



## wwPDB EM Validation Summary Report ⓘ

Nov 26, 2023 – 10:15 PM JST

PDB ID : 8I6P  
EMDB ID : EMD-35202  
Title : The cryo-EM structure of OsCyc1 tetramer state  
Authors : Ma, X.L.; Xu, H.F.; Tong, Y.R.; Luo, Y.F.; Dong, Q.H.; Jiang, T.  
Deposited on : 2023-01-29  
Resolution : 3.50 Å (reported)

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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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev70  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

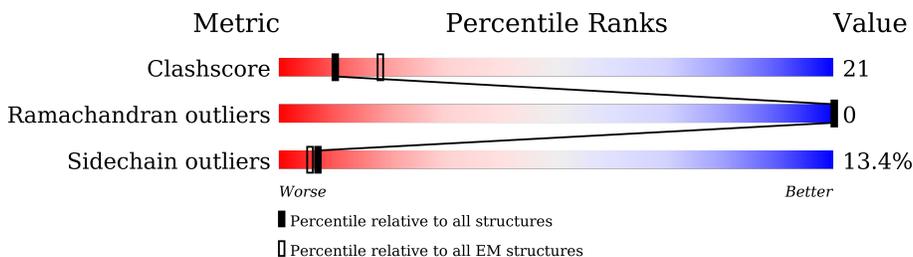
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.50 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	775	 44% 40% 5% 11%
1	B	775	 45% 39% 5% 11%
1	C	775	 46% 38% 5% 11%
1	D	775	 46% 38% 5% 11%

## 2 Entry composition i

There is only 1 type of molecule in this entry. The entry contains 22016 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 Syn-copalyl diphosphate synthase, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	688	Total	C	N	O	S	0	0
			5504	3492	944	1033	35		
1	C	688	Total	C	N	O	S	0	0
			5504	3492	944	1033	35		
1	D	688	Total	C	N	O	S	0	0
			5504	3492	944	1033	35		
1	A	688	Total	C	N	O	S	0	0
			5504	3492	944	1033	35		

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	768	GLU	-	expression tag	UNP Q0JF02
B	769	PHE	-	expression tag	UNP Q0JF02
B	770	HIS	-	expression tag	UNP Q0JF02
B	771	HIS	-	expression tag	UNP Q0JF02
B	772	HIS	-	expression tag	UNP Q0JF02
B	773	HIS	-	expression tag	UNP Q0JF02
B	774	HIS	-	expression tag	UNP Q0JF02
B	775	HIS	-	expression tag	UNP Q0JF02
C	768	GLU	-	expression tag	UNP Q0JF02
C	769	PHE	-	expression tag	UNP Q0JF02
C	770	HIS	-	expression tag	UNP Q0JF02
C	771	HIS	-	expression tag	UNP Q0JF02
C	772	HIS	-	expression tag	UNP Q0JF02
C	773	HIS	-	expression tag	UNP Q0JF02
C	774	HIS	-	expression tag	UNP Q0JF02
C	775	HIS	-	expression tag	UNP Q0JF02
D	768	GLU	-	expression tag	UNP Q0JF02
D	769	PHE	-	expression tag	UNP Q0JF02
D	770	HIS	-	expression tag	UNP Q0JF02
D	771	HIS	-	expression tag	UNP Q0JF02
D	772	HIS	-	expression tag	UNP Q0JF02
D	773	HIS	-	expression tag	UNP Q0JF02

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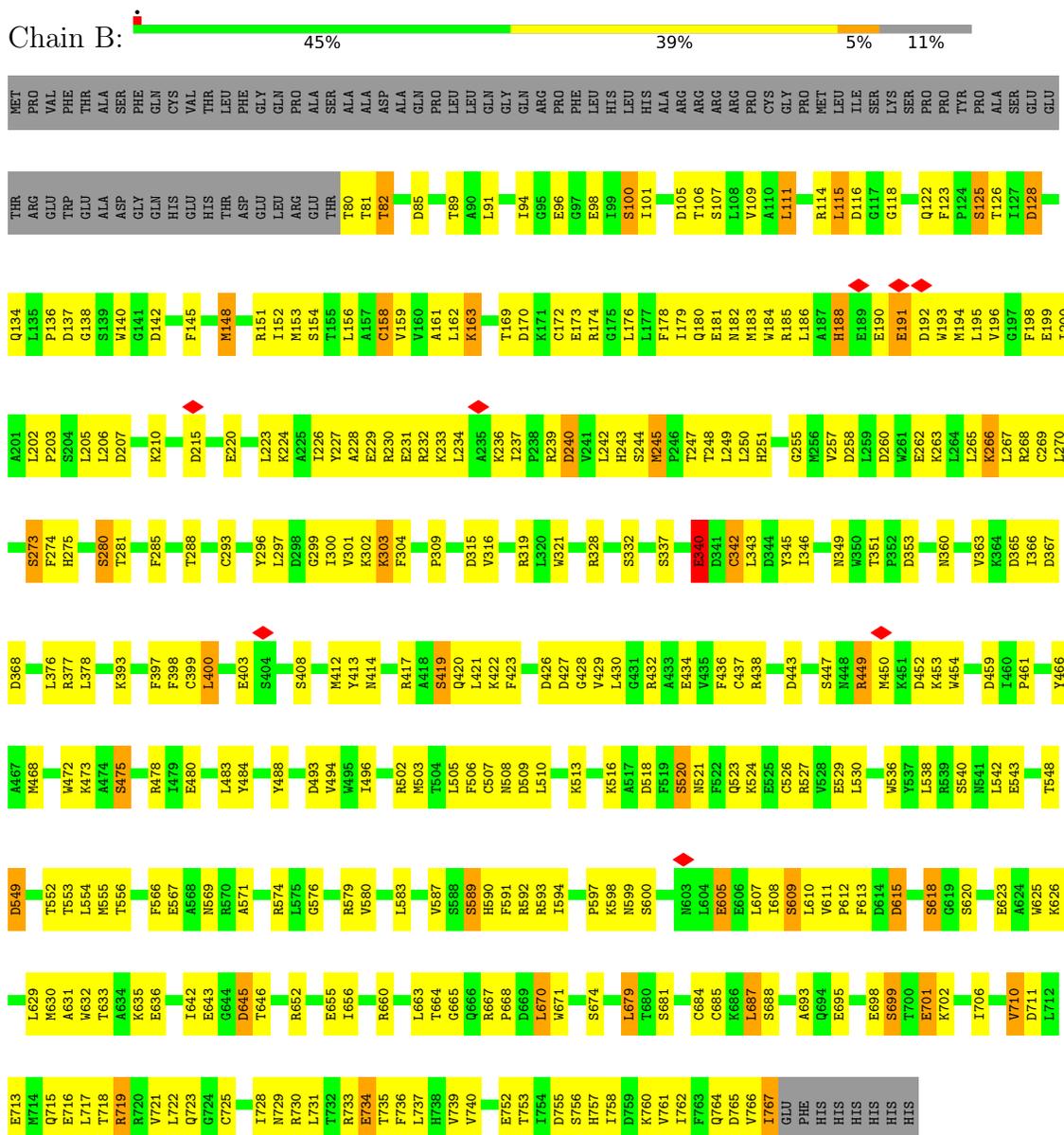
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Chain	Residue	Modelled	Actual	Comment	Reference
D	774	HIS	-	expression tag	UNP Q0JF02
D	775	HIS	-	expression tag	UNP Q0JF02
A	768	GLU	-	expression tag	UNP Q0JF02
A	769	PHE	-	expression tag	UNP Q0JF02
A	770	HIS	-	expression tag	UNP Q0JF02
A	771	HIS	-	expression tag	UNP Q0JF02
A	772	HIS	-	expression tag	UNP Q0JF02
A	773	HIS	-	expression tag	UNP Q0JF02
A	774	HIS	-	expression tag	UNP Q0JF02
A	775	HIS	-	expression tag	UNP Q0JF02

