



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 03:52 PM UTC

PDB ID : 5ZEB / pdb_00005zeb
EMDB ID : EMD-6920
Title : M. Smegmatis P/P state 70S ribosome structure
Authors : Mishra, S.; Ahmed, T.; Tyagi, A.; Shi, J.; Bhushan, S.
Deposited on : 2018-02-27
Resolution : 3.40 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:

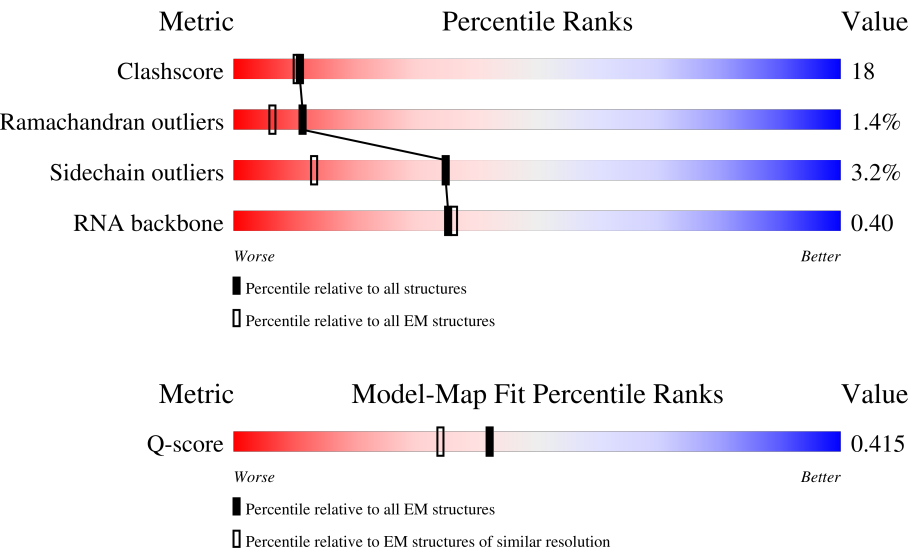
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	a	1528	
2	c	275	
3	e	214	

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Mol	Chain	Length	Quality of chain
4	g	156	
5	h	132	
6	i	150	
7	j	101	
8	k	138	
9	l	124	
10	o	89	
11	q	98	
12	r	84	
13	s	93	
14	t	86	
15	v	77	
16	n	61	
17	b	277	
18	d	201	
19	f	96	
20	m	124	
21	p	156	
22	u	33	
23	C	278	
24	D	217	
25	E	215	
26	F	187	
27	G	179	
28	H	151	

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Mol	Chain	Length	Quality of chain
29	I	175	
30	J	142	
31	K	147	
32	L	122	
33	M	147	
34	N	138	
35	O	199	
36	P	127	
37	Q	113	
38	R	129	
39	S	103	
40	T	153	
41	U	100	
42	V	105	
43	W	215	
44	X	88	
45	Y	64	
46	Z	77	
47	B	118	
48	A	3120	
49	1	61	
50	2	75	
51	3	57	
52	4	55	
53	5	47	

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Mol	Chain	Length	Quality of chain
54	6	64	69%30%.
55	7	37	5% 43%51%. .
56	8	24	12% 79%17%. .

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 150328 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1506	Total	C	N	O	P	0	0
			32341	14404	5921	10510	1506		

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	210	Total	C	N	O	S	0	0
			1672	1043	324	300	5		

- Molecule 3 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	e	198	Total	C	N	O	S	0	0
			1433	885	282	262	4		

- Molecule 4 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	g	156	Total	C	N	O	S	0	0
			1240	773	242	222	3		

- Molecule 5 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	h	130	Total	C	N	O	S	0	0
			1003	629	188	185	1		

- Molecule 6 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	i	126	Total	C	N	O		0	0
			994	630	194	170			

- Molecule 7 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	j	97	Total	C	N	O	S	0	0
			775	488	143	141	3		

- Molecule 8 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	k	117	Total	C	N	O	S	0	0
			871	539	173	158	1		

- Molecule 9 is a protein called 30S ribosomal protein S12.

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

- Molecule 10 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	o	87	Total	C	N	O	0	0
			709	443	143	123		

- Molecule 11 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	q	92	Total	C	N	O	S	0	0
			730	458	138	132	2		

- Molecule 12 is a protein called 30S ribosomal protein S18 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	r	64	Total	C	N	O	S	0	0
			512	319	102	88	3		

- Molecule 13 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	s	78	Total	C	N	O	S	0	0
			630	405	117	107	1		

- Molecule 14 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	t	84	Total	C	N	O	0	0
			655	399	138	118		

- Molecule 15 is a RNA chain called P-tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	v	77	Total	C	N	O	P	0	0
			1643	732	297	537	77		

- Molecule 16 is a protein called 30S ribosomal protein S14 type Z.

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

- Molecule 17 is a protein called 30S ribosomal protein S2.

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

- Molecule 18 is a protein called 30S ribosomal protein S4.

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

- Molecule 19 is a protein called 30S ribosomal protein S6.

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

- Molecule 20 is a protein called 30S ribosomal protein S13.

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

- Molecule 21 is a protein called 30S ribosomal protein S16.

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

- Molecule 22 is a protein called Conserved domain protein.

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

- Molecule 23 is a protein called 50S ribosomal protein L2.

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

- Molecule 24 is a protein called 50S ribosomal protein L3.

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

- Molecule 25 is a protein called 50S ribosomal protein L4.

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

- Molecule 26 is a protein called 50S ribosomal protein L5.

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

- Molecule 27 is a protein called 50S ribosomal protein L6.

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

- Molecule 28 is a protein called 50S ribosomal protein L9.

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

- Molecule 29 is a protein called 50S ribosomal protein L10.

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

- Molecule 30 is a protein called 50S ribosomal protein L11.

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

- Molecule 31 is a protein called 50S ribosomal protein L13.

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

- Molecule 32 is a protein called 50S ribosomal protein L14.

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

- Molecule 33 is a protein called 50S ribosomal protein L15.

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

- Molecule 34 is a protein called 50S ribosomal protein L16.

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

- Molecule 35 is a protein called 50S ribosomal protein L17.

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

- Molecule 36 is a protein called 50S ribosomal protein L18.

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

- Molecule 37 is a protein called 50S ribosomal protein L19.

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

- Molecule 38 is a protein called 50S ribosomal protein L20.

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

- Molecule 39 is a protein called 50S ribosomal protein L21.

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

- Molecule 40 is a protein called 50S ribosomal protein L22.

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

- Molecule 41 is a protein called 50S ribosomal protein L23.

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

- Molecule 42 is a protein called 50S ribosomal protein L24.

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

- Molecule 43 is a protein called 50S ribosomal protein L25.

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

- Molecule 44 is a protein called 50S ribosomal protein L27.

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

- Molecule 45 is a protein called 50S ribosomal protein L28.

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

- Molecule 46 is a protein called 50S ribosomal protein L29.

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

- Molecule 47 is a RNA chain called 5S rRNA.

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

- Molecule 48 is a RNA chain called 23S rRNA.

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

- Molecule 49 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	1	60	Total	C	N	O	0	0
			483	298	97	88		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2	66	Total	C	N	O	S	0	0
			510	316	93	96	5		

- Molecule 51 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 52 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	50	Total	C	N	O	S	0	0
			416	254	86	72	4		

- Molecule 53 is a protein called 50S ribosomal protein L34.

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

- Molecule 54 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	6	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 55 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	7	37	Total	C	N	O	S	0	0
			298	181	66	46	5		

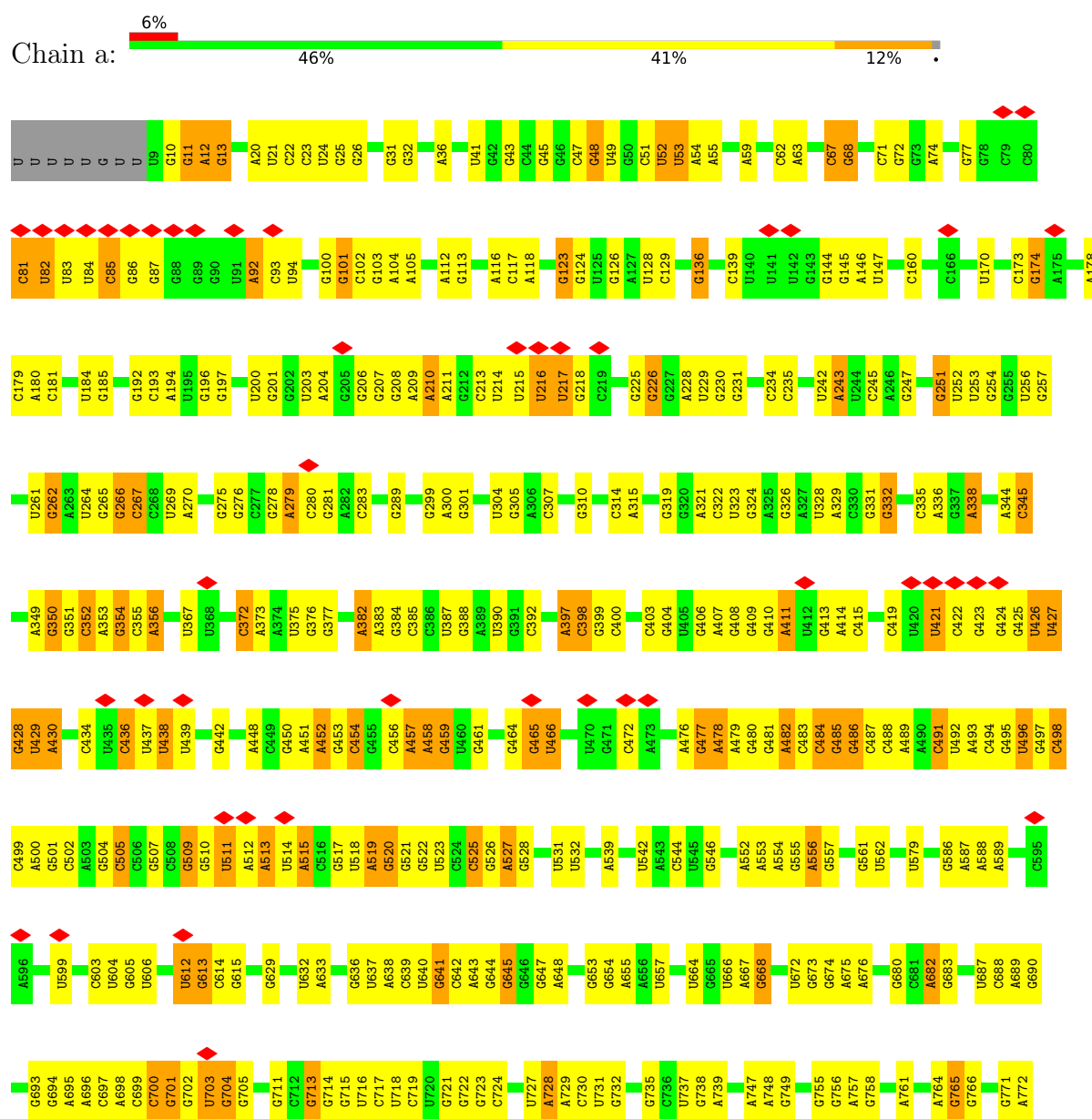
- Molecule 56 is a protein called Uncharacterized protein bL37.

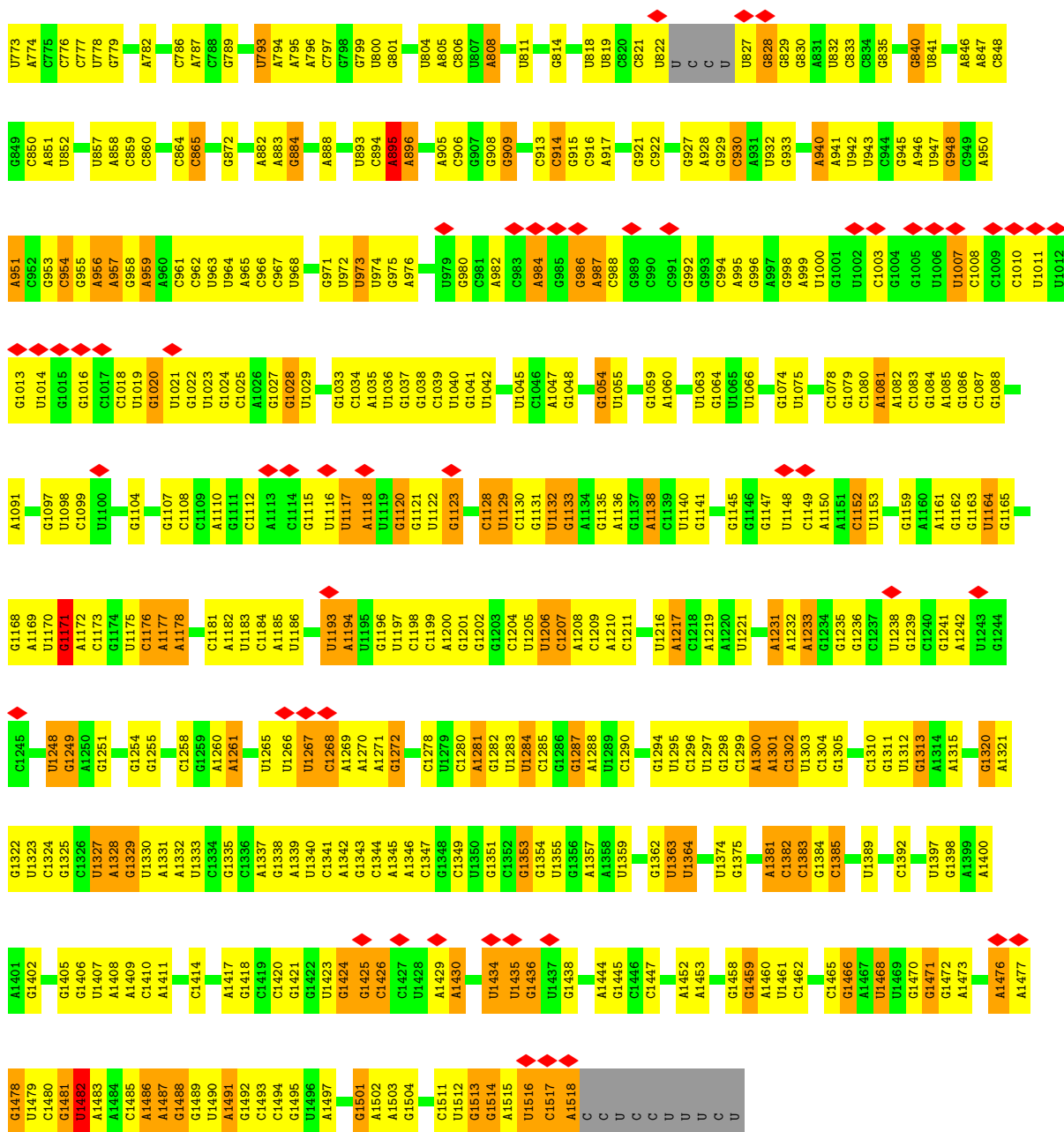
Mol	Chain	Residues	Atoms				AltConf	Trace
56	8	23	Total	C	N	O	0	0
			189	111	50	28		

