



## wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 04:31 PM UTC

PDB ID : 7PHB / pdb\_00007phb  
EMDB ID : EMD-13412  
Title : 70S ribosome with A- and P-site tRNAs in chloramphenicol-treated Mycoplasma pneumoniae cells  
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.  
Deposited on : 2021-08-16  
Resolution : 4.90 Å (reported)  
Based on initial models : 3J9W, 7OOD, 7OOC, 4V7C

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

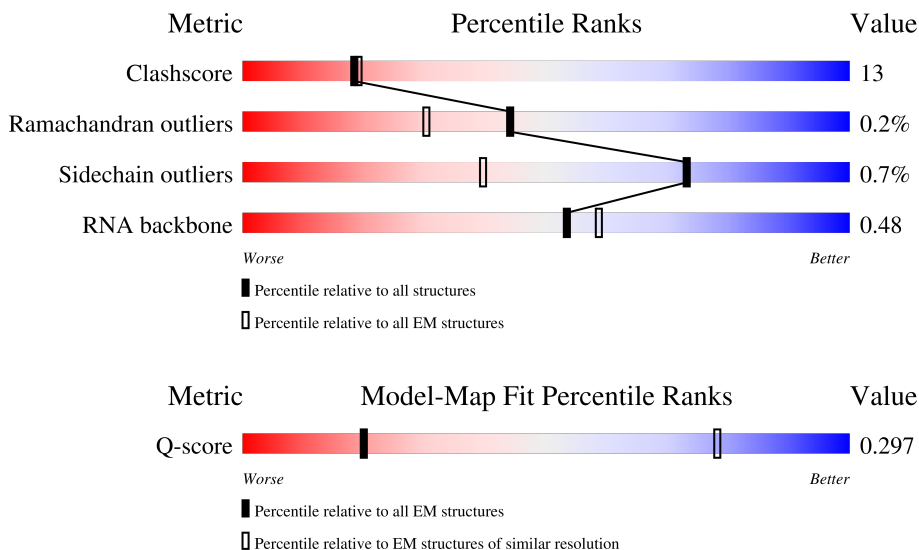
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (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 4.90 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	1274 ( 4.40 - 5.40 )

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  $\geq 3$ , 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	48	6% (red), 75% (green), 23% (yellow), 0% (orange), 0% (grey)
2	1	59	7% (red), 71% (green), 29% (yellow), 0% (orange), 0% (grey)
3	2	37	11% (red), 68% (green), 32% (yellow), 0% (orange), 0% (grey)

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Mol	Chain	Length	Quality of chain
4	A	294	40% 54% 28% 18%
5	B	273	35% 58% 21% 21%
6	C	205	43% 68% 31%
7	D	219	23% 54% 16% 30%
8	E	215	48% 60% 17% 22%
9	F	155	53% 76% 23%
10	G	142	44% 61% 39%
11	H	132	45% 64% 33%
12	I	108	51% 73% 20% 6%
13	J	121	37% 71% 23% 6%
14	K	139	27% 62% 33%
15	L	124	47% 63% 32% 5%
16	M	61	34% 61% 38%
17	N	86	37% 59% 37%
18	O	94	29% 56% 29% 15%
19	P	85	42% 73% 24%
20	Q	104	22% 44% 18% 38%
21	R	87	52% 63% 28%
22	S	87	24% 57% 31% 11%
23	T	60	42% 67% 22% 12%
24	Z	5	100%
25	a	287	16% 80% 19%
26	b	287	17% 55% 25% 20%
27	c	212	21% 77% 22%
28	d	180	58% 66% 31%


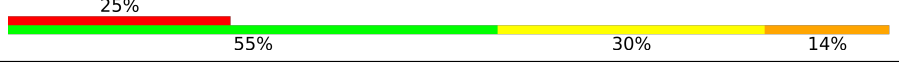

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Mol	Chain	Length	Quality of chain
29	e	184	43% 70% 26% .
30	f	149	85% 60% 36% ..
31	g	161	65% 37% 34% . . 22%
32	h	137	85% 64% 30% 7%
33	i	146	20% 72% 27% .
34	j	122	23% 75% 25%
35	k	151	20% 73% 25% .
36	l	139	14% 73% 25% .
37	m	124	9% 77% 17% ..
38	n	116	27% 64% 33% .
39	o	119	24% 66% 29% ..
40	p	127	13% 63% 27% 10%
41	q	100	25% 59% 40% .
42	r	159	17% 70% 18% 13%
43	s	237	8% 31% 8% 61%
44	t	111	43% 77% 23%
45	u	104	18% 58% 25% 17%
46	v	65	18% 72% 25% .
47	w	111	34% 68% 23% 10%
48	x	97	32% 29% 16% 55%
49	y	57	14% 65% 23% 11% .
50	z	53	21% 66% 28% 6%
51	3	2907	5% 39% 50% 10% .
52	4	108	. 44% 42% 11% .
53	5	1520	. 36% 53% 9% .

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Mol	Chain	Length	Quality of chain
54	6	76	
54	7	76	
55	Y	40	

## 2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 146364 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 L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	47	380	236	81	61	2	0	0

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	59	477	300	99	77	1	0	0

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	37	304	189	65	46	4	0	0

- Molecule 4 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A	240	1921	1226	334	352	9	0	0

- Molecule 5 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	215	1698	1073	313	307	5	0	0

- Molecule 6 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C	203	1660	1051	314	290	5	0	0

- Molecule 7 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	D	153	1173	742	226	202	3	0	0

- Molecule 8 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	E	167	1362	857	240	263	2	0	0

- Molecule 9 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	F	154	1246	785	239	216	6	0	0

- Molecule 10 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	G	141	1110	723	193	192	2	0	0

- Molecule 11 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	H	128	1028	655	191	181	1	0	0

- Molecule 12 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	I	101	809	523	142	143	1	0	0

- Molecule 13 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	J	114	829	514	153	156	6	0	0

- Molecule 14 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	K	136	1076	680	213	181	2	0	0

- Molecule 15 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	L	118	951	594	191	166		0	0

- Molecule 16 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	M	60	474	302	96	72	4	0	0

- Molecule 17 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	N	83	673	428	125	120		0	0

- Molecule 18 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	O	80	646	414	119	111	2	0	0

- Molecule 19 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	P	83	675	425	135	115		0	0

- Molecule 20 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	Q	65	535	342	103	86	4	0	0

- Molecule 21 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	84	Total	C	N	O	S	0	0
			682	435	127	118	2		

- Molecule 22 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	77	Total	C	N	O	S	0	0
			629	383	135	111			

- Molecule 23 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	53	Total	C	N	O	S	0	0
			471	295	103	72	1		

- Molecule 24 is a protein called nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Z	5	Total	C	N	O	0	0
			25	15	5	5		

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	d	175	1388	893	245	246	4	0	0

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	e	176	1396	899	247	250		0	0

- Molecule 30 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	f	145	1182	763	206	210	3	0	0

- Molecule 31 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	g	126	960	612	167	178	3	0	0

- Molecule 32 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	h	128	959	616	160	177	6	0	0

- Molecule 33 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	i	144	1164	737	213	209	5	0	0

- Molecule 34 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	j	122	944	595	178	167	4	0	0

- Molecule 35 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
35	k	148	1153	731	226	196	0	0

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	l	136	1079	694	196	182	7	0	0

- Molecule 37 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	m	119	958	609	175	171	3	0	0

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	n	112	889	557	175	155	2	0	0

- Molecule 39 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	o	115	938	592	180	165	1	0	0

- Molecule 40 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	p	114	947	603	188	154	2	0	0

- Molecule 41 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	q	99	811	525	148	134	4	0	0

- Molecule 42 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 43 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 44 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 45 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 46 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 47 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	w	100	Total	C	N	O	0	0
			818	517	153	148		

- Molecule 48 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

- Molecule 49 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 51 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 52 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

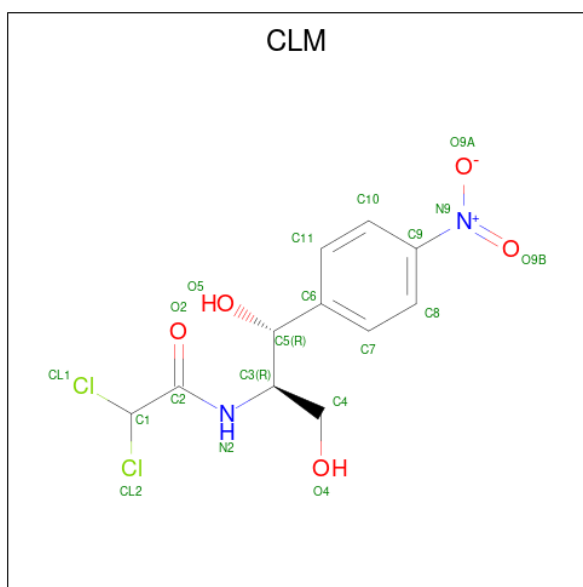
- Molecule 54 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	6	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
54	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

- Molecule 55 is a RNA chain called mRNA.

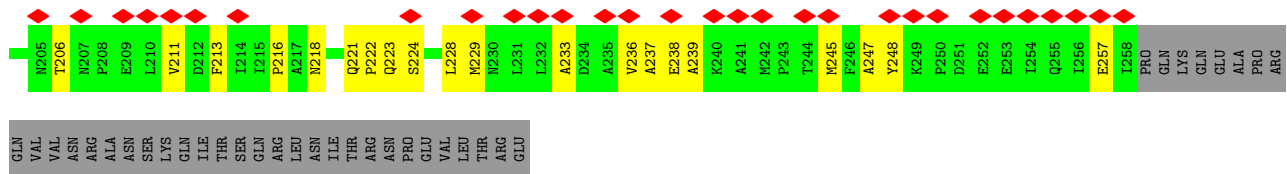
Mol	Chain	Residues	Atoms					AltConf	Trace
55	Y	9	Total	C	N	O	P	0	0
			177	81	18	70	8		

- Molecule 56 is CHLORAMPHENICOL (CCD ID: CLM) (formula: C<sub>11</sub>H<sub>12</sub>Cl<sub>2</sub>N<sub>2</sub>O<sub>5</sub>) (labeled as "Ligand of Interest" by depositor).

