



wwPDB EM Validation Summary Report ⓘ

Dec 19, 2022 – 12:25 am GMT

PDB ID : 7ND2
EMDB ID : EMD-12273
Title : Cryo-EM structure of the human FERRY complex
Authors : Quentin, D.; Klink, B.U.; Raunser, S.
Deposited on : 2021-01-29
Resolution : 4.00 Å(reported)

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<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) : 2.31.3

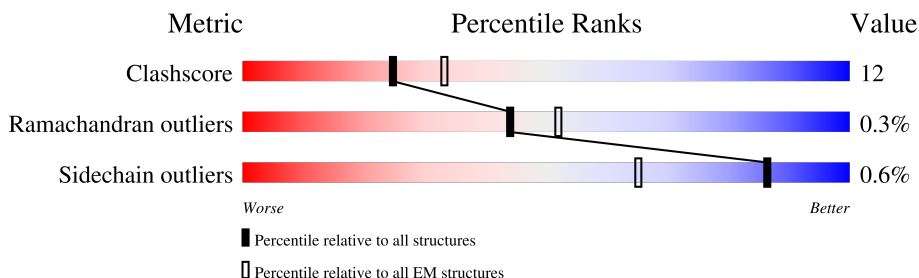
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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	784	
1	B	784	
2	C	356	
2	D	356	
3	E	227	
3	F	227	
3	G	227	
3	H	227	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16824 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 Protein phosphatase 1 regulatory subunit 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	330	Total	C	N	O	S	0	0
			2565	1633	437	483	12		
1	B	330	Total	C	N	O	S	0	0
			2565	1633	437	483	12		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	MET	-	initiating methionine	UNP Q6ZMI0
A	-2	ALA	-	expression tag	UNP Q6ZMI0
A	-1	ALA	-	expression tag	UNP Q6ZMI0
A	0	ALA	-	expression tag	UNP Q6ZMI0
B	-3	MET	-	initiating methionine	UNP Q6ZMI0
B	-2	ALA	-	expression tag	UNP Q6ZMI0
B	-1	ALA	-	expression tag	UNP Q6ZMI0
B	0	ALA	-	expression tag	UNP Q6ZMI0

- Molecule 2 is a protein called Quinone oxidoreductase-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	352	Total	C	N	O	S	0	0
			2721	1734	464	511	12		
2	D	352	Total	C	N	O	S	0	0
			2721	1734	464	511	12		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-6	MET	-	initiating methionine	UNP O95825
C	-5	SER	-	expression tag	UNP O95825
C	-4	HIS	-	expression tag	UNP O95825
C	-3	HIS	-	expression tag	UNP O95825
C	-2	HIS	-	expression tag	UNP O95825

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	HIS	-	expression tag	UNP O95825
C	0	HIS	-	expression tag	UNP O95825
C	1	HIS	-	expression tag	UNP O95825
D	-6	MET	-	initiating methionine	UNP O95825
D	-5	SER	-	expression tag	UNP O95825
D	-4	HIS	-	expression tag	UNP O95825
D	-3	HIS	-	expression tag	UNP O95825
D	-2	HIS	-	expression tag	UNP O95825
D	-1	HIS	-	expression tag	UNP O95825
D	0	HIS	-	expression tag	UNP O95825
D	1	HIS	-	expression tag	UNP O95825

- Molecule 3 is a protein called Glutamine amidotransferase-like class 1 domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	210	Total	C	N	O	S	1	0
			1563	984	273	295	11		
3	F	210	Total	C	N	O	S	1	0
			1563	984	273	295	11		
3	H	210	Total	C	N	O	S	1	0
			1563	984	273	295	11		
3	G	210	Total	C	N	O	S	1	0
			1563	984	273	295	11		

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-6	MET	-	initiating methionine	UNP Q8NB37
E	-5	SER	-	expression tag	UNP Q8NB37
E	-4	HIS	-	expression tag	UNP Q8NB37
E	-3	HIS	-	expression tag	UNP Q8NB37
E	-2	HIS	-	expression tag	UNP Q8NB37
E	-1	HIS	-	expression tag	UNP Q8NB37
E	0	HIS	-	expression tag	UNP Q8NB37
E	1	HIS	-	expression tag	UNP Q8NB37
F	-6	MET	-	initiating methionine	UNP Q8NB37
F	-5	SER	-	expression tag	UNP Q8NB37
F	-4	HIS	-	expression tag	UNP Q8NB37
F	-3	HIS	-	expression tag	UNP Q8NB37
F	-2	HIS	-	expression tag	UNP Q8NB37
F	-1	HIS	-	expression tag	UNP Q8NB37

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Chain	Residue	Modelled	Actual	Comment	Reference
F	0	HIS	-	expression tag	UNP Q8NB37
F	1	HIS	-	expression tag	UNP Q8NB37
H	-6	MET	-	initiating methionine	UNP Q8NB37
H	-5	SER	-	expression tag	UNP Q8NB37
H	-4	HIS	-	expression tag	UNP Q8NB37
H	-3	HIS	-	expression tag	UNP Q8NB37
H	-2	HIS	-	expression tag	UNP Q8NB37
H	-1	HIS	-	expression tag	UNP Q8NB37
H	0	HIS	-	expression tag	UNP Q8NB37
H	1	HIS	-	expression tag	UNP Q8NB37
G	-6	MET	-	initiating methionine	UNP Q8NB37
G	-5	SER	-	expression tag	UNP Q8NB37
G	-4	HIS	-	expression tag	UNP Q8NB37
G	-3	HIS	-	expression tag	UNP Q8NB37
G	-2	HIS	-	expression tag	UNP Q8NB37
G	-1	HIS	-	expression tag	UNP Q8NB37
G	0	HIS	-	expression tag	UNP Q8NB37
G	1	HIS	-	expression tag	UNP Q8NB37

THR	GLU	GLU	LYS	ASN	LYS	LEU	ALA	SER	GLN	ASN	ILE	SER	ARG	LEU	GLN	ASP	GLU	LEU	THR	THR	THR	LYS	ARG	SER	SER	THR	GLU	ASP	GLN	LEU	SER	MET	MET	SER	SER	ASP	HIS	LEU	CYS	SER	MET	ASN	GLU	THR	LEU	SER	LYS	GLN	ARG	GLU	GLU	ILE	ASP	THR	LEU	LYS	MET	SER	SER	SER	LYS	GLY	ASN	GLU	THR
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- Molecule 1: Protein phosphatase 1 regulatory subunit 21



