



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2026 – 02:36 am BST

PDB ID : 28LU / pdb_000028lu
EMDB ID : EMD-56602
Title : Structure of the Chlamydomonas reinhardtii chlororibosome with factor pY
Authors : Waltz, F.; Kater, L.; Engel, B.D.
Deposited on : 2026-02-05
Resolution : 2.60 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:

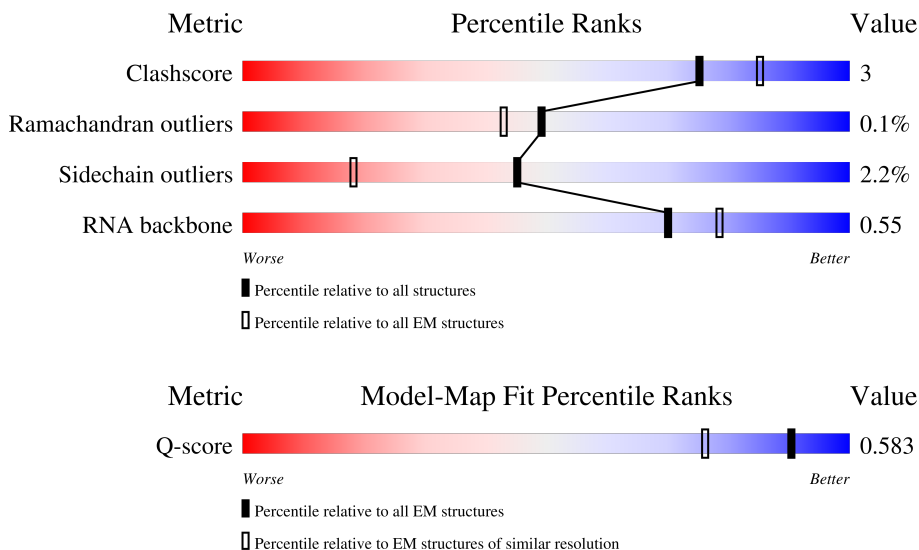
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.60 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.



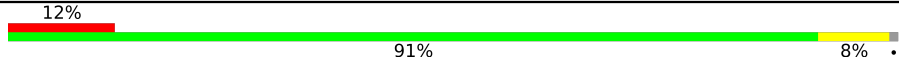







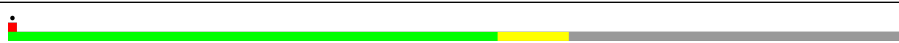

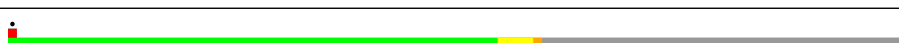


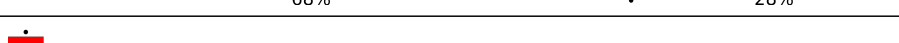
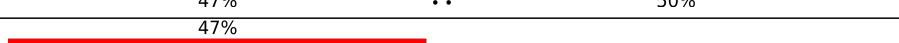
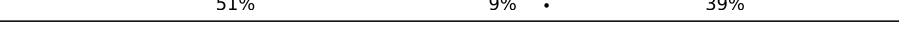
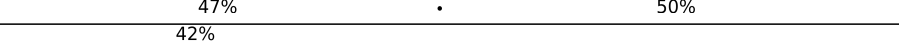
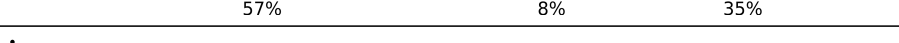
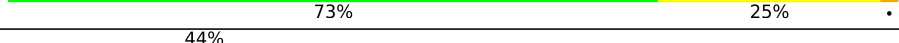




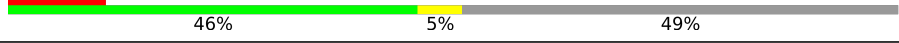

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8728 (2.10 - 3.10)

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	a	436	
2	d	257	
3	f	171	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	g	168	
5	h	141	
6	j	169	
7	k	130	
8	l	133	
9	m	164	
10	n	100	
11	o	141	
12	p	128	
13	q	105	
14	r	137	
15	s	92	
16	t	166	
17	u	184	
18	v	298	
19	x	120	
20	w	560	
21	2	1470	
22	b	910	
23	c	712	
24	e	673	
25	i	191	
26	y	286	
27	0	66	
28	3	121	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	5	47	
30	6	101	
31	7	124	
32	8	114	
33	9	37	
34	B	278	
35	C	259	
36	D	243	
37	E	179	
38	F	207	
39	G	200	
40	H	235	
41	I	176	
42	J	225	
43	K	122	
44	L	241	
45	M	136	
46	N	173	
47	O	145	
48	P	153	
49	Q	112	
50	R	179	
51	S	175	
52	T	111	
53	U	170	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	V	161	<p>6% 66% 6% 29%</p>
55	W	195	<p>6% 65% 6% 29%</p>
56	X	134	<p>6% 72% 7% 21%</p>
57	Z	98	<p>39% 32% 6% 58%</p>
58	Y	136	<p>32% 32% 15% 52%</p>
59	1	2375	<p>6% 77% 21% 6%</p>
60	4	272	<p>6% 79% 18% 6%</p>

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 159560 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 Ribosomal protein S1 homologue.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	a	236	Total	C	N	O	S	0	0
			1868	1175	285	395	13		

- Molecule 2 is a protein called Small ribosomal subunit protein uS4c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	d	256	Total	C	N	O	S	0	0
			2107	1356	403	341	7		

- Molecule 3 is a protein called bS6c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	f	103	Total	C	N	O	S	0	0
			850	543	148	156	3		

- Molecule 4 is a protein called Small ribosomal subunit protein uS7c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	g	167	Total	C	N	O	S	0	0
			1334	846	253	229	6		

- Molecule 5 is a protein called Small ribosomal subunit protein uS8c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	h	141	Total	C	N	O	S	0	0
			1113	698	206	203	6		

- Molecule 6 is a protein called Small ribosomal subunit protein uS10 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	j	122	Total	C	N	O	S	0	0
			957	597	173	178	9		

- Molecule 7 is a protein called Small ribosomal subunit protein uS11c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	k	117	894	560	179	151	4	0	0

- Molecule 8 is a protein called Small ribosomal subunit protein uS12c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	l	121	941	591	190	157	3	0	0

- Molecule 9 is a protein called uS13c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	m	114	924	569	181	172	2	0	0

- Molecule 10 is a protein called Small ribosomal subunit protein uS14c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	n	99	814	513	163	132	6	0	0

- Molecule 11 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	o	101	813	502	156	151	4	0	0

- Molecule 12 is a protein called 30S ribosomal protein S16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	p	80	666	433	120	112	1	0	0

- Molecule 13 is a protein called Small ribosomal subunit protein uS17c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	q	78	621	386	117	116	2	0	0

- Molecule 14 is a protein called Small ribosomal subunit protein bS18c.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	r	81	Total	C	N	O	S	0	0
			664	434	123	106	1		

- Molecule 15 is a protein called Small ribosomal subunit protein uS19c.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	s	81	Total	C	N	O	S	0	0
			645	414	122	106	3		

- Molecule 16 is a protein called bS20c.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	t	119	Total	C	N	O	S	0	0
			935	592	172	167	4		

- Molecule 17 is a protein called bS21c.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	u	92	Total	C	N	O	S	0	0
			789	494	144	147	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	652	ARG	ASP	conflict	UNP A8HPN4

- Molecule 18 is a protein called 30S ribosomal protein 3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	v	181	Total	C	N	O	S	0	0
			1430	907	245	276	2		

- Molecule 19 is a protein called cS26/PSRP8.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	x	60	Total	C	N	O	S	0	0
			462	299	80	81	2		

- Molecule 20 is a protein called Plastid-specific ribosomal protein-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	w	365	2786	1749	429	598	10	0	0

- Molecule 21 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
21	2	1470	31537	14077	5779	10211	1470	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	?	-	C	deletion	GB 41179002
2	?	-	A	deletion	GB 41179002
2	372	A	-	insertion	GB 41179002
2	373	G	-	insertion	GB 41179002
2	871	G	-	insertion	GB 41179002
2	872	G	-	insertion	GB 41179002
2	912	2MG	A	conflict	GB 41179002
2	982	A	-	insertion	GB 41179002
2	983	C	-	insertion	GB 41179002
2	1200	C	-	insertion	GB 41179002
2	1218	A	C	conflict	GB 41179002

- Molecule 22 is a protein called Small ribosomal subunit protein uS2c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	b	685	5545	3581	1010	934	20	0	0

- Molecule 23 is a protein called Small ribosomal subunit protein uS3c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	c	607	4939	3179	905	844	11	0	0

- Molecule 24 is a protein called uS5c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	e	536	3988	2477	658	838	15	0	0

- Molecule 25 is a protein called Small ribosomal subunit protein uS9c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	i	153	1189	750	219	217	3	0	0

- Molecule 26 is a protein called Sigma 54 modulation/S30EA ribosomal protein C-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	y	146	1155	725	203	225	2	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
y	236	ALA	-	insertion	UNP A0A2K3DSW0

- Molecule 27 is a protein called cL38/PSRP6.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
27	0	47	369	233	76	60	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	17	SER	THR	conflict	UNP A0A835SZL0
0	37	ARG	ALA	conflict	UNP A0A835SZL0
0	38	ALA	SER	conflict	UNP A0A835SZL0
0	41	ASN	ARG	conflict	UNP A0A835SZL0
0	63	ALA	GLY	conflict	UNP A0A835SZL0

- Molecule 28 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
28	3	121	2571	1148	449	853	121	0	0

- Molecule 29 is a RNA chain called 3S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
29	5	47	1006	450	185	324	47	0	0

- Molecule 30 is a protein called bL33c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	6	58	473	293	91	86	3	0	0

- Molecule 31 is a protein called bL34c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	7	60	455	271	104	77	3	0	0

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	8	68	520	322	104	91	3	0	0

- Molecule 33 is a protein called Large ribosomal subunit protein bL36c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	9	37	292	177	63	46	6	0	0

- Molecule 34 is a protein called Large ribosomal subunit protein uL2c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	B	276	2159	1347	431	377	4	0	0

- Molecule 35 is a protein called Large ribosomal subunit protein uL3c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	C	223	1681	1057	310	305	9	0	0

- Molecule 36 is a protein called Large ribosomal subunit protein uL4c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	D	216	1599	997	290	306	6	0	0

- Molecule 37 is a protein called Large ribosomal subunit protein uL5c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	E	178	1413	900	247	260	6	0	0

- Molecule 38 is a protein called Plastid ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	F	177	1338	845	245	244	4	0	0

- Molecule 39 is a protein called Large ribosomal subunit protein bL9c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	G	54	418	272	72	73	1	0	0

- Molecule 40 is a protein called uL10c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	H	141	1114	711	189	209	5	0	0

- Molecule 41 is a protein called Large ribosomal subunit protein uL11c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	I	132	980	623	171	181	5	0	0

- Molecule 42 is a protein called uL13c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	J	173	1346	857	243	243	3	0	0

- Molecule 43 is a protein called Large ribosomal subunit protein uL14c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	K	122	942	588	180	169	5	0	0

- Molecule 44 is a protein called uL15c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	L	198	1484	921	282	276	5	0	0

- Molecule 45 is a protein called Large ribosomal subunit protein uL16c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	M	135	1080	689	211	173	7	0	0

- Molecule 46 is a protein called Large ribosomal subunit protein bL17c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	N	117	937	585	185	162	5	0	0

- Molecule 47 is a protein called Large ribosomal subunit protein uL18c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	O	118	902	557	173	168	4	0	0

- Molecule 48 is a protein called bL19c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	P	130	995	620	199	174	2	0	0

- Molecule 49 is a protein called Large ribosomal subunit protein bL20c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	Q	111	943	592	193	152	6	0	0

- Molecule 50 is a protein called bL21c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	R	115	907	585	161	157	4	0	0

- Molecule 51 is a protein called Large ribosomal subunit protein uL22c.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S	115	Total	C	N	O	S	0	0
			903	564	174	157	8		

- Molecule 52 is a protein called uL23c, Large ribosomal subunit protein uL23c.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	T	107	Total	C	N	O	S	0	0
			837	542	148	146	1		

- Molecule 53 is a protein called KOW domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	U	132	Total	C	N	O	S	0	0
			1020	650	189	178	3		

- Molecule 54 is a protein called bL27c.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	V	114	Total	C	N	O	S	0	0
			869	535	172	159	3		

- Molecule 55 is a protein called Large ribosomal subunit protein bL28c.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	W	138	Total	C	N	O	S	0	0
			1104	700	205	193	6		

- Molecule 56 is a protein called uL29c.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	X	106	Total	C	N	O	S	0	0
			843	518	169	153	3		

- Molecule 57 is a protein called bL32c.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	Z	41	Total	C	N	O	0	0
			323	213	57	53		

- Molecule 58 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Y	65	Total	C	N	O	S	0	0
			521	331	90	98	2		

- Molecule 59 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	1	2375	Total	C	N	O	P	0	0
			50934	22751	9345	16463	2375		

- Molecule 60 is a RNA chain called 7S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	4	272	Total	C	N	O	P	0	0
			5856	2616	1106	1862	272		

- Molecule 61 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
61	2	47	Total	K	0
			47	47	
61	U	1	Total	K	0
			1	1	
61	1	86	Total	K	0
			86	86	
61	4	4	Total	K	0
			4	4	

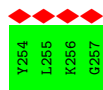
- Molecule 62 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
62	2	98	Total	Mg	0
			98	98	
62	3	5	Total	Mg	0
			5	5	
62	5	4	Total	Mg	0
			4	4	
62	D	1	Total	Mg	0
			1	1	
62	L	1	Total	Mg	0
			1	1	
62	N	1	Total	Mg	0
			1	1	

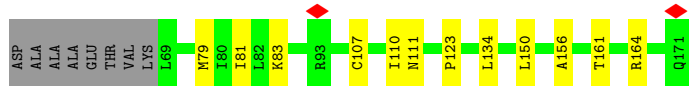
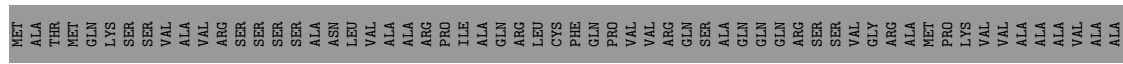
Continued on next page...

