



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:06 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 Full wwPDB EM Validation 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.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

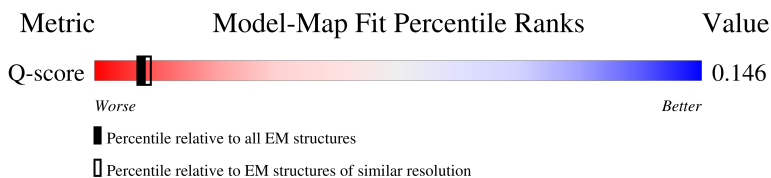
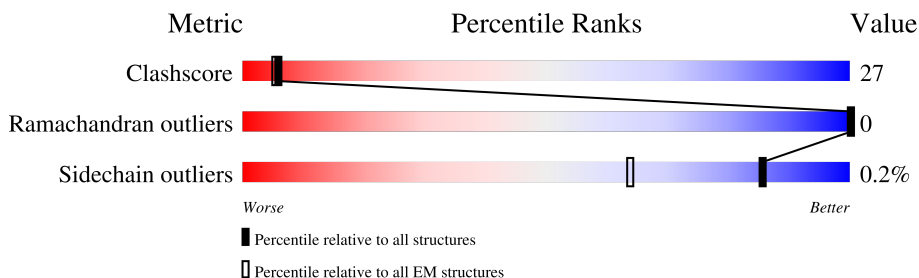
1 Overall quality at a glance

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	

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	D2043	R2043
LYS	A2548	F2426	S2426	L2365	E2303	R2241	M2112	R2044	R2044
THR	C2549	T2427	T2427	I2366	Q2304	W2242	L2113	Q2045	Q2045
TRP	V2550	D2428	D2428	F2367	V2305	E2243	T2114	L2046	L2046
ASN	N2551	I2429	I2429	R2368	K2306	E2244	N2115	C2047	C2047
PRO	Y2552	S2431	S2431	R2369	I2307	I2245	I2116	F2048	F2048
TYR	Y2553	I2432	I2432	R2370	E2310	S2246	E2117	S2049	S2049
GLU	N2554	I2433	I2433	K2371	L2311	K2247	F2118	R2050	R2050
THR	Y2555	K2434	K2434	W2372	E2312	R2248	I2119	I2051	I2051
ASP	L2557	G2435	G2435	F2374	ASP	Y2249	K2187	P2055	P2055
THR	K2558	D2436	D2436	L2373	VAL	K2250	D2120	A2056	A2056
PHE	K2559	D2437	D2437	L2375	ILE	K2251	I2121	R2057	R2057
LYS	K2560	M2438	M2438	D2378	ARG	Y2252	K2122	L2058	L2058
SER	E2561	E2439	E2439	P2379	ILE	M2255	I2123	I2061	I2061
LYS	E2562	E2440	E2440	S2380	LYS	D2256	L2124	N2062	N2062
CYS	Y2563	K2441	K2441	K2381	HIS	D2257	L2125	E2063	E2063
ASP	E2564	N2442	N2442	I2382	GLU	I2257	R2127	F2064	F2064
CYS	V2501	S2443	S2443	C2383	TYR	L2258	L2128	K2065	K2065
PRO	P2502	S2444	S2444	E2384	ASP	K2259	L2129	E2066	E2066
LYS	Q2503	D2445	D2445	Y2385	LYS	D2260	K2197	E2067	E2067
LEU	F2504	K2446	K2446	K2386	GLY	W2261	Q2198	I2068	I2068
PRO	L2505	I2447	I2447	R2387	N2327	K2262	Q2199	L2069	L2069
SER	R2506	G2448	G2448	D2388	D2328	E2263	E2200	K2070	K2070
PRO	W2507	K2449	K2449	P2389	Y2329	PRO	K2201	G2071	G2071
ILE	F2508	I2450	I2450	K2390	I2330	ASP	E2202	A2072	A2072
LYS	Q2509	L2451	L2451	N2391	C2331	ALA	Y2203	Q2073	Q2073
ASP	E2510	G2452	G2452	F2392	N2332	THR	V2204	S2074	S2074
LEU	W2511	D2453	D2453	K2393	K2333	LEU	E2205	K2077	K2077
PRO	S2512	T2454	T2454	F2394	K2335	TYR	K2206	F2078	F2078
PRO	E2513	D2455	D2455	F2395	N2336	LEU	S2206	L2079	L2079
GLN	N2514	G2456	G2456	T2396	I2337	ARG	K2207	G2080	G2080
ALA	F2515	D2457	D2457	I2397	I2338	GLU	C2208	N2081	N2081
ASP	C2516	Q2457	Q2457	K2398	D2339	CYS	S2209	Y2082	Y2082
GLU	D2517	N2458	N2458	W2399	ARG	SER	N2210	Y2083	Y2083
PRO	R2518	E2459	E2459	S2399	MET	LYS	V2211	K2084	K2084
GLY	R2519	K2460	K2460	A2400	LYS	CYS	T2212	E2085	E2085
THR	Q2520	R2461	R2461	F2401	LYS	PRO	T2213	H2086	H2086
LYS	K2521	K2462	K2462	E2402	ASN	GLY	L2214	K2087	K2087
LYS	L2522	K2463	K2463	E2403	ASN	GLY	W2151	W2088	W2088
HIS	Y2523	W2464	W2464	E2405	ASN	PHE	G2215	N2089	N2089
HIS	D2524	W2465	W2465	E2406	ASN	ASP	A2216	E2090	E2090
HIS	K2525	D2466	D2466	L2407	PHE	ASP	Q2217	A2153	A2153
HIS	L2526	M2467	M2467	K2408	V2349	MET	A2218	N2154	N2154
HIS	N2527	N2468	N2468	K2409	T2350	GLU	S2219	K2091	K2091
HIS	S2528	K2469	K2469	A2410	D2351	GLU	G2157	A2092	A2092
HIS	E2529	Y2470	Y2470	Y2411	N2352	MET	Y2158	L2093	L2093
HIS	G2530	H2471	H2471	G2412	F2353	ASN	K2159	E2094	E2094
HIS	I2531	I2472	I2472	G2413	K2356	ASN	K2160	A2095	A2095
HIS	N2532	W2473	W2473	A2414	S2357	K2223	N2163	F2100	F2100
HIS	A2533	E2474	E2474	K2415	N2358	K2229	K2164	Y2101	Y2101
HIS	E2534	S2475	S2475	A2416	W2359	K2230	L2165	D2102	D2102
HIS	E2535	N2476	N2476	K2417	E2359	Y2231	I2166	Y2103	Y2103
HIS	C2536	L2477	L2477	V2418	K2356	Q2232	D2167	E2104	E2104
HIS	T2536	C2478	C2478	Y2419	S2357	E2296	P2168		
HIS	G2479	Y2480	Y2480	H2420	E2359	A2297			
HIS	V2540								
HIS	K2602								

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.

