



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 02:32 PM UTC

PDB ID : 8URH / pdb_00008urh
EMDB ID : EMD-42492
Title : Escherichia coli transcription-translation coupled complex class B (TTC-B) containing RfaH bound to ops signal, mRNA with a 27 nt long spacer, and fMet-tRNAs in E-site and P-site of the ribosome
Authors : Molodtsov, V.; Wang, C.; Ebright, R.H.
Deposited on : 2023-10-26
Resolution : 5.70 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

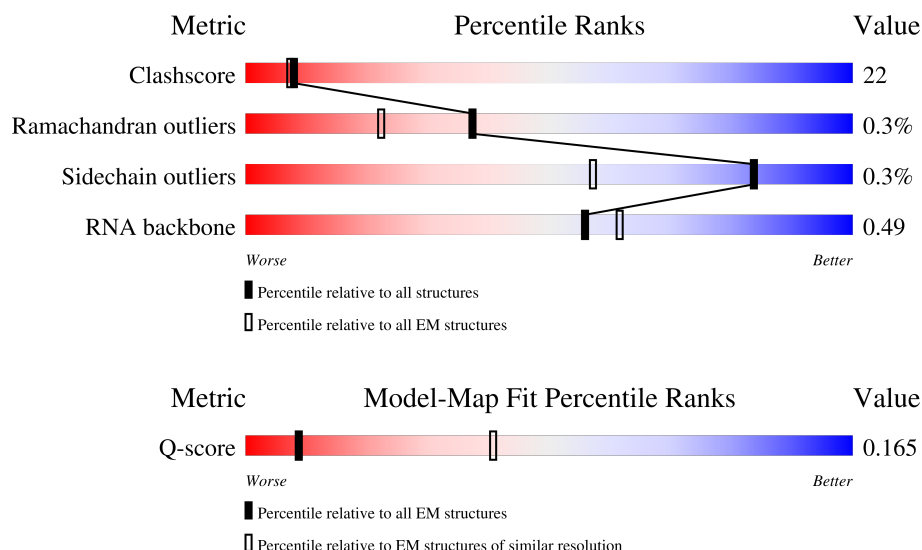
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.70 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.



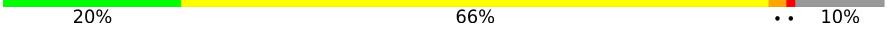
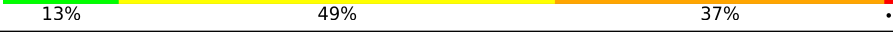
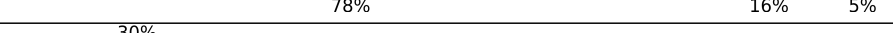
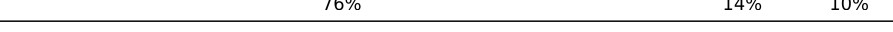
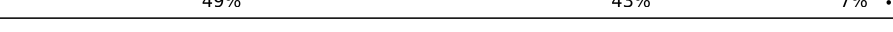
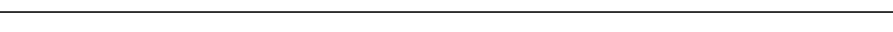
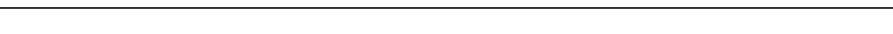
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	503 (5.20 - 6.20)

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	0	103	
2	1	110	
3	2	100	

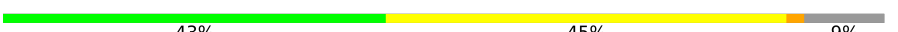
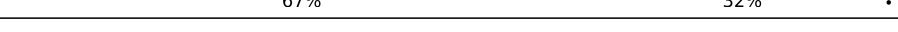
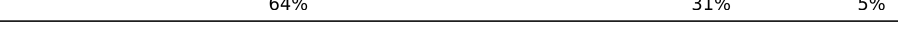
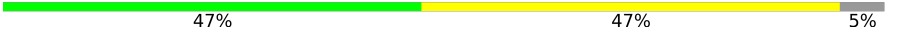
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Mol	Chain	Length	Quality of chain
4	3	104	
5	4	94	
6	5	38	
7	6	38	
8	7	44	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	162	
13	AC	329	
13	AD	329	
14	AE	1407	
15	AF	91	
16	C	75	
17	D	1542	
18	E	87	
19	F	71	
20	G	241	
21	H	557	
22	I	233	
23	J	206	
24	K	167	
25	L	135	
26	M	179	

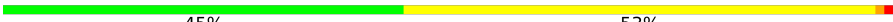
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Mol	Chain	Length	Quality of chain
27	N	130	
28	O	130	
29	P	103	
30	Q	129	
31	R	124	
32	S	101	
33	T	89	
34	U	82	
35	V	84	
36	W	92	
37	X	118	
38	Y	142	
39	Z	121	
40	a	2904	
41	b	85	
42	c	78	
43	d	120	
44	e	63	
45	f	59	
46	g	70	
47	h	273	
48	i	57	
49	j	209	
50	k	55	
51	l	201	

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Mol	Chain	Length	Quality of chain
52	m	46	 59% 41%
53	n	179	 45% 53% ...
54	o	65	 58% 35% 5% .
55	p	177	 67% 32% .
56	q	38	 61% 39%
57	r	149	 68% 32%
58	s	142	 55% 44% ..
59	t	123	 46% 54% .
60	u	144	 62% 37% .
61	v	136	 49% 49% .
62	w	127	 44% 46% . 6%
63	x	117	 63% 36% .
64	y	115	 63% 36% .
65	z	118	 58% 41% ..

2 Entry composition

There are 67 unique types of molecules in this entry. The entry contains 276038 atoms, of which 98638 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 Ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	0	103	Total	C	H	N	O	S	0	0
			1655	516	839	153	145	2		

- Molecule 2 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1	110	Total	C	H	N	O	S	0	0
			1779	532	922	166	156	3		

- Molecule 3 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	2	94	Total	C	H	N	O	S	0	0
			1557	470	811	140	134	2		

- Molecule 4 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	3	103	Total	C	H	N	O		0	0
			1632	498	844	148	142			

- Molecule 5 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	4	94	Total	C	H	N	O	S	0	0
			1533	479	780	137	134	3		

- Molecule 6 is a DNA chain called NT DNA ops.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	5	35	Total	C	N	O	P		0	0
			726	342	141	208	35			

- Molecule 7 is a DNA chain called T DNA ops.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	35	Total	C	N	O	P	0	0
			703	336	117	215	35		

- Molecule 8 is a RNA chain called mRNA with 27 nt long spacer.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	37	Total	C	N	O	P	0	0
			772	345	110	280	37		

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	148	Total	C	N	O	S	0	0
			1117	705	196	209	7		

- Molecule 10 is a RNA chain called E-site and P-site fMet-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	A	76	Total 2446	C 723	H 826	N 295	O 527	P 75	0	0
10	B	76	Total 2433	C 723	H 813	N 295	O 527	P 75	0	0

- Molecule 11 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AA	1316	Total	C	N	O	S	0	0
			10381	6514	1810	2014	43		

- Molecule 12 is a protein called Transcription antitermination protein RfaH.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AB	161	Total	C	N	O	S	0	0
			1286	828	222	232	4		

- Molecule 13 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AC	221	Total	C	N	O	S	0	0
			1698	1060	299	333	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	AD	218	Total	C	N	O	S	0	0
			1677	1048	297	326	6		

- Molecule 14 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AE	1337	Total	C	N	O	S	0	0
			10404	6535	1856	1963	50		

- Molecule 15 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AF	82	Total	C	N	O	S	0	0
			650	396	122	131	1		

- Molecule 16 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	C	66	Total	C	H	N	O	S	
			1103	344	559	102	97	1	0

- Molecule 17 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	D	1524	Total	C	H	N	O	P	
			49126	14585	16423	6003	10591	1524	0

- Molecule 18 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	E	86	Total	C	H	N	O	S	
			1388	414	719	138	114	3	0

- Molecule 19 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	F	70	Total	C	H	N	O	S	
			1218	366	629	125	97	1	0

- Molecule 20 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	G	225	Total	C	H	N	O	S	0	0
			3545	1113	1785	316	323	8		

- Molecule 21 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	H	259	Total	C	H	N	O	S	0	0
			3184	1073	1454	305	349	3		

- Molecule 22 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	I	208	Total	C	H	N	O	S	0	0
			3346	1036	1710	307	290	3		

- Molecule 23 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	J	205	Total	C	H	N	O	S	0	0
			3350	1026	1707	315	298	4		

- Molecule 24 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	K	156	Total	C	H	N	O	S	0	0
			2348	717	1196	217	212	6		

- Molecule 25 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	L	104	Total	C	H	N	O	S	0	0
			1694	536	846	153	152	7		

- Molecule 26 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	M	151	Total	C	H	N	O	S	0	0
			2416	735	1235	227	215	4		

- Molecule 27 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	N	129	Total	C	H	N	O	S	0	0
			2010	616	1031	173	184	6		

- Molecule 28 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	O	127	Total	C	H	N	O	S	0	0
			2092	634	1070	206	179	3		

- Molecule 29 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	P	99	Total	C	H	N	O	S	0	0
			1621	495	831	151	143	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
30	Q	117	Total	C	H	N	O	S	0	0
			1764	540	887	174	160	3		

- Molecule 31 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	R	121	Total	C	H	N	O	S	0	0
			1940	580	1001	194	161	4		

- Molecule 32 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	S	100	Total	C	H	N	O	S	0	0
			1649	499	844	164	139	3		

- Molecule 33 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	T	88	Total	C	H	N	O	S	0	0
			1448	439	734	144	130	1		

- Molecule 34 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	U	82	Total	C	H	N	O	S	0	0
			1315	406	666	128	114	1		

- Molecule 35 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	V	80	Total	C	H	N	O	S	0	0
			1339	411	691	121	113	3		

- Molecule 36 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	W	83	Total	C	H	N	O	S	0	0
			1351	424	688	126	111	2		

- Molecule 37 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	X	116	Total	C	H	N	O	S	0	0
			1864	558	964	181	158	3		

- Molecule 38 is a protein called 50S ribosomal protein L11.

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

- Molecule 39 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Z	30	Total	C	N	O	S	0	0
			227	144	33	47	3		

- Molecule 40 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	a	2880	Total	C	H	N	O	P	0	0
			92918	27587	31077	11398	19976	2880		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	887	A	U	conflict	GB 937521852

- Molecule 41 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	b	76	Total	C	H	N	O	S	0	0
			1181	360	599	117	104	1		

- Molecule 42 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	c	77	Total	C	H	N	O	S	0	0
			1277	388	652	129	106	2		

- Molecule 43 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	d	120	Total	C	H	N	O	P	0	0
			3870	1144	1301	468	837	120		

- Molecule 44 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	e	62	Total	C	H	N	O	S	0	0
			1032	308	531	98	94	1		

- Molecule 45 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	f	58	Total	C	H	N	O	S	0	0
			936	281	488	87	78	2		

- Molecule 46 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	g	66	Total	C	H	N	O	S	0	0
			1042	323	520	99	94	6		

- Molecule 47 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	h	271	Total	C	H	N	O	S	0	0
			4236	1288	2154	423	364	7		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	i	56	Total	C	H	N	O	S	0	0
			903	269	459	94	80	1		

- Molecule 49 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	j	209	Total	C	H	N	O	S	0	0
			3182	979	1617	288	294	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
50	k	52	Total	C	H	N	O		0	0
			890	275	464	78	73			

- Molecule 51 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	l	201	Total	C	H	N	O	S	0	0
			3171	974	1619	283	290	5		

- Molecule 52 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	m	46	Total	C	H	N	O	S	0	0
			795	228	418	90	57	2		

- Molecule 53 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	n	177	Total	C	H	N	O	S	0	0
			2853	899	1443	249	256	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
54	o	64	Total	C	H	N	O	S	0	0
			1076	323	572	105	74	2		

- Molecule 55 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	p	175	Total	C	H	N	O	S	0	0
			2671	826	1358	241	244	2		

- Molecule 56 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	q	38	Total	C	H	N	O	S	0	0
			645	185	343	65	48	4		

- Molecule 57 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	r	149	Total	C	H	N	O	S	0	0
			2259	699	1148	197	214	1		

- Molecule 58 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	s	142	Total	C	H	N	O	S	0	0
			2291	714	1162	212	199	4		

- Molecule 59 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	t	123	Total	C	H	N	O	S	0	0
			1969	593	1023	181	166	6		

- Molecule 60 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	u	144	Total	C	H	N	O	S	0	0
			2182	654	1129	207	190	2		

- Molecule 61 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	v	136	Total	C	H	N	O	S	0	0
			2231	686	1157	205	177	6		

- Molecule 62 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	w	119	Total	C	H	N	O	S	0	0
			1945	588	994	195	163	5		

- Molecule 63 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	x	116	Total	C	H	N	O		0	0
			1815	552	923	178	162			

- Molecule 64 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	y	114	Total	C	H	N	O	S	0	0
			1879	574	962	179	163	1		

- Molecule 65 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	z	117	Total	C	H	N	O		0	0
			1967	604	1020	192	151			

- Molecule 66 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
66	AE	1	Total	Mg	0
			1	1	

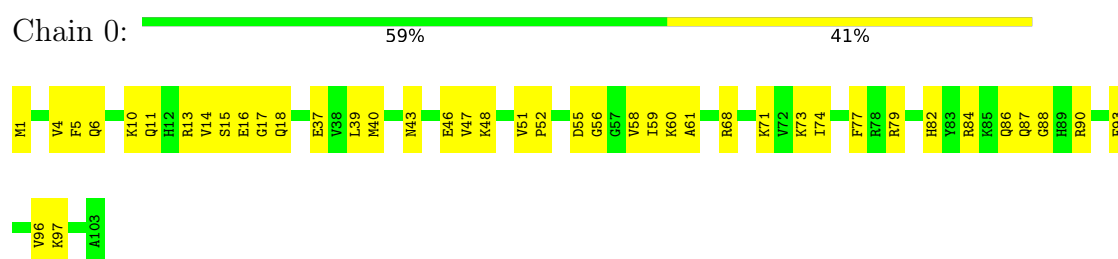
- Molecule 67 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
67	AE	2	Total	Zn	0
			2	2	

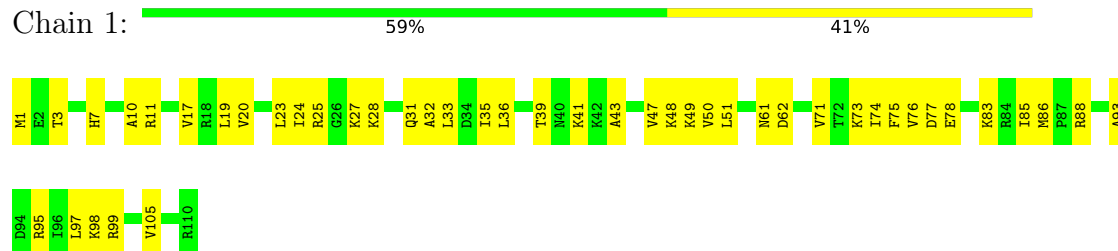
3 Residue-property plots

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.