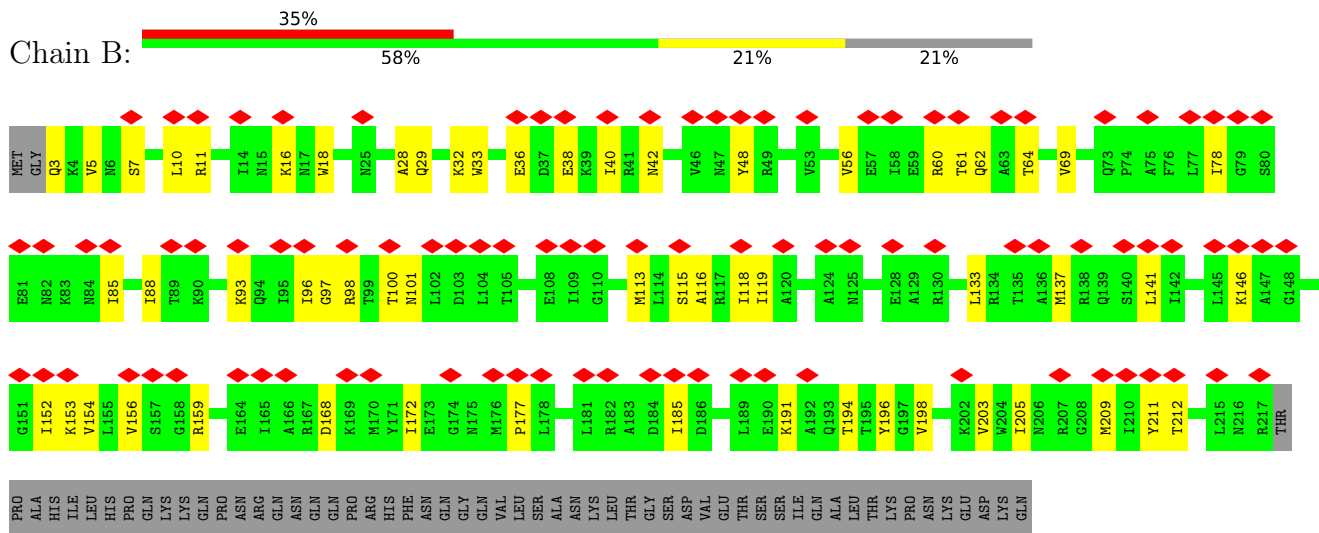


Mol	Chain	Residues	Atoms					AltConf
			Total	C	Cl	N	O	
56	3	1	20	11	2	2	5	0

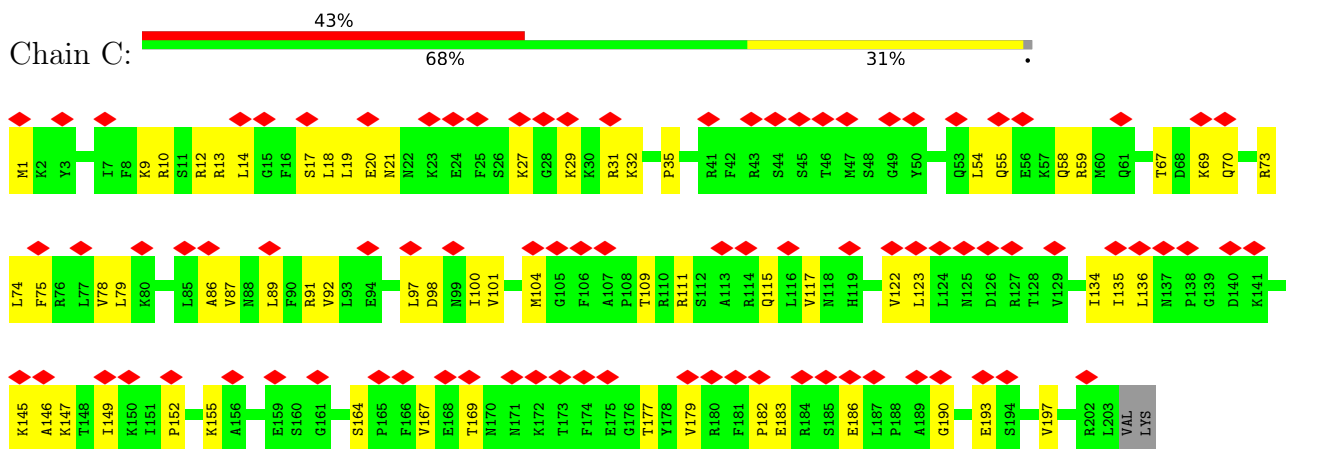




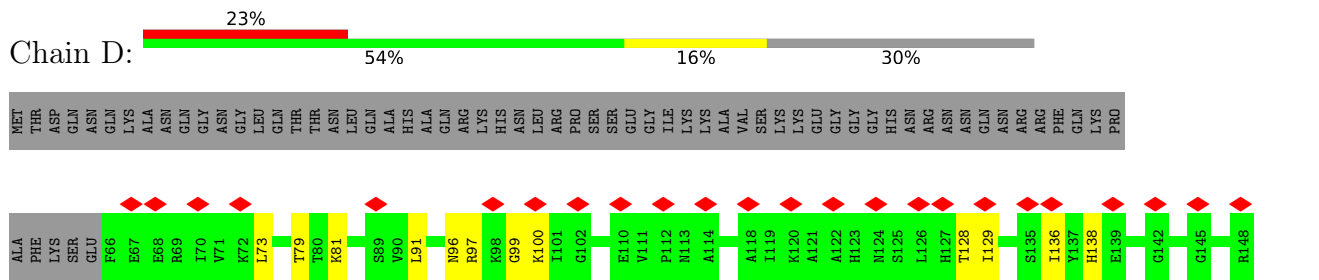
• Molecule 5: 30S ribosomal protein S3

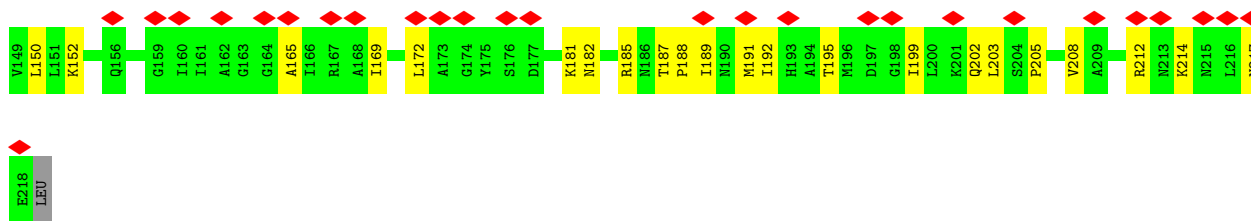


• Molecule 6: 30S ribosomal protein S4

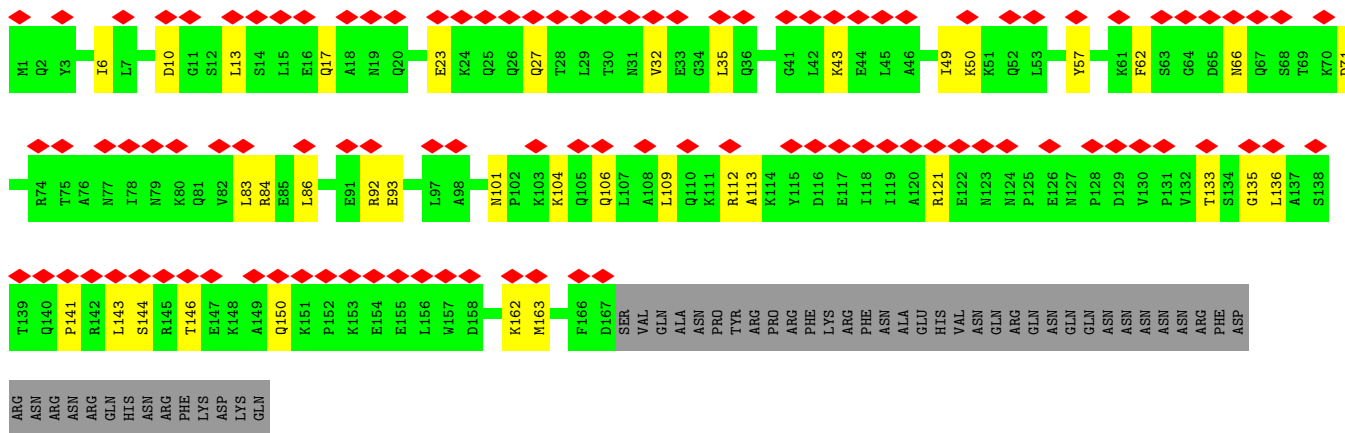


• Molecule 7: 30S ribosomal protein S5

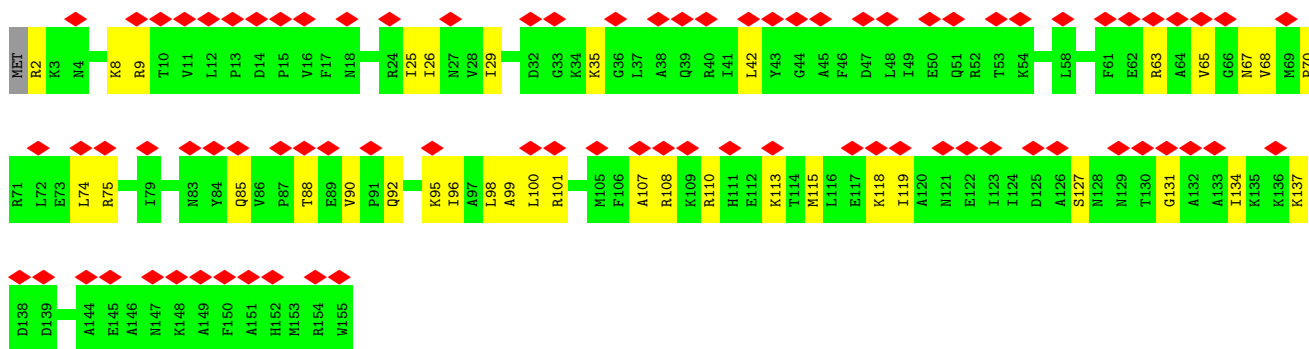
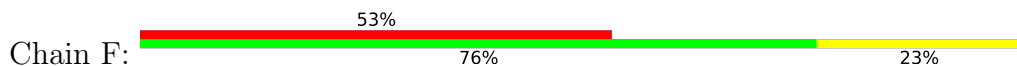




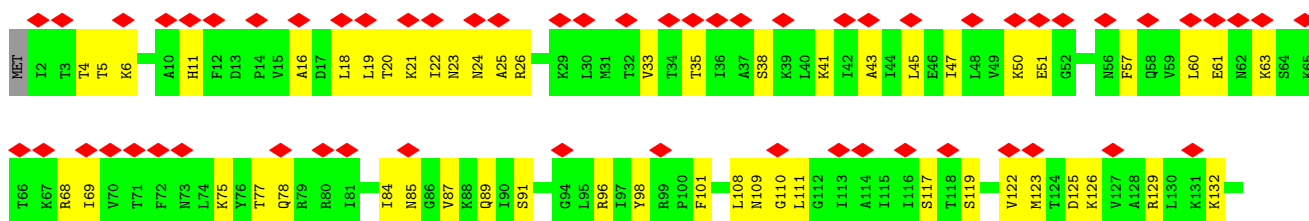
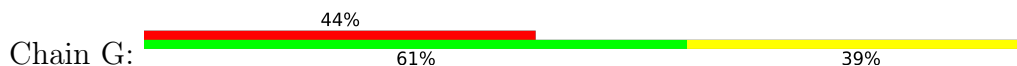
• Molecule 8: 30S ribosomal protein S6

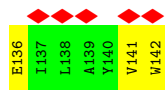


• Molecule 9: 30S ribosomal protein S7

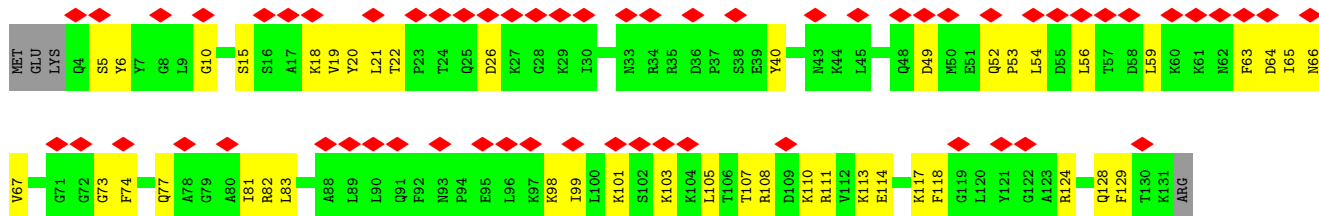
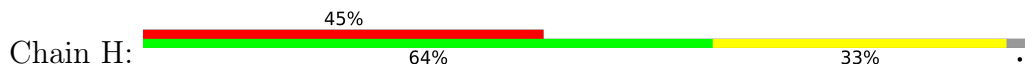


• Molecule 10: 30S ribosomal protein S8

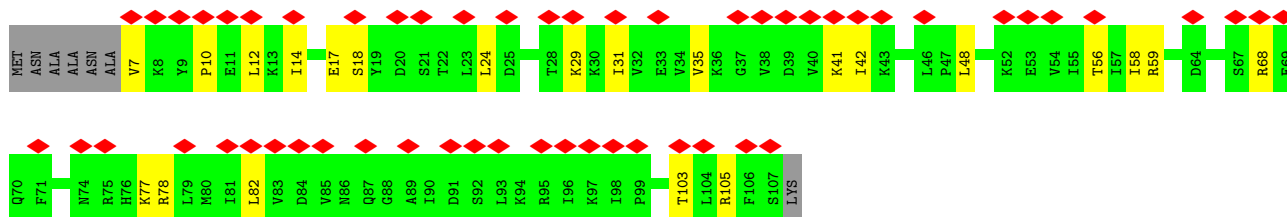
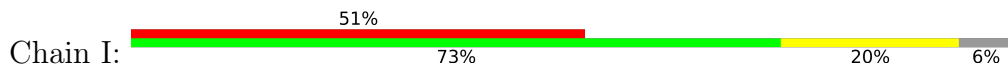




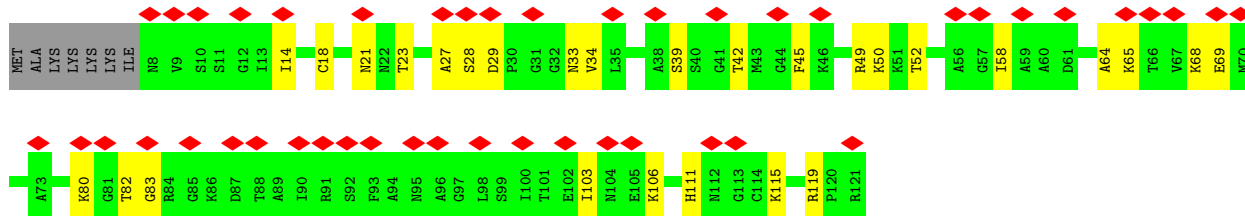
• Molecule 11: 30S ribosomal protein S9



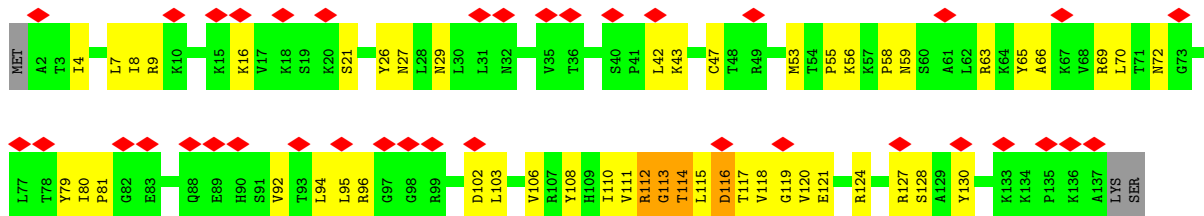
• Molecule 12: 30S ribosomal protein S10



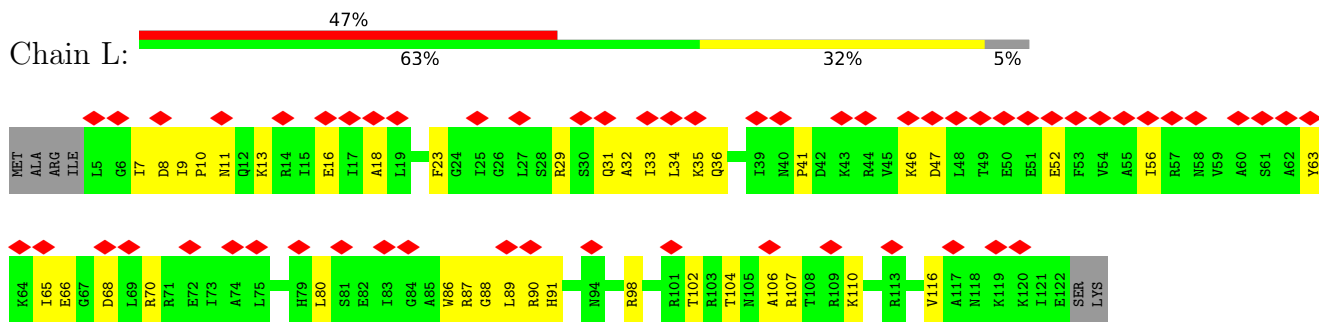
• Molecule 13: 30S ribosomal protein S11



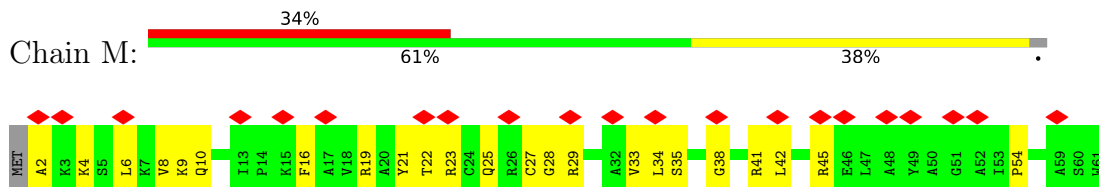
• Molecule 14: 30S ribosomal protein S12



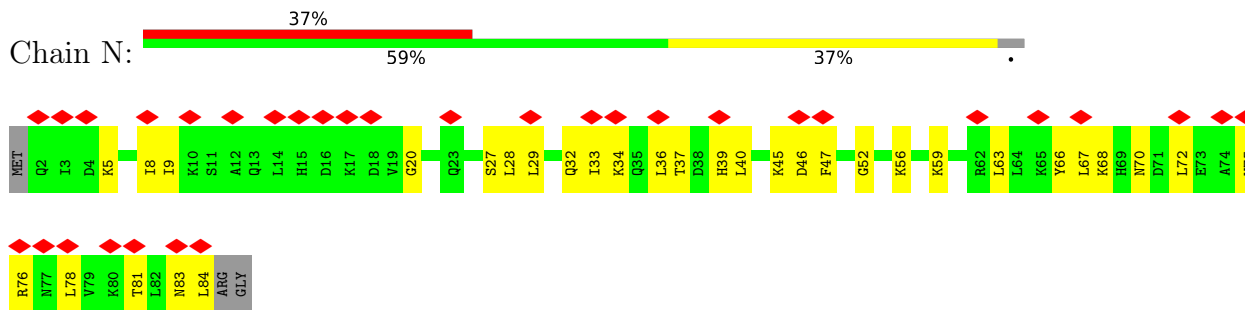
• Molecule 15: 30S ribosomal protein S13



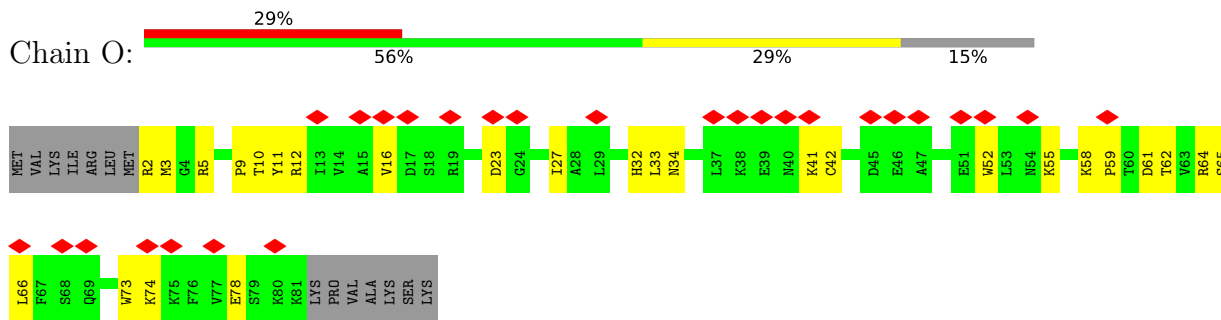
• Molecule 16: 30S ribosomal protein S14 type Z



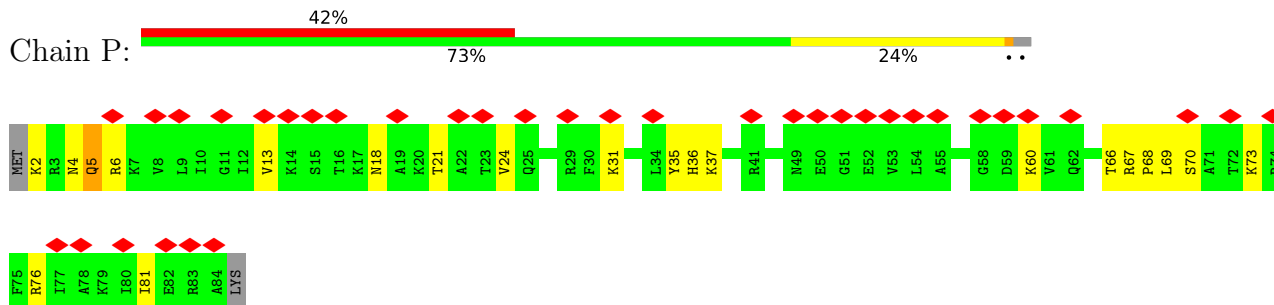
• Molecule 17: 30S ribosomal protein S15



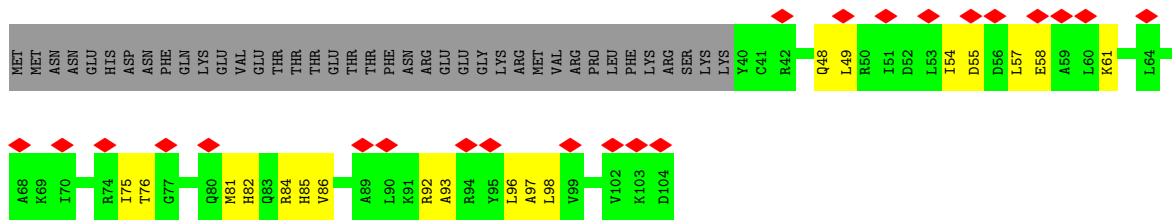
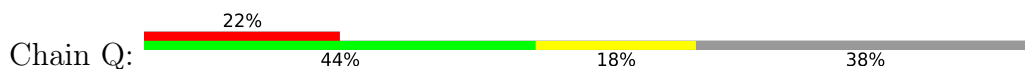
• Molecule 18: 30S ribosomal protein S16



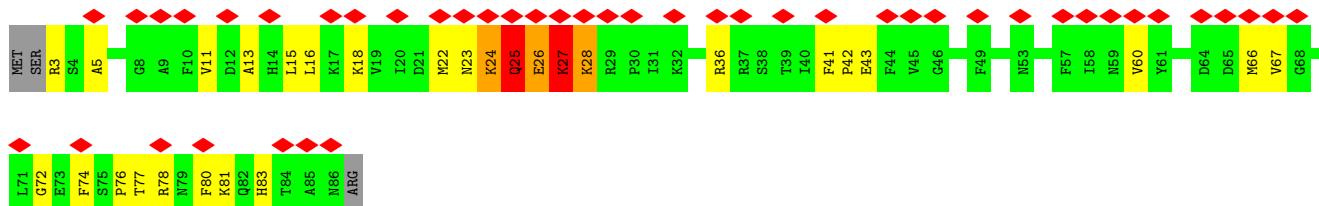
• Molecule 19: 30S ribosomal protein S17



