



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 09:12 PM UTC

PDB ID : 9G9L / pdb_00009g9l
EMDB ID : EMD-51156
Title : DNA-PK + Polymerase lambda
Authors : Chaplin, A.K.; Amin, H.; Zahid, S.; Hardwick, S.W.
Deposited on : 2024-07-25
Resolution : 4.63 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.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

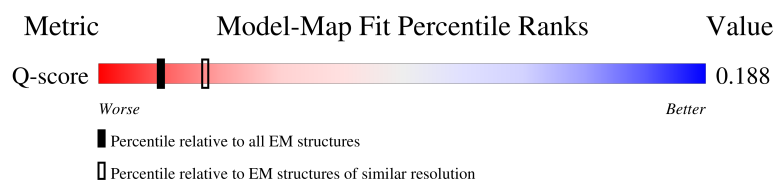
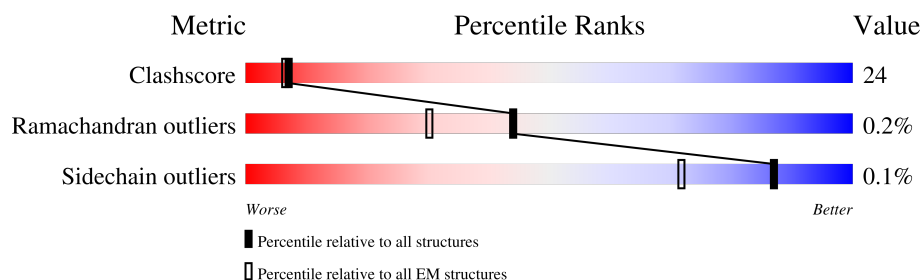
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.63 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.




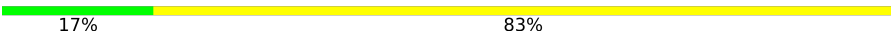

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2068 (4.13 - 5.13)

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	4128	
2	B	609	
3	C	732	
4	F	575	

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Mol	Chain	Length	Quality of chain
5	M	204	 10% 89%
6	D	24	 17% 83%
7	E	23	 17% 83%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 39800 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 DNA-dependent protein kinase catalytic subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3688	Total	C	N	O	S	0	0
			29010	18609	4895	5318	188		

- Molecule 2 is a protein called X-ray repair cross-complementing protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	488	Total	C	N	O	S	0	0
			3825	2453	645	709	18		

- Molecule 3 is a protein called X-ray repair cross-complementing protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	647	Total	C	N	O	S	0	0
			5093	3248	849	970	26		

- Molecule 4 is a protein called DNA polymerase lambda.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	98	Total	C	N	O	S	0	0
			755	482	141	129	3		

- Molecule 5 is a protein called Protein PAXX.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	23	Total	C	N	O	S	0	0
			155	99	25	30	1		

- Molecule 6 is a DNA chain called DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	24	Total	C	N	O	P	0	0
			488	238	89	138	23		

- Molecule 7 is a DNA chain called DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	23	Total	C	N	O	P	0	0
			474	230	79	142	23		

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.