All (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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2233:GLU:HG3	1:A:2237:LYS:HE2	1.55	0.88
1:A:2127:ARG:HA	1:A:2135:ASN:HD21	1.38	0.87
1:A:2183:LEU:HD11	1:A:2187:LYS:HE2	1.58	0.84
1:A:2159:LYS:HG2	1:A:2171:CYS:HB3	1.60	0.83
1:A:2022:TRP:HA	1:A:2044:ARG:HH12	1.42	0.83
1:A:2141:ASP:HA	1:A:2144:LYS:HG2	1.63	0.79
1:A:2440:GLU:HG3	1:A:2443:SER:HB2	1.66	0.78
1:A:2450:ILE:HG13	1:A:2451:LEU:HG	1.71	0.73
1:A:2238:ARG:HE	1:A:2241:ARG:HE	1.34	0.72
1:A:2406:ARG:HH12	1:A:2410:ALA:HB2	1.54	0.72
1:A:2104:GLU:HG2	1:A:2147:LYS:HE2	1.72	0.71
1:A:2254:ARG:HG2	1:A:2257:ILE:HG22	1.72	0.71
1:A:2062:ASN:HA	1:A:2065:LYS:HD2	1.73	0.70
1:A:2064:PHE:HA	1:A:2067:GLU:HG2	1.76	0.68
1:A:2164:LYS:HE3	1:A:2173:ILE:HG23	1.75	0.68
1:A:2366:ILE:HD12	1:A:2371:LYS:HD3	1.76	0.68
1:A:2069:LEU:O	1:A:2073:GLN:N	2.26	0.67
1:A:2516:CYS:HA	1:A:2519:ARG:HB3	1.78	0.65
1:A:2066:GLU:O	1:A:2070:LYS:N	2.24	0.65
1:A:2144:LYS:O	1:A:2148:LYS:NZ	2.30	0.64
1:A:2401:PHE:HA	1:A:2404:VAL:HG22	1.78	0.64
1:A:2418:VAL:HG12	1:A:2422:MET:HE1	1.78	0.64
1:A:2467:MET:O	1:A:2471:HIS:ND1	2.26	0.64
1:A:2244:THR:HB	1:A:2248:ARG:HH12	1.61	0.64
1:A:2565:ILE:O	1:A:2569:LYS:HG2	1.98	0.63
1:A:2334:TYR:HA	1:A:2337:ILE:HG12	1.79	0.63
1:A:2201:LYS:HA	1:A:2204:VAL:HG12	1.82	0.61
1:A:2033:LYS:HD2	1:A:2035:LYS:HE2	1.81	0.61
1:A:2419:VAL:HA	1:A:2422:MET:SD	2.41	0.60
1:A:2062:ASN:HA	1:A:2065:LYS:CD	2.31	0.60
1:A:2424:TYR:HA	1:A:2427:THR:HG22	1.83	0.60
1:A:2353:PHE:O	1:A:2356:LYS:NZ	2.33	0.60
1:A:2396:ILE:O	1:A:2399:SER:OG	2.11	0.59
1:A:2180:PRO:HD2	1:A:2183:LEU:HD23	1.84	0.59
1:A:2243:GLU:O	1:A:2247:LYS:N	2.36	0.59
1:A:2592:CYS:HB3	1:A:2596:LYS:HB3	1.84	0.59
1:A:2433:ILE:HD11	1:A:2465:TRP:CD1	2.38	0.58
1:A:2065:LYS:HG2	1:A:2142:TRP:HZ2	1.69	0.58
1:A:2183:LEU:HD12	1:A:2186:ILE:HD11	1.86	0.58
1:A:2064:PHE:HA	1:A:2067:GLU:CG	2.33	0.58
1:A:2302:LYS:O	1:A:2305:VAL:HG12	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2502:PRO:HD2	1:A:2505:LEU:CD2	2.31	0.57
1:A:2550:VAL:HA	1:A:2553:LYS:HE2	1.86	0.57
1:A:2443:SER:HA	1:A:2446:LYS:HE3	1.87	0.57
1:A:2502:PRO:HB2	1:A:2505:LEU:HD13	1.87	0.57
1:A:2552:TYR:O	1:A:2556:ILE:HG12	2.05	0.57
1:A:2074:SER:O	1:A:2077:LYS:HG3	2.05	0.56
1:A:2471:HIS:O	1:A:2474:GLU:HG2	2.05	0.56
1:A:2535:CYS:SG	1:A:2540:VAL:HG12	2.45	0.56
1:A:2182:PHE:CE2	1:A:2253:LYS:HG2	2.40	0.56
1:A:2250:LYS:HA	1:A:2253:LYS:NZ	2.21	0.56
1:A:2588:LEU:HD12	1:A:2591:LYS:HE2	1.87	0.56
1:A:2233:GLU:O	1:A:2237:LYS:HG3	2.05	0.56
1:A:2061:LEU:HD12	1:A:2064:PHE:CE1	2.41	0.56
1:A:2385:TYR:O	1:A:2389:PRO:HG3	2.06	0.56
1:A:2403:GLU:HA	1:A:2407:LEU:HD23	1.88	0.55
1:A:2597:CYS:SG	1:A:2600:LEU:HD12	2.46	0.55
1:A:2040:PRO:HG2	1:A:2043:ARG:HB2	1.89	0.55
1:A:2446:LYS:O	1:A:2450:ILE:HG12	2.06	0.55
1:A:2124:LYS:HD2	1:A:2127:ARG:HH21	1.71	0.55
1:A:2404:VAL:HG12	1:A:2476:MET:HE3	1.88	0.55
1:A:2050:ARG:HE	1:A:2051:ILE:H	1.55	0.54
1:A:2204:VAL:HB	1:A:2231:TYR:HE1	1.72	0.54
1:A:2083:TYR:CE2	1:A:2092:ALA:HB1	2.43	0.54
1:A:2106:ILE:HG23	1:A:2113:LEU:HG	1.89	0.54
1:A:2192:ASN:O	1:A:2196:GLN:HG2	2.08	0.54
1:A:2563:TYR:O	1:A:2566:GLN:HG3	2.08	0.54
1:A:2224:CYS:O	1:A:2228:ILE:HG12	2.08	0.54
1:A:2197:LYS:O	1:A:2201:LYS:HG2	2.08	0.54
1:A:2303:GLU:HA	1:A:2306:LYS:HG2	1.90	0.53
1:A:2373:LEU:CD2	1:A:2432:ILE:HG21	2.38	0.53
1:A:2039:ILE:HD12	1:A:2043:ARG:O	2.08	0.53
1:A:2061:LEU:HA	1:A:2064:PHE:CE1	2.44	0.53
1:A:2562:GLU:HA	1:A:2565:ILE:HG22	1.90	0.53
1:A:2460:LYS:O	1:A:2463:LYS:HG3	2.09	0.53
1:A:2070:LYS:O	1:A:2074:SER:N	2.37	0.53
1:A:2112:MET:O	1:A:2113:LEU:HD22	2.09	0.53