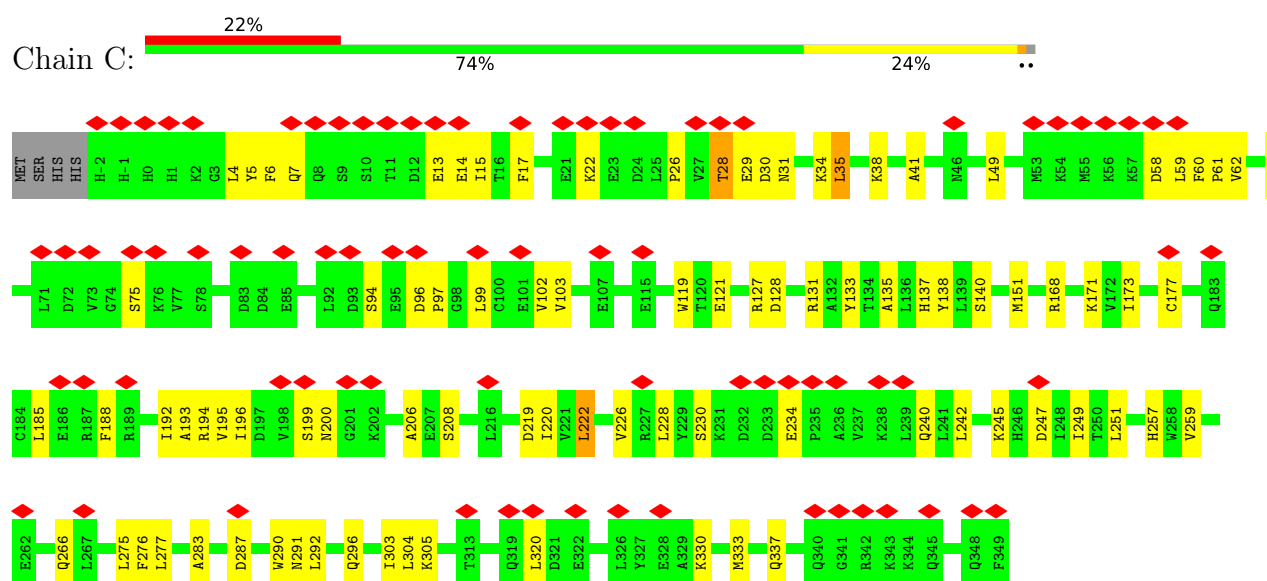
MET	ALA	ALA	ALA	NET	SER	ALA	ALA	GLU	GLN	LEU	GLY	LYS	TYR	GLN	LYS	LEU	LEU	ALA	GLN	GLU	TYR	SER	LYS	LEU	ARG	ALA	GLN	ASN	VAL	VAL	GLY	GLY	VAL	VAL	ASP	GLU	GLN	ALA	ALA	SER	ASN	LYS	LEU	LEU	ALA	MET	LYS	LYS	ASP	GLN	SER	LYS	LEU	ARG	LYS	LEU	GLN
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GLN
GLU
MET
ASP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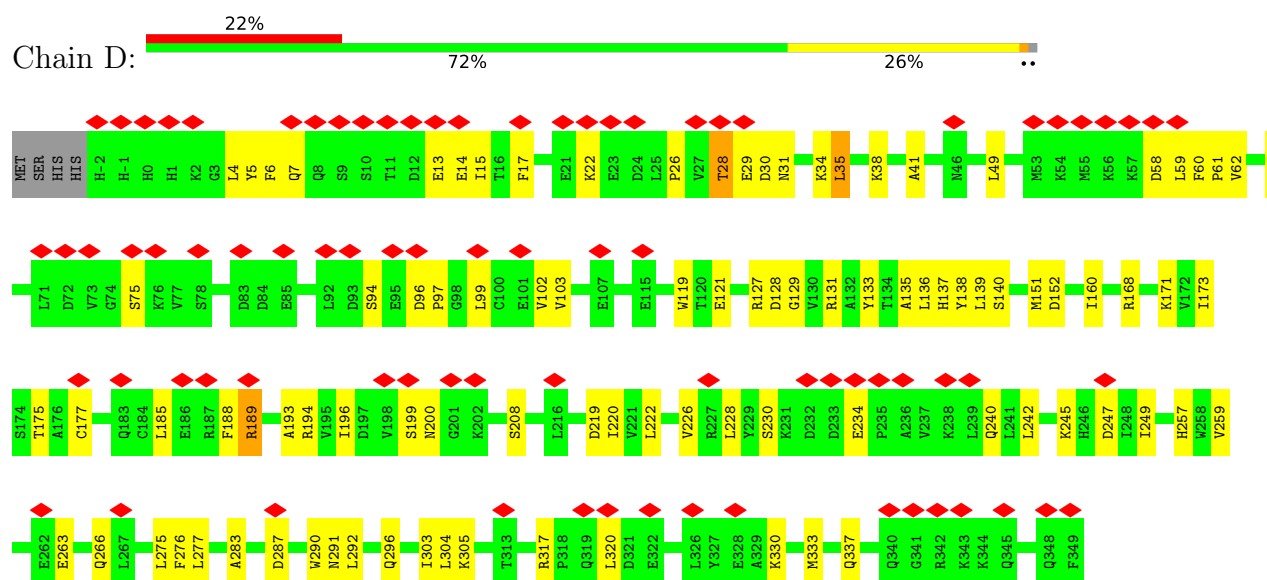
GLU GLU GLU ASN GLN PHE PHE GLU LEU HIS ILE GLN PHE PHE GLU ALA ASP GLU GLN HIS LYS HIS VAL GLU GLU LEU ARG SER ARG ARG LEU LEU THR THR LEU GLU THR ALA ALA GLN HIS GLN ALA VAL VAL ASP GLY LEU THR THR ARG LYS TYR MET GLU THR THR ILE GLU LYS LEU GLN ASN GLN ASP ASP

