



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:40 PM UTC

PDB ID : 4V6K / pdb_00004v6k
EMDB ID : EMD-1849
Title : Structural insights into cognate vs. near-cognate discrimination during decoding.
Authors : Agirrezabala, X.; Schreiner, E.; Trabuco, L.G.; Lei, J.; Ortiz-Meoz, R.F.; Schulten, K.; Green, R.; Frank, J.
Deposited on : 2011-01-07
Resolution : 8.25 Å (reported)
Based on initial model : 2I2V

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

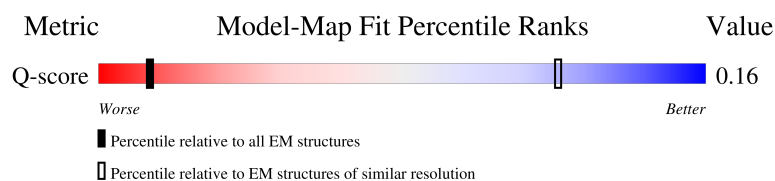
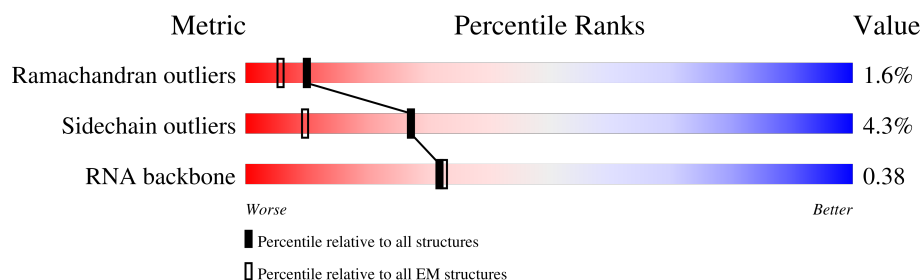
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 8.25 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.



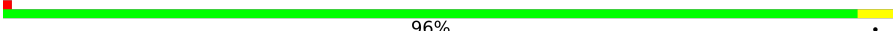
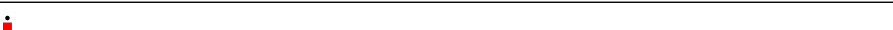
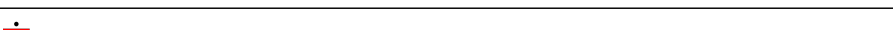
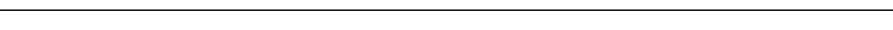
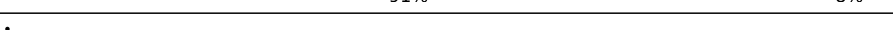
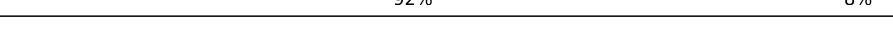
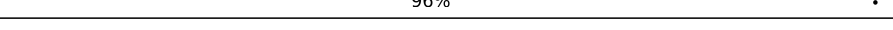
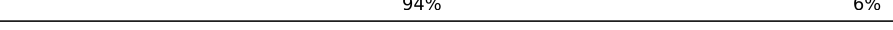
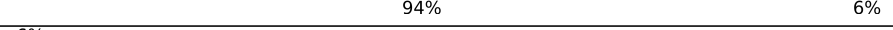
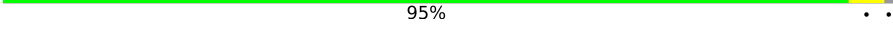
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	306 (7.76 - 8.75)

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	273	

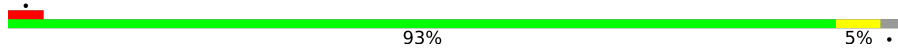
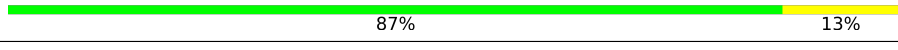
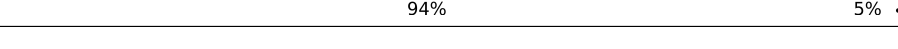
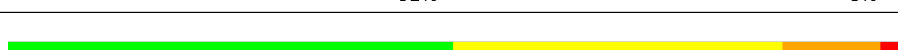
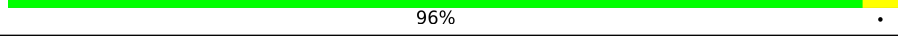
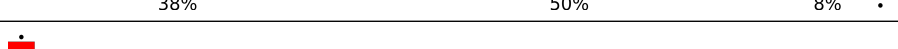
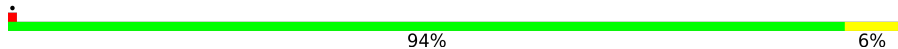
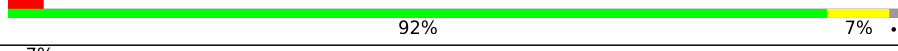
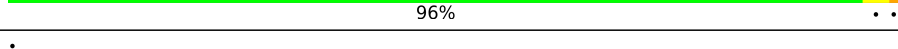
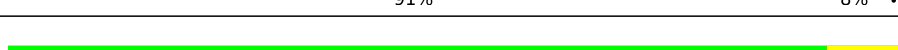
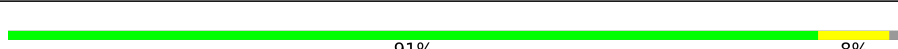
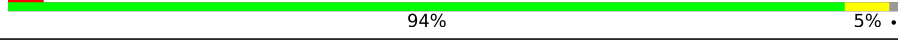
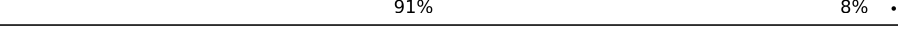
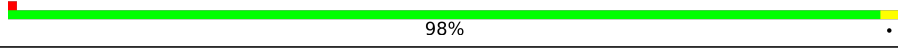
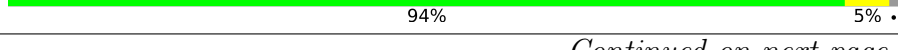
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Mol	Chain	Length	Quality of chain
5	AE	209	 91% 8% .
6	AF	201	 96% .
7	AG	179	 91% 8% ..
8	AH	177	 89% 11% .
9	AI	149	 16% 91% 8% .
10	AJ	142	 94% 5% .
11	AK	142	 96% .
12	AL	123	 90% 10%
13	AM	144	 96% .
14	AN	136	 94% . .
15	AO	127	 96% . .
16	AP	117	 92% 8%
17	AQ	115	 88% 10% ..
18	AR	118	 91% 8% .
19	AS	103	 92% 8%
20	AT	110	 96% .
21	AU	100	 94% 6%
22	AV	104	 90% 9% .
23	AW	94	 94% 6%
24	AX	85	 6% 91% 7% ..
25	AY	78	 95% . .
26	AZ	63	 89% 11%
27	Aa	59	 85% 14% .
28	Ab	70	 6% 86% 11% .
29	Ac	57	 84% 14% .

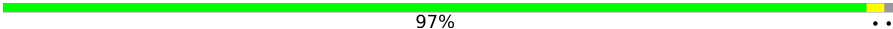
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Mol	Chain	Length	Quality of chain
30	Ad	55	 93% 5%
31	Ae	46	 87% 13%
32	Af	65	 94% 5%
33	Ag	38	 92% 8%
34	BA	1542	 50% 37% 11%
35	BB	76	 57% 30% 11%
35	BE	76	 49% 36% 12%
36	BC	393	 96% 9%
37	BD	24	 38% 50% 8%
38	BF	241	 93% 7%
39	BG	233	 90% 9% 6%
40	BH	206	 94% 6%
41	BI	167	 92% 7%
42	BJ	135	 96% 7%
43	BK	179	 91% 8%
44	BL	130	 92% 8%
45	BM	130	 91% 8%
46	BN	103	 89% 11%
47	BO	129	 94% 5%
48	BP	124	 91% 8%
49	BQ	118	 96%
50	BR	101	 86% 11%
51	BS	89	 97%
52	BT	82	 98%
53	BU	84	94% 5%

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Mol	Chain	Length	Quality of chain
54	BV	75	 87%9%..
55	BW	92	 5%93%5%.
56	BX	87	 97%..
57	BY	71	 11%83%14%..

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 153634 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 ribosomal RNA 5S.

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 ribosomal RNA 23S.

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 L11.

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

- Molecule 11 is a protein called 50S ribosomal protein L13.

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

- Molecule 12 is a protein called 50S ribosomal protein L14.

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

- Molecule 13 is a protein called 50S ribosomal protein L15.

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

- Molecule 14 is a protein called 50S ribosomal protein L16.

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

- Molecule 15 is a protein called 50S ribosomal protein L17.

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

- Molecule 16 is a protein called 50S ribosomal protein L18.

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

- Molecule 17 is a protein called 50S ribosomal protein L19.

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

- Molecule 18 is a protein called 50S ribosomal protein L20.

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

- Molecule 19 is a protein called 50S ribosomal protein L21.

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

- Molecule 20 is a protein called 50S ribosomal protein L22.

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

- Molecule 21 is a protein called 50S ribosomal protein L23.

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

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	103	Total	C	N	O	S	0	0
			789	498	148	143			

- Molecule 23 is a protein called 50S ribosomal protein L25.

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

- Molecule 24 is a protein called 50S ribosomal protein L27.

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

- Molecule 25 is a protein called 50S ribosomal protein L28.

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

- Molecule 26 is a protein called 50S ribosomal protein L29.

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

- Molecule 27 is a protein called 50S ribosomal protein L30.

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

- Molecule 28 is a protein called 50S ribosomal protein L31.

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

- Molecule 29 is a protein called 50S ribosomal protein L32.

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

- Molecule 30 is a protein called 50S ribosomal protein L33.

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

- Molecule 31 is a protein called 50S ribosomal protein L34.

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

- Molecule 32 is a protein called 50S ribosomal protein L35.

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

- Molecule 33 is a protein called 50S ribosomal protein L36.

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

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

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

- Molecule 35 is a RNA chain called A/T-site tRNA Phe.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	BB	76	Total	C	N	O	P	S	0	0
			1635	735	291	532	75	2		
35	BE	76	Total	C	N	O	P	S	0	0
			1635	735	291	532	75	2		

- Molecule 36 is a protein called Elongation factor Tu 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BC	393	Total	C	N	O	S	0	0
			3036	1918	523	582	13		

- Molecule 37 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BD	24	Total	C	N	O	P	0	0
			495	222	68	181	24		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

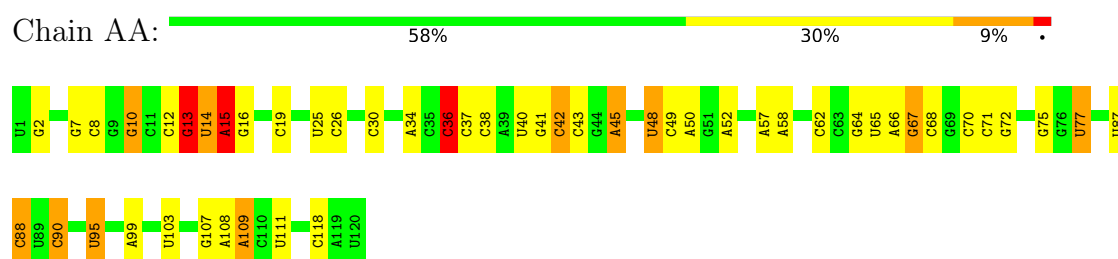
- Molecule 57 is a protein called 30S ribosomal protein S21.

