



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2025 – 01:30 AM EDT

PDB ID : 4V7C
EMDB ID : EMD-5799
Title : Structure of the Ribosome with Elongation Factor G Trapped in the Pre-Translocation State (pre-translocation 70S*tRNA structure)
Authors : Brilot, A.F.; Korostelev, A.A.; Ermolenko, D.N.; Grigorieff, N.
Deposited on : 2013-11-20
Resolution : 7.60 Å(reported)
Based on initial model : 4GD1

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:

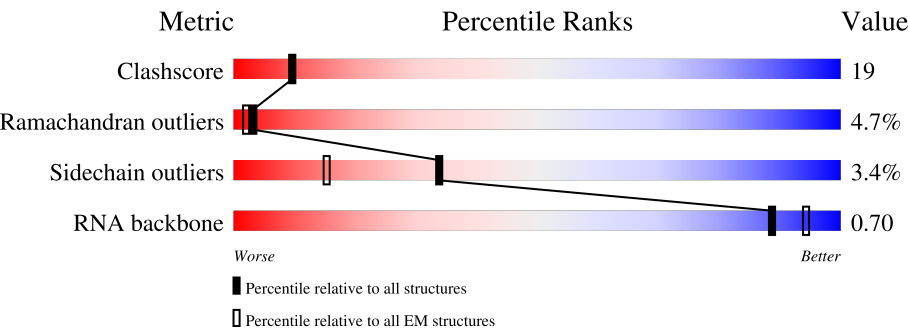
EMDB validation analysis : 0.0.1.dev117
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

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 7.60 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	AA	1542	<div><div>54%</div><div>41%</div><div>5%</div></div>
2	AB	240	<div><div>35%</div><div>21%</div><div>58%</div><div>11%</div><div>9%</div></div>
3	AC	232	<div><div>13%</div><div>38%</div><div>47%</div><div>•</div><div>11%</div></div>
4	AD	205	<div><div>10%</div><div>36%</div><div>53%</div><div>11%</div></div>
5	AE	166	<div><div>5%</div><div>46%</div><div>40%</div><div>•</div><div>10%</div></div>
6	AF	131	<div><div>11%</div><div>28%</div><div>43%</div><div>5%</div><div>24%</div></div>
7	AG	178	<div><div>6%</div><div>40%</div><div>42%</div><div>•</div><div>15%</div></div>

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Mol	Chain	Length	Quality of chain
8	AH	129	
9	AI	129	
10	AJ	103	
11	AK	128	
12	AL	123	
13	AM	117	
14	AN	100	
15	AO	88	
16	AP	82	
17	AQ	83	
18	AR	74	
19	AS	91	
20	AT	86	
21	AU	70	
22	AV	76	
22	AW	76	
23	AX	18	
24	AY	6	
25	BA	2903	
26	BB	119	
27	BC	233	
28	BD	272	
29	BE	209	
30	BF	201	
31	BG	178	

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Mol	Chain	Length	Quality of chain
32	BH	176	
33	BI	149	
34	BJ	165	
35	BK	141	
36	BL	142	
37	BM	123	
38	BN	144	
39	BO	136	
40	BP	127	
41	BQ	117	
42	BR	114	
43	BS	117	
44	BT	103	
45	BU	110	
46	BV	100	
47	BW	103	
48	BX	94	
49	BY	84	
50	BZ	77	
51	B1	63	
52	B2	58	
53	B3	56	
54	B4	54	
55	B5	46	
56	B6	64	

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Mol	Chain	Length	Quality of chain
57	B7	38	<div><div></div><div>61%</div><div>39%</div></div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	5OH	AY	6	-	-	X	-

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 148028 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1538	Total	C	N	O	P	0	0
			32995	14716	6050	10691	1538		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

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

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

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

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	AR	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 22 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		
22	AW	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		

- Molecule 23 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AX	18	Total	C	N	O	P	0	0
			386	173	71	124	18		

- Molecule 24 is a protein called viomycin.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	AY	6	Total	C	N	O	0	0
			48	25	13	10		

- Molecule 25 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BA	2897	Total	C	N	O	P	0	0
			62192	27744	11444	20107	2897		

- Molecule 26 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BB	119	Total	C	N	O	P	0	0
			2548	1135	466	829	118		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BC	225	Total	C	N	O	S	0	0
			1675	1047	305	317	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BD	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BG	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BI	53	Total	C	N	O	S	0	0
			409	261	74	73	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BJ	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BM	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BN	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BP	120	Total	C	N	O	S	0	0
			959	592	196	166	5		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
41	BQ	116	Total	C	N	O	0	0
			892	552	178	162		

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BV	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BW	102	Total	C	N	O	S	0	0
			779	492	146	141			

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BY	76	Total	C	N	O	S	0	0
			575	356	117	101	1		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B1	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 53 is a protein called 50S ribosomal protein L32.

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

- Molecule 54 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	B4	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 55 is a protein called 50S ribosomal protein L34.

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

- Molecule 56 is a protein called 50S ribosomal protein L35.

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

- Molecule 57 is a protein called 50S ribosomal protein L36.

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

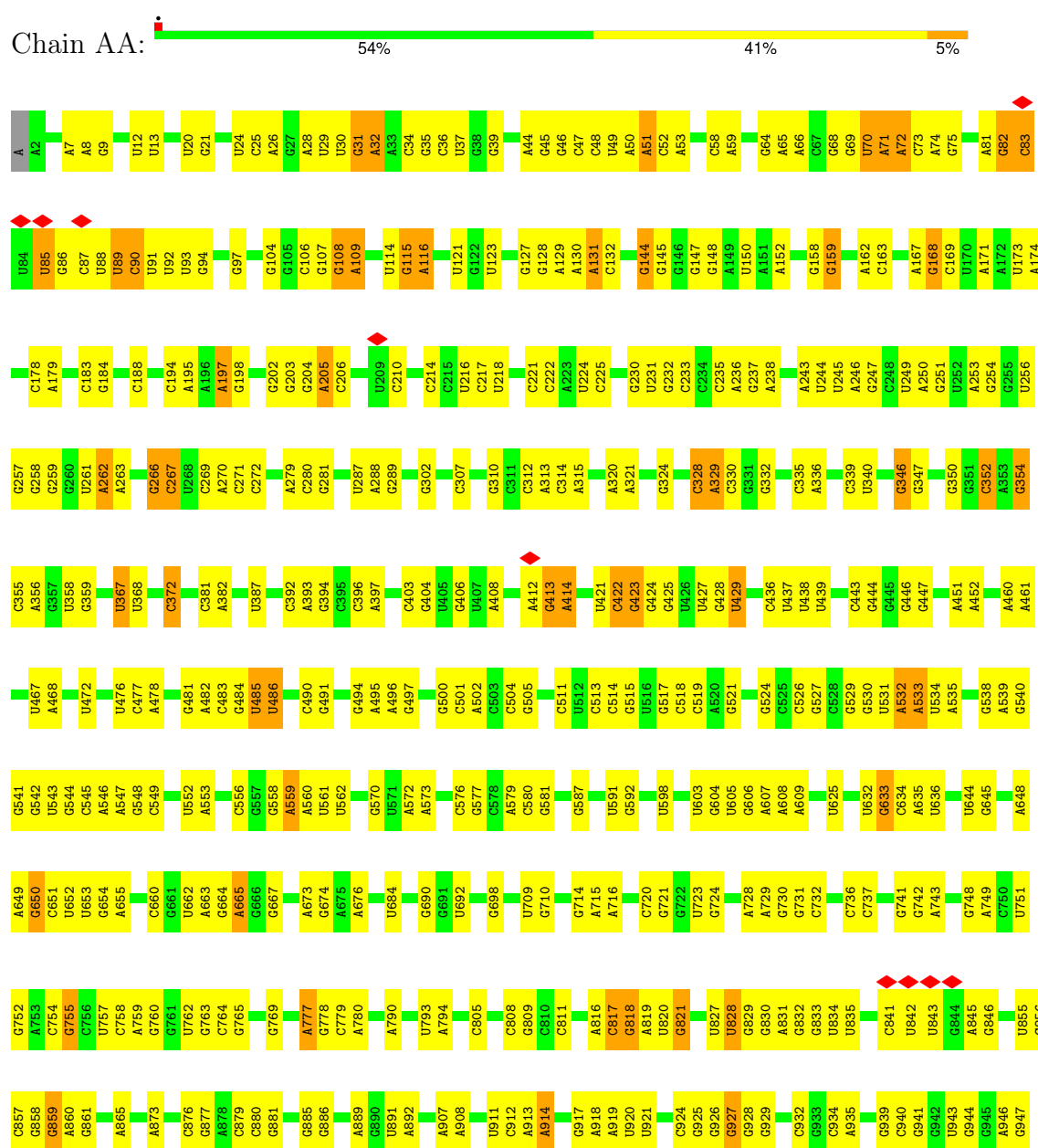
- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

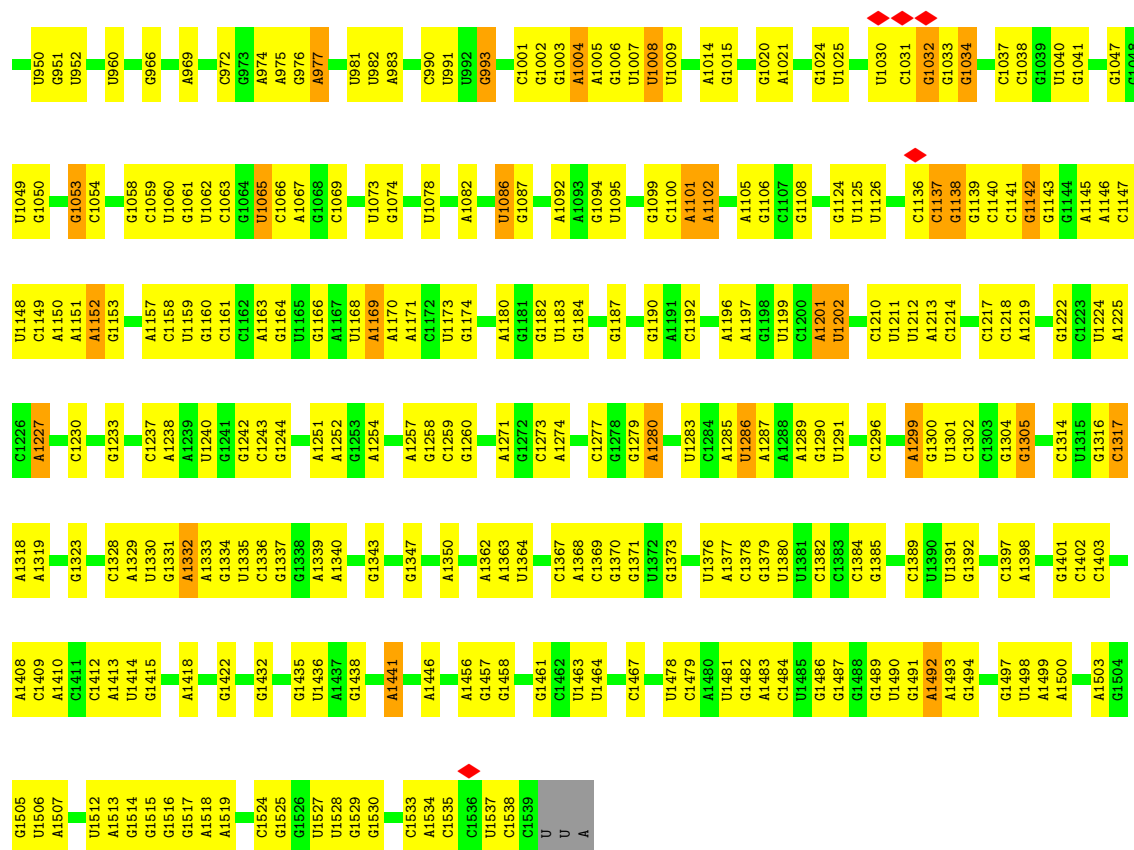
Mol	Chain	Residues	Atoms		AltConf
58	B7	1	Total	Zn	0
			1	1	

3 Residue-property plots

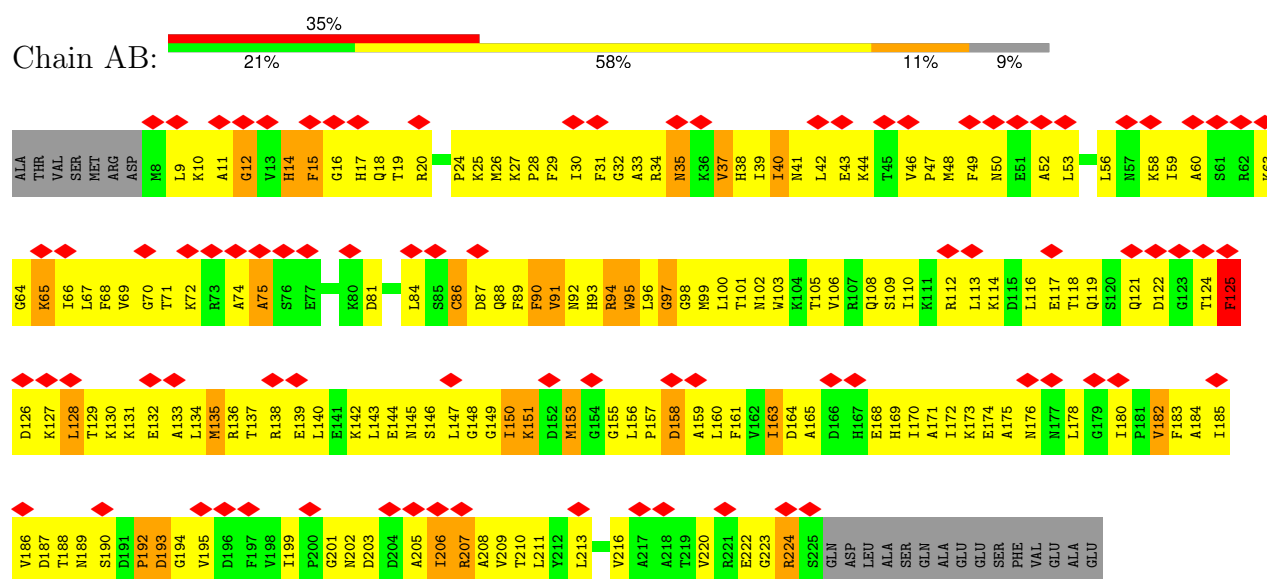
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S ribosomal RNA

