



wwPDB EM Validation Summary Report ⓘ

Mar 14, 2026 – 12:48 AM UTC

PDB ID : 6NBX / pdb_00006nbx
EMDB ID : EMD-0425
Title : T.elongatus NDH (data-set 2)
Authors : Laughlin, T.G.; Bayne, A.; Trempe, J.-F.; Savage, D.F.; Davies, K.M.
Deposited on : 2018-12-10
Resolution : 3.50 Å (reported)
Based on initial model : 6NBQ

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:

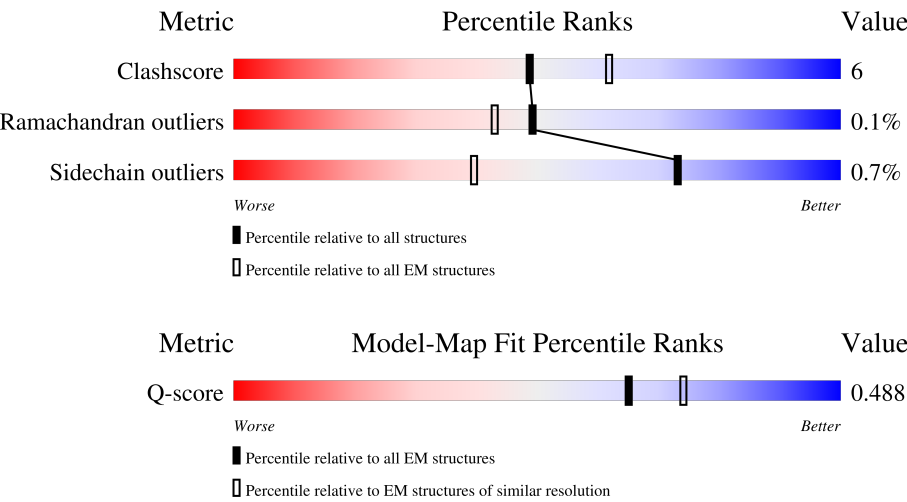
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 i

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

The reported resolution of this entry is 3.50 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.



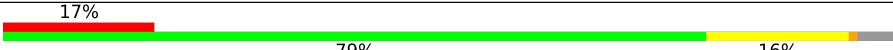
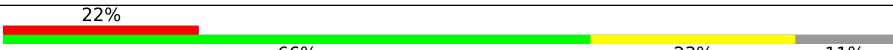
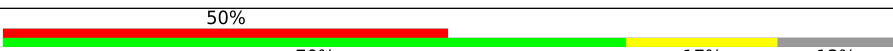
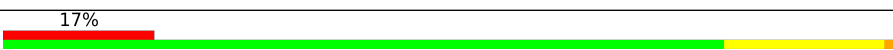
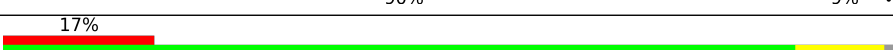
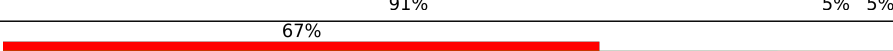
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	19% 74% 16% 10%
2	B	515	82% 11% 6%
3	C	132	18% 67% 9% 24%
4	D	529	8% 84% 10% 5%

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Mol	Chain	Length	Quality of chain
5	E	101	
6	F	656	
7	G	200	
8	H	394	
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
1	A	335	Total	C	N	O	S	0	0
			2494	1685	398	401	10		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

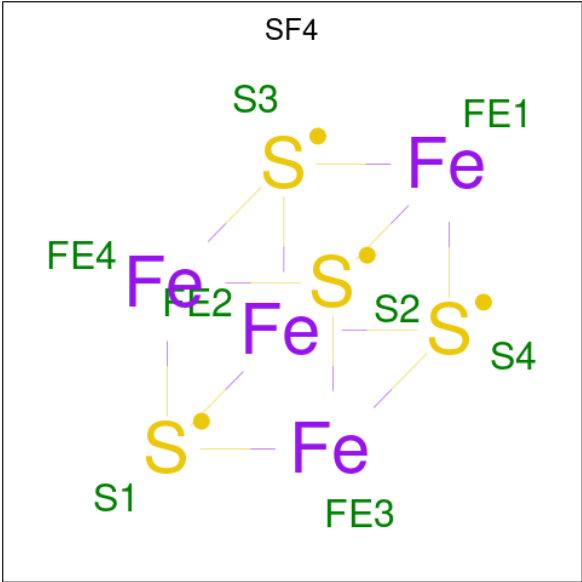
- Molecule 17 is a protein called Proton-translocating NADH-quinone dehydrogenase subunit Q NdhQ.

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

- Molecule 18 is a protein called Tlr0636 protein.

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

- Molecule 19 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).

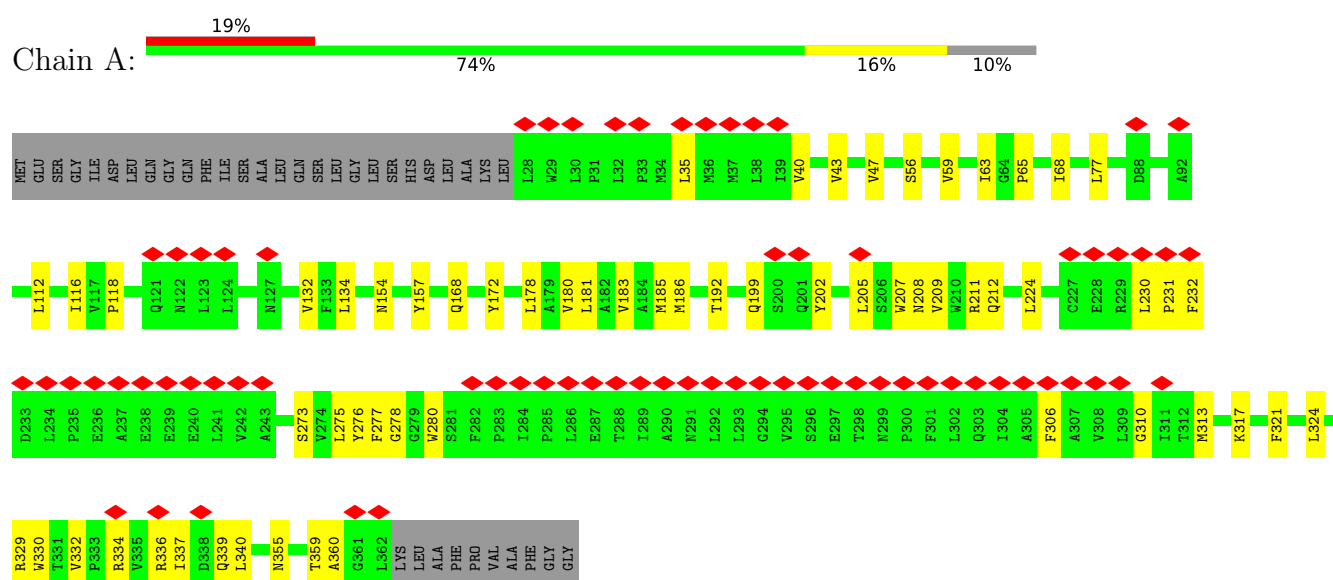


Mol	Chain	Residues	Atoms			AltConf
19	I	1	Total	Fe	S	0
			8	4	4	
19	I	1	Total	Fe	S	0
			8	4	4	
19	K	1	Total	Fe	S	0
			8	4	4	

