



## wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 04:42 PM UTC

PDB ID : 6LT0 / pdb\_00006lt0  
EMDB ID : EMD-0966  
Title : cryo-EM structure of C9ORF72-SMCR8-WDR41  
Authors : Tang, D.; Sheng, J.; Xu, L.; Zhan, X.; Yan, C.; Qi, S.  
Deposited on : 2020-01-21  
Resolution : 3.20 Å(reported)

This is a wwPDB EM Validation Summary 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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

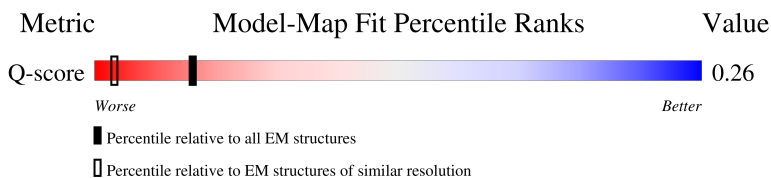
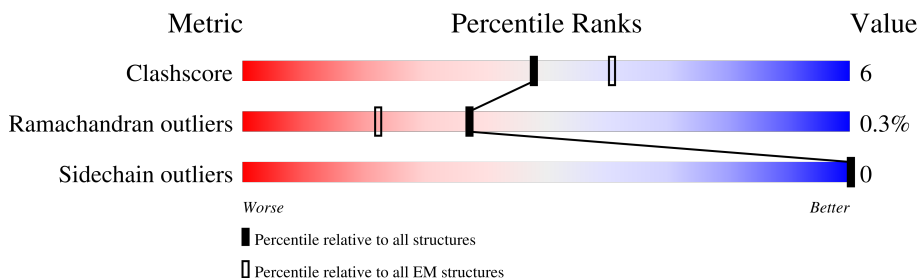
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : 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 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



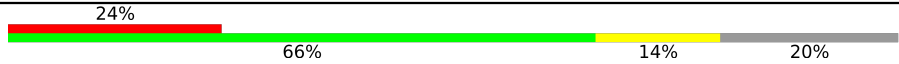

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15020 ( 2.70 - 3.70 )

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	A	459	<p>7% (Poor fit), 63% (0 outliers), 11% (1 outlier), 25% (2+ outliers)</p>
1	D	459	<p>75% (Poor fit), 63% (0 outliers), 11% (1 outlier), 25% (2+ outliers)</p>
2	B	937	<p>16% (Poor fit), 35% (0 outliers), 6% (1 outlier), 59% (2+ outliers)</p>
2	E	937	<p>39% (Poor fit), 35% (0 outliers), 6% (1 outlier), 59% (2+ outliers)</p>

Continued on next page...

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Mol	Chain	Length	Quality of chain
3	C	481	
3	F	481	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 17774 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 WD repeat-containing protein 41.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	343	Total	C	N	O	S	0	0
			2693	1713	471	497	12		
1	D	343	Total	C	N	O	S	0	0
			2693	1713	471	497	12		

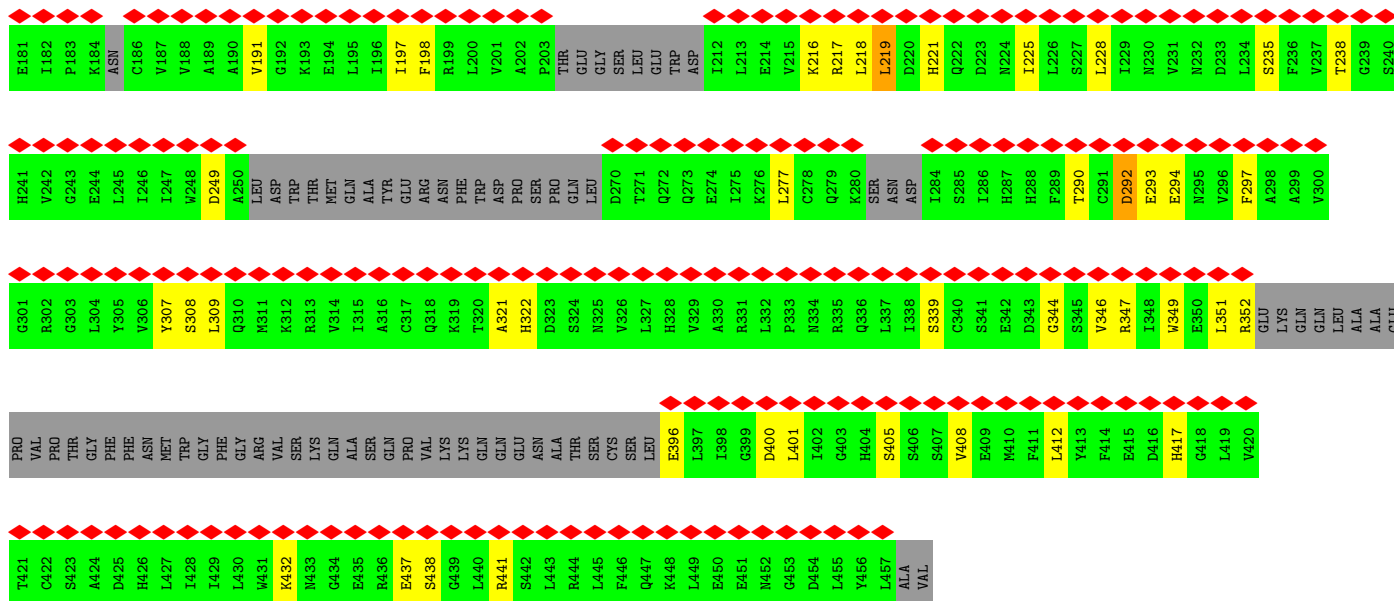
- Molecule 2 is a protein called Guanine nucleotide exchange protein SMCR8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	386	Total	C	N	O	S	0	0
			3134	2026	541	551	16		
2	E	386	Total	C	N	O	S	0	0
			3134	2026	541	551	16		

