



wwPDB EM Validation Summary Report ⓘ

Jan 30, 2023 – 04:54 PM EST

PDB ID : 4V6S
EMDB ID : EMD-5360
Title : Structural characterization of mRNA-tRNA translocation intermediates (class 3 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 : 2011-12-09
Resolution : 13.10 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.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) : 2.32.1

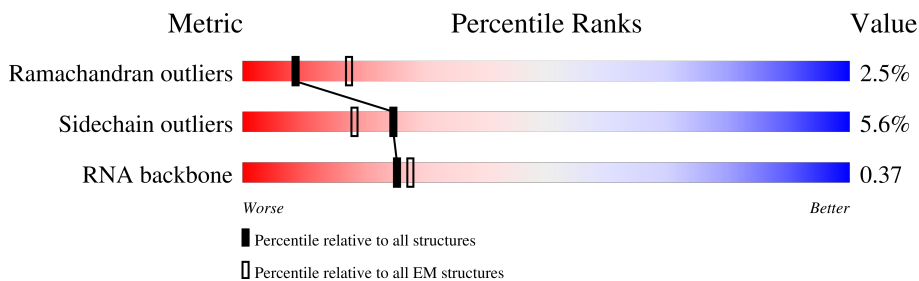
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 13.10 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.



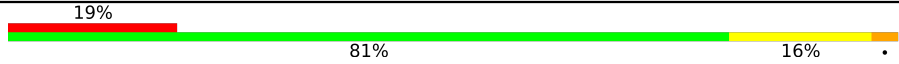
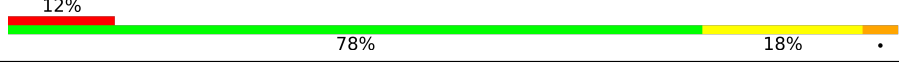
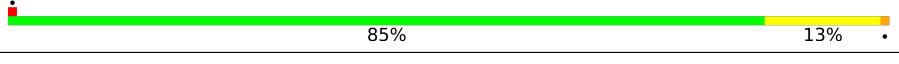


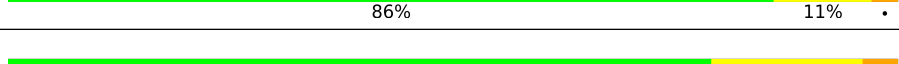
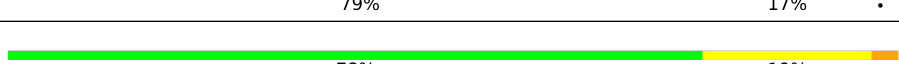
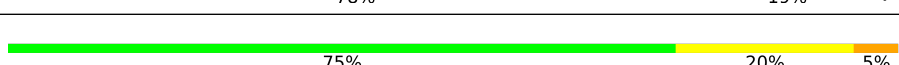
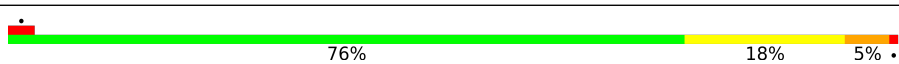


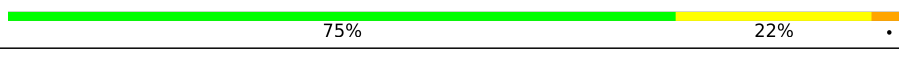
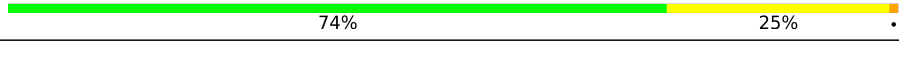

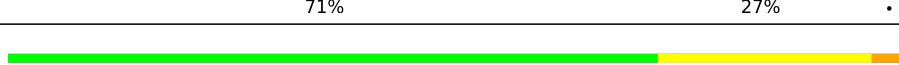










Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 ≥ 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	



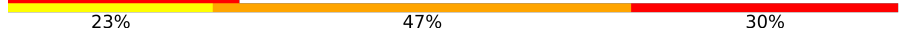





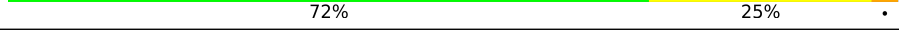
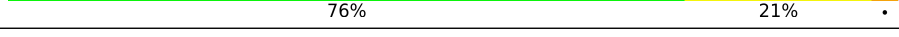
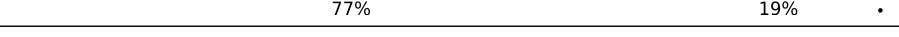

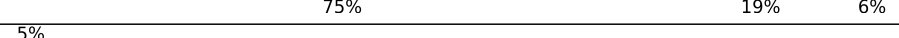
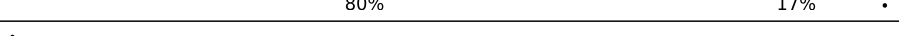
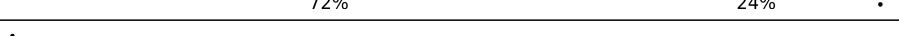


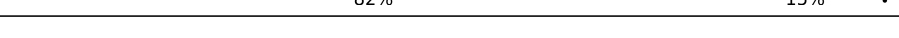
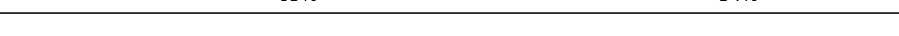

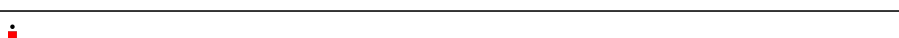

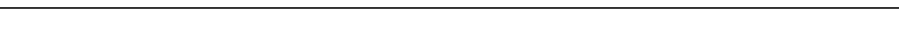
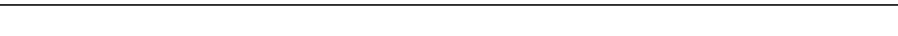
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Mol	Chain	Length	Quality of chain
9	AI	149	
10	AJ	164	
11	AK	141	
12	AL	142	
13	AM	123	
14	AN	144	
15	AO	136	
16	AP	127	
17	AQ	117	
18	AR	114	
19	AS	117	
20	AT	103	
21	AU	110	
22	AV	100	
23	AW	103	
24	AX	94	
25	AY	84	
26	AZ	77	
27	A0	63	
28	A1	58	
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	 68% 29% .
35	BA	1542	 33% 54% 13%
36	BB	47	 26% 23% 47% 30%
37	BC	77	 38% 53% 9%
38	BD	240	 7% 82% 15% .
39	BE	232	 76% 20% .
40	BF	205	 78% 20% .
41	BG	166	 80% 17% .
42	BH	135	 72% 25% .
43	BI	178	 76% 21% .
44	BJ	129	 77% 19% .
45	BK	129	 78% 17% 5% .
46	BL	103	 75% 19% 6%
47	BM	128	 5% 80% 17% .
48	BN	123	 72% 24% .
49	BO	117	 78% 18% . .
50	BP	100	 75% 22% .
51	BQ	88	 82% 15% .
52	BR	82	 65% 34% .
53	BS	83	 75% 20% 5%
54	BT	74	 74% 20% 5%
55	BU	91	 70% 27% .
56	BV	86	 86% 13% .
57	BW	70	 66% 27% 6% .

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 150700 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
			Total	C	N	O	P		
1	AA	120	2566	1144	468	835	119	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	P		
35	BA	1542	33089	14767	6064	10717	1541	0	0

- Molecule 36 is a RNA chain called mRNA.

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

- Molecule 37 is a RNA chain called P site tRNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BO	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	BP	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	BQ	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	BR	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	BS	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	BT	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	BU	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
			Total	C	N	O	S		
56	BV	86	670	414	138	115	3	0	0

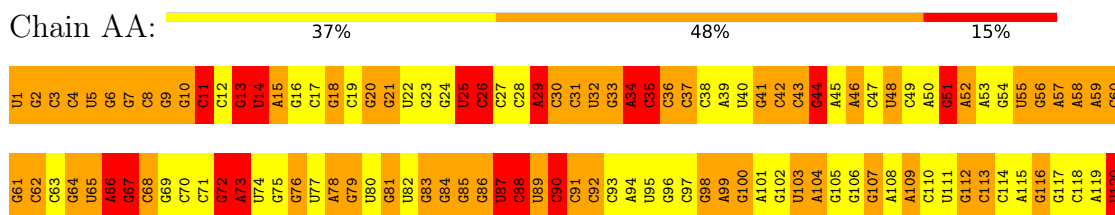
- Molecule 57 is a protein called 30S ribosomal protein S21.

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

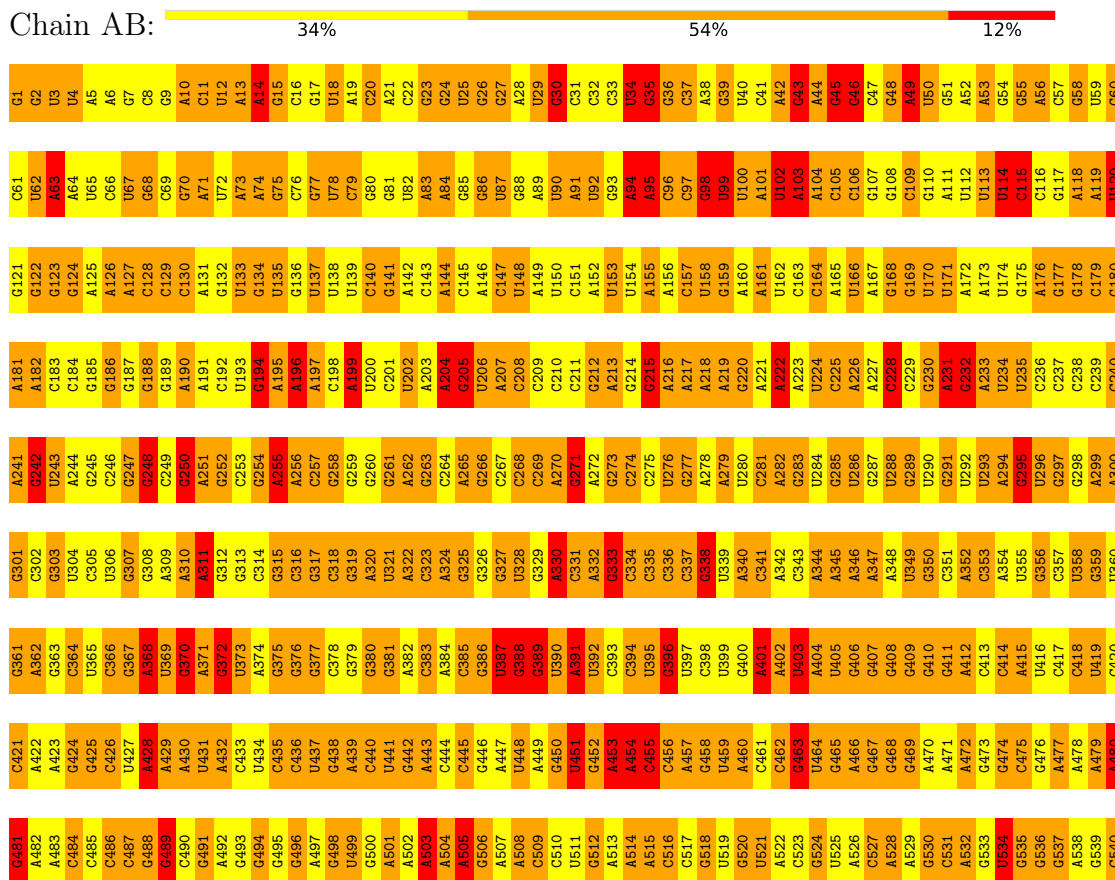
3 Residue-property plots

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.

