



Full wwPDB EM Validation Report ⓘ

Nov 7, 2022 – 04:09 PM JST

PDB ID : 5XXU
EMDB ID : EMD-6780
Title : Small subunit of Toxoplasma gondii ribosome
Authors : LI, Z.; Guo, Q.; Zheng, L.; Ji, Y.; Xie, Y.; Lai, D.; Lun, Z.; Suo, X.; Gao, N.
Deposited on : 2017-07-05
Resolution : 3.35 Å (reported)

This is a Full wwPDB EM Validation 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:

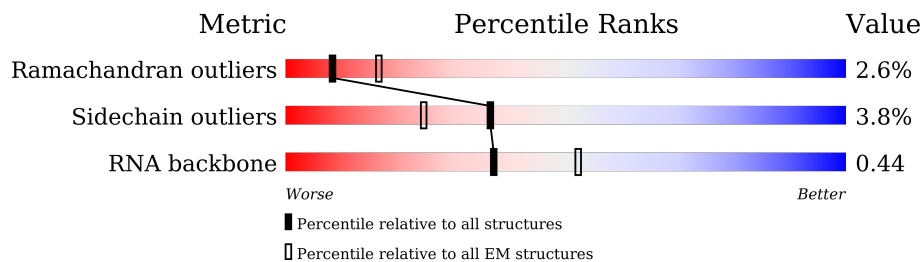
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 3.35 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.



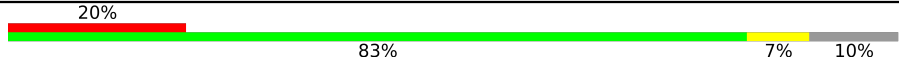
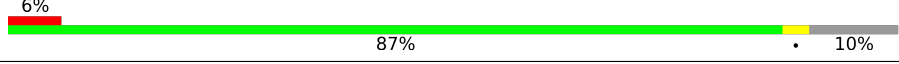
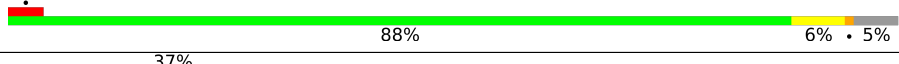


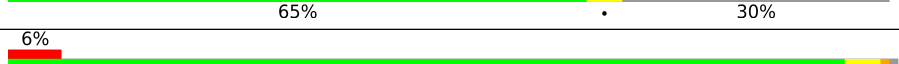
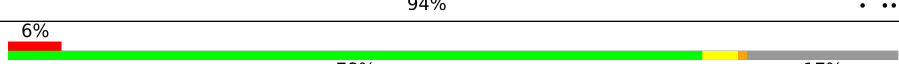
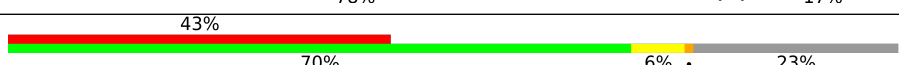
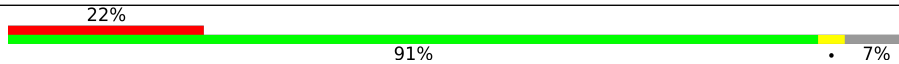


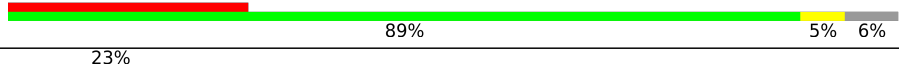


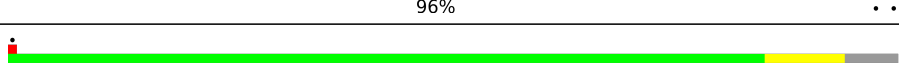
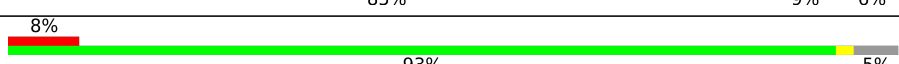
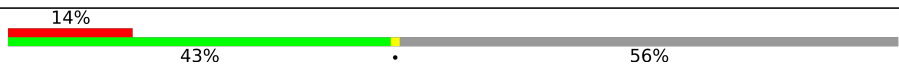

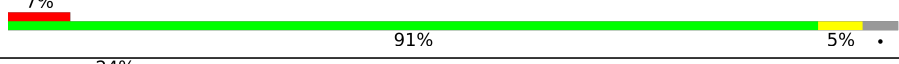

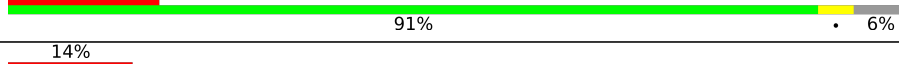




Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	2	1791	
2	A	287	
3	B	259	
4	C	269	
5	D	235	
6	E	263	
7	F	192	
8	G	256	


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Mol	Chain	Length	Quality of chain
9	H	196	
10	I	205	
11	J	188	
12	K	152	
13	L	161	
14	M	142	
15	N	151	
16	O	156	
17	P	150	
18	Q	148	
19	R	132	
20	S	156	
21	T	160	
22	U	233	
23	V	82	
24	W	130	
25	X	143	
26	Y	135	
27	Z	161	
28	a	112	
29	b	82	
30	c	68	
31	d	54	
32	e	59	
33	f	154	

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Mol	Chain	Length	Quality of chain
34	m	39	 85% 10% . .

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 68955 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 RNA chain called 18S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	1619	34513	15429	6130	11335	1619	0	0

- Molecule 2 is a protein called Ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	198	1565	1003	271	279	12	0	0

- Molecule 3 is a protein called Ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	212	1691	1070	301	303	17	0	0

- Molecule 4 is a protein called Ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	C	225	1750	1124	311	306	9	0	0

- Molecule 5 is a protein called Ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	D	200	1568	987	291	279	11	0	0

- Molecule 6 is a protein called Ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	E	259	2085	1325	400	346	14	0	0

- Molecule 7 is a protein called Ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	F	187	1475	921	280	263	11	0	0

- Molecule 8 is a protein called Ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	G	220	1782	1118	354	303	7	0	0

- Molecule 9 is a protein called Ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	H	177	1354	862	250	238	4	0	0

- Molecule 10 is a protein called Ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	I	185	1496	936	298	254	8	0	0

- Molecule 11 is a protein called Ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	J	178	1457	924	286	244	3	0	0

- Molecule 12 is a protein called Ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	K	94	675	433	118	122	2	0	0

- Molecule 13 is a protein called Ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L	147	1206	766	231	203	6	0	0

- Molecule 14 is a protein called Ribosomal protein eS12.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	M	99	Total	C	N	O	0	0
			508	307	99	102		

- Molecule 15 is a protein called Ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	150	Total	C	N	O	S	0	0
			1204	773	225	204	2		

- Molecule 16 is a protein called Ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	129	Total	C	N	O	S	0	0
			966	591	194	177	4		

- Molecule 17 is a protein called Ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	115	Total	C	N	O	S	0	0
			939	603	168	162	6		

- Molecule 18 is a protein called Ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	138	Total	C	N	O	S	0	0
			1086	693	205	185	3		

- Molecule 19 is a protein called Ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	117	Total	C	N	O	S	0	0
			947	590	182	171	4		

- Molecule 20 is a protein called Ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	135	Total	C	N	O	S	0	0
			1091	684	219	186	2		

- Molecule 21 is a protein called Ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	T	151	1236	789	233	210	4	0	0

- Molecule 22 is a protein called Ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	U	103	823	517	153	151	2	0	0

- Molecule 23 is a protein called Ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	V	80	618	379	119	116	4	0	0

- Molecule 24 is a protein called Ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	W	129	1040	660	195	178	7	0	0

- Molecule 25 is a protein called Ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	X	135	1040	659	203	177	1	0	0

- Molecule 26 is a protein called Ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	Y	128	1020	647	200	171	2	0	0

- Molecule 27 is a protein called Ribosomal protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	Z	71	576	365	108	102	1	0	0

- Molecule 28 is a protein called Ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	99	Total	C	N	O	S	0	0
			794	480	171	137	6		

- Molecule 29 is a protein called Ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	79	Total	C	N	O	S	0	0
			605	383	106	107	9		

- Molecule 30 is a protein called Ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	57	Total	C	N	O	S	0	0
			448	279	91	77	1		

- Molecule 31 is a protein called Ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	51	Total	C	N	O	S	0	0
			429	269	90	63	7		

- Molecule 32 is a protein called Ribosomal protein eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	e	50	Total	C	N	O	0	0
			391	242	85	64		

- Molecule 33 is a protein called Ribosomal protein eS31.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	f	45	Total	C	N	O	0	0
			229	139	45	45		

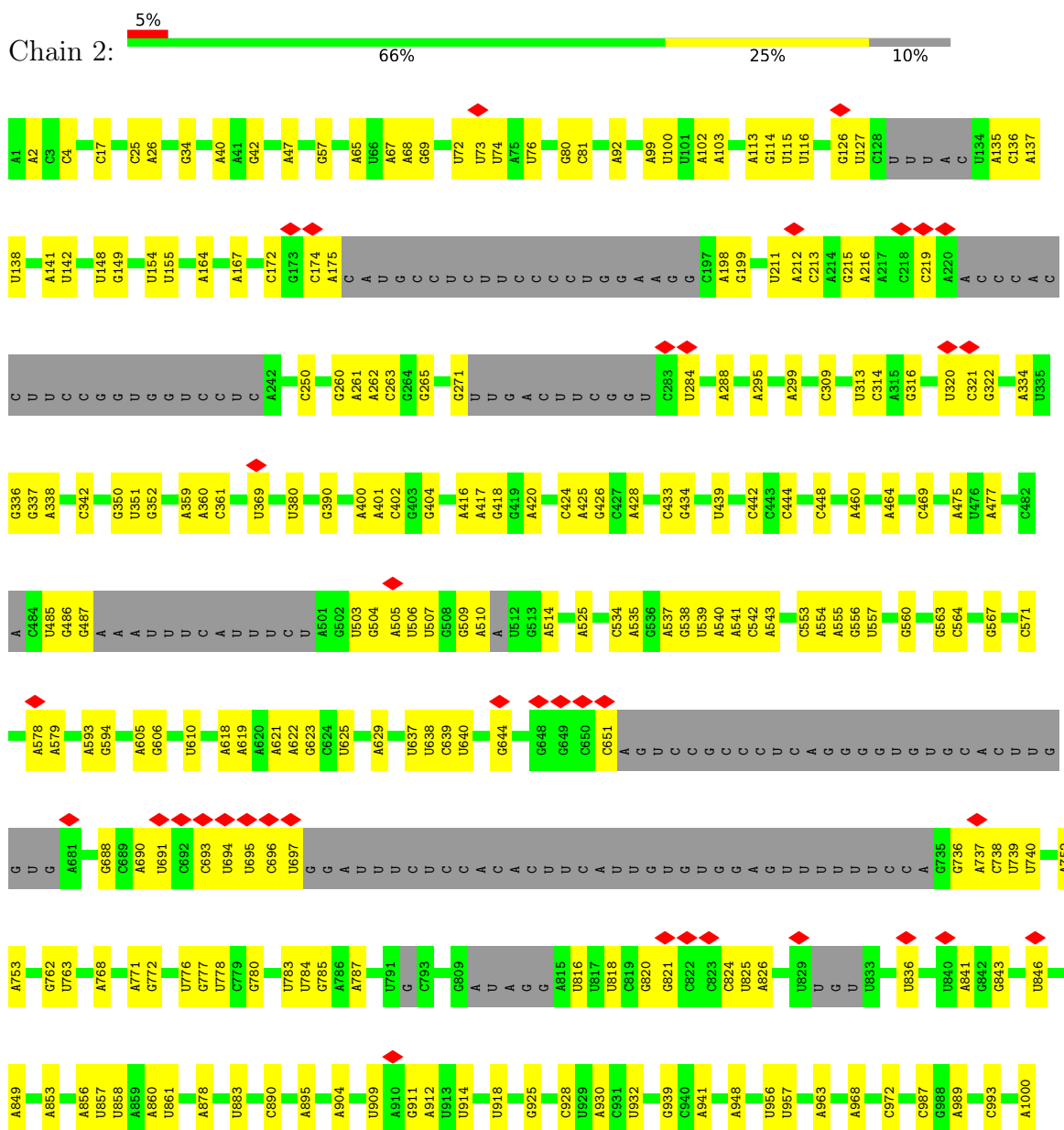
- Molecule 34 is a protein called Ribosomal protein eL41.

