



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:02 AM UTC

PDB ID : 7JGF / pdb_00007jgf
EMDB ID : EMD-22325
Title : Cryo-EM structure of P. falciparum VAR2CSA FCR3 domains DBL5 and DBL6 at 4.69 Å
Authors : Ma, R.; Tolia, N.H.
Deposited on : 2020-07-19
Resolution : 4.69 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

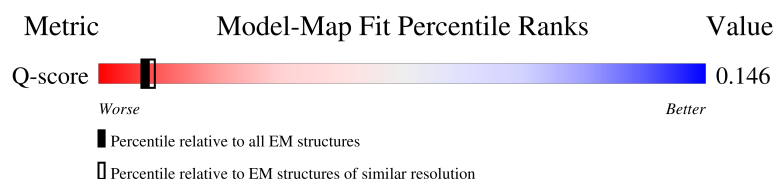
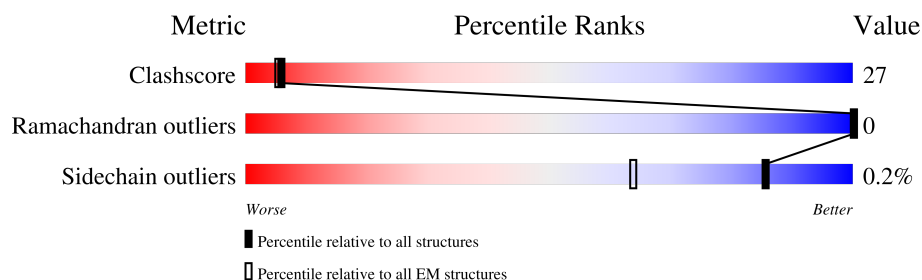
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.69 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	1970 (4.19 - 5.19)

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	2660	12% 10% 10% 80%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4477 atoms, of which 30 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 Erythrocyte membrane protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	532	4477	2808	30	770	839	30	4	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	THR	-	expression tag	UNP Q6UDW7
A	0	GLY	-	expression tag	UNP Q6UDW7
A	2650	GLY	-	expression tag	UNP Q6UDW7
A	2651	THR	-	expression tag	UNP Q6UDW7
A	2652	LYS	-	expression tag	UNP Q6UDW7
A	2653	HIS	-	expression tag	UNP Q6UDW7
A	2654	HIS	-	expression tag	UNP Q6UDW7
A	2655	HIS	-	expression tag	UNP Q6UDW7
A	2656	HIS	-	expression tag	UNP Q6UDW7
A	2657	HIS	-	expression tag	UNP Q6UDW7
A	2658	HIS	-	expression tag	UNP Q6UDW7