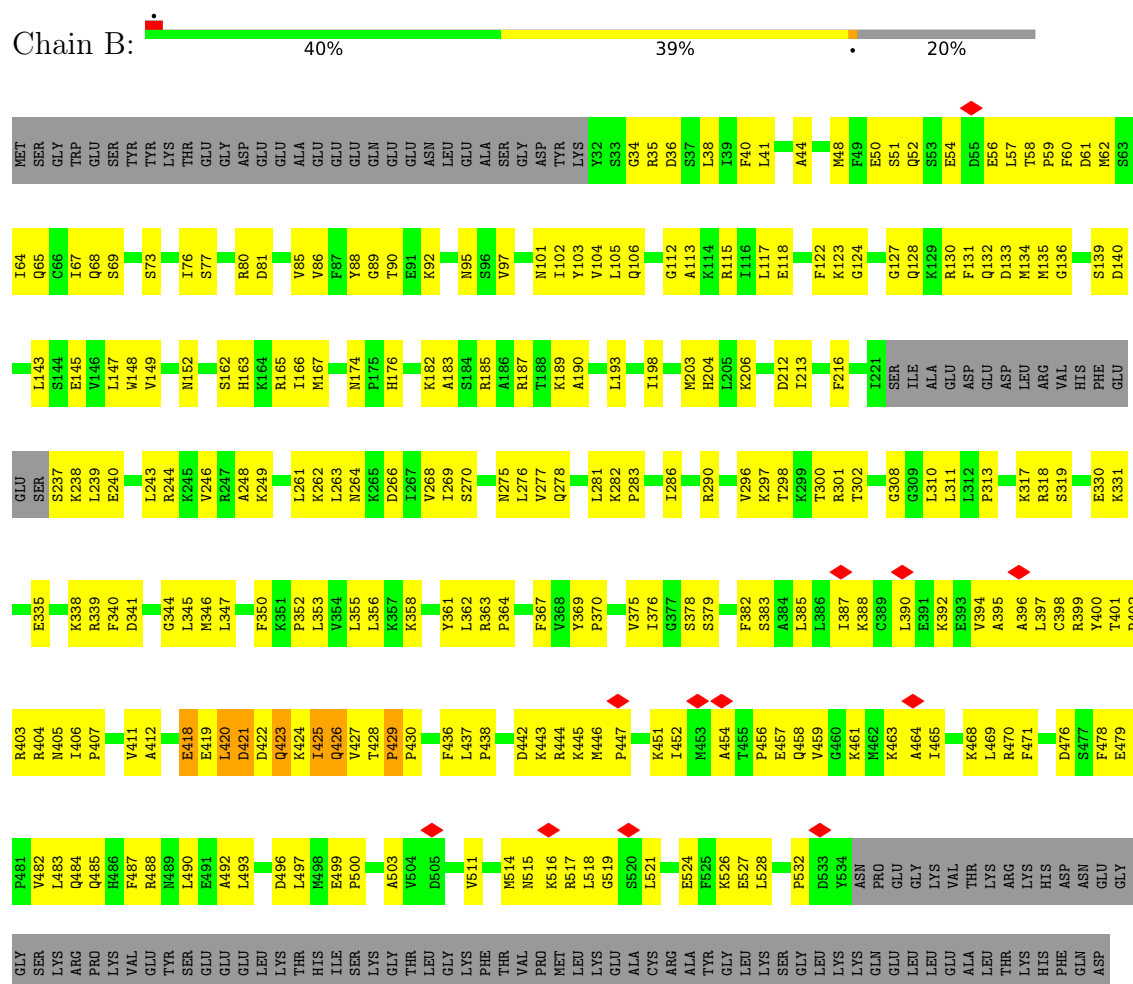
Chain A: 47% 42% 11%



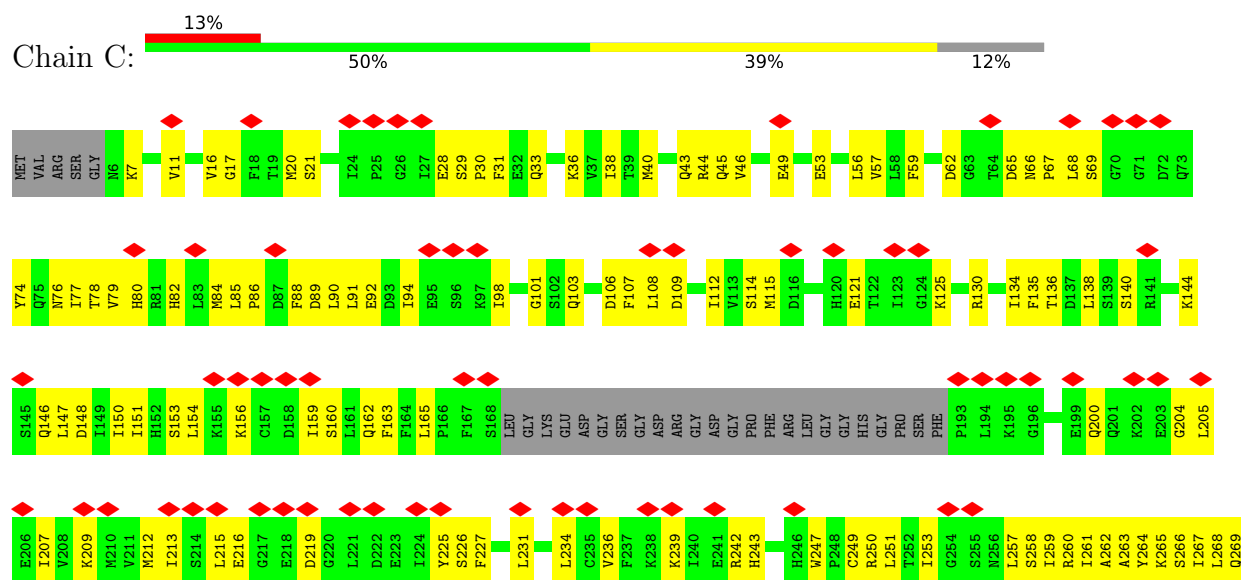
K3008	L2921	F2851	ASP	GLY	LEU	R2576	E2497	Y2412	M2331	G2261	H2163	H2091	A1948
K3009	R2922	F2852	A2767	LEU	THR	F2577	L2501	F2413	E2332	G2262	W2164	E2092	I1949
S3010	W2923	F2853	V2769	PRO	GLN	L2580	L2581	L2414	E2338	R2263	Q2170	C2093	S1950
L3011	F2924	F2854	V2769	GLY	THR	P2580	D2504	L2415	E2339	R2264	L2171	M2094	I1951
E3012	E2925	C2857	R2776	ASP	ALA	L2581	D2504	K2416	E2340	P2265	P2096	A2095	I1952
F3022	L2926	L2858	H2777	GLY	ASP	F2586	Q2508	S2417	S2340	N2266	T2097	T2096	F1956
N3028	A2927	I2861		ARG	GLY			K2418	V2345	G2180	E2180	L2098	F1966
K3029	Y2930	I2861	P2781	THR	ARG	Y2589	P2515	D2419	V2345	G2181	E2181	A2099	L1959
I3030	R2931	H2865	D2782	SER	SER		G2516	F2420	Q2348	L2182	L2182	M2098	L1960
E3033	S2932	H2865	L2783	VAL	PHE	R2596	G2516	W2421	Q2349	S2271	H2183	L2100	F1961
P3034	I2933	A2866	Q2784	LYS	ASP	PHE	Q2518	V2423	L2348	V2272	Y2184	K2102	
F3035	G2934	L2867	I2785	GLY	TRP	ARG	Q2519	V2424	L2349	G2273		T2101	
Y3036	E2935	L2868	K2786	ALA	LEU	SER	I2520	R2425	H2352	I2274		T2102	
Y3037	Y2936	L2869	H2787	ALA	THR	THR	I2521	R2425		Q2275		H2104	
O3037	D2937	S2870		GLY	THR	VAL	R2522		M2356	L2276		E2105	
E3038	L2938	L2871	L2790	THR	SER	LEU	R2522	D2429	E2357			R2106	
Y3040	D2939	L2872	I2791	ARG	SER	LEU	S2526	R2431	K2359	W2281		L2108	
L3041	L2942	P2873	T2792	THR	THR	THR	H2597	E2437	F2360	A2282		S2107	
K3044	I2943	V2876	P2793	ASP	ASP	MET	E2528	Q2432	I2361	P2287		L2108	
L3045	T2944	C2880	L2794	LEU	PRO	GLY	R2530	L2436	V2362	Q2291		GLY	
R3046	T2944	C2880	A2796	ARG	LEU	VAL	R2531	I2438	L2364	C2292		PRO	
L3049	K2950	L2884	V2797	ARG	VAL	GLU	L2531	I2439	N2365	G2293		GLN	
K3050	T2953	F2887	A2798	ARG	VAL	GLU	P2532	I2440	K2366	K2207		GLY	
L3051	F2957	V2888	I2803	THR	THR	THR	R2533	K2441	V2367	D2208		GLU	
L3052	L2957	G2889	A2804	ASP	SER	GLY	T2535	M2442	T2368	E2209		ASP	
L3053	D2964	L2890	K2806	GLN	SER	THR	R2538	M2443		Q2295		VAL	
E2967	E2967	L2892	Q2807	GLU	ASP	LEU	L2542	K2447	P2371	S2296		R2119	
Y2972	Y2972	L2893	L2808	LYS	LEU	THR	N2543	L2451	P2372	S2297		R2120	
S3060	L2976	E2895	F2809	SER	LEU	THR	S2547	R2452	P2373	E2298		D2121	
L3061	N2977	L2897	S2811	NET	ALA	GLN	I2550	E2453	L2374	Y2299		L2122	
L3062	K2978	L2898	L2812	TYR	THR	GLY	E2551	L2454	A2375	F2300		N2126	
T3063	Q2979	R2899	F2813	ARG	ARG	SER	V2552	R2470	D2376	N2217		K2127	
F3064	D2980	L2900	G2815	ALA	SER	LEU	H2553	K2471	L2385	L2215		F2128	
L3065	W2981	L2901	I2816	GLY	GLU	SER	F2554	E2471	L2386	L2219		M2220	
D3066	V2982	L2902	L2817	VAL	ARG	ALA	L2555	Q2472	P2377	L2303		K2221	
K3067	D2983	ALA	K2818	ALA	LEU	TRP	S2556	M2473	F2378	V2304		L2129	
A3068	P2986	LEU	E2819	GLN	GLN	PRO	L2557	Y2474	M2379	N2305		H2130	
M3069	K2991	PRO	M2820	ARG	ARG	VAL	A2558		V2382	N2306		G2131	
E3072	K2991	ALA	K2824	GLN	ALA	VAL	T2559	M2478	K2394	K2307		G2134	
K3075	W2994	LYS		LYS	PRO	ALA	N2560	F2479	T2385	F2239		N2135	
E3079	F2995	ARG	K2829	GLU	LEU	GLY	F2561	K2479	L2396	T2240		V2138	
L3080	L2996	VAL	N2830	LYS	LEU	THR	L2562	H2481	C2397	L2140		F2139	
S3083	A2997	GLY	N2831	VAL	SER	ILE	L2563	H2481	L2398	R2143		THR	
L3086	S2998	GLY	Q2834	VAL	VAL	ARG	E2564	Y2484	E2399	L2144		ASP	
L3089	L2999	LYS	K2835	GLY	GLY	ALA	M2565	R2485	V2400	F2145		VAL	
A3006	D3000	ALA		LYS	PRO	THR	S2569	R2485	C2403	T2153		GLU	
Y3102	H3004	ARG	Q2838	GLU	PHE	GLN	D2570	E2490	R2404	P2252		LEU	
	L3005	LYS	D2839	LEU	GLY	GLN	P2571		Y2253	F2157		GLU	
	F3007	MET	F2918	LYS	LYS	HIS	Y2572	N2493	R2254	R2158		ALA	
	A3006	ARG	P2940	MET	ASP	ASP	Y2573	D2494	F2257	P2159		ALA	
		LYS	D2919	LYS	ARG	PHE	N2574	S2495	F2260	Y2160		ASN	
		GLN	V2920	GLN	LEU	THR	P2575	Q2496		A2161		GLY	
										R2090		ASP	