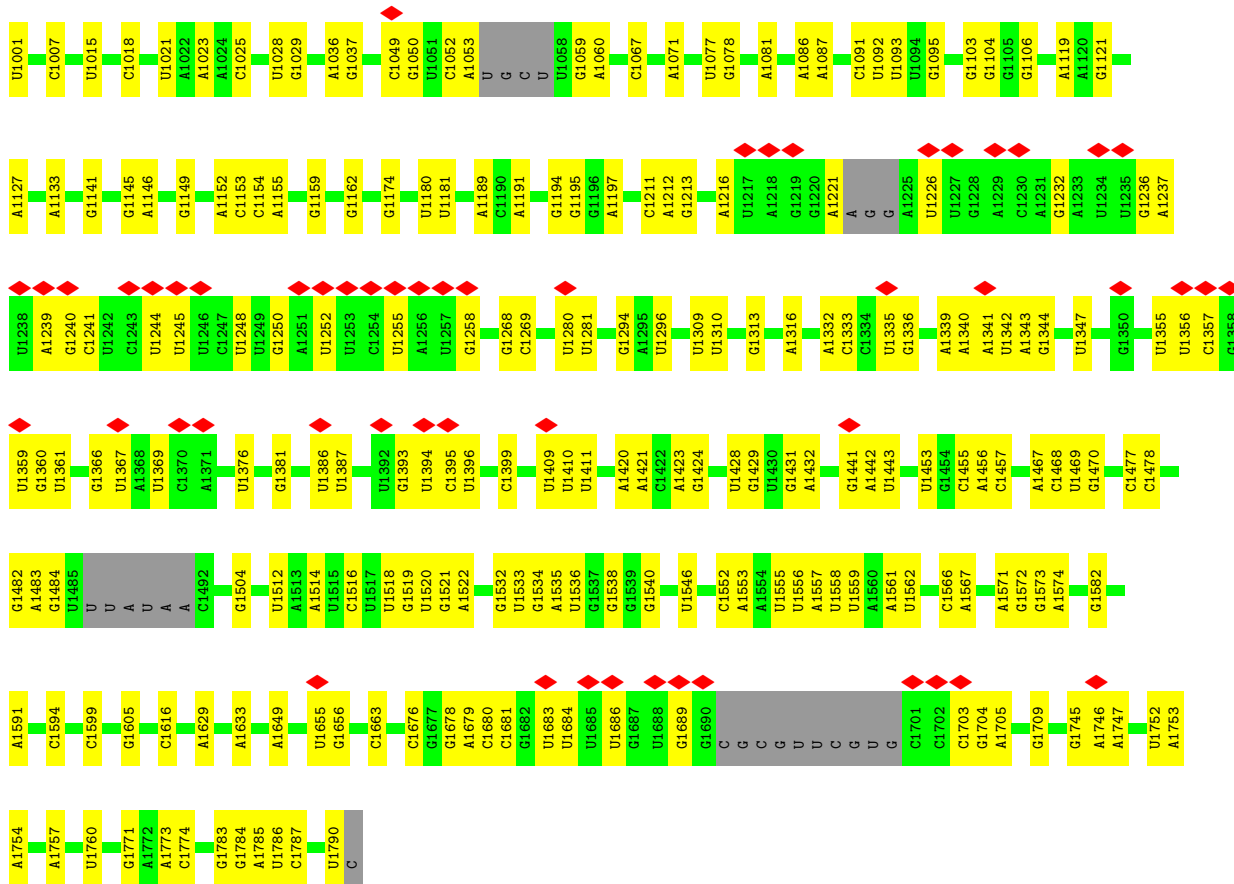
Mol	Chain	Residues	Atoms					AltConf	Trace
34	m	38	Total	C	N	O	S	0	0
			348	213	89	44	2		

3 Residue-property plots

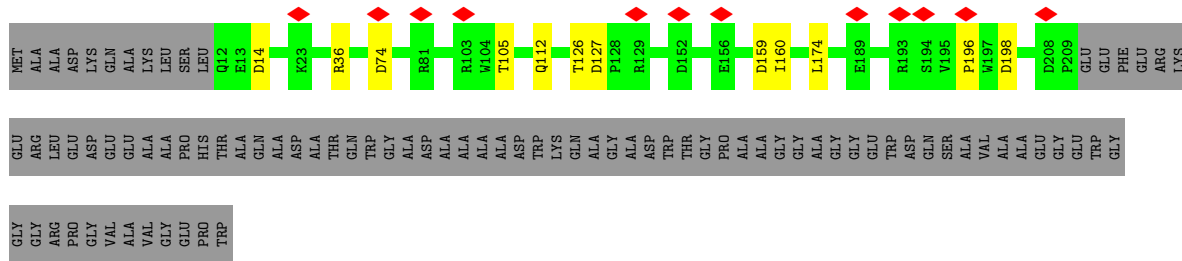
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 18S RNA

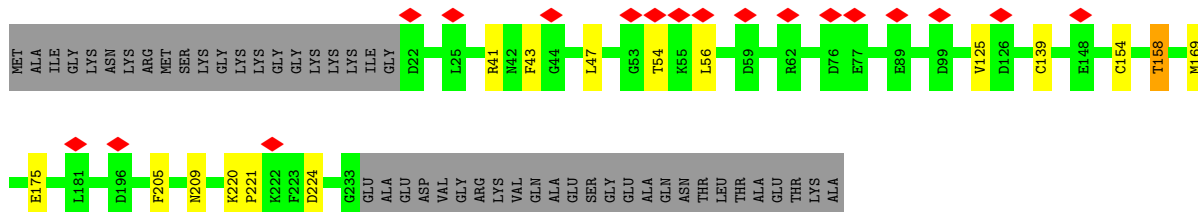
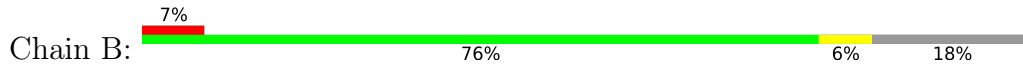




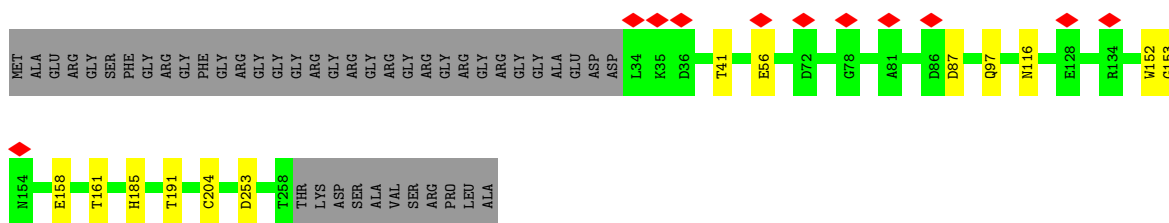
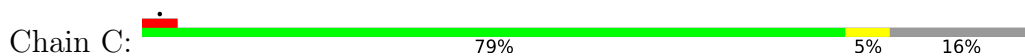
• Molecule 2: Ribosomal protein uS2



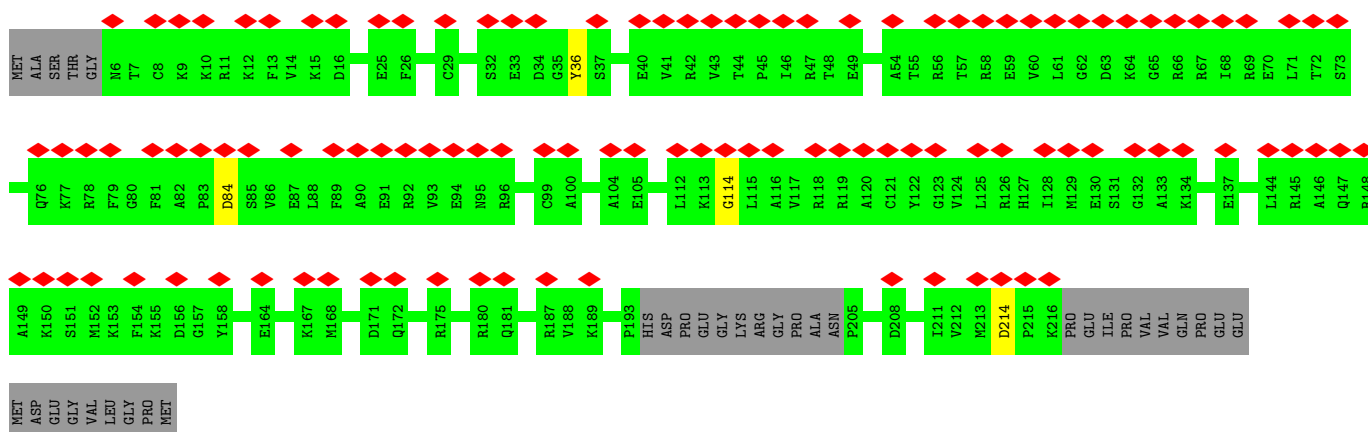
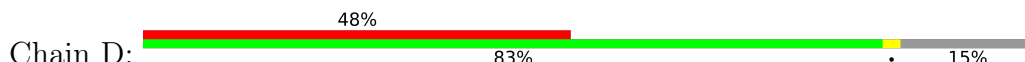
• Molecule 3: Ribosomal protein eS1



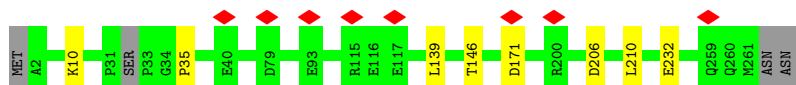
● Molecule 4: Ribosomal protein uS5



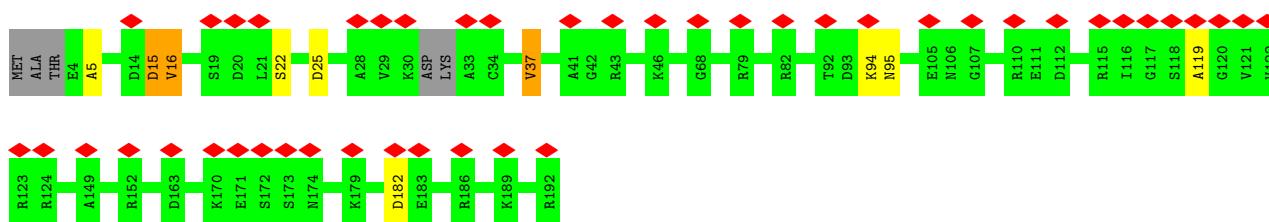
● Molecule 5: Ribosomal protein uS3



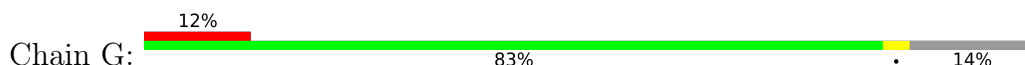
● Molecule 6: Ribosomal protein eS4

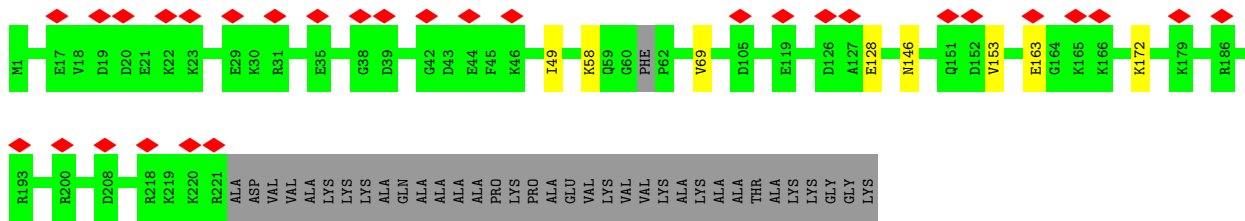


● Molecule 7: Ribosomal protein uS7

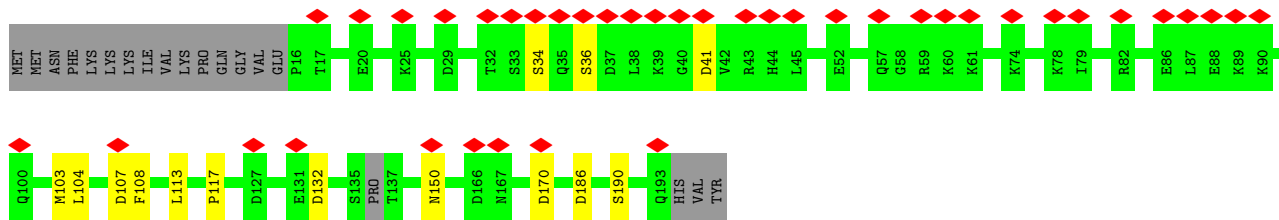
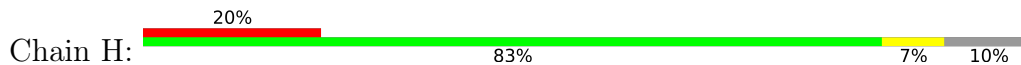


● Molecule 8: Ribosomal protein eS6

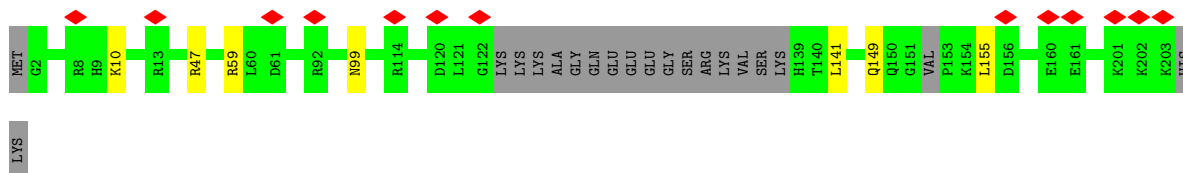
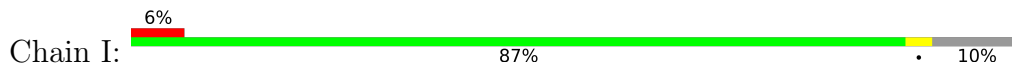