HIS	S2543	R2481	A2421	I2360	F2298	R2236	S2169	D2105	I2039
ILE	K2544	E2482	M2422	S2361	K2299	K2237	W2170	I2106	P2040
ASP	C2545	A2483	K2423	N2362	Q2300	R2238	C2171	I2107	P2041
LYS	T2546	E2484	Y2424	G2363	I2301	S2239	I2172	K2108	R2042
ASN	H2547	G2485	S2425	V2364	K2302	I2240	D2111		R2043
LYS	A2548	D2486	F2426	L2365	E2303	R2241	M2112		R2044
THR	C2549	T2487	T2427	I2366	Q2304	W2242	L2113		Q2045
LYS	V2550	E2488	D2428	F2367	V2305	E2243	T2114		L2046
ASN	N2551	T2489	I2429	R2368	K2306	E2244	N2115		G2047
PRO	Y2552	N2490	G2430	R2369	I2307	I2245	I2116		F2048
THR	K2553	E2491	I2432	R2370	E2310	S2246	E2117		S2049
LEU	Y2555	N2492	I2433	K2371	L2311	K2247	R2184		R2050
GLU	L2556	C2493	K2434	W2372	E2312	R2248	F2185		I2051
ASP	L2557	R2494	G2435	F2374	ASP	Y2249	K2187		
THR	T2558	F2495	D2436	L2373	VAL	K2250	I2186		P2055
PHE	K2559	P2496	D2437	L2375	ILE	K2251	K2187		A2056
LYS	K2560	D2497	M2438		TYR	Y2252	I2187		A2057
SER	T2561	I2498	E2439	D2378	ARG	W2253	E2188		
LYS	E2562	E2499	E2440	P2379	ILE	K2254	W2189		
CYS	Y2563	S2500	M2441	S2380	LYS	W2255	I2191		
ASP	E2564	V2501	N2442	K2381	HIS	D2256	N2192		L2061
CYS	T2565	P2502	S2443	I2382	GLU	I2257	C2194		N2062
PRO	Q2566	Q2503	S2444	C2383	TYR	L2258	I2195		E2063
LYS	T2567	F2504	D2445	E2384	ASP	K2259	Q2196		F2064
LEU	N2568	L2505	K2446	Y2385	LYS	D2260	K2197		E2066
PRO	K2569	R2506	I2447	K2386	GLY	W2261	Q2198		E2067
SER	Y2570	W2507	G2448	K2387	N2327	K2262	Q2199		I2068
PRO	D2571	F2508	K2449	D2388	D2328	E2263	E2200		L2069
ILE	N2572	E2509	I2450	P2389	ASP	PRO	K2201		K2070
LYS	E2573	E2510	L2451	K2390	N2331	ALA	E2202		G2071
ASP	F2574	W2511	G2452	L2391	N2332	THR	Y2203		A2072
LEU	K2575	S2512	D2453	K2393	K2333	TYR	V2204		Q2073
PRO	E2576	E2513	T2454	F2394	K2335	LEU	K2205		S2074
PRO	N2577	N2514	D2455	F2395	N2336	ARG	S2206		K2077
ALA	N2578	F2515	G2456	T2396	I2337	GLU	K2207		F2078
ASP	S2579	C2516	Q2457	T2397	H2338	HIS	C2208		L2079
GLU	N2580	D2517	K2458	W2398	D2339	CYS	S2209		Q2080
PRO	D2581	R2518	E2459	S2399	ARG	SER	N2210		N2081
GLY	K2582	R2519	K2460	A2400	MET	LYS	N2211		Y2082
THR	D2583	Q2520	K2461	F2401	LYS	CYS	T2212		Y2083
LYS	A2584	L2522	K2462	E2402	ASN	PRO	T2213		K2084
HIS	P2585	Y2523	K2463	E2403	ASN	CYS	N2214		E2085
HIS	D2586	D2524	W2464	E2404	GLY	GLY	L2214		H2086
HIS	Y2587	K2525	W2465	E2405	ASN	PHE	Q2215		K2087
HIS	L2588	L2526	D2466	R2406	ASP	ASP	A2216		W2088
HIS	K2589	N2527	M2467	L2407	PHE	MET	Q2217		K2089
	E2590	S2528	N2468	K2408	V2349	GLU	A2218		E2090
	K2591	E2529	K2469	K2409	T2350	GLU	S2219		K2091
	C2592	G2530	Y2470	A2410	D2351	MET	A2092		A2092
	N2593	I2531	H2471	Y2411	N2352	ASN	L2093		L2093
	D2594	W2473	I2472	G2412	F2353	ASN	E2094		E2094
	N2595	E2474	E2473	G2413	K2356	ASN	A2095		A2095
	K2596	S2475	N2476	A2414	S2357		K2160		W2096
	C2597	N2476	M2476	A2415	W2358		N2163		F2100
	E2598	L2477	K2477	A2416	E2359		K2164		Y2101
	C2599	C2478	G2479	A2417			I2165		D2102
	L2600	Y2480		V2418			I2166		Y2103
	N2601			V2419			D2167		E2104
	K2602			H2420			P2168		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	271442	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 ($e^-/\text{\AA}^2$)	71.2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	49.984	Depositor
Minimum map value	-20.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	6.73	Depositor
Map size ($\text{\AA}$)	270.848, 270.848, 270.848	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.058, 1.058, 1.058	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	0.13	0/4564	0.38	0/6120

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	4447	30	4371	236	0
All	All	4447	30	4371	236	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 27.

