



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 06:43 AM UTC

PDB ID : 3IZY / pdb_00003izy
EMDB ID : EMD-1855
Title : Mammalian mitochondrial translation initiation factor 2
Authors : Yassin, A.S.; Haque, E.; Datta, P.P.; Elmore, K.; Banavali, N.K.; Spremulli, L.L.; Agrawal, R.K.
Deposited on : 2011-01-19
Resolution : 10.80 Å(reported)

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

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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
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

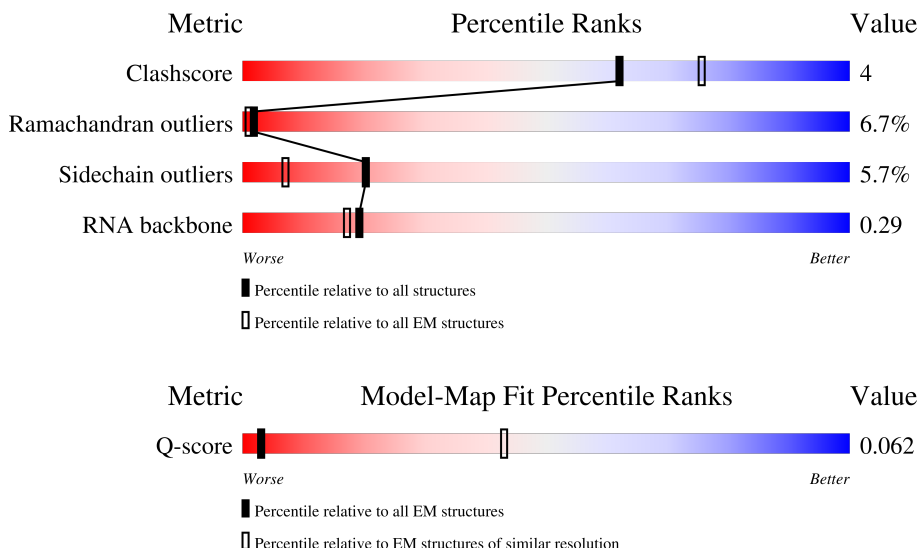
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 10.80 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	98 (10.30 - 11.30)

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	N	76	
2	P	537	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5802 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 RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	N	76	Total	C	N	O	P	0	0
			1622	725	293	529	75		

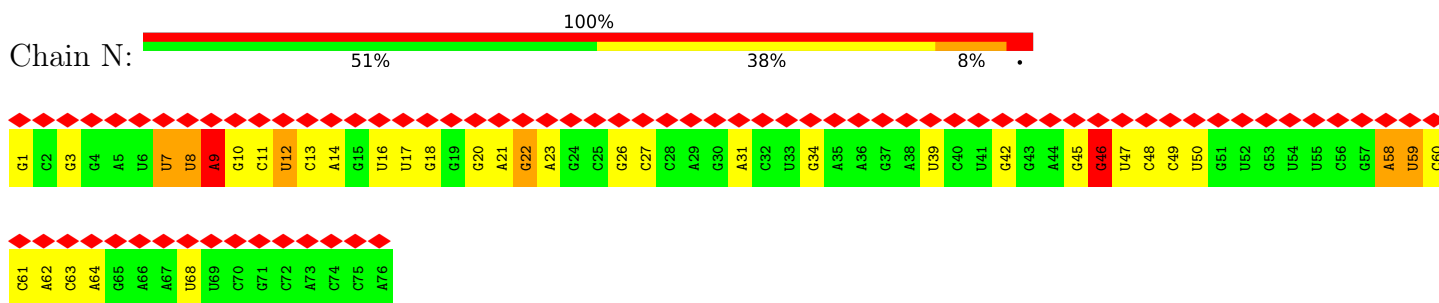
- Molecule 2 is a protein called Translation initiation factor IF-2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	537	Total	C	N	O	S	0	0
			4180	2631	732	799	18		