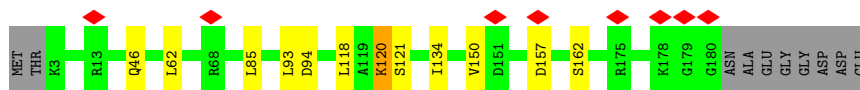
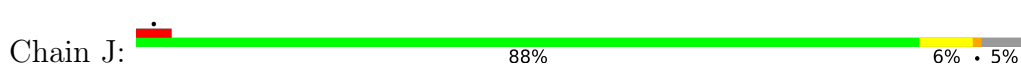
• Molecule 9: Ribosomal protein eS7



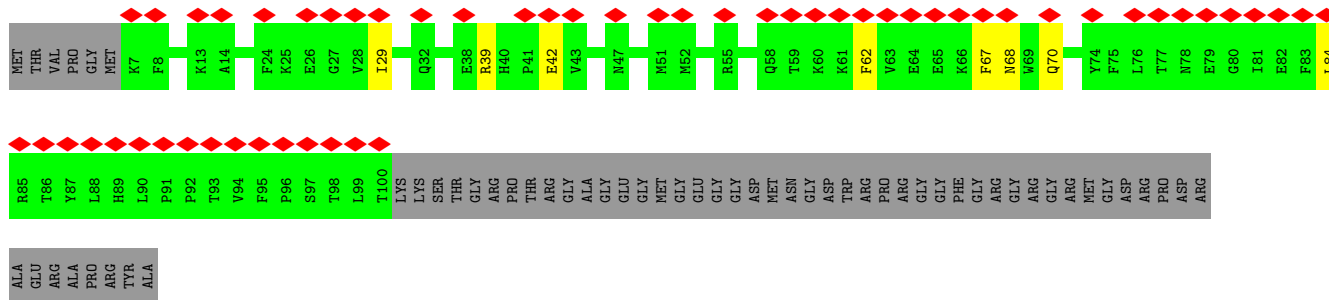
• Molecule 10: Ribosomal protein eS8



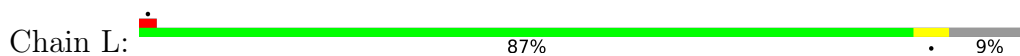
• Molecule 11: Ribosomal protein uS4



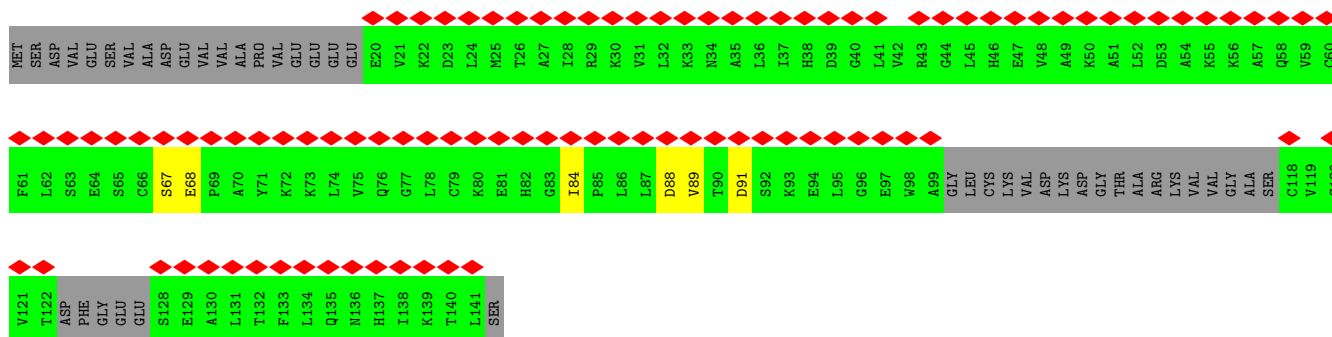
• Molecule 12: Ribosomal protein eS10



• Molecule 13: Ribosomal protein uS17



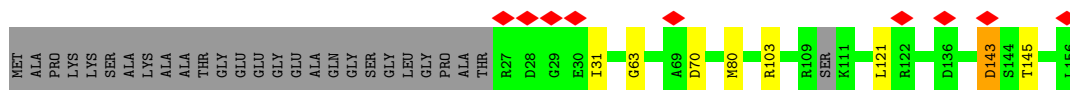
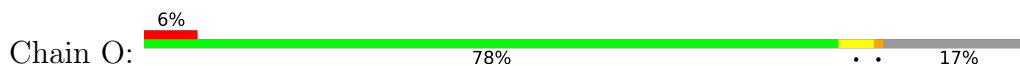
• Molecule 14: Ribosomal protein eS12



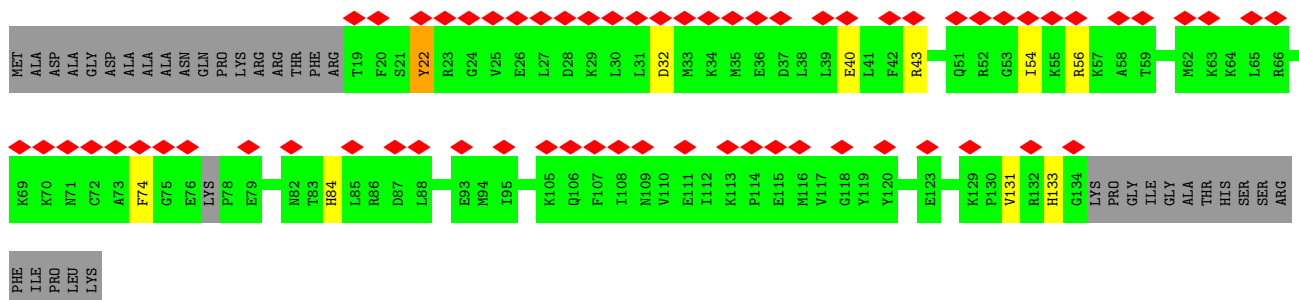
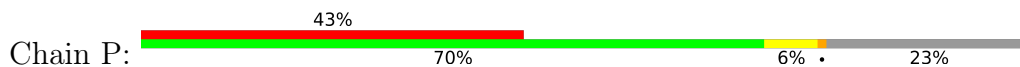
• Molecule 15: Ribosomal protein uS15



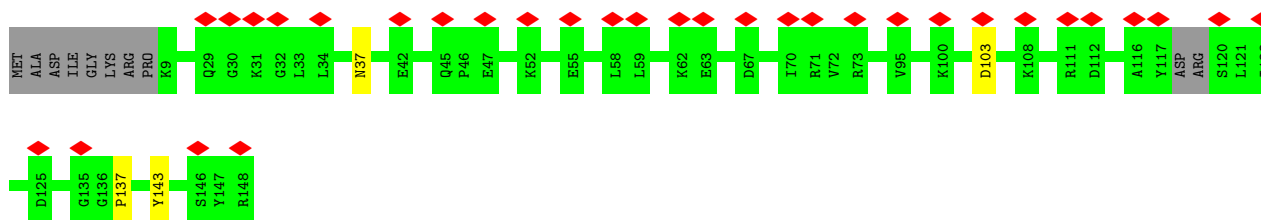
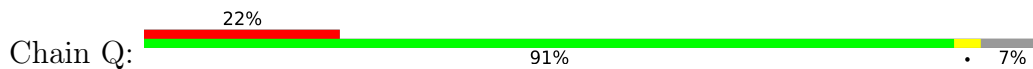
• Molecule 16: Ribosomal protein uS11



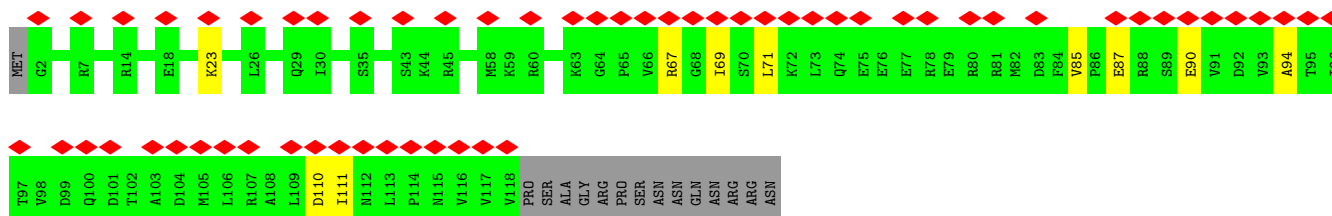
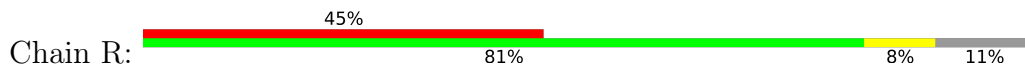
• Molecule 17: Ribosomal protein uS19



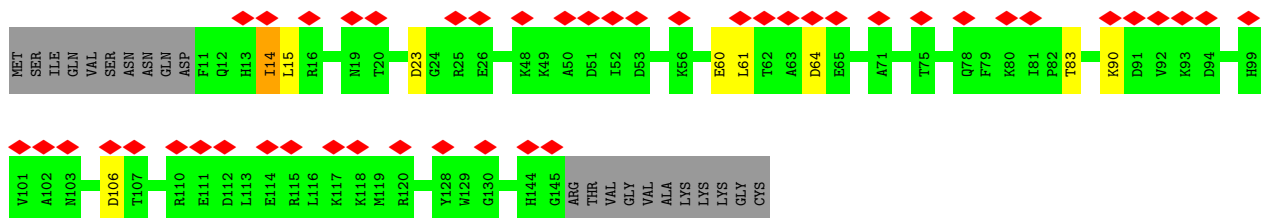
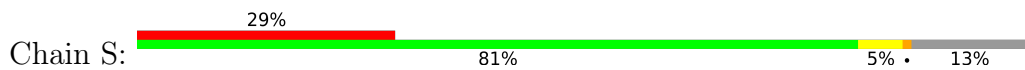
• Molecule 18: Ribosomal protein uS9



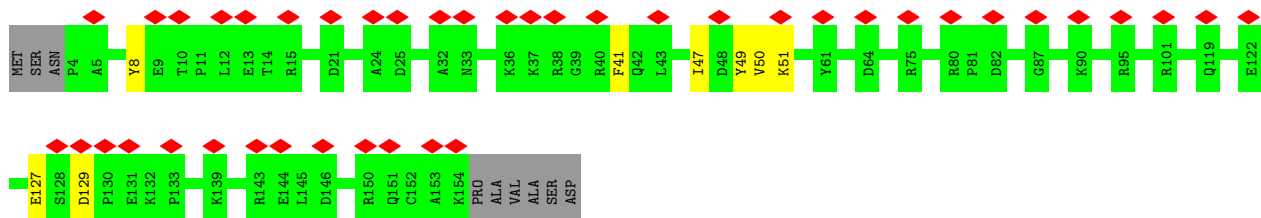
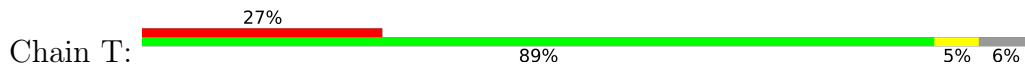
• Molecule 19: Ribosomal protein eS17