3 Residue-property plots

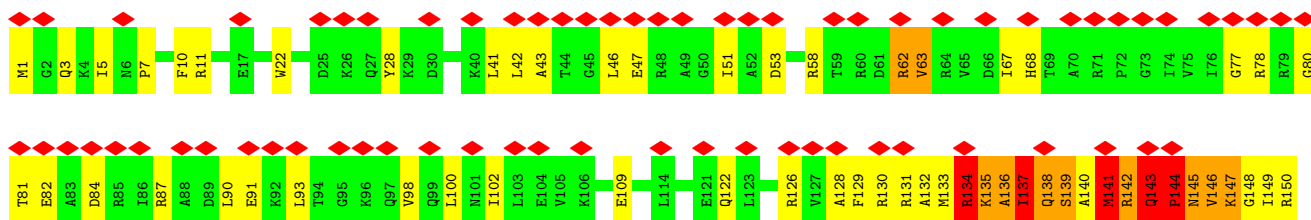
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

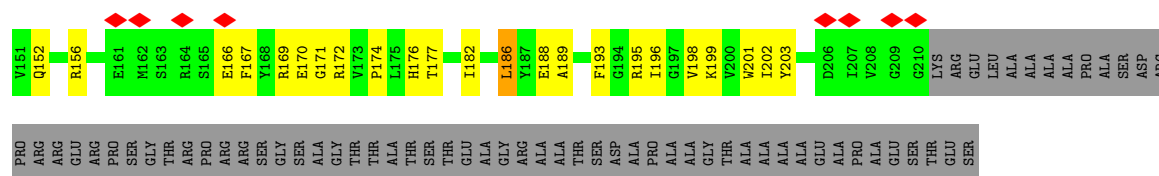
• Molecule 1: 16S rRNA



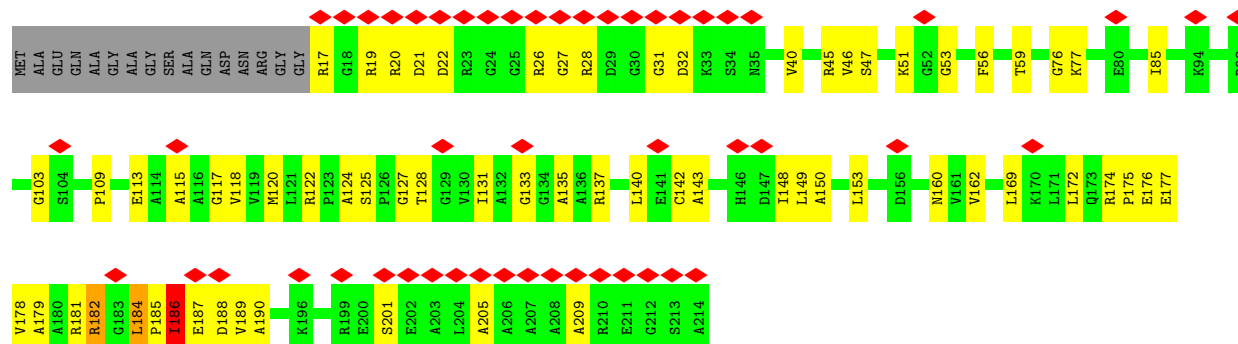


• Molecule 2: 30S ribosomal protein S3

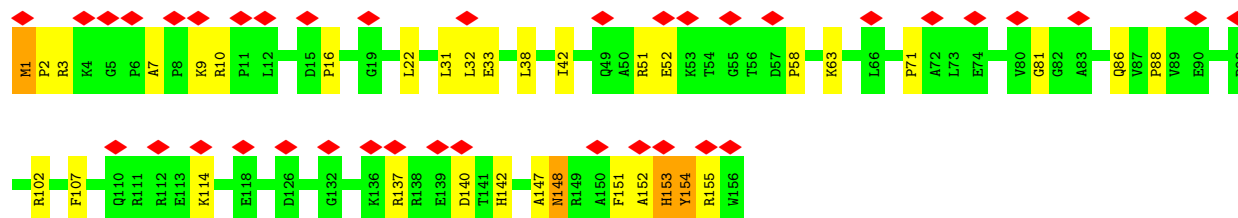
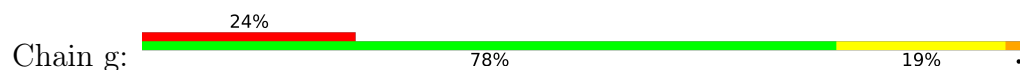




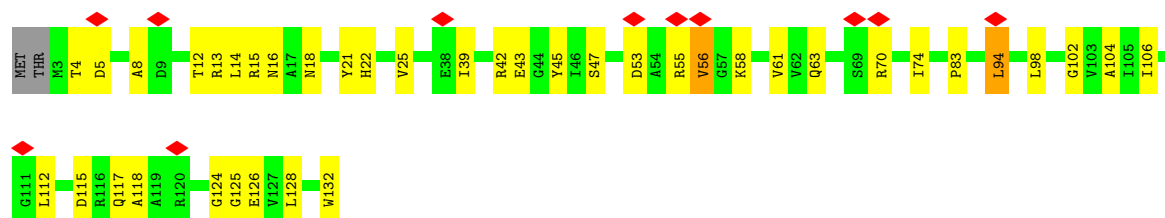
• Molecule 3: 30S ribosomal protein S5



• Molecule 4: 30S ribosomal protein S7

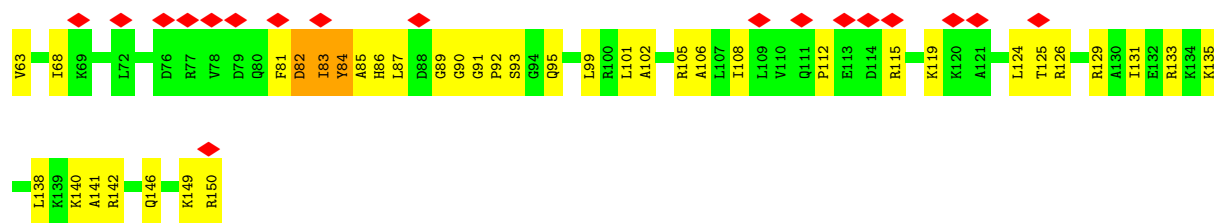


• Molecule 5: 30S ribosomal protein S8

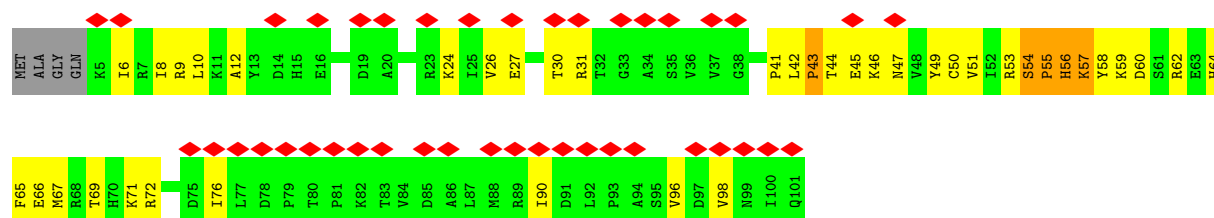
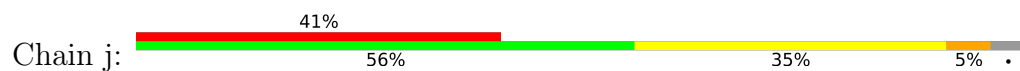


• Molecule 6: 30S ribosomal protein S9

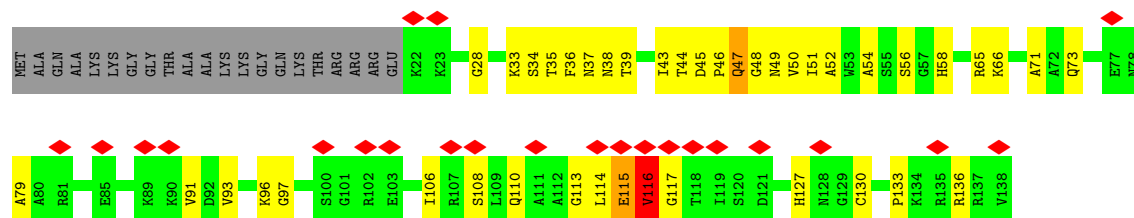




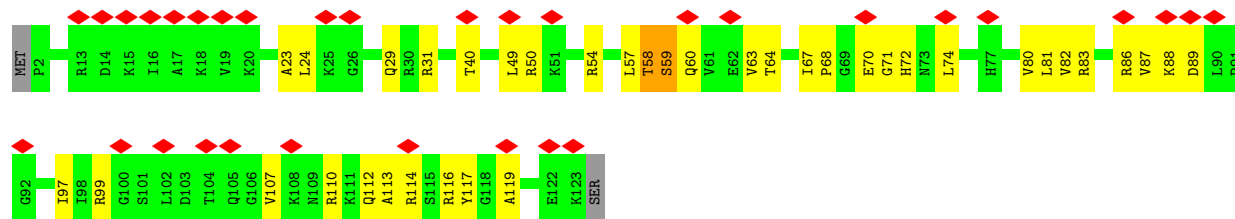
• Molecule 7: 30S ribosomal protein S10



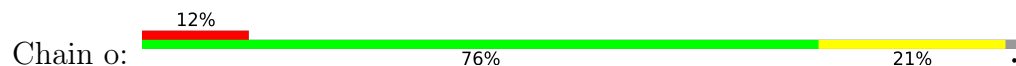
• Molecule 8: 30S ribosomal protein S11



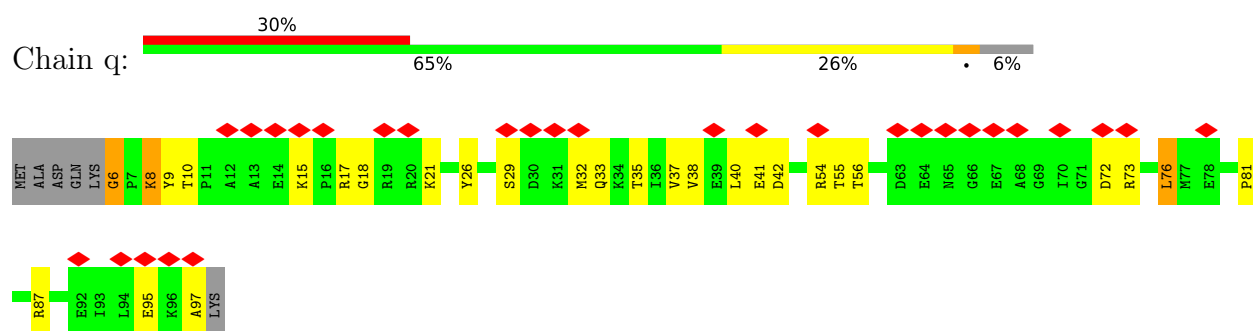
• Molecule 9: 30S ribosomal protein S12



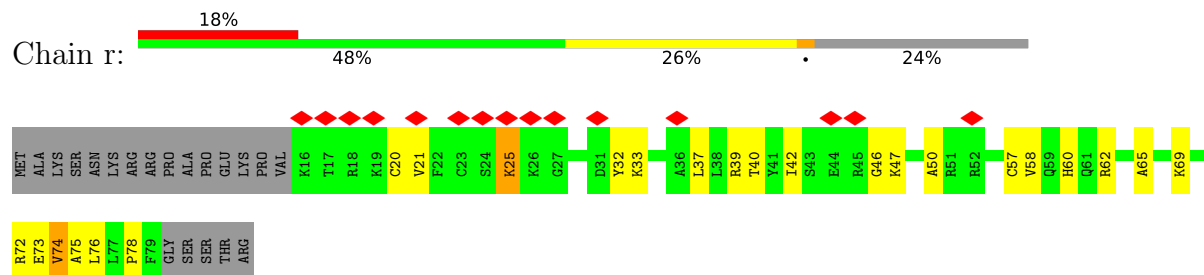
• Molecule 10: 30S ribosomal protein S15



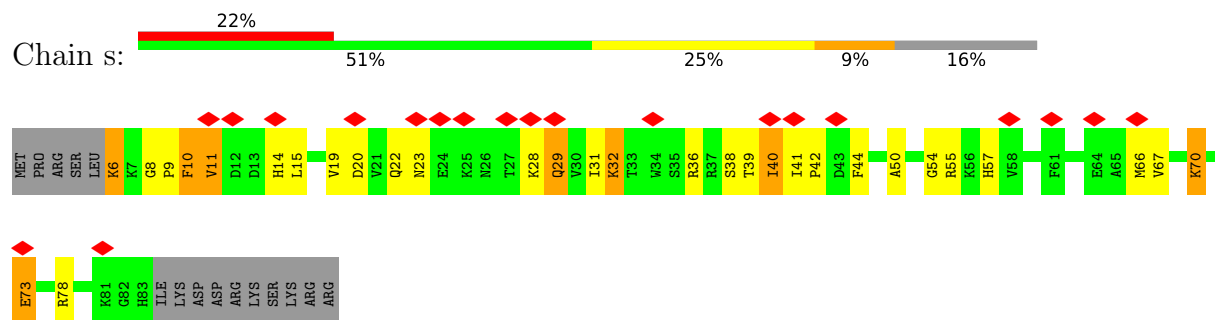
• Molecule 11: 30S ribosomal protein S17



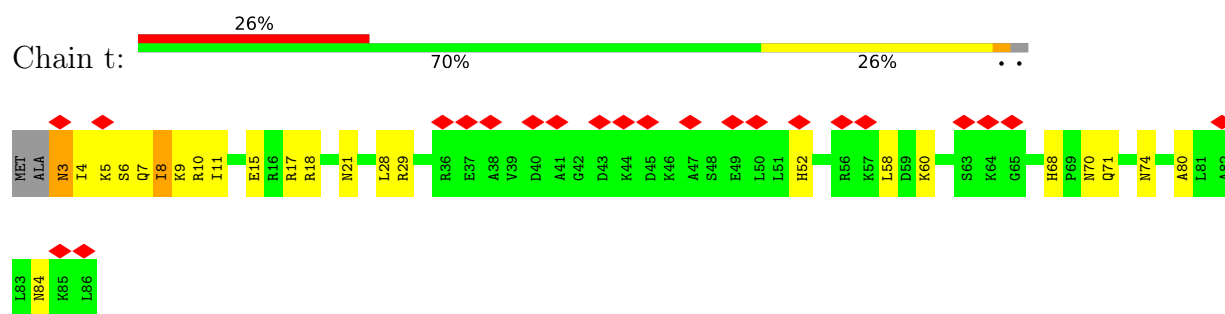
- Molecule 12: 30S ribosomal protein S18 2



