



## Full wwPDB EM Validation Report ⓘ

Nov 6, 2022 – 05:06 AM EST

PDB ID : 6B2Z  
EMDB ID : EMD-7036  
Title : Cryo-EM structure of the dimeric FO region of yeast mitochondrial ATP synthase  
Authors : Guo, H.; Rubinstein, J.L.  
Deposited on : 2017-09-20  
Resolution : 3.60 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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  
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

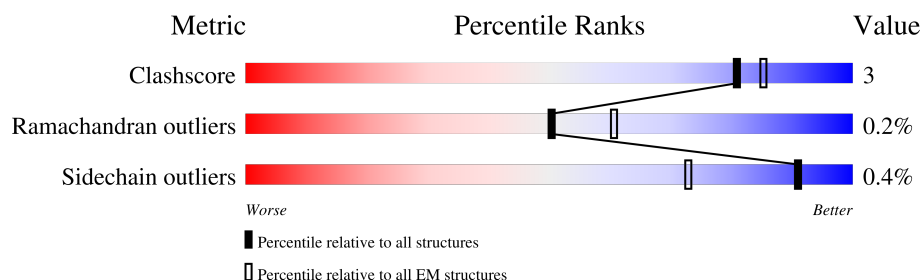
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.60 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.



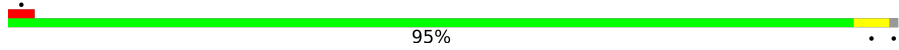
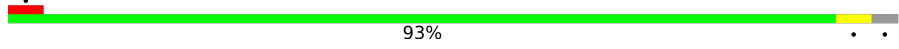
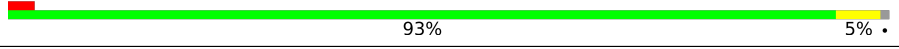
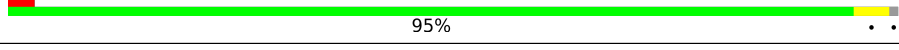

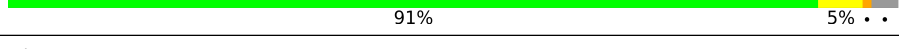
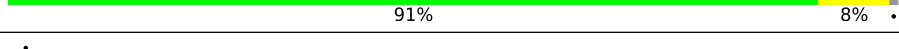
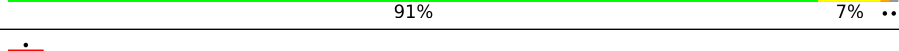
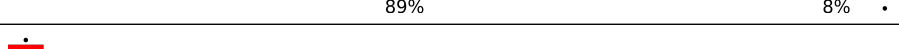
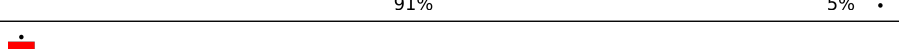
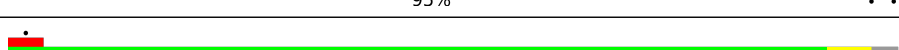
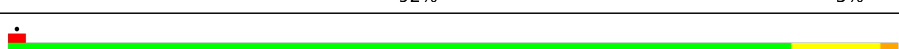
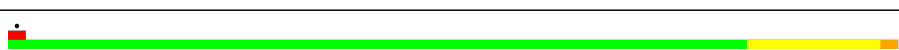

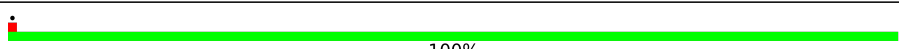




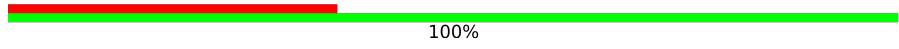
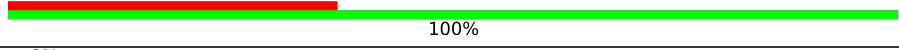
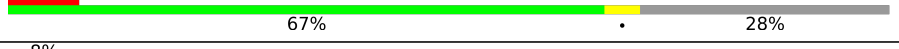

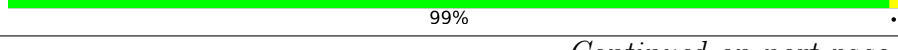

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	0	76	95% ..
1	1	76	96% ..
1	2	76	89% 8% ..
1	3	76	92% . . .
1	4	76	92% 7% .
1	5	76	91% 7% ..
1	6	76	89% 8% .
1	7	76	91% 5% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	8	76	
1	9	76	
1	B	76	
1	C	76	
1	D	76	
1	E	76	
1	F	76	
1	G	76	
1	H	76	
1	I	76	
1	J	76	
1	K	76	
2	A	48	
2	L	48	
3	M	249	
3	a	249	
4	N	209	
4	b	209	
5	O	173	
5	d	173	
6	P	49	
6	e	49	
7	Q	95	
7	f	95	
8	R	106	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	g	106	<div><div></div><div>30%</div><div></div><div>99%</div><div></div></div>
9	S	59	<div><div></div><div></div><div></div><div>97%</div><div></div></div>
9	i	59	<div><div></div><div></div><div></div><div>100%</div><div></div></div>
10	T	68	<div><div></div><div>6%</div><div></div><div>32%</div><div></div><div>65%</div><div></div></div>
10	k	68	<div><div></div><div>6%</div><div></div><div>35%</div><div></div><div>65%</div><div></div></div>

## 2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 21436 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 ATP synthase subunit c, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	75	Total	C	N	O	S	0	0
			537	359	83	91	4		
1	2	75	Total	C	N	O	S	0	0
			537	359	83	91	4		
1	3	74	Total	C	N	O	S	0	0
			529	354	82	90	3		
1	4	75	Total	C	N	O	S	0	0
			537	359	83	91	4		
1	5	75	Total	C	N	O	S	0	0
			537	359	83	91	4		
1	6	74	Total	C	N	O	S	0	0
			529	354	82	90	3		
1	7	73	Total	C	N	O	S	0	0
			522	348	81	89	4		
1	8	75	Total	C	N	O	S	0	0
			537	359	83	91	4		
1	9	74	Total	C	N	O	S	0	0
			529	354	82	90	3		
1	0	75	Total	C	N	O	S	0	0
			537	359	83	91	4		
1	C	75	Total	C	N	O	S	0	0
			537	359	83	91	4		
1	D	75	Total	C	N	O	S	0	0
			537	359	83	91	4		
1	E	74	Total	C	N	O	S	0	0
			529	354	82	90	3		
1	F	75	Total	C	N	O	S	0	0
			537	359	83	91	4		
1	G	75	Total	C	N	O	S	0	0
			537	359	83	91	4		
1	H	74	Total	C	N	O	S	0	0
			529	354	82	90	3		
1	I	73	Total	C	N	O	S	0	0
			522	348	81	89	4		

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					AltConf	Trace
1	J	75	Total	C	N	O	S	0	0
			537	359	83	91	4		
1	K	74	Total	C	N	O	S	0	0
			529	354	82	90	3		
1	B	75	Total	C	N	O	S	0	0
			537	359	83	91	4		

- Molecule 2 is a protein called ATP synthase protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	48	Total	C	N	O	S	0	0
			410	287	59	60	4		
2	L	48	Total	C	N	O	S	0	0
			410	287	59	60	4		

- Molecule 3 is a protein called ATP synthase subunit a.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	a	249	Total	C	N	O	S	0	0
			1971	1338	296	326	11		
3	M	249	Total	C	N	O	S	0	0
			1971	1338	296	326	11		

- Molecule 4 is a protein called ATP synthase subunit b.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	b	97	Total	C	N	O	S	0	0
			639	407	107	124	1		
4	N	97	Total	C	N	O	S	0	0
			639	407	107	124	1		

- Molecule 5 is a protein called ATP synthase subunit d, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	d	53	Total	C	N	O	S	0	0
			411	262	69	78	2		
5	O	53	Total	C	N	O	S	0	0
			411	262	69	78	2		

- Molecule 6 is a protein called ATP synthase subunit e, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	e	49	Total	C	N	O	0	0
			245	147	49	49		
6	P	49	Total	C	N	O	0	0
			245	147	49	49		

- Molecule 7 is a protein called ATP synthase subunit f, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	f	68	Total	C	N	O	S	0	0
			528	349	92	86	1		
7	Q	68	Total	C	N	O	S	0	0
			528	349	92	86	1		

- Molecule 8 is a protein called ATP synthase subunit g.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	g	106	Total	C	N	O	0	0
			530	318	106	106		
8	R	106	Total	C	N	O	0	0
			530	318	106	106		

- Molecule 9 is a protein called ATP synthase subunit j, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	59	Total	C	N	O	S	0	0
			473	313	78	80	2		
9	S	59	Total	C	N	O	S	0	0
			473	313	78	80	2		

- Molecule 10 is a protein called ATP synthase subunit k, mitochondrial.

