



wwPDB EM Validation Summary Report ⓘ

Nov 15, 2022 – 06:41 PM EST

PDB ID : 6XJA
EMDB ID : EMD-22204
Title : Streptococcus Pneumoniae IgA1 Protease with IgA1 substrate
Authors : Eisenmesser, E.Z.; Zheng, H.
Deposited on : 2020-06-23
Resolution : 4.00 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 ⓘ 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) : 2.31.2

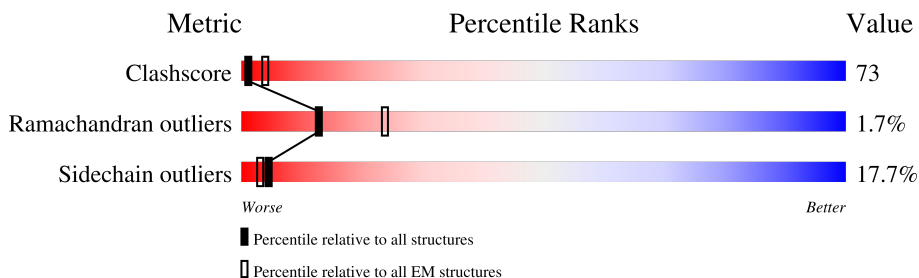
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	P	1299	
2	A	210	
2	B	210	
3	L	219	
4	H	232	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 16441 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 Immunoglobulin A1 protease.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	P	1286	10159	6402	1727	2012	18	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	1605	ALA	GLU	engineered mutation	UNP Q59947

- Molecule 2 is a protein called Immunoglobulin heavy constant alpha 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	209	1598	1007	276	306	9	0	0
2	B	210	1604	1010	277	307	10	0	0

- Molecule 3 is a protein called Immunoglobulin alpha-1 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	L	219	1541	956	267	312	6	0	0

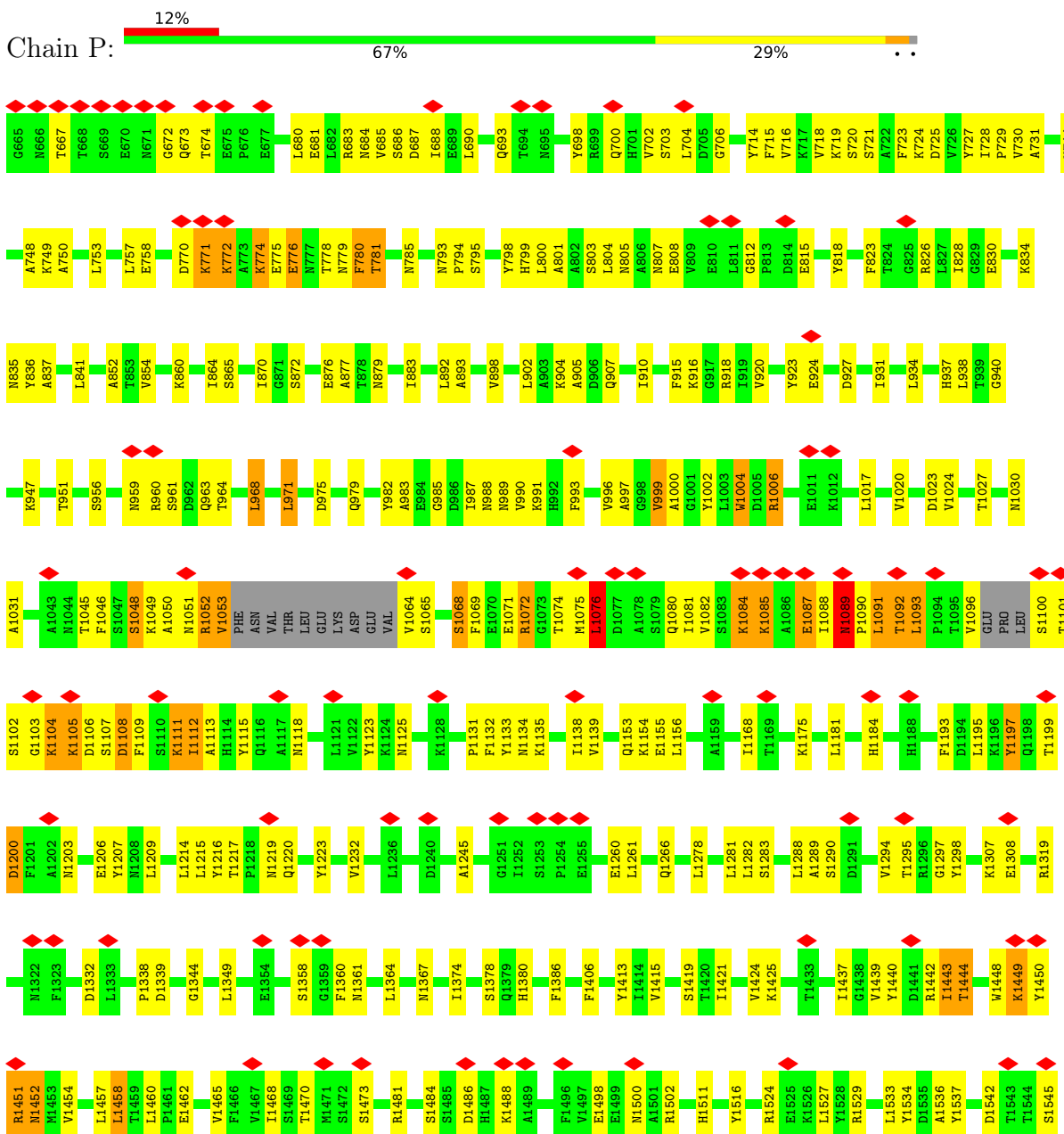
- Molecule 4 is a protein called Immunoglobulin alpha-1 heavy chain.