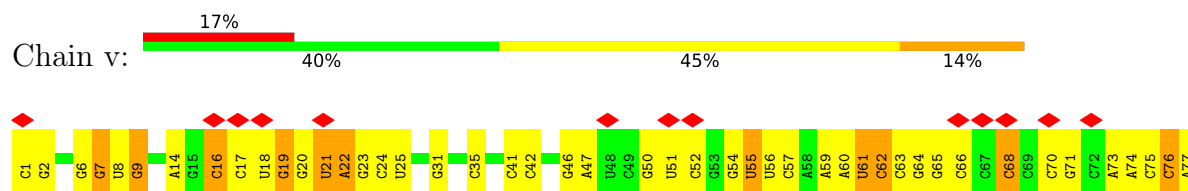
- Molecule 13: 30S ribosomal protein S19



- Molecule 14: 30S ribosomal protein S20



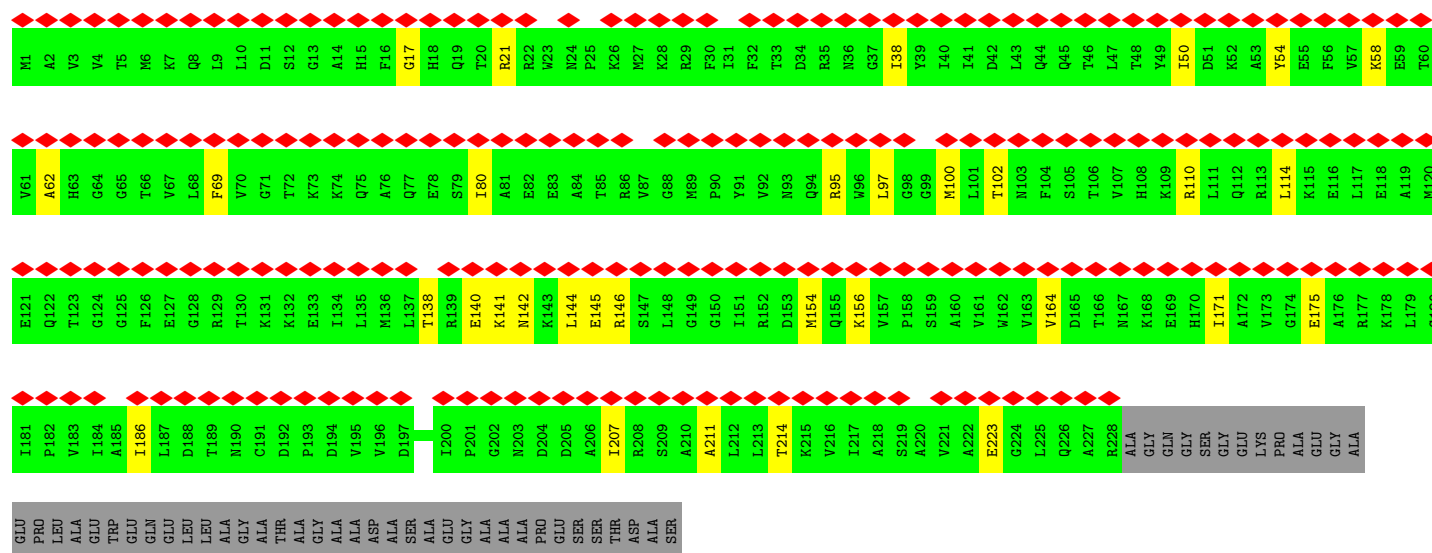
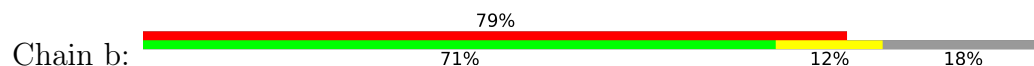
- Molecule 15: P-tRNA^fMet



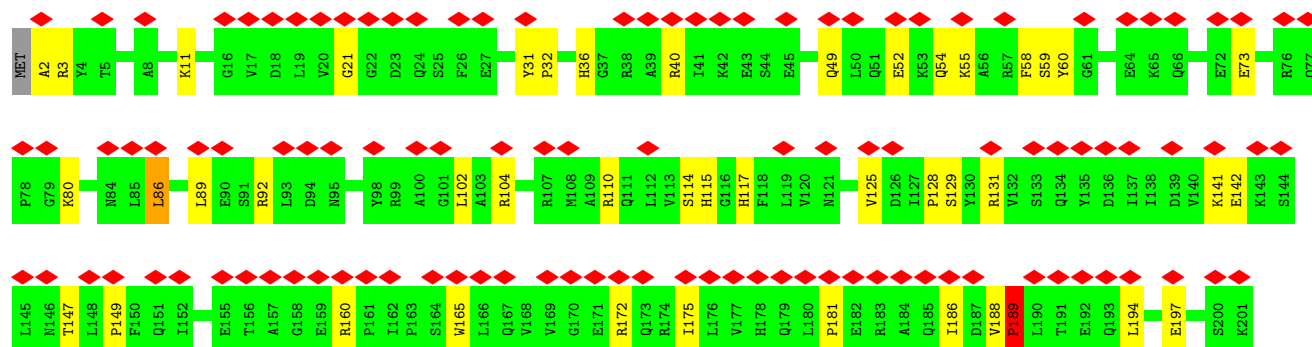
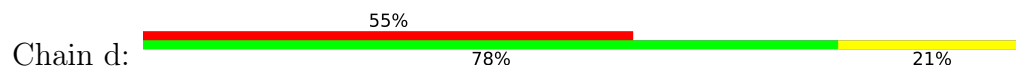
- Molecule 16: 30S ribosomal protein S14 type Z



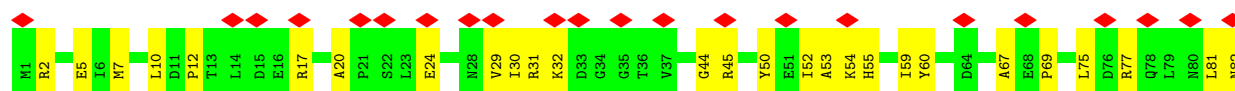
• Molecule 17: 30S ribosomal protein S2



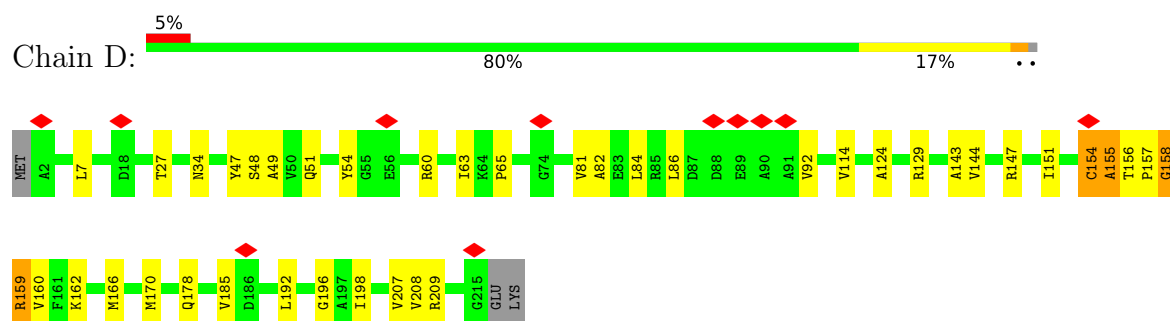
• Molecule 18: 30S ribosomal protein S4



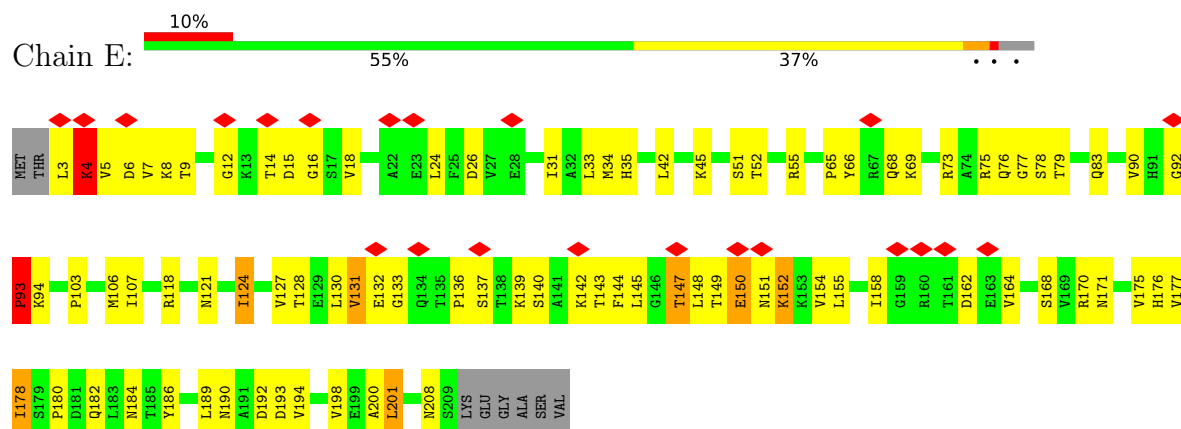
• Molecule 19: 30S ribosomal protein S6



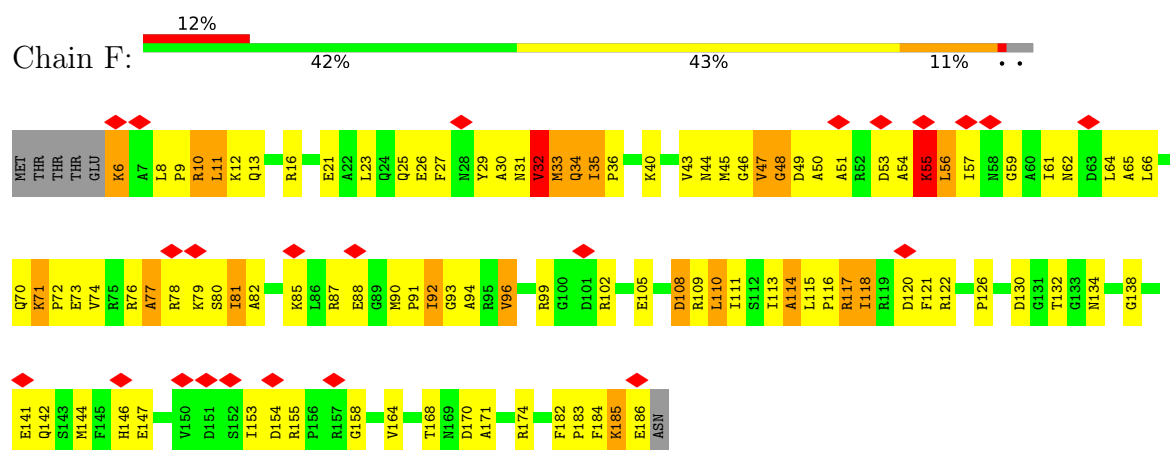
- Molecule 24: 50S ribosomal protein L3



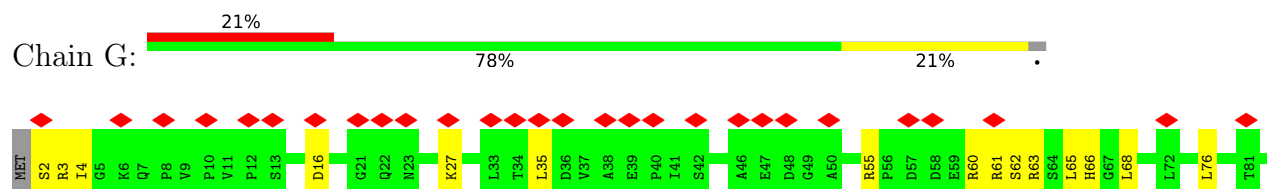
- Molecule 25: 50S ribosomal protein L4

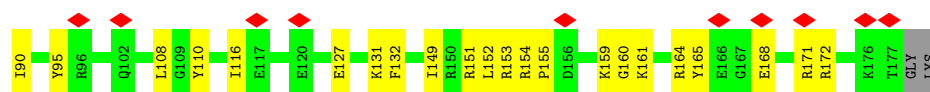


- Molecule 26: 50S ribosomal protein L5

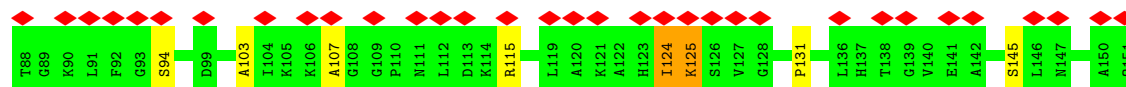
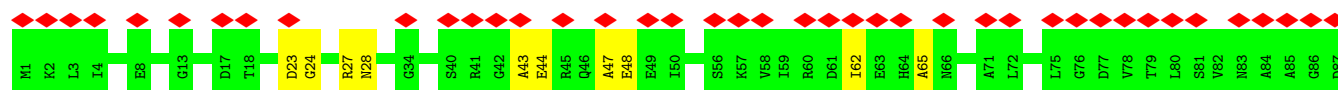
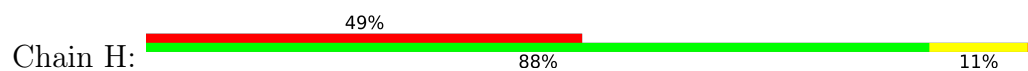


- Molecule 27: 50S ribosomal protein L6

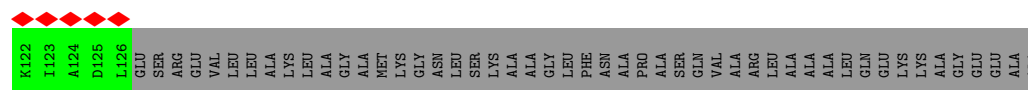
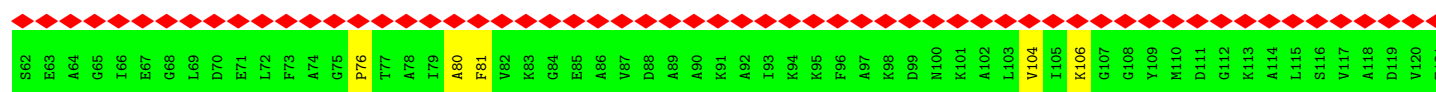
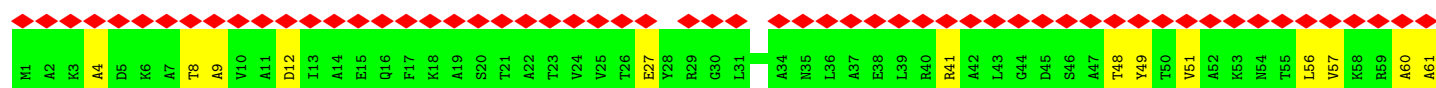