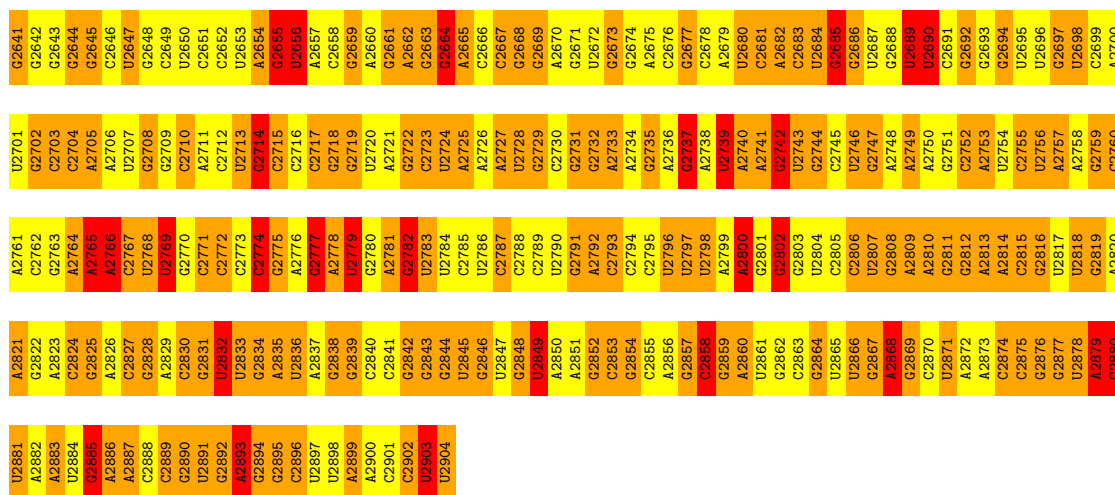
- Molecule 1: 5S ribosomal RNA



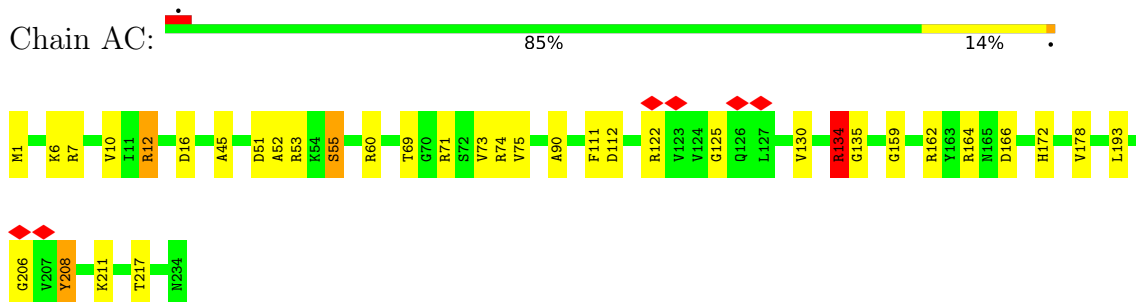
- Molecule 2: 23S ribosomal RNA



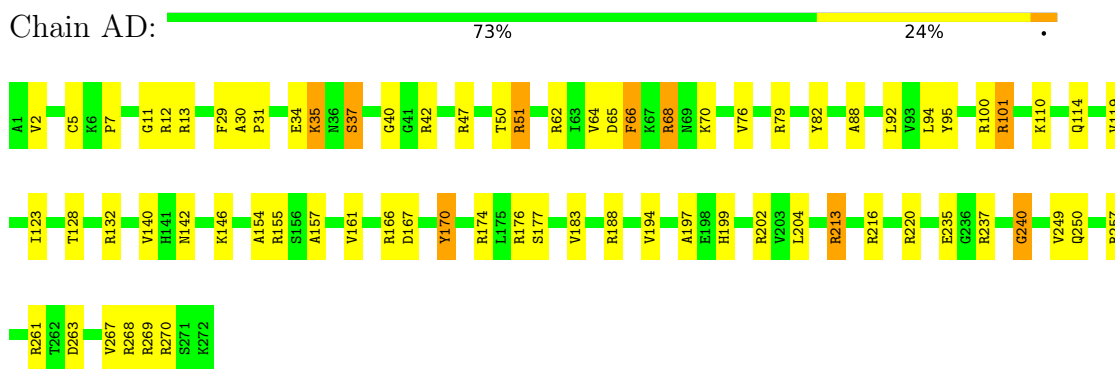
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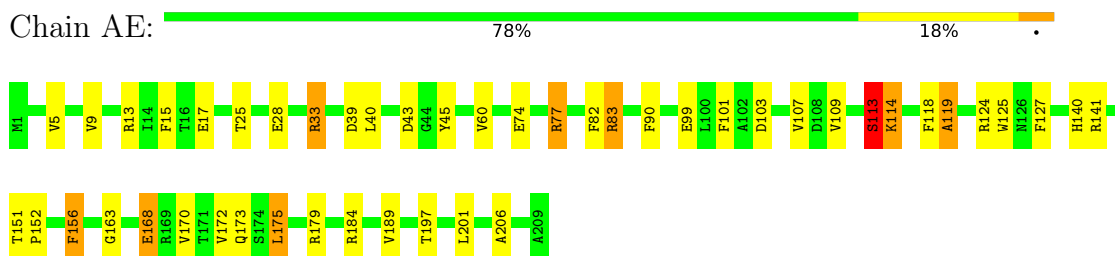
• Molecule 3: 50S ribosomal protein L1



• Molecule 4: 50S ribosomal protein L2




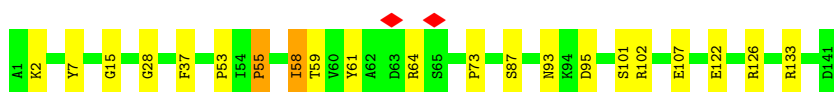
• Molecule 5: 50S ribosomal protein L3




• Molecule 6: 50S ribosomal protein L4

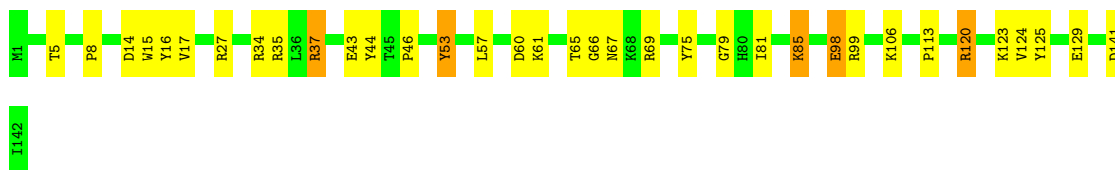
- Molecule 11: 50S ribosomal protein L11

Chain AK:  85% 13%




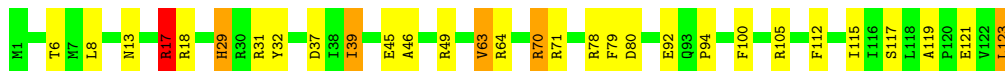
- Molecule 12: 50S ribosomal protein L13

Chain AL:  75% 21%




- Molecule 13: 50S ribosomal protein L14

Chain AM:  76% 20%




- Molecule 14: 50S ribosomal protein L15

Chain AN:  86% 11%




- Molecule 15: 50S ribosomal protein L16

Chain AO:  79% 17%




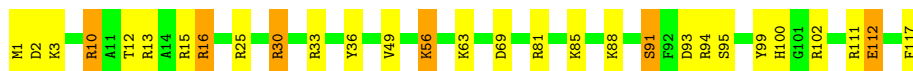
- Molecule 16: 50S ribosomal protein L17

Chain AP:  78% 19%

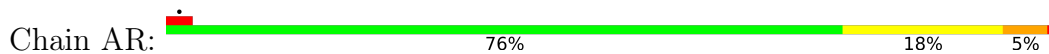


- Molecule 17: 50S ribosomal protein L18

Chain AQ:  75% 20% 5%



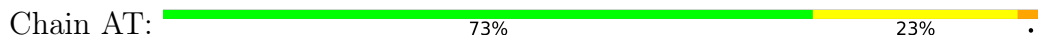
- Molecule 18: 50S ribosomal protein L19



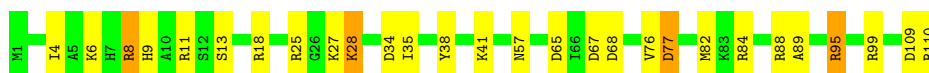
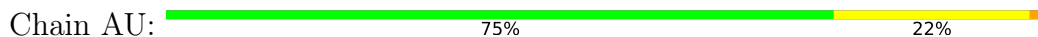
- Molecule 19: 50S ribosomal protein L20



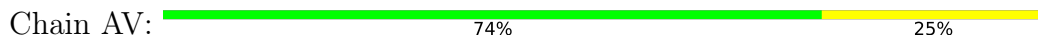
- Molecule 20: 50S ribosomal protein L21



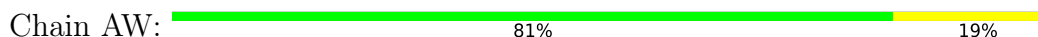
- Molecule 21: 50S ribosomal protein L22



- Molecule 22: 50S ribosomal protein L23



- Molecule 23: 50S ribosomal protein L24



- Molecule 24: 50S ribosomal protein L25

Chain AX:  71% 27%



- Molecule 25: 50S ribosomal protein L27

Chain AY:  73% 24%




- Molecule 26: 50S ribosomal protein L28

Chain AZ:  60% 36%



- Molecule 27: 50S ribosomal protein L29

Chain A0:  79% 14% 6%




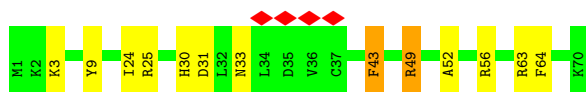
- Molecule 28: 50S ribosomal protein L30

Chain A1:  74% 19% 7%




- Molecule 29: 50S ribosomal protein L31

Chain A2:  6% 81% 16%

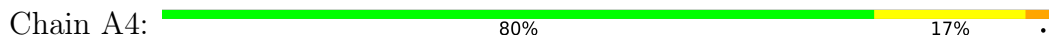


- Molecule 30: 50S ribosomal protein L32

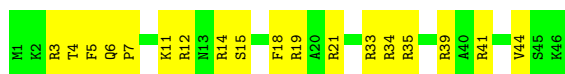
Chain A3:  77% 18%



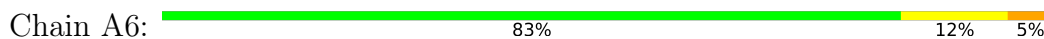
- Molecule 31: 50S ribosomal protein L33



