



wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 01:30 PM EST

PDB ID : 3J92
EMDB ID : EMD-2832
Title : Structure and assembly pathway of the ribosome quality control complex
Authors : Shao, S.; Brown, A.; Santhanam, B.; Hegde, R.S.
Deposited on : 2014-12-02
Resolution : 3.60 Å(reported)
Based on initial models : 4W20, 4W1Z

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:

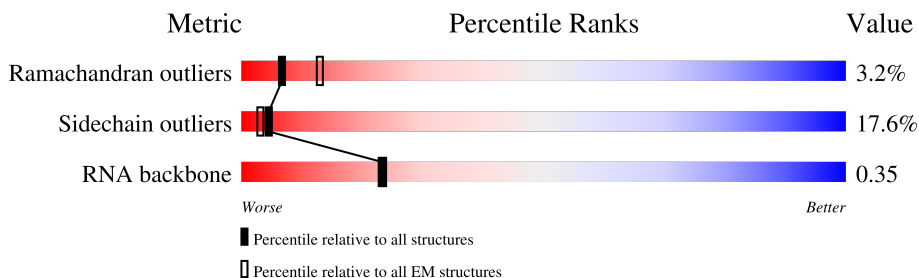
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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 3.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



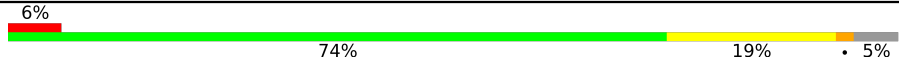
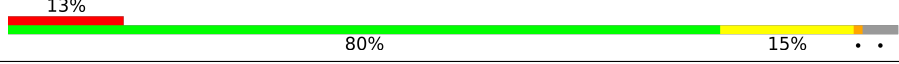
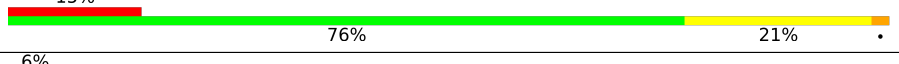


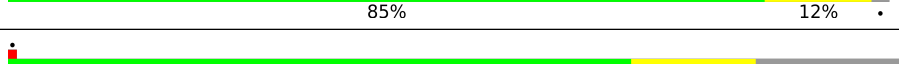
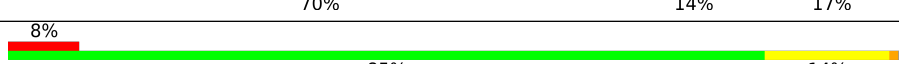
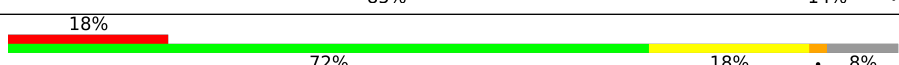
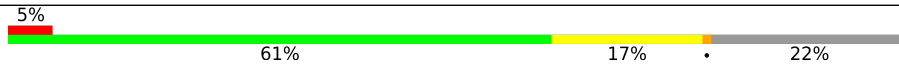


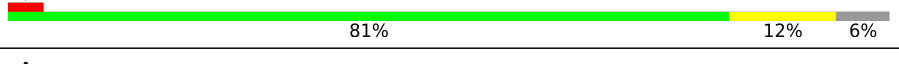


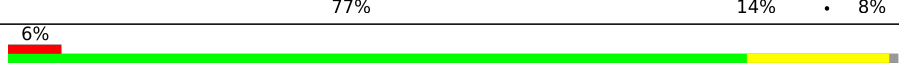

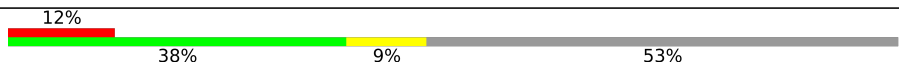








Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	A	257	
2	B	395	
3	C	368	
4	D	297	
5	E	284	
6	F	250	
7	G	266	
8	H	192	

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Mol	Chain	Length	Quality of chain
9	I	214	
10	J	178	
11	L	211	
12	M	213	
13	N	204	
14	O	204	
15	P	184	
16	Q	188	
17	R	196	
18	S	224	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	160	
28	c	115	
29	d	125	
30	e	135	
31	f	110	
32	g	117	
33	h	123	

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Mol	Chain	Length	Quality of chain
34	i	105	10% 81% 14% . .
35	j	97	. 69% 20% 11%
36	k	70	24% 74% 24% .
37	l	51	10% 76% 18% . .
38	m	128	. 30% 9% . 59%
39	o	106	10% 77% 18% . .
40	p	92	9% 82% 16% . .
41	r	137	9% 74% 16% . 9%
42	s	317	47% 52% 10% . 38%
43	t	165	78% 71% 25% . .
44	u	501	26% 24% . 74%
44	v	501	15% 23% . 73%
45	0	1766	. 98%
45	w	1766	. 99%
45	z	1766	. 6% . 93%
46	x	218	53% 100%
46	y	218	59% 97% .
47	1	104	5% 11% . . 86%
48	2	77	91% 55% 43% .
49	5	3664	10% 60% 37% .
50	7	120	. 76% 24%
51	8	156	6% 68% 31% .

2 Entry composition [i](#)

There are 53 unique types of molecules in this entry. The entry contains 146386 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 uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	394	Total	C	N	O	S	0	0
			3147	2005	591	538	13		

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	367	Total	C	N	O	S	0	0
			2919	1836	582	486	15		

- Molecule 4 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	292	Total	C	N	O	S	0	0
			2384	1511	435	426	12		

- Molecule 5 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	236	Total	C	N	O	S	0	0
			1904	1219	364	316	5		

- Molecule 6 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	241	1939	1235	372	328	4	0	0

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	190	1518	956	284	272	6	0	0

- Molecule 9 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	204	1651	1048	318	271	14	0	0

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	170	1359	856	256	241	6	0	0

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L	210	1703	1064	354	280	5	0	0

- Molecule 12 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	M	138	1131	727	216	181	7	0	0

- Molecule 13 is a protein called eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	N	203	1701	1072	359	266	4	0	0

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	O	199	1638	1056	321	256	5	0	0

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	P	153	1242	776	241	216	9	0	0

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	Q	187	1506	941	311	249	5	0	0

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	R	180	1508	933	328	238	9	0	0

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	S	175	1454	925	284	235	10	0	0

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	T	159	1298	823	252	217	6	0	0

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	U	99	808	518	141	147	2	0	0

- Molecule 21 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 24 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	147	Total	C	N	O	S	0	0
			1163	735	239	185	4		

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	c	94	732	465	130	131	6	0	0

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	d	107	888	560	171	155	2	0	0

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	e	128	1053	667	216	165	5	0	0

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	f	109	876	555	174	144	3	0	0

- Molecule 32 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	g	114	906	566	187	147	6	0	0

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	h	122	1015	642	205	167	1	0	0

- Molecule 34 is a protein called eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	i	102	832	521	177	129	5	0	0

- Molecule 35 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	86	Total	C	N	O	S	0	0
			706	436	155	110	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 40 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 41 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	r	125	Total	C	N	O	S	0	0
			1001	622	206	168	5		

- Molecule 42 is a protein called uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	s	198	Total	C	N	O	S	0	0
			1522	968	265	280	9		

- Molecule 43 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	163	Total	C	N	O	S	0	0
			1238	773	230	230	5		

- Molecule 44 is a protein called NEMF.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	130	Total	C	N	O		0	0
			645	385	130	130			
44	v	136	Total	C	N	O	S	0	0
			1092	687	197	206	2		

- Molecule 45 is a protein called Listerin.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	w	15	Total	C	N	O		0	0
			110	67	23	20			
45	z	130	Total	C	N	O	S	0	0
			1057	681	180	189	7		
45	0	36	Total	C	N	O	S	0	0
			293	187	53	48	5		

- Molecule 46 is a protein called Listerin.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	x	218	Total	C	N	O	0	0
			1090	654	218	218		
46	y	211	Total	C	N	O	0	0
			1055	633	211	211		

- Molecule 47 is a protein called nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	1	15	Total	C	N	O	S	0	0
			125	82	20	22	1		

- Molecule 48 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
48	2	75	1601	715	292	520	74	0	0

- Molecule 49 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
49	5	3662	78486	34947	14363	25515	3661	0	0

- Molecule 50 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
50	7	120	2558	1141	456	842	119	0	0

- Molecule 51 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
51	8	156	3314	1480	585	1094	155	0	0

- Molecule 52 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
52	P	1	Total 1	Mg 1	0
52	V	1	Total 1	Mg 1	0
52	g	1	Total 1	Mg 1	0
52	5	150	Total 150	Mg 150	0
52	7	5	Total 5	Mg 5	0
52	8	1	Total 1	Mg 1	0

- Molecule 53 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
53	g	1	Total 1	Zn 1	0

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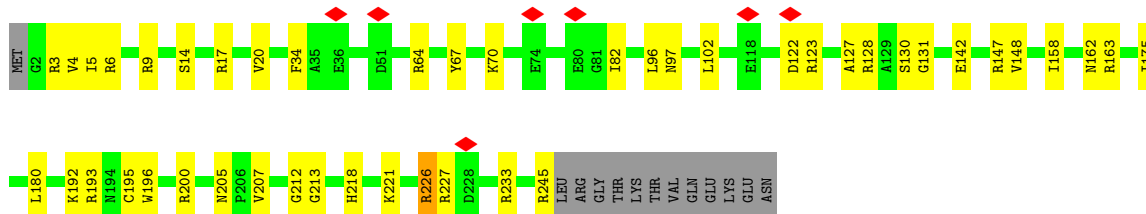
Mol	Chain	Residues	Atoms		AltConf
53	j	1	Total 1	Zn 1	0
53	m	1	Total 1	Zn 1	0
53	o	1	Total 1	Zn 1	0
53	p	1	Total 1	Zn 1	0

3 Residue-property plots


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

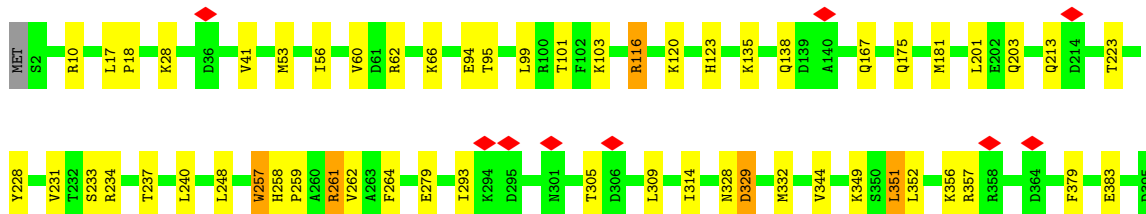
- Molecule 1: uL2

Chain A: 




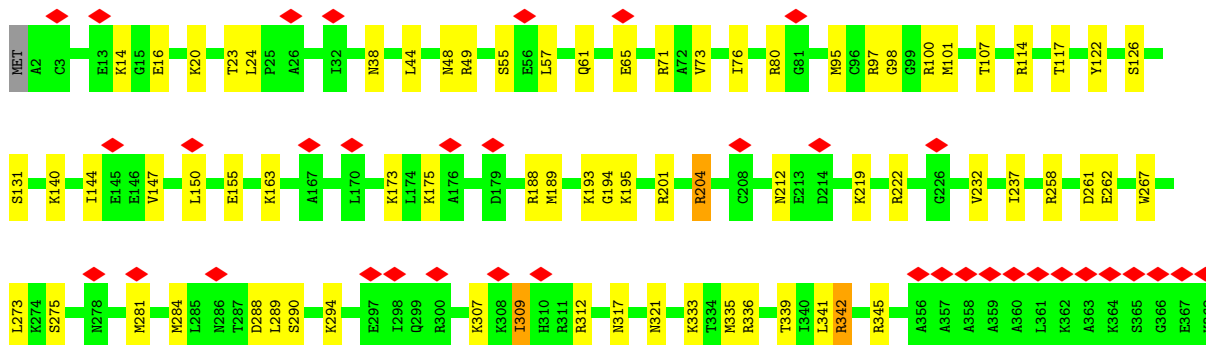
- Molecule 2: uL3

Chain B: 

