



## wwPDB EM Validation Summary Report ⓘ

Jun 1, 2026 – 10:31 AM EDT

PDB ID : 12JP / pdb\_000012jp  
EMDB ID : EMD-76487  
Title : Structural determination of lipid-bound Factor VIII  
Authors : Mohammed, B.M.  
Deposited on : 2026-04-08  
Resolution : 3.46 Å(reported)  
Based on initial models : ., 3CDZ

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  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
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

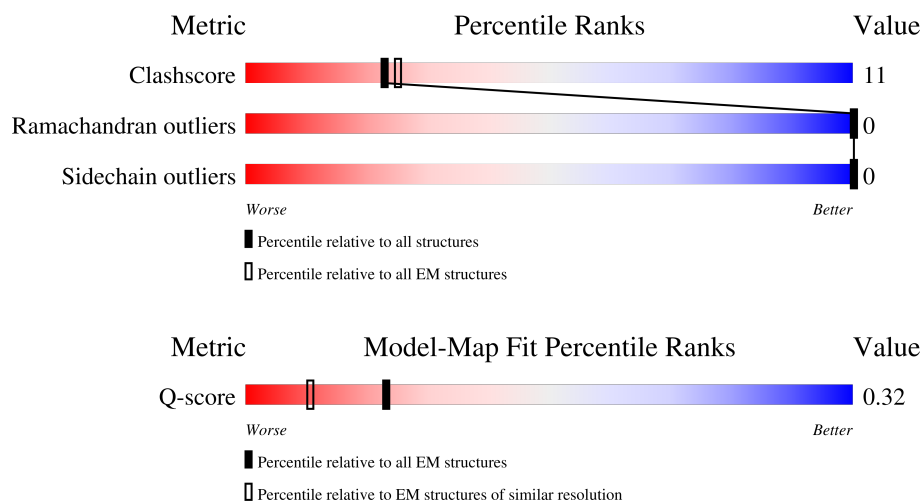
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.46 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	13788 ( 2.96 - 3.96 )

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	2332	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 10272 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 Coagulation factor VIII.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1263	10227	6572	1744	1854	57	0	0

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula:  $C_8H_{15}NO_6$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
2	A	1	14	8	1	5	0
2	A	1	14	8	1	5	0
2	A	1	14	8	1	5	0

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total 1	Ca 1	0

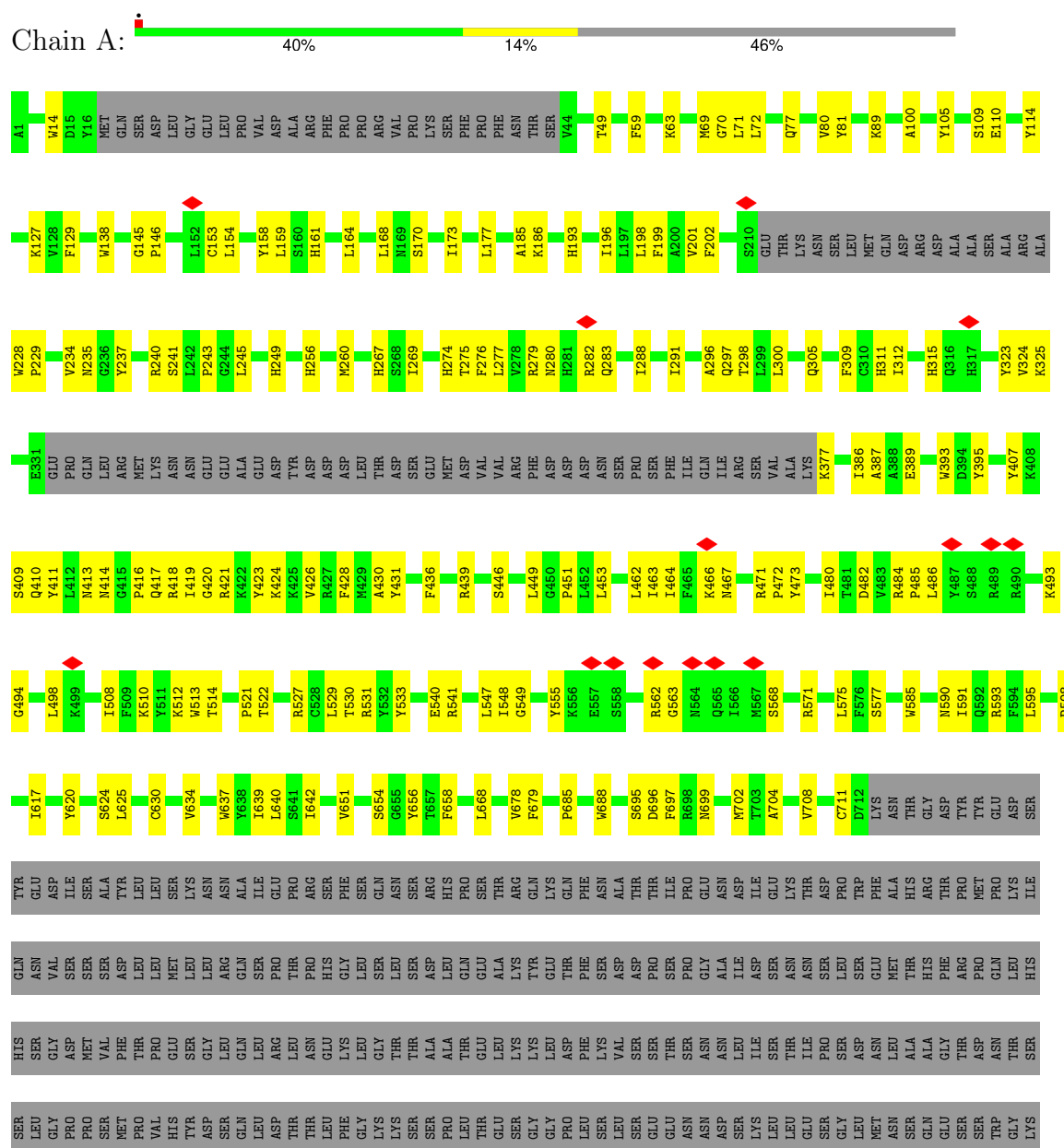
- Molecule 4 is COPPER (II) ION (CCD ID: CU) (formula: Cu) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	A	2	Total 2	Cu 2	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: Coagulation factor VIII



