wwPDB EM Validation Summary Report (i)

Nov 26, 2022 – 06:37 PM EST

PDB ID	:	7SYD
EMDB ID	:	EMD-25522
Title	:	Cryo-EM structure of the extracellular module of the full-length EGFR bound to EGF "tips-juxtaposed" conformation
Authors	:	Huang, Y.; Ognjenovic, J.; Karandur, D.; Miller, K.; Merk, A.; Subramaniam, S.; Kuriyan, J.
Deposited on	:	2021-11-24
Resolution	:	3.10 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

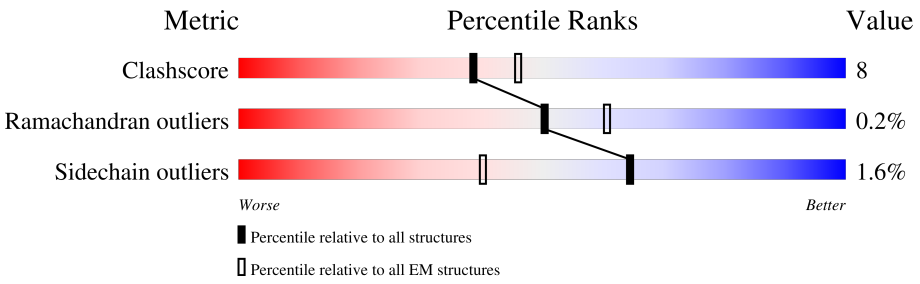
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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 <=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	1210	• 40% 11% 49%
1	B	1210	42% 9% 49%
2	C	53	85% • 11%
2	D	53	85% • 11%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 10216 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 Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	614	4723	2914	842	907	60	1	0
1	B	614	4723	2914	842	907	60	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	232	ASN	ASP	conflict	UNP P00533
B	232	ASN	ASP	conflict	UNP P00533

- Molecule 2 is a protein called Epidermal growth factor.

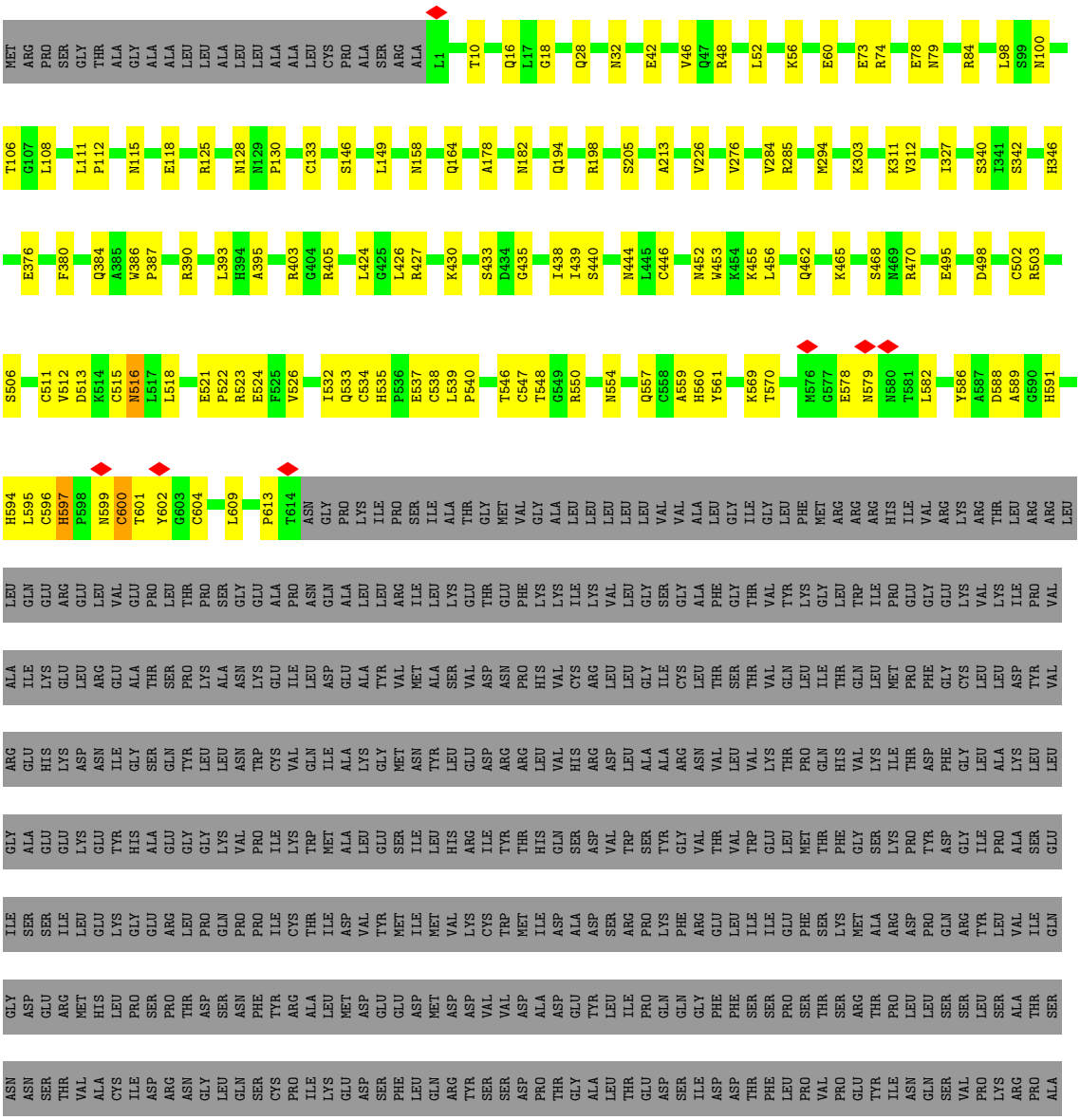
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	47	385	244	63	71	7	0	0
2	D	47	385	244	63	71	7	0	0

