



# wwPDB EM Validation Summary Report ⓘ

Jun 17, 2026 – 03:36 pm BST

PDB ID : 9GR1 / pdb\_00009gr1  
EMDB ID : EMD-51517  
Title : E. coli 70S-TEC complex in delivery state  
Authors : Webster, M.W.; Weixlbaumer, A.  
Deposited on : 2024-09-10  
Resolution : 3.17 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](mailto: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>.

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

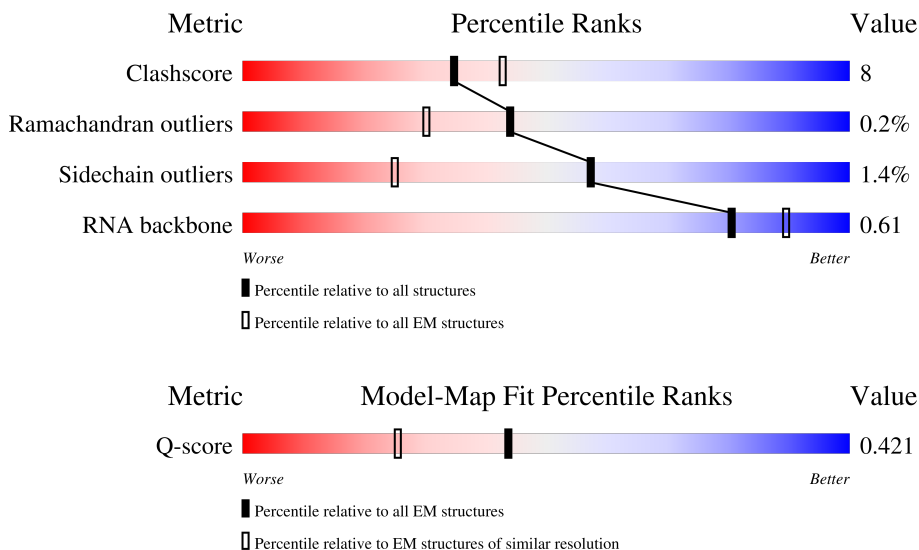
EMDB validation analysis : 0.0.1.dev132  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 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 3.17 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	14465 ( 2.67 - 3.67 )

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  $\geq 3$ , 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	0	55	93% 
2	1	46	15% 
3	2	65	29% 

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Mol	Chain	Length	Quality of chain
4	3	38	50% 82% 18%
5	A	1542	9% 55% 39% ..
6	B	241	8% 79% 13% 7%
7	C	233	18% 75% 13% 12%
8	D	206	67% 59% 40%
9	E	167	. 71% 22% 7%
10	F	135	10% 60% 16% 24%
11	G	179	17% 63% 23% 15%
12	H	130	5% 77% 22% .
13	I	130	12% 71% 27% .
14	J	103	44% 59% 35% 5%
15	K	129	. 71% 19% 9%
16	L	124	14% 82% 11% 6%
17	M	118	40% 68% 29% ..
18	N	101	27% 66% 33% .
19	O	89	9% 82% 17% .
20	P	82	51% 54% 45% .
21	Q	84	35% 76% 17% 6%
22	R	75	5% 56% 17% 27%
23	S	92	39% 62% 29% 9%
24	T	87	49% 78% 21% .
25	U	71	31% 87% 11% .
26	X	16	38% 19% 50% 12% 19%
27	Z	76	75% 47% 38% 13% .
28	a	2925	7% 74% 18% 6%

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Mol	Chain	Length	Quality of chain
29	b	119	14% 81% 18%
30	c	273	6% 84% 15%
31	d	209	53% 89% 11%
32	e	201	61% 88% 12%
33	f	179	72% 75% 23%
34	g	177	92% 78% 20%
35	h	149	95% 71% 25%
36	i	142	59% 78% 21%
37	j	123	35% 89% 11%
38	k	144	51% 92% 8%
39	l	136	42% 85% 14%
40	m	127	50% 87% 6% 7%
41	n	117	69% 84% 15%
42	o	115	57% 90% 9%
43	p	118	42% 90% 9%
44	q	103	64% 92% 8%
45	r	110	64% 88% 12%
46	s	100	67% 74% 19% 7%
47	t	104	81% 82% 14%
48	u	94	81% 89% 10%
49	v	85	49% 84% 8% 8%
50	w	78	31% 86% 13%
51	x	63	75% 92% 6%
52	y	59	66% 92% 7%
53	z	57	68% 79% 18%

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Mol	Chain	Length	Quality of chain
54	4	10	
55	Y	77	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
28	3TD	a	1919	-	-	X	-

## 2 Entry composition [i](#)

There are 59 unique types of molecules in this entry. The entry contains 142297 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 L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	0	51	417	269	76	72	0	0

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	46	377	228	90	57	2	0	0

- Molecule 3 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	64	504	323	105	74	2	0	0

- Molecule 4 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	38	302	185	65	48	4	0	0

- Molecule 5 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	A	1513	32478	14493	5961	10511	1513	0	0

- Molecule 6 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	B	224	1753	1109	315	321	8	0	0

- Molecule 7 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 8 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 9 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	E	156	1152	717	217	212	6	0	0

- Molecule 10 is a protein called Small ribosomal subunit protein bS6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	F	103	839	530	151	151	7	0	0

- Molecule 11 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	G	153	1203	750	231	218	4	0	0

- Molecule 12 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 13 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 14 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 15 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 16 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	116	Total	C	N	O	S	0	0
			902	558	183	156	5		

- Molecule 17 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 18 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 19 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 20 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 21 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 22 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms				AltConf	Trace	
22	R	55	Total	C	N	O	S	0	0
			455	288	86	81			

- Molecule 23 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 24 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 25 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 26 is a RNA chain called mRNA in ribosome channel.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	13	Total	C	N	O	P	0	0
			271	122	44	92	13		

- Molecule 27 is a RNA chain called Phe-NH-tRNA(Phe) A-site.

Mol	Chain	Residues	Atoms					AltConf	Trace	
27	Z	76	Total	C	N	O	P	S	0	0
			1624	724	290	533	76	1		

- Molecule 28 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
28	a	2748	59025	26336	10876	19065	2748	0	0

- Molecule 29 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
29	b	119	2549	1135	466	829	119	0	0

- Molecule 30 is a protein called 50S ribosomal protein L2.

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

- Molecule 31 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	d	209	1566	980	288	294	4	0	0

- Molecule 32 is a protein called 50S ribosomal protein L4.

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

- Molecule 33 is a protein called 50S ribosomal protein L5.

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

- Molecule 34 is a protein called 50S ribosomal protein L6.

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

- Molecule 35 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	h	148	1101	694	196	210	1	0	0

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	j	123	946	593	181	166	6	0	0

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	77	ILE	VAL	conflict	UNP A0A140N711

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	l	136	1075	686	205	178	6	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	m	118	945	585	194	161	5	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	78	Total	C	N	O	S	0	0
			586	362	116	107	1		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

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

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

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

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

- Molecule 54 is a RNA chain called mRNA in SD-aSD duplex.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	10	Total	C	N	O	P	0	0
			223	99	48	66	10		

- Molecule 55 is a RNA chain called tRNA(fmet) P-site.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	N	O	P			S
55	Y	77	1645	734	297	536	77	1	0	0

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	3	1	Total	Zn	0
			1	1	

- Molecule 57 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
57	A	48	Total	K	0
			48	48	
57	a	112	Total	K	0
			112	112	
57	b	1	Total	K	0
			1	1	
57	c	4	Total	K	0
			4	4	
57	d	1	Total	K	0
			1	1	
57	e	1	Total	K	0
			1	1	
57	f	1	Total	K	0
			1	1	

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

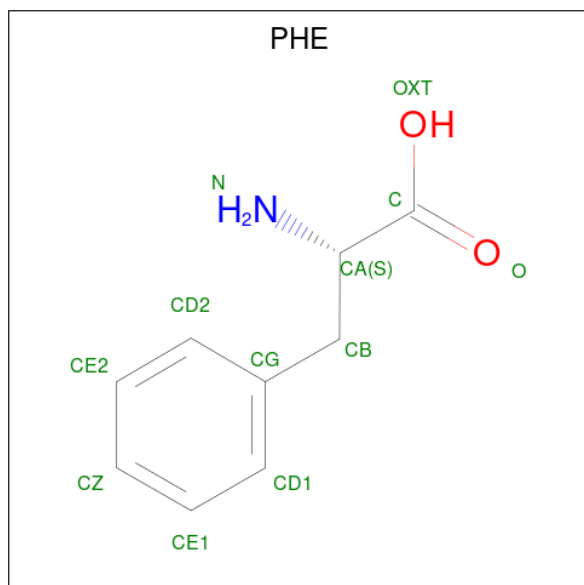
Mol	Chain	Residues	Atoms		AltConf
58	A	95	Total	Mg	0
			95	95	
58	N	1	Total	Mg	0
			1	1	
58	a	254	Total	Mg	0
			254	254	
58	b	5	Total	Mg	0
			5	5	
58	c	1	Total	Mg	0
			1	1	
58	d	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
58	k	1	Total	Mg	0
			1	1	
58	z	1	Total	Mg	0
			1	1	
58	Y	1	Total	Mg	0
			1	1	

- Molecule 59 is PHENYLALANINE (CCD ID: PHE) (formula:  $C_9H_{11}NO_2$ ).

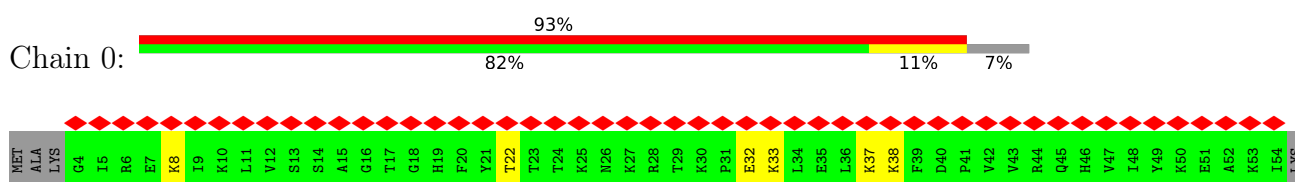


Mol	Chain	Residues	Atoms				AltConf
59	a	1	Total	C	N	O	0
			11	9	1	1	

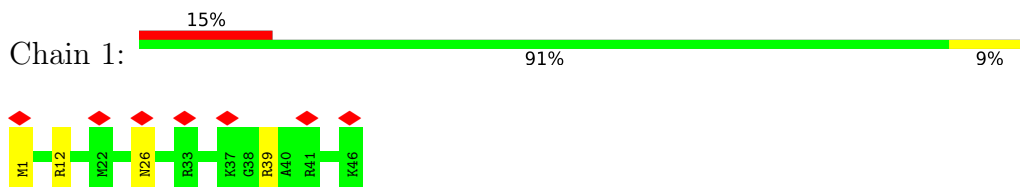
### 3 Residue-property plots [i](#)

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.

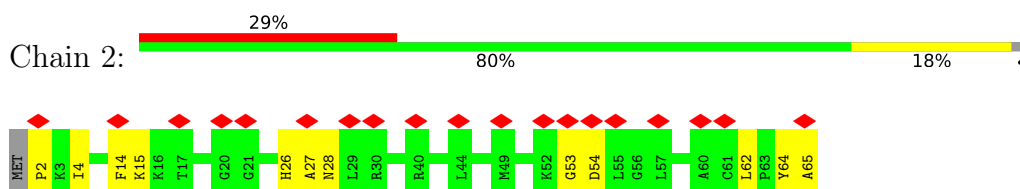
- Molecule 1: 50S ribosomal protein L33



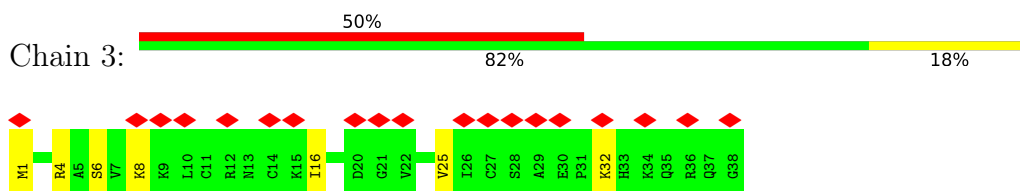
- Molecule 2: 50S ribosomal protein L34



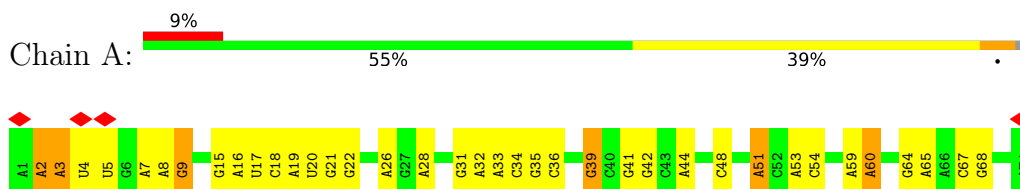
- Molecule 3: 50S ribosomal protein L35

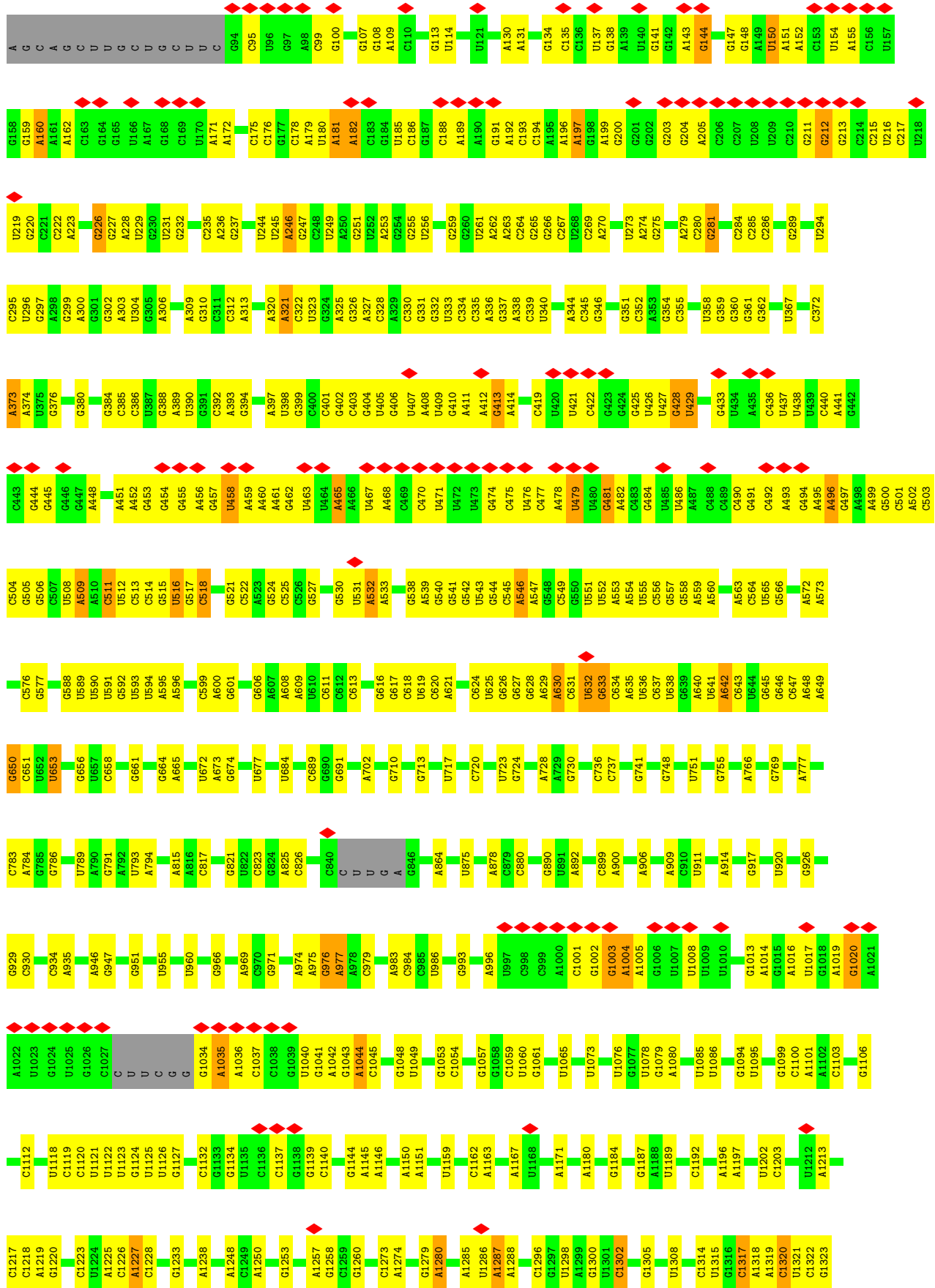


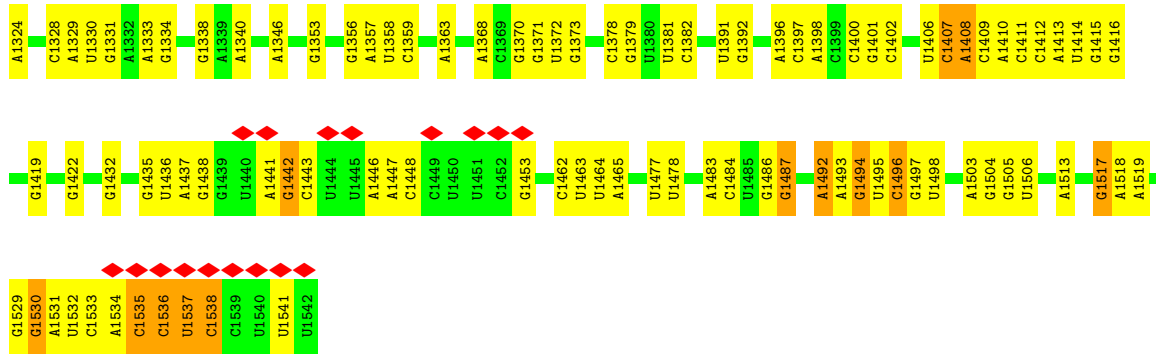
- Molecule 4: 50S ribosomal protein L36



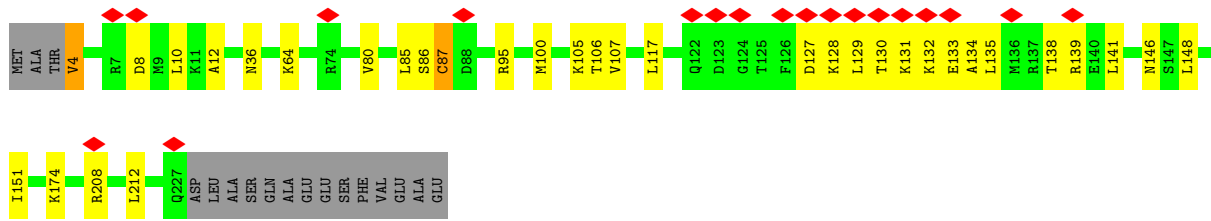
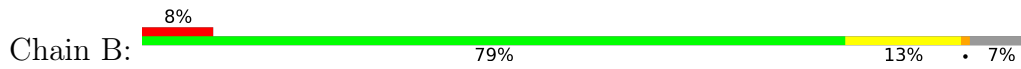
- Molecule 5: 16S ribosomal RNA