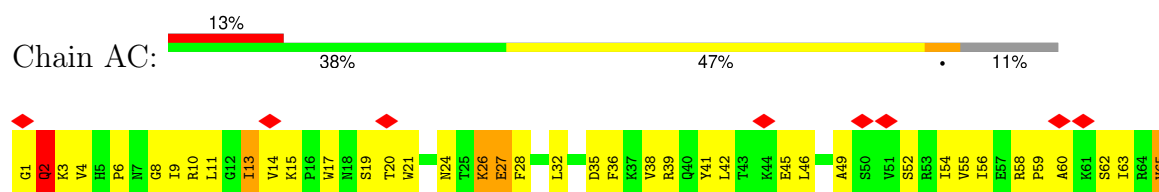


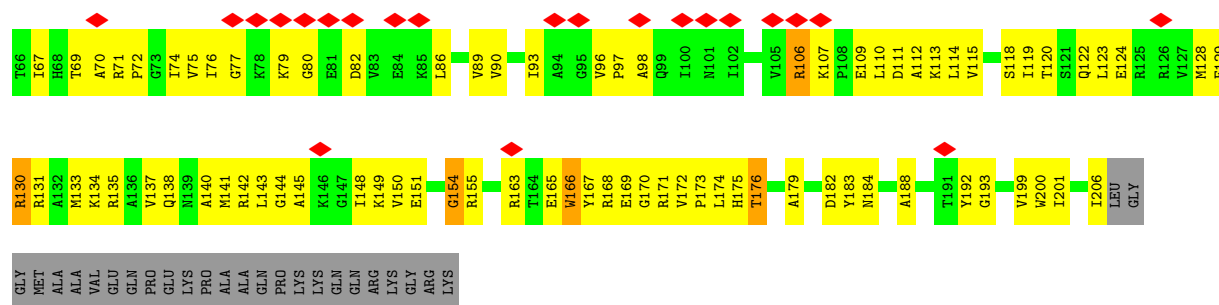


• Molecule 2: 30S ribosomal protein S2

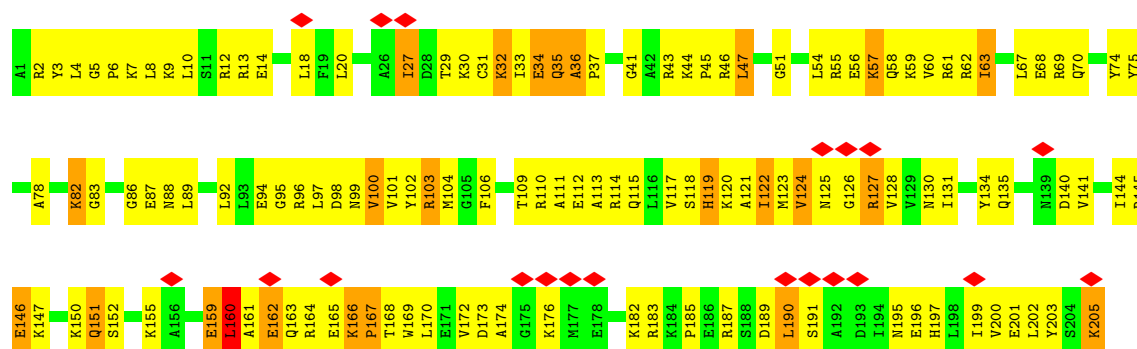


• Molecule 3: 30S ribosomal protein S3

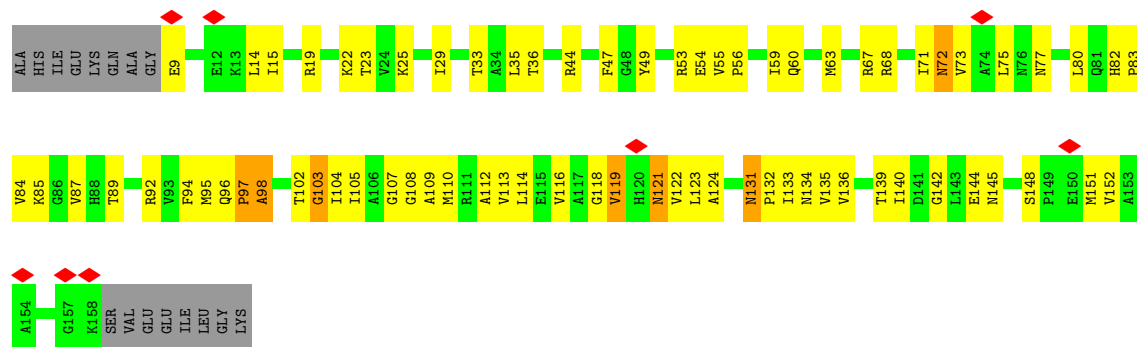




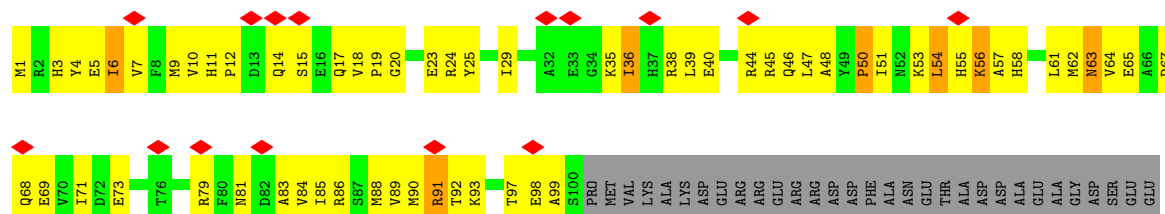
• Molecule 4: 30S ribosomal protein S4



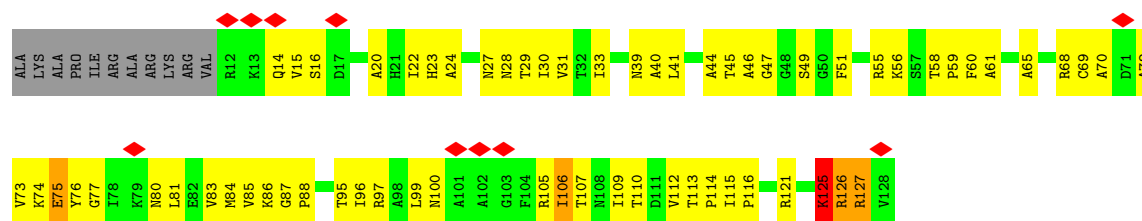
• Molecule 5: 30S ribosomal protein S5



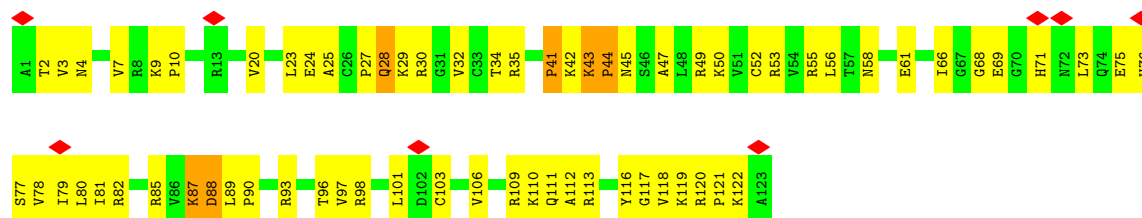
• Molecule 6: 30S ribosomal protein S6



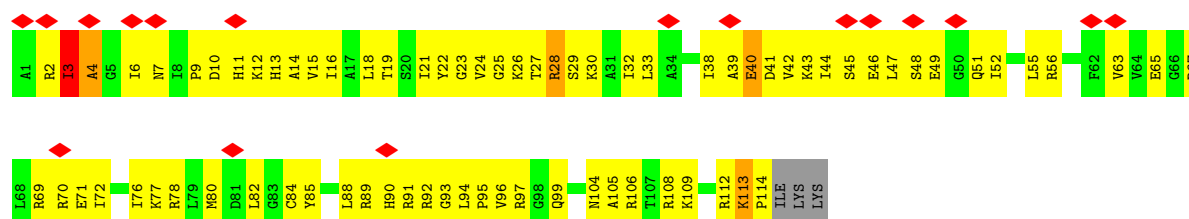




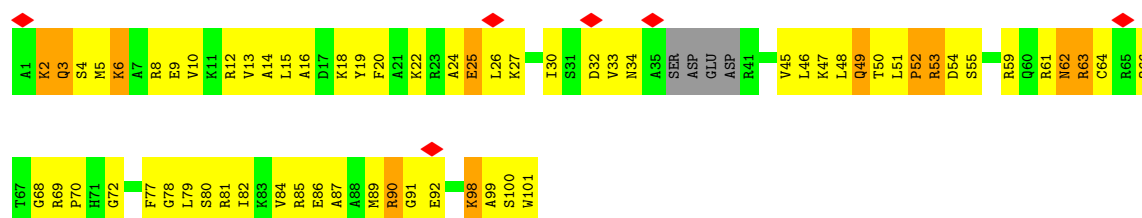
• Molecule 12: 30S ribosomal protein S12



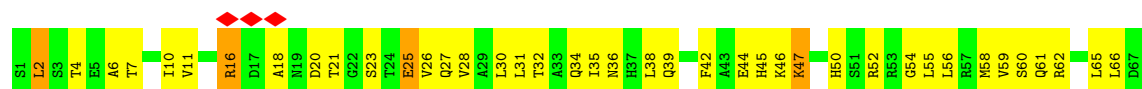
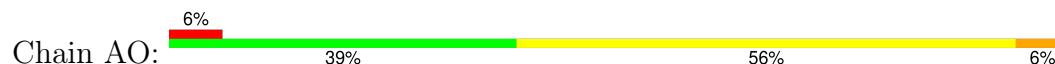
• Molecule 13: 30S ribosomal protein S13

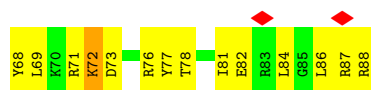


• Molecule 14: 30S ribosomal protein S14

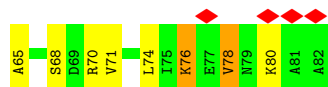
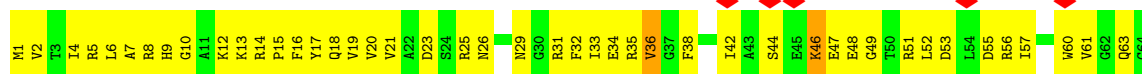


• Molecule 15: 30S ribosomal protein S15





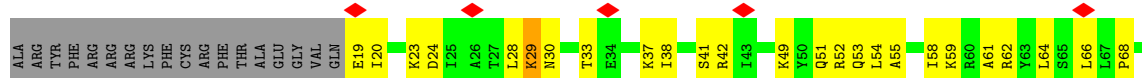
- Molecule 16: 30S ribosomal protein S16



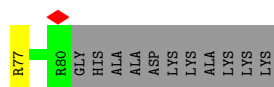
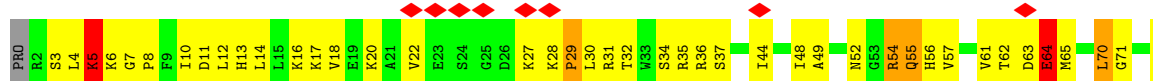
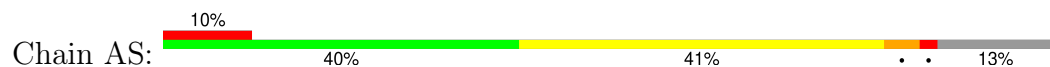
- Molecule 17: 30S ribosomal protein S17



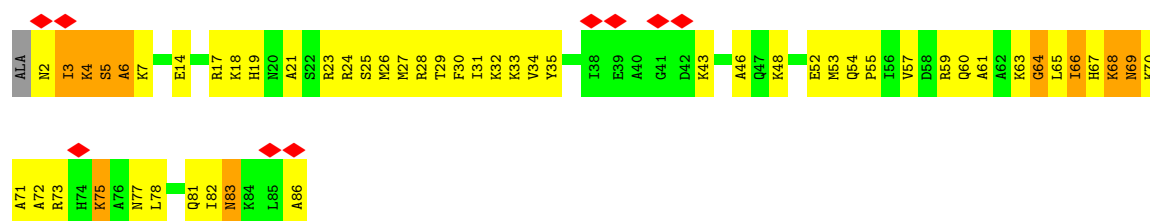
- Molecule 18: 30S ribosomal protein S18



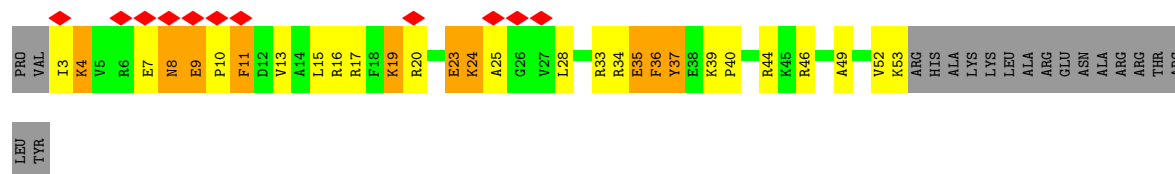
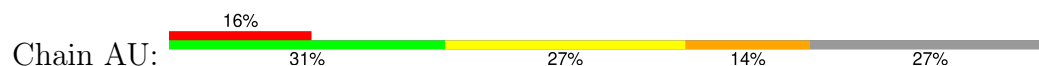
- Molecule 19: 30S ribosomal protein S19



