	U854	A914	A975	A1036	U1095	G1156	C1216	G1276	G1336	C1397	G1457	G1517
C735	C795	U855	A915	G976	A1037	U1097	G1158	C1217	C1277	G1337	A1398	G1458	A1518
A736	G796	C856	A916	A977	C1038	U1097	U1159	C1218	G1278	G1338	C1399	G1459	A1519
C737	C797	C857	A918	A978	C1038	U1098	U1160	C1219	A1280	A1339	C1400	C1460	G1520
C738	U798	C858	A919	C979	G1039	G1099	G1161	G1220	A1281	A1340	G1401	G1461	C1521
C739	G799	C859	U920	C980	U1040	C1100	C1162	G1221	C1282	U1341	C1402	C1462	U1522
U740	G800	C860	U921	U981	C1041	A1101	C1163	G1222	U1283	C1342	C1403	U1463	G1523
G741	U801	G861	C922	U982	A1042	C1102	G1164	C1223	U1284	G1343	G1404	U1464	C1524
G742	A802	C862	A923	A983	G1043	C1103	G1165	C1224	A1285	C1344	G1405	A1465	G1525
A743	G803	U863	C924	C984	A1044	G1104	U1166	A1225	U1286	U1345	U1406	C1466	G1526
C744	U804	A864	G925	C985	C1045	A1105	G1167	C1226	A1287	A1346	C1407	C1467	U1527
G745	C805	A865	G926	C986	A1046	G1106	A1168	C1227	A1288	G1347	A1408	A1468	U1528
A746	C806	C866	G927	G987	G1047	C1109	U1169	C1228	A1289	U1348	C1409	C1469	G1529
C747	A807	C867	G928	G988	A1048	C1109	A1170	C1229	A1290	A1349	A1410	U1470	C1530
G748	C808	C868	G929	U989	U1049	A1110	A1171	C1230	U1291	C1350	C1411	U1471	A1531
A749	G809	G869	C930	C990	C1050	A1111	C1172	G1231	U1292	G1352	C1412	U1472	U1532
C750	C810	U870	C931	U991	C1051	C1112	U1173	U1232	G1293	G1353	A1413	G1473	C1533
U751	C811	U871	C932	U992	A1052	C1113	G1174	C1233	G1294	U1354	U1414	U1474	A1534
G752	G812	A872	G933	U993	G1053	C1114	G1175	C1234	G1295	G1355	G1415	U1475	C1535
A753	U813	C873	C934	A994	C1054	U1115	G1176	U1235	U1296	G1356	G1416	A1476	G1536
C754	G814	G874	A935	C995	A1055	U1116	A1177	C1236	G1297	A1357	G1417	U1477	U1537
G755	A815	U875	C936	A996	U1056	U1117	G1178	C1237	U1298	U1358	A1418	U1478	C1538
C756	A816	C876	A937	U997	G1057	U1118	C1179	A1238	U1299	C1359	G1419	C1479	C1539
U757	C817	G877	A938	C998	G1058	U1119	A1179	C1239	A1300	A1360	U1420	C1480	U1540
C758	G818	A878	G939	C999	U1059	C1120	G1180	U1240	U1301	G1361	G1421	U1481	U1541
A759	A819	C879	C940	U1000	U1060	U1121	G1181	G1241	U1302	A1362	G1422	U1482	A1542
G760	U820	C880	G941	C1001	G1061	U1122	G1182	G1242	C1303	A1363	G1423	A1483	C36
G761	G821	G881	G942	U1002	U1062	U1123	U1183	C1243	C1304	U1364	U1424	C1484	A37
U762	U822	C882	G943	G1003	C1063	G1124	G1184	G1244	G1305	G1365	U1425	U1485	A38
G763	C823	U883	G944	A1004	G1064	U1125	G1185	C1245	G1306	C1366	G1426	G1486	A39
C764	G824	U884	G945	A1005	U1065	U1126	G1186	A1246	A1307	C1367	C1427	G1487	C40
G765	A825	G885	A946	G1006	C1066	G1127	G1187	U1247	U1308	A1368	A1428	G1488	C41
A766	C826	G886	G947	U1007	A1067	C1128	U1188	U1248	U1309	C1369	A1429	G1489	C42
C767	U827	G887	C948	U1008	C1068	C1129	U1189	C1249	G1310	G1370	A1430	U1490	C43
A768	U828	G888	A949	U1009	G1069	A1130	G1190	A1250	G1311	G1371	A1431	G1491	C44
G769	C829	A889	U950	U1010	U1070	G1131	A1191	A1251	A1312	U1372	G1432	A1492	U45
C770	G830	U890	G951	C1011	C1071	G1132	C1192	A1252	G1313	G1373	A1433	A1493	G46
G771	A831	U891	U952	U1012	G1072	G1133	G1193	G1253	U1314	A1374	A1434	G1494	U47
U772	G832	A892	G953	U1013	U1073	U1134	U1194	A1254	C1315	A1375	G1435	U1495	G48
G773	G833	C893	G954	A1014	G1074	U1135	C1195	G1255	U1316	U1376	U1436	C1496	G49
C774	U834	U894	U955	G1015	U1075	G1136	A1196	A1256	G1317	A1377	A1437	G1497	G50
G775	U835	G895	U956	A1016	U1076	C1137	U1197	A1257	C1318	C1378	G1438	U1498	G51
U776	C836	C896	U957	U1017	G1077	G1138	G1198	G1258	A1319	G1379	G1439	A1499	A52
G777	U837	C897	A958	U1018	U1078	G1139	U1199	C1259	U1320	U1380	U1440	A1500	G53
G778	G838	A898	U959	A1019	G1079	C1140	C1200	G1260	C1321	U1381	A1441	C1501	U54
C779	C839	C899	U960	G1020	A1080	G1141	C1201	A1261	U1322	C1382	G1442	A1502	U55
A780	U840	A900	U961	A1021	A1081	G1142	U1202	C1262	C1323	C1383	G1443	A1503	C56
G781	C841	A901	C962	A1022	A1082	G1143	C1203	C1263	G1324	C1384	U1444	G1504	G57
A782	U842	G902	G963	U1023	U1083	G1144	A1204	U1264	A1325	G1385	U1445	G1505	A58
C783	U843	A903	A964	G1024	U1084	G1145	U1205	C1265	C1326	G1386	A1446	U1506	G59
A784	G844	U904	U965	U1025	U1085	G1146	G1206	G1266	U1326	G1387	A1447	A1507	U60

• Molecule 2: A site tRNA

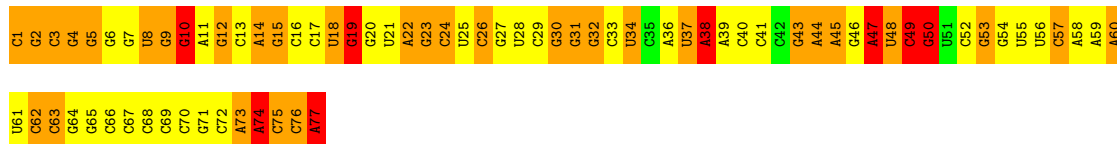
Chain AB:  7% 38% 37% 18%

A1	G2	G3	G4	G5	G6	G7	G8	A9	G10	C71	U72	G73	C74	C75	A76
C61	U62	C63	U64	C65	C66	C67	C68	C69	C70	C71	U72	G73	C74	C75	A76
A81	G82	G83	G84	G85	G86	G87	G88	A89	G90	C91	U92	G93	C94	C95	A96
C97	G98	G99	G100	G101	G102	G103	A104	G105	G106	C107	U108	G109	C110	C111	A112
C113	A114	U115	G116	G117	G118	G119	U120	A121	G122	C123	U124	G125	C126	C127	A128
G129	G130	G131	G132	G133	G134	G135	U136	A137	G138	C139	U140	G141	C142	C143	A144
C145	G146	G147	G148	G149	G150	G151	A152	G153	C154	U155	G156	C157	C158	C159	A160