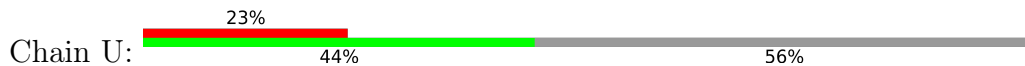
• Molecule 20: Ribosomal protein uS13

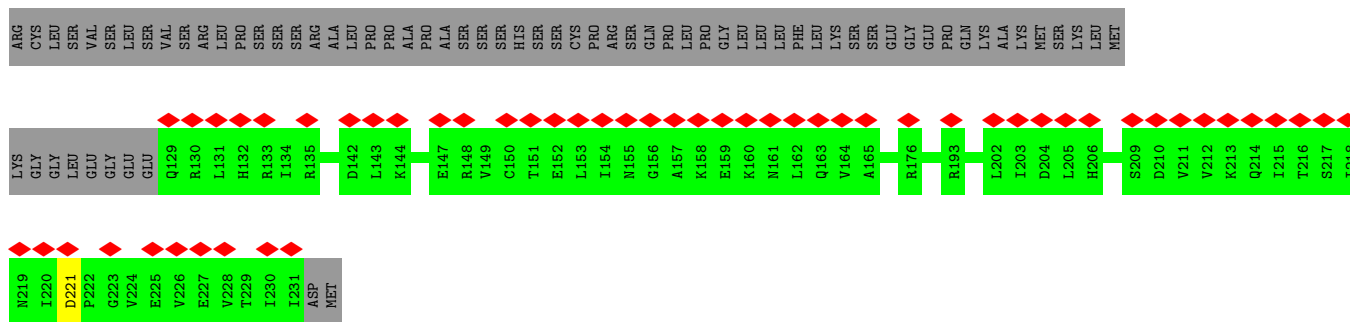


• Molecule 21: Ribosomal protein eS19

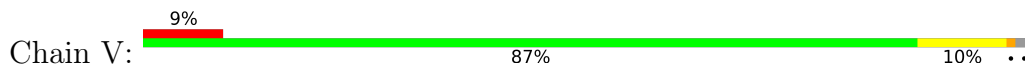


• Molecule 22: Ribosomal protein uS10

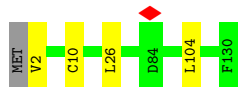




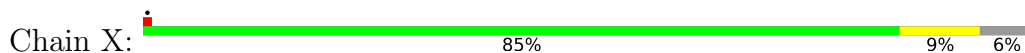
• Molecule 23: Ribosomal protein eS21



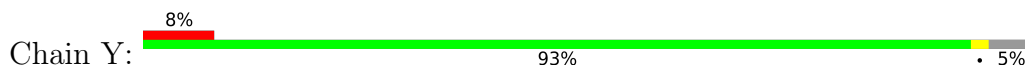
• Molecule 24: Ribosomal protein uS8



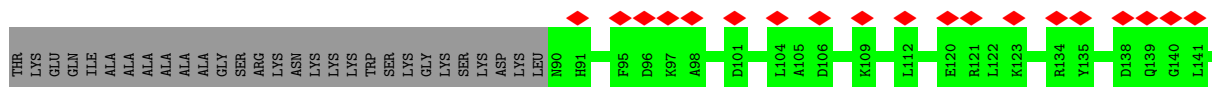
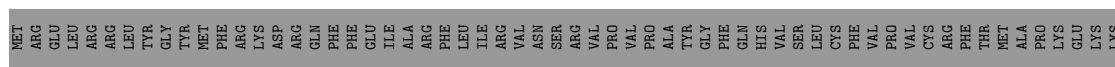
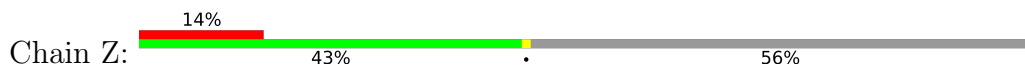
• Molecule 25: Ribosomal protein uS12

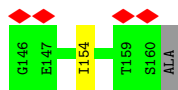


• Molecule 26: Ribosomal protein eS24

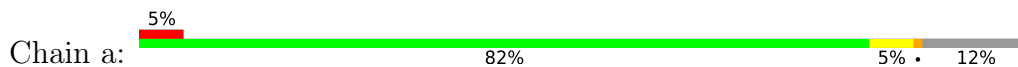


• Molecule 27: Ribosomal protein eS25

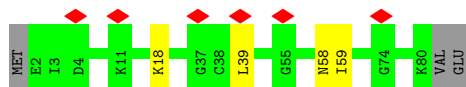
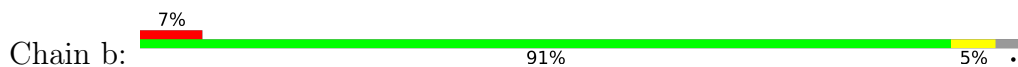




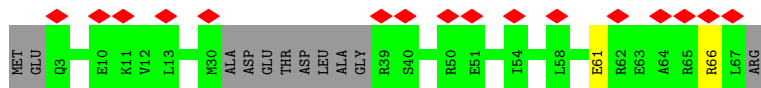
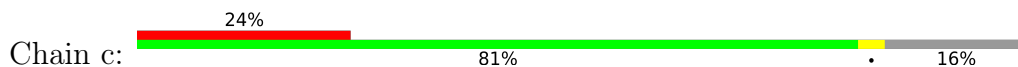
• Molecule 28: Ribosomal protein eS26



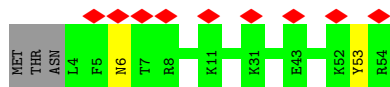
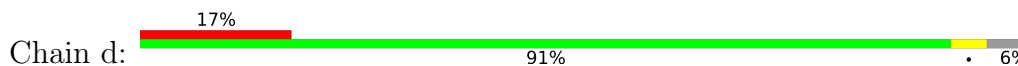
• Molecule 29: Ribosomal protein eS27



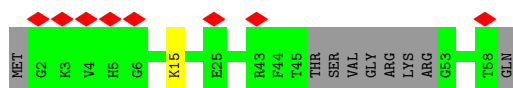
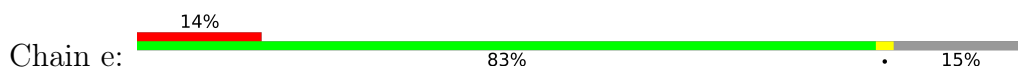
• Molecule 30: Ribosomal protein eS28



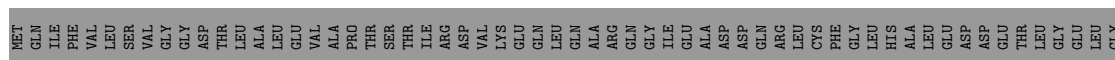
• Molecule 31: Ribosomal protein uS14

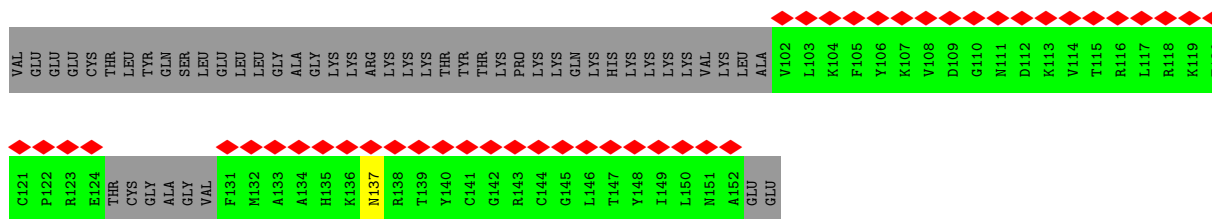


• Molecule 32: Ribosomal protein eS30

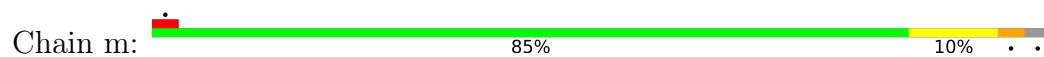


• Molecule 33: Ribosomal protein eS31





• Molecule 34: Ribosomal protein eL41



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	108162	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.209	Depositor
Minimum map value	-0.115	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	2	0.20	0/38592	0.67	0/60102
2	A	0.37	0/1600	0.53	0/2175
3	B	0.35	0/1716	0.55	0/2297
4	C	0.43	0/1792	0.60	0/2423
5	D	0.36	0/1586	0.53	0/2121
6	E	0.38	0/2129	0.58	0/2860
7	F	0.38	0/1495	0.64	0/2007
8	G	0.34	0/1802	0.56	0/2390
9	H	0.37	0/1371	0.60	0/1843
10	I	0.37	0/1523	0.57	0/2031
11	J	0.38	0/1481	0.62	0/1977
12	K	0.52	0/691	0.65	0/946
13	L	0.34	0/1228	0.55	0/1639
14	M	0.42	0/507	0.53	0/703
15	N	0.42	0/1230	0.62	0/1654
16	O	0.35	0/977	0.60	0/1311
17	P	0.38	0/955	0.60	0/1274
18	Q	0.39	0/1102	0.53	0/1477
19	R	0.36	0/956	0.61	0/1283
20	S	0.36	0/1109	0.51	0/1489
21	T	0.39	0/1266	0.58	0/1706
22	U	0.33	0/833	0.49	0/1126
23	V	0.35	0/627	0.56	0/842
24	W	0.35	0/1056	0.53	0/1412
25	X	0.38	0/1057	0.64	0/1412
26	Y	0.35	0/1036	0.51	0/1373
27	Z	0.35	0/587	0.59	0/793
28	a	0.34	0/805	0.63	0/1076
29	b	0.34	0/617	0.49	0/830
30	c	0.35	0/449	0.58	0/597
31	d	0.37	0/438	0.62	0/578
32	e	0.35	0/396	0.52	0/522
33	f	0.35	0/228	0.44	0/315
34	m	0.30	0/353	0.46	0/457

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.30	0/73590	0.63	0/107041

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	
2	A	196/287 (68%)	186 (95%)	6 (3%)	4 (2%)	7	33
3	B	210/259 (81%)	188 (90%)	14 (7%)	8 (4%)	3	21
4	C	223/269 (83%)	207 (93%)	11 (5%)	5 (2%)	6	32
5	D	196/235 (83%)	182 (93%)	13 (7%)	1 (0%)	29	63
6	E	255/263 (97%)	226 (89%)	27 (11%)	2 (1%)	19	53
7	F	183/192 (95%)	168 (92%)	8 (4%)	7 (4%)	3	21
8	G	216/256 (84%)	199 (92%)	12 (6%)	5 (2%)	6	31
9	H	173/196 (88%)	149 (86%)	17 (10%)	7 (4%)	3	20
10	I	179/205 (87%)	168 (94%)	8 (4%)	3 (2%)	9	36
11	J	176/188 (94%)	162 (92%)	9 (5%)	5 (3%)	5	26
12	K	92/152 (60%)	83 (90%)	4 (4%)	5 (5%)	2	13
13	L	143/161 (89%)	132 (92%)	10 (7%)	1 (1%)	22	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	M	93/142 (66%)	73 (78%)	14 (15%)	6 (6%)	1	10
15	N	148/151 (98%)	135 (91%)	9 (6%)	4 (3%)	5	27
16	O	125/156 (80%)	106 (85%)	15 (12%)	4 (3%)	4	24
17	P	111/150 (74%)	99 (89%)	6 (5%)	6 (5%)	2	13
18	Q	134/148 (90%)	120 (90%)	11 (8%)	3 (2%)	6	32
19	R	115/132 (87%)	103 (90%)	7 (6%)	5 (4%)	2	18
20	S	133/156 (85%)	122 (92%)	6 (4%)	5 (4%)	3	21
21	T	149/160 (93%)	134 (90%)	11 (7%)	4 (3%)	5	27
22	U	101/233 (43%)	97 (96%)	4 (4%)	0	100	100
23	V	78/82 (95%)	67 (86%)	8 (10%)	3 (4%)	3	21
24	W	127/130 (98%)	115 (91%)	12 (9%)	0	100	100
25	X	131/143 (92%)	116 (88%)	11 (8%)	4 (3%)	4	25
26	Y	126/135 (93%)	114 (90%)	10 (8%)	2 (2%)	9	38
27	Z	69/161 (43%)	59 (86%)	9 (13%)	1 (1%)	11	40
28	a	97/112 (87%)	85 (88%)	7 (7%)	5 (5%)	2	14
29	b	77/82 (94%)	67 (87%)	7 (9%)	3 (4%)	3	20
30	c	53/68 (78%)	50 (94%)	3 (6%)	0	100	100
31	d	49/54 (91%)	47 (96%)	2 (4%)	0	100	100
32	e	46/59 (78%)	45 (98%)	1 (2%)	0	100	100
33	f	41/154 (27%)	36 (88%)	4 (10%)	1 (2%)	6	30
34	m	36/39 (92%)	31 (86%)	2 (6%)	3 (8%)	1	6
All	All	4281/5310 (81%)	3871 (90%)	298 (7%)	112 (3%)	8	28

All (112) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	158	THR
4	C	116	ASN
6	E	35	PRO
7	F	16	VAL
8	G	58	LYS
8	G	69	VAL
8	G	153	VAL
9	H	108	PHE
10	I	141	LEU

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Mol	Chain	Res	Type
12	K	42	GLU
12	K	68	ASN
14	M	67	SER
17	P	43	ARG
17	P	131	VAL
17	P	133	HIS
19	R	23	LYS
19	R	71	LEU
20	S	14	ILE
21	T	50	VAL
29	b	18	LYS
34	m	7	ARG
2	A	196	PRO
3	B	43	PHE
3	B	154	CYS
7	F	94	LYS
9	H	34	SER
9	H	150	ASN
10	I	155	LEU
13	L	57	ASP
14	M	89	VAL
15	N	4	MET
16	O	70	ASP
16	O	143	ASP
18	Q	37	ASN
18	Q	143	TYR
20	S	60	GLU
21	T	41	PHE
21	T	129	ASP
23	V	10	ASP
25	X	112	VAL
28	a	47	ALA
29	b	58	ASN
29	b	59	ILE
34	m	16	ARG
3	B	54	THR
4	C	185	HIS
7	F	5	ALA
9	H	36	SER
10	I	59	ARG
11	J	120	LYS
12	K	62	PHE

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Mol	Chain	Res	Type
14	M	88	ASP
17	P	22	TYR
17	P	56	ARG
17	P	74	PHE
20	S	61	LEU
20	S	90	LYS
23	V	4	ASP
25	X	95	ASP
28	a	85	ARG
2	A	126	THR
3	B	209	ASN
3	B	220	LYS
3	B	221	PRO
4	C	41	THR
4	C	158	GLU
6	E	232	GLU
7	F	37	VAL
8	G	172	LYS
9	H	113	LEU
9	H	117	PRO
11	J	62	LEU
11	J	121	SER
14	M	68	GLU
14	M	84	ILE
14	M	91	ASP
15	N	28	ILE
15	N	60	VAL
19	R	94	ALA
20	S	83	THR
28	a	36	ILE
33	f	137	ASN
34	m	3	HIS
2	A	105	THR
3	B	224	ASP
7	F	15	ASP
7	F	119	ALA
8	G	146	ASN
9	H	190	SER
11	J	162	SER
12	K	67	PHE
15	N	21	LYS
19	R	87	GLU