Continued from previous page...

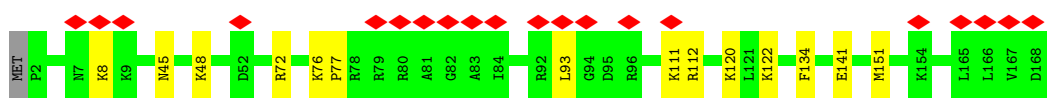
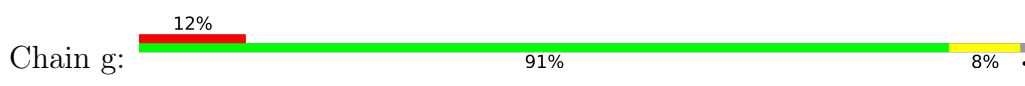
Mol	Chain	Residues	Atoms		AltConf
62	1	205	Total 205	Mg 205	0
62	4	7	Total 7	Mg 7	0



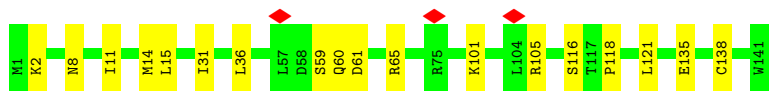
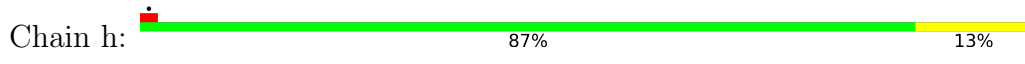
• Molecule 3: bS6c



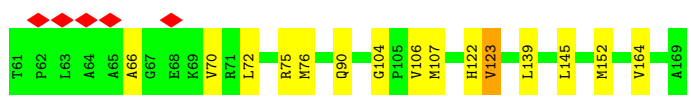
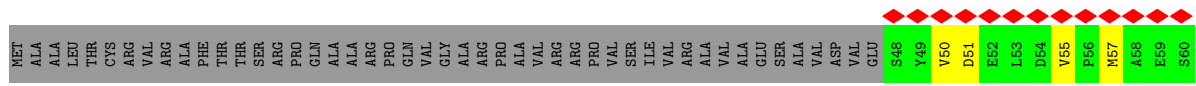
• Molecule 4: Small ribosomal subunit protein uS7c



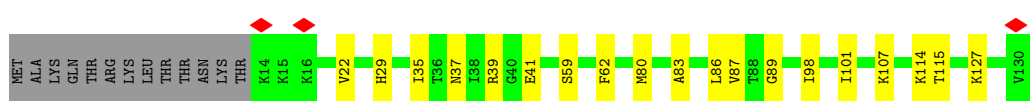
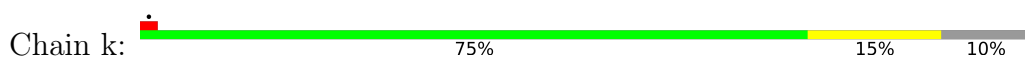
• Molecule 5: Small ribosomal subunit protein uS8c



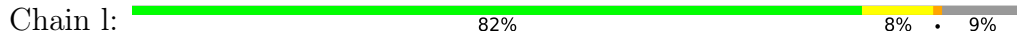
• Molecule 6: Small ribosomal subunit protein uS10 domain-containing protein



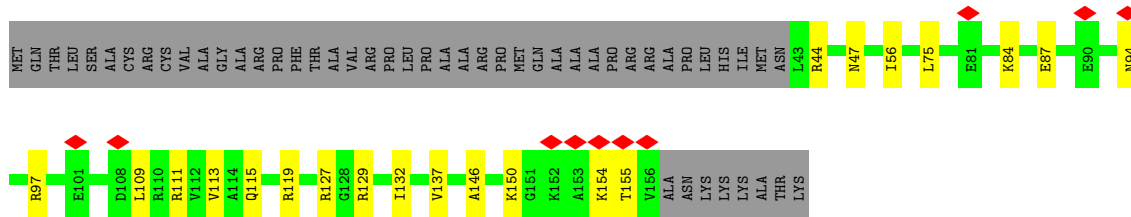
• Molecule 7: Small ribosomal subunit protein uS11c



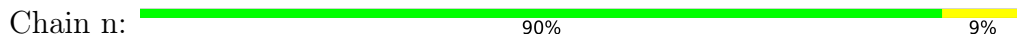
• Molecule 8: Small ribosomal subunit protein uS12c



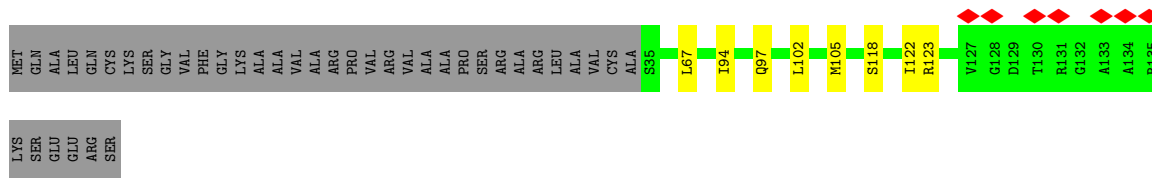
• Molecule 9: uS13c



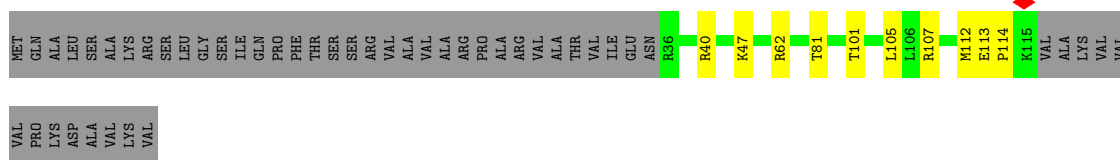
• Molecule 10: Small ribosomal subunit protein uS14c



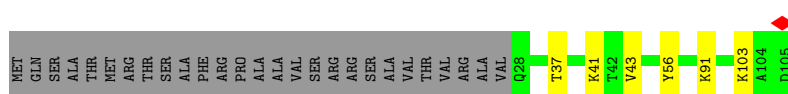
• Molecule 11: 30S ribosomal protein S15

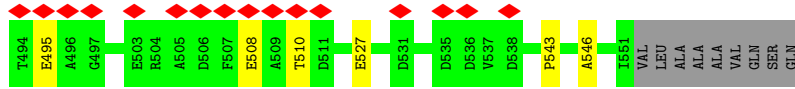


• Molecule 12: 30S ribosomal protein S16, chloroplastic

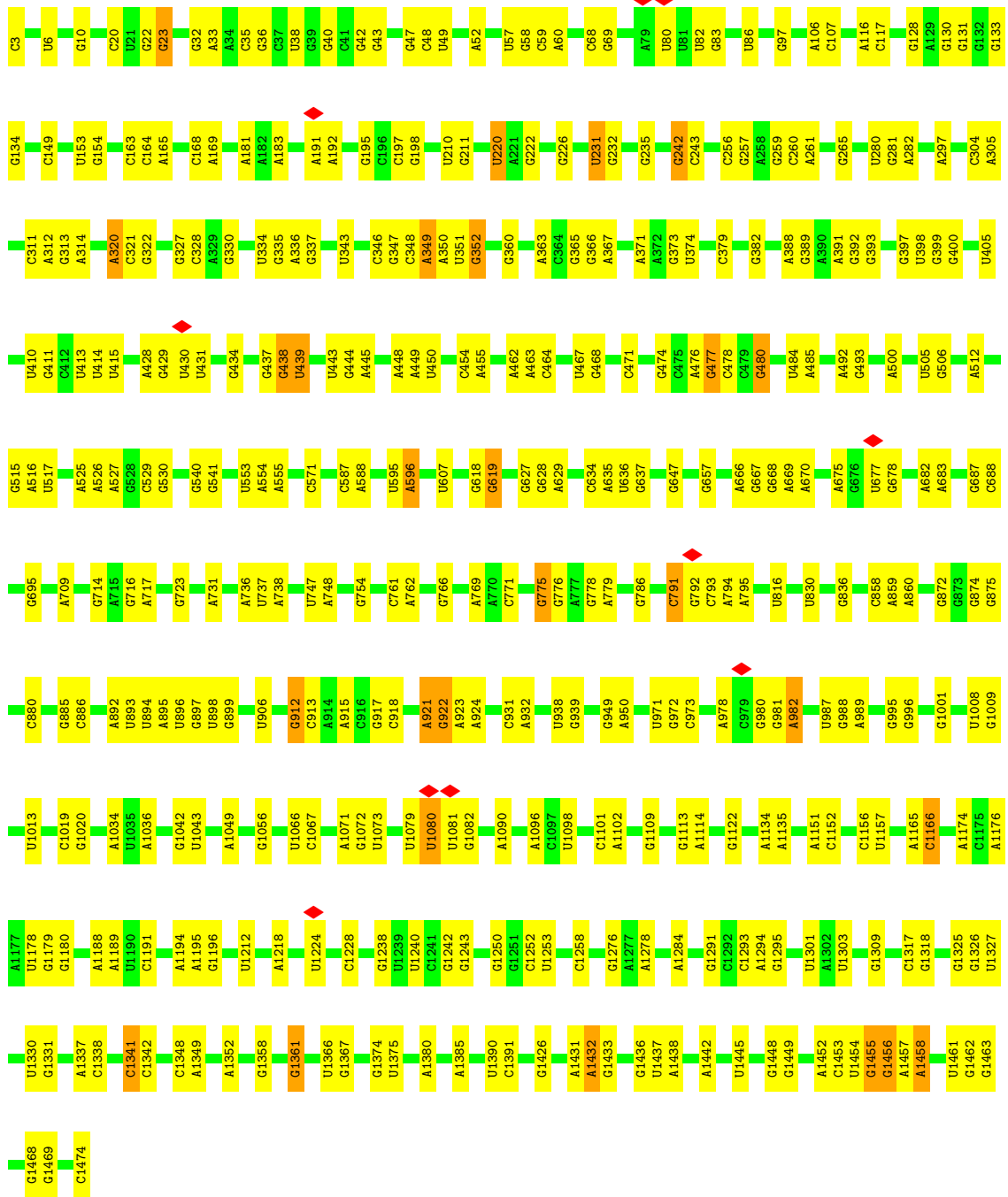


• Molecule 13: Small ribosomal subunit protein uS17c

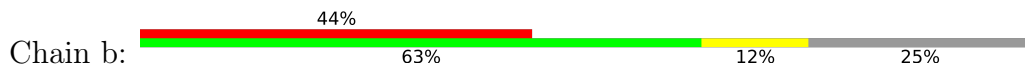


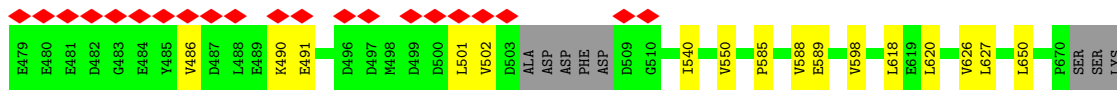


• Molecule 21: 16S rRNA

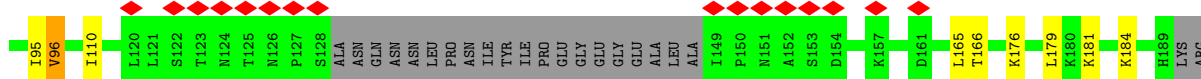
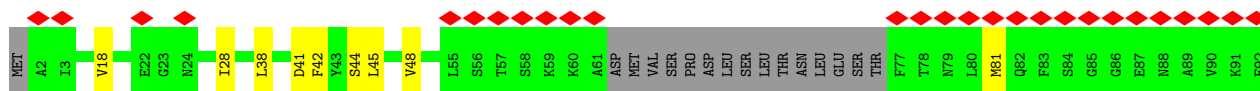


