wwPDB EM Validation Summary Report ⓘ

Dec 10, 2022 – 10:32 am GMT

PDB ID	:	5G06
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)

The following versions of software and data (see references ⓘ) were used in the production of this report:

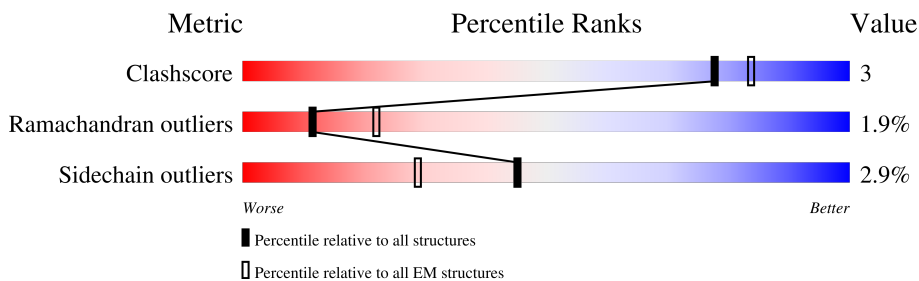|		
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)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

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.
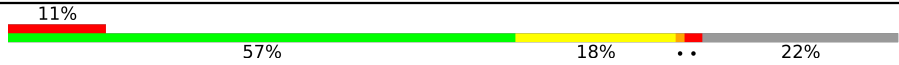
Metric	Percentile Ranks	Value
Clashscore		3
Ramachandran outliers		1.9%
Sidechain outliers		2.9%

Worse   *Better*

▮ Percentile relative to all structures

▯ Percentile relative to all EM structures

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	7% — 79% · 19% ··
2	B	246	· — 73% · 21% · ·
3	C	394	7% — 64% · 17% · · 15%
4	D	223	· — 81% · 18% ·
5	E	265	· — 79% · 19% ·
6	F	250	· — 61% · 20% · · 16%
7	G	240	· — 75% · 20% · ·
8	H	359	· — 58% · 21% · 18%

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Mol	Chain	Length	Quality of chain
9	I	292	11% / 57% / 18% / · · / 22%
10	J	1001	6% / 74% / 22% / · ·
11	P	747	8% / 8% / · · / 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 2350	C 1474	N 402	O 457	S 17	0	0

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

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

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

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

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 1707	C 1073	N 289	O 335	S 10	0	0

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

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

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:

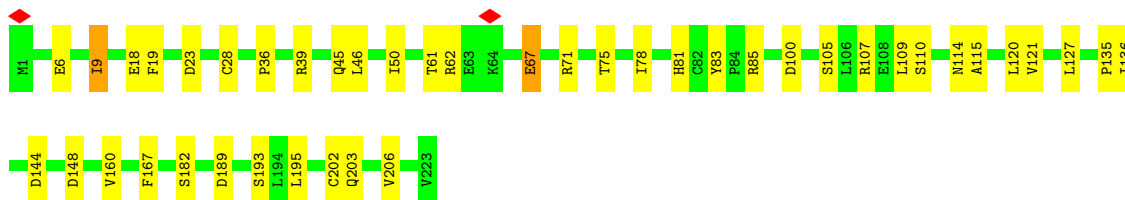| Chain	Residue	Modelled	Actual	Comment	Reference
F	75	SER	THR	conflict	UNP P48240

- 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		

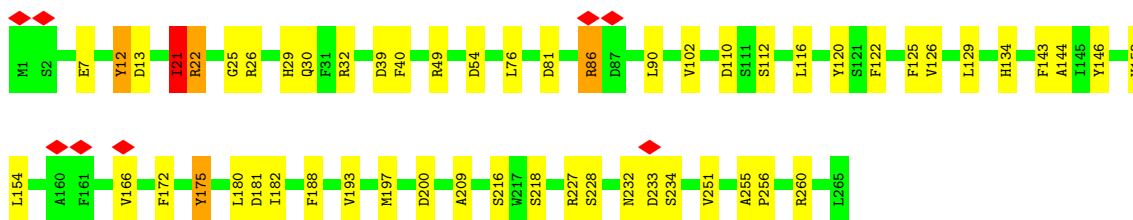- Molecule 8 is a protein called EXOSOME COMPLEX COMPONENT RRP4.

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

Chain A:
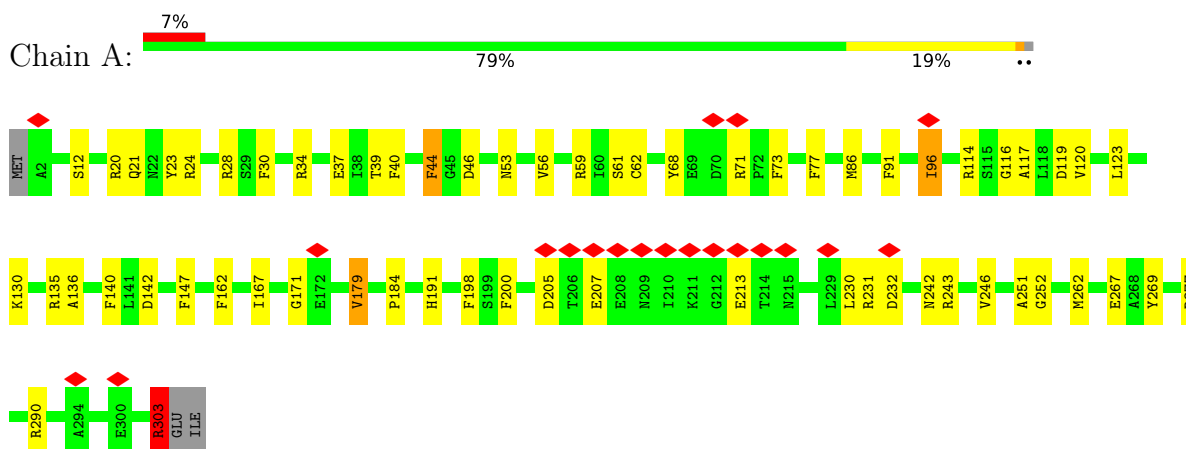
• Molecule 2: EXOSOME COMPLEX COMPONENT SKI6

