



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:47 AM UTC

PDB ID : 5G06 / pdb_00005g06
EMDB ID : EMD-3366
Title : Cryo-EM structure of yeast cytoplasmic exosome
Authors : Liu, J.J.; Niu, C.Y.; Wu, Y.; Tan, D.; Wang, Y.; Ye, M.D.; Liu, Y.; Zhao, W.W.; Zhou, K.; Liu, Q.S.; Dai, J.B.; Yang, X.R.; Dong, M.Q.; Huang, N.; Wang, H.W.
Deposited on : 2016-03-17
Resolution : 4.20 Å(reported)

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:

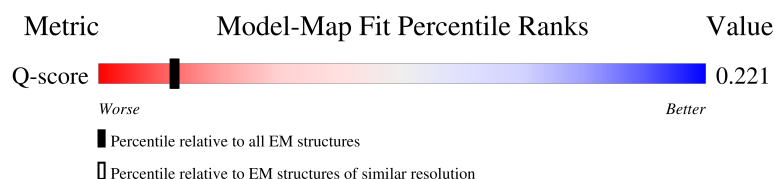
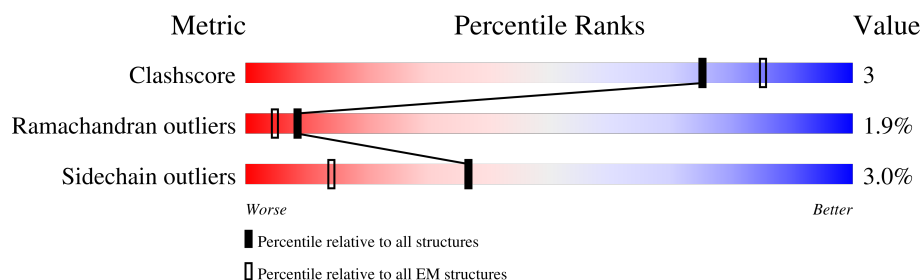
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5410 (3.70 - 4.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	305	
2	B	246	
3	C	394	
4	D	223	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	E	265	43%52%
6	F	250	31%47%6%16%
7	G	240	45%47%5%
8	H	359	37%40%5%18%
9	I	292	11%35%37%5%22%
10	J	1001	6%43%51%5%
11	P	747	8%5%5%87%

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 26794 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called EXOSOME COMPLEX COMPONENT RRP45.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	302	Total	C	N	O	S	0	0
			2350	1474	402	457	17		

- Molecule 2 is a protein called EXOSOME COMPLEX COMPONENT SKI6.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	240	Total	C	N	O	S	0	0
			1890	1182	338	362	8		

- Molecule 3 is a protein called EXOSOME COMPLEX COMPONENT RRP43.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	335	Total	C	N	O	S	0	0
			2622	1653	455	503	11		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	363	MET	VAL	conflict	UNP P25359

- Molecule 4 is a protein called EXOSOME COMPLEX COMPONENT RRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	223	Total	C	N	O	S	0	0
			1707	1073	289	335	10		

- Molecule 5 is a protein called EXOSOME COMPLEX COMPONENT RRP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	265	Total	C	N	O	S	0	0
			2048	1307	336	400	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	138	ILE	VAL	conflict	UNP Q12277

- Molecule 6 is a protein called EXOSOME COMPLEX COMPONENT MTR3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	211	Total	C	N	O	S	0	0
			1627	1018	276	323	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	75	SER	THR	conflict	UNP P48240

- Molecule 7 is a protein called EXOSOME COMPLEX COMPONENT RRP40.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	236	Total	C	N	O	S	0	0
			1831	1169	301	350	11		

- Molecule 8 is a protein called EXOSOME COMPLEX COMPONENT RRP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	293	Total	C	N	O	S	0	0
			2277	1419	411	435	12		

- Molecule 9 is a protein called EXOSOME COMPLEX COMPONENT CSL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	227	Total	C	N	O	S	0	0
			1750	1093	310	338	9		

- Molecule 10 is a protein called EXOSOME COMPLEX EXONUCLEASE DIS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	993	Total	C	N	O	S	0	0
			7942	5002	1395	1509	36		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	171	ASN	ASP	conflict	UNP Q08162
J	551	ASN	ASP	conflict	UNP Q08162

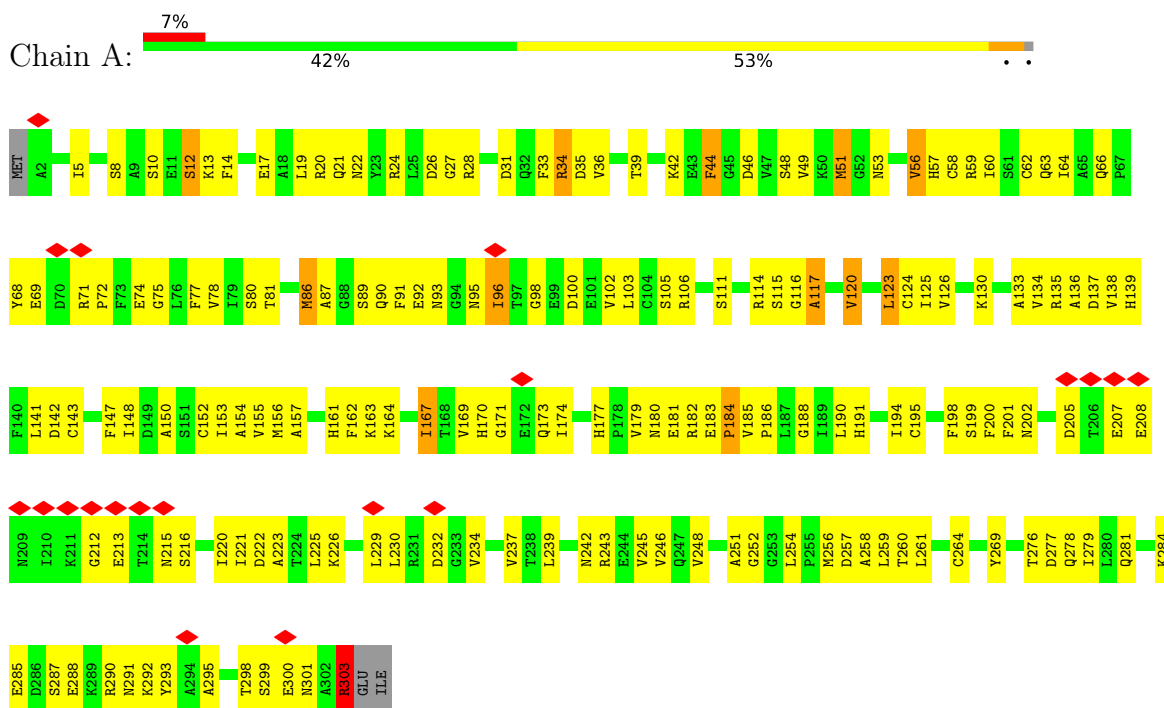
- Molecule 11 is a protein called SUPERKILLER PROTEIN 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	P	95	750	475	128	146	1	0	0

