



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 06:50 PM UTC

PDB ID : 8WYD / pdb_00008wyd
EMDB ID : EMD-37924
Title : Cryo-EM structure of DSR2-DSAD1 complex
Authors : Zhang, J.T.; Jia, N.; Liu, X.Y.
Deposited on : 2023-10-30
Resolution : 2.56 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:

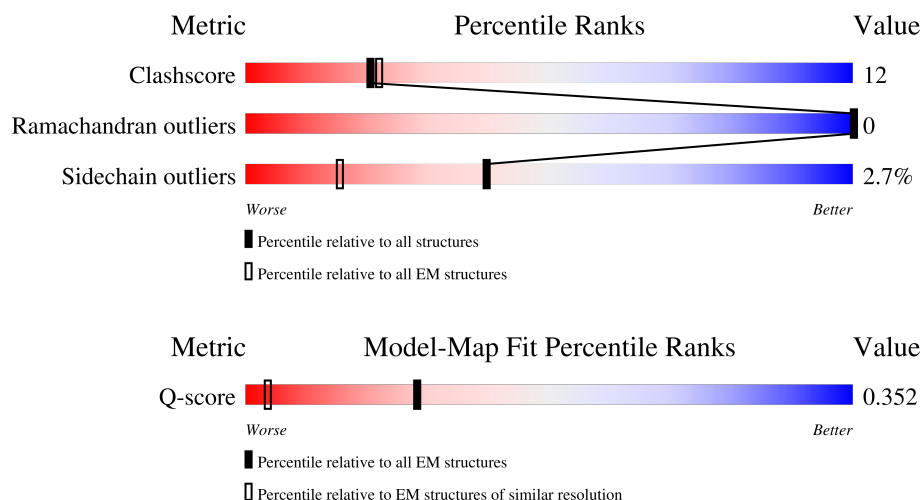
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.56 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	7558 (2.06 - 3.06)

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	1005	
1	B	1005	
1	C	1005	
1	D	1005	

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Mol	Chain	Length	Quality of chain
2	E	146	
2	F	146	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 33765 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 SIR2 family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	953	Total	C	N	O	S	0	0
			7964	5163	1285	1484	32		
1	B	953	Total	C	N	O	S	0	0
			7966	5162	1288	1486	30		
1	C	952	Total	C	N	O	S	0	0
			7955	5157	1283	1483	32		
1	D	953	Total	C	N	O	S	0	0
			7966	5162	1288	1486	30		

- Molecule 2 is a protein called Bacillus phage SPbeta DSAD1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	116	Total	C	N	O	S	0	0
			957	625	154	175	3		
2	F	116	Total	C	N	O	S	0	0
			957	625	154	175	3		

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	121	TRP	-	expression tag	UNP O64191
E	122	SER	-	expression tag	UNP O64191
E	123	HIS	-	expression tag	UNP O64191
E	124	PRO	-	expression tag	UNP O64191
E	125	GLN	-	expression tag	UNP O64191
E	126	PHE	-	expression tag	UNP O64191
E	127	GLU	-	expression tag	UNP O64191
E	128	LYS	-	expression tag	UNP O64191
E	129	GLY	-	expression tag	UNP O64191
E	130	GLY	-	expression tag	UNP O64191
E	131	GLY	-	expression tag	UNP O64191
E	132	SER	-	expression tag	UNP O64191
E	133	GLY	-	expression tag	UNP O64191

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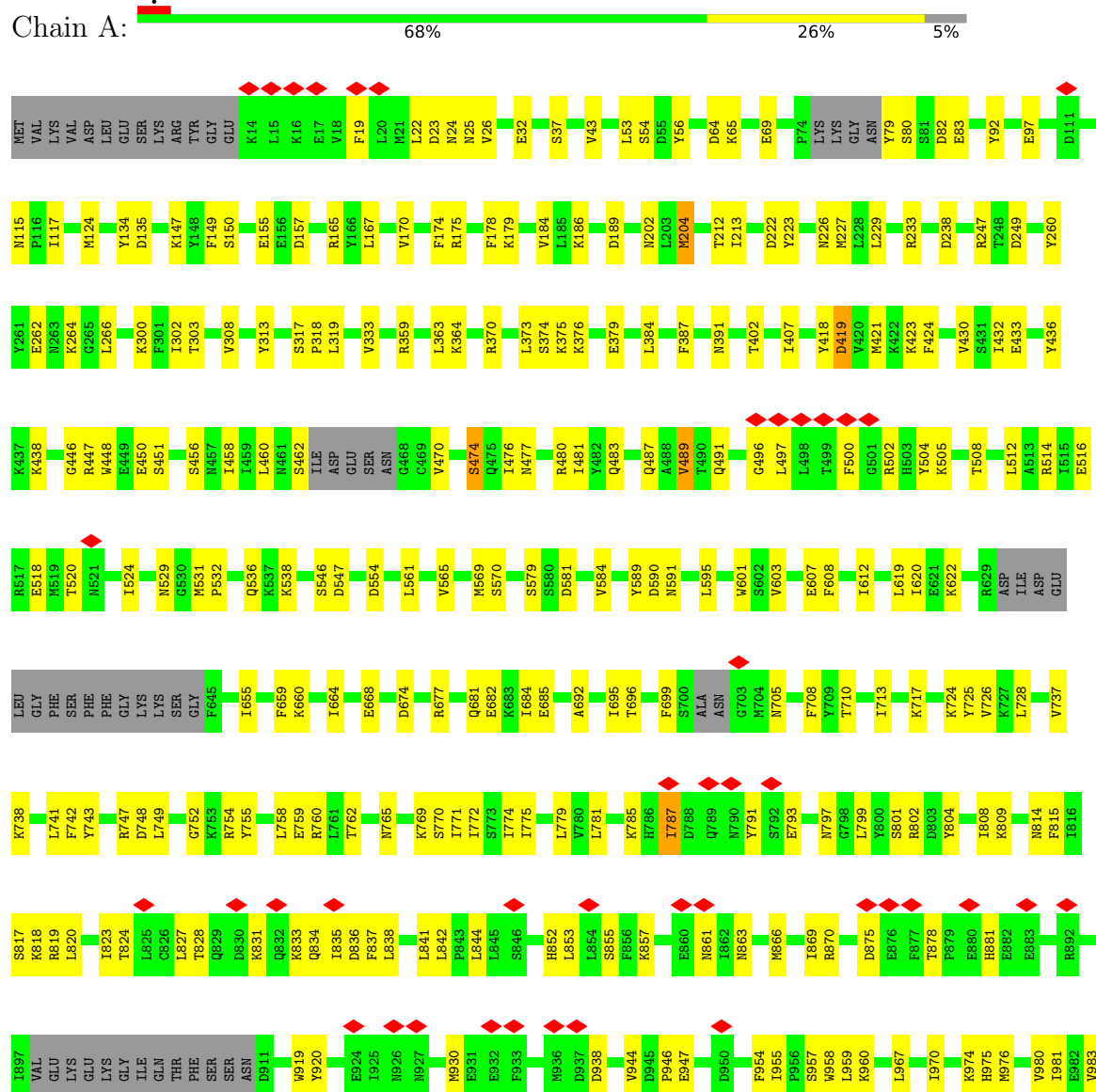
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Chain	Residue	Modelled	Actual	Comment	Reference
E	134	GLY	-	expression tag	UNP O64191
E	135	GLY	-	expression tag	UNP O64191
E	136	SER	-	expression tag	UNP O64191
E	137	GLY	-	expression tag	UNP O64191
E	138	GLY	-	expression tag	UNP O64191
E	139	TRP	-	expression tag	UNP O64191
E	140	SER	-	expression tag	UNP O64191
E	141	HIS	-	expression tag	UNP O64191
E	142	PRO	-	expression tag	UNP O64191
E	143	GLN	-	expression tag	UNP O64191
E	144	PHE	-	expression tag	UNP O64191
E	145	GLU	-	expression tag	UNP O64191
E	146	LYS	-	expression tag	UNP O64191
F	121	TRP	-	expression tag	UNP O64191
F	122	SER	-	expression tag	UNP O64191
F	123	HIS	-	expression tag	UNP O64191
F	124	PRO	-	expression tag	UNP O64191
F	125	GLN	-	expression tag	UNP O64191
F	126	PHE	-	expression tag	UNP O64191
F	127	GLU	-	expression tag	UNP O64191
F	128	LYS	-	expression tag	UNP O64191
F	129	GLY	-	expression tag	UNP O64191
F	130	GLY	-	expression tag	UNP O64191
F	131	GLY	-	expression tag	UNP O64191
F	132	SER	-	expression tag	UNP O64191
F	133	GLY	-	expression tag	UNP O64191
F	134	GLY	-	expression tag	UNP O64191
F	135	GLY	-	expression tag	UNP O64191
F	136	SER	-	expression tag	UNP O64191
F	137	GLY	-	expression tag	UNP O64191
F	138	GLY	-	expression tag	UNP O64191
F	139	TRP	-	expression tag	UNP O64191
F	140	SER	-	expression tag	UNP O64191
F	141	HIS	-	expression tag	UNP O64191
F	142	PRO	-	expression tag	UNP O64191
F	143	GLN	-	expression tag	UNP O64191
F	144	PHE	-	expression tag	UNP O64191
F	145	GLU	-	expression tag	UNP O64191
F	146	LYS	-	expression tag	UNP O64191

