



wwPDB EM Validation Summary Report ⓘ

Oct 21, 2025 – 06:28 PM EDT

PDB ID : 9DAE / pdb_00009dae
EMDB ID : EMD-46690
Title : Cryo-EM Structure of the Multimeric Phosphoenolpyruvate Binding Domain of *Staphylothermus marinus* Phosphoenolpyruvate Synthase
Authors : Legare, S.; Kirby, M.W.; Stetefeld, J.
Deposited on : 2024-08-22
Resolution : 2.24 Å(reported)
Based on initial model : .

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.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

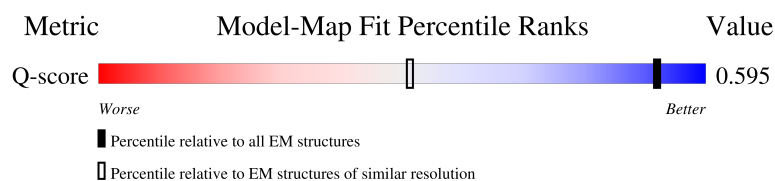
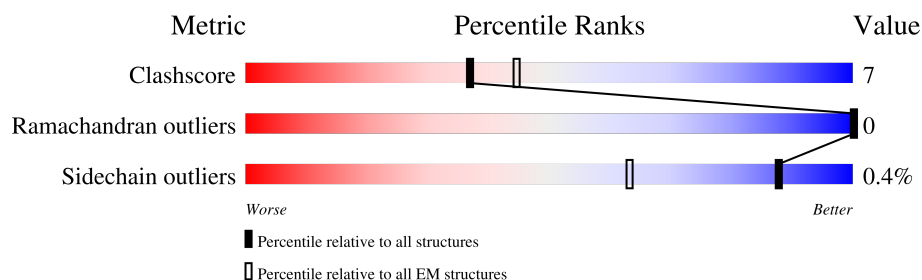
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.24 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.








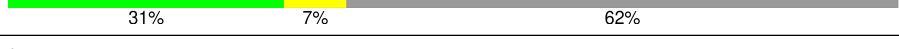

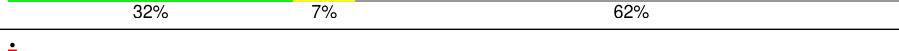
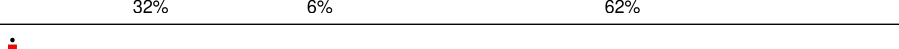
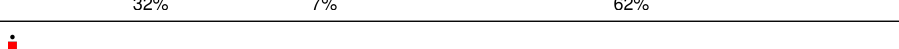










Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	3381 (1.75 - 2.74)

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	846	
1	BA	846	
1	C	846	
1	DA	846	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	E	846	
1	FA	846	
1	G	846	
1	HA	846	
1	I	846	
1	JA	846	
1	K	846	
1	LA	846	
1	M	846	
1	NA	846	
1	O	846	
1	PA	846	
1	Q	846	
1	RA	846	
1	S	846	
1	TA	846	
1	V	846	
1	VA	846	
1	X	846	
1	Z	846	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 62232 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 Phosphoenolpyruvate synthase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	C	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	E	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	G	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	I	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	K	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	M	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	O	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	Q	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	S	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	V	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	X	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	Z	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	BA	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	DA	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	FA	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	HA	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	JA	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	LA	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	NA	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	PA	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	RA	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	TA	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		
1	VA	323	Total	C	N	O	S	0	0
			2592	1678	431	471	12		

There are 312 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	initiating methionine	UNP P46893
A	-10	GLY	-	expression tag	UNP P46893
A	-9	SER	-	expression tag	UNP P46893
A	-8	SER	-	expression tag	UNP P46893
A	-7	HIS	-	expression tag	UNP P46893
A	-6	HIS	-	expression tag	UNP P46893
A	-5	HIS	-	expression tag	UNP P46893
A	-4	HIS	-	expression tag	UNP P46893
A	-3	HIS	-	expression tag	UNP P46893
A	-2	HIS	-	expression tag	UNP P46893
A	-1	SER	-	expression tag	UNP P46893
A	0	SER	-	expression tag	UNP P46893
A	1	GLY	-	expression tag	UNP P46893
C	-11	MET	-	initiating methionine	UNP P46893
C	-10	GLY	-	expression tag	UNP P46893
C	-9	SER	-	expression tag	UNP P46893
C	-8	SER	-	expression tag	UNP P46893
C	-7	HIS	-	expression tag	UNP P46893
C	-6	HIS	-	expression tag	UNP P46893
C	-5	HIS	-	expression tag	UNP P46893
C	-4	HIS	-	expression tag	UNP P46893
C	-3	HIS	-	expression tag	UNP P46893
C	-2	HIS	-	expression tag	UNP P46893
C	-1	SER	-	expression tag	UNP P46893
C	0	SER	-	expression tag	UNP P46893

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	GLY	-	expression tag	UNP P46893
E	-11	MET	-	initiating methionine	UNP P46893
E	-10	GLY	-	expression tag	UNP P46893
E	-9	SER	-	expression tag	UNP P46893
E	-8	SER	-	expression tag	UNP P46893
E	-7	HIS	-	expression tag	UNP P46893
E	-6	HIS	-	expression tag	UNP P46893
E	-5	HIS	-	expression tag	UNP P46893
E	-4	HIS	-	expression tag	UNP P46893
E	-3	HIS	-	expression tag	UNP P46893
E	-2	HIS	-	expression tag	UNP P46893
E	-1	SER	-	expression tag	UNP P46893
E	0	SER	-	expression tag	UNP P46893
E	1	GLY	-	expression tag	UNP P46893
G	-11	MET	-	initiating methionine	UNP P46893
G	-10	GLY	-	expression tag	UNP P46893
G	-9	SER	-	expression tag	UNP P46893
G	-8	SER	-	expression tag	UNP P46893
G	-7	HIS	-	expression tag	UNP P46893
G	-6	HIS	-	expression tag	UNP P46893
G	-5	HIS	-	expression tag	UNP P46893
G	-4	HIS	-	expression tag	UNP P46893
G	-3	HIS	-	expression tag	UNP P46893
G	-2	HIS	-	expression tag	UNP P46893
G	-1	SER	-	expression tag	UNP P46893
G	0	SER	-	expression tag	UNP P46893
G	1	GLY	-	expression tag	UNP P46893
I	-11	MET	-	initiating methionine	UNP P46893
I	-10	GLY	-	expression tag	UNP P46893
I	-9	SER	-	expression tag	UNP P46893
I	-8	SER	-	expression tag	UNP P46893
I	-7	HIS	-	expression tag	UNP P46893
I	-6	HIS	-	expression tag	UNP P46893
I	-5	HIS	-	expression tag	UNP P46893
I	-4	HIS	-	expression tag	UNP P46893
I	-3	HIS	-	expression tag	UNP P46893
I	-2	HIS	-	expression tag	UNP P46893
I	-1	SER	-	expression tag	UNP P46893
I	0	SER	-	expression tag	UNP P46893
I	1	GLY	-	expression tag	UNP P46893
K	-11	MET	-	initiating methionine	UNP P46893
K	-10	GLY	-	expression tag	UNP P46893

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
K	-9	SER	-	expression tag	UNP P46893
K	-8	SER	-	expression tag	UNP P46893
K	-7	HIS	-	expression tag	UNP P46893
K	-6	HIS	-	expression tag	UNP P46893
K	-5	HIS	-	expression tag	UNP P46893
K	-4	HIS	-	expression tag	UNP P46893
K	-3	HIS	-	expression tag	UNP P46893
K	-2	HIS	-	expression tag	UNP P46893
K	-1	SER	-	expression tag	UNP P46893
K	0	SER	-	expression tag	UNP P46893
K	1	GLY	-	expression tag	UNP P46893
M	-11	MET	-	initiating methionine	UNP P46893
M	-10	GLY	-	expression tag	UNP P46893
M	-9	SER	-	expression tag	UNP P46893
M	-8	SER	-	expression tag	UNP P46893
M	-7	HIS	-	expression tag	UNP P46893
M	-6	HIS	-	expression tag	UNP P46893
M	-5	HIS	-	expression tag	UNP P46893
M	-4	HIS	-	expression tag	UNP P46893
M	-3	HIS	-	expression tag	UNP P46893
M	-2	HIS	-	expression tag	UNP P46893
M	-1	SER	-	expression tag	UNP P46893
M	0	SER	-	expression tag	UNP P46893
M	1	GLY	-	expression tag	UNP P46893
O	-11	MET	-	initiating methionine	UNP P46893
O	-10	GLY	-	expression tag	UNP P46893
O	-9	SER	-	expression tag	UNP P46893
O	-8	SER	-	expression tag	UNP P46893
O	-7	HIS	-	expression tag	UNP P46893
O	-6	HIS	-	expression tag	UNP P46893
O	-5	HIS	-	expression tag	UNP P46893
O	-4	HIS	-	expression tag	UNP P46893
O	-3	HIS	-	expression tag	UNP P46893
O	-2	HIS	-	expression tag	UNP P46893
O	-1	SER	-	expression tag	UNP P46893
O	0	SER	-	expression tag	UNP P46893
O	1	GLY	-	expression tag	UNP P46893
Q	-11	MET	-	initiating methionine	UNP P46893
Q	-10	GLY	-	expression tag	UNP P46893
Q	-9	SER	-	expression tag	UNP P46893
Q	-8	SER	-	expression tag	UNP P46893
Q	-7	HIS	-	expression tag	UNP P46893

