



wwPDB EM Validation Summary Report ⓘ

Nov 27, 2022 – 05:33 AM EST

PDB ID : 6NBY
EMDB ID : EMD-0415
Title : T.elongatus NDH (composite model)
Authors : Laughlin, T.G.; Bayne, A.; Trempe, J.-F.; Savage, D.F.; Davies, K.M.
Deposited on : 2018-12-10
Resolution : 3.10 Å (reported)
Based on initial models : 6NBQ, 6NBX

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:

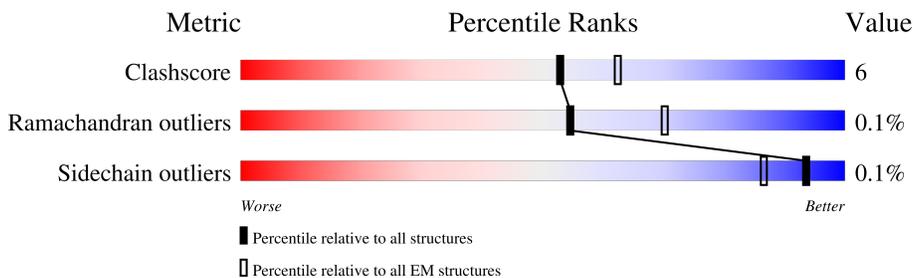
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance

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

The reported resolution of this entry is 3.10 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)
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 $\leq 5\%$. 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	372	
2	B	515	
3	C	132	
4	D	529	
5	E	101	
6	F	656	
7	G	200	
8	H	394	

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Mol	Chain	Length	Quality of chain
9	I	196	
10	J	168	
11	K	237	
12	L	76	
13	M	111	
14	N	150	
15	O	70	
16	P	44	
17	Q	45	
18	S	110	

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 29401 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 NAD(P)H-quinone oxidoreductase subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	335	2494	1685	398	401	10	0	0

- Molecule 2 is a protein called NAD(P)H-quinone oxidoreductase subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	483	3579	2393	563	607	16	0	0

- Molecule 3 is a protein called NAD(P)H-quinone oxidoreductase subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	100	793	560	115	116	2	0	0

- Molecule 4 is a protein called NAD(P)H-quinone oxidoreductase chain 4 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	504	3817	2572	604	620	21	0	0

- Molecule 5 is a protein called NAD(P)H-quinone oxidoreductase subunit 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	101	772	512	128	128	4	0	0

- Molecule 6 is a protein called NADH dehydrogenase subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	655	4902	3253	776	839	34	0	0

- Molecule 7 is a protein called NADH-quinone oxidoreductase subunit J.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	191	1373	914	217	238	4	0	0

- Molecule 8 is a protein called NAD(P)H-quinone oxidoreductase subunit H.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	392	3105	2010	541	535	19	0	0

- Molecule 9 is a protein called NAD(P)H-quinone oxidoreductase subunit I.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	184	1444	922	249	260	13	0	0

- Molecule 10 is a protein called NAD(P)H-quinone oxidoreductase subunit J.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	161	1295	832	223	235	5	0	0

- Molecule 11 is a protein called NAD(P)H-quinone oxidoreductase subunit K.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	212	1615	1040	282	279	14	0	0

- Molecule 12 is a protein called NAD(P)H-quinone oxidoreductase subunit L.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	66	536	369	83	83	1	0	0

- Molecule 13 is a protein called NAD(P)H-quinone oxidoreductase subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	M	111	866	542	161	161	2	0	0

- Molecule 14 is a protein called NAD(P)H-quinone oxidoreductase subunit N.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	N	148	1158	755	201	201	1	0	0

- Molecule 15 is a protein called NAD(P)H-quinone oxidoreductase subunit O.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	O	69	543	352	93	98	0	0

- Molecule 16 is a protein called Proton-translocating NADH-quinone dehydrogenase subunit P NdhP.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	P	42	318	212	51	53	2	0	0

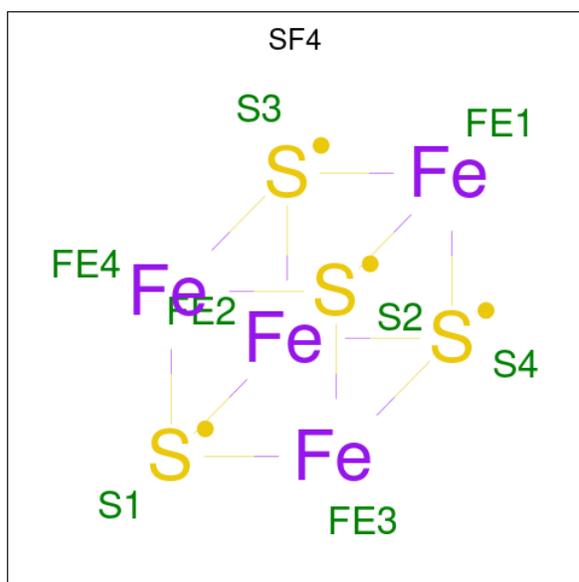
- Molecule 17 is a protein called Proton-translocating NADH-quinone dehydrogenase subunit Q NdhQ.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	Q	43	327	218	52	55	2	0	0

- Molecule 18 is a protein called Thr0636 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	S	57	440	286	71	81	2	0	0

- Molecule 19 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).

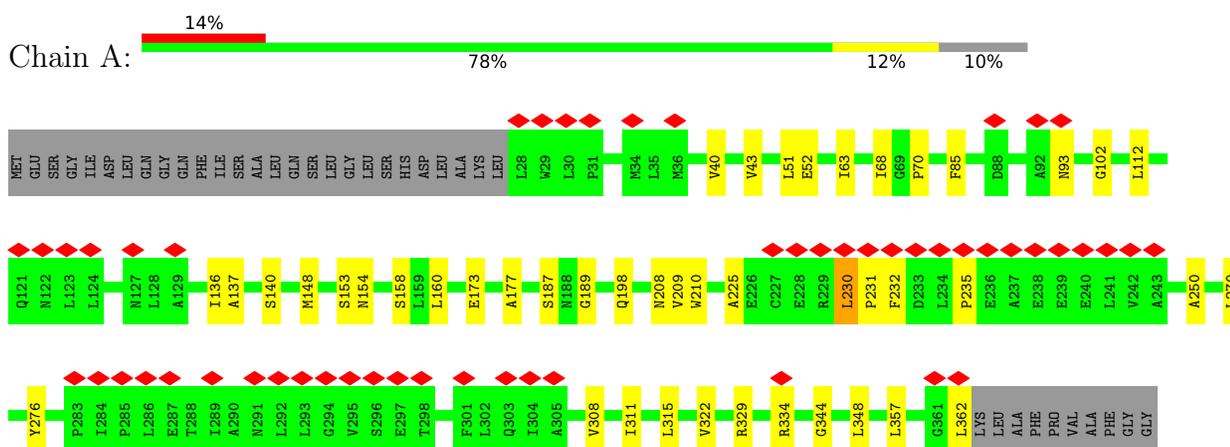


Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
19	I	1	16	8	8	0
19	I	1	16	8	8	0
19	K	1	8	4	4	0

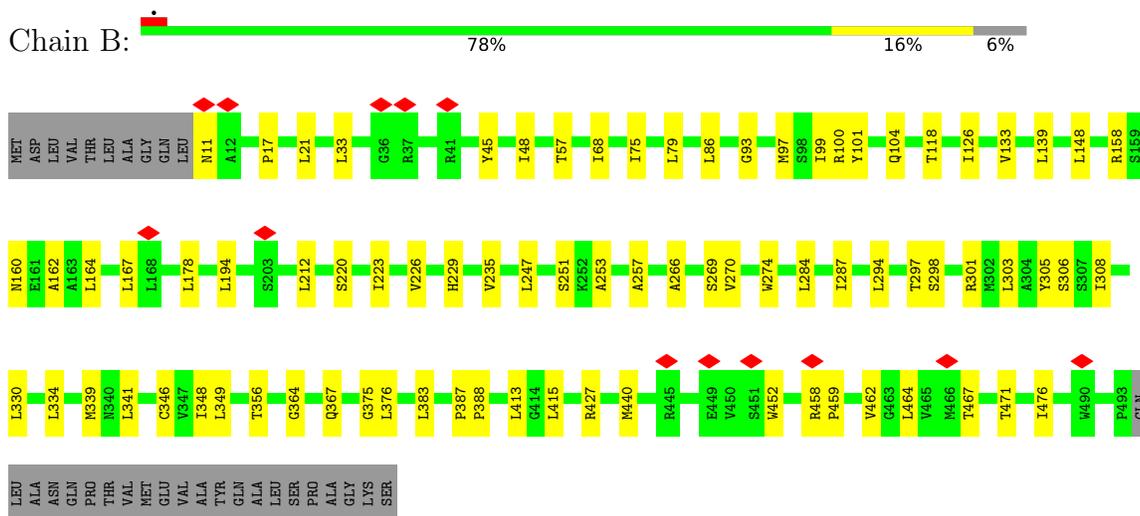
3 Residue-property plots

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: NAD(P)H-quinone oxidoreductase subunit 1

