



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 06:40 PM UTC

PDB ID : 9V26 / pdb_00009v26
EMDB ID : EMD-64718
Title : Cryo- EM structure of 75S ribosome with A/P- & P/E- tRNAs from Entamoeba histolytica bound to antibiotic paromomycin
Authors : Sharma, S.; Mishra, S.; Gourinath, S.; Kaushal, P.S.
Deposited on : 2025-05-19
Resolution : 3.10 Å(reported)
Based on initial model : .

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

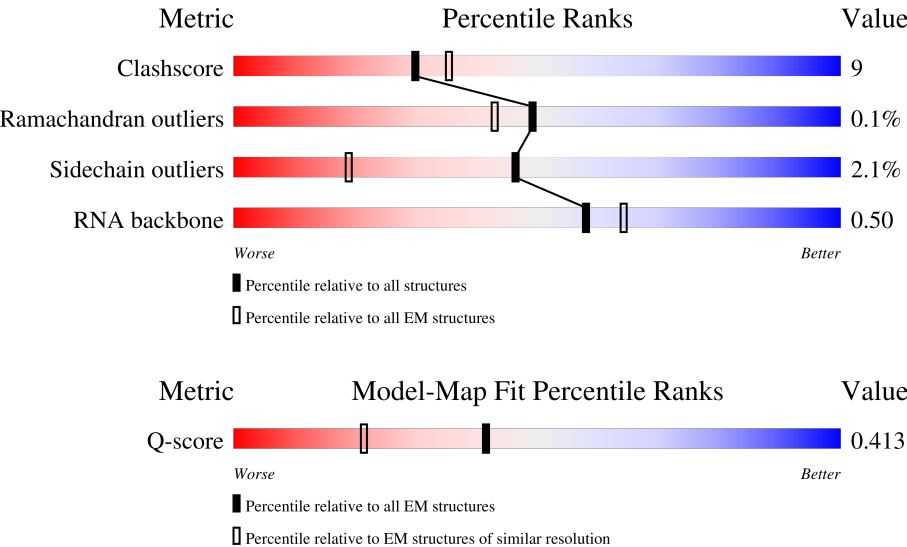
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

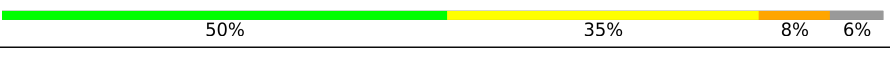
The reported resolution of this entry is 3.10 Å.

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.



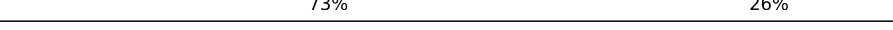
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	1A	3503	
2	1B	155	
3	1C	117	

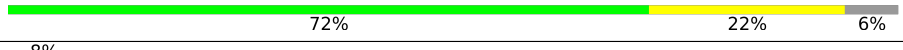
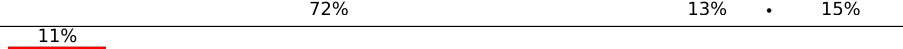
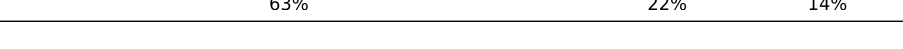
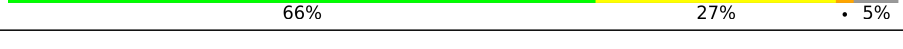
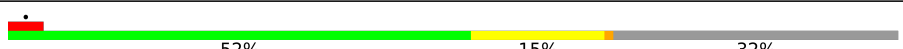
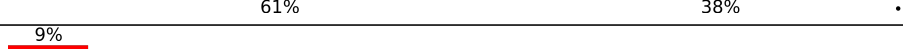
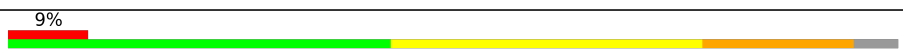
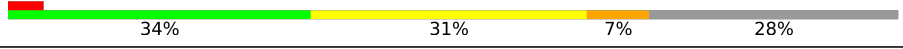
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Mol	Chain	Length	Quality of chain
4	ID	257	
5	IE	402	
6	IF	431	
7	IG	286	
8	IH	204	
9	II	230	
10	IJ	286	
11	IK	197	
12	IL	210	
13	IM	174	
14	IN	291	
15	IO	205	
16	IP	135	
17	IQ	205	
18	IR	179	
19	IS	168	
20	IT	173	
21	IU	198	
22	IV	166	
23	IW	137	
24	IX	140	
25	IY	121	
26	IZ	163	
27	la	213	
28	lb	139	

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Mol	Chain	Length	Quality of chain
29	lc	149	
30	ld	64	
31	le	109	
32	lf	150	
33	lg	134	
34	lh	137	
35	li	122	
36	lj	108	
37	lk	104	
38	ll	77	
39	lm	93	
40	ln	77	
41	lo	51	
42	lp	56	
43	lq	98	
44	sA	137	
45	sB	144	
46	sC	84	
47	sD	69	
48	sE	56	
49	sI	76	
50	sJ	77	
51	sK	10	
52	sa	1947	
53	sc	255	

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Mol	Chain	Length	Quality of chain
54	sd	244	
55	se	256	
56	sf	326	
57	sg	206	
58	sh	266	
59	si	201	
60	sj	237	
61	sk	185	
62	sl	127	
63	sm	156	
64	so	151	
65	sp	146	
66	sq	144	
67	sr	130	
68	ss	158	
69	st	117	
70	su	155	
71	sv	155	
72	sw	118	
73	sx	86	
74	sy	141	

2 Entry composition

There are 75 unique types of molecules in this entry. The entry contains 178778 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	3142	Total	C	N	O	P	0	0
			67153	30106	12192	21713	3142		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1B	145	Total	C	N	O	P	0	0
			3097	1390	560	1002	145		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1C	117	Total	C	N	O	P	0	0
			2477	1108	425	827	117		

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1D	246	Total	C	N	O	S	0	0
			1881	1165	382	326	8		

- Molecule 5 is a protein called 60S ribosomal protein L3, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1E	387	Total	C	N	O	S	0	0
			3076	1956	578	527	15		

- Molecule 6 is a protein called 60S ribosomal protein L4, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1F	425	Total	C	N	O	S	0	0
			3281	2091	624	552	14		

- Molecule 7 is a protein called 60S ribosomal protein L5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	lG	278	Total	C	N	O	S	0	0
			2209	1412	399	390	8		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	lH	203	Total	C	N	O	S	0	0
			1608	1054	272	278	4		

- Molecule 9 is a protein called 60S ribosomal protein L7, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	lI	210	Total	C	N	O	S	0	0
			1658	1067	301	282	8		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	lJ	201	Total	C	N	O	S	0	0
			1640	1058	302	275	5		

- Molecule 11 is a protein called 60S ribosomal protein L9, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	lK	193	Total	C	N	O	S	0	0
			1538	974	279	279	6		

- Molecule 12 is a protein called Ribosomal protein L10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	lL	200	Total	C	N	O	S	0	0
			1597	1017	302	264	14		

- Molecule 13 is a protein called 60S ribosomal protein L11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	lM	170	Total	C	N	O	S	0	0
			1350	857	243	245	5		

- Molecule 14 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	lN	267	Total	C	N	O	S	0	0
			2130	1358	412	352	8		

- Molecule 15 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	lO	204	Total	C	N	O	S	0	0
			1616	1030	302	275	9		

- Molecule 16 is a protein called 60S ribosomal protein L14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	lP	130	Total	C	N	O	S	0	0
			1021	654	188	175	4		

- Molecule 17 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	lQ	204	Total	C	N	O	S	0	0
			1676	1051	356	264	5		

- Molecule 18 is a protein called 60S ribosomal protein L17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	lR	158	Total	C	N	O	S	0	0
			1232	779	238	210	5		

- Molecule 19 is a protein called 60S ribosomal protein L18, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	lS	167	Total	C	N	O	S	0	0
			1321	835	258	219	9		

- Molecule 20 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	lT	173	Total	C	N	O	S	0	0
			1413	910	259	235	9		

- Molecule 21 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	IU	150	Total	C	N	O	S	0	0
			1235	787	246	197	5		

- Molecule 22 is a protein called 60S ribosomal protein L21, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	IV	165	Total	C	N	O	S	0	0
			1320	846	254	217	3		

- Molecule 23 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	IW	93	Total	C	N	O	S	0	0
			763	493	132	133	5		

- Molecule 24 is a protein called 60S ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	IX	133	Total	C	N	O	S	0	0
			1015	629	196	182	8		

- Molecule 25 is a protein called Ribosomal protein L23A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	IY	116	Total	C	N	O	S	0	0
			926	597	166	159	4		

- Molecule 26 is a protein called 60S ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	IZ	57	Total	C	N	O	S	0	0
			481	318	88	73	2		

- Molecule 27 is a protein called 60S ribosomal protein L26, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	la	210	Total	C	N	O	S	0	0
			1651	1055	304	285	7		

- Molecule 28 is a protein called 60S ribosomal protein L27, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	lb	137	Total	C	N	O	S	0	0
			1094	707	196	187	4		

- Molecule 29 is a protein called Large ribosomal subunit protein uL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	lc	148	Total	C	N	O	S	0	0
			1192	757	236	194	5		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	ld	60	Total	C	N	O	S	0	0
			478	297	97	82	2		

- Molecule 31 is a protein called 60S ribosomal protein L30, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	le	93	Total	C	N	O	S	0	0
			693	438	118	135	2		

- Molecule 32 is a protein called 60S ribosomal protein L31, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	lf	126	Total	C	N	O	S	0	0
			1032	662	191	174	5		

- Molecule 33 is a protein called 60S ribosomal protein L32, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	lg	123	Total	C	N	O	S	0	0
			1010	643	200	162	5		

- Molecule 34 is a protein called 60S ribosomal protein L34, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	lh	102	Total	C	N	O	S	0	0
			805	503	166	130	6		

- Molecule 35 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	li	122	Total	C	N	O	S	0	0
			974	620	188	162	4		

- Molecule 36 is a protein called 60S ribosomal protein L35a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	lj	106	Total	C	N	O	S	0	0
			841	545	158	135	3		

- Molecule 37 is a protein called 60S ribosomal protein L36, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	lk	89	Total	C	N	O	S	0	0
			712	447	144	116	5		

- Molecule 38 is a protein called 60S ribosomal protein L37-A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	ll	72	Total	C	N	O	S	0	0
			591	361	132	91	7		

- Molecule 39 is a protein called 60S ribosomal protein L37a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	lm	90	Total	C	N	O	S	0	0
			693	432	136	119	6		

- Molecule 40 is a protein called 60S ribosomal protein L38 putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	ln	73	Total	C	N	O	S	0	0
			584	378	104	100	2		

- Molecule 41 is a protein called Ribosomal protein L39, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	lo	50	Total	C	N	O	S	0	0
			432	275	91	63	3		

- Molecule 42 is a protein called 60S ribosomal protein L40, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	lp	53	Total	C	N	O	S	0	0
			420	259	86	69	6		

- Molecule 43 is a protein called 60S ribosomal protein L44, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	lq	92	Total	C	N	O	S	0	0
			756	480	148	122	6		

- Molecule 44 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	sA	10	Total	C	N	O		0	0
			91	62	15	14			

- Molecule 45 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	sB	98	Total	C	N	O	S	0	0
			787	478	169	134	6		

- Molecule 46 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	sC	32	Total	C	N	O	S	0	0
			249	161	42	45	1		

- Molecule 47 is a protein called 40S ribosomal protein S28, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	sD	60	Total	C	N	O	S	0	0
			468	289	93	84	2		

- Molecule 48 is a protein called Ribosomal protein S29, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	sE	55	Total	C	N	O	S	0	0
			442	273	90	75	4		

- Molecule 49 is a RNA chain called A/P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	sI	73	Total	C	N	O	P	0	0
			1556	695	283	506	72		

- Molecule 50 is a RNA chain called P/E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	sJ	73	Total	C	N	O	P	0	0
			1549	691	271	514	73		

- Molecule 51 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	sK	10	Total	C	N	O	P	0	0
			215	97	41	67	10		

- Molecule 52 is a RNA chain called 17S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	sa	1401	Total	C	N	O	P	0	0
			29968	13412	5443	9712	1401		

- Molecule 53 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	sc	196	Total	C	N	O	S	0	0
			1499	960	267	265	7		

- Molecule 54 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	sd	188	Total	C	N	O	S	0	0
			1440	912	257	260	11		

- Molecule 55 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	se	144	Total	C	N	O	S	0	0
			1166	746	208	205	7		

- Molecule 56 is a protein called 40S ribosomal protein S4, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	sf	256	Total	C	N	O	S	0	0
			2031	1297	378	345	11		

- Molecule 57 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	sg	179	Total	C	N	O	S	0	0
			1424	897	258	258	11		

- Molecule 58 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	sh	52	Total	C	N	O	S	0	0
			400	243	83	70	4		

- Molecule 59 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	si	57	Total	C	N	O	S	0	0
			445	285	82	77	1		

- Molecule 60 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	sj	129	Total	C	N	O	S	0	0
			1009	623	203	179	4		

- Molecule 61 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	sk	82	Total	C	N	O	S	0	0
			677	430	132	110	5		

- Molecule 62 is a protein called 40S ribosomal protein S10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	sl	66	Total	C	N	O	S	0	0
			536	352	90	85	9		

- Molecule 63 is a protein called 40S ribosomal protein S11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	sm	141	Total	C	N	O	S	0	0
			1161	735	224	196	6		

- Molecule 64 is a protein called 40S ribosomal protein S13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	so	76	Total	C	N	O	S	0	0
			644	410	123	108	3		

- Molecule 65 is a protein called Ribosomal protein S14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	sp	128	Total	C	N	O	S	0	0
			964	592	187	179	6		

- Molecule 66 is a protein called 40S ribosomal protein S15, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	sq	105	Total	C	N	O	S	0	0
			842	543	150	144	5		

- Molecule 67 is a protein called 40S ribosomal protein S15a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	sr	129	Total	C	N	O	S	0	0
			1022	650	186	181	5		

- Molecule 68 is a protein called 40S ribosomal protein S16, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	ss	137	Total	C	N	O	S	0	0
			1076	695	193	184	4		

- Molecule 69 is a protein called 40S ribosomal protein S17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	st	81	Total	C	N	O	S	0	0
			676	424	135	116	1		

- Molecule 70 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	su	124	Total	C	N	O	S	0	0
			1006	625	207	170	4		

- Molecule 71 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	sv	127	Total	C	N	O	S	0	0
			1015	646	185	178	6		

- Molecule 72 is a protein called 40S ribosomal protein S20, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	sw	46	Total	C	N	O	S	0	0
			376	238	70	65	3		

- Molecule 73 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	sx	63	Total	C	N	O	S	0	0
			494	313	90	88	3		

- Molecule 74 is a protein called 40S ribosomal protein S23, putative.

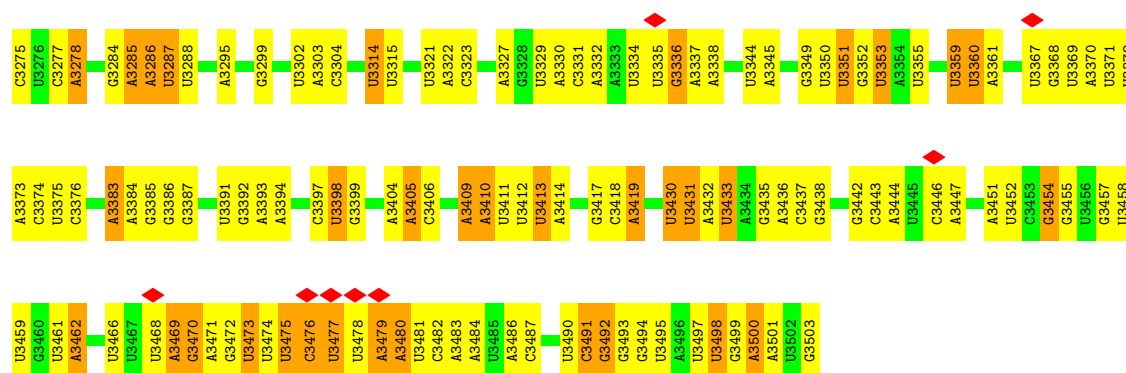
Mol	Chain	Residues	Atoms					AltConf	Trace
74	sy	106	Total	C	N	O	S	0	0
			836	522	169	142	3		

- Molecule 75 is PAROMOMYCIN (CCD ID: PAR) (formula: C₂₃H₄₅N₅O₁₄) (labeled as "Ligand of Interest" by depositor).



