



wwPDB EM Validation Summary Report ⓘ

Mar 13, 2024 – 01:52 PM JST

PDB ID : 3JBU
EMDB ID : EMD-6483
Title : Mechanisms of Ribosome Stalling by SecM at Multiple Elongation Steps
Authors : Zhang, J.; Pan, X.J.; Yan, K.G.; Sun, S.; Gao, N.; Sui, S.F.
Deposited on : 2015-10-16
Resolution : 3.64 Å (reported)
Based on initial model : 4V7T

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.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

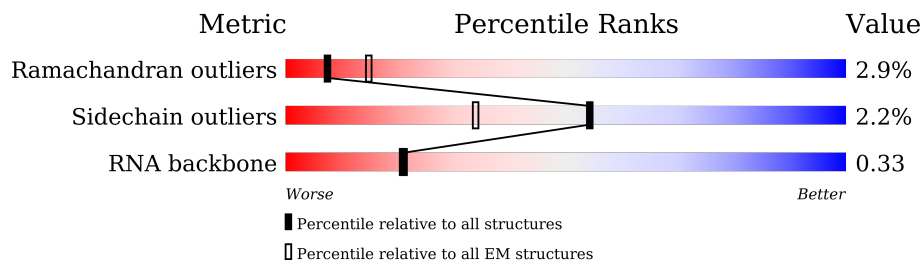
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.64 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	B	241	 85% 87% 10% .
2	C	233	 81% 85% 12% .
3	D	206	 87% 97% .
4	E	167	 65% 87% 10% .
5	F	131	 31% 73% 24% .
6	G	156	 58% 93% . .
7	H	130	 76% 96% . .
8	I	130	 80% 92% 5% .

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Mol	Chain	Length	Quality of chain
9	J	103	85% 87% 8% 5%
10	K	129	33% 90% 9%
11	L	124	39% 94% 5%
12	M	118	56% 94% . .
13	N	101	81% 88% 7% 5%
14	O	89	28% 97% ..
15	P	82	67% 79% 21%
16	Q	84	52% 93% . 5%
17	R	75	37% 73% 27%
18	S	92	54% 84% . 14%
19	T	87	41% 95% ..
20	U	71	51% 66% 6% 28%
21	0	78	5% 95% ..
22	1	63	30% 92% 6% .
23	2	59	. 93% 5% .
24	3	57	19% 93% 5% .
25	4	55	15% 87% . 9%
26	6	46	7% 89% 11%
27	7	65	. 95% ..
28	8	38	8% 100%
29	c	273	5% 96% ..
30	d	209	11% 95% .
31	e	201	22% 94% 5%
32	f	179	26% 92% 6% ..
33	g	177	36% 95% ...

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Mol	Chain	Length	Quality of chain
34	h	149	74% 90% 10%
35	j	142	8% 96% •
36	k	123	16% 94% 5% •
37	l	144	16% 94% 6%
38	m	136	9% 98% ••
39	n	127	9% 91% •• 6%
40	o	117	25% 92% 7% •
41	p	115	18% 95% ••
42	q	118	8% 97% ••
43	r	103	23% 94% 6%
44	s	110	9% 95% 5%
45	t	100	18% 89% • 7%
46	u	104	33% 89% 8% ••
47	w	94	17% 96% •
48	y	85	5% 88% 12%
49	z	87	24% 14% 16% 70%
50	A	1542	15% 70% 29% •
51	X	11	55% 27% 36% 36%
52	a	120	• 62% 34% ••
53	b	2904	6% 55% 37% 6% •
54	v	76	22% 61% 39%

2 Entry composition [i](#)

There are 54 unique types of molecules in this entry. The entry contains 143334 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 30S ribosomal protein S2.

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

- Molecule 2 is a protein called 30S ribosomal protein S3.

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

- Molecule 3 is a protein called 30S ribosomal protein S4.

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

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	150	1105	687	211	201	6	0	0

- Molecule 5 is a protein called 30S ribosomal protein S6.

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

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	150	1174	730	226	214	4	0	0

- Molecule 7 is a protein called 30S ribosomal protein S8.

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

- Molecule 8 is a protein called 30S ribosomal protein S9.

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

- Molecule 9 is a protein called 30S ribosomal protein S10.

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

- Molecule 10 is a protein called 30S ribosomal protein S11.

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

- Molecule 11 is a protein called 30S ribosomal protein S12.

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

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	M	113	876	541	177	155	3	0	0

- Molecule 13 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	N	96	774	483	160	128	3	0	0

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	O	88	716	440	146	129	1	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	79	ARG	GLN	conflict	UNP P0ADZ4

- Molecule 15 is a protein called 30S ribosomal protein S16.

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

- Molecule 16 is a protein called 30S ribosomal protein S17.

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

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	R	55	455	288	86	81	0	0

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	S	79	637	408	120	107	2	0	0

- Molecule 19 is a protein called 30S ribosomal protein S20.

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

- Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 21 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 23 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 24 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 25 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	4	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 26 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 27 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 28 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 29 is a protein called 50S ribosomal protein L2.

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

- Molecule 30 is a protein called 50S ribosomal protein L3.

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

- Molecule 31 is a protein called 50S ribosomal protein L4.

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

- Molecule 32 is a protein called 50S ribosomal protein L5.

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

- Molecule 33 is a protein called 50S ribosomal protein L6.

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

- Molecule 34 is a protein called 50S ribosomal protein L9.

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

- Molecule 35 is a protein called 50S ribosomal protein L13.

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

- Molecule 36 is a protein called 50S ribosomal protein L14.

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

- Molecule 37 is a protein called 50S ribosomal protein L15.

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

- Molecule 38 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	135	Total	C	N	O	S	0	0
			1063	680	201	176	6		

- Molecule 39 is a protein called 50S ribosomal protein L17.

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

- Molecule 40 is a protein called 50S ribosomal protein L18.

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

- Molecule 41 is a protein called 50S ribosomal protein L19.

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

- Molecule 42 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	q	117	947	604	192	151		0	0

- Molecule 43 is a protein called 50S ribosomal protein L21.

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

- Molecule 44 is a protein called 50S ribosomal protein L22.

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

- Molecule 45 is a protein called 50S ribosomal protein L23.

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

- Molecule 46 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	u	102	779	492	146	141		0	0

- Molecule 47 is a protein called 50S ribosomal protein L25.

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

- Molecule 48 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	y	75	569	353	113	102	1	0	0

- Molecule 49 is a protein called SecM-glycine.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
49	z	26	203	129	33	41	0	0

- Molecule 50 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
50	A	1530	32831	14642	6024	10635	1530	0	0

- Molecule 51 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
51	X	11	232	103	39	79	11	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
52	a	118	2528	1126	464	821	117	0	0

- Molecule 53 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
53	b	2903	62321	27801	11467	20150	2903	0	0

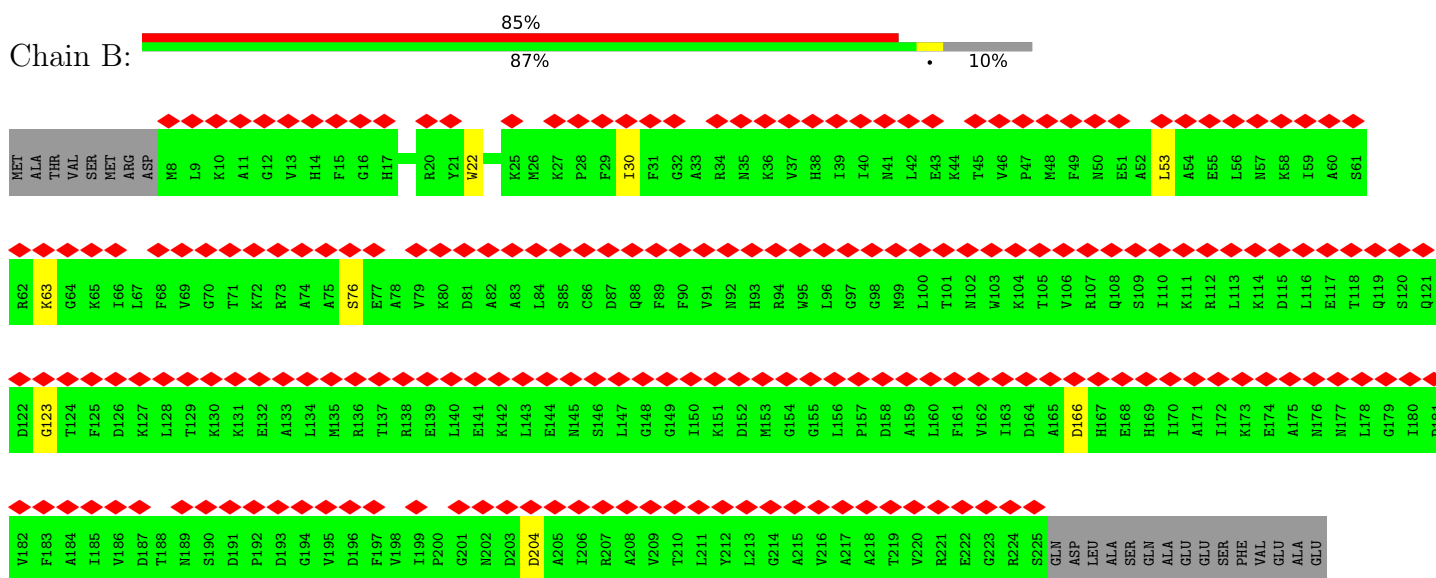
- Molecule 54 is a RNA chain called glycine-tRNA.

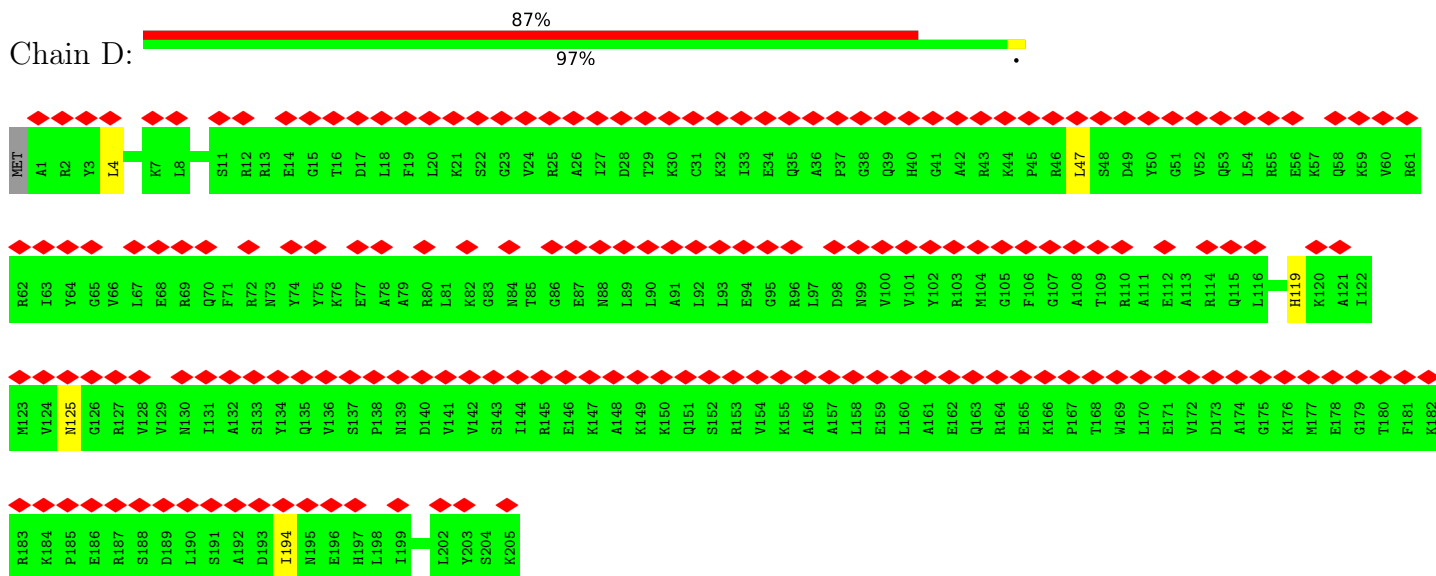
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
54	v	76	1623	722	291	534	76	0	0

3 Residue-property plots

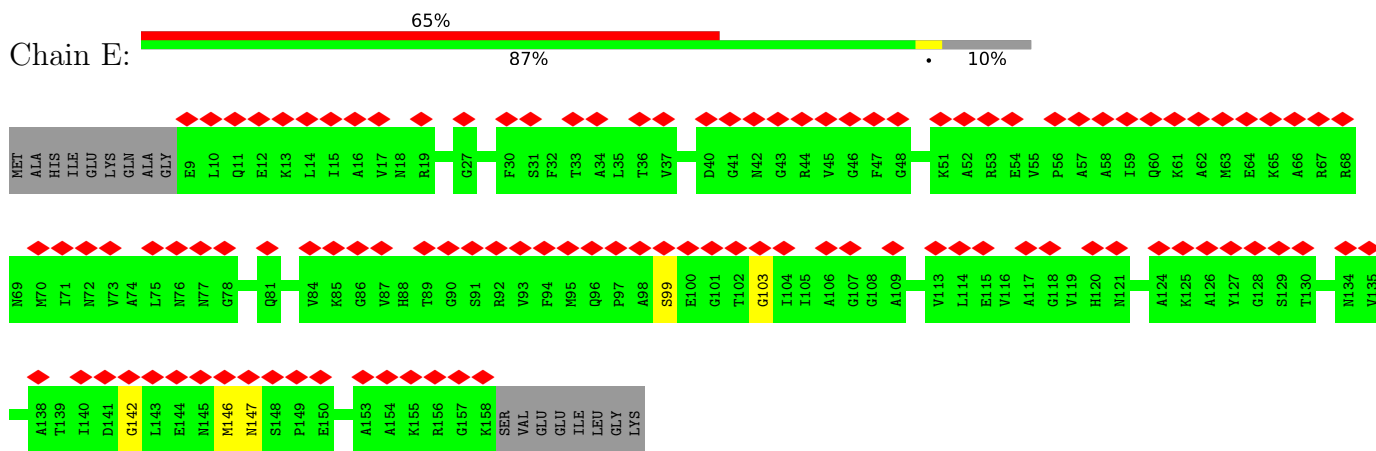
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 30S ribosomal protein S2