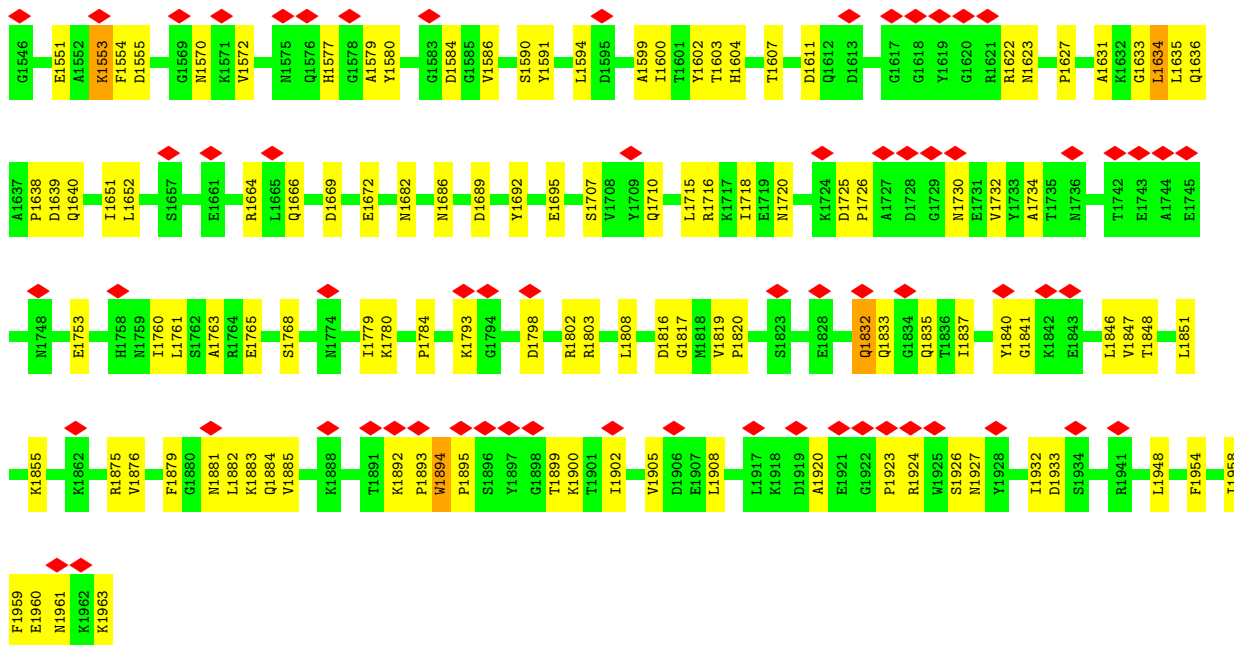
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	H	232	1539	962	263	307	7	0	0

3 Residue-property plots

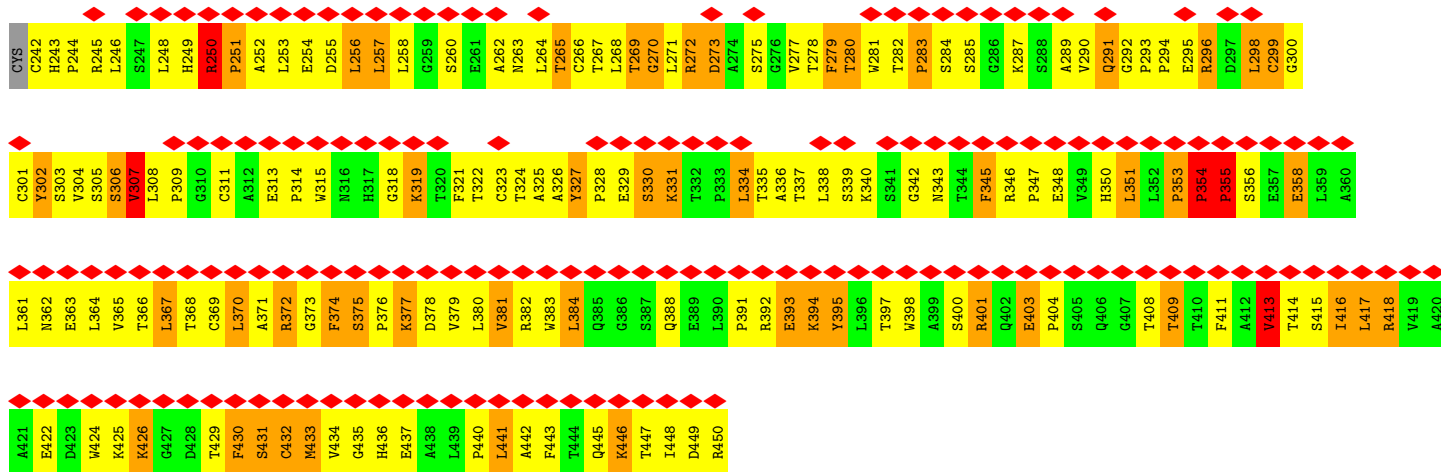
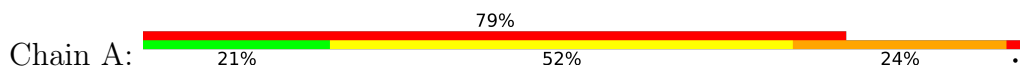
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Immunoglobulin A1 protease

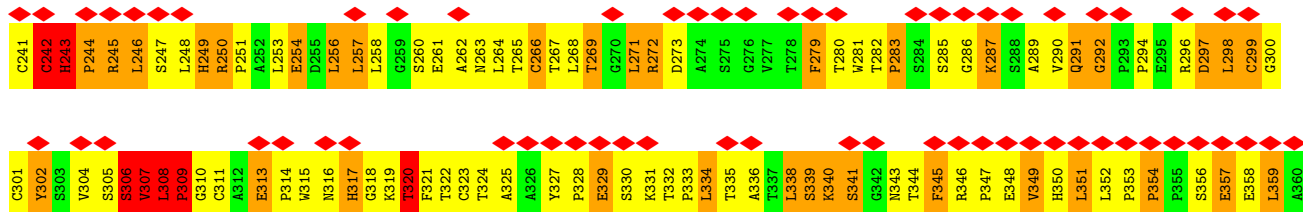
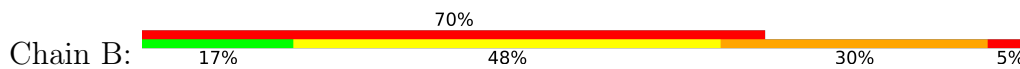