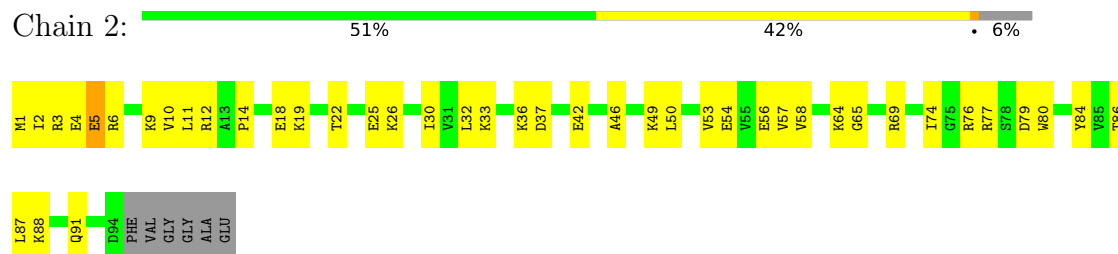
• Molecule 1: Ribosomal protein L21



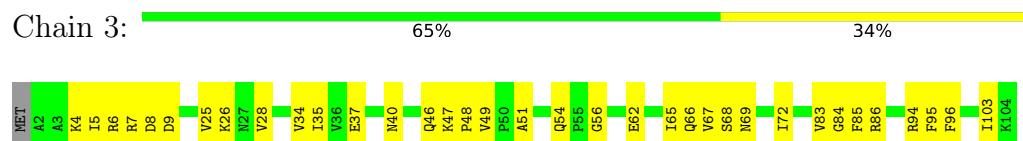
• Molecule 2: 50S ribosomal protein L22



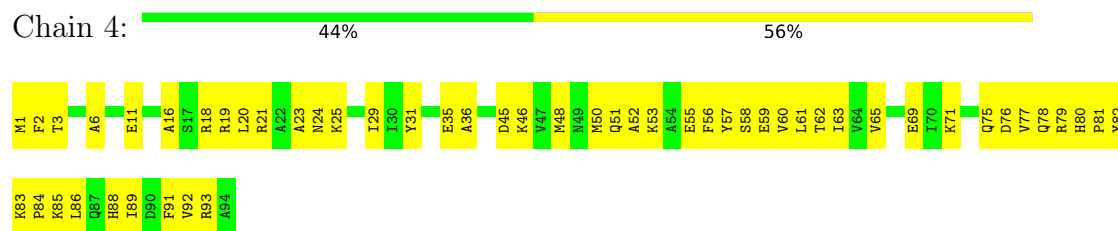
• Molecule 3: 50S ribosomal protein L23



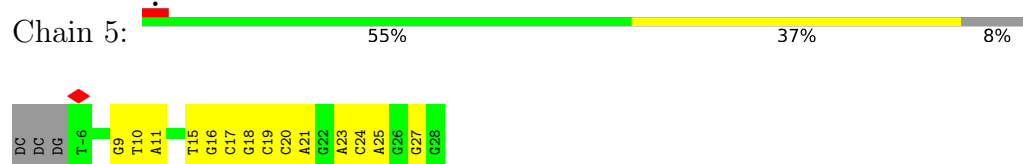
• Molecule 4: 50S ribosomal protein L24



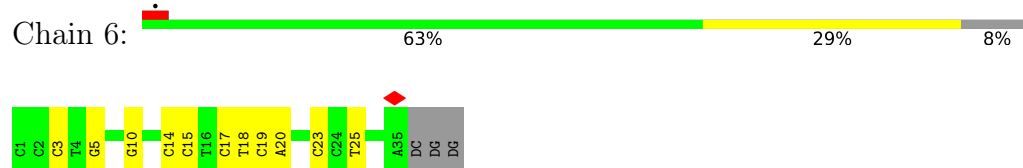
- Molecule 5: 50S ribosomal protein L25



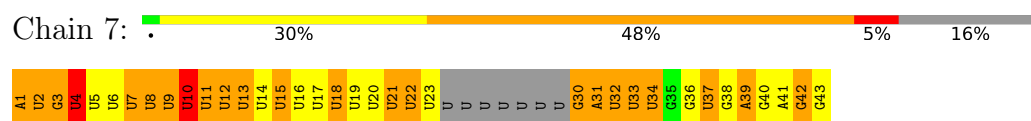
- Molecule 6: NT DNA ops



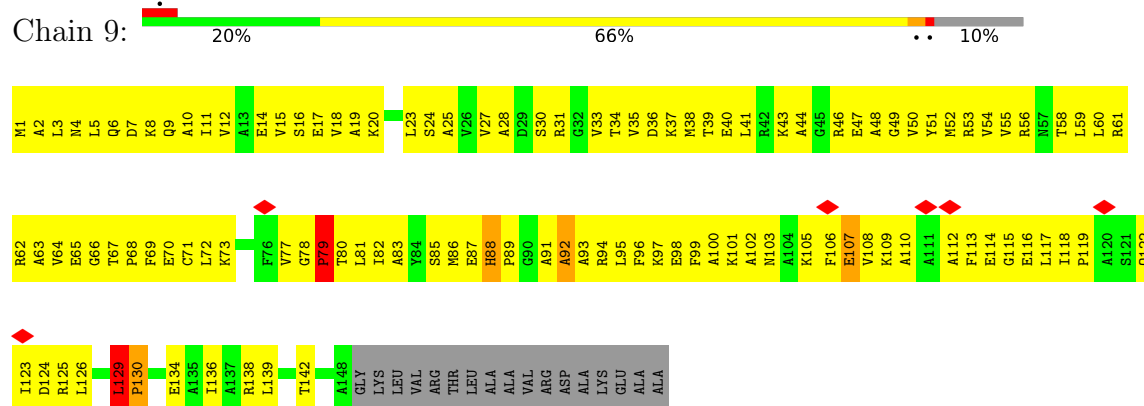
- Molecule 7: T DNA ops



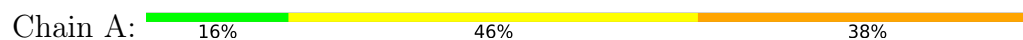
- Molecule 8: mRNA with 27 nt long spacer



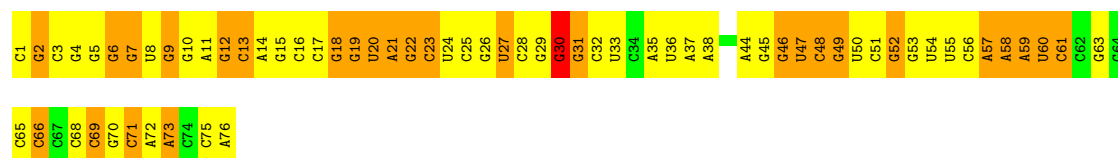
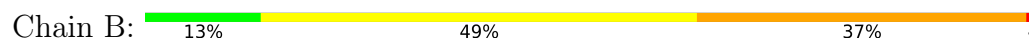
- Molecule 9: 50S ribosomal protein L10



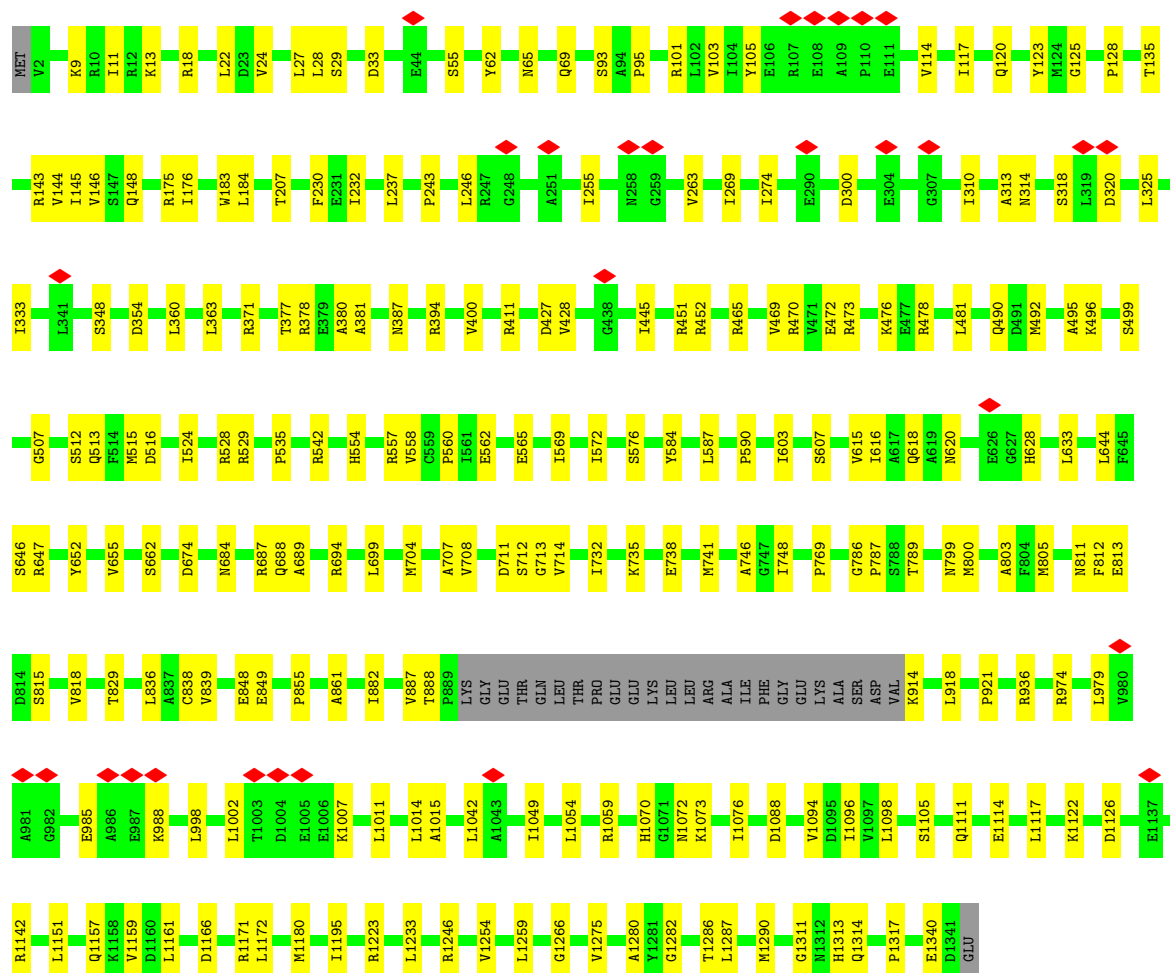
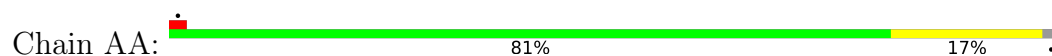
- Molecule 10: E-site and P-site fMet-tRNA



- Molecule 10: E-site and P-site fMet-tRNA



- Molecule 11: DNA-directed RNA polymerase subunit beta



- Molecule 12: Transcription antitermination protein RfaH

G135	A71	MET
L141	T72	Q2
L142	R73	S3
L143	G74	W4
L144	W75	Y5
L145	S76	L6
L146	H77	L7
M147	F78	Y8
K148	R79	C9
L149	G80	K10
L150	F81	
H151	G82	R16
H152	P85	A17
S153		Q18
V154	V88	E19
K155	P89	H20
N156	S90	L21
L157	A91	E22
O158	V92	R23
F159	H93	Q24
R160	H94	A25
K161	O95	V26
L162	L96	N27
		Z28
	Y99	L29
	K100	A30
	P101	P31
	K102	N32
	D103	T33
	V104	T34
	V105	L35
	D106	E36
		K37
		T38
	T109	
	P110	K42
	Y111	R43
	G113	
	D114	S47
	K115	
	V116	L50
	I117	F51
	I118	P52
	T119	N53
	E120	Y54
	G121	L55
	A122	F56
	F123	V57
	E124	E58
	G125	F59
	F126	D60
	O127	P61
	A128	E62
	I129	
	F130	H65
	T131	T66
	E132	T68
	P133	T69
	L134	H70

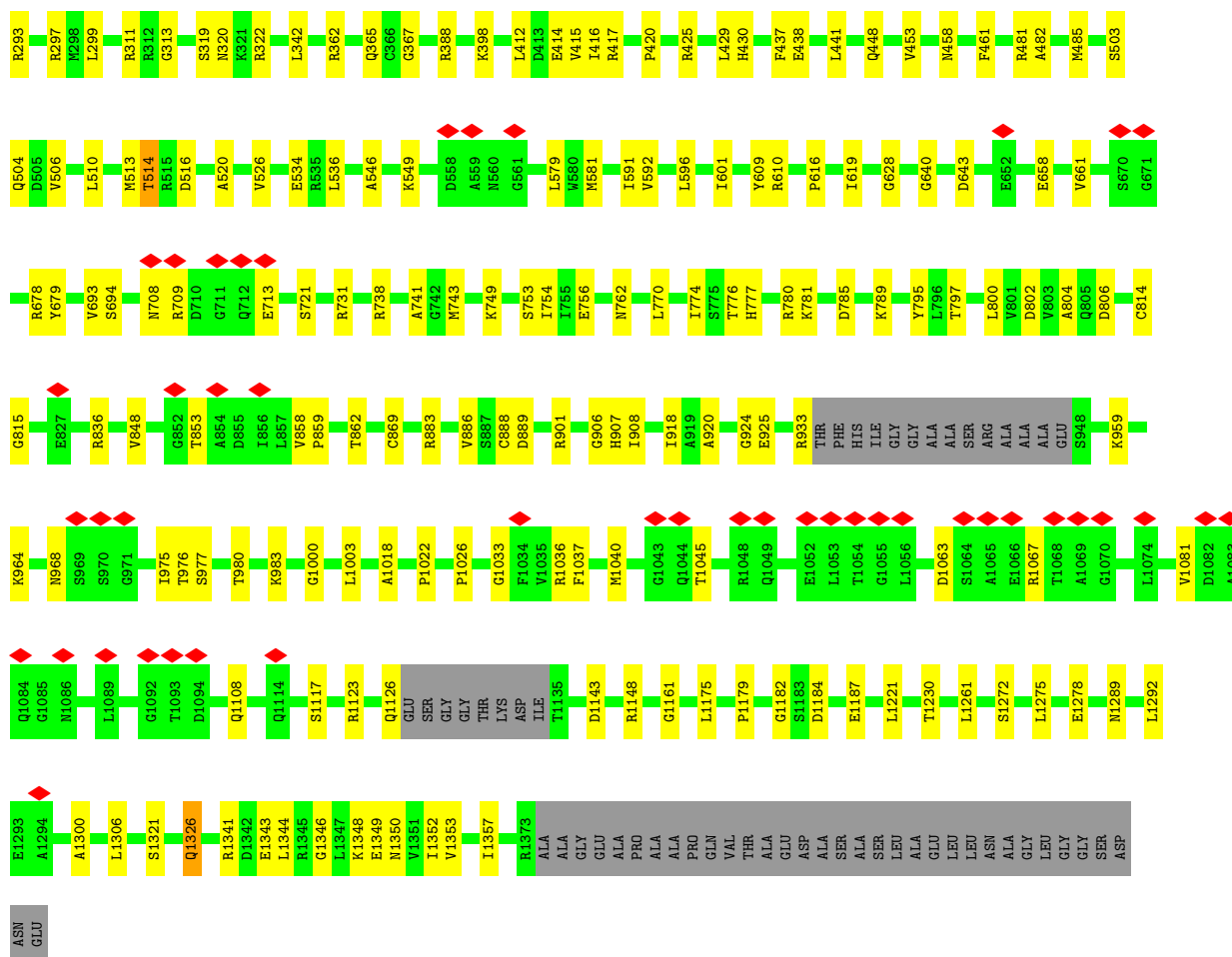
Chain AC:

Amino Acid	Frequency (%)
MET	Low
GLN	Low
GLY	Low
SER	Low
VAL	Low
THR	Low
E7	High
L28	High
L43	High
R44	High
R45	High
L48	High
T57	High
V64	High
T78	High
L79	High
E80	High
I81	High
L82	High
L100	High
T101	High
L102	High
N103	High
K104	High
V110	High
T115	High
I140	High
S141	High
M142	High
R158	High
ILE	Low
HIS	Low
SER	Low
GLU	Low
GLY	Low
ASP	Low
E165	High
L171	High
R191	High
V192	High
E193	High
Q194	High
L201	High
T217	High
P219	High

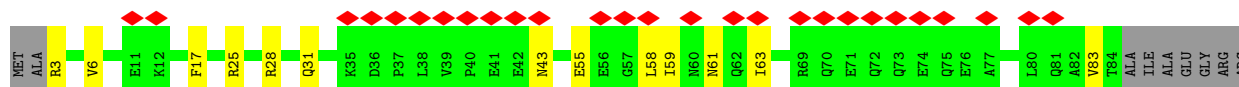
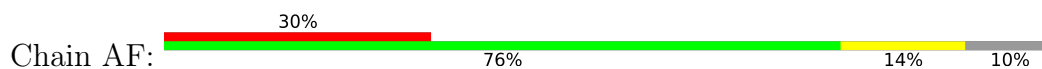
Amino Acid	Frequency (%)
THR	High
PRO	High
ASN	High
LEU	High
LEU	High
GLY	High
LYS	High
LYS	High
SER	High
THR	High
THR	High
ILE	High
LYS	High
ASP	High
VAL	High
LEU	High
LEU	High
ALA	High
SER	High
ARG	High
ARG	High
GLY	High
LEU	High
SER	High
SER	High
LEU	High
LEU	High
GLY	High
MET	High
PRO	High
ARG	High
VAL	High
ASP	High
ASP	High
LEU	High
ASN	High
TRP	High
PRO	High
PRO	High
ALA	High
SER	High
ILE	High
ALA	High
ASP	High
ASP	High
GLY	High

[illegible]

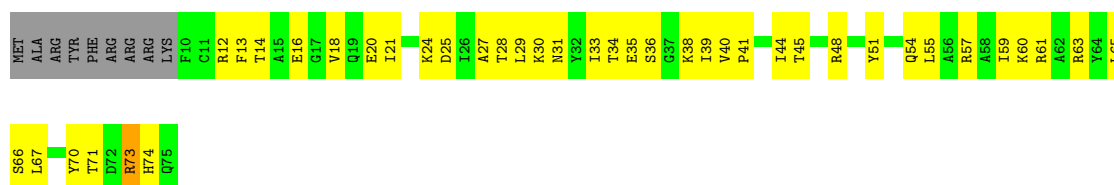
Chain AE:



- Molecule 15: DNA-directed RNA polymerase subunit omega



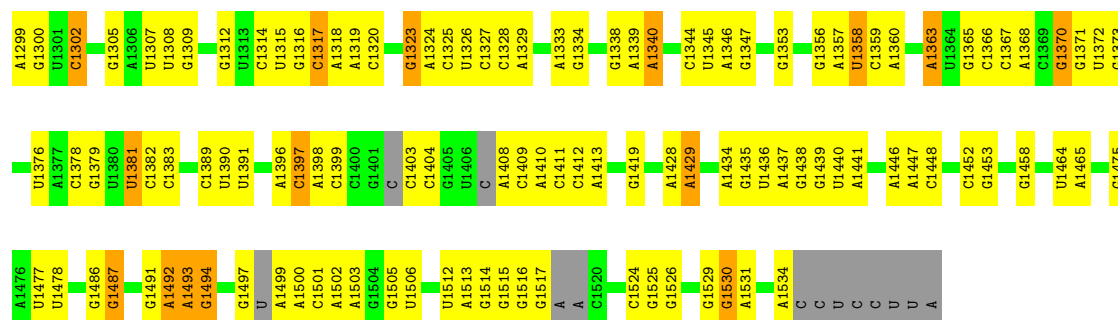
- Molecule 16: 30S ribosomal protein S18



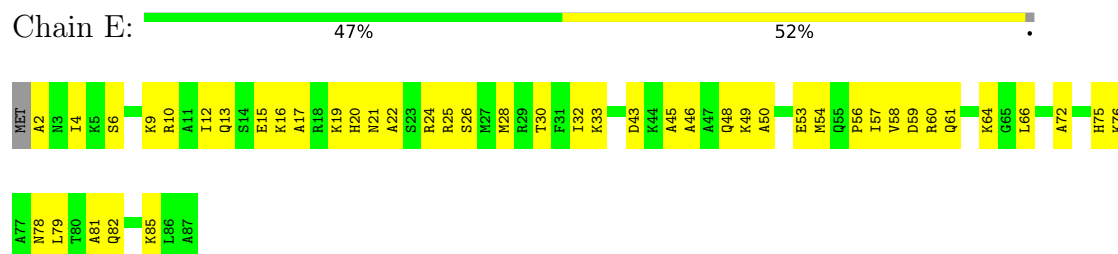
- Molecule 17: 16S rRNA



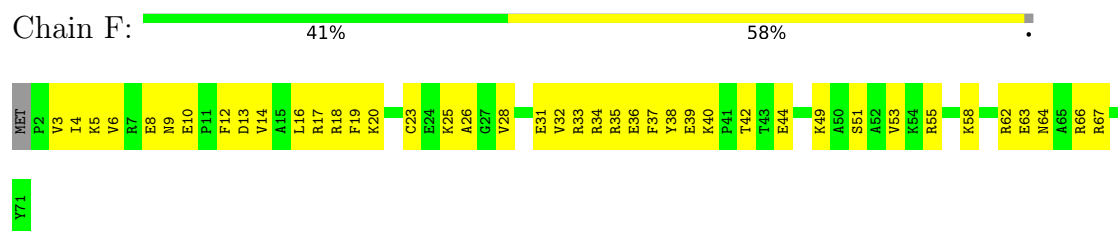
C1208	C1209	C1210	U1211	U1212	A1213	C1214	C1215	C1216	C1217	C1218	A1219	C1223	U1224	A1225	C1226	U1227	C1228	A1229	C1230	C1231	A1238	U1239	U1240	G1241	C1242	U1243	G1244	A1250	A1251	A1252	G1255	A1256	U1257	C1258	U1259	A1261	C1262	A1275	C1276	G1277	G1278	G1279	A1280	A1285	U1286	A1287	A1288	A1289	G1290	G1294	G		
C1132	G1133	U1134	U1135	C1136	C1137	U1138	U1139	C1140	C1141	G1142	U1143	G1144	A1145	A1146	C1147	U1148	C1149	A1150	A1151	A1152	A1157	C1158	U1159	U1160	C1161	A1167	U1168	A1169	A1170	A1171	C1172	U1173	U1174	G1175	A1176	C1177	G1181	U1184	G1185	G1186	U1189	C1190	G1193	U1194	C1195	A1196	A1197	U1202	C1203	G1206	G		
G963	A964	U965	C	G	A968	A969	C972	G973	A974	A975	G976	A977	U978	C979	C980	U981	U982	A983	C984	C985	U986	G987	U991	U992	C993	A996	U997	C998	A1004	U1005	G1006	U1007	U1008	U1009	U1017	G1018	A1021	G1024	U1025	G1026	C1027	C1028	U1029	U1030	C1031	G1032	A1035	A1036	C1037				
A1044	C1045	A1046	A1055	A1060	U1061	U1062	C1063	G1064	U1065	C1071	U1072	U1073	G1074	U1075	U1076	U1077	U1078	U1079	A1080	A1081	A1082	U1085	U1086	G1087	G1094	U1095	C1096	A1099	G1100	A1101	A1102	C1103	G1104	A1105	G1106	C1107	G1108	C1109	A1110	C1113	C1114	C1119	C1120	U1121	G1124	U1125	U1126	G1127	C1128				
G963	A964	U965	C	G	A968	A969	C972	G973	A974	A975	G976	A977	U978	C979	C980	U981	U982	A983	C984	C985	U986	G987	U991	U992	C993	A996	U997	C998	A1004	U1005	G1006	U1007	U1008	U1009	U1017	G1018	A1021	G1024	U1025	G1026	C1027	C1028	U1029	U1030	C1031	G1032	A1035	A1036	C1037				
A878	C882	C883	U884	C887	U890	U891	U892	C893	G894	G902	A906	A907	A908	U909	U911	C912	A913	A914	A915	G916	U917	A918	U919	U920	U921	U922	A923	G925	G926	G927	U928	G929	C932	C933	A935	C936	A937	G945	A946	G947	G951	U952	G953	A958	U959	U960							
U692	A695	A696	U697	G700	U701	A704	C623	C624	U625	G543	C549	G550	U551	U552	A553	A554	U555	C556	A559	U562	A563	C564	G567	C568	U569	G570	A571	A572	A573	C574	G575	G577	C578	A579	C580	G581	C582	A583	G588	A596	U598	C599	U602	U603	G604	U605	A607						
U610	C611	G612	C613	U619	C620	A621	A622	C624	U625	G626	G627	G628	G633	C634	A635	U636	C637	A642	C643	U644	A649	G650	C651	U652	A653	A654	U657	U662	A663	G664	A665	G671	U672	A673	G674	A675	U677	U678	C679	A681	G682	U684	C685	U686	G687	G688	C689	U690	G691				
A777	A790	C791	U792	U793	U794	C795	C796	C797	C808	G809	G812	A815	A816	C817	U820	U821	C822	A823	G824	A825	U827	A828	U829	U832	G836	C841	U842	U843	A844	A845	C846	G849	A860	G861	A864	A865	C868	C869	A872	U873	G874	U875	C876	G877									
A371	C372	A373	A374	U375	G376	G377	C378	C379	C381	A382	A383	C384	A389	C392	A393	G394	A397	U398	C399	C400	C422	G423	G424	U427	G428	U429	A430	A431	A441	G442	G443	G444	U451	U452	C511	U512	G515	U517	C518	C519	A520	G521	C522	A523	G524	C525	C526	C527	U438	U439	C440	A441	
C277	G278	A279	C280	G281	U283	C285	G289	G299	A300	A306	C307	G308	A309	G310	C311	C316	U317	A320	A321	U323	C235	G236	A237	C328	U245	A246	G247	A250	G251	U252	A253	G254	G255	U256	G257	G258	G347	C352	A353	C354	C355	A356	G357	G360	G361	U367							
A182	C183	G184	C193	C194	U195	A196	A197	G198	G204	U208	U209	C210	G211	G108	G212	U216	C217	U218	U219	U114	G220	C221	G226	A119	A120	G39	C43	C47	C48	U49	A50	A51	C52	A53	C54	U55	U56	G57	C58	G61	U62	C63	G68	G69	U70	A71	A72	C73	A74	G75	G76	A77	G82



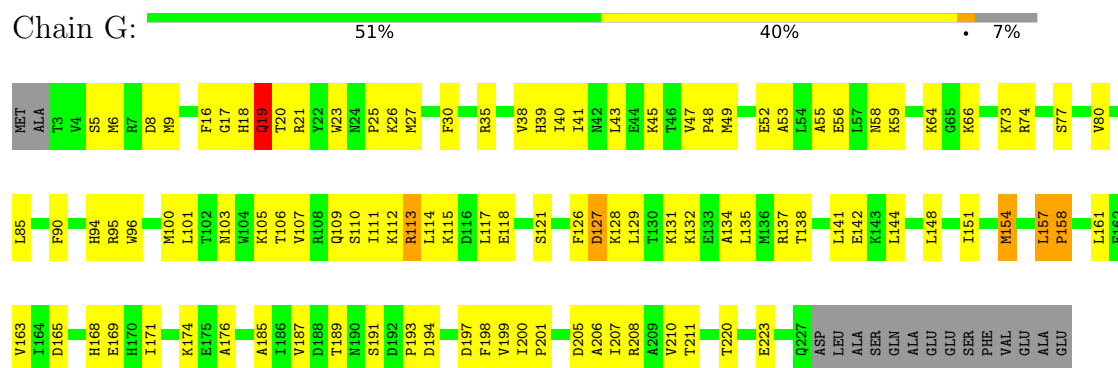
• Molecule 18: 30S ribosomal protein S20



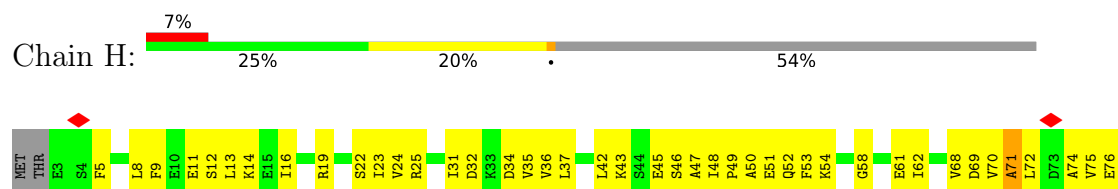
• Molecule 19: 30S ribosomal protein S21

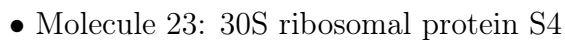
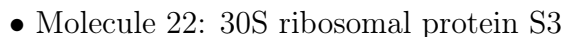


• Molecule 20: 30S ribosomal protein S2

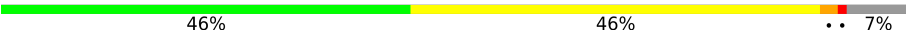


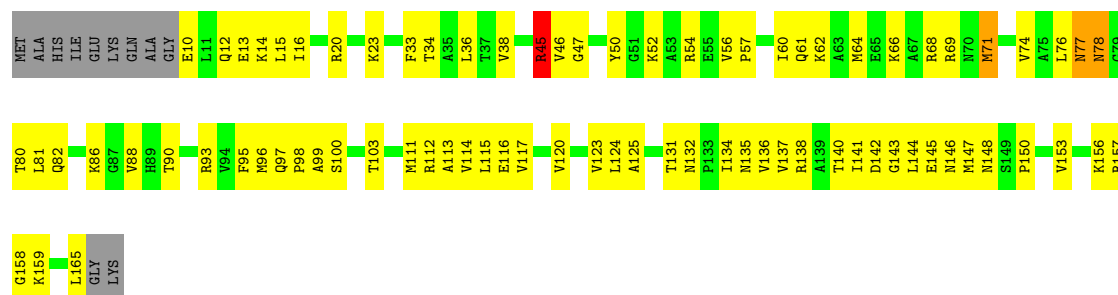
• Molecule 21: 30S ribosomal protein S1



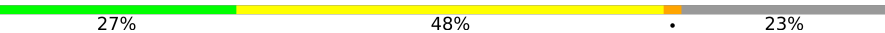


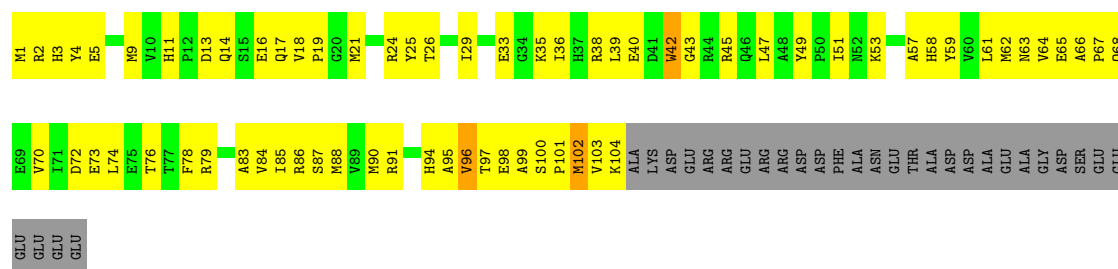
- Molecule 24: 30S ribosomal protein S5

Chain K:  46% 46% .. 7%



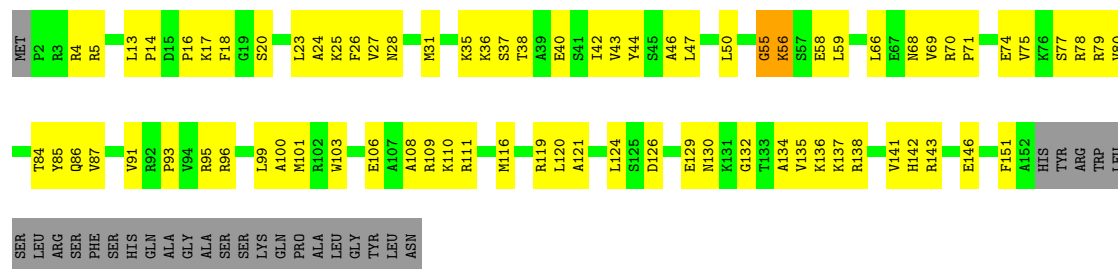
- Molecule 25: 30S ribosomal protein S6

Chain L:  27% 48% • 23%



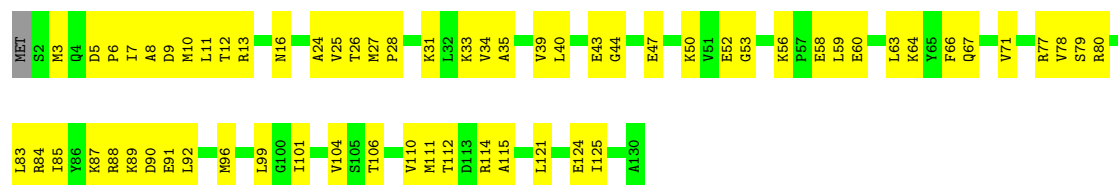
- Molecule 26: 30S ribosomal protein S7

Chain M:  41% 42% • 16%



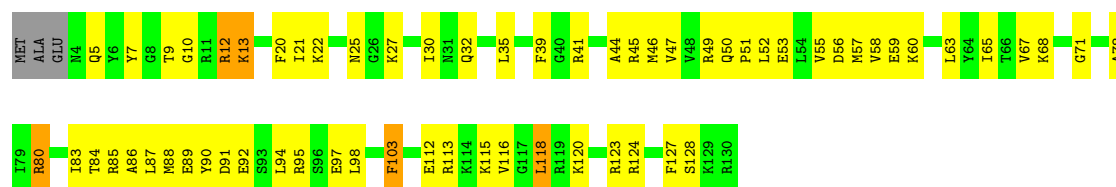
- Molecule 27: 30S ribosomal protein S8

Chain N:  51% 48% •



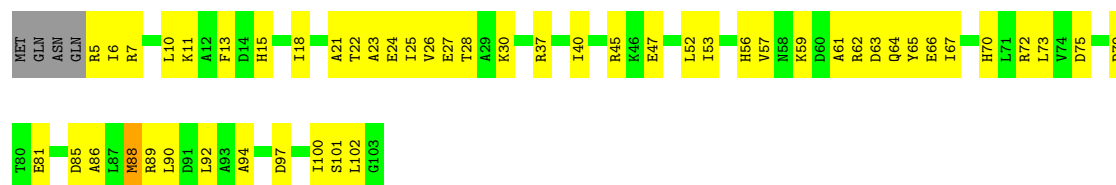
- Molecule 28: 30S ribosomal protein S9

Chain O: 

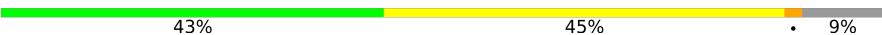


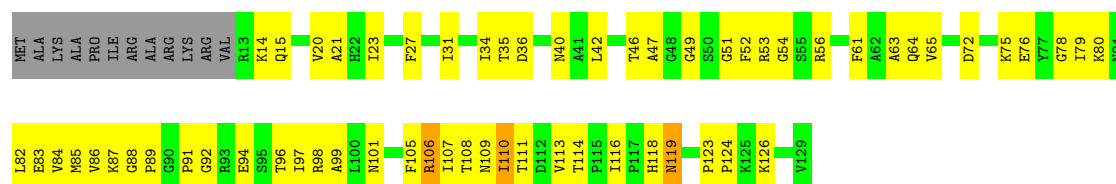
- Molecule 29: 30S ribosomal protein S10

Chain P: 