LYS	GLY	ALA	THR	ARG	ILE	K529	E454	S385	E323	D284	LYS	ALA
ASN	LEU	LEU	SER	THR	LEU	S530	L455	Q386	S324	I255	LEU	LYS
SER	THR	THR	ASP	ASP	GLU	K533	P456	D387	I325		GLU	LEU
LYS	GLU	GLU	SER	SER	LYS	P534	T457		T326	Q288	VAL	GLU
LYS	GLU	GLU	LYS	GLU	ASN	L535	A458	T392	E327	A259	LYS	LYS
ASN	MET	VAL	VAL	VAL	ASN	L536	T459	A393	D328		GLN	SER
LYS	LYS	PRO	ASP	ASP	GLN	E537	Q460	E396	T329	Q264	THR	THR
LEU	LEU	VAL	ILE	ILE	ALA	S538	K461		V330		LEU	LEU
ALA	ARG	VAL	ARG	ARG	ALA	E539	L462	Q399	L333	T268	GLU	GLU
GLN	SER	GLU	GLU	SER	ASP	V539	L463	T400	E394	A269	LYS	LYS
ASN	ASN	ARG	GLU	GLU	LYS	P540	T464	Y401	L271	L270	GLU	GLU
ILE	ILE	ASP	ASP	ASP	LYS	Y541		I402	N272	L271	ALA	ALA
SER	SER	ASP	ASP	ASP	LYS		D467	A403	V337	F273	GLU	GLU
ARG	ARG	LEU	LEU	LEU	ASN	A544		L404	K338	H274	CYS	CYS
LEU	LEU	ILE	THR	THR	THR	L546	L470	L405	L339	T275	ARG	ARG
GLN	GLN	LYS	GLY	GLY	GLY	A546	S471	A406	K340	Y276	LEU	LEU
ASP	ASP	ASN	SER	SER	ALA	N547		L407	T341	T277	ARG	ARG
GLU	LEU	THR	THR	THR	GLN	R548	L476	P408	F342	R280	THR	THR
LEU	THR	THR	THR	THR	VAL	R549	T477	S409	S343	I281	GLU	GLU
LYS	LYS	THR	THR	THR	GLY	I550	H478	T410	E344		GLU	GLU
LYS	LYS	ILE	ILE	ILE	LEU	L551	G479	E411	H345	Q282	GLN	GLN
ARG	ARG	VAL	VAL	VAL	ALA	L552		P412	L346	F284	LEU	LEU
SER	SER	GLU	GLU	GLU	GLN		K482	D412	T347	P285	GLN	GLN
SER	SER	GLU	GLU	GLU	GLU	SER	L483	D413	I350	V286	LEU	LEU
THR	THR	LEU	LEU	LEU	ASN	THR	A484	Q414	C351	ASP	THR	THR
ALA	ALA	ALA	SER	SER	ALA	GLU	S485	L415	F352	SER	LEU	LEU
ALA	ALA	ALA	LYS	LYS	VAL	SER	F486	L416	L353	ALA	HIS	HIS
VAL	VAL	VAL	VAL	VAL	VAL	ARG	F487	R417	R354	ILE	GLU	GLU
SER	SER	GLN	GLN	GLN	ASN	GLU	S488	T418	K355	ASP	ASP	ASP
THR	THR	THR	THR	THR	THR	GLY	H489	N419	I356	LEU	LEU	LEU
ALA	ALA	ALA	ALA	ALA	ALA	LEU	H490	Y420	L357	ASP	SER	SER
ASP	ASP	ASP	ASP	SER	GLY	ALA	L491	S421	P358	T292	GLY	GLY
HIS	LEU	HIS	LYS	LYS	GLN	GLN	D492	S422	Y359	I293	ARG	ARG
VAL	VAL	VAL	SER	SER	ASP	VAL	Y493	V423	Q360	L296	GLU	GLU
GLN	GLN	GLN	GLN	GLN	GLN	GLN	A496	L424	L361	N297	GLU	GLU
GLN	GLN	GLN	THR	THR	THR	SER	S497	T425	K362	Q298	LYS	LYS
ALA	ALA	ALA	ALA	ALA	LYS	LEU	L498	N426	S363	K299	GLU	GLU
LYS	LYS	LYS	LYS	LYS	LYS	GLU		V427	L364	F300	LYS	LYS
ALA	ALA	ALA	ALA	ALA	VAL	LYS	S499	A429	E365	S301	LYS	LYS
THR	THR	THR	THR	THR	VAL	ILE	Y500	A429	E366	Q302	LYS	LYS
LEU	LEU	LEU	LEU	LEU	GLU	SER	G501	A430	E367	I221	LYS	LYS
LYS	LYS	LYS	ARG	ARG	LEU	SER	P502	L431	H305	N223	LYS	LYS
GLN	GLN	GLN	ALA	ALA	PRO	LYS			E368	E306	LYS	LYS
ARG	ARG	SER	LEU	LEU	LEU	LEU	H432	H432	C369	K225	LYS	LYS
GLU	GLU	LYS	GLN	GLN	ILE	GLU	K503	G433	S370		LYS	LYS
GLU	GLU	ARG	SER	SER	THR	GLU	A504	F434	S371	S309	LYS	LYS
LYS	LYS	LEU	LEU	LEU	SER	LYS	A505	H495	L372	Y310	LYS	LYS
GLU	GLU	ALA	ALA	ALA	GLU	GLU	S506		C373	V311	LYS	LYS
LEU	LEU	LEU	LEU	LEU	ILE	LYS	G507	M438	T374	R312	LYS	LYS
THR	THR	THR	THR	THR	ILE	TRP	F508		S375	P313	LYS	LYS
THR	THR	THR	THR	THR	THR	MET			A376	L314	LYS	LYS
LEU	LEU	LEU	LEU	LEU	LEU	LEU	T509	K443	L377	E315	LYS	LYS
LEU	LEU	ALA	ALA	ALA	ALA	GLU	S510	H444	R378	G317	LYS	LYS
ALA	ALA	ALA	ALA	ALA	ALA	ILE	P511	Y445	L377	E316	LYS	LYS
LEU	LEU	LEU	LEU	LEU	GLN	GLN	L512	S446	R378	G317	LYS	LYS
ALA	ALA	LEU	LEU	LEU	THR	THR			A379	M318	LYS	LYS
LYS	LYS	ALA	ALA	ALA	LYS	LYS	F515	K448	R360	L319	LYS	LYS
							C516		N381	H320	LYS	LYS
							K522	A449	E383	F322	LYS	LYS
								A450	L382	L321	LYS	LYS
								I451	L384		LYS	LYS
								E452			LYS	LYS
								H453			LYS	LYS
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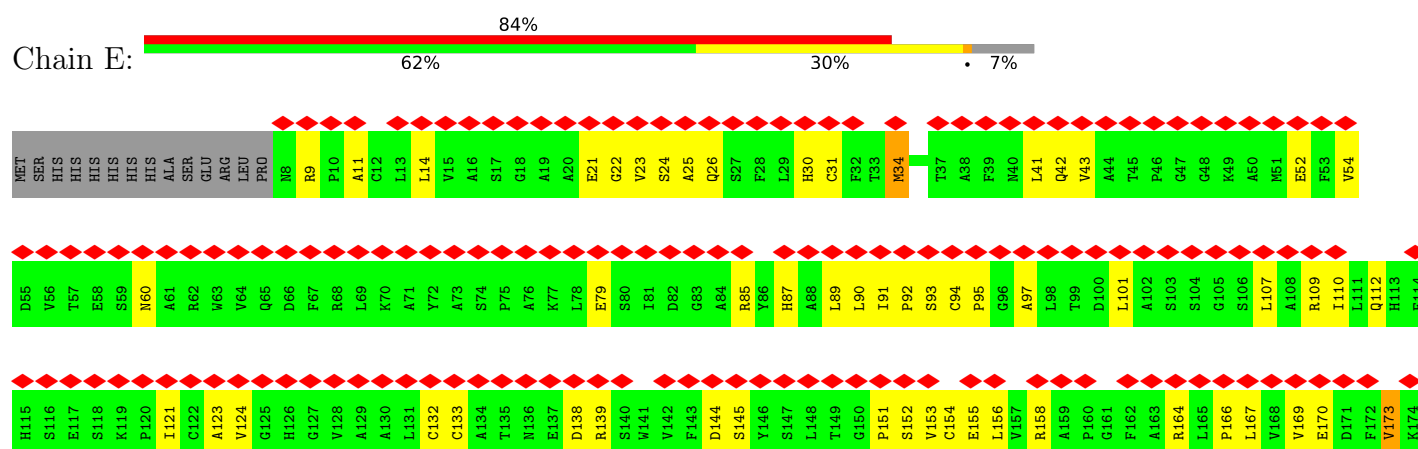
- Molecule 2: Quinone oxidoreductase-like protein 1