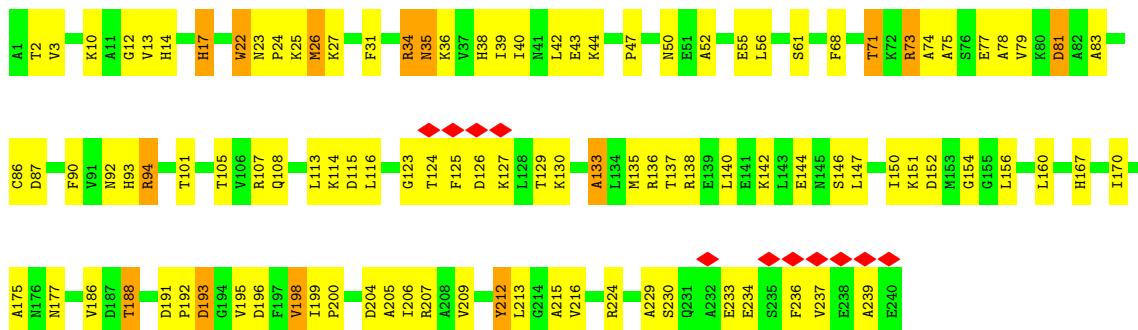
- Molecule 3: mRNA



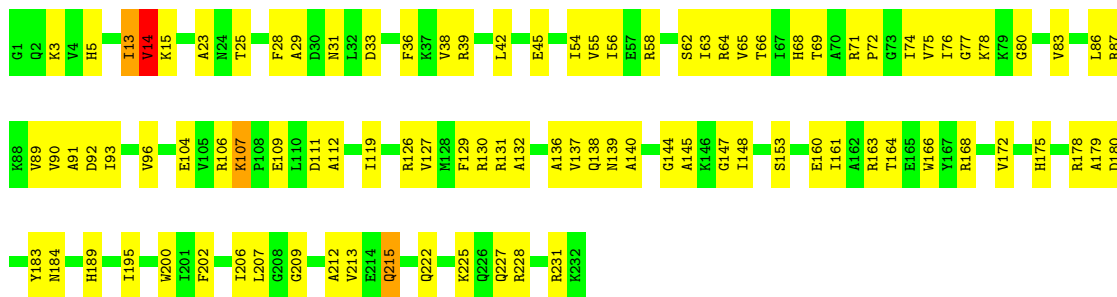
- Molecule 4: P site tRNA



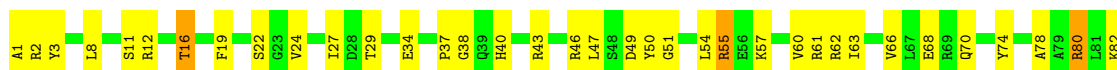
- Molecule 5: 30S ribosomal protein S2

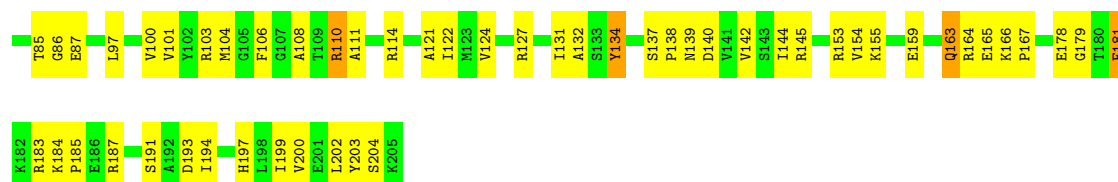


- Molecule 6: 30S ribosomal protein S3



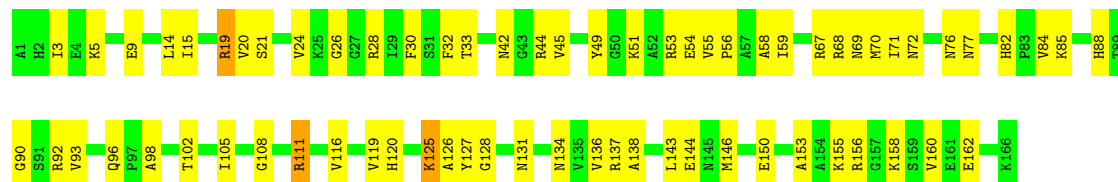
- Molecule 7: 30S ribosomal protein S4





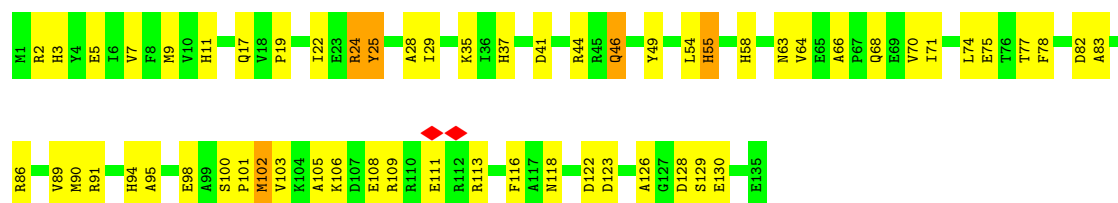
• Molecule 8: 30S ribosomal protein S5

Chain AH: 59% 39%



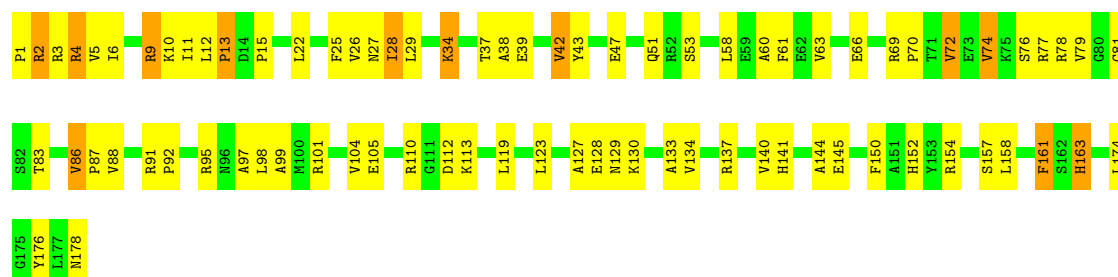
• Molecule 9: 30S ribosomal protein S6

Chain AI: 56% 40%



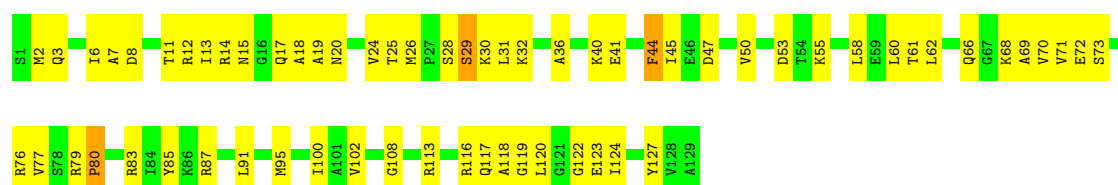
• Molecule 10: 30S ribosomal protein S7

Chain AJ: 55% 38% 7%

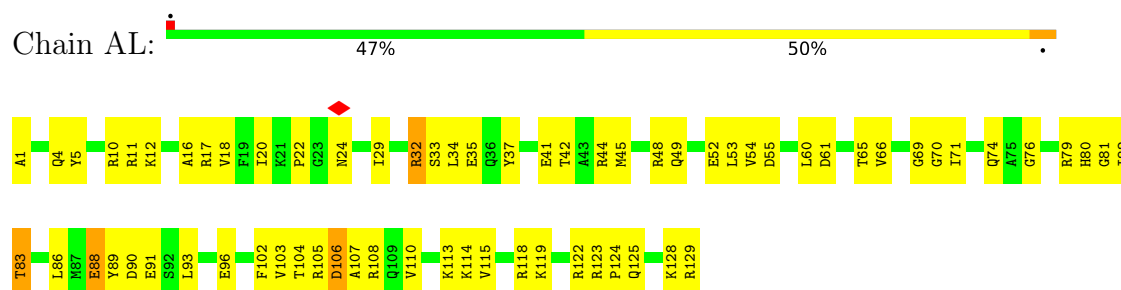


• Molecule 11: 30S ribosomal protein S8

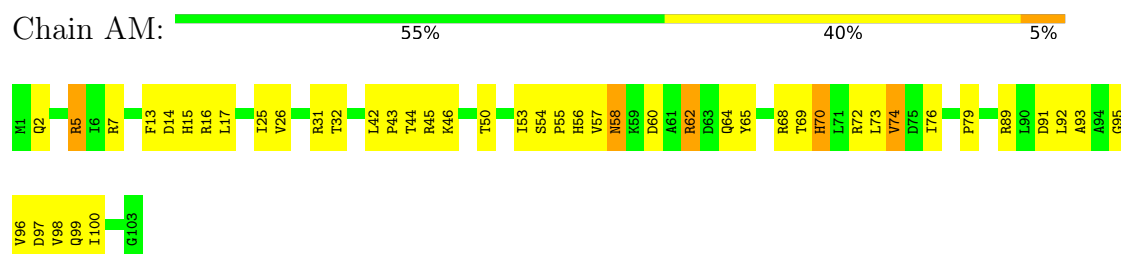
Chain AK: 50% 47%



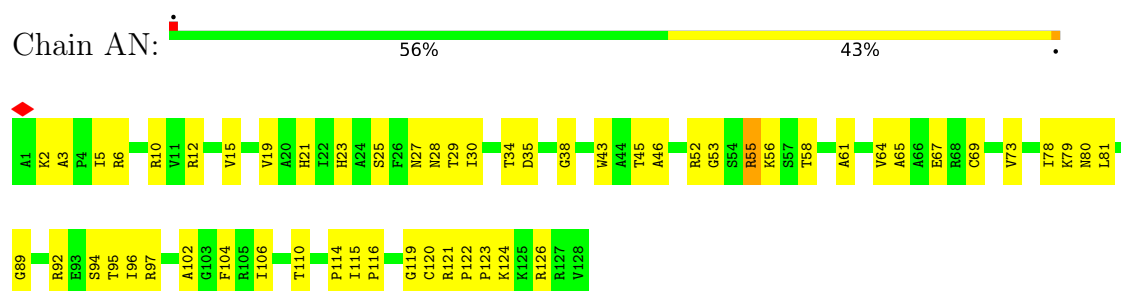
- Molecule 12: 30S ribosomal protein S9



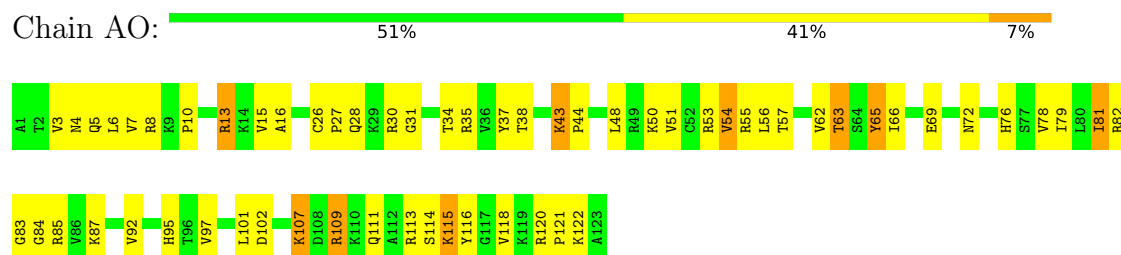
- Molecule 13: 30S ribosomal protein S10



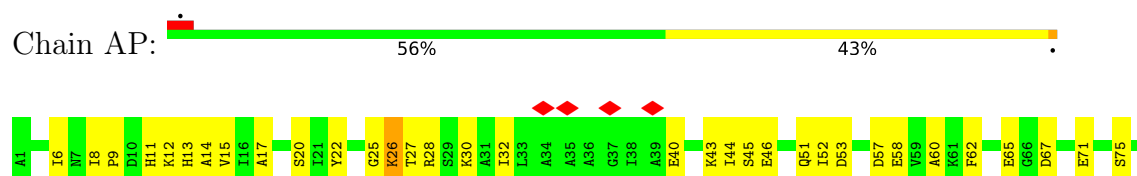
- Molecule 14: 30S ribosomal protein S11



- Molecule 15: 30S ribosomal protein S12



- Molecule 16: 30S ribosomal protein S13

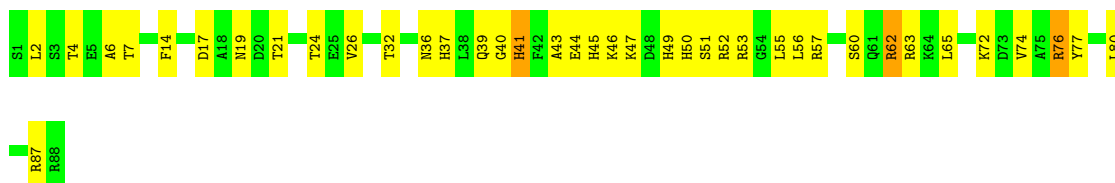




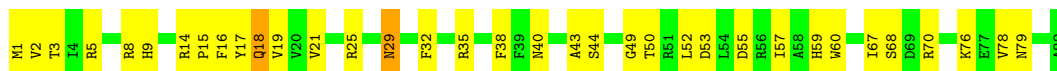
- Molecule 17: 30S ribosomal protein S14



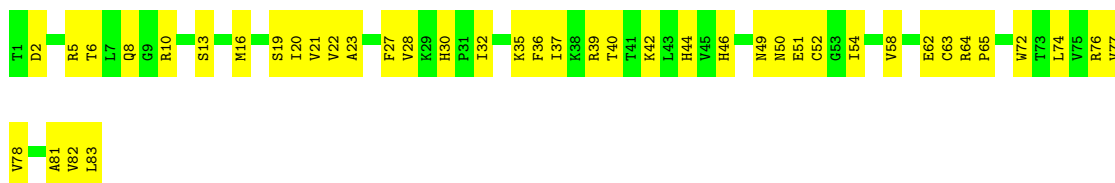
- Molecule 18: 30S ribosomal protein S15



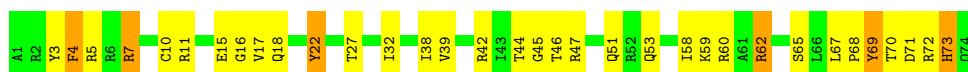
- Molecule 19: 30S ribosomal protein S16



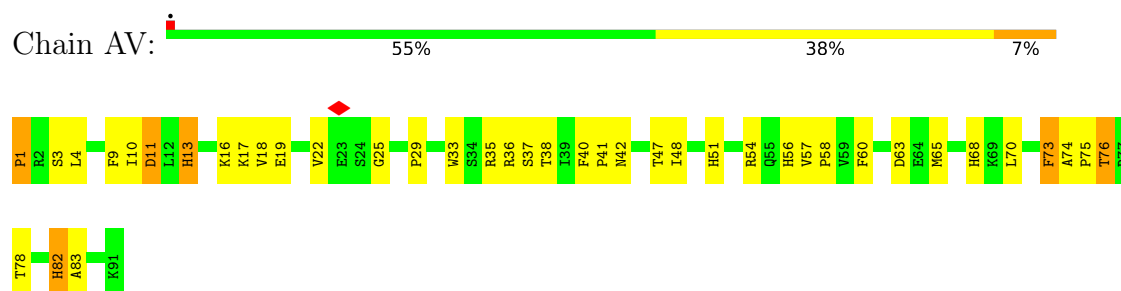
- Molecule 20: 30S ribosomal protein S17



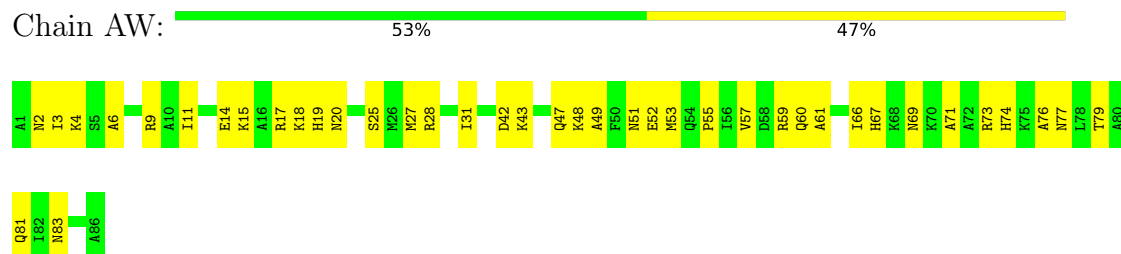
- Molecule 21: 30S ribosomal protein S18



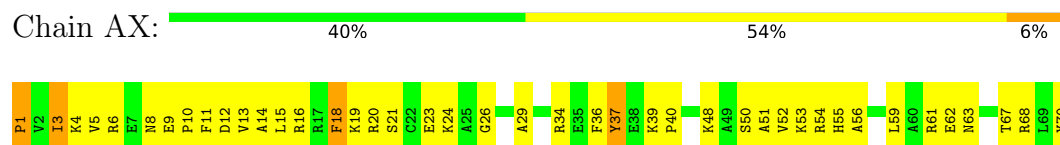
- Molecule 22: 30S ribosomal protein S19



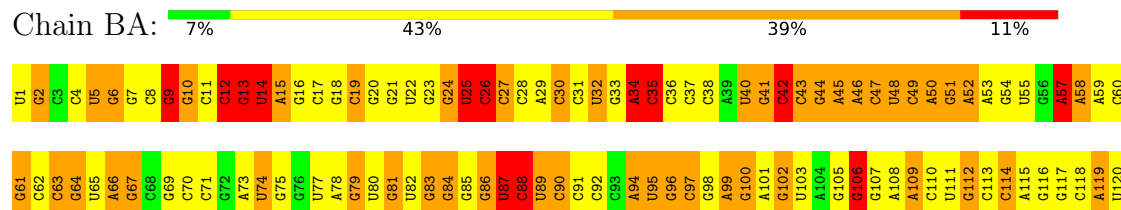
- Molecule 23: 30S ribosomal protein S20



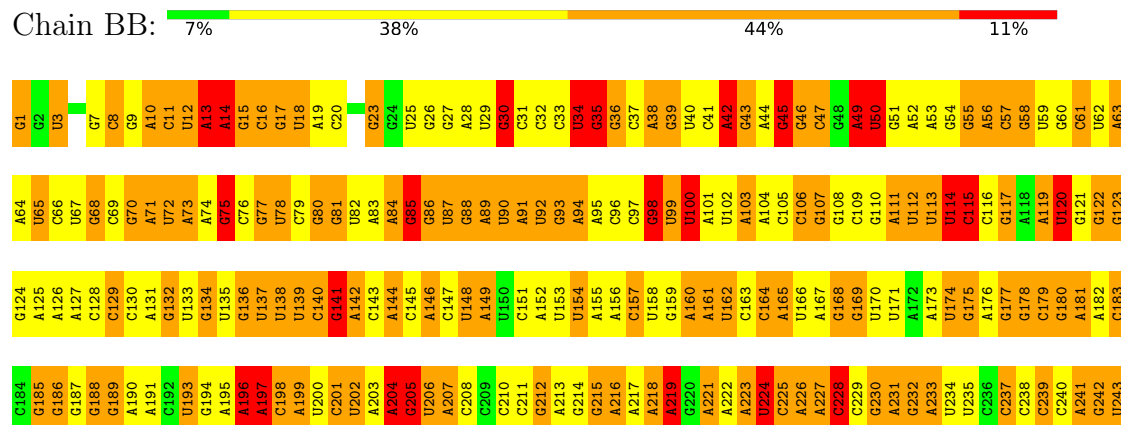
- Molecule 24: 30S ribosomal protein S21