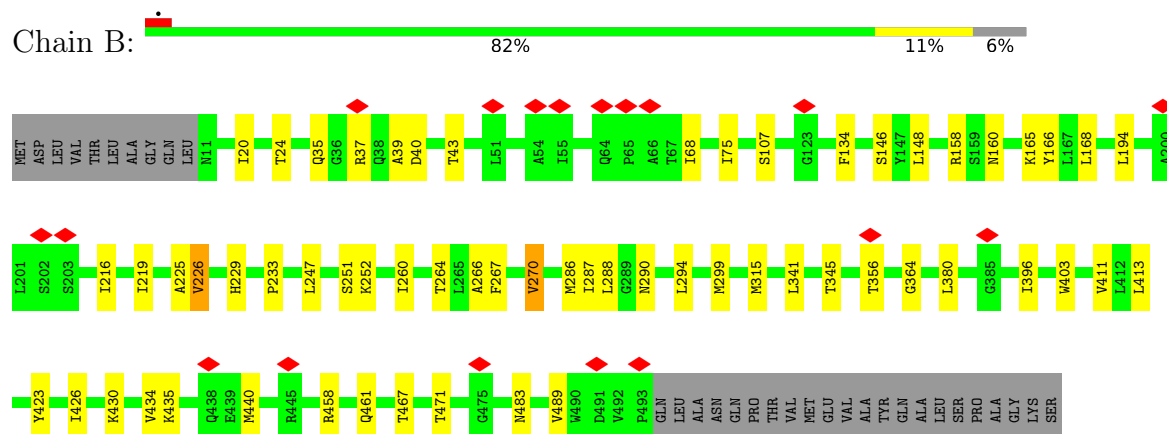
3 Residue-property plots

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

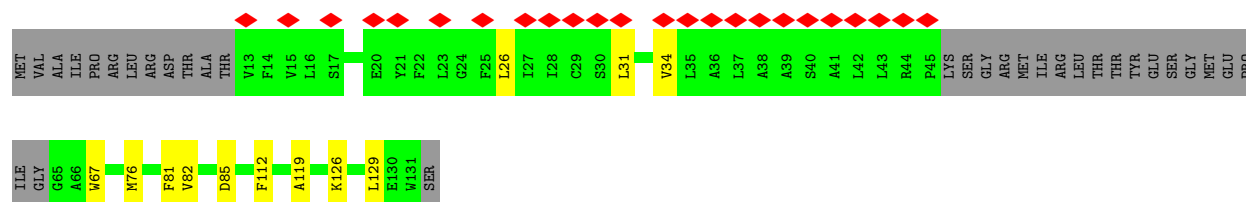


- Molecule 2: NAD(P)H-quinone oxidoreductase subunit 2

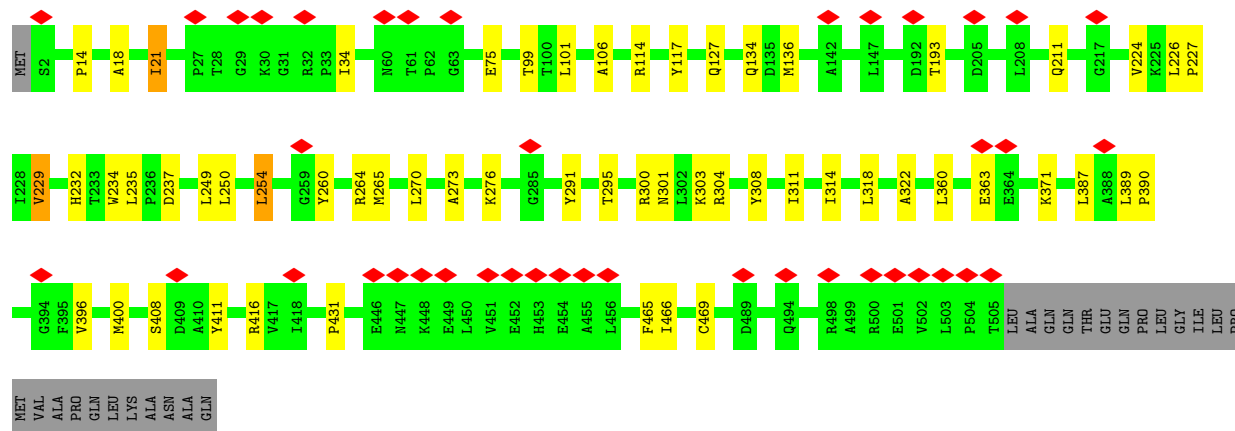
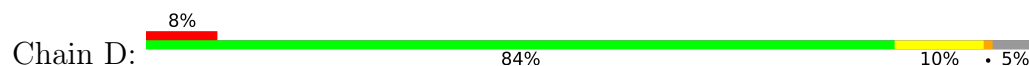


- Molecule 3: NAD(P)H-quinone oxidoreductase subunit 3

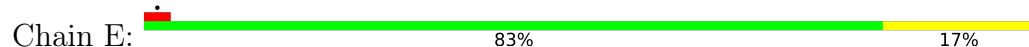




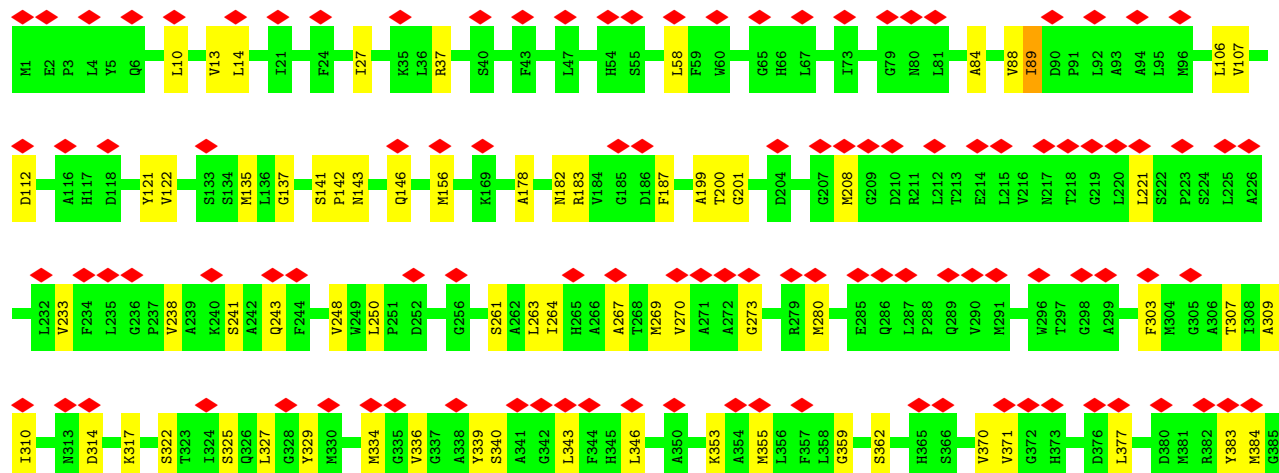
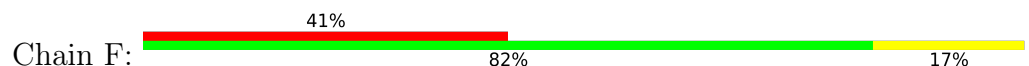
• Molecule 4: NAD(P)H-quinone oxidoreductase chain 4 1

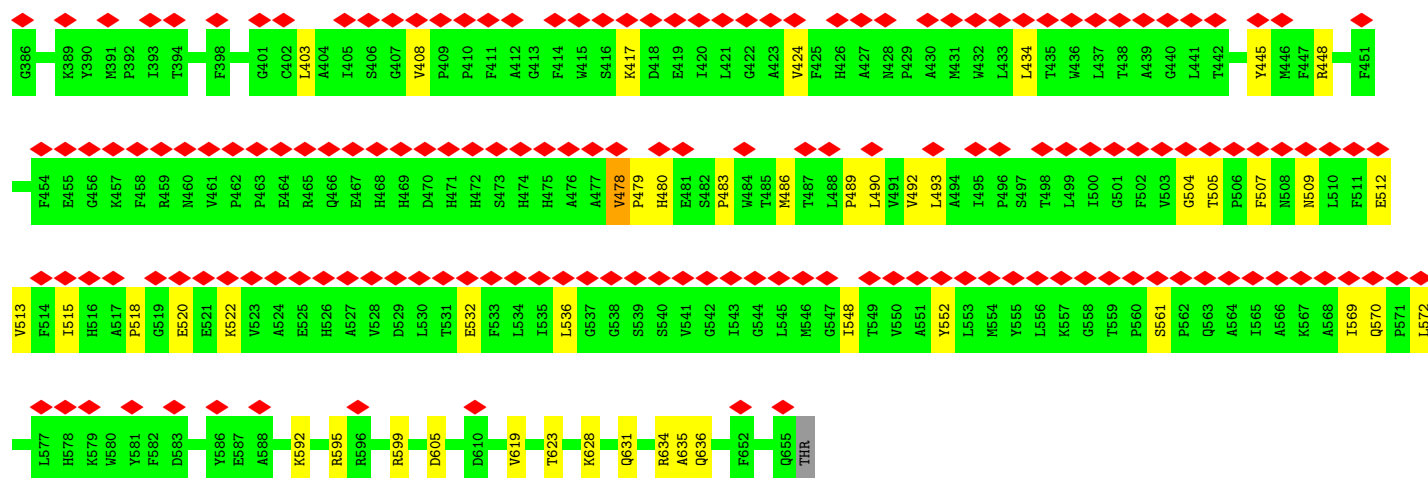


• Molecule 5: NAD(P)H-quinone oxidoreductase subunit 4L

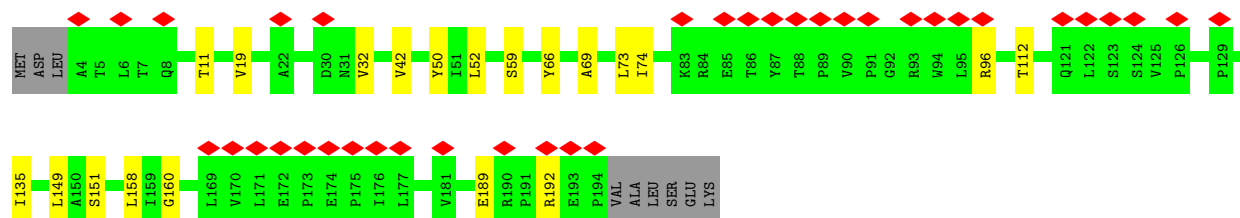
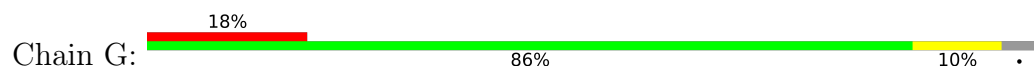


• Molecule 6: NADH dehydrogenase subunit 5

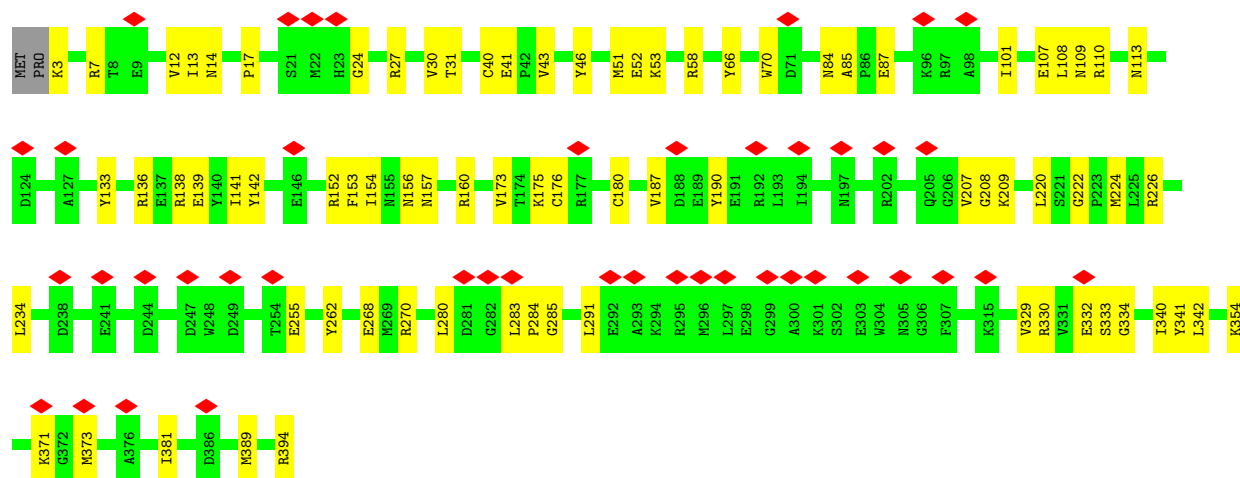
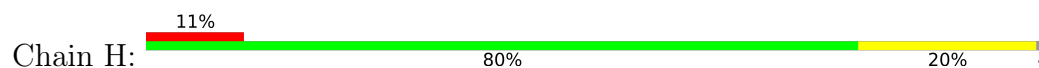