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

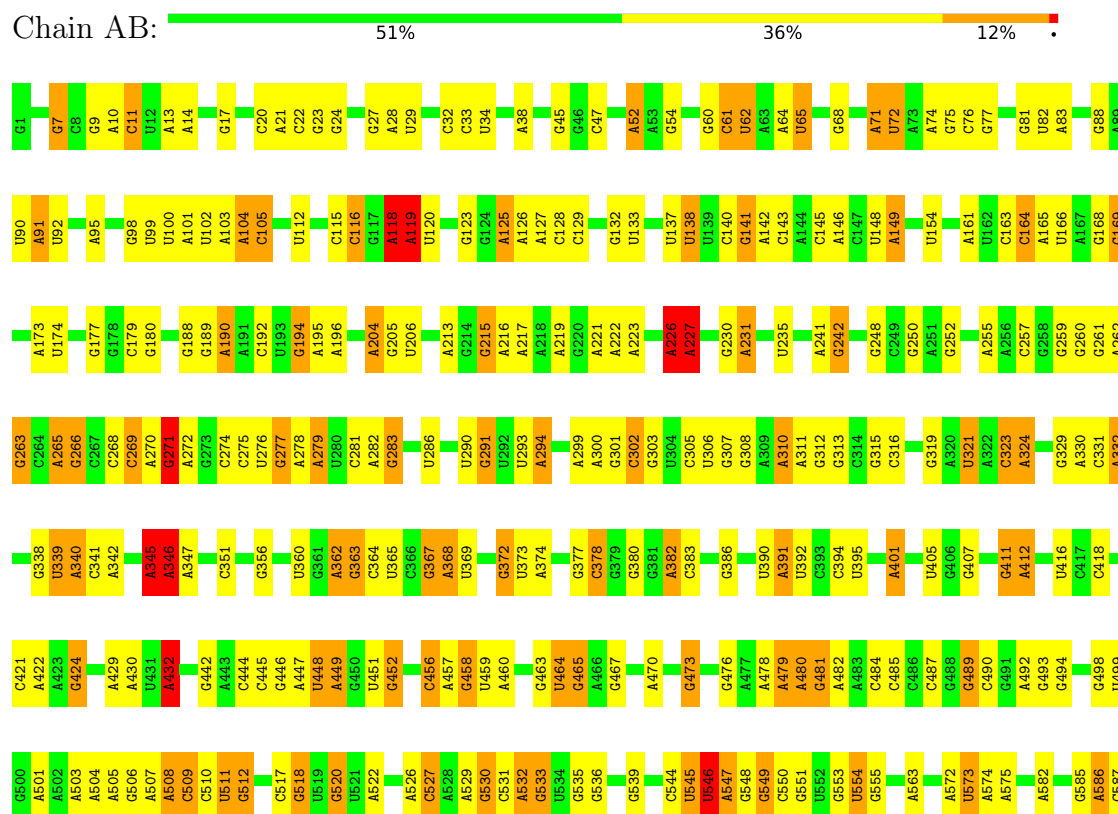
3 Residue-property plots

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

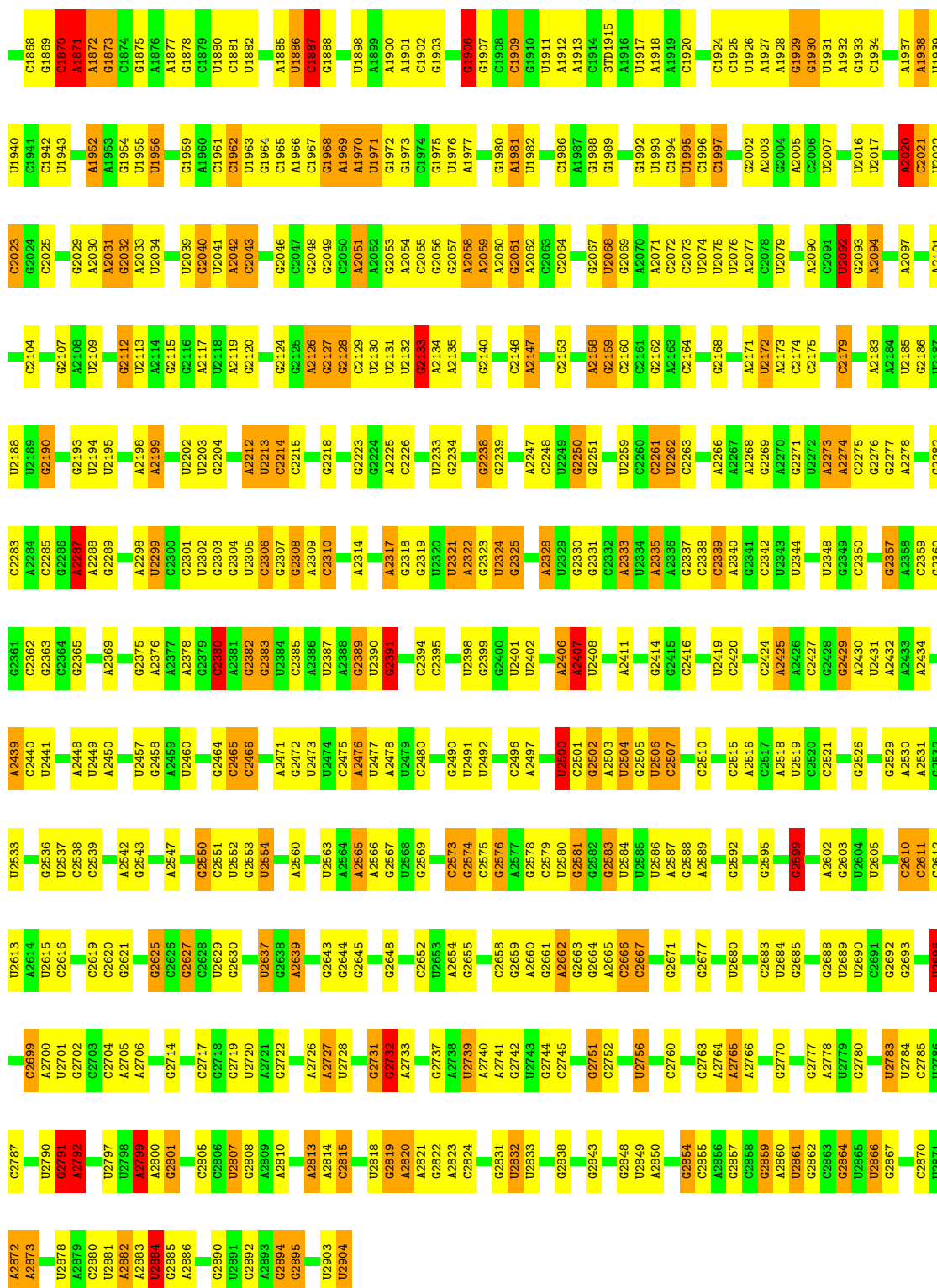
• Molecule 1: ribosomal RNA 5S



• Molecule 2: ribosomal RNA 23S

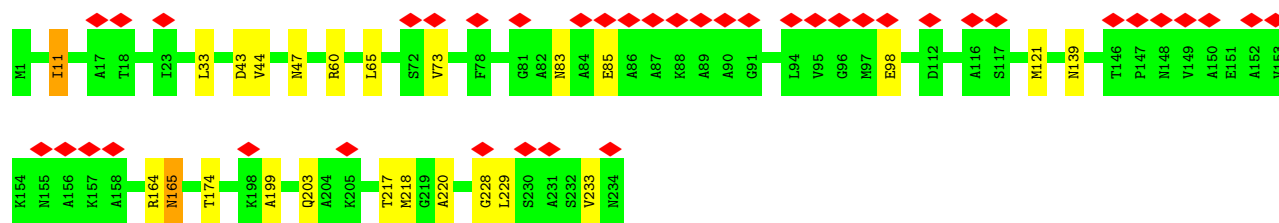


	A1785	A1701	A1603	U1523	G1418	A1327	A1246	A1080	A1010	G924	U839	C758	A676	U588
	G1702	G1702	C1604	G1527	A1419	C1330	A1247	U1081	A1011	A925	C840	C758	A677	U589
	G1703	G1703	C1605	G1527	A1420	G1331	G1248	U1084	U1011	G930	G841	A764	C678	A590
	A1705	C1704	C1606	C1532	G1424	G1332	G1250	A1085	A1012	U931	U842	C765	U686	U591
	C1706	A1608	A1607	C1533	G1425	G1333	A1254	A1086	A1013	U932	A844	U767	U686	U594
		A1609	A1608	G1334	G1426	G1334	A1255	A1087	U1015	U933	A845	C775	C691	C595
	U1709	A1610	A1609	C1335	A1427	C1335	G1256	A1088	G1016	U934	U846	G776	C692	A602
	U1710	C1536	C1611	G1339	G1436	G1339	A1262	A1089	G1017	A936	C848	G776	A693	A603
	A1711			G1345			A1263	U1094	U1018	G940	U852	G777	G696	G604
	U1714	U1440	C1615	C1345	U1440	C1345	U1263	A1095	U1019	A941	U852	G778	G697	U607
	G1715	G1543	A1616	C1349	G1441	C1349	G1266	A1096	A1020		G855	G780	G700	A608
		U1442	U1442	C1349	U1442	C1349	G1267	U1097	G1022	A945	G856	A781	G701	
	G1721	C1446	C1446	A1353	C1446	A1353	A1268	A1098	G1025	C946	G857	A782	U702	C611
	A1722	G1455	G1455	A1353	G1455	A1353	G1268	U1184	A1026	G947	G858	A783	G612	G612
	G1723	C1547	C1547	A1356	G1456	A1356	A1269	A1099	A1027	C948	G859	G784	G704	A613
	G1724	U1458	U1458	G1356	G1457	G1356	G1271	U1108	A1028	G949	G864	C786	U710	A614
	U1725	A1459	A1459	A1359	G1458	A1359	A1272	C1109	A1029		U870	C787	A718	A631
	G1726	C1462	C1462	U1458	G1459	U1458	A1276	G1110	G1041		U871	A794	A632	G630
		A1463	A1463	C1454	U1460	C1454	A1285	G1111	G1042		U872	G798	A719	A616
	C1730	G1455	G1455	A1365	C1455	A1365	G1281	A1112	C1045	U955	C865	A788	U714	
	G1731	C1456	C1456	A1365	G1456	A1365	G1282	U1113	A1032	G956	A866	A789	A714	C623
	C1732	U1457	U1457	G1368	G1457	G1368	G1283	U1114	U1033	C957	C867	U790	C957	
	G1733	U1458	U1458	G1371	G1458	G1371	A1284	G1115	G1034	U958	U868	C791	A716	
	G1734	U1459	U1459	G1371	G1459	G1371	A1285	G1116	G1041	A960	U870	A793	A717	A631
	A1735	C1460	C1460	A1371	U1460	A1371	A1286	G1117	G1042	C962	U871	A794	A718	A632
	U1736	G1455	G1455	A1371	C1455	A1371	G1287	C1118	C1045	C965	A877	G798	U720	C635
	G1737	C1456	C1456	A1371	G1456	A1371	A1288	U1119	A1046	G966	U872	G798	A721	G636
	U1738	U1457	U1457	G1371	G1457	G1371	G1289	G1120	G1047		U873	G798	A722	A637
	G1739	U1458	U1458	A1371	G1458	A1371	G1290	C1121	A1048		G882	G801	U724	G638
	C1740	C1459	C1459	G1380	G1459	G1380	G1291	G1122	C1052	G971	U886	G805	G725	U639
	G1741	U1460	U1460	G1381	G1460	G1381	C1291	C1123	C1053	G974	U887	C806	G726	
	U1742	A1461	A1461	G1382	C1461	G1382	G1292	G1124	U1053	G975	U888	C807	A727	U642
	G1743	C1462	C1462	A1383	G1462	A1383	G1293	U1128	A1054	G976	C889	G808	G728	A643
		U1463	U1463	A1384	G1463	A1384	G1294	A1129	G1055	G977	C890	G809	G729	A644
	A1746	U1464	U1464	A1385	G1464	A1385	G1295	U1130	G1056	G978	C891	U810	A730	C645
		C1465	C1465	G1385	G1465	G1385	G1296	G1131	A1057		G892	U811	G733	U646
	G1750	U1466	U1466	G1389	G1466	G1389	G1299	U1132	U1058	A979	A892	C812	G733	
	U1751	C1467	C1467	U1390	G1467	U1390	G1300	G1133	U1059	A981	C893	U813	G736	G648
	C1752	U1468	U1468	U1391	G1468	U1391	A1301	A1134	U1060	C982	U894	C814	C737	G651
	A1755	A1493	A1493	A1392	C1493	A1392	A1302	G1135	U1061	A983	U895	C815	G738	
	G1756	C1494	C1494	U1393	A1494	U1393	A1303	G1136	G1062	A984	A896	C816	A739	A654
	A1757	A1495	A1495	A1395	G1495	A1395	A1304	G1137	G1063		C897	C817	G738	A655
		C1496	C1496	U1396	G1496	U1396	G1305	U1138	C1064	A990	C898	G818	C740	G656
	G1760	U1501	U1501	U1397	G1501	U1397	A1308	G1139	U1065	C991	C901	A821	A743	U657
	A1761	C1497	C1497	U1398	G1497	U1398	G1309	C1140	U1066	C992	C902	A821	U744	
	C1762	U1504	U1504	C1399	A1504	C1399	G1310	U1141	A1067	C993	A910	U824	G745	C660
	G1763	C1507	C1507	U1400	G1507	U1400	G1310	A1142	G1068	C994	A911	U824	U746	A666
	A1773	A1508	A1508	G1407	A1508	G1407	U1313	A1143	A1070	A996	C912	U827	G747	G669
	C1774	U1509	U1509	G1408	A1509	G1408	C1314	U1144	G1074	A1000	U913	U828	A749	A670
	U1775	G1510	G1510	U1409	A1510	U1409	G1314	C1145	C1075	A917	U913	U828	A750	A671
	G1776	U1511	U1511	G1410	A1511	G1410	G1317	G1153	C1076	G1003	G914	U832	A751	C672
	U1777	G1514	G1514	U1411	A1514	U1411	A1321	G1154	A1077	U1004	A918	U833	A752	C673
		U1515	U1515	U1411	A1515	U1411	A1321	C1161	C1078	C1005	A919	U834	A753	G674
		G1521	G1521	U1416	A1521	U1416	G1324	G1166	C1079		C921	G835	A754	A675
		A1522	A1522	C1417	G1522	C1417	G1324					G836		