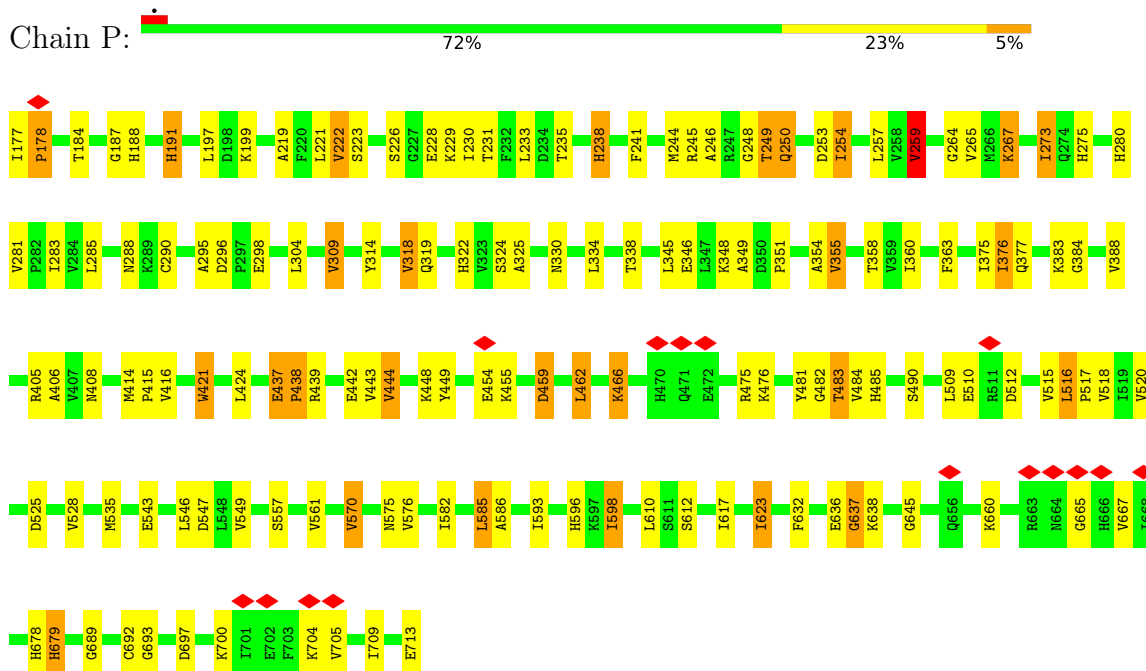
3 Residue-property plots

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: tRNA-Phe



• Molecule 2: Translation initiation factor IF-2, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	121742	Depositor
Resolution determination method	Not provided	
CTF correction method	Every Micrograph	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	50760	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	118750.000	Depositor
Minimum map value	-80468.800	Depositor
Average map value	25.858	Depositor
Map value standard deviation	2548.510	Depositor
Recommended contour level	14825	Depositor
Map size ($\text{\AA}$)	358.8, 358.8, 358.8	wwPDB
Map dimensions	130, 130, 130	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing ($\text{\AA}$)	2.76, 2.76, 2.76	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	N	0.90	0/1814	1.13	2/2827 (0.1%)
2	P	1.33	4/4247 (0.1%)	1.69	83/5726 (1.4%)
All	All	1.22	4/6061 (0.1%)	1.53	85/8553 (1.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	N	0	11
2	P	0	5
All	All	0	16

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	713	GLU	C-OXT	-11.58	1.00	1.23
2	P	713	GLU	C-O	-11.55	1.00	1.23
2	P	693	GLY	CA-C	-5.91	1.48	1.52
2	P	296	ASP	CA-CB	5.51	1.56	1.52

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	709	ILE	N-CA-C	-7.69	95.99	107.37
2	P	406	ALA	N-CA-C	7.63	119.59	111.28
2	P	330	ASN	CA-C-N	6.91	130.23	120.28
2	P	330	ASN	C-N-CA	6.91	130.23	120.28
2	P	490	SER	CA-C-N	6.79	129.38	120.28
2	P	490	SER	C-N-CA	6.79	129.38	120.28
2	P	375	ILE	N-CA-CB	6.77	119.11	110.99
1	N	9	A	P-O5'-C5'	-6.53	111.10	120.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	462	LEU	N-CA-CB	6.47	116.11	109.51
2	P	191	HIS	N-CA-C	-6.46	105.03	113.17
2	P	405	ARG	CA-C-N	6.35	128.79	120.28
2	P	405	ARG	C-N-CA	6.35	128.79	120.28
2	P	199	LYS	CA-C-N	6.33	129.08	120.54
2	P	199	LYS	C-N-CA	6.33	129.08	120.54
2	P	250	GLN	N-CA-C	6.32	118.70	110.43
2	P	557	SER	CA-C-N	6.19	128.58	120.28
2	P	557	SER	C-N-CA	6.19	128.58	120.28
2	P	228	GLU	CA-C-N	6.19	133.37	121.54
2	P	228	GLU	C-N-CA	6.19	133.37	121.54
2	P	244	MET	CG-SD-CE	-6.15	87.36	100.90
2	P	249	THR	N-CA-C	-6.03	97.96	110.80
2	P	184	THR	N-CA-C	-5.99	100.20	109.24
2	P	259	VAL	N-CA-C	-5.90	100.05	109.20
2	P	598	ILE	O-C-N	-5.88	115.22	122.57
2	P	298	GLU	CA-C-N	5.88	128.08	120.44
2	P	298	GLU	C-N-CA	5.88	128.08	120.44
2	P	475	ARG	N-CA-C	-5.83	106.08	113.43
2	P	375	ILE	N-CA-C	-5.82	100.03	108.36
2	P	223	SER	CA-C-N	5.79	127.33	120.09
2	P	223	SER	C-N-CA	5.79	127.33	120.09
2	P	576	VAL	N-CA-C	5.77	116.51	110.62
2	P	267	LYS	N-CA-C	5.77	117.24	111.07
2	P	319	GLN	N-CA-C	-5.68	100.92	109.95
2	P	692	CYS	N-CA-C	-5.68	100.44	109.07
2	P	322	HIS	CA-CB-CG	-5.66	108.14	113.80
2	P	249	THR	N-CA-CB	5.63	120.01	110.49
2	P	637	GLY	N-CA-C	-5.63	106.76	114.64
2	P	177	ILE	CA-C-N	5.61	126.85	119.84
2	P	177	ILE	C-N-CA	5.61	126.85	119.84
2	P	483	THR	CA-C-N	5.58	132.02	121.97
2	P	483	THR	C-N-CA	5.58	132.02	121.97
2	P	376	ILE	N-CA-C	-5.57	99.21	107.51
2	P	187	GLY	N-CA-C	-5.54	105.27	111.63
2	P	454	GLU	CA-C-N	5.50	128.42	120.38
2	P	454	GLU	C-N-CA	5.50	128.42	120.38
2	P	330	ASN	CA-CB-CG	-5.46	107.14	112.60
2	P	264	GLY	CA-C-N	5.45	131.78	121.97
2	P	264	GLY	C-N-CA	5.45	131.78	121.97
2	P	295	ALA	N-CA-C	5.42	117.79	111.02
2	P	632	PHE	CA-CB-CG	-5.41	108.39	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	437	GLU	CA-C-N	5.38	126.57	119.84
2	P	437	GLU	C-N-CA	5.38	126.57	119.84
2	P	406	ALA	CA-C-N	5.38	131.38	121.70
2	P	406	ALA	C-N-CA	5.38	131.38	121.70
2	P	238	HIS	CA-C-N	5.36	128.84	120.75
2	P	238	HIS	C-N-CA	5.36	128.84	120.75
1	N	46	G	P-O3'-C3'	5.34	128.21	120.20
2	P	408	ASN	N-CA-C	-5.32	99.64	108.75
2	P	338	THR	N-CA-CB	5.32	117.94	110.12
2	P	254	ILE	N-CA-C	-5.31	100.79	108.71
2	P	360	ILE	N-CA-C	-5.30	105.23	111.00
2	P	660	LYS	N-CA-C	-5.25	98.47	107.61
2	P	485	HIS	N-CA-C	5.21	117.71	111.71
2	P	585	LEU	CA-C-N	5.21	127.25	120.28
2	P	585	LEU	C-N-CA	5.21	127.25	120.28
2	P	384	GLY	N-CA-C	-5.17	102.90	110.87
2	P	421	TRP	N-CA-CB	5.17	119.23	110.49
2	P	226	SER	N-CA-C	-5.16	100.99	109.40
2	P	363	PHE	CA-CB-CG	-5.15	108.65	113.80
2	P	334	LEU	N-CA-CB	5.13	117.41	109.91
2	P	645	GLY	N-CA-C	-5.13	103.58	111.64
2	P	248	GLY	CA-C-N	5.11	131.30	121.54
2	P	248	GLY	C-N-CA	5.11	131.30	121.54
2	P	455	LYS	N-CA-C	5.11	118.29	111.75
2	P	280	HIS	CA-CB-CG	-5.09	108.71	113.80
2	P	667	VAL	CA-C-N	5.08	127.07	120.88
2	P	667	VAL	C-N-CA	5.08	127.07	120.88
2	P	309	VAL	N-CA-C	-5.07	101.18	108.53
2	P	288	ASN	N-CA-C	-5.06	103.25	110.59
2	P	535	MET	N-CA-C	5.04	116.85	111.36
2	P	700	LYS	N-CA-C	-5.03	101.09	108.99
2	P	528	VAL	N-CA-CB	5.03	118.12	110.58
2	P	549	VAL	N-CA-C	-5.01	108.09	112.90
2	P	636	GLU	N-CA-C	-5.01	104.92	112.99
2	P	235	THR	N-CA-C	-5.00	98.45	109.11