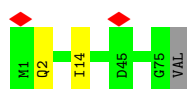
Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	24	Total	C	N	O	S	0	0
			180	122	30	27	1		
10	T	24	Total	C	N	O	S	0	0
			180	122	30	27	1		

### 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.

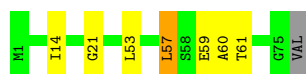
- Molecule 1: ATP synthase subunit c, mitochondrial

Chain 1:  96% ..



- Molecule 1: ATP synthase subunit c, mitochondrial

Chain 2:  89% 8% ..



- Molecule 1: ATP synthase subunit c, mitochondrial

Chain 3:  92% ...




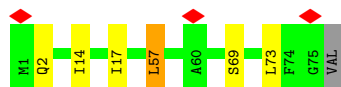
- Molecule 1: ATP synthase subunit c, mitochondrial

Chain 4:  92% 7% .




- Molecule 1: ATP synthase subunit c, mitochondrial

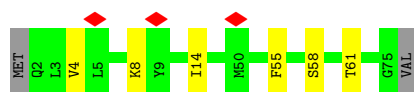
Chain 5:  91% 7% ..




- Molecule 1: ATP synthase subunit c, mitochondrial

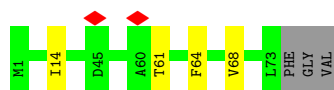


Chain 6:  89% 8% .



- Molecule 1: ATP synthase subunit c, mitochondrial

Chain 7:  91% 5% .



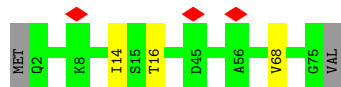
- Molecule 1: ATP synthase subunit c, mitochondrial

Chain 8:  95% . .



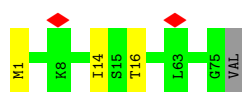
- Molecule 1: ATP synthase subunit c, mitochondrial

Chain 9:  93% . .



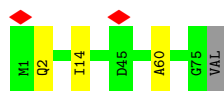
- Molecule 1: ATP synthase subunit c, mitochondrial

Chain 0:  95% . .




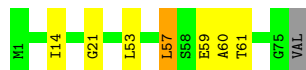
- Molecule 1: ATP synthase subunit c, mitochondrial

Chain C:  95% . .




- Molecule 1: ATP synthase subunit c, mitochondrial

Chain D:  89% 8% . .



- Molecule 1: ATP synthase subunit c, mitochondrial

Chain E:  91% 5% ..



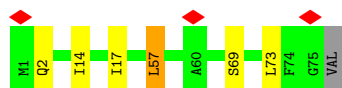
- Molecule 1: ATP synthase subunit c, mitochondrial

Chain F:  91% 8% .




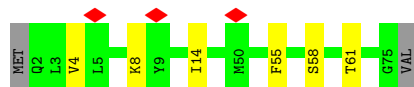
- Molecule 1: ATP synthase subunit c, mitochondrial

Chain G:  91% 7% ..




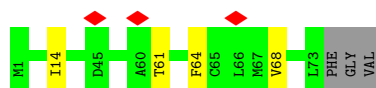
- Molecule 1: ATP synthase subunit c, mitochondrial

Chain H:  89% 8% .



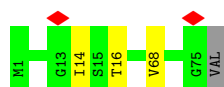
- Molecule 1: ATP synthase subunit c, mitochondrial

Chain I:  91% 5% .



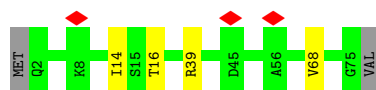
- Molecule 1: ATP synthase subunit c, mitochondrial

Chain J:  95% ..



- Molecule 1: ATP synthase subunit c, mitochondrial

Chain K:  92% 5% .



- Molecule 1: ATP synthase subunit c, mitochondrial

Chain B: 93% 5%



- Molecule 2: ATP synthase protein 8

Chain A: 88% 10%



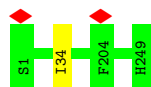
- Molecule 2: ATP synthase protein 8

Chain L: 83% 15%



- Molecule 3: ATP synthase subunit a

Chain a: 100%



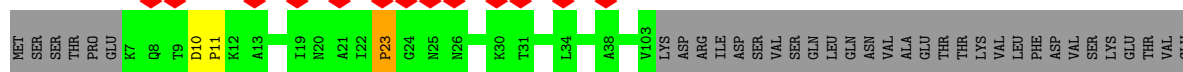
- Molecule 3: ATP synthase subunit a

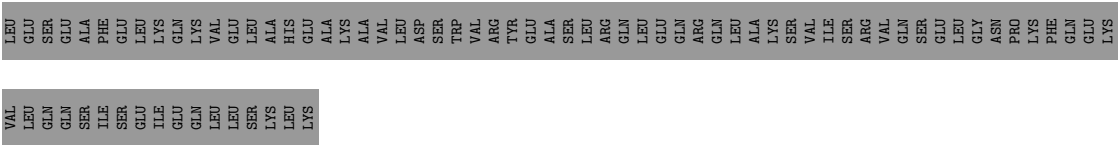
Chain M: 88% 12%



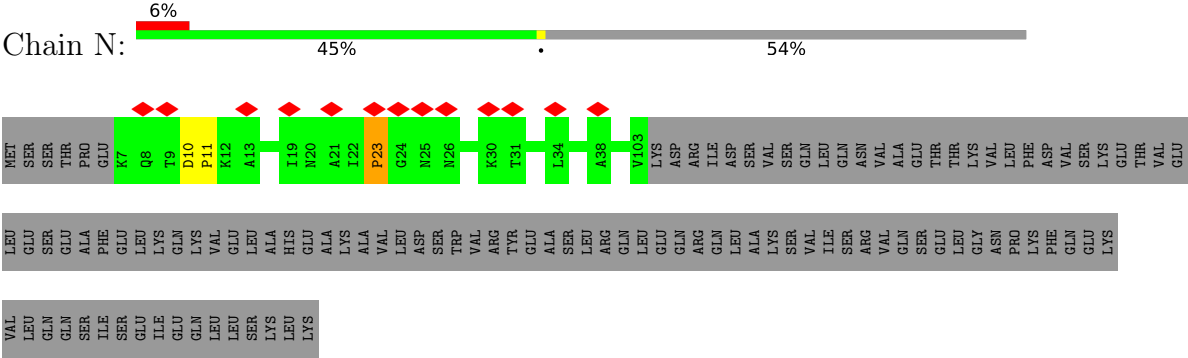
- Molecule 4: ATP synthase subunit b

Chain b: 6% 45% 54%

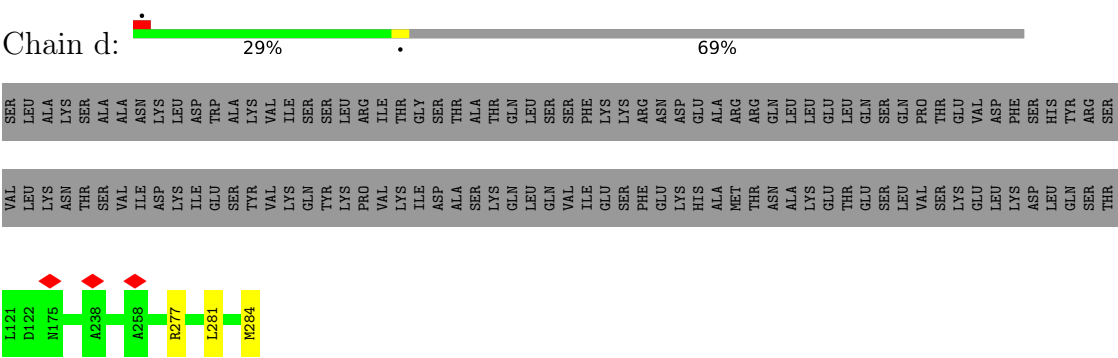




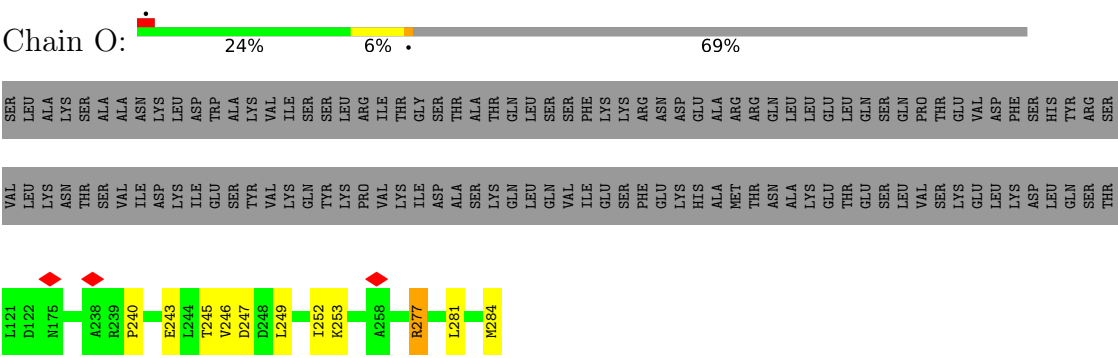
• Molecule 4: ATP synthase subunit b



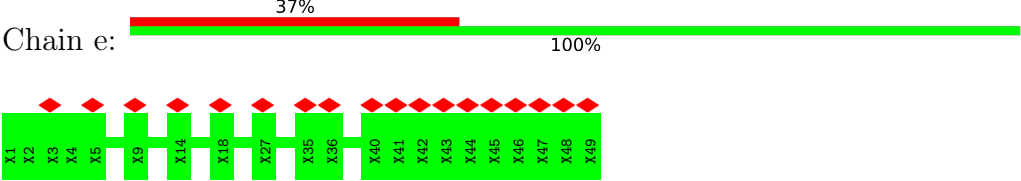
• Molecule 5: ATP synthase subunit d, mitochondrial



