



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 02:40 AM UTC

PDB ID : 8Y3Y / pdb_00008y3y
EMDB ID : EMD-38907
Title : The Cryo-EM structure of anti-phage defense associated DSR2 tetramer bound with two DSAD1 inhibitors (opposite side)
Authors : Wang, R.W.; Xu, Q.; Wu, Z.X.; Li, J.L.; Shi, Z.B.; Li, F.X.
Deposited on : 2024-01-29
Resolution : 3.33 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:

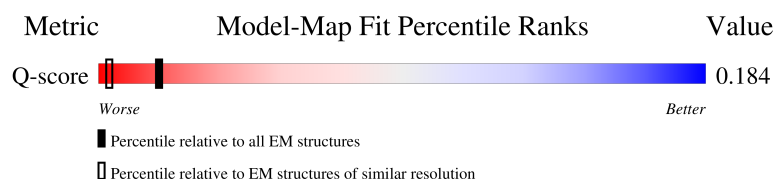
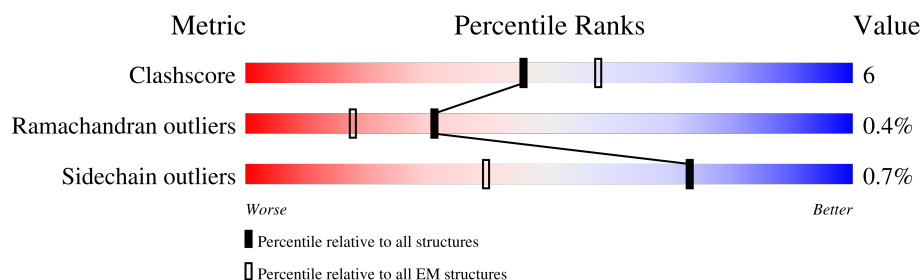
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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

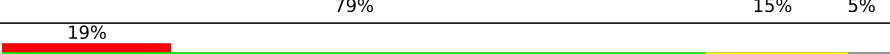
The reported resolution of this entry is 3.33 Å.

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	14484 (2.83 - 3.83)

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	D	1005	
1	E	1005	

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Mol	Chain	Length	Quality of chain			
			5%	66%	19%	15%
2	C	120				
2	F	120				

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 33586 atoms, of which 0 are hydrogens and 0 are deuteriums.

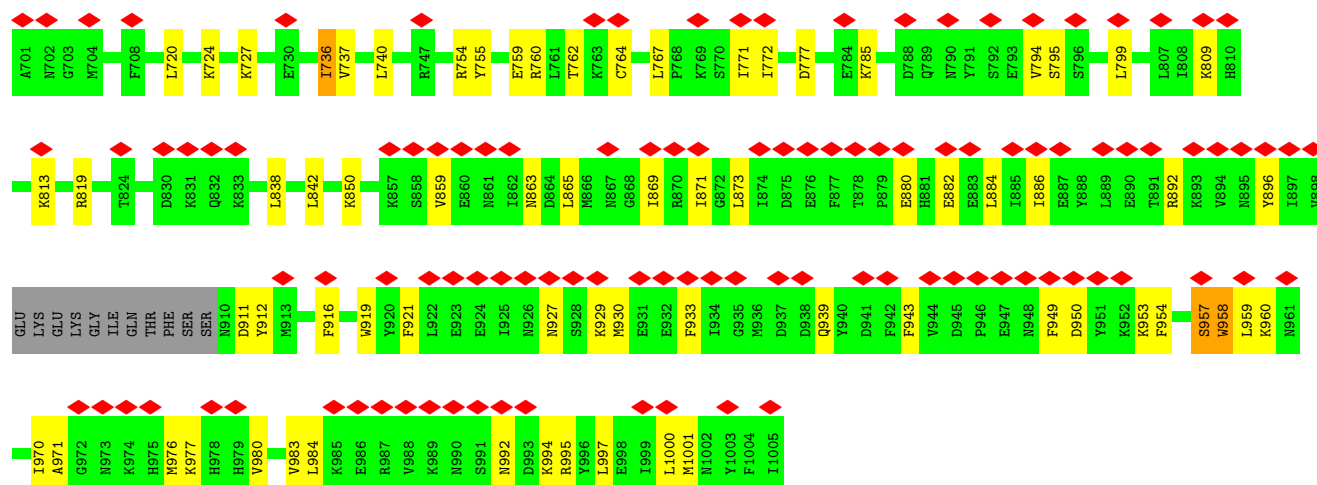
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called SIR2-like domain-containing protein.

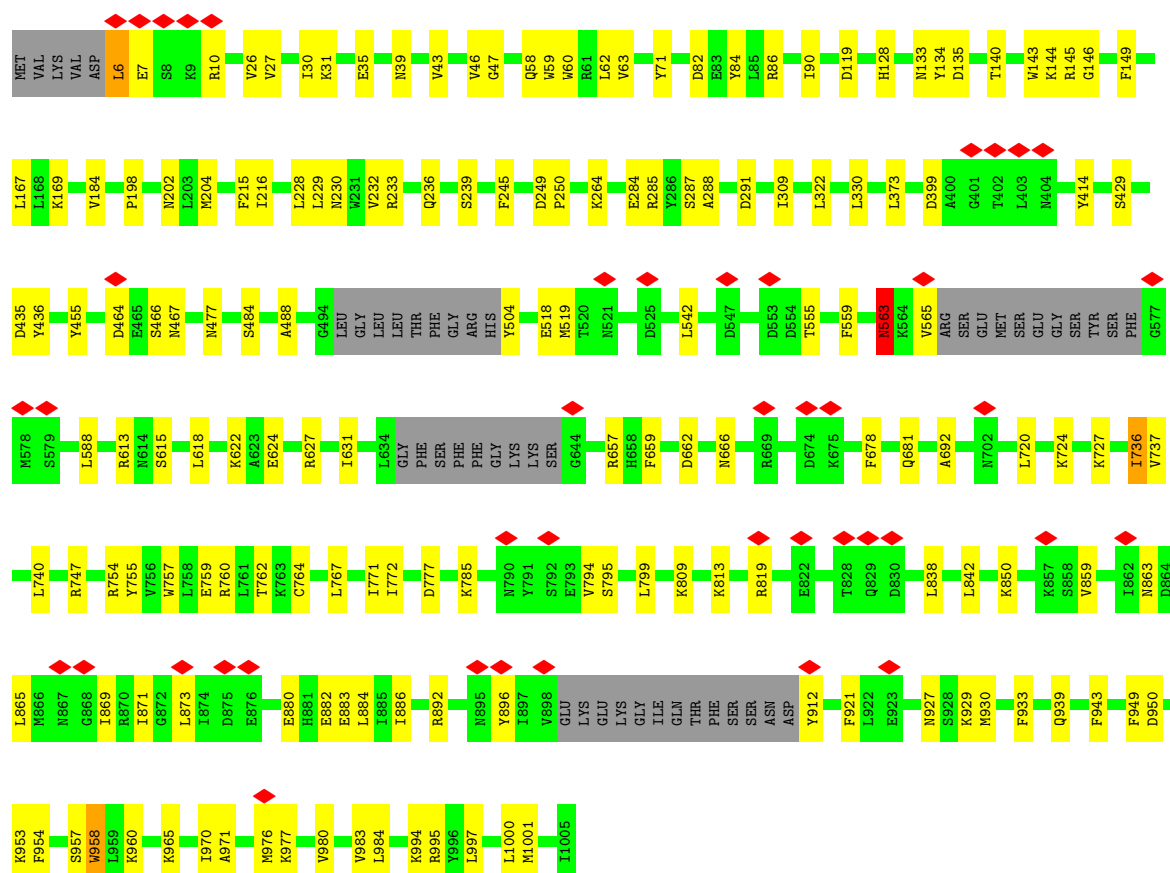
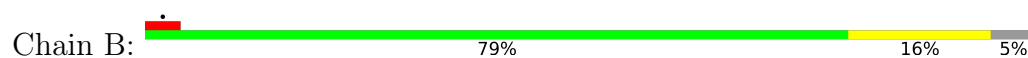
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	957	Total	C	N	O	S	0	0
			7968	5155	1282	1499	32		
1	B	958	Total	C	N	O	S	0	0
			7996	5178	1290	1497	31		
1	D	957	Total	C	N	O	S	0	0
			7968	5155	1282	1499	32		
1	E	958	Total	C	N	O	S	0	0
			7996	5178	1290	1497	31		