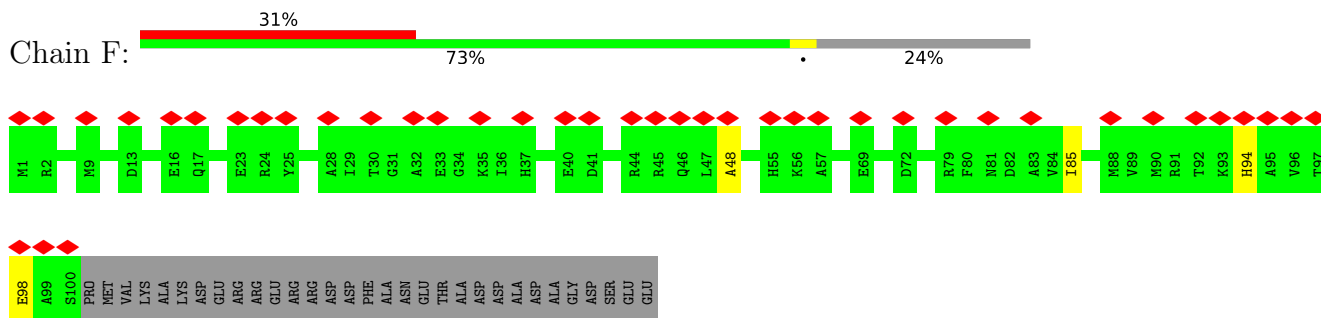




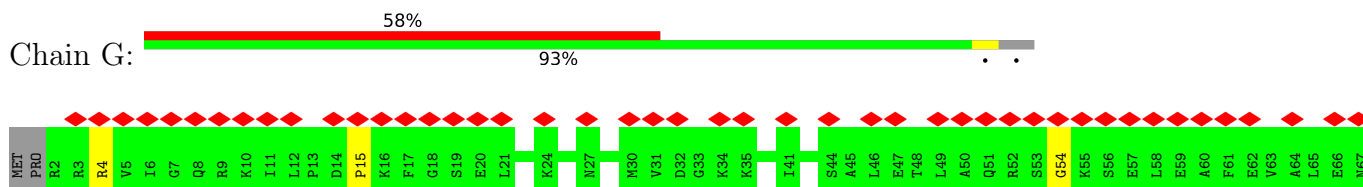
- Molecule 4: 30S ribosomal protein S5

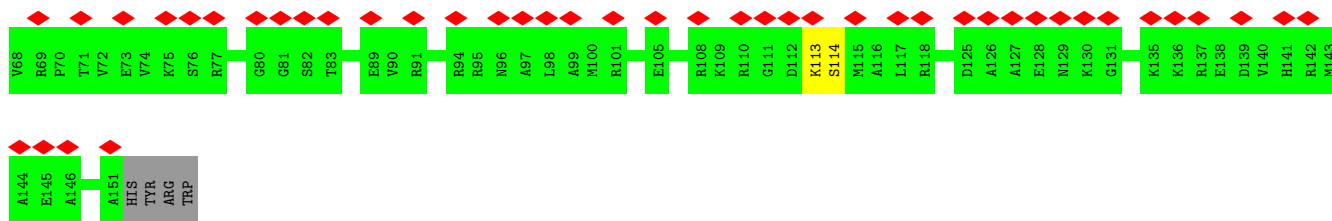


- Molecule 5: 30S ribosomal protein S6

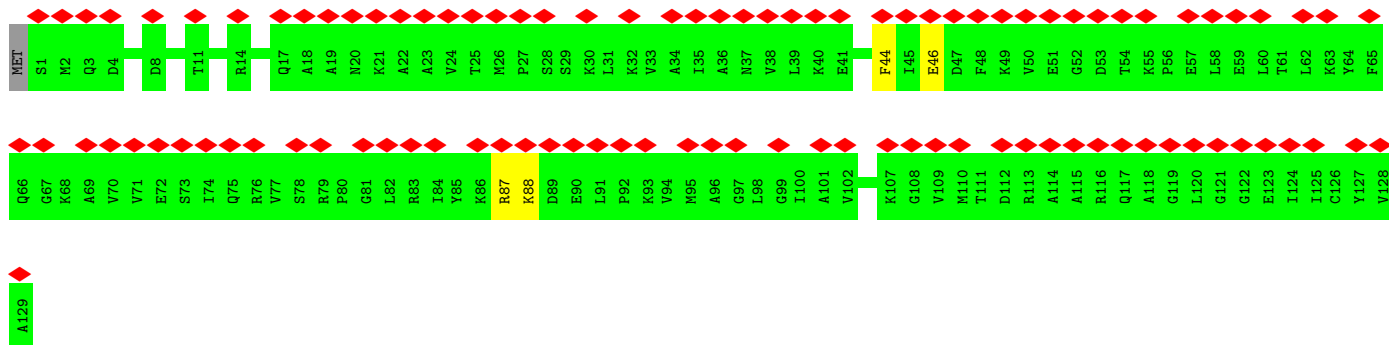
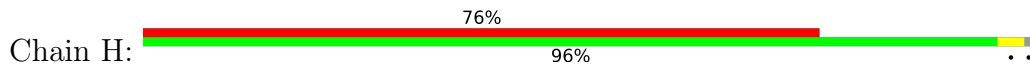


- Molecule 6: 30S ribosomal protein S7

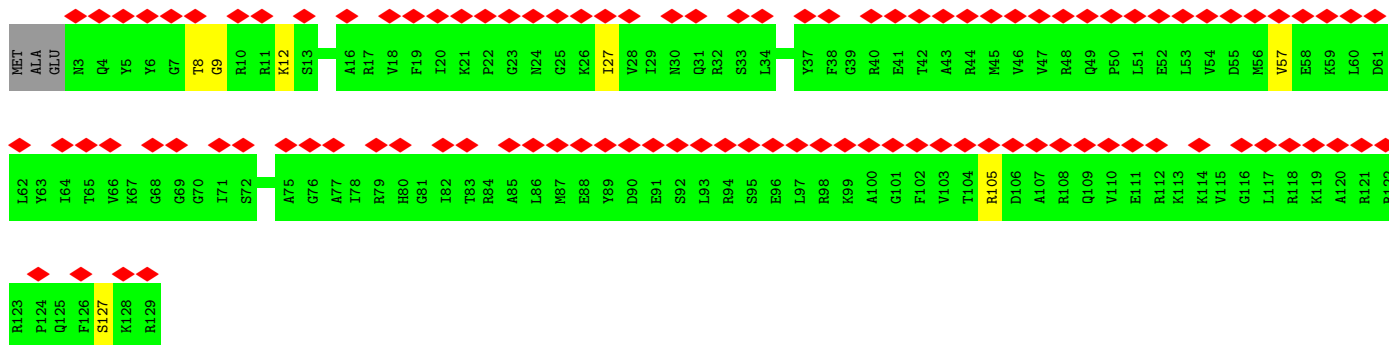
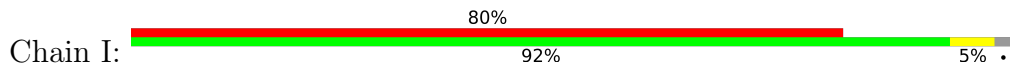




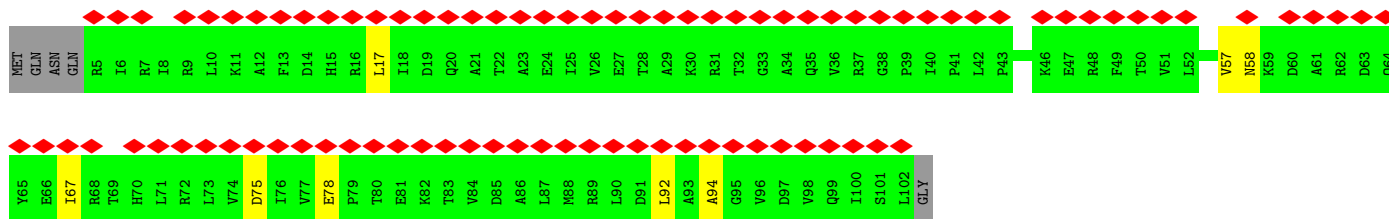
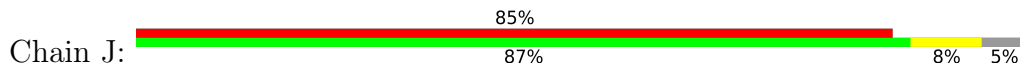
• Molecule 7: 30S ribosomal protein S8



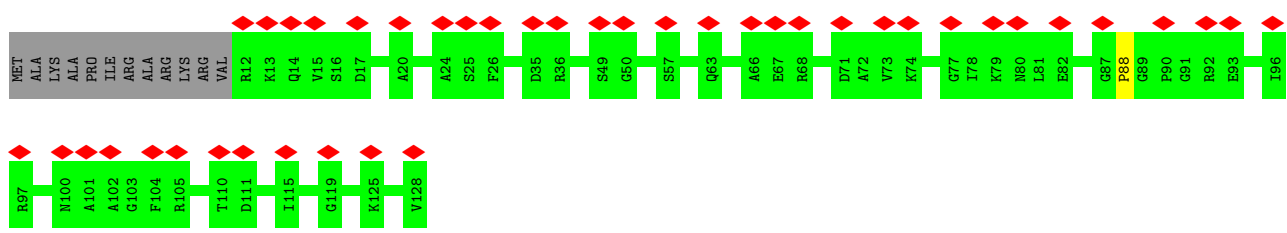
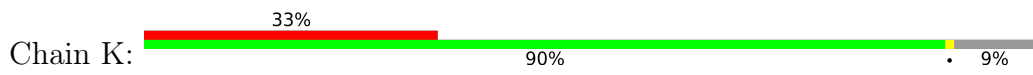
• Molecule 8: 30S ribosomal protein S9



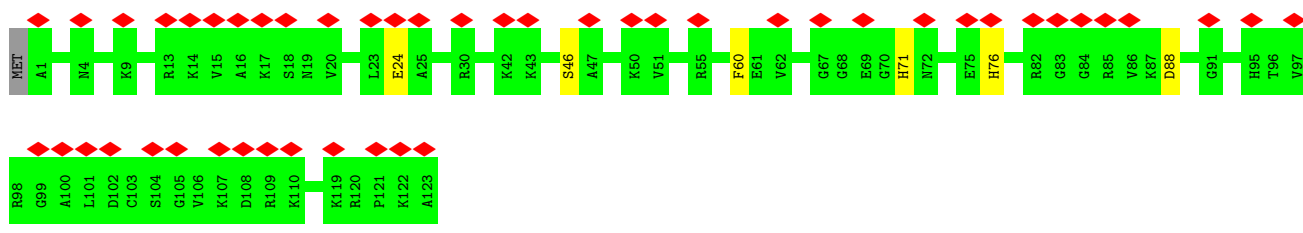
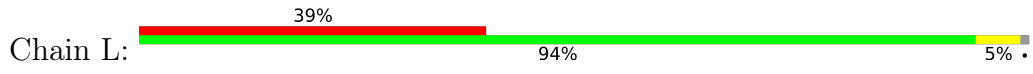
• Molecule 9: 30S ribosomal protein S10



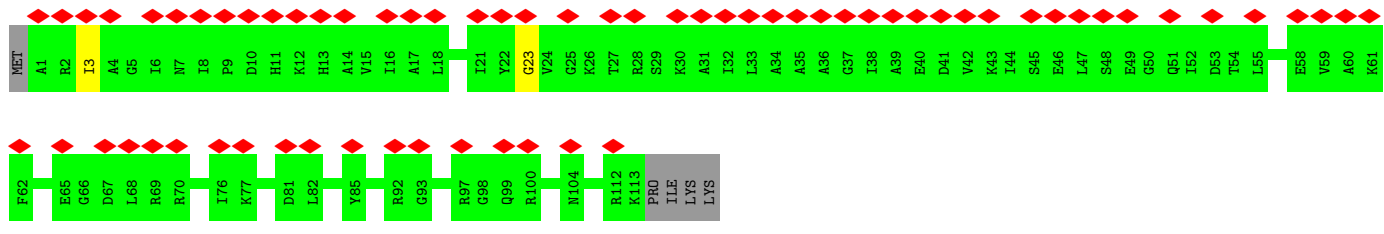
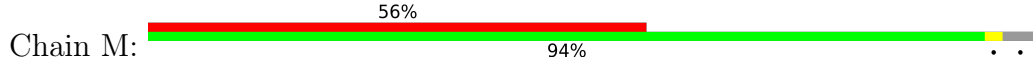
• Molecule 10: 30S ribosomal protein S11



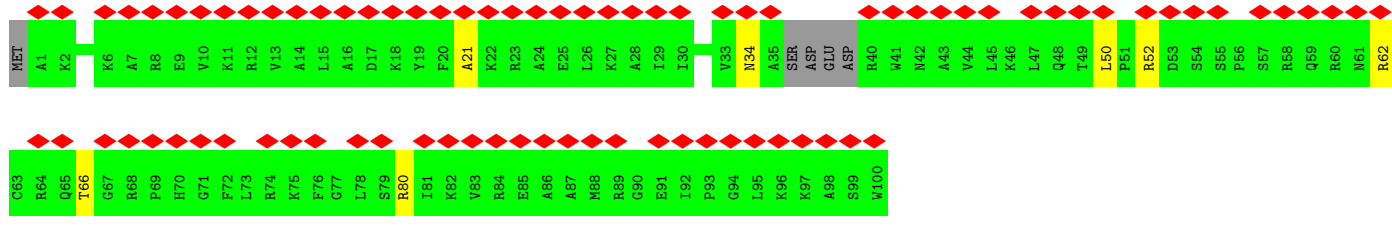
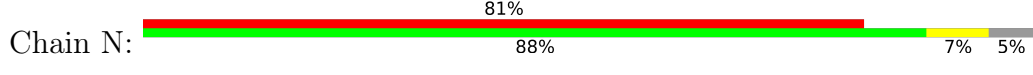
• Molecule 11: 30S ribosomal protein S12



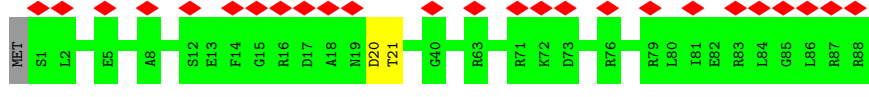
• Molecule 12: 30S ribosomal protein S13



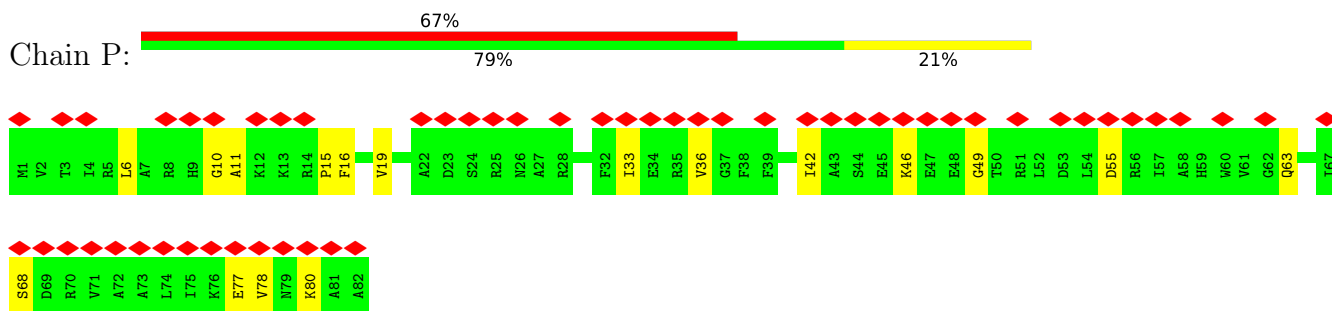
• Molecule 13: 30S ribosomal protein S14