- Molecule 25: 5S ribosomal RNA



- Molecule 26: 23S ribosomal RNA



C1207	A1147	G1087	A1027	U967	G907	U847	G786	G725	U685	G605	C544	C484	G424	C364	U304	A244
C1208	U1148	A1088	A1028	C968	C908	C848	C787	G726	A666	U606	U545	C485	G425	U365	C305	G245
U1209	G1149	A1089	A1029	G969	A909	A849	A788	A727	U687	U607	U546	C486	G426	C366	U306	C246
G1210	C1150	A1090	C1030	U970	A910	U850	A789	G728	A668	A608	A547	C487	U427	G367	G307	G247
C1211	A1151	G1091	G1031	G971	A911	C851	U790	G729	G669	A609	G548	C488	A428	A368	A308	G248
G1212	C1152	C1092	A1032	A972	C912	U852	C791	A730	A670	C610	G549	C489	A429	U369	G309	C249
A1213	G1153	G1093	U1033	A973	U913	C853	A792	C731	C671	C611	C550	C490	A430	G370	A310	G250
G1214	G1154	U1094	U1034	G974	G914	C854	A793	C732	C672	G612	G551	C491	U431	A371	A311	A251
A1215	A1155	A1095	G1035	A975	C915	C855	A794	C733	C673	A613	U552	A492	A432	C372	G312	G252
G1216	A1156	U1096	G1036	G976	A916	C856	C795	A734	G674	A614	G553	C493	C433	U373	G313	C253
U1217	G1157	U1097	G1037	G977	A917	C857	G796	A735	A675	U615	U554	C494	A434	A374	C314	G254
G1218	C1158	A1098	G1038	G978	A918	C858	G797	C736	A676	A616	G555	C495	G435	G375	G315	A255
U1219	U1159	G1099	A1039	A979	U919	C859	G798	C737	A677	G617	A556	C496	C436	G376	C316	A256
G1220	G1160	C1100	A1040	A980	A920	U860	G799	G738	C678	G618	C557	A497	U437	G377	G317	C257
C1221	C1161	U1101	G1041	A981	C921	A861	A800	G739	C679	G619	U558	C498	U438	C378	C318	G258
U1222	G1162	C1102	G1042	C982	C922	C862	G801	C740	C680	G620	U559	C499	A439	G379	G319	G259
G1223	A1163	A1103	C1043	A983	G923	A863	A802	U741	G681	A621	C560	U500	C440	G380	A320	G260
C1224	G1164	G1104	C1044	A984	G924	C864	U803	A742	G682	G622	G561	A501	U441	G381	U321	G261
U1225	A1165	U1105	C1045	C985	A925	C865	A804	A743	U683	C623	A502	A502	G442	A382	A322	A262
G1226	G1166	G1106	A1046	C986	G926	A866	C805	U744	A685	G624	A503	A503	A443	C383	C323	G263
U1227	C1167	G1107	G1047	C987	A927	C867	G806	G745	C686	G625	C504	A504	C444	A384	A324	G264
G1228	G1168	U1108	A1048	A988	A928	U868	U807	U746	U688	A626	C505	A505	G445	C385	G325	A265
C1229	A1169	C1109	C1049	G989	U929	C869	G808	U747	C687	A627	U566	G506	G446	G386	G326	G266
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G1231	G1171	U1111	G1051	C991	U931	U871	U810	A749	A689	G629	U568	A508	U448	G388	U328	C268
C1232	C1172	G1112	C1052	C992	U932	U872	U811	A750	C690	G630	U569	C509	A449	G389	G329	C269
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C1234	A1174	C1114	A1054	C994	U934	C874	U813	A752	C692	A632	U571	U511	U451	A391	C331	G271
G1235	A1175	G1115	G1055	C995	C935	C875	C814	A753	A693	A633	A572	G512	G452	U392	A332	A272
C1236	G1176	G1116	G1056	A996	A936	C876	C815	G754	U694	C634	U573	A513	A453	C393	G333	G273
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C1241	U1181	C1121	A1061	A1001	A941	C881	A820	G760	A699	U639	G578	G518	G458	C398	G338	A278
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C2174	U2113	G2053	U1983	G1933	G1873	G1813	C1752	U1892	G1631	A1571	G1510	G1450	G1389	A1328	U1267
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A2176	G2115	C2055	U1995	G1935	A1875	A1815		C1694	A1633	G1573	C1512	A1452	U1391	A1269	
C2177	G2116	C2056	C1996	A1936	A1876	C1816	G1756	G1695	A1634	C1574	U1513	A1453	A1392	G1331	
C2178	G2117	G2057	C1997	A1937	A1877	U1817	A1757	G1696	A1635	C1575	G1514	A1454	A1393	G1332	
C2179	U2118	A2058	A1998	A1938	G1878	U1818	A1758	G1697	A1636	U1576	A1515	G1455	U1394	A1272	
U2180	A2119	A2059	C1999	U1939	C1879	A1819	A1759	A1698	A1637	C1577	G1516	G1456	A1395	U1273	
U2181	G2120	C2060	C2000	U1940	U1880	U1820	G1760	G1699	C1638	U1578	G1517	U1457	U1396	U1274	
U2182	G2121	G2061	C2001	C1941	C1881	A1821	C1761	A1700	C1639	A1579	C1518	U1458	U1397	A1275	
A2183	G2122	A2062	G2002	C1942	U1882	C1822	A1762	A1701	A1640	A1580	U1519	U1459	C1398	A1276	
C2184	C2063	C2063	A2003	U1943	U1883	G1823	G1763	G1702	A1641	G1581	U1520	U1460	C1399	G1277	
U2185	U2064	C2064	G2004	U1944	G1884	G1824	C1764	G1703	G1642	C1582	G1521	C1461	U1400	A1278	
C2186	G2125	C2065	A2005	G1945	A1885	U1825	G1765	C1704	G1643	A1583	A1522	C1462	U1401	G1341	
U2187	G2127	C2066	C2006	U1946	U1886	G1826	G1766	A1705	C1644	U1584	U1523	C1463	U1402	G1279	
U2188	G2128	U2067	U2007	C1947	C1887	U1827	G1767	C1706	G1645	A1585	G1524	G1464	A1403	A1342	
U2189	U2129	C2068	C2008	G1948	G1888	G1828	C1768	G1707	G1646	A1586	A1525	G1465	A1404	G1343	
U2190	U2130	G2069	A2009	G1949	A1889	A1829	U1769	C1708	U1647	G1587	G1526	U1466	U1405	A1284	
A2191	U2131	A2070	G2010	G1950	A1890	C1830	G1770	U1709	U1648	G1588	G1527	U1467	U1406	A1285	
U2192	U2132	A2071	U2011	U1951	G1891	G1831	C1771	G1710	G1649	U1589	A1528	U1468	G1407	A1286	
G2193	G2133	C2072	G2012	A1952	C1892	C1832	A1772	A1711	A1650	A1590	G1529	A1469	G1408	C1287	
U2194	C2134	C2073	A2013	A1953	C1893	C1833	A1773	U1712	G1651	A1591	G1530	A1470	U1409	G1288	
U2195	A2135	U2074	A2014	G1954	C1894	U1834	C1774	A1713	A1652	C1592	G1531	G1471	G1410	C1289	
C2196	G2136	U2075	A2015	U1955	C1895	G1835	G1775	U1714	G1653	A1593	A1532	C1472	U1411	C1290	
U2197	U2137	U2076	U2016	U1956	G1896	C1836	G1776	G1715	A1654	U1594	G1533	G1473	U1412	C1291	
A2198	G2138	A2077	U2017	G1957	G1897	C1837	U1777	U1716	A1655	C1595	U1534	U1474	A1413	G1292	
A2199	U2139	C2078	G2018	C1958	U1898	C1838	U1778	A1717	C1656	A1596	A1535	G1475	C1414	C1293	
C2200	G2140	U2079	A2019	G1959	A1899	G1839	U1779	G1718	U1657	A1597		A1477	U1415	U1294	
G2201	A2141	A2080	A2020	A1960	A1900	G1840	U1780	G1719	C1658	A1598		G1478	G1416	C1295	
U2202	A2142	U2081	C2021	C1961	A1901	U1841	U1781	U1720	G1659	U1599	U1539	G1479	G1418	C1297	
U2203	C2143	A2082	U2022	C1962	G1902	G1842	U1782	G1721	G1660	G1601	U1541	G1480	A1419	C1298	
G2204	G2144	G2083	C2023	U1963	G1903	C1843	A1783	A1722	G1661	G1602	U1542	U1481	A1420	G1299	
A2205	C2145	C2084	G2024	C1964	G1904	C1844	A1784	G1723	U1662	U1603	U1543	G1482	G1421	G1300	
C2206	C2146	U2085	C2025	C1965	G1905	G1845	A1785	G1724	G1663	A1604	A1544	G1483	G1422	C1362	
C2207	A2147	G2087	U2026	A1966	G1906	G1846	A1786	U1725	A1664	C1605	A1545	U1484	G1423	C1363	
C2208	G2148	G2087	G2027	C1967	G1907	A1847	U1787	G1726	A1665	G1606	G1546	U1485	G1424	G1364	
C2209	U2149	A2088	U2028	G1968	C1908	A1848	C1788	C1727	G1666	C1607	G1547	U1486	G1425	A1304	
U2210	C2150	C2089	G2029	A1969	G1909	G1849	U1789	G1728	G1667	A1608	U1548	U1487	G1426	C1305	
A2211	U2151	A2090	A2030	C1970	G1910	G1850	C1790	U1729	A1668	A1609	U1549	C1488	A1427	A1367	
A2212	G2152	C2091	A2031	U1971	U1911	U1851	A1791	C1730	A1669	A1610	C1550	C1489	G1428	A1307	
U2213	C2153	U2092	G2032	G1972	A1912	U1852	G1792	G1731	C1670	C1611	A1551	A1490	G1429	A1308	
C2214	A2154	G2093	A2033	G1973	A1913	A1853	C1793	C1732	G1671	C1612	A1552	G1491		G1309	
C2215	U2155	A2094	U2034	C1974	A1914	A1854	A1794	G1733	A1672	G1613	A1553	G1492	A1433	G1371	
G2216	G2156	A2095	G2035	G1975	3TD1915	U1855	C1795	G1734	G1673	G1614	U1554	C1493	A1434	U1372	
G2217	G2157	C2096	C2036	U1976	A1916	U1856	U1796	A1735	G1674	A1615	G1555	A1494		G1373	
G2218	A2158	A2097	A2037	A1977	U1917	G1857	G1797	U1736	C1675	C1616	G1556	A1495	G1435	A1374	
U2219	G2159	U2098	U2038	A1978	A1918	U1858	U1798	G1737	A1677	A1617	C1557	A1496	G1436	U1375	
U2220	C2160	U2099	U2039	U1979	A1919	U1859	G1799	G1738	A1678	G1618	C1558	U1497	G1437	C1376	
C2221	C2161	G2100	G2040	G1980	C1920	G1860	A1800	A1739	A1679	A1619	U1559	C1498	U1438	G1377	
G2222	G2162	A2101	U2041	A1981	G1921	G1861	A1801	G1740	A1680	G1620	U1560	C1499	A1439	U1378	
G2223	A2163	G2102	A2042	U1982	G1922	G1862	A1802	C1741	A1681	U1621	C1561	G1500	U1440	U1379	
G2224	C2164	C2103	C2043	G1983	U1923	G1863	A1803	U1742	G1681	G1622	U1562	G1501	G1441	C1380	
A2225	C2165	C2104	C2044	C1984	C1924	U1864	A1804	G1743	A1682	G1623	U1563	A1502	U1442	C1381	
C2226	U2166	U2105	C2045	C1985	C1925	U1865	A1805	A1744	U1683	G1624	U1564	A1503	U1443	G1382	
A2227	U2167	G2106	G2046	C1986	U1926	A1866	G1806	A1745	G1684	G1625	G1565	A1504	G1444	A1383	
G2228	G2168	G2107	C2047	A1987	G1927	G1867	G1807	A1746	C1685	A1626	U1566	A1505	G1445	A1384	
U2229	A2169	A2108	G2048	G1988	A1928	C1868	A1808	U1747	G1686	G1627	G1567	U1506	G1446	A1385	
G2230	A2170	U2109	G2049	G1989	G1929	G1869	A1809	C1748	G1687	G1628	G1568	C1507	G1447	A1386	
U2231	C2171	C2110	C2050	C1990	G1930	A1870	A1810	A1749	U1688	U1629	A1569	G1508	G1448	A1387	
C2232	U2172	U2111	A2051	U1991	G1931	A1871		G1750						U1326	
U2233	A2173	G2112	A2052	G1992	A1932	A1872	U1812	U1751	C1691	A1630	A1570	A1509	G1449	G1388	

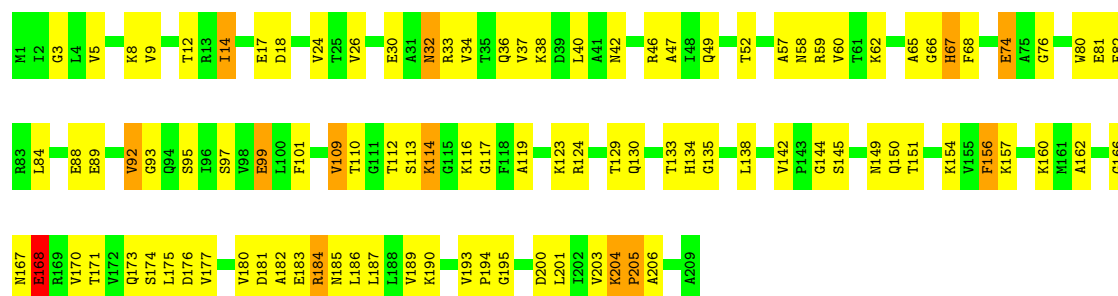
- Molecule 28: 50S ribosomal protein L2

Chain BD: 



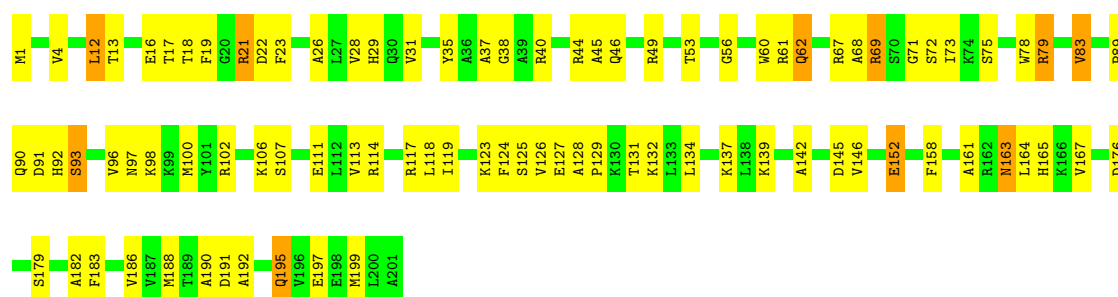
- Molecule 29: 50S ribosomal protein L3

Chain BE: 



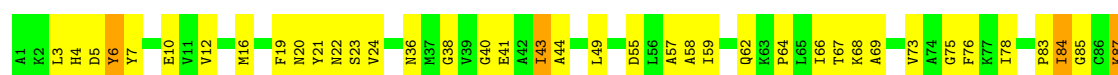
- Molecule 30: 50S ribosomal protein L4

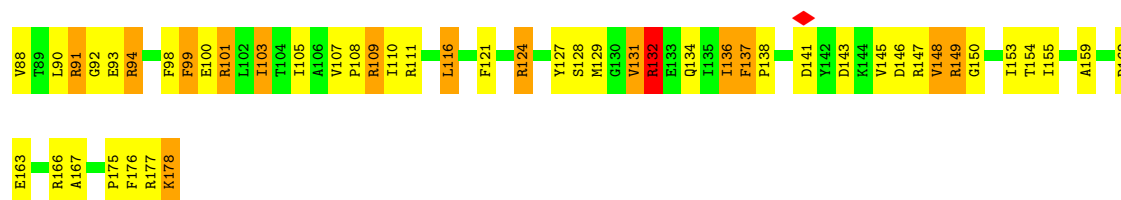
Chain BF: 



