



wwPDB EM Validation Summary Report ⓘ

May 23, 2026 – 05:47 PM EDT

PDB ID : 9PIJ / pdb_00009pij
EMDB ID : EMD-71669
Title : E. coli 70S ribosome bound to Minocycline
Authors : Devarkar, S.C.; Lomakin, I.B.; Bunick, C.G.
Deposited on : 2025-07-10
Resolution : 2.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

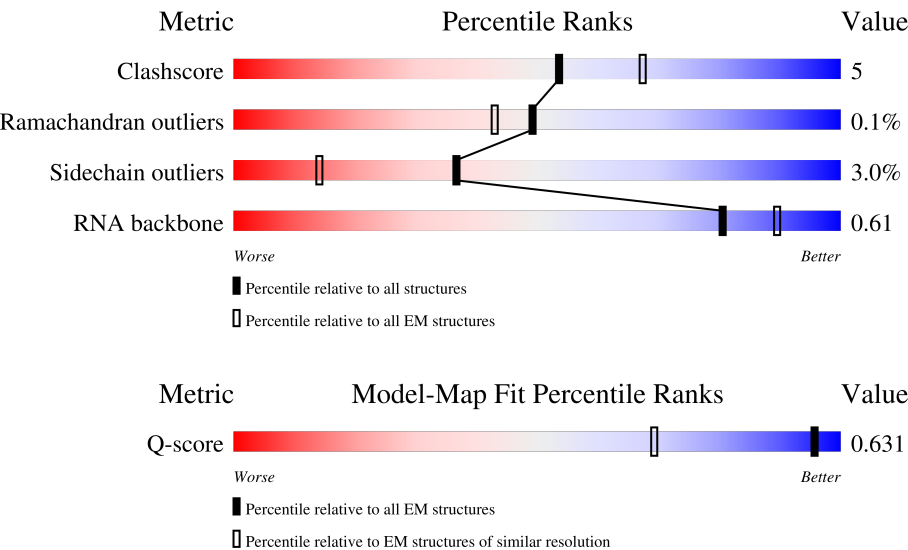
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

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

The reported resolution of this entry is 2.20 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.






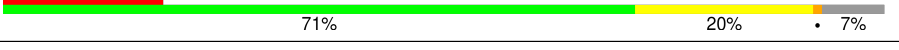
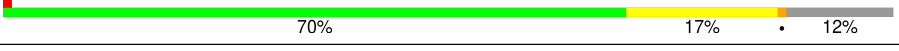








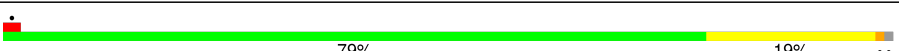
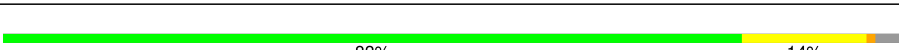

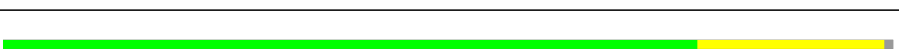




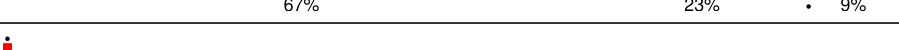
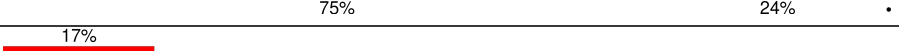


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3184 (1.71 - 2.70)

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	55	
2	1	46	
3	2	65	


























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Mol	Chain	Length	Quality of chain
4	3	38	
5	4	70	
6	A	1542	
7	B	241	
8	C	233	
9	D	206	
10	E	167	
11	F	135	
12	G	179	
13	H	130	
14	I	130	
15	J	103	
16	K	129	
17	L	124	
18	M	118	
19	N	101	
20	O	89	
21	P	82	
22	Q	84	
23	R	75	
24	S	92	
25	T	87	
26	U	71	
27	X	22	
28	Z	75	


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Mol	Chain	Length	Quality of chain
29	a	2904	 71% 22% 5%
30	b	120	 83% 15% ..
31	c	273	 92% 7% .
32	d	209	 90% 9% .
33	e	201	 95% 5%
34	f	179	 74% 24% ..
35	g	177	 74% 23% ..
36	h	149	 21% 5% 72%
37	i	142	 87% 11% .
38	j	123	 83% 16% .
39	k	144	 90% 10%
40	l	136	 79% 21%
41	m	127	 83% 10% 7%
42	n	117	 85% 13% ...
43	o	115	 86% 13% .
44	p	118	 88% 11% .
45	q	103	 81% 18% .
46	r	110	 92% 8%
47	s	100	 78% 15% 7%
48	t	104	 88% 10% .
49	u	94	 81% 18% .
50	v	85	 85% 7% 8%
51	w	78	 87% 12% .
52	x	63	 89% 10% .
53	y	59	 5% 80% 15% ...

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Mol	Chain	Length	Quality of chain
54	z	57	 A horizontal bar chart showing the quality of chain 54. The bar is 88% green and 11% yellow. A small red square is at the start, and a small grey square is at the end. The text '88%' is centered under the green portion, and '11%' is centered under the yellow portion. A small black dot is at the far right end of the bar.

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 141677 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

- Molecule 5 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 6 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	1500	Total	C	N	O	P	0	0
			32211	14373	5919	10419	1500		

- Molecule 7 is a protein called 30S ribosomal protein S2.

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

- Molecule 8 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 9 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 10 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 11 is a protein called Small ribosomal subunit protein bS6.

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

- Molecule 12 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 13 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 14 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 15 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 16 is a protein called 30S ribosomal protein S11.

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

- Molecule 17 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 18 is a protein called Small ribosomal subunit protein uS13.

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

- Molecule 19 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 20 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 21 is a protein called Small ribosomal subunit protein bS16.

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

- Molecule 22 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 23 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 24 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 25 is a protein called Small ribosomal subunit protein bS20.

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

- Molecule 26 is a protein called Small ribosomal subunit protein bS21.

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

- Molecule 27 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	10	Total	C	N	O	P	0	0
			211	95	35	71	10		

- Molecule 28 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	75	Total	C	N	O	P	S	
			1605	716	291	522	75	1	
								0	0

- Molecule 29 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	2753	Total	C	N	O	P		
			59130	26384	10897	19096	2753		
								0	0

- Molecule 30 is a RNA chain called 5S rRNA.

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

- Molecule 31 is a protein called 50S ribosomal protein L2.

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

- Molecule 32 is a protein called 50S ribosomal protein L3.

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

- Molecule 33 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 34 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 35 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 36 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 37 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 38 is a protein called Large ribosomal subunit protein uL14.

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

- Molecule 39 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 40 is a protein called 50S ribosomal protein L16.

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

- Molecule 41 is a protein called Large ribosomal subunit protein bL17.

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

- Molecule 42 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 43 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 44 is a protein called 50S ribosomal protein L20.

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

- Molecule 45 is a protein called Ribosomal protein L21.

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

- Molecule 46 is a protein called 50S ribosomal protein L22.

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

- Molecule 47 is a protein called 50S ribosomal protein L23.

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

- Molecule 48 is a protein called 50S ribosomal protein L24.

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

- Molecule 49 is a protein called Large ribosomal subunit protein bL25.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L28.

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

- Molecule 52 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 53 is a protein called 50S ribosomal protein L30.

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

- Molecule 54 is a protein called 50S ribosomal protein L32.

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

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
55	3	1	Total	Zn	0
			1	1	

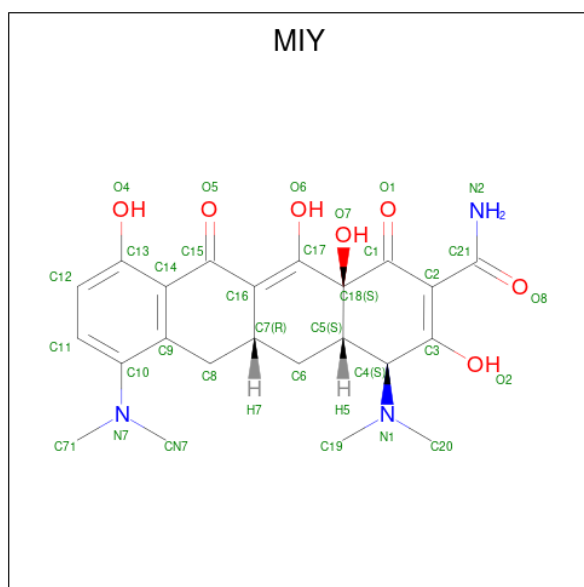
- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	A	85	Total	Mg	0
			85	85	
56	a	248	Total	Mg	0
			248	248	
56	b	5	Total	Mg	0
			5	5	
56	p	2	Total	Mg	0
			2	2	

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

Mol	Chain	Residues	Atoms		AltConf
57	A	37	Total	K	0
			37	37	
57	a	109	Total	K	0
			109	109	
57	b	1	Total	K	0
			1	1	
57	c	1	Total	K	0
			1	1	

- Molecule 58 is (4S,4AS,5AR,12AS)-4,7-BIS(DIMETHYLAMINO)-3,10,12,12A-TETRAHYDROXY-1,11-DIOXO-1,4,4A,5,5A,6,11,12A-OCTAHYDROTETRACENE-2-CARBOXAMIDE (CCD ID: MIY) (formula: C₂₃H₂₇N₃O₇) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
58	A	1	Total	C	N	O	0
			33	23	3	7	
58	a	1	Total	C	N	O	0
			33	23	3	7	

- Molecule 59 is water.

Mol	Chain	Residues	Atoms		AltConf
59	0	1	Total	O	0
			1	1	
59	1	8	Total	O	0
			8	8	
59	3	2	Total	O	0
			2	2	
59	A	119	Total	O	0
			119	119	
59	O	1	Total	O	0
			1	1	
59	U	1	Total	O	0
			1	1	
59	a	1450	Total	O	0
			1450	1450	
59	b	10	Total	O	0
			10	10	
59	c	6	Total	O	0
			6	6	
59	d	3	Total	O	0
			3	3	
59	e	4	Total	O	0
			4	4	
59	h	1	Total	O	0
			1	1	
59	i	2	Total	O	0
			2	2	
59	j	1	Total	O	0
			1	1	
59	k	7	Total	O	0
			7	7	
59	l	1	Total	O	0
			1	1	
59	m	6	Total	O	0
			6	6	
59	p	5	Total	O	0
			5	5	

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Mol	Chain	Residues	Atoms		AltConf
59	q	5	Total 5	O 5	0
59	r	2	Total 2	O 2	0
59	s	2	Total 2	O 2	0
59	t	1	Total 1	O 1	0
59	u	2	Total 2	O 2	0
59	v	2	Total 2	O 2	0
59	w	2	Total 2	O 2	0
59	y	1	Total 1	O 1	0
59	z	4	Total 4	O 4	0

3 Residue-property plots [i](#)


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

• Molecule 1: 50S ribosomal protein L33

Chain 0: 




• Molecule 2: 50S ribosomal protein L34

Chain 1: 




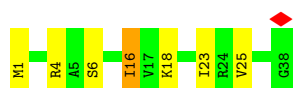
• Molecule 3: 50S ribosomal protein L35

Chain 2: 




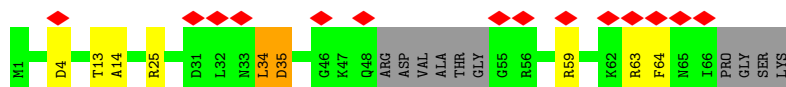
• Molecule 4: 50S ribosomal protein L36

Chain 3: 

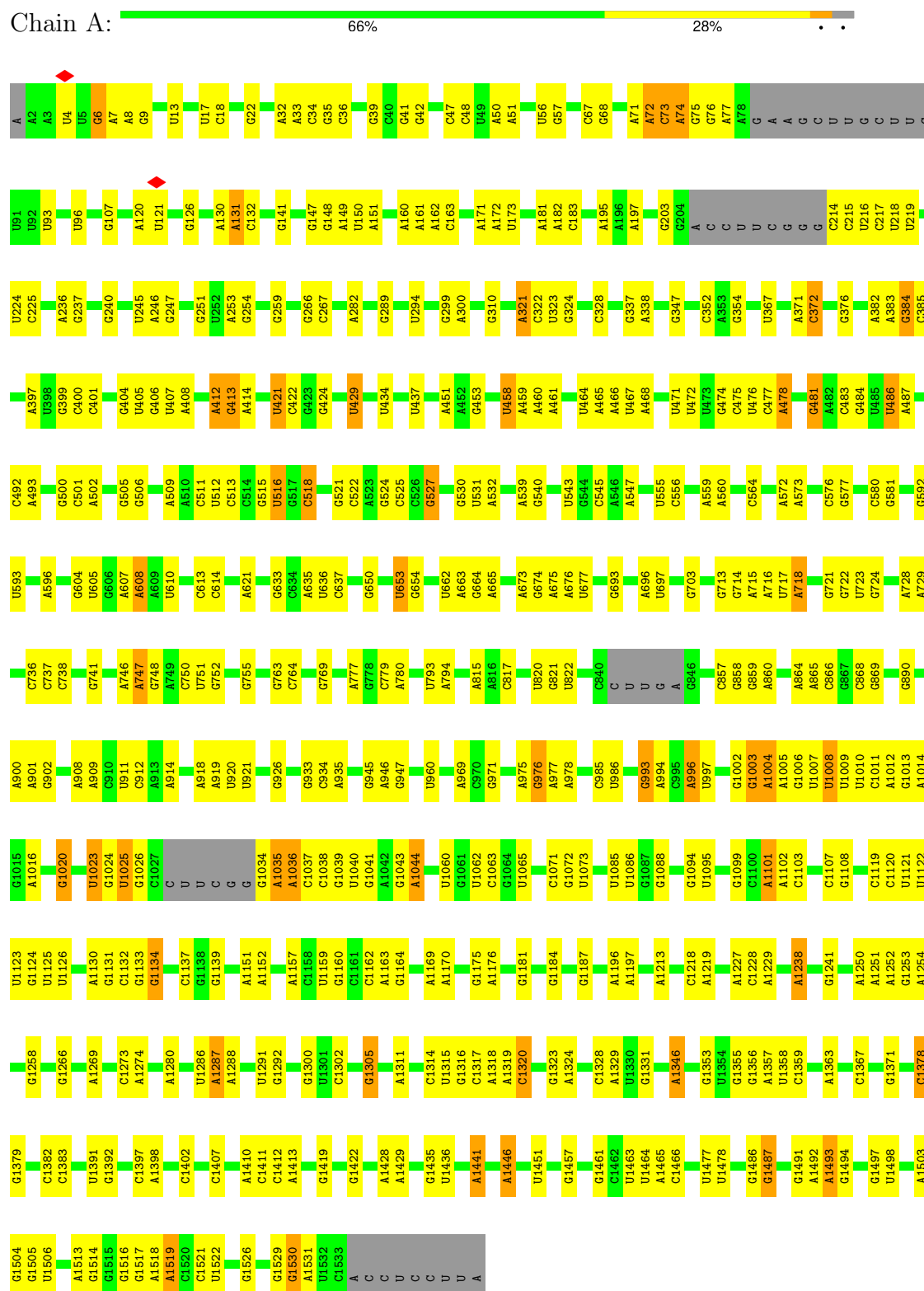


• Molecule 5: 50S ribosomal protein L31

Chain 4: 



