



wwPDB EM Validation Summary Report ⓘ

Jul 3, 2024 – 02:09 am BST

PDB ID : 7OHT
EMDB ID : EMD-12908
Title : Nog1-TAP associated immature ribosomal particles from *S. cerevisiae* after rpL2 expression shut down, population A
Authors : Milkereit, P.; Poell, G.
Deposited on : 2021-05-11
Resolution : 4.70 Å(reported)
Based on initial model : 3JCT

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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

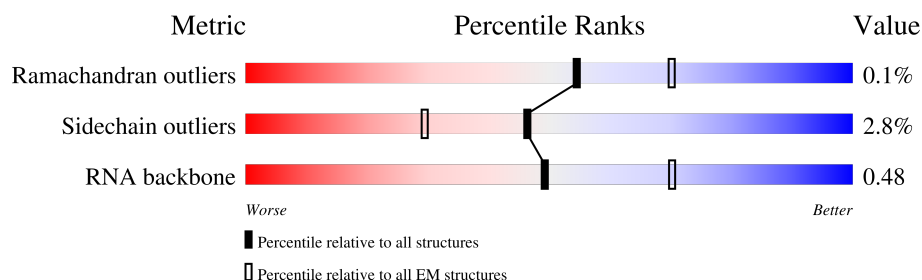
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.70 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.



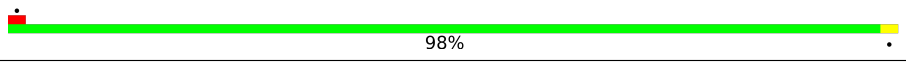
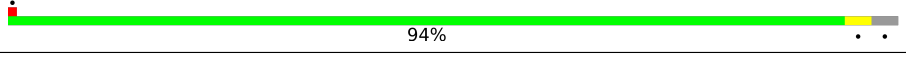
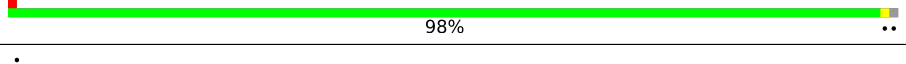
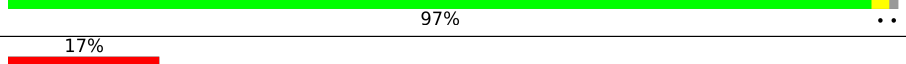
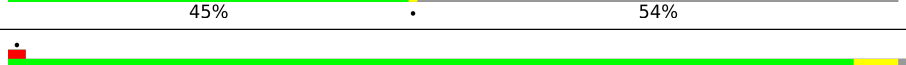
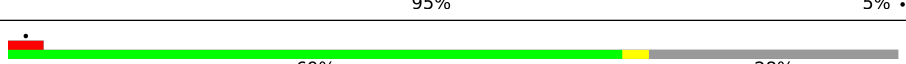
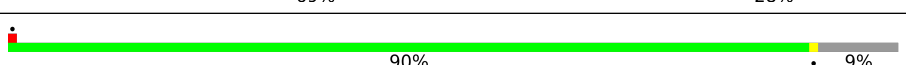
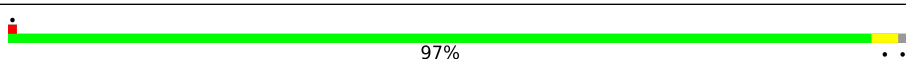


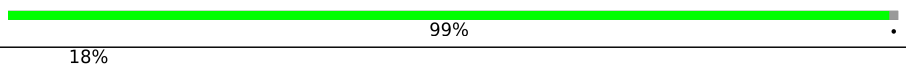
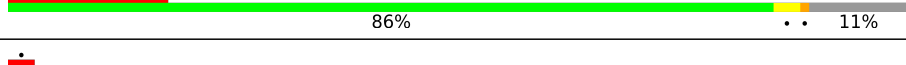

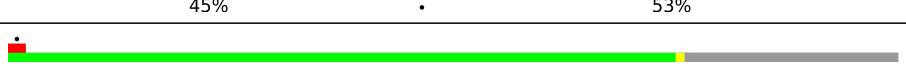
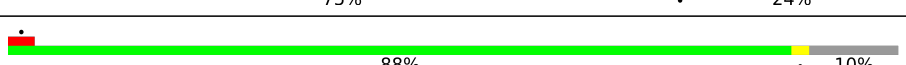
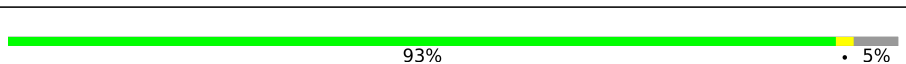
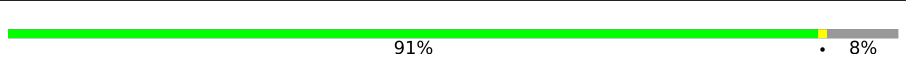


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	1	3396	
2	2	158	
3	3	121	
4	B	387	
5	C	362	
6	D	297	
7	E	176	
8	F	244	

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Mol	Chain	Length	Quality of chain
9	H	191	
10	J	174	
11	M	138	
12	O	199	
13	Q	186	
14	S	172	
15	T	160	
16	V	137	
17	W	236	
18	b	647	
19	e	130	
20	f	107	
21	m	486	
22	r	261	
23	u	199	
24	v	344	
25	w	203	
26	x	515	
27	y	245	

2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 135365 atoms, of which 59714 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 25S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	1	1485	Total	C	H	N	O	P	0	0
			47732	14188	15960	5725	10374	1485		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	2	19	Total	C	H	N	O	P	0	0
			605	180	203	69	134	19		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	3	114	Total	C	H	N	O	P	0	0
			3661	1086	1229	436	796	114		

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	B	350	Total	C	H	N	O	S	0	0
			5624	1763	2849	516	489	7		

- Molecule 5 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	C	239	Total	C	H	N	O		0	0
			3813	1178	1961	348	326			

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	D	265	Total	C	H	N	O	S	0	0
			4236	1352	2098	377	407	2		

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	E	141	Total	C	H	N	O	S	0	0
			2338	724	1217	203	193	1		

- Molecule 8 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	F	222	Total	C	H	N	O	S	0	0
			3647	1151	1863	324	308	1		

- Molecule 9 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	H	191	Total	C	H	N	O	S	0	0
			3105	963	1587	274	277	4		

- Molecule 10 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	169	Total	C	H	N	O	S	0	0
			2738	847	1385	253	249	4		

- Molecule 11 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	M	137	Total	C	H	N	O	S	0	0
			2214	678	1155	200	179	2		

- Molecule 12 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	O	197	Total	C	H	N	O	S	0	0
			3216	1003	1661	289	262	1		

- Molecule 13 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	Q	85	Total	C	H	N	O		0	0
			1357	414	705	123	115			

- Molecule 14 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	S	171	Total	C	H	N	O	S	0	0
			2913	925	1476	266	243	3		

- Molecule 15 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	T	116	Total	C	H	N	O	S	0	0
			1899	583	976	176	161	3		

- Molecule 16 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	V	124	Total	C	H	N	O	S	0	0
			1880	576	963	171	163	7		

- Molecule 17 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	W	234	Total	C	H	N	O	S	0	0
			3806	1194	1921	323	362	6		

- Molecule 18 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	b	453	Total	C	H	N	O	S	0	0
			7406	2340	3727	635	686	18		

- Molecule 19 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	e	39	Total	C	H	N	O	S	0	0
			625	185	331	59	50			

- Molecule 20 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	f	106	Total	C	H	N	O	S	0	0
			1731	540	881	165	144	1		

- Molecule 21 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	m	433	Total	C	H	N	O	S	0	0
			7069	2221	3565	633	641	9		

- Molecule 22 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	r	230	Total	C	H	N	O	S	0	0
			3827	1177	1967	352	324	7		

- Molecule 23 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	u	94	Total	C	H	N	O	S	0	0
			1633	504	833	164	123	9		

- Molecule 24 is a protein called Ribosome biogenesis protein RPF2.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	v	263	Total	C	H	N	O	S	0	0
			4323	1365	2193	372	379	14		

- Molecule 25 is a protein called Regulator of ribosome biosynthesis.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	w	182	Total	C	H	N	O	S	0	0
			2960	911	1512	261	271	5		

- Molecule 26 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	x	488	Total	C	H	N	O	S	0	0
			7606	2398	3799	677	711	21		

- Molecule 27 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	y	225	Total	C	H	N	O	S	0	0
			3398	1056	1697	295	343	7		

- Molecule 28 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
28	b	1	Total 1	Mg 1	0
28	m	1	Total 1	Mg 1	0

