



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 04:12 PM UTC

PDB ID : 9X0F / pdb_00009x0f
EMDB ID : EMD-66433
Title : Cryo-EM structure of EvSS
Authors : Bai, L.; Lyu, R.Q.
Deposited on : 2025-09-30
Resolution : 3.25 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

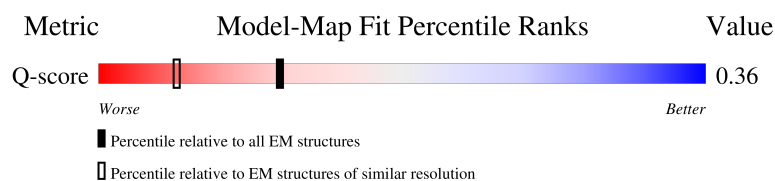
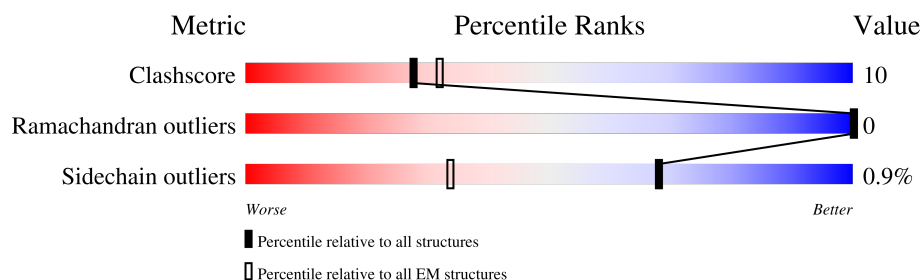
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.25 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	14599 (2.75 - 3.75)

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	714	22% 31% 10% 59%
1	B	714	32% 32% 8% 59%
1	C	714	33% 30% 11% 59%
1	D	714	32% 33% 8% 59%

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Mol	Chain	Length	Quality of chain
1	E	714	
1	F	714	
1	G	714	
1	H	714	
1	I	714	
1	J	714	
1	K	714	
1	L	714	
1	M	714	
1	N	714	
1	O	714	
1	P	714	
1	Q	714	
1	R	714	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 42552 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 Stellatatriene synthase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	B	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	C	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	D	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	E	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	F	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	G	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	H	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	I	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	J	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	K	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	L	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	M	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	N	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	O	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	P	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		
1	Q	294	Total	C	N	O	S	0	0
			2364	1502	407	444	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	R	294	2364	1502	407	444	11	0	0

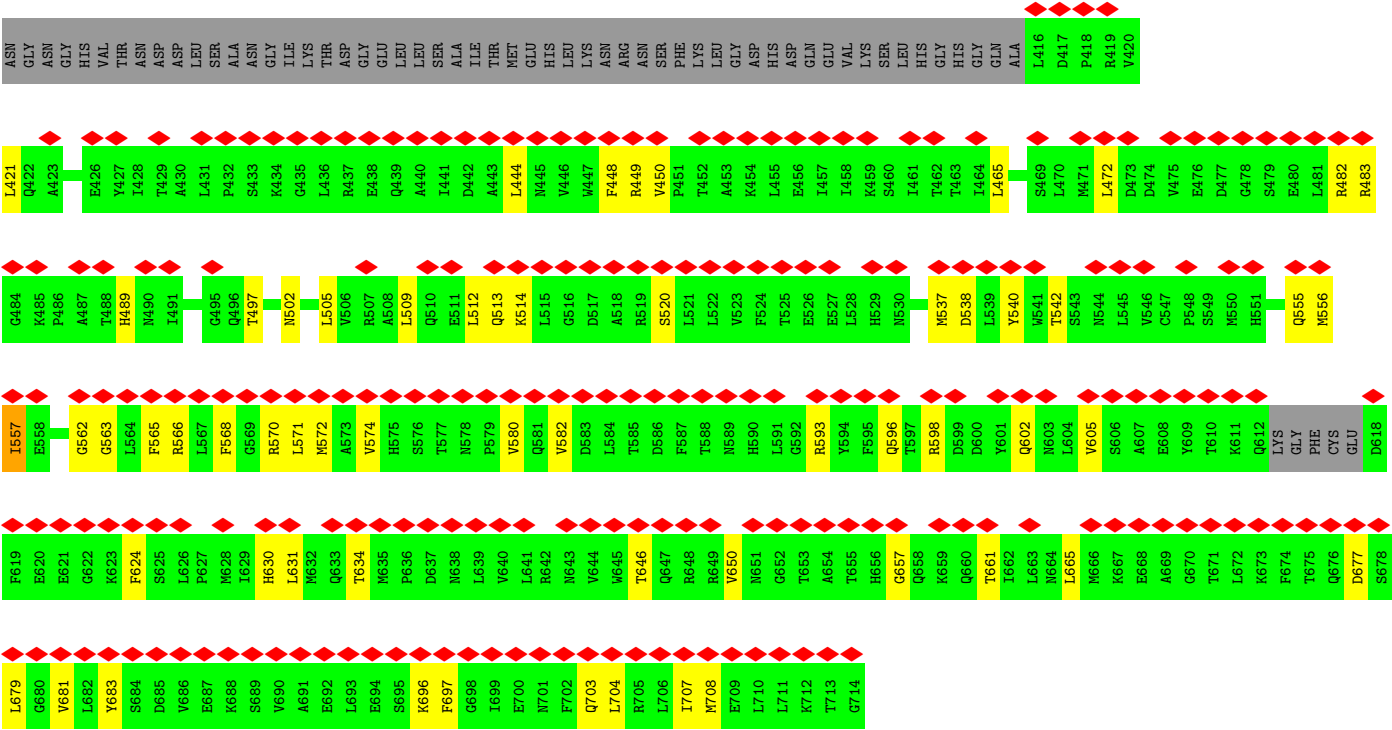
Chain B:

G680	E620	E558	R483	L421	ASN
G681	E621	G562	G484	Q422	GLY
G682	G622	G563	R485	A423	ASN
G683	K623	L564	P486		GLY
G684	F624	F565	A487	E426	VAL
D685	G625	R566	T488	I428	THR
G686	L626	L567	R489	T429	ASN
G687	P627	F568	M490	A430	ASP
G688	M628	F569	I491	L431	ASP
G689	P629	G569			LEU
G690	H630	R570	G495	P432	LEU
A691	L631	L571	Q496	S433	ALA
E692	M632	M572	T497	K434	ASN
G693	G633	A573		G435	GLY
E694	G634	V574	R507	L436	THR
G695	M635	H575	A508	ASP	ASP
G696	P636	R576	L509	E438	GLY
F697	D637	T577	Q510	Q439	GLU
G698	M638	M578	L512	A440	LEU
E699	L639	P579	Q513	I441	LEU
E700	G640	V580	A514	D442	ASN
M701	L641	Q581	L515	A443	ALA
F702	R642	V582	G516	L444	THR
Q703	M643	D583	D517	N445	THR
L704	V644	L584	A518	V446	GLU
R705	G645	T585	R519	V447	GLU
L706	T646	D586	S520	F448	LYS
I707	Q647	T587	L521	R449	ASN
M708	R648	F588	L522	V450	ASN
E709	G649	T589	V523	P451	PHE
L710	V650	H590	F524	T452	LYS
L711	M651	L591	T525	A453	LYS
L712	G652	G592	E526	K454	LEU
K713	G653	R593	E527	L455	GLY
A654	G654	V594	L528	E456	VAL
G655	H655	F595	H529	I457	LYS
H656	P656	Q596	M530	L458	GLY
G657	G657	T597	V533	K459	GLN
Q658	G658	R598		S460	GLN
G659	P659	D599	D538	I461	LEU
G660	M660	V600	L539	T462	HIS
T661	L661	G602	T542	T463	HIS
L662	L662	M603	S543	A467	GLY
L663	L663	L604	N544	A468	GLN
L665	L665	V605	L545	S469	ALA
M666	M666	R606	V546	L470	D417
F667	F667	A607	C547	M471	P418
E668	E668	E608	P548	L472	R419
A669	A669	V609	S549	D473	V420
G670	G670	T610	M550	D474	
T671	T671	K611	H551	L475	
L672	L672	Q612	E552	E476	
K673	K673	L554	F554	A477	
F674	F674	GLY	Q555	D478	
T675	T675	PHE	M556	S479	
Q676	Q676	CYS	I557	E480	
D677	D677	GLU		L481	
S678	S678	P619		R482	
L714	L714				
L715	L715				
L716	L716				
L717	L717				
L718	L718				
L719	L719				
L720	L720				
L721	L721				
L722	L722				
L723	L723				
L724	L724				
L725	L725				
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L799	L799				
L800	L800				

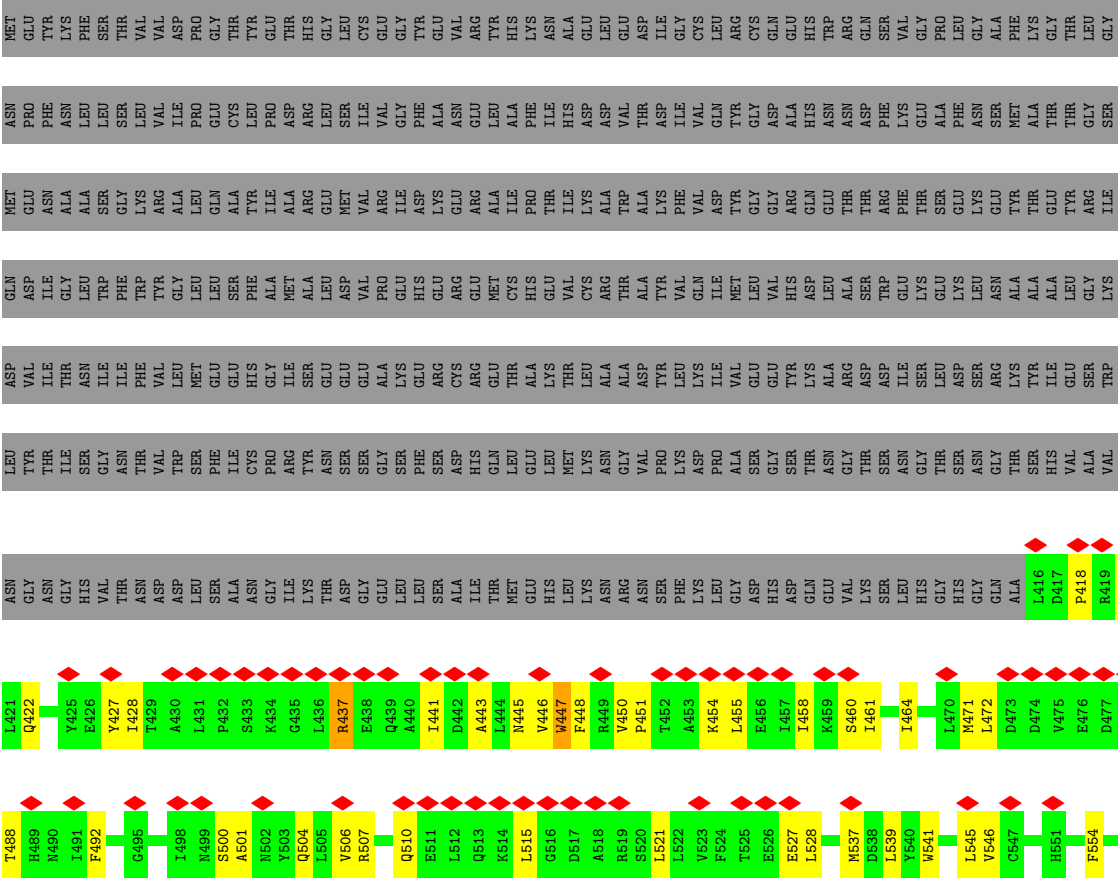
Chain C:

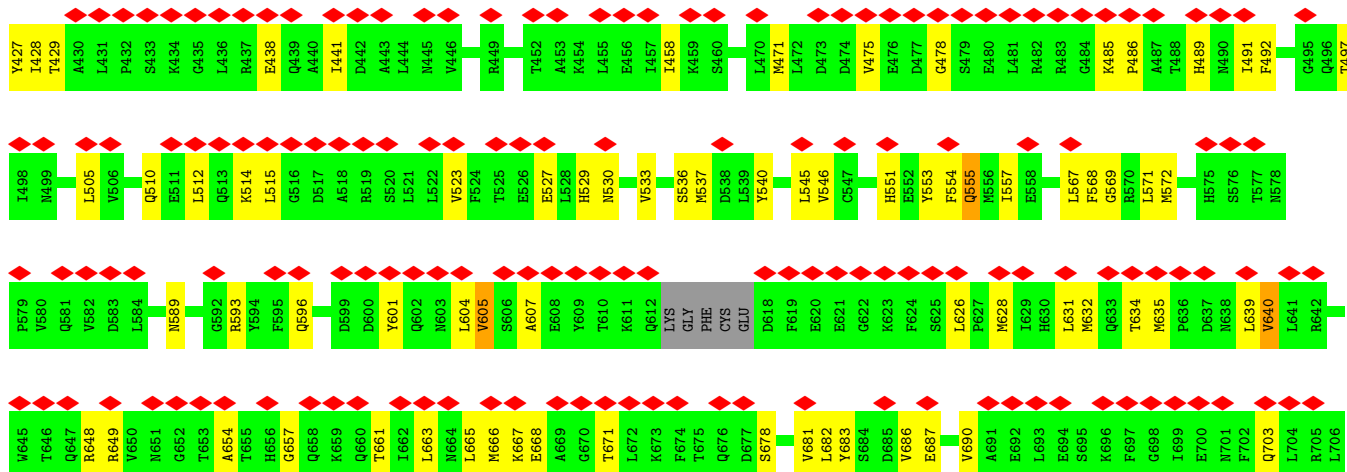


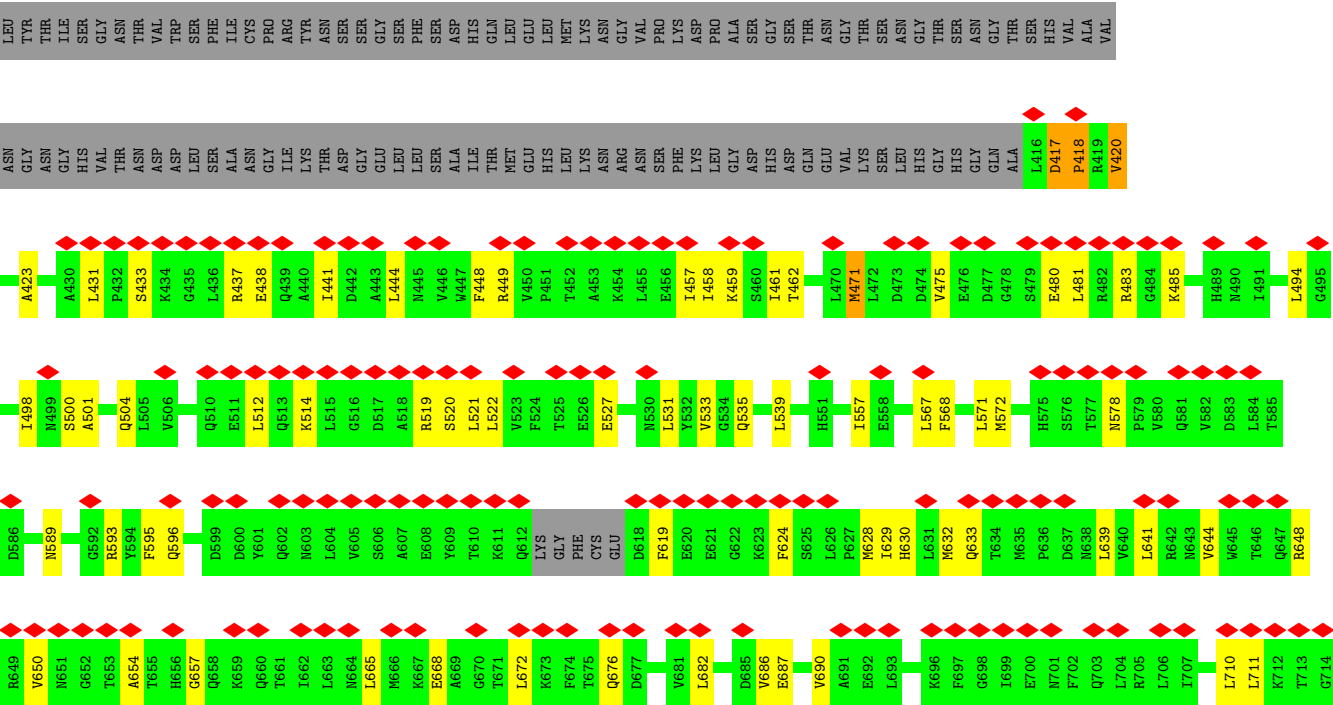
MET	GLU	ASN	ALA	ALA	SER	GLY	LYS	ARG	ALA	LEU	GLN	ALA	ALA	TYR	ILE	ALA	ALA	ARG	GLU	MET	VAL	ARG	ILE	ILE	ASP	LYS	GLU	ALA	ALA	ILE	PRO	THR	ILE	LYS	ALA	ALA	LYS	ALA	PHE	VAL	ASP	GLY	TYR	GLY	GLY	GLN	GLU	THR	THR	ARG	PHE	THR	SER	GLU	LYS	GLU	TYR	THR	GLY	THR	ARG	ILE
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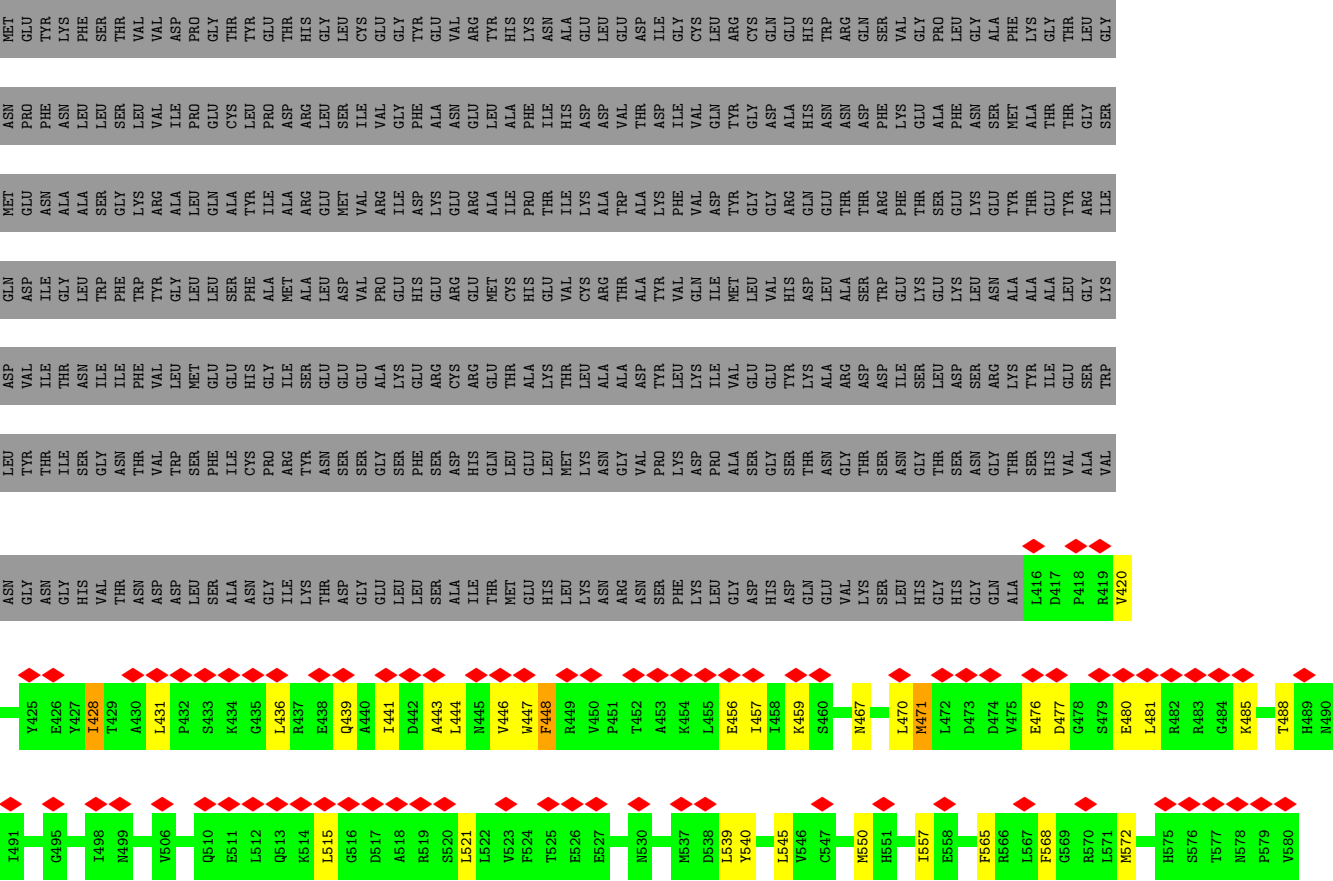
● Molecule 1: Stellatatriene synthase

