



wwPDB EM Validation Summary Report ⓘ

Sep 30, 2026 – 07:49 pm BST

PDB ID : 28RF / pdb_000028rf
EMDB ID : EMD-56766
Title : Cryo-EM single particle structure of the Plastid-Encoded RNA Polymerase (PEP) from *Chlamydomonas reinhardtii*.
Authors : Kumar, A.; Schuller, S.; Schuller, J.
Deposited on : 2026-02-15
Resolution : 2.65 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.dev133
MolProbity : 4-5-2 with Phenix2.2
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) : 2.51

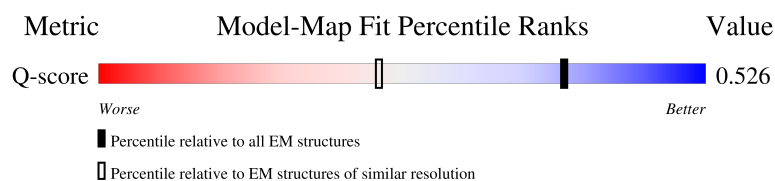
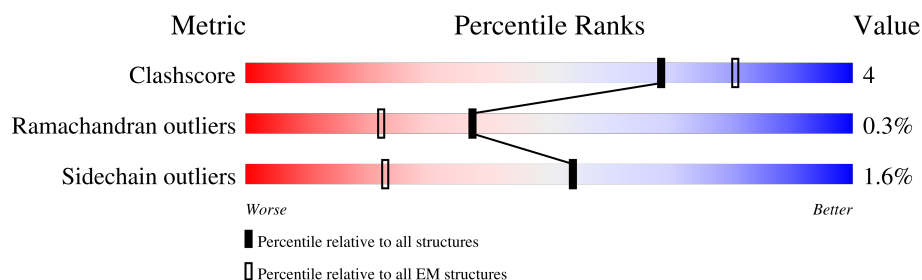
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.65 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	9050 (2.15 - 3.15)

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	737	
1	Z	737	
2	B	822	
3	C	626	

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Mol	Chain	Length	Quality of chain
4	D	3120	
5	E	1932	
6	F	648	
7	G	834	
8	H	609	
8	I	609	
9	J	343	
10	K	2788	
11	M	1801	
12	N	803	
13	Q	414	
14	R	356	
15	S	359	
16	T	381	
17	X	410	
17	Y	410	

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 83535 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 DNA-directed RNA polymerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	421	Total	C	N	O	S	0	0
			3368	2181	558	615	14		
1	Z	453	Total	C	N	O	S	0	0
			3590	2321	594	664	11		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta N-terminal section.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	617	Total	C	N	O	S	0	0
			4970	3213	849	890	18		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta C-terminal section.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	424	Total	C	N	O	S	0	0
			3368	2156	572	625	15		

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit beta”.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	1725	Total	C	N	O	S	0	0
			14136	9263	2372	2469	32		

- Molecule 5 is a protein called DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	696	Total	C	N	O	S	0	0
			5698	3684	1001	992	21		

- Molecule 6 is a protein called Glucose-6-phosphate 1-epimerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	452	Total	C	N	O	S	0	0
			3517	2234	596	672	15		

- Molecule 7 is a protein called Rubisco LSM1 substrate-binding domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	664	Total	C	N	O	S	0	0
			5136	3246	887	980	23		

- Molecule 8 is a protein called UDP-3-O-acyl-N-acetylglucosamine deacetylase.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	441	Total	C	N	O	S	0	0
			3419	2148	593	665	13		
8	I	324	Total	C	N	O	S	0	0
			2506	1590	431	474	11		

- Molecule 9 is a protein called Uncharacterized protein A0A2K3DRS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	135	Total	C	N	O	S	0	0
			1105	697	189	212	7		

- Molecule 10 is a protein called SAP domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	1726	Total	C	N	O	S	0	0
			12323	7722	2159	2397	45		

- Molecule 11 is a protein called Uncharacterized protein A0A2K3D3G3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	375	Total	C	N	O	S	0	0
			2794	1739	485	556	14		

- Molecule 12 is a protein called Mur ligase central domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	623	Total	C	N	O	S	0	0
			4733	2987	814	921	11		

- Molecule 13 is a protein called Coenzyme Q-binding protein COQ10 START domain-containing

protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Q	225	Total	C	N	O	S	0	0
			1730	1098	295	331	6		

- Molecule 14 is a protein called S1 motif domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	R	301	Total	C	N	O	S	0	0
			2438	1534	401	492	11		

- Molecule 15 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	287	Total	C	N	O	S	0	0
			2374	1467	414	484	9		

- Molecule 16 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	104	Total	C	N	O	S	0	0
			809	523	134	146	6		

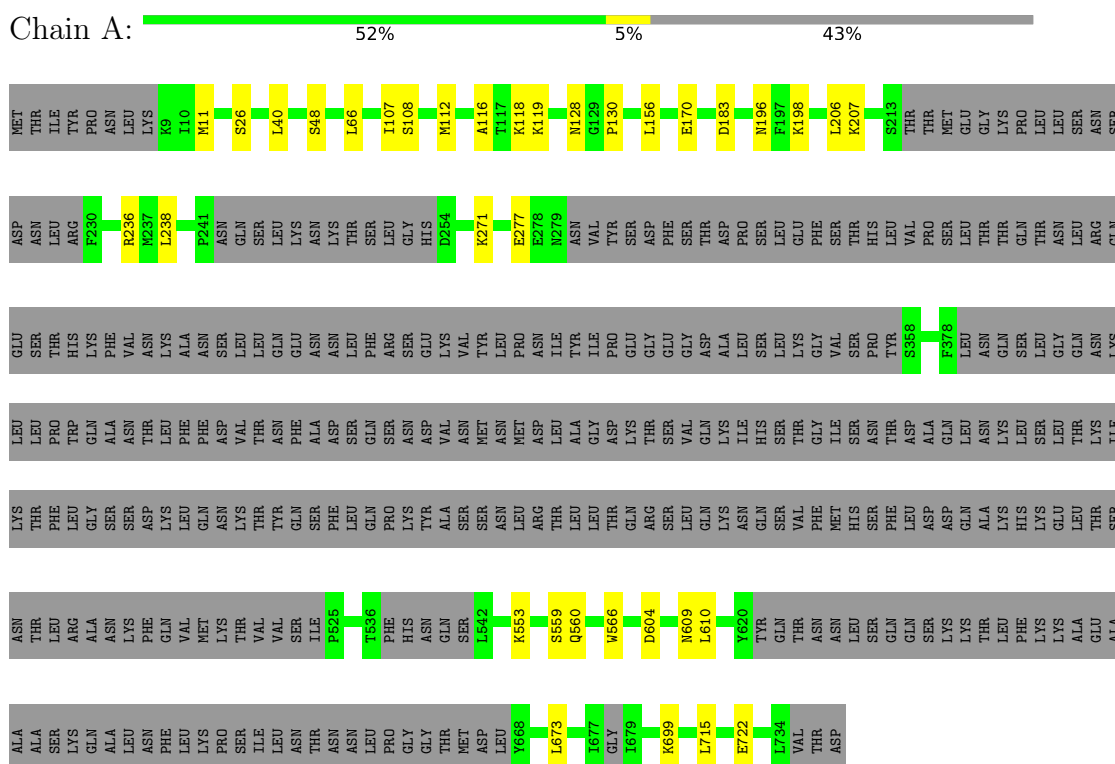
- Molecule 17 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	X	353	Total	C	N	O	S	0	0
			2700	1706	467	510	17		
17	Y	368	Total	C	N	O	S	0	0
			2821	1788	486	530	17		