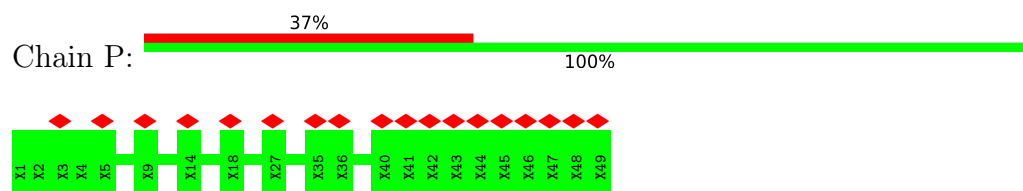
• Molecule 5: ATP synthase subunit d, mitochondrial



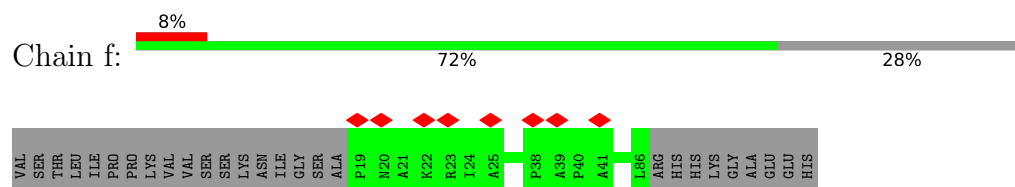
• Molecule 6: ATP synthase subunit e, mitochondrial



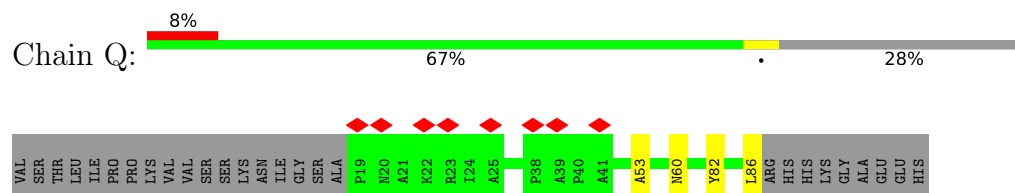
- Molecule 6: ATP synthase subunit e, mitochondrial



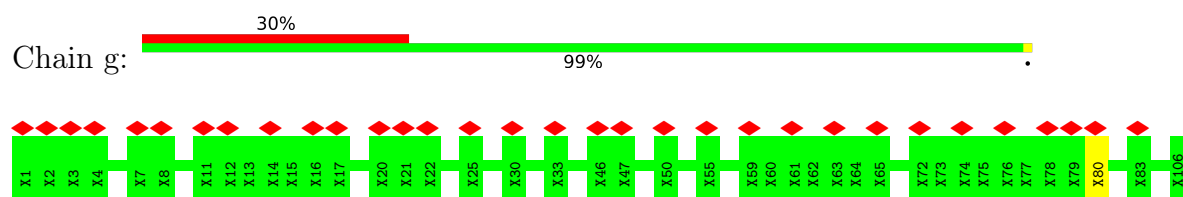
- Molecule 7: ATP synthase subunit f, mitochondrial



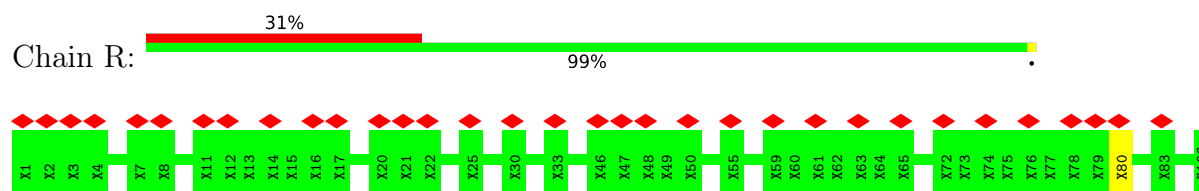
- Molecule 7: ATP synthase subunit f, mitochondrial



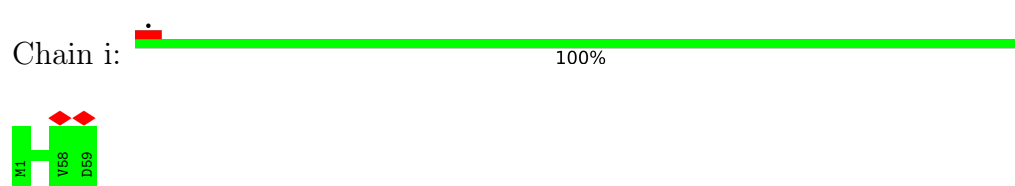
- Molecule 8: ATP synthase subunit g



- Molecule 8: ATP synthase subunit g

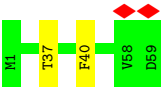


- Molecule 9: ATP synthase subunit j, mitochondrial

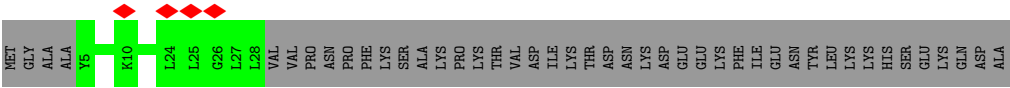


- Molecule 9: ATP synthase subunit j, mitochondrial

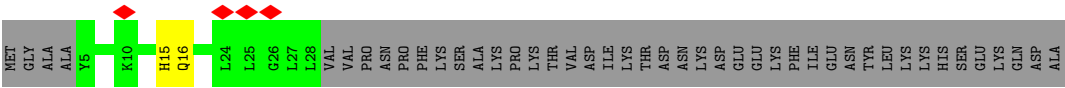




• Molecule 10: ATP synthase subunit k, mitochondrial



• Molecule 10: ATP synthase subunit k, mitochondrial



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	238848	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 ( $e^-/\text{\AA}^2$ )	71	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	47170	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	1.191	Depositor
Minimum map value	-0.737	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.165	Depositor
Map size (Å)	339.19998, 339.19998, 339.19998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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	0	0.34	0/545	0.61	0/737
1	1	0.35	0/545	0.55	0/737
1	2	0.38	0/545	0.67	1/737 (0.1%)
1	3	0.37	0/537	0.61	1/727 (0.1%)
1	4	0.34	0/545	0.60	0/737
1	5	0.32	0/545	0.58	0/737
1	6	0.33	0/537	0.60	0/727
1	7	0.31	0/529	0.56	0/716
1	8	0.31	0/545	0.56	0/737
1	9	0.32	0/537	0.57	0/727
1	B	0.34	0/545	0.60	0/737
1	C	0.34	0/545	0.55	0/737
1	D	0.38	0/545	0.67	1/737 (0.1%)
1	E	0.37	0/537	0.61	1/727 (0.1%)
1	F	0.34	0/545	0.60	0/737
1	G	0.32	0/545	0.58	0/737
1	H	0.33	0/537	0.60	0/727
1	I	0.31	0/529	0.56	0/716
1	J	0.31	0/545	0.56	0/737
1	K	0.32	0/537	0.57	0/727
2	A	0.50	0/422	0.77	1/570 (0.2%)
2	L	0.50	0/422	0.77	1/570 (0.2%)
3	M	0.45	0/2023	0.70	0/2758
3	a	0.45	0/2023	0.70	0/2758
4	N	0.34	0/646	0.58	2/883 (0.2%)
4	b	0.34	0/646	0.58	2/883 (0.2%)
5	O	0.37	0/418	0.60	1/563 (0.2%)
5	d	0.37	0/418	0.60	1/563 (0.2%)
7	Q	0.38	0/546	0.59	0/738
7	f	0.38	0/546	0.59	0/738
9	S	0.42	0/488	0.60	0/659
9	i	0.42	0/488	0.60	0/659
10	T	0.28	0/185	0.68	0/250
10	k	0.28	0/185	0.68	0/250



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
All	All	0.38	0/20276	0.62	12/27480 (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
8	R	0	2
8	g	0	2
All	All	0	4