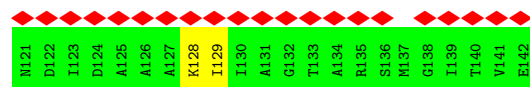
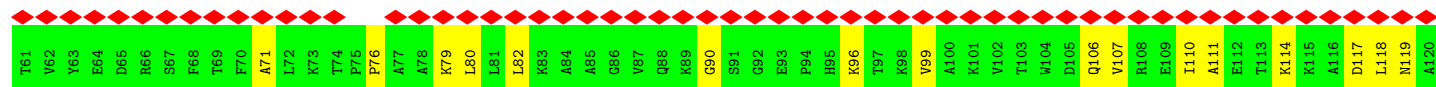
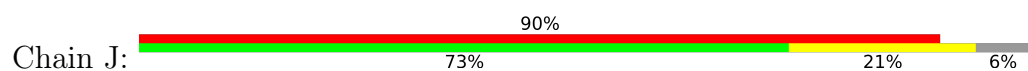
• Molecule 28: 50S ribosomal protein L9



• Molecule 29: 50S ribosomal protein L10

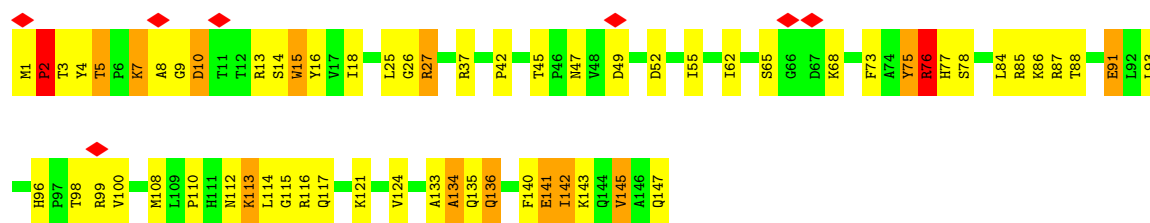


• Molecule 30: 50S ribosomal protein L11

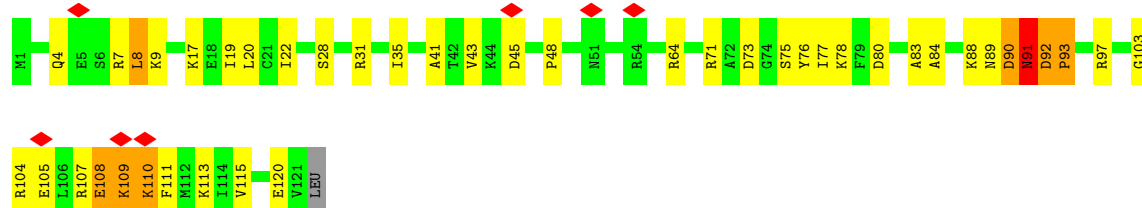


• Molecule 31: 50S ribosomal protein L13

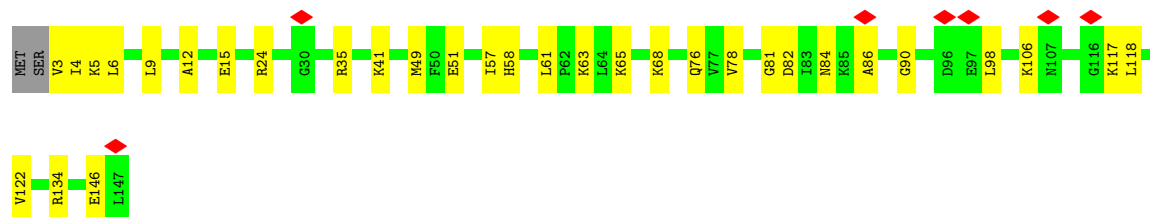
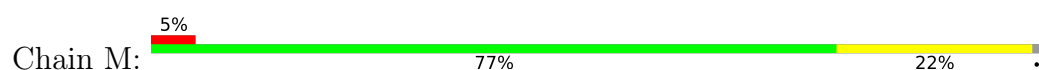




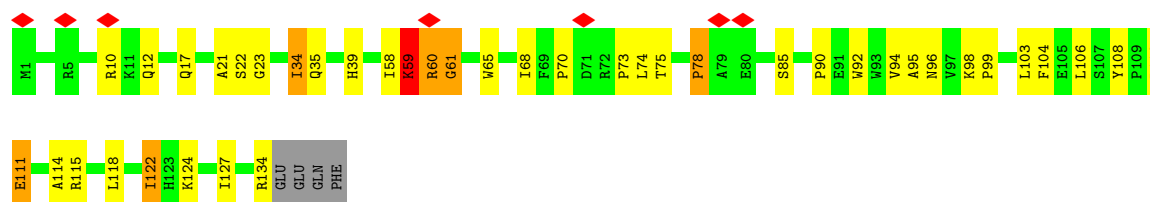
• Molecule 32: 50S ribosomal protein L14



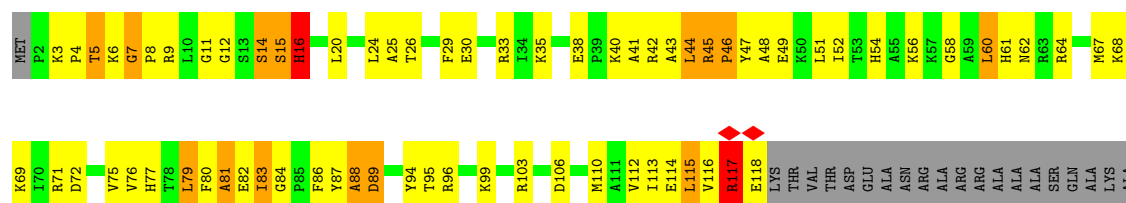
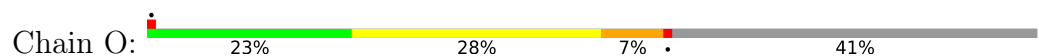
• Molecule 33: 50S ribosomal protein L15

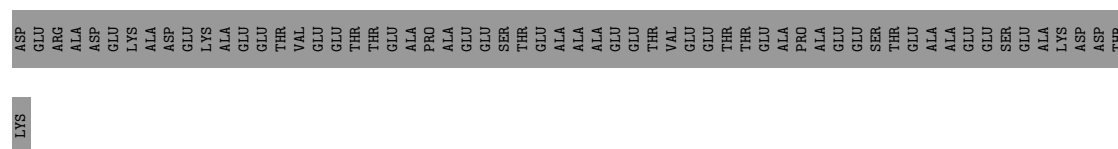


• Molecule 34: 50S ribosomal protein L16

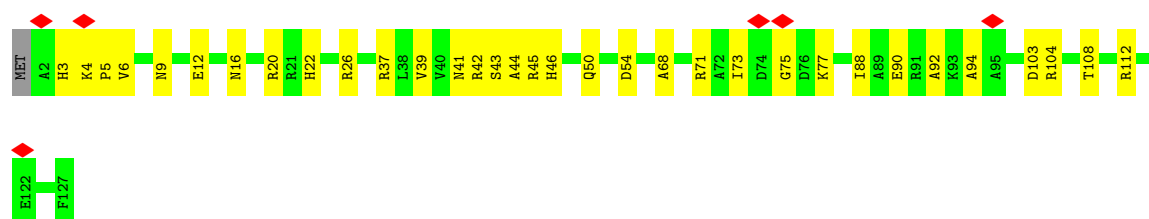


• Molecule 35: 50S ribosomal protein L17





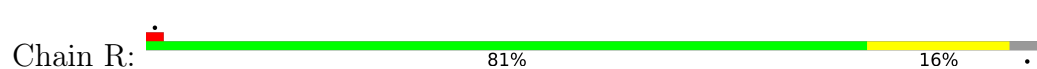
- Molecule 36: 50S ribosomal protein L18



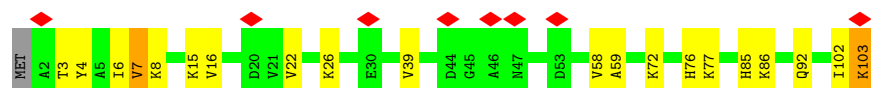
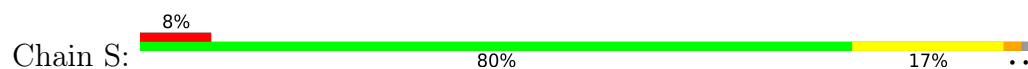
- Molecule 37: 50S ribosomal protein L19



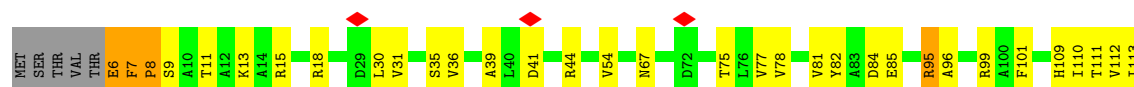
- Molecule 38: 50S ribosomal protein L20

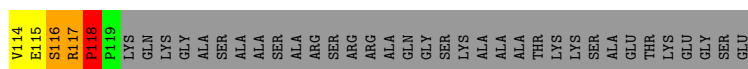


- Molecule 39: 50S ribosomal protein L21

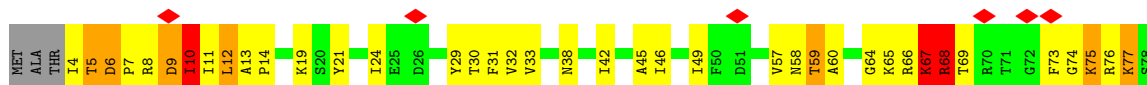
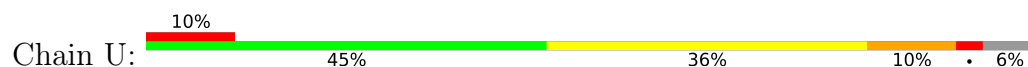


- Molecule 40: 50S ribosomal protein L22

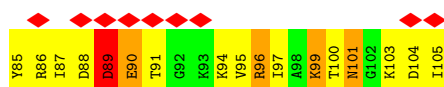




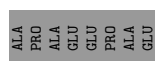
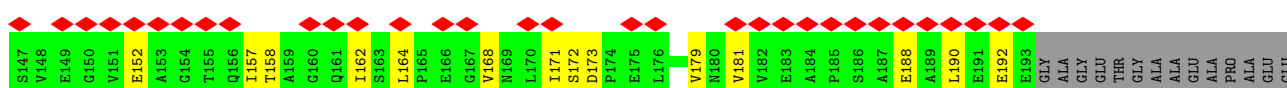
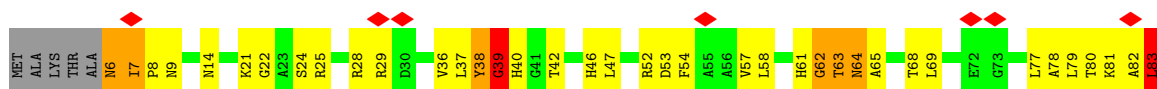
• Molecule 41: 50S ribosomal protein L23



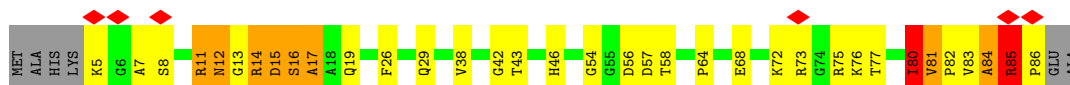
• Molecule 42: 50S ribosomal protein L24



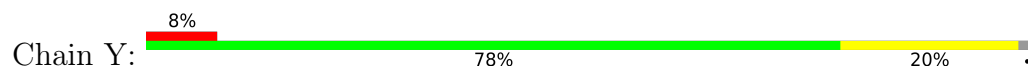
• Molecule 43: 50S ribosomal protein L25



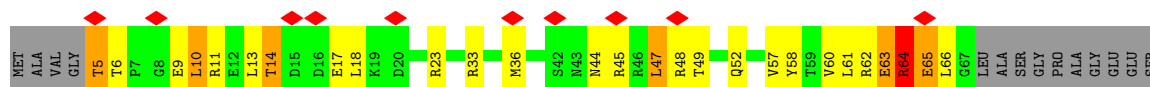
• Molecule 44: 50S ribosomal protein L27



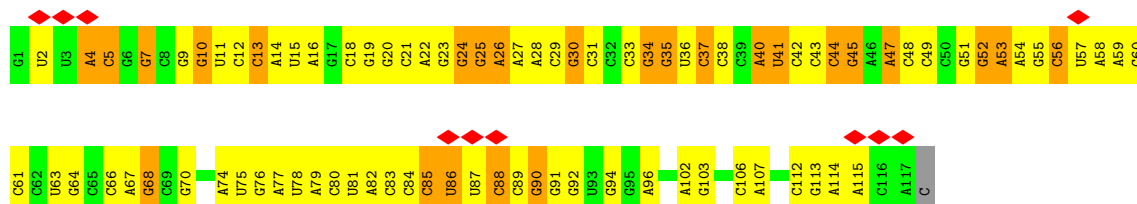
- Molecule 45: 50S ribosomal protein L28