• Molecule 2: X-ray repair cross-complementing protein 6



• Molecule 3: X-ray repair cross-complementing protein 5





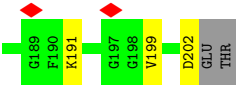
ASP	VAL	LEU	THR	ALA	THR	ALA	GLN	G129	G165	MET
LEU	LEU	THR	THR	GLU	ASN	GLN	GLN	F130	ASP	PRO
ILE	ILE	GLN	PRO	LYS	HIS	PRO	ILE	I132	ARG	GLY
THR	THR	GLN	ILE	ILE	ASN	SER	SER	F133	ILE	ILE
HIS	HIS	ALA	GLU	GLU	LEU	ASP	ASP	I134	G70	LEU
PRO	PRO	ILE	ILE	HIS	THR	ASP	ASP	P135	G71	LYS
ASP	GLY	LEU	LEU	THR	THR	GLU	GLU	L72	L72	ALA
GLY	ARG	LYS	GLU	GLU	GLU	ALA	ALA	S136	G73	ALA
SER	SER	HIS	SER	LYS	LYS	SER	SER	TYR	Q76	PHE
HIS	HIS	TYR	GLY	LEU	LEU	ASP	ASP	LEU	G77	PRO
ARG	ARG	SER	SER	GLU	GLU	GLY	GLY	ASP	P78	LYS
GLY	GLY	LEU	VAL	VAL	VAL	GLU	GLU	HIS	G79	GLN
ILE	ILE	ARG	GLU	ARG	LEU	THR	THR	PRO	V80	ILE
PHE	PHE	LEU	ALA	ALA	LYS	GLN	GLN	GLN	T81	HIS
SER	SER	LEU	LYS	ALA	LYS	VAL	VAL	PRO	H82	ALA
ARG	ARG	ASP	ASP	ALA	ALA	SER	SER	SER	T83	ASP
LEU	LEU	PRO	ILE	SER	SER	ALA	ALA	GLU	D86	SER
LEU	LEU	ILE	ILE	SER	VAL	GLN	ASP	GLU	E87	SER
ASP	ASP	GLU	GLU	GLN	GLN	ASP	LEU	ASP	G88	LYS
GLU	GLU	SER	SER	GLY	GLY	LEU	GLU	ASP	H89	VAL
LEU	VAL	VAL	VAL	ASP	ASP	ALA	ALA	ALA	D90	LEU
THR	THR	THR	THR	LYS	LYS	ALA	SER	SER	Y91	ALA
GLN	GLN	GLU	GLU	TRP	TRP	ILE	ILE	PRO	F92	LYS
GLY	GLY	ILE	ILE	ARG	ARG	ILE	SER	PRO	R93	ILE
PHE	PHE	GLU	GLU	ALA	ALA	SER	GLY	PRO	A94	PRO
LEU	LEU	LEU	LEU	LEU	LEU	GLY	THR	GLY	L97	ARG
THR	THR	PHE	THR	GLY	GLY	HIS	THR	HIS	L98	ARG
ASP	ASP	SER	VAL	ASN	ASN	PRO	GLU	GLU	R99	GLU
GLN	GLN	ILE	LYS	ALA	LYS	SER	ALA	ALA	L100	GLY
LEU	VAL	TRP	ALA	ALA	ILE	THR	LEU	LEU	P101	GLU
SER	SER	GLY	ILE	ILE	ILE	LEU	GLN	GLN	Q102	GLU
GLN	GLN	ALA	ALA	ASN	ALA	GLY	THR	THR	L103	ALA
GLU	GLU	ALA	ALA	GLY	LEU	ASP	ALA	ALA	P104	GLU
GLY	GLY	ASN	LYS	LYS	LYS	CYS	LEU	LEU	P105	ASP
ASN	ASN	SER	THR	SER	SER	GLU	SER	SER	L41	GLY
GLY	GLY	ALA	ALA	PHE	THR	THR	PRO	PRO	G106	GLY
GLN	GLN	LEU	GLN	HIS	HIS	PRO	PRO	PRO	A107	GLY
GLN	GLN	LEU	THR	THR	LYS	PRO	PRO	PRO	Q108	GLY
LYS	LYS	CYS	TRP	PRO	VAL	ALA	PRO	PRO	L109	GLY
TYR	TYR	VAL	TYR	VAL	THR	ALA	THR	THR	V110	GLY
LEU	LEU	ALA	GLN	SER	SER	VAL	VAL	ARG	K111	GLY
GLY	GLY	CYS	GLY	THR	THR	LEU	LEU	PRO	W114	GLY
VAL	VAL	GLY	PHE	GLN	GLN	ASP	ASP	VAL	V49	GLY
SER	SER	SER	SER	GLY	GLY	GLU	THR	SER	L115	GLY
ARG	ARG	THR	ARG	ALA	ALA	ALA	TRP	PRO	S116	GLY
PRO	PRO	LEU	LEU	CYS	CYS	VAL	VAL	PRO	L117	GLY
GLY	GLY	GLY	GLY	SER	SER	GLN	CYS	GLN	C118	GLY
PRO	PRO	LYS	ASP	ILE	ILE	ALA	LYS	LYS	L119	GLY
GLY	GLY	ILE	ILE	PRO	GLY	GLN	ALA	ALA	Q120	GLY
ARG	ARG	THR	ARG	GLY	GLY	PRO	LYS	LYS	E121	GLY
ARG	ARG	CYS	SER	ILE	ILE	SER	SER	GLU	R122	GLY
HIS	HIS	GLY	GLN	GLY	GLY	SER	SER	ALA	R123	GLY
ARG	ARG	ASP	ALA	LYS	LYS	GLN	PRO	PRO	L124	GLY
ARG	ARG	SER	SER	ARG	ARG	ASN	LYS	ASN	V125	GLY
</										

LEU	ASP	ILE	ILE	VAL	PRO	TYR	SER	GLU	PHE	ALA	CYS	ALA	LEU	LEU	TYR	THR	GLY	SER	ALA	HIS	PHE	ASN	ARG	SER	MET	ARG	ALA	LEU	ALA	LYS	THR	LYS	GLY	MET	SER	SER	LEU	SER	GLU	HIS	ALA	LEU	SER	THR	ALA	VAL	VAL	ARG	ASN	THR	HIS	GLY	CYS	LYS	VAL	GLY	PRO	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
ARG	VAL	LEU	THR	PRO	PRO	GLU	LYS	ASP	VAL	PHE	ARG	LEU	LEU	GLY	LEU	PRO	TYR	ARG	GLU	PRO	ALA	GLU	ASP	TRP																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						

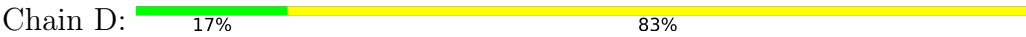
● Molecule 5: Protein PAXX



LEU	ARG	ALA	LEU	THR	LEU	GLY	LEU	ALA	LYS	ARG	VAL	TRP	SER	LEU	GLU	ARG	LEU	ALA	ALA	ALA	GLU	GLU	THR	ALA	VAL	SER	PRO	PRO	ARG	LYS	PRO	ASP	PRO	PHE	LEU	GLN	THR	PRO	ASP	PRO	PHE	PRO	GLN	ARG	GLY	LYS	PRO	GLY	PRO	GLY	VAL	ARG	ARG	ARG	C180	
MET	ASP	PRO	LEU	SER	PRO	PRO	LEU	CYS	THR	GLU	LEU	PRO	PRO	GLY	PRO	ARG	PRO	PHE	VAL	CYS	TYR	CYS	GLU	GLY	GLU	GLU	SER	GLY	GLY	ASP	ARG	GLY	GLY	PHE	ASN	LEU	TYR	VAL	THR	ASP	ALA	ALA	GLU	LEU	TRP	SER	THR	CYS	PHE	PRO	ASP	SER	LEU	ALA	ALA	LEU



● Molecule 6: DNA



T20	A21	A24	A25	A26	C27	T28	A29	A30	A31	A32	A33	C34	T35	A36	T37	T38	A39	T40	T41	A42	T43
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● Molecule 7: DNA



A15	A16	T17	A18	A19	T20	A21	G22	T23	T24	T25	T26	T27	A28	G29	T30	T31	T32	A33	T34	T35	A36	G37
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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	12656	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 ($e^-/\text{\AA}^2$)	51.96	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.640	Depositor
Minimum map value	-0.137	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.18	Depositor
Map size (Å)	417.28, 417.28, 417.28	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.304, 1.304, 1.304	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	0.18	0/29602	0.46	2/40074 (0.0%)
2	B	0.24	0/3900	0.49	2/5268 (0.0%)
3	C	0.15	0/5185	0.39	0/6998
4	F	0.27	0/771	0.50	0/1046
5	M	0.09	0/159	0.34	0/216
6	D	0.23	0/548	0.49	0/843
7	E	0.24	0/530	0.49	0/817
All	All	0.19	0/40695	0.46	4/55262 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	126	PRO	N-CA-CB	6.58	110.57	103.33
1	A	2297	SER	N-CA-C	-5.35	107.77	114.56
2	B	281	LEU	CA-C-N	5.24	130.90	120.94
2	B	281	LEU	C-N-CA	5.24	130.90	120.94

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	29010	0	28916	1364	0
2	B	3825	0	3813	248	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	5093	0	5039	247	0
4	F	755	0	767	54	0
5	M	155	0	135	3	0
6	D	488	0	275	39	0
7	E	474	0	266	29	0
All	All	39800	0	39211	1882	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 24.