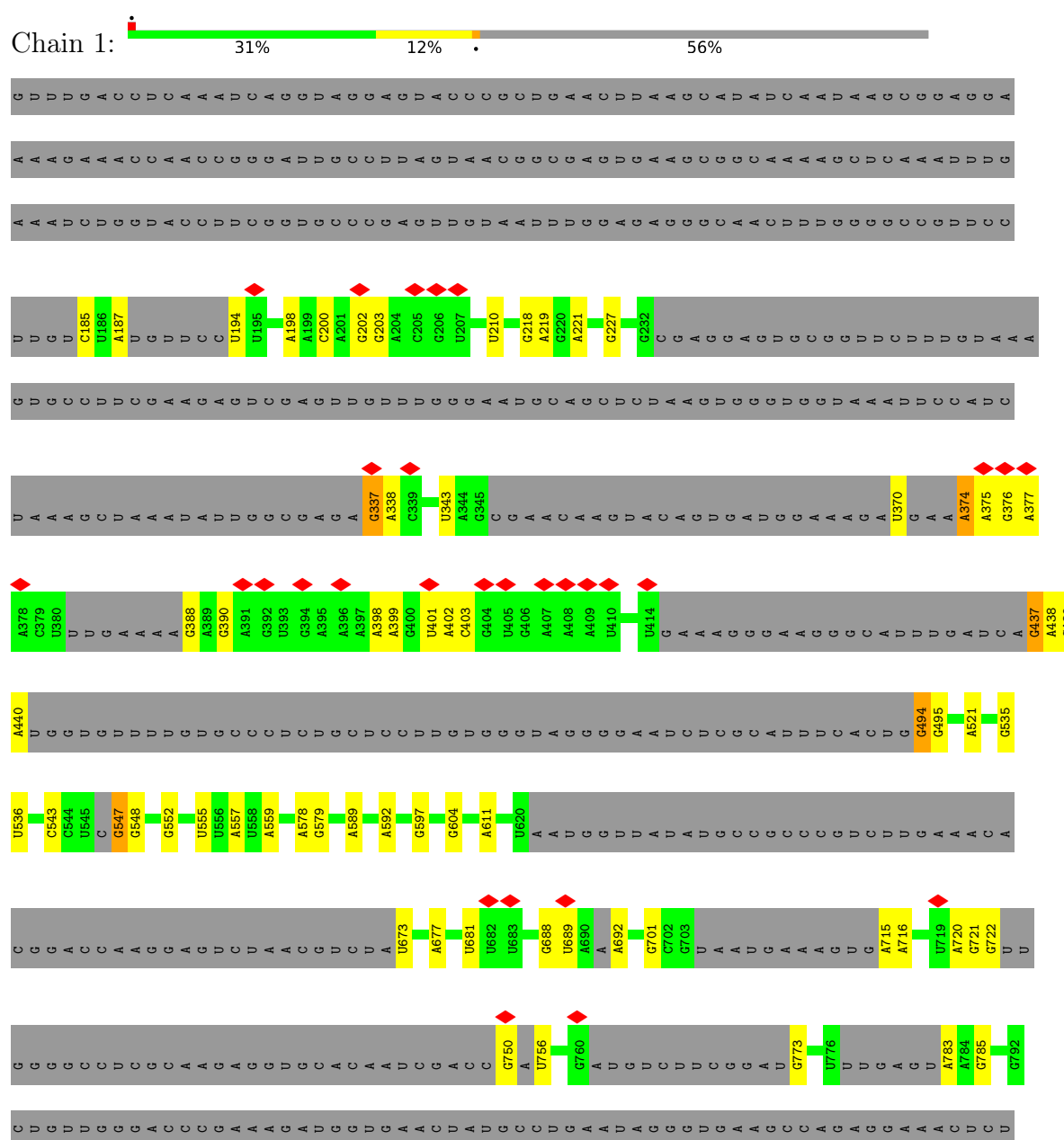
- Molecule 29 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
29	u	1	Total 1	Zn 1	0

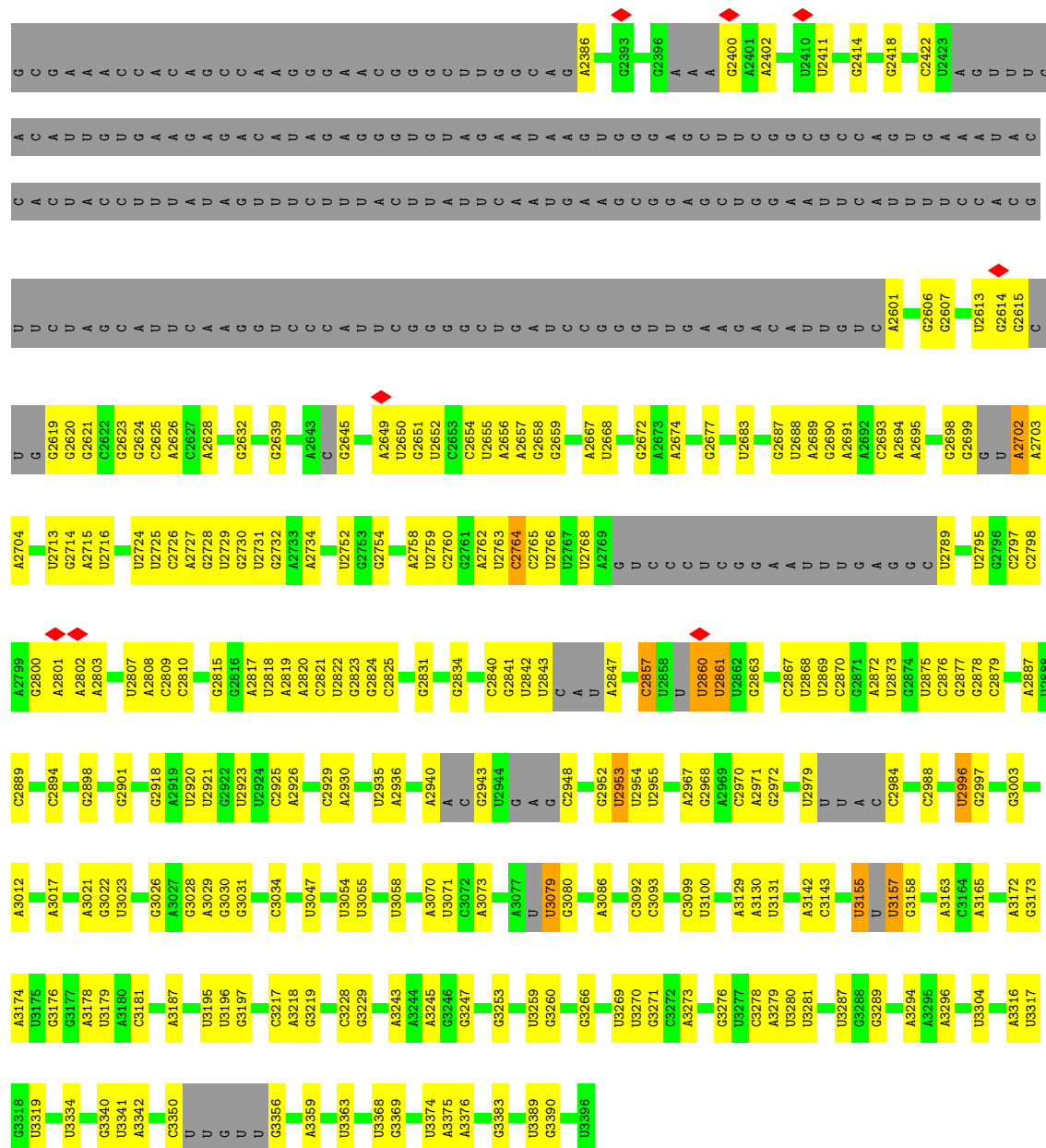
3 Residue-property plots [i](#)

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.

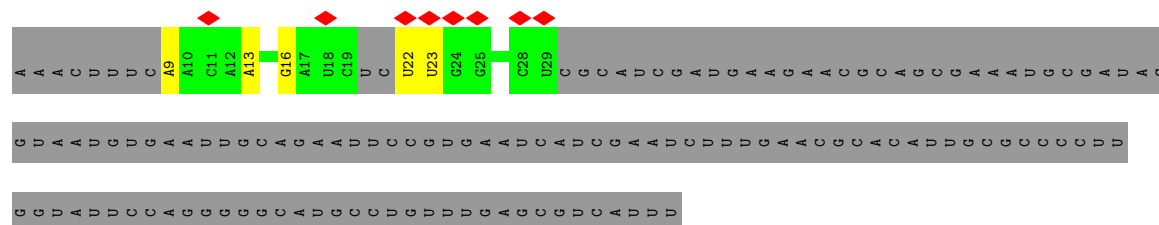
• Molecule 1: 25S rRNA






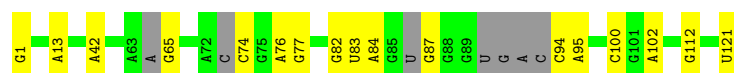


• Molecule 2: 5.8S rRNA




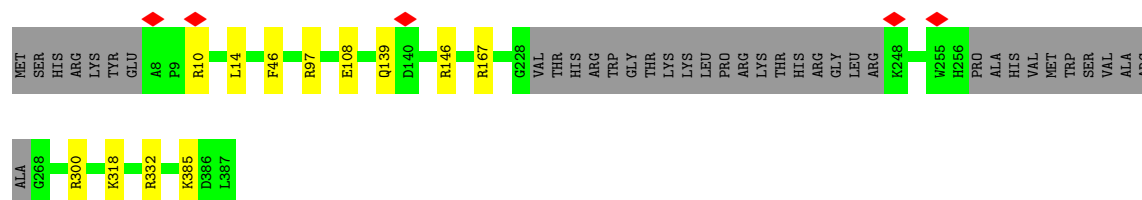
• Molecule 3: 5S rRNA

Chain 3:  80% 14% 6%



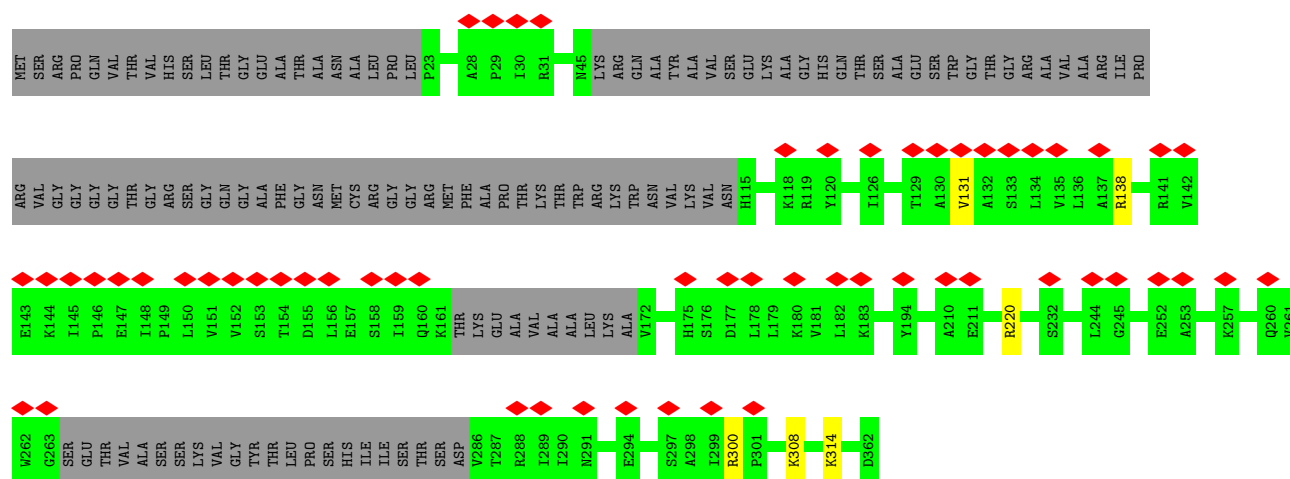
• Molecule 4: 60S ribosomal protein L3

Chain B:  87% 10%




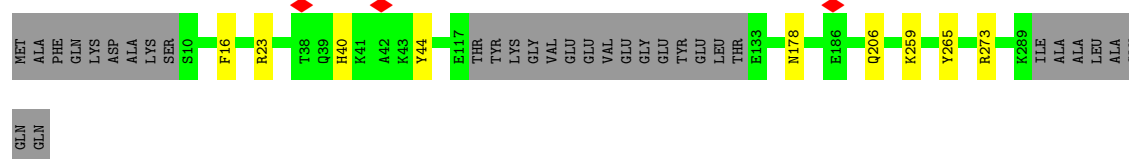
• Molecule 5: 60S ribosomal protein L4-A