• Molecule 2: Quinone oxidoreductase-like protein 1

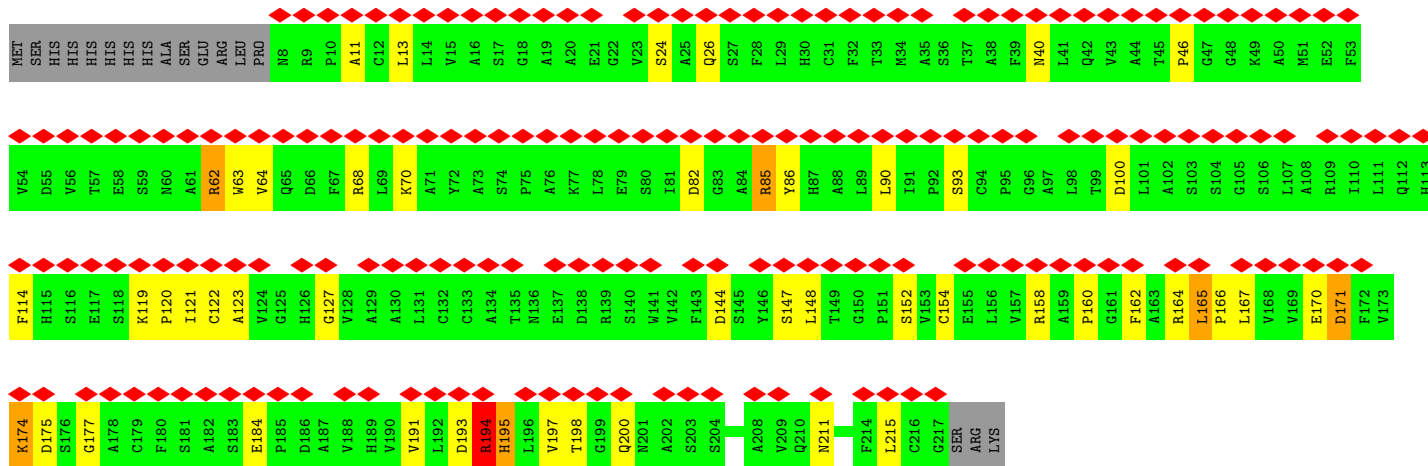
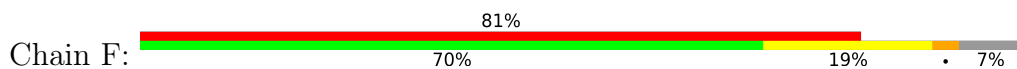


• Molecule 3: Glutamine amidotransferase-like class 1 domain-containing protein 1

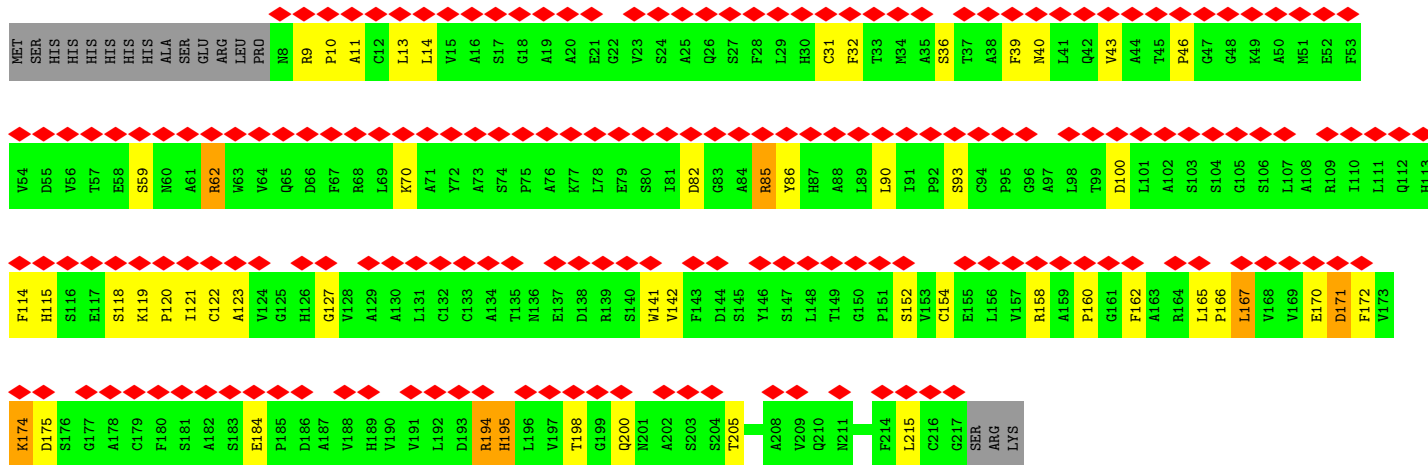
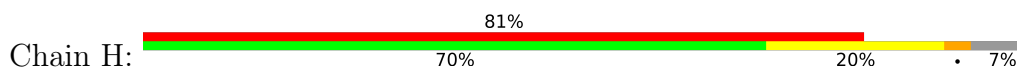




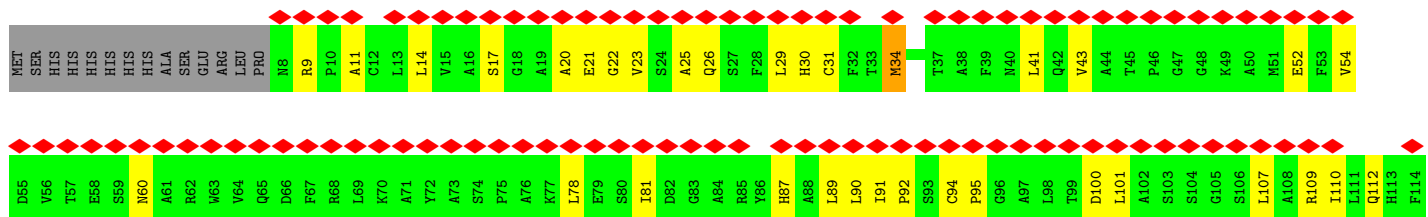
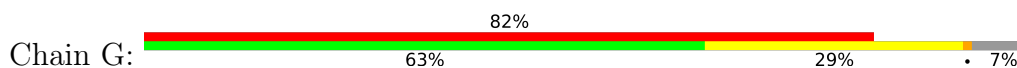
• Molecule 3: Glutamine amidotransferase-like class 1 domain-containing protein 1



• Molecule 3: Glutamine amidotransferase-like class 1 domain-containing protein 1



• Molecule 3: Glutamine amidotransferase-like class 1 domain-containing protein 1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	18300	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	75.8	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.049	Depositor
Minimum map value	-0.026	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.011	Depositor
Map size (Å)	285.12003, 285.12003, 285.12003	wwPDB
Map dimensions	264, 264, 264	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.50	0/2609	0.84	7/3532 (0.2%)
1	B	0.52	0/2609	0.83	4/3532 (0.1%)
2	C	0.62	0/2774	0.87	5/3760 (0.1%)
2	D	0.62	0/2774	0.88	5/3760 (0.1%)
3	E	0.45	0/1599	0.92	6/2179 (0.3%)
3	F	0.42	0/1599	0.85	6/2179 (0.3%)
3	G	0.51	1/1599 (0.1%)	0.97	8/2179 (0.4%)
3	H	0.40	0/1599	0.85	5/2179 (0.2%)
All	All	0.53	1/17162 (0.0%)	0.87	46/23300 (0.2%)

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
3	F	0	1
3	H	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	92	PRO	CG-CD	-8.80	1.21	1.50

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	92	PRO	N-CD-CG	-10.27	87.80	103.20
3	F	165	LEU	CA-CB-CG	9.50	137.16	115.30
3	H	165	LEU	CA-CB-CG	9.15	136.34	115.30
1	A	424	LEU	CA-CB-CG	8.74	135.40	115.30
3	E	21	GLU	CA-CB-CG	8.28	131.62	113.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	F	70	LYS	Peptide
3	H	70	LYS	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2565	0	2564	79	0
1	B	2565	0	2564	81	0
2	C	2721	0	2727	56	0
2	D	2721	0	2727	61	0
3	E	1563	0	1526	41	0
3	F	1563	0	1526	33	0
3	G	1563	0	1526	36	0
3	H	1563	0	1526	32	0
All	All	16824	0	16686	391	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 12.