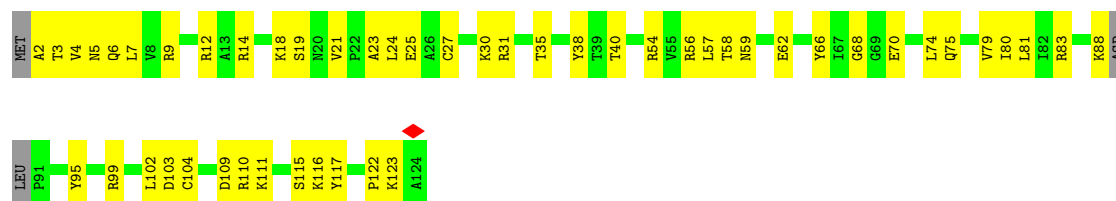
- Molecule 30: 30S ribosomal protein S11

Chain Q: 



- Molecule 31: 30S ribosomal protein S12

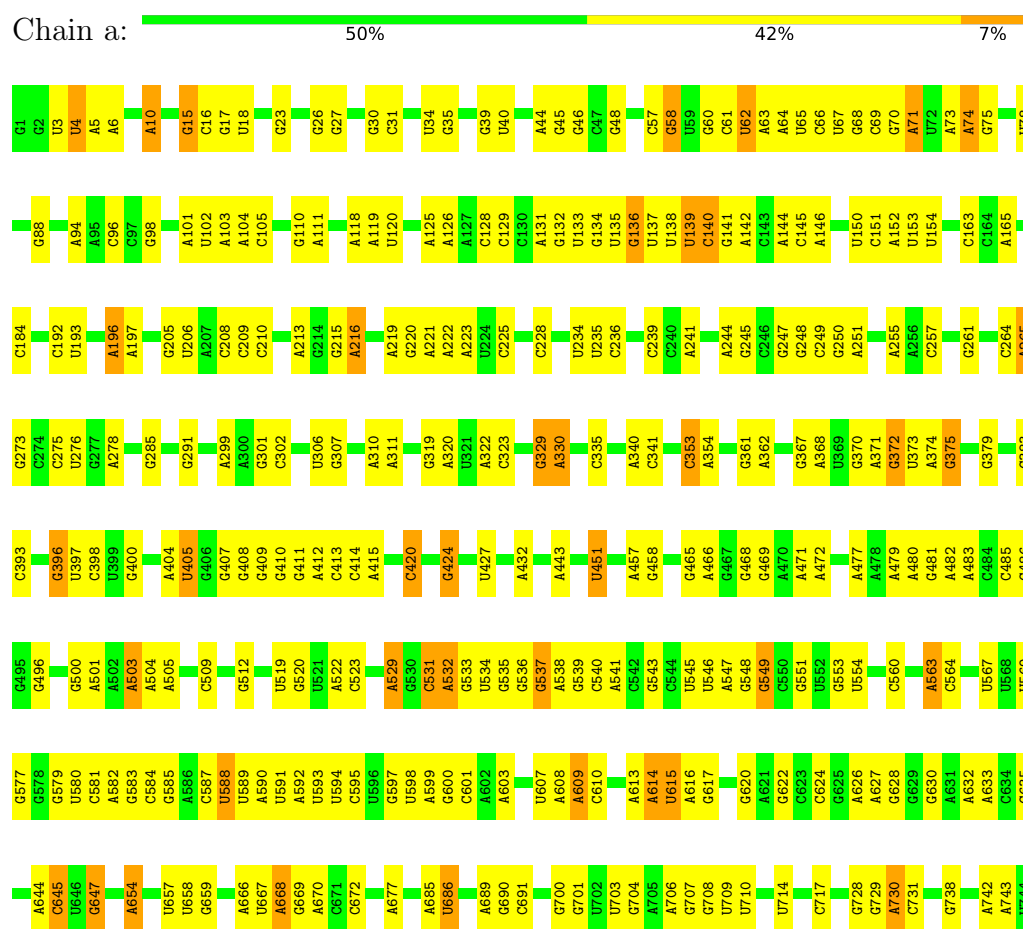
Chain R: 



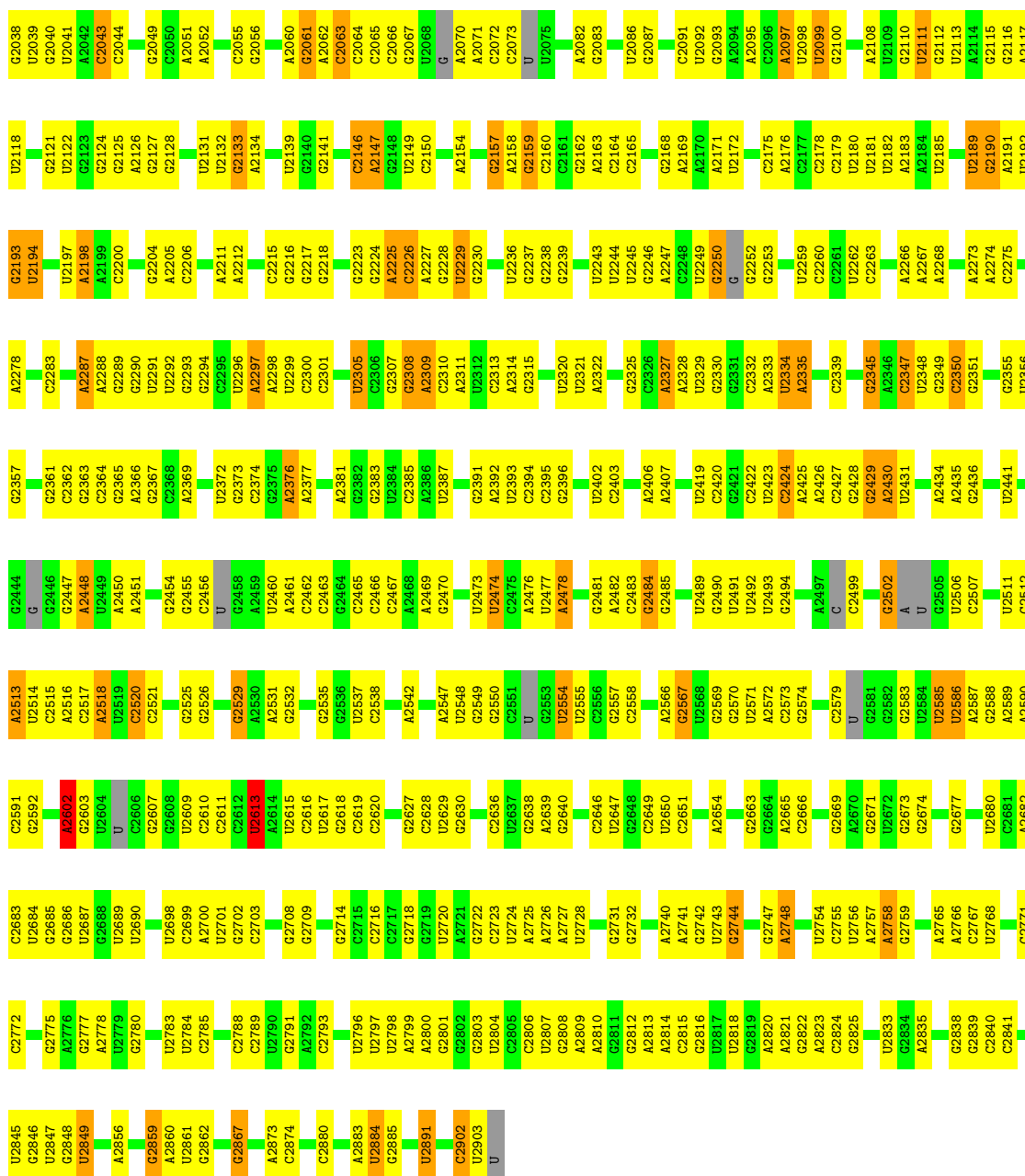
- Molecule 32: 30S ribosomal protein S14

Chain S: 





U1963	C1881	A1808	C1708	C1800	G1410	G1333	G1238	A1144	C1072	A1000	C922	A845	A750
G1964	U1862	G1811	U1709	G1801	U1411	G1334	G1243	C1145	A1073	A1001	G923	U846	A751
C1965	U1883		G1710	U1602	A1412	U1340	C1243	A1146	C1074	C1005	A927	C851	A752
C1967	A1885	G1814	U1714	U1603	A1413	G1341	C1246	C1147	C1075	C1006	A928	U852	A753
A1970	A1889	C1815	G1715	U1607	U1414	G1342	A1247	C1153	C1076	C1007	U929	C856	U754
U1971	A1890	C1816	U1720	A1608	U1415	G1343	A1248	G1154	C1077	A1008	G330	U857	U755
G1972	A1890	G1817	G1721	A1609	U1416	U1344	U1249		U1078	A1009	U931	C858	A756
G1980	A1900	A1819	G1729	U1610	U1417	U1345	G1250	G1160	C1079			G859	G757
U1981	G1906	U1820	U1729	G1613	U1418	G1346	G1251	G1161	A1080	U1012	G938	U860	A760
U1982	G1907	G1730	U1730	A1614	A1420	G1347	G1252	G1162	U1081	C1013	G939	U861	A761
G1983		C1732	G1731	C1617	G1421	C1348	A1253	C1167	U1082	A1014	G940	C862	A764
A1987	G1910		G1738	A	G1422	C1350	G1256	G1168	A1083	U1019	A941		C765
U1991	U		G1738	G1619	A1427	U1351	C1257	G1169	A1085	A1020	A945	G869	U773
G1992	A1912		A1746	G1622	G1428	U1352	A1262	C1170	A1086	A1021	A946	U870	U774
U1993	C1914		U1747	G1622	G1429	A1353	G1266	G1171	G1087	U1022	A947	U871	G775
C1996	U		G1750	U1647	G1430	A1354		C1172	A1088	U1023	C948	U872	G776
C1997	A1916		G1750	U1648	A1431	G1355		U1173	A1089	G1024		C873	
A1998	A1918		G1753	U1649	A1432	G1356		U1174	A1090	G1025	G952	C874	G780
C1999	A1919		A1754	U1651	A1433	G1360		A1175	A1095	G1026	G953	A781	A782
C2000	A1920		G1755	U1652	A1434	G1361		G1176	A1096	A1027	U	A878	A783
C2001	G		G1756	U1653	G1435	C1362		C1177	U1101	A1028	C957	G879	G784
G2002	U		G1756	U1654	G1441	A1365		G1178	C1102	A1029	U958	G880	G785
C2006	A1922		G1758	U1655	U1442	A1366		U1180	A1103	U1033	A959	C881	G786
U2007	U		U1758	U1656	U1443	A1367		U1181	G1106	G1036	A960	U884	C787
C2008	C1924		C1764	U1657	G1444	A1368		U1183	G1107	G1037	C961	C885	C788
A2009	U1941		G1764	U1658	G1445	G1369		G1186	U1108	G1038	G962	C886	A789
G2010	U1942		G1770	U1659	G1452	C1370		G1187	C1109	A1039	U963	C888	A800
U2011	U1943		G1773	U1660	G1453	G1371		U1188	G1110	A1040	C965	C889	A800
A2012	U1931		U1778	U1661	C1454	A1378		U1189	A1111	G1041	G966	G891	G805
A2014	G1932		U1779	U1662	U1460	G1379		G1190	U1112	C1042	U967	A892	C806
A2015	A1936		A1783	U1663	U1467	A1380		C1196	U1113	C1043	C968	C893	U807
U2016	A1937		A1784	U1664	A1468	A1383		G1197	G1114	C1044	G969	U894	U811
U2017	U		A1785	U1665	A1469	A1384		U1198	U1119	A1046	U970	A895	C812
C2020	U		A1786	U1666	A1470	A1385		U1199	G1120	G1047	A973	A896	U813
U2021	U1940		G1789	U1667	U1477	C1386		C1200	G1121	C1049	A974	C897	U814
U2022	U1944		C1790	U1668	G1482	A1387		U1201	G1122	A975	A975	A898	C815
G2023	G1945		A1791	U1669	A1482	A1392		A1204	G1125	C1053	A890	A900	A819
C2024	U1946		G1792	U1670	A1490	A1393		G1205	G1128	G1054	A983	C901	A826
U2025	C1947		U1963	U1671	A1494	U1394		G1206	U1131	G1055	A984	G904	U827
U2026	U1947		G1793	U1672	A1495	U1395		U1209	G1132	U1058	C985	G907	U828
G2027	A1953		A1794	U1673	A1496	U1396		G1212	U1133	G1059	C986	C908	A829
U2028	U1954		C1795	U1674	U1497	C1397		A1213	A1133	U1060	C987	A909	U832
G2029	A		U1796	U1675	C1498	U1400		A1214	A1134	U1061	A990	A910	U833
A2031	U1955		G1797	U1676	U1499	A1403		G1223	G1135	C1064	G993	A911	A834
G2032	C1957		U1798	U1677	G1500	U1404		U1224	G1137	U1065	G994	U912	C837
A2033	U1958		G1800	U1678	G1503	U1405		G1225	G1138	U1066	C995	C915	G914
U2034	G1959		A1801	U1679	A1506	U1406		A1226	G1139	A1067	C996	C916	U839
C2035	A1960		A1802	U1680	U1507	U1407		G1236	G1140	G1068	G997	U917	C840
U2036	C		A1803	U1681	U1508	G1408		A1237	U1141	A1069	C998	A920	G841
A2037				U1682		U1409			A1142	A1070	U999	C921	U842



• Molecule 41: 50S ribosomal protein L27

Chain b: 59% 31% 11%



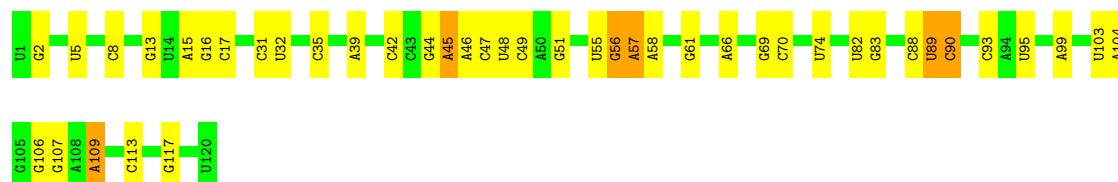
• Molecule 42: 50S ribosomal protein L28

Chain c: 67% 32% 1%

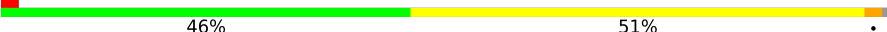


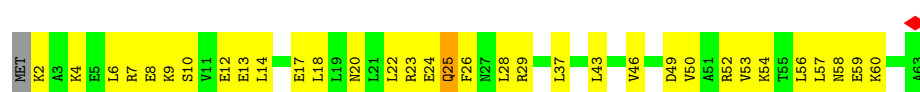
- Molecule 43: 5S rRNA

Chain d: 



- Molecule 44: 50S ribosomal protein L29

Chain e: 

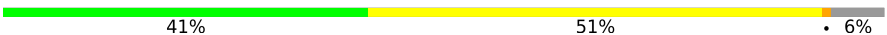


- Molecule 45: 50S ribosomal protein L30

Chain f: 



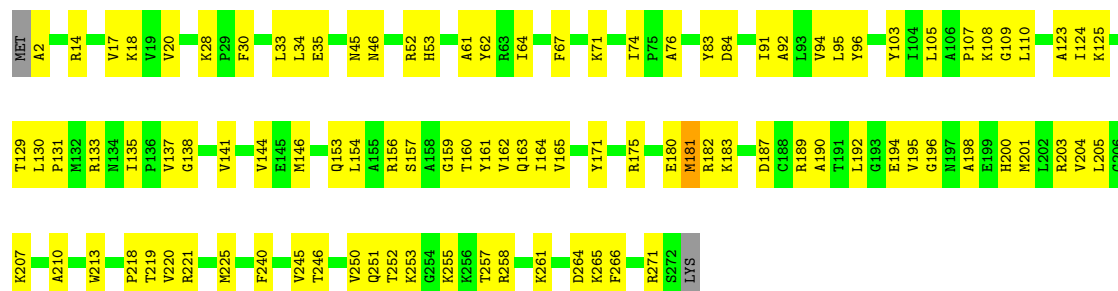
- Molecule 46: 50S ribosomal protein L31

Chain g: 



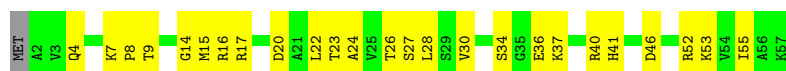
- Molecule 47: 50S ribosomal protein L2

Chain h: 



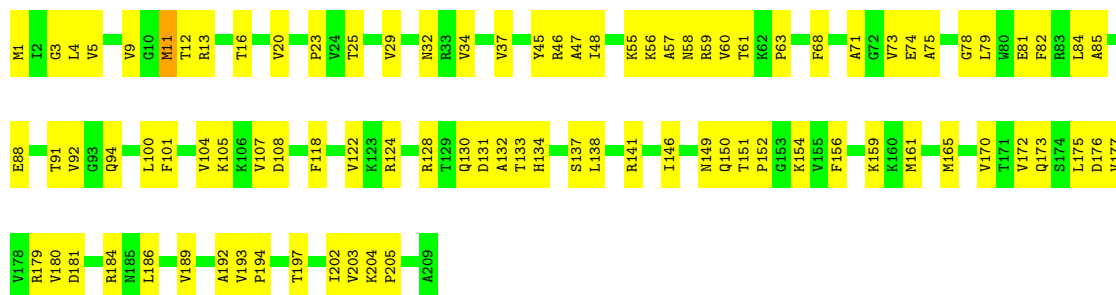
- Molecule 48: 50S ribosomal protein L32

Chain i: 



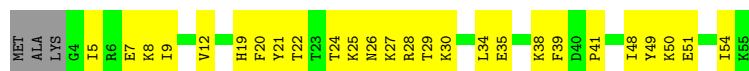
• Molecule 49: 50S ribosomal protein L3

Chain j: 56% 43%



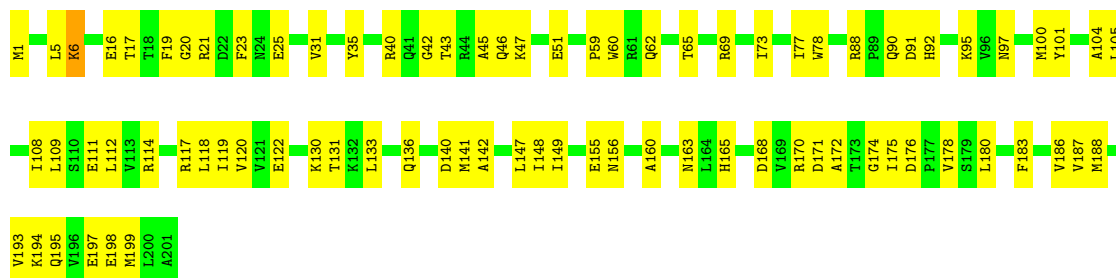
• Molecule 50: 50S ribosomal protein L33

Chain k: 47% 47% 5%



• Molecule 51: 50S ribosomal protein L4

Chain l: 60% 40%



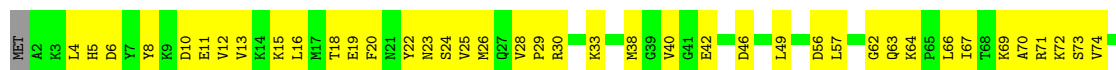
• Molecule 52: 50S ribosomal protein L34

Chain m: 59% 41%



• Molecule 53: 50S ribosomal protein L5

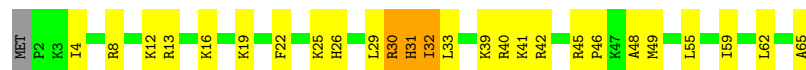
Chain n: 45% 53% ...