The worst 5 of 236 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:2072:ALA:HB1	1:A:2150:ILE:HD12	1.41	1.01
1:A:2464:TRP:HA	1:A:2467:MET:HE2	1.47	0.94
1:A:2373:LEU:HD22	1:A:2432:ILE:HD13	1.51	0.92
1:A:2165:ILE:HG13	1:A:2173:ILE:HG22	1.49	0.92
1:A:2502:PRO:HD2	1:A:2505:LEU:HD22	1.53	0.91

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	529/2660 (20%)	505 (96%)	24 (4%)	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	493/2412 (20%)	491 (100%)	2 (0%)	84	83

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2518[A]	ARG
1	A	2518[B]	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2135	ASN
1	A	2232	GLN
1	A	2503	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2520	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

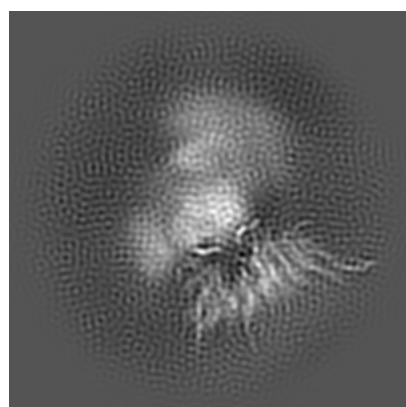
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22325. These allow visual inspection of the internal detail of the map and identification of artifacts.

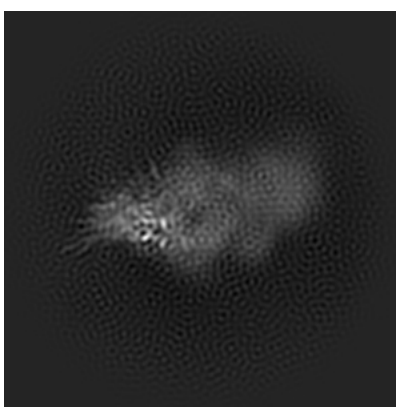
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

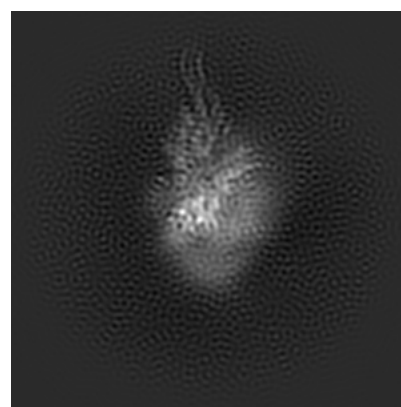
6.1.1 Primary map



X



Y

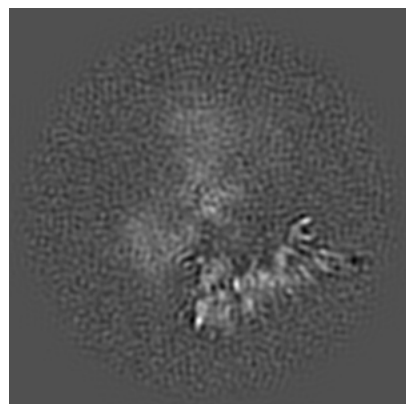


Z

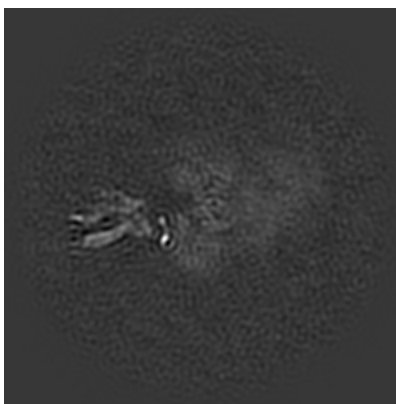
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