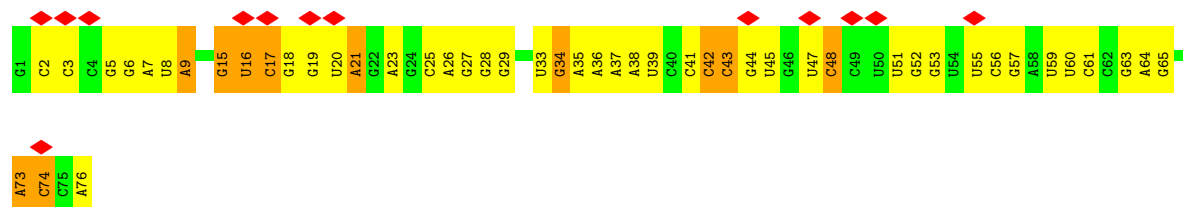
- Molecule 20: 30S ribosomal protein S20



- Molecule 21: 30S ribosomal protein S21



- Molecule 22: tRNA



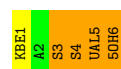
- Molecule 22: tRNA



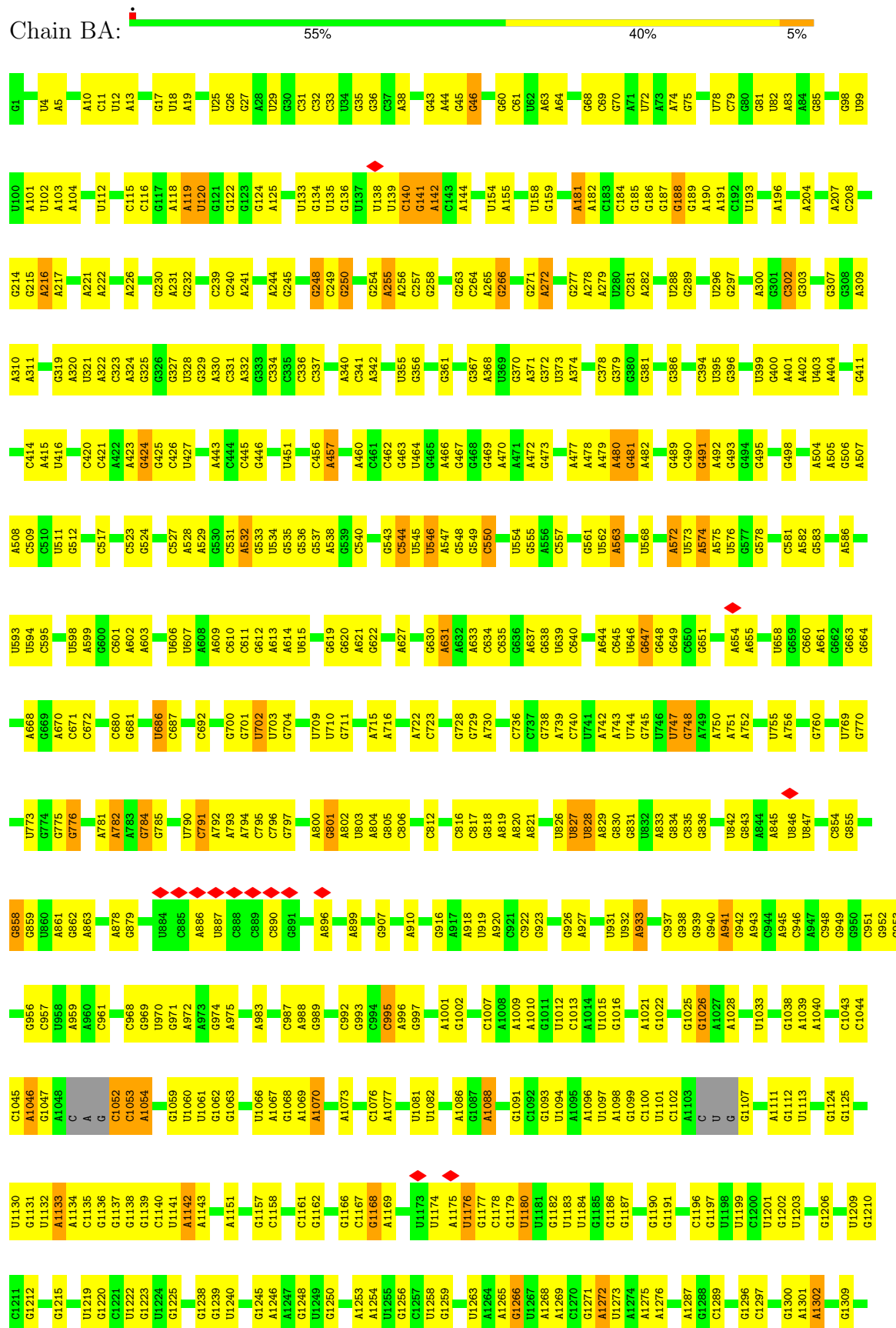
- Molecule 23: mRNA



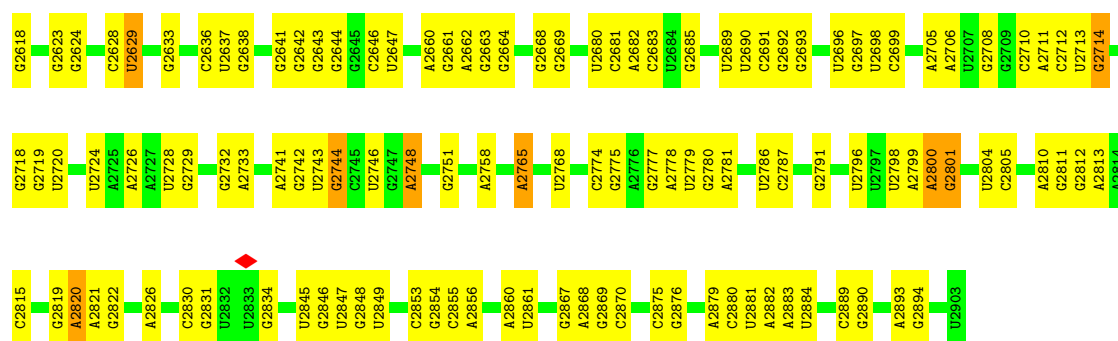
- Molecule 24: viomycin



● Molecule 25: 23S ribosomal RNA







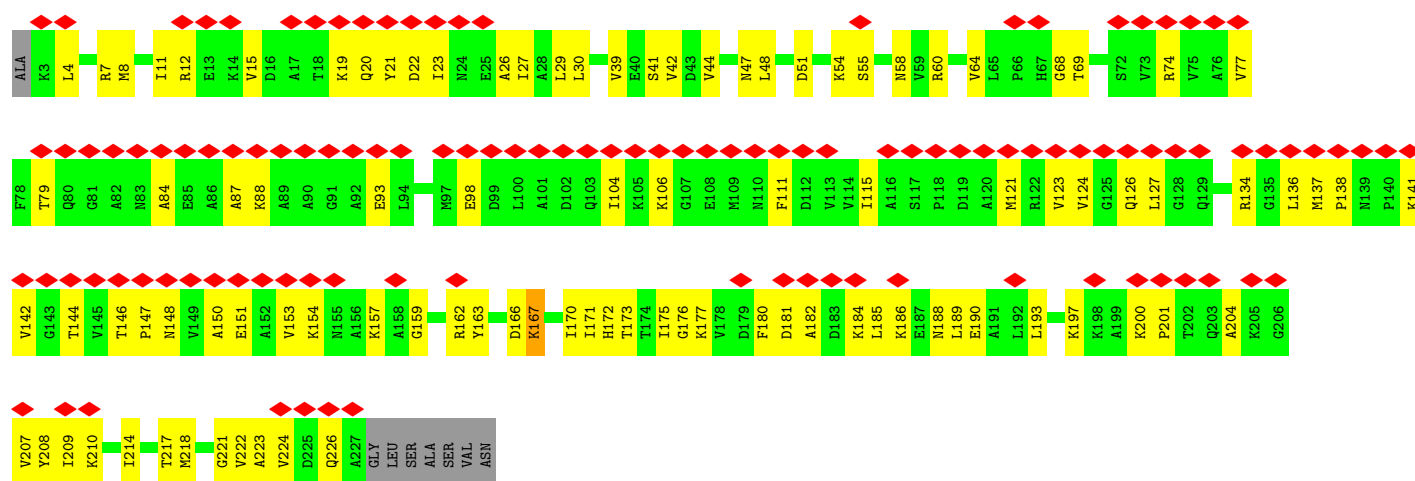
• Molecule 26: 5S ribosomal RNA

Chain BB: 56% 38% 6%



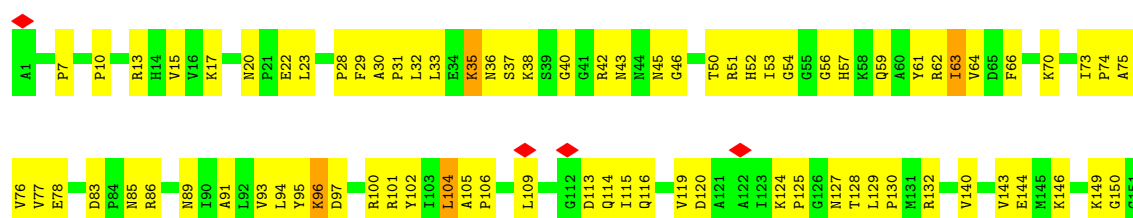
• Molecule 27: 50S ribosomal protein L1

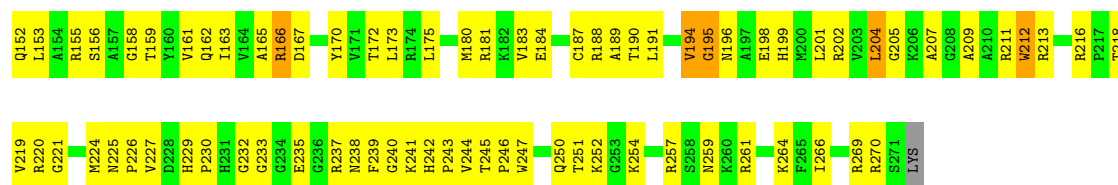
Chain BC: 49% 54% 42%



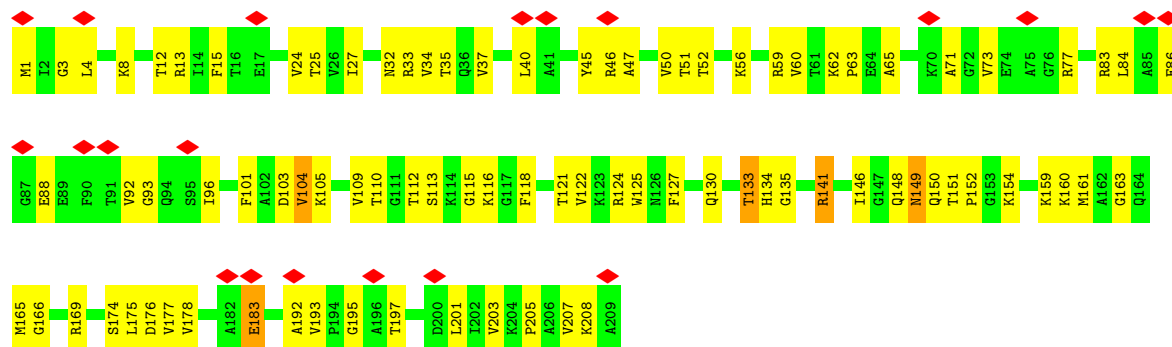
• Molecule 28: 50S ribosomal protein L2

Chain BD: 43% 53%

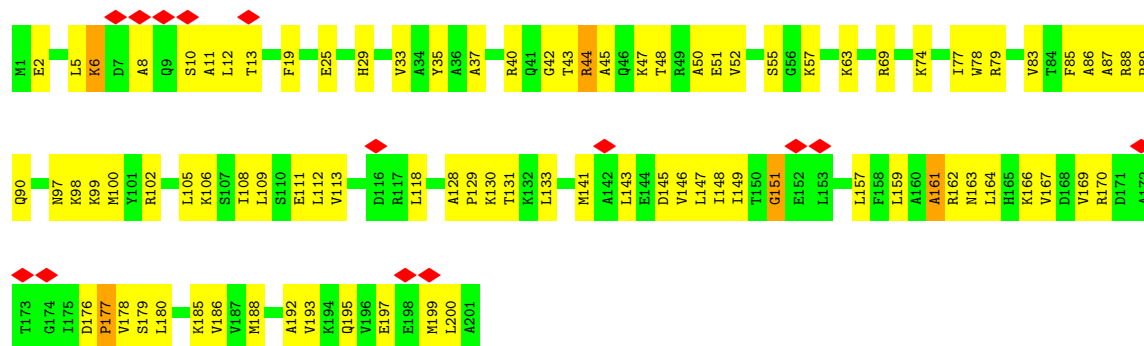




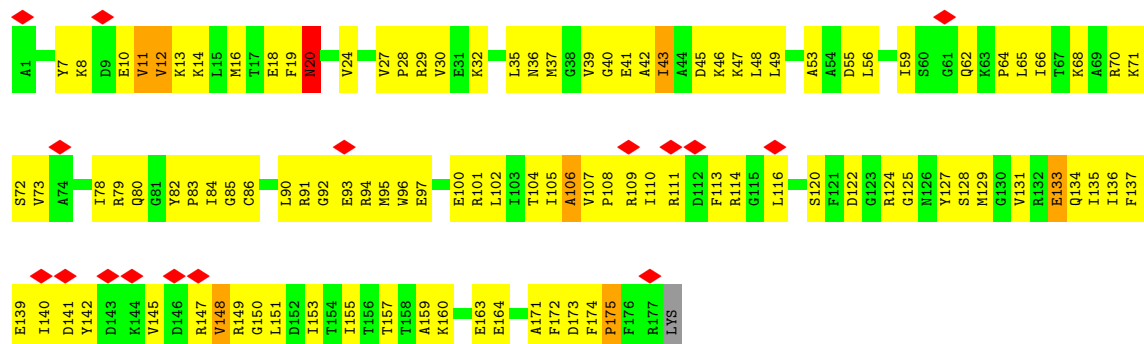
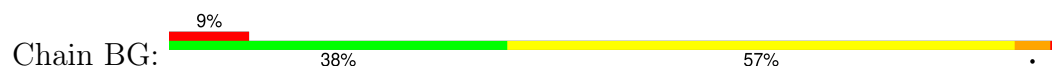
• Molecule 29: 50S ribosomal protein L3