### 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: Syn-copalyl diphosphate synthase, chloroplastic



- Molecule 1: Syn-copalyl diphosphate synthase, chloroplastic

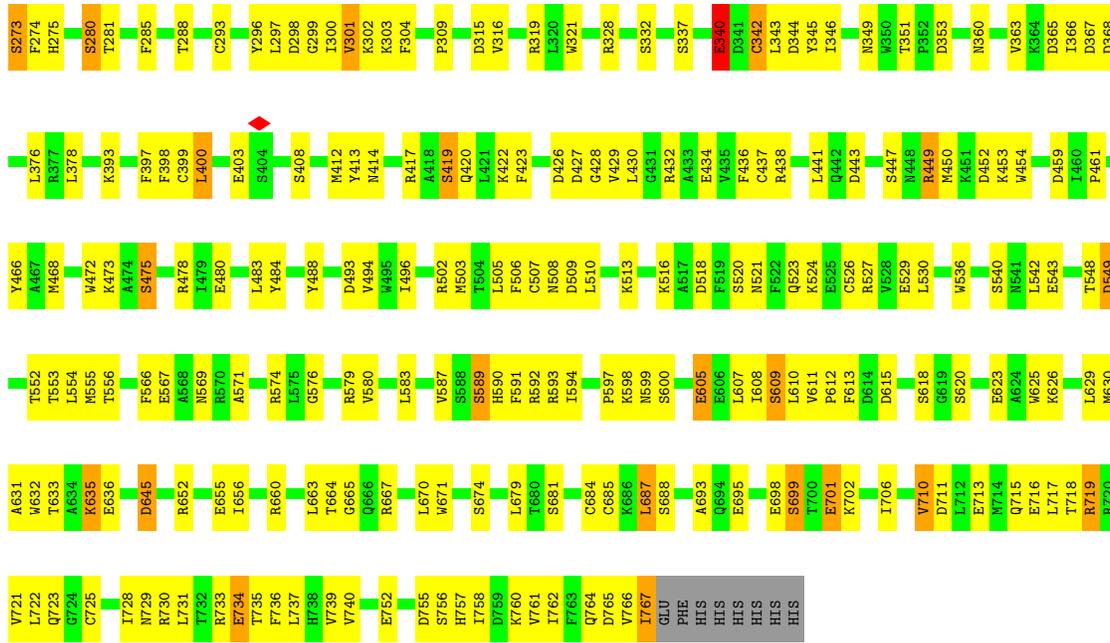


MET	THR	Q134	A201	F274	D365	A467	T556	E636	R720
PRO	ARG	L136	L202	H275	I366	M468	F566	I642	V721
VAL	GLU	P136	P203	H276	D367	W472	E567	D645	L722
PHE	TRP	D137	L206	S280	D368	A474	A568	R652	Q723
THR	GLU	G138	L206	T281	L376	A474	N569	G652	G725
ALA	ALA	S139	D207	F285	R377	S475	R570	R652	C726
SER	ASP	S139	D207	F285	L378	A571	A571	E655	I728
PHE	GLY	G141	K210	T288	K393	R478	R574	I656	N729
GLN	GLN	G142	D215	C293	F397	E480	L575	R730	R730
CYS	HIS	F145	E220	Y296	F398	L483	G576	L731	L731
THR	THR	M148	L223	L297	C399	Y484	R579	R732	R732
LEU	LEU	R151	L223	D298	L400	Y488	V580	E734	E734
PHE	ASP	I152	K224	G299	E403	D493	L583	T735	T735
GLY	LEU	I152	A225	R300	E403	D493	L583	T736	T736
GLN	LEU	M153	L226	I300	S408	V494	V587	V739	V739
PRO	ARG	M153	A226	V301	M412	V494	S588	V740	V740
ALA	GLU	S154	A227	K302	Y413	M503	H590	E752	E752
SER	THR	T155	A228	K303	R417	T504	R592	T753	T753
ALA	THR	L156	E229	F304	A418	L505	R593	I754	I754
ALA	ALA	A157	E229	F304	S419	F506	L594	S756	S756
ASP	ASP	T81	R230	P309	R417	F506	I594	H757	H757
ALA	ALA	V159	R230	P309	A418	F506	I594	T760	T760
GLN	GLN	V160	R232	P309	S419	F506	I594	V761	V761
PRO	PRO	A161	R232	P309	S419	F506	I594	W761	W761
LEU	LEU	L162	R233	D315	R417	T504	L594	S674	S674
LEU	LEU	K163	L234	V316	A418	L505	I594	L679	L679
GLN	GLN	L163	L234	V316	S419	F506	I594	T680	T680
GLY	GLY	T169	K236	R319	R417	F506	I594	C507	C507
GLN	GLN	D170	L320	L320	K422	N508	N599	S681	S681
ARG	ARG	G85	P238	W321	F423	D509	N599	S681	S681
PRO	PRO	E96	R239	R325	D426	D427	S600	C684	C684
PHE	PHE	G97	D240	R325	D427	G428	S600	C685	C685
LEU	LEU	E98	V241	R328	D427	G428	S600	C685	C685
HIS	HIS	I99	G175	L242	D427	G428	S600	C685	C685
LEU	LEU	S100	G175	H243	D427	G428	S600	C685	C685
HIS	HIS	I101	L176	L329	D427	G428	S600	C685	C685
ALA	ALA	I101	L176	L329	D427	G428	S600	C685	C685
ARG	ARG	D105	M245	S332	R432	A433	S609	R690	R690
ARG	ARG	T106	P246	S337	A433	A433	L610	A693	A693
ARG	ARG	Q180	T247	S337	E434	E434	V611	Q694	Q694
ARG	ARG	E181	T248	S337	V435	V435	P612	Q694	Q694
ARG	ARG	N182	L249	E940	F436	K524	F613	E695	E695
PRO	PRO	M183	L250	D341	C437	K524	F613	E695	E695
CYS	CYS	A110	H251	C342	R438	C526	D614	S698	S698
GLY	GLY	L184	G255	L343	D443	C526	D614	S698	S698
PRO	PRO	R185	G255	D344	D443	V528	S618	T700	T700
MET	MET	L186	M256	D344	S447	E529	S618	E701	E701
LEU	LEU	A187	V257	I346	S447	E529	S618	E701	E701
SER	SER	H188	D258	I346	R449	E529	S618	E701	E701
ILE	ILE	E189	E262	N349	M450	L542	E623	I706	I706
LYS	LYS	E190	E262	V350	M450	L542	E623	I706	I706
SER	SER	F123	E262	T351	K451	E543	E623	I706	I706
PRO	PRO	F124	L265	F952	D452	E543	E623	I706	I706
PRO	PRO	S125	K266	D353	K452	E543	E623	I706	I706
TYR	TYR	T126	L267	G354	K452	E543	E623	I706	I706
PRO	PRO	M194	K268	W454	D452	E543	E623	I706	I706
PRO	PRO	I127	R268	L355	D452	E543	E623	I706	I706
TYR	TYR	D128	C269	L355	D452	E543	E623	I706	I706
ALA	ALA	W129	L270	N360	D452	E543	E623	I706	I706
GLU	GLU	Q132	G197	I460	D452	E543	E623	I706	I706
GLU	GLU	N133	F198	P461	D452	E543	E623	I706	I706
			E199	Y466	D452	E543	E623	I706	I706
			I200		D452	E543	E623	I706	I706
			S273		D452	E543	E623	I706	I706