Chain B:
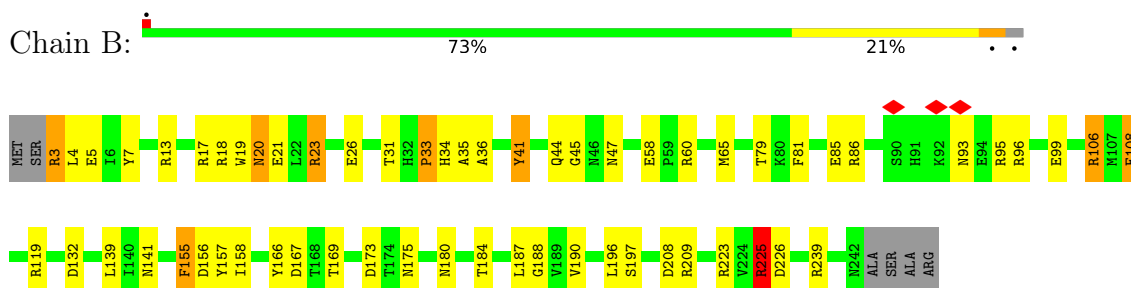
• Molecule 3: EXOSOME COMPLEX COMPONENT RRP43

Chain C:

ASN LEU LYS MET K206 R207 K208 W209 V212 A215 V219 R222 D228 M235 Y236 R245 E250 R251 A252 S253 D254 L255 R256 M257 T258 I259 R260 T261 R262 G263 R264 S265 A266 T267 I268 R269 E270 T271 Y272 E273 K289 Y297 G298 E301 E305 C306 Q307 L308

GLN ASN SER ASP ASN SER GLU GLU GLU GLU VAL ASP ILE ASP MET ASP LYS LEU N327 L334 D335 T336 E337 P353 Y357 K358 Q359 G365 G366 T370 R376 S381 R382 V383 R384 R391 F392 N393 I394

• Molecule 4: EXOSOME COMPLEX COMPONENT RRP46

Chain D: 81% 18%

M1 E6 I9 E18 F19 D23 C28 P36 R39 Q45 L46 I50 T61 R62 E63 K64 E67 R71 T75 I78 H81 C82 Y83 P84 R85 D100 S105 L106 R107 E108 L109 S110 N114 A115 L120 V121 L127 P135 I136

D144 D148 V160 F167 S182 D189 S193 L194 L195 C202 Q203 V206 V223
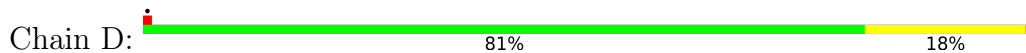
• Molecule 5: EXOSOME COMPLEX COMPONENT RRP42

Chain E: 79% 19%

M1 S2 E7 Y12 D13 I21 R22 G25 R26 H29 Q30 F31 R32 D39 F40 R49 D54 L76 D81 R86 D87 L90 V102 D110 S111 S112 L116 Y120 S121 F122 F125 V126 L129 H134 F143 A144 I145 Y146 Y153

L154 A160 F161 V166 F172 Y175 L180 D181 I182 F188 V193 M197 D200 A209 S216 W217 S218 R227 S228 N232 D233 S234 V251 A255 P256 R260 L265
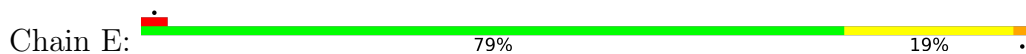
• Molecule 6: EXOSOME COMPLEX COMPONENT MTR3

Chain F: 61% 20% 16%

MET ASN VAL Q4 D5 R6 R7 R8 P12 A13 A14 F20 S21 ASN THR THR THR HIS VAL PRO GLU LYS LYS SER THR ASP LEU THR PRO LYS GLY ASN GLU S42 E43 S47 L48 H49 F52 I53 E54 N55 L61 R65 S75 A76 V77 Y78 G79 P80 R81 R84

G85 K98 L102 E109 S115 F116 F121 R129 F138 V139 Y140 Y143 D144 K145 D146 L147 T148 ASN ASN PRO GLN ASP ASP ASP SER GLN SER LYS MET MET SER S163 Q164 I165 L168 T174 S175 L178 D189 M190 A191 G192 A193 G194 E195 A196 N197

V200 F203 N206 F213 W214 K215 D216 D217 D222 E225 R229 Y234 N235 R236 Y237 R238 D239 I242 Q248 GLU THR

• Molecule 7: EXOSOME COMPLEX COMPONENT RRP40

Chain G: 75% 20%

M1 F6 F11 V19 G22 Y26 P29 R35 N38 L42 G48 K49 Y56 I57 D58 Y59 Y64 V68 N69 D70 F71 I76 F80 Y84 F91 S92 S96 Y99 F102 P103 N104 R110 P111 Q114 D117 L118 V119
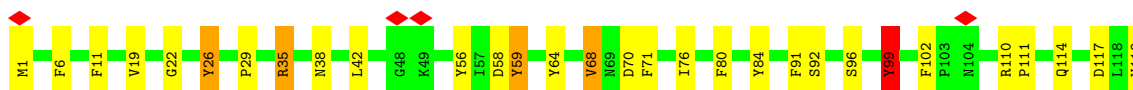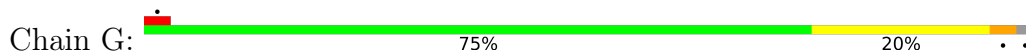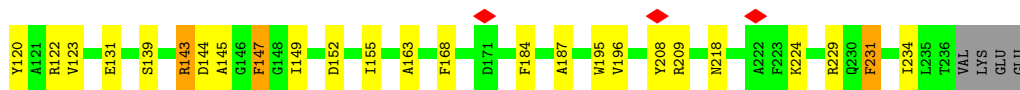
• Molecule 8: EXOSOME COMPLEX COMPONENT RRP4

