



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 01:46 AM UTC

PDB ID : 5O61 / pdb_00005o61
EMDB ID : EMD-3751
Title : The complete structure of the Mycobacterium smegmatis 70S ribosome
Authors : Hentschel, J.; Burnside, C.; Mignot, I.; Leibundgut, M.; Boehringer, D.; Ban, N.
Deposited on : 2017-06-03
Resolution : 3.31 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

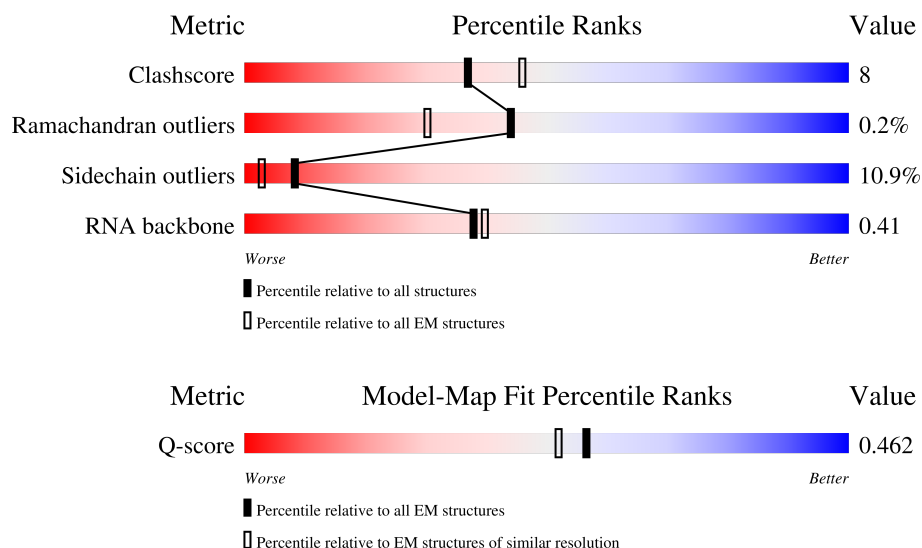
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.31 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14550 (2.81 - 3.81)

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	3	24	
2	A	3120	
3	B	118	

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Mol	Chain	Length	Quality of chain
4	C	278	
5	D	217	
6	E	215	
7	F	187	
8	G	179	
9	H	151	
10	I	175	
11	J	142	
12	K	147	
13	L	122	
14	M	147	
15	N	138	
16	O	199	
17	P	127	
18	Q	113	
19	R	129	
20	S	103	
21	T	153	
22	U	100	
23	V	105	
24	W	215	
25	X	88	
26	Y	64	
27	Z	77	
28	a	61	

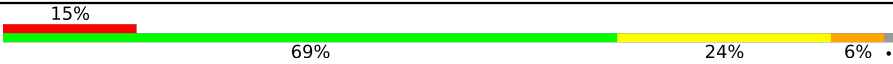
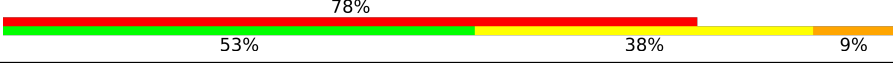
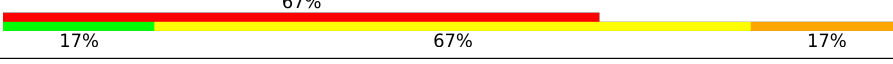
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Mol	Chain	Length	Quality of chain
29	b	57	
30	c	55	
31	d	47	
32	e	64	
33	f	37	
34	g	75	
35	BA	1528	
36	BB	33	
37	BC	275	
38	BD	201	
39	BE	214	
40	BF	96	
41	BG	156	
42	BH	132	
43	BI	150	
44	BJ	101	
45	BK	138	
46	BL	124	
47	BM	124	
48	BN	61	
49	BO	89	
50	BP	156	
51	BQ	98	
52	BR	84	
53	BS	93	

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Mol	Chain	Length	Quality of chain
54	BT	86	
55	BV	277	
56	BW	76	
57	BX	6	

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 151463 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 bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	3	23	Total	C	N	O	0	0
			189	111	50	28		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	3119	Total	C	N	O	P	0	0
			66981	29854	12313	21695	3119		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	100	Total	C	N	O		0	0
			754	478	137	139			

- Molecule 21 is a protein called 50S ribosomal protein L22.

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

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 24 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 26 is a protein called LSU ribosomal protein L28P.

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

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 28 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	a	59	Total	C	N	O	0	0
			474	292	95	87		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 34 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	59	Total	C	N	O	S	0	0
			458	284	84	85	5		

- Molecule 35 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BA	1511	Total	C	N	O	P	0	0
			32439	14448	5930	10550	1511		

- Molecule 36 is a protein called Conserved domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BB	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

- Molecule 37 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BC	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

- Molecule 38 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BD	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 39 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BE	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

- Molecule 40 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BF	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 41 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BG	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

- Molecule 42 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BH	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 43 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BI	126	Total	C	N	O	S	0	0
			994	630	194	170			

- Molecule 44 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BJ	99	Total	C	N	O	S	0	0
			788	495	146	144	3		

- Molecule 45 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BK	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 46 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BL	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 47 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BM	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 48 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BN	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

- Molecule 49 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	BO	88	Total	C	N	O	0	0
			720	449	147	124		

- Molecule 50 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	BP	113	Total	C	N	O	0	0
			891	570	162	159		

- Molecule 51 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BQ	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 52 is a protein called 30S ribosomal protein S18 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BR	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 53 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BS	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 54 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	BT	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 55 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BV	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 56 is a RNA chain called P/P-site Phe-tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BW	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 57 is a RNA chain called mRNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BX	6	Total	C	N	O	P	0	0
			117	54	13	45	5		

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
58	A	390	Total	Mg	0
			390	390	
58	B	9	Total	Mg	0
			9	9	
58	C	4	Total	Mg	0
			4	4	
58	F	1	Total	Mg	0
			1	1	
58	M	1	Total	Mg	0
			1	1	
58	N	1	Total	Mg	0
			1	1	
58	T	1	Total	Mg	0
			1	1	
58	c	1	Total	Mg	0
			1	1	
58	BA	215	Total	Mg	0
			215	215	
58	BF	1	Total	Mg	0
			1	1	
58	BR	1	Total	Mg	0
			1	1	

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
59	Y	1	Total	Zn	0
			1	1	
59	c	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
59	f	1	Total Zn 1 1	0
59	g	1	Total Zn 1 1	0
59	BN	1	Total Zn 1 1	0
59	BR	1	Total Zn 1 1	0

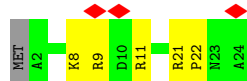
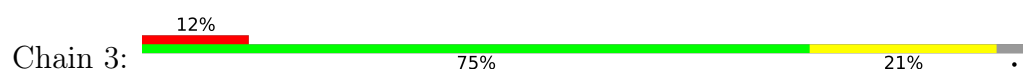
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- Chemical structure of Phenylalanine (PHE) showing the amino acid backbone and the phenyl ring. The structure is labeled with various atoms and groups:
- Backbone:** The central carbon is labeled **CA(S)**. The amino group is labeled **N** and **H₂**. The carboxyl group is labeled **C**, **OH**, and **O**.
 - Side Chain:** The side chain is labeled **CB** (beta carbon) and **CG** (gamma carbon).
 - Phenyl Ring:** The phenyl ring is labeled with **CE1**, **CE2**, and **CZ** (ortho positions) and **CD1**, **CD2** (meta positions).

Mol	Chain	Residues	Atoms				AltConf
60	BW	1	Total	C	N	O	0
			11	9	1	1	

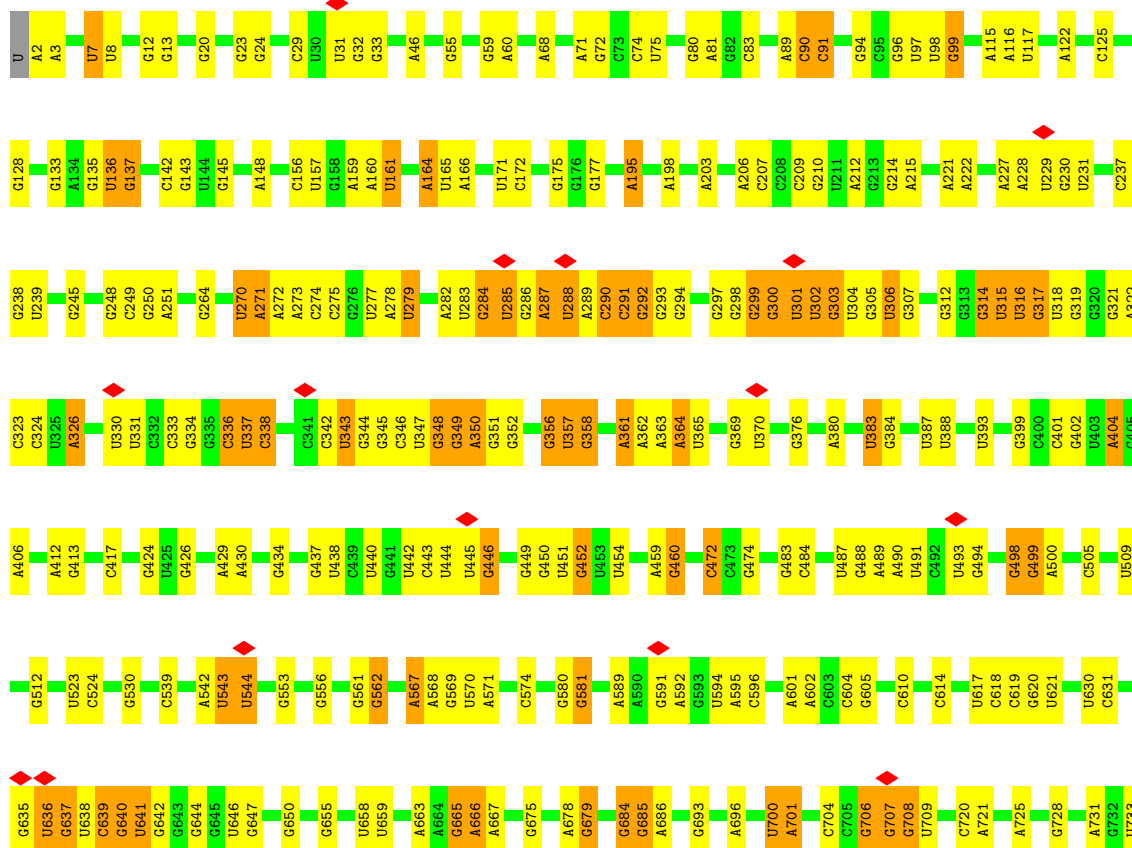
3 Residue-property plots

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: 50S ribosomal protein bL37