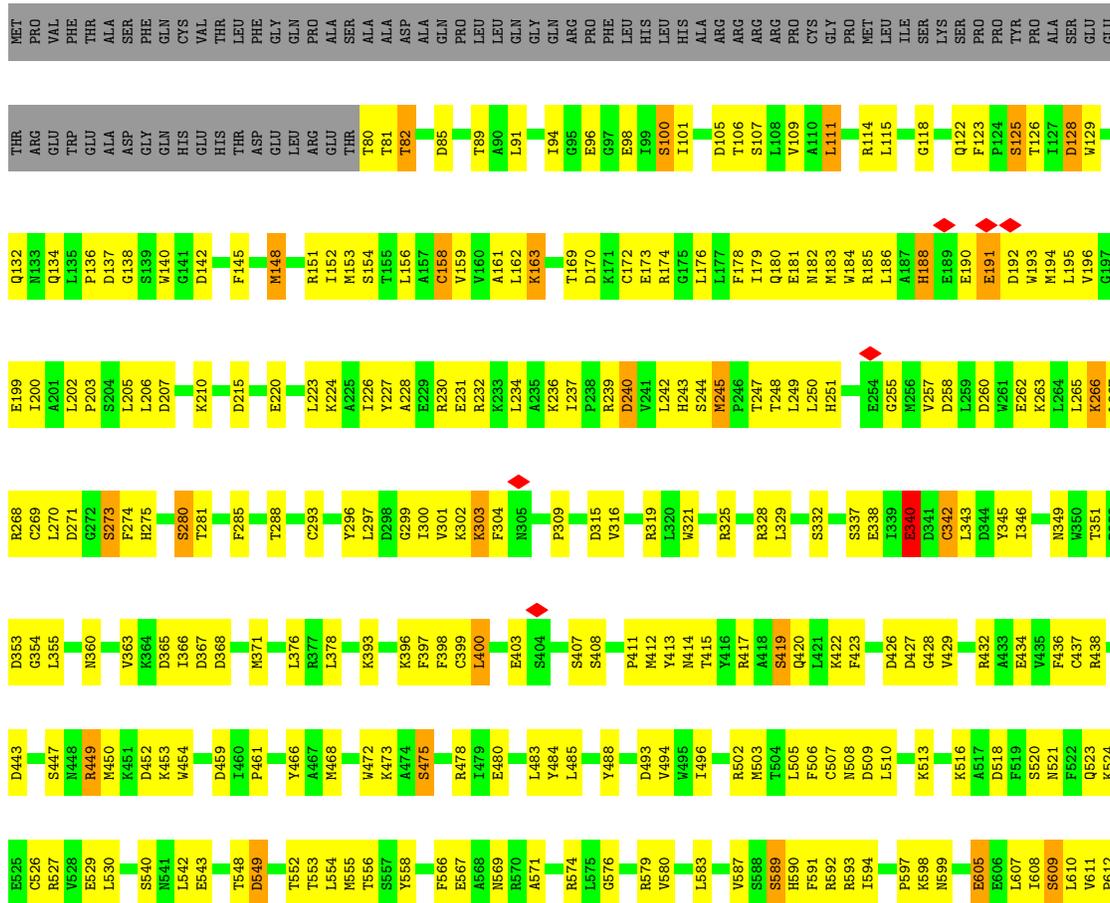
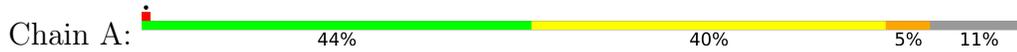
• Molecule 1: Syn-copalyl diphosphate synthase, chloroplastic