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
Q	-6	HIS	-	expression tag	UNP P46893
Q	-5	HIS	-	expression tag	UNP P46893
Q	-4	HIS	-	expression tag	UNP P46893
Q	-3	HIS	-	expression tag	UNP P46893
Q	-2	HIS	-	expression tag	UNP P46893
Q	-1	SER	-	expression tag	UNP P46893
Q	0	SER	-	expression tag	UNP P46893
Q	1	GLY	-	expression tag	UNP P46893
S	-11	MET	-	initiating methionine	UNP P46893
S	-10	GLY	-	expression tag	UNP P46893
S	-9	SER	-	expression tag	UNP P46893
S	-8	SER	-	expression tag	UNP P46893
S	-7	HIS	-	expression tag	UNP P46893
S	-6	HIS	-	expression tag	UNP P46893
S	-5	HIS	-	expression tag	UNP P46893
S	-4	HIS	-	expression tag	UNP P46893
S	-3	HIS	-	expression tag	UNP P46893
S	-2	HIS	-	expression tag	UNP P46893
S	-1	SER	-	expression tag	UNP P46893
S	0	SER	-	expression tag	UNP P46893
S	1	GLY	-	expression tag	UNP P46893
V	-11	MET	-	initiating methionine	UNP P46893
V	-10	GLY	-	expression tag	UNP P46893
V	-9	SER	-	expression tag	UNP P46893
V	-8	SER	-	expression tag	UNP P46893
V	-7	HIS	-	expression tag	UNP P46893
V	-6	HIS	-	expression tag	UNP P46893
V	-5	HIS	-	expression tag	UNP P46893
V	-4	HIS	-	expression tag	UNP P46893
V	-3	HIS	-	expression tag	UNP P46893
V	-2	HIS	-	expression tag	UNP P46893
V	-1	SER	-	expression tag	UNP P46893
V	0	SER	-	expression tag	UNP P46893
V	1	GLY	-	expression tag	UNP P46893
X	-11	MET	-	initiating methionine	UNP P46893
X	-10	GLY	-	expression tag	UNP P46893
X	-9	SER	-	expression tag	UNP P46893
X	-8	SER	-	expression tag	UNP P46893
X	-7	HIS	-	expression tag	UNP P46893
X	-6	HIS	-	expression tag	UNP P46893
X	-5	HIS	-	expression tag	UNP P46893
X	-4	HIS	-	expression tag	UNP P46893

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
X	-3	HIS	-	expression tag	UNP P46893
X	-2	HIS	-	expression tag	UNP P46893
X	-1	SER	-	expression tag	UNP P46893
X	0	SER	-	expression tag	UNP P46893
X	1	GLY	-	expression tag	UNP P46893
Z	-11	MET	-	initiating methionine	UNP P46893
Z	-10	GLY	-	expression tag	UNP P46893
Z	-9	SER	-	expression tag	UNP P46893
Z	-8	SER	-	expression tag	UNP P46893
Z	-7	HIS	-	expression tag	UNP P46893
Z	-6	HIS	-	expression tag	UNP P46893
Z	-5	HIS	-	expression tag	UNP P46893
Z	-4	HIS	-	expression tag	UNP P46893
Z	-3	HIS	-	expression tag	UNP P46893
Z	-2	HIS	-	expression tag	UNP P46893
Z	-1	SER	-	expression tag	UNP P46893
Z	0	SER	-	expression tag	UNP P46893
Z	1	GLY	-	expression tag	UNP P46893
BA	-11	MET	-	initiating methionine	UNP P46893
BA	-10	GLY	-	expression tag	UNP P46893
BA	-9	SER	-	expression tag	UNP P46893
BA	-8	SER	-	expression tag	UNP P46893
BA	-7	HIS	-	expression tag	UNP P46893
BA	-6	HIS	-	expression tag	UNP P46893
BA	-5	HIS	-	expression tag	UNP P46893
BA	-4	HIS	-	expression tag	UNP P46893
BA	-3	HIS	-	expression tag	UNP P46893
BA	-2	HIS	-	expression tag	UNP P46893
BA	-1	SER	-	expression tag	UNP P46893
BA	0	SER	-	expression tag	UNP P46893
BA	1	GLY	-	expression tag	UNP P46893
DA	-11	MET	-	initiating methionine	UNP P46893
DA	-10	GLY	-	expression tag	UNP P46893
DA	-9	SER	-	expression tag	UNP P46893
DA	-8	SER	-	expression tag	UNP P46893
DA	-7	HIS	-	expression tag	UNP P46893
DA	-6	HIS	-	expression tag	UNP P46893
DA	-5	HIS	-	expression tag	UNP P46893
DA	-4	HIS	-	expression tag	UNP P46893
DA	-3	HIS	-	expression tag	UNP P46893
DA	-2	HIS	-	expression tag	UNP P46893
DA	-1	SER	-	expression tag	UNP P46893

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
DA	0	SER	-	expression tag	UNP P46893
DA	1	GLY	-	expression tag	UNP P46893
FA	-11	MET	-	initiating methionine	UNP P46893
FA	-10	GLY	-	expression tag	UNP P46893
FA	-9	SER	-	expression tag	UNP P46893
FA	-8	SER	-	expression tag	UNP P46893
FA	-7	HIS	-	expression tag	UNP P46893
FA	-6	HIS	-	expression tag	UNP P46893
FA	-5	HIS	-	expression tag	UNP P46893
FA	-4	HIS	-	expression tag	UNP P46893
FA	-3	HIS	-	expression tag	UNP P46893
FA	-2	HIS	-	expression tag	UNP P46893
FA	-1	SER	-	expression tag	UNP P46893
FA	0	SER	-	expression tag	UNP P46893
FA	1	GLY	-	expression tag	UNP P46893
HA	-11	MET	-	initiating methionine	UNP P46893
HA	-10	GLY	-	expression tag	UNP P46893
HA	-9	SER	-	expression tag	UNP P46893
HA	-8	SER	-	expression tag	UNP P46893
HA	-7	HIS	-	expression tag	UNP P46893
HA	-6	HIS	-	expression tag	UNP P46893
HA	-5	HIS	-	expression tag	UNP P46893
HA	-4	HIS	-	expression tag	UNP P46893
HA	-3	HIS	-	expression tag	UNP P46893
HA	-2	HIS	-	expression tag	UNP P46893
HA	-1	SER	-	expression tag	UNP P46893
HA	0	SER	-	expression tag	UNP P46893
HA	1	GLY	-	expression tag	UNP P46893
JA	-11	MET	-	initiating methionine	UNP P46893
JA	-10	GLY	-	expression tag	UNP P46893
JA	-9	SER	-	expression tag	UNP P46893
JA	-8	SER	-	expression tag	UNP P46893
JA	-7	HIS	-	expression tag	UNP P46893
JA	-6	HIS	-	expression tag	UNP P46893
JA	-5	HIS	-	expression tag	UNP P46893
JA	-4	HIS	-	expression tag	UNP P46893
JA	-3	HIS	-	expression tag	UNP P46893
JA	-2	HIS	-	expression tag	UNP P46893
JA	-1	SER	-	expression tag	UNP P46893
JA	0	SER	-	expression tag	UNP P46893
JA	1	GLY	-	expression tag	UNP P46893
LA	-11	MET	-	initiating methionine	UNP P46893

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
LA	-10	GLY	-	expression tag	UNP P46893
LA	-9	SER	-	expression tag	UNP P46893
LA	-8	SER	-	expression tag	UNP P46893
LA	-7	HIS	-	expression tag	UNP P46893
LA	-6	HIS	-	expression tag	UNP P46893
LA	-5	HIS	-	expression tag	UNP P46893
LA	-4	HIS	-	expression tag	UNP P46893
LA	-3	HIS	-	expression tag	UNP P46893
LA	-2	HIS	-	expression tag	UNP P46893
LA	-1	SER	-	expression tag	UNP P46893
LA	0	SER	-	expression tag	UNP P46893
LA	1	GLY	-	expression tag	UNP P46893
NA	-11	MET	-	initiating methionine	UNP P46893
NA	-10	GLY	-	expression tag	UNP P46893
NA	-9	SER	-	expression tag	UNP P46893
NA	-8	SER	-	expression tag	UNP P46893
NA	-7	HIS	-	expression tag	UNP P46893
NA	-6	HIS	-	expression tag	UNP P46893
NA	-5	HIS	-	expression tag	UNP P46893
NA	-4	HIS	-	expression tag	UNP P46893
NA	-3	HIS	-	expression tag	UNP P46893
NA	-2	HIS	-	expression tag	UNP P46893
NA	-1	SER	-	expression tag	UNP P46893
NA	0	SER	-	expression tag	UNP P46893
NA	1	GLY	-	expression tag	UNP P46893
PA	-11	MET	-	initiating methionine	UNP P46893
PA	-10	GLY	-	expression tag	UNP P46893
PA	-9	SER	-	expression tag	UNP P46893
PA	-8	SER	-	expression tag	UNP P46893
PA	-7	HIS	-	expression tag	UNP P46893
PA	-6	HIS	-	expression tag	UNP P46893
PA	-5	HIS	-	expression tag	UNP P46893
PA	-4	HIS	-	expression tag	UNP P46893
PA	-3	HIS	-	expression tag	UNP P46893
PA	-2	HIS	-	expression tag	UNP P46893
PA	-1	SER	-	expression tag	UNP P46893
PA	0	SER	-	expression tag	UNP P46893
PA	1	GLY	-	expression tag	UNP P46893
RA	-11	MET	-	initiating methionine	UNP P46893
RA	-10	GLY	-	expression tag	UNP P46893
RA	-9	SER	-	expression tag	UNP P46893
RA	-8	SER	-	expression tag	UNP P46893