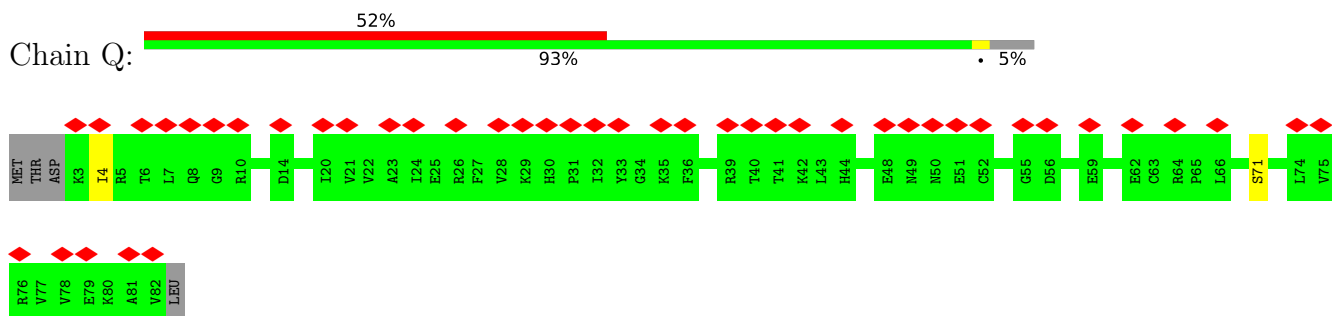
• Molecule 14: 30S ribosomal protein S15



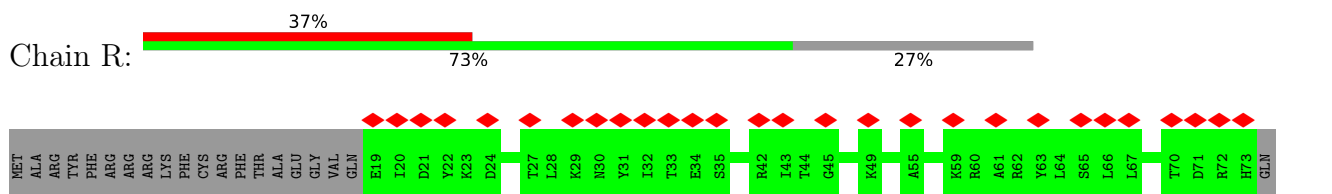
• Molecule 15: 30S ribosomal protein S16



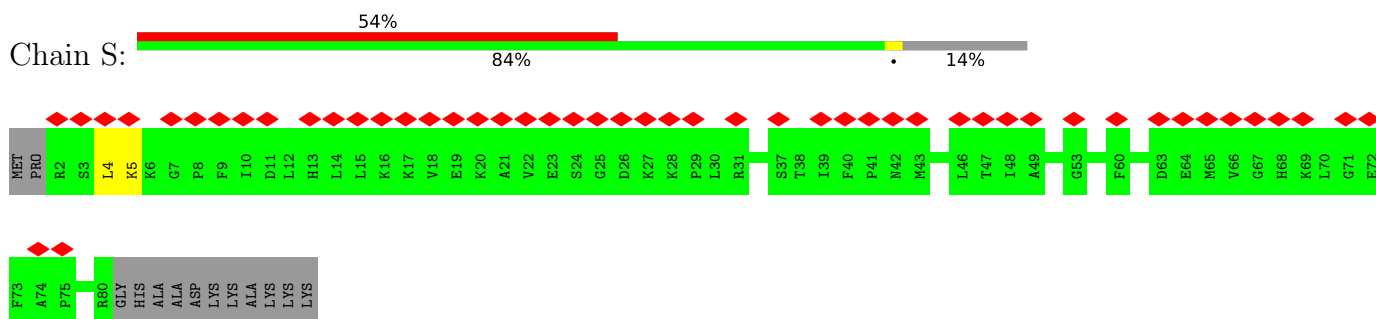
• Molecule 16: 30S ribosomal protein S17



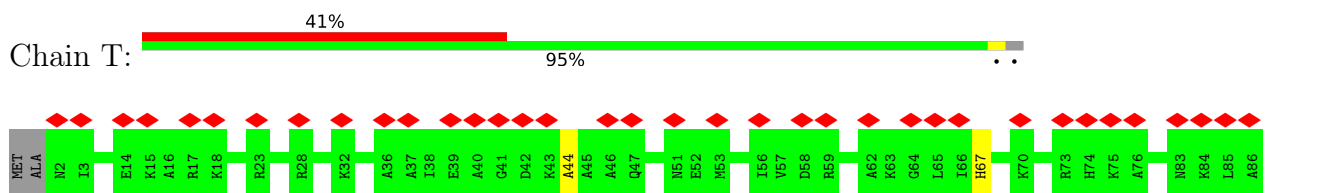
• Molecule 17: 30S ribosomal protein S18



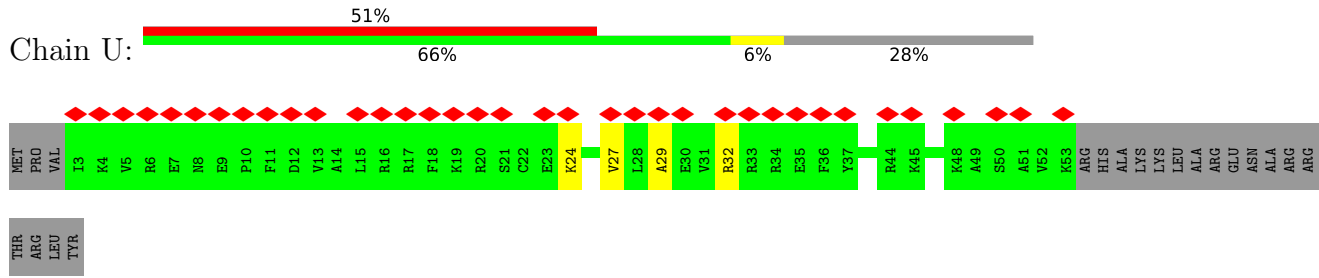
• Molecule 18: 30S ribosomal protein S19



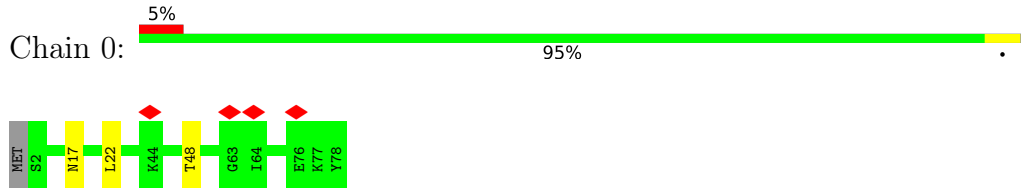
• Molecule 19: 30S ribosomal protein S20



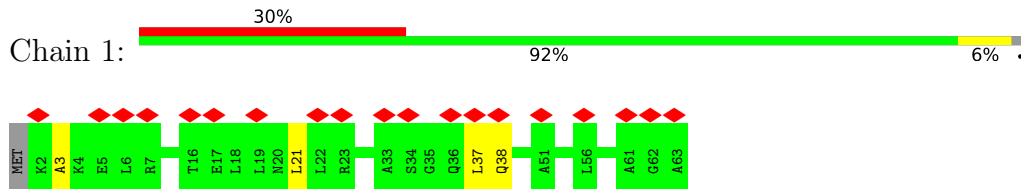
• Molecule 20: 30S ribosomal protein S21



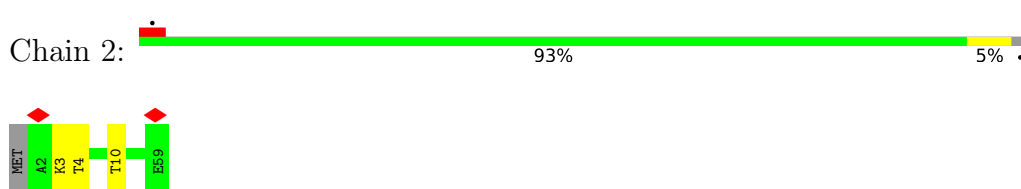
• Molecule 21: 50S ribosomal protein L28



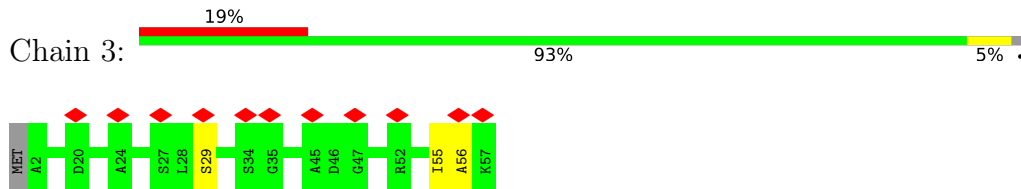
• Molecule 22: 50S ribosomal protein L29



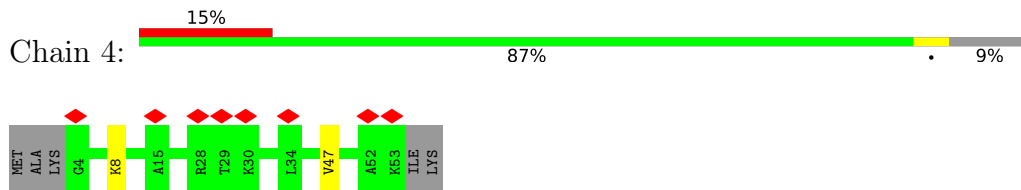
• Molecule 23: 50S ribosomal protein L30



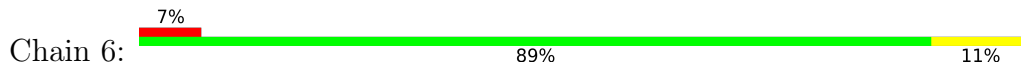
• Molecule 24: 50S ribosomal protein L32

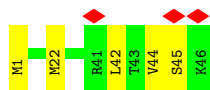


• Molecule 25: 50S ribosomal protein L33

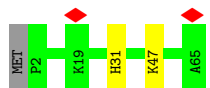


• Molecule 26: 50S ribosomal protein L34

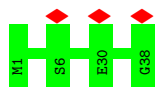




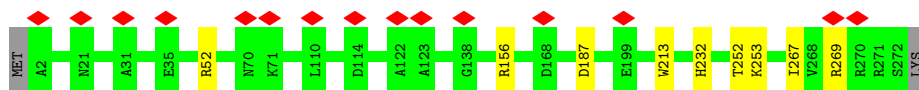
- Molecule 27: 50S ribosomal protein L35



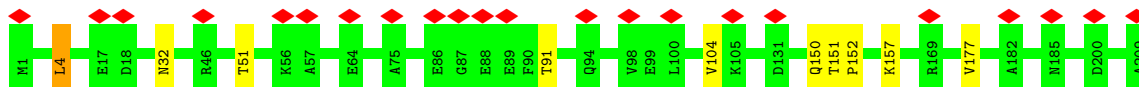
- Molecule 28: 50S ribosomal protein L36



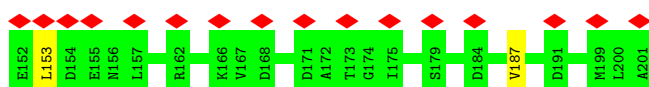
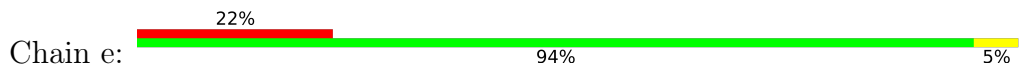
- Molecule 29: 50S ribosomal protein L2



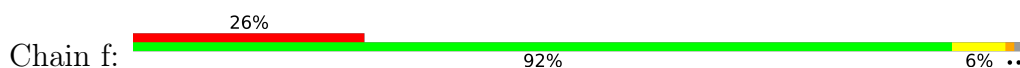
- Molecule 30: 50S ribosomal protein L3

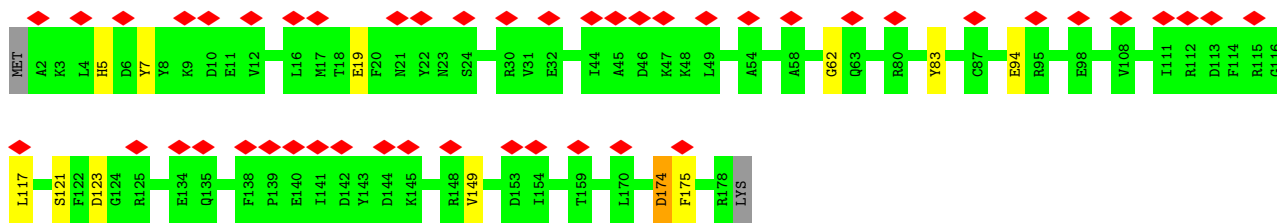


- Molecule 31: 50S ribosomal protein L4

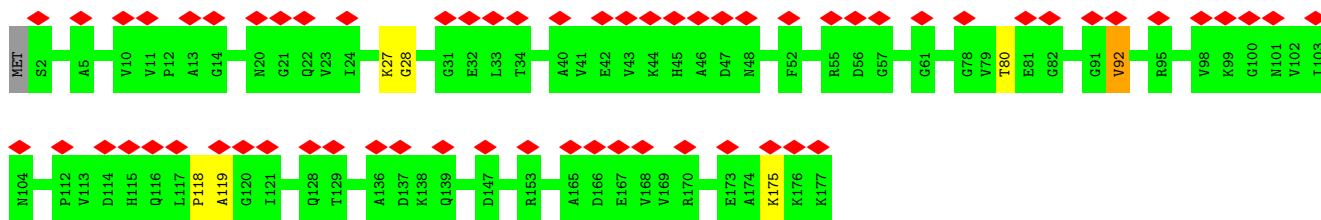


- Molecule 32: 50S ribosomal protein L5

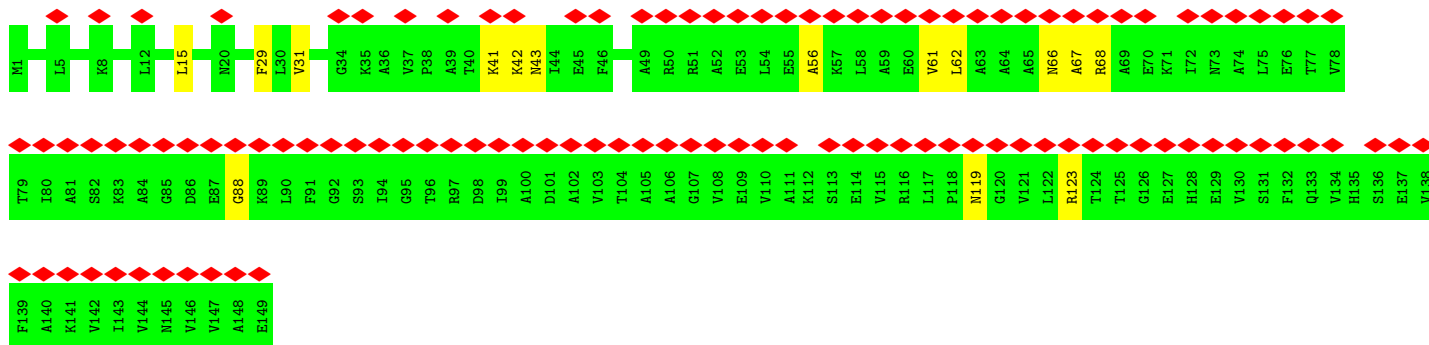
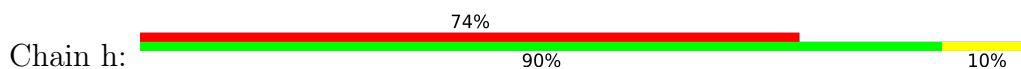




