



## wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 12:16 PM EST

PDB ID : 4V6N  
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](mailto: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>.

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

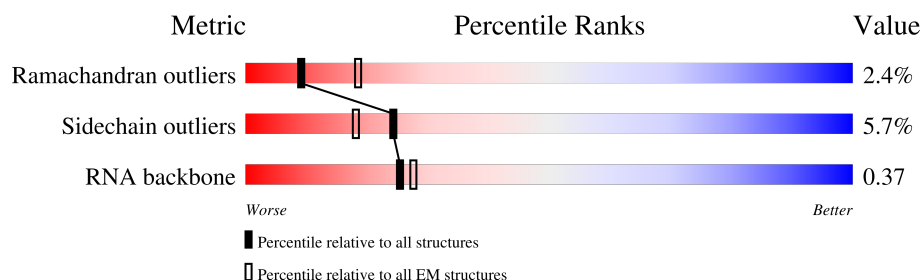
EMDB validation analysis : 0.0.1.dev43  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

# 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.








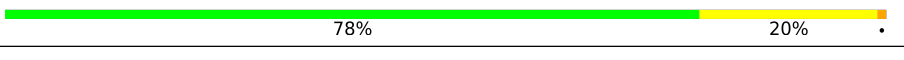

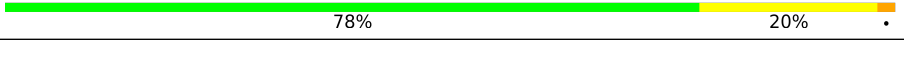

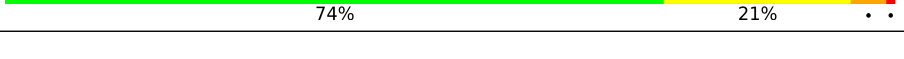
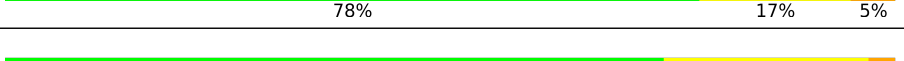
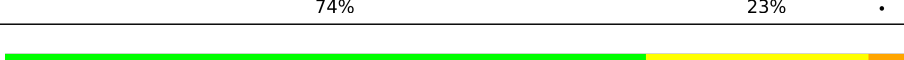
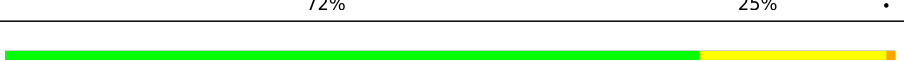
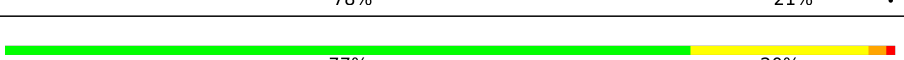
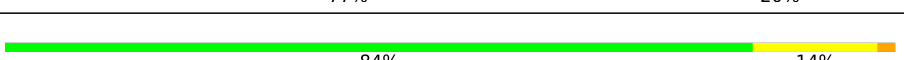
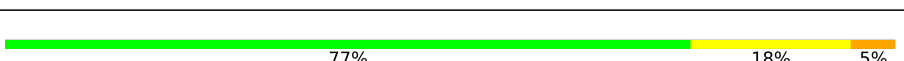
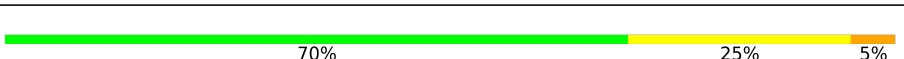
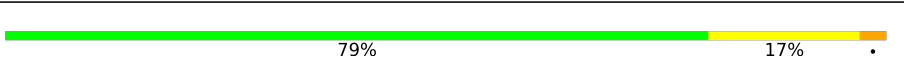



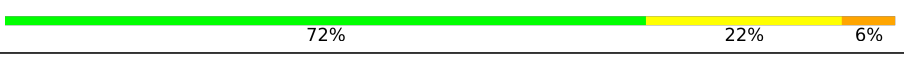
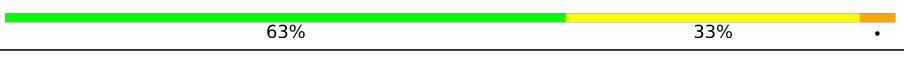
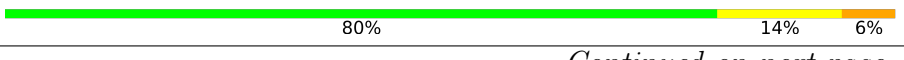

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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	
5	AE	209	
6	AF	201	
7	AG	178	
8	AH	176	

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Mol	Chain	Length	Quality of chain
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	
30	A3	56	
31	A4	54	
32	A5	46	
33	A6	64	

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Mol	Chain	Length	Quality of chain
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	
55	BU	74	
56	BV	91	
57	BW	86	
58	BX	70	

## 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		

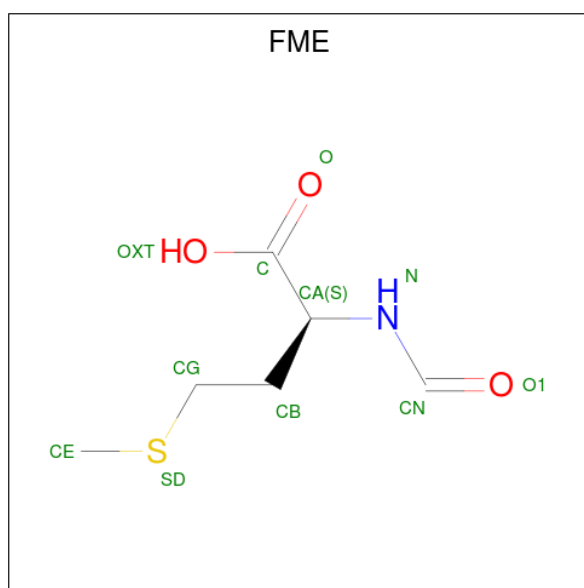
- Molecule 57 is a protein called 30S ribosomal protein S20.

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.

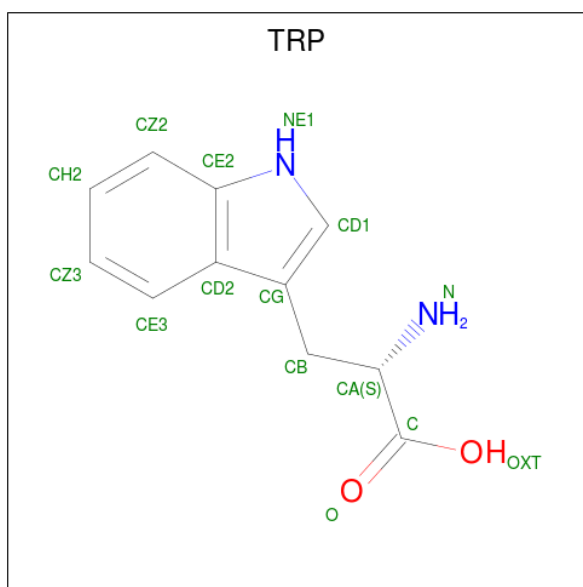
Mol	Chain	Residues	Atoms					AltConf	Trace
58	BX	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 59 is N-FORMYLMETHIONINE (three-letter code: 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 (three-letter code: TRP) (formula:  $C_{11}H_{12}N_2O_2$ ).