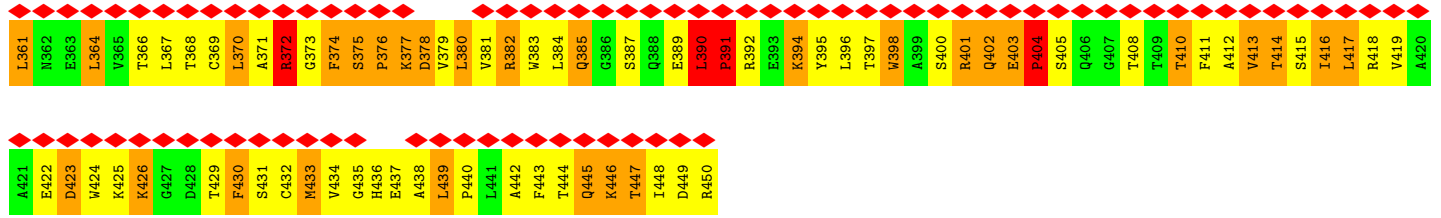


• Molecule 2: Immunoglobulin heavy constant alpha 1

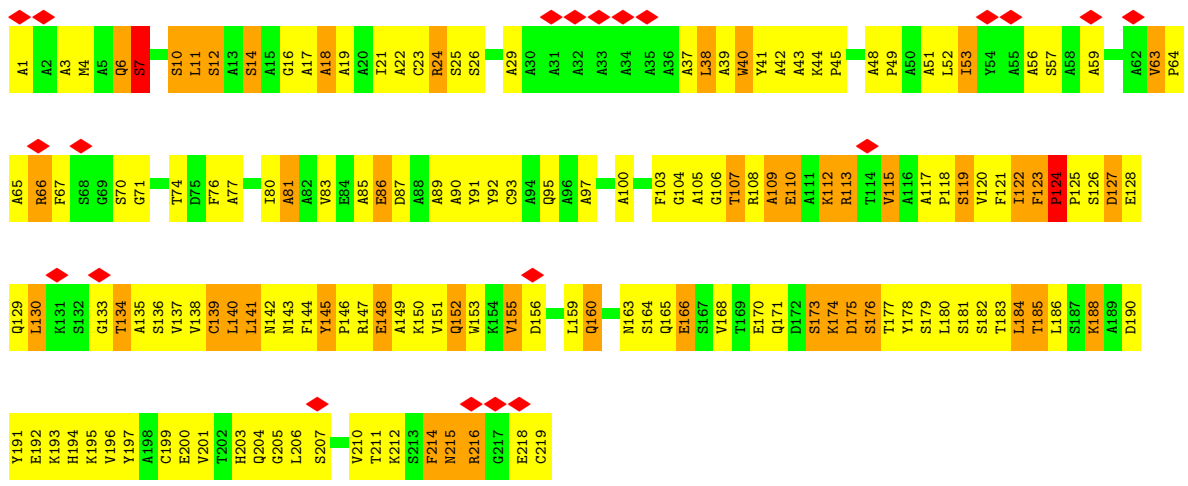


• Molecule 2: Immunoglobulin heavy constant alpha 1

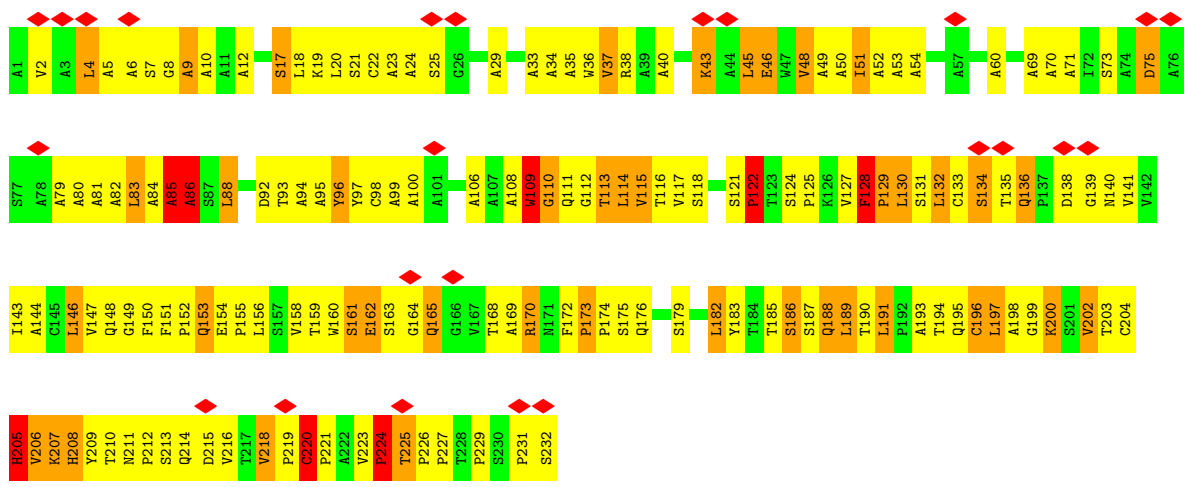




• Molecule 3: Immunoglobulin alpha-1 light chain



• Molecule 4: Immunoglobulin alpha-1 heavy chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	100000	Depositor
Resolution determination method	FSC 3 SIGMA CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.751	Depositor
Minimum map value	-0.401	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.15	Depositor
Map size (\AA)	356.15997, 356.15997, 356.15997	wwPDB
Map dimensions	224, 224, 224	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.5899999, 1.5899999, 1.5899999	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	P	0.41	0/10345	0.55	2/13970 (0.0%)
2	A	0.85	5/1639 (0.3%)	0.79	4/2238 (0.2%)
2	B	1.91	23/1645 (1.4%)	1.80	23/2246 (1.0%)
3	L	0.80	3/1570 (0.2%)	0.74	3/2140 (0.1%)
4	H	1.23	15/1574 (1.0%)	1.15	18/2177 (0.8%)
All	All	0.86	46/16773 (0.3%)	0.87	50/22771 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	P	0	1
2	B	0	6
3	L	0	3
4	H	0	6
All	All	0	16