• Molecule 33: 50S ribosomal protein L6



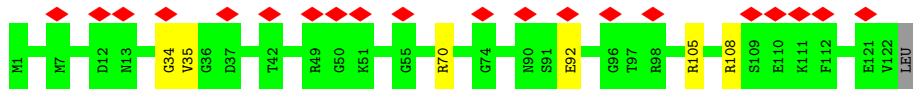
• Molecule 34: 50S ribosomal protein L9



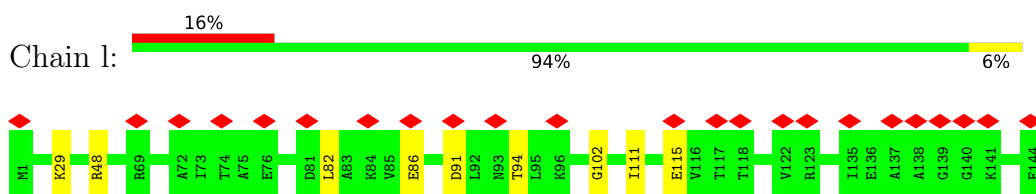
• Molecule 35: 50S ribosomal protein L13



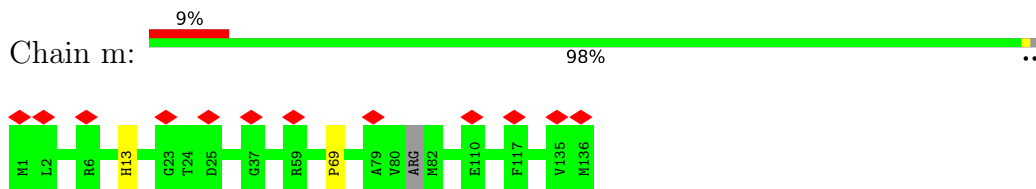
• Molecule 36: 50S ribosomal protein L14



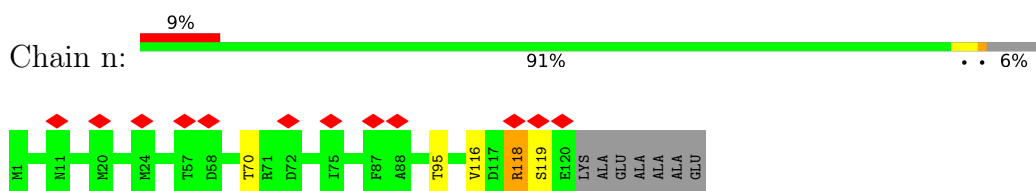
• Molecule 37: 50S ribosomal protein L15



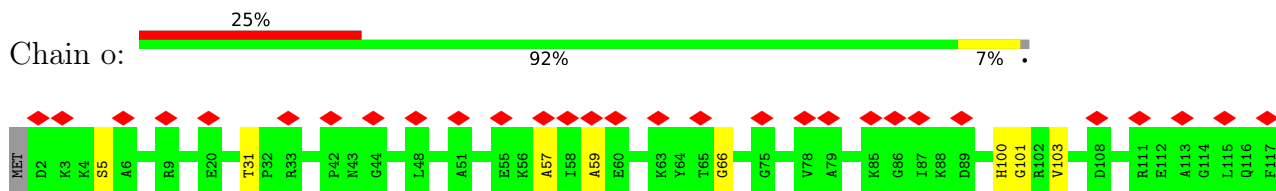
- Molecule 38: 50S ribosomal protein L16



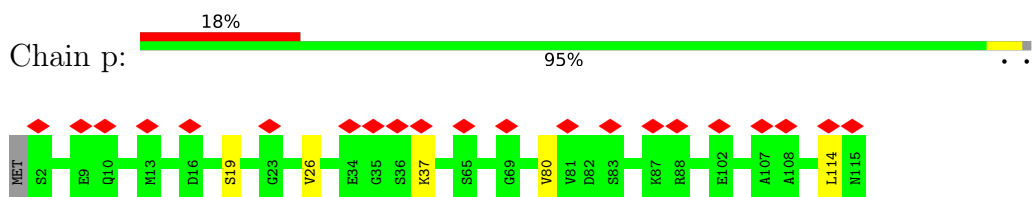
- Molecule 39: 50S ribosomal protein L17



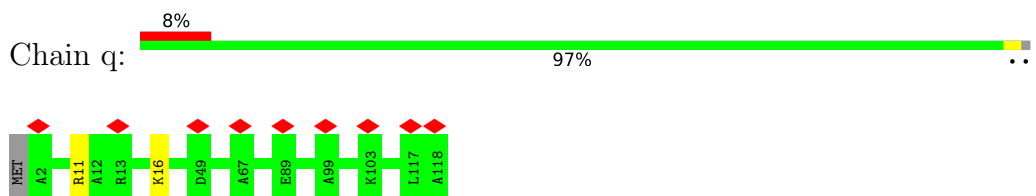
- Molecule 40: 50S ribosomal protein L18



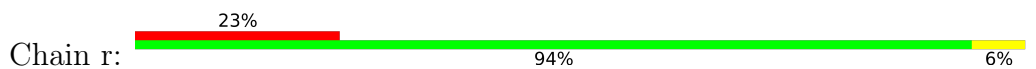
- Molecule 41: 50S ribosomal protein L19

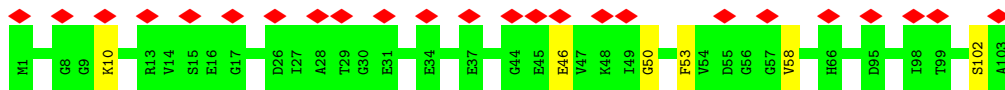


- Molecule 42: 50S ribosomal protein L20

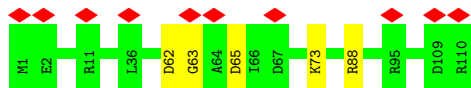


- Molecule 43: 50S ribosomal protein L21

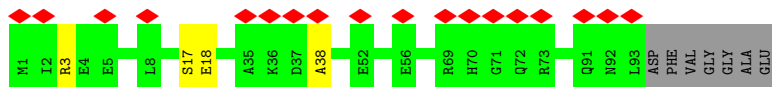
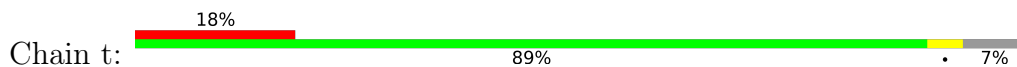




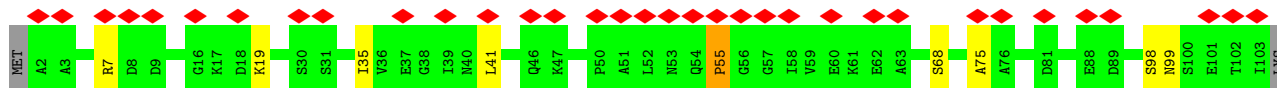
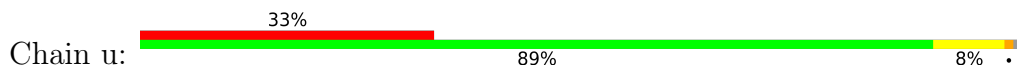
• Molecule 44: 50S ribosomal protein L22



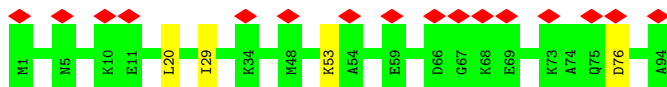
• Molecule 45: 50S ribosomal protein L23



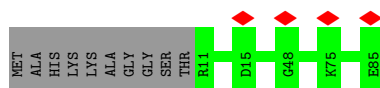
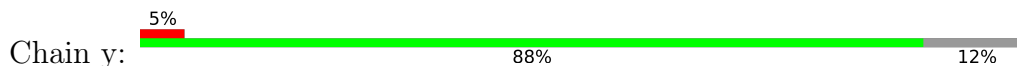
• Molecule 46: 50S ribosomal protein L24