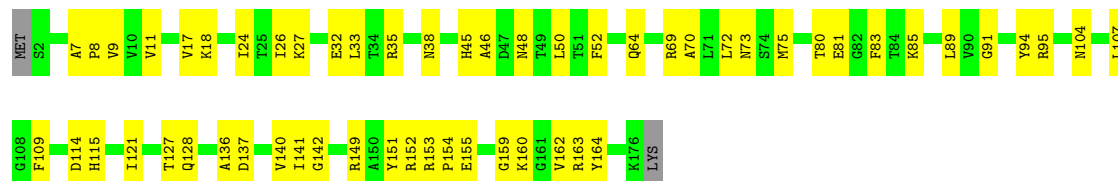
- Molecule 54: 50S ribosomal protein L35

Chain o: 58% 35% 5% .



- Molecule 55: 50S ribosomal protein L6

Chain p: 67% 32% .



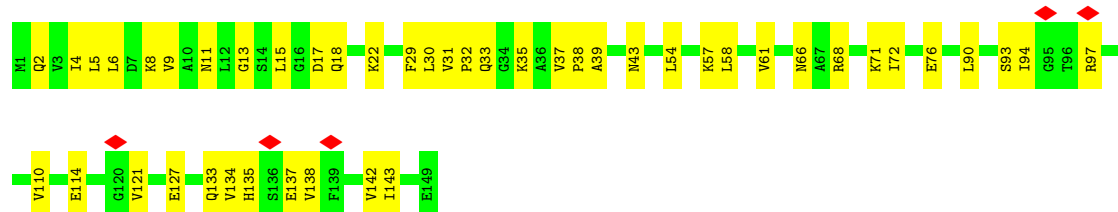
- Molecule 56: 50S ribosomal protein L36

Chain q: 61% 39%



- Molecule 57: 50S ribosomal protein L9

Chain r: 68% 32%



- Molecule 58: 50S ribosomal protein L13

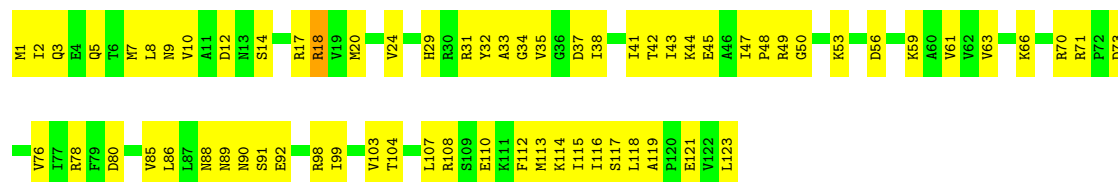
Chain s: 55% 44% .





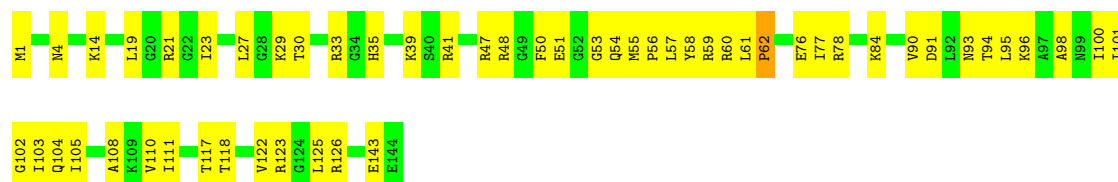
- Molecule 59: 50S ribosomal protein L14

Chain t: 46% 54%



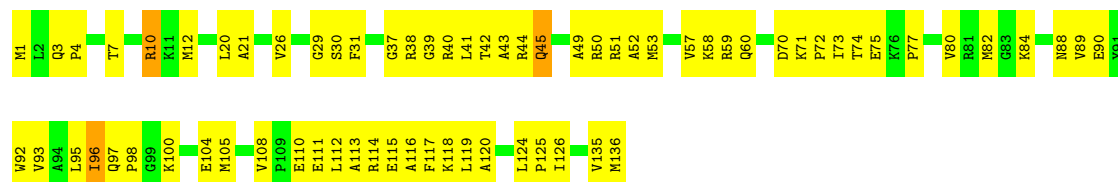
- Molecule 60: 50S ribosomal protein L15

Chain u: 62% 37%



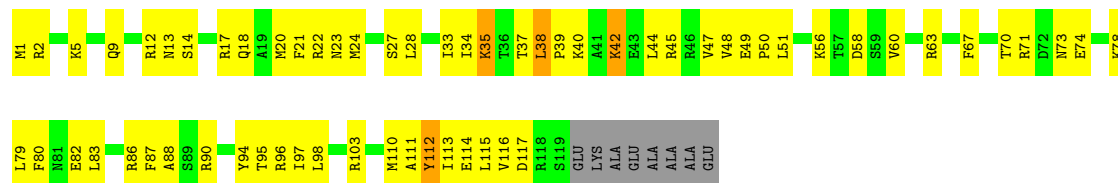
- Molecule 61: 50S ribosomal protein L16

Chain v: 49% 49%



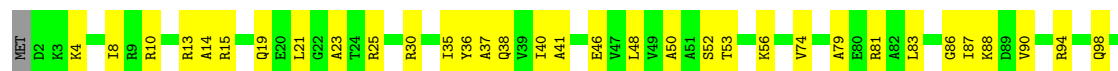
- Molecule 62: 50S ribosomal protein L17

Chain w: 44% 46% 6%



- Molecule 63: 50S ribosomal protein L18

Chain x: 63% 36%





- Molecule 64: 50S ribosomal protein L19

Chain y: 63% 36%



- Molecule 65: 50S ribosomal protein L20

Chain z: 58% 41%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6271	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	1250	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.032	Depositor
Minimum map value	-0.007	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0042	Depositor
Map size (Å)	531.968, 531.968, 531.968	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.039, 1.039, 1.039	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.43	0/829	0.51	0/1107
2	1	0.60	0/864	0.63	0/1156
3	2	0.55	1/752 (0.1%)	0.67	0/1005
4	3	0.35	0/796	0.48	0/1062
5	4	0.57	0/766	0.63	0/1025
6	5	0.56	0/816	0.77	0/1259
7	6	0.56	0/783	0.78	0/1203
8	7	0.56	2/856 (0.2%)	0.88	4/1326 (0.3%)
9	9	0.37	0/1131	0.74	2/1524 (0.1%)
10	A	0.27	0/1810	0.58	0/2821
10	B	0.31	1/1810 (0.1%)	0.63	2/2821 (0.1%)
11	AA	0.38	0/10547	0.62	0/14232
12	AB	0.46	0/1317	1.12	12/1786 (0.7%)
13	AC	0.37	0/1718	0.61	0/2328
13	AD	0.32	0/1696	0.60	0/2298
14	AE	0.38	0/10561	0.64	5/14258 (0.0%)
15	AF	0.29	0/652	0.61	0/879
16	C	0.67	0/553	0.81	1/743 (0.1%)
17	D	0.29	0/36610	0.41	9/57091 (0.0%)
18	E	0.61	0/675	0.72	0/895
19	F	0.53	0/597	0.60	0/792
20	G	0.68	5/1791 (0.3%)	0.79	8/2413 (0.3%)
21	H	0.38	0/1746	0.81	0/2382
22	I	0.57	1/1663 (0.1%)	0.68	4/2241 (0.2%)
23	J	0.46	0/1665	0.58	0/2227
24	K	0.72	2/1165 (0.2%)	0.86	6/1568 (0.4%)
25	L	0.68	1/867 (0.1%)	0.79	1/1171 (0.1%)
26	M	0.56	0/1195	0.69	2/1602 (0.1%)
27	N	0.50	0/989	0.58	0/1326
28	O	0.65	3/1034 (0.3%)	0.79	3/1375 (0.2%)
29	P	0.49	0/800	0.65	1/1082 (0.1%)
30	Q	0.72	2/893 (0.2%)	0.76	2/1205 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	R	0.49	0/952	0.59	0/1274
32	S	0.53	0/817	0.61	0/1088
33	T	0.57	1/722 (0.1%)	0.68	0/964
34	U	0.41	0/659	0.53	0/884
35	V	0.48	0/657	0.63	0/881
36	W	0.56	1/680 (0.1%)	0.62	1/915 (0.1%)
37	X	0.45	0/909	0.72	1/1215 (0.1%)
38	Y	0.38	2/1046 (0.2%)	0.66	2/1410 (0.1%)
39	Z	0.13	0/227	0.40	0/304
40	a	0.30	0/69247	0.43	10/107985 (0.0%)
41	b	0.42	0/589	0.55	0/779
42	c	0.51	0/635	0.61	0/848
43	d	0.25	0/2872	0.37	0/4478
44	e	0.69	2/502 (0.4%)	0.65	1/667 (0.1%)
45	f	0.52	0/452	0.57	0/605
46	g	0.45	1/531 (0.2%)	0.64	0/709
47	h	0.49	1/2121 (0.0%)	0.58	1/2852 (0.0%)
48	i	0.41	0/450	0.55	0/599
49	j	0.51	0/1586	0.57	1/2134 (0.0%)
50	k	0.45	0/433	0.62	0/576
51	l	0.51	1/1571 (0.1%)	0.62	0/2113
52	m	0.45	0/380	0.56	0/498
53	n	0.46	0/1434	0.66	1/1926 (0.1%)
54	o	0.51	0/513	0.71	1/676 (0.1%)
55	p	0.41	0/1333	0.62	2/1805 (0.1%)
56	q	0.46	0/303	0.64	0/397
57	r	0.28	0/1122	0.48	0/1515
58	s	0.70	2/1152 (0.2%)	0.74	2/1551 (0.1%)
59	t	0.52	0/955	0.75	3/1279 (0.2%)
60	u	0.43	0/1062	0.59	0/1413
61	v	0.60	1/1093 (0.1%)	0.77	3/1460 (0.2%)
62	w	0.83	3/964 (0.3%)	0.80	3/1289 (0.2%)
63	x	0.34	0/902	0.50	0/1209
64	y	0.41	0/929	0.54	0/1242
65	z	0.62	2/960 (0.2%)	0.62	0/1278
All	All	0.39	35/190707 (0.0%)	0.53	94/281021 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
9	9	0	3
12	AB	0	10
13	AC	0	1
13	AD	0	1
14	AE	0	4
20	G	0	1
21	H	0	5
22	I	0	1
24	K	0	2
28	O	0	1
37	X	0	1
38	Y	0	1
53	n	0	1
54	o	0	1
58	s	0	1
60	u	0	2
All	All	0	36

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	w	35	LYS	CE-NZ	-12.74	1.11	1.49
28	O	80	ARG	CD-NE	-10.49	1.31	1.46
62	w	42	LYS	CD-CE	-9.39	1.24	1.52
24	K	45	ARG	CG-CD	7.75	1.75	1.52
8	7	42	G	C1'-N9	-7.60	1.36	1.48

The worst 5 of 94 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	K	71	MET	CG-SD-CE	-11.32	75.99	100.90
20	G	158	PRO	N-CD-CG	-10.99	86.72	103.20
12	AB	141	LEU	CA-C-N	-10.55	106.34	122.16
12	AB	141	LEU	C-N-CA	-10.55	106.34	122.16
25	L	102	MET	CA-CB-CG	-9.63	94.84	114.10

There are no chirality outliers.

5 of 36 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	9	107	GLU	Peptide
9	9	79	PRO	Peptide

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Mol	Chain	Res	Type	Group
9	9	92	ALA	Peptide
12	AB	106	ASP	Peptide
12	AB	116	VAL	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	0	816	839	839	54	0
2	1	857	922	922	69	0
3	2	746	811	811	61	0
4	3	788	844	844	46	0
5	4	753	780	780	87	0
6	5	726	0	392	111	0
7	6	703	0	396	34	0
8	7	772	0	382	117	0
9	9	1117	0	1155	256	0
10	A	1620	826	827	108	0
10	B	1620	813	827	114	0
11	AA	10381	0	10390	233	0
12	AB	1286	0	1302	331	0
13	AC	1698	0	1718	13	0
13	AD	1677	0	1713	29	0
14	AE	10404	0	10627	260	0
15	AF	650	0	658	11	0
16	C	544	559	560	109	0
17	D	32703	16423	16453	743	0
18	E	669	719	719	83	0
19	F	589	629	629	59	0
20	G	1760	1785	1787	154	0
21	H	1730	1454	1455	163	0
22	I	1636	1710	1710	153	0
23	J	1643	1707	1707	85	0
24	K	1152	1196	1196	114	0
25	L	848	846	846	106	0
26	M	1181	1235	1238	120	0
27	N	979	1031	1031	93	0
28	O	1022	1070	1070	92	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	P	790	831	831	138	0
30	Q	877	887	887	97	0
31	R	939	1001	1001	93	0
32	S	805	844	844	77	0
33	T	714	734	734	93	0
34	U	649	666	666	63	0
35	V	648	691	691	67	0
36	W	663	688	688	47	0
37	X	900	964	965	111	0
38	Y	1032	0	1088	212	0
39	Z	227	0	237	31	0
40	a	61841	31077	31120	1323	0
41	b	582	599	599	47	0
42	c	625	652	652	33	0
43	d	2569	1301	1301	42	0
44	e	501	531	531	45	0
45	f	448	488	488	38	0
46	g	522	520	520	67	0
47	h	2082	2154	2154	137	0
48	i	444	459	458	48	0
49	j	1565	1617	1616	119	0
50	k	426	464	464	41	0
51	l	1552	1619	1619	124	0
52	m	377	418	418	29	0
53	n	1410	1443	1444	154	0
54	o	504	572	572	51	0
55	p	1313	1358	1358	74	0
56	q	302	343	343	25	0
57	r	1111	1148	1148	52	0
58	s	1129	1162	1162	125	0
59	t	946	1023	1023	102	0
60	u	1053	1129	1129	80	0
61	v	1074	1157	1157	122	0
62	w	951	994	994	101	0
63	x	892	923	923	48	0
64	y	917	962	962	50	0
65	z	947	1020	1019	79	0
66	AE	1	0	0	0	0
67	AE	2	0	0	1	0
All	All	177400	98638	128790	6790	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 22.