A2201	K2207	H2210	H2211	N2217	A2218	N2219	R2220	V2223	N2224	N2225	W2229	K2239	V2240	T2241	T2244	T2245	T2253	S2254	L2261	T2262	S2263	S2264	S2265	L2273	F2274	V2280	K2281	P2300	L2301	Y2305	Q2316	I2317	A2318	L2319	M2321	E2322	G2325	D2330	LEU	TYR					
K1813	T1814	Y1815	F1816	H1822	M1823	A1824	P1825	F1830	K1833	A1834	E1844	P1854	N1864	H1867	G1868	R1869	Q1870	Q1874	W1889	R1897	N1898	C1899	R1900	E1914	N1915	Y1916	R1917	F1918	I1921	T1925	M1926	L1929	Y1933	T1940	L1944	S1949	N1952	I1956	H1957						
V1962	V1965	R1966	K1972	L1975	L1978	F1983	E1984	T1985	V1986	G1994	T1995	W1996	R1997	L2001	H2005	L2006	M2010	F2014	L2015	W2016	Y2017	G2026	H2031	T2032	R2033	Q2036	S2040	G2041	Q2042	P2048	K2049	L2050	Y2055	W2070	L2071	K2072	V2073	D2074	L2075	L2076	A2077				
K2078	K2079	L2080	K2085	T2086	Q2087	G2088	Q2091	K2092	L2096	Y2097	L2098	L2102	W2112	Y2115	R2116	G2117	L2123	W2124	K2136	H2137	N2138	N2141	P2142	P2143	L2144	L2145	Y2148	T2149	L2150	L2151	H2152	R2159	L2162	R2163	K2164	E2165	G2179	H2180	A2184	S2183	T2197	N2198			
ASP	GLU	ASN	GLN	SER	PRO	ARG	SER	F1691	T1695	R1696	H1697	Y1698	F1699	W1707	R1719	M1720	R1721	A1722	Q1723	P1728	W1734	F1743	E1751	E1754	H1755	L1756	G1757	L1758	L1759	G1760	P1761	D1769	W1772	M1777	Y1783	S1787	S1788	L1789	I1790	R1797	Q1798	G1799	K1804		
GLU	VAL	THR	TRP	ALA	TRP	LYS	GLN	ARG	GLY	THR	ARG	LEU	CYS	SER	ASN	GLU	ASP	TRP	LYS	VAL	GLU	GLY	ALA	TYR	ARG	LEU	GLN	GLY	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE
LYS	ASP	LEU	PHE	ALA	TRP	GLU	ASN	HIS	THR	GLY	GLN	ILE	PRO	GLY	PRO	GLN	LYS	GLY	ALA	TYR	ARG	LEU	GLN	GLY	THR	ASP	ILE	ALA	VAL	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE
LEU	THR	ILE	GLN	GLY	LEU	LYS	ARG	ILE	VAL	VAL	GLY	ASP	THR	SER	THR	GLU	ASP	TRP	LYS	VAL	GLU	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
THR	LEU	ILE	GLN	GLY	LEU	LYS	ARG	ILE	VAL	VAL	GLY	ASP	THR	SER	THR	GLU	ASP	TRP	LYS	VAL	GLU	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
GLY	PRO	ILE	PRO	PRO	LYS	ALA	GLN	VAL	VAL	VAL	GLY	MET	GLY	LEU	LYS	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	TYR	ASP	ILE
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
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ASN	VAL	SER	SER	THR	GLU	THR	GLY	ARG	PHE	PHE	GLY	SER	GLY	LYS	ASP	THR	GLU	ASP	TRP	LYS	VAL	GLY	THR	ASP	ILE	ALA	VAL	THR	ASP	GLU	PRO	PHE	ASN	THR	ILE	SER	GLU	GLY	GLN	PHE	ILE	TYR	ASP	ILE	
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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	58291	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	55	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	150000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.681	Depositor
Minimum map value	-0.001	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.149	Depositor
Map size (Å)	386.04797, 386.04797, 386.04797	wwPDB
Map dimensions	416, 416, 416	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.9279999, 0.9279999, 0.9279999	Depositor

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, CU, CA

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	0.14	0/10517	0.37	0/14259

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	10227	0	9975	228	0
2	A	42	0	39	0	0
3	A	1	0	0	0	0
4	A	2	0	0	0	0
All	All	10272	0	10014	228	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 11.

The worst 5 of 228 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:484:ARG:O	1:A:512:LYS:HB3	1.62	0.99
1:A:1797:ARG:HG3	1:A:1798:GLN:H	1.37	0.87
1:A:277:LEU:HD12	1:A:282:ARG:HE	1.40	0.84
1:A:2070:TRP:HA	1:A:2151:LEU:O	1.80	0.80
1:A:1864:ASN:H	1:A:1869:ARG:H	1.29	0.80

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	1253/2332 (54%)	1167 (93%)	86 (7%)	0	100	100

There are no Ramachandran outliers to report.

### 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	1122/2093 (54%)	1122 (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 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	618	ASN
1	A	1770	ASN
1	A	2031	HIS
1	A	1820	GLN
1	A	1954	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 oligosaccharides in this entry.

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

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	NAG	A	2402	1	14,14,15	0.74	0	17,19,21	0.96	0
2	NAG	A	2401	1	14,14,15	0.72	0	17,19,21	0.87	1 (5%)
2	NAG	A	2403	1	14,14,15	0.75	0	17,19,21	0.84	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	2402	1	-	2/6/23/26	0/1/1/1
2	NAG	A	2401	1	-	0/6/23/26	0/1/1/1
2	NAG	A	2403	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2401	NAG	C1-O5-C5	2.08	114.98	112.19

There are no chirality outliers.