- Molecule 2 is a protein called DSR anti-defence 1.

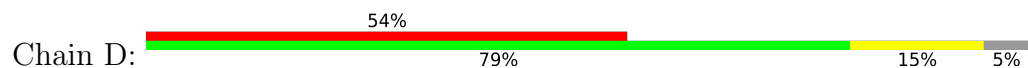
Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	102	Total	C	N	O	S	0	0
			829	544	133	150	2		
2	F	102	Total	C	N	O	S	0	0
			829	544	133	150	2		



• Molecule 1: SIR2-like domain-containing protein



• Molecule 1: SIR2-like domain-containing protein



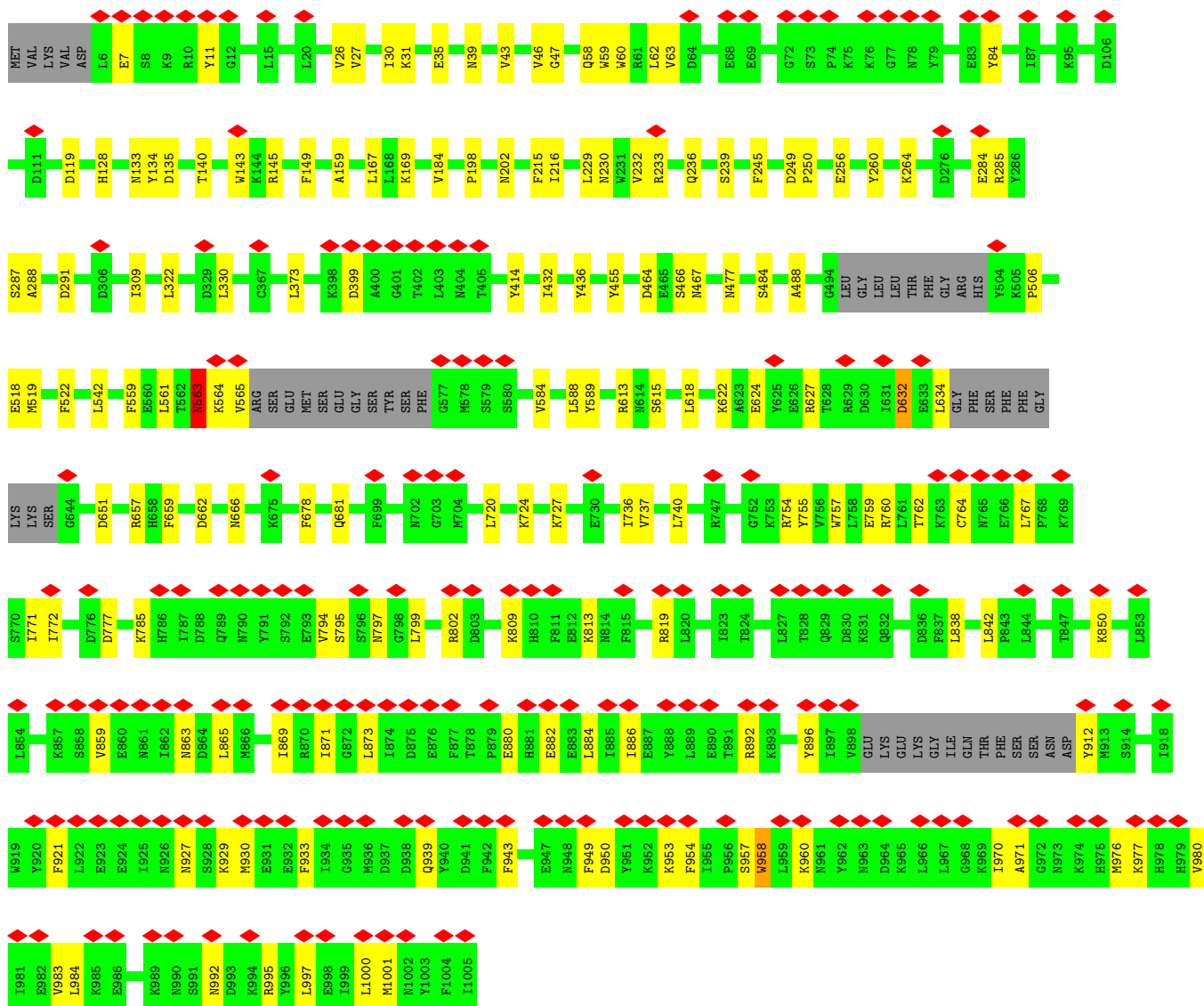
Y940	D941	F942	F943	Y944	D945	F946	E947	N948	F949	D950	Y951	K952	K953	F954	Y955	S957	Y958	N959	K960	N961	Y962	N963	D964	K965	L966	Y970	A971	N973	K974	N975	N976	K977	Y980	Y983	L984	K985	E986	N987	N988	K989	N990	S991	N992	D993	K994	N995	Y996	L997	E998	Y999	L1000	M1001	N1002	Y1003								
E812	F815	I816	S817	K818	R819	L820	H881	S882	E883	I823	L884	L885	I886	E887		E890	T891	R892	D893	K893	Y894	N895	K896	N981	I897	N987	GLU	LYS	LYS	GLY	I891	L841	GLN	L842	THR	PHE	SER	N910	D911	Y912		F916	F921	L922	K985	E924	I925	K987	S988	N927	S928	K929	M930	E931	E932	F933	K996	L996	G935	N936	D937	Q939
L740	F744	P745	E746	R747	D748	I751	R754	Y755	L758	E759	R760	L761	T762	C763	N765	E766	L767	I768	K769	S770	I771	L773	I774		D777	F778	L779	S780	L781	E784	K785	L786	I787	D788	Q789	N790	I791	S792	K793	V794	S795	S796		L799	Y800	S801	L865	M866	N867	G868	I869	R870	H810	F811								
K665	N666	E668	R669	S670	C671	K675		F678	Q681	E686	Y687	Q690	I691	A692	E693	E694	K697	Q698	F699	S700	A701	N702	G703	M704	N705	Q711	F712	I713	S714	E715	L716	A718	A719	L720	F722	N723	K724		K727	L728	S729	E730	E731	G732		K735	I736	V737	K738	A739												
E597	N598	C599	L600	W601	S602	E607	F608		Y611	I612	R613	S615	M616	S617	L618	L619	I620	E621	K622	A623	E624	Y625	E626	R627	T628	R629	D630	I631	ASP	GLU	LEU	GLY	PHE	SER	PHE	GLY	LYS	SER	G644	F645	F646	M647	V653	N654	R657	H658	F659	K660	I661	D662	D663	I664										
P506	F507	T508	D509	E510	F511	L512	A513	R514	E515	E516	R517	E518	M519	T520	N521	F522	I524	M531	P532	F533	E534	F535	Q536	K537	K538	Y539	K540	L542	L545	S546	T555	N563	K564	V565	R566	E571	F576	G577	M578	S579	S580	V583	R587	L588	Y589	D590	F594															