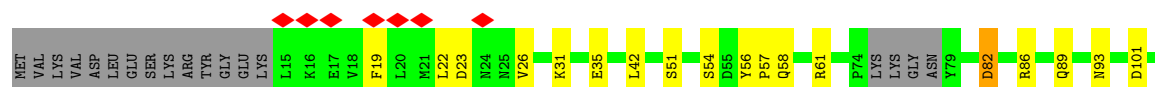
3 Residue-property plots

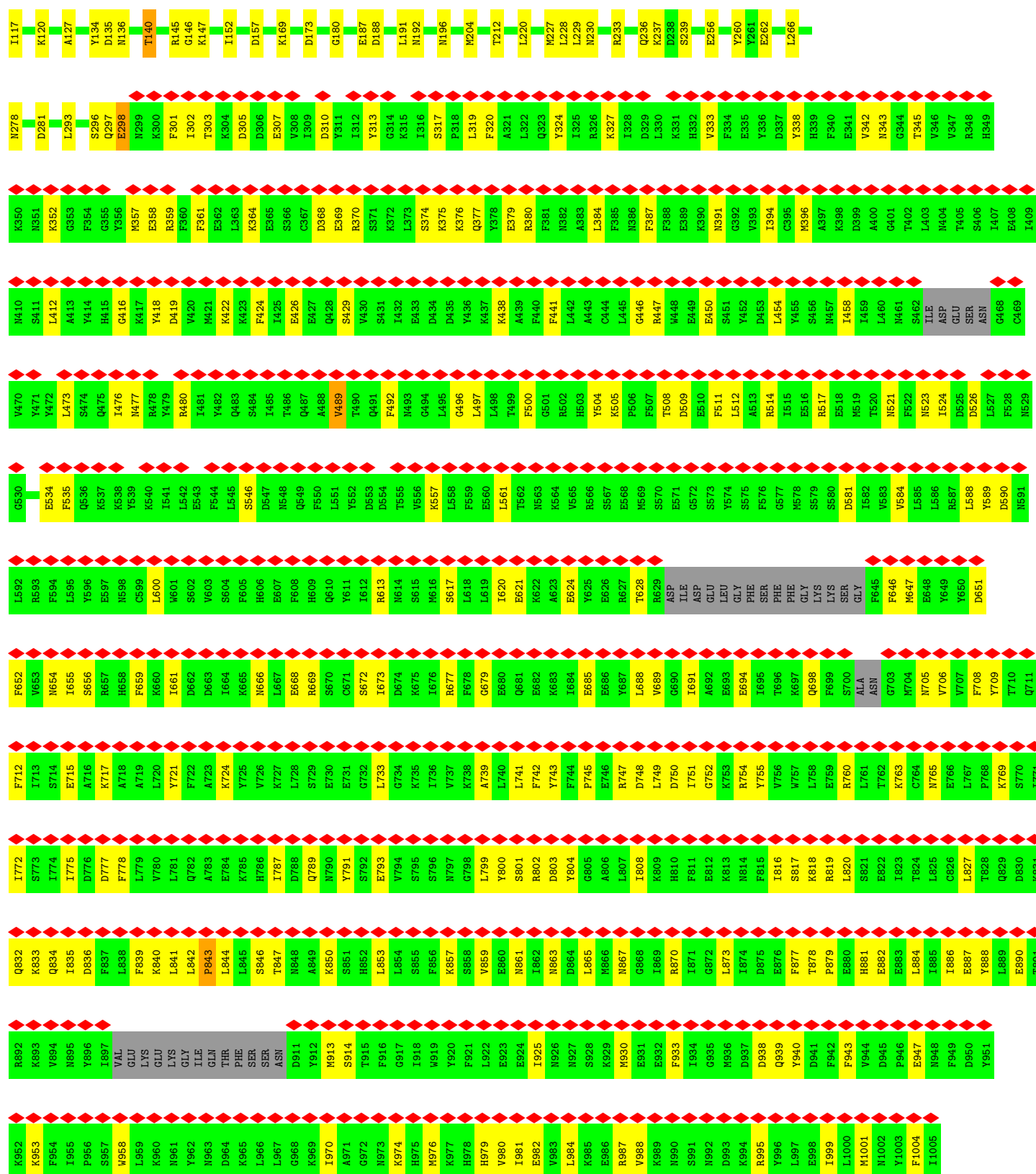
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: SIR2 family protein