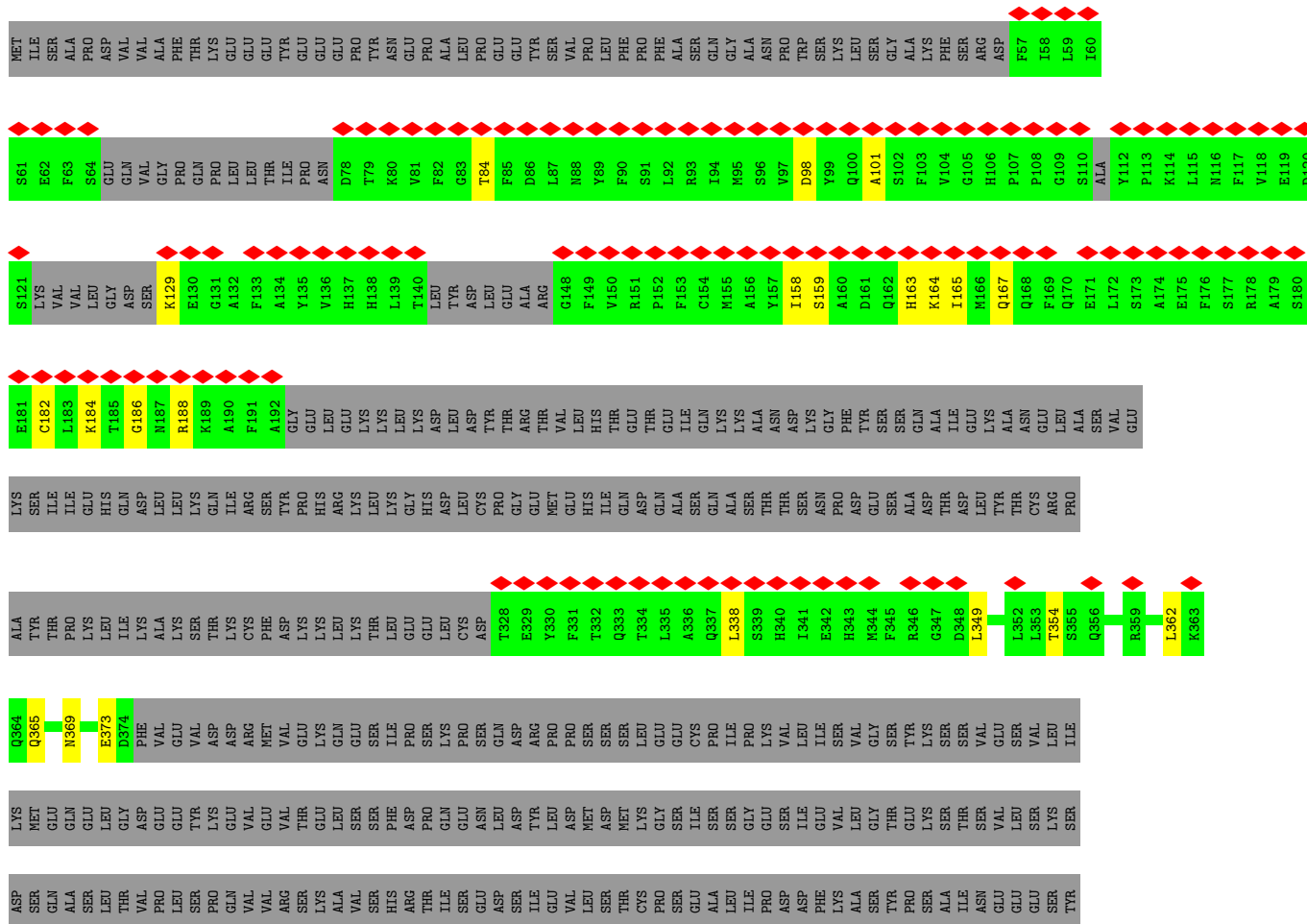
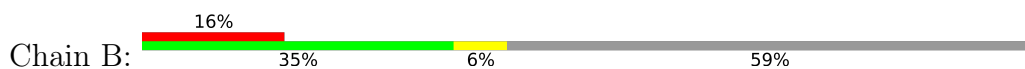
- Molecule 3 is a protein called Guanine nucleotide exchange C9orf72.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	385	Total	C	N	O	S	0	0
			3060	1980	514	550	16		
3	F	385	Total	C	N	O	S	0	0
			3060	1980	514	550	16		