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	d	281	LEU	CA-CB-CG	7.81	133.26	115.30
5	O	281	LEU	CA-CB-CG	7.81	133.26	115.30
2	A	26	LEU	CA-CB-CG	7.72	133.06	115.30
2	L	26	LEU	CA-CB-CG	7.71	133.03	115.30
1	2	57	LEU	CA-CB-CG	5.79	128.62	115.30
1	D	57	LEU	CA-CB-CG	5.79	128.60	115.30
4	N	11	PRO	N-CA-CB	5.78	110.23	103.30
4	b	11	PRO	N-CA-CB	5.78	110.23	103.30
4	N	23	PRO	N-CA-CB	5.65	110.08	103.30
4	b	23	PRO	N-CA-CB	5.63	110.05	103.30
1	E	20	LEU	CA-CB-CG	5.11	127.06	115.30
1	3	20	LEU	CA-CB-CG	5.10	127.02	115.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	R	80	UNK	Mainchain,Peptide
8	g	80	UNK	Mainchain,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	0	537	0	582	4	0
1	1	537	0	582	3	0
1	2	537	0	582	5	0
1	3	529	0	570	4	0
1	4	537	0	582	5	0
1	5	537	0	582	5	0
1	6	529	0	570	5	0
1	7	522	0	570	4	0
1	8	537	0	582	4	0
1	9	529	0	570	4	0
1	B	537	0	582	5	0
1	C	537	0	582	4	0
1	D	537	0	582	6	0
1	E	529	0	570	5	0
1	F	537	0	582	6	0
1	G	537	0	582	5	0
1	H	529	0	570	5	0
1	I	522	0	570	4	0
1	J	537	0	582	4	0
1	K	529	0	570	5	0
2	A	410	0	444	3	0
2	L	410	0	444	5	0
3	M	1971	0	2071	17	0
3	a	1971	0	2071	0	0
4	N	639	0	555	0	0
4	b	639	0	555	0	0
5	O	411	0	397	7	0
5	d	411	0	397	0	0
6	P	245	0	51	0	0
6	e	245	0	51	0	0
7	Q	528	0	494	2	0
7	f	528	0	494	0	0
8	R	530	0	108	0	0
8	g	530	0	108	0	0
9	S	473	0	476	1	0
9	i	473	0	476	0	0
10	T	180	0	192	1	0
10	k	180	0	192	0	0
All	All	21436	0	21120	85	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 3.

All (85) 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)
3:M:27:THR:H	3:M:30:SER:HB3	1.61	0.66
1:8:14:ILE:HG21	1:9:14:ILE:HD13	1.83	0.61
1:J:14:ILE:HG21	1:K:14:ILE:HD13	1.83	0.60
1:F:17:ILE:HB	1:G:17:ILE:HG12	1.87	0.57
3:M:211:VAL:HG23	3:M:212:PRO:HD3	1.87	0.56
2:L:46:SER:OG	5:O:277:ARG:NH1	2.39	0.56
5:O:245:THR:HG22	5:O:247:ASP:H	1.72	0.55
1:1:14:ILE:HG21	1:2:14:ILE:HD13	1.89	0.55
1:4:17:ILE:HB	1:5:17:ILE:HG12	1.87	0.55
1:C:14:ILE:HG21	1:D:14:ILE:HD13	1.89	0.55
3:M:23:CYS:SG	3:M:24:LEU:N	2.81	0.54
3:M:32:TYR:HB3	3:M:111:LEU:HD11	1.91	0.53
3:M:49:ASN:ND2	3:M:56:SER:OG	2.42	0.53
1:G:14:ILE:HG21	1:H:14:ILE:HD13	1.92	0.52
1:4:1:MET:SD	1:5:2:GLN:NE2	2.83	0.51
1:E:65:CYS:SG	1:F:16:THR:OG1	2.68	0.51
1:5:14:ILE:HG21	1:6:14:ILE:HD13	1.92	0.51
3:M:81:ASN:HB2	3:M:84:LEU:HD13	1.93	0.51
1:F:1:MET:SD	1:G:2:GLN:NE2	2.83	0.50
3:M:92:LEU:HD22	3:M:234:TRP:HE1	1.76	0.50
1:2:53:LEU:O	1:2:57:LEU:HB3	2.11	0.50
1:7:68:VAL:HG11	1:8:16:THR:HG21	1.93	0.50
3:M:26:LEU:HD21	3:M:31:LEU:HD12	1.93	0.50
1:D:53:LEU:O	1:D:57:LEU:HB3	2.11	0.50
3:M:233:VAL:HA	3:M:236:ILE:HG22	1.94	0.50
1:K:14:ILE:HG21	1:B:14:ILE:HD13	1.93	0.50
7:Q:53:ALA:O	7:Q:60:ASN:ND2	2.44	0.49
1:I:68:VAL:HG11	1:J:16:THR:HG21	1.93	0.49
1:9:14:ILE:HG21	1:0:14:ILE:HD13	1.93	0.49
10:T:15:HIS:CD2	10:T:16:GLN:H	2.31	0.49
3:M:108:SER:OG	3:M:109:PHE:N	2.46	0.49
1:7:14:ILE:HG21	1:8:14:ILE:HD13	1.96	0.48
3:M:96:ILE:HG21	3:M:177:LEU:HD11	1.96	0.48
1:I:14:ILE:HG21	1:J:14:ILE:HD13	1.96	0.48
3:M:51:ASN:HB3	5:O:246:VAL:HG22	1.96	0.47
2:A:26:LEU:O	2:A:30:PHE:HB2	2.15	0.47
2:L:26:LEU:O	2:L:30:PHE:HB2	2.15	0.47
1:D:60:ALA:HB2	3:M:176:ARG:HE	1.79	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:14:ILE:HD13	1:0:14:ILE:HG21	1.97	0.47
1:C:14:ILE:HD13	1:B:14:ILE:HG21	1.97	0.47
9:S:37:THR:HG23	9:S:40:PHE:H	1.80	0.46
1:5:69:SER:O	1:5:73:LEU:HB2	2.15	0.46
1:8:68:VAL:HG11	1:9:16:THR:HG21	1.98	0.46
1:J:68:VAL:HG11	1:K:16:THR:HG21	1.98	0.46
1:G:69:SER:O	1:G:73:LEU:HB2	2.15	0.45
1:6:14:ILE:HG21	1:7:14:ILE:HD13	1.98	0.45
1:C:2:GLN:HE21	1:B:1:MET:HG2	1.82	0.45
2:A:36:LEU:HA	2:A:39:TYR:HD2	1.81	0.45
3:M:1:SER:OG	3:M:4:ASP:OD2	2.33	0.45
5:O:249:LEU:HA	5:O:252:ILE:HG22	1.99	0.45
2:L:45:ILE:HD11	5:O:249:LEU:HD11	1.99	0.45
1:1:2:GLN:HE21	1:0:1:MET:HG2	1.82	0.44
1:H:14:ILE:HG21	1:I:14:ILE:HD13	1.98	0.44
2:L:36:LEU:HA	2:L:39:TYR:HD2	1.81	0.44
1:I:61:THR:HA	1:I:64:PHE:HD2	1.83	0.44
1:D:21:GLY:HA3	1:E:20:LEU:HA	1.99	0.44
1:G:57:LEU:HD13	1:H:55:PHE:HZ	1.83	0.44
1:2:21:GLY:HA3	1:3:20:LEU:HA	1.99	0.43
1:2:59:GLU:O	1:2:61:THR:N	2.52	0.43
1:5:57:LEU:HD13	1:6:55:PHE:HZ	1.83	0.43
1:7:61:THR:HA	1:7:64:PHE:HD2	1.83	0.43
1:H:58:SER:O	1:H:61:THR:OG1	2.35	0.43
2:L:23:LEU:HD23	2:L:26:LEU:HD22	2.00	0.43
1:2:59:GLU:O	1:2:60:ALA:C	2.57	0.43
1:D:59:GLU:O	1:D:60:ALA:C	2.57	0.43
2:A:23:LEU:HD23	2:A:26:LEU:HD22	2.00	0.42
5:O:240:PRO:HB2	5:O:243:GLU:HG2	2.01	0.42
1:D:59:GLU:O	1:D:61:THR:N	2.52	0.42
3:M:10:THR:HA	3:M:27:THR:HG23	2.01	0.42
1:9:68:VAL:HG11	1:0:16:THR:HG21	2.01	0.42
1:E:33:LEU:HA	1:F:34:ILE:HG21	2.02	0.41
1:6:58:SER:O	1:6:61:THR:OG1	2.34	0.41
1:C:60:ALA:HB2	3:M:222:LEU:HD21	2.02	0.41
1:K:39:ARG:HH12	1:B:39:ARG:HE	1.68	0.41
1:6:4:VAL:O	1:6:8:LYS:HB2	2.20	0.41
7:Q:82:TYR:HA	7:Q:86:LEU:HB2	2.01	0.41
1:3:33:LEU:HA	1:4:34:ILE:HG21	2.02	0.41
5:O:252:ILE:HG23	5:O:253:LYS:HG2	2.01	0.41
1:3:21:GLY:HA3	1:4:20:LEU:HB2	2.02	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:14:ILE:HG21	1:4:14:ILE:HG12	2.02	0.41
1:E:21:GLY:HA3	1:F:20:LEU:HB2	2.03	0.41
1:H:4:VAL:O	1:H:8:LYS:HB2	2.20	0.40
1:K:68:VAL:HG11	1:B:16:THR:HG21	2.01	0.40
1:E:14:ILE:HG21	1:F:14:ILE:HG12	2.02	0.40
3:M:46:LEU:H	3:M:46:LEU:HG	1.73	0.40