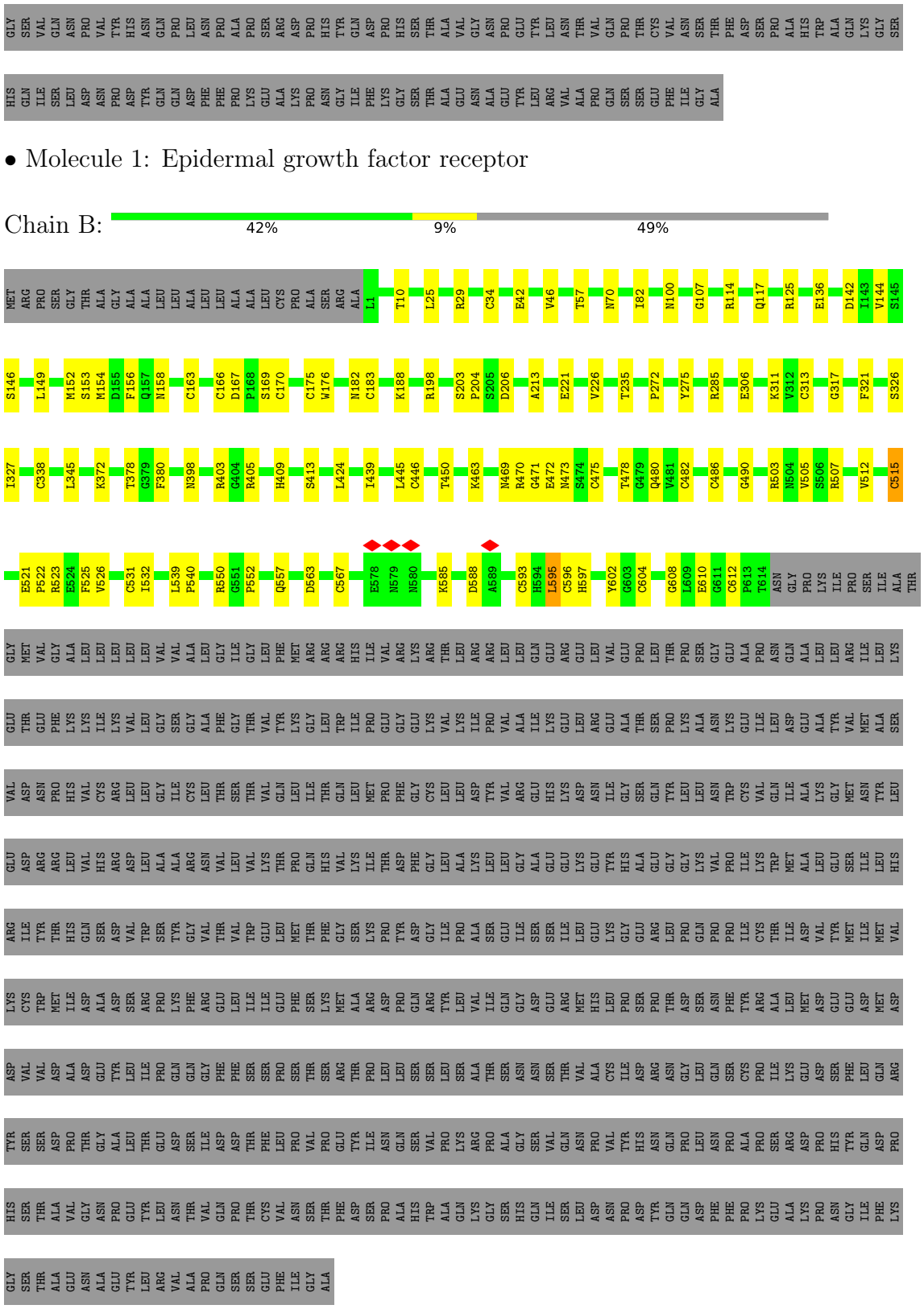
3 Residue-property plots (i)

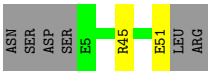
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Epidermal growth factor receptor