- Molecule 32: 50S ribosomal protein L34



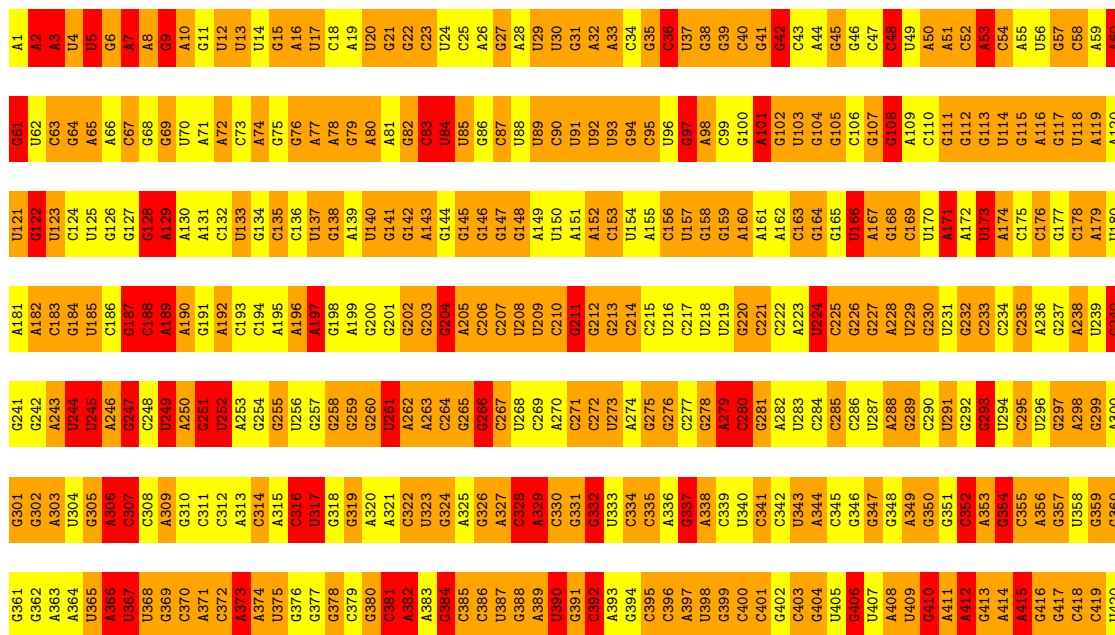
- Molecule 33: 50S ribosomal protein L35



- Molecule 34: 50S ribosomal protein L36



- Molecule 35: 16S ribosomal RNA



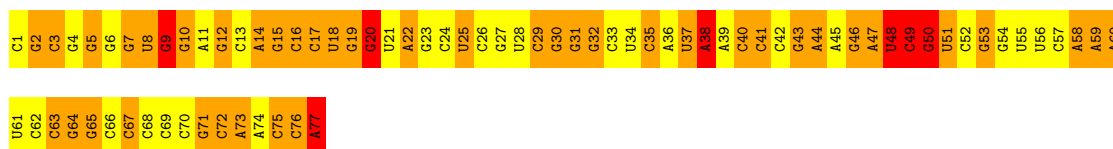
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U1443	C1383	C1203	G1143	U1083	A1023	G963	G903	U843	C783	U723	U663	G603	G543	C463	G423
U1444	C1384	A1204	G1144	G1084	G1024	A964	U904	G844	A784	G724	G664	U604	U544	C464	G424
U1445	G1385	U1205	A1145	U1085	U1025	U965	U905	A845	G785	G725	G665	G605	C545	U485	G425
A1446	G1386	G1206	A1146	U1086	G1026	G966	A906	G846	G786	G726	G666	G606	A546	U486	U426
A1447	G1387	G1207	C1147	G1087	C1027	C967	A907	G847	A787	G727	G667	A607	A547	A487	U427
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U1450	U1390	C1210	A1150	U1090	U1030	C970	C910	U850	A790	G730	G670	A610	G550	A490	A430
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G1459	C1399	A1219	U1159	G1099	U1039	C979	A919	C859	G799	C739	C679	U619	A559	A499	U439
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C1462	C1402	G1222	A1162	A1102	A1042	U982	G922	C862	A802	G742	U682	C622	U562	C502	G442
C1463	C1403	C1223	A1163	C1103	G1043	U983	A923	U863	G803	A743	C683	C623	A563	C503	C443
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A1465	A1405	A1225	A1165	A1105	U1045	C985	G925	A865	C805	G745	G685	U625	U565	C505	G445
C1466	U1406	G1226	G1166	G1106	A1046	U986	G926	C866	C806	A746	U686	G626	C566	G506	G446
C1467	C1407	A1227	A1167	C1107	G1047	U987	G927	C867	A807	A747	A687	G627	G567	C507	G447
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U1471	C1411	G1231	A1171	A1111	U1051	U991	C931	U871	C811	U751	G691	C631	U571	C511	A451
U1472	C1352	U1232	C1172	C1112	U1052	U992	C932	A872	C812	G752	U692	C632	A572	U512	A452
G1473	C1353	G1233	U1173	C1113	G1053	G993	G933	C873	U813	A753	G693	C633	A573	C513	G453
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A1476	G1356	A1236	A1176	U1116	U1056	A996	C936	C876	C816	C756	U696	C636	C576	U516	A456
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A1483	G1423	C1243	U1183	U1123	C1063	C1003	U943	C883	C823	G763	G703	C643	A583	A523	U463
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C1496	U1436	A1256	A1196	C1136	U1076	A1016	U956	C896	G836	G776	A716	G656	A596	C536	U476
G1497	C1317	A1257	A1197	C1137	G1077	U1017	U957	C897	U837	A777	U717	C657	G597	G537	C477
U1498	G1438	G1258	U1198	G1138	U1078	A1018	A958	C898	G838	G778	A718	C658	U598	G538	A478
A1499	U1439	C1259	U1199	G1139	G1079	U1019	A959	C899	G839	C779	A719	C659	U599	C539	U479
A1500	U1440	G1260	C1200	C1140	A1080	G1020	U960	A900	C840	A780	C720	C660	A600	G540	U480



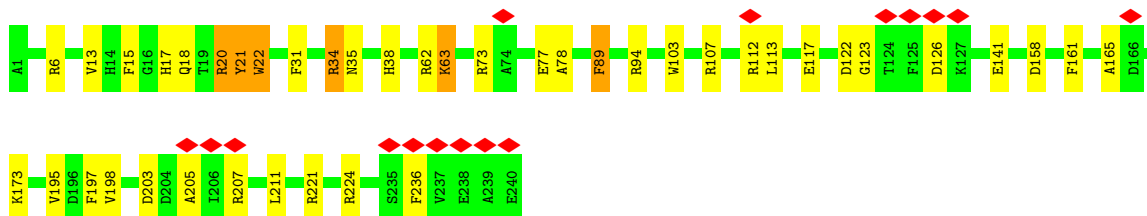
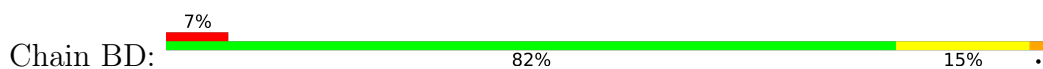
• Molecule 36: mRNA



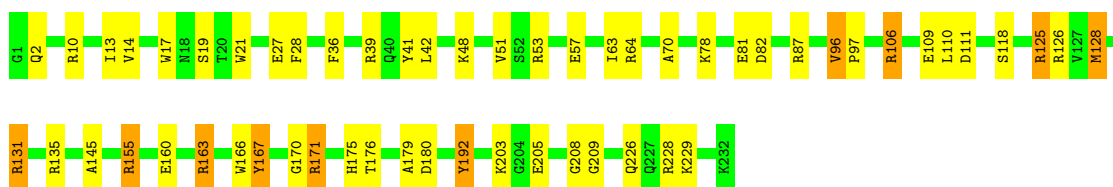
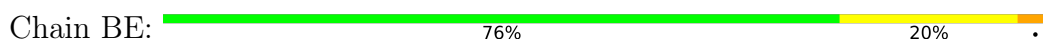
• Molecule 37: P site tRNA



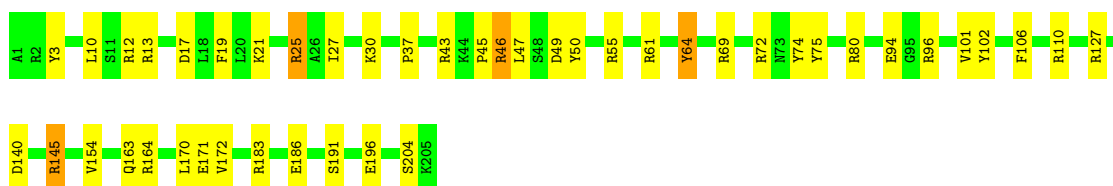
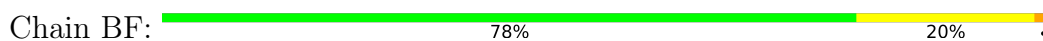
• Molecule 38: 30S ribosomal protein S2




• Molecule 39: 30S ribosomal protein S3

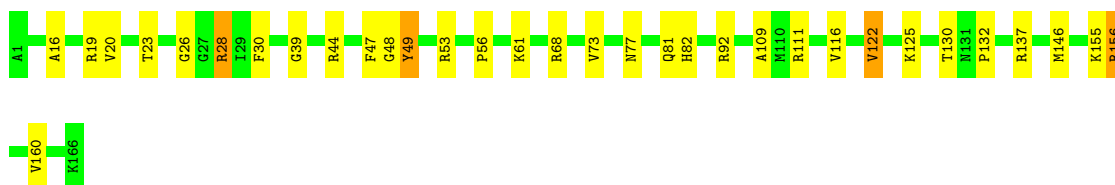


• Molecule 40: 30S ribosomal protein S4



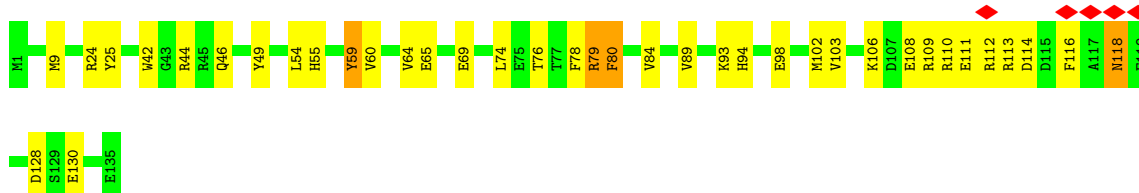
- Molecule 41: 30S ribosomal protein S5

Chain BG:  80% 17%




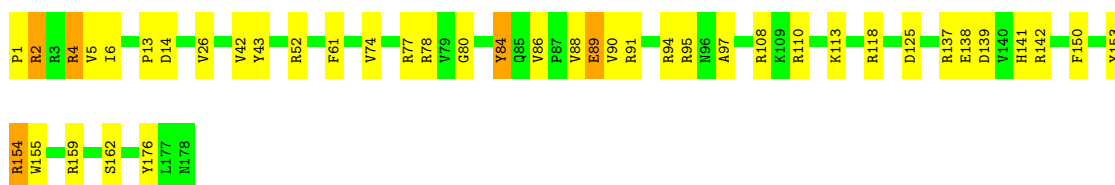
- Molecule 42: 30S ribosomal protein S6

Chain BH:  72% 25%




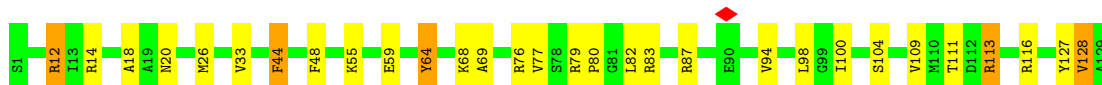
- Molecule 43: 30S ribosomal protein S7

Chain BI:  76% 21%




- Molecule 44: 30S ribosomal protein S8

Chain BJ:  77% 19%



- Molecule 45: 30S ribosomal protein S9

Chain BK:  78% 17% 5%

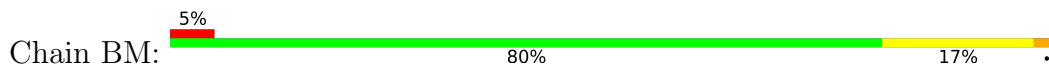


- Molecule 46: 30S ribosomal protein S10

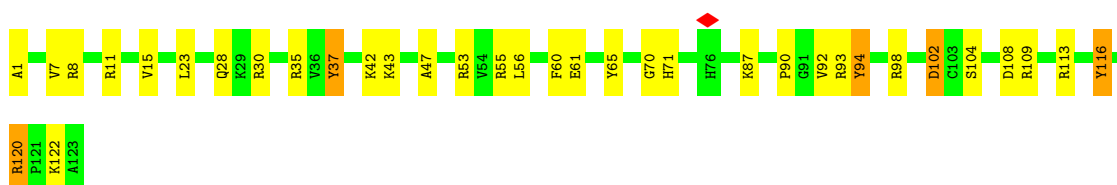
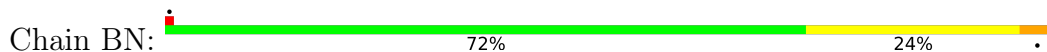
Chain BL:  75% 19% 6%