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	0	73/76 (96%)	73 (100%)	0	0	100	100
1	1	73/76 (96%)	71 (97%)	2 (3%)	0	100	100
1	2	73/76 (96%)	71 (97%)	2 (3%)	0	100	100
1	3	72/76 (95%)	72 (100%)	0	0	100	100
1	4	73/76 (96%)	73 (100%)	0	0	100	100
1	5	73/76 (96%)	72 (99%)	1 (1%)	0	100	100
1	6	72/76 (95%)	72 (100%)	0	0	100	100
1	7	71/76 (93%)	71 (100%)	0	0	100	100
1	8	73/76 (96%)	73 (100%)	0	0	100	100
1	9	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
1	B	73/76 (96%)	73 (100%)	0	0	100	100
1	C	73/76 (96%)	71 (97%)	2 (3%)	0	100	100
1	D	73/76 (96%)	71 (97%)	2 (3%)	0	100	100
1	E	72/76 (95%)	72 (100%)	0	0	100	100
1	F	73/76 (96%)	73 (100%)	0	0	100	100

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	73/76 (96%)	72 (99%)	1 (1%)	0	100	100
1	H	72/76 (95%)	72 (100%)	0	0	100	100
1	I	71/76 (93%)	71 (100%)	0	0	100	100
1	J	73/76 (96%)	73 (100%)	0	0	100	100
1	K	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
2	A	46/48 (96%)	43 (94%)	2 (4%)	1 (2%)	6	39
2	L	46/48 (96%)	43 (94%)	2 (4%)	1 (2%)	6	39
3	M	247/249 (99%)	228 (92%)	19 (8%)	0	100	100
3	a	247/249 (99%)	228 (92%)	19 (8%)	0	100	100
4	N	95/209 (46%)	87 (92%)	6 (6%)	2 (2%)	7	40
4	b	95/209 (46%)	87 (92%)	6 (6%)	2 (2%)	7	40
5	O	51/173 (30%)	50 (98%)	1 (2%)	0	100	100
5	d	51/173 (30%)	50 (98%)	1 (2%)	0	100	100
7	Q	66/95 (70%)	58 (88%)	8 (12%)	0	100	100
7	f	66/95 (70%)	58 (88%)	8 (12%)	0	100	100
9	S	57/59 (97%)	50 (88%)	7 (12%)	0	100	100
9	i	57/59 (97%)	50 (88%)	7 (12%)	0	100	100
10	T	22/68 (32%)	19 (86%)	3 (14%)	0	100	100
10	k	22/68 (32%)	19 (86%)	3 (14%)	0	100	100
All	All	2618/3322 (79%)	2506 (96%)	106 (4%)	6 (0%)	50	79

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	b	10	ASP
4	N	10	ASP
2	A	6	PRO
4	b	23	PRO
2	L	6	PRO
4	N	23	PRO

### 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	0	55/56 (98%)	55 (100%)	0	100	100
1	1	55/56 (98%)	55 (100%)	0	100	100
1	2	55/56 (98%)	55 (100%)	0	100	100
1	3	54/56 (96%)	54 (100%)	0	100	100
1	4	55/56 (98%)	55 (100%)	0	100	100
1	5	55/56 (98%)	54 (98%)	1 (2%)	59	81
1	6	54/56 (96%)	54 (100%)	0	100	100
1	7	54/56 (96%)	54 (100%)	0	100	100
1	8	55/56 (98%)	55 (100%)	0	100	100
1	9	54/56 (96%)	54 (100%)	0	100	100
1	B	55/56 (98%)	55 (100%)	0	100	100
1	C	55/56 (98%)	55 (100%)	0	100	100
1	D	55/56 (98%)	55 (100%)	0	100	100
1	E	54/56 (96%)	54 (100%)	0	100	100
1	F	55/56 (98%)	55 (100%)	0	100	100
1	G	55/56 (98%)	54 (98%)	1 (2%)	59	81
1	H	54/56 (96%)	54 (100%)	0	100	100
1	I	54/56 (96%)	54 (100%)	0	100	100
1	J	55/56 (98%)	55 (100%)	0	100	100
1	K	54/56 (96%)	54 (100%)	0	100	100
2	A	47/47 (100%)	47 (100%)	0	100	100
2	L	47/47 (100%)	47 (100%)	0	100	100
3	M	217/217 (100%)	216 (100%)	1 (0%)	88	95
3	a	217/217 (100%)	216 (100%)	1 (0%)	88	95
4	N	48/182 (26%)	48 (100%)	0	100	100
4	b	48/182 (26%)	48 (100%)	0	100	100
5	O	42/158 (27%)	40 (95%)	2 (5%)	25	60
5	d	42/158 (27%)	40 (95%)	2 (5%)	25	60
7	Q	46/76 (60%)	46 (100%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	f	46/76 (60%)	46 (100%)	0	100	100
9	S	49/49 (100%)	49 (100%)	0	100	100
9	i	49/49 (100%)	49 (100%)	0	100	100
10	T	18/57 (32%)	18 (100%)	0	100	100
10	k	18/57 (32%)	18 (100%)	0	100	100
All	All	2026/2692 (75%)	2018 (100%)	8 (0%)	91	97

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	5	57	LEU
3	a	34	ILE
5	d	277	ARG
5	d	284	MET
1	G	57	LEU
3	M	34	ILE
5	O	277	ARG
5	O	284	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	2	GLN
1	C	2	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.



## 5.6 Ligand geometry

There are no ligands in this entry.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

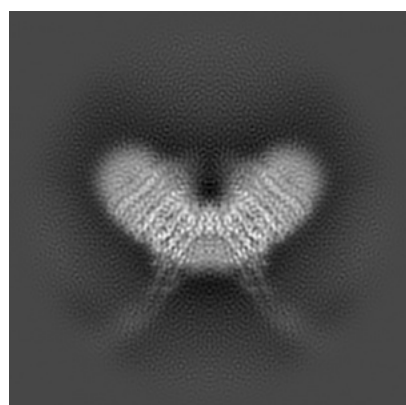
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7036. These allow visual inspection of the internal detail of the map and identification of artifacts.

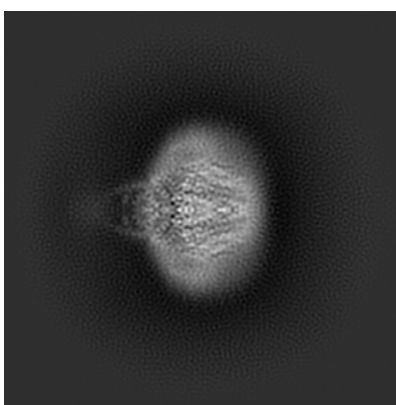
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

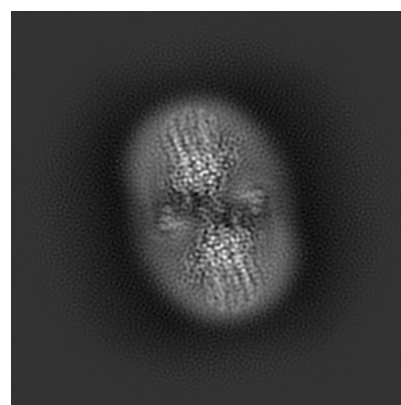
#### 6.1.1 Primary map



X



Y

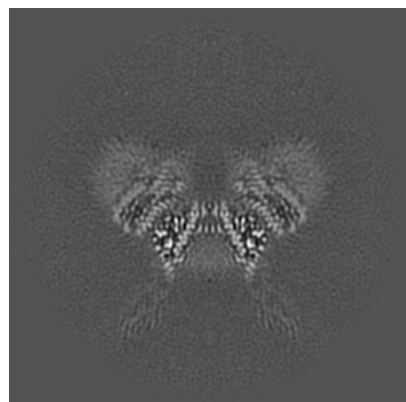


Z

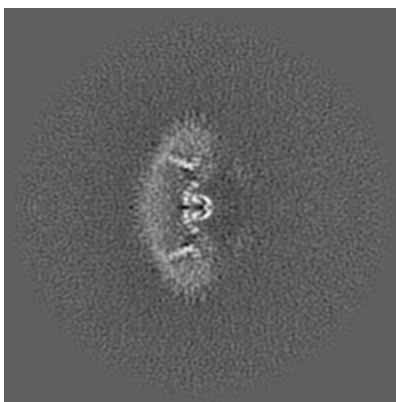
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