K423	F424	E427	Q428	S429	V430	S431	I432	E433	D434	D435	Y436	K437		F441	E450	L454	Y455	N457	L458	L459	L460	N461	S462	I463	D464	E465	S466	N467	G468	C469	V470	Y471	N477	S484	A488	V489	T490	PHE	ASN	GLY	LEU	GLY	LEU	THR	PHE	GLY	ARG	HIS	TYR													
G355	R359	E362	L363	K364	E365	S366	C367	D368	E369	R370	S371	K372	L373	S374	K375	K376	Q377	Y378	E379	R380	F381	N382	F385	N386	F387	F388	E389	K390	I394	C395	M396	A397	K398	D399	Y324	I325	R326	K327	I328	D329	L330	K331	H332	V333	F334	E335	Y336	D337	N343	V347	R348	F354										
Y280	D281	Y282	L283	E284	R285	Y286	S287	A288	V289	M290	D291	L292	L293	I294	E295	S296	Q297	K300	F301	I302	T303	K304	D305	D306	F307	V308	I309	D310	I316	S317	P318	L319	F320	A321	L322	Q323	Y324	I325	R326	K327	I328	D329	L330	K331	H332	V333	F334	E335	Y336	D337	N343	V347	R348	F354								
F215	I216	G217	Y218	G219	L220	G221	D222	Y223	N224	I225	L228	L229	N230	W231	V232	R233	Q236	K237	D238	S239	F240	H241	K242	P243	F244	F245	I246	R247	T248	D249	P250	S251	P252	I253	E254	N255	E256	T257	L258	L259	K264	G265	L266	R267	L268	L269	D270	A271	A272	S273	L274	I275	D276	S277	N278	E279						
H67	E68	E69	L70	Y71	G72	S73	P74	K75	G76	G77	N78	Y79	S80	S81	D82	E83	Y84	L85	B86	F91	Y92	N93	V94	K95	A99	G102	I103	D106	F107	F108	Q109	V110	D111	K112	P113	T114	N115	P116	I117	S201	H118	D119	K120	I121	M124	N125	P126	A127	H128	N133	Y134	D135	T140									
A141	C142	W143	K144	R145	G146	K147	Y148	F149	V151	E156	D157	V158	A159	S163	S164	R165	Y166	L167	K169	G172	D173	F174	K175	K176	G177	F178	K179	V184	L185	K186	E187	Y190	N196	Y197	P198	L199	I200	S201	L203	M204	K205	T206	L207	I208	A209	L210	H211	T212	I213	V214												
MET	VAL	VAL	ASP	LEU	GLU	SER	LYS	ARG	TYR	G12	E13	K14	L15	K16	E17	V18	F19	L20	M21	L22	D23	N24	N25	V26	V27	E28	C29	I30	K31	E32	E35	R38	N39	G40	K41	L42	V43	F44	F45	V46	G47	V50	S54	D55	Q58	W59	W60	R61	L62	V63	D64	K65	Y66									




 F1004
 I1005

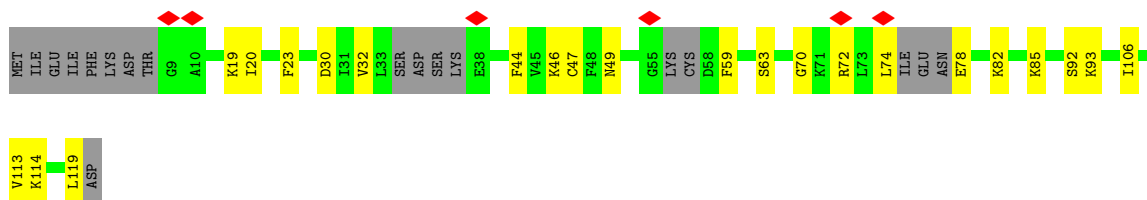
• Molecule 1: SIR2-like domain-containing protein

Chain E: 