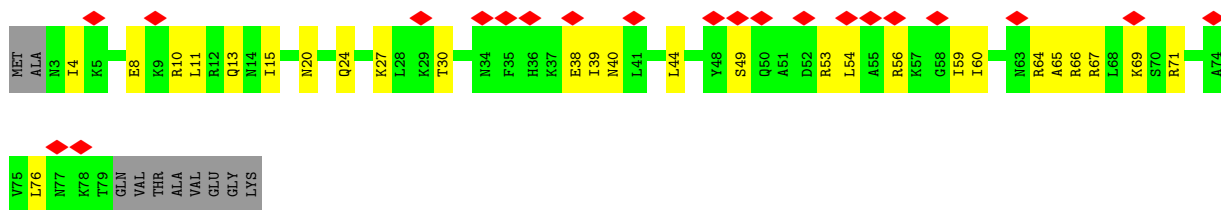
• Molecule 20: 30S ribosomal protein S18



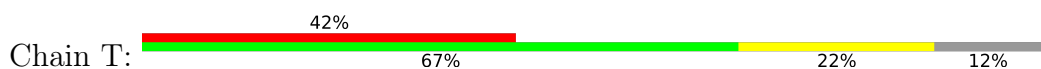
• Molecule 21: 30S ribosomal protein S19



• Molecule 22: 30S ribosomal protein S20



• Molecule 23: 30S ribosomal protein S21

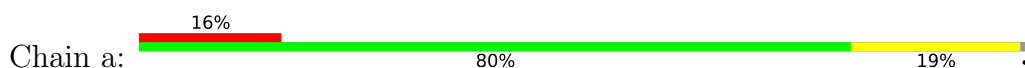


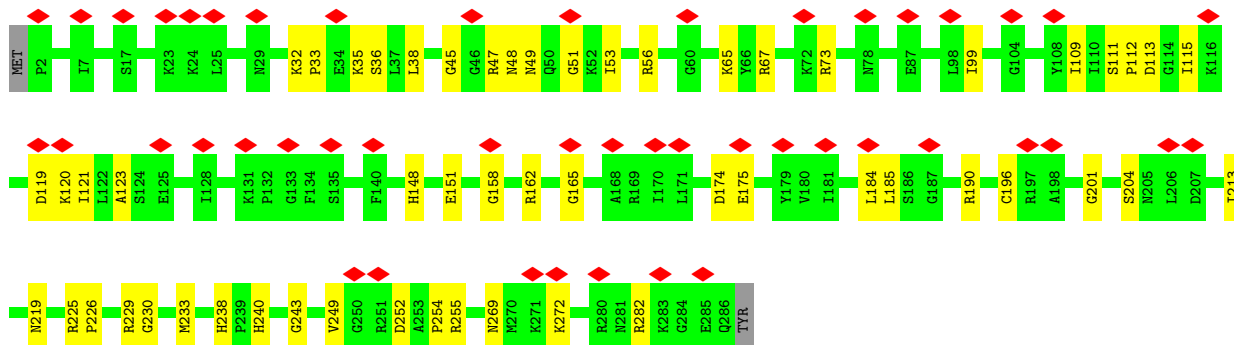
• Molecule 24: nascent peptide



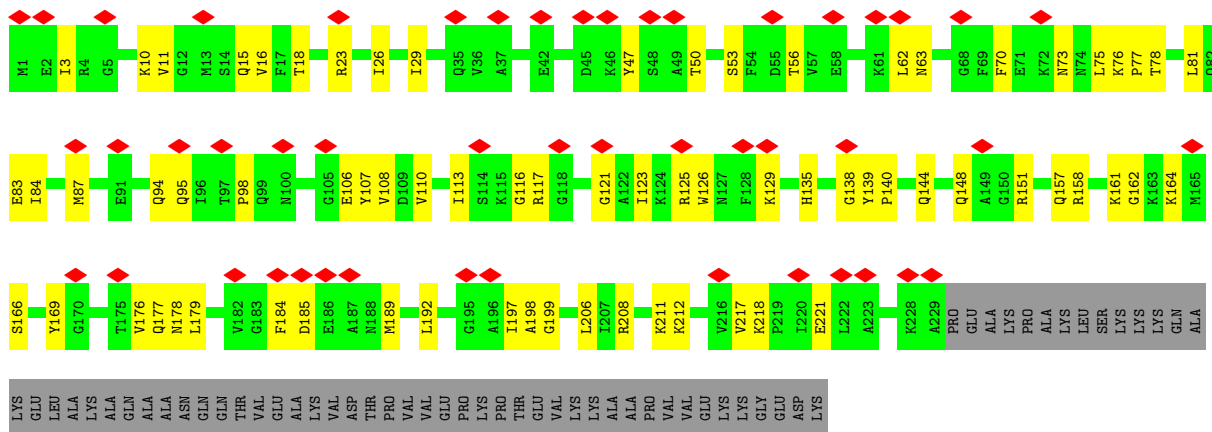
There are no outlier residues recorded for this chain.

• Molecule 25: 50S ribosomal protein L2

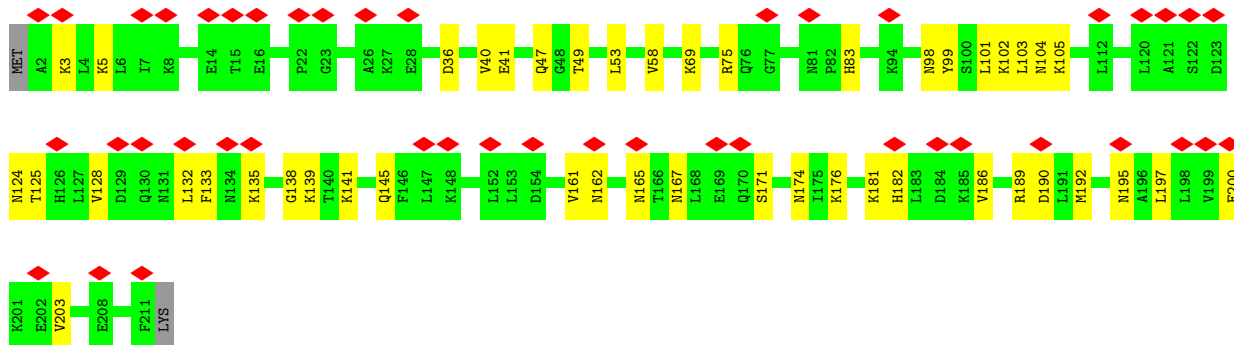
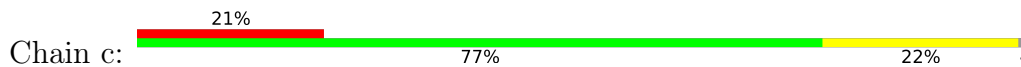




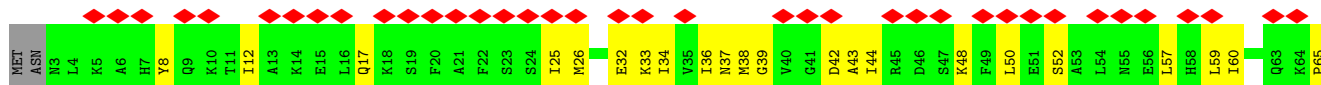
• Molecule 26: 50S ribosomal protein L3

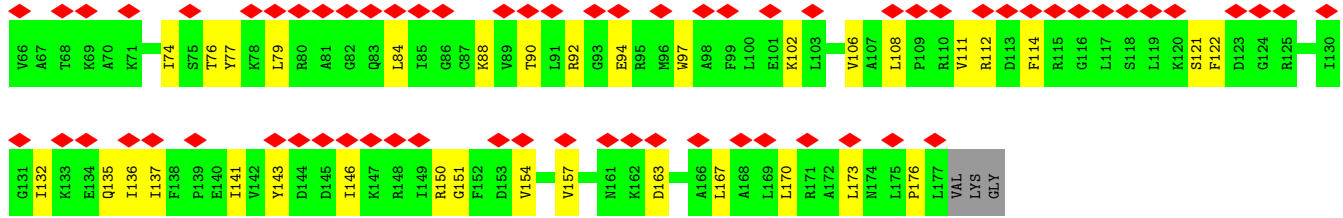


• Molecule 27: 50S ribosomal protein L4

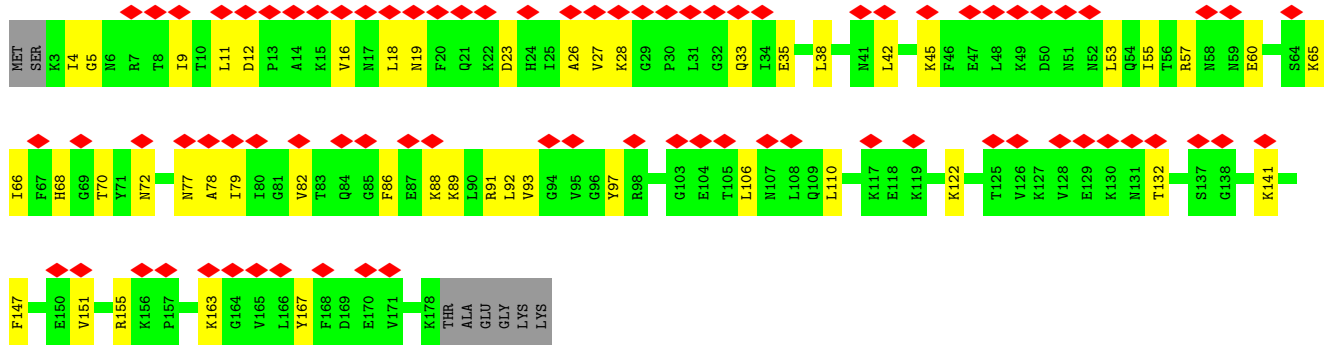
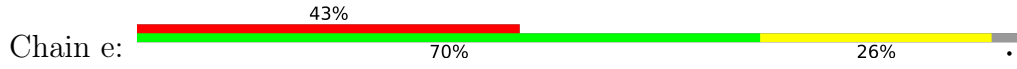


• Molecule 28: 50S ribosomal protein L5

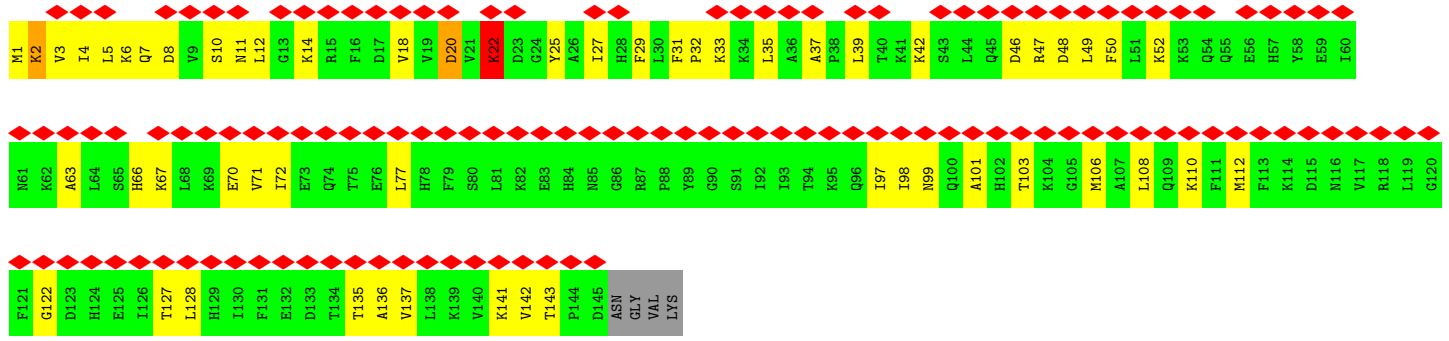
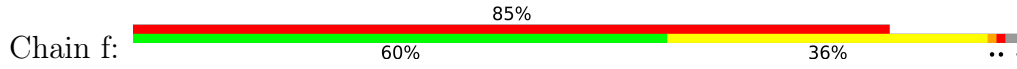




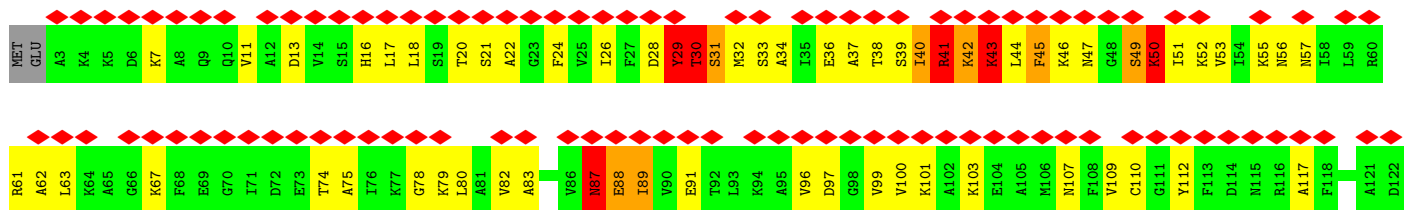
• Molecule 29: 50S ribosomal protein L6

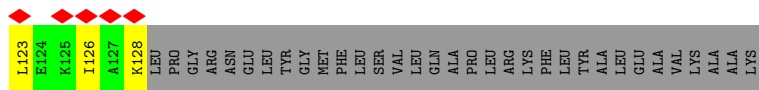


• Molecule 30: 50S ribosomal protein L9

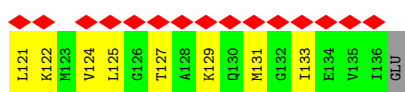
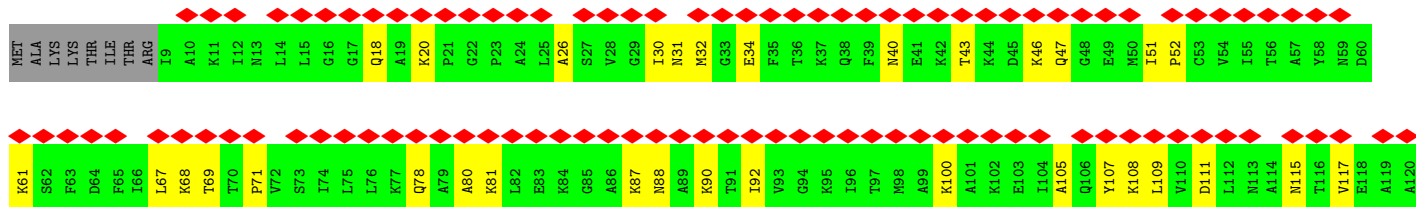
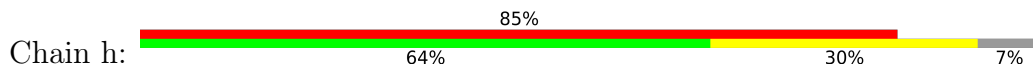


• Molecule 31: 50S ribosomal protein L10

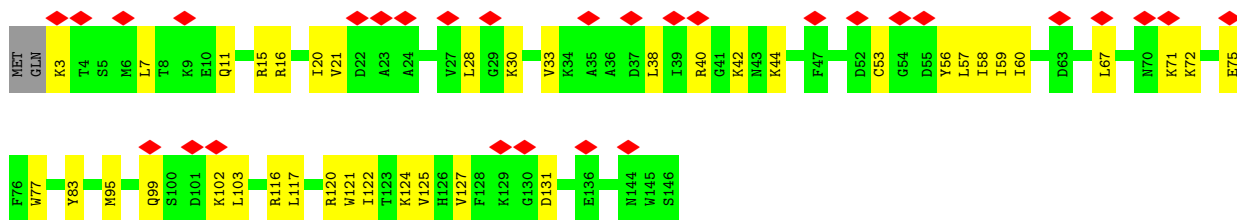




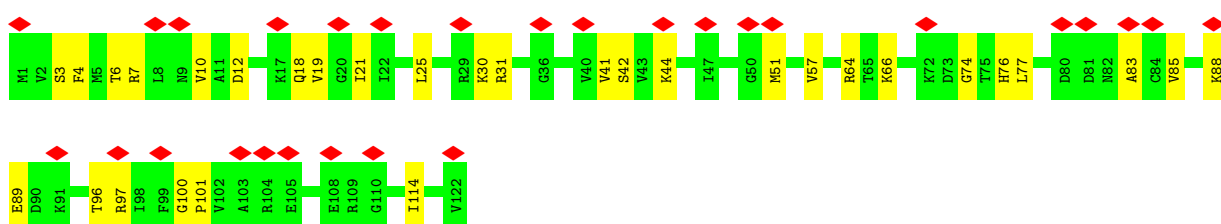
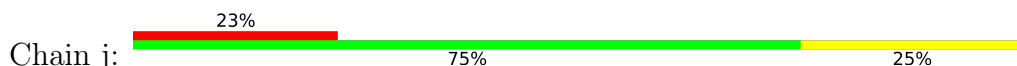
• Molecule 32: 50S ribosomal protein L11



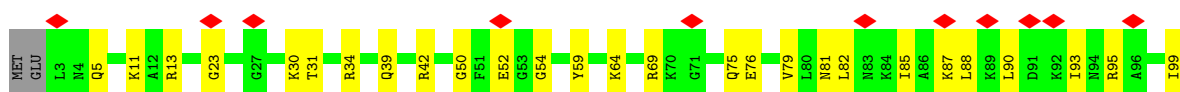
• Molecule 33: 50S ribosomal protein L13