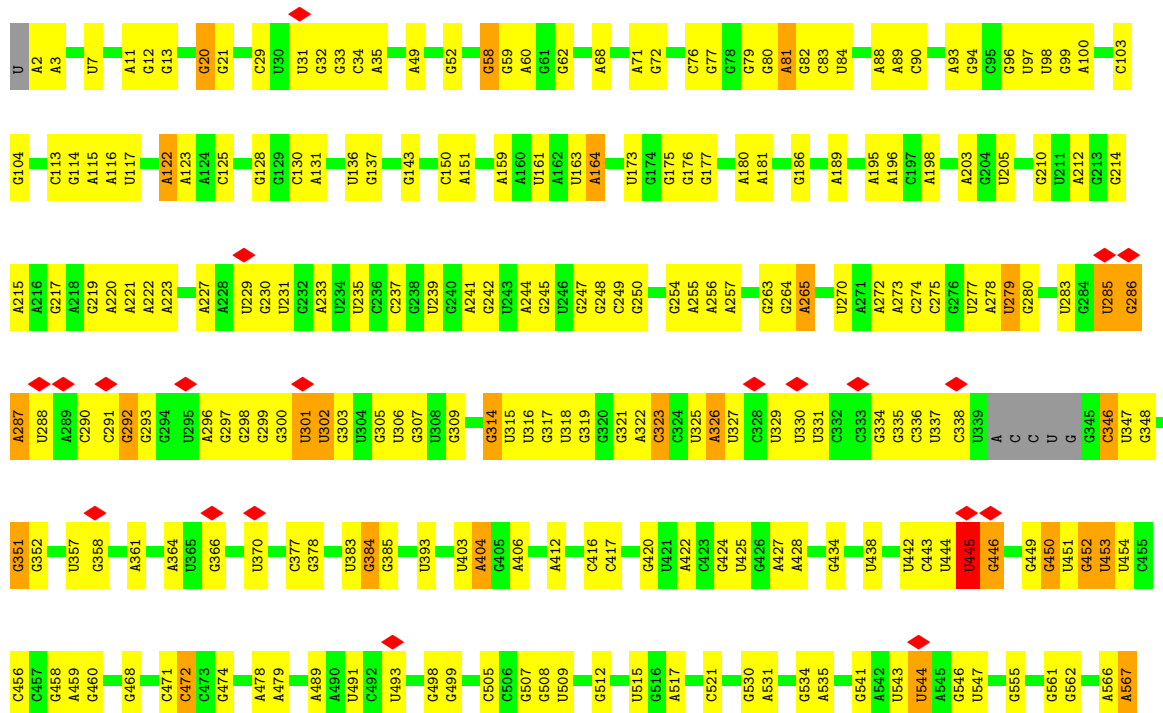
- Molecule 46: 50S ribosomal protein L29

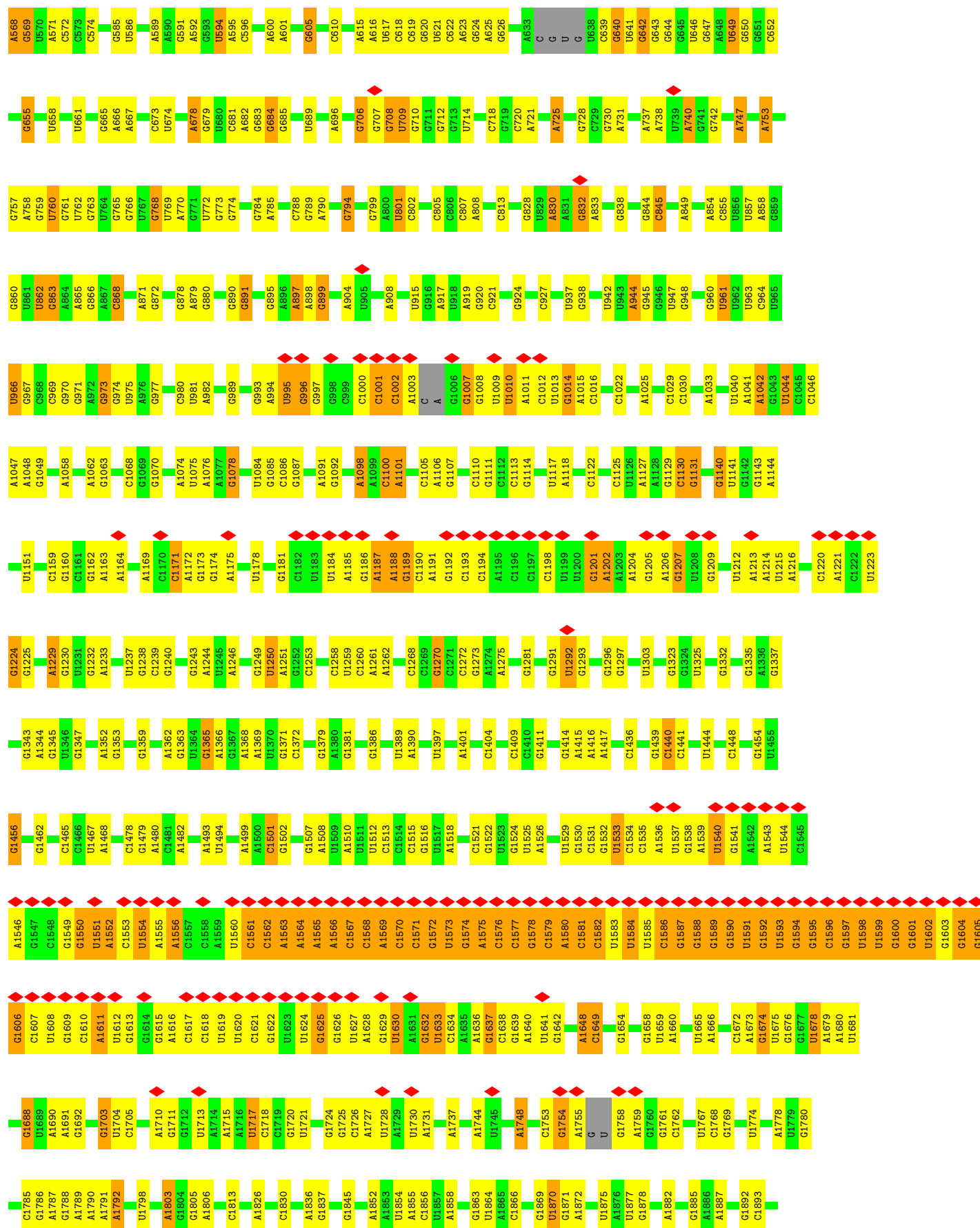


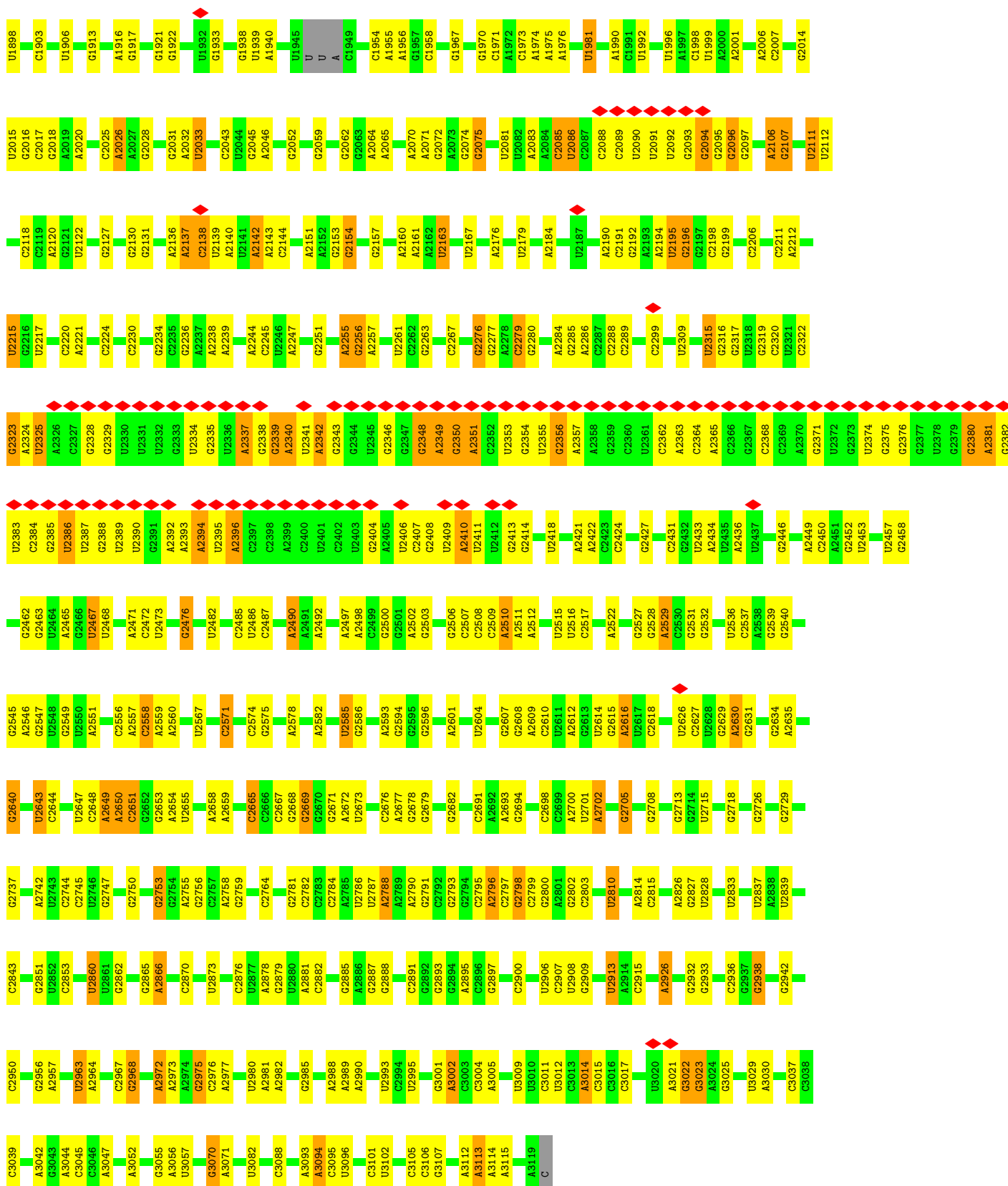
- Molecule 47: 5S rRNA



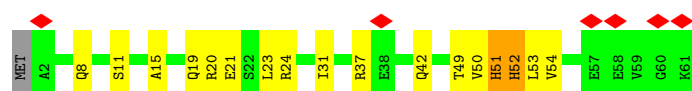
- Molecule 48: 23S rRNA



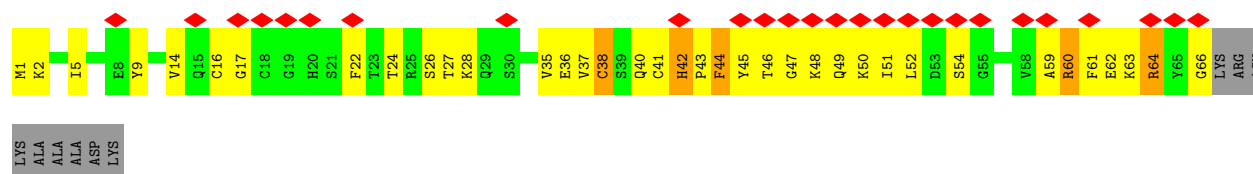




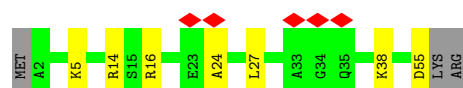
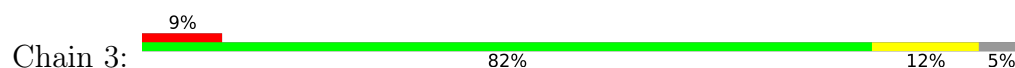
• Molecule 49: 50S ribosomal protein L30



- Molecule 50: 50S ribosomal protein L31



- Molecule 51: 50S ribosomal protein L32



- Molecule 52: 50S ribosomal protein L33 1



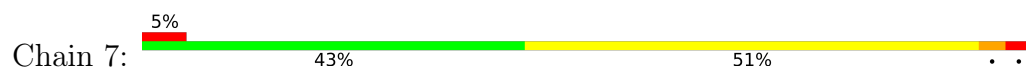
- Molecule 53: 50S ribosomal protein L34

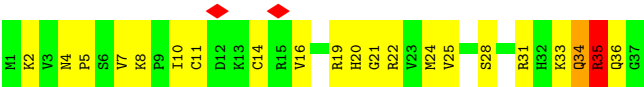


- Molecule 54: 50S ribosomal protein L35

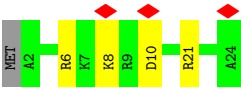
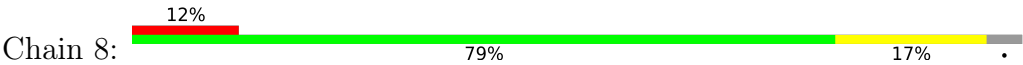


- Molecule 55: 50S ribosomal protein L36





• Molecule 56: Uncharacterized protein bL37



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 ($e^-/\text{\AA}^2$)	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	0.550	Depositor
Minimum map value	-0.382	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.07	Depositor
Map size ($\text{\AA}$)	419.99997, 419.99997, 419.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	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	a	0.40	0/36201	0.52	5/56488 (0.0%)
2	c	0.32	0/1696	0.77	4/2276 (0.2%)
3	e	0.38	0/1449	0.78	3/1949 (0.2%)
4	g	0.30	0/1260	0.71	1/1701 (0.1%)
5	h	0.43	0/1018	0.92	4/1375 (0.3%)
6	i	0.42	1/1012 (0.1%)	0.91	4/1362 (0.3%)
7	j	0.39	0/789	0.78	4/1069 (0.4%)
8	k	0.31	0/889	0.75	2/1201 (0.2%)
9	l	0.41	0/969	0.95	1/1294 (0.1%)
10	o	0.31	0/718	0.66	1/963 (0.1%)
11	q	0.39	0/741	0.74	2/993 (0.2%)
12	r	0.30	0/517	0.78	2/691 (0.3%)
13	s	0.42	0/647	0.96	6/871 (0.7%)
14	t	0.35	0/658	0.68	0/875
15	v	0.21	0/1835	0.38	0/2857
16	n	0.46	0/488	0.67	0/650
17	b	0.25	0/1822	0.62	0/2457
18	d	0.33	0/1672	0.74	2/2251 (0.1%)
19	f	0.35	0/782	0.69	2/1059 (0.2%)
20	m	0.34	0/942	0.75	0/1260
21	p	0.39	0/908	0.69	0/1226
22	u	0.58	0/280	0.93	0/359
23	C	1.01	0/2140	1.15	14/2879 (0.5%)
24	D	0.53	0/1609	0.77	0/2165
25	E	0.86	0/1576	1.06	3/2132 (0.1%)
26	F	0.63	0/1459	1.11	12/1962 (0.6%)
27	G	0.31	0/1369	0.60	0/1848
28	H	0.30	0/1027	0.69	2/1398 (0.1%)
29	I	0.22	0/925	0.56	0/1246
30	J	0.27	0/1006	0.71	0/1364
31	K	0.80	0/1165	1.21	16/1578 (1.0%)
32	L	0.90	0/938	1.11	6/1257 (0.5%)
33	M	0.49	0/1091	0.71	0/1457
34	N	0.91	0/1100	1.19	7/1482 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	O	0.81	1/936 (0.1%)	1.24	13/1256 (1.0%)
36	P	0.38	0/966	0.62	0/1298
37	Q	0.46	0/921	0.70	0/1236
38	R	0.51	0/1000	0.64	0/1341
39	S	0.44	0/778	0.62	0/1048
40	T	0.95	1/887 (0.1%)	1.16	7/1204 (0.6%)
41	U	0.77	0/749	1.18	7/1006 (0.7%)
42	V	0.66	0/737	1.05	4/987 (0.4%)
43	W	0.63	1/1422 (0.1%)	1.17	9/1941 (0.5%)
44	X	0.94	0/613	1.08	1/821 (0.1%)
45	Y	0.52	0/478	0.77	0/641
46	Z	0.69	0/530	0.92	0/708
47	B	0.28	0/2797	0.48	0/4357
48	A	0.47	0/74597	0.51	4/116386 (0.0%)
49	1	0.85	0/486	1.00	1/651 (0.2%)
50	2	0.40	0/520	0.86	1/698 (0.1%)
51	3	0.54	0/427	0.70	0/572
52	4	0.75	0/424	1.10	2/567 (0.4%)
53	5	0.95	0/375	1.34	4/493 (0.8%)
54	6	1.00	0/507	1.03	1/672 (0.1%)
55	7	0.87	0/302	1.03	0/401
56	8	0.46	0/191	0.75	0/247
All	All	0.49	4/163341 (0.0%)	0.63	157/244526 (0.1%)