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
RA	-7	HIS	-	expression tag	UNP P46893
RA	-6	HIS	-	expression tag	UNP P46893
RA	-5	HIS	-	expression tag	UNP P46893
RA	-4	HIS	-	expression tag	UNP P46893
RA	-3	HIS	-	expression tag	UNP P46893
RA	-2	HIS	-	expression tag	UNP P46893
RA	-1	SER	-	expression tag	UNP P46893
RA	0	SER	-	expression tag	UNP P46893
RA	1	GLY	-	expression tag	UNP P46893
TA	-11	MET	-	initiating methionine	UNP P46893
TA	-10	GLY	-	expression tag	UNP P46893
TA	-9	SER	-	expression tag	UNP P46893
TA	-8	SER	-	expression tag	UNP P46893
TA	-7	HIS	-	expression tag	UNP P46893
TA	-6	HIS	-	expression tag	UNP P46893
TA	-5	HIS	-	expression tag	UNP P46893
TA	-4	HIS	-	expression tag	UNP P46893
TA	-3	HIS	-	expression tag	UNP P46893
TA	-2	HIS	-	expression tag	UNP P46893
TA	-1	SER	-	expression tag	UNP P46893
TA	0	SER	-	expression tag	UNP P46893
TA	1	GLY	-	expression tag	UNP P46893
VA	-11	MET	-	initiating methionine	UNP P46893
VA	-10	GLY	-	expression tag	UNP P46893
VA	-9	SER	-	expression tag	UNP P46893
VA	-8	SER	-	expression tag	UNP P46893
VA	-7	HIS	-	expression tag	UNP P46893
VA	-6	HIS	-	expression tag	UNP P46893
VA	-5	HIS	-	expression tag	UNP P46893
VA	-4	HIS	-	expression tag	UNP P46893
VA	-3	HIS	-	expression tag	UNP P46893
VA	-2	HIS	-	expression tag	UNP P46893
VA	-1	SER	-	expression tag	UNP P46893
VA	0	SER	-	expression tag	UNP P46893
VA	1	GLY	-	expression tag	UNP P46893

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
2	A	1	Total Mg 1 1	0
2	C	1	Total Mg 1 1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
2	E	1	Total 1	Mg 1	0
2	G	1	Total 1	Mg 1	0
2	I	1	Total 1	Mg 1	0
2	K	1	Total 1	Mg 1	0
2	M	1	Total 1	Mg 1	0
2	O	1	Total 1	Mg 1	0
2	Q	1	Total 1	Mg 1	0
2	S	1	Total 1	Mg 1	0
2	V	1	Total 1	Mg 1	0
2	X	1	Total 1	Mg 1	0
2	Z	1	Total 1	Mg 1	0
2	BA	1	Total 1	Mg 1	0
2	DA	1	Total 1	Mg 1	0
2	FA	1	Total 1	Mg 1	0
2	HA	1	Total 1	Mg 1	0
2	JA	1	Total 1	Mg 1	0
2	LA	1	Total 1	Mg 1	0
2	NA	1	Total 1	Mg 1	0
2	PA	1	Total 1	Mg 1	0
2	RA	1	Total 1	Mg 1	0
2	TA	1	Total 1	Mg 1	0

Continued on next page...

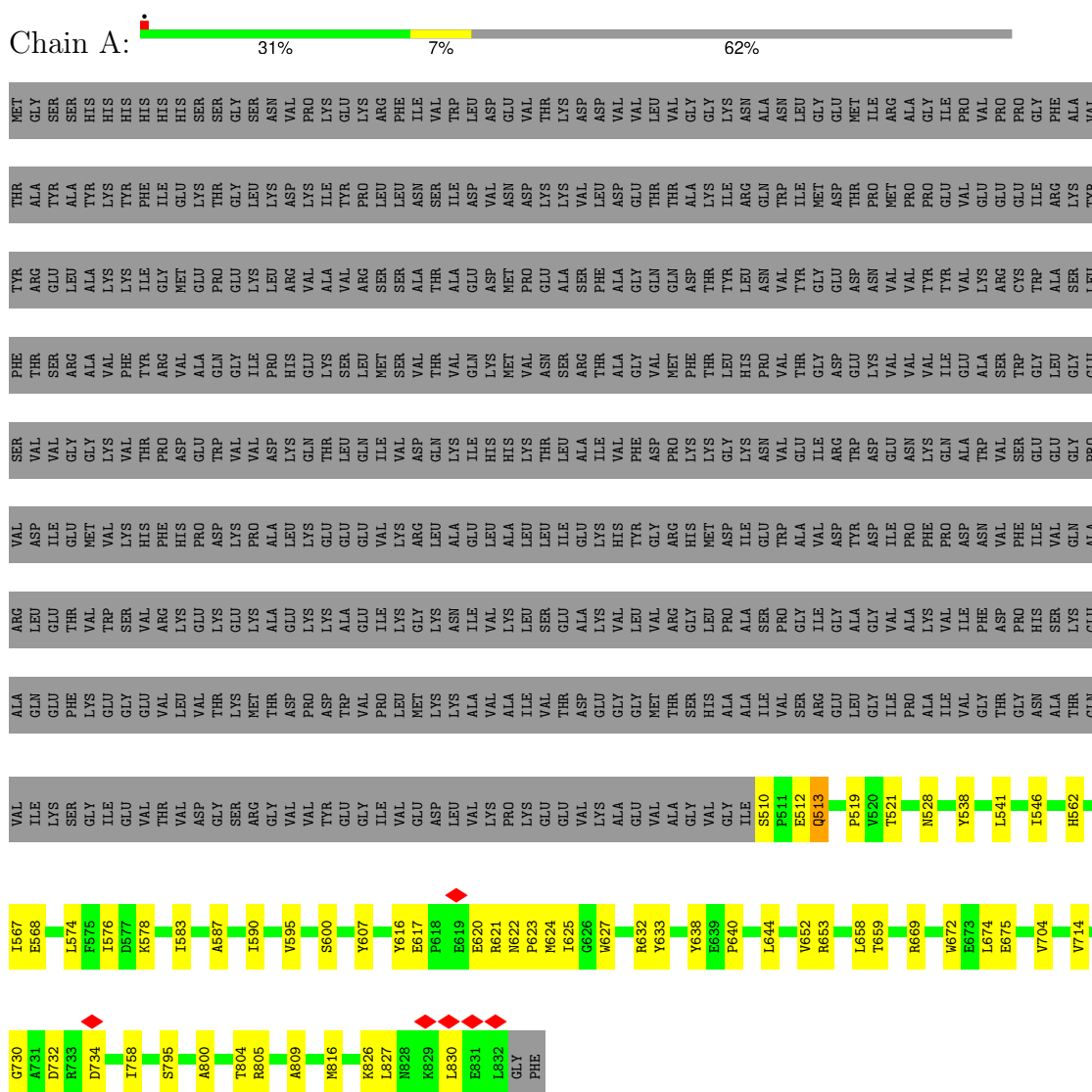
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
2	VA	1	1	1	0

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.