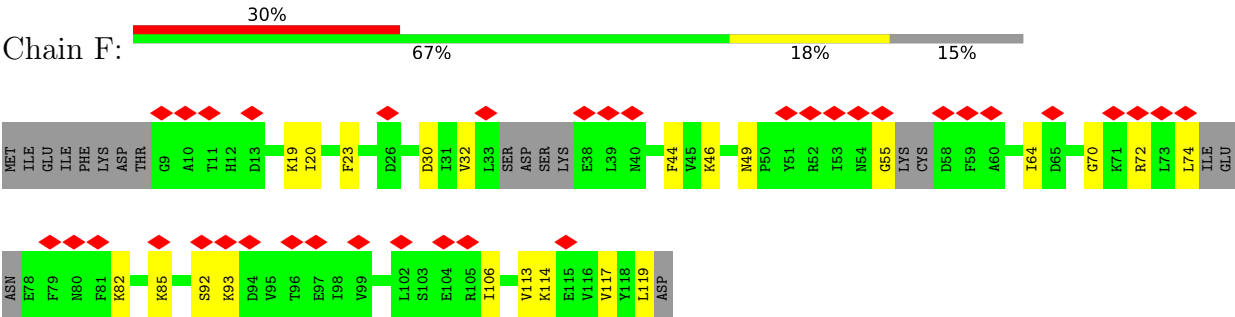


• Molecule 2: DSR anti-defence 1

Chain C: 



● Molecule 2: DSR anti-defence 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	91205	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	13000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.660	Depositor
Minimum map value	-0.368	Depositor
Average map value	0.031	Depositor
Map value standard deviation	0.084	Depositor
Recommended contour level	0.6	Depositor
Map size ($\text{\AA}$)	430.91998, 430.91998, 430.91998	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0773, 1.0773, 1.0773	Depositor

5 Model quality

5.1 Standard geometry

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	0.34	0/8150	0.71	0/10979
1	B	0.33	0/8178	0.70	0/11014
1	D	0.33	0/8150	0.71	1/10979 (0.0%)
1	E	0.33	0/8178	0.70	0/11014
2	C	0.37	0/847	0.85	2/1144 (0.2%)
2	F	0.37	0/847	0.85	2/1144 (0.2%)
All	All	0.33	0/34350	0.71	5/46274 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	6
1	B	0	3
1	D	0	4
1	E	0	4
2	C	0	1
2	F	0	1
All	All	0	19

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	377	GLN	CA-CB-CG	-6.15	101.81	114.10
2	C	70	GLY	N-CA-C	-6.03	105.99	112.08
2	F	70	GLY	N-CA-C	-5.98	106.04	112.08
2	C	32	VAL	N-CA-C	-5.98	107.46	113.20
2	F	32	VAL	N-CA-C	-5.97	107.47	113.20

There are no chirality outliers.

5 of 19 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	563	ASN	Peptide
1	A	565	VAL	Peptide
1	A	568	GLU	Peptide
1	A	794	VAL	Peptide
1	A	911	ASP	Peptide

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	7968	0	7798	105	0
1	B	7996	0	7845	107	0
1	D	7968	0	7798	99	0
1	E	7996	0	7845	103	0
2	C	829	0	820	15	0
2	F	829	0	820	14	0
All	All	33586	0	32926	413	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 6.

The worst 5 of 413 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:B:912:TYR:HH	2:C:78:GLU:N	1.51	1.08
1:A:562:THR:O	1:A:566:ARG:HB2	1.61	0.99
1:D:892:ARG:O	1:D:896:TYR:HB2	1.73	0.88
1:B:892:ARG:O	1:B:896:TYR:HB2	1.73	0.88
1:A:892:ARG:O	1:A:896:TYR:HB2	1.73	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	949/1005 (94%)	872 (92%)	74 (8%)	3 (0%)	36	65
1	B	948/1005 (94%)	871 (92%)	74 (8%)	3 (0%)	36	65
1	D	949/1005 (94%)	870 (92%)	76 (8%)	3 (0%)	36	65
1	E	948/1005 (94%)	870 (92%)	74 (8%)	4 (0%)	30	59
2	C	94/120 (78%)	74 (79%)	19 (20%)	1 (1%)	11	40
2	F	94/120 (78%)	74 (79%)	19 (20%)	1 (1%)	11	40
All	All	3982/4260 (94%)	3631 (91%)	336 (8%)	15 (0%)	31	59

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	958	TRP
1	B	958	TRP
1	D	958	TRP
1	E	958	TRP
1	A	795	SER

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	879/923 (95%)	873 (99%)	6 (1%)	76	79
1	B	881/923 (95%)	874 (99%)	7 (1%)	73	78
1	D	879/923 (95%)	873 (99%)	6 (1%)	76	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	881/923 (95%)	875 (99%)	6 (1%)	76	79
2	C	94/113 (83%)	94 (100%)	0	100	100
2	F	94/113 (83%)	94 (100%)	0	100	100
All	All	3708/3918 (95%)	3683 (99%)	25 (1%)	73	79

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	736	ILE
1	D	838	LEU
1	E	859	VAL
1	D	785	LYS
1	D	859	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	136	ASN
2	F	21	ASN
1	D	658	HIS
2	F	17	HIS
1	E	493	ASN

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 ⓘ

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.

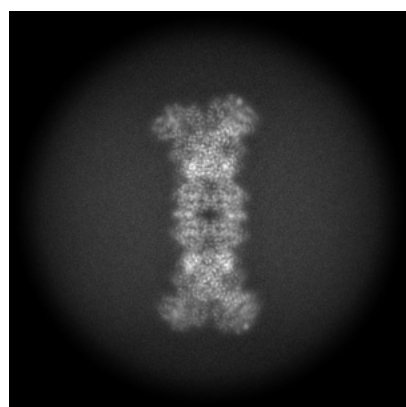
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38907. These allow visual inspection of the internal detail of the map and identification of artifacts.

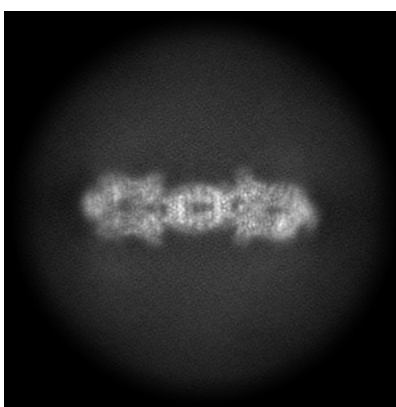
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