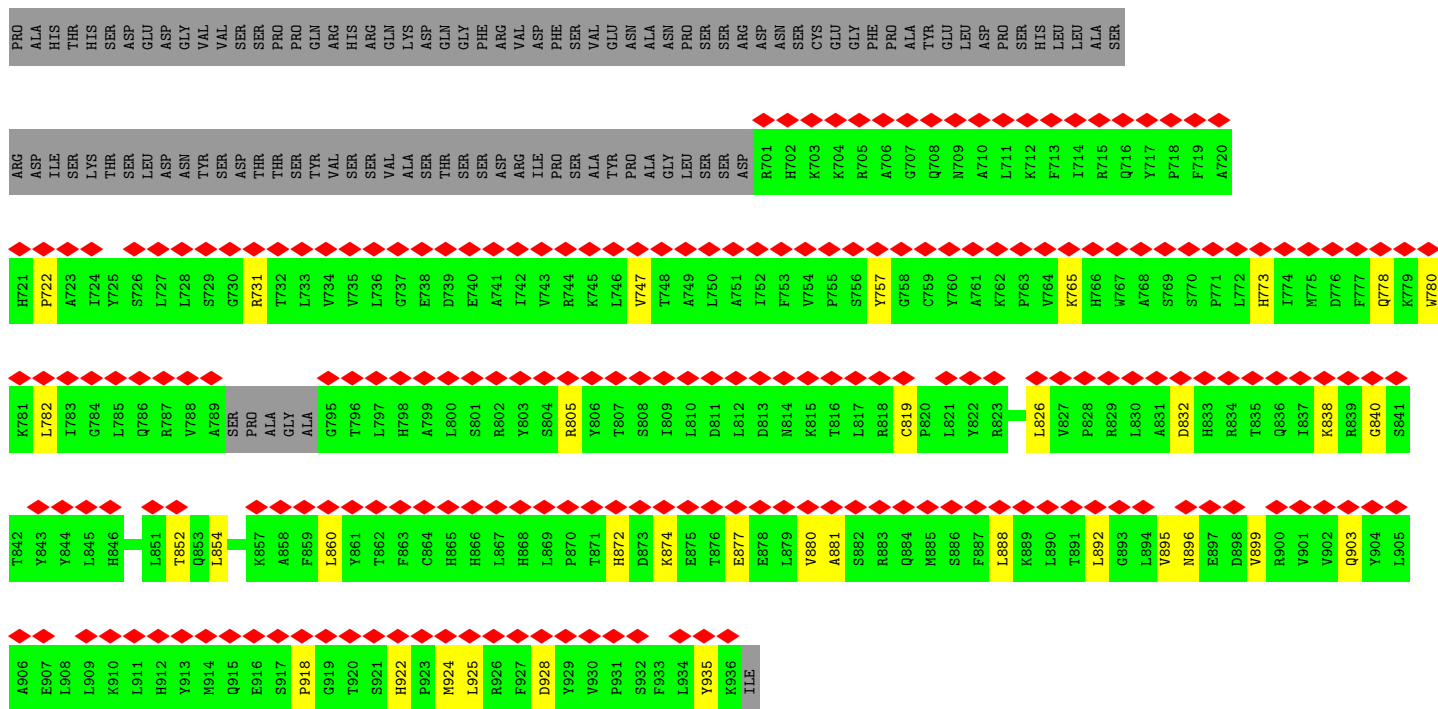




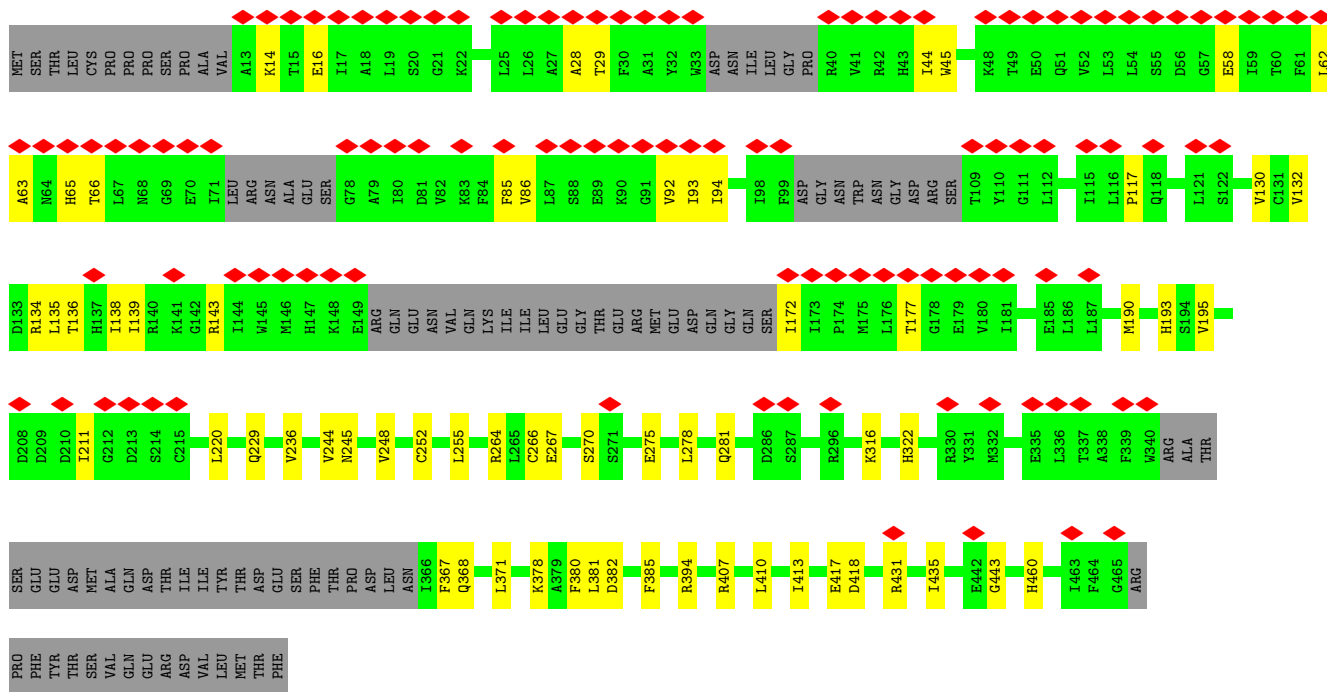
• Molecule 2: Guanine nucleotide exchange protein SMCR8



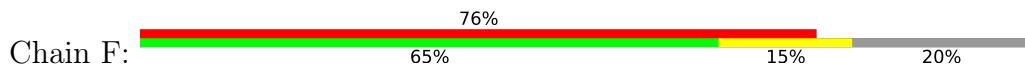




• Molecule 3: Guanine nucleotide exchange C9orf72



• Molecule 3: Guanine nucleotide exchange C9orf72



MET	SER	THR	LEU	CYS	PRO	PRO	SER	PRO	ALA	VAL	A13	K14	T15	E16	I17	A18	L19	S20	G21	K22	S23	P24	L25	L26	A27	A28	T29	F30	A31	Y32	W33	ASP	ASN	ILE	LEU	GLY	PRO	R40	V41	R42	H43	I44	W45	A46	P47	R48	T49	E50	Q51	V52	L53	L54	S55	D56	G57	E58	I59	T60						
F61	L62	A63	N64	H65	T66	L67	N68	G69	E70	I71	LEU	ARG	ASN	ALA	GLU	SER	G78	A79	I80	D81	V82	R83	F84	F85	V86	L87	S88	E89	K90	G91	V92	I93	A94	W95	S96	L97	I98	F99	ASP	GLY	ASN	TRP	ASN	GLY	ASP	R42	H43	I44	W45	A46	P47	R48	T49	E50	Q51	V52	L53	L54	S55	D56	G57	E58	I59	T60
L121	S122	F123	Y124	L125	P126	L127	R128	R129	V130	G131	V132	D133	R134	L135	T136	H137	I138	I139	R140	K141	G142	R143	I144	W145	M146	H147	K148	E149	ARG	GLN	GLU	ASN	VAL	GLN	LYS	ILE	ILE	LEU	GLU	GLY	THR	GLU	ARG	MET	ASP	GLN	GLY	SER	T109	Y110	G111	L112	S113	I114	L115	P117	E118	T119	E120					
I181	P182	V183	M184	E185	L186	L187	S188	S189	M190	K191	S192	H193	S194	V195	P196	E197	E198	I199	D200	I201	A202	D203	T204	V205	L206	M207	D208	D209	D210	I211	G212	D213	S214	C215	H216	E217	G218	F219	L220	L221	N222	A223	I224	S225	S226	H227	L228	Q229	T230	C231	G232	C233	S234	V235	V236	V237	G238	S239	S240					
A241	E242	K243	V244	N245	K246	I247	V248	R249	T250	L251	C252	L253	F254	L255	T256	P257	A258	E259	R260	K261	C262	S263	R264	L265	C266	E267	A268	E269	S270	S271	F272	K273	Y274	E275	S276	G277	L278	F279	V280	Q281	G282	L283	L284	K285	D286	S287	T288	G289	F291	V292	L293	P294	F295	R296	Q297	V298	M299	Y300						
A301	P302	Y303	P304	T305	T306	D309	V310	D311	V312	N313	T314	V315	K316	Q317	M318	P319	P320	C321	H322	E323	H324	I325	Y326	N327	Q328	R329	R330	Y331	M332	R333	S334	E335	L336	T337	A338	F339	W340	ARG	ALA	THR	SER	GLU	GLU	ASP	MET	ALA	GLN	ASP	THR	THR	ILE	ILE	TYR	THR	ASP	GLU	SER	PHE	THR					
PRO	ASP	LEU	ASN	I366	F367	Q368	D369	H372	R373	D374	T375	L376	V377	K378	A379	F380	L381	D382	Q383	V384	F385	Q386	L387	K388	P389	G390	L391	S392	L393	R394	S395	T396	F397	L398	A399	Q400	F401	L402	L403	V404	L405	H406	R407	K408	A409	L410	T411	L412	I413	K414	Y415	I416	E417	D418	D419	T420	Q421	K422						
G423	K424	K425	P426	F427	K428	S429	L430	R431	M432	L433	K434	I435	D436	L437	D438	L439	T440	A441	E442	G443	D444	L445	M446	I447	I448	M449	A450	L451	A452	E453	K454	I455	K456	P457	G458	L459	H460	S461	F462	I463	F464	G465	ARG	PRO	PHE	TYR	THR	SER	THR	VAL	GLN	GLU	ARG	ASP	VAL	LEU	MET	THR	PHE					