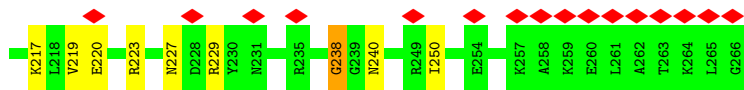


- Molecule 3: uL4

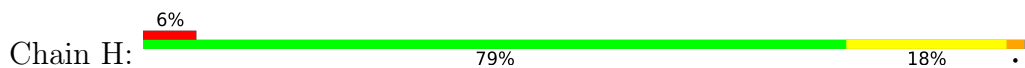
Chain C: 



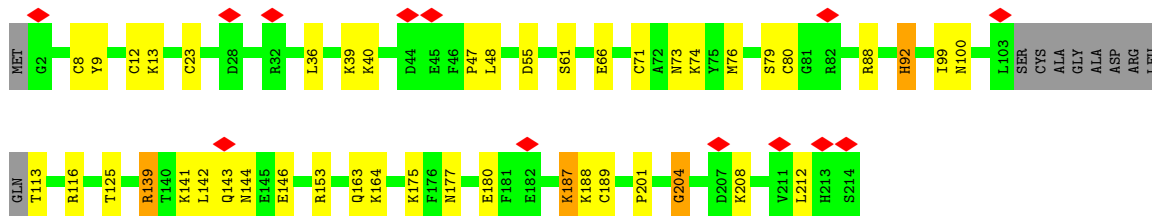
- Molecule 4: uL18



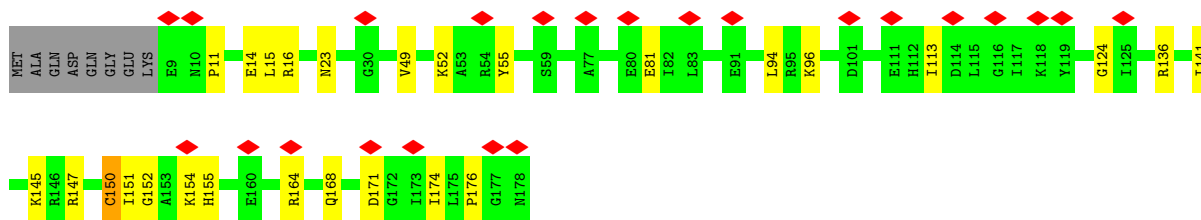
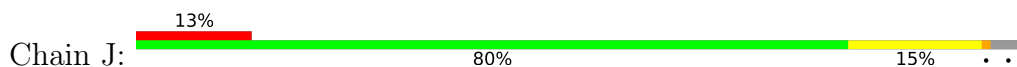
• Molecule 8: uL6



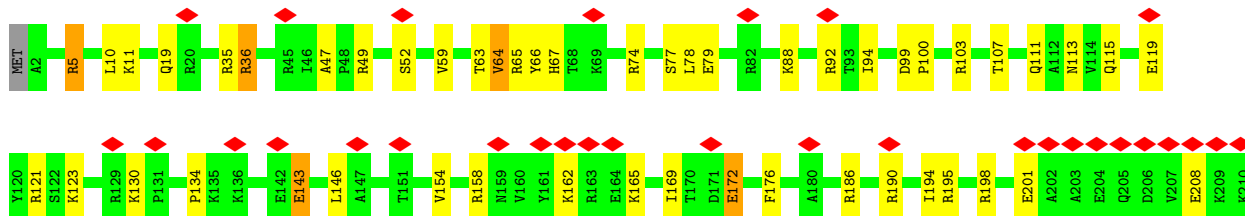
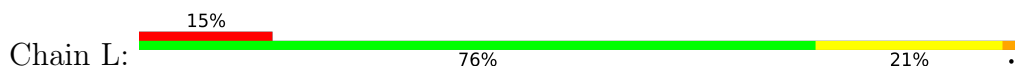
• Molecule 9: uL16



• Molecule 10: uL5

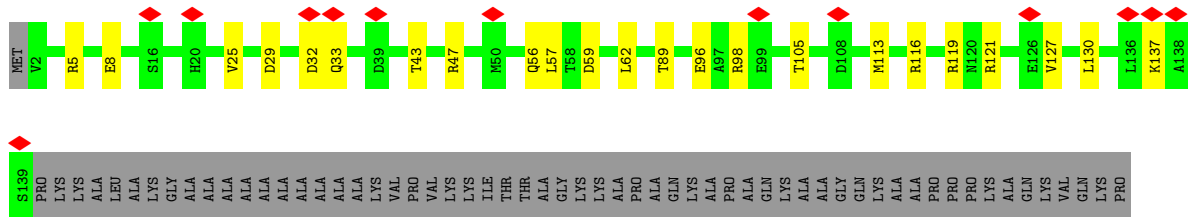


• Molecule 11: eL13



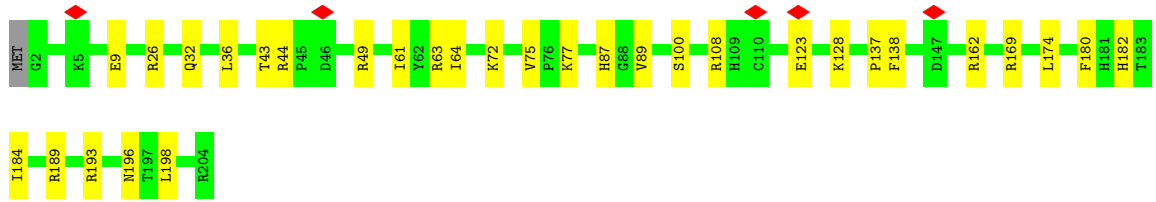
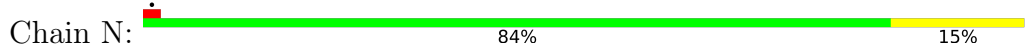
K2L1

Molecule 12: eL14

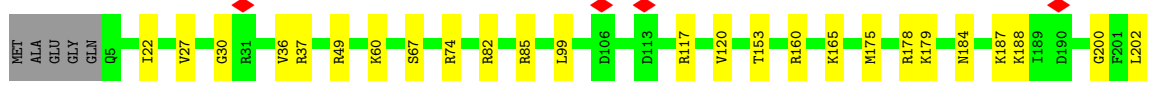
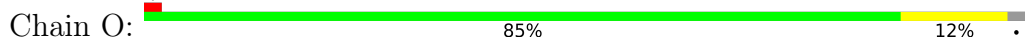


PRO ALA GLN LYS ALA PRO ALA PRO LYS ALA ALA SER GLY GLU LYS ALA

Molecule 13: eL15

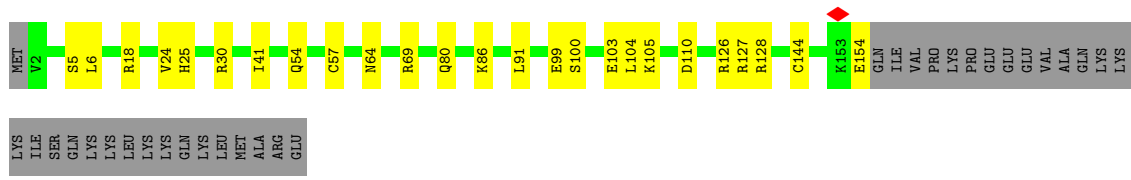


Molecule 14: uL13

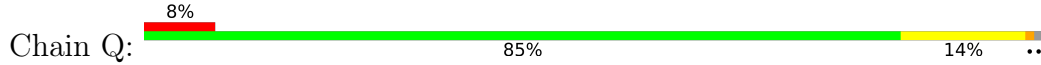


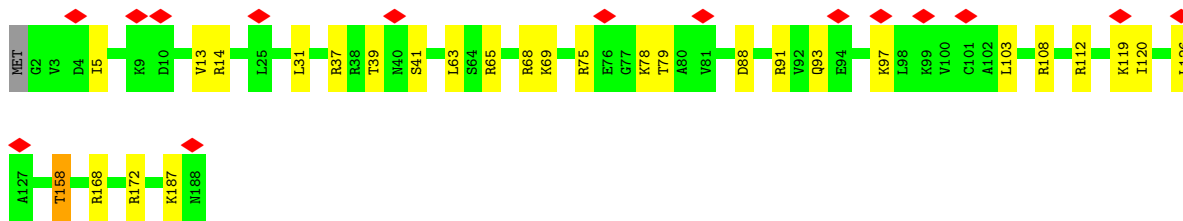
Y203

Molecule 15: uL22

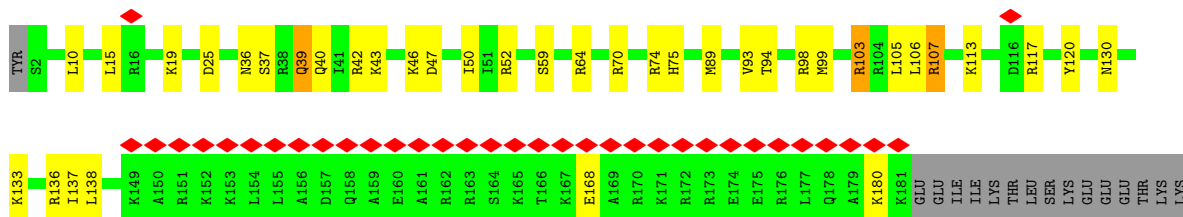


Molecule 16: eL18

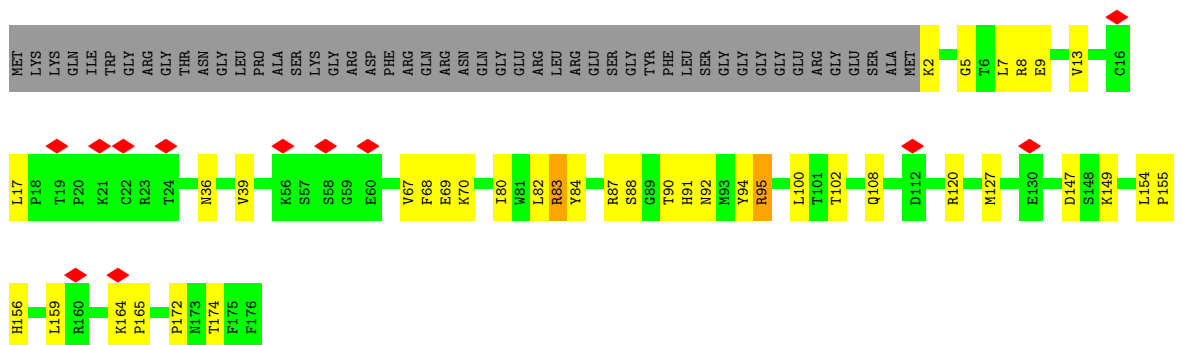




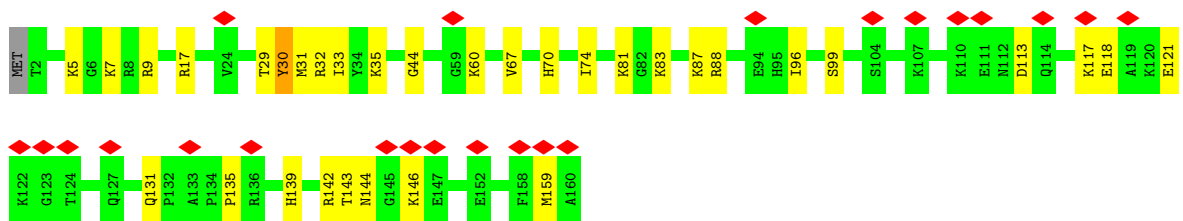
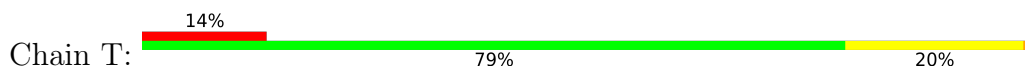
• Molecule 17: eL19