• Molecule 22: Small ribosomal subunit protein uS2c

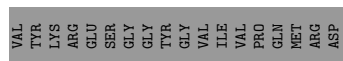
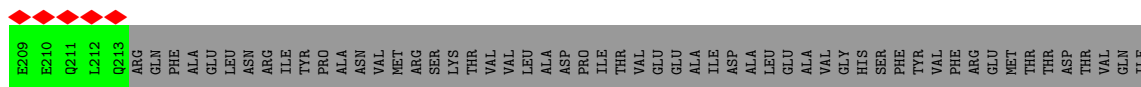
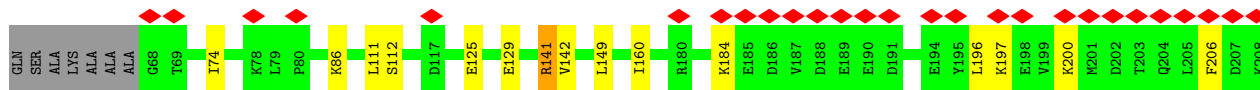
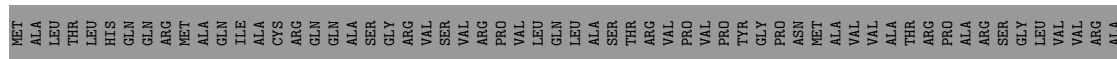




• Molecule 25: Small ribosomal subunit protein uS9c



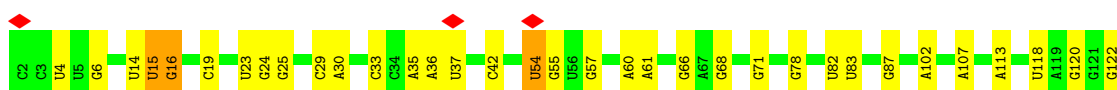
• Molecule 26: Sigma 54 modulation/S30EA ribosomal protein C-terminal domain-containing protein



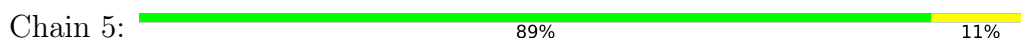
• Molecule 27: cL38/PSRP6



• Molecule 28: 5S rRNA

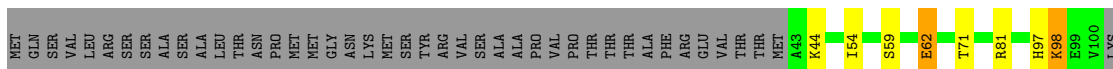


• Molecule 29: 3S rRNA

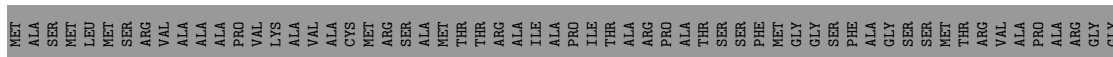




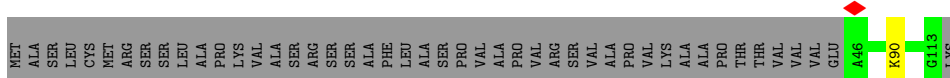
- Molecule 30: bL33c



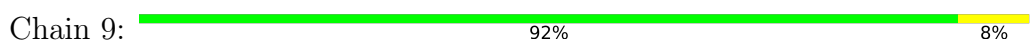
- Molecule 31: bL34c



- Molecule 32: 50S ribosomal protein L35



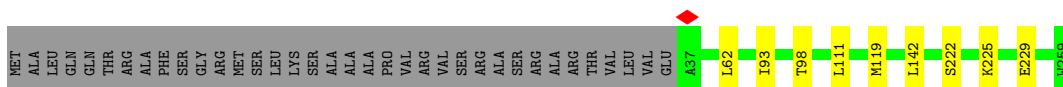
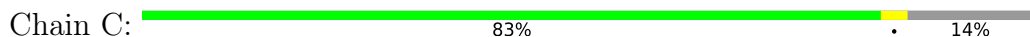
- Molecule 33: Large ribosomal subunit protein bL36c




- Molecule 34: Large ribosomal subunit protein uL2c



- Molecule 35: Large ribosomal subunit protein uL3c




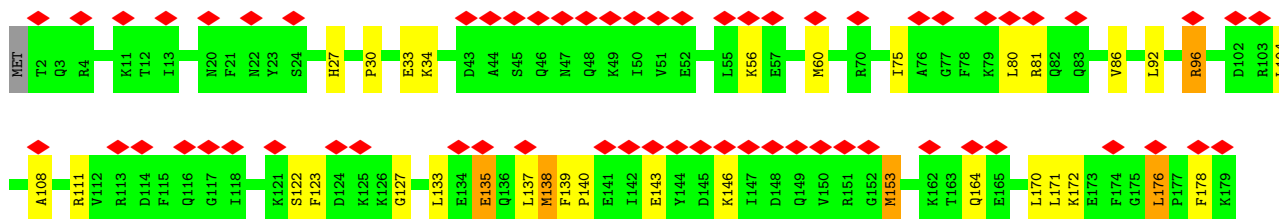
- Molecule 36: Large ribosomal subunit protein uL4c

Chain D:  83% 6% 11%




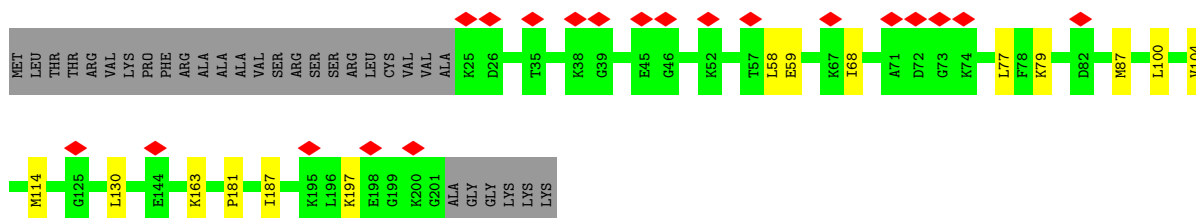
• Molecule 37: Large ribosomal subunit protein uL5c

Chain E:  35% 81% 16% ..



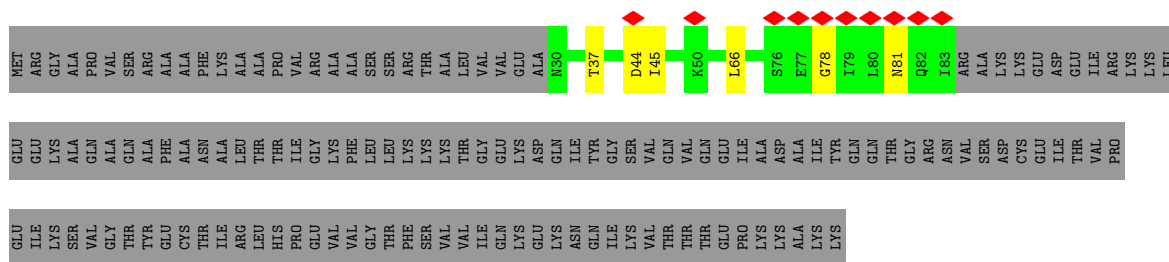
• Molecule 38: Plastid ribosomal protein L6

Chain F:  10% 79% 7% 14%



• Molecule 39: Large ribosomal subunit protein bL9c

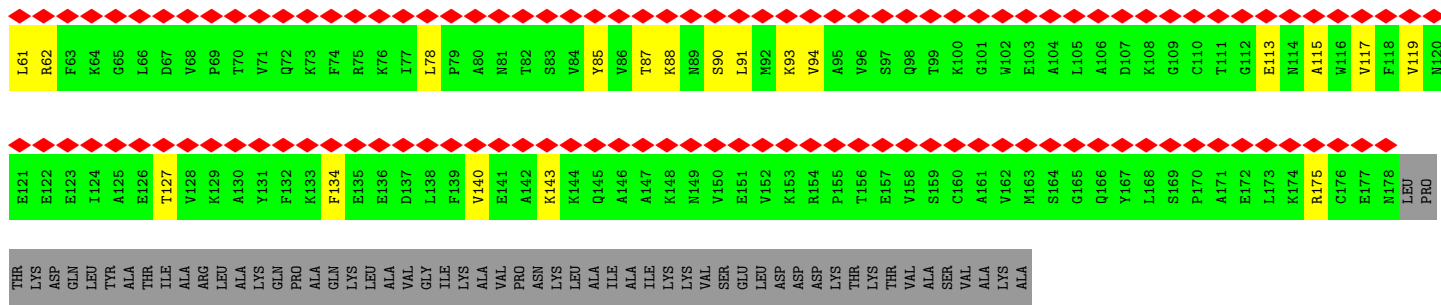
Chain G:  5% 24% 73%



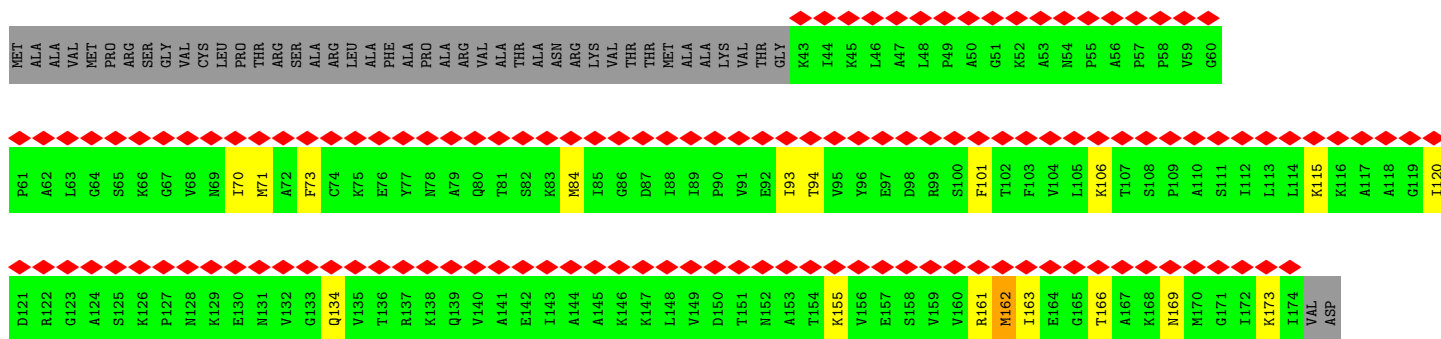
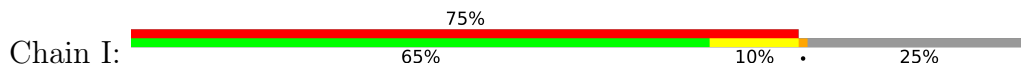
• Molecule 40: uL10c

Chain H:  60% 51% 9% 40%

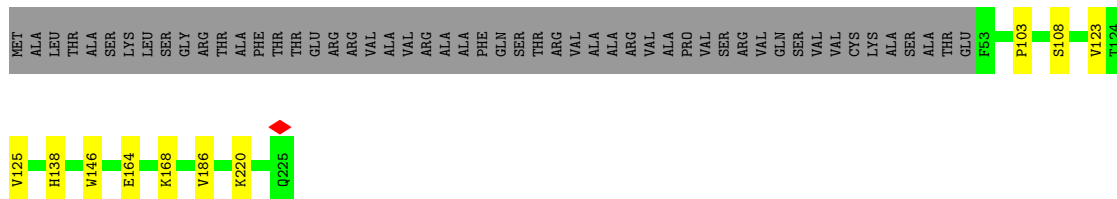




• Molecule 41: Large ribosomal subunit protein uL11c



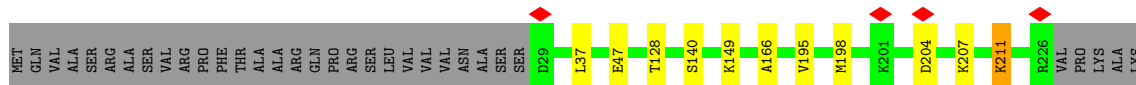
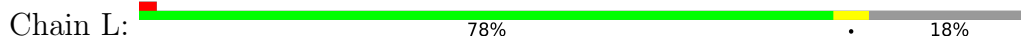
• Molecule 42: uL13c