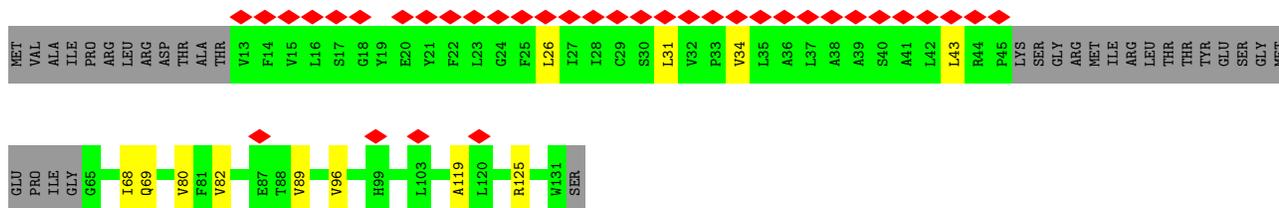


- Molecule 2: NAD(P)H-quinone oxidoreductase subunit 2

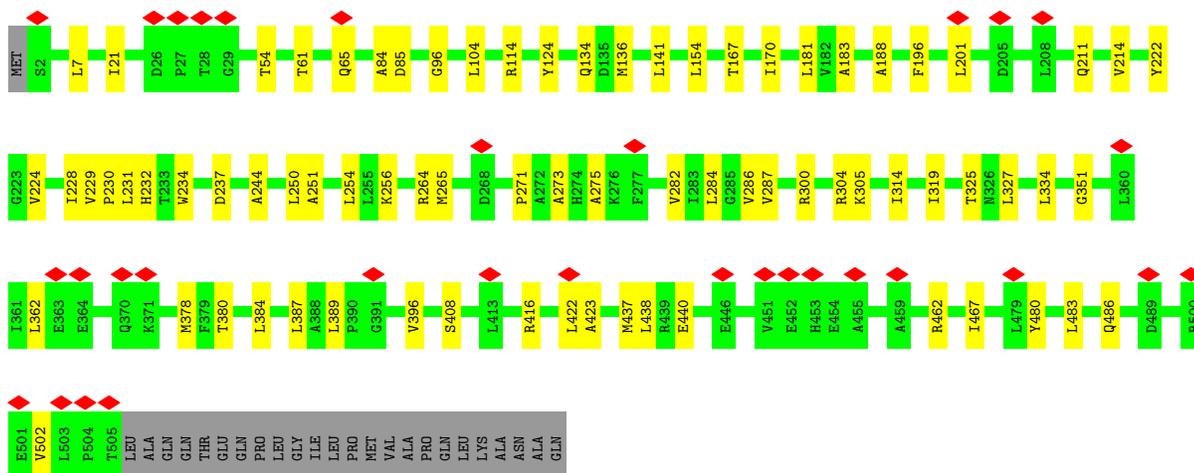
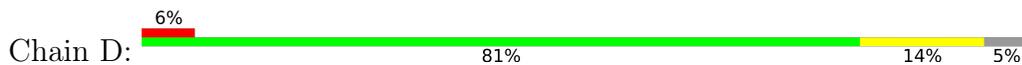


- Molecule 3: NAD(P)H-quinone oxidoreductase subunit 3





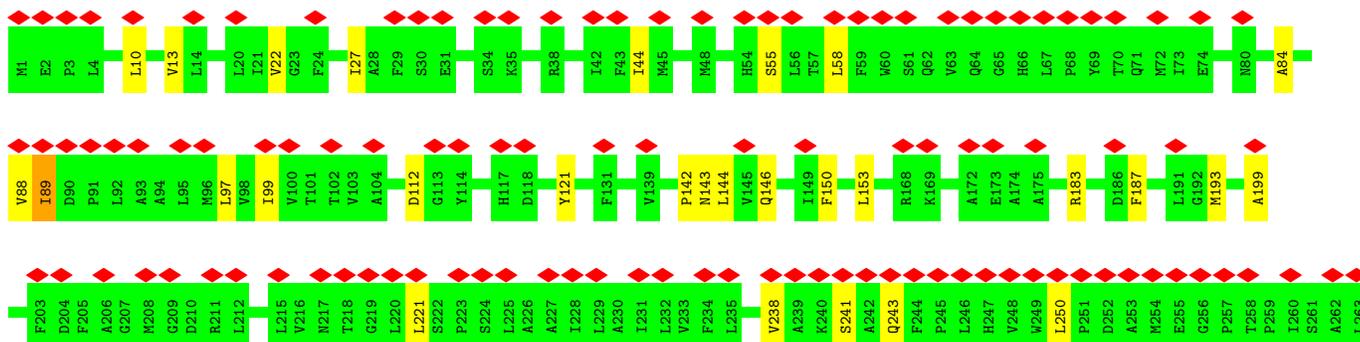
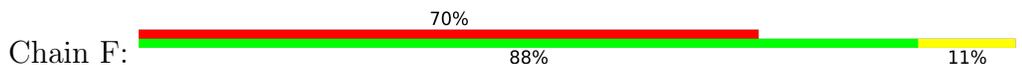
● Molecule 4: NAD(P)H-quinone oxidoreductase chain 4 1

