



wwPDB EM Validation Summary Report ⓘ

Jun 19, 2026 – 07:33 am BST

PDB ID : 6YST / pdb_00006yst
EMDB ID : EMD-10907
Title : Structure of the P+9 ArfB-ribosome complex with P/E hybrid tRNA in the post-hydrolysis state
Authors : Chan, K.-H.; Petrychenko, V.; Mueller, C.; Maracci, C.; Holtkamp, W.; Wilson, D.N.; Fischer, N.; Rodnina, M.V.
Deposited on : 2020-04-23
Resolution : 3.20 Å (reported)
Based on initial models : 4V95, 4RB7, 5O2R, 5AFI

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:

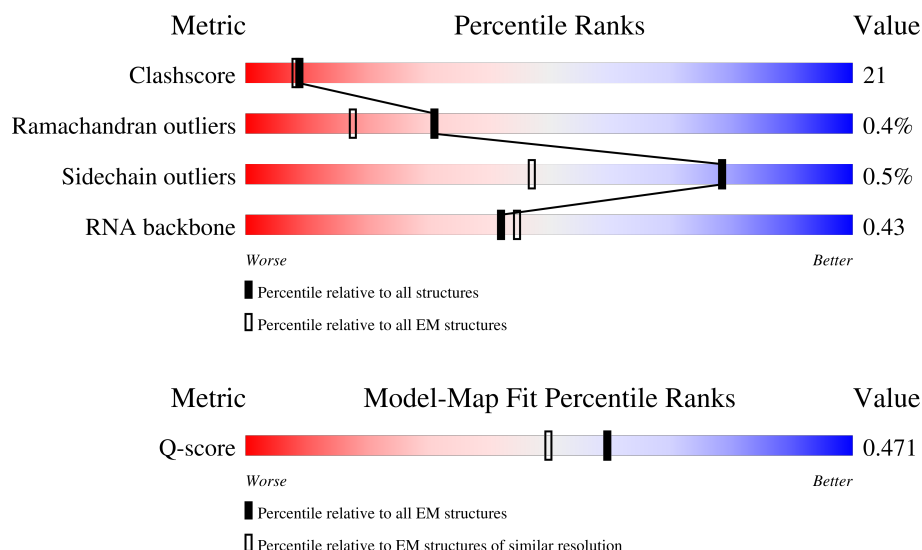
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

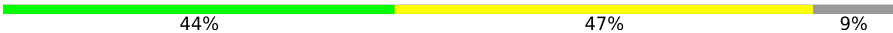
The reported resolution of this entry is 3.20 Å.

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.



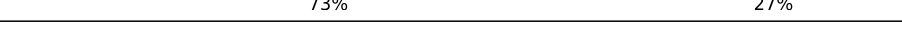
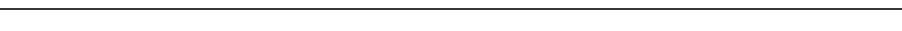
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	57	 63% 35%
2	1	55	 44% 47% 9%
3	2	46	 63% 37%

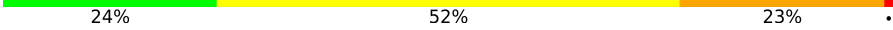
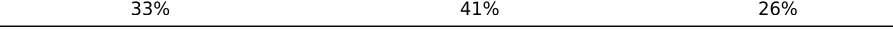
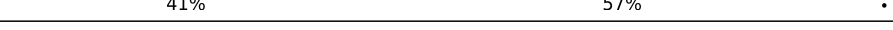
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Mol	Chain	Length	Quality of chain
4	3	65	
5	4	38	
6	5	165	
7	6	70	
8	A	2903	
9	B	120	
10	C	273	
11	D	209	
12	E	201	
13	F	179	
14	G	177	
15	H	149	
16	I	142	
17	J	142	
18	K	123	
19	L	144	
20	M	136	
21	N	127	
22	O	117	
23	P	115	
24	Q	118	
25	R	103	
26	S	110	
27	T	100	
28	U	104	

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Mol	Chain	Length	Quality of chain
29	V	94	 51% 49%
30	W	85	 58% 31% 12%
31	X	78	 53% 46% .
32	Y	63	 59% 37% . .
33	Z	59	 56% 42% .
34	a	1542	 24% 52% 23% .
35	b	240	 40% 50% 9%
36	c	233	 45% 43% 12%
37	d	206	 43% 52% . .
38	e	167	 53% 41% 6%
39	f	135	 33% 41% 26%
40	g	179	 36% 47% . 16%
41	h	130	 59% 40% .
42	i	130	 41% 57% .
43	j	103	 40% 52% . . 5%
44	k	129	 53% 37% 10%
45	l	124	 50% 49% .
46	m	118	 53% 43% .
47	n	102	 54% 45% .
48	o	89	 69% 30% .
49	p	82	 39% 55% . .
50	q	84	 40% 51% . 5%
51	r	75	 51% 36% 13%
52	s	92	 34% 55% 11%
53	t	87	 51% 44% . . .

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Mol	Chain	Length	Quality of chain
54	u	71	
55	v	14	
56	w	76	
57	x	15	
58	y	140	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MIA	w	37	-	-	X	-
8	3TD	A	1915	-	-	X	-

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 146847 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L32.

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

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	5	131	Total	C	N	O	0	0
			647	385	131	131		

- Molecule 7 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 8 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	2903	Total	C	N	O	P	0	0
			62336	27815	11468	20150	2903		

- Molecule 9 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	120	Total	C	N	O	P	0	0
			2570	1144	468	838	120		

- Molecule 10 is a protein called 50S ribosomal protein L2.

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

- Molecule 11 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 12 is a protein called 50S ribosomal protein L4.

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

- Molecule 13 is a protein called 50S ribosomal protein L5.

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

- Molecule 14 is a protein called 50S ribosomal protein L6.

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

- Molecule 15 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 16 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	141	Total	C	N	O	S	0	0
			693	411	141	141			

- Molecule 17 is a protein called 50S ribosomal protein L13.

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

- Molecule 18 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 20 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 21 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 22 is a protein called 50S ribosomal protein L18.

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

- Molecule 23 is a protein called 50S ribosomal protein L19.

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

- Molecule 24 is a protein called 50S ribosomal protein L20.

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

- Molecule 25 is a protein called 50S ribosomal protein L21.

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

- Molecule 26 is a protein called 50S ribosomal protein L22.

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

- Molecule 27 is a protein called 50S ribosomal protein L23.

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

- Molecule 28 is a protein called 50S ribosomal protein L24.

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

- Molecule 29 is a protein called 50S ribosomal protein L25.

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

- Molecule 30 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	W	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 31 is a protein called 50S ribosomal protein L28.

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

- Molecule 32 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 33 is a protein called 50S ribosomal protein L30.

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

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	1540	Total	C	N	O	P	0	0
			33050	14748	6057	10705	1540		

- Molecule 35 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 36 is a protein called 30S ribosomal protein S3.

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

- Molecule 37 is a protein called 30S ribosomal protein S4.

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

- Molecule 38 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

- Molecule 39 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	f	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 40 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	g	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 41 is a protein called 30S ribosomal protein S8.

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

- Molecule 42 is a protein called 30S ribosomal protein S9.

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

- Molecule 43 is a protein called 30S ribosomal protein S10.

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

- Molecule 44 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	k	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 45 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	l	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 46 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	m	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 47 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	n	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	36	ALA	-	insertion	UNP I2X5X6

- Molecule 48 is a protein called 30S ribosomal protein S15.

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

- Molecule 49 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	p	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 50 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 51 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 52 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s	82	Total	C	N	O	S	0	0
			658	421	125	110	2		

- Molecule 53 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	t	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 54 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	65	Total	C	N	O	S	0	0
			506	313	105	87	1		

- Molecule 55 is a protein called Api137.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	v	14	Total	C	N	O	0	0
			121	80	25	16		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	10	ARG	GLN	conflict	UNP Q8WSY8

- Molecule 56 is a RNA chain called P/E-site tRNAPhe.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	w	76	Total	C	N	O	P	S	0	0
			1631	731	291	531	76	2		

- Molecule 57 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	x	4	Total	C	N	O	P	0	0
			82	37	12	29	4		

- Molecule 58 is a protein called Alternative stalled-ribosome rescue factor B.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	y	139	Total	C	N	O	S	0	0
			1078	666	215	195	2		

- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
59	0	1	Total	Mg	0
			1	1	
59	4	1	Total	Mg	0
			1	1	
59	6	1	Total	Mg	0
			1	1	
59	A	206	Total	Mg	0
			206	206	
59	B	6	Total	Mg	0
			6	6	
59	C	1	Total	Mg	0
			1	1	
59	D	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
59	S	1	Total 1	Mg 1	0
59	a	35	Total 35	Mg 35	0

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
60	4	1	Total 1	Zn 1	0
60	6	1	Total 1	Zn 1	0

- Molecule 61 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
61	A	1	Total 1	Na 1	0
61	M	1	Total 1	Na 1	0

3 Residue-property plots

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

- Molecule 1: 50S ribosomal protein L32

Chain 0: 



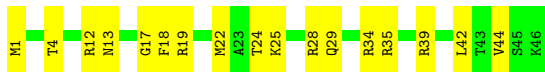
- Molecule 2: 50S ribosomal protein L33

Chain 1: 



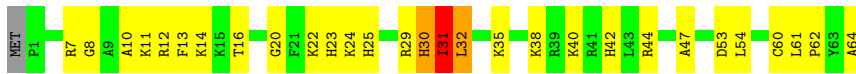
- Molecule 3: 50S ribosomal protein L34

Chain 2: 



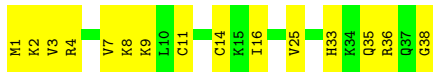
- Molecule 4: 50S ribosomal protein L35

Chain 3: 



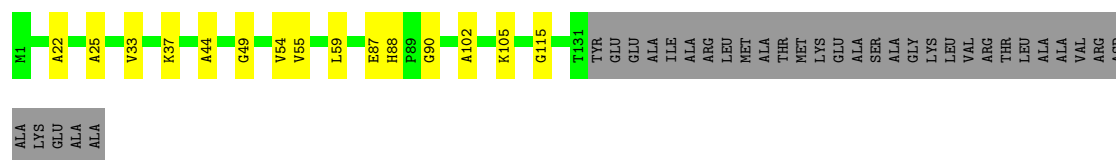
- Molecule 5: 50S ribosomal protein L36

Chain 4: 

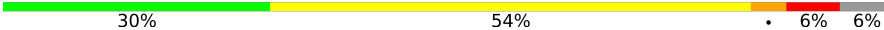


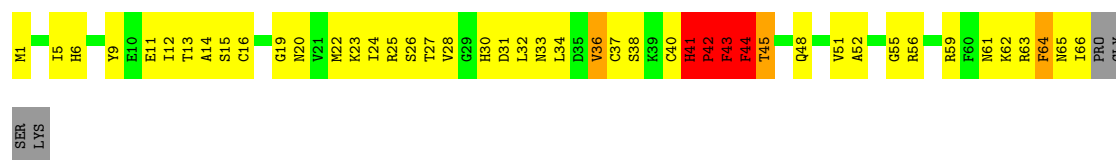
- Molecule 6: 50S ribosomal protein L10

Chain 5:  70% 9% 21%

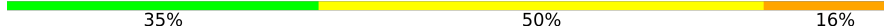


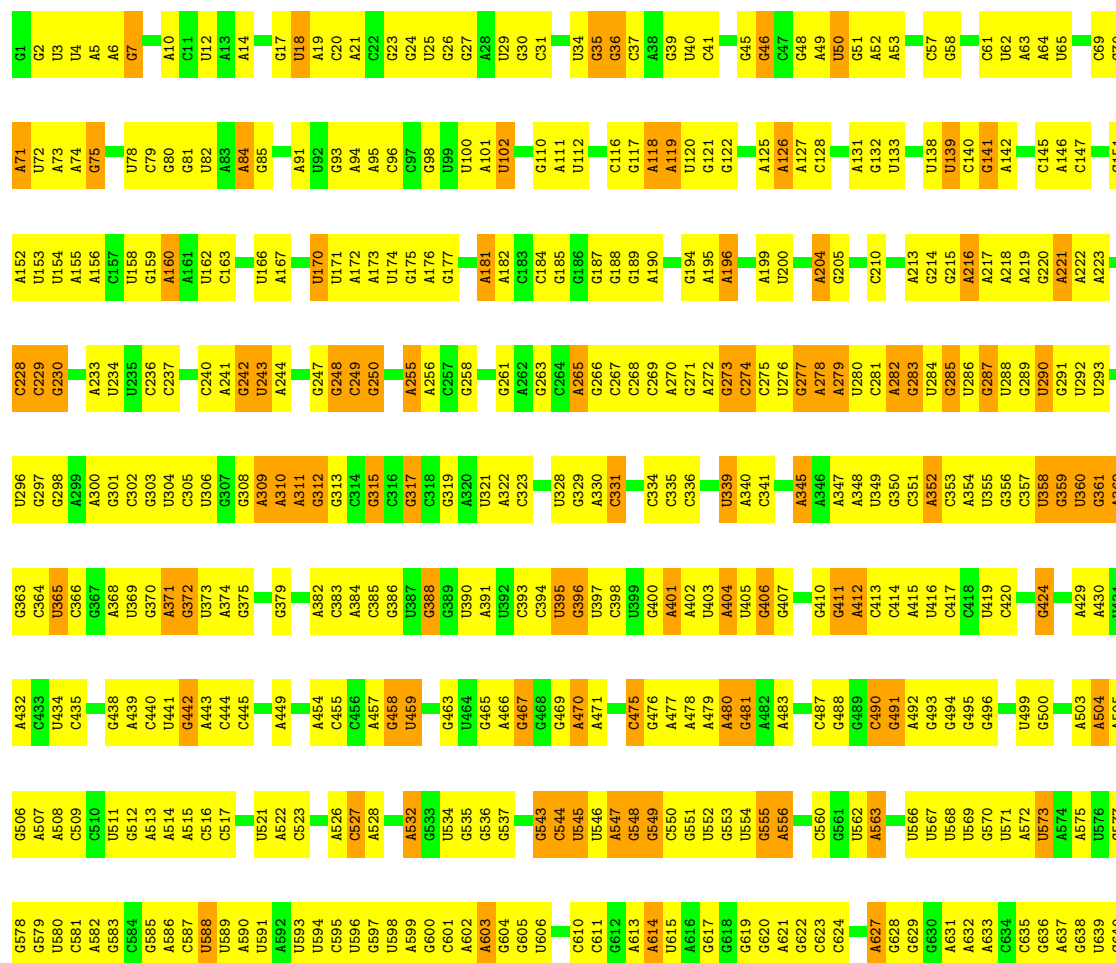
• Molecule 7: 50S ribosomal protein L31

Chain 6:  30% 54% 6% 6%



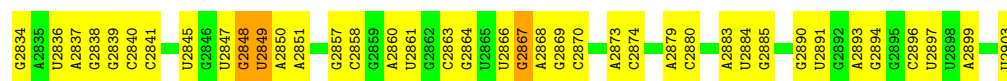
• Molecule 8: 23S ribosomal RNA

Chain A:  35% 50% 16%

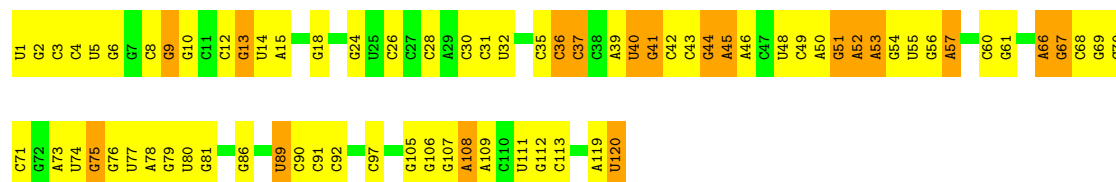


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	U1458		U1393	G1236	C1152	A1087	G1024	G956	G881	C815	G729	G651
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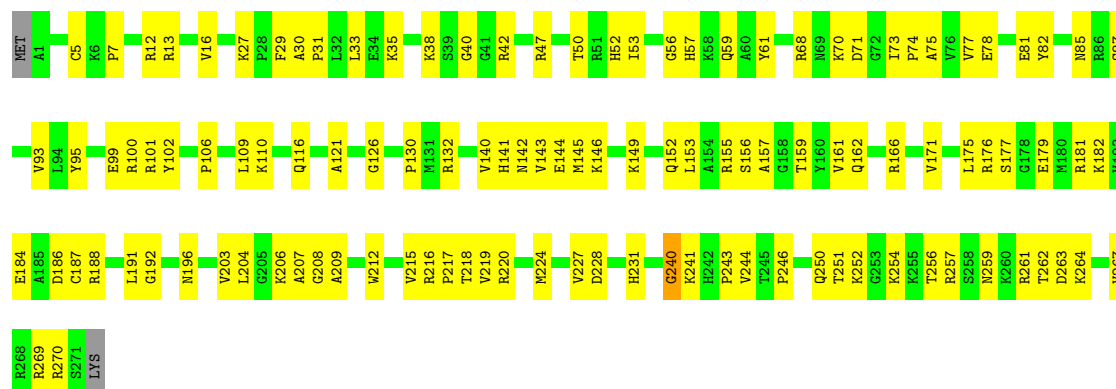
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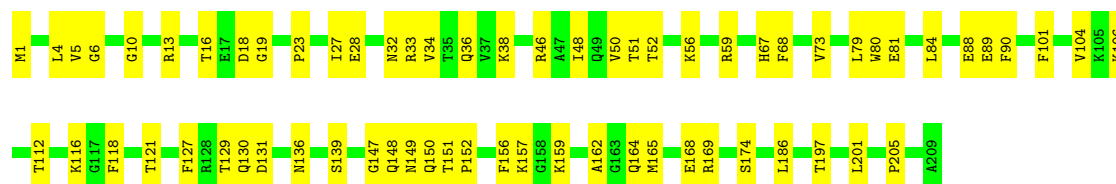
• Molecule 9: 5S ribosomal RNA