Chain B: 69% 25% 5%



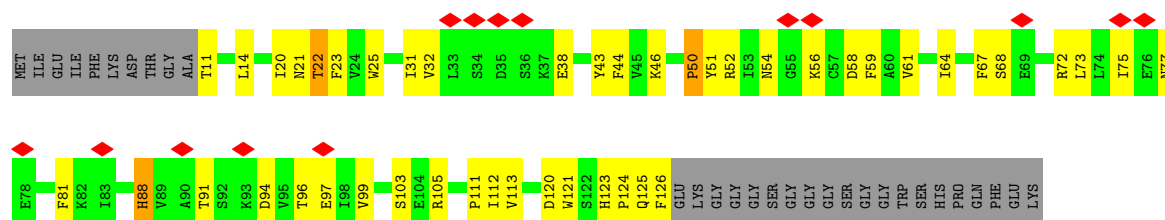


- Molecule 1: SIR2 family protein

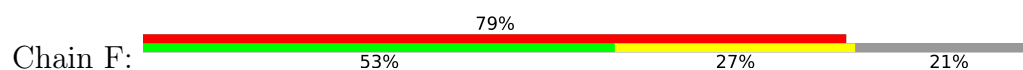


MET	VAL	LYS	VAL	ASP	LEU	GLU	S8	K9	R10	Y11	G12	E13	K14	L15	K16	E17	V18	F19	L20	M21	L22	D23	N24	N25	V26	C29	I30	I33	S37	R38	V43	G47	Y56	P74	LYS	LYS	GLY	ASN	Y79	Y84	Y94	K95	P116	K120	A123	M124															
M133	Y134	D135	N136	L137	I138	D139	T140	R145	G146	K147	Y148	F149	S150	V151	S163	S164	R165	K169	V170	R175	V183	D188	M204	I213	L220	N230	R233	P250	S251	E256	I259	D270	S273	L274	Y282	R285	Y286	S287	M290	D291																					
L292	L293	I294	E295	S296	Q297	E298	N299	K300	F301	I302	T303	K304	D305	D306	E307	V308	I309	D310	Y311	I312	Y313	G314	K315	I316	S317	P318	L319	F320	A321	L322	Q323	Y324	I325	R326	K327	I328	D329	L330	K331	H332	V333	F334	E335	Y336	D337	Y338	H339	F340	E341	V342	N343	G344	T345	V346	V347	R348	H349	K350	N351		
K352	G353	F354	G355	G356	G357	M357	E358	R359	F360	F361	E362	L363	K364	E365	S366	C367	D368	R369	R370	I371	S371	K372	L373	S374	K375	K376	Q377	Y378	E379	R380	F381	N382	A383	L384	F385	N386	F387	F388	E389	K390	N391	G392	G393	I394	C395	M396	A397	K398	D399	A400	G401	T402	L403	M404	T405	S406	I407	E408	I409	M410	S411
L412	A413	Y414	H415	G416	K417	Y418	D419	Y479	V420	M421	K422	K423	F424	I425	E426	E427	Q428	S429	V430	S431	I432	E433	D434	D435	Y436	K437	K438	A439	F440	F441	L442	A443	C444	L445	G446	R447	W448	E449	E450	S451	Y452	D453	L454	Y455	S456	M457	I458	T459	L460	M461	S462	I463	ASP	GLU	SER	N467	G468	C469	V470	Y471	
Y472	L473	S474	Q475	I476	M477	R478	Y479	R480	I481	Y482	Q483	S484	I485	T486	Q487	A488	V489	T490	Q491	F492	M493	G494	L495	GLY	LEU	LEU	THR	PHE	G501	R502	H503	Y504	A443	K505	P506	F507	T508	D509	E510	F511	L512	A513	R514	I515	E516	R517	E518	M519	T520	N521	F522	N523	I524	D525	D526	L527	F528	N529	M531		
F532	F533	K537	K540	I541	L542	E543	F544	L545	S546	D547	N548	Q549	F550	L551	Y552	D553	D554	T555	V556	L557	L558	F559	E560	L561	T562	N563	K564	V565	ARG	SER	GLU	MET	SER	GLU	GLY	SER	TYR	PHE	GLY	MET	S579	S580	D581	L582	V583	V584	L585	L586	R587	L588	Y589	D590	E591	L592	R593	F594					
L595	Y596	E597	N598	C599	L600	M601	S602	S603	S604	F605	H606	E607	F608	H609	Q610	Y611	R612	R613	N614	S615	M616	S617	L618	L619	I620	E621	K622	A623	H603	Y625	E626	R627	T628	R629	D630	I631	D632	E633	L634	Q635	P636	SER	PHE	PHE	GLY	LYS	SER	G644	F645	F646	M647	E648	Y649	V650	D651	F652	V653	N654			
I655	S656	R657	H658	F659	K660	I661	D662	D663	I664	K665	N666	L667	E668	R669	Q670	C671	S672	I673	L674	K675	I676	R677	F678	Q679	E680	Q681	E682	K683	I684	E685	E686	Y687	L688	V689	G690	I691	A692	E693	E694	I695	T696	K697	Q698	F699	S700	A701	N702	G703	M704	N705	V706	V707	F708	Y709	T710	Q711	I712	I713	S714		
E715	A716	K717	A718	A719	L720	Y721	F722	A723	Y725	V726	K727	L728	S729	E730	E731	G732	L733	G734	K735	L736	V737	K738	A739	L740	L741	F742	F743	F744	P745	E746	R747	D748	L749	D750	I751	G752	K753	R754	Y755	V756	W757	L758	E759	R760	L761	T762	K763	C764	N765	E766	L767	P768	K769	S770	I771	S772	S773	I774			
I775	D776	D777	F778	L779	V780	L781	Q782	E783	E784	K785	H786	I787	D788	Q789	N790	Y791	S792	E793	V794	S795	S796	N797	G798	L799	Y800	S801	R802	D803	Y804	G805	A806	L807	I808	K809	H810	F811	E812	R813	N814	F815	T816	S817	K818	R819	L820	S821	E822	L823	T824	L825	C826	L827	T828	Q829	D830	K831	Q832	K833	Q834		
I835	D836	F837	L838	F839	K840	L841	L842	P843	L844	L845	S846	T847	H848	A849	K850	S851	H852	L853	L854	S855	F856	K857	S858	H859	E860	H861	I862	H863	L864	L865	S866	H867	G868	L869	N890	R870	I871	G872	L873	L874	D875	E876	F877	T878	F879	E880	H881	E882	S883	L884	I885	I886	E887	D888	L889	K952	E890	T891	R892	K893	V894
M895	Y896	I897	VAL	GLU	GLY	GLU	LYS	GLY	ILE	THR	PHE	SER	SER	ASN	D911	Y912	N913	S914	T915	F916	G917	V918	Y919	Y920	F921	L922	E923	E924	I925	N926	N927	S928	K929	N930	E931	E932	F933	G935	N936	D937	D938	Q939	Y940	D941	F942	F943	Y944	D945	P946	E947	N948	F949	D950	Y951	K952	K953	F954				
I955	P956	S957	Q958	L959	K960	N961	Y962	N963	D964	K965	L966	L967	G968	K969	I970	S971	G972	N973	K974	H975	M976	K977	H978	H979	Y980	I981	E982	V983	L984	K985	S986	N987	E988	E989	N990	F991	G992	D993	K994	K995	L996	E997	I998	I999	L1000	M1001	N1002	Y1003	F1004	I1005											

● Molecule 2: Bacillus phage SPbeta DSAD1 protein



● Molecule 2: Bacillus phage SPbeta DSAD1 protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	101402	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.225	Depositor
Minimum map value	-2.195	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.070	Depositor
Recommended contour level	0.4	Depositor
Map size ($\text{\AA}$)	463.12003, 463.12003, 463.12003	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.827, 0.827, 0.827	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	0.14	0/8148	0.31	0/10973
1	B	0.15	0/8148	0.33	0/10973
1	C	0.16	1/8139 (0.0%)	0.36	5/10962 (0.0%)
1	D	0.14	0/8148	0.31	0/10973
2	E	0.15	0/983	0.42	1/1333 (0.1%)
2	F	0.12	0/983	0.32	0/1333
All	All	0.15	1/34549 (0.0%)	0.33	6/46547 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	745	PRO	CG-CD	-5.23	1.32	1.50

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	843	PRO	CA-N-CD	-12.23	94.88	112.00
1	C	745	PRO	N-CD-CG	-9.97	88.24	103.20
2	E	50	PRO	CA-N-CD	-6.43	103.00	112.00
1	C	745	PRO	CA-CB-CG	-5.79	93.50	104.50
1	C	745	PRO	CA-N-CD	-5.65	104.09	112.00

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	7964	0	7812	189	0
1	B	7966	0	7811	187	0
1	C	7955	0	7799	192	0
1	D	7966	0	7811	203	0
2	E	957	0	942	41	0
2	F	957	0	942	31	0
All	All	33765	0	33117	806	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 12.

The worst 5 of 806 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:E:52:ARG:HH21	2:E:54:ASN:HA	1.32	0.93
1:C:297:GLN:NE2	1:D:521:ASN:HD21	1.74	0.85
1:C:297:GLN:NE2	1:D:521:ASN:ND2	2.25	0.83
2:F:88:HIS:HD2	2:F:91:THR:H	1.25	0.83
1:C:772:ILE:HD11	1:C:808:ILE:HG23	1.62	0.81

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	941/1005 (94%)	925 (98%)	16 (2%)	0	100	100
1	B	939/1005 (93%)	921 (98%)	18 (2%)	0	100	100
1	C	940/1005 (94%)	928 (99%)	12 (1%)	0	100	100
1	D	939/1005 (93%)	921 (98%)	18 (2%)	0	100	100
2	E	114/146 (78%)	111 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F	114/146 (78%)	108 (95%)	6 (5%)	0	100	100
All	All	3987/4312 (92%)	3914 (98%)	73 (2%)	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	878/923 (95%)	853 (97%)	25 (3%)	38	54
1	B	877/923 (95%)	859 (98%)	18 (2%)	47	63
1	C	877/923 (95%)	856 (98%)	21 (2%)	43	59
1	D	877/923 (95%)	848 (97%)	29 (3%)	33	48
2	E	111/131 (85%)	108 (97%)	3 (3%)	39	55
2	F	111/131 (85%)	108 (97%)	3 (3%)	39	55
All	All	3731/3954 (94%)	3632 (97%)	99 (3%)	40	55

5 of 99 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	497	LEU
1	D	150	SER
1	C	588	LEU
1	C	981	ILE
1	D	274	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	549	GLN
1	D	927	ASN
1	C	606	HIS

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Mol	Chain	Res	Type
1	C	992	ASN
1	D	979	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](#)

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.

