



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 02:59 PM UTC

PDB ID : 6G2H / pdb_00006g2h
EMDB ID : EMD-4343
Title : Filament of acetyl-CoA carboxylase and BRCT domains of BRCA1 (ACC-BRCT) core at 4.6 Å resolution
Authors : Hunkeler, M.; Hagmann, A.; Stutfeld, E.; Chami, M.; Stahlberg, H.; Maier, T.
Deposited on : 2018-03-23
Resolution : 4.60 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

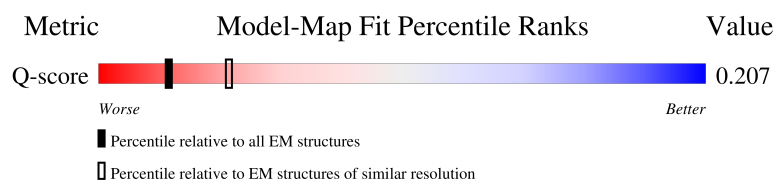
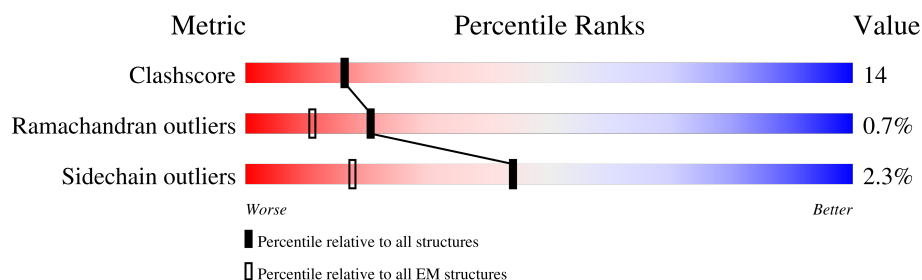
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

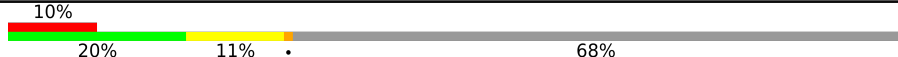
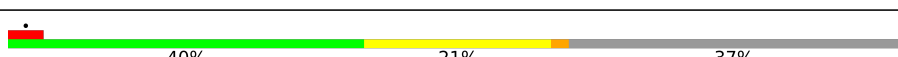
The reported resolution of this entry is 4.60 Å.

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	2407 (4.10 - 5.10)

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	2407	
1	B	2407	
1	C	2407	
1	D	2407	

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Mol	Chain	Length	Quality of chain
1	E	2407	42% 20% 37%
1	F	2407	28% 11% 61%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 103896 atoms, of which 51852 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 Acetyl-CoA carboxylase 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	D	1518	Total	C	H	N	O	S	0	0
			24416	7790	12181	2126	2249	70		
1	E	1518	Total	C	H	N	O	S	0	0
			24416	7790	12181	2126	2249	70		
1	C	948	Total	C	H	N	O	S	0	0
			15171	4850	7561	1318	1403	39		
1	F	948	Total	C	H	N	O	S	0	0
			15171	4850	7561	1318	1403	39		
1	B	761	Total	C	H	N	O	S	0	0
			12361	3935	6184	1076	1125	41		
1	A	761	Total	C	H	N	O	S	0	0
			12361	3935	6184	1076	1125	41		

There are 366 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-60	MET	-	initiating methionine	UNP Q13085
D	-59	ALA	-	expression tag	UNP Q13085
D	-58	HIS	-	expression tag	UNP Q13085
D	-57	HIS	-	expression tag	UNP Q13085
D	-56	HIS	-	expression tag	UNP Q13085
D	-55	HIS	-	expression tag	UNP Q13085
D	-54	HIS	-	expression tag	UNP Q13085
D	-53	HIS	-	expression tag	UNP Q13085
D	-52	HIS	-	expression tag	UNP Q13085
D	-51	HIS	-	expression tag	UNP Q13085
D	-50	HIS	-	expression tag	UNP Q13085
D	-49	HIS	-	expression tag	UNP Q13085
D	-48	GLY	-	expression tag	UNP Q13085
D	-47	SER	-	expression tag	UNP Q13085
D	-46	THR	-	expression tag	UNP Q13085
D	-45	SER	-	expression tag	UNP Q13085
D	-44	GLY	-	expression tag	UNP Q13085
D	-43	SER	-	expression tag	UNP Q13085

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-42	GLY	-	expression tag	UNP Q13085
D	-41	GLU	-	expression tag	UNP Q13085
D	-40	GLN	-	expression tag	UNP Q13085
D	-39	LYS	-	expression tag	UNP Q13085
D	-38	LEU	-	expression tag	UNP Q13085
D	-37	ILE	-	expression tag	UNP Q13085
D	-36	SER	-	expression tag	UNP Q13085
D	-35	GLU	-	expression tag	UNP Q13085
D	-34	GLU	-	expression tag	UNP Q13085
D	-33	ASP	-	expression tag	UNP Q13085
D	-32	LEU	-	expression tag	UNP Q13085
D	-31	GLY	-	expression tag	UNP Q13085
D	-30	SER	-	expression tag	UNP Q13085
D	-29	THR	-	expression tag	UNP Q13085
D	-28	SER	-	expression tag	UNP Q13085
D	-27	GLY	-	expression tag	UNP Q13085
D	-26	SER	-	expression tag	UNP Q13085
D	-25	GLY	-	expression tag	UNP Q13085
D	-24	ASP	-	expression tag	UNP Q13085
D	-23	TYR	-	expression tag	UNP Q13085
D	-22	LYS	-	expression tag	UNP Q13085
D	-21	ASP	-	expression tag	UNP Q13085
D	-20	ASP	-	expression tag	UNP Q13085
D	-19	ASP	-	expression tag	UNP Q13085
D	-18	ASP	-	expression tag	UNP Q13085
D	-17	LYS	-	expression tag	UNP Q13085
D	-16	LEU	-	expression tag	UNP Q13085
D	-15	THR	-	expression tag	UNP Q13085
D	-14	SER	-	expression tag	UNP Q13085
D	-13	LEU	-	expression tag	UNP Q13085
D	-12	TYR	-	expression tag	UNP Q13085
D	-11	LYS	-	expression tag	UNP Q13085
D	-10	LYS	-	expression tag	UNP Q13085
D	-9	ALA	-	expression tag	UNP Q13085
D	-8	GLY	-	expression tag	UNP Q13085
D	-7	LEU	-	expression tag	UNP Q13085
D	-6	GLU	-	expression tag	UNP Q13085
D	-5	ASN	-	expression tag	UNP Q13085
D	-4	LEU	-	expression tag	UNP Q13085
D	-3	TYR	-	expression tag	UNP Q13085
D	-2	PHE	-	expression tag	UNP Q13085
D	-1	GLN	-	expression tag	UNP Q13085

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Chain	Residue	Modelled	Actual	Comment	Reference
D	0	GLY	-	expression tag	UNP Q13085
E	-60	MET	-	initiating methionine	UNP Q13085
E	-59	ALA	-	expression tag	UNP Q13085
E	-58	HIS	-	expression tag	UNP Q13085
E	-57	HIS	-	expression tag	UNP Q13085
E	-56	HIS	-	expression tag	UNP Q13085
E	-55	HIS	-	expression tag	UNP Q13085
E	-54	HIS	-	expression tag	UNP Q13085
E	-53	HIS	-	expression tag	UNP Q13085
E	-52	HIS	-	expression tag	UNP Q13085
E	-51	HIS	-	expression tag	UNP Q13085
E	-50	HIS	-	expression tag	UNP Q13085
E	-49	HIS	-	expression tag	UNP Q13085
E	-48	GLY	-	expression tag	UNP Q13085
E	-47	SER	-	expression tag	UNP Q13085
E	-46	THR	-	expression tag	UNP Q13085
E	-45	SER	-	expression tag	UNP Q13085
E	-44	GLY	-	expression tag	UNP Q13085
E	-43	SER	-	expression tag	UNP Q13085
E	-42	GLY	-	expression tag	UNP Q13085
E	-41	GLU	-	expression tag	UNP Q13085
E	-40	GLN	-	expression tag	UNP Q13085
E	-39	LYS	-	expression tag	UNP Q13085
E	-38	LEU	-	expression tag	UNP Q13085
E	-37	ILE	-	expression tag	UNP Q13085
E	-36	SER	-	expression tag	UNP Q13085
E	-35	GLU	-	expression tag	UNP Q13085
E	-34	GLU	-	expression tag	UNP Q13085
E	-33	ASP	-	expression tag	UNP Q13085
E	-32	LEU	-	expression tag	UNP Q13085
E	-31	GLY	-	expression tag	UNP Q13085
E	-30	SER	-	expression tag	UNP Q13085
E	-29	THR	-	expression tag	UNP Q13085
E	-28	SER	-	expression tag	UNP Q13085
E	-27	GLY	-	expression tag	UNP Q13085
E	-26	SER	-	expression tag	UNP Q13085
E	-25	GLY	-	expression tag	UNP Q13085
E	-24	ASP	-	expression tag	UNP Q13085
E	-23	TYR	-	expression tag	UNP Q13085
E	-22	LYS	-	expression tag	UNP Q13085
E	-21	ASP	-	expression tag	UNP Q13085
E	-20	ASP	-	expression tag	UNP Q13085