Chain H:
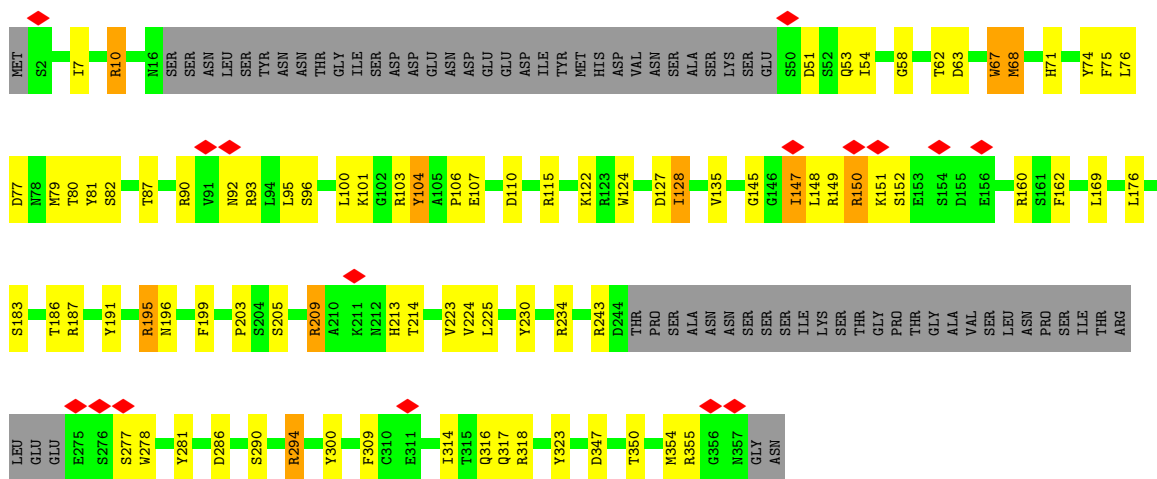
• Molecule 9: EXOSOME COMPLEX COMPONENT CSL4

Chain I:
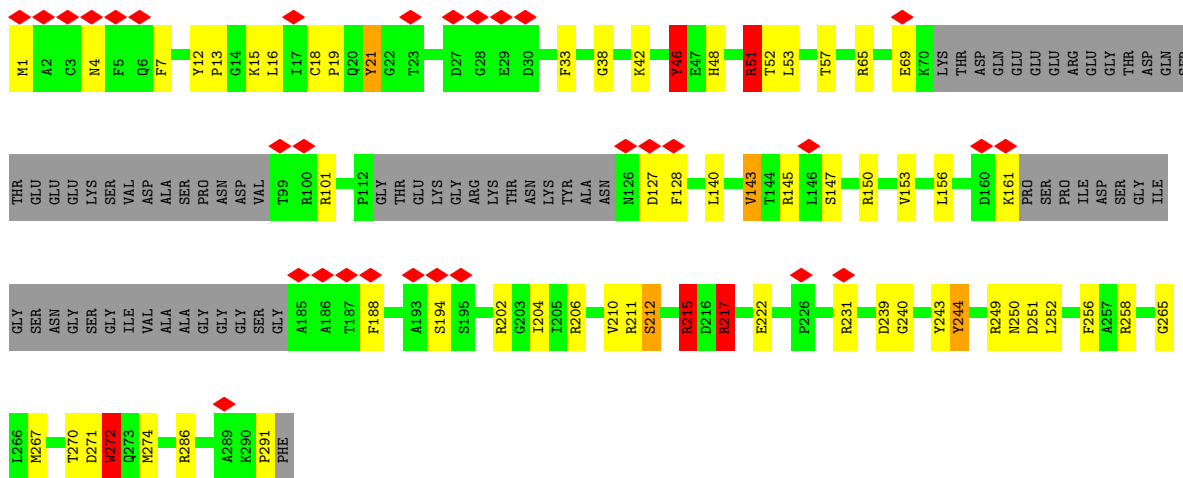
• Molecule 10: EXOSOME COMPLEX EXONUCLEASE DIS3

Chain J:

• Molecule 11: SUPERKILLER PROTEIN 7

LEU LEU ASN LYS ALA ASP LEU ILE SER TRP ASP LYS HIS ARG LEU GLU MET ILE GLN SER GLU LEU ASN TYR VAL LEU LYS GLU ASN PHE GLN TRP THR ASP ALA GLU PHE GLN PHE ILE PRO CYS SER GLY LEU LEU GLY SER ASN LEU ASN LYS THR GLU ASN ILE THR LYS SER LYS

TYR LYS SER GLU PHE ASP SER ILE ASN TYR VAL PRO GLU TRP TYR GLU GLY PRO THR PHE PHE SER GLN LEU GLU TYR LEU GLU VAL GLU HIS ASN MET ILE GLU GLU THR THR GLU GLU GLU PRO PHE VAL GLY THR ILE LEU GLN SER SER VAL LEU GLU GLN PRO ILE ALA GLU ILE ASN

TYR VAL SER LEU LYS VAL LEU LEU ASN GLY TYR GLN SER GLY GLN THR ILE GLU ILE HIS THR GLN TYR GLU ASP PHE HIS TYR GLY ILE VAL SER ARG MET LYS ASN SER LYS GLN ILE LEU GLU THR ASN THR LYS ASN ILE SER VAL GLY LEU ASN PRO ASP ILE

LEU GLU VAL LEU VAL LYS HIS ASN GLU ASP THR GLU ASP PHE THR LYS LYS GLN PHE HIS ILE ARG GLY ASP LYS ILE ILE HIS SER ARG THR ASN THR LEU SER PRO ASN LEU ASN THR LYS LEU GLU LEU ALA LEU ARG LEU LYS LEU SER ILE GLN THR HIS ALA LEU

SER ASP PRO VAL ASP LEU GLY SER GLU LEU LEU LEU TYR HIS ASN LEU THR HIS ALA VAL LYS LEU VAL LYS ILE LEU GLY THR ASN ASP ILE SER ILE ASN PRO ASN GLN SER LEU ILE VAL GLU VAL GLU ILE ILE GLU GLU PRO ASP PHE ALA LEU ASN VAL ILE ASP SER LYS TYR

ILE THR ASN ASN ILE VAL LEU THR SER ILE ASP HIS LYS VAL ILE ALA VAL GLY ARG ILE ALA CYS GLN

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 $(e^-/\text{Å}^2)$	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 (Å)	235.1772, 235.1772, 235.1772	wwPDB
Map dimensions	180, 180, 180	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	1.70	14/2386 (0.6%)	1.91	46/3218 (1.4%)
2	B	1.75	25/1914 (1.3%)	1.91	33/2577 (1.3%)
3	C	1.69	23/2659 (0.9%)	2.01	69/3596 (1.9%)
4	D	1.67	9/1725 (0.5%)	1.86	27/2339 (1.2%)
5	E	1.68	11/2087 (0.5%)	1.90	42/2836 (1.5%)
6	F	1.79	16/1649 (1.0%)	2.04	48/2222 (2.2%)
7	G	1.76	17/1868 (0.9%)	1.99	53/2531 (2.1%)
8	H	1.80	30/2311 (1.3%)	2.02	61/3118 (2.0%)
9	I	1.78	26/1774 (1.5%)	1.98	42/2398 (1.8%)
10	J	1.75	90/8097 (1.1%)	1.98	214/10972 (2.0%)
11	P	1.69	6/763 (0.8%)	1.87	15/1031 (1.5%)
All	All	1.74	267/27233 (1.0%)	1.96	650/36838 (1.8%)