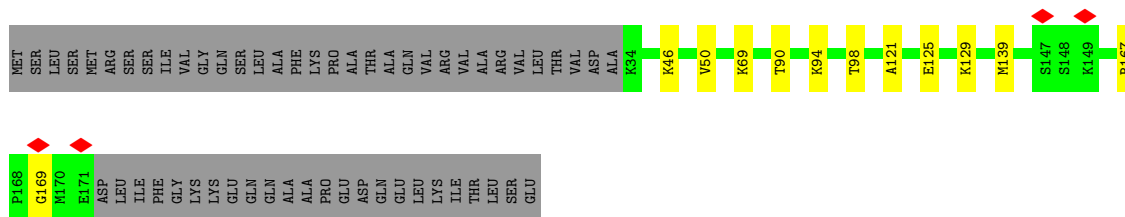


• Molecule 43: Large ribosomal subunit protein uL14c



• Molecule 44: uL15c

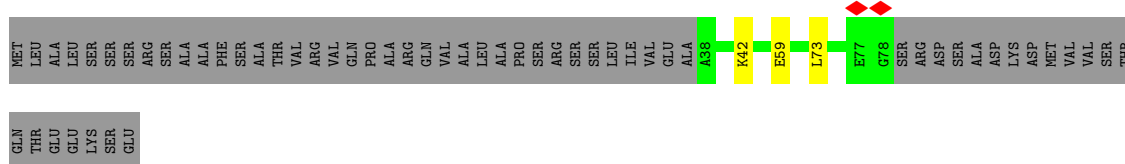




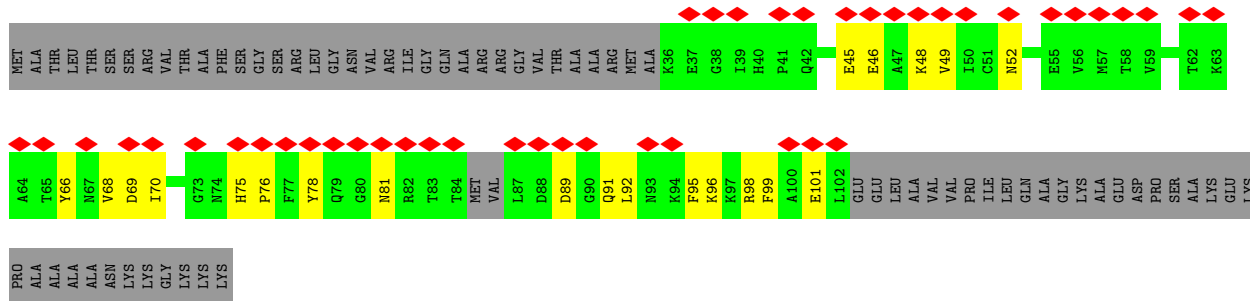
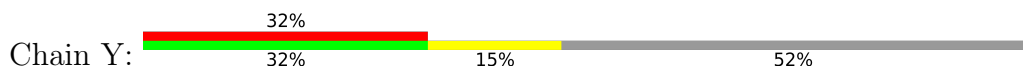
• Molecule 56: uL29c



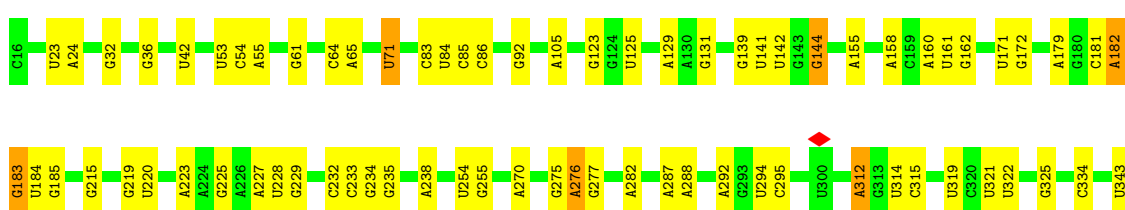
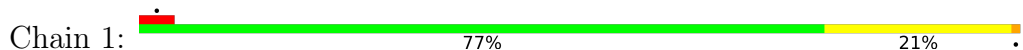
• Molecule 57: bL32c

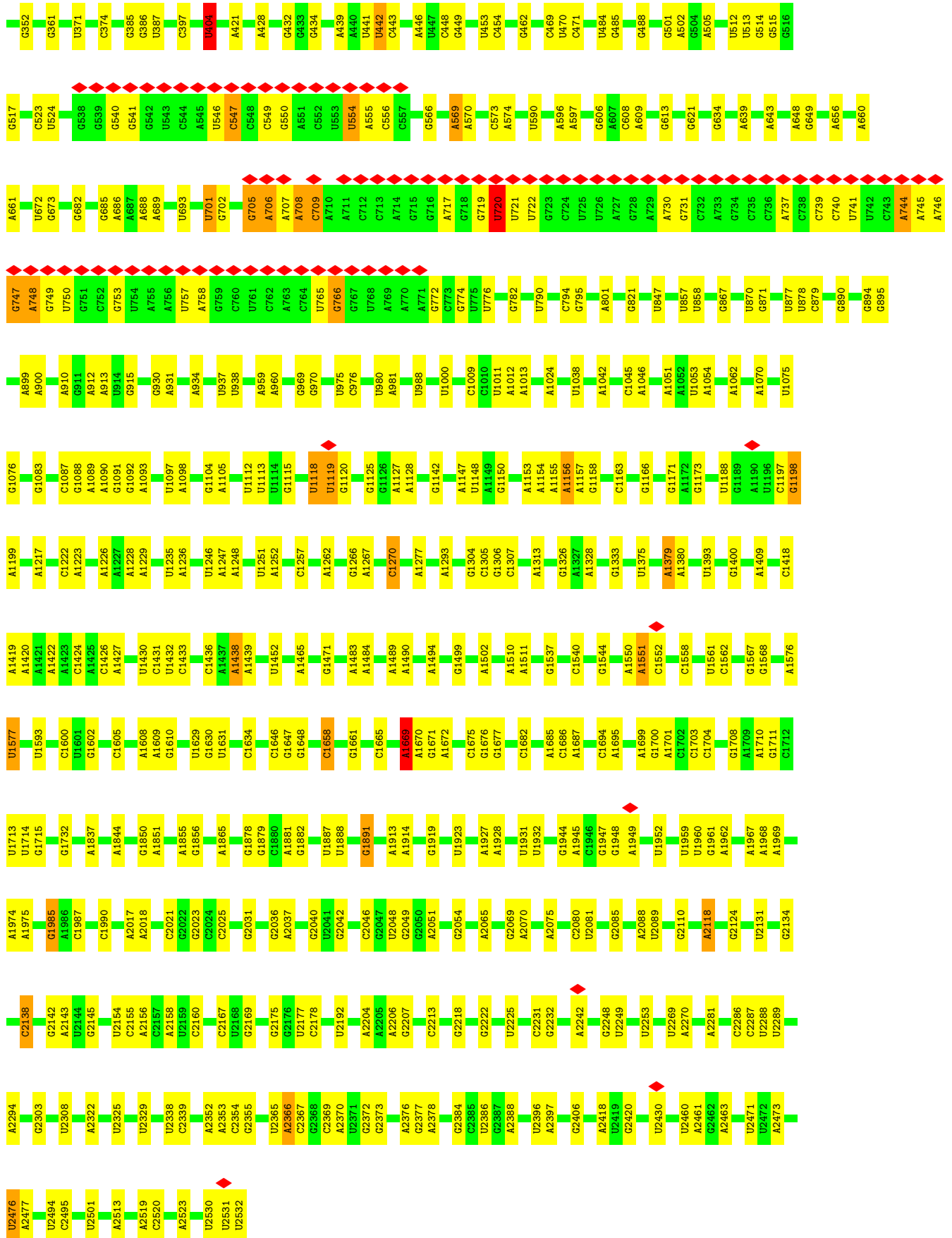


• Molecule 58: 50S ribosomal protein L31

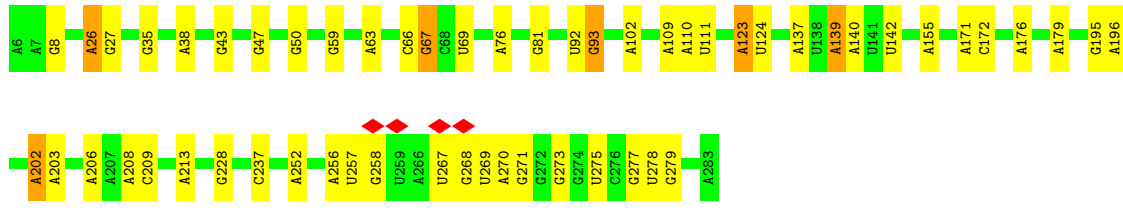
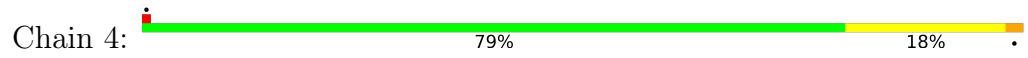


• Molecule 59: 23S rRNA





• Molecule 60: 7S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	175058	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	75000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	1.538	Depositor
Minimum map value	-0.289	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.107	Depositor
Map size (Å)	544.3072, 544.3072, 544.3072	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0631, 1.0631, 1.0631	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: MG, MA6, G7M, 6MZ, OMC, 4OC, 2MA, OMG, H2U, UR3, OMU, 2MG, 5MC, K, 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	a	0.22	0/1899	0.59	0/2570
2	d	0.17	0/2144	0.40	0/2867
3	f	0.14	0/868	0.35	0/1172
4	g	0.19	0/1354	0.47	0/1820
5	h	0.14	0/1125	0.36	0/1505
6	j	0.16	0/974	0.48	0/1316
7	k	0.17	0/908	0.42	0/1210
8	l	0.15	0/955	0.36	0/1282
9	m	0.19	0/931	0.47	0/1246
10	n	0.13	0/827	0.32	0/1097
11	o	0.18	0/822	0.42	0/1098
12	p	0.15	0/682	0.39	0/917
13	q	0.15	0/626	0.35	0/836
14	r	0.17	0/676	0.40	0/907
15	s	0.17	0/661	0.44	0/887
16	t	0.18	0/948	0.40	0/1269
17	u	0.19	0/801	0.70	3/1070 (0.3%)
18	v	0.25	0/1463	0.69	3/1994 (0.2%)
19	x	0.14	0/472	0.37	0/637
20	w	0.18	0/2835	0.43	0/3845
21	2	0.15	2/35103 (0.0%)	0.31	0/54745
22	b	0.22	0/5616	0.53	3/7512 (0.0%)
23	c	0.16	0/5008	0.42	1/6698 (0.0%)
24	e	0.16	0/4029	0.44	1/5461 (0.0%)
25	i	0.20	0/1202	0.54	0/1605
26	y	0.28	1/1168 (0.1%)	0.50	0/1570
27	0	0.20	0/382	0.37	0/518
28	3	0.18	0/2871	0.36	0/4471
29	5	0.22	0/1126	0.38	0/1753
30	6	0.19	0/479	0.39	0/640
31	7	0.23	0/457	0.47	0/595
32	8	0.21	0/528	0.39	0/702