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	347925	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 ( $e^-/\text{\AA}^2$ )	5.3	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.145	Depositor
Minimum map value	-0.094	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.026	Depositor
Map size (Å)	297.08, 297.08, 297.08	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.061, 1.061, 1.061	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.24	0/2735	0.63	0/3705
1	D	0.25	0/2735	0.63	0/3705
2	B	0.25	0/3211	0.62	0/4334
2	E	0.25	0/3211	0.62	0/4334
3	C	0.25	0/3122	0.58	2/4220 (0.0%)
3	F	0.25	0/3122	0.58	2/4220 (0.0%)
All	All	0.25	0/18136	0.61	4/24518 (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
1	A	0	2
1	D	0	2
3	C	0	2
3	F	0	2
All	All	0	8

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	172	ILE	CA-C-N	5.30	124.57	120.33
3	C	172	ILE	C-N-CA	5.30	124.57	120.33
3	F	172	ILE	CA-C-N	5.27	124.55	120.33
3	F	172	ILE	C-N-CA	5.27	124.55	120.33

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	218	LEU	Peptide
1	A	292	ASP	Peptide
3	C	193	HIS	Peptide
3	C	195	VAL	Peptide
1	D	218	LEU	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2693	0	2697	28	0
1	D	2693	0	2697	28	0
2	B	3134	0	3105	47	0
2	E	3134	0	3105	36	0
3	C	3060	0	3134	47	0
3	F	3060	0	3134	59	0
All	All	17774	0	17872	210	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 210 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)
2:B:834:ARG:HG2	3:F:431:ARG:NH2	1.43	1.31
3:C:431:ARG:HD3	3:F:435:ILE:CD1	1.61	1.30
2:B:896:ASN:CG	3:F:368:GLN:OE1	1.91	1.13
3:C:431:ARG:CD	3:F:435:ILE:HD12	1.85	1.05
2:B:834:ARG:O	3:F:431:ARG:NH2	1.90	1.05

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	329/459 (72%)	277 (84%)	50 (15%)	2 (1%)	21	56
1	D	329/459 (72%)	277 (84%)	50 (15%)	2 (1%)	21	56
2	B	370/937 (40%)	315 (85%)	54 (15%)	1 (0%)	36	68
2	E	370/937 (40%)	315 (85%)	54 (15%)	1 (0%)	36	68
3	C	373/481 (78%)	334 (90%)	39 (10%)	0	100	100
3	F	373/481 (78%)	334 (90%)	39 (10%)	0	100	100
All	All	2144/3754 (57%)	1852 (86%)	286 (13%)	6 (0%)	37	68

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	293	GLU
1	D	293	GLU
2	B	840	GLY
2	E	840	GLY
1	A	219	LEU

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	298/405 (74%)	298 (100%)	0	100	100
1	D	298/405 (74%)	298 (100%)	0	100	100
2	B	339/837 (40%)	339 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	339/837 (40%)	339 (100%)	0	100	100
3	C	344/431 (80%)	344 (100%)	0	100	100
3	F	344/431 (80%)	344 (100%)	0	100	100
All	All	1962/3346 (59%)	1962 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	896	ASN
3	F	281	GLN
3	F	245	ASN
3	C	43	HIS
2	E	814	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

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

There are no chain breaks in this entry.

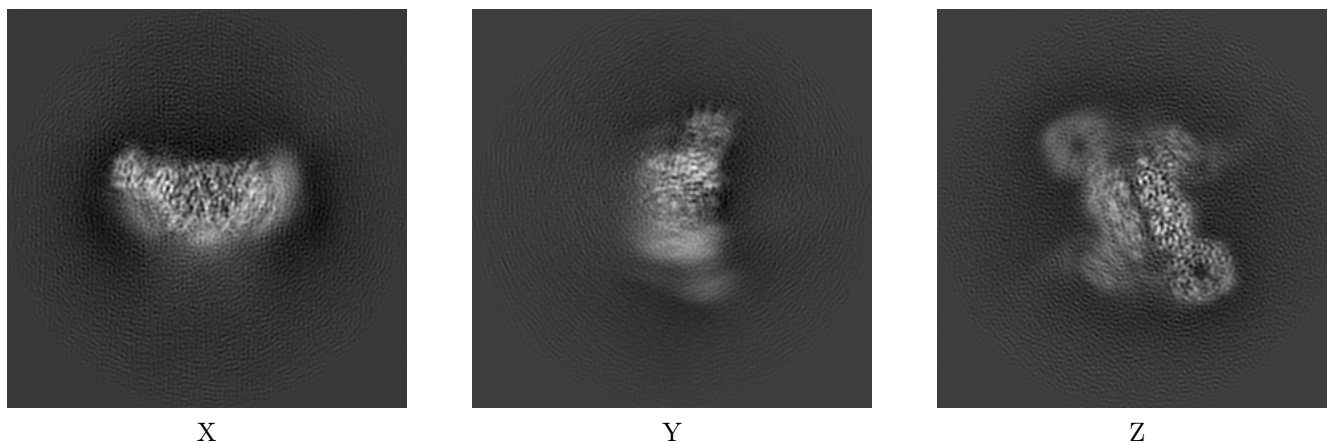
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0966. 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](#)