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
2	c	0	10
3	e	0	1
4	g	0	2
5	h	0	2
7	j	0	1
8	k	0	2
9	l	0	2
11	q	0	1
13	s	0	2
18	d	0	1
20	m	0	1
23	C	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
25	E	0	5
26	F	0	3
31	K	0	1
32	L	0	2
34	N	0	1
35	O	0	4
40	T	0	1
43	W	0	2
44	X	0	4
50	2	0	1
52	4	0	1
All	All	0	55

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	W	7	ILE	C-N	6.28	1.39	1.33
40	T	117	ARG	C-N	5.83	1.40	1.33
35	O	45	ARG	C-N	5.53	1.40	1.34
6	i	42	VAL	C-N	5.09	1.39	1.33

The worst 5 of 157 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	W	62	GLY	N-CA-C	19.05	133.83	111.93
5	h	94	LEU	N-CA-C	-15.76	85.09	109.04
34	N	61	GLY	N-CA-C	14.64	128.49	111.36
43	W	61	HIS	CA-C-N	11.61	131.12	120.10
43	W	61	HIS	C-N-CA	11.61	131.12	120.10

There are no chirality outliers.

5 of 55 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	c	136	ALA	Peptide
2	c	137	ILE	Peptide
2	c	141	MET	Peptide
2	c	142	ARG	Peptide
2	c	62	ARG	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	a	32341	0	16266	942	0
2	c	1672	0	1722	149	0
3	e	1433	0	1485	158	0
4	g	1240	0	1293	78	0
5	h	1003	0	1039	54	0
6	i	994	0	1048	118	0
7	j	775	0	808	62	0
8	k	871	0	885	105	0
9	l	958	0	1045	35	0
10	o	709	0	747	41	0
11	q	730	0	772	38	0
12	r	512	0	543	29	0
13	s	630	0	639	93	0
14	t	655	0	707	103	0
15	v	1643	0	832	69	0
16	n	477	0	501	60	0
17	b	1793	0	1839	29	0
18	d	1641	0	1668	67	0
19	f	771	0	795	43	0
20	m	935	0	983	111	0
21	p	891	0	933	33	0
22	u	280	0	342	15	0
23	C	2097	0	2147	221	0
24	D	1587	0	1629	58	0
25	E	1553	0	1587	149	0
26	F	1437	0	1461	250	0
27	G	1348	0	1399	27	0
28	H	1018	0	988	11	0
29	I	918	0	959	13	0
30	J	990	0	1021	28	0
31	K	1138	0	1174	118	0
32	L	930	0	989	80	0
33	M	1078	0	1151	46	0
34	N	1074	0	1116	73	0
35	O	919	0	959	161	0
36	P	956	0	990	58	0
37	Q	907	0	938	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	R	988	0	1038	20	0
39	S	768	0	820	46	0
40	T	873	0	909	55	0
41	U	739	0	777	100	0
42	V	731	0	782	115	0
43	W	1407	0	1422	151	0
44	X	604	0	622	65	0
45	Y	470	0	484	9	0
46	Z	527	0	537	60	0
47	B	2501	0	1272	232	0
48	A	66623	0	33514	1038	0
49	1	483	0	513	22	0
50	2	510	0	500	121	0
51	3	423	0	463	12	0
52	4	416	0	419	99	0
53	5	372	0	406	38	0
54	6	502	0	541	32	0
55	7	298	0	320	23	0
56	8	189	0	205	4	0
All	All	150328	0	100944	4550	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 4550 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)
39:S:3:THR:CG2	39:S:102:ILE:HD13	1.25	1.65
39:S:58:VAL:HG23	39:S:103:LYS:CG	1.24	1.65
41:U:83:ILE:HD11	48:A:1456:G:C2	1.14	1.64
48:A:1565:A:N3	48:A:1606:G:C5	1.69	1.61
12:r:32:TYR:CE1	19:f:91:LEU:HD11	1.34	1.59

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	
2	c	208/275 (76%)	176 (85%)	24 (12%)	8 (4%)	2	15
3	e	196/214 (92%)	176 (90%)	19 (10%)	1 (0%)	24	54
4	g	154/156 (99%)	144 (94%)	9 (6%)	1 (1%)	21	50
5	h	128/132 (97%)	119 (93%)	8 (6%)	1 (1%)	16	44
6	i	124/150 (83%)	113 (91%)	11 (9%)	0	100	100
7	j	95/101 (94%)	82 (86%)	10 (10%)	3 (3%)	3	17
8	k	115/138 (83%)	103 (90%)	10 (9%)	2 (2%)	7	28
9	l	120/124 (97%)	94 (78%)	25 (21%)	1 (1%)	16	44
10	o	85/89 (96%)	81 (95%)	4 (5%)	0	100	100
11	q	90/98 (92%)	78 (87%)	12 (13%)	0	100	100
12	r	62/84 (74%)	55 (89%)	7 (11%)	0	100	100
13	s	76/93 (82%)	65 (86%)	9 (12%)	2 (3%)	4	21
14	t	82/86 (95%)	77 (94%)	5 (6%)	0	100	100
16	n	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
17	b	226/277 (82%)	212 (94%)	14 (6%)	0	100	100
18	d	198/201 (98%)	185 (93%)	12 (6%)	1 (0%)	24	54
19	f	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
20	m	114/124 (92%)	98 (86%)	15 (13%)	1 (1%)	14	42
21	p	111/156 (71%)	104 (94%)	7 (6%)	0	100	100
22	u	30/33 (91%)	28 (93%)	2 (7%)	0	100	100
23	C	271/278 (98%)	233 (86%)	32 (12%)	6 (2%)	5	24
24	D	212/217 (98%)	197 (93%)	13 (6%)	2 (1%)	14	42
25	E	205/215 (95%)	179 (87%)	20 (10%)	6 (3%)	3	19
26	F	179/187 (96%)	160 (89%)	16 (9%)	3 (2%)	7	28
27	G	174/179 (97%)	166 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	H	149/151 (99%)	139 (93%)	9 (6%)	1 (1%)	18	47
29	I	124/175 (71%)	118 (95%)	6 (5%)	0	100	100
30	J	131/142 (92%)	118 (90%)	13 (10%)	0	100	100
31	K	145/147 (99%)	132 (91%)	10 (7%)	3 (2%)	5	24
32	L	119/122 (98%)	103 (87%)	13 (11%)	3 (2%)	4	21
33	M	143/147 (97%)	128 (90%)	15 (10%)	0	100	100
34	N	132/138 (96%)	113 (86%)	19 (14%)	0	100	100
35	O	115/199 (58%)	98 (85%)	12 (10%)	5 (4%)	2	13
36	P	124/127 (98%)	119 (96%)	5 (4%)	0	100	100
37	Q	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
38	R	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
39	S	100/103 (97%)	94 (94%)	5 (5%)	1 (1%)	12	40
40	T	112/153 (73%)	103 (92%)	6 (5%)	3 (3%)	4	20
41	U	92/100 (92%)	74 (80%)	12 (13%)	6 (6%)	1	6
42	V	93/105 (89%)	83 (89%)	8 (9%)	2 (2%)	5	24
43	W	186/215 (86%)	171 (92%)	10 (5%)	5 (3%)	4	20
44	X	80/88 (91%)	59 (74%)	15 (19%)	6 (8%)	1	5
45	Y	61/64 (95%)	57 (93%)	4 (7%)	0	100	100
46	Z	61/77 (79%)	56 (92%)	1 (2%)	4 (7%)	1	6
49	1	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
50	2	64/75 (85%)	59 (92%)	4 (6%)	1 (2%)	7	29
51	3	52/57 (91%)	51 (98%)	1 (2%)	0	100	100
52	4	48/55 (87%)	41 (85%)	5 (10%)	2 (4%)	2	14
53	5	43/47 (92%)	41 (95%)	2 (5%)	0	100	100
54	6	61/64 (95%)	54 (88%)	7 (12%)	0	100	100
55	7	35/37 (95%)	33 (94%)	1 (3%)	1 (3%)	3	19
56	8	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
All	All	5989/6679 (90%)	5407 (90%)	501 (8%)	81 (1%)	11	31

5 of 81 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	c	137	ILE

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Mol	Chain	Res	Type
2	c	138	GLN
2	c	143	GLN
2	c	144	PRO
2	c	145	ASN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	c	171/212 (81%)	166 (97%)	5 (3%)	37	60
3	e	139/147 (95%)	137 (99%)	2 (1%)	59	70
4	g	132/132 (100%)	131 (99%)	1 (1%)	73	77
5	h	106/108 (98%)	106 (100%)	0	100	100
6	i	102/125 (82%)	96 (94%)	6 (6%)	18	44
7	j	88/90 (98%)	87 (99%)	1 (1%)	65	74
8	k	91/105 (87%)	90 (99%)	1 (1%)	65	74
9	l	103/105 (98%)	103 (100%)	0	100	100
10	o	75/77 (97%)	75 (100%)	0	100	100
11	q	78/83 (94%)	76 (97%)	2 (3%)	40	61
12	r	55/72 (76%)	54 (98%)	1 (2%)	51	67
13	s	69/84 (82%)	67 (97%)	2 (3%)	37	60
14	t	69/70 (99%)	67 (97%)	2 (3%)	37	60
16	n	49/50 (98%)	49 (100%)	0	100	100
17	b	191/218 (88%)	191 (100%)	0	100	100
18	d	175/176 (99%)	174 (99%)	1 (1%)	78	80
19	f	85/85 (100%)	85 (100%)	0	100	100
20	m	99/104 (95%)	94 (95%)	5 (5%)	21	48
21	p	92/118 (78%)	92 (100%)	0	100	100
22	u	30/31 (97%)	23 (77%)	7 (23%)	1	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	C	214/218 (98%)	204 (95%)	10 (5%)	23	50
24	D	160/163 (98%)	157 (98%)	3 (2%)	50	66
25	E	167/173 (96%)	158 (95%)	9 (5%)	20	47
26	F	150/156 (96%)	136 (91%)	14 (9%)	8	29
27	G	148/150 (99%)	147 (99%)	1 (1%)	76	78
28	H	90/116 (78%)	90 (100%)	0	100	100
29	I	89/120 (74%)	89 (100%)	0	100	100
30	J	102/108 (94%)	102 (100%)	0	100	100
31	K	120/120 (100%)	116 (97%)	4 (3%)	33	57
32	L	99/100 (99%)	97 (98%)	2 (2%)	48	65
33	M	112/114 (98%)	111 (99%)	1 (1%)	70	76
34	N	112/116 (97%)	107 (96%)	5 (4%)	24	51
35	O	96/158 (61%)	89 (93%)	7 (7%)	13	39
36	P	93/94 (99%)	93 (100%)	0	100	100
37	Q	100/100 (100%)	99 (99%)	1 (1%)	68	75
38	R	97/99 (98%)	97 (100%)	0	100	100
39	S	82/83 (99%)	81 (99%)	1 (1%)	63	72
40	T	90/117 (77%)	88 (98%)	2 (2%)	45	63
41	U	82/85 (96%)	70 (85%)	12 (15%)	3	12
42	V	81/86 (94%)	71 (88%)	10 (12%)	4	18
43	W	154/168 (92%)	139 (90%)	15 (10%)	8	28
44	X	59/63 (94%)	55 (93%)	4 (7%)	14	40
45	Y	50/51 (98%)	50 (100%)	0	100	100
46	Z	58/66 (88%)	53 (91%)	5 (9%)	10	33
49	1	53/54 (98%)	52 (98%)	1 (2%)	50	66
50	2	57/63 (90%)	54 (95%)	3 (5%)	20	47
51	3	43/46 (94%)	43 (100%)	0	100	100
52	4	48/52 (92%)	38 (79%)	10 (21%)	1	4
53	5	35/36 (97%)	34 (97%)	1 (3%)	37	60
54	6	53/54 (98%)	53 (100%)	0	100	100
55	7	35/35 (100%)	32 (91%)	3 (9%)	10	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	8	18/19 (95%)	18 (100%)	0	100	100
All	All	4946/5375 (92%)	4786 (97%)	160 (3%)	35	58

5 of 160 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	V	95	VAL
50	2	38	CYS
43	W	7	ILE
43	W	146	VAL
52	4	32	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 130 such sidechains are listed below:

Mol	Chain	Res	Type
49	1	42	GLN
50	2	40	GLN
23	C	53	HIS
23	C	38	HIS
52	4	49	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1504/1528 (98%)	394 (26%)	0
15	v	76/77 (98%)	18 (23%)	0
47	B	116/118 (98%)	31 (26%)	1 (0%)
48	A	3096/3120 (99%)	793 (25%)	45 (1%)
All	All	4792/4843 (98%)	1236 (25%)	46 (0%)

5 of 1236 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	11	G
1	a	12	A
1	a	13	G
1	a	26	G
1	a	36	A

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	A	1577	C
48	A	1592	G
48	A	1578	G
48	A	1581	C
48	A	1597	G

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

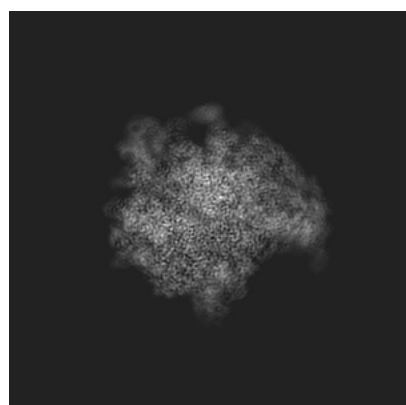
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6920. These allow visual inspection of the internal detail of the map and identification of artifacts.