• Molecule 18: eL20



• Molecule 19: eL21

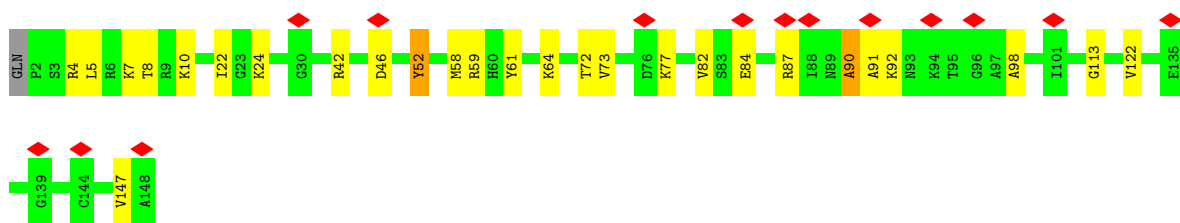
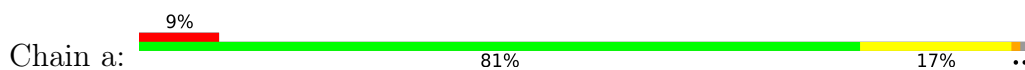


• Molecule 20: eL22

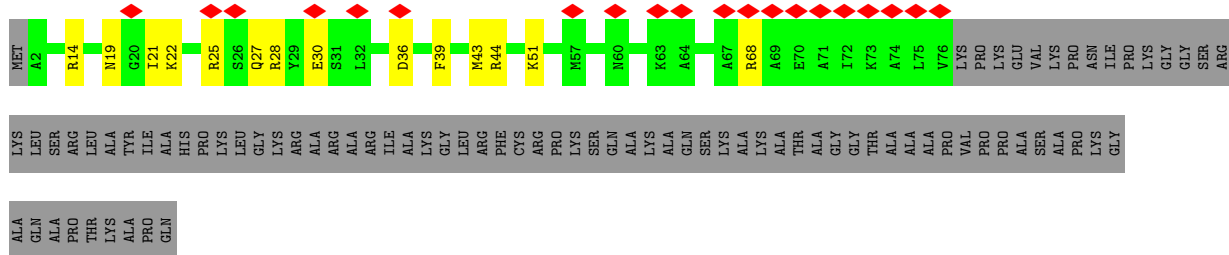
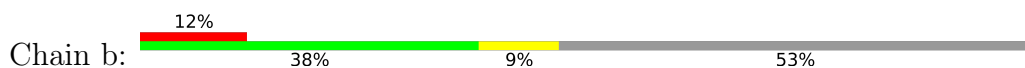




• Molecule 26: uL15



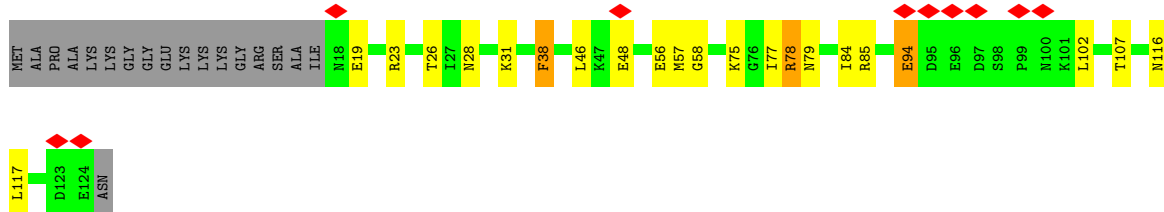
• Molecule 27: eL29



• Molecule 28: eL30



• Molecule 29: eL31

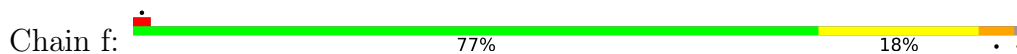


• Molecule 30: eL32

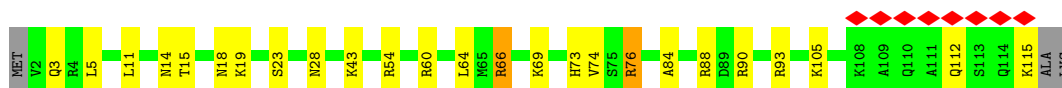
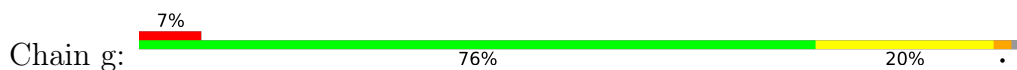




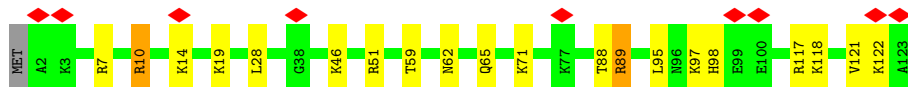
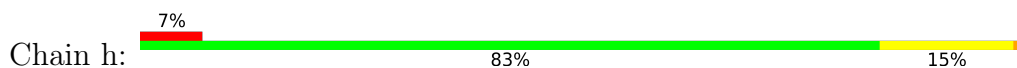
• Molecule 31: eL33



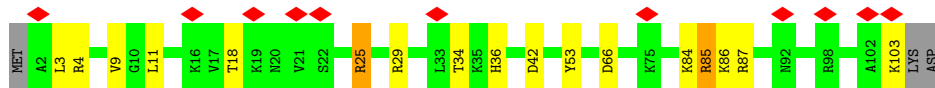
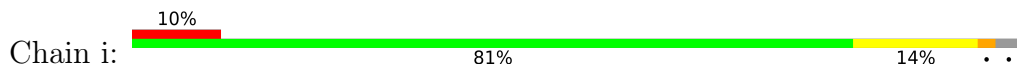
• Molecule 32: eL34



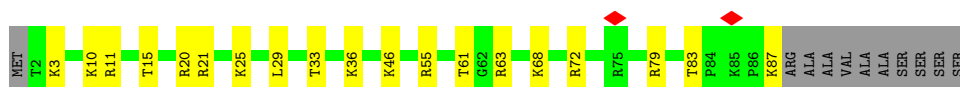
• Molecule 33: uL29



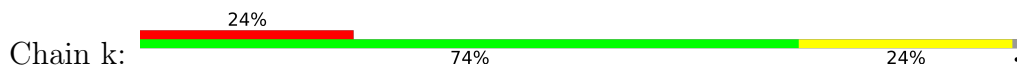
• Molecule 34: eL36

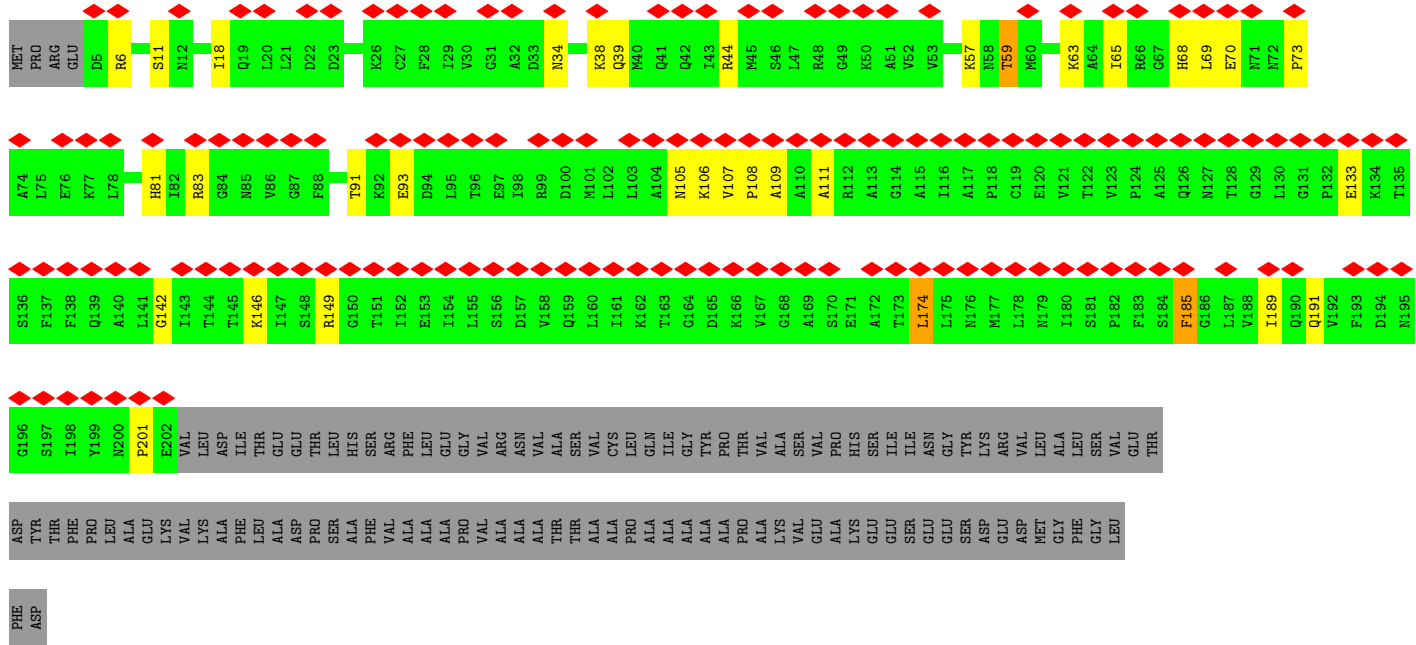


• Molecule 35: eL37

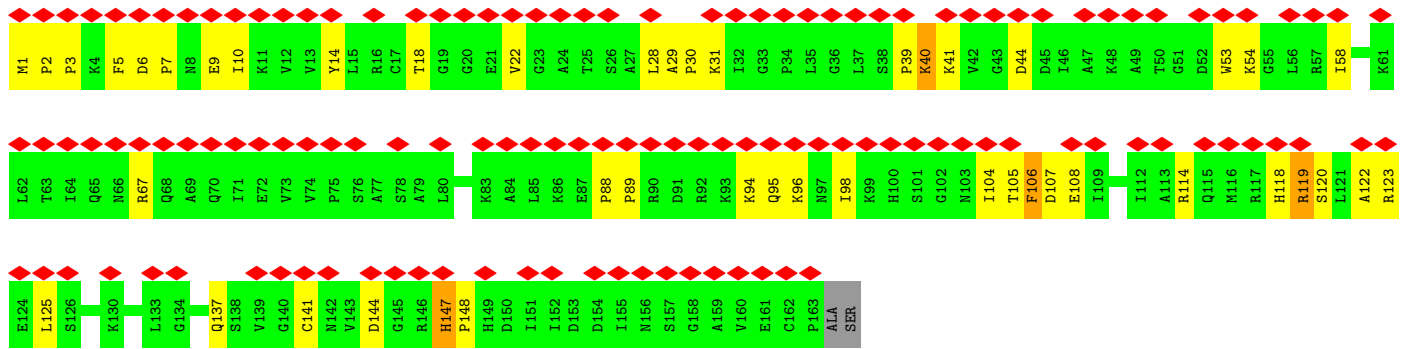
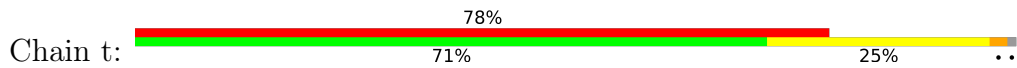