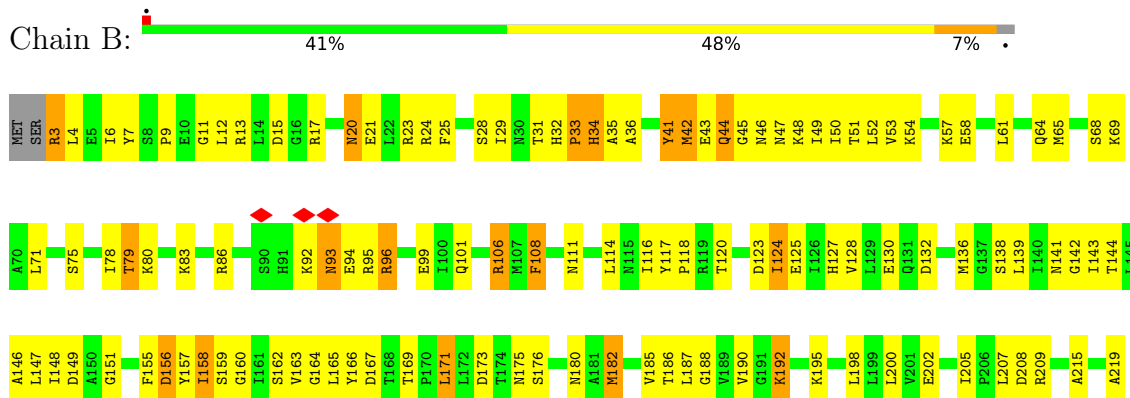
3 Residue-property plots

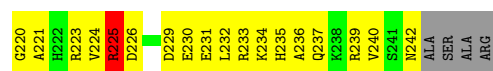
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: EXOSOME COMPLEX COMPONENT RRP45