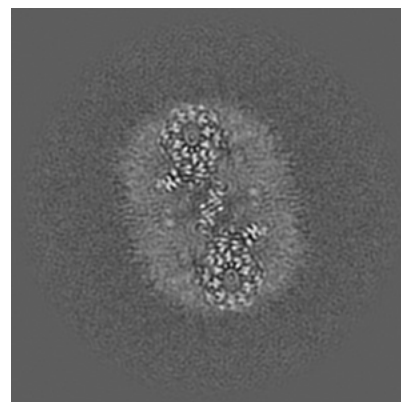
#### 6.2.1 Primary map



X Index: 160



Y Index: 160

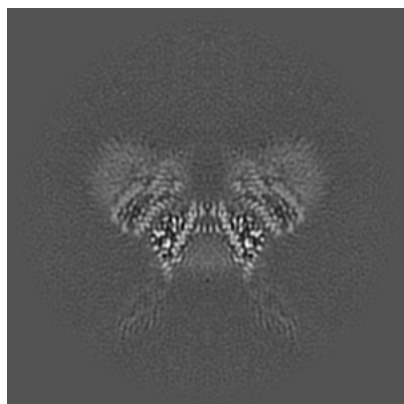


Z Index: 160

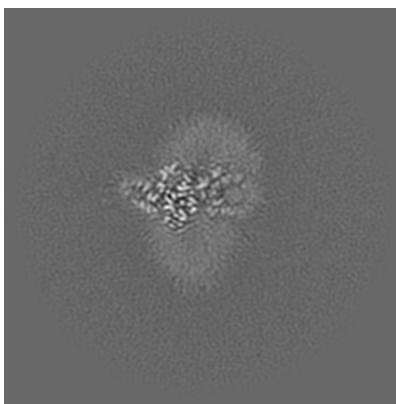
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

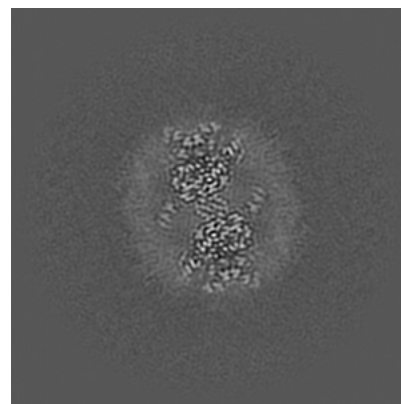
### 6.3.1 Primary map



X Index: 160



Y Index: 128



Z Index: 145

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

## 6.4 Orthogonal surface views [i](#)

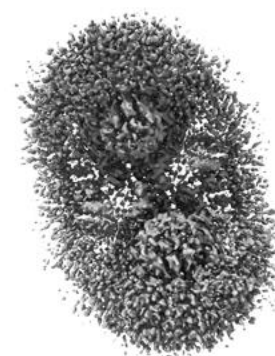
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.165. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

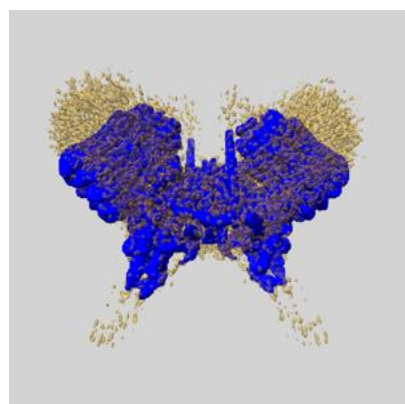
## 6.5 Mask visualisation [i](#)

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

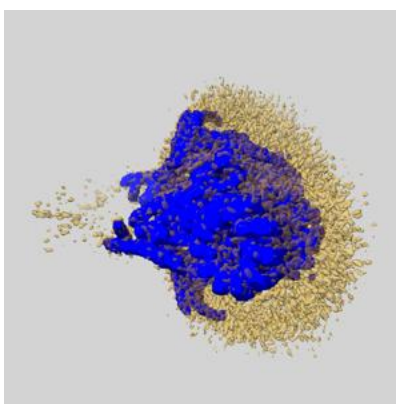
A mask typically either:

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

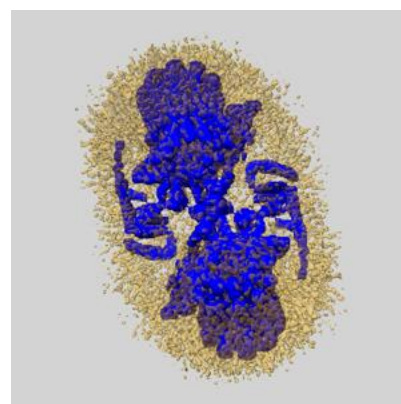
### 6.5.1 emd\_7036\_msk\_1.map [i](#)



