



wwPDB EM Validation Summary Report ⓘ

Nov 21, 2022 – 04:41 PM JST

PDB ID : 7D68
EMDB ID : EMD-30590
Title : Cryo-EM structure of the human glucagon-like peptide-2 receptor-Gs protein complex
Authors : Sun, W.; Chen, L.; Zhou, Q.; Zhao, L.; Zhang, H.; Cong, Z.; Shen, D.; Zhao, F.; Zhou, F.; Cai, X.; Chen, Y.; Zhou, Y.; Gadgaard, S.; van der Velden, W.J.; Zhao, S.; Jiang, Y.; Rosenkilde, M.M.; Yang, D.; Xu, H.E.; Zhang, Y.; Wang, M.
Deposited on : 2020-09-29
Resolution : 3.00 Å(reported)

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We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.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

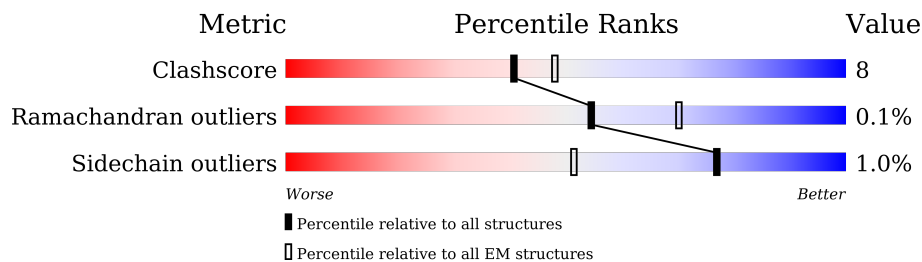
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	378	
2	B	371	
3	G	71	
4	N	126	
5	P	33	
6	R	664	

2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 8564 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 Guanine nucleotide-binding protein G(s) subunit alpha isoforms short.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	226	1885	1190	343	345	7	0	0

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	338	2600	1604	467	508	21	0	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	MET	-	initiating methionine	UNP P62871
B	-3	GLY	-	expression tag	UNP P62871
B	-2	SER	-	expression tag	UNP P62871
B	-1	LEU	-	expression tag	UNP P62871
B	0	LEU	-	expression tag	UNP P62871
B	1	GLN	-	expression tag	UNP P62871
B	341	GLY	-	expression tag	UNP P62871
B	342	SER	-	expression tag	UNP P62871
B	343	SER	-	expression tag	UNP P62871
B	344	GLY	-	expression tag	UNP P62871
B	345	GLY	-	expression tag	UNP P62871
B	346	GLY	-	expression tag	UNP P62871
B	347	GLY	-	expression tag	UNP P62871
B	348	SER	-	expression tag	UNP P62871
B	349	GLY	-	expression tag	UNP P62871
B	350	GLY	-	expression tag	UNP P62871
B	351	GLY	-	expression tag	UNP P62871
B	352	GLY	-	expression tag	UNP P62871
B	353	SER	-	expression tag	UNP P62871
B	354	SER	-	expression tag	UNP P62871

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Chain	Residue	Modelled	Actual	Comment	Reference
B	355	GLY	-	expression tag	UNP P62871
B	356	VAL	-	expression tag	UNP P62871
B	357	SER	-	expression tag	UNP P62871
B	358	GLY	-	expression tag	UNP P62871
B	359	TRP	-	expression tag	UNP P62871
B	360	ARG	-	expression tag	UNP P62871
B	361	LEU	-	expression tag	UNP P62871
B	362	PHE	-	expression tag	UNP P62871
B	363	LYS	-	expression tag	UNP P62871
B	364	LYS	-	expression tag	UNP P62871
B	365	ILE	-	expression tag	UNP P62871
B	366	SER	-	expression tag	UNP P62871

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	G	57	436	273	77	83	3	0	0

- Molecule 4 is a protein called Nanobody-35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	N	126	961	599	168	188	6	0	0

- Molecule 5 is a protein called Pro-glucagon.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	P	31	249	157	42	49	1	0	0

- Molecule 6 is a protein called Glucagon-like peptide 2 receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	R	292	2426	1624	399	391	12	0	0

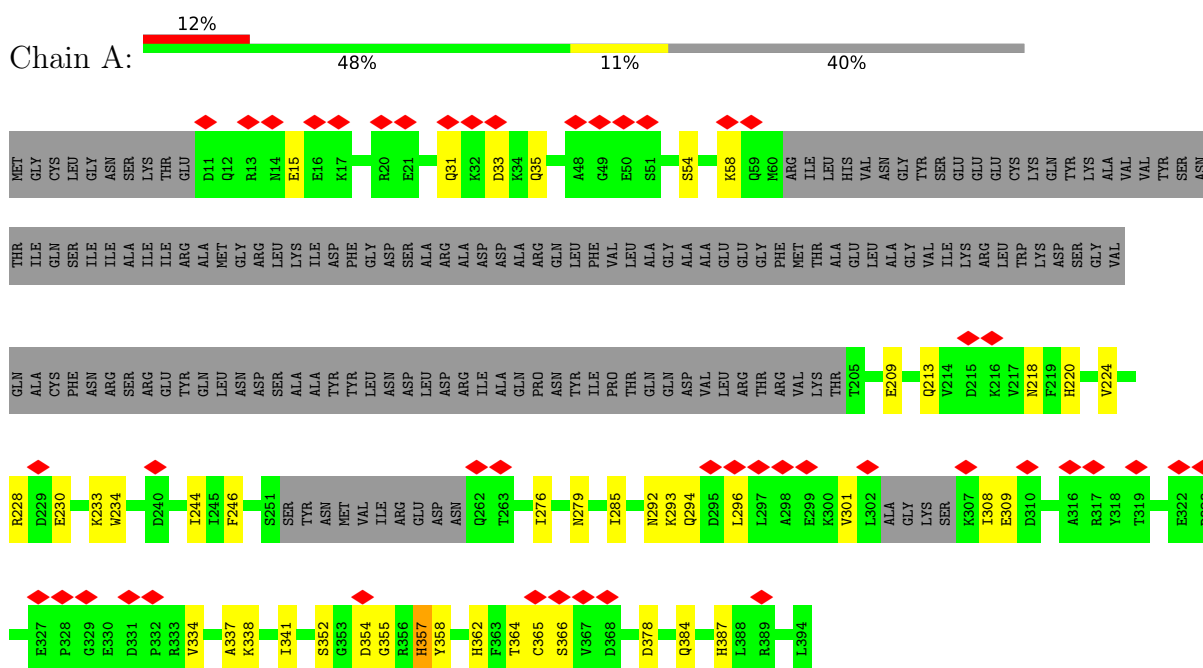
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		AltConf
7	A	1	Total 1	O 1	0
7	R	6	Total 6	O 6	0