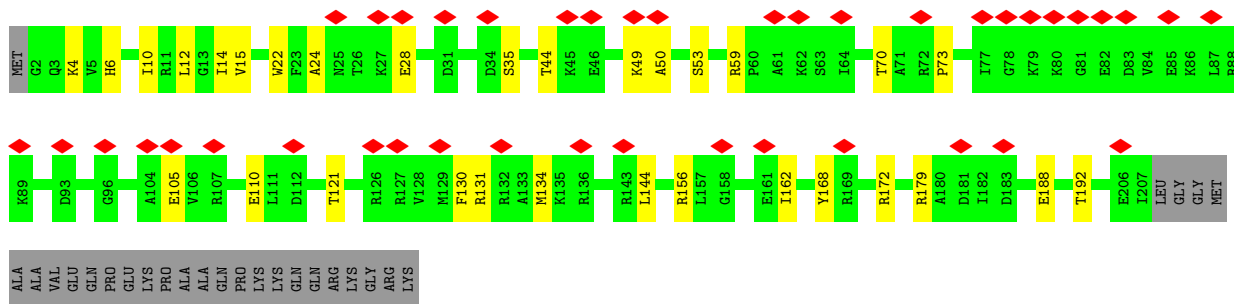
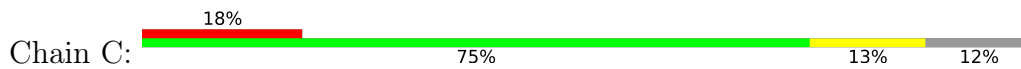




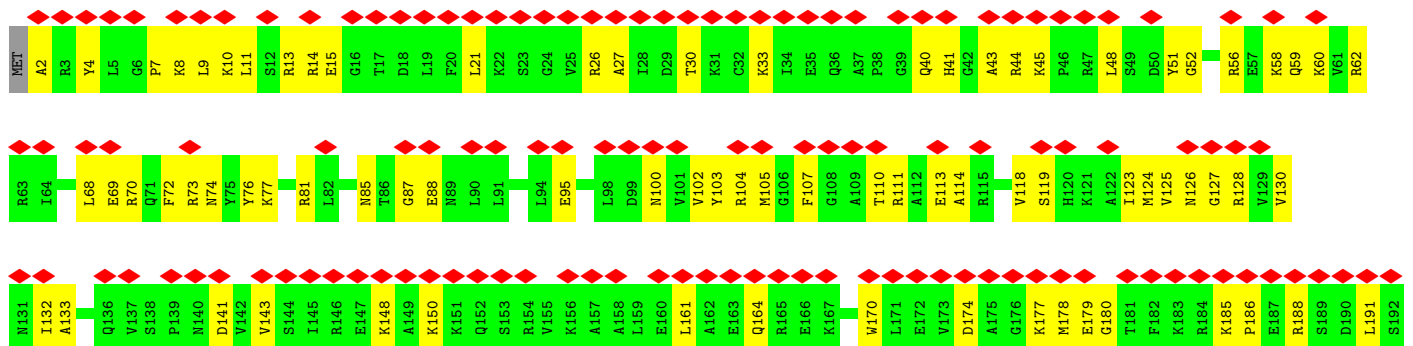
• Molecule 6: Small ribosomal subunit protein uS2



• Molecule 7: Small ribosomal subunit protein uS3



• Molecule 8: Small ribosomal subunit protein uS4

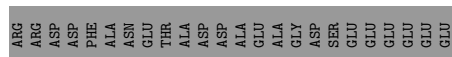
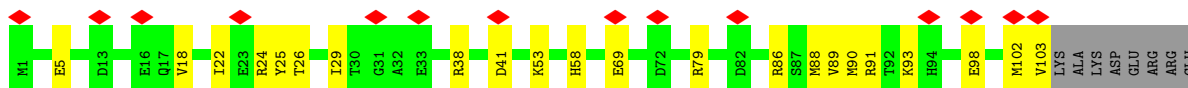




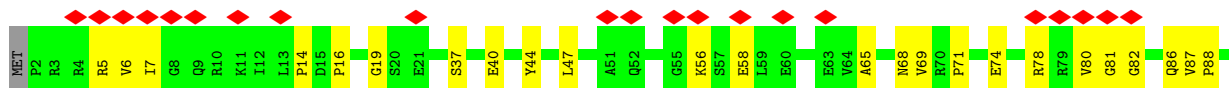
• Molecule 9: Small ribosomal subunit protein uS5



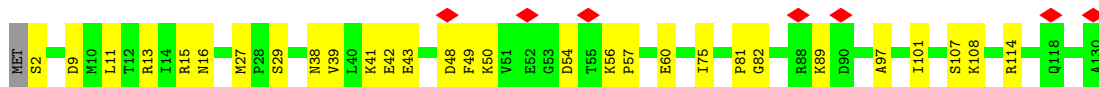
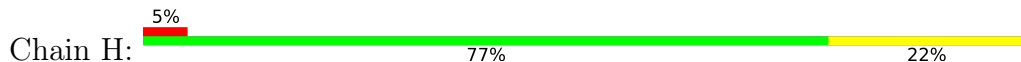
• Molecule 10: Small ribosomal subunit protein bS6, fully modified isoform



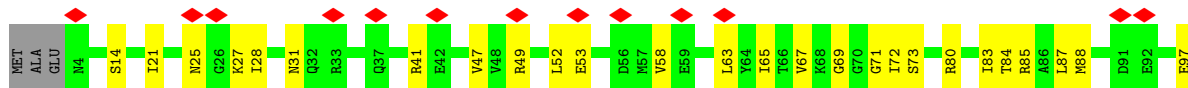
• Molecule 11: Small ribosomal subunit protein uS7



• Molecule 12: Small ribosomal subunit protein uS8

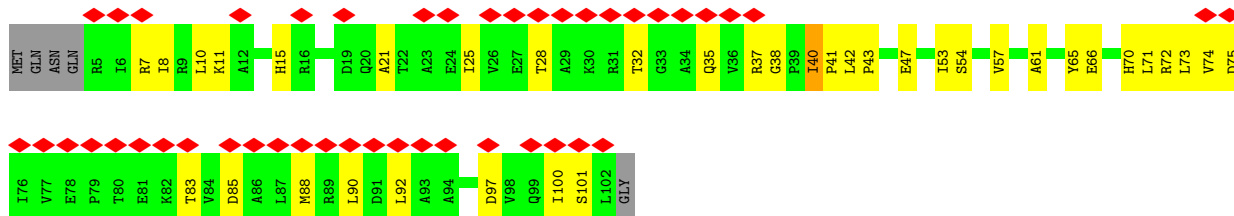
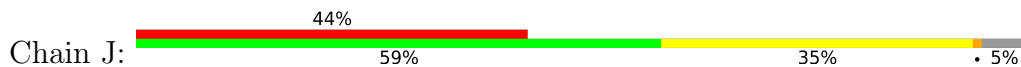


• Molecule 13: Small ribosomal subunit protein uS9

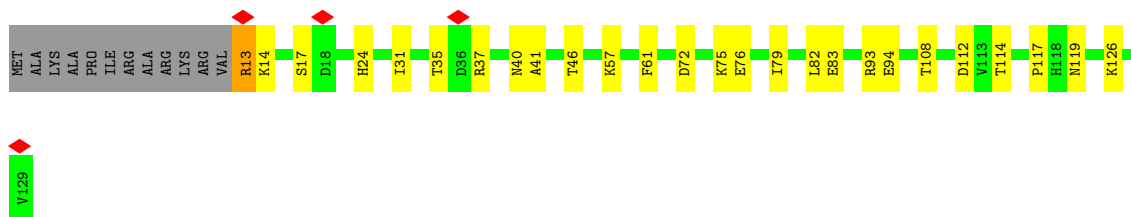




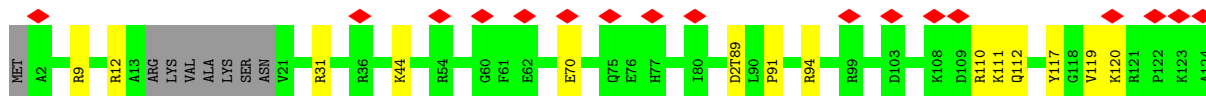
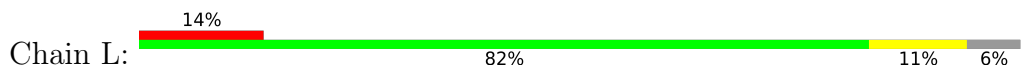
• Molecule 14: Small ribosomal subunit protein uS10



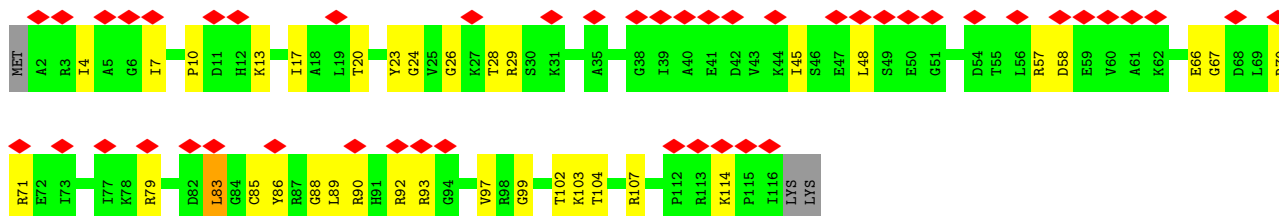
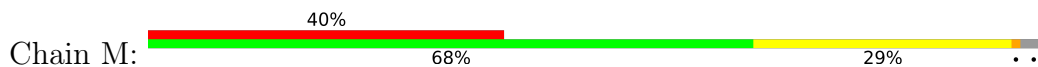
• Molecule 15: Small ribosomal subunit protein uS11



• Molecule 16: Small ribosomal subunit protein uS12

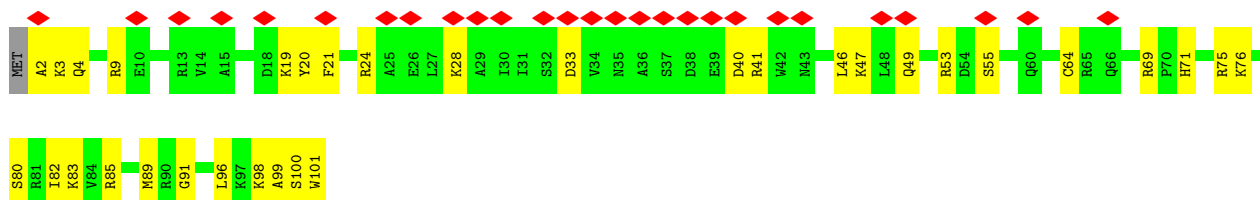


• Molecule 17: Small ribosomal subunit protein uS13

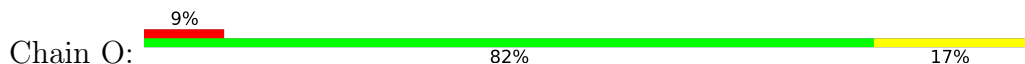


• Molecule 18: Small ribosomal subunit protein uS14

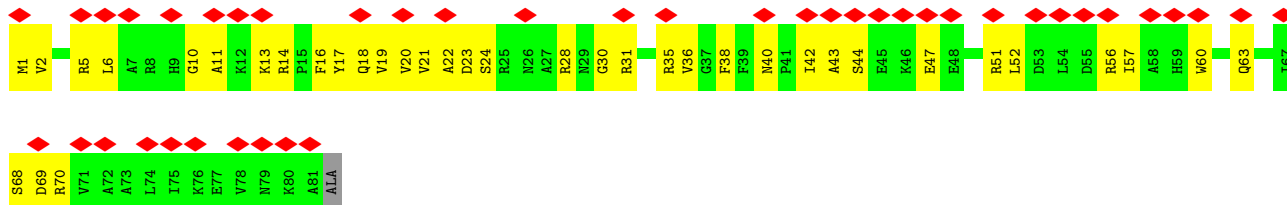




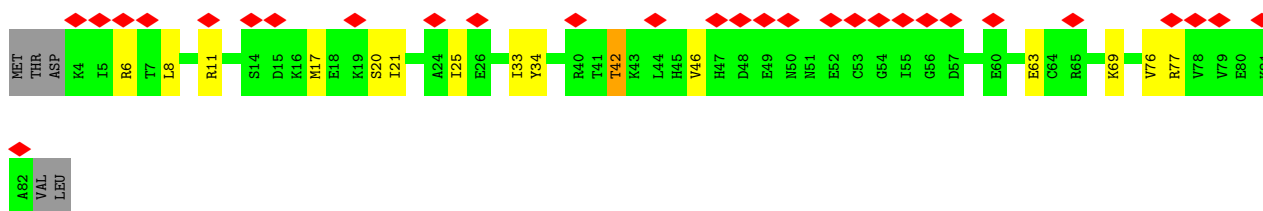
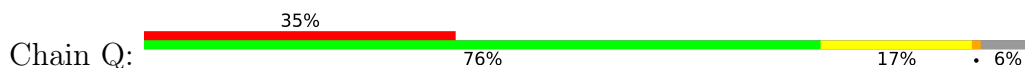
- Molecule 19: Small ribosomal subunit protein uS15



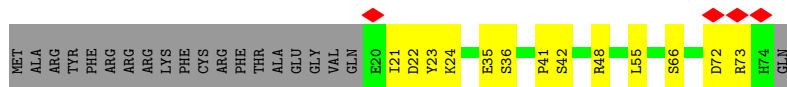
- Molecule 20: 30S ribosomal protein S16



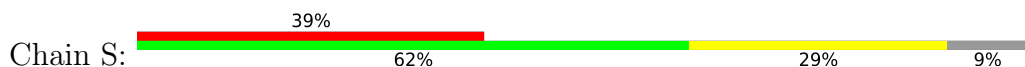
- Molecule 21: Small ribosomal subunit protein uS17



- Molecule 22: Small ribosomal subunit protein bS18

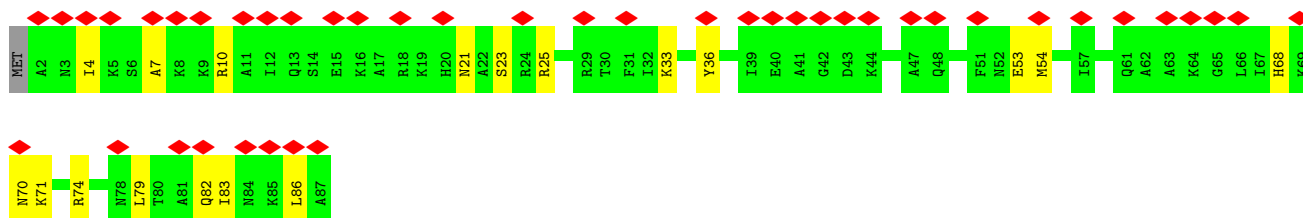
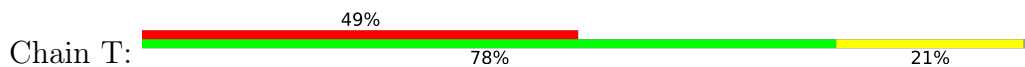


