wwPDB EM Validation Summary Report ⓘ

Nov 8, 2022 – 09:57 AM JST

PDB ID	:	5ZET
EMDB ID	:	EMD-6922
Title	:	M. smegmatis P/P state 50S ribosomal subunit
Authors	:	Mishra, S.; Ahmed, T.; Tyagi, A.; Shi, J.; Bhushan, S.
Deposited on	:	2018-02-28
Resolution	:	3.20 Å(reported)

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

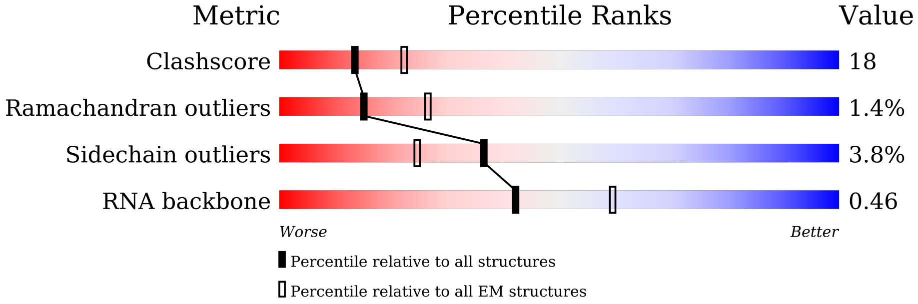
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance ⓘ

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

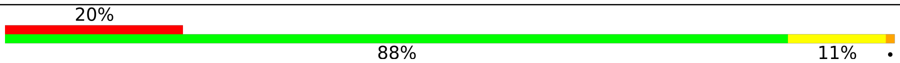
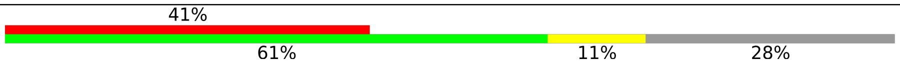
The reported resolution of this entry is 3.20 Å.

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	158937	4297
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 <=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	C	278	
2	D	217	
3	E	215	
4	F	187	
5	G	179	
6	H	151	
7	I	175	

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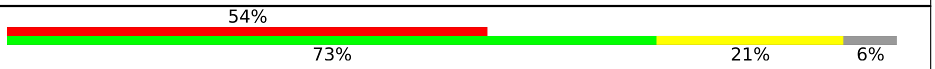
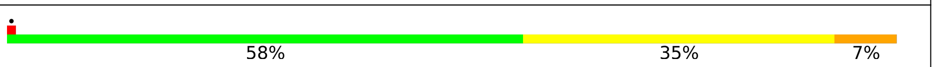
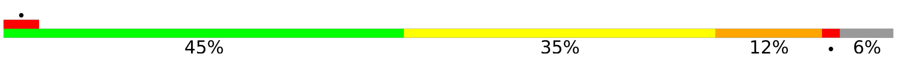
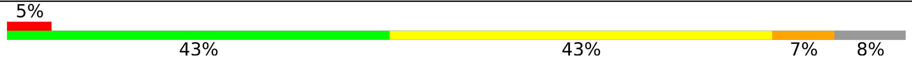
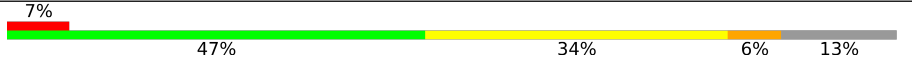
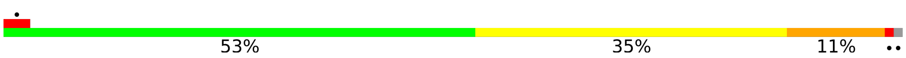
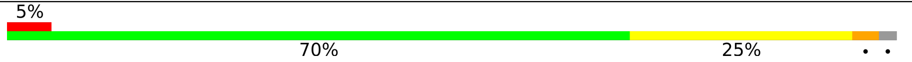
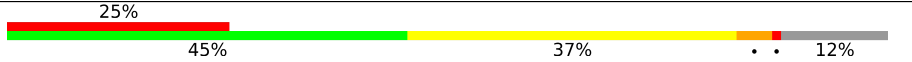
Mol	Chain	Length	Quality of chain
8	J	142	
9	K	147	
10	L	122	
11	M	147	
12	N	138	
13	O	199	
14	P	127	
15	Q	113	
16	R	129	
17	S	103	
18	T	153	
19	U	100	
20	V	105	
21	W	215	
22	X	88	
23	Y	64	
24	Z	77	
25	B	118	
26	A	3120	
27	1	61	
28	2	75	
29	3	57	
30	4	55	
31	5	47	
32	6	64	

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Mol	**Chain**	**Length**	**Quality of chain**
33	7	37	
34	8	24	

2 Entry composition ⓘ

There are 34 unique types of molecules in this entry. The entry contains 97374 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 protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	C	273	2097	1290	435	368	4	0	0

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	D	214	1587	982	310	290	5	0	0

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	E	207	1553	959	292	300	2	0	0

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	F	181	1437	903	269	259	6	0	0

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	G	176	1348	845	249	253	1	0	0

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	H	151	1018	635	188	194	1	0	0

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	I	126	918	580	156	180	2	0	0

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	J	133	990	625	175	187	3	0	0

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	K	147	1138	727	208	201	2	0	0

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	L	121	930	580	178	169	3	0	0

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	M	145	1078	676	205	194	3	0	0

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	N	134	1074	680	211	181	2	0	0

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	O	117	919	577	178	162	2	0	0

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	P	126	956	586	199	171	0	0

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	Q	113	907	570	171	165	1	0	0

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	R	124	988	613	203	172	0	0

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	S	102	768	487	140	141	0	0

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	T	114	873	543	171	159	0	0

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
19	U	94	739	469	135	135	0	0

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	V	97	731	456	137	136	2	0	0

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
21	W	188	1407	869	251	287	0	0

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
22	X	82	604	372	127	105	0	0

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	Y	63	470	283	103	80	4	0	0

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Z	63	527	322	102	102	1	0	0

- Molecule 25 is a RNA chain called P-tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
25	B	117	2501	1116	462	806	117	0	0

- Molecule 26 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
26	A	3102	66623	29694	12253	21574	3102	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
27	1	60	483	298	97	88	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	2	66	510	316	93	96	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	3	54	423	260	93	69	1	0	0

- Molecule 30 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	4	50	416	254	86	72	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	5	45	372	222	96	53	1	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
32	6	63	502	302	115	85	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	7	37	298	181	66	46	5	0	0

- Molecule 34 is a protein called Uncharacterized protein bL37.

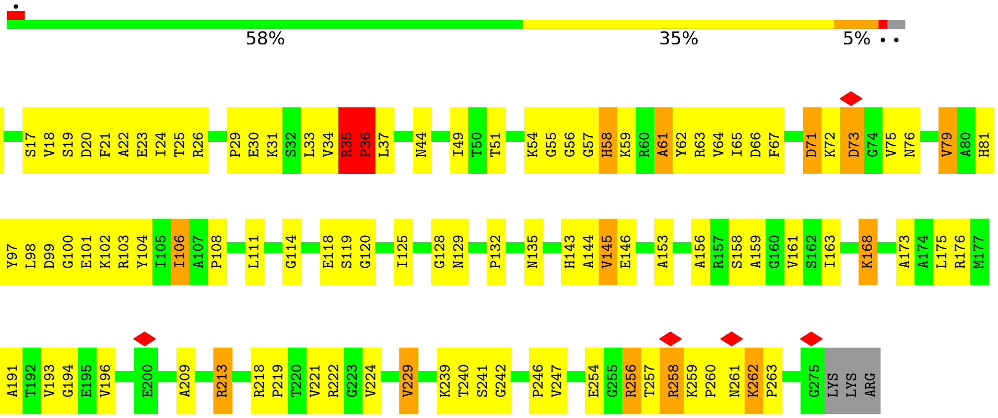
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
34	8	23	189	111	50	28	0	0

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.

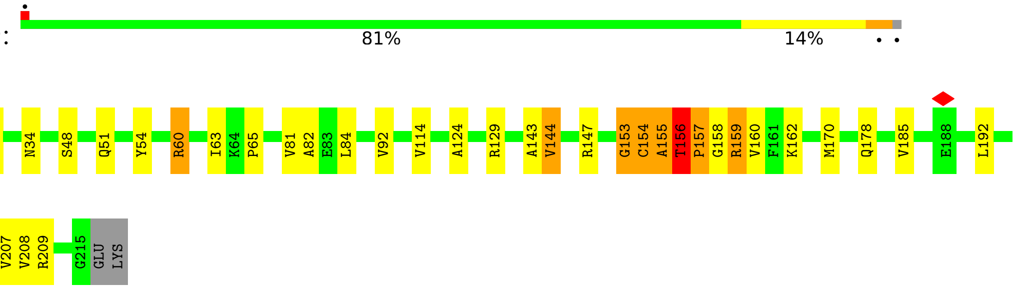
- Molecule 1: 50S ribosomal protein L2

Chain C:



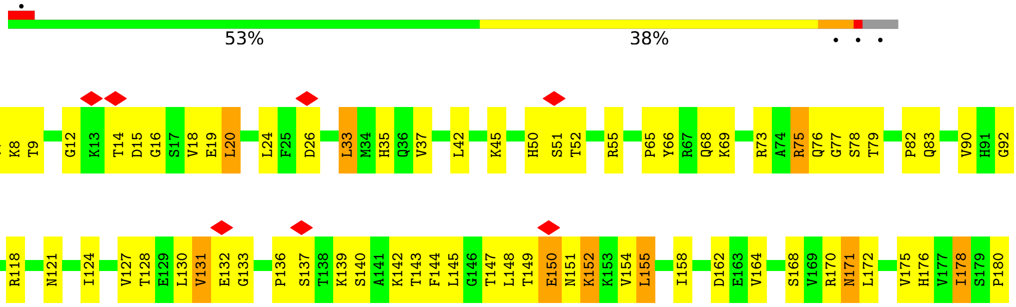
- Molecule 2: 50S ribosomal protein L3

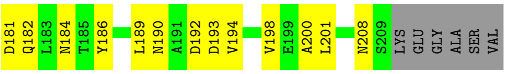
Chain D:



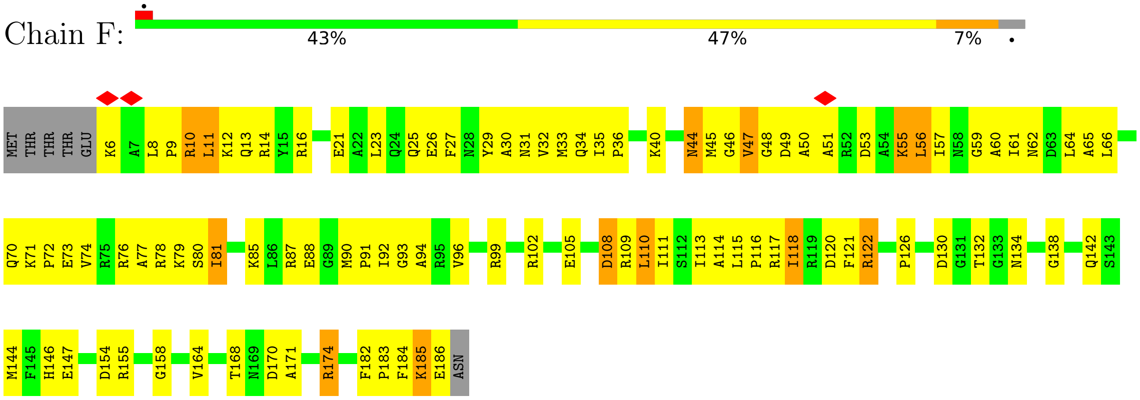
- Molecule 3: 50S ribosomal protein L4

Chain E:

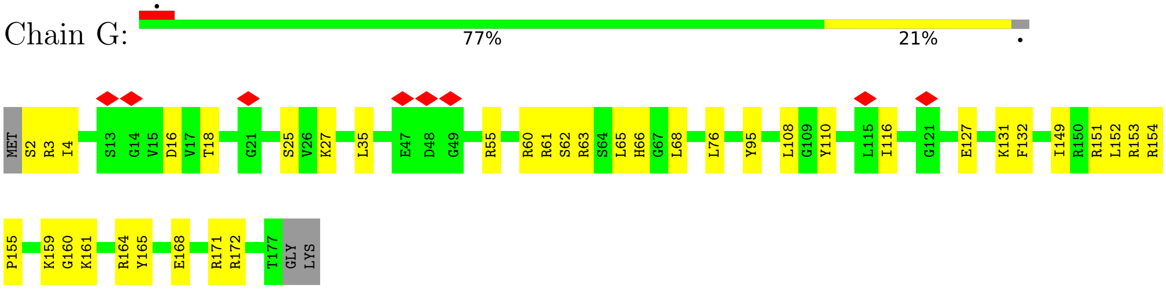




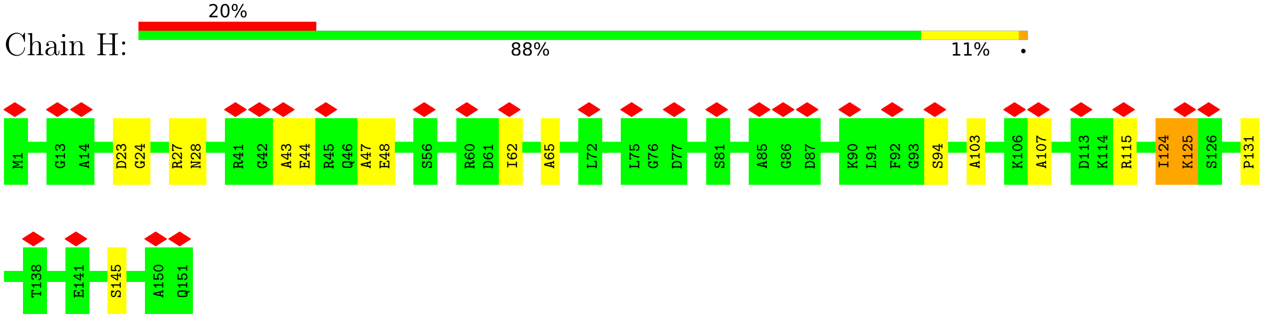
- Molecule 4: 50S ribosomal protein L5



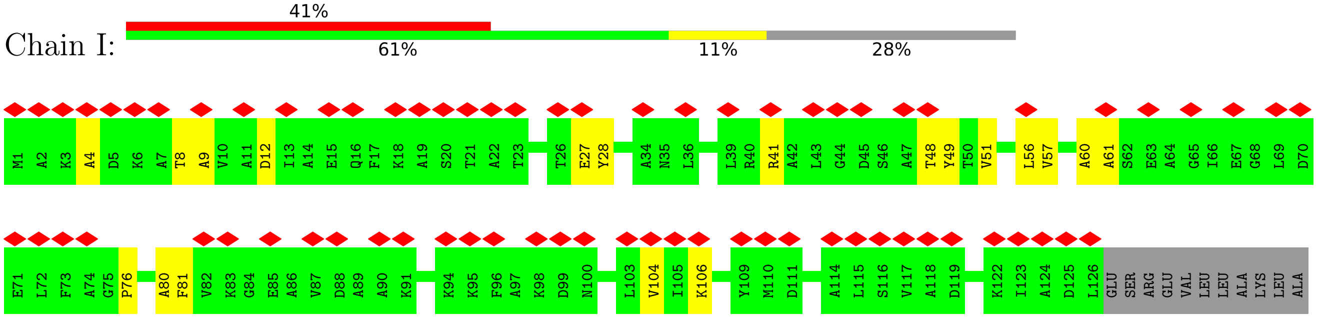
- Molecule 5: 50S ribosomal protein L6



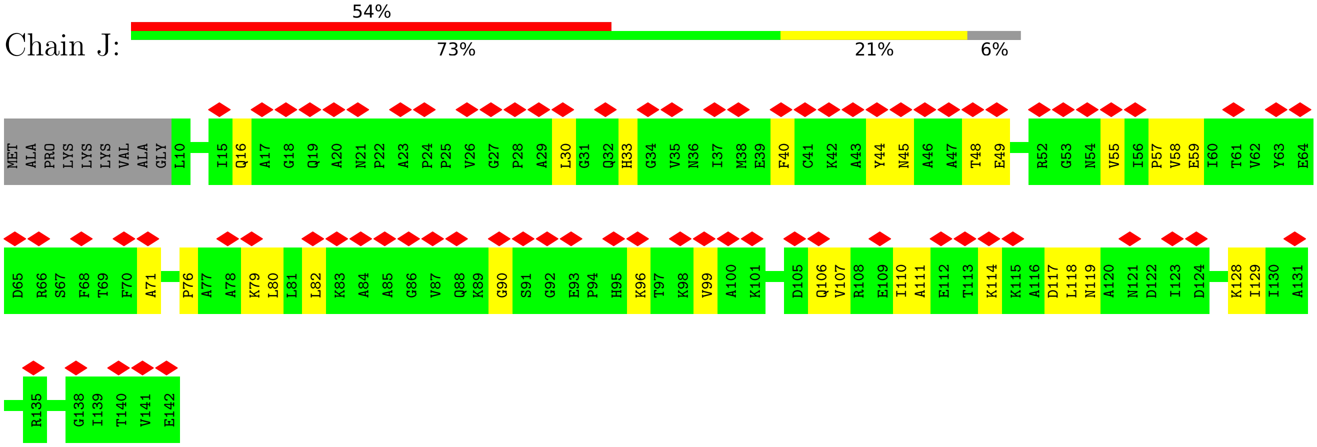
- Molecule 6: 50S ribosomal protein L9



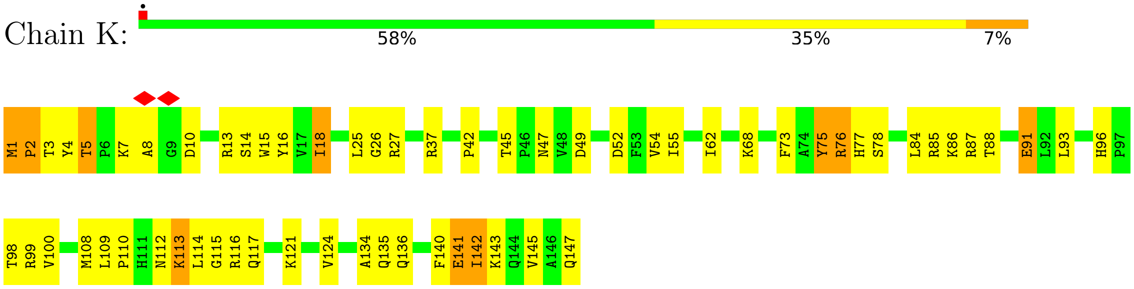
- Molecule 7: 50S ribosomal protein L10



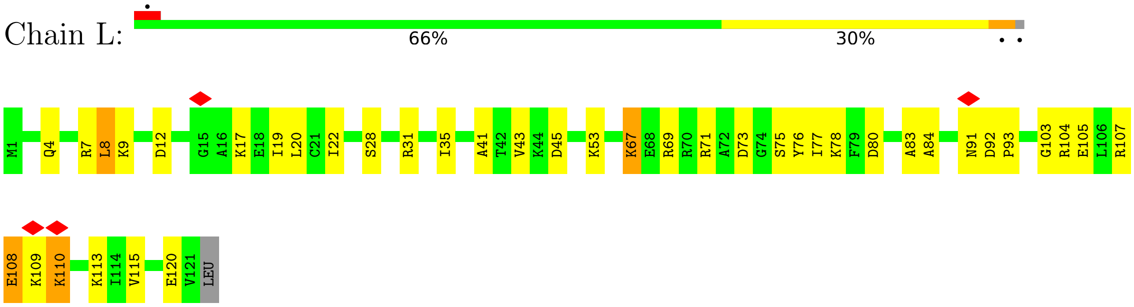
- Molecule 8: 50S ribosomal protein L11



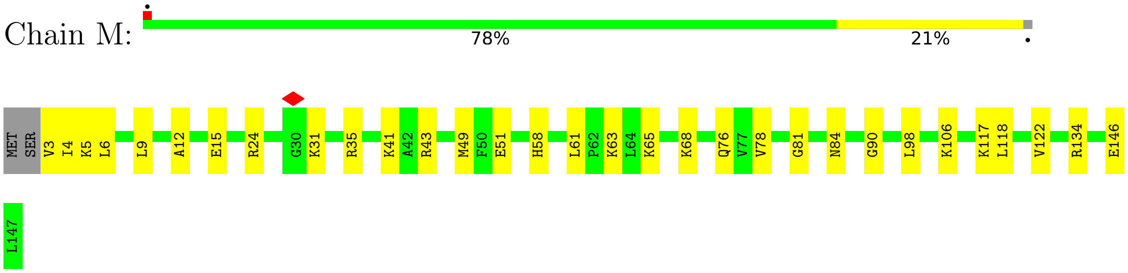
- Molecule 9: 50S ribosomal protein L13



- Molecule 10: 50S ribosomal protein L14

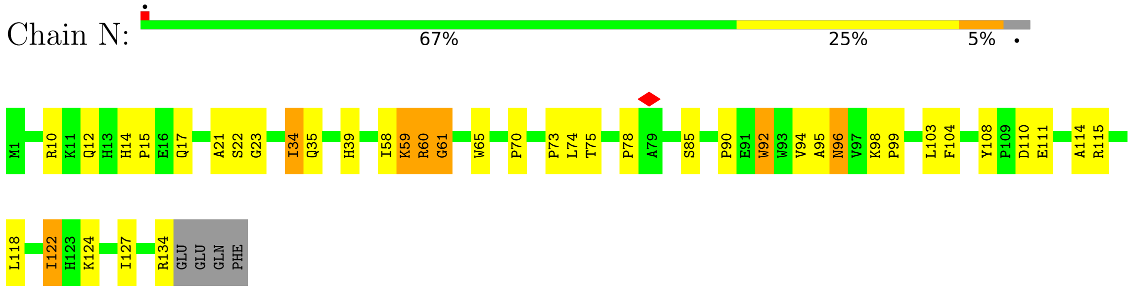


- Molecule 11: 50S ribosomal protein L15



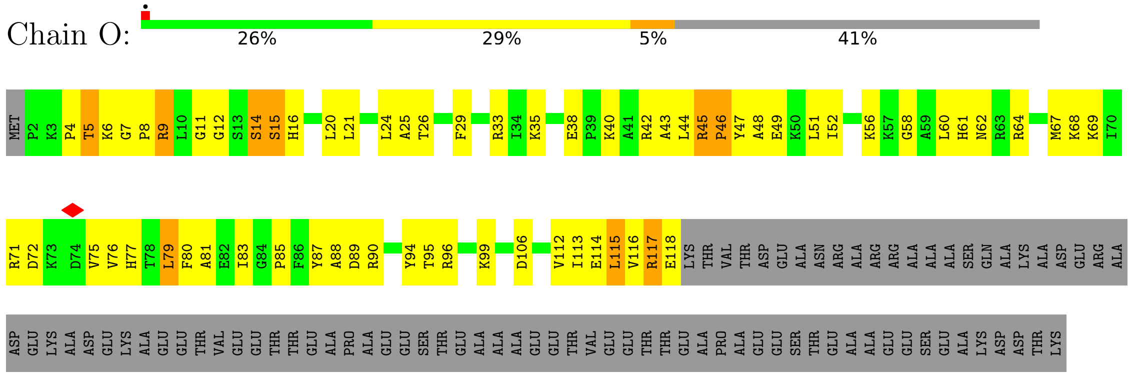
- Molecule 12: 50S ribosomal protein L16

Chain N:



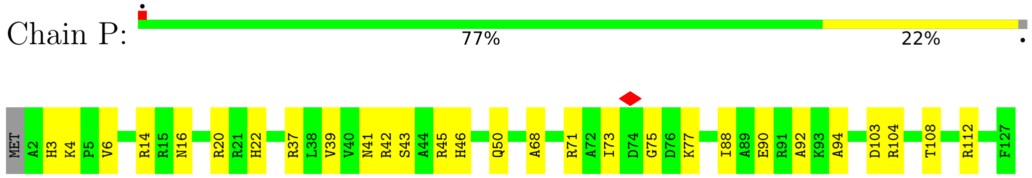