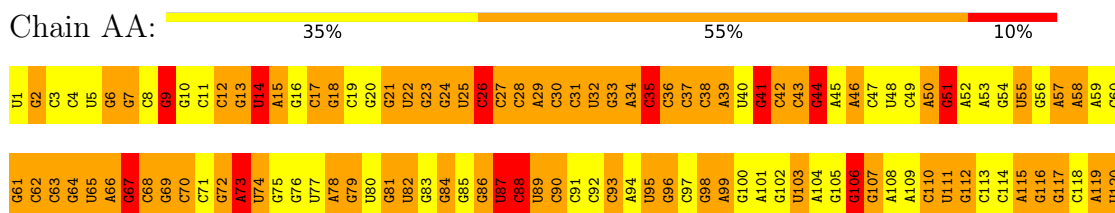


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
60	BB	1	14	11	2	1	0

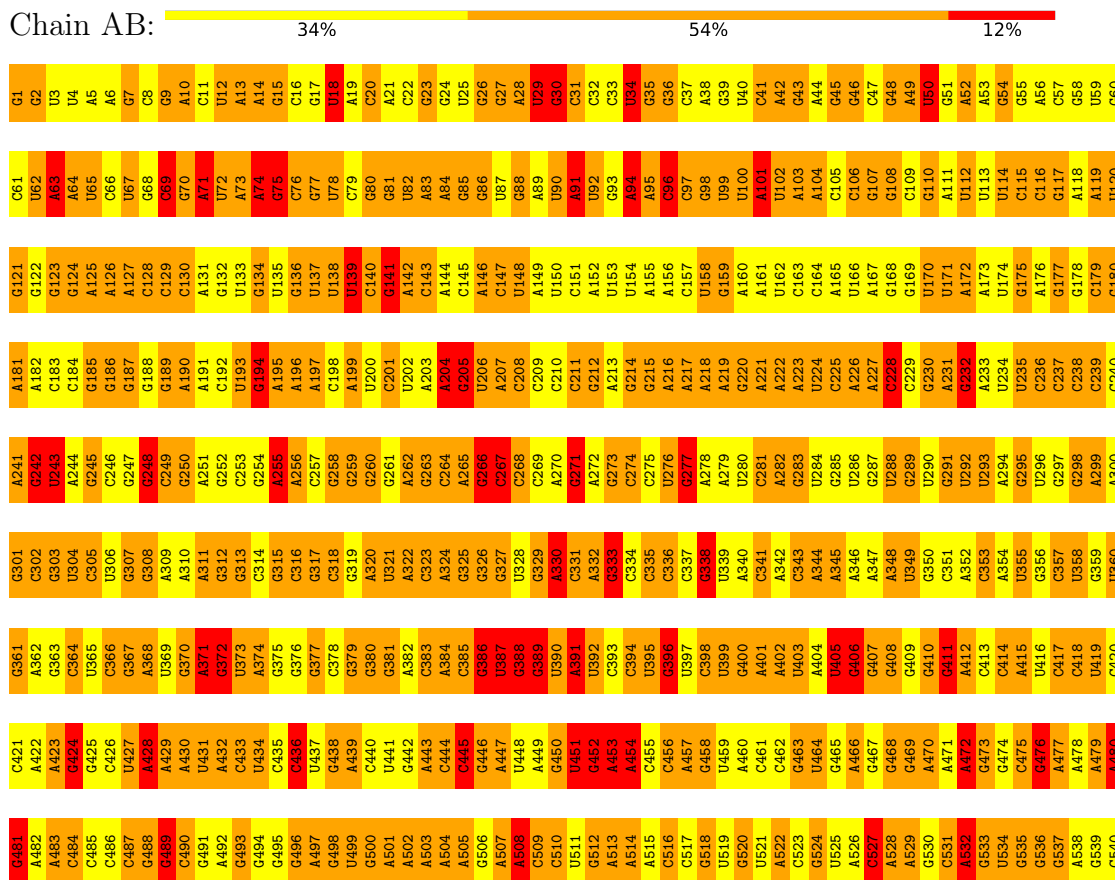
### 3 Residue-property plots

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



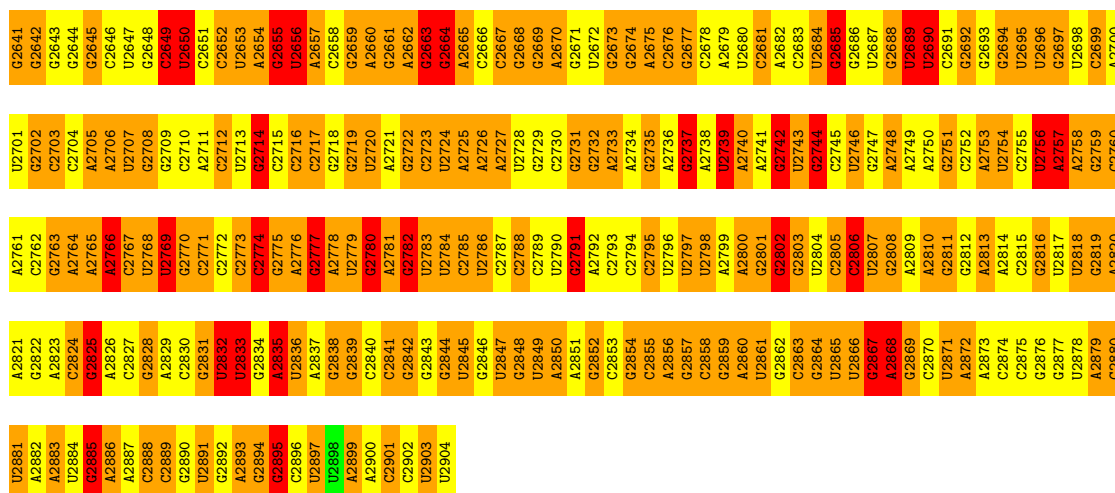
#### • Molecule 2: 23S ribosomal RNA



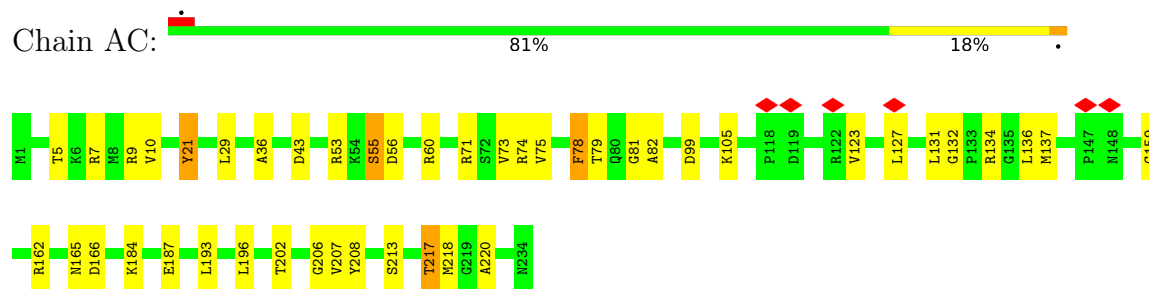
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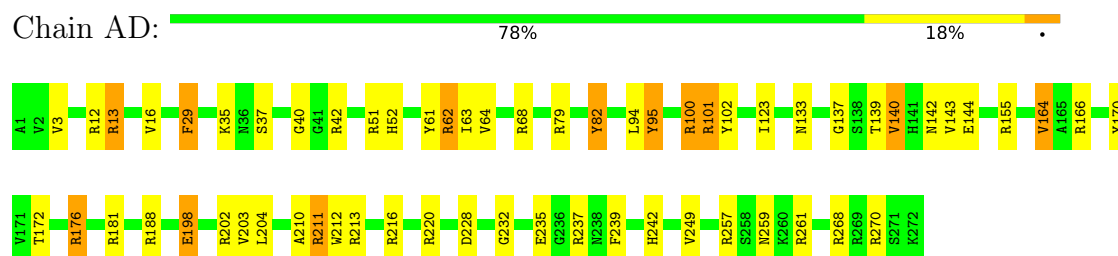
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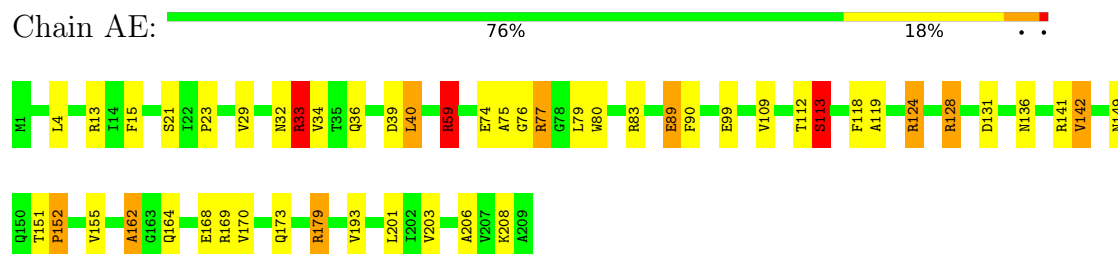
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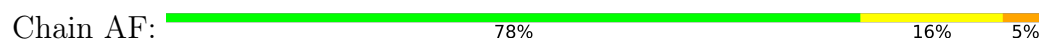
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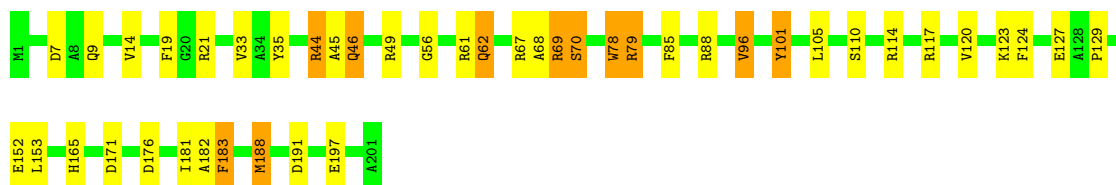


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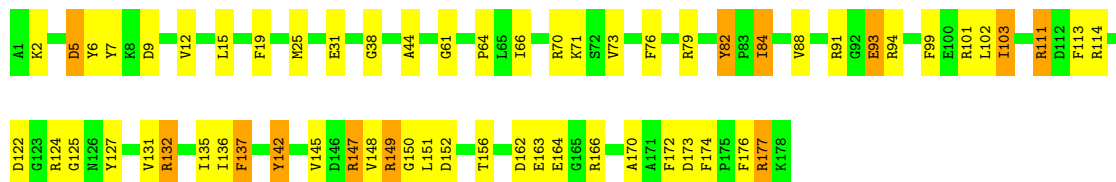
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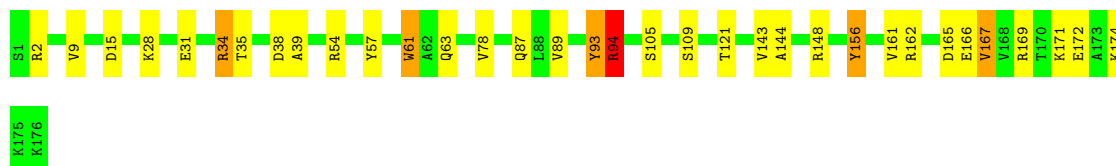
- Molecule 7: 50S ribosomal protein L5

Chain AG: 66% 28% 7%



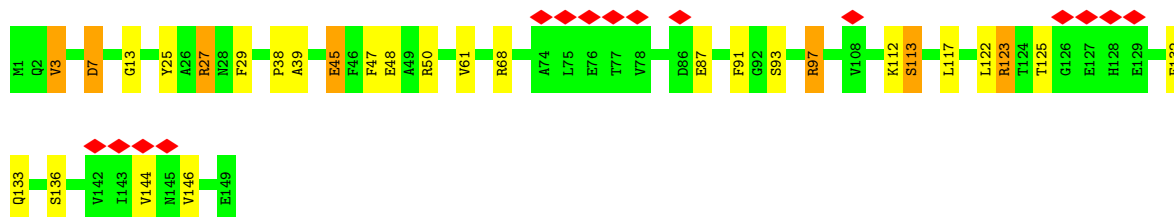
- Molecule 8: 50S ribosomal protein L6

Chain AH: 81% 16% ..



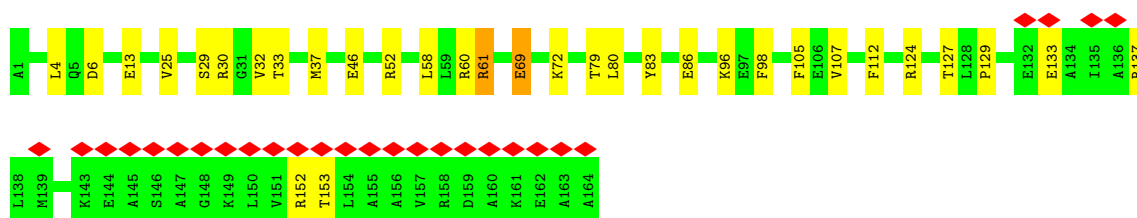
- Molecule 9: 50S ribosomal protein L9

Chain AI: 10% 81% 15% 5%




- Molecule 10: 50S ribosomal protein L10

Chain AJ: 16% 80% 18%



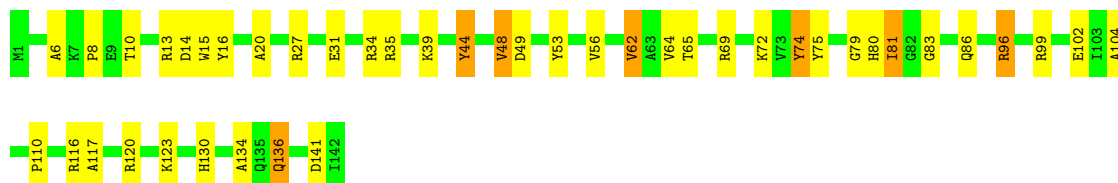
- Molecule 11: 50S ribosomal protein L11

Chain AK:  84% 14%




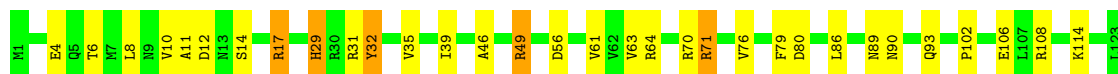
- Molecule 12: 50S ribosomal protein L13

Chain AL:  70% 25% 5%




- Molecule 13: 50S ribosomal protein L14

Chain AM:  74% 22%




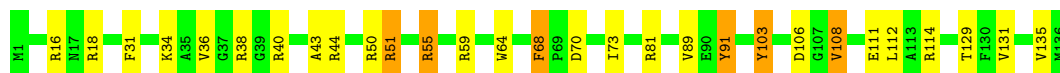
- Molecule 14: 50S ribosomal protein L15

Chain AN:  78% 20%




- Molecule 15: 50S ribosomal protein L16

Chain AO:  79% 17%




- Molecule 16: 50S ribosomal protein L17

Chain AP:  78% 20%

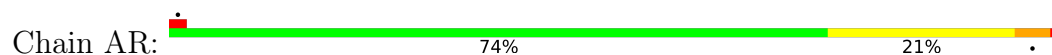


- Molecule 17: 50S ribosomal protein L18

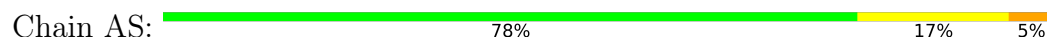
Chain AQ:  78% 20%



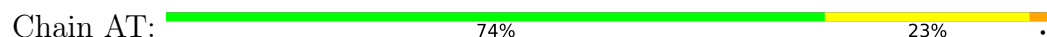
- Molecule 18: 50S ribosomal protein L19



- Molecule 19: 50S ribosomal protein L20



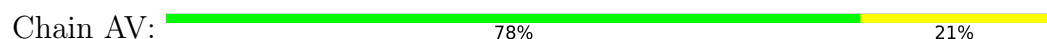
- Molecule 20: 50S ribosomal protein L21



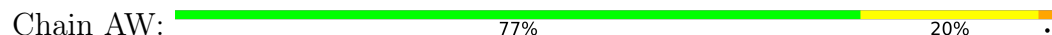
- Molecule 21: 50S ribosomal protein L22



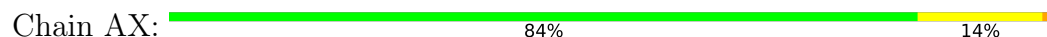
- Molecule 22: 50S ribosomal protein L23

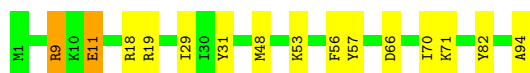


- Molecule 23: 50S ribosomal protein L24



- Molecule 24: 50S ribosomal protein L25





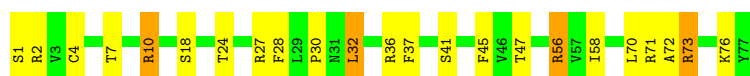
- Molecule 25: 50S ribosomal protein L27

Chain AY: 77% 18% 5%



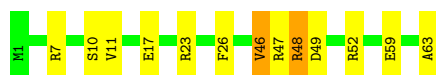
- Molecule 26: 50S ribosomal protein L28

Chain AZ: 70% 25% 5%



- Molecule 27: 50S ribosomal protein L29

Chain A0: 79% 17% 4%



- Molecule 28: 50S ribosomal protein L30

Chain A1: 78% 21% 1%



- Molecule 29: 50S ribosomal protein L31

Chain A2: 77% 14% 9%



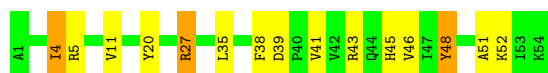
- Molecule 30: 50S ribosomal protein L32