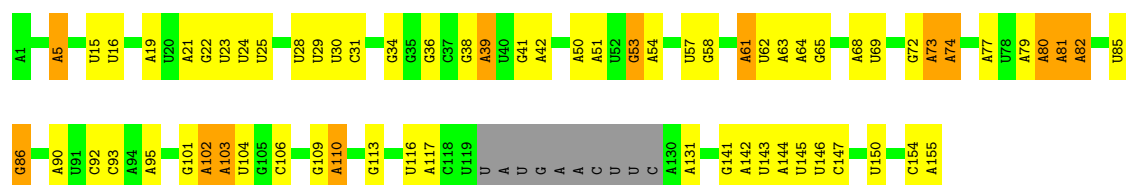


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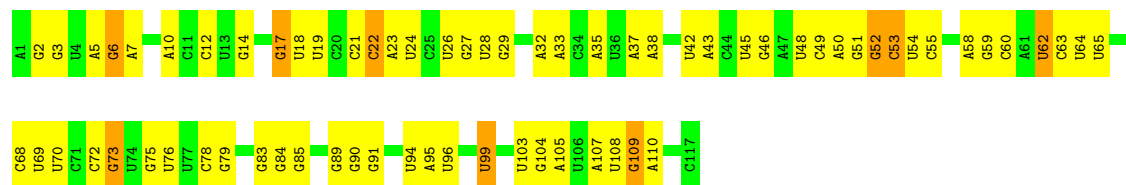
• Molecule 2: 5.8S rRNA

Chain IB: 50% 35% 8% 6%



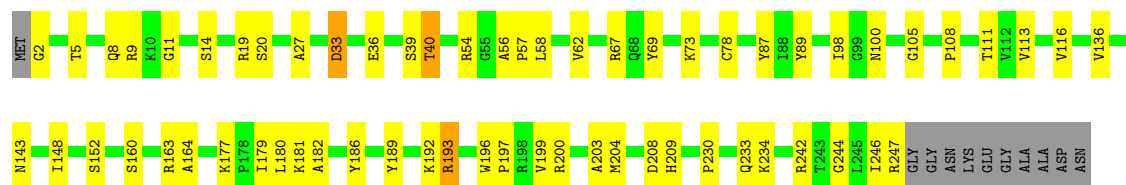
• Molecule 3: 5S rRNA

Chain IC: 41% 51% 8%



• Molecule 4: Large ribosomal subunit protein uL2

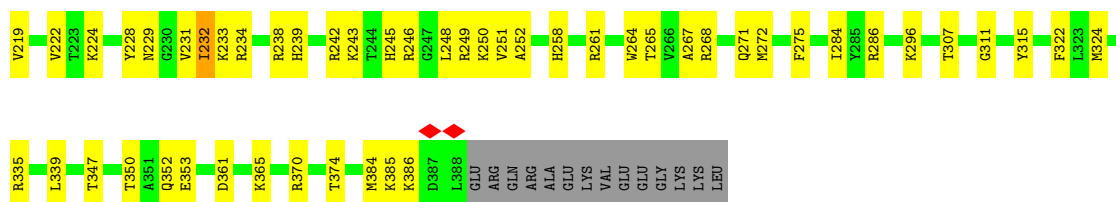
Chain ID: 72% 23% 5%



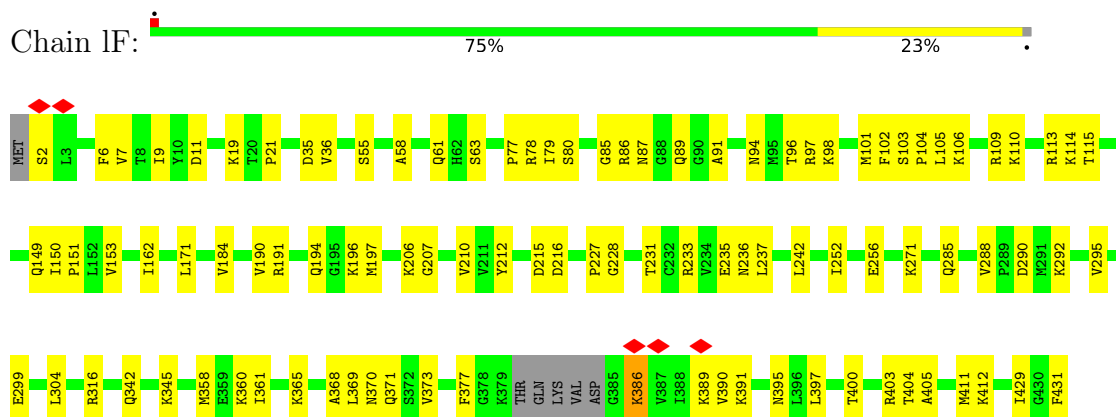
• Molecule 5: 60S ribosomal protein L3, putative

Chain IE: 76% 19% 5%

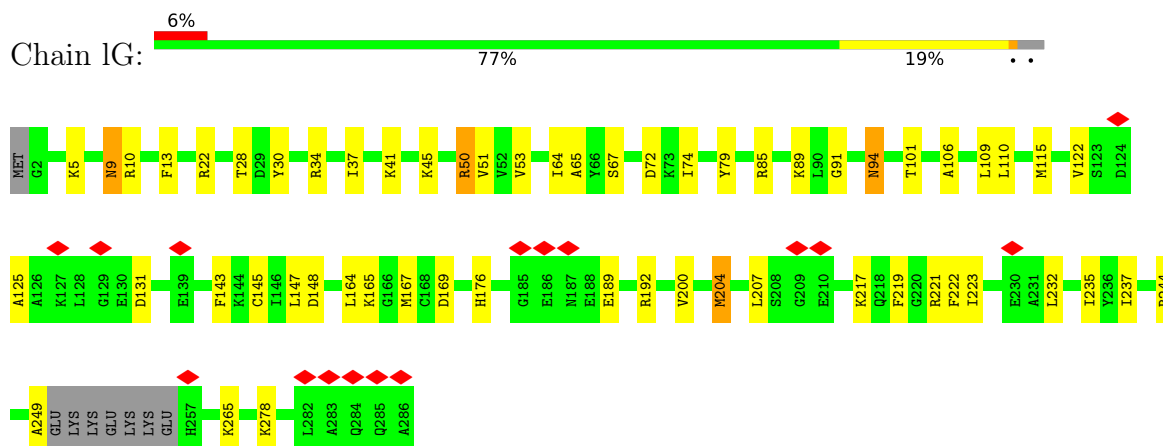




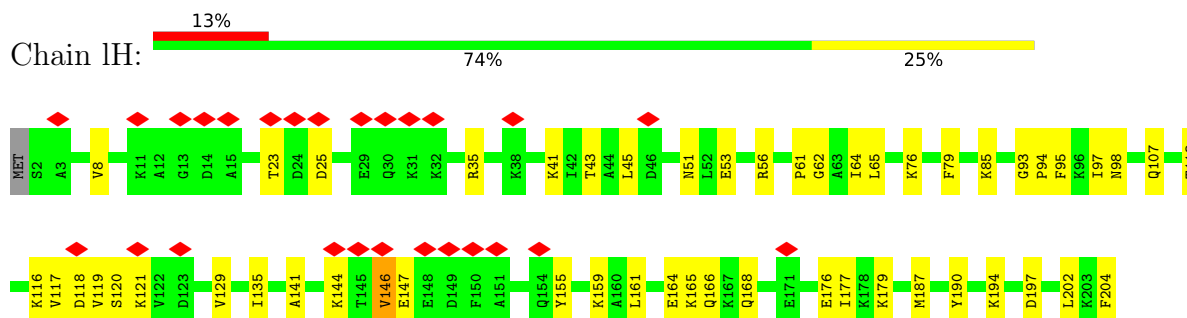
- Molecule 6: 60S ribosomal protein L4, putative



- Molecule 7: 60S ribosomal protein L5, putative

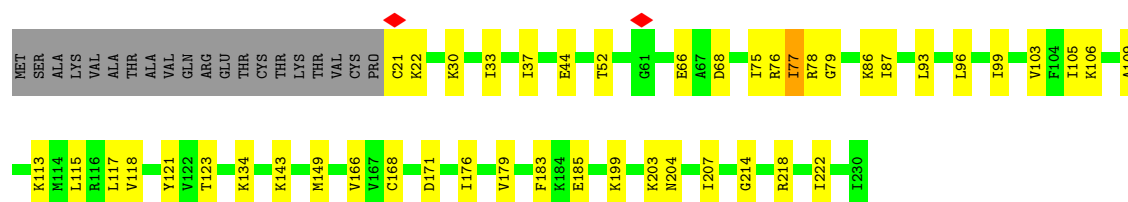


- Molecule 8: Large ribosomal subunit protein eL6

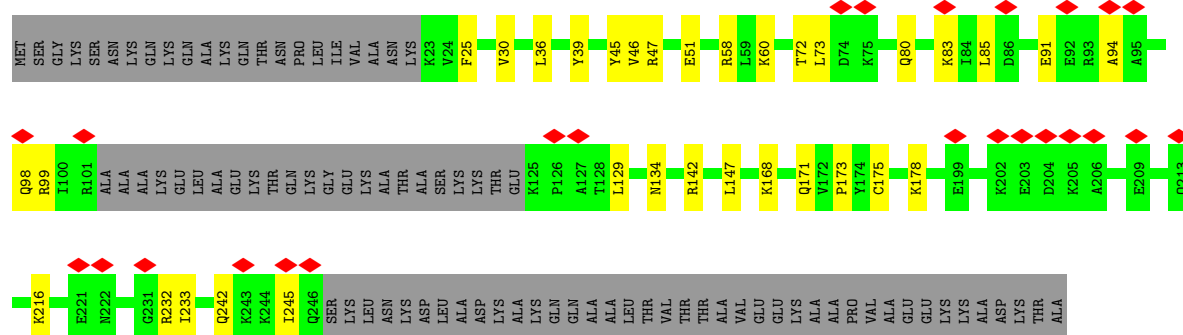


- Molecule 9: 60S ribosomal protein L7, putative

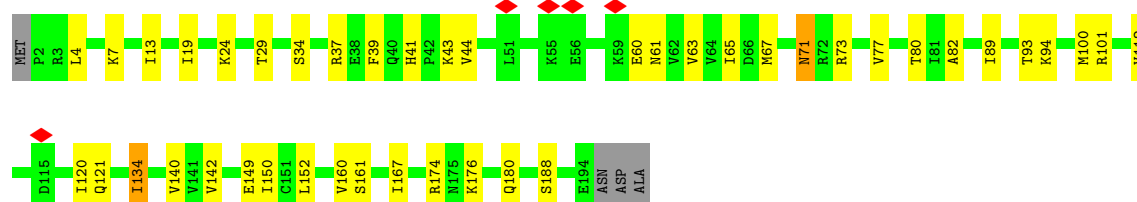
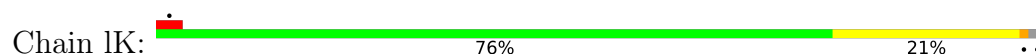




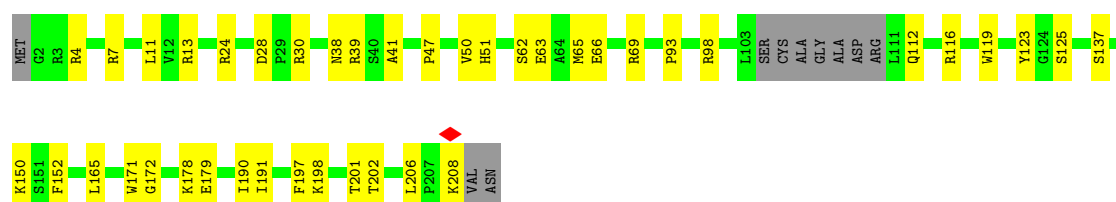
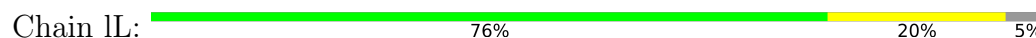
- Molecule 10: 60S ribosomal protein L7a



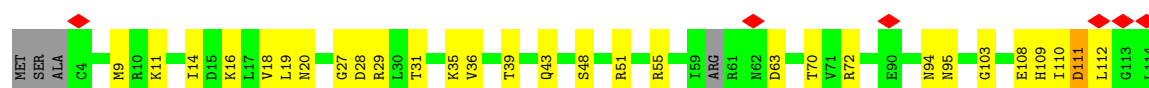
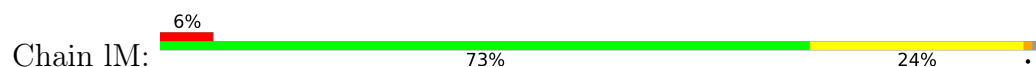
- Molecule 11: 60S ribosomal protein L9, putative



- Molecule 12: Ribosomal protein L10, putative

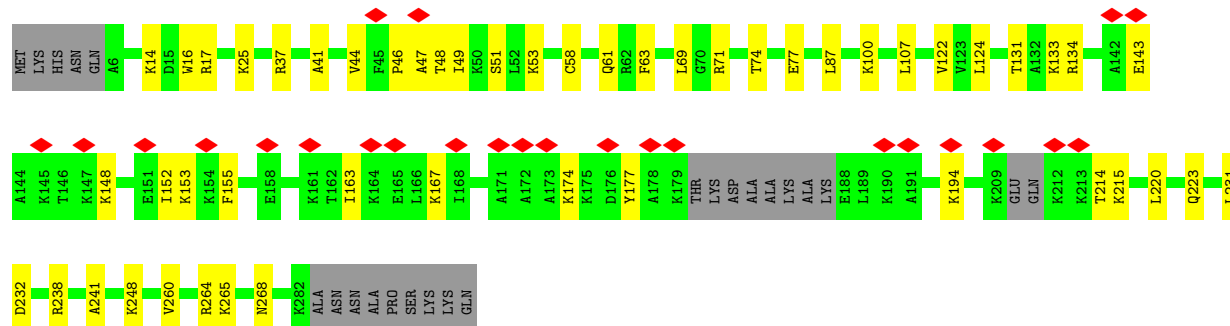
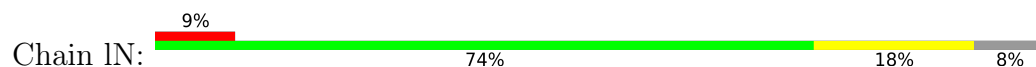


- Molecule 13: 60S ribosomal protein L11, putative

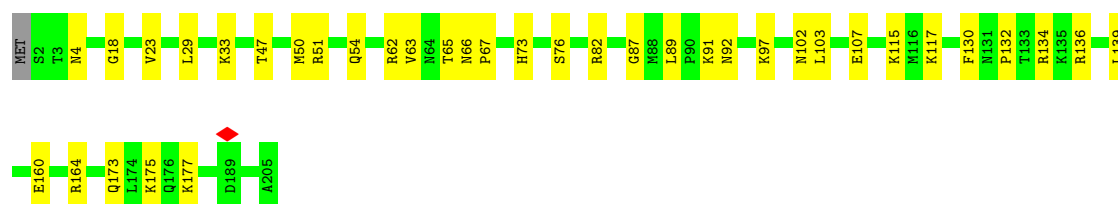
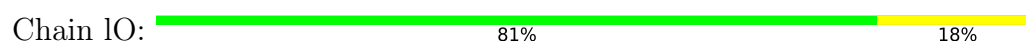