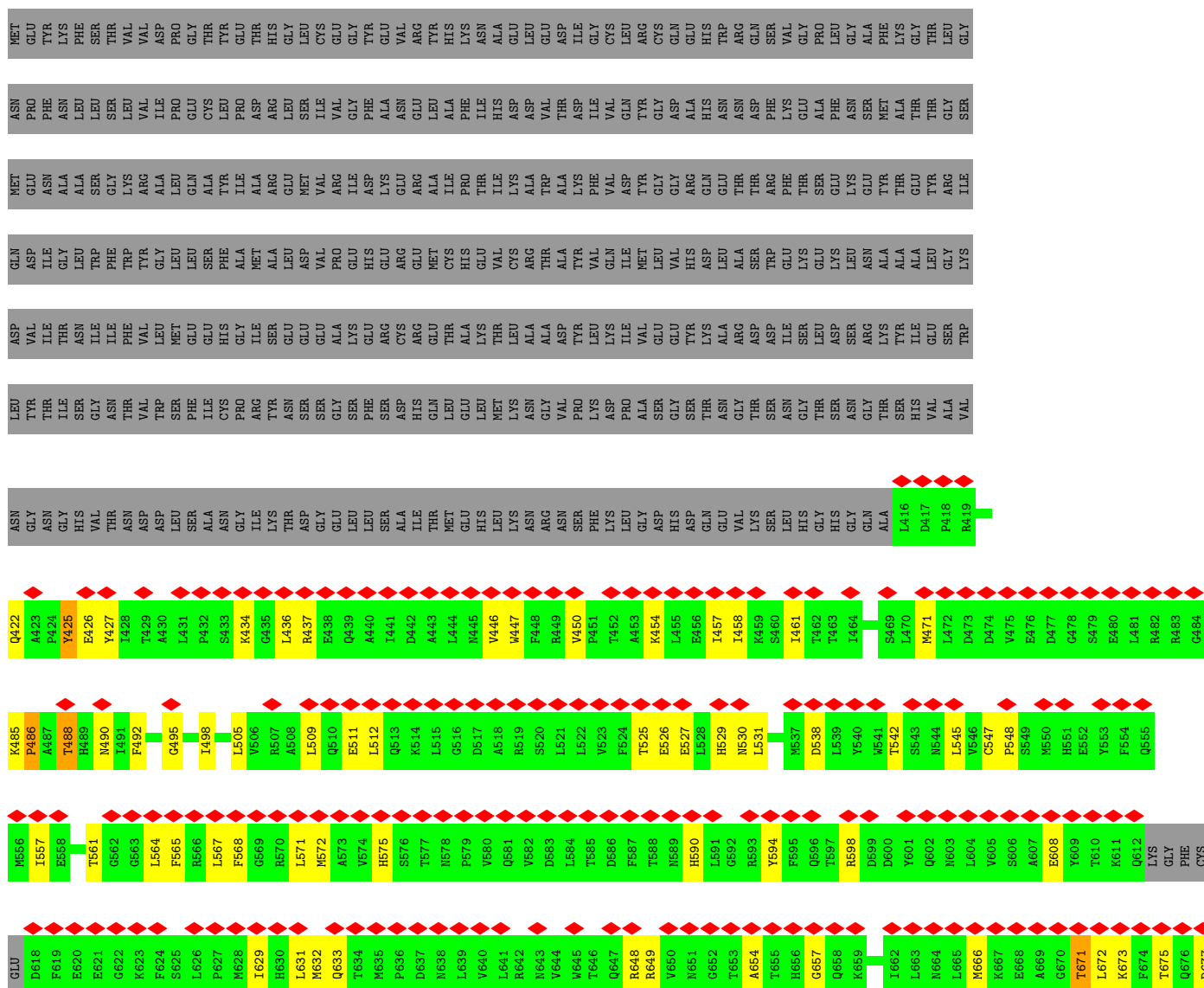


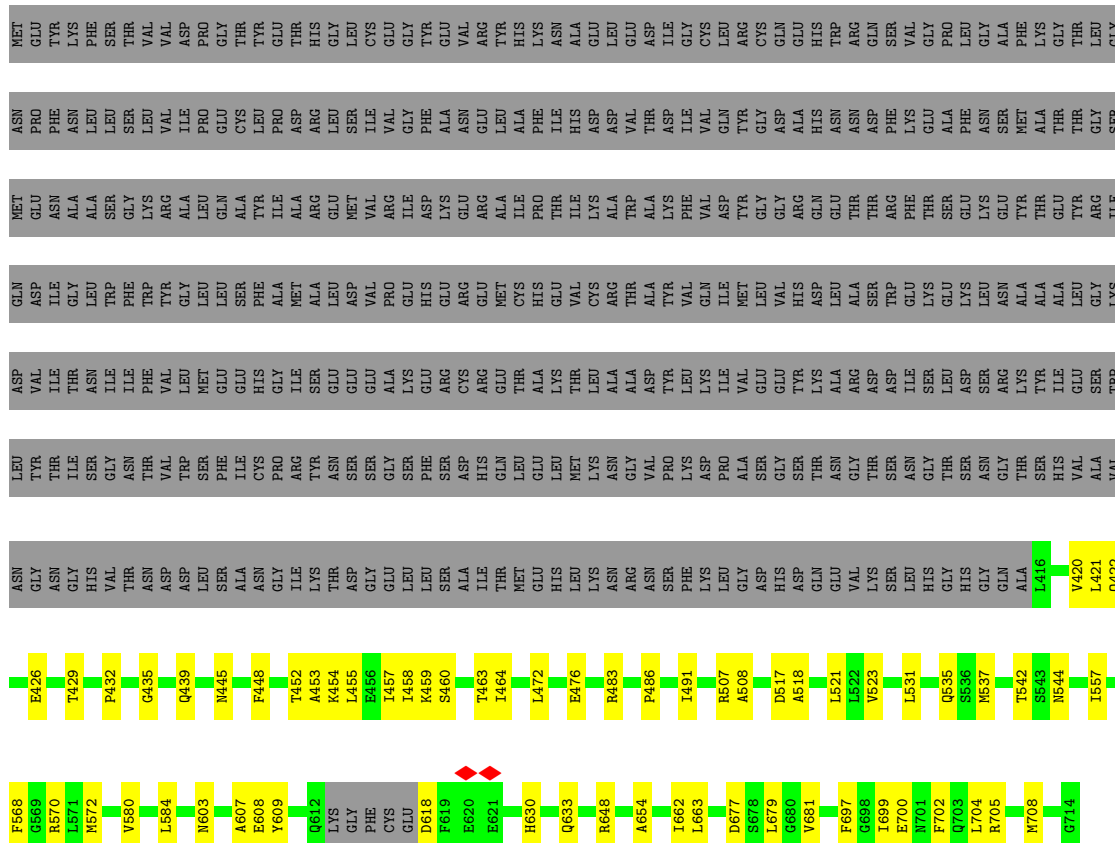




● Molecule 1: Steltatriene synthase







Chain O:



E621	E438	ASN	GLN	ASP	GLN	MET	ASN	MET	ASN
L626	I441	ASN	GLY	THR	ILE	GLU	PRO	GLU	TYR
M635	K459	HIS	VAL	THR	GLY	ASN	LEU	LEU	PHE
L639	L470	ASN	THR	ASN	ILE	ILE	SER	LEU	ASN
V640	M471	ASN	THR	THR	PHE	THR	VAL	VAL	VAL
V644	L472	ASP	TRP	VAL	GLY	THR	ILE	ASP	ASP
R648	V475	LEU	SER	THR	GLY	GLU	PRO	PRO	PRO
A654	R482	SER	PHE	ILE	GLU	GLN	GLY	GLY	GLY
G657	T488	ASN	ILE	THR	THR	THR	ALA	ALA	THR
T661	H489	GLY	THR	THR	THR	THR	ASP	CYS	TYR
L662	S500	GLY	THR	SER	GLU	MET	GLY	GLY	CYS
L663	Q504	LEU	GLY	SER	GLU	ARG	VAL	VAL	GLY
N664	L512	LEU	LEU	PHE	GLU	HIS	GLY	GLY	TYR
K667	D517	SER	ALA	SER	ASP	LYS	ALA	ALA	GLU
E668	A518	ALA	ILE	ASN	CYS	ARG	GLU	ASN	VAL
F674	R519	ILE	THR	GLN	ARG	GLU	GLU	GLU	ARG
D677	S520	MET	THR	HIS	GLU	THR	ALA	LEU	TYR
V681	L521	GLY	GLU	GLU	ALA	CYS	ILE	ALA	HIS
E687	M537	HIS	LEU	LYS	LYS	THR	THR	ILE	ASN
K688	M550	LEU	LYS	THR	VAL	ILE	HIS	HIS	ALA
S689	ASN	ASN	ASN	GLY	THR	ASP	TRP	ASP	GLU
K696	V563	ASN	VAL	VAL	ASP	ALA	ALA	THR	ASP
L704	F564	SER	PRO	THR	TYR	LYS	ASP	ILE	ILE
L707	Q555	PHE	LYS	LEU	LEU	VAL	PHE	GLY	GLY
M708	R556	LYS	ASP	ASP	ILE	GLN	VAL	LEU	CYS
L711	I557	LEU	GLY	ILE	ILE	THR	THR	TYR	ARG
G714	V582	ASP	GLY	GLU	VAL	GLY	ASP	CYS	GLN
	D586	HIS	THR	THR	HIS	ARG	ALA	ALA	HIS
	F587	GLN	THR	ASN	ASP	GLU	THR	TRP	ARG
	T597	VAL	GLY	GLY	ALA	LEU	THR	ASN	GLN
	R598	LYS	THR	SER	ASP	SER	THR	ASP	SER
	Q602	SER	ASN	ILE	ASP	THR	ARG	PHE	LYS
	N603	LEU	ASN	GLU	THR	THR	THR	GLY	VAL
		HIS	GLY	LYS	LYS	GLU	SER	ALA	PRO
	R612	HIS	SER	ASP	LEU	GLY	GLU	PHE	GLY
	LYS	GLY	ASN	SER	ASN	LYS	ASN	ASN	ASN
	GLY	GLN	GLY	THR	GLY	THR	GLY	SER	ALA
	PHE	ALA	THR	THR	THR	THR	THR	THR	PHE
	CYS	ALA	SER	ILE	ILE	ALA	ALA	ALA	LYS
	GLU	GLY	VAL	GLU	GLU	GLY	THR	THR	GLY
	D618	GLY	VAL	GLU	GLY	THR	THR	THR	THR
	F619	GLY	VAL	THR	THR	THR	THR	THR	GLY
		THR	THR	THR	THR	THR	THR	THR	THR

