



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 11:46 PM UTC

PDB ID : 4V6N / pdb_00004v6n
EMDB ID : EMD-5361
Title : Structural characterization of mRNA-tRNA translocation intermediates (50S ribosome of class2 of the six classes)
Authors : Agirrezabala, X.; Liao, H.; Schreiner, E.; Fu, J.; Ortiz-Meoz, R.F.; Schulten, K.; Green, R.; Frank, J.
Deposited on : 2011-12-07
Resolution : 12.10 Å (reported)
Based on initial models : 1MZP, 1ZAV, 2I2V

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

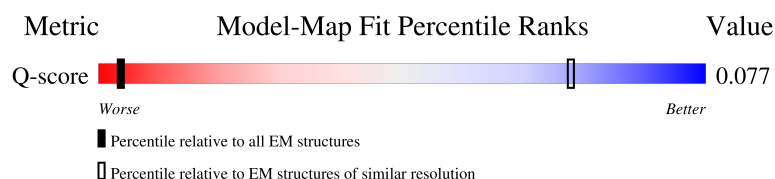
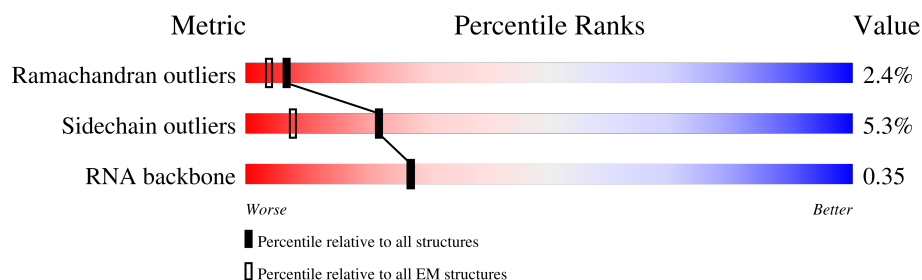
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 12.10 Å.

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



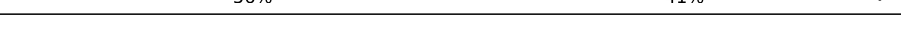
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	85 (11.60 - 12.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	120	
2	AB	2904	
3	AC	234	
4	AD	272	

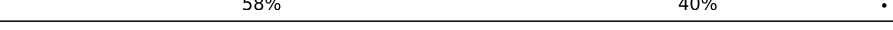
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Mol	Chain	Length	Quality of chain
5	AE	209	
6	AF	201	
7	AG	178	
8	AH	176	
9	AI	149	
10	AJ	164	
11	AK	141	
12	AL	142	
13	AM	123	
14	AN	144	
15	AO	136	
16	AP	127	
17	AQ	117	
18	AR	114	
19	AS	117	
20	AT	103	
21	AU	110	
22	AV	100	
23	AW	103	
24	AX	94	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

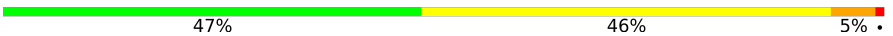
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Mol	Chain	Length	Quality of chain
30	A3	56	
31	A4	54	
32	A5	46	
33	A6	64	
34	A7	38	
35	BA	1542	
36	BB	76	
37	BC	47	
38	BD	77	
39	BE	240	
40	BF	232	
41	BG	205	
42	BH	166	
43	BI	135	
44	BJ	178	
45	BK	129	
46	BL	129	
47	BM	103	
48	BN	128	
49	BO	123	
50	BP	117	
51	BQ	100	
52	BR	88	
53	BS	82	
54	BT	83	

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Mol	Chain	Length	Quality of chain
55	BU	74	 49% 46% 5%
56	BV	91	 47% 46% 5% •
57	BW	86	 52% 45% ••
58	BX	70	 60% 34% 6%

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 5S ribosomal RNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 36 is a RNA chain called A site tRNA.

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

- Molecule 37 is a RNA chain called mRNA.

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

- Molecule 38 is a RNA chain called P site tRNA.

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

- Molecule 39 is a protein called 30S ribosomal protein S2.

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

- Molecule 40 is a protein called 30S ribosomal protein S3.

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

- Molecule 41 is a protein called 30S ribosomal protein S4.

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

- Molecule 42 is a protein called 30S ribosomal protein S5.

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

- Molecule 43 is a protein called 30S ribosomal protein S6.

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

- Molecule 44 is a protein called 30S ribosomal protein S7.

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

- Molecule 45 is a protein called 30S ribosomal protein S8.

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

- Molecule 46 is a protein called 30S ribosomal protein S9.

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

- Molecule 47 is a protein called 30S ribosomal protein S10.

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

- Molecule 48 is a protein called 30S ribosomal protein S11.

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

- Molecule 49 is a protein called 30S ribosomal protein S12.

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

- Molecule 50 is a protein called 30S ribosomal protein S13.

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

- Molecule 51 is a protein called 30S ribosomal protein S14.

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

- Molecule 52 is a protein called 30S ribosomal protein S15.

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

- Molecule 53 is a protein called 30S ribosomal protein S16.

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

- Molecule 54 is a protein called 30S ribosomal protein S17.

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

- Molecule 55 is a protein called 30S ribosomal protein S18.

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

- Molecule 56 is a protein called 30S ribosomal protein S19.

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

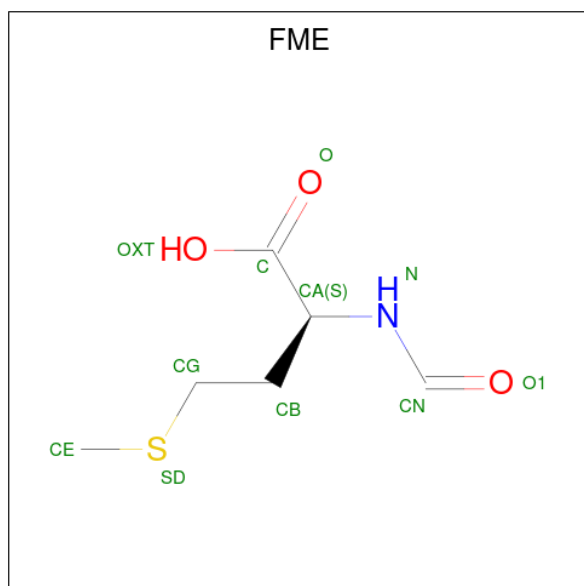
- Molecule 57 is a protein called 30S ribosomal protein S20.

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

- Molecule 58 is a protein called 30S ribosomal protein S21.

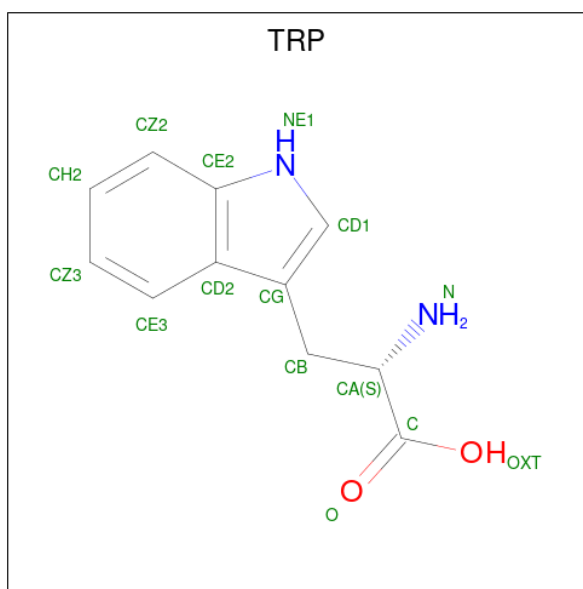
Mol	Chain	Residues	Atoms					AltConf	Trace
58	BX	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 59 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: $C_6H_{11}NO_3S$).



Mol	Chain	Residues	Atoms					AltConf
59	AB	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 60 is TRYPTOPHAN (CCD ID: TRP) (formula: $C_{11}H_{12}N_2O_2$).