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Mol	Chain	Res	Type
19	R	111	ILE
25	X	129	SER
28	a	46	ASP
4	C	153	GLY
7	F	22	SER
11	J	134	ILE
23	V	7	ARG
26	Y	54	ASP
27	Z	154	ILE
28	a	61	THR
2	A	160	ILE
18	Q	137	PRO
25	X	39	ASN
16	O	31	ILE
16	O	63	GLY
5	D	114	GLY
26	Y	81	ASN
12	K	29	ILE
21	T	47	ILE

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	
2	A	171/225 (76%)	163 (95%)	8 (5%)	26	58
3	B	188/225 (84%)	179 (95%)	9 (5%)	25	57
4	C	187/213 (88%)	179 (96%)	8 (4%)	29	60
5	D	171/199 (86%)	168 (98%)	3 (2%)	59	80
6	E	225/229 (98%)	219 (97%)	6 (3%)	44	72
7	F	158/162 (98%)	152 (96%)	6 (4%)	33	63
8	G	189/212 (89%)	186 (98%)	3 (2%)	62	81
9	H	139/181 (77%)	132 (95%)	7 (5%)	24	56
10	I	159/176 (90%)	155 (98%)	4 (2%)	47	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	J	154/161 (96%)	146 (95%)	8 (5%)	23	55
12	K	60/128 (47%)	57 (95%)	3 (5%)	24	56
13	L	133/144 (92%)	127 (96%)	6 (4%)	27	59
14	M	8/120 (7%)	8 (100%)	0	100	100
15	N	128/129 (99%)	122 (95%)	6 (5%)	26	58
16	O	98/114 (86%)	93 (95%)	5 (5%)	24	55
17	P	103/129 (80%)	98 (95%)	5 (5%)	25	57
18	Q	111/119 (93%)	110 (99%)	1 (1%)	78	89
19	R	104/118 (88%)	99 (95%)	5 (5%)	25	57
20	S	116/134 (87%)	111 (96%)	5 (4%)	29	60
21	T	128/135 (95%)	124 (97%)	4 (3%)	40	69
22	U	96/211 (46%)	95 (99%)	1 (1%)	76	87
23	V	64/65 (98%)	57 (89%)	7 (11%)	6	25
24	W	113/114 (99%)	109 (96%)	4 (4%)	36	66
25	X	106/115 (92%)	97 (92%)	9 (8%)	10	36
26	Y	106/111 (96%)	105 (99%)	1 (1%)	78	89
27	Z	63/139 (45%)	63 (100%)	0	100	100
28	a	88/97 (91%)	85 (97%)	3 (3%)	37	66
29	b	72/75 (96%)	71 (99%)	1 (1%)	67	83
30	c	48/56 (86%)	46 (96%)	2 (4%)	30	60
31	d	45/48 (94%)	43 (96%)	2 (4%)	28	59
32	e	40/48 (83%)	39 (98%)	1 (2%)	47	73
33	f	3/130 (2%)	3 (100%)	0	100	100
34	m	33/34 (97%)	30 (91%)	3 (9%)	9	33
All	All	3607/4496 (80%)	3471 (96%)	136 (4%)	36	63

All (136) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	14	ASP
2	A	36	ARG
2	A	74	ASP
2	A	112	GLN
2	A	127	ASP

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Mol	Chain	Res	Type
2	A	159	ASP
2	A	174	LEU
2	A	198	ASP
3	B	41	ARG
3	B	47	LEU
3	B	56	LEU
3	B	125	VAL
3	B	139	CYS
3	B	158	THR
3	B	169	MET
3	B	175	GLU
3	B	205	PHE
4	C	56	GLU
4	C	87	ASP
4	C	97	GLN
4	C	152	TRP
4	C	161	THR
4	C	191	THR
4	C	204	CYS
4	C	253	ASP
5	D	36	TYR
5	D	84	ASP
5	D	214	ASP
6	E	10	LYS
6	E	139	LEU
6	E	146	THR
6	E	171	ASP
6	E	206	ASP
6	E	210	LEU
7	F	15	ASP
7	F	16	VAL
7	F	25	ASP
7	F	37	VAL
7	F	95	ASN
7	F	182	ASP
8	G	49	ILE
8	G	128	GLU
8	G	163	GLU
9	H	41	ASP
9	H	103	MET
9	H	104	LEU
9	H	107	ASP

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Mol	Chain	Res	Type
9	H	132	ASP
9	H	170	ASP
9	H	186	ASP
10	I	10	LYS
10	I	47	ARG
10	I	99	ASN
10	I	149	GLN
11	J	46	GLN
11	J	85	LEU
11	J	93	LEU
11	J	94	ASP
11	J	118	LEU
11	J	120	LYS
11	J	150	VAL
11	J	157	ASP
12	K	39	ARG
12	K	70	GLN
12	K	84	LEU
13	L	9	GLU
13	L	49	LEU
13	L	72	VAL
13	L	110	THR
13	L	113	LEU
13	L	146	GLU
15	N	21	LYS
15	N	60	VAL
15	N	84	LEU
15	N	94	LYS
15	N	121	ARG
15	N	125	LEU
16	O	80	MET
16	O	103	ARG
16	O	121	LEU
16	O	143	ASP
16	O	145	THR
17	P	22	TYR
17	P	32	ASP
17	P	40	GLU
17	P	54	ILE
17	P	84	HIS
18	Q	103	ASP
19	R	67	ARG

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Mol	Chain	Res	Type
19	R	69	ILE
19	R	85	VAL
19	R	90	GLU
19	R	110	ASP
20	S	14	ILE
20	S	15	LEU
20	S	23	ASP
20	S	64	ASP
20	S	106	ASP
21	T	8	TYR
21	T	49	TYR
21	T	51	LYS
21	T	127	GLU
22	U	221	ASP
23	V	10	ASP
23	V	11	LEU
23	V	12	TYR
23	V	13	ILE
23	V	41	GLU
23	V	44	ARG
23	V	63	GLU
24	W	2	VAL
24	W	10	CYS
24	W	26	LEU
24	W	104	LEU
25	X	55	LEU
25	X	57	ILE
25	X	60	LYS
25	X	71	ARG
25	X	77	ASN
25	X	98	ASP
25	X	101	LEU
25	X	105	PHE
25	X	137	LYS
26	Y	19	LEU
28	a	10	ARG
28	a	15	ARG
28	a	85	ARG
29	b	39	LEU
30	c	61	GLU
30	c	66	ARG
31	d	6	ASN

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Mol	Chain	Res	Type
31	d	53	TYR
32	e	15	LYS
34	m	12	ARG
34	m	15	MET
34	m	16	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
3	B	74	ASN
3	B	180	GLN
4	C	76	GLN
4	C	102	GLN
4	C	118	HIS
4	C	185	HIS
7	F	17	ASN
7	F	39	HIS
7	F	71	ASN
7	F	95	ASN
7	F	136	ASN
7	F	167	ASN
8	G	59	GLN
8	G	192	GLN
9	H	80	GLN
10	I	139	HIS
11	J	155	HIS
15	N	62	GLN
15	N	105	ASN
15	N	134	GLN
16	O	48	HIS
19	R	31	ASN
20	S	77	GLN
20	S	87	ASN
23	V	38	GLN
24	W	56	HIS
25	X	63	ASN
25	X	73	GLN
29	b	47	HIS
29	b	49	GLN
31	d	18	GLN
31	d	26	HIS
32	e	57	GLN

Continued on next page...

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Mol	Chain	Res	Type
34	m	3	HIS
34	m	28	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1602/1791 (89%)	428 (26%)	48 (2%)

All (428) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	17	C
1	2	25	C
1	2	26	A
1	2	34	G
1	2	40	A
1	2	42	G
1	2	47	A
1	2	57	G
1	2	65	A
1	2	67	A
1	2	68	A
1	2	69	G
1	2	72	U
1	2	73	U
1	2	74	U
1	2	76	U
1	2	81	C
1	2	92	A
1	2	99	A
1	2	100	U
1	2	103	A
1	2	113	A
1	2	114	G
1	2	115	U
1	2	116	U
1	2	126	G
1	2	127	U
1	2	135	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	2	136	C
1	2	137	A
1	2	138	U
1	2	141	A
1	2	142	U
1	2	148	U
1	2	149	G
1	2	154	U
1	2	155	U
1	2	164	A
1	2	167	A
1	2	172	C
1	2	174	C
1	2	175	A
1	2	199	G
1	2	212	A
1	2	213	C
1	2	215	G
1	2	216	A
1	2	219	C
1	2	250	C
1	2	260	G
1	2	261	A
1	2	262	A
1	2	263	C
1	2	265	G
1	2	271	G
1	2	284	U
1	2	288	A
1	2	295	A
1	2	299	A
1	2	309	C
1	2	313	U
1	2	314	C
1	2	316	G
1	2	320	U
1	2	321	C
1	2	322	G
1	2	334	A
1	2	336	G
1	2	337	G
1	2	338	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	2	342	C
1	2	350	G
1	2	351	U
1	2	352	G
1	2	359	A
1	2	360	A
1	2	361	C
1	2	369	U
1	2	380	U
1	2	390	G
1	2	400	A
1	2	401	A
1	2	402	C
1	2	404	G
1	2	416	A
1	2	417	A
1	2	418	G
1	2	420	A
1	2	424	C
1	2	425	A
1	2	426	G
1	2	428	A
1	2	433	C
1	2	434	G
1	2	439	U
1	2	442	C
1	2	444	C
1	2	448	C
1	2	460	A
1	2	464	A
1	2	469	C
1	2	475	A
1	2	477	A
1	2	485	U
1	2	486	G
1	2	487	G
1	2	503	U
1	2	504	G
1	2	505	A
1	2	506	U
1	2	507	U
1	2	509	G

Continued on next page...

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Mol	Chain	Res	Type
1	2	510	A
1	2	514	A
1	2	525	A
1	2	534	C
1	2	535	A
1	2	537	A
1	2	538	G
1	2	539	U
1	2	540	A
1	2	541	A
1	2	542	C
1	2	543	A
1	2	553	C
1	2	554	A
1	2	555	A
1	2	556	G
1	2	557	U
1	2	560	G
1	2	563	G
1	2	564	C
1	2	567	G
1	2	571	C
1	2	578	A
1	2	579	A
1	2	593	A
1	2	594	G
1	2	605	A
1	2	610	U
1	2	618	A
1	2	619	A
1	2	621	A
1	2	622	A
1	2	623	G
1	2	625	U
1	2	629	A
1	2	638	U
1	2	639	C
1	2	640	U
1	2	644	G
1	2	651	C
1	2	688	G
1	2	690	A

Continued on next page...

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Mol	Chain	Res	Type
1	2	691	U
1	2	693	C
1	2	694	U
1	2	695	U
1	2	696	C
1	2	697	U
1	2	736	G
1	2	737	A
1	2	738	C
1	2	739	U
1	2	740	U
1	2	752	A
1	2	753	A
1	2	762	G
1	2	763	U
1	2	768	A
1	2	771	A
1	2	772	G
1	2	776	U
1	2	777	G
1	2	778	U
1	2	780	G
1	2	783	U
1	2	784	U
1	2	785	G
1	2	787	A
1	2	816	U
1	2	818	U
1	2	820	G
1	2	821	G
1	2	824	C
1	2	825	U
1	2	826	A
1	2	836	U
1	2	841	A
1	2	843	G
1	2	846	U
1	2	849	A
1	2	853	A
1	2	856	A
1	2	857	U
1	2	858	U

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Mol	Chain	Res	Type
1	2	860	A
1	2	861	U
1	2	878	A
1	2	883	U
1	2	890	C
1	2	895	A
1	2	904	A
1	2	909	U
1	2	911	G
1	2	912	A
1	2	914	U
1	2	918	U
1	2	925	G
1	2	928	C
1	2	930	A
1	2	932	U
1	2	939	G
1	2	941	A
1	2	948	A
1	2	957	U
1	2	963	A
1	2	968	A
1	2	972	C
1	2	987	C
1	2	989	A
1	2	993	C
1	2	1000	A
1	2	1001	U
1	2	1007	C
1	2	1015	U
1	2	1018	C
1	2	1021	U
1	2	1023	A
1	2	1025	C
1	2	1028	U
1	2	1029	G
1	2	1036	A
1	2	1037	G
1	2	1049	C
1	2	1050	G
1	2	1052	C
1	2	1053	A

Continued on next page...