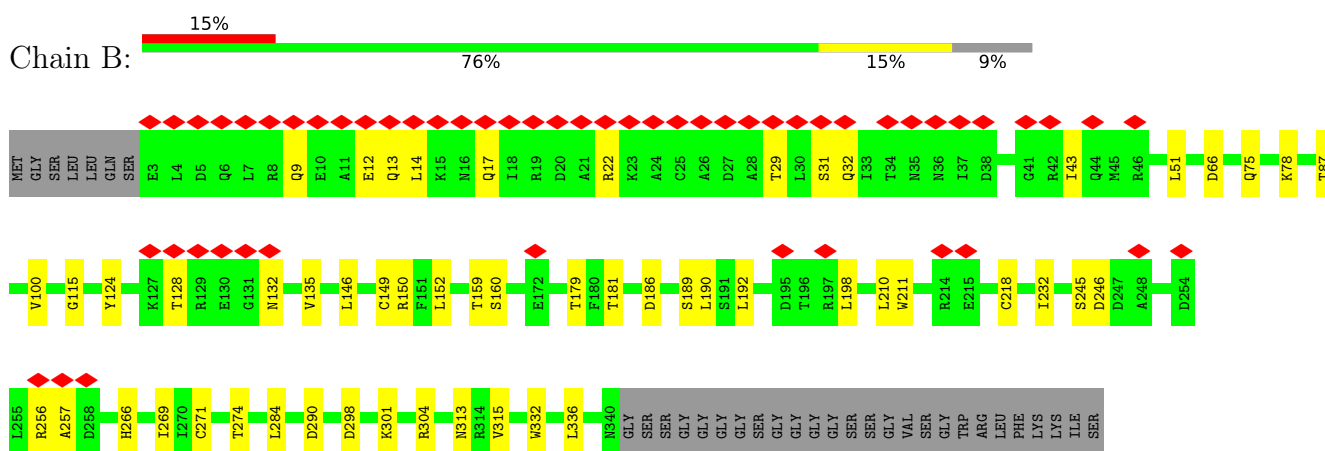
3 Residue-property plots

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.

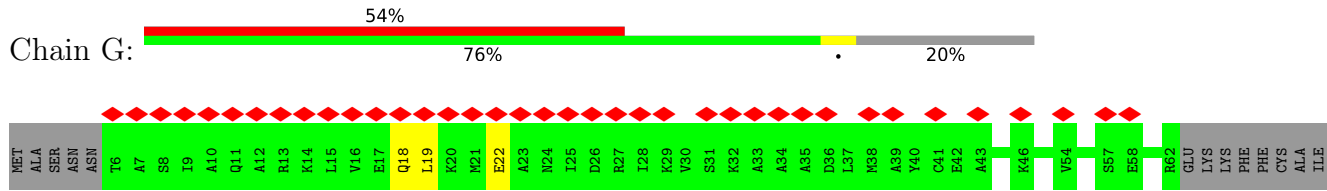
- Molecule 1: Guanine nucleotide-binding protein G(s) subunit alpha isoforms short



- Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

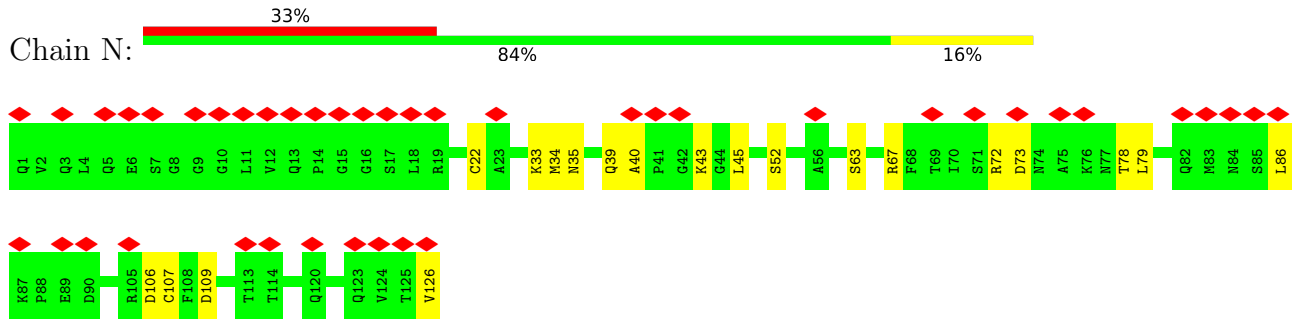


- Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2

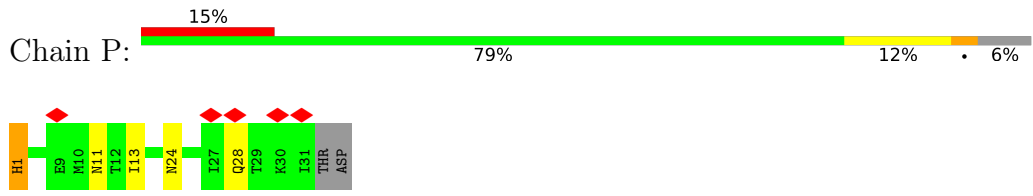


LEU

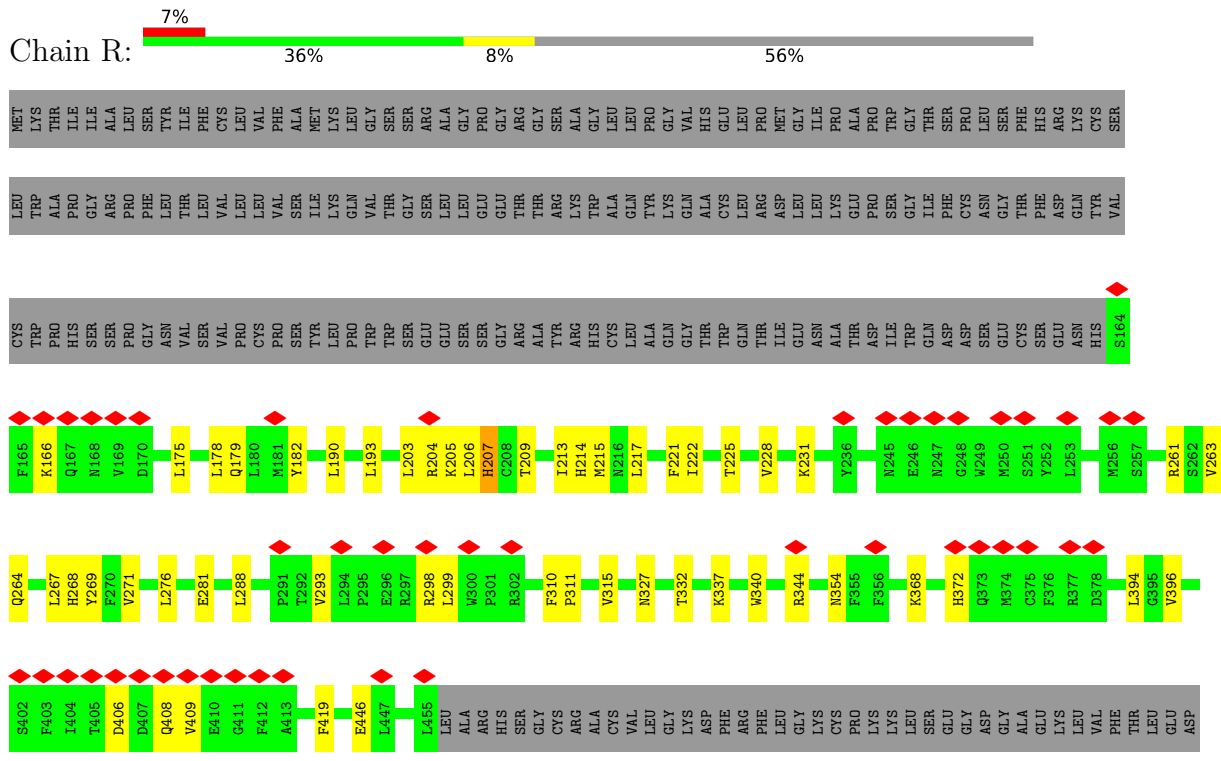
• Molecule 4: Nanobody-35



• Molecule 5: Pro-glucagon



• Molecule 6: Glucagon-like peptide 2 receptor



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

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

THR VAL
THR THR
GLY GLY
THR THR
LEU LEU
TRP TRP
ASN ASN
GLY GLY
ASN ASN
LYS LYS
ILE ILE
ILE ILE
ASP ASP
GLU GLU
ARG ARG
LEU LEU
ILE ILE
THR THR
PRO PRO
ASP ASP
GLY GLY
SER SER
SER SER
MET MET
LEU LEU
PHE PHE
ARG ARG
VAL VAL
THR THR
ILE ILE
ILE ILE
ASN ASN
SER SER

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	284669	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 ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.410	Depositor
Minimum map value	-0.299	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	227.13602, 227.13602, 227.13602	wwPDB
Map dimensions	224, 224, 224	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.014, 1.014, 1.014	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	0.28	0/1919	0.42	0/2577
2	B	0.28	0/2647	0.49	0/3589
3	G	0.25	0/442	0.42	0/597
4	N	0.28	0/981	0.46	0/1329
5	P	0.24	0/253	0.40	0/342
6	R	0.28	0/2497	0.44	0/3389
All	All	0.28	0/8739	0.45	0/11823

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1885	0	1865	31	0
2	B	2600	0	2505	34	0
3	G	436	0	448	3	0
4	N	961	0	930	11	0
5	P	249	0	239	14	0
6	R	2426	0	2497	58	0
7	A	1	0	0	0	0
7	R	6	0	0	0	0
All	All	8564	0	8484	128	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 8.