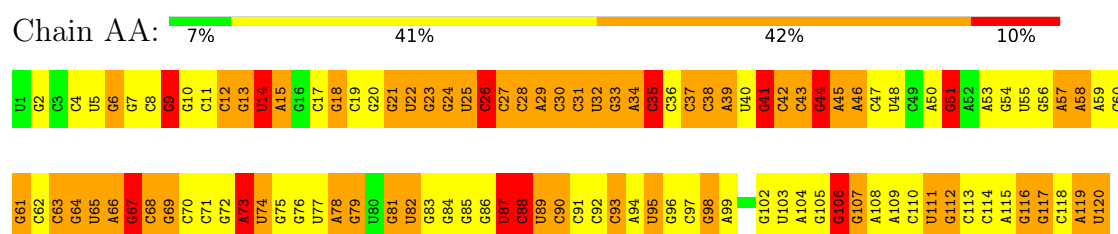


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
60	BB	1	14	11	2	1	0

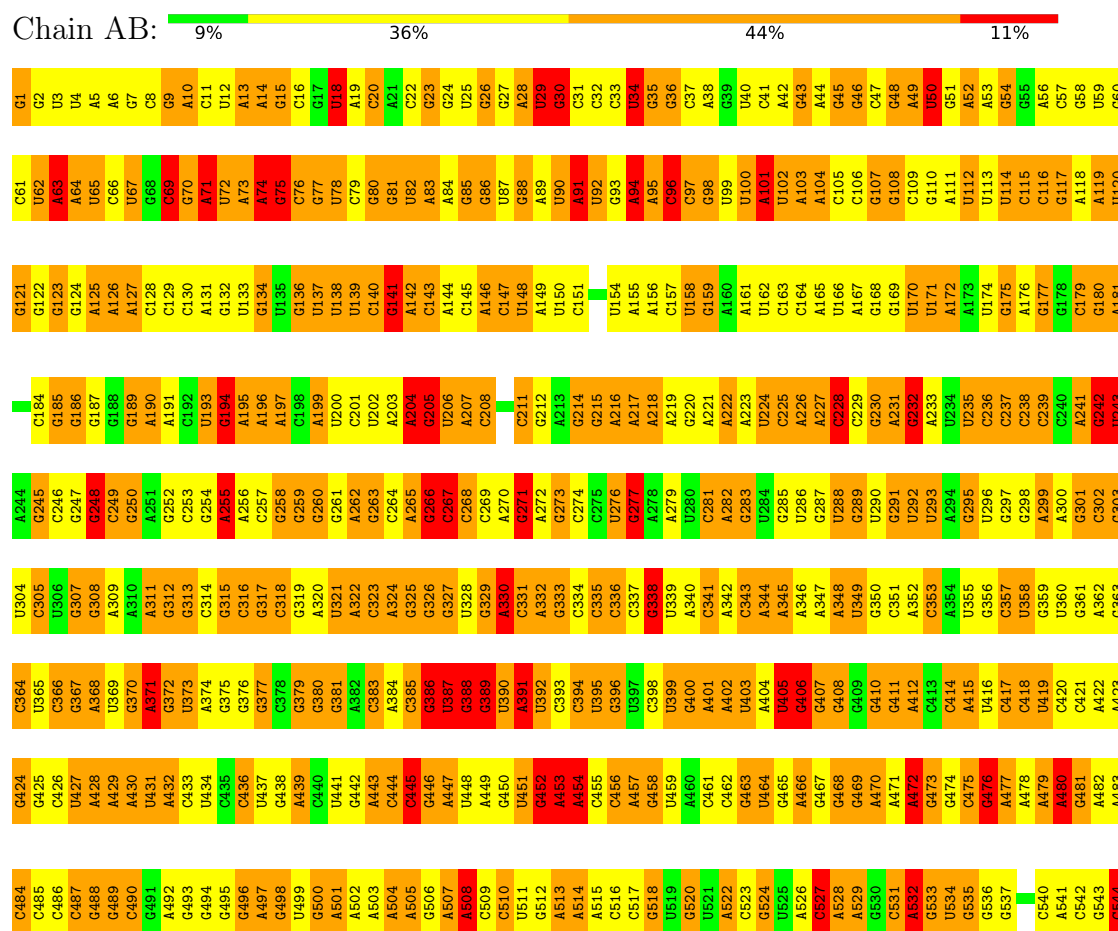
3 Residue-property plots

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: 5S ribosomal RNA

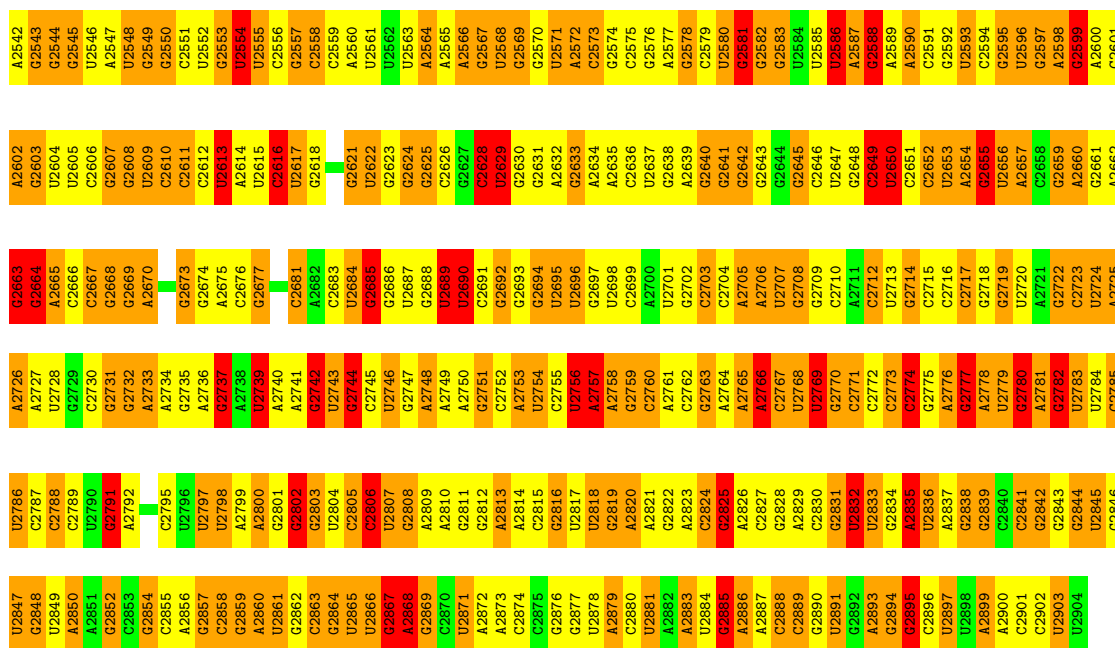


• Molecule 2: 23S ribosomal RNA

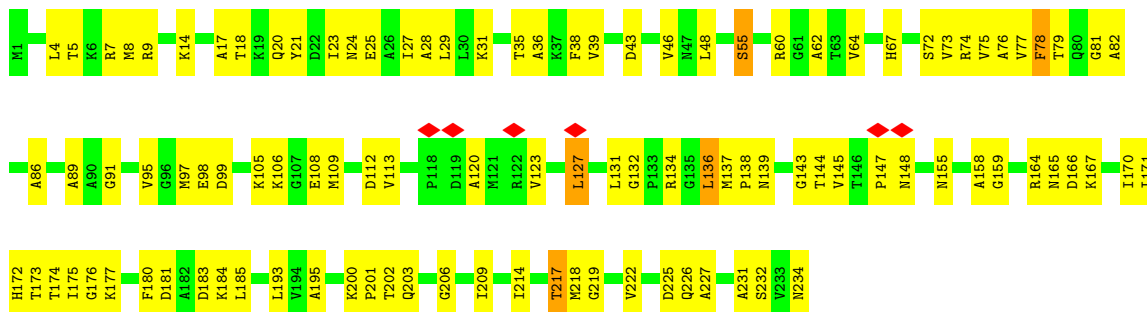


G1514	G1515	G1453	G1391	G1331	G1270	G1210	G1150	A1089	A909	A849	A788	G728	U665	G605	U545
G1454	G1516	G1455	A1392	G1332	G1271	G1211	A1151	A1090	A910	U850	A789	G729	A666	U606	U546
G1456	G1517	G1456	A1393	G1333	A1272	G1212	G1152	G1091	A911	C851	U790	A730	U667	U607	A547
G1457	G1518	G1457	U1394	G1334	U1273	A1213	G1153	C1092	C912	U852	C791	C731	A668	A608	G548
G1458	G1519	G1458	A1395	A1335	A1274	A1214	G1154	U1093	U913	G669	A792	C732	G669	A609	G549
G1459	U1520	G1459	U1396	A1336	A1275	G1215	U1155	U1094	G914	C854	A793	G733	C670	C610	C550
U1460	U1397	A1276	A1276	G1337	A1276	G1216	A1156	A1095	C915	G855	A794	A734	C671	C611	G551
U1398	G1398	G1277	G1277	G1338	G1278	U1217	G1157	A1096	G916	G856	C795	A735	C672	G612	U552
C1399	C1399	G1278	G1278	G1339	G1278	U1218	G1158	U1097	A917	G857	C796	G736	C673	A613	G553
U1400	U1400	G1279	G1279	U1340	G1279	U1219	G1159	A1098	A918	G858	C797	C737	G674	G614	U554
G1401	G1401	G1280	G1280	G1341	G1280	G1220	G1160	G1099	U919	G859	G798	G738	A675	G615	G555
A1402	A1402	G1281	G1281	A1342	G1281	C1221	C1161	U1100	A920	U860	G799	A739	A676	U616	A556
A1403	A1403	U1282	U1282	G1343	U1282	C1222	G1162	U1101	C921	A861	A800	A740	A677	G617	C557
C1404	C1404	G1283	G1283	U1344	G1283	G1223	G1163	C1102	C922	G862	C801	U741	C678	G618	U558
U1405	U1405	A1284	A1284	G1345	A1284	U1224	C1164	A1103	G923	A863	A802	A742	C679	G619	G559
A1406	A1406	G1285	G1285	G1346	A1285	G1225	A1165	C1104	G924	G864	U803	A743	C680	C560	C560
A1407	A1407	A1286	A1286	A1347	A1286	A1226	G1166	U1105	C925	C865	A804	U744	G681	A621	U561
G1408	G1408	A1287	A1287	C1348	A1287	G1227	C1167	G1106	G926	A866	G745	U745	G682	G622	U562
U1409	U1409	G1288	G1288	C1349	G1288	G1228	G1168	G1107	A927	C867	U746	U746	U683	C623	A563
G1410	G1410	C1289	C1289	C1350	C1289	G1229	A1169	U1108	A928	U868	U747	U747	G684	C624	C564
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C1414	C1414	U1294	U1294	A1355	U1294	C1233	U1173	G1112	U932	U872	C812	A751	U688	G628	U568
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G1420	G1420	U1300	U1300	C1360	U1300	G1239	G1179	G1120	U938	A878	C818	G757	A694	C634	A574
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G1422	G1422	A1302	A1302	C1362	A1302	A1241	U1181	G1122	U940	U880	A820	C759	G696	G636	U576
U1423	U1423	G1303	G1303	C1363	G1303	U1242	G1182	U1061	A941	C881	A821	G760	C697	A637	G577
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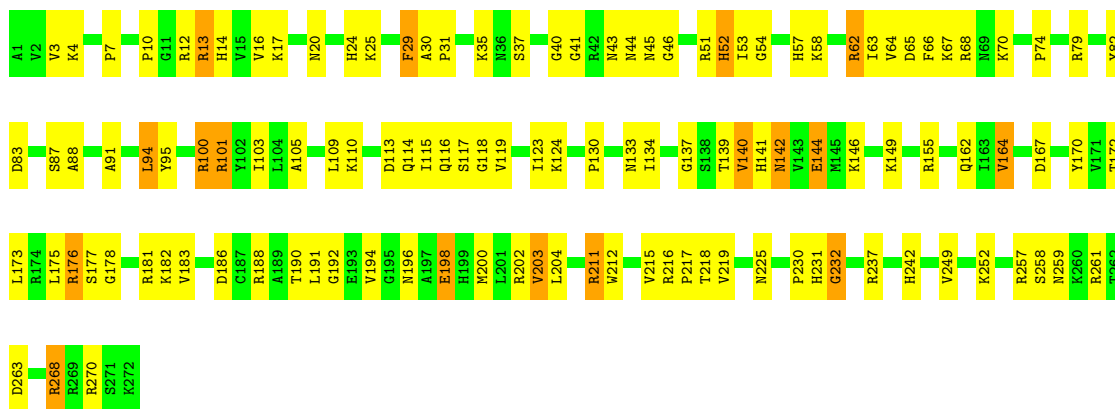
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• Molecule 3: 50S ribosomal protein L1

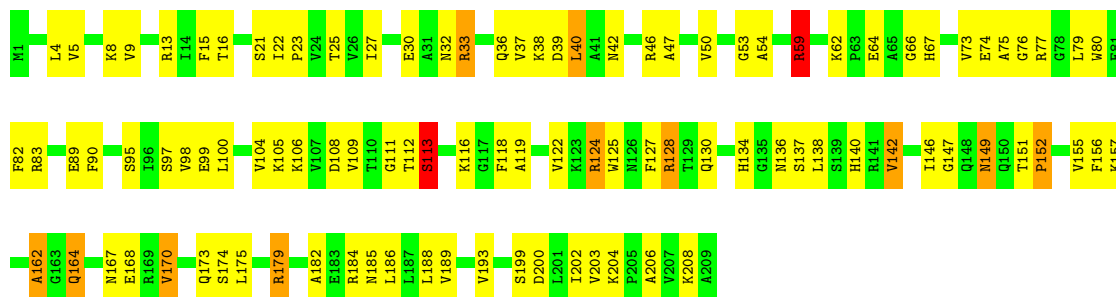


• Molecule 4: 50S ribosomal protein L2



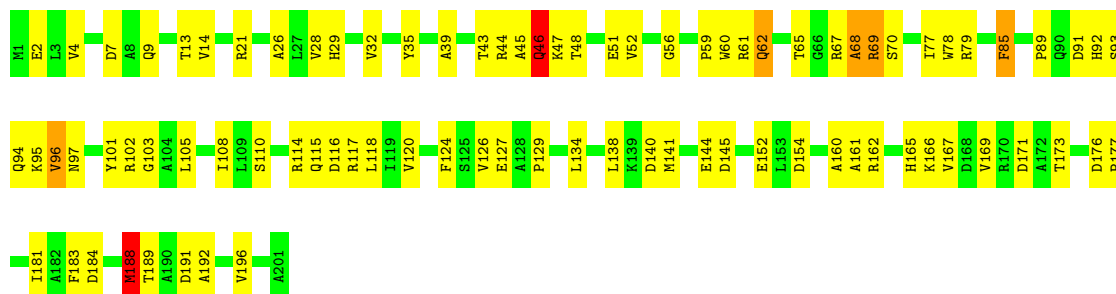
• Molecule 5: 50S ribosomal protein L3

Chain AE:  52% 42% 5% .

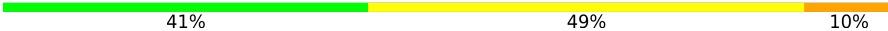


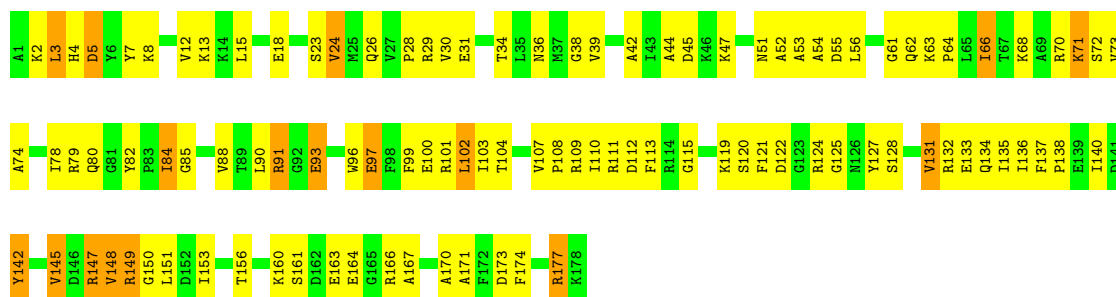
• Molecule 6: 50S ribosomal protein L4

Chain AF:  57% 39% ..



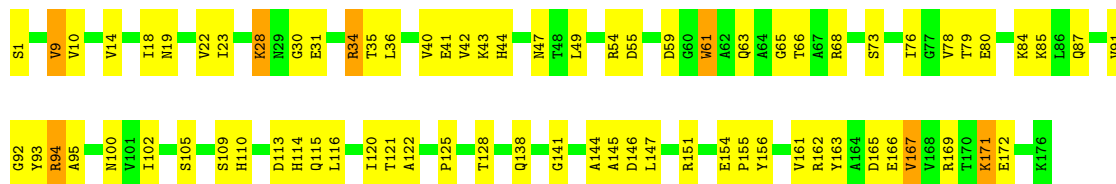
• Molecule 7: 50S ribosomal protein L5

Chain AG:  41% 49% 10%

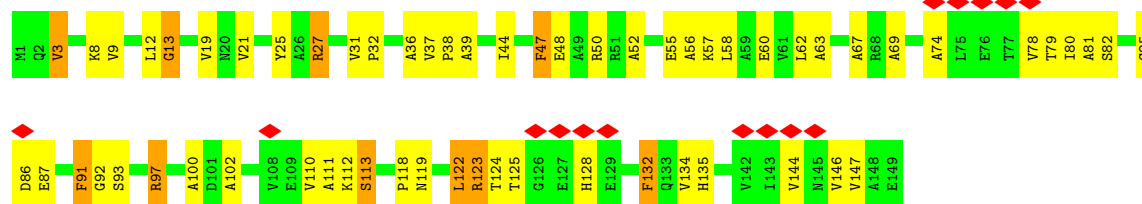


• Molecule 8: 50S ribosomal protein L6

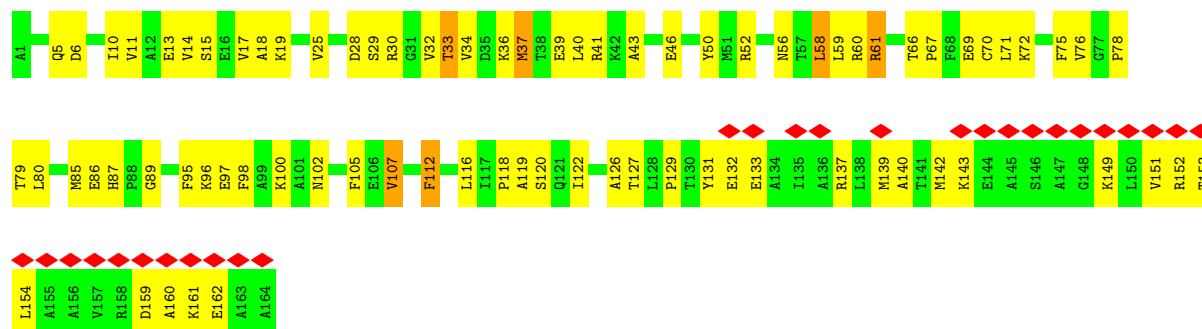
Chain AH:  57% 39% .



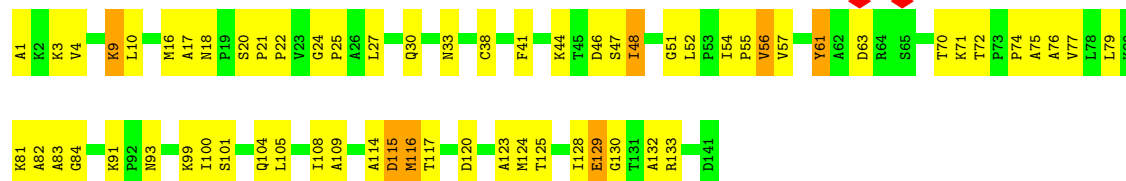
• Molecule 9: 50S ribosomal protein L9



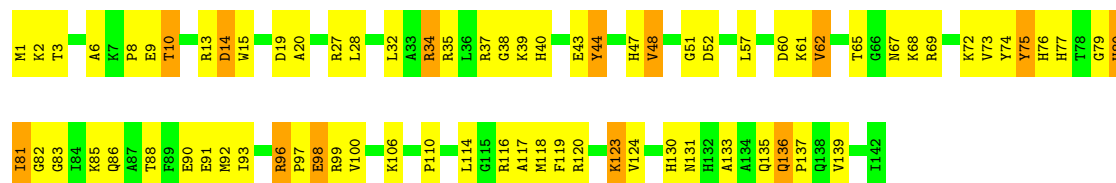
• Molecule 10: 50S ribosomal protein L10



• Molecule 11: 50S ribosomal protein L11

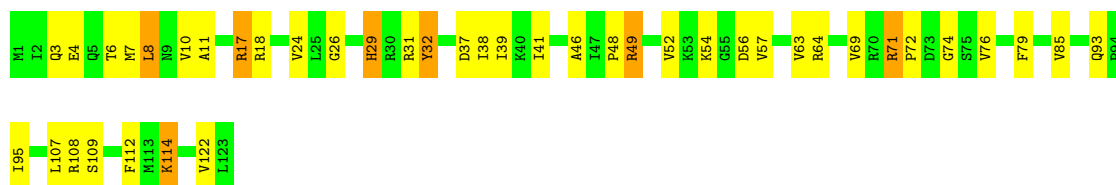


• Molecule 12: 50S ribosomal protein L13



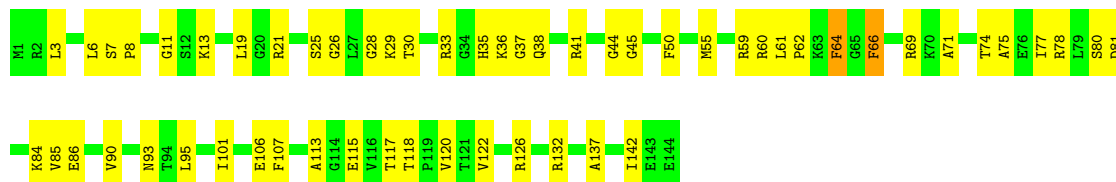
• Molecule 13: 50S ribosomal protein L14





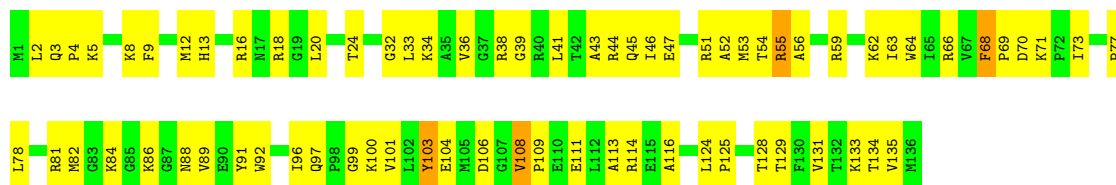
- Molecule 14: 50S ribosomal protein L15

Chain AN: 61% 38% .