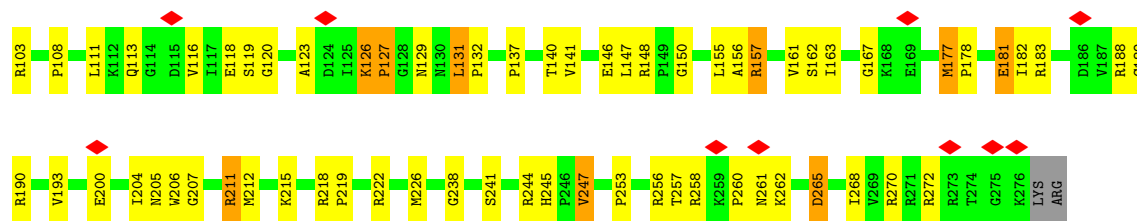


- Molecule 2: 23S rRNA

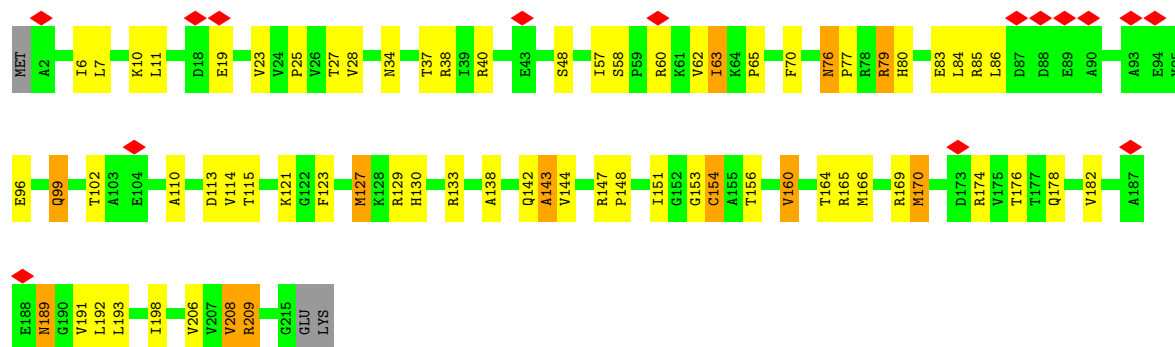




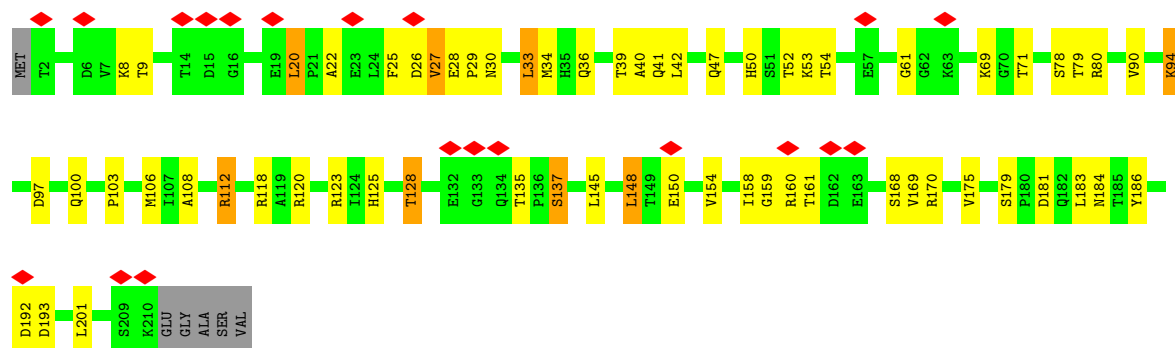




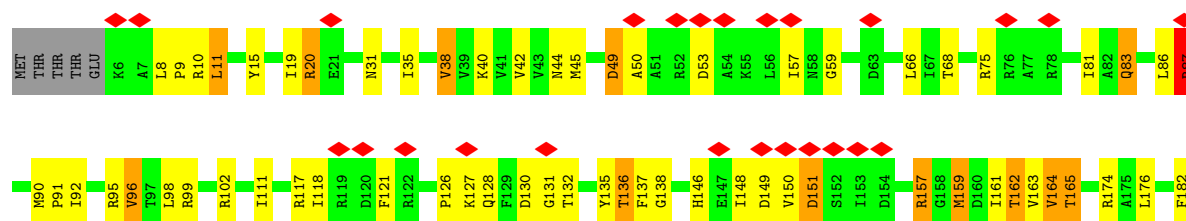
• Molecule 5: 50S ribosomal protein L3



• Molecule 6: 50S ribosomal protein L4

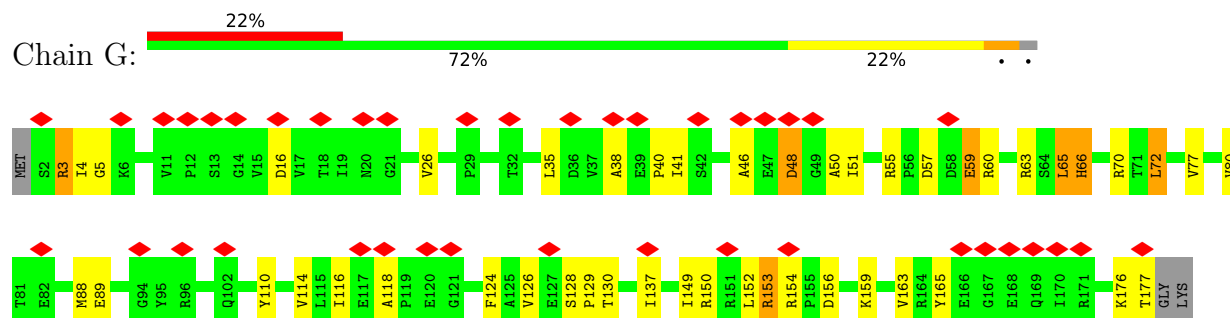


• Molecule 7: 50S ribosomal protein L5

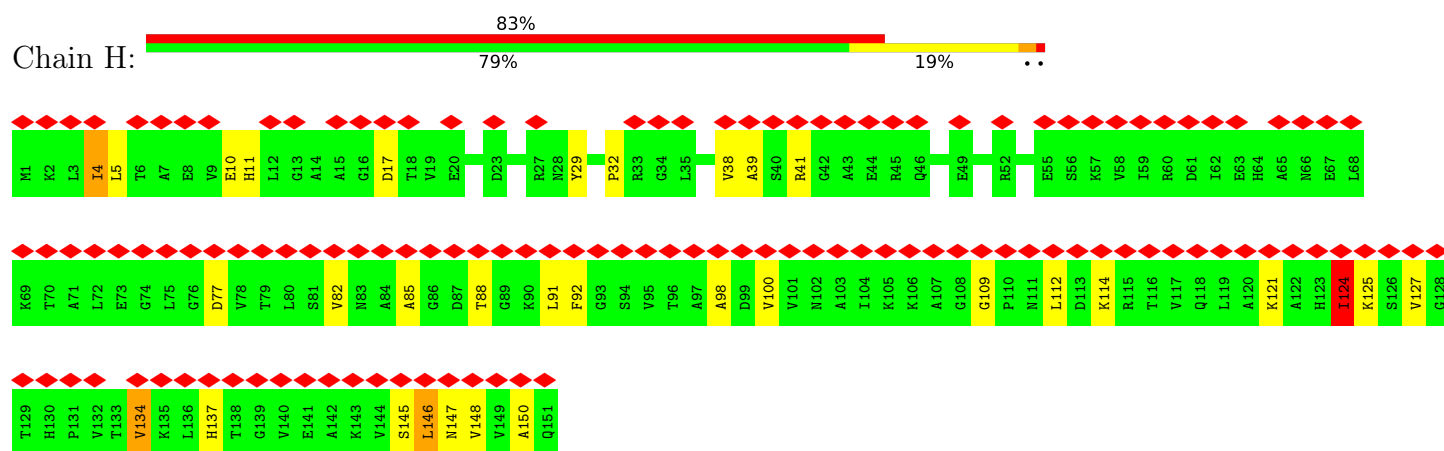




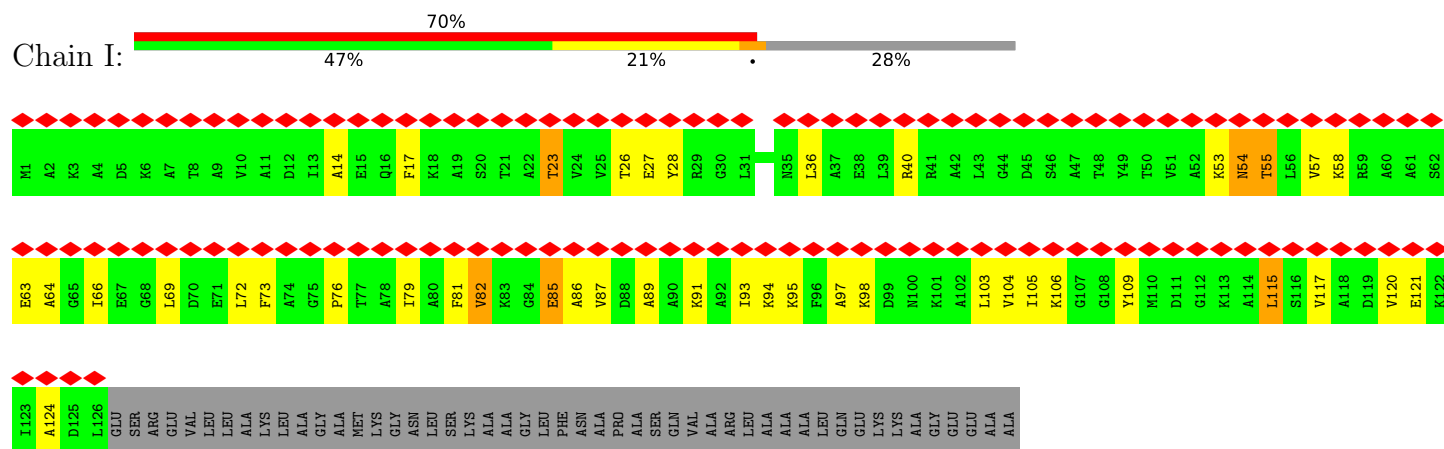
• Molecule 8: 50S ribosomal protein L6



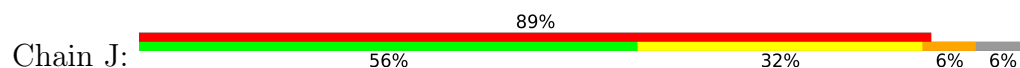
• Molecule 9: 50S ribosomal protein L9

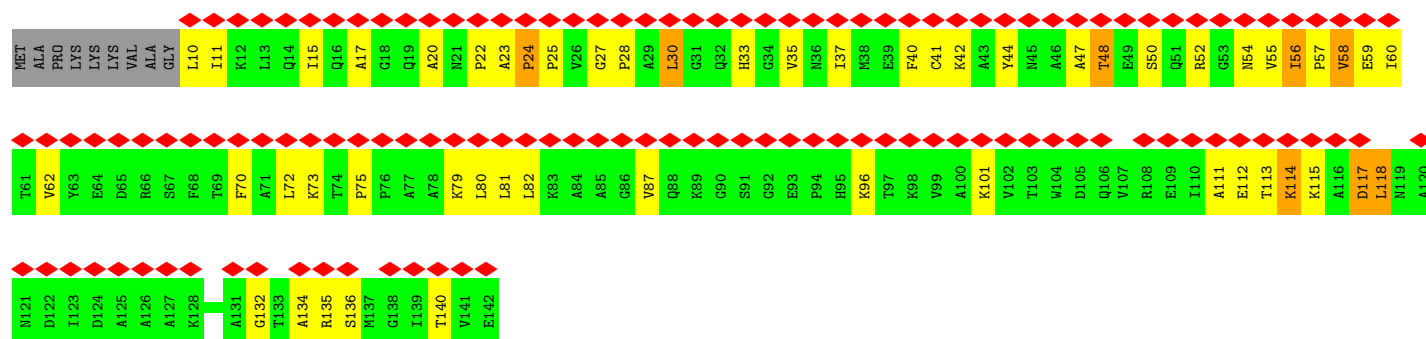


• Molecule 10: 50S ribosomal protein L10

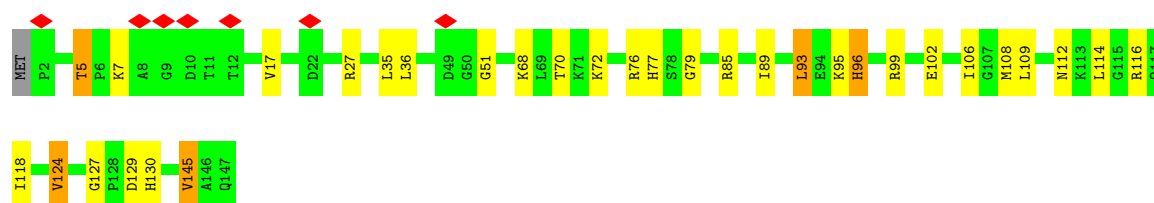
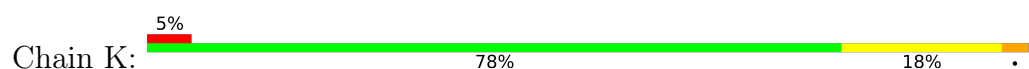


• Molecule 11: 50S ribosomal protein L11

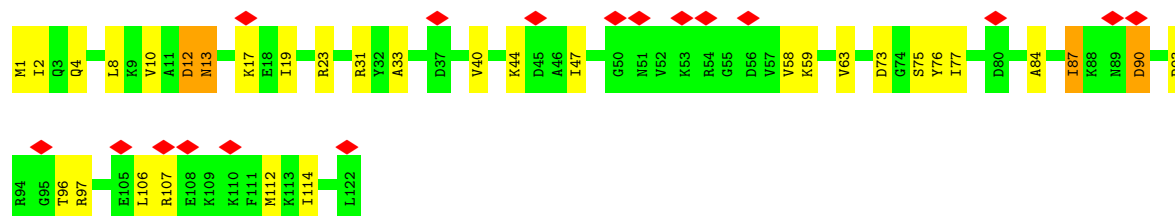
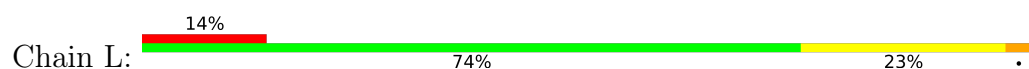




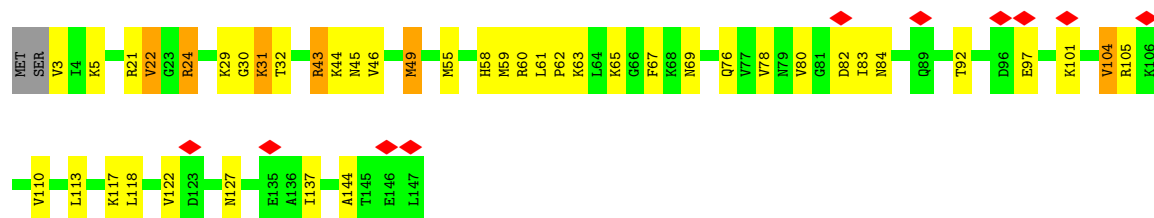
• Molecule 12: 50S ribosomal protein L13



• Molecule 13: 50S ribosomal protein L14

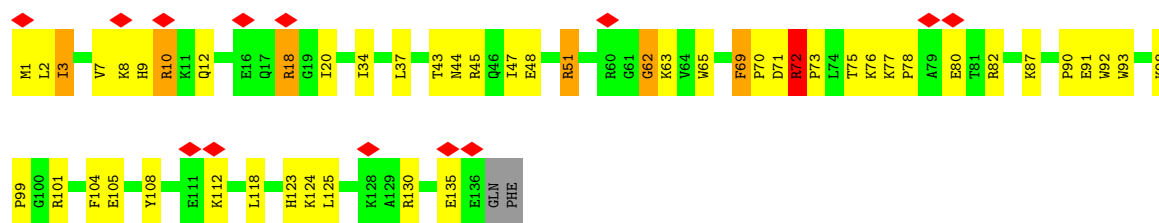


• Molecule 14: 50S ribosomal protein L15

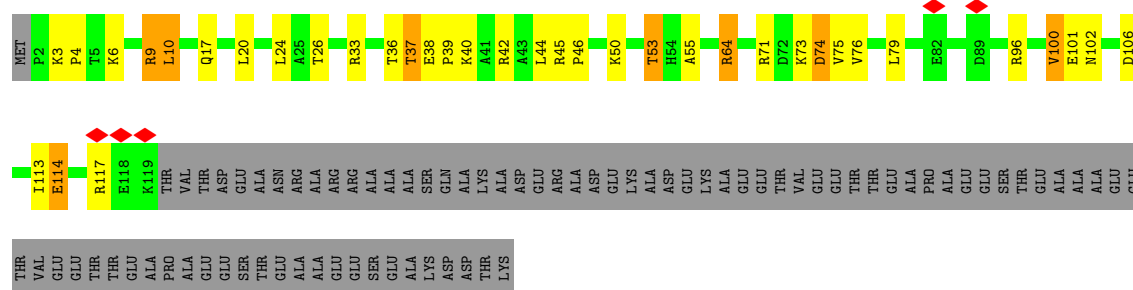


• Molecule 15: 50S ribosomal protein L16

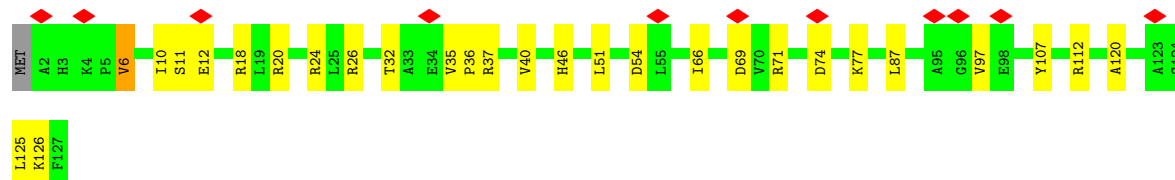
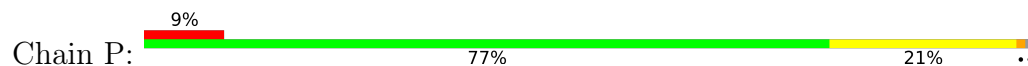




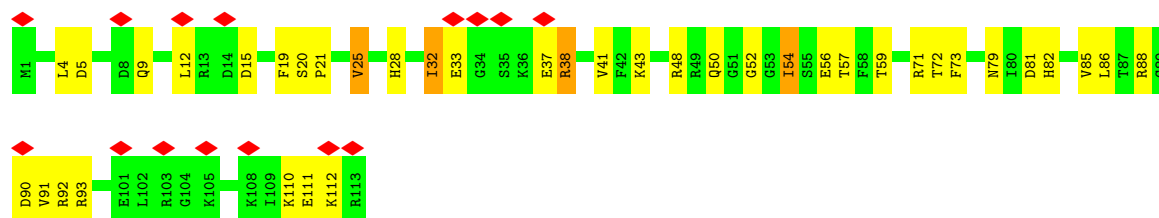
• Molecule 16: 50S ribosomal protein L17