MET	THR	Q134	I200	A201	THR	Q134	A201	F274	D365	A467	T556	E636	R720
PRO	ARG	L136	A201	L202	ARG	L136	A201	H275	I366	M468	F566	I642	V721
VAL	GLU	P136	L202	P203	GLU	P136	L202	H276	D367	W472	E567	D645	L722
PHE	TRP	D137	P203	L206	TRP	D137	P203	S280	D368	A474	A568	R652	Q723
THR	GLU	G138	L206	L206	GLU	G138	L206	T281	D368	A474	A568	R652	G725
ALA	ALA	S139	L206	D207	ALA	S139	L206	F285	D368	A474	A568	R652	C726
SER	ASP	S139	D207	K210	ASP	S139	D207	F285	D368	A474	A568	R652	I728
PHE	GLY	G141	K210	D215	GLY	G141	K210	T288	D368	A474	A568	R652	N729
GLN	GLN	G142	D215	E220	GLN	G142	D215	C293	D368	A474	A568	R652	R730
CYS	HIS	F145	E220	L223	CYS	F145	E220	Y296	D368	A474	A568	R652	L731
THR	THR	M148	L223	K224	THR	M148	L223	L297	D368	A474	A568	R652	R731
LEU	LEU	R151	L223	A225	LEU	R151	L223	D298	D368	A474	A568	R652	R732
PHE	ASP	I152	K224	A226	PHE	I152	K224	G299	D368	A474	A568	R652	E734
GLY	LEU	I152	M153	A227	GLY	I152	M153	R300	D368	A474	A568	R652	T735
GLN	LEU	M153	L226	A228	GLN	M153	L226	I300	D368	A474	A568	R652	T736
PRO	ARG	S154	L226	A227	PRO	S154	L226	V301	D368	A474	A568	R652	V739
SER	THR	T155	Y227	E229	SER	T155	Y227	K302	D368	A474	A568	R652	V740
ALA	ALA	L156	A228	E229	ALA	L156	A228	F304	D368	A474	A568	R652	W740
ALA	ALA	A157	E229	E229	ALA	A157	E229	F304	D368	A474	A568	R652	E752
ASP	ASP	T81	R230	R230	ASP	T81	R230	P309	D368	A474	A568	R652	T753
ALA	ALA	V159	R230	R230	ALA	V159	R230	P309	D368	A474	A568	R652	I754
GLN	GLN	V160	R232	R232	GLN	V160	R232	P309	D368	A474	A568	R652	S756
PRO	PRO	A161	R232	R232	PRO	A161	R232	P309	D368	A474	A568	R652	H757
LEU	LEU	L162	R233	R233	LEU	L162	R233	D315	D368	A474	A568	R652	T760
LEU	LEU	K163	L234	L234	LEU	K163	L234	V316	D368	A474	A568	R652	V761
GLN	GLN	L163	L234	L234	GLN	L163	L234	V316	D368	A474	A568	R652	W761
GLY	GLY	T169	K236	K236	GLY	T169	K236	L320	D368	A474	A568	R652	S674
GLN	GLN	D170	L320	L320	GLN	D170	L320	L320	D368	A474	A568	R652	L679
ARG	ARG	G85	P238	P238	ARG	G85	P238	W321	D368	A474	A568	R652	T680
PRO	PRO	E96	R239	R239	PRO	E96	R239	R325	D368	A474	A568	R652	C507
PHE	PHE	G97	D240	D240	PHE	G97	D240	R325	D368	A474	A568	R652	S681
LEU	LEU	E98	V241	V241	LEU	E98	V241	R328	D368	A474	A568	R652	S681
HIS	HIS	I99	G175	G175	HIS	I99	G175	L242	D368	A474	A568	R652	S681
LEU	LEU	S100	G175	G175	LEU	S100	G175	H243	D368	A474	A568	R652	S681
HIS	HIS	I101	L176	L176	HIS	I101	L176	L329	D368	A474	A568	R652	S681
ALA	ALA	I101	L176	L176	ALA	I101	L176	L329	D368	A474	A568	R652	S681
ARG	ARG	D105	M245	M245	ARG	D105	M245	S332	D368	A474	A568	R652	S681
ARG	ARG	T106	P246	P246	ARG	T106	P246	S337	D368	A474	A568	R652	S681
ARG	ARG	Q180	T247	T247	ARG	Q180	T247	S337	D368	A474	A568	R652	S681
ARG	ARG	E181	T248	T248	ARG	E181	T248	S337	D368	A474	A568	R652	S681
ARG	ARG	N182	L249	L249	ARG	N182	L249	S337	D368	A474	A568	R652	S681
PRO	PRO	M183	L250	L250	PRO	M183	L250	S337	D368	A474	A568	R652	S681
CYS	CYS	A110	H251	H251	CYS	A110	H251	S337	D368	A474	A568	R652	S681
GLY	GLY	L184	G255	G255	GLY	L184	G255	S337	D368	A474	A568	R652	S681
PRO	PRO	R185	M256	M256	PRO	R185	M256	S337	D368	A474	A568	R652	S681
MET	MET	L186	V257	V257	MET	L186	V257	S337	D368	A474	A568	R652	S681
LEU	LEU	A187	D258	D258	LEU	A187	D258	S337	D368	A474	A568	R652	S681
SER	SER	H188	E262	E262	SER	H188	E262	S337	D368	A474	A568	R652	S681
LYS	LYS	E190	E262	E262	LYS	E190	E262	S337	D368	A474	A568	R652	S681
SER	SER	F123	E262	E262	SER	F123	E262	S337	D368	A474	A568	R652	S681
PRO	PRO	F124	L265	L265	PRO	F124	L265	S337	D368	A474	A568	R652	S681
PRO	PRO	S125	K266	K266	PRO	S125	K266	S337	D368	A474	A568	R652	S681
TYR	TYR	T126	L267	L267	TYR	T126	L267	S337	D368	A474	A568	R652	S681
PRO	PRO	M194	R268	R268	PRO	M194	R268	S337	D368	A474	A568	R652	S681
PRO	PRO	I127	R268	R268	PRO	I127	R268	S337	D368	A474	A568	R652	S681
TYR	TYR	D128	C269	C269	TYR	D128	C269	S337	D368	A474	A568	R652	S681
ALA	ALA	W129	L270	L270	ALA	W129	L270	S337	D368	A474	A568	R652	S681
SER	SER	T126	L270	L270	SER	T126	L270	S337	D368	A474	A568	R652	S681
GLU	GLU	Q132	G197	G197	GLU	Q132	G197	S337	D368	A474	A568	R652	S681
GLU	GLU	F198	F198	F198	GLU	F198	F198	S337	D368	A474	A568	R652	S681
		E199	E199	E199									



● Molecule 1: Syn-copalyl diphosphate synthase, chloroplastic





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	149837	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 ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.065	Depositor
Minimum map value	-0.036	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0137	Depositor
Map size (Å)	299.6, 299.6, 299.6	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	0.34	0/5627	0.47	1/7615 (0.0%)
1	B	0.34	0/5627	0.47	1/7615 (0.0%)
1	C	0.34	0/5627	0.47	1/7615 (0.0%)
1	D	0.34	0/5627	0.47	1/7615 (0.0%)
All	All	0.34	0/22508	0.47	4/30460 (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	B	340	GLU	CA-CB-CG	5.32	125.10	113.40
1	C	340	GLU	CA-CB-CG	5.31	125.08	113.40
1	A	340	GLU	CA-CB-CG	5.31	125.08	113.40
1	D	340	GLU	CA-CB-CG	5.30	125.06	113.40

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	5504	0	5413	237	0
1	B	5504	0	5413	249	0
1	C	5504	0	5413	229	0
1	D	5504	0	5413	236	0
All	All	22016	0	21652	938	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 21.

The worst 5 of 938 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:D:297:LEU:O	1:D:301:VAL:CG1	1.94	1.16
1:D:297:LEU:O	1:D:301:VAL:HG12	1.44	1.11
1:D:631:ALA:C	1:D:635:LYS:HE2	1.77	1.05
1:A:631:ALA:C	1:A:635:LYS:HE2	1.82	0.98
1:B:631:ALA:O	1:B:635:LYS:HE3	1.67	0.93

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	686/775 (88%)	647 (94%)	39 (6%)	0	100	100
1	B	686/775 (88%)	647 (94%)	39 (6%)	0	100	100
1	C	686/775 (88%)	647 (94%)	39 (6%)	0	100	100
1	D	686/775 (88%)	646 (94%)	40 (6%)	0	100	100
All	All	2744/3100 (88%)	2587 (94%)	157 (6%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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	597/672 (89%)	517 (87%)	80 (13%)	4	21
1	B	597/672 (89%)	518 (87%)	79 (13%)	4	21
1	C	597/672 (89%)	517 (87%)	80 (13%)	4	21
1	D	597/672 (89%)	516 (86%)	81 (14%)	3	20
All	All	2388/2688 (89%)	2068 (87%)	320 (13%)	7	21

5 of 320 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	688	SER
1	A	493	ASP
1	D	734	GLU
1	A	245	MET
1	A	615	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	709	GLN
1	A	531	ASN
1	D	723	GLN
1	A	291	GLN
1	A	678	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 monosaccharides 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.

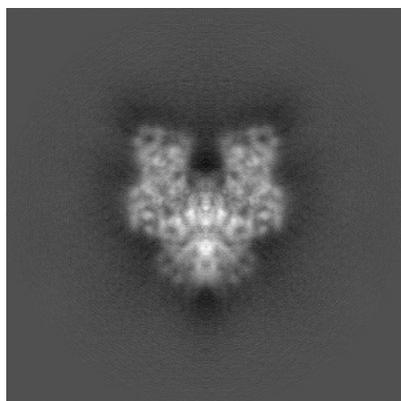
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35202. These allow visual inspection of the internal detail of the map and identification of artifacts.