There are no chirality outliers.

All (16) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	N	10	G	Sidechain
1	N	12	U	Sidechain

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Mol	Chain	Res	Type	Group
1	N	22	G	Sidechain
1	N	23	A	Sidechain
1	N	31	A	Sidechain
1	N	42	G	Sidechain
1	N	45	G	Sidechain
1	N	58	A	Sidechain
1	N	59	U	Sidechain
1	N	7	U	Sidechain
1	N	8	U	Sidechain
2	P	245	ARG	Sidechain
2	P	414	MET	Peptide
2	P	424	LEU	Peptide
2	P	449	TYR	Sidechain
2	P	481	TYR	Sidechain

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	N	1622	0	821	21	0
2	P	4180	0	4249	40	0
All	All	5802	0	5070	47	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (47) 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:N:1:G:C5'	2:P:637:GLY:HA2	1.46	1.46
1:N:1:G:H5'	2:P:637:GLY:CA	1.44	1.45
1:N:1:G:C4'	2:P:637:GLY:HA2	1.45	1.43
1:N:1:G:C4'	2:P:637:GLY:CA	2.41	0.97
1:N:1:G:C5'	2:P:637:GLY:CA	2.19	0.93
1:N:1:G:H5'	2:P:637:GLY:HA3	1.53	0.90
1:N:1:G:H5'	2:P:637:GLY:C	1.96	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:1:G:H4'	2:P:637:GLY:HA2	1.57	0.86
1:N:1:G:O4'	2:P:637:GLY:HA2	1.75	0.85
1:N:68:U:OP1	2:P:638:LYS:HA	1.81	0.81
1:N:13:C:H42	1:N:46:G:H21	1.43	0.67
1:N:1:G:O4'	2:P:637:GLY:CA	2.46	0.64
1:N:1:G:H5'	2:P:637:GLY:O	2.00	0.62
2:P:304:LEU:HD22	2:P:304:LEU:H	1.69	0.57
2:P:575:ASN:HD22	2:P:596:HIS:CD2	2.24	0.55
2:P:246:ALA:HB1	2:P:377:GLN:HE22	1.70	0.55
1:N:1:G:C5'	2:P:637:GLY:O	2.55	0.54
2:P:518:VAL:HG12	2:P:570:VAL:H	1.74	0.53
2:P:257:LEU:HD13	2:P:273:ILE:HG12	1.93	0.51
2:P:241:PHE:HB2	2:P:275:HIS:CD2	2.46	0.50
2:P:354:ALA:HB2	2:P:444:VAL:H	1.78	0.48
1:N:11:C:C4	1:N:12:U:C5	3.03	0.47
2:P:355:VAL:HG22	2:P:376:ILE:HG23	1.97	0.47
1:N:11:C:C5	1:N:12:U:C5	3.04	0.46
2:P:191:HIS:CE1	2:P:259:VAL:HA	2.51	0.46
1:N:1:G:C5'	2:P:637:GLY:C	2.72	0.46
1:N:8:U:H2'	1:N:14:A:H62	1.80	0.46
2:P:561:VAL:HG11	2:P:586:ALA:HB2	1.98	0.46
2:P:222:VAL:HG13	2:P:231:THR:H	1.81	0.45
2:P:678:HIS:CG	2:P:679:HIS:H	2.35	0.45
2:P:283:ILE:HB	2:P:318:VAL:HA	1.98	0.44
2:P:221:LEU:HD11	2:P:233:LEU:HD23	2.00	0.43
2:P:257:LEU:HD11	2:P:283:ILE:HG21	1.99	0.43
1:N:9:A:OP2	1:N:12:U:C5	2.72	0.43
2:P:285:LEU:HD11	2:P:309:VAL:HB	2.01	0.42
2:P:253:ASP:HA	2:P:345:LEU:HD23	2.02	0.42
2:P:516:LEU:H	2:P:517:PRO:CD	2.33	0.42
2:P:178:PRO:HA	2:P:349:ALA:HB3	2.02	0.41
2:P:250:GLN:HG3	2:P:281:VAL:HG21	2.02	0.41
1:N:11:C:C4	1:N:12:U:C4	3.09	0.41
2:P:290:CYS:H	2:P:324:SER:HA	1.84	0.41
2:P:358:THR:HA	2:P:439:ARG:HA	2.02	0.41
2:P:275:HIS:CE1	2:P:459:ASP:O	2.74	0.41
2:P:462:LEU:HD23	2:P:462:LEU:HA	1.97	0.41
1:N:63:C:H2'	1:N:64:A:C8	2.55	0.40
2:P:466:LYS:HE3	2:P:547:ASP:H	1.86	0.40
2:P:188:HIS:HA	2:P:238:HIS:CD2	2.57	0.40

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
2	P	535/537 (100%)	440 (82%)	59 (11%)	36 (7%)	1 12