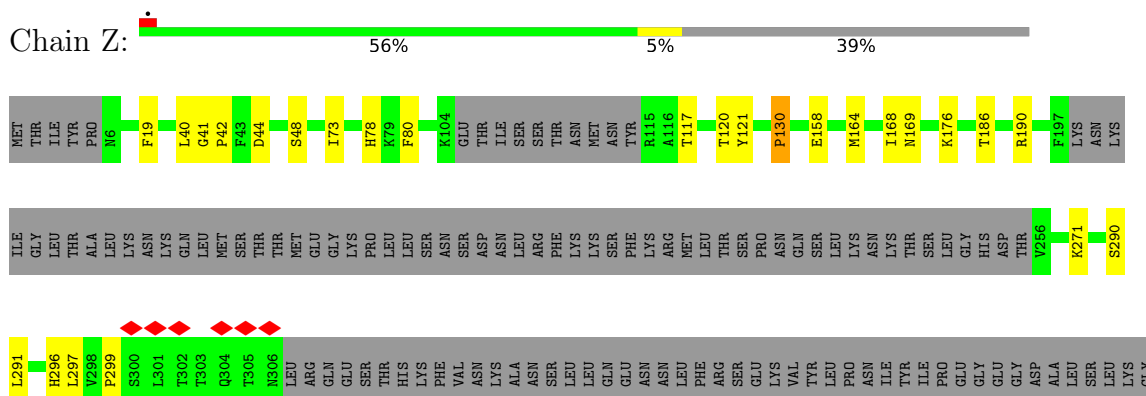
3 Residue-property plots [i](#)

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: DNA-directed RNA polymerase

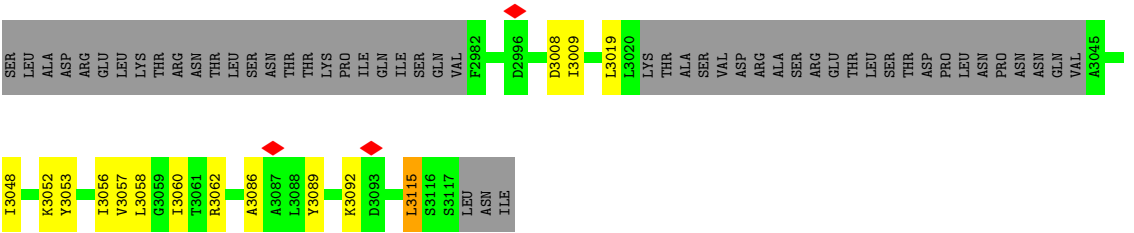


• Molecule 1: DNA-directed RNA polymerase

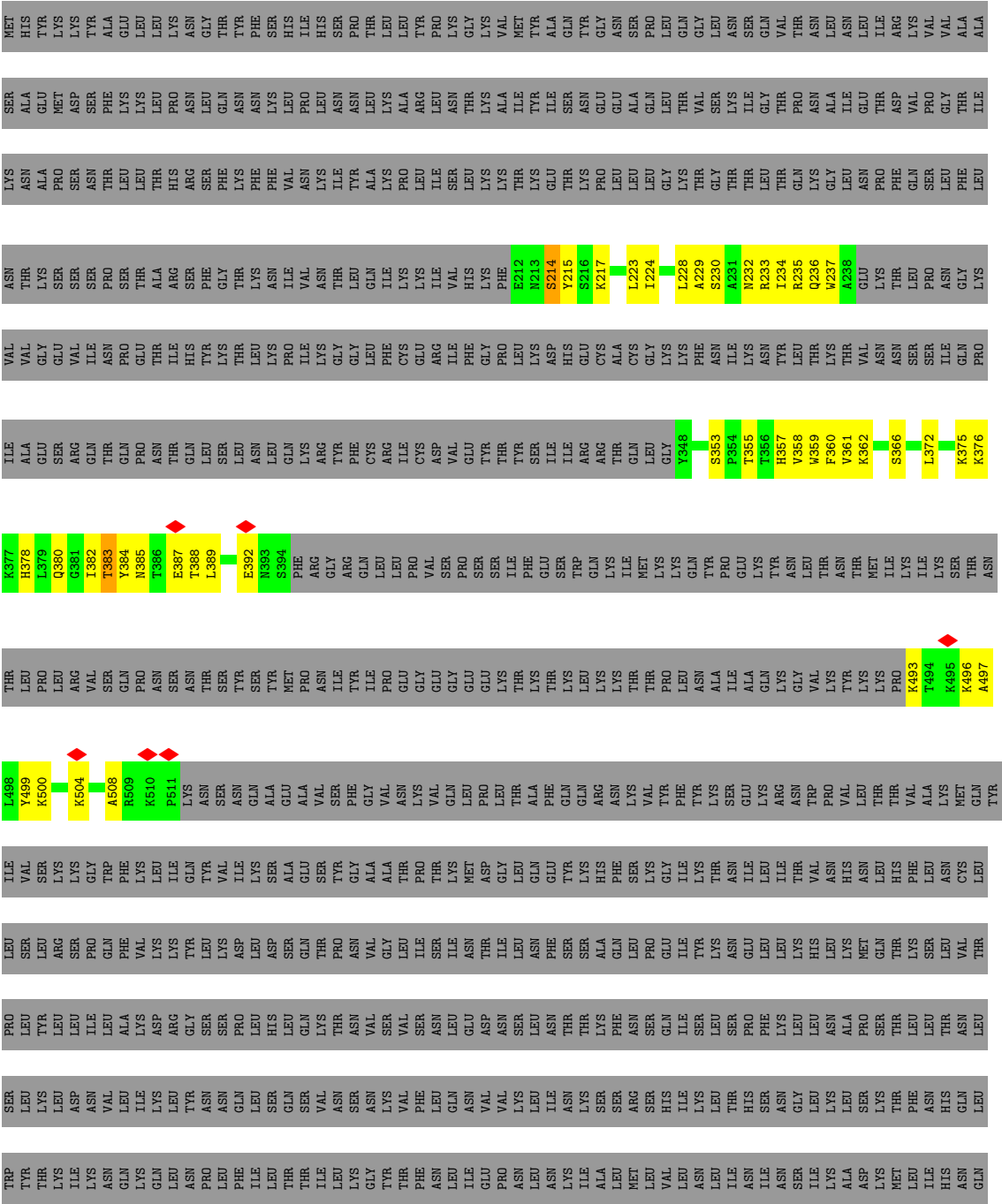


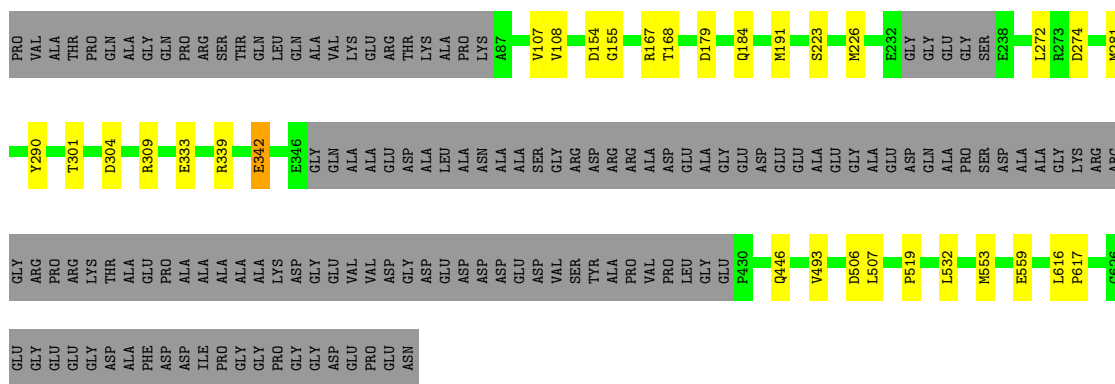
[illegible]