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-19	ASP	-	expression tag	UNP Q13085
E	-18	ASP	-	expression tag	UNP Q13085
E	-17	LYS	-	expression tag	UNP Q13085
E	-16	LEU	-	expression tag	UNP Q13085
E	-15	THR	-	expression tag	UNP Q13085
E	-14	SER	-	expression tag	UNP Q13085
E	-13	LEU	-	expression tag	UNP Q13085
E	-12	TYR	-	expression tag	UNP Q13085
E	-11	LYS	-	expression tag	UNP Q13085
E	-10	LYS	-	expression tag	UNP Q13085
E	-9	ALA	-	expression tag	UNP Q13085
E	-8	GLY	-	expression tag	UNP Q13085
E	-7	LEU	-	expression tag	UNP Q13085
E	-6	GLU	-	expression tag	UNP Q13085
E	-5	ASN	-	expression tag	UNP Q13085
E	-4	LEU	-	expression tag	UNP Q13085
E	-3	TYR	-	expression tag	UNP Q13085
E	-2	PHE	-	expression tag	UNP Q13085
E	-1	GLN	-	expression tag	UNP Q13085
E	0	GLY	-	expression tag	UNP Q13085
C	-60	MET	-	initiating methionine	UNP Q13085
C	-59	ALA	-	expression tag	UNP Q13085
C	-58	HIS	-	expression tag	UNP Q13085
C	-57	HIS	-	expression tag	UNP Q13085
C	-56	HIS	-	expression tag	UNP Q13085
C	-55	HIS	-	expression tag	UNP Q13085
C	-54	HIS	-	expression tag	UNP Q13085
C	-53	HIS	-	expression tag	UNP Q13085
C	-52	HIS	-	expression tag	UNP Q13085
C	-51	HIS	-	expression tag	UNP Q13085
C	-50	HIS	-	expression tag	UNP Q13085
C	-49	HIS	-	expression tag	UNP Q13085
C	-48	GLY	-	expression tag	UNP Q13085
C	-47	SER	-	expression tag	UNP Q13085
C	-46	THR	-	expression tag	UNP Q13085
C	-45	SER	-	expression tag	UNP Q13085
C	-44	GLY	-	expression tag	UNP Q13085
C	-43	SER	-	expression tag	UNP Q13085
C	-42	GLY	-	expression tag	UNP Q13085
C	-41	GLU	-	expression tag	UNP Q13085
C	-40	GLN	-	expression tag	UNP Q13085
C	-39	LYS	-	expression tag	UNP Q13085

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-38	LEU	-	expression tag	UNP Q13085
C	-37	ILE	-	expression tag	UNP Q13085
C	-36	SER	-	expression tag	UNP Q13085
C	-35	GLU	-	expression tag	UNP Q13085
C	-34	GLU	-	expression tag	UNP Q13085
C	-33	ASP	-	expression tag	UNP Q13085
C	-32	LEU	-	expression tag	UNP Q13085
C	-31	GLY	-	expression tag	UNP Q13085
C	-30	SER	-	expression tag	UNP Q13085
C	-29	THR	-	expression tag	UNP Q13085
C	-28	SER	-	expression tag	UNP Q13085
C	-27	GLY	-	expression tag	UNP Q13085
C	-26	SER	-	expression tag	UNP Q13085
C	-25	GLY	-	expression tag	UNP Q13085
C	-24	ASP	-	expression tag	UNP Q13085
C	-23	TYR	-	expression tag	UNP Q13085
C	-22	LYS	-	expression tag	UNP Q13085
C	-21	ASP	-	expression tag	UNP Q13085
C	-20	ASP	-	expression tag	UNP Q13085
C	-19	ASP	-	expression tag	UNP Q13085
C	-18	ASP	-	expression tag	UNP Q13085
C	-17	LYS	-	expression tag	UNP Q13085
C	-16	LEU	-	expression tag	UNP Q13085
C	-15	THR	-	expression tag	UNP Q13085
C	-14	SER	-	expression tag	UNP Q13085
C	-13	LEU	-	expression tag	UNP Q13085
C	-12	TYR	-	expression tag	UNP Q13085
C	-11	LYS	-	expression tag	UNP Q13085
C	-10	LYS	-	expression tag	UNP Q13085
C	-9	ALA	-	expression tag	UNP Q13085
C	-8	GLY	-	expression tag	UNP Q13085
C	-7	LEU	-	expression tag	UNP Q13085
C	-6	GLU	-	expression tag	UNP Q13085
C	-5	ASN	-	expression tag	UNP Q13085
C	-4	LEU	-	expression tag	UNP Q13085
C	-3	TYR	-	expression tag	UNP Q13085
C	-2	PHE	-	expression tag	UNP Q13085
C	-1	GLN	-	expression tag	UNP Q13085
C	0	GLY	-	expression tag	UNP Q13085
F	-60	MET	-	initiating methionine	UNP Q13085
F	-59	ALA	-	expression tag	UNP Q13085
F	-58	HIS	-	expression tag	UNP Q13085

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-57	HIS	-	expression tag	UNP Q13085
F	-56	HIS	-	expression tag	UNP Q13085
F	-55	HIS	-	expression tag	UNP Q13085
F	-54	HIS	-	expression tag	UNP Q13085
F	-53	HIS	-	expression tag	UNP Q13085
F	-52	HIS	-	expression tag	UNP Q13085
F	-51	HIS	-	expression tag	UNP Q13085
F	-50	HIS	-	expression tag	UNP Q13085
F	-49	HIS	-	expression tag	UNP Q13085
F	-48	GLY	-	expression tag	UNP Q13085
F	-47	SER	-	expression tag	UNP Q13085
F	-46	THR	-	expression tag	UNP Q13085
F	-45	SER	-	expression tag	UNP Q13085
F	-44	GLY	-	expression tag	UNP Q13085
F	-43	SER	-	expression tag	UNP Q13085
F	-42	GLY	-	expression tag	UNP Q13085
F	-41	GLU	-	expression tag	UNP Q13085
F	-40	GLN	-	expression tag	UNP Q13085
F	-39	LYS	-	expression tag	UNP Q13085
F	-38	LEU	-	expression tag	UNP Q13085
F	-37	ILE	-	expression tag	UNP Q13085
F	-36	SER	-	expression tag	UNP Q13085
F	-35	GLU	-	expression tag	UNP Q13085
F	-34	GLU	-	expression tag	UNP Q13085
F	-33	ASP	-	expression tag	UNP Q13085
F	-32	LEU	-	expression tag	UNP Q13085
F	-31	GLY	-	expression tag	UNP Q13085
F	-30	SER	-	expression tag	UNP Q13085
F	-29	THR	-	expression tag	UNP Q13085
F	-28	SER	-	expression tag	UNP Q13085
F	-27	GLY	-	expression tag	UNP Q13085
F	-26	SER	-	expression tag	UNP Q13085
F	-25	GLY	-	expression tag	UNP Q13085
F	-24	ASP	-	expression tag	UNP Q13085
F	-23	TYR	-	expression tag	UNP Q13085
F	-22	LYS	-	expression tag	UNP Q13085
F	-21	ASP	-	expression tag	UNP Q13085
F	-20	ASP	-	expression tag	UNP Q13085
F	-19	ASP	-	expression tag	UNP Q13085
F	-18	ASP	-	expression tag	UNP Q13085
F	-17	LYS	-	expression tag	UNP Q13085
F	-16	LEU	-	expression tag	UNP Q13085

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-15	THR	-	expression tag	UNP Q13085
F	-14	SER	-	expression tag	UNP Q13085
F	-13	LEU	-	expression tag	UNP Q13085
F	-12	TYR	-	expression tag	UNP Q13085
F	-11	LYS	-	expression tag	UNP Q13085
F	-10	LYS	-	expression tag	UNP Q13085
F	-9	ALA	-	expression tag	UNP Q13085
F	-8	GLY	-	expression tag	UNP Q13085
F	-7	LEU	-	expression tag	UNP Q13085
F	-6	GLU	-	expression tag	UNP Q13085
F	-5	ASN	-	expression tag	UNP Q13085
F	-4	LEU	-	expression tag	UNP Q13085
F	-3	TYR	-	expression tag	UNP Q13085
F	-2	PHE	-	expression tag	UNP Q13085
F	-1	GLN	-	expression tag	UNP Q13085
F	0	GLY	-	expression tag	UNP Q13085
B	-60	MET	-	initiating methionine	UNP Q13085
B	-59	ALA	-	expression tag	UNP Q13085
B	-58	HIS	-	expression tag	UNP Q13085
B	-57	HIS	-	expression tag	UNP Q13085
B	-56	HIS	-	expression tag	UNP Q13085
B	-55	HIS	-	expression tag	UNP Q13085
B	-54	HIS	-	expression tag	UNP Q13085
B	-53	HIS	-	expression tag	UNP Q13085
B	-52	HIS	-	expression tag	UNP Q13085
B	-51	HIS	-	expression tag	UNP Q13085
B	-50	HIS	-	expression tag	UNP Q13085
B	-49	HIS	-	expression tag	UNP Q13085
B	-48	GLY	-	expression tag	UNP Q13085
B	-47	SER	-	expression tag	UNP Q13085
B	-46	THR	-	expression tag	UNP Q13085
B	-45	SER	-	expression tag	UNP Q13085
B	-44	GLY	-	expression tag	UNP Q13085
B	-43	SER	-	expression tag	UNP Q13085
B	-42	GLY	-	expression tag	UNP Q13085
B	-41	GLU	-	expression tag	UNP Q13085
B	-40	GLN	-	expression tag	UNP Q13085
B	-39	LYS	-	expression tag	UNP Q13085
B	-38	LEU	-	expression tag	UNP Q13085
B	-37	ILE	-	expression tag	UNP Q13085
B	-36	SER	-	expression tag	UNP Q13085
B	-35	GLU	-	expression tag	UNP Q13085