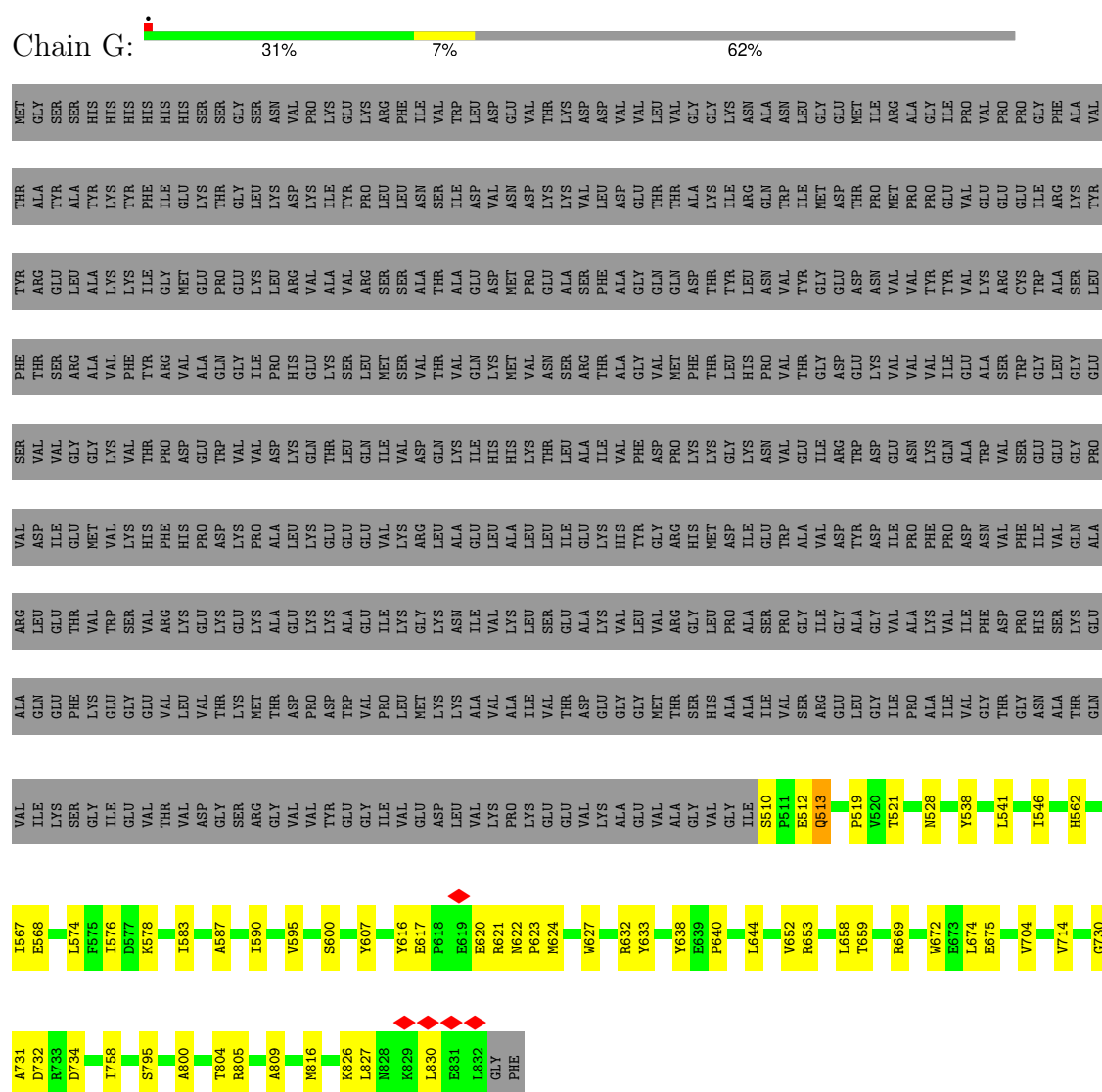
• Molecule 1: Phosphoenolpyruvate synthase