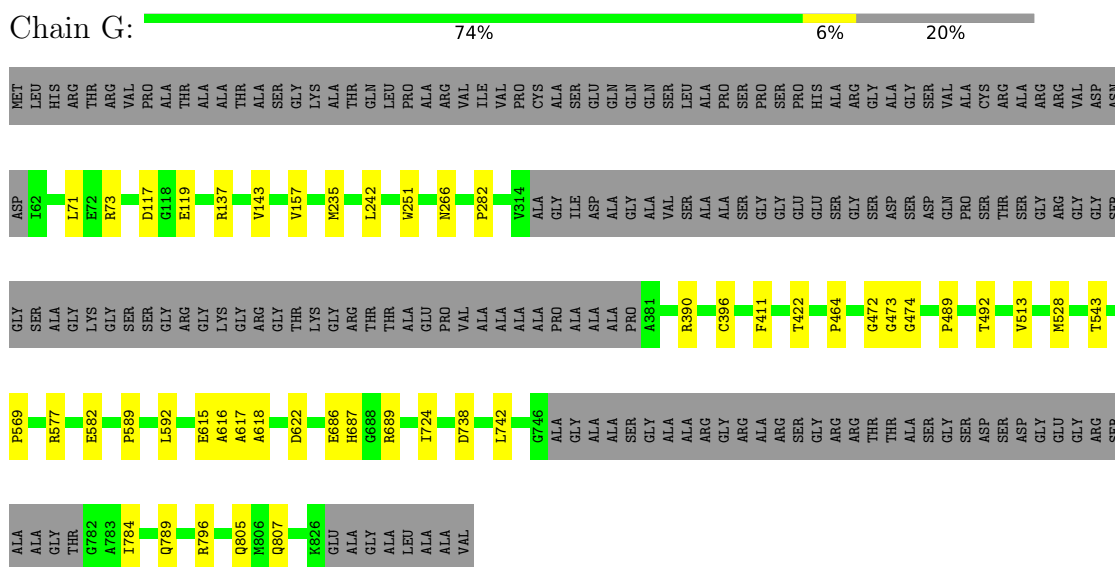


● Molecule 5: DNA-directed RNA polymerase subunit

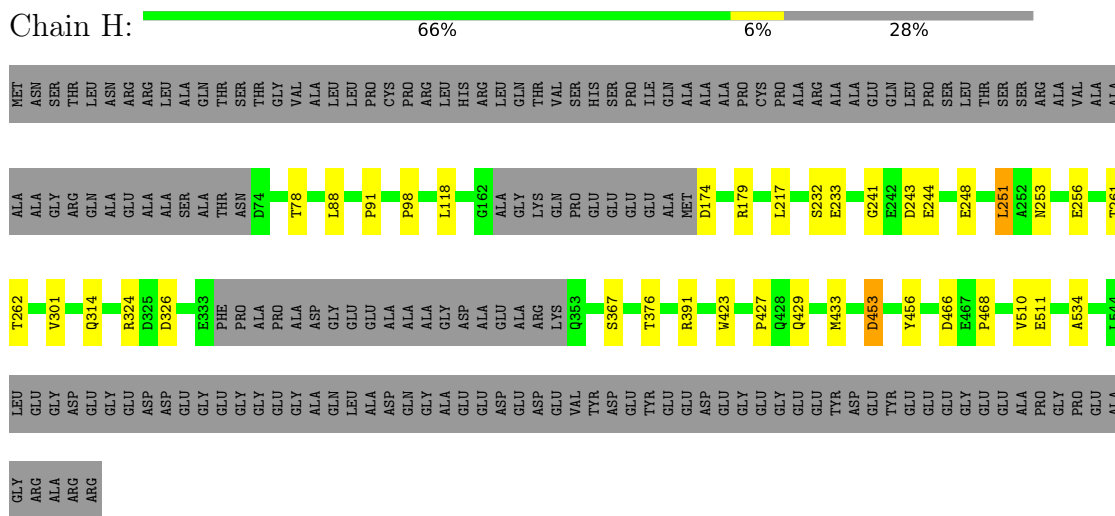




- Molecule 7: Rubisco LSMT substrate-binding domain-containing protein



- Molecule 8: UDP-3-O-acyl-N-acetylglucosamine deacetylase



- Molecule 8: UDP-3-O-acyl-N-acetylglucosamine deacetylase

Response	Percentage
Yes, more action is needed	47%
No, the U.S. is doing enough	6%
Don't know	47%



Opinion	Percentage
Doing a good job	35%
Doing a bad job	61%

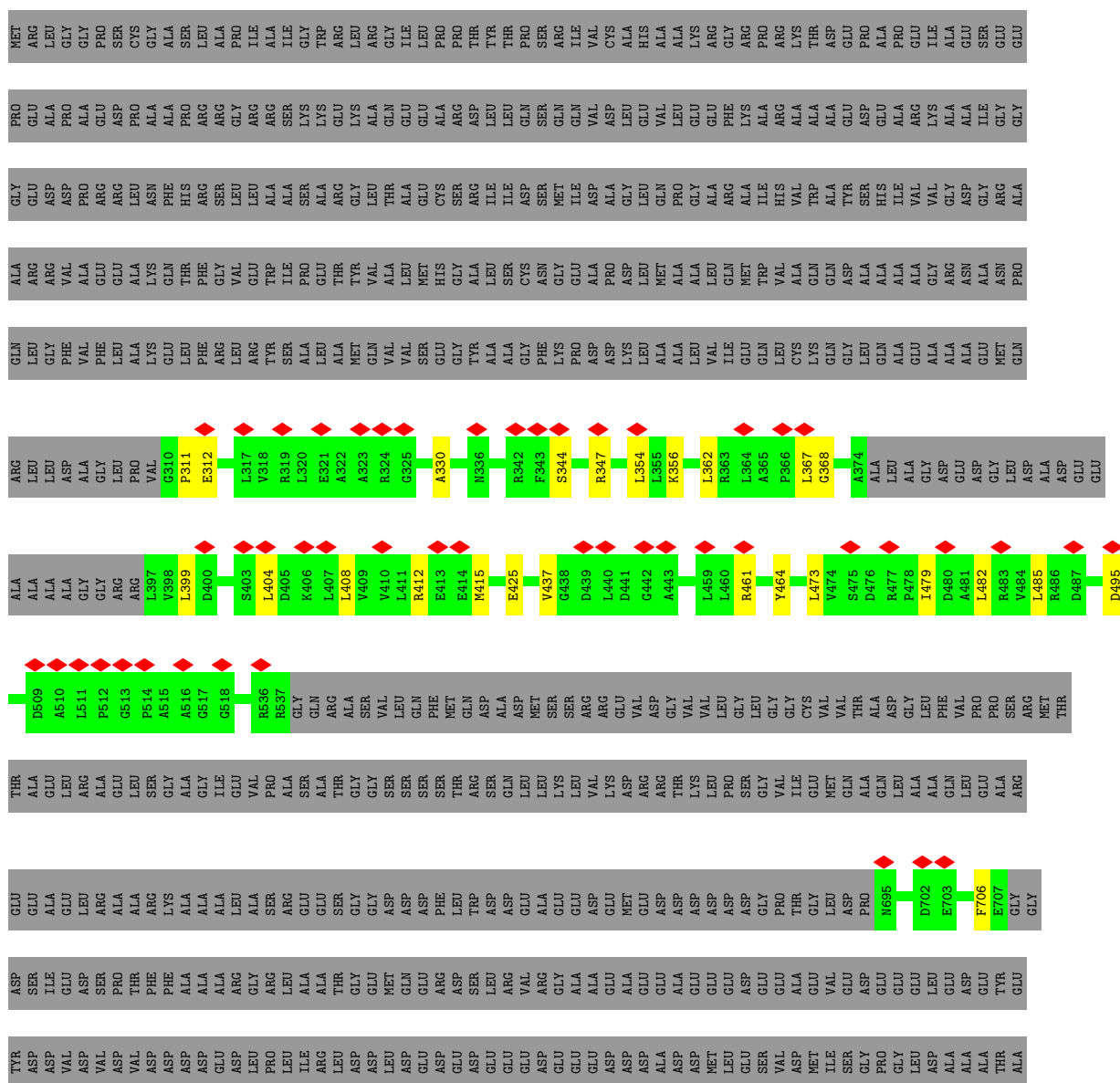


58% 38%





- Molecule 11: Uncharacterized protein A0A2K3D3G3

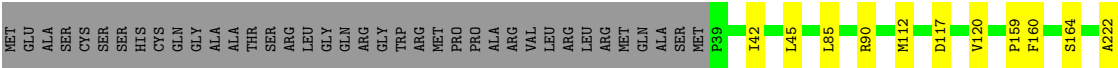
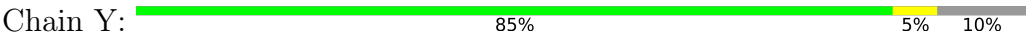