• Molecule 7: NADH-quinone oxidoreductase subunit J

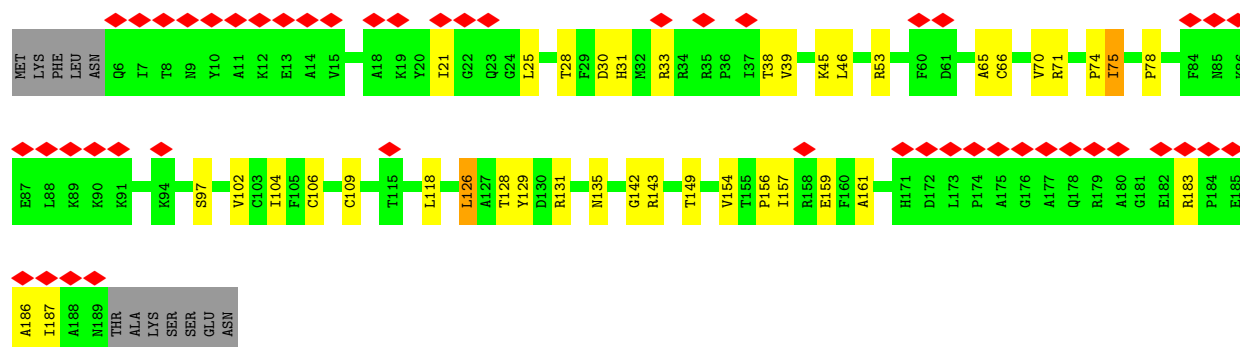


• Molecule 8: NAD(P)H-quinone oxidoreductase subunit H

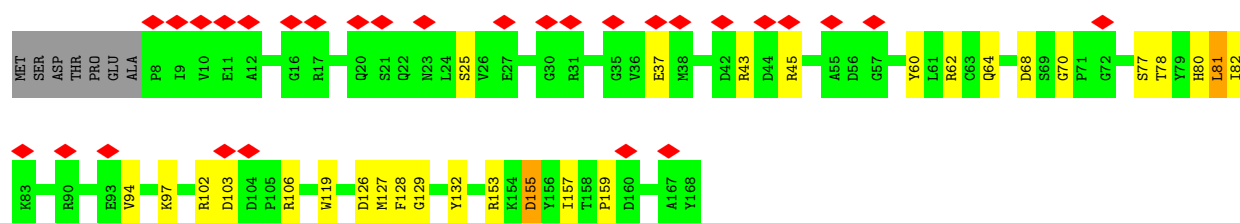
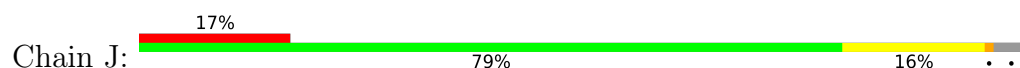


• Molecule 9: NAD(P)H-quinone oxidoreductase subunit I

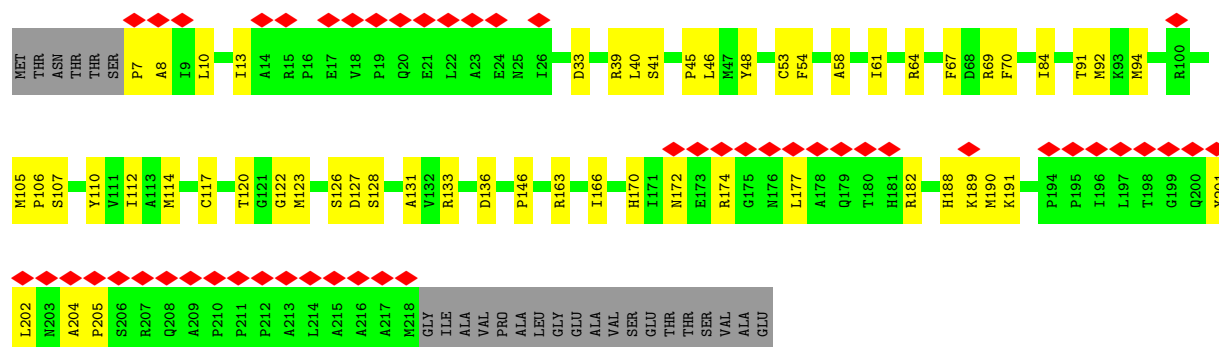




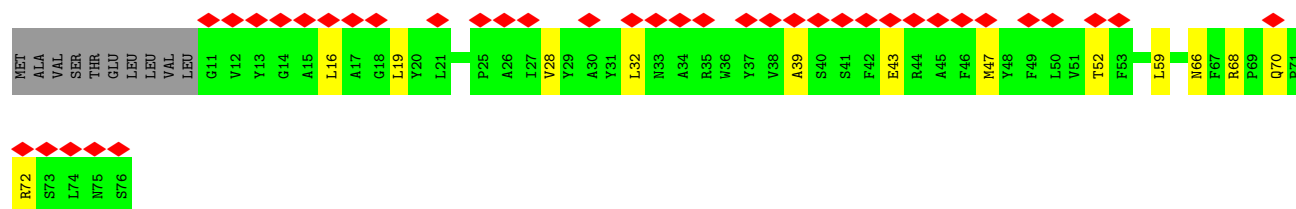
• Molecule 10: NAD(P)H-quinone oxidoreductase subunit J



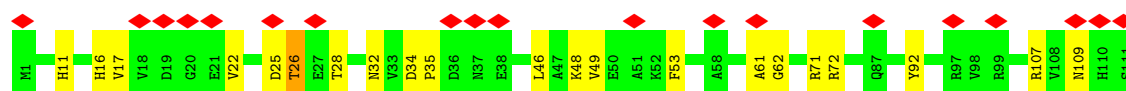
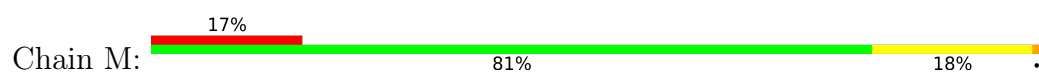
• Molecule 11: NAD(P)H-quinone oxidoreductase subunit K



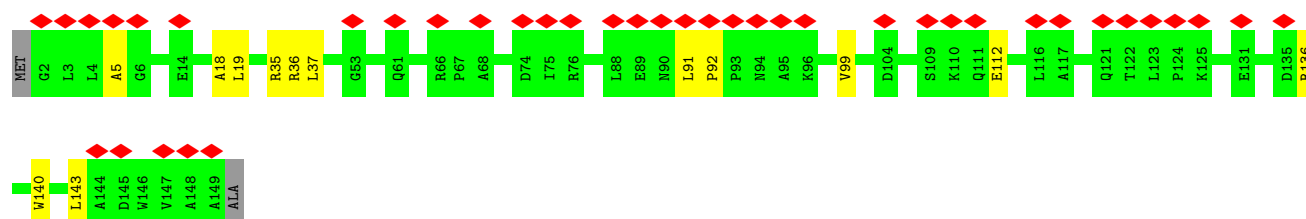
• Molecule 12: NAD(P)H-quinone oxidoreductase subunit L



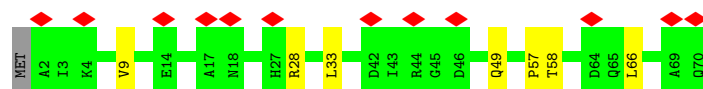
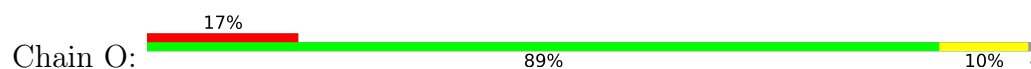
• Molecule 13: NAD(P)H-quinone oxidoreductase subunit M



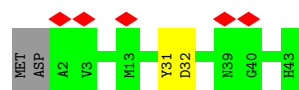
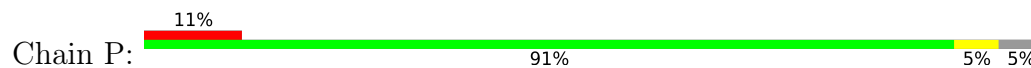
• Molecule 14: NAD(P)H-quinone oxidoreductase subunit N



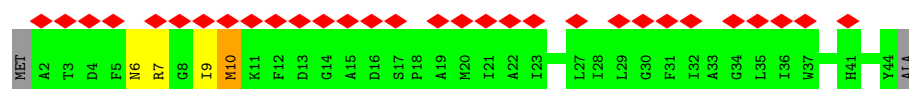
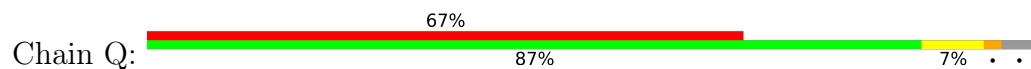
• Molecule 15: NAD(P)H-quinone oxidoreductase subunit O



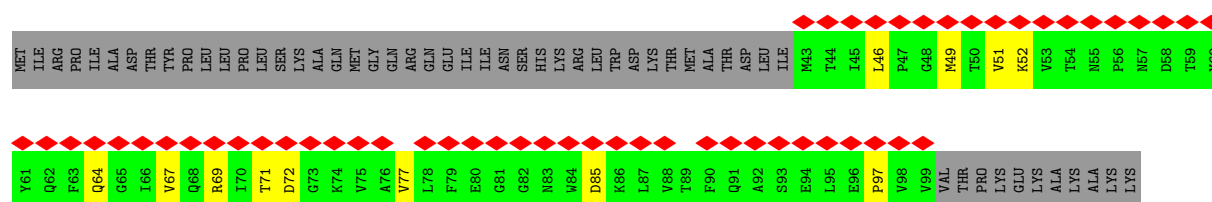
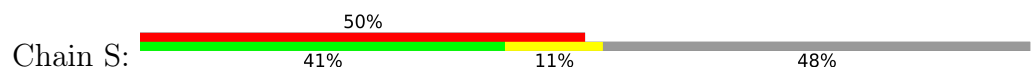
• Molecule 16: Proton-translocating NADH-quinone dehydrogenase subunit P NdhP