• Molecule 47: 50S ribosomal protein L25

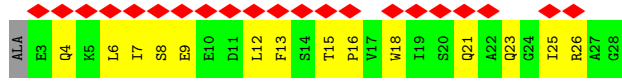


• Molecule 48: 50S ribosomal protein L27

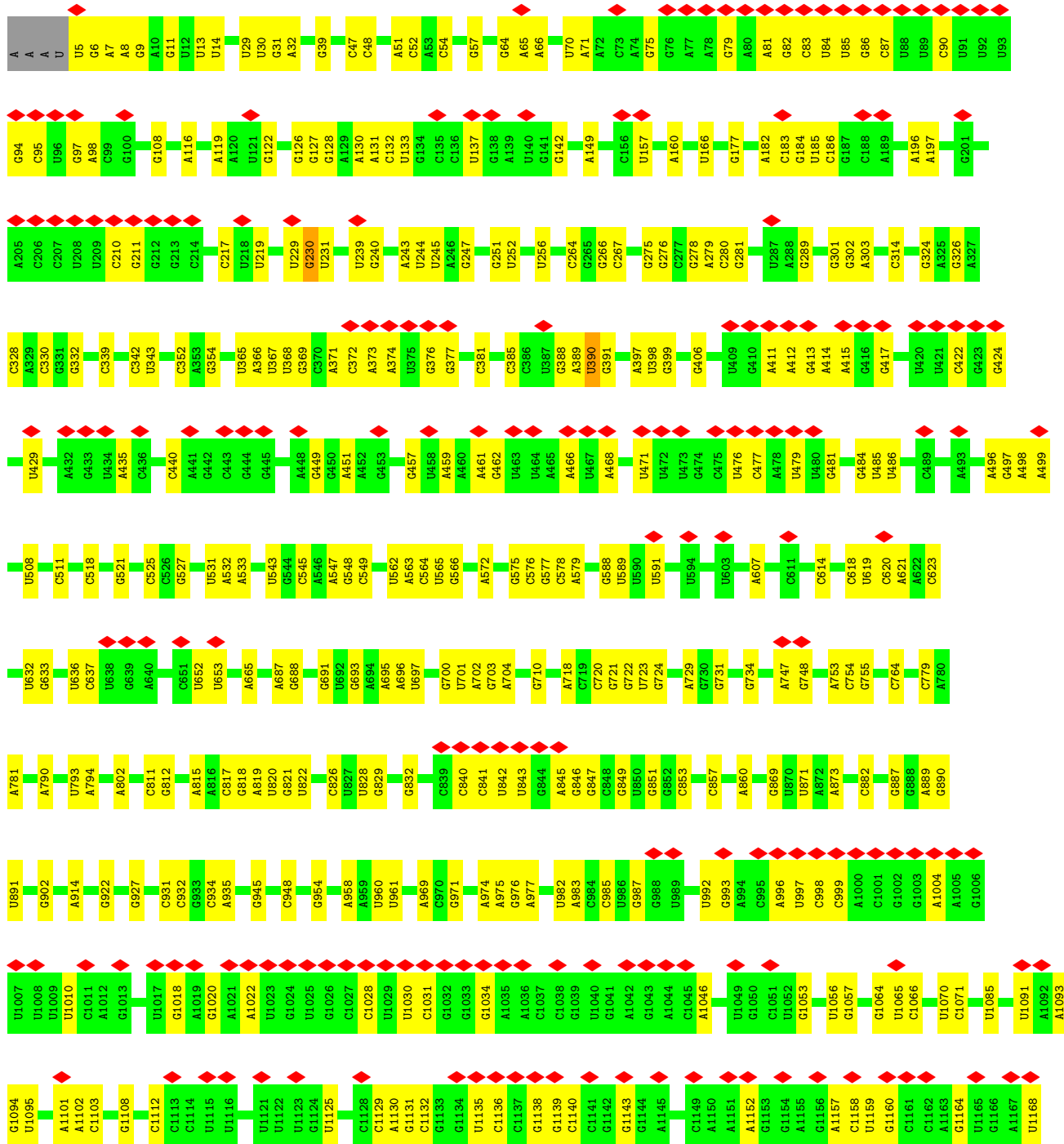


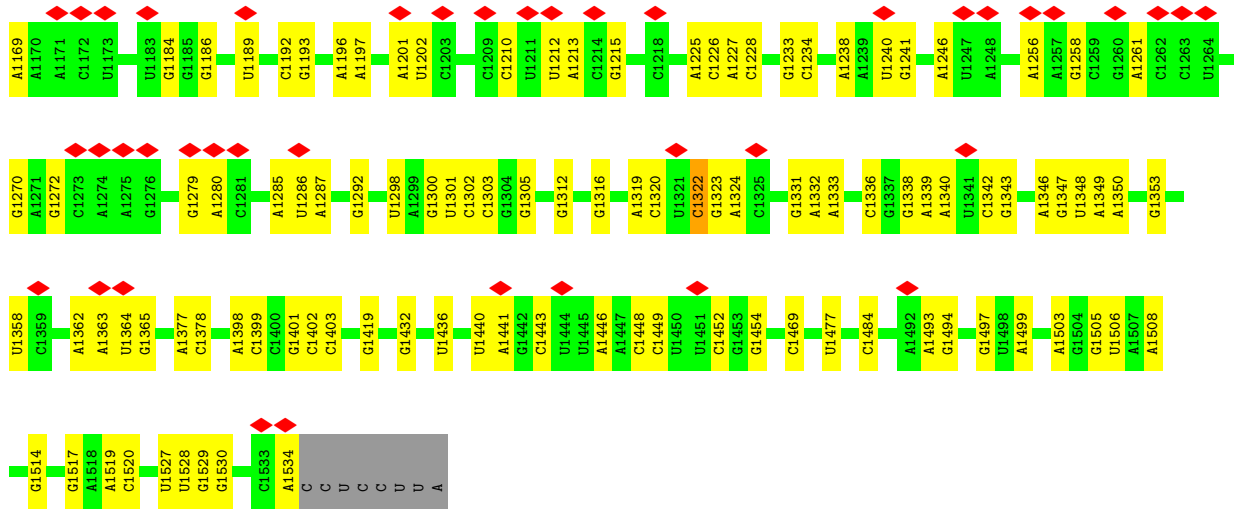
• Molecule 49: SecM-glycine



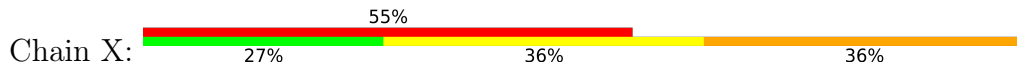


• Molecule 50: 16S rRNA

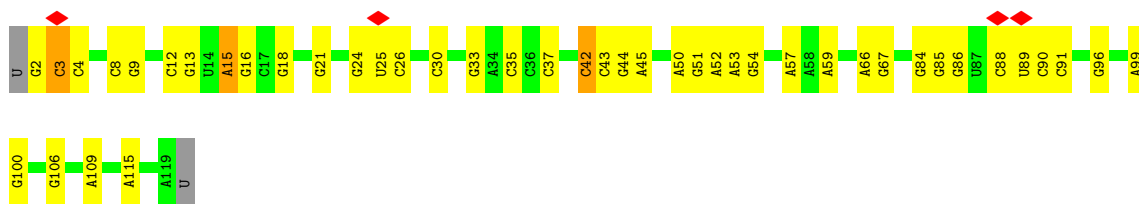




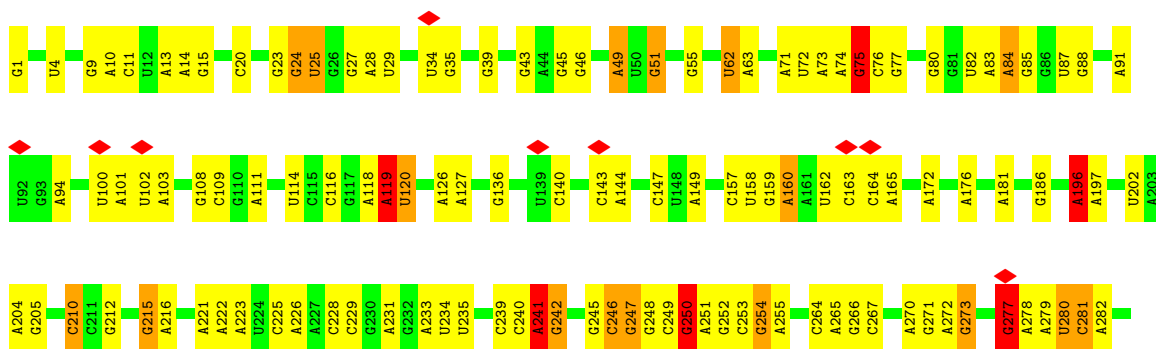
• Molecule 51: mRNA

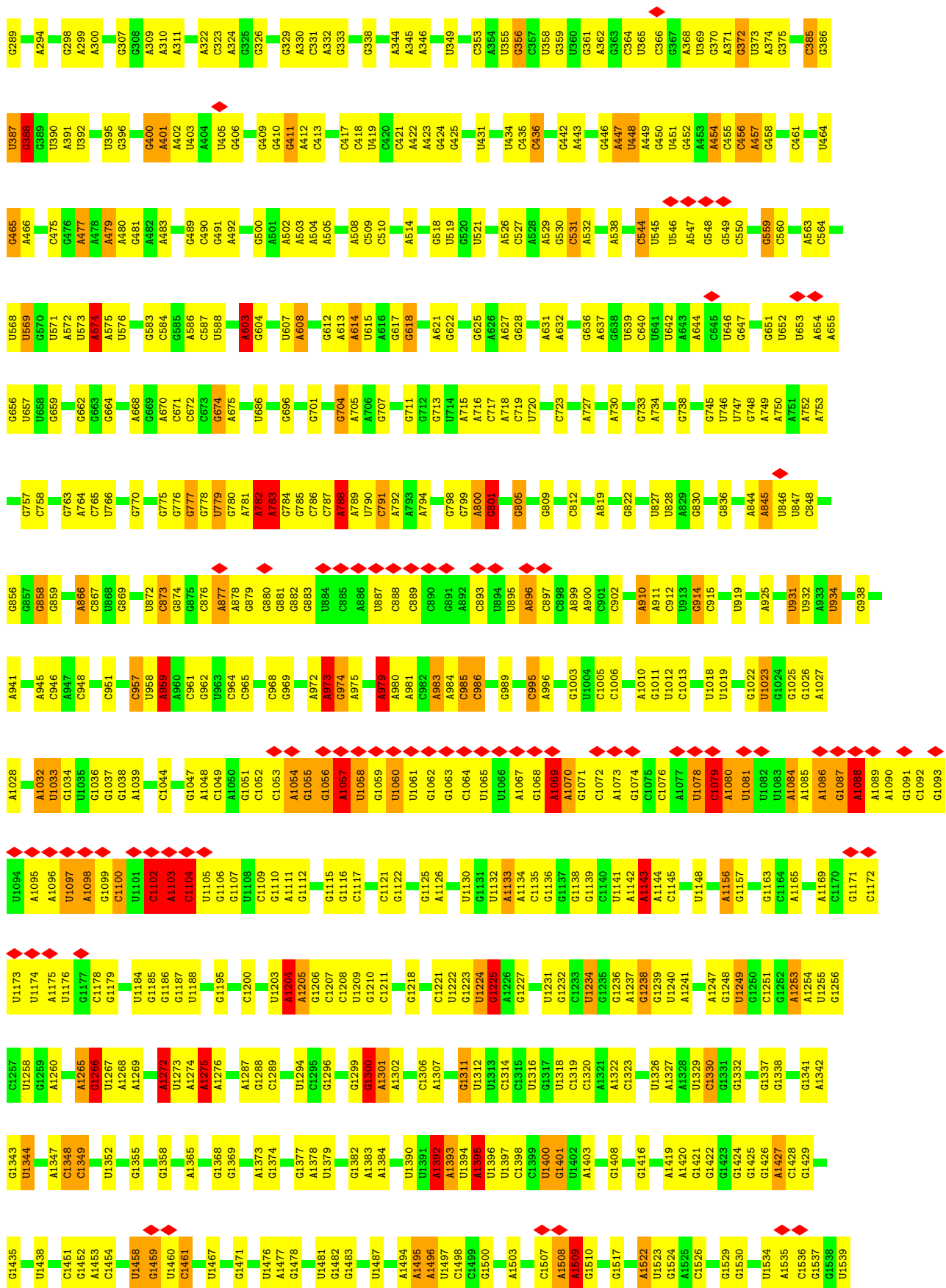


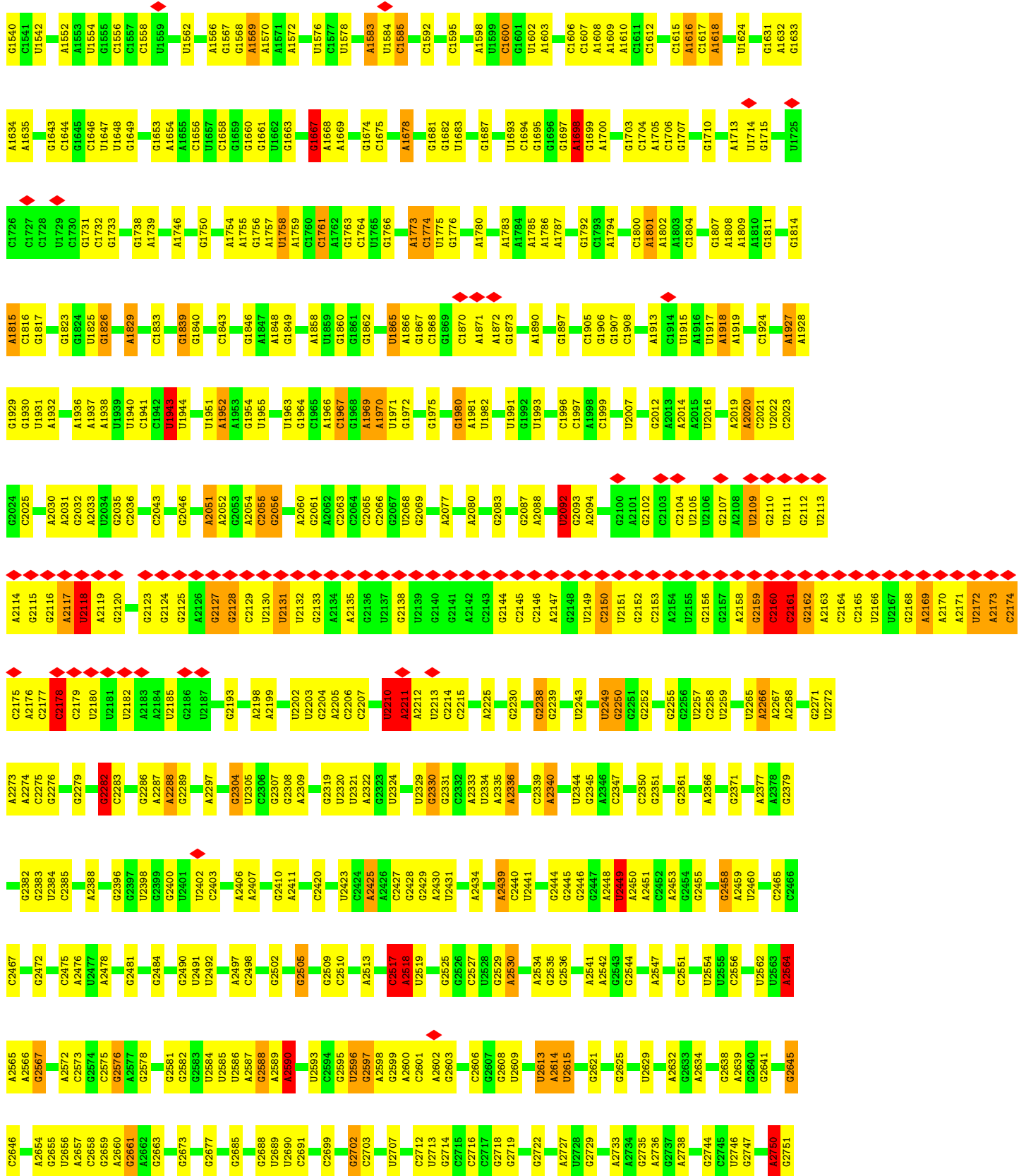
• Molecule 52: 5S rRNA

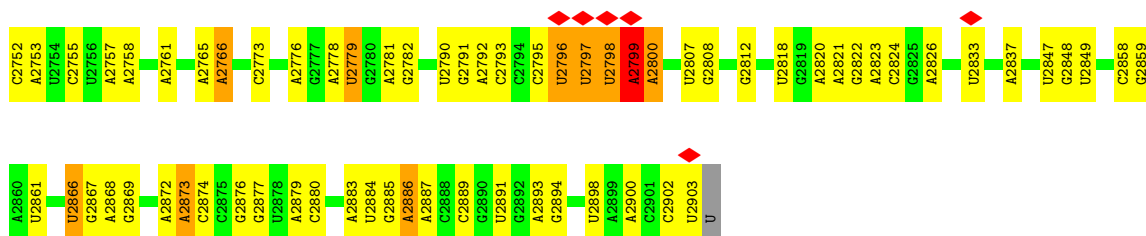


• Molecule 53: 23S rRNA









- Molecule 54: glycine-tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	60354	Depositor
Resolution determination method	Not provided	
CTF correction method	CTFFIND	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	16	Depositor
Minimum defocus (nm)	3500	Depositor
Maximum defocus (nm)	1000	Depositor
Magnification	37878	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.180	Depositor
Minimum map value	-0.099	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.03	Depositor
Map size (\AA)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.32, 1.32, 1.32	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	B	0.29	0/1735	0.51	0/2338
2	C	0.33	0/1651	0.55	0/2225
3	D	0.34	0/1665	0.55	0/2227
4	E	0.38	0/1118	0.56	0/1504
5	F	0.32	0/835	0.56	0/1128
6	G	0.31	0/1187	0.53	0/1591
7	H	0.35	0/989	0.55	0/1326
8	I	0.32	0/1034	0.61	0/1375
9	J	0.33	0/796	0.59	0/1077
10	K	0.30	0/893	0.53	0/1205
11	L	0.36	0/969	0.59	0/1300
12	M	0.31	0/884	0.52	0/1181
13	N	0.34	0/785	0.54	0/1043
14	O	0.33	0/724	0.54	0/966
15	P	0.29	0/659	0.49	0/884
16	Q	0.34	0/657	0.53	0/881
17	R	0.37	0/462	0.58	0/621
18	S	0.32	0/652	0.55	0/877
19	T	0.33	0/671	0.52	0/888
20	U	0.33	0/430	0.63	0/570
21	0	0.38	0/635	0.67	0/848
22	1	0.37	0/502	0.65	0/667
23	2	0.39	0/453	0.61	0/605
24	3	0.41	0/450	0.73	0/599
25	4	0.38	0/416	0.58	0/554
26	6	0.44	0/380	0.77	0/498
27	7	0.37	0/513	0.62	0/676
28	8	0.38	0/303	0.74	0/397
29	c	0.39	0/2121	0.70	1/2852 (0.0%)
30	d	0.38	0/1586	0.63	1/2134 (0.0%)
31	e	0.39	0/1571	0.62	1/2113 (0.0%)
32	f	0.39	0/1434	0.66	0/1926
33	g	0.37	0/1343	0.56	0/1816
34	h	0.37	0/1122	0.68	5/1515 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	j	0.37	0/1152	0.58	0/1551
36	k	0.38	0/947	0.68	1/1268 (0.1%)
37	l	0.38	0/1062	0.68	0/1413
38	m	0.38	0/1081	0.63	0/1443
39	n	0.39	0/973	0.67	0/1301
40	o	0.39	0/902	0.70	0/1209
41	p	0.37	0/929	0.66	0/1242
42	q	0.39	0/960	0.69	1/1278 (0.1%)
43	r	0.40	0/829	0.67	1/1107 (0.1%)
44	s	0.35	0/864	0.67	1/1156 (0.1%)
45	t	0.40	0/744	0.66	1/994 (0.1%)
46	u	0.39	0/787	0.67	0/1051
47	w	0.36	0/766	0.58	0/1025
48	y	0.37	0/576	0.60	0/762
49	z	0.49	0/206	0.83	2/277 (0.7%)
50	A	0.87	6/36762 (0.0%)	0.86	20/57350 (0.0%)
51	X	1.07	4/257 (1.6%)	0.91	0/396
52	a	0.45	1/2824 (0.0%)	0.93	7/4402 (0.2%)
53	b	0.55	52/69800 (0.1%)	1.03	441/108892 (0.4%)
54	v	0.36	1/1812 (0.1%)	0.85	4/2822 (0.1%)
All	All	0.60	64/155858 (0.0%)	0.89	487/233346 (0.2%)

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
11	L	0	1
23	2	0	1
29	c	0	1
30	d	0	1
36	k	0	1
37	l	0	1
43	r	0	1
52	a	0	1
53	b	0	72
All	All	0	80

The worst 5 of 64 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	A	230	G	C6-N1	60.83	1.82	1.39
50	A	230	G	N3-C4	58.56	1.76	1.35
50	A	230	G	C2-N3	55.19	1.76	1.32
50	A	230	G	N1-C2	53.83	1.80	1.37
50	A	230	G	C5-C4	53.10	1.75	1.38

The worst 5 of 487 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	A	230	G	N7-C8-N9	21.72	123.96	113.10
50	A	230	G	C2-N3-C4	19.69	121.75	111.90
50	A	230	G	N3-C4-N9	18.99	137.39	126.00
53	b	1509	A	N9-C1'-C2'	17.94	137.32	114.00
53	b	1275	A	N9-C1'-C2'	17.27	136.46	114.00

There are no chirality outliers.