The worst 5 of 128 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)
6:R:206:LEU:HD21	6:R:446:GLU:HG3	1.64	0.78
6:R:203:LEU:HD12	6:R:206:LEU:HD11	1.66	0.78
6:R:344:ARG:NH1	6:R:406:ASP:HB3	2.01	0.75
2:B:22:ARG:NH1	2:B:257:ALA:O	2.21	0.73
4:N:35:ASN:ND2	4:N:109:ASP:OD2	2.23	0.71

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	218/378 (58%)	212 (97%)	6 (3%)	0	100	100
2	B	336/371 (91%)	319 (95%)	17 (5%)	0	100	100
3	G	55/71 (78%)	54 (98%)	1 (2%)	0	100	100
4	N	124/126 (98%)	118 (95%)	6 (5%)	0	100	100
5	P	29/33 (88%)	29 (100%)	0	0	100	100
6	R	290/664 (44%)	268 (92%)	21 (7%)	1 (0%)	41	76
All	All	1052/1643 (64%)	1000 (95%)	51 (5%)	1 (0%)	54	85

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	R	207	HIS

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	204/331 (62%)	201 (98%)	3 (2%)	65	87
2	B	281/302 (93%)	279 (99%)	2 (1%)	84	94
3	G	46/58 (79%)	46 (100%)	0	100	100
4	N	104/104 (100%)	104 (100%)	0	100	100
5	P	27/29 (93%)	26 (96%)	1 (4%)	34	70
6	R	264/582 (45%)	261 (99%)	3 (1%)	73	90
All	All	926/1406 (66%)	917 (99%)	9 (1%)	77	91

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	R	214	HIS
6	R	215	MET
2	B	256	ARG
2	B	304	ARG
5	P	1	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	220	GLN
2	B	230	ASN
6	R	408	GLN
6	R	264	GLN
6	R	372	HIS

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 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.

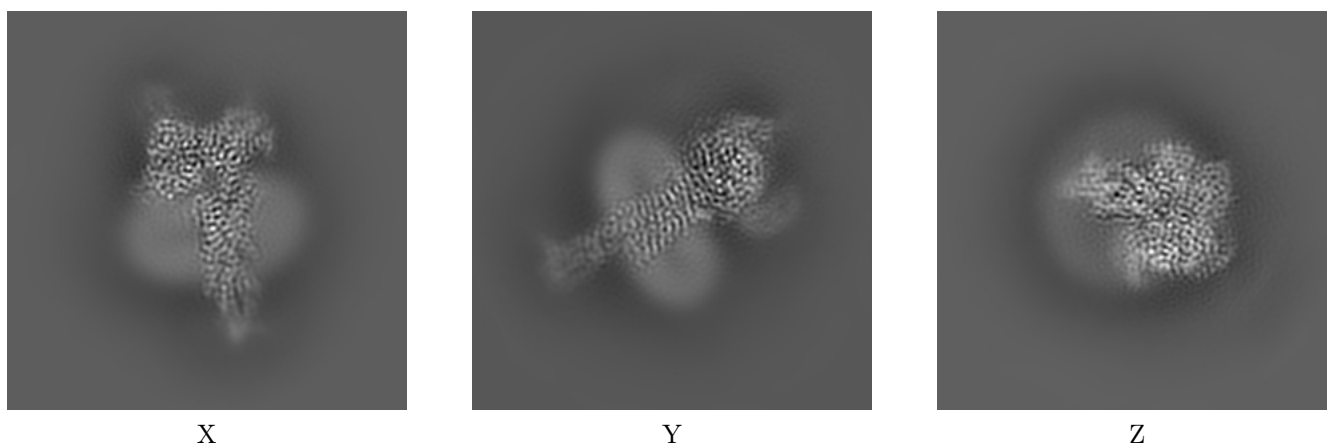
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30590. 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](#)

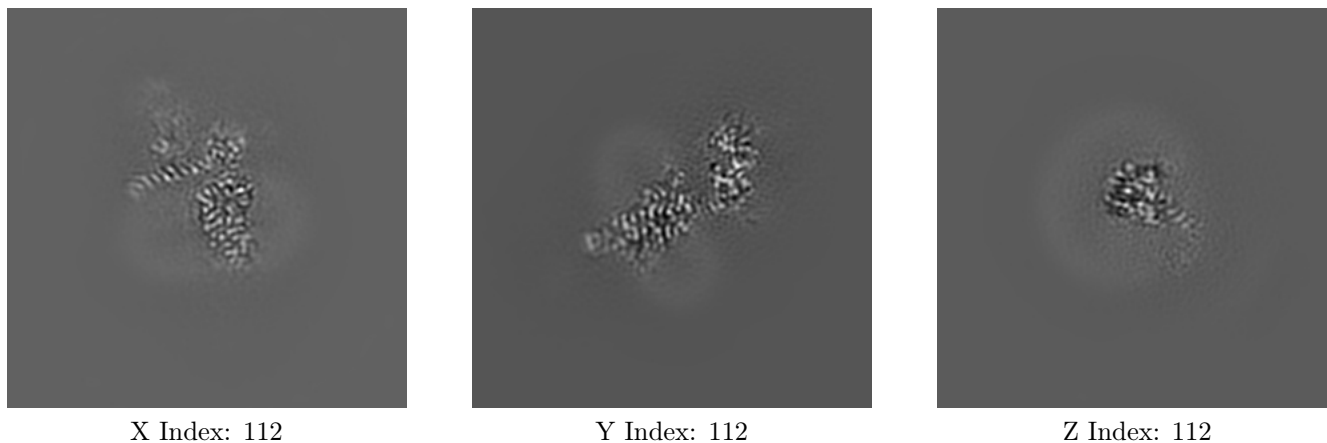
6.1.1 Primary map



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

6.2 Central slices [i](#)

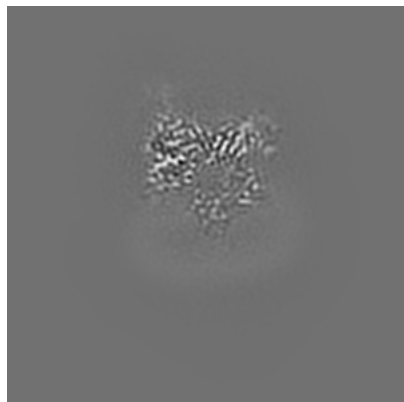
6.2.1 Primary map



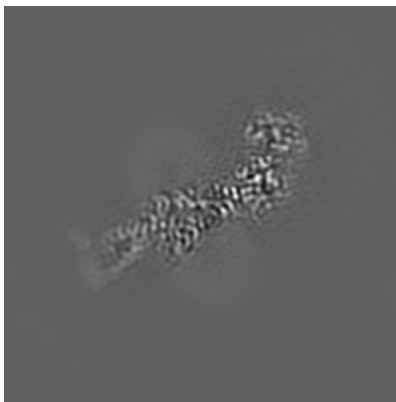
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