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-34	GLU	-	expression tag	UNP Q13085
B	-33	ASP	-	expression tag	UNP Q13085
B	-32	LEU	-	expression tag	UNP Q13085
B	-31	GLY	-	expression tag	UNP Q13085
B	-30	SER	-	expression tag	UNP Q13085
B	-29	THR	-	expression tag	UNP Q13085
B	-28	SER	-	expression tag	UNP Q13085
B	-27	GLY	-	expression tag	UNP Q13085
B	-26	SER	-	expression tag	UNP Q13085
B	-25	GLY	-	expression tag	UNP Q13085
B	-24	ASP	-	expression tag	UNP Q13085
B	-23	TYR	-	expression tag	UNP Q13085
B	-22	LYS	-	expression tag	UNP Q13085
B	-21	ASP	-	expression tag	UNP Q13085
B	-20	ASP	-	expression tag	UNP Q13085
B	-19	ASP	-	expression tag	UNP Q13085
B	-18	ASP	-	expression tag	UNP Q13085
B	-17	LYS	-	expression tag	UNP Q13085
B	-16	LEU	-	expression tag	UNP Q13085
B	-15	THR	-	expression tag	UNP Q13085
B	-14	SER	-	expression tag	UNP Q13085
B	-13	LEU	-	expression tag	UNP Q13085
B	-12	TYR	-	expression tag	UNP Q13085
B	-11	LYS	-	expression tag	UNP Q13085
B	-10	LYS	-	expression tag	UNP Q13085
B	-9	ALA	-	expression tag	UNP Q13085
B	-8	GLY	-	expression tag	UNP Q13085
B	-7	LEU	-	expression tag	UNP Q13085
B	-6	GLU	-	expression tag	UNP Q13085
B	-5	ASN	-	expression tag	UNP Q13085
B	-4	LEU	-	expression tag	UNP Q13085
B	-3	TYR	-	expression tag	UNP Q13085
B	-2	PHE	-	expression tag	UNP Q13085
B	-1	GLN	-	expression tag	UNP Q13085
B	0	GLY	-	expression tag	UNP Q13085
A	-60	MET	-	initiating methionine	UNP Q13085
A	-59	ALA	-	expression tag	UNP Q13085
A	-58	HIS	-	expression tag	UNP Q13085
A	-57	HIS	-	expression tag	UNP Q13085
A	-56	HIS	-	expression tag	UNP Q13085
A	-55	HIS	-	expression tag	UNP Q13085
A	-54	HIS	-	expression tag	UNP Q13085

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-53	HIS	-	expression tag	UNP Q13085
A	-52	HIS	-	expression tag	UNP Q13085
A	-51	HIS	-	expression tag	UNP Q13085
A	-50	HIS	-	expression tag	UNP Q13085
A	-49	HIS	-	expression tag	UNP Q13085
A	-48	GLY	-	expression tag	UNP Q13085
A	-47	SER	-	expression tag	UNP Q13085
A	-46	THR	-	expression tag	UNP Q13085
A	-45	SER	-	expression tag	UNP Q13085
A	-44	GLY	-	expression tag	UNP Q13085
A	-43	SER	-	expression tag	UNP Q13085
A	-42	GLY	-	expression tag	UNP Q13085
A	-41	GLU	-	expression tag	UNP Q13085
A	-40	GLN	-	expression tag	UNP Q13085
A	-39	LYS	-	expression tag	UNP Q13085
A	-38	LEU	-	expression tag	UNP Q13085
A	-37	ILE	-	expression tag	UNP Q13085
A	-36	SER	-	expression tag	UNP Q13085
A	-35	GLU	-	expression tag	UNP Q13085
A	-34	GLU	-	expression tag	UNP Q13085
A	-33	ASP	-	expression tag	UNP Q13085
A	-32	LEU	-	expression tag	UNP Q13085
A	-31	GLY	-	expression tag	UNP Q13085
A	-30	SER	-	expression tag	UNP Q13085
A	-29	THR	-	expression tag	UNP Q13085
A	-28	SER	-	expression tag	UNP Q13085
A	-27	GLY	-	expression tag	UNP Q13085
A	-26	SER	-	expression tag	UNP Q13085
A	-25	GLY	-	expression tag	UNP Q13085
A	-24	ASP	-	expression tag	UNP Q13085
A	-23	TYR	-	expression tag	UNP Q13085
A	-22	LYS	-	expression tag	UNP Q13085
A	-21	ASP	-	expression tag	UNP Q13085
A	-20	ASP	-	expression tag	UNP Q13085
A	-19	ASP	-	expression tag	UNP Q13085
A	-18	ASP	-	expression tag	UNP Q13085
A	-17	LYS	-	expression tag	UNP Q13085
A	-16	LEU	-	expression tag	UNP Q13085
A	-15	THR	-	expression tag	UNP Q13085
A	-14	SER	-	expression tag	UNP Q13085
A	-13	LEU	-	expression tag	UNP Q13085
A	-12	TYR	-	expression tag	UNP Q13085

Continued on next page...

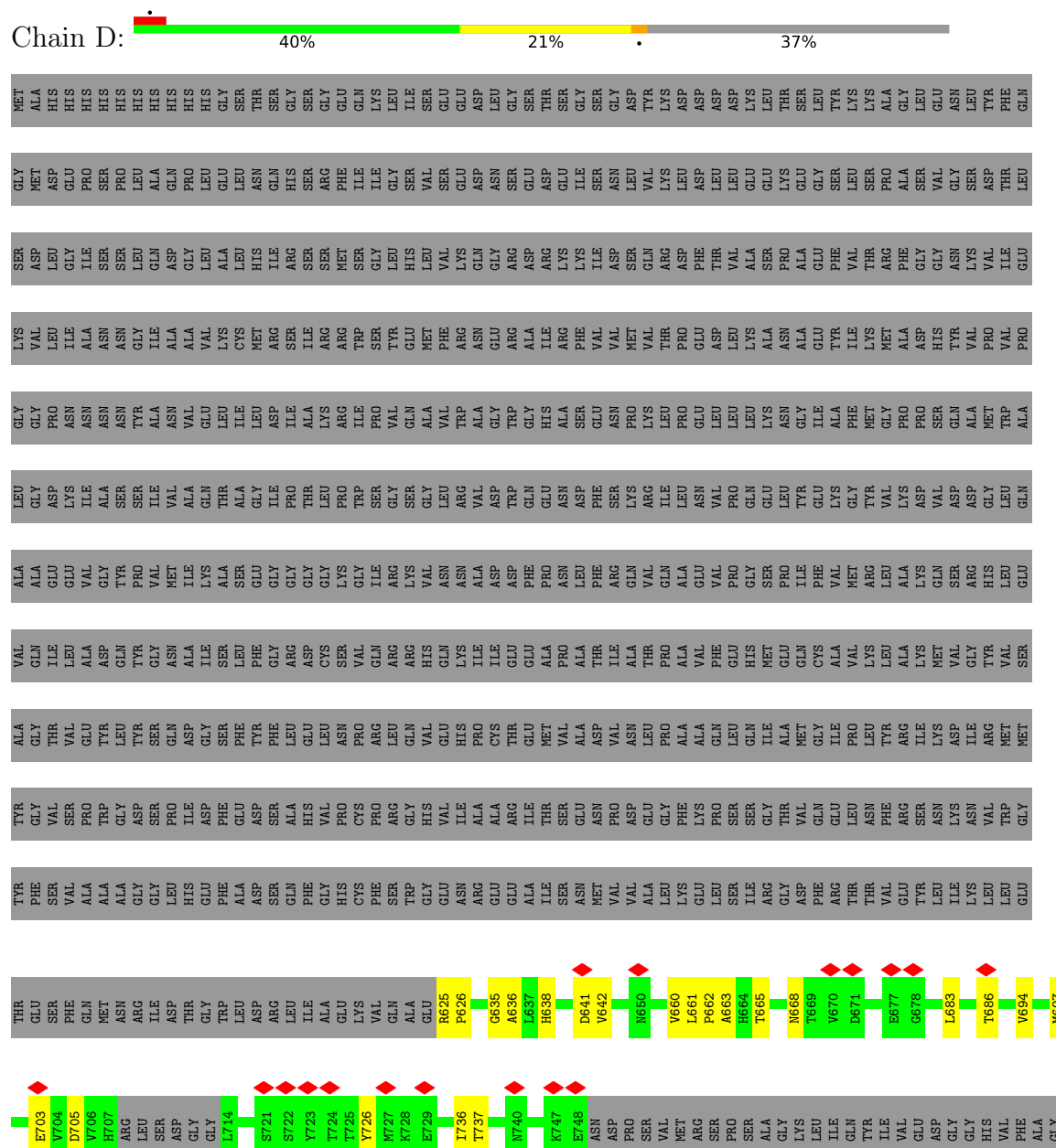
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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A	-10	LYS	-	expression tag	UNP Q13085
A	-9	ALA	-	expression tag	UNP Q13085
A	-8	GLY	-	expression tag	UNP Q13085
A	-7	LEU	-	expression tag	UNP Q13085
A	-6	GLU	-	expression tag	UNP Q13085
A	-5	ASN	-	expression tag	UNP Q13085
A	-4	LEU	-	expression tag	UNP Q13085
A	-3	TYR	-	expression tag	UNP Q13085
A	-2	PHE	-	expression tag	UNP Q13085
A	-1	GLN	-	expression tag	UNP Q13085
A	0	GLY	-	expression tag	UNP Q13085