Chain A3: 70% 21% 9%



- Molecule 31: 50S ribosomal protein L33

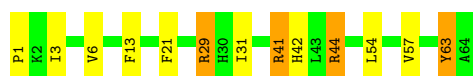
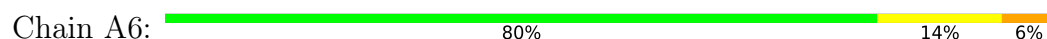
Chain A4: 72% 22% 6%



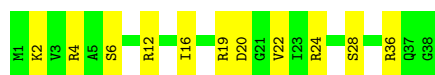
- Molecule 32: 50S ribosomal protein L34



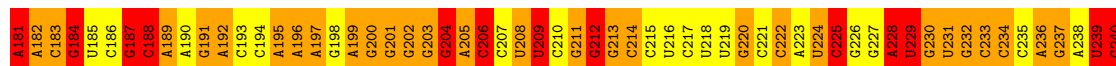
- Molecule 33: 50S ribosomal protein L35



- Molecule 34: 50S ribosomal protein L36



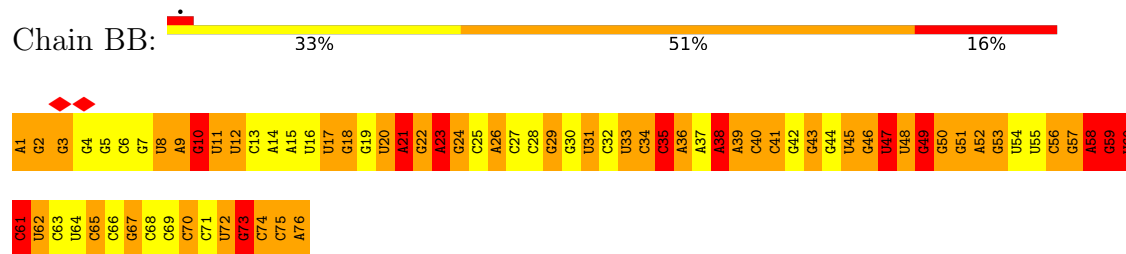
- Molecule 35: 16S ribosomal RNA



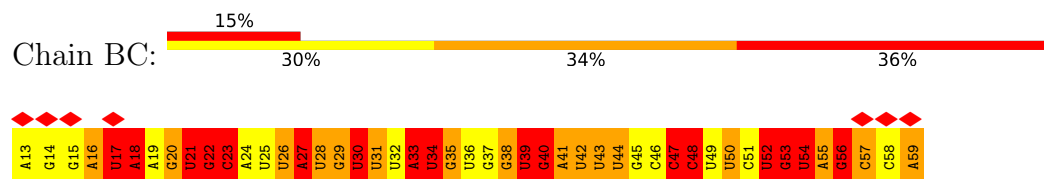
C1501	A1441	U1381	U1321	A1261	A1201	C1141	A1081	A1021	U961	A901	C841	A781	G721	G661	G601	G541	G481
A1502	G1442	C1362	C1322	C1262	U1202	G1142	A1082	A1022	C962	G902	U842	A782	G722	U662	A602	G542	A482
A1503	C1443	C1363	G1323	U1263	C1203	G1143	U1083	G1023	G963	G903	U843	C783	G723	A663	G603	U543	A483
U1504	C1444	C1364	A1324	U1264	A1204	G1144	G1084	G1024	A964	U904	G844	A784	G724	G664	G604	G544	G484
G1505	U1445	G1365	C1325	C1265	G1205	A1145	U1085	U1025	U965	U905	A845	G785	G725	A665	G605	C545	U485
U1506	A1446	G1366	U1326	G1266	G1206	A1146	U1086	C1026	G966	A906	G846	G786	G726	G666	G606	A546	U486
A1507	U1447	G1367	C1327	U1267	G1207	C1147	G1087	C1027	C967	A907	G847	A787	G727	A667	A607	A547	A487
U1508	C1448	C1368	C1328	G1268	C1208	U1148	G1088	U1028	A968	A908	C848	U788	A728	G668	A608	C548	C488
A1509	A1449	C1369	A1329	A1269	C1209	U1149	U1089	U1029	A969	A909	G849	U789	A729	G669	A609	C549	C489
U1510	U1450	C1370	U1330	G1270	C1210	A1150	U1090	C1030	C970	U910	U850	G790	G730	G670	U610	G550	C490
G1511	A1451	C1371	G1331	A1271	G1211	A1151	U1091	C1031	C971	U911	G851	G791	G731	G671	C611	U551	G491
U1512	C1452	G1372	A1332	C1272	U1212	A1152	A1092	G1032	C972	C912	G852	A792	G732	U672	C612	U552	A492
A1513	G1453	C1373	A1333	C1273	C1213	G1153	A1093	G1033	G973	A913	C853	U793	G733	G673	C613	A493	A493
G1514	C1454	A1374	G1334	A1274	C1214	G1154	G1094	G1034	A974	A914	U854	A794	G734	G674	C614	A544	G494
U1515	A1455	C1395	U1335	A1275	G1215	A1155	U1095	A1035	A975	A915	U855	C795	G735	A675	G615	U555	A495
G1516	C1456	C1396	C1336	G1276	A1216	U1156	C1096	A1036	C976	U916	C856	G796	G736	A676	G616	C556	A496
U1517	A1457	C1397	G1337	C1277	G1217	A1157	C1097	C1037	A977	A917	C857	G797	G737	U677	G617	G557	A497
A1518	U1458	C1398	A1338	G1278	C1218	C1158	C1098	C1038	A978	A918	G858	U798	G738	U678	C618	G558	A498
U1519	A1459	C1399	A1339	G1279	C1219	U1159	C1099	C1039	C979	A919	C859	G799	G739	C679	U619	A559	A499
C1520	C1460	C1400	A1340	U1280	G1220	G1160	C1100	U1040	C980	U920	A860	G800	U740	C620	A620	A560	G500
U1521	G1461	G1401	U1341	C1281	G1221	C1161	A1101	G1041	C981	U921	G861	U801	G741	A621	U561	C501	C501
C1522	C1462	C1402	C1342	U1282	G1222	C1162	A1102	A1042	U982	G922	C862	A802	G742	A622	U562	A502	A502
U1523	A1463	C1403	G1343	U1283	C1223	A1163	C1103	G1043	A983	A923	U863	G803	A743	C623	C563	C503	C503
C1524	U1464	C1404	C1344	C1284	U1224	G1164	G1104	A1044	C984	C924	A864	U804	C744	G624	C564	C504	C504
U1525	A1465	G1405	U1345	A1285	A1225	U1165	A1105	C1045	C985	G925	A865	C805	G745	U625	U565	G505	G505
G1526	C1466	U1406	A1346	U1286	C1226	G1166	G1106	A1046	U986	G926	C866	C806	A746	G626	C566	G506	G506
U1527	U1467	C1407	G1347	A1287	C1227	C1167	C1107	G1047	C987	G927	G867	A807	A747	G627	C567	C507	C507
U1528	A1468	C1408	U1348	U1288	C1228	U1168	C1108	C1048	G988	G928	C868	G808	G748	A627	G567	A507	A507
C1529	C1469	A1409	A1349	A1289	G1229	G1169	C1109	U1049	C989	G929	C869	G809	A749	A629	C569	A509	A509
U1530	U1470	C1410	C1350	U1290	G1230	A1170	A1110	G1050	C990	C930	U870	C810	C750	A630	A510	A510	A510
A1531	C1471	C1411	U1351	U1291	G1231	A1171	A1111	C1051	U991	C931	U871	C811	U751	C631	C511	C511	C511
U1532	U1472	C1412	C1352	G1292	U1232	C1172	C1112	U1052	U992	C932	A872	C812	G752	U632	U512	U512	U512
C1533	G1473	A1413	G1353	C1293	G1233	U1173	C1113	G1053	C993	G933	A873	U813	A753	C633	C513	C513	C513
A1534	U1474	C1414	U1354	G1294	C1234	G1174	C1114	A1054	A994	A934	C874	A814	C754	A634	C514	C514	C514
U1535	G1475	G1415	C1355	U1295	U1235	G1175	U1115	A1055	C995	A935	U875	A815	G755	A635	G515	G515	G515
C1536	A1476	C1416	G1356	C1296	A1236	A1176	U1116	U1056	A996	C936	C876	A816	C756	U636	C516	C516	C516
U1537	U1477	G1417	A1357	G1297	G1237	G1177	A1117	C1057	U997	A937	G877	C817	U757	C637	G517	G517	G517
C1538	U1478	A1418	U1358	U1298	A1238	G1178	U1118	C1058	C998	A938	A878	G818	C758	U638	C518	C518	C518
U1539	C1479	U1419	C1359	A1299	A1239	A1179	C1119	C1059	C999	G939	C879	A819	A759	G639	C519	C519	C519
U1540	A1480	U1420	A1360	G1300	U1240	A1180	C1120	U1060	A1000	C940	C880	U820	G760	A640	A520	A520	A520
U1541	U1481	G1421	G1361	U1301	G1241	G1181	U1121	C1061	C1001	G941	C881	G821	G761	U641	C521	C521	C521
A1482	C1482	G1422	A1362	C1302	G1242	C1182	U1122	U1062	G1002	G942	C882	U822	U762	A642	C522	C522	C522
A1483	U1483	G1423	A1363	G1303	C1243	U1183	U1123	C1063	G1003	U943	C883	G823	G763	C643	A523	A523	A523
C1484	U1484	U1424	U1364	G1304	G1244	G1184	G1124	G1064	A1004	C944	U884	G824	C764	U644	G524	G524	G524
U1485	U1485	U1425	G1365	G1305	C1245	G1185	U1125	U1065	A1005	G945	C885	A825	G765	G645	C525	C525	C525
A1486	C1486	G1426	C1366	A1306	A1246	G1186	U1126	C1066	G1006	A946	G886	C826	A766	G646	C526	C526	C526
U1487	U1487	C1427	C1367	U1307	G1247	G1187	G1127	A1067	U1007	G947	G887	U827	A767	G647	C527	C527	C527
A1488	G1488	A1428	A1368	U1308	A1248	A1188	C1128	G1068	U1008	A948	C888	U828	A768	A648	C528	C528	C528
U1489	U1489	A1429	C1369	G1309	C1249	U1189	C1129	C1069	U1009	A949	C889	G829	G769	U649	G529	G529	G529
U1490	A1490	A1430	G1370	G1310	A1250	G1190	A1130	U1070	U1010	U950	C890	G830	C770	G650	G530	G530	G530
G1491	C1491	A1431	G1371	A1311	A1251	A1191	G1131	C1071	C1011	G951	U891	A831	G771	C651	U531	U531	U531
A1492	U1492	G1432	U1372	C1312	A1252	C1192	C1132	G1072	A1012	U952	A892	A832	U772	U652	A532	A532	A532
A1493	C1493	A1433	G1373	U1313	G1253	G1193	G1133	U1073	G1013	G953	C893	G833	G773	U653	A533	A533	A533
G1494	A1494	A1434	A1374	C1314	A1254	U1194	G1134	G1074	A1014	G954	C894	U834	G774	G654	U534	U534	U534
U1495	U1495	G1435	A1375	U1315	G1255	C1195	U1135	U1075	G1015	U955	C895	U835	G775	A655	A535	A535	A535
A1496	C1496	A1436	U1376	A1316	A1256	A1196	C1136	U1076	A1016	U956	C896	G836	G776	G656	C536	C536	C536
G1497	U1497	A1437	A1377	C1317	A1257	A1197	C1137	G1077	U1017	U957	C897	U837	A777	U657	G537	G537	G537
U1498	U1498	G1438	C1378	A1318	G1258	U1198	G1138	U1078	G1018	A958	C898	G838	G778	C658	A538	A538	A538
A1499	A1499	C1379	A1319	U1199	U1259	U1199	G1139	G1079	A1019	A959	C899	G839	C779	U659	A539	A539	A539
A1500	C1500	U1440	U1380	C1320	G1260	C1200	C1140	A1080	G1020	U960	A900	C840	A780	C720	C660	A600	A600