The worst 5 of 1882 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:420:LEU:HA	2:B:426:GLN:CA	1.78	1.12
2:B:420:LEU:CA	2:B:426:GLN:HA	1.79	1.11
1:A:3226:ASP:N	1:A:3229:SER:HG	1.69	0.89
1:A:3868:VAL:HG12	1:A:3872:ARG:HE	1.38	0.88
2:B:407:PRO:HG2	3:C:486:ARG:HD2	1.54	0.88

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	3652/4128 (88%)	3389 (93%)	258 (7%)	5 (0%)	48	83
2	B	484/609 (80%)	434 (90%)	44 (9%)	6 (1%)	10	42
3	C	639/732 (87%)	586 (92%)	52 (8%)	1 (0%)	43	77
4	F	96/575 (17%)	91 (95%)	5 (5%)	0	100	100
5	M	21/204 (10%)	21 (100%)	0	0	100	100
All	All	4892/6248 (78%)	4521 (92%)	359 (7%)	12 (0%)	44	77

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	426	GLN
2	B	418	GLU
2	B	420	LEU
2	B	425	ILE
2	B	429	PRO

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	3158/3671 (86%)	3157 (100%)	1 (0%)	100	100
2	B	414/548 (76%)	412 (100%)	2 (0%)	81	81
3	C	559/649 (86%)	559 (100%)	0	100	100
4	F	78/480 (16%)	78 (100%)	0	100	100
5	M	15/160 (9%)	15 (100%)	0	100	100
All	All	4224/5508 (77%)	4221 (100%)	3 (0%)	87	88

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	855	VAL
2	B	421	ASP
2	B	423	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 70 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	68	GLN
2	B	458	GLN
3	C	359	ASN
1	A	1941	HIS
1	A	1771	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.

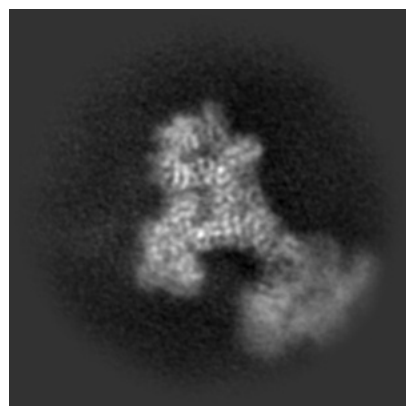
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51156. These allow visual inspection of the internal detail of the map and identification of artifacts.

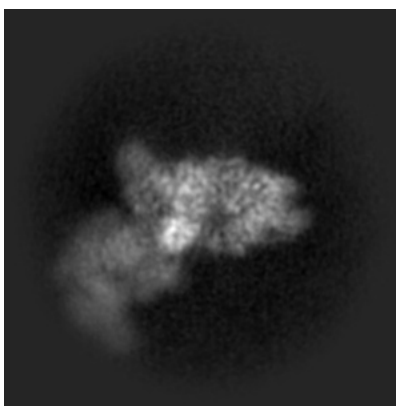
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

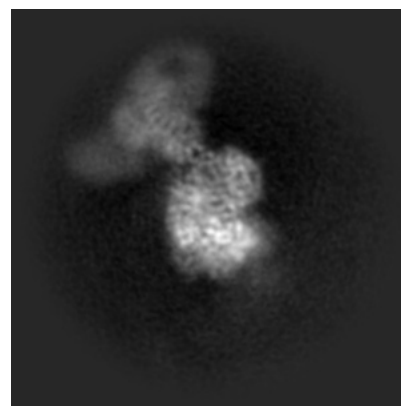
6.1.1 Primary map



X

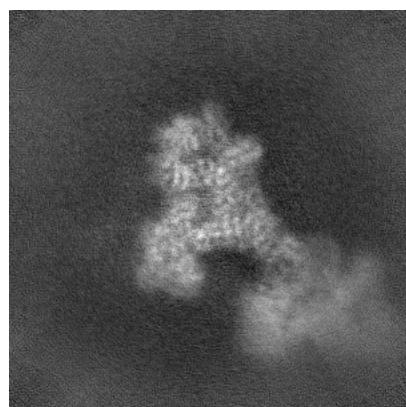


Y

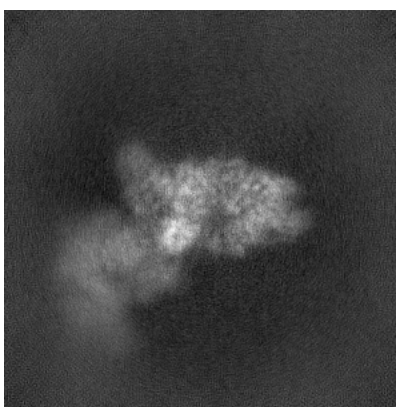


Z

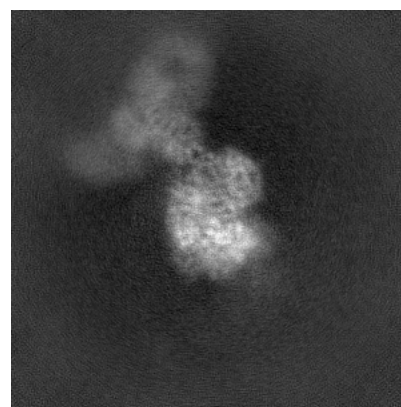
6.1.2 Raw map



X



Y

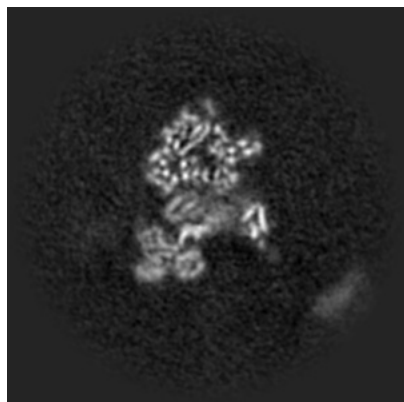


Z

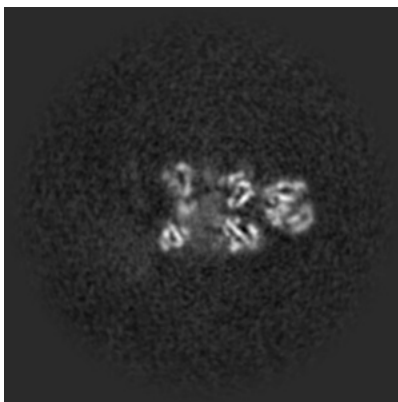
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