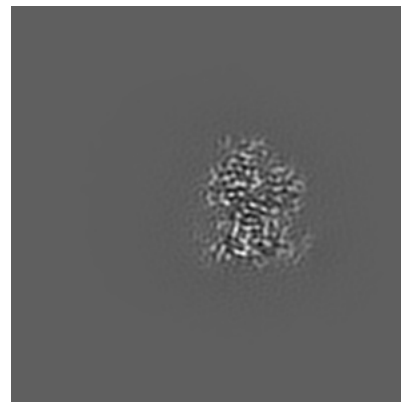
6.3.1 Primary map



X Index: 124



Y Index: 124



Z Index: 148

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

6.4 Orthogonal surface views [i](#)

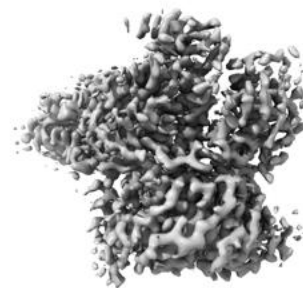
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

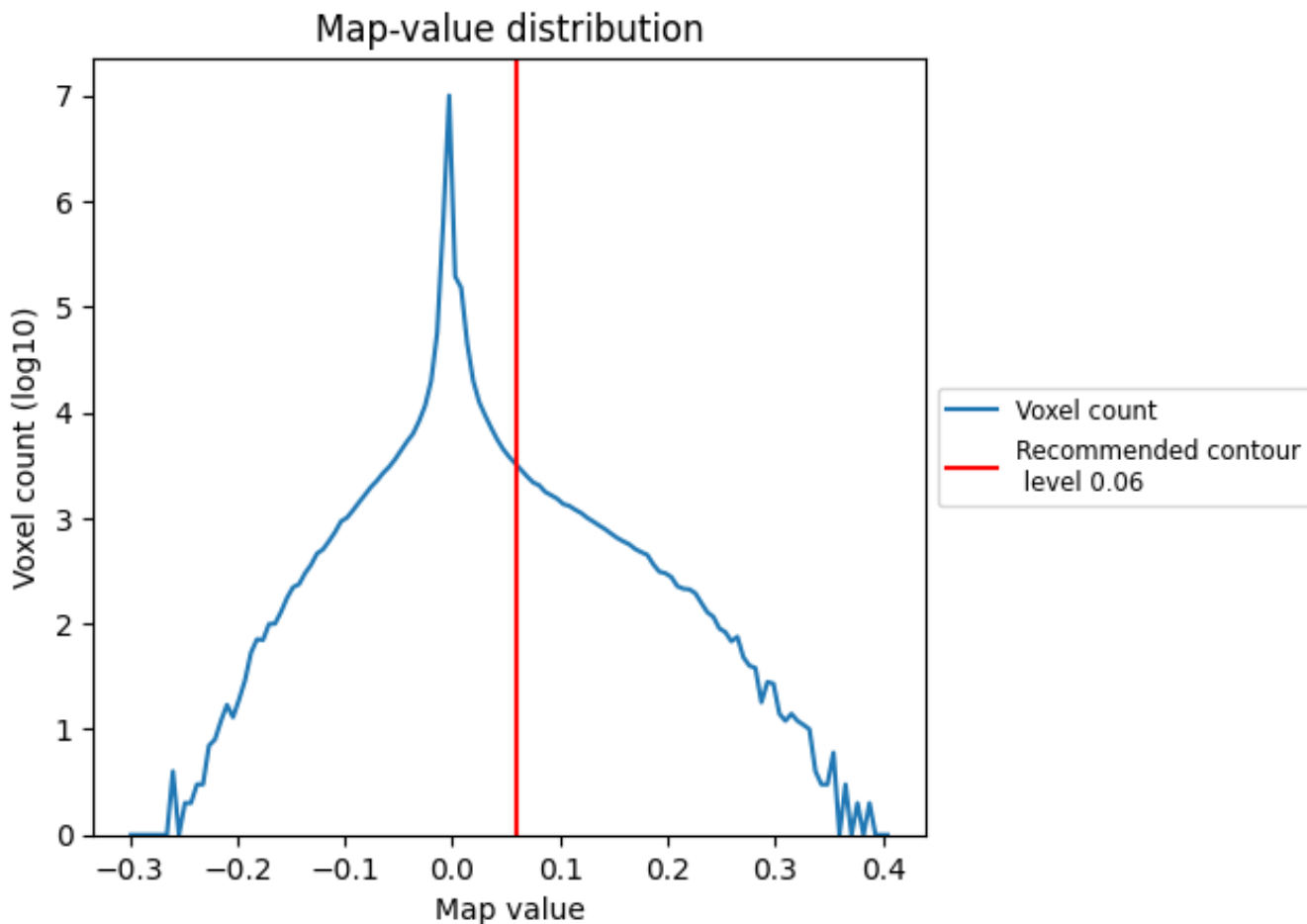
6.5 Mask visualisation

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