The worst 5 of 391 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)
1:A:412:PRO:HD2	1:A:511:PRO:HG3	1.71	0.73
1:B:412:PRO:HD2	1:B:511:PRO:HG3	1.73	0.70
3:H:59:SER:O	3:H:62:ARG:NH1	2.25	0.70
1:B:420:TYR:HA	1:B:423:VAL:HB	1.73	0.69
3:E:154:CYS:SG	3:E:155:GLU:N	2.67	0.67

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	326/784 (42%)	313 (96%)	13 (4%)	0	100	100
1	B	326/784 (42%)	313 (96%)	13 (4%)	0	100	100
2	C	350/356 (98%)	333 (95%)	15 (4%)	2 (1%)	25	63
2	D	350/356 (98%)	332 (95%)	16 (5%)	2 (1%)	25	63
3	E	209/227 (92%)	194 (93%)	15 (7%)	0	100	100
3	F	209/227 (92%)	198 (95%)	10 (5%)	1 (0%)	29	67
3	G	209/227 (92%)	193 (92%)	15 (7%)	1 (0%)	29	67
3	H	209/227 (92%)	196 (94%)	12 (6%)	1 (0%)	29	67
All	All	2188/3188 (69%)	2072 (95%)	109 (5%)	7 (0%)	44	75

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	29	GLU
3	F	152	SER
2	D	29	GLU
3	H	152	SER
3	G	20	ALA

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	278/694 (40%)	278 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	278/694 (40%)	277 (100%)	1 (0%)	91	94
2	C	298/310 (96%)	298 (100%)	0	100	100
2	D	298/310 (96%)	298 (100%)	0	100	100
3	E	168/183 (92%)	165 (98%)	3 (2%)	59	77
3	F	168/183 (92%)	163 (97%)	5 (3%)	41	64
3	G	168/183 (92%)	166 (99%)	2 (1%)	71	84
3	H	168/183 (92%)	164 (98%)	4 (2%)	49	69
All	All	1824/2740 (67%)	1809 (99%)	15 (1%)	86	89

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	195[B]	HIS
3	G	195[A]	HIS
1	B	419	ASN
3	G	195[B]	HIS
3	H	195[A]	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	297	GLN
1	B	419	ASN
3	G	60	ASN
3	G	26	GLN
3	E	42	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 [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

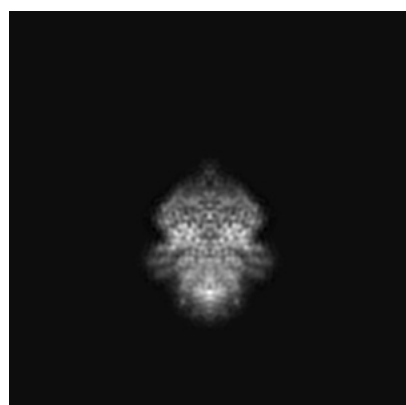
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12273. These allow visual inspection of the internal detail of the map and identification of artifacts.

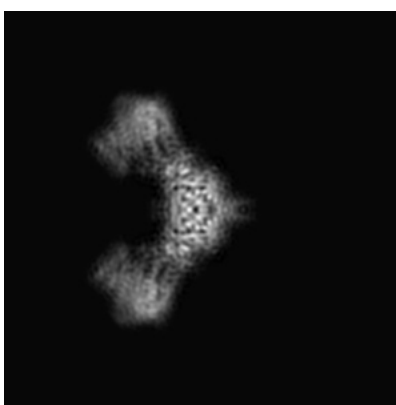
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

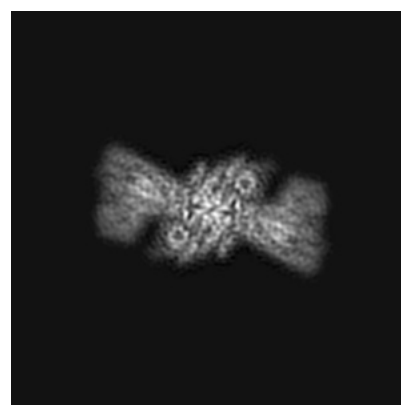
6.1.1 Primary map



X



Y



Z

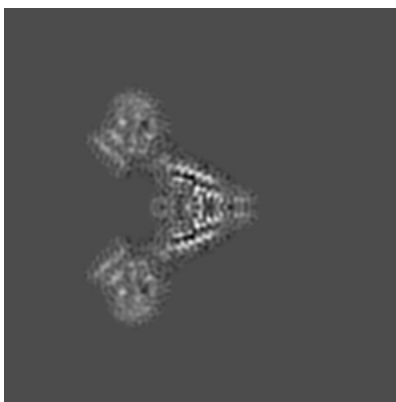
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

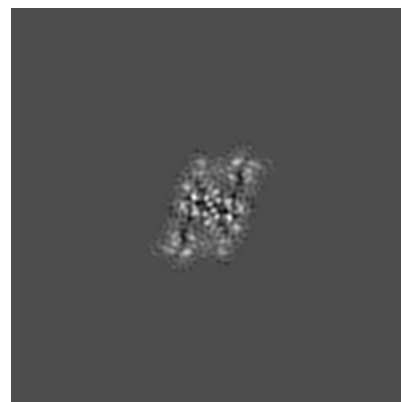
6.2.1 Primary map



X Index: 132



Y Index: 132

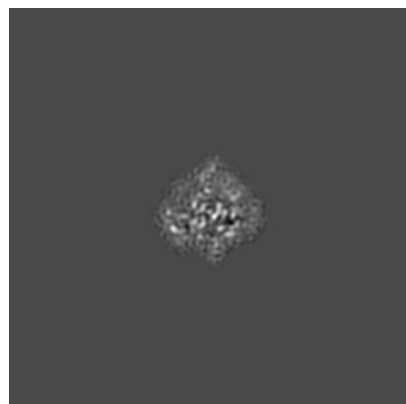


Z Index: 132

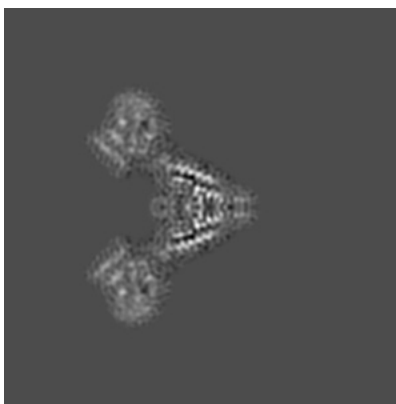
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

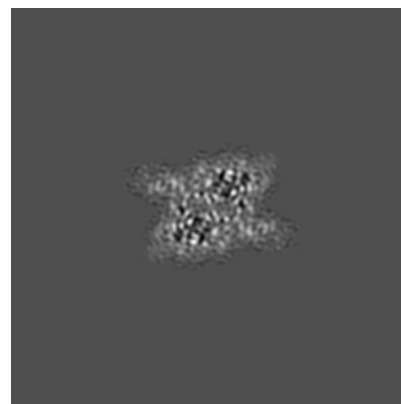
6.3.1 Primary map



X Index: 128



Y Index: 132



Z Index: 119

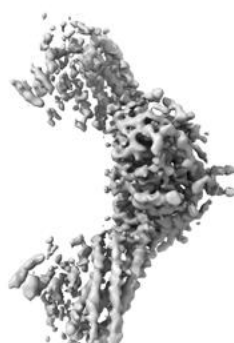
The images above show the largest variance slices of the map in three orthogonal directions.