- Molecule 23: 30S ribosomal protein S19

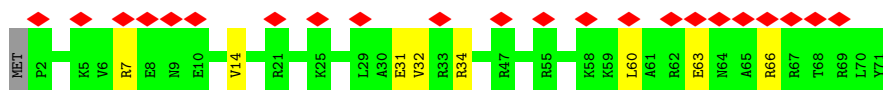
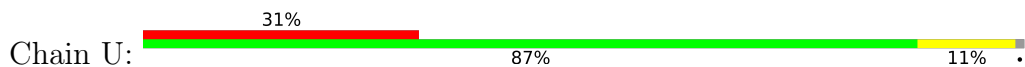




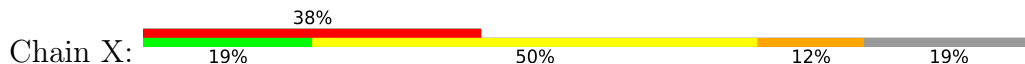
- Molecule 24: Small ribosomal subunit protein bS20



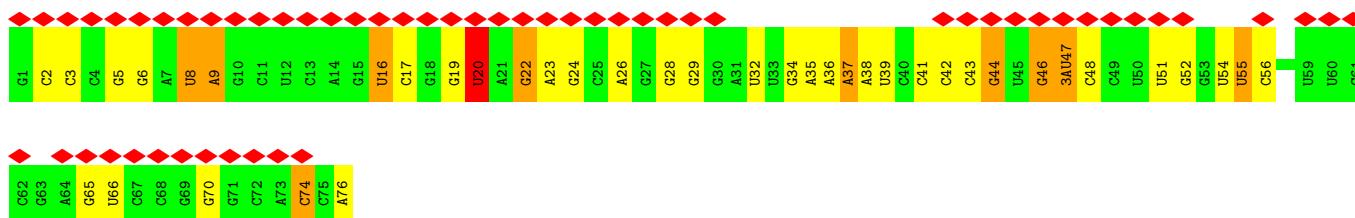
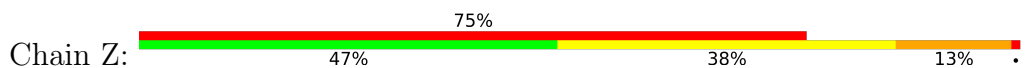
- Molecule 25: Small ribosomal subunit protein bS21



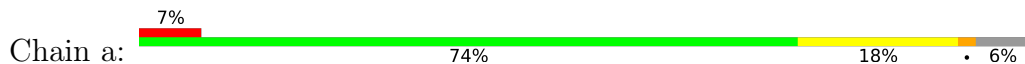
- Molecule 26: mRNA in ribosome channel



- Molecule 27: Phe-NH-tRNA(Phe) A-site

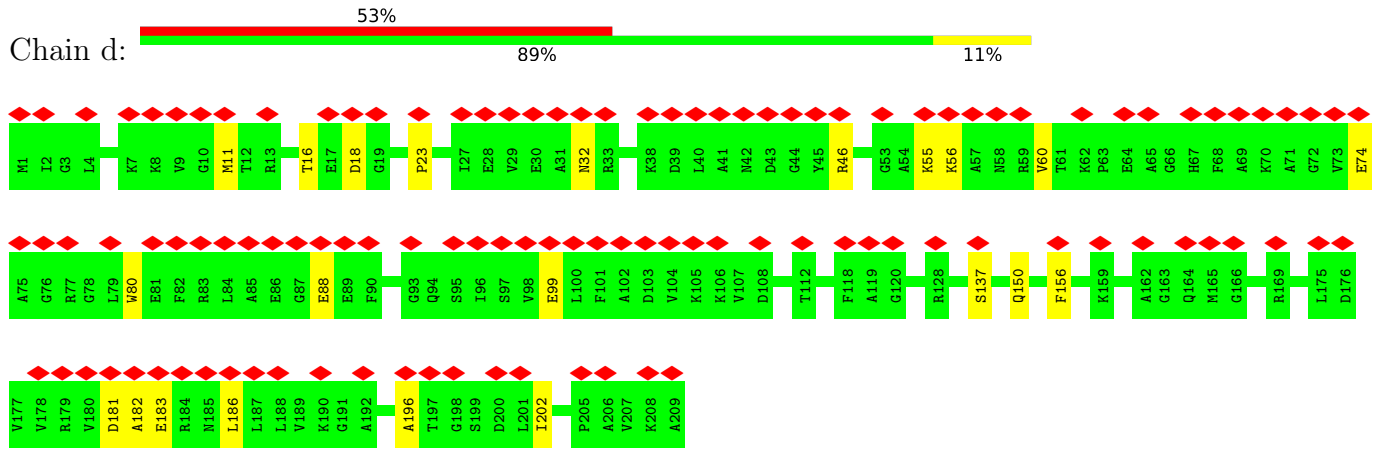


- Molecule 28: 23S ribosomal RNA

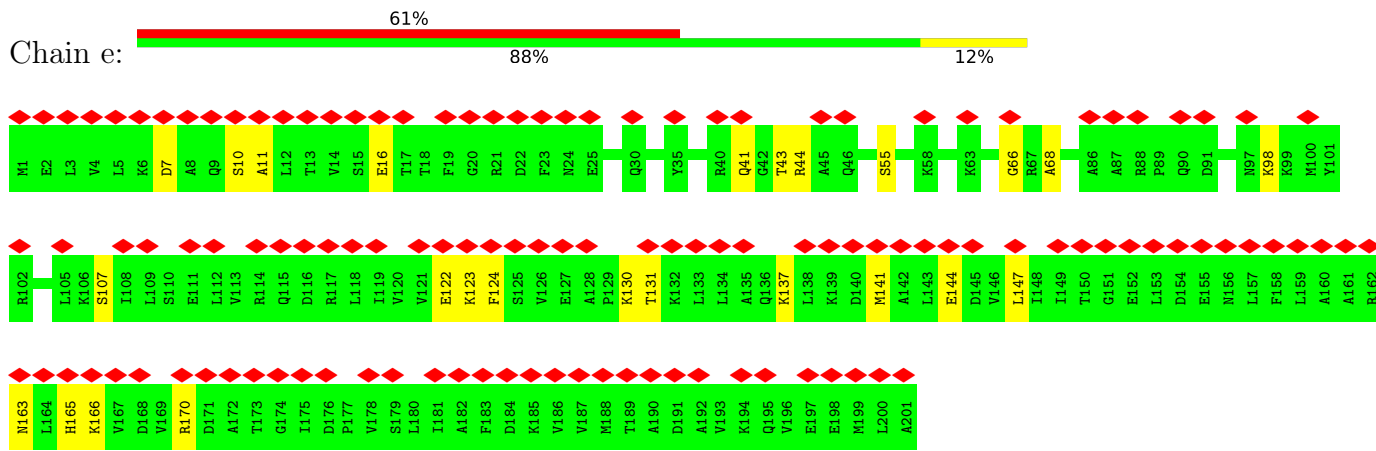




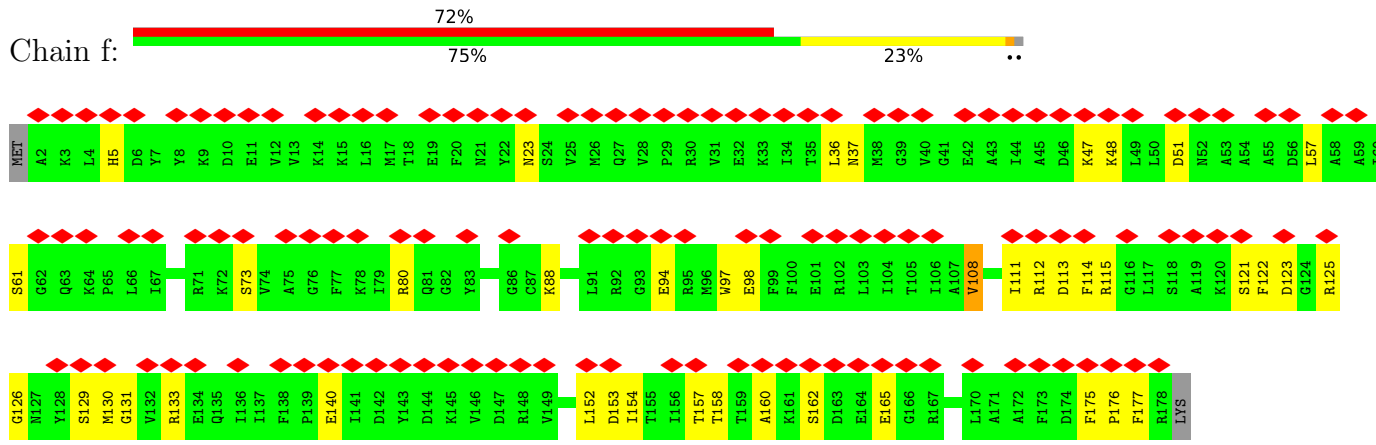




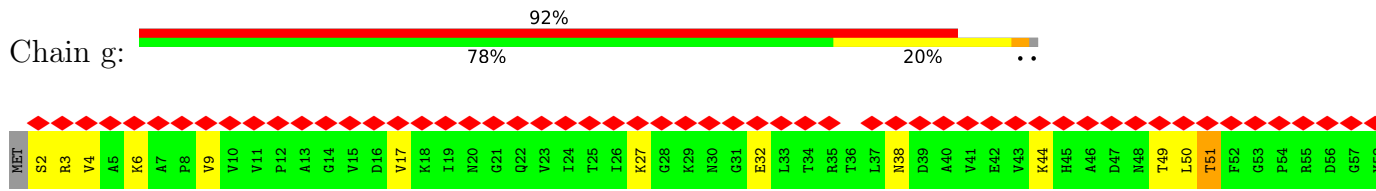
• Molecule 32: 50S ribosomal protein L4

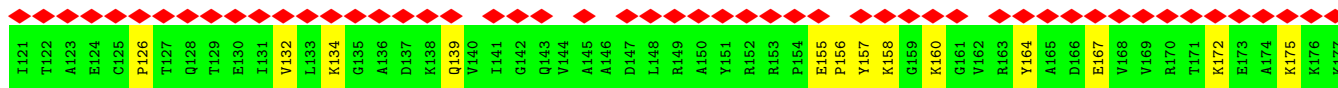


• Molecule 33: 50S ribosomal protein L5

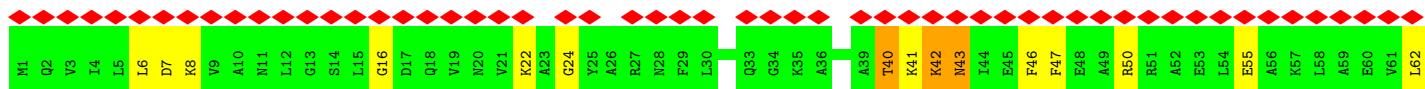


• Molecule 34: 50S ribosomal protein L6

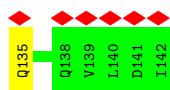
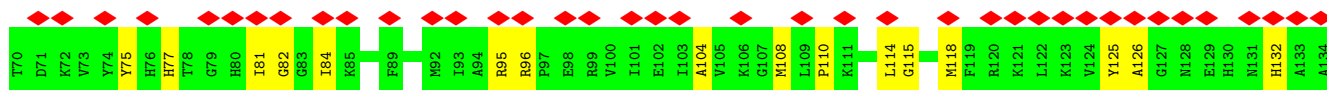
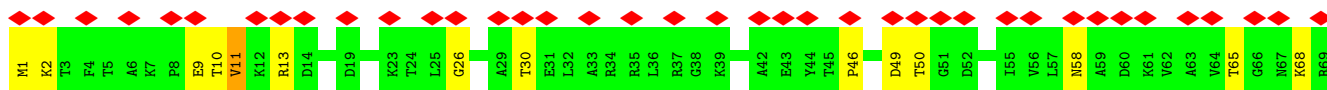
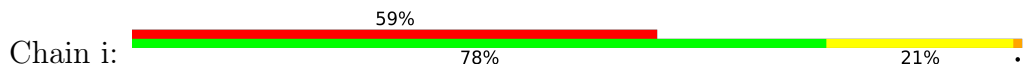




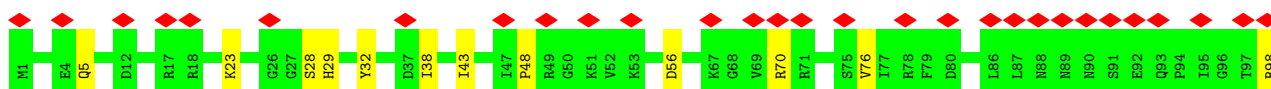
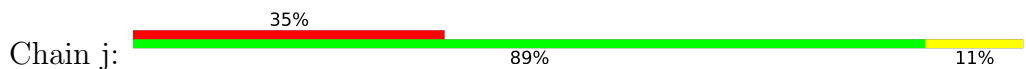
- Molecule 35: 50S ribosomal protein L9



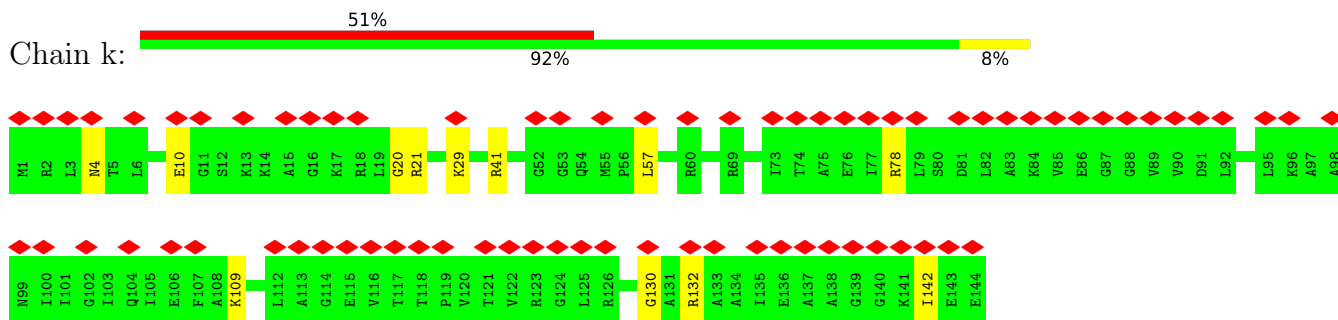
- Molecule 36: 50S ribosomal protein L13



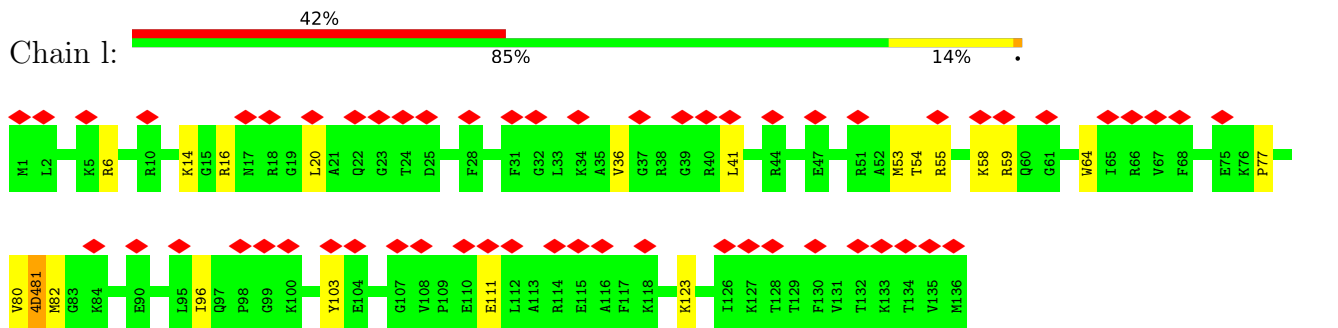
- Molecule 37: 50S ribosomal protein L14



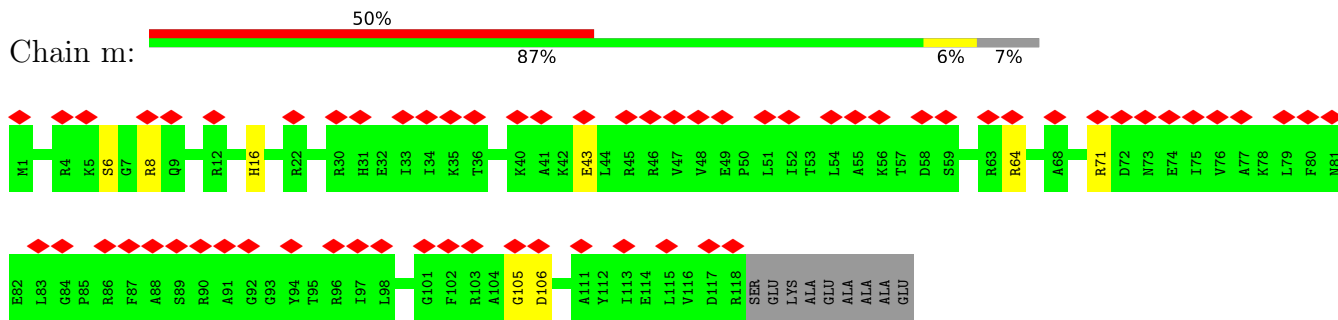
- Molecule 38: 50S ribosomal protein L15