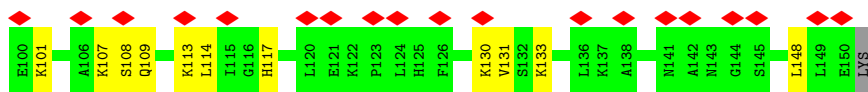


• Molecule 34: 50S ribosomal protein L14

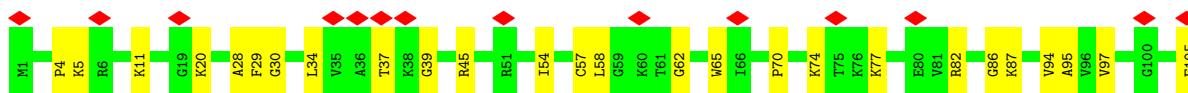


• Molecule 35: 50S ribosomal protein L15

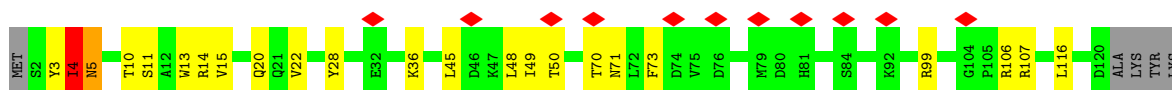
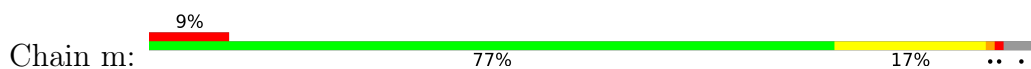




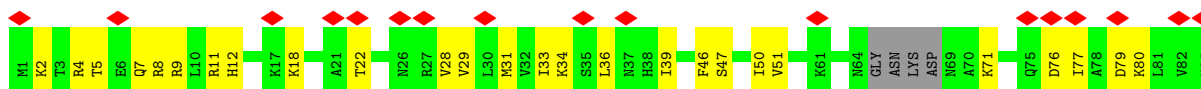
- Molecule 36: 50S ribosomal protein L16



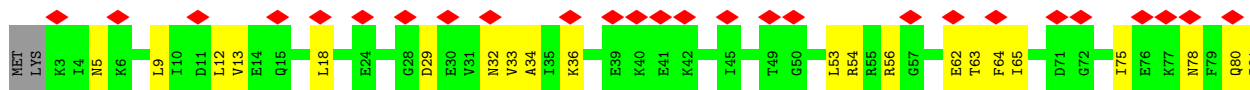
- Molecule 37: 50S ribosomal protein L17



- Molecule 38: 50S ribosomal protein L18



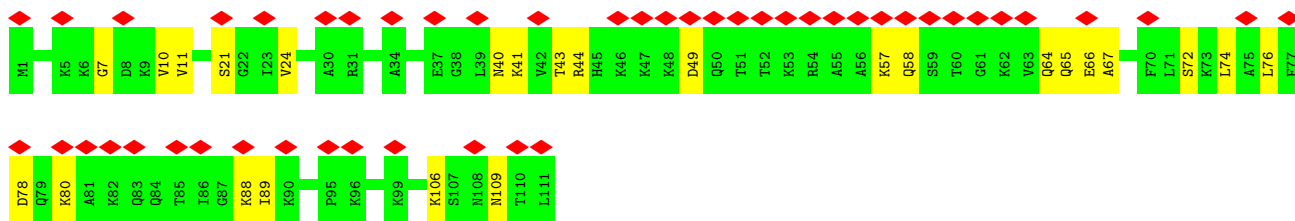
- Molecule 39: 50S ribosomal protein L19



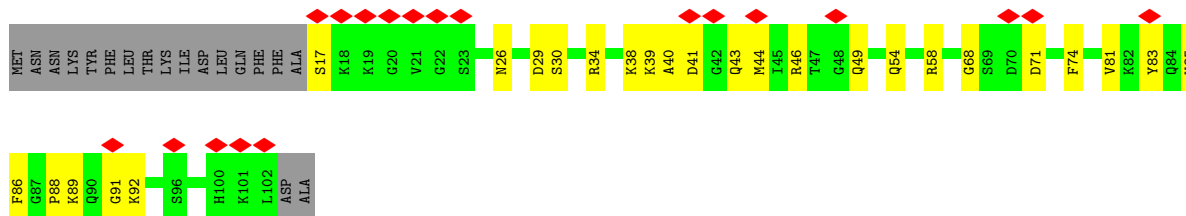
- Molecule 40: 50S ribosomal protein L20



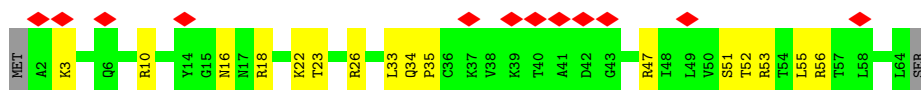




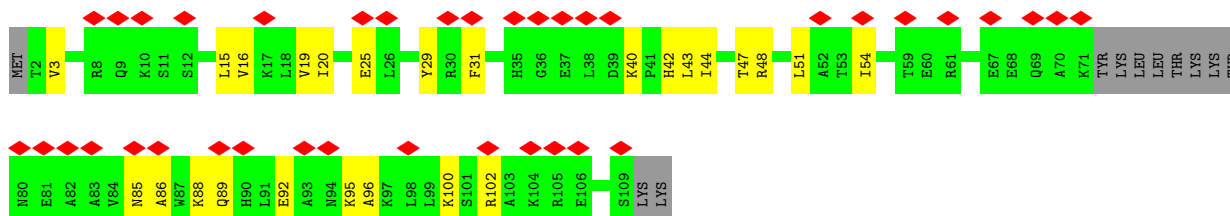
• Molecule 45: 50S ribosomal protein L27



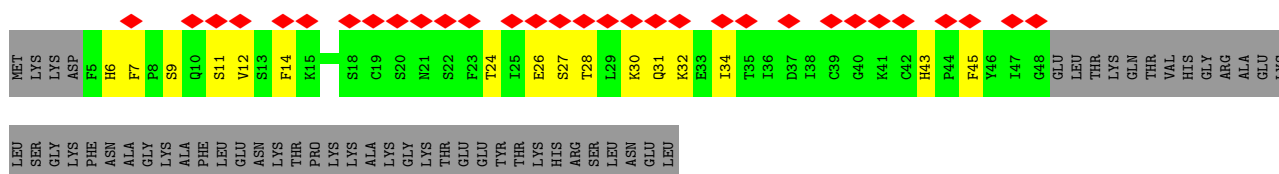
• Molecule 46: 50S ribosomal protein L28



• Molecule 47: 50S ribosomal protein L29

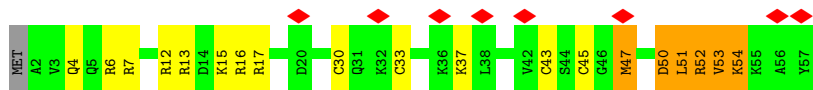


• Molecule 48: 50S ribosomal protein L31



• Molecule 49: 50S ribosomal protein L32

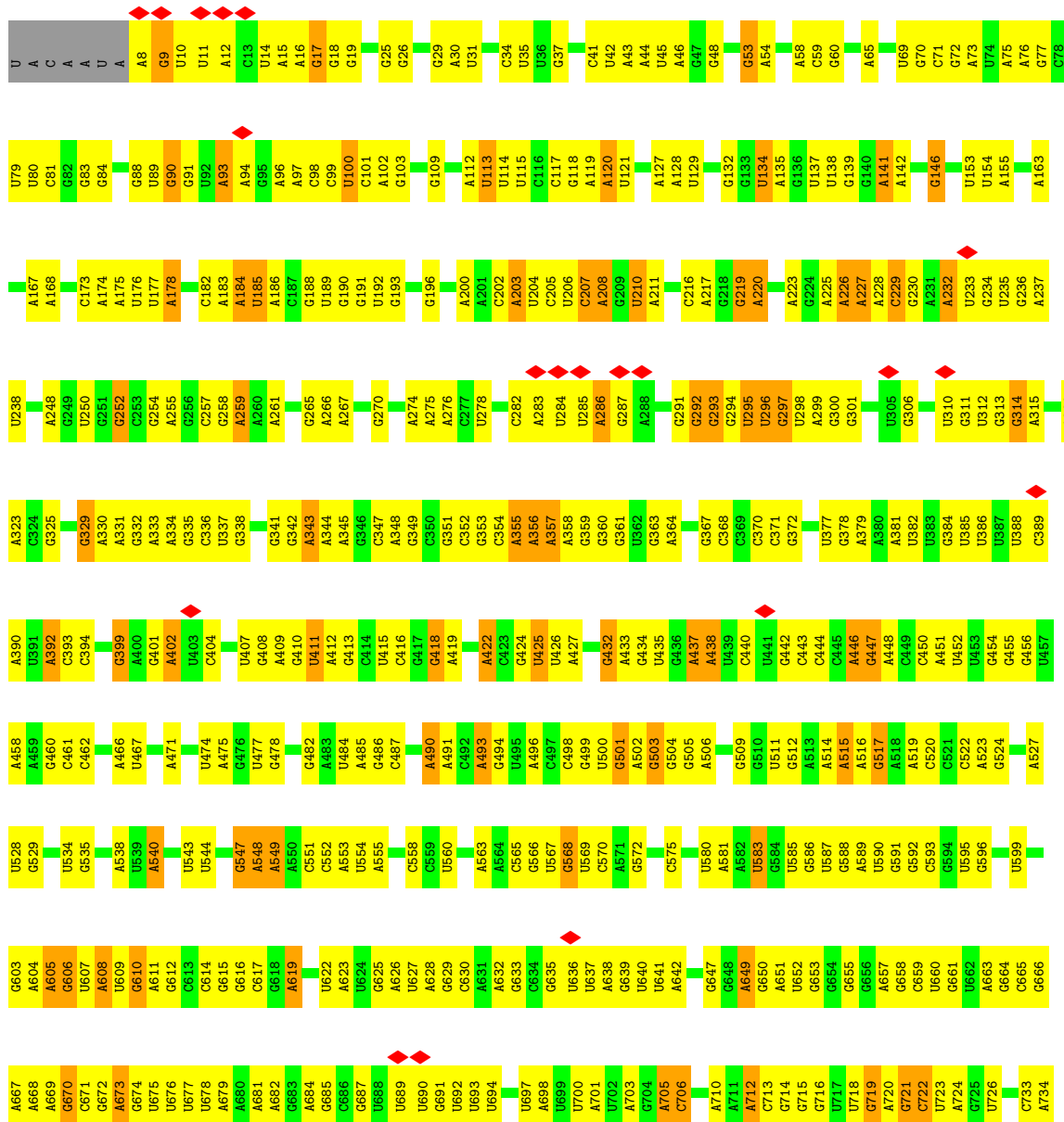


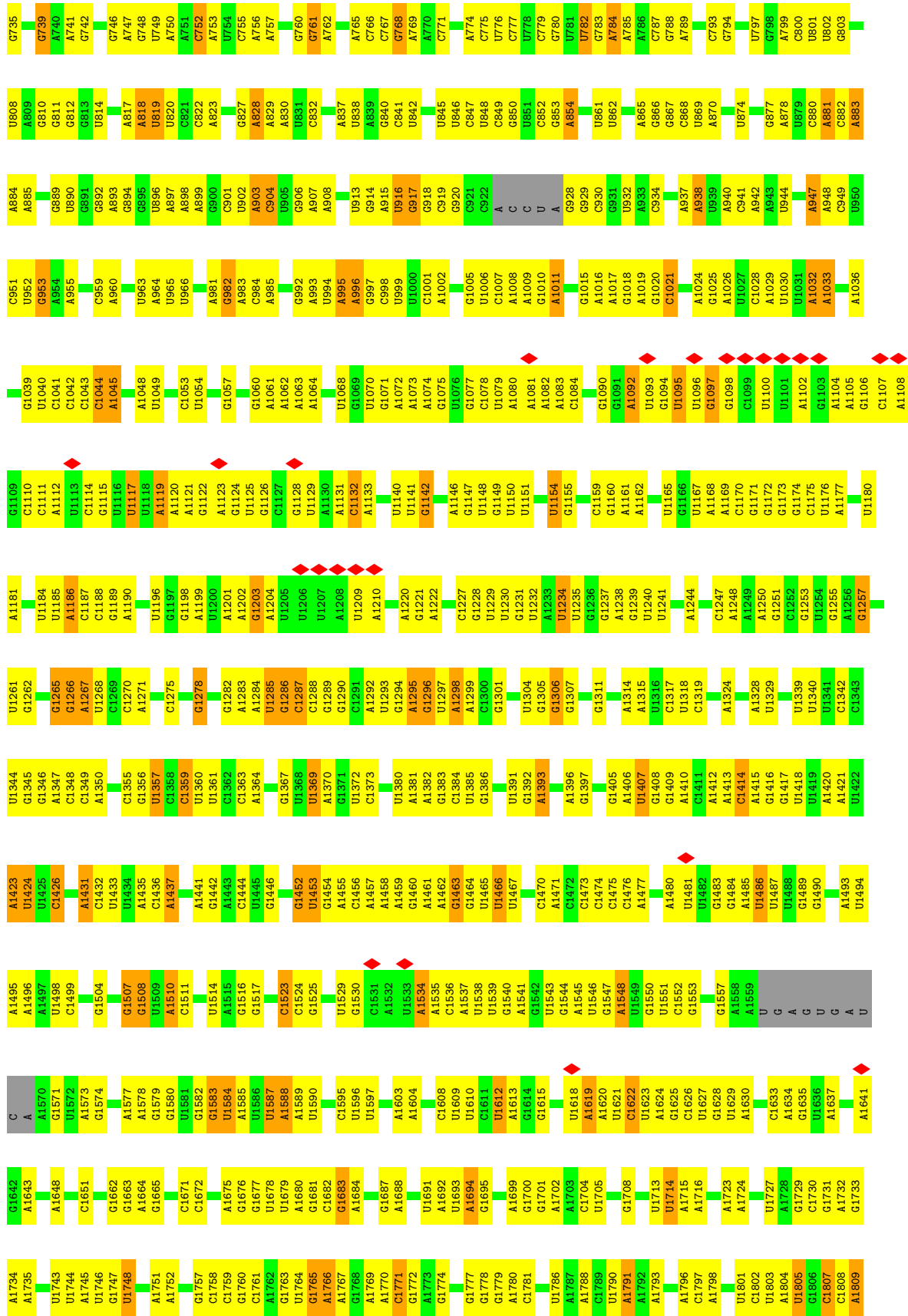


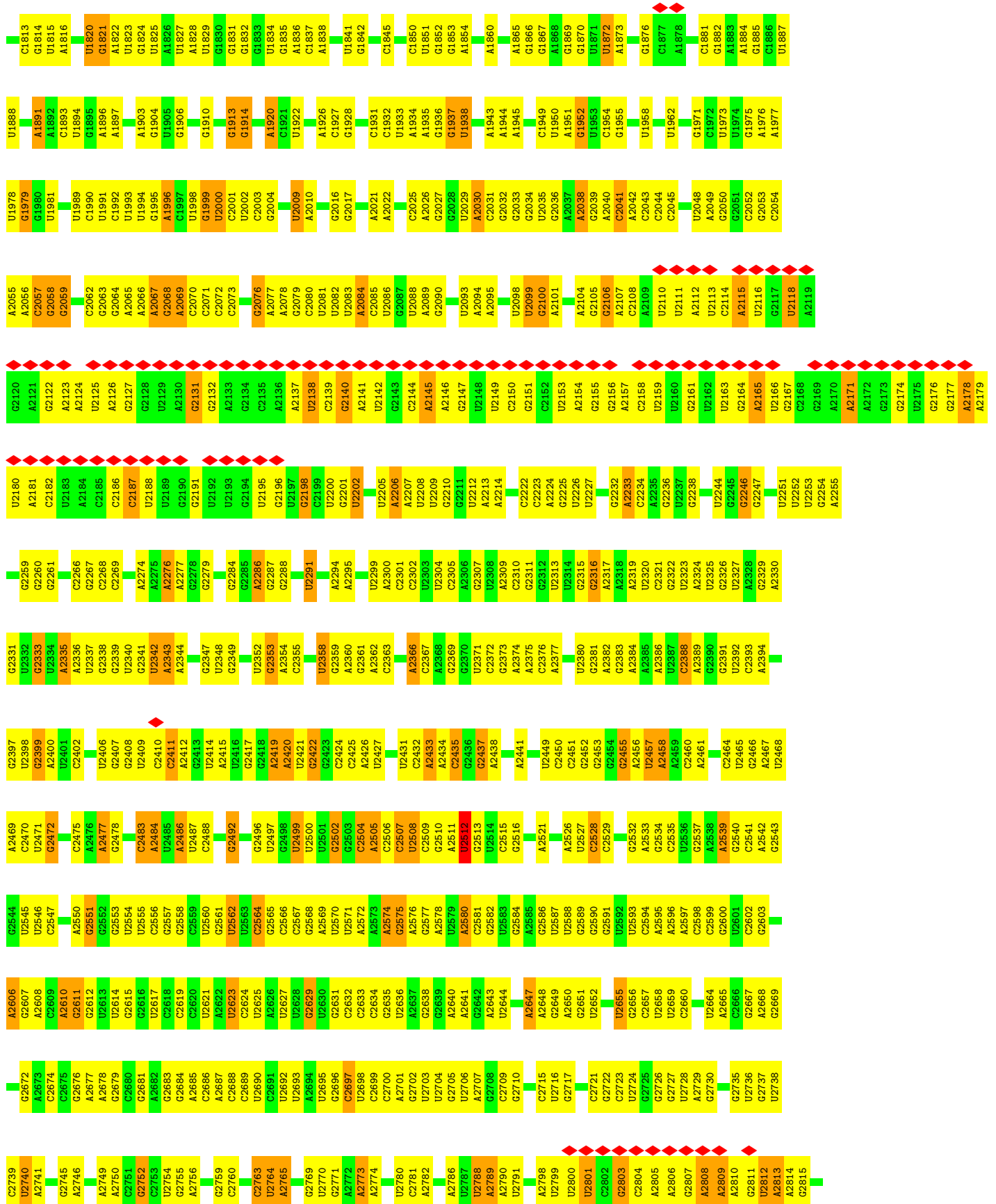
• Molecule 50: 50S ribosomal protein L33 1