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 267 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	110	ARG	CZ-NH2	9.83	1.45	1.33
10	J	886	ARG	CZ-NH2	9.40	1.45	1.33
8	H	74	TYR	CZ-OH	8.53	1.52	1.37
10	J	590	ARG	NE-CZ	8.02	1.43	1.33
1	A	34	ARG	CZ-NH2	7.95	1.43	1.33

The worst 5 of 650 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	7	TYR	CB-CG-CD2	20.64	133.39	121.00
8	H	281	TYR	CB-CG-CD2	-16.23	111.26	121.00
3	C	44	ARG	NE-CZ-NH2	-15.84	112.38	120.30
7	G	110	ARG	NE-CZ-NH1	15.73	128.16	120.30
3	C	262	ARG	NE-CZ-NH1	15.64	128.12	120.30

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 ⓘ

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	4	0
2	B	1890	0	1943	5	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	50	0
7	G	1831	0	1829	2	0
8	H	2277	0	2283	9	0
9	I	1750	0	1755	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	7942	0	7947	12	0
11	P	750	0	759	112	0
All	All	26794	0	27001	157	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 157 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　ⓘ

5.3.1　Protein backbone　ⓘ

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%)	12	48
2	B	238/246 (97%)	223 (94%)	11 (5%)	4 (2%)	9	44
3	C	327/394 (83%)	294 (90%)	22 (7%)	11 (3%)	3	30
4	D	221/223 (99%)	211 (96%)	9 (4%)	1 (0%)	29	68
5	E	263/265 (99%)	248 (94%)	10 (4%)	5 (2%)	8	41
6	F	205/250 (82%)	194 (95%)	8 (4%)	3 (2%)	10	46
7	G	234/240 (98%)	219 (94%)	14 (6%)	1 (0%)	34	72
8	H	287/359 (80%)	263 (92%)	15 (5%)	9 (3%)	4	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	219/292 (75%)	200 (91%)	14 (6%)	5 (2%)	6	37
10	J	991/1001 (99%)	905 (91%)	68 (7%)	18 (2%)	8	42
11	P	93/747 (12%)	82 (88%)	9 (10%)	2 (2%)	6	38
All	All	3378/4322 (78%)	3117 (92%)	198 (6%)	63 (2%)	11	41

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%)	259 (98%)	4 (2%)	65	80
2	B	214/218 (98%)	207 (97%)	7 (3%)	38	61
3	C	294/349 (84%)	286 (97%)	8 (3%)	44	66
4	D	197/197 (100%)	193 (98%)	4 (2%)	55	73
5	E	240/240 (100%)	233 (97%)	7 (3%)	42	64
6	F	181/219 (83%)	174 (96%)	7 (4%)	32	57
7	G	205/209 (98%)	197 (96%)	8 (4%)	32	57
8	H	252/311 (81%)	245 (97%)	7 (3%)	43	65
9	I	190/240 (79%)	184 (97%)	6 (3%)	39	62
10	J	895/901 (99%)	865 (97%)	30 (3%)	37	61
11	P	89/702 (13%)	88 (99%)	1 (1%)	73	84
All	All	3020/3852 (78%)	2931 (97%)	89 (3%)	45	64

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	I	272	TRP
10	J	552	ASP
10	J	74	ASP
10	J	251	SER
10	J	671	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
10	J	871	HIS
10	J	888	HIS
11	P	16	ASN
6	F	171	HIS
6	F	99	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

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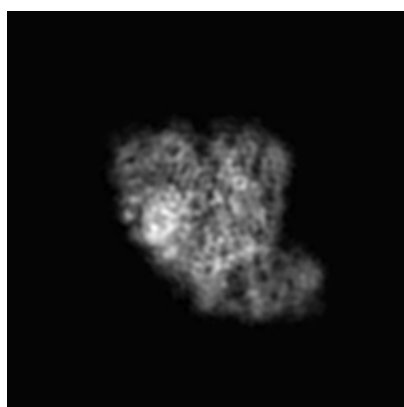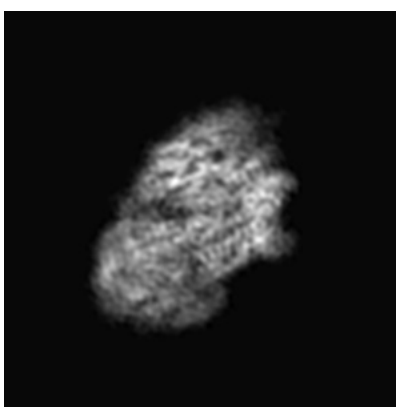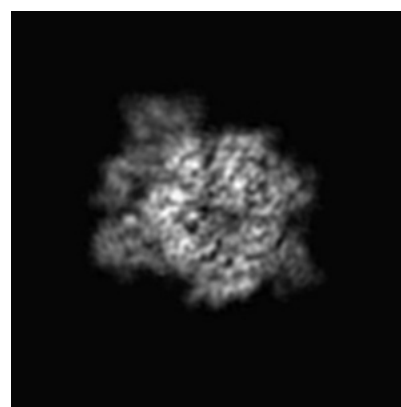
The images above show the map projected in three orthogonal directions.