All (4) torsion outliers are listed below:

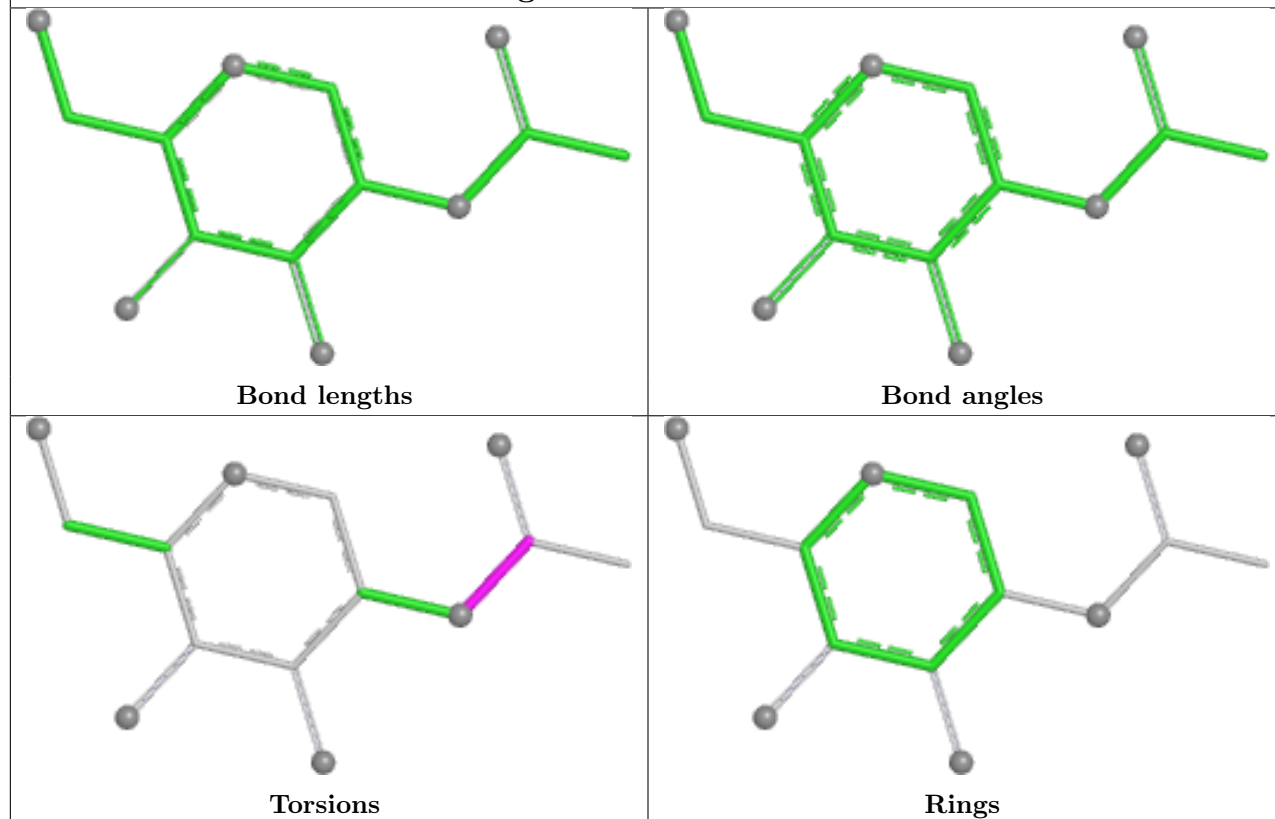
Mol	Chain	Res	Type	Atoms
2	A	2402	NAG	C8-C7-N2-C2
2	A	2402	NAG	O7-C7-N2-C2
2	A	2403	NAG	O5-C5-C6-O6
2	A	2403	NAG	C4-C5-C6-O6

There are no ring outliers.

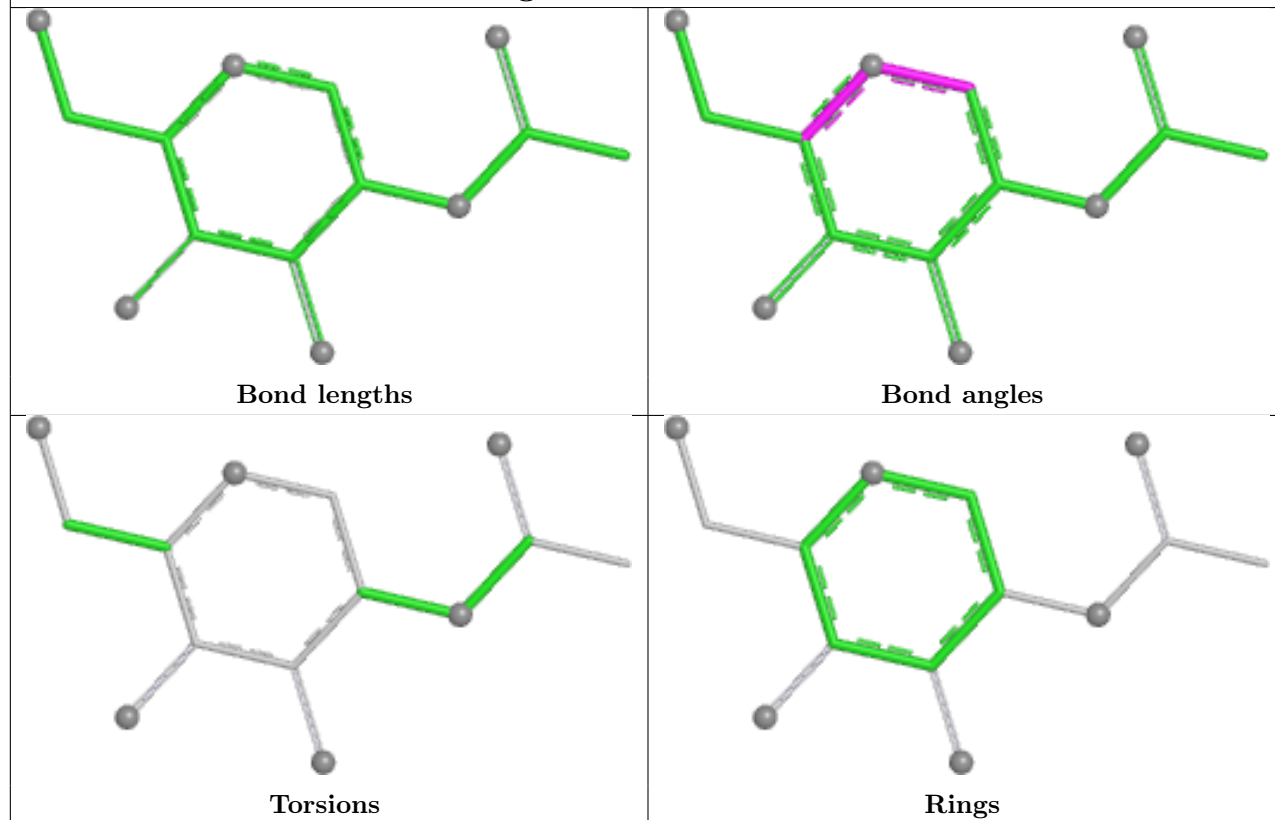
No monomer is involved in short contacts.