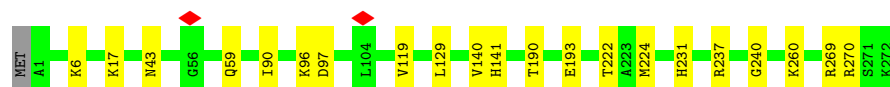


• Molecule 3: 50S ribosomal protein L1





- Molecule 4: 50S ribosomal protein L2



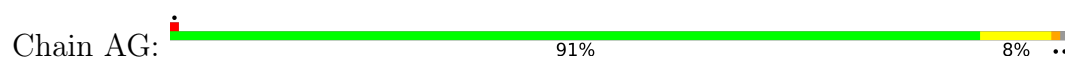
- Molecule 5: 50S ribosomal protein L3



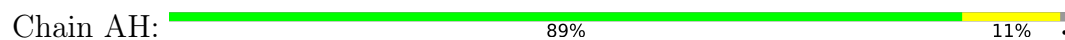
- Molecule 6: 50S ribosomal protein L4



- Molecule 7: 50S ribosomal protein L5

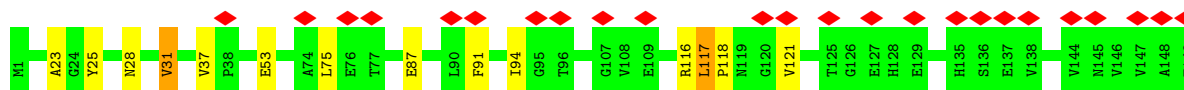


- Molecule 8: 50S ribosomal protein L6



- Molecule 9: 50S ribosomal protein L9





- Molecule 10: 50S ribosomal protein L11



- Molecule 11: 50S ribosomal protein L13



- Molecule 12: 50S ribosomal protein L14



- Molecule 13: 50S ribosomal protein L15



- Molecule 14: 50S ribosomal protein L16

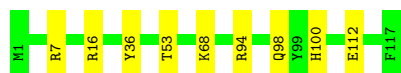


- Molecule 15: 50S ribosomal protein L17



- Molecule 16: 50S ribosomal protein L18

Chain AP:  92% 8%



- Molecule 17: 50S ribosomal protein L19

Chain AQ:  88% 10% ..



- Molecule 18: 50S ribosomal protein L20

Chain AR:  91% 8% .

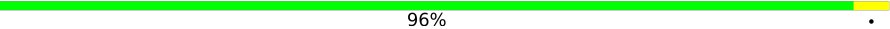


- Molecule 19: 50S ribosomal protein L21

Chain AS:  92% 8%

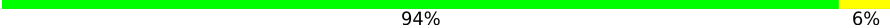


- Molecule 20: 50S ribosomal protein L22

Chain AT:  96% .



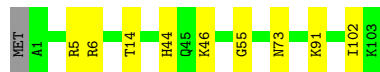
- Molecule 21: 50S ribosomal protein L23

Chain AU:  94% 6%

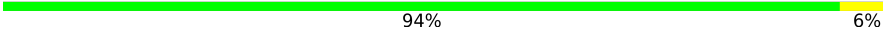


- Molecule 22: 50S ribosomal protein L24

Chain AV:  90% 9% .



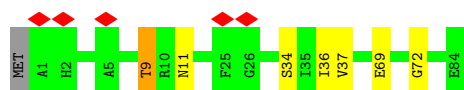
- Molecule 23: 50S ribosomal protein L25

Chain AW:  94% 6%

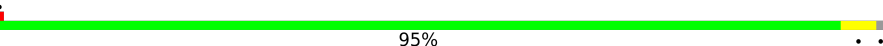


- Molecule 24: 50S ribosomal protein L27

Chain AX:  6% 91% 7% ..



- Molecule 25: 50S ribosomal protein L28

Chain AY:  95% ..



- Molecule 26: 50S ribosomal protein L29

Chain AZ:  89% 11%



- Molecule 27: 50S ribosomal protein L30

Chain Aa:  85% 14%



- Molecule 28: 50S ribosomal protein L31

Chain Ab:  6% 86% 11%



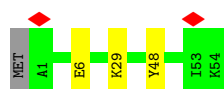
- Molecule 29: 50S ribosomal protein L32

Chain Ac:  84% 14%



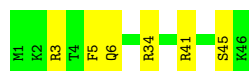
- Molecule 30: 50S ribosomal protein L33

Chain Ad:  93% 5%



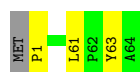
- Molecule 31: 50S ribosomal protein L34

Chain Ae:  87% 13%



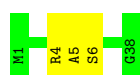
- Molecule 32: 50S ribosomal protein L35

Chain Af:  94% 5%



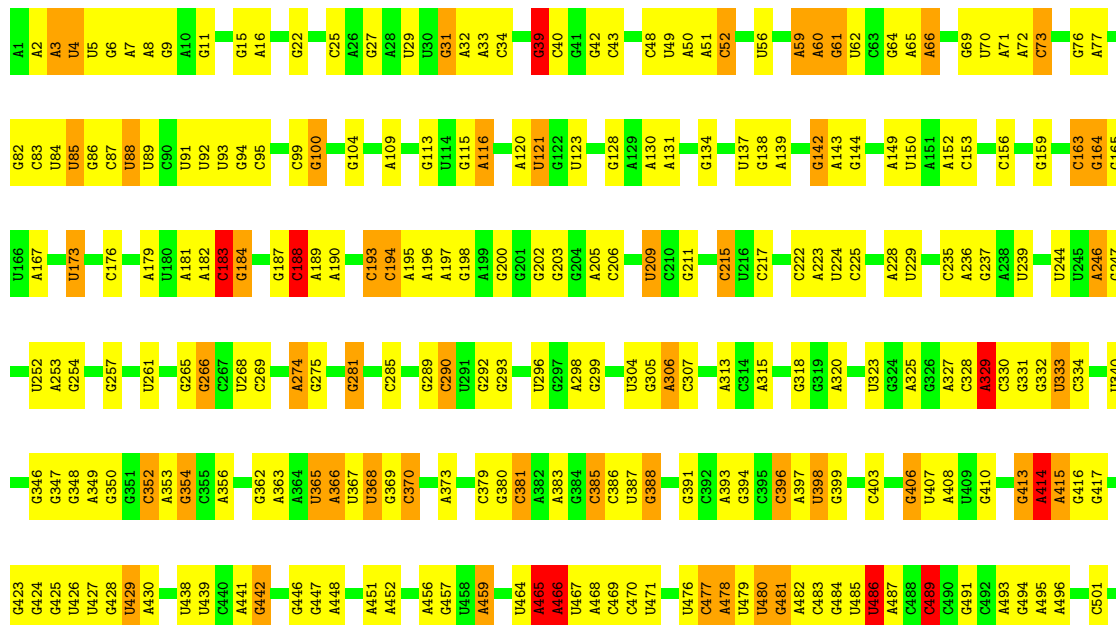
- Molecule 33: 50S ribosomal protein L36

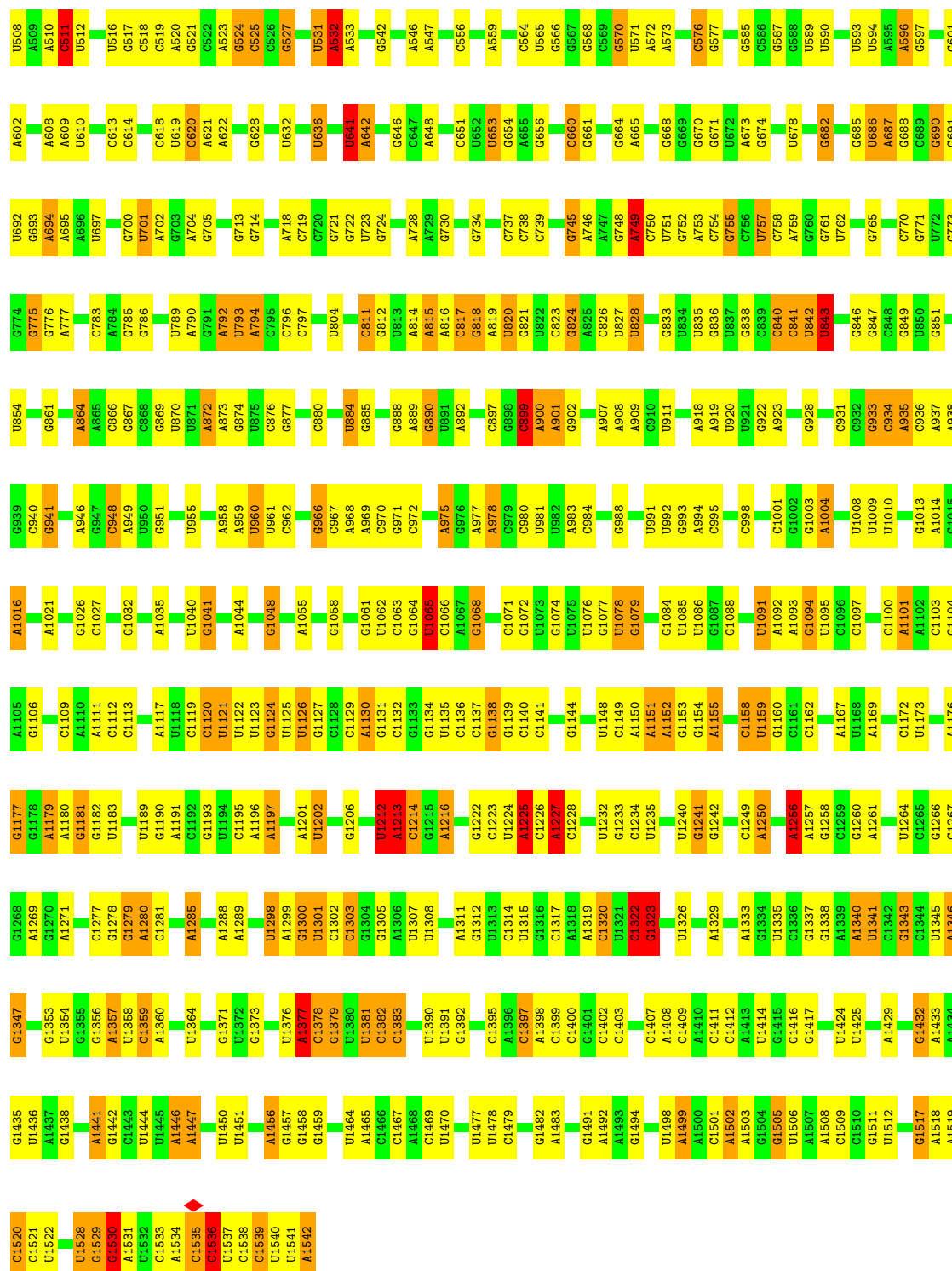
Chain Ag:  92% 8%



- Molecule 34: 16S ribosomal RNA

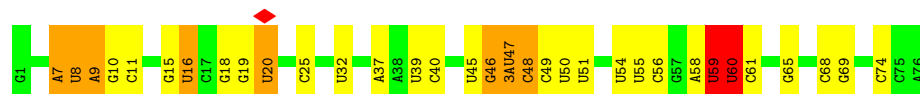
Chain BA:  50% 37% 11%





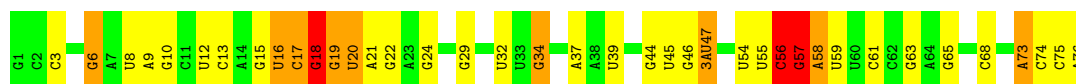
• Molecule 35: A/T-site tRNA Phe

Chain BB: 57% 30% 11%

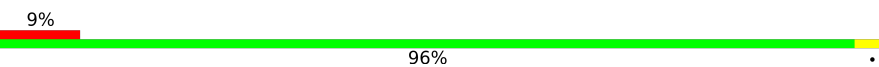


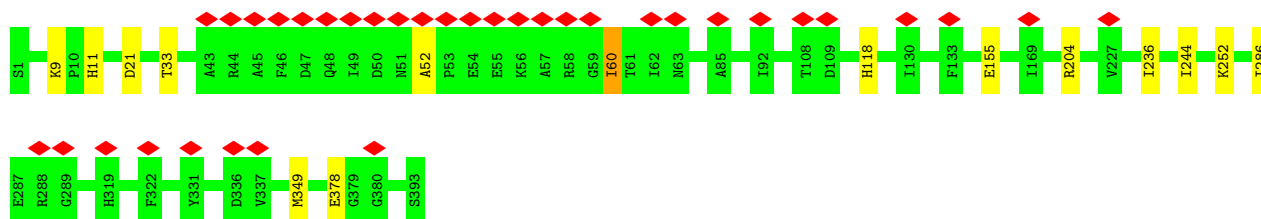
- Molecule 35: A/T-site tRNA Phe

Chain BE: 