1:A:2120:ASP:O	1:A:2124:LYS:HD3	2.09	0.52
1:A:2041:PRO:HA	1:A:2044:ARG:CZ	2.39	0.52
1:A:2136:THR:O	1:A:2139:ALA:HB3	2.10	0.52
1:A:2335:LYS:HA	1:A:2338:HIS:ND1	2.24	0.52
1:A:2338:HIS:HA	1:A:2401:PHE:CZ	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2137:LYS:HA	1:A:2140:GLU:OE2	2.10	0.52
1:A:2198:GLN:NE2	1:A:2199:GLU:HG3	2.25	0.52
1:A:2429:ILE:O	1:A:2433:ILE:HG12	2.09	0.52
1:A:2458:ASN:HB2	1:A:2461:ARG:HB2	1.92	0.52
1:A:2451:LEU:HB2	1:A:2453:ASP:OD1	2.10	0.51
1:A:2141:ASP:O	1:A:2145:THR:N	2.43	0.51
1:A:2422:MET:HE2	1:A:2480:TYR:OH	2.09	0.51
1:A:2400:ALA:HA	1:A:2403:GLU:OE1	2.10	0.51
1:A:2201:LYS:O	1:A:2205:LYS:HE3	2.11	0.51
1:A:2445:ASP:OD1	1:A:2449:LYS:HE3	2.11	0.51
1:A:2440:GLU:CG	1:A:2443:SER:HB2	2.40	0.51
1:A:2481:ARG:NH1	1:A:2489:THR:HG21	2.25	0.50
1:A:2179:PRO:HD2	1:A:2184:ARG:HH11	1.77	0.50
1:A:2093:LEU:HA	1:A:2096:MET:HG3	1.92	0.50
1:A:2183:LEU:CD1	1:A:2186:ILE:HD11	2.42	0.50
1:A:2560:LYS:O	1:A:2564:GLU:HG2	2.12	0.50
1:A:2090:GLU:O	1:A:2093:LEU:HG	2.11	0.50
1:A:2124:LYS:O	1:A:2128:LEU:HD23	2.11	0.50
1:A:2140:GLU:HA	1:A:2143:TRP:CD1	2.46	0.50
1:A:2140:GLU:HA	1:A:2143:TRP:HD1	1.77	0.50
1:A:2165:ILE:HB	1:A:2172:THR:O	2.12	0.50
1:A:2404:VAL:HG12	1:A:2476:MET:CE	2.42	0.50
1:A:2505:LEU:HG	1:A:2587:TYR:OH	2.12	0.50
1:A:2257:ILE:O	1:A:2262:LYS:NZ	2.45	0.50
1:A:2260:ASP:OD1	1:A:2260:ASP:N	2.45	0.50
1:A:2496:PRO:O	1:A:2499:GLU:HG3	2.12	0.50
1:A:2373:LEU:HD12	1:A:2374:PHE:H	1.77	0.49
1:A:2201:LYS:O	1:A:2205:LYS:HG2	2.12	0.49
1:A:2225:THR:O	1:A:2229:LYS:HG2	2.12	0.49
1:A:2232:GLN:O	1:A:2236:ARG:HG3	2.12	0.49
1:A:2426:PHE:HA	1:A:2429:ILE:HG12	1.93	0.49
1:A:2232:GLN:HG3	1:A:2236:ARG:HE	1.78	0.49
1:A:2242:TRP:O	1:A:2246:SER:N	2.40	0.49
1:A:2101:TYR:OH	1:A:2184:ARG:HA	2.13	0.49
1:A:2107:ILE:HB	1:A:2143:TRP:CZ3	2.48	0.48
1:A:2349:VAL:CG1	1:A:2406:ARG:HD3	2.43	0.48
1:A:2531:ILE:H	1:A:2531:ILE:HD12	1.78	0.48
1:A:2086:HIS:CD2	1:A:2092:ALA:HA	2.48	0.48
1:A:2307:ILE:H	1:A:2307:ILE:HD12	1.78	0.48
1:A:2120:ASP:OD2	1:A:2124:LYS:NZ	2.47	0.47
1:A:2473:TRP:CZ3	1:A:2495:PHE:HA	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2502:PRO:CG	1:A:2505:LEU:HD13	2.44	0.47
1:A:2246:SER:O	1:A:2250:LYS:HG3	2.14	0.47
1:A:2472:ILE:O	1:A:2476:MET:HG2	2.14	0.47
1:A:2039:ILE:HG13	1:A:2044:ARG:HD2	1.96	0.47
1:A:2236:ARG:HG2	1:A:2299:LYS:HZ3	1.80	0.47
1:A:2417:LYS:HE3	1:A:2418:VAL:HG23	1.96	0.47
1:A:2469:LYS:HA	1:A:2472:ILE:HG22	1.96	0.47
1:A:2581:ASP:OD2	1:A:2582:LYS:NZ	2.43	0.47
1:A:2291:GLU:N	1:A:2291:GLU:OE1	2.47	0.47
1:A:2510:GLU:O	1:A:2513:GLU:HG3	2.15	0.47
1:A:2108:LYS:HE2	1:A:2147:LYS:HB2	1.96	0.47
1:A:2183:LEU:CD1	1:A:2187:LYS:HE2	2.38	0.47
1:A:2115:ASN:HB3	1:A:2118:PHE:CD1	2.49	0.47
1:A:2430:GLY:O	1:A:2434:LYS:HG2	2.15	0.47
1:A:2257:ILE:O	1:A:2259:LYS:HG2	2.15	0.46
1:A:2508:PHE:CZ	1:A:2588:LEU:HD13	2.50	0.46
1:A:2031:TYR:HD2	1:A:2033:LYS:HE3	1.80	0.46
1:A:2040:PRO:HB3	1:A:2192:ASN:OD1	2.15	0.46
1:A:2312:GLU:N	1:A:2312:GLU:OE1	2.49	0.46
1:A:2406:ARG:NH1	1:A:2410:ALA:HB2	2.25	0.46
1:A:2547:HIS:O	1:A:2550:VAL:HG22	2.15	0.46
1:A:2332:ASN:HA	1:A:2335:LYS:HG2	1.97	0.46
1:A:2447:ILE:HA	1:A:2450:ILE:HG12	1.98	0.46
1:A:2104:GLU:HA	1:A:2107:ILE:HG12	1.97	0.46
1:A:2065:LYS:HG2	1:A:2142:TRP:CZ2	2.49	0.46
1:A:2236:ARG:HG2	1:A:2299:LYS:NZ	2.31	0.46
1:A:2414:ALA:HB3	1:A:2417:LYS:CG	2.46	0.46
1:A:2358:TRP:HH2	1:A:2368:PRO:HD3	1.79	0.46
1:A:2183:LEU:O	1:A:2187:LYS:HG2	2.16	0.46
1:A:2379:PRO:HA	1:A:2382:ILE:HG12	1.98	0.45
1:A:2443:SER:O	1:A:2446:LYS:HG2	2.15	0.45
1:A:2077:LYS:HE3	1:A:2078:PHE:CE1	2.52	0.45