• Molecule 1: Phosphoenolpyruvate synthase



- Molecule 1: Phosphoenolpyruvate synthase



- Molecule 1: Phosphoenolpyruvate synthase

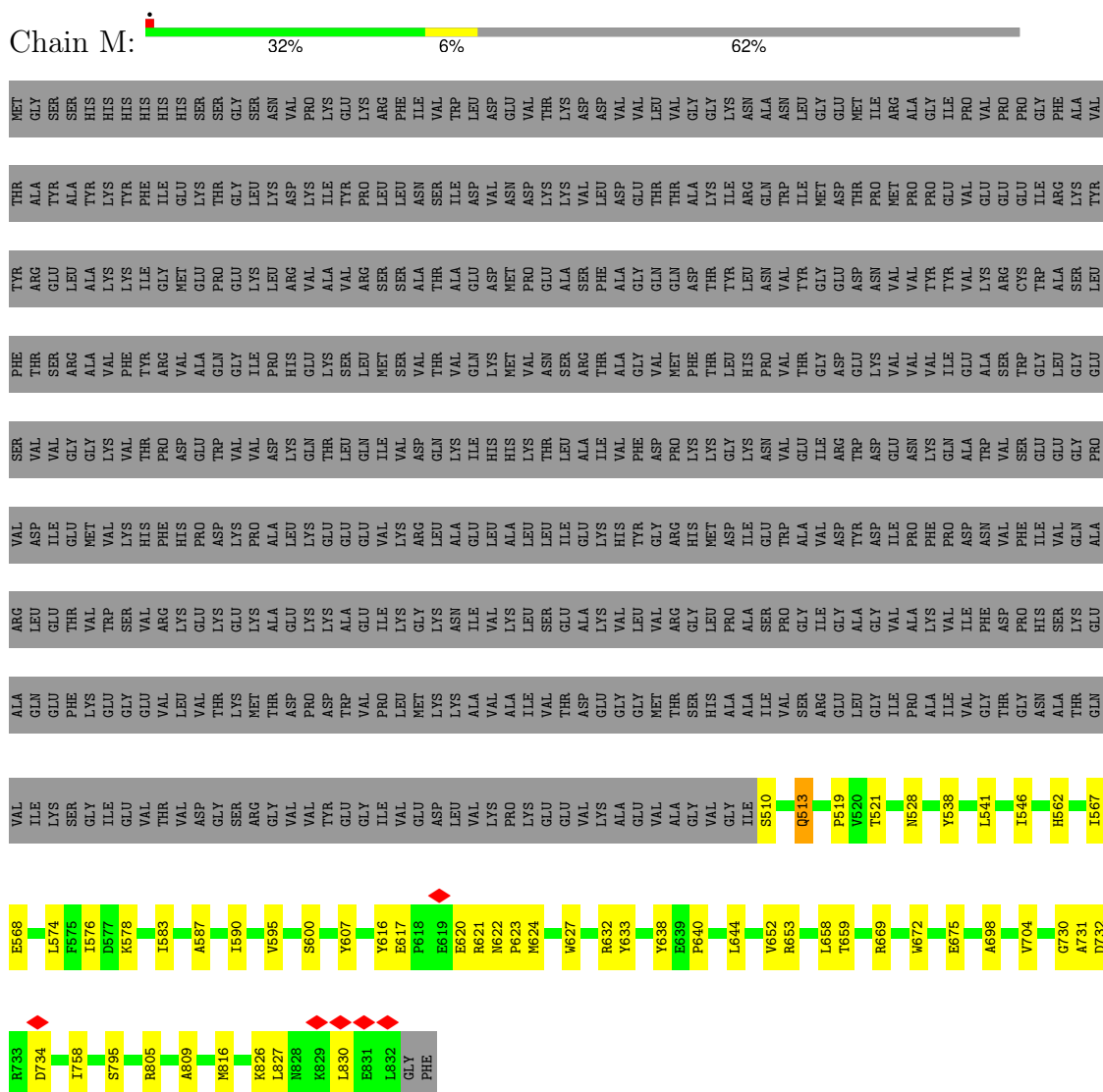


- Molecule 1: Phosphoenolpyruvate synthase



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

- Molecule 1: Phosphoenolpyruvate synthase

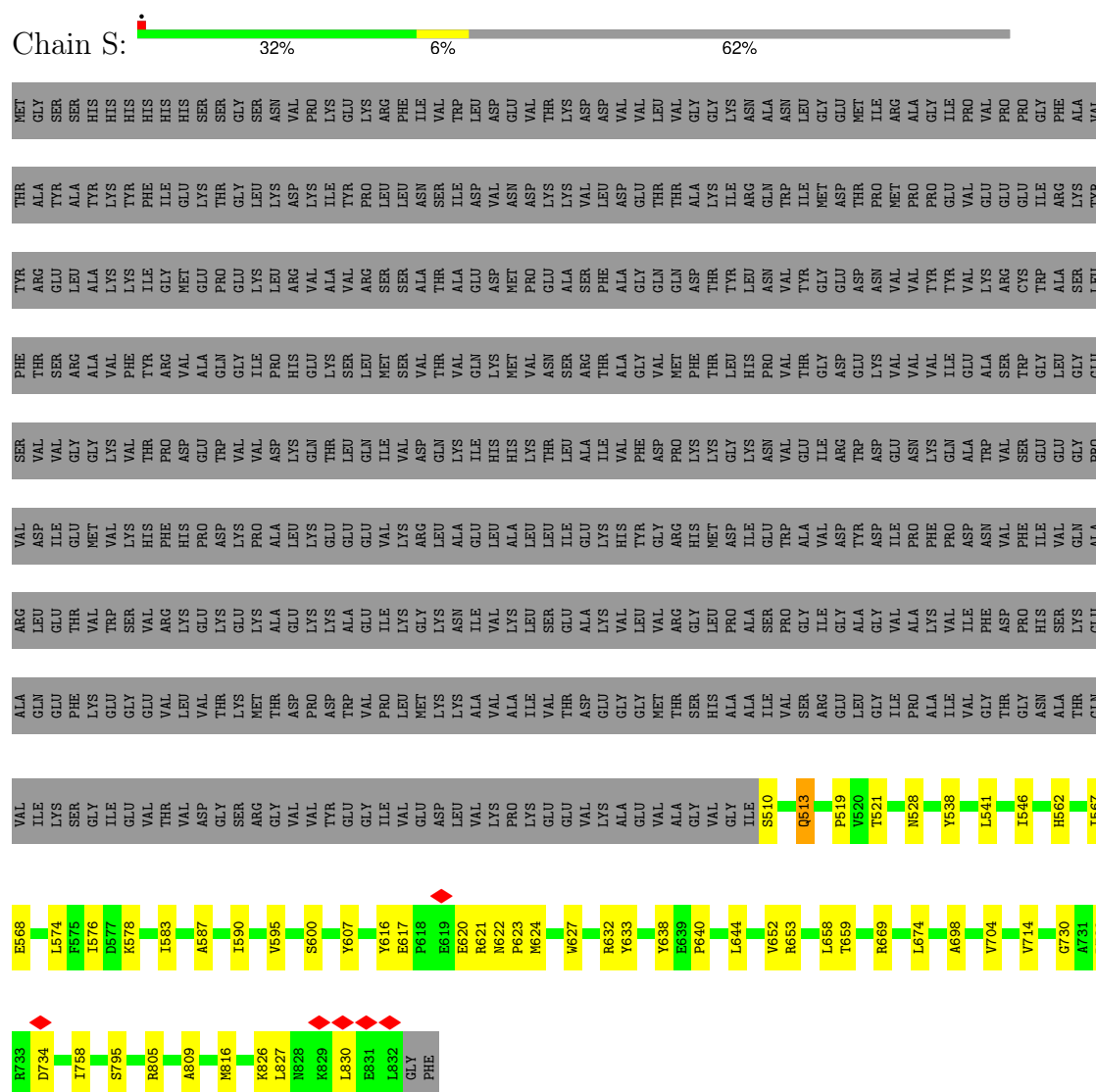


- Molecule 1: Phosphoenolpyruvate synthase



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

- Molecule 1: Phosphoenolpyruvate synthase