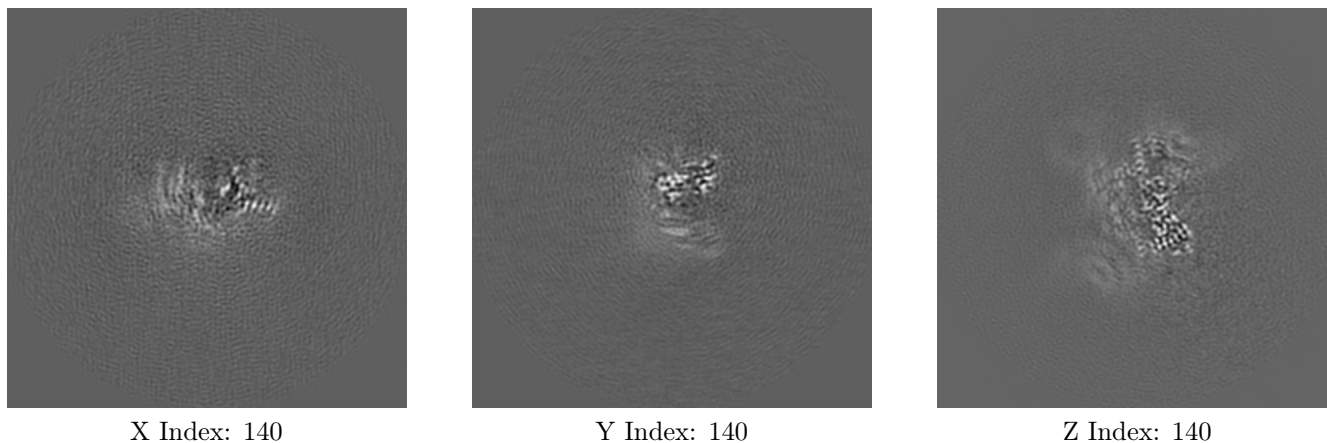
#### 6.1.1 Primary map



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

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

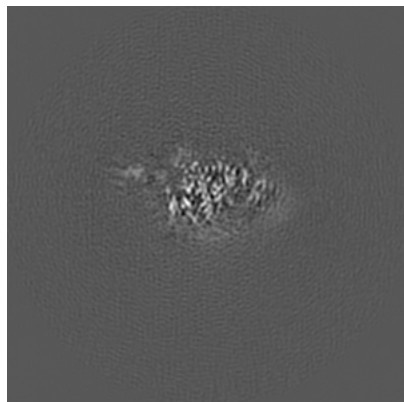
#### 6.2.1 Primary map



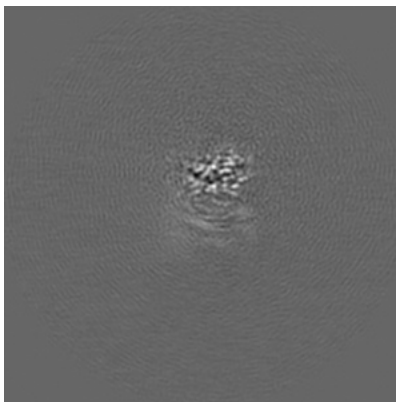
The images above show central slices of the map in three orthogonal directions.

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

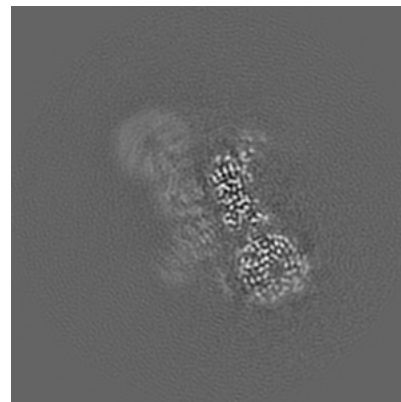
### 6.3.1 Primary map



X Index: 159



Y Index: 130

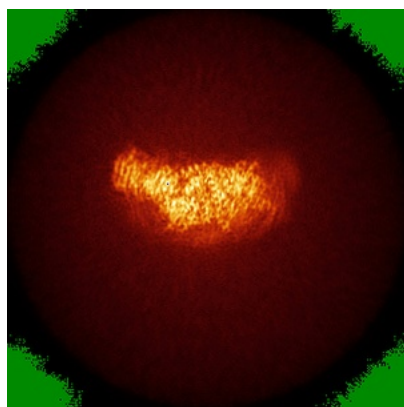


Z Index: 159

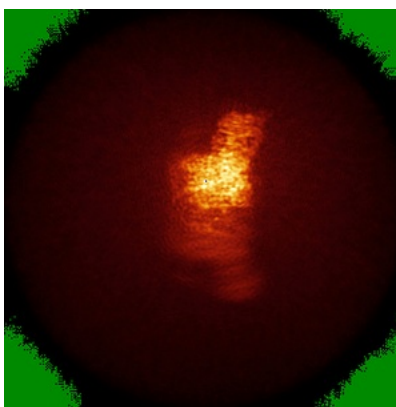
The images above show the largest variance slices of the map in three orthogonal directions.