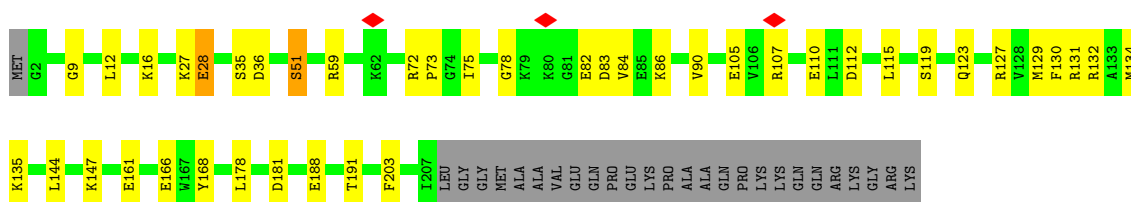
• Molecule 6: 16S rRNA



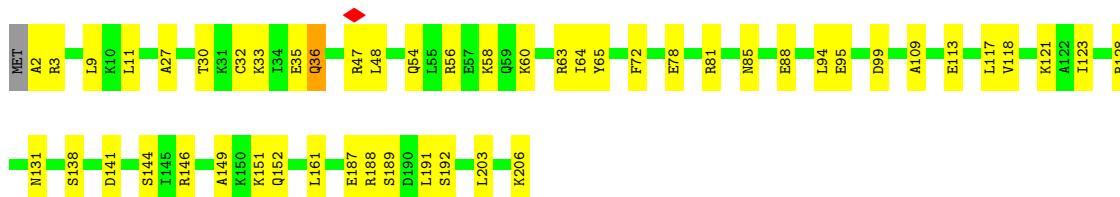
• Molecule 7: 30S ribosomal protein S2



- Molecule 8: Small ribosomal subunit protein uS3



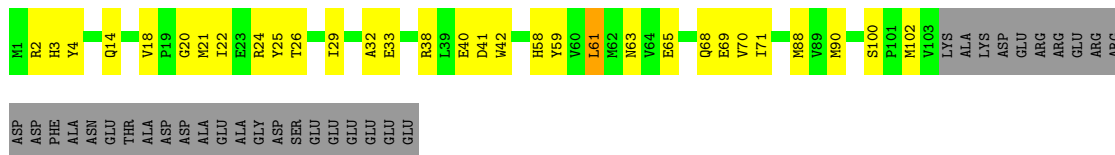
- Molecule 9: Small ribosomal subunit protein uS4



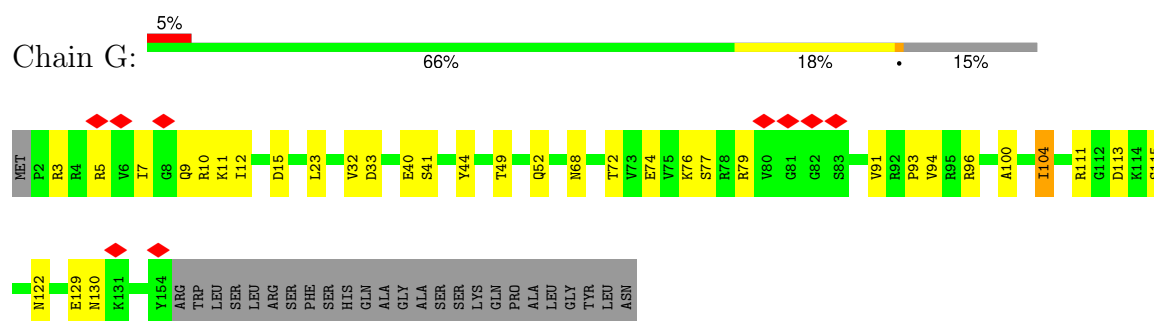
- Molecule 10: Small ribosomal subunit protein uS5



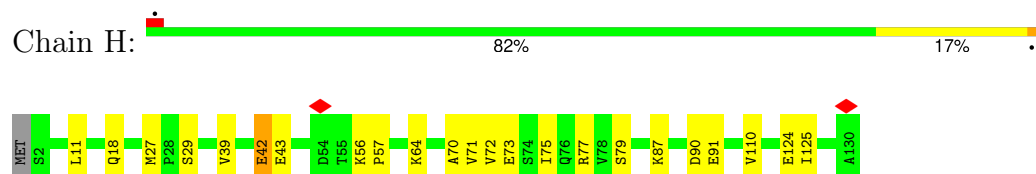
- Molecule 11: Small ribosomal subunit protein bS6



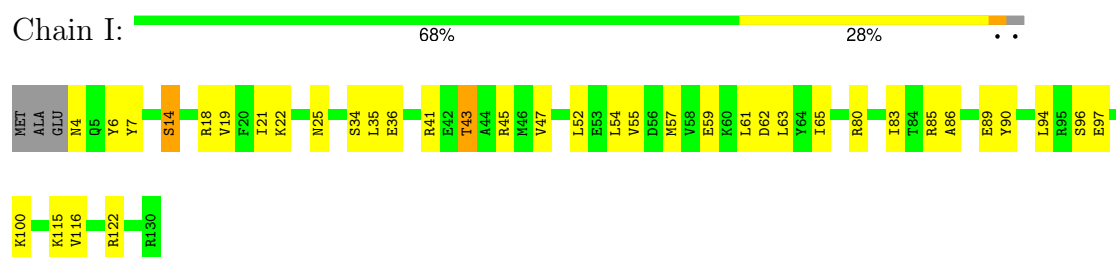
- Molecule 12: Small ribosomal subunit protein uS7



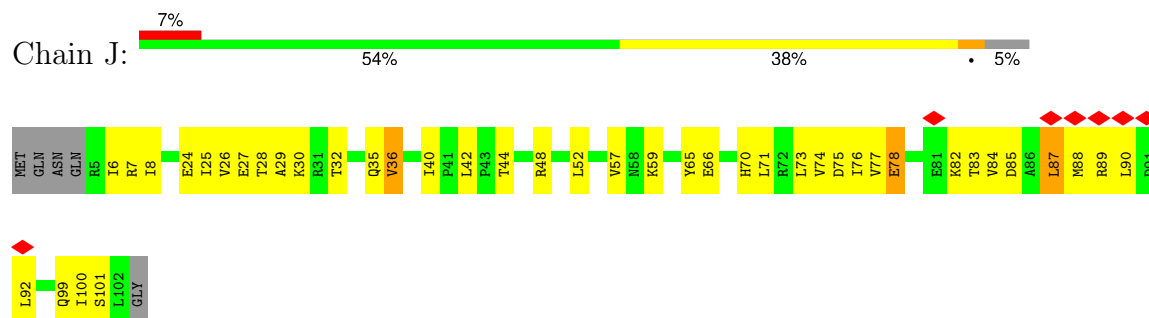
- Molecule 13: Small ribosomal subunit protein uS8



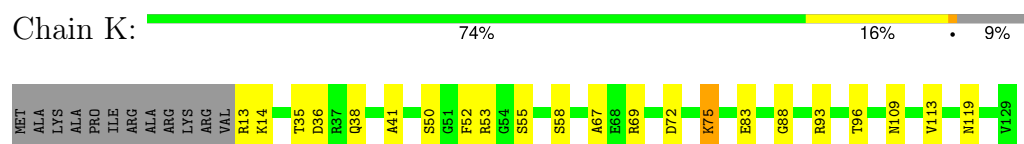
- Molecule 14: Small ribosomal subunit protein uS9



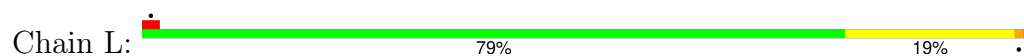
- Molecule 15: Small ribosomal subunit protein uS10

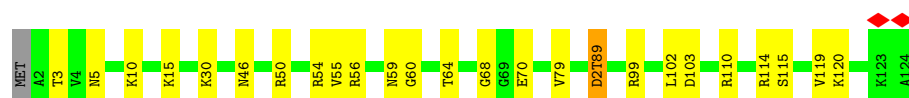


- Molecule 16: 30S ribosomal protein S11



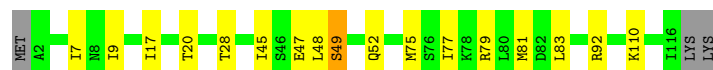
- Molecule 17: Small ribosomal subunit protein uS12





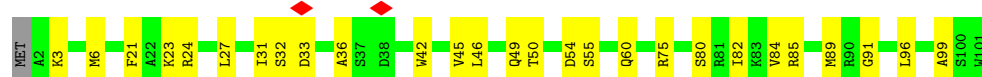
- Molecule 18: Small ribosomal subunit protein uS13

Chain M: 83% 14% . .



- Molecule 19: Small ribosomal subunit protein uS14

Chain N: 72% 27% .



- Molecule 20: Small ribosomal subunit protein uS15

Chain O: 78% 21% .



- Molecule 21: Small ribosomal subunit protein bS16

Chain P: 82% 17% .



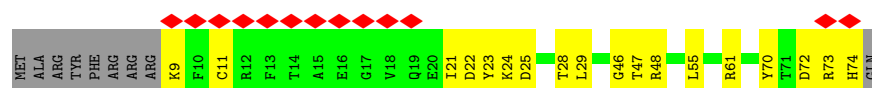
- Molecule 22: Small ribosomal subunit protein uS17

Chain Q: 71% 21% . 6%

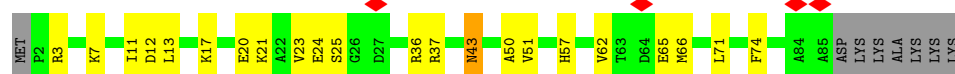


- Molecule 23: Small ribosomal subunit protein bS18

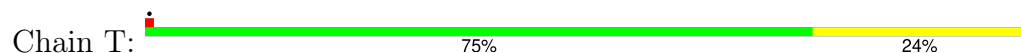
Chain R: 17% 64% 24% 12%



- Molecule 24: Small ribosomal subunit protein uS19



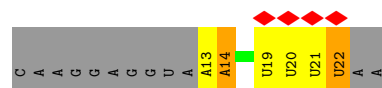
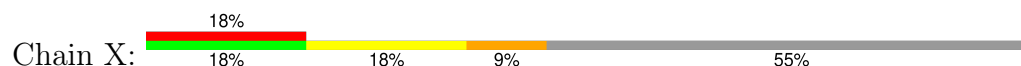
- Molecule 25: Small ribosomal subunit protein bS20



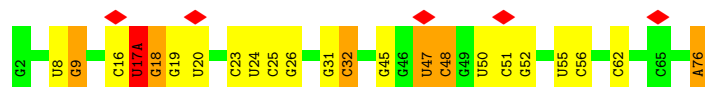
- Molecule 26: Small ribosomal subunit protein bS21