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



• Molecule 18: Tlr0636 protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	34655	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 ($e^-/\text{\AA}^2$)	60	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	41.702	Depositor
Minimum map value	-14.495	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.842	Depositor
Recommended contour level	5.5	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	0.40	0/2560	0.59	0/3510
2	B	0.44	0/3665	0.61	1/5008 (0.0%)
3	C	0.35	0/820	0.54	0/1125
4	D	0.42	0/3924	0.60	0/5364
5	E	0.44	0/782	0.52	0/1063
6	F	0.33	1/5040 (0.0%)	0.63	2/6882 (0.0%)
7	G	0.39	0/1401	0.62	0/1926
8	H	0.41	0/3187	0.59	0/4325
9	I	0.37	0/1481	0.59	0/2013
10	J	0.37	0/1332	0.55	1/1816 (0.1%)
11	K	0.48	0/1657	0.63	0/2258
12	L	0.26	0/556	0.54	0/760
13	M	0.37	0/882	0.53	0/1198
14	N	0.32	0/1190	0.50	0/1619
15	O	0.32	0/555	0.51	0/755
16	P	0.33	0/327	0.65	0/445
17	Q	0.23	0/336	0.62	0/457
18	S	0.27	0/449	0.57	0/612
All	All	0.39	1/30144 (0.0%)	0.59	4/41136 (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	3
11	K	0	1
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	89	ILE	C-N	-5.06	1.23	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
10	J	119	TRP	CA-CB-CG	6.33	125.62	113.60
2	B	489	VAL	CB-CA-C	5.75	117.15	110.88
6	F	504	GLY	CA-C-N	5.00	129.93	121.92
6	F	504	GLY	C-N-CA	5.00	129.93	121.92

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	F	383	TYR	Peptide
6	F	384	MET	Peptide
6	F	561	SER	Peptide
11	K	106	PRO	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	38	0
2	B	3579	0	3707	38	0
3	C	793	0	808	10	0
4	D	3817	0	3937	36	0
5	E	772	0	827	13	0
6	F	4902	0	4841	68	0
7	G	1373	0	1396	17	0
8	H	3105	0	3060	53	0
9	I	1444	0	1399	27	0
10	J	1295	0	1254	18	0
11	K	1615	0	1657	40	0
12	L	536	0	539	10	0
13	M	866	0	847	18	0
14	N	1158	0	1170	9	0
15	O	543	0	553	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	P	318	0	309	2	0
17	Q	327	0	326	4	0
18	S	440	0	440	6	0
19	I	16	0	0	0	0
19	K	8	0	0	0	0
All	All	29401	0	29640	343	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 343 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)
4:D:21:ILE:HG23	4:D:34:ILE:HD11	1.71	0.71
4:D:211:GLN:HB3	4:D:273:ALA:HB2	1.74	0.68
10:J:62:ARG:HH21	10:J:80:HIS:HE1	1.41	0.68
2:B:364:GLY:HA3	2:B:440:MET:HB3	1.77	0.66
8:H:24:GLY:HA3	8:H:389:MET:HB2	1.79	0.64

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%)	299 (90%)	34 (10%)	0	100	100
2	B	481/515 (93%)	445 (92%)	36 (8%)	0	100	100
3	C	96/132 (73%)	88 (92%)	8 (8%)	0	100	100
4	D	502/529 (95%)	465 (93%)	37 (7%)	0	100	100
5	E	99/101 (98%)	94 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	653/656 (100%)	599 (92%)	51 (8%)	3 (0%)	24	57
7	G	189/200 (94%)	168 (89%)	21 (11%)	0	100	100
8	H	390/394 (99%)	359 (92%)	31 (8%)	0	100	100
9	I	182/196 (93%)	164 (90%)	17 (9%)	1 (0%)	24	57
10	J	159/168 (95%)	148 (93%)	11 (7%)	0	100	100
11	K	210/237 (89%)	181 (86%)	29 (14%)	0	100	100
12	L	64/76 (84%)	59 (92%)	5 (8%)	0	100	100
13	M	109/111 (98%)	95 (87%)	14 (13%)	0	100	100
14	N	146/150 (97%)	139 (95%)	7 (5%)	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%)	34 (83%)	6 (15%)	1 (2%)	4	29
18	S	55/110 (50%)	42 (76%)	13 (24%)	0	100	100
All	All	3816/4106 (93%)	3475 (91%)	336 (9%)	5 (0%)	49	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	479	PRO
9	I	65	ALA
6	F	478	VAL
17	Q	10	MET
6	F	570	GLN

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	245/302 (81%)	245 (100%)	0	100	100
2	B	367/413 (89%)	364 (99%)	3 (1%)	73	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	76/109 (70%)	75 (99%)	1 (1%)	61	72
4	D	381/424 (90%)	377 (99%)	4 (1%)	68	75
5	E	79/82 (96%)	79 (100%)	0	100	100
6	F	484/527 (92%)	481 (99%)	3 (1%)	78	79
7	G	137/166 (82%)	136 (99%)	1 (1%)	76	78
8	H	317/338 (94%)	317 (100%)	0	100	100
9	I	153/172 (89%)	151 (99%)	2 (1%)	61	72
10	J	137/148 (93%)	135 (98%)	2 (2%)	57	71
11	K	172/196 (88%)	169 (98%)	3 (2%)	53	70
12	L	54/63 (86%)	54 (100%)	0	100	100
13	M	91/96 (95%)	90 (99%)	1 (1%)	65	74
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%)	32 (100%)	0	100	100
17	Q	31/32 (97%)	31 (100%)	0	100	100
18	S	48/97 (50%)	47 (98%)	1 (2%)	47	66
All	All	2978/3381 (88%)	2957 (99%)	21 (1%)	73	78

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	J	81	LEU
11	K	112	ILE
18	S	85	ASP
11	K	120	THR
11	K	84	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
8	H	113	ASN
11	K	80	GLN
8	H	157	ASN
9	I	178	GLN
11	K	179	GLN

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](#)

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	I	201	-	0,12,12	-	-	-		
19	SF4	I	202	-	0,12,12	-	-	-		
19	SF4	K	301	-	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	I	201	-	-	-	0/6/5/5
19	SF4	I	202	-	-	-	0/6/5/5
19	SF4	K	301	-	-	-	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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

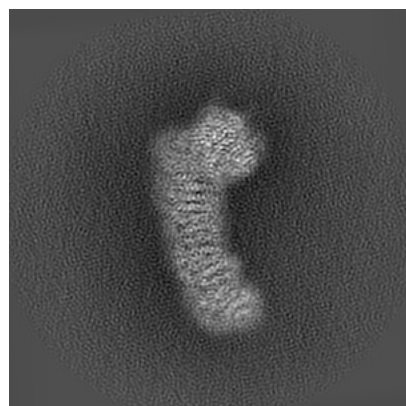
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0425. These allow visual inspection of the internal detail of the map and identification of artifacts.

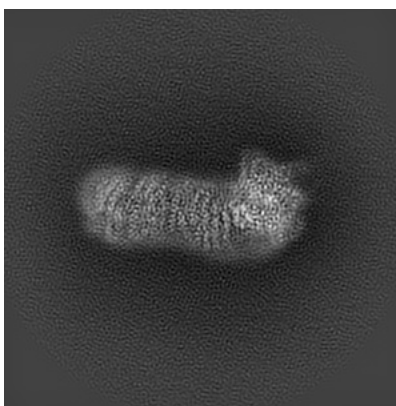
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

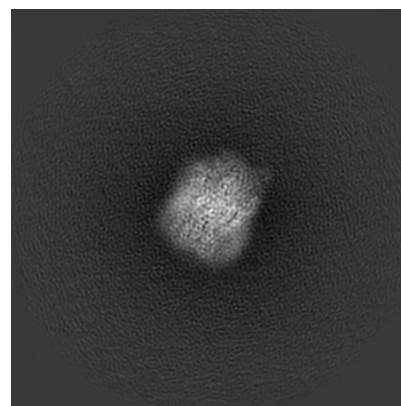
6.1.1 Primary map



X

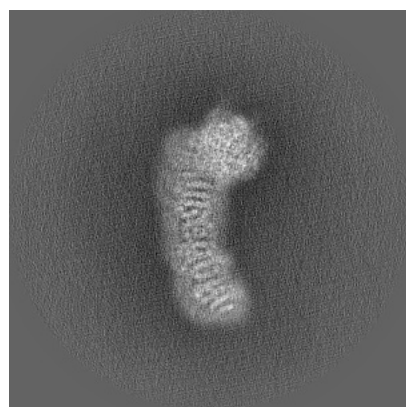


Y

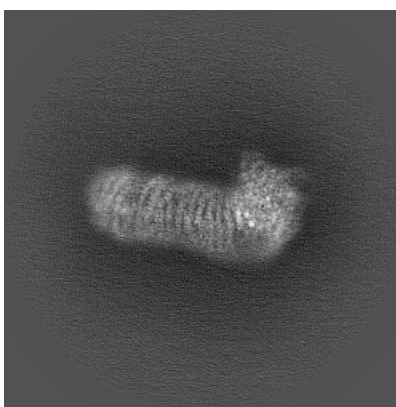


Z

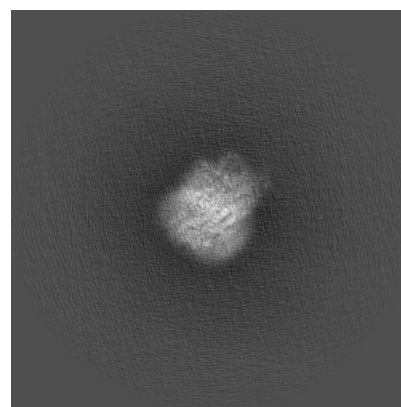
6.1.2 Raw map



X



Y

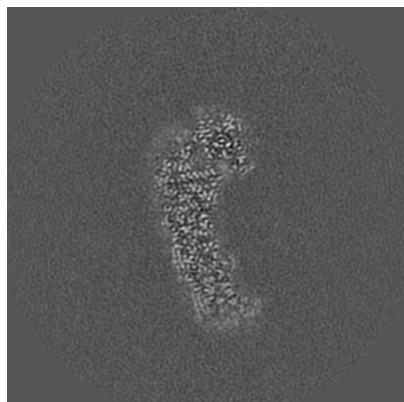


Z

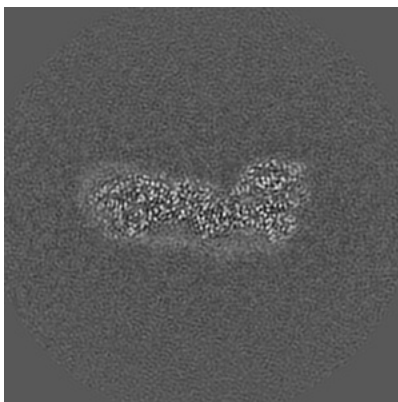
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