7 Map analysis [i](#)

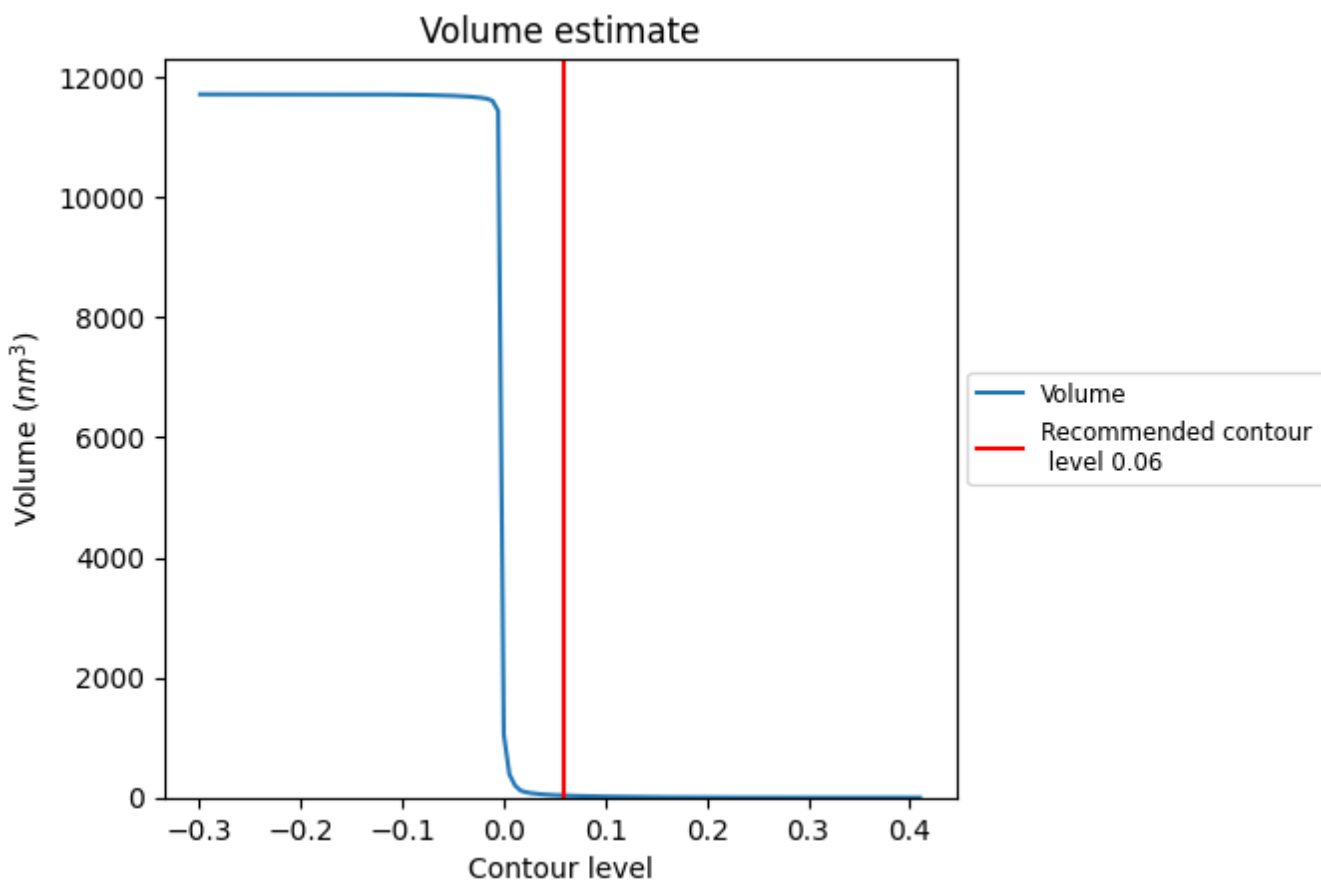
This section contains the results of statistical analysis of the map.

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.

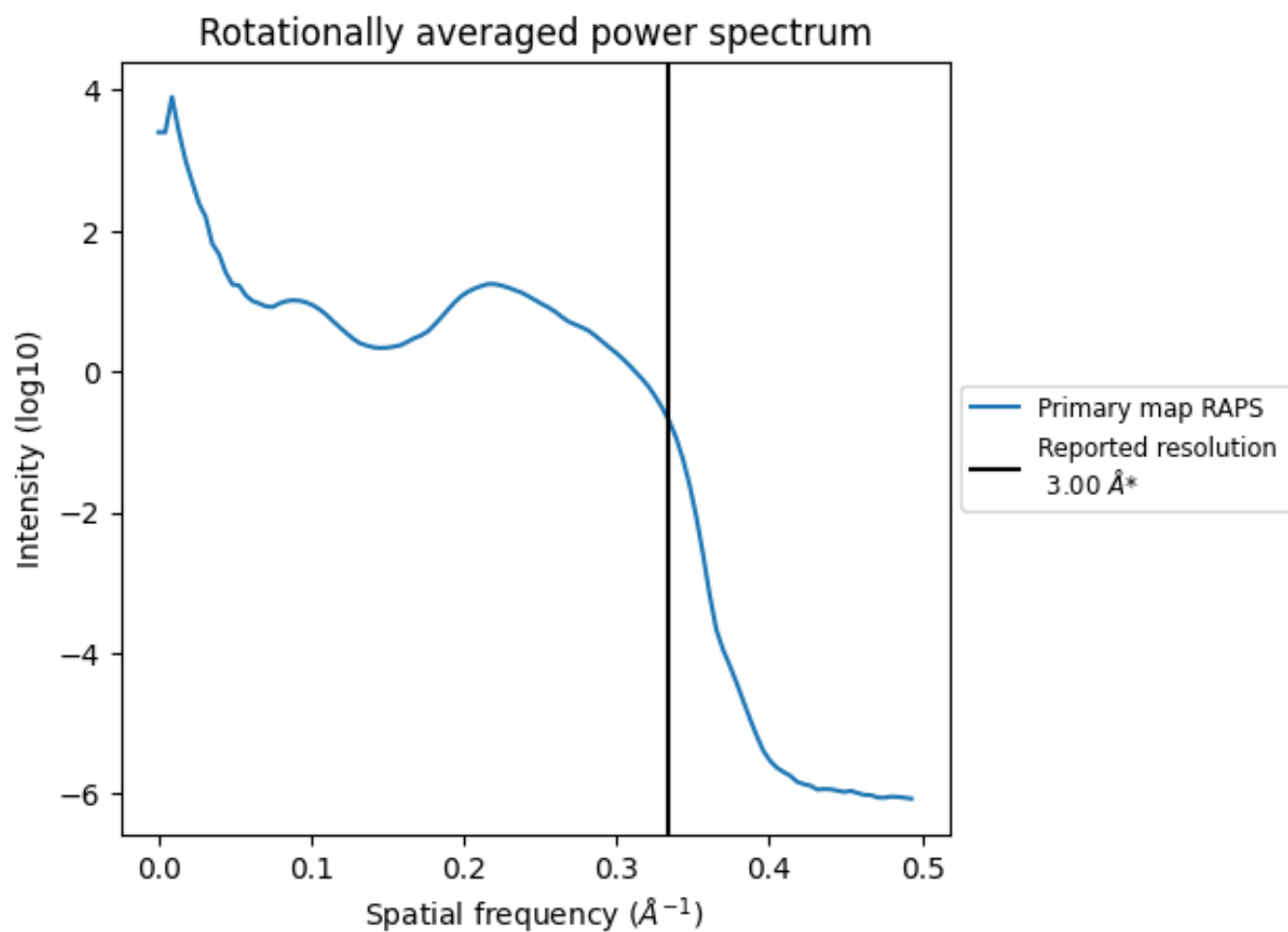
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 34 nm³; this corresponds to an approximate mass of 30 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 0.333\AA^{-1}