Chain A: 40% 11% 49%

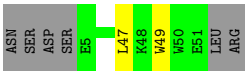



GLY SER VAL GLN ASN PRO VAL TYR HIS ASN GLN PRO LEU ASN PRO ALA PRO SER ARG ASP PRO HIS TYR GLN ASP PRO HIS SER THR ALA VAL GLY ASN PRO GLU TYR LEU ASN THR VAL GLN PRO THR CYS VAL ASN SER THR PHE ASP SER PRO ALA HIS TRP ALA GLN LYS GLY SER
HIS GLN ILE SER LEU ASP ASN PRO ASP TYR GLN GLN ASP PHE PHE PRO LYS GLU ALA LYS PRO ASN GLY ILE PHE LYS GLY SER THR ALA GLU ASN ALA GLU TYR LEU ARG VAL ALA PRO GLN SER SER GLU PHE ILE GLY ALA
Chain B:
42%
9%
49%
MET ARG PRO SER GLY THR ALA GLY ALA ALA LEU LEU ALA LEU LEU ALA ALA LEU CYS PRO ALA SER ARG ALA L1 T10 L25 R29 C34 E42 V46 T57 N70 I82 N100 G107 R114 Q117 R125 E136 D142 I143 V144 S145
S146 L149 M152 S153 M154 D155 F156 Q157 N158 C163 C166 D167 P168 S169 C170 C175 W176 N182 C183 K188 R198 S203 P204 S205 D206 A213 E221 V226 T235 P272 Y275 R285 E306 K311 V312 C313 G317 F321 S326
I327 C338 L345 K372 T378 G379 F380 N398 R403 G404 R405 H409 S413 L424 I439 L445 C446 T450 K463 N469 R470 G471 E472 N473 S474 C475 T478 G479 Q480 V481 C482 C486 G490 R503 N504 V505 S506 R507 V512 C515
E521 P522 R523 E524 F525 V526 C531 I532 L539 P540 R550 G551 P552 Q557 D563 C567 E578 N579 N580 K585 D588 A589 C593 H594 L595 C596 H597 Y602 G603 C604 G608 L609 E610 G611 C612 P613 T614 ASN GLY PRO LYS ILE PRO SER ILE ALA THR
GLY MET VAL GLY ALA LEU LEU LEU LEU LEU VAL VAL ALA LEU GLY ILE GLY LEU PHE MET ARG ARG ARG HIS ILE VAL ARG LYS ARG THR LEU ARG ARG LEU LEU GLN GLU ARG GLU LEU VAL GLU PRO LEU THR PRO SER GLY GLU ALA PRO ASN GLN ALA LEU LEU ARG ILE LEU LYS
GLU THR GLU PHE LYS LYS ILE LYS VAL LEU GLY SER GLY ALA PHE GLY THR VAL TYR LYS GLY LEU TRP ILE PRO GLU GLY GLU LYS VAL LYS ILE PRO VAL ALA ILE LYS GLU LEU ARG GLU ALA THR SER PRO LYS ALA ASN LYS GLU ILE LEU ASP GLU ALA TYR VAL MET ALA SER
VAL ASP ASN PRO HIS VAL CYS ARG LEU LEU GLY ILE CYS LEU THR SER THR VAL GLN LEU ILE THR GLN LEU MET PRO PHE GLY CYS LEU LEU ASP TYR VAL ARG GLU HIS LYS ASP ASN ILE GLY SER GLN TYR LEU LEU ASN TRP CYS VAL GLN ILE ALA LYS GLY MET ASN TYR LEU
GLU ASP ARG ARG LEU VAL HIS HIS ARG ASP LEU ALA ALA ARG ASN VAL LEU VAL LYS THR PRO GLN HIS VAL LYS ILE THR ASP PHE GLY LEU ALA LYS LEU LEU GLY ALA GLU GLU LYS GLU TYR HIS ALA GLU GLY GLY LYS VAL PRO ILE LYS TRP MET ALA LEU GLU SER ILE LEU HIS
ARG ILE TYR THR HIS GLN SER ASP VAL TRP SER TYR GLY VAL THR VAL TRP GLU LEU MET THR PHE GLY SER LYS PRO TYR ASP GLY ILE PRO ALA SER GLU ILE SER SER ILE LEU GLU LYS GLY GLU ARG LEU PRO GLN PRO PRO ILE CYS THR ILE ASP VAL LEU MET ASP VAL
LYS CYS TRP MET ILE ASP ALA ASP SER ARG PRO LYS PHE ARG GLU LEU ILE ILE GLU PHE SER LYS MET ALA ARG ASP PRO GLN ARG TYR LEU VAL ILE GLN GLY ASP GLU ARG MET HIS LEU PRO SER PRO THR ASP SER ASN PHE TYR ARG ALA LEU MET ASP GLU GLU ASP ASP
ASP VAL VAL ASP ALA ASP GLU TYR LEU ILE PRO GLN GLN GLY PHE PHE SER SER PRO SER THR SER ARG THR PRO LEU LEU LEU SER ALA THR SER ASN ASN SER THR VAL ALA CYS ILE ASP ARG ASN GLY LEU GLN SER CYS PRO ILE LYS ARG GLU ASP SER PHE LEU GLN ARG
TYR SER SER ASP PRO THR GLY ALA LEU THR GLU ASP SER ILE ASP ASP THR PHE LEU PRO VAL PRO GLU TYR ILE ASN GLN SER SER VAL PRO LYS ARG PRO ALA GLY SER VAL GLN ASN PRO VAL TYR HIS ASN GLN PRO LEU ASN PRO ALA PRO SER ILE LYS ARG ASP PRO HIS TYR GLN ASP PRO
HIS SER THR ALA VAL GLY ASN PRO GLU TYR LEU ASN THR VAL GLN PRO THR CYS VAL ASN SER THR PHE ASP SER PRO ALA HIS TRP ALA GLN LYS GLY SER HIS GLN ILE SER LEU ASP ASN PRO ASP TYR GLN GLN ASP PHE PHE PRO LYS GLU ALA LYS PRO ASN GLY ILE PHE LYS
GLY SER THR ALA GLU ASN ALA GLU TYR LEU ARG VAL ALA PRO GLN SER SER GLU PHE ILE GLY ALA
• Molecule 1: Epidermal growth factor receptor
Chain B:
42%
9%
49%
MET ARG PRO SER GLY THR ALA GLY ALA ALA LEU LEU ALA LEU LEU ALA ALA LEU CYS PRO ALA SER ARG ALA L1 T10 L25 R29 C34 E42 V46 T57 N70 I82 N100 G107 R114 Q117 R125 E136 D142 I143 V144 S145
S146 L149 M152 S153 M154 D155 F156 Q157 N158 C163 C166 D167 P168 S169 C170 C175 W176 N182 C183 K188 R198 S203 P204 S205 D206 A213 E221 V226 T235 P272 Y275 R285 E306 K311 V312 C313 G317 F321 S326
I327 C338 L345 K372 T378 G379 F380 N398 R403 G404 R405 H409 S413 L424 I439 L445 C446 T450 K463 N469 R470 G471 E472 N473 S474 C475 T478 G479 Q480 V481 C482 C486 G490 R503 N504 V505 S506 R507 V512 C515
E521 P522 R523 E524 F525 V526 C531 I532 L539 P540 R550 G551 P552 Q557 D563 C567 E578 N579 N580 K585 D588 A589 C593 H594 L595 C596 H597 Y602 G603 C604 G608 L609 E610 G611 C612 P613 T614 ASN GLY PRO LYS ILE PRO SER ILE ALA THR
GLY MET VAL GLY ALA LEU LEU LEU LEU LEU VAL VAL ALA LEU GLY ILE GLY LEU PHE MET ARG ARG ARG HIS ILE VAL ARG LYS ARG THR LEU ARG ARG LEU LEU GLN GLU ARG GLU LEU VAL GLU PRO LEU THR PRO SER GLY GLU ALA PRO ASN GLN ALA LEU LEU ARG ILE LEU LYS
GLU THR GLU PHE LYS LYS ILE LYS VAL LEU GLY SER GLY ALA PHE GLY THR VAL TYR LYS GLY LEU TRP ILE PRO GLU GLY GLU LYS VAL LYS ILE PRO VAL ALA ILE LYS GLU LEU ARG GLU ALA THR SER PRO LYS ALA ASN LYS GLU ILE LEU ASP GLU ALA TYR VAL MET ALA SER
VAL ASP ASN PRO HIS VAL CYS ARG LEU LEU GLY ILE CYS LEU THR SER THR VAL GLN LEU ILE THR GLN LEU MET PRO PHE GLY CYS LEU LEU ASP TYR VAL ARG GLU HIS LYS ASP ASN ILE GLY SER GLN TYR LEU LEU ASN TRP CYS VAL GLN ILE ALA LYS GLY MET ASN TYR LEU
GLU ASP ARG ARG LEU VAL HIS HIS ARG ASP LEU ALA ALA ARG ASN VAL LEU VAL LYS THR PRO GLN HIS VAL LYS ILE THR ASP PHE GLY LEU ALA LYS LEU LEU GLY ALA GLU GLU LYS GLU TYR HIS ALA GLU GLY GLY LYS VAL PRO ILE LYS TRP MET ALA LEU GLU SER ILE LEU HIS
ARG ILE TYR THR HIS GLN SER ASP VAL TRP SER TYR GLY VAL THR VAL TRP GLU LEU MET THR PHE GLY SER LYS PRO TYR ASP GLY ILE PRO ALA SER GLU ILE SER SER ILE LEU GLU LYS GLY GLU ARG LEU PRO GLN PRO PRO ILE CYS THR ILE ASP VAL LEU MET ASP VAL
LYS CYS TRP MET ILE ASP ALA ASP SER ARG PRO LYS PHE ARG GLU LEU ILE ILE GLU PHE SER LYS MET ALA ARG ASP PRO GLN ARG TYR LEU VAL ILE GLN GLY ASP GLU ARG MET HIS LEU PRO SER PRO THR ASP SER ASN PHE TYR ARG ALA LEU MET ASP GLU GLU ASP ASP
ASP VAL VAL ASP ALA ASP GLU TYR LEU ILE PRO GLN GLN GLY PHE PHE SER SER PRO SER THR SER ARG THR PRO LEU LEU LEU SER ALA THR SER ASN ASN SER THR VAL ALA CYS ILE ASP ARG ASN GLY LEU GLN SER CYS PRO ILE LYS ARG GLU ASP SER PHE LEU GLN ARG
TYR SER SER ASP PRO THR GLY ALA LEU THR GLU ASP SER ILE ASP ASP THR PHE LEU PRO VAL PRO GLU TYR ILE ASN GLN SER SER VAL PRO LYS ARG PRO ALA GLY SER VAL GLN ASN PRO VAL TYR HIS ASN GLN PRO LEU ASN PRO ALA PRO SER ILE LYS ARG ASP PRO HIS TYR GLN ASP PRO
HIS SER THR ALA VAL GLY ASN PRO GLU TYR LEU ASN THR VAL GLN PRO THR CYS VAL ASN SER THR PHE ASP SER PRO ALA HIS TRP ALA GLN LYS GLY SER HIS GLN ILE SER LEU ASP ASN PRO ASP TYR GLN GLN ASP PHE PHE PRO LYS GLU ALA LYS PRO ASN GLY ILE PHE LYS
GLY SER THR ALA GLU ASN ALA GLU TYR LEU ARG VAL ALA PRO GLN SER SER GLU PHE ILE GLY ALA
• Molecule 2: Epidermal growth factor
Chain C:
85%
•
11%