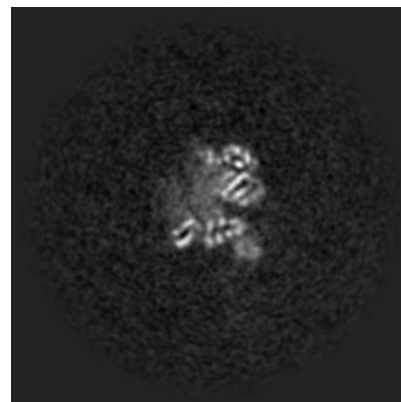
6.2.1 Primary map



X Index: 160

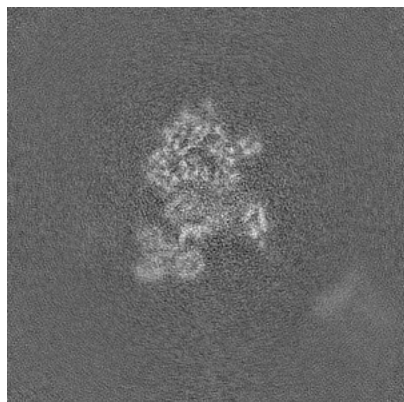


Y Index: 160

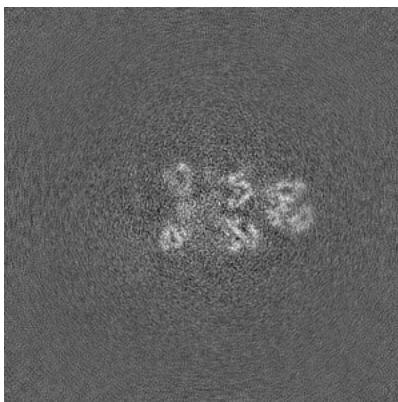


Z Index: 160

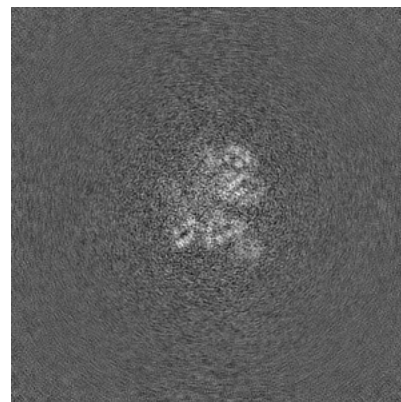
6.2.2 Raw map



X Index: 160



Y Index: 160

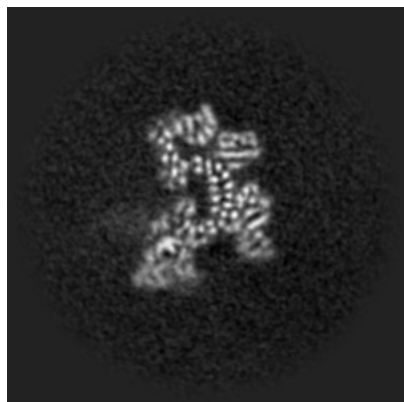


Z Index: 160

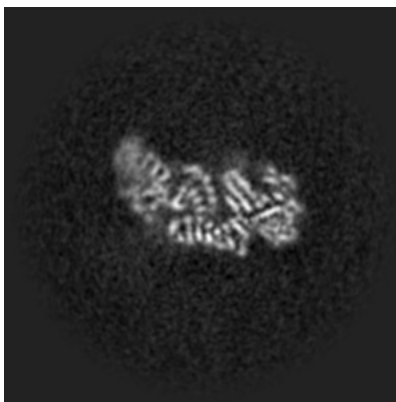
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

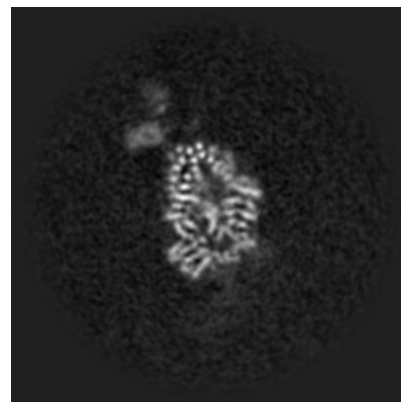
6.3.1 Primary map



X Index: 176

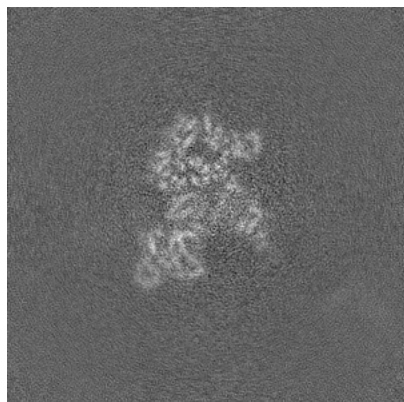


Y Index: 141

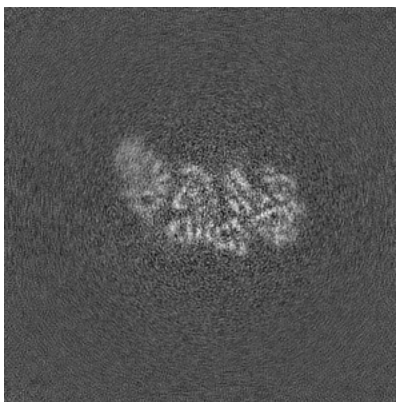


Z Index: 141

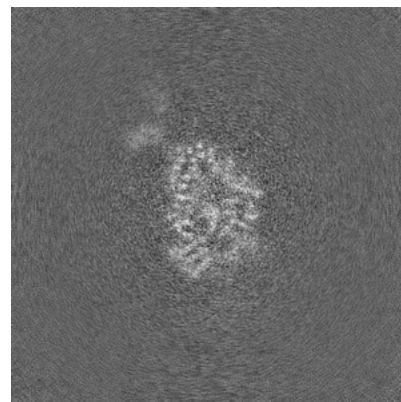
6.3.2 Raw map



X Index: 165



Y Index: 142

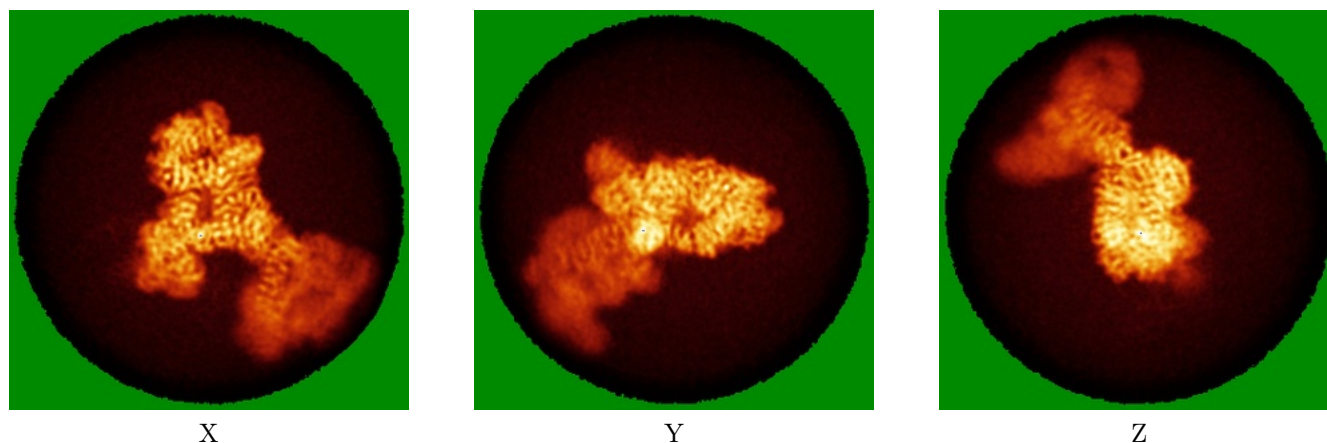


Z Index: 142

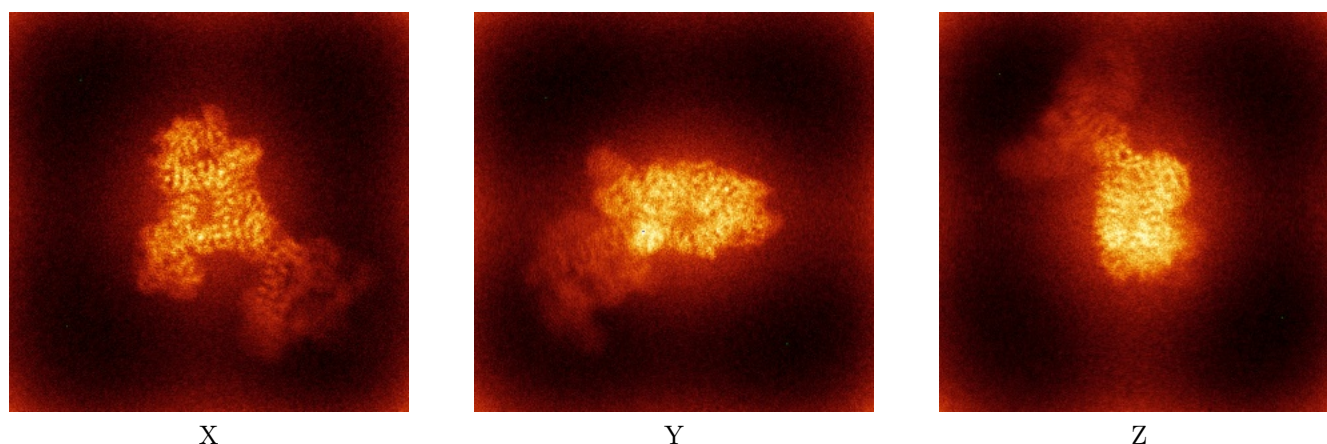
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