Chain C:  16% 64% 34%




• Molecule 6: 60S ribosomal protein L5

Chain D:  86% 11%



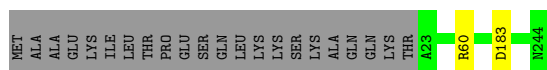
• Molecule 7: 60S ribosomal protein L6-A

Chain E:  78% 20%



- Molecule 8: 60S ribosomal protein L7-A

Chain F: 90% 9%



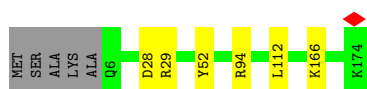
- Molecule 9: 60S ribosomal protein L9-A

Chain H: 98%



- Molecule 10: 60S ribosomal protein L11-A

Chain J: 94%



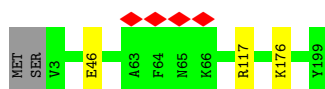
- Molecule 11: 60S ribosomal protein L14-A

Chain M: 98%



- Molecule 12: 60S ribosomal protein L16-A

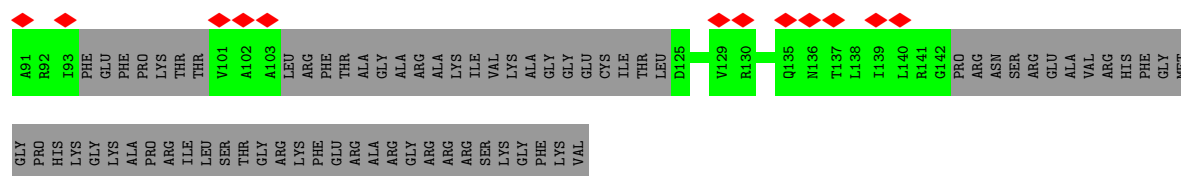
Chain O: 97%



- Molecule 13: 60S ribosomal protein L18-A

Chain Q: 17% 45% 54%

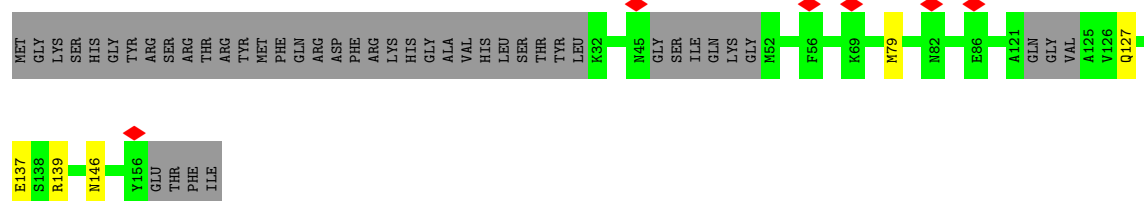




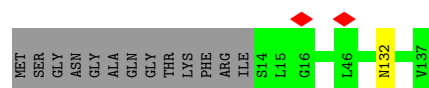
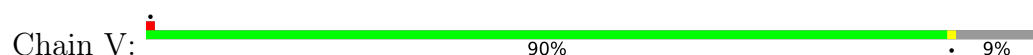
- Molecule 14: 60S ribosomal protein L20-A



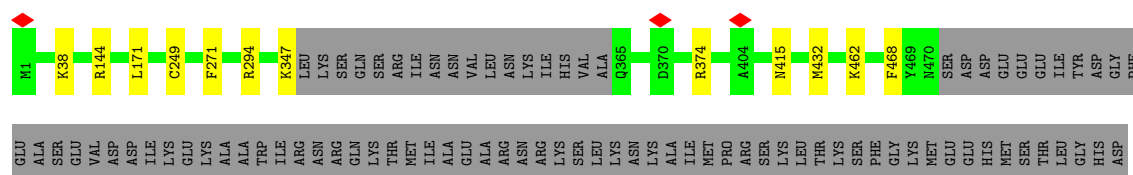
- Molecule 15: 60S ribosomal protein L21-A



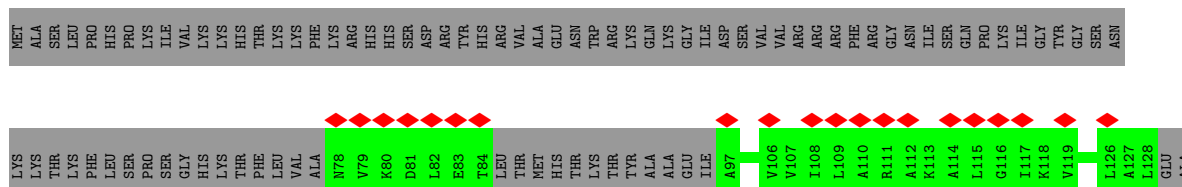
- Molecule 16: 60S ribosomal protein L23-A



- Molecule 17: Ribosome assembly factor MRT4



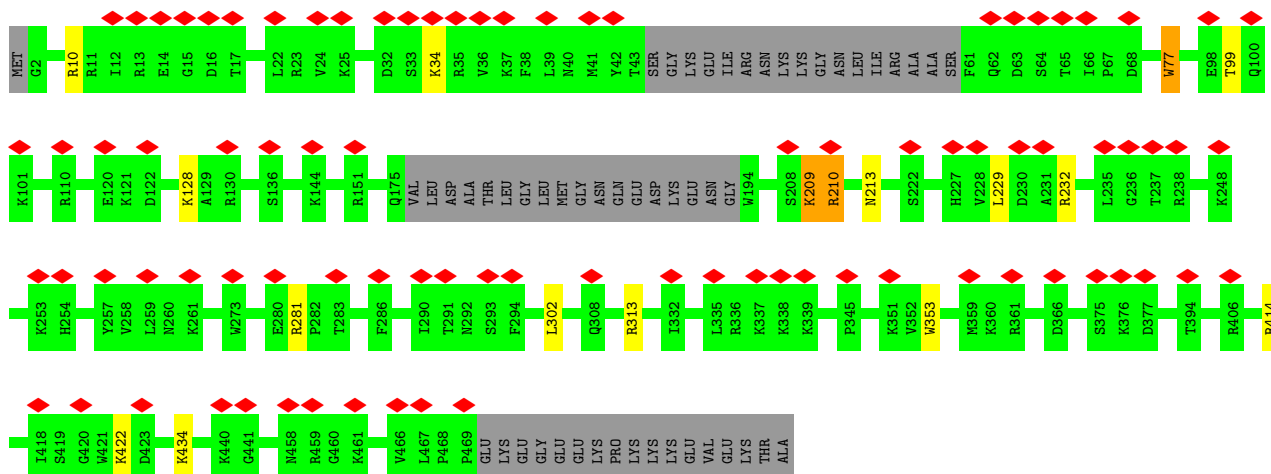
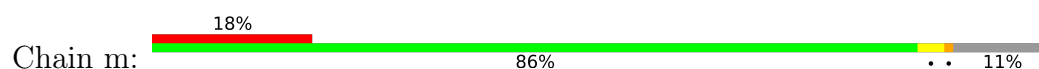
- Molecule 19: 60S ribosomal protein L32



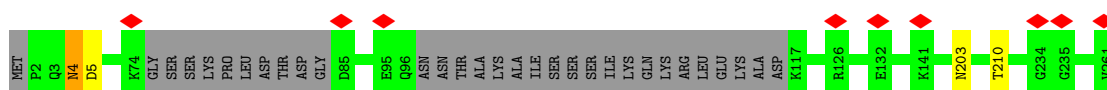
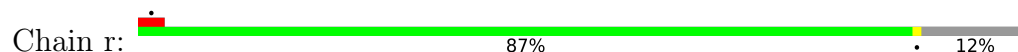
- Molecule 20: 60S ribosomal protein L33-A



- Molecule 21: Nucleolar GTP-binding protein 2

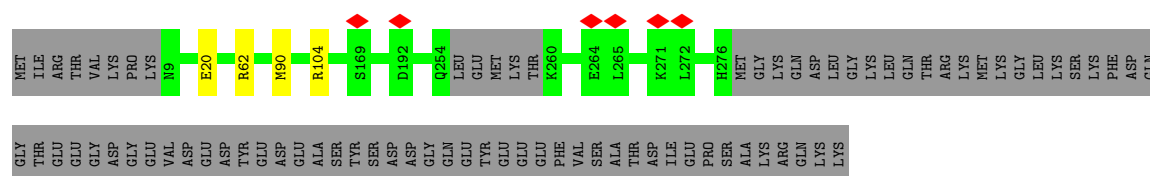


- Molecule 22: Ribosome biogenesis protein NSA2

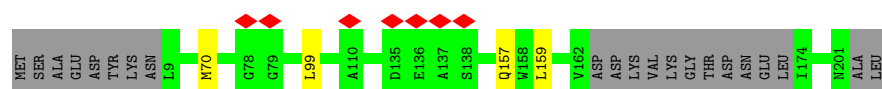


- Molecule 23: Ribosome biogenesis protein RLP24

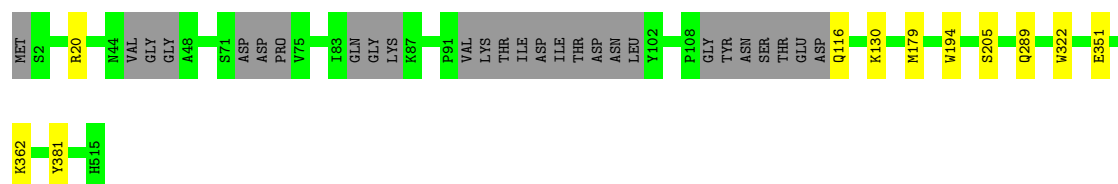
- Molecule 24: Ribosome biogenesis protein RPF2