• Molecule 2: Epidermal growth factor

Chain D:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	105728	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	7500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.465	Depositor
Minimum map value	-0.542	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.038	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	323.81998, 323.81998, 323.81998	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0794, 1.0794, 1.0794	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	0.38	0/4806	0.49	0/6501
1	B	0.38	0/4815	0.50	0/6514
2	C	0.41	0/396	0.45	0/536
2	D	0.45	0/396	0.47	0/536
All	All	0.38	0/10413	0.50	0/14087

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	4723	0	4556	96	0
1	B	4723	0	4556	77	0
2	C	385	0	344	1	0
2	D	385	0	344	2	0
All	All	10216	0	9800	159	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 159 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:602:TYR:HB3	1:B:602:TYR:CD1	1.41	1.52
1:A:602:TYR:HB3	1:B:602:TYR:CE1	1.71	1.25
1:A:602:TYR:CB	1:B:602:TYR:CD1	2.31	1.13
1:A:602:TYR:CB	1:B:602:TYR:HD1	1.73	0.98
1:A:602:TYR:CB	1:B:602:TYR:CE1	2.45	0.97

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	612/1210 (51%)	543 (89%)	67 (11%)	2 (0%)	41	73
1	B	612/1210 (51%)	549 (90%)	63 (10%)	0	100	100
2	C	45/53 (85%)	42 (93%)	3 (7%)	0	100	100
2	D	45/53 (85%)	41 (91%)	4 (9%)	0	100	100
All	All	1314/2526 (52%)	1175 (89%)	137 (10%)	2 (0%)	50	79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	516	ASN
1	A	613	PRO

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	535/1053 (51%)	526 (98%)	9 (2%)	60	83
1	B	536/1053 (51%)	527 (98%)	9 (2%)	60	83
2	C	41/47 (87%)	40 (98%)	1 (2%)	49	76
2	D	41/47 (87%)	41 (100%)	0	100	100
All	All	1153/2200 (52%)	1134 (98%)	19 (2%)	64	84

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	557	GLN
1	B	596	CYS
1	B	610	GLU
1	B	595	LEU
1	A	601	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	409	HIS
1	B	384	GLN
1	A	544	ASN
1	B	134	ASN
1	A	541	GLN

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.

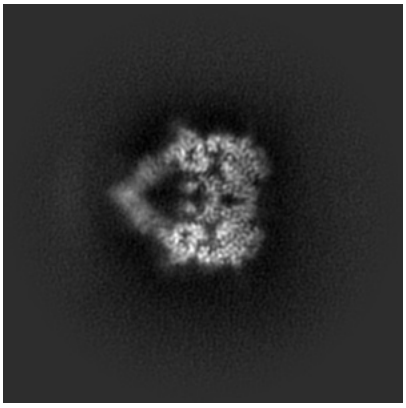
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-25522. These allow visual inspection of the internal detail of the map and identification of artifacts.

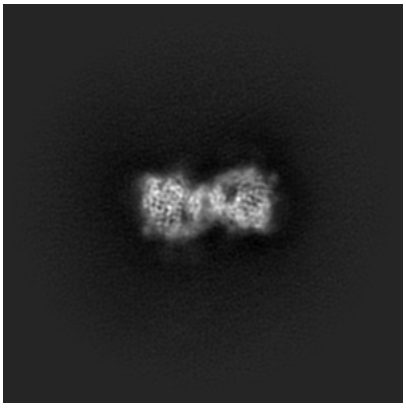
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