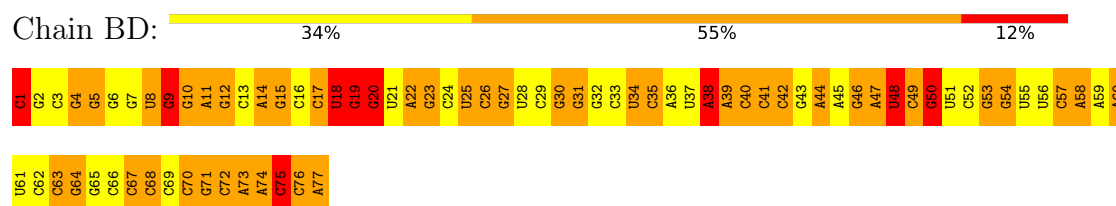
- Molecule 36: A site tRNA



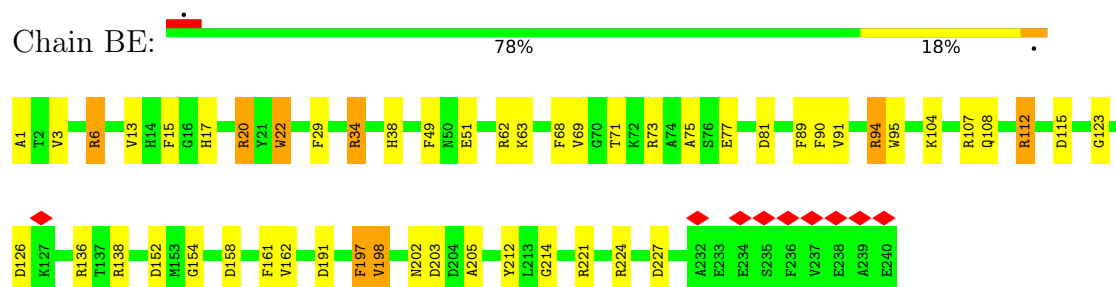
- Molecule 37: mRNA



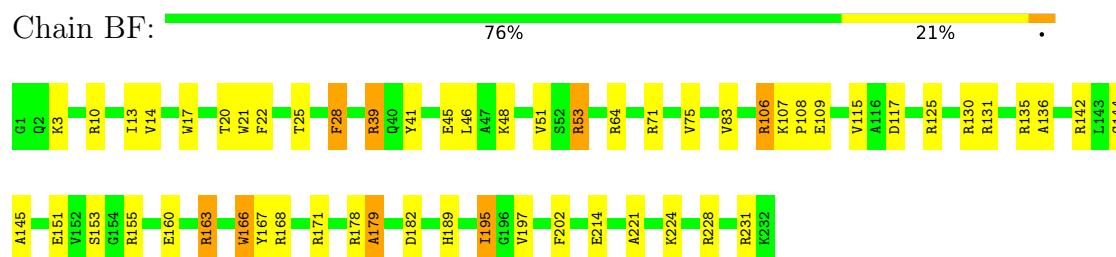
- Molecule 38: P site tRNA



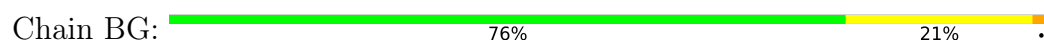
- Molecule 39: 30S ribosomal protein S2

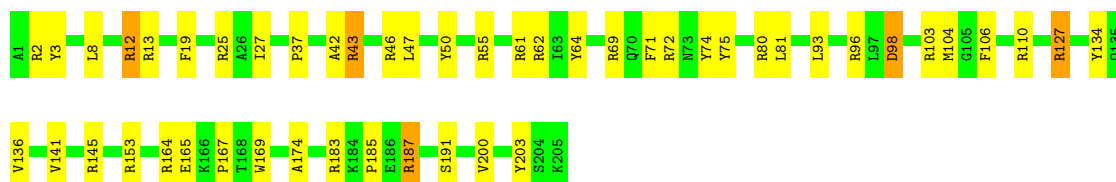


- Molecule 40: 30S ribosomal protein S3



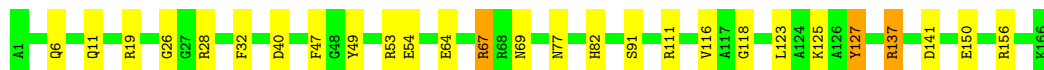
- Molecule 41: 30S ribosomal protein S4





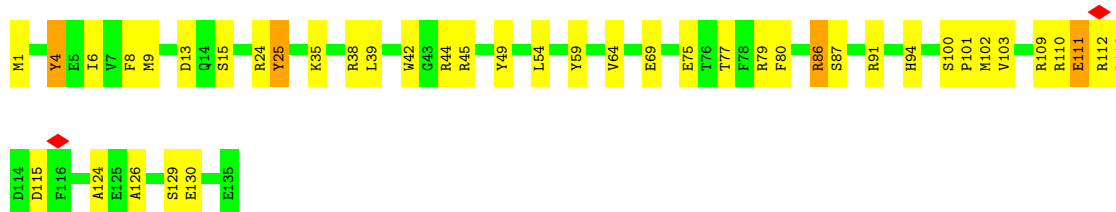
- Molecule 42: 30S ribosomal protein S5

Chain BH: 84% 14% .



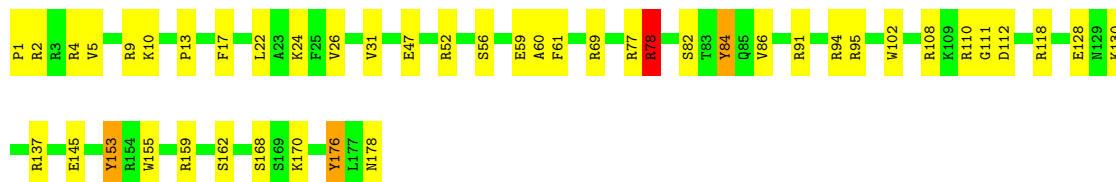
- Molecule 43: 30S ribosomal protein S6

Chain BI: 69% 28% .



- Molecule 44: 30S ribosomal protein S7

Chain BJ: 75% 23% ..



- Molecule 45: 30S ribosomal protein S8

Chain BK: 78% 16% 5%



- Molecule 46: 30S ribosomal protein S9

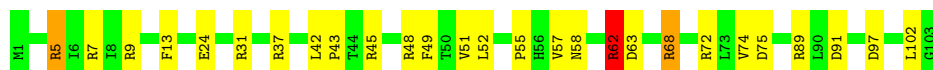
Chain BL: 68% 27% 5%





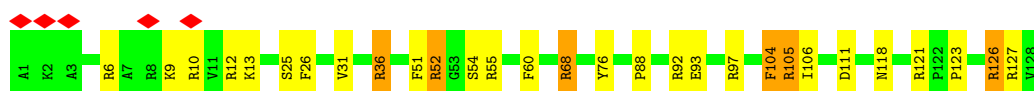
- Molecule 47: 30S ribosomal protein S10

Chain BM: 74% 23%



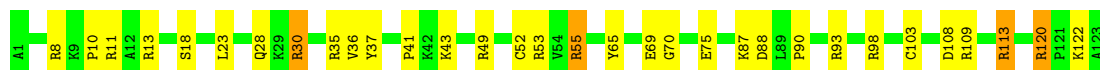
- Molecule 48: 30S ribosomal protein S11

Chain BN: 77% 18% 5%



- Molecule 49: 30S ribosomal protein S12

Chain BO: 74% 23%



- Molecule 50: 30S ribosomal protein S13

Chain BP: 77% 19%



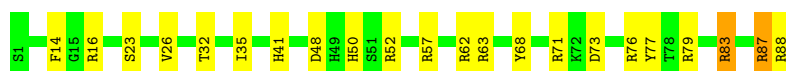
- Molecule 51: 30S ribosomal protein S14

Chain BQ: 67% 31%



- Molecule 52: 30S ribosomal protein S15

Chain BR: 75% 23%



- Molecule 53: 30S ribosomal protein S16

Chain BS: 77% 20%



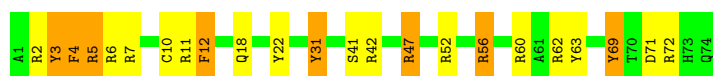
- Molecule 54: 30S ribosomal protein S17

Chain BT: 75% 24% .



- Molecule 55: 30S ribosomal protein S18

Chain BU: 69% 20% 11% .



- Molecule 56: 30S ribosomal protein S19

Chain BV: 79% 19% .



- Molecule 57: 30S ribosomal protein S20

Chain BW: 86% 13% .



- Molecule 58: 30S ribosomal protein S21

Chain BX: 69% 26% 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: 1MG, CH, OMC, MA6, OMG, 7MG, 3TD, 5MC, UR3, 6MZ, FME, 2MA, 4SU, H2U, 4OC, OMU, PSU, 5MU, MIA, 2MG

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	3.14	330/2869 (11.5%)	3.60	681/4474 (15.2%)
2	AB	3.07	7254/69257 (10.5%)	3.51	15515/108040 (14.4%)
3	AC	1.50	7/1748 (0.4%)	1.83	37/2355 (1.6%)
4	AD	1.51	4/2131 (0.2%)	1.99	62/2863 (2.2%)
5	AE	1.50	6/1586 (0.4%)	1.92	28/2134 (1.3%)
6	AF	1.47	5/1571 (0.3%)	1.92	37/2113 (1.8%)
7	AG	1.60	10/1444 (0.7%)	2.03	49/1937 (2.5%)
8	AH	1.53	3/1343 (0.2%)	1.92	28/1816 (1.5%)
9	AI	1.45	3/1122 (0.3%)	1.96	24/1515 (1.6%)
10	AJ	1.56	7/1247 (0.6%)	1.92	21/1679 (1.3%)
11	AK	1.50	3/1046 (0.3%)	1.84	19/1410 (1.3%)
12	AL	1.52	7/1152 (0.6%)	1.94	33/1551 (2.1%)
13	AM	1.41	1/956 (0.1%)	1.89	24/1279 (1.9%)
14	AN	1.52	2/1062 (0.2%)	1.98	27/1413 (1.9%)
15	AO	1.48	2/1093 (0.2%)	2.19	34/1460 (2.3%)
16	AP	1.48	4/1021 (0.4%)	2.00	21/1364 (1.5%)
17	AQ	1.49	3/910 (0.3%)	1.93	24/1219 (2.0%)
18	AR	1.56	6/929 (0.6%)	2.07	25/1242 (2.0%)
19	AS	1.57	5/960 (0.5%)	2.21	34/1278 (2.7%)
20	AT	1.56	1/829 (0.1%)	1.93	19/1107 (1.7%)
21	AU	1.47	4/864 (0.5%)	2.01	27/1156 (2.3%)
22	AV	1.49	4/794 (0.5%)	1.86	17/1060 (1.6%)
23	AW	1.53	4/797 (0.5%)	1.94	20/1062 (1.9%)
24	AX	1.46	2/766 (0.3%)	1.80	14/1025 (1.4%)
25	AY	1.51	0/642	1.97	16/848 (1.9%)
26	AZ	1.57	3/635 (0.5%)	2.13	20/848 (2.4%)
27	A0	1.51	1/510 (0.2%)	1.90	10/677 (1.5%)
28	A1	1.41	1/453 (0.2%)	2.05	17/605 (2.8%)
29	A2	1.55	1/559 (0.2%)	2.18	16/745 (2.1%)
30	A3	1.53	4/450 (0.9%)	2.15	17/599 (2.8%)
31	A4	1.50	0/448	1.96	12/594 (2.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	A5	1.49	4/380 (1.1%)	2.28	17/498 (3.4%)
33	A6	1.49	3/513 (0.6%)	1.89	11/676 (1.6%)
34	A7	1.42	1/303 (0.3%)	2.16	11/397 (2.8%)
35	BA	3.10	3971/36769 (10.8%)	3.53	8378/57354 (14.6%)
36	BB	3.03	178/1600 (11.1%)	3.53	372/2492 (14.9%)
37	BC	3.13	119/1108 (10.7%)	3.48	238/1724 (13.8%)
38	BD	3.05	179/1721 (10.4%)	3.56	400/2683 (14.9%)
39	BE	1.49	8/1904 (0.4%)	1.96	46/2565 (1.8%)
40	BF	1.49	6/1852 (0.3%)	1.99	48/2490 (1.9%)
41	BG	1.57	9/1665 (0.5%)	2.08	56/2227 (2.5%)
42	BH	1.50	5/1239 (0.4%)	1.87	27/1664 (1.6%)
43	BI	1.55	5/1121 (0.4%)	2.04	41/1509 (2.7%)
44	BJ	1.54	8/1422 (0.6%)	1.94	39/1908 (2.0%)
45	BK	1.42	7/989 (0.7%)	1.98	21/1326 (1.6%)
46	BL	1.56	8/1048 (0.8%)	2.24	44/1394 (3.2%)
47	BM	1.49	3/835 (0.4%)	2.00	25/1127 (2.2%)
48	BN	1.48	2/982 (0.2%)	2.08	28/1323 (2.1%)
49	BO	1.52	4/969 (0.4%)	1.90	23/1300 (1.8%)
50	BP	1.52	5/919 (0.5%)	2.05	25/1226 (2.0%)
51	BQ	1.62	9/817 (1.1%)	2.10	30/1088 (2.8%)
52	BR	1.47	1/724 (0.1%)	2.09	29/966 (3.0%)
53	BS	1.52	1/659 (0.2%)	2.18	22/884 (2.5%)
54	BT	1.55	4/681 (0.6%)	2.06	19/913 (2.1%)
55	BU	1.55	4/637 (0.6%)	2.18	28/851 (3.3%)
56	BV	1.52	2/744 (0.3%)	1.90	13/995 (1.3%)
57	BW	1.49	2/676 (0.3%)	1.78	7/895 (0.8%)
58	BX	1.58	2/598 (0.3%)	2.02	22/792 (2.8%)
All	All	2.70	12237/164069 (7.5%)	3.17	26948/244735 (11.0%)