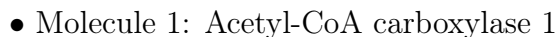
3 Residue-property plots

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: Acetyl-CoA carboxylase 1

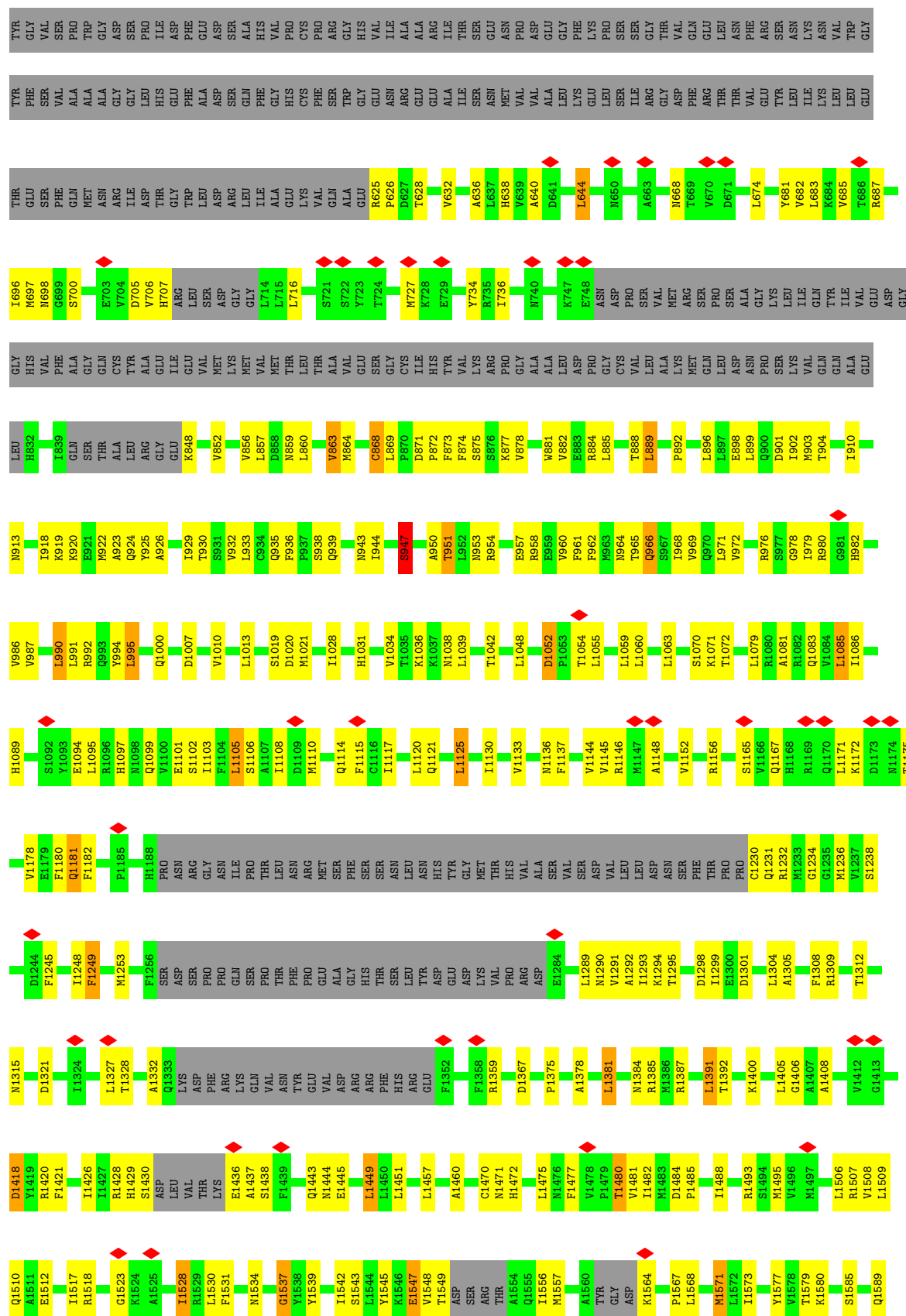


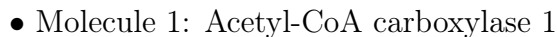
Y925	Y926	Y929	Y930	L933	Q934	Q935	S938	Q939	Q940	Y984	L995	E998	Q1000	Y1006	D1007	V1010	E1016	S1019	D1020	N1021	N1022	L1025	M1026	S1030	H1031	A1032	G1033	V1034	T1035	K1036	H1037	H1038	T1042	M1043	L1044	Q966	S967	I968	V969	Q972	Q973	R974	R975	R976	I979	R980	G981	H982	M983	V986	V987	M988	D989	E991	M992	R992	Q993
SER	THR	ALA	LEU	ARG	GLY	GLU	K648	F852	F853	V856	V863	M864	N865	G866	Y867	C868	P870	F873	F874	K877	V878	W881	V882	E883	R884	M886	K887	T888	L889	P892	E898	L899	Q900	D901	I902	M903	T904	N913	V914	E915	I918	K919	K920	E921	M922	A923	Q924										
CYS	TTR	ALA	LEU	ILE	GLU	VAL	MET	MET	VAL	THR	LEU	THR	ALA	GLU	SER	GLY	CYS	ILE	HIS	TYR	VAL	LYS	ARG	PRO	GLY	ALA	LEU	ASP	PRO	GLY	CYS	VAL	LEU	ALA	LYS	MET	GLN	LEU	H832	T833	G834	I839	GLN														
G1768	C1769	E1770	D1774	R1779	I1782	T1783	D1784	I1785	I1786	G1787	K1788	E1789	G1790	G1791	I1792	N1796	L1797	R1798	I1803	A1804	G1805	S1808	L1809	M1812	E1813	I1814	I1817	S1818	L1819	F1734	H1735	V1736	A1737	W1738	P1741	E1742	Y1745	Y1748	R1749	Y1750	L1751	V1761	S1762	A1763	L1764	N1765	T1864	S1865									
T1480	M1483	D1484	P1485	E1489	R1493	Y1499	G1500	S1501	R1502	L1503	R1507	V1508	L1509	Q1510	A1511	E1512	T1517	R1518	G1523	K1524	I1526	P1529	D1630	M1631	L1632	E1636	L1639	D1640	D1641	Q1642	G1643	M1648	N1649	A1661	W1662	K1663	M1664	E1670	Y1671	D1676	V1679	I1680	G1681														
K1400	H1401	H1402	L1403	Y1404	L1405	A1408	V1412	G1413	T1417	D1418	Y1419	R1420	F1421	F1422	V1423	R1424	A1425	T1426	I1427	R1428	H1429	S1430	ASP	LEU	VAL	THR	LYS	E1436	A1437	S1438	Y1441	M1444	E1445	R1448	L1449	L1450	L1457	E1458	V1459	A1460	F1461	G1470	N1471	H1472	I1473	F1474	L1475	N1476	F1477	V1478	P1479						
T1312	M1315	L1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA	GLY	HIS	THR	SER	LEU	TYR	ASP	GLU	ASP	LYS	VAL	PRO	ARG	ASP	E1284	L1289	N1290	V1291	A1292	I1293	K1294	T1295	D1298	I1299	E1300	D1301	L1304	R1309										
T1312	M1315	D1321	E1243	R1247	I1248	F1249	M1253	F1256	SER	ASP	PRO	GLN	ASN	PRO	THR	PHE	PRO	GLU	ALA</																																						



Frequency	Percentage
Daily	42%
Weekly	20%
Monthly	37%
Other	1%







Frequency	Percentage
Daily	28%
Weekly	11%
Monthly	61%







- Molecule 1: Acetyl-CoA carboxylase 1

[illegible]





[illegible]

- Molecule 1: Acetyl-CoA carboxylase 1



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

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

[illegible]

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

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

VAL	GLN	ILE	LEU	ALA	ASP	GLN	TYR	GLY	ASN	ILE	ALA	ILE	SER	LEU	PHE	GLY	ARG	ASP	CYS	SER	VAL	GLN	GLN	ARG	ARG	HIS	LYS	ILE	ILE	GLU	GLU	ALA	ALA	ALA	ALA	ALA	VAL	VAL	PHE	GLU	HIS	GLY	MET	GLU	GLN	GLN	CYS	ALA	ALA	LYS	LYS	LEU	GLY	TYR	VAL	VAL	SER
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[illegible]

Tyr	Gly	Val	Ser	Pro	Trp	Gly	Asp	Ser	Pro	Pro	Ile	Asp	Phe	Glu	Asp	Ser	Ala	Ala	His	Val	Pro	Cys	Pro	Arg	Gly	His	Val	Ile	Ala	Ala	Ala	Arg	Ile	Thr	Ser	Glu	Pro	Pro	Asp	Glu	Gly	Phe	Lys	Pro	Ser	Ser	Gly	Thr	Val	Gln	Glu	Leu	Asn	Asn	Phe	Arg	Ser	Asn	Lys	Val	Val	Trp	Tyr
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Tyr	Phe	Ser	Ser	Val	Ala	Ala	Gly	Leu	His	Glu	Phe	Ala	Asn	Ser	Gln	Phe	Gly	His	Cys	Phe	Ser	Trp	Ser	Tyr	Gly	Glu	Asn	Arg	Glu	Glu	Ala	Ile	Ser	Asn	Met	Val	Val	Ala	Ala	Leu	Lys	Glu	Leu	Ser	Ile	Arg	Gly	ASP	PHE	ARG	THR	Thr	Val	Val	Glu	Tyr	Leu	Lys	Lys	Leu	Leu
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[illegible]