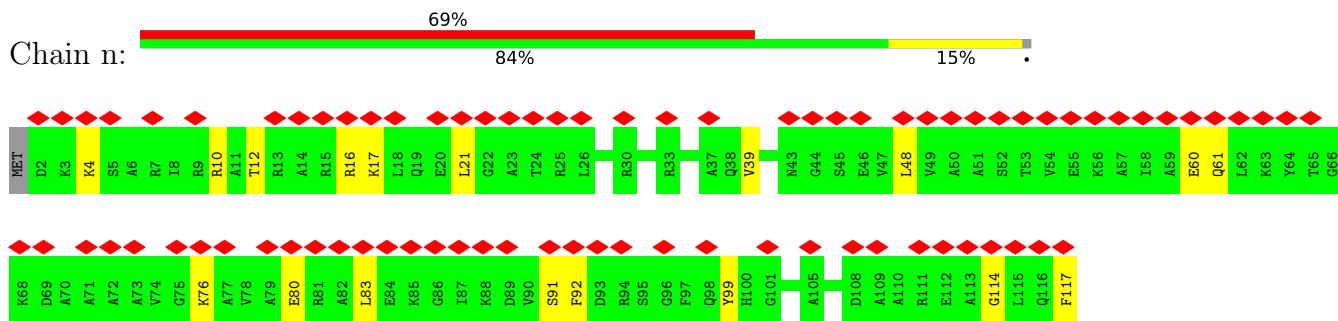
• Molecule 39: 50S ribosomal protein L16



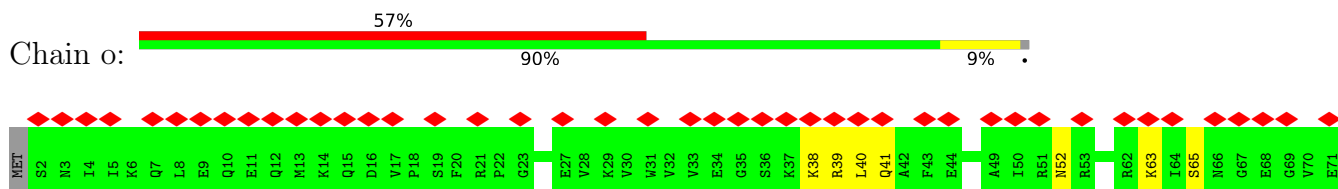
• Molecule 40: 50S ribosomal protein L17

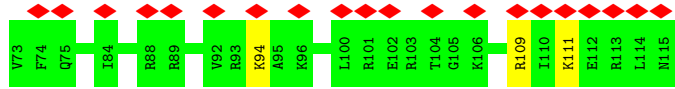


• Molecule 41: 50S ribosomal protein L18

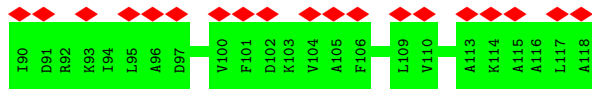
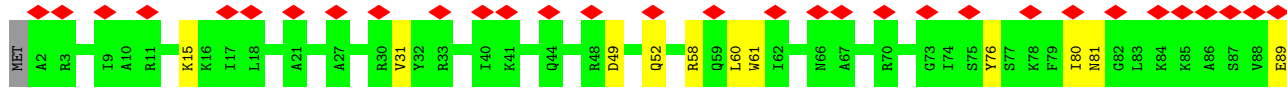
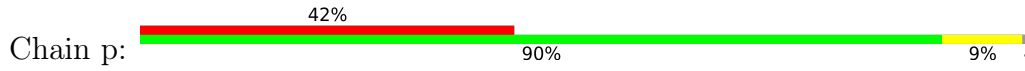


• Molecule 42: 50S ribosomal protein L19

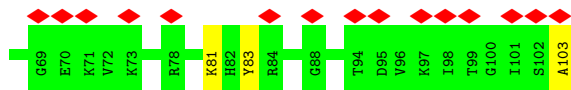
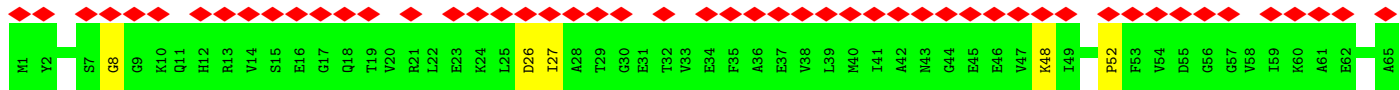
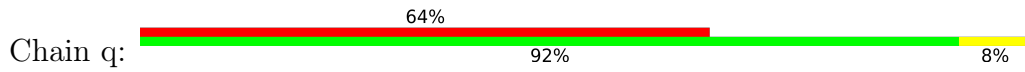




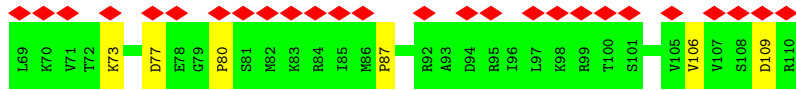
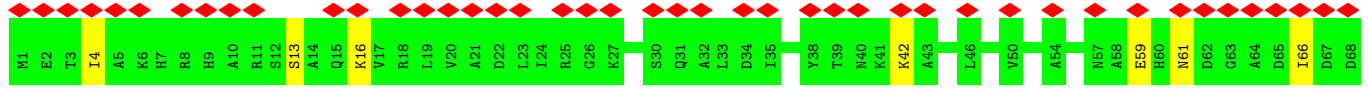
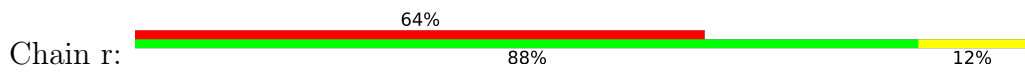
• Molecule 43: 50S ribosomal protein L20



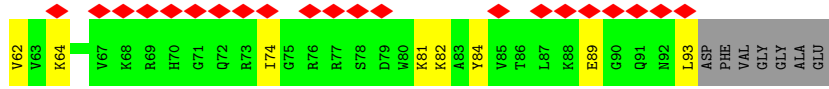
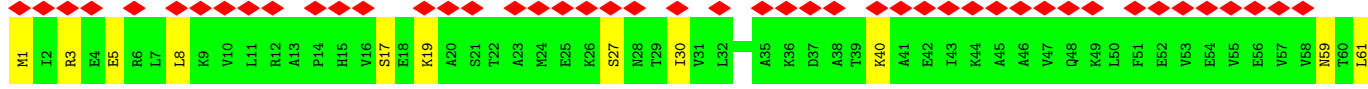
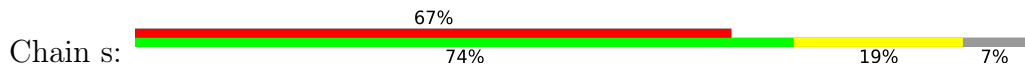
• Molecule 44: 50S ribosomal protein L21



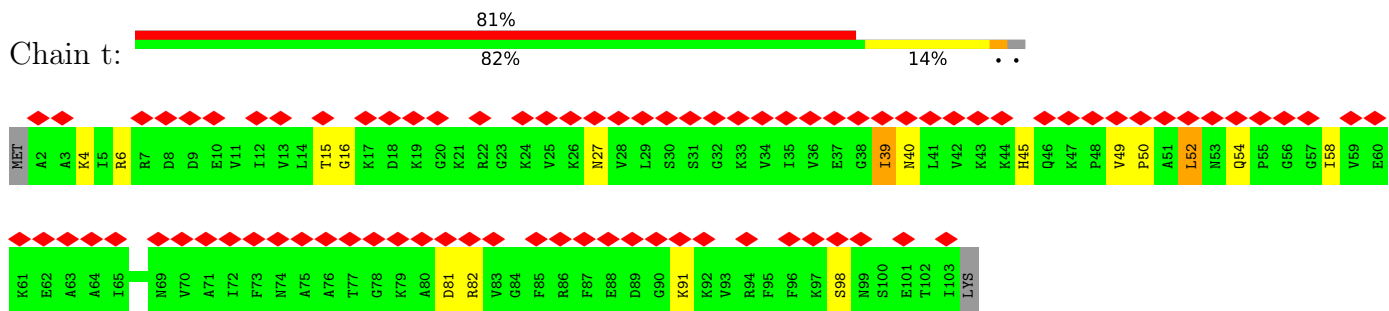
• Molecule 45: 50S ribosomal protein L22



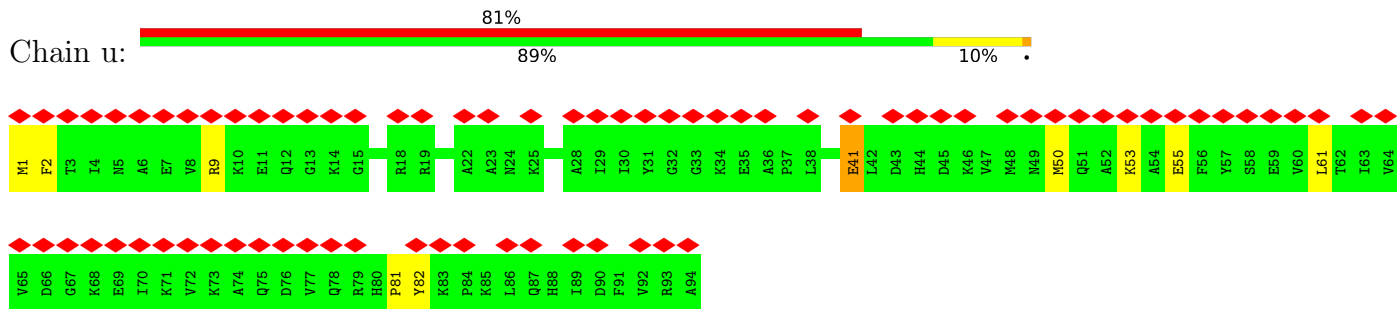
• Molecule 46: 50S ribosomal protein L23



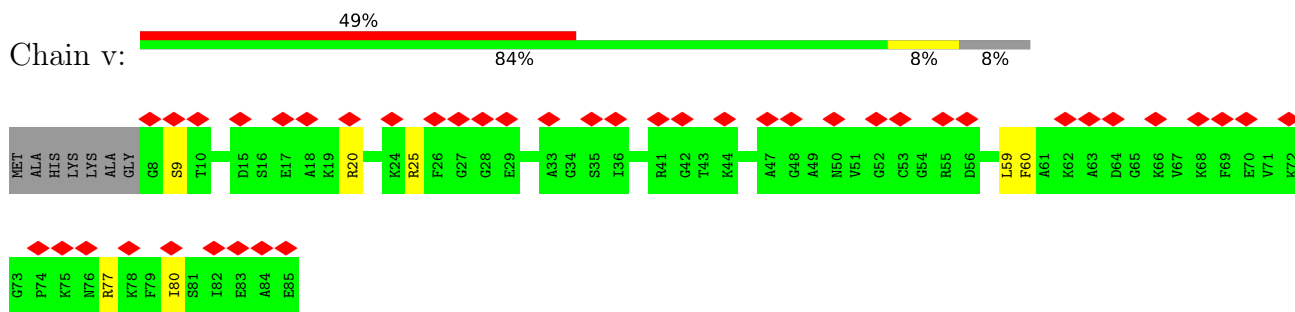
• Molecule 47: 50S ribosomal protein L24



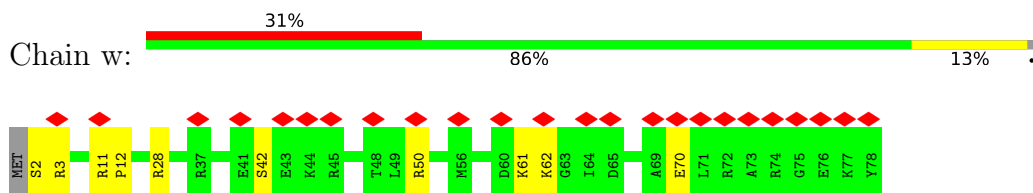
• Molecule 48: 50S ribosomal protein L25



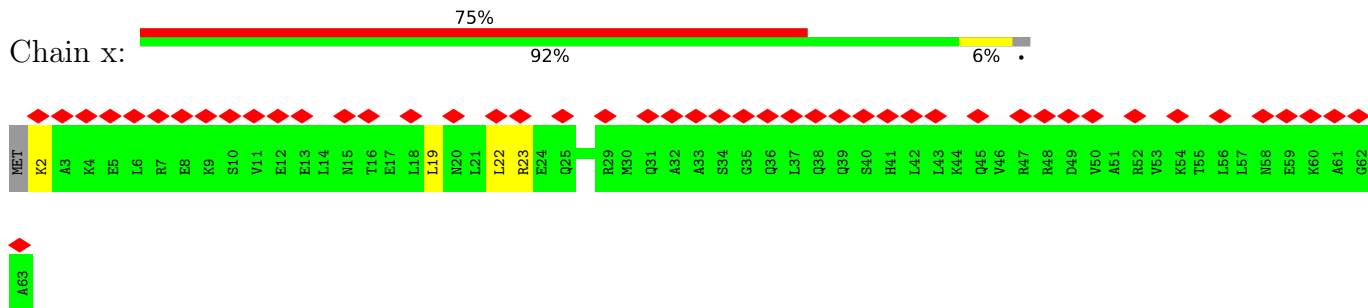
• Molecule 49: 50S ribosomal protein L27



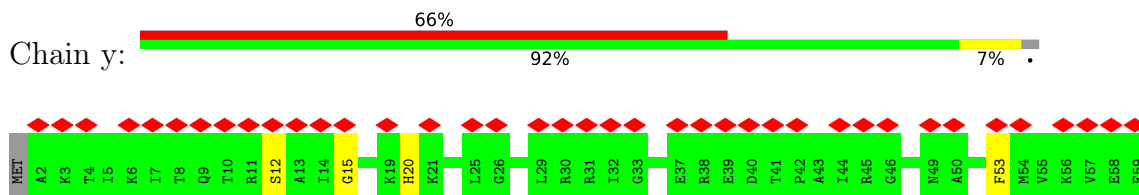
• Molecule 50: 50S ribosomal protein L28



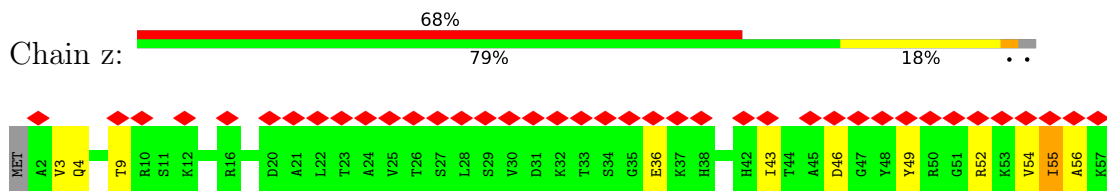
• Molecule 51: 50S ribosomal protein L29



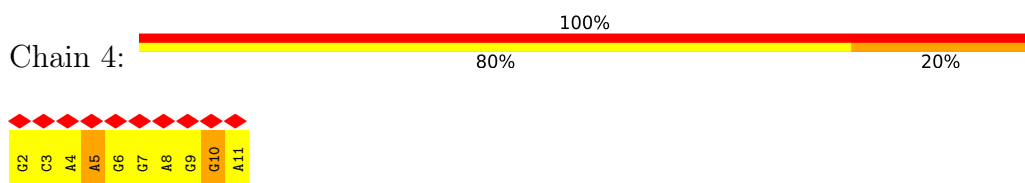
• Molecule 52: 50S ribosomal protein L30



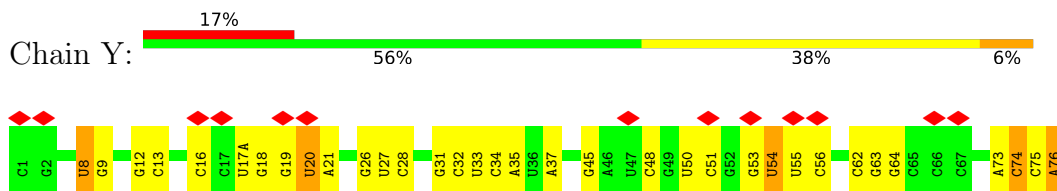
• Molecule 53: 50S ribosomal protein L32



• Molecule 54: mRNA in SD-aSD duplex



• Molecule 55: tRNA(fmet) P-site



## 4 Experimental information i

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39139	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.147	Depositor
Minimum map value	-0.078	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.025	Depositor
Map size ( $\text{\AA}$ )	673.28, 673.28, 673.28	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.052, 1.052, 1.052	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: D2T, OMC, MEQ, MG, 5MU, UR3, 2MA, OMG, H2U, G7M, PSU, 2MG, ZN, 4SU, 4D4, 1MG, MA6, 7MG, MIA, 6MZ, 4OC, K, OMU, 3AU, 3TD, 5MC