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	243	HIS	CA-CB	44.50	2.51	1.53
2	B	307	VAL	CA-CB	26.19	2.09	1.54
2	B	243	HIS	CB-CG	21.19	1.88	1.50
2	B	308	LEU	C-O	19.47	1.60	1.23
2	B	307	VAL	N-CA	16.87	1.80	1.46

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	242	CYS	O-C-N	-39.03	60.26	122.70
2	B	307	VAL	CG1-CB-CG2	-26.52	68.48	110.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	307	VAL	CA-CB-CG1	26.40	150.50	110.90
2	B	243	HIS	CA-CB-CG	23.12	152.90	113.60
2	B	307	VAL	CA-CB-CG2	19.70	140.44	110.90

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	242	CYS	Mainchain
2	B	243	HIS	Peptide
2	B	306	SER	Peptide
2	B	307	VAL	Peptide
1	P	1093	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	P	10159	0	9932	674	0
2	A	1598	0	1576	395	0
2	B	1604	0	1577	715	0
3	L	1541	0	1490	388	0
4	H	1539	0	1508	448	0
All	All	16441	0	16083	2371	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 73.

The worst 5 of 2371 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:385:GLN:HG2	2:B:430:PHE:CB	1.20	1.67
1:P:836:TYR:CD1	1:P:1093:LEU:HD22	1.29	1.62
2:B:307:VAL:CA	2:B:307:VAL:HB	1.20	1.61
3:L:11:LEU:CD1	3:L:19:ALA:HB1	1.21	1.60
4:H:71:ALA:HB3	4:H:84:ALA:CB	1.16	1.60

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	P	1272/1299 (98%)	1197 (94%)	69 (5%)	6 (0%)	29	67
2	A	207/210 (99%)	178 (86%)	19 (9%)	10 (5%)	2	23
2	B	208/210 (99%)	178 (86%)	20 (10%)	10 (5%)	2	23
3	L	217/219 (99%)	205 (94%)	8 (4%)	4 (2%)	8	41
4	H	230/232 (99%)	209 (91%)	14 (6%)	7 (3%)	4	32
All	All	2134/2170 (98%)	1967 (92%)	130 (6%)	37 (2%)	13	43

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	P	779	ASN
1	P	1089	ASN
2	A	354	PRO
2	B	244	PRO
2	B	302	TYR

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	P	1096/1118 (98%)	1030 (94%)	66 (6%)	19	47
2	A	179/180 (99%)	110 (62%)	69 (38%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	180/180 (100%)	109 (61%)	71 (39%)	0	0
3	L	145/145 (100%)	93 (64%)	52 (36%)	0	1
4	H	142/142 (100%)	91 (64%)	51 (36%)	0	1
All	All	1742/1765 (99%)	1433 (82%)	309 (18%)	4	12

5 of 309 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	L	134	THR
4	H	170	ARG
3	L	156	ASP
4	H	25	SER
4	H	202	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	P	1640	GLN
4	H	205	HIS
2	A	249	HIS
4	H	140	ASN
1	P	1961	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 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	P	4

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	P	1106:ASP	C	1107:SER	N	3.16
1	P	673:GLN	C	674:THR	N	2.88
1	P	1091:LEU	C	1092:THR	N	2.39
1	P	1958:ILE	C	1959:PHE	N	2.01

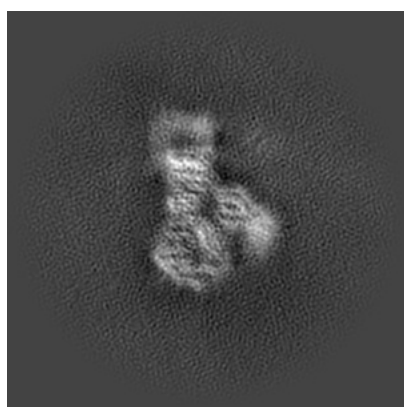
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22204. These allow visual inspection of the internal detail of the map and identification of artifacts.

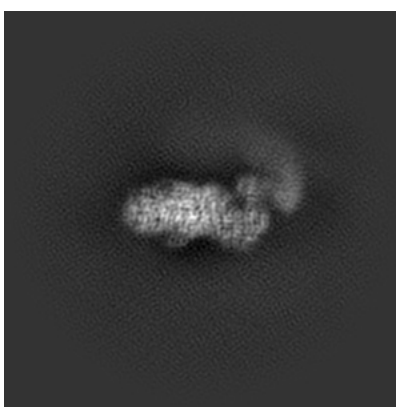
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

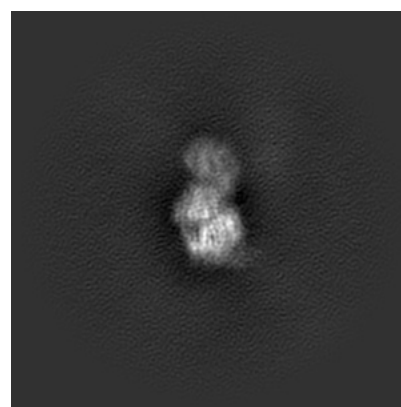
6.1.1 Primary map



X



Y

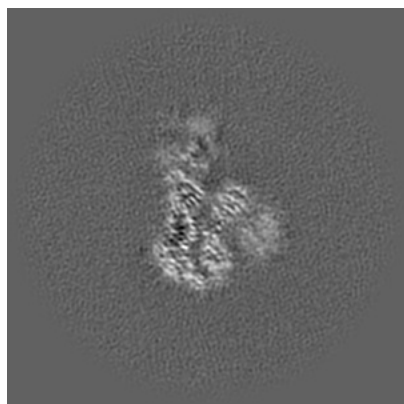


Z

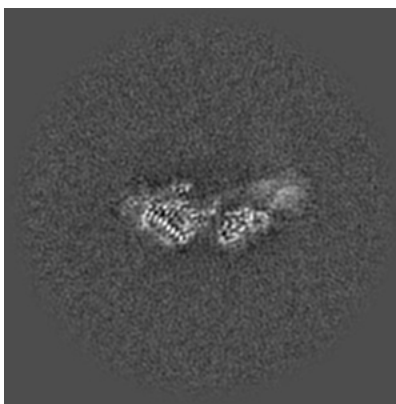
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