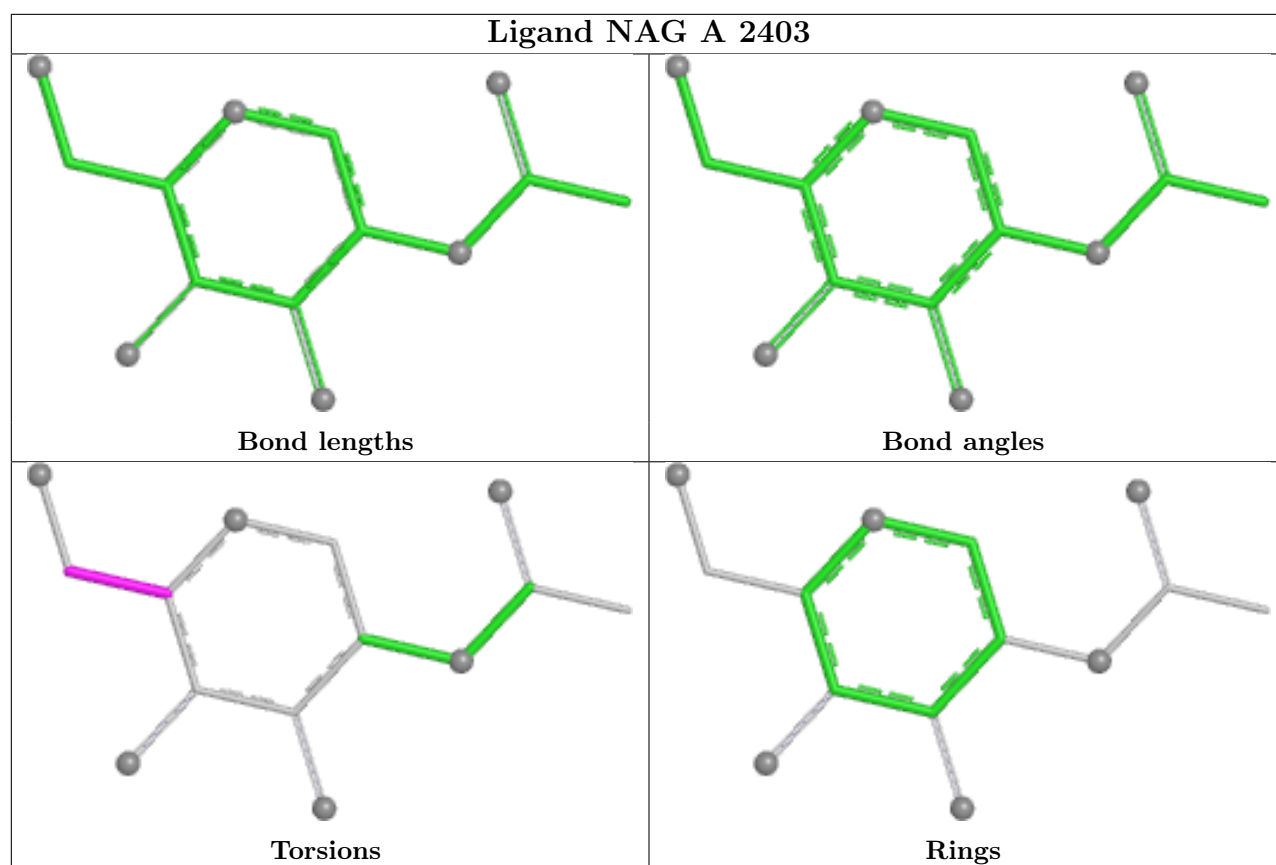
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

## Ligand NAG A 2402



## Ligand NAG A 2401





## 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.

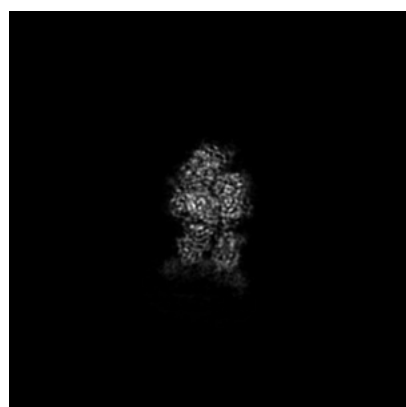
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-76487. These allow visual inspection of the internal detail of the map and identification of artifacts.

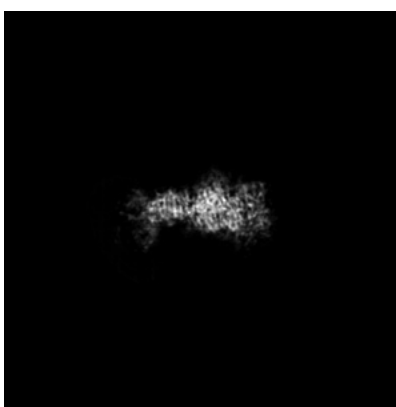
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