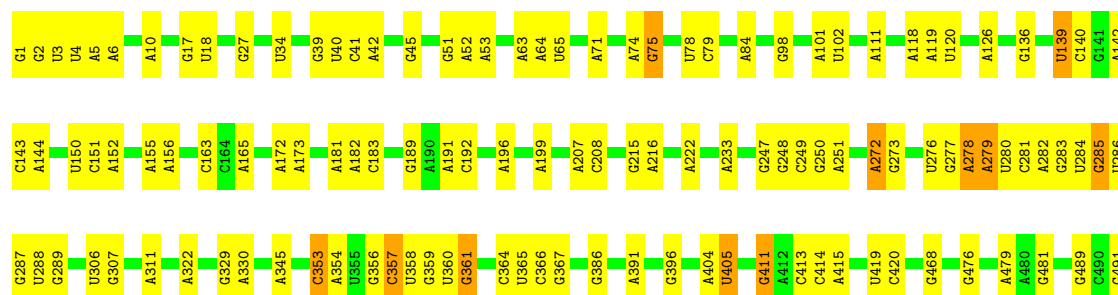
- Molecule 27: mRNA



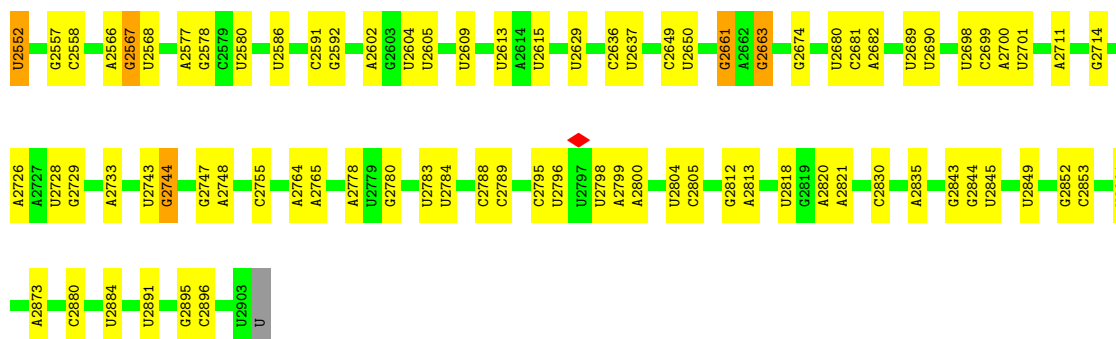
- Molecule 28: P-site tRNA



- Molecule 29: 23S rRNA



U2441	A2287	A	U	G2012	C1800	A1618	G1482	A1301	G1115	C	C898	G776	C635	U499
C2442	A2288	U	G	A2013	A1801	A1641	G1483	G1311	G1116	A	A899	A782	G636	G500
G2443	U2291	A	U	A2014	A1802	A1642	U1484	C1315	U1130	G	G907	G783	G637	A505
G2444	U2292	C	G	A2015	A1803	G1645	U1485	U1329	G1125	A	C908	G784	G638	A508
A2445	C2295	A	G	A2020	A1808	C1646	C1493	U1362	U1130	U	A909	G805	C640	C509
A2448	U2296	C	A	C2023	A1809	U1647	A1494	U1365	G1131	G	A910	A644	A644	C509
U2449	U2297	C	U	C2023	A1810	U1648	A1495	A1366	G1132	U	A911	C645	C510	C510
A2450	A2298	C	A	A2030	C1816	U1649	A1496	C1370	U1133	G	C912	U646	U646	U511
A2451	U2299	U	G	A2031	C1816	G1649	C1497	C1371	A1134	U	U934	G647	U512	G512
G2455	U2305	U	U	G2032	A1829	C1656	U1506	U1371	G1135	C	C935	U811	G530	G530
C2456	C2306	A	G	A2033	A1848	U1657	C1507	U1382	G1136	U	C936	U812	C531	C531
U2457	G2307	A	G	G2038	U1856	A1664	A1508	A1387	G1137	U	C937	U813	A532	A532
G2461	G2308	G	G	U2039	U1857	G1667	A1509	C1386	G1138	G	A933	U827	A533	G533
A2461	U2312	U	G	C2043	A1858	G1674	G1510	A1383	U1141	A	U934	U828	A555	G539
A2462	U2312	U	G	C2043	A1858	G1674	G1510	A1383	U1141	A	U934	U828	A555	G539
C2466	A2322	U	C	A2052	C1868	G1674	A1515	C1386	U1142	C	A936	U829	U657	U657
A2469	G2325	U	U	U2052	G1869	U1680	A1528	A1387	G1149	C	C937	U832	U686	U686
G2470	C2326	U	U	C2055	C1870	G1681	G1529	A1387	C1150	C	G938	U833	U687	U687
A2481	A2327	A	A	G2056	A1871	G1682	A1535	C1386	C1172	G	C946	U834	G697	G697
G2481	A2328	A	A	A2060	A1872	U1683	A1536	A1386	U	C	A947	U839	G698	G549
A2482	U2329	G	G	G2061	A1889	G1715	G1537	C1386	U	U	C948	U840	U709	A563
G2484	G2330	U	U	A2062	A1890	U1720	C1538	A1387	A	C	U955	U846	U710	U573
U2491	U2334	U	U	C2063	G1906	G1721	U1539	A1392	G1177	A	C961	U847	G711	U573
C2498	A2335	A	A	G2066	U1911	G1724	A1548	U1394	C1178	U	G969	C948	C717	A574
C2499	G2345	C	C	G2069	A1912	U1729	A1549	A1395	U1180	U	U970	U851	A721	A575
G2502	C2346	G	G	A2070	A1913	C1730	U1563	U1406	G1181	A	G974	U852	A722	U576
U2504	C2347	C	C	C2072	C1914	U1736	C1564	U1406	U1182	A	A983	G856	C723	G577
G2505	C2350	C	C	C2073	3TD1915	G1737	C1565	U1411	U1183	C	A986	G857	C724	U580
U2514	C2360	A	A	U2074	U1917	U1738	A1569	U1411	U1199	A	U987	G858	U724	C581
C2515	A2381	U	U	U2075	A1928	G1738	A1570	U1411	U1199	A	A987	G859	C725	A586
U2518	G2382	C	C	U2079	G1929	U1743	U1578	G1416	G1212	C	A1000	U870	A730	C587
U2519	U2384	C	C	U2086	U1931	G1743	U1579	C1417	A1226	G	A1001	U871	C740	U588
C2520	C2385	A	A	G2087	A1932	A1746	A1583	C1428	U1239	U	C1005	U872	U593	U593
G2523	G2395	U	U	G2093	G1933	U1747	U1584	G1429	U1240	A	U1012	A877	C594	U594
G2526	U2402	G	G	U2098	U1946	C1748	C1585	G1430	A1253	U	C1013	A878	C595	C595
G2529	A2406	C	C	U2098	C1947	G1764	A1586	G1432	A1254	A	G1022	G879	A743	U596
G2532	C2420	C	C	U2098	U1955	A1773	A1587	A1434	U1255	C	G1026	G880	U744	G597
U2537	A2425	U	U	U2098	C1967	U1782	A1597	G1435	G1256	U	A1027	G881	G745	A603
C2538	G2429	C	C	U2098	A1970	G1790	A1598	G1441	U1266	C	A1028	C887	U747	A608
A2547	A2430	A	A	U2098	A1971	A1791	U1602	U1442	G1266	A	A1029	C888	A753	A609
U2548	U2548	U	U	U2098	G1972	A1794	C1604	U1443	G1271	U	U1033	C889	U754	A614
		A	A	U2098	U1991	C1796	C1605	U1452	A1272	G	U1046	C890	U755	U615
		U	U	U2098	U1992	U1796	C1606	A1469	U1282		G1047	C891	A761	A627
		G	G	U2098	U1993	G1797	A1608	A1470	G1283		A1048	C893	A764	A632
		A	A	U2098	U1993	G1797	A1614	A1470	G1300		C1052	C895	A764	A633
		A	A	U2098	U1993	G1797	A1614	A1470	G1300		C1052	C897	A764	C634



• Molecule 30: 5S rRNA

Chain b: 83% 15% ..



• Molecule 31: 50S ribosomal protein L2

Chain c: 92% 7% .



• Molecule 32: 50S ribosomal protein L3

Chain d: 90% 9% .



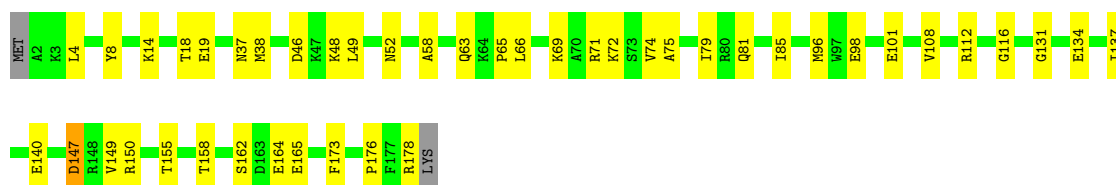
• Molecule 33: Large ribosomal subunit protein uL4

Chain e: 95% 5%




• Molecule 34: Large ribosomal subunit protein uL5

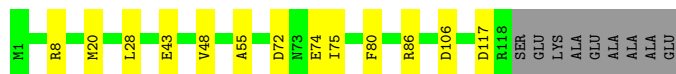
Chain f: 74% 24% ..




• Molecule 35: Large ribosomal subunit protein uL6

- Molecule 41: Large ribosomal subunit protein bL17

Chain m:  83% 10% 7%




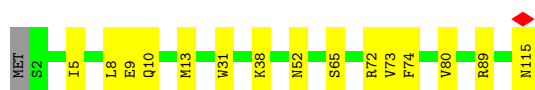
- Molecule 42: Large ribosomal subunit protein uL18

Chain n:  85% 13% ...




- Molecule 43: Large ribosomal subunit protein bL19

Chain o:  86% 13% .




- Molecule 44: 50S ribosomal protein L20

Chain p:  88% 11% .



- Molecule 45: Ribosomal protein L21

Chain q:  81% 18% .



- Molecule 46: 50S ribosomal protein L22

Chain r:  92% 8%

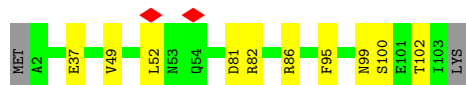
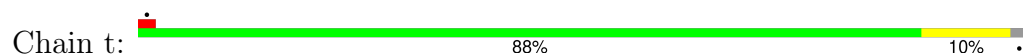


- Molecule 47: 50S ribosomal protein L23

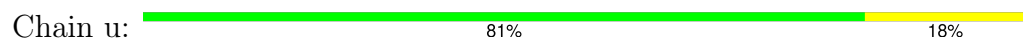
Chain s:  78% 15% 7%



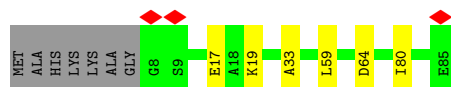
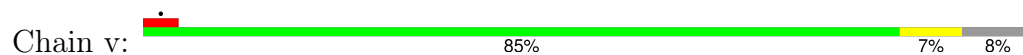
- Molecule 48: 50S ribosomal protein L24



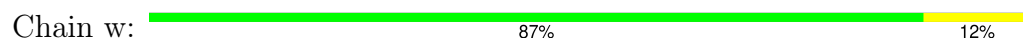
- Molecule 49: Large ribosomal subunit protein bL25



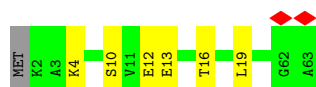
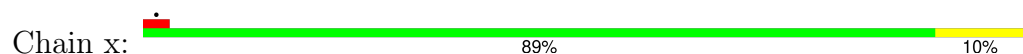
- Molecule 50: 50S ribosomal protein L27



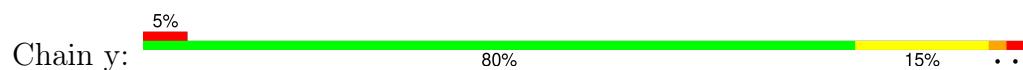
- Molecule 51: 50S ribosomal protein L28



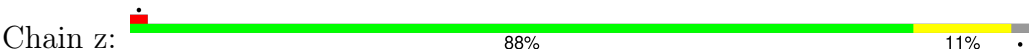
- Molecule 52: Large ribosomal subunit protein uL29



- Molecule 53: 50S ribosomal protein L30



- Molecule 54: 50S ribosomal protein L32



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	628487	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)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.864	Depositor
Minimum map value	-0.232	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	470.80002, 470.80002, 470.80002	wwPDB
Map dimensions	440, 440, 440	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: MG, 6MZ, OMC, PSU, 5MU, 2MG, G7M, D2T, MEQ, 4OC, OMG, 4SU, H2U, 3TD, K, ZN, MA6, UR3, 5MC, MIY, 2MA, 1MG, OMU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	0	0.29	0/424	0.36	0/565
2	1	0.36	0/380	0.35	0/498
3	2	0.35	0/513	0.35	0/676
4	3	0.33	0/303	0.39	0/397
5	4	0.16	0/488	0.39	0/649
6	A	0.33	0/35787	0.30	0/55816
7	B	0.20	0/1784	0.35	0/2403
8	C	0.24	0/1651	0.33	0/2225
9	D	0.24	0/1665	0.35	0/2227
10	E	0.38	0/1165	0.48	0/1568
11	F	0.26	0/858	0.42	0/1160
12	G	0.22	0/1219	0.37	0/1635
13	H	0.32	0/989	0.45	0/1326
14	I	0.31	0/1034	0.58	0/1375
15	J	0.25	0/796	0.48	0/1077
16	K	0.28	0/893	0.41	0/1205
17	L	0.27	0/960	0.33	0/1286
18	M	0.22	0/900	0.37	0/1204
19	N	0.38	0/817	0.58	0/1088
20	O	0.26	0/722	0.40	0/964
21	P	0.28	0/653	0.41	0/877
22	Q	0.26	0/650	0.37	0/871
23	R	0.26	0/553	0.39	0/742
24	S	0.40	0/685	0.48	0/922
25	T	0.26	0/676	0.40	0/895
26	U	0.20	0/597	0.34	0/792
27	X	0.52	0/235	0.60	0/363
28	Z	0.58	0/1703	0.72	1/2655 (0.0%)
29	a	0.44	0/65651	0.36	0/102413
30	b	0.32	0/2850	0.27	0/4444
31	c	0.34	0/2121	0.37	0/2852

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	d	0.34	0/1576	0.34	0/2119
33	e	0.31	0/1571	0.34	0/2113
34	f	0.23	0/1434	0.40	0/1926
35	g	0.36	0/1343	0.57	0/1816
36	h	0.26	0/306	0.57	0/413
37	i	0.33	0/1152	0.33	0/1551
38	j	0.32	0/955	0.38	0/1279
39	k	0.32	0/1062	0.39	0/1413
40	l	0.37	0/1093	0.44	0/1460
41	m	0.36	0/958	0.43	0/1281
42	n	0.54	0/902	0.76	0/1209
43	o	0.33	0/929	0.33	0/1242
44	p	0.55	1/960 (0.1%)	0.54	1/1278 (0.1%)
45	q	0.34	0/829	0.44	0/1107
46	r	0.33	0/864	0.35	0/1156
47	s	0.31	0/744	0.42	0/994
48	t	0.38	0/787	0.51	0/1051
49	u	0.28	0/766	0.37	0/1025
50	v	0.33	0/593	0.33	0/785
51	w	0.35	0/635	0.43	0/848
52	x	0.26	0/502	0.35	0/667
53	y	0.79	0/453	1.04	0/605
54	z	0.32	0/450	0.35	0/599
All	All	0.38	1/150586 (0.0%)	0.37	2/225107 (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
42	n	0	1
53	y	0	2
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	p	47	TYR	C-O	7.81	1.33	1.24

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	Z	17(A)	U	C2'-C3'-O3'	5.76	118.14	109.50
44	p	46	ALA	CA-C-O	-5.08	115.49	120.82

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
42	n	94	ARG	Sidechain
53	y	11	ARG	Sidechain
53	y	31	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	417	0	451	2	0
2	1	377	0	418	4	0
3	2	504	0	572	6	0
4	3	302	0	340	4	0
5	4	480	0	482	8	0
6	A	32211	0	16224	273	0
7	B	1753	0	1780	30	0
8	C	1624	0	1696	28	0
9	D	1643	0	1707	33	0
10	E	1152	0	1196	19	0
11	F	839	0	833	21	0
12	G	1203	0	1254	21	0
13	H	979	0	1031	14	0
14	I	1022	0	1070	31	0
15	J	786	0	828	31	0
16	K	877	0	887	17	0
17	L	957	0	1017	17	0
18	M	891	0	952	13	0
19	N	805	0	844	25	0
20	O	714	0	734	16	0
21	P	643	0	661	12	0
22	Q	641	0	682	12	0
23	R	544	0	565	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	S	668	0	693	21	0
25	T	670	0	719	15	0
26	U	589	0	629	14	0
27	X	211	0	106	3	0
28	Z	1605	0	818	10	0
29	a	59130	0	29748	337	0
30	b	2549	0	1290	10	0
31	c	2082	0	2154	13	0
32	d	1566	0	1618	15	0
33	e	1552	0	1619	7	0
34	f	1410	0	1444	34	0
35	g	1323	0	1371	30	0
36	h	303	0	327	7	0
37	i	1129	0	1162	14	0
38	j	946	0	1023	15	0
39	k	1053	0	1129	10	0
40	l	1074	0	1157	19	0
41	m	945	0	989	8	0
42	n	892	0	923	9	0
43	o	917	0	962	12	0
44	p	947	0	1019	7	0
45	q	816	0	839	10	0
46	r	857	0	922	5	0
47	s	738	0	807	13	0
48	t	779	0	831	7	0
49	u	753	0	780	13	0
50	v	586	0	596	3	0
51	w	625	0	652	6	0
52	x	501	0	531	3	0
53	y	449	0	488	6	0
54	z	444	0	458	4	0
55	3	1	0	0	0	0
56	A	85	0	0	0	0
56	a	248	0	0	0	0
56	b	5	0	0	0	0
56	p	2	0	0	0	0
57	A	37	0	0	0	0
57	a	109	0	0	0	0
57	b	1	0	0	0	0
57	c	1	0	0	0	0
58	A	33	0	24	2	0
58	a	33	0	24	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	0	1	0	0	0	0
59	1	8	0	0	1	0
59	3	2	0	0	0	0
59	A	119	0	0	2	0
59	O	1	0	0	0	0
59	U	1	0	0	0	0
59	a	1450	0	0	5	0
59	b	10	0	0	0	0
59	c	6	0	0	0	0
59	d	3	0	0	0	0
59	e	4	0	0	0	0
59	h	1	0	0	0	0
59	i	2	0	0	0	0
59	j	1	0	0	0	0
59	k	7	0	0	0	0
59	l	1	0	0	0	0
59	m	6	0	0	0	0
59	p	5	0	0	0	0
59	q	5	0	0	1	0
59	r	2	0	0	0	0
59	s	2	0	0	0	0
59	t	1	0	0	0	0
59	u	2	0	0	0	0
59	v	2	0	0	0	0
59	w	2	0	0	0	0
59	y	1	0	0	0	0
59	z	4	0	0	0	0
All	All	141677	0	94076	1204	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 5.