5 of 80 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
23	2	3	LYS	Peptide
11	L	71	HIS	Peptide
29	c	232	HIS	Peptide
30	d	151	THR	Peptide
36	k	34	GLY	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	B	216/241 (90%)	186 (86%)	22 (10%)	8 (4%)	3	28
2	C	204/233 (88%)	173 (85%)	22 (11%)	9 (4%)	2	23
3	D	203/206 (98%)	179 (88%)	19 (9%)	5 (2%)	5	35
4	E	148/167 (89%)	125 (84%)	18 (12%)	5 (3%)	3	30
5	F	98/131 (75%)	82 (84%)	12 (12%)	4 (4%)	3	25
6	G	148/156 (95%)	128 (86%)	15 (10%)	5 (3%)	3	30
7	H	127/130 (98%)	111 (87%)	12 (9%)	4 (3%)	4	32
8	I	125/130 (96%)	99 (79%)	20 (16%)	6 (5%)	2	21
9	J	96/103 (93%)	77 (80%)	11 (12%)	8 (8%)	1	10
10	K	115/129 (89%)	101 (88%)	13 (11%)	1 (1%)	17	56
11	L	121/124 (98%)	100 (83%)	16 (13%)	5 (4%)	3	25
12	M	111/118 (94%)	100 (90%)	9 (8%)	2 (2%)	8	42
13	N	92/101 (91%)	78 (85%)	7 (8%)	7 (8%)	1	12
14	O	86/89 (97%)	79 (92%)	5 (6%)	2 (2%)	6	37
15	P	80/82 (98%)	56 (70%)	15 (19%)	9 (11%)	0	6
16	Q	78/84 (93%)	67 (86%)	9 (12%)	2 (3%)	5	34
17	R	53/75 (71%)	49 (92%)	4 (8%)	0	100	100
18	S	77/92 (84%)	66 (86%)	9 (12%)	2 (3%)	5	34
19	T	83/87 (95%)	78 (94%)	3 (4%)	2 (2%)	6	36
20	U	49/71 (69%)	39 (80%)	6 (12%)	4 (8%)	1	10
21	0	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
22	1	60/63 (95%)	51 (85%)	7 (12%)	2 (3%)	4	30
23	2	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	8	42
24	3	54/57 (95%)	49 (91%)	3 (6%)	2 (4%)	3	28
25	4	48/55 (87%)	41 (85%)	7 (15%)	0	100	100
26	6	44/46 (96%)	41 (93%)	1 (2%)	2 (4%)	2	22
27	7	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
28	8	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
29	c	269/273 (98%)	252 (94%)	16 (6%)	1 (0%)	34	70
30	d	207/209 (99%)	195 (94%)	10 (5%)	2 (1%)	15	54
31	e	199/201 (99%)	186 (94%)	5 (2%)	8 (4%)	3	26
32	f	175/179 (98%)	154 (88%)	15 (9%)	6 (3%)	3	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	g	174/177 (98%)	139 (80%)	30 (17%)	5 (3%)	4	33
34	h	147/149 (99%)	120 (82%)	19 (13%)	8 (5%)	2	19
35	j	140/142 (99%)	129 (92%)	9 (6%)	2 (1%)	11	47
36	k	120/123 (98%)	112 (93%)	6 (5%)	2 (2%)	9	43
37	l	142/144 (99%)	128 (90%)	9 (6%)	5 (4%)	3	29
38	m	131/136 (96%)	125 (95%)	5 (4%)	1 (1%)	19	58
39	n	118/127 (93%)	111 (94%)	4 (3%)	3 (2%)	5	35
40	o	114/117 (97%)	107 (94%)	2 (2%)	5 (4%)	2	23
41	p	112/115 (97%)	106 (95%)	5 (4%)	1 (1%)	17	56
42	q	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
43	r	101/103 (98%)	94 (93%)	6 (6%)	1 (1%)	15	54
44	s	108/110 (98%)	103 (95%)	2 (2%)	3 (3%)	5	33
45	t	91/100 (91%)	82 (90%)	6 (7%)	3 (3%)	4	30
46	u	100/104 (96%)	82 (82%)	12 (12%)	6 (6%)	1	17
47	w	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
48	y	73/85 (86%)	72 (99%)	1 (1%)	0	100	100
49	z	24/87 (28%)	21 (88%)	3 (12%)	0	100	100
All	All	5497/5903 (93%)	4898 (89%)	440 (8%)	159 (3%)	7	33

5 of 159 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	76	SER
2	C	7	ASN
2	C	61	LYS
4	E	99	SER
4	E	146	MET

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	B	180/199 (90%)	180 (100%)	0	100	100
2	C	170/190 (90%)	170 (100%)	0	100	100
3	D	172/173 (99%)	172 (100%)	0	100	100
4	E	113/126 (90%)	113 (100%)	0	100	100
5	F	87/112 (78%)	87 (100%)	0	100	100
6	G	123/129 (95%)	123 (100%)	0	100	100
7	H	104/105 (99%)	104 (100%)	0	100	100
8	I	105/107 (98%)	104 (99%)	1 (1%)	76	88
9	J	86/90 (96%)	86 (100%)	0	100	100
10	K	90/99 (91%)	90 (100%)	0	100	100
11	L	103/104 (99%)	103 (100%)	0	100	100
12	M	91/96 (95%)	91 (100%)	0	100	100
13	N	79/84 (94%)	79 (100%)	0	100	100
14	O	76/77 (99%)	76 (100%)	0	100	100
15	P	65/65 (100%)	57 (88%)	8 (12%)	4	25
16	Q	74/78 (95%)	74 (100%)	0	100	100
17	R	48/65 (74%)	48 (100%)	0	100	100
18	S	70/79 (89%)	70 (100%)	0	100	100
19	T	65/66 (98%)	65 (100%)	0	100	100
20	U	44/61 (72%)	44 (100%)	0	100	100
21	0	67/68 (98%)	64 (96%)	3 (4%)	27	61
22	1	54/55 (98%)	52 (96%)	2 (4%)	34	65
23	2	48/49 (98%)	47 (98%)	1 (2%)	53	77
24	3	47/48 (98%)	46 (98%)	1 (2%)	53	77
25	4	45/49 (92%)	43 (96%)	2 (4%)	28	62
26	6	38/38 (100%)	35 (92%)	3 (8%)	12	43
27	7	51/52 (98%)	49 (96%)	2 (4%)	32	64
28	8	34/34 (100%)	34 (100%)	0	100	100
29	c	216/218 (99%)	210 (97%)	6 (3%)	43	71
30	d	164/164 (100%)	157 (96%)	7 (4%)	29	62
31	e	165/165 (100%)	158 (96%)	7 (4%)	30	62
32	f	148/150 (99%)	141 (95%)	7 (5%)	26	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	g	137/138 (99%)	134 (98%)	3 (2%)	52	76
34	h	114/114 (100%)	112 (98%)	2 (2%)	59	80
35	j	116/116 (100%)	113 (97%)	3 (3%)	46	73
36	k	103/104 (99%)	101 (98%)	2 (2%)	57	79
37	l	103/103 (100%)	100 (97%)	3 (3%)	42	71
38	m	108/109 (99%)	107 (99%)	1 (1%)	78	89
39	n	100/103 (97%)	97 (97%)	3 (3%)	41	70
40	o	86/87 (99%)	83 (96%)	3 (4%)	36	67
41	p	99/100 (99%)	95 (96%)	4 (4%)	31	64
42	q	89/90 (99%)	88 (99%)	1 (1%)	73	87
43	r	84/84 (100%)	81 (96%)	3 (4%)	35	66
44	s	93/93 (100%)	92 (99%)	1 (1%)	73	87
45	t	80/84 (95%)	80 (100%)	0	100	100
46	u	83/85 (98%)	79 (95%)	4 (5%)	25	59
47	w	78/78 (100%)	74 (95%)	4 (5%)	24	58
48	y	56/63 (89%)	56 (100%)	0	100	100
49	z	21/62 (34%)	9 (43%)	12 (57%)	0	0
All	All	4572/4808 (95%)	4473 (98%)	99 (2%)	54	76

5 of 99 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	j	142	ILE
41	p	26	VAL
36	k	105	ARG
39	n	116	VAL
43	r	46	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

Mol	Chain	Res	Type
15	P	26	ASN
44	s	61	ASN
18	S	56	HIS
44	s	15	GLN

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Mol	Chain	Res	Type
34	h	43	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	A	1530/1542 (99%)	427 (27%)	36 (2%)
51	X	11/11 (100%)	7 (63%)	2 (18%)
52	a	116/120 (96%)	40 (34%)	0
53	b	2902/2904 (99%)	1211 (41%)	0
54	v	75/76 (98%)	27 (36%)	0
All	All	4634/4653 (99%)	1712 (36%)	38 (0%)

5 of 1712 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	A	6	G
50	A	7	A
50	A	8	A
50	A	9	G
50	A	11	G

5 of 38 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	A	1302	C
50	A	1527	U
50	A	1332	A
50	A	1348	U
51	X	14	U

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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
53	b	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	b	1087:G	O3'	1088:A	P	1.81
1	b	2055:C	O3'	2056:G	P	1.80

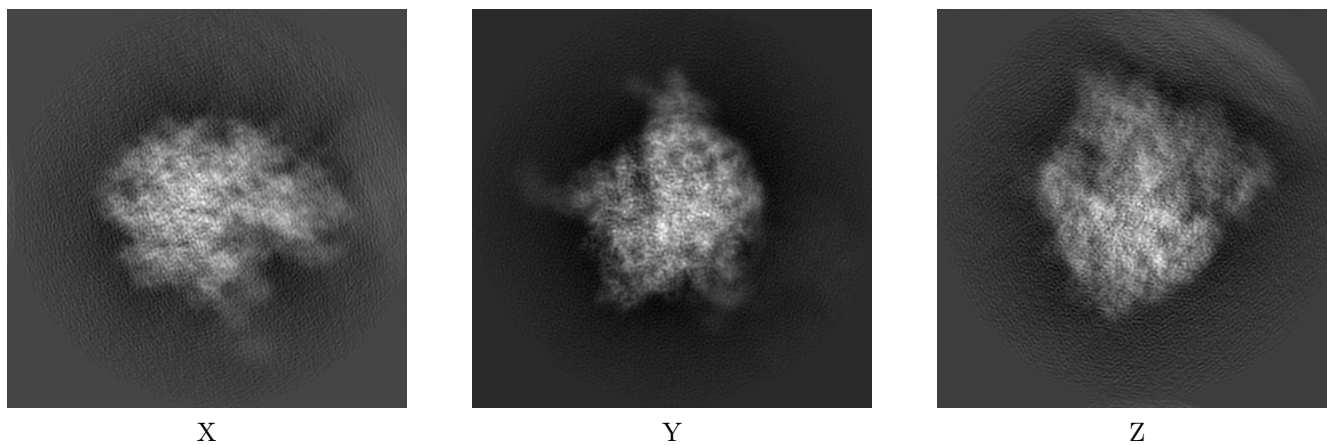
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6483. 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](#)

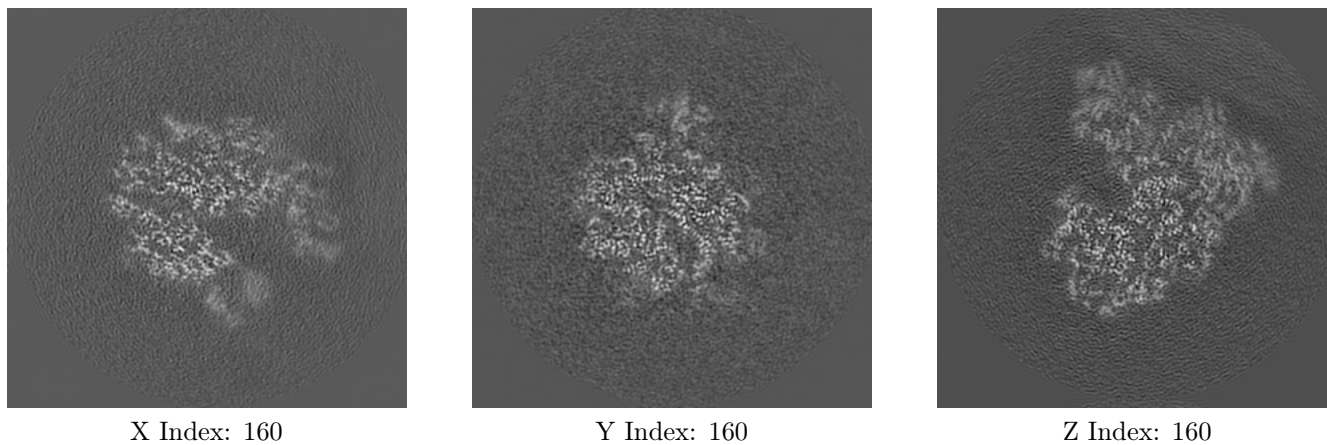
6.1.1 Primary map



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

6.2 Central slices [i](#)

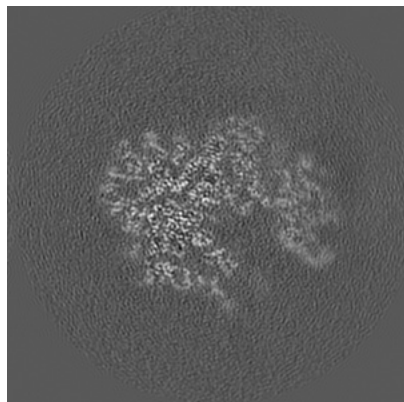
6.2.1 Primary map



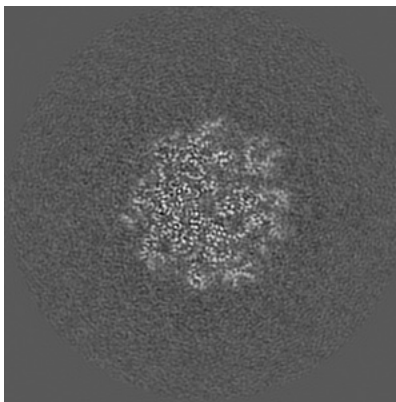
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

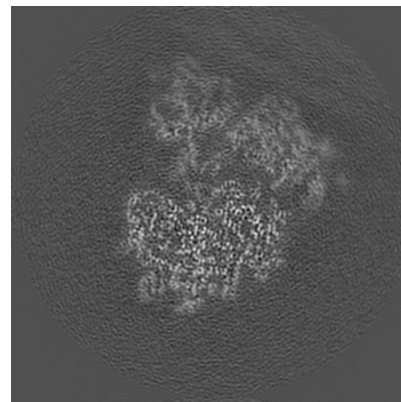
6.3.1 Primary map



X Index: 153



Y Index: 138

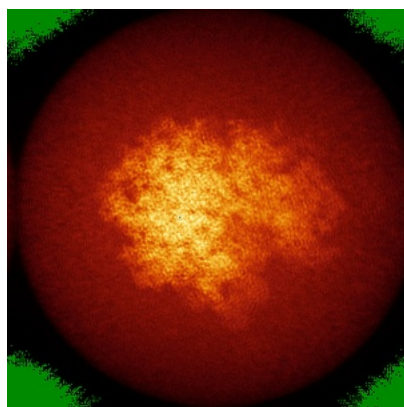


Z Index: 153

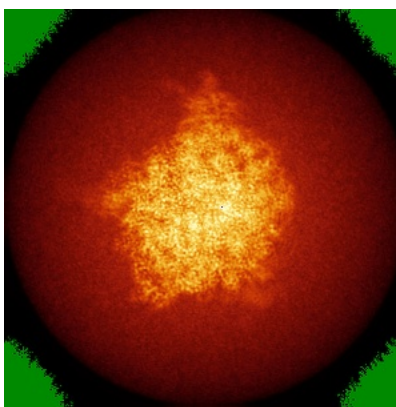
The images above show the largest variance slices of the map in three orthogonal directions.