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	0	0.29	0/424	0.37	0/565
2	1	0.38	0/380	0.42	0/498
3	2	0.35	0/513	0.39	0/676
4	3	0.34	0/303	0.36	0/397
5	A	0.29	1/36083 (0.0%)	0.32	7/56274 (0.0%)
6	B	0.20	0/1784	0.33	0/2403
7	C	0.24	0/1651	0.31	0/2225
8	D	0.18	0/1665	0.36	0/2227
9	E	0.30	0/1165	0.34	0/1568
10	F	0.25	0/858	0.32	0/1160
11	G	0.20	0/1219	0.31	0/1635
12	H	0.28	0/989	0.31	0/1326
13	I	0.22	0/1034	0.33	0/1375
14	J	0.26	0/796	0.36	0/1077
15	K	0.27	0/893	0.40	0/1205
16	L	0.27	0/904	0.38	0/1211
17	M	0.19	0/900	0.29	0/1204
18	N	0.23	0/817	0.30	0/1088
19	O	0.25	0/722	0.24	0/964
20	P	0.18	0/653	0.48	0/877
21	Q	0.26	0/650	0.35	0/871
22	R	0.30	0/462	0.36	0/621
23	S	0.20	0/685	0.33	0/922
24	T	0.22	0/676	0.31	0/895
25	U	0.20	0/597	0.26	0/792
26	X	0.33	0/301	0.84	1/465 (0.2%)
27	Z	0.16	0/1584	0.20	0/2463
28	a	0.47	0/65531	0.41	1/102222 (0.0%)
29	b	0.37	0/2850	0.31	0/4444
30	c	0.35	0/2121	0.39	0/2852
31	d	0.35	0/1576	0.39	0/2119

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	e	0.33	0/1571	0.37	0/2113
33	f	0.23	0/1434	0.29	0/1926
34	g	0.26	0/1343	0.32	0/1816
35	h	0.27	0/1112	0.40	0/1503
36	i	0.34	0/1152	0.36	0/1551
37	j	0.34	0/955	0.38	0/1279
38	k	0.34	0/1062	0.39	0/1413
39	l	0.34	0/1081	0.39	0/1443
40	m	0.35	0/958	0.42	0/1281
41	n	0.27	0/902	0.34	0/1209
42	o	0.34	0/929	0.35	0/1242
43	p	0.35	0/960	0.38	0/1278
44	q	0.34	0/829	0.37	0/1107
45	r	0.34	0/864	0.36	0/1156
46	s	0.31	0/744	0.35	0/994
47	t	0.29	0/787	0.32	0/1051
48	u	0.31	0/766	0.34	0/1025
49	v	0.33	0/593	0.35	0/785
50	w	0.34	0/635	0.37	0/848
51	x	0.28	0/502	0.26	0/667
52	y	0.32	0/453	0.32	0/605
53	z	0.35	0/450	0.42	0/599
54	4	0.13	0/251	0.23	0/391
55	Y	0.18	0/1725	0.27	0/2687
All	All	0.38	1/152844 (0.0%)	0.37	9/228590 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1407	5MC	O3'-P	16.30	1.85	1.61

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1495	U	P-O3'-C3'	11.69	137.74	120.20
5	A	1495	U	OP2-P-O3'	-11.53	73.40	108.00
5	A	1407	5MC	O3'-P-O5'	10.72	120.08	104.00
26	X	21	C	O3'-P-O5'	-9.80	89.30	104.00
5	A	1495	U	O3'-P-O5'	8.59	116.88	104.00

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	417	0	451	6	0
2	1	377	0	417	5	0
3	2	504	0	572	10	0
4	3	302	0	340	10	0
5	A	32478	0	16356	766	0
6	B	1753	0	1780	23	0
7	C	1624	0	1696	31	0
8	D	1643	0	1707	116	0
9	E	1152	0	1196	41	0
10	F	839	0	833	21	0
11	G	1203	0	1254	31	0
12	H	979	0	1031	25	0
13	I	1022	0	1070	35	0
14	J	786	0	828	36	0
15	K	877	0	887	20	0
16	L	902	0	952	22	0
17	M	891	0	952	78	0
18	N	805	0	844	40	0
19	O	714	0	734	35	0
20	P	643	0	661	42	0
21	Q	641	0	682	14	0
22	R	455	0	478	12	0
23	S	668	0	693	43	0
24	T	670	0	719	31	0
25	U	589	0	629	3	0
26	X	271	0	139	20	0
27	Z	1624	0	823	56	0
28	a	59025	0	29690	579	0
29	b	2549	0	1291	14	0
30	c	2082	0	2153	56	0
31	d	1566	0	1618	16	0
32	e	1552	0	1619	18	0
33	f	1410	0	1444	101	0
34	g	1323	0	1370	57	0
35	h	1101	0	1142	32	0
36	i	1129	0	1162	45	0
37	j	946	0	1023	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	k	1053	0	1129	13	0
39	l	1075	0	1154	24	0
40	m	945	0	989	6	0
41	n	892	0	923	36	0
42	o	917	0	962	13	0
43	p	947	0	1019	8	0
44	q	816	0	839	6	0
45	r	857	0	922	12	0
46	s	738	0	807	23	0
47	t	779	0	831	26	0
48	u	753	0	780	7	0
49	v	586	0	596	10	0
50	w	625	0	652	9	0
51	x	501	0	531	4	0
52	y	449	0	488	6	0
53	z	444	0	458	9	0
54	4	223	0	108	39	0
55	Y	1645	0	842	47	0
56	3	1	0	0	0	0
57	A	48	0	0	0	0
57	a	112	0	0	0	0
57	b	1	0	0	0	0
57	c	4	0	0	0	0
57	d	1	0	0	0	0
57	e	1	0	0	0	0
57	f	1	0	0	0	0
58	A	95	0	0	0	0
58	N	1	0	0	0	0
58	Y	1	0	0	0	0
58	a	254	0	0	0	0
58	b	5	0	0	0	0
58	c	1	0	0	0	0
58	d	1	0	0	0	0
58	k	1	0	0	0	0
58	z	1	0	0	0	0
59	a	11	0	8	2	0
All	All	142297	0	95274	1844	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 1844 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:M:71:ARG:NH1	33:f:115:ARG:HD2	1.24	1.41
5:A:1532:U:C4	5:A:1533:C:N4	1.90	1.39
17:M:71:ARG:CZ	33:f:115:ARG:HD2	1.57	1.35
27:Z:74:C:N4	28:a:2511:C:O2'	1.59	1.34
5:A:1054:C:N4	27:Z:34:G:C8	2.03	1.25

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	0	49/55 (89%)	49 (100%)	0	0	100	100
2	1	44/46 (96%)	44 (100%)	0	0	100	100
3	2	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
4	3	36/38 (95%)	36 (100%)	0	0	100	100
6	B	222/241 (92%)	210 (95%)	9 (4%)	3 (1%)	9	36
7	C	204/233 (88%)	193 (95%)	11 (5%)	0	100	100
8	D	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
9	E	154/167 (92%)	150 (97%)	4 (3%)	0	100	100
10	F	101/135 (75%)	99 (98%)	2 (2%)	0	100	100
11	G	151/179 (84%)	136 (90%)	13 (9%)	2 (1%)	9	38
12	H	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
13	I	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
14	J	96/103 (93%)	88 (92%)	7 (7%)	1 (1%)	12	43
15	K	115/129 (89%)	109 (95%)	6 (5%)	0	100	100
16	L	111/124 (90%)	107 (96%)	3 (3%)	1 (1%)	14	45
17	M	113/118 (96%)	109 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	N	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
19	O	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
20	P	79/82 (96%)	73 (92%)	6 (8%)	0	100	100
21	Q	77/84 (92%)	70 (91%)	7 (9%)	0	100	100
22	R	53/75 (71%)	51 (96%)	1 (2%)	1 (2%)	6	30
23	S	82/92 (89%)	74 (90%)	8 (10%)	0	100	100
24	T	84/87 (97%)	84 (100%)	0	0	100	100
25	U	68/71 (96%)	67 (98%)	1 (2%)	0	100	100
30	c	269/273 (98%)	259 (96%)	10 (4%)	0	100	100
31	d	206/209 (99%)	200 (97%)	6 (3%)	0	100	100
32	e	199/201 (99%)	194 (98%)	5 (2%)	0	100	100
33	f	175/179 (98%)	165 (94%)	10 (6%)	0	100	100
34	g	174/177 (98%)	160 (92%)	13 (8%)	1 (1%)	21	53
35	h	146/149 (98%)	134 (92%)	10 (7%)	2 (1%)	9	36
36	i	140/142 (99%)	140 (100%)	0	0	100	100
37	j	121/123 (98%)	118 (98%)	3 (2%)	0	100	100
38	k	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
39	l	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
40	m	116/127 (91%)	112 (97%)	4 (3%)	0	100	100
41	n	114/117 (97%)	113 (99%)	1 (1%)	0	100	100
42	o	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
43	p	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
44	q	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
45	r	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
46	s	91/100 (91%)	90 (99%)	1 (1%)	0	100	100
47	t	100/104 (96%)	96 (96%)	3 (3%)	1 (1%)	12	43
48	u	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
49	v	76/85 (89%)	75 (99%)	1 (1%)	0	100	100
50	w	75/78 (96%)	75 (100%)	0	0	100	100
51	x	60/63 (95%)	60 (100%)	0	0	100	100
52	y	56/59 (95%)	55 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	z	54/57 (95%)	53 (98%)	1 (2%)	0	100	100
All	All	5515/5843 (94%)	5313 (96%)	190 (3%)	12 (0%)	44	72

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	B	87	CYS
6	B	131	LYS
11	G	81	GLY
14	J	57	VAL
34	g	126	PRO

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	46/49 (94%)	46 (100%)	0	100	100
2	1	38/38 (100%)	38 (100%)	0	100	100
3	2	51/52 (98%)	51 (100%)	0	100	100
4	3	34/34 (100%)	34 (100%)	0	100	100
6	B	186/199 (94%)	179 (96%)	7 (4%)	29	59
7	C	170/190 (90%)	166 (98%)	4 (2%)	43	67
8	D	172/173 (99%)	172 (100%)	0	100	100
9	E	119/126 (94%)	118 (99%)	1 (1%)	73	80
10	F	90/116 (78%)	89 (99%)	1 (1%)	65	77
11	G	126/147 (86%)	125 (99%)	1 (1%)	73	80
12	H	104/105 (99%)	103 (99%)	1 (1%)	68	78
13	I	105/107 (98%)	105 (100%)	0	100	100
14	J	86/90 (96%)	83 (96%)	3 (4%)	32	61
15	K	90/99 (91%)	87 (97%)	3 (3%)	33	62
16	L	96/103 (93%)	96 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	M	93/96 (97%)	91 (98%)	2 (2%)	45	68
18	N	83/84 (99%)	82 (99%)	1 (1%)	63	76
19	O	76/77 (99%)	75 (99%)	1 (1%)	61	75
20	P	65/65 (100%)	65 (100%)	0	100	100
21	Q	73/78 (94%)	72 (99%)	1 (1%)	59	74
22	R	48/65 (74%)	46 (96%)	2 (4%)	26	56
23	S	72/79 (91%)	70 (97%)	2 (3%)	38	64
24	T	65/66 (98%)	64 (98%)	1 (2%)	57	73
25	U	60/61 (98%)	57 (95%)	3 (5%)	22	52
30	c	216/218 (99%)	216 (100%)	0	100	100
31	d	163/163 (100%)	163 (100%)	0	100	100
32	e	165/165 (100%)	162 (98%)	3 (2%)	51	71
33	f	148/150 (99%)	146 (99%)	2 (1%)	59	74
34	g	137/138 (99%)	131 (96%)	6 (4%)	25	55
35	h	113/114 (99%)	105 (93%)	8 (7%)	13	41
36	i	116/116 (100%)	115 (99%)	1 (1%)	70	79
37	j	104/104 (100%)	104 (100%)	0	100	100
38	k	103/103 (100%)	102 (99%)	1 (1%)	68	78
39	l	108/108 (100%)	107 (99%)	1 (1%)	70	79
40	m	98/103 (95%)	97 (99%)	1 (1%)	68	78
41	n	86/87 (99%)	86 (100%)	0	100	100
42	o	99/100 (99%)	99 (100%)	0	100	100
43	p	89/90 (99%)	89 (100%)	0	100	100
44	q	84/84 (100%)	84 (100%)	0	100	100
45	r	93/93 (100%)	92 (99%)	1 (1%)	65	77
46	s	80/84 (95%)	79 (99%)	1 (1%)	61	75
47	t	83/85 (98%)	80 (96%)	3 (4%)	31	60
48	u	78/78 (100%)	76 (97%)	2 (3%)	40	66
49	v	58/63 (92%)	58 (100%)	0	100	100
50	w	67/68 (98%)	66 (98%)	1 (2%)	57	73
51	x	54/55 (98%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	y	48/49 (98%)	48 (100%)	0	100	100
53	z	47/48 (98%)	46 (98%)	1 (2%)	47	69
All	All	4585/4765 (96%)	4519 (99%)	66 (1%)	57	74

5 of 66 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	r	109	ASP
47	t	15	THR
53	z	55	ILE
19	O	80	GLN
18	N	49	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
33	f	5	HIS
37	j	29	HIS
33	f	37	ASN
35	h	66	ASN
41	n	116	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	X	12/16 (75%)	5 (41%)	0
27	Z	75/76 (98%)	13 (17%)	1 (1%)
28	a	2742/2925 (93%)	260 (9%)	0
29	b	118/119 (99%)	10 (8%)	0
5	A	1508/1542 (97%)	191 (12%)	5 (0%)
54	4	9/10 (90%)	5 (55%)	0
55	Y	76/77 (98%)	12 (15%)	0
All	All	4540/4765 (95%)	496 (10%)	6 (0%)

5 of 496 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	A	2	A
5	A	3	A

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Mol	Chain	Res	Type
5	A	4	U
5	A	5	U
5	A	9	G

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	A	1035	A
5	A	1535	C
27	Z	19	G
5	A	766	A
5	A	641	U