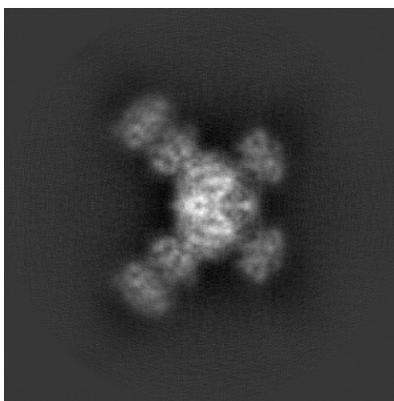
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

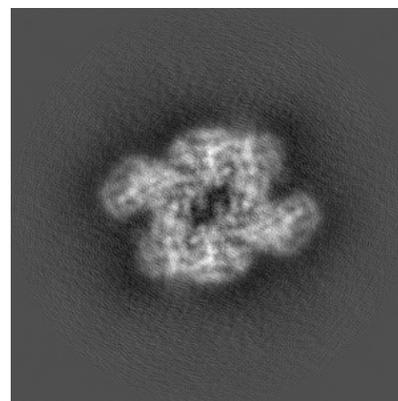
#### 6.1.1 Primary map



X



Y

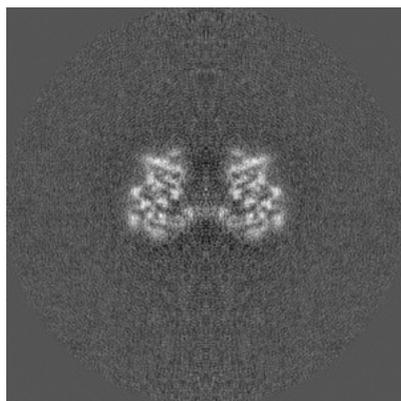


Z

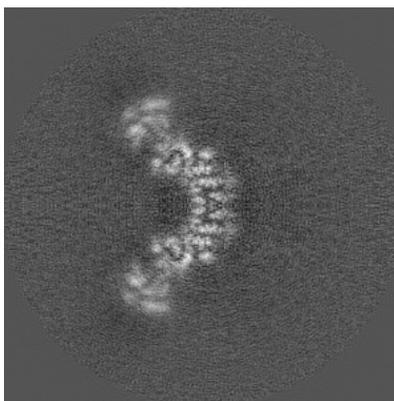
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

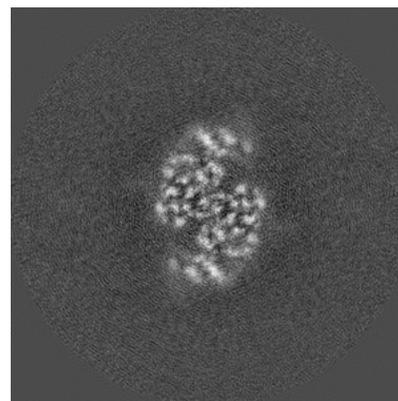
#### 6.2.1 Primary map



X Index: 140



Y Index: 140

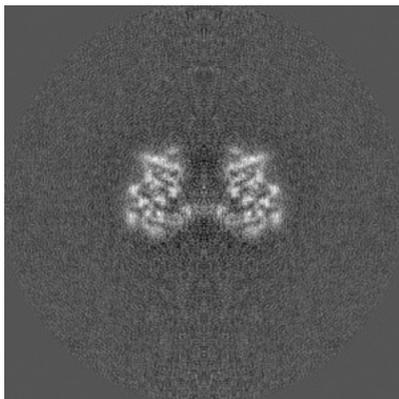


Z Index: 140

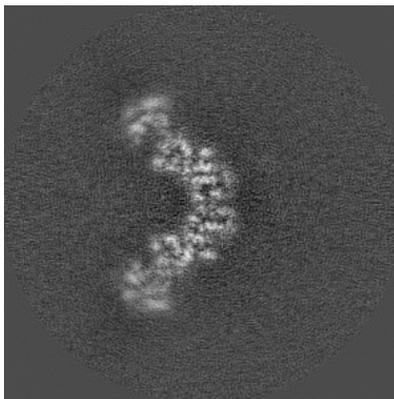
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

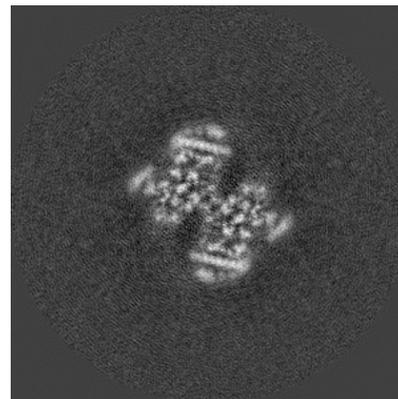
### 6.3.1 Primary map



X Index: 140



Y Index: 141

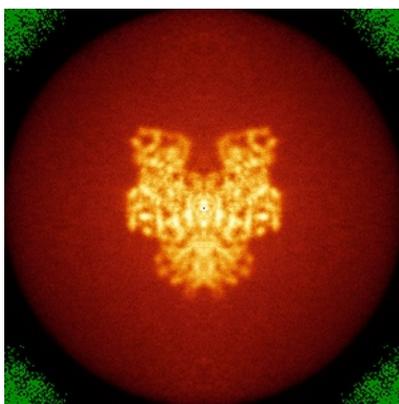


Z Index: 133

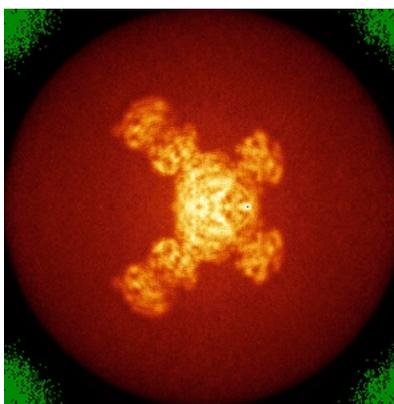
The images above show the largest variance slices of the map in three orthogonal directions.

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

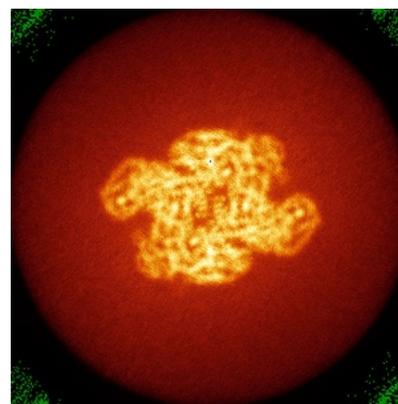
### 6.4.1 Primary map



X



Y

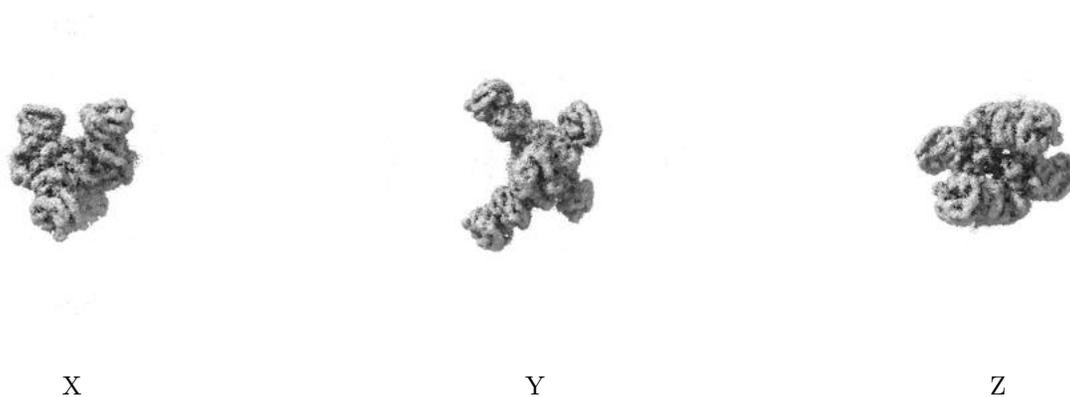


Z

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 [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0137. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