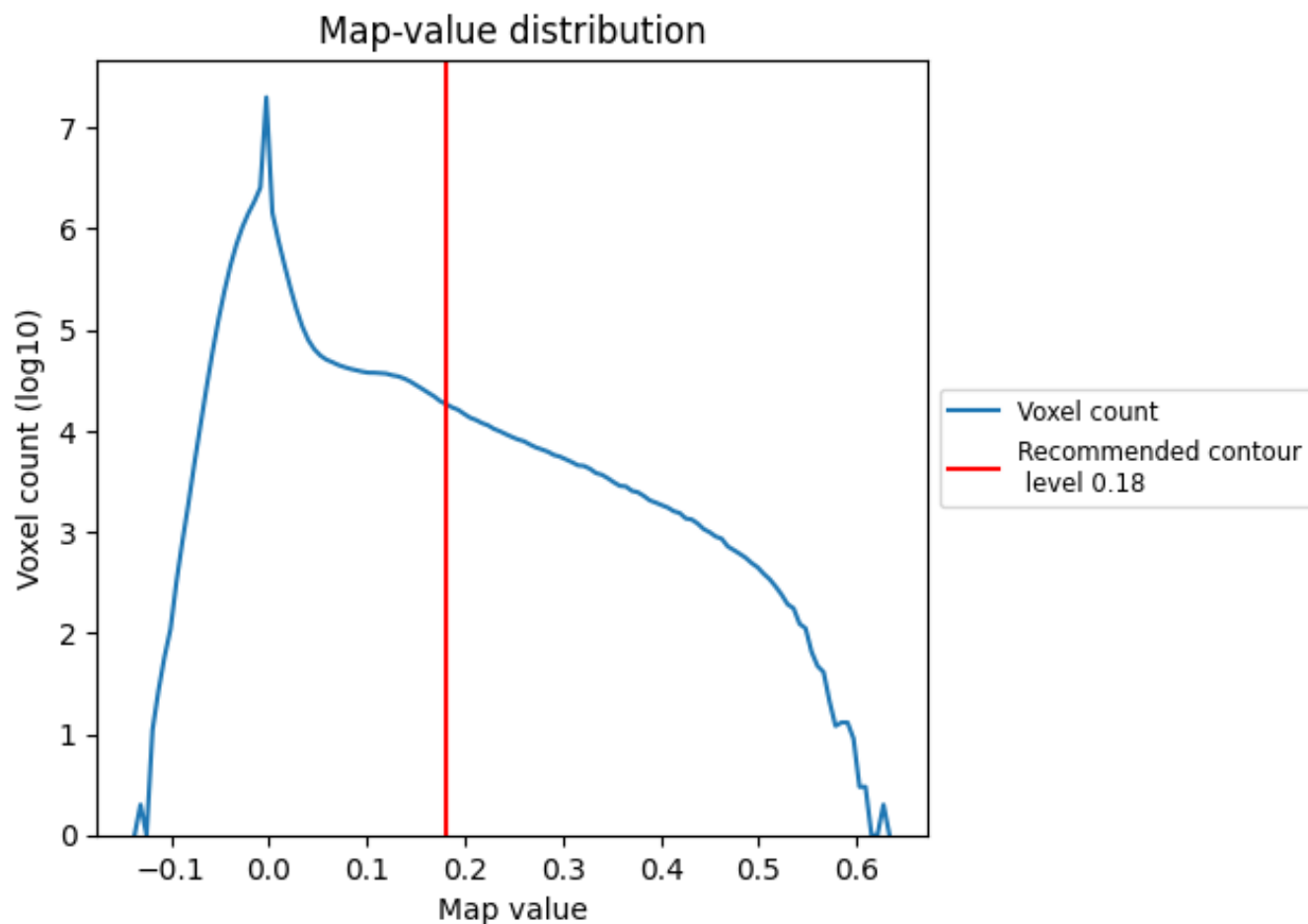
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

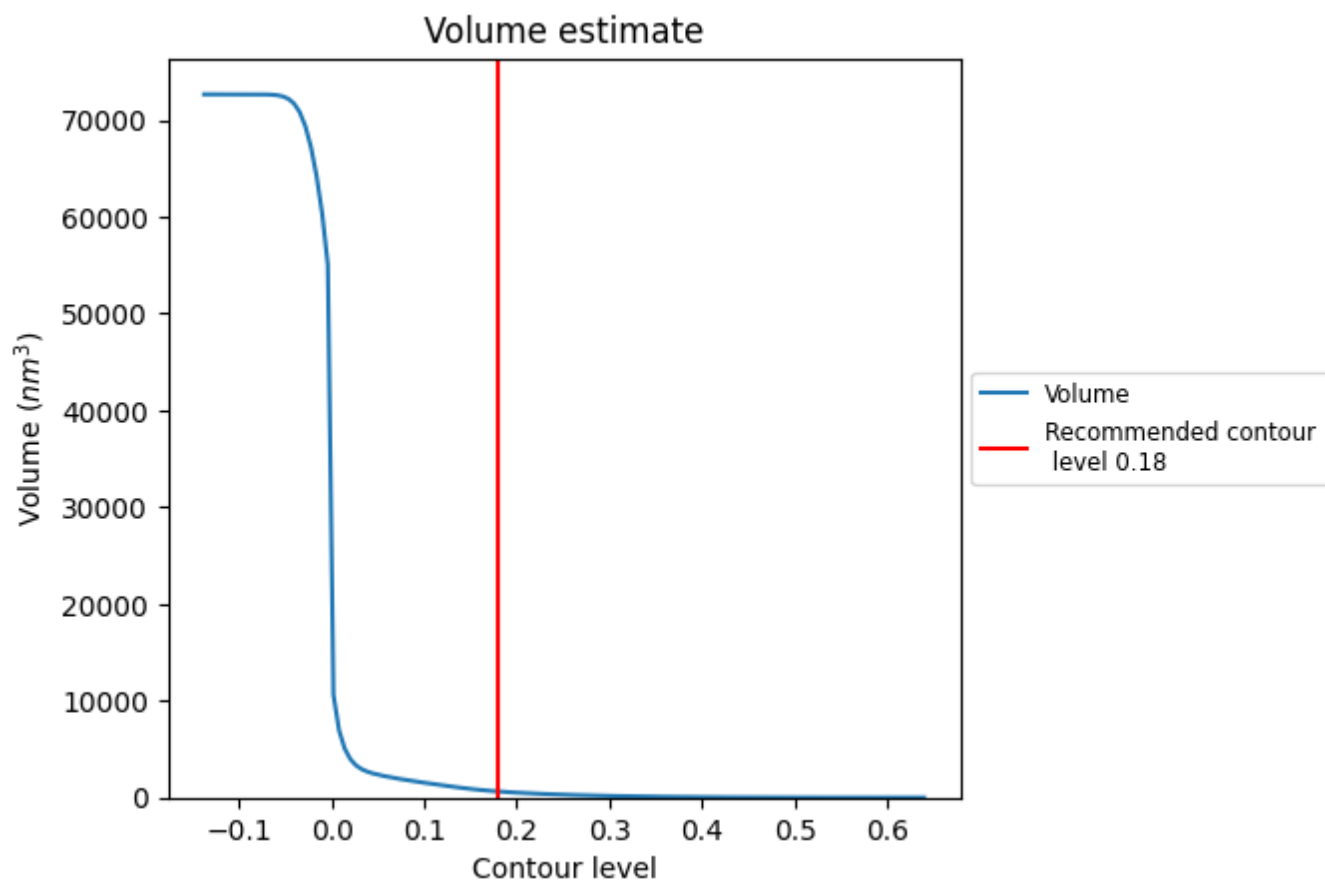
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