- Molecule 31: 50S ribosomal protein L5

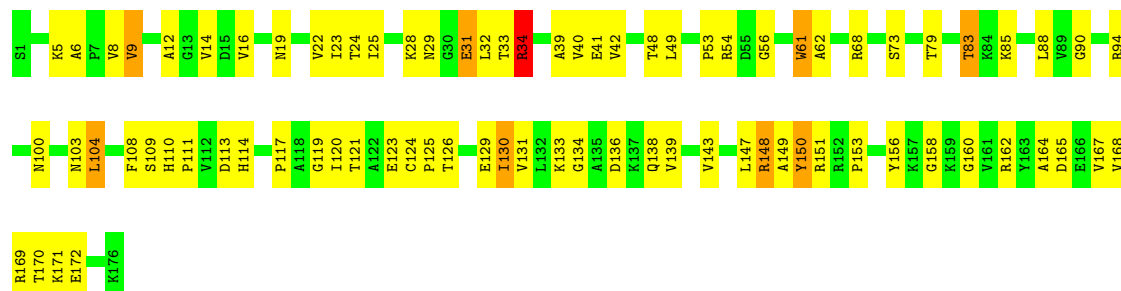
Chain BG: 





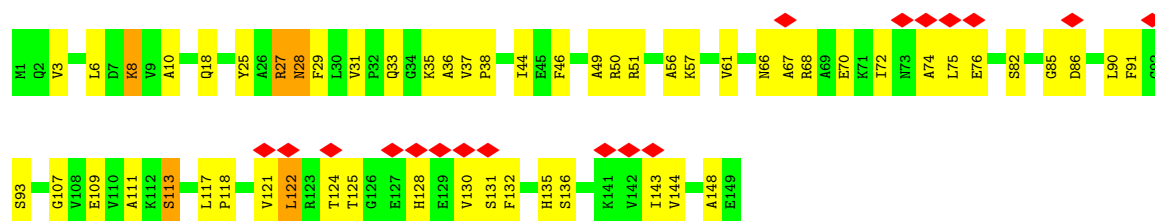
• Molecule 32: 50S ribosomal protein L6

Chain BH: 54% 41% 5% .



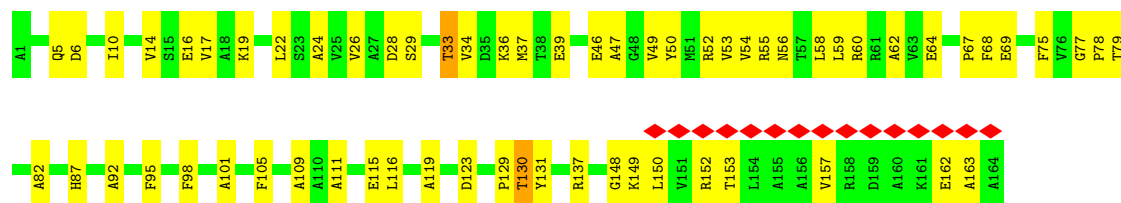
• Molecule 33: 50S ribosomal protein L9

Chain BI: 12% 62% 34% .



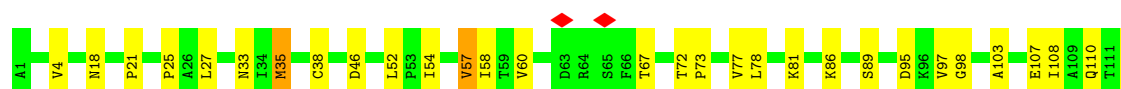
• Molecule 34: 50S ribosomal protein L10

Chain BJ: 9% 62% 37% .



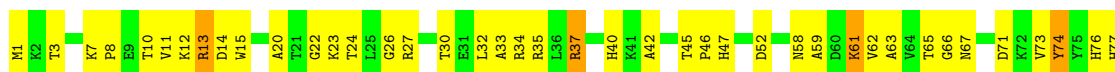
• Molecule 35: 50S ribosomal protein L11

Chain BK: 67% 31% .

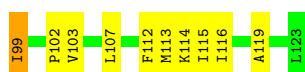
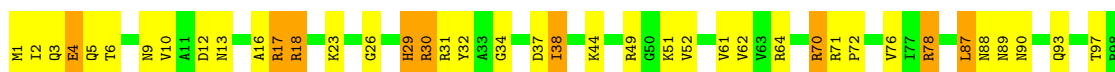




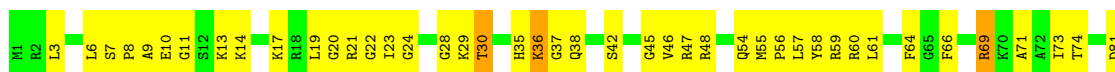
• Molecule 36: 50S ribosomal protein L13



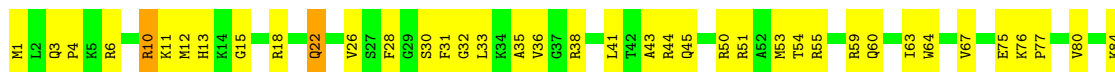
• Molecule 37: 50S ribosomal protein L14



• Molecule 38: 50S ribosomal protein L15



• Molecule 39: 50S ribosomal protein L16



• Molecule 40: 50S ribosomal protein L17





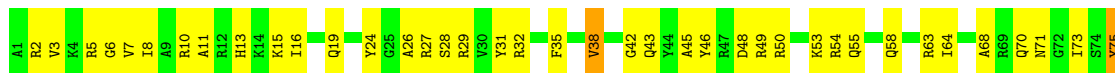
- Molecule 41: 50S ribosomal protein L18



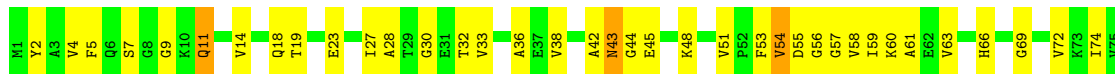
- Molecule 42: 50S ribosomal protein L19



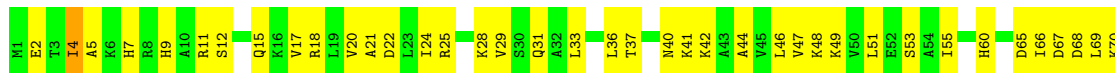
- Molecule 43: 50S ribosomal protein L20



- Molecule 44: 50S ribosomal protein L21



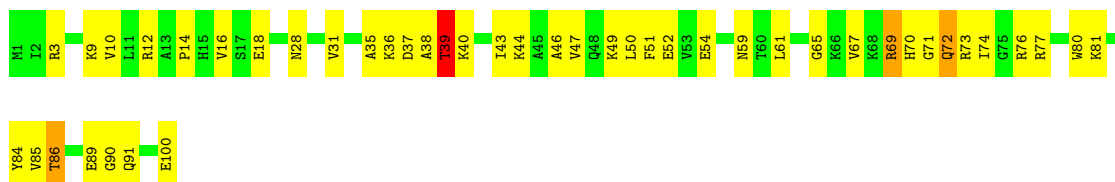
- Molecule 45: 50S ribosomal protein L22





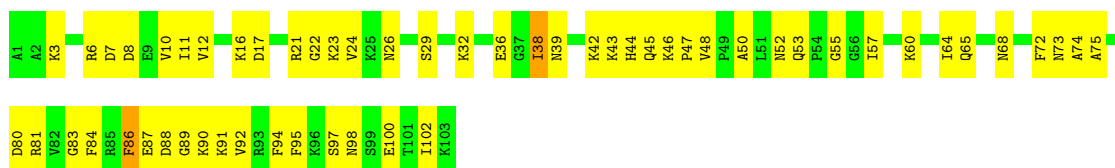
- Molecule 46: 50S ribosomal protein L23

Chain BV: 55% 41%



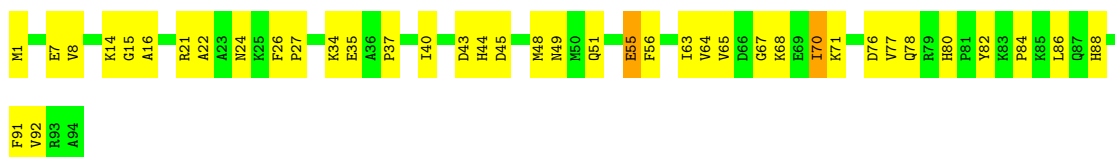
- Molecule 47: 50S ribosomal protein L24

Chain BW: 46% 52%



- Molecule 48: 50S ribosomal protein L25

Chain BX: 57% 40%



- Molecule 49: 50S ribosomal protein L27

Chain BY: 62% 31% 7%



- Molecule 50: 50S ribosomal protein L28

Chain BZ: 51% 48%



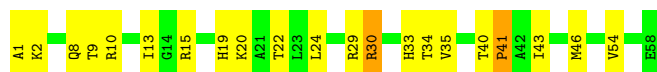
- Molecule 51: 50S ribosomal protein L29

Chain B0: 48% 48% 5%



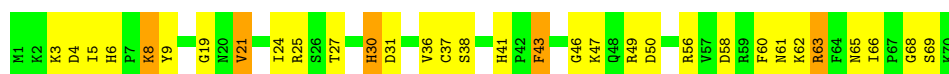
- Molecule 52: 50S ribosomal protein L30

Chain B1: 64% 33% .



- Molecule 53: 50S ribosomal protein L31

Chain B2: 54% 39% 7%



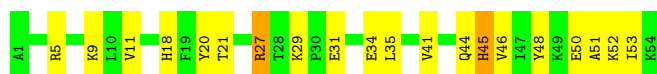
- Molecule 54: 50S ribosomal protein L32

Chain B3: 55% 39% 5%



- Molecule 55: 50S ribosomal protein L33

Chain B4: 63% 33% .



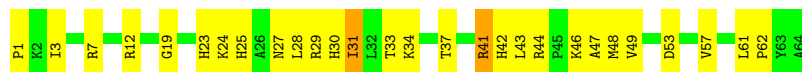
- Molecule 56: 50S ribosomal protein L34

Chain B5: 54% 39% . .



- Molecule 57: 50S ribosomal protein L35

Chain B6: 56% 41% .



- Molecule 58: 50S ribosomal protein L36

Chain B7: 55% 39% 5%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	40000	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	1.481	Depositor
Minimum map value	-0.504	Depositor
Average map value	0.029	Depositor
Map value standard deviation	0.201	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: OMC, H2U, OMU, 6MZ, 3TD, 7MG, MA6, OMG, FME, 2MG, CH, 5MU, PSU, UR3, 4SU, MIA, 2MA, 4OC, 5MC, 1MG

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	578/36769 (1.6%)	2.00	1955/57354 (3.4%)
2	AB	1.94	31/1600 (1.9%)	2.08	106/2492 (4.3%)
3	AC	1.91	15/1108 (1.4%)	2.07	63/1724 (3.7%)
4	AD	1.89	38/1721 (2.2%)	1.98	89/2683 (3.3%)
5	AE	1.99	37/1904 (1.9%)	2.43	113/2565 (4.4%)
6	AF	1.97	28/1852 (1.5%)	2.36	98/2490 (3.9%)
7	AG	1.99	33/1665 (2.0%)	2.39	91/2227 (4.1%)
8	AH	2.04	27/1239 (2.2%)	2.39	62/1664 (3.7%)
9	AI	2.01	20/1121 (1.8%)	2.51	67/1509 (4.4%)
10	AJ	2.00	30/1422 (2.1%)	2.40	76/1908 (4.0%)
11	AK	2.02	22/989 (2.2%)	2.39	56/1326 (4.2%)
12	AL	2.03	31/1048 (3.0%)	2.41	64/1394 (4.6%)
13	AM	2.03	20/835 (2.4%)	2.32	40/1127 (3.5%)
14	AN	2.06	29/982 (3.0%)	2.44	54/1323 (4.1%)
15	AO	2.11	30/969 (3.1%)	2.32	45/1300 (3.5%)
16	AP	1.98	18/919 (2.0%)	2.34	54/1226 (4.4%)
17	AQ	2.01	13/817 (1.6%)	2.42	51/1088 (4.7%)
18	AR	2.11	19/724 (2.6%)	2.43	35/966 (3.6%)
19	AS	2.02	11/659 (1.7%)	2.44	44/884 (5.0%)
20	AT	2.08	25/681 (3.7%)	2.35	35/913 (3.8%)
21	AU	1.89	9/637 (1.4%)	2.46	42/851 (4.9%)
22	AV	1.98	12/744 (1.6%)	2.50	56/995 (5.6%)
23	AW	2.05	14/676 (2.1%)	2.55	56/895 (6.3%)
24	AX	2.01	11/598 (1.8%)	2.42	37/792 (4.7%)
25	BA	1.91	49/2869 (1.7%)	2.00	155/4474 (3.5%)
26	BB	1.90	1161/69257 (1.7%)	1.98	3536/108040 (3.3%)
27	BC	1.95	31/1748 (1.8%)	2.45	112/2355 (4.8%)
28	BD	2.14	63/2131 (3.0%)	2.39	114/2863 (4.0%)
29	BE	2.04	38/1586 (2.4%)	2.42	101/2134 (4.7%)
30	BF	1.95	32/1571 (2.0%)	2.50	100/2113 (4.7%)
31	BG	1.97	29/1444 (2.0%)	2.43	89/1937 (4.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	BH	2.04	35/1343 (2.6%)	2.38	69/1816 (3.8%)
33	BI	1.92	13/1122 (1.2%)	2.44	69/1515 (4.6%)
34	BJ	1.94	17/1247 (1.4%)	2.35	71/1679 (4.2%)
35	BK	2.09	25/1046 (2.4%)	2.33	47/1410 (3.3%)
36	BL	2.02	24/1152 (2.1%)	2.39	65/1551 (4.2%)
37	BM	1.94	15/956 (1.6%)	2.31	46/1279 (3.6%)
38	BN	2.13	29/1062 (2.7%)	2.40	60/1413 (4.2%)
39	BO	2.05	24/1093 (2.2%)	2.42	60/1460 (4.1%)
40	BP	2.03	18/1021 (1.8%)	2.39	73/1364 (5.4%)
41	BQ	1.98	17/910 (1.9%)	2.40	50/1219 (4.1%)
42	BR	1.97	18/929 (1.9%)	2.36	36/1242 (2.9%)
43	BS	2.00	21/960 (2.2%)	2.46	68/1278 (5.3%)
44	BT	1.99	19/829 (2.3%)	2.26	42/1107 (3.8%)
45	BU	2.05	21/864 (2.4%)	2.40	52/1156 (4.5%)
46	BV	1.96	12/794 (1.5%)	2.30	45/1060 (4.2%)
47	BW	1.95	15/797 (1.9%)	2.43	54/1062 (5.1%)
48	BX	1.97	12/766 (1.6%)	2.34	39/1025 (3.8%)
49	BY	1.93	9/642 (1.4%)	2.37	31/848 (3.7%)
50	BZ	2.00	13/635 (2.0%)	2.40	38/848 (4.5%)
51	B0	2.04	12/510 (2.4%)	2.57	47/677 (6.9%)
52	B1	2.09	12/453 (2.6%)	2.38	25/605 (4.1%)
53	B2	1.99	9/559 (1.6%)	2.58	47/745 (6.3%)
54	B3	2.05	14/450 (3.1%)	2.40	24/599 (4.0%)
55	B4	1.95	6/448 (1.3%)	2.26	19/594 (3.2%)
56	B5	1.98	7/380 (1.8%)	2.49	25/498 (5.0%)
57	B6	2.06	10/513 (1.9%)	2.49	37/676 (5.5%)
58	B7	1.93	6/303 (2.0%)	2.46	16/397 (4.0%)
All	All	1.94	2937/164069 (1.8%)	2.11	8851/244735 (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	907
2	AB	0	36
3	AC	0	31
4	AD	0	44
5	AE	0	5
6	AF	0	2
7	AG	0	7