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	9	0.20	0/292	0.32	0/379
34	B	0.23	0/2200	0.42	0/2965
35	C	0.22	0/1711	0.41	0/2304
36	D	0.21	0/1619	0.40	0/2183
37	E	0.25	0/1433	0.63	2/1920 (0.1%)
38	F	0.17	0/1354	0.40	0/1821
39	G	0.20	0/424	0.46	0/570
40	H	0.19	0/1131	0.48	0/1520
41	I	2.27	3/992 (0.3%)	0.97	6/1336 (0.4%)
42	J	0.20	0/1375	0.40	0/1855
43	K	0.21	0/952	0.41	0/1280
44	L	0.21	0/1505	0.46	0/2009
45	M	0.19	0/1105	0.39	0/1482
46	N	0.22	0/951	0.43	0/1275
47	O	0.19	0/913	0.52	0/1222
48	P	0.18	0/1005	0.37	0/1351
49	Q	0.25	0/958	0.43	0/1272
50	R	0.21	0/927	0.39	0/1247
51	S	0.20	0/915	0.43	0/1221
52	T	0.22	0/772	0.44	0/1043
53	U	0.18	0/1036	0.35	0/1381
54	V	0.20	0/884	0.44	0/1187
55	W	0.19	0/1126	0.40	0/1507
56	X	0.20	0/853	0.36	0/1141
57	Z	0.21	0/328	0.39	0/436
58	Y	0.29	0/532	0.69	0/715
59	1	0.53	6/56765 (0.0%)	0.38	4/88499 (0.0%)
60	4	0.24	0/6566	0.37	0/10240
All	All	0.38	12/170564 (0.0%)	0.40	23/251176 (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
1	a	0	1
6	j	0	1
17	u	0	1
18	v	0	1
26	y	0	1
44	L	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
59	1	2	0
All	All	2	6

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	I	162	MET	CA-C	70.08	2.45	1.52
59	1	720	U	N3-C4	50.68	2.39	1.38
59	1	720	U	C2-N3	47.91	2.33	1.37
59	1	720	U	N1-C2	47.81	2.34	1.38
59	1	720	U	N1-C6	45.43	2.28	1.38

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	I	162	MET	O-C-N	-18.55	97.64	122.49
41	I	162	MET	CB-CA-C	13.76	134.34	109.29
17	u	583	ARG	CB-CG-CD	11.32	137.34	111.30
41	I	162	MET	CA-C-O	9.23	129.30	119.14
41	I	162	MET	N-CA-C	8.91	124.46	113.50

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
59	1	312	A	C1'
59	1	1379	A	C1'

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	a	291	VAL	Peptide
6	j	122	HIS	Peptide
17	u	583	ARG	Sidechain
18	v	141	ASP	Peptide
26	y	141	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	a	1868	0	1762	20	0
2	d	2107	0	2303	16	0
3	f	850	0	852	7	0
4	g	1334	0	1441	9	0
5	h	1113	0	1184	13	0
6	j	957	0	968	10	0
7	k	894	0	956	10	0
8	l	941	0	1029	7	0
9	m	924	0	971	32	0
10	n	814	0	877	7	0
11	o	813	0	828	4	0
12	p	666	0	697	7	0
13	q	621	0	658	5	0
14	r	664	0	743	6	0
15	s	645	0	677	24	0
16	t	935	0	1008	3	0
17	u	789	0	794	4	0
18	v	1430	0	1333	18	0
19	x	462	0	480	1	0
20	w	2786	0	2612	27	0
21	2	31537	0	15884	168	0
22	b	5545	0	6140	68	0
23	c	4939	0	5339	41	0
24	e	3988	0	3837	35	0
25	i	1189	0	1243	6	0
26	y	1155	0	1181	11	0
27	0	369	0	381	4	0
28	3	2571	0	1300	11	0
29	5	1006	0	508	1	0
30	6	473	0	498	3	0
31	7	455	0	500	0	0
32	8	520	0	543	0	0
33	9	292	0	332	3	0
34	B	2159	0	2239	7	0
35	C	1681	0	1736	4	0
36	D	1599	0	1659	9	0
37	E	1413	0	1479	17	0
38	F	1338	0	1434	7	0
39	G	418	0	456	2	0
40	H	1114	0	1149	11	0
41	I	980	0	1056	34	0
42	J	1346	0	1389	4	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	K	942	0	998	5	0
44	L	1484	0	1530	6	0
45	M	1080	0	1143	5	0
46	N	937	0	978	4	0
47	O	902	0	920	6	0
48	P	995	0	1057	5	0
49	Q	943	0	992	7	0
50	R	907	0	951	11	0
51	S	903	0	948	7	0
52	T	837	0	823	6	0
53	U	1020	0	1097	8	0
54	V	869	0	882	4	0
55	W	1104	0	1151	6	0
56	X	843	0	884	6	0
57	Z	323	0	367	2	0
58	Y	521	0	498	45	0
59	1	50934	0	25627	210	0
60	4	5856	0	2947	25	0
61	1	86	0	0	0	0
61	2	47	0	0	0	0
61	4	4	0	0	0	0
61	U	1	0	0	0	0
62	1	205	0	0	0	0
62	2	98	0	0	0	0
62	3	5	0	0	0	0
62	4	7	0	0	0	0
62	5	4	0	0	0	0
62	D	1	0	0	0	0
62	L	1	0	0	0	0
62	N	1	0	0	0	0
All	All	159560	0	116249	862	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 3.

The worst 5 of 862 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)
59:1:1577:5MU:C5	59:1:1577:5MU:C4	1.82	1.62
59:1:404:5MU:C5	59:1:404:5MU:C4	1.82	1.61
59:1:720:U:C6	59:1:720:U:C5	2.11	1.37

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:1:720:U:C5	59:1:720:U:C4	2.25	1.24
41:I:162:MET:HA	59:1:720:U:C2	1.77	1.19

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	a	234/436 (54%)	225 (96%)	8 (3%)	1 (0%)	30	51
2	d	254/257 (99%)	248 (98%)	6 (2%)	0	100	100
3	f	101/171 (59%)	99 (98%)	2 (2%)	0	100	100
4	g	165/168 (98%)	160 (97%)	5 (3%)	0	100	100
5	h	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
6	j	120/169 (71%)	114 (95%)	3 (2%)	3 (2%)	4	8
7	k	115/130 (88%)	113 (98%)	2 (2%)	0	100	100
8	l	119/133 (90%)	113 (95%)	6 (5%)	0	100	100
9	m	112/164 (68%)	110 (98%)	2 (2%)	0	100	100
10	n	97/100 (97%)	97 (100%)	0	0	100	100
11	o	99/141 (70%)	96 (97%)	3 (3%)	0	100	100
12	p	78/128 (61%)	78 (100%)	0	0	100	100
13	q	76/105 (72%)	74 (97%)	2 (3%)	0	100	100
14	r	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
15	s	79/92 (86%)	79 (100%)	0	0	100	100
16	t	117/166 (70%)	116 (99%)	1 (1%)	0	100	100
17	u	90/184 (49%)	87 (97%)	3 (3%)	0	100	100
18	v	179/298 (60%)	162 (90%)	14 (8%)	3 (2%)	7	15

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	x	58/120 (48%)	57 (98%)	1 (2%)	0	100	100
20	w	361/560 (64%)	351 (97%)	10 (3%)	0	100	100
22	b	679/910 (75%)	658 (97%)	20 (3%)	1 (0%)	48	70
23	c	597/712 (84%)	584 (98%)	13 (2%)	0	100	100
24	e	528/673 (78%)	505 (96%)	22 (4%)	1 (0%)	43	66
25	i	147/191 (77%)	132 (90%)	14 (10%)	1 (1%)	18	38
26	y	144/286 (50%)	142 (99%)	2 (1%)	0	100	100
27	0	45/66 (68%)	45 (100%)	0	0	100	100
30	6	56/101 (55%)	56 (100%)	0	0	100	100
31	7	58/124 (47%)	57 (98%)	1 (2%)	0	100	100
32	8	66/114 (58%)	64 (97%)	2 (3%)	0	100	100
33	9	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
34	B	274/278 (99%)	270 (98%)	4 (2%)	0	100	100
35	C	221/259 (85%)	217 (98%)	4 (2%)	0	100	100
36	D	214/243 (88%)	213 (100%)	1 (0%)	0	100	100
37	E	176/179 (98%)	169 (96%)	7 (4%)	0	100	100
38	F	175/207 (84%)	170 (97%)	5 (3%)	0	100	100
39	G	52/200 (26%)	52 (100%)	0	0	100	100
40	H	139/235 (59%)	135 (97%)	4 (3%)	0	100	100
41	I	130/176 (74%)	125 (96%)	5 (4%)	0	100	100
42	J	171/225 (76%)	165 (96%)	6 (4%)	0	100	100
43	K	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
44	L	196/241 (81%)	190 (97%)	6 (3%)	0	100	100
45	M	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
46	N	115/173 (66%)	112 (97%)	3 (3%)	0	100	100
47	O	116/145 (80%)	114 (98%)	2 (2%)	0	100	100
48	P	128/153 (84%)	123 (96%)	5 (4%)	0	100	100
49	Q	109/112 (97%)	109 (100%)	0	0	100	100
50	R	113/179 (63%)	112 (99%)	1 (1%)	0	100	100
51	S	113/175 (65%)	111 (98%)	2 (2%)	0	100	100
52	T	90/111 (81%)	88 (98%)	2 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	U	130/170 (76%)	129 (99%)	1 (1%)	0	100	100
54	V	112/161 (70%)	109 (97%)	3 (3%)	0	100	100
55	W	136/195 (70%)	134 (98%)	2 (2%)	0	100	100
56	X	104/134 (78%)	104 (100%)	0	0	100	100
57	Z	39/98 (40%)	37 (95%)	2 (5%)	0	100	100
58	Y	61/136 (45%)	51 (84%)	10 (16%)	0	100	100
All	All	8394/11457 (73%)	8152 (97%)	232 (3%)	10 (0%)	49	70

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	j	123	VAL
1	a	71	VAL
6	j	50	VAL
6	j	51	ASP
18	v	142	PHE

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	a	206/368 (56%)	202 (98%)	4 (2%)	50	75
2	d	233/234 (100%)	226 (97%)	7 (3%)	36	64
3	f	89/140 (64%)	88 (99%)	1 (1%)	65	84
4	g	146/147 (99%)	144 (99%)	2 (1%)	59	81
5	h	125/125 (100%)	122 (98%)	3 (2%)	43	70
6	j	107/143 (75%)	104 (97%)	3 (3%)	38	66
7	k	93/105 (89%)	91 (98%)	2 (2%)	45	72
8	l	103/111 (93%)	100 (97%)	3 (3%)	37	65
9	m	101/138 (73%)	101 (100%)	0	100	100
10	n	88/89 (99%)	87 (99%)	1 (1%)	65	84

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	o	86/115 (75%)	84 (98%)	2 (2%)	44	71
12	p	69/108 (64%)	69 (100%)	0	100	100
13	q	69/90 (77%)	69 (100%)	0	100	100
14	r	73/128 (57%)	72 (99%)	1 (1%)	59	81
15	s	71/80 (89%)	68 (96%)	3 (4%)	26	52
16	t	99/133 (74%)	98 (99%)	1 (1%)	68	86
17	u	85/149 (57%)	84 (99%)	1 (1%)	63	83
18	v	143/246 (58%)	142 (99%)	1 (1%)	76	89
19	x	50/95 (53%)	48 (96%)	2 (4%)	28	55
20	w	287/434 (66%)	279 (97%)	8 (3%)	38	66
22	b	620/807 (77%)	606 (98%)	14 (2%)	44	71
23	c	541/634 (85%)	533 (98%)	8 (2%)	57	80
24	e	411/527 (78%)	402 (98%)	9 (2%)	45	72
25	i	126/159 (79%)	120 (95%)	6 (5%)	23	47
26	y	124/238 (52%)	122 (98%)	2 (2%)	55	79
27	0	39/54 (72%)	38 (97%)	1 (3%)	40	68
30	6	53/90 (59%)	48 (91%)	5 (9%)	8	18
31	7	45/90 (50%)	43 (96%)	2 (4%)	25	50
32	8	55/92 (60%)	54 (98%)	1 (2%)	51	76
33	9	33/33 (100%)	33 (100%)	0	100	100
34	B	228/230 (99%)	223 (98%)	5 (2%)	45	72
35	C	176/204 (86%)	173 (98%)	3 (2%)	53	78
36	D	167/187 (89%)	165 (99%)	2 (1%)	63	83
37	E	156/157 (99%)	150 (96%)	6 (4%)	29	56
38	F	145/168 (86%)	142 (98%)	3 (2%)	47	73
39	G	46/167 (28%)	44 (96%)	2 (4%)	26	51
40	H	122/197 (62%)	116 (95%)	6 (5%)	22	47
41	I	106/138 (77%)	103 (97%)	3 (3%)	38	66
42	J	140/180 (78%)	136 (97%)	4 (3%)	37	65
43	K	101/101 (100%)	98 (97%)	3 (3%)	36	64
44	L	149/180 (83%)	147 (99%)	2 (1%)	61	82