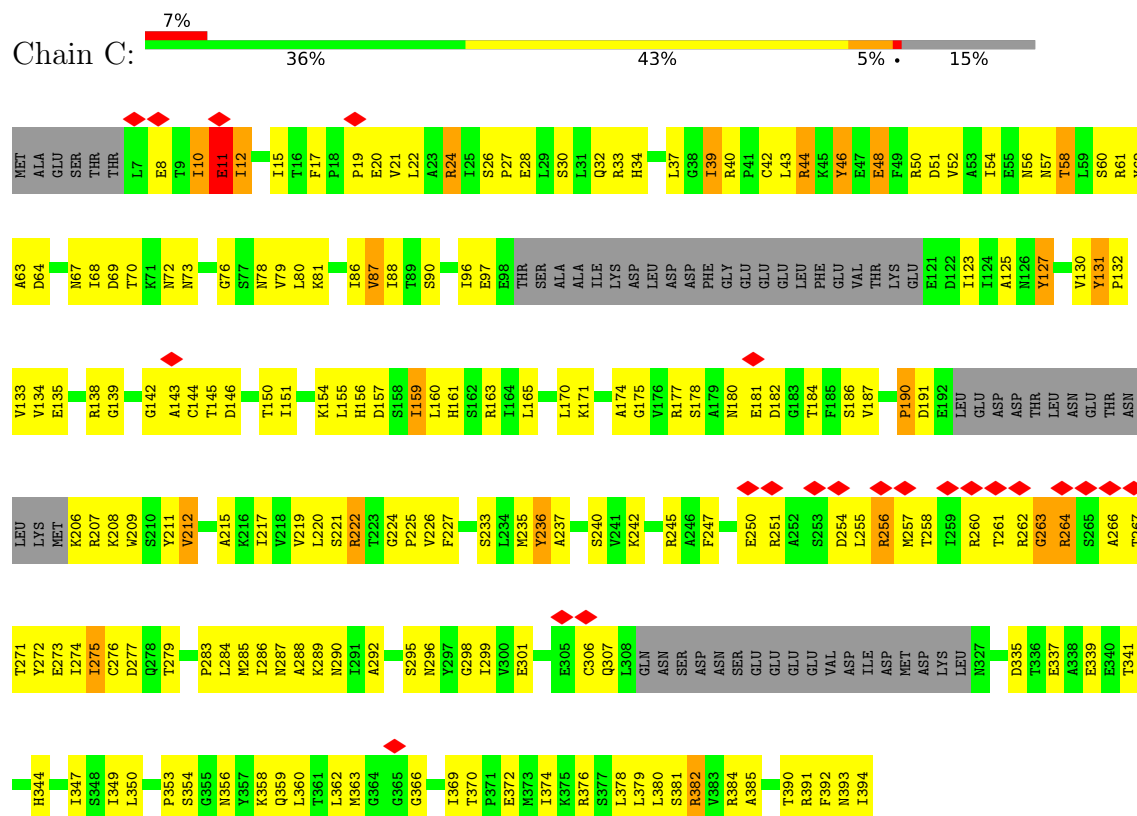


• Molecule 2: EXOSOME COMPLEX COMPONENT SKI6

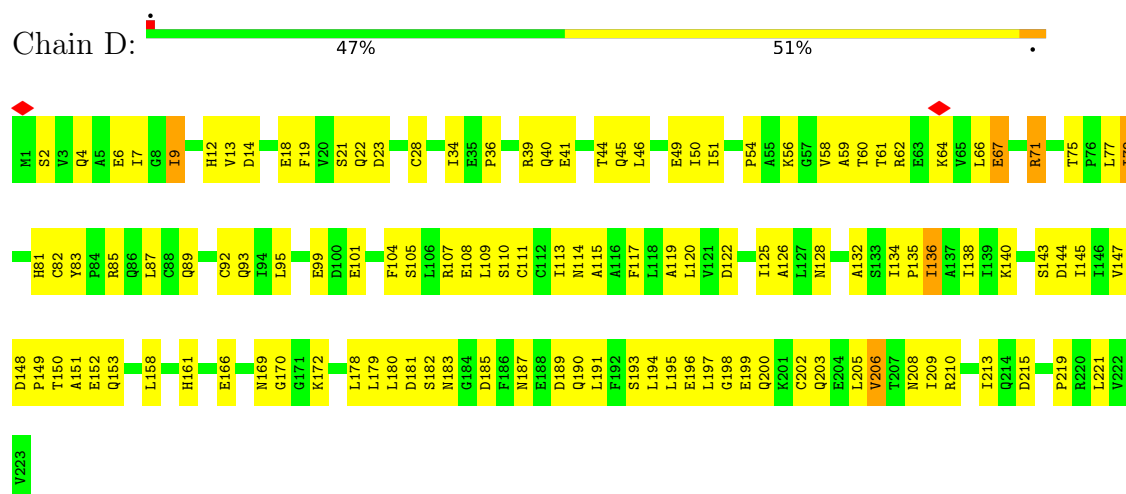




• Molecule 3: EXOSOME COMPLEX COMPONENT RRP43

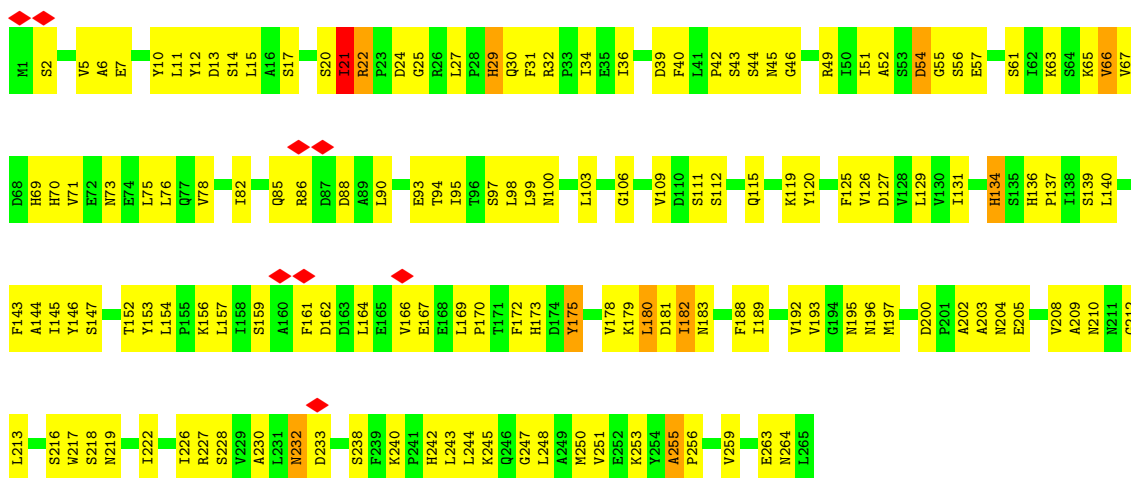


• Molecule 4: EXOSOME COMPLEX COMPONENT RRP46

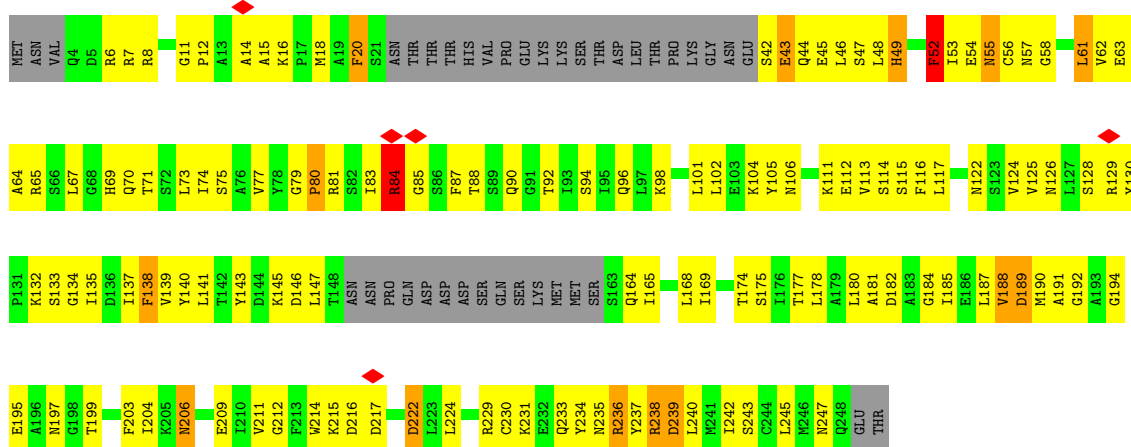


• Molecule 5: EXOSOME COMPLEX COMPONENT RRP42

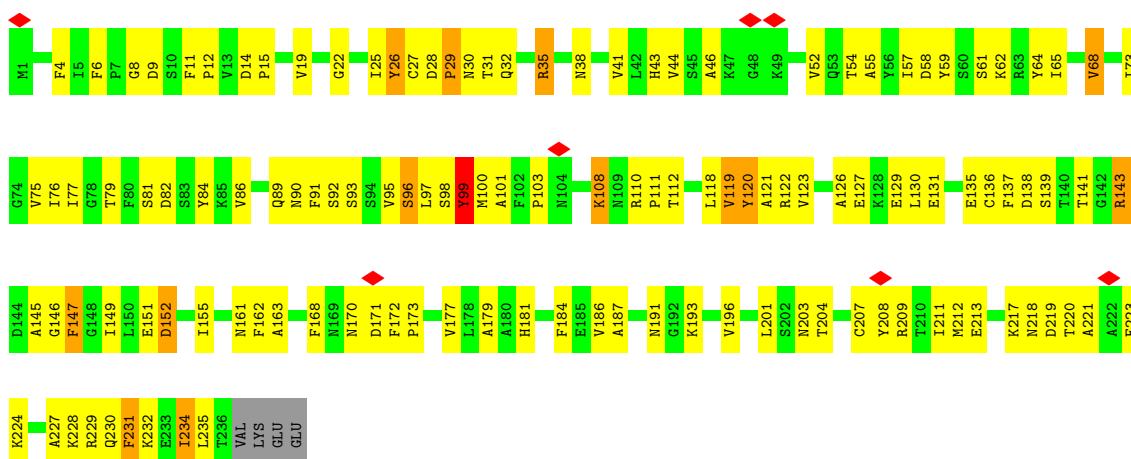




• Molecule 6: EXOSOME COMPLEX COMPONENT MTR3

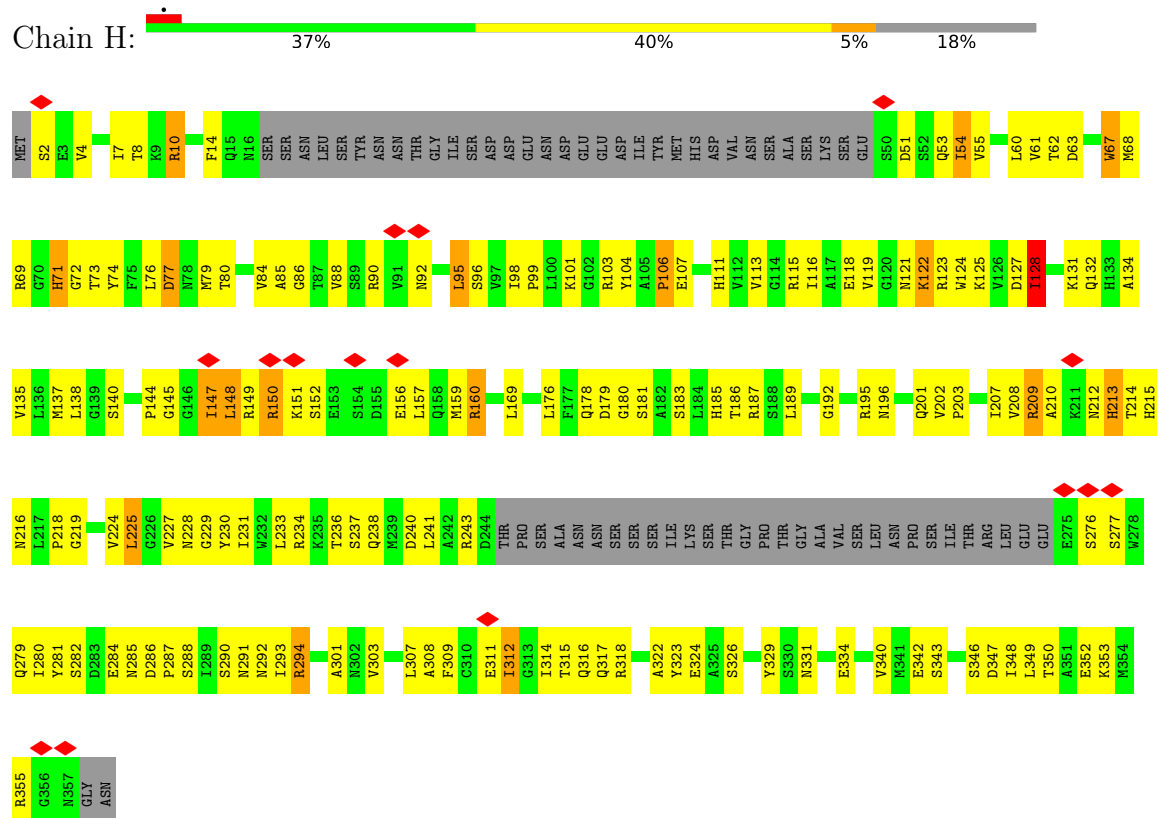


• Molecule 7: EXOSOME COMPLEX COMPONENT RRP40



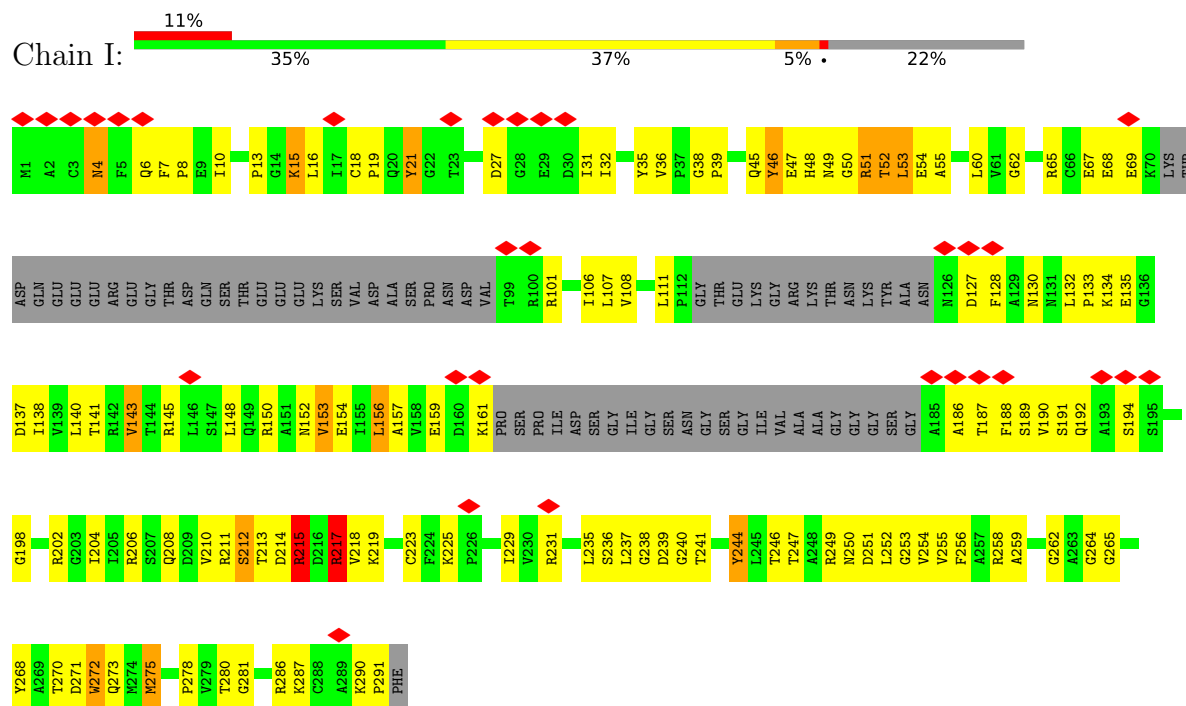
- Molecule 8: EXOSOME COMPLEX COMPONENT RRP4

Chain H:



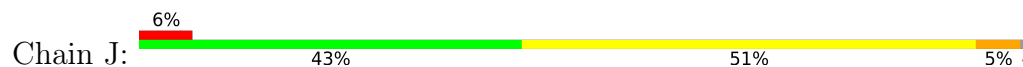
- Molecule 9: EXOSOME COMPLEX COMPONENT CSL4

Chain I:



- Molecule 10: EXOSOME COMPLEX EXONUCLEASE DIS3

Chain J:





Chain P:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	25000	Depositor
Resolution determination method	Not provided	
CTF correction method	MICROGRAPHS	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	21	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.112	Depositor
Minimum map value	-0.050	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	235.1772, 235.1772, 235.1772	wwPDB
Map dimensions	180, 180, 180	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.30654, 1.30654, 1.30654	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	2.33	97/2386 (4.1%)	2.49	168/3218 (5.2%)
2	B	2.33	79/1914 (4.1%)	2.43	118/2577 (4.6%)
3	C	2.25	91/2659 (3.4%)	2.50	185/3596 (5.1%)
4	D	2.33	64/1725 (3.7%)	2.48	124/2339 (5.3%)
5	E	2.32	85/2087 (4.1%)	2.43	133/2836 (4.7%)
6	F	2.36	80/1649 (4.9%)	2.50	120/2222 (5.4%)
7	G	2.30	83/1868 (4.4%)	2.38	123/2531 (4.9%)
8	H	2.32	92/2311 (4.0%)	2.46	153/3118 (4.9%)
9	I	2.33	76/1774 (4.3%)	2.35	95/2398 (4.0%)
10	J	2.32	347/8097 (4.3%)	2.44	534/10972 (4.9%)
11	P	2.32	30/763 (3.9%)	2.59	72/1031 (7.0%)
All	All	2.32	1124/27233 (4.1%)	2.45	1825/36838 (5.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
2	B	0	7
3	C	0	10
4	D	0	2
5	E	0	4
6	F	0	5
7	G	0	7
8	H	0	5
9	I	0	6
10	J	0	26
11	P	0	1
All	All	0	76

The worst 5 of 1124 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	I	265	GLY	CA-C	-11.10	1.42	1.52
10	J	113	VAL	N-CA	-10.84	1.38	1.46
1	A	130	LYS	CA-C	-10.60	1.39	1.52
2	B	188	GLY	CA-C	-10.53	1.40	1.51
3	C	298	GLY	CA-C	-10.48	1.39	1.51

The worst 5 of 1825 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	J	641	PHE	CA-CB-CG	-14.26	99.54	113.80
10	J	225	LEU	CA-C-O	-12.16	108.32	119.75
2	B	132	ASP	N-CA-C	-11.84	96.52	112.03
1	A	125	ILE	N-CA-C	-11.41	100.84	111.45
1	A	252	GLY	N-CA-C	-11.36	100.45	112.04