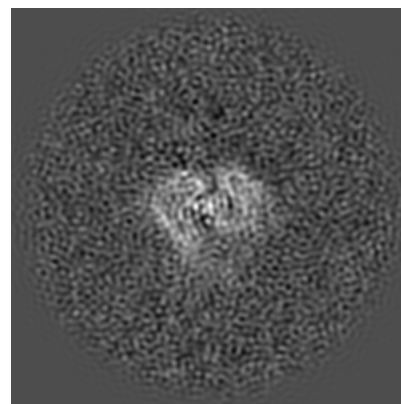
6.2.1 Primary map



X Index: 128



Y Index: 128

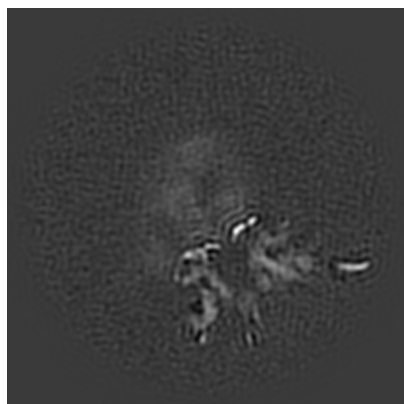


Z Index: 128

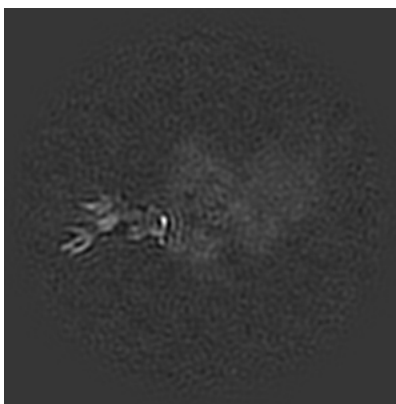
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

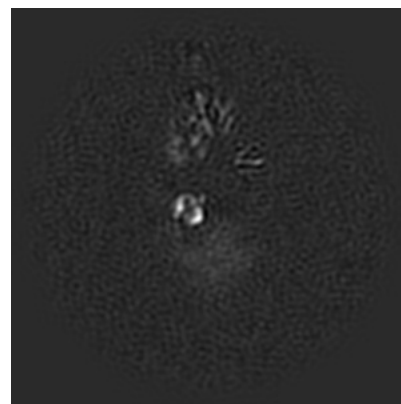
6.3.1 Primary map



X Index: 110



Y Index: 121

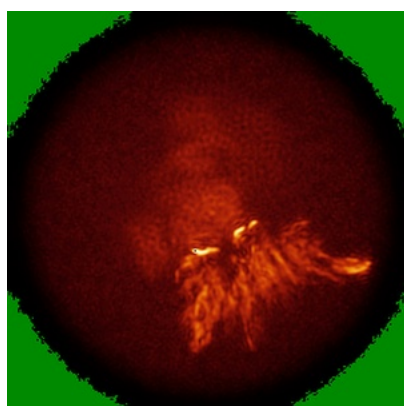


Z Index: 102

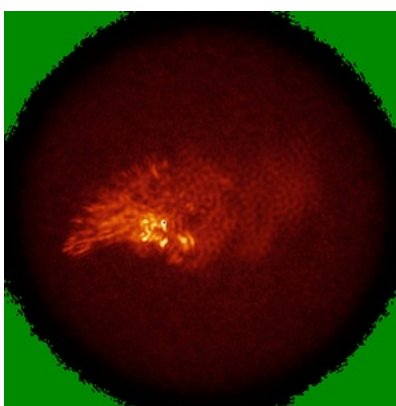
The images above show the largest variance slices of the map in three orthogonal directions.

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

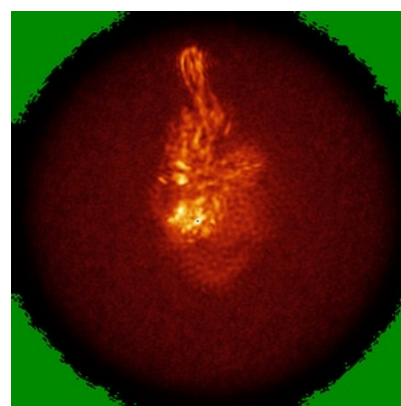
6.4.1 Primary map



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

This section was not generated.