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Mol	Chain	Res	Type
1	2	1060	A
1	2	1067	C
1	2	1071	A
1	2	1077	U
1	2	1078	G
1	2	1081	A
1	2	1086	A
1	2	1087	A
1	2	1091	C
1	2	1092	U
1	2	1093	U
1	2	1095	G
1	2	1103	G
1	2	1104	G
1	2	1106	G
1	2	1119	A
1	2	1121	G
1	2	1127	A
1	2	1133	A
1	2	1141	G
1	2	1145	G
1	2	1146	A
1	2	1149	G
1	2	1152	A
1	2	1153	C
1	2	1154	C
1	2	1155	A
1	2	1159	G
1	2	1162	G
1	2	1174	G
1	2	1180	U
1	2	1181	U
1	2	1189	A
1	2	1191	A
1	2	1194	G
1	2	1195	G
1	2	1197	A
1	2	1212	A
1	2	1213	G
1	2	1216	A
1	2	1221	A
1	2	1226	U

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Mol	Chain	Res	Type
1	2	1232	G
1	2	1236	G
1	2	1237	A
1	2	1239	A
1	2	1240	G
1	2	1241	C
1	2	1244	U
1	2	1245	U
1	2	1248	U
1	2	1250	G
1	2	1252	U
1	2	1255	U
1	2	1258	G
1	2	1269	C
1	2	1280	U
1	2	1281	U
1	2	1294	G
1	2	1296	U
1	2	1309	U
1	2	1310	U
1	2	1313	G
1	2	1316	A
1	2	1332	A
1	2	1333	C
1	2	1335	U
1	2	1336	G
1	2	1340	A
1	2	1341	A
1	2	1342	U
1	2	1343	A
1	2	1344	G
1	2	1347	U
1	2	1355	U
1	2	1356	U
1	2	1357	C
1	2	1359	U
1	2	1360	G
1	2	1361	U
1	2	1366	G
1	2	1367	U
1	2	1369	U
1	2	1376	U

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Mol	Chain	Res	Type
1	2	1381	G
1	2	1386	U
1	2	1387	U
1	2	1393	G
1	2	1394	U
1	2	1395	C
1	2	1396	U
1	2	1399	C
1	2	1409	U
1	2	1411	U
1	2	1420	A
1	2	1421	A
1	2	1423	A
1	2	1424	G
1	2	1428	U
1	2	1429	G
1	2	1431	G
1	2	1432	A
1	2	1441	G
1	2	1442	A
1	2	1443	U
1	2	1453	U
1	2	1455	C
1	2	1456	A
1	2	1457	C
1	2	1467	A
1	2	1468	C
1	2	1469	U
1	2	1470	G
1	2	1478	C
1	2	1482	G
1	2	1483	A
1	2	1484	G
1	2	1504	G
1	2	1512	U
1	2	1514	A
1	2	1516	C
1	2	1518	U
1	2	1519	G
1	2	1520	U
1	2	1521	G
1	2	1522	A

Continued on next page...

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Mol	Chain	Res	Type
1	2	1533	U
1	2	1534	G
1	2	1535	A
1	2	1536	U
1	2	1538	G
1	2	1540	G
1	2	1546	U
1	2	1552	C
1	2	1553	A
1	2	1555	U
1	2	1557	A
1	2	1558	U
1	2	1559	U
1	2	1561	A
1	2	1562	U
1	2	1566	C
1	2	1567	A
1	2	1571	A
1	2	1572	G
1	2	1573	G
1	2	1574	A
1	2	1582	G
1	2	1591	A
1	2	1594	C
1	2	1599	C
1	2	1605	G
1	2	1616	C
1	2	1629	A
1	2	1633	A
1	2	1649	A
1	2	1655	U
1	2	1656	G
1	2	1663	C
1	2	1676	C
1	2	1679	A
1	2	1680	C
1	2	1681	C
1	2	1683	U
1	2	1684	U
1	2	1686	U
1	2	1689	G
1	2	1703	C

Continued on next page...

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Mol	Chain	Res	Type
1	2	1704	G
1	2	1705	A
1	2	1709	G
1	2	1745	G
1	2	1746	A
1	2	1747	A
1	2	1752	U
1	2	1753	A
1	2	1754	A
1	2	1757	A
1	2	1760	U
1	2	1771	G
1	2	1773	A
1	2	1774	C
1	2	1783	G
1	2	1784	G
1	2	1785	A
1	2	1786	U
1	2	1787	C
1	2	1790	U

All (48) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	68	A
1	2	80	G
1	2	102	A
1	2	135	A
1	2	154	U
1	2	198	A
1	2	211	U
1	2	213	C
1	2	260	G
1	2	261	A
1	2	350	G
1	2	400	A
1	2	417	A
1	2	425	A
1	2	540	A
1	2	541	A
1	2	553	C
1	2	554	A

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Mol	Chain	Res	Type
1	2	555	A
1	2	606	G
1	2	637	U
1	2	739	U
1	2	777	G
1	2	956	U
1	2	1001	U
1	2	1059	G
1	2	1077	U
1	2	1103	G
1	2	1152	A
1	2	1211	C
1	2	1268	G
1	2	1280	U
1	2	1339	A
1	2	1359	U
1	2	1393	G
1	2	1410	U
1	2	1453	U
1	2	1468	C
1	2	1469	U
1	2	1477	C
1	2	1532	G
1	2	1535	A
1	2	1556	U
1	2	1566	C
1	2	1571	A
1	2	1678	G
1	2	1752	U
1	2	1753	A

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](#)

There are no chain breaks in this entry.

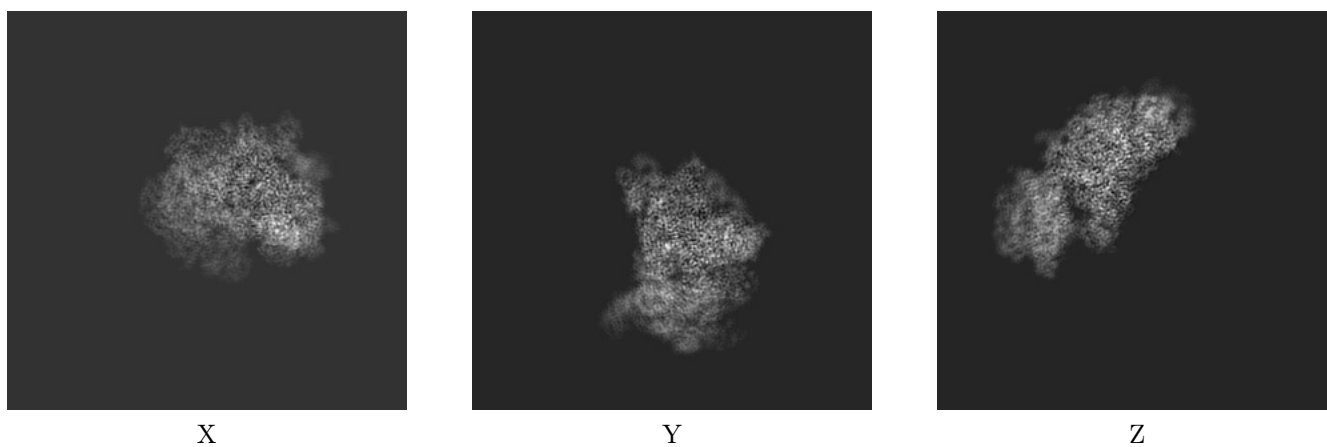
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6780. 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](#)

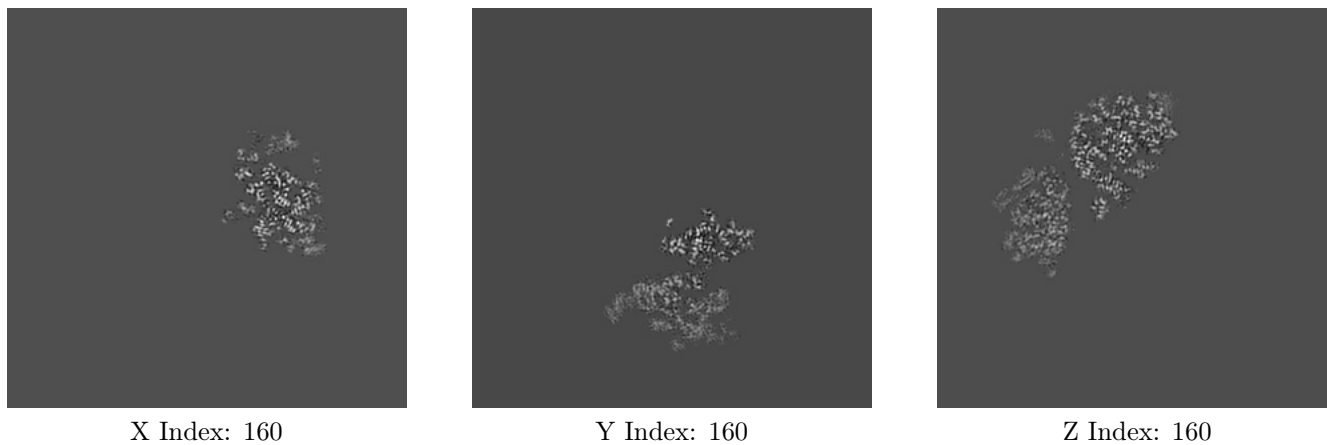
6.1.1 Primary map



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

6.2 Central slices [i](#)

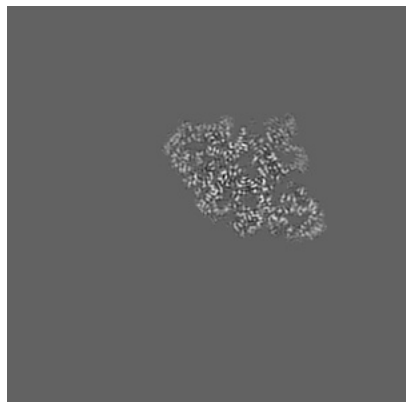
6.2.1 Primary map



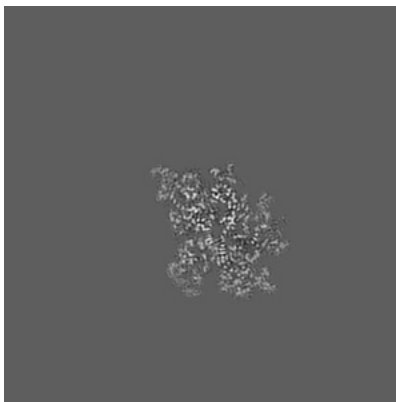
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

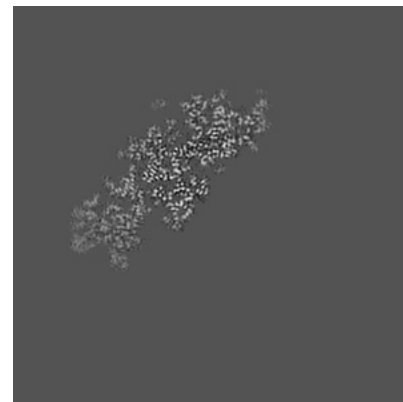
6.3.1 Primary map



X Index: 130



Y Index: 209

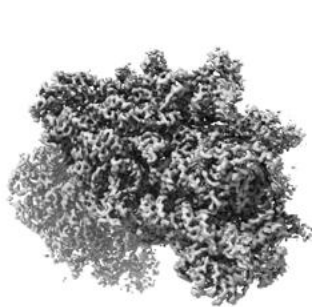


Z Index: 179

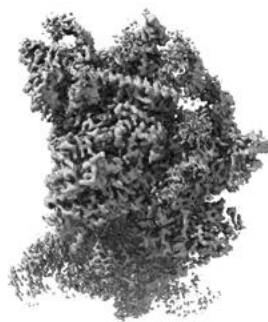
The images above show the largest variance slices of the map in three orthogonal directions.