There are no chirality outliers.

5 of 76 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	269	TYR	Sidechain
1	A	303	ARG	Sidechain
1	A	44	PHE	Sidechain
2	B	23	ARG	Sidechain
2	B	3	ARG	Sidechain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2350	0	2345	6	0
2	B	1890	0	1943	7	0
3	C	2622	0	2688	25	0
4	D	1707	0	1766	4	0
5	E	2048	0	2079	4	0
6	F	1627	0	1607	51	0
7	G	1831	0	1829	2	0
8	H	2277	0	2283	9	0
9	I	1750	0	1755	46	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	7942	0	7947	13	0
11	P	750	0	759	113	0
All	All	26794	0	27001	164	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 164 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:49:HIS:NE2	11:P:36:LYS:HD2	1.28	1.43
3:C:51:ASP:CB	11:P:47:PRO:HD3	1.49	1.41
9:I:250:ASN:OD1	11:P:86:LEU:CD1	1.71	1.38
3:C:81:LYS:HE2	11:P:35:LYS:CB	1.45	1.38
6:F:52:PHE:CD2	11:P:32:LEU:HD22	1.61	1.34

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	300/305 (98%)	278 (93%)	18 (6%)	4 (1%)	9	41
2	B	238/246 (97%)	223 (94%)	11 (5%)	4 (2%)	7	35
3	C	327/394 (83%)	294 (90%)	22 (7%)	11 (3%)	3	21
4	D	221/223 (99%)	211 (96%)	9 (4%)	1 (0%)	24	62
5	E	263/265 (99%)	248 (94%)	10 (4%)	5 (2%)	6	32
6	F	205/250 (82%)	194 (95%)	8 (4%)	3 (2%)	8	38
7	G	234/240 (98%)	219 (94%)	14 (6%)	1 (0%)	30	66
8	H	287/359 (80%)	263 (92%)	15 (5%)	9 (3%)	3	23

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	219/292 (75%)	200 (91%)	14 (6%)	5 (2%)	5	29
10	J	991/1001 (99%)	905 (91%)	68 (7%)	18 (2%)	6	33
11	P	93/747 (12%)	82 (88%)	9 (10%)	2 (2%)	5	29
All	All	3378/4322 (78%)	3117 (92%)	198 (6%)	63 (2%)	8	32

5 of 63 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	251	ALA
3	C	10	ILE
3	C	11	GLU
3	C	12	ILE
3	C	143	ALA

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	
1	A	263/266 (99%)	260 (99%)	3 (1%)	65	73
2	B	214/218 (98%)	206 (96%)	8 (4%)	30	51
3	C	294/349 (84%)	283 (96%)	11 (4%)	30	51
4	D	197/197 (100%)	194 (98%)	3 (2%)	57	70
5	E	240/240 (100%)	231 (96%)	9 (4%)	29	51
6	F	181/219 (83%)	175 (97%)	6 (3%)	33	55
7	G	205/209 (98%)	197 (96%)	8 (4%)	28	50
8	H	252/311 (81%)	247 (98%)	5 (2%)	48	65
9	I	190/240 (79%)	186 (98%)	4 (2%)	47	65
10	J	895/901 (99%)	862 (96%)	33 (4%)	30	51
11	P	89/702 (13%)	88 (99%)	1 (1%)	65	73
All	All	3020/3852 (78%)	2929 (97%)	91 (3%)	37	57

5 of 91 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	J	68	PRO
10	J	486	LEU
10	J	107	CYS
10	J	254	THR
10	J	642	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 67 such sidechains are listed below:

Mol	Chain	Res	Type
10	J	771	ASN
10	J	841	HIS
11	P	37	HIS
6	F	70	GLN
5	E	235	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no chain breaks in this entry.