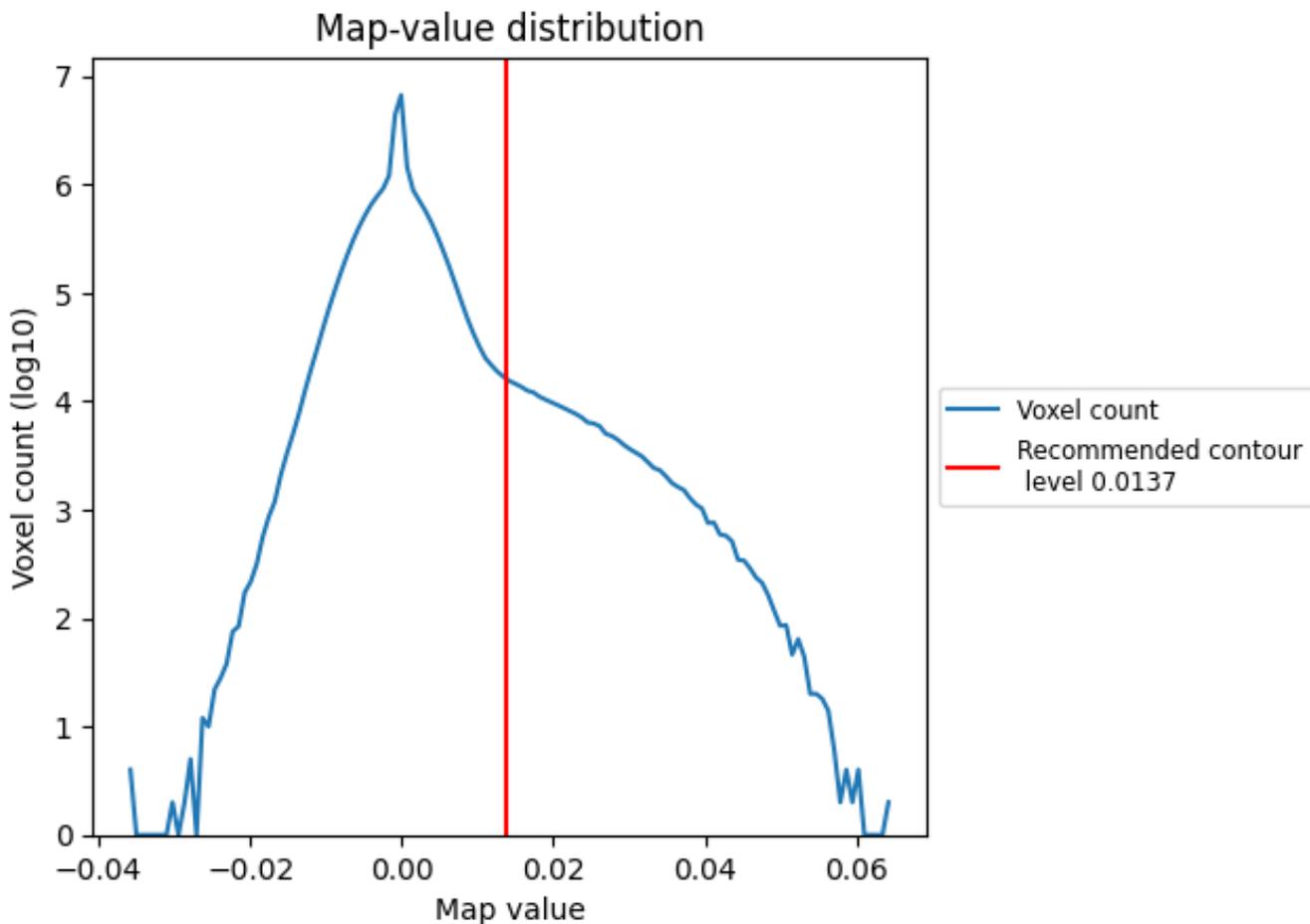
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

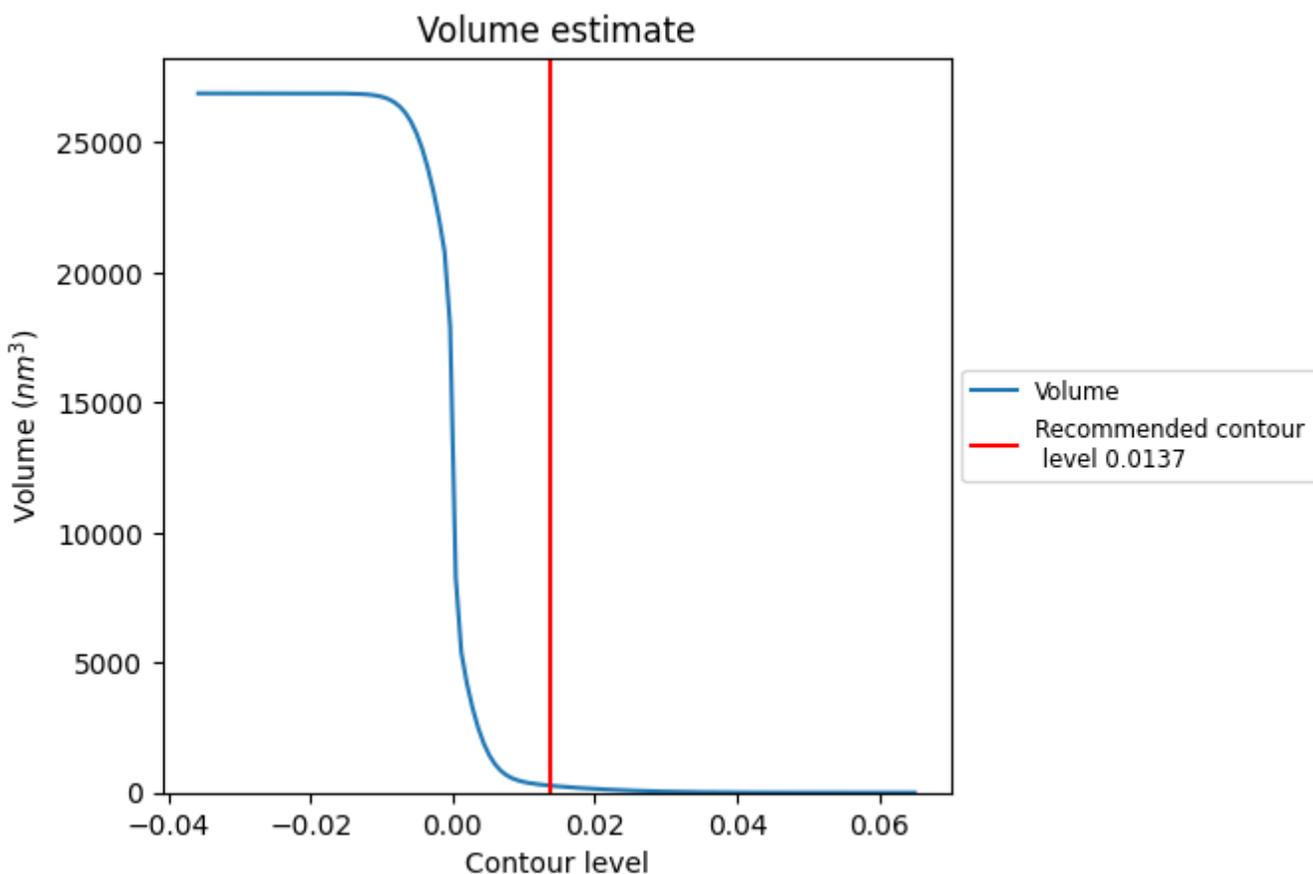
This section contains the results of statistical analysis of the map.