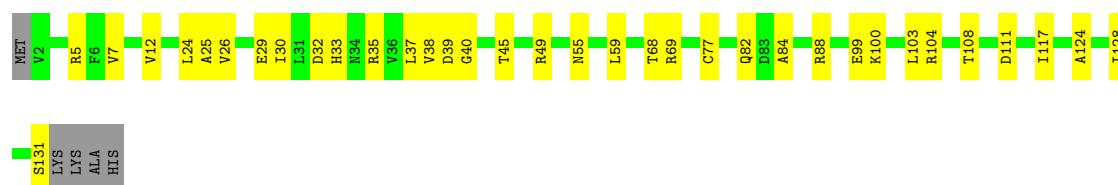
- Molecule 14: 60S ribosomal protein L13, putative



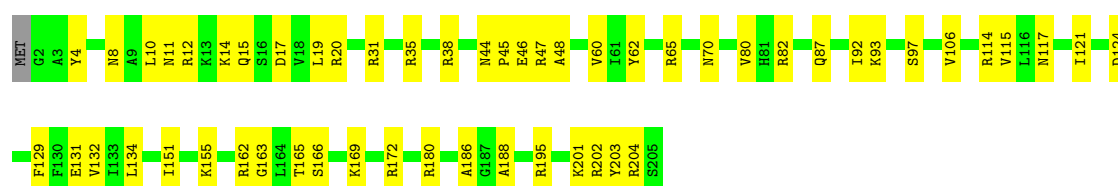
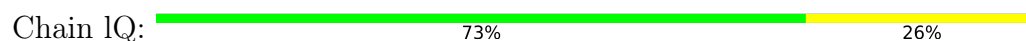
- Molecule 15: 60S ribosomal protein L13, putative



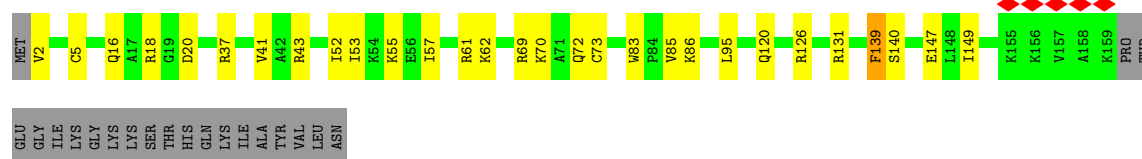
- Molecule 16: 60S ribosomal protein L14, putative



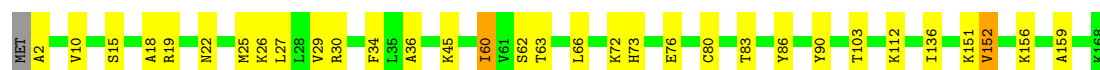
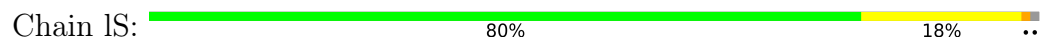
- Molecule 17: Ribosomal protein L15



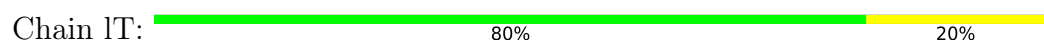
- Molecule 18: 60S ribosomal protein L17, putative



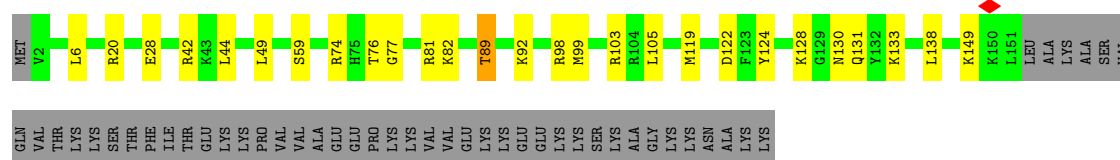
- Molecule 19: 60S ribosomal protein L18, putative



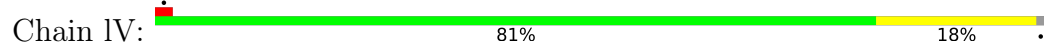
- Molecule 20: 60S ribosomal protein L18a



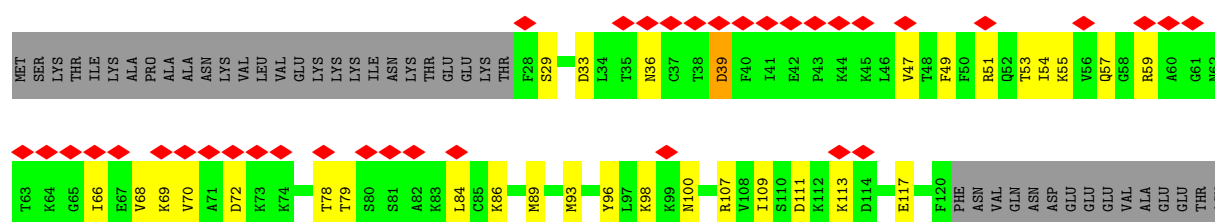
- Molecule 21: Ribosomal protein L19

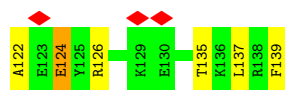


- Molecule 22: 60S ribosomal protein L21, putative

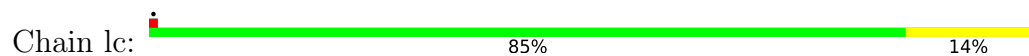


- Molecule 23: Large ribosomal subunit protein eL22

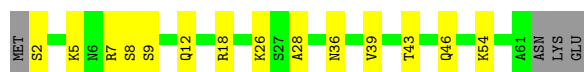




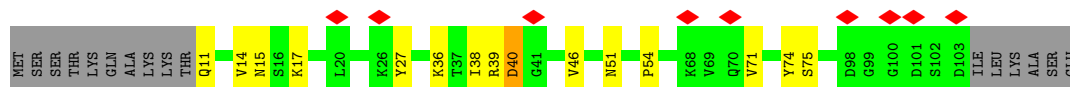
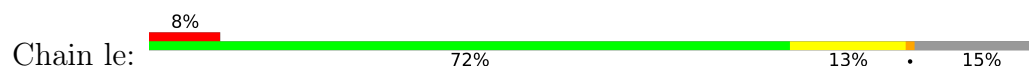
- Molecule 29: Large ribosomal subunit protein uL15A



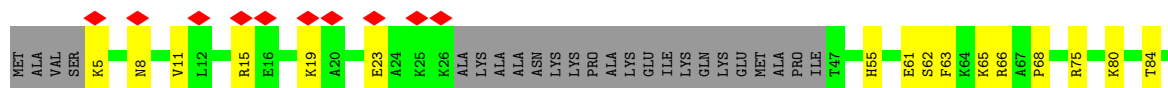
- Molecule 30: 60S ribosomal protein L29



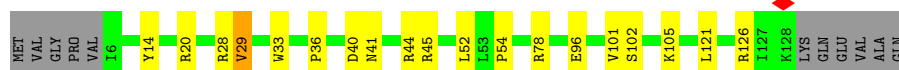
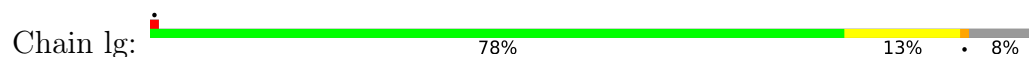
- Molecule 31: 60S ribosomal protein L30, putative



- Molecule 32: 60S ribosomal protein L31, putative

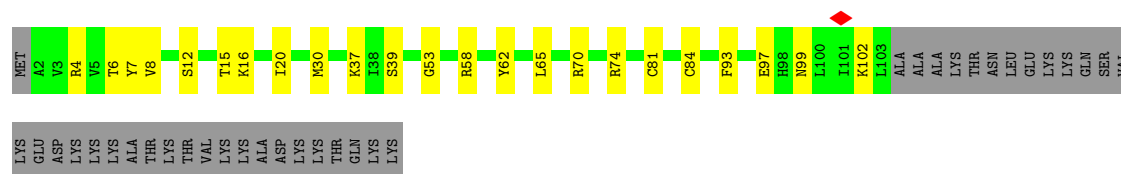


- Molecule 33: 60S ribosomal protein L32, putative

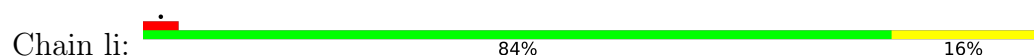


- Molecule 34: 60S ribosomal protein L34, putative

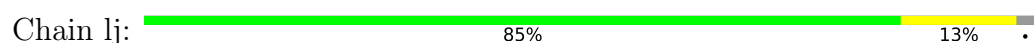




- Molecule 35: uL29



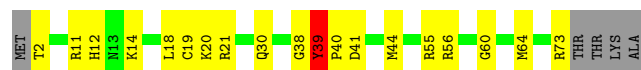
- Molecule 36: 60S ribosomal protein L35a, putative



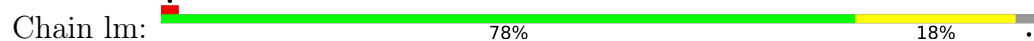
- Molecule 37: 60S ribosomal protein L36, putative



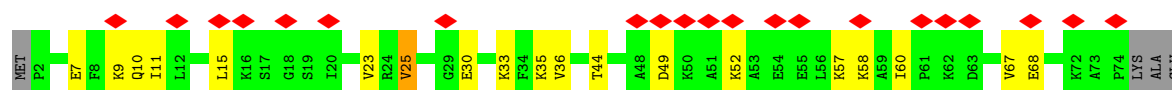
- Molecule 38: 60S ribosomal protein L37-A, putative

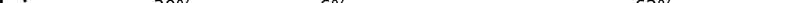


- Molecule 39: 60S ribosomal protein L37a, putative

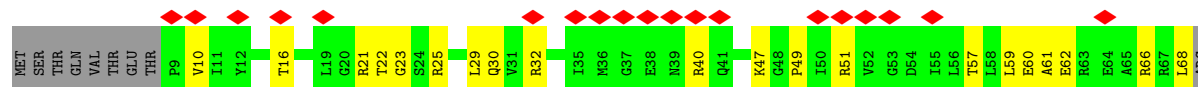


- Molecule 40: 60S ribosomal protein L38 putative



- Chain sC: 

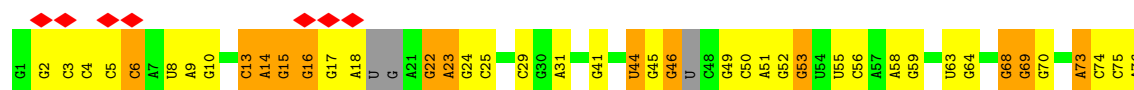
- Molecule 47: 40S ribosomal protein S28, putative



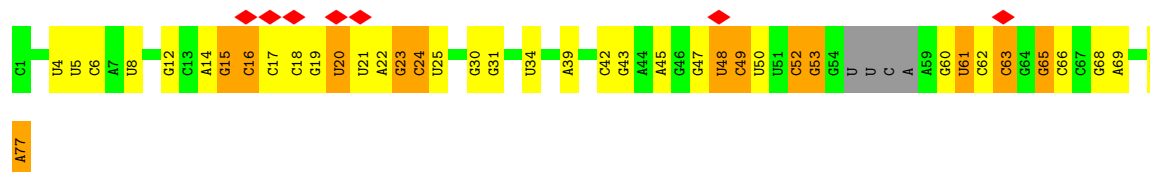
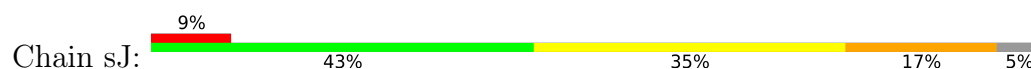
- Molecule 48: Ribosomal protein S29, putative



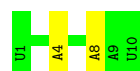
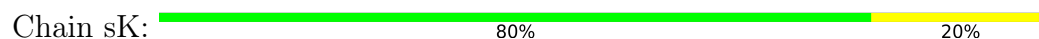
- Molecule 49: A/P-tRNA



- Molecule 50: P/E-tRNA

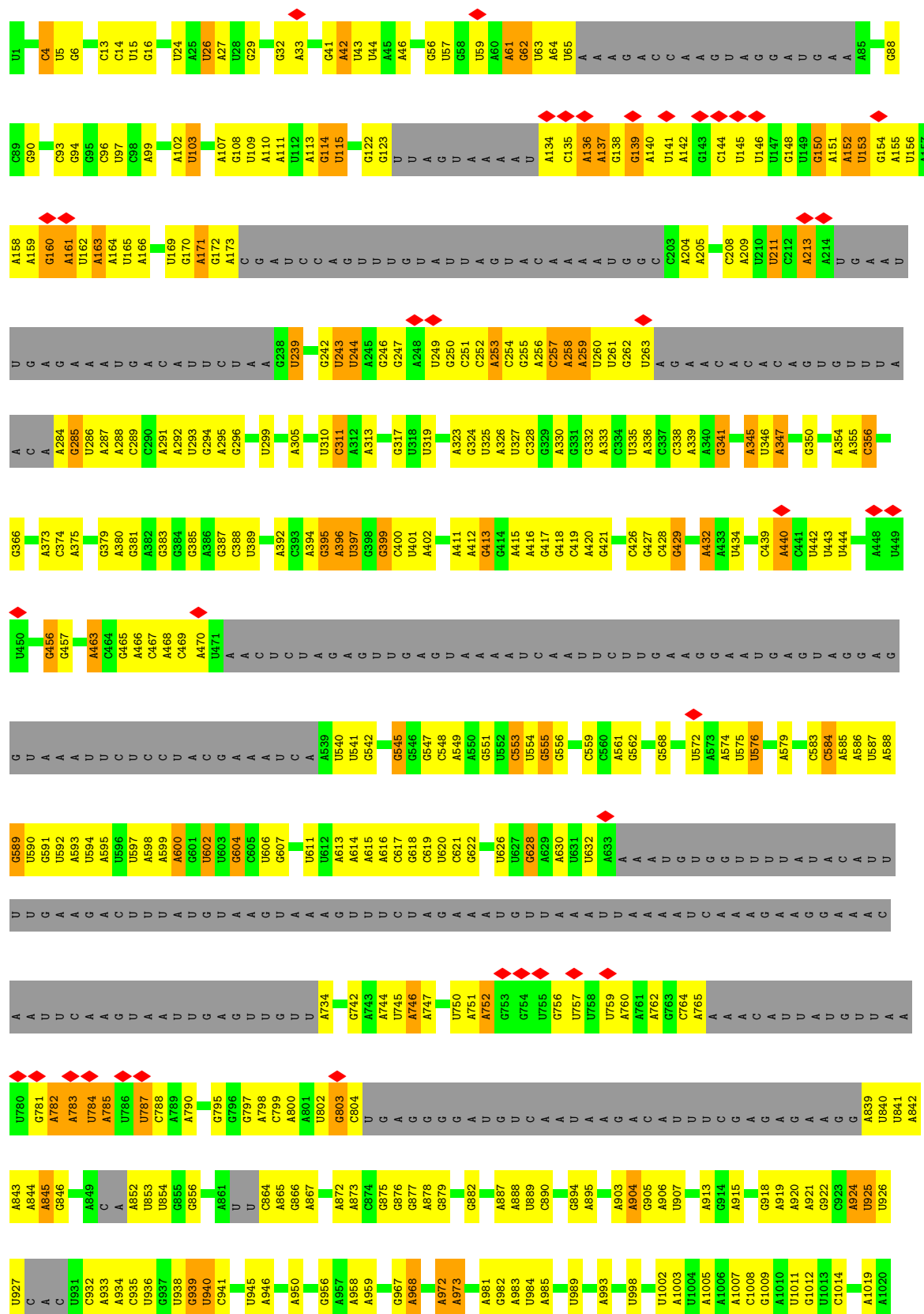


- Molecule 51: mRNA



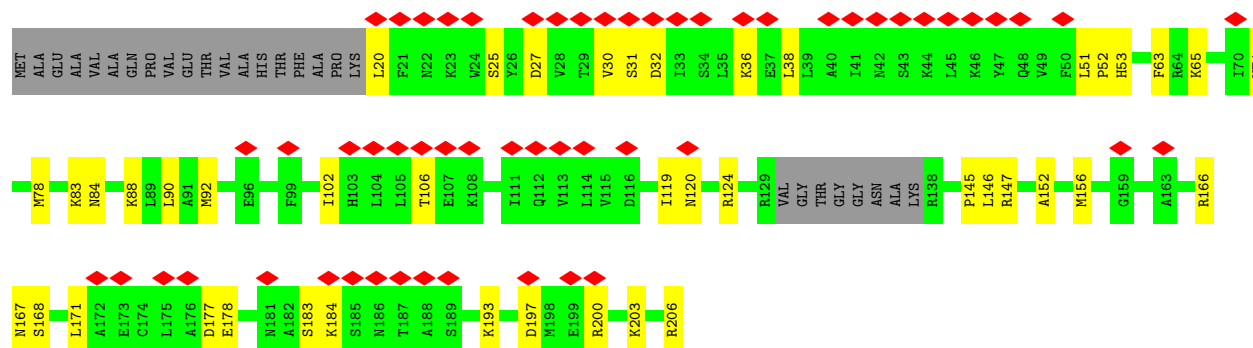
- Molecule 52: 17S rRNA







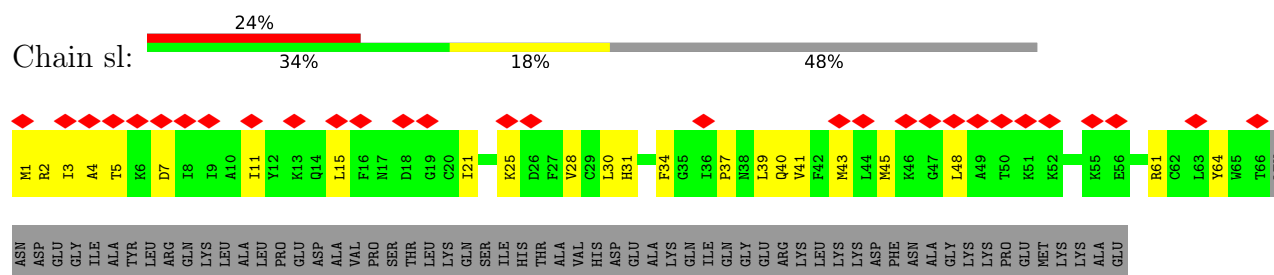
- Molecule 57: Small ribosomal subunit protein uS7