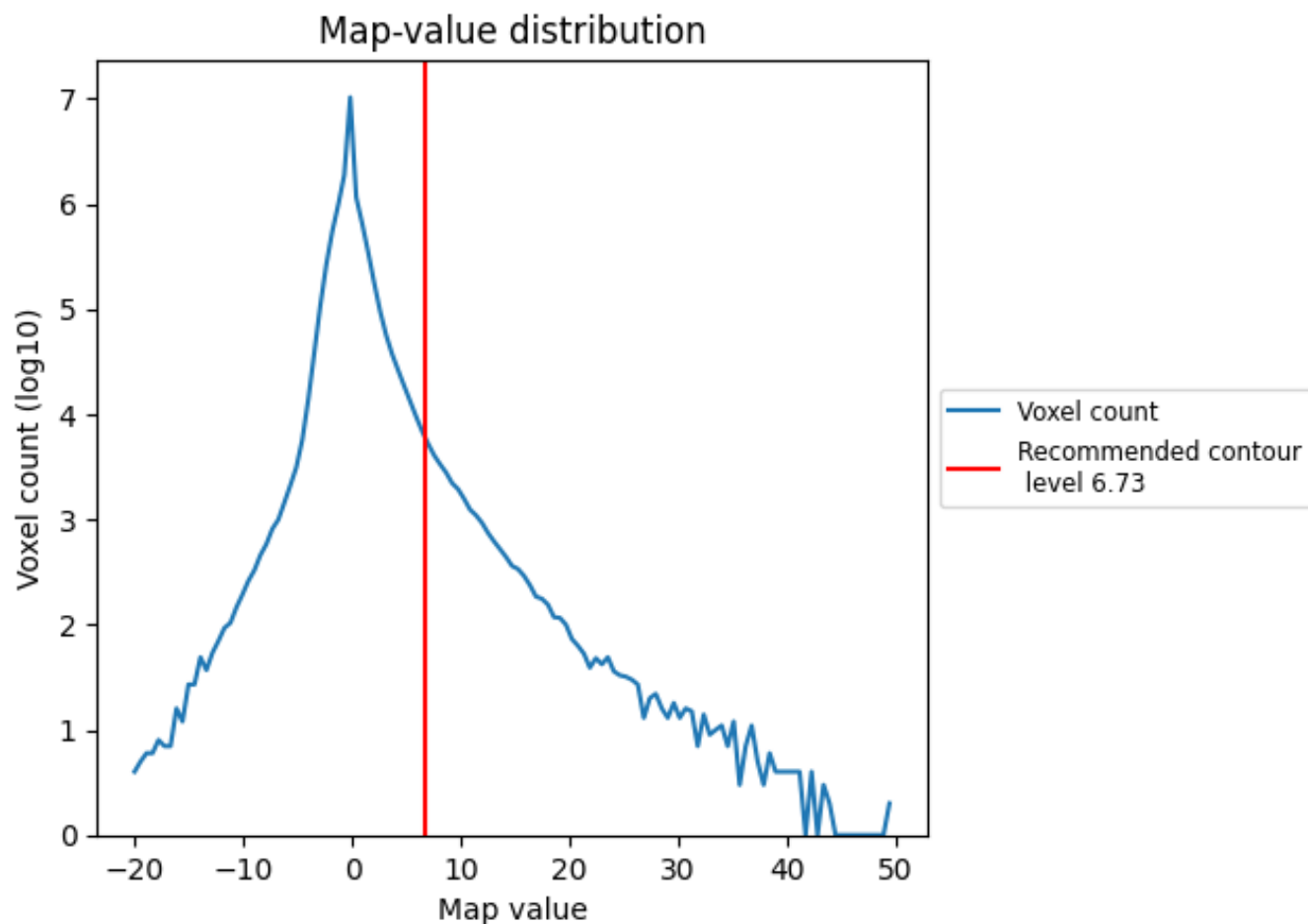
6.6 Mask visualisation

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

7 Map analysis [i](#)