• Molecule 36: eL38

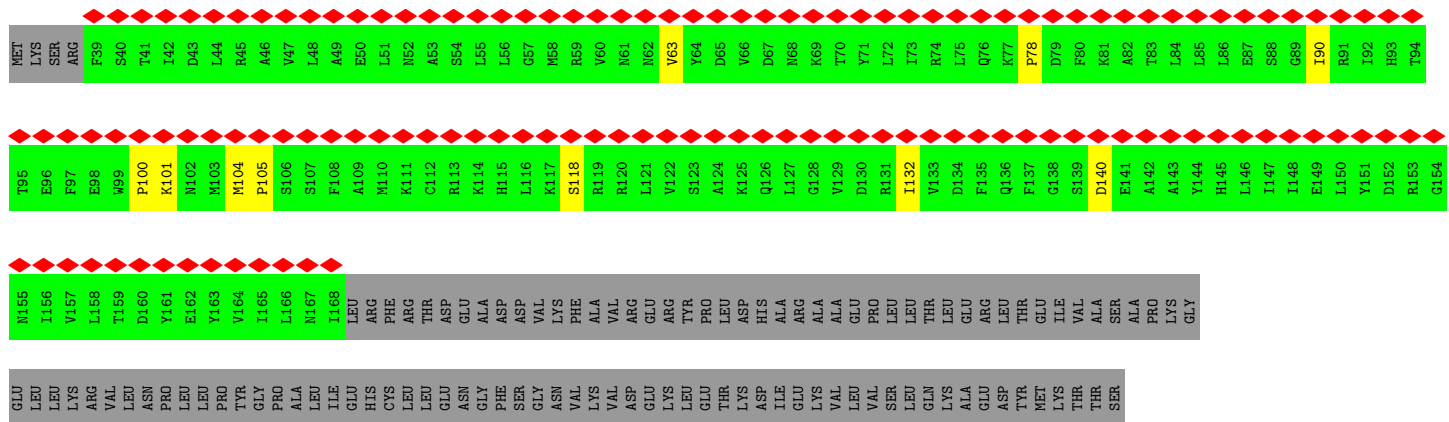


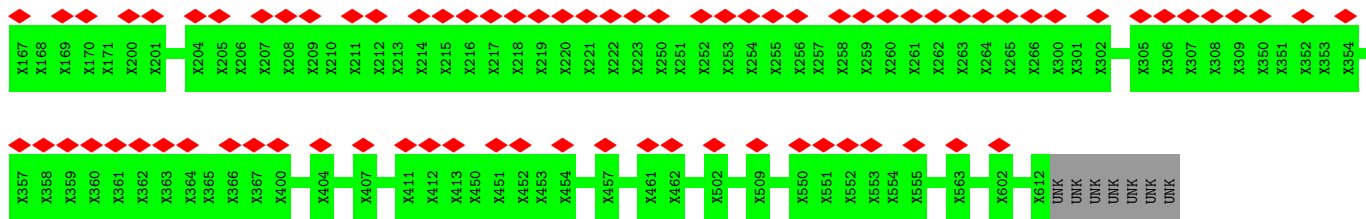


• Molecule 43: uL11

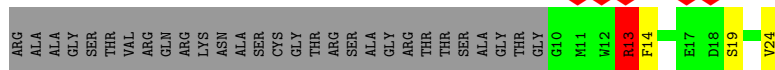


• Molecule 44: NEMF





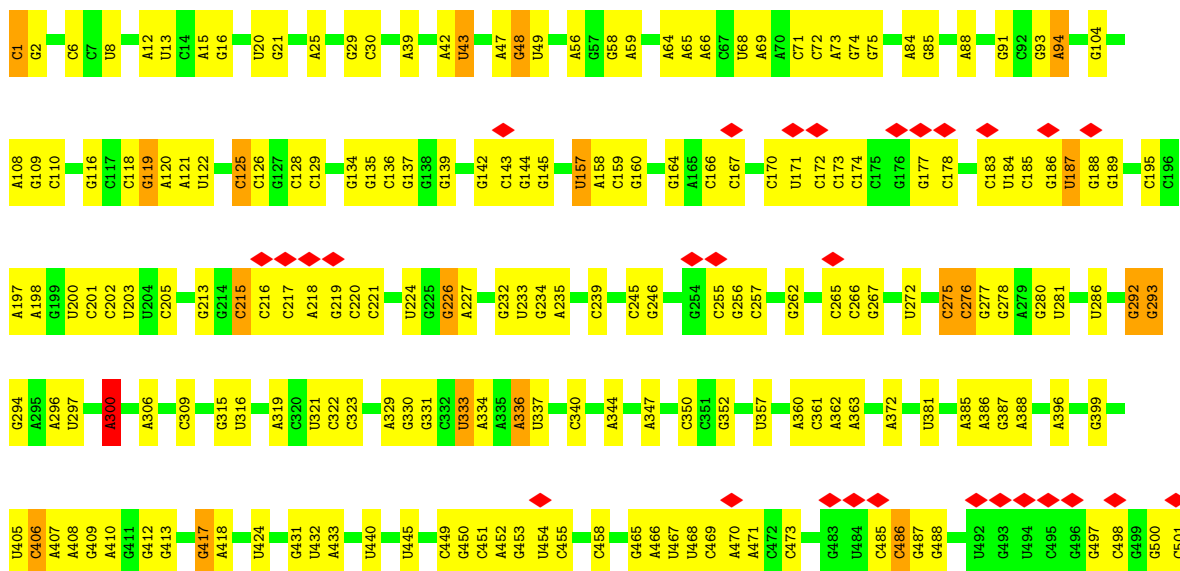
• Molecule 47: nascent chain

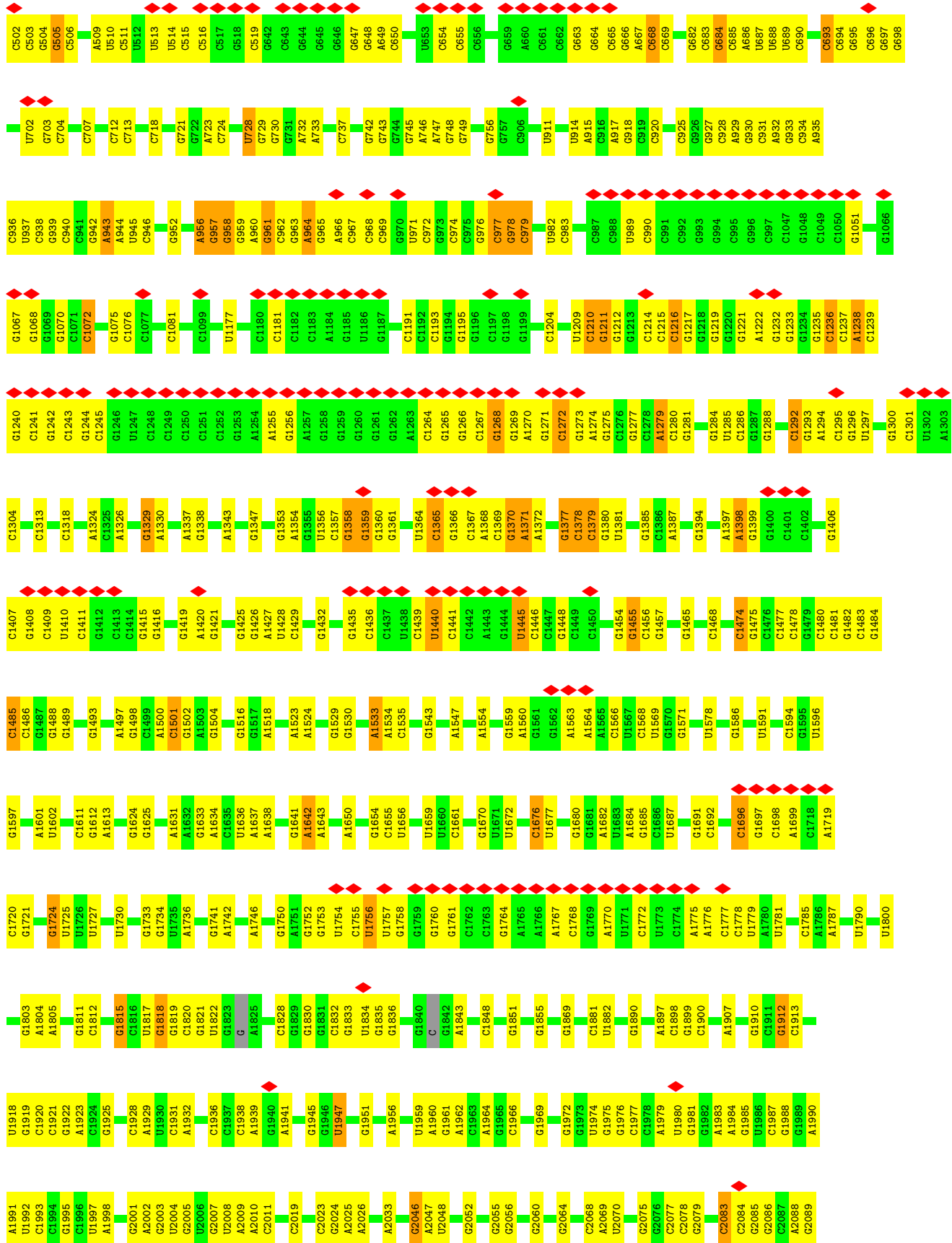


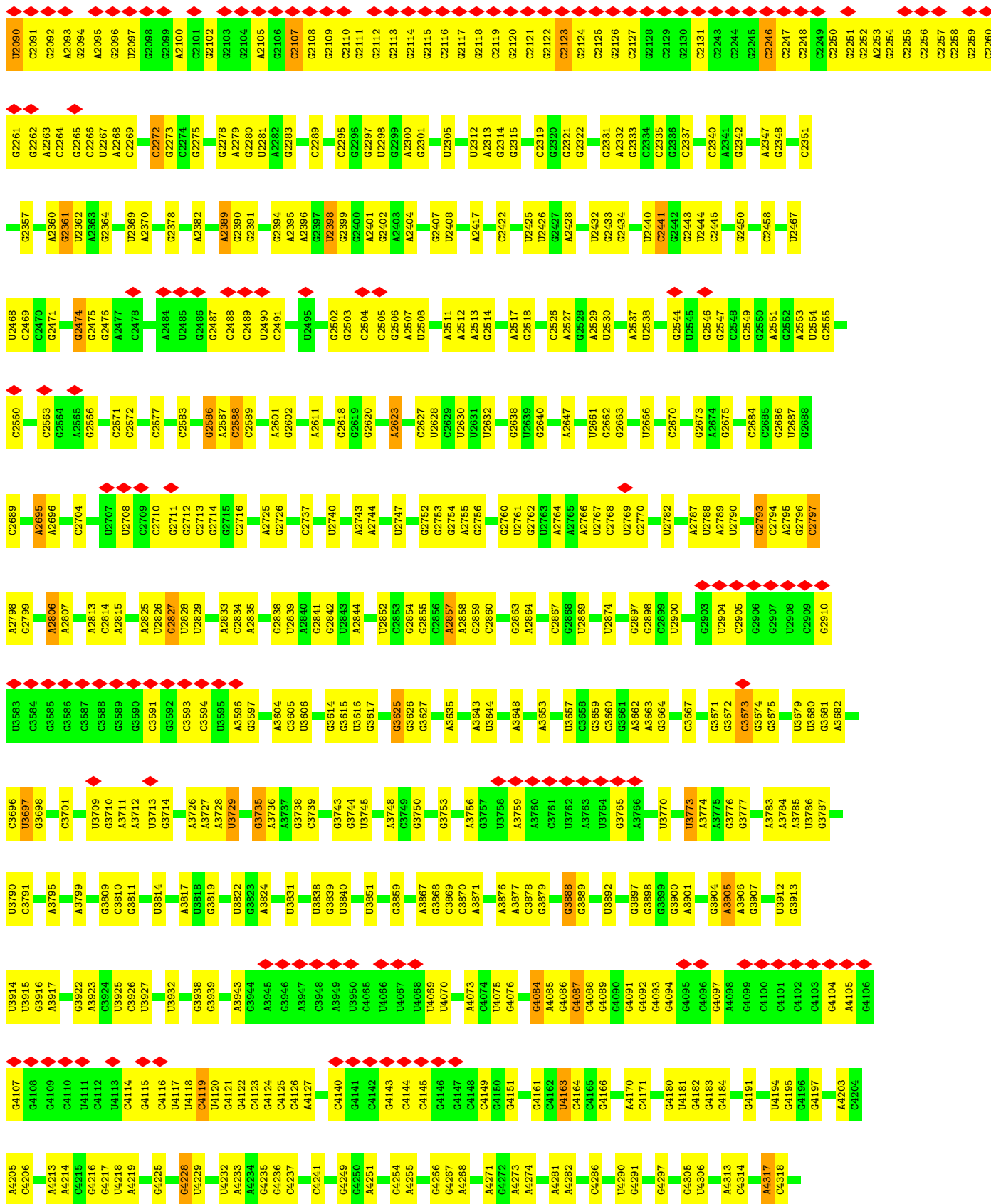
• Molecule 48: tRNA

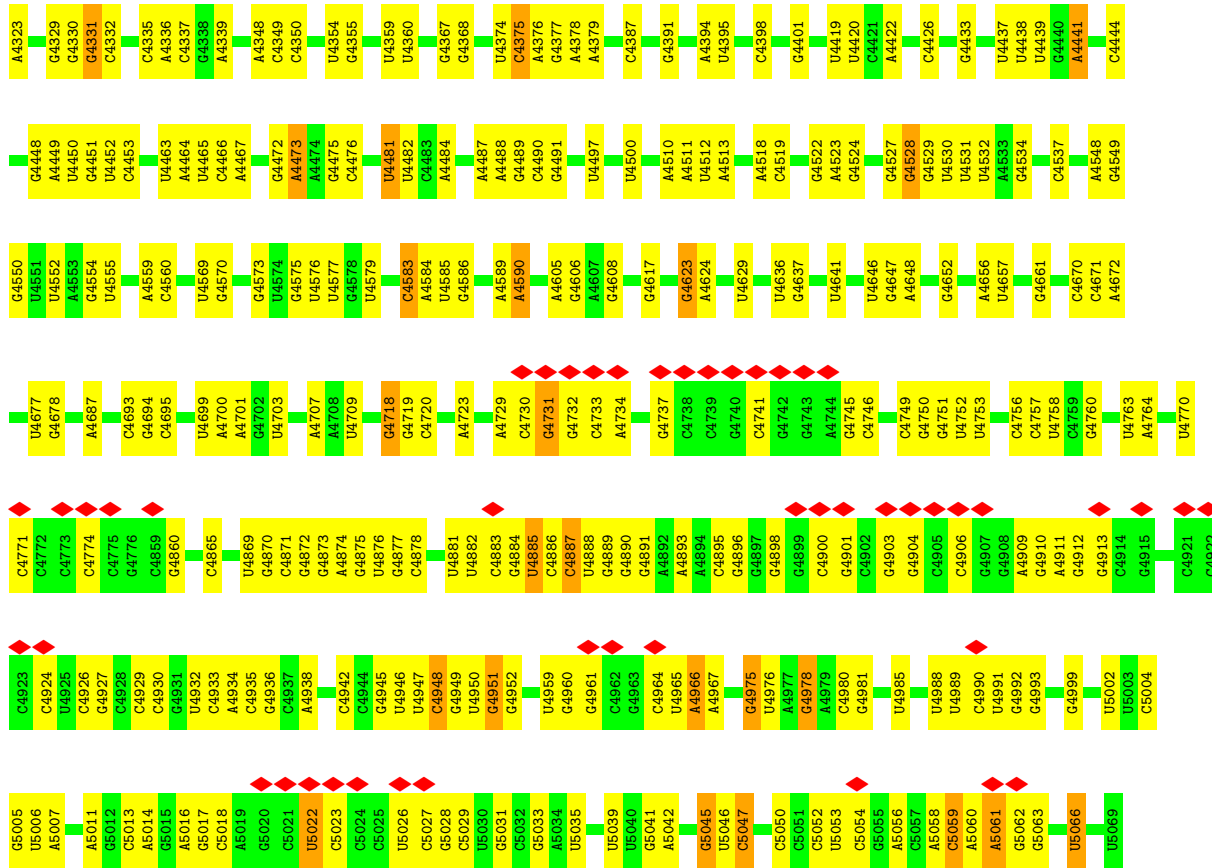


• Molecule 49: 28S rRNA

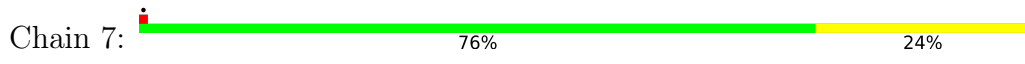




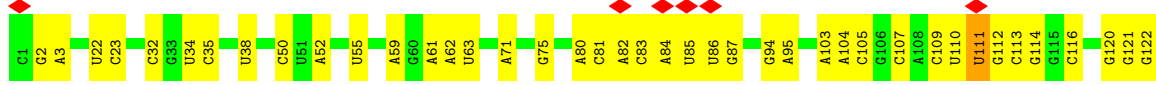




- Molecule 50: 5S rRNA



- Molecule 51: 5.8S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	63826	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS, FEI TITAN KRIOS	Depositor
Voltage (kV)	300, 300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	2000, 2000	Depositor
Maximum defocus (nm)	3500, 3500	Depositor
Magnification	104478, 104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.494	Depositor
Minimum map value	-0.237	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.08	Depositor
Map size (\AA)	428.80002, 428.80002, 428.80002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.34, 1.34, 1.34	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, MG, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.59	0/1906	0.90	2/2556 (0.1%)
2	B	0.57	0/3214	0.88	1/4308 (0.0%)
3	C	0.61	0/2973	0.95	5/3990 (0.1%)
4	D	0.51	0/2430	0.85	3/3256 (0.1%)
5	E	0.52	0/1941	0.95	3/2601 (0.1%)
6	F	0.66	0/1905	1.00	4/2539 (0.2%)
7	G	0.51	0/1971	0.90	2/2652 (0.1%)
8	H	0.52	0/1537	0.91	1/2066 (0.0%)
9	I	0.56	0/1690	0.89	2/2257 (0.1%)
10	J	0.47	0/1382	0.83	1/1849 (0.1%)
11	L	0.59	0/1734	0.98	2/2318 (0.1%)
12	M	0.59	0/1152	0.89	0/1539
13	N	0.62	0/1746	0.97	0/2338
14	O	0.68	0/1671	1.01	1/2234 (0.0%)
15	P	0.62	0/1268	0.89	0/1701
16	Q	0.59	0/1530	0.99	1/2041 (0.0%)
17	R	0.51	0/1524	1.02	3/2013 (0.1%)
18	S	0.62	0/1493	0.97	3/2002 (0.1%)
19	T	0.60	0/1326	0.88	1/1770 (0.1%)
20	U	0.46	0/822	0.83	0/1103
21	V	0.59	0/993	0.86	0/1332
22	W	0.53	0/541	0.90	1/720 (0.1%)
23	X	0.50	0/993	0.85	0/1334
24	Y	0.53	0/1132	0.98	4/1504 (0.3%)
25	Z	0.51	0/1130	0.82	0/1507
26	a	0.68	0/1192	0.95	3/1591 (0.2%)
27	b	0.57	0/620	0.97	1/819 (0.1%)
28	c	0.51	0/742	0.78	0/996
29	d	0.58	0/903	1.03	3/1216 (0.2%)
30	e	0.62	0/1071	0.97	4/1429 (0.3%)
31	f	0.68	0/895	1.00	1/1198 (0.1%)
32	g	0.51	0/916	0.96	3/1220 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.51	0/1023	0.96	3/1350 (0.2%)
34	i	0.50	0/843	1.05	4/1115 (0.4%)
35	j	0.69	0/721	1.00	1/953 (0.1%)
36	k	0.41	0/575	0.83	0/761
37	l	0.57	0/454	0.98	1/599 (0.2%)
38	m	0.56	0/435	0.96	1/575 (0.2%)
39	o	0.53	0/864	0.90	1/1140 (0.1%)
40	p	0.54	0/718	0.89	1/953 (0.1%)
41	r	0.60	0/1017	0.96	0/1365
42	s	0.50	0/1546	0.77	2/2087 (0.1%)
43	t	0.52	0/1257	0.87	1/1697 (0.1%)
44	u	0.46	0/644	0.61	0/897
44	v	0.44	0/1099	0.82	1/1470 (0.1%)
45	0	0.53	0/301	0.69	0/400
45	w	0.47	0/110	0.78	0/146
45	z	0.45	0/1076	0.80	0/1451
47	1	0.59	0/129	0.83	0/173
48	2	0.26	0/1765	0.73	0/2749
49	5	0.49	11/87791 (0.0%)	0.88	177/136941 (0.1%)
50	7	0.42	0/2858	0.72	1/4455 (0.0%)
51	8	0.45	1/3701 (0.0%)	0.77	1/5766 (0.0%)
All	All	0.52	12/155270 (0.0%)	0.88	250/229042 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	4
3	C	0	2
4	D	0	1
5	E	0	4
6	F	0	1
7	G	0	2
8	H	0	1
9	I	0	3
11	L	0	2
13	N	0	1
14	O	0	1
17	R	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
18	S	0	3
19	T	0	3
21	V	0	1
24	Y	0	1
25	Z	0	1
26	a	0	2
27	b	0	1
31	f	0	2
33	h	0	1
34	i	0	1