Chain P:

[illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	108639	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.482	Depositor
Minimum map value	-0.295	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	296.0, 296.0, 296.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.74, 0.74, 0.74	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	0.18	1/2409 (0.0%)	0.51	7/3257 (0.2%)
1	B	0.18	0/2409	0.66	12/3257 (0.4%)
1	C	0.17	0/2409	0.54	5/3257 (0.2%)
1	D	0.15	0/2409	0.42	2/3257 (0.1%)
1	E	0.20	0/2409	0.56	6/3257 (0.2%)
1	F	0.22	0/2409	0.64	11/3257 (0.3%)
1	G	0.15	0/2409	0.51	6/3257 (0.2%)
1	H	0.27	2/2409 (0.1%)	0.59	12/3257 (0.4%)
1	I	0.23	1/2409 (0.0%)	0.38	3/3257 (0.1%)
1	J	0.21	1/2409 (0.0%)	0.63	9/3257 (0.3%)
1	K	0.24	1/2409 (0.0%)	0.68	11/3257 (0.3%)
1	L	0.19	1/2409 (0.0%)	0.46	2/3257 (0.1%)
1	M	0.15	0/2409	0.46	8/3257 (0.2%)
1	N	0.20	1/2409 (0.0%)	0.51	6/3257 (0.2%)
1	O	0.15	0/2409	0.48	6/3257 (0.2%)
1	P	0.16	0/2409	0.49	6/3257 (0.2%)
1	Q	0.20	1/2409 (0.0%)	0.53	4/3257 (0.1%)
1	R	0.17	0/2409	0.52	9/3257 (0.3%)
All	All	0.19	9/43362 (0.0%)	0.54	125/58626 (0.2%)

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	418	PRO	N-CD	9.71	1.61	1.47
1	I	418	PRO	N-CD	9.19	1.60	1.47
1	L	636	PRO	N-CD	-6.14	1.39	1.47
1	N	608	GLU	CA-C	6.03	1.60	1.52
1	Q	451	PRO	N-CD	-6.02	1.39	1.47

The worst 5 of 125 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	588	THR	N-CA-C	11.31	123.61	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	618	ASP	N-CA-CB	11.12	129.41	110.50
1	K	633	GLN	N-CA-C	10.90	123.24	111.36
1	B	476	GLU	N-CA-C	10.43	122.73	111.36
1	B	618	ASP	N-CA-C	-10.29	82.20	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2364	0	2359	48	0
1	B	2364	0	2360	49	0
1	C	2364	0	2360	66	0
1	D	2364	0	2360	60	0
1	E	2364	0	2360	60	0
1	F	2364	0	2360	63	0
1	G	2364	0	2360	40	0
1	H	2364	0	2360	49	0
1	I	2364	0	2360	57	0
1	J	2364	0	2360	65	0
1	K	2364	0	2360	46	0
1	L	2364	0	2360	59	0
1	M	2364	0	2360	37	0
1	N	2364	0	2360	40	0
1	O	2364	0	2360	39	0
1	P	2364	0	2360	29	0
1	Q	2364	0	2359	44	0
1	R	2364	0	2360	22	0
All	All	42552	0	42478	823	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 10.

The worst 5 of 823 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:447:TRP:CZ2	1:A:701:ASN:ND2	1.71	1.55
1:F:427:TYR:OH	1:F:485:LYS:HG2	1.20	1.31
1:C:582:VAL:HG11	1:C:697:PHE:CZ	1.67	1.29
1:O:470:LEU:HD22	1:O:482:ARG:HH22	1.06	1.18
1:B:582:VAL:HG11	1:B:697:PHE:HE1	1.05	1.18

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	290/714 (41%)	287 (99%)	3 (1%)	0	100	100
1	B	290/714 (41%)	286 (99%)	4 (1%)	0	100	100
1	C	290/714 (41%)	283 (98%)	7 (2%)	0	100	100
1	D	290/714 (41%)	284 (98%)	6 (2%)	0	100	100
1	E	290/714 (41%)	284 (98%)	6 (2%)	0	100	100
1	F	290/714 (41%)	280 (97%)	10 (3%)	0	100	100
1	G	290/714 (41%)	287 (99%)	3 (1%)	0	100	100
1	H	290/714 (41%)	286 (99%)	4 (1%)	0	100	100
1	I	290/714 (41%)	286 (99%)	4 (1%)	0	100	100
1	J	290/714 (41%)	286 (99%)	4 (1%)	0	100	100
1	K	290/714 (41%)	281 (97%)	9 (3%)	0	100	100
1	L	290/714 (41%)	281 (97%)	9 (3%)	0	100	100
1	M	290/714 (41%)	288 (99%)	2 (1%)	0	100	100
1	N	290/714 (41%)	287 (99%)	3 (1%)	0	100	100
1	O	290/714 (41%)	286 (99%)	4 (1%)	0	100	100
1	P	290/714 (41%)	283 (98%)	7 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	290/714 (41%)	284 (98%)	6 (2%)	0	100	100
1	R	290/714 (41%)	285 (98%)	5 (2%)	0	100	100
All	All	5220/12852 (41%)	5124 (98%)	96 (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	261/616 (42%)	259 (99%)	2 (1%)	73	78
1	B	261/616 (42%)	261 (100%)	0	100	100
1	C	261/616 (42%)	260 (100%)	1 (0%)	84	84
1	D	261/616 (42%)	260 (100%)	1 (0%)	84	84
1	E	261/616 (42%)	258 (99%)	3 (1%)	65	75
1	F	261/616 (42%)	257 (98%)	4 (2%)	57	71
1	G	261/616 (42%)	257 (98%)	4 (2%)	57	71
1	H	261/616 (42%)	260 (100%)	1 (0%)	84	84
1	I	261/616 (42%)	257 (98%)	4 (2%)	57	71
1	J	261/616 (42%)	258 (99%)	3 (1%)	65	75
1	K	261/616 (42%)	261 (100%)	0	100	100
1	L	261/616 (42%)	259 (99%)	2 (1%)	73	78
1	M	261/616 (42%)	259 (99%)	2 (1%)	73	78
1	N	261/616 (42%)	259 (99%)	2 (1%)	73	78
1	O	261/616 (42%)	258 (99%)	3 (1%)	65	75
1	P	261/616 (42%)	258 (99%)	3 (1%)	65	75
1	Q	261/616 (42%)	259 (99%)	2 (1%)	73	78
1	R	261/616 (42%)	258 (99%)	3 (1%)	65	75
All	All	4698/11088 (42%)	4658 (99%)	40 (1%)	68	76

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	N	663	LEU
1	Q	704	LEU
1	O	438	GLU
1	P	420	VAL
1	R	428	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
1	P	660	GLN
1	R	489	HIS
1	F	660	GLN
1	F	529	HIS
1	R	490	ASN

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

There are no chain breaks in this entry.

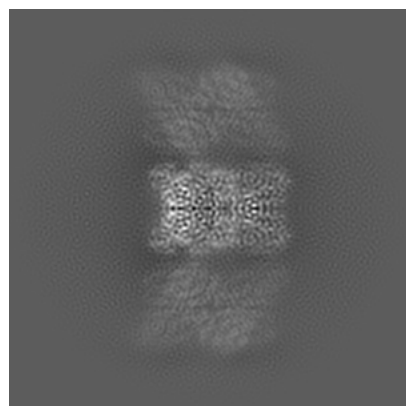
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66433. These allow visual inspection of the internal detail of the map and identification of artifacts.

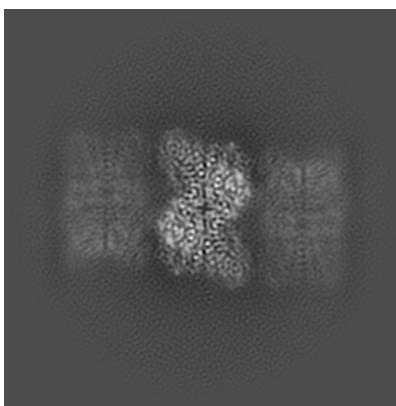
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