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 12237 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	2225	A	N3-C4	18.05	1.45	1.34
2	AB	2615	U	C2-N3	17.29	1.49	1.37
35	BA	729	A	P-O5'	15.61	1.75	1.59
2	AB	1970	A	N9-C4	15.52	1.47	1.37
2	AB	1008	A	N3-C4	15.09	1.44	1.34

The worst 5 of 26948 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AB	2855	C	N3-C4-C5	-23.45	112.52	121.90
2	AB	1264	A	N9-C4-C5	22.40	114.76	105.80
29	A2	25	ARG	NE-CZ-NH1	21.63	131.12	120.30
2	AB	248	G	C2-N3-C4	20.59	122.19	111.90
2	AB	6	A	C8-N9-C4	-20.57	97.57	105.80

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	768	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	103775	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%)	5	31
4	AD	270/272 (99%)	237 (88%)	24 (9%)	9 (3%)	4	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	AE	207/209 (99%)	171 (83%)	28 (14%)	8 (4%)	3	23
6	AF	199/201 (99%)	172 (86%)	18 (9%)	9 (4%)	2	22
7	AG	176/178 (99%)	151 (86%)	16 (9%)	9 (5%)	2	19
8	AH	174/176 (99%)	158 (91%)	13 (8%)	3 (2%)	9	42
9	AI	147/149 (99%)	131 (89%)	10 (7%)	6 (4%)	3	23
10	AJ	162/164 (99%)	156 (96%)	5 (3%)	1 (1%)	25	66
11	AK	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
12	AL	140/142 (99%)	119 (85%)	16 (11%)	5 (4%)	3	25
13	AM	121/123 (98%)	107 (88%)	9 (7%)	5 (4%)	3	23
14	AN	142/144 (99%)	127 (89%)	12 (8%)	3 (2%)	7	36
15	AO	134/136 (98%)	123 (92%)	8 (6%)	3 (2%)	6	35
16	AP	125/127 (98%)	114 (91%)	10 (8%)	1 (1%)	19	60
17	AQ	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
18	AR	112/114 (98%)	97 (87%)	13 (12%)	2 (2%)	8	40
19	AS	115/117 (98%)	107 (93%)	4 (4%)	4 (4%)	3	25
20	AT	101/103 (98%)	91 (90%)	8 (8%)	2 (2%)	7	38
21	AU	108/110 (98%)	100 (93%)	5 (5%)	3 (3%)	5	30
22	AV	98/100 (98%)	75 (76%)	20 (20%)	3 (3%)	4	27
23	AW	101/103 (98%)	89 (88%)	10 (10%)	2 (2%)	7	38
24	AX	92/94 (98%)	87 (95%)	4 (4%)	1 (1%)	14	52
25	AY	82/84 (98%)	63 (77%)	17 (21%)	2 (2%)	6	33
26	AZ	75/77 (97%)	66 (88%)	7 (9%)	2 (3%)	5	31
27	A0	61/63 (97%)	56 (92%)	4 (7%)	1 (2%)	9	44
28	A1	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
29	A2	68/70 (97%)	64 (94%)	3 (4%)	1 (2%)	10	46
30	A3	54/56 (96%)	47 (87%)	4 (7%)	3 (6%)	2	19
31	A4	52/54 (96%)	49 (94%)	1 (2%)	2 (4%)	3	24
32	A5	44/46 (96%)	39 (89%)	3 (7%)	2 (4%)	2	22
33	A6	62/64 (97%)	59 (95%)	2 (3%)	1 (2%)	9	44
34	A7	36/38 (95%)	29 (81%)	5 (14%)	2 (6%)	2	19
39	BE	238/240 (99%)	220 (92%)	12 (5%)	6 (2%)	5	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	BF	230/232 (99%)	217 (94%)	8 (4%)	5 (2%)	6	35
41	BG	203/205 (99%)	189 (93%)	11 (5%)	3 (2%)	10	46
42	BH	164/166 (99%)	149 (91%)	13 (8%)	2 (1%)	13	50
43	BI	133/135 (98%)	123 (92%)	9 (7%)	1 (1%)	19	60
44	BJ	176/178 (99%)	164 (93%)	9 (5%)	3 (2%)	9	42
45	BK	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	19	60
46	BL	127/129 (98%)	115 (91%)	9 (7%)	3 (2%)	6	33
47	BM	101/103 (98%)	90 (89%)	6 (6%)	5 (5%)	2	20
48	BN	126/128 (98%)	112 (89%)	11 (9%)	3 (2%)	6	33
49	BO	121/123 (98%)	107 (88%)	12 (10%)	2 (2%)	9	42
50	BP	115/117 (98%)	110 (96%)	3 (3%)	2 (2%)	9	42
51	BQ	98/100 (98%)	84 (86%)	9 (9%)	5 (5%)	2	19
52	BR	86/88 (98%)	81 (94%)	4 (5%)	1 (1%)	13	50
53	BS	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
54	BT	81/83 (98%)	72 (89%)	8 (10%)	1 (1%)	13	50
55	BU	72/74 (97%)	62 (86%)	7 (10%)	3 (4%)	3	22
56	BV	89/91 (98%)	82 (92%)	6 (7%)	1 (1%)	14	52
57	BW	84/86 (98%)	79 (94%)	4 (5%)	1 (1%)	13	50
58	BX	68/70 (97%)	61 (90%)	4 (6%)	3 (4%)	2	22
All	All	6319/6423 (98%)	5710 (90%)	457 (7%)	152 (2%)	9	33

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%)	177 (98%)	4 (2%)	52	71
4	AD	217/217 (100%)	212 (98%)	5 (2%)	50	70
5	AE	164/164 (100%)	148 (90%)	16 (10%)	8	26
6	AF	165/165 (100%)	156 (94%)	9 (6%)	21	47
7	AG	149/149 (100%)	140 (94%)	9 (6%)	19	44
8	AH	137/137 (100%)	125 (91%)	12 (9%)	10	31
9	AI	114/114 (100%)	107 (94%)	7 (6%)	18	44
10	AJ	122/122 (100%)	111 (91%)	11 (9%)	9	30
11	AK	109/109 (100%)	104 (95%)	5 (5%)	27	52
12	AL	116/116 (100%)	104 (90%)	12 (10%)	7	25
13	AM	104/104 (100%)	96 (92%)	8 (8%)	13	37
14	AN	103/103 (100%)	98 (95%)	5 (5%)	25	50
15	AO	109/109 (100%)	106 (97%)	3 (3%)	43	65
16	AP	103/103 (100%)	100 (97%)	3 (3%)	42	64
17	AQ	87/87 (100%)	81 (93%)	6 (7%)	15	40
18	AR	99/99 (100%)	91 (92%)	8 (8%)	11	35
19	AS	89/89 (100%)	87 (98%)	2 (2%)	52	71
20	AT	84/84 (100%)	77 (92%)	7 (8%)	11	34
21	AU	93/93 (100%)	87 (94%)	6 (6%)	17	42
22	AV	84/84 (100%)	80 (95%)	4 (5%)	25	51
23	AW	84/84 (100%)	79 (94%)	5 (6%)	19	44
24	AX	78/78 (100%)	74 (95%)	4 (5%)	24	48
25	AY	62/62 (100%)	60 (97%)	2 (3%)	39	61
26	AZ	67/67 (100%)	61 (91%)	6 (9%)	9	30
27	A0	55/55 (100%)	52 (94%)	3 (6%)	21	47
28	A1	48/48 (100%)	46 (96%)	2 (4%)	30	54
29	A2	62/62 (100%)	56 (90%)	6 (10%)	8	27
30	A3	47/47 (100%)	45 (96%)	2 (4%)	29	53
31	A4	48/48 (100%)	44 (92%)	4 (8%)	11	34
32	A5	38/38 (100%)	34 (90%)	4 (10%)	7	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	A6	51/51 (100%)	50 (98%)	1 (2%)	55	74
34	A7	34/34 (100%)	33 (97%)	1 (3%)	42	64
39	BE	198/198 (100%)	187 (94%)	11 (6%)	21	46
40	BF	189/189 (100%)	176 (93%)	13 (7%)	15	40
41	BG	172/172 (100%)	165 (96%)	7 (4%)	30	55
42	BH	125/125 (100%)	120 (96%)	5 (4%)	31	55
43	BI	116/116 (100%)	109 (94%)	7 (6%)	19	44
44	BJ	146/146 (100%)	138 (94%)	8 (6%)	21	47
45	BK	104/104 (100%)	93 (89%)	11 (11%)	6	24
46	BL	106/106 (100%)	99 (93%)	7 (7%)	16	41
47	BM	90/90 (100%)	87 (97%)	3 (3%)	38	61
48	BN	98/98 (100%)	93 (95%)	5 (5%)	24	48
49	BO	103/103 (100%)	96 (93%)	7 (7%)	16	41
50	BP	95/95 (100%)	90 (95%)	5 (5%)	22	47
51	BQ	83/83 (100%)	81 (98%)	2 (2%)	49	69
52	BR	76/76 (100%)	74 (97%)	2 (3%)	46	66
53	BS	65/65 (100%)	64 (98%)	1 (2%)	65	80
54	BT	77/77 (100%)	72 (94%)	5 (6%)	17	42
55	BU	64/64 (100%)	61 (95%)	3 (5%)	26	51
56	BV	78/78 (100%)	73 (94%)	5 (6%)	17	42
57	BW	65/65 (100%)	63 (97%)	2 (3%)	40	62
58	BX	60/60 (100%)	56 (93%)	4 (7%)	16	41
All	All	5213/5213 (100%)	4918 (94%)	295 (6%)	24	45

5 of 295 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	BJ	145	GLU
56	BV	56	HIS
45	BK	60	LEU
49	BO	49	ARG
13	AM	114	LYS

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%)	17 (14%)	10 (8%)
2	AB	2898/2904 (99%)	529 (18%)	183 (6%)
35	BA	1538/1542 (99%)	299 (19%)	117 (7%)
36	BB	74/76 (97%)	25 (33%)	5 (6%)
37	BC	46/47 (97%)	16 (34%)	7 (15%)
38	BD	77/77 (100%)	14 (18%)	2 (2%)
All	All	4752/4766 (99%)	900 (18%)	324 (6%)