- Molecule 13: 50S ribosomal protein L17

Chain O:



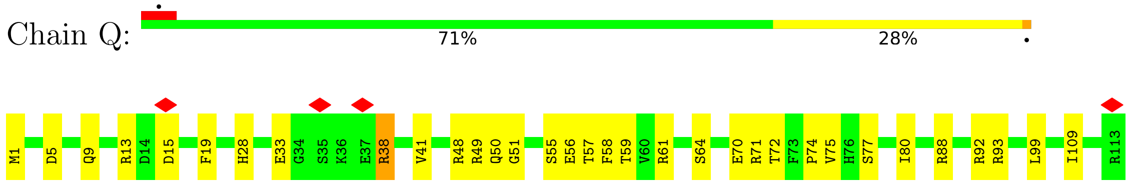
- Molecule 14: 50S ribosomal protein L18

Chain P:



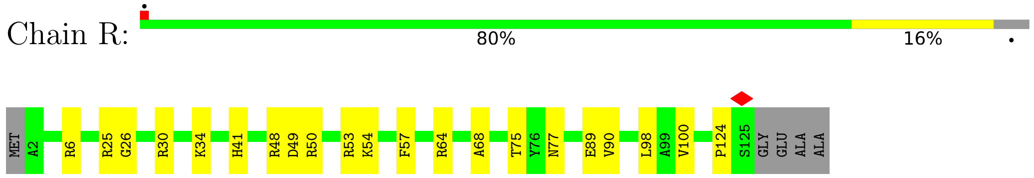
- Molecule 15: 50S ribosomal protein L19

Chain Q:



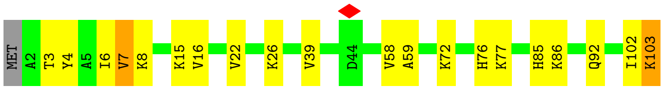
- Molecule 16: 50S ribosomal protein L20

Chain R:

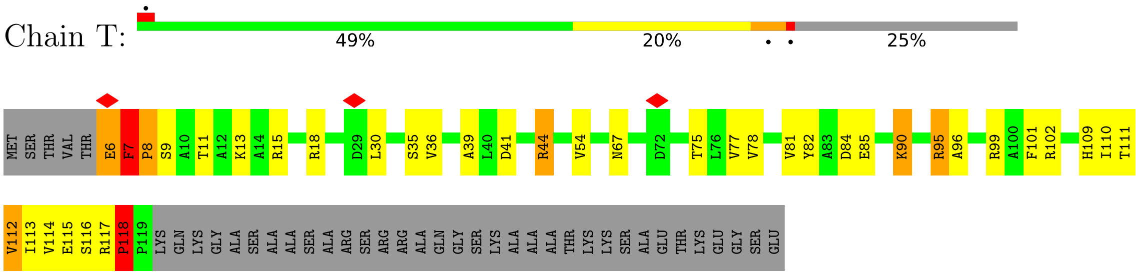


- Molecule 17: 50S ribosomal protein L21

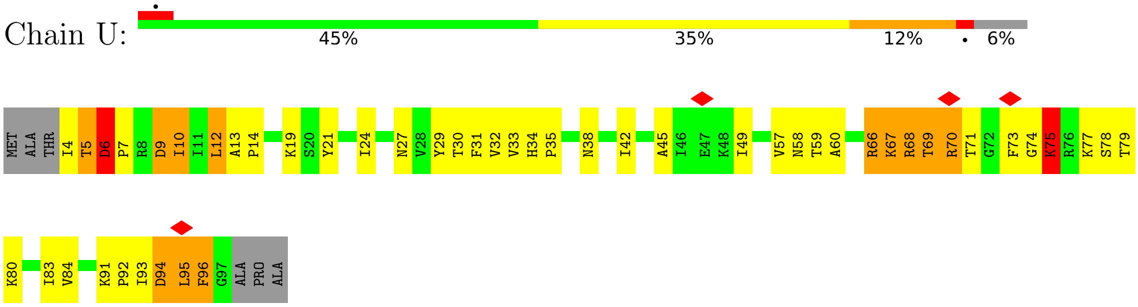
Chain S:



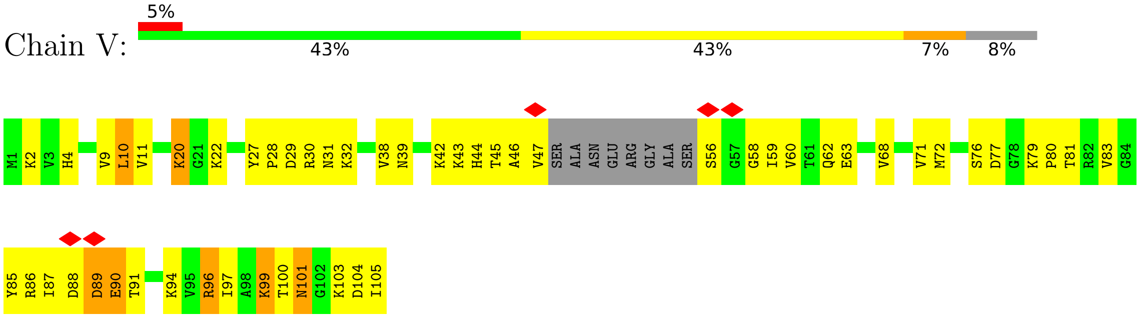
- Molecule 18: 50S ribosomal protein L22



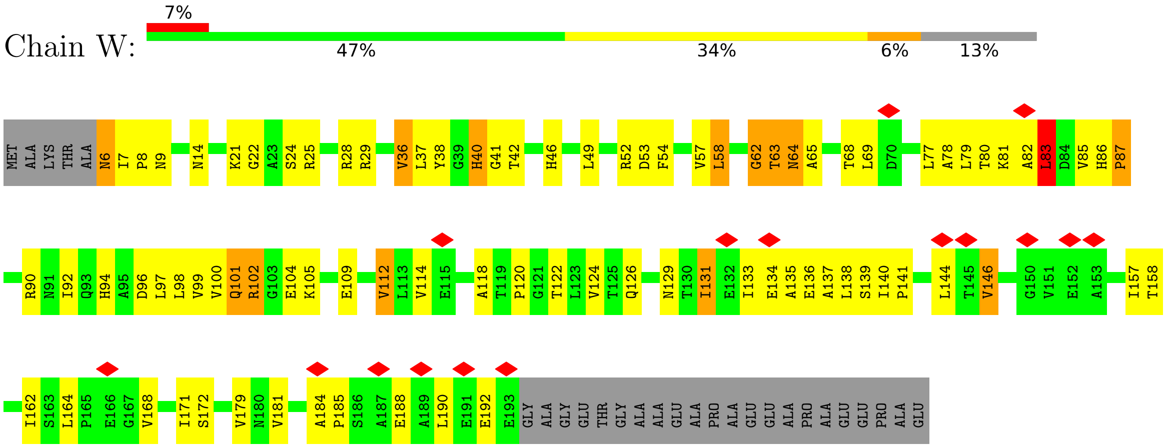
- Molecule 19: 50S ribosomal protein L23



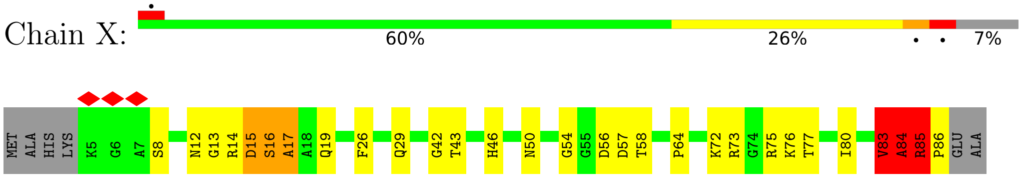
- Molecule 20: 50S ribosomal protein L24



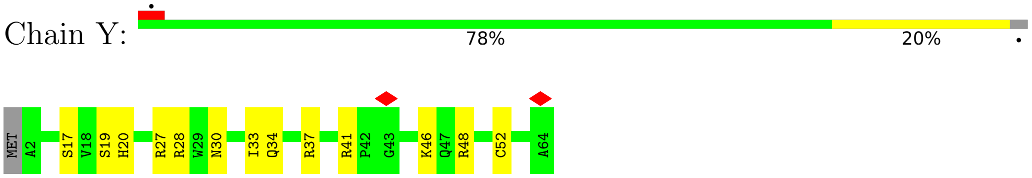
- Molecule 21: 50S ribosomal protein L25