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Mol	Chain	#Chirality outliers	#Planarity outliers
8	AH	0	6
9	AI	0	5
10	AJ	0	5
11	AK	0	2
12	AL	0	6
13	AM	0	1
14	AN	0	1
15	AO	0	7
16	AP	0	1
17	AQ	0	3
18	AR	0	5
19	AS	0	2
21	AU	0	5
22	AV	0	3
23	AW	0	1
24	AX	0	3
25	BA	0	66
26	BB	0	1683
27	BC	0	3
28	BD	0	10
29	BE	0	5
30	BF	0	3
31	BG	0	9
32	BH	0	4
33	BI	0	2
34	BJ	0	5
35	BK	0	1
36	BL	0	9
37	BM	0	7
38	BN	0	5
39	BO	0	2
40	BP	0	3
41	BQ	0	4
42	BR	0	2
43	BS	0	2
44	BT	0	2
45	BU	0	4
46	BV	0	2
47	BW	0	2
48	BX	0	1
49	BY	0	7
50	BZ	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
52	B1	0	1
53	B2	0	4
54	B3	0	2
55	B4	0	2
56	B5	0	1
57	B6	0	1
58	B7	0	1
All	All	0	2945

The worst 5 of 2937 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	1498	UR3	O3'-P	16.25	1.72	1.56
53	B2	66	ILE	CA-CB	12.85	1.61	1.54
35	BK	21	PRO	CA-C	11.87	1.63	1.52
27	BC	67	HIS	ND1-CE1	10.32	1.42	1.32
26	BB	1872	A	O3'-P	10.07	1.76	1.61

The worst 5 of 8851 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	AI	100	SER	CA-C-N	15.48	135.35	119.56
9	AI	100	SER	C-N-CA	15.48	135.35	119.56
22	AV	57	VAL	CA-C-O	-14.44	110.56	119.51
1	AA	746	A	O4'-C4'-C3'	13.36	117.36	104.00
29	BE	181	ASP	CA-CB-CG	13.25	125.85	112.60

There are no chirality outliers.

5 of 2945 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	11	G	Sidechain
1	AA	2	A	Sidechain
1	AA	4	U	Sidechain
1	AA	8	A	Sidechain
1	AA	9	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	16596	0	0
2	AB	1627	0	840	0	0
3	AC	993	0	501	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	1295	0	0
26	BB	62351	0	31202	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	103728	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%)	217 (91%)	14 (6%)	7 (3%)	3	23
6	AF	230/232 (99%)	217 (94%)	8 (4%)	5 (2%)	5	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	AG	203/205 (99%)	187 (92%)	13 (6%)	3 (2%)	8	40
8	AH	164/166 (99%)	148 (90%)	14 (8%)	2 (1%)	10	44
9	AI	133/135 (98%)	122 (92%)	10 (8%)	1 (1%)	16	54
10	AJ	176/178 (99%)	165 (94%)	9 (5%)	2 (1%)	11	46
11	AK	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	16	54
12	AL	127/129 (98%)	112 (88%)	12 (9%)	3 (2%)	4	27
13	AM	101/103 (98%)	90 (89%)	6 (6%)	5 (5%)	1	16
14	AN	126/128 (98%)	111 (88%)	14 (11%)	1 (1%)	16	54
15	AO	121/123 (98%)	106 (88%)	14 (12%)	1 (1%)	16	54
16	AP	115/117 (98%)	109 (95%)	5 (4%)	1 (1%)	14	51
17	AQ	98/100 (98%)	84 (86%)	7 (7%)	7 (7%)	1	11
18	AR	86/88 (98%)	81 (94%)	4 (5%)	1 (1%)	10	44
19	AS	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
20	AT	81/83 (98%)	72 (89%)	8 (10%)	1 (1%)	10	44
21	AU	72/74 (97%)	61 (85%)	7 (10%)	4 (6%)	1	14
22	AV	89/91 (98%)	82 (92%)	6 (7%)	1 (1%)	11	46
23	AW	84/86 (98%)	78 (93%)	6 (7%)	0	100	100
24	AX	68/70 (97%)	61 (90%)	4 (6%)	3 (4%)	2	17
27	BC	232/234 (99%)	216 (93%)	11 (5%)	5 (2%)	5	29
28	BD	270/272 (99%)	235 (87%)	25 (9%)	10 (4%)	2	20
29	BE	207/209 (99%)	174 (84%)	26 (13%)	7 (3%)	3	21
30	BF	199/201 (99%)	174 (87%)	15 (8%)	10 (5%)	1	16
31	BG	176/178 (99%)	151 (86%)	16 (9%)	9 (5%)	1	15
32	BH	174/176 (99%)	157 (90%)	12 (7%)	5 (3%)	3	23
33	BI	147/149 (99%)	130 (88%)	12 (8%)	5 (3%)	3	21
34	BJ	162/164 (99%)	157 (97%)	4 (2%)	1 (1%)	21	59
35	BK	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
36	BL	140/142 (99%)	120 (86%)	16 (11%)	4 (3%)	3	23
37	BM	121/123 (98%)	109 (90%)	8 (7%)	4 (3%)	3	21
38	BN	142/144 (99%)	124 (87%)	14 (10%)	4 (3%)	4	24
39	BO	134/136 (98%)	123 (92%)	10 (8%)	1 (1%)	18	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	BP	125/127 (98%)	116 (93%)	8 (6%)	1 (1%)	16	54
41	BQ	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
42	BR	112/114 (98%)	98 (88%)	11 (10%)	3 (3%)	4	25
43	BS	115/117 (98%)	108 (94%)	4 (4%)	3 (3%)	4	25
44	BT	101/103 (98%)	90 (89%)	7 (7%)	4 (4%)	2	18
45	BU	108/110 (98%)	98 (91%)	6 (6%)	4 (4%)	2	20
46	BV	98/100 (98%)	76 (78%)	19 (19%)	3 (3%)	3	22
47	BW	101/103 (98%)	88 (87%)	10 (10%)	3 (3%)	3	23
48	BX	92/94 (98%)	87 (95%)	4 (4%)	1 (1%)	11	46
49	BY	82/84 (98%)	64 (78%)	16 (20%)	2 (2%)	4	27
50	BZ	75/77 (97%)	68 (91%)	4 (5%)	3 (4%)	2	18
51	B0	61/63 (97%)	57 (93%)	3 (5%)	1 (2%)	7	38
52	B1	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
53	B2	68/70 (97%)	65 (96%)	2 (3%)	1 (2%)	8	40
54	B3	54/56 (96%)	48 (89%)	4 (7%)	2 (4%)	2	20
55	B4	52/54 (96%)	49 (94%)	1 (2%)	2 (4%)	2	19
56	B5	44/46 (96%)	40 (91%)	2 (4%)	2 (4%)	2	17
57	B6	62/64 (97%)	58 (94%)	3 (5%)	1 (2%)	7	38
58	B7	36/38 (95%)	30 (83%)	3 (8%)	3 (8%)	0	9
All	All	6319/6423 (98%)	5706 (90%)	460 (7%)	153 (2%)	7	27

5 of 153 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	AF	163	ARG
8	AH	77	ASN
13	AM	57	VAL
14	AN	52	ARG
17	AQ	2	LYS

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%)	188 (95%)	10 (5%)	21	42
6	AF	189/189 (100%)	179 (95%)	10 (5%)	20	41
7	AG	172/172 (100%)	166 (96%)	6 (4%)	32	53
8	AH	125/125 (100%)	118 (94%)	7 (6%)	19	40
9	AI	116/116 (100%)	111 (96%)	5 (4%)	26	47
10	AJ	146/146 (100%)	134 (92%)	12 (8%)	10	31
11	AK	104/104 (100%)	98 (94%)	6 (6%)	18	40
12	AL	106/106 (100%)	101 (95%)	5 (5%)	23	45
13	AM	90/90 (100%)	86 (96%)	4 (4%)	25	47
14	AN	98/98 (100%)	94 (96%)	4 (4%)	27	49
15	AO	103/103 (100%)	96 (93%)	7 (7%)	14	36
16	AP	95/95 (100%)	93 (98%)	2 (2%)	47	65
17	AQ	83/83 (100%)	80 (96%)	3 (4%)	31	52
18	AR	76/76 (100%)	74 (97%)	2 (3%)	40	62
19	AS	65/65 (100%)	61 (94%)	4 (6%)	16	38
20	AT	77/77 (100%)	74 (96%)	3 (4%)	28	49
21	AU	64/64 (100%)	61 (95%)	3 (5%)	23	45
22	AV	78/78 (100%)	74 (95%)	4 (5%)	21	42
23	AW	65/65 (100%)	65 (100%)	0	100	100
24	AX	60/60 (100%)	57 (95%)	3 (5%)	22	43
27	BC	181/181 (100%)	170 (94%)	11 (6%)	17	38
28	BD	217/217 (100%)	209 (96%)	8 (4%)	30	51
29	BE	164/164 (100%)	150 (92%)	14 (8%)	10	29
30	BF	165/165 (100%)	157 (95%)	8 (5%)	23	44
31	BG	149/149 (100%)	137 (92%)	12 (8%)	11	31
32	BH	137/137 (100%)	123 (90%)	14 (10%)	7	23
33	BI	114/114 (100%)	111 (97%)	3 (3%)	40	62
34	BJ	122/122 (100%)	121 (99%)	1 (1%)	73	80
35	BK	109/109 (100%)	106 (97%)	3 (3%)	38	60
36	BL	116/116 (100%)	110 (95%)	6 (5%)	21	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	BM	104/104 (100%)	100 (96%)	4 (4%)	29	50
38	BN	103/103 (100%)	98 (95%)	5 (5%)	22	43
39	BO	109/109 (100%)	107 (98%)	2 (2%)	51	68
40	BP	103/103 (100%)	98 (95%)	5 (5%)	22	43
41	BQ	87/87 (100%)	79 (91%)	8 (9%)	8	27
42	BR	99/99 (100%)	93 (94%)	6 (6%)	17	38
43	BS	89/89 (100%)	82 (92%)	7 (8%)	11	32
44	BT	84/84 (100%)	80 (95%)	4 (5%)	23	44
45	BU	93/93 (100%)	89 (96%)	4 (4%)	26	47
46	BV	84/84 (100%)	77 (92%)	7 (8%)	10	30
47	BW	84/84 (100%)	79 (94%)	5 (6%)	17	39
48	BX	78/78 (100%)	73 (94%)	5 (6%)	16	37
49	BY	62/62 (100%)	58 (94%)	4 (6%)	15	37
50	BZ	67/67 (100%)	64 (96%)	3 (4%)	24	46
51	B0	55/55 (100%)	50 (91%)	5 (9%)	9	27
52	B1	48/48 (100%)	46 (96%)	2 (4%)	26	48
53	B2	62/62 (100%)	60 (97%)	2 (3%)	34	56
54	B3	47/47 (100%)	47 (100%)	0	100	100
55	B4	48/48 (100%)	44 (92%)	4 (8%)	10	30
56	B5	38/38 (100%)	35 (92%)	3 (8%)	11	32
57	B6	51/51 (100%)	50 (98%)	1 (2%)	48	66
58	B7	34/34 (100%)	33 (97%)	1 (3%)	37	58
All	All	5213/5213 (100%)	4946 (95%)	267 (5%)	23	42

5 of 267 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	BV	100	GLU
48	BX	7	GLU
55	B4	46	VAL
24	AX	1	PRO
22	AV	13	HIS

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%)	321 (20%)	98 (6%)
2	AB	75/76 (98%)	28 (37%)	8 (10%)
25	BA	119/120 (99%)	17 (14%)	11 (9%)
26	BB	2901/2904 (99%)	558 (19%)	181 (6%)
3	AC	46/47 (97%)	21 (45%)	7 (15%)
4	AD	76/77 (98%)	13 (17%)	3 (3%)
All	All	4758/4766 (99%)	958 (20%)	308 (6%)

5 of 958 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	A
1	AA	3	A
1	AA	5	U
1	AA	6	G
1	AA	7	A

5 of 308 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	BB	1715	G
26	BB	2585	U
26	BB	1828	G
26	BB	2236	U
26	BB	2791	G