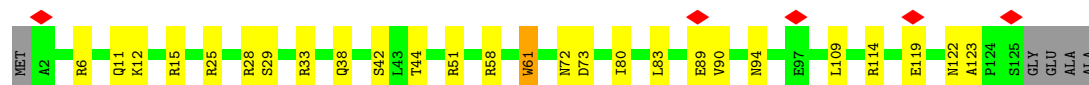
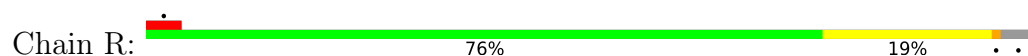
• Molecule 17: 50S ribosomal protein L18



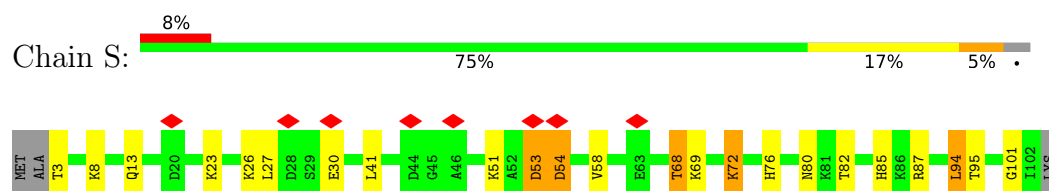
• Molecule 18: 50S ribosomal protein L19



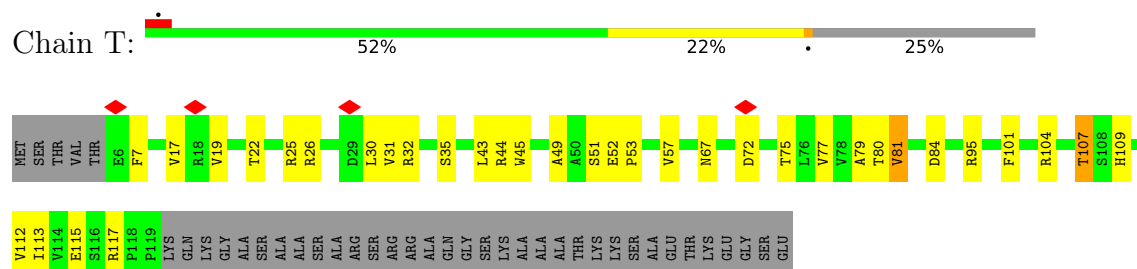
• Molecule 19: 50S ribosomal protein L20



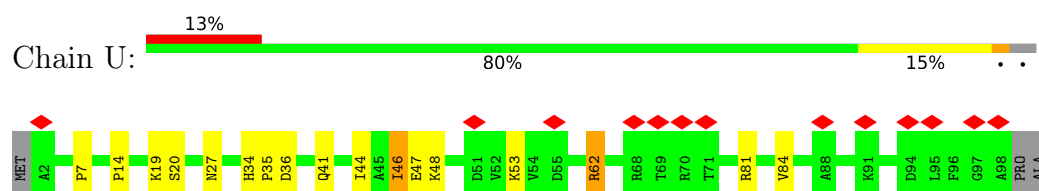
- Molecule 20: 50S ribosomal protein L21



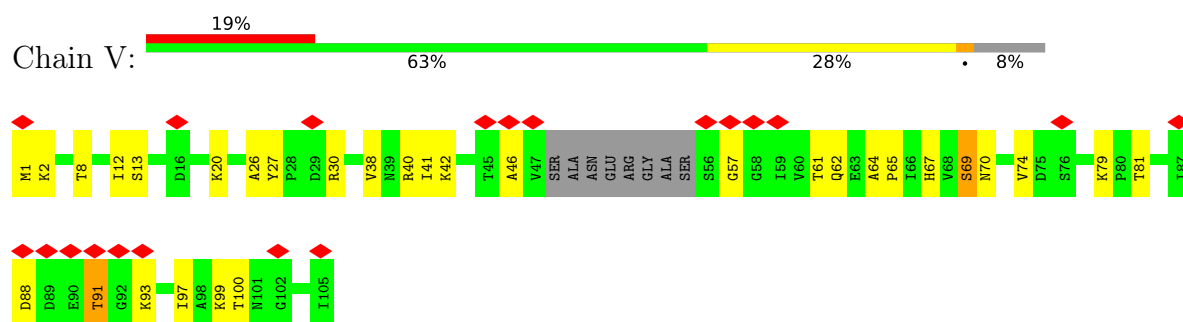
- Molecule 21: 50S ribosomal protein L22



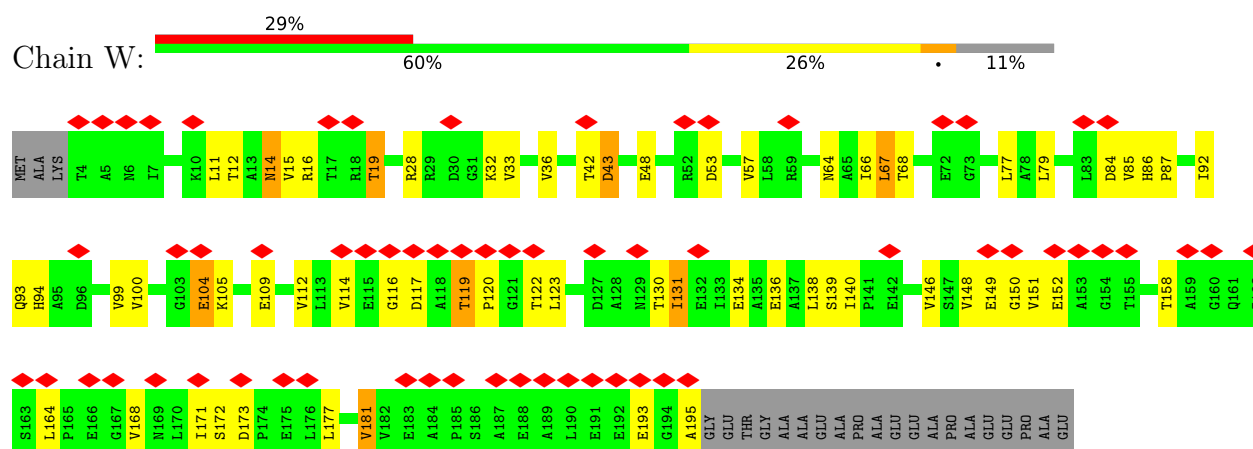
- Molecule 22: 50S ribosomal protein L23



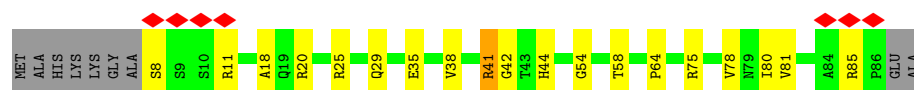
- Molecule 23: 50S ribosomal protein L24



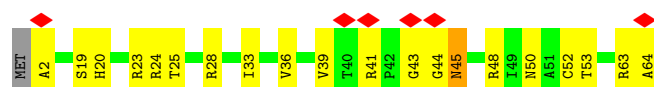
- Molecule 24: 50S ribosomal protein L25



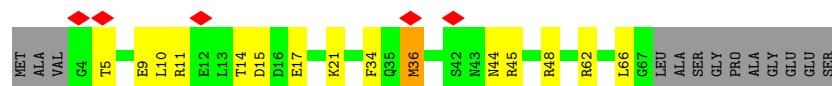
- Molecule 25: 50S ribosomal protein L27



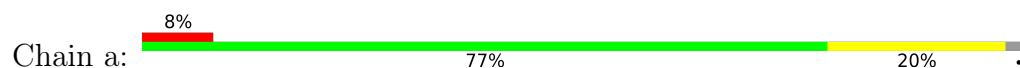
- Molecule 26: LSU ribosomal protein L28P



- Molecule 27: 50S ribosomal protein L29



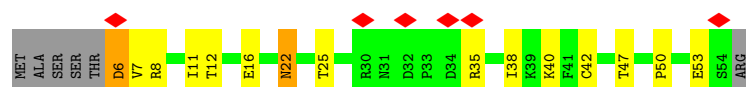
- Molecule 28: 50S ribosomal protein L30



- Molecule 29: 50S ribosomal protein L32

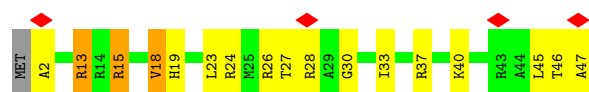


- Molecule 30: 50S ribosomal protein L33 1

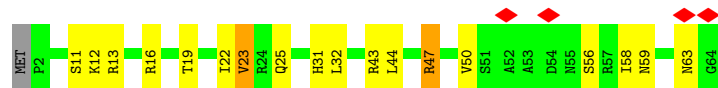


- Molecule 31: 50S ribosomal protein L34

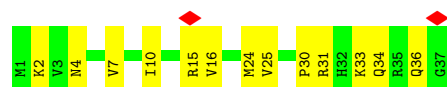




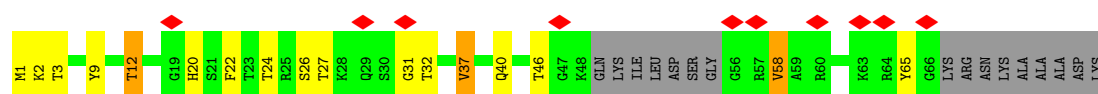
- Molecule 32: 50S ribosomal protein L35



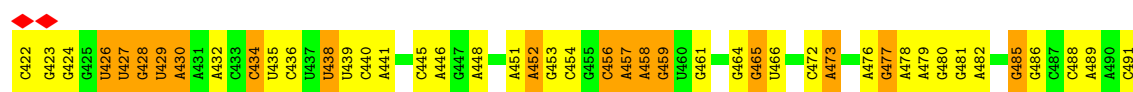
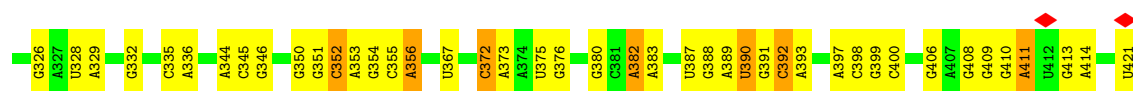
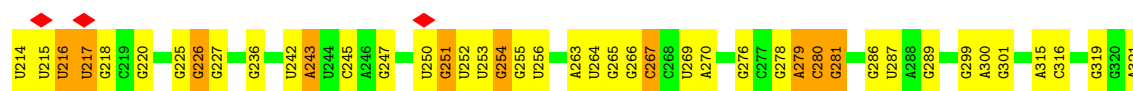
- Molecule 33: 50S ribosomal protein L36