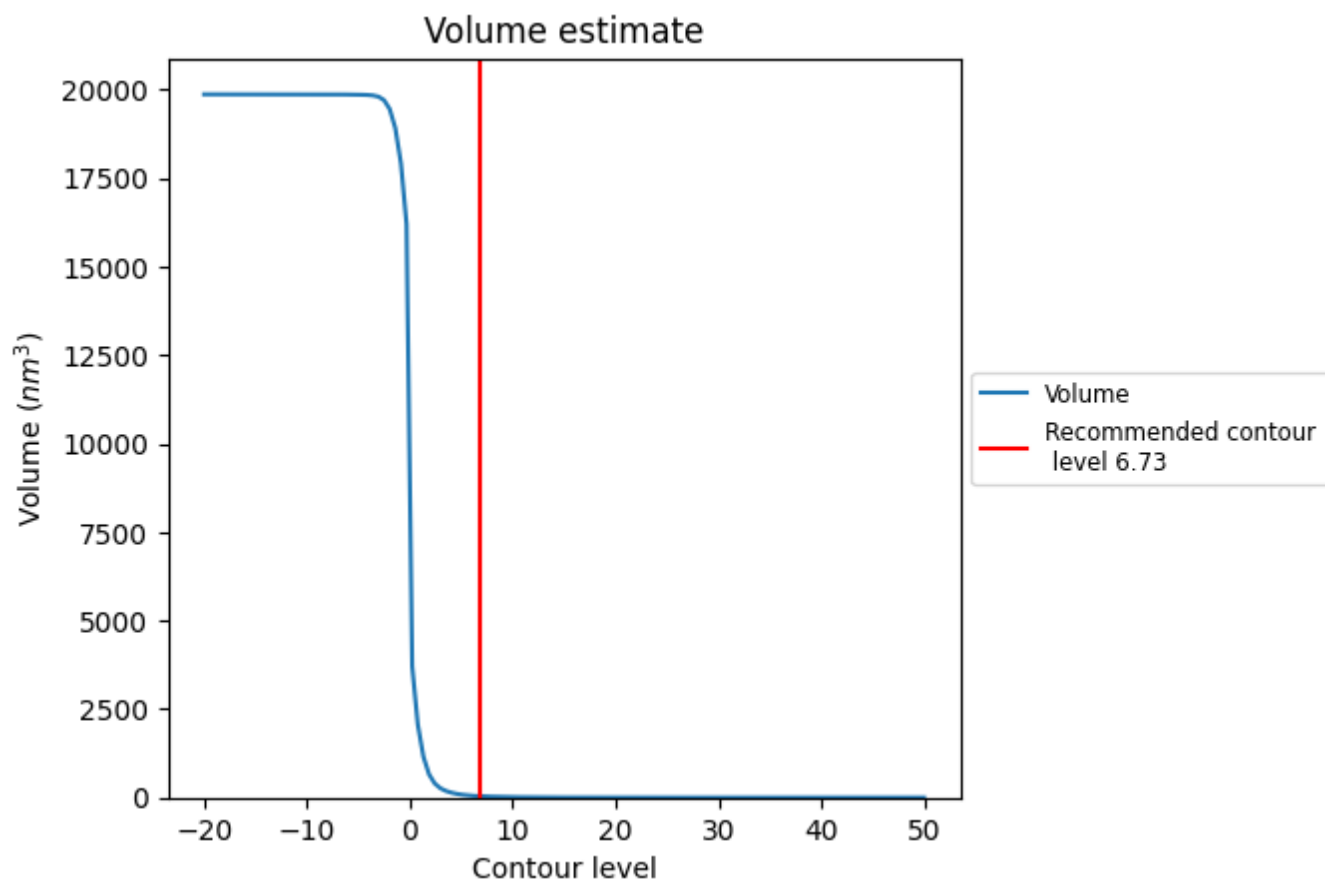
This section contains the results of statistical analysis of the map.

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.