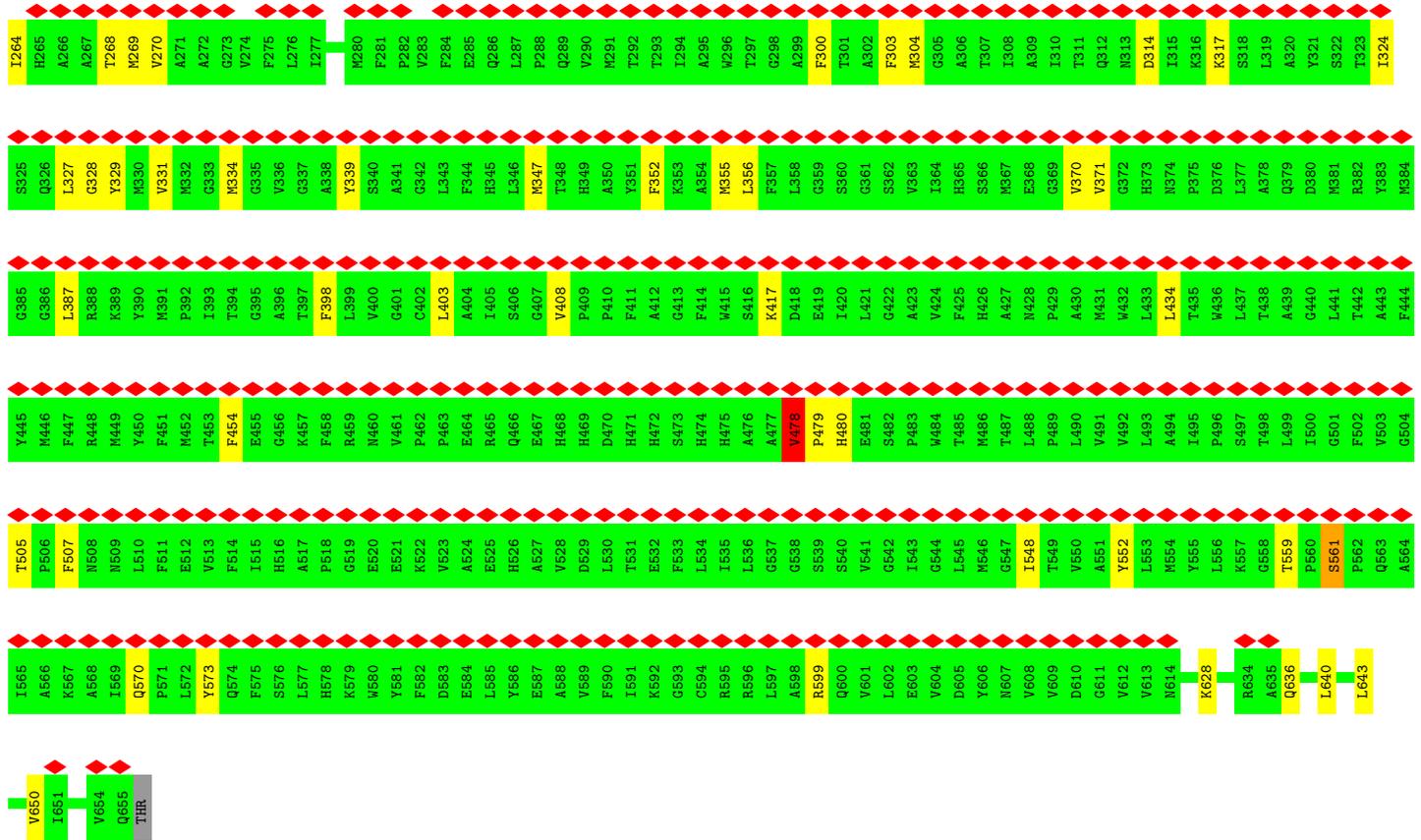


● Molecule 5: NAD(P)H-quinone oxidoreductase subunit 4L

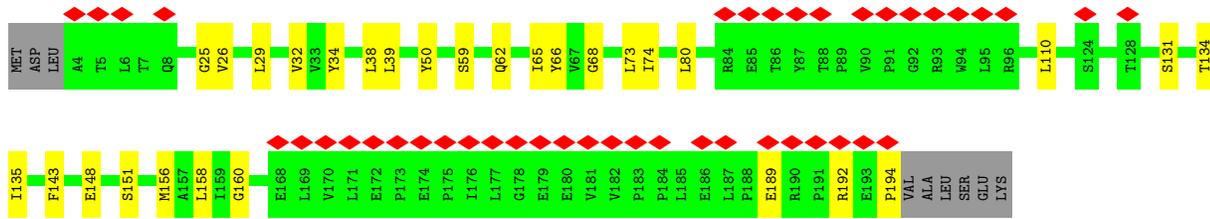
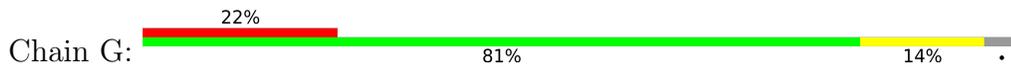


● Molecule 6: NADH dehydrogenase subunit 5

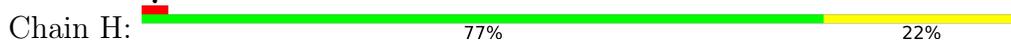




• Molecule 7: NADH-quinone oxidoreductase subunit J

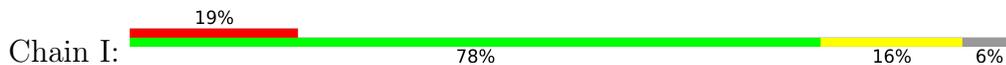


• Molecule 8: NAD(P)H-quinone oxidoreductase subunit H

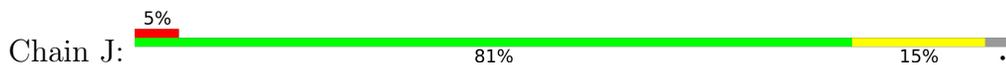




- Molecule 9: NAD(P)H-quinone oxidoreductase subunit I



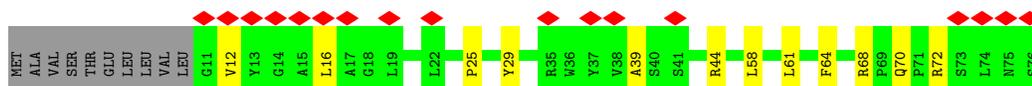
- Molecule 10: NAD(P)H-quinone oxidoreductase subunit J



- Molecule 11: NAD(P)H-quinone oxidoreductase subunit K



- Molecule 12: NAD(P)H-quinone oxidoreductase subunit L



- Molecule 13: NAD(P)H-quinone oxidoreductase subunit M

Chain M:  85% 14%



- Molecule 14: NAD(P)H-quinone oxidoreductase subunit N

Chain N:  7% 89% 10%



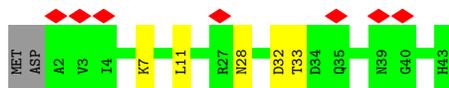
- Molecule 15: NAD(P)H-quinone oxidoreductase subunit O

Chain O:  6% 86% 13%

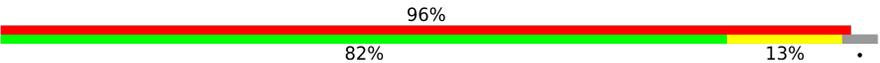


- Molecule 16: Proton-translocating NADH-quinone dehydrogenase subunit P NdhP

Chain P:  16% 84% 11% 5%

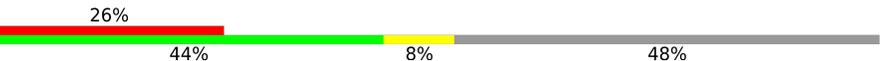


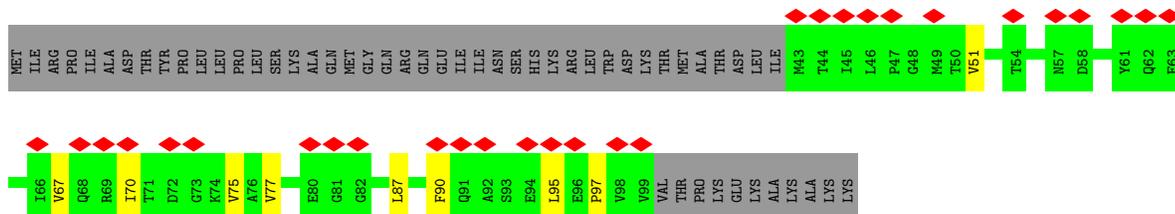
- Molecule 17: Proton-translocating NADH-quinone dehydrogenase subunit Q NdhQ

Chain Q:  96% 82% 13%



- Molecule 18: Tlr0636 protein

Chain S:  26% 44% 8% 48%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	81670	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.324	Depositor
Minimum map value	-0.132	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	384.47998, 384.47998, 384.47998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.068, 1.068, 1.068	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: SF4

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	0.29	0/2560	0.53	1/3510 (0.0%)
2	B	0.29	0/3665	0.53	0/5008
3	C	0.32	0/820	0.52	0/1125
4	D	0.29	0/3924	0.53	1/5364 (0.0%)
5	E	0.26	0/782	0.50	0/1063
6	F	0.28	0/5040	0.56	1/6882 (0.0%)
7	G	0.28	0/1401	0.54	0/1926
8	H	0.30	0/3187	0.51	0/4325
9	I	0.31	0/1481	0.57	2/2013 (0.1%)
10	J	0.28	0/1332	0.49	0/1816
11	K	0.31	0/1657	0.58	0/2258
12	L	0.30	0/556	0.54	0/760
13	M	0.27	0/882	0.47	0/1198
14	N	0.28	0/1190	0.50	0/1619
15	O	0.28	0/555	0.50	0/755
16	P	0.28	0/327	0.56	0/445
17	Q	0.25	0/336	0.45	0/457
18	S	0.30	0/449	0.60	1/612 (0.2%)
All	All	0.29	0/30144	0.53	6/41136 (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
6	F	0	2
9	I	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
6	F	89	ILE	C-N-CA	8.65	143.34	121.70
4	D	362	LEU	CA-CB-CG	6.59	130.45	115.30
1	A	230	LEU	CA-CB-CG	6.28	129.74	115.30
9	I	88	LEU	CA-CB-CG	5.63	128.25	115.30
9	I	126	LEU	CA-CB-CG	5.14	127.12	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	F	478	VAL	Peptide
6	F	561	SER	Peptide
9	I	64	ILE	Peptide

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	2494	0	2570	29	0
2	B	3579	0	3707	52	0
3	C	793	0	808	11	0
4	D	3817	0	3937	47	0
5	E	772	0	827	16	0
6	F	4902	0	4842	41	0
7	G	1373	0	1396	24	0
8	H	3105	0	3060	59	0
9	I	1444	0	1399	23	0
10	J	1295	0	1254	18	0
11	K	1615	0	1657	34	0
12	L	536	0	539	8	0
13	M	866	0	847	12	0
14	N	1158	0	1170	12	0
15	O	543	0	553	7	0
16	P	318	0	309	4	0
17	Q	327	0	326	5	0
18	S	440	0	440	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	I	16	0	0	0	0
19	K	8	0	0	0	0
All	All	29401	0	29641	331	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 6.