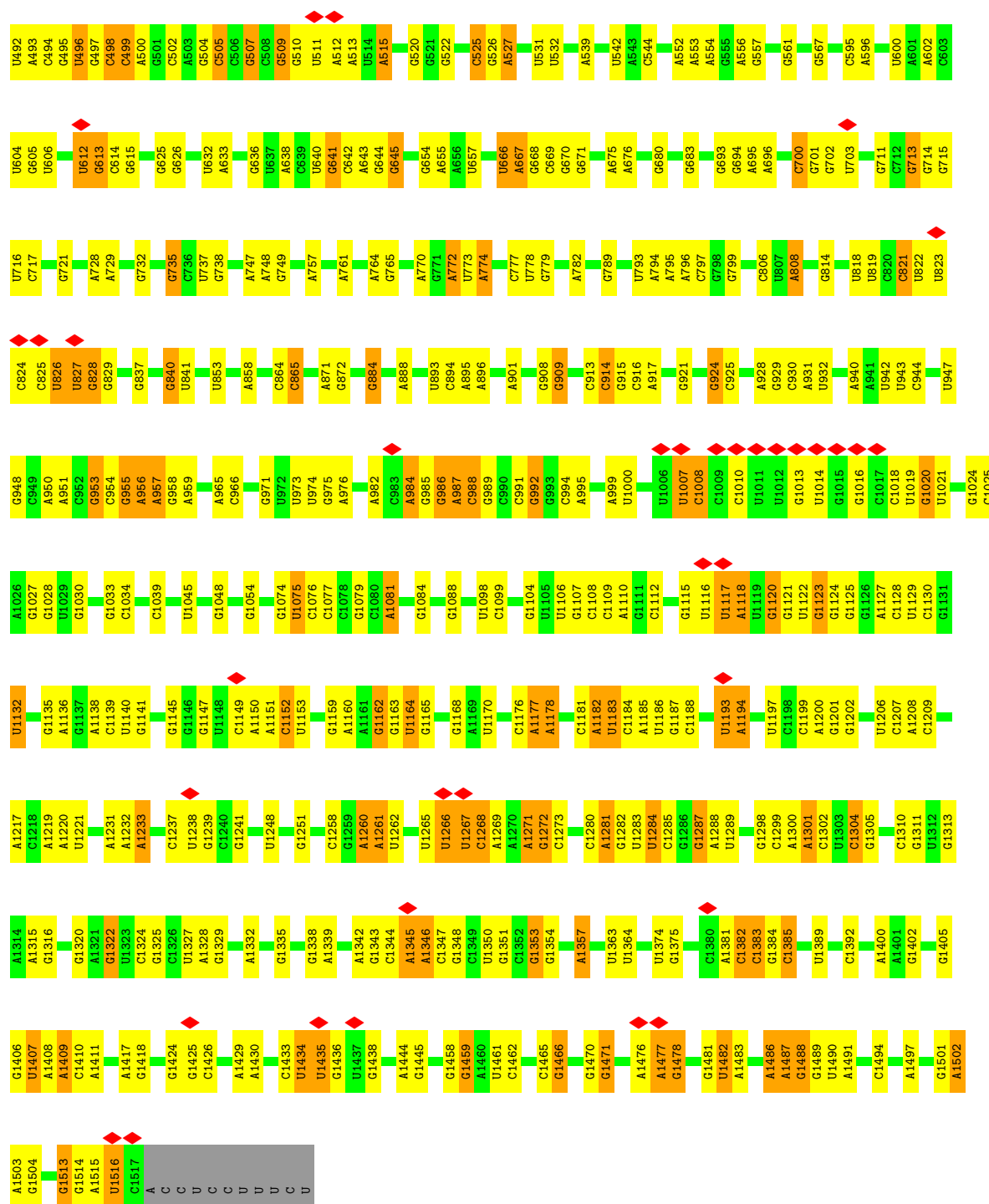


- Molecule 34: 50S ribosomal protein L31



- Molecule 35: 16S rRNA

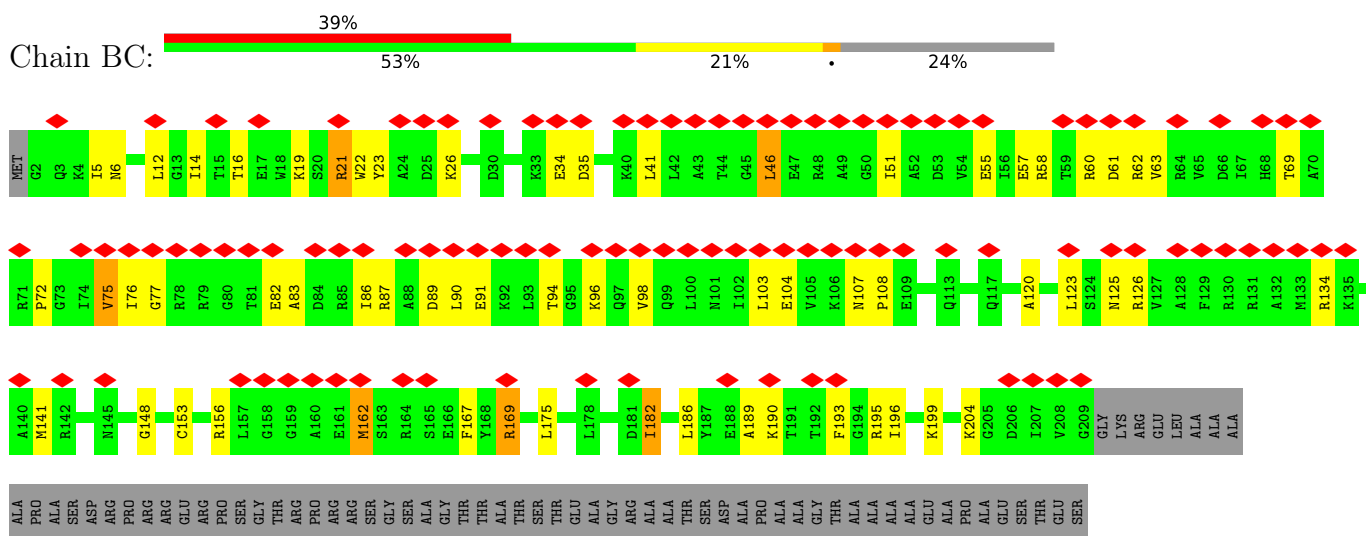




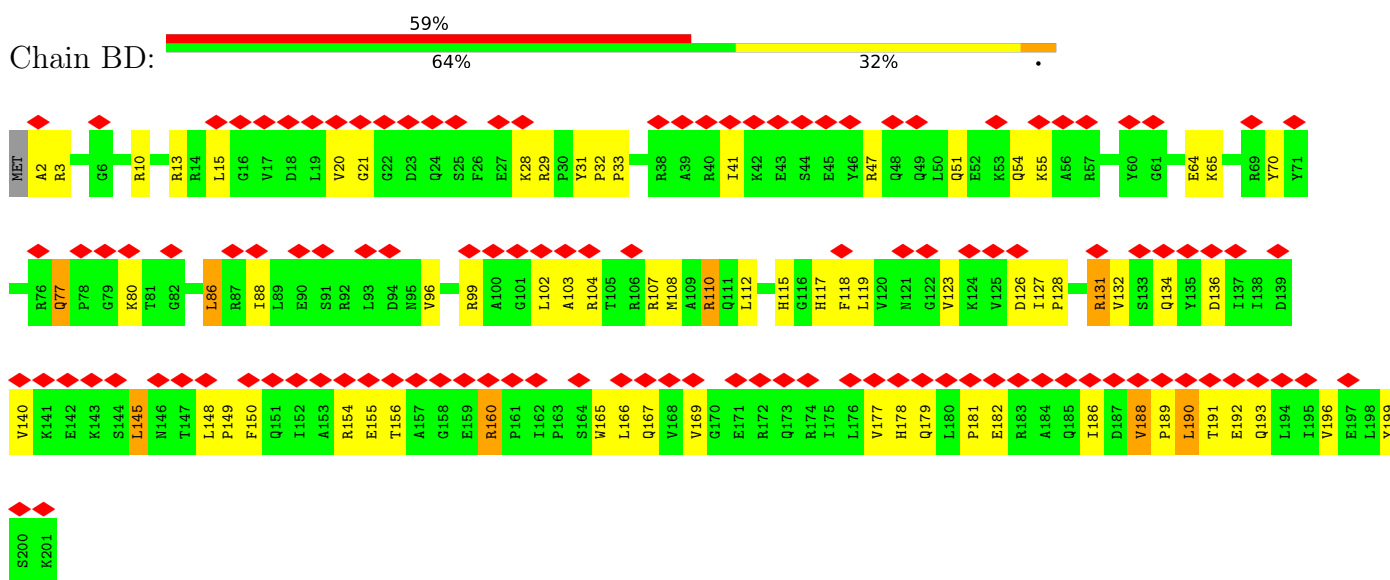
- Molecule 36: Conserved domain protein



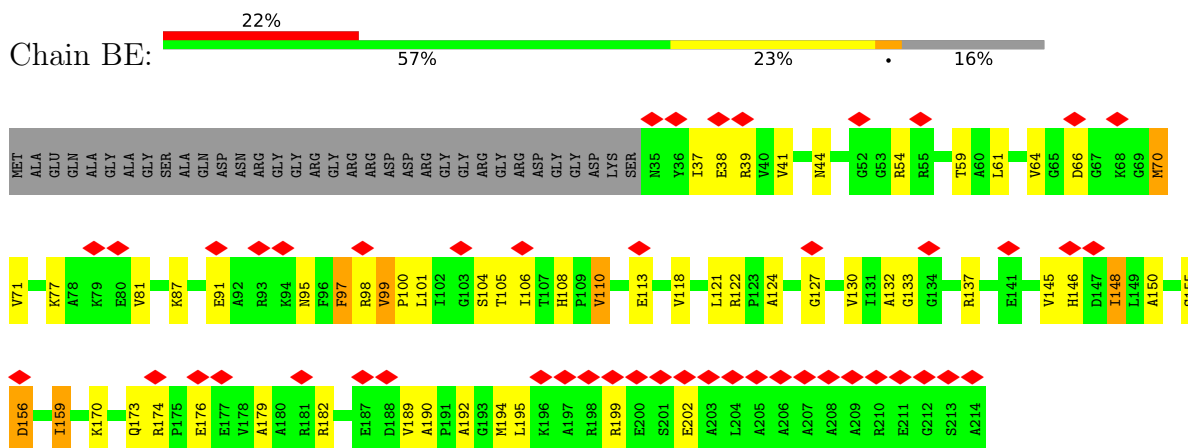
- Molecule 37: 30S ribosomal protein S3



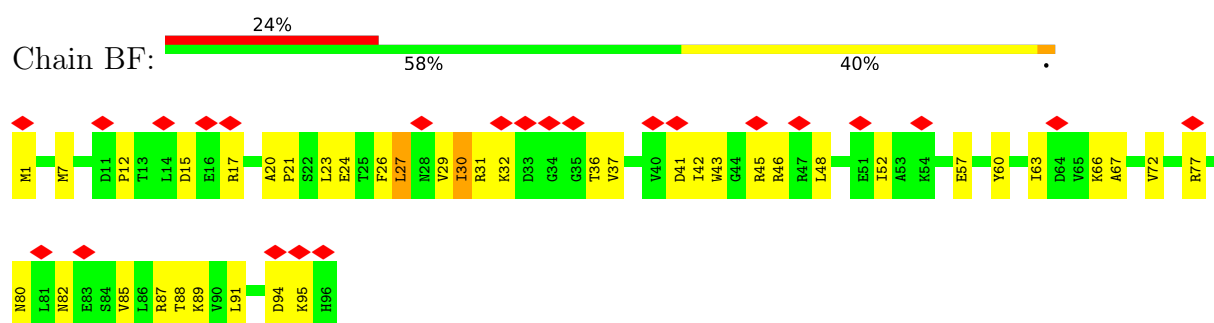
• Molecule 38: 30S ribosomal protein S4



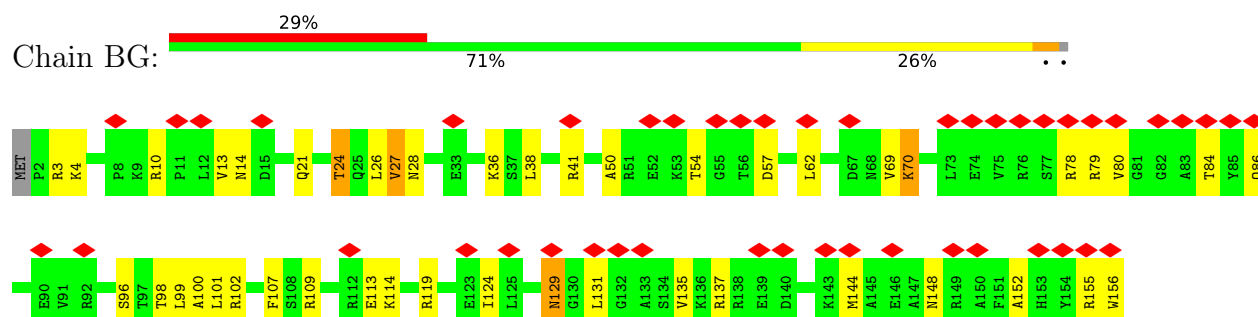
• Molecule 39: 30S ribosomal protein S5



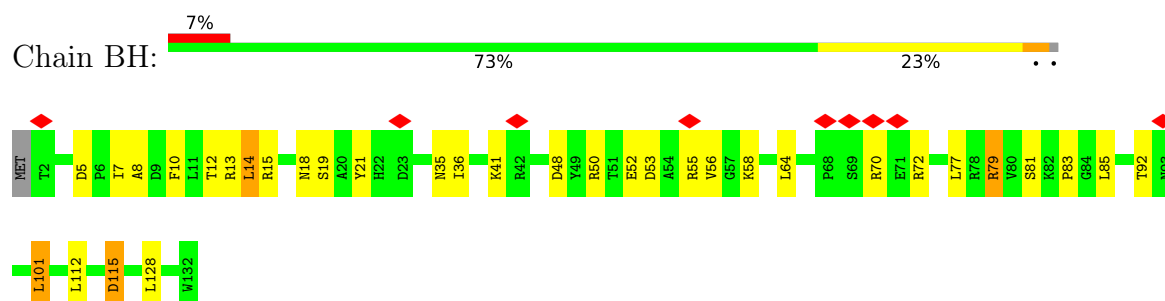
• Molecule 40: 30S ribosomal protein S6



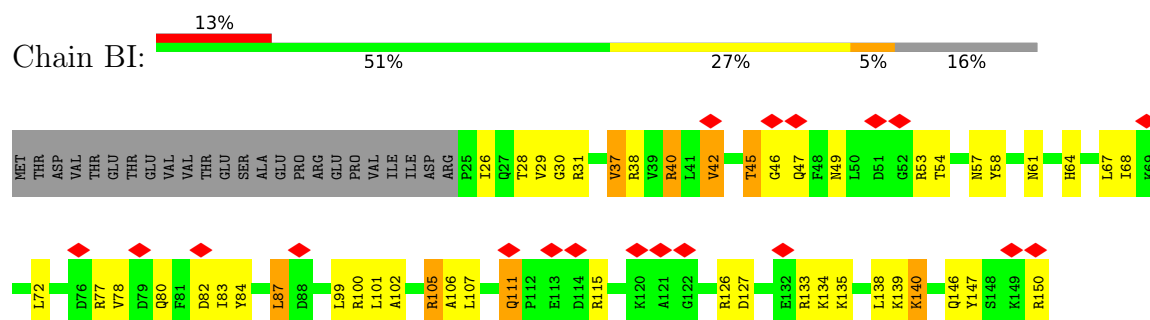
• Molecule 41: 30S ribosomal protein S7



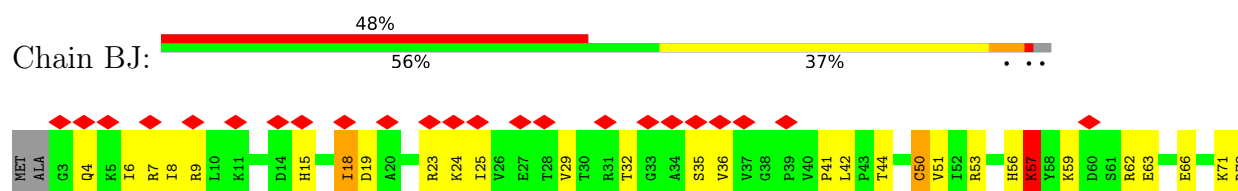
• Molecule 42: 30S ribosomal protein S8



• Molecule 43: 30S ribosomal protein S9

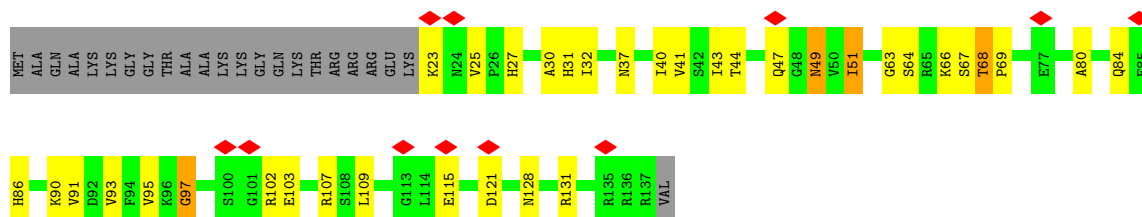


• Molecule 44: 30S ribosomal protein S10

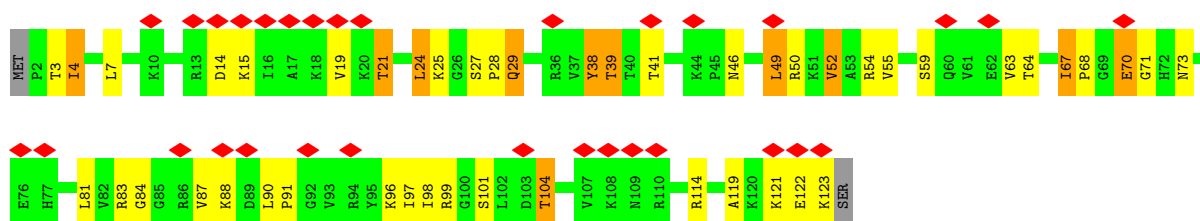




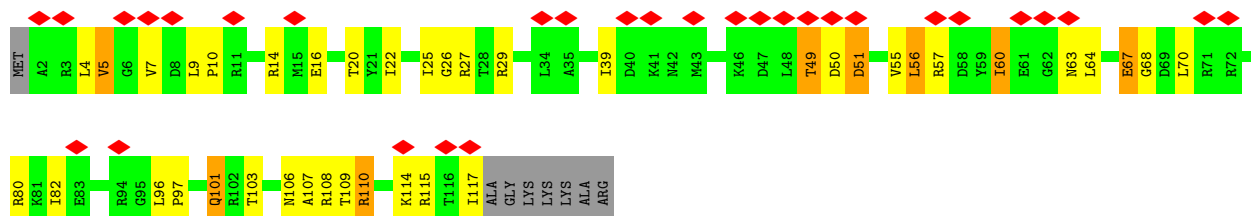
- Molecule 45: 30S ribosomal protein S11