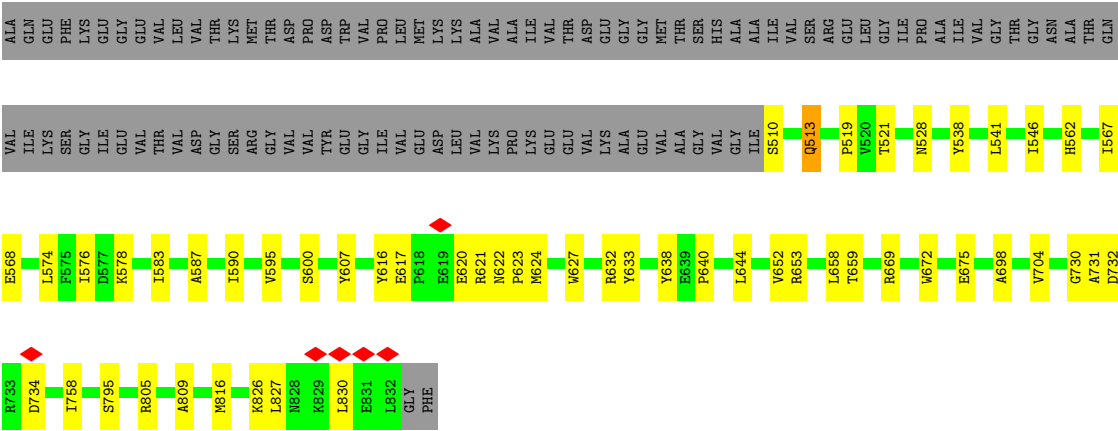


- Molecule 1: Phosphoenolpyruvate synthase

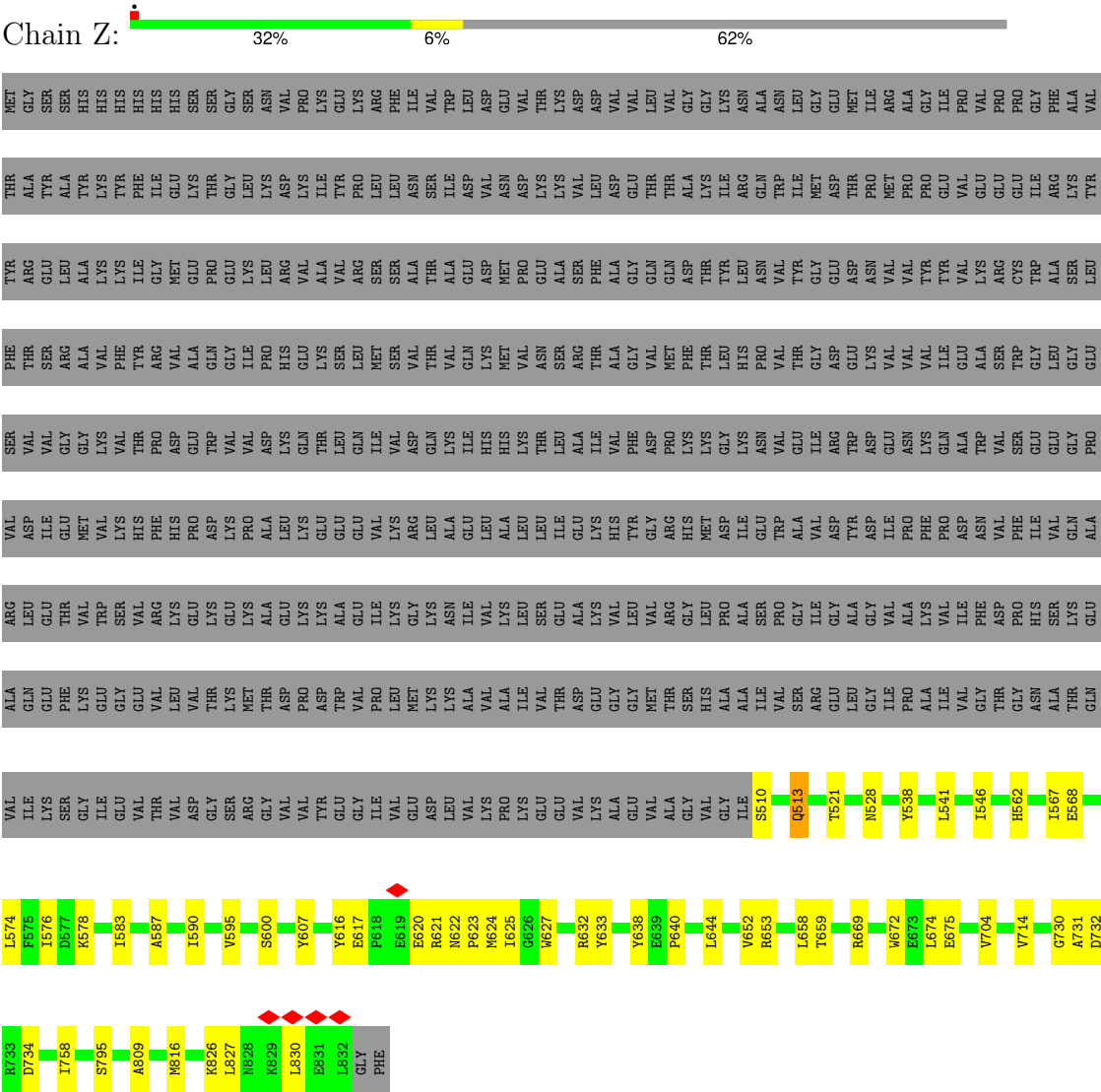


- Molecule 1: Phosphoenolpyruvate synthase

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

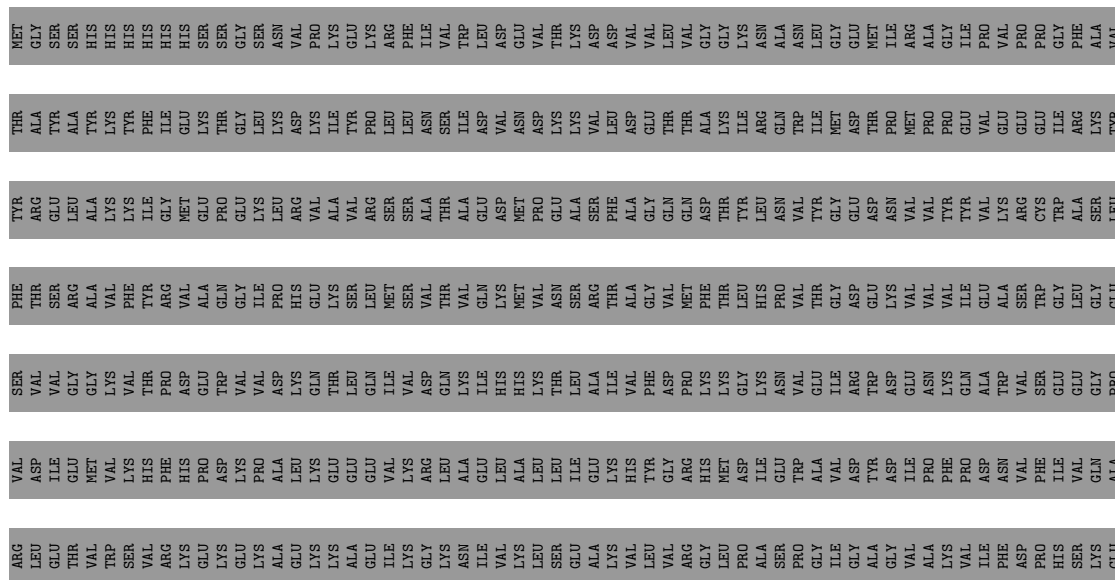


● Molecule 1: Phosphoenolpyruvate synthase

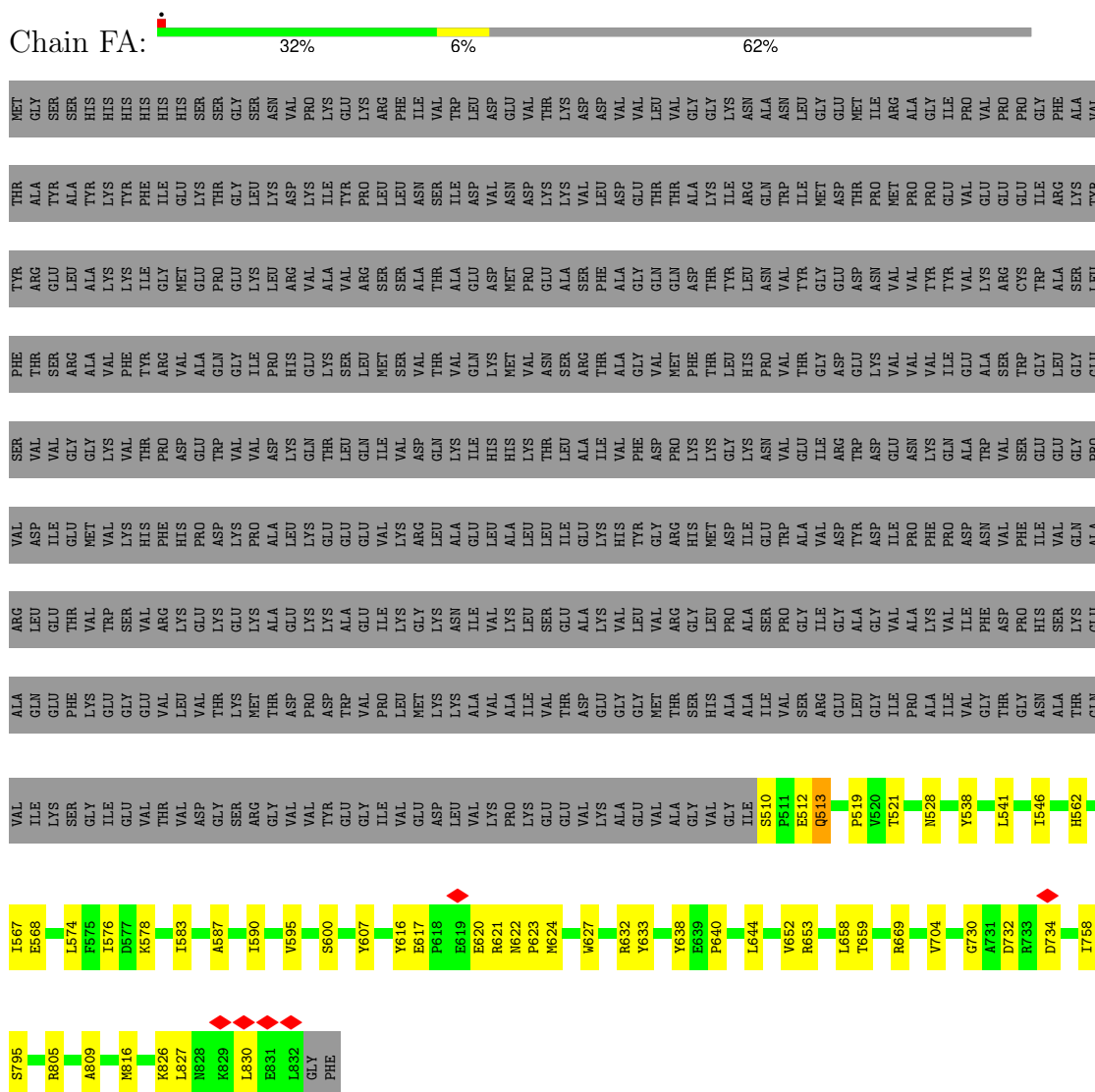


● Molecule 1: Phosphoenolpyruvate synthase





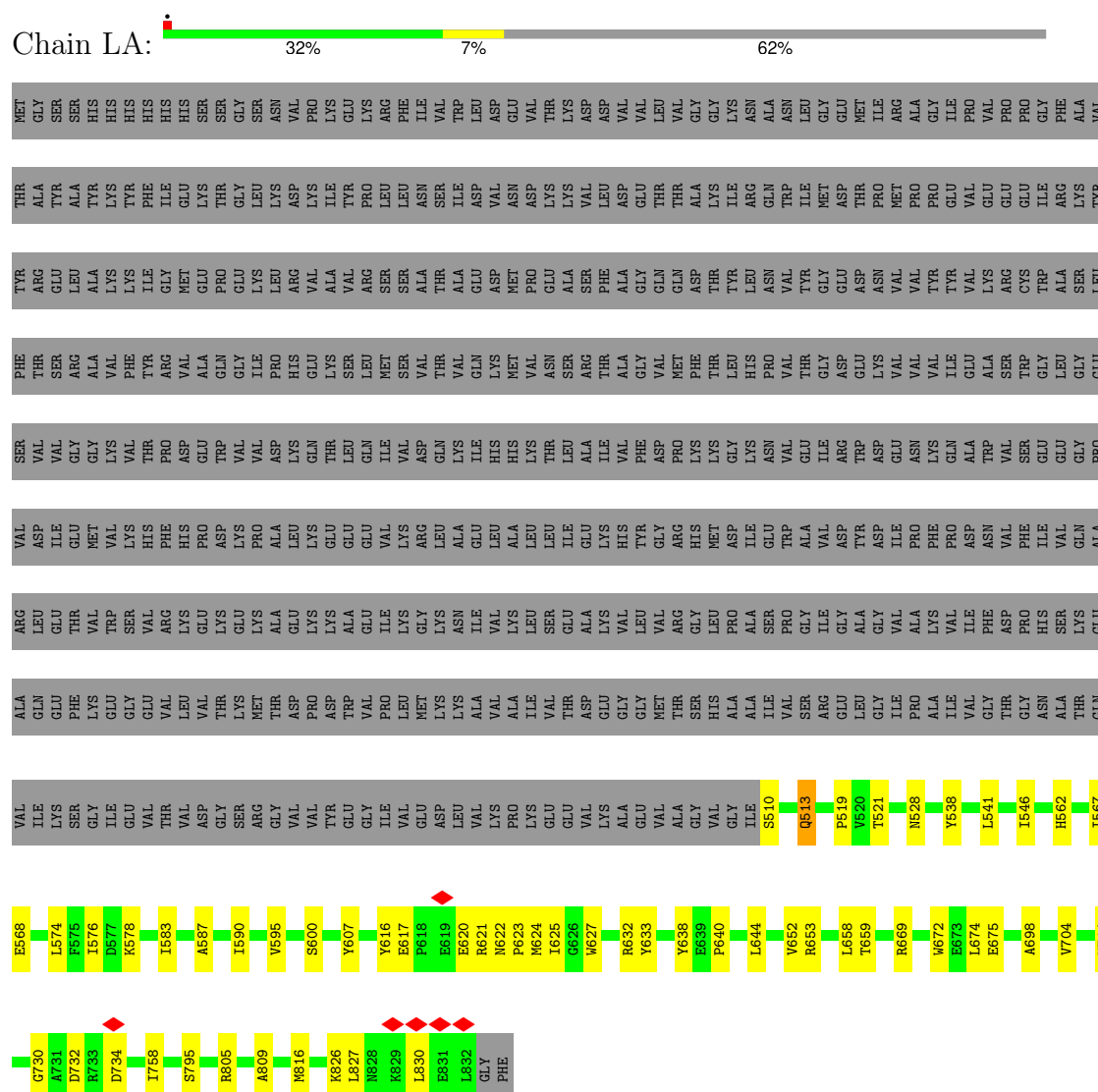
- Molecule 1: Phosphoenolpyruvate synthase