MET	GLU	ALA	SER	CYS	SER	HIS	CYS	GLN	GLY	ALA	ALA	THR	SER	SER	ARG	LEU	GLY	GLN	ARG	GLY	TRP	GLY	GLY	GLN	MET	PRO	PRO	ALA	ALA	ARG	VAL	LEU	ARG	LEU	ARG	MET	MET	GLN	ALA	SER	SER	MET	PRO	MET	VAL	VAL	GLU	GLU	ILE	GLY	LYS	GLU	LEU	GLN	PRO	PRO	GLN	LYS	ASP	THR	LYS	LYS	SSG
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● Molecule 17: Uncharacterized protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	650394	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.623	Depositor
Minimum map value	0.093	Depositor
Average map value	0.201	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.235	Depositor
Map size (Å)	558.6, 558.6, 558.6	wwPDB
Map dimensions	588, 588, 588	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	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	0.15	0/3422	0.35	0/4605
1	Z	0.15	0/3649	0.41	1/4929 (0.0%)
2	B	0.17	0/5073	0.36	1/6846 (0.0%)
3	C	0.16	0/3434	0.38	0/4633
4	D	0.16	0/14417	0.38	0/19397
5	E	0.20	0/5810	0.51	0/7825
6	F	0.18	0/3607	0.40	1/4909 (0.0%)
7	G	0.15	0/5252	0.32	0/7154
8	H	0.14	0/3499	0.34	0/4760
8	I	0.14	0/2568	0.38	0/3500
9	J	0.16	0/1131	0.37	0/1530
10	K	0.15	0/12566	0.34	0/17224
11	M	0.13	0/2824	0.36	0/3817
12	N	0.17	0/4829	0.55	2/6586 (0.0%)
13	Q	0.12	0/1768	0.35	0/2400
14	R	0.15	0/2502	0.32	0/3404
15	S	0.29	0/2433	0.36	0/3308
16	T	0.47	1/825 (0.1%)	0.80	4/1114 (0.4%)
17	X	0.18	0/2761	0.37	0/3767
17	Y	0.16	0/2887	0.37	0/3938
All	All	0.17	1/85257 (0.0%)	0.39	9/115646 (0.0%)

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	1
5	E	0	2
8	I	0	1
10	K	0	3
12	N	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	8

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	T	305	VAL	CA-C	-7.21	1.44	1.52

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	T	305	VAL	N-CA-C	-13.36	97.59	110.42
12	N	638	GLU	CA-C-N	8.76	137.47	121.70
12	N	638	GLU	C-N-CA	8.76	137.47	121.70
16	T	305	VAL	CB-CA-C	-7.03	102.97	111.97
16	T	298	ALA	N-CA-C	5.64	118.42	107.71

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	40	LEU	Peptide
5	E	1224	ASP	Peptide
5	E	383	THR	Peptide
8	I	142	VAL	Peptide
10	K	1161	THR	Peptide

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	3368	0	3524	21	0
1	Z	3590	0	3698	22	0
2	B	4970	0	5159	27	0
3	C	3368	0	3379	32	0
4	D	14136	0	14711	93	0
5	E	5698	0	5930	108	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	3517	0	3392	17	0
7	G	5136	0	5032	22	0
8	H	3419	0	3274	23	0
8	I	2506	0	2418	19	0
9	J	1105	0	1045	11	0
10	K	12323	0	12188	57	0
11	M	2794	0	2758	31	0
12	N	4733	0	4669	105	0
13	Q	1730	0	1693	17	0
14	R	2438	0	2273	10	0
15	S	2374	0	2168	15	0
16	T	809	0	826	30	0
17	X	2700	0	2694	11	0
17	Y	2821	0	2829	15	0
All	All	83535	0	83660	621	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 4.

The worst 5 of 621 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)
8:I:353:GLN:HE21	8:I:353:GLN:N	1.33	1.27
8:I:353:GLN:N	8:I:353:GLN:NE2	2.12	0.98
16:T:307:GLN:HB2	16:T:308:PRO:HD2	1.45	0.94
5:E:380:GLN:O	5:E:384:TYR:HB2	1.71	0.89
5:E:380:GLN:O	5:E:383:THR:O	1.93	0.87

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	405/737 (55%)	397 (98%)	8 (2%)	0	100	100
1	Z	439/737 (60%)	411 (94%)	26 (6%)	2 (0%)	24	39
2	B	603/822 (73%)	590 (98%)	12 (2%)	1 (0%)	43	60
3	C	410/626 (66%)	383 (93%)	27 (7%)	0	100	100
4	D	1655/3120 (53%)	1591 (96%)	62 (4%)	2 (0%)	48	66
5	E	674/1932 (35%)	617 (92%)	52 (8%)	5 (1%)	18	30
6	F	446/648 (69%)	433 (97%)	13 (3%)	0	100	100
7	G	658/834 (79%)	643 (98%)	13 (2%)	2 (0%)	36	52
8	H	435/609 (71%)	421 (97%)	14 (3%)	0	100	100
8	I	314/609 (52%)	293 (93%)	20 (6%)	1 (0%)	36	52
9	J	133/343 (39%)	128 (96%)	5 (4%)	0	100	100
10	K	1704/2788 (61%)	1658 (97%)	44 (3%)	2 (0%)	48	66
11	M	357/1801 (20%)	344 (96%)	12 (3%)	1 (0%)	36	52
12	N	617/803 (77%)	519 (84%)	90 (15%)	8 (1%)	9	16
13	Q	223/414 (54%)	222 (100%)	1 (0%)	0	100	100
14	R	299/356 (84%)	296 (99%)	3 (1%)	0	100	100
15	S	285/359 (79%)	285 (100%)	0	0	100	100
16	T	98/381 (26%)	88 (90%)	4 (4%)	6 (6%)	1	1
17	X	351/410 (86%)	342 (97%)	9 (3%)	0	100	100
17	Y	366/410 (89%)	353 (96%)	12 (3%)	1 (0%)	36	52
All	All	10472/18739 (56%)	10014 (96%)	427 (4%)	31 (0%)	37	52

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	1433	PRO
5	E	508	ALA
5	E	1254	ASP
8	I	143	PRO
10	K	1878	TRP