• Molecule 51: 23S ribosomal RNA

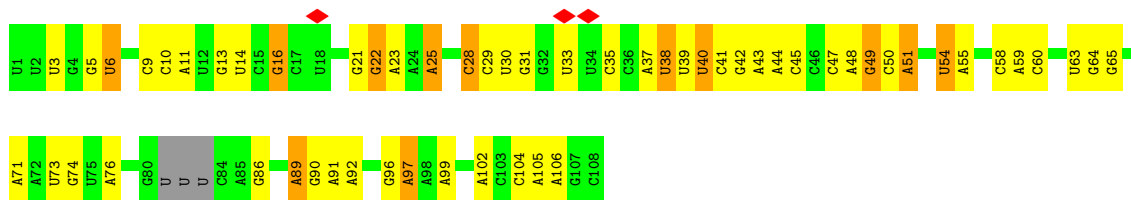




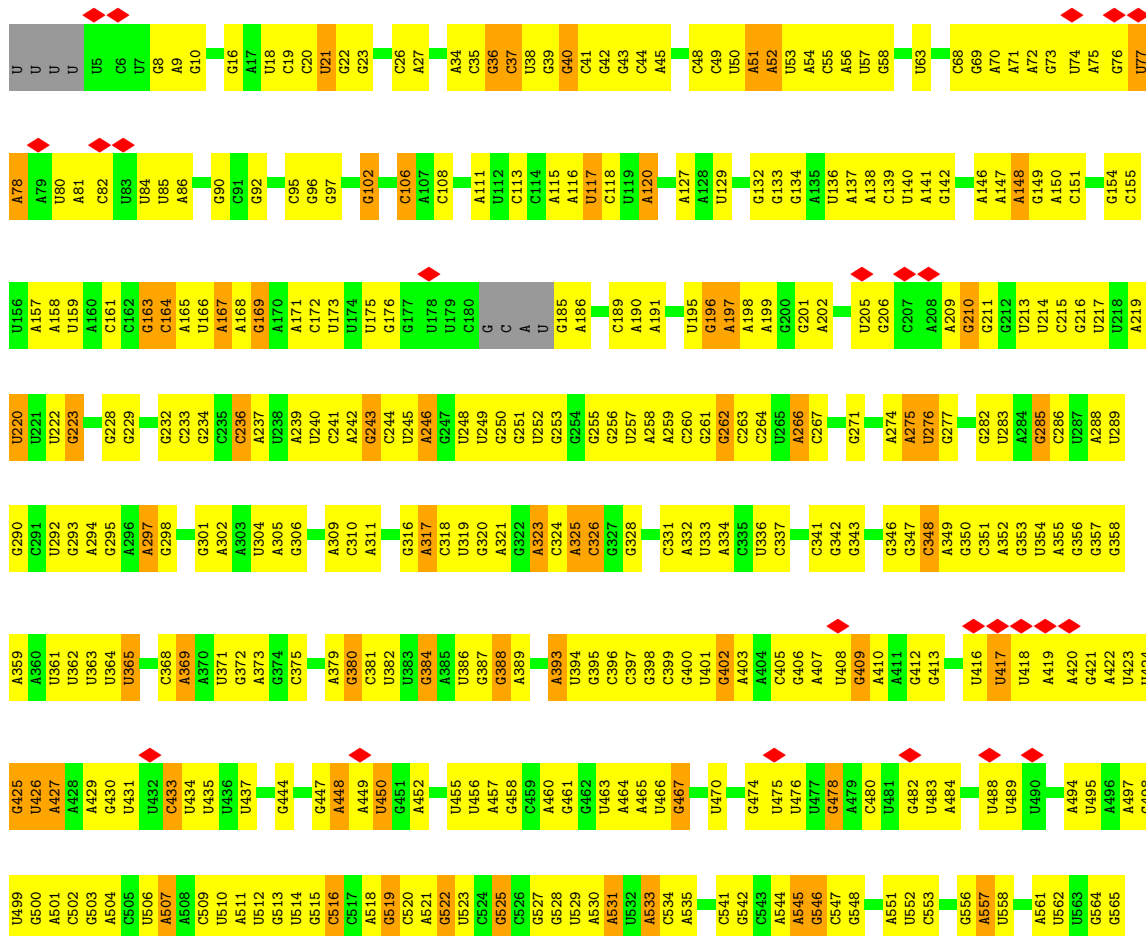




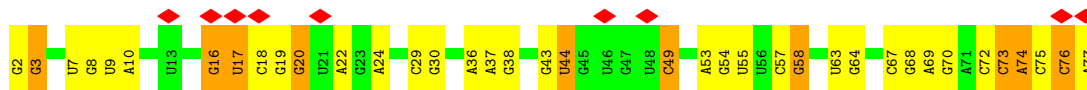
• Molecule 52: 5S ribosomal RNA



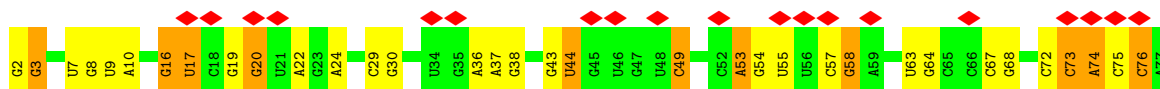
• Molecule 53: 16S ribosomal RNA







• Molecule 54: tRNA-Phe



• Molecule 55: mRNA



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	12915	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.826	Depositor
Minimum map value	-1.600	Depositor
Average map value	0.024	Depositor
Map value standard deviation	0.152	Depositor
Recommended contour level	0.7	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	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: CLM

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	0.15	0/383	0.42	0/504
2	1	0.16	0/484	0.40	0/637
3	2	0.15	0/306	0.38	0/401
4	A	0.15	0/1954	0.41	0/2642
5	B	0.14	0/1721	0.44	0/2323
6	C	0.14	0/1691	0.40	0/2267
7	D	0.16	0/1188	0.44	0/1593
8	E	0.14	0/1384	0.38	0/1867
9	F	0.13	0/1266	0.44	0/1700
10	G	0.14	0/1126	0.45	0/1517
11	H	0.16	0/1044	0.44	0/1395
12	I	0.15	0/820	0.42	0/1103
13	J	0.13	0/844	0.37	0/1136
14	K	0.27	0/1094	0.66	1/1468 (0.1%)
15	L	0.15	0/962	0.45	0/1289
16	M	0.14	0/483	0.40	0/643
17	N	0.12	0/679	0.37	0/907
18	O	0.14	0/659	0.43	0/885
19	P	0.15	0/684	0.40	0/913
20	Q	0.14	0/545	0.45	0/730
21	R	0.24	0/698	0.64	2/936 (0.2%)
22	S	0.15	0/631	0.37	0/838
23	T	0.13	0/475	0.43	0/621
25	a	0.15	0/2267	0.41	0/3044
26	b	0.13	0/1795	0.40	0/2412
27	c	0.12	0/1671	0.36	0/2246
28	d	0.15	0/1409	0.46	1/1894 (0.1%)
29	e	0.14	0/1420	0.39	0/1912
30	f	0.23	0/1205	0.47	0/1616
31	g	0.49	0/969	0.93	5/1295 (0.4%)
32	h	0.15	0/968	0.40	0/1298
33	i	0.12	0/1186	0.35	0/1592

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
34	j	0.15	0/953	0.39	0/1275
35	k	0.14	0/1170	0.42	0/1559
36	l	0.15	0/1104	0.40	0/1481
37	m	0.22	0/973	0.45	0/1309
38	n	0.13	0/897	0.43	0/1198
39	o	0.22	0/948	0.51	0/1262
40	p	0.12	0/961	0.36	0/1278
41	q	0.13	0/828	0.40	0/1111
42	r	0.17	0/1077	0.37	0/1441
43	s	0.14	0/732	0.42	0/988
44	t	0.13	0/879	0.36	0/1165
45	u	0.14	0/665	0.45	0/884
46	v	0.15	0/519	0.42	0/695
47	w	0.12	0/826	0.41	0/1104
48	x	0.13	0/353	0.32	0/474
49	y	0.39	0/457	0.77	0/601
50	z	0.14	0/412	0.40	0/547
51	3	0.09	0/69073	0.23	1/107710 (0.0%)
52	4	0.08	0/2505	0.21	0/3902
53	5	0.09	0/35768	0.21	0/55764
54	6	0.13	0/1808	0.35	0/2817
54	7	0.12	0/1808	0.35	0/2817
55	Y	0.51	1/194 (0.5%)	0.57	0/298
All	All	0.12	1/158921 (0.0%)	0.30	10/237304 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	Y	22	U	C1'-N1	6.26	1.57	1.48

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	3	2512	U	C2'-C3'-O3'	-11.09	97.06	113.70
14	K	116	ASP	CB-CA-C	9.23	125.42	111.85
31	g	50	LYS	N-CA-C	8.29	119.18	108.24
28	d	137	ILE	N-CA-C	-6.46	107.57	113.71
31	g	40	ILE	CB-CA-C	-6.33	103.89	111.81

There are no chirality outliers.

There are no planarity outliers.

## 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	380	0	429	10	0
2	1	477	0	530	18	0
3	2	304	0	350	11	0
4	A	1921	0	1973	52	0
5	B	1698	0	1768	43	0
6	C	1660	0	1719	46	0
7	D	1173	0	1267	30	0
8	E	1362	0	1377	33	0
9	F	1246	0	1308	29	0
10	G	1110	0	1226	42	0
11	H	1028	0	1094	36	0
12	I	809	0	894	16	0
13	J	829	0	855	19	0
14	K	1076	0	1170	40	0
15	L	951	0	1014	29	0
16	M	474	0	509	21	0
17	N	673	0	730	24	0
18	O	646	0	677	21	0
19	P	675	0	728	18	0
20	Q	535	0	562	14	0
21	R	682	0	691	29	0
22	S	629	0	681	23	0
23	T	471	0	522	14	0
24	Z	25	0	8	0	0
25	a	2225	0	2301	42	0
26	b	1762	0	1808	54	0
27	c	1644	0	1731	37	0
28	d	1388	0	1469	41	0
29	e	1396	0	1481	33	0
30	f	1182	0	1227	72	0
31	g	960	0	1014	65	0
32	h	959	0	1039	27	0
33	i	1164	0	1192	36	0
34	j	944	0	1019	26	0
35	k	1153	0	1256	36	0
36	l	1079	0	1134	28	0
37	m	958	0	1011	18	0

*Continued on next page...*

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	n	889	0	952	30	0
39	o	938	0	1008	29	0
40	p	947	0	1028	35	0
41	q	811	0	858	31	0
42	r	1068	0	1150	20	0
43	s	720	0	803	18	0
44	t	872	0	972	17	0
45	u	657	0	695	22	0
46	v	513	0	560	15	0
47	w	818	0	870	17	0
48	x	344	0	333	11	0
49	y	452	0	472	17	0
50	z	408	0	440	12	0
51	3	61664	0	30954	1260	0
52	4	2239	0	1137	36	0
53	5	31943	0	16058	722	0
54	6	1618	0	821	20	0
54	7	1618	0	821	20	0
55	Y	177	0	92	10	0
56	3	20	0	11	2	0
All	All	146364	0	99799	3083	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 13.

The worst 5 of 3083 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)
30:f:2:LYS:NZ	30:f:4:ILE:CB	1.96	1.24
30:f:2:LYS:NZ	30:f:4:ILE:HB	1.51	1.18
30:f:2:LYS:HE3	30:f:6:LYS:HE3	1.16	1.11
30:f:2:LYS:HE3	30:f:6:LYS:CE	1.84	1.08
53:5:661:G:H1	53:5:738:A:H61	1.07	1.02

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	45/48 (94%)	45 (100%)	0	0	100	100
2	1	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
3	2	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
4	A	238/294 (81%)	220 (92%)	18 (8%)	0	100	100
5	B	213/273 (78%)	201 (94%)	12 (6%)	0	100	100
6	C	201/205 (98%)	185 (92%)	16 (8%)	0	100	100
7	D	151/219 (69%)	146 (97%)	5 (3%)	0	100	100
8	E	165/215 (77%)	153 (93%)	12 (7%)	0	100	100
9	F	152/155 (98%)	143 (94%)	9 (6%)	0	100	100
10	G	139/142 (98%)	126 (91%)	13 (9%)	0	100	100
11	H	126/132 (96%)	109 (86%)	17 (14%)	0	100	100
12	I	99/108 (92%)	89 (90%)	10 (10%)	0	100	100
13	J	112/121 (93%)	111 (99%)	1 (1%)	0	100	100
14	K	134/139 (96%)	115 (86%)	16 (12%)	3 (2%)	5	28
15	L	116/124 (94%)	102 (88%)	14 (12%)	0	100	100
16	M	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
17	N	81/86 (94%)	77 (95%)	4 (5%)	0	100	100
18	O	78/94 (83%)	70 (90%)	8 (10%)	0	100	100
19	P	81/85 (95%)	75 (93%)	6 (7%)	0	100	100
20	Q	63/104 (61%)	57 (90%)	6 (10%)	0	100	100
21	R	82/87 (94%)	74 (90%)	5 (6%)	3 (4%)	2	19
22	S	75/87 (86%)	74 (99%)	1 (1%)	0	100	100
23	T	51/60 (85%)	49 (96%)	2 (4%)	0	100	100
25	a	283/287 (99%)	263 (93%)	20 (7%)	0	100	100
26	b	227/287 (79%)	216 (95%)	11 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	c	208/212 (98%)	201 (97%)	7 (3%)	0	100	100
28	d	173/180 (96%)	163 (94%)	10 (6%)	0	100	100
29	e	174/184 (95%)	164 (94%)	10 (6%)	0	100	100
30	f	143/149 (96%)	128 (90%)	14 (10%)	1 (1%)	18	55
31	g	124/161 (77%)	106 (86%)	13 (10%)	5 (4%)	2	18
32	h	126/137 (92%)	113 (90%)	13 (10%)	0	100	100
33	i	142/146 (97%)	136 (96%)	6 (4%)	0	100	100
34	j	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
35	k	146/151 (97%)	137 (94%)	9 (6%)	0	100	100
36	l	134/139 (96%)	129 (96%)	5 (4%)	0	100	100
37	m	117/124 (94%)	112 (96%)	4 (3%)	1 (1%)	14	49
38	n	108/116 (93%)	101 (94%)	7 (6%)	0	100	100
39	o	113/119 (95%)	104 (92%)	9 (8%)	0	100	100
40	p	112/127 (88%)	109 (97%)	3 (3%)	0	100	100
41	q	97/100 (97%)	92 (95%)	5 (5%)	0	100	100
42	r	137/159 (86%)	132 (96%)	5 (4%)	0	100	100
43	s	90/237 (38%)	82 (91%)	8 (9%)	0	100	100
44	t	109/111 (98%)	107 (98%)	2 (2%)	0	100	100
45	u	84/104 (81%)	80 (95%)	4 (5%)	0	100	100
46	v	61/65 (94%)	60 (98%)	1 (2%)	0	100	100
47	w	96/111 (86%)	92 (96%)	4 (4%)	0	100	100
48	x	42/97 (43%)	37 (88%)	5 (12%)	0	100	100
49	y	54/57 (95%)	48 (89%)	5 (9%)	1 (2%)	6	31
50	z	48/53 (91%)	48 (100%)	0	0	100	100
All	All	5820/6670 (87%)	5441 (94%)	365 (6%)	14 (0%)	44	77

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	K	118	VAL
21	R	27	LYS
31	g	41	ARG
31	g	87	ASN
30	f	22	LYS