5 of 900 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
38	OMC	BD	33	38	19,22,23	1.09	1 (5%)	26,31,34	1.52	3 (11%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	2MG	AB	1835	2	18,26,27	1.75	5 (27%)	16,38,41	1.37	2 (12%)
2	PSU	AB	955	2	18,21,22	1.80	4 (22%)	22,30,33	2.43	2 (9%)
38	5MU	BD	55	38	19,22,23	1.43	4 (21%)	28,32,35	1.58	4 (14%)
2	2MG	AB	2445	2	18,26,27	2.19	4 (22%)	16,38,41	0.91	0
35	MA6	BA	1518	35	19,26,27	1.45	2 (10%)	18,38,41	1.32	2 (11%)
2	6MZ	AB	2030	2	18,25,26	1.39	4 (22%)	16,36,39	2.59	4 (25%)
36	H2U	BB	17	36	18,21,22	1.27	3 (16%)	21,30,33	2.09	8 (38%)
36	OMC	BB	32	36	19,22,23	1.03	1 (5%)	26,31,34	1.77	7 (26%)
2	3TD	AB	1915	2	18,22,23	1.94	5 (27%)	22,32,35	1.52	3 (13%)
36	MIA	BB	37	36	24,31,32	1.86	5 (20%)	26,44,47	1.99	7 (26%)
2	PSU	AB	746	2	18,21,22	1.27	1 (5%)	22,30,33	1.80	3 (13%)
2	5MC	AB	1962	2	18,22,23	1.95	6 (33%)	26,32,35	2.60	9 (34%)
35	UR3	BA	1498	35	19,22,23	1.23	2 (10%)	26,32,35	1.42	3 (11%)
36	H2U	BB	16	36	18,21,22	1.50	4 (22%)	21,30,33	1.40	4 (19%)
38	H2U	BD	21	38	18,21,22	0.99	1 (5%)	21,30,33	1.63	3 (14%)
2	5MU	AB	747	2	19,22,23	1.51	4 (21%)	28,32,35	2.31	9 (32%)
2	7MG	AB	2069	2	22,26,27	5.35	4 (18%)	29,39,42	1.51	6 (20%)
36	H2U	BB	20	36	18,21,22	1.86	5 (27%)	21,30,33	1.97	5 (23%)
36	4SU	BB	8	36	18,21,22	2.27	5 (27%)	26,30,33	3.27	9 (34%)
35	MA6	BA	1519	35	19,26,27	1.52	5 (26%)	18,38,41	1.18	2 (11%)
2	6MZ	AB	1618	2	18,25,26	1.40	2 (11%)	16,36,39	1.50	1 (6%)
2	PSU	AB	1917	2	18,21,22	1.59	3 (16%)	22,30,33	1.63	2 (9%)
35	5MC	BA	967	35	18,22,23	1.37	2 (11%)	26,32,35	1.81	4 (15%)
36	7MG	BB	46	36	22,26,27	6.66	3 (13%)	29,39,42	1.36	4 (13%)
2	PSU	AB	2504	2	18,21,22	1.91	6 (33%)	22,30,33	1.74	4 (18%)
35	7MG	BA	527	35	22,26,27	5.58	7 (31%)	29,39,42	1.43	3 (10%)
35	4OC	BA	1402	35	20,23,24	1.61	3 (15%)	26,32,35	2.03	7 (26%)
2	H2U	AB	2449	2	18,21,22	1.51	3 (16%)	21,30,33	1.69	4 (19%)
35	2MG	BA	966	35	18,26,27	2.40	6 (33%)	16,38,41	1.52	4 (25%)
35	PSU	BA	516	35	18,21,22	1.70	6 (33%)	22,30,33	2.12	7 (31%)
2	PSU	AB	2580	2	18,21,22	2.30	6 (33%)	22,30,33	2.76	5 (22%)
2	5MU	AB	1939	2	19,22,23	1.51	4 (21%)	28,32,35	1.62	7 (25%)
2	OMC	AB	2498	2	19,22,23	1.07	1 (5%)	26,31,34	1.47	5 (19%)
35	2MG	BA	1207	35	18,26,27	2.21	6 (33%)	16,38,41	1.70	5 (31%)
35	5MC	BA	1407	35	18,22,23	1.44	2 (11%)	26,32,35	1.46	4 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	PSU	AB	1911	2	18,21,22	1.98	4 (22%)	22,30,33	1.94	7 (31%)
36	PSU	BB	55	36	18,21,22	2.04	6 (33%)	22,30,33	2.58	11 (50%)
2	OMU	AB	2552	2	19,22,23	1.61	3 (15%)	26,31,34	1.63	9 (34%)
2	1MG	AB	745	2	18,26,27	1.96	6 (33%)	19,39,42	2.08	6 (31%)
2	2MA	AB	2503	2	17,25,26	1.08	1 (5%)	17,37,40	1.59	4 (23%)
2	OMG	AB	2251	2	18,26,27	1.65	4 (22%)	19,38,41	1.12	1 (5%)
2	PSU	AB	2605	2	18,21,22	1.22	3 (16%)	22,30,33	1.40	3 (13%)
35	2MG	BA	1516	35	18,26,27	1.78	6 (33%)	16,38,41	1.22	1 (6%)
36	5MU	BB	54	36	19,22,23	1.44	4 (21%)	28,32,35	2.42	5 (17%)
38	4SU	BD	8	38	18,21,22	1.97	4 (22%)	26,30,33	1.50	5 (19%)
2	CH	AB	2575	2	16,21,22	1.08	0	20,30,33	1.35	3 (15%)
38	PSU	BD	56	38	18,21,22	1.94	4 (22%)	22,30,33	1.54	4 (18%)
2	PSU	AB	2457	2	18,21,22	1.85	6 (33%)	22,30,33	1.66	6 (27%)

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
38	OMC	BD	33	38	-	0/9/27/28	0/2/2/2
2	2MG	AB	1835	2	-	0/5/27/28	0/3/3/3
2	PSU	AB	955	2	-	0/7/25/26	0/2/2/2
38	5MU	BD	55	38	-	0/7/25/26	0/2/2/2
2	2MG	AB	2445	2	-	0/5/27/28	0/3/3/3
35	MA6	BA	1518	35	-	0/7/29/30	0/3/3/3
2	6MZ	AB	2030	2	-	1/5/27/28	0/3/3/3
36	H2U	BB	17	36	-	1/7/38/39	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
36	MIA	BB	37	36	-	3/11/33/34	0/3/3/3
2	PSU	AB	746	2	-	2/7/25/26	0/2/2/2
2	5MC	AB	1962	2	-	0/7/25/26	0/2/2/2
35	UR3	BA	1498	35	-	1/7/25/26	0/2/2/2
36	H2U	BB	16	36	-	0/7/38/39	0/2/2/2
38	H2U	BD	21	38	-	0/7/38/39	0/2/2/2
2	5MU	AB	747	2	-	0/7/25/26	0/2/2/2
2	7MG	AB	2069	2	-	0/7/37/38	0/3/3/3
36	H2U	BB	20	36	-	0/7/38/39	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	4SU	BB	8	36	-	1/7/25/26	0/2/2/2
35	MA6	BA	1519	35	-	0/7/29/30	0/3/3/3
2	6MZ	AB	1618	2	-	0/5/27/28	0/3/3/3
2	PSU	AB	1917	2	-	1/7/25/26	0/2/2/2
35	5MC	BA	967	35	-	1/7/25/26	0/2/2/2
36	7MG	BB	46	36	-	1/7/37/38	0/3/3/3
2	PSU	AB	2504	2	-	1/7/25/26	0/2/2/2
35	7MG	BA	527	35	-	2/7/37/38	0/3/3/3
35	4OC	BA	1402	35	-	0/9/29/30	0/2/2/2
2	H2U	AB	2449	2	-	0/7/38/39	0/2/2/2
35	2MG	BA	966	35	-	0/5/27/28	0/3/3/3
35	PSU	BA	516	35	-	0/7/25/26	0/2/2/2
2	PSU	AB	2580	2	-	2/7/25/26	0/2/2/2
2	5MU	AB	1939	2	-	0/7/25/26	0/2/2/2
2	OMC	AB	2498	2	-	1/9/27/28	0/2/2/2
35	2MG	BA	1207	35	-	0/5/27/28	0/3/3/3
35	5MC	BA	1407	35	-	0/7/25/26	0/2/2/2
2	PSU	AB	1911	2	-	0/7/25/26	0/2/2/2
36	PSU	BB	55	36	-	2/7/25/26	0/2/2/2
2	OMU	AB	2552	2	-	0/9/27/28	0/2/2/2
2	1MG	AB	745	2	-	0/3/25/26	0/3/3/3
2	2MA	AB	2503	2	-	0/3/25/26	0/3/3/3
2	OMG	AB	2251	2	-	0/5/27/28	0/3/3/3
2	PSU	AB	2605	2	-	2/7/25/26	0/2/2/2
35	2MG	BA	1516	35	-	2/5/27/28	0/3/3/3
36	5MU	BB	54	36	-	0/7/25/26	0/2/2/2
38	4SU	BD	8	38	-	0/7/25/26	0/2/2/2
2	CH	AB	2575	2	-	0/5/25/26	0/2/2/2
38	PSU	BD	56	38	-	0/7/25/26	0/2/2/2
2	PSU	AB	2457	2	-	0/7/25/26	0/2/2/2

The worst 5 of 186 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	BB	46	7MG	C8-N9	-30.44	1.29	1.46
35	BA	527	7MG	C8-N9	-24.50	1.32	1.46
2	AB	2069	7MG	C8-N9	-24.06	1.32	1.46
36	BB	8	4SU	C4-N3	6.72	1.44	1.37
2	AB	1911	PSU	C2-N1	6.03	1.44	1.36

The worst 5 of 226 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	BB	8	4SU	S4-C4-N3	-10.65	109.72	120.21
2	AB	2580	PSU	C3'-C2'-C1'	10.33	113.66	101.64
2	AB	955	PSU	C3'-C2'-C1'	-8.60	91.61	101.64
36	BB	8	4SU	C5-C4-N3	8.36	122.44	114.69
2	AB	2030	6MZ	C9-N6-C6	8.13	129.87	122.87

There are no chirality outliers.

5 of 24 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	2580	PSU	O4'-C1'-C5-C4
2	AB	2580	PSU	O4'-C1'-C5-C6
2	AB	2605	PSU	C2'-C1'-C5-C6

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides 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	59,36	13,15,16	1.37	1 (7%)	13,20,22	2.26	5 (38%)
59	FME	AB	3001	60	8,9,10	1.94	3 (37%)	7,9,11	2.18	3 (42%)

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	59,36	-	2/4/6/8	0/2/2/2
59	FME	AB	3001	60	-	3/7/9/11	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	AB	3001	FME	CA-N	-4.28	1.40	1.46
60	BB	101	TRP	CD1-NE1	2.41	1.41	1.36
59	AB	3001	FME	O-C	2.35	1.29	1.19
59	AB	3001	FME	CB-CA	2.17	1.57	1.53

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	BB	101	TRP	CB-CG-CD1	-4.76	122.09	127.97
60	BB	101	TRP	CB-CG-CD2	4.39	133.07	126.25
59	AB	3001	FME	O-C-CA	-4.19	113.79	124.78
59	AB	3001	FME	C-CA-N	2.91	114.98	109.73
60	BB	101	TRP	CD2-CE2-NE1	-2.59	102.16	107.92

There are no chirality outliers.

All (5) 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
59	AB	3001	FME	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AA	1

All chain breaks are listed below:

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

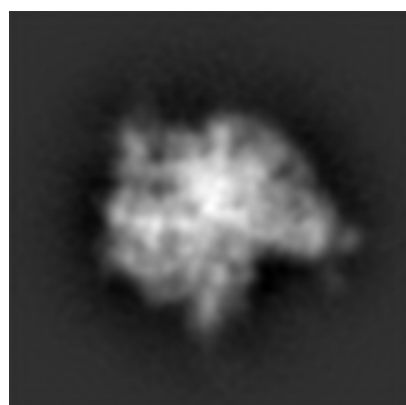
## 6 Map visualisation [i](#)

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.