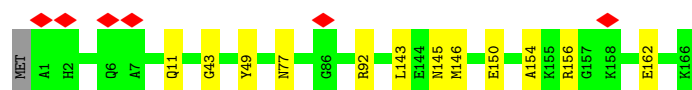
- Molecule 36: Elongation factor Tu 2

Chain BC: 

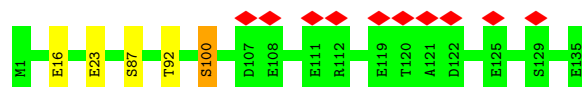




- Molecule 41: 30S ribosomal protein S5



- Molecule 42: 30S ribosomal protein S6



- Molecule 43: 30S ribosomal protein S7



- Molecule 44: 30S ribosomal protein S8



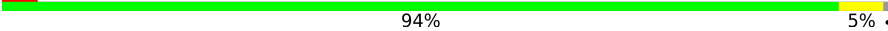
- Molecule 45: 30S ribosomal protein S9



- Molecule 46: 30S ribosomal protein S10



- Molecule 47: 30S ribosomal protein S11

Chain BO:  94% 5%

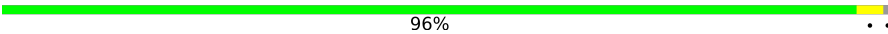


- Molecule 48: 30S ribosomal protein S12

Chain BP:  91% 8%



- Molecule 49: 30S ribosomal protein S13

Chain BQ:  96% ..

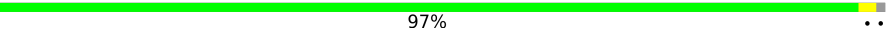


- Molecule 50: 30S ribosomal protein S14

Chain BR:  86% 11% ..

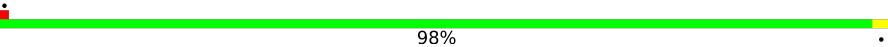


- Molecule 51: 30S ribosomal protein S15

Chain BS:  97% ..

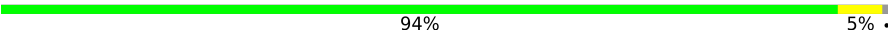


- Molecule 52: 30S ribosomal protein S16

Chain BT:  98% .



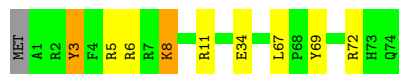
- Molecule 53: 30S ribosomal protein S17

Chain BU:  94% 5%

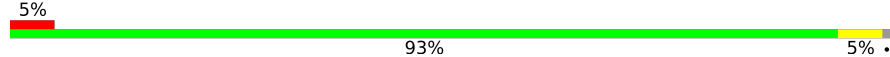


- Molecule 54: 30S ribosomal protein S18

Chain BV:  87% 9% ..

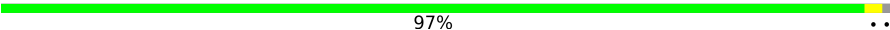


- Molecule 55: 30S ribosomal protein S19

Chain BW:  5% 93% 5% .



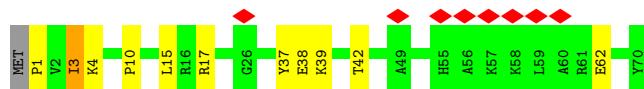
- Molecule 56: 30S ribosomal protein S20

Chain BX:  97% ..



- Molecule 57: 30S ribosomal protein S21

Chain BY:  11% 83% 14% ..



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	359223	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	59000	Depositor
Image detector	TVIPS TEMCAM-F415 (4k x 4k)	Depositor
Maximum map value	299.406	Depositor
Minimum map value	-102.404	Depositor
Average map value	5.380	Depositor
Map value standard deviation	28.487	Depositor
Recommended contour level	32.4	Depositor
Map size ($\text{\AA}$)	375, 375, 375	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing ($\text{\AA}$)	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: 2MG, 4OC, UR3, 3TD, 7MG, 4SU, OMU, 5MC, MIA, 5MU, 6MZ, OMC, 1MG, 2MA, CH, OMG, MA6, 3AU, H2U, PSU

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	0.76	0/2869	1.37	29/4474 (0.6%)
2	AB	0.76	1/69257 (0.0%)	1.35	654/108040 (0.6%)
3	AC	0.69	0/1748	1.46	18/2355 (0.8%)
4	AD	0.75	0/2131	1.43	5/2863 (0.2%)
5	AE	0.68	0/1586	1.37	7/2134 (0.3%)
6	AF	0.68	0/1571	1.39	1/2113 (0.0%)
7	AG	0.71	0/1444	1.46	9/1937 (0.5%)
8	AH	0.68	0/1343	1.42	4/1816 (0.2%)
9	AI	0.69	0/1122	1.45	9/1515 (0.6%)
10	AJ	0.69	0/1046	1.39	4/1410 (0.3%)
11	AK	0.76	0/1152	1.42	4/1551 (0.3%)
12	AL	0.68	0/956	1.26	4/1279 (0.3%)
13	AM	0.70	0/1062	1.40	2/1413 (0.1%)
14	AN	0.72	0/1093	1.43	2/1460 (0.1%)
15	AO	0.71	0/1021	1.40	5/1364 (0.4%)
16	AP	0.68	0/910	1.35	3/1219 (0.2%)
17	AQ	0.69	0/929	1.40	6/1242 (0.5%)
18	AR	0.70	0/960	1.43	8/1278 (0.6%)
19	AS	0.71	0/829	1.32	2/1107 (0.2%)
20	AT	0.66	0/864	1.37	0/1156
21	AU	0.63	0/794	1.36	2/1060 (0.2%)
22	AV	0.63	0/797	1.45	7/1062 (0.7%)
23	AW	0.67	0/766	1.36	2/1025 (0.2%)
24	AX	0.76	0/642	1.51	4/848 (0.5%)
25	AY	0.74	0/635	1.41	2/848 (0.2%)
26	AZ	0.67	0/510	1.61	0/677
27	Aa	0.72	0/453	1.49	6/605 (1.0%)
28	Ab	0.79	0/559	1.67	10/745 (1.3%)
29	Ac	0.76	0/450	1.49	4/599 (0.7%)
30	Ad	0.67	0/448	1.35	0/594
31	Ae	0.74	0/380	1.42	1/498 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Af	0.74	0/513	1.48	3/676 (0.4%)
33	Ag	0.66	0/303	1.32	1/397 (0.3%)
34	BA	0.76	1/36769 (0.0%)	1.34	319/57354 (0.6%)
35	BB	0.80	1/1580 (0.1%)	1.26	9/2459 (0.4%)
35	BE	0.79	1/1580 (0.1%)	1.39	14/2459 (0.6%)
36	BC	0.71	0/3092	1.36	8/4183 (0.2%)
37	BD	0.86	0/548	1.33	5/848 (0.6%)
38	BF	0.70	0/1904	1.44	10/2565 (0.4%)
39	BG	0.72	0/1852	1.42	10/2490 (0.4%)
40	BH	0.71	0/1665	1.40	4/2227 (0.2%)
41	BI	0.68	0/1239	1.40	4/1664 (0.2%)
42	BJ	0.72	0/1121	1.42	2/1509 (0.1%)
43	BK	0.72	0/1422	1.48	6/1908 (0.3%)
44	BL	0.66	0/989	1.39	5/1326 (0.4%)
45	BM	0.69	0/1048	1.37	3/1394 (0.2%)
46	BN	0.73	0/835	1.46	0/1127
47	BO	0.76	0/982	1.36	2/1323 (0.2%)
48	BP	0.73	0/969	1.40	4/1300 (0.3%)
49	BQ	0.71	0/919	1.35	0/1226
50	BR	0.74	0/817	1.48	3/1088 (0.3%)
51	BS	0.71	0/724	1.40	2/966 (0.2%)
52	BT	0.72	0/659	1.41	2/884 (0.2%)
53	BU	0.68	0/681	1.31	2/913 (0.2%)
54	BV	0.73	0/637	1.45	4/851 (0.5%)
55	BW	0.77	0/744	1.38	1/995 (0.1%)
56	BX	0.67	0/676	1.35	2/895 (0.2%)
57	BY	0.80	0/598	1.52	5/792 (0.6%)
All	All	0.74	4/165193 (0.0%)	1.36	1244/246106 (0.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	27
2	AB	0	821
3	AC	0	2
5	AE	0	3
6	AF	0	1
8	AH	0	2
9	AI	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
11	AK	0	2
15	AO	0	1
17	AQ	0	1
18	AR	0	1
28	Ab	0	1
30	Ad	0	1
31	Ae	0	2
34	BA	0	473
35	BB	0	12
35	BE	0	15
37	BD	0	4
38	BF	0	1
39	BG	0	2
40	BH	0	2
41	BI	0	3
42	BJ	0	1
43	BK	0	2
45	BM	0	2
47	BO	0	1
48	BP	0	1
50	BR	0	1
54	BV	0	1
55	BW	0	1
57	BY	0	3
All	All	0	1392

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	BE	8	4SU	O3'-P	6.50	1.62	1.56
34	BA	1498	UR3	O3'-P	5.72	1.61	1.56
35	BB	8	4SU	O3'-P	5.47	1.61	1.56
2	AB	2552	OMU	O3'-P	5.05	1.61	1.56

The worst 5 of 1244 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	BA	899	C	O3'-P-O5'	-13.12	84.33	104.00
2	AB	279	A	O3'-P-O5'	-11.19	87.22	104.00
2	AB	2175	C	O3'-P-O5'	-10.65	88.03	104.00
2	AB	1588	G	O3'-P-O5'	-10.61	88.08	104.00
2	AB	1394	U	C5'-C4'-C3'	-9.86	101.21	116.00

There are no chirality outliers.