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

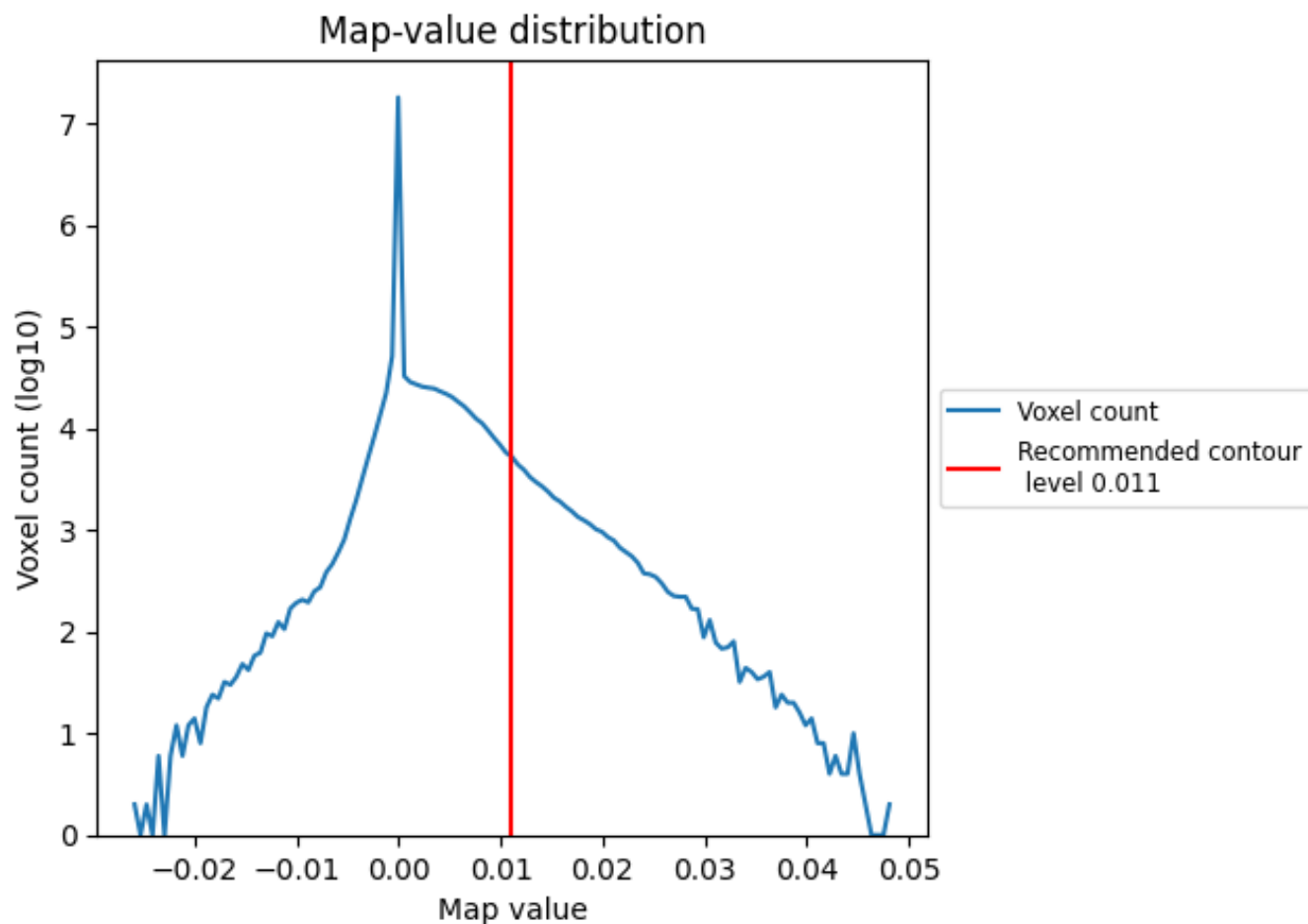
6.5 Mask visualisation

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

7 Map analysis [i](#)

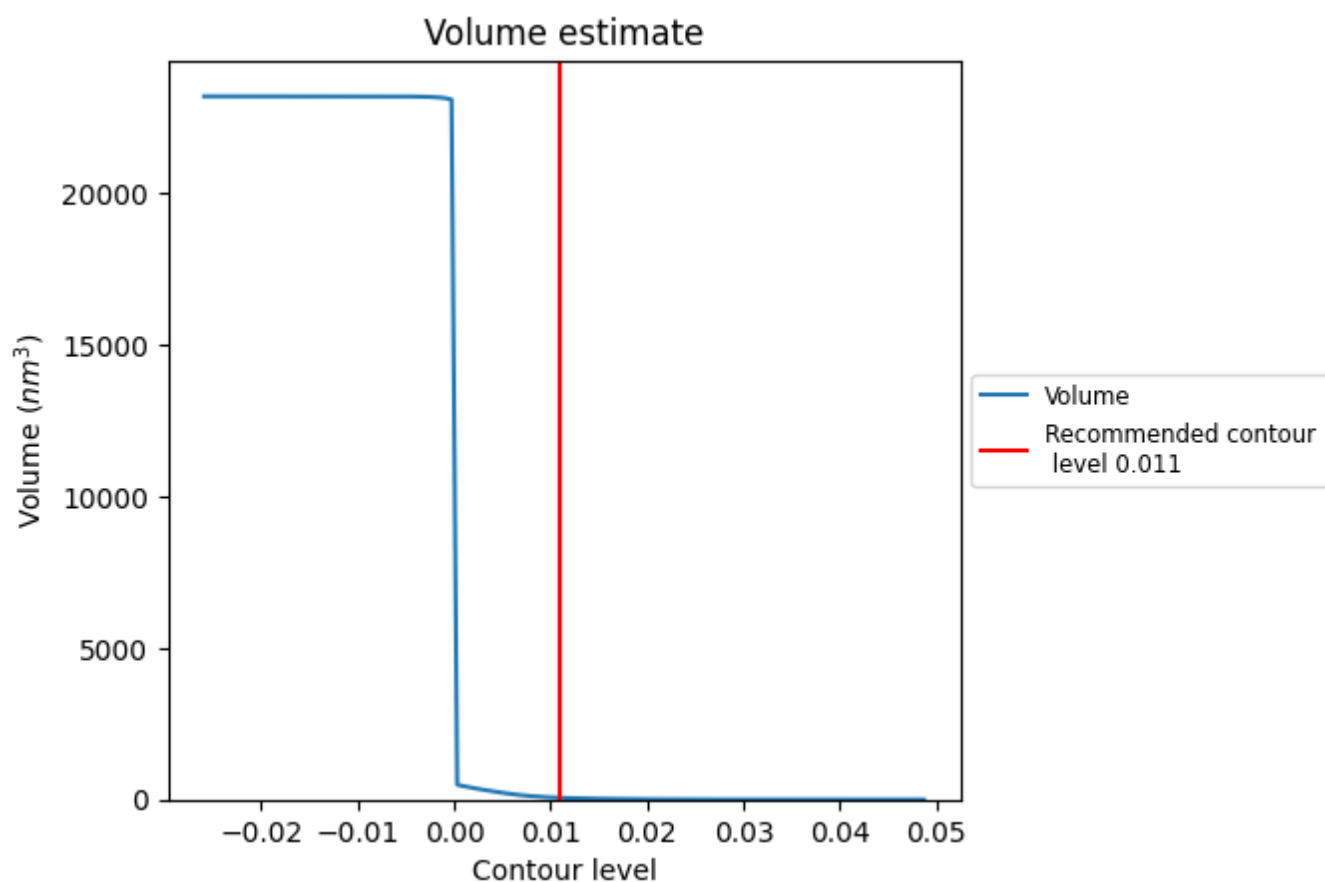
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