• Molecule 30: 50S ribosomal protein L4

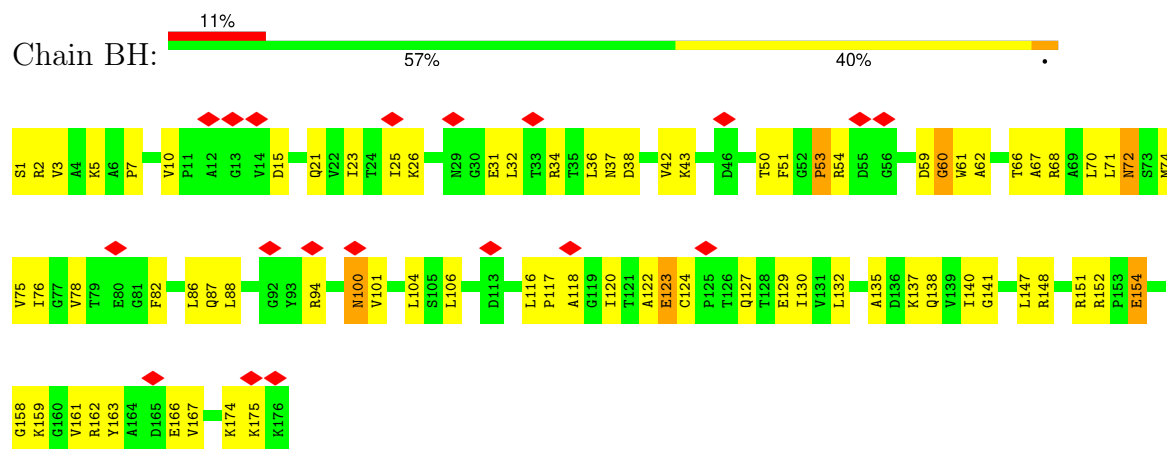


• Molecule 31: 50S ribosomal protein L5



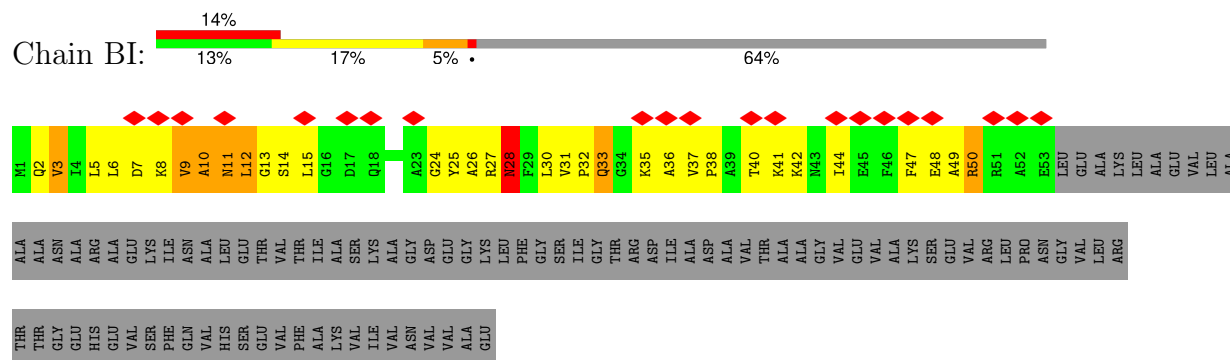
- Molecule 32: 50S ribosomal protein L6

Chain BH:



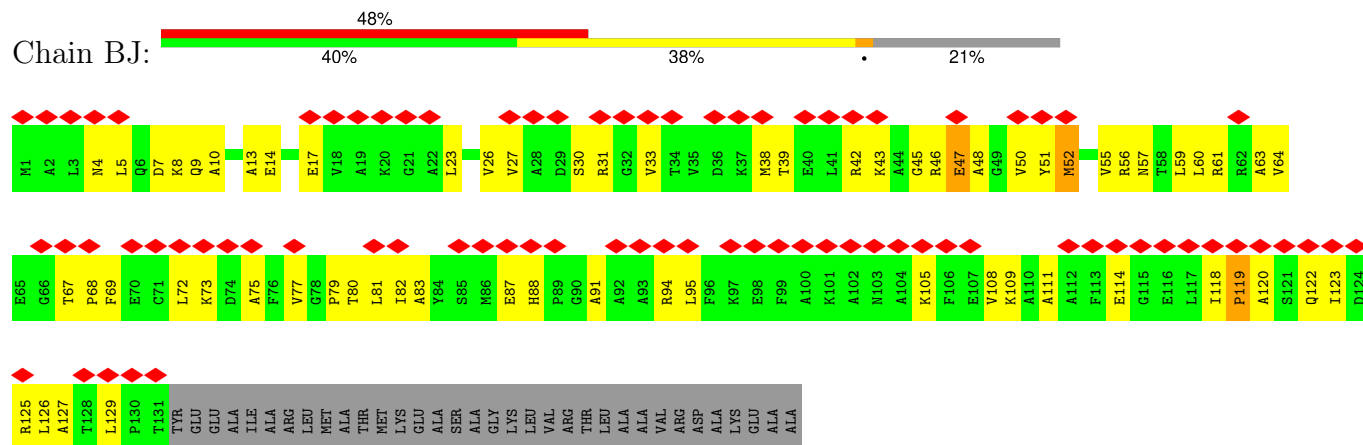
- Molecule 33: 50S ribosomal protein L9

Chain BI:



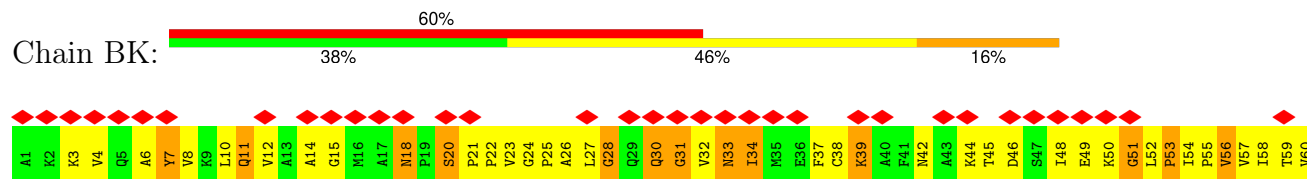
- Molecule 34: 50S ribosomal protein L10

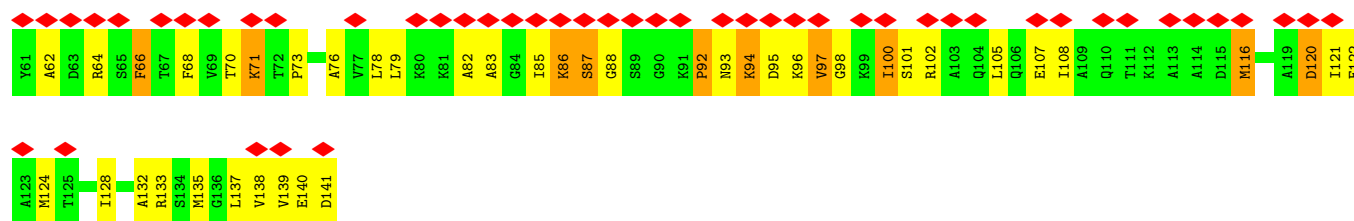
Chain BJ:



- Molecule 35: 50S ribosomal protein L11

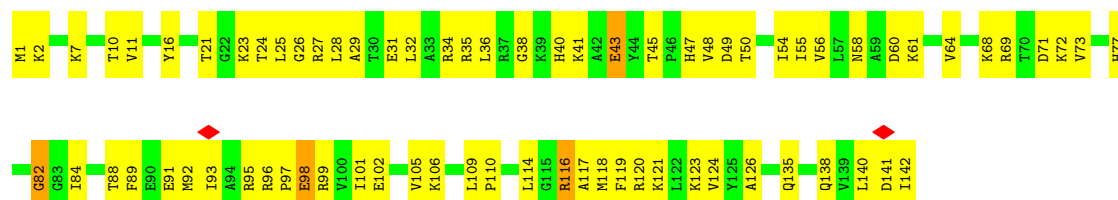
Chain BK:





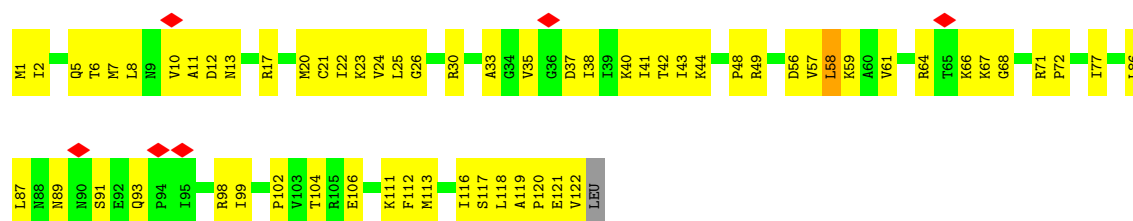
• Molecule 36: 50S ribosomal protein L13

Chain BL: 48% 49%



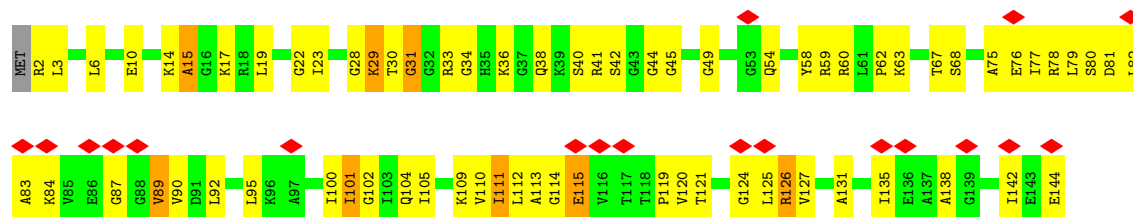
• Molecule 37: 50S ribosomal protein L14

Chain BM: 5% 49% 50%



• Molecule 38: 50S ribosomal protein L15

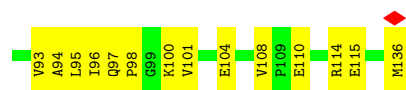
Chain BN: 13% 50% 44% 6%



• Molecule 39: 50S ribosomal protein L16

Chain BO: 60% 38%





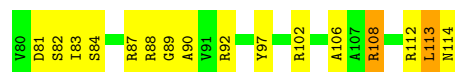
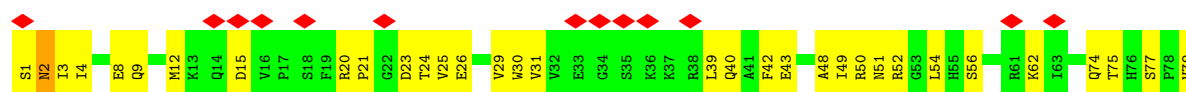
- Molecule 40: 50S ribosomal protein L17



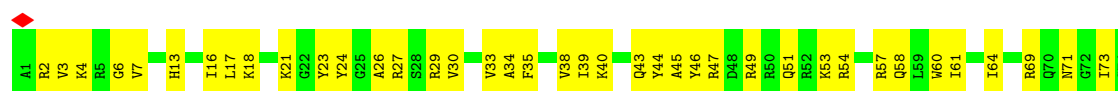
- Molecule 41: 50S ribosomal protein L18



- Molecule 42: 50S ribosomal protein L19

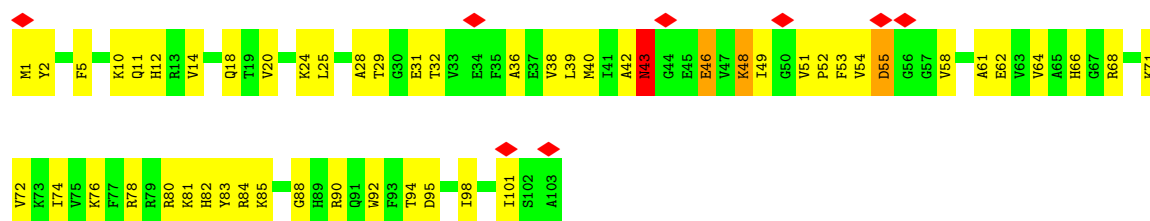


- Molecule 43: 50S ribosomal protein L20

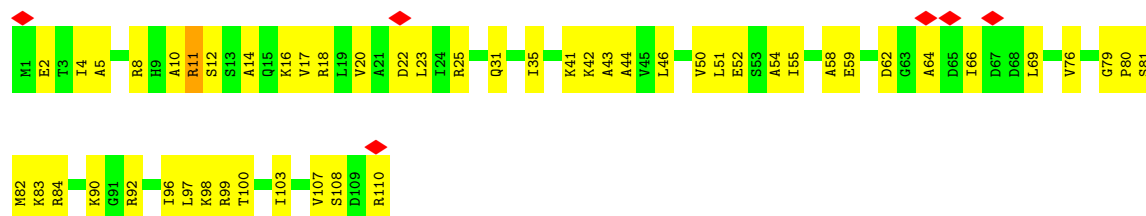


- Molecule 44: 50S ribosomal protein L21

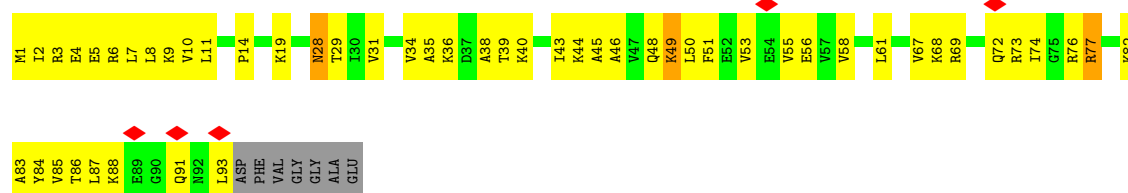
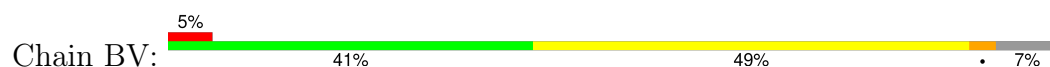