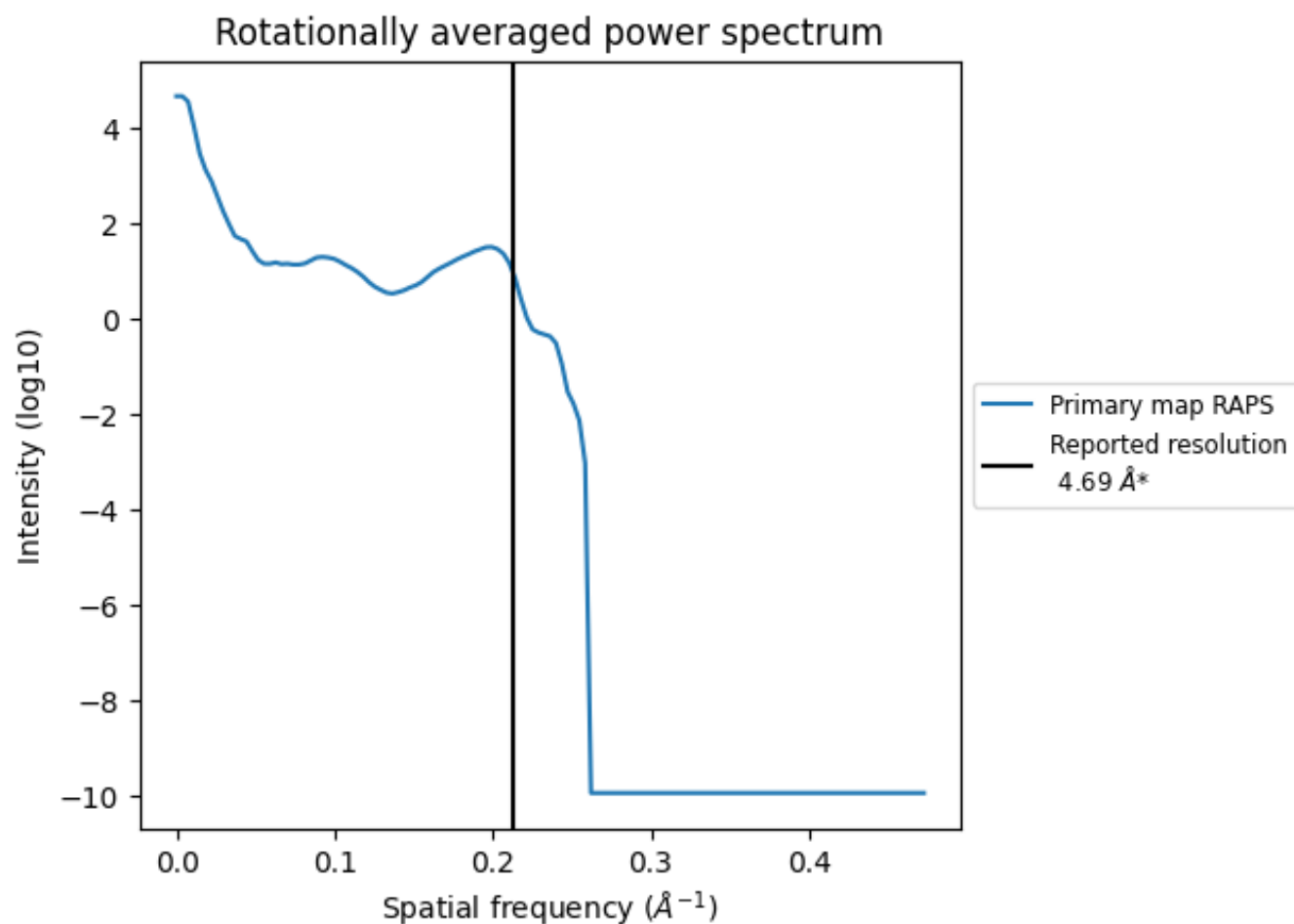
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 39 nm³; this corresponds to an approximate mass of 35 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 0.213 Å⁻¹

8 Fourier-Shell correlation

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

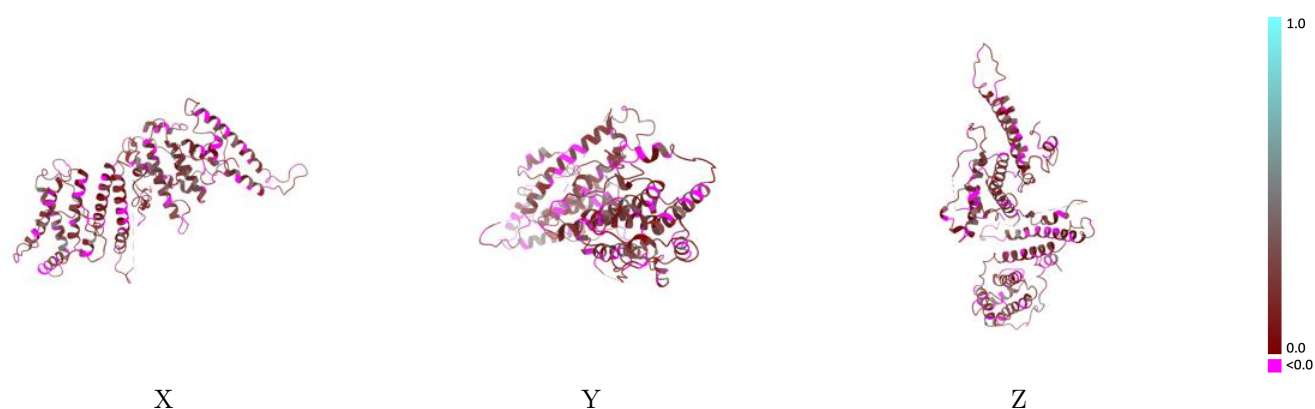
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22325 and PDB model 7JGF. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

This section was not generated.