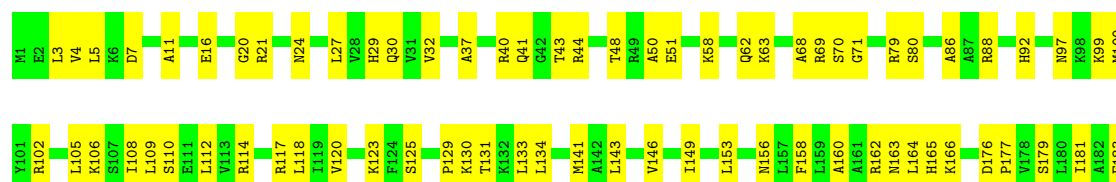
• Molecule 10: 50S ribosomal protein L2

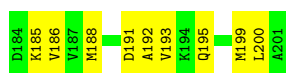


• Molecule 11: 50S ribosomal protein L3



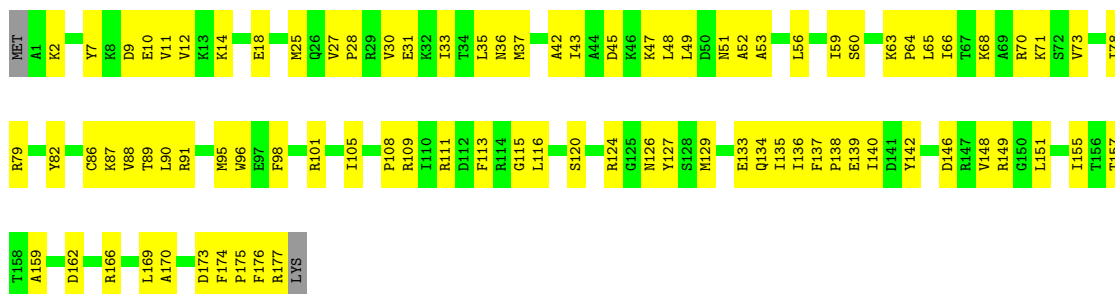
• Molecule 12: 50S ribosomal protein L4





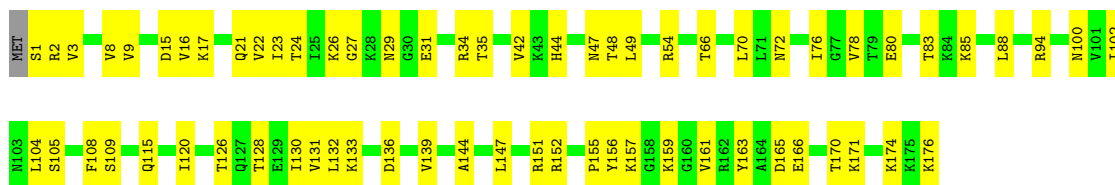
• Molecule 13: 50S ribosomal protein L5

Chain F: 50% 49%



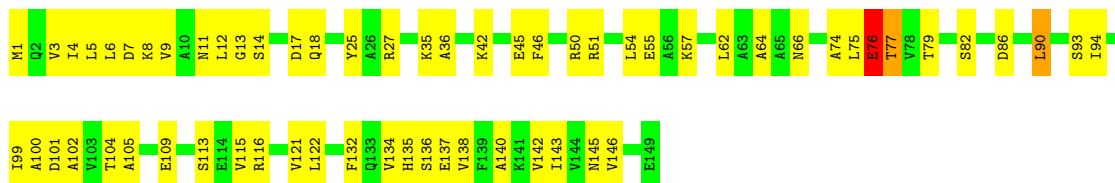
• Molecule 14: 50S ribosomal protein L6

Chain G: 62% 37%



• Molecule 15: 50S ribosomal protein L9

Chain H: 58% 40%



• Molecule 16: 50S ribosomal protein L11

Chain I: 91% 8%



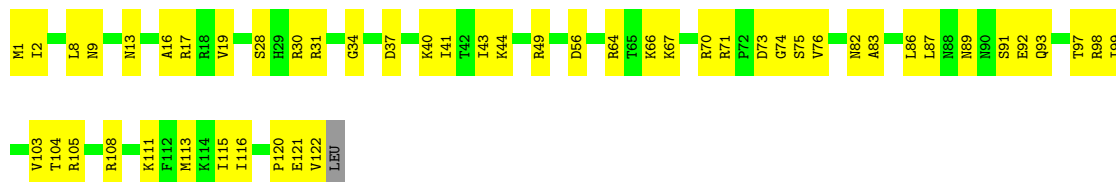
• Molecule 17: 50S ribosomal protein L13

Chain J: 73% 27%



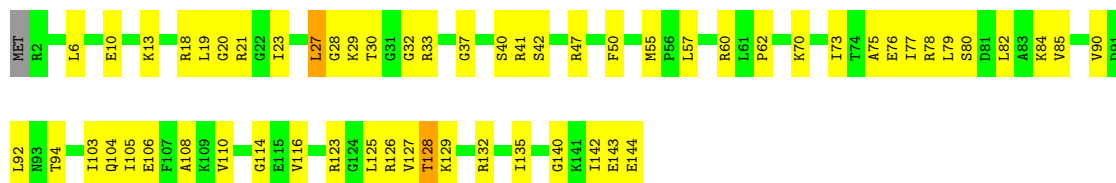
- Molecule 18: 50S ribosomal protein L14

Chain K: 59% 41%



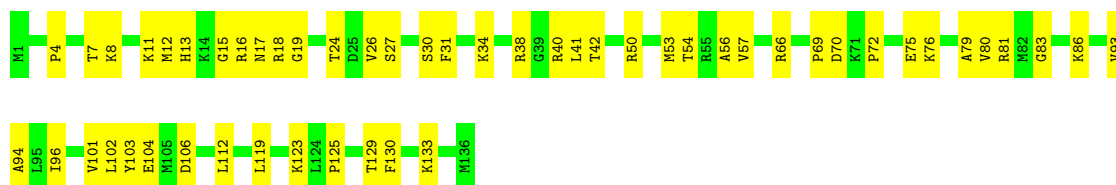
- Molecule 19: 50S ribosomal protein L15

Chain L: 59% 39%



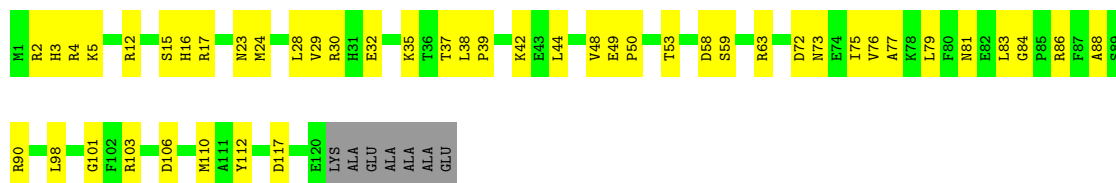
- Molecule 20: 50S ribosomal protein L16

Chain M: 62% 38%



- Molecule 21: 50S ribosomal protein L17

Chain N: 58% 36% 6%



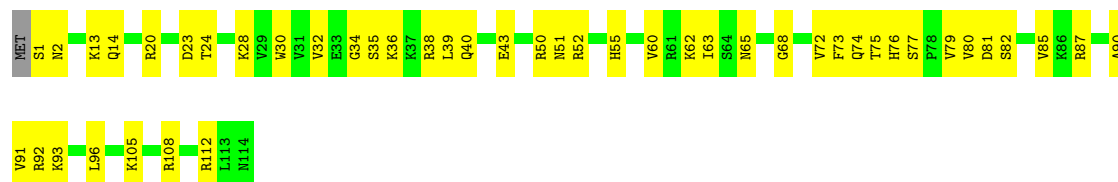
- Molecule 22: 50S ribosomal protein L18

Chain O: 68% 31%



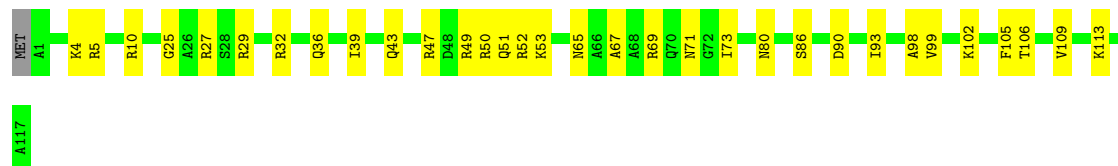
- Molecule 23: 50S ribosomal protein L19

Chain P: 59% 40%



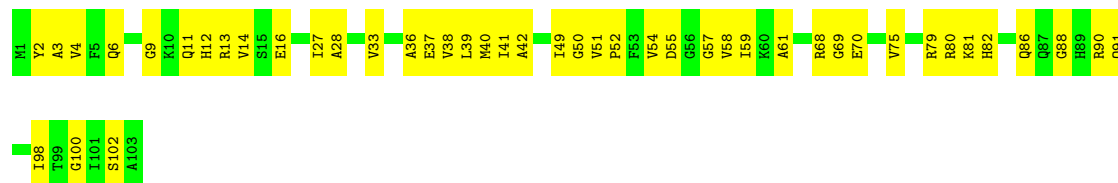
- Molecule 24: 50S ribosomal protein L20

Chain Q: 72% 27%



- Molecule 25: 50S ribosomal protein L21

Chain R: 56% 44%



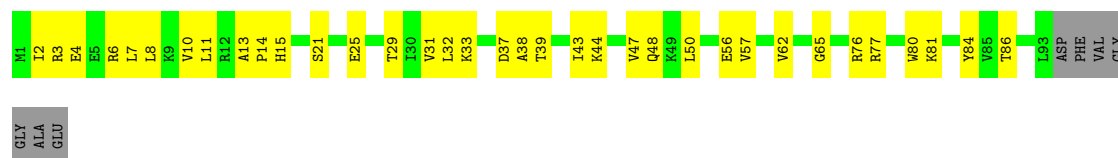
- Molecule 26: 50S ribosomal protein L22

Chain S: 67% 33%

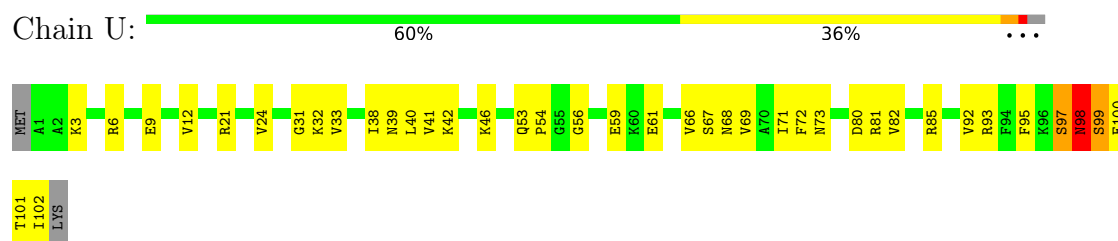


- Molecule 27: 50S ribosomal protein L23

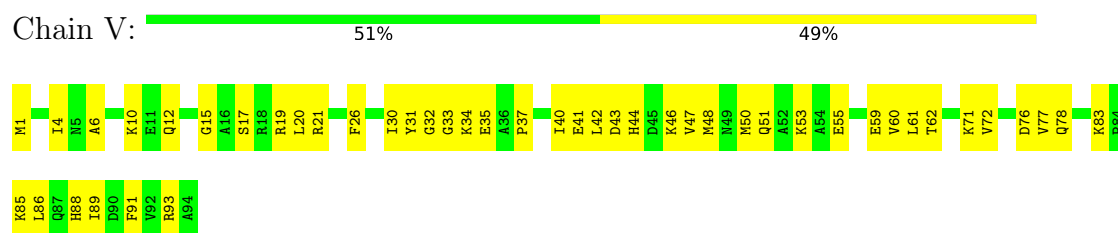
Chain T: 58% 35% 7%



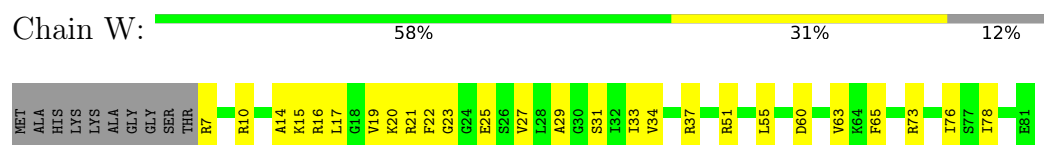
- Molecule 28: 50S ribosomal protein L24



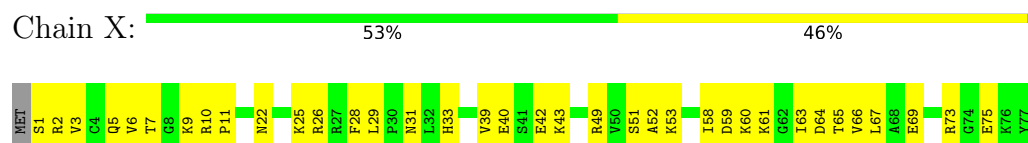
- Molecule 29: 50S ribosomal protein L25



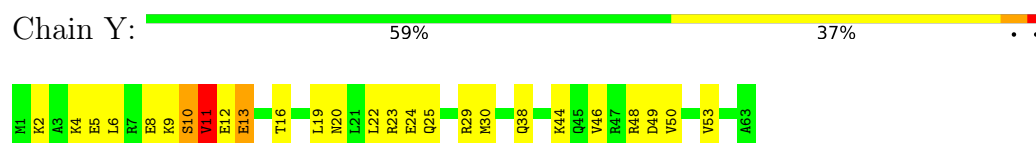
- Molecule 30: 50S ribosomal protein L27