6.2   Central slices (i)

6.2.1   Primary map
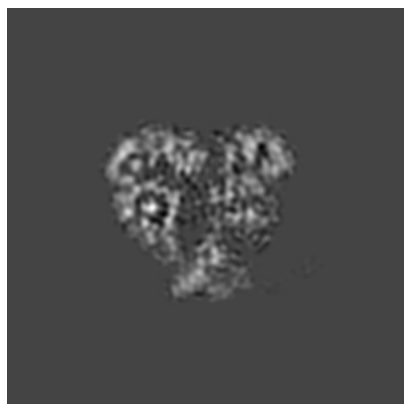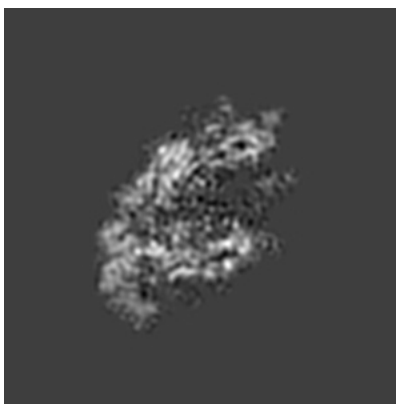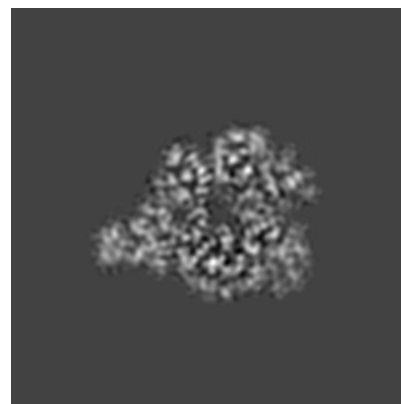
| X Index: 90 | Y Index: 90 | Z Index: 90 |

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

6.3　Largest variance slices ⓘ
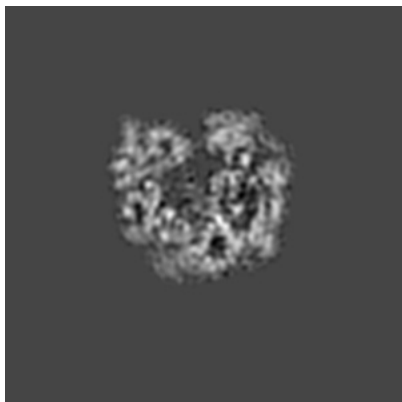
6.3.1　Primary map
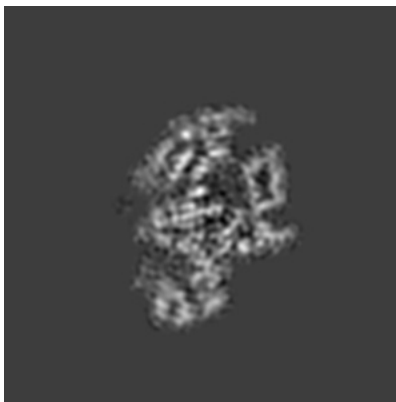
| X Index: 103 | Y Index: 72 | Z Index: 88 |
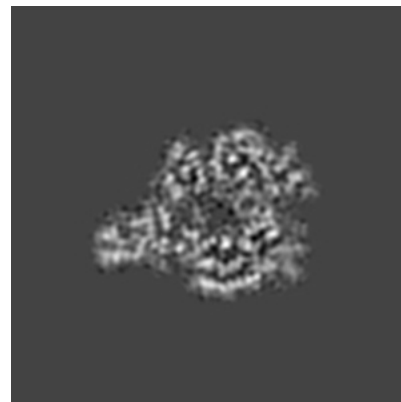
The images above show the largest variance slices of the map in three orthogonal directions.

6.4　Orthogonal surface views ⓘ
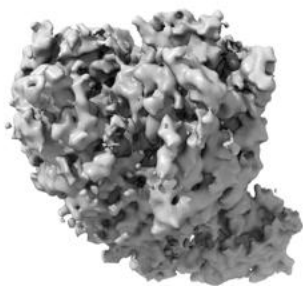
6.4.1　Primary map

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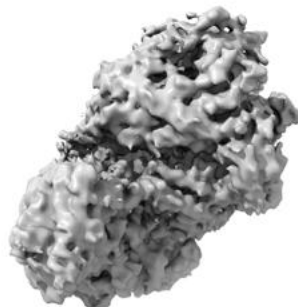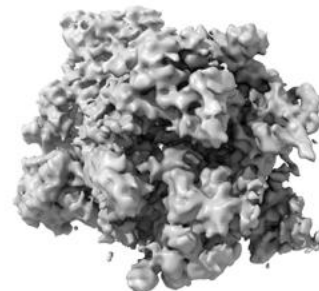
The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5 Mask visualisation (i)