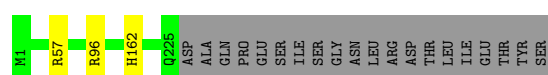
- Molecule 25: Regulator of ribosome biosynthesis



- Molecule 26: Ribosome assembly protein 4



- Molecule 27: Eukaryotic translation initiation factor 6



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21053	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 ($e^-/\text{\AA}^2$)	86.45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.099	Depositor
Minimum map value	-0.026	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	425.40002, 425.40002, 425.40002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0635, 1.0635, 1.0635	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	1	0.16	0/35525	0.76	57/55297 (0.1%)
2	2	0.16	0/447	0.78	2/691 (0.3%)
3	3	0.14	0/2715	0.74	5/4220 (0.1%)
4	B	0.23	0/2833	0.43	0/3806
5	C	0.23	0/1883	0.40	0/2544
6	D	0.24	0/2184	0.40	0/2945
7	E	0.24	0/1137	0.40	0/1525
8	F	0.24	0/1821	0.39	0/2451
9	H	0.24	0/1539	0.42	0/2073
10	J	0.24	0/1374	0.42	0/1842
11	M	0.23	0/1074	0.38	0/1446
12	O	0.24	0/1585	0.38	0/2128
13	Q	0.24	0/656	0.42	0/886
14	S	0.24	0/1473	0.44	0/1980
15	T	0.24	0/936	0.41	0/1255
16	V	0.25	0/931	0.43	0/1254
17	W	0.24	0/1918	0.41	0/2586
18	b	0.24	0/3748	0.41	0/5056
19	e	0.24	0/294	0.40	0/393
20	f	0.24	0/868	0.40	0/1168
21	m	0.23	0/3577	0.41	0/4820
22	r	0.23	0/1892	0.42	0/2528
23	u	0.25	0/816	0.39	0/1078
24	v	0.24	0/2172	0.39	0/2908
25	w	0.23	0/1471	0.39	0/1980
26	x	0.23	0/3897	0.41	0/5282
27	y	0.24	0/1722	0.43	0/2343
All	All	0.20	0/80488	0.62	64/116485 (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
9	H	0	1
21	m	0	1
22	r	0	1
All	All	0	3

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2857	C	N1-C2-O2	8.68	124.11	118.90
1	1	2857	C	N3-C2-O2	-7.37	116.74	121.90
1	1	3278	C	C2-N1-C1'	7.32	126.86	118.80
1	1	3157	U	OP1-P-OP2	-7.03	109.05	119.60
1	1	2645	G	OP1-P-OP2	-6.83	109.35	119.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	H	22	SER	Peptide
21	m	77	TRP	Peptide
22	r	4	ASN	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	
4	B	344/387 (89%)	323 (94%)	21 (6%)	0	100	100
5	C	231/362 (64%)	209 (90%)	21 (9%)	1 (0%)	34	72
6	D	261/297 (88%)	249 (95%)	12 (5%)	0	100	100
7	E	137/176 (78%)	135 (98%)	2 (2%)	0	100	100
8	F	220/244 (90%)	211 (96%)	9 (4%)	0	100	100
9	H	189/191 (99%)	180 (95%)	9 (5%)	0	100	100
10	J	167/174 (96%)	160 (96%)	7 (4%)	0	100	100
11	M	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
12	O	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
13	Q	77/186 (41%)	76 (99%)	1 (1%)	0	100	100
14	S	169/172 (98%)	159 (94%)	10 (6%)	0	100	100
15	T	110/160 (69%)	106 (96%)	4 (4%)	0	100	100
16	V	122/137 (89%)	121 (99%)	1 (1%)	0	100	100
17	W	232/236 (98%)	224 (97%)	8 (3%)	0	100	100
18	b	449/647 (69%)	413 (92%)	36 (8%)	0	100	100
19	e	35/130 (27%)	35 (100%)	0	0	100	100
20	f	104/107 (97%)	98 (94%)	6 (6%)	0	100	100
21	m	427/486 (88%)	386 (90%)	39 (9%)	2 (0%)	29	68
22	r	224/261 (86%)	193 (86%)	29 (13%)	2 (1%)	17	56
23	u	90/199 (45%)	89 (99%)	1 (1%)	0	100	100
24	v	259/344 (75%)	255 (98%)	4 (2%)	0	100	100
25	w	178/203 (88%)	171 (96%)	7 (4%)	0	100	100
26	x	476/515 (92%)	449 (94%)	27 (6%)	0	100	100
27	y	223/245 (91%)	215 (96%)	8 (4%)	0	100	100
All	All	5054/6196 (82%)	4781 (95%)	268 (5%)	5 (0%)	54	85

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	m	209	LYS
22	r	4	ASN
22	r	5	ASP
21	m	210	ARG
5	C	131	VAL

5.3.2 Protein sidechains ⓘ

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	
4	B	291/323 (90%)	279 (96%)	12 (4%)	30	56
5	C	197/289 (68%)	192 (98%)	5 (2%)	47	68
6	D	221/245 (90%)	212 (96%)	9 (4%)	30	56
7	E	122/153 (80%)	118 (97%)	4 (3%)	38	61
8	F	186/205 (91%)	184 (99%)	2 (1%)	73	85
9	H	171/171 (100%)	168 (98%)	3 (2%)	59	77
10	J	147/150 (98%)	141 (96%)	6 (4%)	30	56
11	M	108/109 (99%)	106 (98%)	2 (2%)	57	75
12	O	160/162 (99%)	157 (98%)	3 (2%)	57	75
13	Q	70/151 (46%)	69 (99%)	1 (1%)	67	81
14	S	155/156 (99%)	147 (95%)	8 (5%)	23	50
15	T	100/137 (73%)	95 (95%)	5 (5%)	24	51
16	V	96/105 (91%)	95 (99%)	1 (1%)	76	86
17	W	211/213 (99%)	205 (97%)	6 (3%)	43	65
18	b	408/573 (71%)	396 (97%)	12 (3%)	42	64
19	e	31/111 (28%)	31 (100%)	0	100	100
20	f	90/91 (99%)	90 (100%)	0	100	100
21	m	385/428 (90%)	368 (96%)	17 (4%)	28	54
22	r	203/229 (89%)	201 (99%)	2 (1%)	76	86
23	u	82/180 (46%)	77 (94%)	5 (6%)	18	46
24	v	238/309 (77%)	234 (98%)	4 (2%)	60	78
25	w	161/179 (90%)	157 (98%)	4 (2%)	47	68
26	x	428/451 (95%)	417 (97%)	11 (3%)	46	67
27	y	193/211 (92%)	190 (98%)	3 (2%)	62	79
All	All	4454/5331 (84%)	4329 (97%)	125 (3%)	46	65

5 of 125 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	T	137	GLU
25	w	159	LEU
18	b	271	PHE
25	w	157	GLN
26	x	322	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
21	m	455	ASN
24	v	64	ASN
26	x	44	ASN
24	v	61	ASN
15	T	127	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1458/3396 (42%)	375 (25%)	58 (3%)
2	2	17/158 (10%)	3 (17%)	0
3	3	109/121 (90%)	11 (10%)	1 (0%)
All	All	1584/3675 (43%)	389 (24%)	59 (3%)

5 of 389 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	187	A
1	1	198	A
1	1	200	C
1	1	202	G
1	1	203	G

5 of 59 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1306	G
1	1	3269	U
1	1	2658	G
1	1	3228	C
1	1	3030	G

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

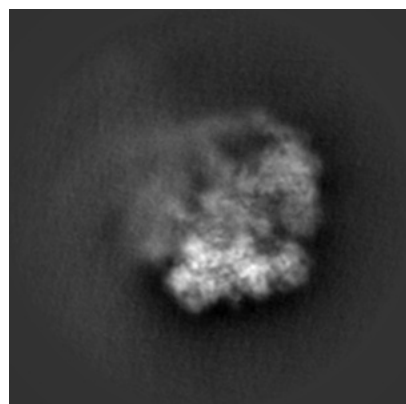
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12908. These allow visual inspection of the internal detail of the map and identification of artifacts.