### 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	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	A	212/262 (81%)	212 (100%)	0	100	100
5	B	180/232 (78%)	180 (100%)	0	100	100
6	C	181/183 (99%)	181 (100%)	0	100	100
7	D	123/178 (69%)	123 (100%)	0	100	100
8	E	150/196 (76%)	150 (100%)	0	100	100
9	F	131/132 (99%)	131 (100%)	0	100	100
10	G	123/124 (99%)	123 (100%)	0	100	100
11	H	111/115 (96%)	111 (100%)	0	100	100
12	I	95/99 (96%)	95 (100%)	0	100	100
13	J	91/97 (94%)	91 (100%)	0	100	100
14	K	117/120 (98%)	113 (97%)	4 (3%)	32	54
15	L	100/105 (95%)	100 (100%)	0	100	100
16	M	47/48 (98%)	47 (100%)	0	100	100
17	N	76/78 (97%)	76 (100%)	0	100	100
18	O	69/82 (84%)	69 (100%)	0	100	100
19	P	73/75 (97%)	72 (99%)	1 (1%)	59	72
20	Q	56/94 (60%)	56 (100%)	0	100	100
21	R	74/77 (96%)	70 (95%)	4 (5%)	20	42
22	S	70/77 (91%)	70 (100%)	0	100	100
23	T	49/56 (88%)	49 (100%)	0	100	100
25	a	241/243 (99%)	241 (100%)	0	100	100
26	b	186/233 (80%)	186 (100%)	0	100	100
27	c	182/184 (99%)	182 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	d	150/154 (97%)	150 (100%)	0	100	100
29	e	153/159 (96%)	153 (100%)	0	100	100
30	f	131/134 (98%)	128 (98%)	3 (2%)	44	63
31	g	101/129 (78%)	86 (85%)	15 (15%)	3	14
32	h	102/110 (93%)	102 (100%)	0	100	100
33	i	126/128 (98%)	126 (100%)	0	100	100
34	j	103/103 (100%)	103 (100%)	0	100	100
35	k	123/126 (98%)	123 (100%)	0	100	100
36	l	113/115 (98%)	113 (100%)	0	100	100
37	m	105/109 (96%)	103 (98%)	2 (2%)	50	66
38	n	96/99 (97%)	96 (100%)	0	100	100
39	o	101/105 (96%)	98 (97%)	3 (3%)	36	57
40	p	100/108 (93%)	100 (100%)	0	100	100
41	q	90/91 (99%)	90 (100%)	0	100	100
42	r	116/132 (88%)	116 (100%)	0	100	100
43	s	82/208 (39%)	82 (100%)	0	100	100
44	t	96/96 (100%)	96 (100%)	0	100	100
45	u	69/85 (81%)	69 (100%)	0	100	100
46	v	58/60 (97%)	58 (100%)	0	100	100
47	w	87/98 (89%)	87 (100%)	0	100	100
48	x	41/86 (48%)	41 (100%)	0	100	100
49	y	48/49 (98%)	42 (88%)	6 (12%)	4	17
50	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5101/5751 (89%)	5063 (99%)	38 (1%)	73	79

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	m	5	ASN
49	y	52	ARG
39	o	91	LYS
49	y	47	MET
49	y	54	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
25	a	159	GLN
42	r	7	GLN
26	b	157	GLN
40	p	40	GLN
44	t	65	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	3	2875/2907 (98%)	614 (21%)	24 (0%)
52	4	103/108 (95%)	28 (27%)	0
53	5	1490/1520 (98%)	308 (20%)	8 (0%)
54	6	75/76 (98%)	22 (29%)	2 (2%)
54	7	75/76 (98%)	22 (29%)	2 (2%)
55	Y	9/40 (22%)	4 (44%)	1 (11%)
All	All	4627/4727 (97%)	998 (21%)	37 (0%)

5 of 998 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	3	9	G
51	3	11	U
51	3	14	U
51	3	15	A
51	3	16	A

5 of 37 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	5	716	C
54	7	57	C
53	5	839	U
54	6	16	G
51	3	1507	G

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
56	CLM	3	3001	-	20,20,20	1.29	1 (5%)	23,27,27	0.91	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
56	CLM	3	3001	-	-	0/20/22/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	3	3001	CLM	C9-N9	-4.34	1.34	1.45

There are no bond angle outliers.

There are no chirality outliers.

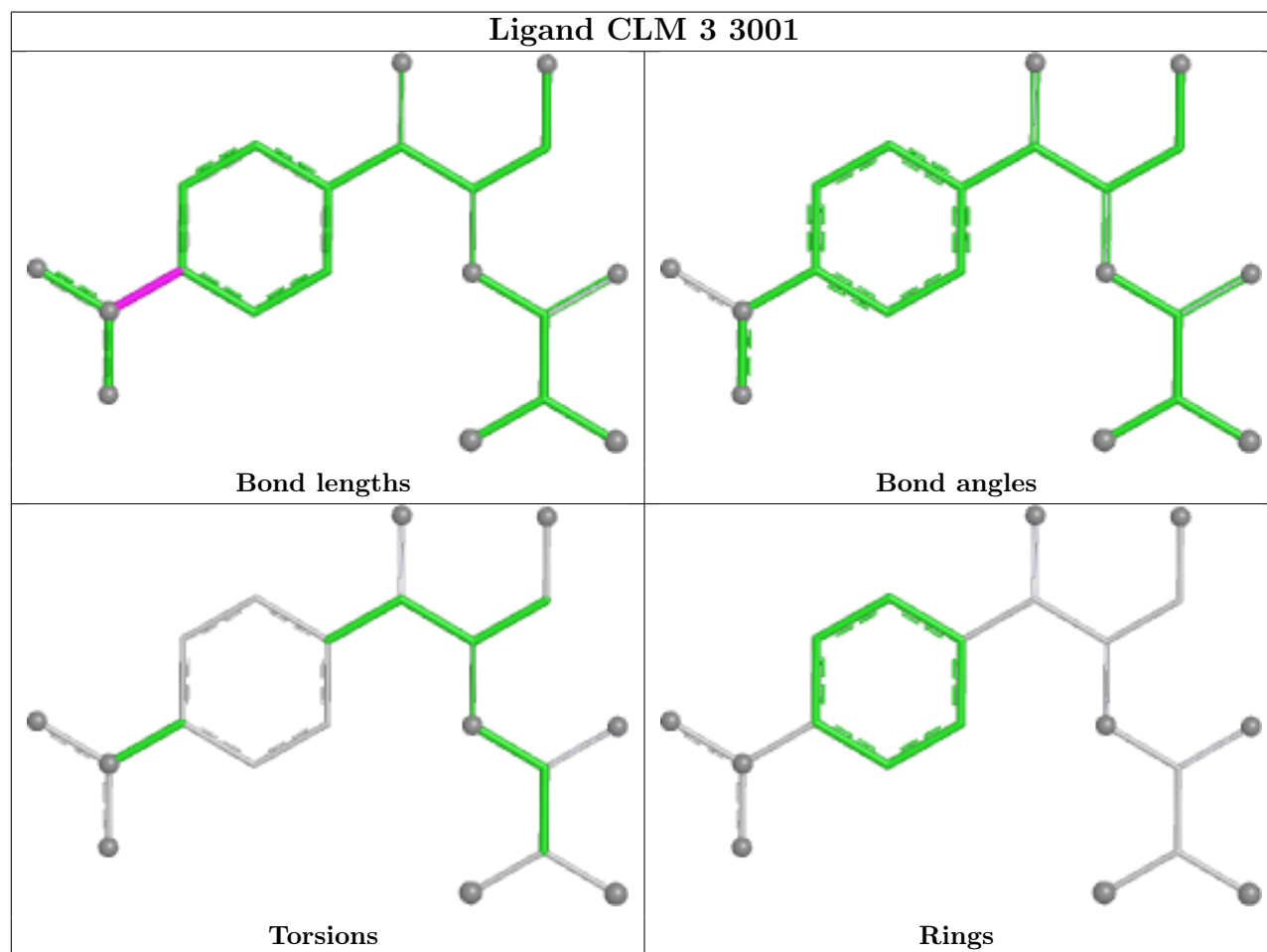
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	3	3001	CLM	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 purple. 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.

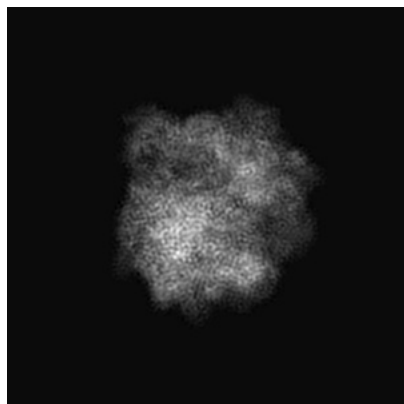
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13412. These allow visual inspection of the internal detail of the map and identification of artifacts.

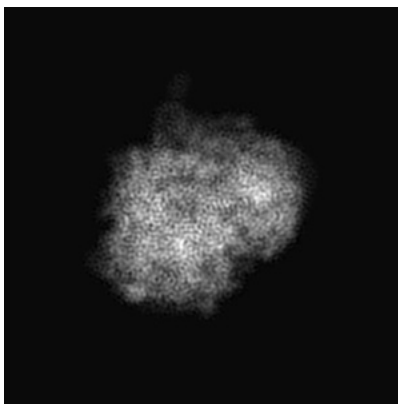
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

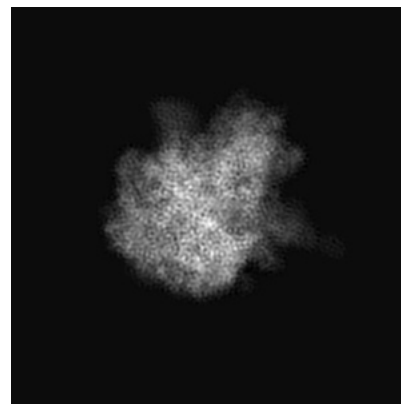
#### 6.1.1 Primary map



X

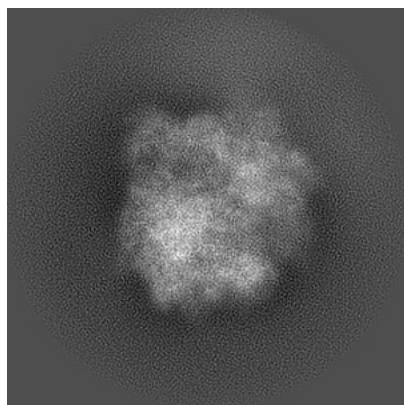


Y

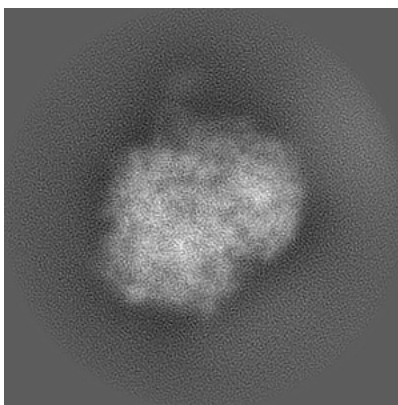


Z

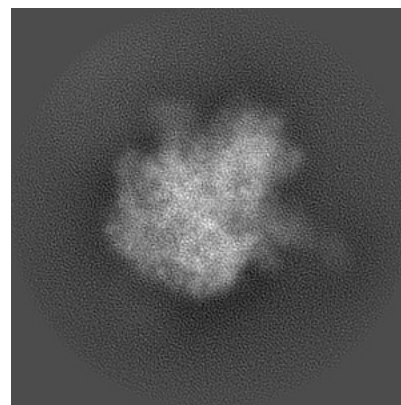
#### 6.1.2 Raw map



X



Y

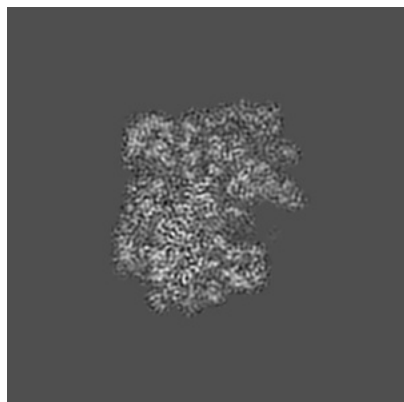


Z

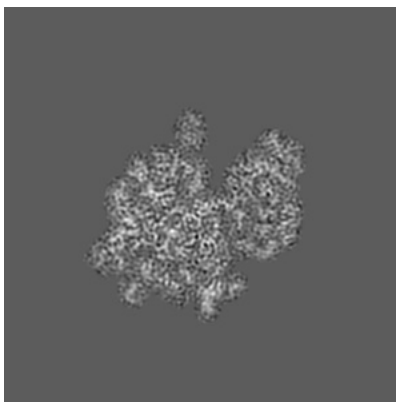
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

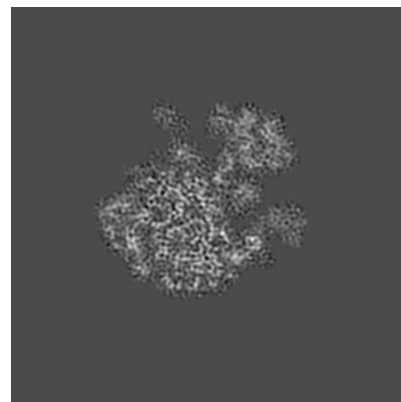
### 6.2.1 Primary map



X Index: 128

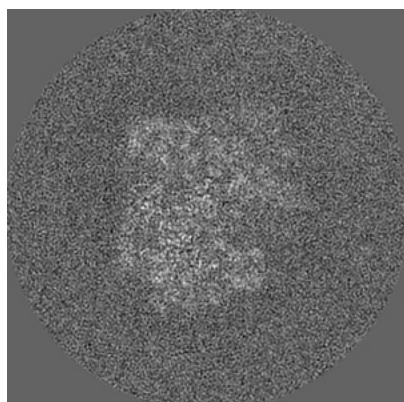


Y Index: 128

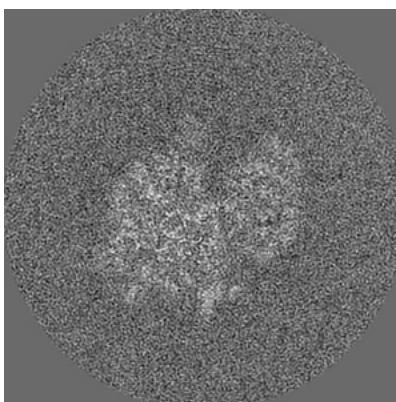


Z Index: 128

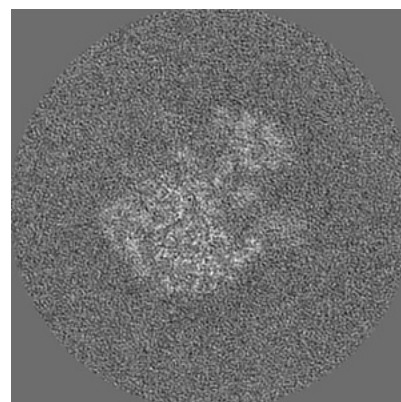
### 6.2.2 Raw map



X Index: 128



Y Index: 128

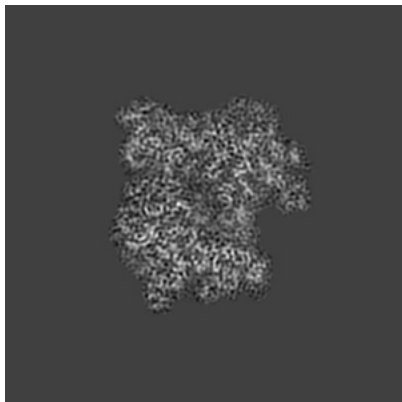


Z Index: 128

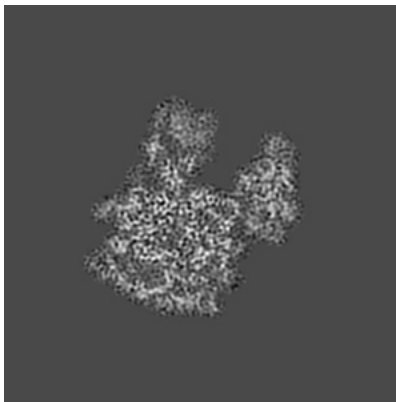
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

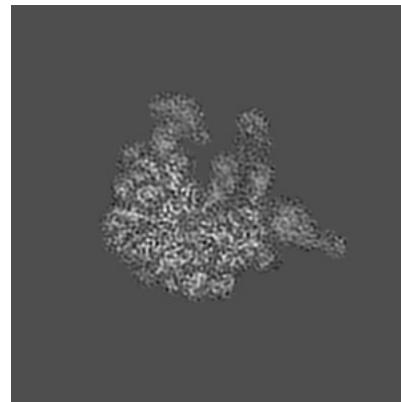
### 6.3.1 Primary map



X Index: 135

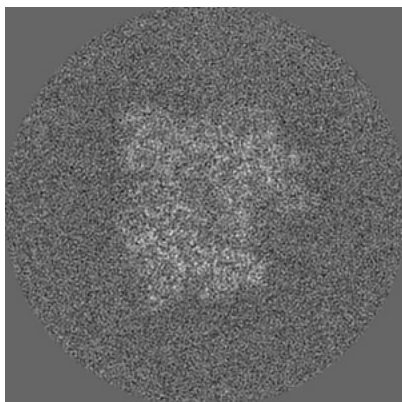


Y Index: 116

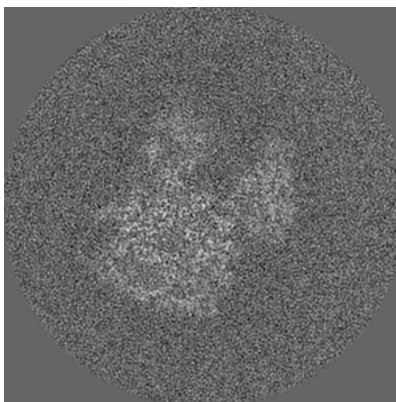


Z Index: 113

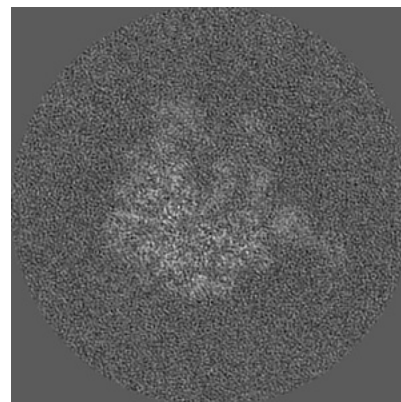
### 6.3.2 Raw map



X Index: 135



Y Index: 116

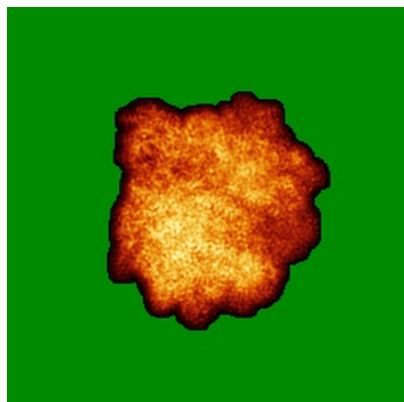


Z Index: 113

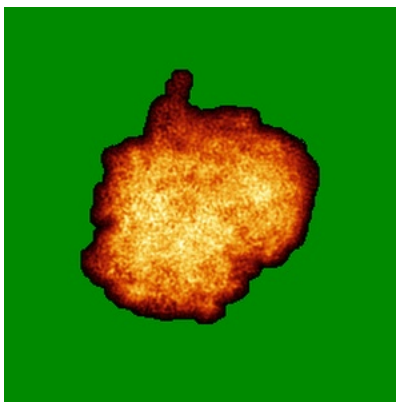
The images above show the largest variance slices of the map in three orthogonal directions.