The worst 5 of 1204 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:76:G:H1	6:A:93:U:H3	1.23	0.86
42:n:90:VAL:HG23	42:n:117:PHE:HB3	1.60	0.83
29:a:881:G:H1	29:a:895:U:H3	1.26	0.83
15:J:66:GLU:HB2	19:N:99:ALA:HB2	1.62	0.82
6:A:1086:U:H3	6:A:1099:G:H22	1.28	0.79

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	49/55 (89%)	49 (100%)	0	0	100	100
2	1	44/46 (96%)	44 (100%)	0	0	100	100
3	2	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
4	3	36/38 (95%)	36 (100%)	0	0	100	100
5	4	56/70 (80%)	54 (96%)	2 (4%)	0	100	100
7	B	222/241 (92%)	211 (95%)	11 (5%)	0	100	100
8	C	204/233 (88%)	196 (96%)	8 (4%)	0	100	100
9	D	203/206 (98%)	202 (100%)	1 (0%)	0	100	100
10	E	154/167 (92%)	147 (96%)	7 (4%)	0	100	100
11	F	101/135 (75%)	97 (96%)	4 (4%)	0	100	100
12	G	151/179 (84%)	140 (93%)	11 (7%)	0	100	100
13	H	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
14	I	125/130 (96%)	118 (94%)	7 (6%)	0	100	100
15	J	96/103 (93%)	92 (96%)	3 (3%)	1 (1%)	12	11
16	K	115/129 (89%)	110 (96%)	5 (4%)	0	100	100
17	L	120/124 (97%)	115 (96%)	5 (4%)	0	100	100
18	M	113/118 (96%)	108 (96%)	5 (4%)	0	100	100
19	N	98/101 (97%)	93 (95%)	5 (5%)	0	100	100
20	O	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
21	P	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
22	Q	77/84 (92%)	75 (97%)	2 (3%)	0	100	100
23	R	64/75 (85%)	61 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	S	82/92 (89%)	79 (96%)	3 (4%)	0	100	100
25	T	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
26	U	68/71 (96%)	68 (100%)	0	0	100	100
31	c	269/273 (98%)	262 (97%)	7 (3%)	0	100	100
32	d	206/209 (99%)	200 (97%)	6 (3%)	0	100	100
33	e	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
34	f	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
35	g	174/177 (98%)	159 (91%)	15 (9%)	0	100	100
36	h	39/149 (26%)	34 (87%)	5 (13%)	0	100	100
37	i	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
38	j	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
39	k	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
40	l	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
41	m	116/127 (91%)	110 (95%)	6 (5%)	0	100	100
42	n	114/117 (97%)	109 (96%)	4 (4%)	1 (1%)	14	14
43	o	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
44	p	115/118 (98%)	115 (100%)	0	0	100	100
45	q	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
46	r	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
47	s	91/100 (91%)	87 (96%)	4 (4%)	0	100	100
48	t	100/104 (96%)	95 (95%)	5 (5%)	0	100	100
49	u	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
50	v	76/85 (89%)	75 (99%)	1 (1%)	0	100	100
51	w	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
52	x	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
53	y	56/59 (95%)	54 (96%)	1 (2%)	1 (2%)	6	4
54	z	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
All	All	5485/5913 (93%)	5292 (96%)	190 (4%)	3 (0%)	49	57

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
42	n	89	ASP

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Mol	Chain	Res	Type
15	J	57	VAL
53	y	4	THR

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	46/49 (94%)	46 (100%)	0	100	100
2	1	38/38 (100%)	37 (97%)	1 (3%)	40	55
3	2	51/52 (98%)	51 (100%)	0	100	100
4	3	34/34 (100%)	32 (94%)	2 (6%)	18	22
5	4	55/62 (89%)	52 (94%)	3 (6%)	19	24
7	B	186/199 (94%)	181 (97%)	5 (3%)	39	53
8	C	170/190 (90%)	164 (96%)	6 (4%)	32	43
9	D	172/173 (99%)	166 (96%)	6 (4%)	32	43
10	E	119/126 (94%)	116 (98%)	3 (2%)	42	56
11	F	90/116 (78%)	89 (99%)	1 (1%)	65	79
12	G	126/147 (86%)	120 (95%)	6 (5%)	23	30
13	H	104/105 (99%)	101 (97%)	3 (3%)	37	51
14	I	105/107 (98%)	100 (95%)	5 (5%)	23	30
15	J	86/90 (96%)	80 (93%)	6 (7%)	14	16
16	K	90/99 (91%)	86 (96%)	4 (4%)	25	34
17	L	102/103 (99%)	101 (99%)	1 (1%)	68	81
18	M	93/96 (97%)	90 (97%)	3 (3%)	34	47
19	N	83/84 (99%)	79 (95%)	4 (5%)	23	30
20	O	76/77 (99%)	76 (100%)	0	100	100
21	P	65/65 (100%)	62 (95%)	3 (5%)	24	32
22	Q	73/78 (94%)	69 (94%)	4 (6%)	19	24
23	R	57/65 (88%)	57 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	S	72/79 (91%)	68 (94%)	4 (6%)	19	24
25	T	65/66 (98%)	64 (98%)	1 (2%)	57	73
26	U	60/61 (98%)	57 (95%)	3 (5%)	22	28
31	c	216/218 (99%)	214 (99%)	2 (1%)	70	84
32	d	163/163 (100%)	159 (98%)	4 (2%)	42	56
33	e	165/165 (100%)	164 (99%)	1 (1%)	78	89
34	f	148/150 (99%)	143 (97%)	5 (3%)	32	44
35	g	137/138 (99%)	128 (93%)	9 (7%)	15	18
36	h	32/114 (28%)	30 (94%)	2 (6%)	16	19
37	i	116/116 (100%)	111 (96%)	5 (4%)	26	35
38	j	104/104 (100%)	103 (99%)	1 (1%)	68	81
39	k	103/103 (100%)	102 (99%)	1 (1%)	68	81
40	l	109/109 (100%)	105 (96%)	4 (4%)	30	41
41	m	98/103 (95%)	98 (100%)	0	100	100
42	n	86/87 (99%)	79 (92%)	7 (8%)	11	12
43	o	99/100 (99%)	99 (100%)	0	100	100
44	p	89/90 (99%)	88 (99%)	1 (1%)	65	79
45	q	84/84 (100%)	76 (90%)	8 (10%)	8	8
46	r	93/93 (100%)	90 (97%)	3 (3%)	34	47
47	s	80/84 (95%)	78 (98%)	2 (2%)	42	56
48	t	83/85 (98%)	83 (100%)	0	100	100
49	u	78/78 (100%)	72 (92%)	6 (8%)	12	13
50	v	58/63 (92%)	58 (100%)	0	100	100
51	w	67/68 (98%)	67 (100%)	0	100	100
52	x	54/55 (98%)	53 (98%)	1 (2%)	50	66
53	y	48/49 (98%)	47 (98%)	1 (2%)	47	63
54	z	47/48 (98%)	46 (98%)	1 (2%)	47	63
All	All	4575/4828 (95%)	4437 (97%)	138 (3%)	37	49

5 of 138 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	p	89	GLU

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Mol	Chain	Res	Type
45	q	33	VAL
49	u	10	LYS
16	K	58	SER
16	K	55	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
33	e	165	HIS
42	n	29	HIS
34	f	27	GLN
37	i	80	HIS
44	p	20	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	X	9/22 (40%)	5 (55%)	0
28	Z	74/75 (98%)	8 (10%)	3 (4%)
29	a	2749/2904 (94%)	267 (9%)	0
30	b	118/120 (98%)	10 (8%)	0
6	A	1495/1542 (96%)	159 (10%)	2 (0%)
All	All	4445/4663 (95%)	449 (10%)	5 (0%)

5 of 449 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	A	4	U
6	A	6	G
6	A	9	G
6	A	13	U
6	A	22	G

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	A	182	A
6	A	1035	A
28	Z	17(A)	U
28	Z	19	G

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Mol	Chain	Res	Type
28	Z	48	C

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
17	D2T	L	89	17	8,9,10	1.80	2 (25%)	6,11,13	1.56	1 (16%)
29	PSU	a	2457	29	18,21,22	1.15	3 (16%)	21,30,33	2.22	6 (28%)
6	MA6	A	1518	6	23,26,27	1.69	6 (26%)	33,38,41	4.25	14 (42%)
28	PSU	Z	55	28	18,21,22	0.92	1 (5%)	21,30,33	0.75	1 (4%)
29	G7M	a	2069	57,29	23,26,27	0.70	1 (4%)	34,39,42	0.62	1 (2%)
29	PSU	a	2605	29	18,21,22	1.10	2 (11%)	21,30,33	2.09	5 (23%)
6	G7M	A	527	57,6	23,26,27	2.59	8 (34%)	34,39,42	2.40	11 (32%)
29	PSU	a	2580	29	18,21,22	1.10	3 (16%)	21,30,33	2.04	5 (23%)
29	PSU	a	1911	29	18,21,22	1.08	1 (5%)	21,30,33	2.07	5 (23%)
29	OMG	a	2251	28,57,29	23,26,27	0.64	0	32,38,41	0.50	0
28	5MC	Z	32	28	19,22,23	0.77	1 (5%)	26,32,35	0.50	0
29	1MG	a	745	29	23,26,27	2.76	8 (34%)	33,39,42	1.76	8 (24%)
6	2MG	A	966	6	23,26,27	0.57	0	33,38,41	0.51	0
29	6MZ	a	1618	29	22,25,26	2.30	7 (31%)	29,36,39	2.47	9 (31%)
29	2MG	a	2445	29	23,26,27	0.75	0	33,38,41	0.52	0
29	2MA	a	2503	57,29,56	22,25,26	1.70	6 (27%)	32,37,40	3.44	12 (37%)
29	5MU	a	1939	57,29	19,22,23	0.71	0	27,32,35	0.53	0
6	2MG	A	1516	6	23,26,27	0.59	0	33,38,41	0.59	0
29	OMC	a	2498	56,29	19,22,23	0.76	1 (5%)	25,31,34	0.67	0
6	UR3	A	1498	6	19,22,23	2.61	8 (42%)	26,32,35	1.67	3 (11%)
29	PSU	a	955	29	18,21,22	1.04	1 (5%)	21,30,33	1.93	4 (19%)
6	2MG	A	1207	57,6	23,26,27	0.51	0	33,38,41	0.50	0
29	PSU	a	2604	29	18,21,22	1.08	2 (11%)	21,30,33	2.03	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
28	4SU	Z	8	28	18,21,22	3.81	8 (44%)	25,30,33	2.41	5 (20%)
32	MEQ	d	150	32	8,9,10	0.94	0	5,10,12	0.72	0
29	PSU	a	2504	57,29	18,21,22	1.06	1 (5%)	21,30,33	1.90	4 (19%)
29	6MZ	a	2030	29	22,25,26	2.27	8 (36%)	29,36,39	2.66	14 (48%)
6	PSU	A	516	56,6	18,21,22	1.07	3 (16%)	21,30,33	1.90	5 (23%)
29	OMU	a	2552	57,29	19,22,23	2.82	6 (31%)	25,31,34	1.97	5 (20%)
6	5MC	A	1407	6	19,22,23	0.82	1 (5%)	26,32,35	0.61	0
6	MA6	A	1519	6	23,26,27	1.66	6 (26%)	33,38,41	4.39	14 (42%)
6	4OC	A	1402	6	20,23,24	3.12	8 (40%)	25,32,35	0.94	2 (8%)
28	5MU	Z	54	28	19,22,23	0.25	0	27,32,35	0.35	0
29	5MU	a	747	29	19,22,23	0.65	0	27,32,35	0.59	0
29	2MG	a	1835	29	23,26,27	0.66	0	33,38,41	0.47	0
29	PSU	a	1917	29	18,21,22	1.01	1 (5%)	21,30,33	1.95	4 (19%)
6	5MC	A	967	6	19,22,23	0.69	0	26,32,35	0.64	0
29	5MC	a	1962	57,29	19,22,23	0.79	0	26,32,35	0.59	0
29	3TD	a	1915	29	19,22,23	4.12	7 (36%)	23,32,35	1.83	3 (13%)
29	PSU	a	746	56,29	18,21,22	1.09	2 (11%)	21,30,33	1.85	3 (14%)
29	H2U	a	2449	29	18,21,22	0.65	0	19,30,33	0.98	1 (5%)