All (36) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	P	219	ALA
2	P	229	LYS
2	P	249	THR
2	P	265	VAL
2	P	437	GLU
2	P	459	ASP
2	P	483	THR
2	P	484	VAL
2	P	346	GLU
2	P	348	LYS
2	P	476	LYS
2	P	516	LEU
2	P	610	LEU
2	P	612	SER
2	P	617	ILE
2	P	623	ILE
2	P	697	ASP
2	P	705	VAL
2	P	314	TYR
2	P	325	ALA
2	P	351	PRO
2	P	383	LYS
2	P	438	PRO
2	P	448	LYS
2	P	482	GLY
2	P	665	GLY
2	P	689	GLY
2	P	178	PRO

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Mol	Chain	Res	Type
2	P	442	GLU
2	P	512	ASP
2	P	543	GLU
2	P	598	ILE
2	P	679	HIS
2	P	444	VAL
2	P	704	LYS
2	P	515	VAL

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	
2	P	453/453 (100%)	427 (94%)	26 (6%)	18	40

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	P	197	LEU
2	P	222	VAL
2	P	230	ILE
2	P	254	ILE
2	P	259	VAL
2	P	267	LYS
2	P	273	ILE
2	P	318	VAL
2	P	355	VAL
2	P	388	VAL
2	P	415	PRO
2	P	416	VAL
2	P	421	TRP
2	P	438	PRO
2	P	443	VAL
2	P	466	LYS
2	P	509	LEU
2	P	510	GLU

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Mol	Chain	Res	Type
2	P	520	VAL
2	P	525	ASP
2	P	546	LEU
2	P	570	VAL
2	P	582	ILE
2	P	585	LEU
2	P	593	ILE
2	P	623	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
2	P	191	HIS
2	P	216	HIS
2	P	238	HIS
2	P	275	HIS
2	P	280	HIS
2	P	408	ASN
2	P	470	HIS
2	P	501	GLN
2	P	533	ASN
2	P	542	HIS
2	P	559	ASN
2	P	575	ASN
2	P	584	GLN
2	P	596	HIS
2	P	621	HIS
2	P	656	GLN
2	P	666	HIS
2	P	679	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	N	75/76 (98%)	21 (28%)	4 (5%)

All (21) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	N	3	G

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Mol	Chain	Res	Type
1	N	7	U
1	N	9	A
1	N	16	U
1	N	17	U
1	N	18	G
1	N	20	G
1	N	21	A
1	N	22	G
1	N	26	G
1	N	27	C
1	N	34	G
1	N	39	U
1	N	47	U
1	N	48	C
1	N	49	C
1	N	50	U
1	N	59	U
1	N	60	C
1	N	61	C
1	N	62	A

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	N	16	U
1	N	46	G
1	N	58	A
1	N	60	C

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

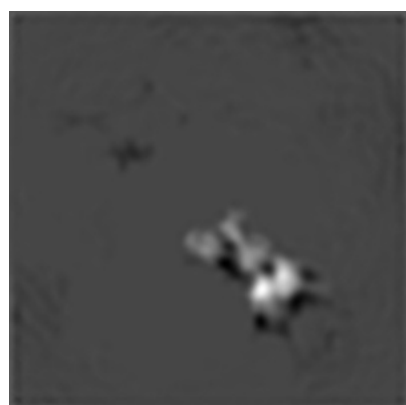
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1855. These allow visual inspection of the internal detail of the map and identification of artifacts.

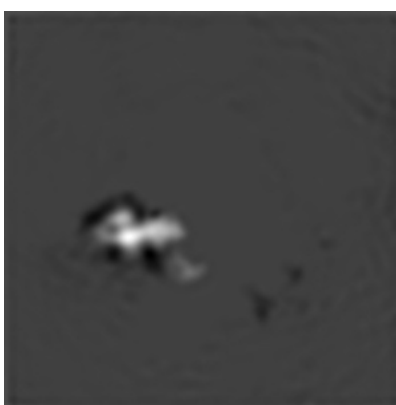
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