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

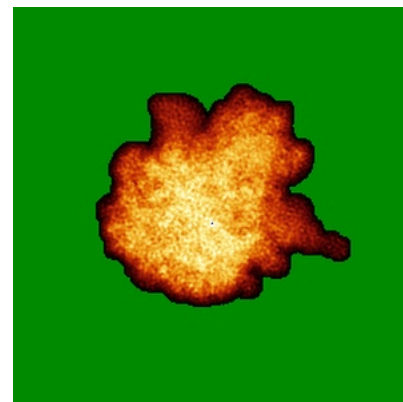
### 6.4.1 Primary map



X

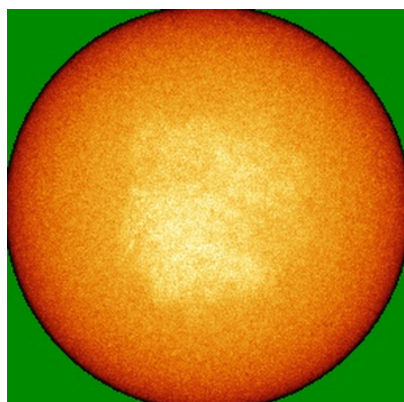


Y

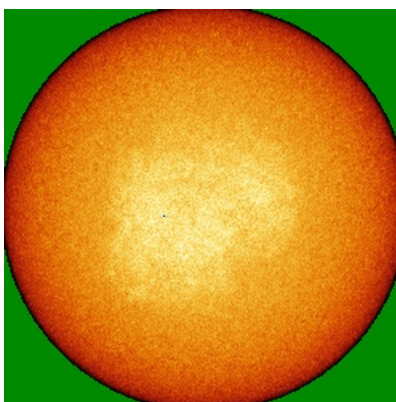


Z

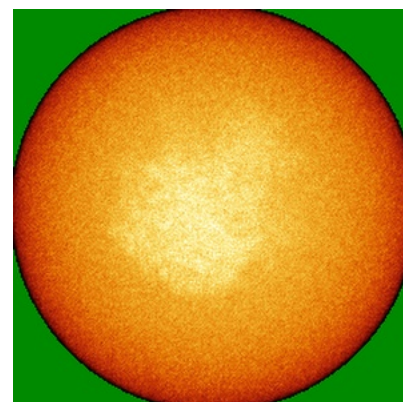
### 6.4.2 Raw map



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.

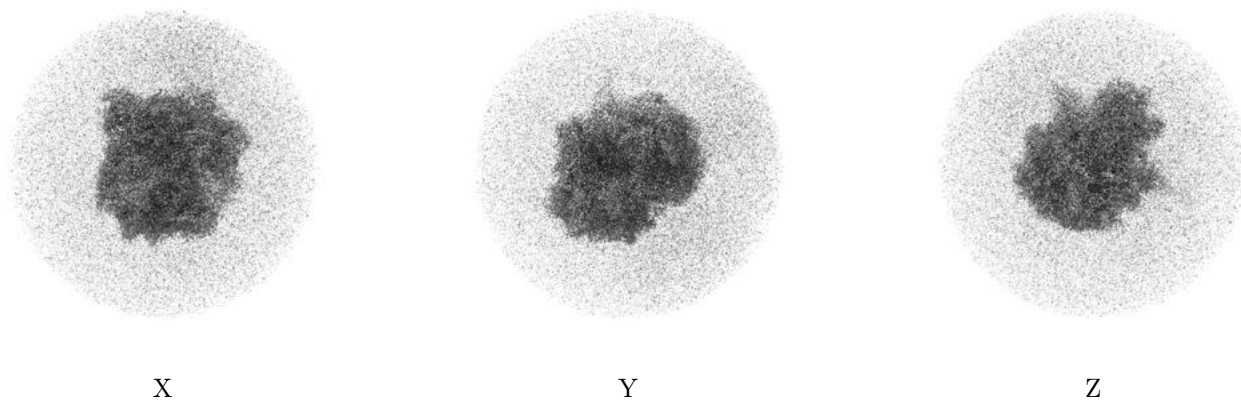
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.7. 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.

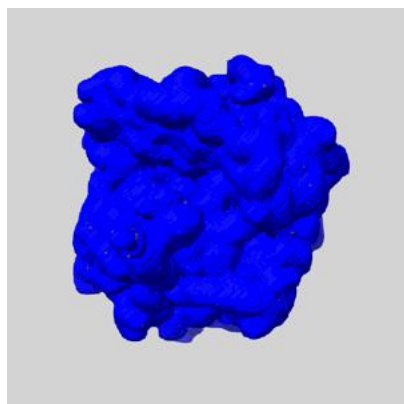
## 6.6 Mask visualisation [i](#)

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

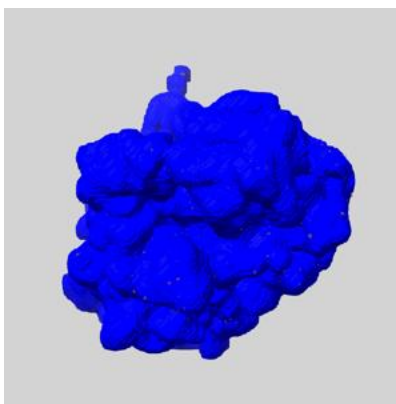
A mask typically either:

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

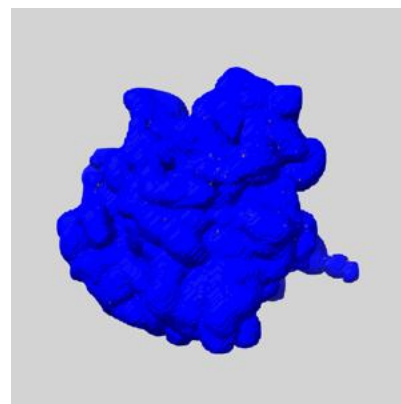
### 6.6.1 emd\_13412\_msk\_1.map [i](#)



X



Y

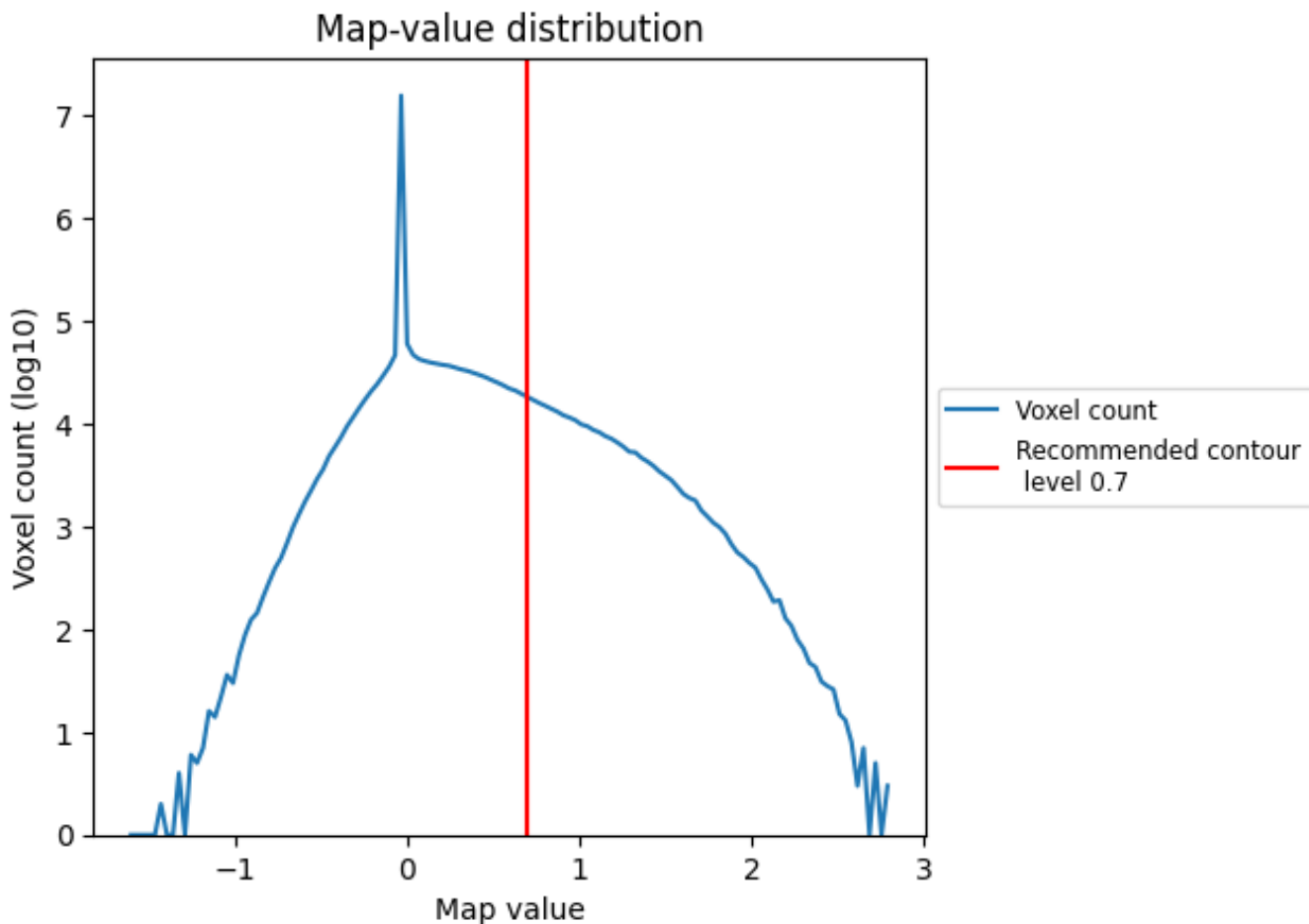


Z

## 7 Map analysis [i](#)

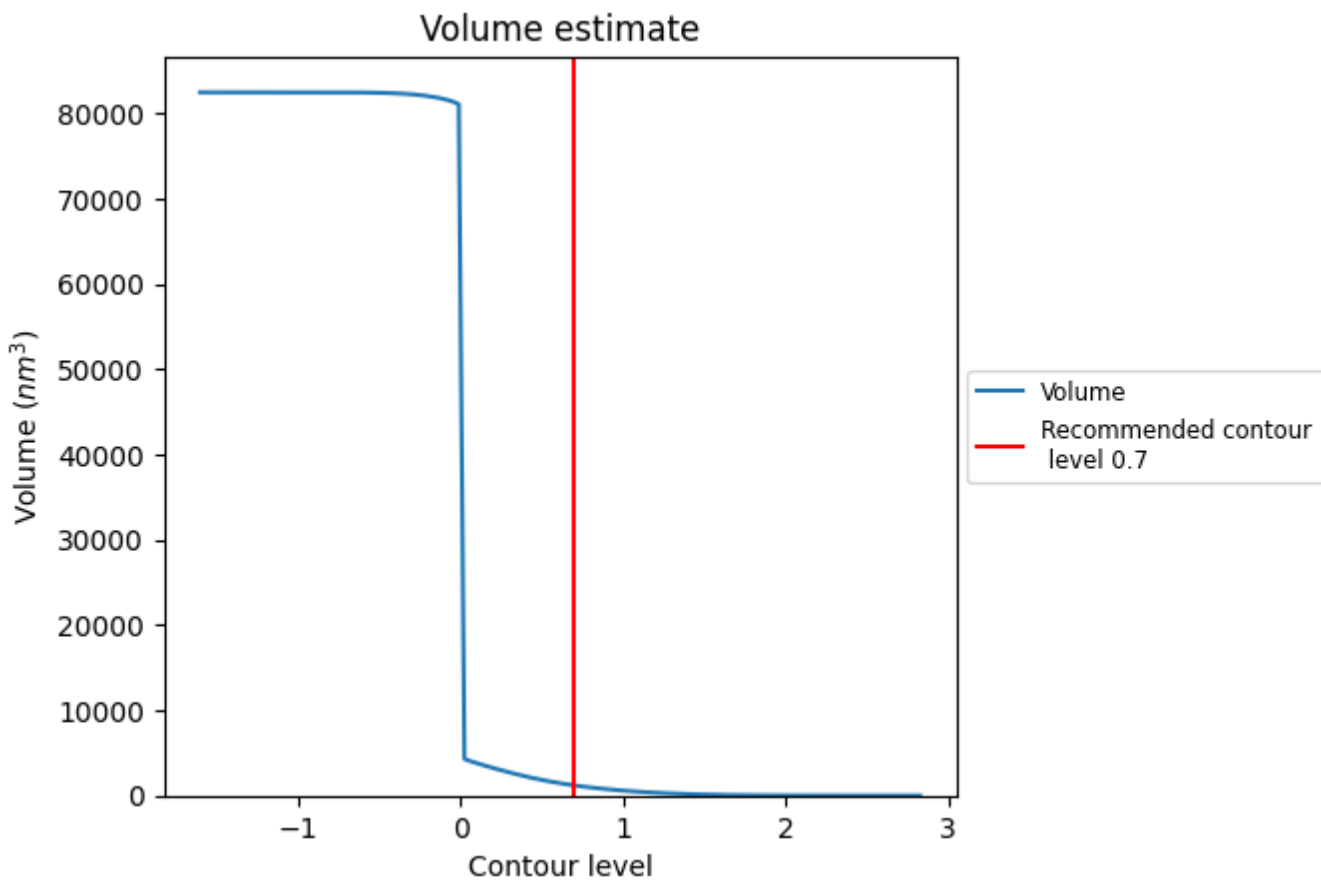
This section contains the results of statistical analysis of the map.