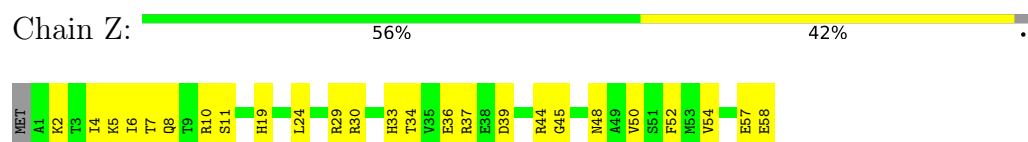
- Molecule 31: 50S ribosomal protein L28



- Molecule 32: 50S ribosomal protein L29



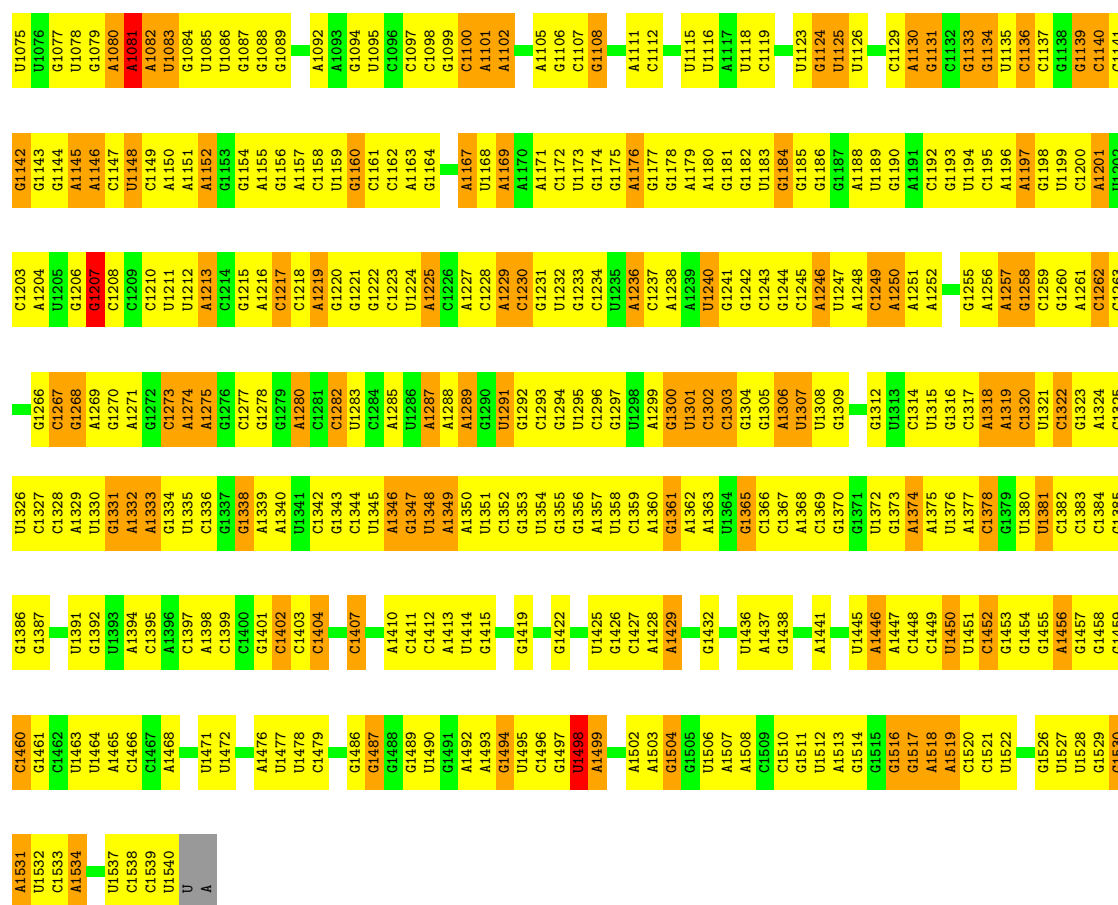
- Molecule 33: 50S ribosomal protein L30



- Molecule 34: 16S ribosomal RNA

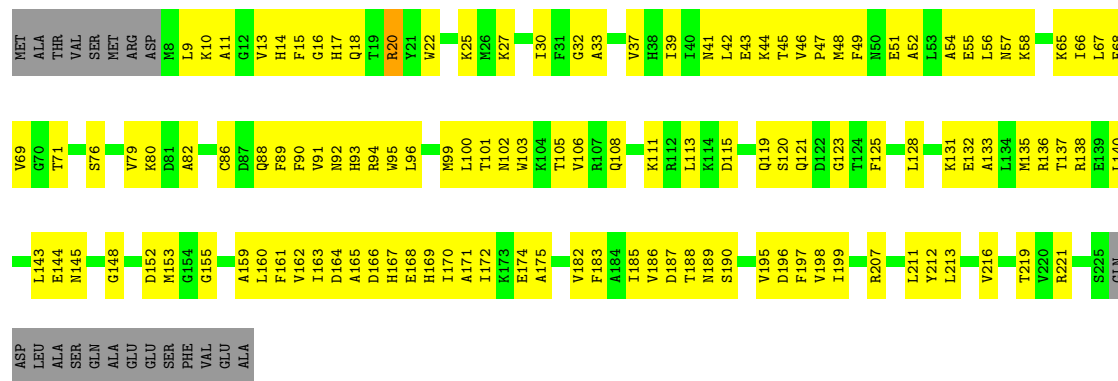


C948	C949	C950	C951	C952	C953	C954	C955	C956	C957	C958	C959	C960	C961	C962	C963	C964	C965	C966	C967	C968	C969	C970	C971	C972	C973	C974	C975	C976	C977	C978	C979	C980	C981	C982	C983	C984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999	C1000	C1001	C1002	C1003	C1004	C1005	C1006	C1007	C1008	C1009	C1010																																																																																																																																																																																																																																																																																								
G1011	G1012	G1013	G1014	G1015	G1016	G1017	G1018	G1019	G1020	G1021	G1022	G1023	G1024	G1025	G1026	G1027	G1028	G1029	G1030	G1031	G1032	G1033	G1034	G1035	G1036	G1037	G1038	G1039	G1040	G1041	G1042	G1043	G1044	G1045	G1046	G1047	G1048	G1049	G1050	G1051	G1052	G1053	G1054	G1055	G1056	G1057	G1058	G1059	G1060	G1061	G1062	G1063	G1064	G1065	G1066	G1067	G1068	G1069	G1070	G1071	G1072	G1073	G1074																																																																																																																																																																																																																																																																																							
U875	U876	U877	U878	U879	U880	U881	U882	U883	U884	U885	U886	U887	U888	U889	U890	U891	U892	U893	U894	U895	U896	U897	U898	U899	U900	U901	U902	U903	U904	U905	U906	U907	U908	U909	U910	U911	U912	U913	U914	U915	U916	U917	U918	U919	U920	U921	U922	U923	U924	U925	U926	U927	U928	U929	U930	U931	U932	U933	U934	U935	U936	U937	U938	U939	U940	U941	U942	U943	U944	U945	U946	U947																																																																																																																																																																																																																																																																														
U723	U724	U725	U726	U727	U728	U729	U730	U731	U732	U733	U734	U735	U736	U737	U738	U739	U740	U741	U742	U743	U744	U745	U746	U747	U748	U749	U750	U751	U752	U753	U754	U755	U756	U757	U758	U759	U760	U761	U762	U763	U764	U765	U766	U767	U768	U769	U770	U771	U772	U773	U774	U775	U776	U777	U778	U779	U780	U781	U782	U783	U784	U785	U786	U787	U788	U789	U790	U791	U792	U793	U794	U795																																																																																																																																																																																																																																																																														
G812	G813	G814	G815	G816	G817	G818	G819	G820	G821	G822	G823	G824	G825	G826	G827	G828	G829	G830	G831	G832	G833	G834	G835	G836	G837	G838	G839	G840	G841	G842	G843	G844	G845	G846	G847	G848	G849	G850	G851	G852	G853	G854	G855	G856	G857	G858	G859	G860	G861	G862	G863	G864	G865	G866	G867	G868	G869	G870	G871	G872	G873	G874	G875	G876	G877	G878	G879	G880	G881	G882	G883	G884	G885	G886	G887	G888	G889	G890	G891	G892	G893	G894	G895	G896	G897	G898	G899	G900	G901	G902	G903	G904	G905	G906	G907	G908	G909	G910	G911	G912	G913	G914	G915	G916	G917	G918	G919	G920	G921	G922	G923	G924	G925	G926	G927	G928	G929	G930	G931	G932	G933	G934	G935	G936	G937	G938	G939	G940	G941	G942	G943	G944	G945	G946	G947	G948	G949	G950	G951	G952	G953	G954	G955	G956	G957	G958	G959	G960	G961	G962	G963	G964	G965	G966	G967	G968	G969	G970	G971	G972	G973	G974	G975	G976	G977	G978	G979	G980	G981	G982	G983	G984	G985	G986	G987	G988	G989	G990	G991	G992	G993	G994	G995	G996	G997	G998	G999	G1000	G1001	G1002	G1003	G1004	G1005	G1006	G1007	G1008	G1009	G1010																																																																																																																																																
U659	U660	U661	U662	U663	U664	U665	U666	U667	U668	U669	U670	U671	U672	U673	U674	U675	U676	U677	U678	U679	U680	U681	U682	U683	U684	U685	U686	U687	U688	U689	U690	U691	U692	U693	U694	U695	U696	U697	U698	U699	U700	U701	U702	U703	U704	U705	U706	U707	U708	U709	U710	U711	U712	U713	U714	U715	U716	U717	U718	U719	U720	U721	U722	U723	U724	U725	U726	U727	U728	U729	U730	U731	U732	U733	U734	U735	U736	U737	U738	U739	U740	U741	U742	U743	U744	U745	U746	U747	U748	U749	U750	U751	U752	U753	U754	U755	U756	U757	U758	U759	U760	U761	U762	U763	U764	U765	U766	U767	U768	U769	U770	U771	U772	U773	U774	U775	U776	U777	U778	U779	U780	U781	U782	U783	U784	U785	U786	U787	U788	U789	U790	U791	U792	U793	U794	U795																																																																																																																																																																																																														
A595	A596	A597	A598	A599	A600	A601	A602	A603	A604	A605	A606	A607	A608	A609	A610	A611	A612	A613	A614	A615	A616	A617	A618	A619	A620	A621	A622	A623	A624	A625	A626	A627	A628	A629	A630	A631	A632	A633	A634	A635	A636	A637	A638	A639	A640	A641	A642	A643	A644	A645	A646	A647	A648	A649	A650	A651	A652	A653	A654	A655	A656	A657	A658	A659	A660	A661	A662	A663	A664	A665	A666	A667	A668	A669	A670	A671	A672	A673	A674	A675	A676	A677	A678	A679	A680	A681	A682	A683	A684	A685	A686	A687	A688	A689	A690	A691	A692	A693	A694	A695	A696	A697	A698	A699	A700	A701	A702	A703	A704	A705	A706	A707	A708	A709	A710	A711	A712	A713	A714	A715	A716	A717	A718	A719	A720	A721	A722	A723	A724	A725	A726	A727	A728	A729	A730	A731	A732	A733	A734	A735	A736	A737	A738	A739	A740	A741	A742	A743	A744	A745	A746	A747	A748	A749	A750	A751	A752	A753	A754	A755	A756	A757	A758	A759	A760	A761	A762	A763	A764	A765	A766	A767	A768	A769	A770	A771	A772	A773	A774	A775	A776	A777	A778	A779	A780	A781	A782	A783	A784	A785	A786	A787	A788	A789	A790	A791	A792	A793	A794	A795																																																																																																																																														
A468	A469	A470	A471	A472	A473	A474	A475	A476	A477	A478	A479	A480	A481	A482	A483	A484	A485	A486	A487	A488	A489	A490	A491	A492	A493	A494	A495	A496	A497	A498	A499	A500	A501	A502	A503	A504	A505	A506	A507	A508	A509	A510	A511	A512	A513	A514	A515	A516	A517	A518	A519	A520	A521	A522	A523	A524	A525	A526	A527	A528	A529	A530	A531	A532	A533	A534	A535	A536	A537	A538	A539	A540	A541	A542	A543	A544	A545	A546	A547	A548	A549	A550	A551	A552	A553	A554	A555	A556	A557	A558	A559	A560	A561	A562	A563	A564	A565	A566	A567	A568	A569	A570	A571	A572	A573	A574	A575	A576	A577	A578	A579	A580	A581	A582	A583	A584	A585	A586	A587	A588	A589	A590	A591	A592	A593	A594	A595	A596	A597	A598	A599	A600	A601	A602	A603	A604	A605	A606	A607	A608	A609	A610	A611	A612	A613	A614	A615	A616	A617	A618	A619	A620	A621	A622	A623	A624	A625	A626	A627	A628	A629	A630	A631	A632	A633	A634	A635	A636	A637	A638	A639	A640	A641	A642	A643	A644	A645	A646	A647	A648	A649	A650	A651	A652	A653	A654	A655	A656	A657	A658	A659	A660	A661	A662	A663	A664	A665	A666	A667	A668	A669	A670	A671	A672	A673	A674	A675	A676	A677	A678	A679	A680	A681	A682	A683	A684	A685	A686	A687	A688	A689	A690	A691	A692	A693	A694	A695	A696	A697	A698	A699	A700	A701	A702	A703	A704	A705	A706	A707	A708	A709	A710	A711	A712	A713	A714	A715	A716	A717	A718	A719	A720	A721	A722	A723	A724	A725	A726	A727	A728	A729	A730	A731	A732	A733	A734	A735	A736	A737	A738	A739	A740	A741	A742	A743	A744	A745	A746	A747	A748	A749	A750	A751	A752	A753	A754	A755	A756	A757	A758	A759	A760	A761	A762	A763	A764	A765	A766	A767	A768	A769	A770	A771	A772	A773	A774	A775	A776	A777	A778	A779	A780	A781	A782	A783	A784	A785	A786	A787	A788	A789	A790	A791	A792	A793	A794	A795															
A344	A345	A346	A347	A348	A349	A350	A351	A352	A353	A354	A355	A356	A357	A358	A359	A360	A361	A362	A363	A364	A365	A366	A367	A368	A369	A370	A371	A372	A373	A374	A375	A376	A377	A378	A379	A380	A381	A382	A383	A384	A385	A386	A387	A388	A389	A390	A391	A392	A393	A394	A395	A396	A397	A398	A399	A400	A401	A402	A403	A404	A405	A406	A407	A408	A409	A410	A411	A412	A413	A414	A415	A416	A417	A418	A419	A420	A421	A422	A423	A424	A425	A426	A427	A428	A429	A430	A431	A432	A433	A434	A435	A436	A437	A438	A439	A440	A441	A442	A443	A444	A445	A446	A447	A448	A449	A450	A451	A452	A453	A454	A455	A456	A457	A458	A459	A460	A461	A462	A463	A464	A465	A466	A467	A468	A469	A470	A471	A472	A473	A474	A475	A476	A477	A478	A479	A480	A481	A482	A483	A484	A485	A486	A487	A488	A489	A490	A491	A492	A493	A494	A495	A496	A497	A498	A499	A500	A501	A502	A503	A504	A505	A506	A507	A508	A509	A510	A511	A512	A513	A514	A515	A516	A517	A518	A519	A520	A521	A522	A523	A524	A525	A526	A527	A528	A529	A530	A531	A532	A533	A534	A535	A536	A537	A538	A539	A540	A541	A542	A543	A544	A545	A546	A547	A548	A549	A550	A551	A552	A553	A554	A555	A556	A557	A558	A559	A560	A561	A562	A563	A564	A565	A566	A567	A568	A569	A570	A571	A572	A573	A574	A575	A576	A577	A578	A579	A580	A581	A582	A583	A584	A585	A586	A587	A588	A589	A590	A591	A592	A593	A594	A595	A596	A597	A598	A599	A600	A601	A602	A603	A604	A605	A606	A607	A608	A609	A610	A611	A612	A613	A614	A615	A616	A617	A618	A619	A620	A621	A622	A623	A624	A625	A626	A627	A628	A629	A630	A631	A632	A633	A634	A635	A636	A637	A638	A639	A640	A641	A642	A643	A644	A645	A646	A647	A648	A649	A650	A651	A652	A653	A654	A655	A656	A657	A658	A659	A660	A661	A662	A663	A664	A665	A666	A667	A668	A669	A670	A671	A672	A673	A674	A675	A676	A677	A678	A679	A680	A681	A682	A683	A684	A685	A686</