1:A:2329:TYR:HA	1:A:2332:ASN:OD1	2.16	0.45
1:A:2207:LYS:HB3	1:A:2207:LYS:HE2	1.72	0.45
1:A:2043:ARG:C	1:A:2044:ARG:HD3	2.41	0.45
1:A:2350:THR:HA	1:A:2406:ARG:NH2	2.32	0.45
1:A:2502:PRO:CB	1:A:2505:LEU:HD13	2.45	0.45
1:A:2062:ASN:OD1	1:A:2065:LYS:HD2	2.16	0.45
1:A:2237:LYS:O	1:A:2240:ILE:HG12	2.17	0.45
1:A:2403:GLU:HG3	1:A:2407:LEU:HD23	1.97	0.45
1:A:2375:LEU:HD21	1:A:2446:LYS:HE2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2101:TYR:O	1:A:2184:ARG:NH2	2.51	0.44
1:A:2163:ASN:O	1:A:2164:LYS:HD2	2.17	0.44
1:A:2464:TRP:HA	1:A:2467:MET:CE	2.33	0.44
1:A:2516:CYS:HB2	1:A:2599:CYS:HB2	1.50	0.44
1:A:2392:PHE:CE2	1:A:2396:ILE:HD11	2.52	0.44
1:A:2502:PRO:HD2	1:A:2505:LEU:HD13	1.99	0.44
1:A:2208:CYS:HB2	1:A:2224:CYS:HB3	1.61	0.44
1:A:2241:ARG:NH1	1:A:2245:ILE:HD12	2.33	0.44
1:A:2366:ILE:O	1:A:2366:ILE:HG13	2.17	0.44
1:A:2123:ILE:HG22	1:A:2127:ARG:CZ	2.48	0.44
1:A:2041:PRO:HA	1:A:2044:ARG:NH2	2.33	0.44
1:A:2045:GLN:C	1:A:2046:LEU:HD12	2.43	0.44
1:A:2476:MET:HB3	1:A:2480:TYR:CE2	2.53	0.44
1:A:2108:LYS:HD3	1:A:2143:TRP:HB3	1.99	0.44
1:A:2063:GLU:O	1:A:2067:GLU:HG2	2.18	0.43
1:A:2558:THR:O	1:A:2561:THR:HG22	2.19	0.43
1:A:2086:HIS:HD2	1:A:2092:ALA:HA	1.81	0.43
1:A:2023:ASN:O	1:A:2027:LEU:HB2	2.18	0.43
1:A:2498:ILE:HD13	1:A:2596:LYS:NZ	2.32	0.43
1:A:2061:LEU:HD12	1:A:2064:PHE:HE1	1.84	0.43
1:A:2383:CYS:O	1:A:2387:LYS:HG2	2.18	0.43
1:A:2529:GLU:HB3	1:A:2531:ILE:CD1	2.48	0.43
1:A:2093:LEU:HD12	1:A:2094:GLU:N	2.33	0.43
1:A:2101:TYR:OH	1:A:2179:PRO:HG2	2.19	0.43
1:A:2115:ASN:HB3	1:A:2118:PHE:HD1	1.82	0.43
1:A:2417:LYS:CE	1:A:2418:VAL:HG23	2.49	0.43
1:A:2024:ASP:O	1:A:2028:ARG:HG2	2.18	0.43
1:A:2525:LYS:HE2	1:A:2525:LYS:HB3	1.85	0.43
1:A:2416:ALA:HA	1:A:2419:VAL:HG12	2.00	0.42
1:A:2498:ILE:O	1:A:2501:VAL:HG13	2.19	0.42
1:A:2521:LYS:HB3	1:A:2521:LYS:HE2	1.88	0.42
1:A:2392:PHE:O	1:A:2395:PHE:HB3	2.19	0.42
1:A:2411:TYR:HB3	1:A:2418:VAL:HG22	2.01	0.42
1:A:2045:GLN:HE22	1:A:2082:TYR:HE1	1.68	0.42
1:A:2033:LYS:HD2	1:A:2035:LYS:CE	2.49	0.42
1:A:2311:LEU:HD23	1:A:2312:GLU:N	2.34	0.42
1:A:2469:LYS:O	1:A:2472:ILE:HG22	2.20	0.42
1:A:2143:TRP:O	1:A:2147:LYS:N	2.42	0.42
1:A:2382:ILE:HD13	1:A:2385:TYR:CE2	2.55	0.42
1:A:2093:LEU:HA	1:A:2096:MET:CG	2.50	0.42
1:A:2244:THR:HB	1:A:2248:ARG:NH1	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2250:LYS:HA	1:A:2253:LYS:HZ1	1.84	0.41
1:A:2195:ILE:O	1:A:2198:GLN:HG3	2.19	0.41
1:A:2381:LYS:HB2	1:A:2384:GLU:OE1	2.20	0.41
1:A:2090:GLU:O	1:A:2094:GLU:HG2	2.20	0.41
1:A:2398:TRP:O	1:A:2401:PHE:HB3	2.20	0.41
1:A:2328:ASP:OD2	1:A:2331:CYS:HB3	2.21	0.41
1:A:2430:GLY:HA3	1:A:2465:TRP:CE2	2.56	0.41
1:A:2566:GLN:HA	1:A:2569:LYS:HG2	2.02	0.41
1:A:2586:ASP:O	1:A:2590:GLU:HG2	2.21	0.41
1:A:2356:LYS:HZ1	1:A:2368:PRO:HB3	1.86	0.41
1:A:2414:ALA:HB3	1:A:2417:LYS:HG3	2.03	0.41
1:A:2503:GLN:HE21	1:A:2506:ARG:NH2	2.19	0.41
1:A:2165:ILE:CG1	1:A:2173:ILE:HG22	2.36	0.41
1:A:2502:PRO:CD	1:A:2505:LEU:HD13	2.50	0.41
1:A:2582:LYS:HE2	1:A:2587:TYR:HD1	1.86	0.41
1:A:2350:THR:HA	1:A:2406:ARG:HH21	1.86	0.41
1:A:2522:LEU:HD12	1:A:2555:TYR:CD1	2.55	0.41
1:A:2064:PHE:O	1:A:2067:GLU:HB2	2.21	0.40
1:A:2431:SER:HB2	1:A:2506:ARG:NH1	2.36	0.40
1:A:2104:GLU:HA	1:A:2107:ILE:CG1	2.51	0.40
1:A:2379:PRO:O	1:A:2382:ILE:HG12	2.21	0.40
1:A:2194:CYS:HA	1:A:2197:LYS:NZ	2.36	0.40
1:A:2488:GLU:OE2	1:A:2490:ASN:HB3	2.22	0.40
1:A:2041:PRO:HA	1:A:2044:ARG:NE	2.37	0.40
1:A:2250:LYS:HA	1:A:2253:LYS:HZ3	1.84	0.40
1:A:2334:TYR:HE1	1:A:2404:VAL:HG21	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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 ⓘ