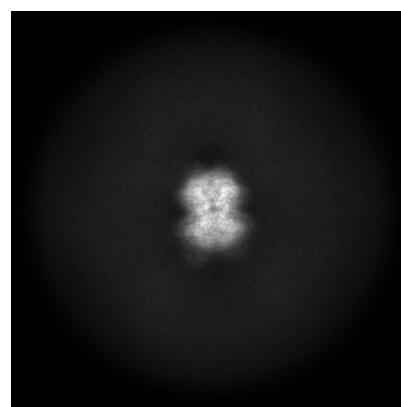
6.1.1 Primary map



X



Y

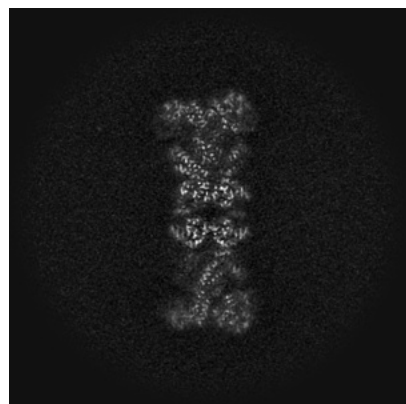


Z

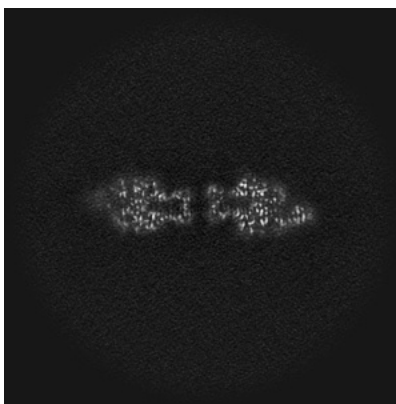
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

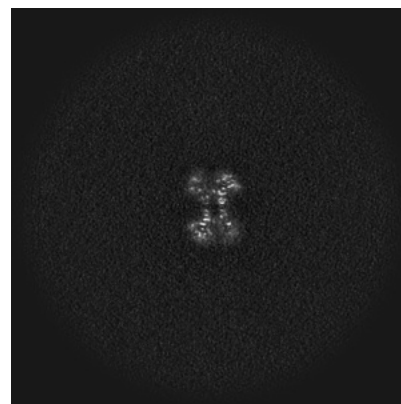
6.2.1 Primary map



X Index: 200



Y Index: 200

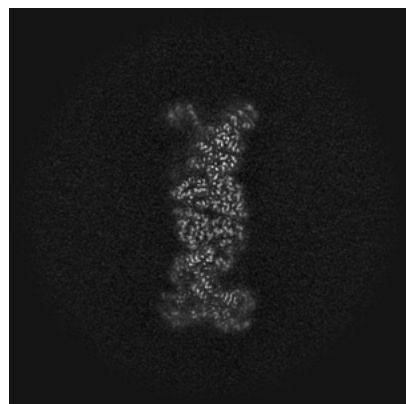


Z Index: 200

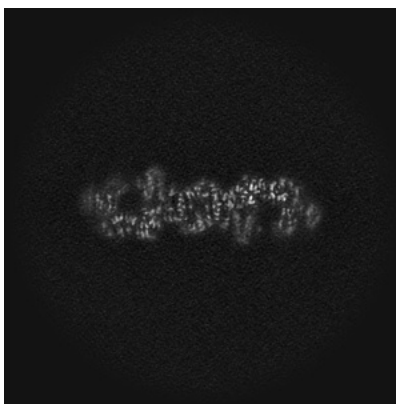
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

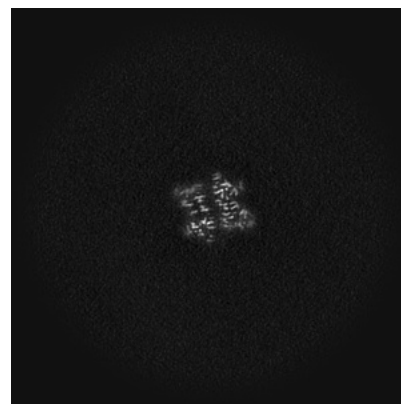
6.3.1 Primary map



X Index: 212



Y Index: 219

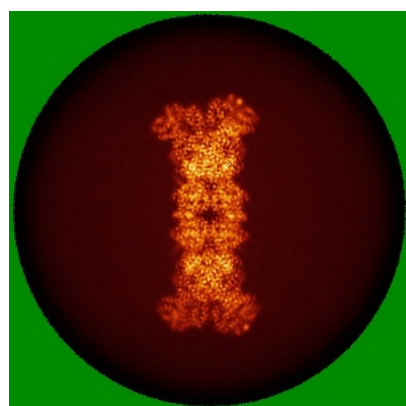


Z Index: 242

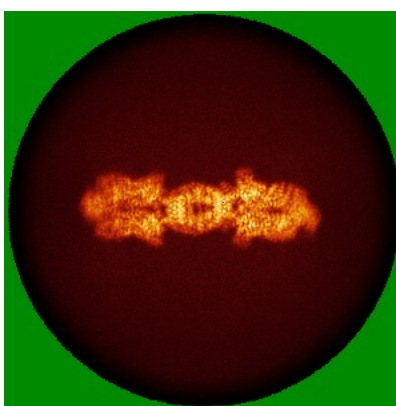
The images above show the largest variance slices of the map in three orthogonal directions.

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

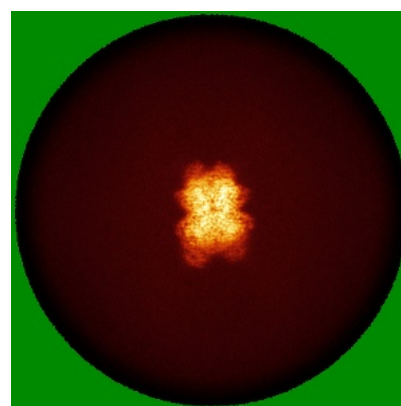
6.4.1 Primary map



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.