- Molecule 1: Phosphoenolpyruvate synthase

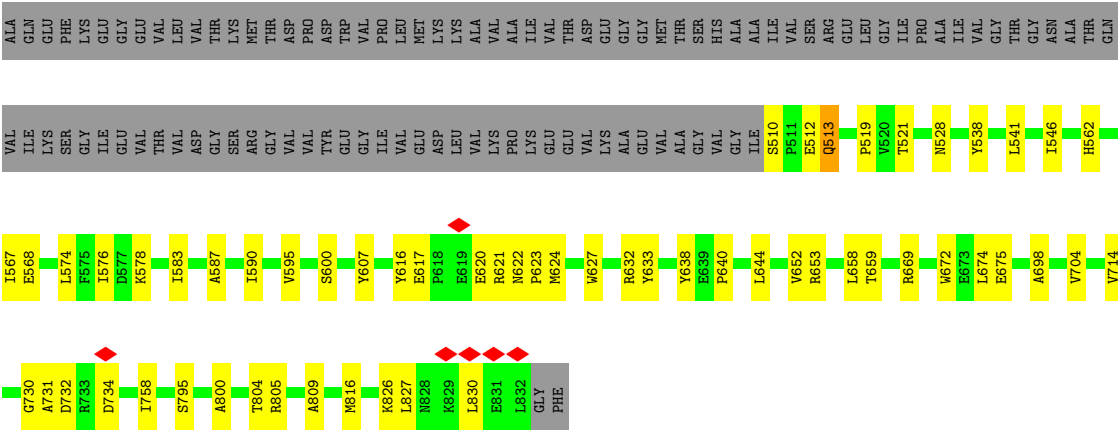


- Molecule 1: Phosphoenolpyruvate synthase

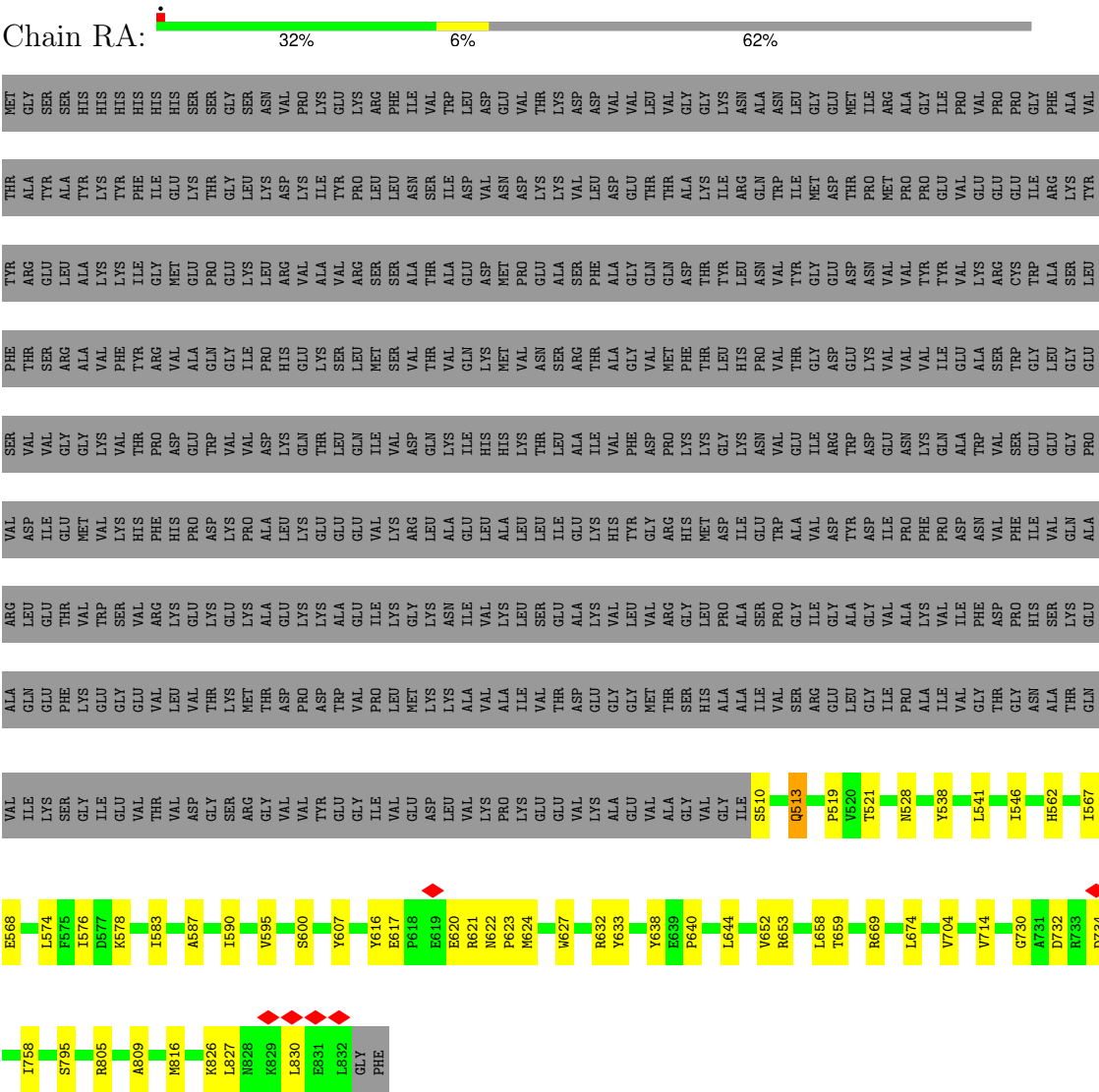


- Molecule 1: Phosphoenolpyruvate synthase





● Molecule 1: Phosphoenolpyruvate synthase



● Molecule 1: Phosphoenolpyruvate synthase





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, O	Depositor
Number of particles used	1138254	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 ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.178	Depositor
Minimum map value	-0.040	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	403.75998, 403.75998, 403.75998	wwPDB
Map dimensions	392, 392, 392	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.03, 1.03, 1.03	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	0.12	0/2648	0.30	0/3578
1	BA	0.12	0/2648	0.30	0/3578
1	C	0.12	0/2648	0.30	0/3578
1	DA	0.12	0/2648	0.30	0/3578
1	E	0.12	0/2648	0.30	0/3578
1	FA	0.12	0/2648	0.30	0/3578
1	G	0.12	0/2648	0.30	0/3578
1	HA	0.12	0/2648	0.30	0/3578
1	I	0.12	0/2648	0.30	0/3578
1	JA	0.12	0/2648	0.30	0/3578
1	K	0.12	0/2648	0.30	0/3578
1	LA	0.12	0/2648	0.30	0/3578
1	M	0.12	0/2648	0.30	0/3578
1	NA	0.12	0/2648	0.30	0/3578
1	O	0.12	0/2648	0.30	0/3578
1	PA	0.12	0/2648	0.30	0/3578
1	Q	0.12	0/2648	0.30	0/3578
1	RA	0.12	0/2648	0.30	0/3578
1	S	0.12	0/2648	0.30	0/3578
1	TA	0.12	0/2648	0.30	0/3578
1	V	0.12	0/2648	0.30	0/3578
1	VA	0.12	0/2648	0.30	0/3578
1	X	0.12	0/2648	0.30	0/3578
1	Z	0.12	0/2648	0.30	0/3578
All	All	0.12	0/63552	0.30	0/85872

There are no bond length outliers.

There are no bond angle outliers.

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	2592	0	2650	49	0
1	BA	2592	0	2650	49	0
1	C	2592	0	2650	48	0
1	DA	2592	0	2650	51	0
1	E	2592	0	2650	47	0
1	FA	2592	0	2650	45	0
1	G	2592	0	2650	50	0
1	HA	2592	0	2650	48	0
1	I	2592	0	2650	49	0
1	JA	2592	0	2650	49	0
1	K	2592	0	2650	48	0
1	LA	2592	0	2650	48	0
1	M	2592	0	2650	47	0
1	NA	2592	0	2650	48	0
1	O	2592	0	2650	50	0
1	PA	2592	0	2650	50	0
1	Q	2592	0	2650	51	0
1	RA	2592	0	2650	46	0
1	S	2592	0	2650	47	0
1	TA	2592	0	2650	47	0
1	V	2592	0	2650	47	0
1	VA	2592	0	2650	45	0
1	X	2592	0	2650	47	0
1	Z	2592	0	2650	49	0
2	A	1	0	0	0	0
2	BA	1	0	0	0	0
2	C	1	0	0	0	0
2	DA	1	0	0	0	0
2	E	1	0	0	0	0
2	FA	1	0	0	0	0
2	G	1	0	0	0	0
2	HA	1	0	0	0	0
2	I	1	0	0	0	0
2	JA	1	0	0	0	0
2	K	1	0	0	0	0
2	LA	1	0	0	0	0
2	M	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	NA	1	0	0	0	0
2	O	1	0	0	0	0
2	PA	1	0	0	0	0
2	Q	1	0	0	0	0
2	RA	1	0	0	0	0
2	S	1	0	0	0	0
2	TA	1	0	0	0	0
2	V	1	0	0	0	0
2	VA	1	0	0	0	0
2	X	1	0	0	0	0
2	Z	1	0	0	0	0
All	All	62232	0	63600	925	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 7.

The worst 5 of 925 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:C:621:ARG:HH12	1:NA:624:MET:H	1.32	0.78
1:E:624:MET:H	1:LA:621:ARG:HH12	1.32	0.78
1:A:624:MET:H	1:PA:621:ARG:HH12	1.32	0.78
1:O:621:ARG:HH12	1:JA:624:MET:H	1.32	0.78
1:E:621:ARG:HH12	1:LA:624:MET:H	1.32	0.78

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	321/846 (38%)	315 (98%)	6 (2%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BA	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	C	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	DA	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	E	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	FA	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	G	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	HA	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	I	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	JA	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	K	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	LA	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	M	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	NA	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	O	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	PA	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	Q	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	RA	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	S	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	TA	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	V	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	VA	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	X	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
1	Z	321/846 (38%)	315 (98%)	6 (2%)	0	100	100
All	All	7704/20304 (38%)	7560 (98%)	144 (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	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	BA	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	C	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	DA	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	E	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	FA	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	G	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	HA	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	I	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	JA	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	K	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	LA	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	M	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	NA	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	O	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	PA	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	Q	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	RA	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	S	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	TA	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	V	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	VA	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	X	278/723 (38%)	277 (100%)	1 (0%)	89	92
1	Z	278/723 (38%)	277 (100%)	1 (0%)	89	92
All	All	6672/17352 (38%)	6648 (100%)	24 (0%)	88	92

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	DA	513	GLN
1	JA	513	GLN
1	HA	513	GLN
1	LA	513	GLN
1	M	513	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	FA	726	GLN
1	TA	726	GLN
1	VA	726	GLN
1	S	726	GLN
1	A	726	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 24 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

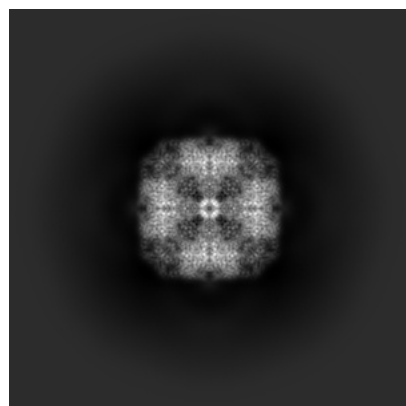
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-46690. These allow visual inspection of the internal detail of the map and identification of artifacts.