- Molecule 46: 30S ribosomal protein S12



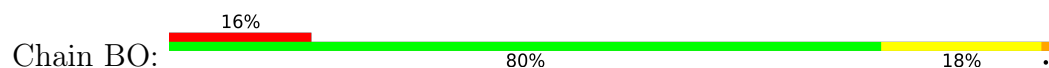
- Molecule 47: 30S ribosomal protein S13

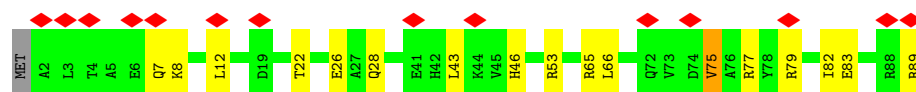


- Molecule 48: 30S ribosomal protein S14 type Z

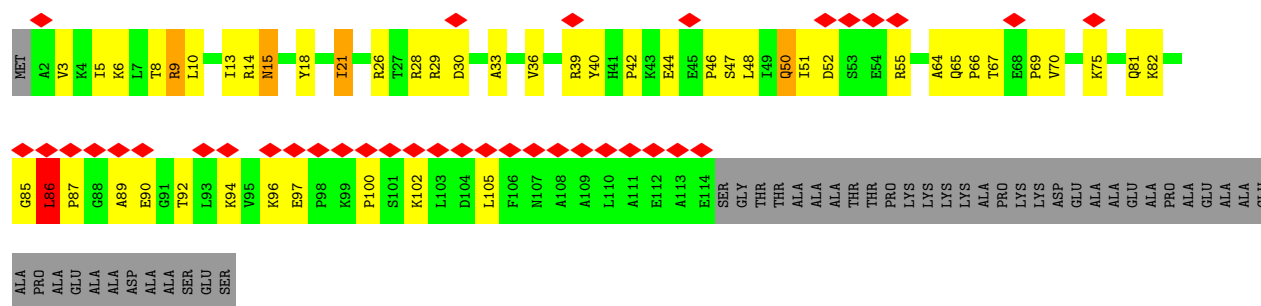
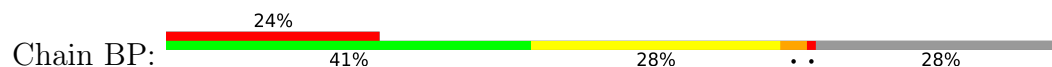


- Molecule 49: 30S ribosomal protein S15

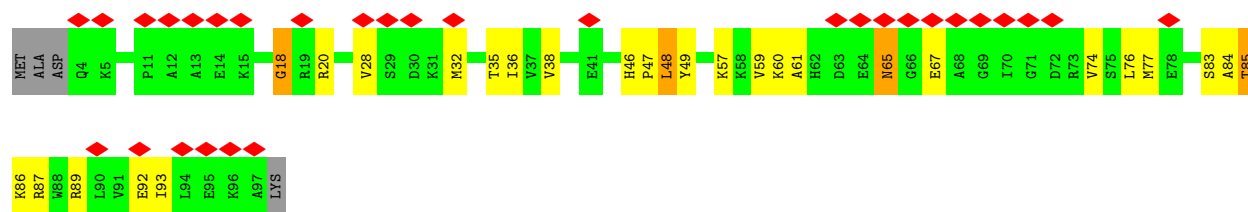




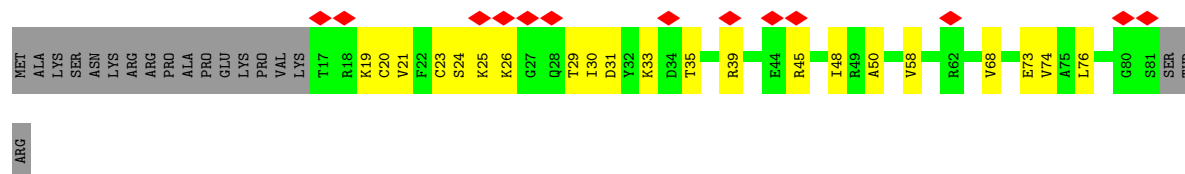
- Molecule 50: 30S ribosomal protein S16



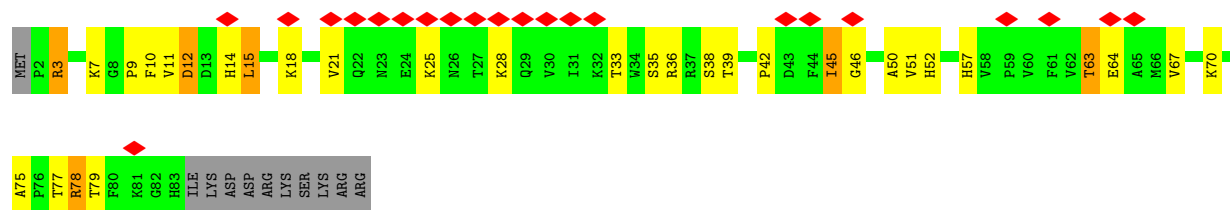
- Molecule 51: 30S ribosomal protein S17



- Molecule 52: 30S ribosomal protein S18 2

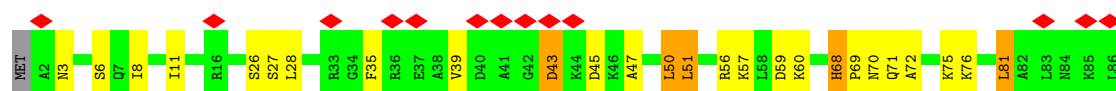


- Molecule 53: 30S ribosomal protein S19



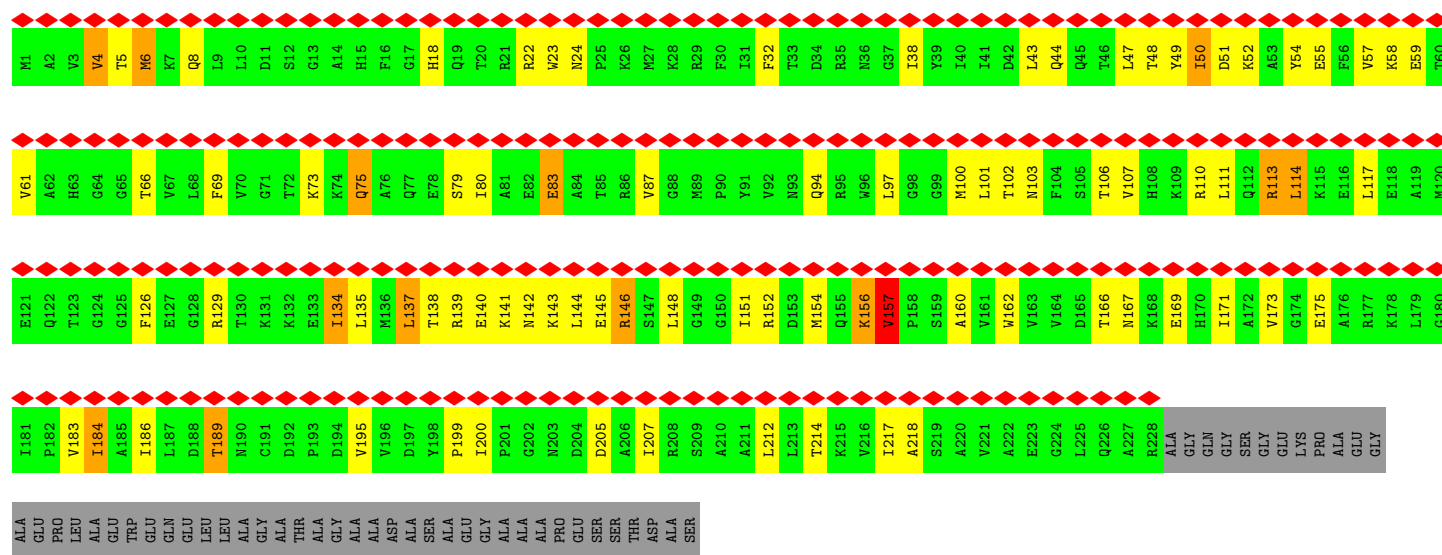
- Molecule 54: 30S ribosomal protein S20

Chain BT: 



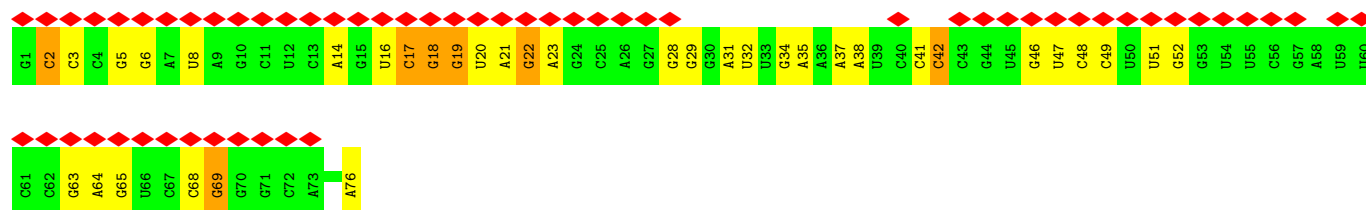
• Molecule 55: 30S ribosomal protein S2

Chain BV: 

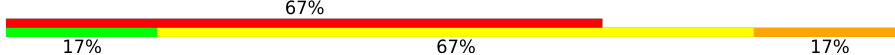


• Molecule 56: P/P-site Phe-tRNA(Phe)

Chain BW: 



• Molecule 57: mRNA fragment

Chain BX: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	224584	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; CTF correction in Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	100719	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.437	Depositor
Minimum map value	-0.187	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.034	Depositor
Recommended contour level	0.08	Depositor
Map size ($\text{\AA}$)	300.24, 300.24, 300.24	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.39, 1.39, 1.39	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	3	0.58	0/191	0.85	0/247
2	A	0.37	0/75001	0.42	1/117027 (0.0%)
3	B	0.25	0/2821	0.36	0/4396
4	C	0.64	0/2153	1.00	4/2895 (0.1%)
5	D	0.64	0/1609	0.96	3/2165 (0.1%)
6	E	0.53	0/1592	0.95	4/2153 (0.2%)
7	F	0.47	0/1467	0.93	2/1973 (0.1%)
8	G	0.48	0/1369	0.90	2/1848 (0.1%)
9	H	0.64	0/1027	0.89	1/1398 (0.1%)
10	I	0.90	0/925	0.95	2/1246 (0.2%)
11	J	0.98	1/1006 (0.1%)	1.06	5/1364 (0.4%)
12	K	0.58	0/1157	0.98	8/1567 (0.5%)
13	L	0.59	0/946	0.90	1/1268 (0.1%)
14	M	0.57	0/1091	1.08	0/1457
15	N	0.62	0/1118	1.05	9/1506 (0.6%)
16	O	0.57	0/945	0.94	0/1267
17	P	0.47	0/966	0.91	3/1298 (0.2%)
18	Q	0.55	0/921	0.97	1/1236 (0.1%)
19	R	0.73	1/1000 (0.1%)	0.92	5/1341 (0.4%)
20	S	0.55	0/764	0.98	1/1030 (0.1%)
21	T	0.87	5/887 (0.6%)	1.03	6/1204 (0.5%)
22	U	0.56	0/766	0.93	0/1030
23	V	0.47	0/738	0.89	2/987 (0.2%)
24	W	0.50	0/1443	0.91	3/1970 (0.2%)
25	X	0.63	0/595	0.97	4/798 (0.5%)
26	Y	0.63	0/478	0.98	1/641 (0.2%)
27	Z	0.51	0/534	0.81	0/713
28	a	0.59	0/477	0.94	1/640 (0.2%)
29	b	0.60	0/427	0.85	0/572
30	c	0.53	0/413	1.02	2/553 (0.4%)
31	d	0.63	0/380	0.96	1/500 (0.2%)
32	e	0.56	0/507	0.88	0/672

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.62	0/303	1.06	1/401 (0.2%)
34	g	0.49	0/467	0.92	1/626 (0.2%)
35	BA	0.30	0/36309	0.41	1/56657 (0.0%)
36	BB	0.49	0/280	0.82	0/359
37	BC	0.49	0/1684	0.91	2/2261 (0.1%)
38	BD	0.74	4/1672 (0.2%)	1.02	10/2251 (0.4%)
39	BE	0.50	0/1312	0.97	4/1772 (0.2%)
40	BF	0.50	0/782	0.90	1/1059 (0.1%)
41	BG	0.52	0/1252	0.84	2/1690 (0.1%)
42	BH	0.46	0/1025	0.89	0/1385
43	BI	0.55	0/1012	0.88	4/1362 (0.3%)
44	BJ	0.59	0/802	0.93	2/1086 (0.2%)
45	BK	0.50	0/873	0.94	2/1180 (0.2%)
46	BL	0.53	0/969	0.95	3/1294 (0.2%)
47	BM	0.47	0/942	0.84	2/1260 (0.2%)
48	BN	0.40	0/488	0.97	3/650 (0.5%)
49	BO	0.45	0/729	0.82	0/977
50	BP	0.53	0/908	1.08	4/1226 (0.3%)
51	BQ	0.49	0/759	0.94	1/1016 (0.1%)
52	BR	0.52	0/518	0.90	1/693 (0.1%)
53	BS	0.71	3/680 (0.4%)	0.87	0/915
54	BT	0.52	0/663	0.90	2/882 (0.2%)
55	BV	0.77	1/1822 (0.1%)	0.88	0/2457
56	BW	0.36	0/1809	0.42	0/2819
57	BX	0.38	0/128	0.39	0/196
All	All	0.43	15/163902 (0.0%)	0.60	118/245436 (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
21	T	0	1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	BD	115	HIS	ND1-CE1	-13.58	1.19	1.32
21	T	109	HIS	CG-ND1	8.41	1.47	1.38
21	T	109	HIS	CE1-NE2	7.79	1.40	1.32
21	T	109	HIS	ND1-CE1	-7.78	1.24	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	BD	115	HIS	CG-CD2	7.22	1.43	1.35

The worst 5 of 118 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	20	LEU	CA-C-N	9.70	129.79	119.90
6	E	20	LEU	C-N-CA	9.70	129.79	119.90
19	R	61	TRP	CG-CD2-CE3	9.34	143.24	133.90
30	c	42	CYS	CA-C-N	9.27	128.61	118.97
30	c	42	CYS	C-N-CA	9.27	128.61	118.97