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
1	A	2520	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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.

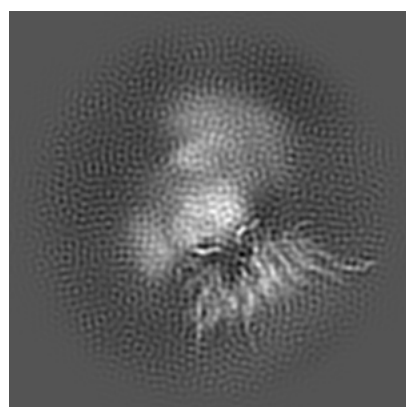
6 Map visualisation [i](#)

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.

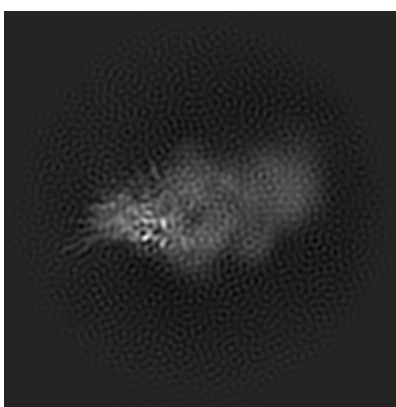
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

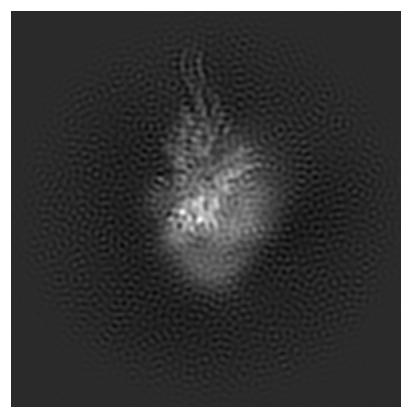
6.1.1 Primary map



X



Y

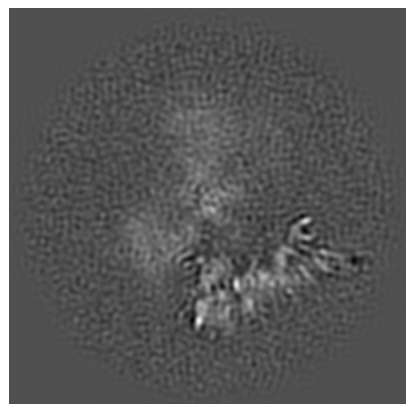


Z

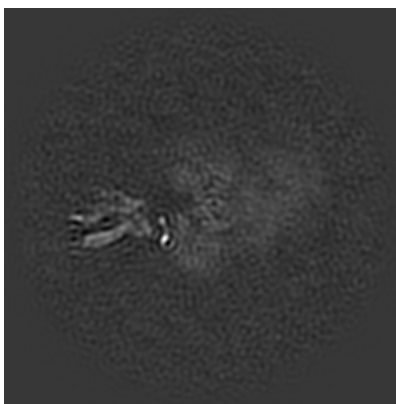
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

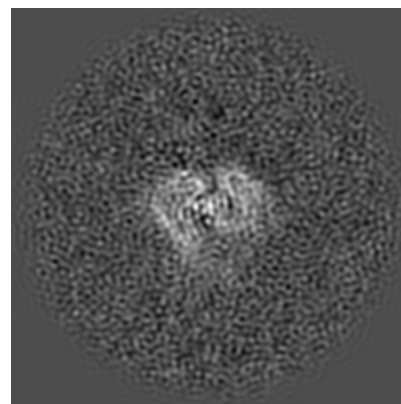
6.2.1 Primary map



X Index: 128



Y Index: 128

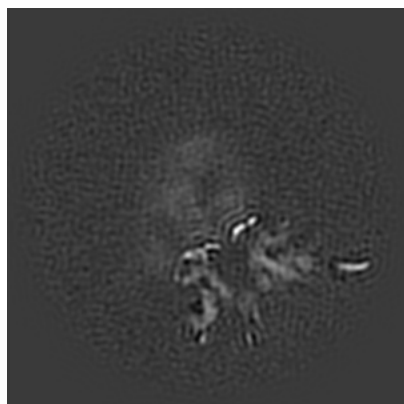


Z Index: 128

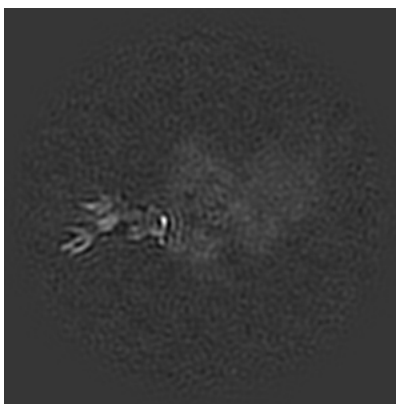
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