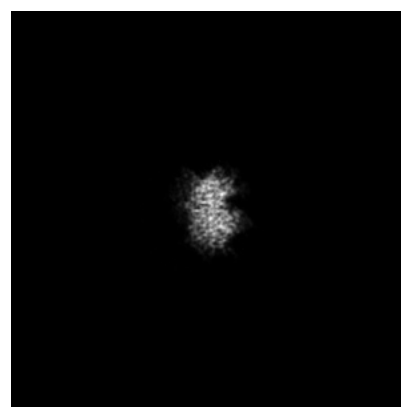
#### 6.1.1 Primary map



X



Y



Z

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

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

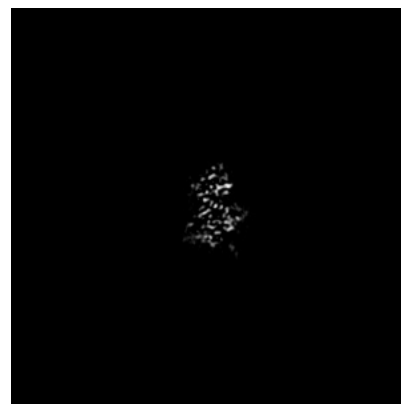
#### 6.2.1 Primary map



X Index: 208



Y Index: 208



Z Index: 208

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

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

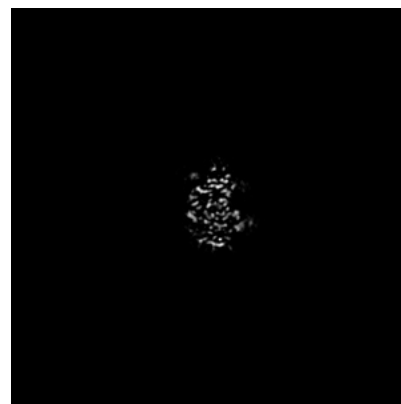
### 6.3.1 Primary map



X Index: 209



Y Index: 192

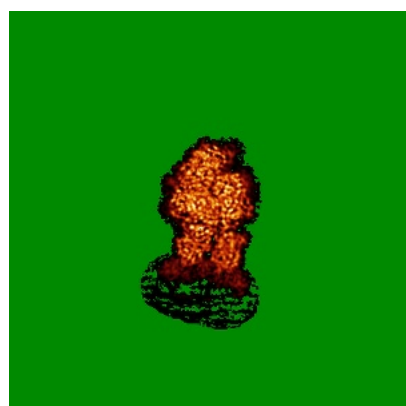


Z Index: 218

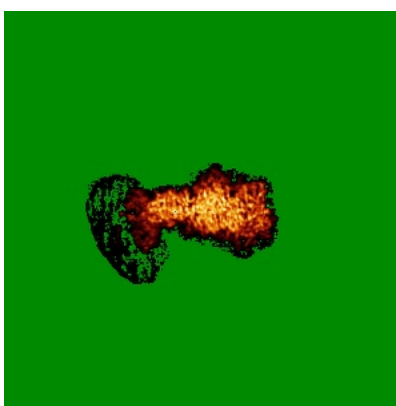
The images above show the largest variance slices of the map in three orthogonal directions.

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

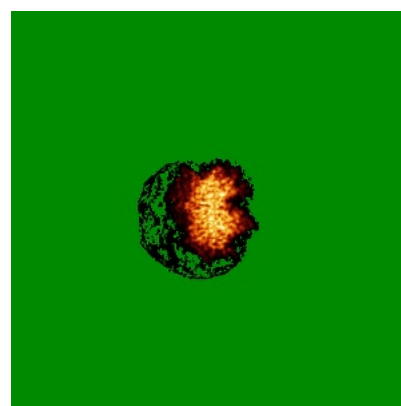
### 6.4.1 Primary map



X



Y

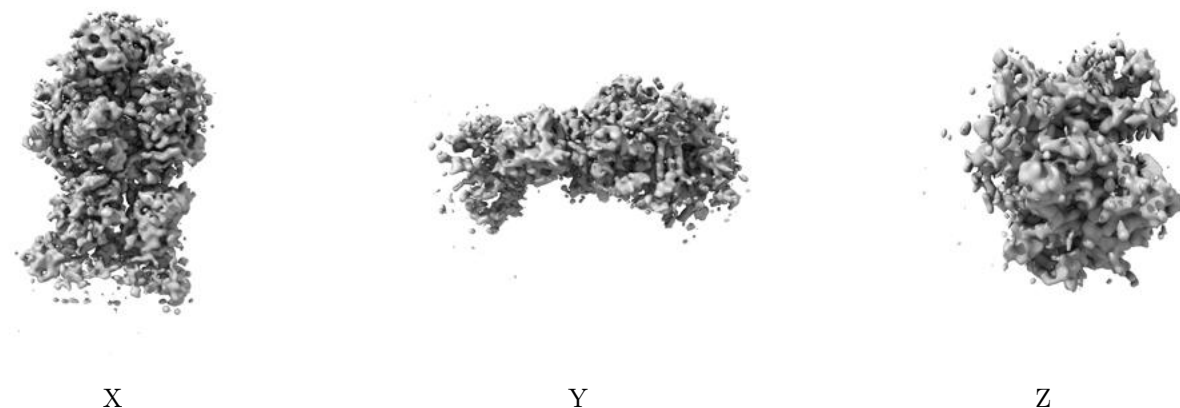


Z

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 0.149. 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](#)

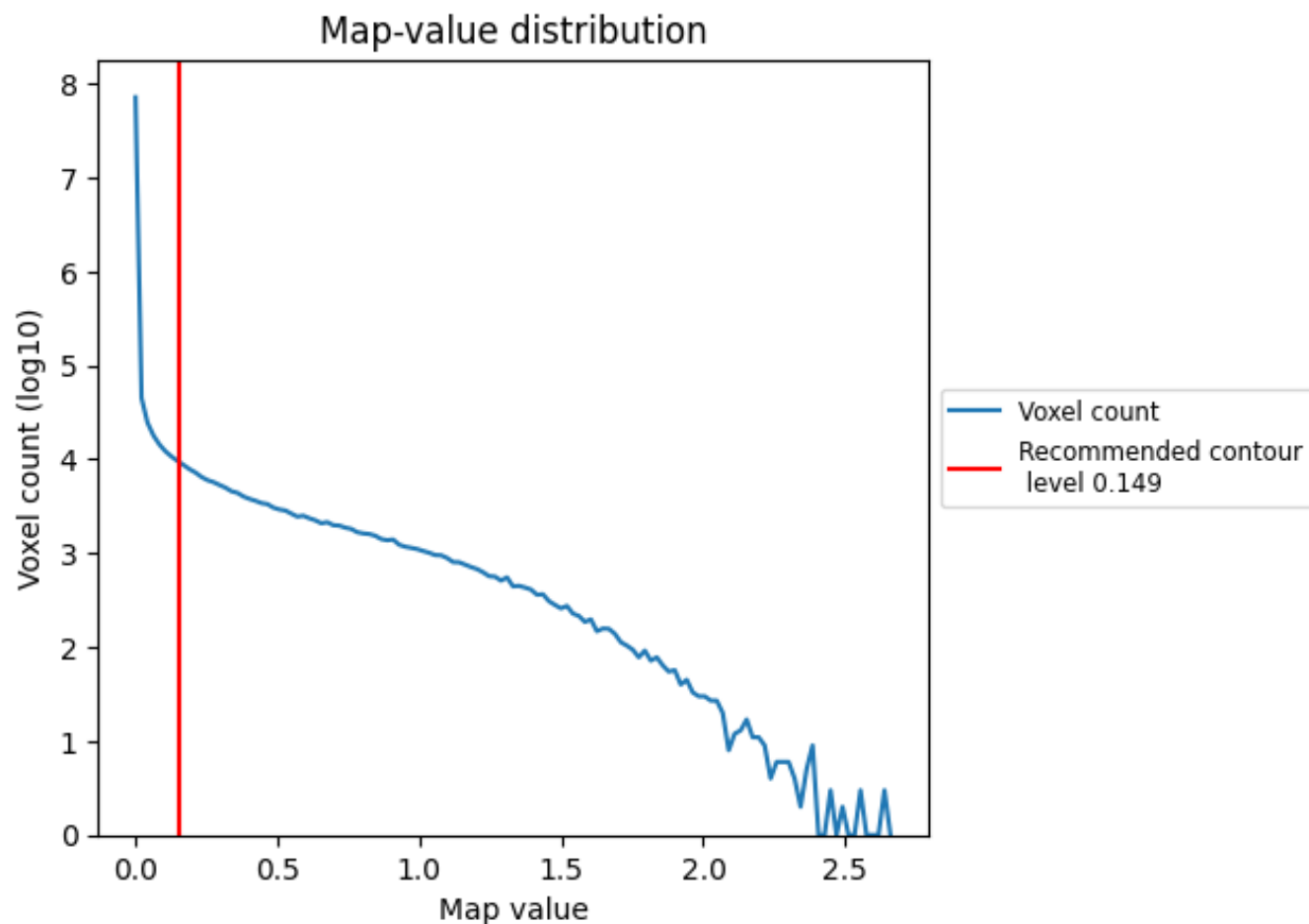
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis ⓘ