The worst 5 of 331 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:334:MET:HG2	6:F:339:TYR:HB2	1.78	0.66
8:H:69:ARG:NH2	11:K:148:CYS:SG	2.70	0.65
2:B:364:GLY:HA3	2:B:440:MET:HB3	1.79	0.64
1:A:225:ALA:HA	1:A:231:PRO:HG2	1.80	0.63
9:I:187:ILE:HG22	9:I:187:ILE:O	1.97	0.63

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	333/372 (90%)	310 (93%)	23 (7%)	0	100	100
2	B	481/515 (93%)	454 (94%)	27 (6%)	0	100	100
3	C	96/132 (73%)	91 (95%)	5 (5%)	0	100	100
4	D	502/529 (95%)	465 (93%)	37 (7%)	0	100	100
5	E	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
6	F	653/656 (100%)	601 (92%)	50 (8%)	2 (0%)	41	73
7	G	189/200 (94%)	169 (89%)	20 (11%)	0	100	100
8	H	390/394 (99%)	361 (93%)	29 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	182/196 (93%)	168 (92%)	13 (7%)	1 (0%)	29	64
10	J	159/168 (95%)	148 (93%)	11 (7%)	0	100	100
11	K	210/237 (89%)	185 (88%)	25 (12%)	0	100	100
12	L	64/76 (84%)	60 (94%)	4 (6%)	0	100	100
13	M	109/111 (98%)	101 (93%)	8 (7%)	0	100	100
14	N	146/150 (97%)	143 (98%)	3 (2%)	0	100	100
15	O	67/70 (96%)	60 (90%)	7 (10%)	0	100	100
16	P	40/44 (91%)	36 (90%)	4 (10%)	0	100	100
17	Q	41/45 (91%)	36 (88%)	5 (12%)	0	100	100
18	S	55/110 (50%)	46 (84%)	9 (16%)	0	100	100
All	All	3816/4106 (93%)	3527 (92%)	286 (8%)	3 (0%)	54	83

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	I	65	ALA
6	F	479	PRO
6	F	478	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	245/302 (81%)	245 (100%)	0	100	100
2	B	367/413 (89%)	367 (100%)	0	100	100
3	C	76/109 (70%)	76 (100%)	0	100	100
4	D	381/424 (90%)	381 (100%)	0	100	100
5	E	79/82 (96%)	78 (99%)	1 (1%)	69	87
6	F	484/527 (92%)	484 (100%)	0	100	100
7	G	137/166 (82%)	137 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	317/338 (94%)	316 (100%)	1 (0%)	92	96
9	I	153/172 (89%)	153 (100%)	0	100	100
10	J	137/148 (93%)	137 (100%)	0	100	100
11	K	172/196 (88%)	172 (100%)	0	100	100
12	L	54/63 (86%)	54 (100%)	0	100	100
13	M	91/96 (95%)	90 (99%)	1 (1%)	73	89
14	N	117/120 (98%)	117 (100%)	0	100	100
15	O	57/59 (97%)	57 (100%)	0	100	100
16	P	32/37 (86%)	31 (97%)	1 (3%)	40	70
17	Q	31/32 (97%)	31 (100%)	0	100	100
18	S	48/97 (50%)	48 (100%)	0	100	100
All	All	2978/3381 (88%)	2974 (100%)	4 (0%)	93	98

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	91	VAL
8	H	330	ARG
13	M	97	ARG
16	P	33	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
9	I	150	GLN
11	K	203	ASN
15	O	65	GLN
13	M	11	HIS
6	F	54	HIS

5.3.3 RNA ⓘ

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
19	SF4	K	301	-	0,12,12	-	-	-		
19	SF4	I	202	-	0,12,12	-	-	-		
19	SF4	I	201	-	0,12,12	-	-	-		

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
19	SF4	K	301	-	-	-	0/6/5/5
19	SF4	I	202	-	-	-	0/6/5/5
19	SF4	I	201	-	-	-	0/6/5/5

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-0415. These allow visual inspection of the internal detail of the map and identification of artifacts.

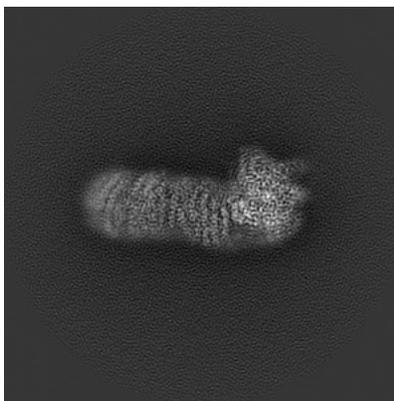
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

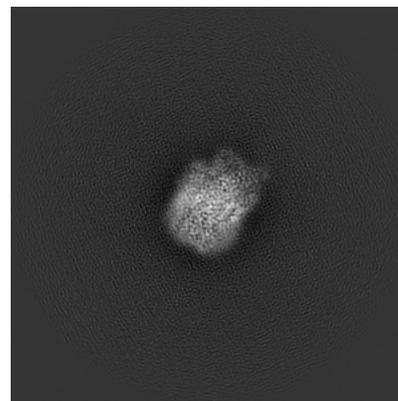
6.1.1 Primary map



X



Y

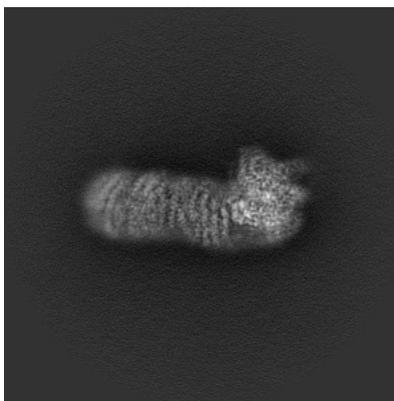


Z

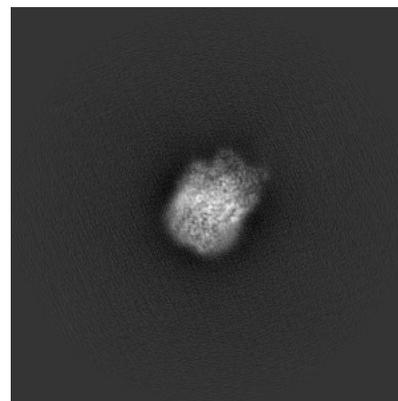
6.1.2 Raw map



X



Y

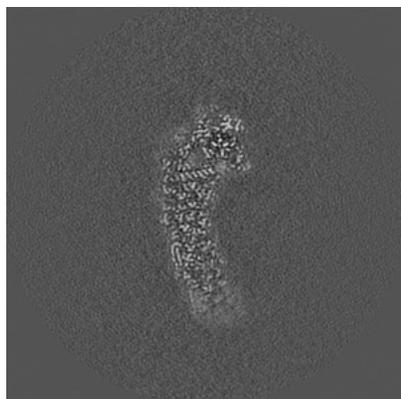


Z

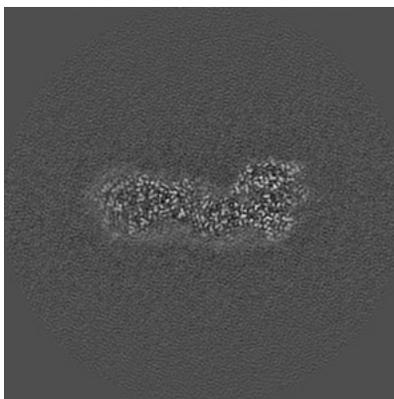
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