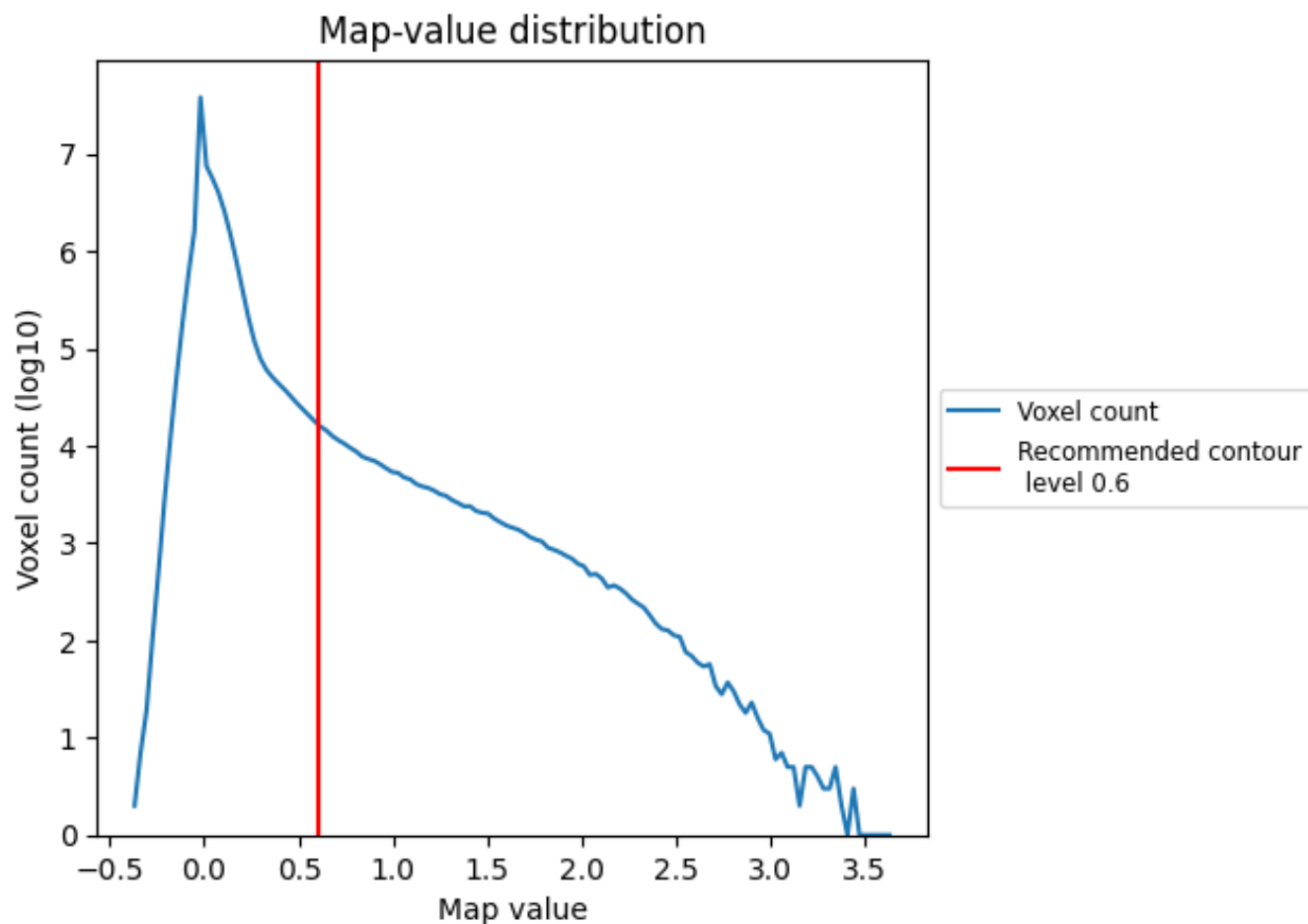
6.6 Mask visualisation

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

7 Map analysis [i](#)

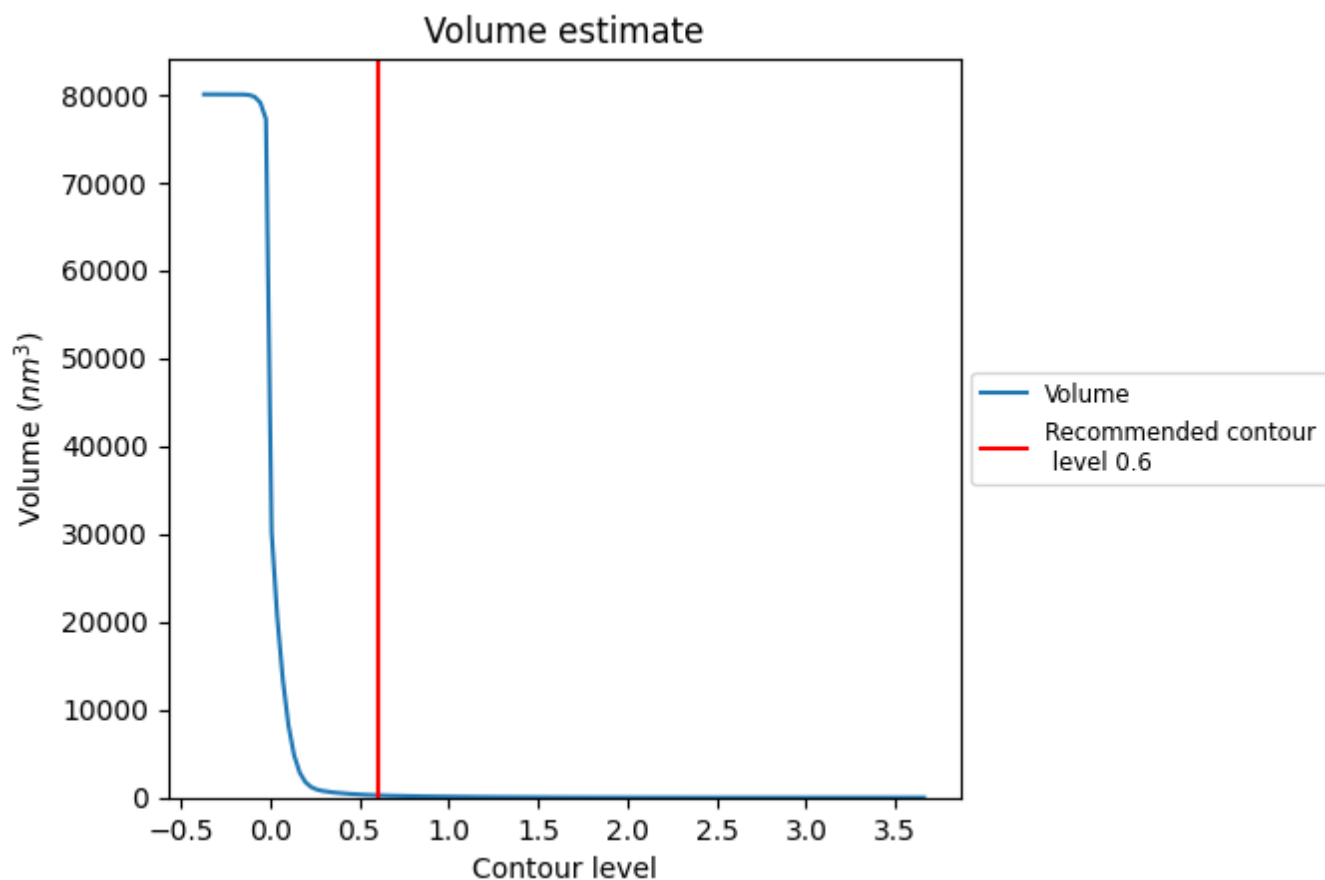
This section contains the results of statistical analysis of the map.

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.