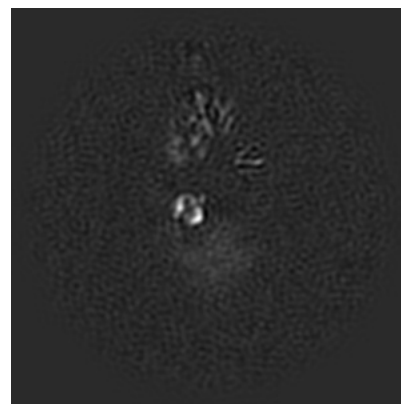
6.3.1 Primary map



X Index: 110



Y Index: 121

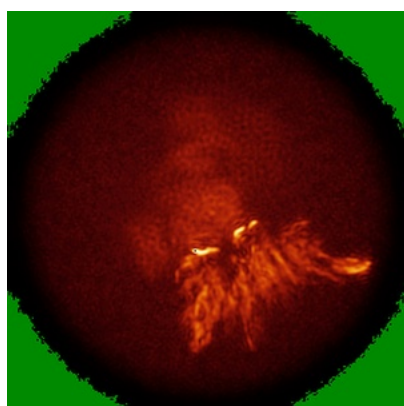


Z Index: 102

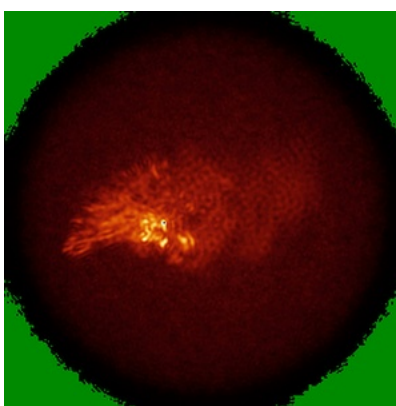
The images above show the largest variance slices of the map in three orthogonal directions.

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

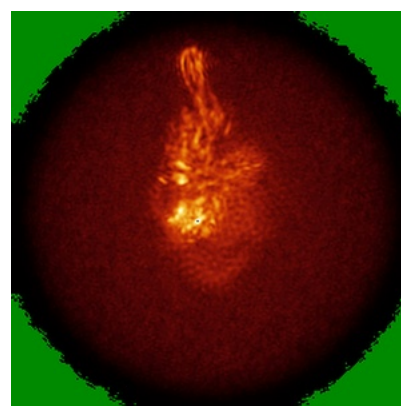
6.4.1 Primary map



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.