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	384/674 (57%)	379 (99%)	5 (1%)	61	77
1	Z	405/674 (60%)	401 (99%)	4 (1%)	68	81
2	B	554/737 (75%)	546 (99%)	8 (1%)	59	76
3	C	364/551 (66%)	358 (98%)	6 (2%)	55	74
4	D	1574/2864 (55%)	1545 (98%)	29 (2%)	51	72
5	E	629/1769 (36%)	616 (98%)	13 (2%)	47	69
6	F	362/499 (72%)	359 (99%)	3 (1%)	73	85
7	G	526/629 (84%)	520 (99%)	6 (1%)	65	80
8	H	354/473 (75%)	352 (99%)	2 (1%)	78	88
8	I	264/473 (56%)	256 (97%)	8 (3%)	36	57
9	J	114/277 (41%)	112 (98%)	2 (2%)	51	72
10	K	1182/1841 (64%)	1159 (98%)	23 (2%)	50	71
11	M	279/1296 (22%)	276 (99%)	3 (1%)	65	80
12	N	495/634 (78%)	482 (97%)	13 (3%)	40	63
13	Q	186/312 (60%)	184 (99%)	2 (1%)	65	80
14	R	262/303 (86%)	261 (100%)	1 (0%)	84	93
15	S	251/305 (82%)	247 (98%)	4 (2%)	55	74
16	T	89/300 (30%)	85 (96%)	4 (4%)	24	42
17	X	298/346 (86%)	291 (98%)	7 (2%)	44	66
17	Y	312/346 (90%)	310 (99%)	2 (1%)	78	88
All	All	8884/15303 (58%)	8739 (98%)	145 (2%)	54	74

5 of 145 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	N	370	GLN
1	Z	297	LEU
12	N	648	VAL
16	T	303	ARG
5	E	1244	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
16	T	269	ASN
17	X	145	GLN
1	Z	592	GLN
4	D	2364	GLN
4	D	2361	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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
8	I	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	501:ALA	C	502:ASP	N	4.51

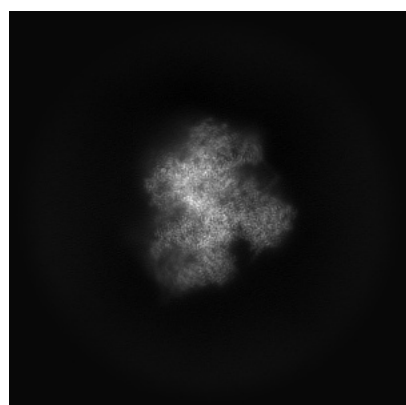
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-56766. These allow visual inspection of the internal detail of the map and identification of artifacts.

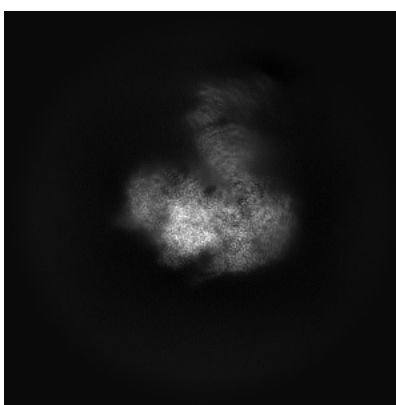
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

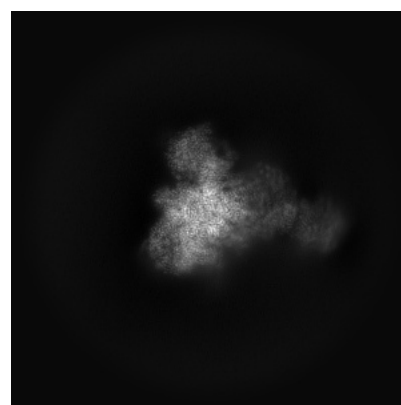
6.1.1 Primary map



X



Y

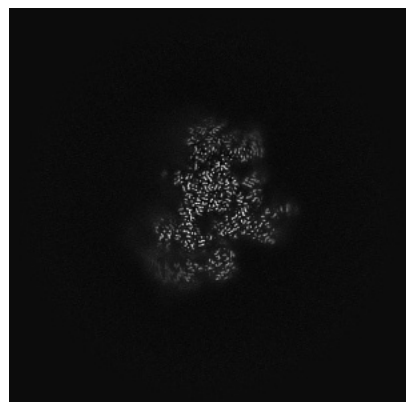


Z

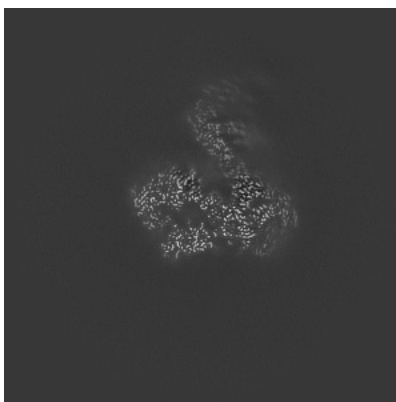
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 294



Y Index: 294

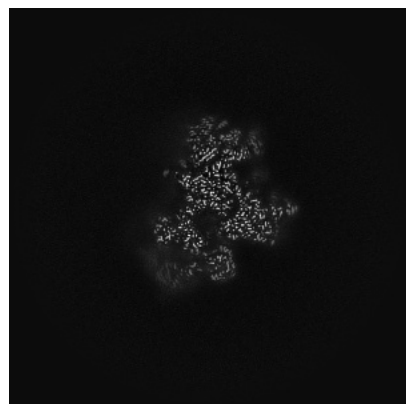


Z Index: 294

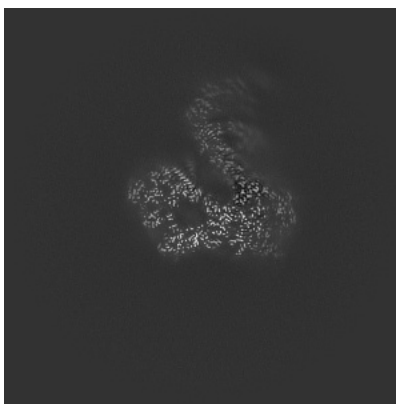
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

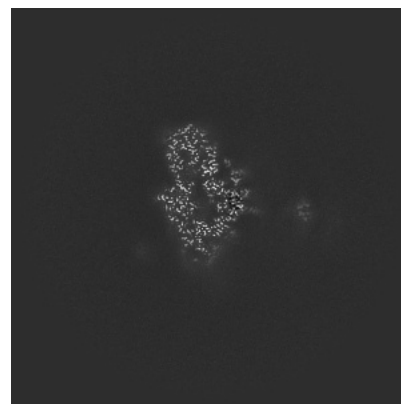
6.3.1 Primary map



X Index: 289



Y Index: 288

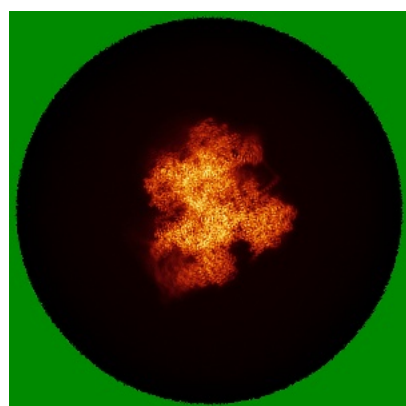


Z Index: 272

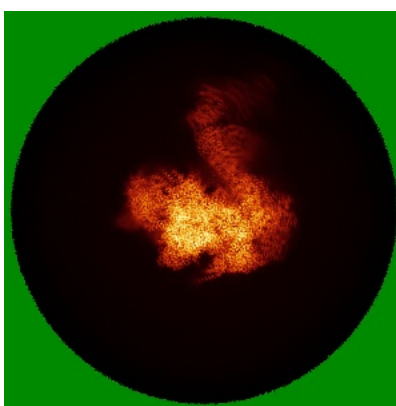
The images above show the largest variance slices of the map in three orthogonal directions.