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

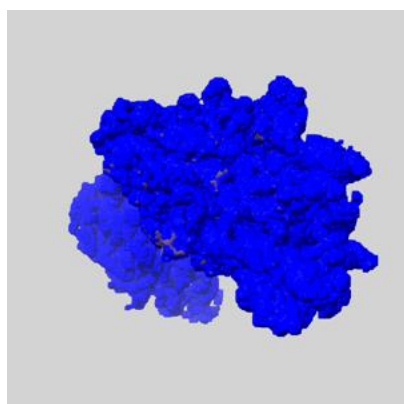
6.5 Mask visualisation [i](#)

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

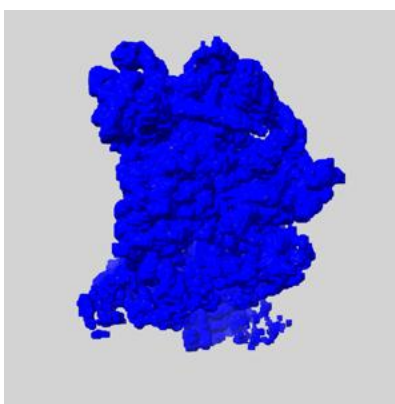
A mask typically either:

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

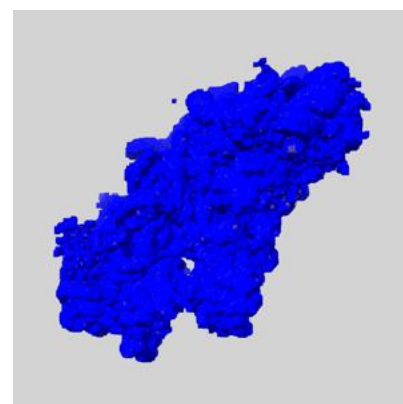
6.5.1 emd_6780_msk_1.map [i](#)



X



Y

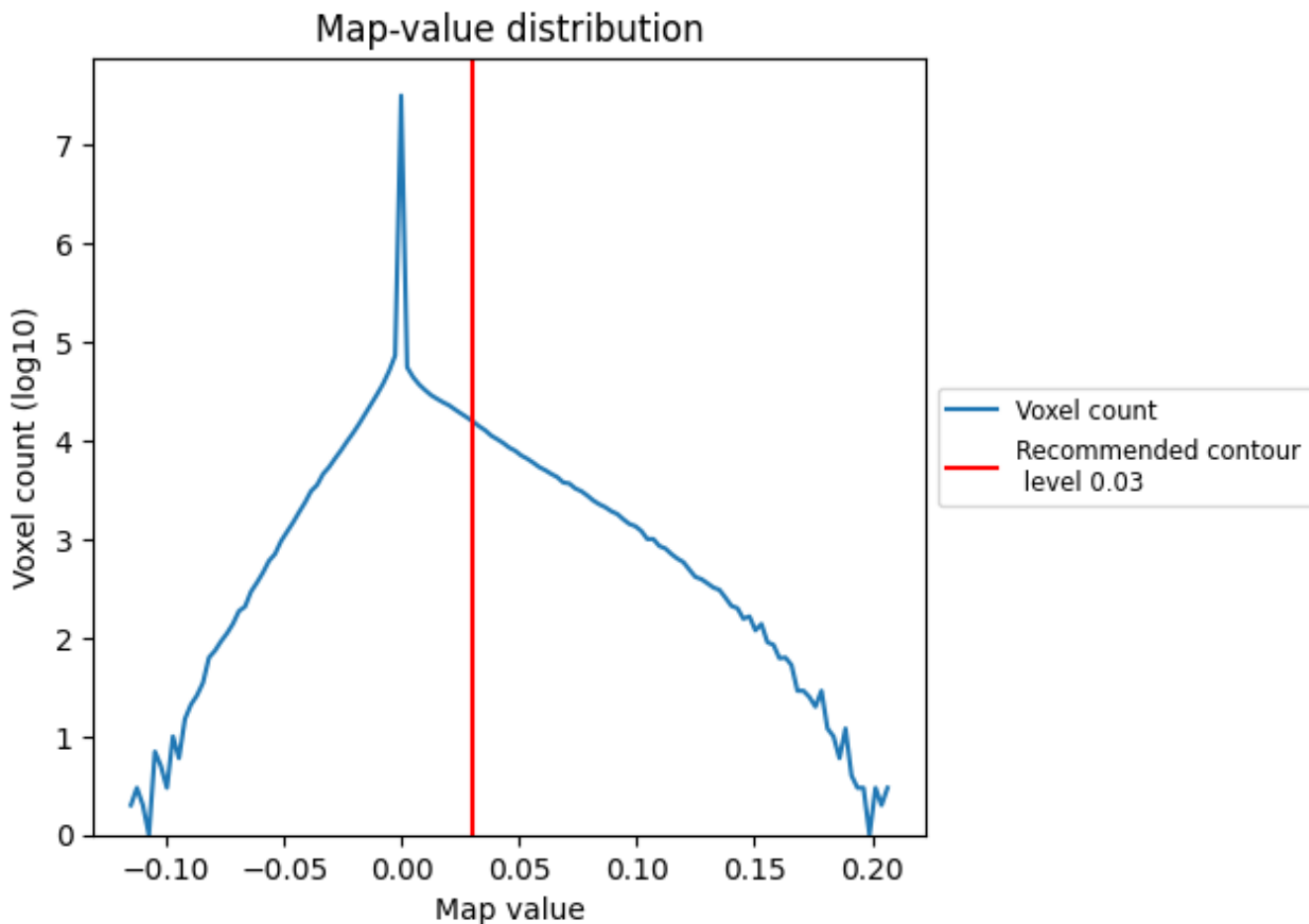


Z

7 Map analysis [i](#)

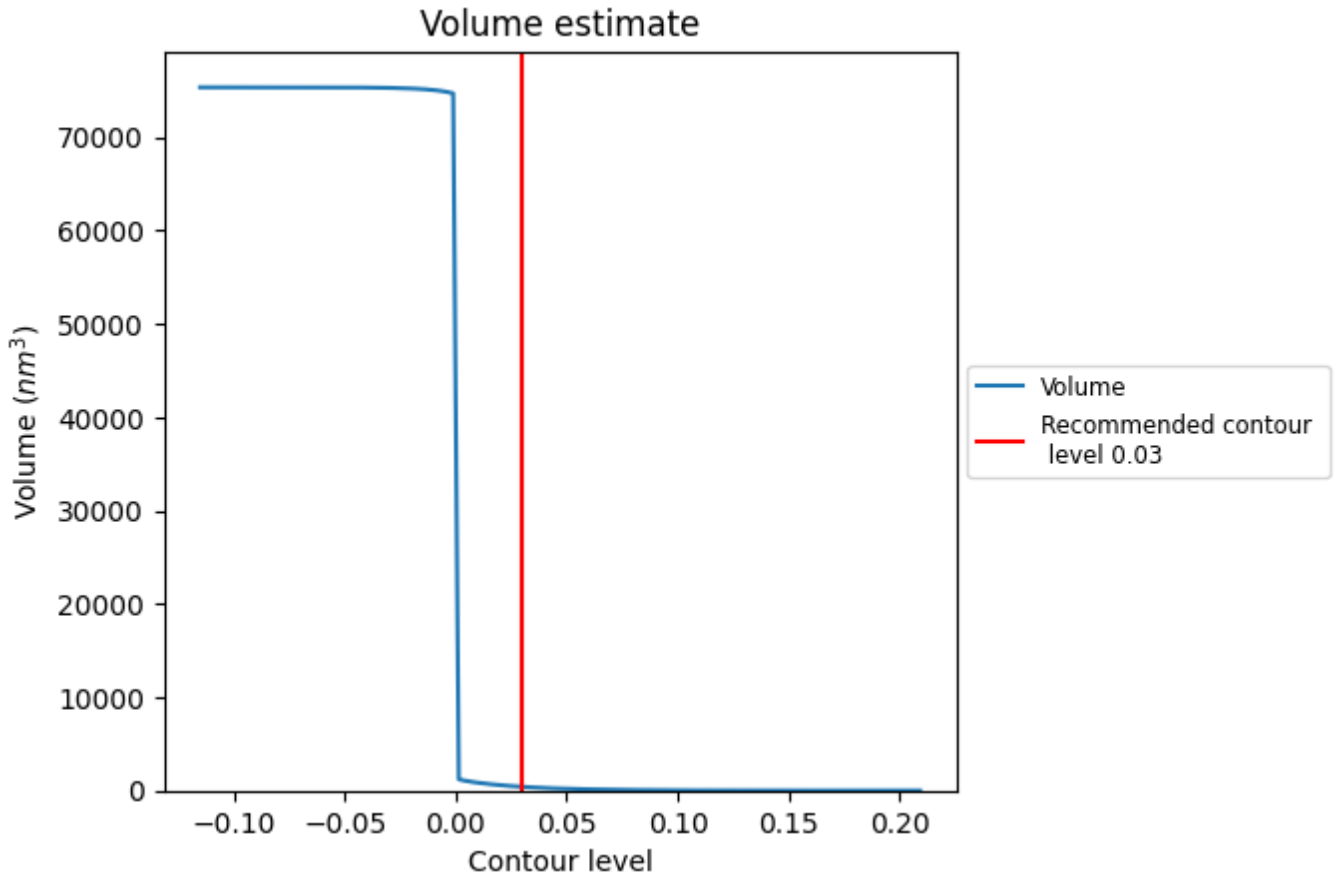
This section contains the results of statistical analysis of the map.

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.

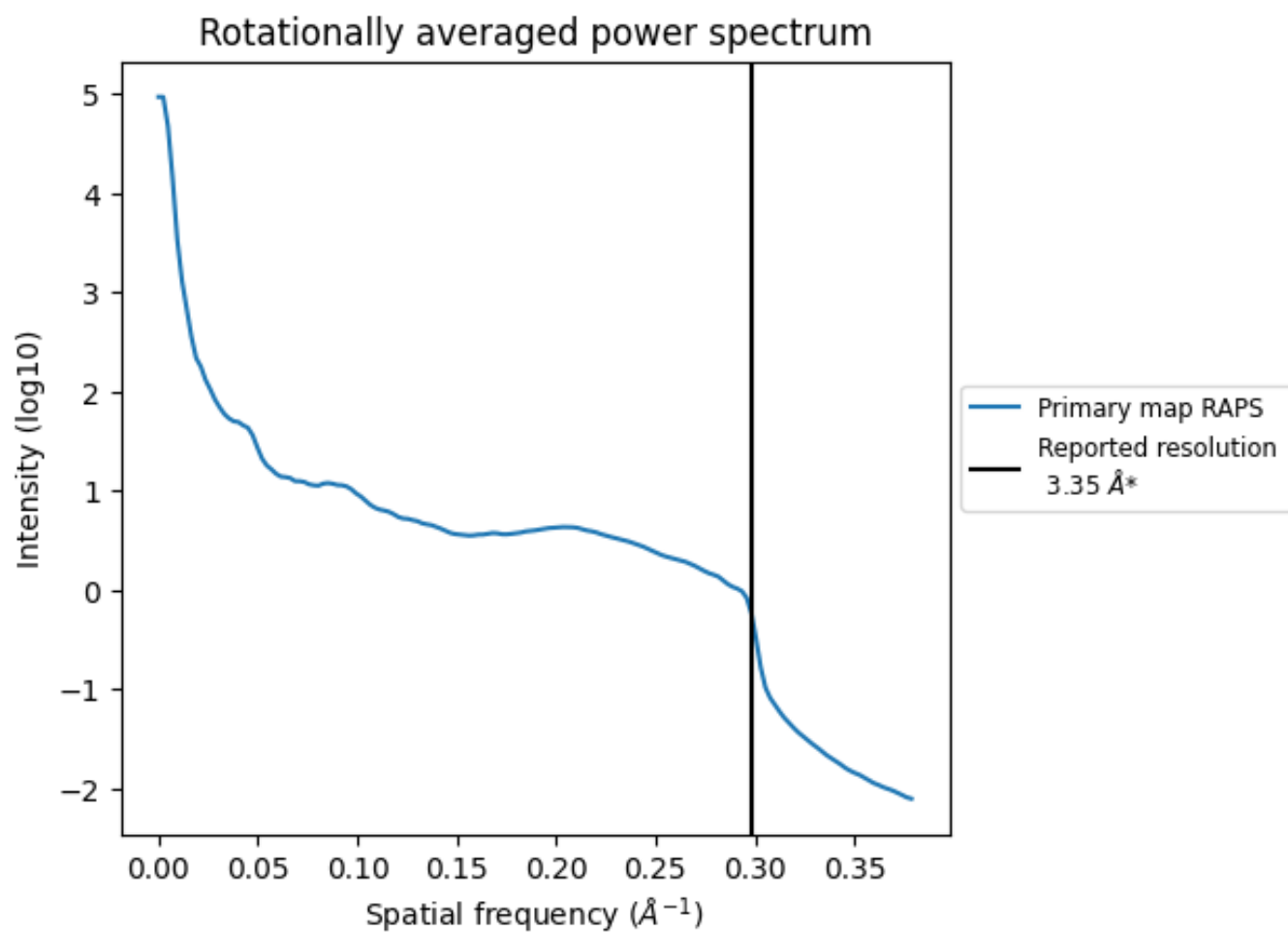
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 401 nm³; this corresponds to an approximate mass of 362 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