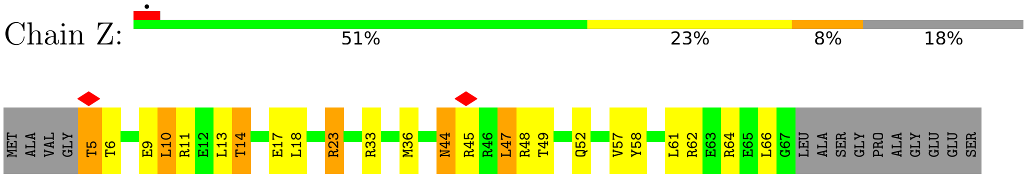
- Molecule 22: 50S ribosomal protein L27



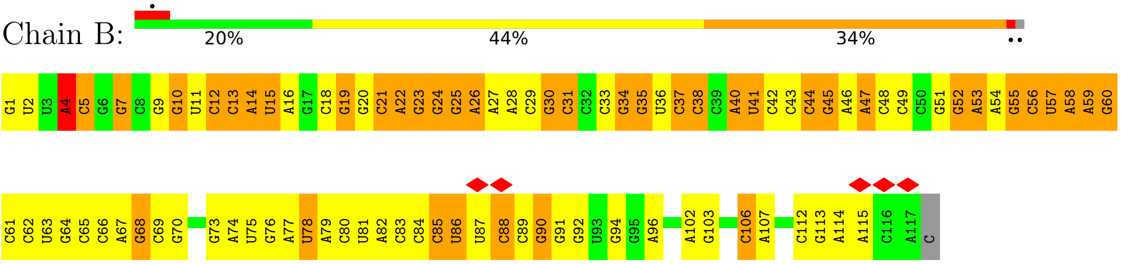
- Molecule 23: 50S ribosomal protein L28



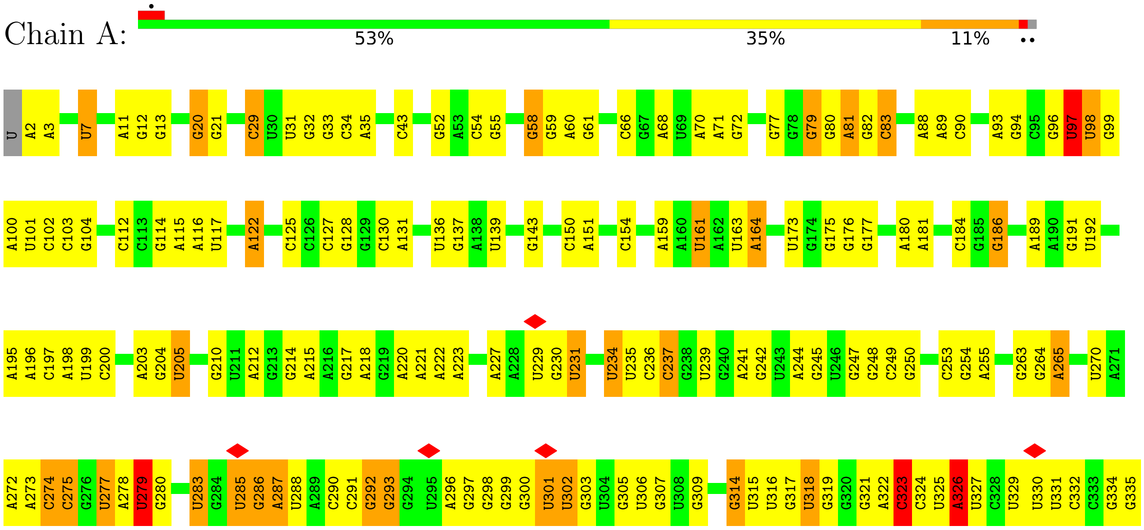
- Molecule 24: 50S ribosomal protein L29