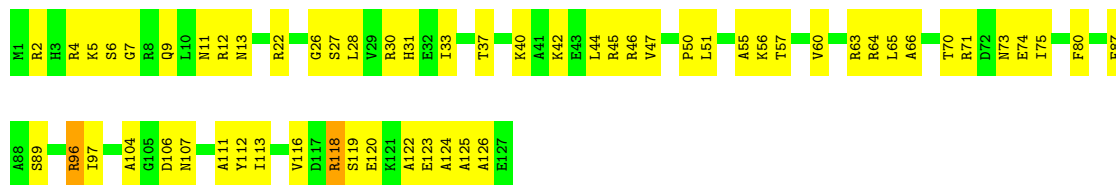
- Molecule 15: 50S ribosomal protein L16

Chain AO: 47% 50% .



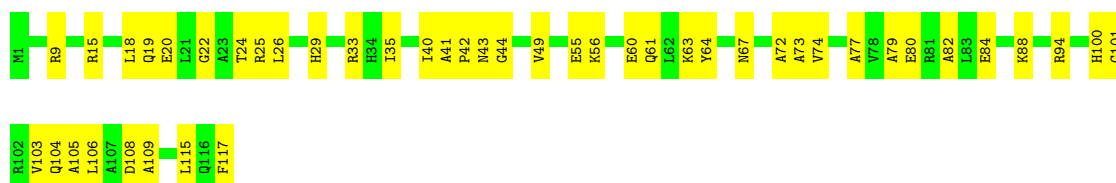
- Molecule 16: 50S ribosomal protein L17

Chain AP: 54% 44% .



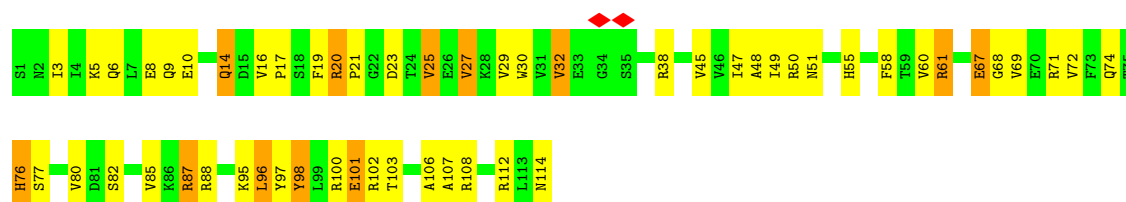
- Molecule 17: 50S ribosomal protein L18

Chain AQ: 62% 38%



- Molecule 18: 50S ribosomal protein L19

Chain AR: 52% 38% 11%



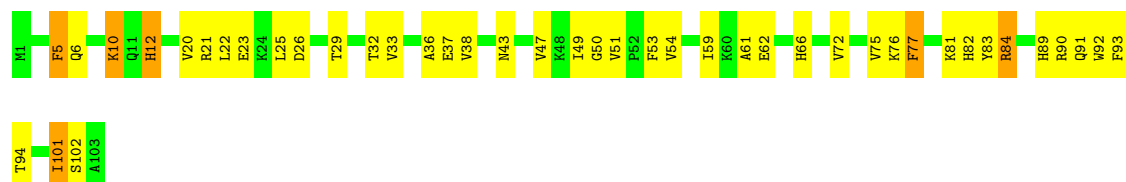
- Molecule 19: 50S ribosomal protein L20

Chain AS: 56% 41% .



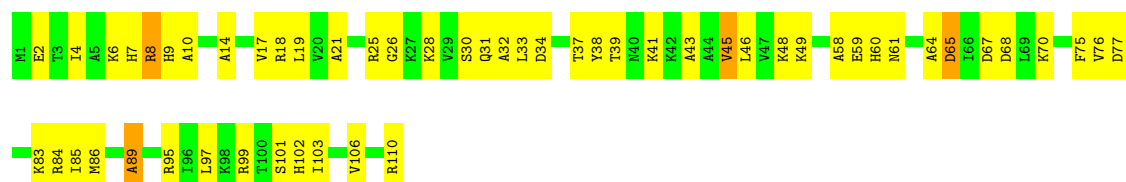
- Molecule 20: 50S ribosomal protein L21

Chain AT: 58% 36% 6%



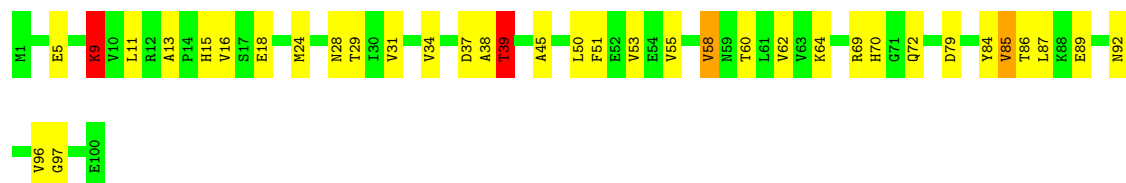
- Molecule 21: 50S ribosomal protein L22

Chain AU: 51% 45% .



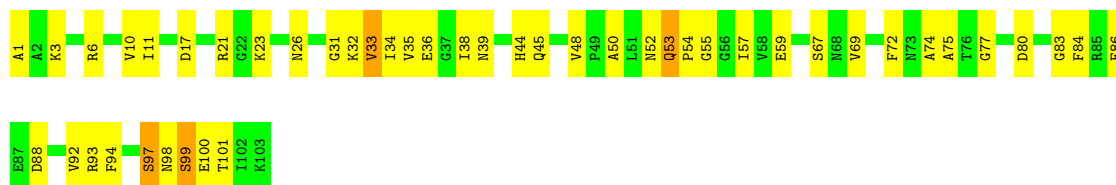
- Molecule 22: 50S ribosomal protein L23

Chain AV: 64% 32% . .



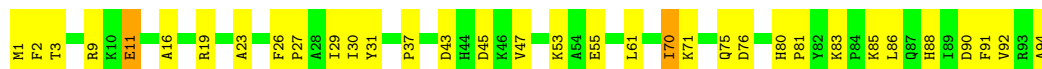
- Molecule 23: 50S ribosomal protein L24

Chain AW:  55% 41% .



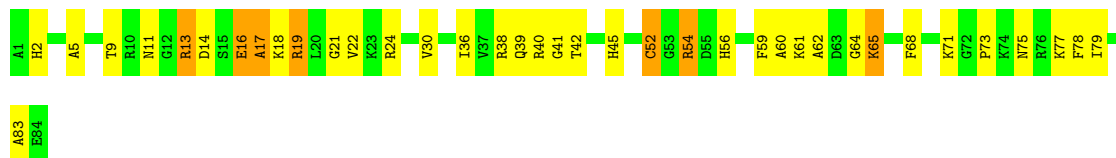
- Molecule 24: 50S ribosomal protein L25

Chain AX:  64% 34% .

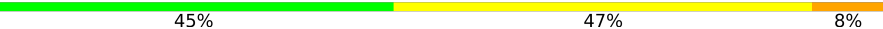


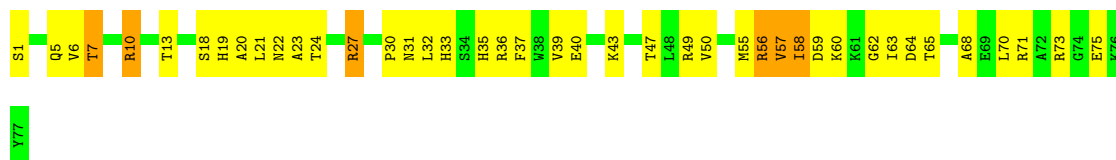
- Molecule 25: 50S ribosomal protein L27

Chain AY:  55% 37% 8%



- Molecule 26: 50S ribosomal protein L28

Chain AZ:  45% 47% 8%



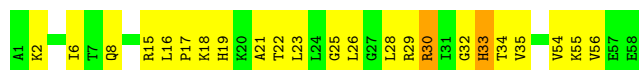
- Molecule 27: 50S ribosomal protein L29

Chain A0:  51% 43% 6%



- Molecule 28: 50S ribosomal protein L30

Chain A1:  60% 36% .



- Molecule 29: 50S ribosomal protein L31

Chain A2:  51% 46%



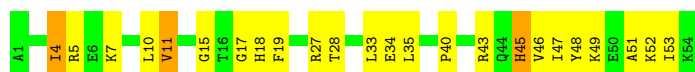
- Molecule 30: 50S ribosomal protein L32