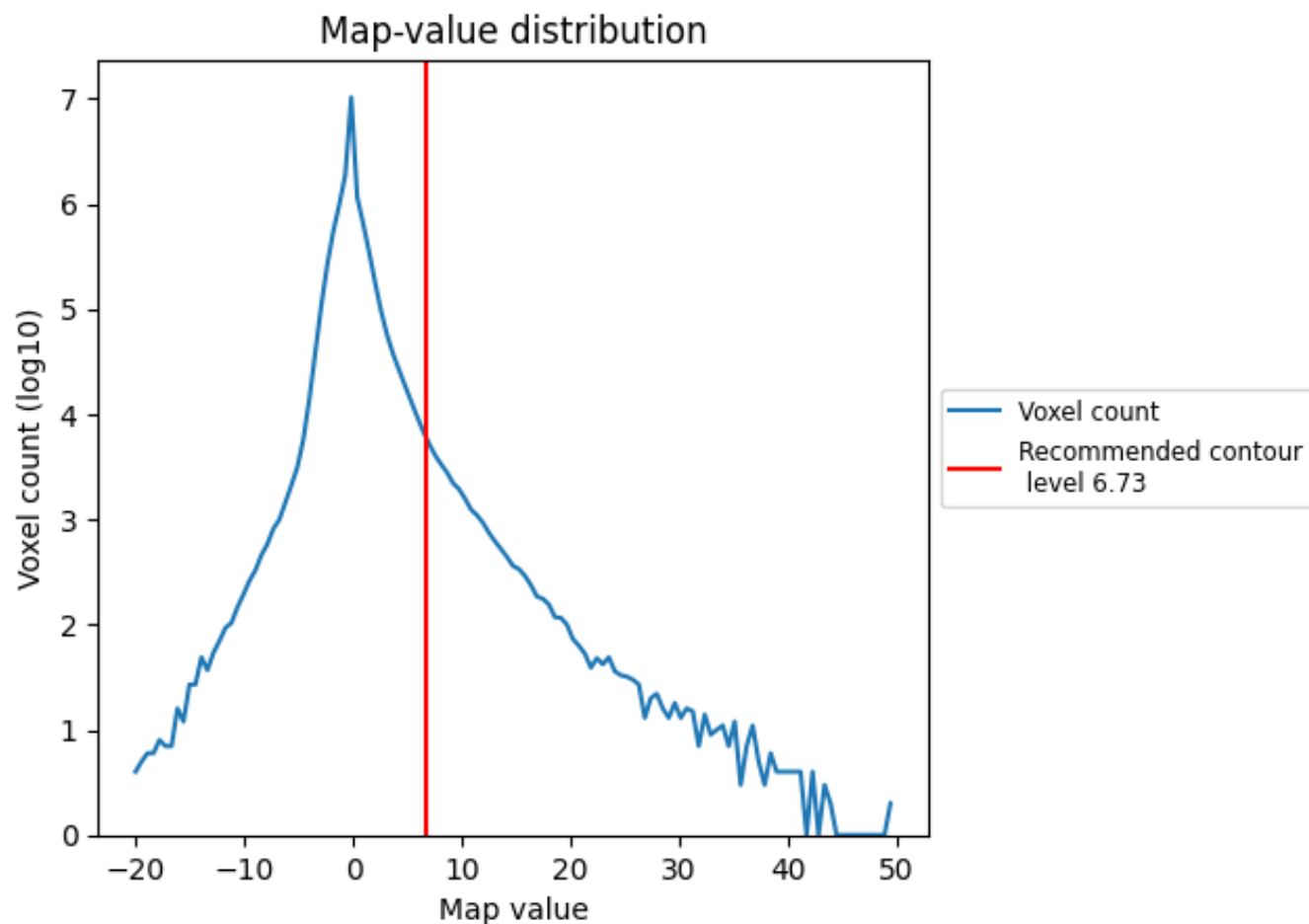
6.6 Mask visualisation

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

7 Map analysis [i](#)

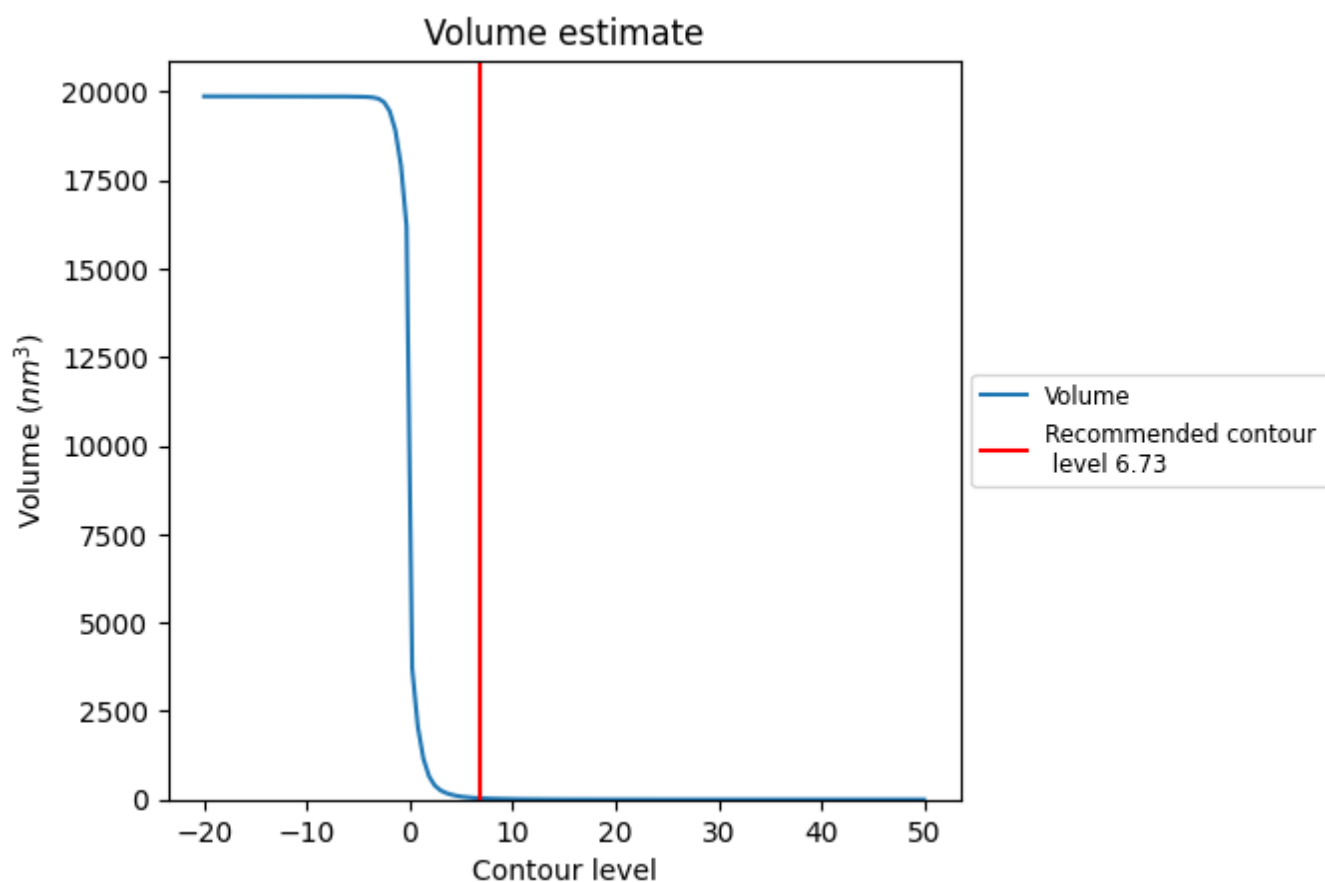
This section contains the results of statistical analysis of the map.

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.

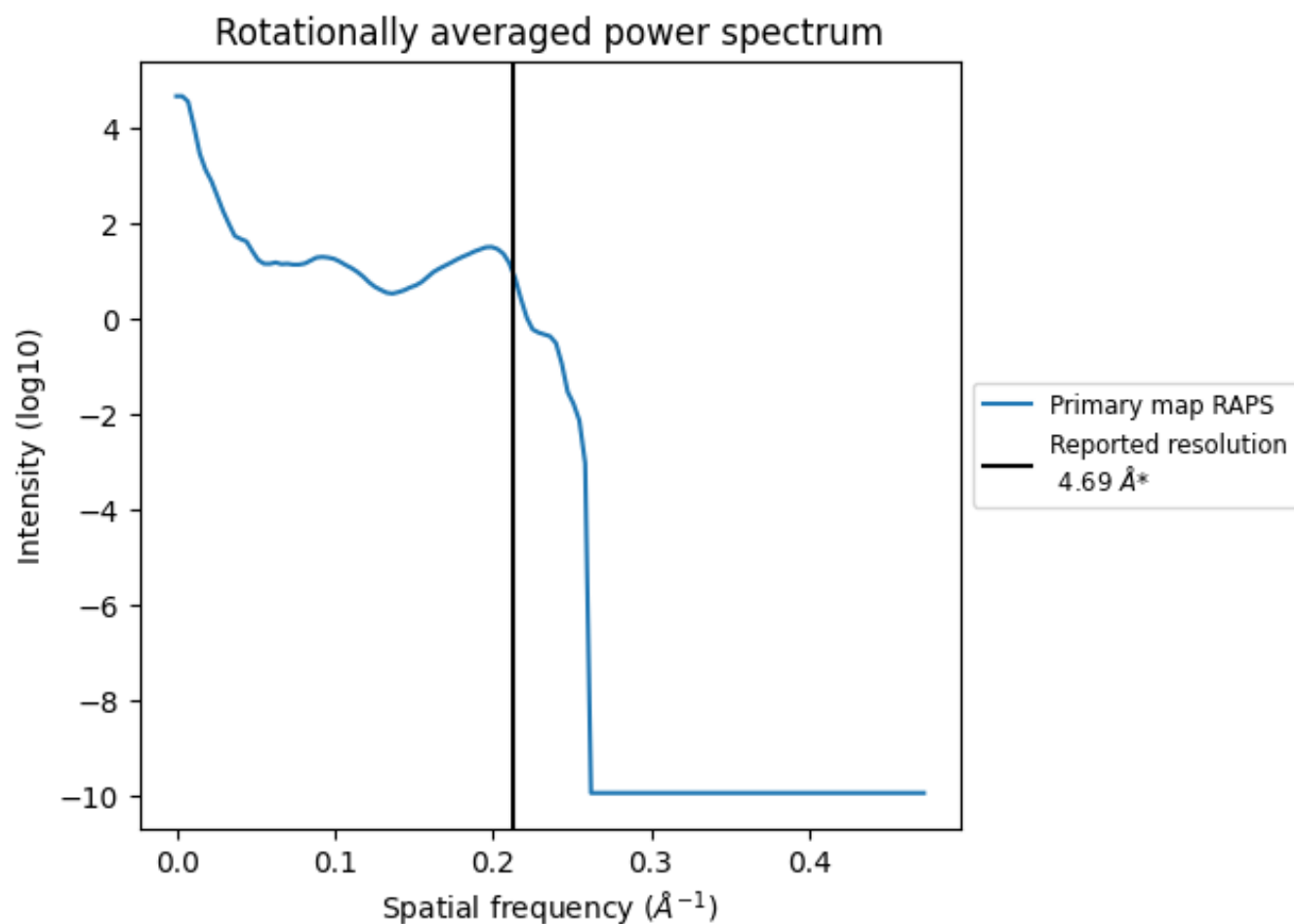
7.2 Volume estimate [i](#)



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.