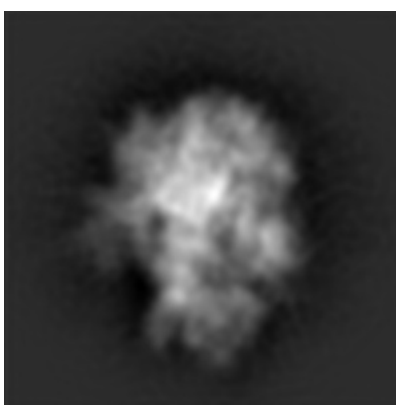
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

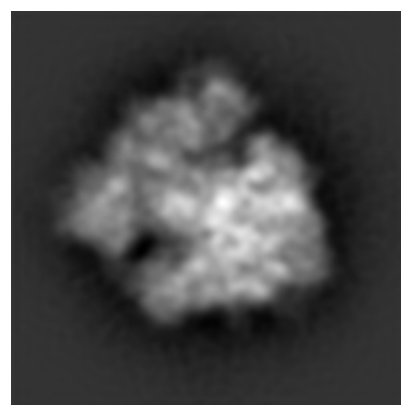
#### 6.1.1 Primary map



X



Y

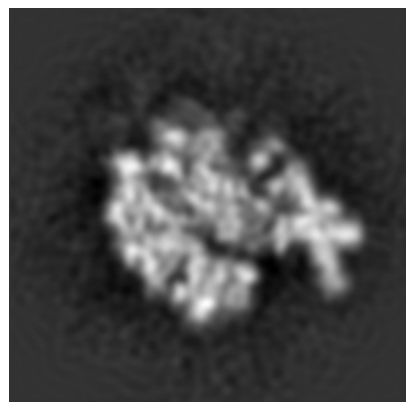


Z

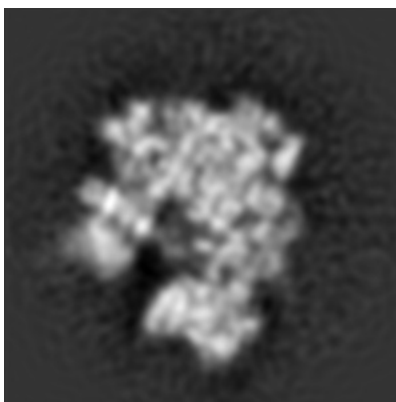
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

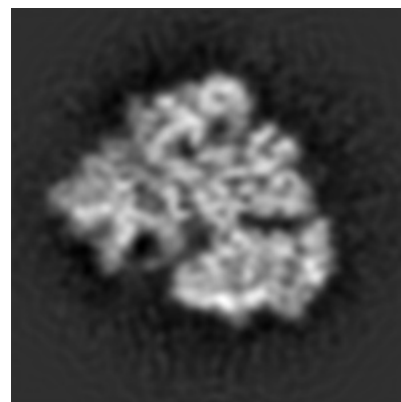
#### 6.2.1 Primary map



X Index: 125



Y Index: 125

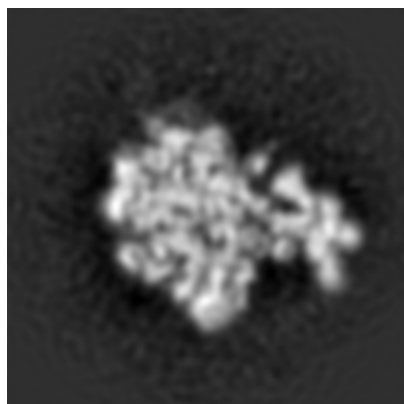


Z Index: 125

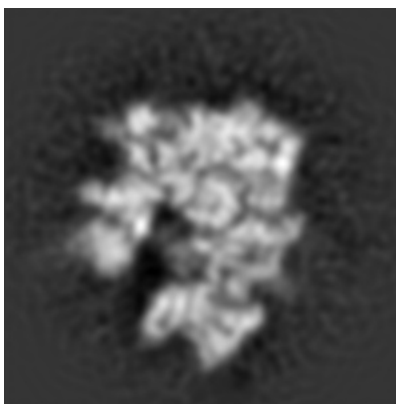
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

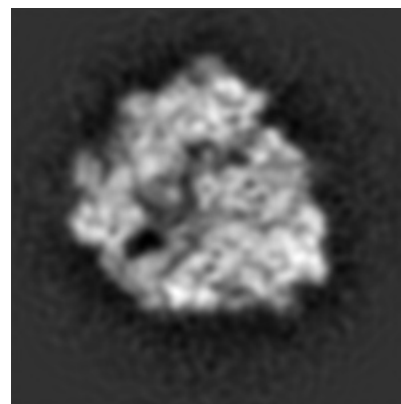
### 6.3.1 Primary map



X Index: 130



Y Index: 129

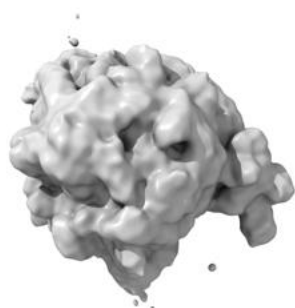


Z Index: 116

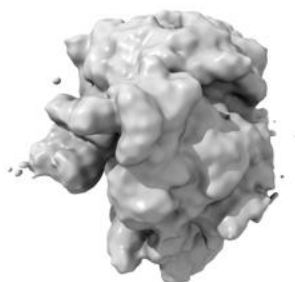
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

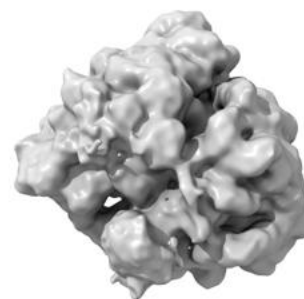
### 6.4.1 Primary map



X



Y



Z

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.



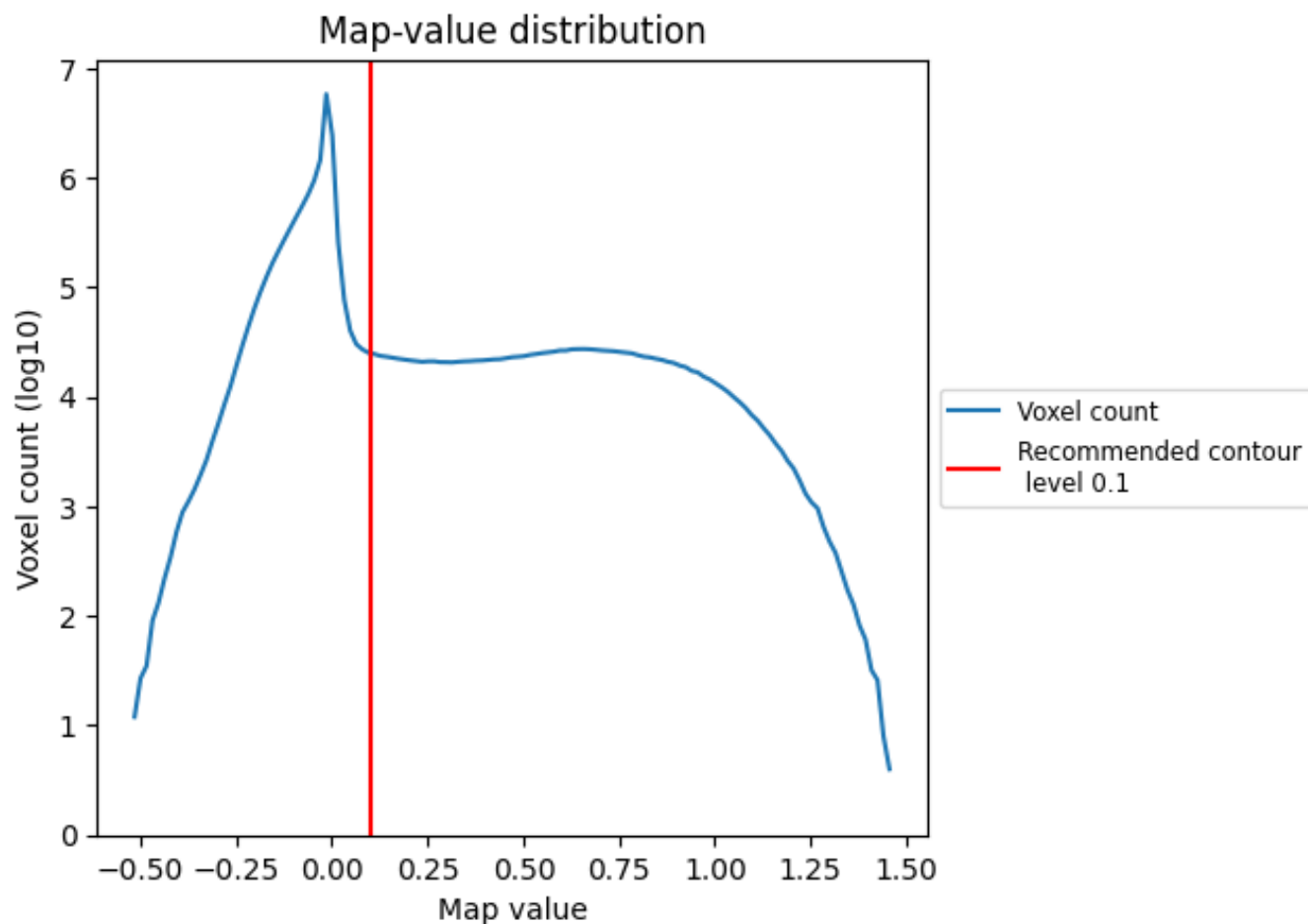
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

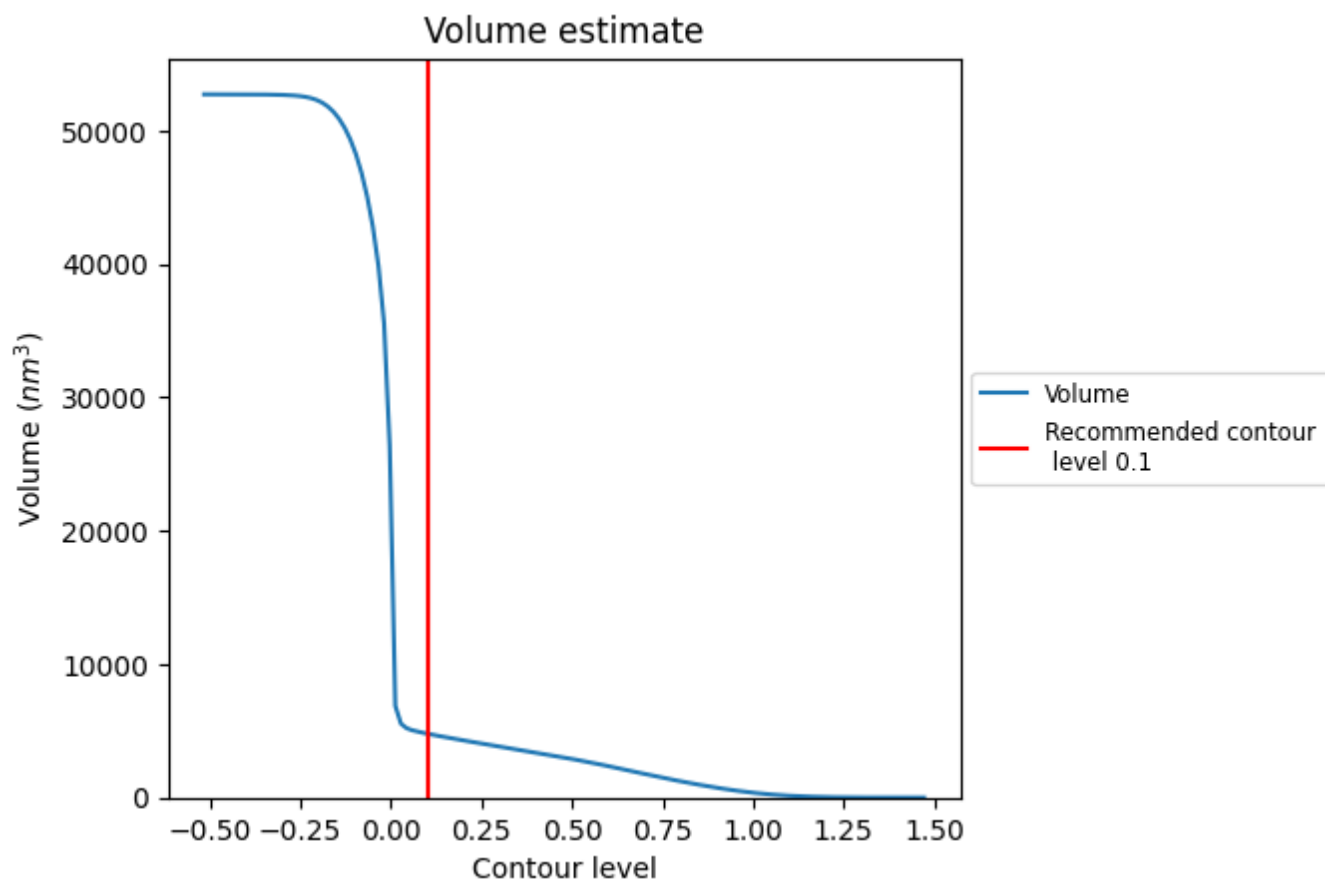
This section contains the results of statistical analysis of the map.