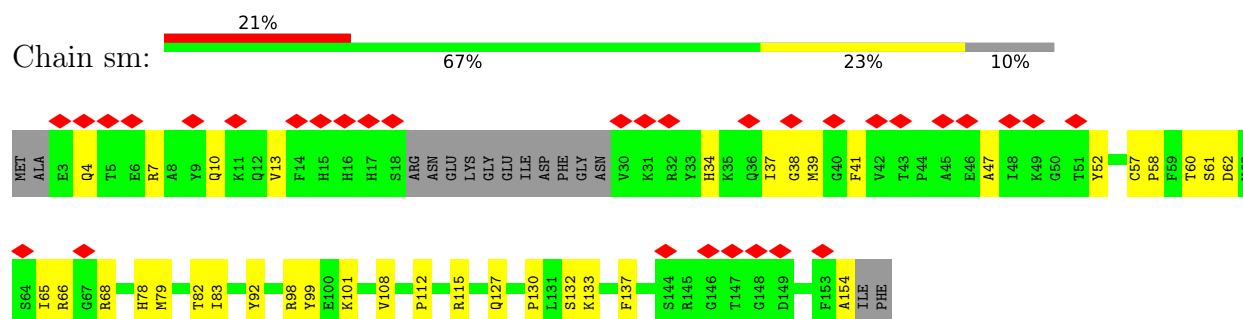
- Molecule 58: 40S ribosomal protein S6



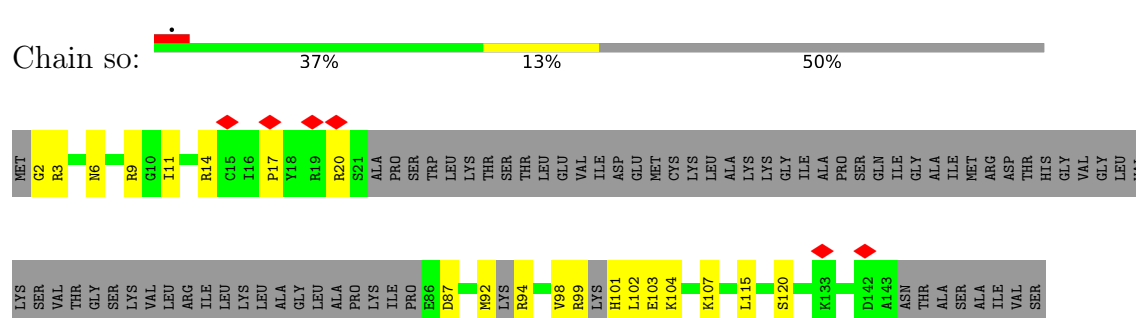
- Molecule 62: 40S ribosomal protein S10, putative



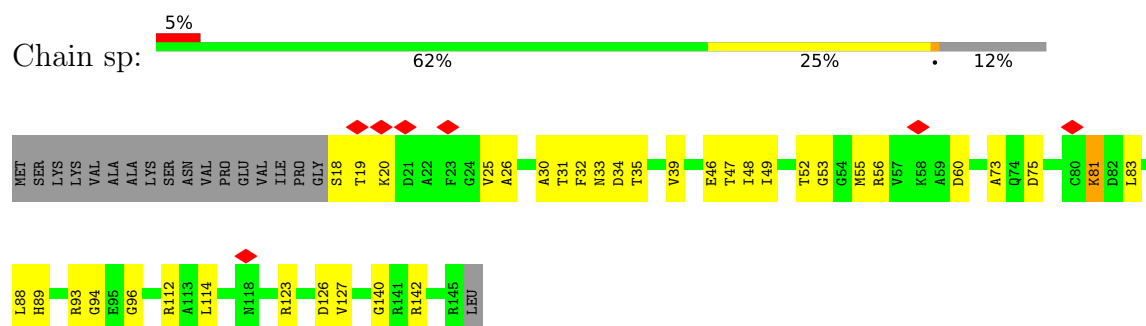
- Molecule 63: 40S ribosomal protein S11, putative



- Molecule 64: 40S ribosomal protein S13, putative

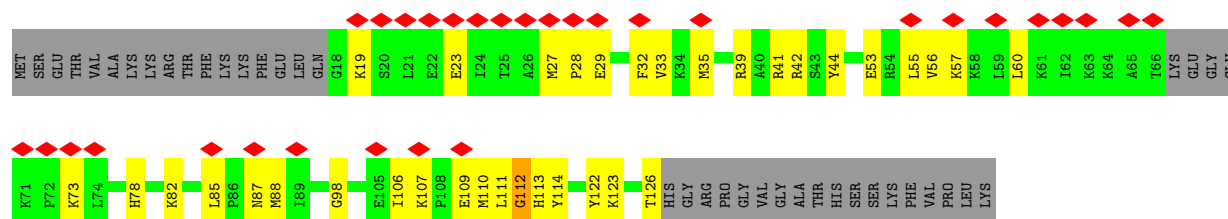


- Molecule 65: Ribosomal protein S14, putative



- Molecule 66: 40S ribosomal protein S15, putative





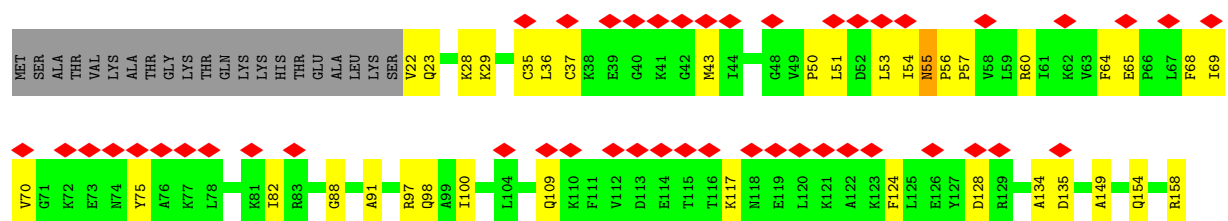
- Molecule 67: 40S ribosomal protein S15a, putative

Chain sr: 74% 25% ..



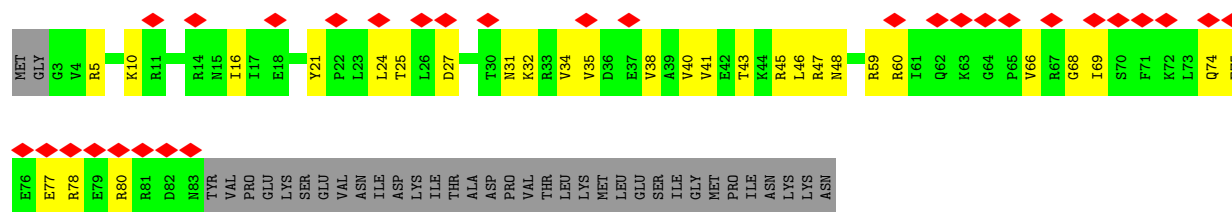
- Molecule 68: 40S ribosomal protein S16, putative

Chain ss: 29% 63% 23% 13%



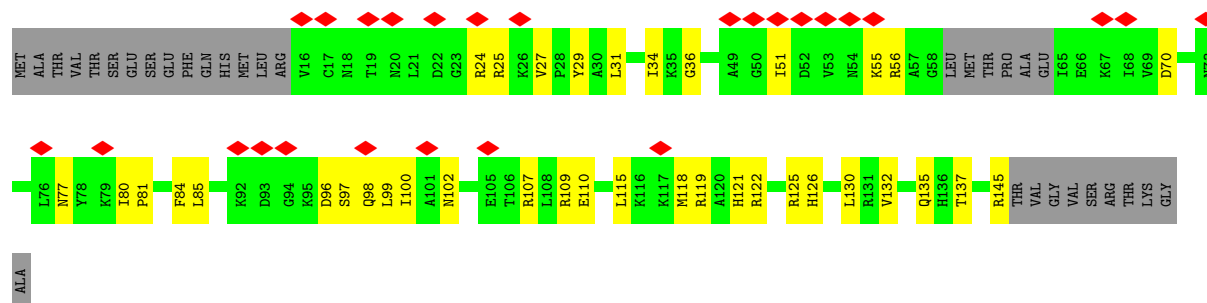
- Molecule 69: 40S ribosomal protein S17, putative

Chain st: 26% 44% 25% 31%

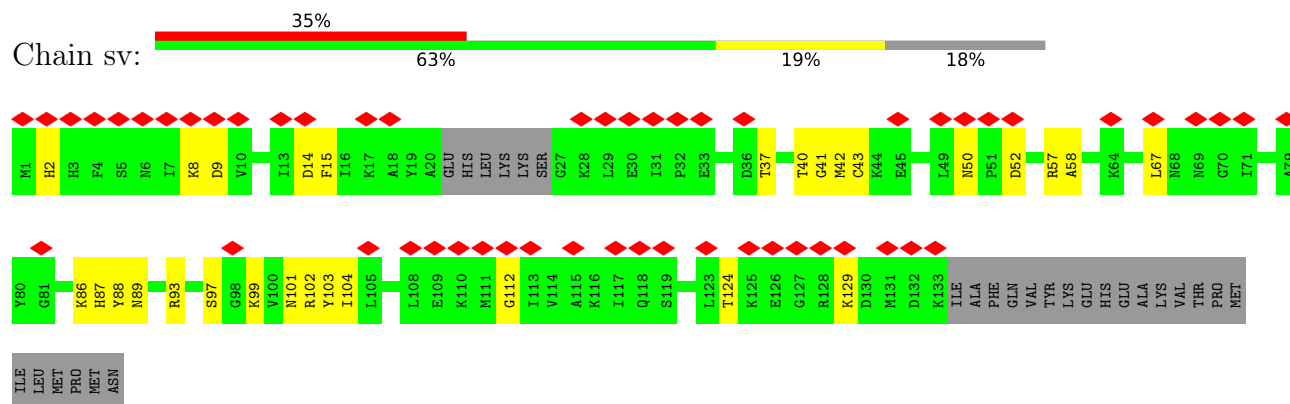


- Molecule 70: Small ribosomal subunit protein uS13

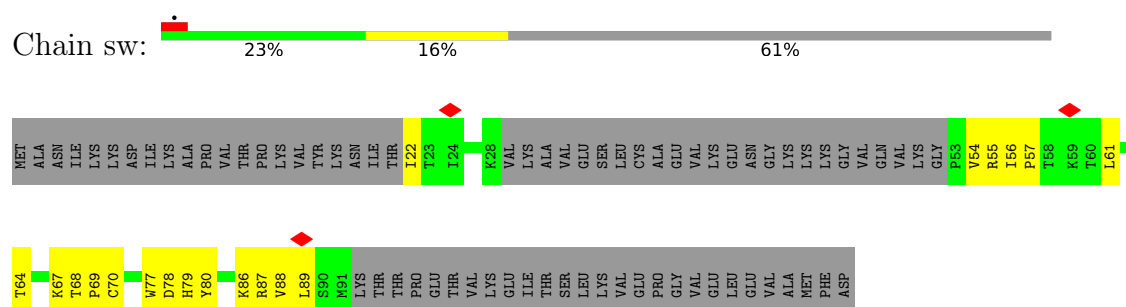
Chain su: 17% 56% 24% 20%



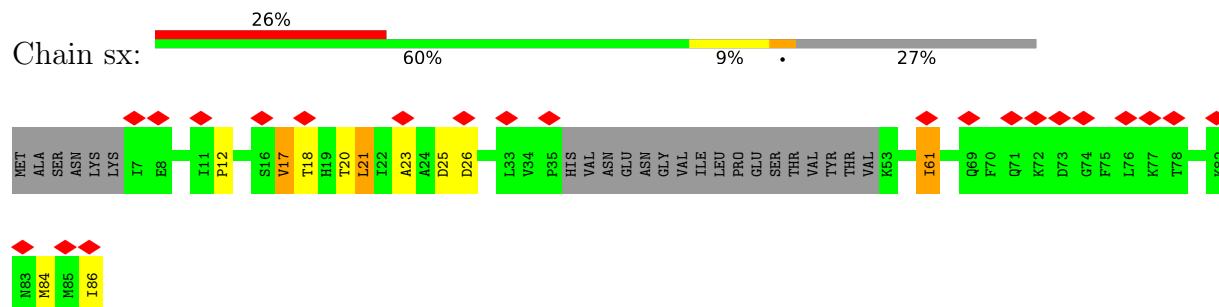
- Molecule 71: Small ribosomal subunit protein eS19



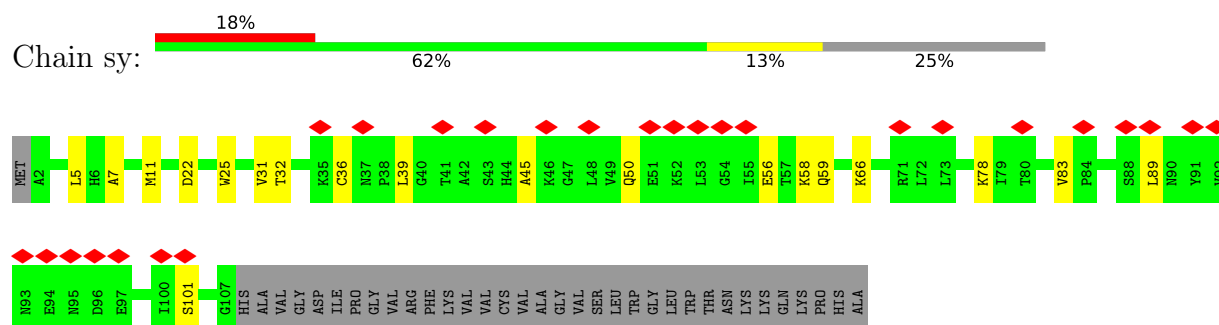
- Molecule 72: 40S ribosomal protein S20, putative



- Molecule 73: 40S ribosomal protein S21



- Molecule 74: 40S ribosomal protein S23, putative



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	54889	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 ($e^-/\text{\AA}^2$)	1.09	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	23.075	Depositor
Minimum map value	-9.423	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.8	Depositor
Map size (Å)	428.00003, 428.00003, 428.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality

5.1 Standard geometry

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

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	1A	0.25	0/75250	0.33	2/117222 (0.0%)
2	1B	0.24	0/3470	0.32	0/5401
3	1C	0.25	0/2765	0.38	2/4303 (0.0%)
4	1D	0.25	0/1920	0.32	0/2582
5	1E	0.23	0/3140	0.30	0/4216
6	1F	0.22	0/3339	0.32	0/4479
7	1G	0.19	0/2248	0.28	0/3013
8	1H	0.17	0/1640	0.33	0/2204
9	1I	0.22	0/1680	0.29	0/2252
10	1J	0.17	0/1670	0.29	0/2243
11	1K	0.19	0/1562	0.27	0/2103
12	1L	0.20	0/1633	0.30	0/2184
13	1M	0.15	0/1369	0.24	0/1834
14	1N	0.19	0/2158	0.28	0/2875
15	1O	0.23	0/1646	0.30	0/2209
16	1P	0.21	0/1033	0.28	0/1389
17	1Q	0.26	0/1707	0.29	0/2276
18	1R	0.25	0/1251	0.29	0/1675
19	1S	0.24	0/1342	0.32	0/1796
20	1T	0.22	0/1445	0.29	0/1946
21	1U	0.21	0/1253	0.28	0/1666
22	1V	0.22	0/1351	0.30	0/1819
23	1W	0.14	0/774	0.37	0/1031
24	1X	0.23	0/1030	0.33	0/1384
25	1Y	0.19	0/941	0.25	0/1262
26	1Z	0.20	0/492	0.28	0/656
27	1a	0.18	0/1673	0.26	0/2236
28	1b	0.17	0/1112	0.26	0/1489
29	1c	0.26	0/1223	0.29	0/1636
30	1d	0.22	0/485	0.25	0/639
31	1e	0.20	0/701	0.29	0/945
32	1f	0.22	0/1050	0.27	0/1402

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	lg	0.24	0/1027	0.28	0/1370
34	lh	0.22	0/818	0.29	0/1094
35	li	0.17	0/984	0.22	0/1310
36	lj	0.27	0/862	0.30	0/1163
37	lk	0.17	0/721	0.24	0/955
38	ll	0.27	0/602	0.35	0/797
39	lm	0.22	0/701	0.34	0/934
40	ln	0.18	0/592	0.29	0/789
41	lo	0.26	0/444	0.29	0/587
42	lp	0.23	0/425	0.48	1/563 (0.2%)
43	lq	0.23	0/770	0.27	0/1019
44	sA	0.14	0/94	0.44	0/128
45	sB	0.14	0/797	0.25	0/1062
46	sC	0.13	0/255	0.29	0/346
47	sD	0.15	0/470	0.30	0/630
48	sE	0.14	0/449	0.31	0/595
49	sI	0.16	0/1737	0.38	0/2702
50	sJ	0.17	0/1727	0.40	0/2684
51	sK	0.16	0/241	0.27	0/373
52	sa	0.15	0/33554	0.28	0/52257
53	sc	0.13	0/1528	0.24	0/2064
54	sd	0.11	0/1456	0.27	0/1949
55	se	0.14	0/1174	0.31	0/1555
56	sf	0.11	0/2072	0.28	0/2792
57	sg	0.11	0/1443	0.26	0/1938
58	sh	0.11	0/402	0.26	0/535
59	si	0.11	0/453	0.28	0/610
60	sj	0.12	0/1021	0.27	0/1366
61	sk	0.09	0/688	0.25	0/916
62	sl	0.11	0/549	0.26	0/740
63	sm	0.12	0/1187	0.25	0/1586
64	so	0.13	0/654	0.22	0/866
65	sp	0.14	0/977	0.28	0/1311
66	sq	0.12	0/856	0.33	0/1143
67	sr	0.15	0/1040	0.31	0/1404
68	ss	0.11	0/1093	0.25	0/1466
69	st	0.11	0/684	0.24	0/914
70	su	0.13	0/1020	0.33	0/1364
71	sv	0.11	0/1034	0.23	0/1388
72	sw	0.12	0/382	0.24	0/512
73	sx	0.13	0/502	0.28	0/676
74	sy	0.12	0/848	0.30	0/1131
All	All	0.21	0/192686	0.31	5/283951 (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
6	lF	0	1
38	ll	0	1
48	sE	0	1
67	sr	0	1
All	All	0	4

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	lC	62	U	OP2-P-O3'	-8.61	82.16	108.00
3	lC	62	U	OP1-P-O3'	-8.53	82.42	108.00
42	lp	24	CYS	CA-CB-SG	7.16	130.87	114.40
1	lA	2468	C	P-O3'-C3'	-5.13	112.50	120.20
1	lA	2468	C	O3'-P-O5'	5.10	111.66	104.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	lF	368	ALA	Peptide
38	ll	39	TYR	Peptide
48	sE	15	GLY	Peptide
67	sr	76	SER	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	lA	67153	0	33687	1002	0
2	lB	3097	0	1552	49	0
3	lC	2477	0	1252	71	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	ID	1881	0	1928	53	0
5	IE	3076	0	3209	63	0
6	IF	3281	0	3513	75	0
7	IG	2209	0	2287	43	0
8	IH	1608	0	1728	33	0
9	II	1658	0	1802	31	0
10	IJ	1640	0	1749	20	0
11	IK	1538	0	1598	28	0
12	IL	1597	0	1654	29	0
13	IM	1350	0	1390	34	0
14	IN	2130	0	2338	41	0
15	IO	1616	0	1700	25	0
16	IP	1021	0	1107	25	0
17	IQ	1676	0	1777	45	0
18	IR	1232	0	1307	22	0
19	IS	1321	0	1427	25	0
20	IT	1413	0	1479	26	0
21	IU	1235	0	1369	25	0
22	IV	1320	0	1406	23	0
23	IW	763	0	818	20	0
24	IX	1015	0	1054	23	0
25	IY	926	0	997	16	0
26	IZ	481	0	518	11	0
27	la	1651	0	1822	30	0
28	lb	1094	0	1174	27	0
29	lc	1192	0	1205	18	0
30	ld	478	0	507	13	0
31	le	693	0	721	9	0
32	lf	1032	0	1095	20	0
33	lg	1010	0	1091	16	0
34	lh	805	0	849	19	0
35	li	974	0	1093	13	0
36	lj	841	0	878	7	0
37	lk	712	0	755	21	0
38	ll	591	0	617	16	0
39	lm	693	0	738	10	0
40	ln	584	0	643	13	0
41	lo	432	0	444	10	0
42	lp	420	0	450	16	0
43	lq	756	0	821	16	0
44	sA	91	0	88	2	0
45	sB	787	0	833	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	sC	249	0	259	6	0
47	sD	468	0	500	15	0
48	sE	442	0	444	15	0
49	sI	1556	0	795	18	0
50	sJ	1549	0	789	20	0
51	sK	215	0	108	2	0
52	sa	29968	0	15064	504	0
53	sc	1499	0	1565	23	0
54	sd	1440	0	1522	29	0
55	se	1166	0	1227	29	0
56	sf	2031	0	2145	63	0
57	sg	1424	0	1485	38	0
58	sh	400	0	415	12	0
59	si	445	0	466	10	0
60	sj	1009	0	1055	40	0
61	sk	677	0	724	14	0
62	sl	536	0	559	19	0
63	sm	1161	0	1181	28	0
64	so	644	0	664	15	0
65	sp	964	0	988	27	0
66	sq	842	0	913	30	0
67	sr	1022	0	1051	28	0
68	ss	1076	0	1151	29	0
69	st	676	0	718	19	0
70	su	1006	0	1049	28	0
71	sv	1015	0	1043	20	0
72	sw	376	0	405	16	0
73	sx	494	0	508	8	0
74	sy	836	0	885	14	0
75	sa	42	0	45	1	0
All	All	178778	0	130193	2752	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 9.

The worst 5 of 2752 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)
1:lA:805:G:H21	1:lA:1496:A:N6	1.45	1.13
1:lA:869:G:N2	1:lA:872:A:H62	1.48	1.11
52:sa:139:G:H1	52:sa:166:A:N6	1.48	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:869:G:H21	1:1A:872:A:N6	1.52	1.07
3:1C:79:G:N1	3:1C:95:A:C2	2.24	1.03

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	
4	1D	244/257 (95%)	226 (93%)	18 (7%)	0	100	100
5	1E	385/402 (96%)	362 (94%)	23 (6%)	0	100	100
6	1F	421/431 (98%)	392 (93%)	28 (7%)	1 (0%)	43	73
7	1G	274/286 (96%)	255 (93%)	19 (7%)	0	100	100
8	1H	201/204 (98%)	185 (92%)	14 (7%)	2 (1%)	12	41
9	1I	208/230 (90%)	199 (96%)	8 (4%)	1 (0%)	24	57
10	1J	197/286 (69%)	188 (95%)	9 (5%)	0	100	100
11	1K	191/197 (97%)	184 (96%)	6 (3%)	1 (0%)	24	57
12	1L	196/210 (93%)	184 (94%)	12 (6%)	0	100	100
13	1M	166/174 (95%)	162 (98%)	3 (2%)	1 (1%)	21	52
14	1N	261/291 (90%)	247 (95%)	14 (5%)	0	100	100
15	1O	202/205 (98%)	192 (95%)	10 (5%)	0	100	100
16	1P	128/135 (95%)	124 (97%)	4 (3%)	0	100	100
17	1Q	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
18	1R	156/179 (87%)	148 (95%)	8 (5%)	0	100	100
19	1S	165/168 (98%)	151 (92%)	14 (8%)	0	100	100
20	1T	171/173 (99%)	162 (95%)	9 (5%)	0	100	100
21	1U	148/198 (75%)	145 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	IV	163/166 (98%)	157 (96%)	6 (4%)	0	100	100
23	IW	91/137 (66%)	83 (91%)	8 (9%)	0	100	100
24	IX	131/140 (94%)	125 (95%)	6 (5%)	0	100	100
25	IY	114/121 (94%)	112 (98%)	2 (2%)	0	100	100
26	IZ	55/163 (34%)	54 (98%)	1 (2%)	0	100	100
27	la	208/213 (98%)	197 (95%)	11 (5%)	0	100	100
28	lb	135/139 (97%)	132 (98%)	3 (2%)	0	100	100
29	lc	146/149 (98%)	134 (92%)	12 (8%)	0	100	100
30	ld	58/64 (91%)	54 (93%)	4 (7%)	0	100	100
31	le	91/109 (84%)	81 (89%)	10 (11%)	0	100	100
32	lf	122/150 (81%)	115 (94%)	7 (6%)	0	100	100
33	lg	121/134 (90%)	118 (98%)	3 (2%)	0	100	100
34	lh	100/137 (73%)	98 (98%)	2 (2%)	0	100	100
35	li	120/122 (98%)	118 (98%)	1 (1%)	1 (1%)	16	47
36	lj	104/108 (96%)	98 (94%)	6 (6%)	0	100	100
37	lk	83/104 (80%)	81 (98%)	2 (2%)	0	100	100
38	ll	70/77 (91%)	63 (90%)	5 (7%)	2 (3%)	3	19
39	lm	88/93 (95%)	82 (93%)	6 (7%)	0	100	100
40	ln	71/77 (92%)	68 (96%)	3 (4%)	0	100	100
41	lo	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
42	lp	51/56 (91%)	48 (94%)	3 (6%)	0	100	100
43	lq	90/98 (92%)	89 (99%)	1 (1%)	0	100	100
44	sA	8/137 (6%)	6 (75%)	2 (25%)	0	100	100
45	sB	96/144 (67%)	93 (97%)	3 (3%)	0	100	100
46	sC	30/84 (36%)	30 (100%)	0	0	100	100
47	sD	58/69 (84%)	52 (90%)	6 (10%)	0	100	100
48	sE	53/56 (95%)	50 (94%)	3 (6%)	0	100	100
53	sc	194/255 (76%)	184 (95%)	10 (5%)	0	100	100
54	sd	184/244 (75%)	174 (95%)	10 (5%)	0	100	100
55	se	126/256 (49%)	121 (96%)	4 (3%)	1 (1%)	16	47
56	sf	254/326 (78%)	231 (91%)	23 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	sg	175/206 (85%)	166 (95%)	9 (5%)	0	100	100
58	sh	49/266 (18%)	48 (98%)	1 (2%)	0	100	100
59	si	53/201 (26%)	53 (100%)	0	0	100	100
60	sj	125/237 (53%)	120 (96%)	5 (4%)	0	100	100
61	sk	80/185 (43%)	79 (99%)	1 (1%)	0	100	100
62	sl	64/127 (50%)	63 (98%)	1 (2%)	0	100	100
63	sm	137/156 (88%)	127 (93%)	10 (7%)	0	100	100
64	so	68/151 (45%)	66 (97%)	2 (3%)	0	100	100
65	sp	126/146 (86%)	119 (94%)	7 (6%)	0	100	100
66	sq	101/144 (70%)	92 (91%)	8 (8%)	1 (1%)	12	41
67	sr	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
68	ss	135/158 (85%)	129 (96%)	6 (4%)	0	100	100
69	st	79/117 (68%)	79 (100%)	0	0	100	100
70	su	120/155 (77%)	108 (90%)	12 (10%)	0	100	100
71	sv	123/155 (79%)	116 (94%)	7 (6%)	0	100	100
72	sw	42/118 (36%)	42 (100%)	0	0	100	100
73	sx	59/86 (69%)	57 (97%)	2 (3%)	0	100	100
74	sy	104/141 (74%)	97 (93%)	7 (7%)	0	100	100
All	All	8946/11289 (79%)	8471 (95%)	464 (5%)	11 (0%)	49	78

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	ll	40	PRO
55	se	193	ASN
6	lF	390	VAL
8	lH	119	VAL
13	lM	28	ASP