36	k	0	1
42	s	0	2
43	t	0	4
47	l	0	1
49	5	0	3
All	All	0	52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	5	957	G	O3'-P	8.72	1.71	1.61
49	5	1358	G	O3'-P	7.41	1.70	1.61
49	5	956	A	O3'-P	7.15	1.69	1.61
49	5	1370	G	O3'-P	6.23	1.68	1.61
49	5	4375	C	O3'-P	-5.70	1.54	1.61

The worst 5 of 250 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	5	1358	G	C4'-C3'-O3'	11.60	136.20	113.00
24	Y	87	ARG	NE-CZ-NH2	10.23	125.41	120.30
34	i	25	ARG	NE-CZ-NH1	10.20	125.40	120.30
18	S	83	ARG	NE-CZ-NH2	9.56	125.08	120.30
49	5	336	A	O4'-C1'-N9	9.31	115.65	108.20

There are no chirality outliers.

5 of 52 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	131	GLY	Peptide
2	B	17	LEU	Peptide

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Mol	Chain	Res	Type	Group
2	B	257	TRP	Peptide
2	B	332	MET	Peptide
2	B	351	LEU	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	A	242/257 (94%)	203 (84%)	28 (12%)	11 (4%)	2	23
2	B	392/395 (99%)	342 (87%)	44 (11%)	6 (2%)	10	47
3	C	365/368 (99%)	315 (86%)	43 (12%)	7 (2%)	8	42
4	D	290/297 (98%)	266 (92%)	18 (6%)	6 (2%)	7	40
5	E	232/284 (82%)	176 (76%)	39 (17%)	17 (7%)	1	13
6	F	223/250 (89%)	203 (91%)	16 (7%)	4 (2%)	8	43
7	G	239/266 (90%)	196 (82%)	36 (15%)	7 (3%)	4	33
8	H	188/192 (98%)	164 (87%)	17 (9%)	7 (4%)	3	28
9	I	200/214 (94%)	171 (86%)	22 (11%)	7 (4%)	3	30
10	J	168/178 (94%)	143 (85%)	17 (10%)	8 (5%)	2	22
11	L	208/211 (99%)	174 (84%)	22 (11%)	12 (6%)	1	18
12	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	10	47
13	N	201/204 (98%)	172 (86%)	28 (14%)	1 (0%)	29	68
14	O	197/204 (97%)	173 (88%)	23 (12%)	1 (0%)	29	68
15	P	151/184 (82%)	133 (88%)	17 (11%)	1 (1%)	22	61
16	Q	185/188 (98%)	161 (87%)	22 (12%)	2 (1%)	14	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	R	178/196 (91%)	160 (90%)	14 (8%)	4 (2%)	6	39
18	S	173/224 (77%)	153 (88%)	16 (9%)	4 (2%)	6	38
19	T	157/160 (98%)	136 (87%)	19 (12%)	2 (1%)	12	50
20	U	97/128 (76%)	84 (87%)	9 (9%)	4 (4%)	3	26
21	V	129/140 (92%)	112 (87%)	16 (12%)	1 (1%)	19	59
22	W	61/157 (39%)	55 (90%)	5 (8%)	1 (2%)	9	46
23	X	117/156 (75%)	105 (90%)	11 (9%)	1 (1%)	17	57
24	Y	132/145 (91%)	121 (92%)	9 (7%)	2 (2%)	10	47
25	Z	133/136 (98%)	115 (86%)	13 (10%)	5 (4%)	3	27
26	a	145/148 (98%)	118 (81%)	20 (14%)	7 (5%)	2	22
27	b	73/160 (46%)	68 (93%)	4 (6%)	1 (1%)	11	48
28	c	92/115 (80%)	86 (94%)	5 (5%)	1 (1%)	14	53
29	d	105/125 (84%)	93 (89%)	9 (9%)	3 (3%)	4	33
30	e	126/135 (93%)	113 (90%)	11 (9%)	2 (2%)	9	46
31	f	107/110 (97%)	93 (87%)	10 (9%)	4 (4%)	3	28
32	g	112/117 (96%)	98 (88%)	12 (11%)	2 (2%)	8	43
33	h	120/123 (98%)	103 (86%)	16 (13%)	1 (1%)	19	59
34	i	100/105 (95%)	92 (92%)	5 (5%)	3 (3%)	4	33
35	j	84/97 (87%)	70 (83%)	12 (14%)	2 (2%)	6	37
36	k	67/70 (96%)	56 (84%)	8 (12%)	3 (4%)	2	23
37	l	48/51 (94%)	38 (79%)	8 (17%)	2 (4%)	3	25
38	m	50/128 (39%)	45 (90%)	3 (6%)	2 (4%)	3	26
39	o	102/106 (96%)	88 (86%)	11 (11%)	3 (3%)	4	33
40	p	89/92 (97%)	74 (83%)	13 (15%)	2 (2%)	6	39
41	r	123/137 (90%)	102 (83%)	18 (15%)	3 (2%)	6	37
42	s	196/317 (62%)	159 (81%)	22 (11%)	15 (8%)	1	12
43	t	161/165 (98%)	93 (58%)	39 (24%)	29 (18%)	0	2
44	u	128/501 (26%)	88 (69%)	30 (23%)	10 (8%)	1	11
44	v	130/501 (26%)	125 (96%)	3 (2%)	2 (2%)	10	47
45	0	34/1766 (2%)	29 (85%)	3 (9%)	2 (6%)	1	18
45	w	13/1766 (1%)	13 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	z	120/1766 (7%)	106 (88%)	10 (8%)	4 (3%)	4	31
47	1	13/104 (12%)	9 (69%)	1 (8%)	3 (23%)	0	0
All	All	7132/14052 (51%)	6110 (86%)	793 (11%)	229 (3%)	7	31