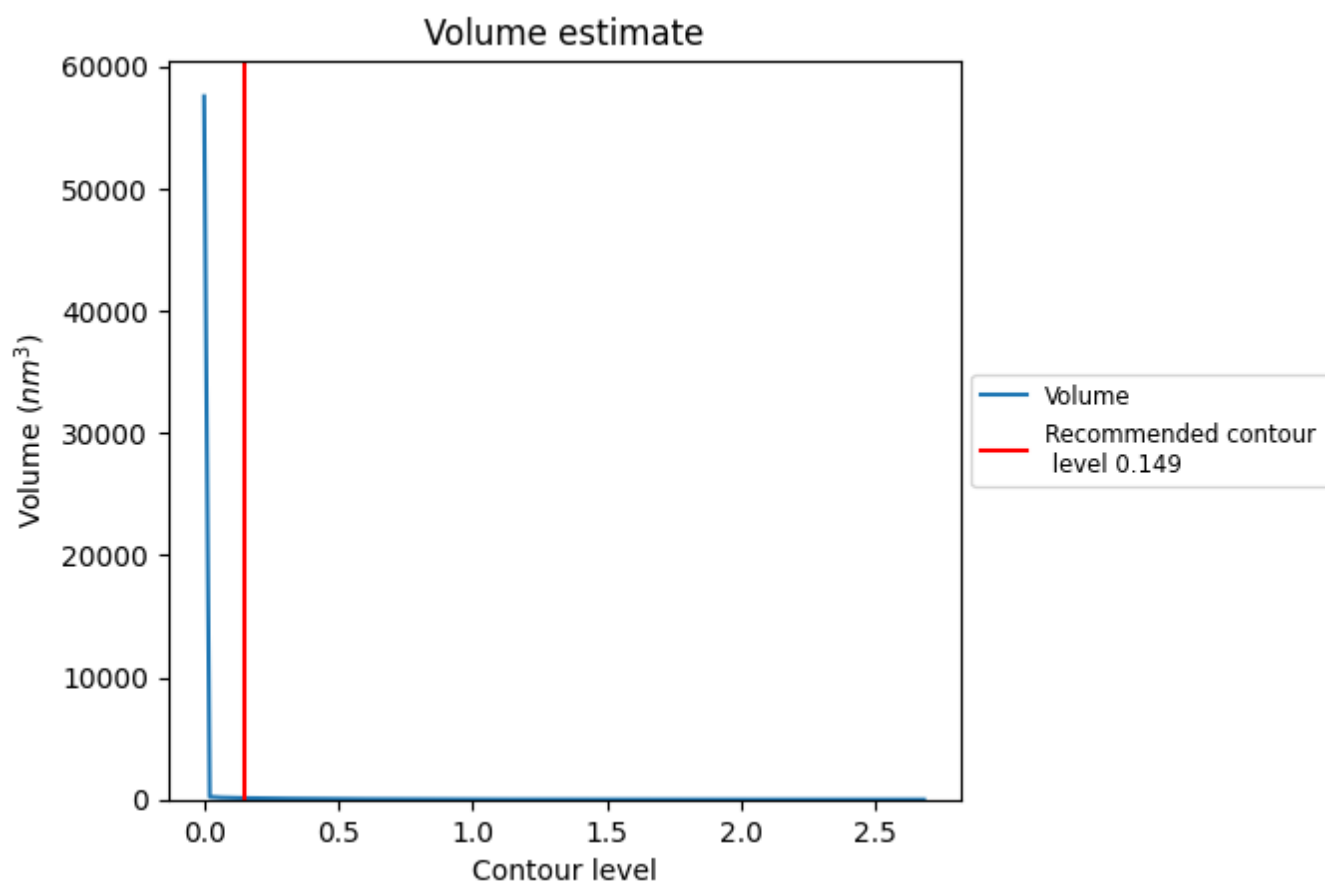
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution ⓘ



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.