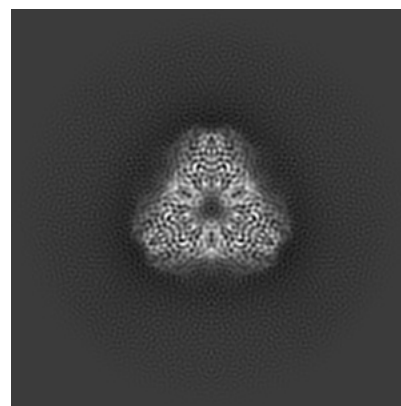
6.1.1 Primary map



X

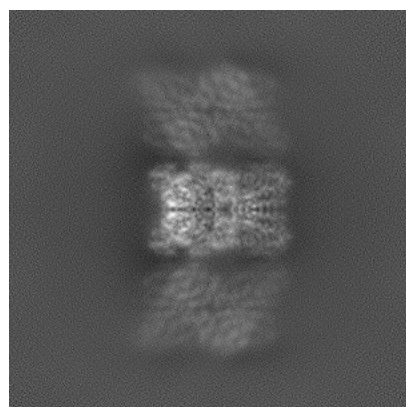


Y

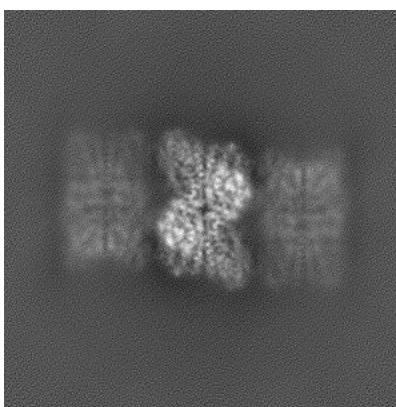


Z

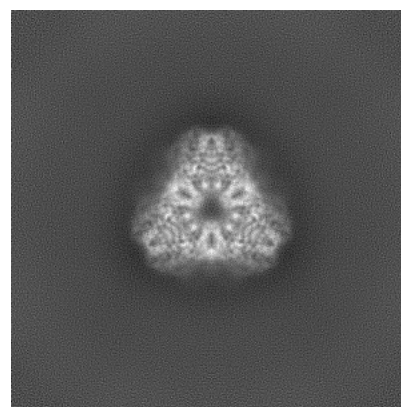
6.1.2 Raw map



X



Y

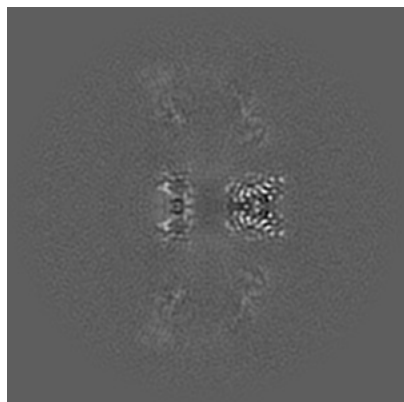


Z

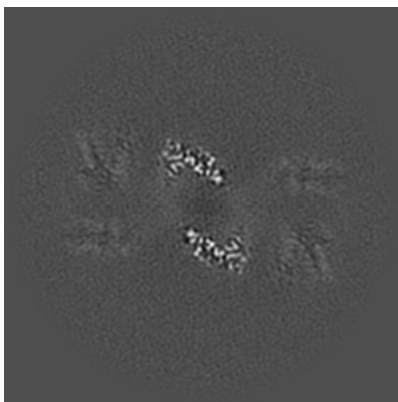
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

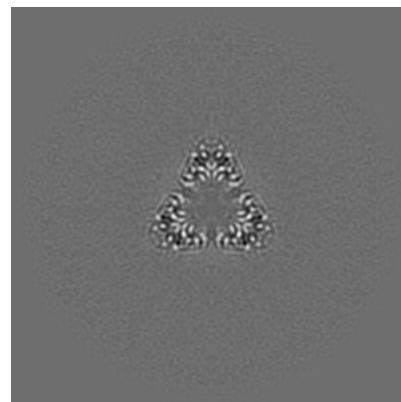
6.2.1 Primary map



X Index: 200

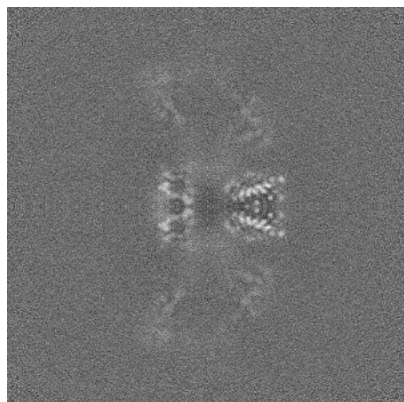


Y Index: 200

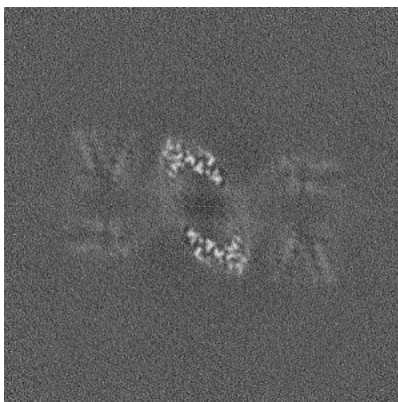


Z Index: 200

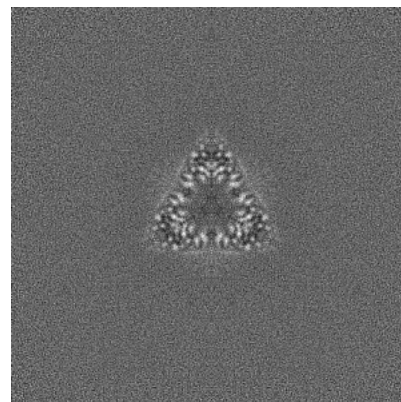
6.2.2 Raw map



X Index: 200



Y Index: 200

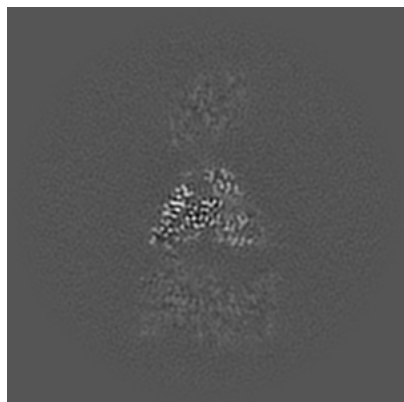


Z Index: 200

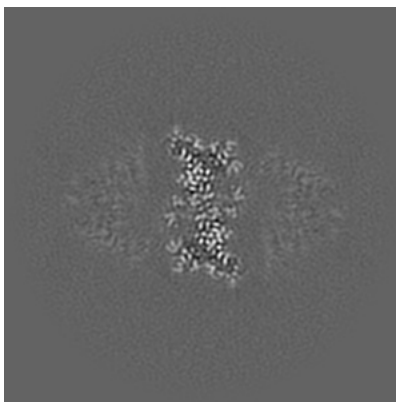
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

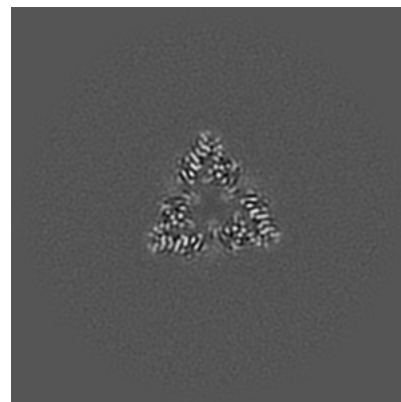
6.3.1 Primary map



X Index: 165

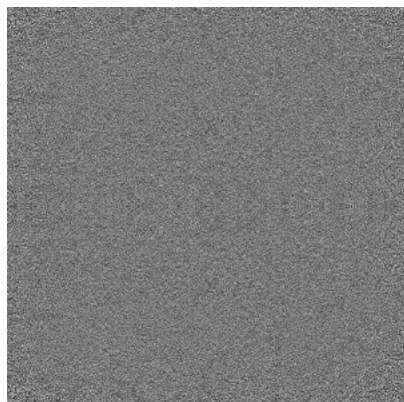


Y Index: 171

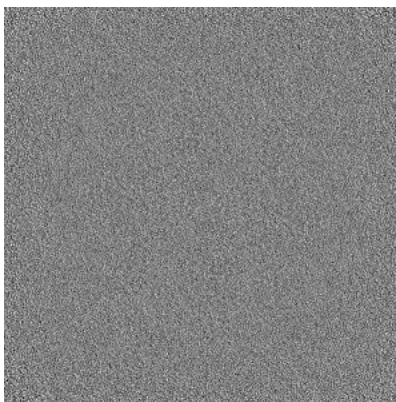


Z Index: 193

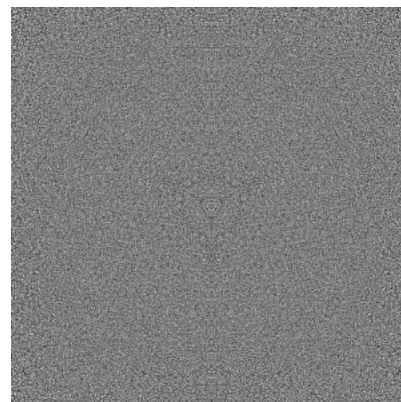
6.3.2 Raw map



X Index: 0



Y Index: 0

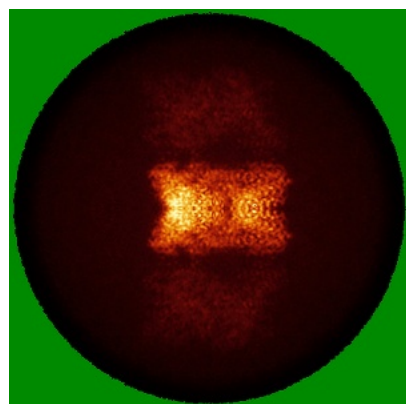


Z Index: 0

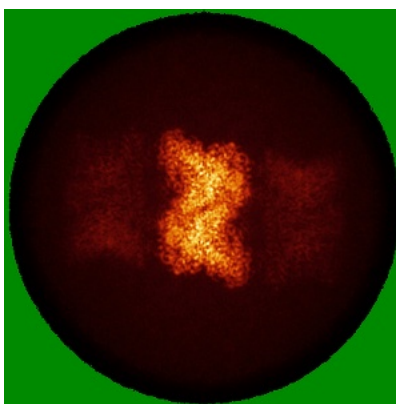
The images above show the largest variance slices of the map in three orthogonal directions.