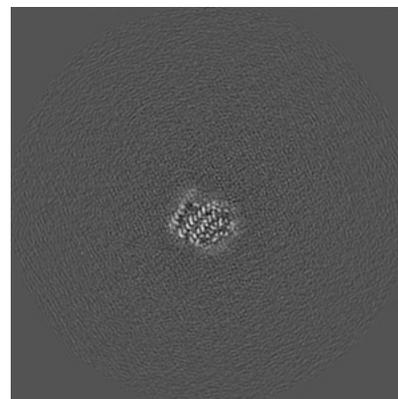
6.2.1 Primary map



X Index: 180

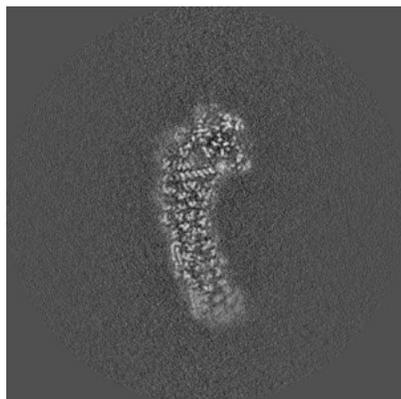


Y Index: 180

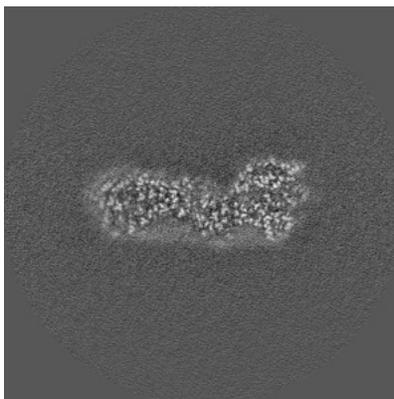


Z Index: 180

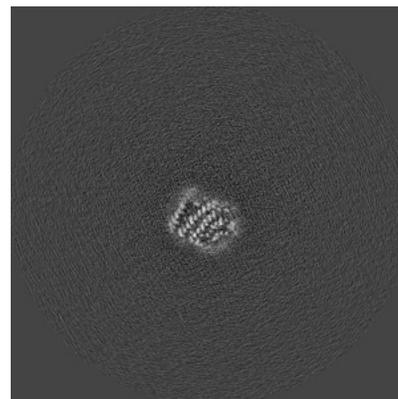
6.2.2 Raw map



X Index: 180



Y Index: 180

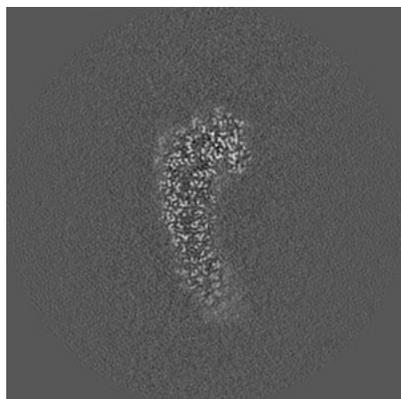


Z Index: 180

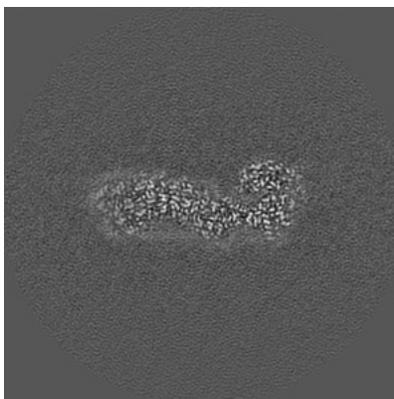
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

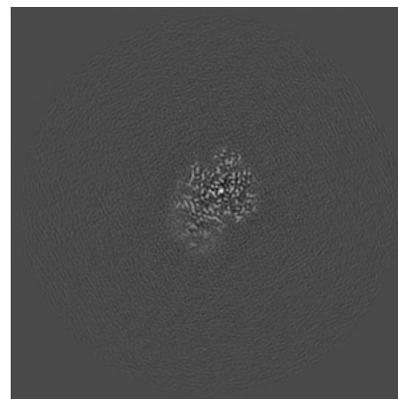
6.3.1 Primary map



X Index: 173



Y Index: 178

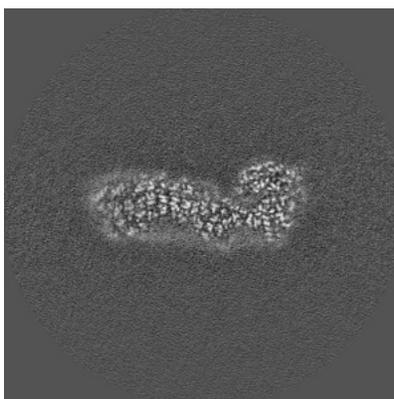


Z Index: 239

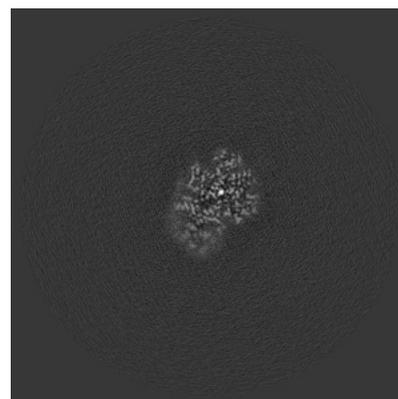
6.3.2 Raw map



X Index: 181



Y Index: 178



Z Index: 239

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



X



Y



Z

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.

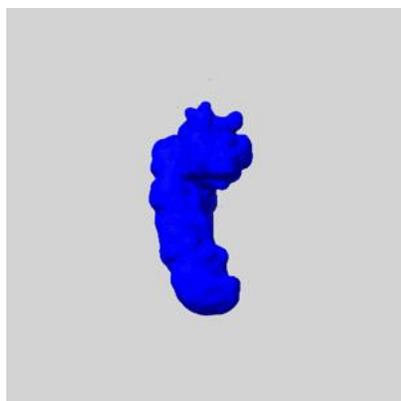
6.5 Mask visualisation [i](#)

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

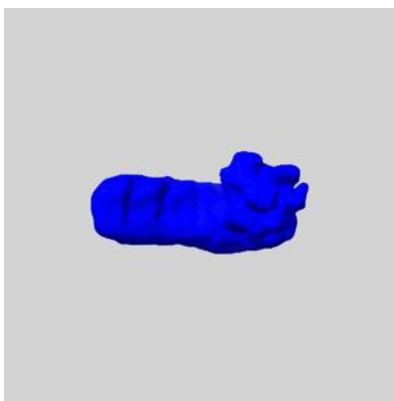
A mask typically either:

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

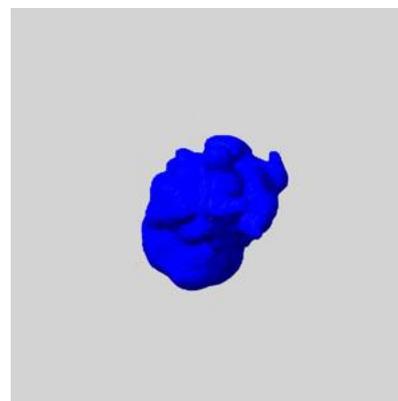
6.5.1 emd_0415_msk_1.map [i](#)