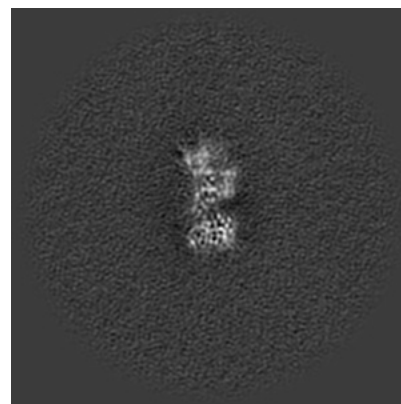
6.2.1 Primary map



X Index: 112



Y Index: 112

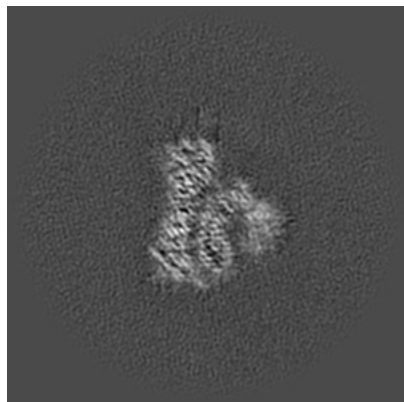


Z Index: 112

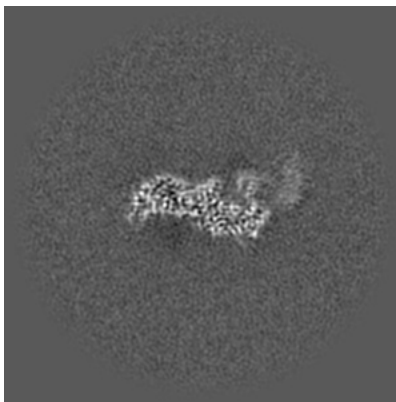
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

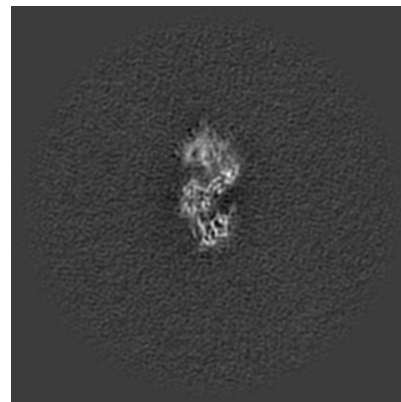
6.3.1 Primary map



X Index: 108



Y Index: 99



Z Index: 105

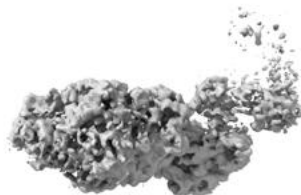
The images above show the largest variance slices of the map in three orthogonal directions.