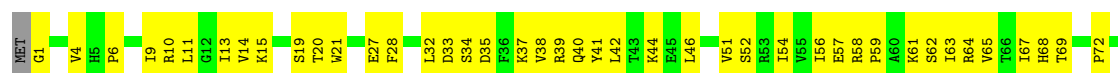
• Molecule 35: 30S ribosomal protein S2

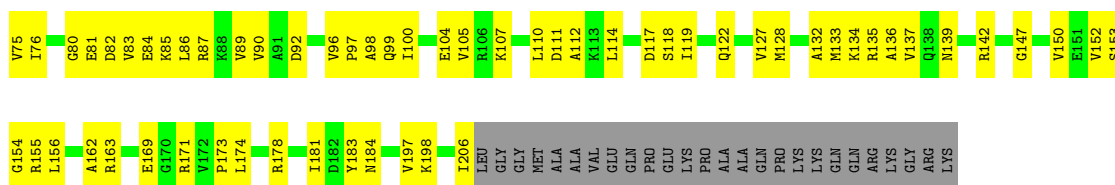
Chain b: 40% 50% 9%



• Molecule 36: 30S ribosomal protein S3

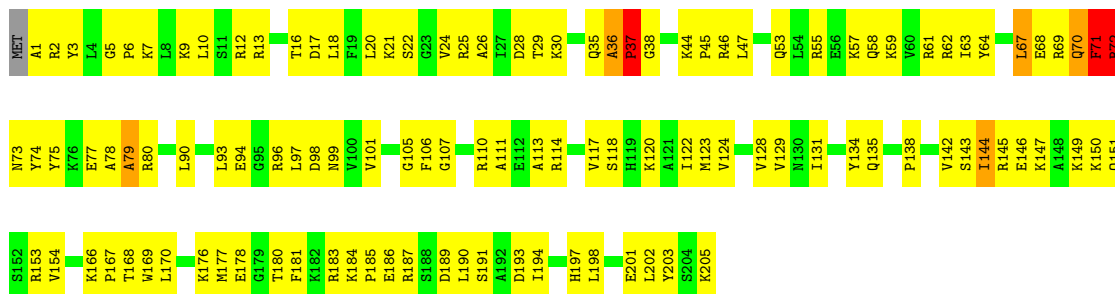
Chain c: 45% 43% 12%





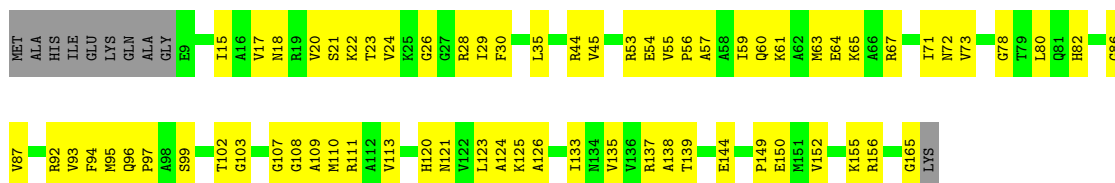
- Molecule 37: 30S ribosomal protein S4

Chain d: 43% 52% ..



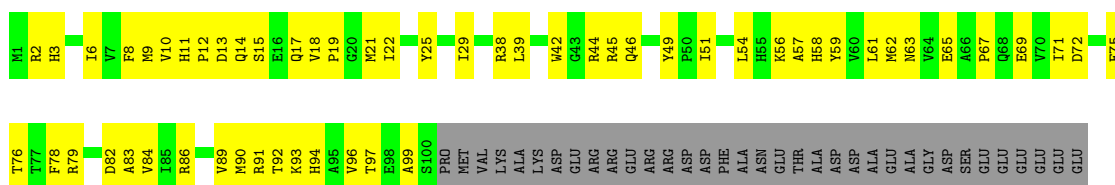
- Molecule 38: 30S ribosomal protein S5

Chain e: 53% 41% 6%



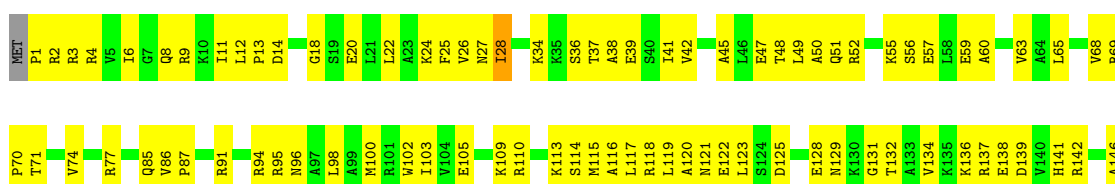
- Molecule 39: 30S ribosomal protein S6

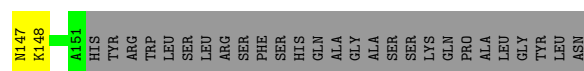
Chain f: 33% 41% 26%



- Molecule 40: 30S ribosomal protein S7

Chain g: 36% 47% 16%





• Molecule 41: 30S ribosomal protein S8

Chain h: 59% 40%



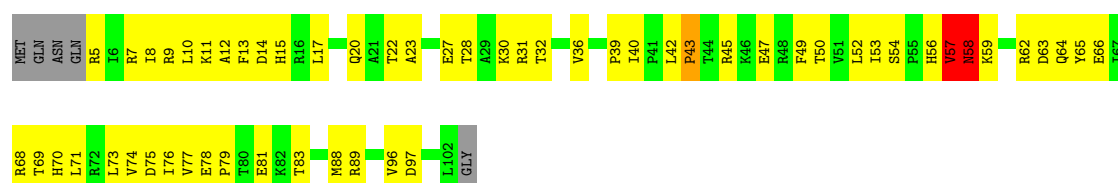
• Molecule 42: 30S ribosomal protein S9

Chain i: 41% 57%



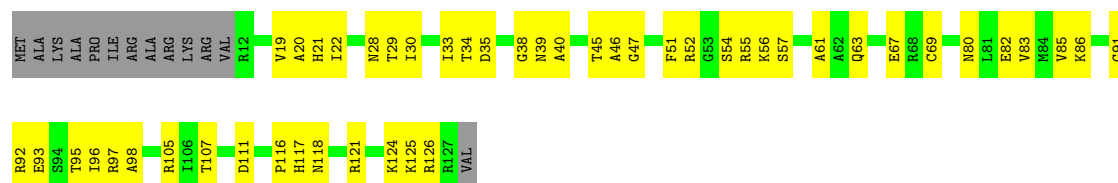
• Molecule 43: 30S ribosomal protein S10

Chain j: 40% 52% 5%



• Molecule 44: 30S ribosomal protein S11

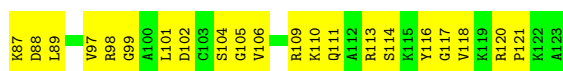
Chain k: 53% 37% 10%



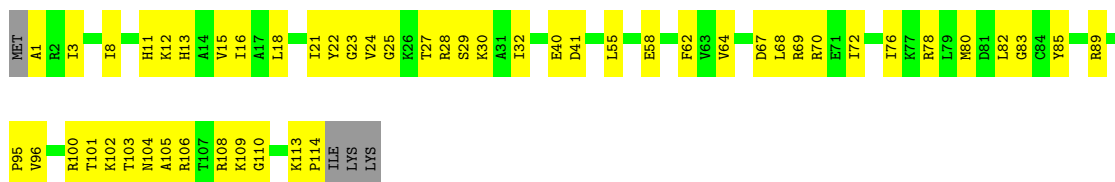
• Molecule 45: 30S ribosomal protein S12

Chain l: 50% 49%

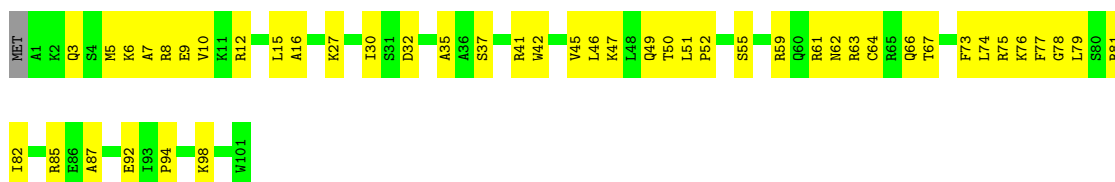




• Molecule 46: 30S ribosomal protein S13



• Molecule 47: 30S ribosomal protein S14



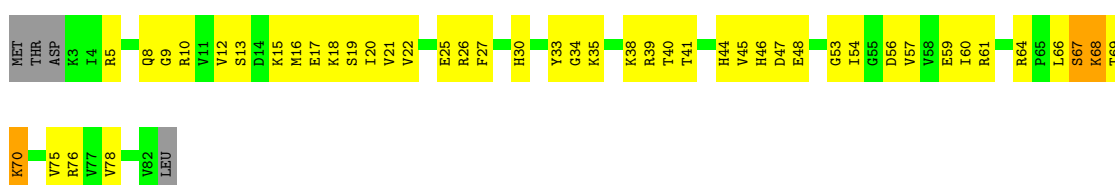
• Molecule 48: 30S ribosomal protein S15



• Molecule 49: 30S ribosomal protein S16

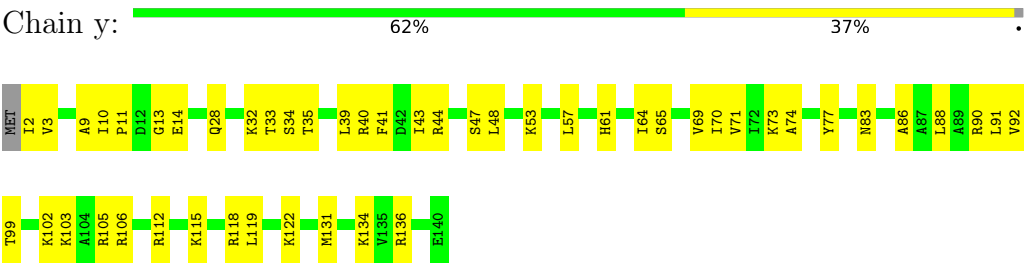


• Molecule 50: 30S ribosomal protein S17





● Molecule 58: Alternative stalled-ribosome rescue factor B



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	23340	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	2.5	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	14.075	Depositor
Minimum map value	-5.703	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	334.08, 334.08, 334.08	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.37	0/450	0.41	0/599
2	1	0.34	0/416	0.44	0/554
3	2	0.43	0/380	0.47	0/498
4	3	0.41	0/513	0.76	4/676 (0.6%)
5	4	0.35	0/303	0.53	0/397
6	5	0.19	0/646	0.56	0/898
7	6	0.98	2/531 (0.4%)	1.63	17/709 (2.4%)
8	A	0.44	2/69263 (0.0%)	0.39	0/108050
9	B	0.38	1/2873 (0.0%)	0.37	0/4478
10	C	0.44	0/2121	0.52	1/2852 (0.0%)
11	D	0.39	0/1586	0.44	0/2134
12	E	0.36	0/1571	0.46	0/2113
13	F	0.27	0/1434	0.49	0/1926
14	G	0.30	0/1343	0.41	0/1816
15	H	0.37	1/1122 (0.1%)	0.73	7/1515 (0.5%)
16	I	0.18	0/692	0.54	0/960
17	J	0.39	0/1152	0.40	0/1551
18	K	0.41	0/947	0.49	0/1268
19	L	0.39	0/1054	0.54	0/1403
20	M	0.39	0/1093	0.44	0/1460
21	N	0.40	0/973	0.51	0/1301
22	O	0.31	0/902	0.44	0/1209
23	P	0.36	0/929	0.49	0/1242
24	Q	0.45	0/960	0.46	0/1278
25	R	0.39	0/829	0.49	0/1107
26	S	0.37	0/864	0.46	0/1156
27	T	0.33	0/744	0.46	0/994
28	U	0.50	2/787 (0.3%)	0.81	7/1051 (0.7%)
29	V	0.36	0/766	0.48	0/1025
30	W	0.41	0/582	0.43	0/769
31	X	0.39	0/635	0.44	0/848

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	0.43	0/510	0.77	3/677 (0.4%)
33	Z	0.38	0/453	0.44	0/605
34	a	0.34	5/36725 (0.0%)	0.41	16/57285 (0.0%)
35	b	0.20	0/1735	0.48	0/2338
36	c	0.25	0/1651	0.46	0/2225
37	d	0.34	0/1665	0.97	19/2227 (0.9%)
38	e	0.29	0/1154	0.44	0/1554
39	f	0.29	0/835	0.48	0/1128
40	g	0.22	0/1195	0.43	0/1602
41	h	0.31	0/989	0.45	0/1326
42	i	0.22	0/1034	0.51	0/1375
43	j	0.64	4/796 (0.5%)	0.90	7/1077 (0.6%)
44	k	0.30	0/885	0.43	0/1195
45	l	0.30	0/969	0.48	0/1300
46	m	0.21	0/892	0.45	0/1193
47	n	0.25	0/811	0.47	0/1081
48	o	0.31	0/722	0.42	0/964
49	p	0.72	2/659 (0.3%)	0.99	9/884 (1.0%)
50	q	0.34	0/657	0.53	0/881
51	r	0.30	0/544	0.47	0/731
52	s	0.21	0/675	0.39	0/908
53	t	0.67	3/671 (0.4%)	0.99	11/888 (1.2%)
54	u	0.75	5/512 (1.0%)	1.02	5/683 (0.7%)
55	v	0.35	0/128	0.43	0/175
56	w	0.55	7/1650 (0.4%)	0.50	3/2569 (0.1%)
57	x	0.18	0/90	0.42	0/137
58	y	0.32	0/1090	0.43	0/1461
All	All	0.40	34/158158 (0.0%)	0.45	109/236306 (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
7	6	0	1
43	j	0	1
49	p	0	3
All	All	0	5

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	6	42	PRO	N-CA	17.72	1.70	1.47
49	p	48	GLU	C-O	-12.08	1.09	1.23
43	j	58	ASN	C-O	-11.16	1.09	1.24
53	t	6	ALA	C-O	-9.56	1.11	1.24
7	6	44	PHE	C-N	9.16	1.44	1.33

The worst 5 of 109 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	6	44	PHE	CA-C-O	-17.00	98.86	119.43
37	d	72	ARG	CB-CA-C	16.23	143.92	109.99
7	6	41	HIS	CA-C-N	13.99	137.32	119.84
7	6	41	HIS	C-N-CA	13.99	137.32	119.84
7	6	41	HIS	O-C-N	-13.80	108.78	121.20

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	6	41	HIS	Mainchain
43	j	58	ASN	Mainchain
49	p	45	GLU	Mainchain
49	p	48	GLU	Mainchain
49	p	50	THR	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	444	0	461	24	0
2	1	409	0	440	22	0
3	2	377	0	418	17	0
4	3	504	0	574	25	0
5	4	302	0	340	12	0
6	5	647	0	336	9	0
7	6	522	0	522	98	0
8	A	62336	0	31370	1659	0
9	B	2570	0	1301	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	C	2082	0	2157	102	0
11	D	1565	0	1616	51	0
12	E	1552	0	1618	76	0
13	F	1410	0	1447	76	0
14	G	1323	0	1374	54	0
15	H	1111	0	1148	50	0
16	I	693	0	347	11	0
17	J	1129	0	1162	35	0
18	K	938	0	1012	41	0
19	L	1045	0	1117	55	0
20	M	1074	0	1157	35	0
21	N	960	0	1000	37	0
22	O	892	0	923	26	0
23	P	917	0	965	38	0
24	Q	947	0	1022	32	0
25	R	816	0	839	37	0
26	S	857	0	922	30	0
27	T	738	0	807	25	0
28	U	779	0	834	42	0
29	V	753	0	780	35	0
30	W	575	0	592	20	0
31	X	625	0	655	32	0
32	Y	509	0	543	22	0
33	Z	449	0	491	16	0
34	a	33050	0	16648	1415	0
35	b	1704	0	1732	102	0
36	c	1624	0	1699	79	0
37	d	1643	0	1710	139	0
38	e	1141	0	1170	59	0
39	f	817	0	808	51	0
40	g	1181	0	1240	85	0
41	h	979	0	1034	48	0
42	i	1022	0	1070	82	0
43	j	786	0	828	65	0
44	k	869	0	878	43	0
45	l	955	0	1019	57	0
46	m	883	0	944	53	0
47	n	799	0	841	48	0
48	o	714	0	737	22	0
49	p	649	0	666	61	0
50	q	648	0	691	53	0
51	r	535	0	552	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	s	658	0	685	53	0
53	t	665	0	714	51	0
54	u	506	0	502	19	0
55	v	121	0	128	3	0
56	w	1631	0	836	83	0
57	x	82	0	43	3	0
58	y	1078	0	1134	50	0
59	0	1	0	0	0	0
59	4	1	0	0	0	0
59	6	1	0	0	0	0
59	A	206	0	0	0	0
59	B	6	0	0	0	0
59	C	1	0	0	0	0
59	D	1	0	0	0	0
59	S	1	0	0	0	0
59	a	35	0	0	0	0
60	4	1	0	0	0	0
60	6	1	0	0	0	0
61	A	1	0	0	0	0
61	M	1	0	0	0	0
All	All	146847	0	98599	4991	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 21.