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	H2U	AB	20	2	18,21,22	1.43	3 (16%)	19,30,33	1.94	5 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MC	AA	967	1	19,22,23	1.42	1 (5%)	26,32,35	2.06	8 (30%)
1	2MG	AA	1207	1	23,26,27	1.50	3 (13%)	33,38,41	1.48	4 (12%)
26	PSU	BB	2605	26	18,21,22	1.77	4 (22%)	21,30,33	2.32	6 (28%)
26	PSU	BB	2504	26	18,21,22	1.81	3 (16%)	21,30,33	2.34	6 (28%)
26	H2U	BB	2449	26	18,21,22	1.51	4 (22%)	19,30,33	1.17	3 (15%)
26	OMC	BB	2498	26	19,22,23	1.16	4 (21%)	25,31,34	1.89	7 (28%)
4	5MU	AD	55	4	19,22,23	1.49	5 (26%)	27,32,35	1.51	5 (18%)
1	UR3	AA	1498	1	19,22,23	1.47	3 (15%)	26,32,35	2.03	12 (46%)
2	MIA	AB	37	2	28,31,32	2.94	3 (10%)	38,44,47	1.84	7 (18%)
26	2MG	BB	1835	26	23,26,27	1.19	1 (4%)	33,38,41	1.52	4 (12%)
26	PSU	BB	1917	26	18,21,22	1.85	4 (22%)	21,30,33	1.34	2 (9%)
2	PSU	AB	55	2	18,21,22	1.94	5 (27%)	21,30,33	1.75	6 (28%)
1	4OC	AA	1402	1	20,23,24	1.34	3 (15%)	25,32,35	1.49	5 (20%)
26	PSU	BB	2457	26	18,21,22	1.66	4 (22%)	21,30,33	1.33	2 (9%)
1	2MG	AA	966	1	23,26,27	1.33	4 (17%)	33,38,41	1.22	3 (9%)
2	H2U	AB	16	2	18,21,22	2.01	5 (27%)	19,30,33	1.46	3 (15%)
26	1MG	BB	745	26	23,26,27	1.46	3 (13%)	33,39,42	2.39	14 (42%)
26	5MU	BB	1939	26	19,22,23	1.31	2 (10%)	27,32,35	1.92	9 (33%)
1	MA6	AA	1519	1	23,26,27	1.79	5 (21%)	33,38,41	2.04	7 (21%)
1	5MC	AA	1407	1	19,22,23	1.86	4 (21%)	26,32,35	1.48	5 (19%)
2	5MU	AB	54	2	19,22,23	1.52	3 (15%)	27,32,35	2.66	8 (29%)
4	4SU	AD	8	4	18,21,22	2.26	4 (22%)	25,30,33	2.53	9 (36%)
4	PSU	AD	56	4	18,21,22	1.99	4 (22%)	21,30,33	1.30	1 (4%)
26	6MZ	BB	2030	26	22,25,26	1.22	3 (13%)	29,36,39	2.27	9 (31%)
1	7MG	AA	527	1	23,26,27	3.02	5 (21%)	27,39,42	1.54	1 (3%)
26	PSU	BB	1911	26	18,21,22	1.80	5 (27%)	21,30,33	1.63	5 (23%)
26	OMU	BB	2552	26	19,22,23	1.00	2 (10%)	25,31,34	1.64	5 (20%)
26	7MG	BB	2069	26	23,26,27	3.67	5 (21%)	27,39,42	2.01	5 (18%)
26	2MA	BB	2503	26	22,25,26	1.99	4 (18%)	32,37,40	1.81	6 (18%)
26	PSU	BB	2580	26	18,21,22	1.90	4 (22%)	21,30,33	1.91	5 (23%)
26	6MZ	BB	1618	26	22,25,26	1.59	4 (18%)	29,36,39	1.78	7 (24%)
1	MA6	AA	1518	1	23,26,27	1.39	5 (21%)	33,38,41	1.51	7 (21%)
2	H2U	AB	17	2	18,21,22	1.62	4 (22%)	19,30,33	1.54	5 (26%)
2	4SU	AB	8	2	18,21,22	2.12	5 (27%)	25,30,33	1.60	6 (24%)
4	H2U	AD	21	4	18,21,22	1.40	2 (11%)	19,30,33	2.36	5 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
26	5MU	BB	747	26	19,22,23	1.59	3 (15%)	27,32,35	2.13	10 (37%)
1	2MG	AA	1516	1	23,26,27	1.31	4 (17%)	33,38,41	1.24	3 (9%)
4	OMC	AD	33	4	19,22,23	1.02	2 (10%)	25,31,34	1.75	4 (16%)
2	7MG	AB	46	2	23,26,27	3.69	5 (21%)	27,39,42	1.81	4 (14%)
26	PSU	BB	746	26	18,21,22	1.79	5 (27%)	21,30,33	1.96	7 (33%)
2	OMC	AB	32	2	19,22,23	1.12	3 (15%)	25,31,34	1.79	6 (24%)
26	CH	BB	2575	26	16,21,22	1.57	2 (12%)	19,30,33	1.32	2 (10%)
1	PSU	AA	516	1	18,21,22	1.56	4 (22%)	21,30,33	2.01	5 (23%)
26	PSU	BB	955	26	18,21,22	2.03	3 (16%)	21,30,33	2.29	5 (23%)
26	3TD	BB	1915	26	19,22,23	1.92	5 (26%)	23,32,35	1.74	5 (21%)
26	5MC	BB	1962	26	19,22,23	2.81	5 (26%)	26,32,35	1.79	4 (15%)
26	2MG	BB	2445	26	23,26,27	1.11	2 (8%)	33,38,41	1.86	10 (30%)
26	OMG	BB	2251	26	23,26,27	1.07	1 (4%)	32,38,41	1.77	9 (28%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	H2U	AB	20	2	-	0/7/38/39	0/2/2/2
1	5MC	AA	967	1	-	0/7/25/26	0/2/2/2
1	2MG	AA	1207	1	-	0/9/27/28	0/3/3/3
26	PSU	BB	2605	26	-	2/7/25/26	0/2/2/2
26	PSU	BB	2504	26	-	0/7/25/26	0/2/2/2
26	H2U	BB	2449	26	-	0/7/38/39	0/2/2/2
26	OMC	BB	2498	26	-	1/9/27/28	0/2/2/2
4	5MU	AD	55	4	-	0/7/25/26	0/2/2/2
1	UR3	AA	1498	1	-	1/7/25/26	0/2/2/2
2	MIA	AB	37	2	-	1/15/33/34	0/3/3/3
26	2MG	BB	1835	26	-	0/9/27/28	0/3/3/3
26	PSU	BB	1917	26	-	1/7/25/26	0/2/2/2
2	PSU	AB	55	2	-	0/7/25/26	0/2/2/2
1	4OC	AA	1402	1	-	0/9/29/30	0/2/2/2
26	PSU	BB	2457	26	-	0/7/25/26	0/2/2/2
1	2MG	AA	966	1	-	0/9/27/28	0/3/3/3
2	H2U	AB	16	2	-	0/7/38/39	0/2/2/2
26	1MG	BB	745	26	-	0/7/25/26	0/3/3/3
26	5MU	BB	1939	26	-	0/7/25/26	0/2/2/2

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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	5MC	AA	1407	1	-	0/7/25/26	0/2/2/2
2	5MU	AB	54	2	-	0/7/25/26	0/2/2/2
4	4SU	AD	8	4	-	0/7/25/26	0/2/2/2
4	PSU	AD	56	4	-	0/7/25/26	0/2/2/2
26	6MZ	BB	2030	26	-	1/9/27/28	0/3/3/3
1	7MG	AA	527	1	-	1/7/37/38	0/3/3/3
26	PSU	BB	1911	26	-	0/7/25/26	0/2/2/2
26	OMU	BB	2552	26	-	0/9/27/28	0/2/2/2
26	7MG	BB	2069	26	-	1/7/37/38	0/3/3/3
26	2MA	BB	2503	26	-	2/7/25/26	0/3/3/3
26	PSU	BB	2580	26	-	0/7/25/26	0/2/2/2
26	6MZ	BB	1618	26	-	0/9/27/28	0/3/3/3
1	MA6	AA	1518	1	-	0/11/29/30	0/3/3/3
2	H2U	AB	17	2	-	2/7/38/39	0/2/2/2
2	4SU	AB	8	2	-	5/7/25/26	0/2/2/2
4	H2U	AD	21	4	-	0/7/38/39	0/2/2/2
26	5MU	BB	747	26	-	0/7/25/26	0/2/2/2
1	2MG	AA	1516	1	-	1/9/27/28	0/3/3/3
4	OMC	AD	33	4	-	0/9/27/28	0/2/2/2
2	7MG	AB	46	2	-	0/7/37/38	0/3/3/3
26	PSU	BB	746	26	-	3/7/25/26	0/2/2/2
2	OMC	AB	32	2	-	1/9/27/28	0/2/2/2
26	CH	BB	2575	26	-	0/5/25/26	0/2/2/2
1	PSU	AA	516	1	-	1/7/25/26	0/2/2/2
26	PSU	BB	955	26	-	0/7/25/26	0/2/2/2
26	3TD	BB	1915	26	-	1/7/25/26	0/2/2/2
26	5MC	BB	1962	26	-	0/7/25/26	0/2/2/2
26	2MG	BB	2445	26	-	0/9/27/28	0/3/3/3
26	OMG	BB	2251	26	-	0/9/27/28	0/3/3/3

The worst 5 of 176 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	BB	2069	7MG	C8-N9	-16.15	1.35	1.45
2	AB	46	7MG	C8-N9	-15.37	1.35	1.45
2	AB	37	MIA	C2-S10	14.33	1.87	1.75
1	AA	527	7MG	C8-N9	-11.97	1.38	1.45
26	BB	1962	5MC	C5-C4	9.74	1.51	1.44

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AB	46	7MG	N9-C8-N7	6.95	113.21	103.37
26	BB	2069	7MG	N9-C8-N7	6.89	113.13	103.37
1	AA	1519	MA6	N1-C6-N6	6.89	125.25	116.86
4	AD	21	H2U	O4'-C1'-N1	6.33	117.92	109.30
4	AD	8	4SU	C6-N1-C2	-6.27	113.36	121.00

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	AA	1516	2MG	N3-C2-N2-CM2
2	AB	8	4SU	C2'-C1'-N1-C2
2	AB	32	OMC	C1'-C2'-O2'-CM2
26	BB	746	PSU	C2'-C1'-C5-C4
26	BB	2503	2MA	O4'-C1'-N9-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	2,60	15,15,16	2.09	5 (33%)	17,20,22	1.82	4 (23%)
60	FME	BB	3001	59	8,9,10	0.86	0	8,9,11	1.17	1 (12%)

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	2,60	-	0/6/6/8	0/2/2/2
60	FME	BB	3001	59	-	1/7/9/11	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	AB	101	TRP	OXT-C	-4.67	1.22	1.42
59	AB	101	TRP	CZ3-CE3	3.34	1.44	1.38
59	AB	101	TRP	CB-CG	3.11	1.56	1.50
59	AB	101	TRP	C-CA	2.99	1.57	1.52
59	AB	101	TRP	CE3-CD2	2.09	1.43	1.39

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	AB	101	TRP	CD2-CE2-NE1	-3.46	104.64	107.52
59	AB	101	TRP	CE2-NE1-CD1	3.18	111.91	109.08
59	AB	101	TRP	CZ2-CE2-CD2	3.11	125.20	122.19
59	AB	101	TRP	OXT-C-CA	2.52	121.20	111.52
60	BB	3001	FME	CB-CA-N	-2.32	106.29	110.52

There are no chirality outliers.

All (1) torsion outliers are listed below:

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

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
26	BB	2
1	AA	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BB	1872:A	O3'	1873:G	P	1.76
1	AA	1017:U	O3'	1018:G	P	1.75
1	BB	600:G	O3'	601:C	P	1.75

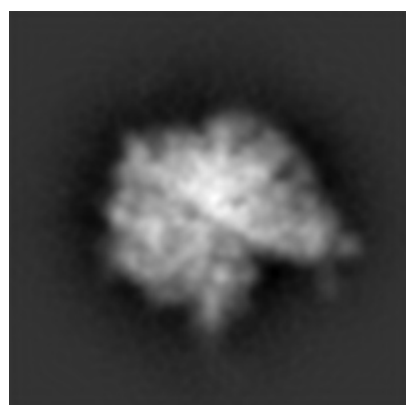
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5363. These allow visual inspection of the internal detail of the map and identification of artifacts.