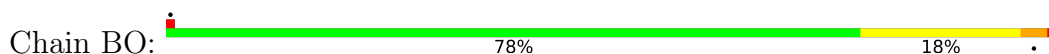
• Molecule 47: 30S ribosomal protein S11



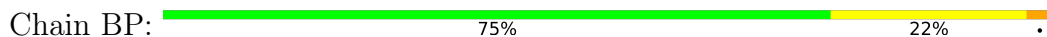
• Molecule 48: 30S ribosomal protein S12



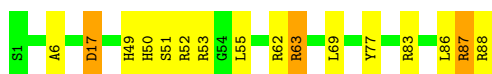
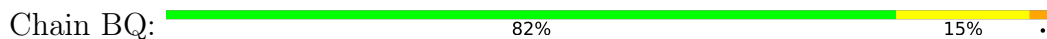
• Molecule 49: 30S ribosomal protein S13



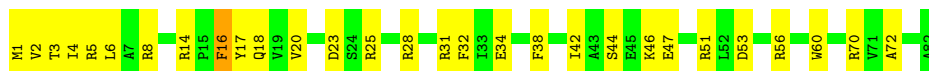
• Molecule 50: 30S ribosomal protein S14




• Molecule 51: 30S ribosomal protein S15

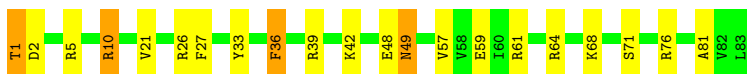


• Molecule 52: 30S ribosomal protein S16




- Molecule 53: 30S ribosomal protein S17

Chain BS:  75% 20% 5%



- Molecule 54: 30S ribosomal protein S18

Chain BT:  74% 20% 5%



- Molecule 55: 30S ribosomal protein S19

Chain BU:  70% 27% 3%



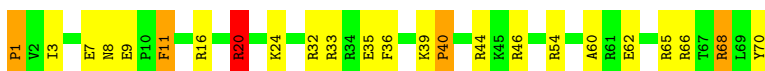
- Molecule 56: 30S ribosomal protein S20

Chain BV:  86% 13% 1%



- Molecule 57: 30S ribosomal protein S21

Chain BW:  66% 27% 6%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21000	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	1.443	Depositor
Minimum map value	-0.456	Depositor
Average map value	0.028	Depositor
Map value standard deviation	0.182	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 i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 2MA, 5MC, OMC, CH, OMG, 1MG, PSU, 3TD, 4OC, UR3, MA6, 4SU, 2MG, 7MG, 6MZ, H2U, 5MU, OMU

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	3.07	298/2869 (10.4%)	3.56	669/4474 (15.0%)
2	AB	3.08	7422/69257 (10.7%)	3.52	15483/108040 (14.3%)
3	AC	1.42	3/1748 (0.2%)	1.86	30/2355 (1.3%)
4	AD	1.56	11/2131 (0.5%)	2.03	60/2863 (2.1%)
5	AE	1.49	5/1586 (0.3%)	1.92	39/2134 (1.8%)
6	AF	1.52	7/1571 (0.4%)	1.92	42/2113 (2.0%)
7	AG	1.53	3/1444 (0.2%)	2.02	45/1937 (2.3%)
8	AH	1.53	6/1343 (0.4%)	1.96	35/1816 (1.9%)
9	AI	1.45	3/1122 (0.3%)	1.94	25/1515 (1.7%)
10	AJ	1.52	5/1247 (0.4%)	1.94	27/1679 (1.6%)
11	AK	1.44	5/1046 (0.5%)	1.86	18/1410 (1.3%)
12	AL	1.50	6/1152 (0.5%)	2.08	30/1551 (1.9%)
13	AM	1.53	5/956 (0.5%)	1.95	25/1279 (2.0%)
14	AN	1.52	5/1062 (0.5%)	1.89	20/1413 (1.4%)
15	AO	1.49	3/1093 (0.3%)	2.07	38/1460 (2.6%)
16	AP	1.48	5/1021 (0.5%)	2.09	28/1364 (2.1%)
17	AQ	1.57	4/910 (0.4%)	1.90	27/1219 (2.2%)
18	AR	1.54	2/929 (0.2%)	1.95	26/1242 (2.1%)
19	AS	1.52	6/960 (0.6%)	2.20	39/1278 (3.1%)
20	AT	1.60	5/829 (0.6%)	1.89	18/1107 (1.6%)
21	AU	1.49	1/864 (0.1%)	1.96	21/1156 (1.8%)
22	AV	1.54	3/794 (0.4%)	1.90	17/1060 (1.6%)
23	AW	1.44	2/797 (0.3%)	1.90	13/1062 (1.2%)
24	AX	1.49	5/766 (0.7%)	1.79	15/1025 (1.5%)
25	AY	1.48	2/642 (0.3%)	1.92	14/848 (1.7%)
26	AZ	1.50	3/635 (0.5%)	2.21	25/848 (2.9%)
27	A0	1.37	1/510 (0.2%)	1.90	12/677 (1.8%)
28	A1	1.52	2/453 (0.4%)	2.11	13/605 (2.1%)
29	A2	1.55	3/559 (0.5%)	1.96	12/745 (1.6%)
30	A3	1.49	1/450 (0.2%)	2.05	15/599 (2.5%)
31	A4	1.46	1/448 (0.2%)	1.82	7/594 (1.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	A5	1.53	1/380 (0.3%)	2.15	14/498 (2.8%)
33	A6	1.55	4/513 (0.8%)	1.80	7/676 (1.0%)
34	A7	1.57	2/303 (0.7%)	1.98	6/397 (1.5%)
35	BA	3.07	3871/36769 (10.5%)	3.53	8462/57354 (14.8%)
36	BB	3.23	131/1108 (11.8%)	3.61	262/1724 (15.2%)
37	BC	3.09	176/1721 (10.2%)	3.61	392/2683 (14.6%)
38	BD	1.43	2/1904 (0.1%)	1.86	32/2565 (1.2%)
39	BE	1.55	11/1852 (0.6%)	1.94	38/2490 (1.5%)
40	BF	1.51	8/1665 (0.5%)	1.96	51/2227 (2.3%)
41	BG	1.54	5/1239 (0.4%)	2.01	27/1664 (1.6%)
42	BH	1.50	3/1121 (0.3%)	1.92	27/1509 (1.8%)
43	BI	1.54	5/1422 (0.4%)	2.05	48/1908 (2.5%)
44	BJ	1.49	3/989 (0.3%)	2.00	23/1326 (1.7%)
45	BK	1.55	5/1048 (0.5%)	2.08	34/1394 (2.4%)
46	BL	1.47	1/835 (0.1%)	2.19	25/1127 (2.2%)
47	BM	1.52	7/982 (0.7%)	2.02	28/1323 (2.1%)
48	BN	1.52	4/969 (0.4%)	2.10	39/1300 (3.0%)
49	BO	1.51	8/919 (0.9%)	1.98	30/1226 (2.4%)
50	BP	1.53	1/817 (0.1%)	2.02	23/1088 (2.1%)
51	BQ	1.43	1/724 (0.1%)	1.93	16/966 (1.7%)
52	BR	1.53	2/659 (0.3%)	2.14	25/884 (2.8%)
53	BS	1.55	6/681 (0.9%)	1.99	18/913 (2.0%)
54	BT	1.60	6/637 (0.9%)	2.07	18/851 (2.1%)
55	BU	1.53	3/744 (0.4%)	1.84	16/995 (1.6%)
56	BV	1.39	1/676 (0.1%)	1.86	14/895 (1.6%)
57	BW	1.46	5/598 (0.8%)	2.19	23/792 (2.9%)
All	All	2.69	12105/162469 (7.5%)	3.17	26586/242243 (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	69
2	AB	0	1654
3	AC	0	3
4	AD	0	11
5	AE	0	7
6	AF	0	2
7	AG	0	1
8	AH	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	AI	0	3
10	AJ	0	8
11	AK	0	1
12	AL	0	3
13	AM	0	3
14	AN	0	2
15	AO	0	3
16	AP	0	5
17	AQ	0	4
18	AR	0	6
19	AS	0	3
20	AT	0	5
21	AU	0	5
22	AV	0	1
24	AX	0	5
25	AY	0	4
26	AZ	0	2
27	A0	0	4
28	A1	0	4
29	A2	0	3
30	A3	0	1
31	A4	0	2
32	A5	0	2
33	A6	0	2
34	A7	0	2
35	BA	0	882
36	BB	0	30
37	BC	0	41
38	BD	0	4
39	BE	0	9
40	BF	0	3
41	BG	0	3
42	BH	0	9
43	BI	0	3
44	BJ	0	7
45	BK	0	5
46	BL	0	2
47	BM	0	1
48	BN	0	6
49	BO	0	4
50	BP	0	1
51	BQ	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
52	BR	0	2
53	BS	0	1
54	BT	0	2
55	BU	0	4
57	BW	0	4
All	All	0	2857

The worst 5 of 12105 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	504	A	N3-C4	18.22	1.45	1.34
2	AB	2682	A	N3-C4	18.21	1.45	1.34
2	AB	744	U	C2-N3	17.97	1.50	1.37
35	BA	1484	C	N1-C6	16.21	1.46	1.37
2	AB	2829	A	P-O5'	15.96	1.75	1.59

The worst 5 of 26586 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	AL	120	ARG	NE-CZ-NH2	24.50	132.55	120.30
2	AB	1193	G	C8-N9-C4	-23.95	96.82	106.40
35	BA	581	G	N9-C4-C5	22.36	114.35	105.40
46	BL	45	ARG	NE-CZ-NH1	21.76	131.18	120.30
44	BJ	116	ARG	NE-CZ-NH2	-21.74	109.43	120.30

There are no chirality outliers.