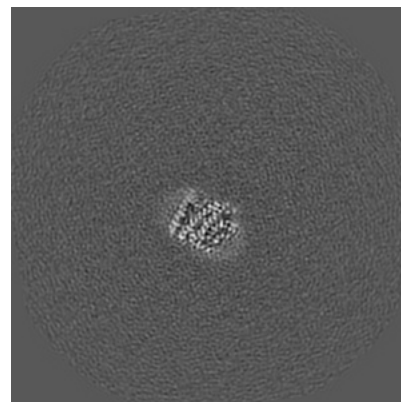
6.2.1 Primary map



X Index: 180

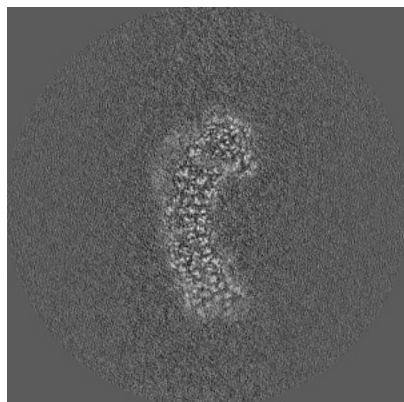


Y Index: 180

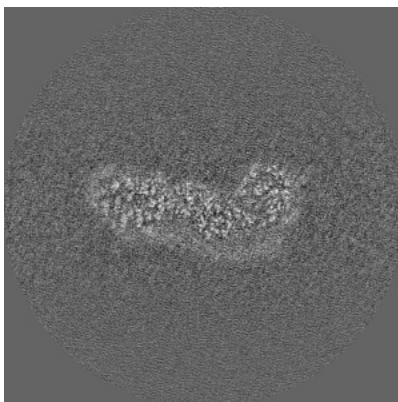


Z Index: 180

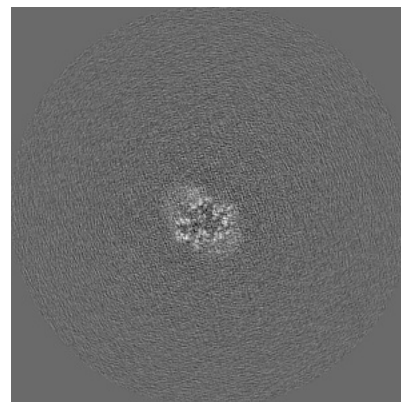
6.2.2 Raw map



X Index: 180



Y Index: 180

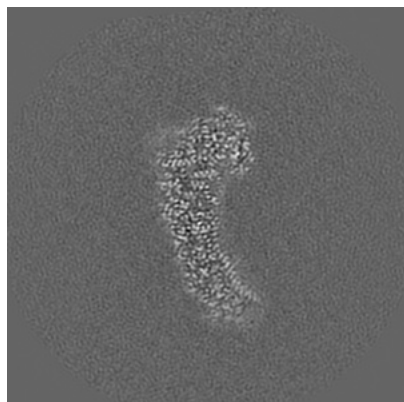


Z Index: 180

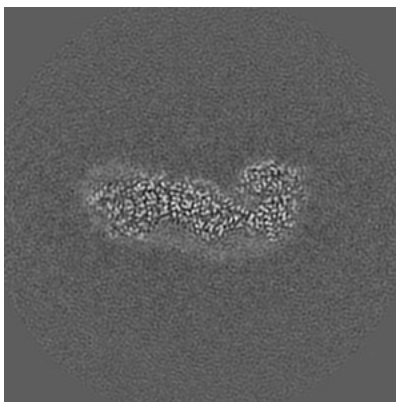
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

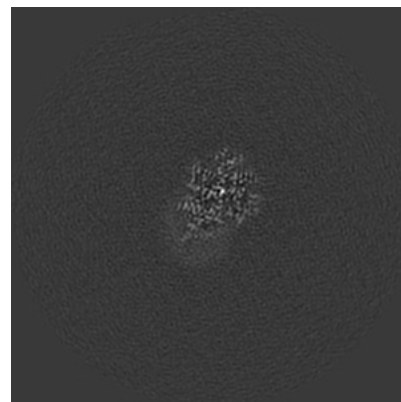
6.3.1 Primary map



X Index: 172

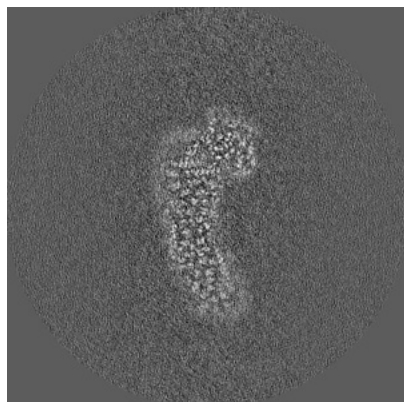


Y Index: 178

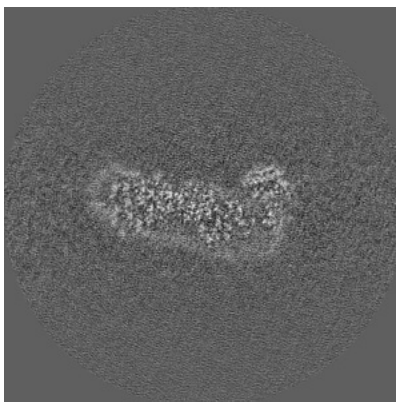


Z Index: 239

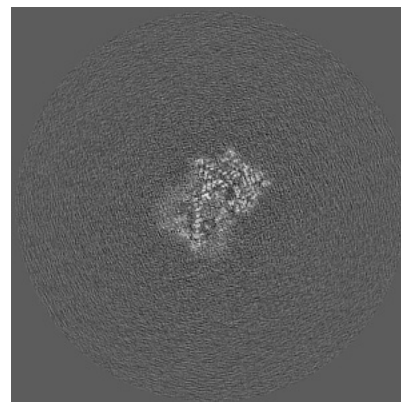
6.3.2 Raw map



X Index: 176



Y Index: 177

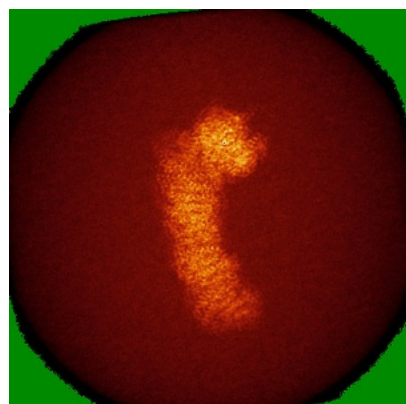


Z Index: 224

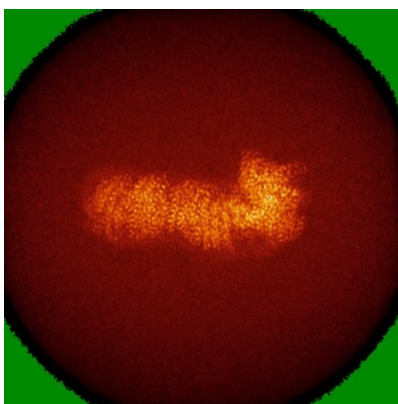
The images above show the largest variance slices of the map in three orthogonal directions.