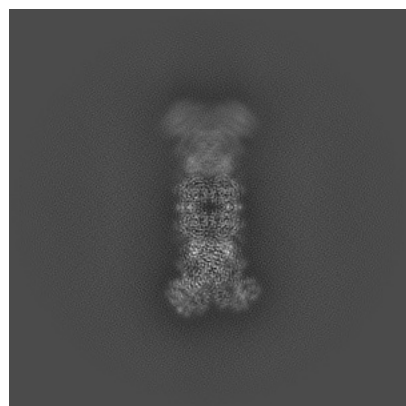
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37924. These allow visual inspection of the internal detail of the map and identification of artifacts.

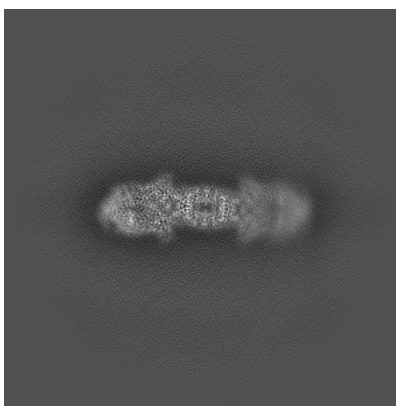
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

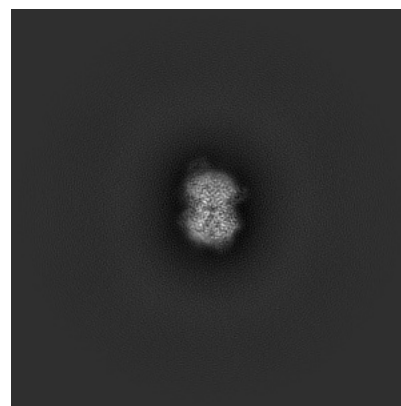
6.1.1 Primary map



X

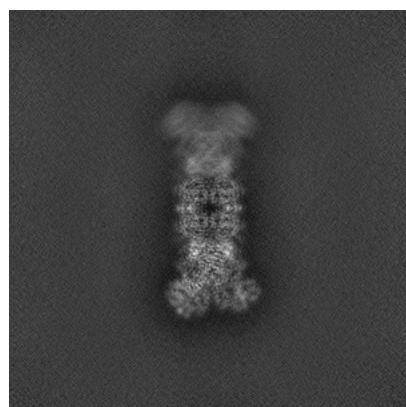


Y

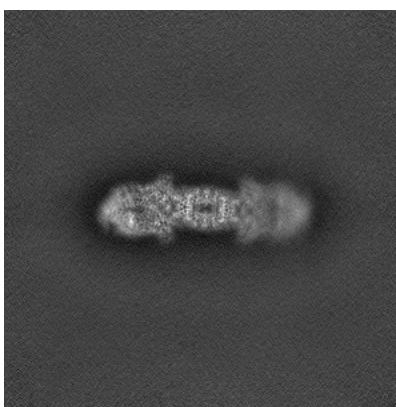


Z

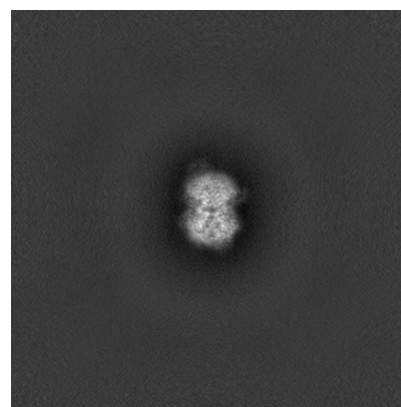
6.1.2 Raw map



X



Y

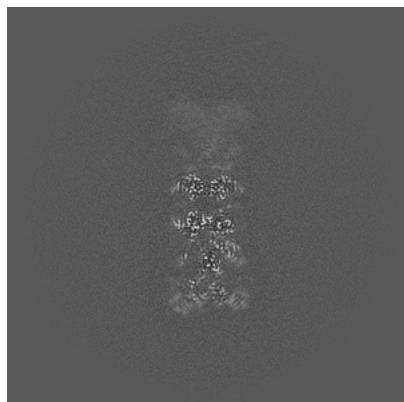


Z

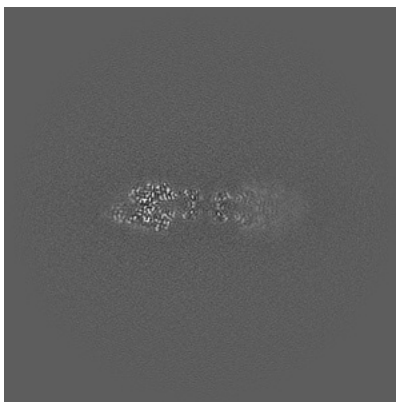
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

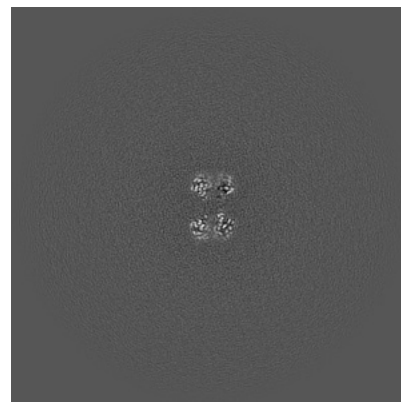
6.2.1 Primary map



X Index: 280

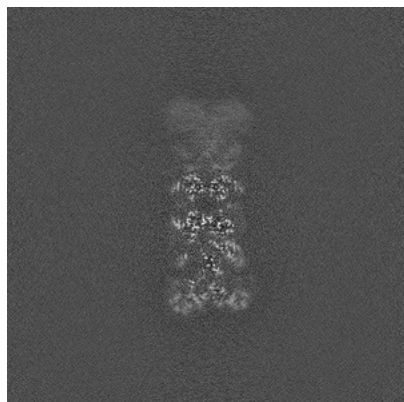


Y Index: 280

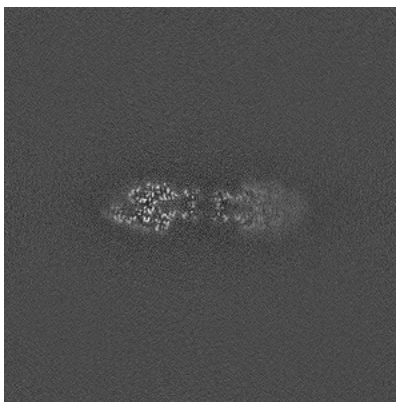


Z Index: 280

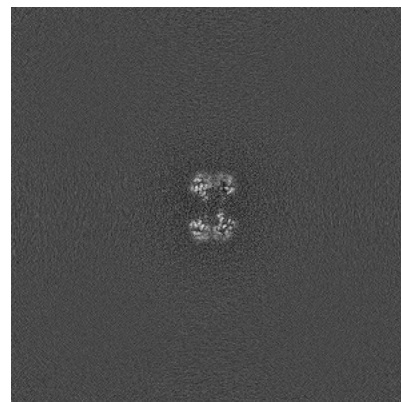
6.2.2 Raw map



X Index: 280



Y Index: 280

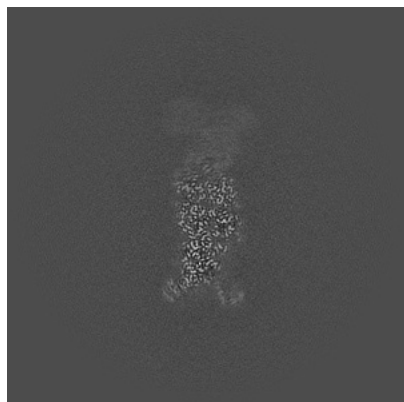


Z Index: 280

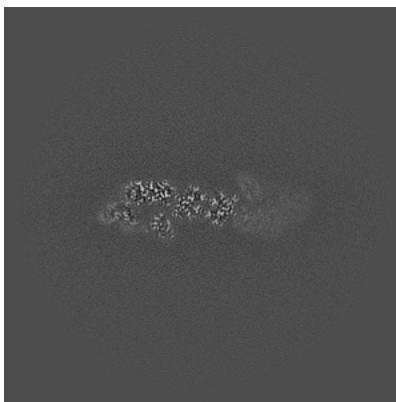
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