5 of 1392 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	13	G	Sidechain
1	AA	14	U	Sidechain
1	AA	15	A	Sidechain
1	AA	2	G	Sidechain
1	AA	7	G	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	2566	0	1302	0	0
2	AB	62351	0	31387	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	1032	0	1088	0	0
11	AK	1129	0	1162	0	0
12	AL	947	0	1023	0	0
13	AM	1053	0	1129	0	0
14	AN	1074	0	1157	0	0
15	AO	1008	0	1045	0	0
16	AP	900	0	935	0	0
17	AQ	917	0	965	0	0
18	AR	947	0	1022	0	0
19	AS	816	0	839	0	0
20	AT	857	0	922	0	0
21	AU	787	0	846	0	0
22	AV	789	0	847	0	0
23	AW	753	0	780	0	0
24	AX	634	0	656	0	0
25	AY	625	0	655	0	0
26	AZ	509	0	543	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	Aa	449	0	491	0	0
28	Ab	549	0	552	0	0
29	Ac	444	0	461	0	0
30	Ad	441	0	485	0	0
31	Ae	377	0	418	0	0
32	Af	504	0	574	0	0
33	Ag	302	0	343	0	0
34	BA	33089	0	16678	0	0
35	BB	1635	0	849	0	0
35	BE	1635	0	849	0	0
36	BC	3036	0	3052	0	0
37	BD	495	0	249	0	0
38	BF	1872	0	1885	0	0
39	BG	1822	0	1913	0	0
40	BH	1643	0	1710	0	0
41	BI	1225	0	1273	0	0
42	BJ	1101	0	1050	0	0
43	BK	1400	0	1449	0	0
44	BL	979	0	1034	0	0
45	BM	1036	0	1084	0	0
46	BN	825	0	865	0	0
47	BO	965	0	997	0	0
48	BP	955	0	1019	0	0
49	BQ	910	0	981	0	0
50	BR	805	0	847	0	0
51	BS	716	0	742	0	0
52	BT	649	0	666	0	0
53	BU	672	0	716	0	0
54	BV	626	0	651	0	0
55	BW	727	0	769	0	0
56	BX	670	0	722	0	0
57	BY	590	0	631	0	0
All	All	153634	0	105519	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 ⓘ

5.3.1 Protein backbone ⓘ

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%)	204 (88%)	25 (11%)	3 (1%)	9	42
4	AD	270/273 (99%)	239 (88%)	23 (8%)	8 (3%)	3	23
5	AE	207/209 (99%)	186 (90%)	15 (7%)	6 (3%)	3	23
6	AF	199/201 (99%)	182 (92%)	14 (7%)	3 (2%)	8	40
7	AG	176/179 (98%)	147 (84%)	27 (15%)	2 (1%)	11	46
8	AH	174/177 (98%)	163 (94%)	8 (5%)	3 (2%)	7	36
9	AI	147/149 (99%)	126 (86%)	16 (11%)	5 (3%)	3	21
10	AJ	139/142 (98%)	123 (88%)	15 (11%)	1 (1%)	18	56
11	AK	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
12	AL	121/123 (98%)	106 (88%)	13 (11%)	2 (2%)	7	36
13	AM	142/144 (99%)	125 (88%)	15 (11%)	2 (1%)	9	40
14	AN	134/136 (98%)	122 (91%)	9 (7%)	3 (2%)	5	29
15	AO	125/127 (98%)	117 (94%)	7 (6%)	1 (1%)	16	54
16	AP	115/117 (98%)	104 (90%)	10 (9%)	1 (1%)	14	51
17	AQ	112/115 (97%)	100 (89%)	10 (9%)	2 (2%)	6	34
18	AR	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	14	51
19	AS	101/103 (98%)	91 (90%)	6 (6%)	4 (4%)	2	18
20	AT	108/110 (98%)	98 (91%)	9 (8%)	1 (1%)	14	51
21	AU	98/100 (98%)	85 (87%)	11 (11%)	2 (2%)	6	31
22	AV	101/104 (97%)	89 (88%)	11 (11%)	1 (1%)	12	49
23	AW	92/94 (98%)	85 (92%)	5 (5%)	2 (2%)	5	29
24	AX	82/85 (96%)	67 (82%)	12 (15%)	3 (4%)	2	20
25	AY	75/78 (96%)	64 (85%)	9 (12%)	2 (3%)	4	25
26	AZ	61/63 (97%)	49 (80%)	9 (15%)	3 (5%)	1	16
27	Aa	56/59 (95%)	54 (96%)	1 (2%)	1 (2%)	6	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	Ab	68/70 (97%)	57 (84%)	10 (15%)	1 (2%)	8	40
29	Ac	54/57 (95%)	47 (87%)	5 (9%)	2 (4%)	2	20
30	Ad	52/55 (94%)	45 (86%)	7 (14%)	0	100	100
31	Ae	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
32	Af	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
33	Ag	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	4	24
36	BC	391/393 (100%)	368 (94%)	20 (5%)	3 (1%)	16	54
38	BF	238/241 (99%)	215 (90%)	20 (8%)	3 (1%)	9	42
39	BG	230/233 (99%)	211 (92%)	17 (7%)	2 (1%)	14	51
40	BH	203/206 (98%)	191 (94%)	10 (5%)	2 (1%)	12	49
41	BI	164/167 (98%)	144 (88%)	17 (10%)	3 (2%)	6	34
42	BJ	133/135 (98%)	128 (96%)	3 (2%)	2 (2%)	8	40
43	BK	176/179 (98%)	160 (91%)	14 (8%)	2 (1%)	11	46
44	BL	127/130 (98%)	117 (92%)	8 (6%)	2 (2%)	7	38
45	BM	127/130 (98%)	111 (87%)	14 (11%)	2 (2%)	7	38
46	BN	101/103 (98%)	86 (85%)	11 (11%)	4 (4%)	2	18
47	BO	126/129 (98%)	113 (90%)	11 (9%)	2 (2%)	7	38
48	BP	121/124 (98%)	104 (86%)	12 (10%)	5 (4%)	2	18
49	BQ	115/118 (98%)	108 (94%)	7 (6%)	0	100	100
50	BR	98/101 (97%)	83 (85%)	8 (8%)	7 (7%)	1	11
51	BS	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
52	BT	80/82 (98%)	79 (99%)	1 (1%)	0	100	100
53	BU	81/84 (96%)	73 (90%)	8 (10%)	0	100	100
54	BV	72/75 (96%)	65 (90%)	5 (7%)	2 (3%)	4	24
55	BW	89/92 (97%)	80 (90%)	9 (10%)	0	100	100
56	BX	84/87 (97%)	78 (93%)	6 (7%)	0	100	100
57	BY	68/71 (96%)	60 (88%)	7 (10%)	1 (2%)	8	40
All	All	6548/6682 (98%)	5904 (90%)	536 (8%)	108 (2%)	10	38

5 of 108 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AD	260	LYS

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Mol	Chain	Res	Type
5	AE	122	VAL
5	AE	150	GLN
5	AE	170	VAL
9	AI	23	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AC	181/181 (100%)	170 (94%)	11 (6%)	17	38
4	AD	217/218 (100%)	207 (95%)	10 (5%)	24	45
5	AE	164/164 (100%)	156 (95%)	8 (5%)	22	43
6	AF	165/165 (100%)	162 (98%)	3 (2%)	51	68
7	AG	149/150 (99%)	140 (94%)	9 (6%)	17	39
8	AH	137/138 (99%)	125 (91%)	12 (9%)	9	28
9	AI	114/114 (100%)	109 (96%)	5 (4%)	25	47
10	AJ	109/110 (99%)	105 (96%)	4 (4%)	30	51
11	AK	116/116 (100%)	114 (98%)	2 (2%)	53	69
12	AL	104/104 (100%)	96 (92%)	8 (8%)	12	32
13	AM	103/103 (100%)	100 (97%)	3 (3%)	37	58
14	AN	109/109 (100%)	104 (95%)	5 (5%)	24	45
15	AO	103/103 (100%)	102 (99%)	1 (1%)	68	78
16	AP	87/87 (100%)	81 (93%)	6 (7%)	14	36
17	AQ	99/100 (99%)	91 (92%)	8 (8%)	11	31
18	AR	89/90 (99%)	85 (96%)	4 (4%)	24	46
19	AS	84/84 (100%)	81 (96%)	3 (4%)	31	52
20	AT	93/93 (100%)	90 (97%)	3 (3%)	34	56
21	AU	84/84 (100%)	81 (96%)	3 (4%)	31	52
22	AV	84/85 (99%)	80 (95%)	4 (5%)	23	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	AW	78/78 (100%)	75 (96%)	3 (4%)	29	50
24	AX	62/63 (98%)	60 (97%)	2 (3%)	34	56
25	AY	67/68 (98%)	67 (100%)	0	100	100
26	AZ	55/55 (100%)	51 (93%)	4 (7%)	13	34
27	Aa	48/49 (98%)	44 (92%)	4 (8%)	10	30
28	Ab	62/62 (100%)	58 (94%)	4 (6%)	15	37
29	Ac	47/48 (98%)	43 (92%)	4 (8%)	10	29
30	Ad	48/49 (98%)	46 (96%)	2 (4%)	26	48
31	Ae	38/38 (100%)	35 (92%)	3 (8%)	11	32
32	Af	51/52 (98%)	50 (98%)	1 (2%)	48	66
33	Ag	34/34 (100%)	33 (97%)	1 (3%)	37	58
36	BC	326/326 (100%)	318 (98%)	8 (2%)	42	63
38	BF	198/199 (100%)	193 (98%)	5 (2%)	42	63
39	BG	189/190 (100%)	177 (94%)	12 (6%)	16	37
40	BH	172/173 (99%)	166 (96%)	6 (4%)	32	53
41	BI	125/126 (99%)	120 (96%)	5 (4%)	28	49
42	BJ	116/116 (100%)	114 (98%)	2 (2%)	53	69
43	BK	146/147 (99%)	139 (95%)	7 (5%)	23	44
44	BL	104/105 (99%)	99 (95%)	5 (5%)	23	44
45	BM	106/107 (99%)	101 (95%)	5 (5%)	23	45
46	BN	90/90 (100%)	83 (92%)	7 (8%)	11	32
47	BO	98/99 (99%)	95 (97%)	3 (3%)	35	56
48	BP	103/104 (99%)	101 (98%)	2 (2%)	50	67
49	BQ	95/96 (99%)	91 (96%)	4 (4%)	26	48
50	BR	83/84 (99%)	78 (94%)	5 (6%)	17	39
51	BS	76/77 (99%)	76 (100%)	0	100	100
52	BT	65/65 (100%)	64 (98%)	1 (2%)	57	72
53	BU	77/78 (99%)	74 (96%)	3 (4%)	28	49
54	BV	64/65 (98%)	58 (91%)	6 (9%)	8	26
55	BW	78/79 (99%)	75 (96%)	3 (4%)	29	50
56	BX	65/66 (98%)	64 (98%)	1 (2%)	57	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	BY	60/61 (98%)	55 (92%)	5 (8%)	10	30
All	All	5417/5447 (99%)	5182 (96%)	235 (4%)	27	47

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

Mol	Chain	Res	Type
24	AX	9	THR
54	BV	6	ARG
36	BC	236	ILE
53	BU	70	LYS
46	BN	77	VAL

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%)	15 (12%)	3 (2%)
2	AB	2901/2904 (99%)	430 (14%)	130 (4%)
34	BA	1541/1542 (99%)	206 (13%)	77 (4%)
35	BB	75/76 (98%)	13 (17%)	2 (2%)
35	BE	75/76 (98%)	15 (20%)	6 (8%)
37	BD	24/24 (100%)	8 (33%)	5 (20%)
All	All	4735/4742 (99%)	687 (14%)	223 (4%)

5 of 687 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	10	G
1	AA	13	G
1	AA	15	A
1	AA	16	G
1	AA	36	C

5 of 223 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	AB	2602	A
35	BE	56	C

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Mol	Chain	Res	Type
34	BA	193	C
35	BE	18	G
34	BA	1302	C