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	M	110/111 (99%)	108 (98%)	2 (2%)	51	76
46	N	97/140 (69%)	95 (98%)	2 (2%)	47	73
47	O	93/116 (80%)	93 (100%)	0	100	100
48	P	104/122 (85%)	101 (97%)	3 (3%)	37	65
49	Q	100/101 (99%)	98 (98%)	2 (2%)	48	74
50	R	97/145 (67%)	95 (98%)	2 (2%)	47	73
51	S	94/136 (69%)	90 (96%)	4 (4%)	26	51
52	T	85/89 (96%)	83 (98%)	2 (2%)	43	70
53	U	109/137 (80%)	107 (98%)	2 (2%)	51	76
54	V	90/127 (71%)	89 (99%)	1 (1%)	65	84
55	W	116/164 (71%)	113 (97%)	3 (3%)	40	68
56	X	89/109 (82%)	88 (99%)	1 (1%)	65	84
57	Z	33/81 (41%)	32 (97%)	1 (3%)	36	64
58	Y	55/106 (52%)	54 (98%)	1 (2%)	51	76
All	All	7178/9495 (76%)	7020 (98%)	158 (2%)	45	72

5 of 158 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	H	85	TYR
51	S	133	VAL
40	H	175	ARG
44	L	128	THR
53	U	126	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
53	U	77	GLN
54	V	127	GLN
23	c	462	ASN
23	c	215	GLN
55	W	45	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
21	2	1468/1470 (99%)	202 (13%)	3 (0%)
28	3	120/121 (99%)	20 (16%)	1 (0%)
29	5	46/47 (97%)	3 (6%)	0
59	1	2362/2375 (99%)	331 (14%)	5 (0%)
60	4	270/272 (99%)	35 (12%)	1 (0%)
All	All	4266/4285 (99%)	591 (13%)	10 (0%)

5 of 591 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
21	2	6	U
21	2	10	G
21	2	20	C
21	2	23	G
21	2	32	G

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
59	1	1961	G
59	1	2396	U
60	4	277	G
28	3	15	U
59	1	484	U

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

19 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
21	MA6	2	1458	21	23,26,27	1.67	5 (21%)	34,38,41	3.46	12 (35%)
59	OMC	1	2138	62,59	19,22,23	2.85	8 (42%)	26,31,34	0.83	0
59	2MG	1	1471	59	23,26,27	2.86	7 (30%)	32,38,41	2.88	13 (40%)
21	2MG	2	1455	21	23,26,27	2.85	7 (30%)	32,38,41	2.93	11 (34%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
21	5MC	2	913	21	18,22,23	3.62	7 (38%)	26,32,35	0.99	2 (7%)
59	5MU	1	1577	61,59	19,22,23	7.65	9 (47%)	28,32,35	3.42	10 (35%)
59	6MZ	1	1669	59	22,25,26	4.32	13 (59%)	30,36,39	3.02	13 (43%)
21	UR3	2	1437	21	19,22,23	2.78	8 (42%)	26,32,35	1.33	2 (7%)
59	H2U	1	2089	59	18,21,22	0.52	0	21,30,33	0.92	1 (4%)
21	G7M	2	480	61,21	23,26,27	2.27	7 (30%)	35,39,42	2.99	10 (28%)
21	2MG	2	912	21	23,26,27	3.11	7 (30%)	32,38,41	3.18	13 (40%)
59	OMG	1	1891	61,59	23,26,27	2.39	7 (30%)	33,38,41	2.26	10 (30%)
21	MA6	2	1457	21	23,26,27	1.62	5 (21%)	34,38,41	3.38	11 (32%)
59	2MA	1	2143	61,59,62	22,25,26	4.07	7 (31%)	33,37,40	2.41	9 (27%)
59	5MC	1	1600	61,59	18,22,23	3.48	7 (38%)	26,32,35	0.99	2 (7%)
59	OMU	1	2192	61,59	19,22,23	3.02	8 (42%)	26,31,34	1.74	5 (19%)
59	2MG	1	2085	59	23,26,27	2.72	7 (30%)	32,38,41	2.52	14 (43%)
59	5MU	1	404	59	19,22,23	7.68	8 (42%)	28,32,35	3.24	12 (42%)
21	4OC	2	1341	21	20,23,24	3.41	8 (40%)	26,32,35	0.87	1 (3%)

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
21	MA6	2	1458	21	-	2/11/29/30	0/3/3/3
59	OMC	1	2138	62,59	-	0/9/27/28	0/2/2/2
59	2MG	1	1471	59	-	0/9/27/28	0/3/3/3
21	2MG	2	1455	21	-	0/9/27/28	0/3/3/3
21	5MC	2	913	21	-	0/7/25/26	0/2/2/2
59	5MU	1	1577	61,59	-	0/7/25/26	0/2/2/2
59	6MZ	1	1669	59	-	2/9/27/28	0/3/3/3
21	UR3	2	1437	21	-	0/7/25/26	0/2/2/2
59	H2U	1	2089	59	-	0/7/38/39	0/2/2/2
21	G7M	2	480	61,21	-	3/7/25/26	0/3/3/3
21	2MG	2	912	21	-	0/9/27/28	0/3/3/3
59	OMG	1	1891	61,59	-	3/9/27/28	0/3/3/3
21	MA6	2	1457	21	-	0/11/29/30	0/3/3/3
59	2MA	1	2143	61,59,62	-	2/7/25/26	0/3/3/3
59	5MC	1	1600	61,59	-	0/7/25/26	0/2/2/2
59	OMU	1	2192	61,59	-	0/9/27/28	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	2MG	1	2085	59	-	1/9/27/28	0/3/3/3
59	5MU	1	404	59	-	1/7/25/26	0/2/2/2
21	4OC	2	1341	21	-	1/9/29/30	0/2/2/2

The worst 5 of 135 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	1	1577	5MU	C4-C5	22.49	1.82	1.44
59	1	404	5MU	C4-C5	22.39	1.82	1.44
59	1	1577	5MU	C6-N1	15.73	1.64	1.38
59	1	404	5MU	C6-N1	15.62	1.64	1.38
59	1	1669	6MZ	C6-N6	13.74	1.49	1.34

The worst 5 of 151 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	2	1457	MA6	N1-C6-N6	-13.09	102.77	117.08
21	2	1458	MA6	N1-C6-N6	-13.02	102.85	117.08
59	1	1577	5MU	C5-C4-N3	10.78	124.51	115.31
59	1	404	5MU	C5-C4-N3	9.62	123.53	115.31
21	2	480	G7M	CN7-N7-C5	9.36	138.40	126.77

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	1	1669	6MZ	C3'-C4'-C5'-O5'
59	1	1891	OMG	C1'-C2'-O2'-CM2
59	1	1669	6MZ	O4'-C4'-C5'-O5'
21	2	480	G7M	C3'-C4'-C5'-O5'
59	1	1891	OMG	O4'-C4'-C5'-O5'

There are no ring outliers.

8 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
21	2	1458	MA6	1	0
21	2	1455	2MG	2	0
59	1	1577	5MU	1	0
59	1	1669	6MZ	1	0
21	2	912	2MG	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	1	1891	OMG	1	0
59	1	404	5MU	2	0
21	2	1341	4OC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 460 ligands modelled in this entry, 460 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
59	1	12
21	2	2
24	e	1
60	4	1

The worst 5 of 16 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	e	187:GLY	C	227:ALA	N	25.55
1	1	1190:A	O3'	1196:U	P	16.56

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	4	259:U	O3'	266:A	P	16.51
1	1	1506:C	O3'	1509:G	P	16.30
1	1	1738:G	O3'	1830:G	P	15.17

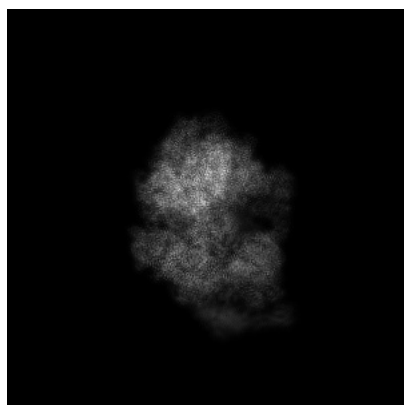
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-56602. These allow visual inspection of the internal detail of the map and identification of artifacts.

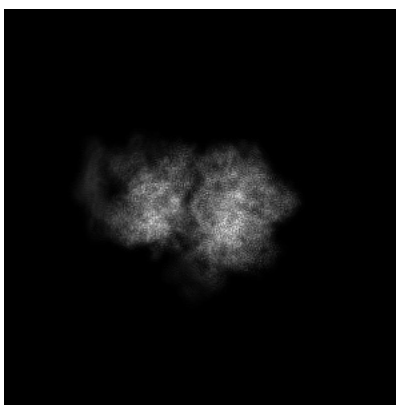
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

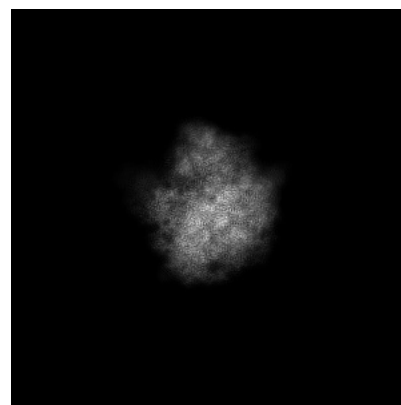
6.1.1 Primary map



X



Y



Z

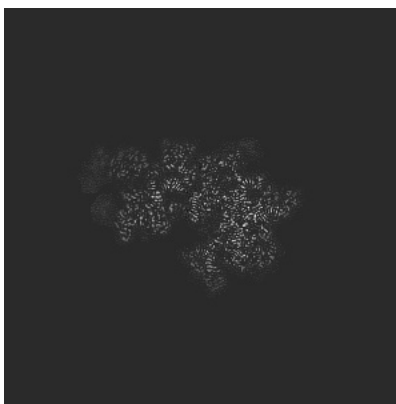
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 256



Y Index: 256

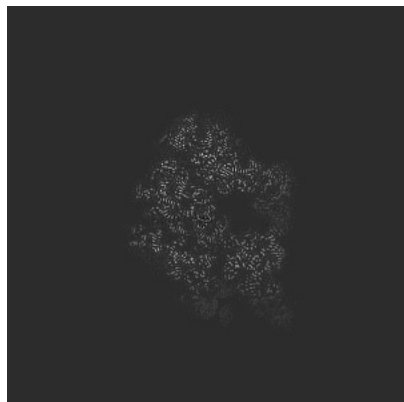


Z Index: 256

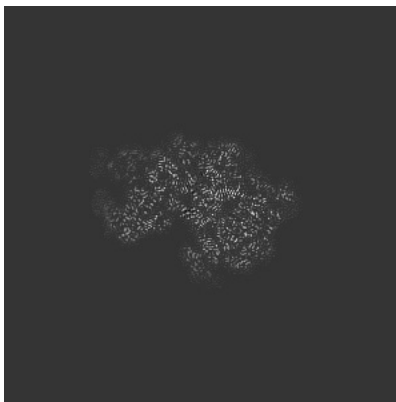
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

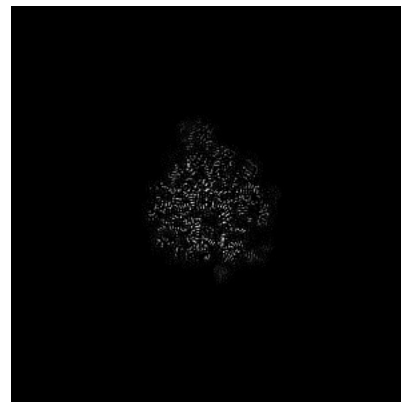
6.3.1 Primary map



X Index: 251



Y Index: 244

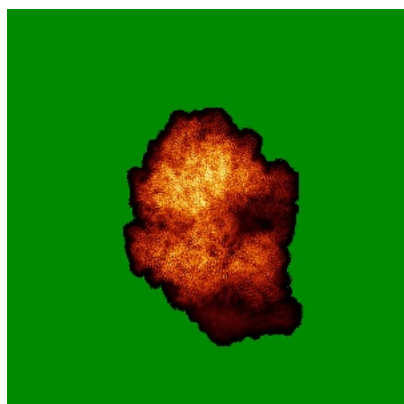


Z Index: 299

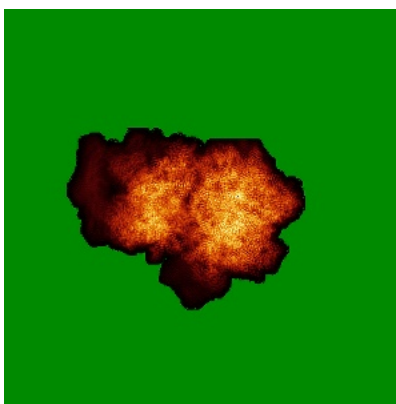
The images above show the largest variance slices of the map in three orthogonal directions.