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

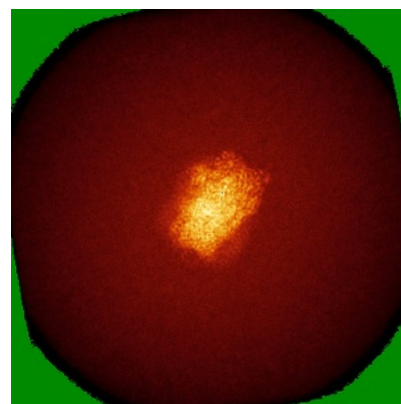
6.4.1 Primary map



X

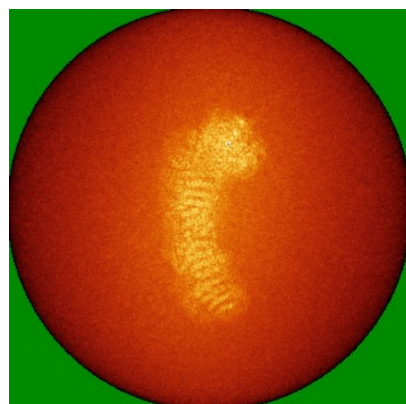


Y

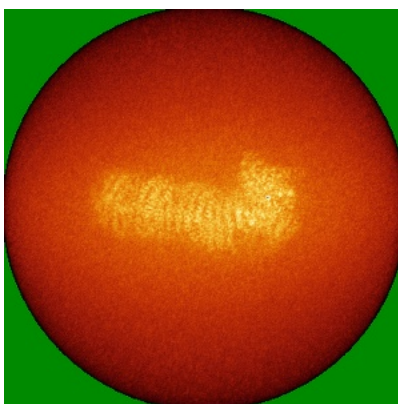


Z

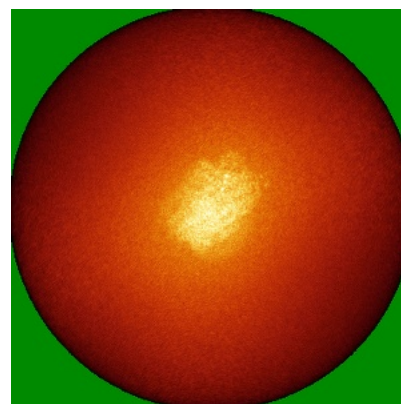
6.4.2 Raw map



X



Y

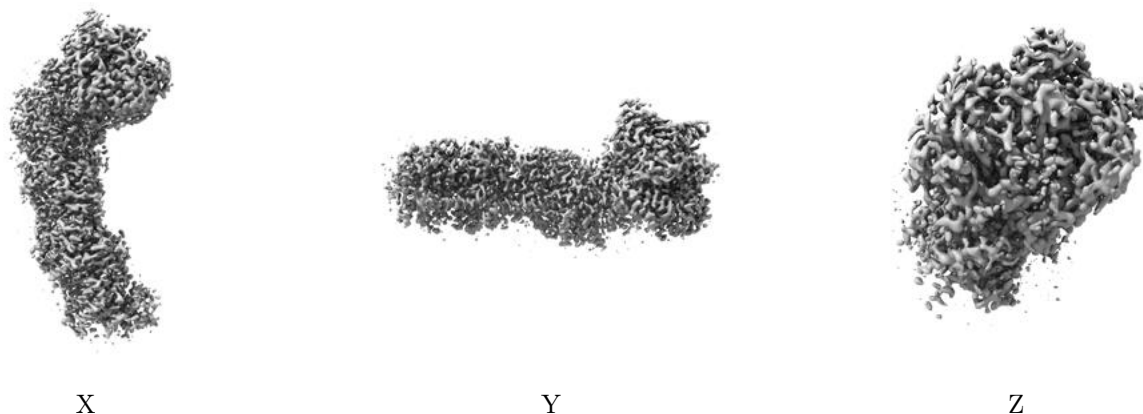


Z

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

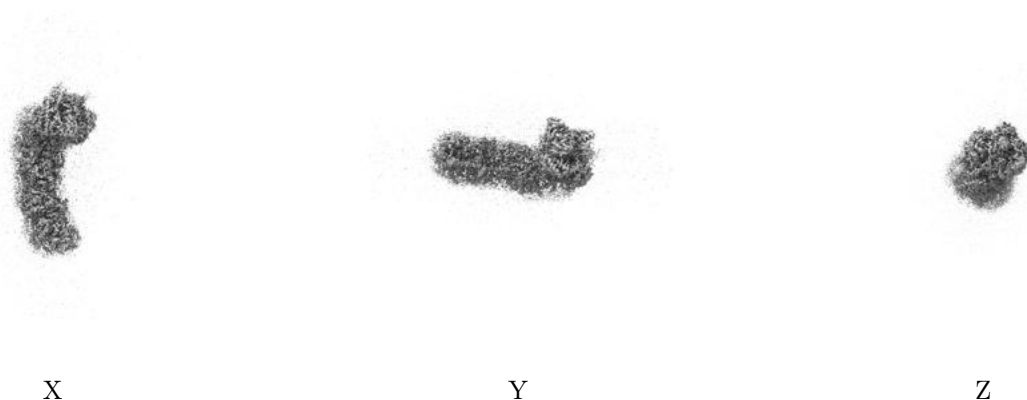
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 5.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

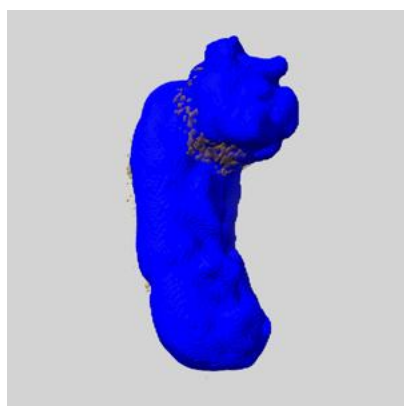
6.6 Mask visualisation [i](#)

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

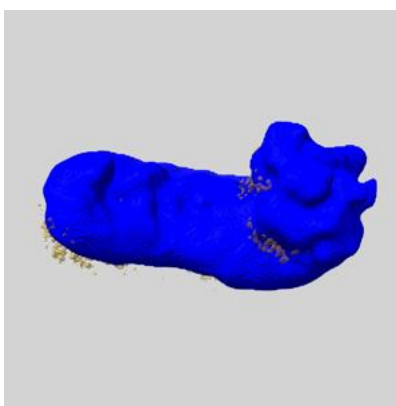
A mask typically either:

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

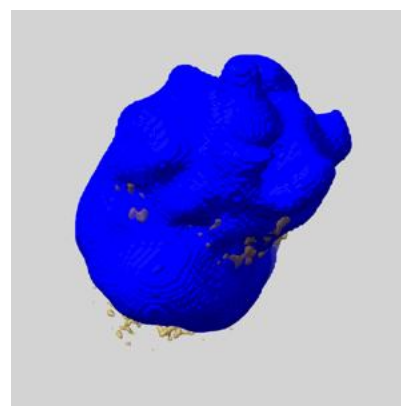
6.6.1 emd_0425_msk_1.map [i](#)