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

55 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	$\# Z > 2$
35	4SU	BE	8	35	18,21,22	1.46	1 (5%)	25,30,33	1.65	6 (24%)
2	5MC	AB	1962	2	19,22,23	0.59	0	26,32,35	1.26	4 (15%)
35	5MU	BB	54	35	19,22,23	0.63	0	27,32,35	1.25	3 (11%)
34	2MG	BA	1207	34	23,26,27	0.79	0	33,38,41	0.88	0
34	2MG	BA	1516	34	23,26,27	0.70	0	33,38,41	0.76	0
35	7MG	BB	46	35	23,26,27	3.94	2 (8%)	27,39,42	1.39	2 (7%)
2	2MG	AB	1835	2	23,26,27	0.76	0	33,38,41	0.87	1 (3%)
2	CH	AB	2575	2	16,21,22	1.04	1 (6%)	19,30,33	1.23	2 (10%)
35	H2U	BE	16	35	18,21,22	0.82	0	19,30,33	1.06	1 (5%)
2	2MG	AB	2445	2	23,26,27	0.80	0	33,38,41	0.80	0
35	4SU	BB	8	35	18,21,22	1.48	2 (11%)	25,30,33	1.16	3 (12%)
2	PSU	AB	2504	2	18,21,22	1.09	2 (11%)	21,30,33	1.31	2 (9%)
35	PSU	BB	39	35	18,21,22	0.86	0	21,30,33	0.99	1 (4%)
34	MA6	BA	1519	34	23,26,27	0.71	0	33,38,41	1.29	3 (9%)
34	4OC	BA	1402	34	20,23,24	0.67	0	25,32,35	1.13	2 (8%)
2	6MZ	AB	2030	2	22,25,26	0.60	0	29,36,39	1.06	3 (10%)
2	5MU	AB	747	2	19,22,23	0.69	0	27,32,35	1.42	3 (11%)
2	1MG	AB	745	2	23,26,27	0.72	0	33,39,42	1.32	4 (12%)
34	MA6	BA	1518	34	23,26,27	0.69	0	33,38,41	0.98	1 (3%)
35	7MG	BE	46	35	23,26,27	3.90	2 (8%)	27,39,42	1.47	2 (7%)
2	7MG	AB	2069	2	23,26,27	3.91	2 (8%)	27,39,42	1.38	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	H2U	AB	2449	2	18,21,22	0.81	0	19,30,33	0.82	0
35	PSU	BE	39	35	18,21,22	0.93	1 (5%)	21,30,33	1.07	1 (4%)
35	MIA	BB	37	35	28,31,32	0.84	1 (3%)	38,44,47	1.28	2 (5%)
34	5MC	BA	1407	34	19,22,23	0.61	0	26,32,35	0.99	1 (3%)
2	PSU	AB	2580	2	18,21,22	0.95	1 (5%)	21,30,33	1.31	2 (9%)
2	5MU	AB	1939	2	19,22,23	0.62	0	27,32,35	1.27	3 (11%)
35	5MU	BE	54	35	19,22,23	0.63	0	27,32,35	1.18	3 (11%)
2	3TD	AB	1915	2	19,22,23	0.77	0	23,32,35	0.96	1 (4%)
35	3AU	BB	47	-	24,28,29	0.87	1 (4%)	30,40,43	0.91	1 (3%)
2	PSU	AB	955	2	18,21,22	0.87	1 (5%)	21,30,33	1.14	1 (4%)
2	6MZ	AB	1618	2	22,25,26	0.62	0	29,36,39	0.90	2 (6%)
2	PSU	AB	2605	2	18,21,22	0.89	1 (5%)	21,30,33	0.97	1 (4%)
35	PSU	BB	55	35	18,21,22	0.94	1 (5%)	21,30,33	1.08	1 (4%)
2	PSU	AB	746	2	18,21,22	0.99	1 (5%)	21,30,33	1.37	2 (9%)
35	H2U	BB	16	35	18,21,22	0.80	0	19,30,33	1.09	1 (5%)
2	PSU	AB	2457	2	18,21,22	0.98	1 (5%)	21,30,33	1.42	3 (14%)
34	7MG	BA	527	34	23,26,27	3.88	2 (8%)	27,39,42	1.39	2 (7%)
35	H2U	BE	20	35	18,21,22	0.78	0	19,30,33	1.27	2 (10%)
34	PSU	BA	516	34	18,21,22	0.93	1 (5%)	21,30,33	1.17	1 (4%)
35	PSU	BB	32	35	18,21,22	0.95	1 (5%)	21,30,33	1.16	2 (9%)
34	2MG	BA	966	34	23,26,27	0.74	0	33,38,41	1.06	2 (6%)
2	PSU	AB	1917	2	18,21,22	0.90	0	21,30,33	0.76	1 (4%)
35	H2U	BB	20	35	18,21,22	0.79	0	19,30,33	0.95	1 (5%)
34	UR3	BA	1498	34	19,22,23	0.71	0	26,32,35	0.94	1 (3%)
35	MIA	BE	37	35	28,31,32	0.84	1 (3%)	38,44,47	1.25	4 (10%)
35	3AU	BE	47	-	24,28,29	0.88	1 (4%)	30,40,43	1.24	4 (13%)
2	2MA	AB	2503	2	22,25,26	0.69	0	32,37,40	0.82	0
2	OMU	AB	2552	2	19,22,23	0.67	0	25,31,34	0.97	2 (8%)
2	OMC	AB	2498	2	19,22,23	0.53	0	25,31,34	0.85	0
35	PSU	BE	55	35	18,21,22	0.99	1 (5%)	21,30,33	1.00	1 (4%)
34	5MC	BA	967	34	19,22,23	0.62	0	26,32,35	0.88	1 (3%)
2	PSU	AB	1911	2	18,21,22	0.89	0	21,30,33	0.86	1 (4%)
2	OMG	AB	2251	2	23,26,27	0.52	0	32,38,41	0.81	1 (3%)
35	PSU	BE	32	35	18,21,22	0.95	1 (5%)	21,30,33	1.13	2 (9%)

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
35	4SU	BE	8	35	-	0/7/25/26	0/2/2/2
2	5MC	AB	1962	2	-	5/7/25/26	0/2/2/2
35	5MU	BB	54	35	-	0/7/25/26	0/2/2/2
34	2MG	BA	1207	34	-	0/9/27/28	0/3/3/3
34	2MG	BA	1516	34	-	0/9/27/28	0/3/3/3
35	7MG	BB	46	35	-	1/7/37/38	0/3/3/3
2	2MG	AB	1835	2	-	0/9/27/28	0/3/3/3
2	CH	AB	2575	2	-	1/5/25/26	0/2/2/2
35	H2U	BE	16	35	-	0/7/38/39	0/2/2/2
2	2MG	AB	2445	2	-	0/9/27/28	0/3/3/3
35	4SU	BB	8	35	-	0/7/25/26	0/2/2/2
2	PSU	AB	2504	2	-	1/7/25/26	0/2/2/2
35	PSU	BB	39	35	-	0/7/25/26	0/2/2/2
34	MA6	BA	1519	34	-	0/11/29/30	0/3/3/3
34	4OC	BA	1402	34	-	0/9/29/30	0/2/2/2
2	6MZ	AB	2030	2	-	3/9/27/28	0/3/3/3
2	5MU	AB	747	2	-	4/7/25/26	0/2/2/2
2	1MG	AB	745	2	-	0/7/25/26	0/3/3/3
34	MA6	BA	1518	34	-	0/11/29/30	0/3/3/3
35	7MG	BE	46	35	-	0/7/37/38	0/3/3/3
2	7MG	AB	2069	2	-	0/7/37/38	0/3/3/3
2	H2U	AB	2449	2	-	0/7/38/39	0/2/2/2
35	PSU	BE	39	35	-	0/7/25/26	0/2/2/2
35	MIA	BB	37	35	-	1/15/33/34	0/3/3/3
34	5MC	BA	1407	34	-	0/7/25/26	0/2/2/2
2	PSU	AB	2580	2	-	0/7/25/26	0/2/2/2
2	5MU	AB	1939	2	-	0/7/25/26	0/2/2/2
35	5MU	BE	54	35	-	0/7/25/26	0/2/2/2
2	3TD	AB	1915	2	-	0/7/25/26	0/2/2/2
35	3AU	BB	47	-	-	2/16/34/35	0/2/2/2
2	PSU	AB	955	2	-	0/7/25/26	0/2/2/2
2	6MZ	AB	1618	2	-	0/9/27/28	0/3/3/3
2	PSU	AB	2605	2	-	0/7/25/26	0/2/2/2
35	PSU	BB	55	35	-	1/7/25/26	0/2/2/2
2	PSU	AB	746	2	-	2/7/25/26	0/2/2/2
35	H2U	BB	16	35	-	0/7/38/39	0/2/2/2
2	PSU	AB	2457	2	-	0/7/25/26	0/2/2/2
34	7MG	BA	527	34	-	1/7/37/38	0/3/3/3
35	H2U	BE	20	35	-	0/7/38/39	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	PSU	BA	516	34	-	0/7/25/26	0/2/2/2
35	PSU	BB	32	35	-	2/7/25/26	0/2/2/2
34	2MG	BA	966	34	-	0/9/27/28	0/3/3/3
2	PSU	AB	1917	2	-	0/7/25/26	0/2/2/2
35	H2U	BB	20	35	-	0/7/38/39	0/2/2/2
34	UR3	BA	1498	34	-	0/7/25/26	0/2/2/2
35	MIA	BE	37	35	-	0/15/33/34	0/3/3/3
35	3AU	BE	47	-	-	4/16/34/35	0/2/2/2
2	2MA	AB	2503	2	-	2/7/25/26	0/3/3/3
2	OMU	AB	2552	2	-	0/9/27/28	0/2/2/2
2	OMC	AB	2498	2	-	1/9/27/28	0/2/2/2
35	PSU	BE	55	35	-	2/7/25/26	0/2/2/2
34	5MC	BA	967	34	-	0/7/25/26	0/2/2/2
2	PSU	AB	1911	2	-	0/7/25/26	0/2/2/2
2	OMG	AB	2251	2	-	0/9/27/28	0/3/3/3
35	PSU	BE	32	35	-	0/7/25/26	0/2/2/2

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	BB	46	7MG	C8-N9	-18.42	1.33	1.45
2	AB	2069	7MG	C8-N9	-18.33	1.34	1.45
35	BE	46	7MG	C8-N9	-18.29	1.34	1.45
34	BA	527	7MG	C8-N9	-18.17	1.34	1.45
35	BB	8	4SU	C5-C4	-5.34	1.36	1.42

The worst 5 of 97 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	BB	37	MIA	C11-S10-C2	5.98	106.73	102.25
35	BE	46	7MG	N9-C8-N7	5.97	111.82	103.37
2	AB	2069	7MG	N9-C8-N7	5.88	111.70	103.37
34	BA	527	7MG	N9-C8-N7	5.78	111.56	103.37
35	BB	46	7MG	N9-C8-N7	5.66	111.39	103.37

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AB	747	5MU	C2'-C1'-N1-C2
2	AB	2503	2MA	O4'-C1'-N9-C4

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Mol	Chain	Res	Type	Atoms
34	BA	527	7MG	C4'-C5'-O5'-P
35	BB	37	MIA	N6-C12-C13-C14
35	BB	46	7MG	C4'-C5'-O5'-P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

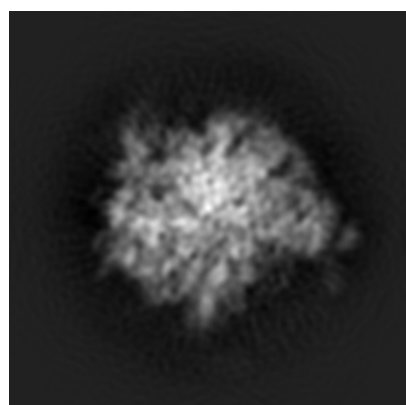
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1849. These allow visual inspection of the internal detail of the map and identification of artifacts.

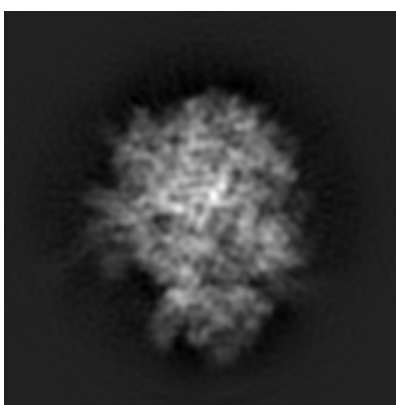
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

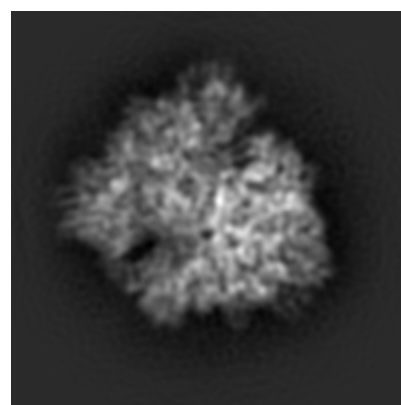
6.1.1 Primary map



X



Y

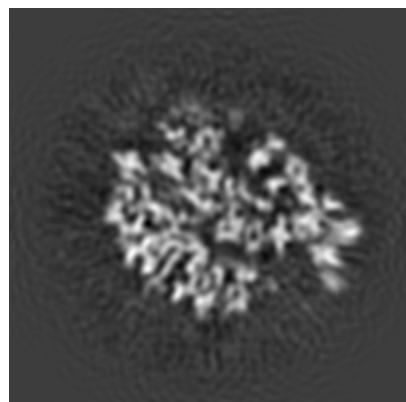


Z

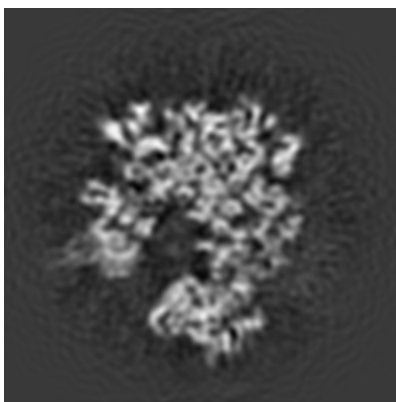
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