X



Y

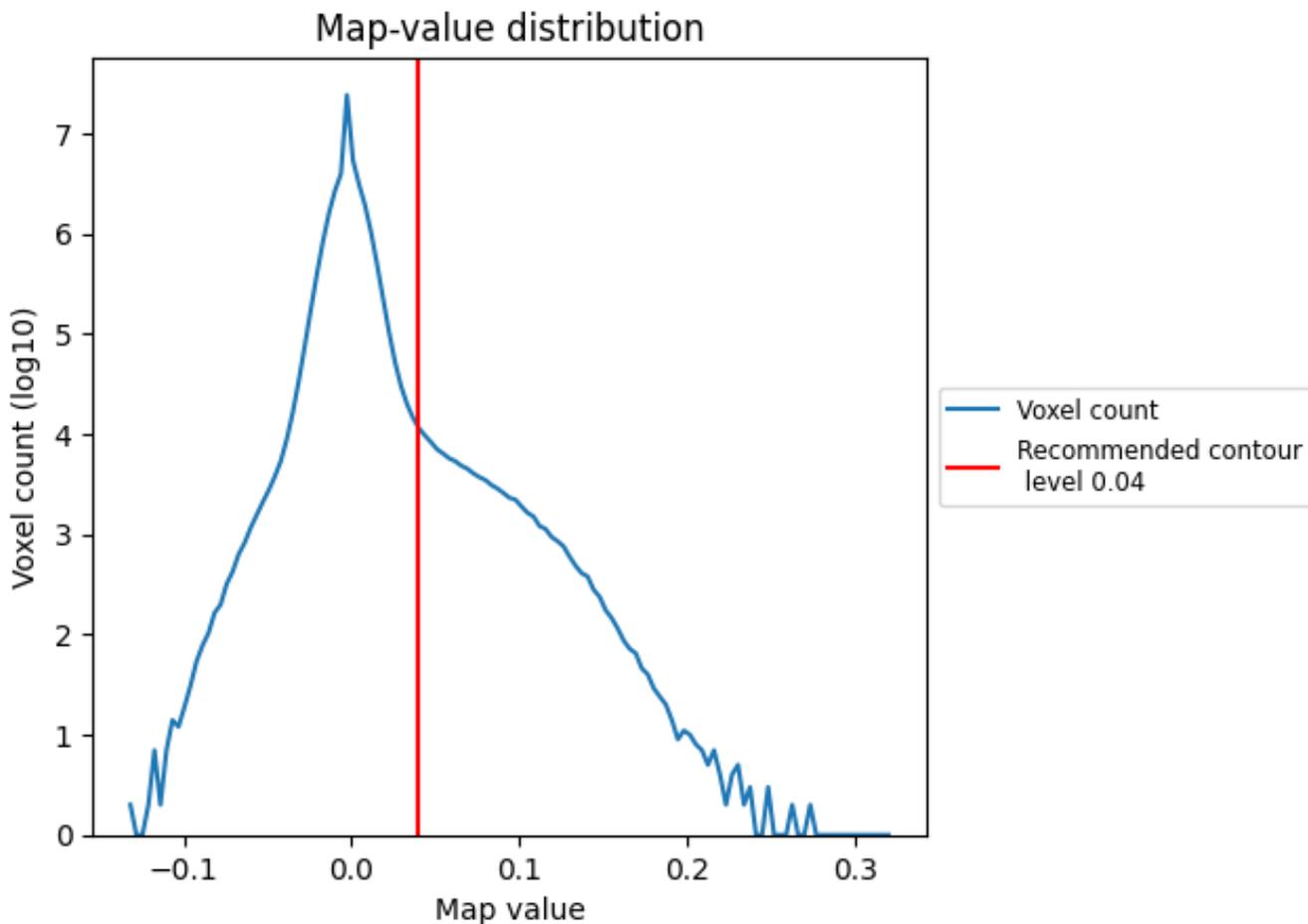


Z

7 Map analysis [i](#)

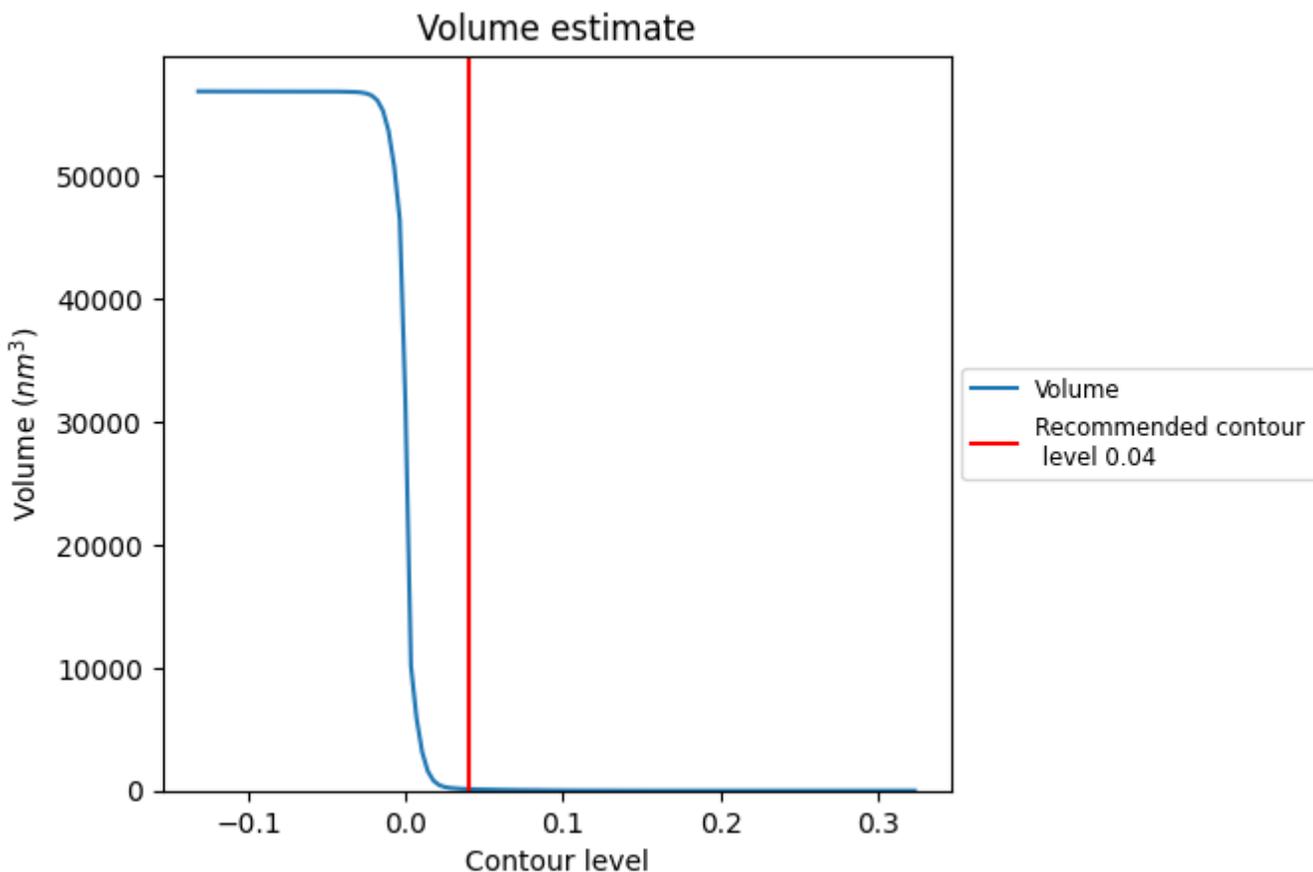
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