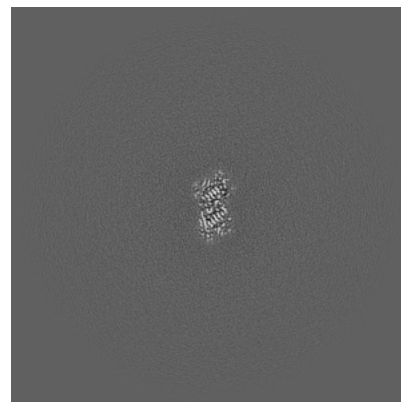
6.3.1 Primary map



X Index: 295

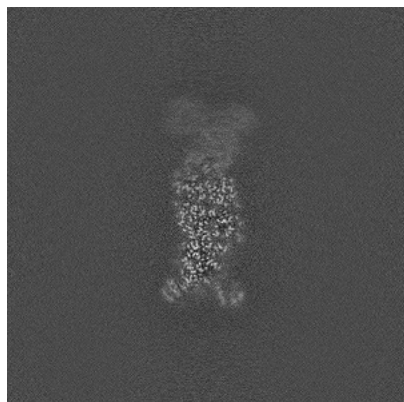


Y Index: 265

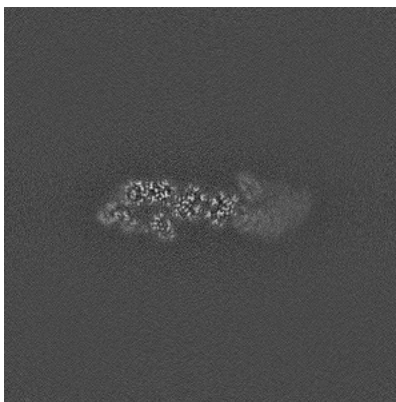


Z Index: 257

6.3.2 Raw map



X Index: 295



Y Index: 265

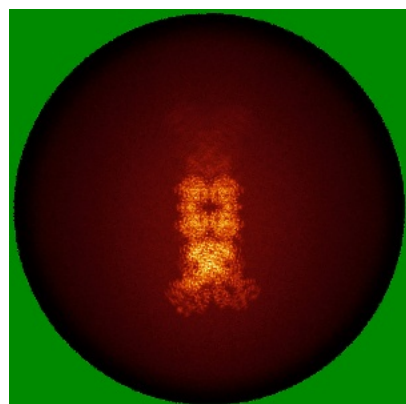


Z Index: 257

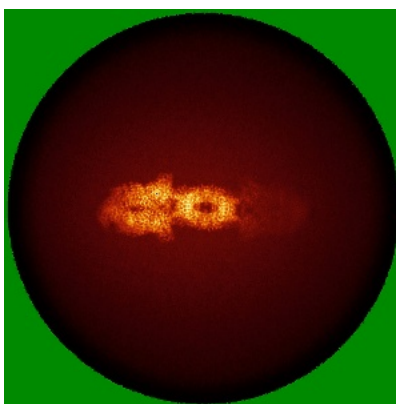
The images above show the largest variance slices of the map in three orthogonal directions.

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

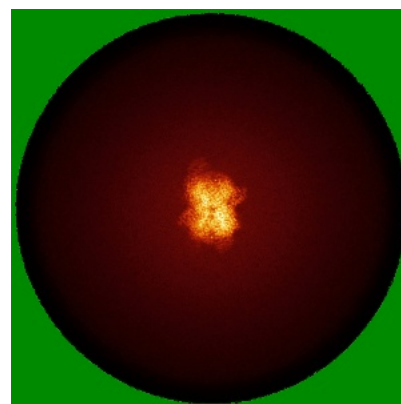
6.4.1 Primary map



X

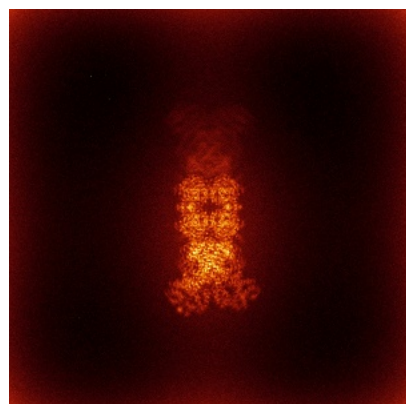


Y

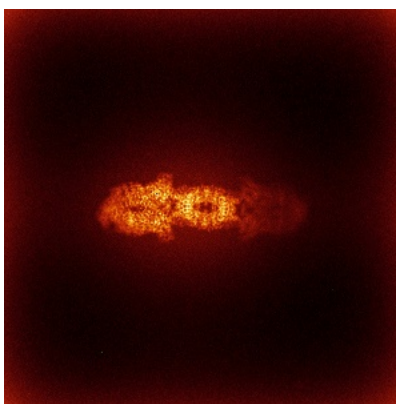


Z

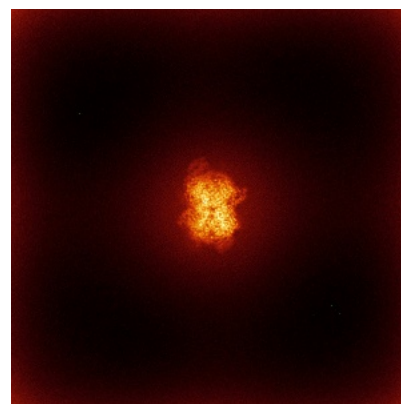
6.4.2 Raw map



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](#)

This section was not generated.

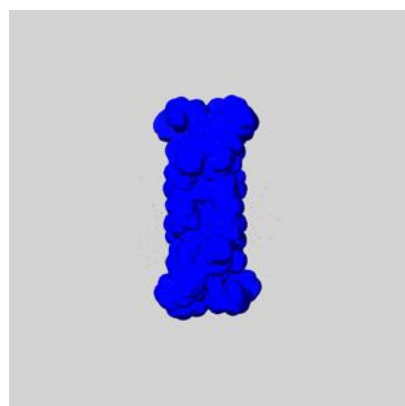
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

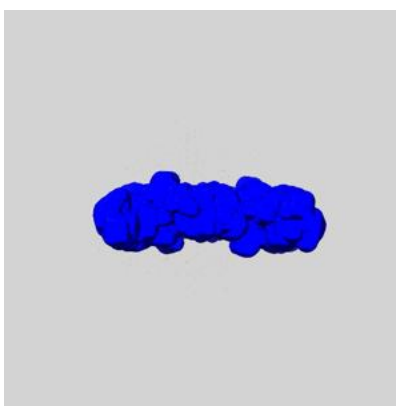
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

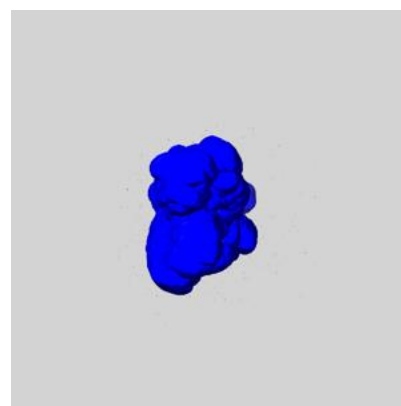
6.6.1 emd_37924_msk_1.map [i](#)