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

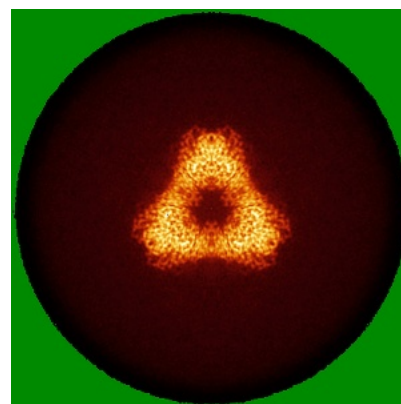
6.4.1 Primary map



X

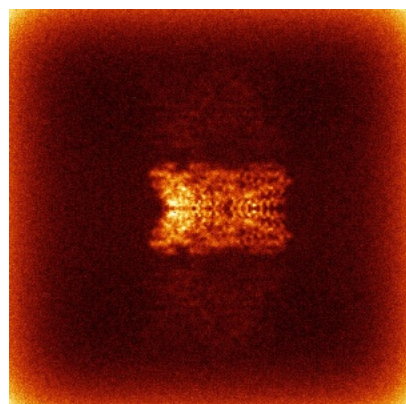


Y

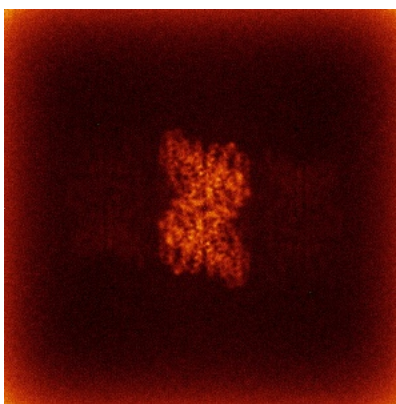


Z

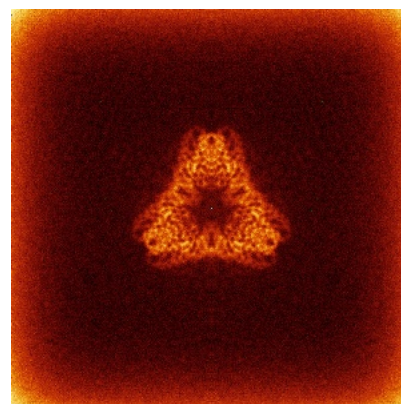
6.4.2 Raw map



X



Y

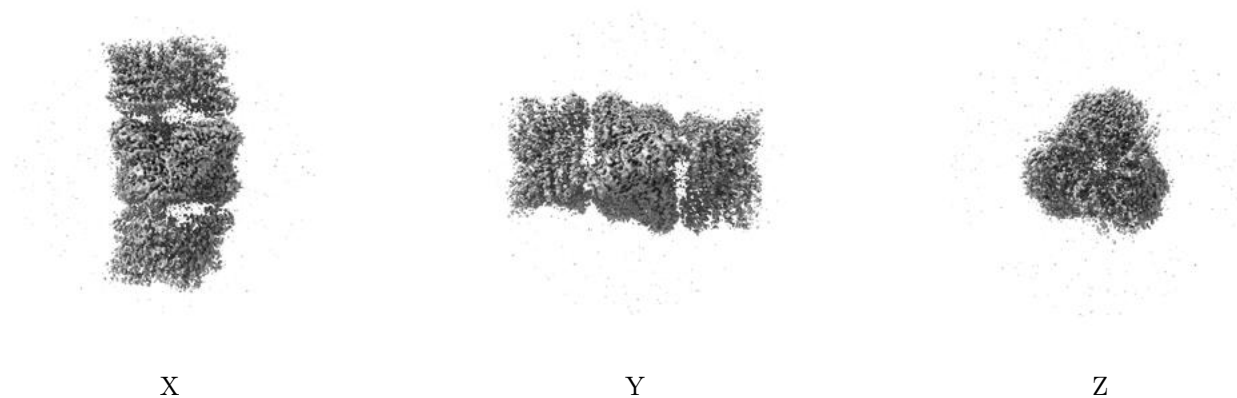


Z

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.

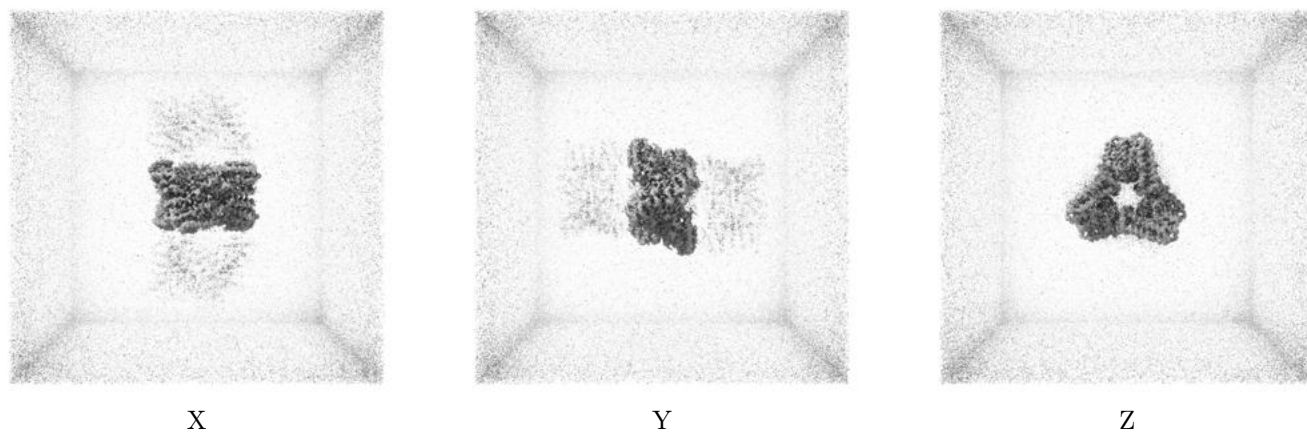
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

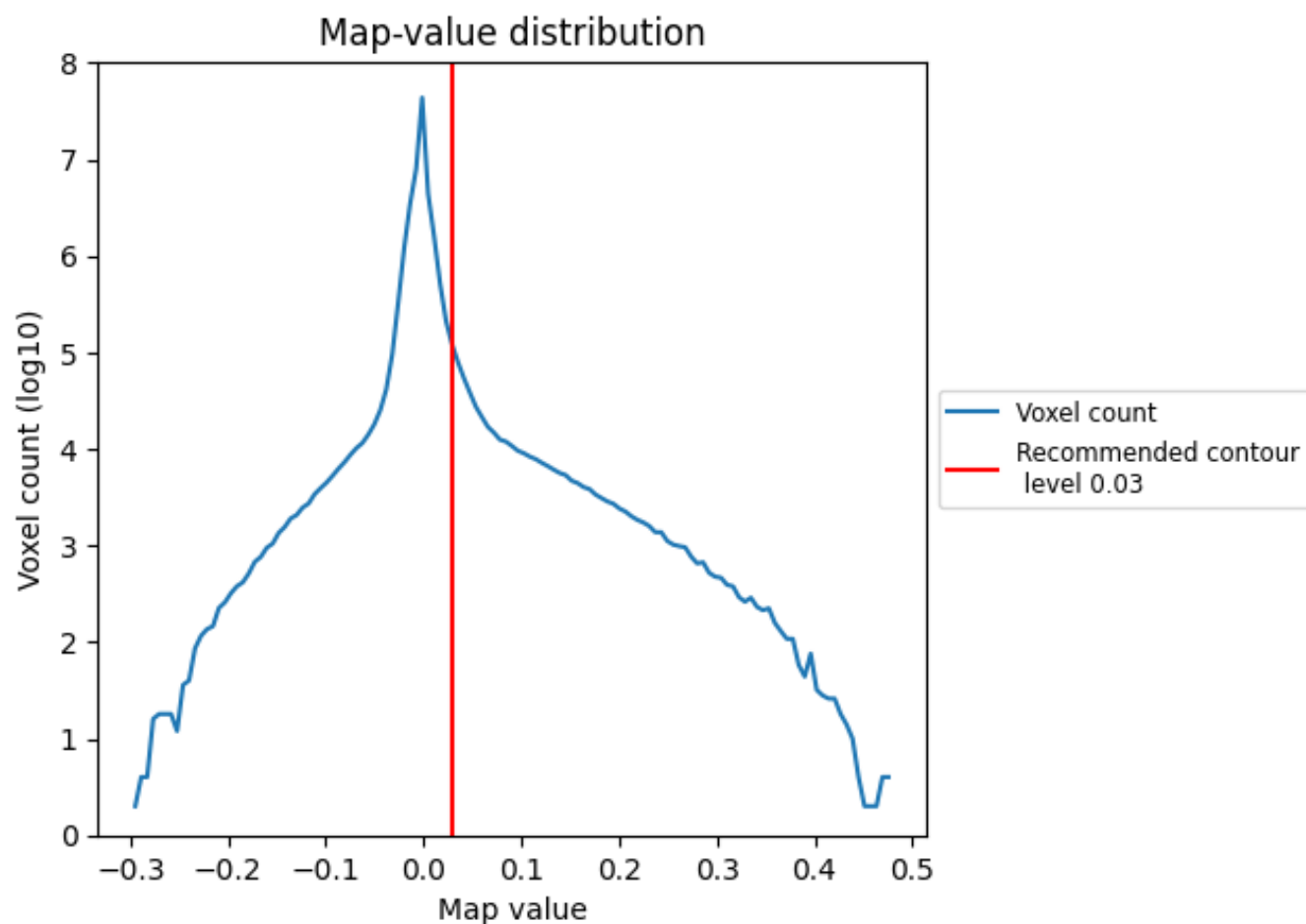
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