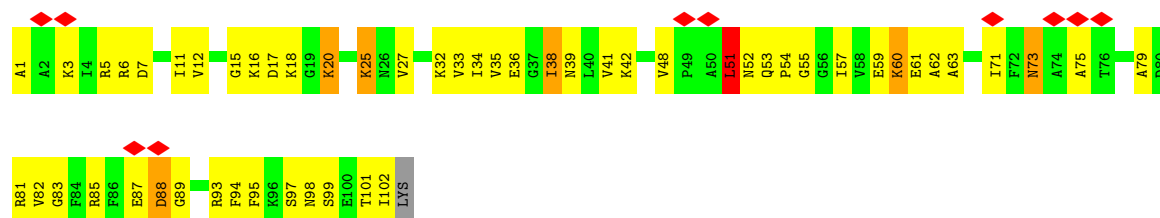
- Molecule 45: 50S ribosomal protein L22



- Molecule 46: 50S ribosomal protein L23



- Molecule 47: 50S ribosomal protein L24



- Molecule 48: 50S ribosomal protein L25

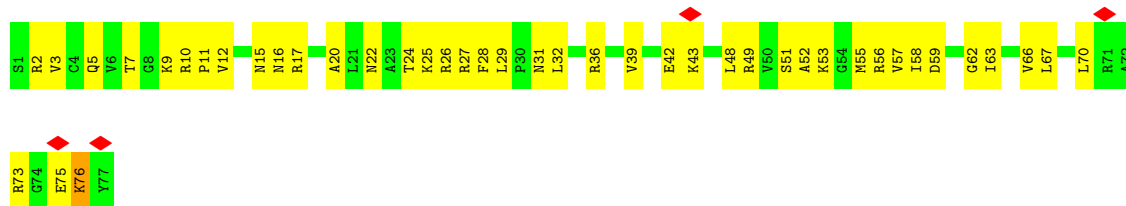
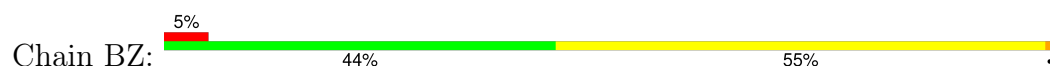




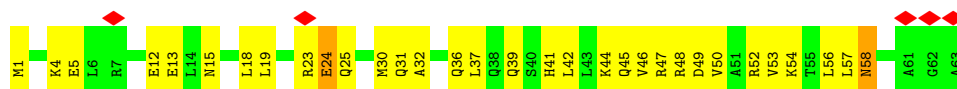
- Molecule 49: 50S ribosomal protein L27



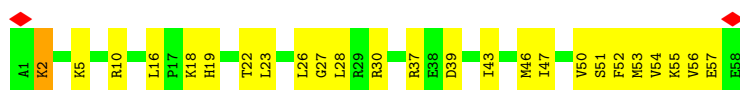
- Molecule 50: 50S ribosomal protein L28



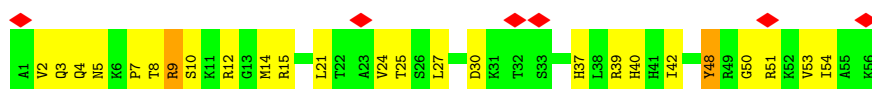
- Molecule 51: 50S ribosomal protein L29



- Molecule 52: 50S ribosomal protein L30

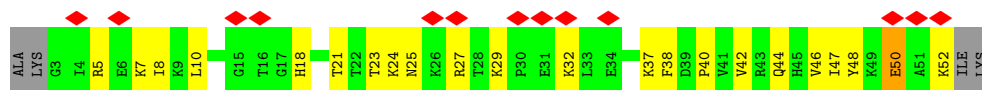


- Molecule 53: 50S ribosomal protein L32

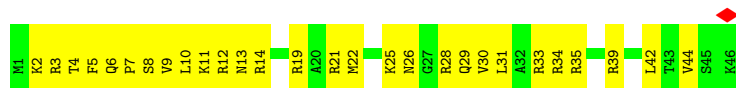


- Molecule 54: 50S ribosomal protein L33

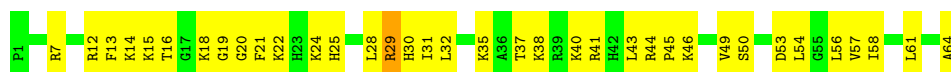




- Molecule 55: 50S ribosomal protein L34



- Molecule 56: 50S ribosomal protein L35



- Molecule 57: 50S ribosomal protein L36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	85115	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	CTFFIND3, FREALIGN per micrograph	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1150	Depositor
Maximum defocus (nm)	6950	Depositor
Magnification	134615	Depositor
Image detector	FEI FALCON I (4k x 4k)	Depositor
Maximum map value	1.302	Depositor
Minimum map value	-0.460	Depositor
Average map value	-0.027	Depositor
Map value standard deviation	0.175	Depositor
Recommended contour level	0.32	Depositor
Map size (\AA)	332.8, 332.8, 332.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.04, 1.04, 1.04	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5OH, DPP, UAL, KBE, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.21	0/36944	0.62	0/57632
2	AB	0.25	0/1735	0.42	0/2338
3	AC	0.23	0/1651	0.41	0/2225
4	AD	0.22	0/1665	0.40	0/2227
5	AE	0.23	0/1118	0.42	0/1504
6	AF	0.24	0/835	0.43	0/1128
7	AG	0.22	0/1195	0.42	0/1602
8	AH	0.23	0/989	0.41	0/1326
9	AI	0.23	0/1034	0.42	0/1375
10	AJ	0.22	0/796	0.45	0/1077
11	AK	0.24	0/893	0.41	0/1205
12	AL	0.22	0/969	0.42	0/1300
13	AM	0.21	0/892	0.42	0/1193
14	AN	0.24	0/785	0.38	0/1043
15	AO	0.23	0/722	0.40	0/964
16	AP	0.25	0/659	0.39	0/884
17	AQ	0.23	0/657	0.43	0/881
18	AR	0.23	0/462	0.41	0/621
19	AS	0.25	0/652	0.42	0/877
20	AT	0.24	0/671	0.41	0/888
21	AU	0.26	0/430	0.42	0/570
22	AV	0.30	0/1809	0.67	0/2819
22	AW	0.24	0/1812	0.62	0/2823
23	AX	0.32	0/432	0.65	0/671
24	AY	2.44	2/11 (18.2%)	0.74	0/13
25	BA	0.26	1/69653 (0.0%)	0.62	3/108657 (0.0%)
26	BB	0.21	0/2847	0.61	0/4440
27	BC	0.21	0/1690	0.40	0/2278
28	BD	0.21	0/2121	0.41	0/2852
29	BE	0.24	0/1586	0.41	0/2134
30	BF	0.23	0/1571	0.40	0/2113
31	BG	0.25	0/1434	0.40	0/1926

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	BH	0.22	0/1343	0.41	0/1816
33	BI	0.27	0/414	0.42	0/556
34	BJ	0.24	0/1001	0.41	0/1350
35	BK	0.24	0/1046	0.43	0/1410
36	BL	0.23	0/1152	0.40	0/1551
37	BM	0.22	0/947	0.42	0/1268
38	BN	0.23	0/1054	0.42	0/1403
39	BO	0.25	0/1093	0.41	0/1460
40	BP	0.24	0/970	0.38	0/1295
41	BQ	0.22	0/902	0.38	0/1209
42	BR	0.23	0/929	0.40	0/1242
43	BS	0.24	0/960	0.36	0/1278
44	BT	0.25	0/829	0.43	0/1107
45	BU	0.21	0/864	0.41	0/1156
46	BV	0.22	0/744	0.41	0/994
47	BW	0.24	0/787	0.40	0/1051
48	BX	0.24	0/766	0.38	0/1025
49	BY	0.26	0/582	0.37	0/769
50	BZ	0.24	0/635	0.39	0/848
51	B1	0.23	0/510	0.41	0/677
52	B2	0.23	0/453	0.42	0/605
53	B3	0.22	0/450	0.40	0/599
54	B4	0.26	0/416	0.41	0/554
55	B5	0.25	0/380	0.39	0/498
56	B6	0.24	0/513	0.41	0/676
57	B7	0.22	0/303	0.39	0/397
All	All	0.24	3/160763 (0.0%)	0.57	3/240380 (0.0%)

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
25	BA	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BA	1911	U	O3'-P	-40.57	1.12	1.61
24	AY	3	SER	CA-C	-5.17	1.39	1.52
24	AY	4	SER	CA-C	-5.17	1.39	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1911	U	P-O3'-C3'	-14.37	102.45	119.70
25	BA	1911	U	OP1-P-O3'	-9.93	83.36	105.20
25	BA	1911	U	OP2-P-O3'	9.58	126.28	105.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
25	BA	1915	U	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	32995	0	16607	584	0
2	AB	1704	0	1732	189	0
3	AC	1624	0	1699	125	0
4	AD	1643	0	1710	168	0
5	AE	1105	0	1148	78	0
6	AF	817	0	808	67	0
7	AG	1181	0	1240	93	0
8	AH	979	0	1034	86	0
9	AI	1022	0	1070	109	0
10	AJ	786	0	828	79	0
11	AK	877	0	887	72	0
12	AL	955	0	1019	84	0
13	AM	883	0	944	79	0
14	AN	774	0	827	84	0
15	AO	714	0	737	53	0
16	AP	649	0	666	57	0
17	AQ	648	0	691	56	0
18	AR	455	0	478	32	0
19	AS	637	0	665	43	0
20	AT	665	0	714	63	0
21	AU	425	0	449	32	0
22	AV	1619	0	822	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	AW	1622	0	821	39	0
23	AX	386	0	194	8	0
24	AY	48	0	40	13	0
25	BA	62192	0	31283	1057	0
26	BB	2548	0	1292	44	0
27	BC	1675	0	1763	92	0
28	BD	2082	0	2157	170	0
29	BE	1565	0	1616	92	0
30	BF	1552	0	1619	99	0
31	BG	1410	0	1447	115	0
32	BH	1323	0	1374	67	0
33	BI	409	0	429	34	0
34	BJ	988	0	1025	53	0
35	BK	1032	0	1088	92	0
36	BL	1129	0	1162	71	0
37	BM	938	0	1012	51	0
38	BN	1045	0	1117	92	0
39	BO	1074	0	1157	48	0
40	BP	959	0	998	73	0
41	BQ	892	0	923	51	0
42	BR	917	0	965	54	0
43	BS	947	0	1022	61	0
44	BT	816	0	839	54	0
45	BU	857	0	922	48	0
46	BV	738	0	807	49	0
47	BW	779	0	834	49	0
48	BX	753	0	780	42	0
49	BY	575	0	589	33	0
50	BZ	625	0	655	39	0
51	B1	509	0	543	37	0
52	B2	449	0	491	27	0
53	B3	444	0	461	31	0
54	B4	409	0	440	22	0
55	B5	377	0	418	37	0
56	B6	504	0	574	49	0
57	B7	302	0	343	22	0
58	B7	1	0	0	0	0
All	All	148028	0	99975	4831	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 19.