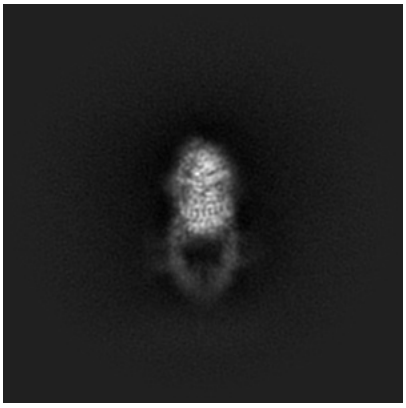
6.1.1 Primary map



X



Y

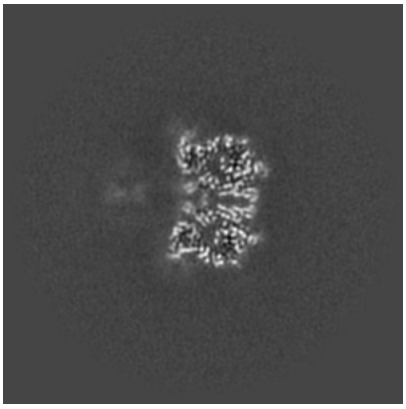


Z

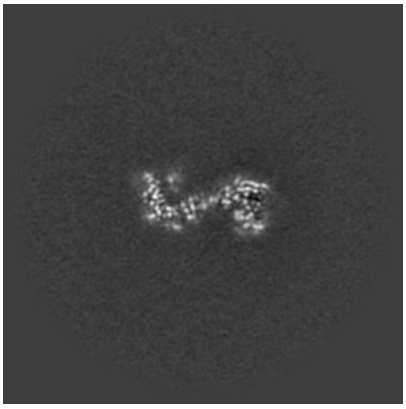
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

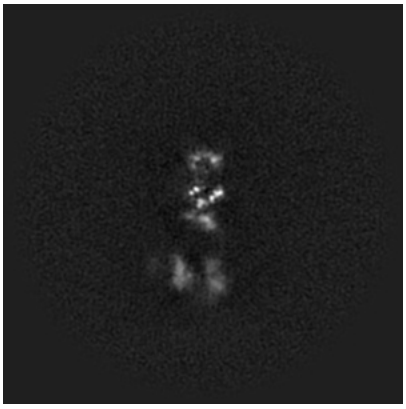
6.2.1 Primary map



X Index: 150



Y Index: 150

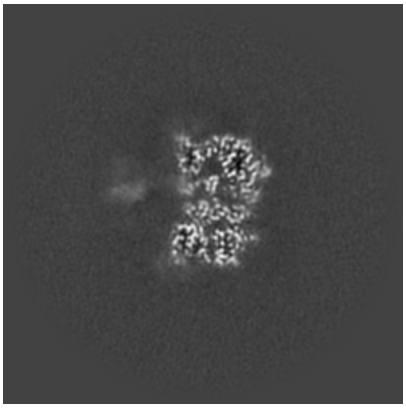


Z Index: 150

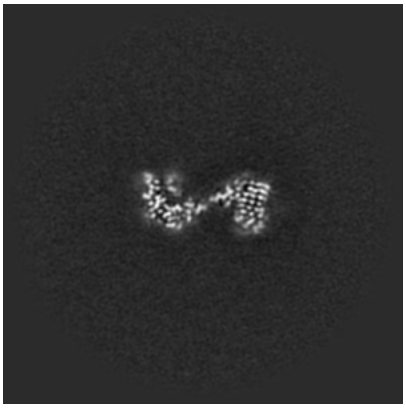
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

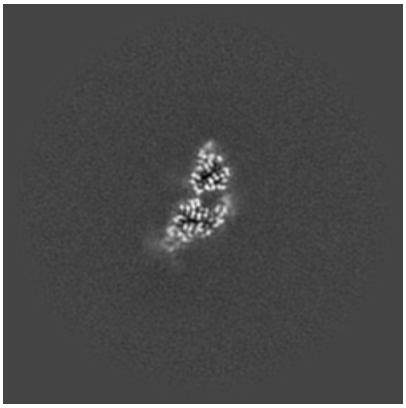
6.3.1 Primary map



X Index: 147



Y Index: 148



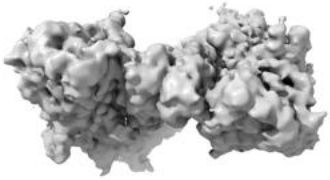
Z Index: 124

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

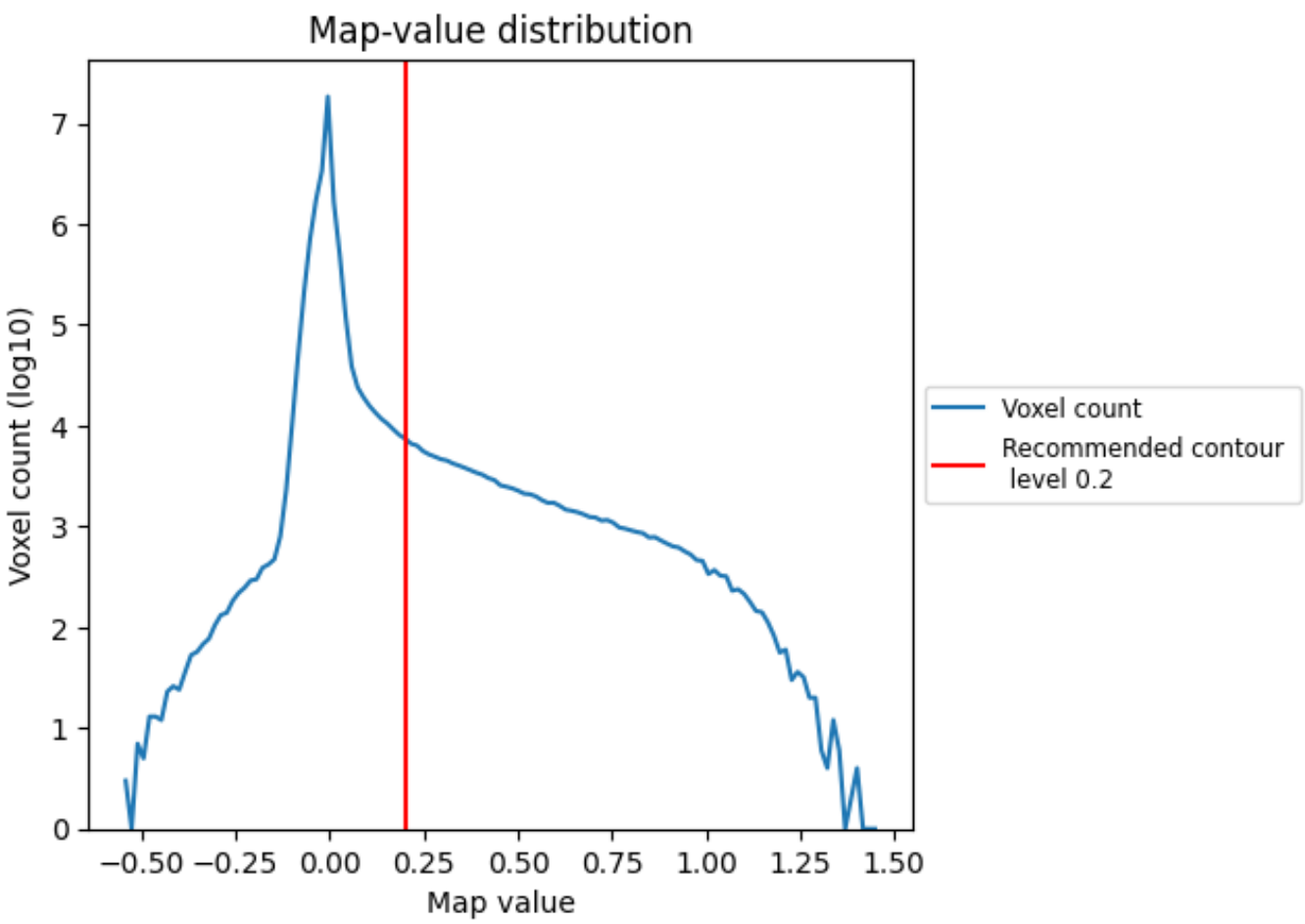
6.5 Mask visualisation (i)