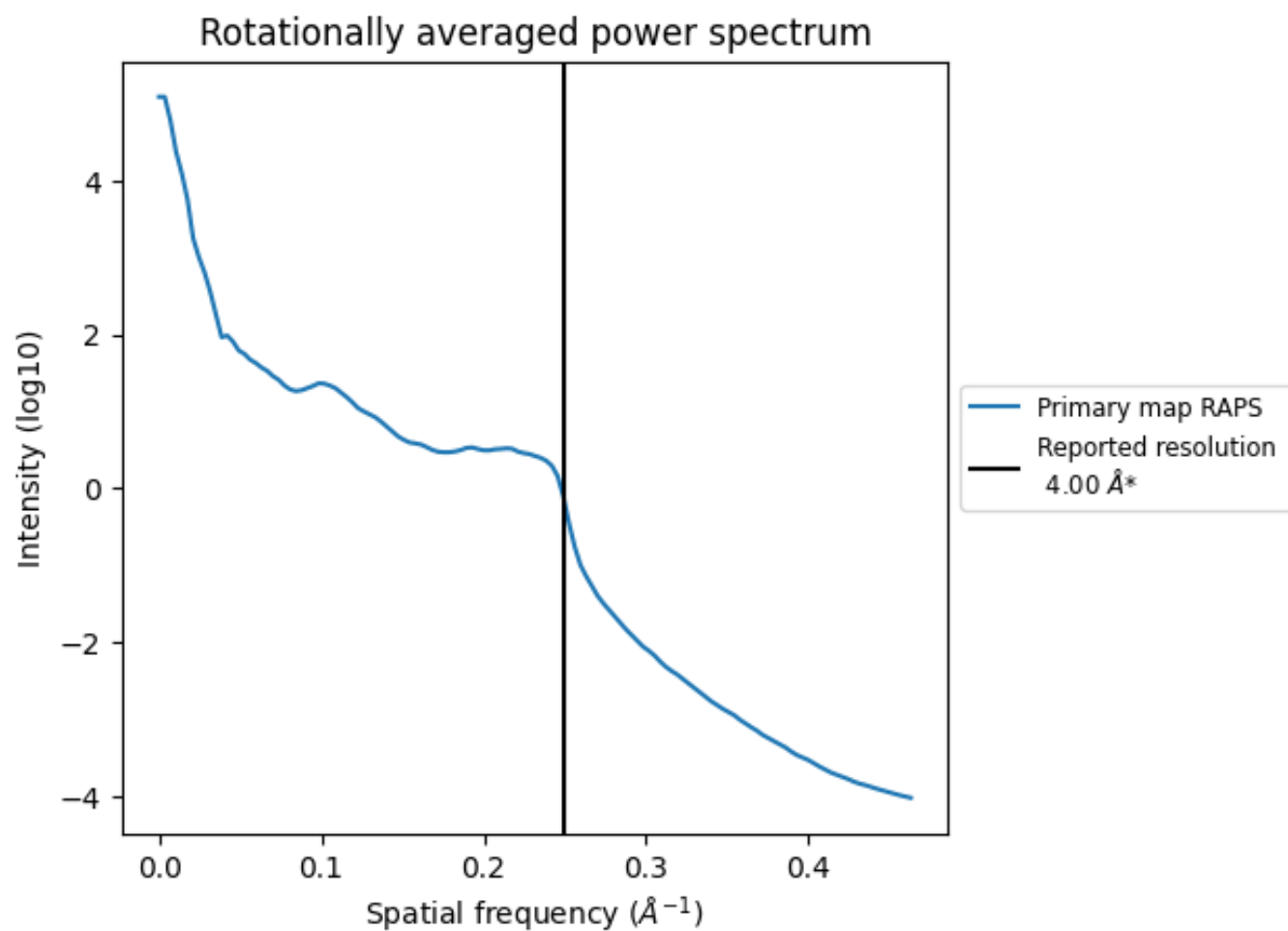
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 58 nm^3 ; this corresponds to an approximate mass of 53 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 0.250 Å⁻¹

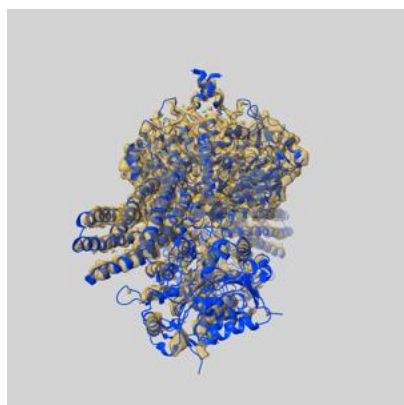
8 Fourier-Shell correlation

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

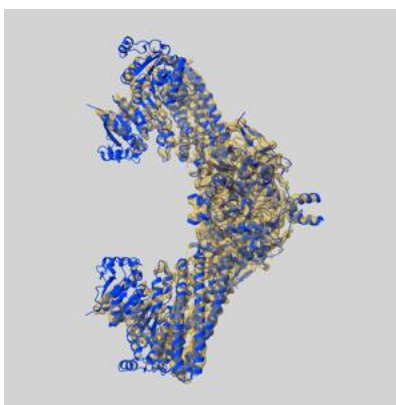
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12273 and PDB model 7ND2. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

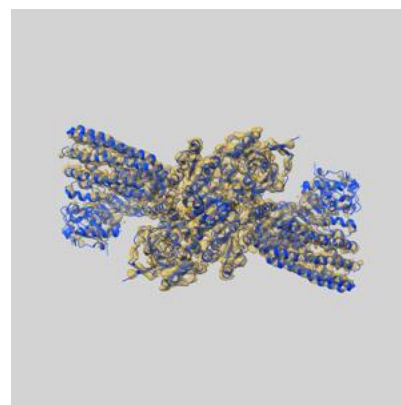
9.1 Map-model overlay [i](#)