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

53 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
28	PSU	a	748	28,58	18,21,22	1.10	2 (11%)	22,30,33	1.60	3 (13%)
28	PSU	a	1921	28	18,21,22	1.04	1 (5%)	22,30,33	1.84	4 (18%)
5	MA6	A	1519	5	23,26,27	1.38	5 (21%)	34,38,41	2.87	13 (38%)
55	OMC	Y	32	55	19,22,23	3.01	8 (42%)	26,31,34	0.90	2 (7%)
5	4OC	A	1402	5	20,23,24	2.98	8 (40%)	26,32,35	0.94	1 (3%)
28	PSU	a	1915	28	18,21,22	1.01	1 (5%)	22,30,33	1.78	3 (13%)
27	5MU	Z	54	27	19,22,23	1.38	5 (26%)	28,32,35	2.09	6 (21%)
28	OMU	a	2556	57,28,58	19,22,23	3.07	7 (36%)	26,31,34	1.66	4 (15%)
55	4SU	Y	8	55	18,21,22	4.19	8 (44%)	26,30,33	2.26	5 (19%)
5	5MC	A	1407	5	18,22,23	0.83	1 (5%)	26,32,35	0.58	0
27	4SU	Z	8	27	18,21,22	4.19	8 (44%)	26,30,33	2.25	4 (15%)
55	H2U	Y	20	55	18,21,22	3.11	5 (27%)	21,30,33	1.97	5 (23%)
39	4D4	l	81	39	9,11,12	0.54	0	8,13,15	1.03	1 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
31	MEQ	d	150	31	8,9,10	0.82	0	5,10,12	0.76	0
28	5MU	a	749	28	19,22,23	0.72	0	28,32,35	0.56	0
27	H2U	Z	20	27	18,21,22	3.13	5 (27%)	21,30,33	1.99	5 (23%)
28	2MG	a	2449	28	23,26,27	0.78	0	32,38,41	0.57	0
5	2MG	A	1516	5	23,26,27	0.65	0	32,38,41	0.62	0
28	PSU	a	957	28	18,21,22	1.07	1 (5%)	22,30,33	1.79	2 (9%)
27	PSU	Z	32	27	18,21,22	1.07	1 (5%)	22,30,33	1.77	5 (22%)
28	1MG	a	747	28	22,26,27	2.59	6 (27%)	33,39,42	2.07	7 (21%)
27	PSU	Z	55	27	18,21,22	1.10	1 (5%)	22,30,33	1.81	5 (22%)
28	2MA	a	2507	57,28,58	22,25,26	3.74	11 (50%)	33,37,40	2.78	12 (36%)
28	5MU	a	1943	57,28	19,22,23	0.81	0	28,32,35	0.46	0
28	OMC	a	2502	28,58	19,22,23	0.81	1 (5%)	26,31,34	0.66	0
27	7MG	Z	46	27	20,25,27	3.36	10 (50%)	27,37,42	2.11	8 (29%)
28	PSU	a	2508	57,28	18,21,22	1.03	1 (5%)	22,30,33	1.87	4 (18%)
16	D2T	L	89	16	7,9,10	1.36	1 (14%)	6,11,13	1.79	2 (33%)
5	PSU	A	516	5	18,21,22	0.99	1 (5%)	22,30,33	1.71	5 (22%)
28	OMG	a	2255	57,28,55	23,26,27	0.71	0	33,38,41	0.53	0
55	5MU	Y	54	55	19,22,23	1.39	5 (26%)	28,32,35	2.07	6 (21%)
5	5MC	A	967	5	18,22,23	0.76	0	26,32,35	0.61	0
28	6MZ	a	1620	28	22,25,26	2.86	5 (22%)	30,36,39	2.72	11 (36%)
28	2MG	a	1837	28	23,26,27	0.69	0	32,38,41	0.56	0
28	PSU	a	2584	28	18,21,22	1.07	2 (11%)	22,30,33	1.77	3 (13%)
27	3AU	Z	47	27	18,21,29	3.38	8 (44%)	26,30,43	1.64	5 (19%)
27	MIA	Z	37	27	21,24,32	1.74	4 (19%)	31,35,47	2.13	10 (32%)
28	6MZ	a	2034	28	22,25,26	2.81	6 (27%)	30,36,39	2.84	11 (36%)
5	MA6	A	1518	5	23,26,27	1.37	5 (21%)	34,38,41	2.81	14 (41%)
28	3TD	a	1919	28	18,22,23	4.02	7 (38%)	22,32,35	1.79	3 (13%)
27	H2U	Z	16	27	18,21,22	3.06	5 (27%)	21,30,33	2.09	5 (23%)
5	G7M	A	527	5	23,26,27	2.61	9 (39%)	35,39,42	2.63	11 (31%)
5	2MG	A	1207	57,5	23,26,27	0.56	0	32,38,41	0.54	0
28	5MC	a	1966	57,28	18,22,23	0.81	0	26,32,35	0.53	0
28	H2U	a	2453	28	18,21,22	0.63	0	21,30,33	1.07	3 (14%)
28	G7M	a	2073	57,28	23,26,27	2.67	9 (39%)	35,39,42	1.69	9 (25%)
28	PSU	a	2609	28	18,21,22	1.08	1 (5%)	22,30,33	1.89	4 (18%)
28	PSU	a	2608	28	18,21,22	1.05	1 (5%)	22,30,33	1.85	3 (13%)
5	2MG	A	966	5	23,26,27	0.57	0	32,38,41	0.55	0
27	PSU	Z	39	27	18,21,22	1.05	1 (5%)	22,30,33	1.80	5 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
55	PSU	Y	55	55	18,21,22	1.12	1 (5%)	22,30,33	1.76	4 (18%)
28	PSU	a	2461	28	18,21,22	1.10	1 (5%)	22,30,33	1.84	4 (18%)
5	UR3	A	1498	5	19,22,23	2.57	6 (31%)	26,32,35	1.37	3 (11%)

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
28	PSU	a	748	28,58	-	1/7/25/26	0/2/2/2
28	PSU	a	1921	28	-	0/7/25/26	0/2/2/2
5	MA6	A	1519	5	-	3/11/29/30	0/3/3/3
55	OMC	Y	32	55	-	3/9/27/28	0/2/2/2
5	4OC	A	1402	5	-	0/9/29/30	0/2/2/2
28	PSU	a	1915	28	-	0/7/25/26	0/2/2/2
27	5MU	Z	54	27	-	0/7/25/26	0/2/2/2
28	OMU	a	2556	57,28,58	-	0/9/27/28	0/2/2/2
55	4SU	Y	8	55	-	2/7/25/26	0/2/2/2
5	5MC	A	1407	5	-	0/7/25/26	0/2/2/2
27	4SU	Z	8	27	-	2/7/25/26	0/2/2/2
55	H2U	Y	20	55	-	7/7/38/39	0/2/2/2
39	4D4	l	81	39	-	6/11/12/14	-
31	MEQ	d	150	31	-	2/8/9/11	-
28	5MU	a	749	28	-	0/7/25/26	0/2/2/2
27	H2U	Z	20	27	-	2/7/38/39	0/2/2/2
28	2MG	a	2449	28	-	0/9/27/28	0/3/3/3
5	2MG	A	1516	5	-	0/9/27/28	0/3/3/3
28	PSU	a	957	28	-	0/7/25/26	0/2/2/2
27	PSU	Z	32	27	-	0/7/25/26	0/2/2/2
28	1MG	a	747	28	-	0/7/25/26	0/3/3/3
27	PSU	Z	55	27	-	0/7/25/26	0/2/2/2
28	2MA	a	2507	57,28,58	-	2/7/25/26	0/3/3/3
28	5MU	a	1943	57,28	-	0/7/25/26	0/2/2/2
28	OMC	a	2502	28,58	-	0/9/27/28	0/2/2/2
27	7MG	Z	46	27	-	2/7/34/38	0/3/3/3
28	PSU	a	2508	57,28	-	0/7/25/26	0/2/2/2
16	D2T	L	89	16	-	3/7/12/14	-
5	PSU	A	516	5	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	OMG	a	2255	57,28,55	-	1/9/27/28	0/3/3/3
55	5MU	Y	54	55	-	0/7/25/26	0/2/2/2
5	5MC	A	967	5	-	0/7/25/26	0/2/2/2
28	6MZ	a	1620	28	-	0/9/27/28	0/3/3/3
28	2MG	a	1837	28	-	0/9/27/28	0/3/3/3
28	PSU	a	2584	28	-	0/7/25/26	0/2/2/2
27	3AU	Z	47	27	-	2/7/25/35	0/2/2/2
27	MIA	Z	37	27	-	0/7/25/34	0/3/3/3
28	6MZ	a	2034	28	-	2/9/27/28	0/3/3/3
5	MA6	A	1518	5	-	0/11/29/30	0/3/3/3
28	3TD	a	1919	28	-	2/7/25/26	0/2/2/2
27	H2U	Z	16	27	-	0/7/38/39	0/2/2/2
5	G7M	A	527	5	-	0/7/25/26	0/3/3/3
5	2MG	A	1207	57,5	-	0/9/27/28	0/3/3/3
28	5MC	a	1966	57,28	-	0/7/25/26	0/2/2/2
28	H2U	a	2453	28	-	0/7/38/39	0/2/2/2
28	G7M	a	2073	57,28	-	2/7/25/26	0/3/3/3
28	PSU	a	2609	28	-	0/7/25/26	0/2/2/2
28	PSU	a	2608	28	-	0/7/25/26	0/2/2/2
5	2MG	A	966	5	-	0/9/27/28	0/3/3/3
27	PSU	Z	39	27	-	0/7/25/26	0/2/2/2
55	PSU	Y	55	55	-	0/7/25/26	0/2/2/2
28	PSU	a	2461	28	-	0/7/25/26	0/2/2/2
5	UR3	A	1498	5	-	0/7/25/26	0/2/2/2

The worst 5 of 174 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	a	1919	3TD	C6-C5	12.08	1.49	1.35
28	a	1620	6MZ	C6-N6	11.66	1.46	1.34
28	a	2034	6MZ	C6-N6	11.18	1.46	1.34
28	a	2507	2MA	C4-N3	10.44	1.47	1.34
27	Z	20	H2U	C2-N1	9.70	1.49	1.35

The worst 5 of 220 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1519	MA6	N1-C6-N6	-9.37	106.84	117.08
5	A	1518	MA6	N1-C6-N6	-8.90	107.36	117.08
28	a	2507	2MA	C1'-N9-C8	-8.83	107.21	127.14
55	Y	8	4SU	C4-N3-C2	-7.98	119.59	127.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	Z	8	4SU	C4-N3-C2	-7.85	119.72	127.34

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
27	Z	46	7MG	O4'-C4'-C5'-O5'
39	l	81	4D4	NH1-CZ-NE-CD
55	Y	20	H2U	O4'-C1'-N1-C6
55	Y	32	OMC	C1'-C2'-O2'-CM2
28	a	2034	6MZ	O4'-C4'-C5'-O5'

There are no ring outliers.

12 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1407	5MC	4	0
39	l	81	4D4	1	0
31	d	150	MEQ	1	0
27	Z	20	H2U	1	0
27	Z	55	PSU	1	0
5	A	516	PSU	1	0
28	a	2255	OMG	2	0
55	Y	54	5MU	2	0
28	a	2584	PSU	1	0
27	Z	37	MIA	3	0
28	a	2034	6MZ	1	0
28	a	1919	3TD	9	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 530 ligands modelled in this entry, 529 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
59	PHE	a	3001	-	10,11,12	0.43	0	10,13,15	0.30	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
59	PHE	a	3001	-	-	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.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	a	3001	PHE	2	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
5	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1532:U	O3'	1533:C	P	3.52

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1407:5MC	O3'	1408:A	P	1.85

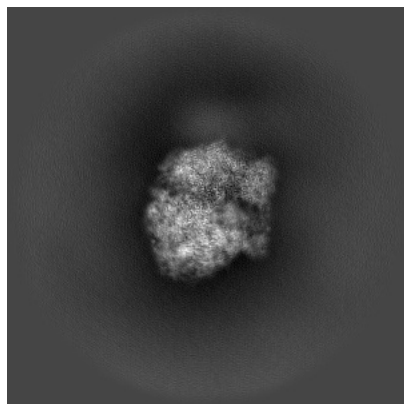
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51517. These allow visual inspection of the internal detail of the map and identification of artifacts.

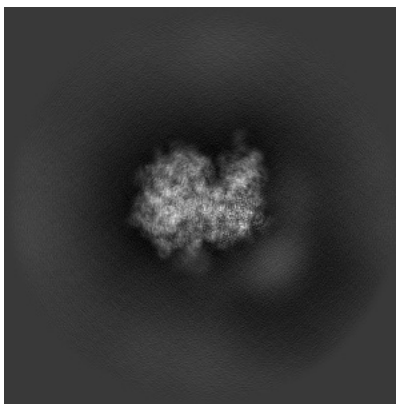
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

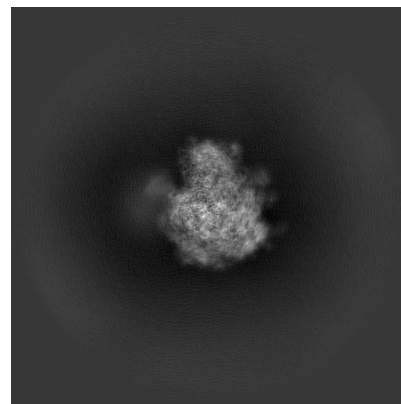
#### 6.1.1 Primary map



X

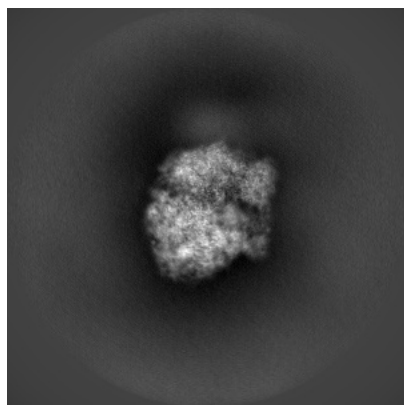


Y

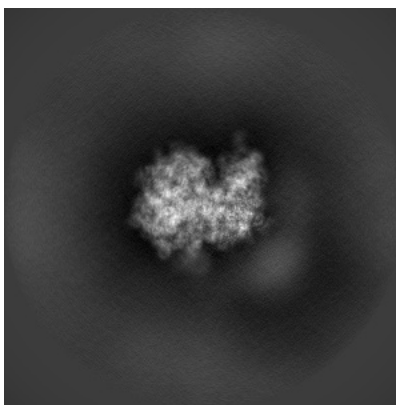


Z

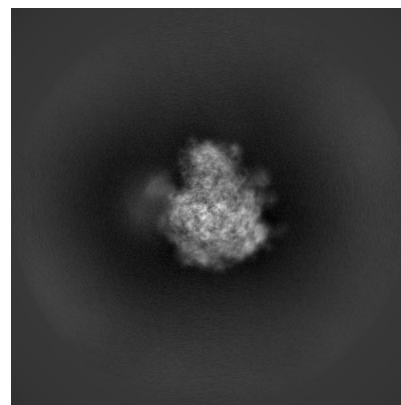
#### 6.1.2 Raw map



X



Y

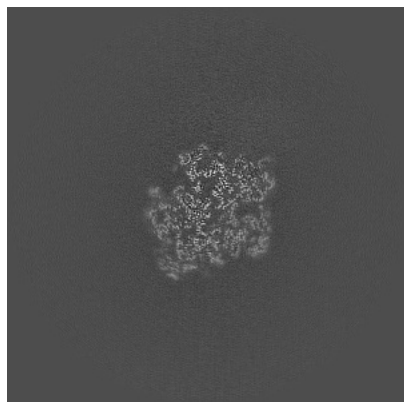


Z

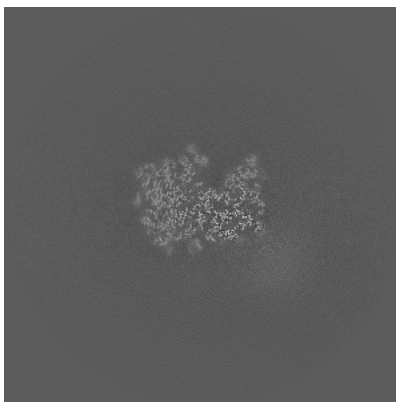
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

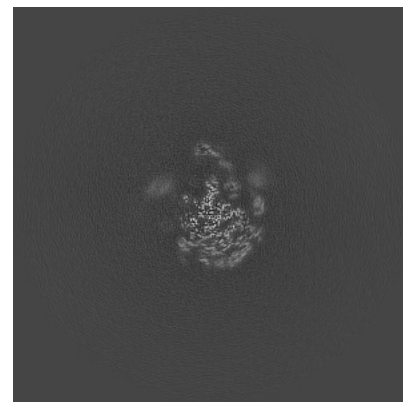
### 6.2.1 Primary map



X Index: 320

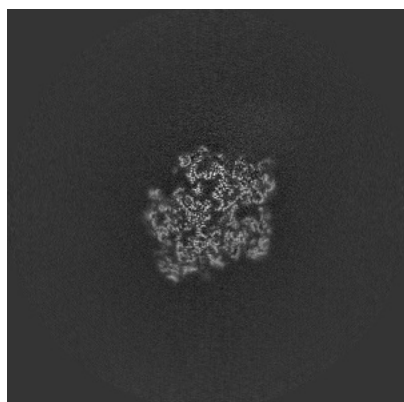


Y Index: 320

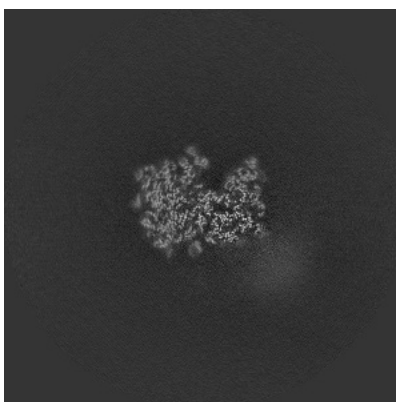


Z Index: 320

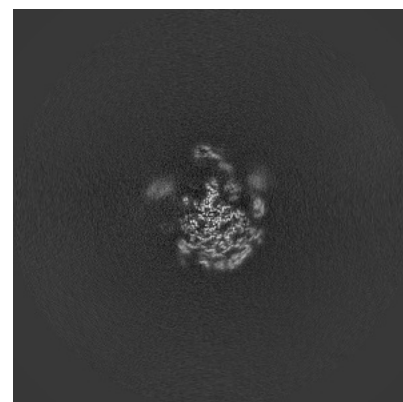
### 6.2.2 Raw map



X Index: 320



Y Index: 320

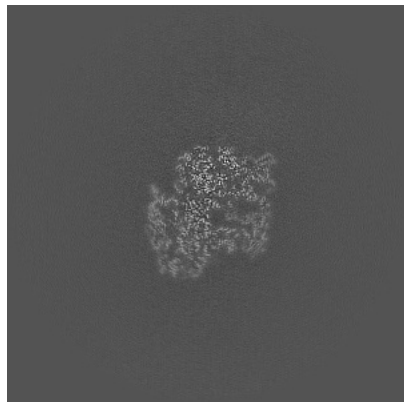


Z Index: 320

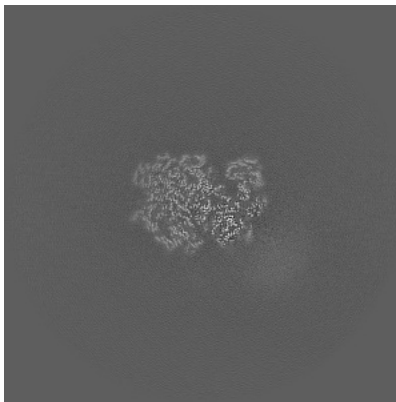
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