Chain A3:  57% 34% 9%



- Molecule 31: 50S ribosomal protein L33

Chain A4:  56% 39% 6%

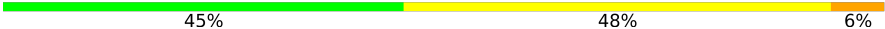


- Molecule 32: 50S ribosomal protein L34

Chain A5:  37% 54%



- Molecule 33: 50S ribosomal protein L35

Chain A6:  45% 48% 6%



- Molecule 34: 50S ribosomal protein L36

Chain A7:  50% 47%

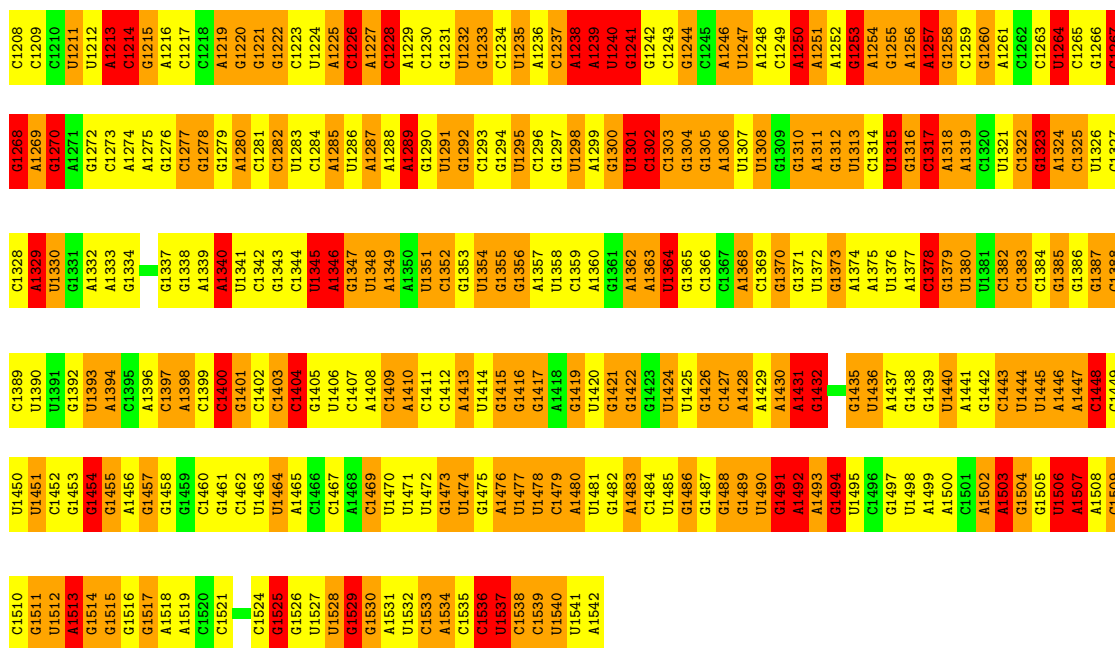


- Molecule 35: 16S ribosomal RNA

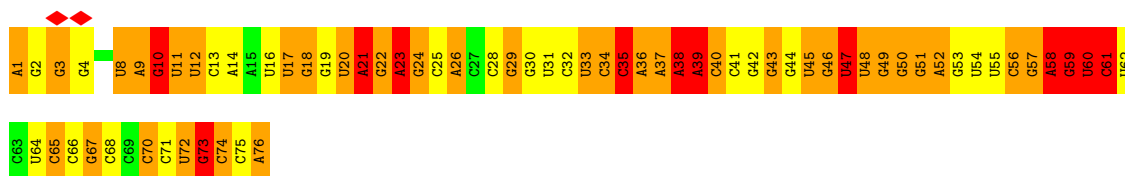
Chain BA:  7% 37% 44% 12%



U1148	U1086	G1026	G966	A906	A845	G785	G725	A665	U605	C545	U485	G424	A364	A303	A243	C183	U123
C1149	G1087	C1027	C967	A907	G846	G786	C726	G666	G606	A546	U486	G425	U365	U304	U244	C184	C124
A1150	G1088	U1028	A968	A908	G847	A787	G727	G667	A607	A547	A487	U426	U366	G305	U245	U185	U126
A1151	G1089	U1029	A969	A909	C948	U788	A728	G668	A608	A548	C488	U427	U367	A306	A246	C186	G126
A1152	U1090	U1030	C970	C910	G849	U789	A729	G669	A609	A549	C489	G428	U368	G307	G247	G187	G127
G1153	U1091	C1031	G971	U911	U850	A790	G730	G670	U610	G550	C490	U429	G369	C308	C248	C188	G128
A1154	A1092	G1032	C972	C912	G851	G791	G731	G671	C611	U551	A491	A430	C370	A309	U249	A189	A129
A1155	A1093	G1033	G973	A913	G852	A792	G732	U672	C612	U552	C492	A431	A371	G310	A250	A190	A130
G1156	G1094	U1034	A974	A914	C953	U793	G733	A673	C613	A553	A493		C372	C311	A251	G191	A131
A1157	U1095	A1035	A975	A915	U854	A794	G734	G674	C614	A554	G494	U434	A373	C312	U252	A192	A132
C1158	C1096	A1036	G976	U916	U855	C795	G735	A675	C615	U555	A495	A435	A374	A313	A253	C193	U133
U1159	C1097	C1037	A977	G917	C856	G796	G736	A676	C616	C556	A496	C436	U375	C314	G254	C194	G134
U1160	G1098	U1038	A978	A918	C857	G797	C737	U677	C617	G557	G497	U437	G376	A315	G255	A195	C135
C1161	G1099	G1039	C979	A919		U798	C738	U678	C618	G558	A498	U438	G377	C316	U256	A196	C136
C1162	U1100	U1040	C980	U920	A960	G799	C739	C679	U619	A559	A499	U439	G378	U317	G257	A197	
A1163	A1101	A1041	U981	U921	G861	G800	U740	C680	U620	A560	G500	U440	C379	U318	G258	G198	G138
G1164	C1102	A1042	U982	G922	C862	A801	G741	A681	A621	U561	C501	A441	G380	A320	G259	A199	A139
U1165	U1103	G1043	A983	A923	U863	A802	G742	G682	C622	U562	A502	C442	A381	A321	G260	G200	U140
A1166	G1104	A1044	C984	G924	A864	G803	A743	G683	C623	C564	C503	C443	A382	A322	U261	G201	G141
A1167	A1105	C1045	C985	G925	A865	U804	G744	U684	C624	C565	C504	A444	A383	C322	A262	G202	G142
U1168	G1106	U1046	U986	G926	C866	C805	G745	U685	U625	U566	G505	G445	A384	U323	A263	G203	A143
A1169	C1107	G1047	G987	G927	C867	C806	A746	U686	C626	C566	G506	G446	C385	G324	C264	G204	G144
A1170	G1108	U1048	G988	G928	C868	A807	A747	A687	C627	G567	C507	G447	C386	A325	G265	A205	G145
A1171	C1109	U1049	U989	G929	G869	C808	G748	C688	C628	U568	U508	A448	U387	G326	G266	C206	G146
C1172	A1110	G1050	C990	U930	U870	G809	A749	C689	A629	C569	A509	G449	G388	A327	C267	G207	G147
U1173	A1111	C1051	U991	C931	U871	C810	C750	C690	A630	G570	A510	G450	A389	C328	U268	U208	G148
G1174	C1112	U1052	U992	C932	A872	C811	U751	C691	C631	U571	C511	A451	U390	A329	C289	U209	A149
G1175	G1113	G1053	G993	G933	A873	C812	G752	U692	U632	A572	U512	A452	C390	C330	A270	C210	U150
A1176	C1114	C1054	A994	A934	G874	U813	A753	G693	C633	A573	C513	G453	C392	G331	C271	G211	A151
G1177	U1115	A1055	C995	A935	U875	A814	C754	A694	C634	A574	C514	G454	A393	G332	C272	G212	A152
U1178	U1116	U1056	A996	C936	C876	A815	G755	A695	C635	G575	G515	G455	G394	U333	U273	G213	C153
A1179	A1117	G1057	U997	A937	G877	A816	C756	A696	U636	C576	U516	A456	C395	C334	A274	C214	U154
A1180	U1118	C1058	C998	A938	A878	C817	U757	U697	C637	G577	G517	A457	C396	C335	G275	C215	A185
G1181	C1119	U1059	C999	G939	C879	G818	C758	G698	U638	C578	C518	U458	U397	A336	G276	U216	C156
U1182	C1120	U1060	A1000	C940	C880	A819	A759	C699	C639	A579	C519	A459	U398	G337	C277	C217	U157
U1183		G1061	C1001	G941	G881	U820	G760	G700	A640	C580	A520	A460	G399		G278	U218	G158
G1184	U1123	U1062	G1002	G942	C882	G821	U761	U701	U641	G581	G521	A461	C400	U340	A279	U219	G159
G1185	G1124	C1063	C1003	U943	C883	U822	U762	A702	A642	C582	G522	G462	C401	C341	C280	G220	A160
U1186	U1125	G1064	A1004	G944	U884	C823	G763	G703	C643	A583	A523	U463	C402	C342	C281	C221	A161
G1187	U1126	U1065	A1005	G945	G885	G824	C764	A704	U644	G584	G524	U464	C403	U343	A282	C222	A162
A1188	G1127	C1066	G1006	A946	G886	A825	G765	G705	C645	C585	C525	A465	C404	A344	U283	A223	C163
U1189	C1128	A1067	U1007	G947	G887	C826	A766	A706	C646	C586	C526	A466	U405	A345	C284	U224	G164
G1190	C1129	G1068	U1008	C948	G888	U827	A767	U707	C647	G587	G527	U467	U406	G346	C285	G225	G165
A1191	A1130	C1069	U1009	A949	A889	U828	A768	C708	A648	C588	C528	A468	U407	G347	C286	U226	U166
C1192	G1131	U1070	U1010	U950	G890	G829	G769	U709	A649	U589	G529	C469	A408	G348	U287	G227	A167
U1193	C1132	C1071	C1011	G951	U891	G830	C770	U710	C650	U590	G530	C470	U409	A349	A288	A228	G168
U1194	G1133	G1072	A1012	U952	A892	A831	G771	G711	C651	U591	U531	U471	G410	G350	G289	U229	C169
C1195	G1134	U1073	G1013	G953	C993	G832	U772	A712	U652	G592	A532	U472	A411	C351	C290	G230	U170
A1196	U1135	G1074	A1014	G954	G894	G833	G773	G713	U653	U593	A533	U473	A412	C352	U291	U231	A171
A1197	C1136	U1075	G1015	U955	G895	U834	G774	G714	C654	U594	U534	G474	G413	A353	G292	G232	A172
G1198	C1137	U1076	A1016	U956	C996	U835	G775	A715	A655	A595	A535	C475	A414	C354	C293	C233	U173
U1199	G1138	G1077	U1017	U957	C997	G836	G776	A716	C656	A596	C536	U476	A415	C355	U294	C234	G175
C1200	G1139	U1078	G1018	A958	G898	U837	A777	U717	U657	G597	G537	C477	A416	A356	C295	A235	C176
U1202		G1079	A1019	A959	C999	G838	G778	A718	C658	U598	G538	A478	G417	C357	G296	A236	G177
C1203	U1202	A1080	G1020	U960	A900	C839	C779	C719	U659	C599	A539	U479	C418	U358	G297	G237	G178
A1204	G1143	A1081	A1021	U961	A901	C840	C780	C720	C660	A600	G540	U480	C419	G359	A298	A238	A179
U1205	G1144	A1082	A1022	C962	G902	C841	A781	G721	C661	G601	G541	C481	U420	G360	C299	U239	G240
G1206	A1145	U1083	U1023	G963	G903	U842	A782	G722	U662	A602	G542	A482	U421	G361	A300	G241	A181
G1207	C1147	U1084	G1024	A964	U904	U843	C783	U723	C663	U603	G543	C483	C422	A362	G301	G242	G243



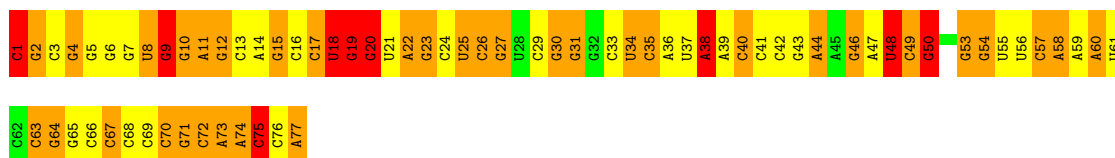
• Molecule 36: A site tRNA



• Molecule 37: mRNA

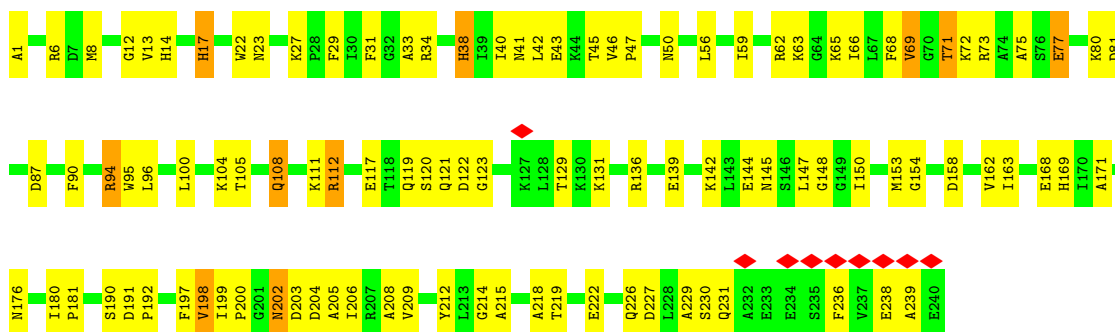


• Molecule 38: P site tRNA



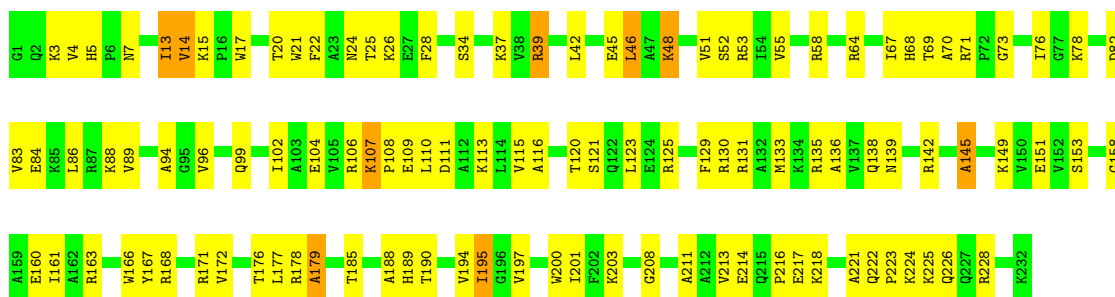
• Molecule 39: 30S ribosomal protein S2





• Molecule 40: 30S ribosomal protein S3

Chain BF: 53% 44% .



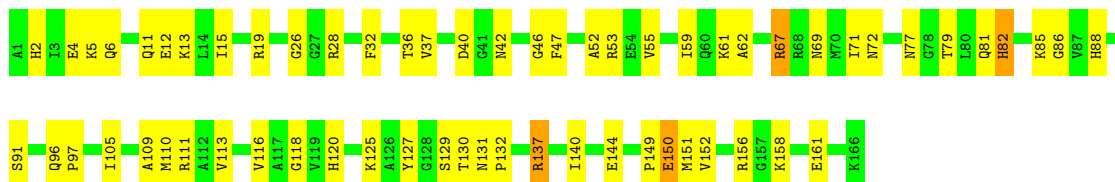
• Molecule 41: 30S ribosomal protein S4

Chain BG: 61% 38% .



• Molecule 42: 30S ribosomal protein S5

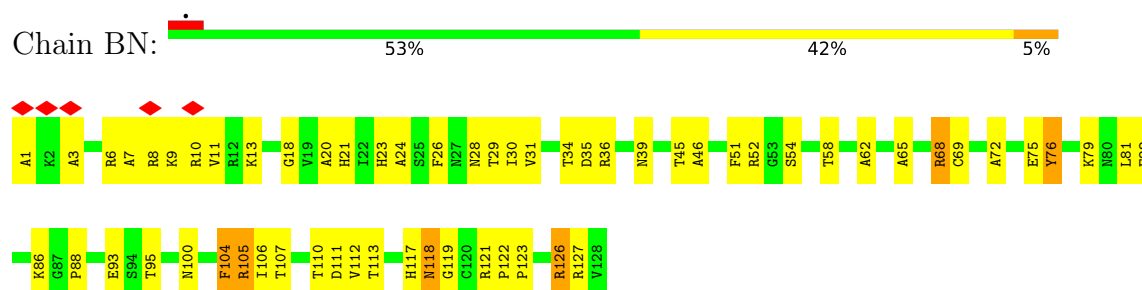
Chain BH: 63% 35% .



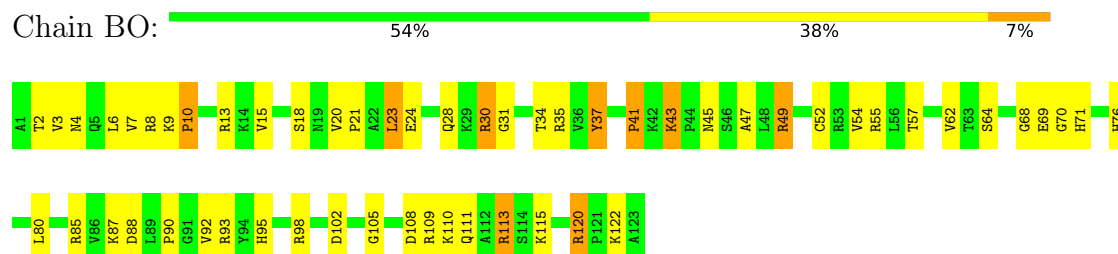
• Molecule 43: 30S ribosomal protein S6

Chain BI: 58% 40% .

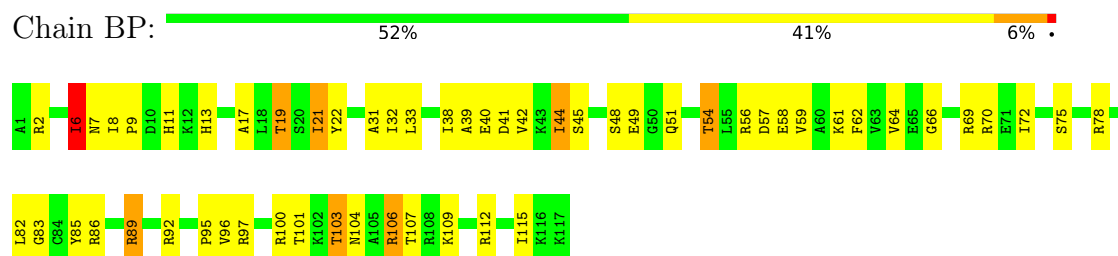
- Molecule 48: 30S ribosomal protein S11



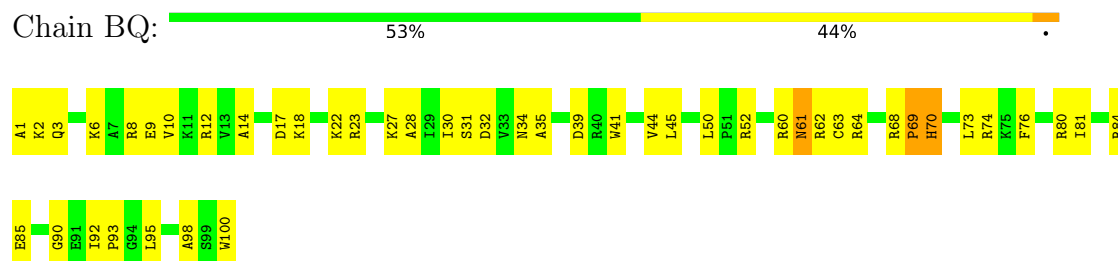
- Molecule 49: 30S ribosomal protein S12



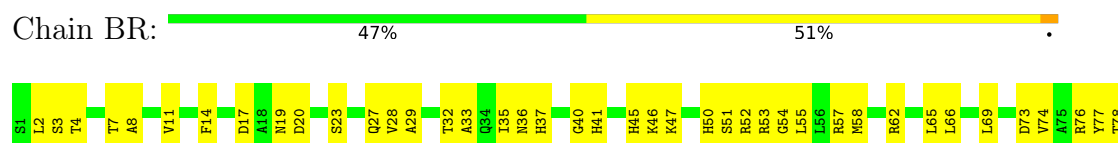
- Molecule 50: 30S ribosomal protein S13



- Molecule 51: 30S ribosomal protein S14



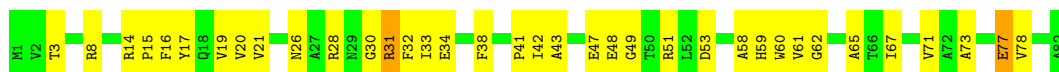
- Molecule 52: 30S ribosomal protein S15





- Molecule 53: 30S ribosomal protein S16

Chain BS: 56% 41%



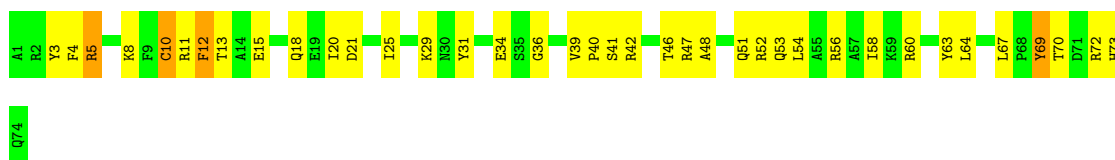
- Molecule 54: 30S ribosomal protein S17

Chain BT: 63% 35%



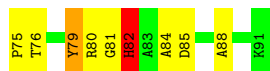
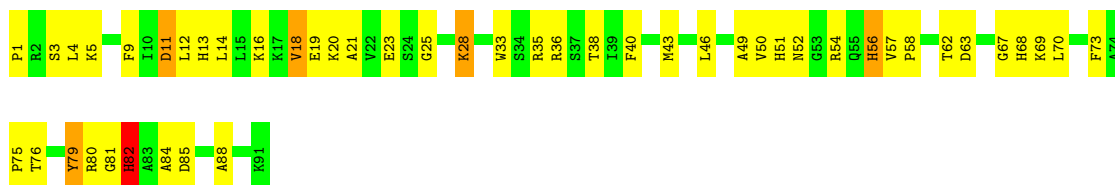
- Molecule 55: 30S ribosomal protein S18