The worst 5 of 6790 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)
6:5:10:DT:C7	11:AA:62:TYR:CD2	1.84	1.60
6:5:9:DG:H5''	11:AA:473:ARG:CB	1.29	1.58
6:5:11:DA:C5'	12:AB:67:THR:HG22	1.20	1.57
24:K:45:ARG:CD	24:K:45:ARG:CG	1.75	1.56
6:5:9:DG:C5'	11:AA:473:ARG:HB3	1.34	1.55

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	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
2	1	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
3	2	92/100 (92%)	87 (95%)	5 (5%)	0	100	100
4	3	101/104 (97%)	98 (97%)	3 (3%)	0	100	100
5	4	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
9	9	146/165 (88%)	100 (68%)	43 (30%)	3 (2%)	5	29
11	AA	1312/1342 (98%)	1198 (91%)	113 (9%)	1 (0%)	48	83
12	AB	159/162 (98%)	109 (69%)	44 (28%)	6 (4%)	2	19
13	AC	217/329 (66%)	203 (94%)	12 (6%)	2 (1%)	14	50
13	AD	214/329 (65%)	198 (92%)	16 (8%)	0	100	100
14	AE	1331/1407 (95%)	1211 (91%)	115 (9%)	5 (0%)	30	67
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
16	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
18	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	F	68/71 (96%)	68 (100%)	0	0	100	100
20	G	223/241 (92%)	212 (95%)	10 (4%)	1 (0%)	30	67
21	H	255/557 (46%)	182 (71%)	66 (26%)	7 (3%)	4	25
22	I	206/233 (88%)	193 (94%)	13 (6%)	0	100	100
23	J	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
24	K	154/167 (92%)	145 (94%)	8 (5%)	1 (1%)	21	59
25	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	48
26	M	149/179 (83%)	140 (94%)	8 (5%)	1 (1%)	18	55
27	N	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
28	O	125/130 (96%)	116 (93%)	8 (6%)	1 (1%)	16	53
29	P	97/103 (94%)	89 (92%)	8 (8%)	0	100	100
30	Q	115/129 (89%)	107 (93%)	8 (7%)	0	100	100
31	R	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
32	S	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
33	T	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
34	U	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
35	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
36	W	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
37	X	114/118 (97%)	103 (90%)	9 (8%)	2 (2%)	6	33
38	Y	139/142 (98%)	101 (73%)	38 (27%)	0	100	100
39	Z	28/121 (23%)	22 (79%)	6 (21%)	0	100	100
41	b	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
42	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
44	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
45	f	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
46	g	64/70 (91%)	62 (97%)	2 (3%)	0	100	100
47	h	269/273 (98%)	255 (95%)	14 (5%)	0	100	100
48	i	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
49	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
50	k	50/55 (91%)	50 (100%)	0	0	100	100
51	l	199/201 (99%)	188 (94%)	11 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
53	n	175/179 (98%)	161 (92%)	13 (7%)	1 (1%)	21	59
54	o	62/65 (95%)	57 (92%)	4 (6%)	1 (2%)	7	37
55	p	173/177 (98%)	162 (94%)	11 (6%)	0	100	100
56	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
57	r	147/149 (99%)	139 (95%)	8 (5%)	0	100	100
58	s	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
59	t	121/123 (98%)	114 (94%)	7 (6%)	0	100	100
60	u	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
61	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
62	w	117/127 (92%)	112 (96%)	5 (4%)	0	100	100
63	x	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
64	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
65	z	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
All	All	9486/10558 (90%)	8739 (92%)	714 (8%)	33 (0%)	37	72

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	AB	127	GLN
12	AB	141	LEU
12	AB	152	HIS
20	G	127	ASP
21	H	304	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	84 (100%)	0	100	100
2	1	93/93 (100%)	93 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	2	81/84 (96%)	81 (100%)	0	100	100
4	3	84/85 (99%)	84 (100%)	0	100	100
5	4	78/78 (100%)	78 (100%)	0	100	100
9	9	112/123 (91%)	112 (100%)	0	100	100
11	AA	1135/1157 (98%)	1130 (100%)	5 (0%)	84	83
12	AB	141/142 (99%)	139 (99%)	2 (1%)	59	71
13	AC	186/286 (65%)	186 (100%)	0	100	100
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1122/1168 (96%)	1111 (99%)	11 (1%)	68	77
15	AF	70/75 (93%)	69 (99%)	1 (1%)	59	71
16	C	57/65 (88%)	57 (100%)	0	100	100
18	E	65/66 (98%)	65 (100%)	0	100	100
19	F	60/61 (98%)	60 (100%)	0	100	100
20	G	187/199 (94%)	187 (100%)	0	100	100
21	H	137/461 (30%)	137 (100%)	0	100	100
22	I	171/190 (90%)	171 (100%)	0	100	100
23	J	172/173 (99%)	171 (99%)	1 (1%)	78	82
24	K	119/126 (94%)	119 (100%)	0	100	100
25	L	91/116 (78%)	91 (100%)	0	100	100
26	M	124/147 (84%)	124 (100%)	0	100	100
27	N	104/105 (99%)	104 (100%)	0	100	100
28	O	105/107 (98%)	105 (100%)	0	100	100
29	P	86/90 (96%)	86 (100%)	0	100	100
30	Q	90/99 (91%)	90 (100%)	0	100	100
31	R	101/104 (97%)	101 (100%)	0	100	100
32	S	83/84 (99%)	83 (100%)	0	100	100
33	T	76/77 (99%)	76 (100%)	0	100	100
34	U	65/65 (100%)	65 (100%)	0	100	100
35	V	74/78 (95%)	74 (100%)	0	100	100
36	W	72/79 (91%)	72 (100%)	0	100	100
37	X	94/96 (98%)	94 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	Y	109/110 (99%)	109 (100%)	0	100	100
39	Z	26/85 (31%)	26 (100%)	0	100	100
41	b	58/63 (92%)	58 (100%)	0	100	100
42	c	67/68 (98%)	67 (100%)	0	100	100
44	e	54/55 (98%)	54 (100%)	0	100	100
45	f	48/49 (98%)	48 (100%)	0	100	100
46	g	59/62 (95%)	59 (100%)	0	100	100
47	h	216/218 (99%)	216 (100%)	0	100	100
48	i	47/48 (98%)	47 (100%)	0	100	100
49	j	164/164 (100%)	164 (100%)	0	100	100
50	k	47/49 (96%)	47 (100%)	0	100	100
51	l	165/165 (100%)	165 (100%)	0	100	100
52	m	38/38 (100%)	38 (100%)	0	100	100
53	n	148/150 (99%)	148 (100%)	0	100	100
54	o	51/52 (98%)	51 (100%)	0	100	100
55	p	136/138 (99%)	136 (100%)	0	100	100
56	q	34/34 (100%)	34 (100%)	0	100	100
57	r	114/114 (100%)	114 (100%)	0	100	100
58	s	116/116 (100%)	116 (100%)	0	100	100
59	t	104/104 (100%)	104 (100%)	0	100	100
60	u	103/103 (100%)	103 (100%)	0	100	100
61	v	109/109 (100%)	109 (100%)	0	100	100
62	w	99/103 (96%)	99 (100%)	0	100	100
63	x	86/87 (99%)	86 (100%)	0	100	100
64	y	99/100 (99%)	99 (100%)	0	100	100
65	z	89/90 (99%)	89 (100%)	0	100	100
All	All	7890/8723 (90%)	7870 (100%)	20 (0%)	84	85

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	AE	291	ILE
14	AE	1261	LEU

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Mol	Chain	Res	Type
23	J	47	ARG
15	AF	63	ILE
12	AB	146	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 109 such sidechains are listed below:

Mol	Chain	Res	Type
22	I	190	HIS
32	S	4	GLN
61	v	97	GLN
23	J	131	ASN
26	M	86	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	8 (10%)
10	B	75/76 (98%)	31 (41%)	9 (12%)
17	D	1514/1542 (98%)	290 (19%)	20 (1%)
40	a	2859/2904 (98%)	511 (17%)	0
43	d	119/120 (99%)	15 (12%)	0
8	7	36/44 (81%)	26 (72%)	5 (13%)
All	All	4678/4762 (98%)	902 (19%)	42 (0%)

5 of 902 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	3	G
8	7	4	U
8	7	5	U
8	7	7	U
8	7	8	U

5 of 42 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
17	D	496	A
17	D	1212	U
17	D	517	G
17	D	1145	A

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Mol	Chain	Res	Type
17	D	1214	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

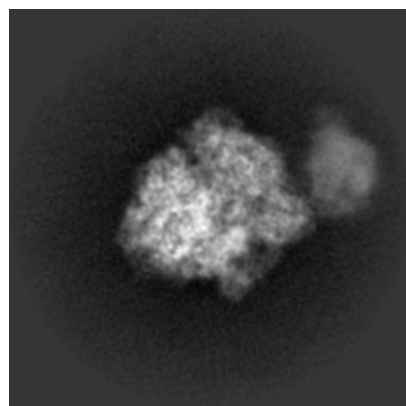
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42492. These allow visual inspection of the internal detail of the map and identification of artifacts.

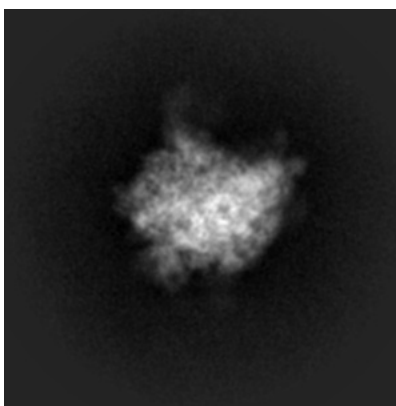
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

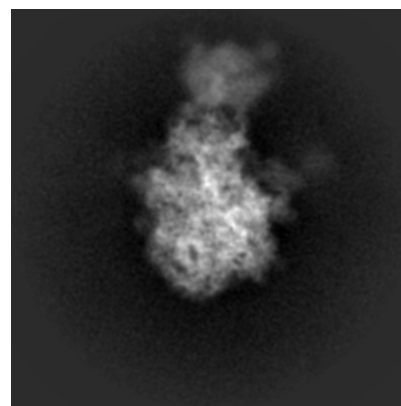
6.1.1 Primary map



X

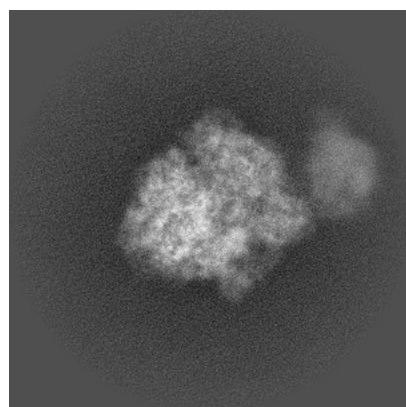


Y

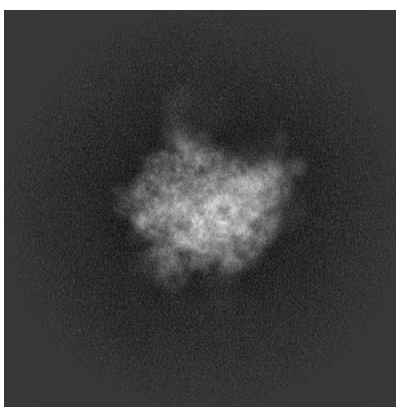


Z

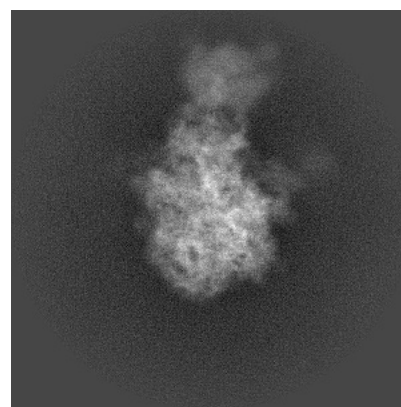
6.1.2 Raw map



X



Y

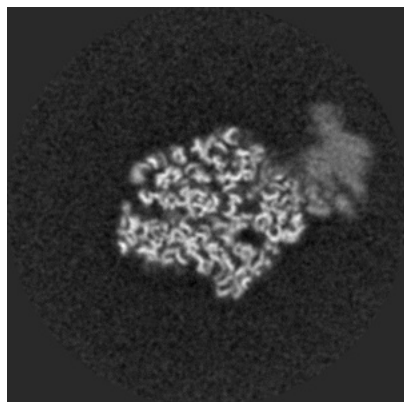


Z

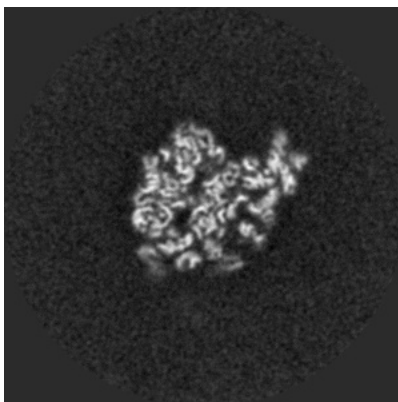
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

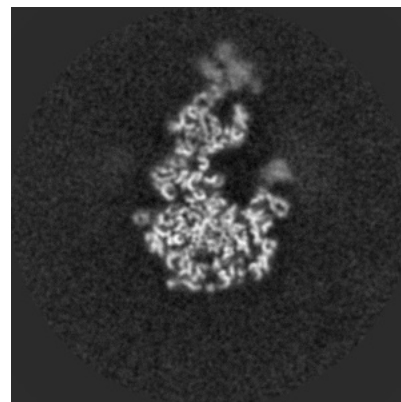
6.2.1 Primary map



X Index: 256

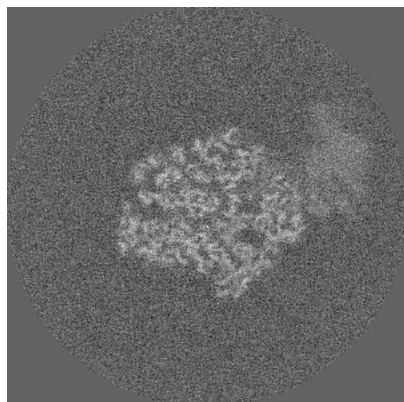


Y Index: 256

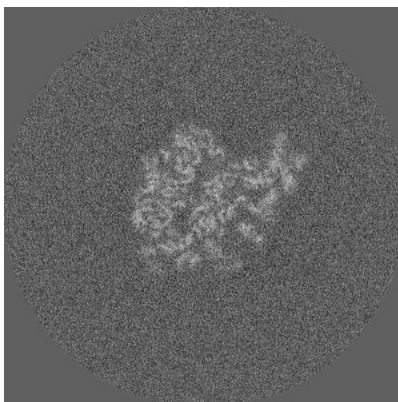


Z Index: 256

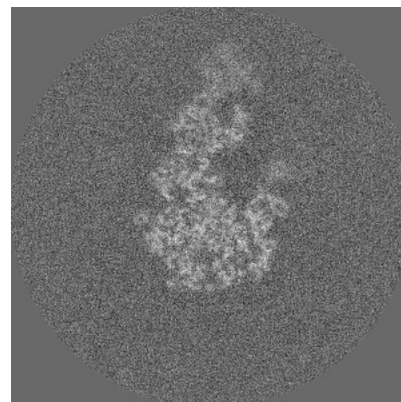
6.2.2 Raw map



X Index: 256



Y Index: 256

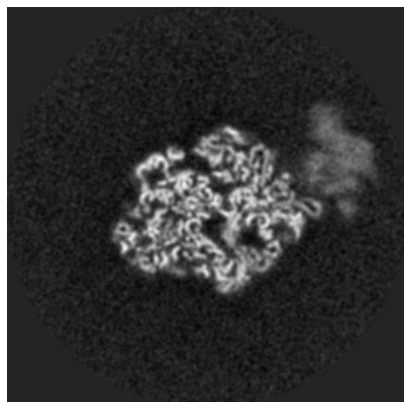


Z Index: 256

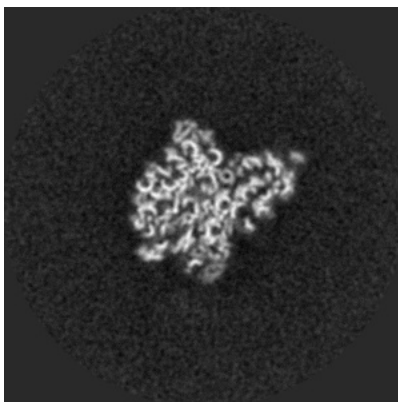
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