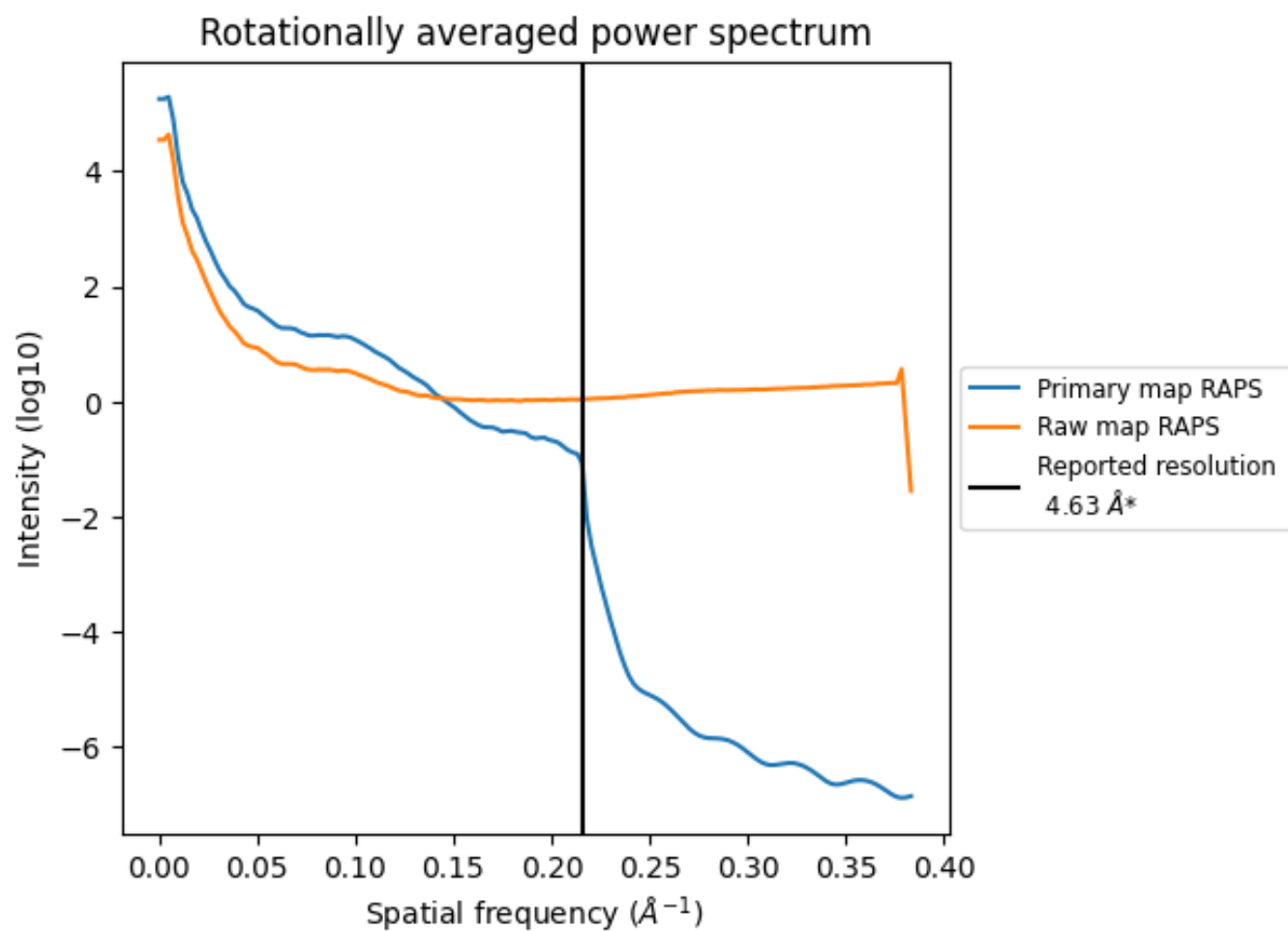
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 632 nm³; this corresponds to an approximate mass of 570 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 ⓘ

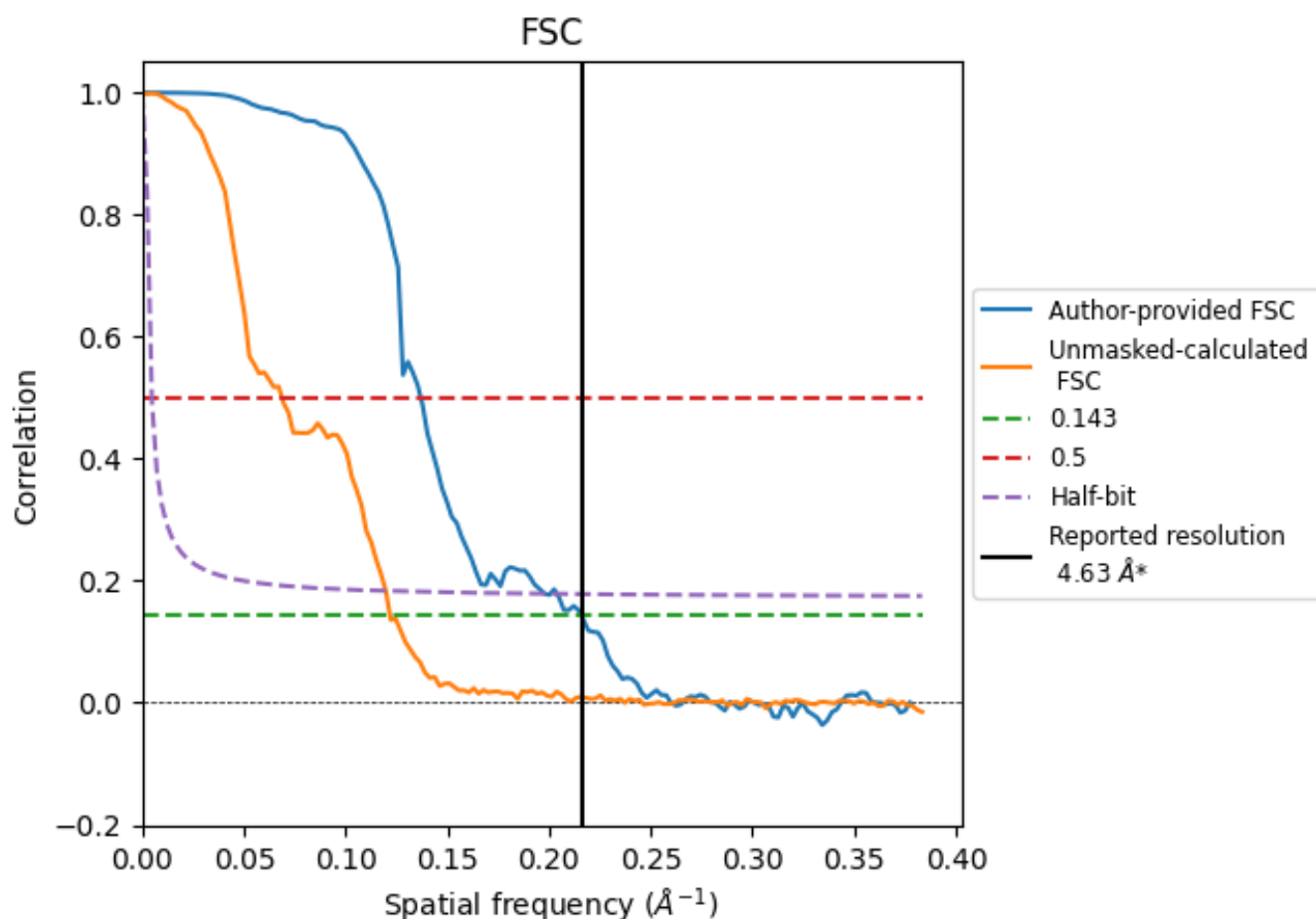


*Reported resolution corresponds to spatial frequency of 0.216 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.216 \AA^{-1}

8.2 Resolution estimates [i](#)

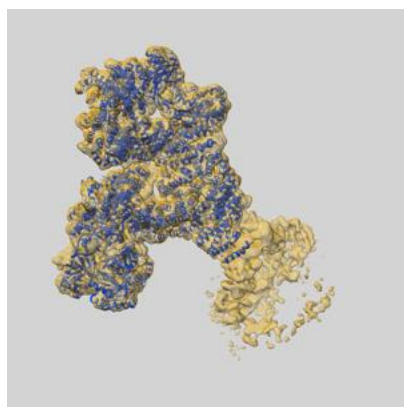
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.63	-	-
Author-provided FSC curve	4.63	7.30	5.05
Unmasked-calculated*	8.20	14.56	8.35

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.20 differs from the reported value 4.63 by more than 10 %

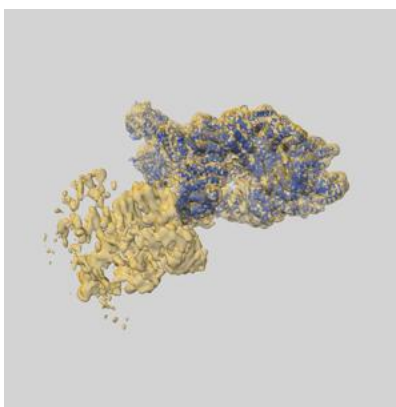
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51156 and PDB model 9G9L. Per-residue inclusion information can be found in section [3](#) on page [6](#).