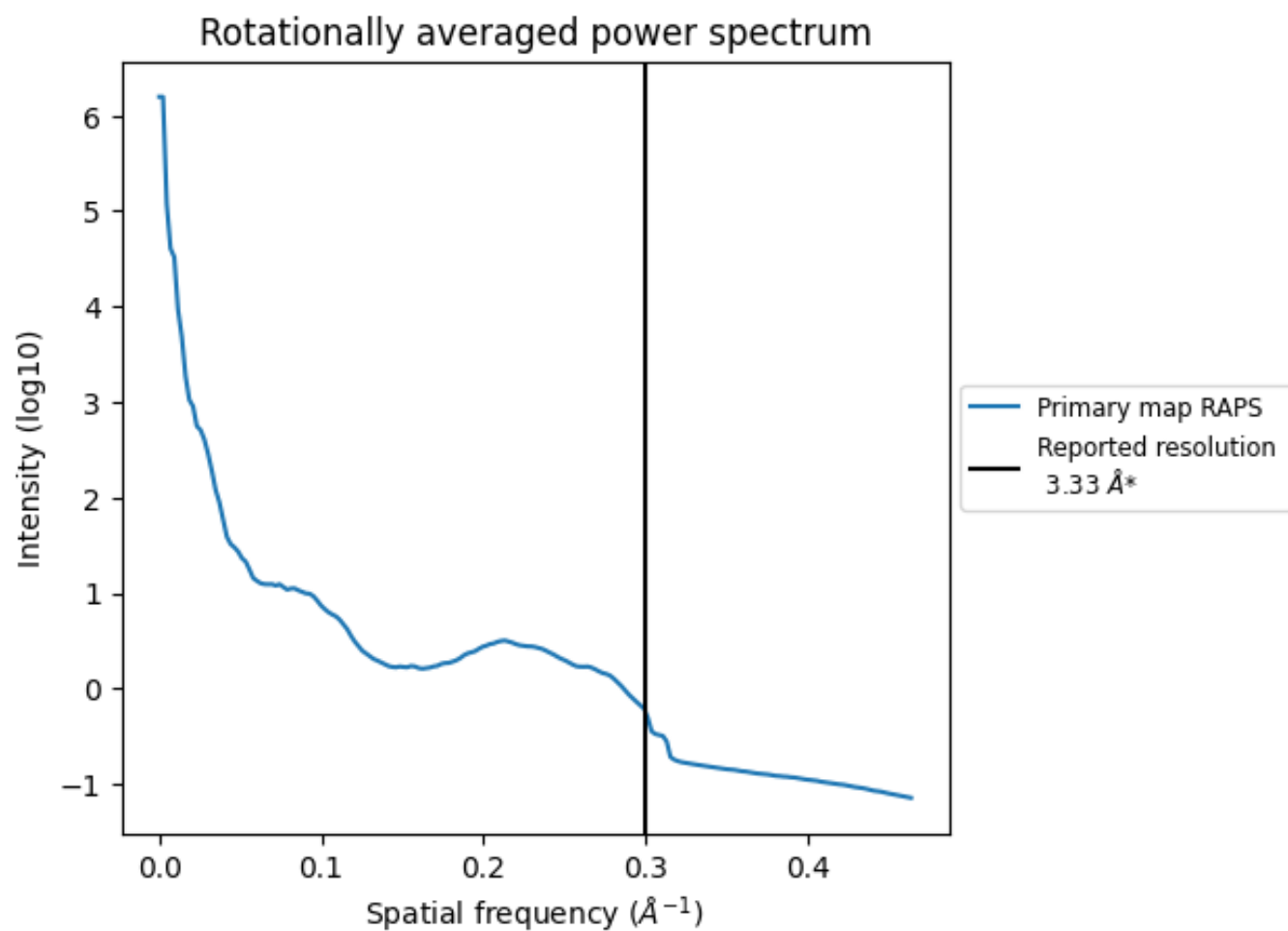
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 258 nm^3 ; this corresponds to an approximate mass of 233 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 0.300 Å⁻¹

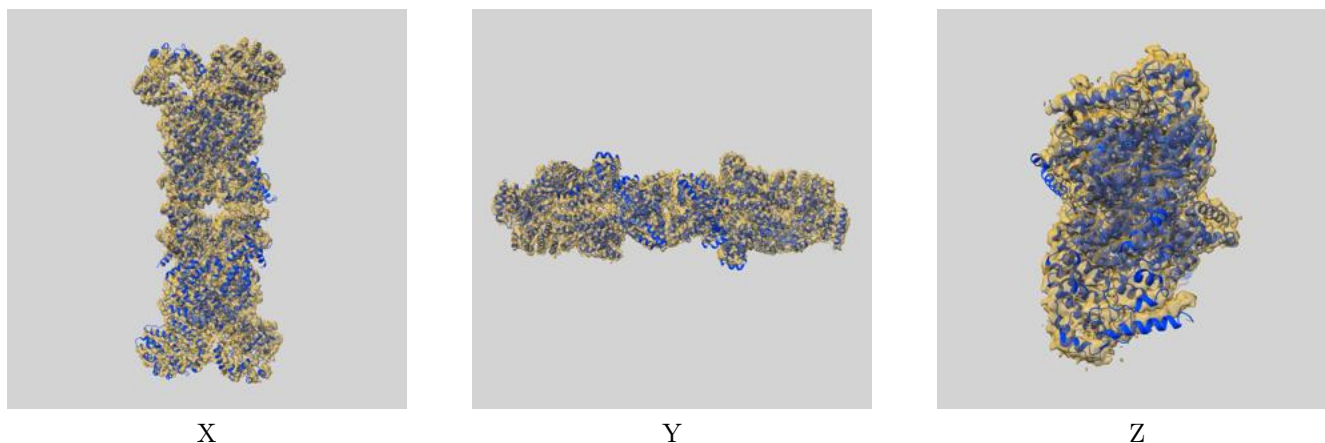
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

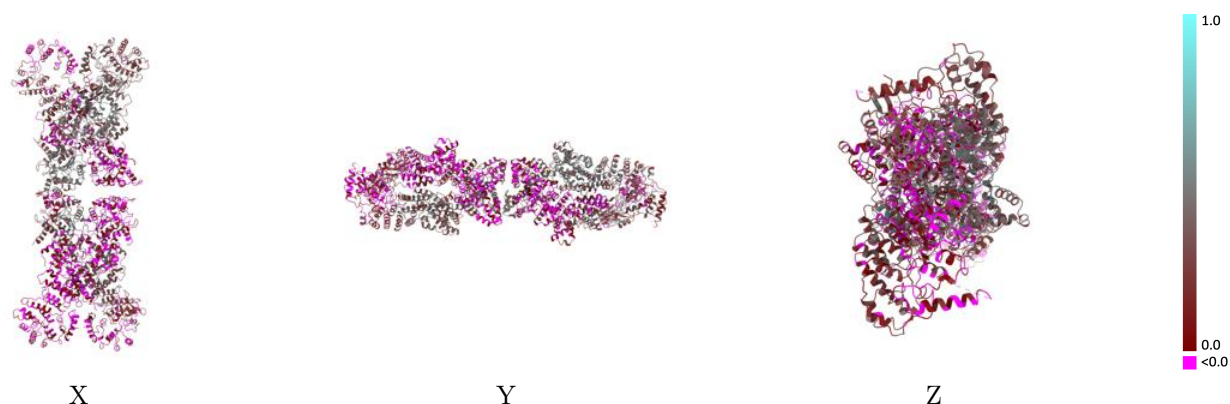
This section contains information regarding the fit between EMDB map EMD-38907 and PDB model 8Y3Y. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