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

7 Map analysis (i)

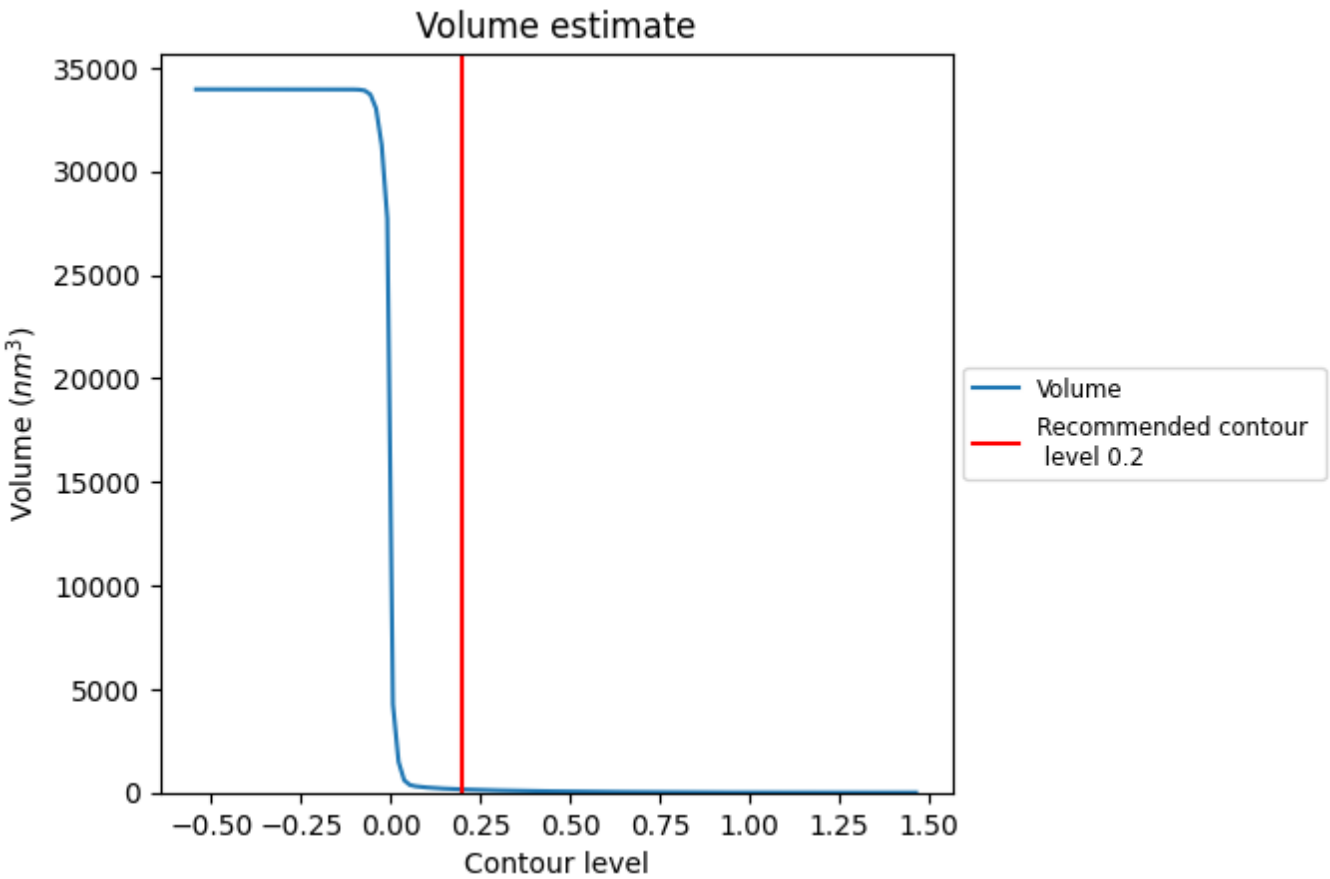
This section contains the results of statistical analysis of the map.

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.