The worst 5 of 4831 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:45:G:H5'	25:BA:46:G:H5'	1.24	1.16
25:BA:1912:A:C2	25:BA:1919:A:C5	2.33	1.16
1:AA:1033:G:H2'	1:AA:1034:G:H5''	1.31	1.10
48:BX:10:LYS:HE2	48:BX:10:LYS:H	1.16	1.09
27:BC:201:PRO:HG2	27:BC:204:ALA:HB2	1.39	1.02

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	
2	AB	216/240 (90%)	140 (65%)	51 (24%)	25 (12%)	0	5
3	AC	204/232 (88%)	169 (83%)	28 (14%)	7 (3%)	3	21
4	AD	203/205 (99%)	161 (79%)	26 (13%)	16 (8%)	1	10
5	AE	148/166 (89%)	111 (75%)	28 (19%)	9 (6%)	1	13
6	AF	98/131 (75%)	72 (74%)	19 (19%)	7 (7%)	1	11
7	AG	149/178 (84%)	120 (80%)	25 (17%)	4 (3%)	4	25
8	AH	127/129 (98%)	113 (89%)	10 (8%)	4 (3%)	3	22
9	AI	125/129 (97%)	94 (75%)	25 (20%)	6 (5%)	2	16
10	AJ	96/103 (93%)	66 (69%)	18 (19%)	12 (12%)	0	4
11	AK	115/128 (90%)	88 (76%)	22 (19%)	5 (4%)	2	17
12	AL	121/123 (98%)	96 (79%)	17 (14%)	8 (7%)	1	12
13	AM	112/117 (96%)	94 (84%)	12 (11%)	6 (5%)	1	15
14	AN	92/100 (92%)	66 (72%)	19 (21%)	7 (8%)	1	10
15	AO	86/88 (98%)	72 (84%)	12 (14%)	2 (2%)	5	28
16	AP	80/82 (98%)	60 (75%)	15 (19%)	5 (6%)	1	13
17	AQ	78/83 (94%)	57 (73%)	13 (17%)	8 (10%)	0	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	AR	53/74 (72%)	48 (91%)	5 (9%)	0	100	100
19	AS	77/91 (85%)	59 (77%)	11 (14%)	7 (9%)	0	8
20	AT	83/86 (96%)	70 (84%)	6 (7%)	7 (8%)	0	9
21	AU	49/70 (70%)	29 (59%)	13 (26%)	7 (14%)	0	3
24	AY	2/6 (33%)	1 (50%)	1 (50%)	0	100	100
27	BC	223/233 (96%)	204 (92%)	18 (8%)	1 (0%)	30	68
28	BD	269/272 (99%)	220 (82%)	41 (15%)	8 (3%)	3	23
29	BE	207/209 (99%)	180 (87%)	22 (11%)	5 (2%)	5	27
30	BF	199/201 (99%)	170 (85%)	23 (12%)	6 (3%)	3	23
31	BG	175/178 (98%)	147 (84%)	19 (11%)	9 (5%)	1	15
32	BH	174/176 (99%)	144 (83%)	24 (14%)	6 (3%)	3	21
33	BI	51/149 (34%)	29 (57%)	14 (28%)	8 (16%)	0	3
34	BJ	129/165 (78%)	111 (86%)	14 (11%)	4 (3%)	3	22
35	BK	139/141 (99%)	77 (55%)	40 (29%)	22 (16%)	0	2
36	BL	140/142 (99%)	117 (84%)	22 (16%)	1 (1%)	19	57
37	BM	120/123 (98%)	101 (84%)	14 (12%)	5 (4%)	2	17
38	BN	141/144 (98%)	107 (76%)	24 (17%)	10 (7%)	1	11
39	BO	134/136 (98%)	116 (87%)	14 (10%)	4 (3%)	3	23
40	BP	116/127 (91%)	96 (83%)	14 (12%)	6 (5%)	1	15
41	BQ	114/117 (97%)	94 (82%)	16 (14%)	4 (4%)	3	20
42	BR	112/114 (98%)	94 (84%)	15 (13%)	3 (3%)	4	25
43	BS	115/117 (98%)	102 (89%)	13 (11%)	0	100	100
44	BT	101/103 (98%)	82 (81%)	15 (15%)	4 (4%)	2	18
45	BU	108/110 (98%)	87 (81%)	19 (18%)	2 (2%)	6	32
46	BV	91/100 (91%)	79 (87%)	11 (12%)	1 (1%)	12	47
47	BW	100/103 (97%)	78 (78%)	15 (15%)	7 (7%)	1	11
48	BX	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
49	BY	74/84 (88%)	63 (85%)	10 (14%)	1 (1%)	9	41
50	BZ	75/77 (97%)	65 (87%)	10 (13%)	0	100	100
51	B1	61/63 (97%)	51 (84%)	8 (13%)	2 (3%)	3	21
52	B2	56/58 (97%)	53 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	B3	54/56 (96%)	46 (85%)	8 (15%)	0	100	100
54	B4	48/54 (89%)	38 (79%)	9 (19%)	1 (2%)	5	30
55	B5	44/46 (96%)	39 (89%)	5 (11%)	0	100	100
56	B6	62/64 (97%)	53 (86%)	8 (13%)	1 (2%)	8	38
57	B7	36/38 (95%)	28 (78%)	7 (19%)	1 (3%)	4	24
All	All	5874/6355 (92%)	4742 (81%)	858 (15%)	274 (5%)	3	16

5 of 274 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	15	PHE
2	AB	33	ALA
2	AB	86	CYS
2	AB	94	ARG
2	AB	163	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	
2	AB	180/198 (91%)	169 (94%)	11 (6%)	15	37
3	AC	170/189 (90%)	162 (95%)	8 (5%)	22	44
4	AD	172/172 (100%)	160 (93%)	12 (7%)	12	32
5	AE	113/125 (90%)	109 (96%)	4 (4%)	31	51
6	AF	87/112 (78%)	84 (97%)	3 (3%)	32	51
7	AG	124/146 (85%)	120 (97%)	4 (3%)	34	53
8	AH	104/104 (100%)	102 (98%)	2 (2%)	52	69
9	AI	105/106 (99%)	95 (90%)	10 (10%)	7	22
10	AJ	86/90 (96%)	83 (96%)	3 (4%)	31	51
11	AK	90/98 (92%)	84 (93%)	6 (7%)	13	34
12	AL	103/103 (100%)	101 (98%)	2 (2%)	52	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	AM	92/95 (97%)	89 (97%)	3 (3%)	33	52
14	AN	79/83 (95%)	72 (91%)	7 (9%)	8	25
15	AO	76/76 (100%)	73 (96%)	3 (4%)	27	48
16	AP	65/65 (100%)	62 (95%)	3 (5%)	23	44
17	AQ	74/77 (96%)	69 (93%)	5 (7%)	13	34
18	AR	48/64 (75%)	47 (98%)	1 (2%)	48	66
19	AS	70/78 (90%)	66 (94%)	4 (6%)	17	38
20	AT	65/65 (100%)	62 (95%)	3 (5%)	23	44
21	AU	44/60 (73%)	40 (91%)	4 (9%)	7	24
24	AY	2/2 (100%)	2 (100%)	0	100	100
27	BC	175/180 (97%)	173 (99%)	2 (1%)	70	80
28	BD	216/217 (100%)	213 (99%)	3 (1%)	62	75
29	BE	164/164 (100%)	162 (99%)	2 (1%)	67	78
30	BF	165/165 (100%)	165 (100%)	0	100	100
31	BG	148/149 (99%)	145 (98%)	3 (2%)	50	68
32	BH	137/137 (100%)	132 (96%)	5 (4%)	30	50
33	BI	42/114 (37%)	39 (93%)	3 (7%)	12	32
34	BJ	100/123 (81%)	99 (99%)	1 (1%)	73	82
35	BK	109/109 (100%)	98 (90%)	11 (10%)	6	20
36	BL	116/116 (100%)	113 (97%)	3 (3%)	41	59
37	BM	103/104 (99%)	102 (99%)	1 (1%)	73	82
38	BN	102/103 (99%)	100 (98%)	2 (2%)	50	68
39	BO	109/109 (100%)	106 (97%)	3 (3%)	38	57
40	BP	100/103 (97%)	96 (96%)	4 (4%)	27	47
41	BQ	86/87 (99%)	85 (99%)	1 (1%)	67	78
42	BR	99/99 (100%)	97 (98%)	2 (2%)	50	68
43	BS	89/89 (100%)	89 (100%)	0	100	100
44	BT	84/84 (100%)	82 (98%)	2 (2%)	44	62
45	BU	93/93 (100%)	93 (100%)	0	100	100
46	BV	80/84 (95%)	77 (96%)	3 (4%)	28	49
47	BW	83/84 (99%)	78 (94%)	5 (6%)	16	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	BX	78/78 (100%)	76 (97%)	2 (3%)	41	59
49	BY	56/62 (90%)	55 (98%)	1 (2%)	54	71
50	BZ	67/67 (100%)	66 (98%)	1 (2%)	60	75
51	B1	55/55 (100%)	54 (98%)	1 (2%)	54	71
52	B2	48/48 (100%)	47 (98%)	1 (2%)	48	66
53	B3	47/47 (100%)	44 (94%)	3 (6%)	14	35
54	B4	45/48 (94%)	45 (100%)	0	100	100
55	B5	38/38 (100%)	38 (100%)	0	100	100
56	B6	51/51 (100%)	50 (98%)	1 (2%)	50	68
57	B7	34/34 (100%)	34 (100%)	0	100	100
All	All	4868/5149 (94%)	4704 (97%)	164 (3%)	34	51

5 of 164 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	BI	50	ARG
42	BR	108	ARG
35	BK	18	ASN
36	BL	116	ARG
47	BW	25	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 152 such sidechains are listed below:

Mol	Chain	Res	Type
41	BQ	98	GLN
51	B1	31	GLN
42	BR	74	GLN
46	BV	28	ASN
55	B5	6	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1537/1542 (99%)	163 (10%)	3 (0%)
22	AV	75/76 (98%)	20 (26%)	2 (2%)
22	AW	75/76 (98%)	12 (16%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
23	AX	17/18 (94%)	3 (17%)	0
25	BA	2894/2903 (99%)	293 (10%)	6 (0%)
26	BB	118/119 (99%)	11 (9%)	0
All	All	4716/4734 (99%)	502 (10%)	11 (0%)

5 of 502 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	9	G
1	AA	31	G
1	AA	32	A
1	AA	39	G
1	AA	47	C

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	BA	1645	G
25	BA	1911	U
25	BA	2425	A
25	BA	2157	G
22	AV	73	A

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

4 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	$\# Z > 2$
24	DPP	AY	2	24	4,5,6	0.49	0	1,5,7	0.27	0
24	5OH	AY	6	24	7,12,13	0.62	0	4,16,18	1.76	1 (25%)
24	KBE	AY	1	24	8,8,9	0.56	0	6,8,10	0.90	0
24	UAL	AY	5	24	6,8,9	2.14	2 (33%)	4,9,11	1.62	1 (25%)

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
24	DPP	AY	2	24	-	0/2/4/6	-
24	5OH	AY	6	24	-	0/2/18/20	0/1/1/1
24	KBE	AY	1	24	-	0/7/7/8	-
24	UAL	AY	5	24	-	0/3/7/9	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	AY	5	UAL	C1-N1	-3.78	1.34	1.40
24	AY	5	UAL	C-CA	-3.46	1.39	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AY	6	5OH	CR-CB-CA	-3.18	109.24	112.61
24	AY	5	UAL	O-C-CA	-2.96	121.68	125.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	AY	6	5OH	8	0
24	AY	1	KBE	2	0
24	AY	5	UAL	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
25	BA	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BA	1916:A	O3'	1917:U	P	2.60
1	BA	1911:U	O3'	1912:A	P	1.12

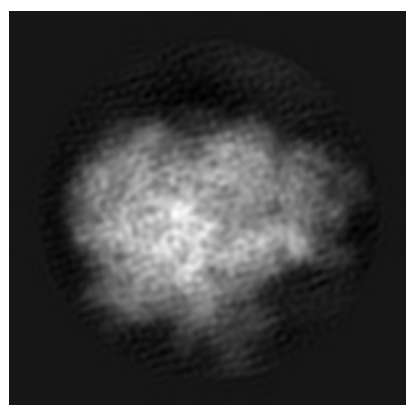
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5799. These allow visual inspection of the internal detail of the map and identification of artifacts.

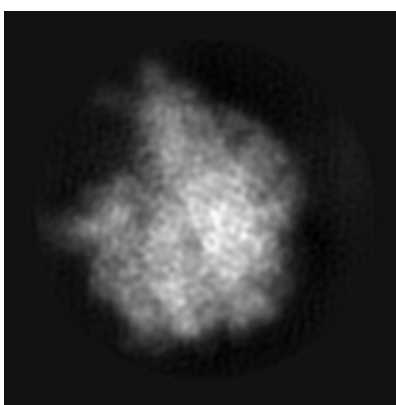
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

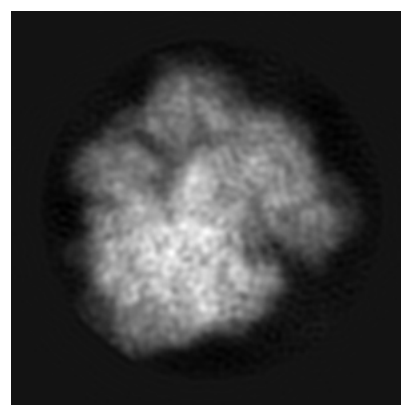
6.1.1 Primary map



X



Y

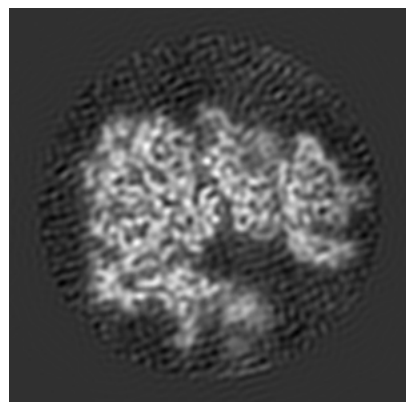


Z

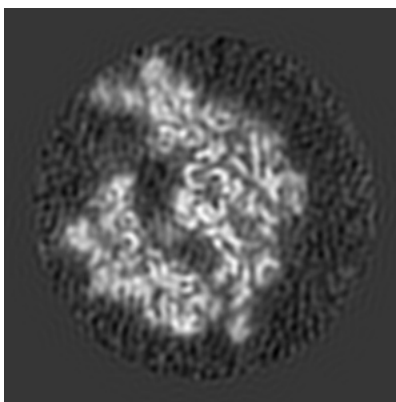
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

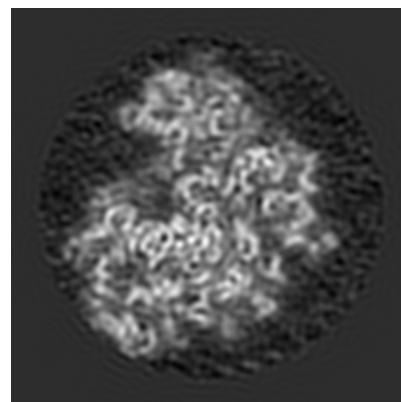
6.2.1 Primary map



X Index: 160



Y Index: 160

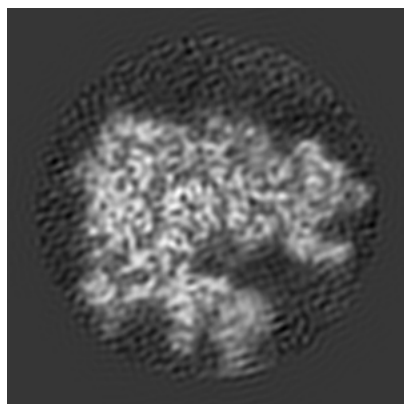


Z Index: 160

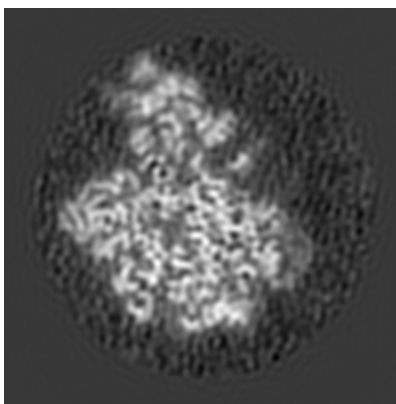
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