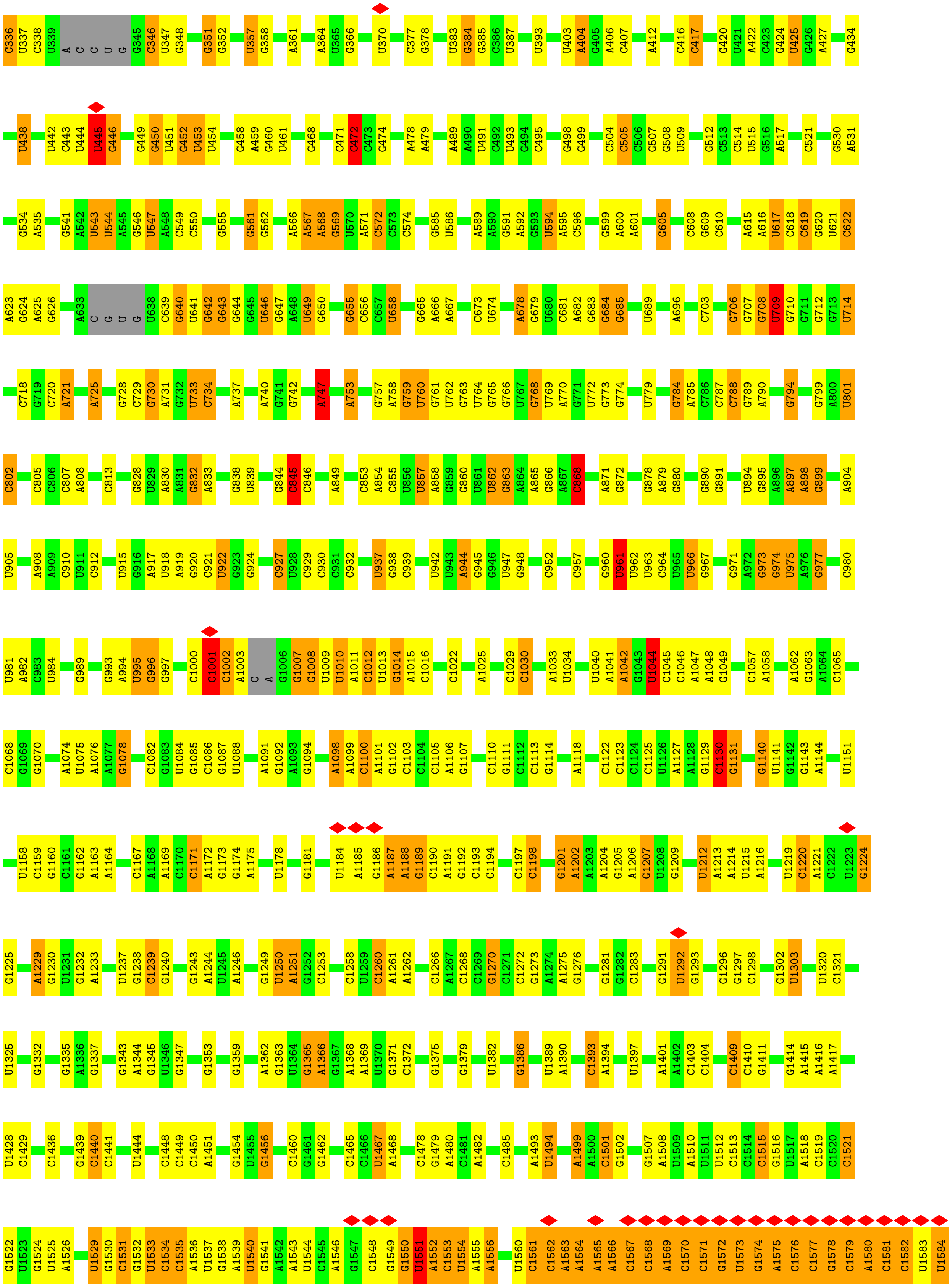


- Molecule 25: P-tRNAfMet



- Molecule 26: 23S rRNA

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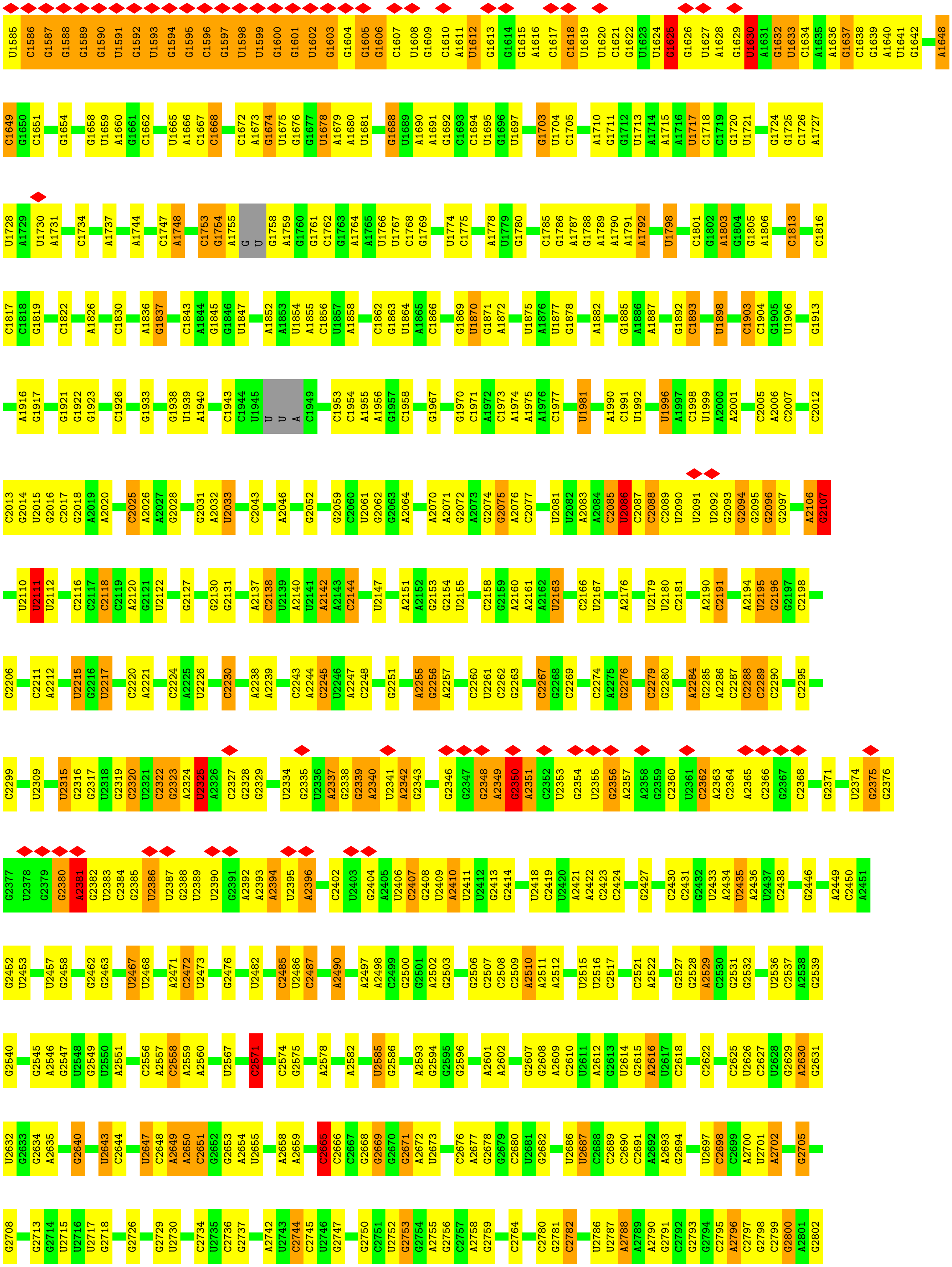
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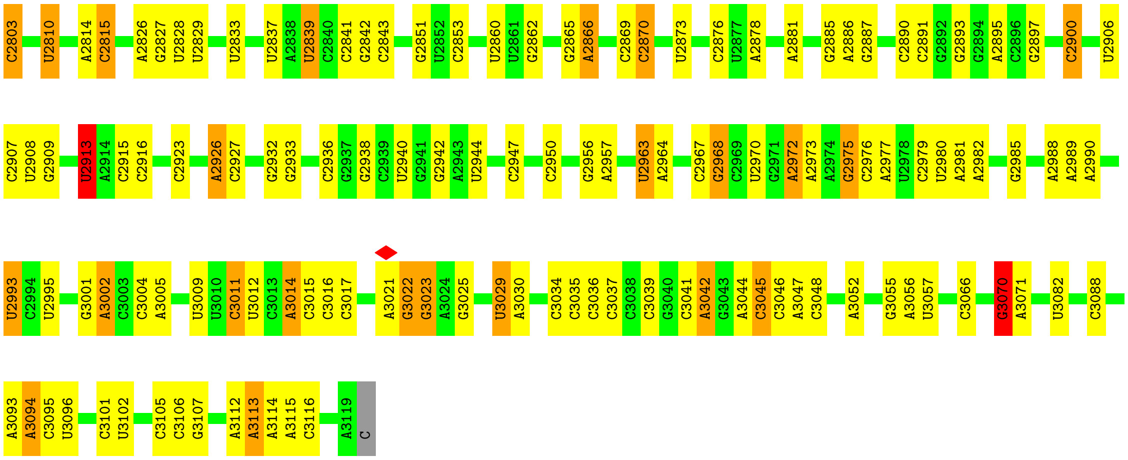
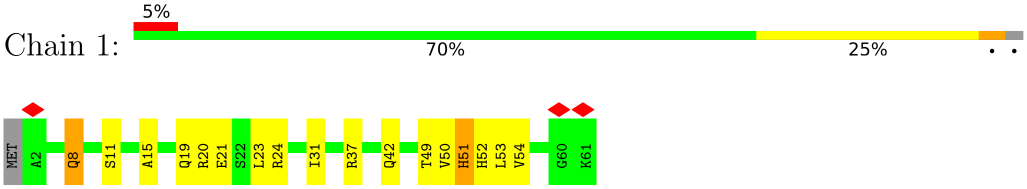
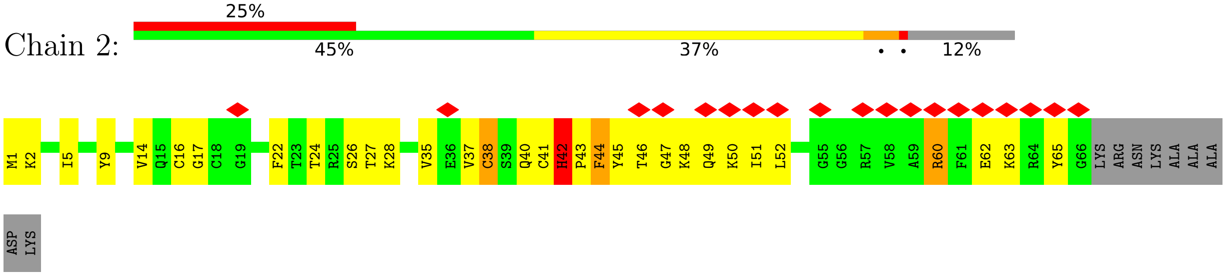


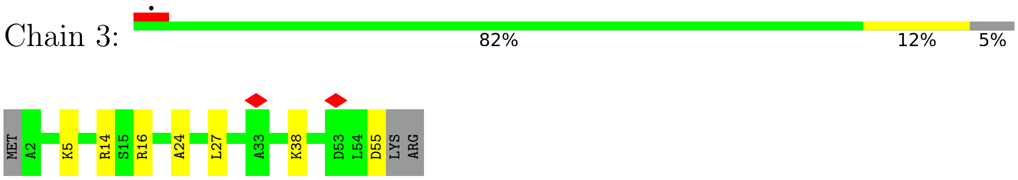
- Molecule 27: 50S ribosomal protein L30



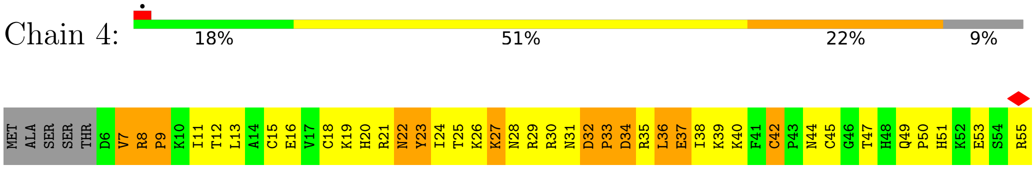
- Molecule 28: 50S ribosomal protein L31



- Molecule 29: 50S ribosomal protein L32



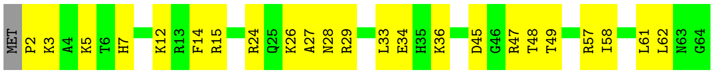
- Molecule 30: 50S ribosomal protein L33 1



- Molecule 31: 50S ribosomal protein L34

- Molecule 32: 50S ribosomal protein L35

Chain 6:

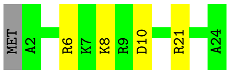


- Molecule 33: 50S ribosomal protein L36

Chain 7:

- Molecule 34: Uncharacterized protein bL37

Chain 8:



4 Experimental information ⓘ

Property	**Value**	**Source**
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	391837	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	1.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.781	Depositor
Minimum map value	-0.495	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	361.19998, 361.19998, 361.19998	wwPDB
Map dimensions	344, 344, 344	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	C	1.01	5/2140 (0.2%)	0.94	5/2879 (0.2%)
2	D	0.55	0/1609	0.66	2/2165 (0.1%)
3	E	0.84	1/1576 (0.1%)	0.87	4/2132 (0.2%)
4	F	0.59	0/1459	0.79	0/1962
5	G	0.36	0/1369	0.57	0/1848
6	H	0.33	0/1027	0.61	1/1398 (0.1%)
7	I	0.29	0/925	0.52	0/1246
8	J	0.29	0/1006	0.60	0/1364
9	K	0.76	1/1165 (0.1%)	0.88	4/1578 (0.3%)
10	L	0.92	0/938	0.95	4/1257 (0.3%)
11	M	0.53	0/1091	0.65	0/1457
12	N	0.91	1/1100 (0.1%)	0.91	2/1482 (0.1%)
13	O	0.75	0/936	0.94	4/1256 (0.3%)
14	P	0.43	0/966	0.57	0/1298
15	Q	0.51	0/921	0.60	1/1236 (0.1%)
16	R	0.55	0/1000	0.58	0/1341
17	S	0.48	0/778	0.57	0/1048
18	T	0.96	1/887 (0.1%)	0.93	3/1204 (0.2%)
19	U	0.74	0/749	0.83	2/1006 (0.2%)
20	V	0.65	0/737	0.78	1/987 (0.1%)
21	W	0.53	0/1422	0.81	4/1941 (0.2%)
22	X	0.94	0/613	0.85	1/821 (0.1%)
23	Y	0.55	0/478	0.70	0/641
24	Z	0.69	0/530	0.75	0/708
25	B	0.56	1/2797 (0.0%)	1.13	18/4357 (0.4%)
26	A	1.00	1/74597 (0.0%)	1.24	633/116386 (0.5%)
27	1	0.80	0/486	0.89	0/651
28	2	0.37	0/520	0.60	1/698 (0.1%)
29	3	0.55	0/427	0.61	0/572
30	4	0.73	1/424 (0.2%)	0.78	2/567 (0.4%)
31	5	0.85	0/375	1.00	1/493 (0.2%)
32	6	0.91	0/507	0.94	2/672 (0.3%)
33	7	0.83	0/302	0.80	0/401
34	8	0.44	0/191	0.60	0/247

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
All	All	0.92	12/106048 (0.0%)	1.14	695/159299 (0.4%)

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	C	0	4
2	D	0	2
3	E	0	5
4	F	0	1
9	K	0	1
12	N	0	1
13	O	0	1
18	T	0	1
22	X	0	2
All	All	0	18

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	B	1	G	OP3-P	-10.43	1.48	1.61
1	C	79	VAL	CB-CG2	-6.92	1.38	1.52
18	T	112	VAL	CB-CG2	-6.68	1.38	1.52
1	C	224	VAL	CB-CG2	-6.23	1.39	1.52
12	N	92	TRP	CB-CG	-6.01	1.39	1.50

The worst 5 of 695 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	A	323	C	N1-C2-O2	11.55	125.83	118.90
26	A	1130	C	N1-C2-O2	11.20	125.62	118.90
26	A	2245	C	N1-C2-O2	11.08	125.55	118.90
26	A	2245	C	C2-N1-C1'	10.64	130.51	118.80
26	A	323	C	C2-N1-C1'	10.56	130.42	118.80

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	144	ALA	Peptide
1	C	229	VAL	Peptide
1	C	246	PRO	Peptide
1	C	61	ALA	Peptide
2	D	153	GLY	Peptide

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	C	2097	0	2147	211	0
2	D	1587	0	1629	66	0
3	E	1553	0	1586	145	0
4	F	1437	0	1463	210	0
5	G	1348	0	1399	27	0
6	H	1018	0	988	12	0
7	I	918	0	959	14	0
8	J	990	0	1021	28	0
9	K	1138	0	1174	115	0
10	L	930	0	989	57	0
11	M	1078	0	1151	46	0
12	N	1074	0	1116	63	0
13	O	919	0	959	151	0
14	P	956	0	989	41	0
15	Q	907	0	938	30	0
16	R	988	0	1038	19	0
17	S	768	0	820	46	0
18	T	873	0	909	57	0
19	U	739	0	777	119	0
20	V	731	0	782	114	0
21	W	1407	0	1423	155	0
22	X	604	0	622	56	0
23	Y	470	0	484	9	0
24	Z	527	0	537	54	0
25	B	2501	0	1269	297	0
26	A	66623	0	33514	1028	0
27	1	483	0	513	22	0
28	2	510	0	497	61	0
29	3	423	0	463	12	0

Continued on next page...

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	4	416	0	421	95	0
31	5	372	0	406	41	0
32	6	502	0	541	32	0
33	7	298	0	320	25	0
34	8	189	0	205	4	0
All	All	97374	0	64049	2838	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 18.