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

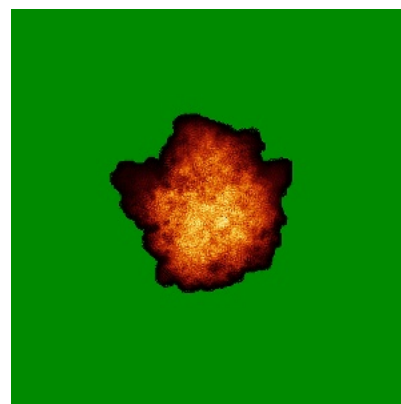
6.4.1 Primary map



X



Y

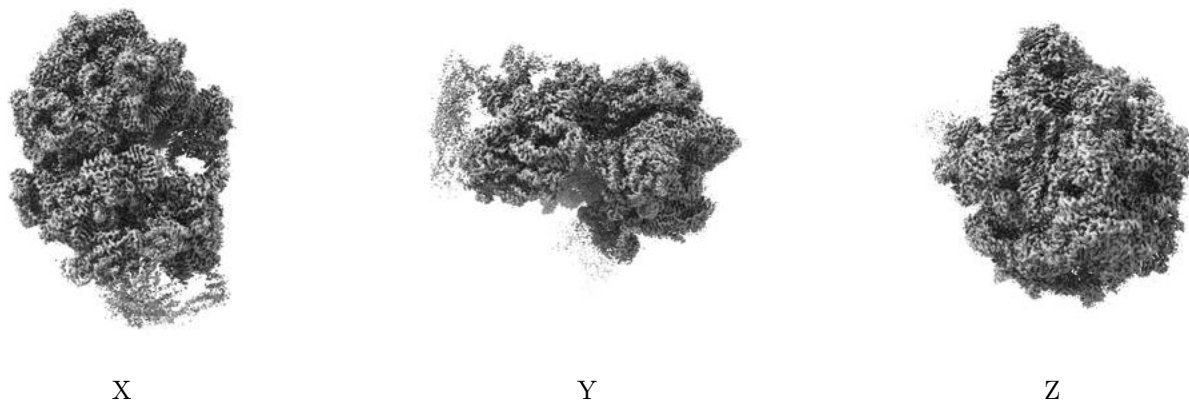


Z

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 0.107. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

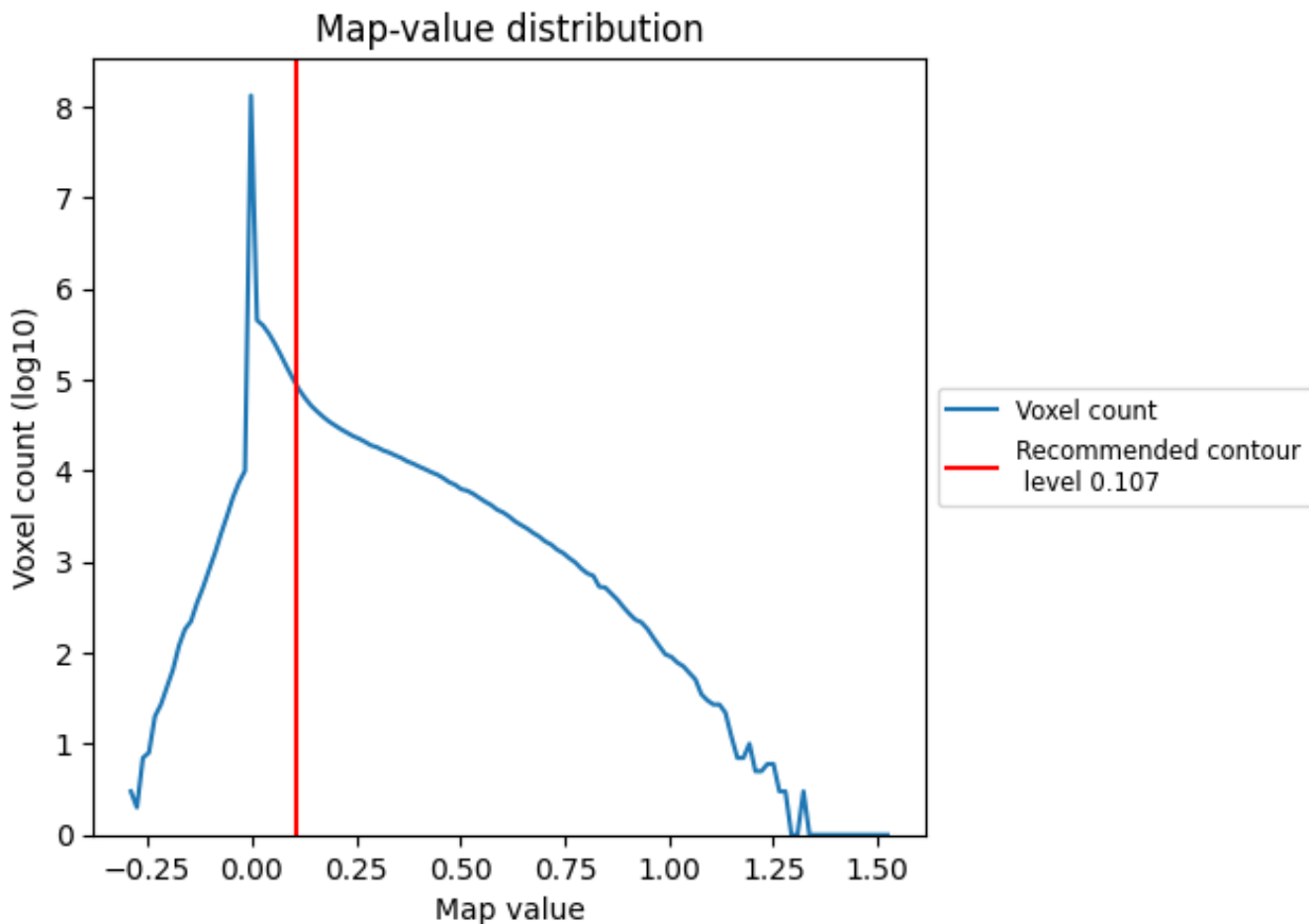
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

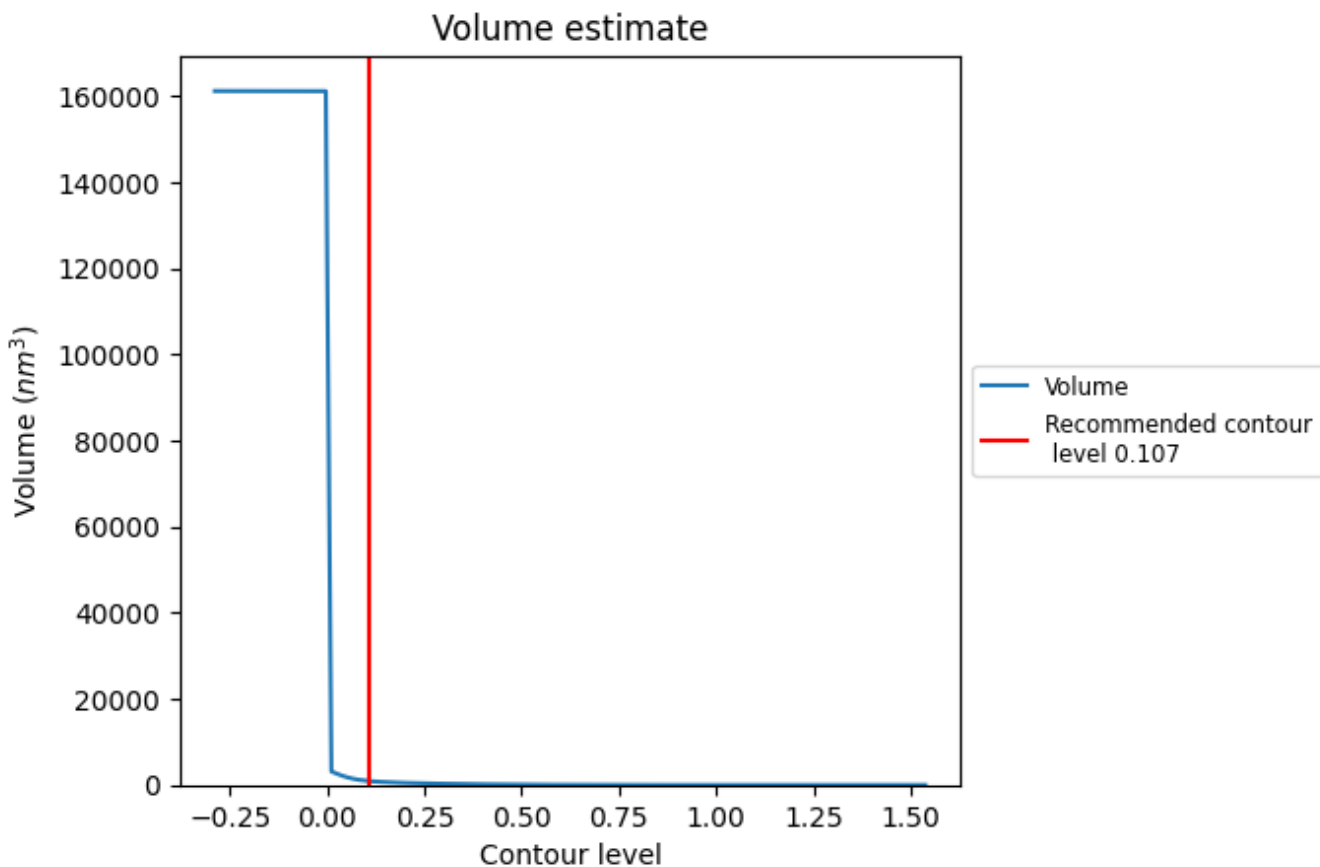
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

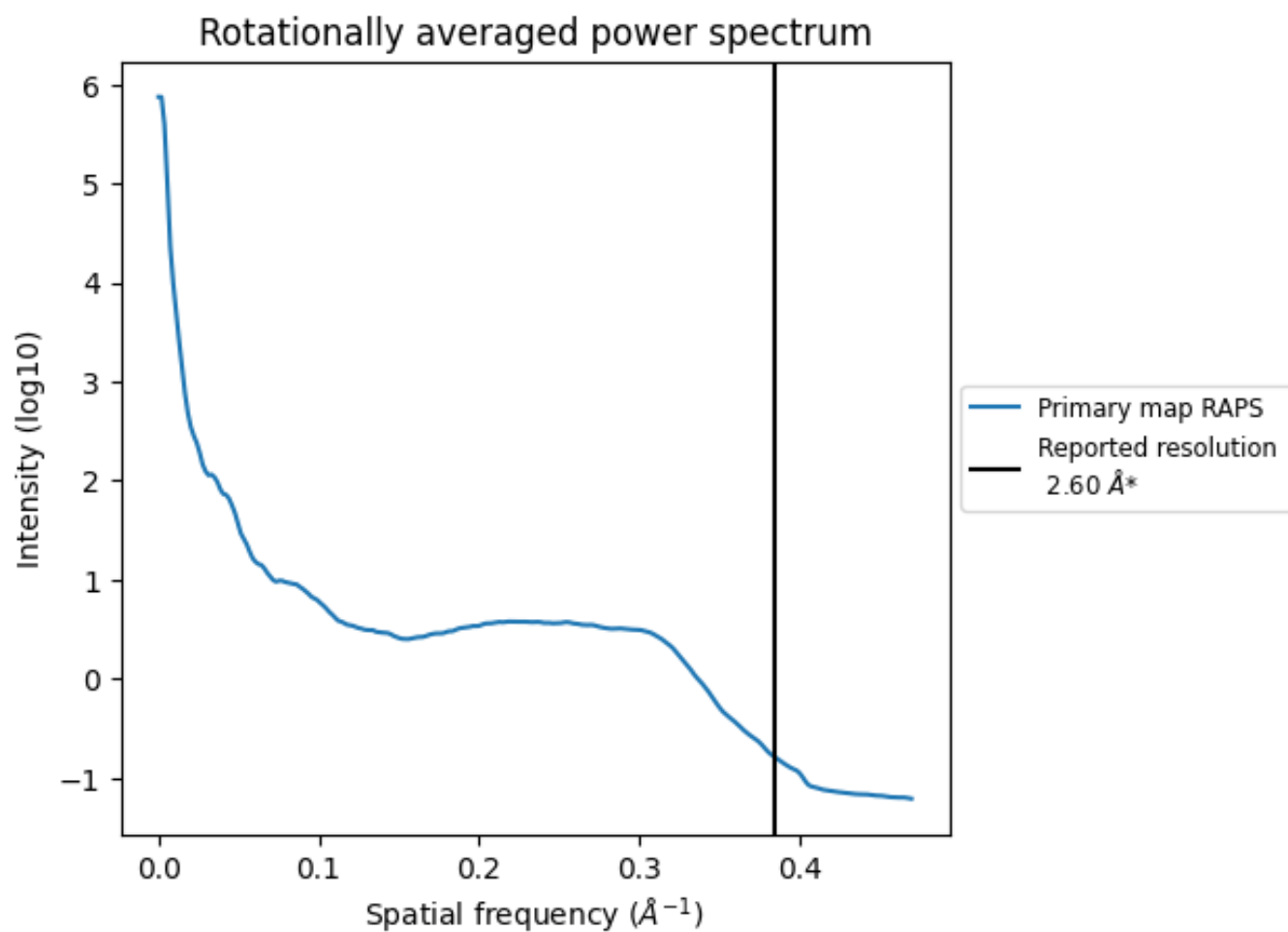
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 915 nm³; this corresponds to an approximate mass of 826 kDa.