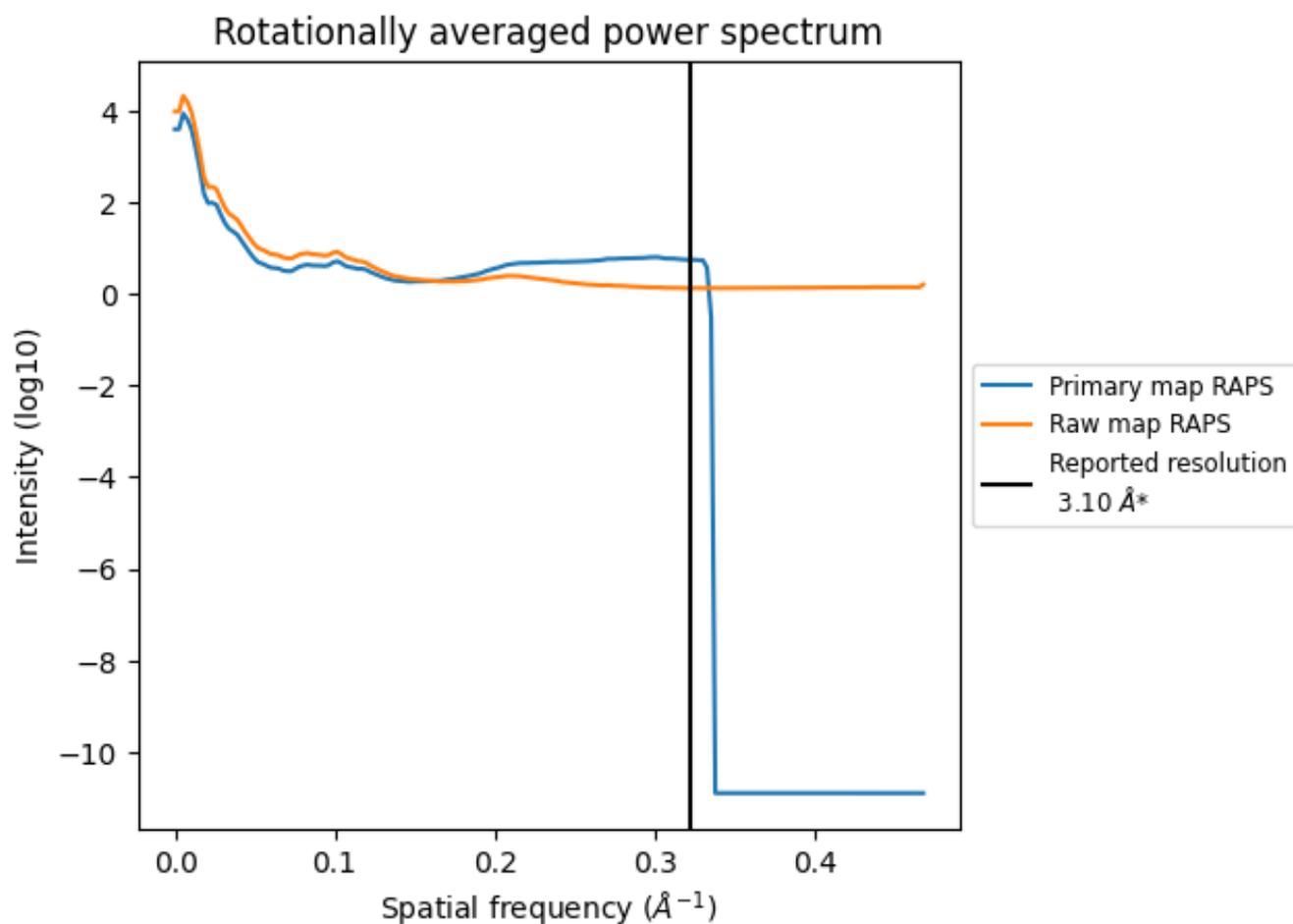
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 125 nm³; this corresponds to an approximate mass of 113 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

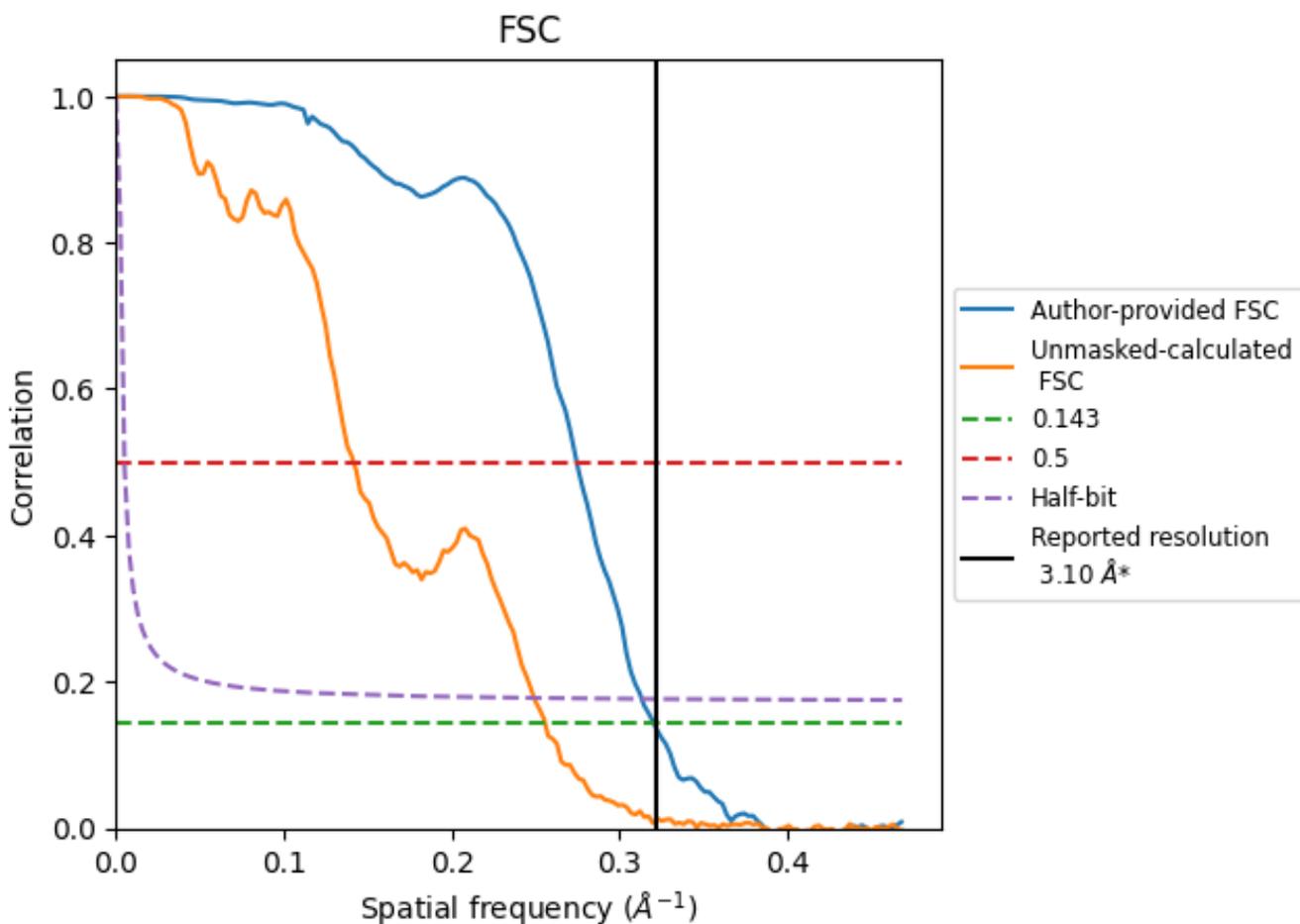


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 \AA^{-1}

8.2 Resolution estimates [i](#)

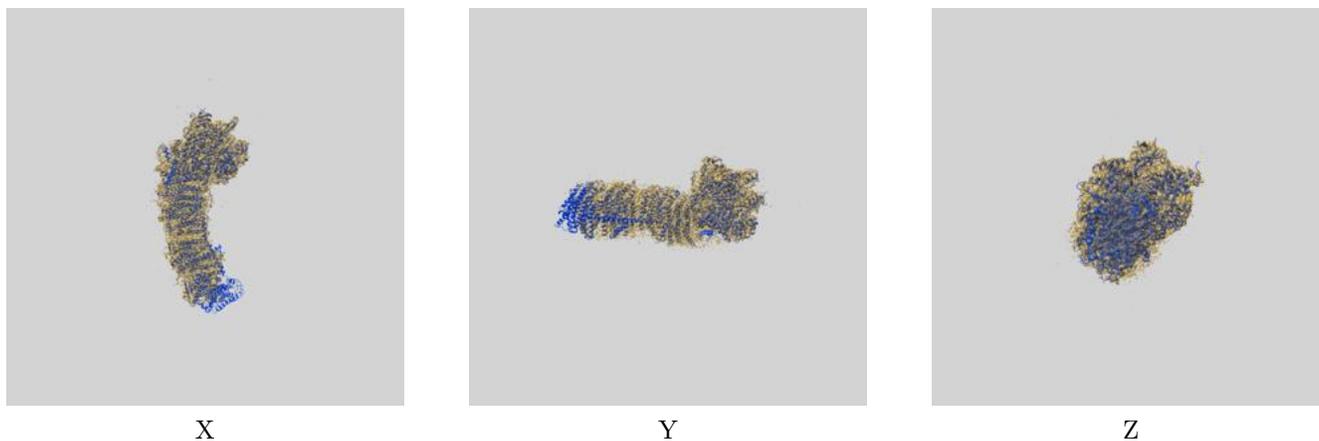
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.12	3.64	3.19
Unmasked-calculated*	3.91	7.06	4.01