X



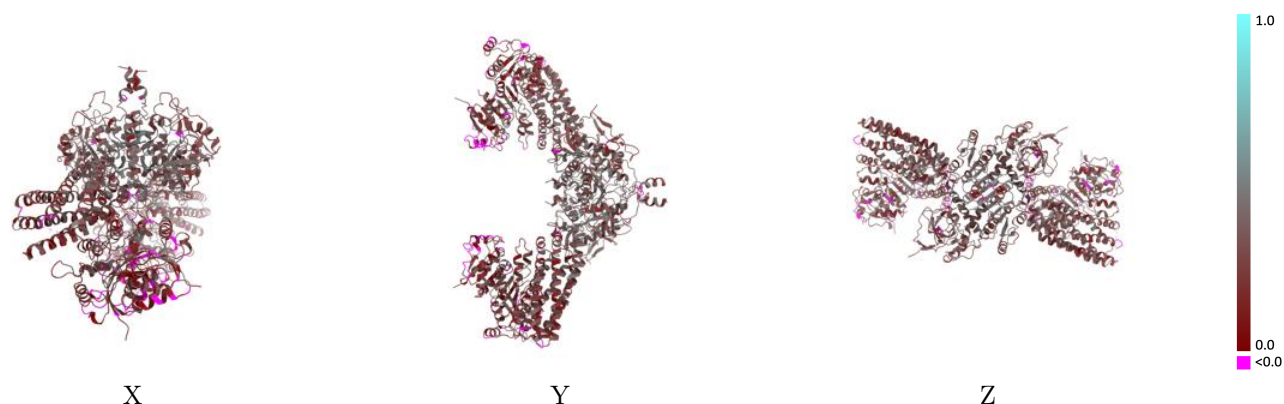
Y



Z

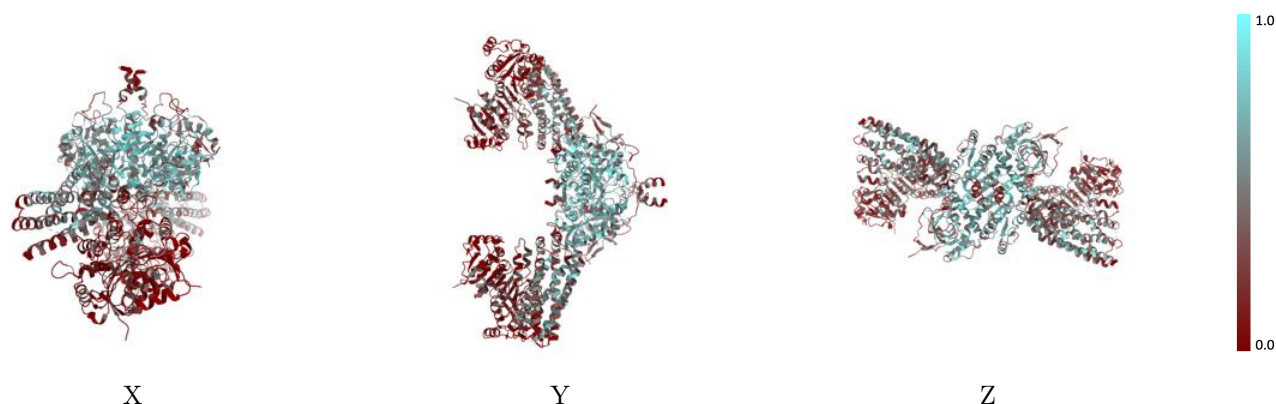
The images above show the 3D surface view of the map at the recommended contour level 0.011 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



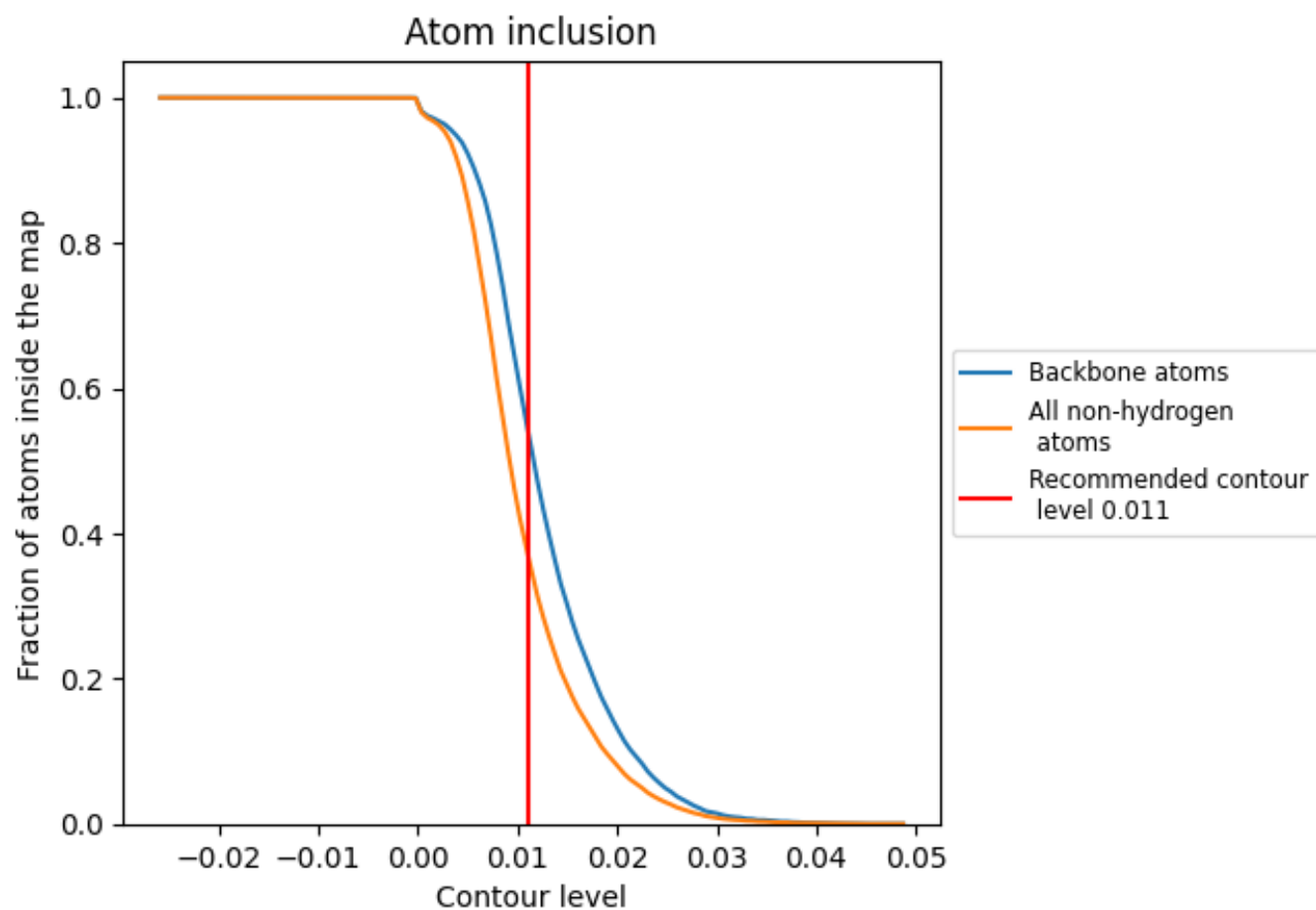
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.011).

9.4 Atom inclusion [i](#)



At the recommended contour level, 54% of all backbone atoms, 37% 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 (0.011) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.3724	<div></div> 0.2850
A	<div></div> 0.4363	<div></div> 0.2990
B	<div></div> 0.4391	<div></div> 0.3020
C	<div></div> 0.5738	<div></div> 0.3540
D	<div></div> 0.5731	<div></div> 0.3530
E	<div></div> 0.1405	<div></div> 0.2010
F	<div></div> 0.1405	<div></div> 0.2240
G	<div></div> 0.1438	<div></div> 0.2020
H	<div></div> 0.1425	<div></div> 0.2230