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	T	117	ARG	Mainchain

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	3	189	0	205	4	0
2	A	66981	0	33699	520	0
3	B	2522	0	1285	13	0
4	C	2110	0	2165	75	0
5	D	1587	0	1630	41	0
6	E	1569	0	1607	43	0
7	F	1445	0	1476	44	0
8	G	1348	0	1399	32	0
9	H	1018	0	988	20	0
10	I	918	0	959	38	0
11	J	990	0	1021	30	0
12	K	1130	0	1167	24	0
13	L	938	0	1000	20	0
14	M	1078	0	1151	44	0
15	N	1092	0	1128	38	0
16	O	928	0	972	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	P	956	0	991	11	0
18	Q	907	0	938	27	0
19	R	988	0	1038	23	0
20	S	754	0	802	17	0
21	T	873	0	909	22	0
22	U	756	0	802	12	0
23	V	732	0	782	20	0
24	W	1428	0	1443	29	0
25	X	586	0	601	12	0
26	Y	470	0	480	15	0
27	Z	531	0	541	18	0
28	a	474	0	500	6	0
29	b	423	0	463	20	0
30	c	405	0	407	6	0
31	d	377	0	411	16	0
32	e	502	0	541	12	0
33	f	299	0	321	7	0
34	g	458	0	443	9	0
35	BA	32439	0	16320	337	0
36	BB	280	0	342	9	0
37	BC	1660	0	1707	39	0
38	BD	1641	0	1668	57	0
39	BE	1296	0	1360	37	0
40	BF	771	0	797	27	0
41	BG	1232	0	1282	30	0
42	BH	1010	0	1046	25	0
43	BI	994	0	1050	35	0
44	BJ	788	0	819	32	0
45	BK	855	0	863	19	0
46	BL	958	0	1045	32	0
47	BM	935	0	986	24	0
48	BN	477	0	499	15	0
49	BO	720	0	760	10	0
50	BP	891	0	935	35	0
51	BQ	748	0	795	17	0
52	BR	513	0	537	16	0
53	BS	662	0	677	22	0
54	BT	660	0	712	15	0
55	BV	1793	0	1839	54	0
56	BW	1619	0	821	23	0
57	BX	117	0	63	3	0
58	A	390	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	B	9	0	0	0	0
58	BA	215	0	0	0	0
58	BF	1	0	0	0	0
58	BR	1	0	0	0	0
58	C	4	0	0	0	0
58	F	1	0	0	0	0
58	M	1	0	0	0	0
58	N	1	0	0	0	0
58	T	1	0	0	0	0
58	c	1	0	0	0	0
59	BN	1	0	0	0	0
59	BR	1	0	0	0	0
59	Y	1	0	0	0	0
59	c	1	0	0	0	0
59	f	1	0	0	0	0
59	g	1	0	0	0	0
60	BW	11	0	8	0	0
All	All	151463	0	101196	1890	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 8.

The worst 5 of 1890 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)
35:BA:531:U:O2'	46:BL:83:ARG:NH1	1.92	1.01
2:A:1786:G:OP1	4:C:211:ARG:NH1	1.97	0.98
2:A:2509:C:OP2	30:c:8:ARG:NH1	1.97	0.98
2:A:2772:G:H1'	13:L:23:ARG:HH12	1.29	0.96
2:A:2279:C:OP1	29:b:5:LYS:NZ	1.98	0.96

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	
1	3	21/24 (88%)	21 (100%)	0	0	100	100
4	C	273/278 (98%)	261 (96%)	12 (4%)	0	100	100
5	D	212/217 (98%)	199 (94%)	12 (6%)	1 (0%)	24	56
6	E	207/215 (96%)	201 (97%)	5 (2%)	1 (0%)	24	56
7	F	180/187 (96%)	167 (93%)	12 (7%)	1 (1%)	21	52
8	G	174/179 (97%)	167 (96%)	7 (4%)	0	100	100
9	H	149/151 (99%)	139 (93%)	9 (6%)	1 (1%)	18	49
10	I	124/175 (71%)	115 (93%)	9 (7%)	0	100	100
11	J	131/142 (92%)	124 (95%)	6 (5%)	1 (1%)	16	45
12	K	144/147 (98%)	136 (94%)	8 (6%)	0	100	100
13	L	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
14	M	143/147 (97%)	135 (94%)	7 (5%)	1 (1%)	18	49
15	N	134/138 (97%)	123 (92%)	11 (8%)	0	100	100
16	O	116/199 (58%)	111 (96%)	5 (4%)	0	100	100
17	P	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
18	Q	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
19	R	122/129 (95%)	117 (96%)	5 (4%)	0	100	100
20	S	98/103 (95%)	96 (98%)	2 (2%)	0	100	100
21	T	112/153 (73%)	109 (97%)	3 (3%)	0	100	100
22	U	95/100 (95%)	91 (96%)	4 (4%)	0	100	100
23	V	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
24	W	190/215 (88%)	185 (97%)	5 (3%)	0	100	100
25	X	77/88 (88%)	73 (95%)	4 (5%)	0	100	100
26	Y	61/64 (95%)	61 (100%)	0	0	100	100
27	Z	62/77 (80%)	60 (97%)	2 (3%)	0	100	100
28	a	57/61 (93%)	56 (98%)	1 (2%)	0	100	100
29	b	52/57 (91%)	51 (98%)	1 (2%)	0	100	100
30	c	47/55 (86%)	45 (96%)	1 (2%)	1 (2%)	5	27
31	d	44/47 (94%)	42 (96%)	2 (4%)	0	100	100
32	e	61/64 (95%)	61 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	f	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
34	g	55/75 (73%)	54 (98%)	1 (2%)	0	100	100
36	BB	30/33 (91%)	28 (93%)	2 (7%)	0	100	100
37	BC	206/275 (75%)	190 (92%)	14 (7%)	2 (1%)	12	41
38	BD	198/201 (98%)	186 (94%)	12 (6%)	0	100	100
39	BE	178/214 (83%)	170 (96%)	8 (4%)	0	100	100
40	BF	94/96 (98%)	91 (97%)	3 (3%)	0	100	100
41	BG	153/156 (98%)	146 (95%)	7 (5%)	0	100	100
42	BH	129/132 (98%)	124 (96%)	5 (4%)	0	100	100
43	BI	124/150 (83%)	119 (96%)	5 (4%)	0	100	100
44	BJ	97/101 (96%)	90 (93%)	7 (7%)	0	100	100
45	BK	113/138 (82%)	106 (94%)	7 (6%)	0	100	100
46	BL	120/124 (97%)	112 (93%)	8 (7%)	0	100	100
47	BM	114/124 (92%)	106 (93%)	8 (7%)	0	100	100
48	BN	58/61 (95%)	52 (90%)	6 (10%)	0	100	100
49	BO	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
50	BP	111/156 (71%)	106 (96%)	5 (4%)	0	100	100
51	BQ	92/98 (94%)	88 (96%)	4 (4%)	0	100	100
52	BR	63/84 (75%)	62 (98%)	1 (2%)	0	100	100
53	BS	80/93 (86%)	76 (95%)	4 (5%)	0	100	100
54	BT	83/86 (96%)	81 (98%)	2 (2%)	0	100	100
55	BV	226/277 (82%)	207 (92%)	18 (8%)	1 (0%)	30	60
All	All	5979/6679 (90%)	5688 (95%)	281 (5%)	10 (0%)	44	72

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	c	7	VAL
37	BC	125	ASN
5	D	143	ALA
14	M	31	LYS
6	E	90	VAL

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	3	18/19 (95%)	17 (94%)	1 (6%)	19	47
4	C	215/218 (99%)	191 (89%)	24 (11%)	6	22
5	D	160/163 (98%)	135 (84%)	25 (16%)	2	12
6	E	169/173 (98%)	149 (88%)	20 (12%)	5	21
7	F	151/156 (97%)	130 (86%)	21 (14%)	3	15
8	G	148/150 (99%)	134 (90%)	14 (10%)	8	30
9	H	90/116 (78%)	83 (92%)	7 (8%)	11	37
10	I	89/120 (74%)	79 (89%)	10 (11%)	6	22
11	J	102/108 (94%)	89 (87%)	13 (13%)	4	18
12	K	119/120 (99%)	109 (92%)	10 (8%)	10	35
13	L	100/100 (100%)	91 (91%)	9 (9%)	9	32
14	M	112/114 (98%)	102 (91%)	10 (9%)	9	32
15	N	114/116 (98%)	102 (90%)	12 (10%)	6	25
16	O	97/158 (61%)	87 (90%)	10 (10%)	7	26
17	P	93/94 (99%)	83 (89%)	10 (11%)	6	24
18	Q	100/100 (100%)	90 (90%)	10 (10%)	7	27
19	R	97/99 (98%)	92 (95%)	5 (5%)	21	49
20	S	81/83 (98%)	71 (88%)	10 (12%)	4	19
21	T	90/117 (77%)	82 (91%)	8 (9%)	9	32
22	U	83/85 (98%)	77 (93%)	6 (7%)	13	40
23	V	81/86 (94%)	74 (91%)	7 (9%)	10	34
24	W	155/168 (92%)	123 (79%)	32 (21%)	1	6
25	X	58/63 (92%)	53 (91%)	5 (9%)	10	34
26	Y	50/51 (98%)	45 (90%)	5 (10%)	7	27
27	Z	58/66 (88%)	55 (95%)	3 (5%)	21	49
28	a	52/54 (96%)	49 (94%)	3 (6%)	18	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	b	43/46 (94%)	36 (84%)	7 (16%)	2	11
30	c	47/52 (90%)	40 (85%)	7 (15%)	3	14
31	d	35/36 (97%)	32 (91%)	3 (9%)	10	34
32	e	53/54 (98%)	47 (89%)	6 (11%)	5	22
33	f	35/35 (100%)	33 (94%)	2 (6%)	18	47
34	g	51/63 (81%)	43 (84%)	8 (16%)	2	12
36	BB	30/31 (97%)	24 (80%)	6 (20%)	1	6
37	BC	170/212 (80%)	157 (92%)	13 (8%)	12	38
38	BD	175/176 (99%)	164 (94%)	11 (6%)	16	44
39	BE	127/147 (86%)	113 (89%)	14 (11%)	6	23
40	BF	85/85 (100%)	76 (89%)	9 (11%)	6	25
41	BG	131/132 (99%)	119 (91%)	12 (9%)	8	31
42	BH	107/108 (99%)	99 (92%)	8 (8%)	12	38
43	BI	102/125 (82%)	87 (85%)	15 (15%)	3	14
44	BJ	89/90 (99%)	81 (91%)	8 (9%)	9	32
45	BK	89/105 (85%)	80 (90%)	9 (10%)	7	27
46	BL	103/105 (98%)	86 (84%)	17 (16%)	2	11
47	BM	99/104 (95%)	85 (86%)	14 (14%)	3	15
48	BN	49/50 (98%)	45 (92%)	4 (8%)	10	36
49	BO	76/77 (99%)	71 (93%)	5 (7%)	15	43
50	BP	92/118 (78%)	80 (87%)	12 (13%)	4	17
51	BQ	80/83 (96%)	71 (89%)	9 (11%)	5	22
52	BR	55/72 (76%)	53 (96%)	2 (4%)	31	58
53	BS	73/84 (87%)	63 (86%)	10 (14%)	3	16
54	BT	69/70 (99%)	59 (86%)	10 (14%)	3	14
55	BV	191/218 (88%)	163 (85%)	28 (15%)	3	14
All	All	4938/5375 (92%)	4399 (89%)	539 (11%)	8	24

5 of 539 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
49	BO	46	HIS
50	BP	70	VAL

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Mol	Chain	Res	Type
48	BN	56	VAL
55	BV	73	LYS
17	P	74	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 126 such sidechains are listed below:

Mol	Chain	Res	Type
24	W	46	HIS
50	BP	41	HIS
32	e	31	HIS
49	BO	28	GLN
54	BT	52	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	A	3118/3120 (99%)	740 (23%)	29 (0%)
3	B	117/118 (99%)	23 (19%)	1 (0%)
35	BA	1510/1528 (98%)	363 (24%)	13 (0%)
56	BW	75/76 (98%)	20 (26%)	0
57	BX	5/6 (83%)	2 (40%)	0
All	All	4825/4848 (99%)	1148 (23%)	43 (0%)

5 of 1148 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	A	7	U
2	A	12	G
2	A	20	G
2	A	29	C
2	A	31	U

5 of 43 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A	3113	A
35	BA	895	A
3	B	10	G
35	BA	456	C
35	BA	1116	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 632 ligands modelled in this entry, 631 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
60	PHE	BW	101	-	10,11,12	0.87	0	8,13,15	0.22	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	PHE	BW	101	-	-	0/5/6/8	0/1/1/1

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](#)

There are no chain breaks in this entry.

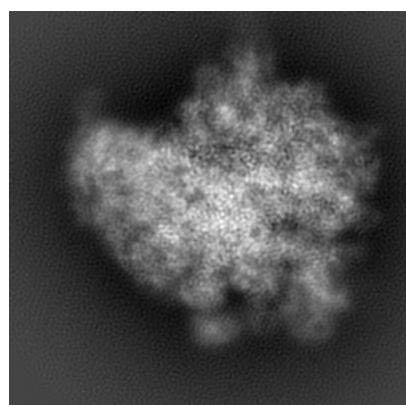
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3751. These allow visual inspection of the internal detail of the map and identification of artifacts.