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
17	D2T	L	89	17	-	5/7/12/14	-
29	PSU	a	2457	29	-	0/7/25/26	0/2/2/2
6	MA6	A	1518	6	-	0/11/29/30	0/3/3/3
28	PSU	Z	55	28	-	0/7/25/26	0/2/2/2
29	G7M	a	2069	57,29	-	0/7/25/26	0/3/3/3
29	PSU	a	2605	29	-	0/7/25/26	0/2/2/2
6	G7M	A	527	57,6	-	3/7/25/26	0/3/3/3
29	PSU	a	2580	29	-	0/7/25/26	0/2/2/2
29	PSU	a	1911	29	-	0/7/25/26	0/2/2/2
29	OMG	a	2251	28,57,29	-	1/9/27/28	0/3/3/3
28	5MC	Z	32	28	-	0/7/25/26	0/2/2/2
29	1MG	a	745	29	-	0/7/25/26	0/3/3/3
6	2MG	A	966	6	-	0/9/27/28	0/3/3/3
29	6MZ	a	1618	29	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
29	2MG	a	2445	29	-	2/9/27/28	0/3/3/3
29	2MA	a	2503	57,29,56	-	2/7/25/26	0/3/3/3
29	5MU	a	1939	57,29	-	0/7/25/26	0/2/2/2
6	2MG	A	1516	6	-	0/9/27/28	0/3/3/3
29	OMC	a	2498	56,29	-	0/9/27/28	0/2/2/2
6	UR3	A	1498	6	-	0/7/25/26	0/2/2/2
29	PSU	a	955	29	-	0/7/25/26	0/2/2/2
6	2MG	A	1207	57,6	-	0/9/27/28	0/3/3/3
29	PSU	a	2604	29	-	0/7/25/26	0/2/2/2
28	4SU	Z	8	28	-	0/7/25/26	0/2/2/2
32	MEQ	d	150	32	-	4/8/9/11	-
29	PSU	a	2504	57,29	-	2/7/25/26	0/2/2/2
29	6MZ	a	2030	29	-	2/9/27/28	0/3/3/3
6	PSU	A	516	56,6	-	0/7/25/26	0/2/2/2
29	OMU	a	2552	57,29	-	0/9/27/28	0/2/2/2
6	5MC	A	1407	6	-	0/7/25/26	0/2/2/2
6	MA6	A	1519	6	-	2/11/29/30	0/3/3/3
6	4OC	A	1402	6	-	0/9/29/30	0/2/2/2
28	5MU	Z	54	28	-	0/7/25/26	0/2/2/2
29	5MU	a	747	29	-	1/7/25/26	0/2/2/2
29	2MG	a	1835	29	-	0/9/27/28	0/3/3/3
29	PSU	a	1917	29	-	0/7/25/26	0/2/2/2
6	5MC	A	967	6	-	0/7/25/26	0/2/2/2
29	5MC	a	1962	57,29	-	2/7/25/26	0/2/2/2
29	3TD	a	1915	29	-	0/7/25/26	0/2/2/2
29	PSU	a	746	56,29	-	2/7/25/26	0/2/2/2
29	H2U	a	2449	29	-	0/7/38/39	0/2/2/2

The worst 5 of 112 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	a	1915	3TD	C6-C5	12.83	1.49	1.35
29	a	1915	3TD	C2-N1	9.18	1.48	1.37
28	Z	8	4SU	C4-N3	8.42	1.46	1.37
29	a	1618	6MZ	C6-N6	7.81	1.43	1.34
29	a	745	1MG	C2-N3	7.22	1.45	1.33

The worst 5 of 149 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1519	MA6	N1-C6-N6	-16.07	97.28	116.86
6	A	1518	MA6	N1-C6-N6	-15.49	97.99	116.86
6	A	1519	MA6	C5-C6-N6	11.18	143.03	125.33
6	A	1518	MA6	C5-C6-N6	10.62	142.14	125.33
29	a	2503	2MA	CM2-C2-N3	10.10	132.25	117.13

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	L	89	D2T	O-C-CA-CB
17	L	89	D2T	CA-CB-CG-OD1
17	L	89	D2T	CA-CB-CG-OD2
32	d	150	MEQ	C-CA-CB-CG
32	d	150	MEQ	O-C-CA-CB

There are no ring outliers.

9 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	L	89	D2T	1	0
29	a	2251	OMG	1	0
28	Z	32	5MC	1	0
29	a	2503	2MA	1	0
6	A	1516	2MG	1	0
29	a	2030	6MZ	1	0
6	A	516	PSU	1	0
29	a	2552	OMU	1	0
6	A	1519	MA6	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 491 ligands modelled in this entry, 489 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
58	MIY	a	3005	-	36,36,36	1.36	4 (11%)	42,58,58	1.89	11 (26%)
58	MIY	A	1635	56	36,36,36	1.50	8 (22%)	42,58,58	1.88	10 (23%)

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
58	MIY	a	3005	-	-	7/12/70/70	0/4/4/4
58	MIY	A	1635	56	-	1/12/70/70	0/4/4/4

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	a	3005	MIY	C18-C5	3.98	1.56	1.53
58	A	1635	MIY	C18-C1	-3.66	1.50	1.55
58	A	1635	MIY	C7-C16	-3.38	1.48	1.51
58	a	3005	MIY	C7-C16	-3.17	1.48	1.51
58	A	1635	MIY	O7-C18	-3.08	1.37	1.42

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	A	1635	MIY	C21-C2-C1	-5.66	114.27	120.97
58	a	3005	MIY	C21-C2-C1	-5.33	114.67	120.97
58	a	3005	MIY	C11-C10-N7	-4.21	115.86	121.65
58	A	1635	MIY	C11-C12-C13	-4.16	116.34	120.50
58	A	1635	MIY	C11-C10-N7	-3.93	116.23	121.65

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	a	3005	MIY	C1-C2-C21-O8
58	a	3005	MIY	C3-C2-C21-O8
58	a	3005	MIY	C1-C2-C21-N2

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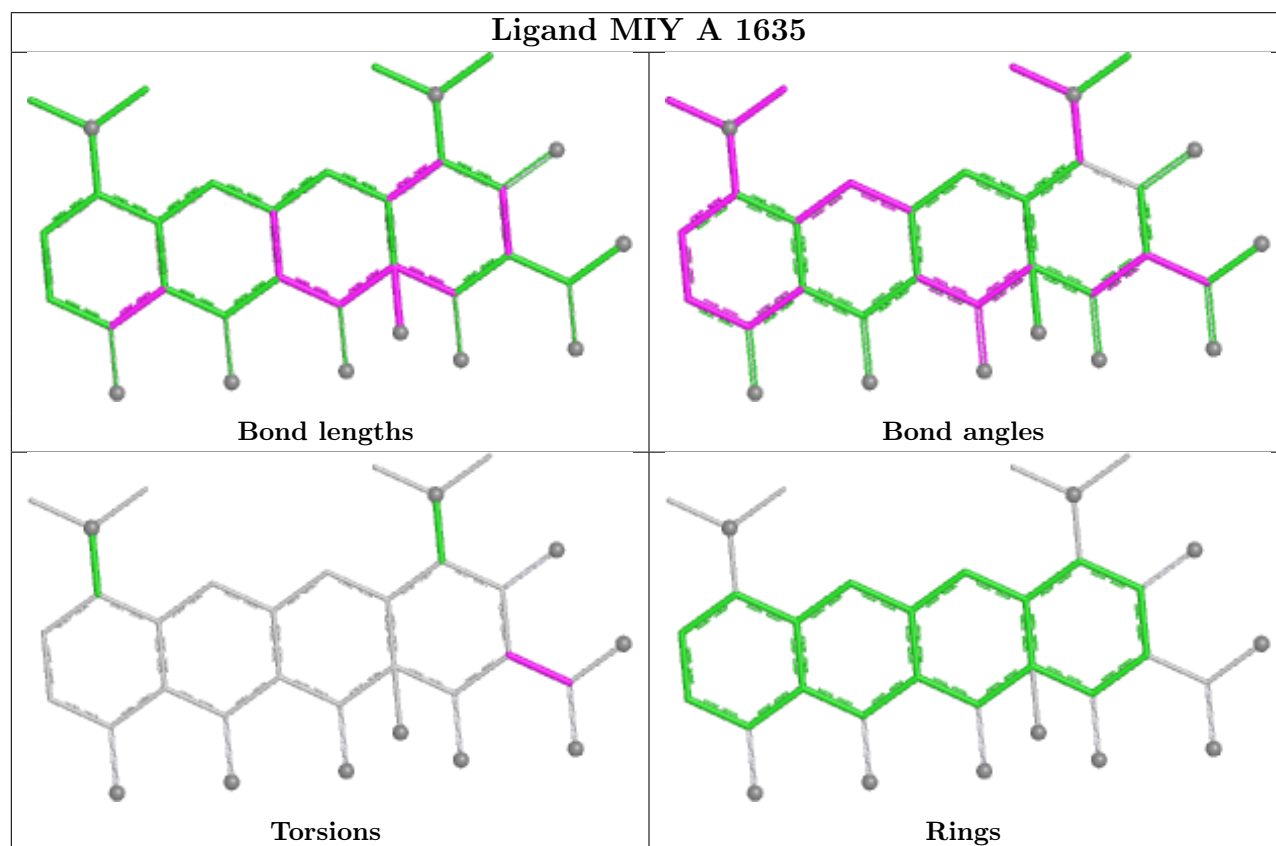
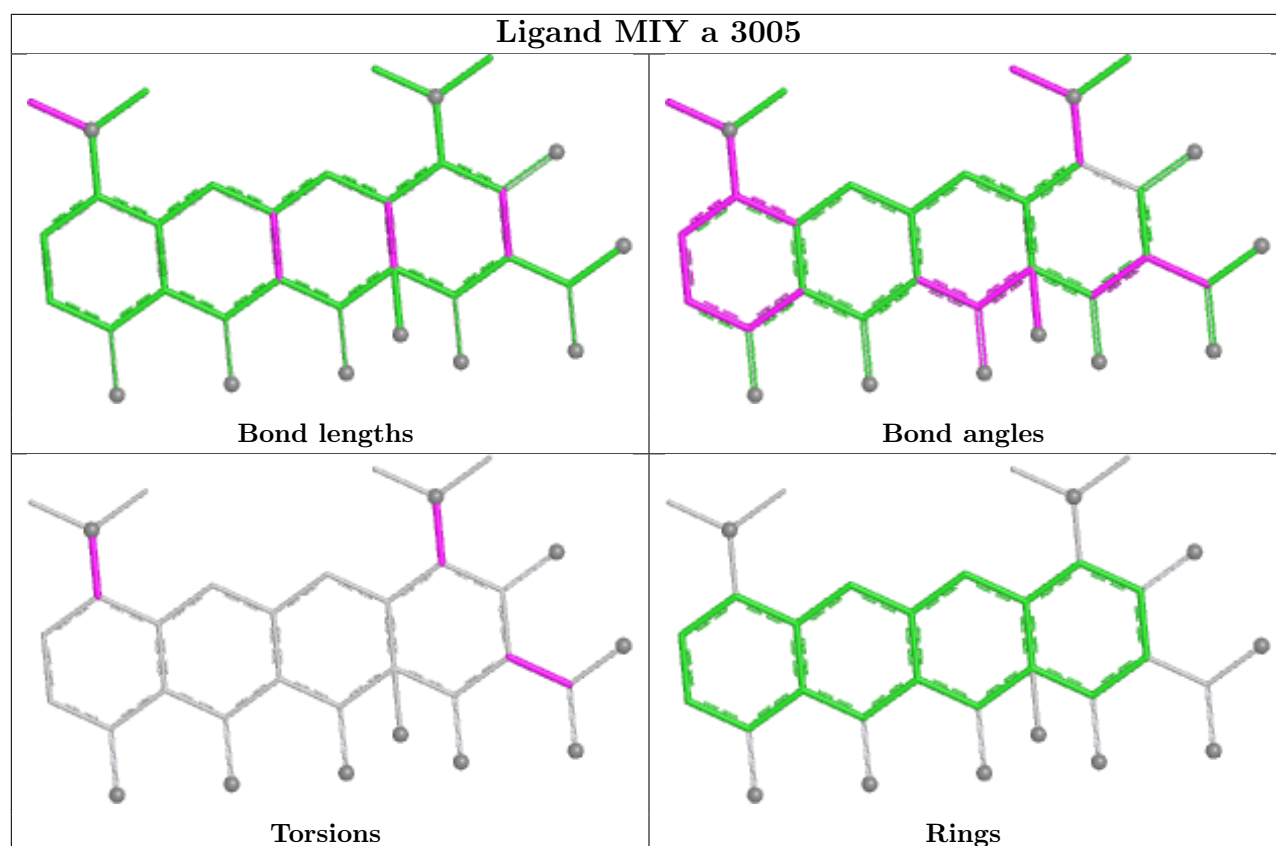
Mol	Chain	Res	Type	Atoms
58	a	3005	MIY	C3-C2-C21-N2
58	a	3005	MIY	C3-C4-N1-C20

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	a	3005	MIY	2	0
58	A	1635	MIY	2	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.

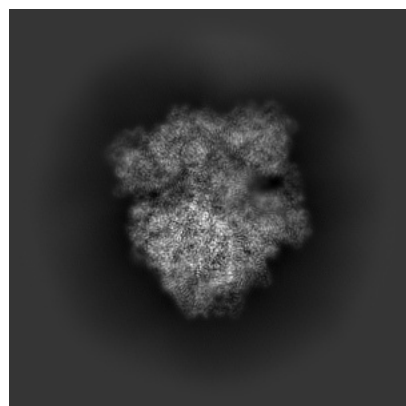
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71669. These allow visual inspection of the internal detail of the map and identification of artifacts.