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	
4	ID	195/201 (97%)	191 (98%)	4 (2%)	47	71
5	IE	330/343 (96%)	325 (98%)	5 (2%)	57	75
6	IF	339/345 (98%)	331 (98%)	8 (2%)	43	69
7	IG	223/231 (96%)	217 (97%)	6 (3%)	39	67
8	IH	172/173 (99%)	168 (98%)	4 (2%)	44	70
9	II	178/195 (91%)	176 (99%)	2 (1%)	65	78
10	IJ	177/242 (73%)	175 (99%)	2 (1%)	65	78
11	IK	171/174 (98%)	170 (99%)	1 (1%)	78	83
12	IL	169/176 (96%)	166 (98%)	3 (2%)	51	73
13	IM	144/147 (98%)	135 (94%)	9 (6%)	16	45
14	IN	224/243 (92%)	221 (99%)	3 (1%)	61	77
15	IO	167/168 (99%)	166 (99%)	1 (1%)	78	83
16	IP	114/118 (97%)	113 (99%)	1 (1%)	70	80
17	IQ	171/172 (99%)	171 (100%)	0	100	100
18	IR	129/147 (88%)	126 (98%)	3 (2%)	44	70
19	IS	142/143 (99%)	138 (97%)	4 (3%)	38	66
20	IT	156/156 (100%)	156 (100%)	0	100	100
21	IU	132/174 (76%)	130 (98%)	2 (2%)	57	75
22	IV	144/145 (99%)	141 (98%)	3 (2%)	47	71
23	IW	86/125 (69%)	83 (96%)	3 (4%)	32	62
24	IX	109/113 (96%)	105 (96%)	4 (4%)	30	61
25	IY	99/102 (97%)	98 (99%)	1 (1%)	68	79
26	IZ	52/137 (38%)	51 (98%)	1 (2%)	50	73
27	la	177/179 (99%)	173 (98%)	4 (2%)	44	70
28	lb	121/123 (98%)	119 (98%)	2 (2%)	53	74
29	lc	120/121 (99%)	116 (97%)	4 (3%)	33	63
30	ld	50/54 (93%)	50 (100%)	0	100	100
31	le	78/92 (85%)	75 (96%)	3 (4%)	29	60
32	lf	110/128 (86%)	107 (97%)	3 (3%)	39	67
33	lg	107/116 (92%)	106 (99%)	1 (1%)	70	80
34	lh	86/116 (74%)	85 (99%)	1 (1%)	63	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	li	103/103 (100%)	100 (97%)	3 (3%)	37	66
36	lj	89/91 (98%)	88 (99%)	1 (1%)	65	78
37	lk	71/82 (87%)	70 (99%)	1 (1%)	59	76
38	ll	60/64 (94%)	60 (100%)	0	100	100
39	lm	73/75 (97%)	70 (96%)	3 (4%)	27	59
40	ln	63/66 (96%)	60 (95%)	3 (5%)	23	54
41	lo	44/45 (98%)	42 (96%)	2 (4%)	24	56
42	lp	45/48 (94%)	45 (100%)	0	100	100
43	lq	85/91 (93%)	84 (99%)	1 (1%)	63	78
44	sA	10/112 (9%)	9 (90%)	1 (10%)	7	29
45	sB	87/127 (68%)	83 (95%)	4 (5%)	24	55
46	sC	28/73 (38%)	25 (89%)	3 (11%)	6	25
47	sD	50/59 (85%)	46 (92%)	4 (8%)	11	37
48	sE	45/46 (98%)	43 (96%)	2 (4%)	25	56
53	sc	157/199 (79%)	153 (98%)	4 (2%)	42	69
54	sd	156/206 (76%)	151 (97%)	5 (3%)	34	64
55	se	130/225 (58%)	127 (98%)	3 (2%)	44	70
56	sf	223/283 (79%)	220 (99%)	3 (1%)	61	77
57	sg	160/178 (90%)	160 (100%)	0	100	100
58	sh	42/220 (19%)	39 (93%)	3 (7%)	13	41
59	si	48/167 (29%)	46 (96%)	2 (4%)	26	58
60	sj	108/205 (53%)	106 (98%)	2 (2%)	50	73
61	sk	72/164 (44%)	72 (100%)	0	100	100
62	sl	60/111 (54%)	60 (100%)	0	100	100
63	sm	126/138 (91%)	124 (98%)	2 (2%)	55	75
64	so	68/129 (53%)	67 (98%)	1 (2%)	57	75
65	sp	99/114 (87%)	96 (97%)	3 (3%)	36	65
66	sq	94/127 (74%)	94 (100%)	0	100	100
67	sr	112/113 (99%)	109 (97%)	3 (3%)	39	67
68	ss	111/128 (87%)	108 (97%)	3 (3%)	39	67
69	st	73/106 (69%)	72 (99%)	1 (1%)	59	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	su	104/130 (80%)	101 (97%)	3 (3%)	37	66
71	sv	106/132 (80%)	104 (98%)	2 (2%)	50	73
72	sw	44/107 (41%)	44 (100%)	0	100	100
73	sx	56/77 (73%)	53 (95%)	3 (5%)	20	50
74	sy	86/114 (75%)	85 (99%)	1 (1%)	63	78
All	All	7760/9554 (81%)	7600 (98%)	160 (2%)	46	71

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

Mol	Chain	Res	Type
48	sE	55	LEU
65	sp	126	ASP
53	sc	216	THR
56	sf	214	ASN
69	st	69	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 67 such sidechains are listed below:

Mol	Chain	Res	Type
61	sk	33	GLN
62	sl	17	ASN
74	sy	59	GLN
18	lR	25	HIS
17	lQ	156	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	lA	3127/3503 (89%)	593 (18%)	0
2	lB	143/155 (92%)	31 (21%)	0
3	lC	116/117 (99%)	18 (15%)	0
49	sI	70/76 (92%)	30 (42%)	0
50	sJ	71/77 (92%)	30 (42%)	0
51	sK	9/10 (90%)	0	0
52	sa	1383/1947 (71%)	305 (22%)	0
All	All	4919/5885 (83%)	1007 (20%)	0

5 of 1007 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	lA	18	G
1	lA	22	A
1	lA	29	U
1	lA	30	A
1	lA	36	A

There are no RNA pucker outliers to report.

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](#)

1 ligand is 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	$\# Z > 2$
75	PAR	sa	5101	-	44,45,45	0.71	0	63,67,67	0.83	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
75	PAR	sa	5101	-	-	3/18/94/94	0/4/4/4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

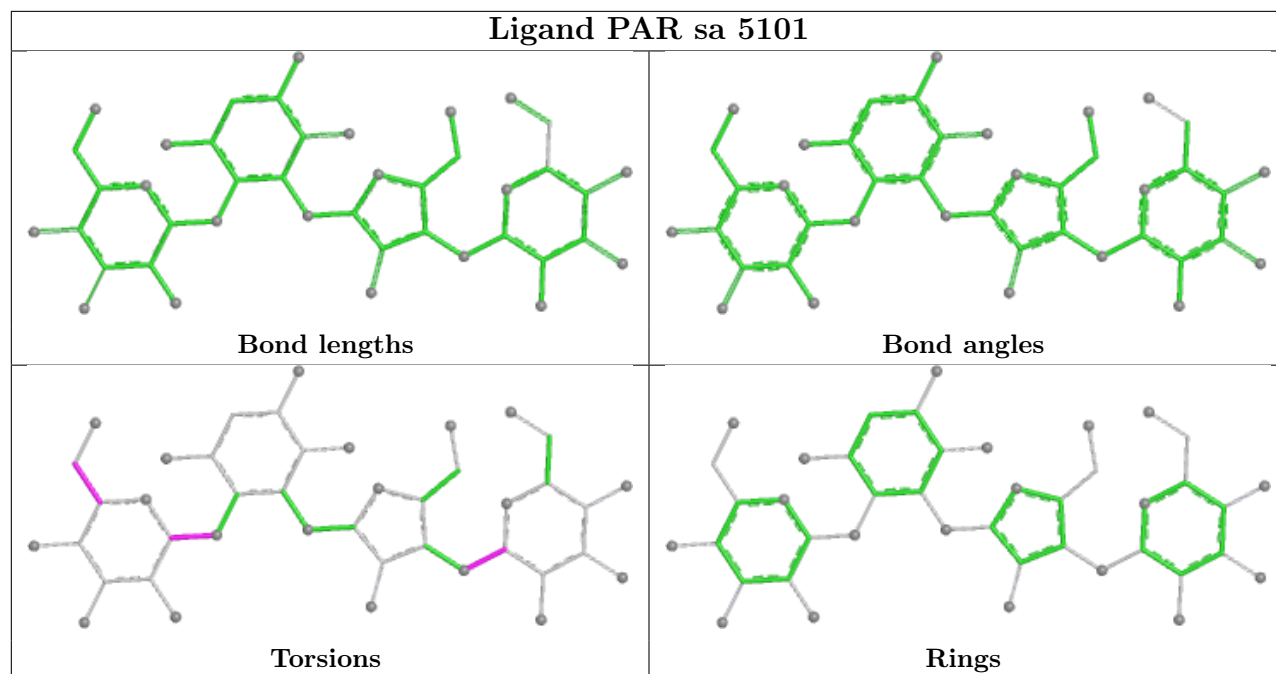
Mol	Chain	Res	Type	Atoms
75	sa	5101	PAR	O54-C14-O33-C33
75	sa	5101	PAR	O51-C51-C61-O61
75	sa	5101	PAR	O51-C11-O11-C42

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
75	sa	5101	PAR	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

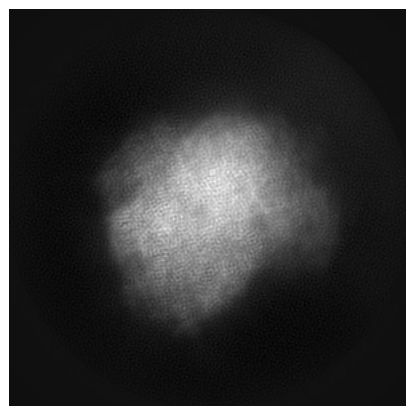
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64718. These allow visual inspection of the internal detail of the map and identification of artifacts.

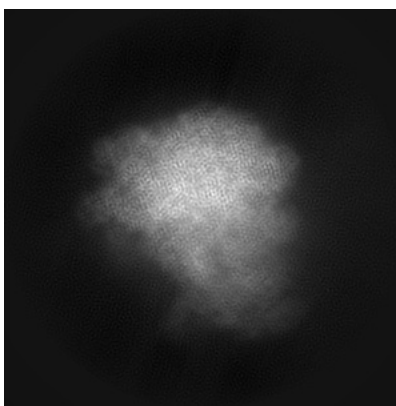
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

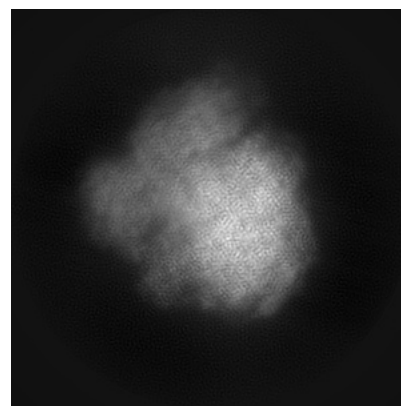
6.1.1 Primary map



X

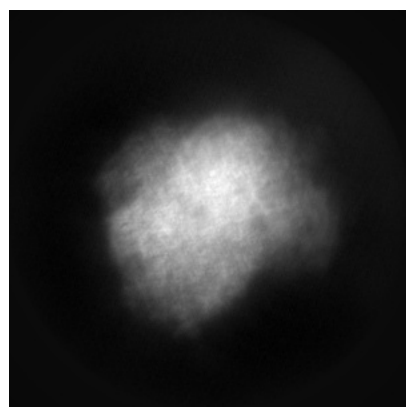


Y

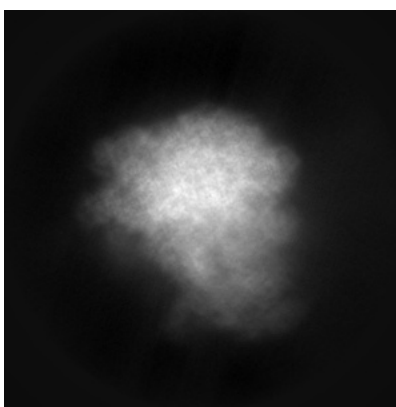


Z

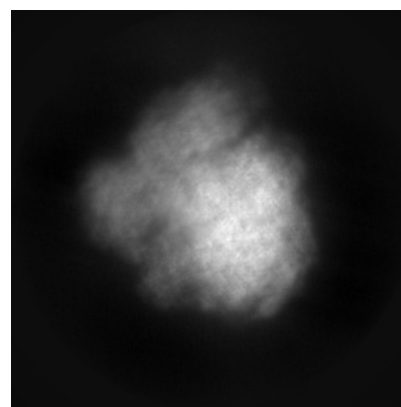
6.1.2 Raw map



X



Y

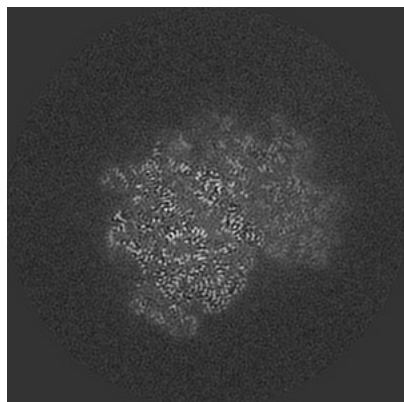


Z

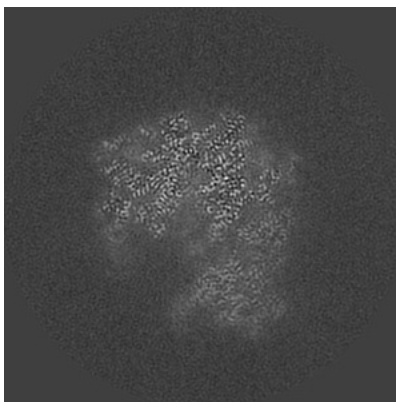
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

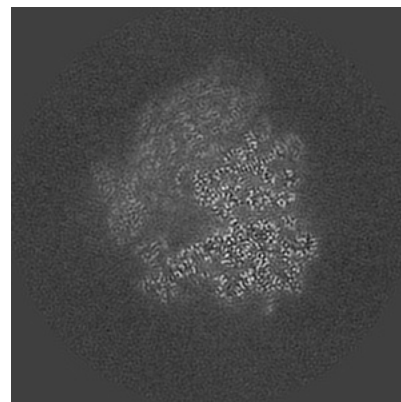
6.2.1 Primary map



X Index: 200

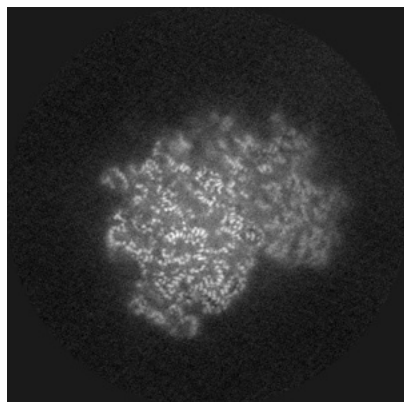


Y Index: 200

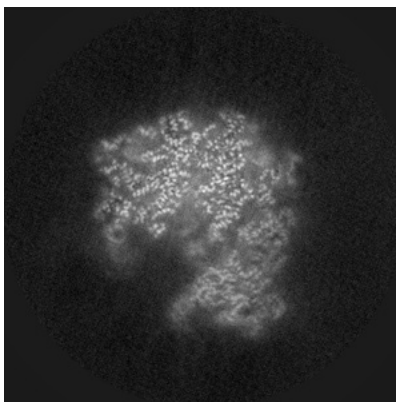


Z Index: 200

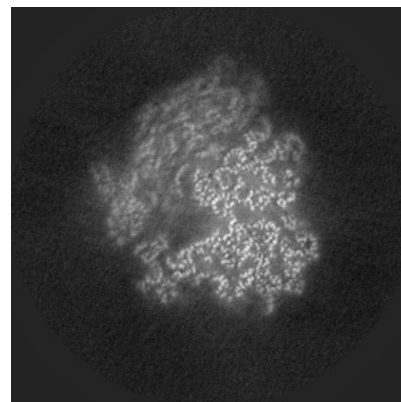
6.2.2 Raw map



X Index: 200



Y Index: 200

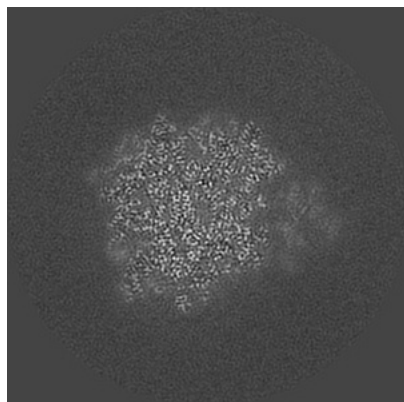


Z Index: 200

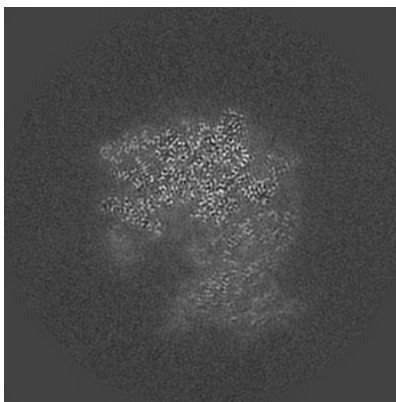
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