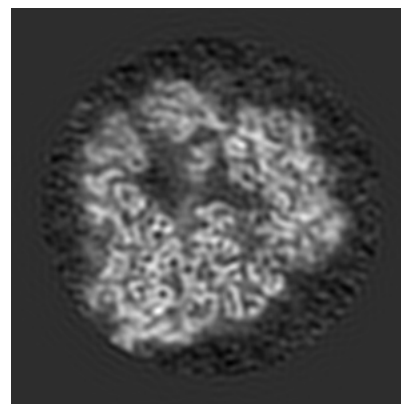
6.3.1 Primary map



X Index: 154



Y Index: 144

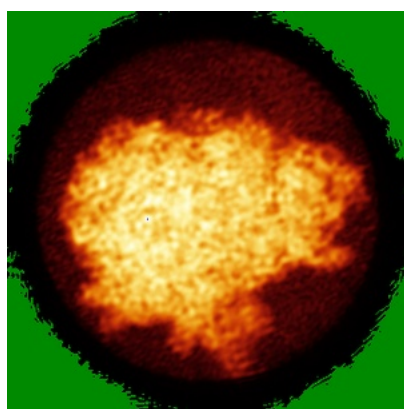


Z Index: 138

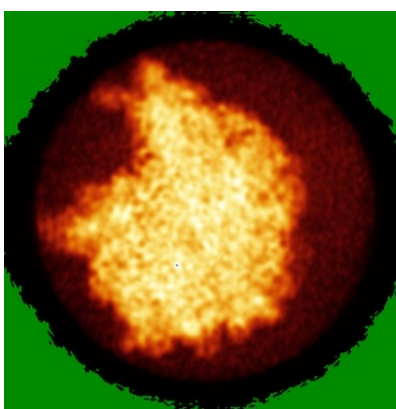
The images above show the largest variance slices of the map in three orthogonal directions.

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

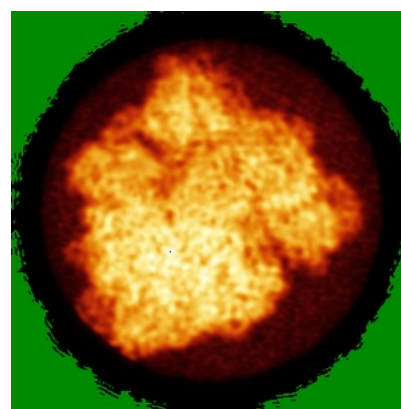
6.4.1 Primary map



X



Y

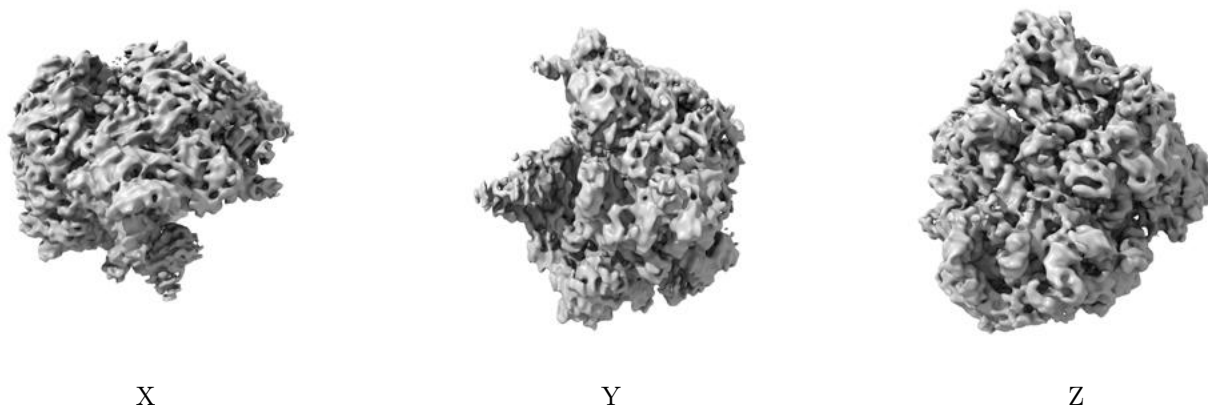


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.32. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

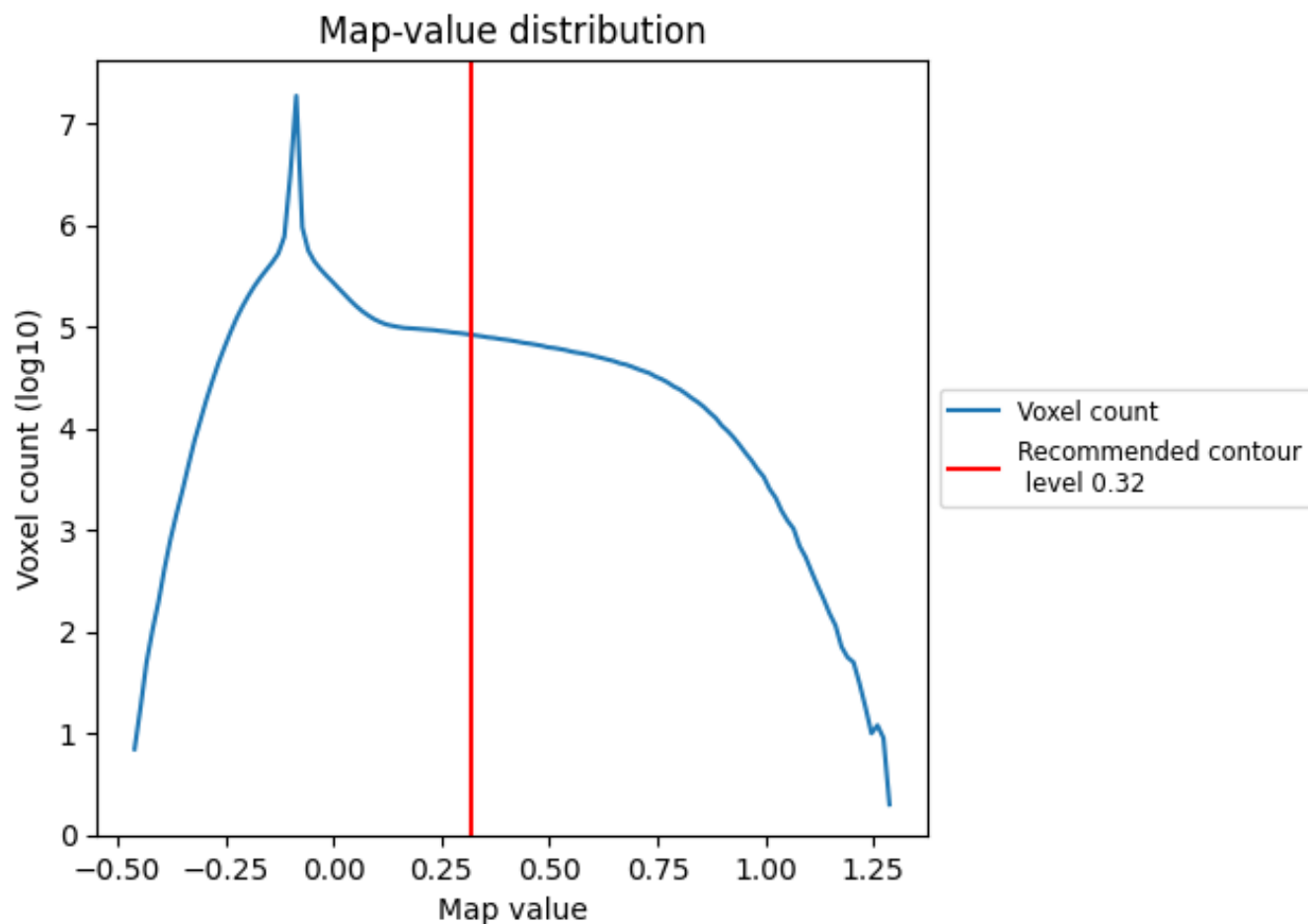
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

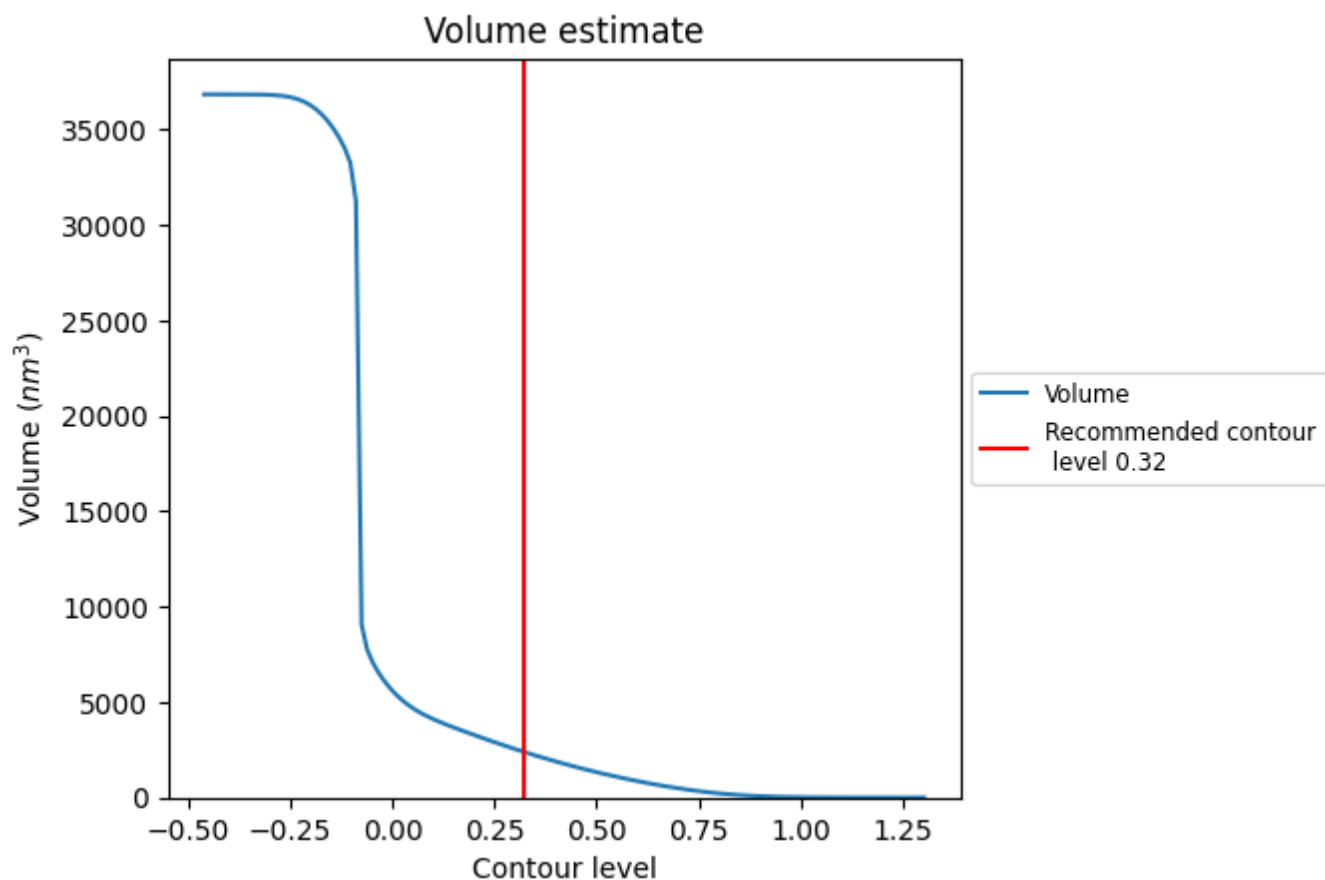
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