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

7.3 Rotationally averaged power spectrum i



*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

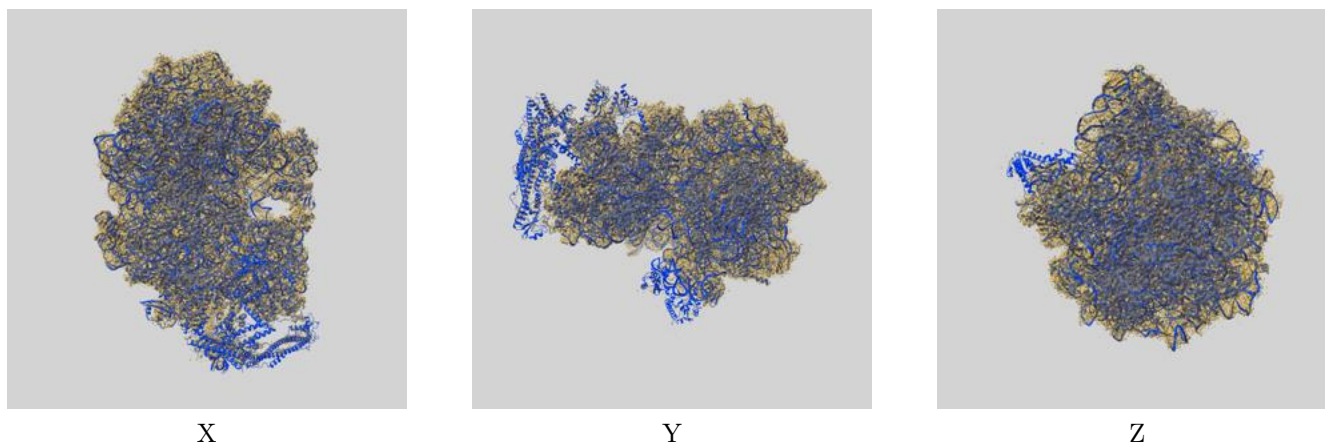
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

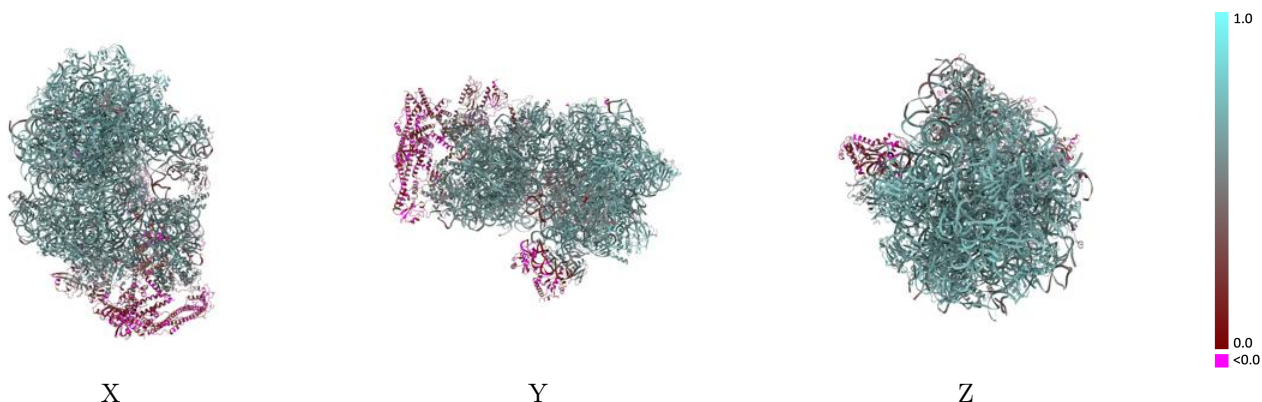
This section contains information regarding the fit between EMDB map EMD-56602 and PDB model 28LU. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



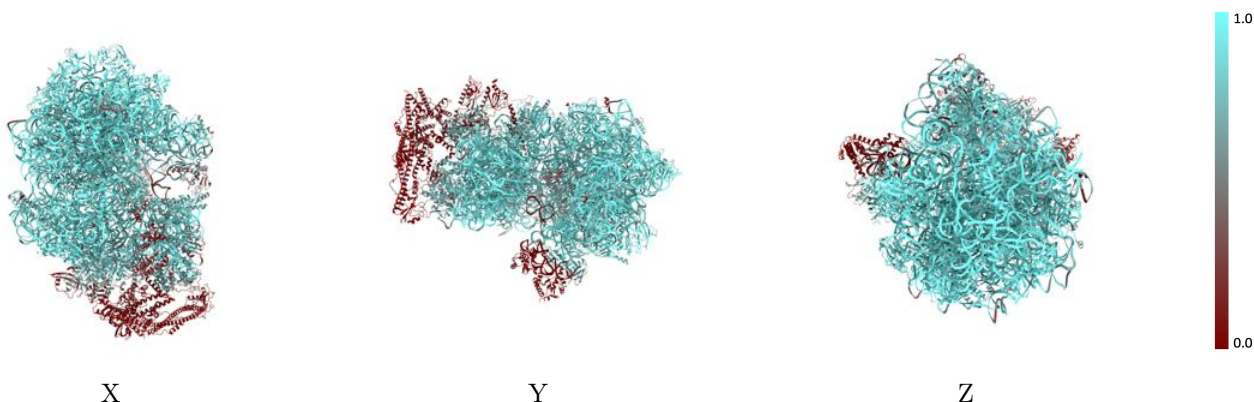
The images above show the 3D surface view of the map at the recommended contour level 0.107 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



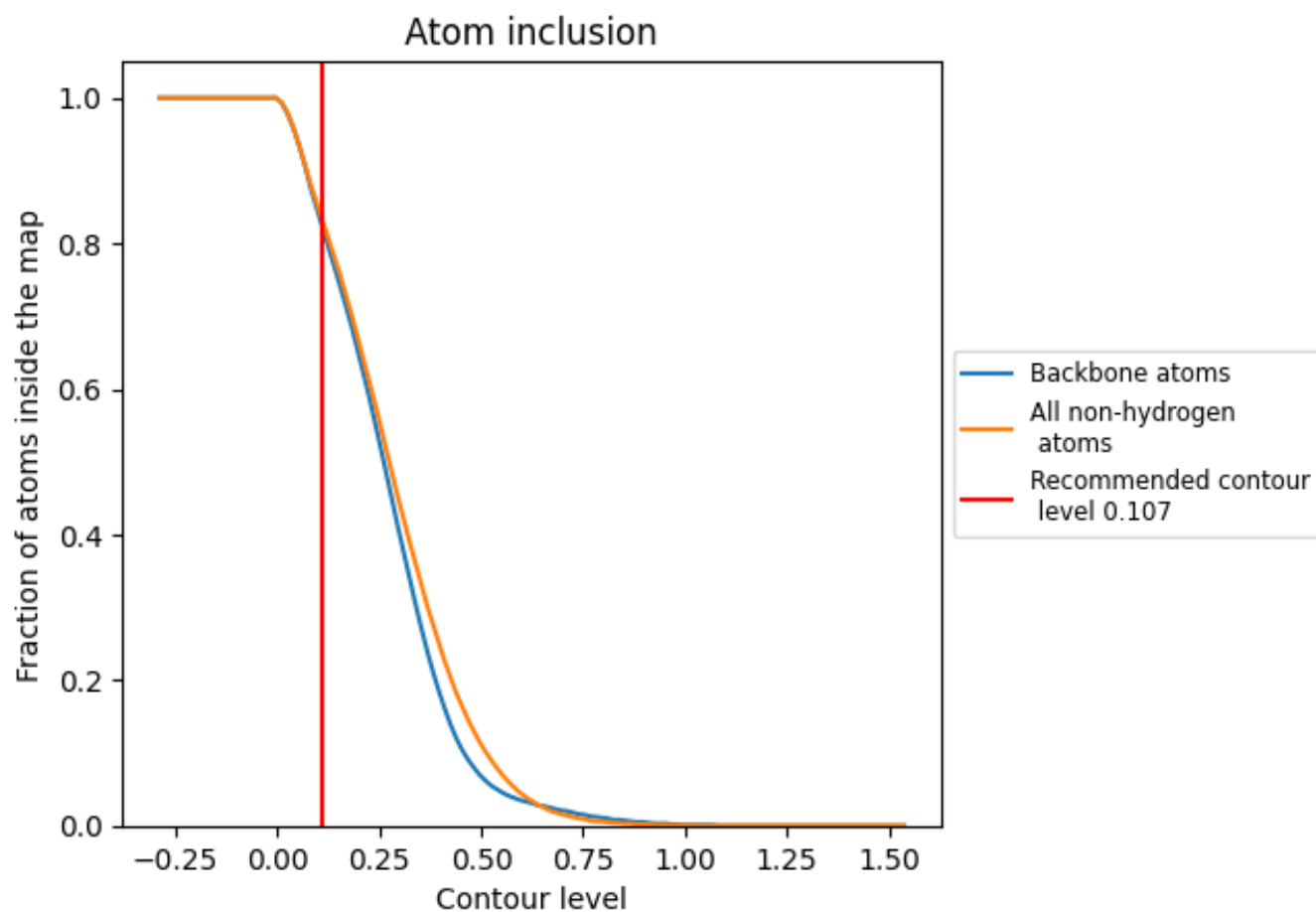
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.107).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 84% 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 (0.107) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8360	 0.5830
0	 0.9050	 0.6620
1	 0.9410	 0.6390
2	 0.9670	 0.6200
3	 0.8380	 0.5420
4	 0.9630	 0.6490
5	 0.9830	 0.6630
6	 0.9210	 0.6630
7	 0.9660	 0.6860
8	 0.9690	 0.6800
9	 0.9610	 0.6730
B	 0.9610	 0.6880
C	 0.9520	 0.6800
D	 0.9430	 0.6770
E	 0.4940	 0.4600
F	 0.7450	 0.5770
G	 0.7320	 0.5630
H	 0.0100	 0.1190
I	 0.0060	 0.0740
J	 0.9350	 0.6700
K	 0.9430	 0.6770
L	 0.8970	 0.6530
M	 0.9370	 0.6750
N	 0.9650	 0.6800
O	 0.7800	 0.5850
P	 0.8820	 0.6400
Q	 0.9860	 0.6900
R	 0.9380	 0.6740
S	 0.9260	 0.6710
T	 0.9540	 0.6670
U	 0.8860	 0.6510
V	 0.8510	 0.6120
W	 0.9110	 0.6570
X	 0.8910	 0.6490
Y	 0.3120	 0.3680



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Z	 0.9370	 0.6630
a	 0.3650	 0.3400
b	 0.3670	 0.3470
c	 0.5000	 0.3990
d	 0.6720	 0.4920
e	 0.4100	 0.3370
f	 0.8350	 0.6060
g	 0.6950	 0.5370
h	 0.9100	 0.6370
i	 0.5910	 0.4800
j	 0.7850	 0.5760
k	 0.8600	 0.6120
l	 0.9330	 0.6460
m	 0.7700	 0.5620
n	 0.9330	 0.6330
o	 0.8630	 0.6030
p	 0.9350	 0.6380
q	 0.8740	 0.6210
r	 0.8940	 0.6230
s	 0.8650	 0.6080
t	 0.8260	 0.5770
u	 0.7740	 0.5800
v	 0.2530	 0.3050
w	 0.2890	 0.2770
x	 0.8960	 0.6180
y	 0.6690	 0.5580