### 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.

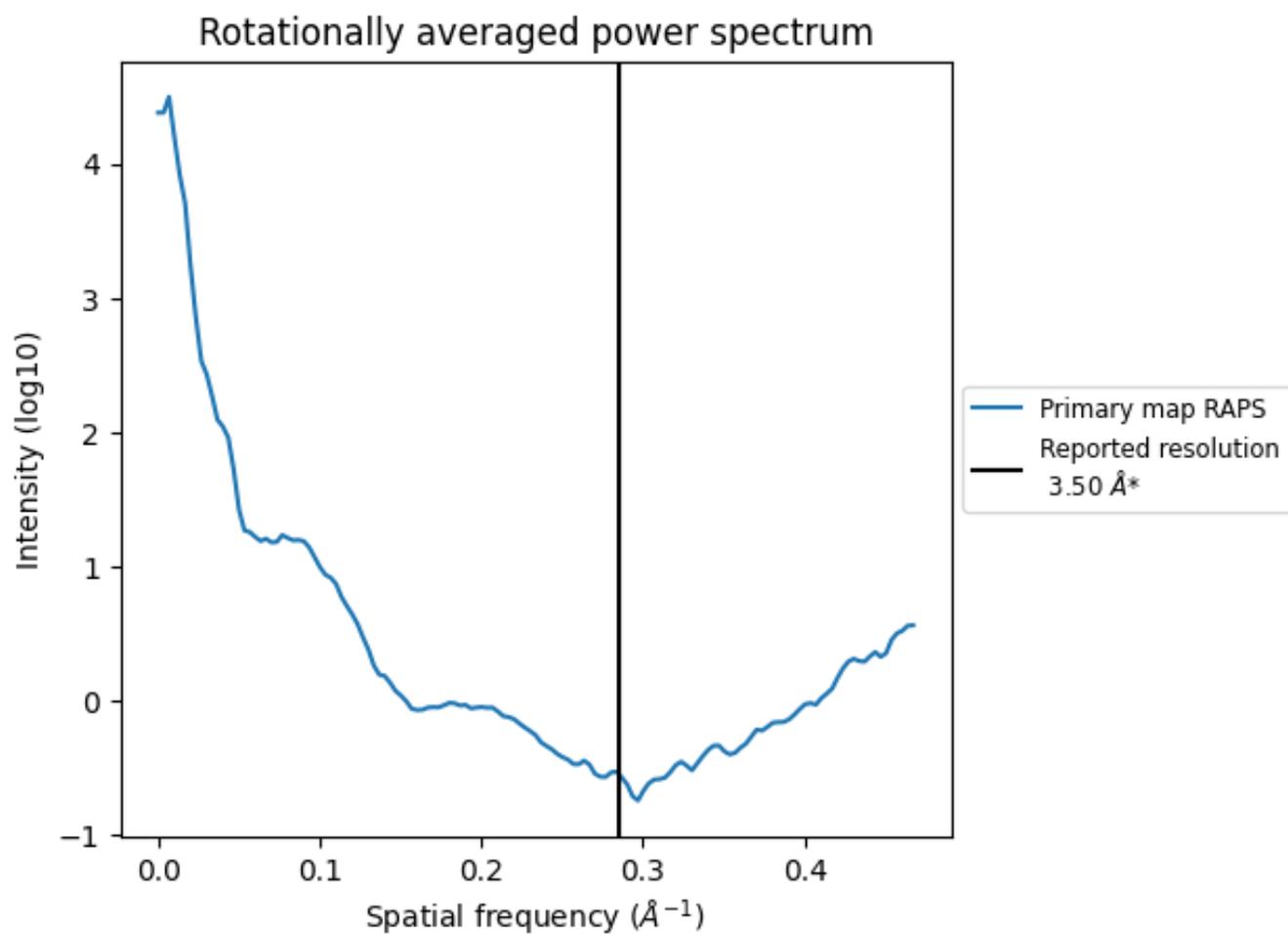
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 270 nm<sup>3</sup>; this corresponds to an approximate mass of 244 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 [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.286 \text{\AA}^{-1}$

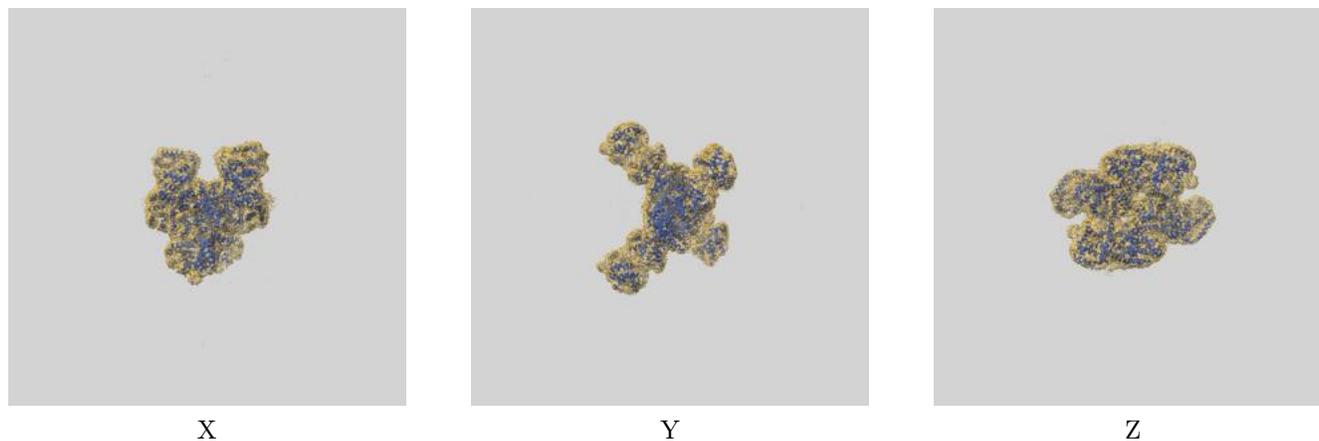
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