The worst 5 of 4991 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)
34:a:151:A:C6	34:a:171:A:N1	1.85	1.45
50:q:19:SER:OG	50:q:70:LYS:HD2	1.23	1.36
34:a:151:A:N7	34:a:170:U:N3	1.73	1.35
7:6:42:PRO:N	7:6:42:PRO:CA	1.70	1.32
49:p:43:ALA:HB1	49:p:48:GLU:CB	1.58	1.31

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	54/57 (95%)	47 (87%)	7 (13%)	0	100	100
2	1	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
3	2	44/46 (96%)	38 (86%)	6 (14%)	0	100	100
4	3	62/65 (95%)	54 (87%)	6 (10%)	2 (3%)	3	21
5	4	36/38 (95%)	27 (75%)	9 (25%)	0	100	100
6	5	129/165 (78%)	94 (73%)	35 (27%)	0	100	100
7	6	64/70 (91%)	47 (73%)	14 (22%)	3 (5%)	2	14
10	C	269/273 (98%)	230 (86%)	38 (14%)	1 (0%)	30	62
11	D	207/209 (99%)	187 (90%)	20 (10%)	0	100	100
12	E	199/201 (99%)	177 (89%)	22 (11%)	0	100	100
13	F	175/179 (98%)	157 (90%)	18 (10%)	0	100	100
14	G	174/177 (98%)	156 (90%)	18 (10%)	0	100	100
15	H	147/149 (99%)	116 (79%)	29 (20%)	2 (1%)	9	39
16	I	139/142 (98%)	103 (74%)	36 (26%)	0	100	100
17	J	140/142 (99%)	129 (92%)	11 (8%)	0	100	100
18	K	120/123 (98%)	98 (82%)	22 (18%)	0	100	100
19	L	141/144 (98%)	123 (87%)	17 (12%)	1 (1%)	18	52
20	M	134/136 (98%)	124 (92%)	10 (8%)	0	100	100
21	N	118/127 (93%)	109 (92%)	9 (8%)	0	100	100
22	O	114/117 (97%)	99 (87%)	15 (13%)	0	100	100
23	P	112/115 (97%)	97 (87%)	15 (13%)	0	100	100
24	Q	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
25	R	101/103 (98%)	82 (81%)	19 (19%)	0	100	100
26	S	108/110 (98%)	91 (84%)	17 (16%)	0	100	100
27	T	91/100 (91%)	75 (82%)	16 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	U	100/104 (96%)	86 (86%)	12 (12%)	2 (2%)	6	31
29	V	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
30	W	73/85 (86%)	67 (92%)	6 (8%)	0	100	100
31	X	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
32	Y	61/63 (97%)	53 (87%)	5 (8%)	3 (5%)	1	13
33	Z	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
35	b	216/240 (90%)	176 (82%)	39 (18%)	1 (0%)	24	59
36	c	204/233 (88%)	185 (91%)	19 (9%)	0	100	100
37	d	203/206 (98%)	162 (80%)	37 (18%)	4 (2%)	6	31
38	e	155/167 (93%)	141 (91%)	14 (9%)	0	100	100
39	f	98/135 (73%)	86 (88%)	12 (12%)	0	100	100
40	g	149/179 (83%)	132 (89%)	17 (11%)	0	100	100
41	h	127/130 (98%)	115 (91%)	12 (9%)	0	100	100
42	i	125/130 (96%)	103 (82%)	22 (18%)	0	100	100
43	j	96/103 (93%)	71 (74%)	23 (24%)	2 (2%)	5	31
44	k	114/129 (88%)	103 (90%)	11 (10%)	0	100	100
45	l	121/124 (98%)	93 (77%)	28 (23%)	0	100	100
46	m	112/118 (95%)	98 (88%)	14 (12%)	0	100	100
47	n	99/102 (97%)	87 (88%)	12 (12%)	0	100	100
48	o	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
49	p	80/82 (98%)	58 (72%)	21 (26%)	1 (1%)	9	40
50	q	78/84 (93%)	63 (81%)	14 (18%)	1 (1%)	9	40
51	r	63/75 (84%)	49 (78%)	14 (22%)	0	100	100
52	s	80/92 (87%)	69 (86%)	11 (14%)	0	100	100
53	t	83/87 (95%)	79 (95%)	3 (4%)	1 (1%)	10	42
54	u	63/71 (89%)	44 (70%)	18 (29%)	1 (2%)	7	36
55	v	12/14 (86%)	11 (92%)	1 (8%)	0	100	100
58	y	137/140 (98%)	125 (91%)	12 (9%)	0	100	100
All	All	5999/6374 (94%)	5166 (86%)	808 (14%)	25 (0%)	31	62

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	3	31	ILE
7	6	42	PRO
28	U	98	ASN
28	U	99	SER
37	d	37	PRO

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	47/48 (98%)	47 (100%)	0	100	100
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	38 (100%)	0	100	100
4	3	51/52 (98%)	50 (98%)	1 (2%)	48	72
5	4	34/34 (100%)	34 (100%)	0	100	100
7	6	59/62 (95%)	56 (95%)	3 (5%)	21	54
10	C	216/218 (99%)	216 (100%)	0	100	100
11	D	164/164 (100%)	164 (100%)	0	100	100
12	E	165/165 (100%)	165 (100%)	0	100	100
13	F	148/150 (99%)	148 (100%)	0	100	100
14	G	137/138 (99%)	137 (100%)	0	100	100
15	H	114/114 (100%)	112 (98%)	2 (2%)	51	74
17	J	116/116 (100%)	116 (100%)	0	100	100
18	K	103/104 (99%)	103 (100%)	0	100	100
19	L	102/103 (99%)	101 (99%)	1 (1%)	68	80
20	M	109/109 (100%)	108 (99%)	1 (1%)	70	81
21	N	100/103 (97%)	100 (100%)	0	100	100
22	O	86/87 (99%)	86 (100%)	0	100	100
23	P	99/100 (99%)	99 (100%)	0	100	100
24	Q	89/90 (99%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	R	84/84 (100%)	84 (100%)	0	100	100
26	S	93/93 (100%)	93 (100%)	0	100	100
27	T	80/84 (95%)	80 (100%)	0	100	100
28	U	83/85 (98%)	83 (100%)	0	100	100
29	V	78/78 (100%)	78 (100%)	0	100	100
30	W	57/63 (90%)	57 (100%)	0	100	100
31	X	67/68 (98%)	67 (100%)	0	100	100
32	Y	55/55 (100%)	55 (100%)	0	100	100
33	Z	48/49 (98%)	48 (100%)	0	100	100
35	b	180/198 (91%)	180 (100%)	0	100	100
36	c	170/190 (90%)	170 (100%)	0	100	100
37	d	172/173 (99%)	169 (98%)	3 (2%)	53	75
38	e	114/126 (90%)	114 (100%)	0	100	100
39	f	87/116 (75%)	87 (100%)	0	100	100
40	g	124/147 (84%)	123 (99%)	1 (1%)	73	82
41	h	104/105 (99%)	103 (99%)	1 (1%)	68	80
42	i	105/107 (98%)	105 (100%)	0	100	100
43	j	86/90 (96%)	85 (99%)	1 (1%)	63	79
44	k	89/99 (90%)	89 (100%)	0	100	100
45	l	103/104 (99%)	102 (99%)	1 (1%)	68	80
46	m	92/96 (96%)	92 (100%)	0	100	100
47	n	79/84 (94%)	79 (100%)	0	100	100
48	o	76/77 (99%)	76 (100%)	0	100	100
49	p	65/65 (100%)	62 (95%)	3 (5%)	24	58
50	q	74/78 (95%)	72 (97%)	2 (3%)	39	68
51	r	56/65 (86%)	56 (100%)	0	100	100
52	s	72/79 (91%)	72 (100%)	0	100	100
53	t	65/66 (98%)	64 (98%)	1 (2%)	57	76
54	u	46/61 (75%)	45 (98%)	1 (2%)	45	71
55	v	14/14 (100%)	13 (93%)	1 (7%)	13	44
58	y	112/115 (97%)	112 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	4752/4958 (96%)	4729 (100%)	23 (0%)	78 85

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	l	102	ASP
49	p	48	GLU
49	p	47	GLU
50	q	68	LYS
19	L	27	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 82 such sidechains are listed below:

Mol	Chain	Res	Type
43	j	15	HIS
49	p	63	GLN
43	j	58	ASN
47	n	34	ASN
52	s	68	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	a	1539/1542 (99%)	508 (33%)	0
56	w	75/76 (98%)	31 (41%)	0
57	x	3/15 (20%)	3 (100%)	0
8	A	2902/2903 (99%)	689 (23%)	53 (1%)
9	B	119/120 (99%)	28 (23%)	4 (3%)
All	All	4638/4656 (99%)	1259 (27%)	57 (1%)

5 of 1259 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	A	7	G
8	A	10	A
8	A	12	U
8	A	14	A
8	A	18	U

5 of 57 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	A	1451	C
9	B	66	A
8	A	2128	G
9	B	52	A
8	A	2790	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	PSU	A	2604	8	18,21,22	1.10	2 (11%)	22,30,33	1.95	5 (22%)
8	6MZ	A	1618	8	22,25,26	3.05	5 (22%)	30,36,39	4.17	11 (36%)
34	2MG	a	1516	34	23,26,27	2.96	8 (34%)	32,38,41	2.34	12 (37%)
8	PSU	A	1911	8	18,21,22	1.07	2 (11%)	22,30,33	1.87	4 (18%)
8	6MZ	A	2030	8	22,25,26	2.93	6 (27%)	30,36,39	4.57	14 (46%)
8	OMG	A	2251	8	23,26,27	2.39	9 (39%)	33,38,41	1.81	7 (21%)
8	PSU	A	2504	8	18,21,22	1.05	3 (16%)	22,30,33	1.71	4 (18%)
8	PSU	A	2580	8	18,21,22	1.18	3 (16%)	22,30,33	2.07	6 (27%)
8	OMU	A	2552	8	19,22,23	2.80	8 (42%)	26,31,34	1.82	5 (19%)
8	PSU	A	746	8	18,21,22	1.07	2 (11%)	22,30,33	1.84	4 (18%)
34	4OC	a	1402	34	20,23,24	2.90	8 (40%)	26,32,35	0.94	2 (7%)
34	2MG	a	966	56,34	23,26,27	3.03	7 (30%)	32,38,41	2.13	10 (31%)
34	PSU	a	516	34	18,21,22	0.88	1 (5%)	22,30,33	1.67	5 (22%)
8	G7M	A	2069	8	23,26,27	3.34	10 (43%)	35,39,42	1.62	7 (20%)
56	G7M	w	46	56	23,26,27	2.60	8 (34%)	35,39,42	2.33	10 (28%)
56	5MU	w	54	56	19,22,23	4.85	7 (36%)	28,32,35	3.61	9 (32%)
34	MA6	a	1518	34	23,26,27	1.54	6 (26%)	34,38,41	2.69	11 (32%)
56	MIA	w	37	56,34	28,31,32	2.61	6 (21%)	40,44,47	3.78	14 (35%)
34	2MG	a	1207	34	23,26,27	2.98	8 (34%)	32,38,41	2.20	11 (34%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	PSU	A	2457	8	18,21,22	1.06	3 (16%)	22,30,33	2.14	6 (27%)
8	5MC	A	747	8	18,22,23	3.52	7 (38%)	26,32,35	1.16	2 (7%)
8	OMC	A	2498	8,59	19,22,23	2.74	7 (36%)	26,31,34	0.77	0
8	PSU	A	955	8	18,21,22	1.14	2 (11%)	22,30,33	1.88	4 (18%)
34	G7M	a	527	34	23,26,27	3.48	10 (43%)	35,39,42	1.66	6 (17%)
34	5MC	a	967	34	18,22,23	3.72	7 (38%)	26,32,35	1.09	1 (3%)
8	2MA	A	2503	8,59	22,25,26	3.63	9 (40%)	33,37,40	2.16	7 (21%)
8	2MG	A	1835	8	23,26,27	2.85	7 (30%)	32,38,41	2.35	10 (31%)
8	PSU	A	2605	8	18,21,22	1.12	2 (11%)	22,30,33	1.80	4 (18%)
34	MA6	a	1519	34	23,26,27	1.48	6 (26%)	34,38,41	2.72	11 (32%)
56	4SU	w	8	56	18,21,22	3.75	8 (44%)	26,30,33	2.16	5 (19%)
56	PSU	w	39	56	18,21,22	1.01	1 (5%)	22,30,33	1.73	3 (13%)
34	UR3	a	1498	59,34	19,22,23	2.74	7 (36%)	26,32,35	1.50	4 (15%)
8	5MU	A	1939	8	19,22,23	4.60	7 (36%)	28,32,35	3.88	10 (35%)
34	5MC	a	1407	34	18,22,23	3.54	7 (38%)	26,32,35	1.15	2 (7%)
8	1MG	A	745	8	22,26,27	2.57	6 (27%)	33,39,42	2.08	9 (27%)
8	5MC	A	1962	8	18,22,23	3.58	7 (38%)	26,32,35	1.17	2 (7%)
8	PSU	A	1917	8	18,21,22	1.11	3 (16%)	22,30,33	1.93	5 (22%)
56	PSU	w	32	56	18,21,22	1.04	1 (5%)	22,30,33	1.73	4 (18%)
8	2MG	A	2445	8	23,26,27	1.88	6 (26%)	32,38,41	2.84	12 (37%)
56	PSU	w	55	56	18,21,22	1.08	1 (5%)	22,30,33	1.80	4 (18%)
8	3TD	A	1915	8	18,22,23	4.25	5 (27%)	22,32,35	1.49	2 (9%)