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

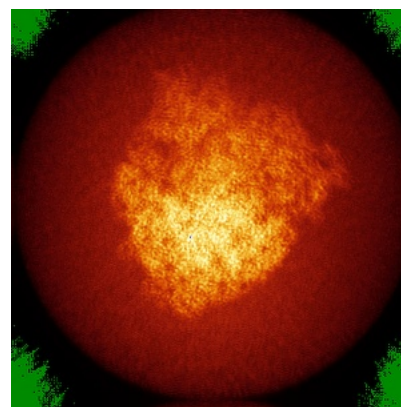
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

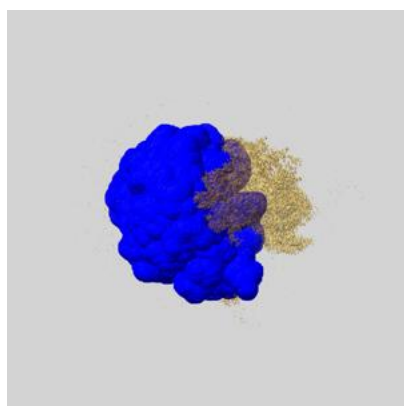
6.6 Mask visualisation [i](#)

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

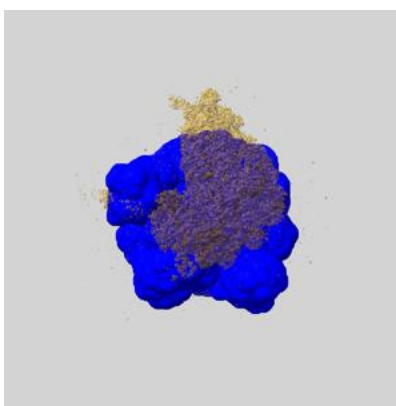
A mask typically either:

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

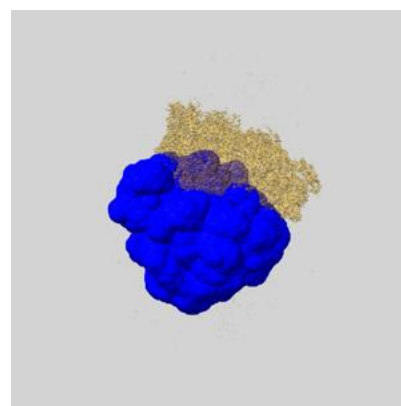
6.6.1 emd_6483_msk_1.map [i](#)



X



Y

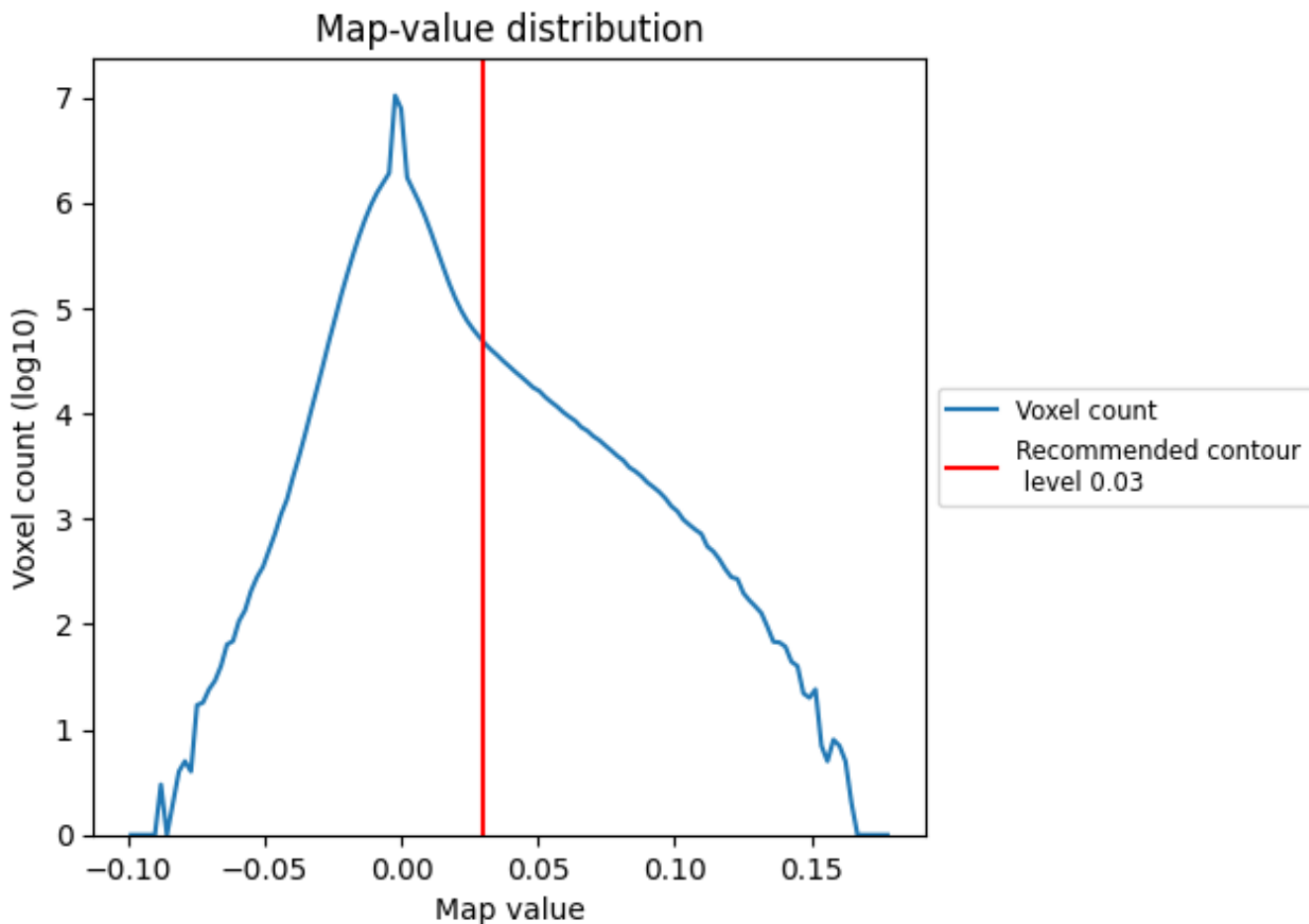


Z

7 Map analysis [i](#)

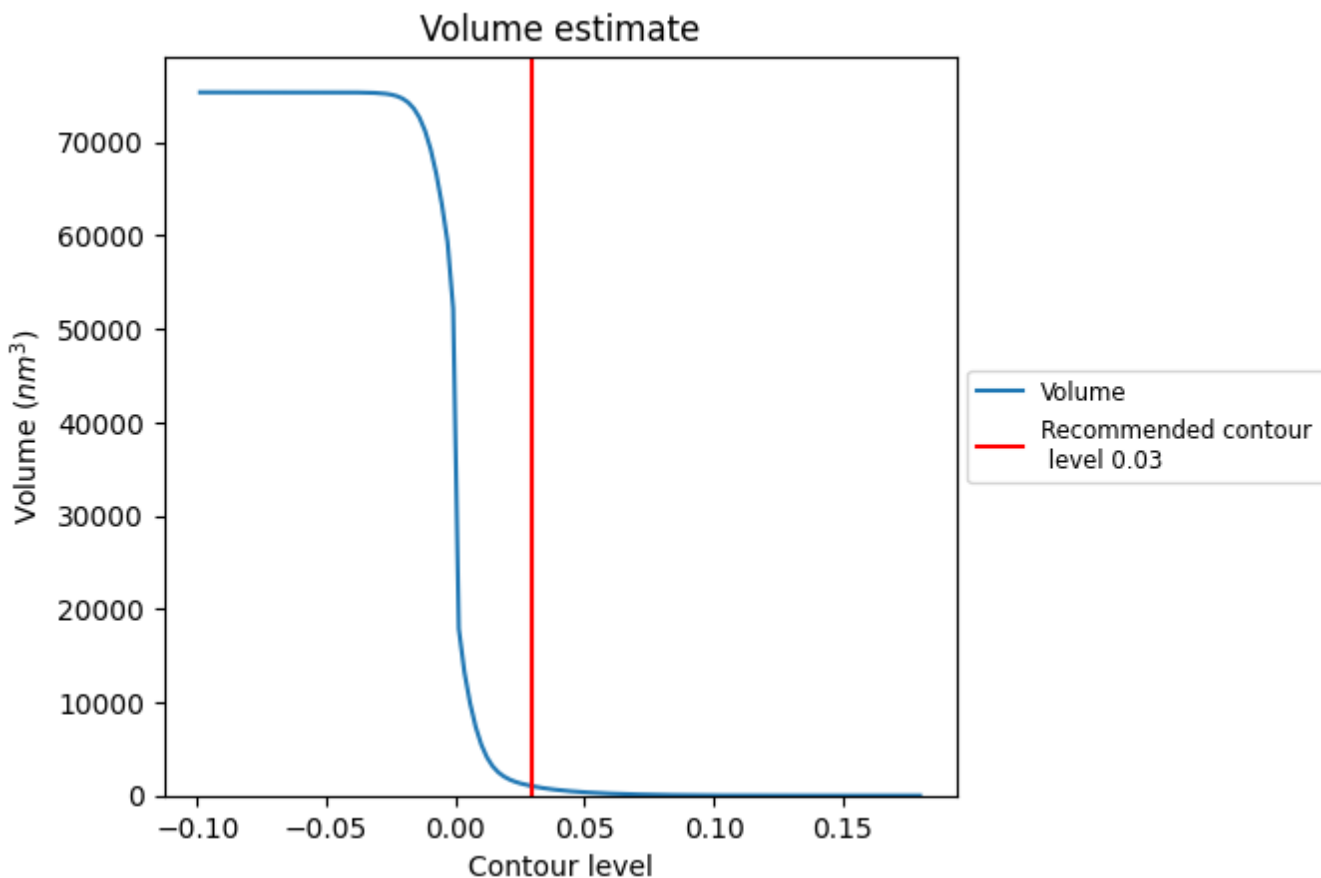
This section contains the results of statistical analysis of the map.

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.

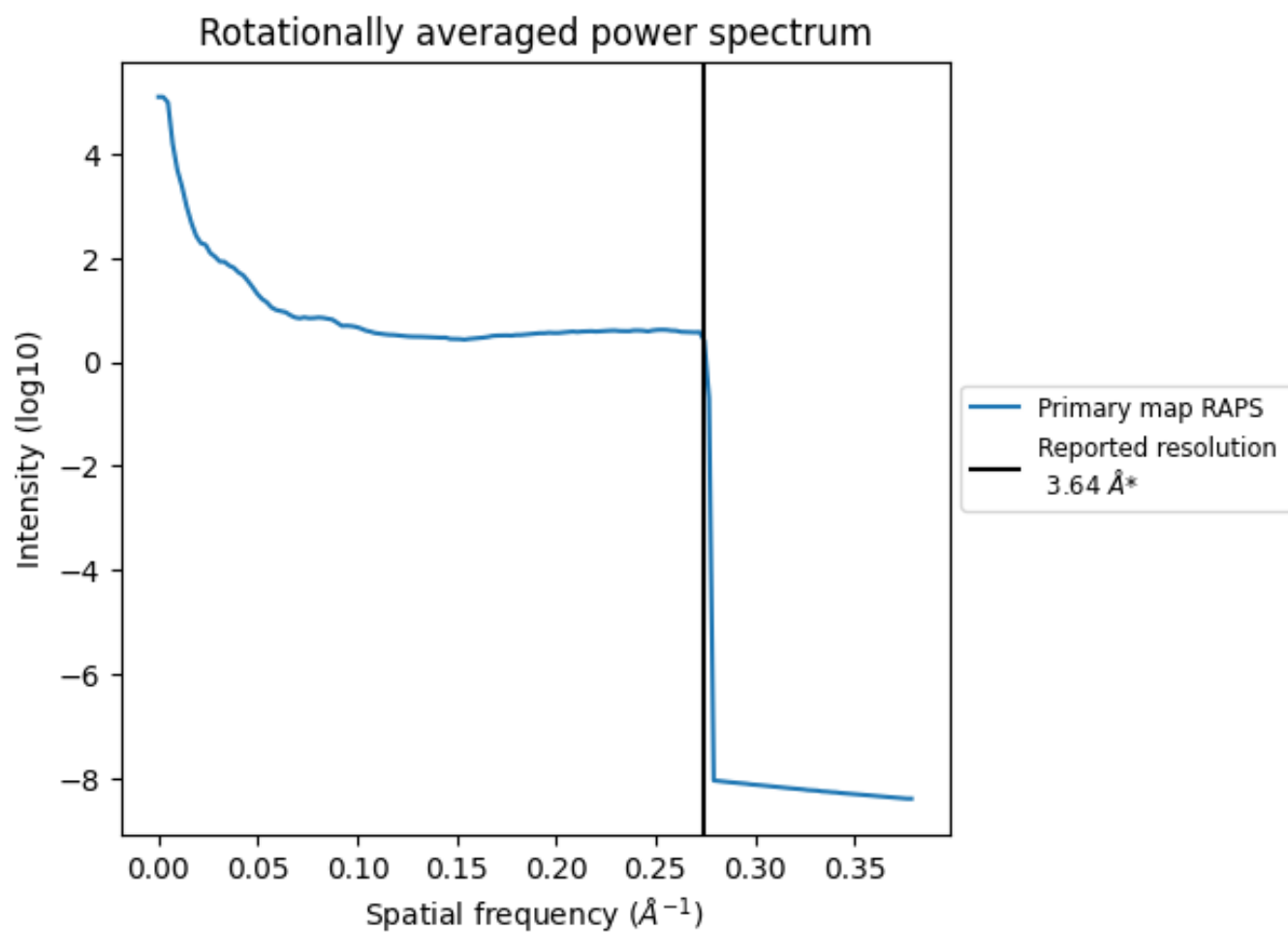
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 995 nm^3 ; this corresponds to an approximate mass of 899 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](#)