5 of 2857 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1	U	Sidechain
1	AA	2	G	Sidechain
1	AA	3	C	Sidechain
1	AA	4	C	Sidechain
1	AA	5	U	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	1299	0	0
2	AB	62351	0	31248	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	16599	0	0
36	BB	993	0	501	0	0
37	BC	1641	0	841	0	0
38	BD	1872	0	1885	0	0
39	BE	1822	0	1913	0	0
40	BF	1643	0	1710	0	0
41	BG	1225	0	1273	0	0
42	BH	1101	0	1050	0	0
43	BI	1400	0	1449	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BJ	979	0	1034	0	0
45	BK	1036	0	1084	0	0
46	BL	825	0	865	0	0
47	BM	965	0	997	0	0
48	BN	955	0	1019	0	0
49	BO	910	0	981	0	0
50	BP	805	0	847	0	0
51	BQ	716	0	742	0	0
52	BR	649	0	666	0	0
53	BS	672	0	716	0	0
54	BT	626	0	651	0	0
55	BU	727	0	769	0	0
56	BV	670	0	722	0	0
57	BW	590	0	631	0	0
All	All	150700	0	102924	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%)	215 (93%)	12 (5%)	5 (2%)	6	35
4	AD	270/272 (99%)	237 (88%)	24 (9%)	9 (3%)	4	26
5	AE	207/209 (99%)	175 (84%)	24 (12%)	8 (4%)	3	23
6	AF	199/201 (99%)	173 (87%)	16 (8%)	10 (5%)	2	20
7	AG	176/178 (99%)	151 (86%)	15 (8%)	10 (6%)	1	18
8	AH	174/176 (99%)	159 (91%)	11 (6%)	4 (2%)	6	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	AI	147/149 (99%)	131 (89%)	12 (8%)	4 (3%)	5	31
10	AJ	162/164 (99%)	155 (96%)	6 (4%)	1 (1%)	25	66
11	AK	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	22	63
12	AL	140/142 (99%)	120 (86%)	15 (11%)	5 (4%)	3	25
13	AM	121/123 (98%)	105 (87%)	12 (10%)	4 (3%)	4	26
14	AN	142/144 (99%)	125 (88%)	14 (10%)	3 (2%)	7	36
15	AO	134/136 (98%)	124 (92%)	8 (6%)	2 (2%)	10	46
16	AP	125/127 (98%)	115 (92%)	9 (7%)	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%)	108 (94%)	3 (3%)	4 (4%)	3	25
20	AT	101/103 (98%)	89 (88%)	9 (9%)	3 (3%)	4	28
21	AU	108/110 (98%)	99 (92%)	5 (5%)	4 (4%)	3	24
22	AV	98/100 (98%)	77 (79%)	18 (18%)	3 (3%)	4	27
23	AW	101/103 (98%)	89 (88%)	9 (9%)	3 (3%)	4	28
24	AX	92/94 (98%)	84 (91%)	7 (8%)	1 (1%)	14	52
25	AY	82/84 (98%)	64 (78%)	14 (17%)	4 (5%)	2	20
26	AZ	75/77 (97%)	68 (91%)	4 (5%)	3 (4%)	3	23
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%)	48 (89%)	4 (7%)	2 (4%)	3	24
31	A4	52/54 (96%)	49 (94%)	1 (2%)	2 (4%)	3	24
32	A5	44/46 (96%)	40 (91%)	2 (4%)	2 (4%)	2	22
33	A6	62/64 (97%)	58 (94%)	3 (5%)	1 (2%)	9	44
34	A7	36/38 (95%)	29 (81%)	4 (11%)	3 (8%)	1	12
38	BD	238/240 (99%)	218 (92%)	14 (6%)	6 (2%)	5	32
39	BE	230/232 (99%)	217 (94%)	9 (4%)	4 (2%)	9	42
40	BF	203/205 (99%)	186 (92%)	13 (6%)	4 (2%)	7	38
41	BG	164/166 (99%)	150 (92%)	12 (7%)	2 (1%)	13	50
42	BH	133/135 (98%)	123 (92%)	9 (7%)	1 (1%)	19	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	BI	176/178 (99%)	168 (96%)	5 (3%)	3 (2%)	9	42
44	BJ	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	19	60
45	BK	127/129 (98%)	114 (90%)	10 (8%)	3 (2%)	6	33
46	BL	101/103 (98%)	91 (90%)	4 (4%)	6 (6%)	1	17
47	BM	126/128 (98%)	109 (86%)	15 (12%)	2 (2%)	9	44
48	BN	121/123 (98%)	103 (85%)	16 (13%)	2 (2%)	9	42
49	BO	115/117 (98%)	109 (95%)	5 (4%)	1 (1%)	17	57
50	BP	98/100 (98%)	85 (87%)	6 (6%)	7 (7%)	1	14
51	BQ	86/88 (98%)	81 (94%)	4 (5%)	1 (1%)	13	50
52	BR	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
53	BS	81/83 (98%)	73 (90%)	7 (9%)	1 (1%)	13	50
54	BT	72/74 (97%)	62 (86%)	7 (10%)	3 (4%)	3	22
55	BU	89/91 (98%)	82 (92%)	6 (7%)	1 (1%)	14	52
56	BV	84/86 (98%)	79 (94%)	4 (5%)	1 (1%)	13	50
57	BW	68/70 (97%)	61 (90%)	4 (6%)	3 (4%)	2	22
All	All	6319/6423 (98%)	5708 (90%)	453 (7%)	158 (2%)	9	32

5 of 158 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AD	94	LEU
6	AF	62	GLN
6	AF	188	MET
7	AG	136	ILE
9	AI	3	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AC	181/181 (100%)	176 (97%)	5 (3%)	43	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AD	217/217 (100%)	205 (94%)	12 (6%)	21	47
5	AE	164/164 (100%)	152 (93%)	12 (7%)	14	39
6	AF	165/165 (100%)	160 (97%)	5 (3%)	41	63
7	AG	149/149 (100%)	140 (94%)	9 (6%)	19	44
8	AH	137/137 (100%)	123 (90%)	14 (10%)	7	25
9	AI	114/114 (100%)	109 (96%)	5 (4%)	28	53
10	AJ	122/122 (100%)	115 (94%)	7 (6%)	20	45
11	AK	109/109 (100%)	104 (95%)	5 (5%)	27	52
12	AL	116/116 (100%)	107 (92%)	9 (8%)	12	36
13	AM	104/104 (100%)	98 (94%)	6 (6%)	20	45
14	AN	103/103 (100%)	102 (99%)	1 (1%)	76	86
15	AO	109/109 (100%)	101 (93%)	8 (7%)	14	39
16	AP	103/103 (100%)	99 (96%)	4 (4%)	32	56
17	AQ	87/87 (100%)	79 (91%)	8 (9%)	9	29
18	AR	99/99 (100%)	94 (95%)	5 (5%)	24	48
19	AS	89/89 (100%)	86 (97%)	3 (3%)	37	60
20	AT	84/84 (100%)	78 (93%)	6 (7%)	14	39
21	AU	93/93 (100%)	88 (95%)	5 (5%)	22	47
22	AV	84/84 (100%)	78 (93%)	6 (7%)	14	39
23	AW	84/84 (100%)	80 (95%)	4 (5%)	25	51
24	AX	78/78 (100%)	73 (94%)	5 (6%)	17	42
25	AY	62/62 (100%)	57 (92%)	5 (8%)	11	35
26	AZ	67/67 (100%)	60 (90%)	7 (10%)	7	24
27	A0	55/55 (100%)	52 (94%)	3 (6%)	21	47
28	A1	48/48 (100%)	42 (88%)	6 (12%)	4	19
29	A2	62/62 (100%)	61 (98%)	1 (2%)	62	79
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%)	35 (92%)	3 (8%)	12	35
33	A6	51/51 (100%)	50 (98%)	1 (2%)	55	74
34	A7	34/34 (100%)	33 (97%)	1 (3%)	42	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	BD	198/198 (100%)	188 (95%)	10 (5%)	24	48
39	BE	189/189 (100%)	174 (92%)	15 (8%)	12	35
40	BF	172/172 (100%)	168 (98%)	4 (2%)	50	70
41	BG	125/125 (100%)	118 (94%)	7 (6%)	21	46
42	BH	116/116 (100%)	107 (92%)	9 (8%)	12	36
43	BI	146/146 (100%)	139 (95%)	7 (5%)	25	51
44	BJ	104/104 (100%)	99 (95%)	5 (5%)	25	51
45	BK	106/106 (100%)	100 (94%)	6 (6%)	20	45
46	BL	90/90 (100%)	83 (92%)	7 (8%)	12	36
47	BM	98/98 (100%)	96 (98%)	2 (2%)	55	74
48	BN	103/103 (100%)	99 (96%)	4 (4%)	32	56
49	BO	95/95 (100%)	89 (94%)	6 (6%)	18	43
50	BP	83/83 (100%)	79 (95%)	4 (5%)	25	51
51	BQ	76/76 (100%)	75 (99%)	1 (1%)	69	81
52	BR	65/65 (100%)	57 (88%)	8 (12%)	4	19
53	BS	77/77 (100%)	72 (94%)	5 (6%)	17	42
54	BT	64/64 (100%)	61 (95%)	3 (5%)	26	51
55	BU	78/78 (100%)	69 (88%)	9 (12%)	5	21
56	BV	65/65 (100%)	65 (100%)	0	100	100
57	BW	60/60 (100%)	55 (92%)	5 (8%)	11	34
All	All	5213/5213 (100%)	4919 (94%)	294 (6%)	25	46

5 of 294 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	BJ	68	LYS
55	BU	47	THR
45	BK	88	GLU
50	BP	66	THR
15	AO	136	MET

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

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	119/120 (99%)	18 (15%)	13 (10%)
2	AB	2898/2904 (99%)	527 (18%)	180 (6%)
35	BA	1538/1542 (99%)	294 (19%)	112 (7%)
36	BB	46/47 (97%)	15 (32%)	6 (13%)
37	BC	76/77 (98%)	14 (18%)	1 (1%)
All	All	4677/4690 (99%)	868 (18%)	312 (6%)

5 of 868 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 312 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	BA	552	U
35	BA	1302	C
35	BA	681	A
35	BA	944	G
35	BA	1465	A

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

40 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
37	OMC	BC	33	37	19,22,23	1.24	3 (15%)	26,31,34	1.38	5 (19%)
35	MA6	BA	1519	35	19,26,27	1.46	4 (21%)	18,38,41	2.25	5 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PSU	AB	746	2	18,21,22	2.04	5 (27%)	22,30,33	2.03	6 (27%)
2	2MA	AB	2503	2	17,25,26	1.22	2 (11%)	17,37,40	1.78	3 (17%)
35	5MC	BA	967	35	18,22,23	1.05	1 (5%)	26,32,35	1.33	4 (15%)
35	2MG	BA	1516	35	18,26,27	1.64	4 (22%)	16,38,41	1.47	3 (18%)
2	PSU	AB	955	2	18,21,22	1.90	3 (16%)	22,30,33	1.56	4 (18%)
2	PSU	AB	2457	2	18,21,22	1.56	3 (16%)	22,30,33	2.33	5 (22%)
2	3TD	AB	1915	2	18,22,23	1.38	3 (16%)	22,32,35	2.17	7 (31%)
2	OMG	AB	2251	2	18,26,27	1.71	5 (27%)	19,38,41	1.37	1 (5%)
2	OMU	AB	2552	2	19,22,23	0.82	1 (5%)	26,31,34	1.36	3 (11%)
35	PSU	BA	516	35	18,21,22	1.67	4 (22%)	22,30,33	2.34	4 (18%)
2	5MC	AB	1962	2	18,22,23	1.31	2 (11%)	26,32,35	1.51	6 (23%)
2	CH	AB	2575	2	16,21,22	1.64	2 (12%)	20,30,33	1.55	4 (20%)
35	5MC	BA	1407	35	18,22,23	1.58	3 (16%)	26,32,35	1.49	6 (23%)
37	H2U	BC	21	37	18,21,22	1.65	6 (33%)	21,30,33	2.23	9 (42%)
2	OMC	AB	2498	2	19,22,23	1.30	5 (26%)	26,31,34	1.57	6 (23%)
2	2MG	AB	1835	2	18,26,27	1.79	4 (22%)	16,38,41	1.83	3 (18%)
2	7MG	AB	2069	2	22,26,27	4.67	4 (18%)	29,39,42	1.64	5 (17%)
35	UR3	BA	1498	35	19,22,23	1.23	3 (15%)	26,32,35	1.91	7 (26%)
35	4OC	BA	1402	35	20,23,24	1.24	4 (20%)	26,32,35	1.97	8 (30%)
37	5MU	BC	55	37	19,22,23	1.01	1 (5%)	28,32,35	1.97	8 (28%)
2	5MU	AB	747	2	19,22,23	1.52	3 (15%)	28,32,35	2.79	17 (60%)
2	PSU	AB	2504	2	18,21,22	1.71	3 (16%)	22,30,33	2.17	5 (22%)
35	2MG	BA	966	35	18,26,27	1.87	6 (33%)	16,38,41	1.50	4 (25%)
2	PSU	AB	1911	2	18,21,22	2.38	8 (44%)	22,30,33	1.33	4 (18%)
2	6MZ	AB	2030	2	18,25,26	1.85	3 (16%)	16,36,39	1.95	3 (18%)
35	2MG	BA	1207	35	18,26,27	1.59	4 (22%)	16,38,41	1.44	2 (12%)
2	PSU	AB	2605	2	18,21,22	1.79	3 (16%)	22,30,33	1.92	7 (31%)
2	H2U	AB	2449	2	18,21,22	1.23	1 (5%)	21,30,33	2.82	9 (42%)
2	6MZ	AB	1618	2	18,25,26	1.81	6 (33%)	16,36,39	1.60	4 (25%)
35	MA6	BA	1518	35	19,26,27	1.51	2 (10%)	18,38,41	1.32	3 (16%)
37	4SU	BC	8	37	18,21,22	1.95	6 (33%)	26,30,33	1.77	7 (26%)
2	5MU	AB	1939	2	19,22,23	1.35	2 (10%)	28,32,35	2.31	9 (32%)
37	PSU	BC	56	37	18,21,22	2.23	5 (27%)	22,30,33	1.22	1 (4%)
2	PSU	AB	2580	2	18,21,22	1.85	5 (27%)	22,30,33	1.48	4 (18%)
2	PSU	AB	1917	2	18,21,22	1.39	4 (22%)	22,30,33	1.82	5 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	2MG	AB	2445	2	18,26,27	1.77	4 (22%)	16,38,41	1.76	4 (25%)
2	1MG	AB	745	2	18,26,27	2.01	9 (50%)	19,39,42	1.89	6 (31%)
35	7MG	BA	527	35	22,26,27	3.39	7 (31%)	29,39,42	1.61	2 (6%)