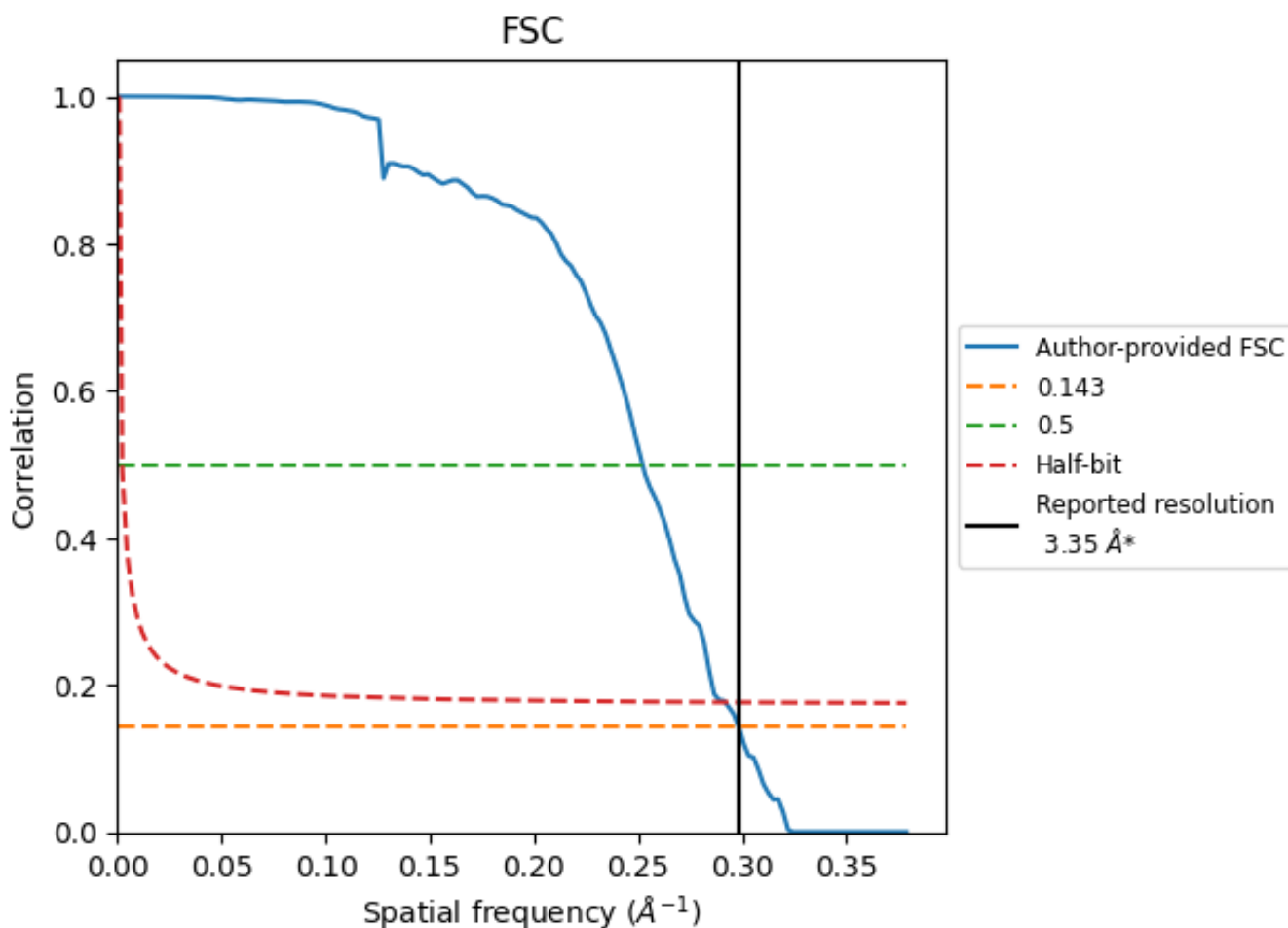


*Reported resolution corresponds to spatial frequency of 0.299 Å⁻¹

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 0.299 Å⁻¹

8.2 Resolution estimates [i](#)

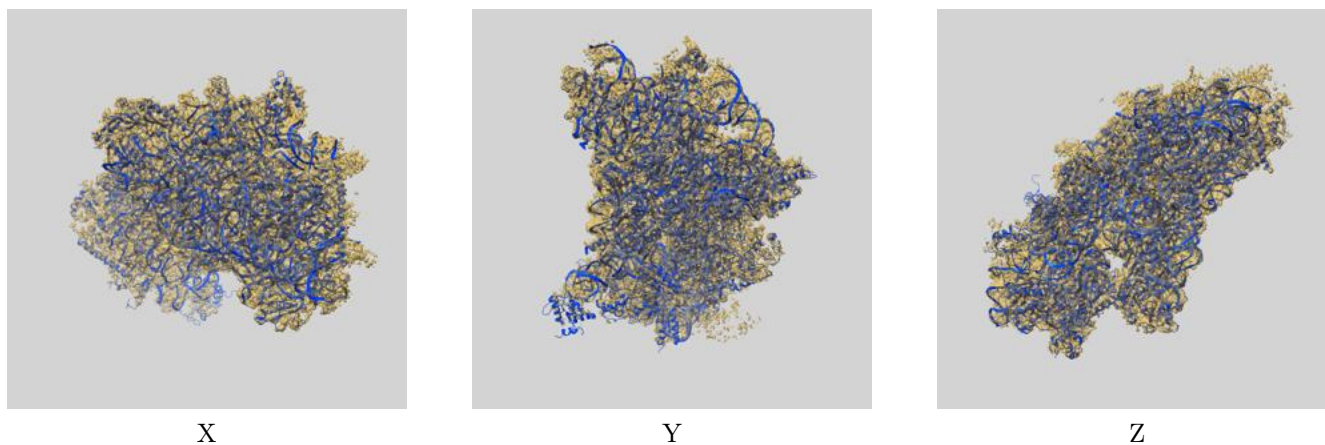
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.35	-	-
Author-provided FSC curve	3.35	3.97	3.43
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

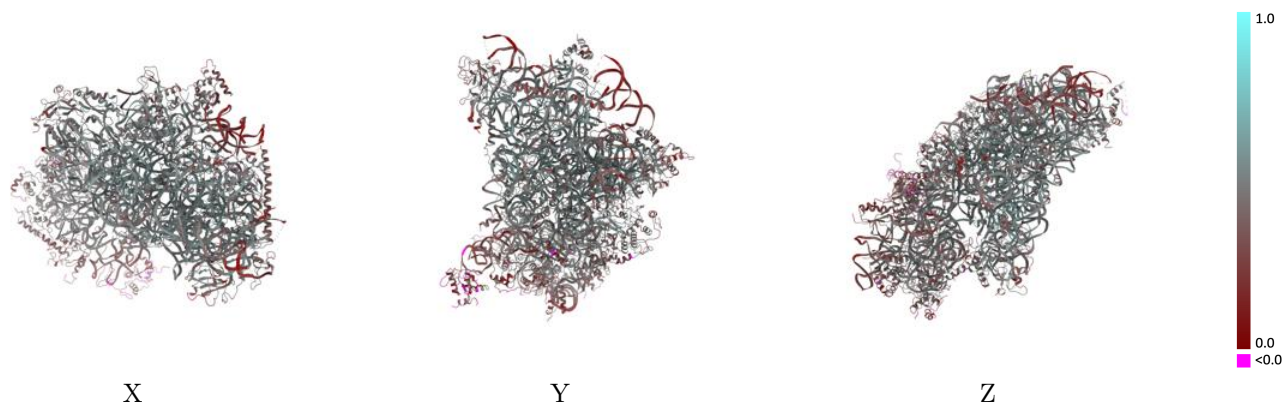
This section contains information regarding the fit between EMDB map EMD-6780 and PDB model 5XXU. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



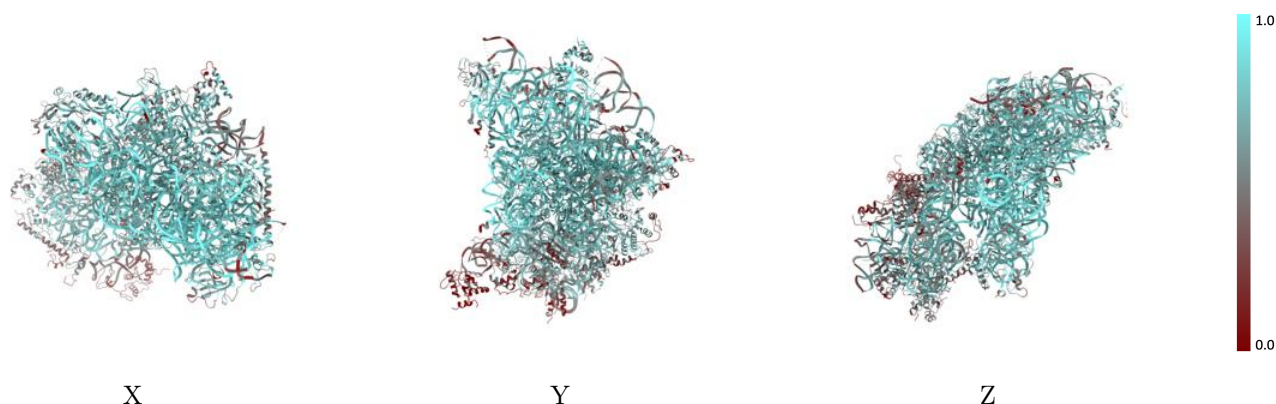
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



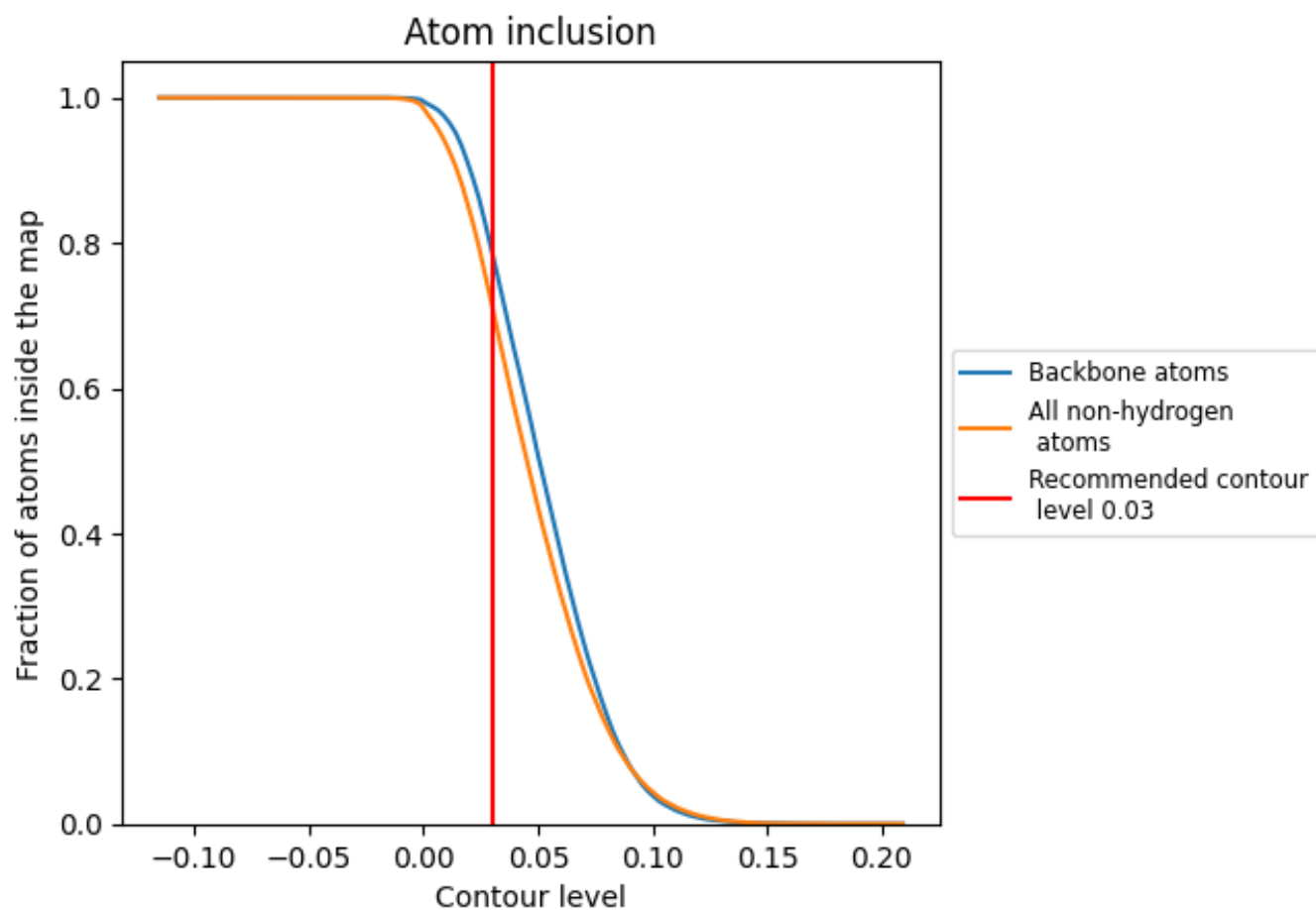
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 71% 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	 0.7129	 0.4440
2	 0.8154	 0.4650
A	 0.6634	 0.4400
B	 0.6757	 0.4540
C	 0.7287	 0.4750
D	 0.3739	 0.3360
E	 0.7252	 0.4760
F	 0.5534	 0.4100
G	 0.6185	 0.4090
H	 0.5896	 0.4250
I	 0.7361	 0.4860
J	 0.7197	 0.4570
K	 0.3503	 0.3020
L	 0.7472	 0.4960
M	 0.0886	 0.1730
N	 0.6963	 0.4690
O	 0.6731	 0.4710
P	 0.3731	 0.3120
Q	 0.5455	 0.4110
R	 0.3858	 0.3370
S	 0.5042	 0.3630
T	 0.5184	 0.3760
U	 0.3920	 0.3460
V	 0.6572	 0.4420
W	 0.7280	 0.4990
X	 0.7525	 0.5030
Y	 0.7078	 0.4590
Z	 0.5107	 0.3400
a	 0.7282	 0.4680
b	 0.7005	 0.4640
c	 0.5442	 0.4160
d	 0.6088	 0.4210
e	 0.6430	 0.4230
f	 0.1179	 0.1380
m	 0.7664	 0.5120