The worst 5 of 2838 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)
17:S:3:THR:CG2	17:S:102:ILE:HD13	1.26	1.66
19:U:83:ILE:HD11	26:A:1456:G:C2	1.14	1.64
26:A:1561:C:C4	26:A:1562:C:C5	1.86	1.62
26:A:1565:A:N3	26:A:1606:G:C5	1.69	1.60
17:S:58:VAL:HG23	17:S:103:LYS:CG	1.24	1.60

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	271/278 (98%)	233 (86%)	33 (12%)	5 (2%)	8	41
2	D	212/217 (98%)	199 (94%)	11 (5%)	2 (1%)	17	56
3	E	205/215 (95%)	179 (87%)	20 (10%)	6 (3%)	4	28
4	F	179/187 (96%)	162 (90%)	15 (8%)	2 (1%)	14	51
5	G	174/179 (97%)	166 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	H	149/151 (99%)	139 (93%)	9 (6%)	1 (1%)	22	61
7	I	124/175 (71%)	118 (95%)	6 (5%)	0	100	100
8	J	131/142 (92%)	118 (90%)	13 (10%)	0	100	100
9	K	145/147 (99%)	133 (92%)	9 (6%)	3 (2%)	7	37
10	L	119/122 (98%)	107 (90%)	12 (10%)	0	100	100
11	M	143/147 (97%)	128 (90%)	15 (10%)	0	100	100
12	N	132/138 (96%)	113 (86%)	19 (14%)	0	100	100
13	O	115/199 (58%)	102 (89%)	10 (9%)	3 (3%)	5	31
14	P	124/127 (98%)	119 (96%)	5 (4%)	0	100	100
15	Q	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
16	R	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
17	S	100/103 (97%)	94 (94%)	5 (5%)	1 (1%)	15	54
18	T	112/153 (73%)	103 (92%)	6 (5%)	3 (3%)	5	30
19	U	92/100 (92%)	70 (76%)	16 (17%)	6 (6%)	1	10
20	V	93/105 (89%)	83 (89%)	8 (9%)	2 (2%)	6	35
21	W	186/215 (86%)	171 (92%)	10 (5%)	5 (3%)	5	30
22	X	80/88 (91%)	61 (76%)	13 (16%)	6 (8%)	1	7
23	Y	61/64 (95%)	57 (93%)	4 (7%)	0	100	100
24	Z	61/77 (79%)	59 (97%)	1 (2%)	1 (2%)	9	43
27	1	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
28	2	64/75 (85%)	61 (95%)	2 (3%)	1 (2%)	9	43
29	3	52/57 (91%)	51 (98%)	1 (2%)	0	100	100
30	4	48/55 (87%)	37 (77%)	7 (15%)	4 (8%)	1	5
31	5	43/47 (92%)	41 (95%)	2 (5%)	0	100	100
32	6	61/64 (95%)	54 (88%)	7 (12%)	0	100	100
33	7	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
34	8	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
All	All	3623/3991 (91%)	3287 (91%)	285 (8%)	51 (1%)	15	46

5 of 51 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	58	HIS

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Mol	Chain	Res	Type
1	C	145	VAL
1	C	262	LYS
3	E	94	LYS
3	E	152	LYS

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	
1	C	214/218 (98%)	207 (97%)	7 (3%)	38	71
2	D	160/163 (98%)	155 (97%)	5 (3%)	40	72
3	E	167/173 (96%)	158 (95%)	9 (5%)	22	58
4	F	150/156 (96%)	137 (91%)	13 (9%)	10	37
5	G	148/150 (99%)	148 (100%)	0	100	100
6	H	90/116 (78%)	90 (100%)	0	100	100
7	I	89/120 (74%)	89 (100%)	0	100	100
8	J	102/108 (94%)	102 (100%)	0	100	100
9	K	120/120 (100%)	116 (97%)	4 (3%)	38	71
10	L	99/100 (99%)	97 (98%)	2 (2%)	55	80
11	M	112/114 (98%)	111 (99%)	1 (1%)	78	91
12	N	112/116 (97%)	107 (96%)	5 (4%)	27	63
13	O	96/158 (61%)	91 (95%)	5 (5%)	23	59
14	P	93/94 (99%)	93 (100%)	0	100	100
15	Q	100/100 (100%)	99 (99%)	1 (1%)	76	90
16	R	97/99 (98%)	96 (99%)	1 (1%)	76	90
17	S	82/83 (99%)	81 (99%)	1 (1%)	71	88
18	T	90/117 (77%)	86 (96%)	4 (4%)	28	64
19	U	82/85 (96%)	71 (87%)	11 (13%)	4	18
20	V	81/86 (94%)	75 (93%)	6 (7%)	13	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	W	154/168 (92%)	139 (90%)	15 (10%)	8	31
22	X	59/63 (94%)	58 (98%)	1 (2%)	60	83
23	Y	50/51 (98%)	50 (100%)	0	100	100
24	Z	58/66 (88%)	53 (91%)	5 (9%)	10	38
27	1	53/54 (98%)	51 (96%)	2 (4%)	33	67
28	2	57/63 (90%)	54 (95%)	3 (5%)	22	58
29	3	43/46 (94%)	43 (100%)	0	100	100
30	4	48/52 (92%)	40 (83%)	8 (17%)	2	10
31	5	35/36 (97%)	33 (94%)	2 (6%)	20	56
32	6	53/54 (98%)	53 (100%)	0	100	100
33	7	35/35 (100%)	33 (94%)	2 (6%)	20	56
34	8	18/19 (95%)	18 (100%)	0	100	100
All	All	2947/3183 (93%)	2834 (96%)	113 (4%)	36	67

5 of 113 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	T	118	PRO
31	5	27	THR
20	V	39	ASN
31	5	6	ARG
28	2	44	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
30	4	20	HIS
30	4	49	GLN
34	8	17	ASN
10	L	4	GLN
9	K	135	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	B	116/118 (98%)	42 (36%)	3 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	A	3096/3120 (99%)	788 (25%)	44 (1%)
All	All	3212/3238 (99%)	830 (25%)	47 (1%)

5 of 830 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
25	B	4	A
25	B	5	C
25	B	7	G
25	B	10	G
25	B	12	C

5 of 47 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	A	1575	A
26	A	1590	G
26	A	1576	C
26	A	1579	C
26	A	1596	C

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

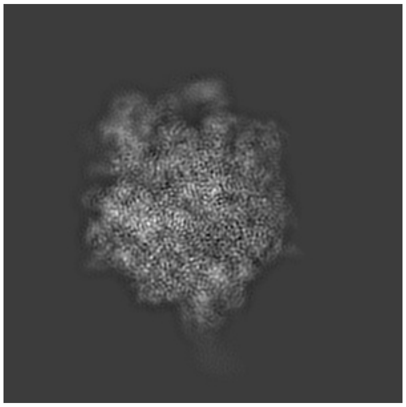
6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-6922. These allow visual inspection of the internal detail of the map and identification of artifacts.

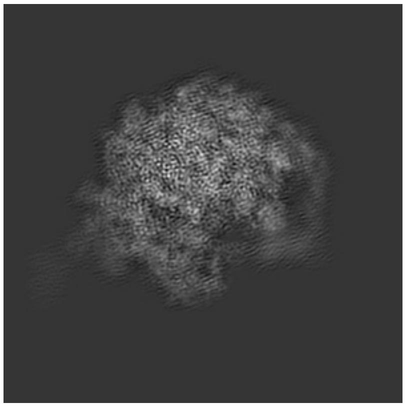
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections ⓘ

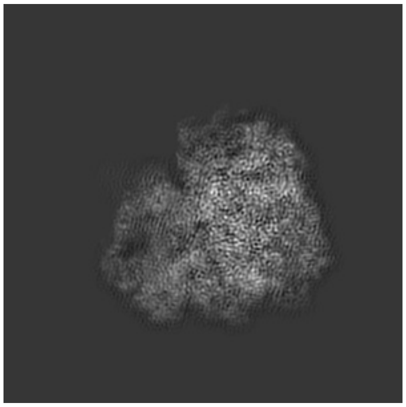
6.1.1 Primary map



X



Y

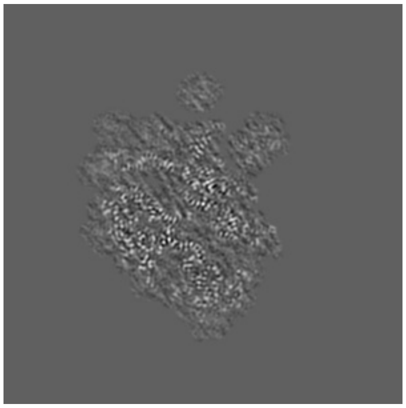


Z

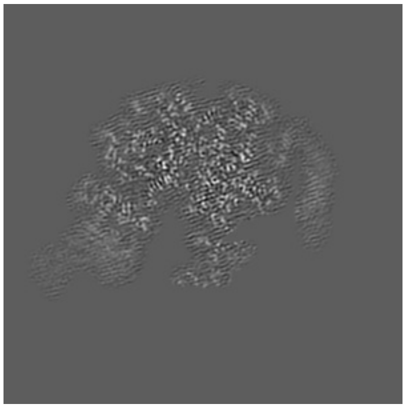
The images above show the map projected in three orthogonal directions.