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

7 Map analysis ⓘ

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

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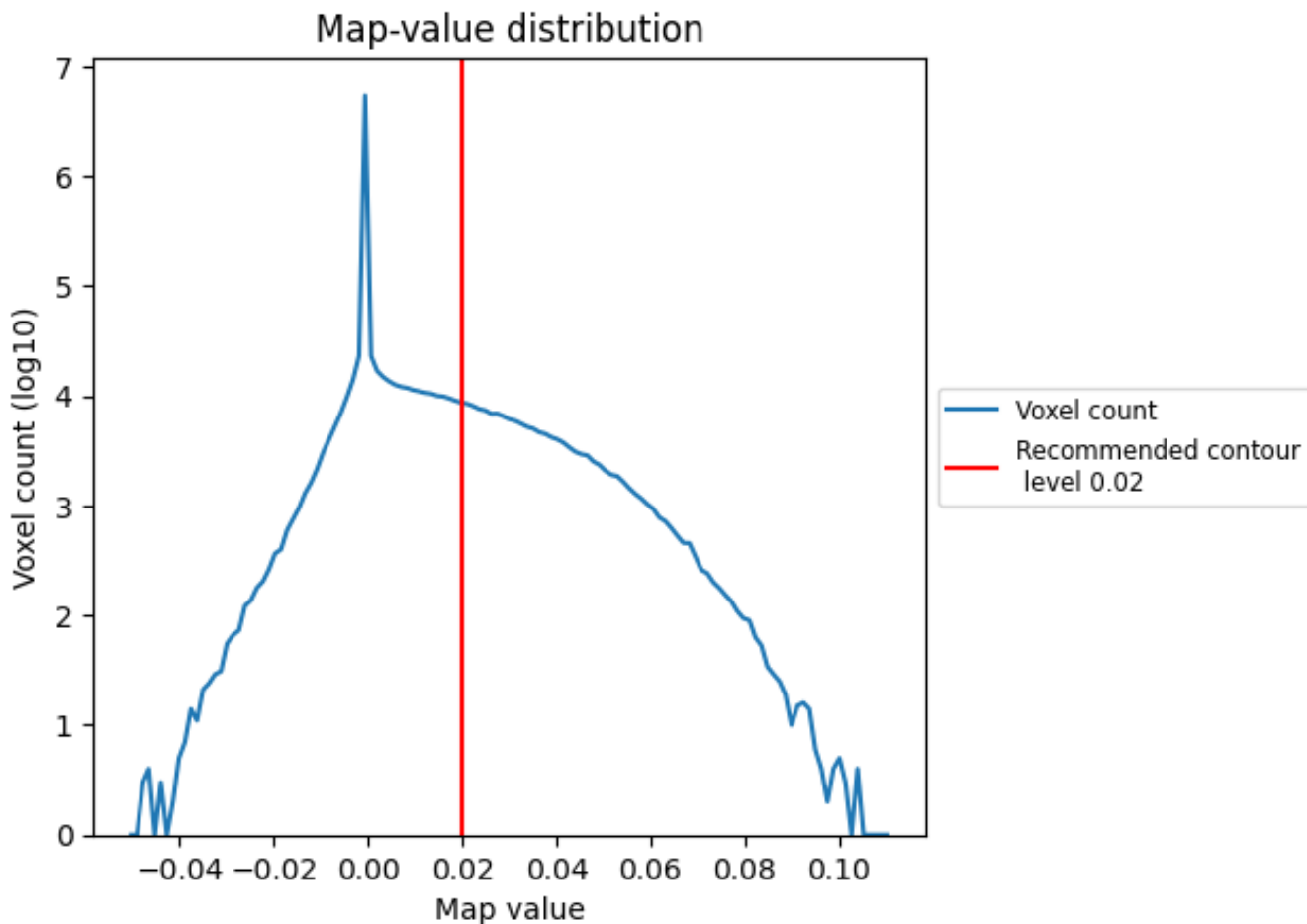
The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2　Volume estimate ⓘ
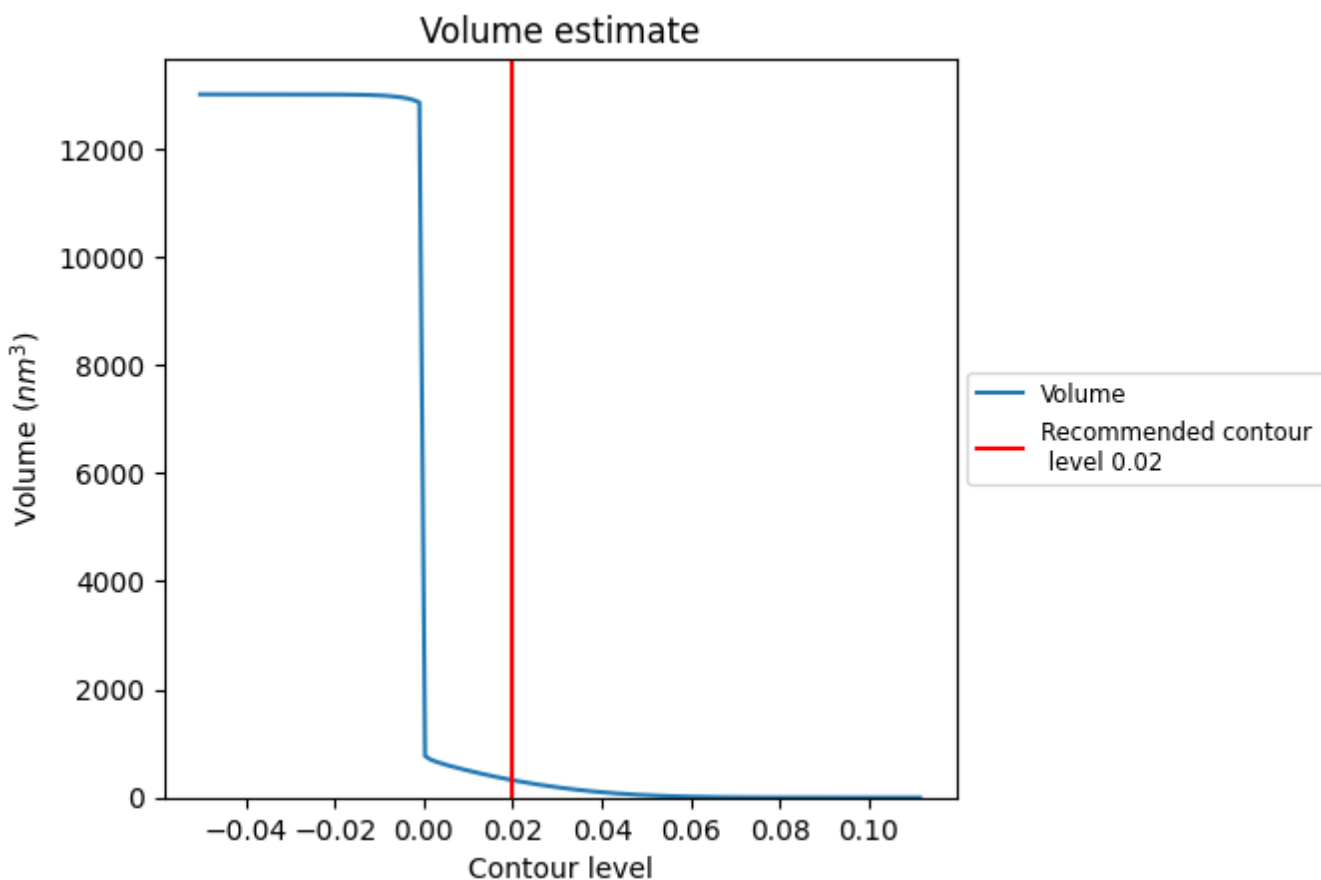
The volume at the recommended contour level is 321 nm^3; this corresponds to an approximate mass of 290 kDa.