T665	T666	L667	L668	T669	D670	V671	E672	E673	L674	I675	V676	E677	E678	V679	K680	E681	V682	L683	K684	V685	T686	R687	Q688	S689	S690	V691	V692	E693	V694	V695	I696	M697	V702	D705	V706	H707	ARG	LEU	SER	ASP	GLY	GLY	L714	S717	V718	D719	G720	S721	S722	V723	T724	T725	V726	K727	K728	E729	E730
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V731	D732	Y733	Y734	R735	I736	T737	I738	G739	N740	K741	T742	E746	K747	E748	ASN	ASP	PRO	SER	VAL	MET	ARG	SER	PRO	SER	SER	ALA	GLY	LYS	LEU	ILE	GLN	TVR	ILE	VAL	GLU	GLU	ASP	GLY	GLY	HIS	VAL	PHE	ALA	ALA	GLN	CYS	TYR	ALA	GLU	ILE	GLU	VAL	MET	LYS	LYS	MET	VAL	MET	THR	LEU	THR
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ALA	VAL	GLU	SER	GLY	CYS	ILE	HIS	TYR	VAL	LYS	ARG	PRO	GLY	ALA	ALA	LEU	LEU	ASP	PRO	GLY	CYS	VAL	LEU	ALA	LYS	MET	GLN	LEU	ASP	ASN	PRO	SER	LYS	VAL	GLN	GLN	ALA	GLU	LEU	H832	H833	H834	S835	L836	F837	R838	T839	GLN	SER	THR	ALA	LEU	ARG	GLY	GLU	K848	H849	L850	R851	R852
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CYS	ASN	PHE	ARG	LYS	GLU	PRO	ILE	TLE
ILE	ALA	GLY	GLY	ASP	LEU	ARG	MET	THR
SER	ASN	ILE	SER	ASP	SER	TRP	HIS	THR
ARG	PRO	ILE	VAL	TYR	ILE	MET	ASN	ILE
ASP	GLU	ILE	LEU	ASP	GLN	PRO	ASN	SER
TYR	LEU	TYR	GLU	GLN	ALA	ALA	GLY	LEU
VAL	THR	HIS	PRO	VAL	ASP	GLY	VAL	VAL
LEU	THR	GLN	GLU	LEU	GLU	PRO	ARG	THR
LYS	GLY	VAL	GLY	LYS	ALA	ALA	HIS	CYS
GLN	GLN	ALA	THR	PHE	ASN	HIS	CYS	ARG
ILE	ILE	VAL	VAL	GLY	LEU	THR	THR	ALA
ARG	GLN	GLN	GLU	ALA	ASP	THR	VAL	ILE
SER	ALA	PHE	ILE	TYR	SER	GLN	CYS	GLY
LEU	MET	ALA	ILE	LYS	GLU	LYS	ASP	ILE
VAL	LEU	ASP	PHE	VAL	ALA	GLY	ASP	GLY
GLN	ARG	GLN	ARG	ASP	GLN	PHE	THR	VAL
ALA	ARG	HIS	ARG	GLY	ILE	LEU	GLU	GLY
ASN	TRP	ASP	LYS	LEU	ILE	LEU	GLY	THR
PRO	PHE	PRO	ASP	ARG	GLN	SER	VAL	LEU
GLU	VAL	THR	LEU	GLU	GLN	PHE	PHE	ARG
VAL	GLU	GLY	VAL	CYS	ALA	PHE	THR	LEU
ALA	VAL	ALA	LYS	CYS	GLY	PHE	VAL	GLY
MET	GLU	MET	THR	GLN	GLN	ASP	LEU	GLN
ASP	GLY	GLN	MET	PRO	VAL	TYR	HIS	ARG
SER	THR	GLU	GLU	VAL	THR	GLY	THR	THR
ILE	VAL	LYS	ARG	LEU	PHE	SER	SEU	ILE
ILE	VAL	GLY	VAL	VAL	PRO	PHE	SER	GLN
HIS	ALA	VAL	VAL	TYR	ASP	SER	TYR	VAL
MET	THR	ILE	SER	ILE	ALA	GLU	MET	GLU
THR	VAL	SER	VAL	PRO	VAL	ILE	PRO	ASN
GLN	THR	ASP	LYS	PRO	GLN	ALA	SER	LEU
LEU	LEU	THR	LYS	LEU	ALA	GLN	SER	THR
ARG	ALA	SER	SER	GLY	ILE	THR	VAL	GLY
ALA	GLU	ARG	GLY	SER	VAL	VAL	PRO	ALA
GLU	TRP	THR	THR	TRP	PHE	VAL	LEU	GLY
VAL	LEU	PHE	PRO	VAL	GLY	GLY	ASN	LEU
ILE	GLU	PHE	GLU	VAL	ARG	ARG	SER	ASN
ILE	LYS	TYR	LEU	VAL	ILE	ALA	SER	LYS
ILE	GLN	TRP	SER	ASP	GLY	ARG	ASP	VAL
LEU	LEU	ARG	THR	SER	LEU	LEU	PRO	VAL
SER	THR	LEU	ALA	SER	PRO	GLY	ILE	GLY
THR	GLU	ARG	GLY	ILE	GLY	GLY	ASP	ARG
MET	GLU	ARG	ARG	ASN	MET	ILE	ARG	GLU
ASP	GLU	LEU	LEU	PRO	VAL	PRO	ILE	VAL
SER	GLY	LEU	GLU	ARG	PHE	VAL	ILE	THR
PRO	VAL	LEU	LEU	HIS	ALA	GLY	GLY	THR
SER	HIS	GLU	GLU	MET	ASN	VAL	PHE	SER
THR	VAL	LEU	ASP	GLY	TRP	VAL	VAL	ASN
		THR	LEU	MET	ARG	ALA	PRO	ASN
		VAL	VAL	TYR	GLY	THR	THR	GLN
		LYS	LYS	THR	GLY	VAL	THR	LEU
		ASN	LYS	ASP	THR	ARG	THR	GLY
		ILE	THR	ARG	GLY	THR	THR	GLY
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		THR	THR	GLU	THR	THR	THR</	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	48483	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 ($e^-/\text{\AA}^2$)	80.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.091	Depositor
Minimum map value	-0.045	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.014	Depositor
Map size (Å)	397.80798, 397.80798, 397.80798	wwPDB
Map dimensions	376, 376, 376	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.058, 1.058, 1.058	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	0.51	0/6291	1.21	25/8496 (0.3%)
1	B	0.52	0/6291	1.18	24/8496 (0.3%)
1	C	0.63	0/7780	1.07	14/10540 (0.1%)
1	D	0.66	2/12491 (0.0%)	1.21	60/16905 (0.4%)
1	E	0.65	1/12491 (0.0%)	1.15	30/16905 (0.2%)
1	F	0.63	1/7780 (0.0%)	1.07	17/10540 (0.2%)
All	All	0.62	4/53124 (0.0%)	1.15	170/71882 (0.2%)

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	12
1	B	0	10
1	C	0	1
1	D	0	16
1	E	0	11
1	F	0	1
All	All	0	51

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	1601	ILE	CA-CB	-9.81	1.49	1.54
1	E	1625	PRO	CA-C	-9.24	1.46	1.51
1	F	1625	PRO	CA-C	-7.18	1.48	1.51
1	D	1625	PRO	CA-C	-5.97	1.48	1.51

The worst 5 of 170 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	1545	TYR	CA-C-N	10.74	139.60	122.21
1	D	1545	TYR	C-N-CA	10.74	139.60	122.21
1	A	1052	ASP	CA-C-N	10.71	133.23	119.84
1	A	1052	ASP	C-N-CA	10.71	133.23	119.84
1	D	1500	GLY	CA-C-N	8.23	131.31	120.28

There are no chirality outliers.

5 of 51 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	1052	ASP	Peptide
1	D	924	GLN	Peptide
1	D	952	LEU	Peptide
1	D	957	GLU	Peptide
1	D	965	THR	Mainchain

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	6177	6184	6209	193	0
1	B	6177	6184	6209	180	0
1	C	7610	7561	7585	211	0
1	D	12235	12181	12225	388	0
1	E	12235	12181	12225	368	0
1	F	7610	7561	7585	218	0
All	All	52044	51852	52038	1476	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 14.

The worst 5 of 1476 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:1679:VAL:HG22	1:D:1714:ILE:HD11	1.54	0.88
1:C:2067:ILE:HD11	1:C:2095:VAL:HG12	1.54	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:668:ASN:ND2	1:E:868:CYS:SG	2.47	0.87
1:F:1545:TYR:OH	1:F:1567:PRO:O	1.92	0.87
1:B:864:MET:HE2	1:B:1040:LEU:HD22	1.54	0.87

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	741/2407 (31%)	640 (86%)	93 (13%)	8 (1%)	11	45
1	B	741/2407 (31%)	641 (86%)	93 (13%)	7 (1%)	14	49
1	C	940/2407 (39%)	882 (94%)	51 (5%)	7 (1%)	18	55
1	D	1498/2407 (62%)	1367 (91%)	123 (8%)	8 (0%)	24	63
1	E	1498/2407 (62%)	1371 (92%)	117 (8%)	10 (1%)	18	55
1	F	940/2407 (39%)	883 (94%)	51 (5%)	6 (1%)	21	58
All	All	6358/14442 (44%)	5784 (91%)	528 (8%)	46 (1%)	20	55

5 of 46 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	868	CYS
1	D	1304	LEU
1	E	868	CYS
1	E	1304	LEU
1	C	2326	ILE

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	694/2108 (33%)	673 (97%)	21 (3%)	36	57
1	B	694/2108 (33%)	676 (97%)	18 (3%)	40	60
1	C	830/2108 (39%)	813 (98%)	17 (2%)	48	65
1	D	1354/2108 (64%)	1323 (98%)	31 (2%)	44	63
1	E	1354/2108 (64%)	1322 (98%)	32 (2%)	43	63
1	F	830/2108 (39%)	817 (98%)	13 (2%)	55	69
All	All	5756/12648 (46%)	5624 (98%)	132 (2%)	44	63

5 of 132 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	863	VAL
1	A	986	VAL
1	A	1514	LYS
1	E	1391	LEU
1	E	1381	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 112 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	2291	ASN
1	A	1388	ASN
1	F	1534	ASN
1	A	1315	ASN
1	A	650	ASN

5.3.3 RNA ⓘ

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.