*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 3.91 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

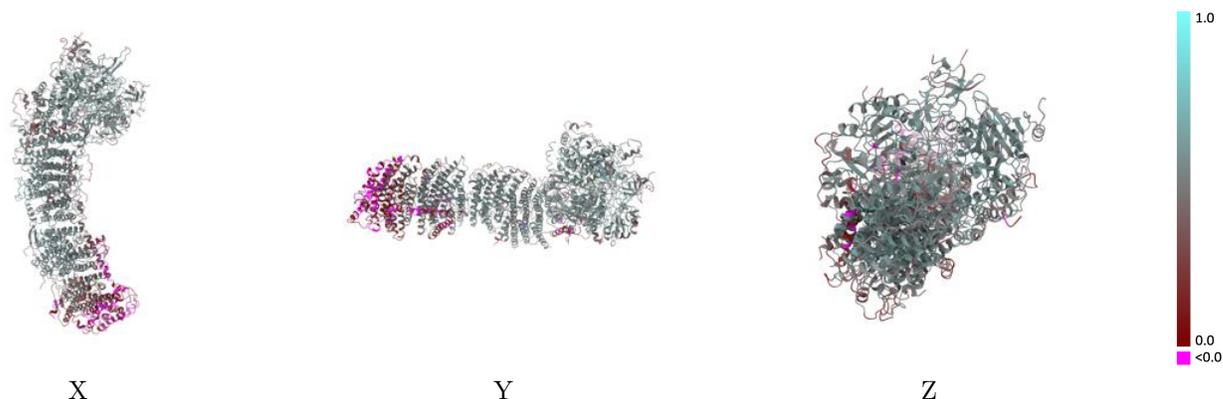
This section contains information regarding the fit between EMDB map EMD-0415 and PDB model 6NBY. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



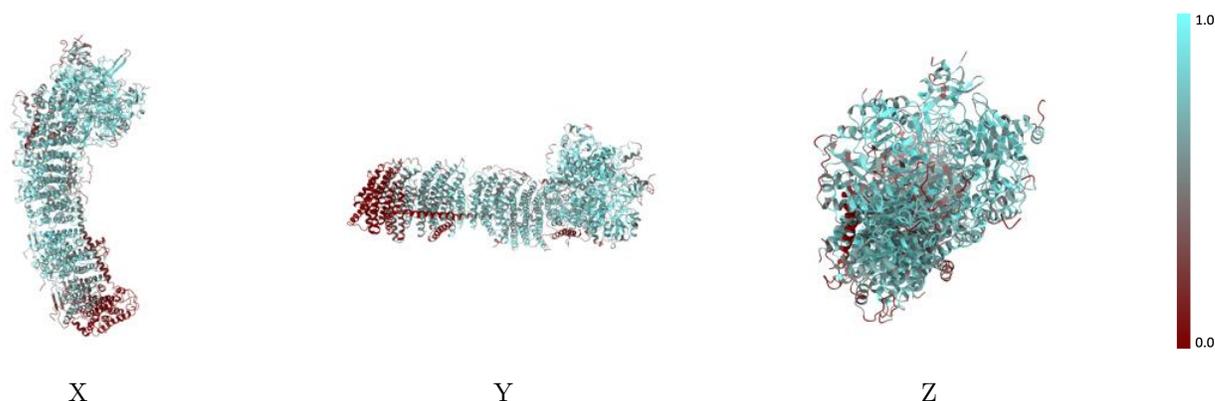
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



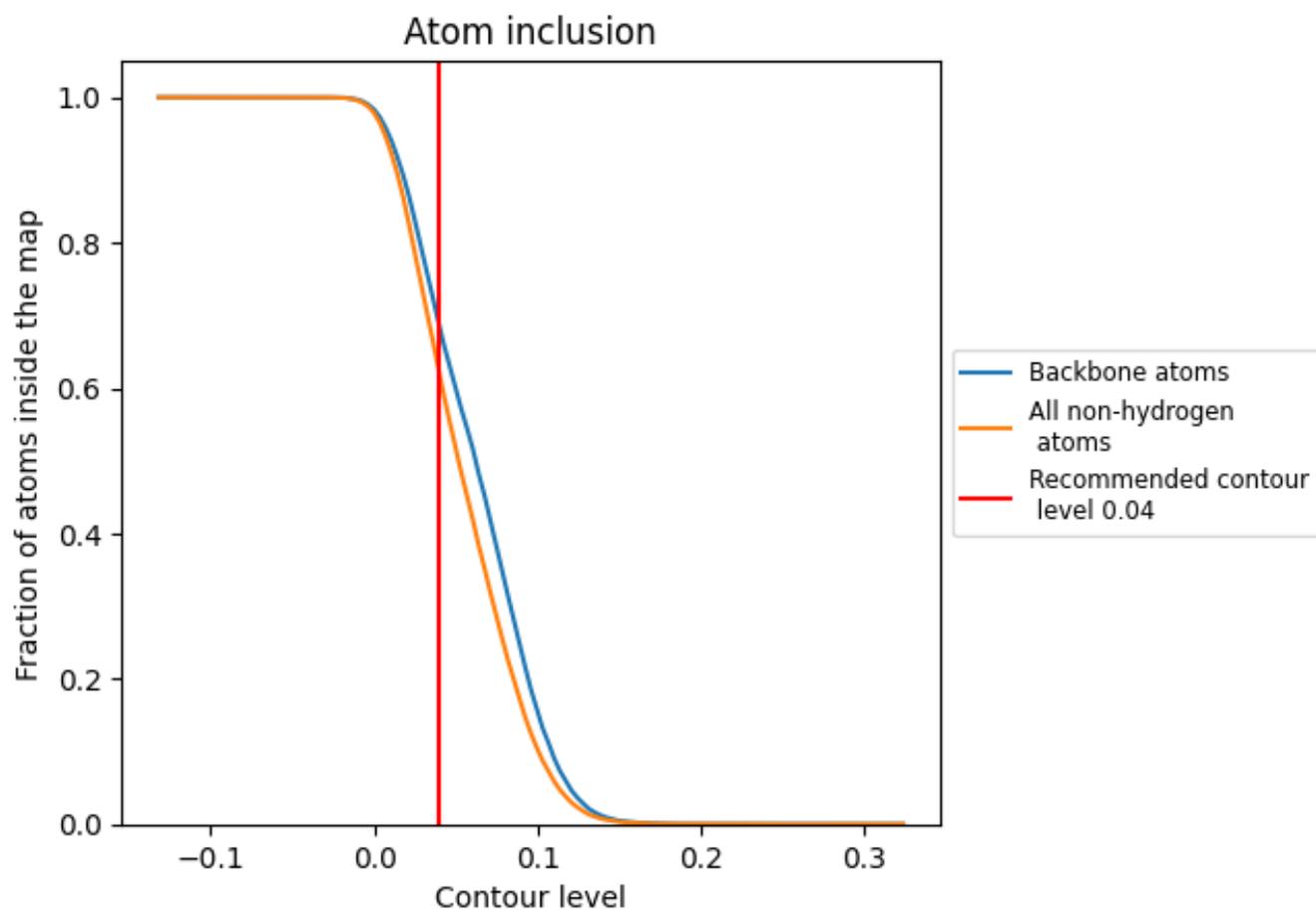
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 62% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6187	 0.4590
A	 0.6635	 0.4880
B	 0.7506	 0.5370
C	 0.5315	 0.4080
D	 0.7133	 0.5180
E	 0.7497	 0.5320
F	 0.2413	 0.2200
G	 0.6334	 0.4870
H	 0.7683	 0.5380
I	 0.6950	 0.4980
J	 0.7476	 0.5250
K	 0.7204	 0.5170
L	 0.5893	 0.4820
M	 0.7385	 0.5270
N	 0.7150	 0.5160
O	 0.7307	 0.5150
P	 0.6306	 0.4650
Q	 0.0155	 0.1440
S	 0.3816	 0.4280