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

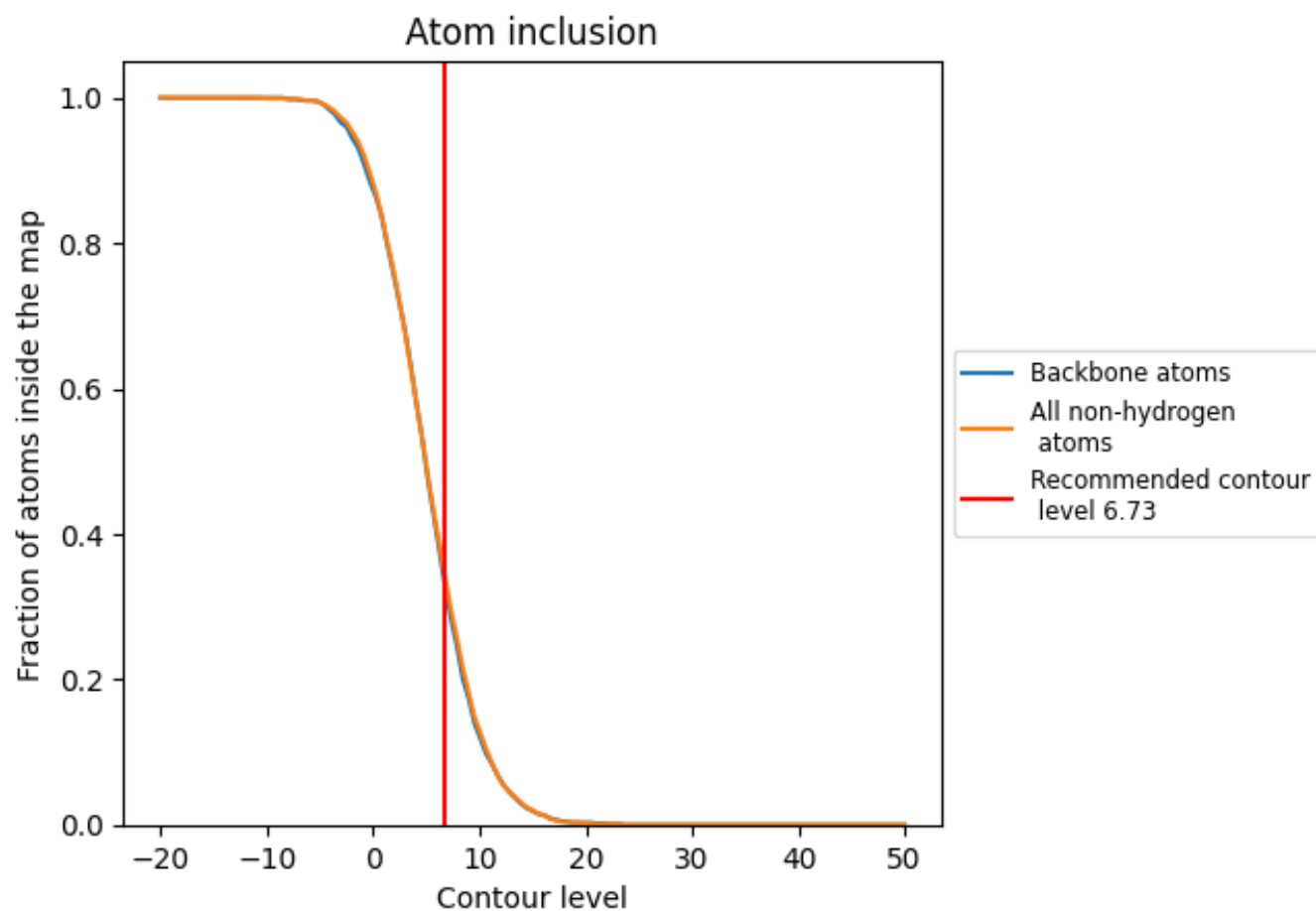


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 33% of all backbone atoms, 34% 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 (6.73) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3430	0.1460
A	0.3450	0.1460