X



Y

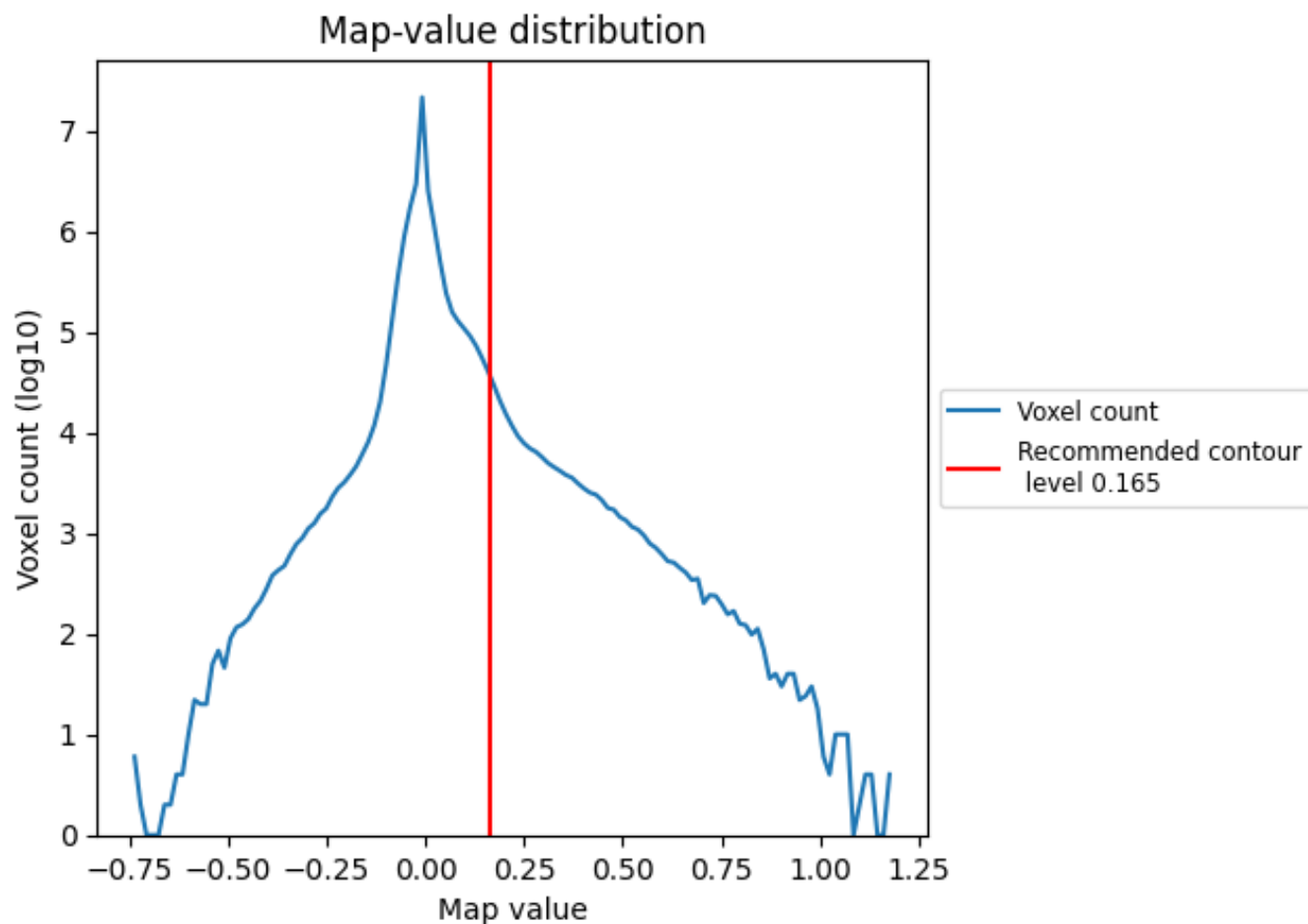


Z

## 7 Map analysis [i](#)

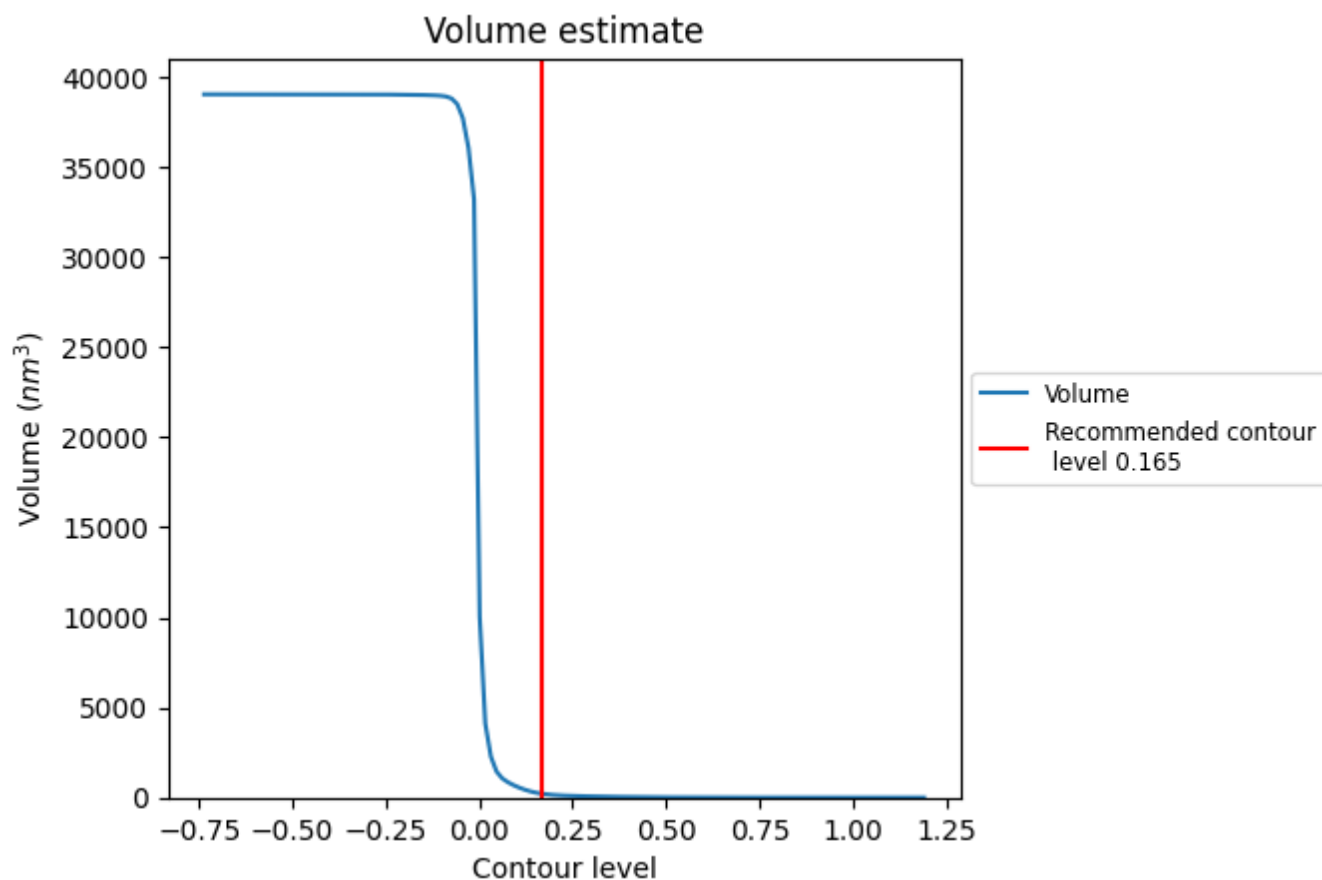
This section contains the results of statistical analysis of the map.

### 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.

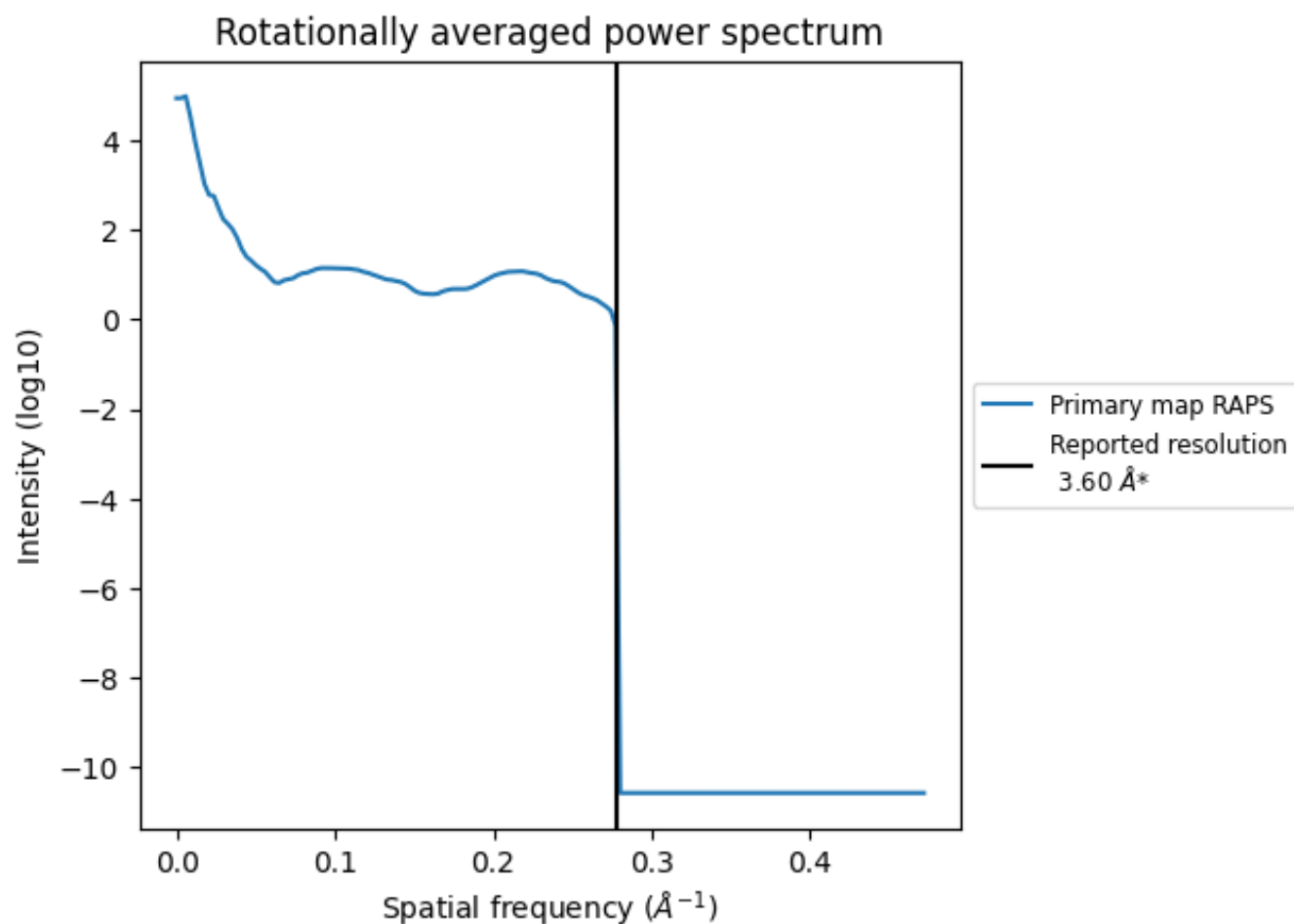
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 221 nm<sup>3</sup>; this corresponds to an approximate mass of 200 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 0.278  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation ⓘ

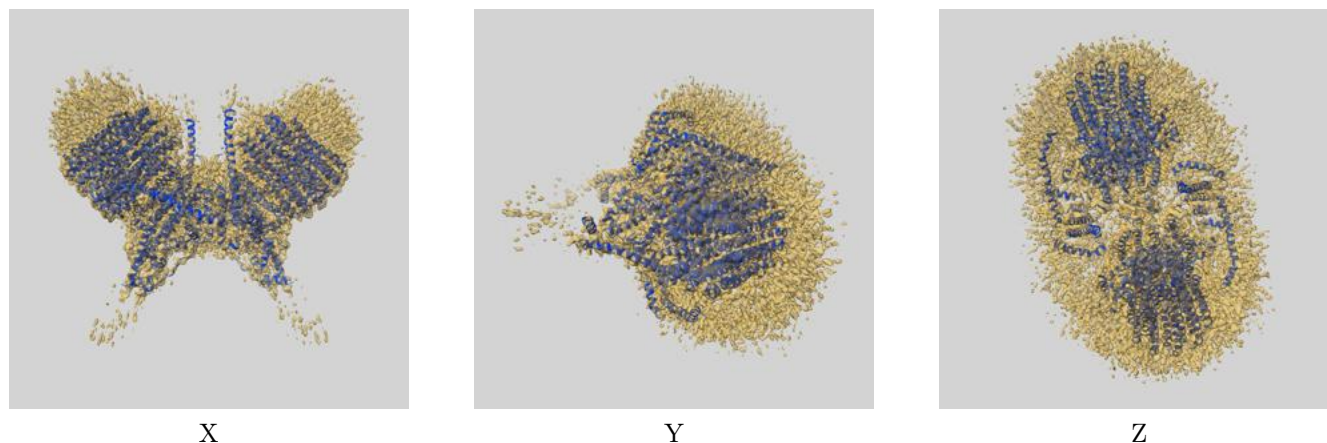
This section was not generated. No FSC curve or half-maps provided.