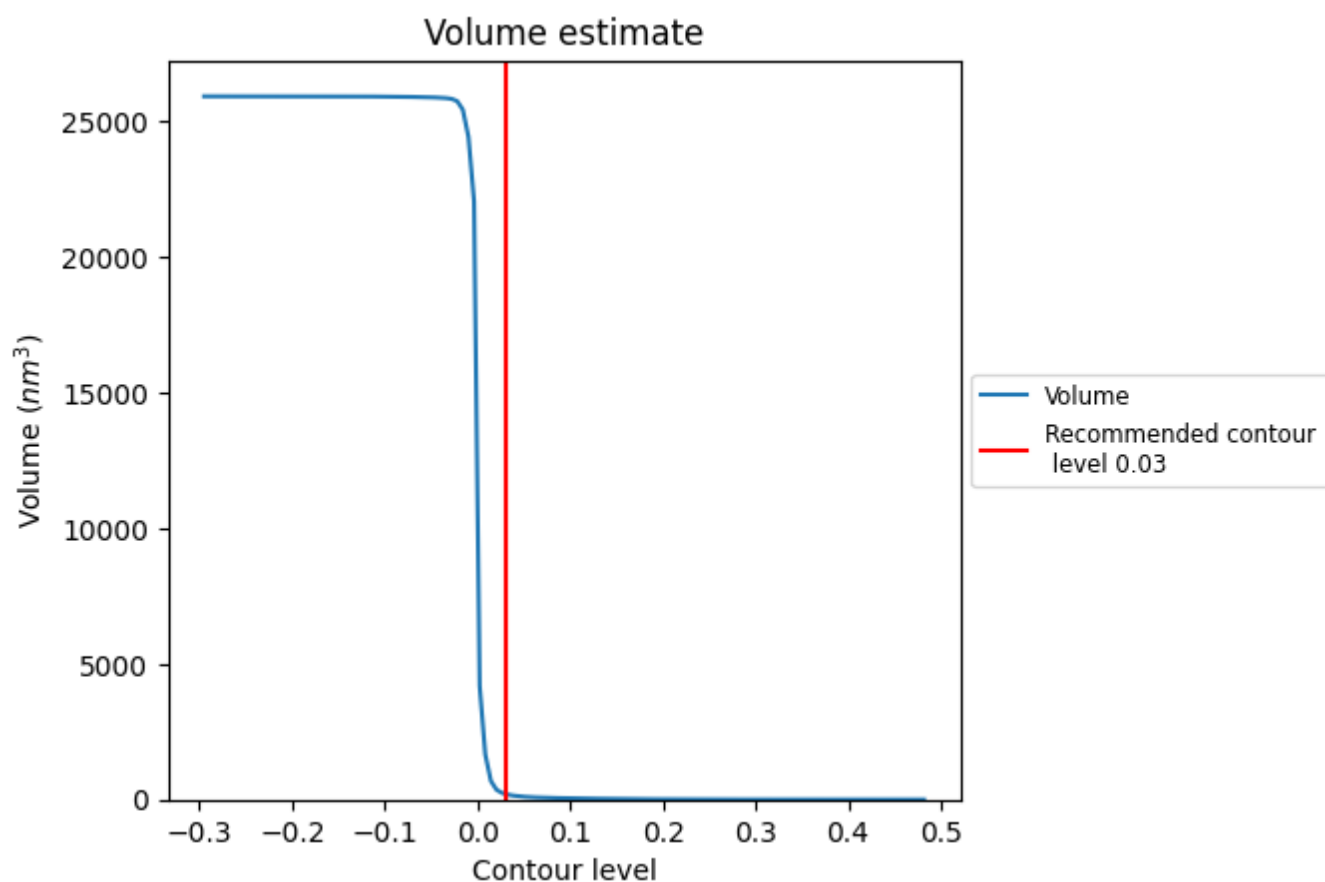
This section contains the results of statistical analysis of the map.

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.

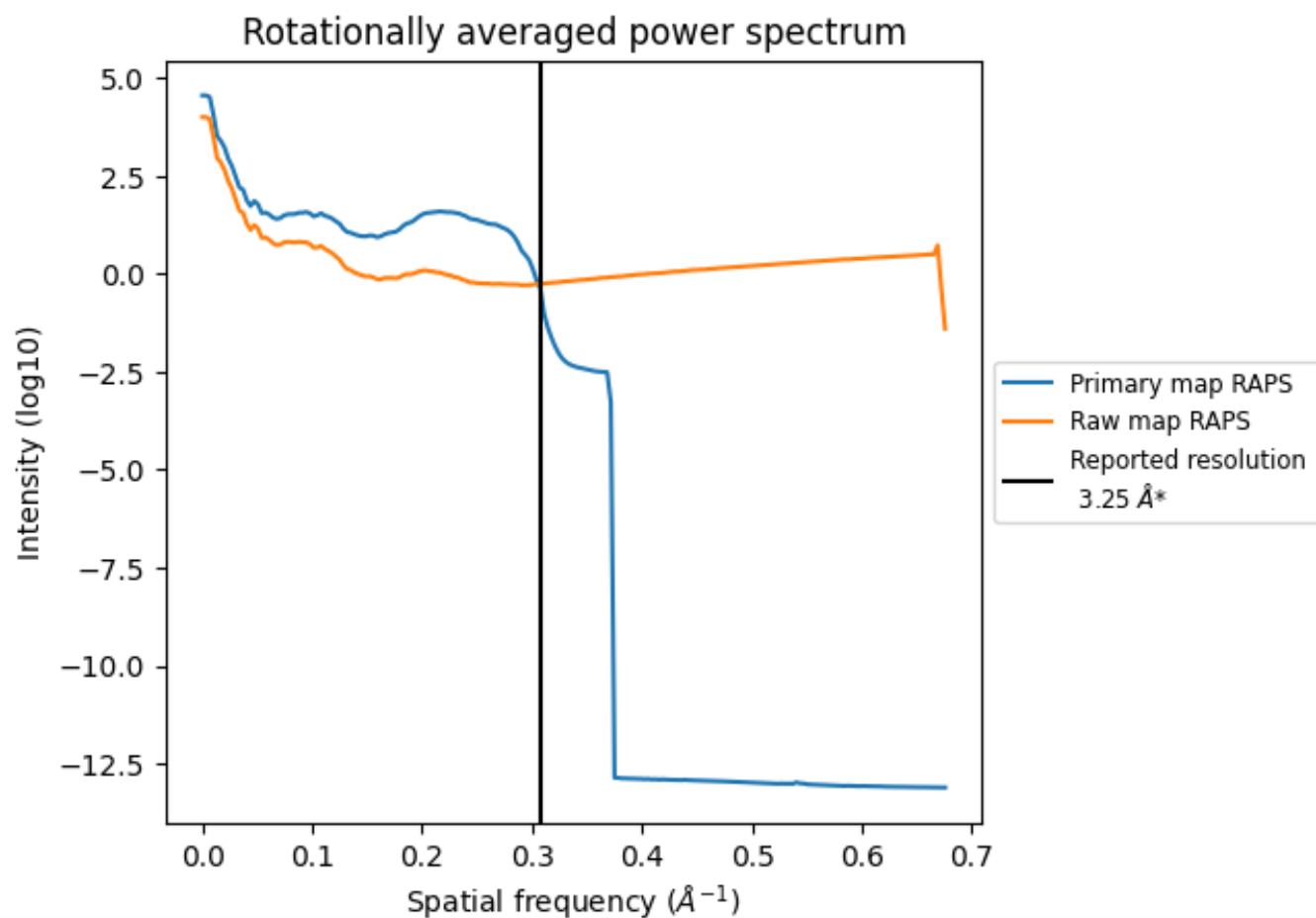
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 209 nm³; this corresponds to an approximate mass of 189 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 ⓘ