Chain BU: 49% 46% 5%



- Molecule 56: 30S ribosomal protein S19

Chain BV: 47% 46% 5%



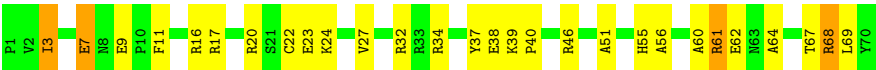
- Molecule 57: 30S ribosomal protein S20

Chain BW: 52% 45%



- Molecule 58: 30S ribosomal protein S21

Chain BX: 60% 34% 6%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	36204	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	1.471	Depositor
Minimum map value	-0.515	Depositor
Average map value	0.030	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: 5MU, 6MZ, 2MG, H2U, 5MC, 4OC, OMC, 4SU, 3TD, OMU, FME, 1MG, MA6, 7MG, OMG, UR3, 2MA, PSU, CH, MIA

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	1.94	50/2869 (1.7%)	1.97	128/4474 (2.9%)
2	AB	1.90	1105/69257 (1.6%)	1.97	3457/108040 (3.2%)
3	AC	2.05	41/1748 (2.3%)	2.42	104/2355 (4.4%)
4	AD	2.03	49/2131 (2.3%)	2.42	134/2863 (4.7%)
5	AE	2.03	43/1586 (2.7%)	2.40	78/2134 (3.7%)
6	AF	1.97	31/1571 (2.0%)	2.38	87/2113 (4.1%)
7	AG	2.07	39/1444 (2.7%)	2.43	103/1937 (5.3%)
8	AH	2.10	35/1343 (2.6%)	2.36	68/1816 (3.7%)
9	AI	1.92	16/1122 (1.4%)	2.41	71/1515 (4.7%)
10	AJ	2.06	32/1247 (2.6%)	2.48	87/1679 (5.2%)
11	AK	2.08	23/1046 (2.2%)	2.42	72/1410 (5.1%)
12	AL	1.99	34/1152 (3.0%)	2.40	77/1551 (5.0%)
13	AM	1.91	11/956 (1.2%)	2.24	37/1279 (2.9%)
14	AN	2.05	17/1062 (1.6%)	2.33	57/1413 (4.0%)
15	AO	1.97	22/1093 (2.0%)	2.56	88/1460 (6.0%)
16	AP	1.95	15/1021 (1.5%)	2.39	59/1364 (4.3%)
17	AQ	1.94	9/910 (1.0%)	2.38	52/1219 (4.3%)
18	AR	2.05	20/929 (2.2%)	2.46	70/1242 (5.6%)
19	AS	2.01	15/960 (1.6%)	2.55	72/1278 (5.6%)
20	AT	2.02	18/829 (2.2%)	2.35	36/1107 (3.3%)
21	AU	2.06	20/864 (2.3%)	2.50	52/1156 (4.5%)
22	AV	2.03	17/794 (2.1%)	2.31	32/1060 (3.0%)
23	AW	2.00	14/797 (1.8%)	2.39	50/1062 (4.7%)
24	AX	1.91	12/766 (1.6%)	2.27	25/1025 (2.4%)
25	AY	1.98	12/642 (1.9%)	2.38	39/848 (4.6%)
26	AZ	2.08	14/635 (2.2%)	2.63	55/848 (6.5%)
27	A0	2.00	12/510 (2.4%)	2.45	29/677 (4.3%)
28	A1	2.02	9/453 (2.0%)	2.57	33/605 (5.5%)
29	A2	1.99	14/559 (2.5%)	2.52	42/745 (5.6%)
30	A3	2.10	12/450 (2.7%)	2.39	19/599 (3.2%)
31	A4	1.97	6/448 (1.3%)	2.20	15/594 (2.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	A5	1.97	9/380 (2.4%)	2.62	37/498 (7.4%)
33	A6	2.06	18/513 (3.5%)	2.30	26/676 (3.8%)
34	A7	2.02	8/303 (2.6%)	2.48	15/397 (3.8%)
35	BA	1.91	600/36769 (1.6%)	2.00	1992/57354 (3.5%)
36	BB	1.94	35/1600 (2.2%)	2.04	91/2492 (3.7%)
37	BC	1.93	17/1108 (1.5%)	2.11	70/1724 (4.1%)
38	BD	1.92	38/1721 (2.2%)	2.04	94/2683 (3.5%)
39	BE	2.02	40/1904 (2.1%)	2.44	112/2565 (4.4%)
40	BF	1.97	35/1852 (1.9%)	2.40	121/2490 (4.9%)
41	BG	2.00	29/1665 (1.7%)	2.34	85/2227 (3.8%)
42	BH	2.04	28/1239 (2.3%)	2.27	50/1664 (3.0%)
43	BI	2.02	24/1121 (2.1%)	2.32	59/1509 (3.9%)
44	BJ	2.01	26/1422 (1.8%)	2.45	88/1908 (4.6%)
45	BK	1.92	15/989 (1.5%)	2.42	62/1326 (4.7%)
46	BL	1.95	20/1048 (1.9%)	2.47	65/1394 (4.7%)
47	BM	2.06	19/835 (2.3%)	2.43	49/1127 (4.3%)
48	BN	2.03	25/982 (2.5%)	2.50	78/1323 (5.9%)
49	BO	2.03	22/969 (2.3%)	2.37	55/1300 (4.2%)
50	BP	2.01	16/919 (1.7%)	2.49	67/1226 (5.5%)
51	BQ	2.06	14/817 (1.7%)	2.44	50/1088 (4.6%)
52	BR	2.02	17/724 (2.3%)	2.62	58/966 (6.0%)
53	BS	1.97	11/659 (1.7%)	2.46	42/884 (4.8%)
54	BT	2.00	12/681 (1.8%)	2.32	26/913 (2.8%)
55	BU	1.96	9/637 (1.4%)	2.33	39/851 (4.6%)
56	BV	2.13	23/744 (3.1%)	2.42	46/995 (4.6%)
57	BW	2.10	18/676 (2.7%)	2.49	42/895 (4.7%)
58	BX	1.95	9/598 (1.5%)	2.28	22/792 (2.8%)
All	All	1.94	2904/164069 (1.8%)	2.11	8869/244735 (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	68
2	AB	0	1652
3	AC	0	2
4	AD	0	11
5	AE	0	11
6	AF	0	3
7	AG	0	8

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Mol	Chain	#Chirality outliers	#Planarity outliers
8	AH	0	5
9	AI	0	3
10	AJ	0	3
11	AK	0	2
12	AL	0	4
13	AM	0	5
14	AN	0	4
15	AO	0	3
16	AP	0	8
17	AQ	0	2
18	AR	0	7
19	AS	0	5
20	AT	0	5
21	AU	0	2
22	AV	0	1
23	AW	0	1
24	AX	0	1
25	AY	0	7
26	AZ	0	2
27	A0	0	4
28	A1	0	1
29	A2	0	3
30	A3	0	3
31	A4	0	2
33	A6	0	5
35	BA	0	910
36	BB	0	37
37	BC	0	28
38	BD	0	45
39	BE	0	4
40	BF	0	7
41	BG	0	2
42	BH	0	3
43	BI	0	5
44	BJ	0	6
45	BK	0	4
46	BL	0	4
47	BM	0	2
48	BN	0	3
49	BO	0	8
50	BP	0	2
51	BQ	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
52	BR	0	1
53	BS	0	4
54	BT	0	1
55	BU	0	5
56	BV	0	4
57	BW	0	2
58	BX	0	3
All	All	0	2936

The worst 5 of 2904 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	39	A	O3'-P	11.11	1.77	1.61
20	AT	51	VAL	CA-C	10.55	1.61	1.53
35	BA	729	A	P-O5'	10.40	1.75	1.59
25	AY	22	VAL	CA-C	10.01	1.63	1.52
8	AH	110	HIS	ND1-CE1	9.85	1.42	1.32

The worst 5 of 8869 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	BL	69	GLY	CA-C-N	16.36	138.79	121.45
46	BL	69	GLY	C-N-CA	16.36	138.79	121.45
37	BC	52	U	O3'-P-O5'	-12.91	84.64	104.00
5	AE	204	LYS	CA-C-N	12.70	132.85	119.90
5	AE	204	LYS	C-N-CA	12.70	132.85	119.90

There are no chirality outliers.

5 of 2936 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	12	C	Sidechain
1	AA	2	G	Sidechain
1	AA	6	G	Sidechain
1	AA	7	G	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	2566	0	1294	0	0
2	AB	62351	0	31238	0	0
3	AC	1733	0	1824	0	0
4	AD	2092	0	2170	0	0
5	AE	1565	0	1616	0	0
6	AF	1552	0	1619	0	0
7	AG	1420	0	1460	0	0
8	AH	1323	0	1374	0	0
9	AI	1111	0	1148	0	0
10	AJ	1233	0	1283	0	0
11	AK	1032	0	1088	0	0
12	AL	1129	0	1162	0	0
13	AM	947	0	1023	0	0
14	AN	1053	0	1129	0	0
15	AO	1074	0	1157	0	0
16	AP	1008	0	1045	0	0
17	AQ	900	0	935	0	0
18	AR	917	0	965	0	0
19	AS	947	0	1022	0	0
20	AT	816	0	839	0	0
21	AU	857	0	922	0	0
22	AV	787	0	846	0	0
23	AW	789	0	847	0	0
24	AX	753	0	780	0	0
25	AY	634	0	656	0	0
26	AZ	625	0	655	0	0
27	A0	509	0	543	0	0
28	A1	449	0	491	0	0
29	A2	549	0	552	0	0
30	A3	444	0	461	0	0
31	A4	441	0	485	0	0
32	A5	377	0	418	0	0
33	A6	504	0	574	0	0
34	A7	302	0	343	0	0
35	BA	33089	0	16604	0	0
36	BB	1627	0	845	0	0
37	BC	993	0	499	0	0
38	BD	1641	0	841	0	0
39	BE	1872	0	1885	0	0
40	BF	1822	0	1913	0	0
41	BG	1643	0	1710	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	BH	1225	0	1273	0	0
43	BI	1101	0	1050	0	0
44	BJ	1400	0	1449	0	0
45	BK	979	0	1034	0	0
46	BL	1036	0	1084	0	0
47	BM	825	0	865	0	0
48	BN	965	0	997	0	0
49	BO	955	0	1019	0	0
50	BP	910	0	981	0	0
51	BQ	805	0	847	0	0
52	BR	716	0	742	0	0
53	BS	649	0	666	0	0
54	BT	672	0	716	0	0
55	BU	626	0	651	0	0
56	BV	727	0	769	0	0
57	BW	670	0	722	0	0
58	BX	590	0	631	0	0
59	AB	10	0	10	0	0
60	BB	14	0	9	0	0
All	All	152351	0	103776	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AC	232/234 (99%)	214 (92%)	12 (5%)	6 (3%)	4	25
4	AD	270/272 (99%)	237 (88%)	24 (9%)	9 (3%)	3	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	AE	207/209 (99%)	171 (83%)	28 (14%)	8 (4%)	2	19
6	AF	199/201 (99%)	172 (86%)	18 (9%)	9 (4%)	2	17
7	AG	176/178 (99%)	151 (86%)	16 (9%)	9 (5%)	1	15
8	AH	174/176 (99%)	158 (91%)	13 (8%)	3 (2%)	7	36
9	AI	147/149 (99%)	131 (89%)	10 (7%)	6 (4%)	2	18
10	AJ	162/164 (99%)	156 (96%)	5 (3%)	1 (1%)	21	59
11	AK	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
12	AL	140/142 (99%)	119 (85%)	16 (11%)	5 (4%)	2	20
13	AM	121/123 (98%)	107 (88%)	9 (7%)	5 (4%)	2	18
14	AN	142/144 (99%)	127 (89%)	12 (8%)	3 (2%)	5	30
15	AO	134/136 (98%)	123 (92%)	8 (6%)	3 (2%)	5	29
16	AP	125/127 (98%)	114 (91%)	10 (8%)	1 (1%)	16	54
17	AQ	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
18	AR	112/114 (98%)	97 (87%)	13 (12%)	2 (2%)	6	34
19	AS	115/117 (98%)	107 (93%)	4 (4%)	4 (4%)	3	20
20	AT	101/103 (98%)	91 (90%)	8 (8%)	2 (2%)	6	31
21	AU	108/110 (98%)	100 (93%)	5 (5%)	3 (3%)	4	24
22	AV	98/100 (98%)	75 (76%)	20 (20%)	3 (3%)	3	22
23	AW	101/103 (98%)	89 (88%)	10 (10%)	2 (2%)	6	31
24	AX	92/94 (98%)	87 (95%)	4 (4%)	1 (1%)	11	46
25	AY	82/84 (98%)	63 (77%)	17 (21%)	2 (2%)	4	27
26	AZ	75/77 (97%)	66 (88%)	7 (9%)	2 (3%)	4	25
27	A0	61/63 (97%)	56 (92%)	4 (7%)	1 (2%)	7	38
28	A1	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
29	A2	68/70 (97%)	64 (94%)	3 (4%)	1 (2%)	8	40
30	A3	54/56 (96%)	47 (87%)	4 (7%)	3 (6%)	1	14
31	A4	52/54 (96%)	49 (94%)	1 (2%)	2 (4%)	2	19
32	A5	44/46 (96%)	39 (89%)	3 (7%)	2 (4%)	2	17
33	A6	62/64 (97%)	59 (95%)	2 (3%)	1 (2%)	7	38
34	A7	36/38 (95%)	29 (81%)	5 (14%)	2 (6%)	1	14
39	BE	238/240 (99%)	220 (92%)	12 (5%)	6 (2%)	4	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	BF	230/232 (99%)	217 (94%)	8 (4%)	5 (2%)	5	29
41	BG	203/205 (99%)	189 (93%)	11 (5%)	3 (2%)	8	40
42	BH	164/166 (99%)	149 (91%)	13 (8%)	2 (1%)	10	44
43	BI	133/135 (98%)	123 (92%)	9 (7%)	1 (1%)	16	54
44	BJ	176/178 (99%)	164 (93%)	9 (5%)	3 (2%)	7	36
45	BK	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	16	54
46	BL	127/129 (98%)	115 (91%)	9 (7%)	3 (2%)	4	27
47	BM	101/103 (98%)	90 (89%)	6 (6%)	5 (5%)	1	16
48	BN	126/128 (98%)	112 (89%)	11 (9%)	3 (2%)	4	27
49	BO	121/123 (98%)	107 (88%)	12 (10%)	2 (2%)	7	36
50	BP	115/117 (98%)	110 (96%)	3 (3%)	2 (2%)	7	36
51	BQ	98/100 (98%)	84 (86%)	9 (9%)	5 (5%)	1	15
52	BR	86/88 (98%)	81 (94%)	4 (5%)	1 (1%)	10	44
53	BS	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
54	BT	81/83 (98%)	72 (89%)	8 (10%)	1 (1%)	10	44
55	BU	72/74 (97%)	62 (86%)	7 (10%)	3 (4%)	2	17
56	BV	89/91 (98%)	82 (92%)	6 (7%)	1 (1%)	11	46
57	BW	84/86 (98%)	79 (94%)	4 (5%)	1 (1%)	10	44
58	BX	68/70 (97%)	61 (90%)	4 (6%)	3 (4%)	2	17
All	All	6319/6423 (98%)	5710 (90%)	457 (7%)	152 (2%)	7	27