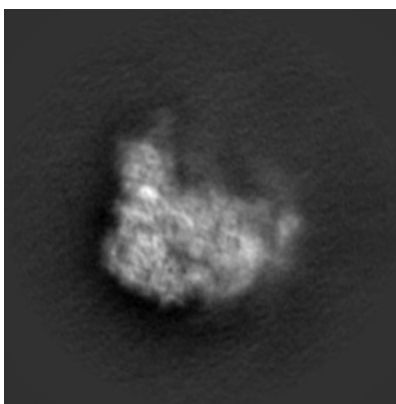
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

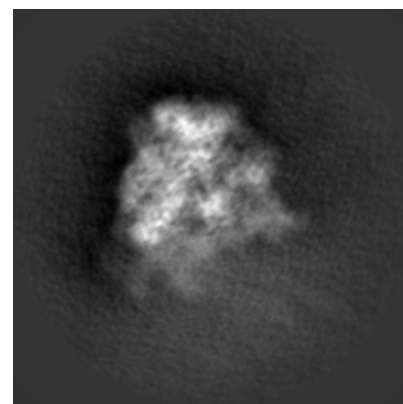
6.1.1 Primary map



X

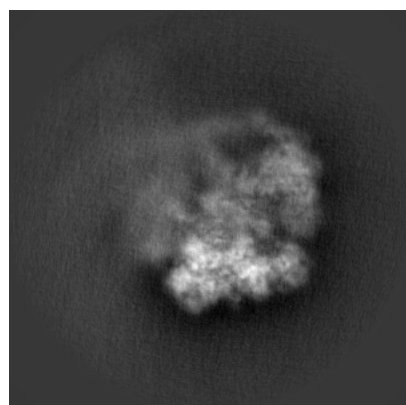


Y

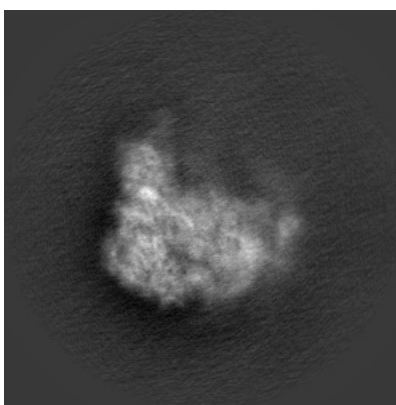


Z

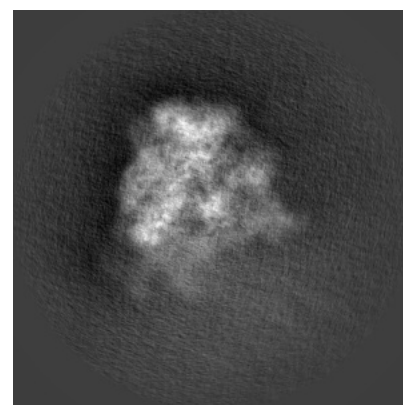
6.1.2 Raw map



X



Y

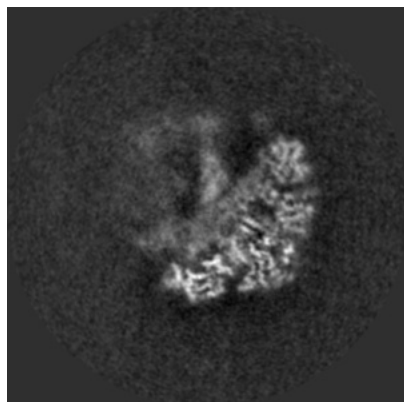


Z

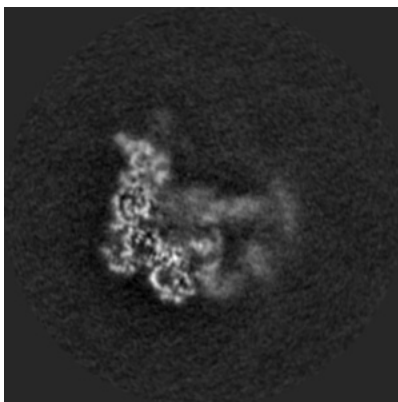
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

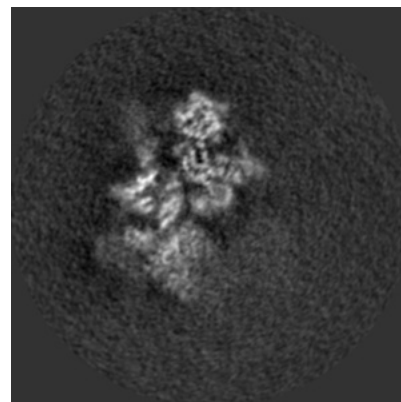
6.2.1 Primary map



X Index: 200

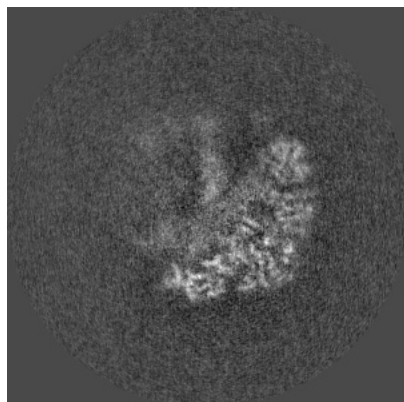


Y Index: 200

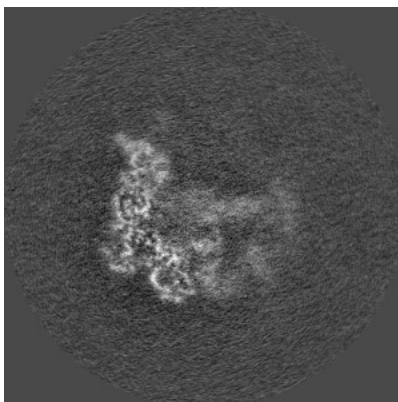


Z Index: 200

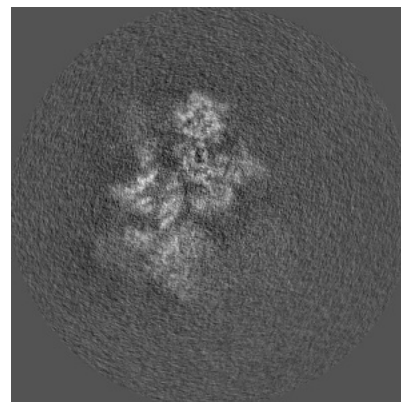
6.2.2 Raw map



X Index: 200



Y Index: 200

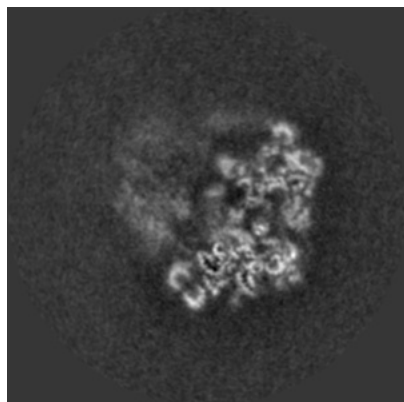


Z Index: 200

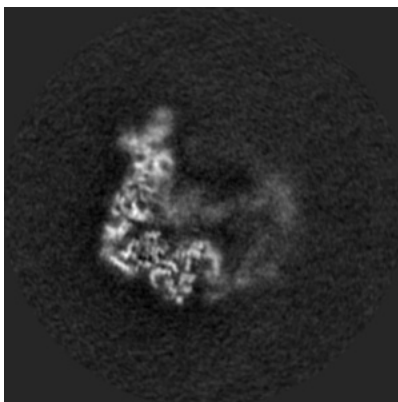
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

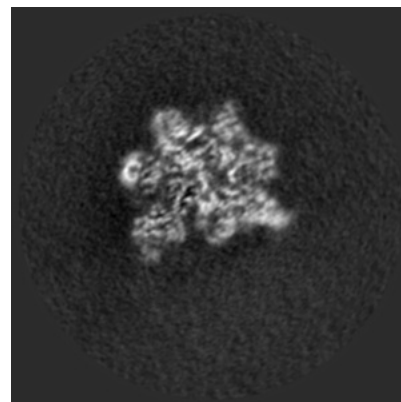
6.3.1 Primary map



X Index: 171

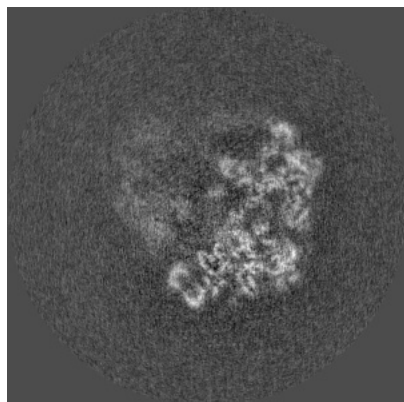


Y Index: 193

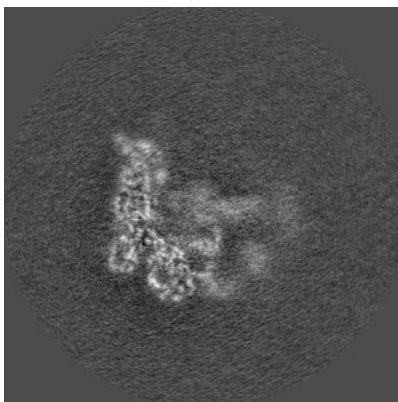


Z Index: 142

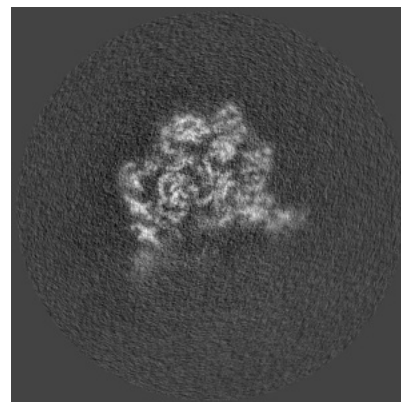
6.3.2 Raw map



X Index: 172



Y Index: 203

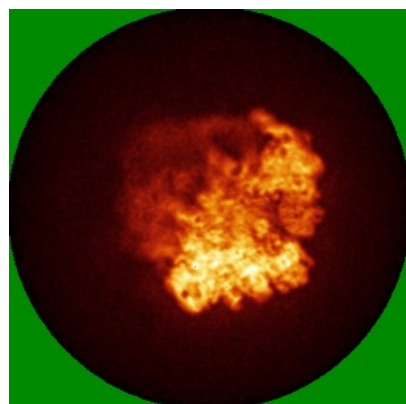


Z Index: 150

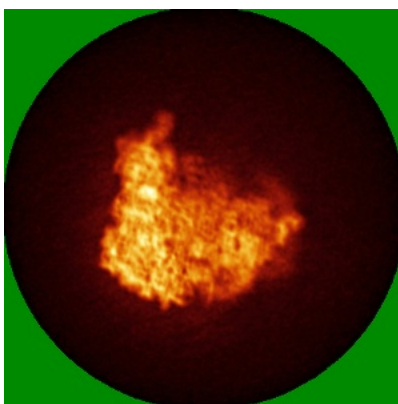
The images above show the largest variance slices of the map in three orthogonal directions.