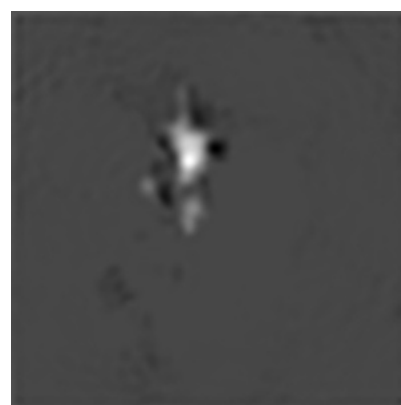
6.1.1 Primary map



X



Y

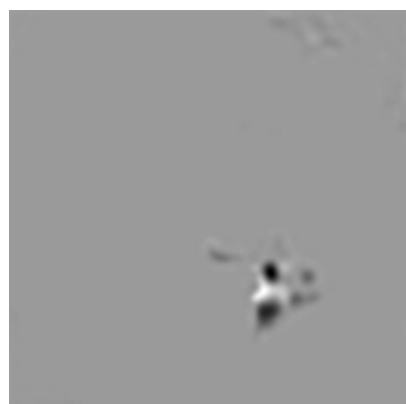


Z

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

6.2 Central slices [i](#)

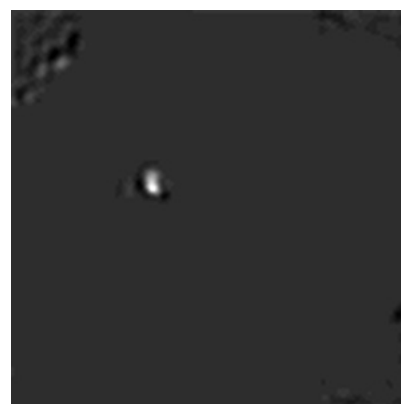
6.2.1 Primary map



X Index: 65



Y Index: 65

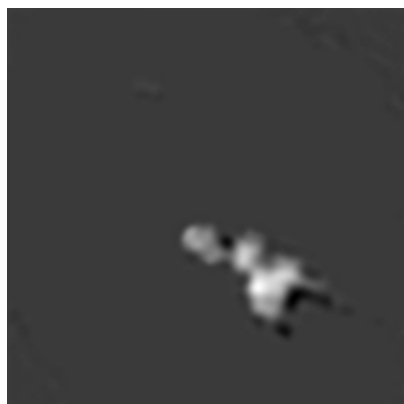


Z Index: 65

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: 57



Y Index: 82

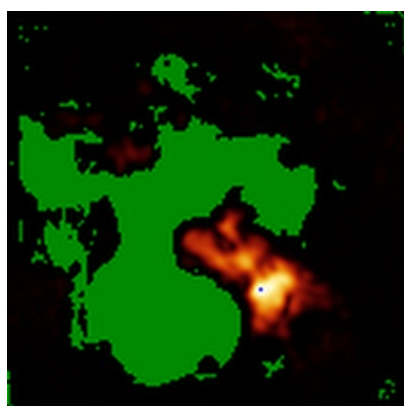


Z Index: 39

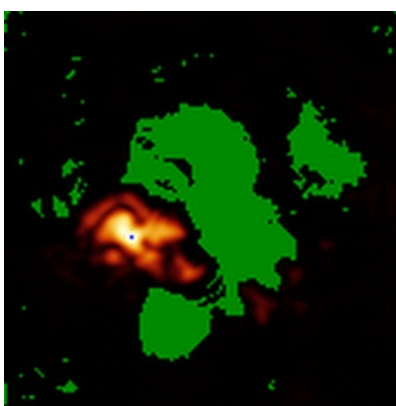
The images above show the largest variance slices of the map in three orthogonal directions.

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

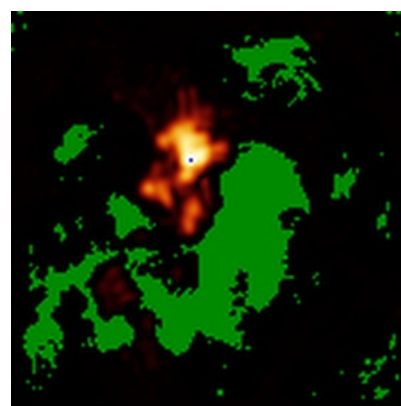
6.4.1 Primary map



X



Y

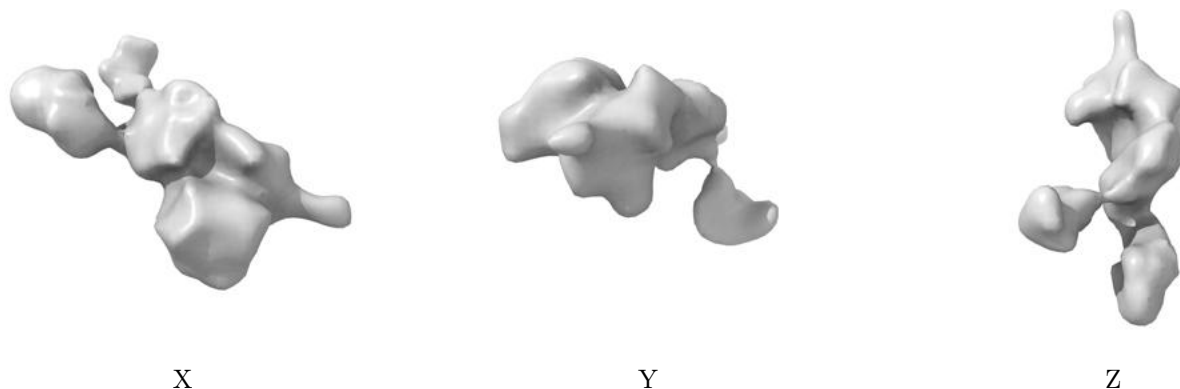


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 14825.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

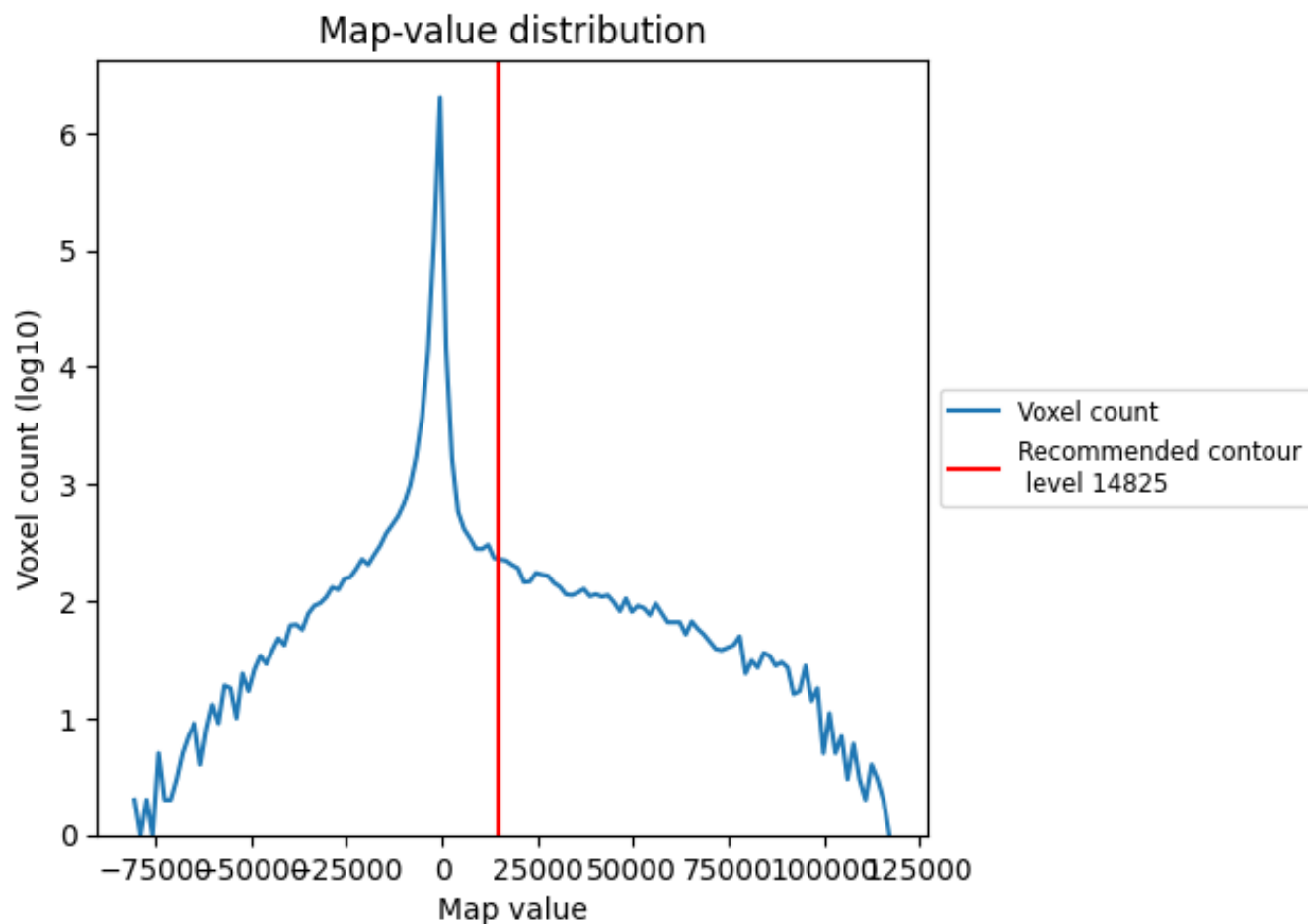
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