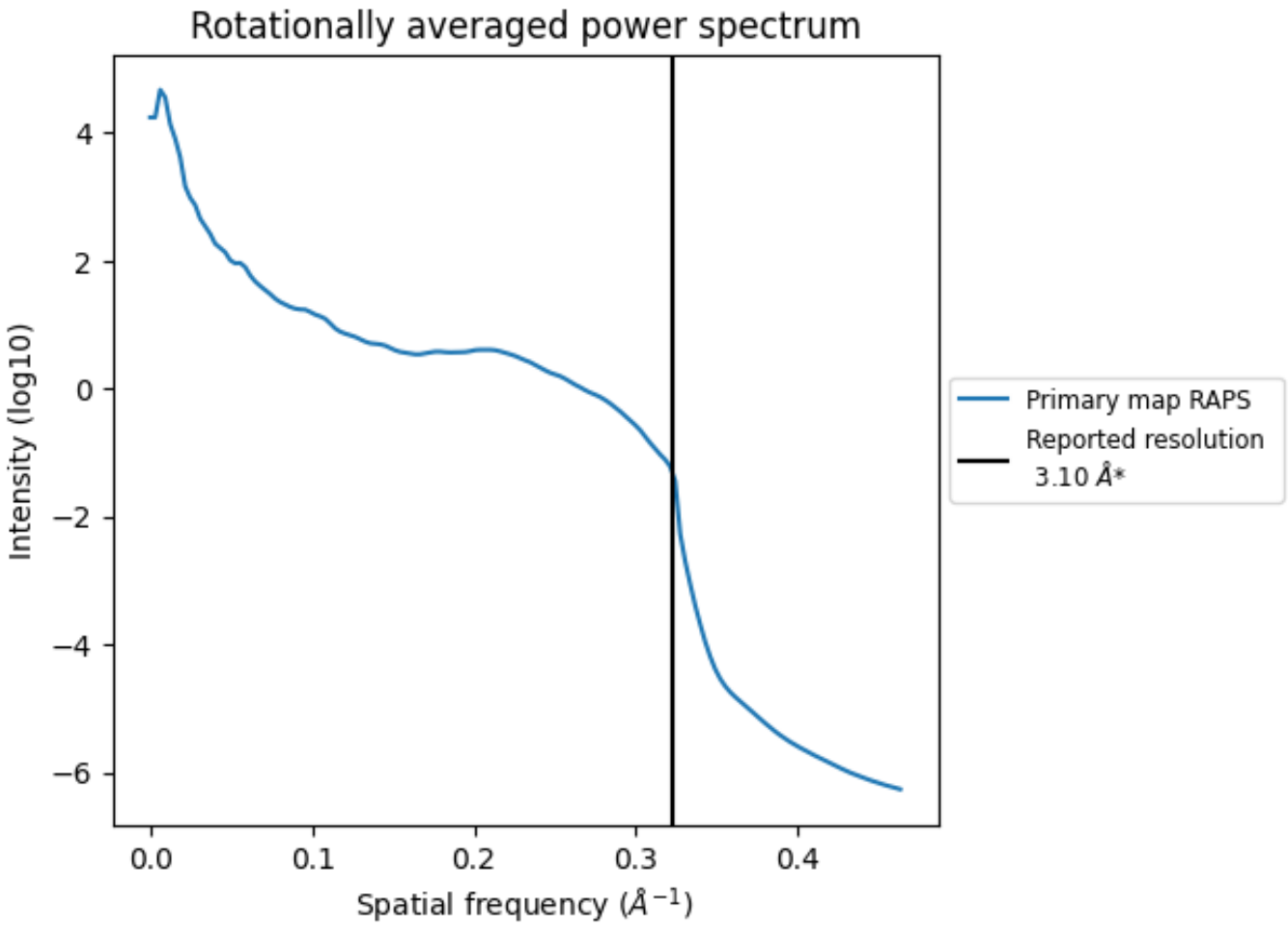
7.2 Volume estimate (i)



The volume at the recommended contour level is 153 nm^3; this corresponds to an approximate mass of 138 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 0.323 Å^{-1}

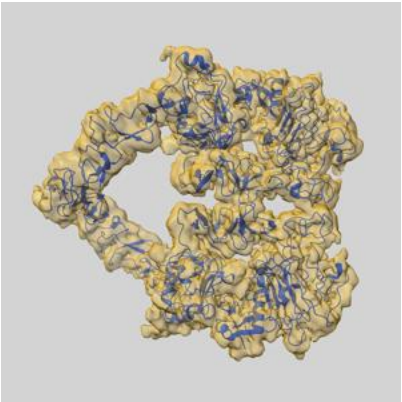
8 Fourier-Shell correlation (i)

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

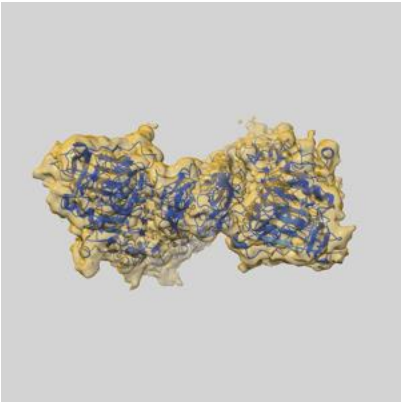
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-25522 and PDB model 7SYD. Per-residue inclusion information can be found in section 3 on page 4.

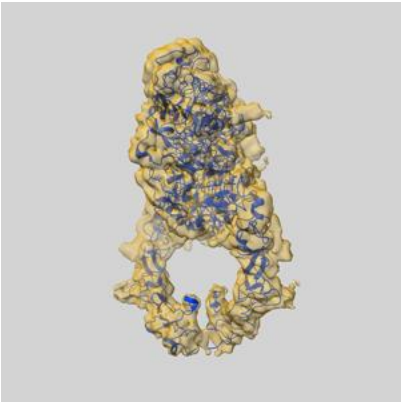
9.1 Map-model overlay (i)