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

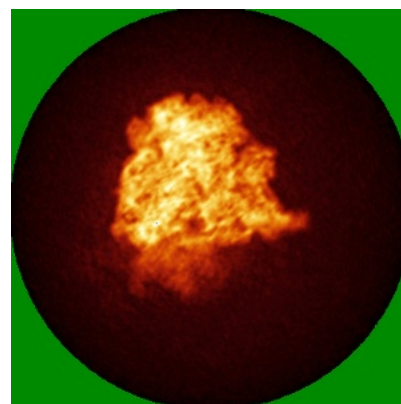
6.4.1 Primary map



X

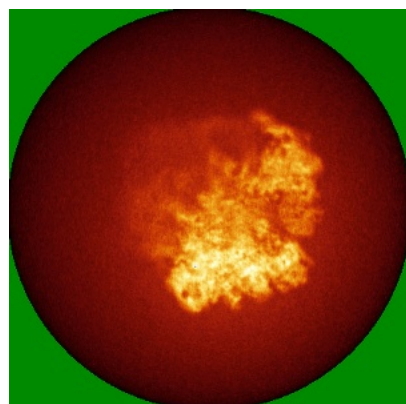


Y

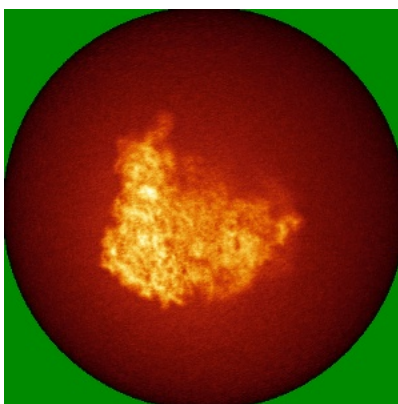


Z

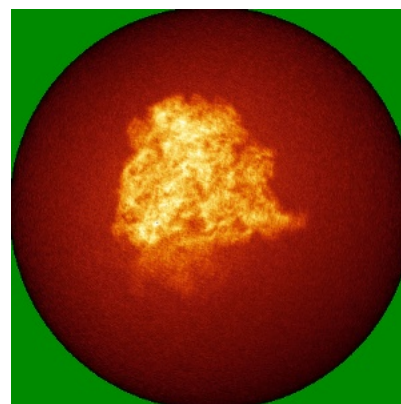
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

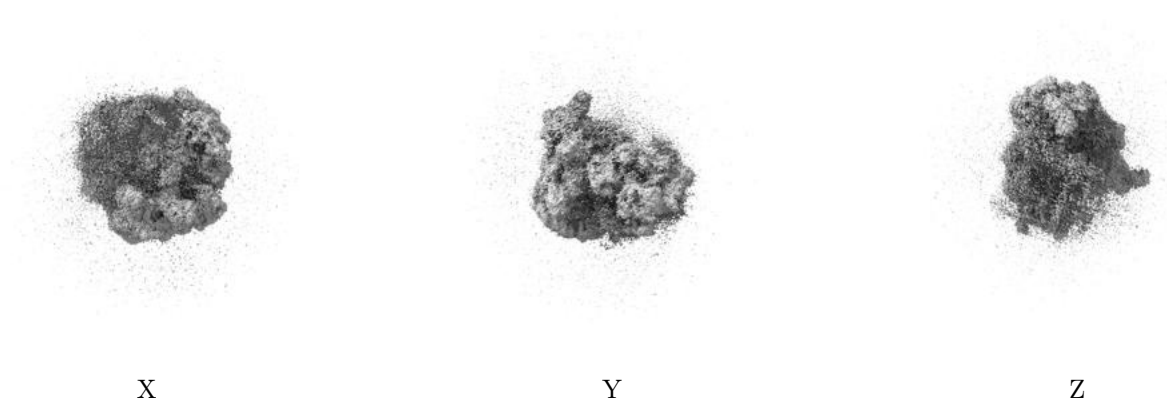
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

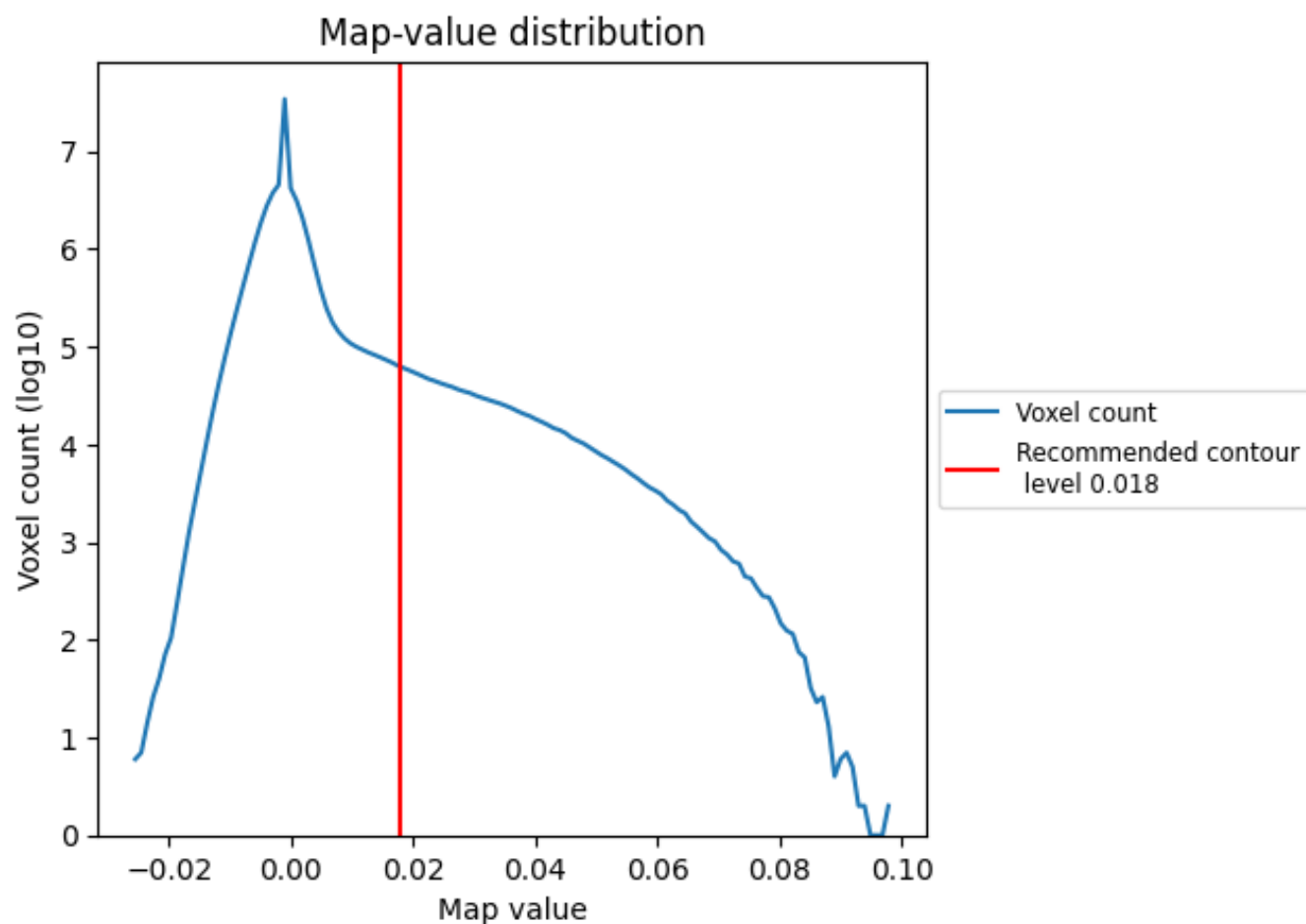
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

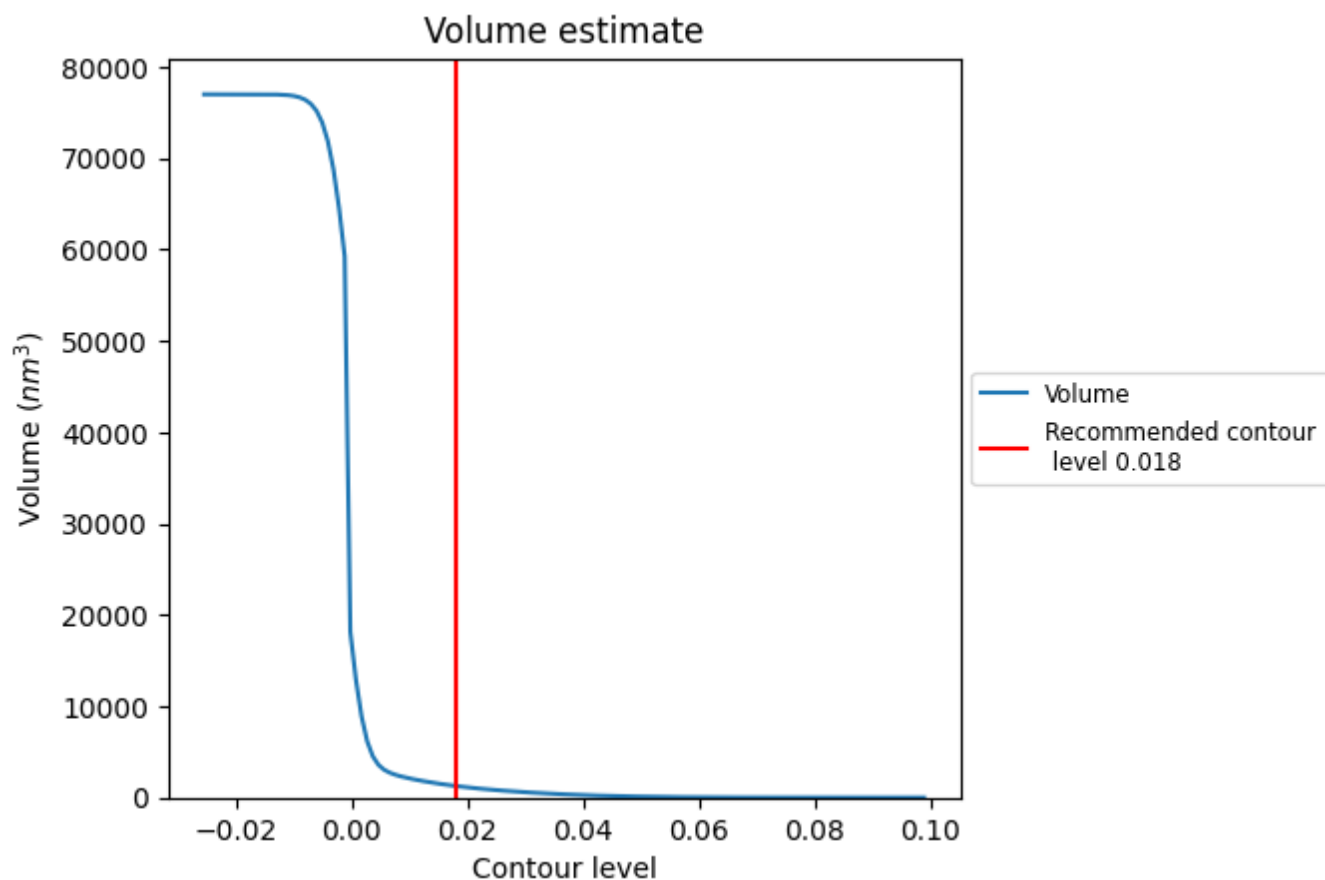
This section contains the results of statistical analysis of the map.