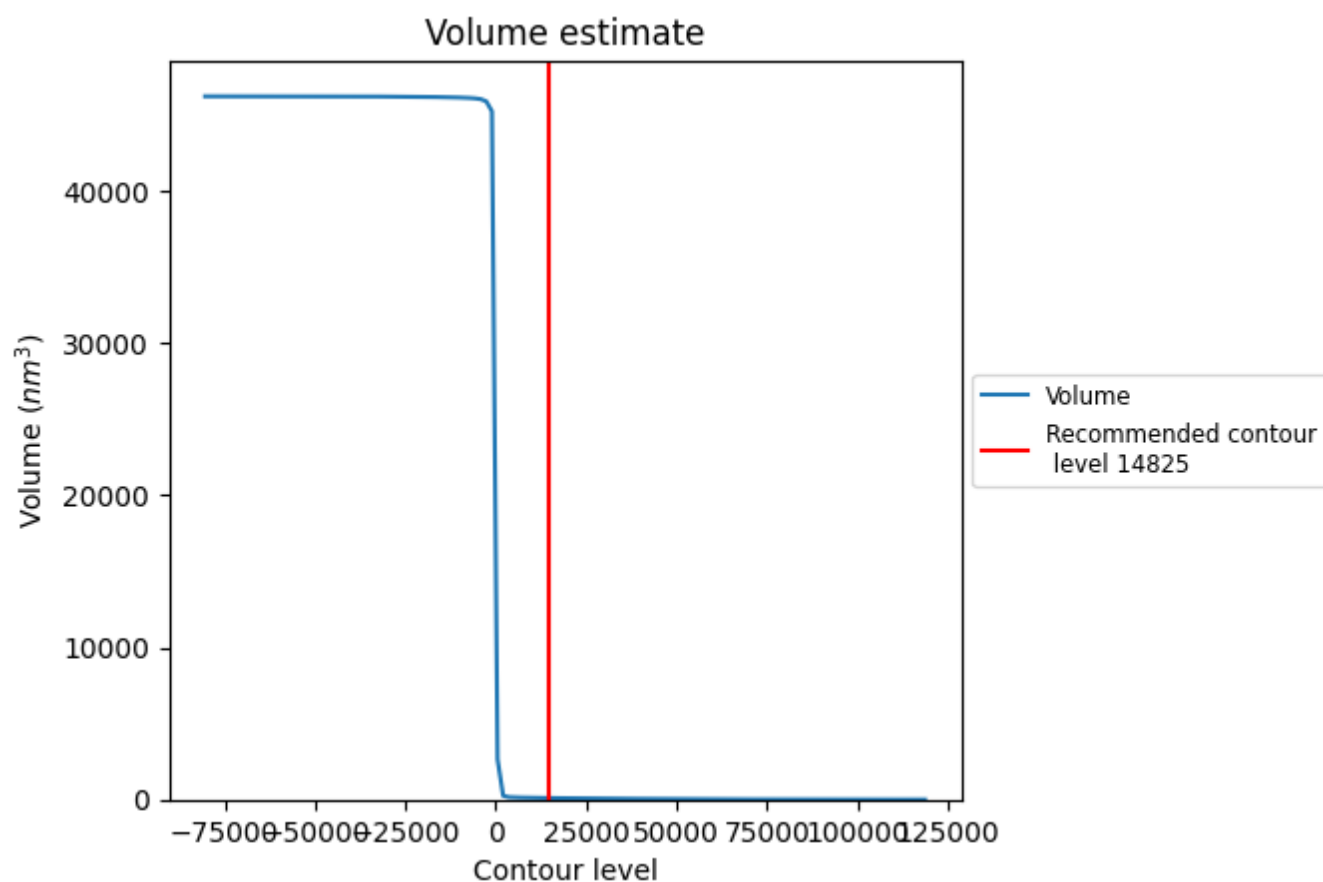
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