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

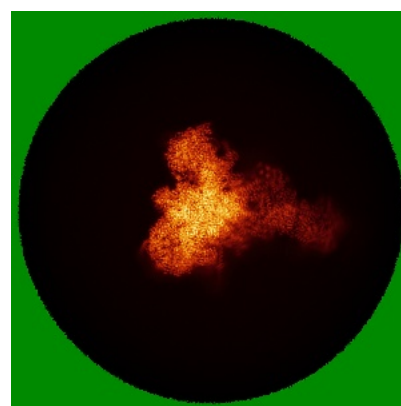
6.4.1 Primary map



X



Y

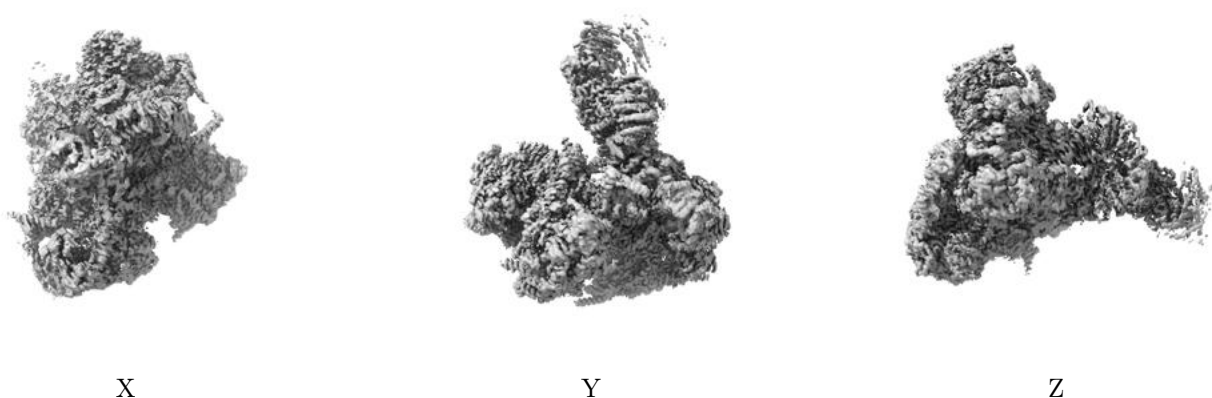


Z

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

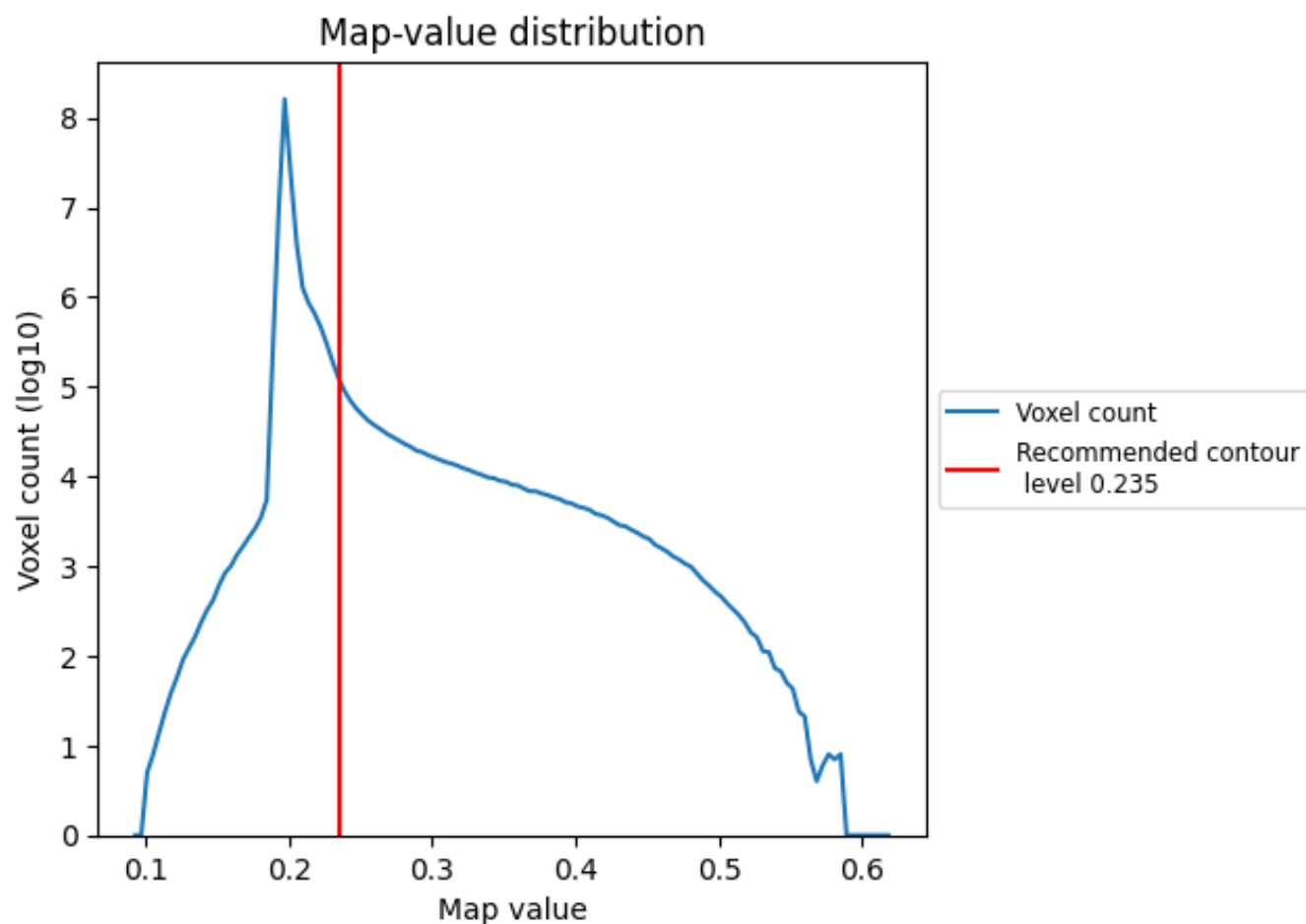
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

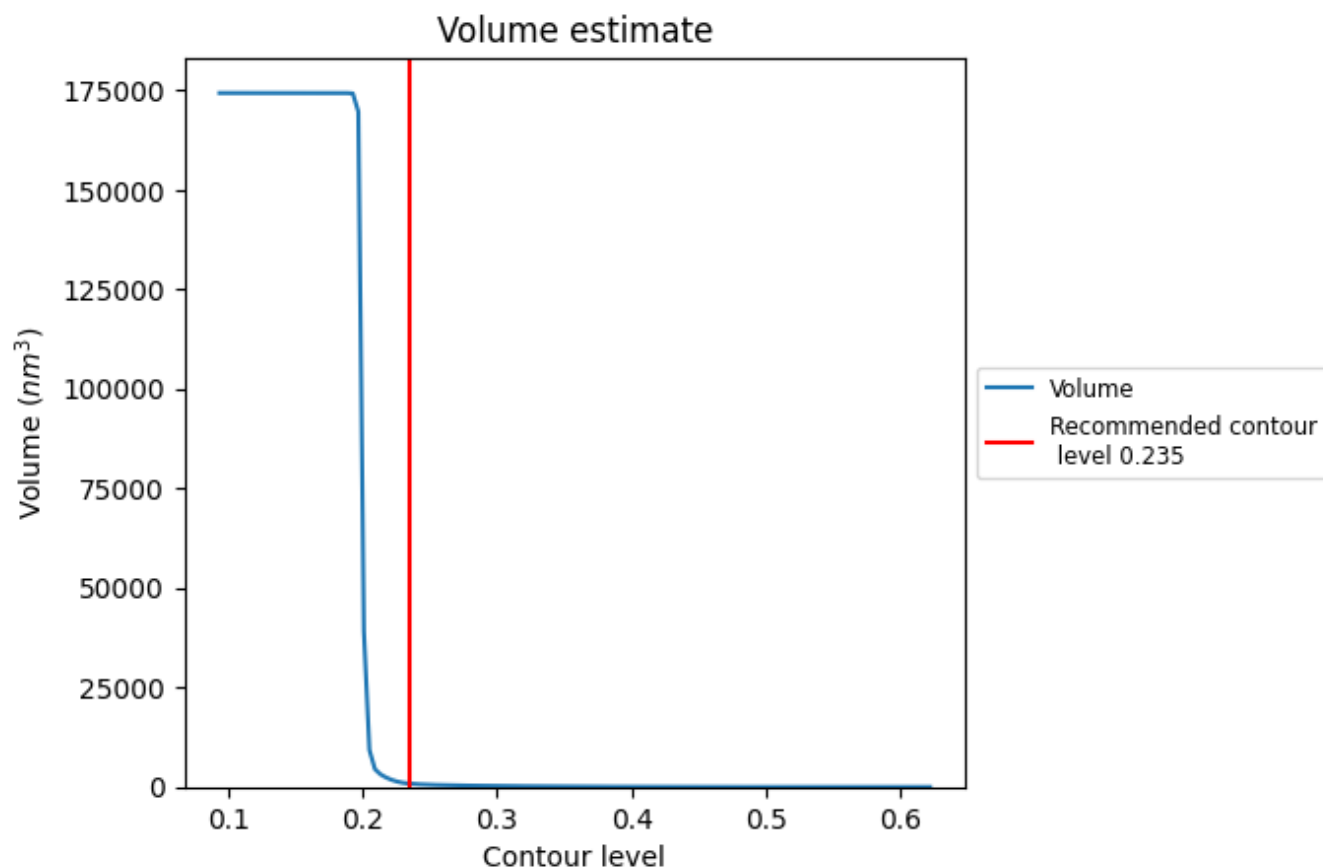
This section contains the results of statistical analysis of the map.