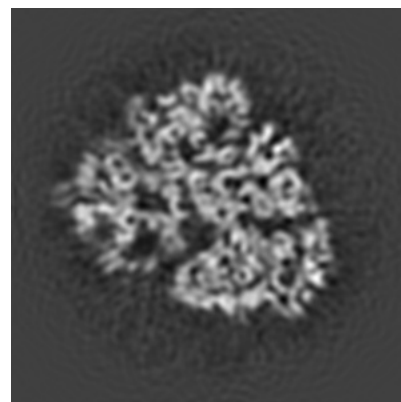
6.2.1 Primary map



X Index: 125



Y Index: 125

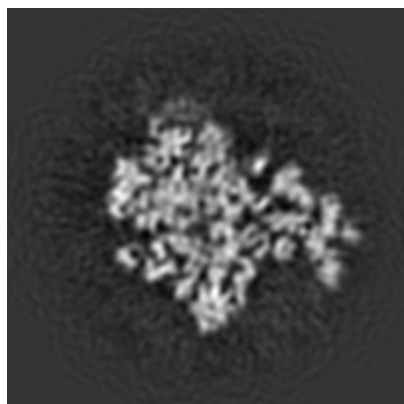


Z Index: 125

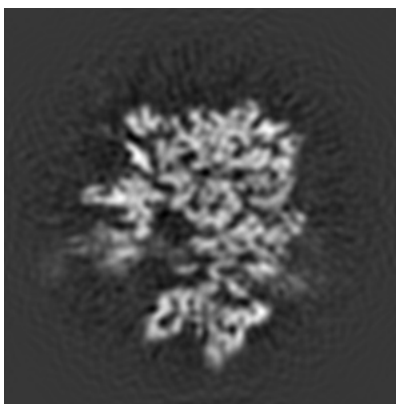
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

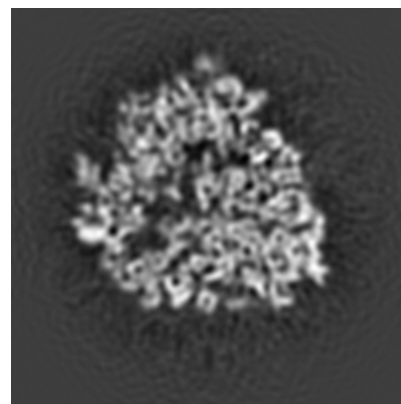
6.3.1 Primary map



X Index: 130



Y Index: 130

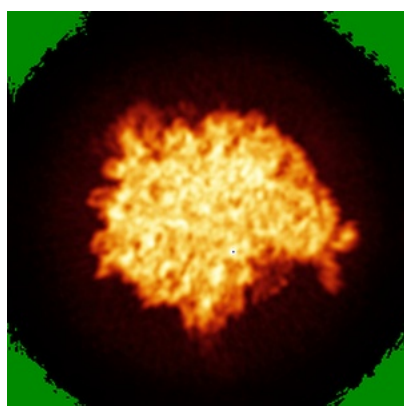


Z Index: 117

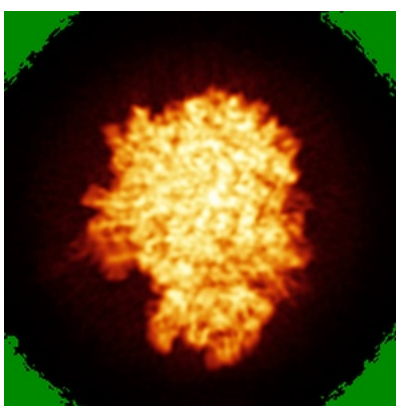
The images above show the largest variance slices of the map in three orthogonal directions.

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

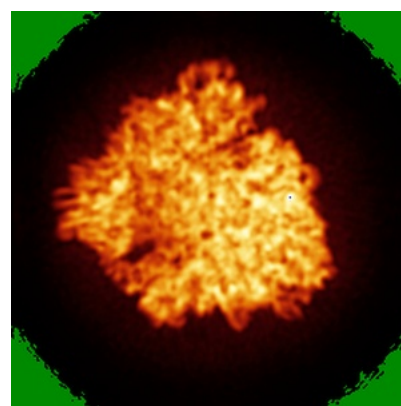
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

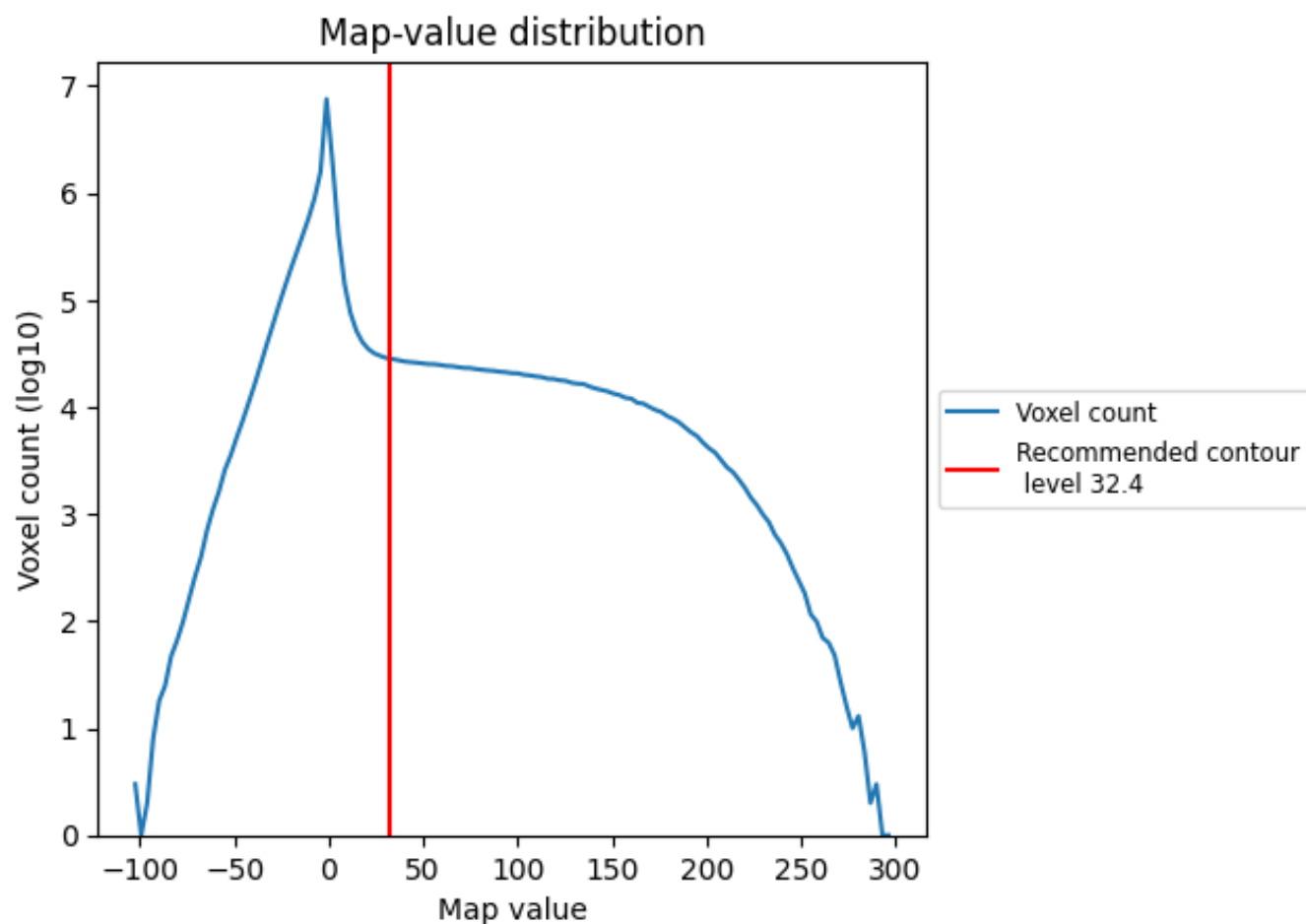
6.6 Mask visualisation

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

7 Map analysis [i](#)

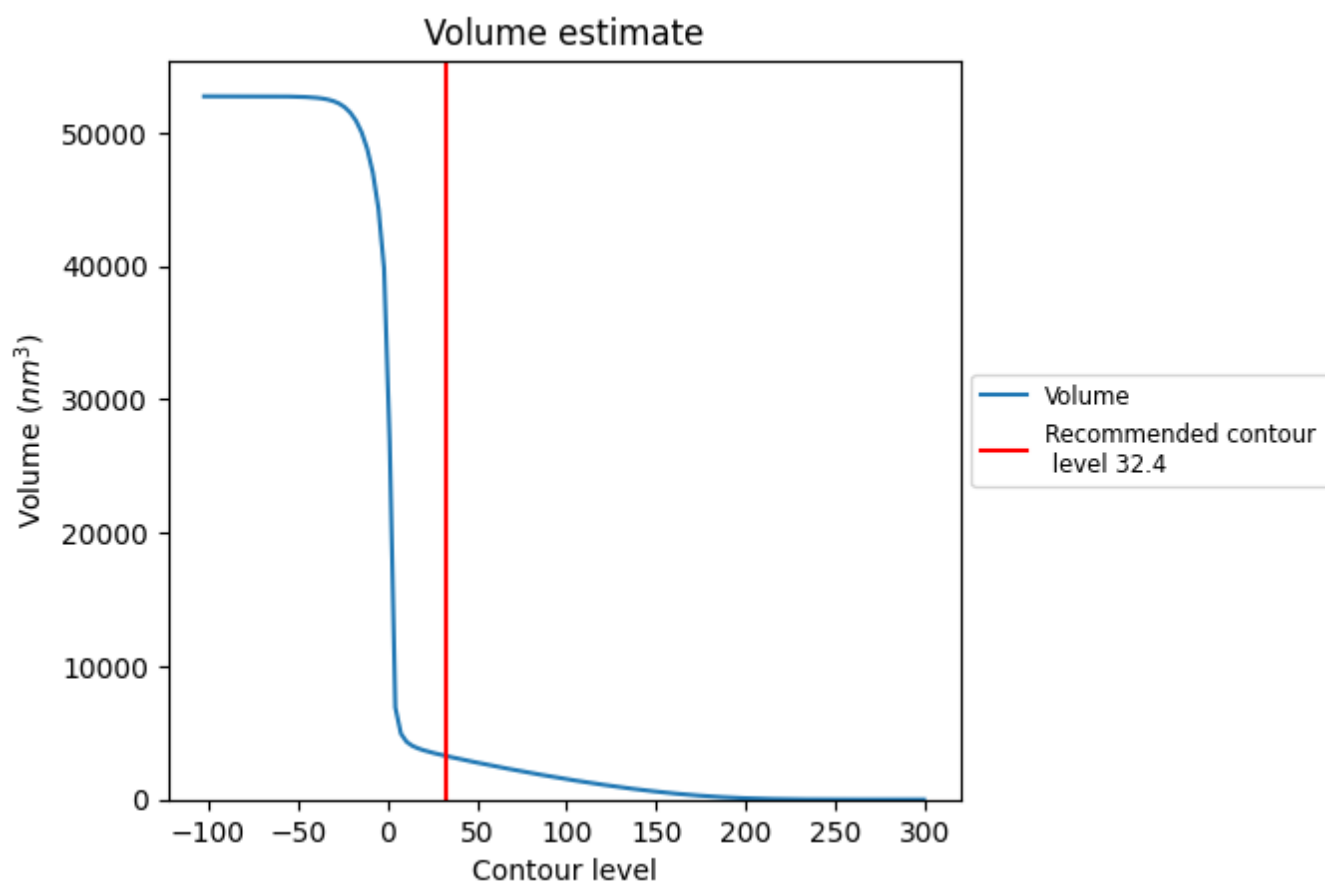
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