5 of 229 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	PHE
1	A	195	CYS
2	B	18	PRO
3	C	273	LEU
5	E	91	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	187/199 (94%)	155 (83%)	32 (17%)	2	13
2	B	335/336 (100%)	285 (85%)	50 (15%)	3	19
3	C	305/306 (100%)	243 (80%)	62 (20%)	1	8
4	D	247/250 (99%)	207 (84%)	40 (16%)	2	15
5	E	209/246 (85%)	172 (82%)	37 (18%)	2	11
6	F	194/217 (89%)	156 (80%)	38 (20%)	1	8
7	G	208/226 (92%)	170 (82%)	38 (18%)	1	10
8	H	169/171 (99%)	135 (80%)	34 (20%)	1	8
9	I	174/181 (96%)	137 (79%)	37 (21%)	1	7
10	J	143/149 (96%)	124 (87%)	19 (13%)	4	23
11	L	176/177 (99%)	137 (78%)	39 (22%)	1	6
12	M	116/160 (72%)	95 (82%)	21 (18%)	1	11
13	N	171/172 (99%)	142 (83%)	29 (17%)	2	14
14	O	171/174 (98%)	149 (87%)	22 (13%)	4	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	P	134/163 (82%)	110 (82%)	24 (18%)	2	11
16	Q	163/164 (99%)	137 (84%)	26 (16%)	2	16
17	R	159/175 (91%)	126 (79%)	33 (21%)	1	7
18	S	156/192 (81%)	125 (80%)	31 (20%)	1	8
19	T	139/140 (99%)	111 (80%)	28 (20%)	1	8
20	U	89/114 (78%)	72 (81%)	17 (19%)	1	9
21	V	101/107 (94%)	86 (85%)	15 (15%)	3	19
22	W	55/126 (44%)	49 (89%)	6 (11%)	6	32
23	X	107/133 (80%)	91 (85%)	16 (15%)	3	19
24	Y	124/135 (92%)	104 (84%)	20 (16%)	2	16
25	Z	117/118 (99%)	101 (86%)	16 (14%)	3	22
26	a	119/120 (99%)	102 (86%)	17 (14%)	3	21
27	b	63/123 (51%)	52 (82%)	11 (18%)	2	12
28	c	79/97 (81%)	69 (87%)	10 (13%)	4	24
29	d	98/110 (89%)	78 (80%)	20 (20%)	1	8
30	e	114/121 (94%)	83 (73%)	31 (27%)	0	3
31	f	88/89 (99%)	67 (76%)	21 (24%)	0	4
32	g	98/100 (98%)	75 (76%)	23 (24%)	1	5
33	h	109/110 (99%)	90 (83%)	19 (17%)	2	12
34	i	86/89 (97%)	73 (85%)	13 (15%)	3	19
35	j	73/80 (91%)	57 (78%)	16 (22%)	1	6
36	k	64/65 (98%)	51 (80%)	13 (20%)	1	8
37	l	47/48 (98%)	37 (79%)	10 (21%)	1	7
38	m	48/116 (41%)	37 (77%)	11 (23%)	1	5
39	o	92/94 (98%)	71 (77%)	21 (23%)	1	5
40	p	74/75 (99%)	60 (81%)	14 (19%)	1	9
41	r	109/121 (90%)	88 (81%)	21 (19%)	1	9
42	s	166/258 (64%)	148 (89%)	18 (11%)	6	32
43	t	136/137 (99%)	120 (88%)	16 (12%)	5	28
44	v	116/445 (26%)	99 (85%)	17 (15%)	3	20
45	0	34/1611 (2%)	30 (88%)	4 (12%)	5	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	w	11/1611 (1%)	9 (82%)	2 (18%)	1	10
45	z	119/1611 (7%)	103 (87%)	16 (13%)	4	23
47	1	13/79 (16%)	11 (85%)	2 (15%)	2	18
All	All	6105/11841 (52%)	5029 (82%)	1076 (18%)	4	12

5 of 1076 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	l	16	LYS
39	o	44	LYS
37	l	8	ARG
44	v	342	GLU
11	L	10	LEU

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

Mol	Chain	Res	Type
33	h	96	ASN
39	o	90	HIS
12	M	56	GLN
11	L	28	GLN
41	r	6	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
48	2	73/77 (94%)	31 (42%)	2 (2%)
49	5	3646/3664 (99%)	1364 (37%)	373 (10%)
50	7	119/120 (99%)	27 (22%)	1 (0%)
51	8	155/156 (99%)	50 (32%)	9 (5%)
All	All	3993/4017 (99%)	1472 (36%)	385 (9%)

5 of 1472 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
48	2	3	C
48	2	5	G
48	2	7	G
48	2	11	A

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Mol	Chain	Res	Type
48	2	13	C

5 of 385 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	5	2513	A
49	5	3888	G
49	5	2588	C
49	5	2857	A
49	5	4124	G

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

1 non-standard protein/DNA/RNA residue 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
48	5MU	2	54	48	19,22,23	1.49	4 (21%)	28,32,35	1.98	8 (28%)

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
48	5MU	2	54	48	-	2/7/25/26	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	2	54	5MU	C6-C5	3.34	1.40	1.34
48	2	54	5MU	C2-N1	3.13	1.43	1.38
48	2	54	5MU	C4-C5	2.69	1.49	1.44
48	2	54	5MU	C4-N3	-2.13	1.34	1.38

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
48	2	54	5MU	N3-C2-N1	4.82	121.28	114.89
48	2	54	5MU	C4-N3-C2	-4.22	121.89	127.35
48	2	54	5MU	C5-C4-N3	3.88	118.62	115.31
48	2	54	5MU	O4-C4-C5	-3.33	121.04	124.90
48	2	54	5MU	C5M-C5-C4	2.83	121.88	118.77

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
48	2	54	5MU	O4'-C4'-C5'-O5'
48	2	54	5MU	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 164 ligands modelled in this entry, 164 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
46	x	14
49	5	13
46	y	12

The worst 5 of 39 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	x	1211:UNK	C	1300:UNK	N	25.67
1	x	608:UNK	C	700:UNK	N	22.35
1	x	1014:UNK	C	1100:UNK	N	19.48
1	x	817:UNK	C	900:UNK	N	18.97
1	y	223:UNK	C	250:UNK	N	18.15

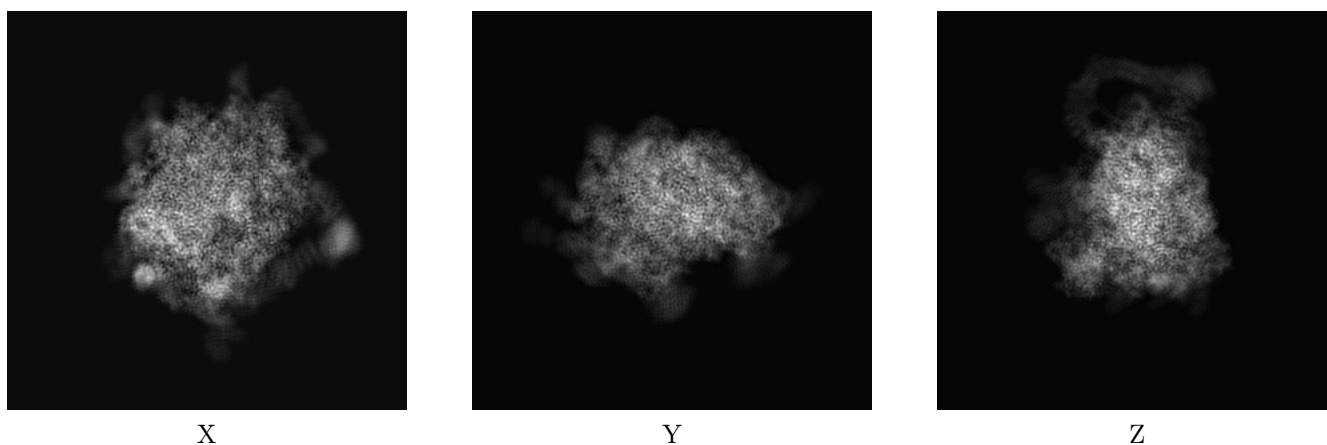
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2832. 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](#)

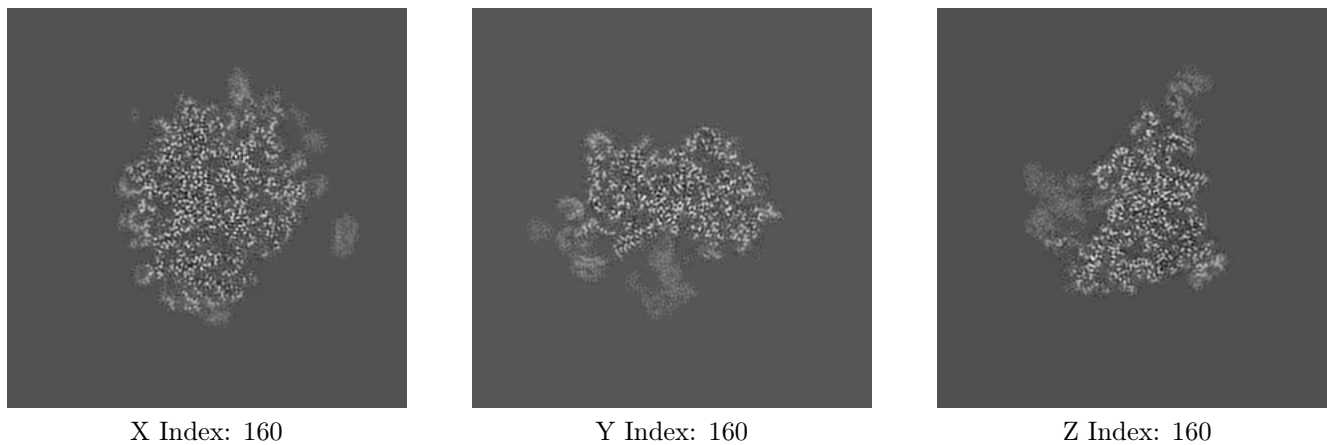
6.1.1 Primary map



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

6.2 Central slices [i](#)

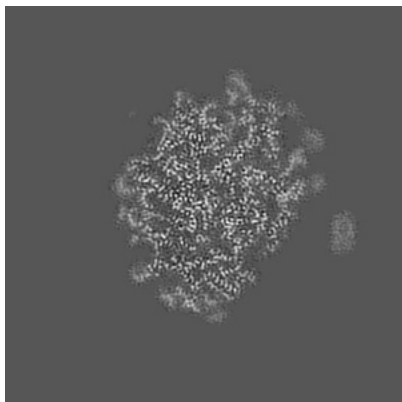
6.2.1 Primary map



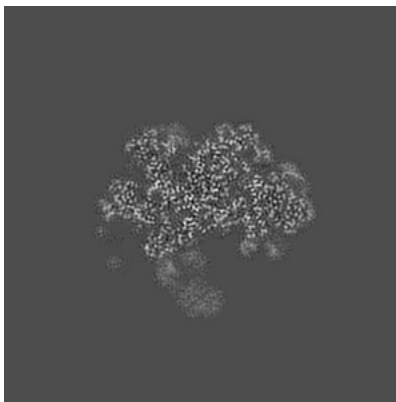
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