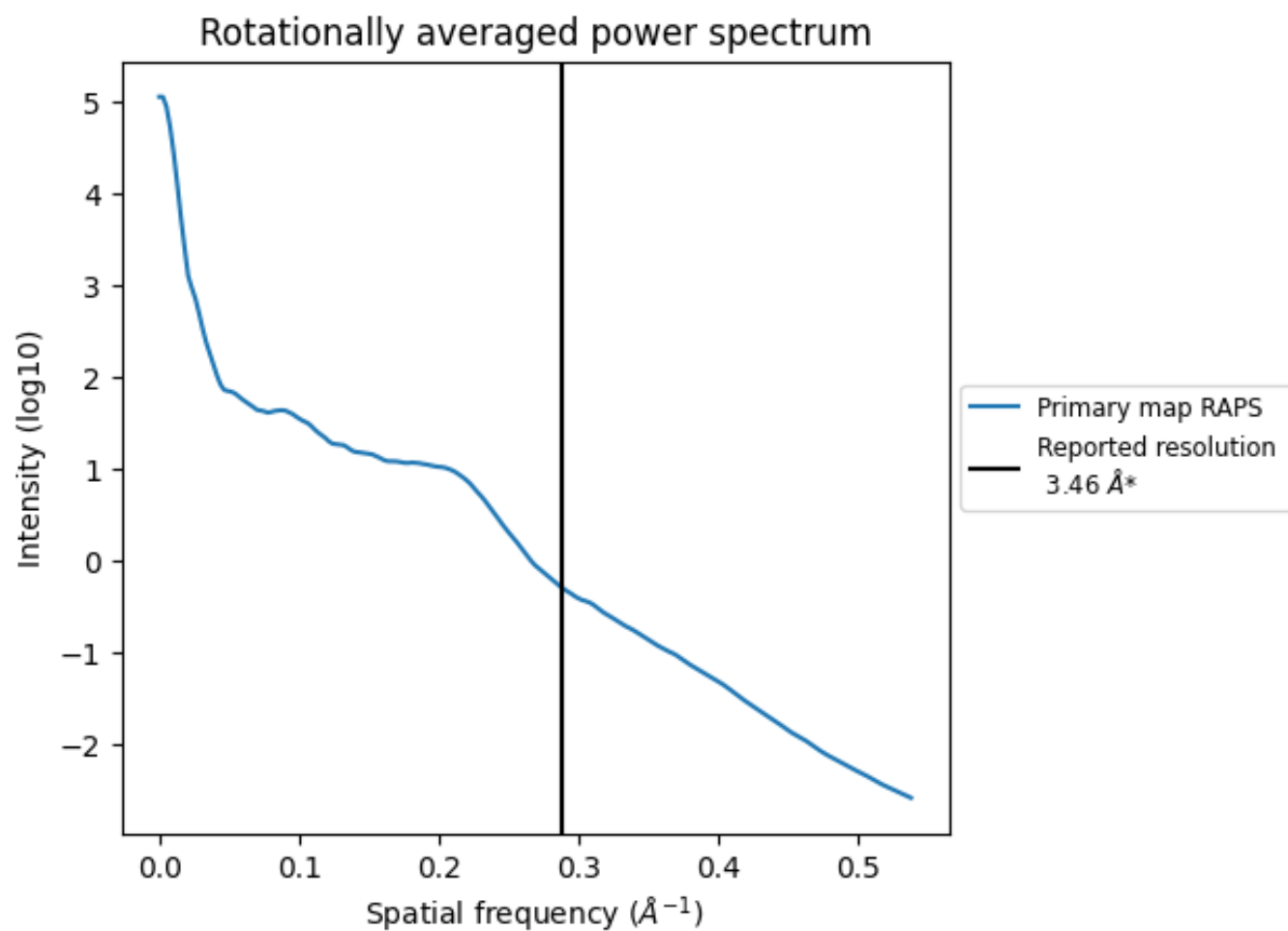
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 123 nm<sup>3</sup>; this corresponds to an approximate mass of 111 kDa.

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

### 7.3 Rotationally averaged power spectrum ⓘ



\*Reported resolution corresponds to spatial frequency of 0.289 Å<sup>-1</sup>

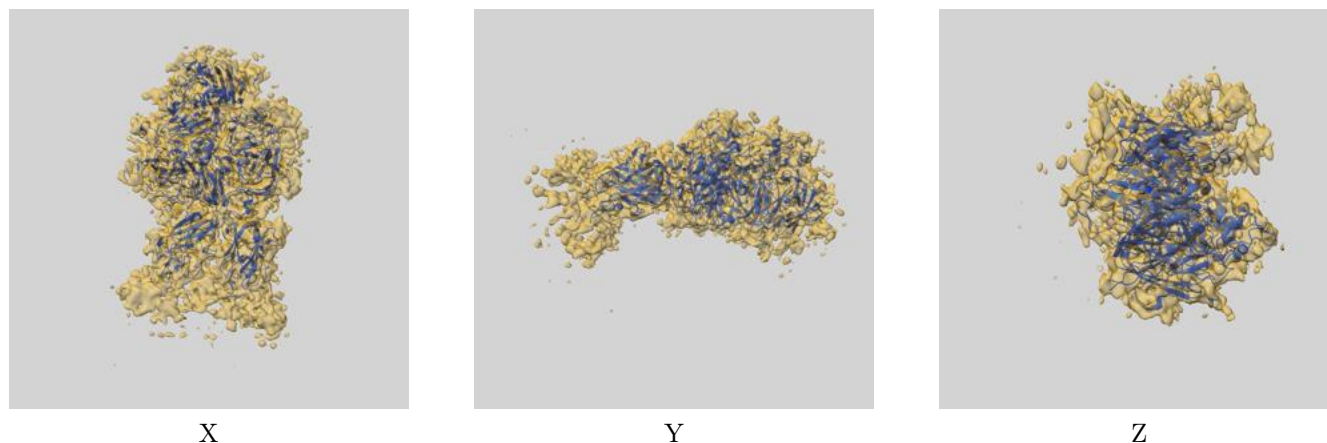
## 8 Fourier-Shell correlation

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

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

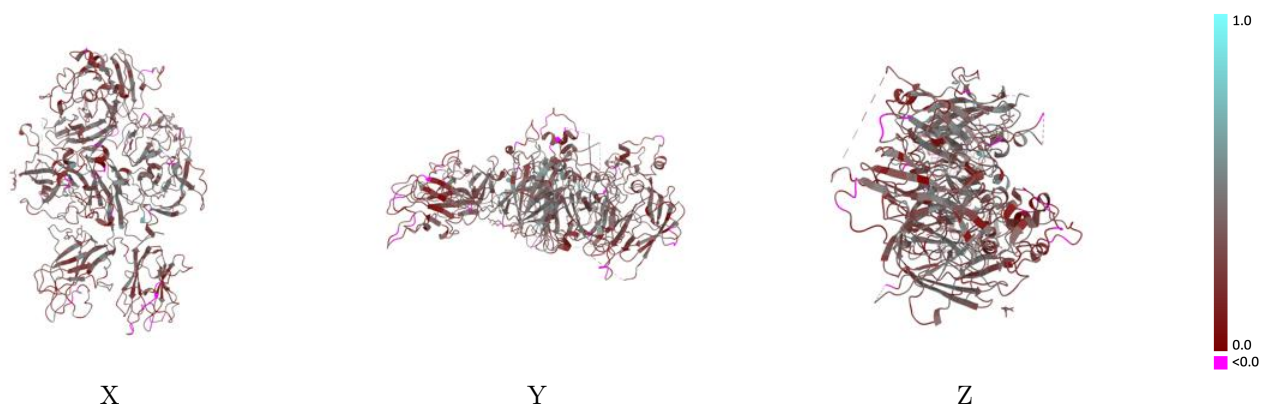
This section contains information regarding the fit between EMDB map EMD-76487 and PDB model 12JP. Per-residue inclusion information can be found in section [3](#) on page [5](#).