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

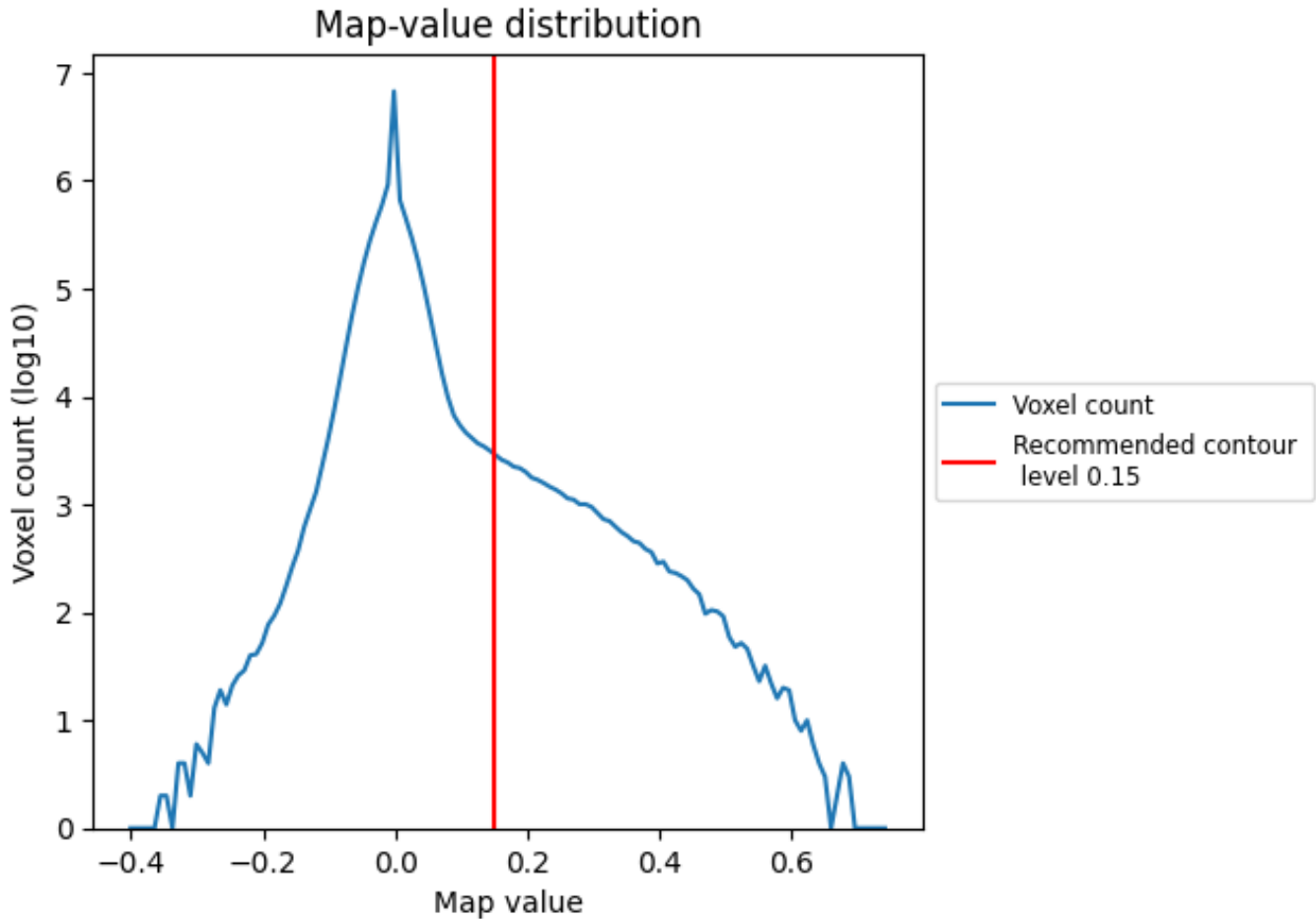
6.5 Mask visualisation

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

7 Map analysis [i](#)

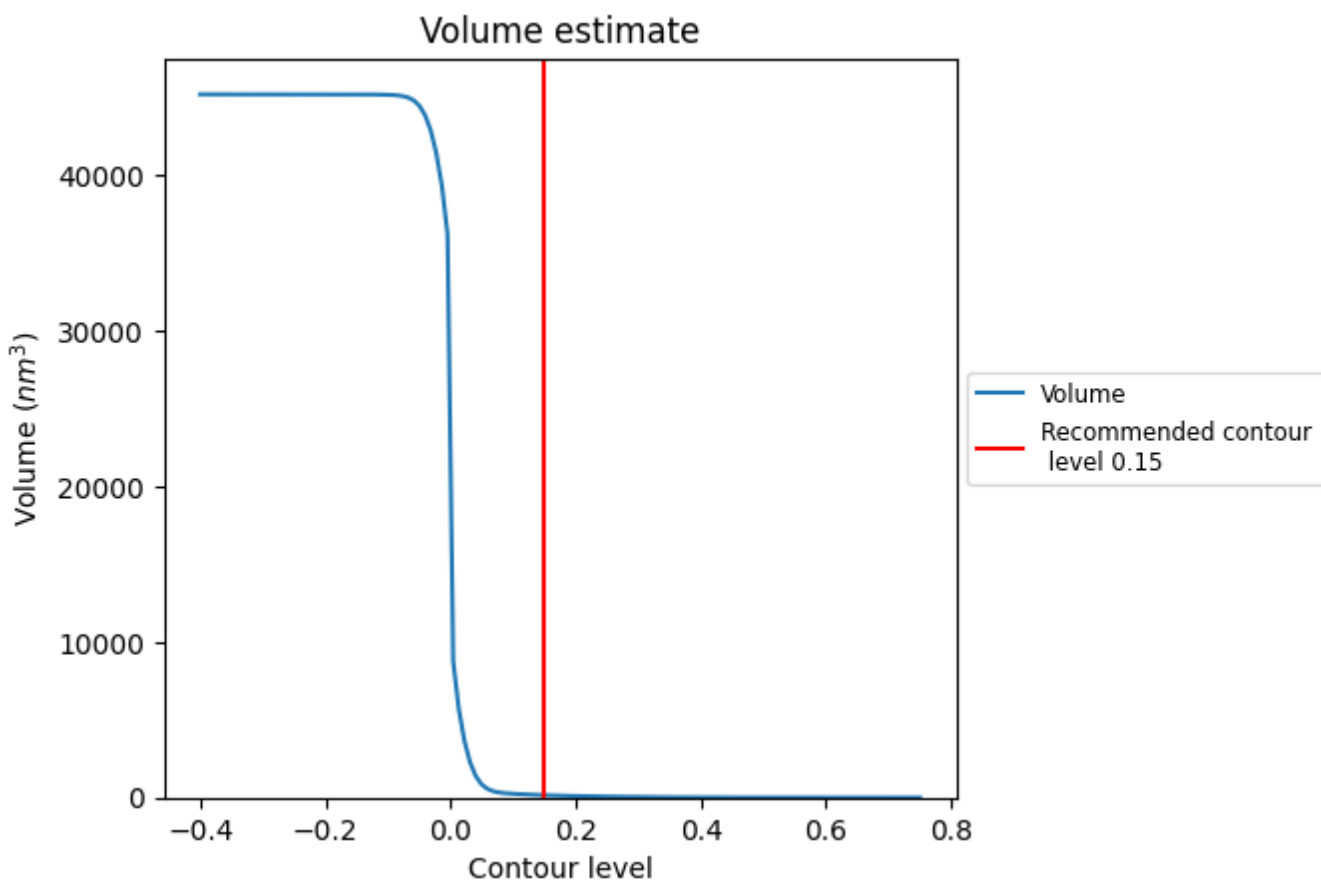
This section contains the results of statistical analysis of the map.

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.