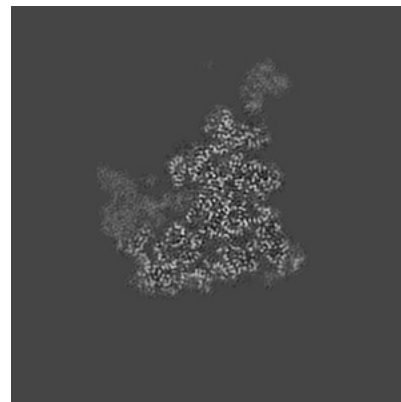
6.3.1 Primary map



X Index: 158



Y Index: 149



Z Index: 156

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

6.4 Orthogonal surface views [i](#)

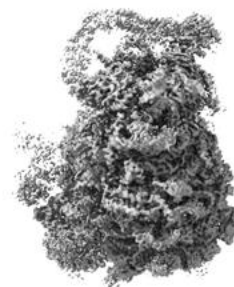
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

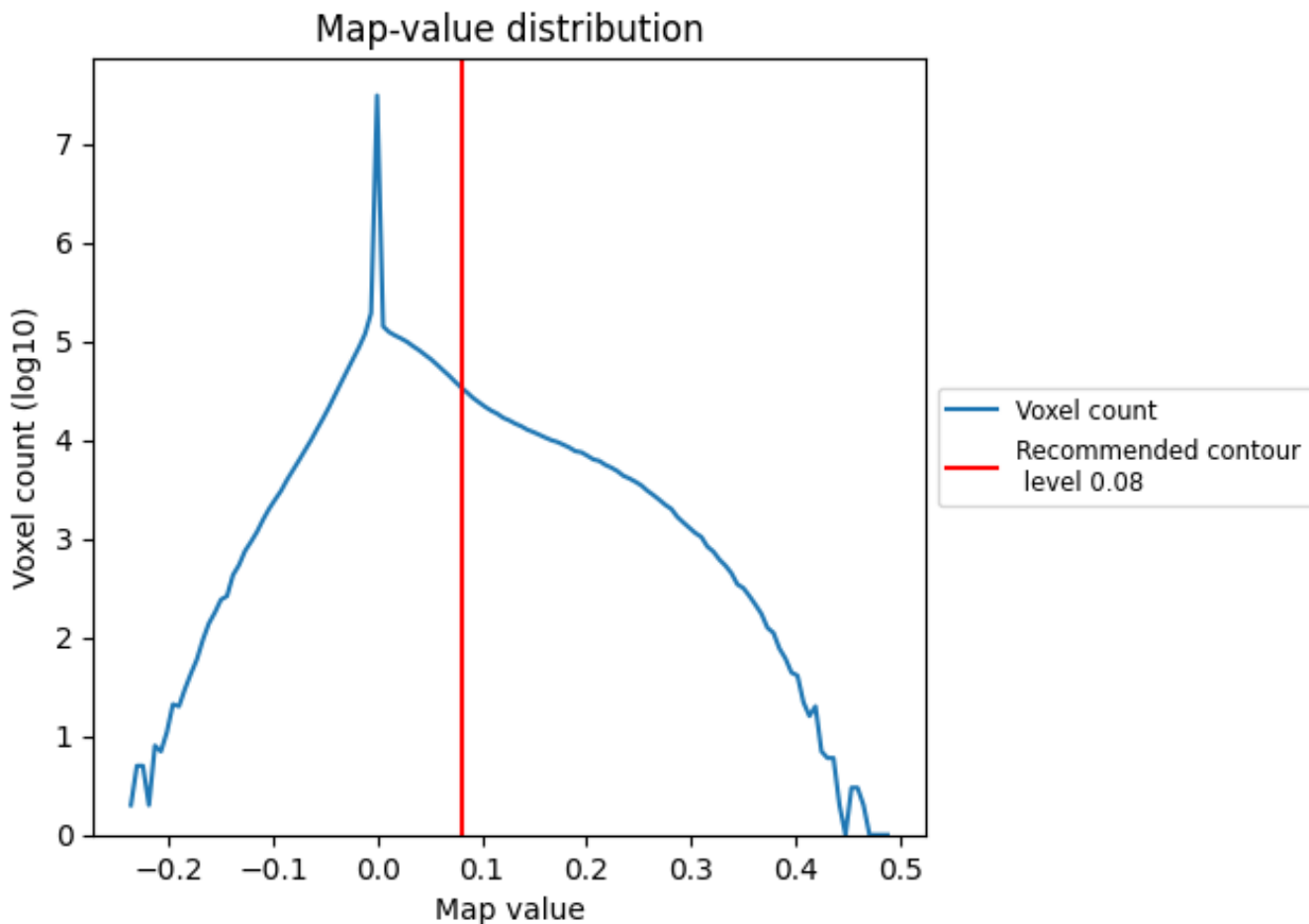
6.5 Mask visualisation

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

7 Map analysis [i](#)

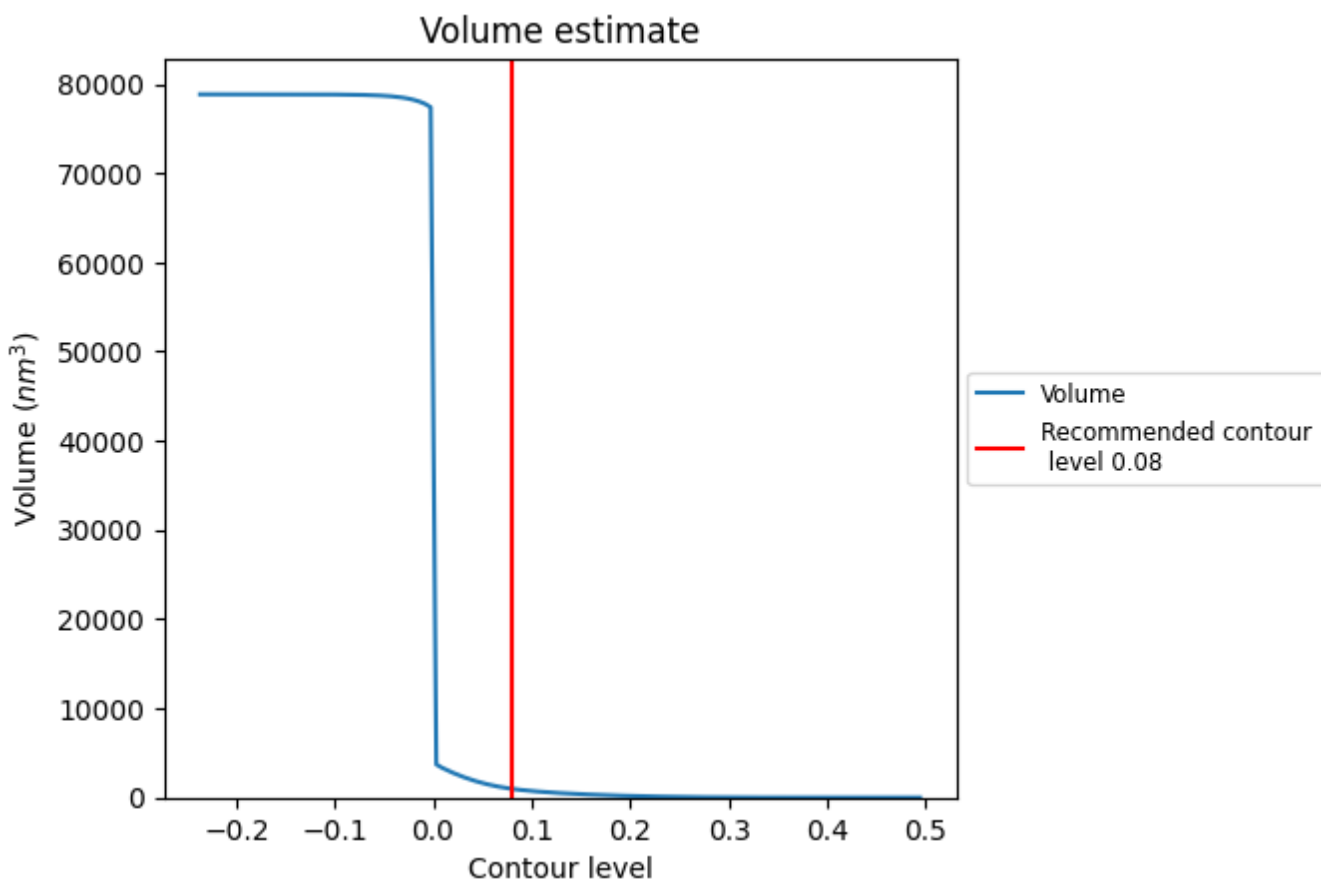
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

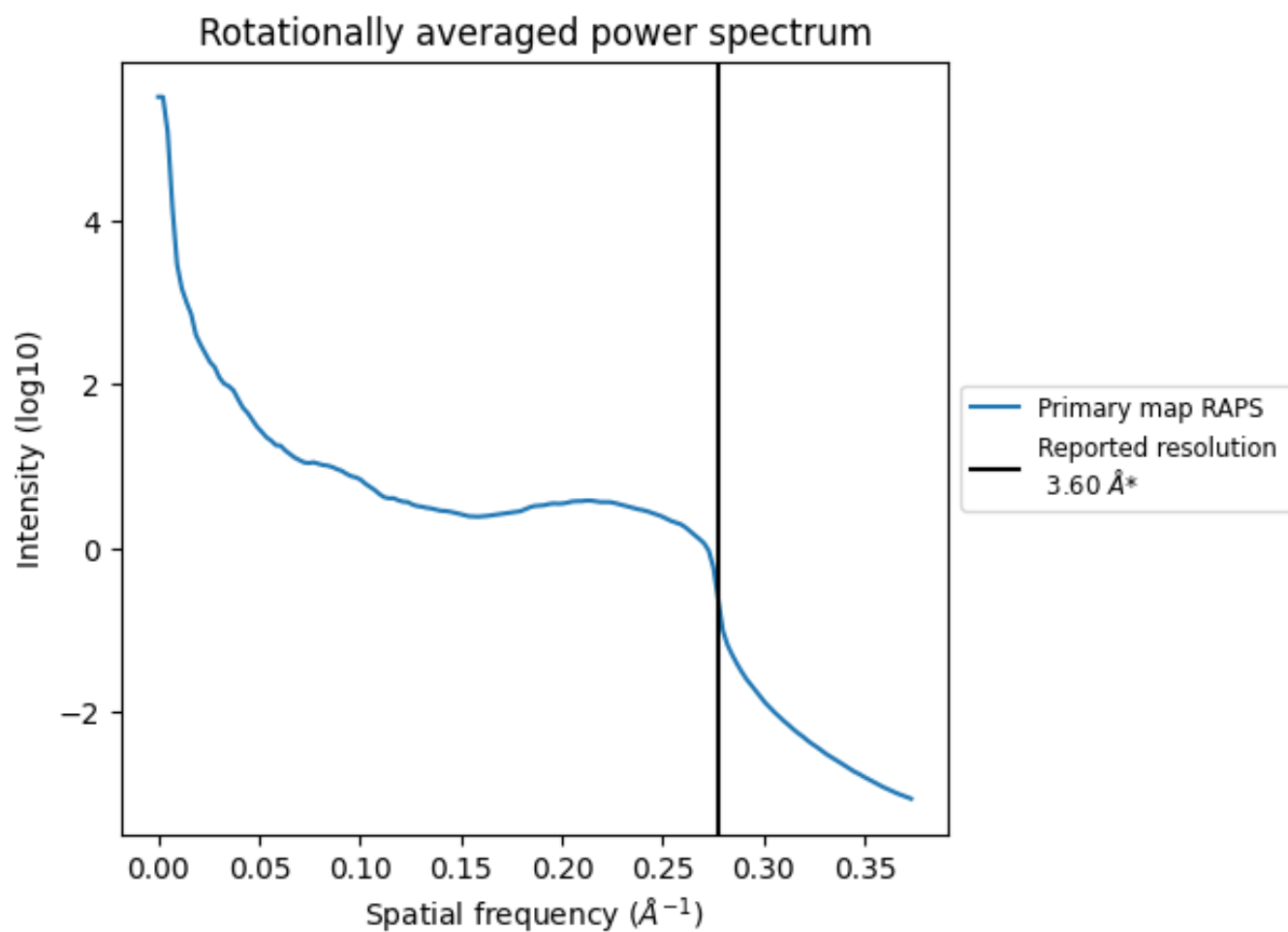
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 982 nm³; this corresponds to an approximate mass of 887 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 0.278\AA^{-1}