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
8	PSU	A	2604	8	-	0/7/25/26	0/2/2/2
8	6MZ	A	1618	8	-	2/9/27/28	0/3/3/3
34	2MG	a	1516	34	-	0/9/27/28	0/3/3/3
8	PSU	A	1911	8	-	1/7/25/26	0/2/2/2
8	6MZ	A	2030	8	-	3/9/27/28	0/3/3/3
8	OMG	A	2251	8	-	1/9/27/28	0/3/3/3
8	PSU	A	2504	8	-	2/7/25/26	0/2/2/2
8	PSU	A	2580	8	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	OMU	A	2552	8	-	5/9/27/28	0/2/2/2
8	PSU	A	746	8	-	4/7/25/26	0/2/2/2
34	4OC	a	1402	34	-	0/9/29/30	0/2/2/2
34	2MG	a	966	56,34	-	2/9/27/28	0/3/3/3
34	PSU	a	516	34	-	2/7/25/26	0/2/2/2
8	G7M	A	2069	8	-	1/7/25/26	0/3/3/3
56	G7M	w	46	56	-	3/7/25/26	0/3/3/3
56	5MU	w	54	56	-	0/7/25/26	0/2/2/2
34	MA6	a	1518	34	-	3/11/29/30	0/3/3/3
56	MIA	w	37	56,34	-	8/15/33/34	0/3/3/3
34	2MG	a	1207	34	-	3/9/27/28	0/3/3/3
8	PSU	A	2457	8	-	0/7/25/26	0/2/2/2
8	5MC	A	747	8	-	3/7/25/26	0/2/2/2
8	OMC	A	2498	8,59	-	2/9/27/28	0/2/2/2
8	PSU	A	955	8	-	3/7/25/26	0/2/2/2
34	G7M	a	527	34	-	1/7/25/26	0/3/3/3
34	5MC	a	967	34	-	4/7/25/26	0/2/2/2
8	2MA	A	2503	8,59	-	2/7/25/26	0/3/3/3
8	2MG	A	1835	8	-	2/9/27/28	0/3/3/3
8	PSU	A	2605	8	-	2/7/25/26	0/2/2/2
34	MA6	a	1519	34	-	0/11/29/30	0/3/3/3
56	4SU	w	8	56	-	0/7/25/26	0/2/2/2
56	PSU	w	39	56	-	3/7/25/26	0/2/2/2
34	UR3	a	1498	59,34	-	6/7/25/26	0/2/2/2
8	5MU	A	1939	8	-	0/7/25/26	0/2/2/2
34	5MC	a	1407	34	-	0/7/25/26	0/2/2/2
8	1MG	A	745	8	-	0/7/25/26	0/3/3/3
8	5MC	A	1962	8	-	0/7/25/26	0/2/2/2
8	PSU	A	1917	8	-	0/7/25/26	0/2/2/2
56	PSU	w	32	56	-	5/7/25/26	0/2/2/2
8	2MG	A	2445	8	-	2/9/27/28	0/3/3/3
56	PSU	w	55	56	-	1/7/25/26	0/2/2/2
8	3TD	A	1915	8	-	3/7/25/26	0/2/2/2

The worst 5 of 228 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1915	3TD	C6-C5	12.78	1.50	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1618	6MZ	C6-N6	12.41	1.47	1.34
8	A	2030	6MZ	C6-N6	11.54	1.46	1.34
8	A	2503	2MA	C4-N3	11.22	1.48	1.34
56	w	54	5MU	C2-N1	11.06	1.56	1.38

The worst 5 of 264 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	w	37	MIA	C11-S10-C2	17.08	115.02	102.27
8	A	2030	6MZ	C4-N9-C8	14.01	120.91	105.73
8	A	1618	6MZ	C4-N9-C8	12.93	119.74	105.73
8	A	1939	5MU	C5-C4-N3	12.70	126.15	115.31
56	w	54	5MU	C5-C4-N3	12.05	125.60	115.31

There are no chirality outliers.

5 of 79 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	746	PSU	C2'-C1'-C5-C4
8	A	746	PSU	C2'-C1'-C5-C6
8	A	746	PSU	O4'-C1'-C5-C6
8	A	955	PSU	C2'-C1'-C5-C4
8	A	1618	6MZ	C5-C6-N6-C9

There are no ring outliers.

29 monomers are involved in 67 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	a	1516	2MG	2	0
8	A	2030	6MZ	4	0
8	A	2251	OMG	1	0
8	A	2504	PSU	2	0
8	A	2552	OMU	2	0
8	A	746	PSU	1	0
34	a	1402	4OC	1	0
34	a	966	2MG	2	0
34	a	516	PSU	4	0
56	w	54	5MU	2	0
34	a	1518	MA6	3	0
56	w	37	MIA	9	0
34	a	1207	2MG	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	2457	PSU	2	0
8	A	747	5MC	1	0
8	A	955	PSU	2	0
34	a	527	G7M	2	0
34	a	967	5MC	5	0
34	a	1519	MA6	1	0
56	w	8	4SU	2	0
56	w	39	PSU	2	0
34	a	1498	UR3	2	0
8	A	1939	5MU	1	0
34	a	1407	5MC	1	0
8	A	1962	5MC	1	0
56	w	32	PSU	1	0
8	A	2445	2MG	1	0
56	w	55	PSU	5	0
8	A	1915	3TD	9	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 257 ligands modelled in this entry, 257 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 ⓘ

There are no chain breaks in this entry.

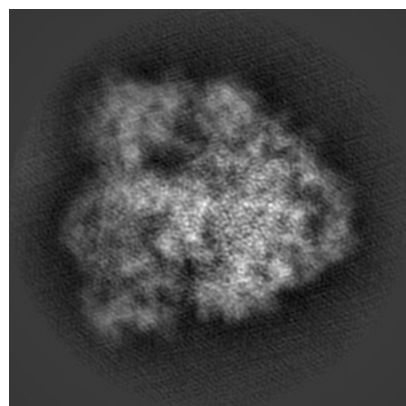
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10907. These allow visual inspection of the internal detail of the map and identification of artifacts.

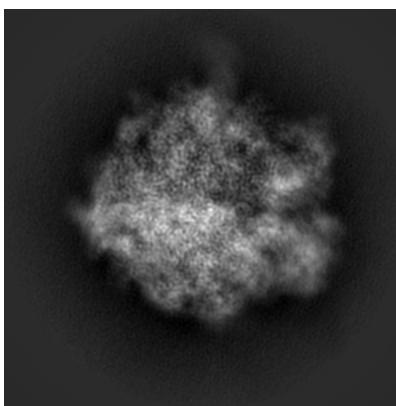
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

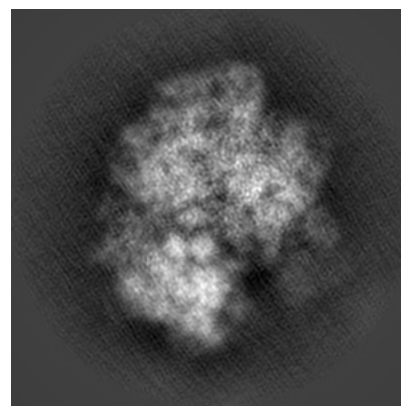
6.1.1 Primary map



X

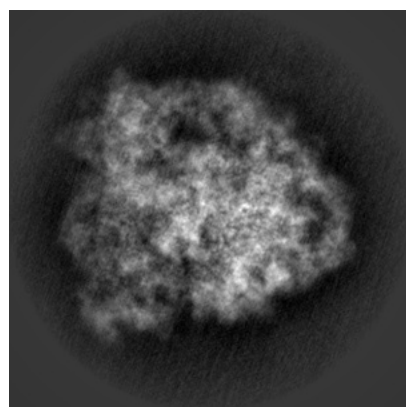


Y

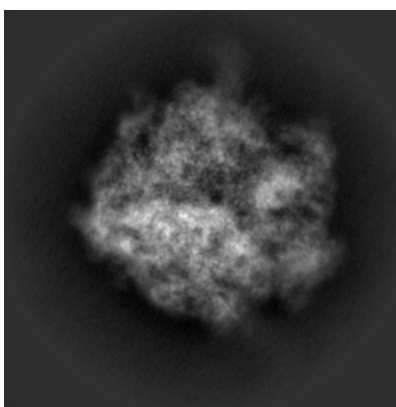


Z

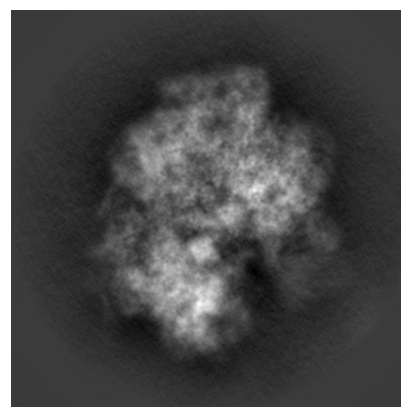
6.1.2 Raw map



X



Y

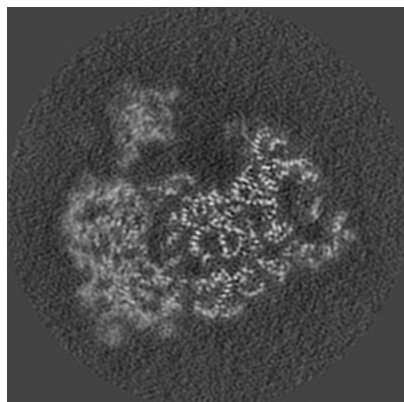


Z

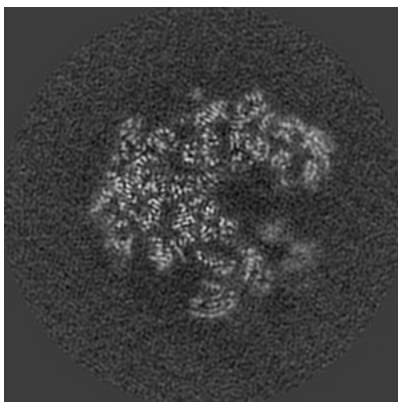
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

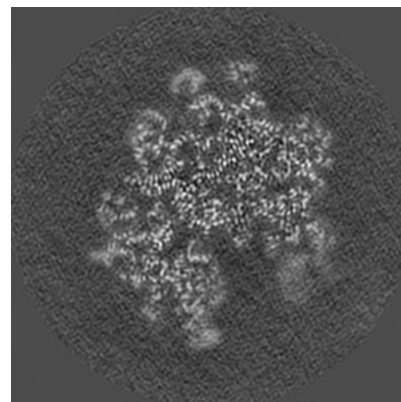
6.2.1 Primary map



X Index: 144

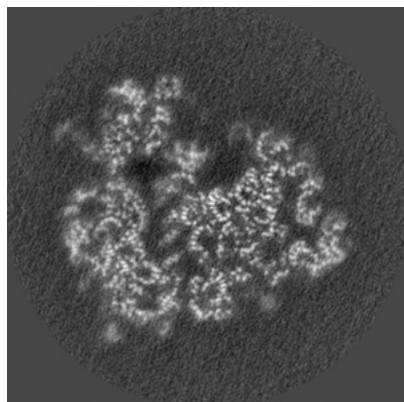


Y Index: 144

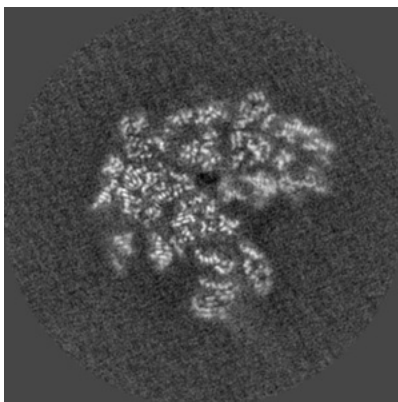


Z Index: 144

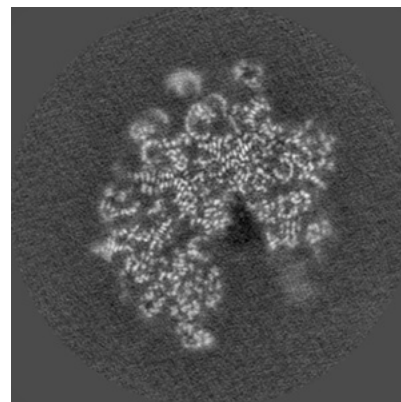
6.2.2 Raw map



X Index: 144



Y Index: 144

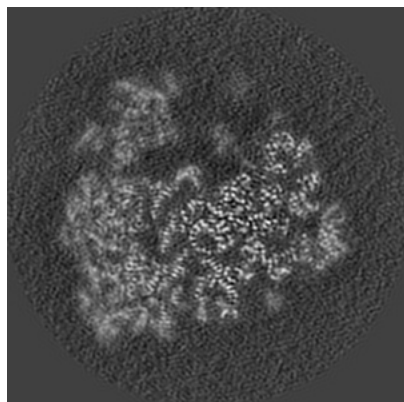


Z Index: 144

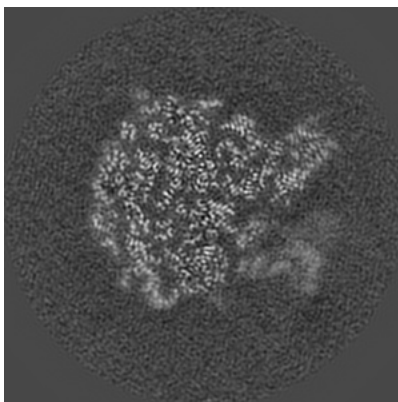
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

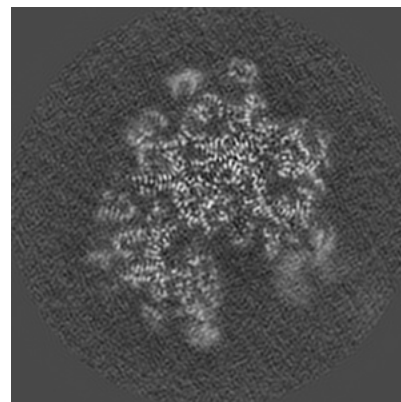
6.3.1 Primary map



X Index: 138

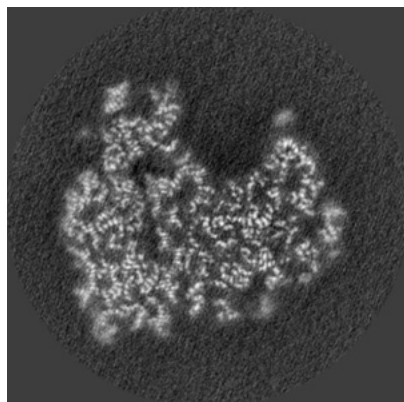


Y Index: 165

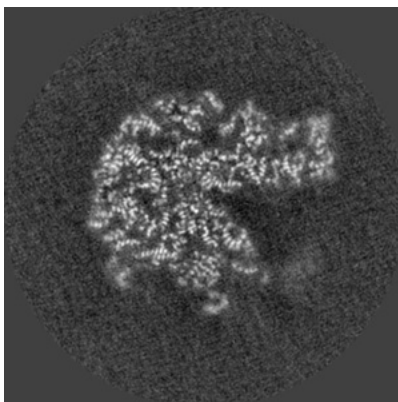


Z Index: 146

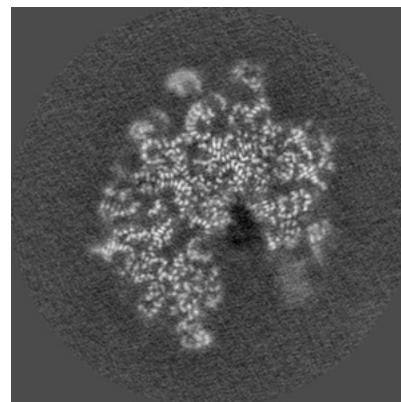
6.3.2 Raw map



X Index: 136



Y Index: 157

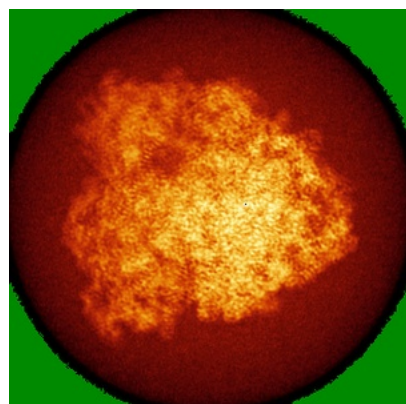


Z Index: 145

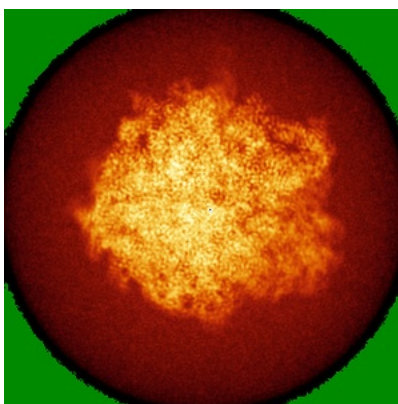
The images above show the largest variance slices of the map in three orthogonal directions.