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
37	OMC	BC	33	37	-	0/9/27/28	0/2/2/2
35	MA6	BA	1519	35	-	0/7/29/30	0/3/3/3
2	PSU	AB	746	2	-	1/7/25/26	0/2/2/2
2	2MA	AB	2503	2	-	0/3/25/26	0/3/3/3
35	5MC	BA	967	35	-	1/7/25/26	0/2/2/2
35	2MG	BA	1516	35	-	0/5/27/28	0/3/3/3
2	PSU	AB	955	2	-	0/7/25/26	0/2/2/2
2	PSU	AB	2457	2	-	0/7/25/26	0/2/2/2
2	3TD	AB	1915	2	-	0/7/25/26	0/2/2/2
2	OMG	AB	2251	2	-	0/5/27/28	0/3/3/3
2	OMU	AB	2552	2	-	1/9/27/28	0/2/2/2
35	PSU	BA	516	35	-	1/7/25/26	0/2/2/2
2	5MC	AB	1962	2	-	0/7/25/26	0/2/2/2
2	CH	AB	2575	2	-	0/5/25/26	0/2/2/2
35	5MC	BA	1407	35	-	0/7/25/26	0/2/2/2
37	H2U	BC	21	37	-	0/7/38/39	0/2/2/2
2	OMC	AB	2498	2	-	0/9/27/28	0/2/2/2
2	2MG	AB	1835	2	-	0/5/27/28	0/3/3/3
2	7MG	AB	2069	2	-	0/7/37/38	0/3/3/3
35	UR3	BA	1498	35	-	0/7/25/26	0/2/2/2
35	4OC	BA	1402	35	-	0/9/29/30	0/2/2/2
37	5MU	BC	55	37	-	0/7/25/26	0/2/2/2
2	5MU	AB	747	2	-	0/7/25/26	0/2/2/2
2	PSU	AB	2504	2	-	2/7/25/26	0/2/2/2
35	2MG	BA	966	35	-	0/5/27/28	0/3/3/3
2	PSU	AB	1911	2	-	2/7/25/26	0/2/2/2
2	6MZ	AB	2030	2	-	0/5/27/28	0/3/3/3
35	2MG	BA	1207	35	-	0/5/27/28	0/3/3/3
2	PSU	AB	2605	2	-	0/7/25/26	0/2/2/2
2	H2U	AB	2449	2	-	0/7/38/39	0/2/2/2
2	6MZ	AB	1618	2	-	1/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	MA6	BA	1518	35	-	0/7/29/30	0/3/3/3
37	4SU	BC	8	37	-	0/7/25/26	0/2/2/2
2	5MU	AB	1939	2	-	0/7/25/26	0/2/2/2
37	PSU	BC	56	37	-	0/7/25/26	0/2/2/2
2	PSU	AB	2580	2	-	3/7/25/26	0/2/2/2
2	PSU	AB	1917	2	-	3/7/25/26	0/2/2/2
2	2MG	AB	2445	2	-	0/5/27/28	0/3/3/3
2	1MG	AB	745	2	-	0/3/25/26	0/3/3/3
35	7MG	BA	527	35	-	1/7/37/38	0/3/3/3

The worst 5 of 153 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	2069	7MG	C8-N9	-20.69	1.34	1.46
35	BA	527	7MG	C8-N9	-14.00	1.38	1.46
2	AB	2030	6MZ	C6-N1	5.79	1.42	1.34
2	AB	1911	PSU	C2'-C1'	-5.36	1.46	1.53
2	AB	955	PSU	C2'-C1'	-5.26	1.46	1.53

The worst 5 of 208 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AB	2457	PSU	C6-C5-C4	7.75	123.62	118.20
35	BA	516	PSU	C3'-C2'-C1'	7.65	110.55	101.64
2	AB	2449	H2U	O2-C2-N1	-7.16	114.12	123.11
2	AB	1939	5MU	C5M-C5-C4	6.70	126.14	118.77
2	AB	2504	PSU	C6-C5-C4	6.64	122.84	118.20

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AB	746	PSU	C2'-C1'-C5-C4
2	AB	2552	OMU	C1'-C2'-O2'-CM2
2	AB	1917	PSU	O4'-C4'-C5'-O5'
2	AB	1917	PSU	C3'-C4'-C5'-O5'
35	BA	527	7MG	C4'-C5'-O5'-P

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](#)

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	AB	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AB	2831:G	O3'	2832:U	P	1.76

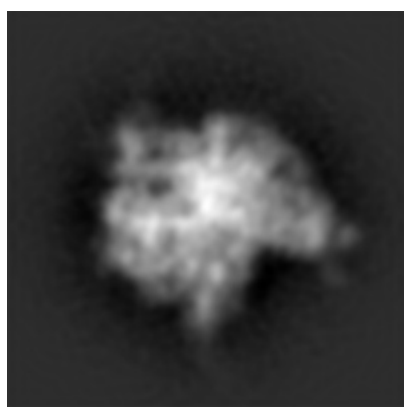
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5360. These allow visual inspection of the internal detail of the map and identification of artifacts.

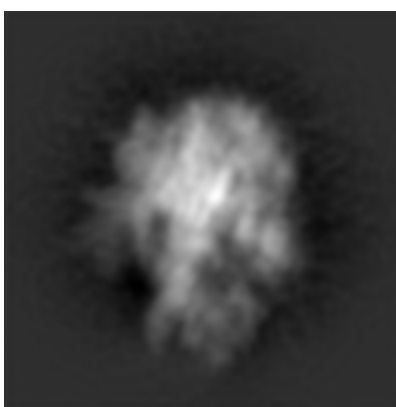
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

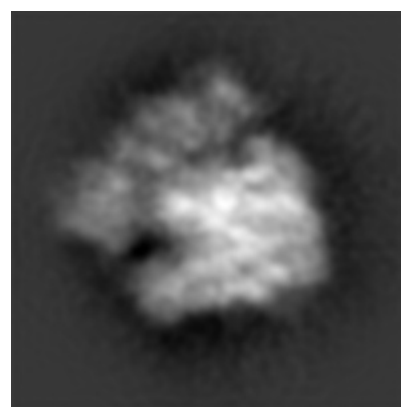
6.1.1 Primary map



X



Y

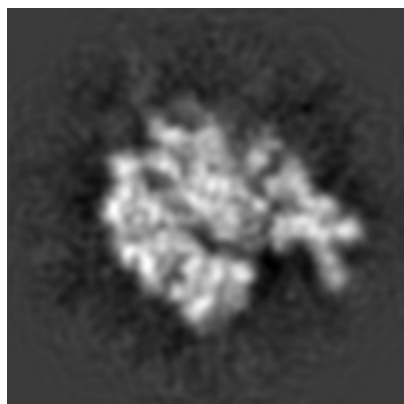


Z

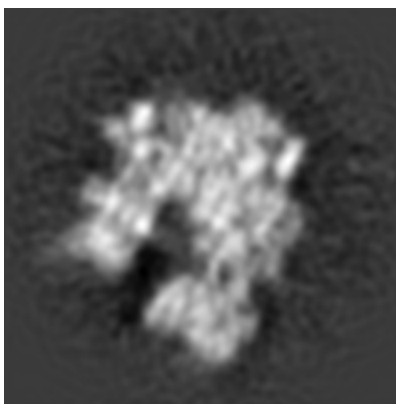
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

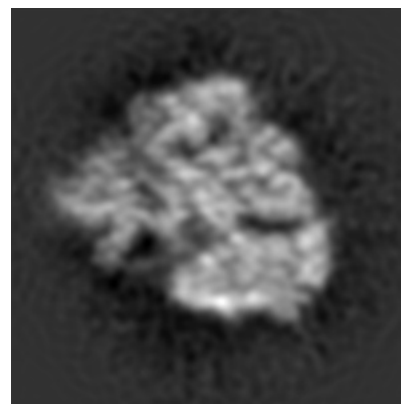
6.2.1 Primary map



X Index: 125



Y Index: 125

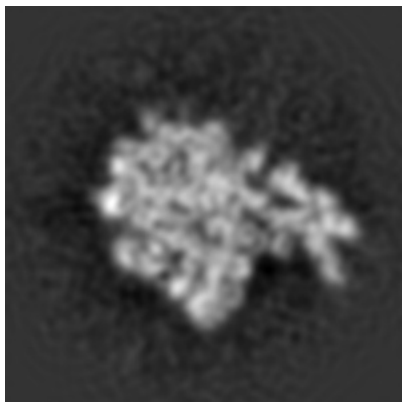


Z Index: 125

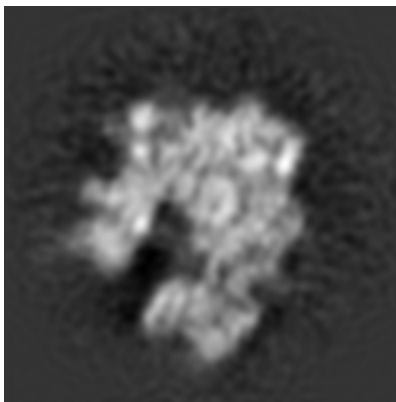
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

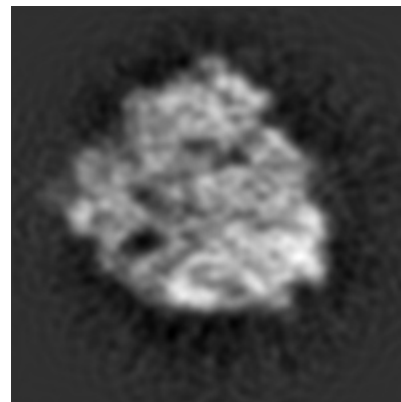
6.3.1 Primary map



X Index: 131



Y Index: 128

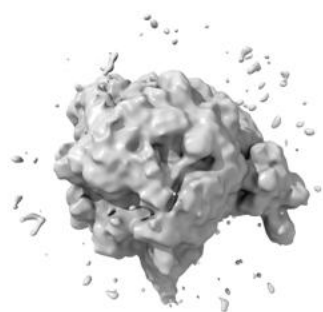


Z Index: 118

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

6.4 Orthogonal surface views [i](#)

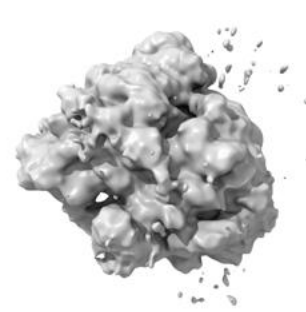
6.4.1 Primary map



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.