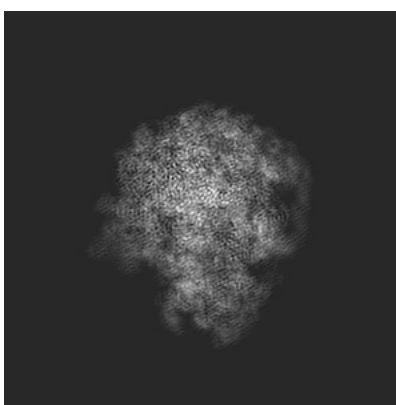
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

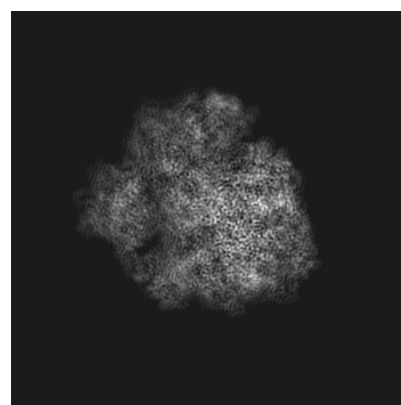
6.1.1 Primary map



X



Y

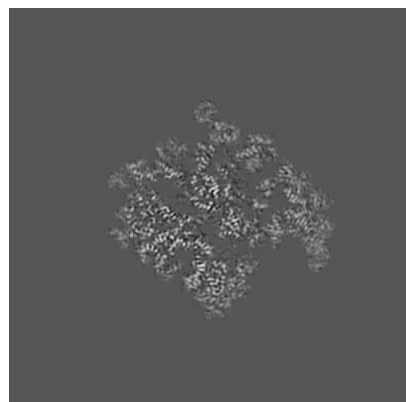


Z

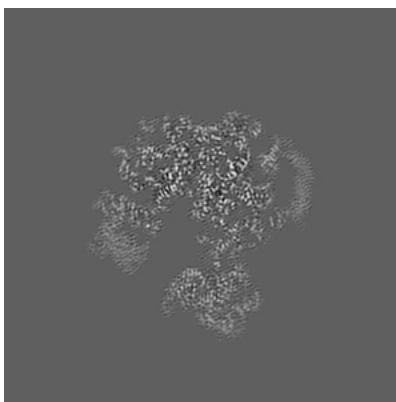
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

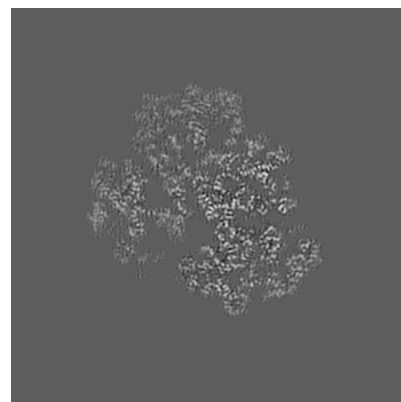
6.2.1 Primary map



X Index: 200



Y Index: 200

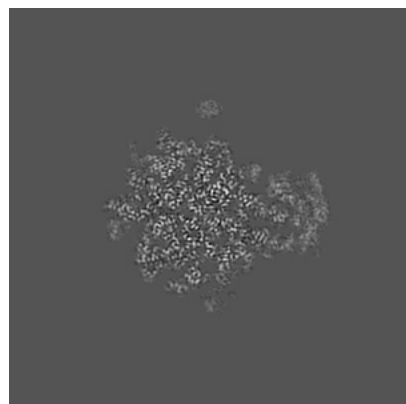


Z Index: 200

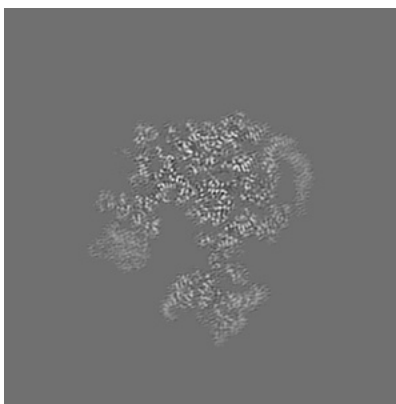
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

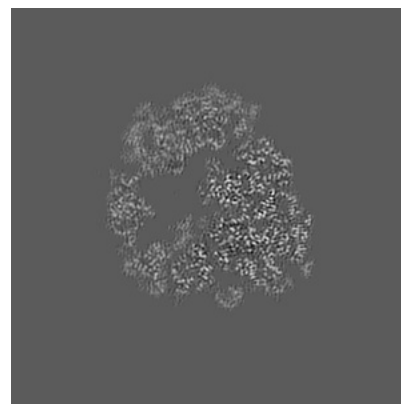
6.3.1 Primary map



X Index: 215



Y Index: 206

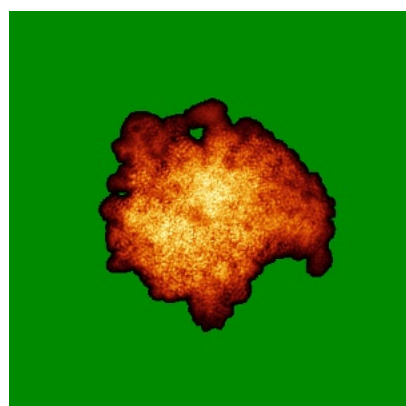


Z Index: 183

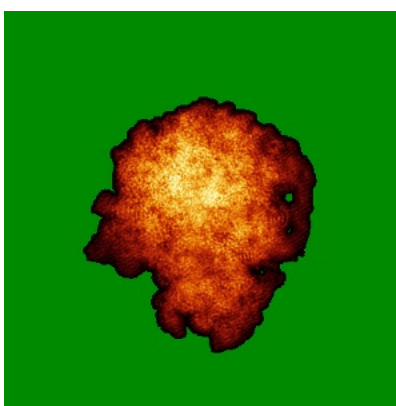
The images above show the largest variance slices of the map in three orthogonal directions.

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

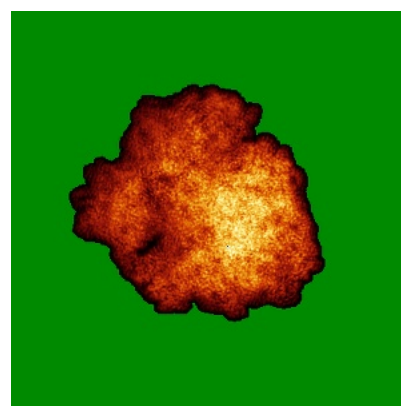
6.4.1 Primary map



X



Y

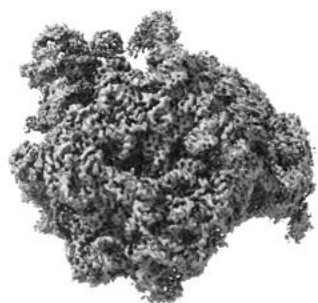


Z

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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

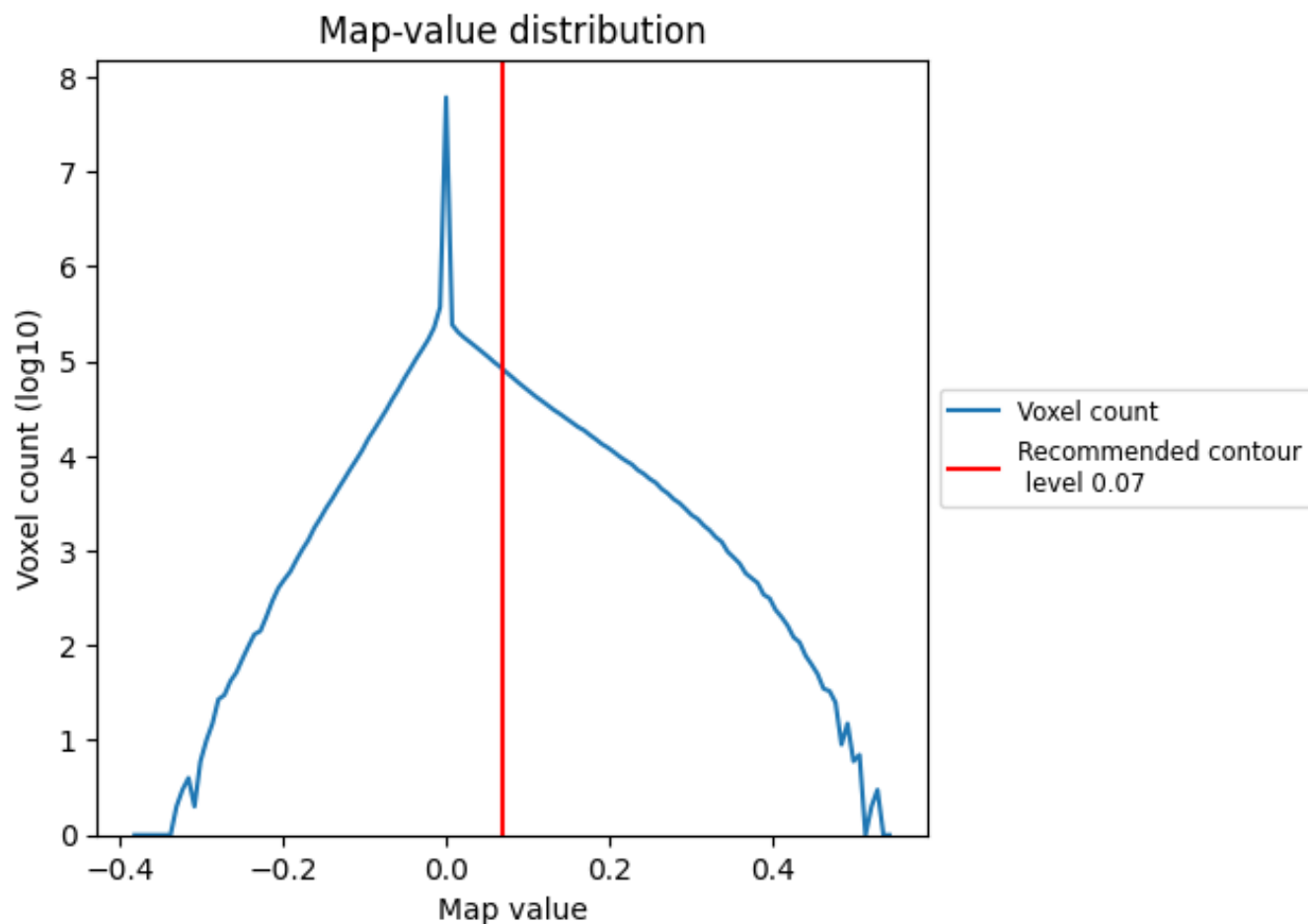
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

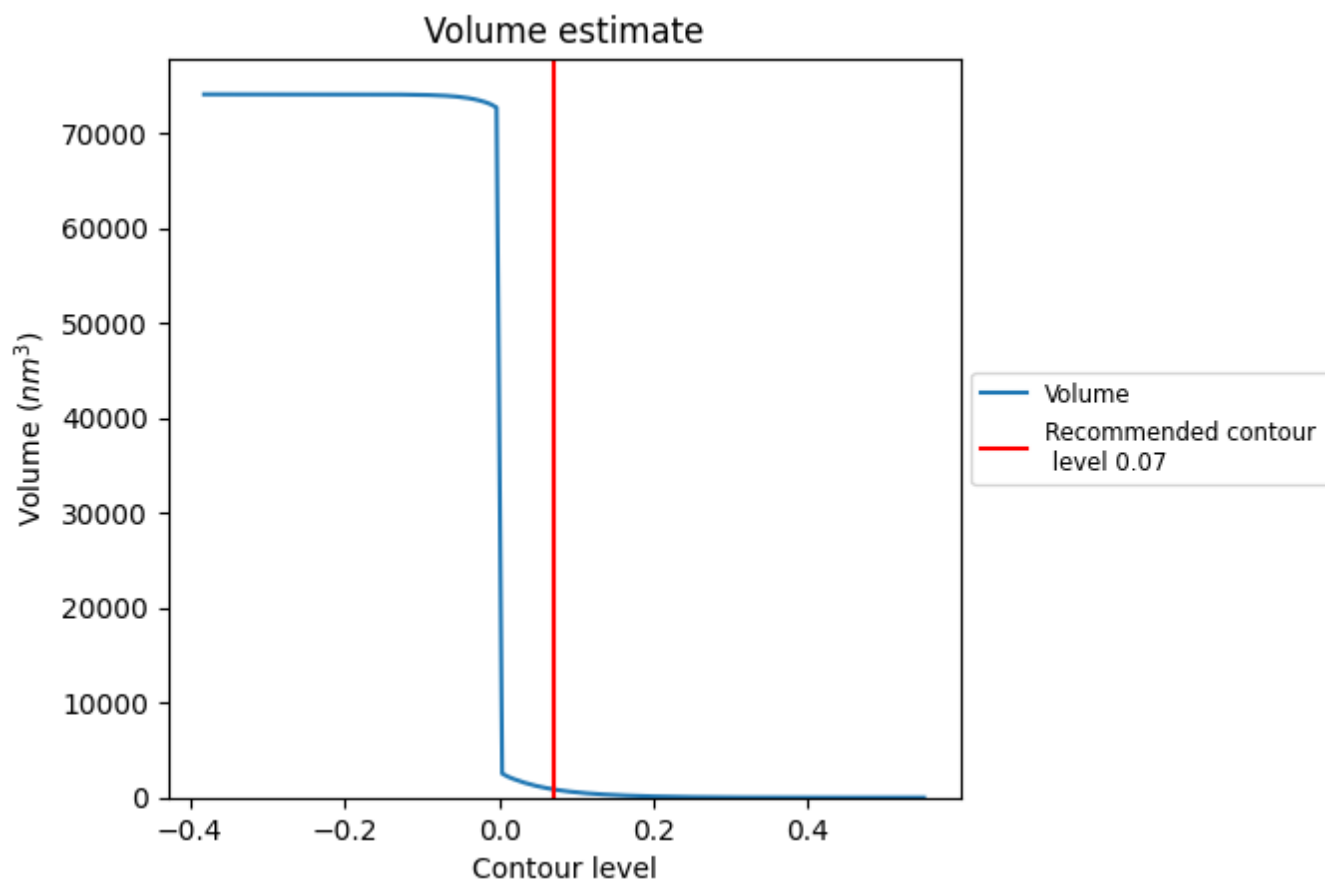
This section contains the results of statistical analysis of the map.

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.