## 9 Map-model fit [i](#)

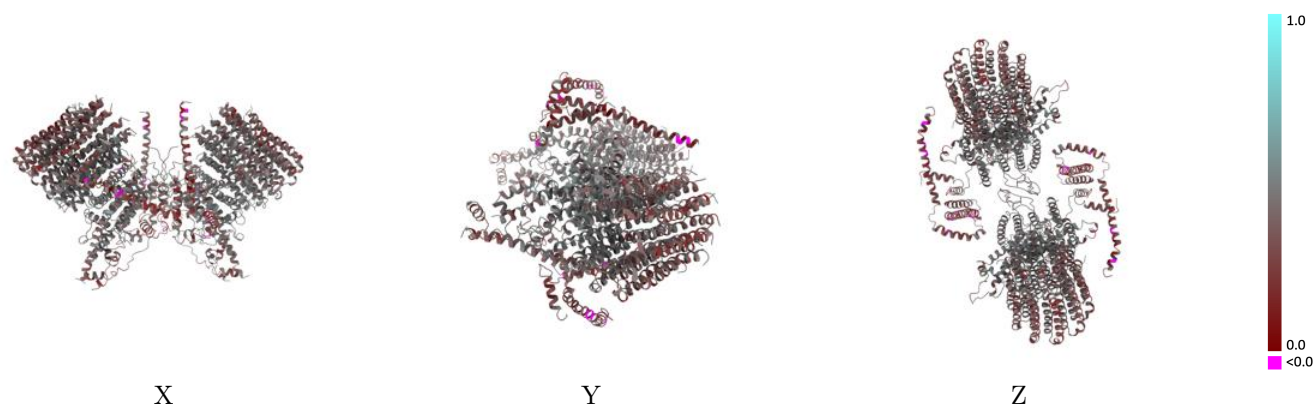
This section contains information regarding the fit between EMDB map EMD-7036 and PDB model 6B2Z. Per-residue inclusion information can be found in section [3](#) on page [8](#).

### 9.1 Map-model overlay [i](#)



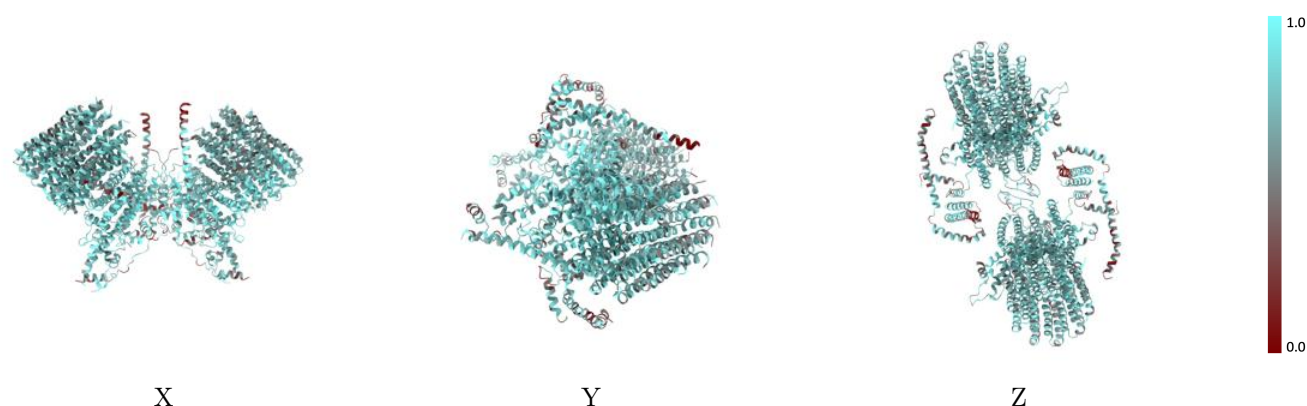
The images above show the 3D surface view of the map at the recommended contour level 0.165 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



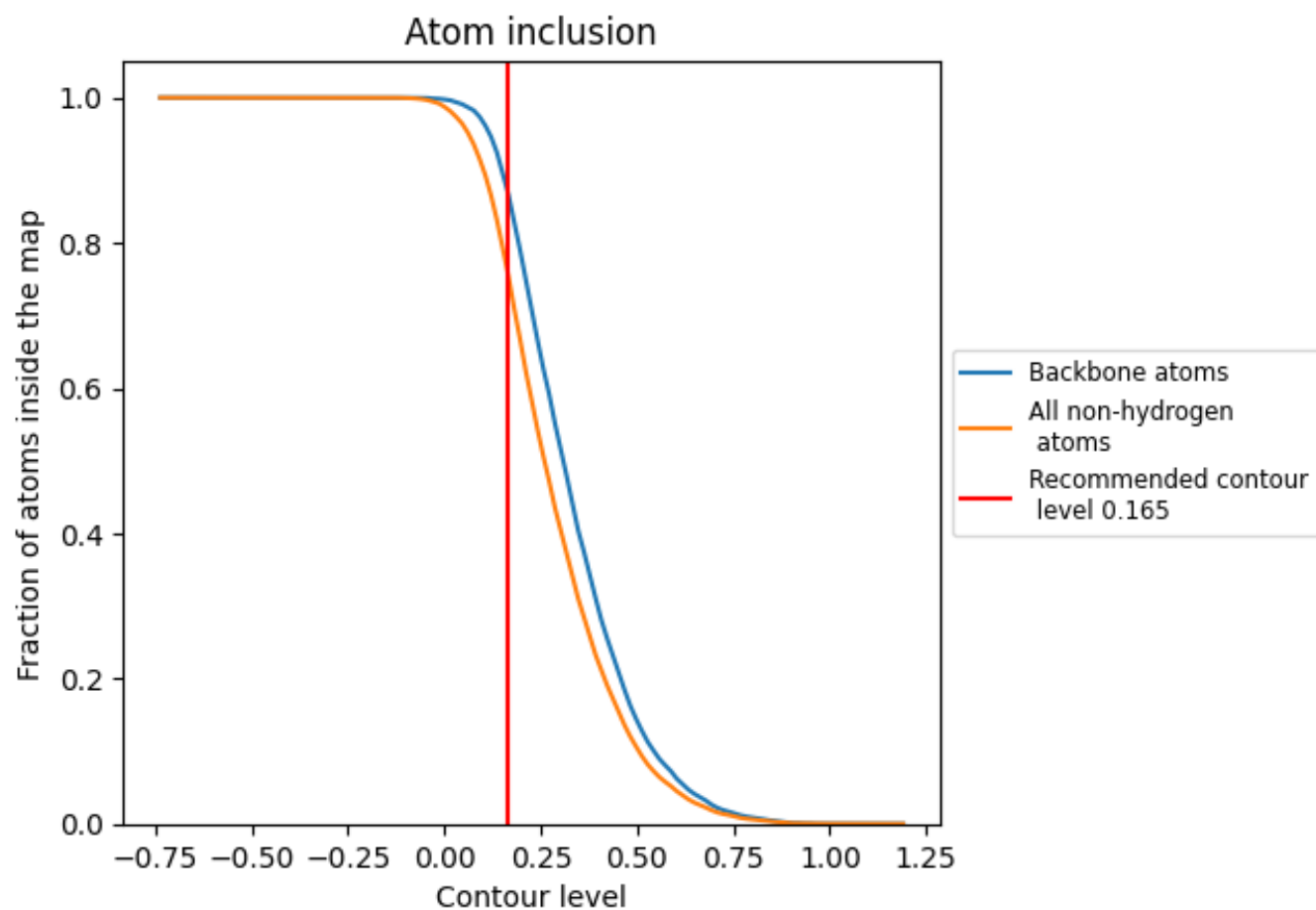
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.165).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ






The table lists the average atom inclusion at the recommended contour level (0.165) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7585	 0.4140
0	 0.7566	 0.4240
1	 0.7828	 0.4590
2	 0.8127	 0.4720
3	 0.7814	 0.4670
4	 0.7547	 0.4280
5	 0.7266	 0.3910
6	 0.7091	 0.3590
7	 0.7110	 0.3480
8	 0.7079	 0.3830
9	 0.7319	 0.3740
A	 0.8288	 0.4480
B	 0.7603	 0.4200
C	 0.7828	 0.4610
D	 0.8052	 0.4730
E	 0.7833	 0.4690
F	 0.7547	 0.4300
G	 0.7322	 0.3910
H	 0.7110	 0.3610
I	 0.7052	 0.3500
J	 0.7041	 0.3840
K	 0.7319	 0.3720
L	 0.8288	 0.4520
M	 0.8332	 0.4710
N	 0.7425	 0.3920
O	 0.7951	 0.4070
P	 0.5918	 0.2700
Q	 0.7709	 0.4190
R	 0.6075	 0.2680
S	 0.7732	 0.4410
T	 0.6760	 0.4040
a	 0.8337	 0.4700
b	 0.7378	 0.3910
d	 0.7975	 0.4070
e	 0.6000	 0.2680



*Continued on next page...*

*Continued from previous page...*

Chain	Atom inclusion	Q-score
f	 0.7709	 0.4190
g	 0.6170	 0.2690
i	 0.7732	 0.4430
k	 0.6760	 0.4070