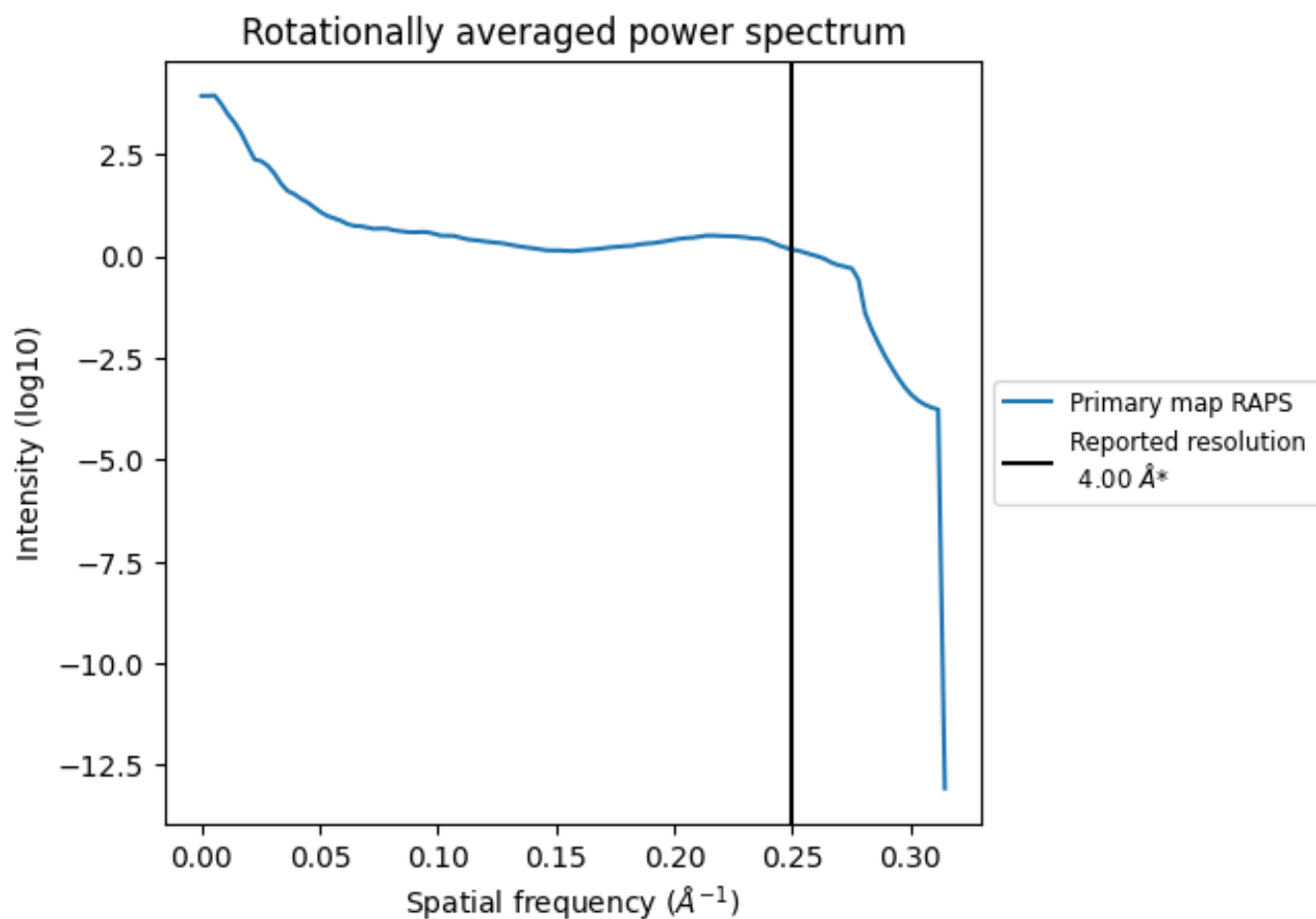
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 152 nm³; this corresponds to an approximate mass of 137 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 0.250 Å⁻¹

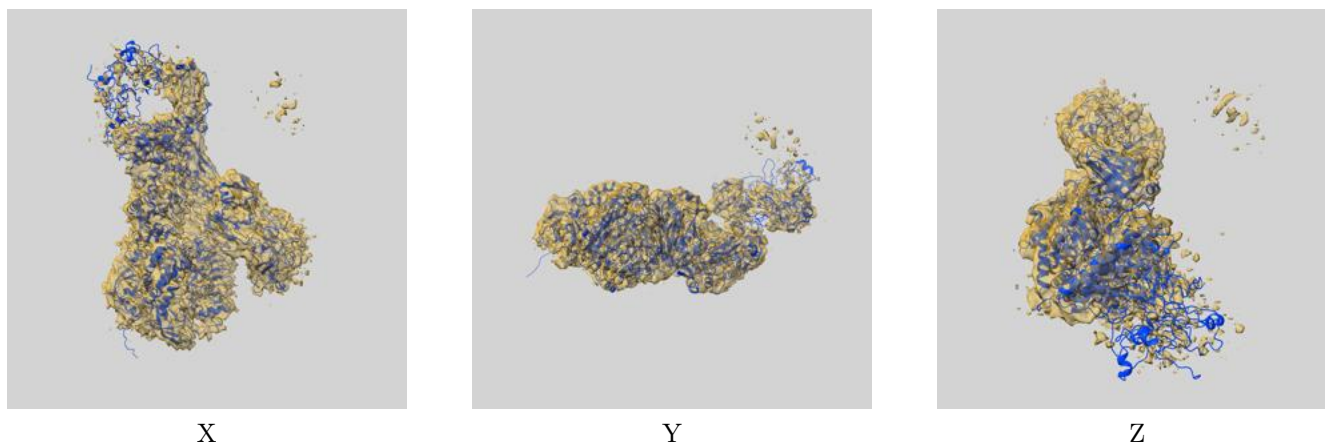
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

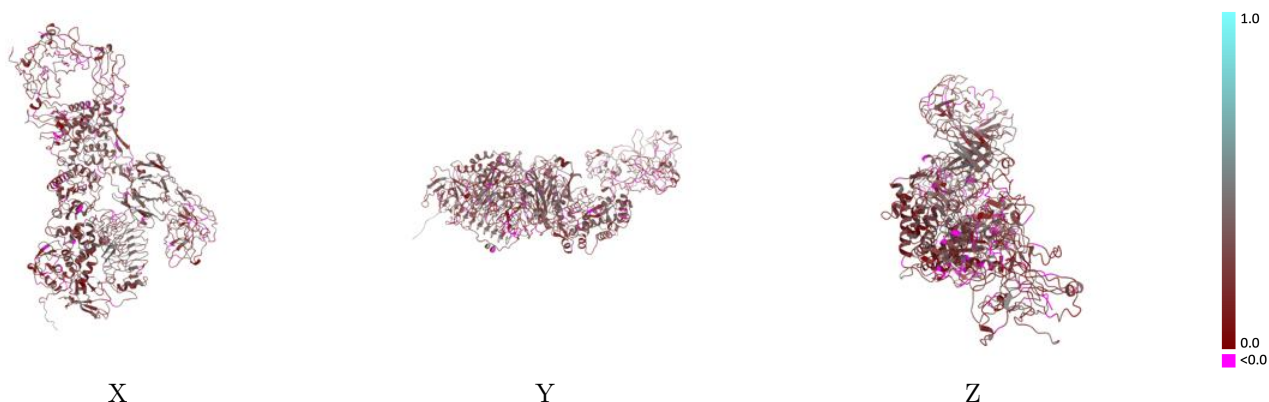
This section contains information regarding the fit between EMDB map EMD-22204 and PDB model 6XJA. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)