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

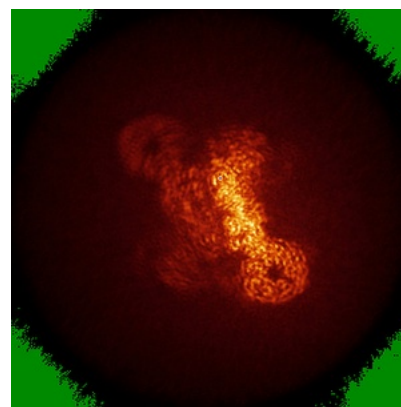
### 6.4.1 Primary map



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

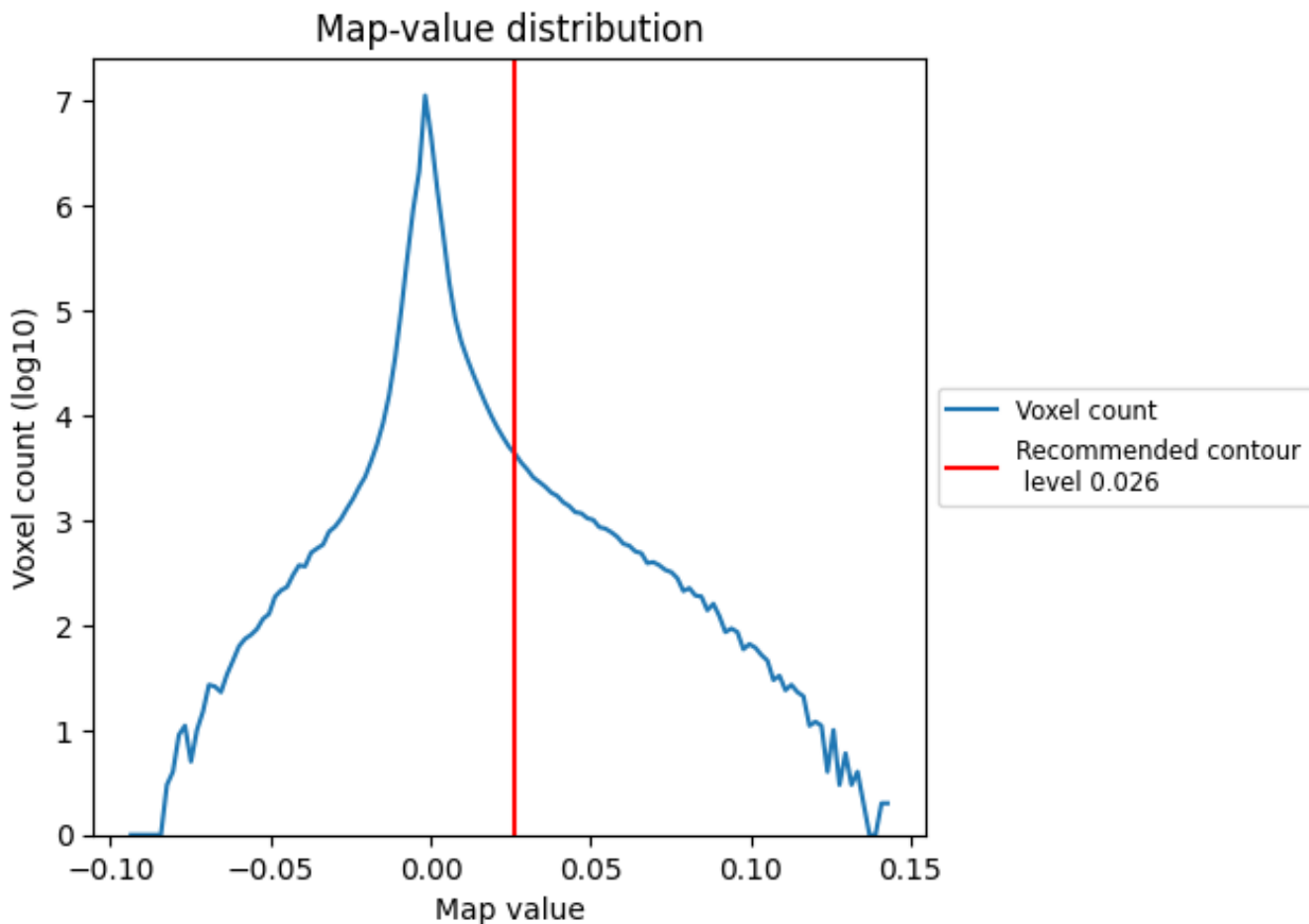
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

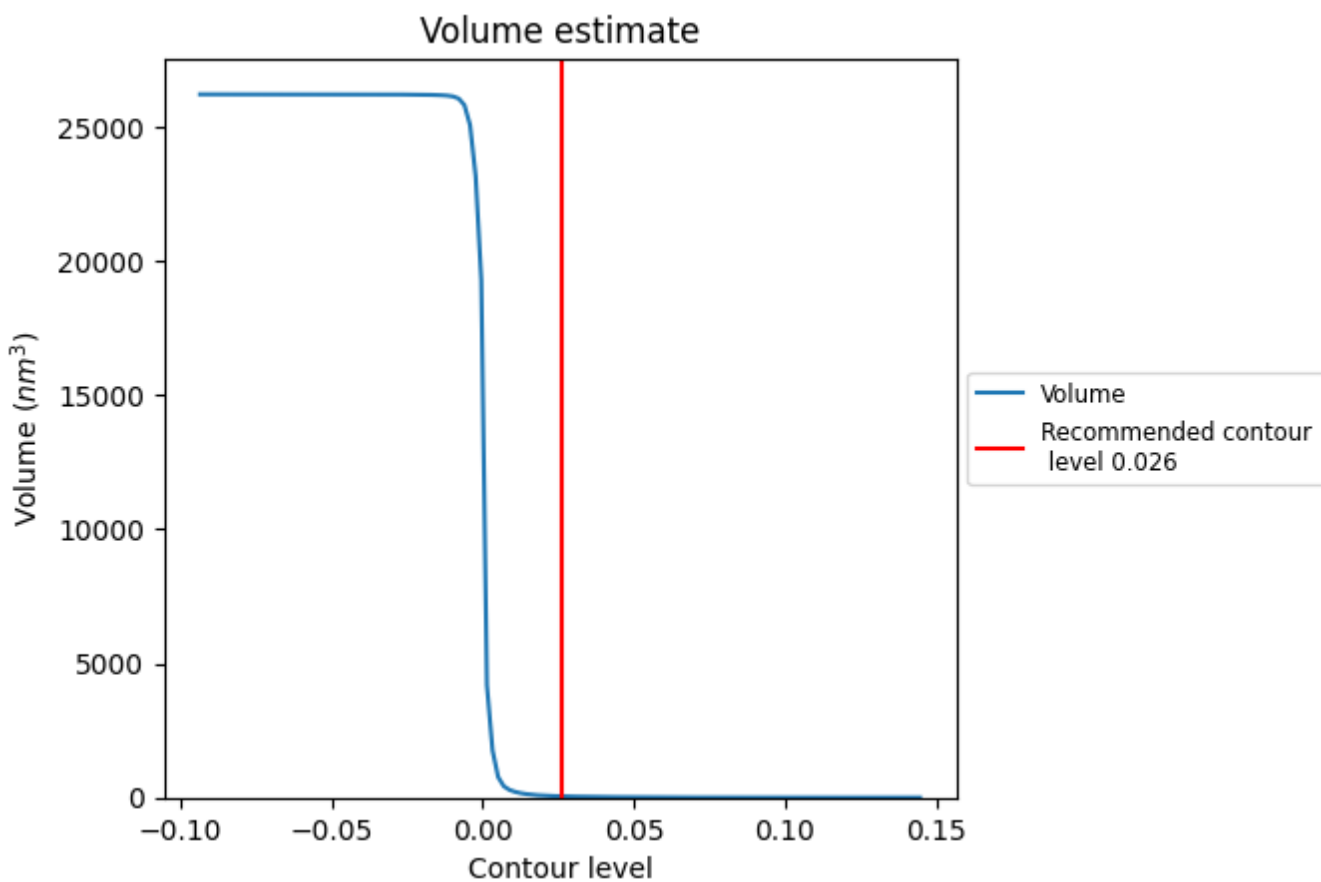
This section contains the results of statistical analysis of the map.