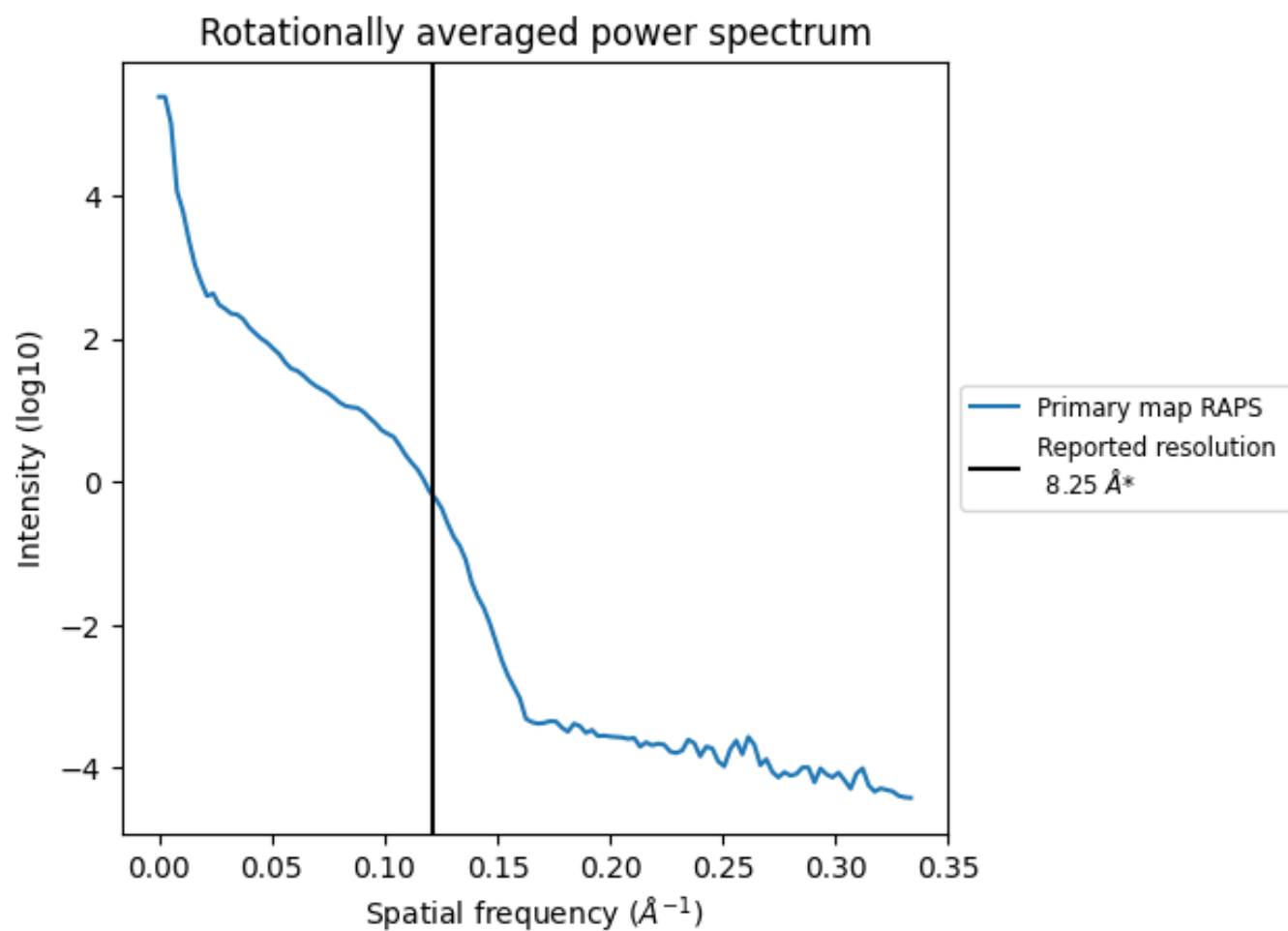
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3278 nm³; this corresponds to an approximate mass of 2961 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 0.121 Å⁻¹

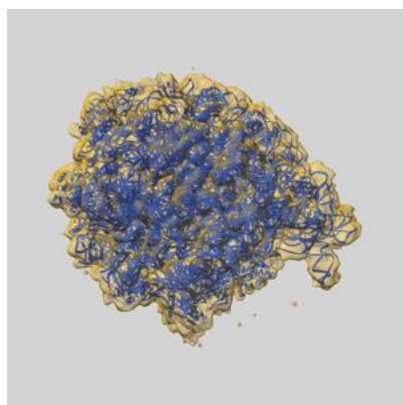
8 Fourier-Shell correlation

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

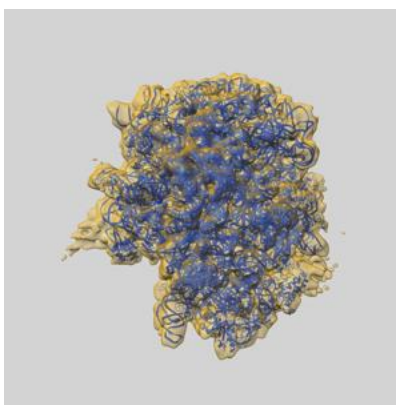
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1849 and PDB model 4V6K. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

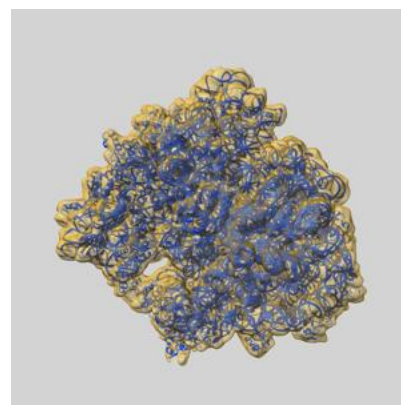
9.1 Map-model overlay [i](#)



X



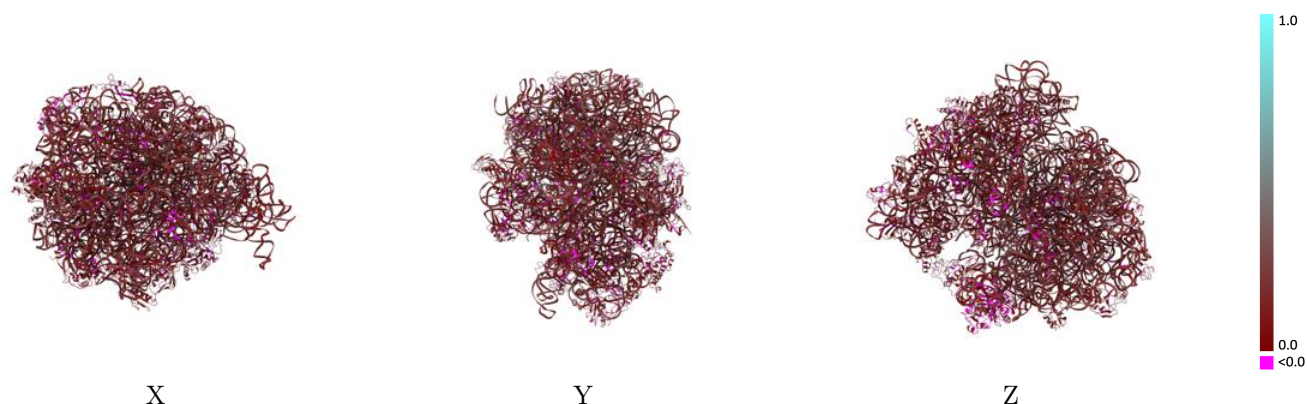
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 32.4 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](#)

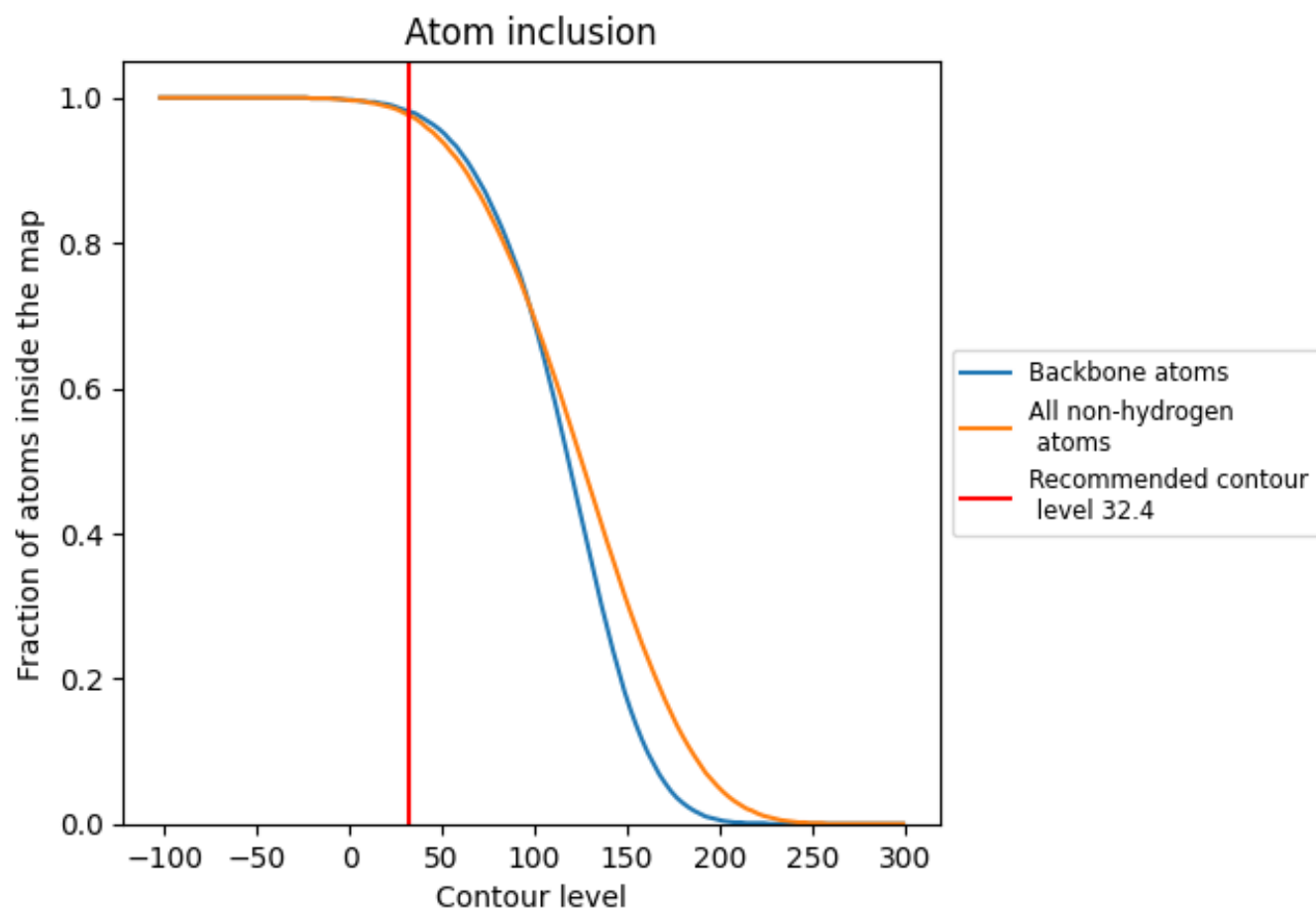


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (32.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9750	 0.1600
AA	 0.9980	 0.1930
AB	 0.9960	 0.1830
AC	 0.7850	 0.0430
AD	 0.9680	 0.1080
AE	 0.9690	 0.1100
AF	 0.9620	 0.1180
AG	 0.9740	 0.1250
AH	 0.9830	 0.1540
AI	 0.7900	 0.1140
AJ	 0.9600	 0.0990
AK	 0.9330	 0.1130
AL	 0.9500	 0.1230
AM	 0.9670	 0.1220
AN	 0.9610	 0.1210
AO	 0.9800	 0.1190
AP	 0.9900	 0.1380
AQ	 0.9410	 0.1510
AR	 0.9570	 0.1030
AS	 0.9440	 0.1270
AT	 0.9700	 0.1360
AU	 0.9700	 0.1300
AV	 0.9820	 0.1410
AW	 0.9850	 0.1560
AX	 0.8980	 0.0680
AY	 0.9520	 0.1110
AZ	 0.9520	 0.1250
Aa	 0.9790	 0.1460
Ab	 0.8830	 0.0890
Ac	 0.9860	 0.0910
Ad	 0.9610	 0.1000
Ae	 0.9750	 0.0930
Af	 0.9800	 0.1240
Ag	 0.9660	 0.0680
BA	 0.9960	 0.1780



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Chain	Atom inclusion	Q-score
BB	 0.9310	 0.1780
BC	 0.8140	 0.1240
BD	 0.9780	 0.1760
BE	 0.9800	 0.1800
BF	 0.9340	 0.1320
BG	 0.9010	 0.1260
BH	 0.9430	 0.1040
BI	 0.9240	 0.1220
BJ	 0.8730	 0.1110
BK	 0.9650	 0.1270
BL	 0.9810	 0.1450
BM	 0.9690	 0.1090
BN	 0.9250	 0.0960
BO	 0.9390	 0.1190
BP	 0.9500	 0.1150
BQ	 0.9780	 0.1320
BR	 0.9790	 0.1030
BS	 0.9860	 0.1310
BT	 0.9700	 0.1100
BU	 0.9790	 0.1210
BV	 0.9880	 0.1210
BW	 0.9060	 0.0800
BX	 0.9850	 0.1370
BY	 0.8660	 0.0860