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 ⓘ
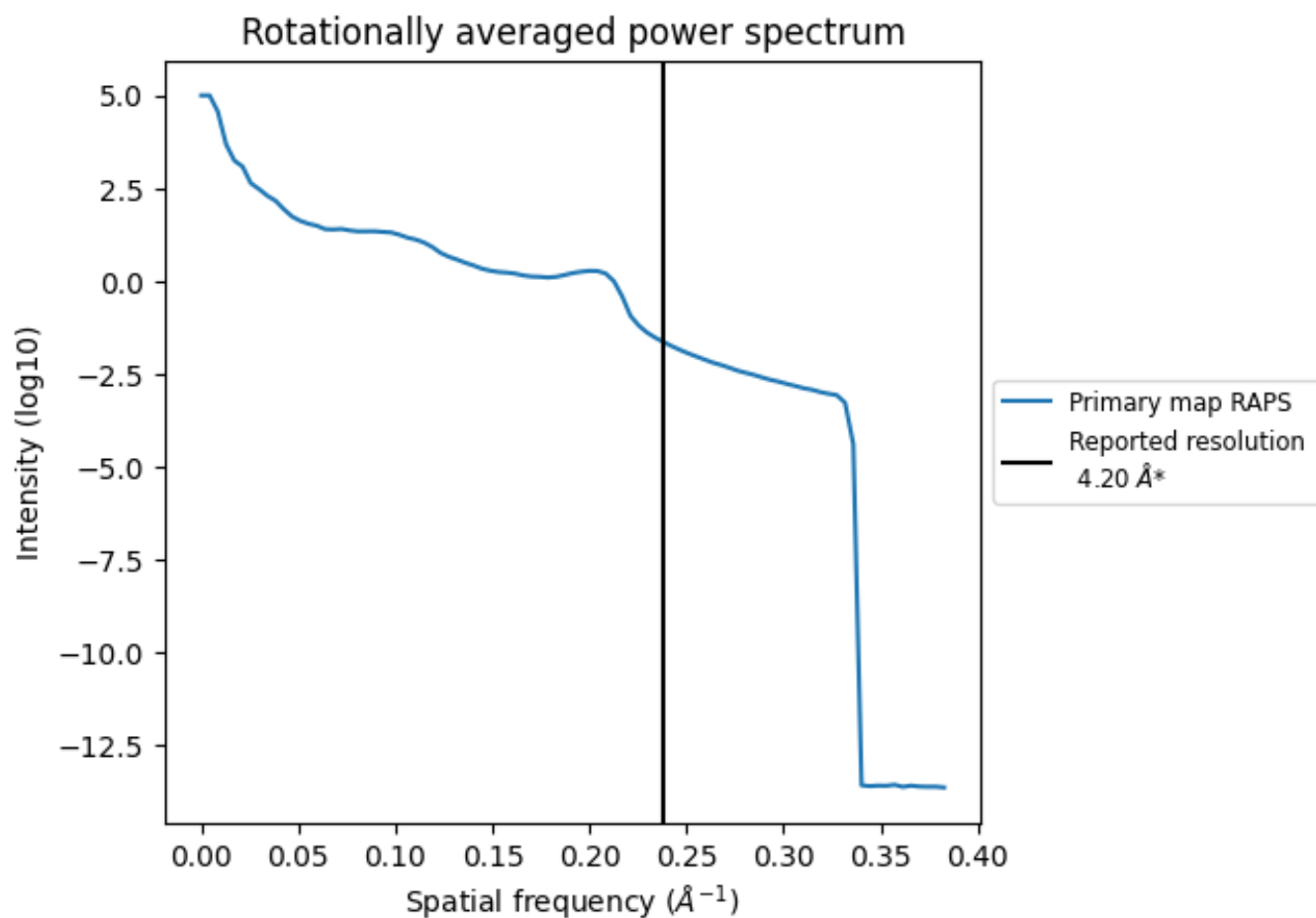
*Reported resolution corresponds to spatial frequency of 0.238 Å^{-1}

8   Fourier-Shell correlation ⓘ

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

9   Map-model fit   ⓘ

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   ⓘ

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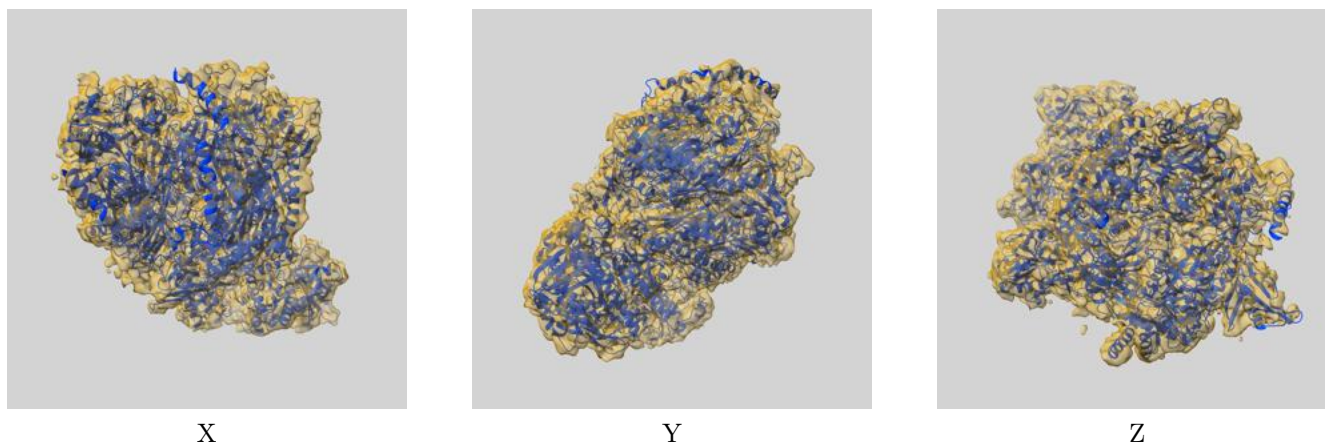
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2   Q-score mapped to coordinate model ⓘ