### 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.

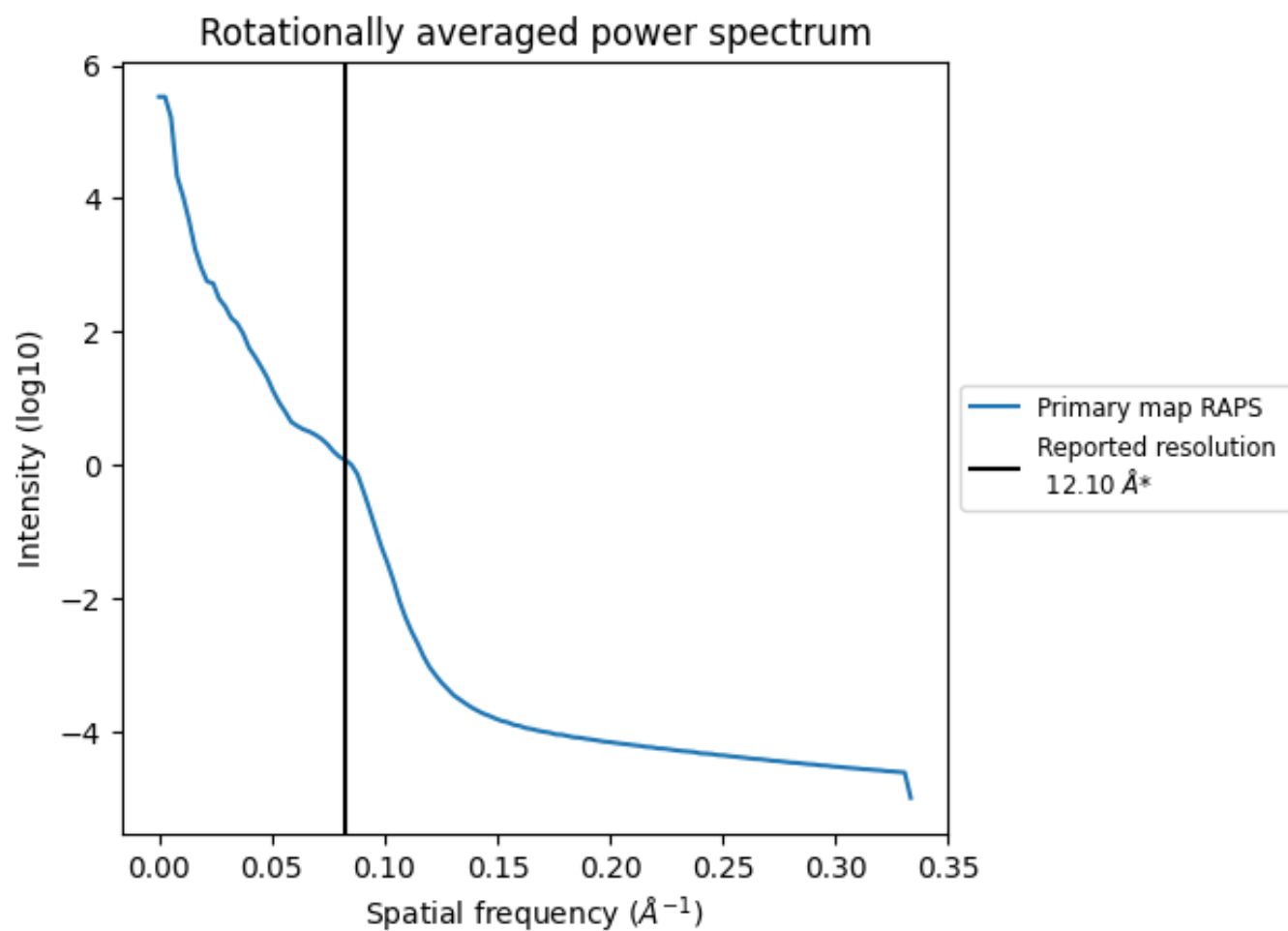
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4792  $\text{nm}^3$ ; 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<sup>-1</sup>

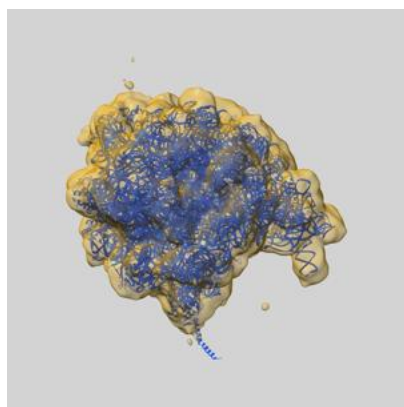
## 8 Fourier-Shell correlation

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

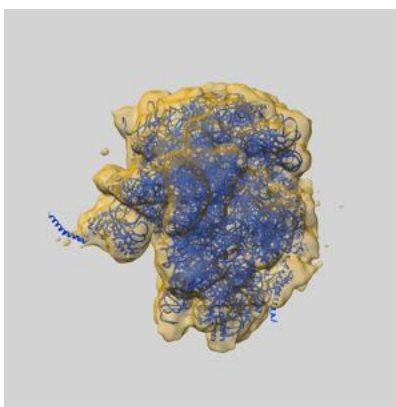
## 9 Map-model fit [i](#)

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 15](#).

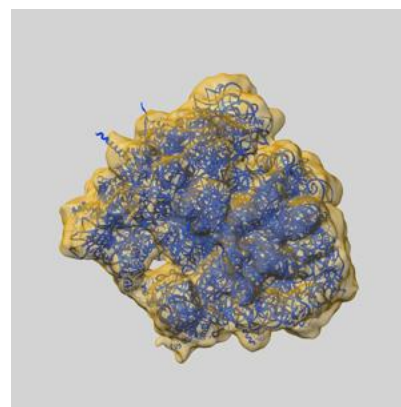
### 9.1 Map-model overlay [i](#)



X



Y



Z

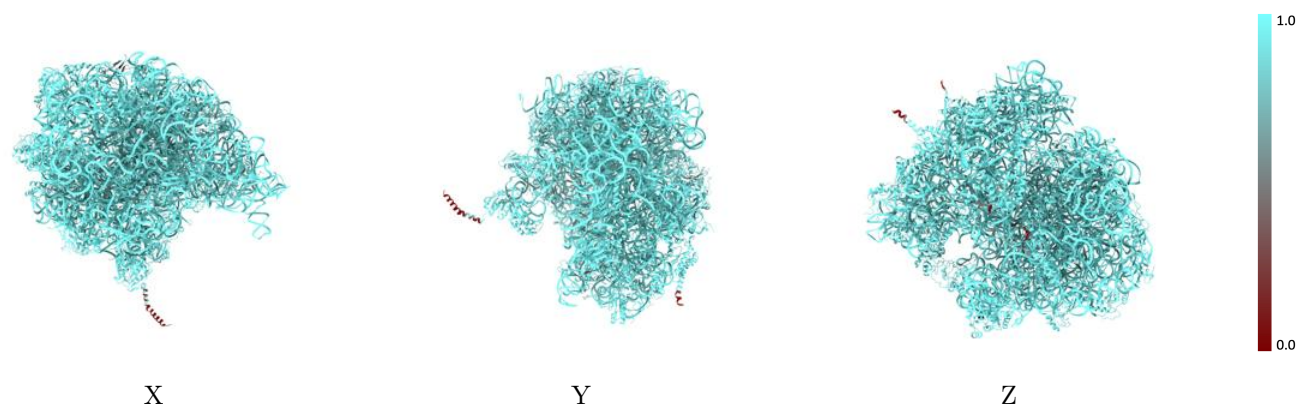
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



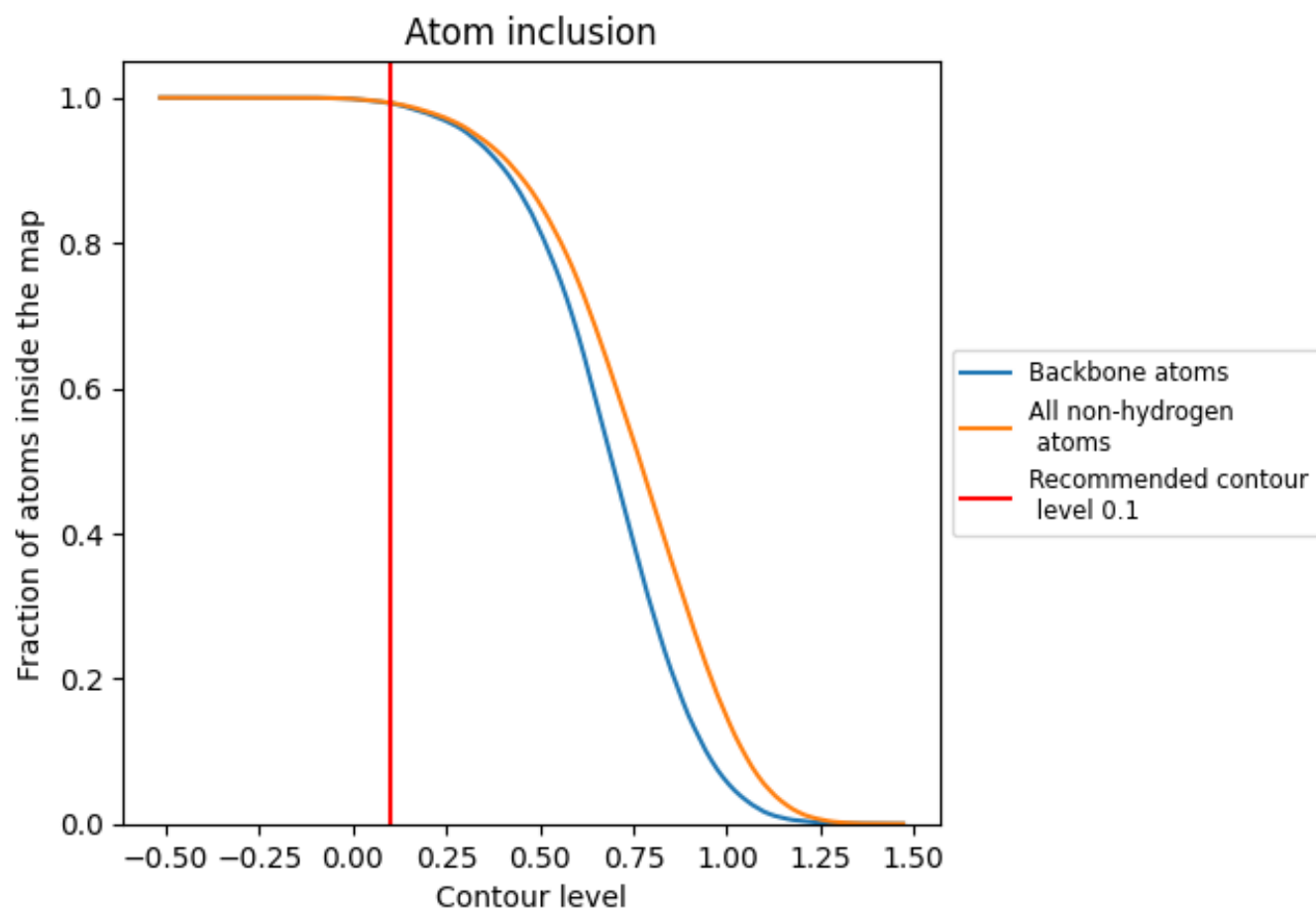
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.9929	 0.0770
A0	 1.0000	 0.0300
A1	 0.9977	 0.0550
A2	 0.9572	 0.0330
A3	 1.0000	 0.0210
A4	 0.9908	 0.0590
A5	 1.0000	 0.0300
A6	 1.0000	 -0.0280
A7	 1.0000	 0.0160
AA	 1.0000	 0.1100
AB	 0.9998	 0.0960
AC	 0.9573	 0.0360
AD	 0.9990	 0.0260
AE	 1.0000	 0.0340
AF	 0.9987	 0.0560
AG	 0.9986	 0.0640
AH	 0.9992	 0.0270
AI	 0.8677	 0.0300
AJ	 0.8284	 0.0480
AK	 0.9785	 0.0430
AL	 1.0000	 0.0270
AM	 0.9935	 0.0380
AN	 1.0000	 0.0070
AO	 1.0000	 0.0400
AP	 1.0000	 0.0310
AQ	 0.9989	 0.0630
AR	 0.9876	 0.0320
AS	 1.0000	 0.0200
AT	 0.9962	 0.0540
AU	 0.9976	 0.0440
AV	 0.9987	 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	 0.9998	 0.0940
BB	 0.9018	 0.0390
BC	 0.8389	 0.0110
BD	 0.9854	 0.0780
BE	 0.9593	 0.0610
BF	 0.9949	 0.0750
BG	 1.0000	 0.0510
BH	 0.9992	 0.0410
BI	 0.9683	 0.0490
BJ	 0.9963	 0.0660
BK	 1.0000	 0.0410
BL	 0.9879	 0.0510
BM	 1.0000	 0.0420
BN	 0.9529	 0.0590
BO	 0.9805	 0.0230
BP	 1.0000	 0.0770
BQ	 1.0000	 0.0340
BR	 1.0000	 0.0520
BS	 0.9984	 0.0180
BT	 1.0000	 0.0580
BU	 1.0000	 0.0370
BV	 0.9958	 0.0330
BW	 1.0000	 0.0310
BX	 0.9964	 0.0380