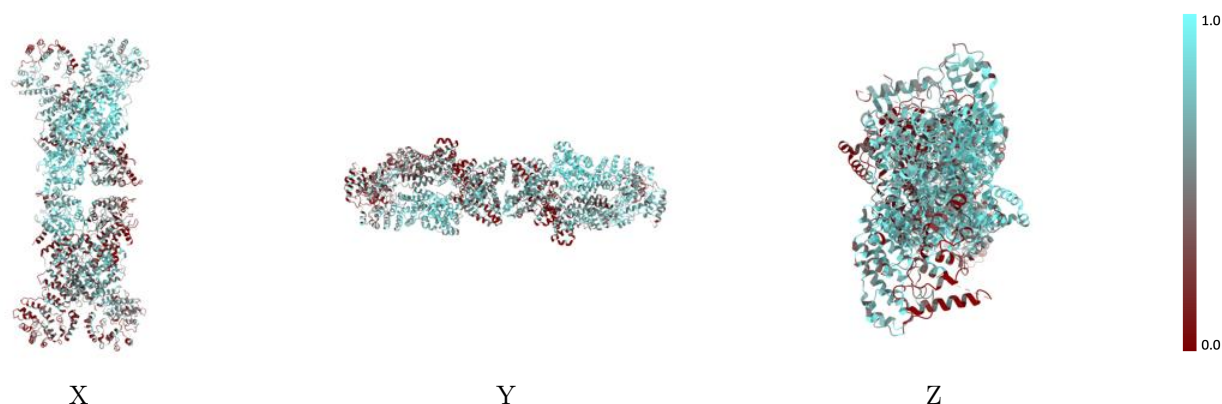
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



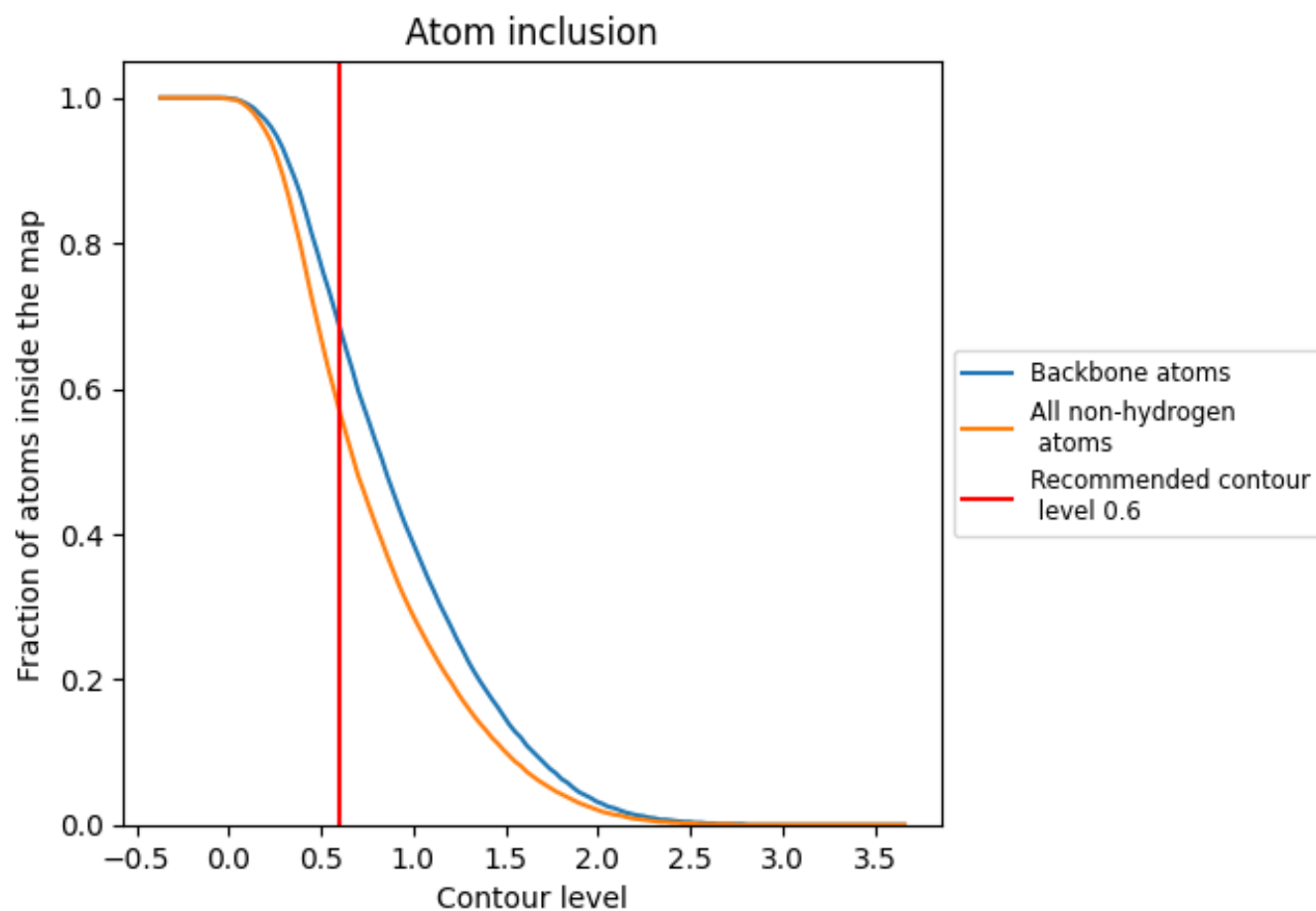
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 57% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5700	0.1840
A	0.4570	0.0680
B	0.7900	0.3750
C	0.7200	0.3560
D	0.3710	0.0170
E	0.6490	0.2540
F	0.5240	0.2310

1.0

0.0

<0.0