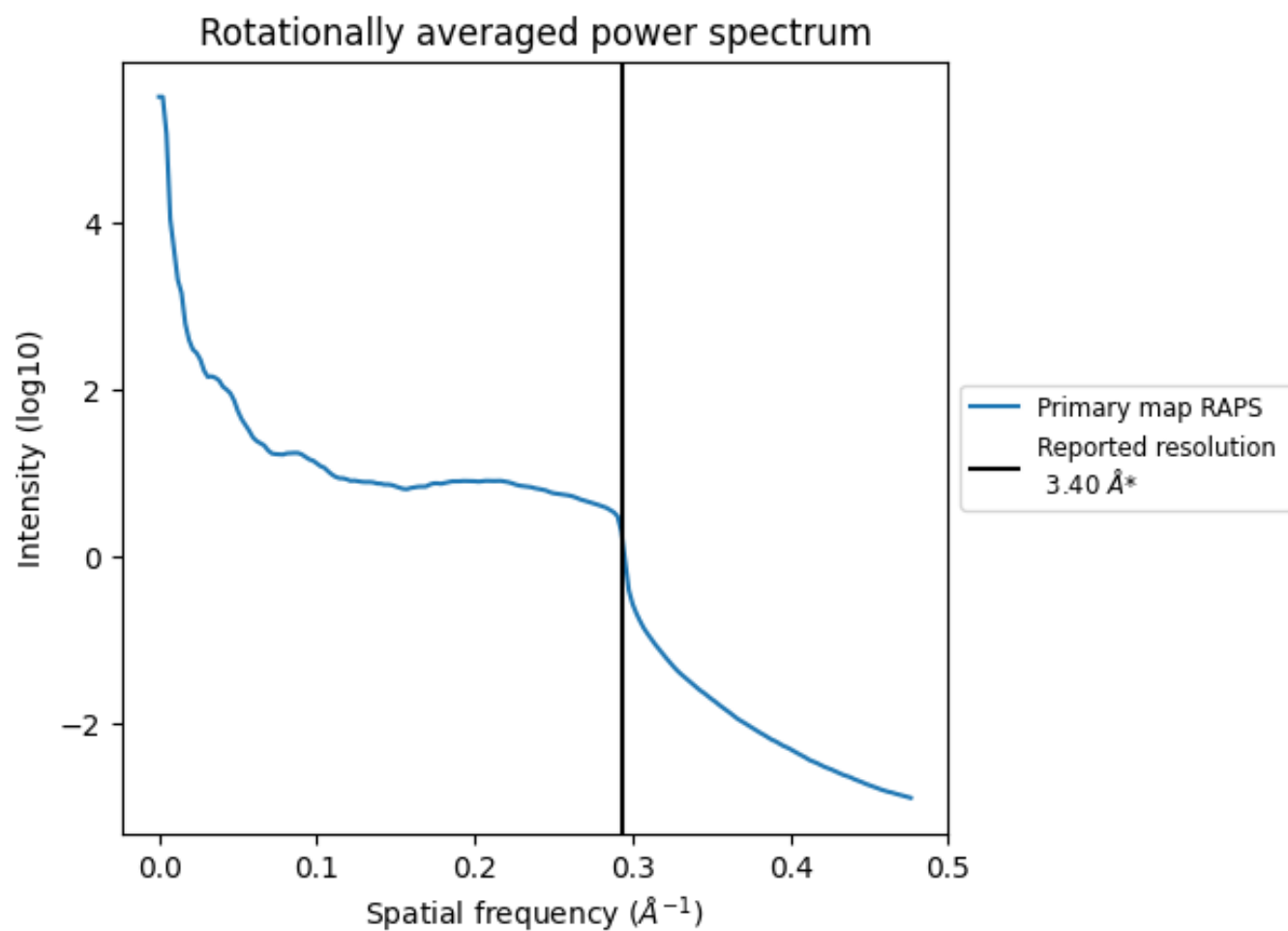
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 871 nm^3 ; this corresponds to an approximate mass of 787 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 0.294 Å⁻¹

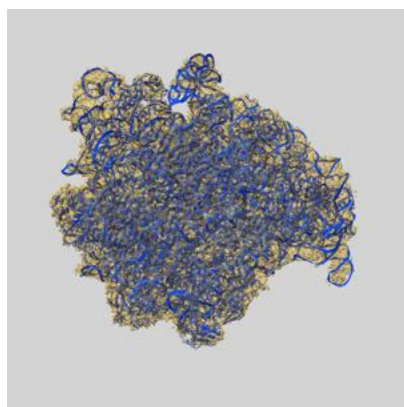
8 Fourier-Shell correlation

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

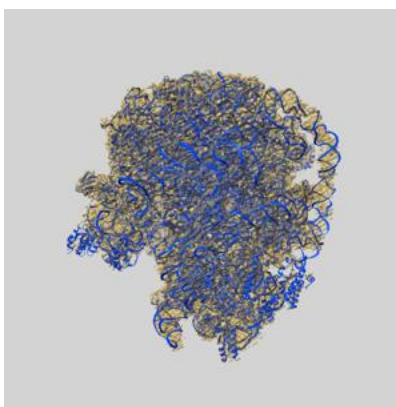
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6920 and PDB model 5ZEB. Per-residue inclusion information can be found in section [3](#) on page [15](#).

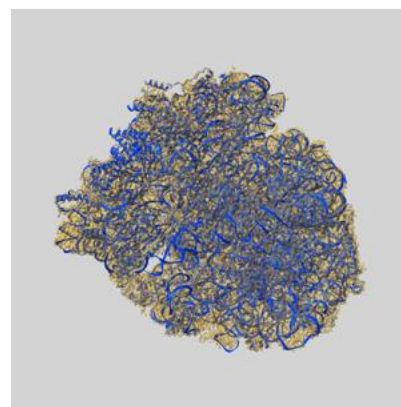
9.1 Map-model overlay [i](#)



X



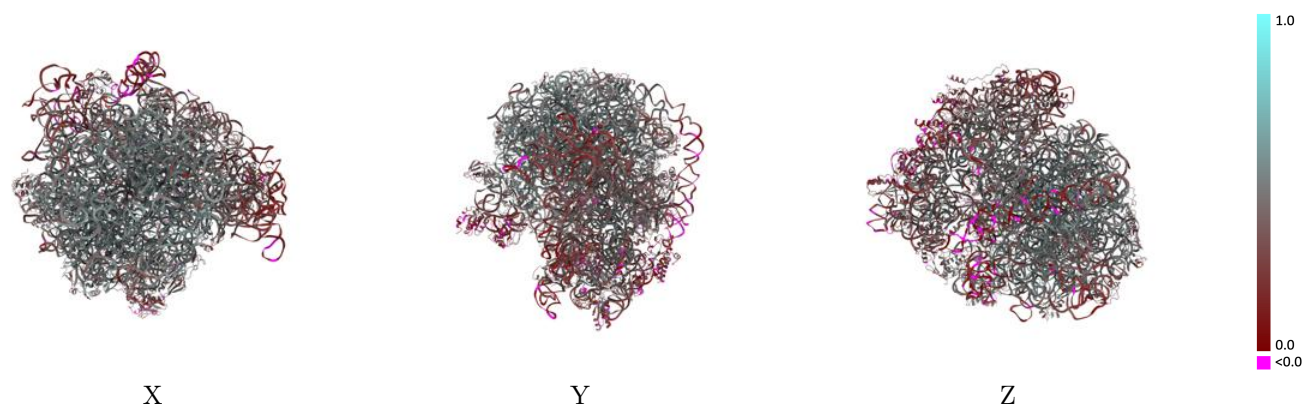
Y



Z

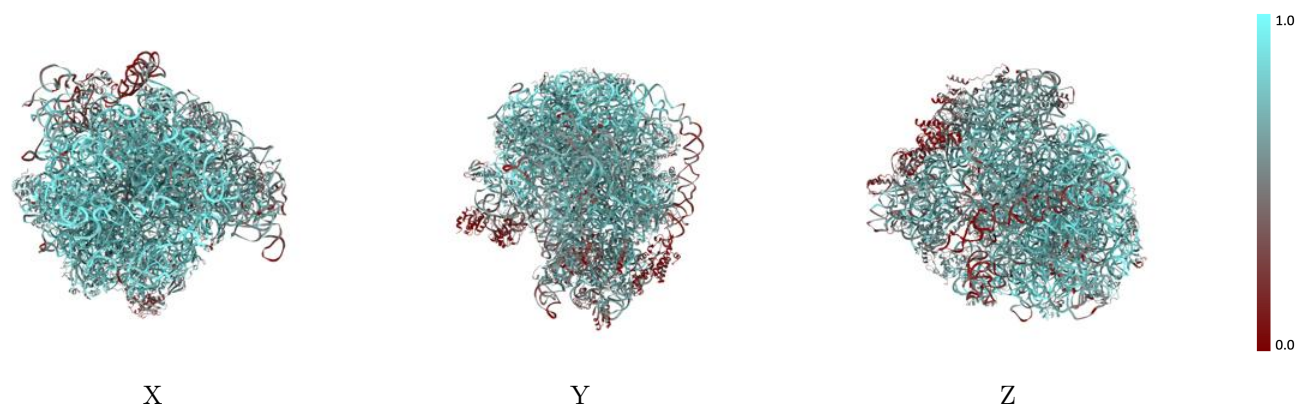
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



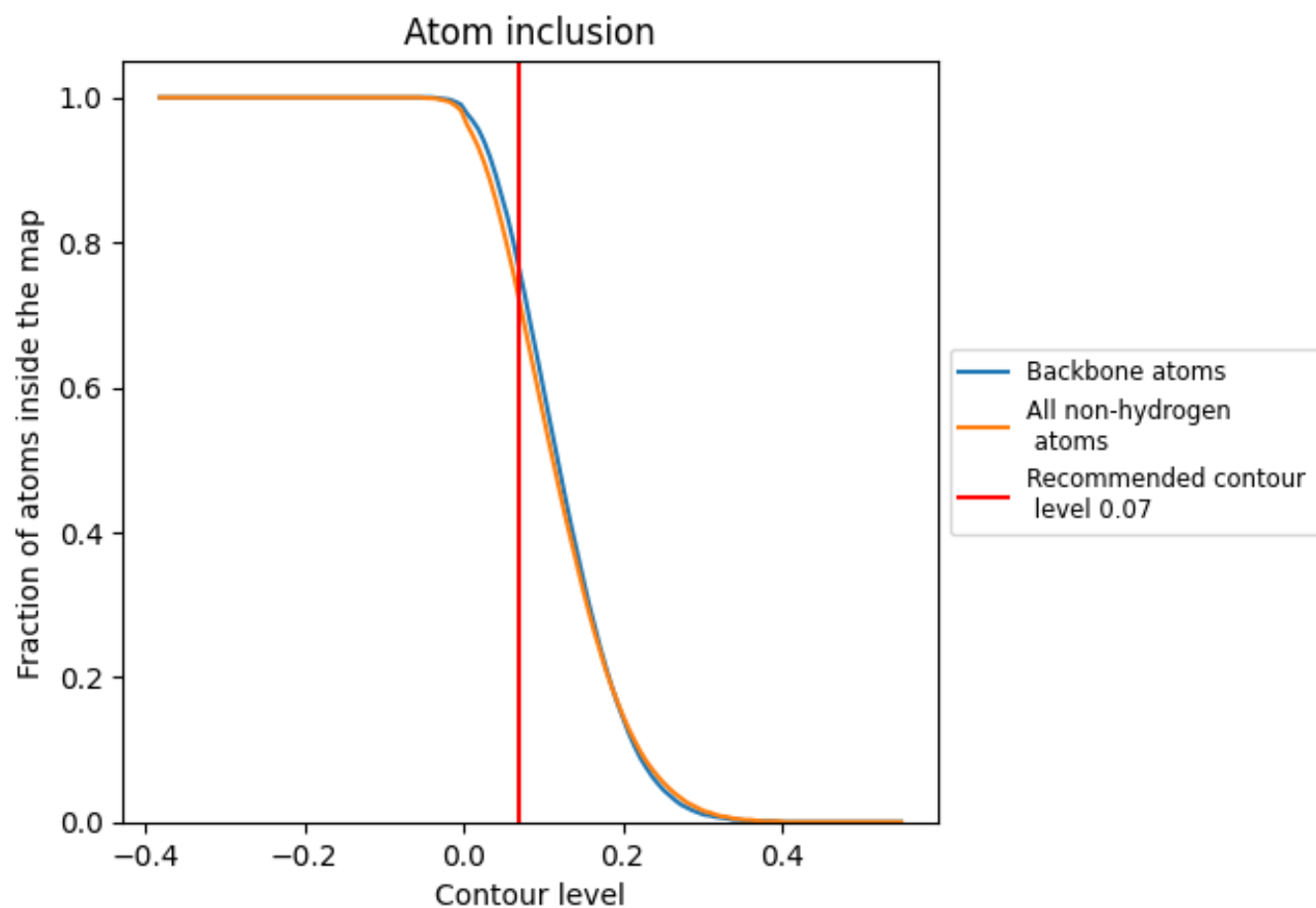
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 72% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7200	 0.4150
1	 0.7090	 0.4820
2	 0.4670	 0.2940
3	 0.7310	 0.4870
4	 0.6900	 0.4390
5	 0.7760	 0.5240
6	 0.8040	 0.5320
7	 0.7830	 0.5100
8	 0.6980	 0.5040
A	 0.8090	 0.4590
B	 0.7450	 0.4000
C	 0.7680	 0.5110
D	 0.7600	 0.4990
E	 0.7170	 0.4590
F	 0.6500	 0.4210
G	 0.5800	 0.3830
H	 0.4160	 0.3470
I	 0.0730	 0.1380
J	 0.0980	 0.1370
K	 0.7540	 0.5000
L	 0.7230	 0.4840
M	 0.7100	 0.4630
N	 0.7410	 0.5010
O	 0.7650	 0.4870
P	 0.7100	 0.4510
Q	 0.6760	 0.4500
R	 0.7850	 0.5020
S	 0.7180	 0.4950
T	 0.7510	 0.5120
U	 0.7050	 0.4680
V	 0.6250	 0.4400
W	 0.5320	 0.3570
X	 0.7410	 0.4930
Y	 0.7060	 0.4800
Z	 0.6660	 0.4120



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Chain	Atom inclusion	Q-score
a	 0.7230	 0.3610
b	 0.1100	 0.1740
c	 0.5060	 0.3440
d	 0.3890	 0.2660
e	 0.5280	 0.3480
f	 0.5590	 0.3710
g	 0.5470	 0.3400
h	 0.6780	 0.4170
i	 0.6000	 0.3650
j	 0.4710	 0.3300
k	 0.5980	 0.3630
l	 0.5360	 0.3630
m	 0.5720	 0.3610
n	 0.6950	 0.4410
o	 0.6840	 0.4230
p	 0.4700	 0.3130
q	 0.5280	 0.3410
r	 0.5910	 0.3640
s	 0.5470	 0.3320
t	 0.5450	 0.3150
u	 0.4240	 0.3470
v	 0.5860	 0.3080