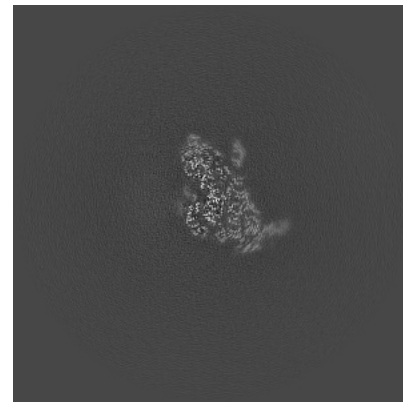
### 6.3.1 Primary map



X Index: 309

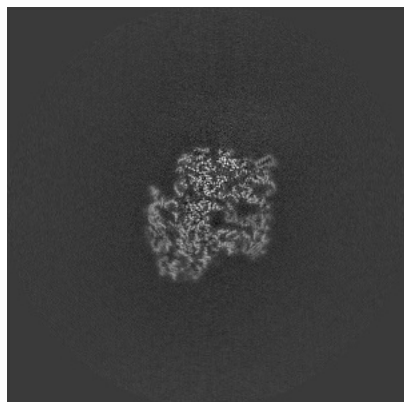


Y Index: 310

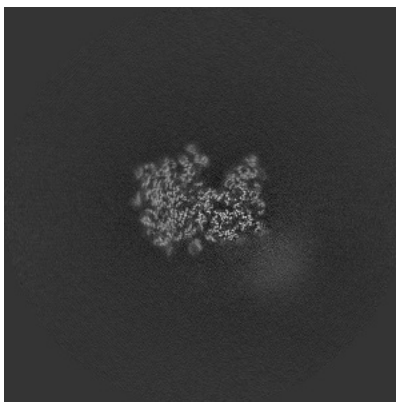


Z Index: 377

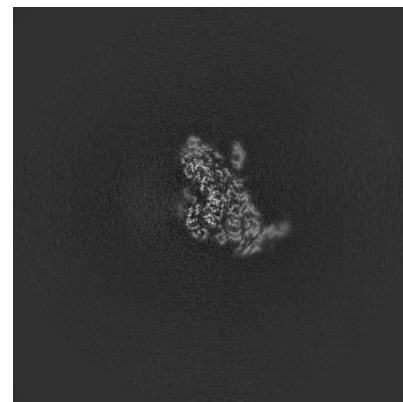
### 6.3.2 Raw map



X Index: 310



Y Index: 320

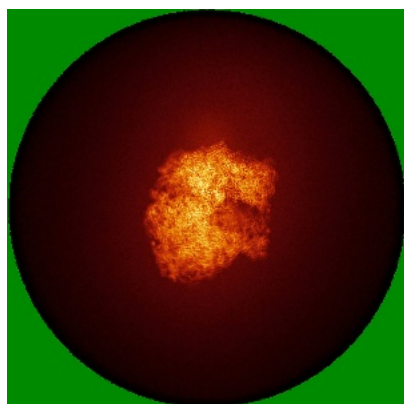


Z Index: 377

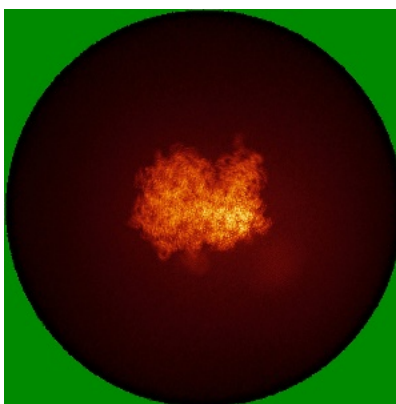
The images above show the largest variance slices of the map in three orthogonal directions.

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

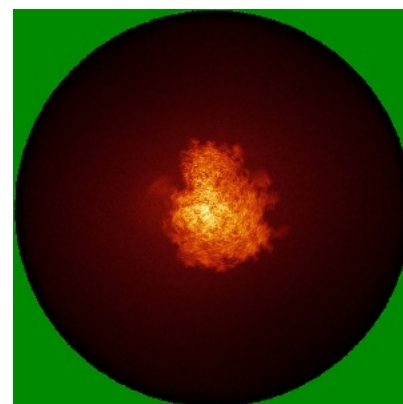
### 6.4.1 Primary map



X

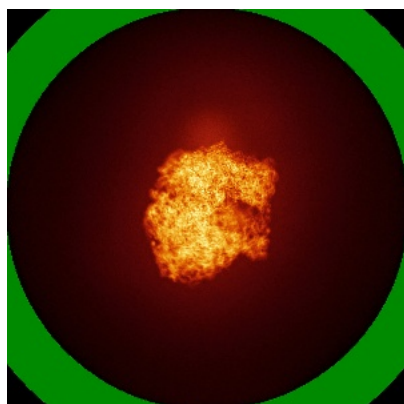


Y

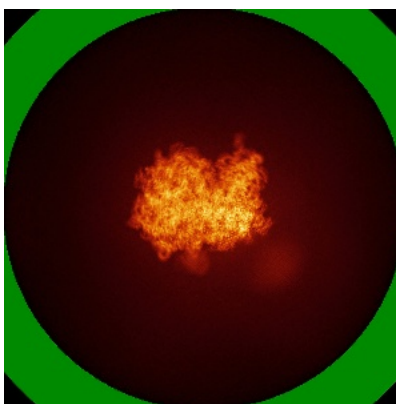


Z

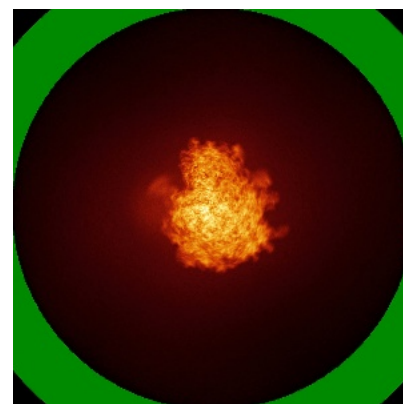
### 6.4.2 Raw map



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.

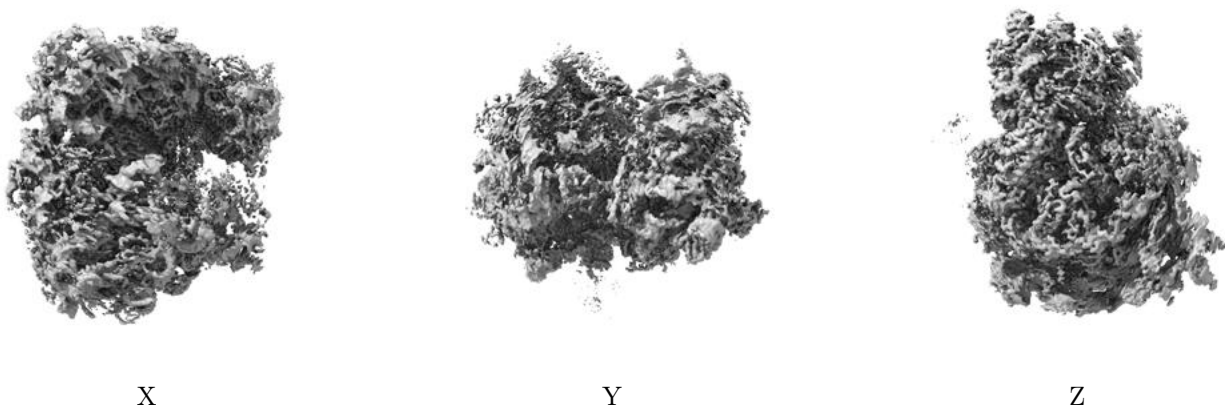
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

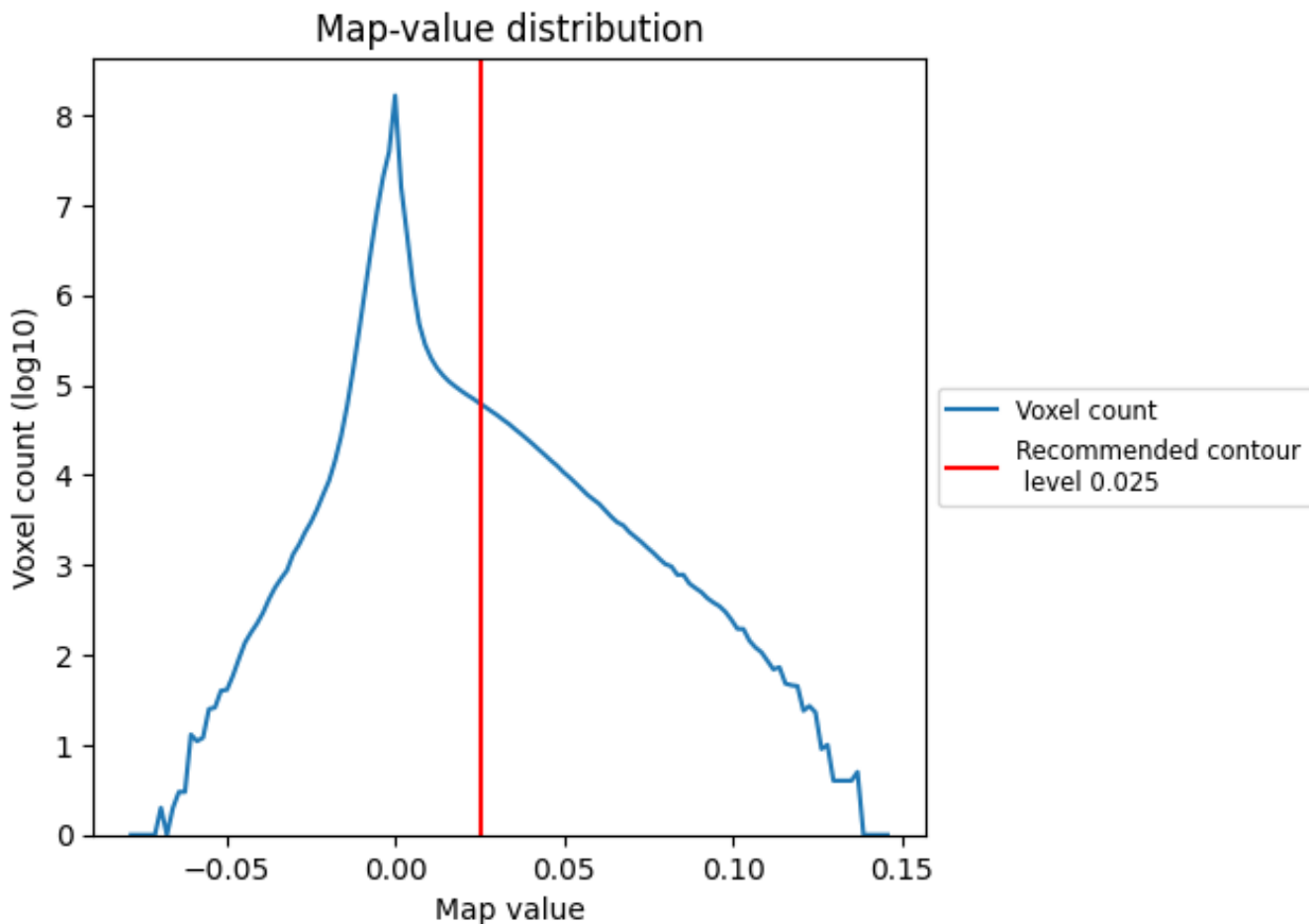
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

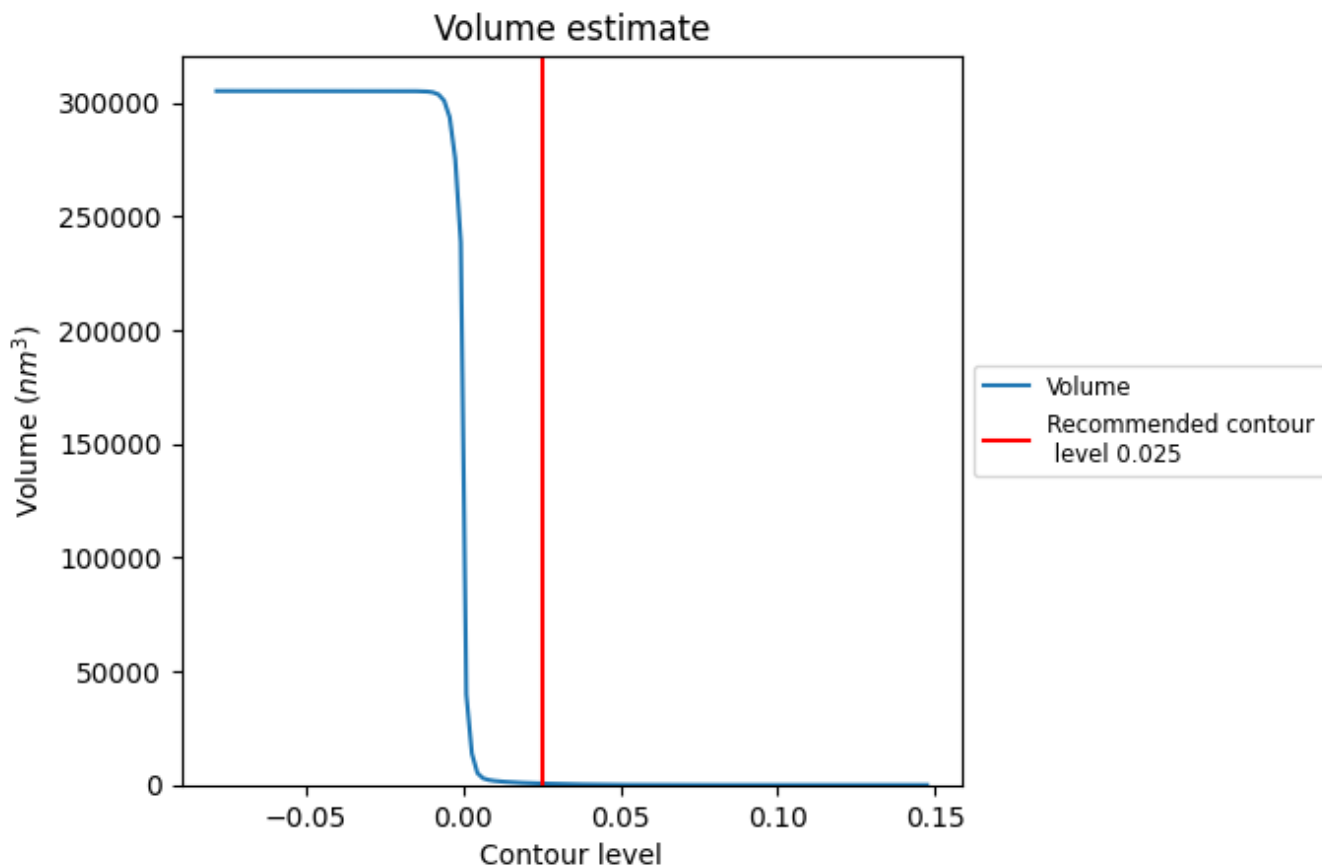
This section contains the results of statistical analysis of the map.