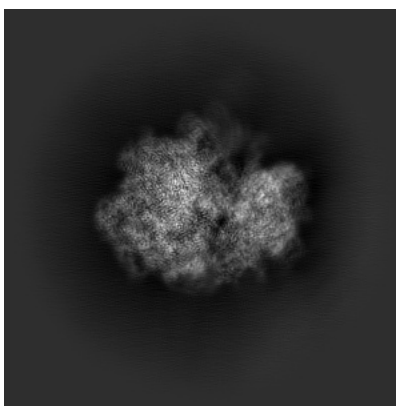
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

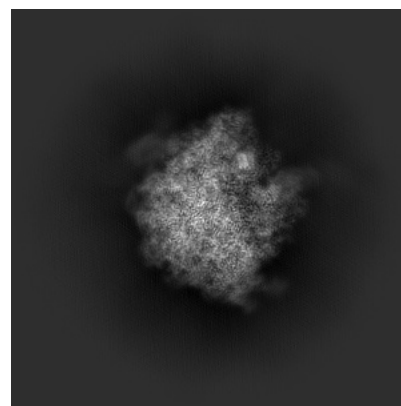
6.1.1 Primary map



X

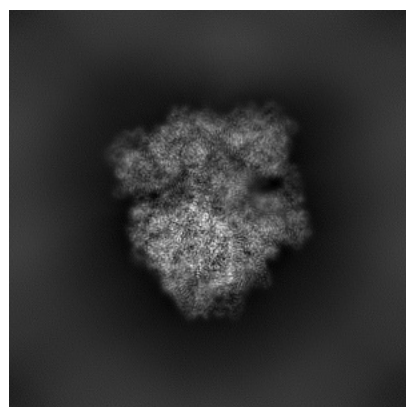


Y

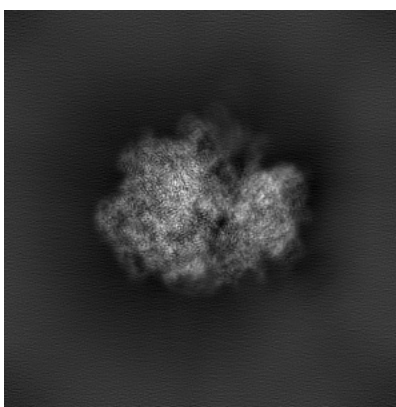


Z

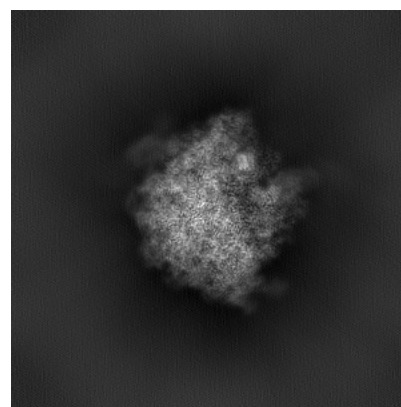
6.1.2 Raw map



X



Y

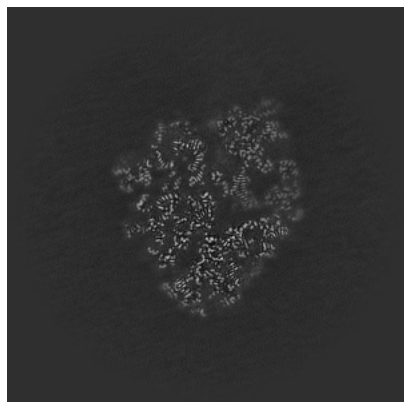


Z

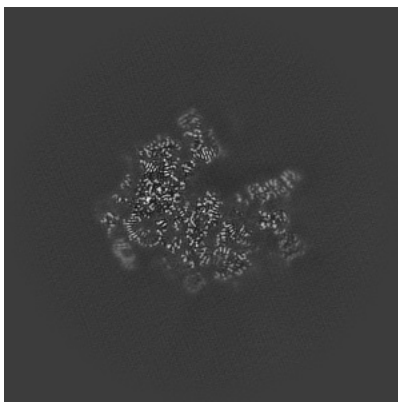
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

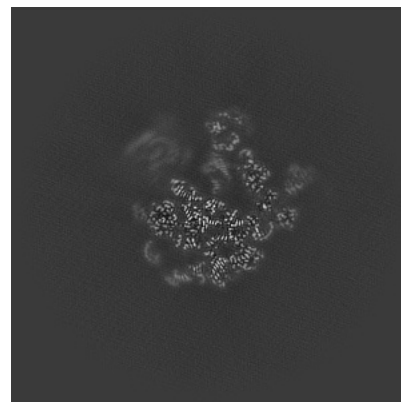
6.2.1 Primary map



X Index: 220

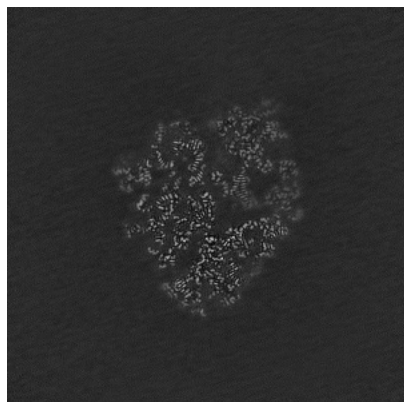


Y Index: 220

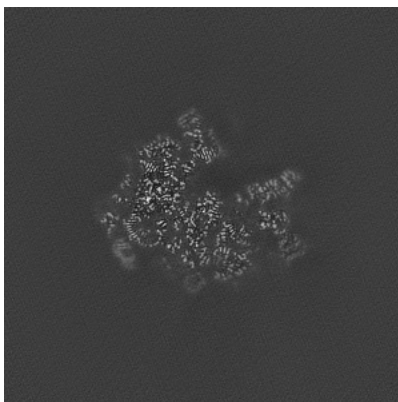


Z Index: 220

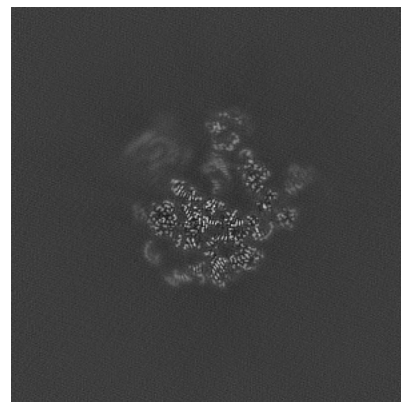
6.2.2 Raw map



X Index: 220



Y Index: 220

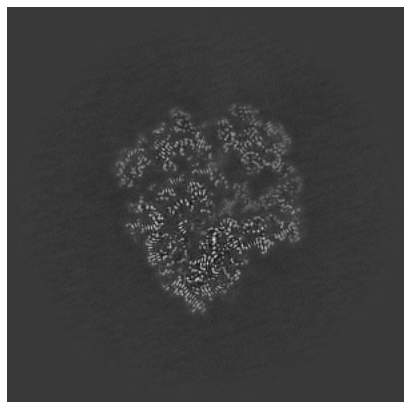


Z Index: 220

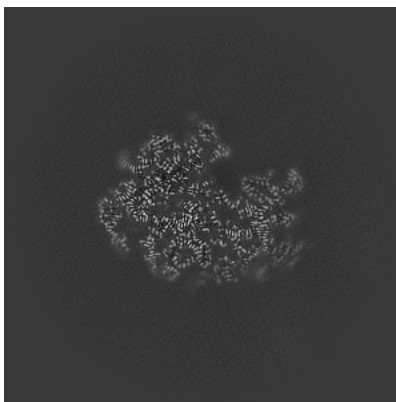
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

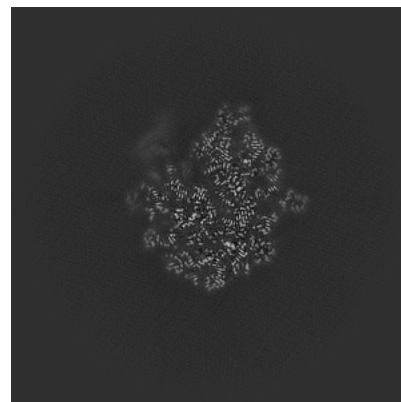
6.3.1 Primary map



X Index: 227

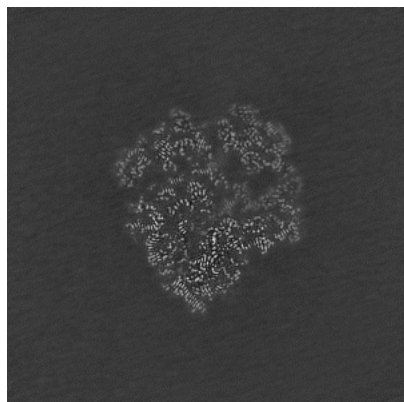


Y Index: 210

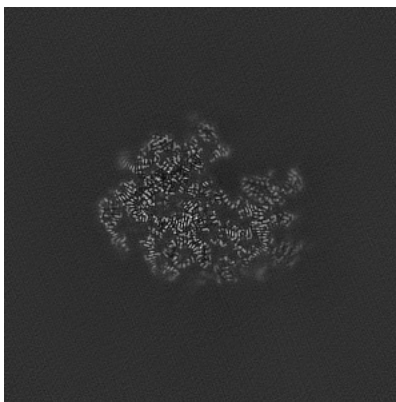


Z Index: 199

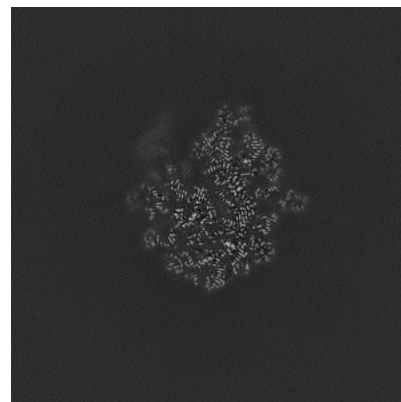
6.3.2 Raw map



X Index: 227



Y Index: 210

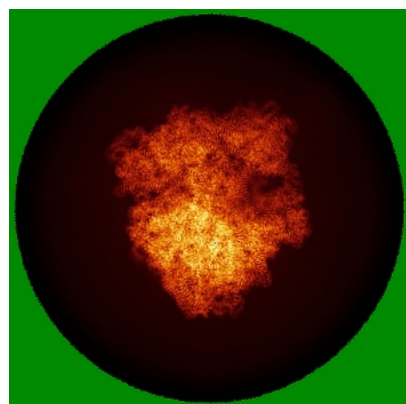


Z Index: 199

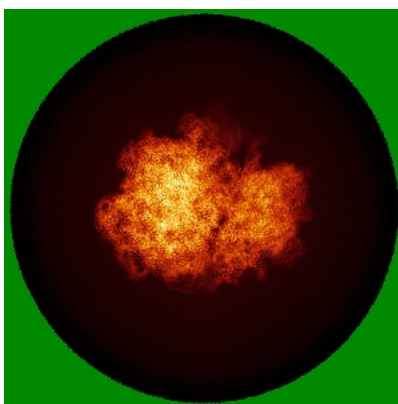
The images above show the largest variance slices of the map in three orthogonal directions.

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

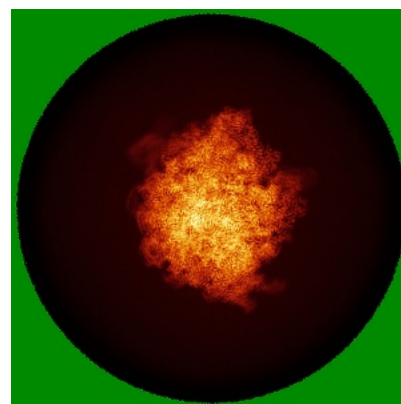
6.4.1 Primary map



X

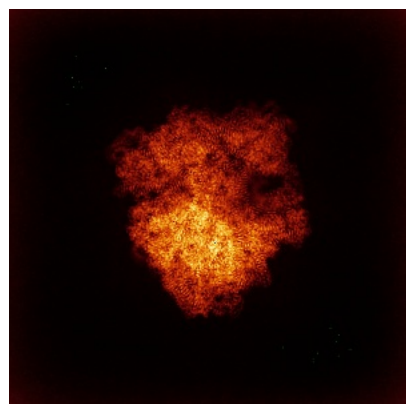


Y

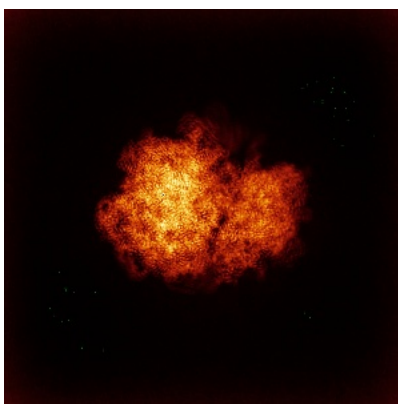


Z

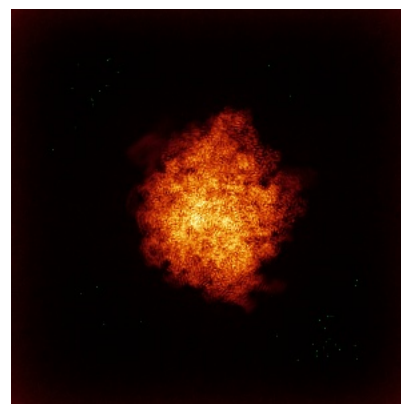
6.4.2 Raw map



X



Y

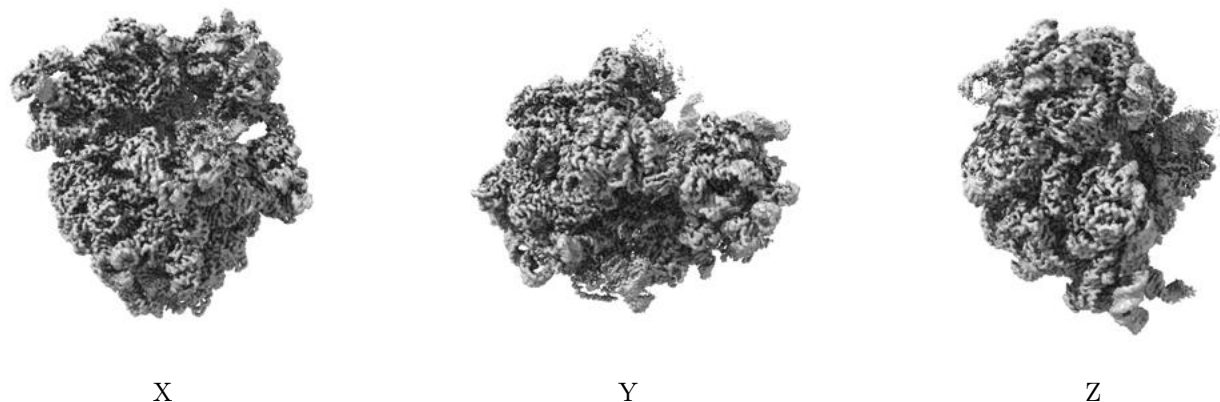


Z

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.

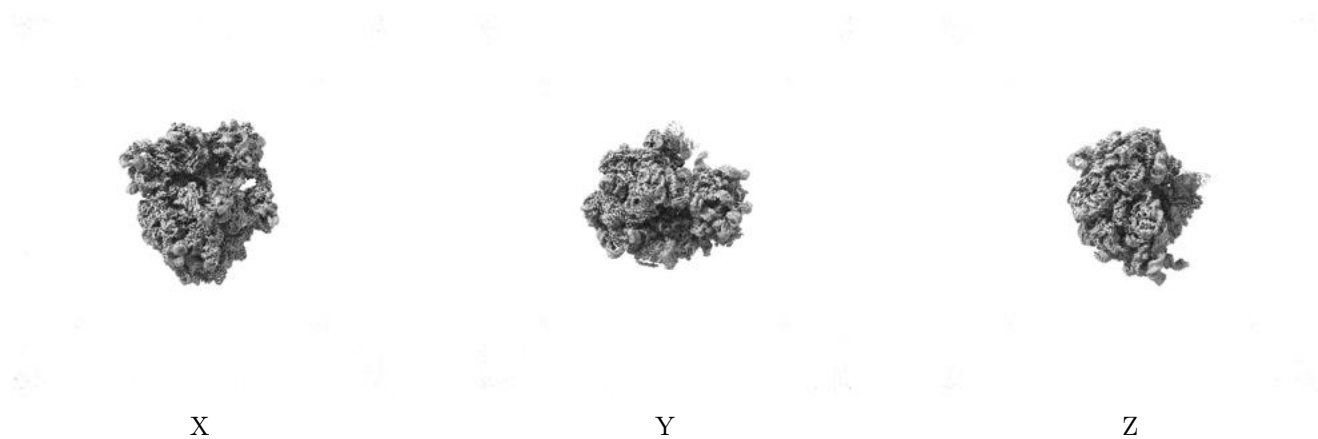
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. 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.