6.2 Central slices ⓘ

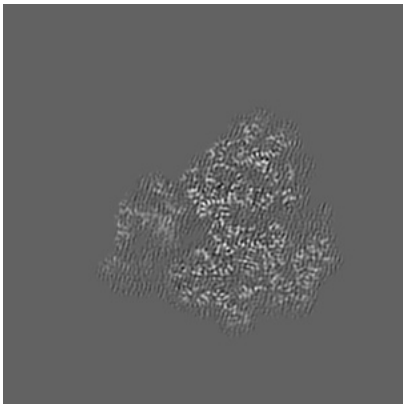
6.2.1 Primary map



X Index: 172



Y Index: 172

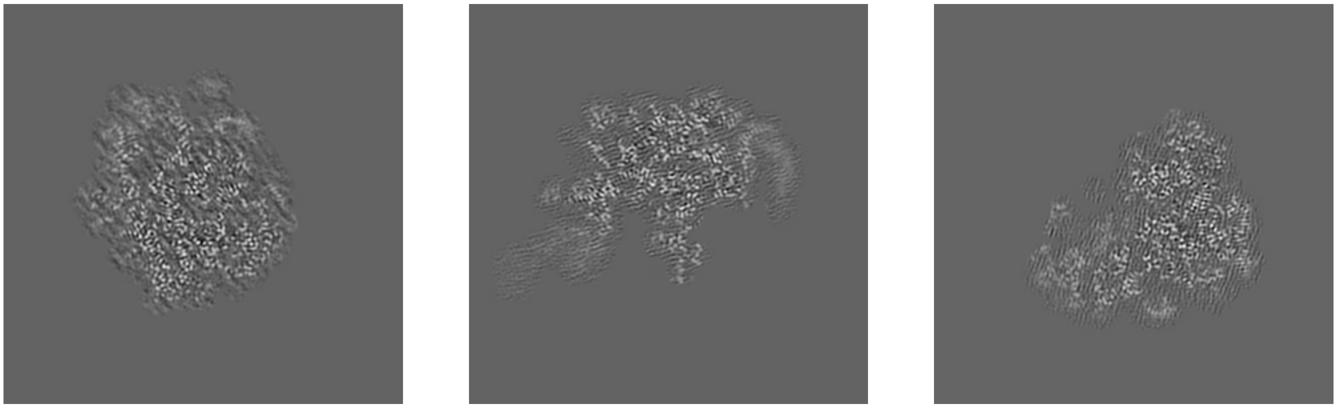


Z Index: 172

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

6.3 Largest variance slices

6.3.1 Primary map



X Index: 205

Y Index: 181

Z Index: 154

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

6.4 Orthogonal surface views

6.4.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

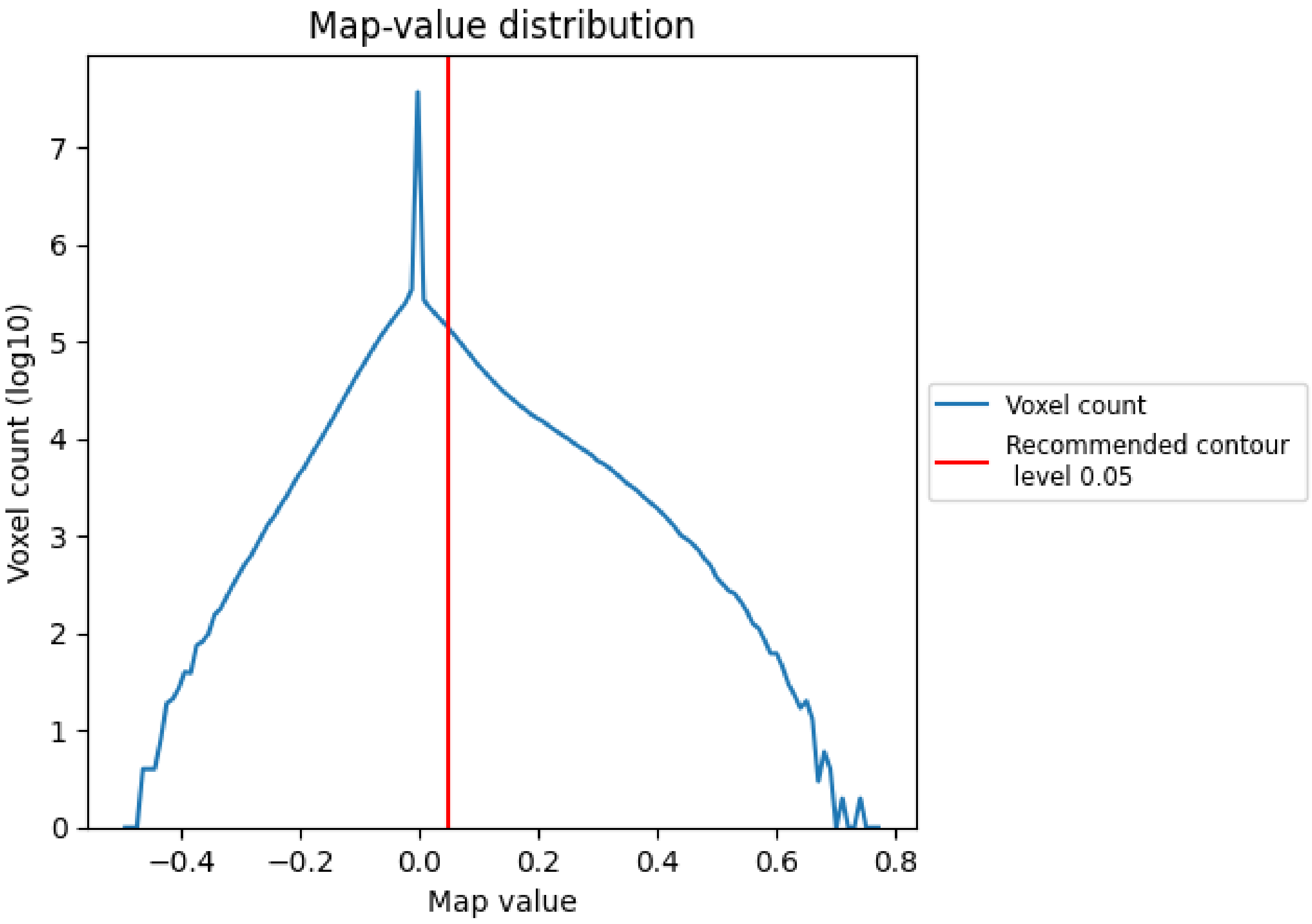
6.5 Mask visualisation ⓘ

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

7 Map analysis ⓘ

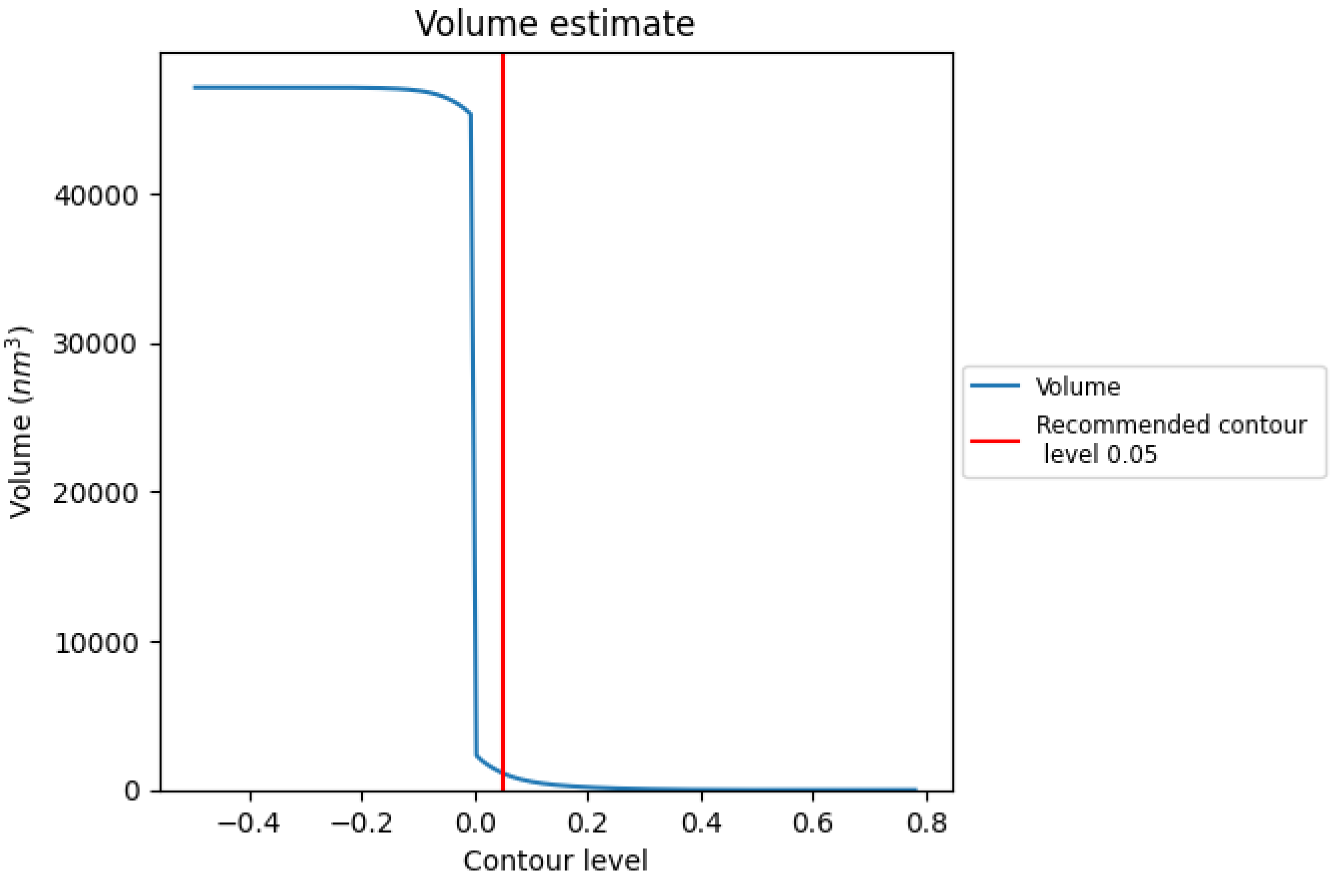
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

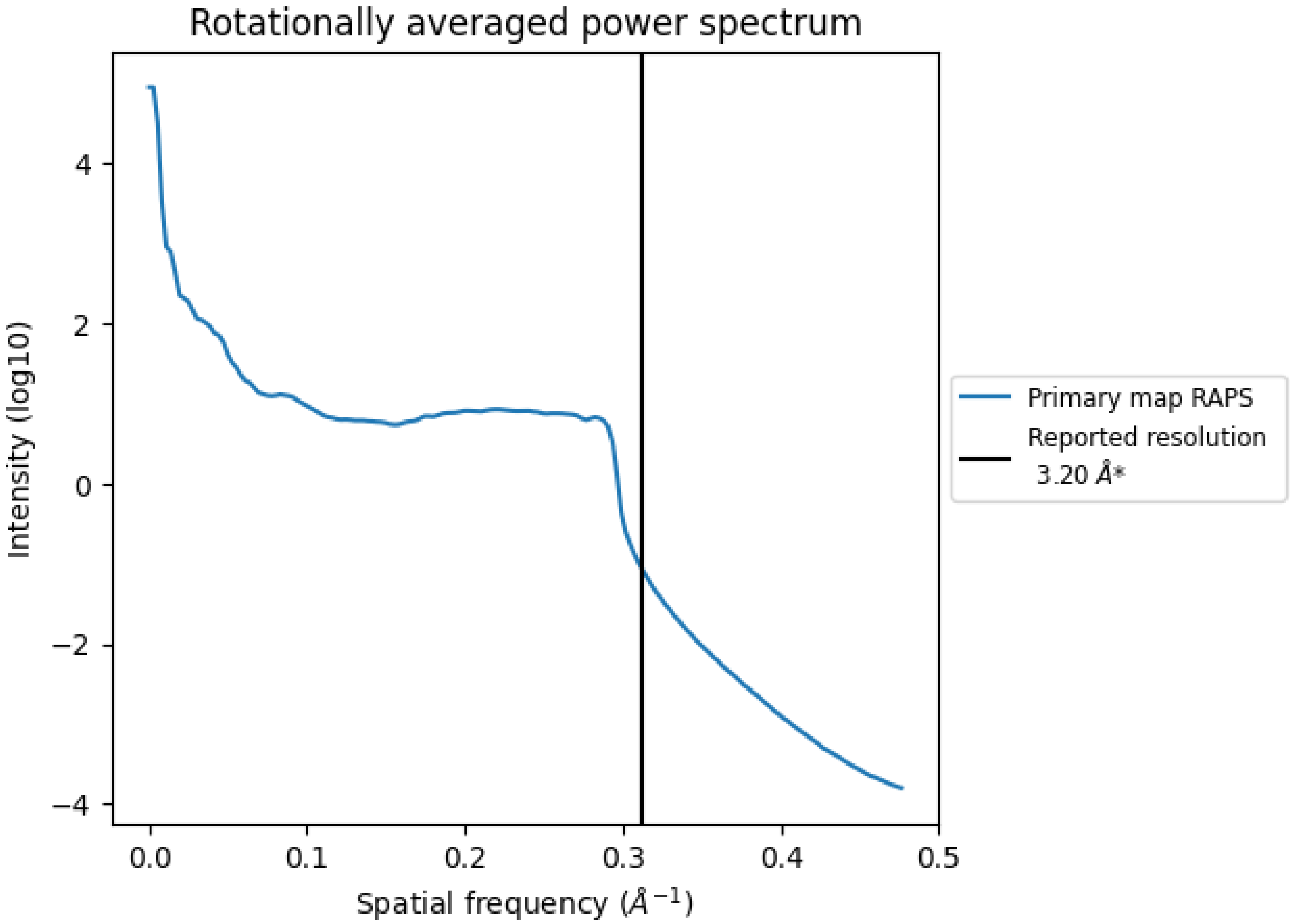
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 1134 nm^3; this corresponds to an approximate mass of 1024 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 0.312 Å^{-1}