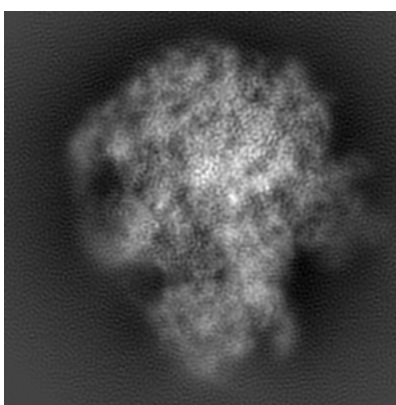
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

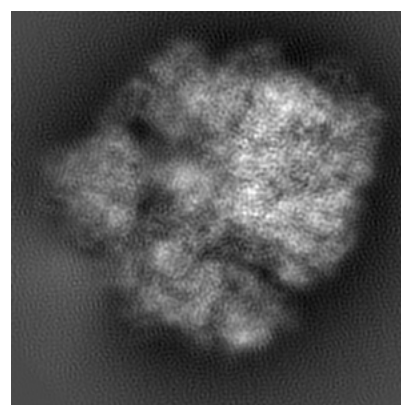
6.1.1 Primary map



X



Y

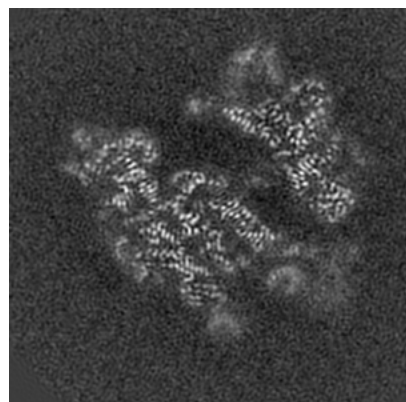


Z

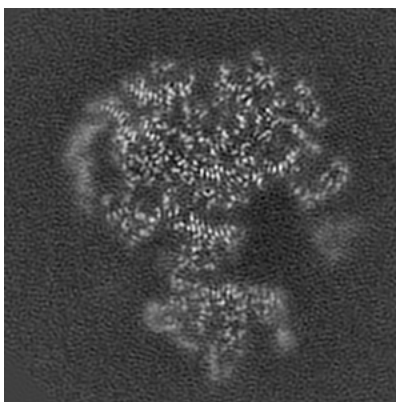
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

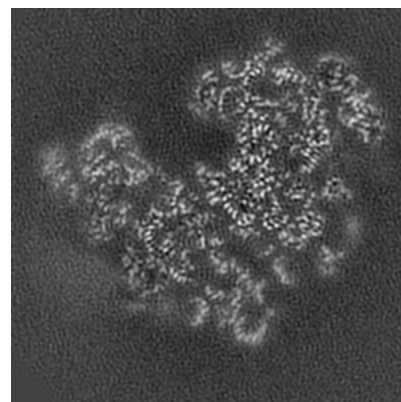
6.2.1 Primary map



X Index: 108



Y Index: 108

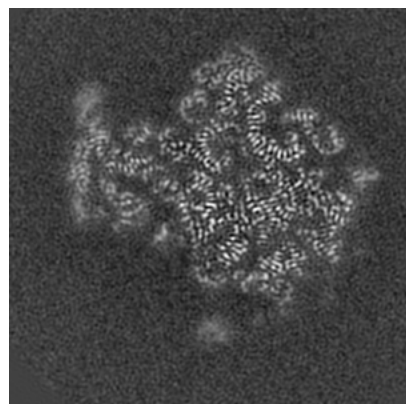


Z Index: 108

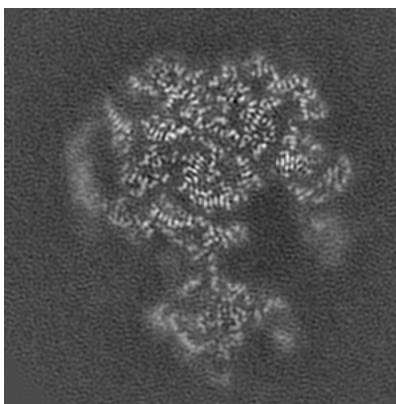
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

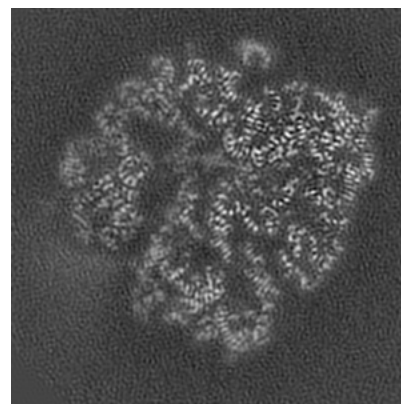
6.3.1 Primary map



X Index: 126



Y Index: 112

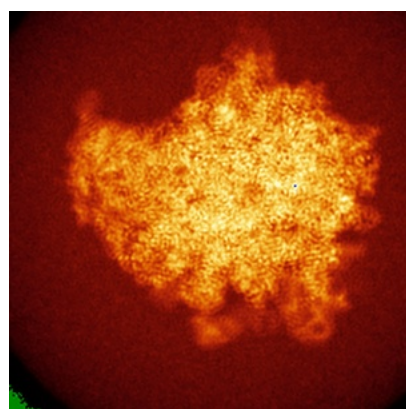


Z Index: 123

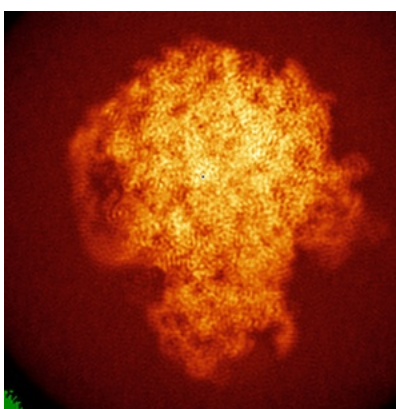
The images above show the largest variance slices of the map in three orthogonal directions.

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

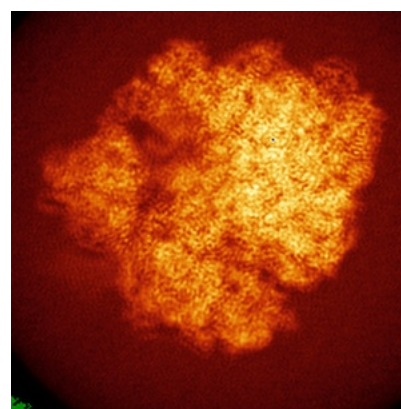
6.4.1 Primary map



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 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

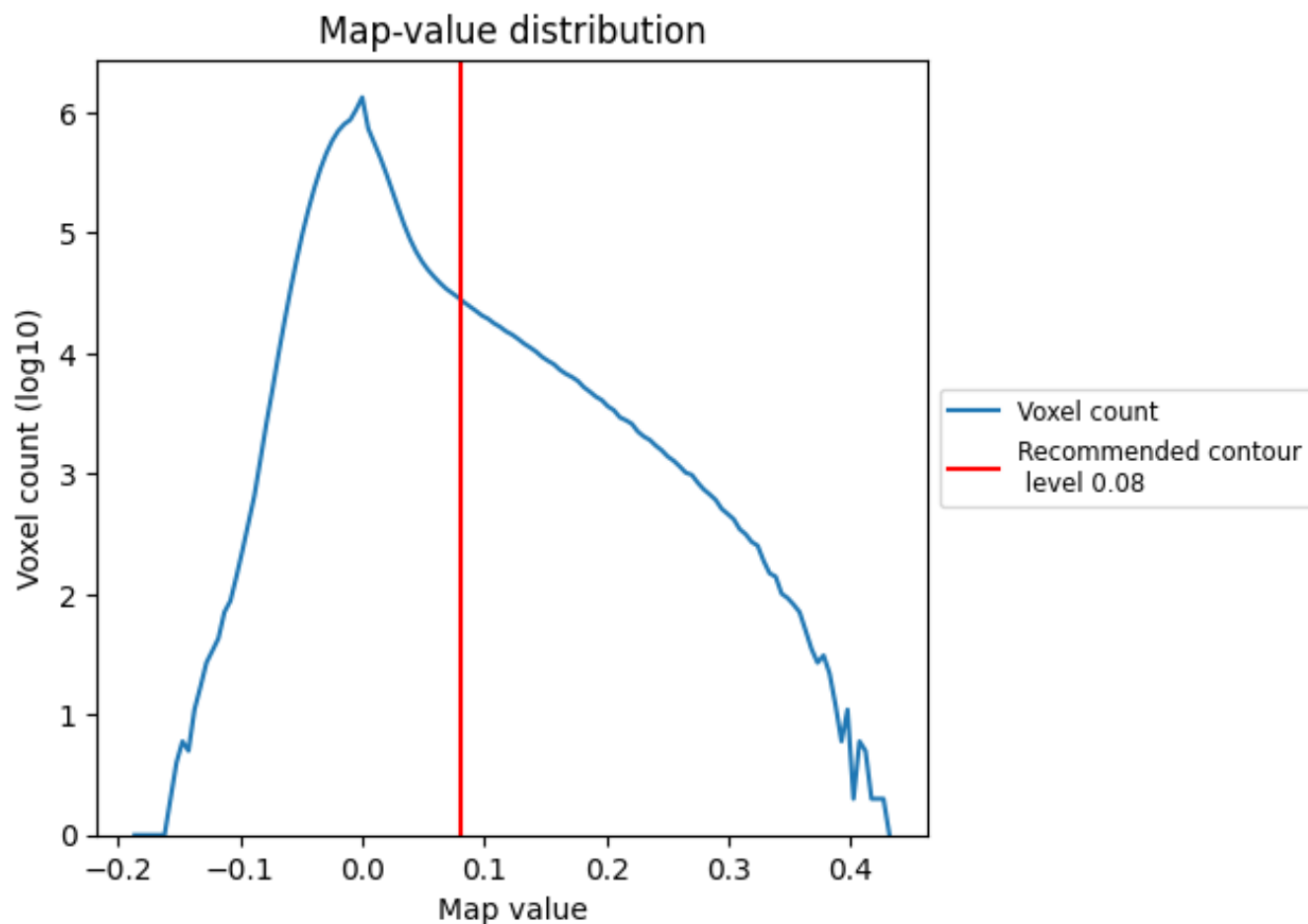
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

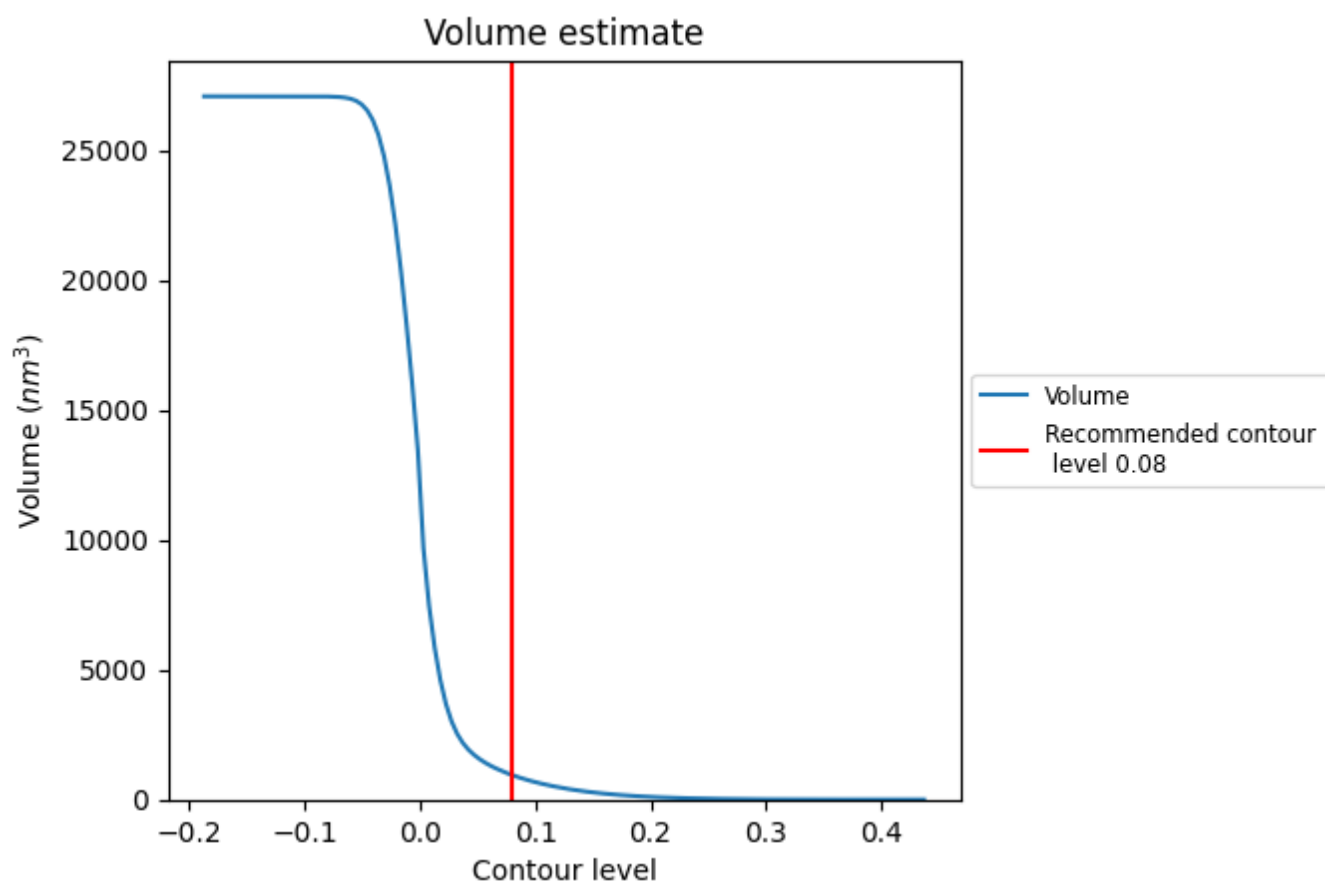
This section contains the results of statistical analysis of the map.

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.

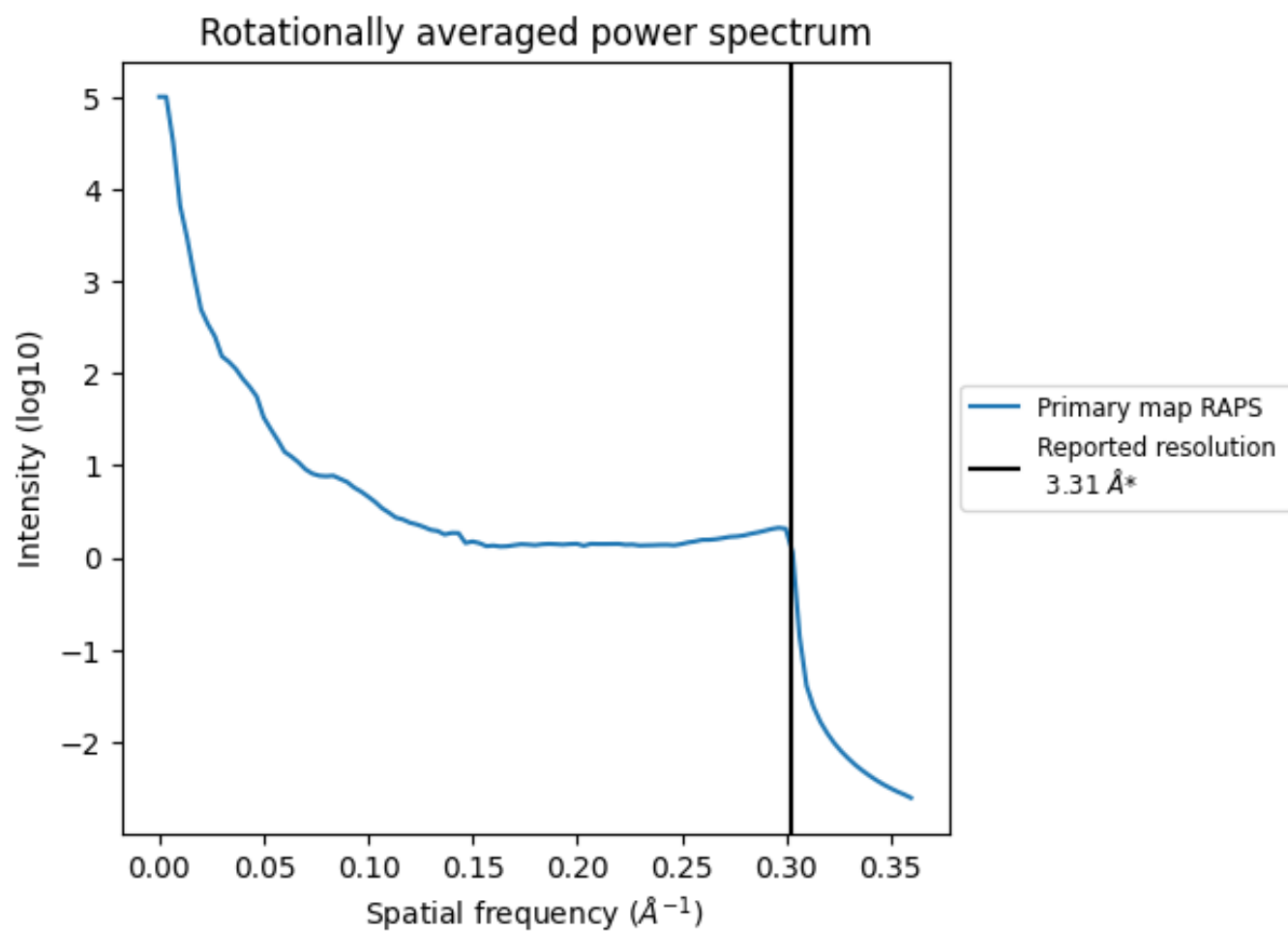
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 945 nm³; this corresponds to an approximate mass of 853 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 ⓘ