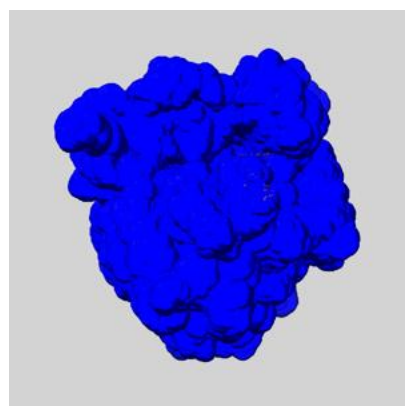
6.6 Mask visualisation [i](#)

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

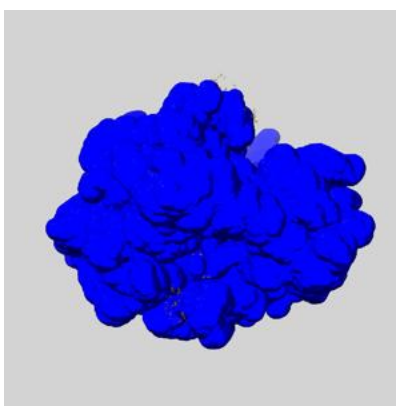
A mask typically either:

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

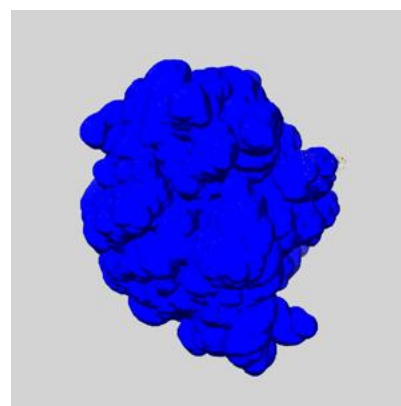
6.6.1 emd_71669_msk_1.map [i](#)



X



Y

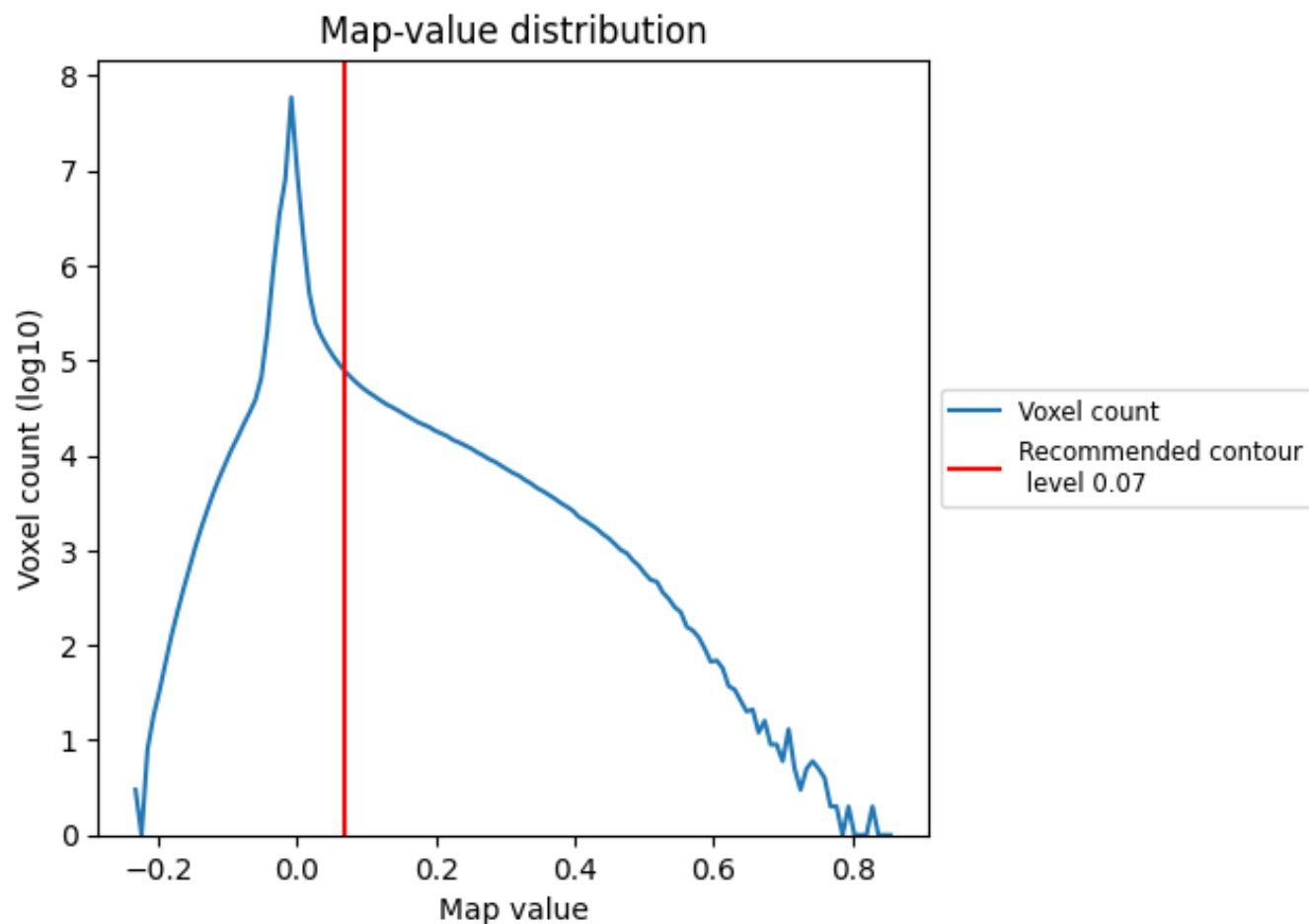


Z

7 Map analysis [i](#)

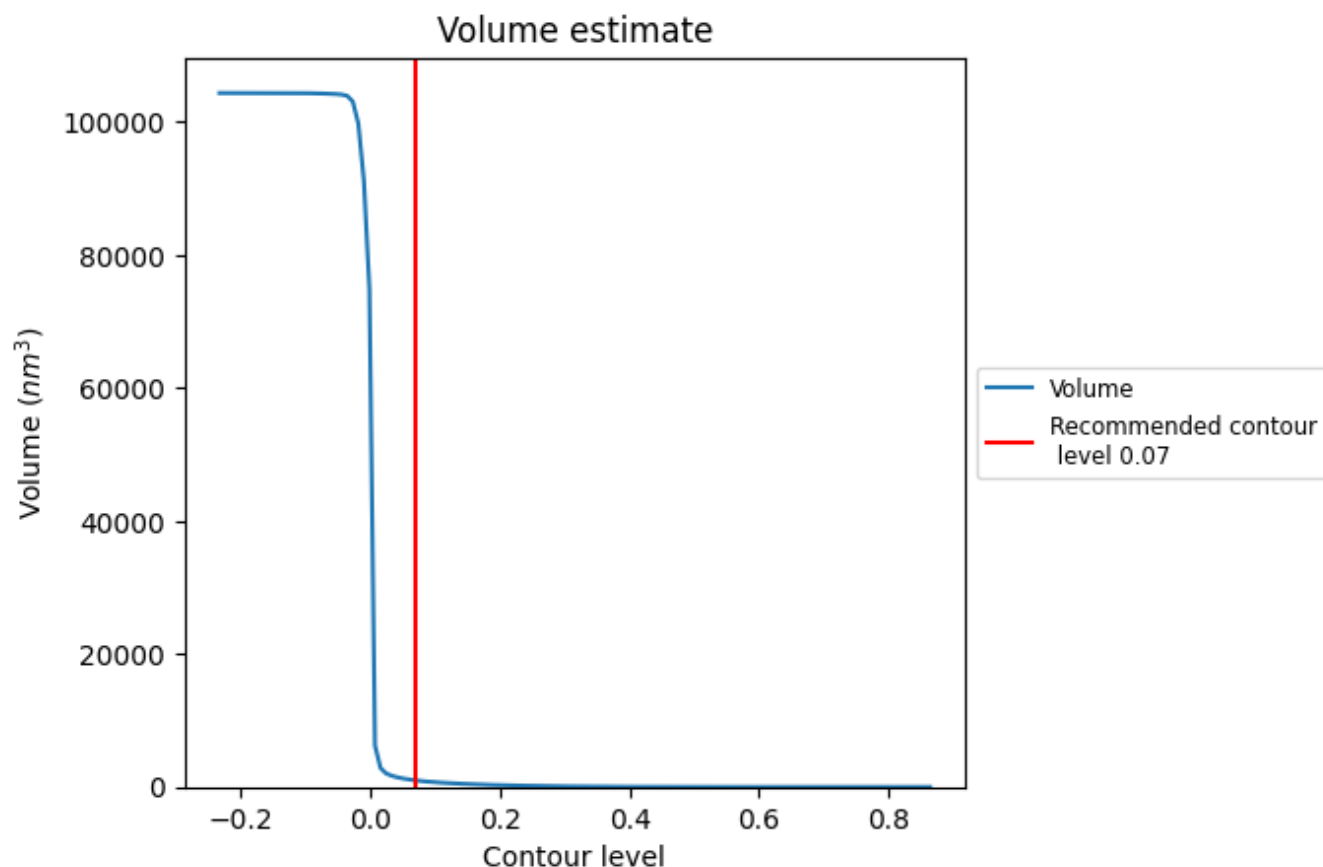
This section contains the results of statistical analysis of the map.

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.

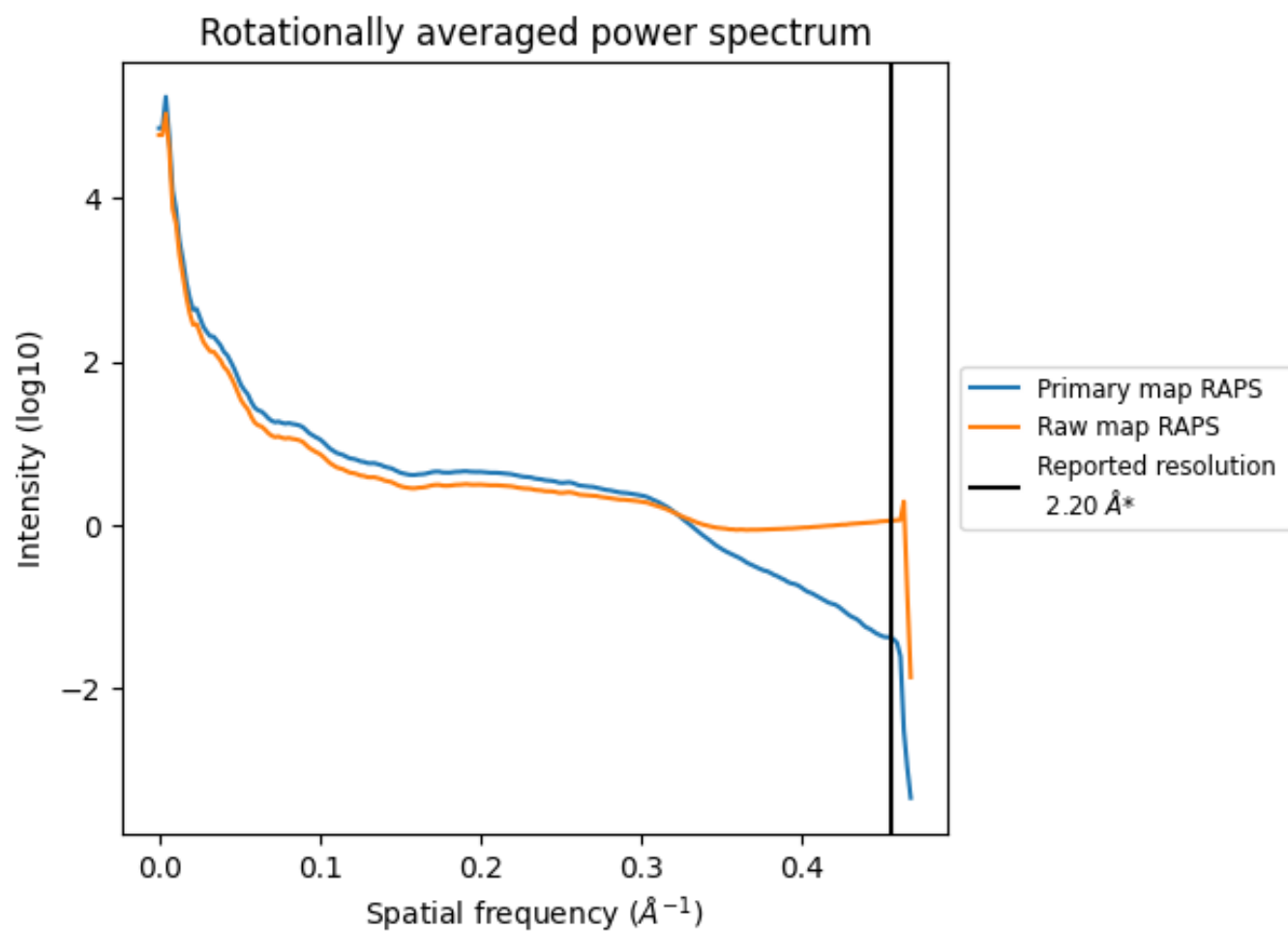
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 989 nm^3 ; this corresponds to an approximate mass of 893 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 ⓘ