5 of 152 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AC	217	THR
4	AD	94	LEU
6	AF	62	GLN
6	AF	188	MET
7	AG	136	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AC	181/181 (100%)	176 (97%)	5 (3%)	38	60
4	AD	217/217 (100%)	211 (97%)	6 (3%)	38	60
5	AE	164/164 (100%)	150 (92%)	14 (8%)	10	29
6	AF	165/165 (100%)	157 (95%)	8 (5%)	23	44
7	AG	149/149 (100%)	135 (91%)	14 (9%)	8	26
8	AH	137/137 (100%)	128 (93%)	9 (7%)	15	37
9	AI	114/114 (100%)	109 (96%)	5 (4%)	25	47
10	AJ	122/122 (100%)	110 (90%)	12 (10%)	7	24
11	AK	109/109 (100%)	103 (94%)	6 (6%)	19	41
12	AL	116/116 (100%)	105 (90%)	11 (10%)	8	25
13	AM	104/104 (100%)	97 (93%)	7 (7%)	15	36
14	AN	103/103 (100%)	99 (96%)	4 (4%)	28	49
15	AO	109/109 (100%)	106 (97%)	3 (3%)	38	60
16	AP	103/103 (100%)	100 (97%)	3 (3%)	37	58
17	AQ	87/87 (100%)	84 (97%)	3 (3%)	32	54
18	AR	99/99 (100%)	92 (93%)	7 (7%)	13	35
19	AS	89/89 (100%)	88 (99%)	1 (1%)	65	76
20	AT	84/84 (100%)	80 (95%)	4 (5%)	23	44
21	AU	93/93 (100%)	88 (95%)	5 (5%)	20	41
22	AV	84/84 (100%)	77 (92%)	7 (8%)	10	30
23	AW	84/84 (100%)	81 (96%)	3 (4%)	31	52
24	AX	78/78 (100%)	74 (95%)	4 (5%)	21	42
25	AY	62/62 (100%)	59 (95%)	3 (5%)	23	44
26	AZ	67/67 (100%)	61 (91%)	6 (9%)	9	27
27	A0	55/55 (100%)	52 (94%)	3 (6%)	19	41
28	A1	48/48 (100%)	47 (98%)	1 (2%)	47	65
29	A2	62/62 (100%)	60 (97%)	2 (3%)	34	56
30	A3	47/47 (100%)	45 (96%)	2 (4%)	26	47
31	A4	48/48 (100%)	41 (85%)	7 (15%)	3	13
32	A5	38/38 (100%)	34 (90%)	4 (10%)	6	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	A6	51/51 (100%)	51 (100%)	0	100	100
34	A7	34/34 (100%)	32 (94%)	2 (6%)	18	39
39	BE	198/198 (100%)	192 (97%)	6 (3%)	36	57
40	BF	189/189 (100%)	177 (94%)	12 (6%)	16	37
41	BG	172/172 (100%)	168 (98%)	4 (2%)	44	64
42	BH	125/125 (100%)	120 (96%)	5 (4%)	28	49
43	BI	116/116 (100%)	113 (97%)	3 (3%)	40	62
44	BJ	146/146 (100%)	135 (92%)	11 (8%)	12	33
45	BK	104/104 (100%)	96 (92%)	8 (8%)	12	32
46	BL	106/106 (100%)	98 (92%)	8 (8%)	12	33
47	BM	90/90 (100%)	85 (94%)	5 (6%)	19	40
48	BN	98/98 (100%)	94 (96%)	4 (4%)	27	49
49	BO	103/103 (100%)	97 (94%)	6 (6%)	18	40
50	BP	95/95 (100%)	84 (88%)	11 (12%)	5	18
51	BQ	83/83 (100%)	81 (98%)	2 (2%)	43	64
52	BR	76/76 (100%)	76 (100%)	0	100	100
53	BS	65/65 (100%)	64 (98%)	1 (2%)	57	72
54	BT	77/77 (100%)	73 (95%)	4 (5%)	21	42
55	BU	64/64 (100%)	63 (98%)	1 (2%)	55	70
56	BV	78/78 (100%)	72 (92%)	6 (8%)	12	32
57	BW	65/65 (100%)	63 (97%)	2 (3%)	35	56
58	BX	60/60 (100%)	56 (93%)	4 (7%)	15	36
All	All	5213/5213 (100%)	4939 (95%)	274 (5%)	22	41

5 of 274 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	BM	96	VAL
49	BO	41	PRO
54	BT	68	LYS
14	AN	6	LEU
13	AM	49	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	119/120 (99%)	18 (15%)	10 (8%)
2	AB	2901/2904 (99%)	556 (19%)	183 (6%)
35	BA	1541/1542 (99%)	307 (19%)	117 (7%)
36	BB	75/76 (98%)	28 (37%)	5 (6%)
37	BC	46/47 (97%)	16 (34%)	7 (15%)
38	BD	77/77 (100%)	15 (19%)	2 (2%)
All	All	4759/4766 (99%)	940 (19%)	324 (6%)

5 of 940 RNA backbone outliers are listed below:

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

5 of 324 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	BA	497	G
35	BA	1226	C
35	BA	622	A
35	BA	937	A
35	BA	1362	A

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
36	7MG	BB	46	36	23,26,27	5.61	3 (13%)	27,39,42	1.39	4 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
35	2MG	BA	1516	35	23,26,27	1.36	3 (13%)	33,38,41	1.78	6 (18%)
2	OMC	AB	2498	2	19,22,23	1.09	2 (10%)	25,31,34	1.45	4 (16%)
35	MA6	BA	1518	35	23,26,27	1.47	2 (8%)	33,38,41	1.34	3 (9%)
2	CH	AB	2575	2	16,21,22	1.10	0	19,30,33	1.38	3 (15%)
2	PSU	AB	1911	2	18,21,22	2.01	4 (22%)	21,30,33	2.09	7 (33%)
35	7MG	BA	527	35	23,26,27	4.75	6 (26%)	27,39,42	1.50	3 (11%)
36	4SU	BB	8	36	18,21,22	2.30	5 (27%)	25,30,33	3.23	9 (36%)
38	PSU	BD	56	38	18,21,22	1.97	4 (22%)	21,30,33	1.66	4 (19%)
2	5MC	AB	1962	2	19,22,23	1.97	7 (36%)	26,32,35	2.71	10 (38%)
2	PSU	AB	746	2	18,21,22	1.24	1 (5%)	21,30,33	1.85	3 (14%)
38	H2U	BD	21	38	18,21,22	1.00	1 (5%)	19,30,33	1.41	2 (10%)
2	2MA	AB	2503	2	22,25,26	1.01	1 (4%)	32,37,40	1.54	6 (18%)
38	OMC	BD	33	38	19,22,23	1.10	1 (5%)	25,31,34	1.58	3 (12%)
36	OMC	BB	32	36	19,22,23	1.02	2 (10%)	25,31,34	1.79	6 (24%)
2	3TD	AB	1915	2	19,22,23	1.93	5 (26%)	23,32,35	1.56	4 (17%)
35	4OC	BA	1402	35	20,23,24	1.52	3 (15%)	25,32,35	2.07	7 (28%)
2	2MG	AB	2445	2	23,26,27	1.82	4 (17%)	33,38,41	1.24	5 (15%)
36	H2U	BB	17	36	18,21,22	1.28	3 (16%)	19,30,33	2.18	7 (36%)
36	5MU	BB	54	36	19,22,23	1.44	4 (21%)	27,32,35	2.45	5 (18%)
2	PSU	AB	2580	2	18,21,22	2.36	6 (33%)	21,30,33	2.80	5 (23%)
35	5MC	BA	967	35	19,22,23	1.34	3 (15%)	26,32,35	1.85	5 (19%)
36	PSU	BB	55	36	18,21,22	2.03	5 (27%)	21,30,33	2.73	12 (57%)
2	PSU	AB	2457	2	18,21,22	1.85	6 (33%)	21,30,33	1.76	6 (28%)
2	OMG	AB	2251	2,38	23,26,27	1.20	2 (8%)	32,38,41	0.90	0
38	5MU	BD	55	38	19,22,23	1.45	4 (21%)	27,32,35	1.60	4 (14%)
2	2MG	AB	1835	2	23,26,27	1.30	2 (8%)	33,38,41	1.49	8 (24%)
2	6MZ	AB	1618	2	22,25,26	1.56	3 (13%)	29,36,39	2.14	7 (24%)
2	H2U	AB	2449	2	18,21,22	1.55	3 (16%)	19,30,33	1.50	3 (15%)
36	H2U	BB	20	36	18,21,22	1.91	5 (27%)	19,30,33	1.69	3 (15%)
36	H2U	BB	16	36	18,21,22	1.48	4 (22%)	19,30,33	1.43	5 (26%)
35	MA6	BA	1519	35	23,26,27	1.20	3 (13%)	33,38,41	1.31	3 (9%)
2	6MZ	AB	2030	2	22,25,26	1.25	2 (9%)	29,36,39	2.17	7 (24%)
35	PSU	BA	516	35	18,21,22	1.64	5 (27%)	21,30,33	2.25	8 (38%)
35	2MG	BA	1207	35	23,26,27	1.86	5 (21%)	33,38,41	1.30	3 (9%)
2	7MG	AB	2069	2	23,26,27	4.55	5 (21%)	27,39,42	1.56	6 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PSU	AB	2605	2	18,21,22	1.22	2 (11%)	21,30,33	1.45	3 (14%)
2	PSU	AB	955	2	18,21,22	1.84	4 (22%)	21,30,33	2.51	3 (14%)
35	UR3	BA	1498	35	19,22,23	1.24	2 (10%)	26,32,35	1.41	4 (15%)
2	PSU	AB	1917	2	18,21,22	1.61	4 (22%)	21,30,33	1.69	2 (9%)
35	2MG	BA	966	35	23,26,27	1.94	4 (17%)	33,38,41	1.25	5 (15%)
2	PSU	AB	2504	2	18,21,22	1.92	4 (22%)	21,30,33	1.75	4 (19%)
38	4SU	BD	8	38	18,21,22	2.04	4 (22%)	25,30,33	1.51	6 (24%)
2	5MU	AB	747	2	19,22,23	1.52	4 (21%)	27,32,35	2.36	9 (33%)
35	5MC	BA	1407	35	19,22,23	1.43	2 (10%)	26,32,35	1.62	6 (23%)
2	1MG	AB	745	2	23,26,27	1.43	4 (17%)	33,39,42	1.64	11 (33%)
2	5MU	AB	1939	2	19,22,23	1.51	4 (21%)	27,32,35	1.66	7 (25%)
36	MIA	BB	37	36	28,31,32	1.70	4 (14%)	38,44,47	1.58	5 (13%)
2	OMU	AB	2552	2	19,22,23	1.60	4 (21%)	25,31,34	1.66	9 (36%)

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
36	7MG	BB	46	36	-	0/7/37/38	0/3/3/3
35	2MG	BA	1516	35	-	2/9/27/28	0/3/3/3
2	OMC	AB	2498	2	-	1/9/27/28	0/2/2/2
35	MA6	BA	1518	35	-	0/11/29/30	0/3/3/3
2	CH	AB	2575	2	-	0/5/25/26	0/2/2/2
2	PSU	AB	1911	2	-	1/7/25/26	0/2/2/2
35	7MG	BA	527	35	-	2/7/37/38	0/3/3/3
36	4SU	BB	8	36	-	1/7/25/26	0/2/2/2
38	PSU	BD	56	38	-	0/7/25/26	0/2/2/2
2	5MC	AB	1962	2	-	0/7/25/26	0/2/2/2
2	PSU	AB	746	2	-	2/7/25/26	0/2/2/2
38	H2U	BD	21	38	-	0/7/38/39	0/2/2/2
2	2MA	AB	2503	2	-	2/7/25/26	0/3/3/3
38	OMC	BD	33	38	-	0/9/27/28	0/2/2/2
36	OMC	BB	32	36	-	0/9/27/28	0/2/2/2
2	3TD	AB	1915	2	-	0/7/25/26	0/2/2/2
35	4OC	BA	1402	35	-	0/9/29/30	0/2/2/2
2	2MG	AB	2445	2	-	0/9/27/28	0/3/3/3
36	H2U	BB	17	36	-	0/7/38/39	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	5MU	BB	54	36	-	0/7/25/26	0/2/2/2
2	PSU	AB	2580	2	-	2/7/25/26	0/2/2/2
35	5MC	BA	967	35	-	1/7/25/26	0/2/2/2
36	PSU	BB	55	36	-	1/7/25/26	0/2/2/2
2	PSU	AB	2457	2	-	0/7/25/26	0/2/2/2
2	OMG	AB	2251	2,38	-	0/9/27/28	0/3/3/3
38	5MU	BD	55	38	-	0/7/25/26	0/2/2/2
2	2MG	AB	1835	2	-	0/9/27/28	0/3/3/3
2	6MZ	AB	1618	2	-	0/9/27/28	0/3/3/3
2	H2U	AB	2449	2	-	0/7/38/39	0/2/2/2
36	H2U	BB	20	36	-	0/7/38/39	0/2/2/2
36	H2U	BB	16	36	-	0/7/38/39	0/2/2/2
35	MA6	BA	1519	35	-	0/11/29/30	0/3/3/3
2	6MZ	AB	2030	2	-	3/9/27/28	0/3/3/3
35	PSU	BA	516	35	-	0/7/25/26	0/2/2/2
35	2MG	BA	1207	35	-	0/9/27/28	0/3/3/3
2	7MG	AB	2069	2	-	0/7/37/38	0/3/3/3
2	PSU	AB	2605	2	-	0/7/25/26	0/2/2/2
2	PSU	AB	955	2	-	0/7/25/26	0/2/2/2
35	UR3	BA	1498	35	-	1/7/25/26	0/2/2/2
2	PSU	AB	1917	2	-	0/7/25/26	0/2/2/2
35	2MG	BA	966	35	-	0/9/27/28	0/3/3/3
2	PSU	AB	2504	2	-	0/7/25/26	0/2/2/2
38	4SU	BD	8	38	-	1/7/25/26	0/2/2/2
2	5MU	AB	747	2	-	0/7/25/26	0/2/2/2
35	5MC	BA	1407	35	-	0/7/25/26	0/2/2/2
2	1MG	AB	745	2	-	0/7/25/26	0/3/3/3
2	5MU	AB	1939	2	-	0/7/25/26	0/2/2/2
36	MIA	BB	37	36	-	3/15/33/34	0/3/3/3
2	OMU	AB	2552	2	-	0/9/27/28	0/2/2/2

The worst 5 of 170 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	BB	46	7MG	C8-N9	-26.03	1.29	1.45
35	BA	527	7MG	C8-N9	-20.92	1.32	1.45
2	AB	2069	7MG	C8-N9	-20.54	1.32	1.45
36	BB	8	4SU	C4-N3	6.97	1.44	1.37
2	AB	1911	PSU	C2-N1	6.30	1.44	1.36

The worst 5 of 260 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AB	2580	PSU	C3'-C2'-C1'	10.15	113.66	101.69
36	BB	8	4SU	S4-C4-N3	-10.02	109.72	120.20
2	AB	955	PSU	C3'-C2'-C1'	-8.53	91.61	101.69
36	BB	8	4SU	C5-C4-N3	8.27	122.44	114.75
2	AB	1962	5MC	CM5-C5-C6	-7.59	112.57	122.85

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AB	746	PSU	O4'-C1'-C5-C4
2	AB	746	PSU	O4'-C1'-C5-C6
2	AB	2503	2MA	O4'-C1'-N9-C8
2	AB	2503	2MA	O4'-C1'-N9-C4
2	AB	2580	PSU	O4'-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	TRP	BB	101	36,59	14,15,16	1.79	4 (28%)	15,20,22	3.01	8 (53%)
59	FME	AB	3001	60	8,9,10	1.92	2 (25%)	8,9,11	2.10	3 (37%)

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	TRP	BB	101	36,59	-	3/5/6/8	0/2/2/2
59	FME	AB	3001	60	-	3/7/9/11	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	AB	3001	FME	CA-N	-4.33	1.40	1.46
60	BB	101	TRP	CE3-CD2	3.28	1.44	1.39
60	BB	101	TRP	CD2-CE2	2.76	1.44	1.41
60	BB	101	TRP	CD1-NE1	2.72	1.41	1.37
59	AB	3001	FME	O-C	2.45	1.29	1.20

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	BB	101	TRP	CD2-CE2-NE1	-6.43	102.16	107.52
60	BB	101	TRP	CE2-NE1-CD1	5.83	114.26	109.08
59	AB	3001	FME	O-C-CA	-4.27	113.79	124.77
60	BB	101	TRP	CZ2-CE2-NE1	4.15	137.38	130.74
60	BB	101	TRP	CE2-CD2-CG	3.32	110.52	107.17

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

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

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AA	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	39:A	O3'	40:U	P	1.77

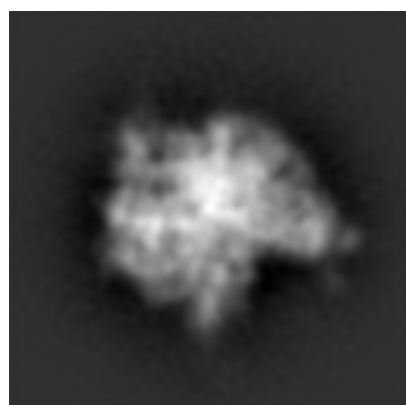
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5361. These allow visual inspection of the internal detail of the map and identification of artifacts.