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



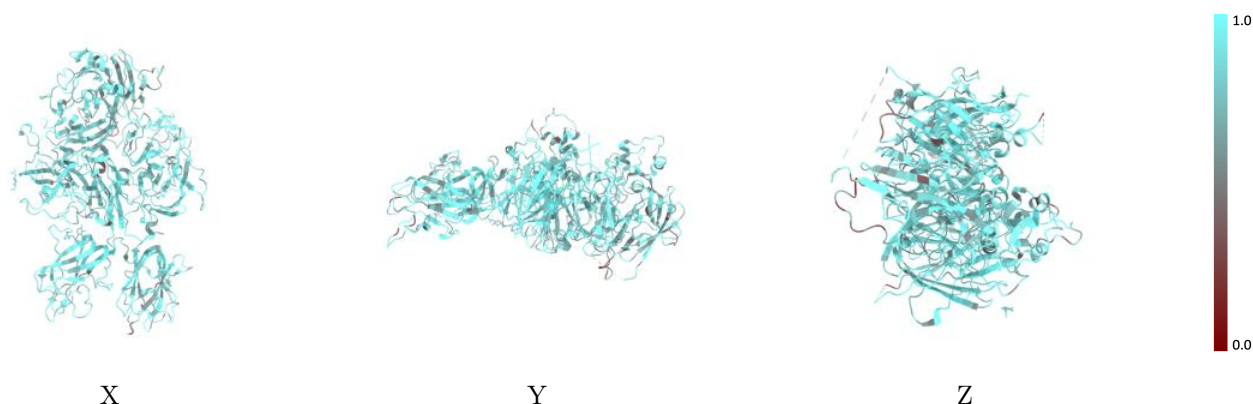
The images above show the 3D surface view of the map at the recommended contour level 0.149 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



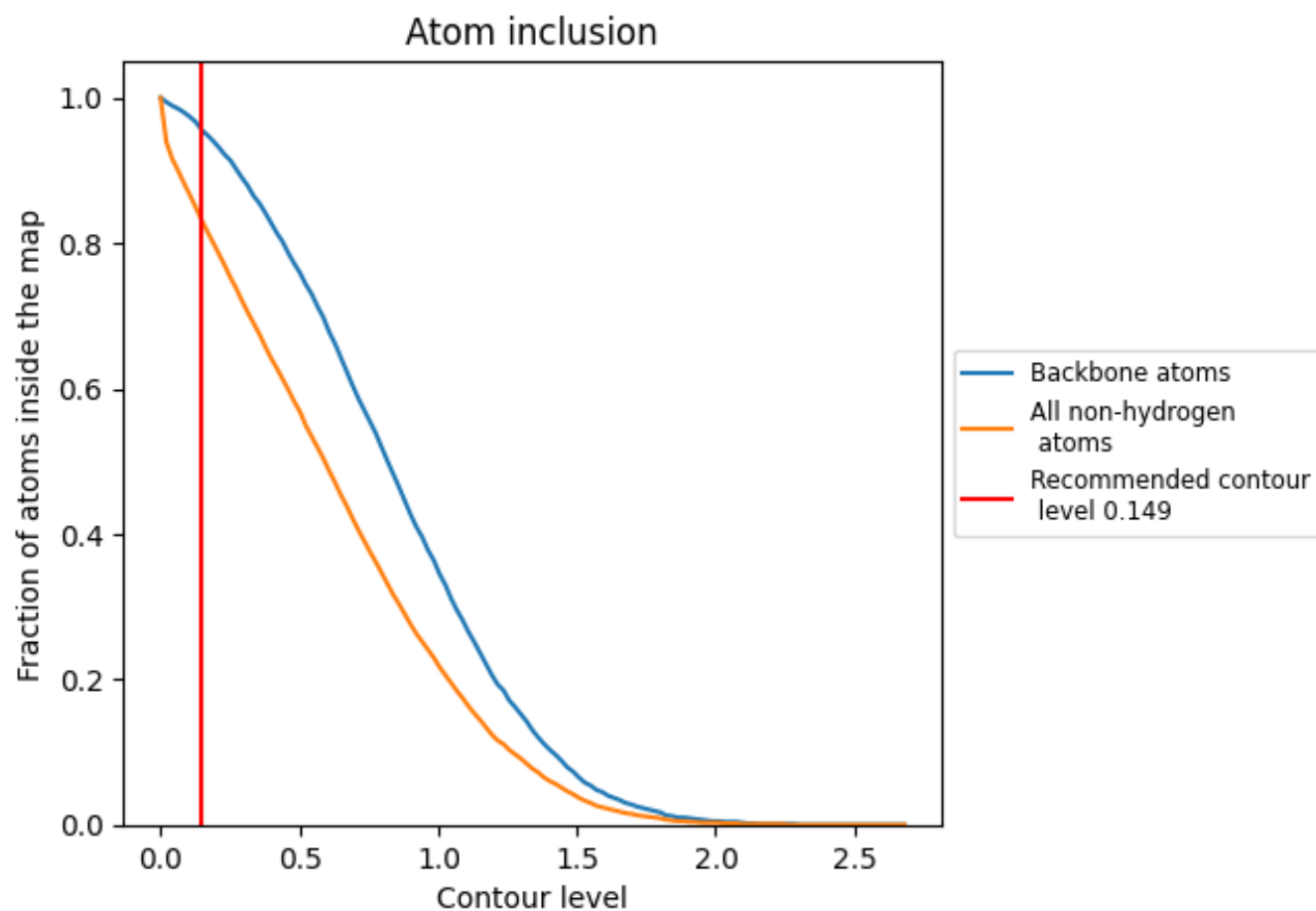
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.149).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 83% 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 (0.149) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8300	<div><div></div></div> 0.3200
A	<div><div></div></div> 0.8300	<div><div></div></div> 0.3200