X



Y

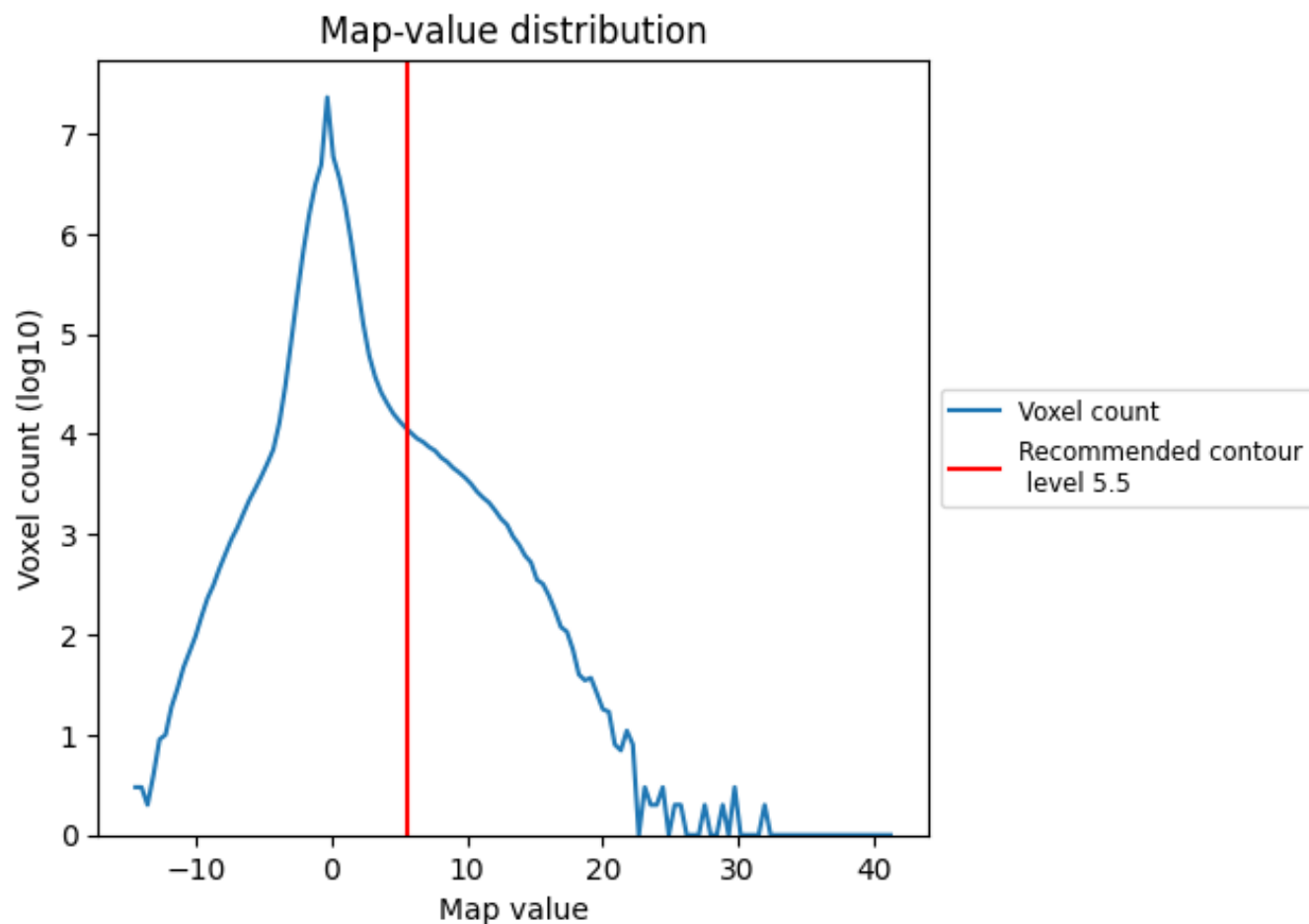


Z

7 Map analysis [i](#)

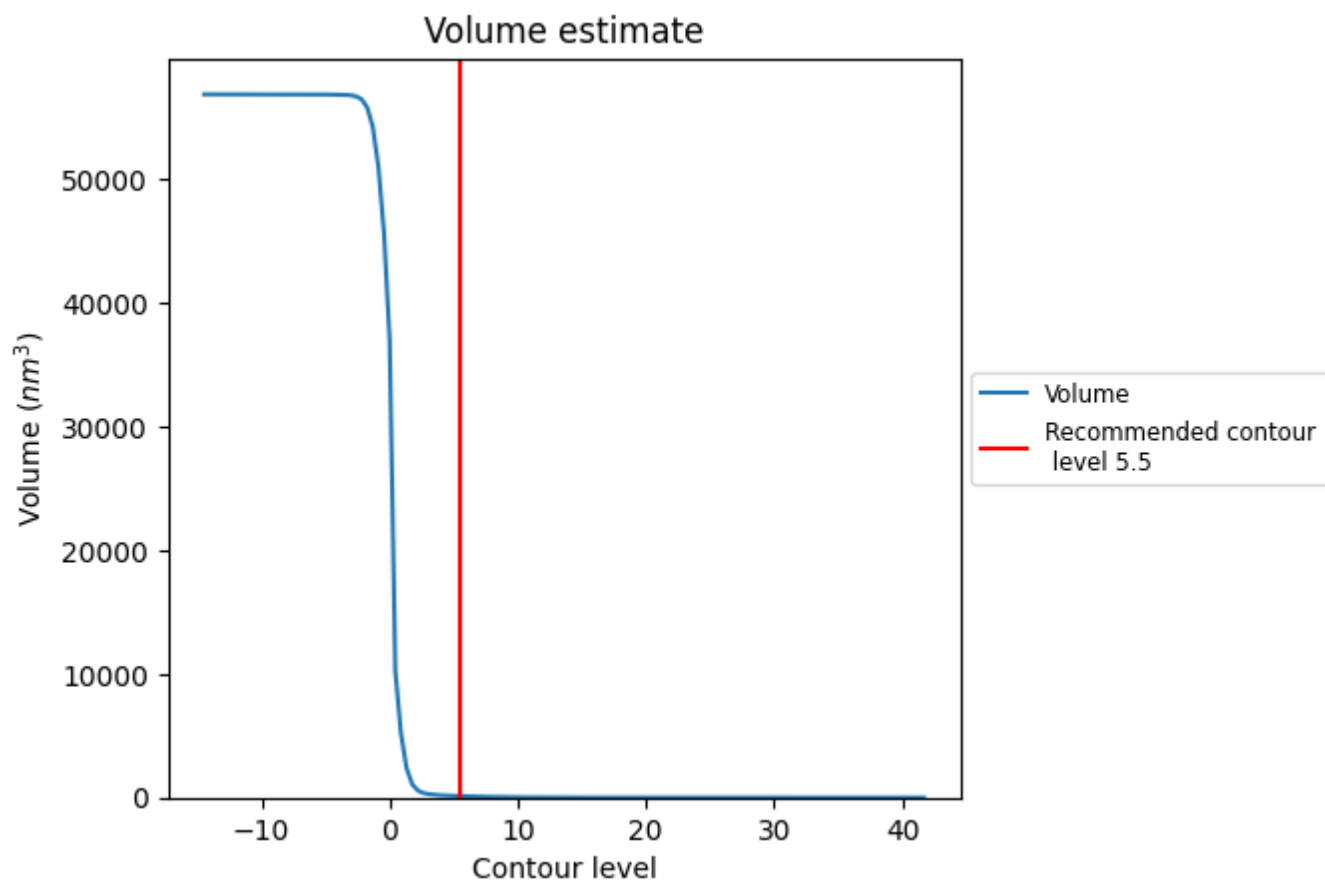
This section contains the results of statistical analysis of the map.

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.

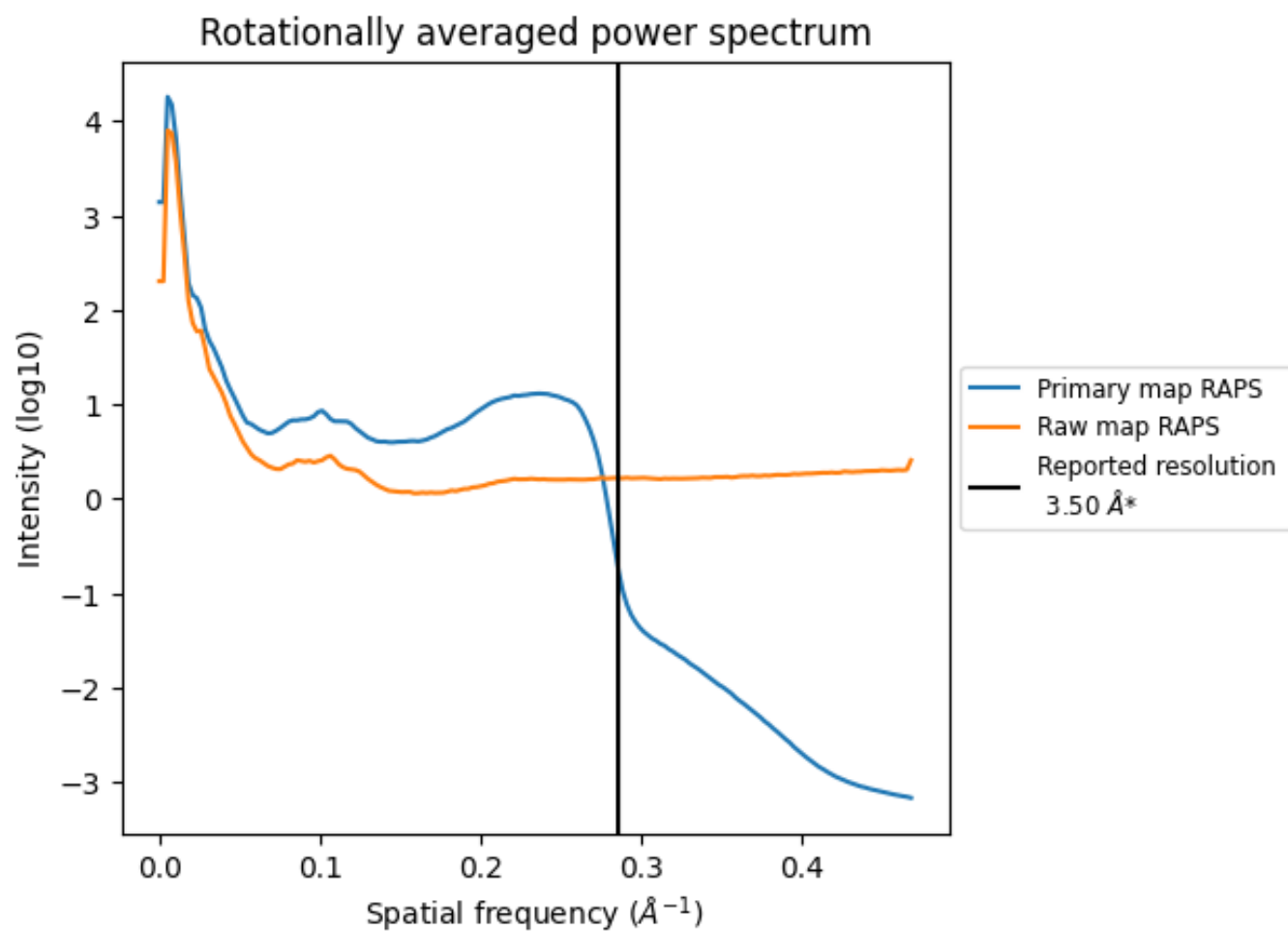
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 115 nm^3 ; this corresponds to an approximate mass of 104 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 ⓘ

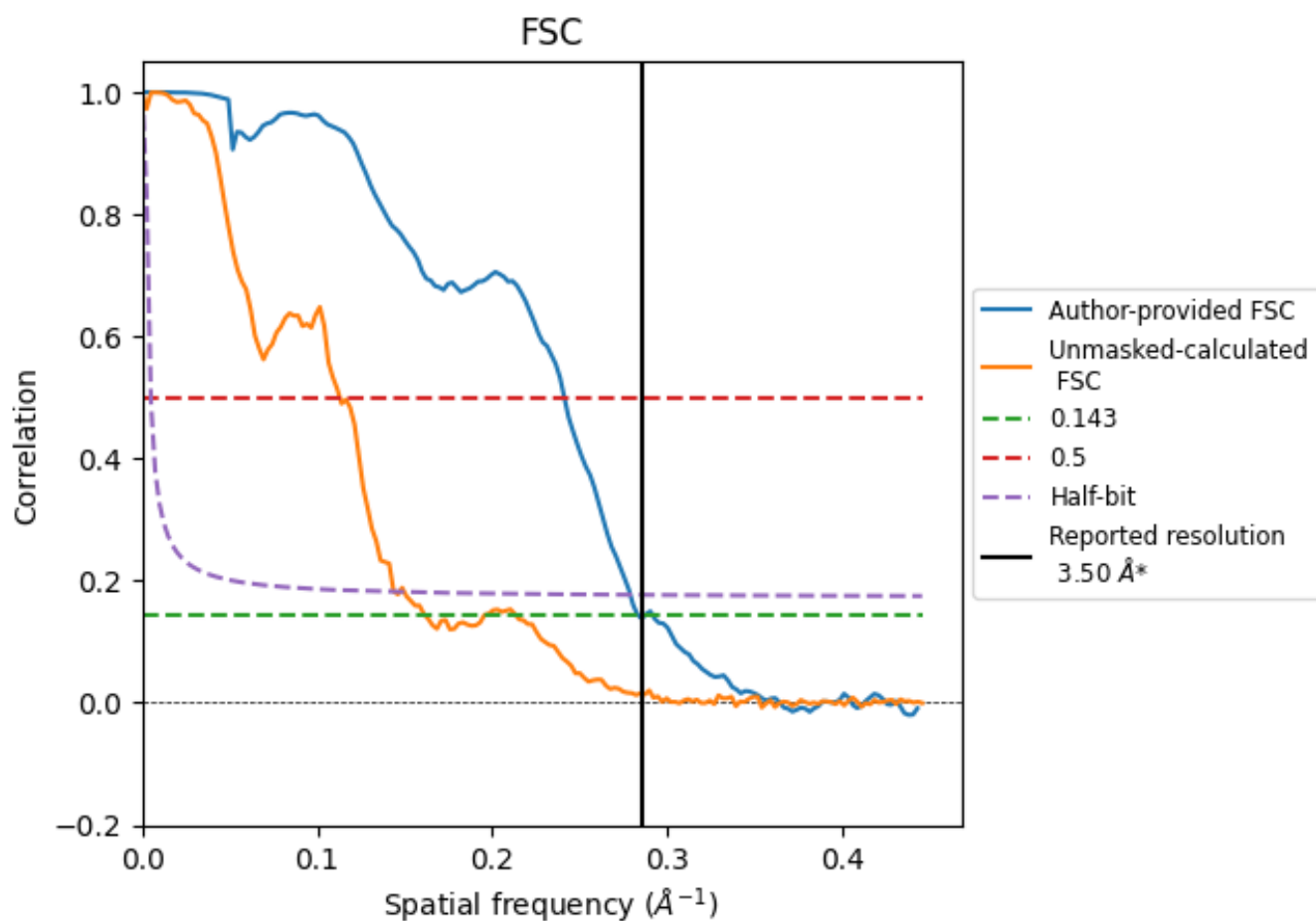


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates

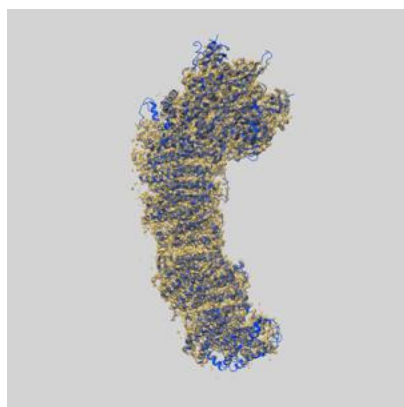
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.53	4.15	3.59
Unmasked-calculated*	6.18	8.87	6.93