### 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.

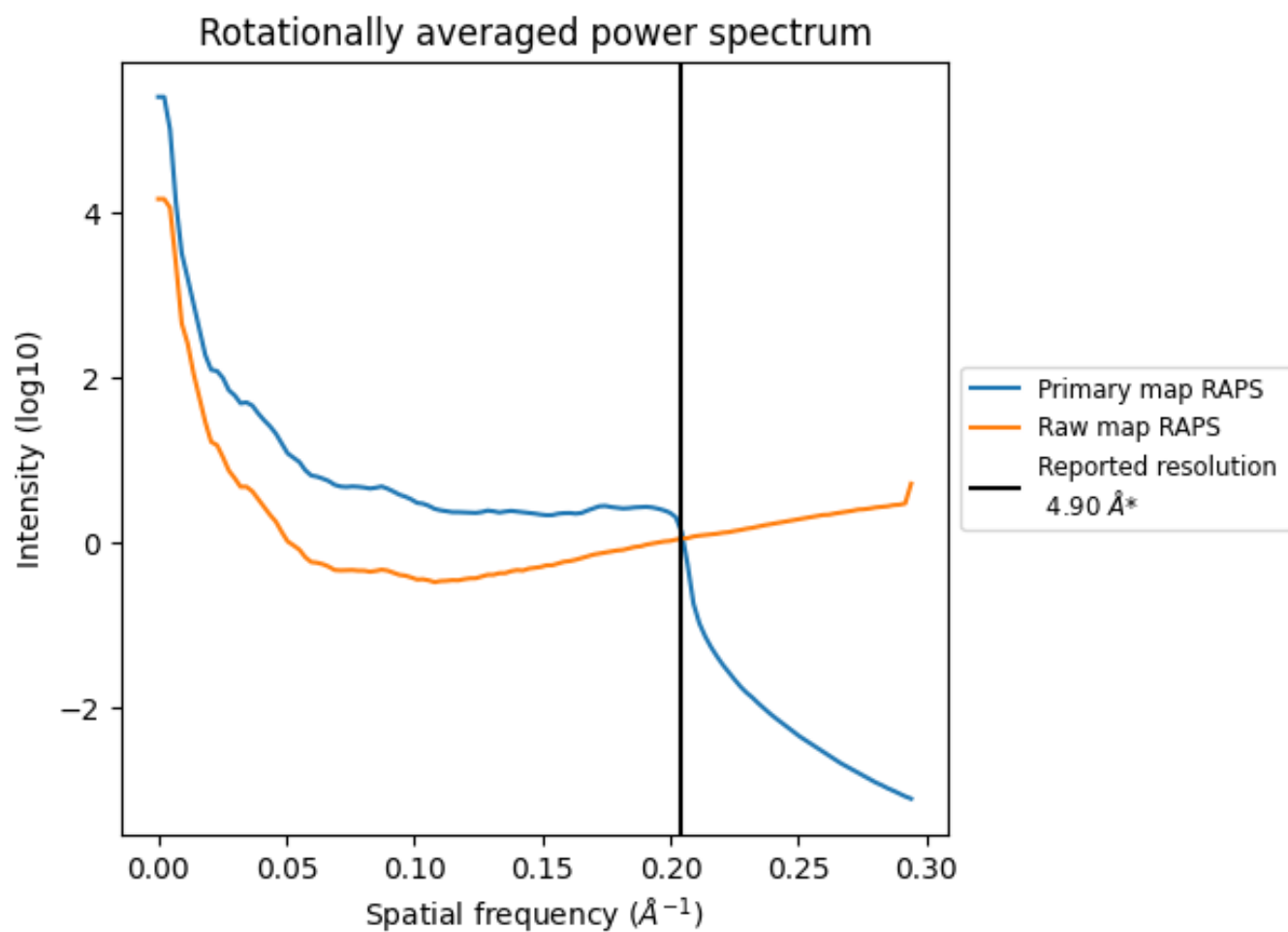
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1192 nm<sup>3</sup>; this corresponds to an approximate mass of 1076 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

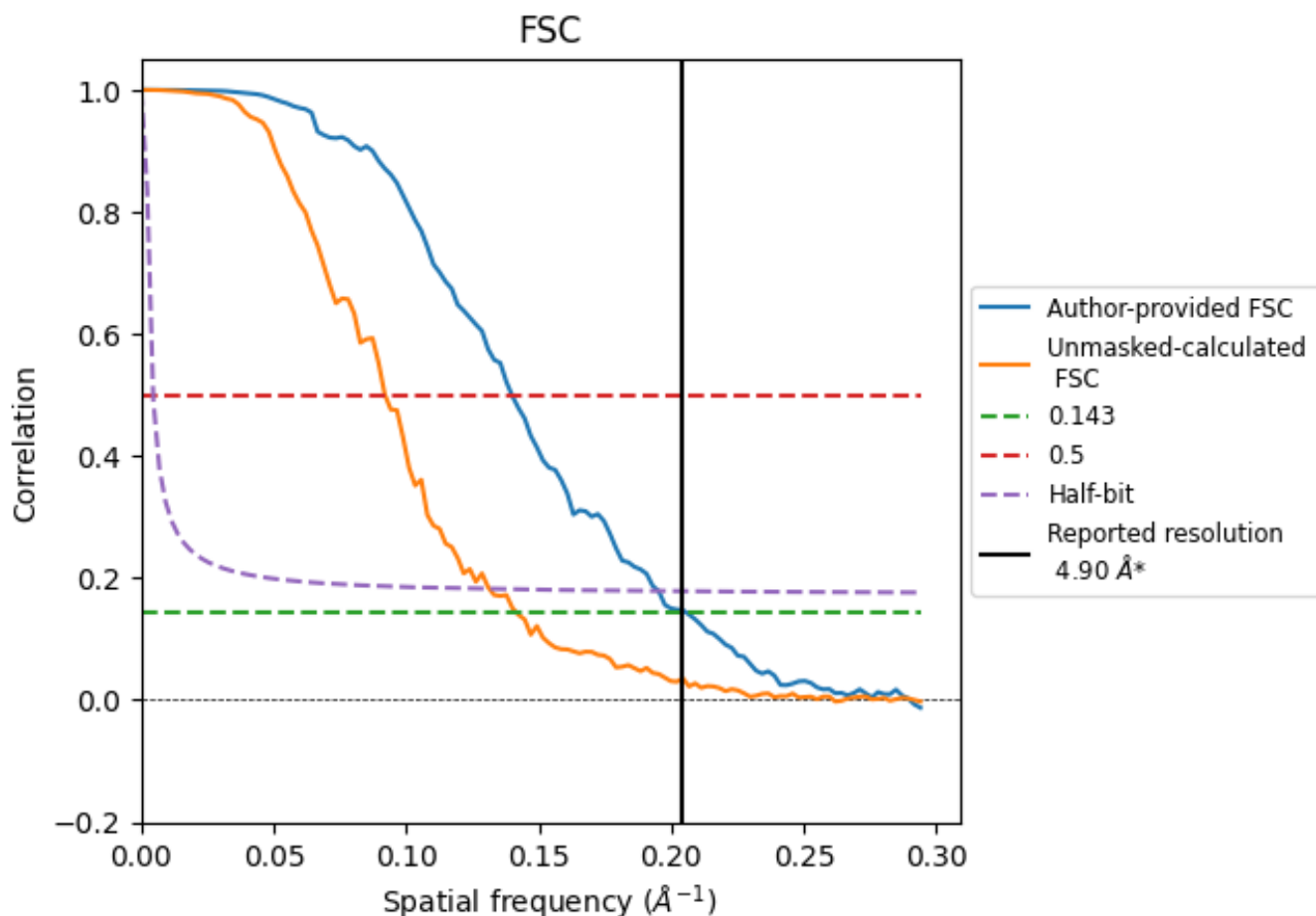


\*Reported resolution corresponds to spatial frequency of 0.204 Å<sup>-1</sup>

## 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 0.204 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

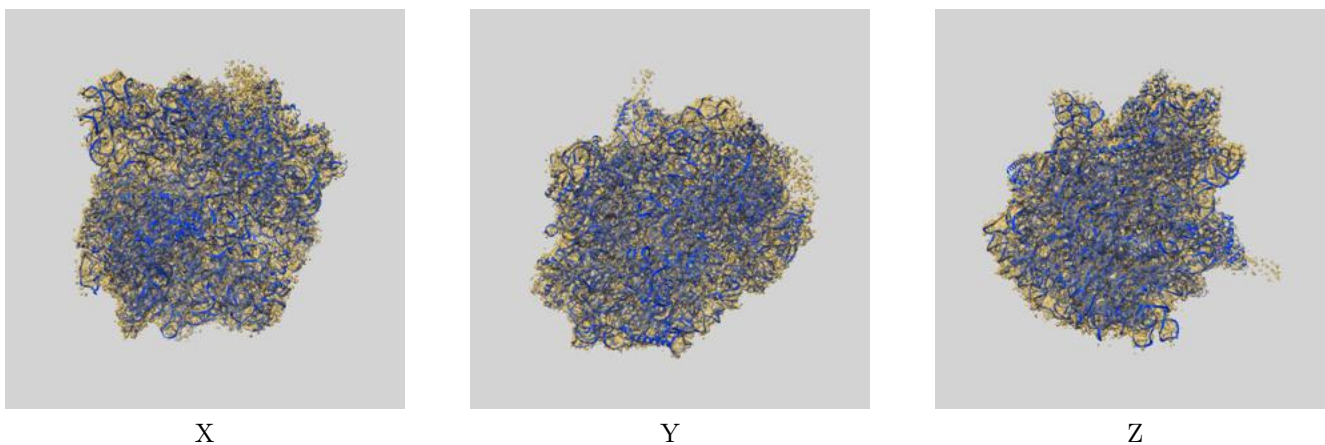
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.90	-	-
Author-provided FSC curve	4.86	7.15	5.12
Unmasked-calculated*	7.06	10.87	7.60

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.06 differs from the reported value 4.9 by more than 10 %

## 9 Map-model fit [i](#)

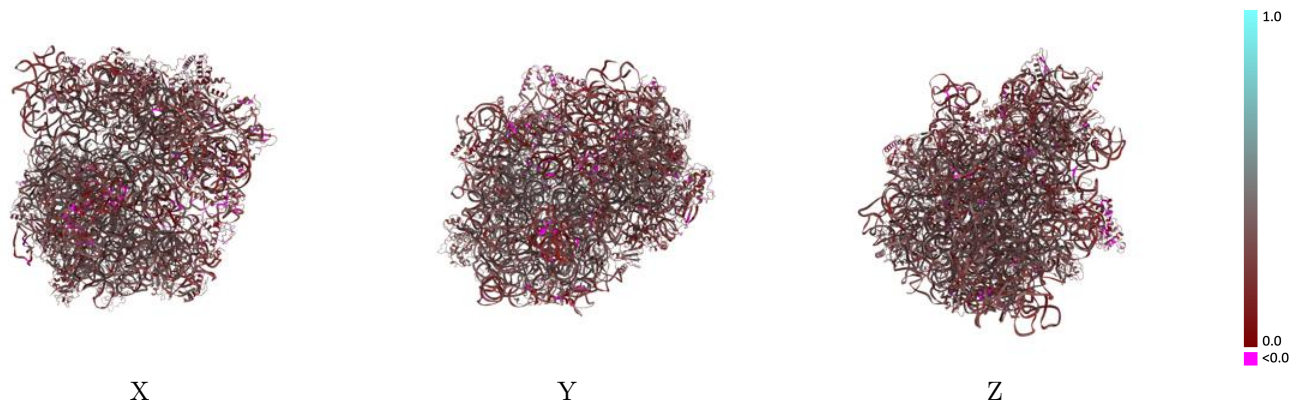
This section contains information regarding the fit between EMDB map EMD-13412 and PDB model 7PHB. Per-residue inclusion information can be found in section 3 on page 15.

### 9.1 Map-model overlay [i](#)



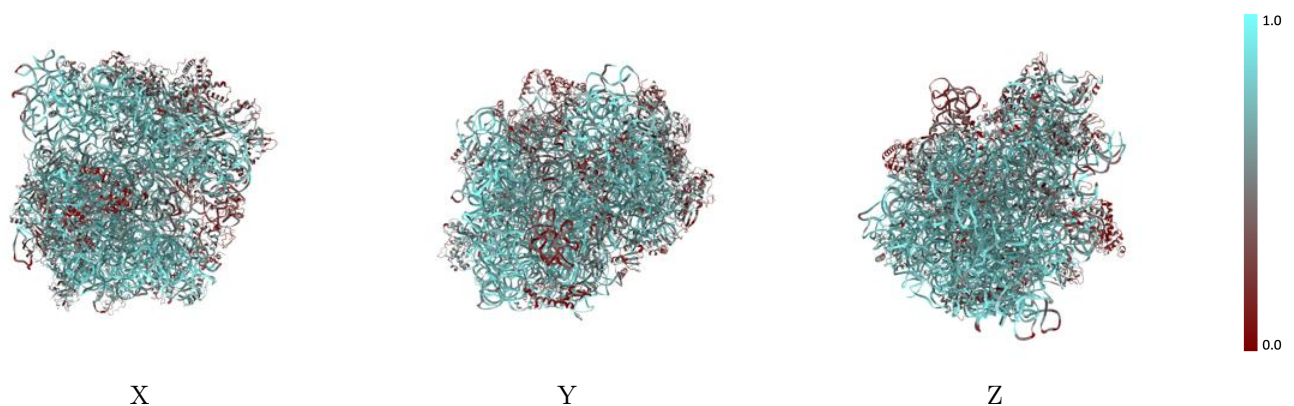
The images above show the 3D surface view of the map at the recommended contour level 0.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



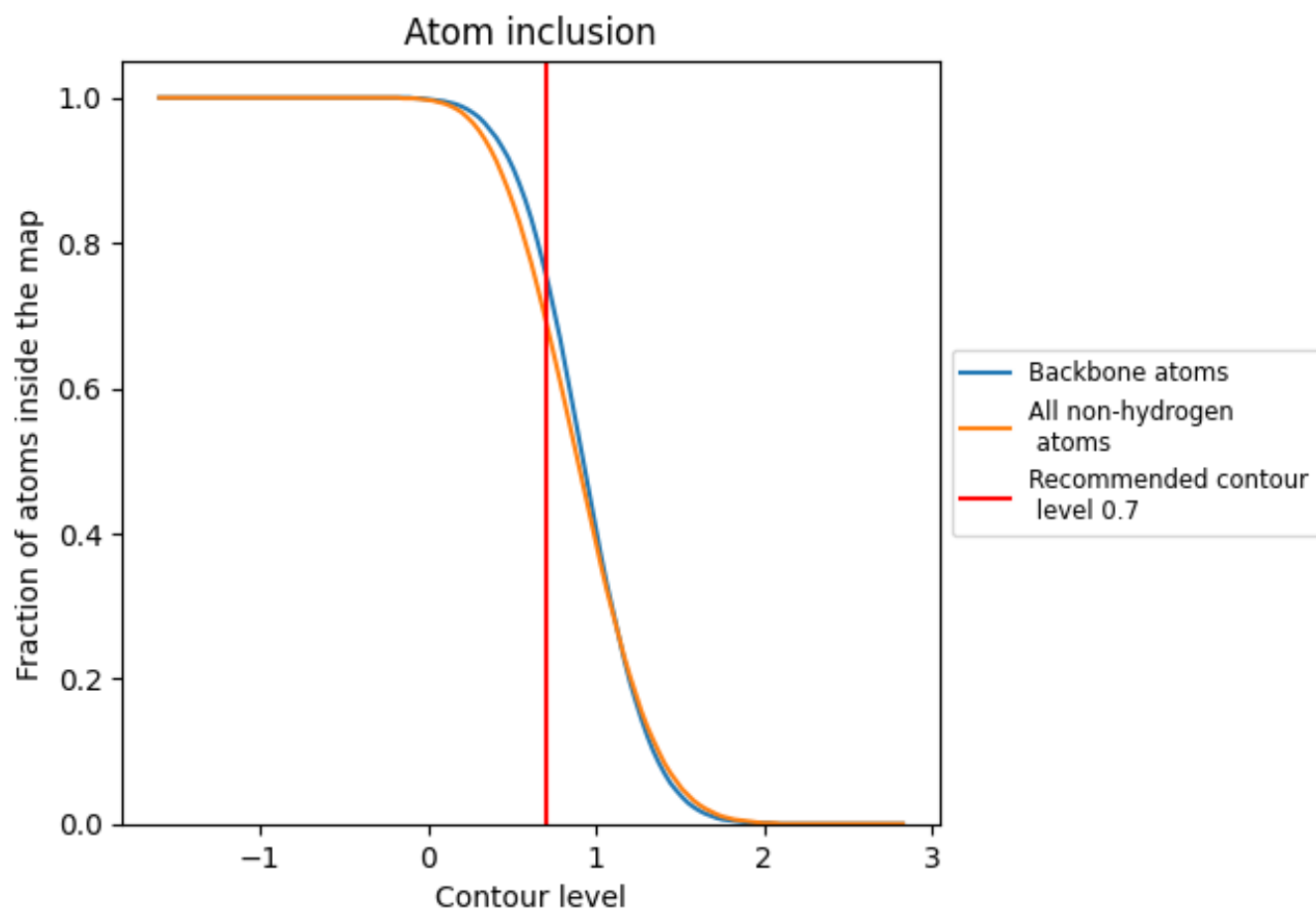
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.7).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 69% 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 (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6930	 0.2970
0	 0.6710	 0.3510
1	 0.6460	 0.3330
2	 0.6550	 0.3400
3	 0.8070	 0.3080
4	 0.7660	 0.2840
5	 0.7860	 0.2890
6	 0.6450	 0.2580
7	 0.5340	 0.1350
A	 0.4020	 0.2670
B	 0.4540	 0.2930
C	 0.4390	 0.2770
D	 0.4950	 0.3030
E	 0.3330	 0.2720
F	 0.3780	 0.2420
G	 0.4480	 0.2670
H	 0.4150	 0.2730
I	 0.3890	 0.2680
J	 0.4590	 0.2930
K	 0.5490	 0.3310
L	 0.4120	 0.2730
M	 0.4990	 0.2860
N	 0.4670	 0.2640
O	 0.5150	 0.2760
P	 0.4340	 0.2850
Q	 0.5120	 0.2710
R	 0.4130	 0.2480
S	 0.5560	 0.2660
T	 0.4350	 0.2730
Y	 0.8640	 0.3470
Z	 0.8800	 0.4790
a	 0.6150	 0.3320
b	 0.5810	 0.3240
c	 0.5610	 0.3290
d	 0.3600	 0.2420



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Chain	Atom inclusion	Q-score
e	 0.4400	 0.3080
f	 0.1410	 0.2150
g	 0.2020	 0.2110
h	 0.1250	 0.2030
i	 0.5770	 0.3220
j	 0.5690	 0.3440
k	 0.5730	 0.3430
l	 0.6000	 0.3290
m	 0.6350	 0.3220
n	 0.5580	 0.2840
o	 0.5460	 0.3320
p	 0.5870	 0.2830
q	 0.5730	 0.3410
r	 0.6030	 0.3380
s	 0.5710	 0.3240
t	 0.4120	 0.3200
u	 0.5830	 0.3290
v	 0.6080	 0.3440
w	 0.4930	 0.2840
x	 0.2830	 0.2270
y	 0.6340	 0.3500
z	 0.5590	 0.3290