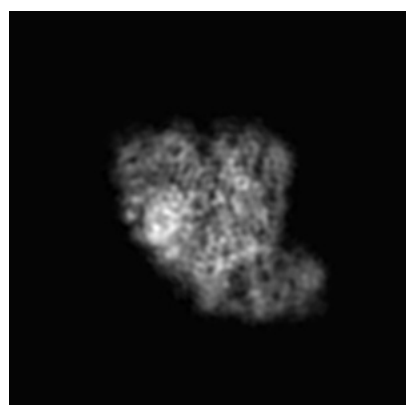
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3366. These allow visual inspection of the internal detail of the map and identification of artifacts.

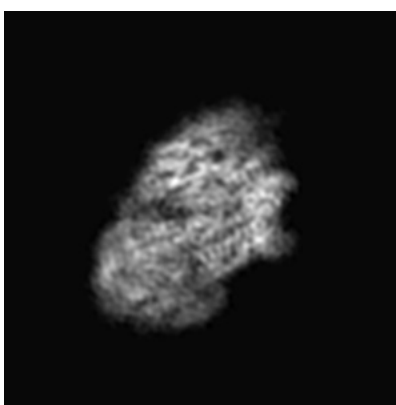
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

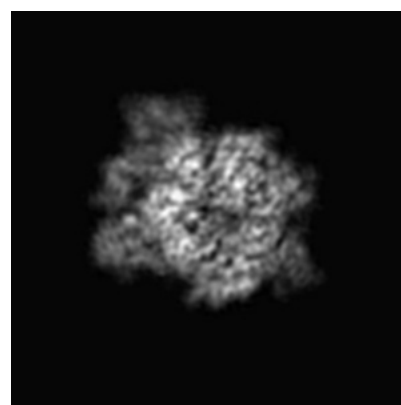
6.1.1 Primary map



X



Y

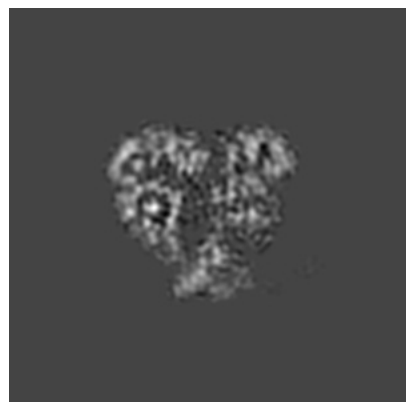


Z

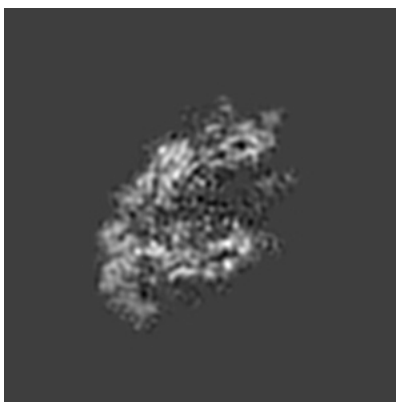
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

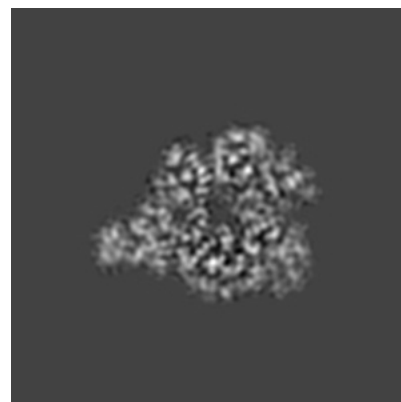
6.2.1 Primary map



X Index: 90



Y Index: 90

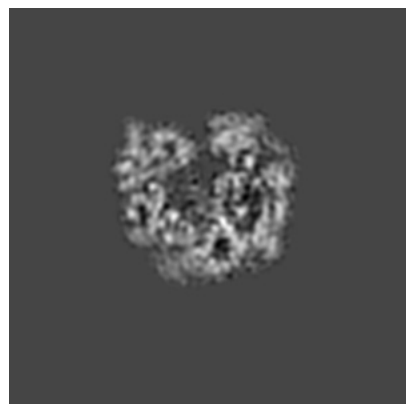


Z Index: 90

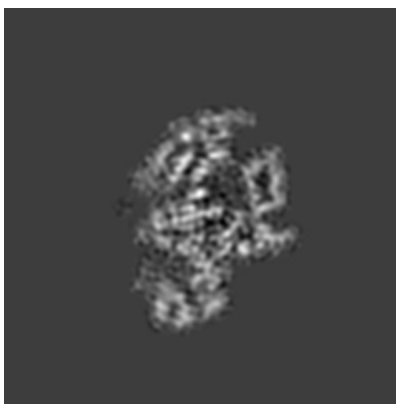
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

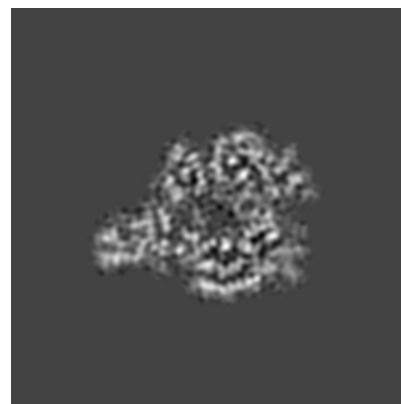
6.3.1 Primary map



X Index: 103



Y Index: 72

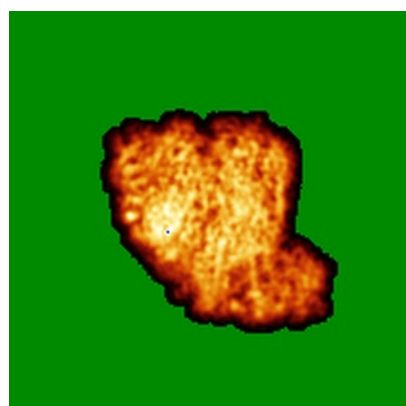


Z Index: 88

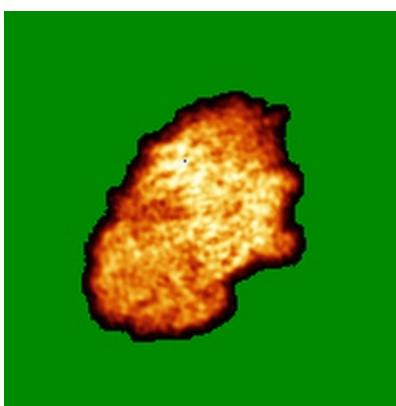
The images above show the largest variance slices of the map in three orthogonal directions.