### 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.

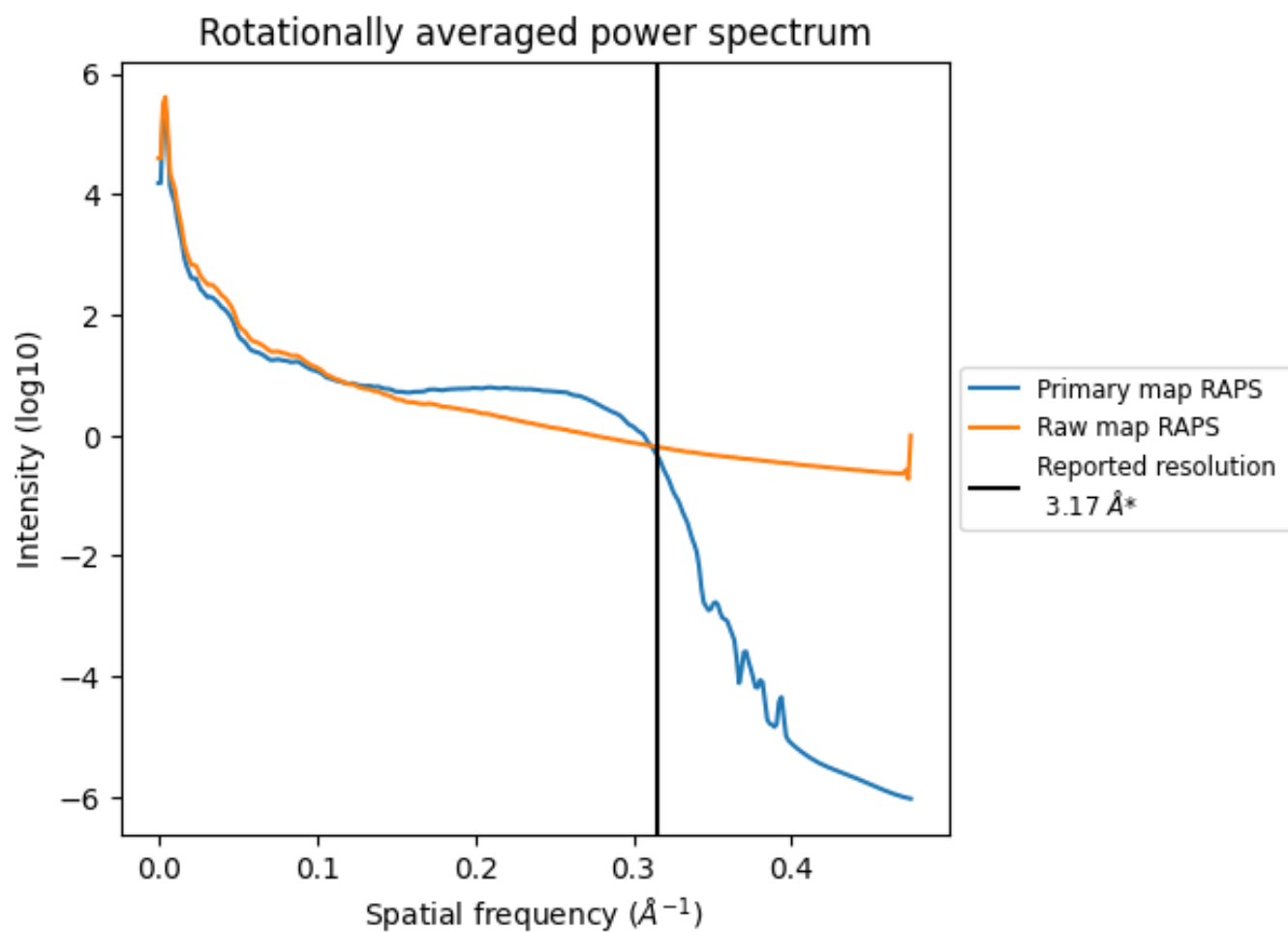
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 631  $\text{nm}^3$ ; this corresponds to an approximate mass of 570 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum i

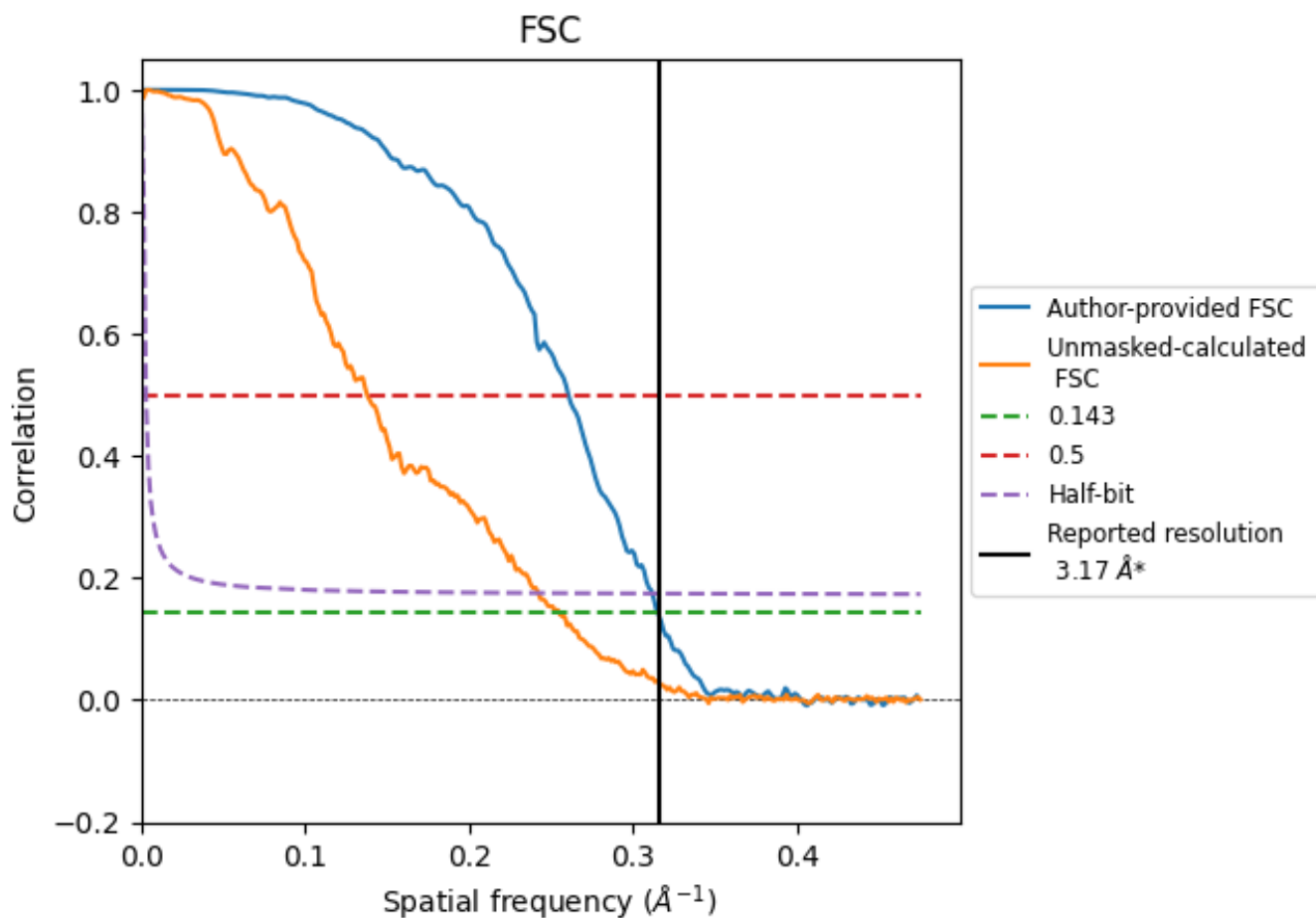


\*Reported resolution corresponds to spatial frequency of  $0.315 \text{ \AA}^{-1}$

## 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 0.315 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

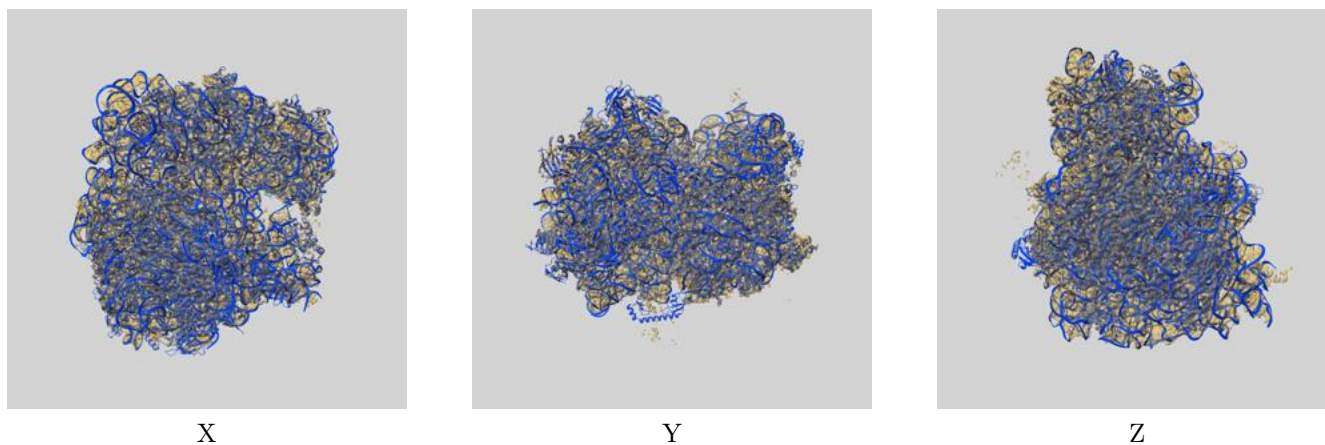
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.17	-	-
Author-provided FSC curve	3.17	3.84	3.21
Unmasked-calculated*	3.92	7.25	4.13

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.92 differs from the reported value 3.17 by more than 10 %

## 9 Map-model fit [i](#)

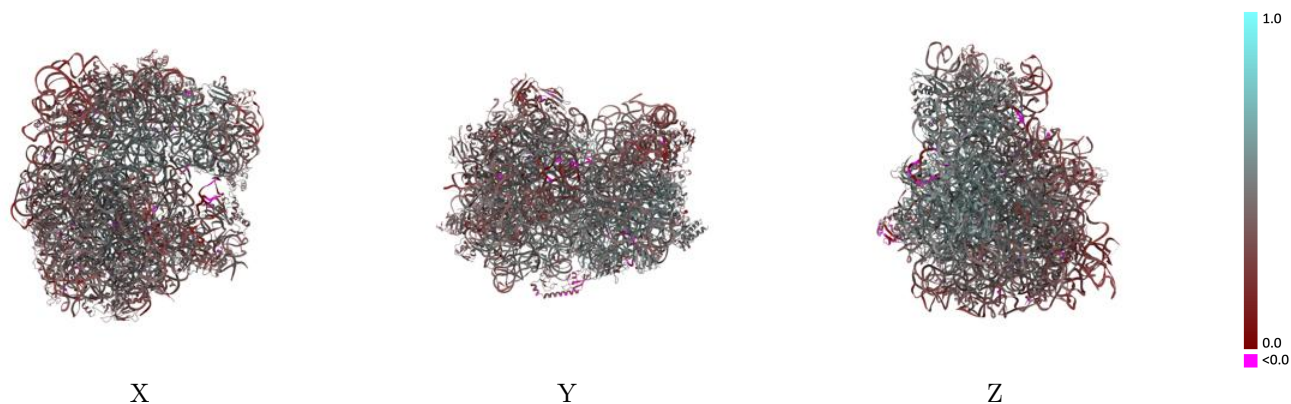
This section contains information regarding the fit between EMDB map EMD-51517 and PDB model 9GR1. Per-residue inclusion information can be found in section 3 on page 16.

### 9.1 Map-model overlay [i](#)



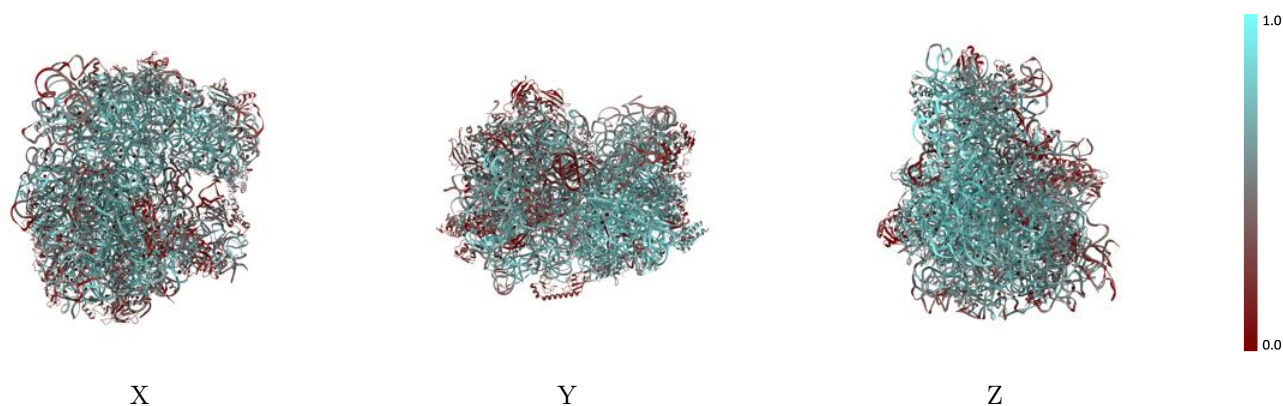
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



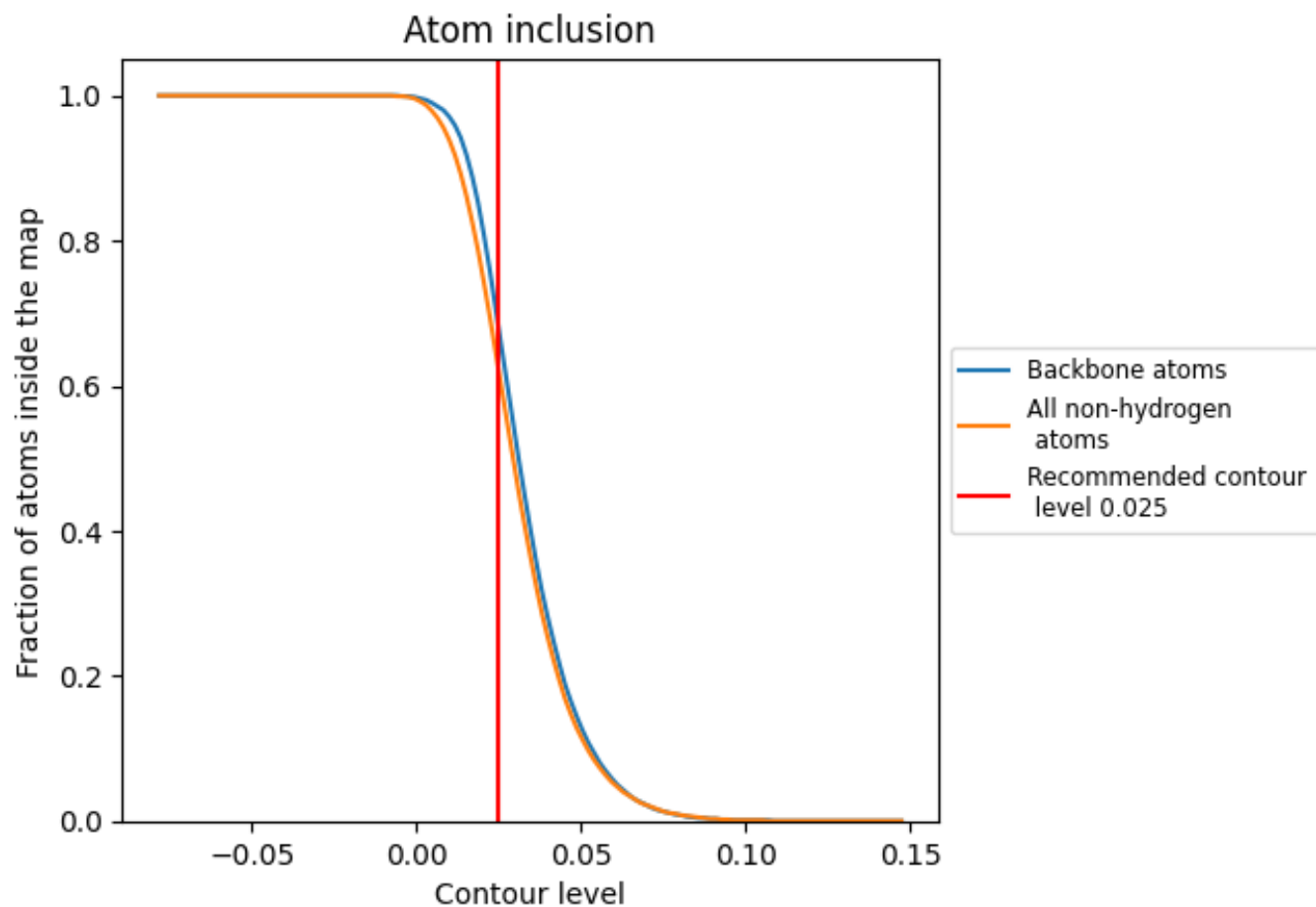
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 62% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6190	 0.4210
0	 0.0390	 0.3730
1	 0.5580	 0.4810
2	 0.4890	 0.4880
3	 0.4200	 0.4080
4	 0.0990	 0.1170
A	 0.7280	 0.4270
B	 0.6860	 0.4950
C	 0.5820	 0.4940
D	 0.3010	 0.3440
E	 0.6720	 0.5250
F	 0.6410	 0.5020
G	 0.5770	 0.4630
H	 0.6650	 0.5190
I	 0.6540	 0.5010
J	 0.4110	 0.4280
K	 0.7020	 0.5210
L	 0.5830	 0.4940
M	 0.4820	 0.4510
N	 0.5340	 0.4640
O	 0.6420	 0.5090
P	 0.3960	 0.3770
Q	 0.4780	 0.4130
R	 0.7180	 0.5230
S	 0.4290	 0.4080
T	 0.4210	 0.3530
U	 0.5010	 0.4110
X	 0.4980	 0.4400
Y	 0.6020	 0.4140
Z	 0.3090	 0.3770
a	 0.6990	 0.4200
b	 0.5960	 0.3880
c	 0.6740	 0.5320
d	 0.3700	 0.4050
e	 0.3260	 0.3840



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Chain	Atom inclusion	Q-score
f	 0.2900	 0.3580
g	 0.1180	 0.2880
h	 0.0410	 0.1850
i	 0.3680	 0.3960
j	 0.4650	 0.4520
k	 0.3990	 0.4280
l	 0.4550	 0.4530
m	 0.4050	 0.4000
n	 0.2860	 0.3450
o	 0.3660	 0.3860
p	 0.4540	 0.4170
q	 0.3200	 0.4040
r	 0.3590	 0.4090
s	 0.2920	 0.3690
t	 0.1750	 0.2940
u	 0.2340	 0.3460
v	 0.4140	 0.4330
w	 0.4990	 0.4510
x	 0.2560	 0.2910
y	 0.3300	 0.3700
z	 0.3430	 0.3950