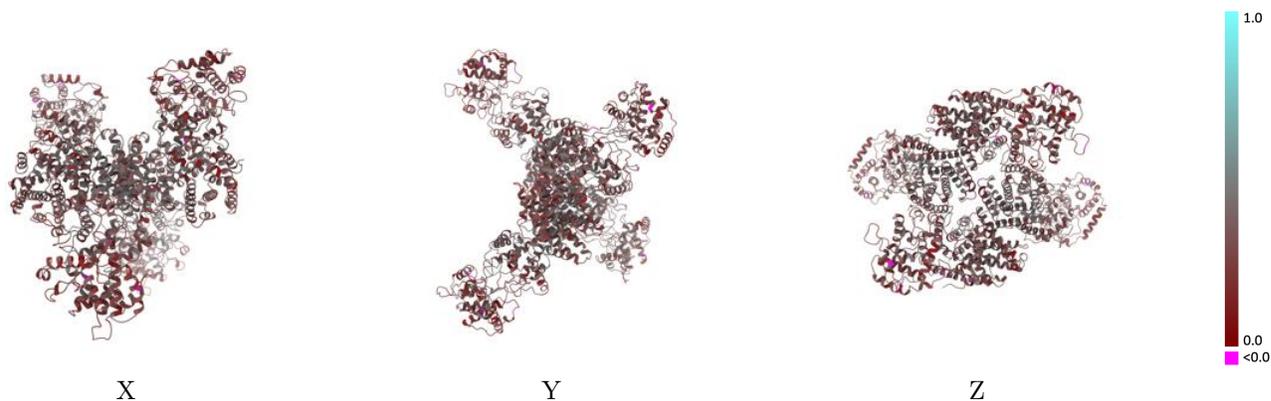
This section contains information regarding the fit between EMDB map EMD-35202 and PDB model 8I6P. Per-residue inclusion information can be found in section 3 on page 5.

### 9.1 Map-model overlay [i](#)



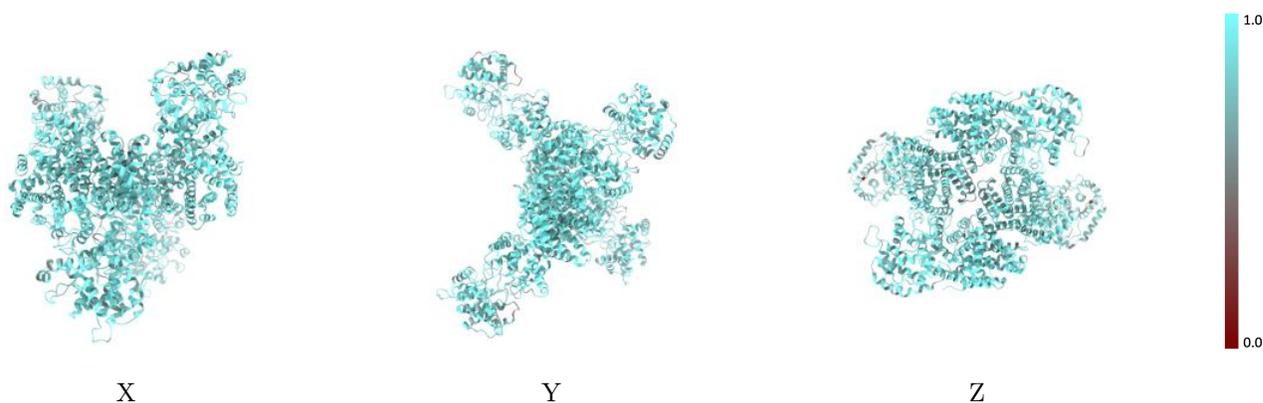
The images above show the 3D surface view of the map at the recommended contour level 0.0137 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



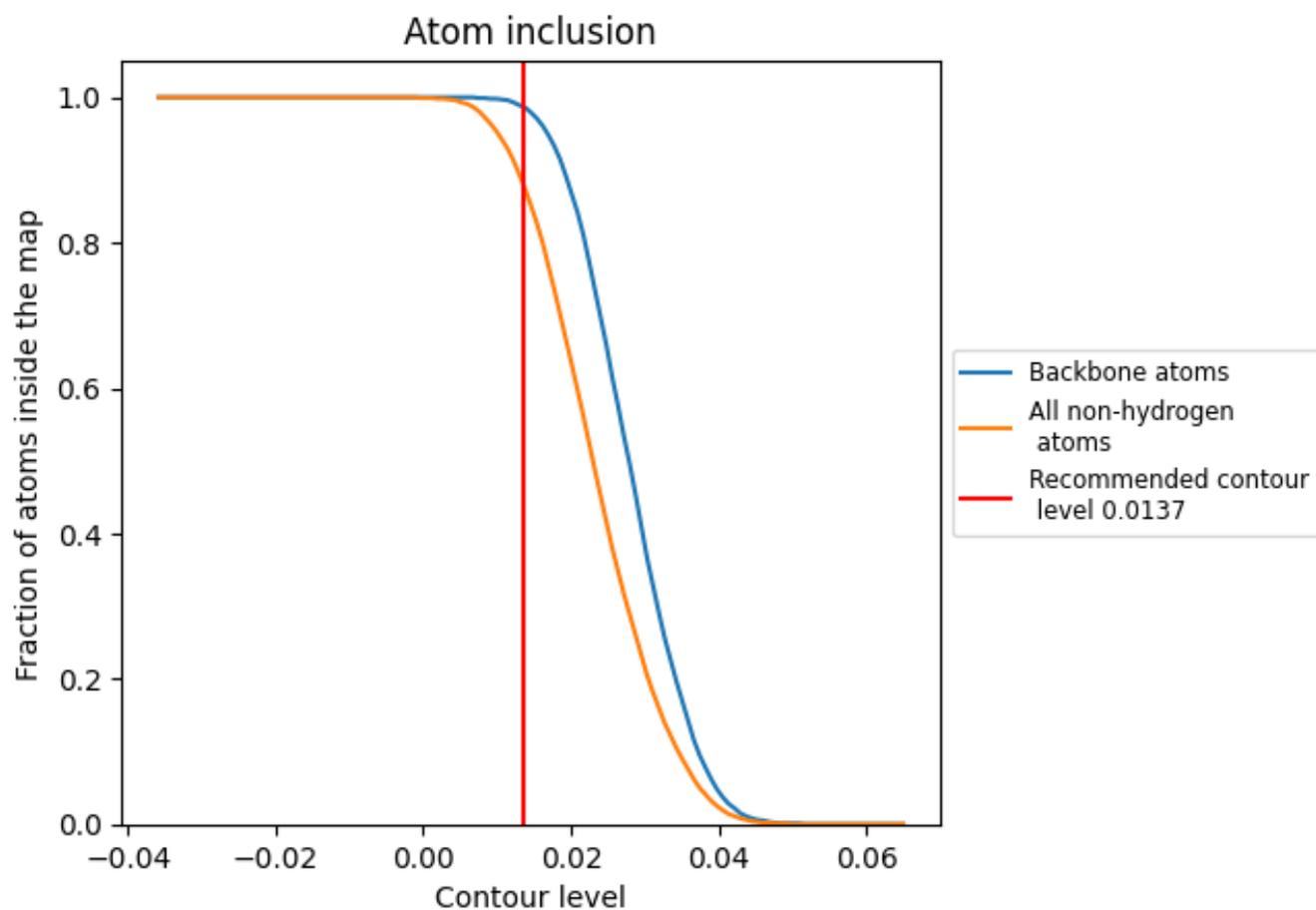
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0137).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.0137) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8770	 0.3190
A	 0.8840	 0.3140
B	 0.8700	 0.3210
C	 0.8700	 0.3270
D	 0.8860	 0.3130