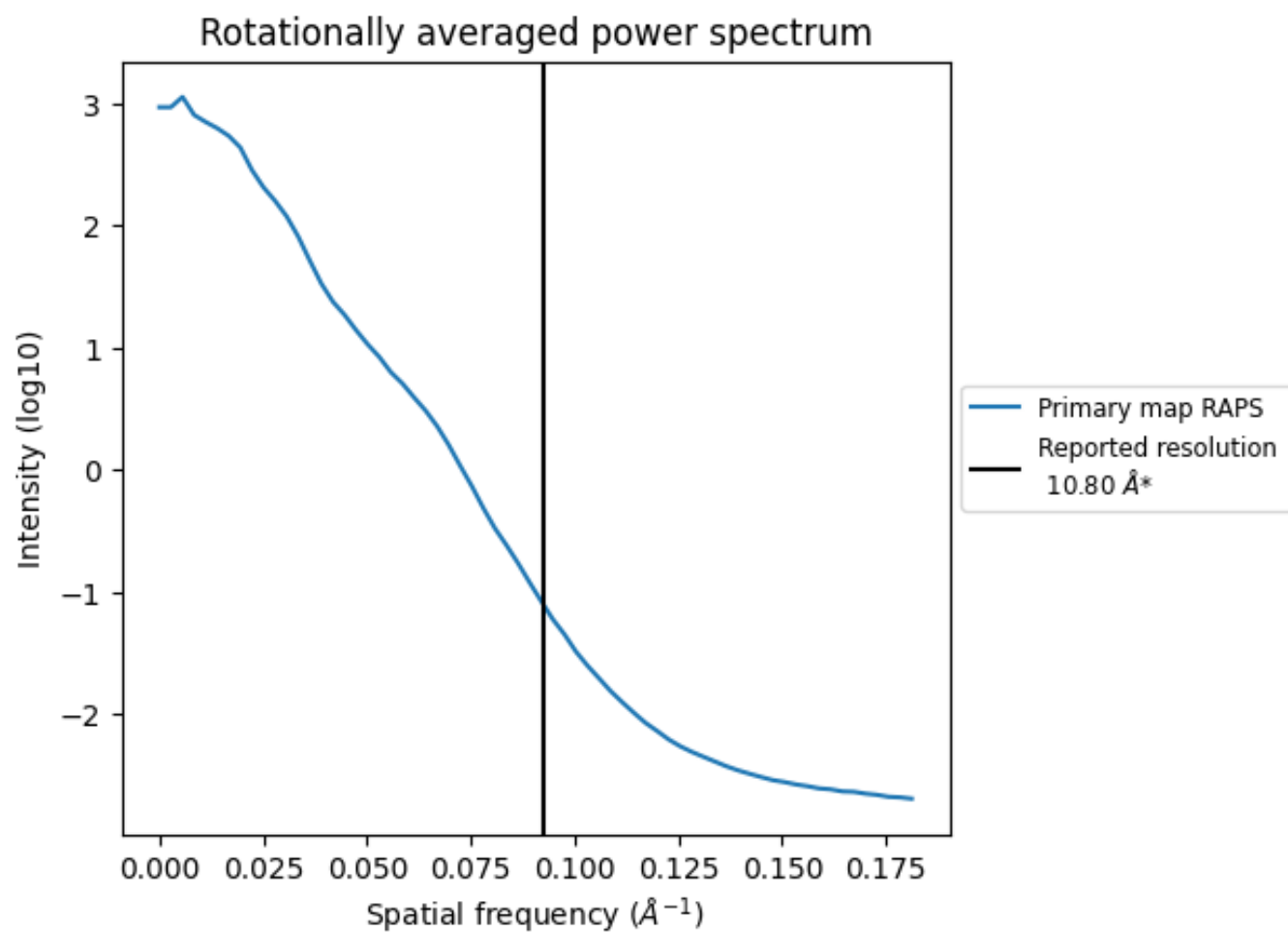
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 100 nm^3 ; this corresponds to an approximate mass of 90 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 0.093 $\text{\AA}^{-1}$

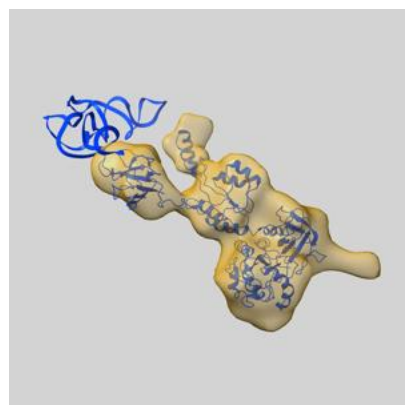
8 Fourier-Shell correlation

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

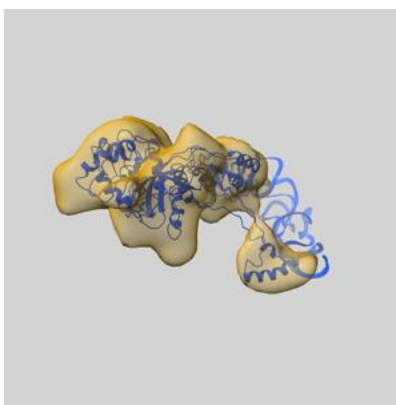
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1855 and PDB model 3IZY. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

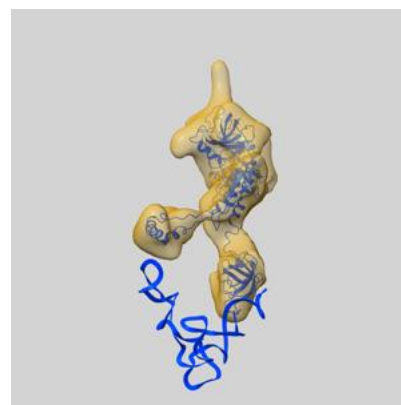
9.1 Map-model overlay [i](#)