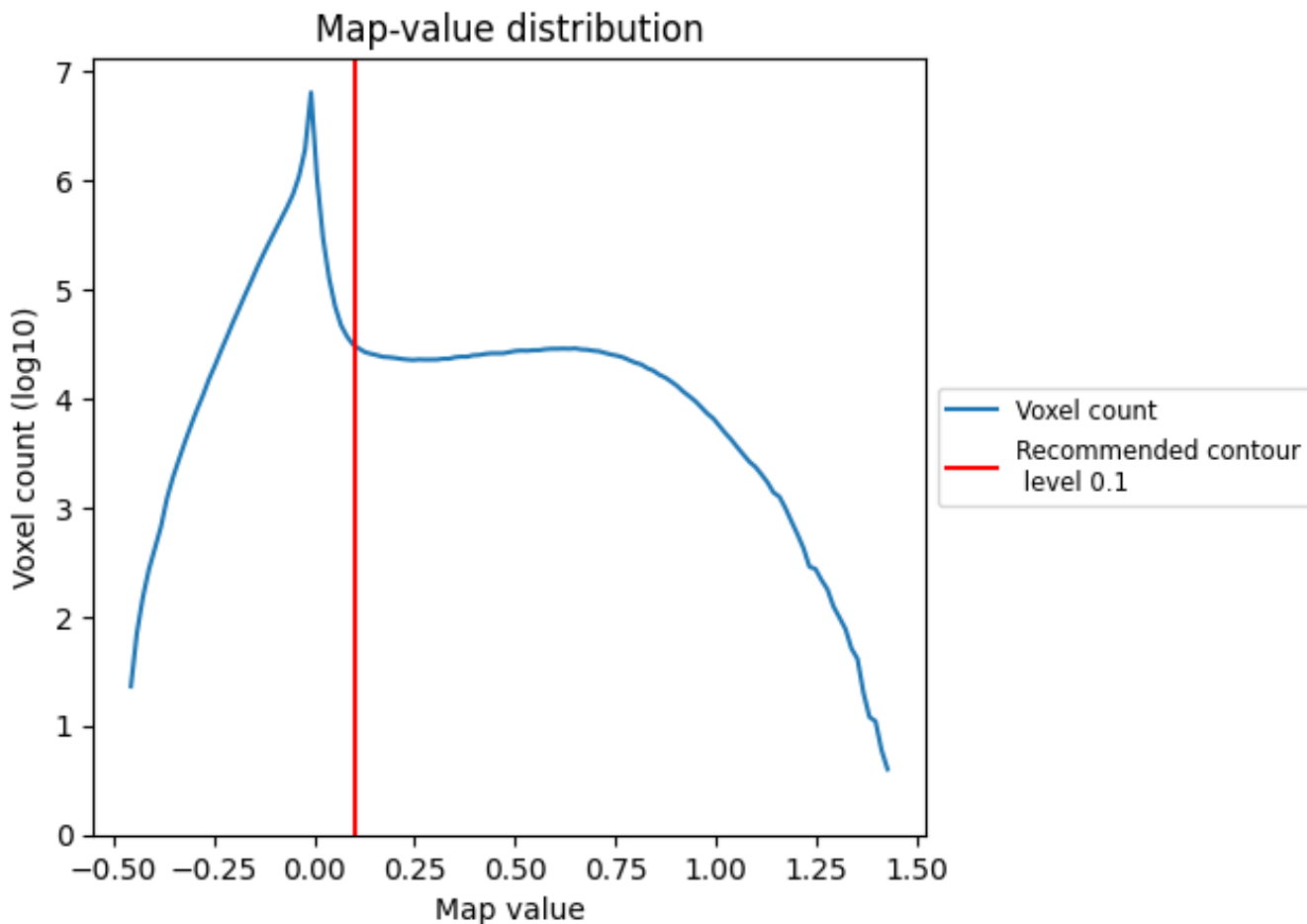
6.5 Mask visualisation

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

7 Map analysis [i](#)

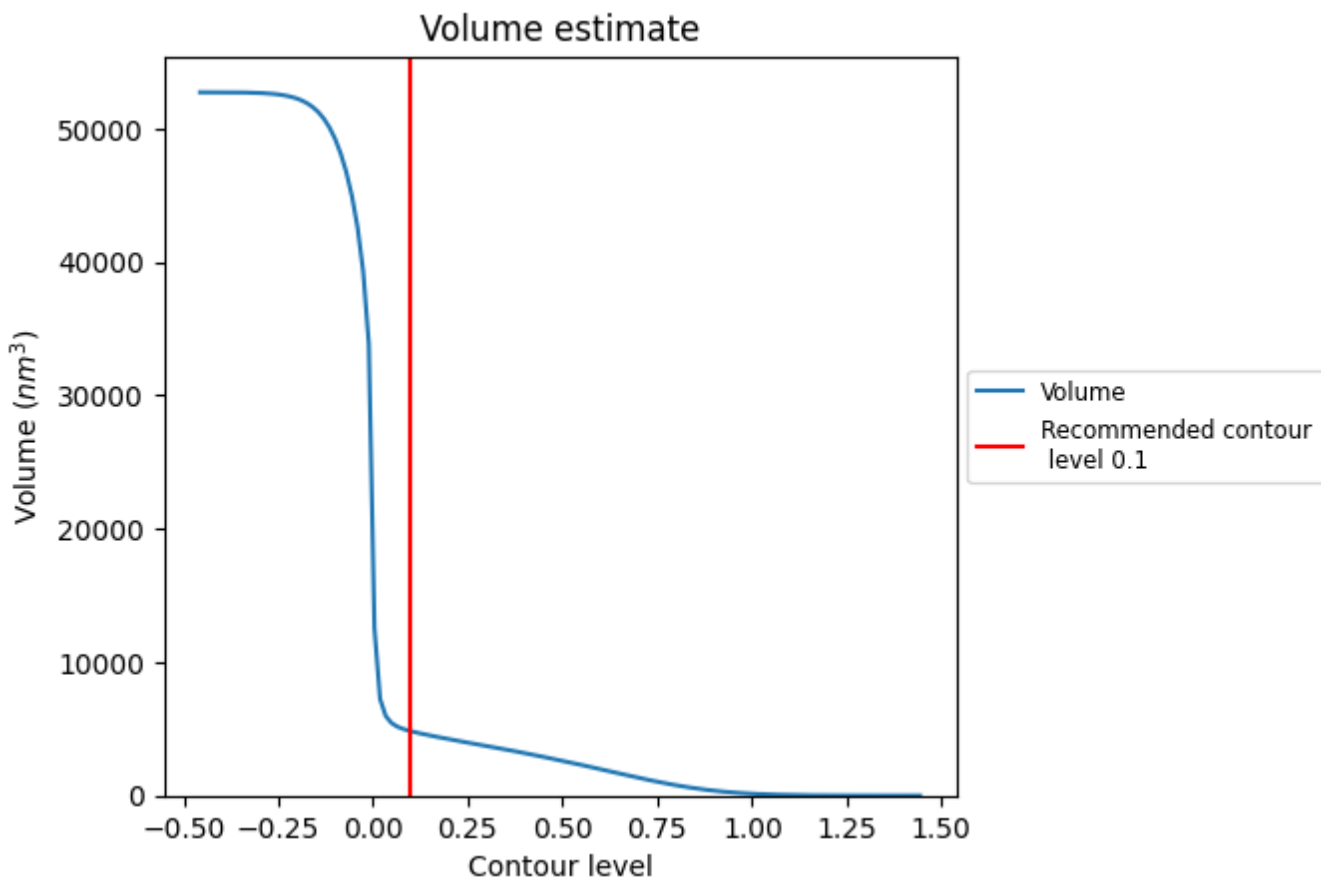
This section contains the results of statistical analysis of the map.

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.

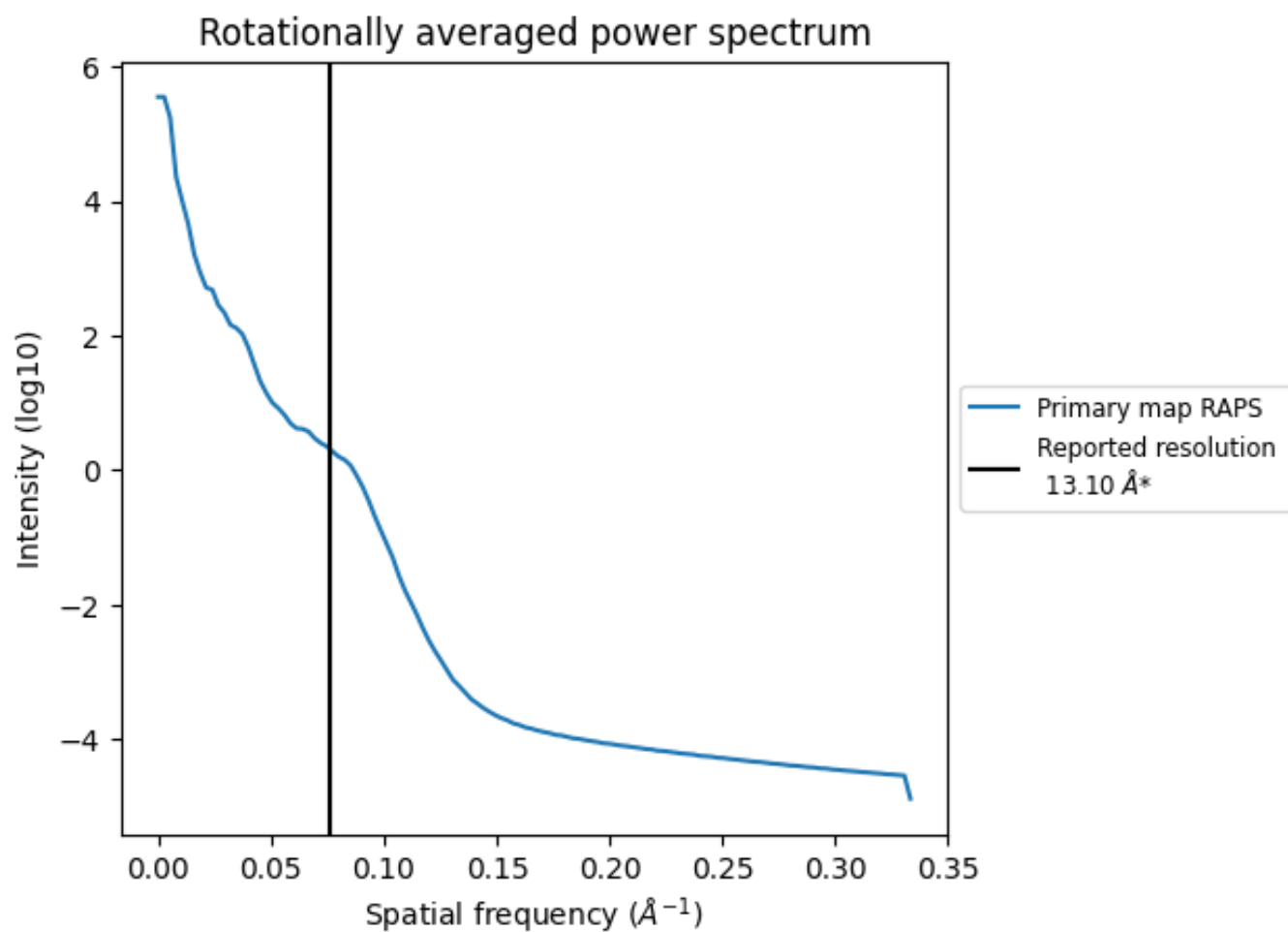
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4825 nm^3 ; this corresponds to an approximate mass of 4359 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.076\AA^{-1}