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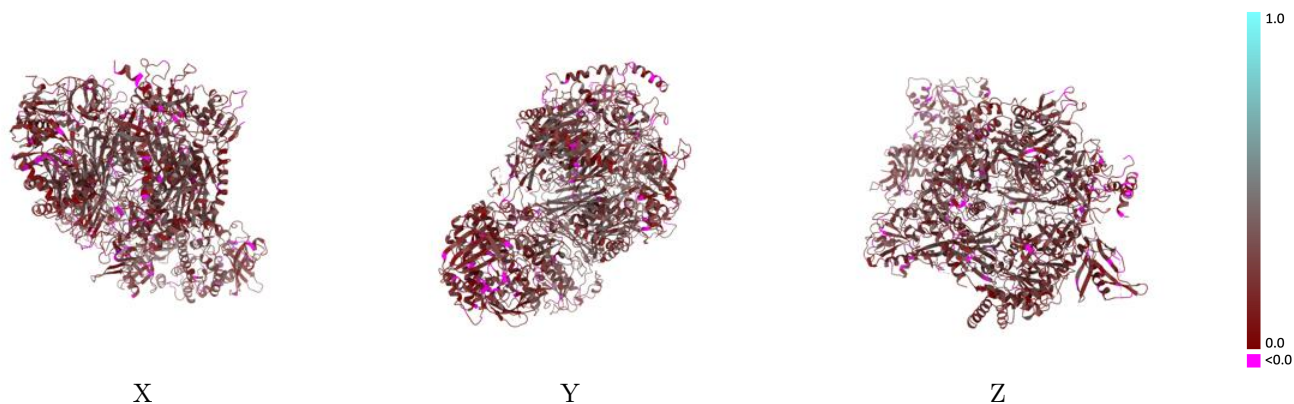
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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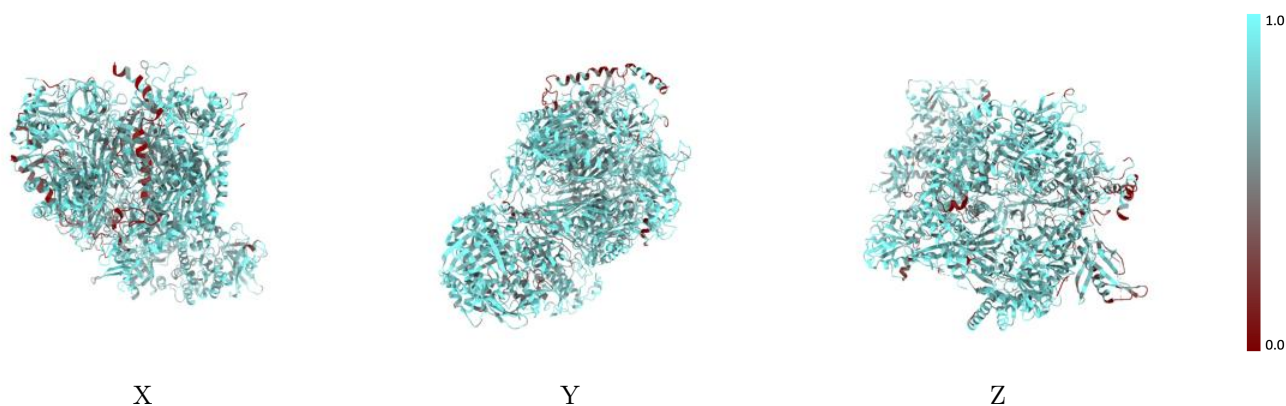
The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

## 9.4   Atom inclusion ⓘ
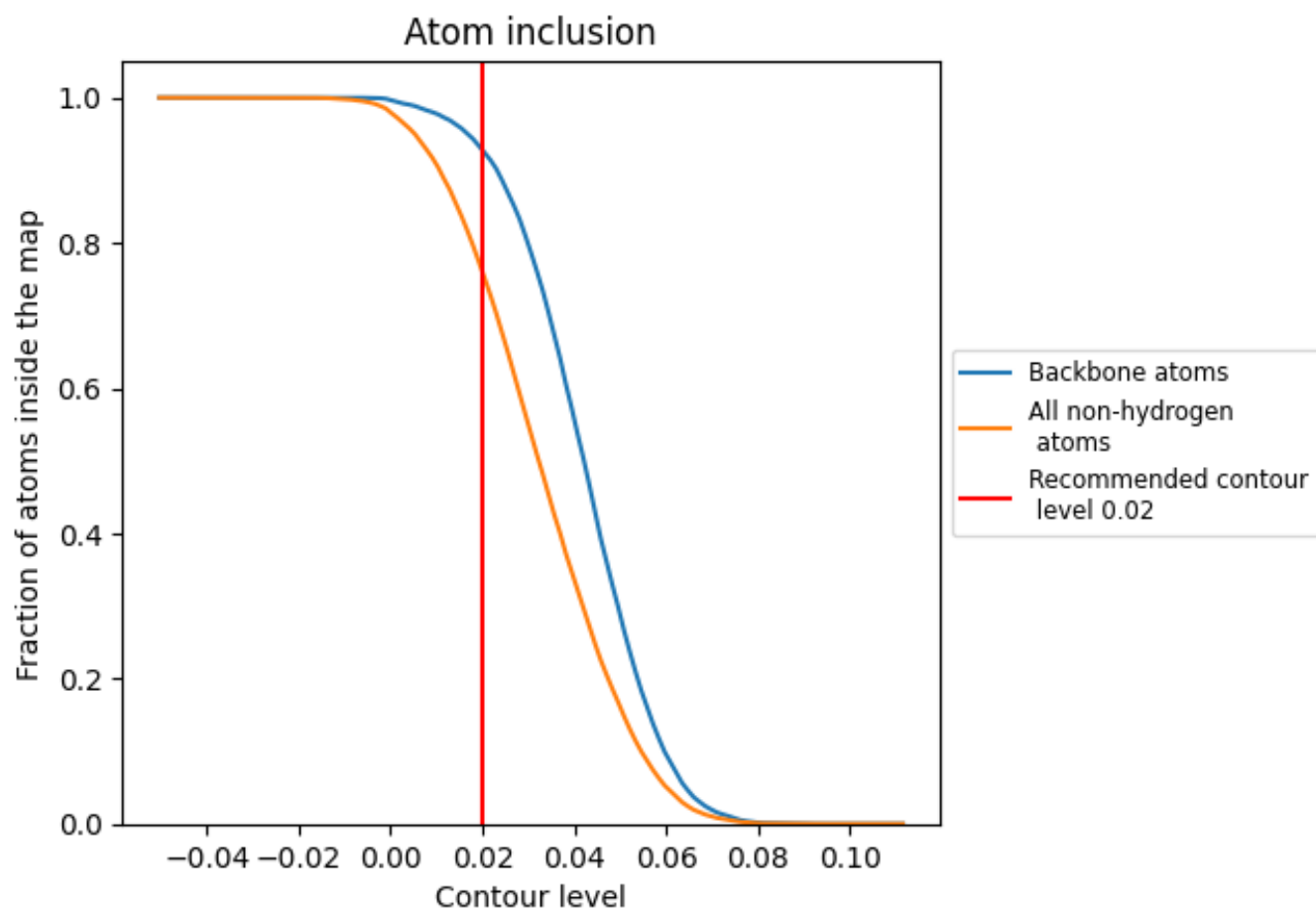
At the recommended contour level, 93% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

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	0.7609	0.2210
A	0.7728	0.2500
B	0.7973	0.2640
C	0.7608	0.2210
D	0.7871	0.2500
E	0.7833	0.2560
F	0.7886	0.2430
G	0.8117	0.2240
H	0.7978	0.2180
I	0.6842	0.1960
J	0.7695	0.1990
P	0.3070	0.1120

1.0

0.0
<0.0