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.

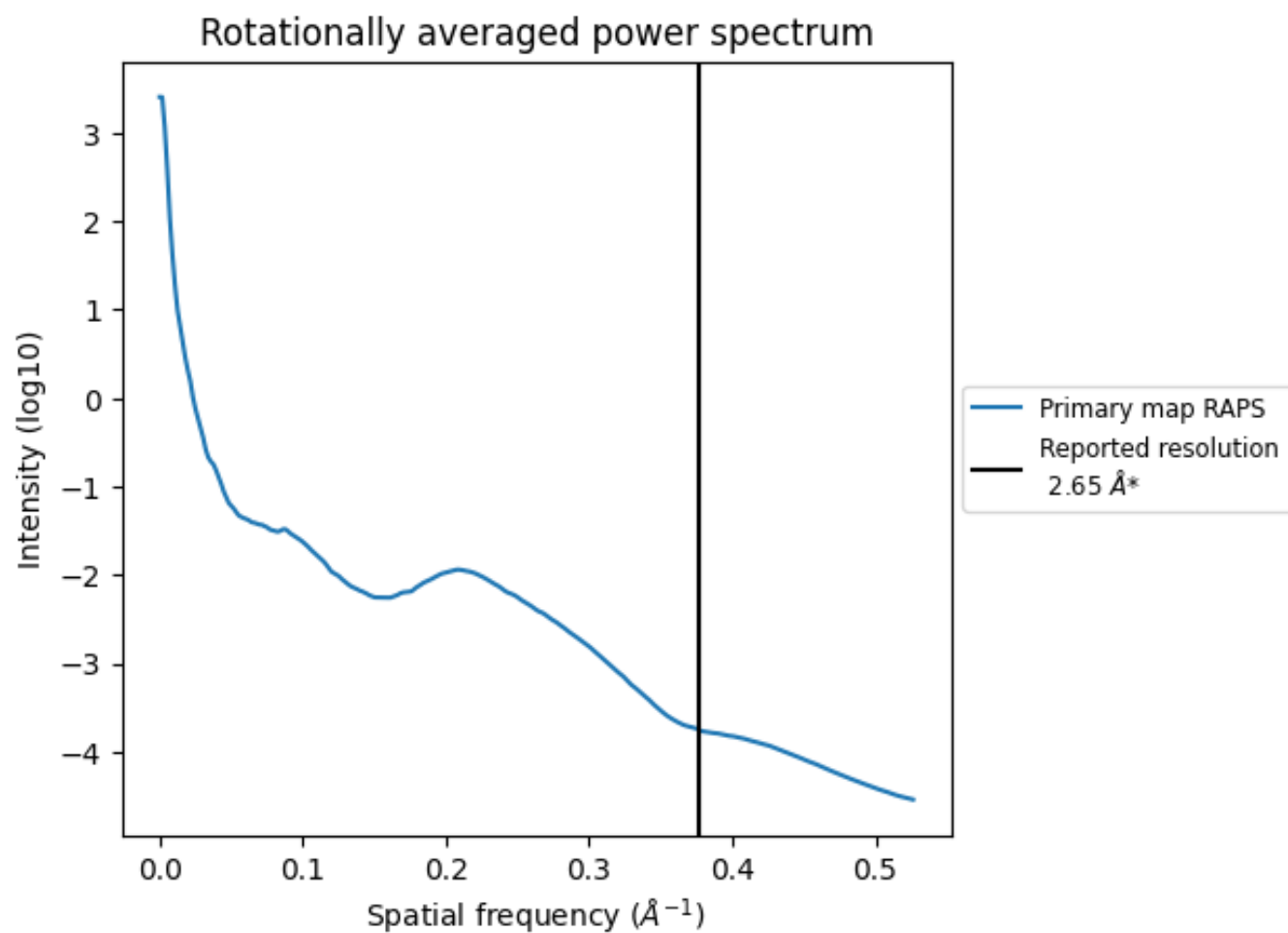
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 833 nm^3 ; this corresponds to an approximate mass of 752 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 0.377 Å⁻¹

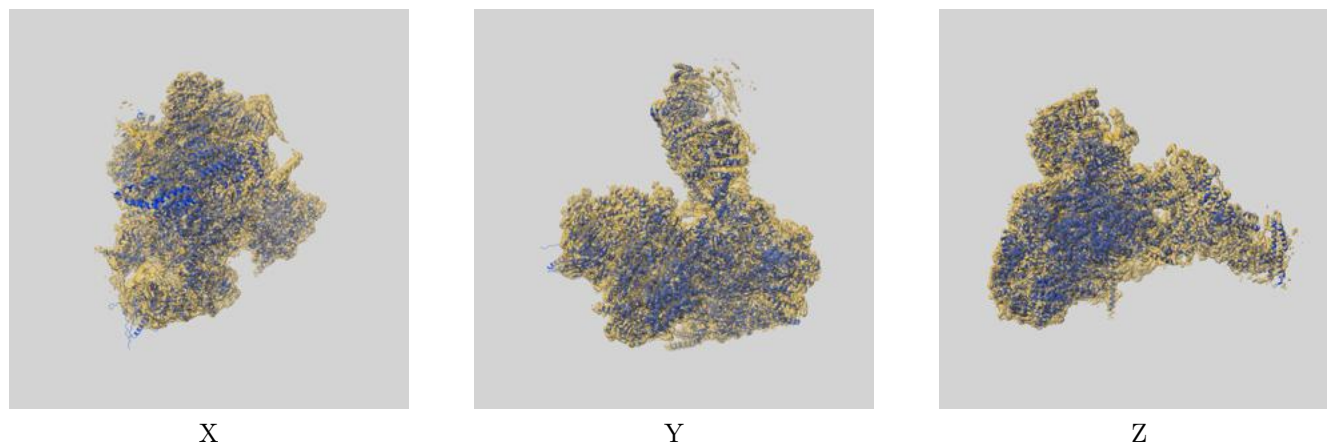
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