*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 6.18 differs from the reported value 3.5 by more than 10 %

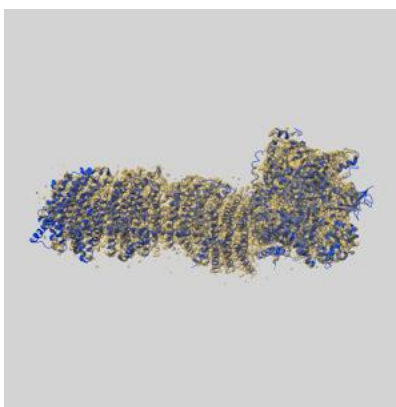
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0425 and PDB model 6NBX. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

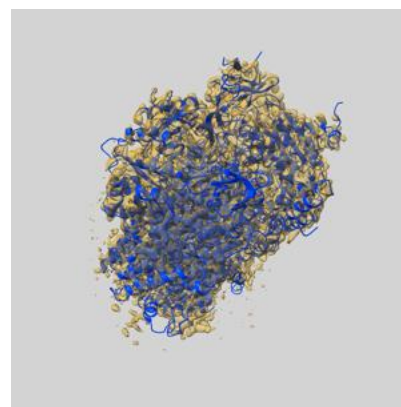
9.1 Map-model overlay [i](#)



X



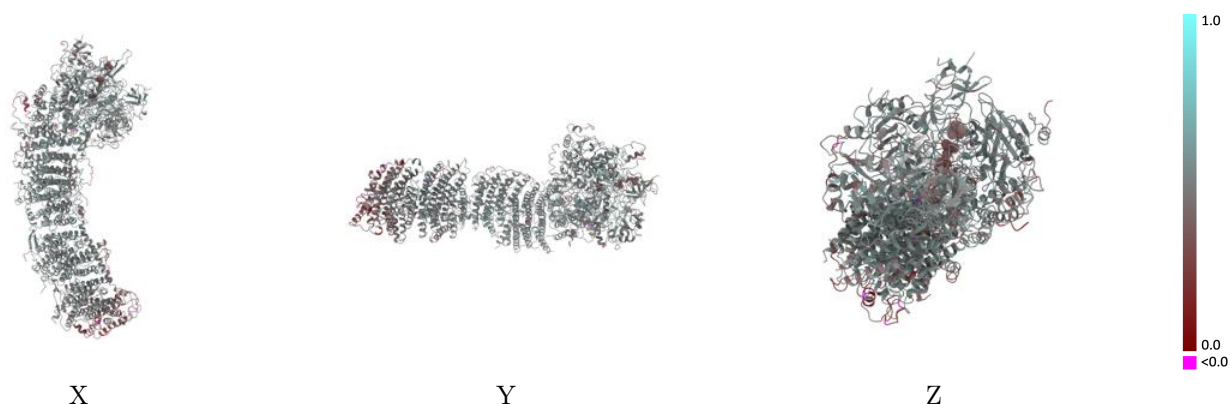
Y



Z

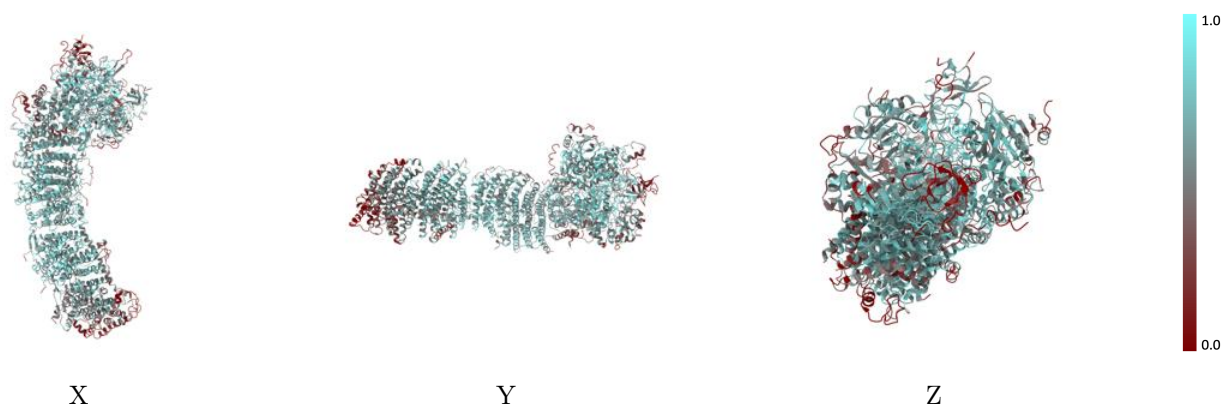
The images above show the 3D surface view of the map at the recommended contour level 5.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



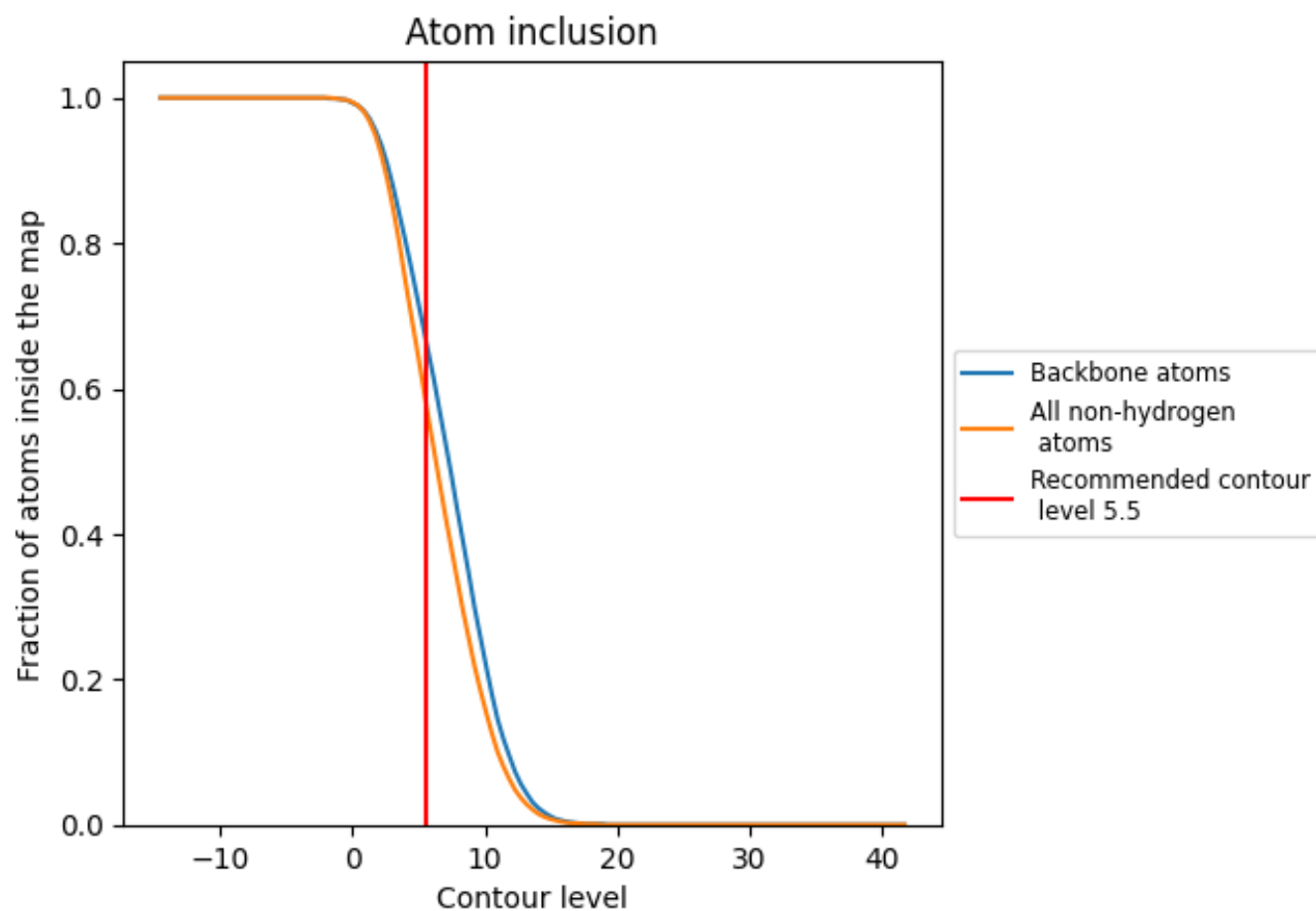
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5.5).

9.4 Atom inclusion ⓘ



At the recommended contour level, 67% of all backbone atoms, 58% 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 (5.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5850	 0.4880
A	 0.5740	 0.4760
B	 0.7090	 0.5250
C	 0.5820	 0.5130
D	 0.6730	 0.5110
E	 0.7130	 0.5260
F	 0.4410	 0.4270
G	 0.6010	 0.4810
H	 0.6410	 0.5100
I	 0.5640	 0.4840
J	 0.6380	 0.5060
K	 0.5980	 0.4950
L	 0.3900	 0.4460
M	 0.6430	 0.5130
N	 0.5340	 0.4980
O	 0.5760	 0.5150
P	 0.6460	 0.4880
Q	 0.3350	 0.4400
S	 0.0830	 0.4370