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.

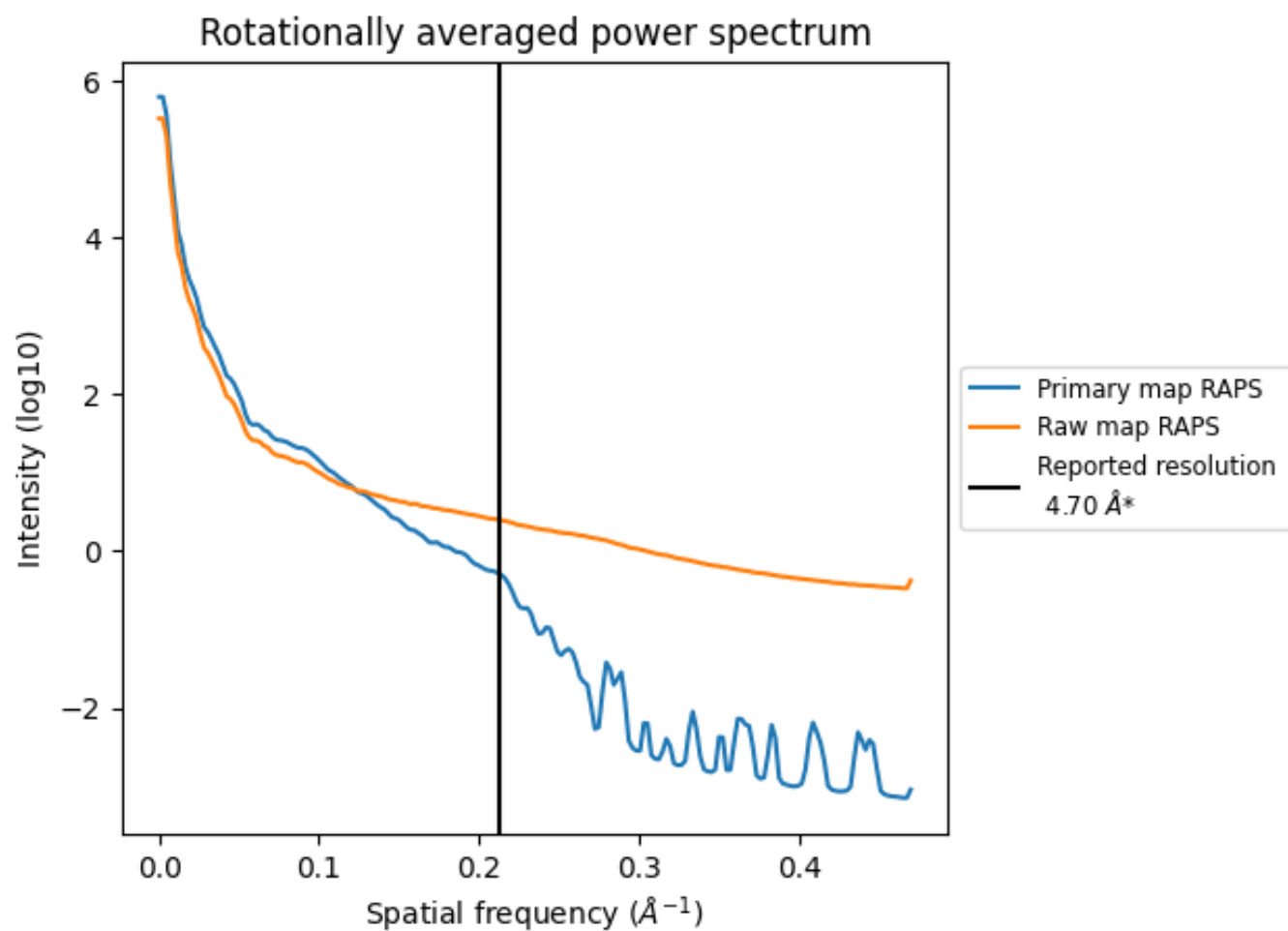
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1261 nm³; this corresponds to an approximate mass of 1139 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 ⓘ