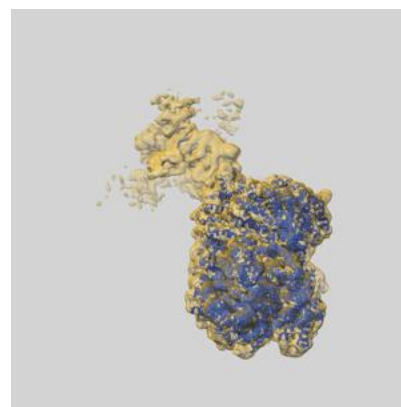
9.1 Map-model overlay [i](#)



X



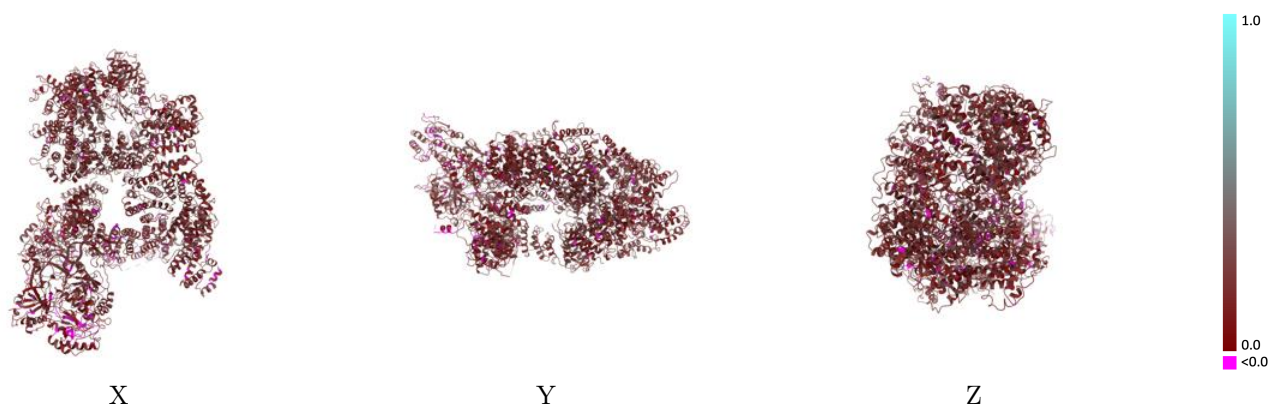
Y



Z

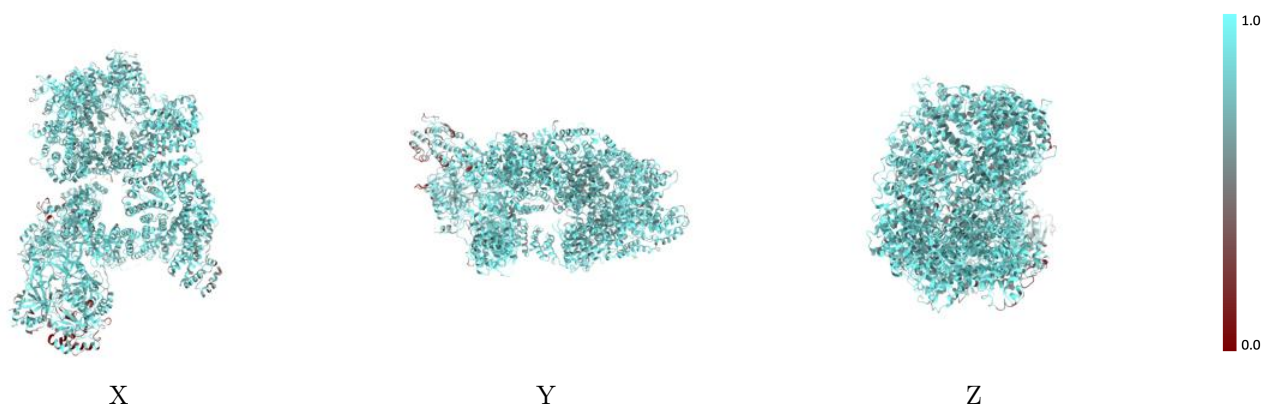
The images above show the 3D surface view of the map at the recommended contour level 0.18 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



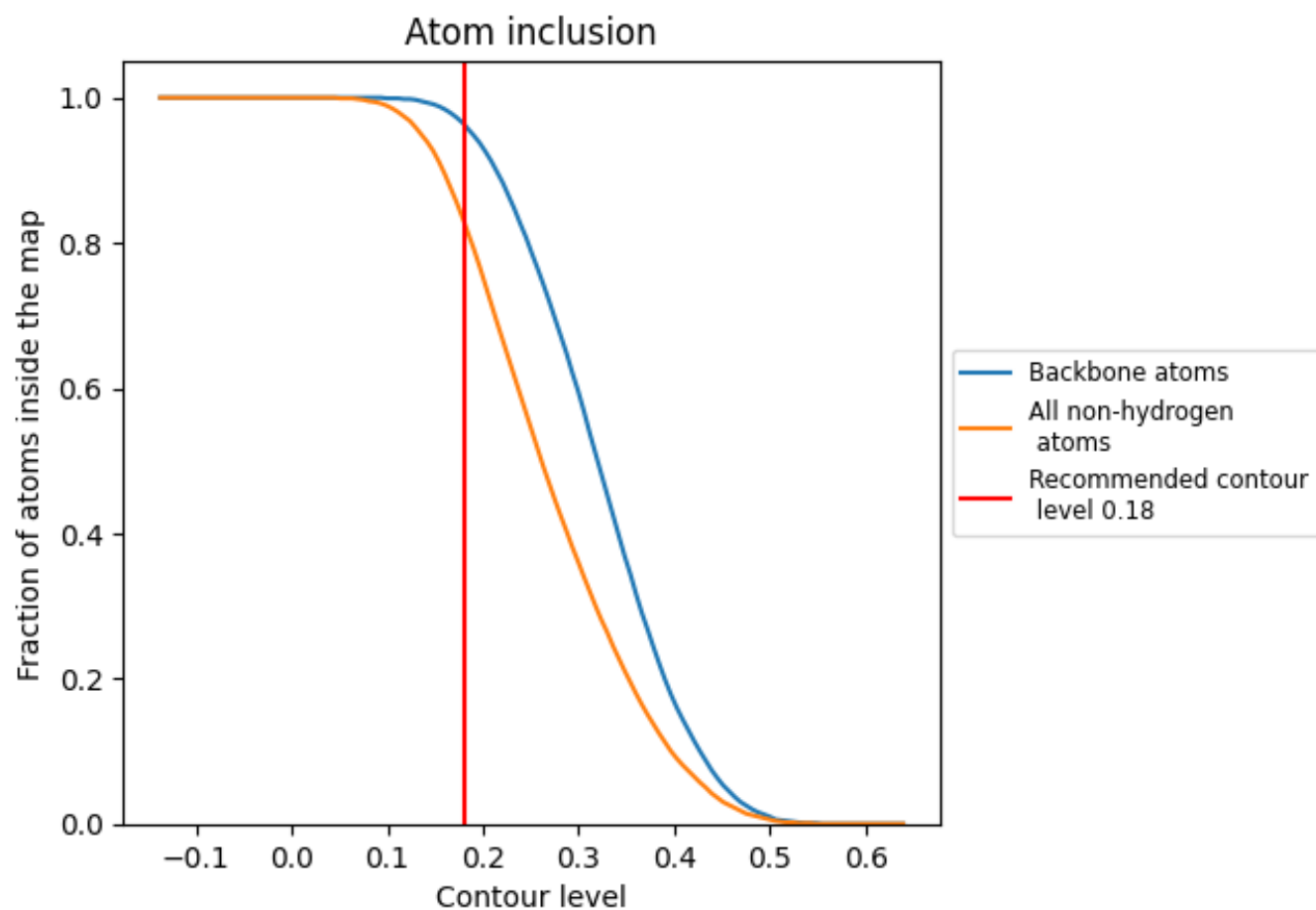
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.18).

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 (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8300</div>	<div><div></div>0.1880</div>
A	<div><div></div>0.8470</div>	<div><div></div>0.1930</div>
B	<div><div></div>0.8470</div>	<div><div></div>0.1870</div>
C	<div><div></div>0.7270</div>	<div><div></div>0.1580</div>
D	<div><div></div>0.9570</div>	<div><div></div>0.2320</div>
E	<div><div></div>0.9410</div>	<div><div></div>0.2140</div>
F	<div><div></div>0.6190</div>	<div><div></div>0.1540</div>
M	<div><div></div>0.8520</div>	<div><div></div>0.2220</div>

1.0

0.0

<0.0