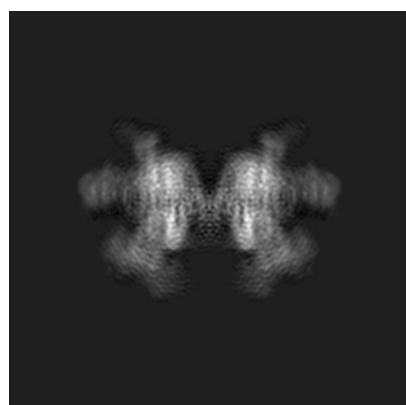
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4343. These allow visual inspection of the internal detail of the map and identification of artifacts.

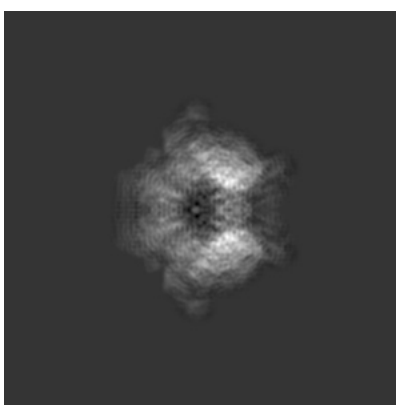
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

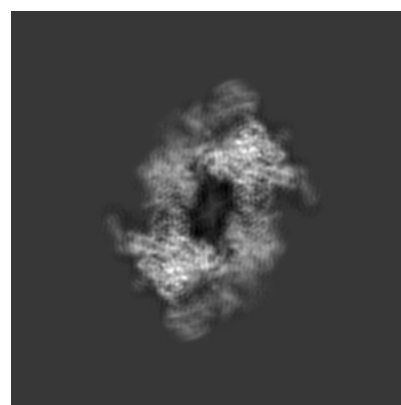
6.1.1 Primary map



X



Y

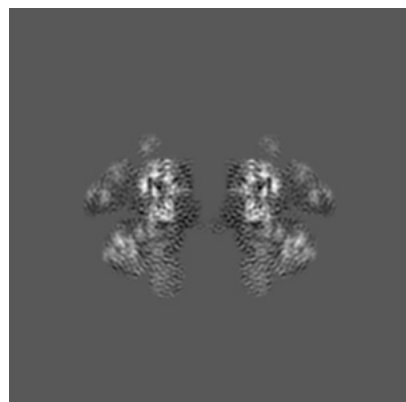


Z

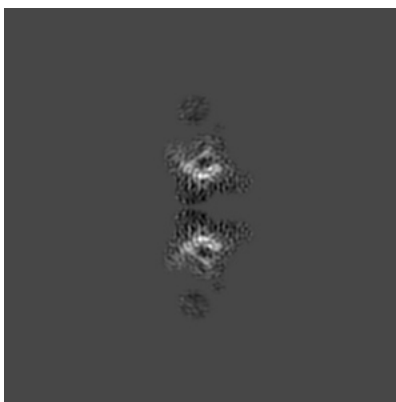
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

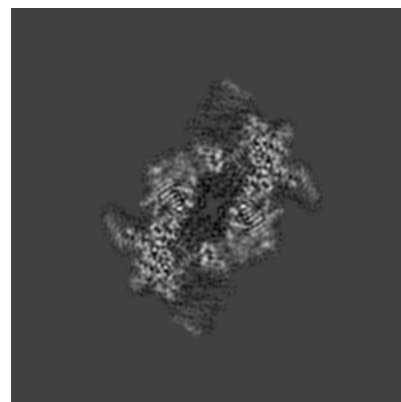
6.2.1 Primary map



X Index: 188



Y Index: 188

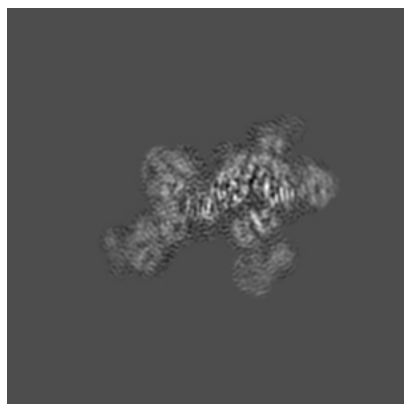


Z Index: 188

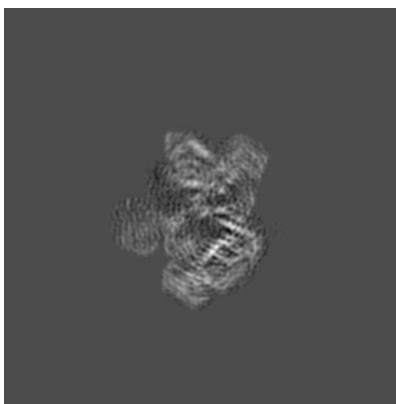
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

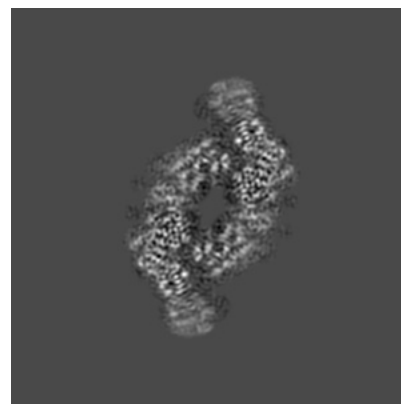
6.3.1 Primary map



X Index: 219



Y Index: 153

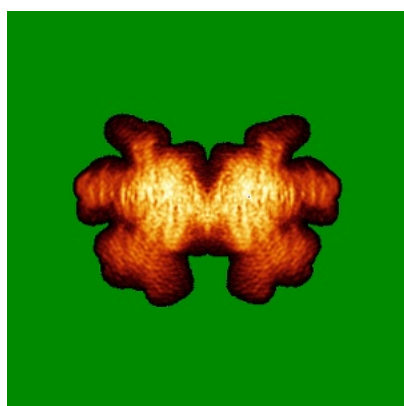


Z Index: 201

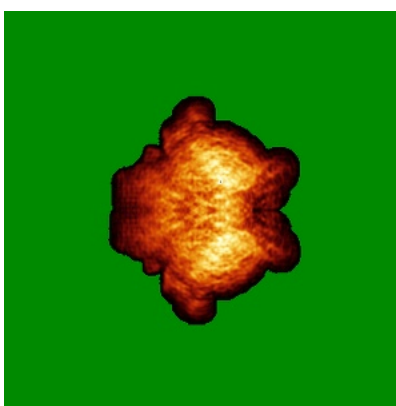
The images above show the largest variance slices of the map in three orthogonal directions.

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

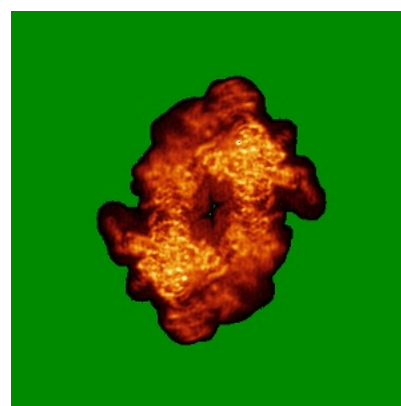
6.4.1 Primary map



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 0.014. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