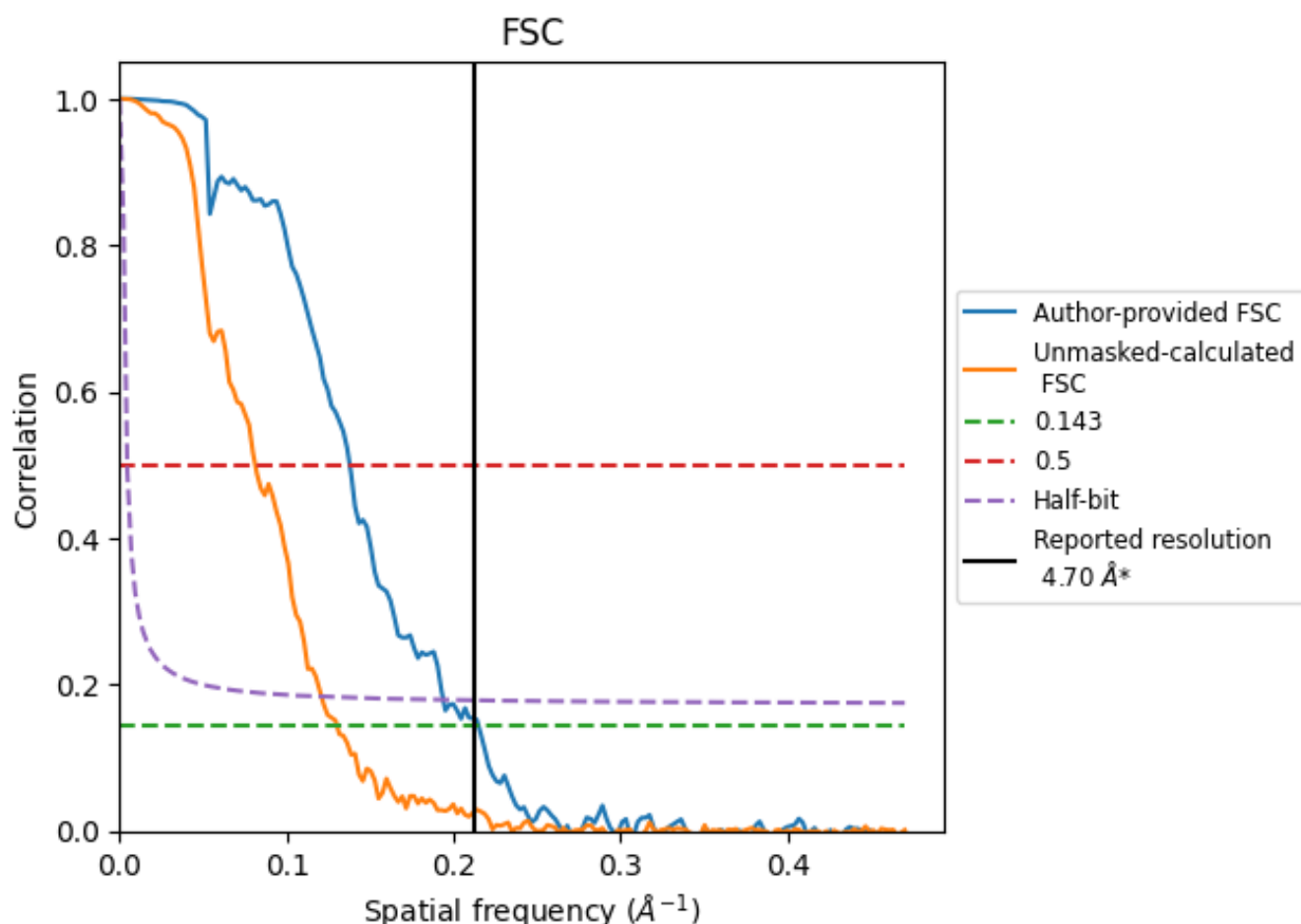


*Reported resolution corresponds to spatial frequency of 0.213 Å⁻¹

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 0.213 Å⁻¹

8.2 Resolution estimates [i](#)

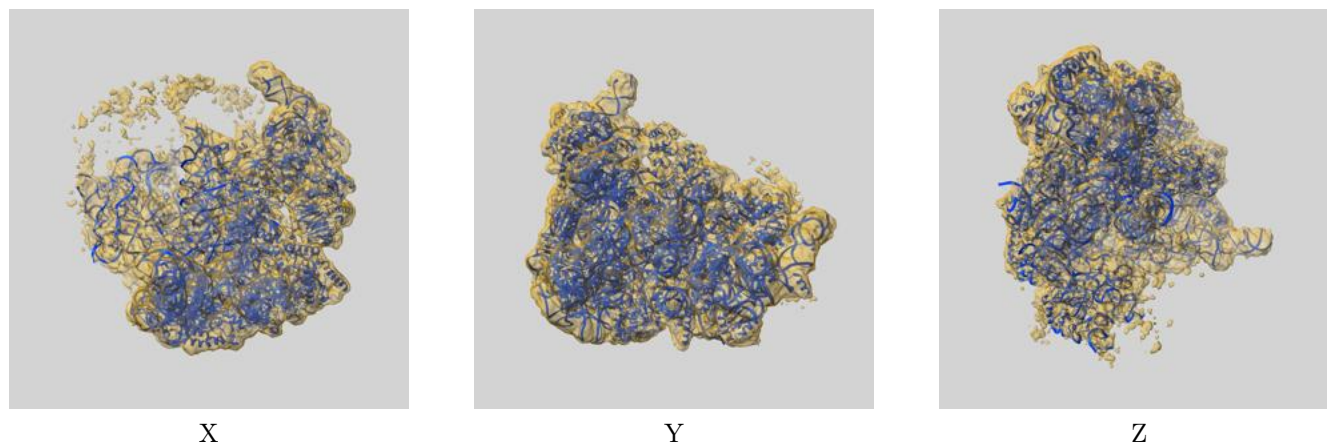
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	4.65	7.26	5.16
Unmasked-calculated*	7.68	12.30	8.27

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.68 differs from the reported value 4.7 by more than 10 %

9 Map-model fit [i](#)

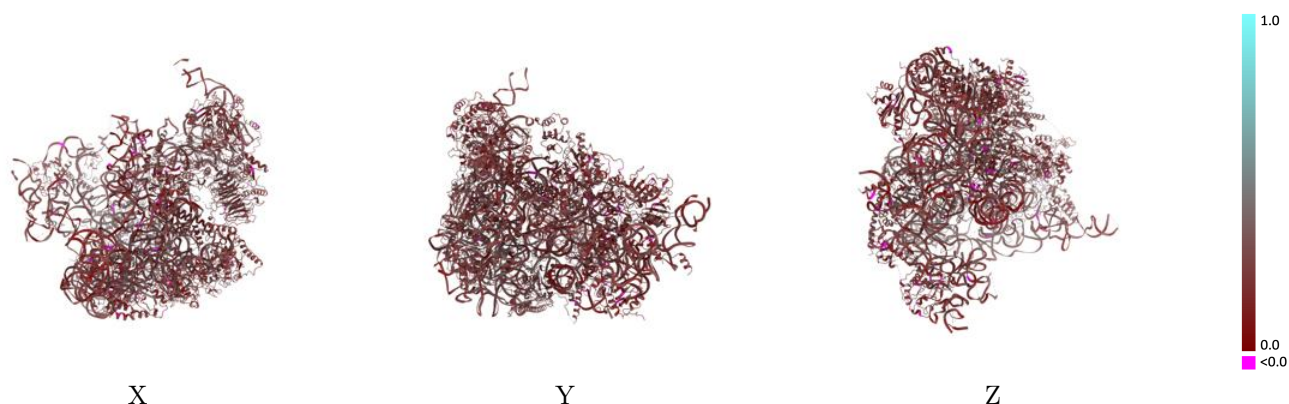
This section contains information regarding the fit between EMDB map EMD-12908 and PDB model 7OHT. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

9.1 Map-model overlay [i](#)



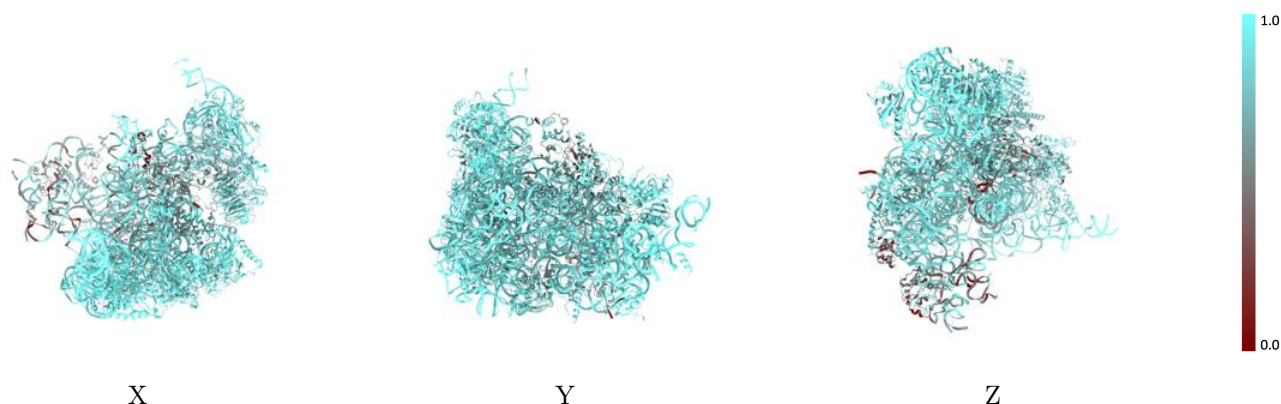
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



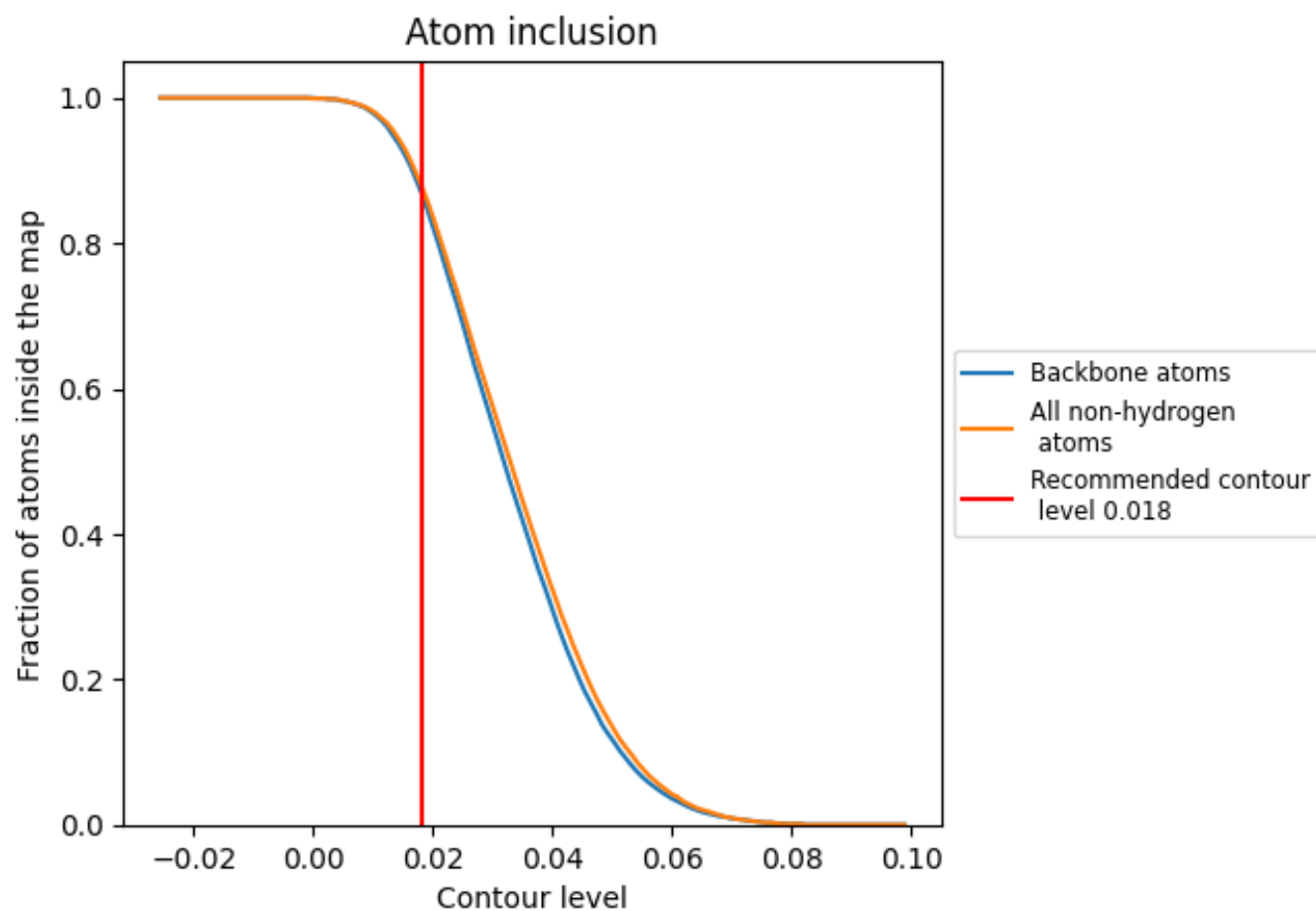
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.018).

























































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 88% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8810	 0.2450
1	 0.9150	 0.2400
2	 0.5550	 0.2080
3	 0.9990	 0.2450
B	 0.9260	 0.2660
C	 0.6310	 0.2350
D	 0.9040	 0.2240
E	 0.9200	 0.2720
F	 0.8660	 0.2730
H	 0.8860	 0.2880
J	 0.9340	 0.2000
M	 0.8890	 0.2870
O	 0.8480	 0.2890
Q	 0.4970	 0.2190
S	 0.8720	 0.2880
T	 0.7790	 0.2650
V	 0.9030	 0.2320
W	 0.9320	 0.2480
b	 0.8810	 0.2300
e	 0.3990	 0.2760
f	 0.8650	 0.3130
m	 0.6400	 0.2240
r	 0.7660	 0.2480
u	 0.9690	 0.2030
v	 0.8910	 0.2470
w	 0.8270	 0.2340
x	 0.8830	 0.2520
y	 0.9470	 0.2340