X



Y

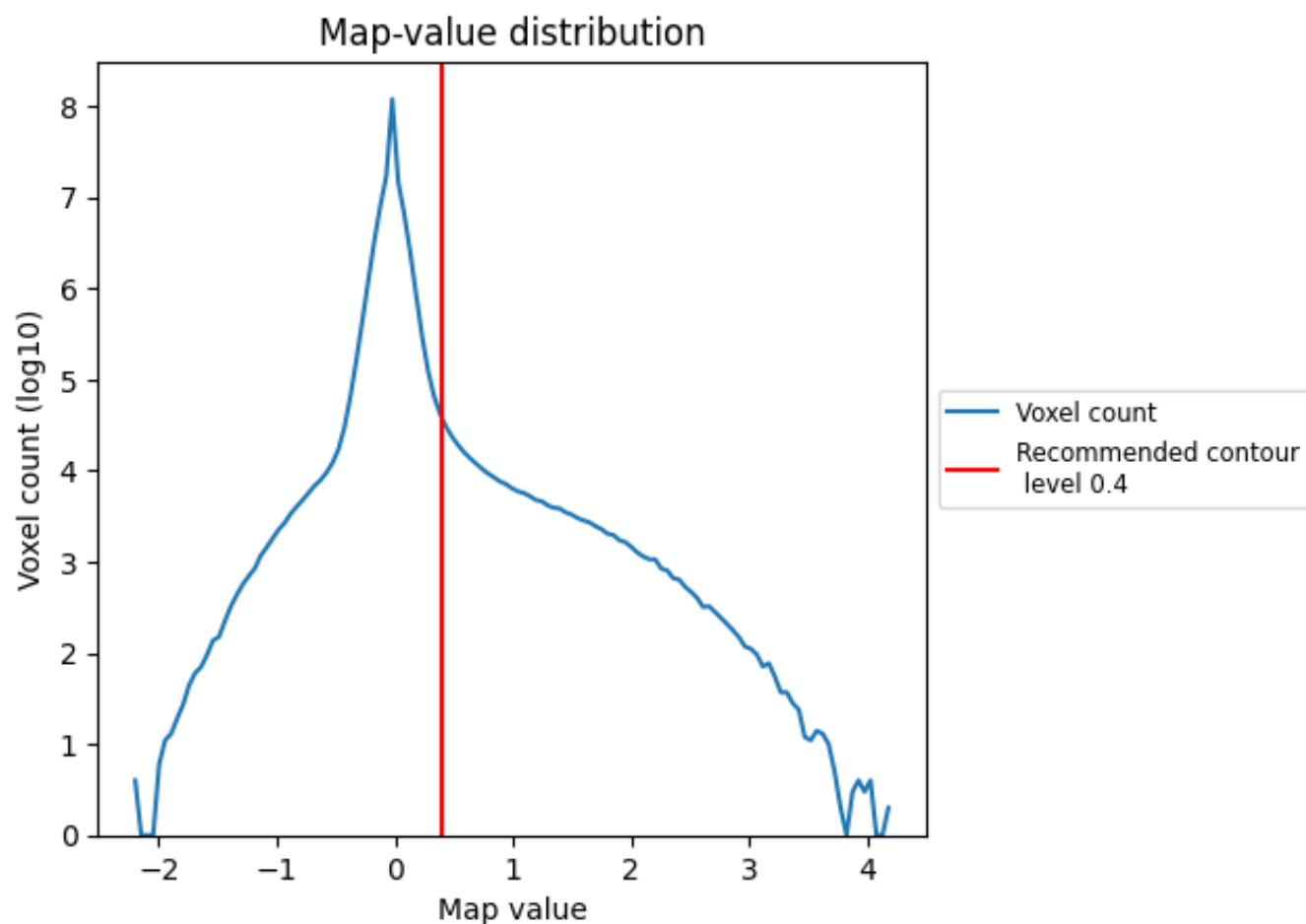


Z

7 Map analysis [i](#)

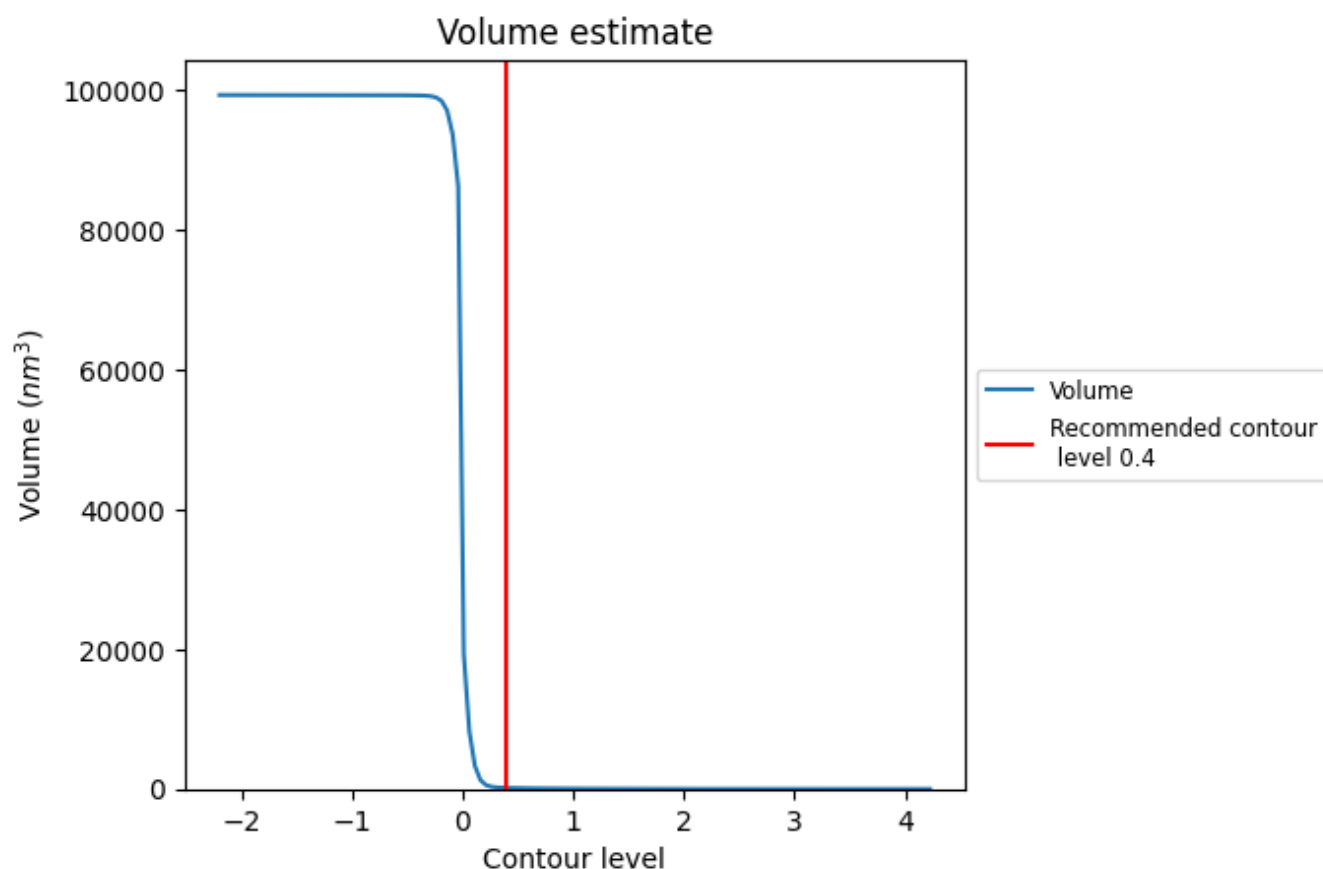
This section contains the results of statistical analysis of the map.

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.