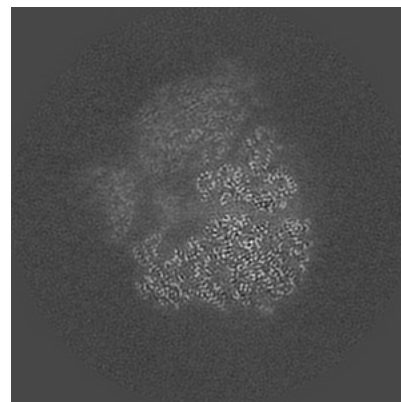
6.3.1 Primary map



X Index: 226

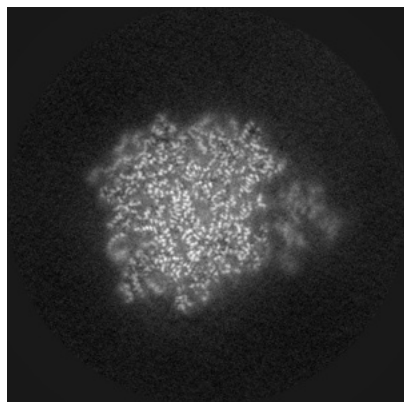


Y Index: 208

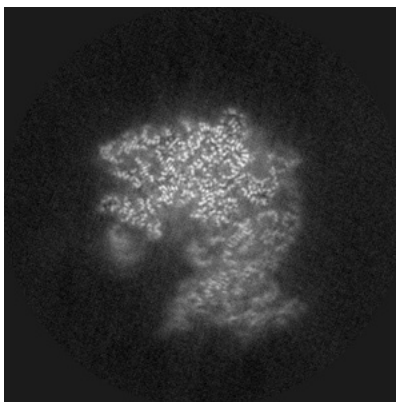


Z Index: 189

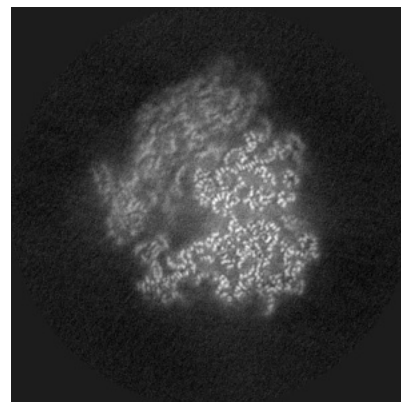
6.3.2 Raw map



X Index: 226



Y Index: 208

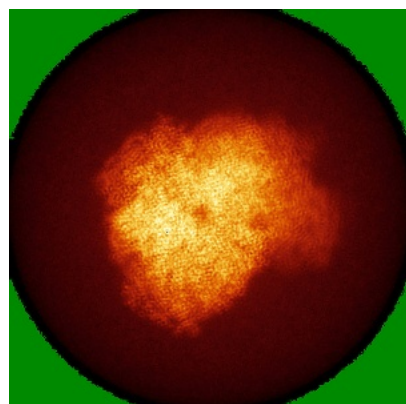


Z Index: 199

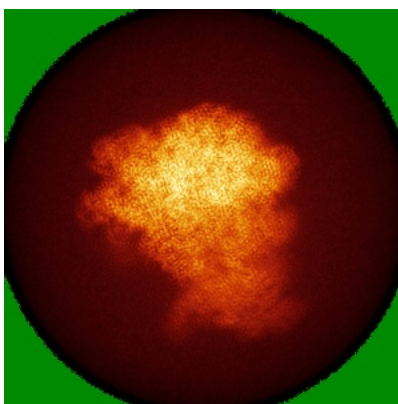
The images above show the largest variance slices of the map in three orthogonal directions.

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

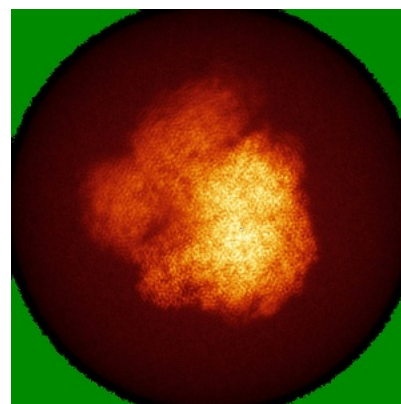
6.4.1 Primary map



X

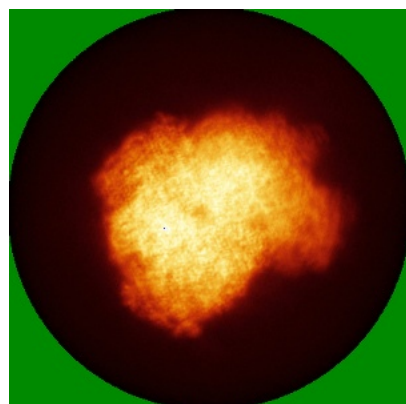


Y

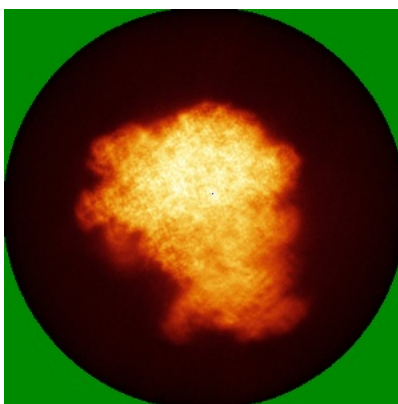


Z

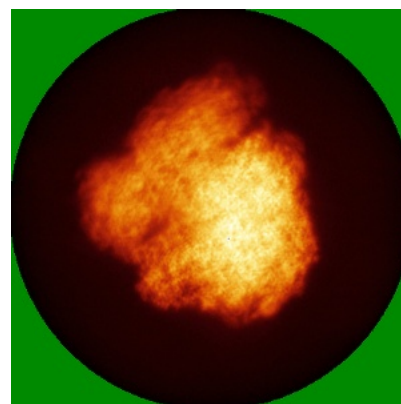
6.4.2 Raw map



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 2.8. 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.

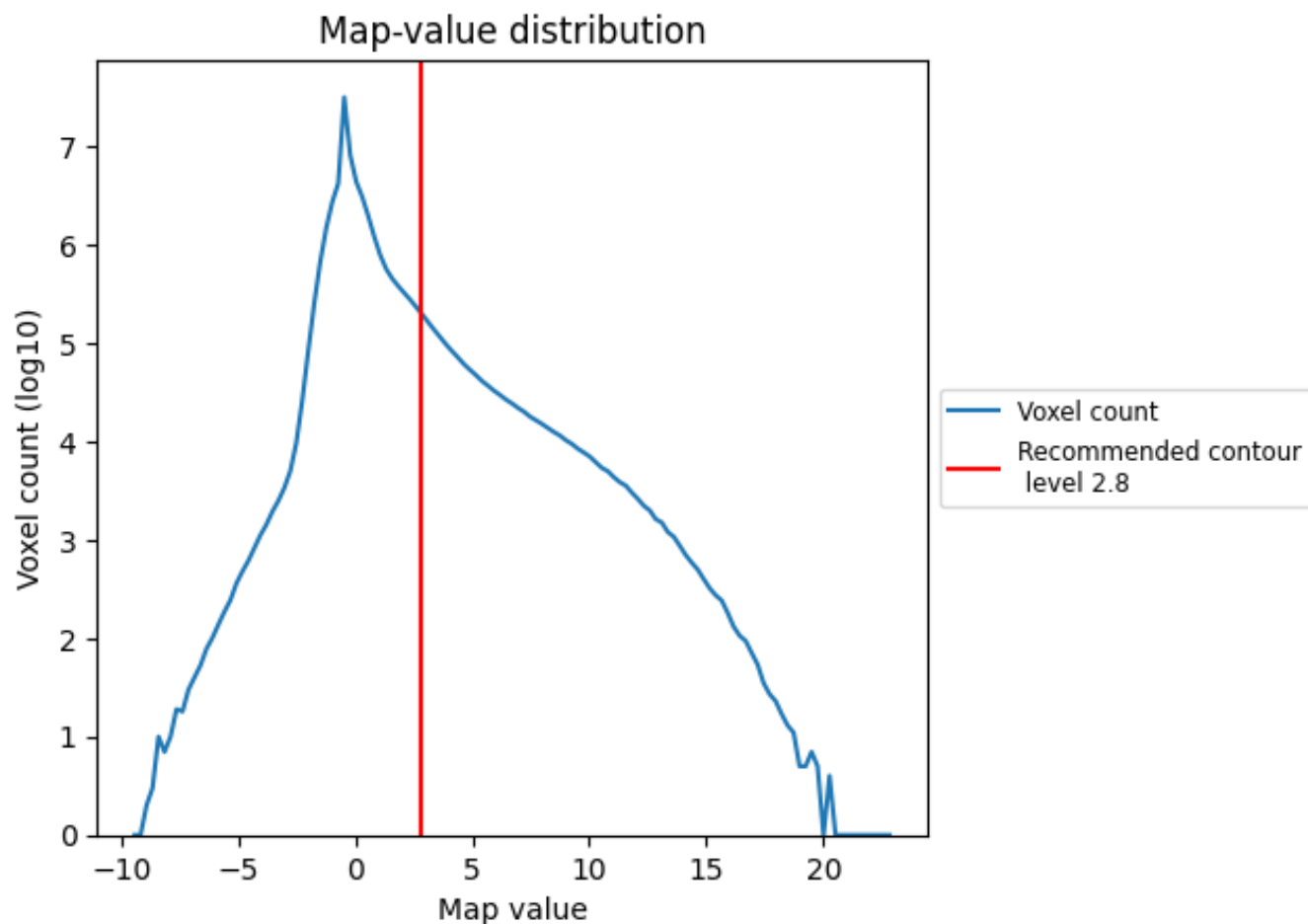
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

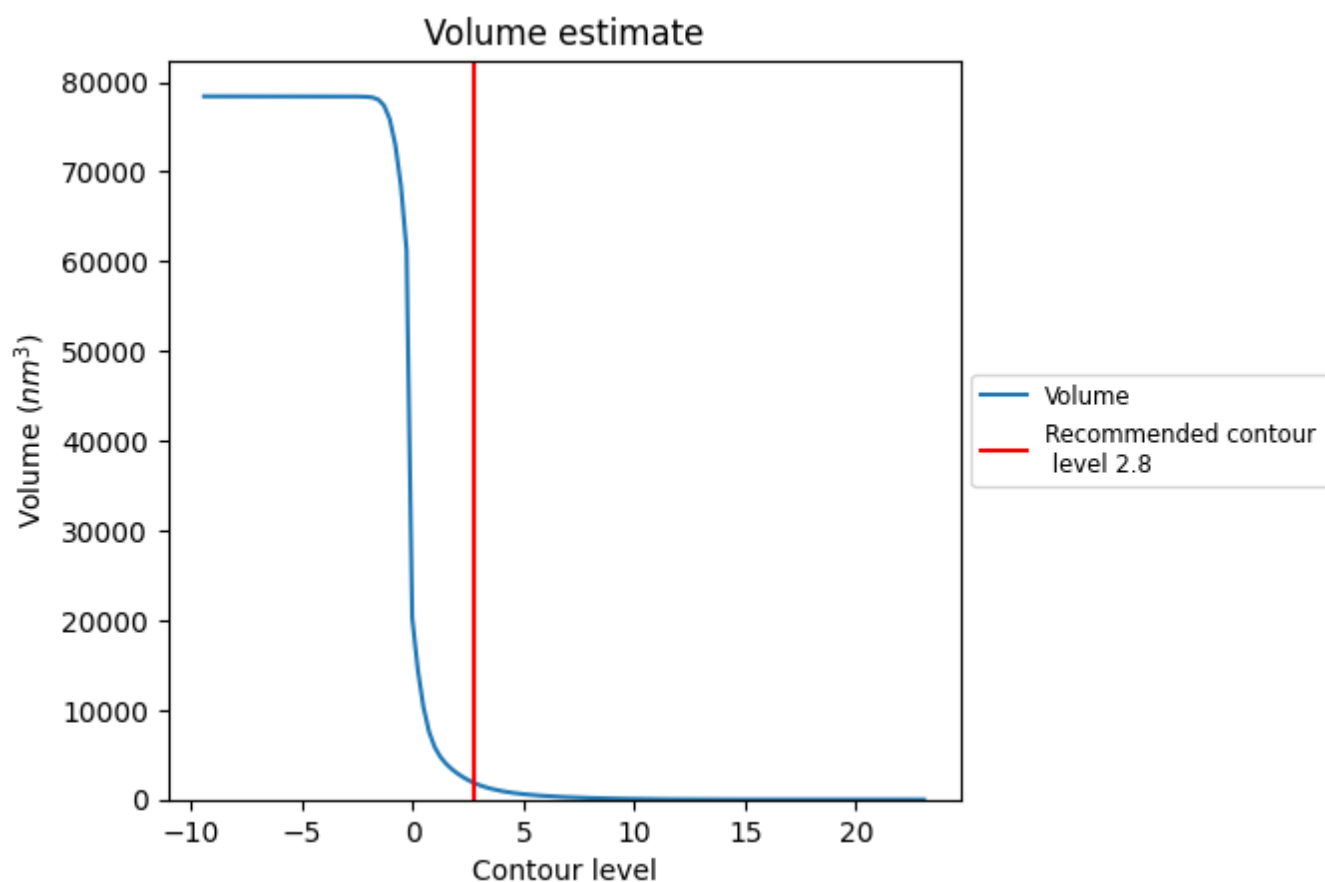
This section contains the results of statistical analysis of the map.

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.

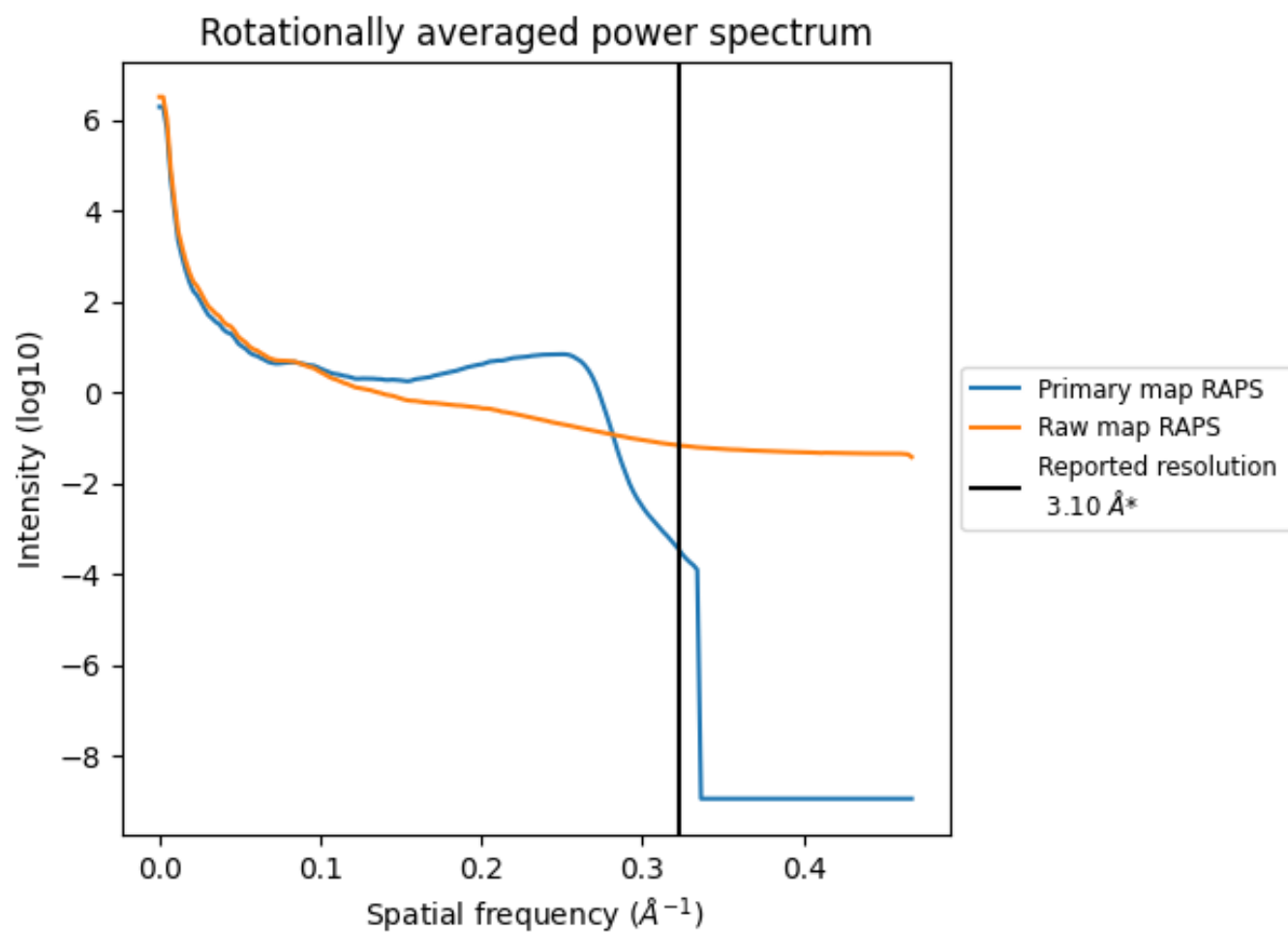
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1820 nm^3 ; this corresponds to an approximate mass of 1644 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 ⓘ