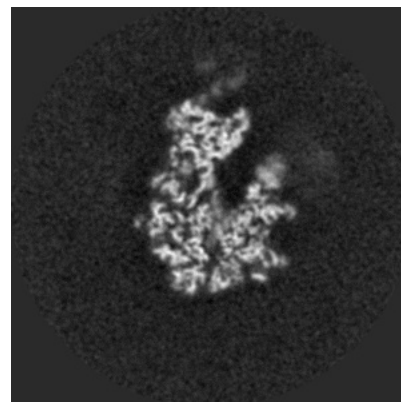
6.3.1 Primary map



X Index: 248

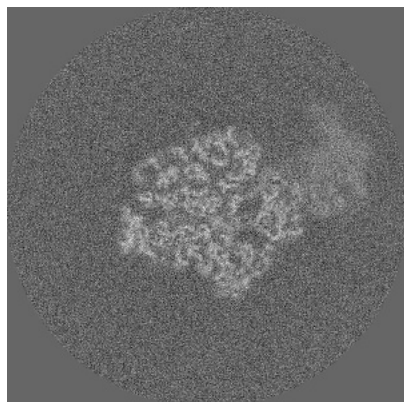


Y Index: 248

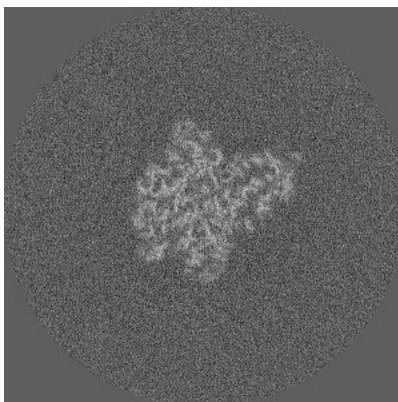


Z Index: 243

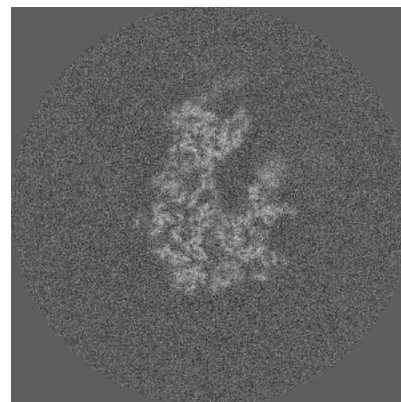
6.3.2 Raw map



X Index: 259



Y Index: 246

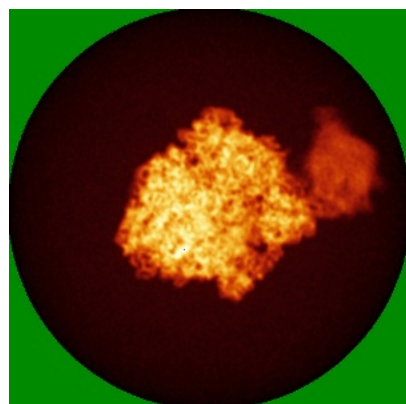


Z Index: 244

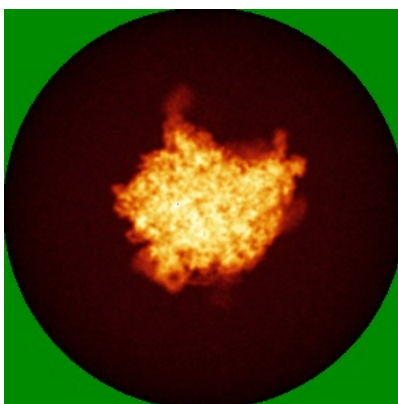
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

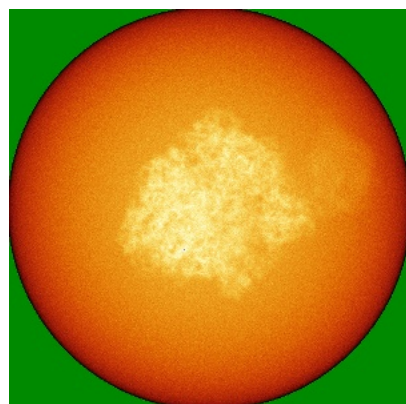


Y

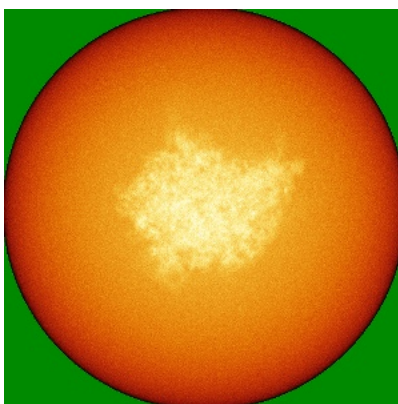


Z

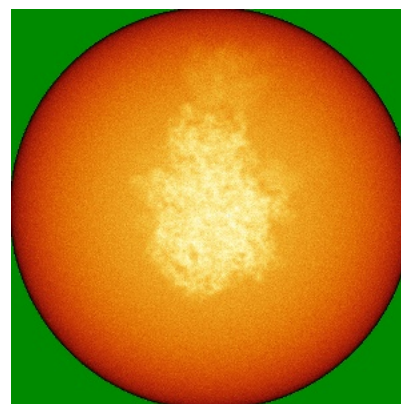
6.4.2 Raw map



X



Y

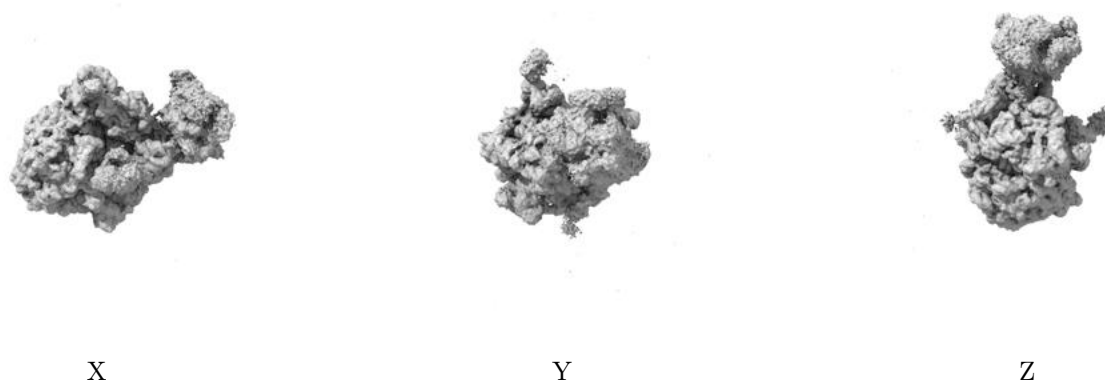


Z

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.

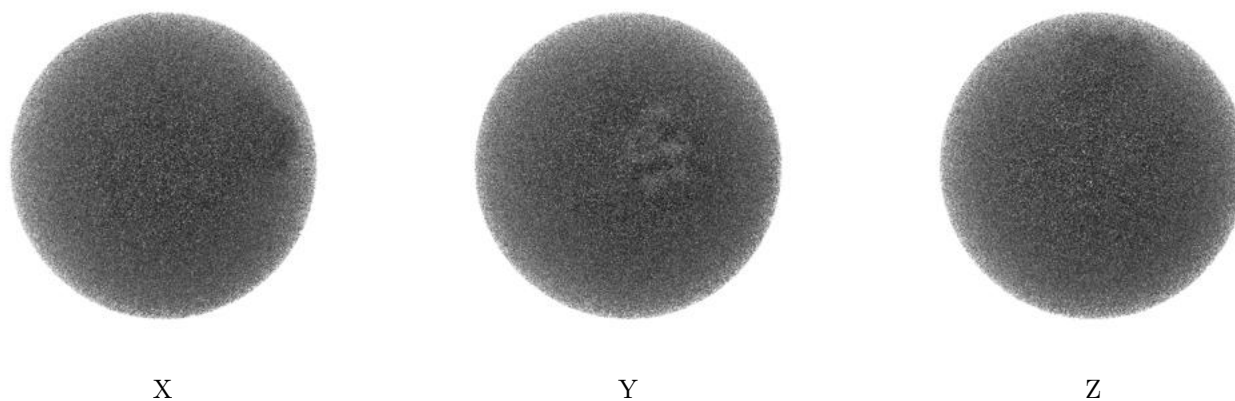
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0042. 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.

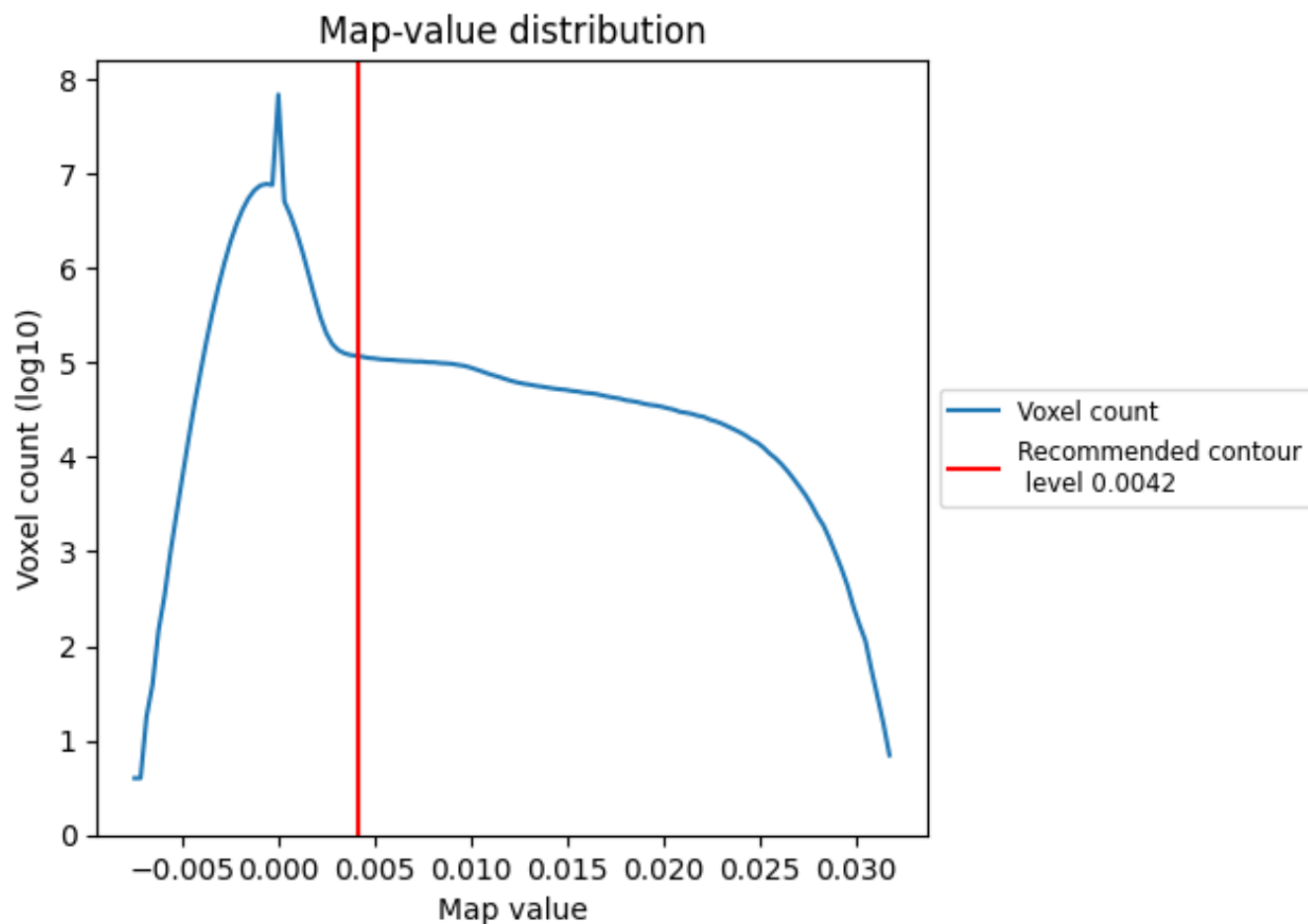
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

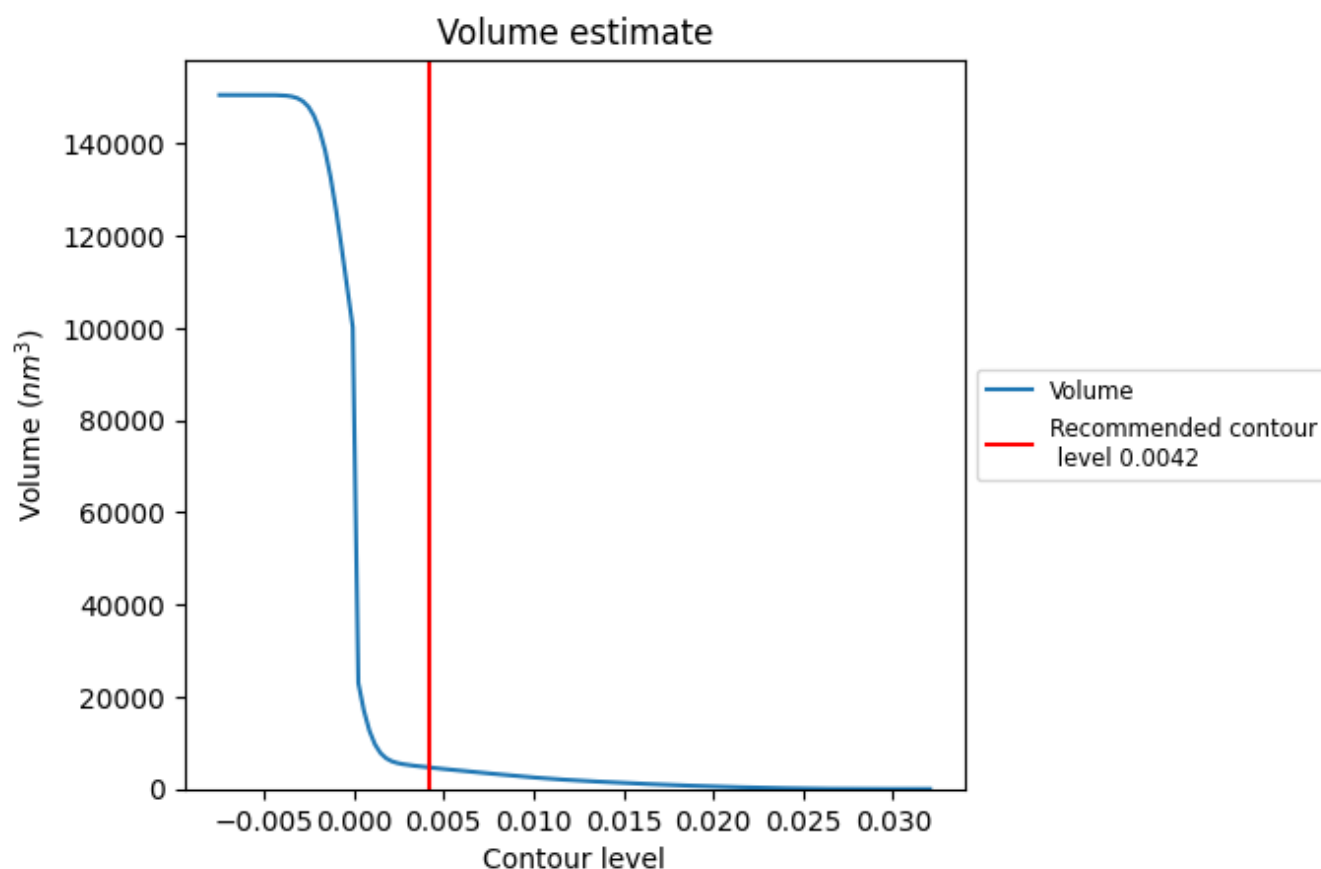
This section contains the results of statistical analysis of the map.

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.