### 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.

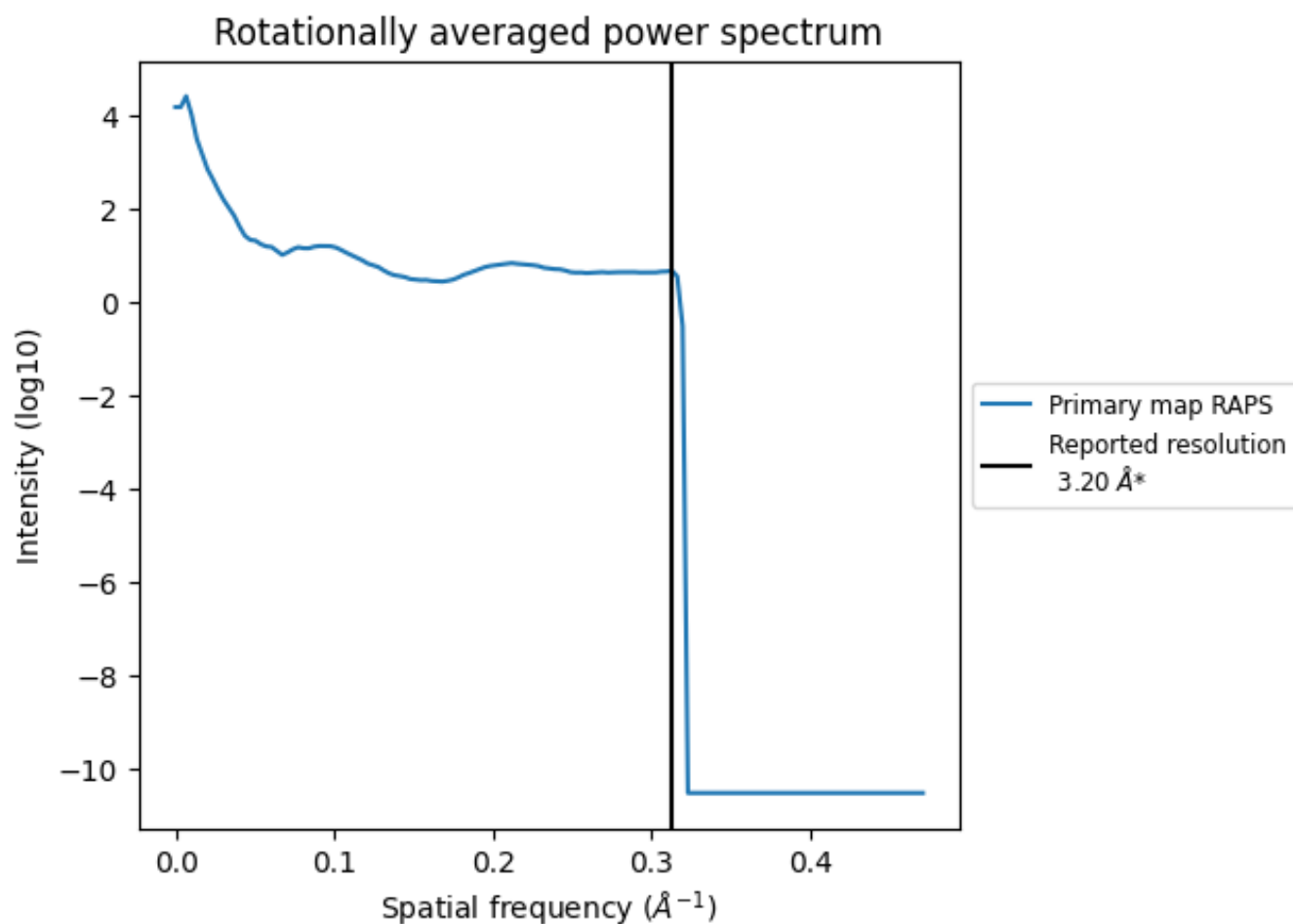
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 47  $\text{nm}^3$ ; this corresponds to an approximate mass of 43 kDa.

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

### 7.3 Rotationally averaged power spectrum [\(i\)](#)



\*Reported resolution corresponds to spatial frequency of 0.312 Å<sup>-1</sup>

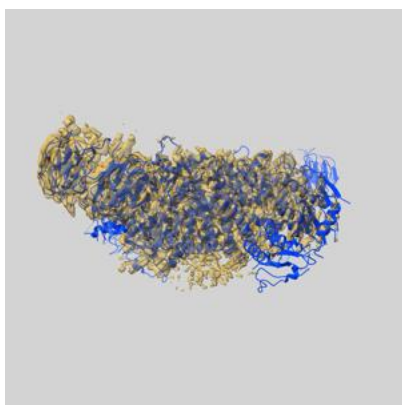
## 8 Fourier-Shell correlation

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

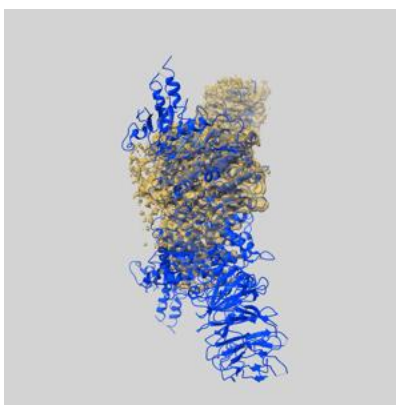
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0966 and PDB model 6LT0. Per-residue inclusion information can be found in section 3 on page 5.