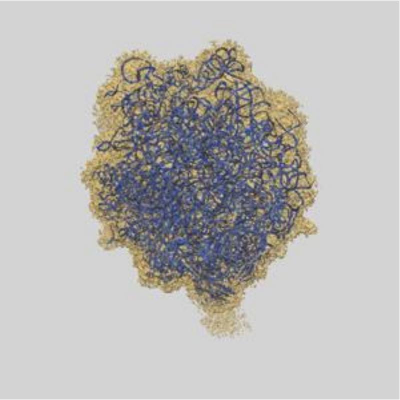
8 Fourier-Shell correlation ⓘ

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

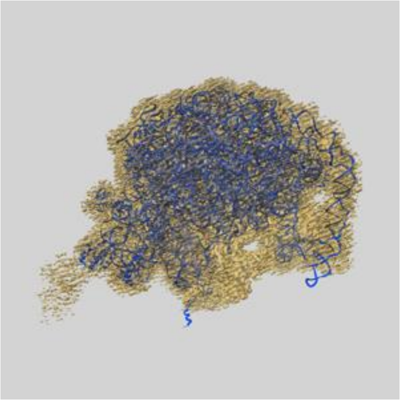
9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-6922 and PDB model 5ZET. Per-residue inclusion information can be found in section 3 on page 10.

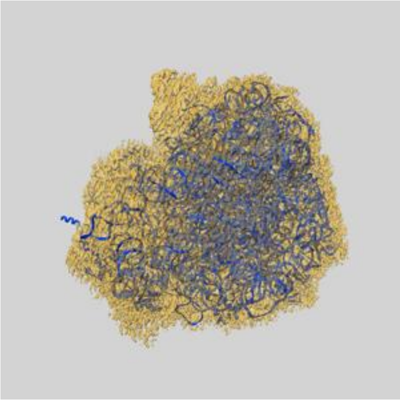
9.1 Map-model overlay ⓘ



X



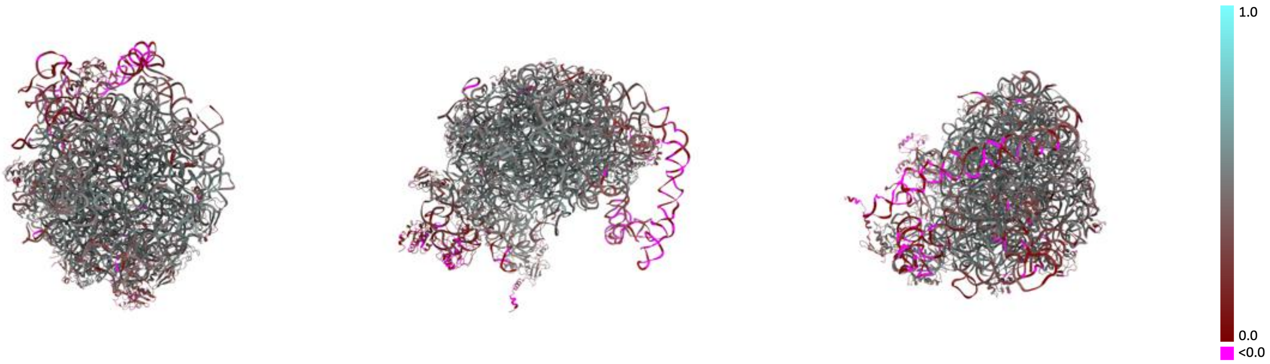
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05 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.

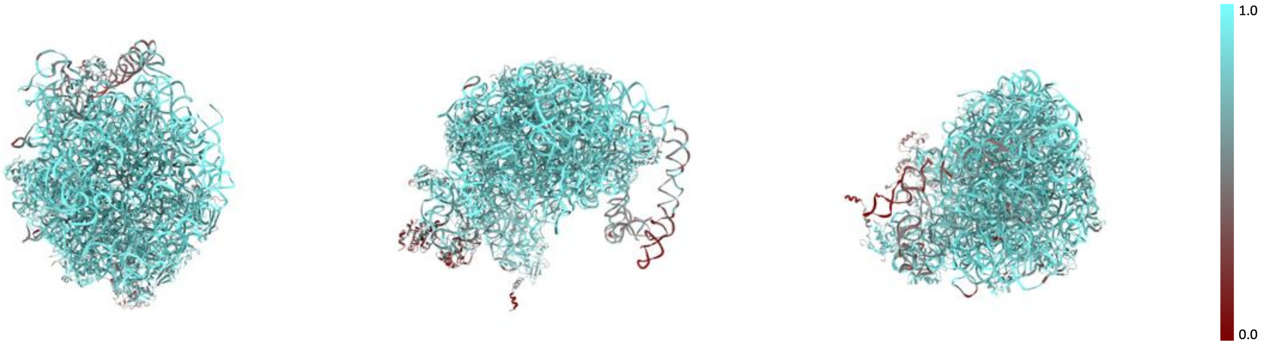
9.2 Q-score mapped to coordinate model ⓘ



X Y Z

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.

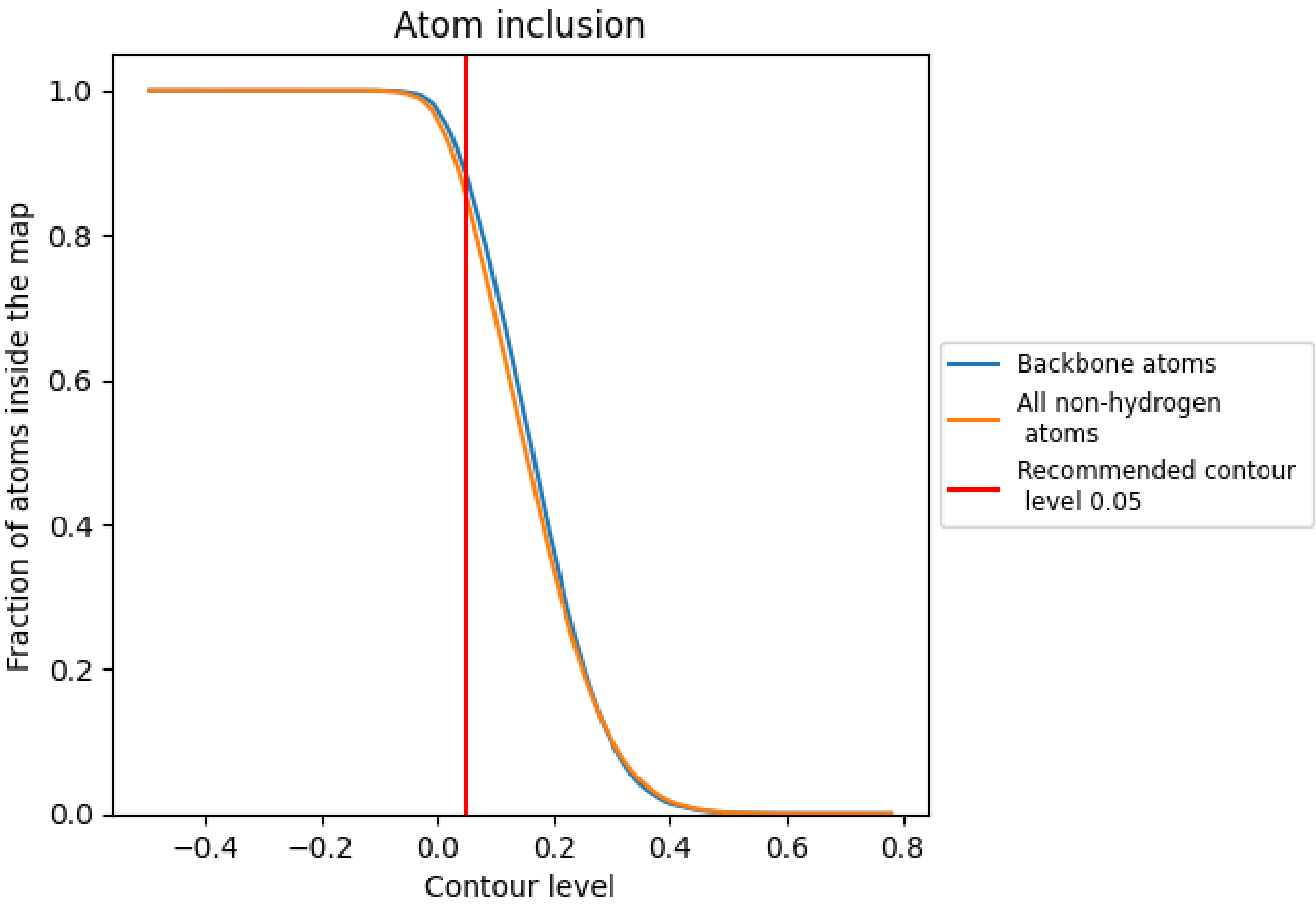
9.3 Atom inclusion mapped to coordinate model ⓘ



X Y Z

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 (0.05).

9.4 Atom inclusion ⓘ



At the recommended contour level, 88% of all backbone atoms, 85% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8512	0.4220
1	0.8205	0.4500
2	0.5391	0.1860
3	0.8358	0.4500
4	0.8040	0.3790
5	0.8605	0.4740
6	0.8688	0.4850
7	0.8811	0.4790
8	0.7933	0.4410
A	0.8825	0.4320
B	0.8617	0.3920
C	0.8531	0.4810
D	0.8518	0.4720
E	0.8199	0.4230
F	0.7933	0.3790
G	0.7669	0.3570
H	0.6300	0.3000
I	0.3451	0.1310
J	0.3718	0.0990
K	0.8396	0.4650
L	0.8259	0.4500
M	0.8215	0.4320
N	0.8413	0.4600
O	0.8221	0.4380
P	0.8330	0.4300
Q	0.8045	0.4390
R	0.8668	0.4750
S	0.8393	0.4340
T	0.8124	0.4440
U	0.7911	0.4080
V	0.7677	0.3650
W	0.6948	0.3140
X	0.8339	0.4650
Y	0.8366	0.4520
Z	0.8182	0.4000