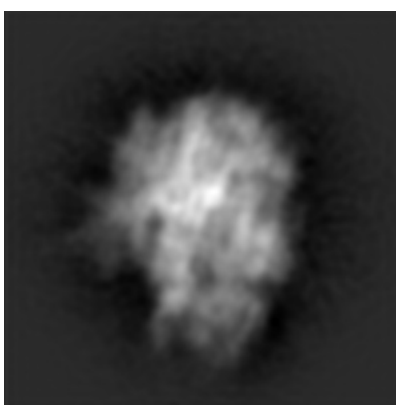
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

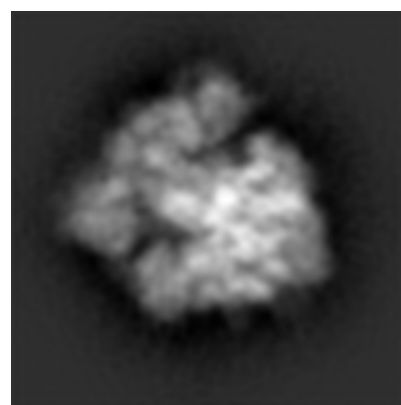
6.1.1 Primary map



X



Y

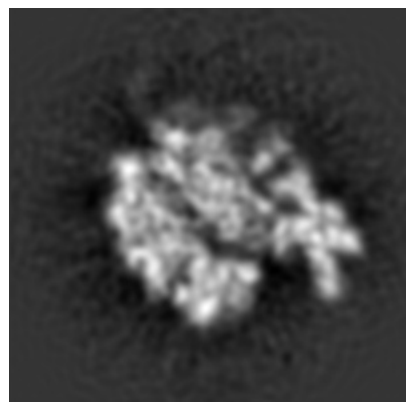


Z

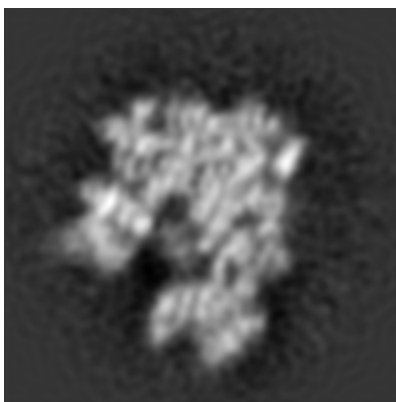
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

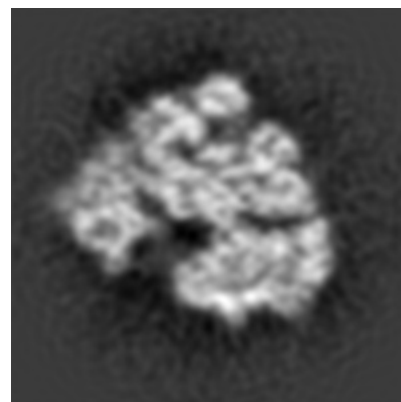
6.2.1 Primary map



X Index: 125



Y Index: 125

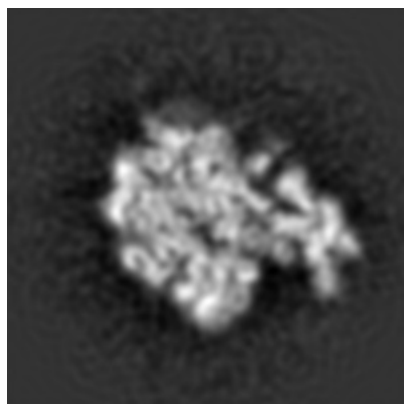


Z Index: 125

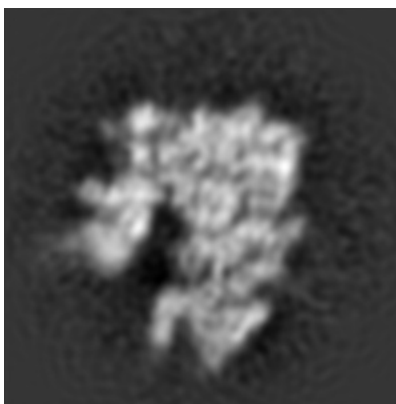
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

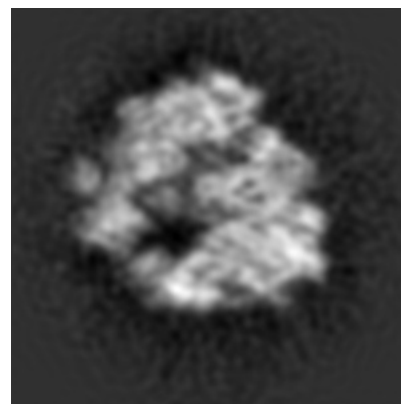
6.3.1 Primary map



X Index: 129



Y Index: 131

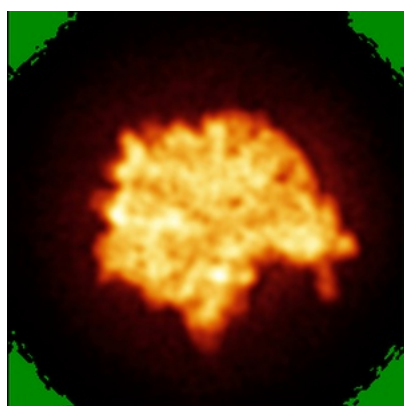


Z Index: 115

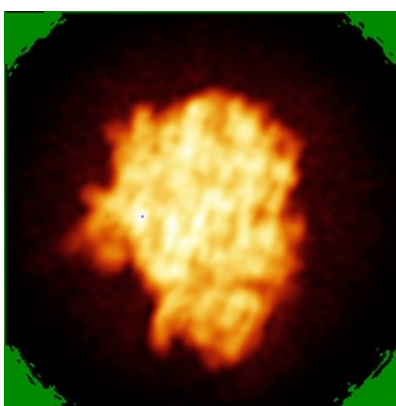
The images above show the largest variance slices of the map in three orthogonal directions.

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

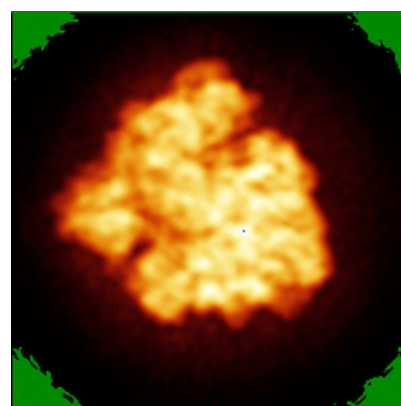
6.4.1 Primary map



X



Y

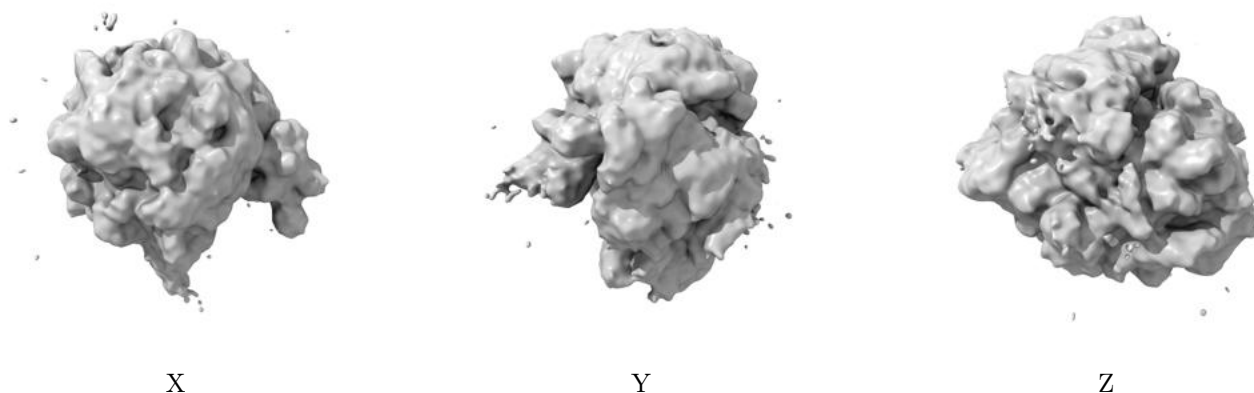


Z

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.

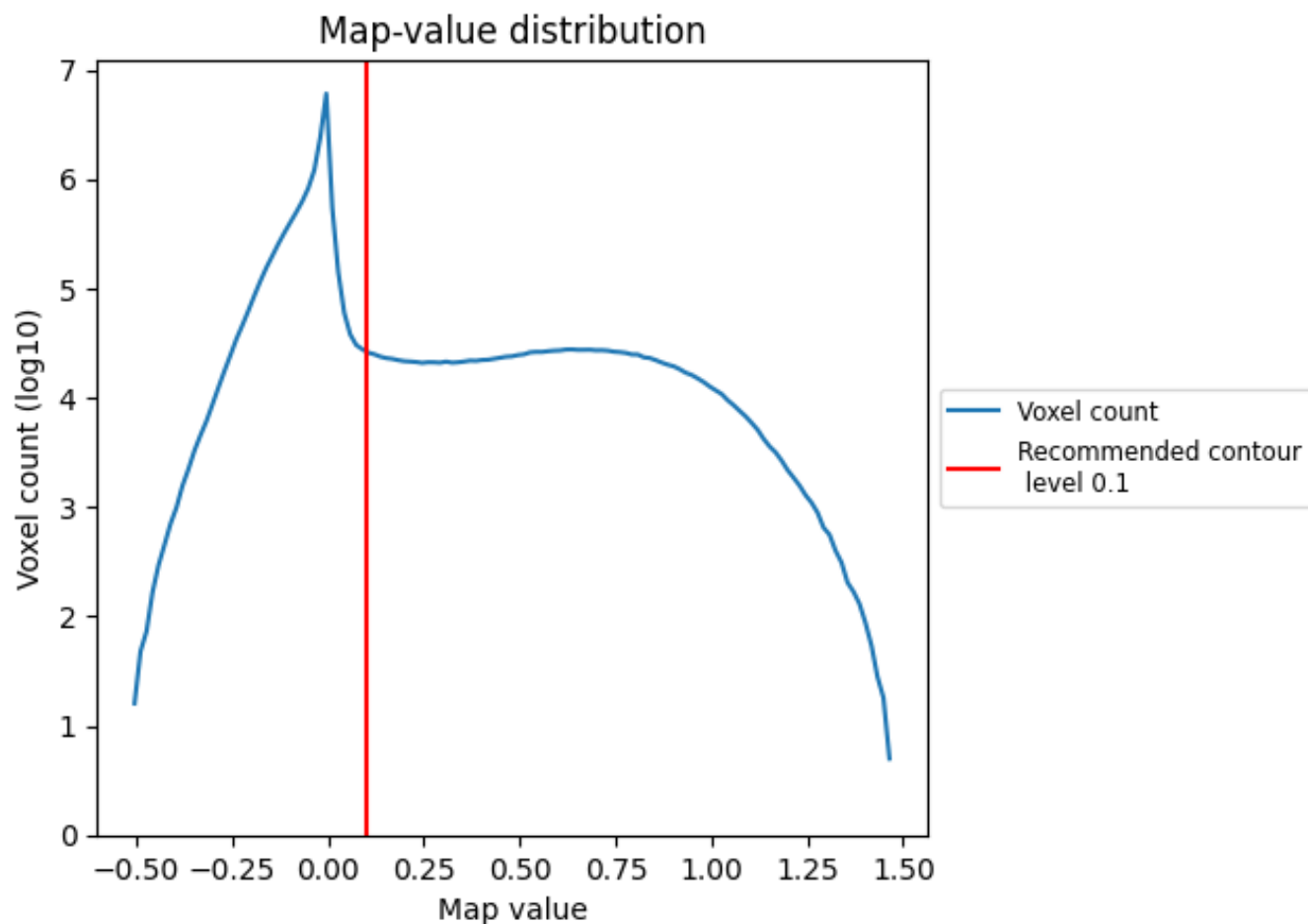
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

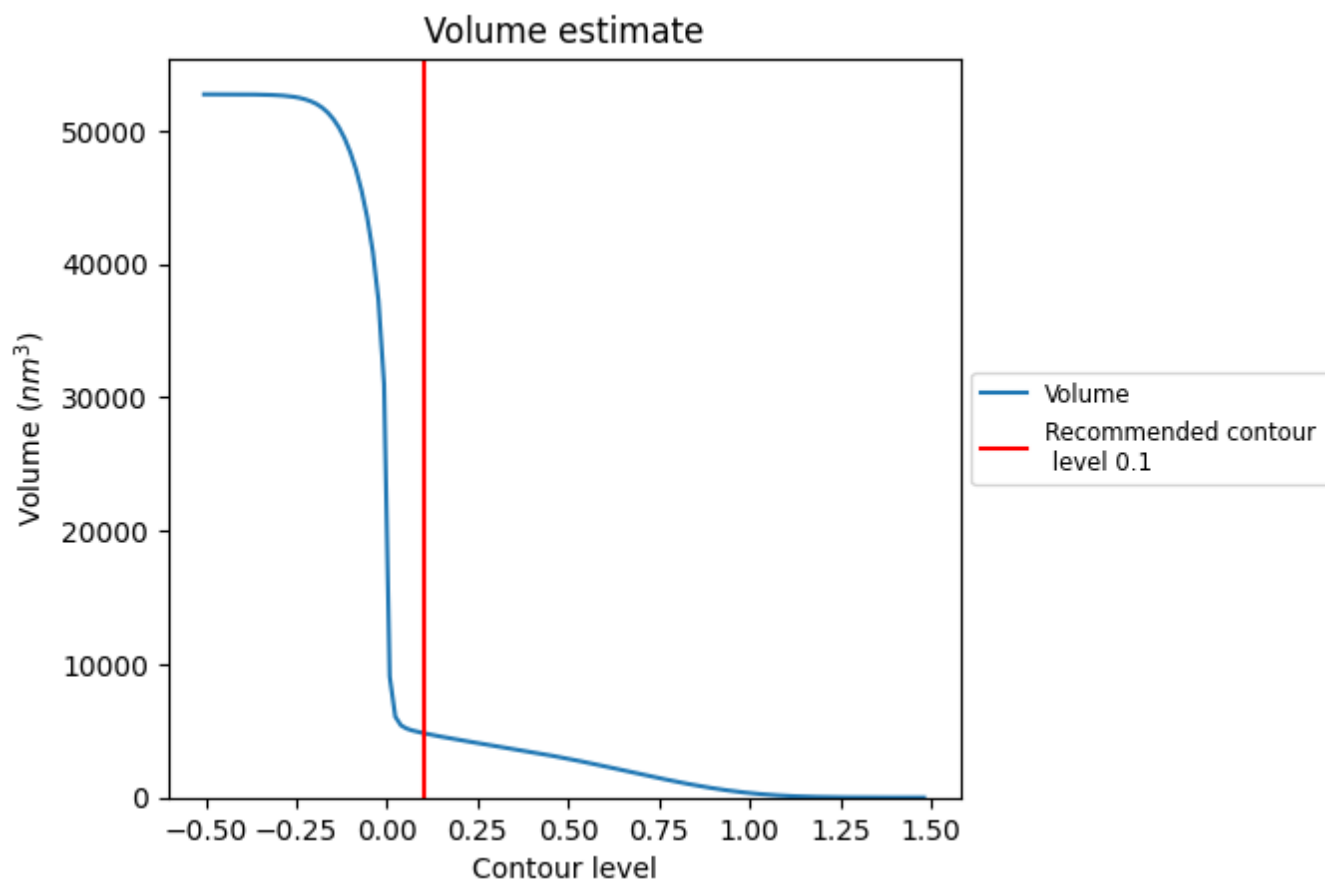
This section contains the results of statistical analysis of the map.

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.