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

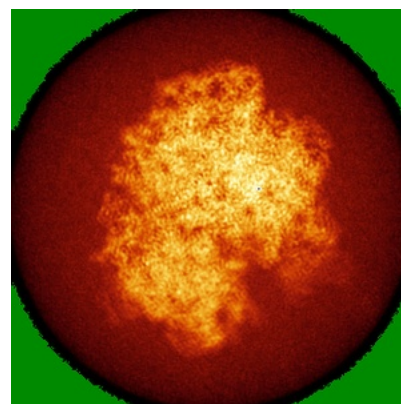
6.4.1 Primary map



X

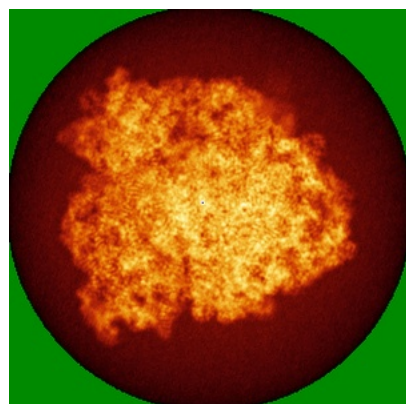


Y

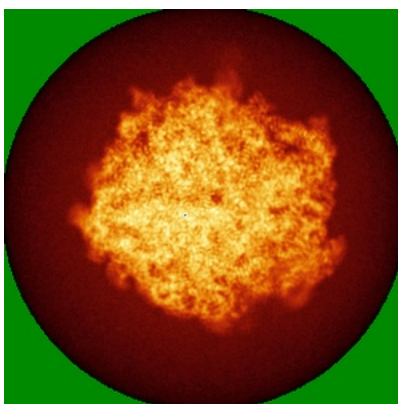


Z

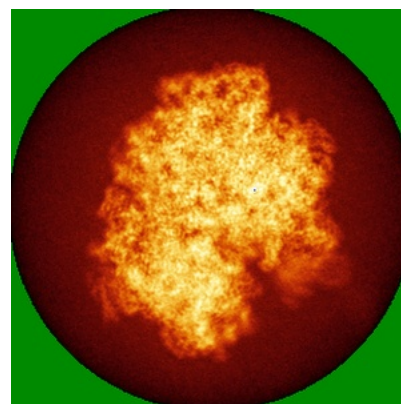
6.4.2 Raw map



X



Y



Z

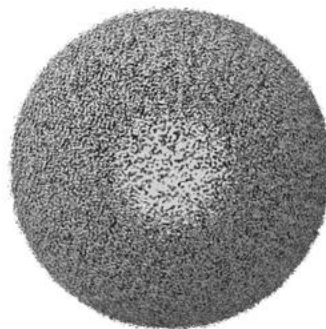
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

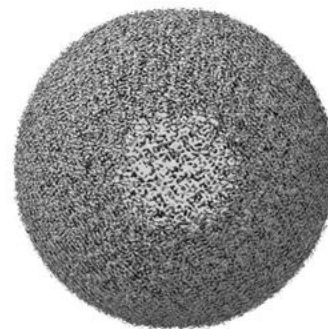
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. 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



X



Y



Z

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.

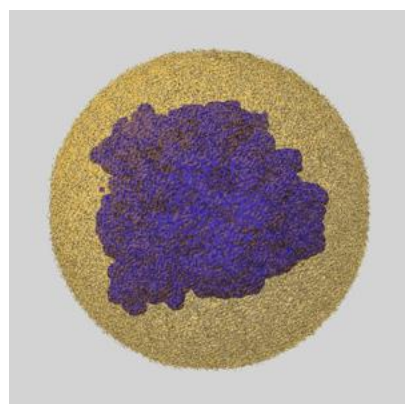
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

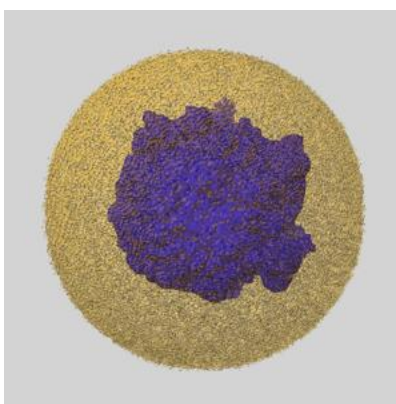
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

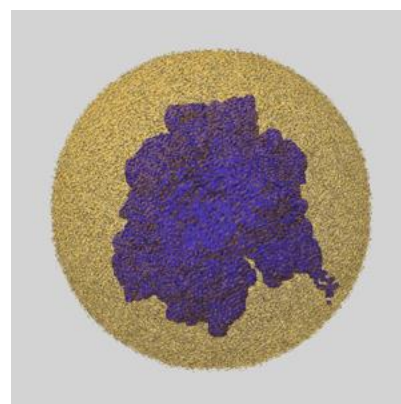
6.6.1 emd_10907_msk_1.map [i](#)



X



Y

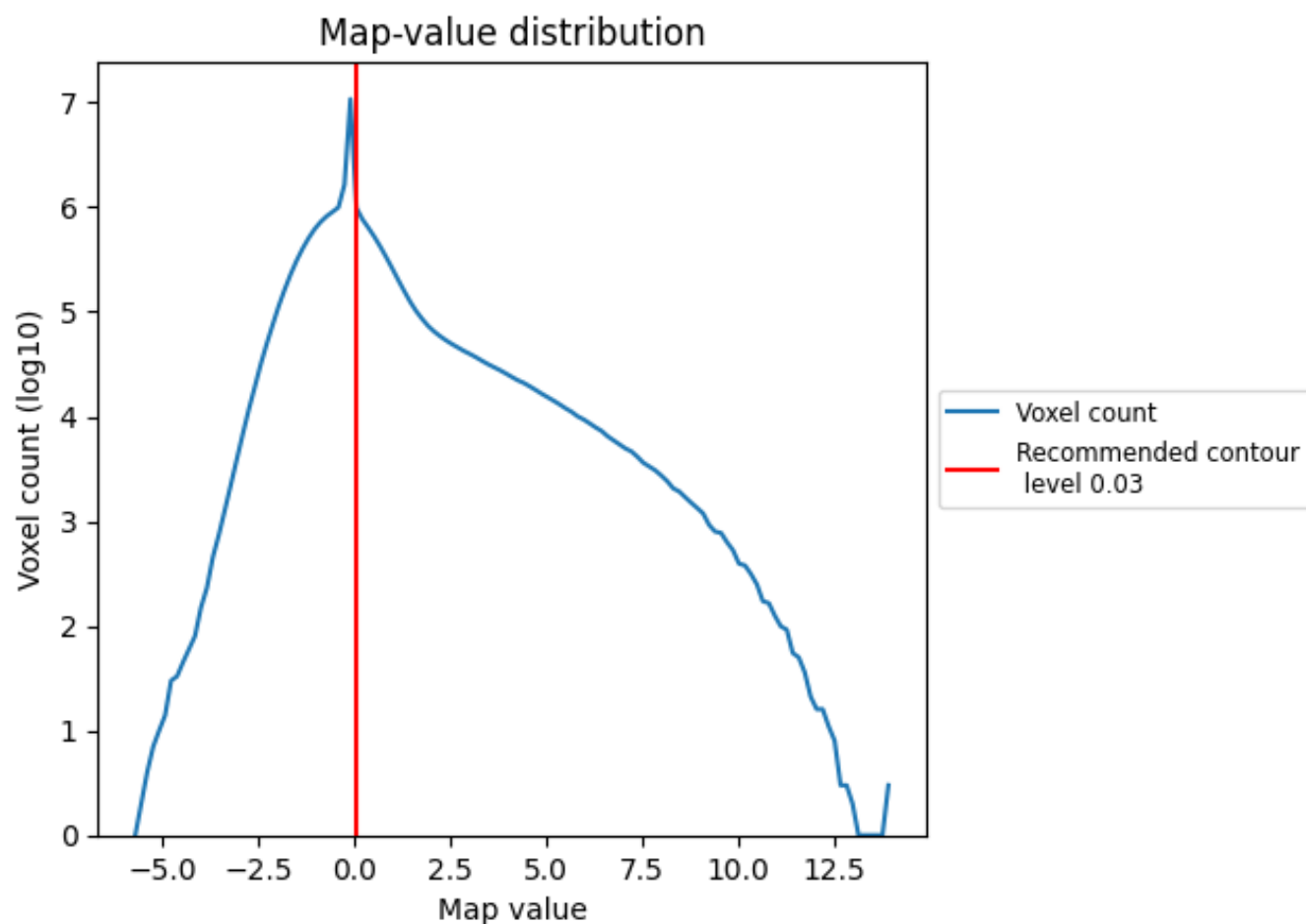


Z

7 Map analysis [i](#)

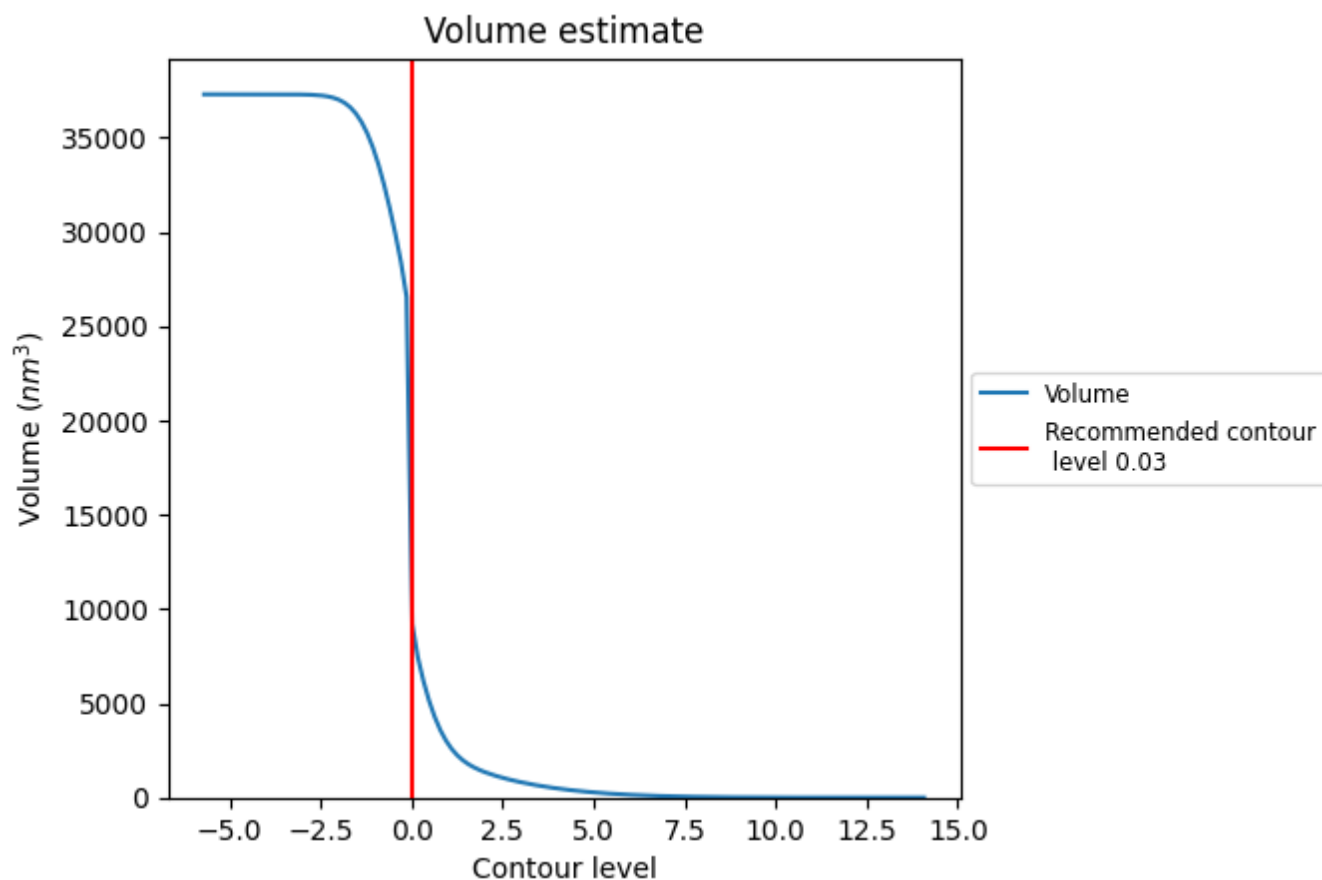
This section contains the results of statistical analysis of the map.

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.

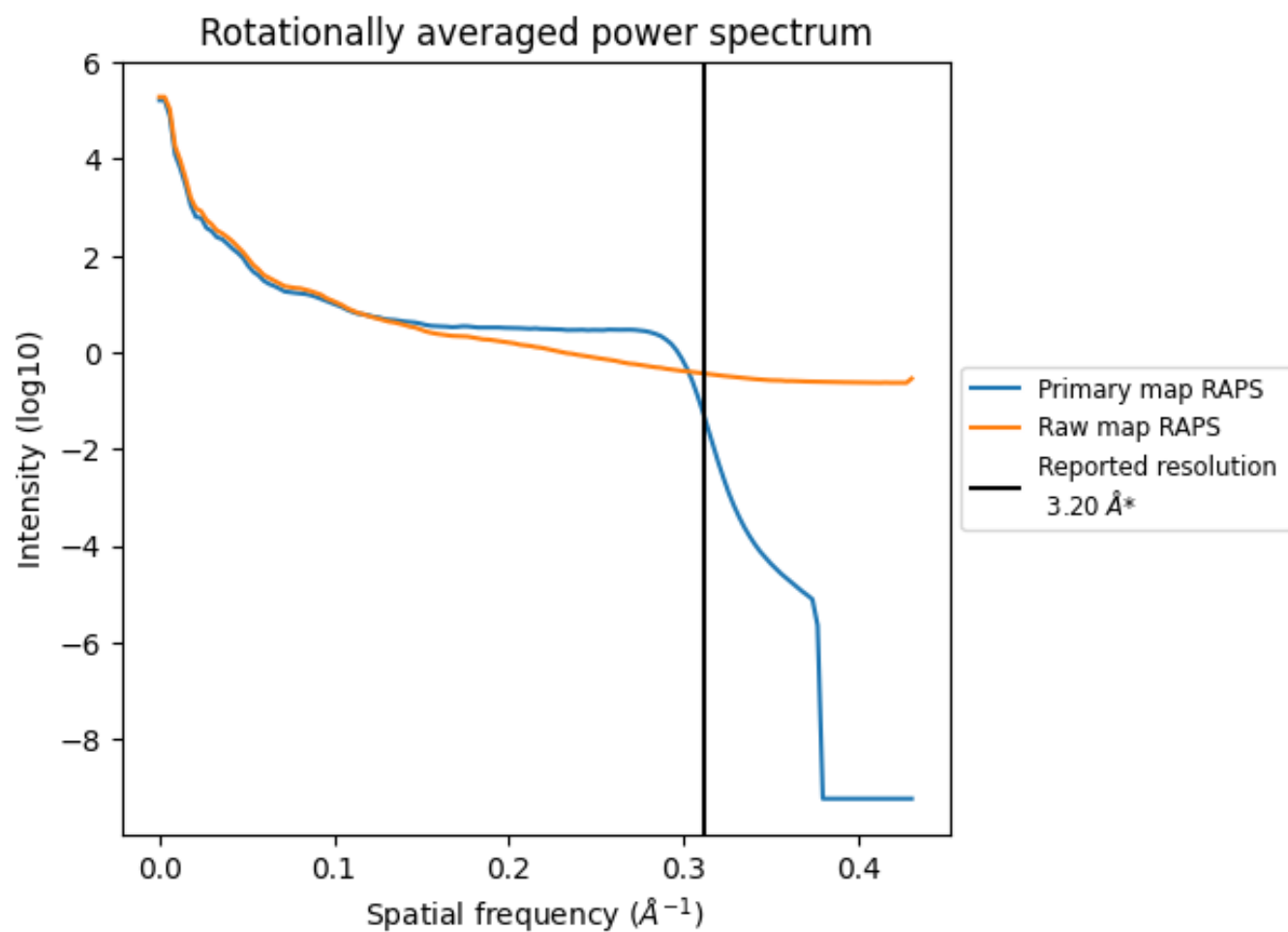
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 9022 nm^3 ; this corresponds to an approximate mass of 8149 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 ⓘ