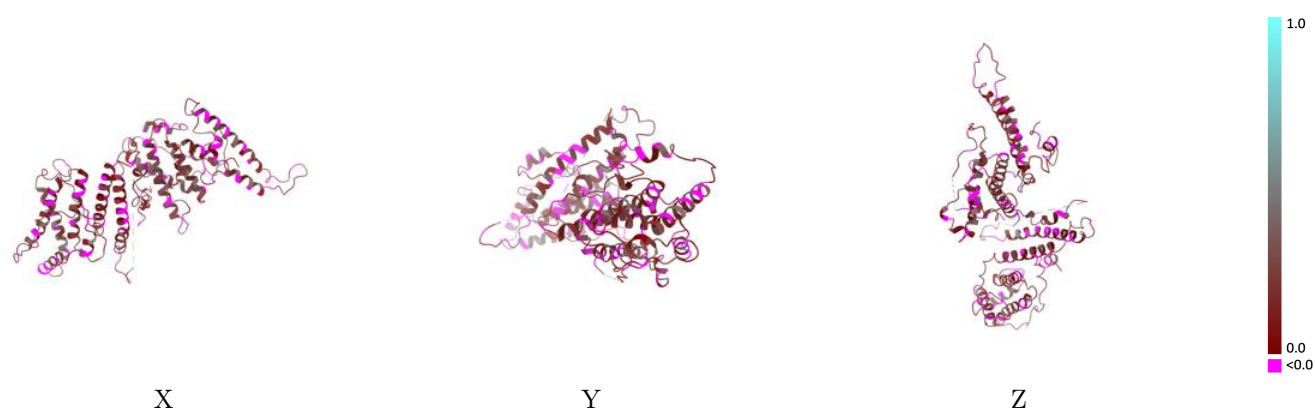
9 Map-model fit [i](#)

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](#)

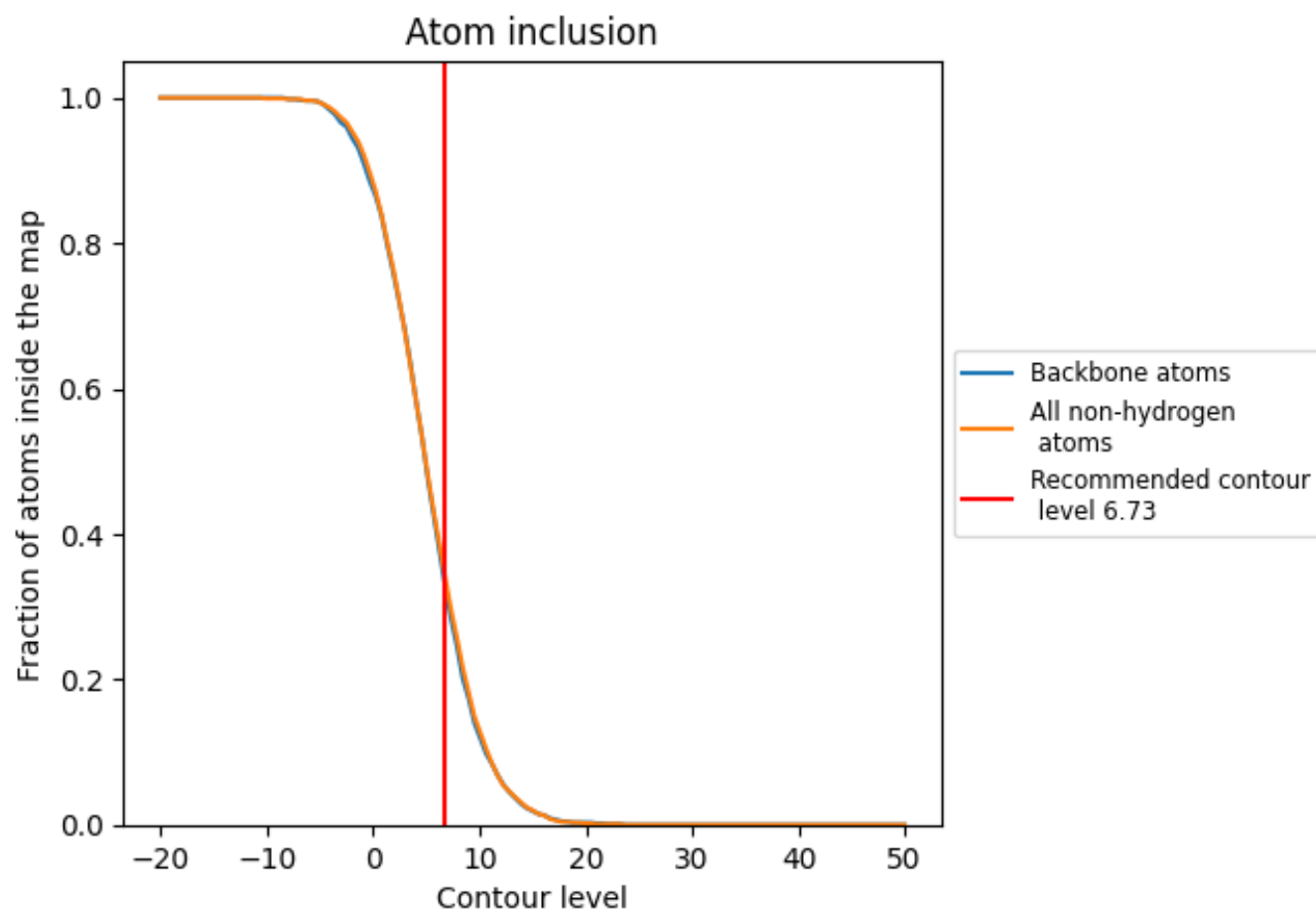


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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