X



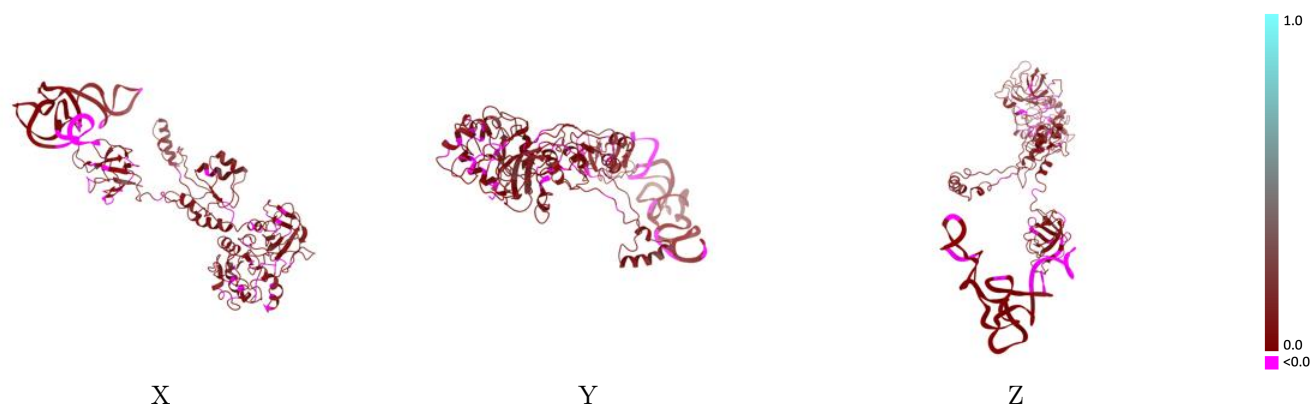
Y



Z

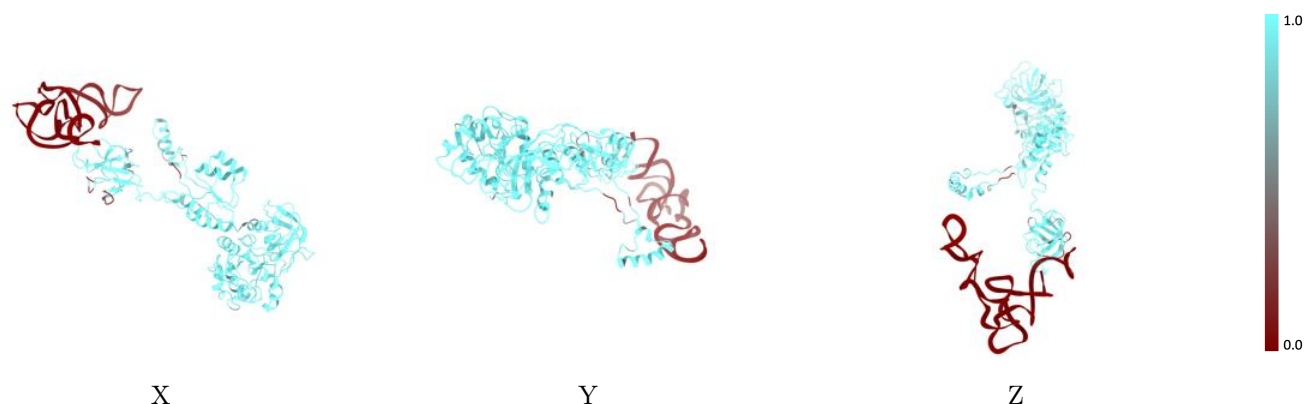
The images above show the 3D surface view of the map at the recommended contour level 14825.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



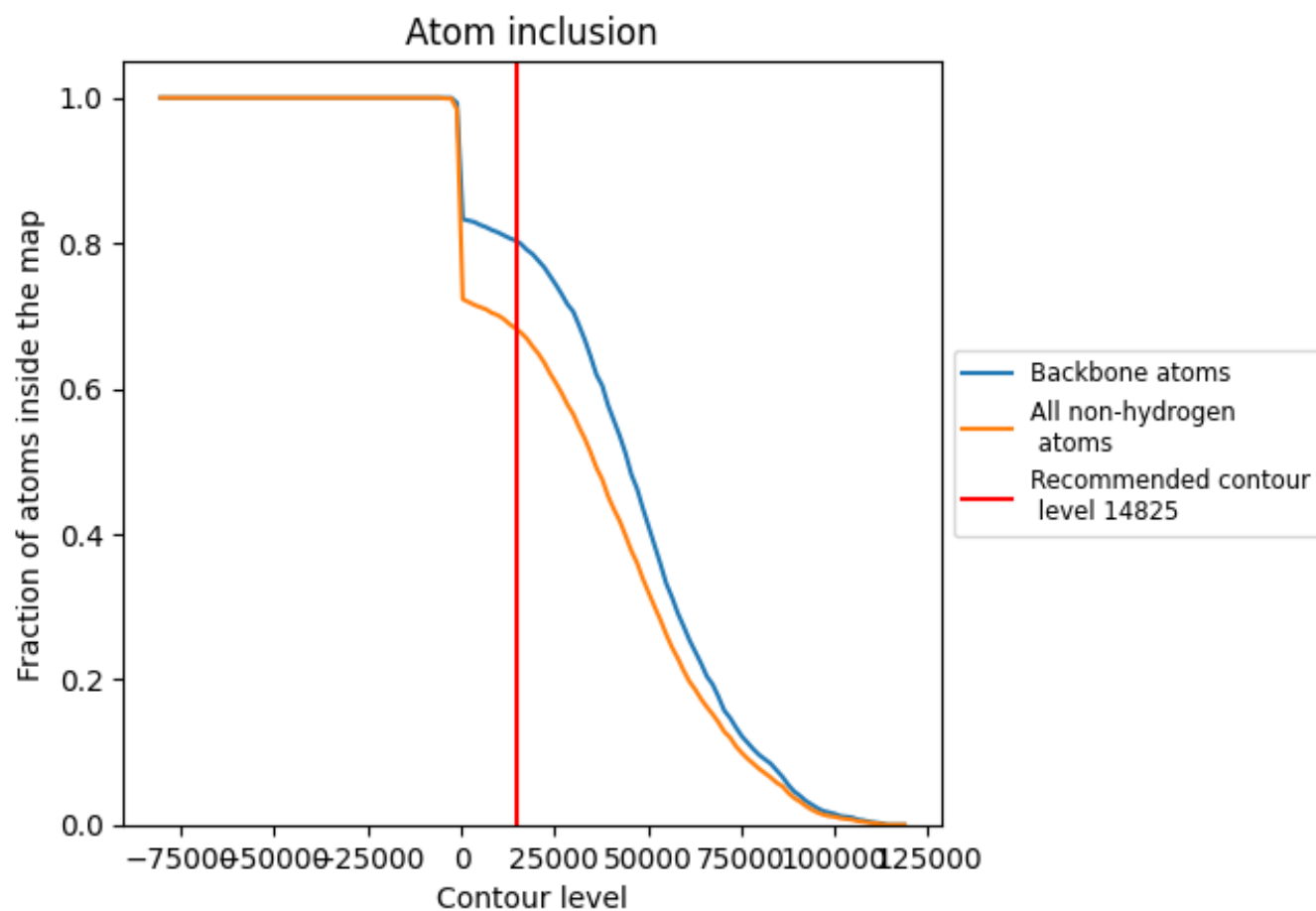
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (14825).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 68% 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 (14825) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6820	0.0620
N	0.0030	-0.0080
P	0.9500	0.0890