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

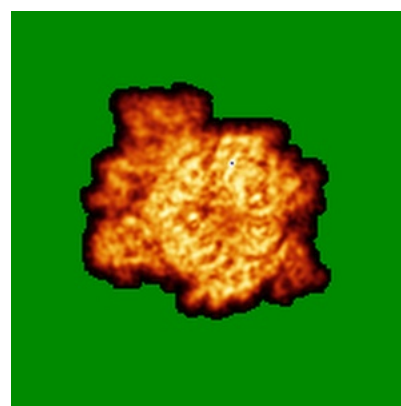
6.4.1 Primary map



X



Y

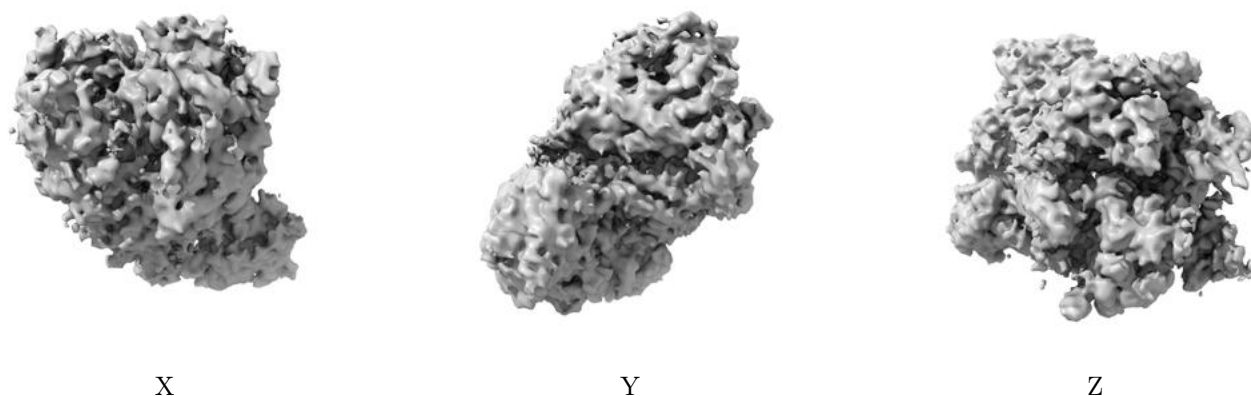


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

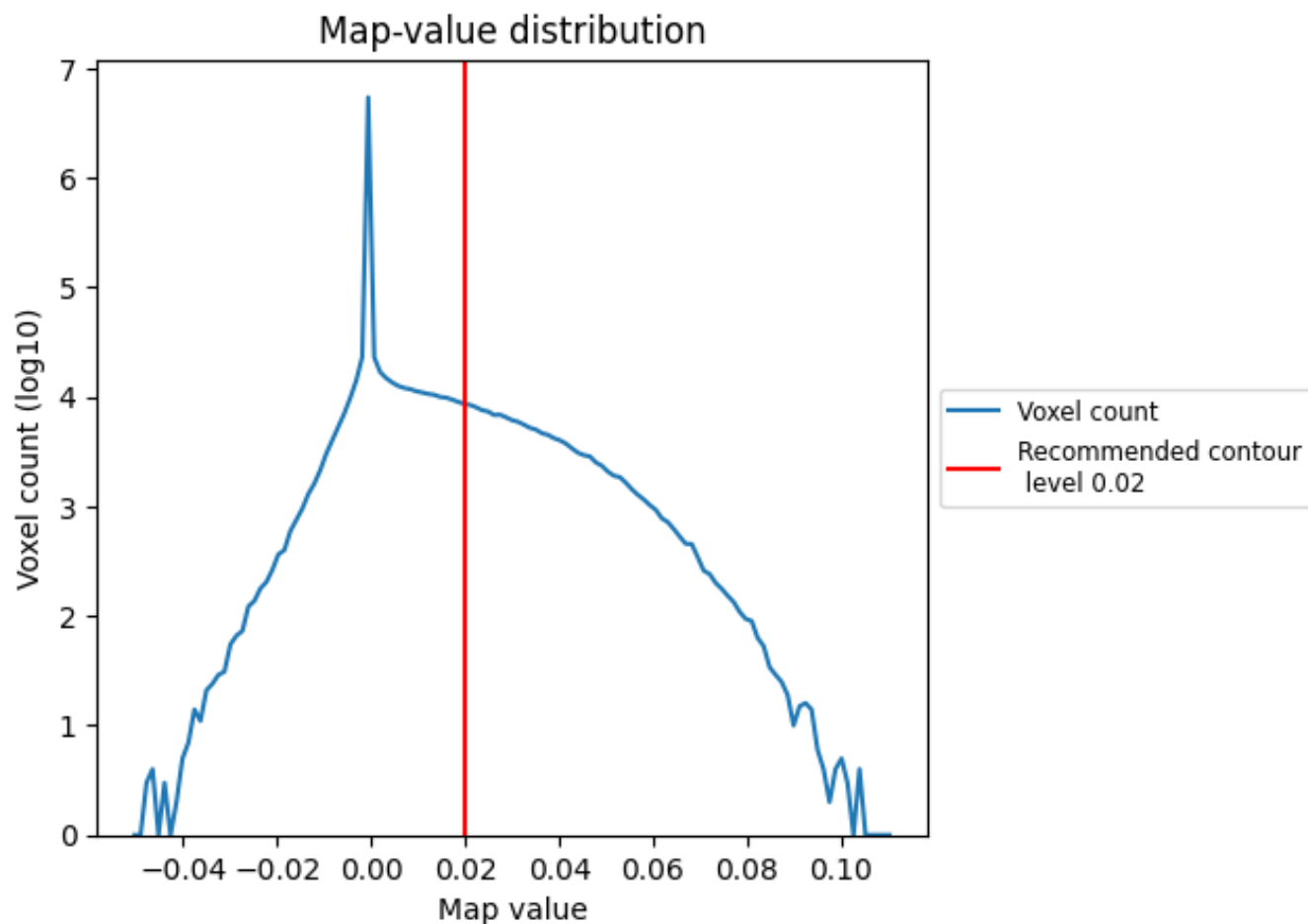
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