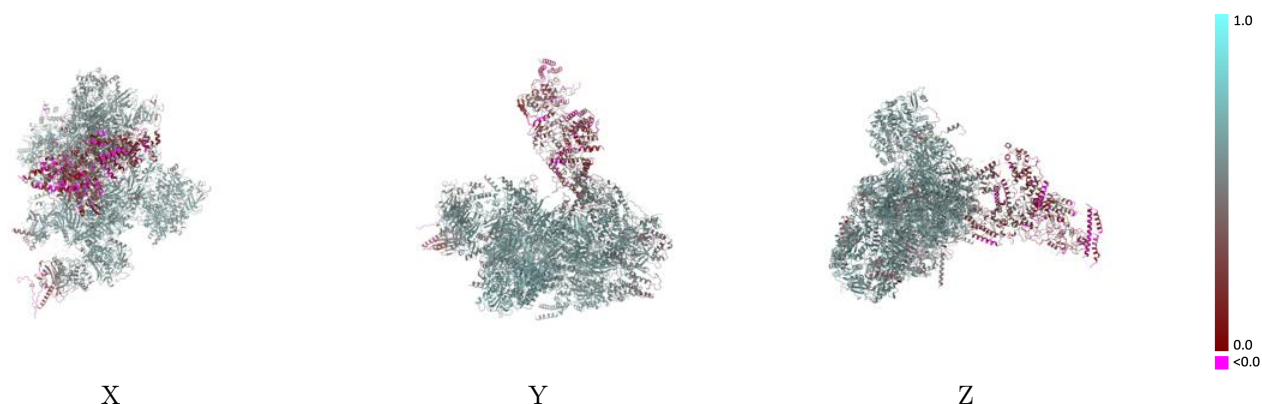
This section contains information regarding the fit between EMDB map EMD-56766 and PDB model 28RF. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



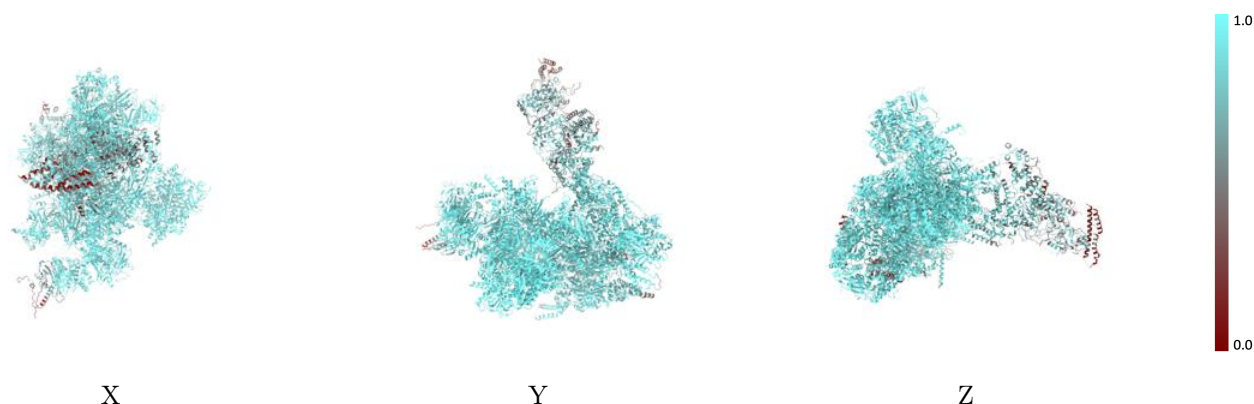
The images above show the 3D surface view of the map at the recommended contour level 0.235 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



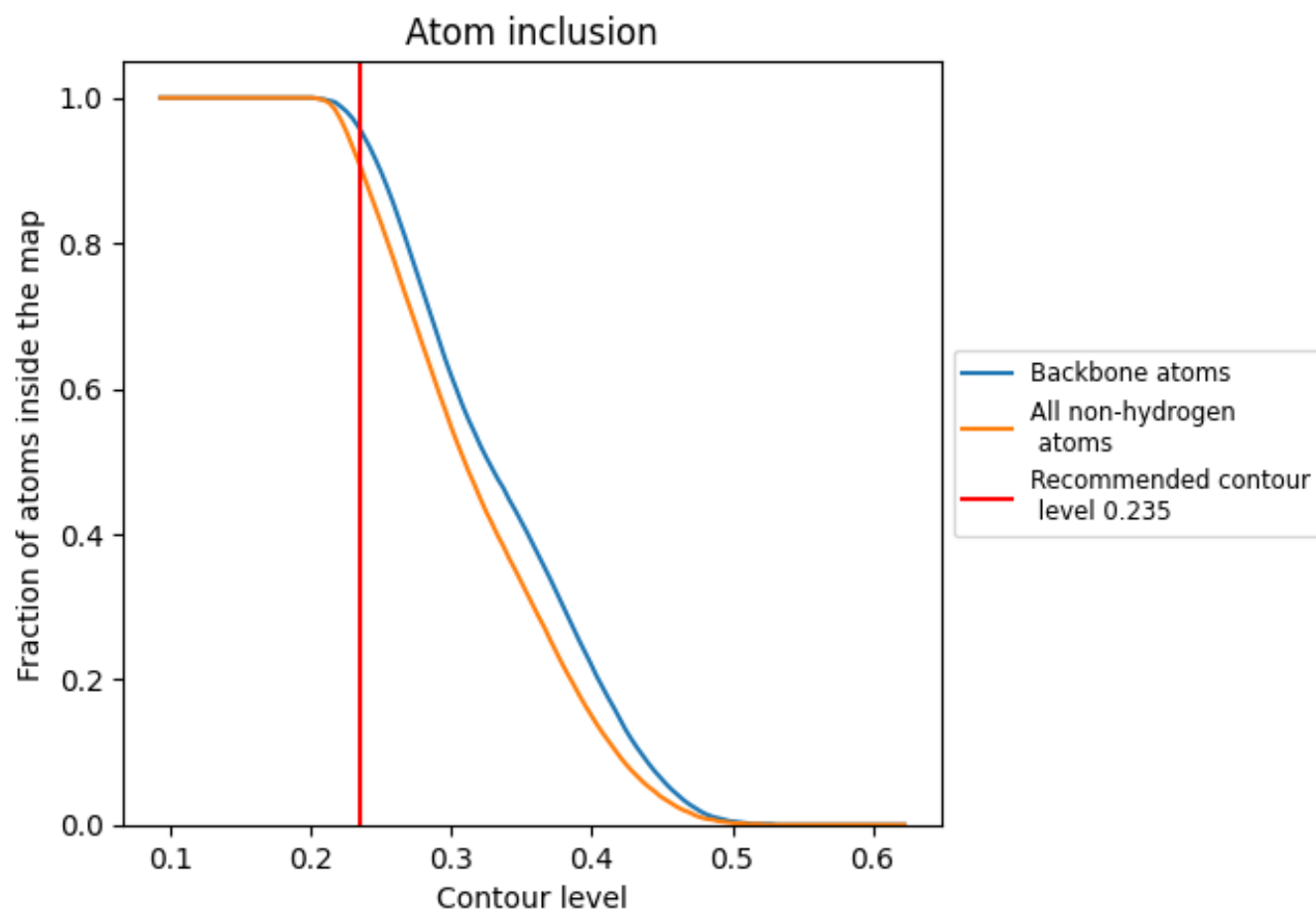
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.235).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 91% 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 (0.235) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9070	 0.5260
A	 0.9480	 0.5850
B	 0.9820	 0.6160
C	 0.9620	 0.5870
D	 0.9490	 0.5580
E	 0.8150	 0.3960
F	 0.9660	 0.5960
G	 0.9740	 0.5870
H	 0.9690	 0.5760
I	 0.9520	 0.5230
J	 0.9480	 0.5540
K	 0.9430	 0.5740
M	 0.5210	 0.1720
N	 0.6520	 0.2340
Q	 0.5390	 0.2210
R	 0.9670	 0.6100
S	 0.9610	 0.6080
T	 0.9520	 0.4880
X	 0.9900	 0.6350
Y	 0.9870	 0.6190
Z	 0.9060	 0.5560