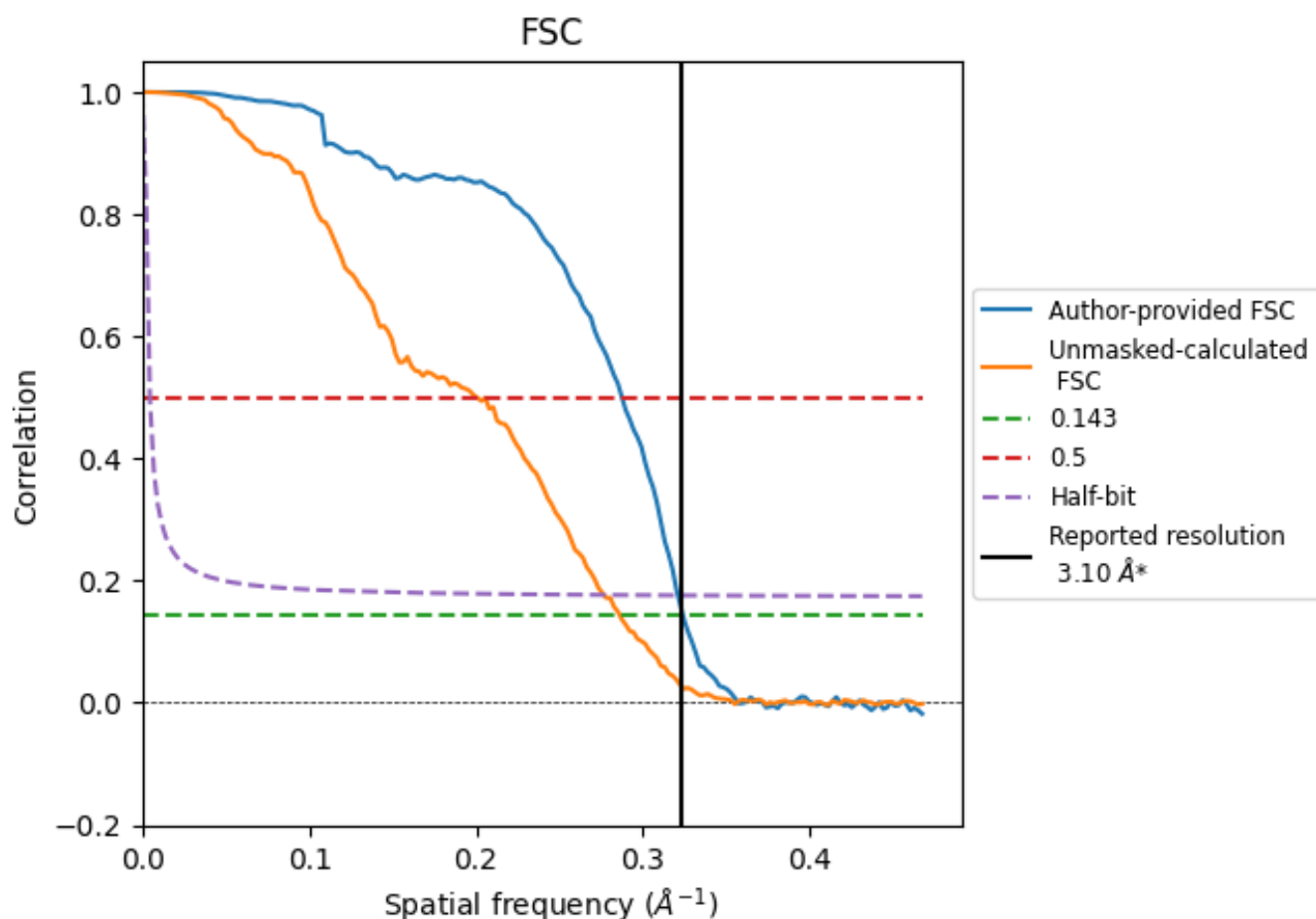


*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

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 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

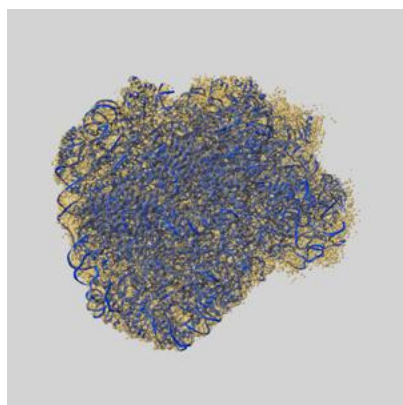
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.09	3.48	3.12
Unmasked-calculated*	3.49	4.99	3.61

*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 3.49 differs from the reported value 3.1 by more than 10 %

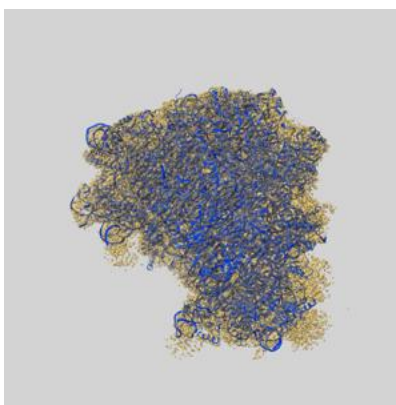
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-64718 and PDB model 9V26. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

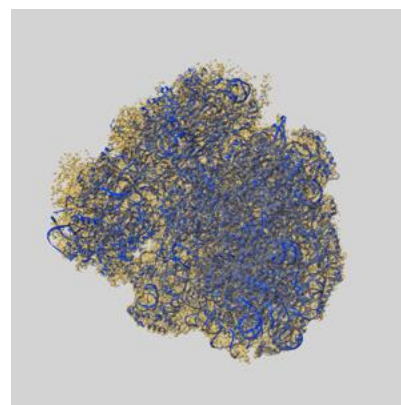
9.1 Map-model overlay [i](#)



X



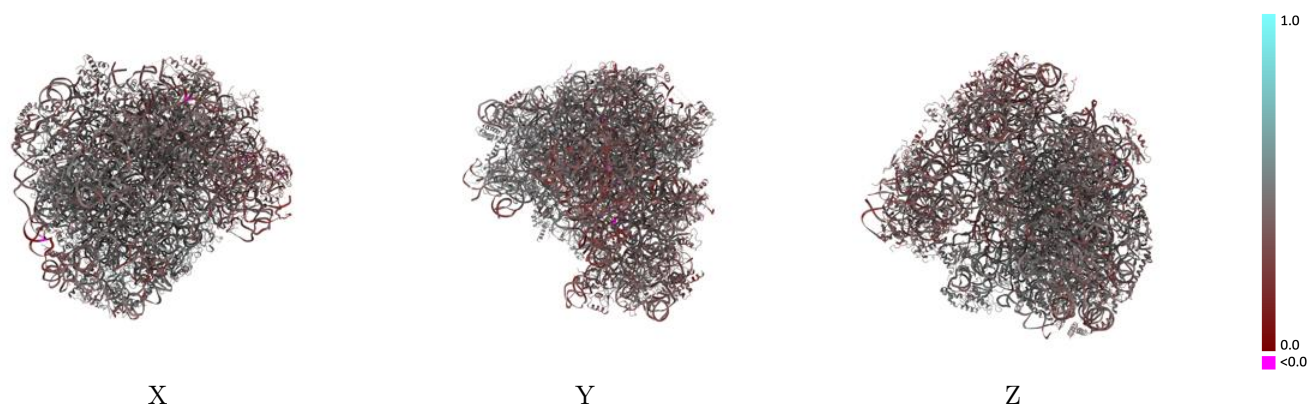
Y



Z

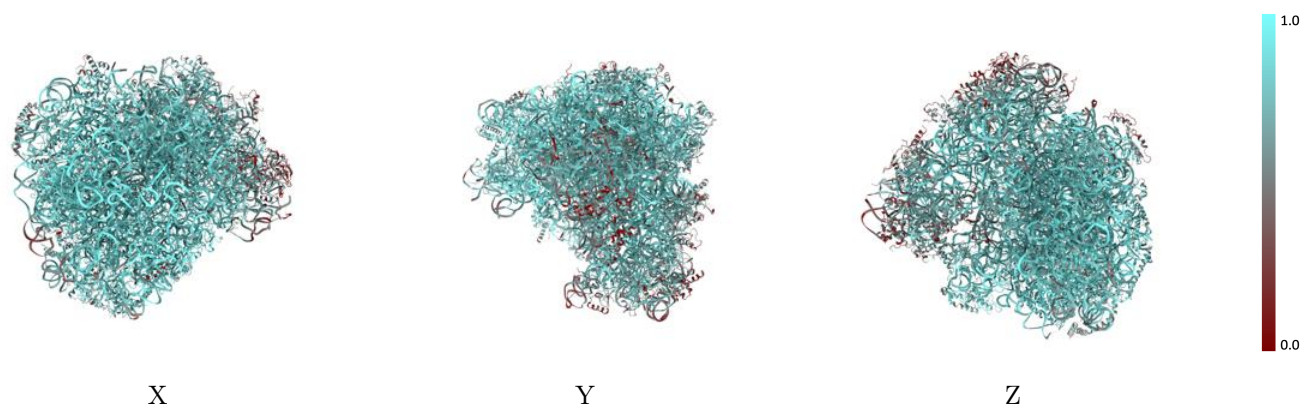
The images above show the 3D surface view of the map at the recommended contour level 2.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



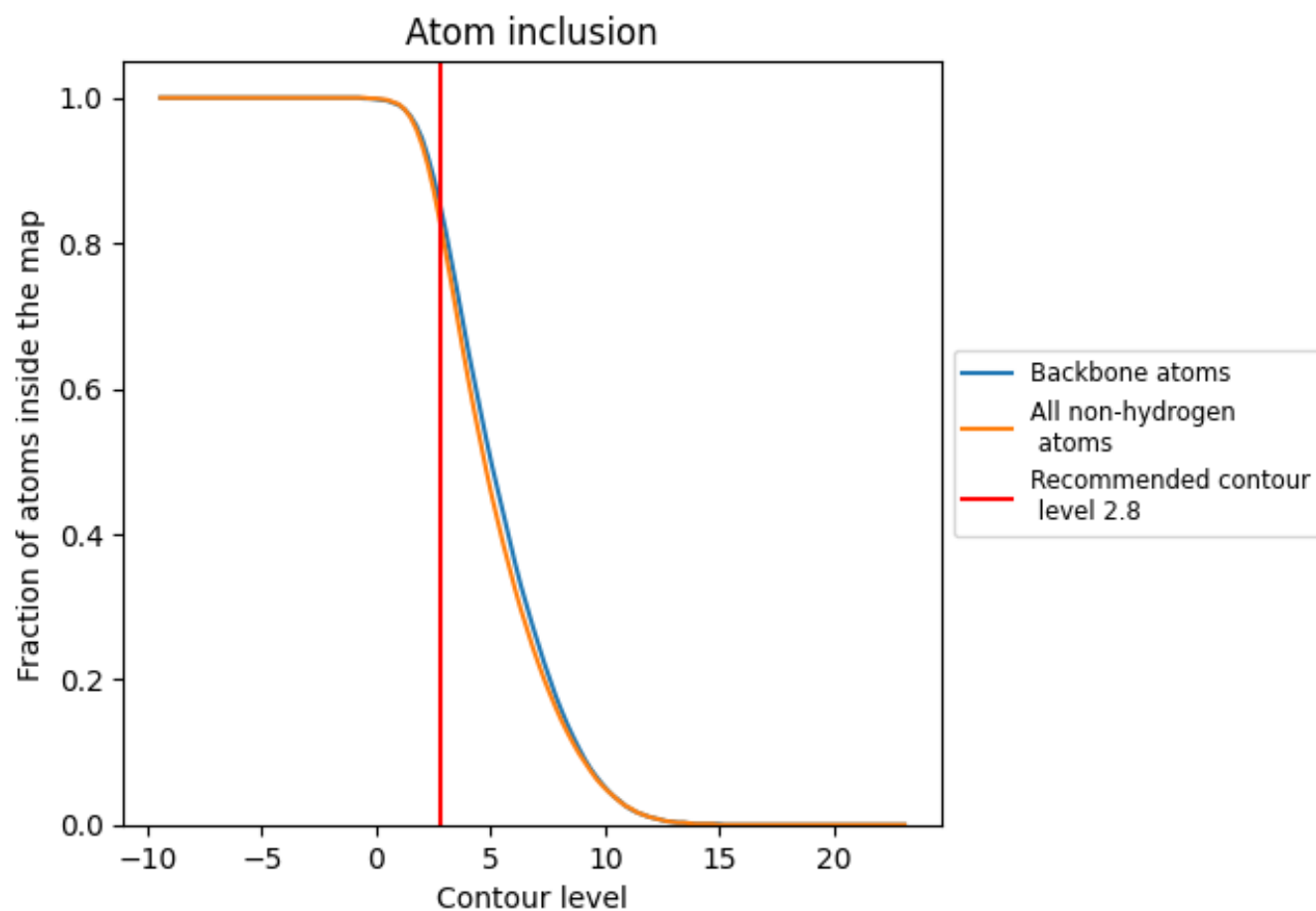
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.8).

9.4 Atom inclusion ⓘ



At the recommended contour level, 85% of all backbone atoms, 83% 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 (2.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8270	 0.4130
1A	 0.9070	 0.4200
1B	 0.9120	 0.4080
1C	 0.9100	 0.4230
1D	 0.9230	 0.4450
1E	 0.8900	 0.4610
1F	 0.8670	 0.4670
1G	 0.8250	 0.4750
1H	 0.6880	 0.4270
1I	 0.8840	 0.4840
1J	 0.7470	 0.4160
1K	 0.8330	 0.4650
1L	 0.8960	 0.4660
1M	 0.7560	 0.4500
1N	 0.7680	 0.4370
1O	 0.8830	 0.4700
1P	 0.8530	 0.4830
1Q	 0.9420	 0.4580
1R	 0.8720	 0.4480
1S	 0.9280	 0.4750
1T	 0.9250	 0.4890
1U	 0.8370	 0.4160
1V	 0.8980	 0.4880
1W	 0.4810	 0.3410
1X	 0.9260	 0.4520
1Y	 0.8150	 0.4240
1Z	 0.8800	 0.4470
1a	 0.7930	 0.4400
1b	 0.6850	 0.3910
1c	 0.9270	 0.4860
1d	 0.9320	 0.4920
1e	 0.7350	 0.4120
1f	 0.7430	 0.3900
1g	 0.9260	 0.4690
1h	 0.8770	 0.4200



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Chain	Atom inclusion	Q-score
li	 0.8150	 0.4280
lj	 0.9170	 0.4820
lk	 0.8470	 0.4520
ll	 0.9480	 0.4640
lm	 0.8700	 0.4310
ln	 0.5970	 0.3630
lo	 0.9350	 0.4390
lp	 0.8810	 0.4530
lq	 0.9050	 0.4670
sA	 0.4610	 0.3600
sB	 0.8250	 0.4330
sC	 0.5320	 0.3900
sD	 0.5410	 0.3950
sE	 0.8100	 0.4150
sI	 0.6790	 0.3060
sJ	 0.7450	 0.3500
sK	 0.9580	 0.4280
sa	 0.7950	 0.3650
sc	 0.6840	 0.4040
sd	 0.5750	 0.3790
se	 0.6700	 0.4030
sf	 0.3170	 0.3220
sg	 0.5430	 0.3810
sh	 0.6080	 0.3640
si	 0.3450	 0.3330
sj	 0.5530	 0.3520
sk	 0.4740	 0.3600
sl	 0.4260	 0.3510
sm	 0.6350	 0.3450
so	 0.7490	 0.3860
sp	 0.7710	 0.4280
sq	 0.5660	 0.3800
sr	 0.7420	 0.4050
ss	 0.5220	 0.3870
st	 0.4880	 0.3460
su	 0.6230	 0.4100
sv	 0.4890	 0.3920
sw	 0.7330	 0.4070
sx	 0.5400	 0.3940
sy	 0.6470	 0.3740