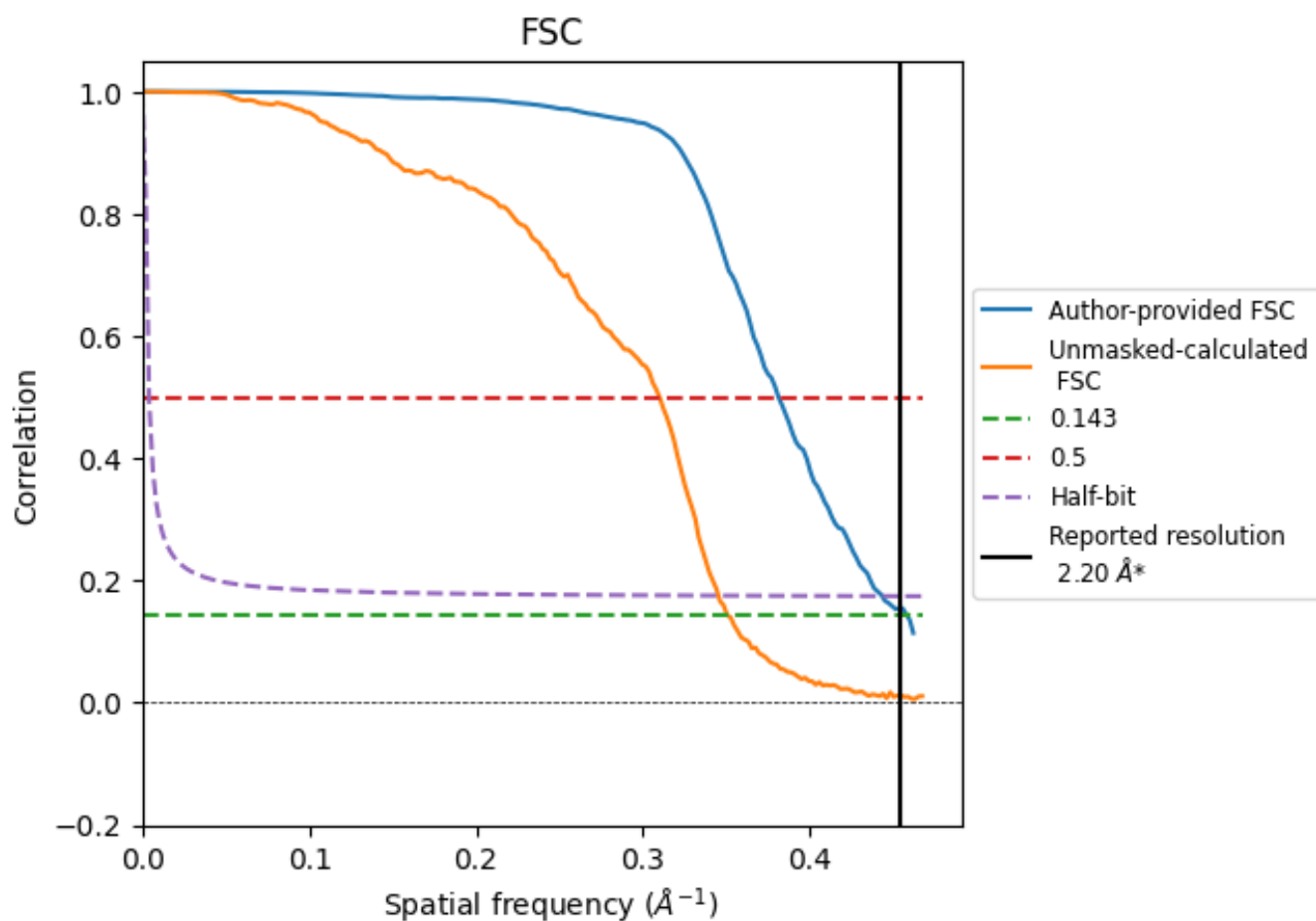


*Reported resolution corresponds to spatial frequency of 0.455 Å⁻¹

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 0.455 \AA^{-1}

8.2 Resolution estimates [i](#)

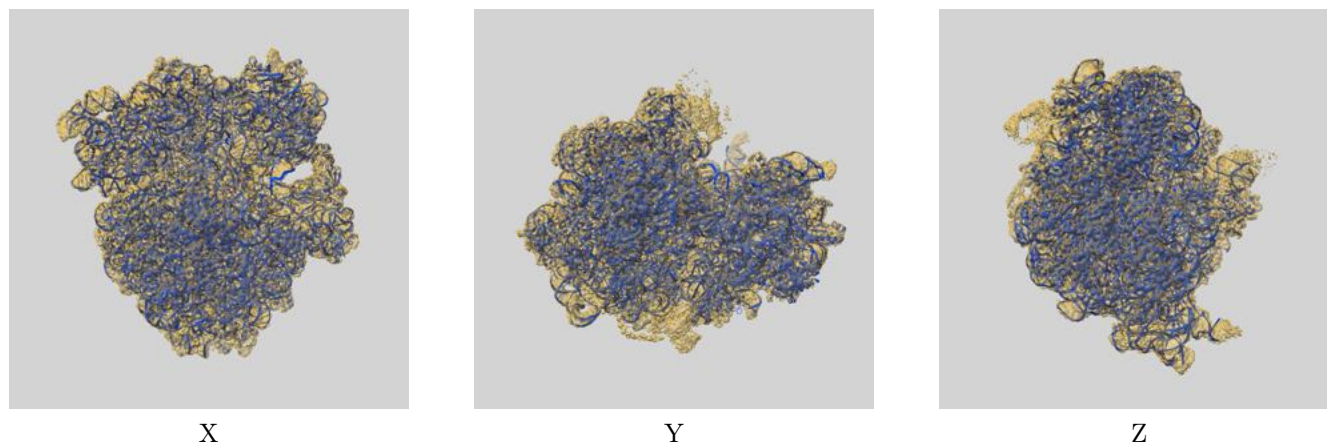
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.20	-	-
Author-provided FSC curve	2.18	2.62	2.26
Unmasked-calculated*	2.85	3.23	2.90

*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 2.85 differs from the reported value 2.2 by more than 10 %

9 Map-model fit [i](#)

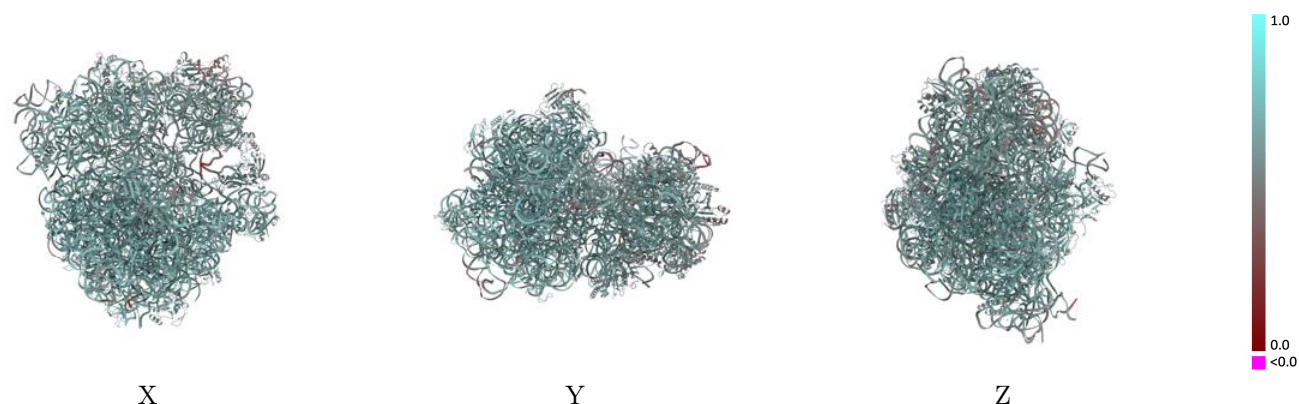
This section contains information regarding the fit between EMDB map EMD-71669 and PDB model 9PIJ. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



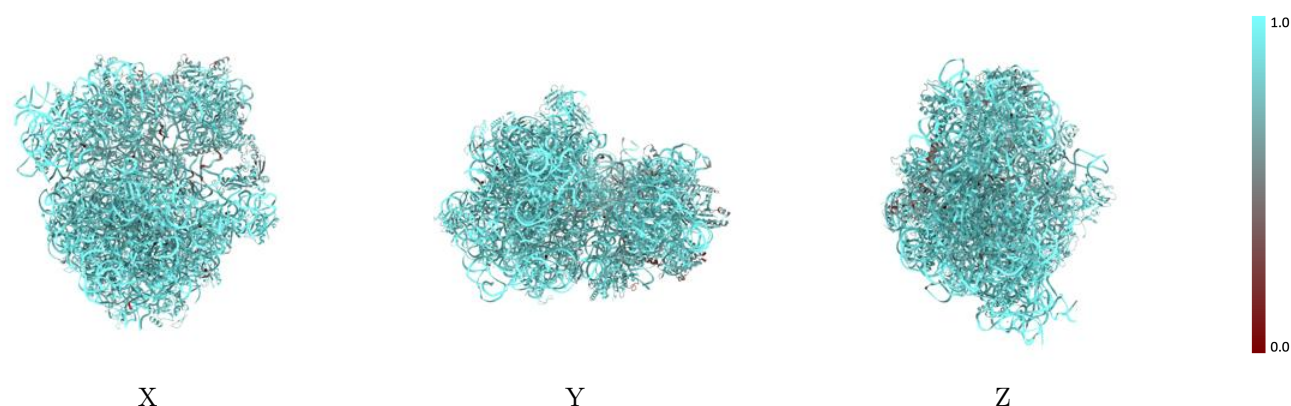
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



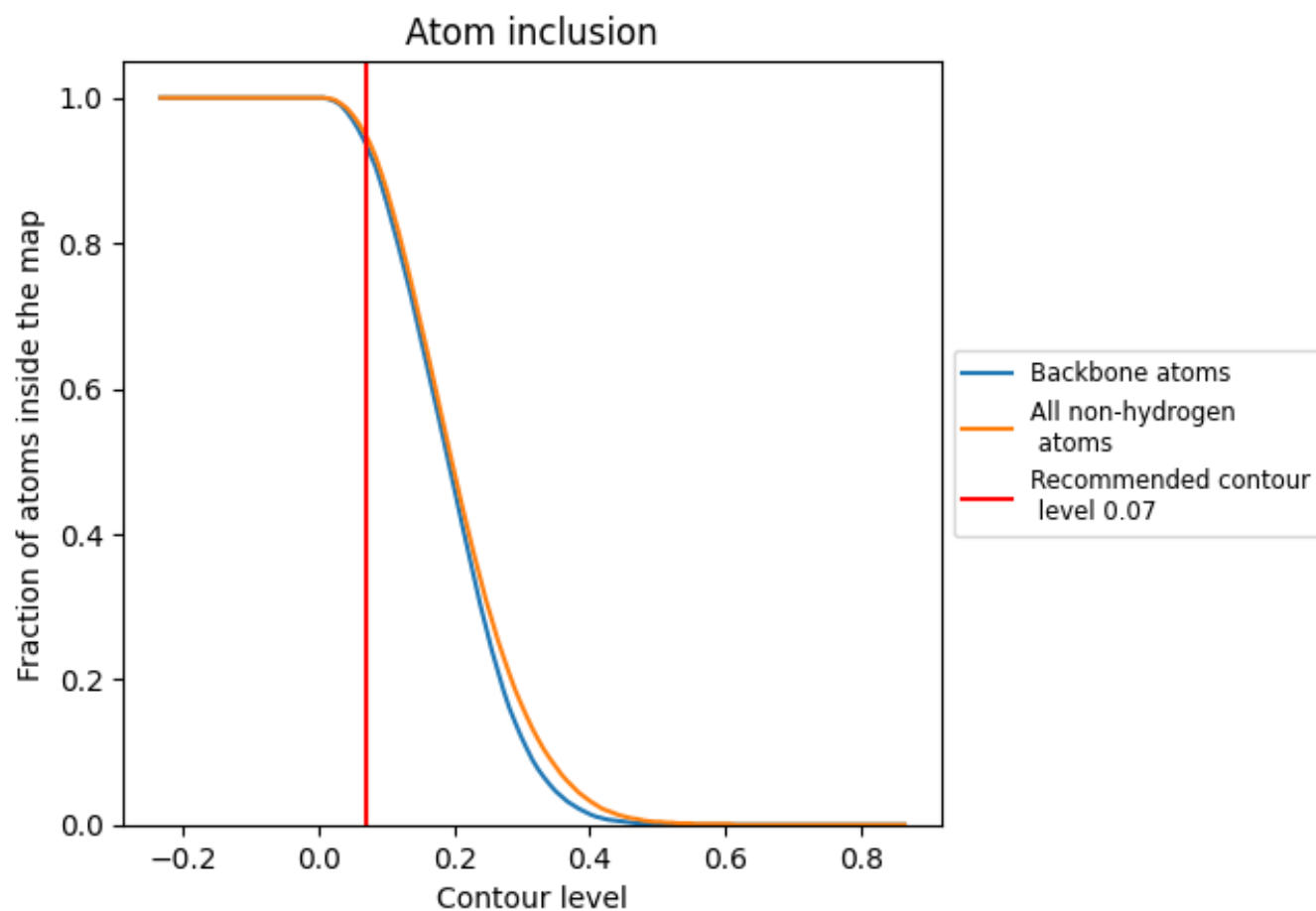
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.07).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 95% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ









































The table lists the average atom inclusion at the recommended contour level (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9490	 0.6310
0	 0.9000	 0.6430
1	 0.9660	 0.6850
2	 0.9700	 0.6800
3	 0.9390	 0.6540
4	 0.5750	 0.5310
A	 0.9830	 0.6190
B	 0.6130	 0.5450
C	 0.8580	 0.5910
D	 0.8660	 0.5960
E	 0.9170	 0.6310
F	 0.8580	 0.5810
G	 0.7770	 0.5510
H	 0.9150	 0.6280
I	 0.8590	 0.5710
J	 0.7740	 0.5370
K	 0.9040	 0.6110
L	 0.9020	 0.6310
M	 0.8370	 0.5720
N	 0.8750	 0.5820
O	 0.9120	 0.6070
P	 0.9190	 0.6200
Q	 0.8800	 0.5990
R	 0.7360	 0.5510
S	 0.8250	 0.5580
T	 0.8950	 0.6050
U	 0.7000	 0.5460
X	 0.6020	 0.4330
Z	 0.8140	 0.5700
a	 0.9850	 0.6510
b	 0.9830	 0.6180
c	 0.9570	 0.6730
d	 0.9460	 0.6610
e	 0.9200	 0.6370
f	 0.8460	 0.5680



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Chain	Atom inclusion	Q-score
g	 0.8540	 0.5650
h	 0.8470	 0.5880
i	 0.9460	 0.6600
j	 0.9330	 0.6580
k	 0.9440	 0.6580
l	 0.9290	 0.6530
m	 0.9710	 0.6680
n	 0.9200	 0.6050
o	 0.9190	 0.6510
p	 0.9740	 0.6750
q	 0.9370	 0.6450
r	 0.9290	 0.6550
s	 0.9130	 0.6220
t	 0.9090	 0.6160
u	 0.9000	 0.6180
v	 0.9180	 0.6610
w	 0.9380	 0.6530
x	 0.8850	 0.6010
y	 0.9150	 0.6370
z	 0.9370	 0.6650