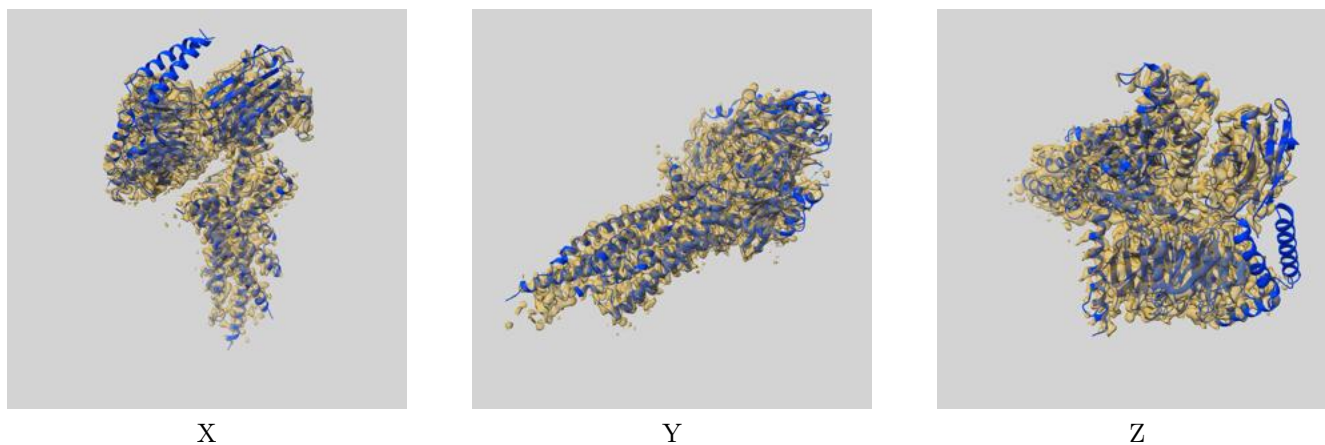
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

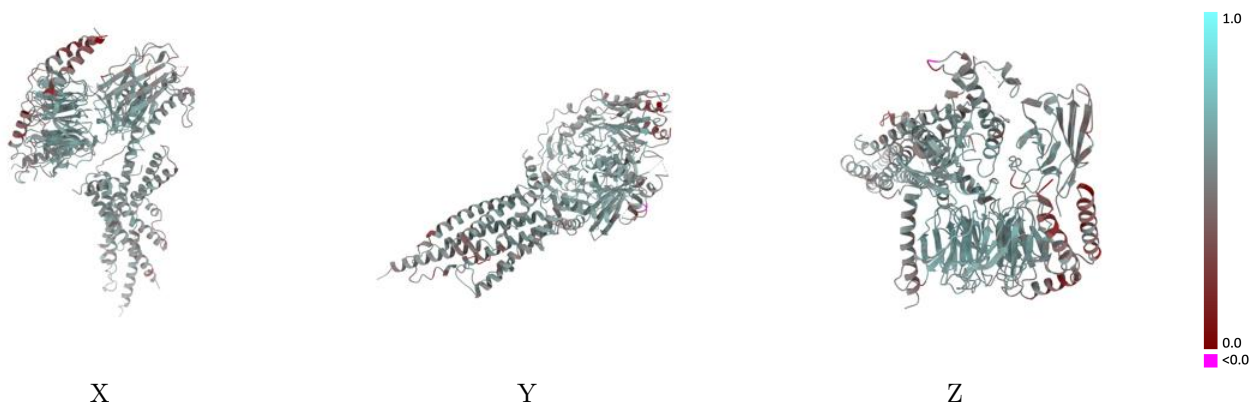
This section contains information regarding the fit between EMDB map EMD-30590 and PDB model 7D68. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