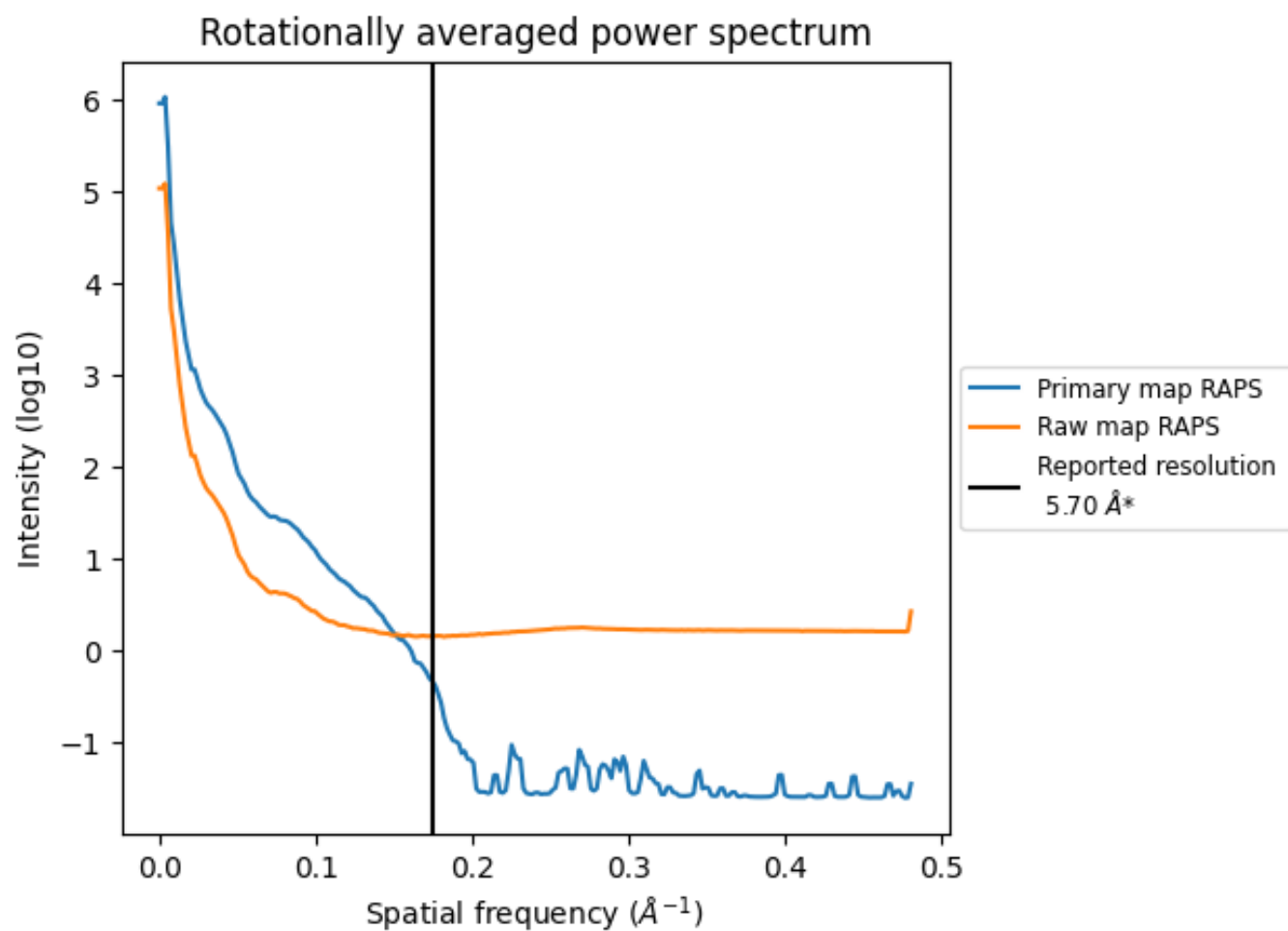
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4667 nm^3 ; this corresponds to an approximate mass of 4216 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 ⓘ

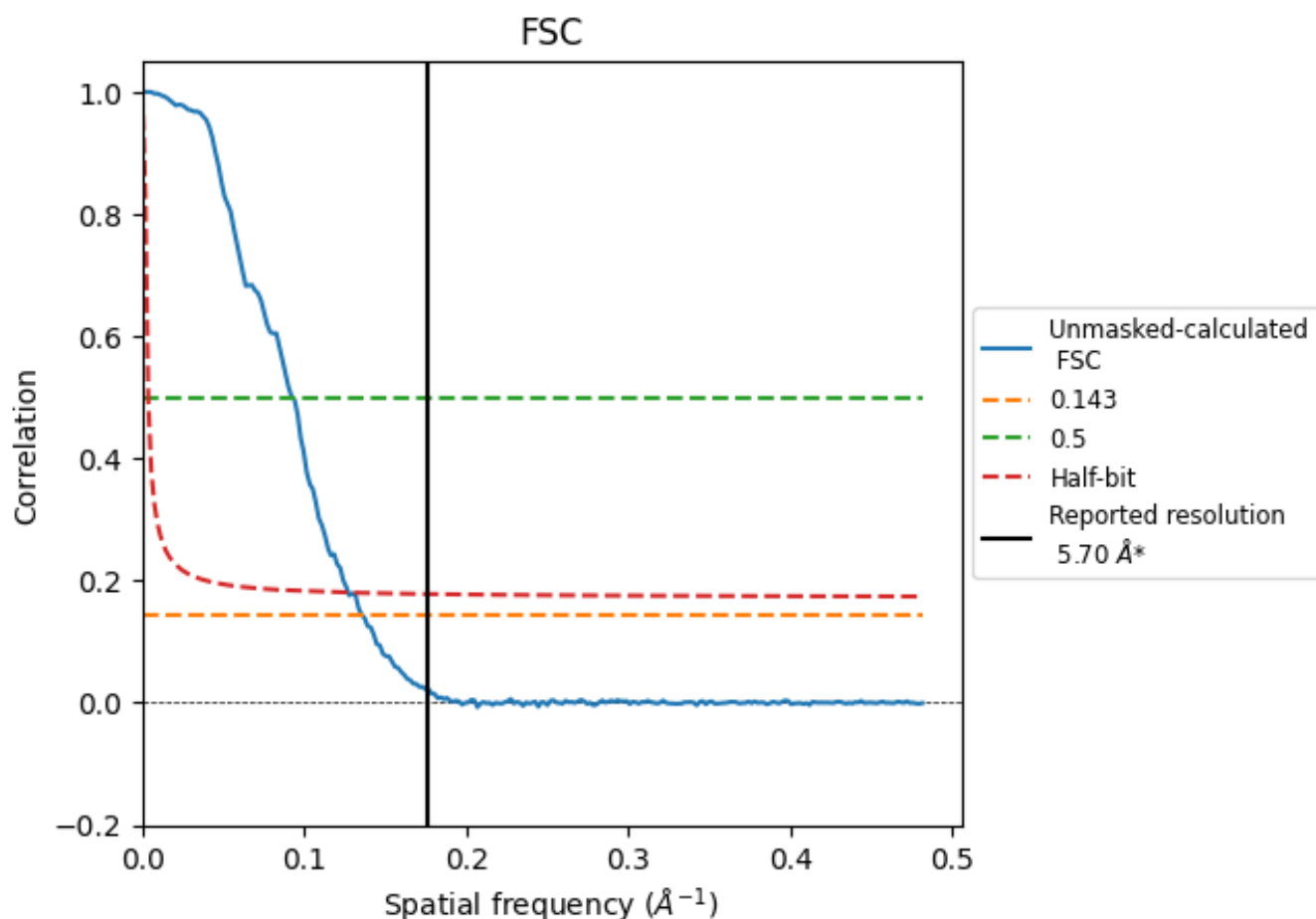


*Reported resolution corresponds to spatial frequency of 0.175 $\text{\AA}^{-1}$

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 0.175 Å⁻¹

8.2 Resolution estimates [i](#)

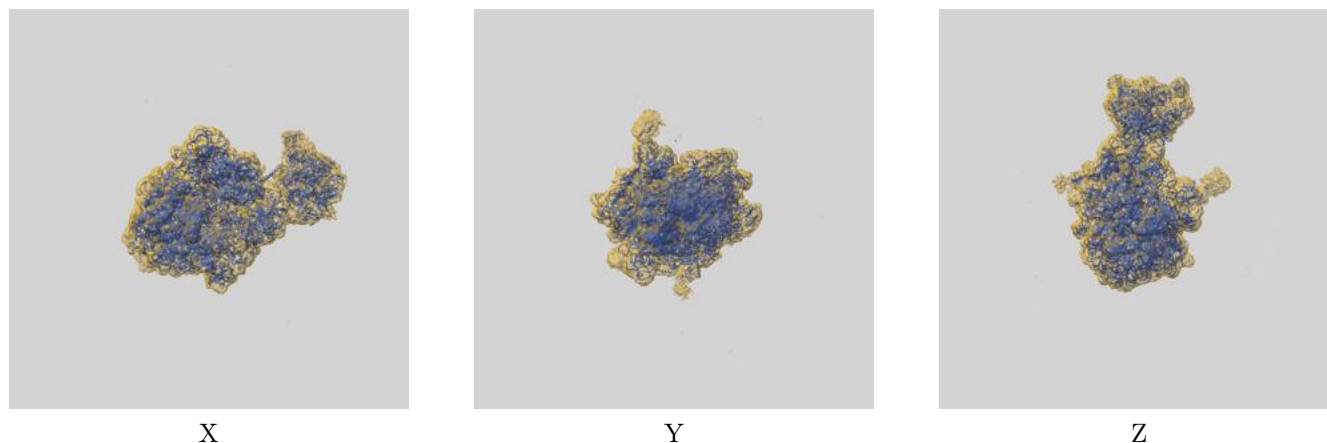
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.36	10.80	7.86

*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 7.36 differs from the reported value 5.7 by more than 10 %

9 Map-model fit [i](#)

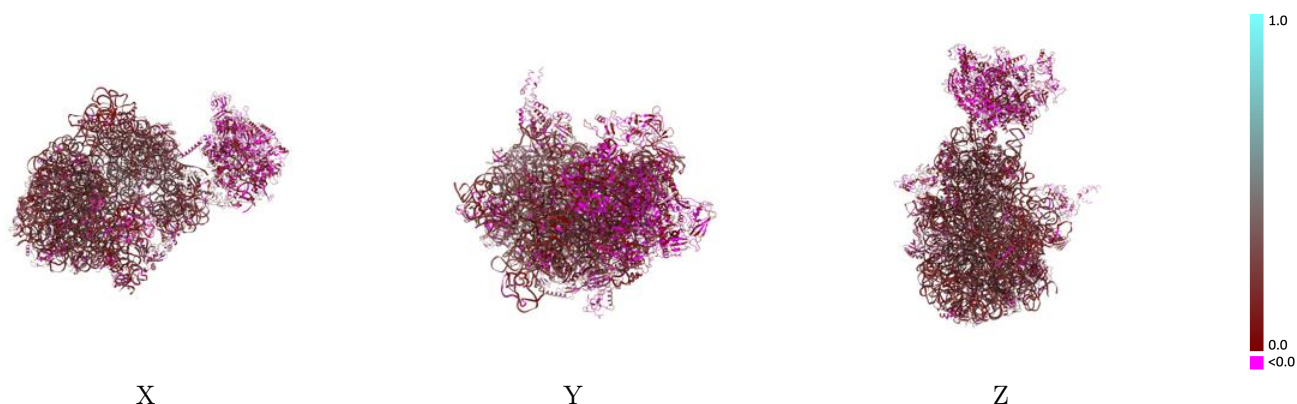
This section contains information regarding the fit between EMDB map EMD-42492 and PDB model 8URH. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



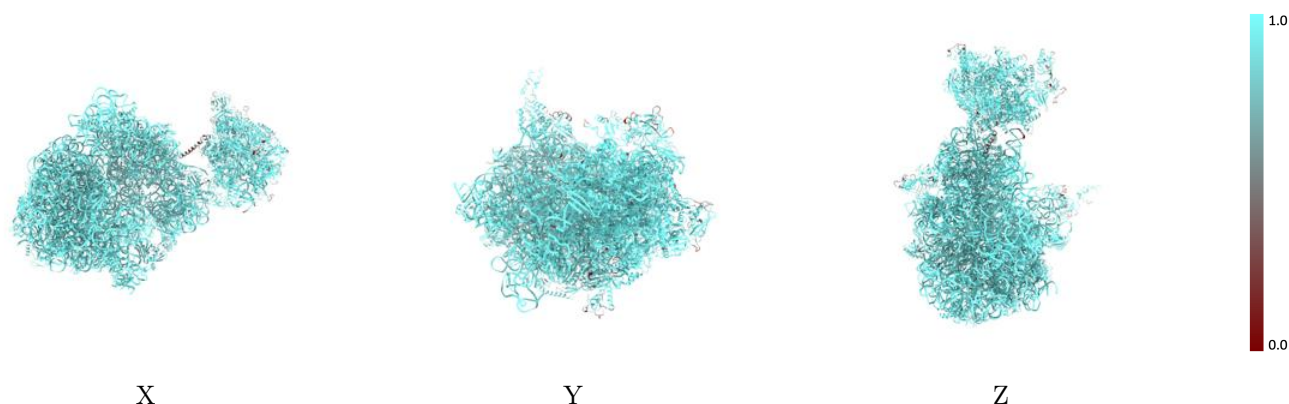
The images above show the 3D surface view of the map at the recommended contour level 0.0042 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



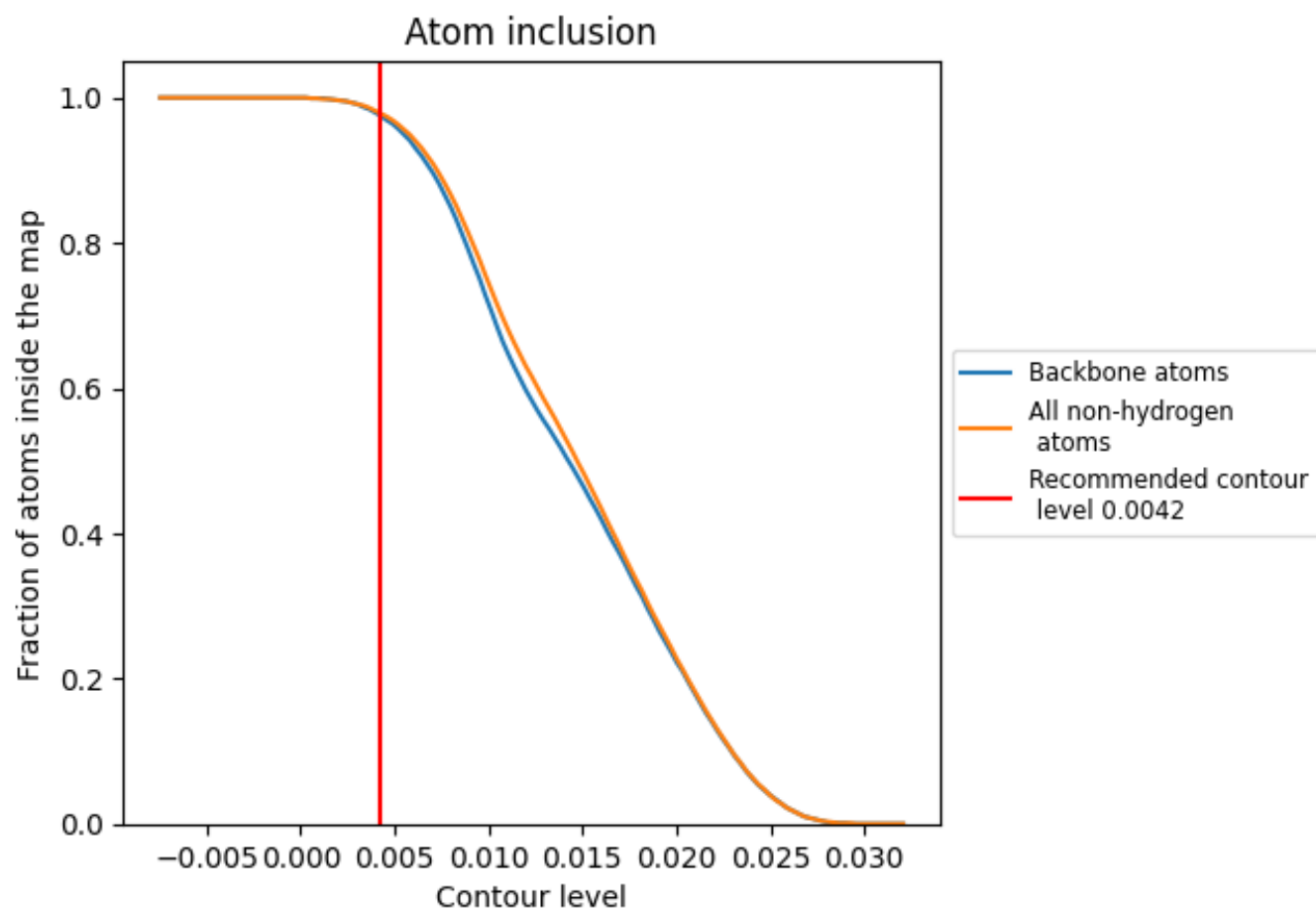
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0042).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.0042) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9790	 0.1650
0	 0.9850	 0.1450
1	 0.9750	 0.1600
2	 0.9750	 0.1360
3	 0.9910	 0.1240
4	 0.9840	 0.1400
5	 0.9530	 0.1190
6	 0.9430	 0.1080
7	 0.9830	 0.1160
9	 0.9520	 0.0690
A	 0.9980	 0.1590
AA	 0.9620	 0.0620
AB	 0.9870	 0.1090
AC	 0.9740	 0.0440
AD	 0.8920	 0.0340
AE	 0.9500	 0.0690
AF	 0.6140	 0.0150
B	 0.9680	 0.1150
C	 0.9960	 0.1410
D	 0.9970	 0.2140
E	 0.9910	 0.1500
F	 0.9750	 0.1620
G	 0.9770	 0.1540
H	 0.8170	 0.0580
I	 0.9840	 0.1840
J	 0.9960	 0.1740
K	 0.9950	 0.2000
L	 0.9920	 0.1540
M	 0.9910	 0.1530
N	 0.9770	 0.1690
O	 0.9860	 0.1330
P	 0.9800	 0.1570
Q	 0.9920	 0.1450
R	 0.9950	 0.2010
S	 0.9940	 0.1520



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Chain	Atom inclusion	Q-score
T	 0.9930	 0.1470
U	 0.9950	 0.1530
V	 0.9810	 0.1610
W	 0.9470	 0.1150
X	 0.9790	 0.1380
Y	 0.8410	 0.0650
Z	 0.9070	 0.0410
a	 0.9970	 0.2030
b	 0.9910	 0.1190
c	 0.9800	 0.1510
d	 0.9990	 0.1740
e	 0.9780	 0.1200
f	 0.9860	 0.1720
g	 0.9690	 0.0970
h	 0.9890	 0.1430
i	 0.9840	 0.1630
j	 0.9940	 0.1520
k	 0.9930	 0.1390
l	 0.9820	 0.1330
m	 0.9920	 0.1750
n	 0.9720	 0.1190
o	 0.9880	 0.1260
p	 0.9880	 0.1400
q	 1.0000	 0.1360
r	 0.9250	 0.1160
s	 0.9870	 0.1640
t	 0.9790	 0.1680
u	 0.9890	 0.1280
v	 0.9870	 0.1750
w	 0.9850	 0.1460
x	 0.9850	 0.0960
y	 0.9800	 0.1570
z	 0.9970	 0.1340