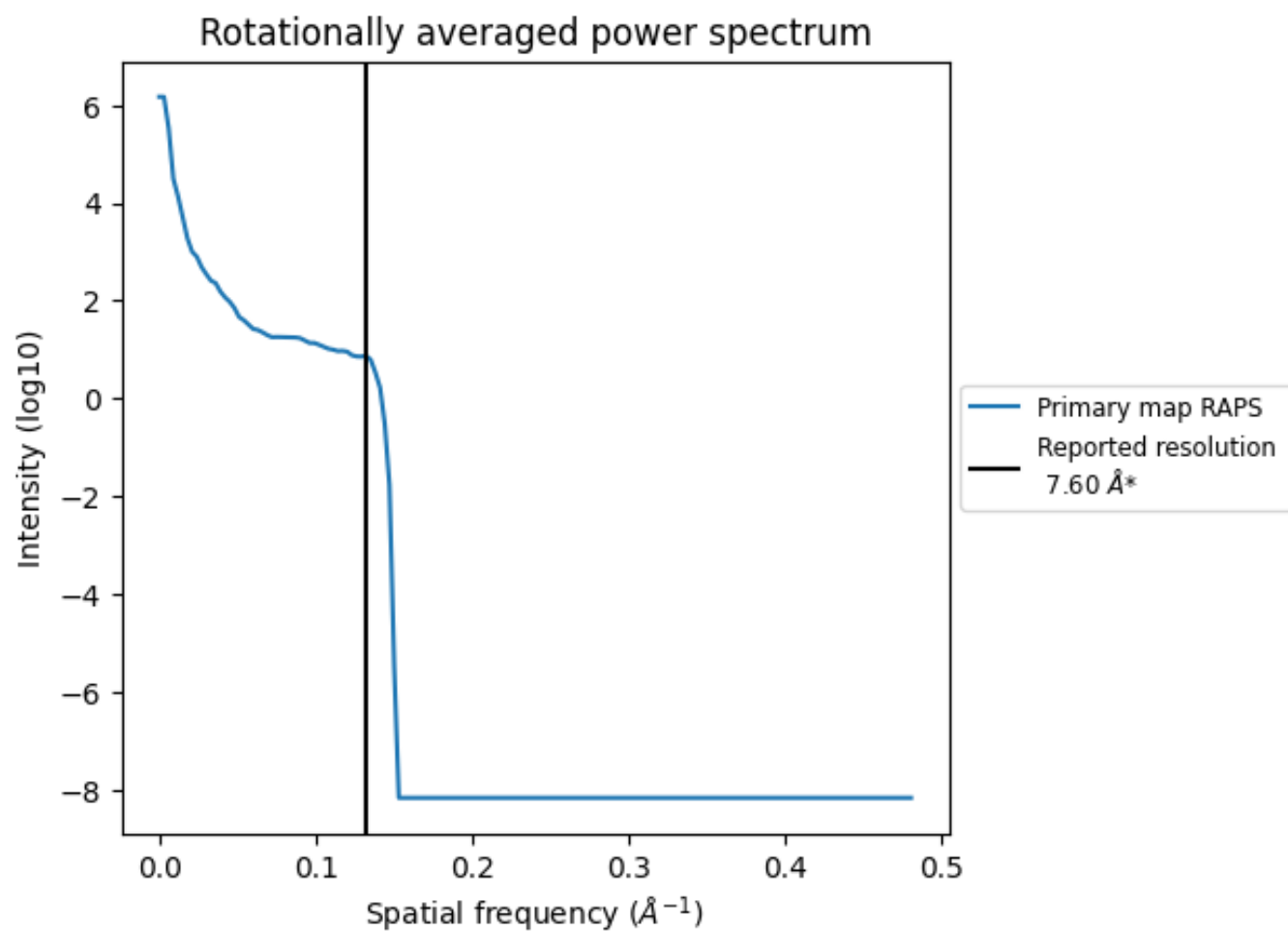
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2409 nm³; this corresponds to an approximate mass of 2176 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 0.132 Å⁻¹

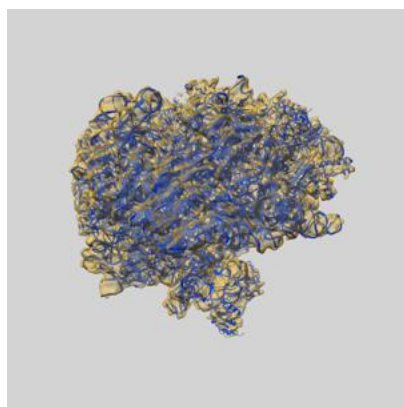
8 Fourier-Shell correlation

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

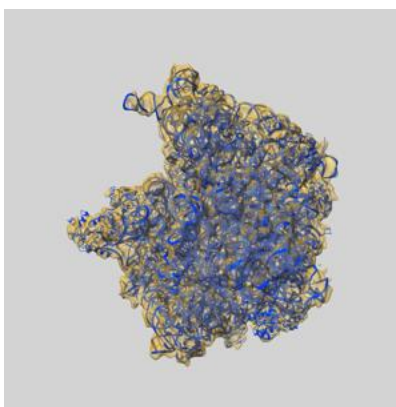
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5799 and PDB model 4V7C. Per-residue inclusion information can be found in section [3](#) on page [15](#).

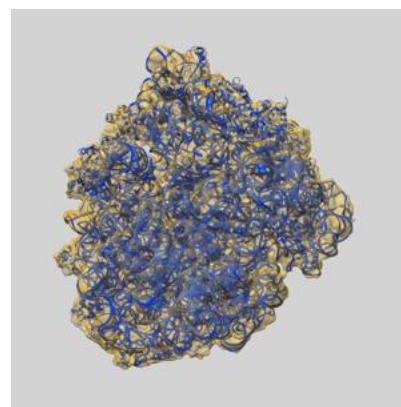
9.1 Map-model overlay [i](#)



X



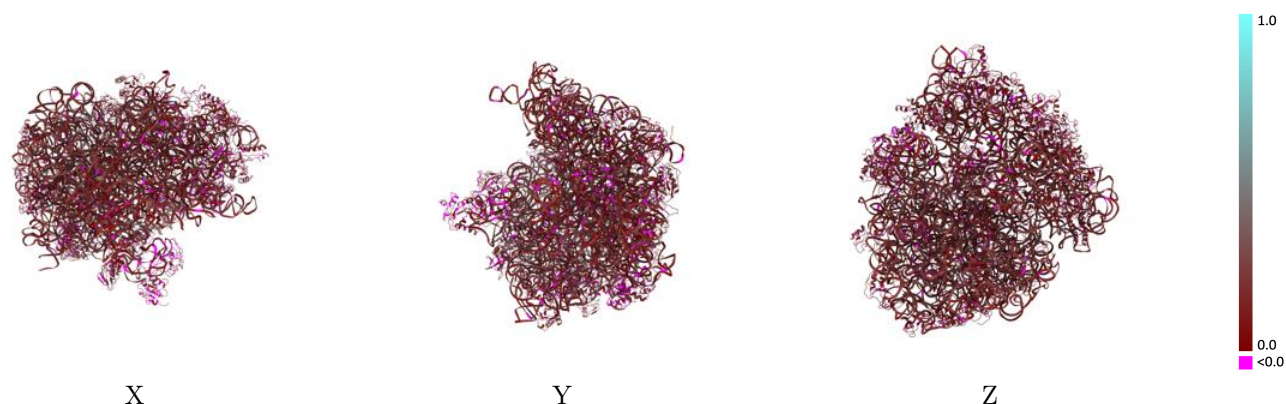
Y



Z

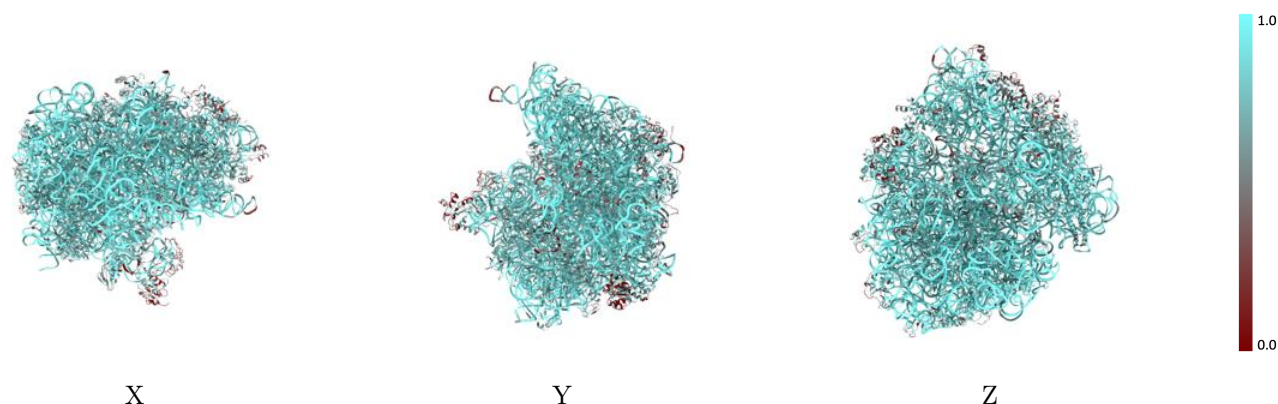
The images above show the 3D surface view of the map at the recommended contour level 0.32 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



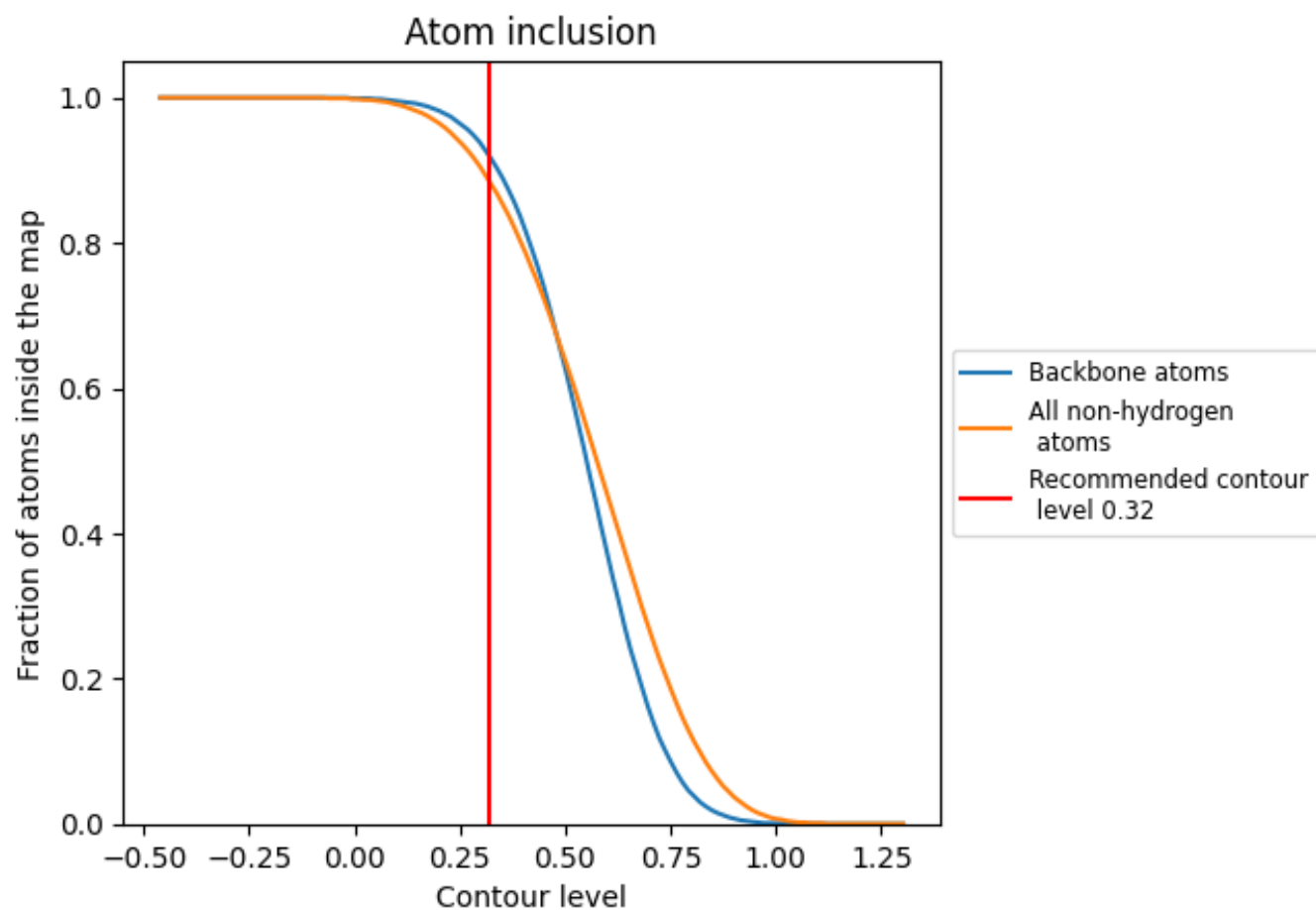
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.32).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 92% of all backbone atoms, 88% 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 (0.32) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8850	 0.1640
AA	 0.9510	 0.1790
AB	 0.4870	 0.1330
AC	 0.6840	 0.1140
AD	 0.7790	 0.1240
AE	 0.7460	 0.1410
AF	 0.6470	 0.1480
AG	 0.7460	 0.1500
AH	 0.7390	 0.1440
AI	 0.8000	 0.1080
AJ	 0.6430	 0.0890
AK	 0.7630	 0.1270
AL	 0.7870	 0.1370
AM	 0.7070	 0.1470
AN	 0.8160	 0.1210
AO	 0.7650	 0.1450
AP	 0.8180	 0.1070
AQ	 0.7610	 0.1190
AR	 0.7520	 0.1290
AS	 0.7570	 0.0980
AT	 0.7920	 0.1500
AU	 0.5940	 0.1420
AV	 0.6730	 0.1250
AW	 0.9350	 0.2010
AX	 0.9090	 0.1630
AY	 0.9580	 0.1680
B1	 0.7260	 0.1340
B2	 0.8310	 0.1480
B3	 0.7940	 0.1240
B4	 0.6110	 0.1100
B5	 0.8990	 0.1220
B6	 0.8450	 0.1130
B7	 0.9450	 0.1070
BA	 0.9660	 0.1880
BB	 0.9580	 0.1790



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Chain	Atom inclusion	Q-score
BC	 0.4040	 0.0770
BD	 0.8660	 0.1290
BE	 0.7810	 0.1150
BF	 0.7570	 0.1190
BG	 0.7700	 0.1220
BH	 0.7520	 0.1310
BI	 0.4680	 0.1260
BJ	 0.3550	 0.0340
BK	 0.3520	 0.0340
BL	 0.8570	 0.1450
BM	 0.7130	 0.1340
BN	 0.7610	 0.1230
BO	 0.7900	 0.1370
BP	 0.8460	 0.1210
BQ	 0.8370	 0.1350
BR	 0.7100	 0.1330
BS	 0.8840	 0.1040
BT	 0.7930	 0.1400
BU	 0.7660	 0.1280
BV	 0.8070	 0.1320
BW	 0.7430	 0.1200
BX	 0.7900	 0.1360
BY	 0.8440	 0.1100
BZ	 0.8040	 0.1200