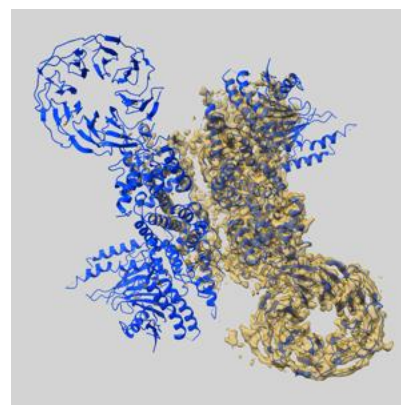
### 9.1 Map-model overlay [i](#)



X



Y



Z

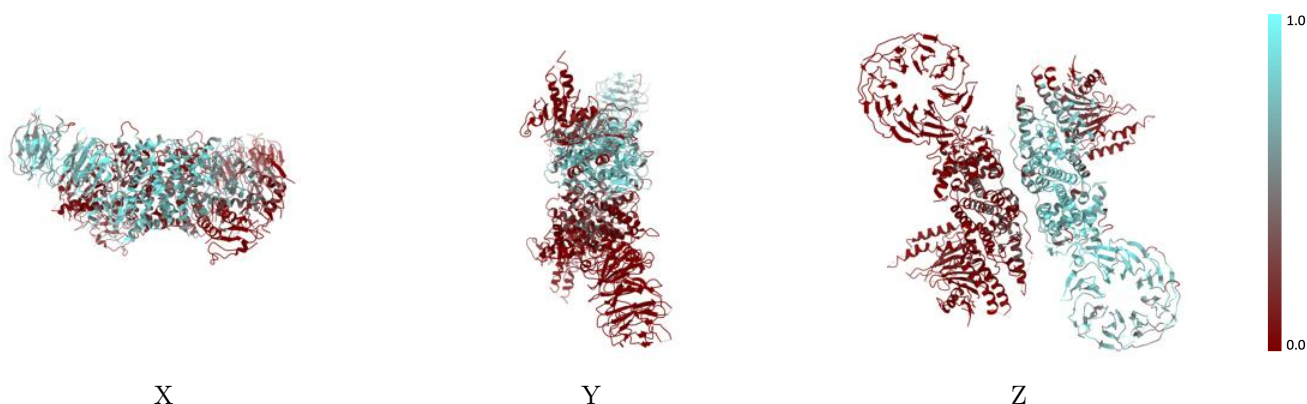
The images above show the 3D surface view of the map at the recommended contour level 0.026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



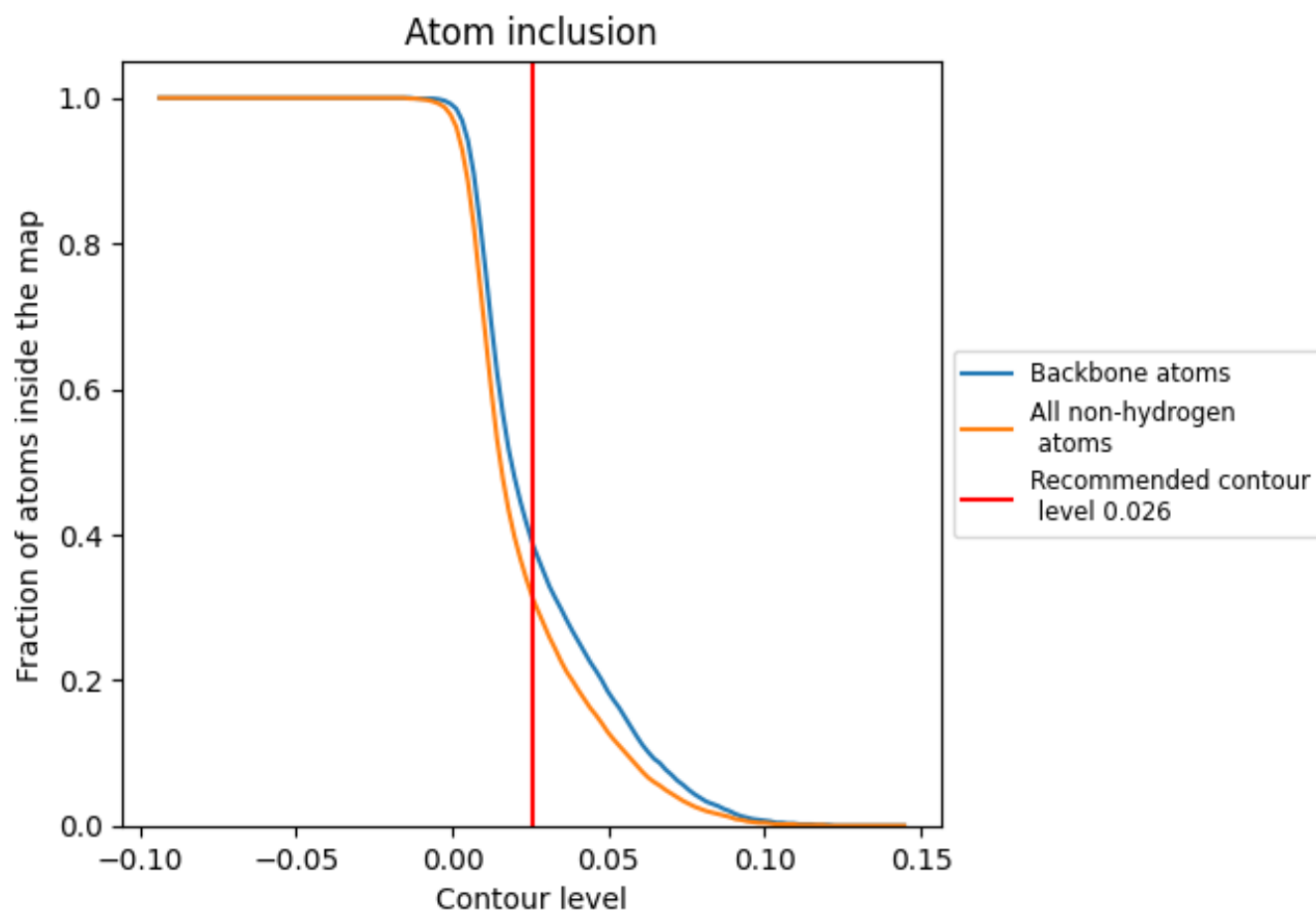
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.026).















## 9.4 Atom inclusion [i](#)



At the recommended contour level, 38% of all backbone atoms, 31% 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 (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3100	 0.2600
A	 0.6850	 0.4600
B	 0.5130	 0.4030
C	 0.5480	 0.4170
D	 0.0000	 0.0590
E	 0.0520	 0.0690
F	 0.0680	 0.1540