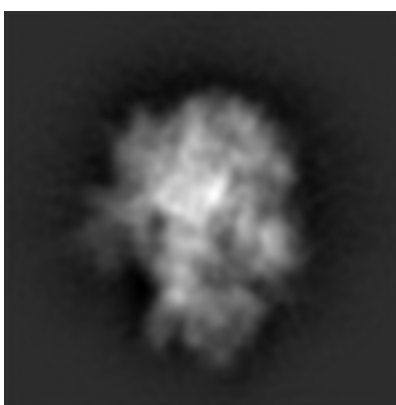
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

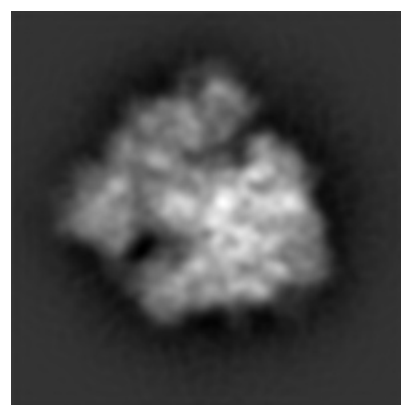
6.1.1 Primary map



X



Y

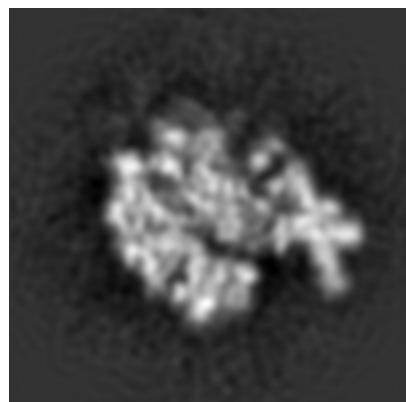


Z

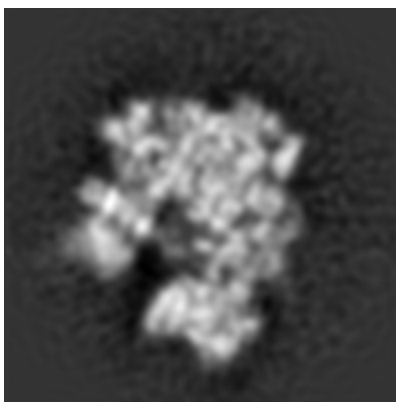
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

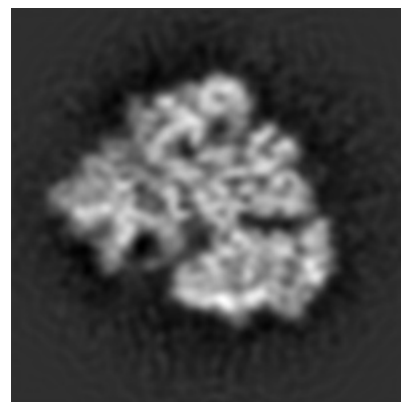
6.2.1 Primary map



X Index: 125



Y Index: 125

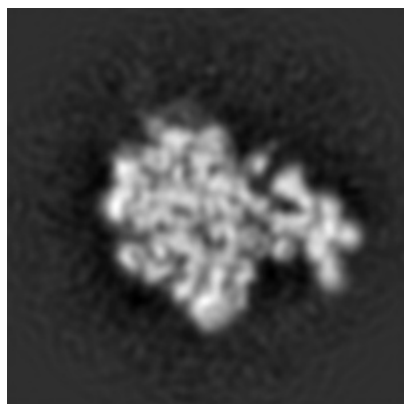


Z Index: 125

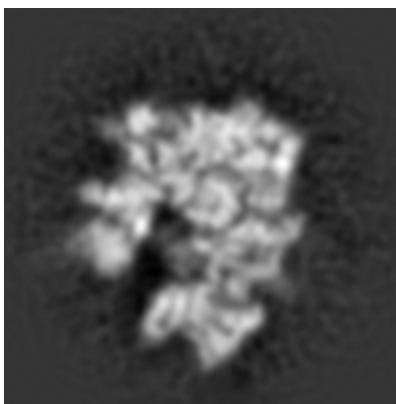
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

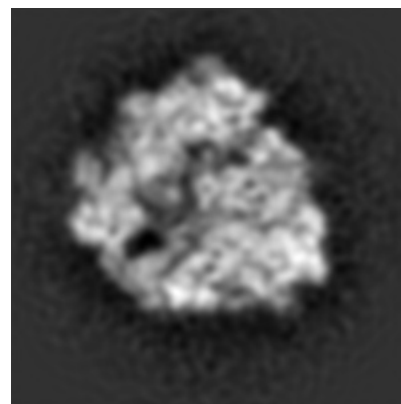
6.3.1 Primary map



X Index: 130



Y Index: 129

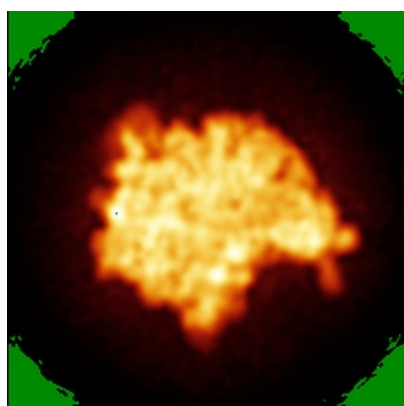


Z Index: 116

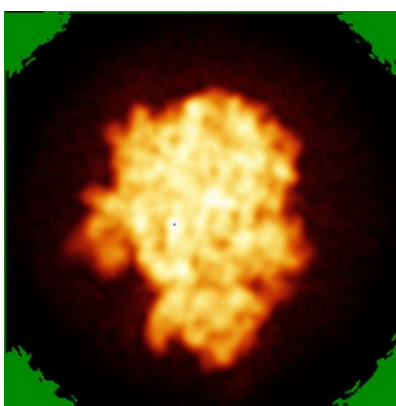
The images above show the largest variance slices of the map in three orthogonal directions.

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

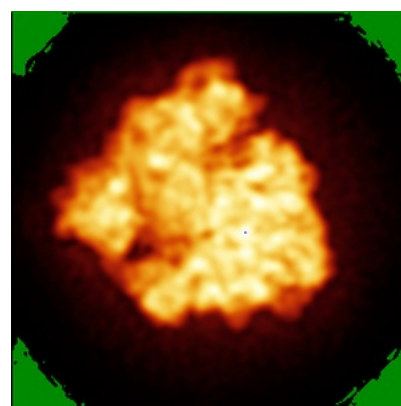
6.4.1 Primary map



X



Y

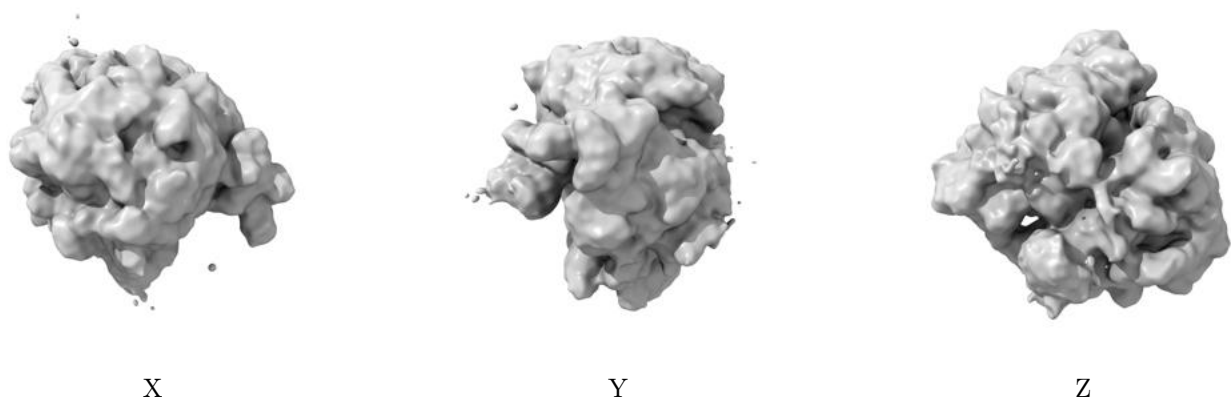


Z

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.

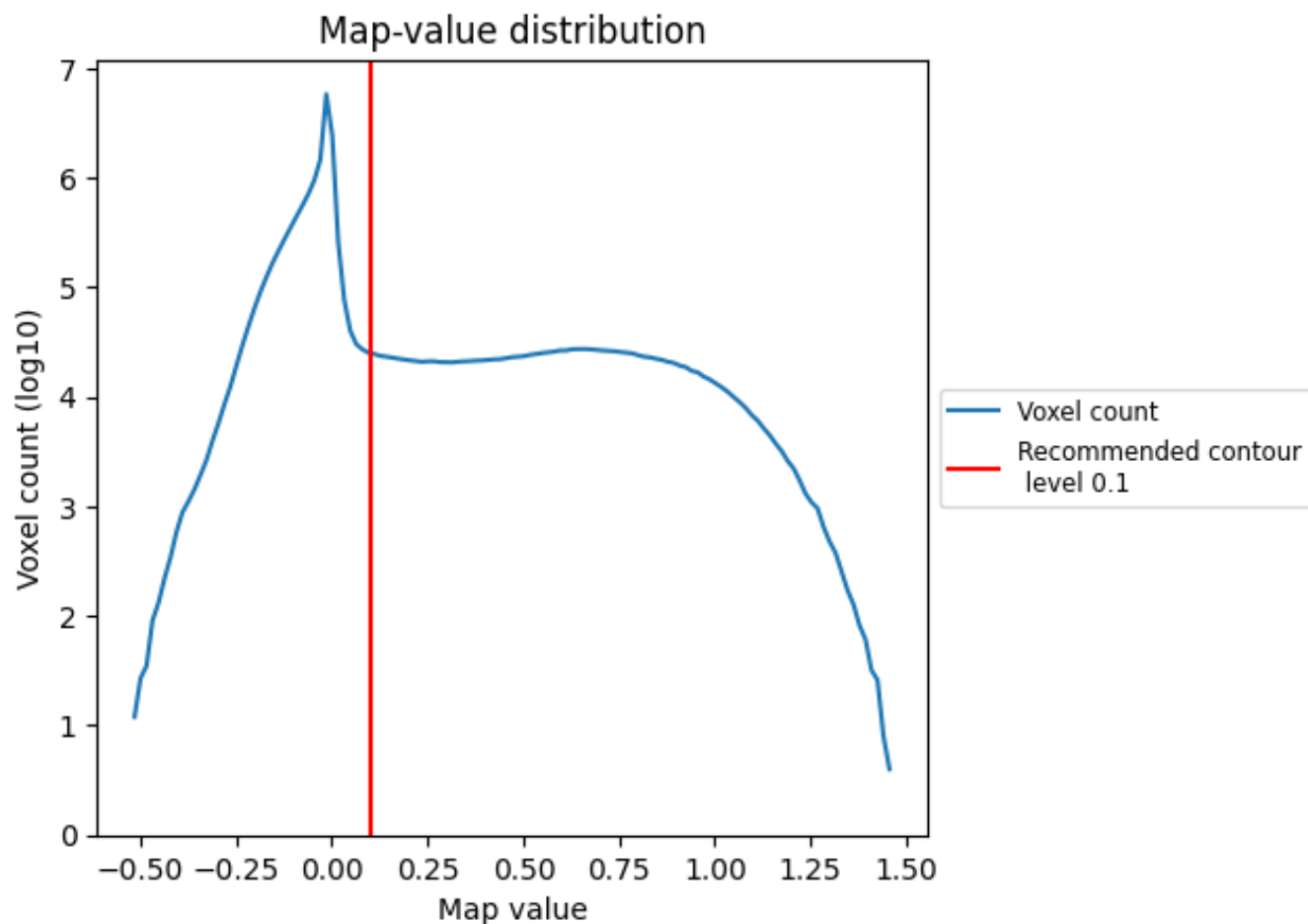
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

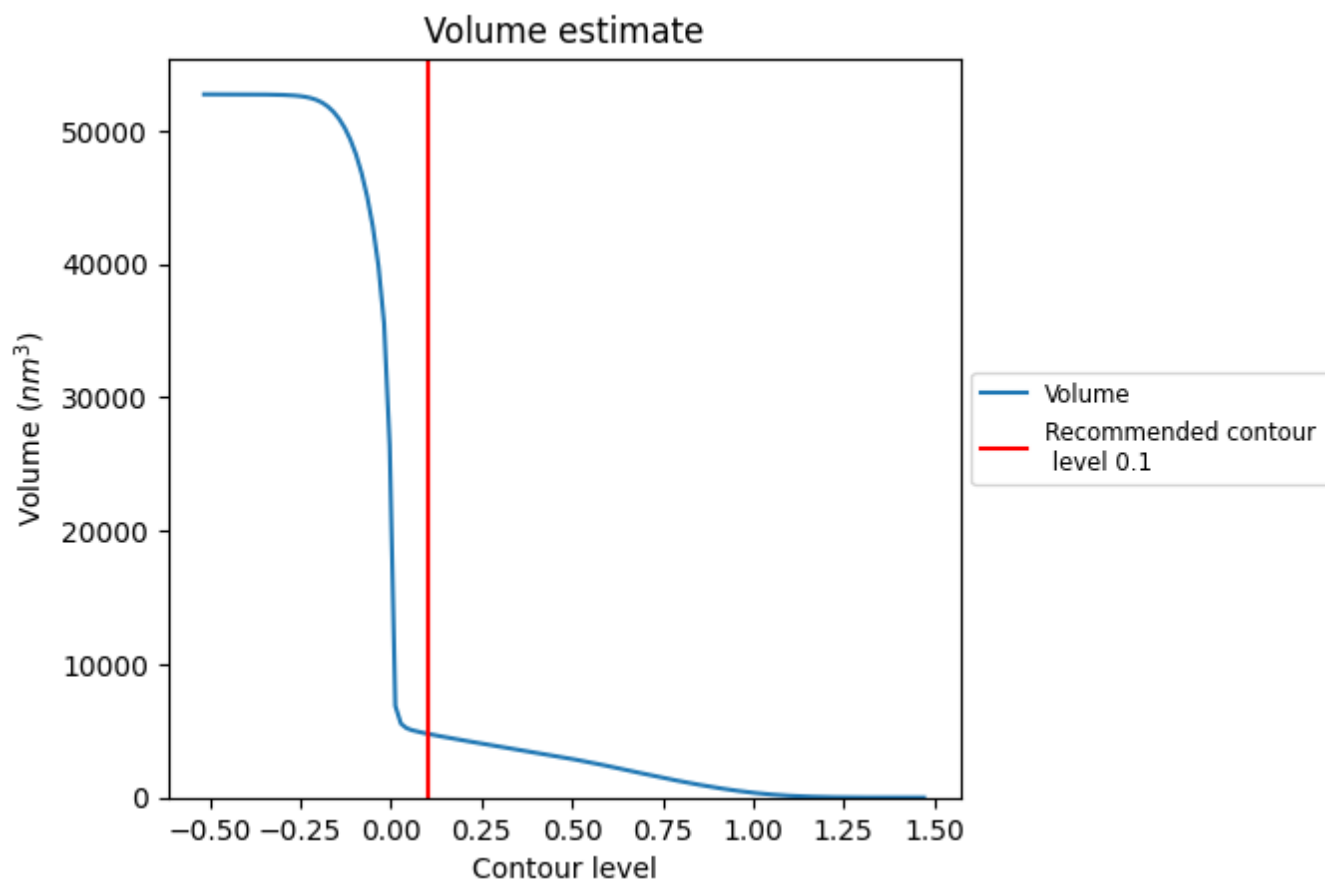
This section contains the results of statistical analysis of the map.