X



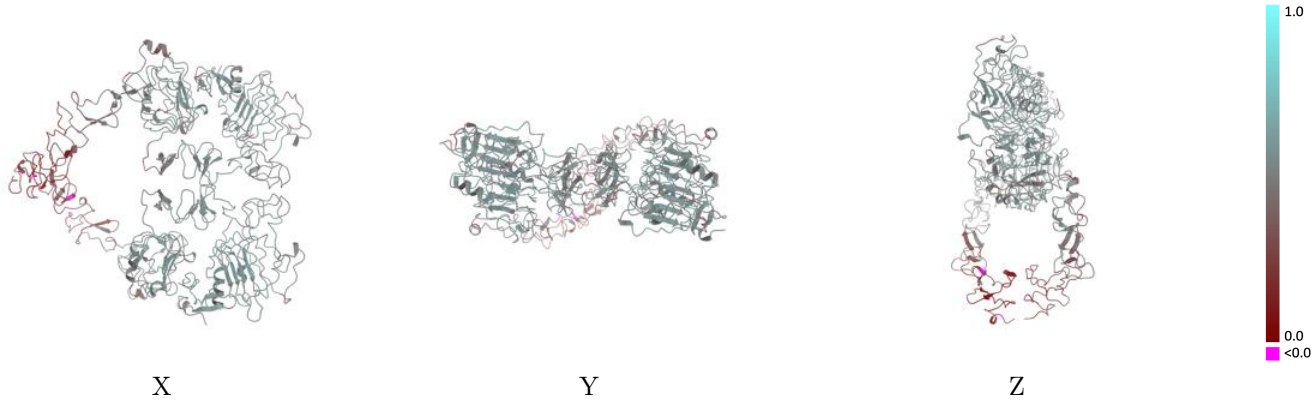
Y



Z

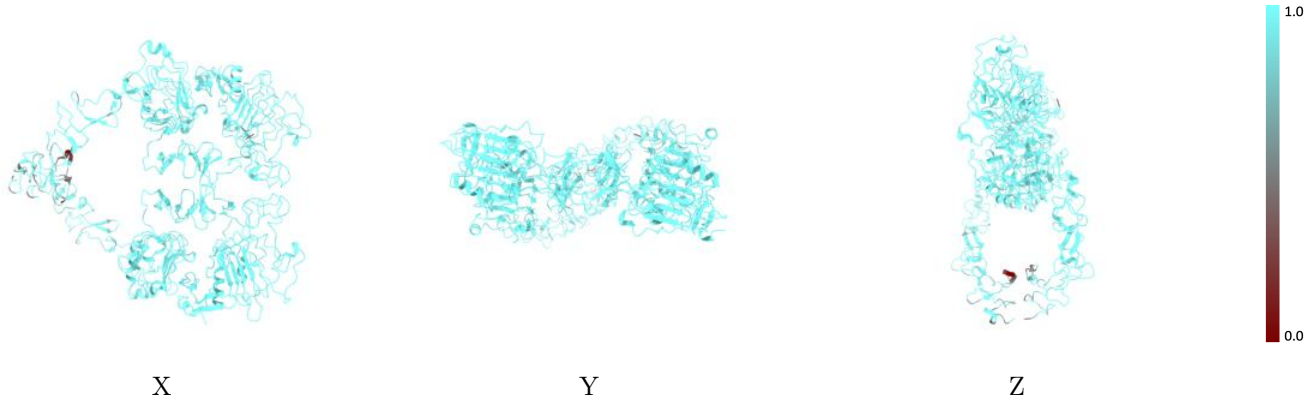
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



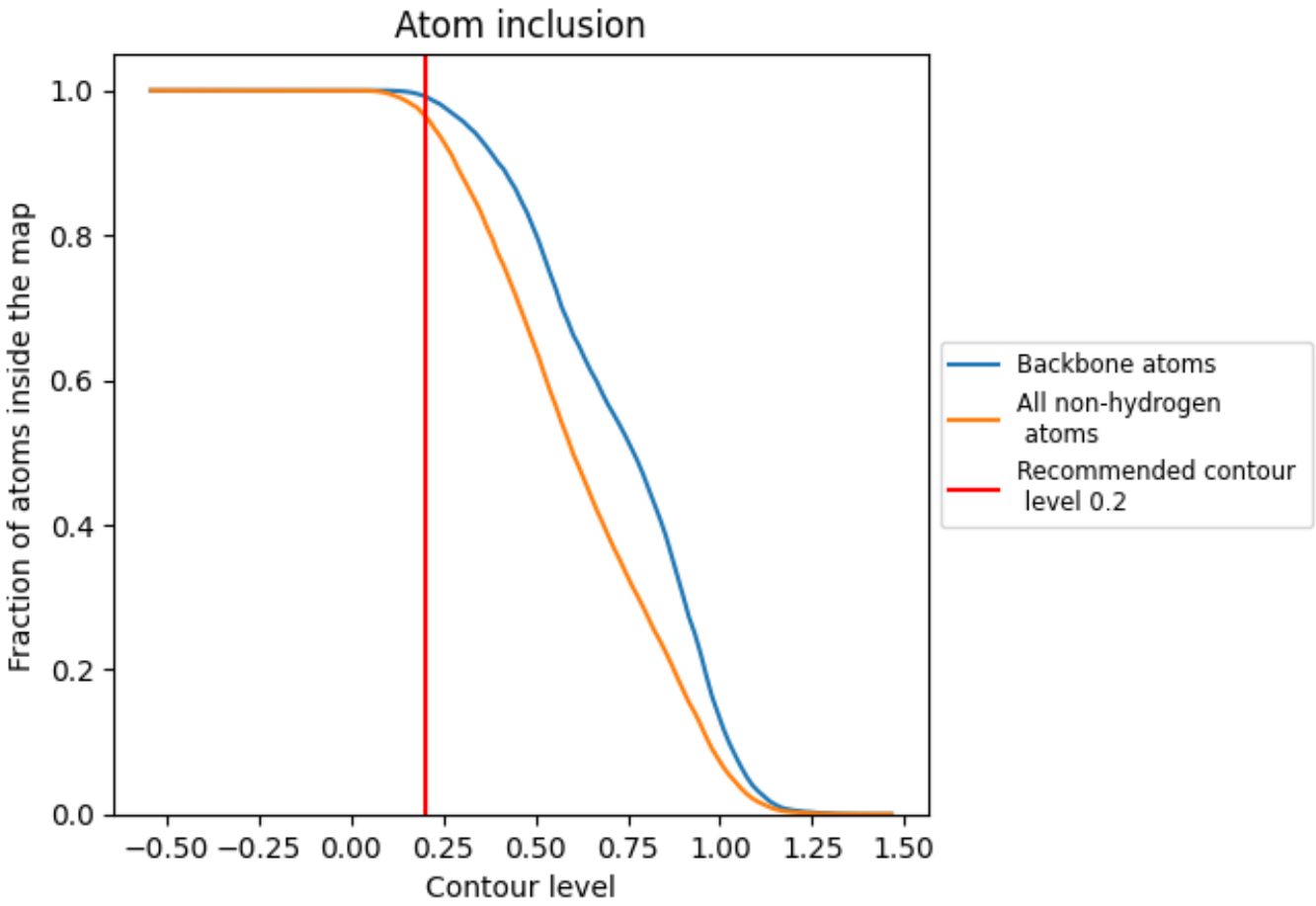
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion (i)



At the recommended contour level, 99% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9649	0.4810
A	0.9640	0.4830
B	0.9628	0.4750
C	0.9733	0.5070
D	0.9947	0.5230