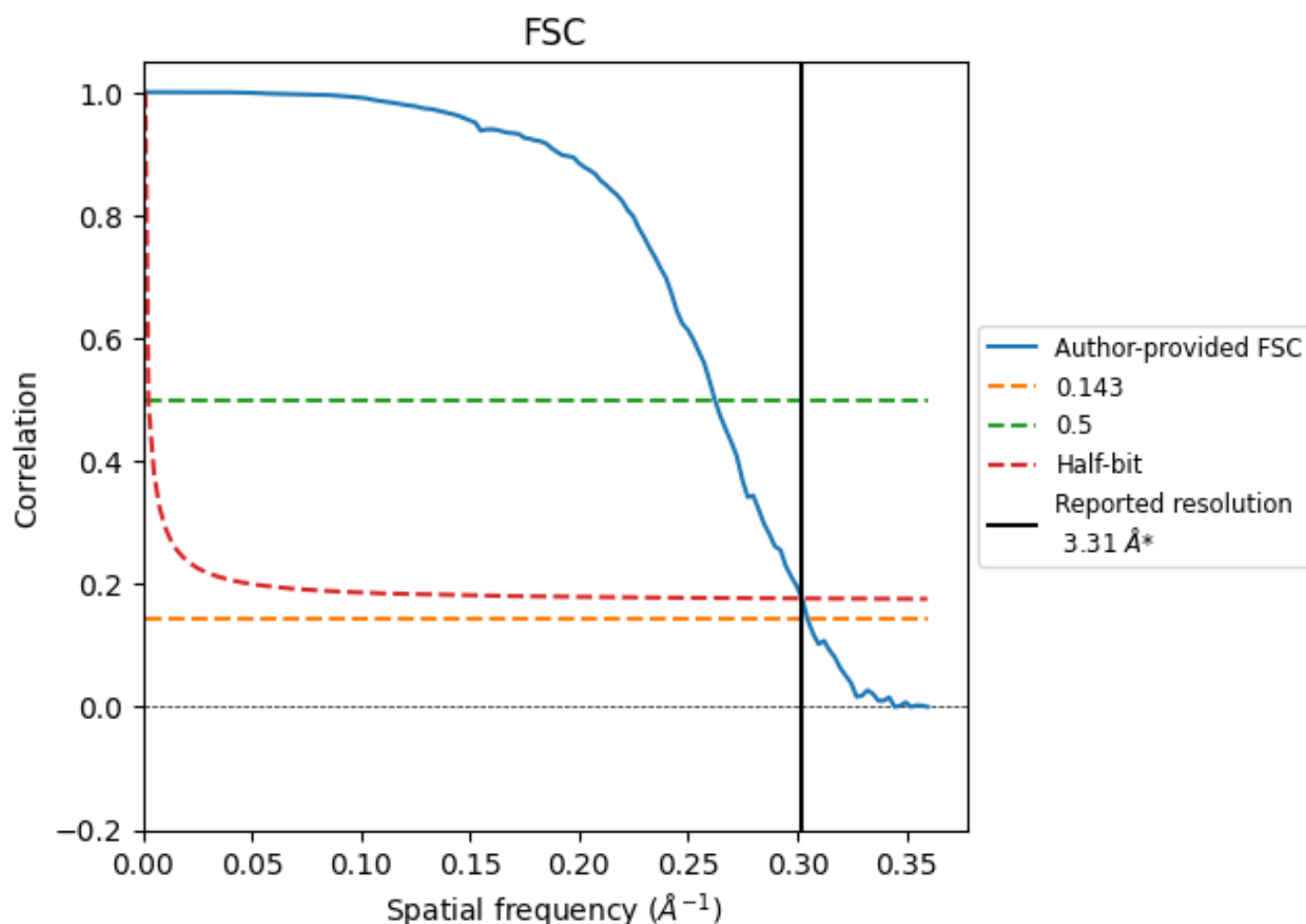


*Reported resolution corresponds to spatial frequency of 0.302 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.302 Å⁻¹

8.2 Resolution estimates [i](#)

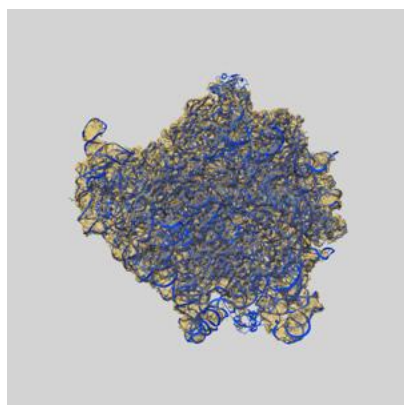
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.31	-	-
Author-provided FSC curve	3.28	3.81	3.31
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

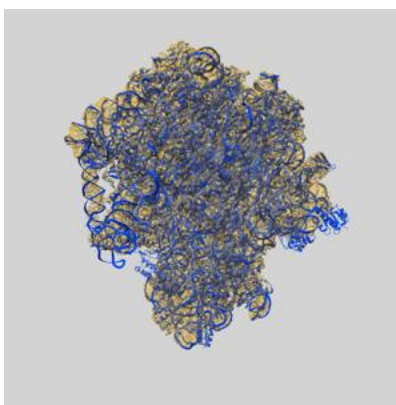
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3751 and PDB model 5O61. Per-residue inclusion information can be found in section [3](#) on page [16](#).

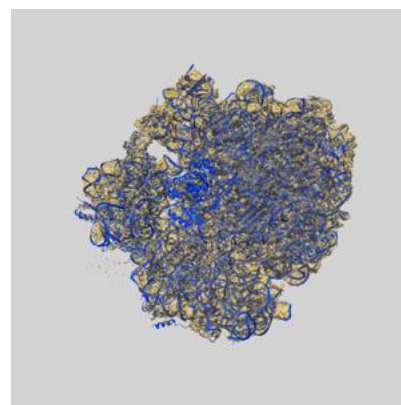
9.1 Map-model overlay [i](#)



X



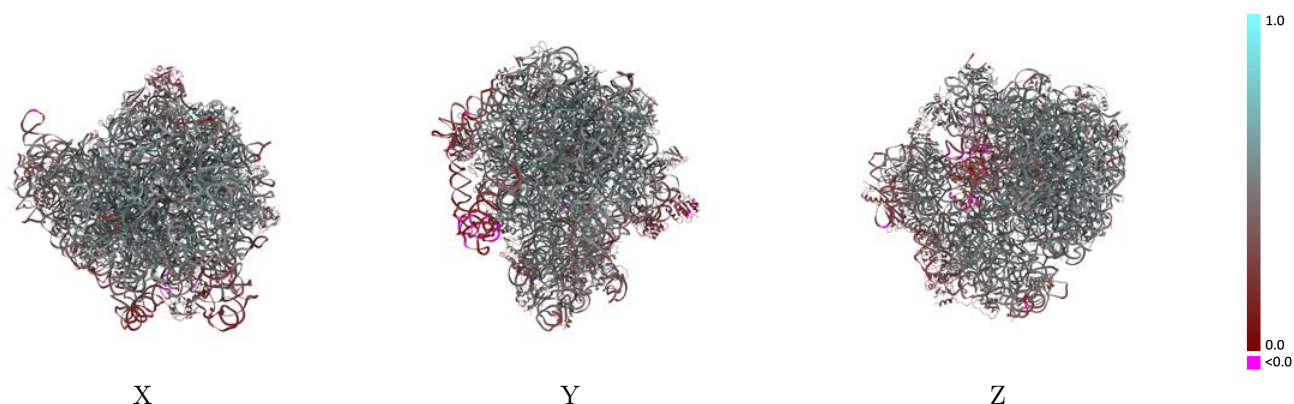
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.08 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](#)



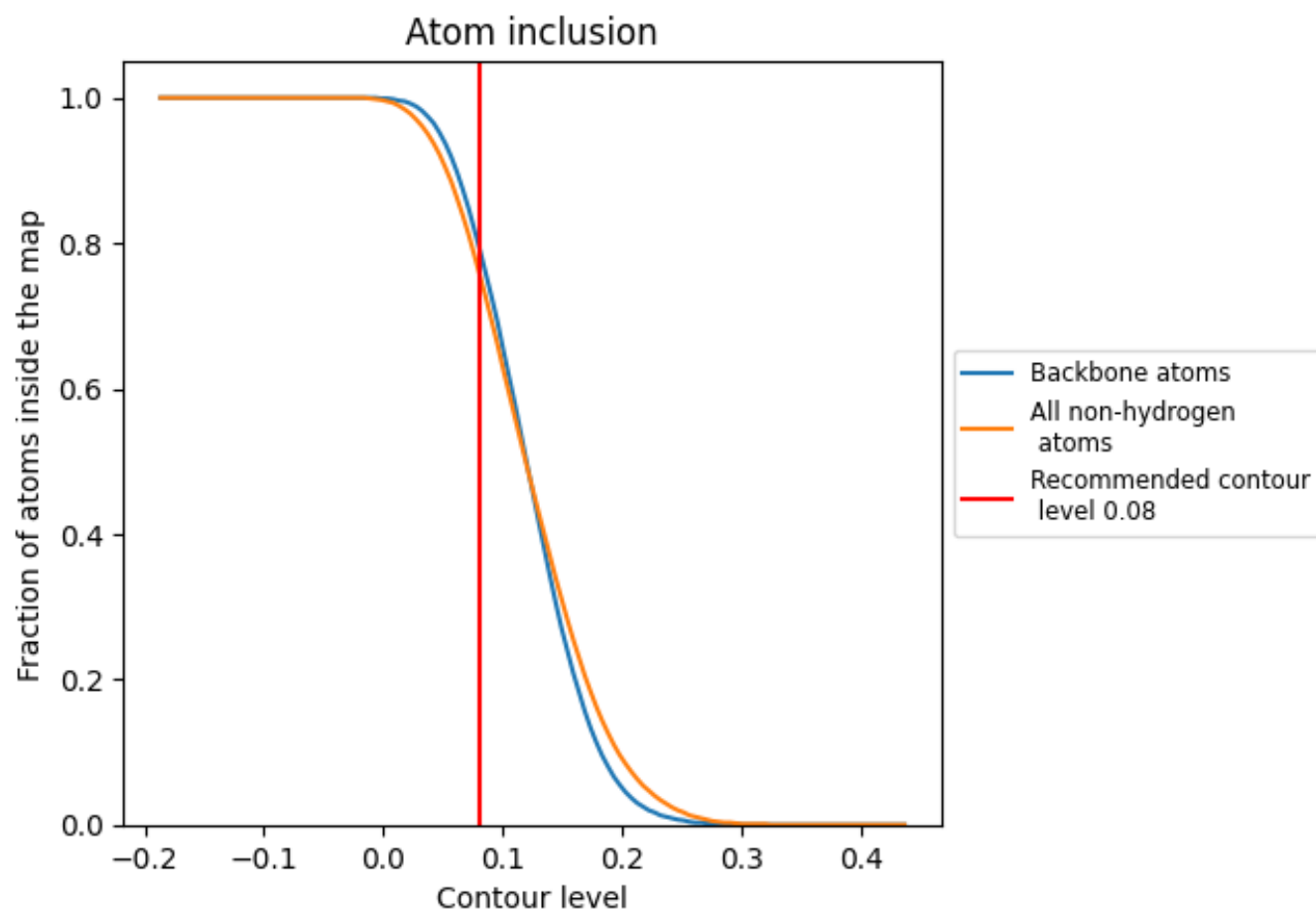
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 76% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7620	 0.4620
3	 0.7040	 0.5240
A	 0.8590	 0.4800
B	 0.9020	 0.4840
BA	 0.8550	 0.4660
BB	 0.3780	 0.4470
BC	 0.3910	 0.3980
BD	 0.3610	 0.3230
BE	 0.5240	 0.4420
BF	 0.5210	 0.4160
BG	 0.5020	 0.4050
BH	 0.6810	 0.4830
BI	 0.6010	 0.4290
BJ	 0.4170	 0.3740
BK	 0.6170	 0.4460
BL	 0.5590	 0.4300
BM	 0.5590	 0.4240
BN	 0.6410	 0.4820
BO	 0.6410	 0.4570
BP	 0.5360	 0.4050
BQ	 0.5220	 0.4060
BR	 0.6180	 0.4440
BS	 0.5380	 0.4370
BT	 0.6340	 0.4150
BV	 0.0260	 0.2650
BW	 0.2710	 0.3630
BX	 0.4620	 0.4330
C	 0.7050	 0.5220
D	 0.7460	 0.5190
E	 0.6900	 0.4870
F	 0.6260	 0.4240
G	 0.5840	 0.4130
H	 0.1910	 0.3450
I	 0.0490	 0.1790
J	 0.0730	 0.1860



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Chain	Atom inclusion	Q-score
K	 0.7330	 0.5090
L	 0.6170	 0.4860
M	 0.6860	 0.4880
N	 0.6710	 0.5050
O	 0.7430	 0.5120
P	 0.7310	 0.4750
Q	 0.6540	 0.4760
R	 0.7770	 0.5130
S	 0.6970	 0.5070
T	 0.7050	 0.5050
U	 0.6310	 0.4680
V	 0.5920	 0.4510
W	 0.5160	 0.4180
X	 0.7470	 0.5240
Y	 0.7050	 0.5150
Z	 0.6670	 0.4380
a	 0.7060	 0.4950
b	 0.6870	 0.5100
c	 0.7000	 0.4940
d	 0.7540	 0.5350
e	 0.7350	 0.5290
f	 0.7600	 0.5130
g	 0.6030	 0.3980