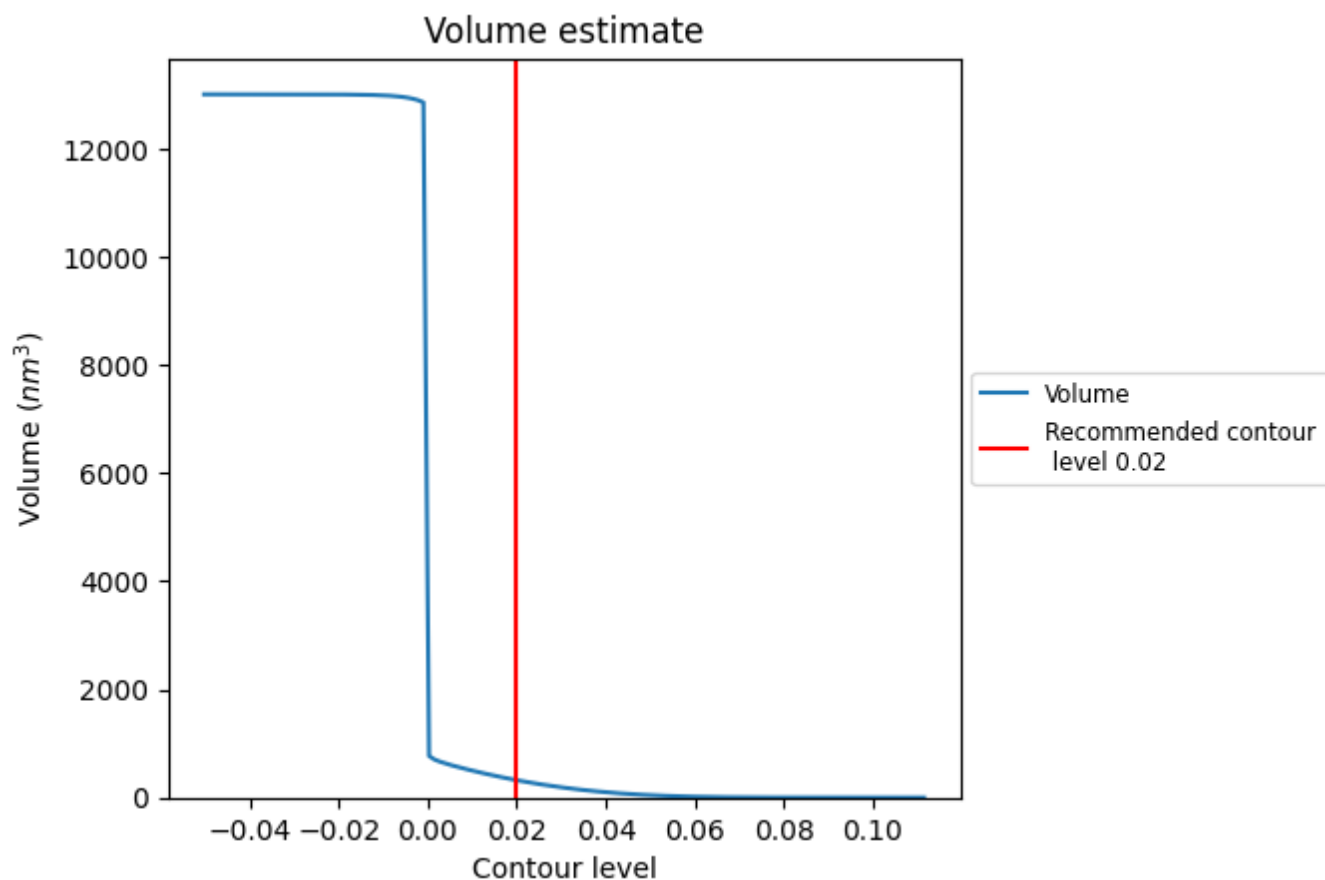
This section contains the results of statistical analysis of the map.

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.

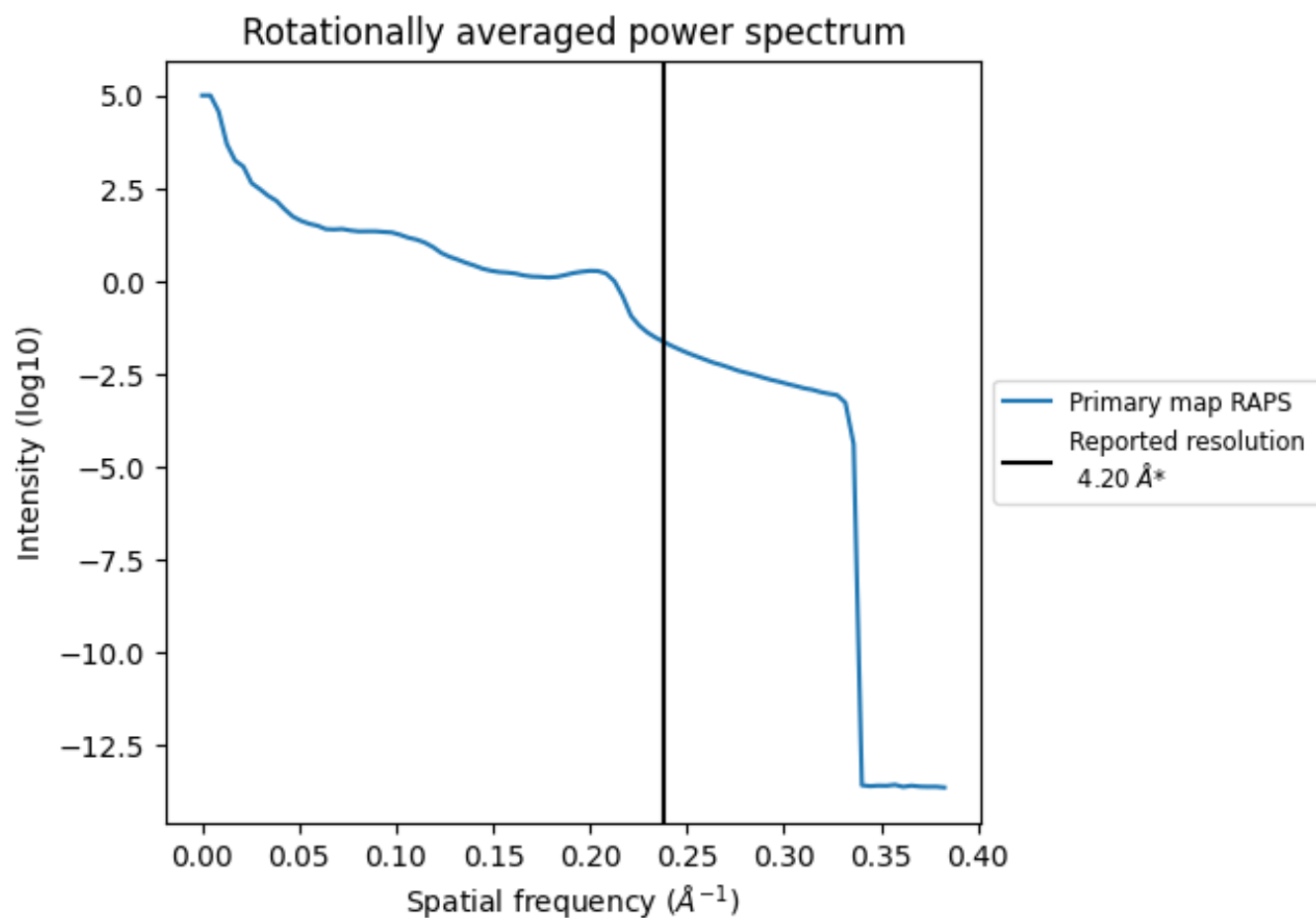
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 321 nm^3 ; this corresponds to an approximate mass of 290 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 0.238 Å⁻¹

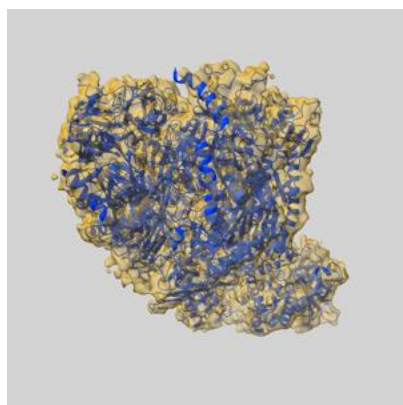
8 Fourier-Shell correlation

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

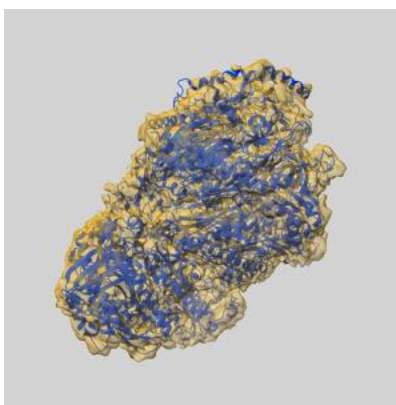
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3366 and PDB model 5G06. Per-residue inclusion information can be found in section [3](#) on page [7](#).