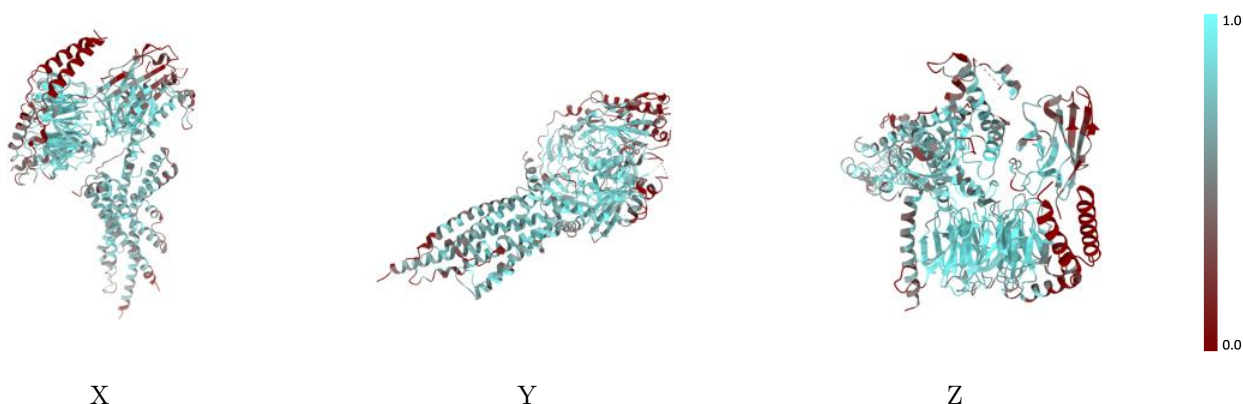
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



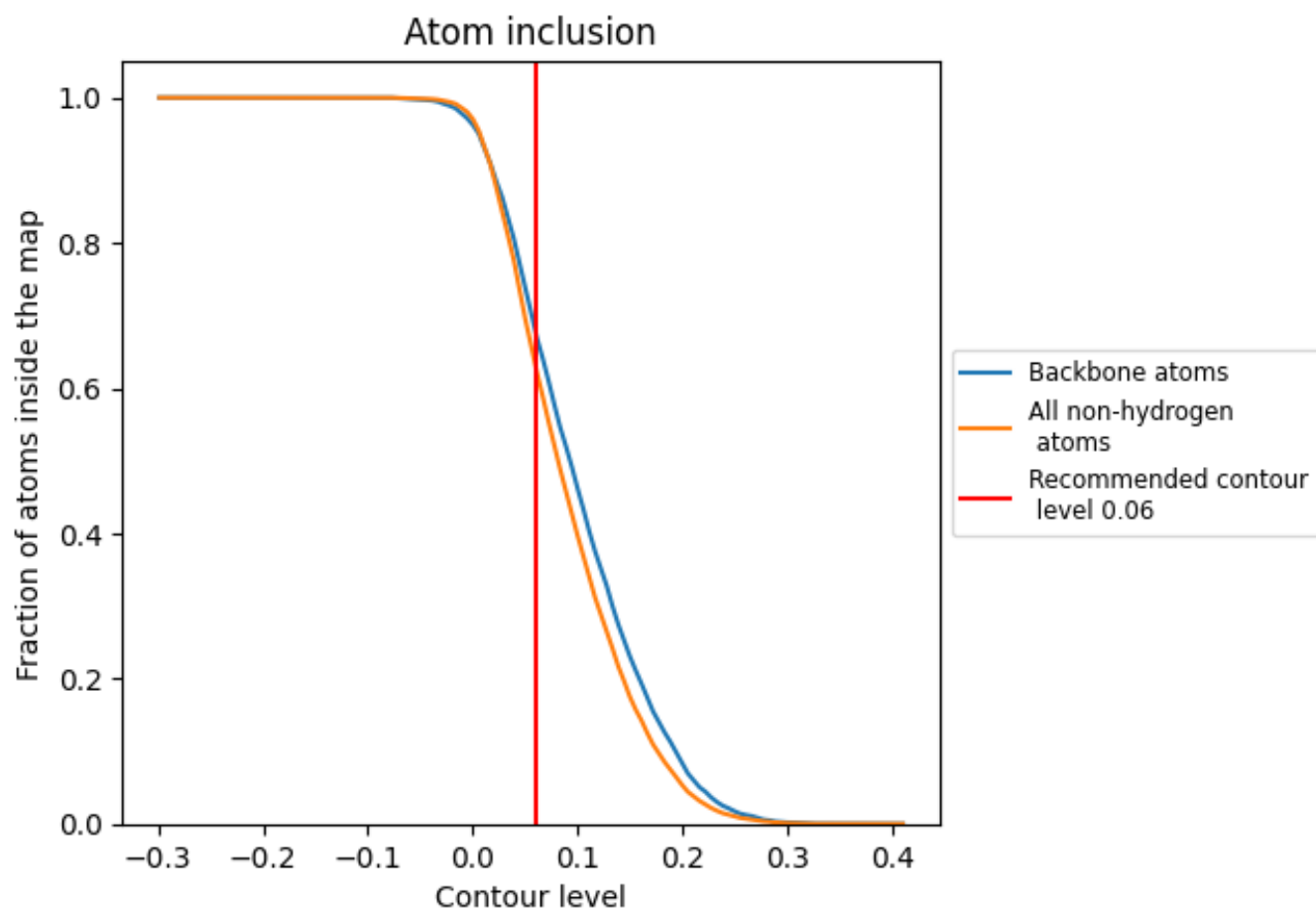
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).















9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 63% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6290	 0.5240
A	 0.6563	 0.5380
B	 0.7083	 0.5520
G	 0.2821	 0.4050
N	 0.5789	 0.5230
P	 0.5813	 0.4950
R	 0.6295	 0.5060