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.

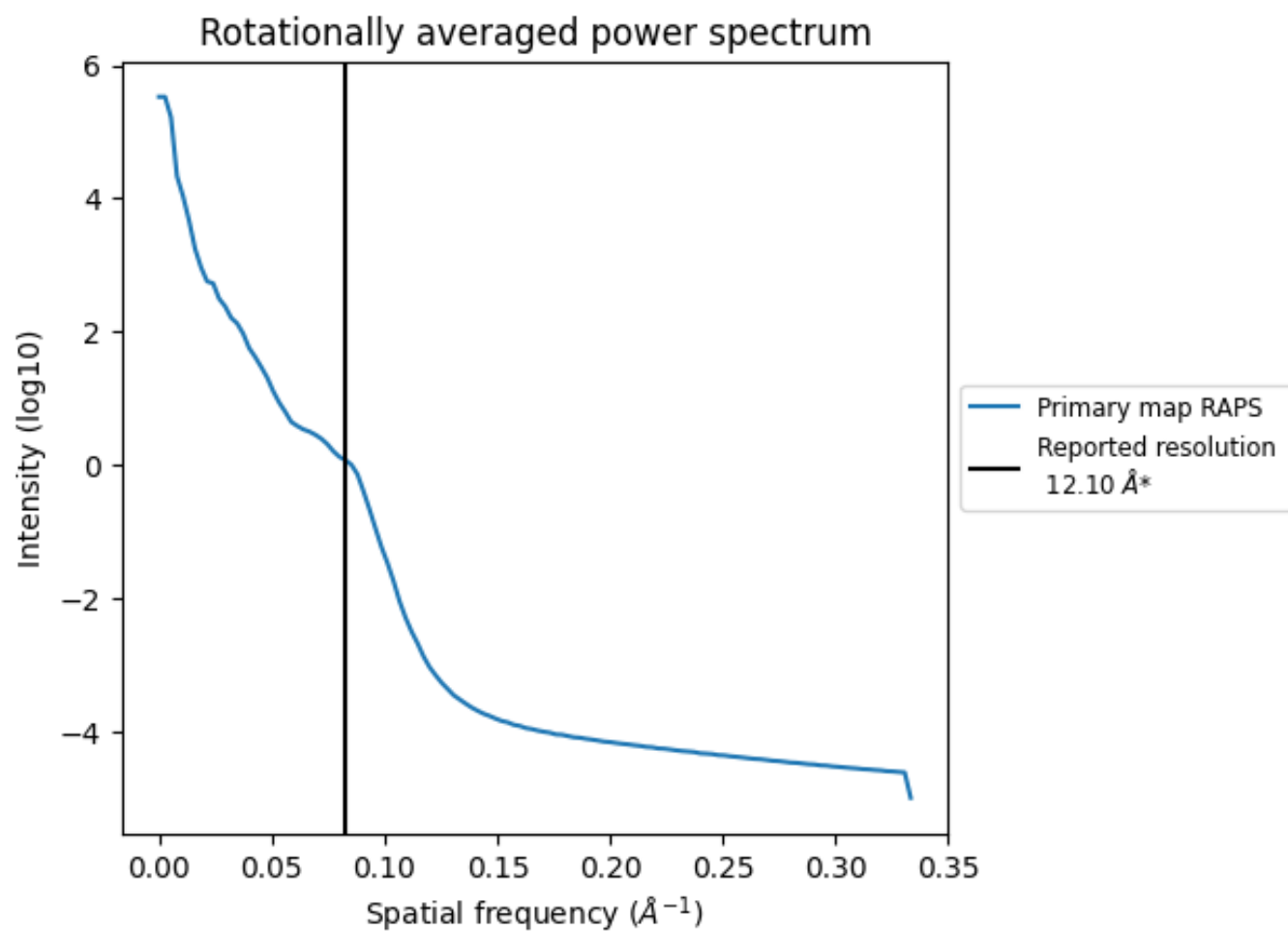
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4792 nm^3 ; this corresponds to an approximate mass of 4329 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 0.083 Å⁻¹

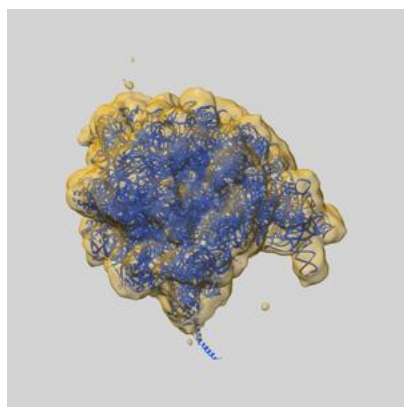
8 Fourier-Shell correlation ⓘ

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

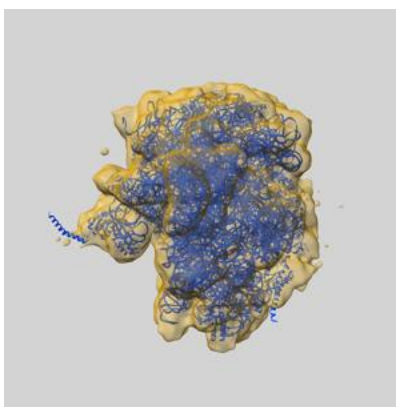
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5361 and PDB model 4V6N. Per-residue inclusion information can be found in section [3](#) on page [16](#).

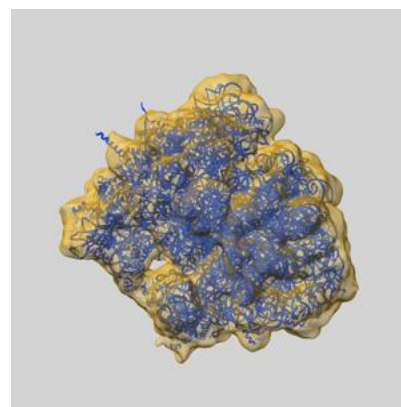
9.1 Map-model overlay [i](#)



X



Y



Z

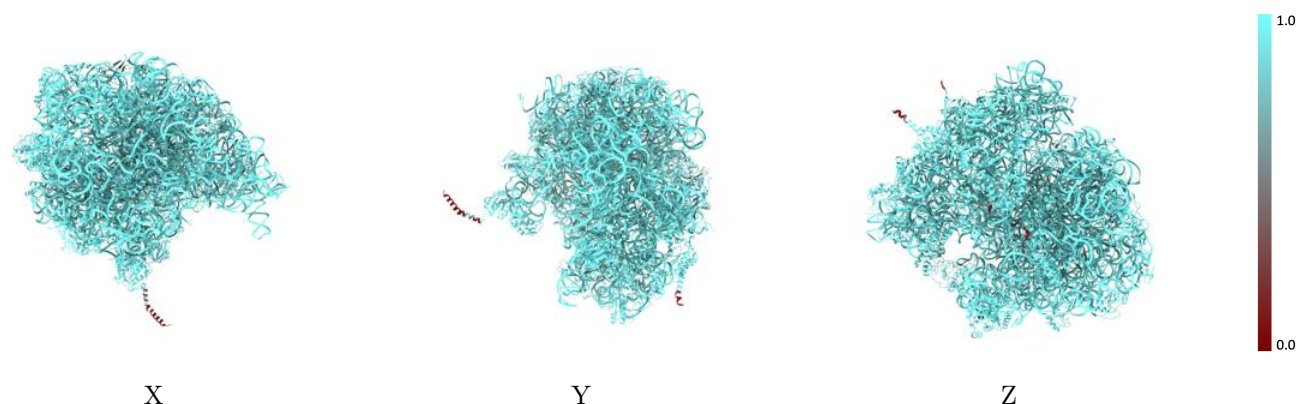
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



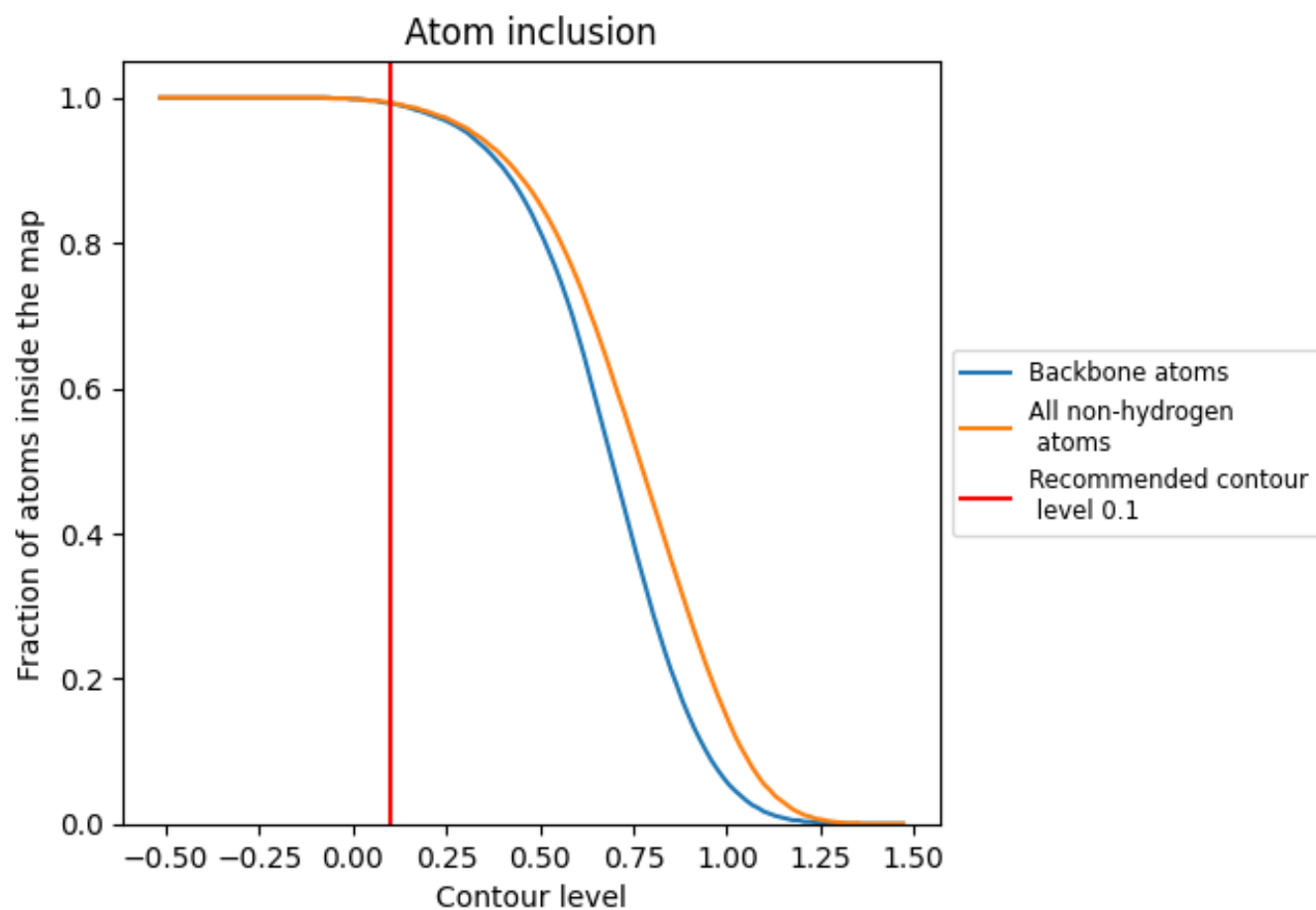
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 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	 0.9930	 0.0770
A0	 1.0000	 0.0300
A1	 0.9980	 0.0550
A2	 0.9570	 0.0330
A3	 1.0000	 0.0210
A4	 0.9910	 0.0590
A5	 1.0000	 0.0300
A6	 1.0000	 -0.0280
A7	 1.0000	 0.0160
AA	 1.0000	 0.1100
AB	 1.0000	 0.0960
AC	 0.9570	 0.0360
AD	 0.9990	 0.0260
AE	 1.0000	 0.0340
AF	 0.9990	 0.0560
AG	 0.9990	 0.0640
AH	 0.9990	 0.0270
AI	 0.8680	 0.0300
AJ	 0.8280	 0.0480
AK	 0.9790	 0.0430
AL	 1.0000	 0.0270
AM	 0.9940	 0.0380
AN	 1.0000	 0.0070
AO	 1.0000	 0.0400
AP	 1.0000	 0.0310
AQ	 0.9990	 0.0630
AR	 0.9880	 0.0320
AS	 1.0000	 0.0200
AT	 0.9960	 0.0540
AU	 0.9980	 0.0440
AV	 0.9990	 0.0140
AW	 1.0000	 0.0530
AX	 1.0000	 0.0660
AY	 1.0000	 0.0020
AZ	 1.0000	 0.0440



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Chain	Atom inclusion	Q-score
BA	 1.0000	 0.0940
BB	 0.9020	 0.0390
BC	 0.8390	 0.0110
BD	 0.9850	 0.0780
BE	 0.9590	 0.0610
BF	 0.9950	 0.0750
BG	 1.0000	 0.0510
BH	 0.9990	 0.0410
BI	 0.9680	 0.0490
BJ	 0.9960	 0.0660
BK	 1.0000	 0.0410
BL	 0.9880	 0.0510
BM	 1.0000	 0.0420
BN	 0.9530	 0.0590
BO	 0.9810	 0.0230
BP	 1.0000	 0.0770
BQ	 1.0000	 0.0340
BR	 1.0000	 0.0520
BS	 0.9980	 0.0180
BT	 1.0000	 0.0580
BU	 1.0000	 0.0370
BV	 0.9960	 0.0330
BW	 1.0000	 0.0310
BX	 0.9960	 0.0380