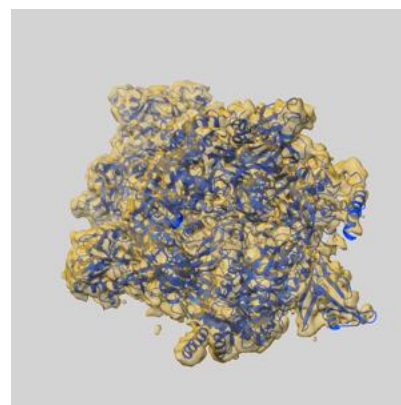
9.1 Map-model overlay [i](#)



X



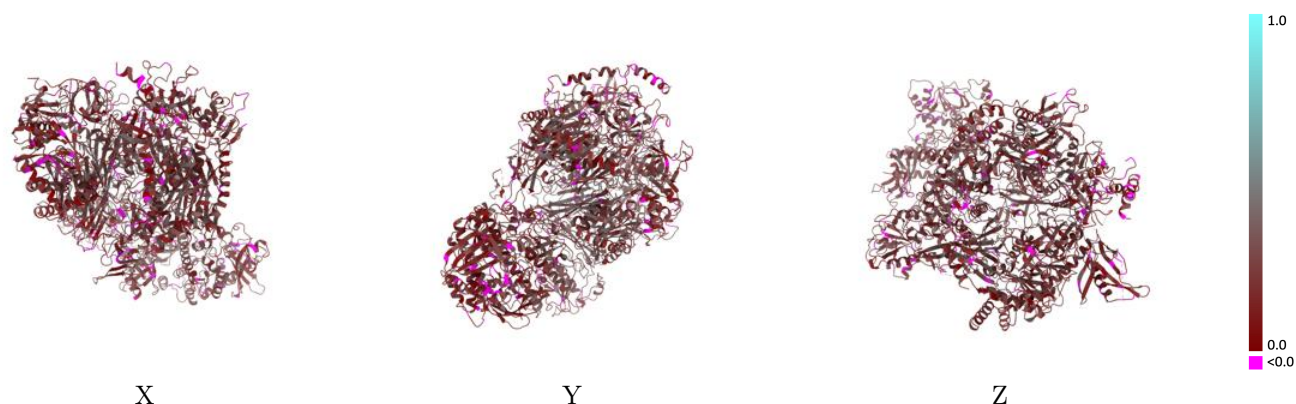
Y



Z

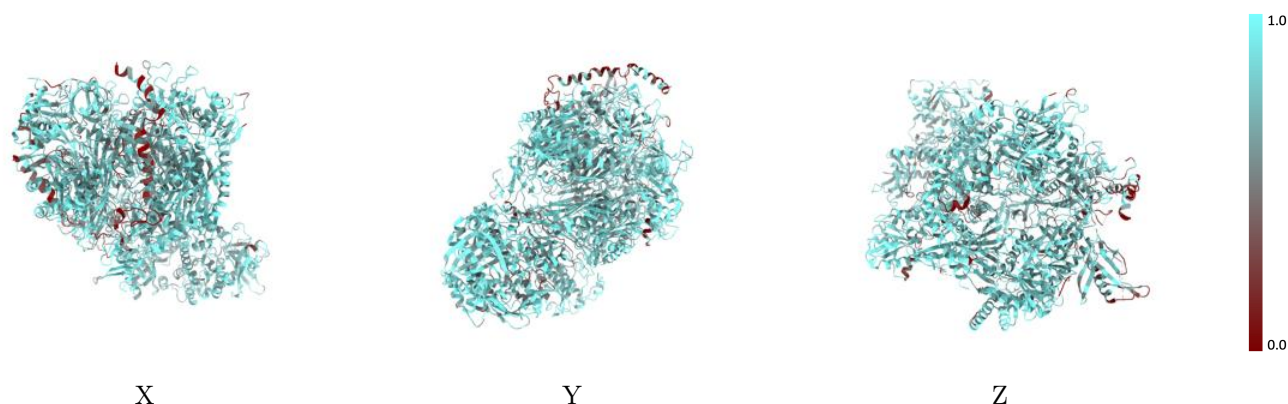
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



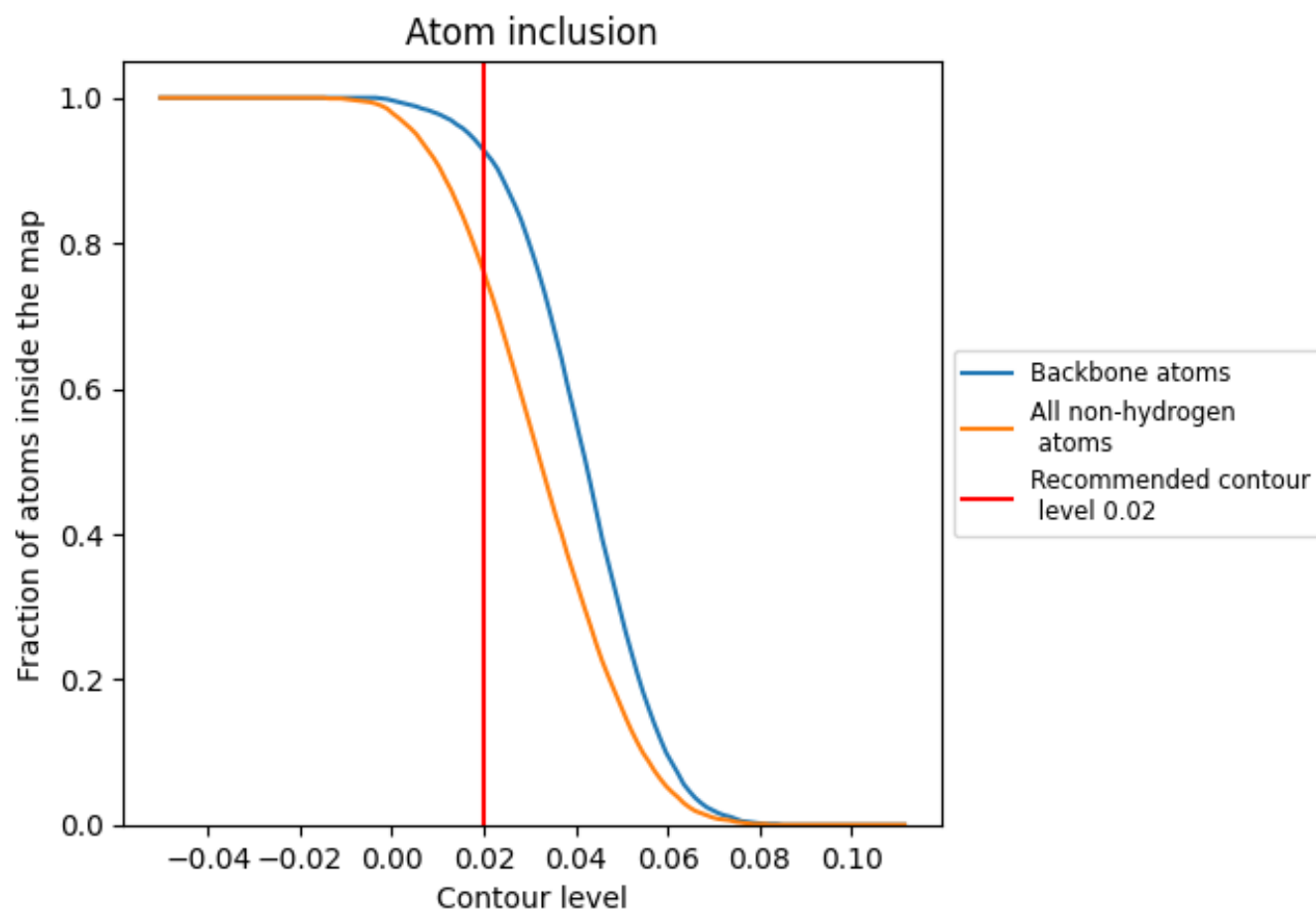
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 76% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7610	0.2210
A	0.7730	0.2500
B	0.7970	0.2640
C	0.7610	0.2210
D	0.7870	0.2500
E	0.7830	0.2560
F	0.7890	0.2430
G	0.8120	0.2240
H	0.7980	0.2180
I	0.6840	0.1960
J	0.7690	0.1990
P	0.3070	0.1120

1.0

0.0

<0.0