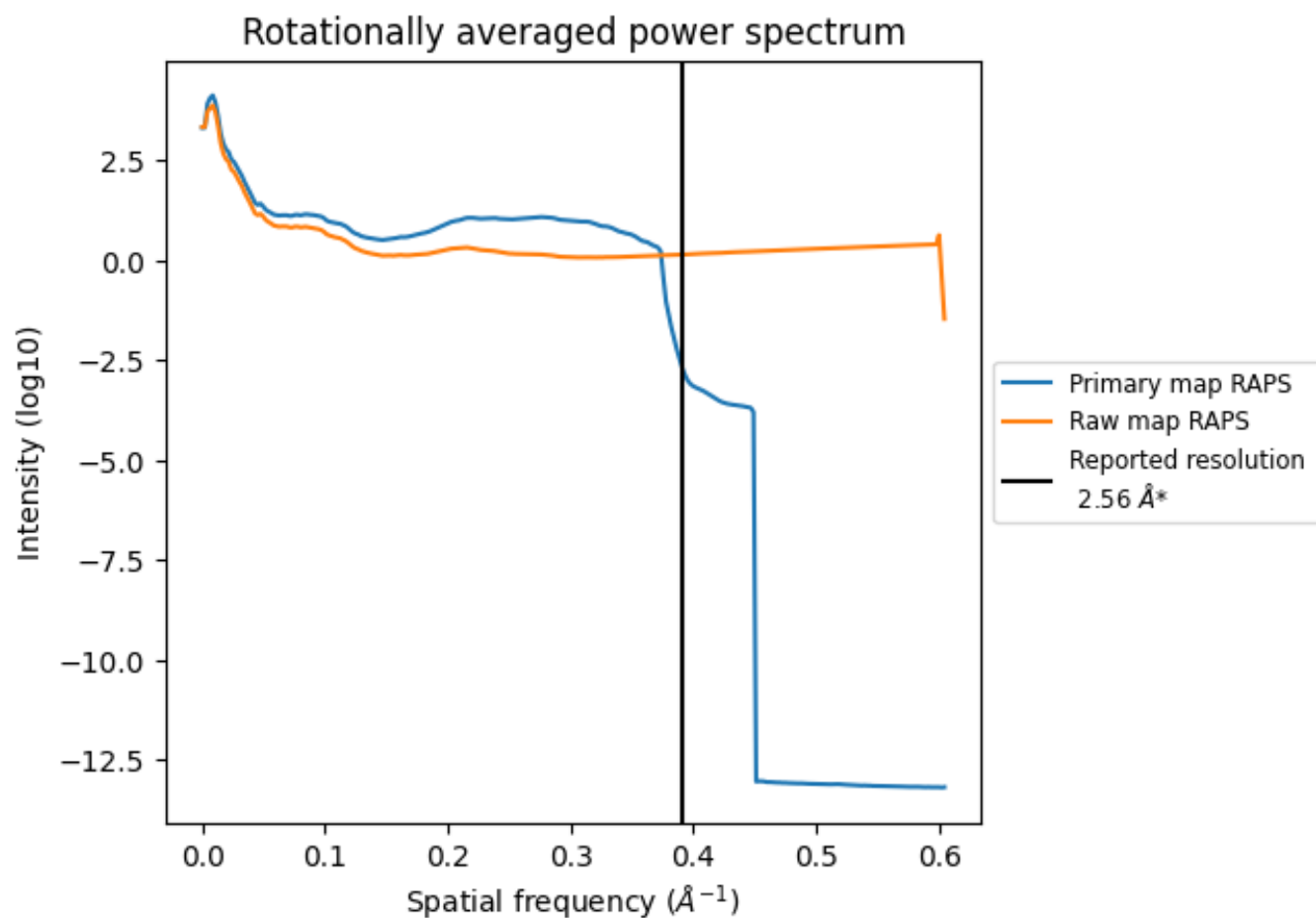
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 153 nm^3 ; this corresponds to an approximate mass of 138 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 ⓘ

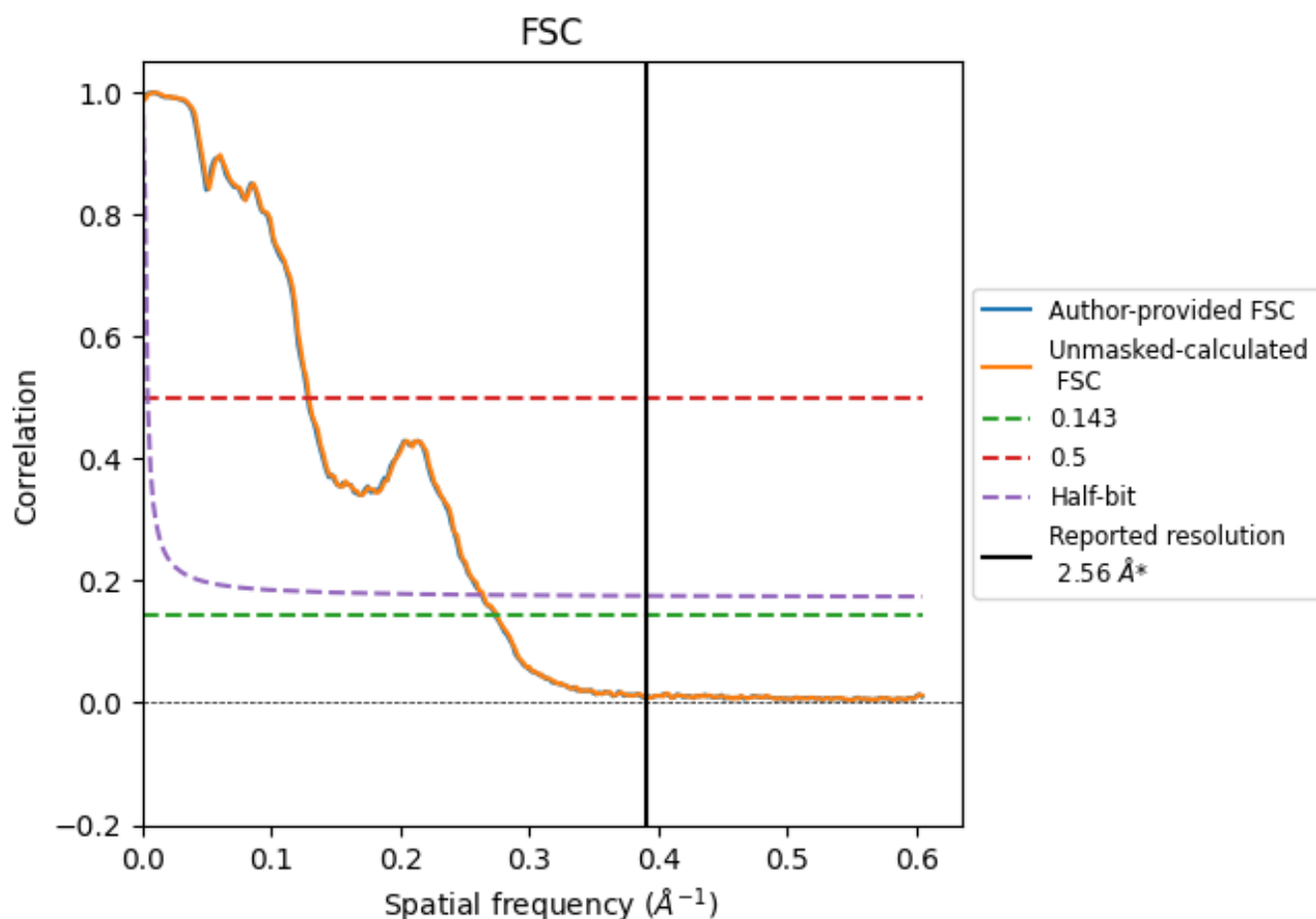


*Reported resolution corresponds to spatial frequency of 0.391 Å⁻¹

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 0.391 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.56	-	-
Author-provided FSC curve	3.65	7.80	3.80
Unmasked-calculated*	3.64	7.74	3.78

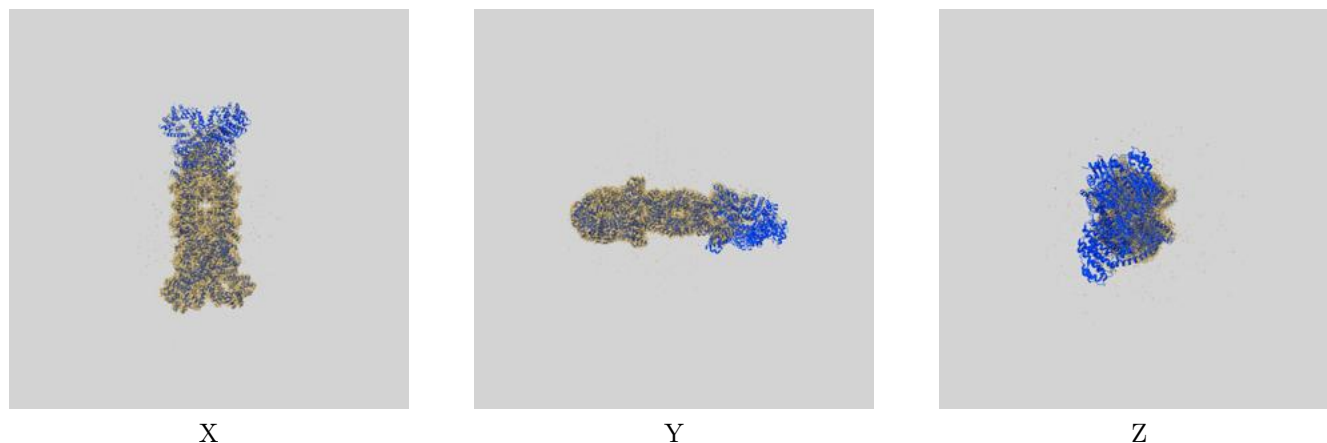
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.65 differs from the reported value 2.56 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.64 differs from the reported value 2.56 by more than 10 %