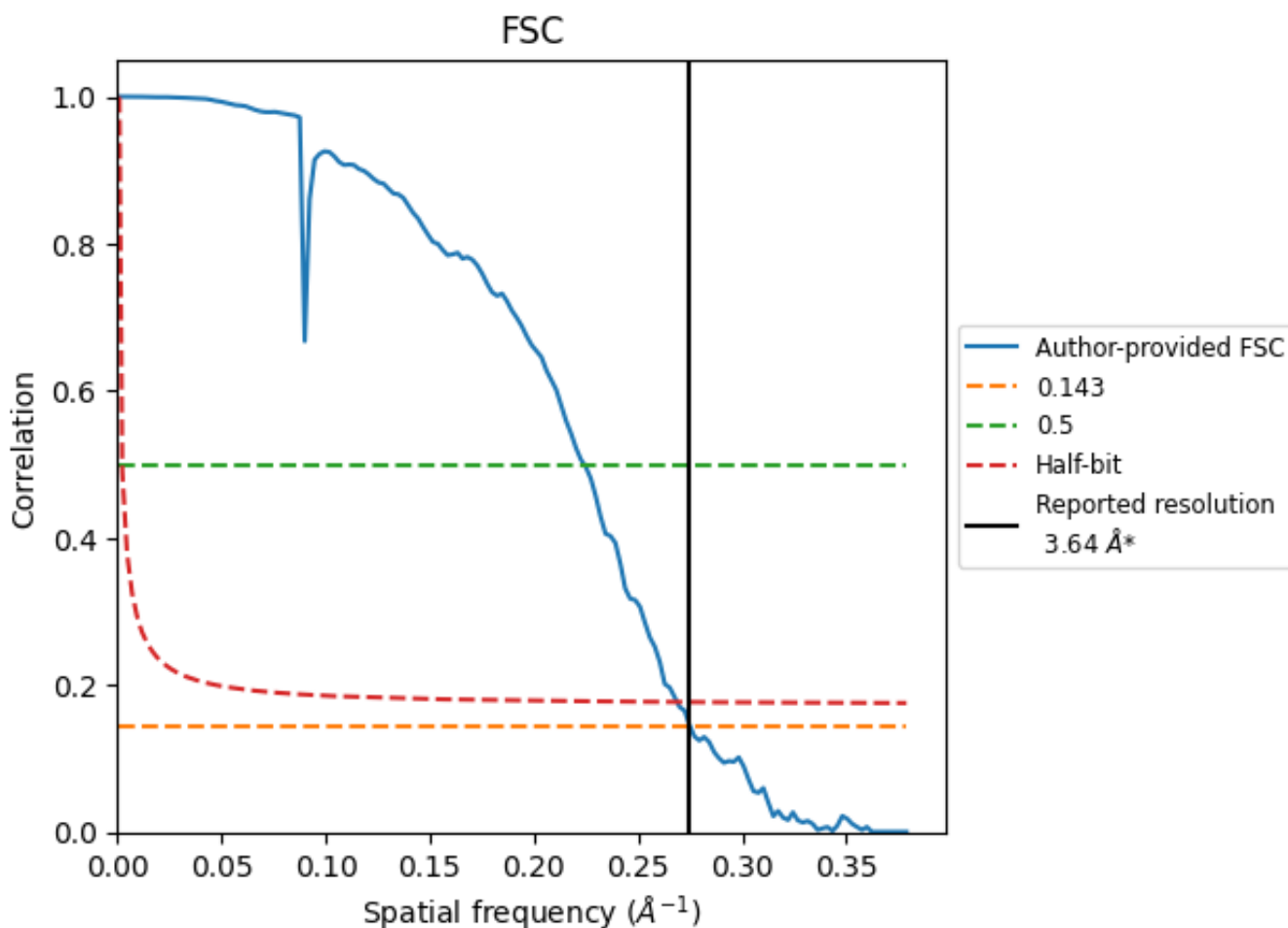


*Reported resolution corresponds to spatial frequency of 0.275 Å⁻¹

8 Fourier-Shell correlation [\(i\)](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.275 Å⁻¹

8.2 Resolution estimates [i](#)

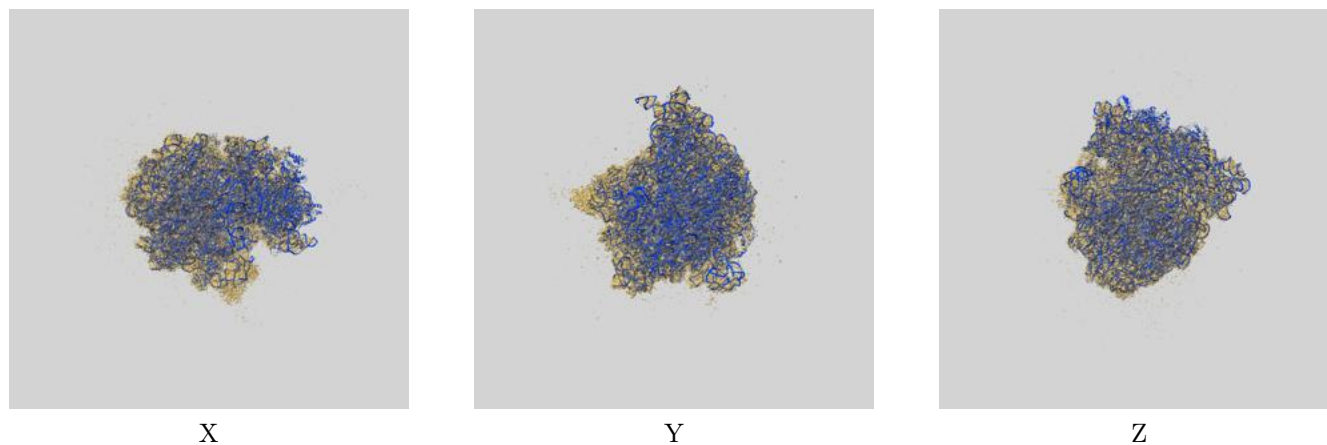
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	3.64	4.46	3.72
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

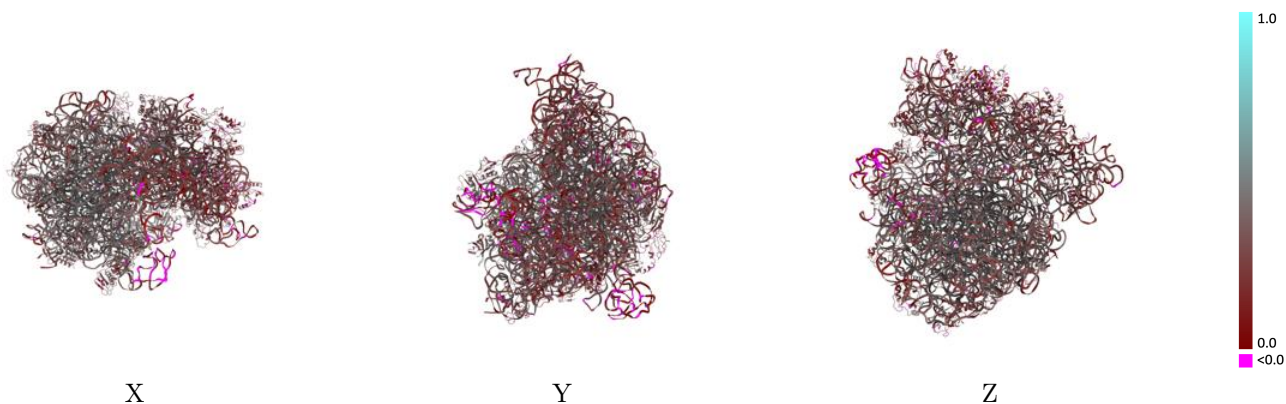
This section contains information regarding the fit between EMDB map EMD-6483 and PDB model 3JBU. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



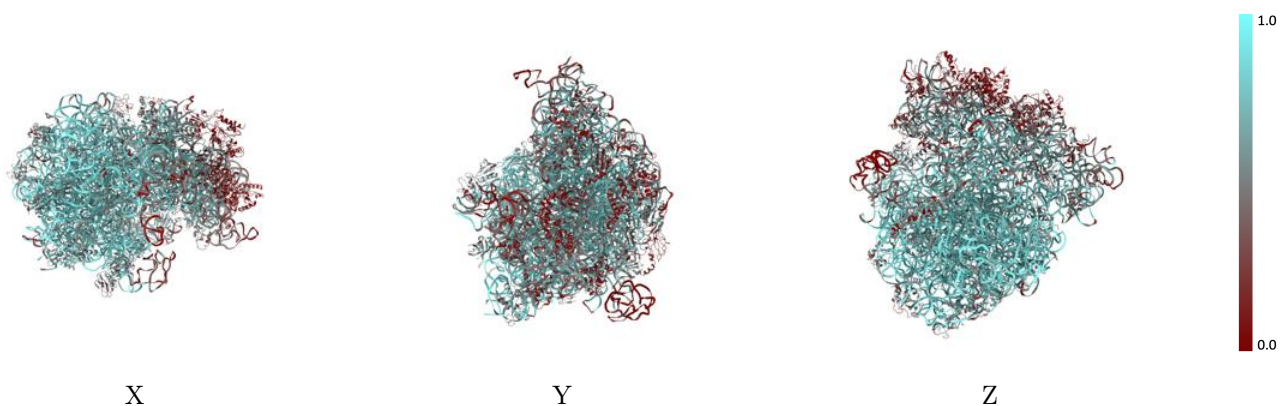
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



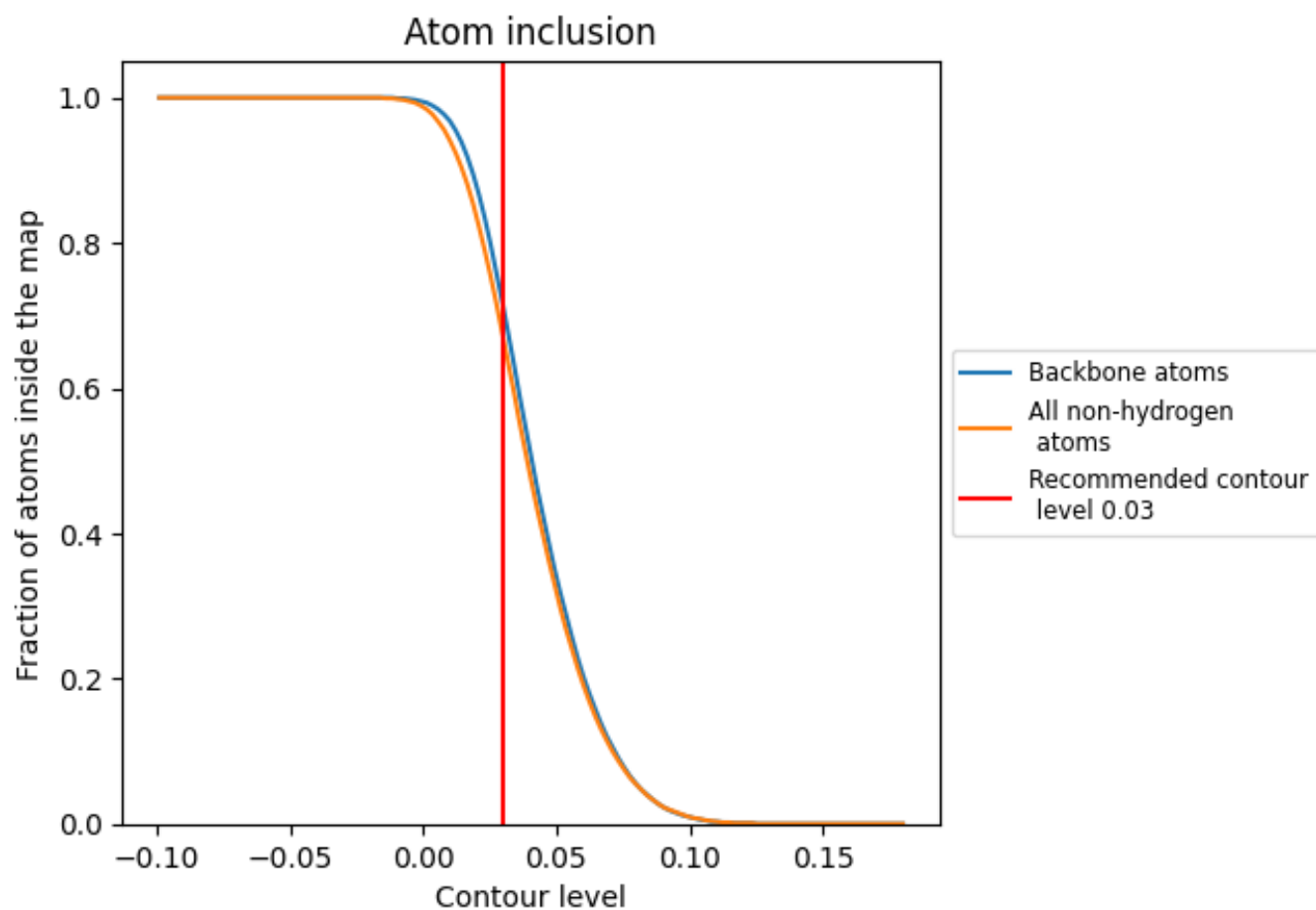
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 67% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary









































The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6710	 0.3410
0	 0.6670	 0.3850
1	 0.4720	 0.2700
2	 0.6660	 0.3800
3	 0.6280	 0.3380
4	 0.6230	 0.3710
6	 0.7470	 0.4140
7	 0.7350	 0.4340
8	 0.6880	 0.4020
A	 0.6530	 0.3220
B	 0.1160	 0.2000
C	 0.1570	 0.1960
D	 0.1660	 0.1960
E	 0.2730	 0.2450
F	 0.4640	 0.3230
G	 0.3450	 0.2520
H	 0.2660	 0.2590
I	 0.2180	 0.1810
J	 0.1410	 0.1890
K	 0.4950	 0.3390
L	 0.4650	 0.3250
M	 0.3820	 0.2680
N	 0.2220	 0.2110
O	 0.5200	 0.2980
P	 0.3000	 0.2170
Q	 0.4000	 0.2910
R	 0.4380	 0.3410
S	 0.3240	 0.2680
T	 0.4570	 0.2500
U	 0.3130	 0.2140
X	 0.4480	 0.2590
a	 0.8220	 0.3620
b	 0.8130	 0.3760
c	 0.7110	 0.3900
d	 0.6570	 0.3880



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Chain	Atom inclusion	Q-score
e	 0.5800	 0.3340
f	 0.5290	 0.2630
g	 0.4890	 0.3040
h	 0.2420	 0.1940
j	 0.6860	 0.3860
k	 0.6070	 0.3850
l	 0.6440	 0.3720
m	 0.6620	 0.3920
n	 0.6630	 0.3710
o	 0.5840	 0.2880
p	 0.5890	 0.3400
q	 0.7090	 0.3910
r	 0.6050	 0.3710
s	 0.6590	 0.3890
t	 0.5650	 0.3130
u	 0.5060	 0.2760
v	 0.5580	 0.2800
w	 0.6060	 0.3440
y	 0.7050	 0.4020
z	 0.1850	 0.3150