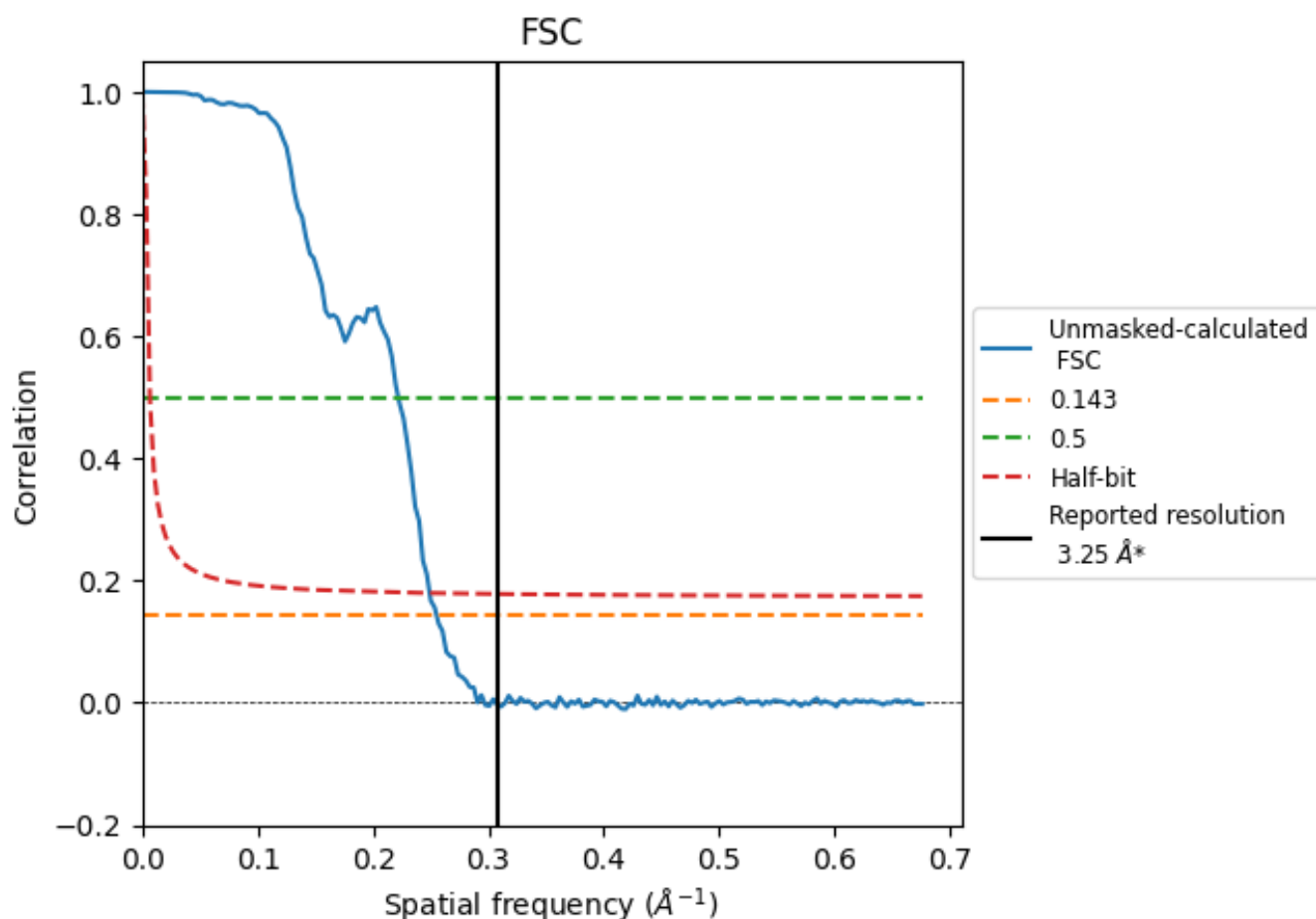


*Reported resolution corresponds to spatial frequency of 0.308 Å⁻¹

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 0.308 Å⁻¹

8.2 Resolution estimates [i](#)

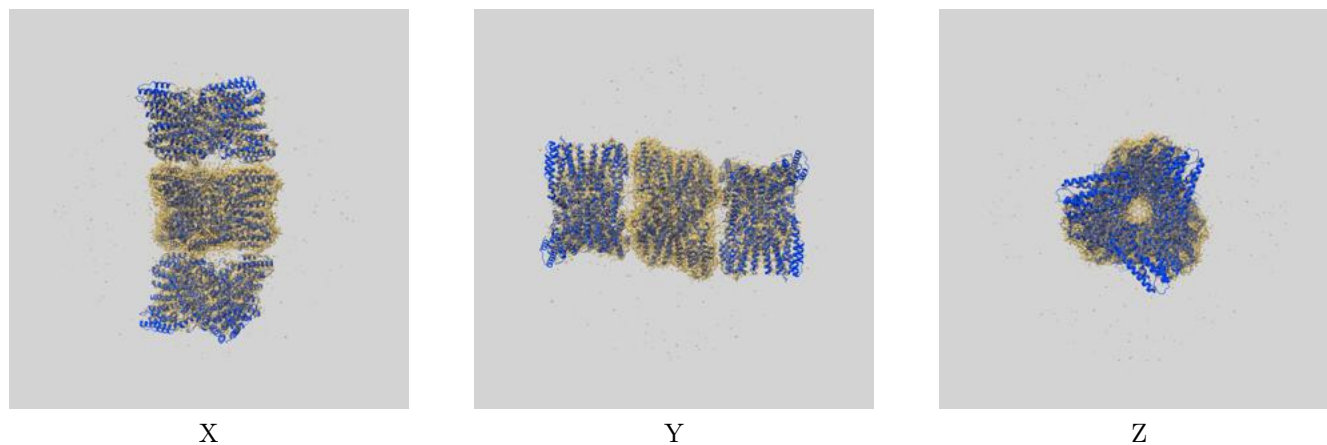
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.25	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.92	4.51	4.02

*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 3.92 differs from the reported value 3.25 by more than 10 %

9 Map-model fit [i](#)

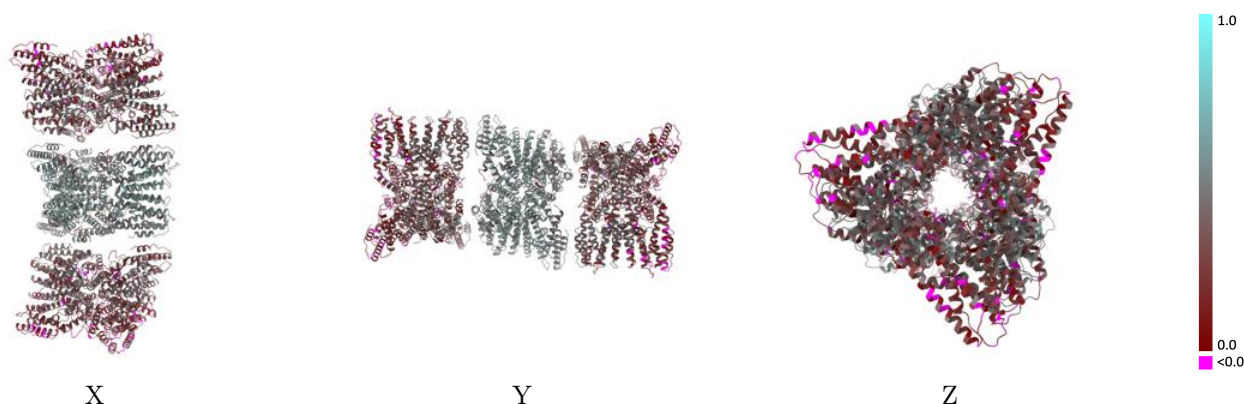
This section contains information regarding the fit between EMDB map EMD-66433 and PDB model 9X0F. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



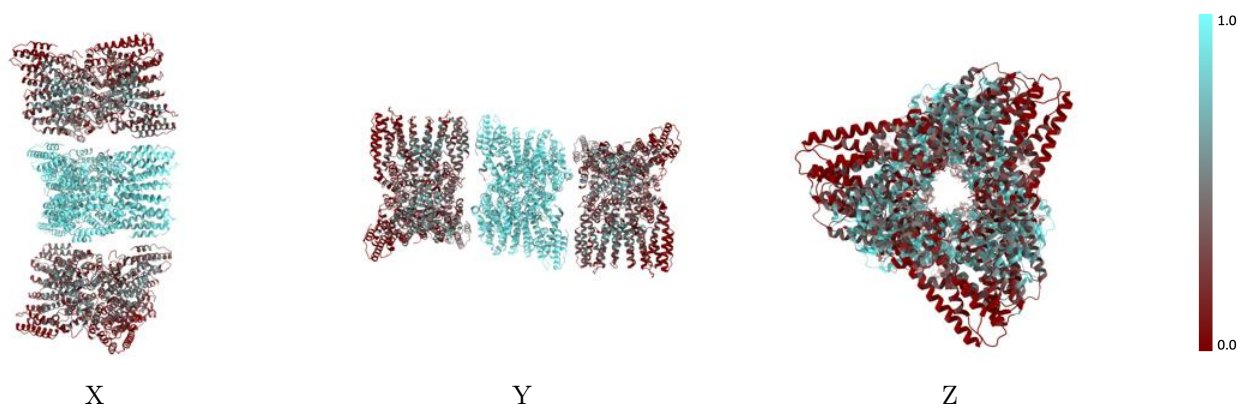
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



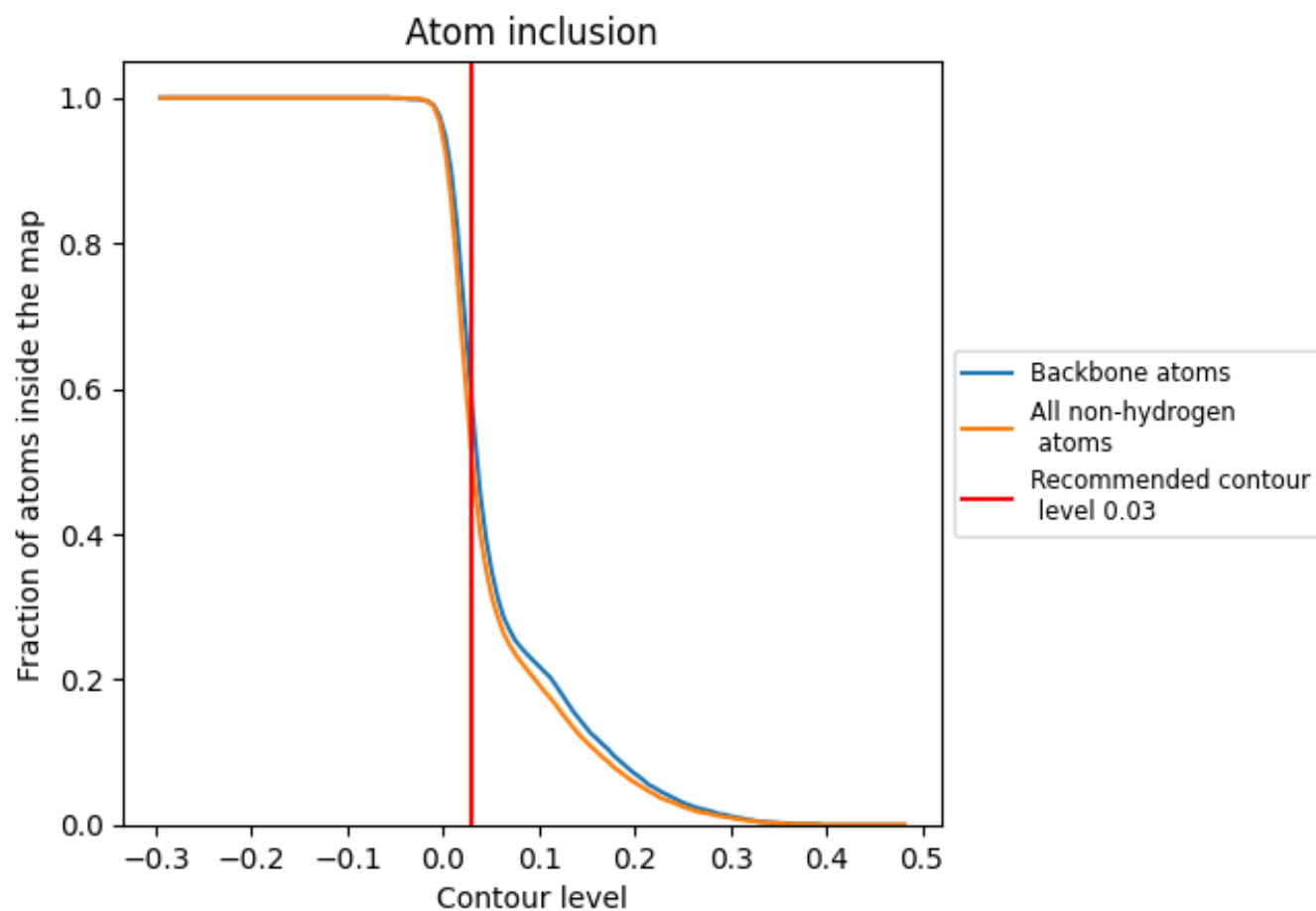
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 58% of all backbone atoms, 50% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5050	 0.3600
A	 0.3860	 0.3470
B	 0.2310	 0.2390
C	 0.2260	 0.2370
D	 0.2310	 0.2380
E	 0.3700	 0.3220
F	 0.3790	 0.3400
G	 0.2310	 0.2370
H	 0.3880	 0.3480
I	 0.3870	 0.3380
J	 0.3860	 0.3450
K	 0.2190	 0.2400
L	 0.2260	 0.2330
M	 0.9060	 0.5060
N	 0.9110	 0.5070
O	 0.9040	 0.5060
P	 0.9040	 0.5040
Q	 0.8970	 0.4900
R	 0.9020	 0.5040