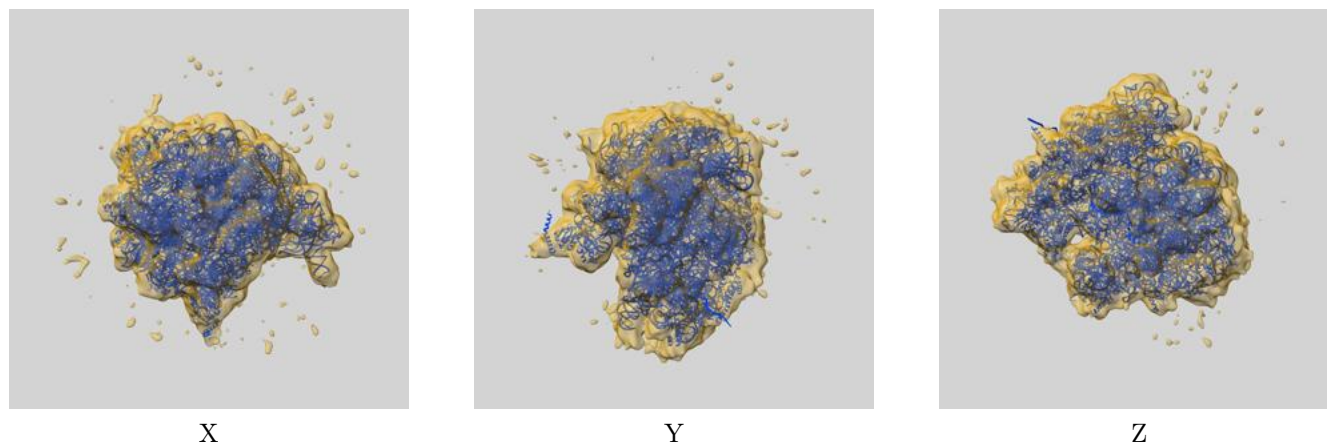
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

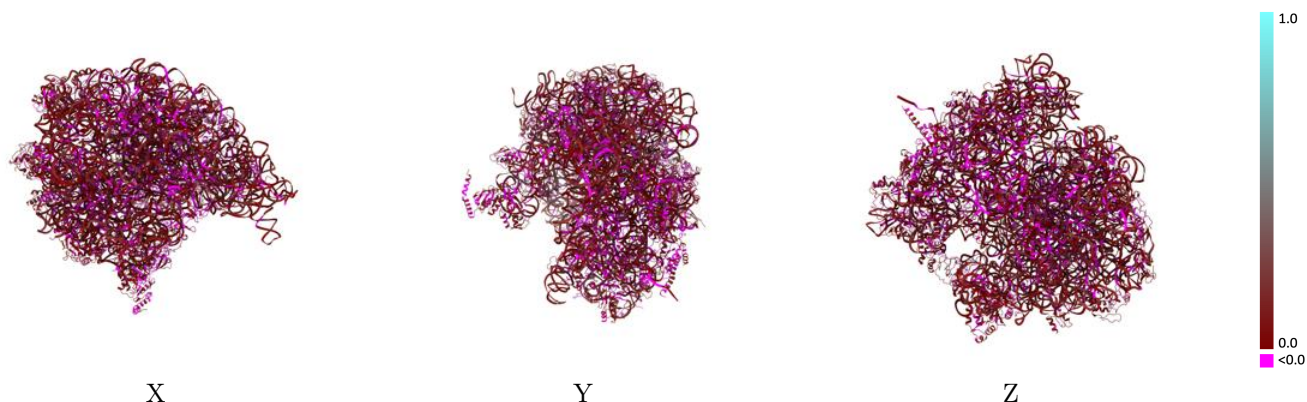
This section contains information regarding the fit between EMDB map EMD-5360 and PDB model 4V6S. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



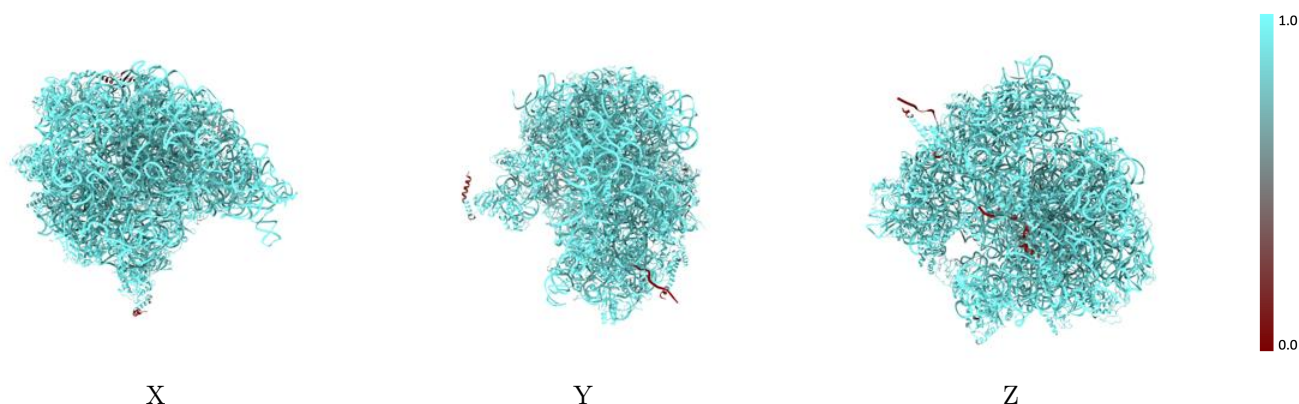
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



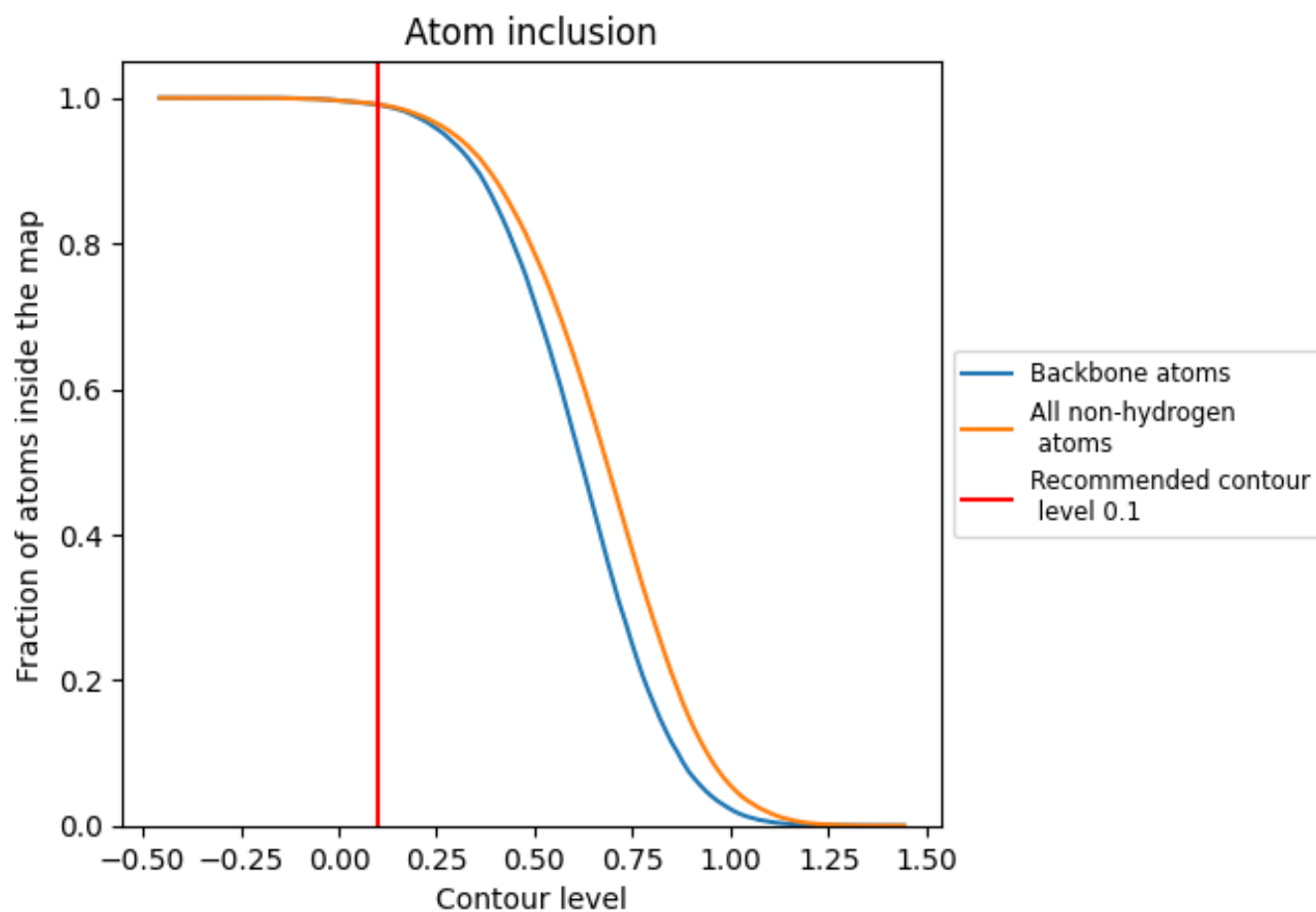
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	0.9912	0.0680
A0	1.0000	0.0510
A1	0.9954	0.0290
A2	0.9108	0.0270
A3	1.0000	0.0260
A4	1.0000	0.0490
A5	1.0000	-0.0180
A6	1.0000	-0.0250
A7	1.0000	0.0160
AA	0.9996	0.0850
AB	0.9991	0.0850
AC	0.9614	0.0370
AD	1.0000	0.0210
AE	0.9961	0.0150
AF	0.9974	0.0470
AG	0.9978	0.0730
AH	0.9992	0.0210
AI	0.7901	0.0300
AJ	0.8698	0.0350
AK	0.9795	0.0440
AL	0.9991	0.0250
AM	0.9902	0.0340
AN	0.9941	0.0100
AO	1.0000	0.0310
AP	1.0000	0.0080
AQ	0.9931	0.0550
AR	0.9786	0.0230
AS	0.9978	0.0170
AT	1.0000	0.0470
AU	1.0000	0.0140
AV	1.0000	0.0310
AW	1.0000	0.0770
AX	1.0000	0.0740
AY	0.9984	0.0080
AZ	1.0000	0.0600



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Chain	Atom inclusion	Q-score
BA	 0.9992	 0.0840
BB	 0.7341	 -0.0130
BC	 1.0000	 0.0980
BD	 0.9093	 0.0220
BE	 0.9983	 0.0640
BF	 1.0000	 0.0460
BG	 0.9967	 0.0420
BH	 0.9618	 0.0290
BI	 0.9926	 0.0680
BJ	 0.9729	 0.0280
BK	 0.9879	 0.0480
BL	 1.0000	 0.0400
BM	 0.9369	 0.0550
BN	 0.9772	 0.0330
BO	 0.9715	 0.0480
BP	 1.0000	 0.0270
BQ	 1.0000	 0.0410
BR	 1.0000	 0.0480
BS	 1.0000	 0.0660
BT	 1.0000	 0.0540
BU	 0.9817	 0.0270
BV	 1.0000	 0.0460
BW	 0.9964	 0.0570