9 Map-model fit [i](#)

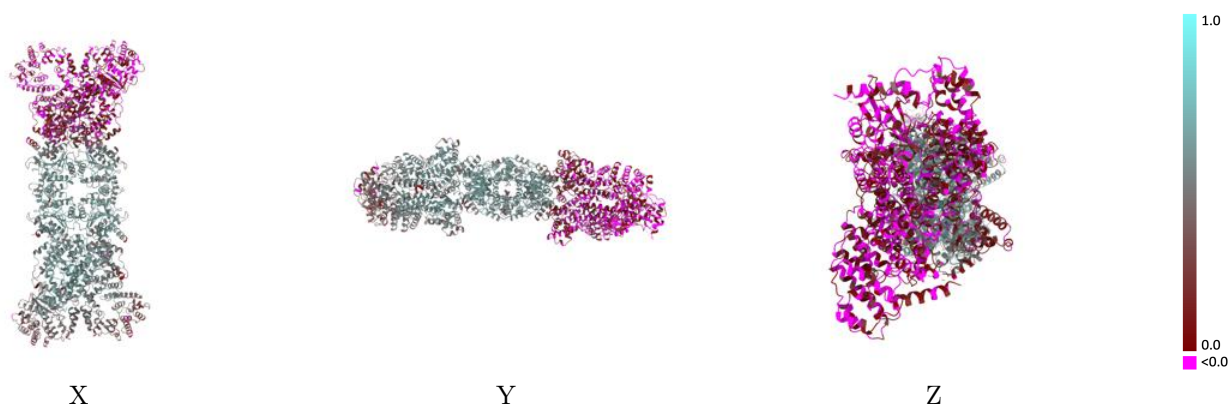
This section contains information regarding the fit between EMDB map EMD-37924 and PDB model 8WYD. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



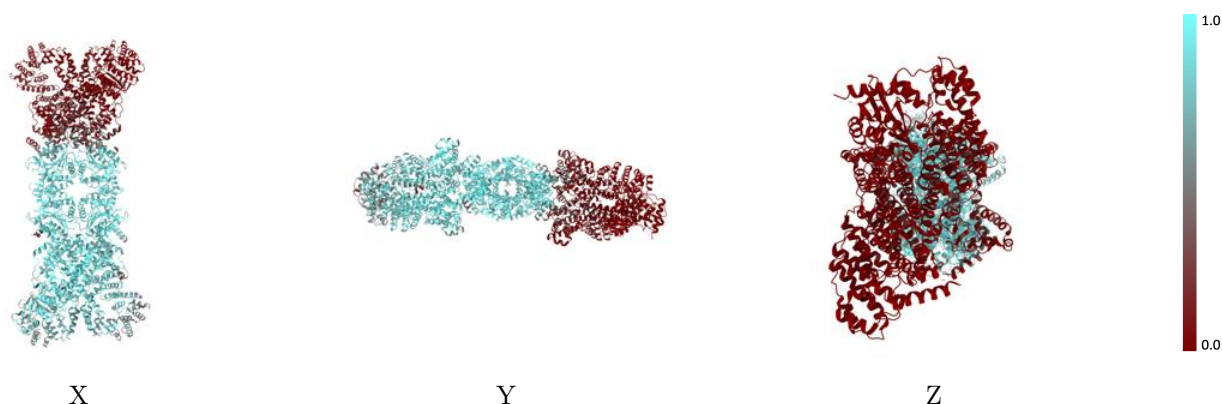
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



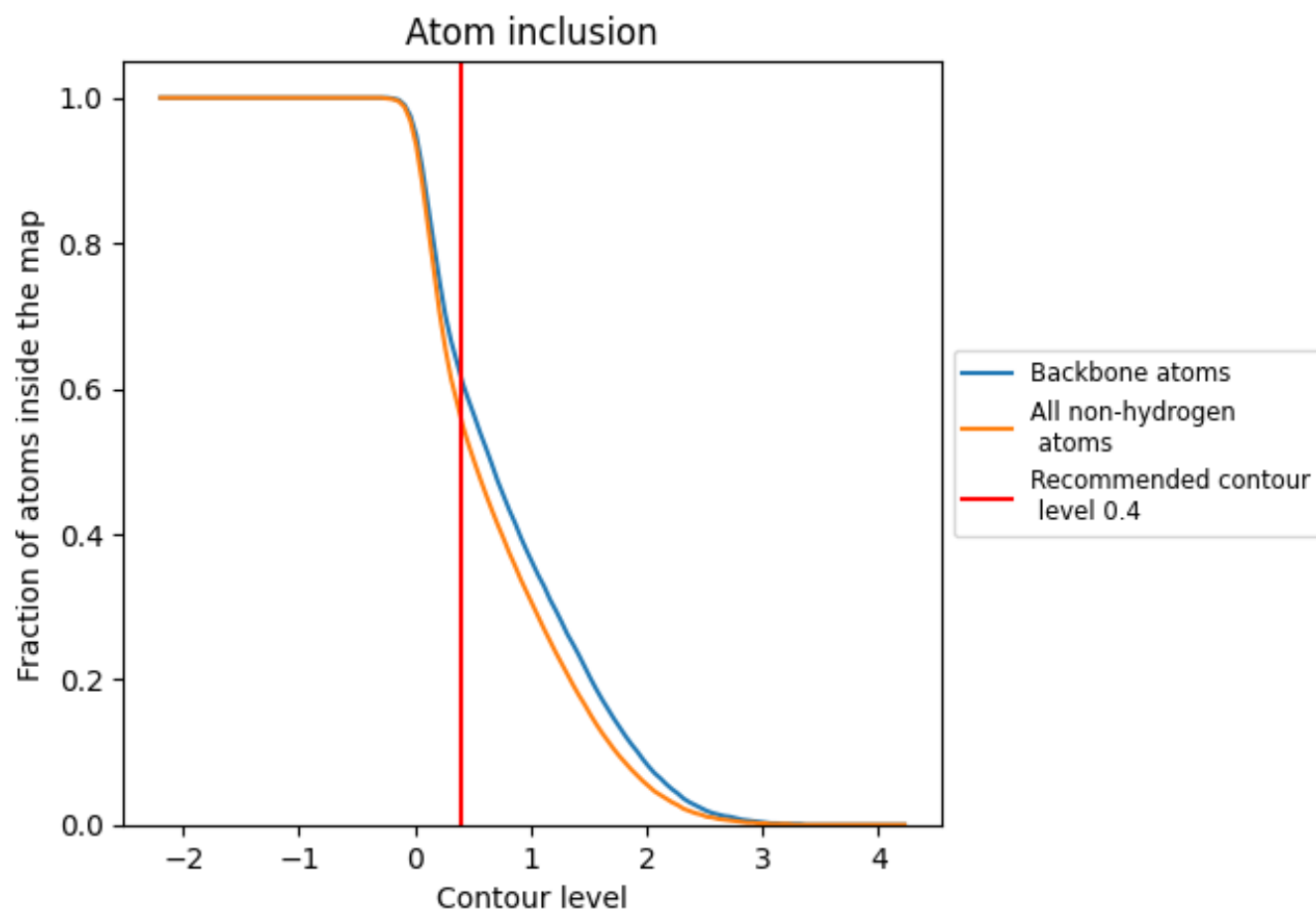
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 56% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5570	0.3520
A	0.8330	0.5110
B	0.8510	0.5300
C	0.2890	0.1860
D	0.3050	0.2140
E	0.6880	0.4290
F	0.0020	0.0130

1.0

0.0

<0.0