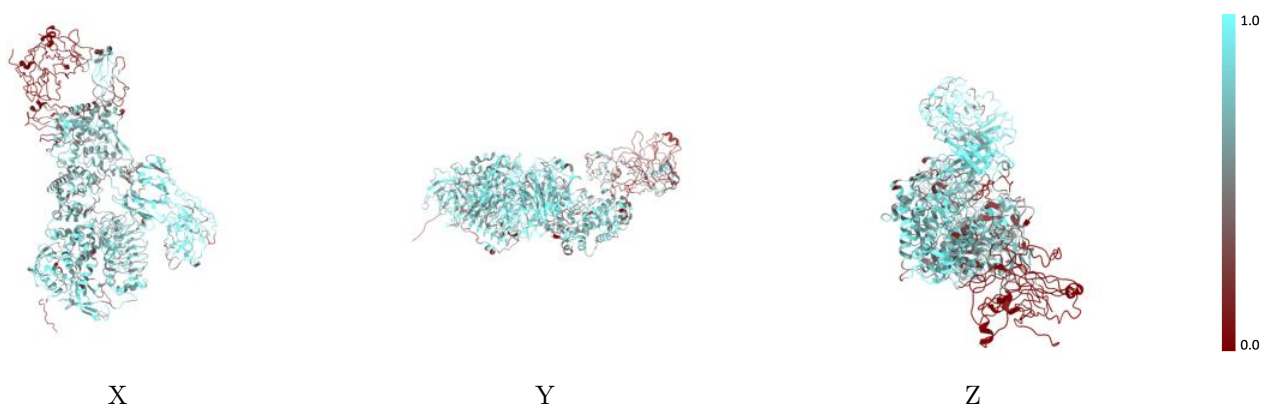
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



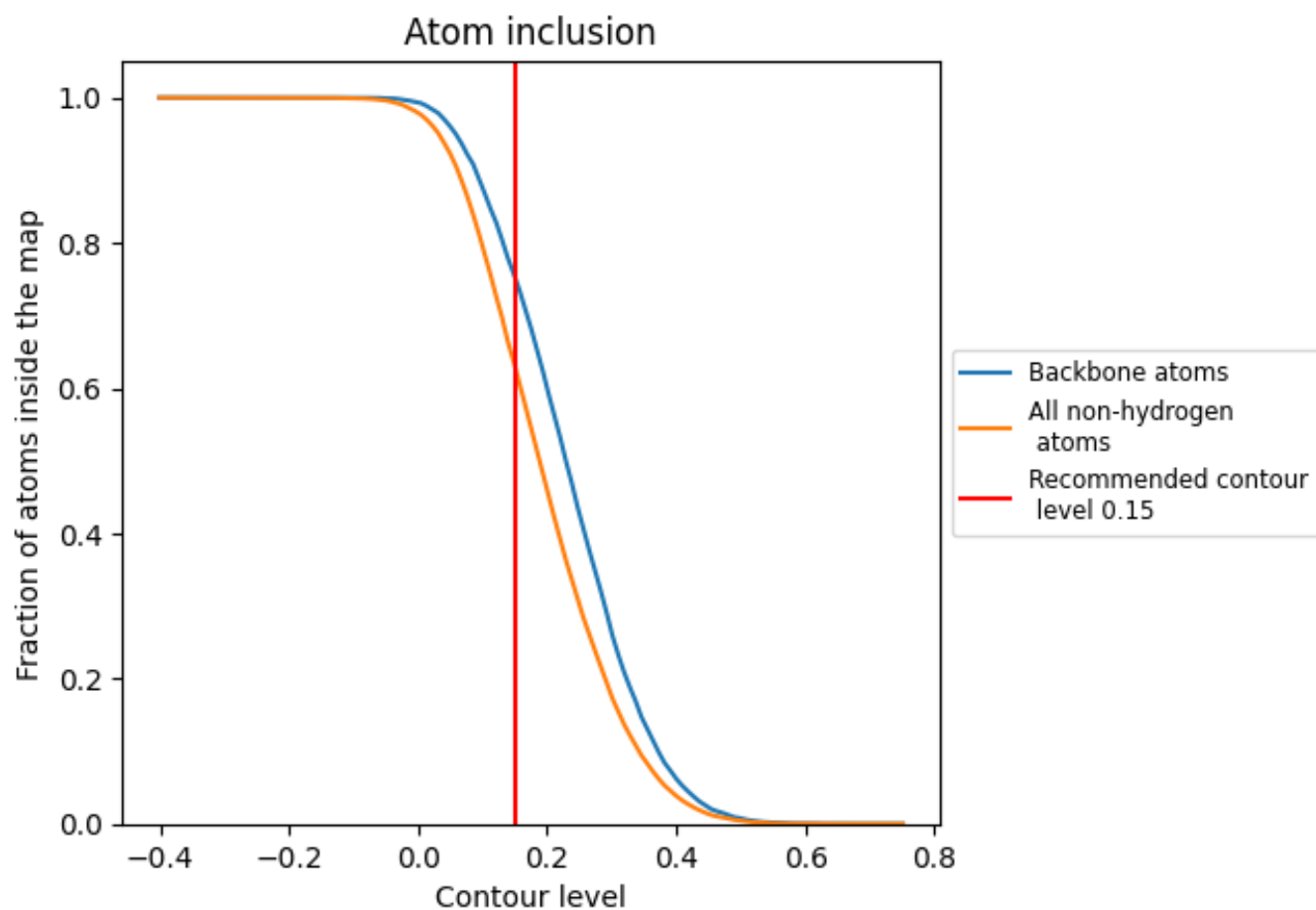
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).













9.4 Atom inclusion [i](#)



At the recommended contour level, 75% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6303	 0.2430
A	 0.2015	 0.2520
B	 0.2884	 0.1810
H	 0.8042	 0.2800
L	 0.8045	 0.2640
P	 0.6984	 0.2430