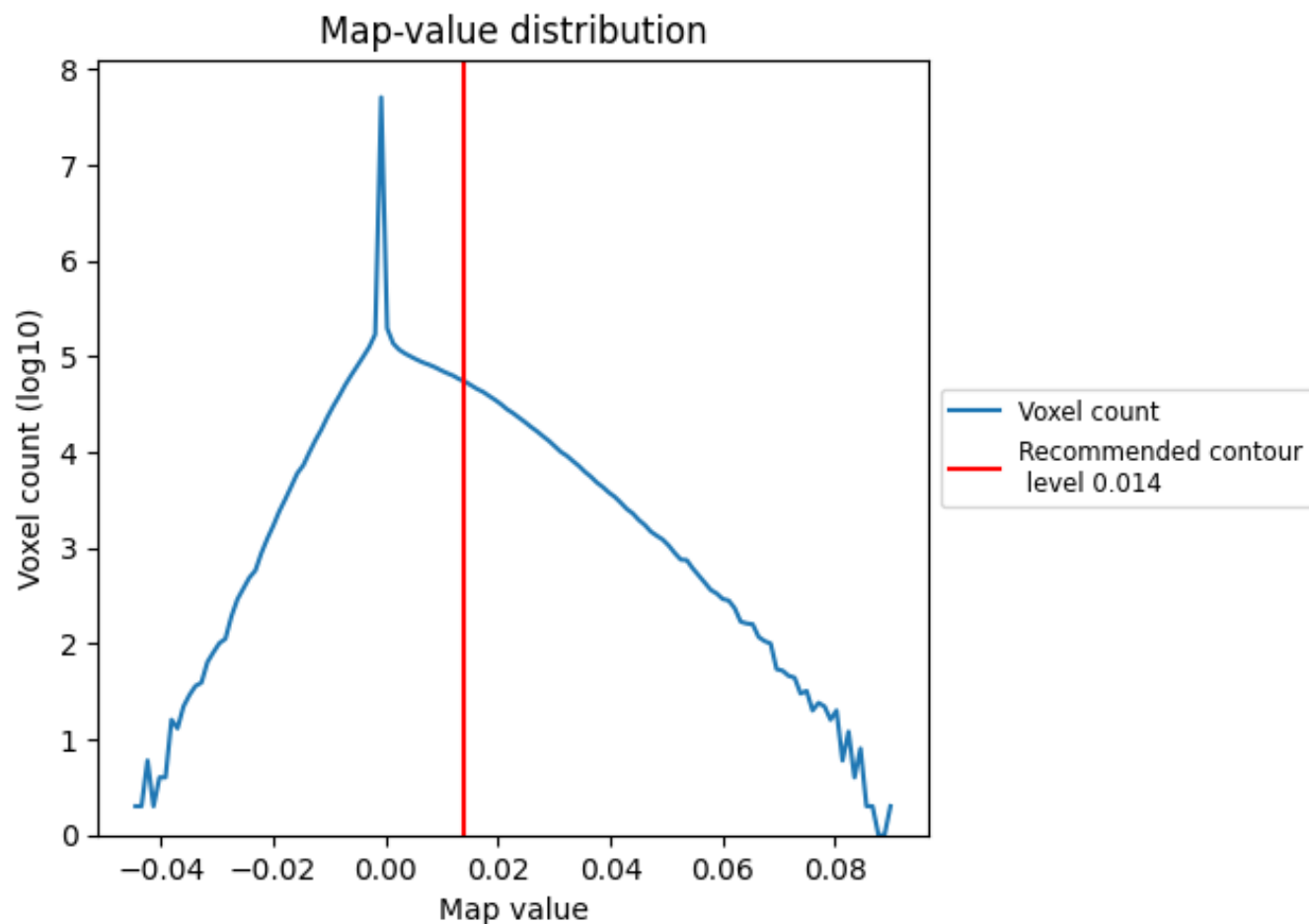
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

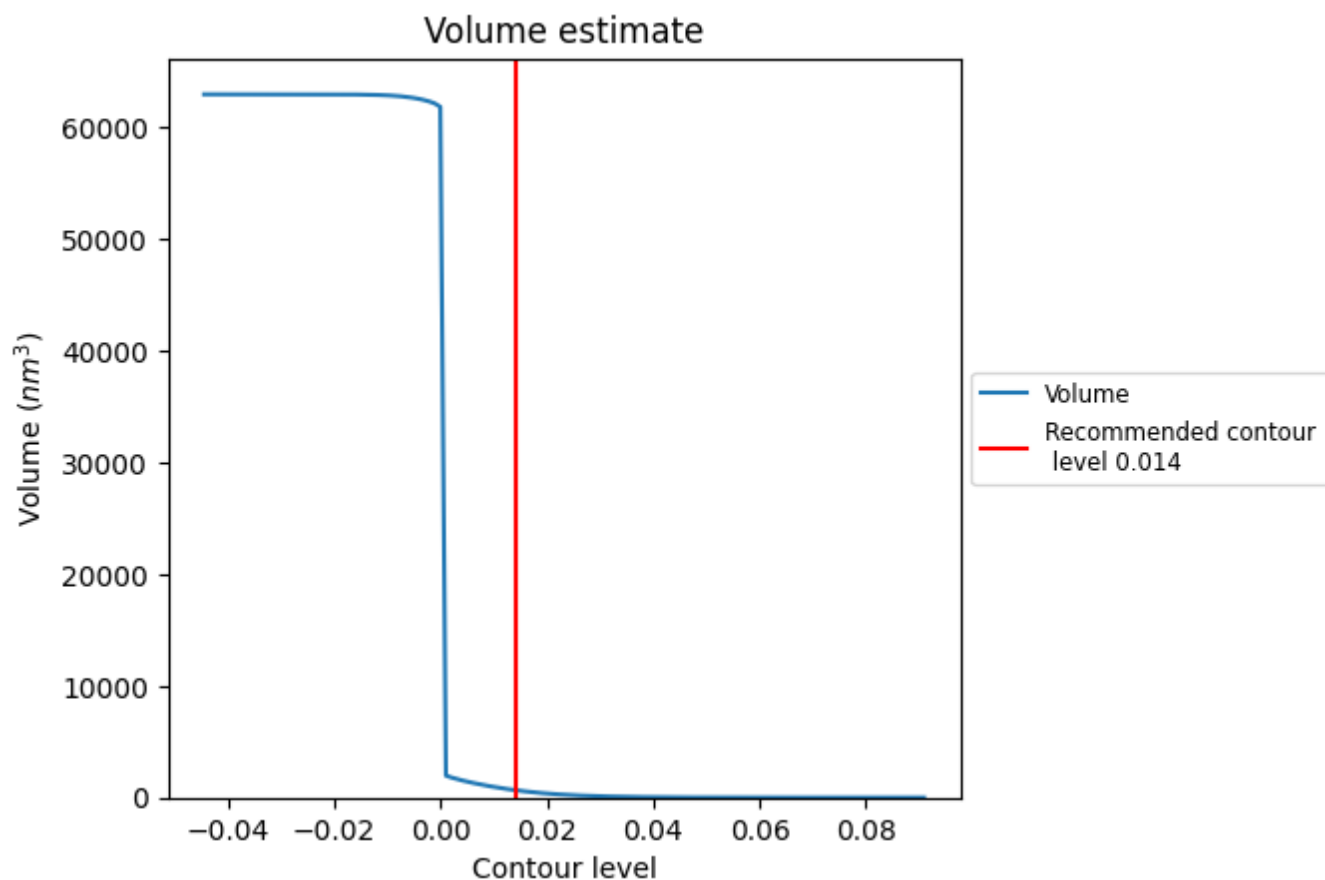
This section contains the results of statistical analysis of the map.

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.

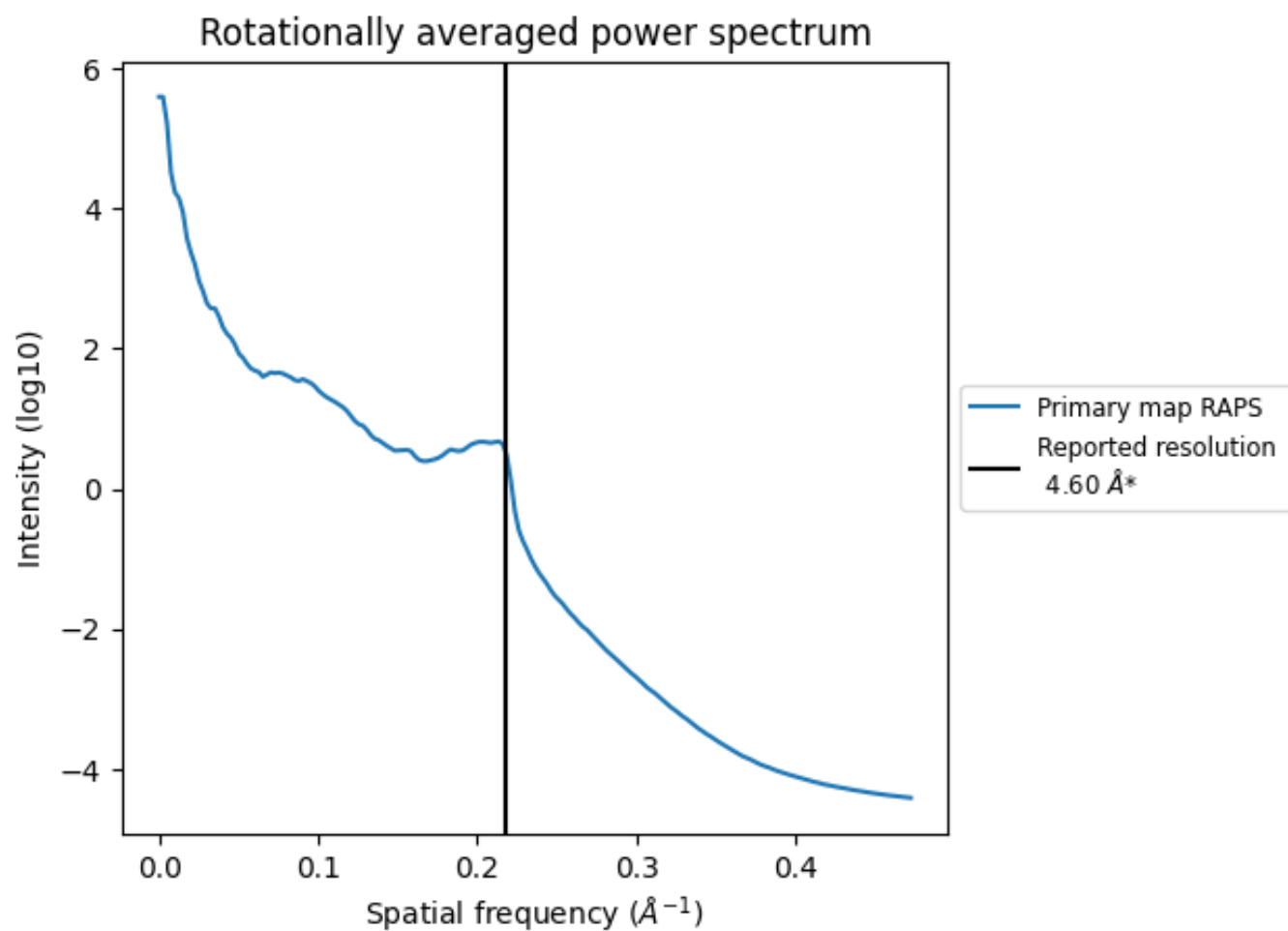
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 664 nm³; this corresponds to an approximate mass of 600 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 0.217 Å⁻¹