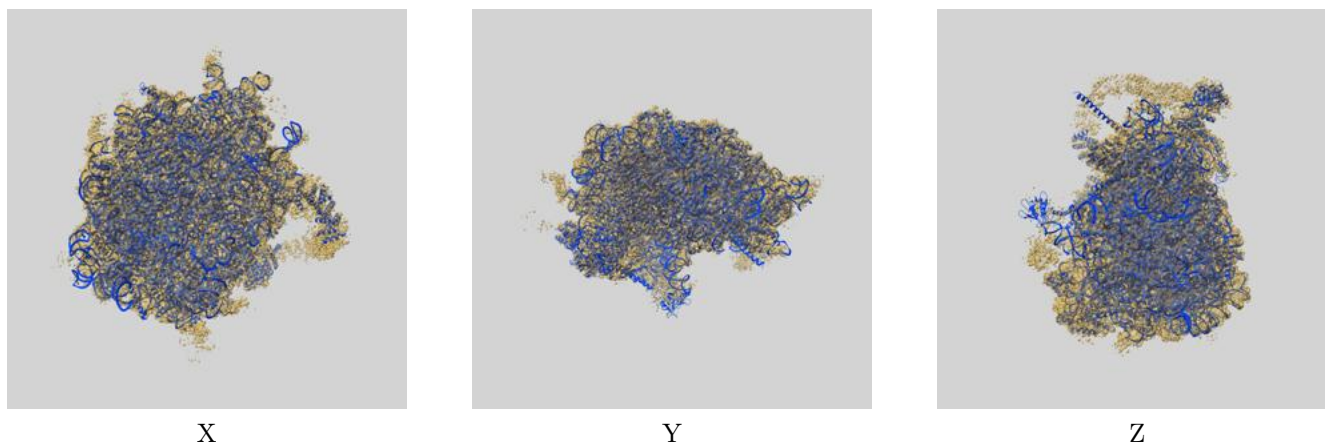
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

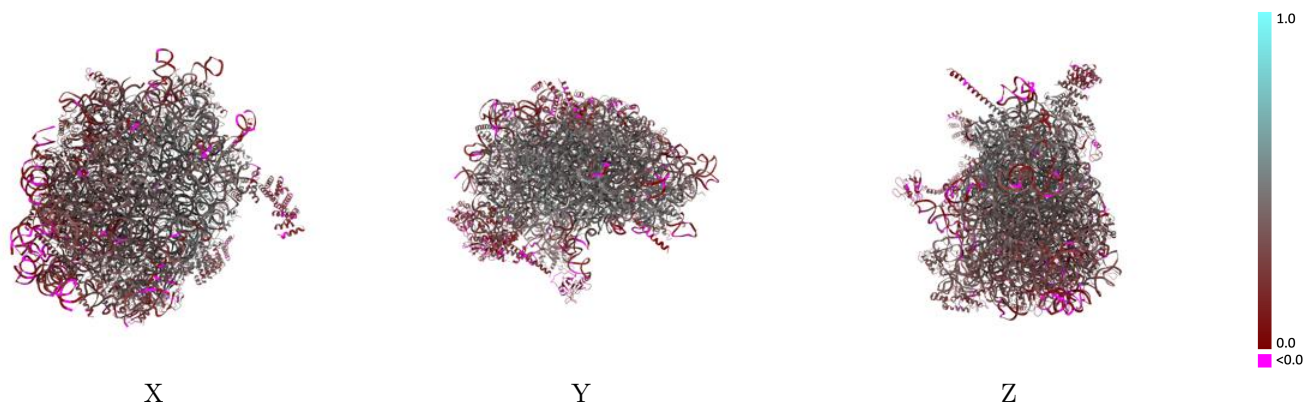
This section contains information regarding the fit between EMDB map EMD-2832 and PDB model 3J92. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



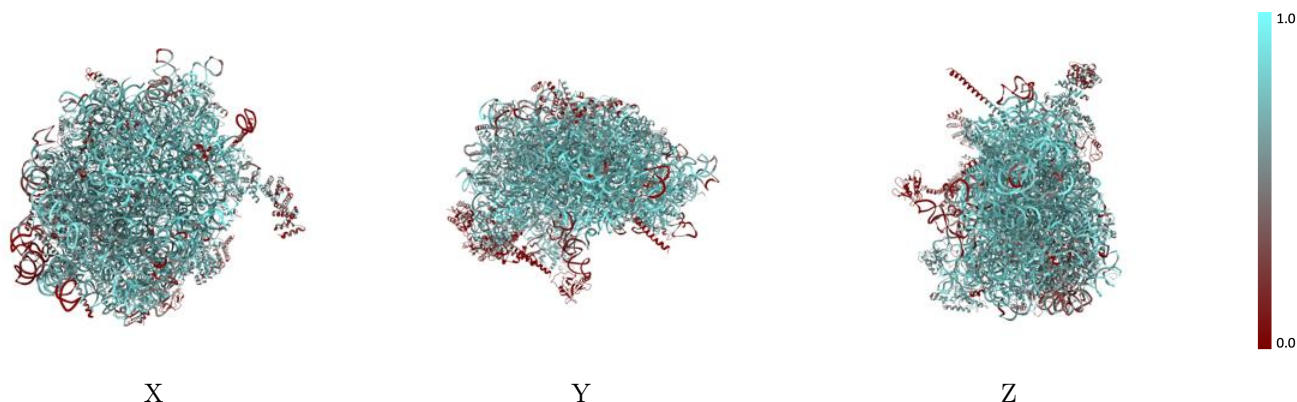
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



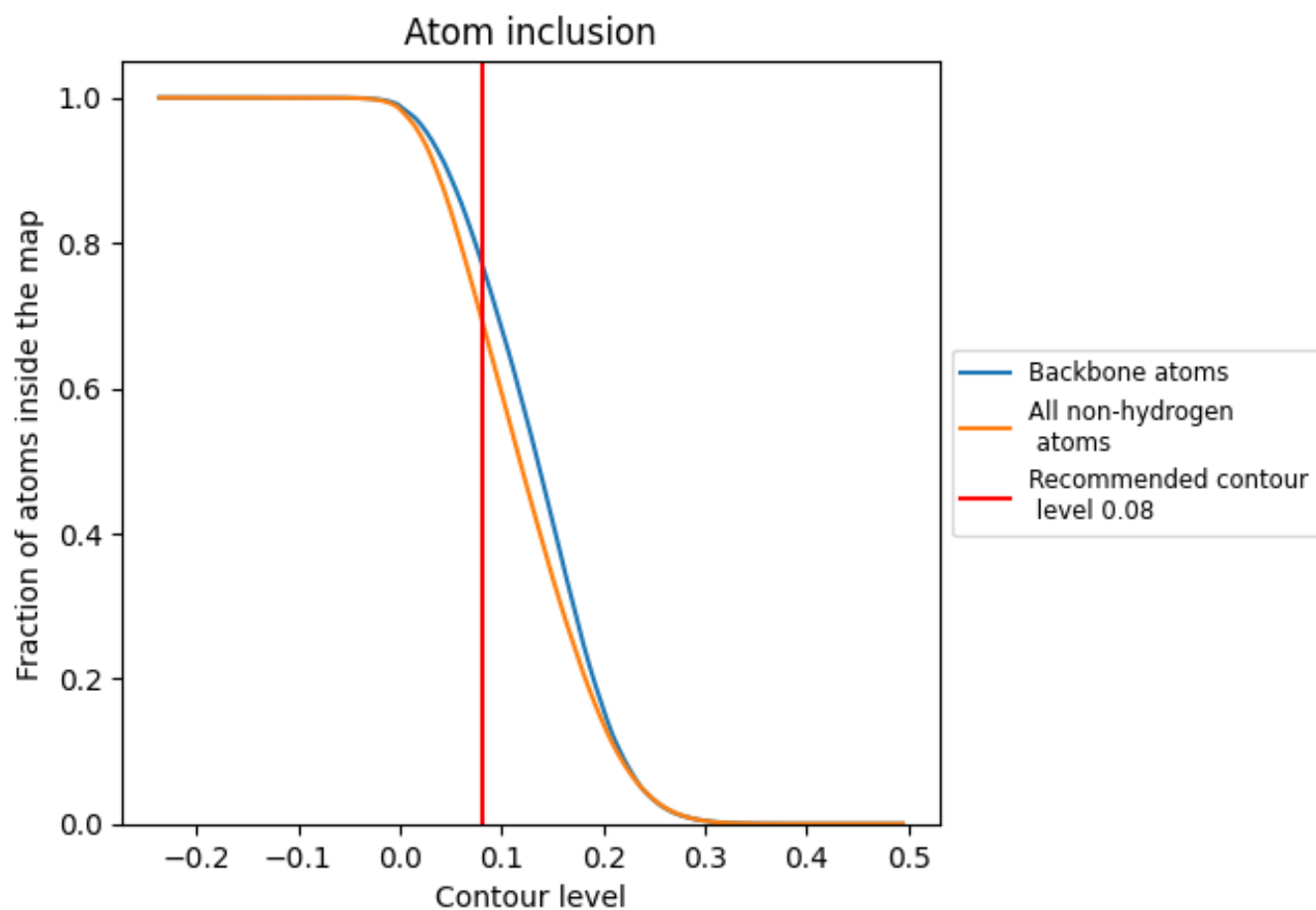
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).







































































9.4 Atom inclusion [i](#)

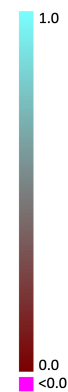


At the recommended contour level, 77% of all backbone atoms, 70% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary











































The table lists the average atom inclusion at the recommended contour level (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6966	 0.3400
0	 0.1045	 0.1200
1	 0.4959	 0.3720
2	 0.1424	 0.1480
5	 0.7507	 0.3290
7	 0.7885	 0.3270
8	 0.7774	 0.3580
A	 0.7643	 0.4550
B	 0.7693	 0.4700
C	 0.6623	 0.3490
D	 0.6232	 0.2770
E	 0.6089	 0.3340
F	 0.6591	 0.3210
G	 0.5915	 0.3360
H	 0.6804	 0.3990
I	 0.6843	 0.3810
J	 0.6240	 0.3070
L	 0.6224	 0.3110
M	 0.6946	 0.3750
N	 0.7327	 0.3860
O	 0.7359	 0.4310
P	 0.7531	 0.4430
Q	 0.6542	 0.3320
R	 0.6343	 0.3880
S	 0.6957	 0.3580
T	 0.6469	 0.3510
U	 0.6785	 0.4340
V	 0.7526	 0.4820
W	 0.7112	 0.4620
X	 0.6828	 0.4060
Y	 0.6809	 0.3670
Z	 0.6887	 0.4210
a	 0.6953	 0.3540
b	 0.5505	 0.2830
c	 0.7259	 0.4490



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Chain	Atom inclusion	Q-score
d	 0.7001	 0.4590
e	 0.7050	 0.3930
f	 0.7387	 0.4080
g	 0.7084	 0.4350
h	 0.6487	 0.3590
i	 0.6391	 0.3470
j	 0.7493	 0.4210
k	 0.5799	 0.3760
l	 0.7021	 0.4410
m	 0.7091	 0.4040
o	 0.6477	 0.3570
p	 0.7184	 0.4660
r	 0.6774	 0.3480
s	 0.2367	 0.1680
t	 0.2130	 0.1390
u	 0.0109	 0.0690
v	 0.3544	 0.2610
w	 0.4906	 0.3660
x	 0.4688	 0.2410
y	 0.4038	 0.2100
z	 0.4927	 0.3510