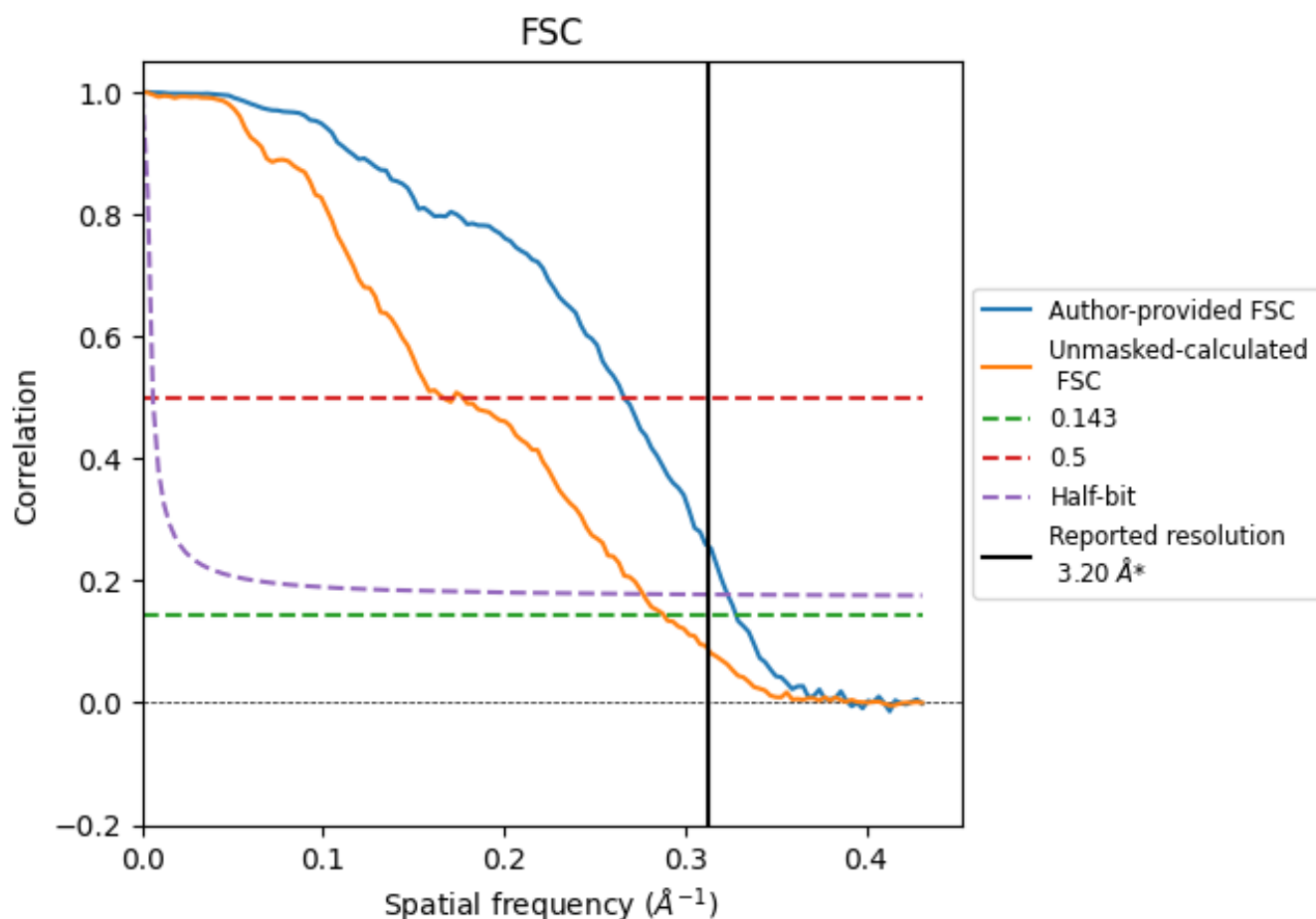


*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

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 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

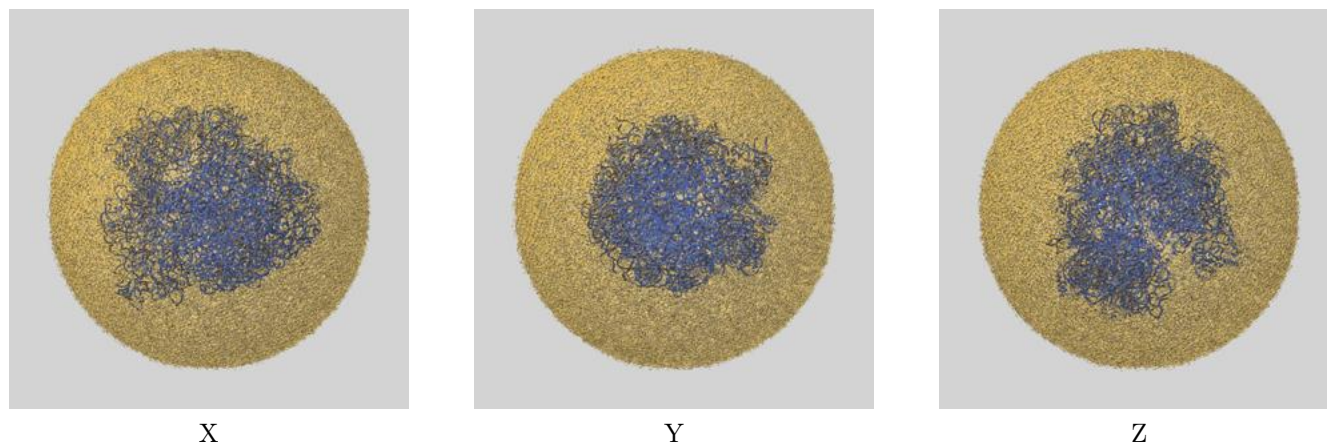
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.05	3.76	3.09
Unmasked-calculated*	3.47	6.02	3.61

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

9 Map-model fit [i](#)

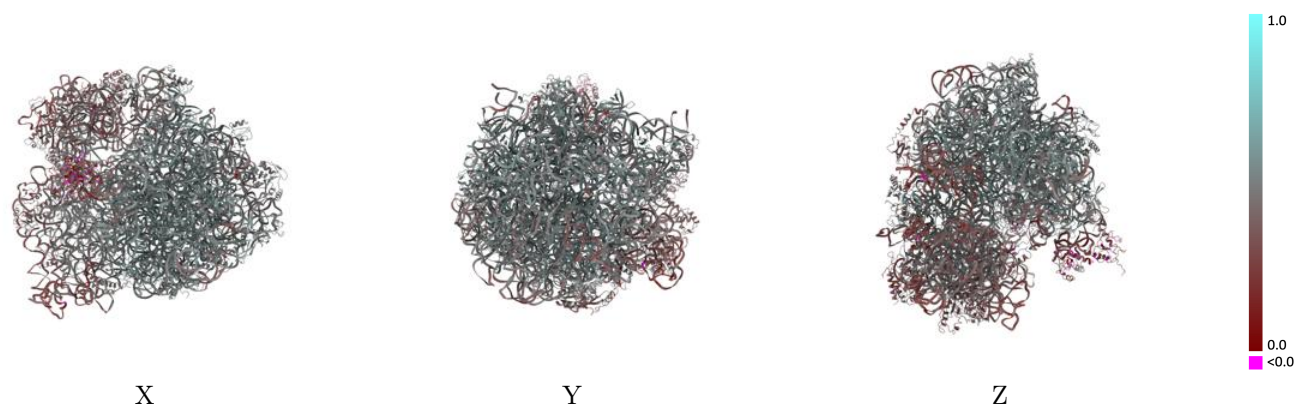
This section contains information regarding the fit between EMDB map EMD-10907 and PDB model 6YST. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



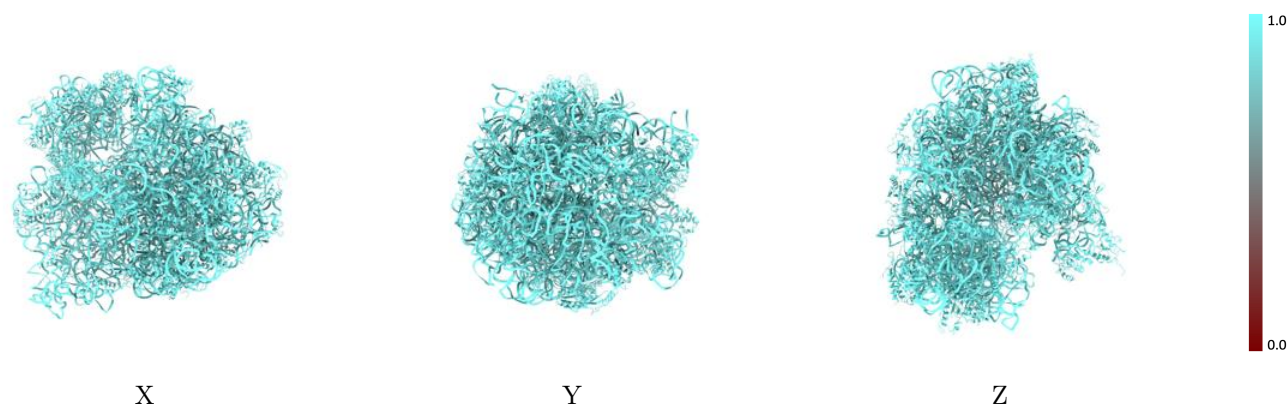
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



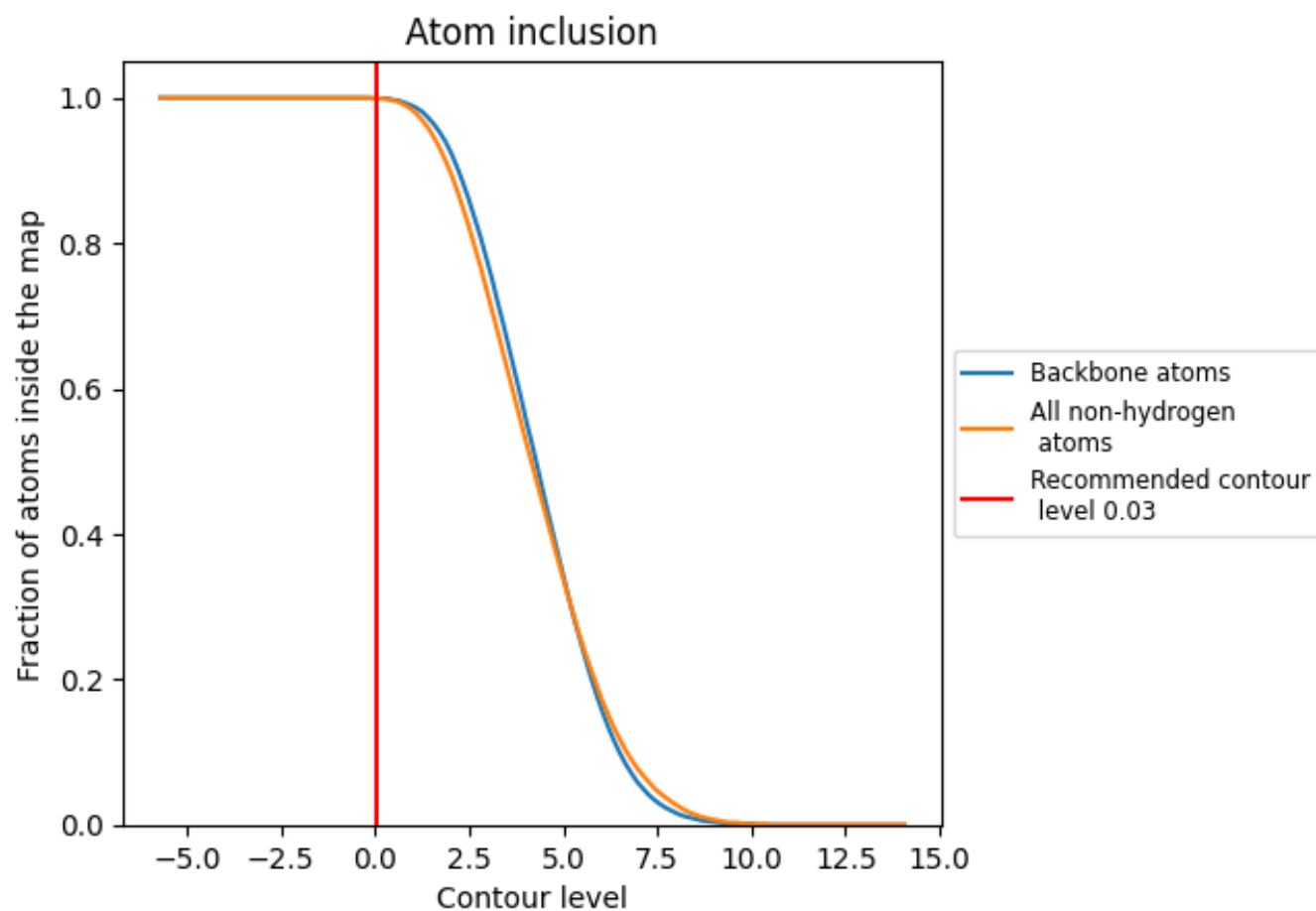
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9990	 0.4710
0	 1.0000	 0.5460
1	 0.9980	 0.5240
2	 0.9920	 0.5500
3	 0.9980	 0.5580
4	 1.0000	 0.5380
5	 0.9990	 0.2450
6	 0.9980	 0.3760
A	 1.0000	 0.4980
B	 1.0000	 0.4810
C	 0.9990	 0.5550
D	 0.9990	 0.5400
E	 1.0000	 0.5020
F	 1.0000	 0.4230
G	 1.0000	 0.4820
H	 0.9930	 0.3990
I	 0.9700	 0.2290
J	 1.0000	 0.5400
K	 0.9980	 0.5350
L	 1.0000	 0.5280
M	 0.9990	 0.5420
N	 0.9990	 0.5420
O	 1.0000	 0.5020
P	 1.0000	 0.5300
Q	 0.9990	 0.5360
R	 1.0000	 0.5190
S	 0.9950	 0.5390
T	 0.9990	 0.5110
U	 1.0000	 0.4900
V	 1.0000	 0.5150
W	 0.9980	 0.5480
X	 1.0000	 0.5250
Y	 1.0000	 0.4480
Z	 1.0000	 0.5390
a	 1.0000	 0.4290



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Chain	Atom inclusion	Q-score
b	 0.9930	 0.3760
c	 0.9990	 0.4270
d	 0.9990	 0.3810
e	 0.9990	 0.4730
f	 1.0000	 0.4460
g	 0.9970	 0.3300
h	 1.0000	 0.4940
i	 1.0000	 0.3800
j	 0.9990	 0.3760
k	 0.9990	 0.4910
l	 0.9990	 0.4710
m	 1.0000	 0.3700
n	 1.0000	 0.4140
o	 0.9990	 0.4950
p	 1.0000	 0.4230
q	 1.0000	 0.4770
r	 0.9980	 0.4800
s	 1.0000	 0.3990
t	 1.0000	 0.4170
u	 1.0000	 0.4470
v	 1.0000	 0.5450
w	 0.9930	 0.3510
x	 1.0000	 0.4270
y	 0.9980	 0.4990