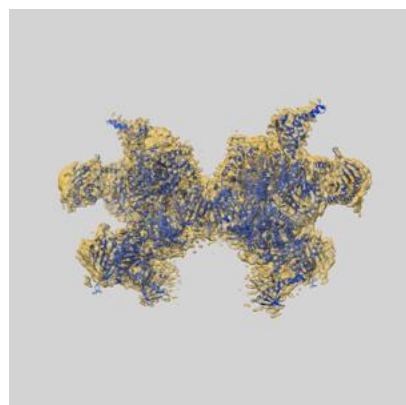
8 Fourier-Shell correlation

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

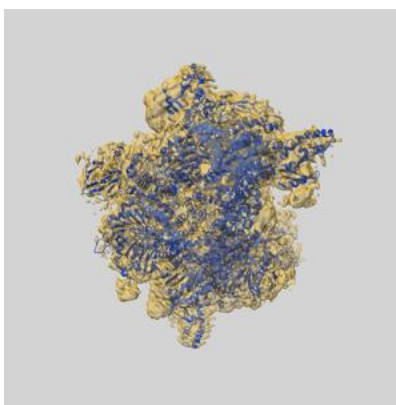
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4343 and PDB model 6G2H. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

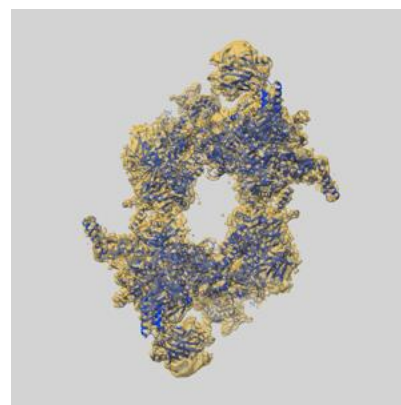
9.1 Map-model overlay [i](#)



X



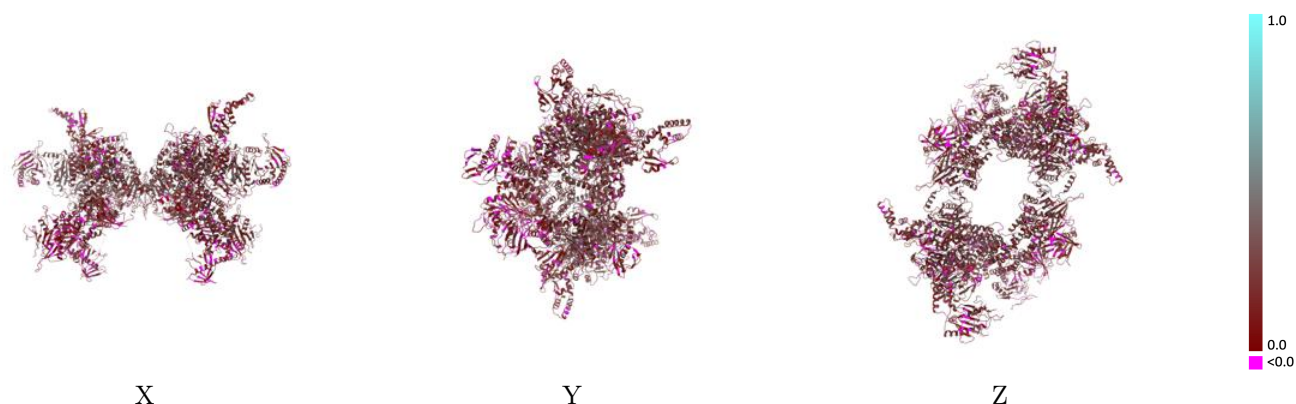
Y



Z

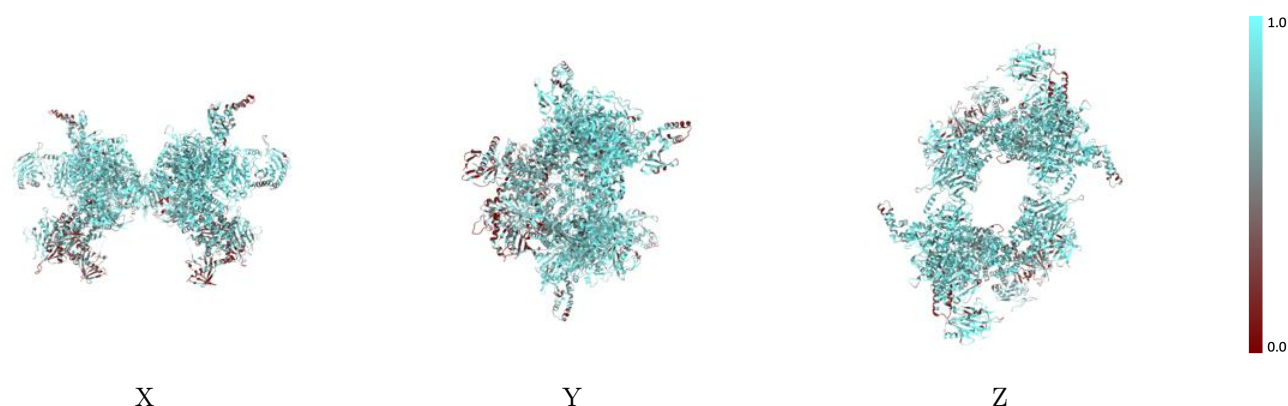
The images above show the 3D surface view of the map at the recommended contour level 0.014 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



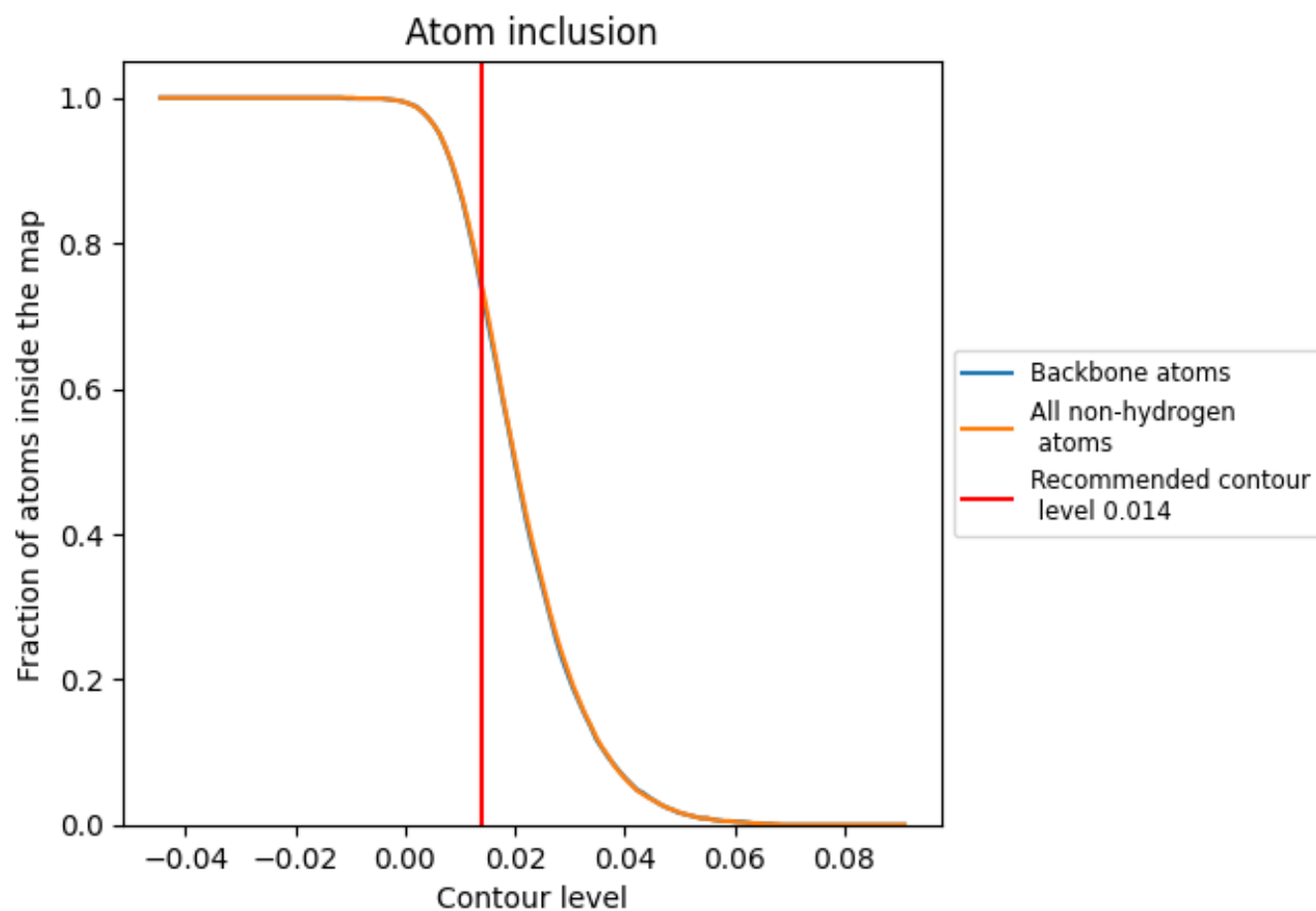
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.014).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 74% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7410	0.2070
A	0.5560	0.1510
B	0.5520	0.1490
C	0.8000	0.2210
D	0.8040	0.2250
E	0.8040	0.2280
F	0.7990	0.2210