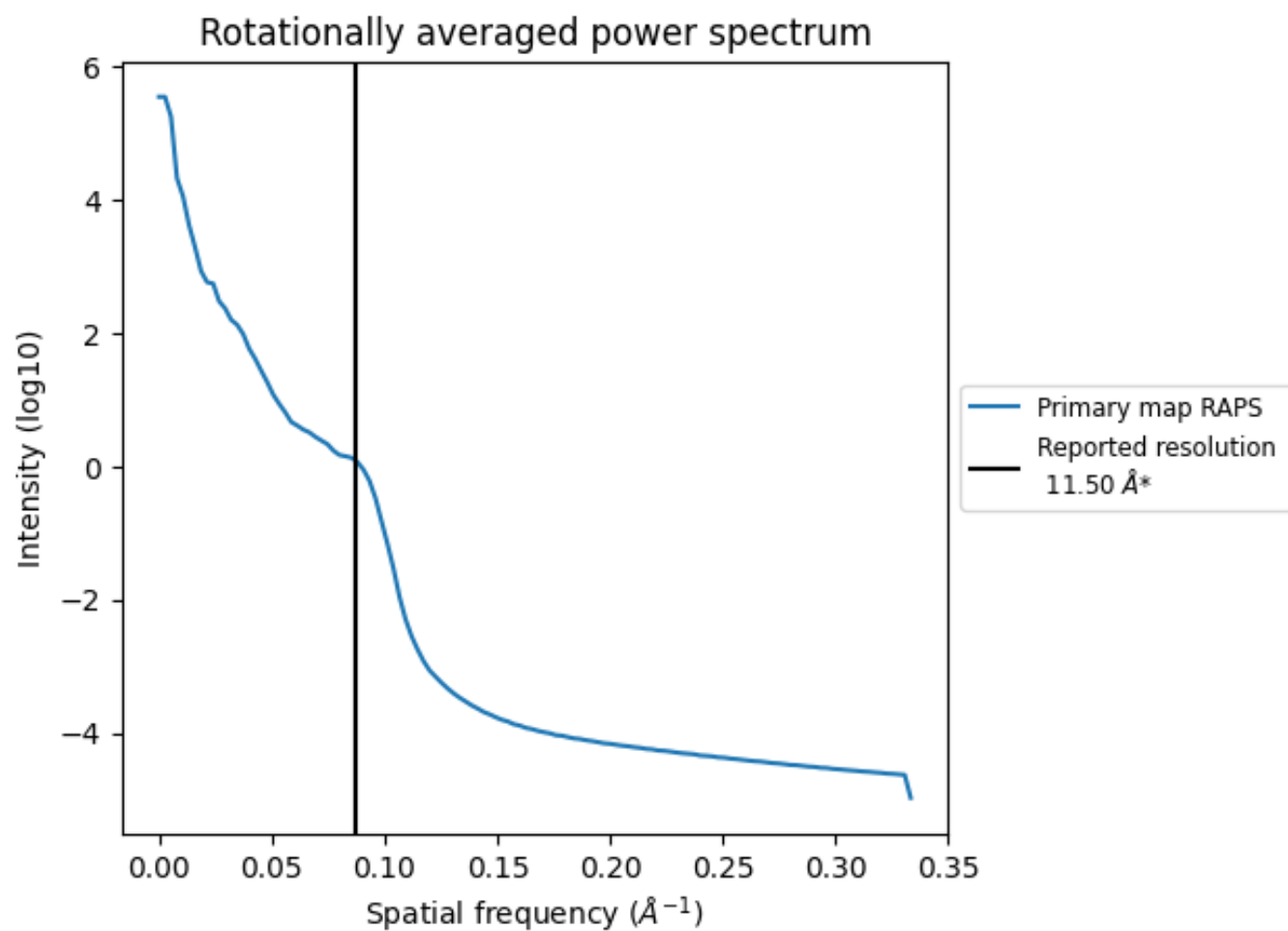
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4835 nm³; this corresponds to an approximate mass of 4367 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

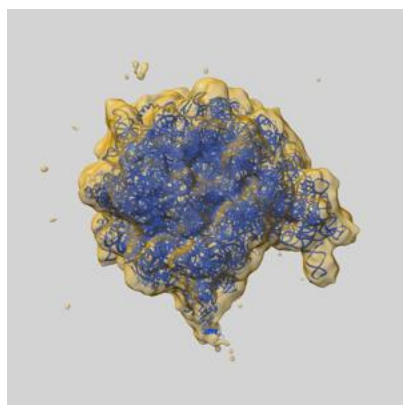
8 Fourier-Shell correlation

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

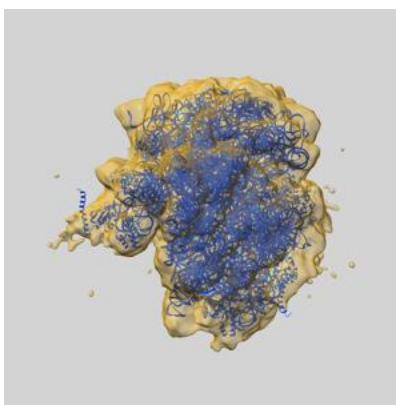
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5363 and PDB model 4V6Q. Per-residue inclusion information can be found in section 3 on page 16.

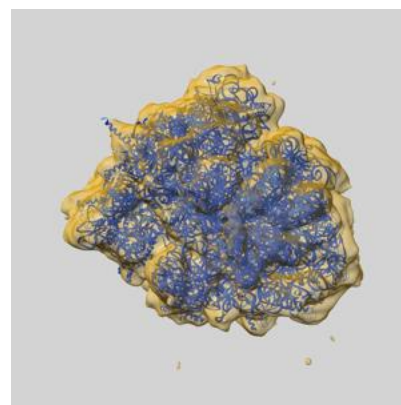
9.1 Map-model overlay [i](#)



X



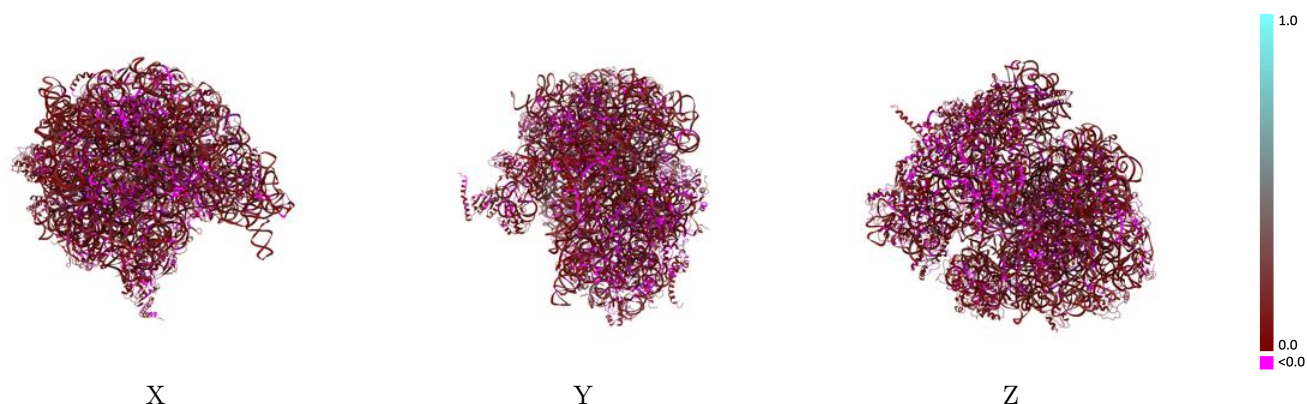
Y



Z

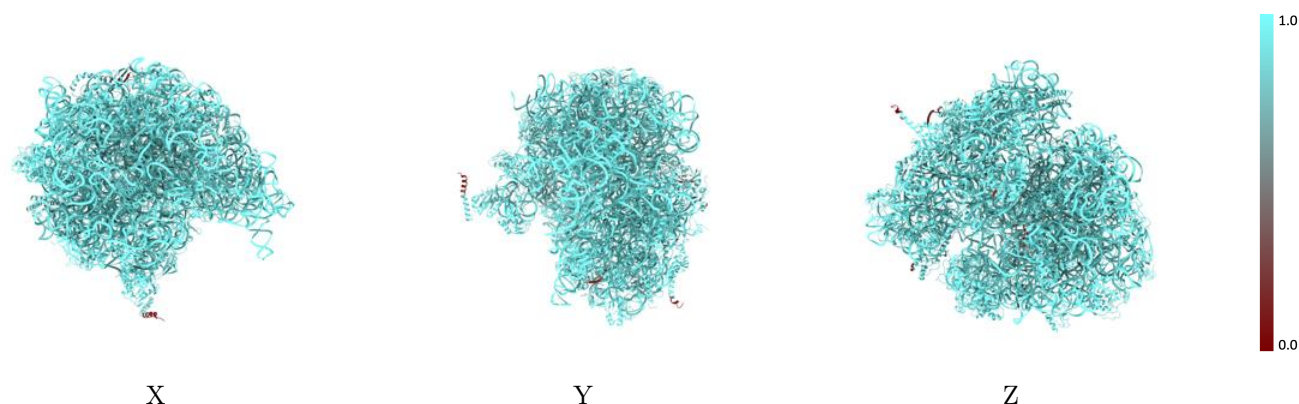
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



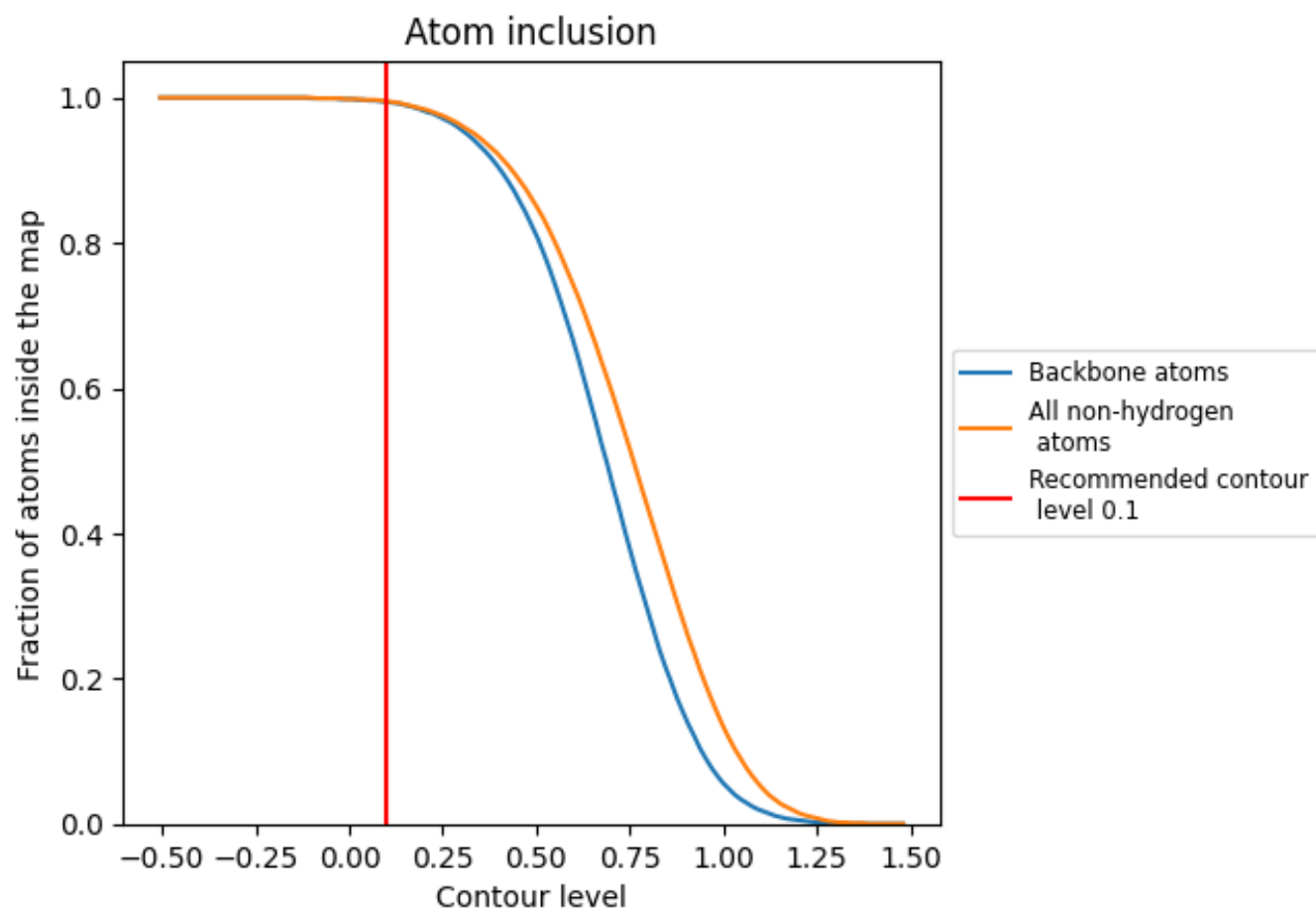
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



At the recommended contour level, 99% of all backbone atoms, 100% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9950	0.0740
AA	1.0000	0.0910
AB	0.9860	0.0530
AC	0.8950	0.0140
AD	0.9940	0.0980
AE	0.9470	0.0370
AF	0.9990	0.0630
AG	0.9990	0.0450
AH	0.9930	0.0430
AI	0.9810	0.0410
AJ	0.9910	0.0540
AK	0.9980	0.0400
AL	0.9810	0.0480
AM	1.0000	0.0220
AN	0.9930	0.0420
AO	0.9890	0.0400
AP	0.9750	0.0410
AQ	1.0000	0.0400
AR	1.0000	0.0540
AS	0.9980	0.0100
AT	1.0000	0.0560
AU	1.0000	0.0290
AV	0.9790	0.0360
AW	1.0000	0.0460
AX	1.0000	0.0290
B0	1.0000	0.0320
B1	1.0000	0.0430
B2	0.9810	0.0180
B3	1.0000	0.0280
B4	0.9980	0.0540
B5	1.0000	0.0030
B6	1.0000	0.0370
B7	1.0000	0.0320
BA	1.0000	0.1010
BB	1.0000	0.0910



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Chain	Atom inclusion	Q-score
BC	 0.9910	 0.0420
BD	 1.0000	 0.0180
BE	 0.9990	 0.0240
BF	 0.9990	 0.0650
BG	 0.9910	 0.0460
BH	 1.0000	 0.0250
BI	 0.8510	 0.0260
BJ	 0.9000	 0.0450
BK	 0.9730	 0.0380
BL	 1.0000	 0.0330
BM	 0.9960	 0.0600
BN	 0.9990	 0.0160
BO	 1.0000	 0.0440
BP	 1.0000	 0.0250
BQ	 0.9950	 0.0580
BR	 0.9980	 0.0280
BS	 0.9980	 0.0250
BT	 0.9950	 0.0480
BU	 0.9980	 0.0270
BV	 0.9990	 0.0330
BW	 1.0000	 0.0690
BX	 1.0000	 0.0740
BY	 0.9980	 0.0240
BZ	 1.0000	 0.0350