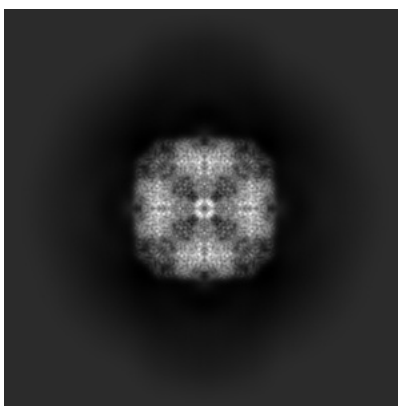
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

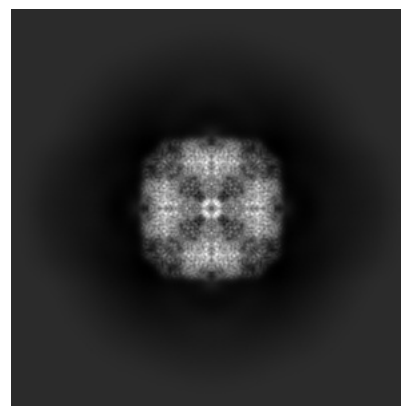
6.1.1 Primary map



X

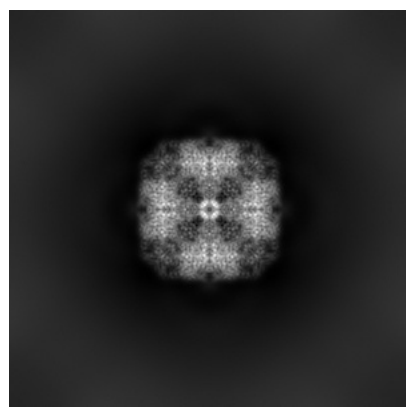


Y

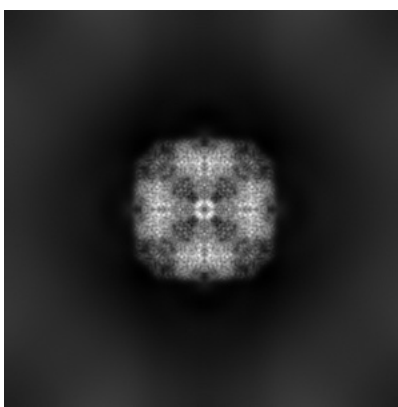


Z

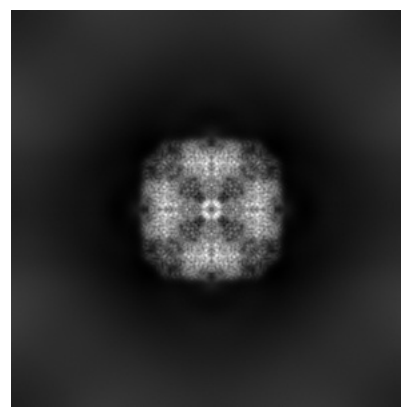
6.1.2 Raw map



X



Y

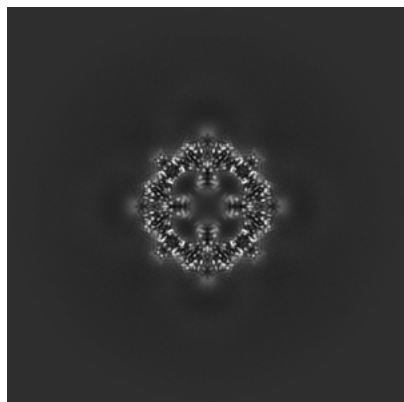


Z

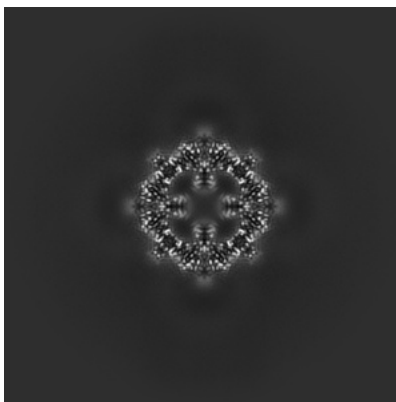
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

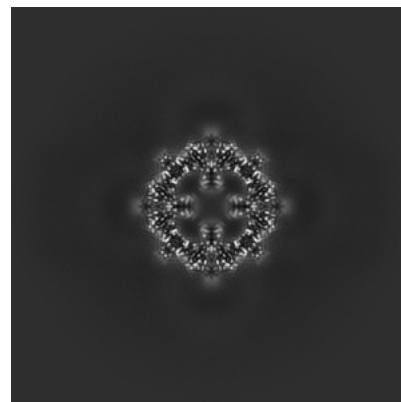
6.2.1 Primary map



X Index: 196

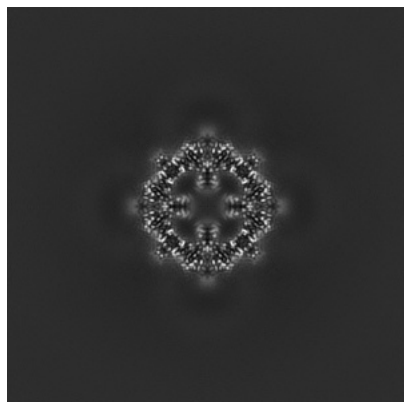


Y Index: 196

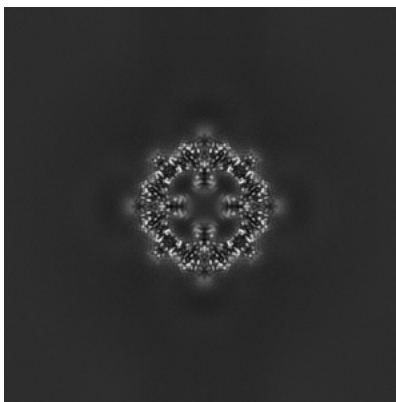


Z Index: 196

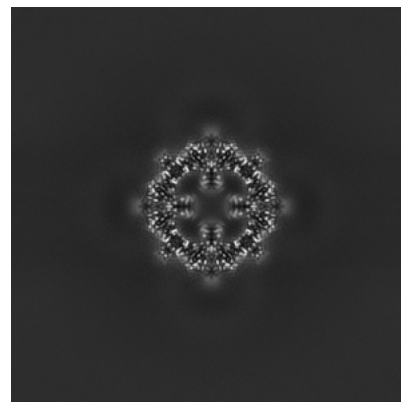
6.2.2 Raw map



X Index: 196



Y Index: 196

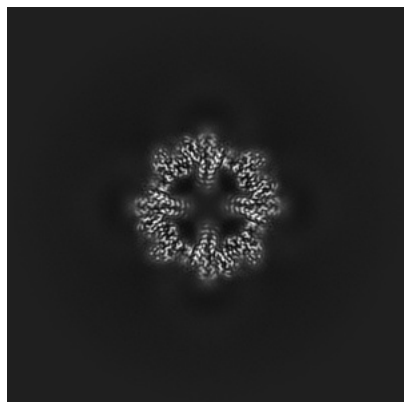


Z Index: 196

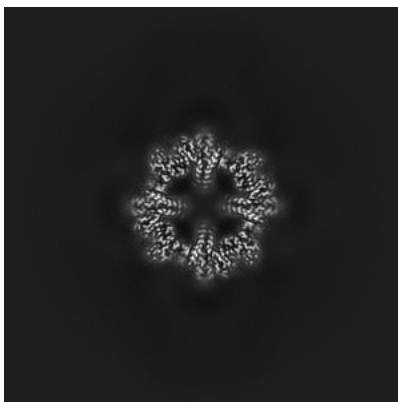
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

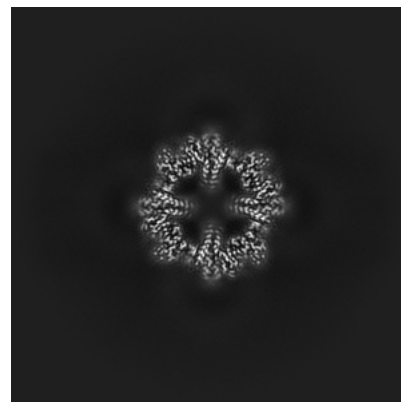
6.3.1 Primary map



X Index: 191

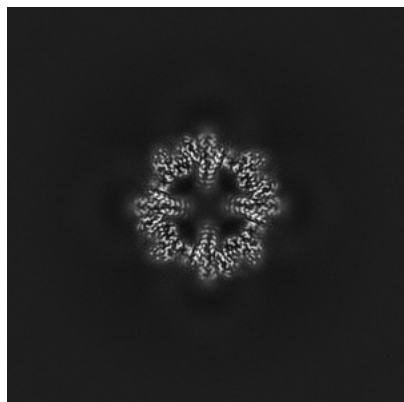


Y Index: 191

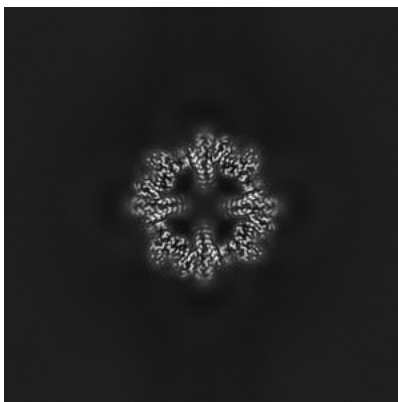


Z Index: 191

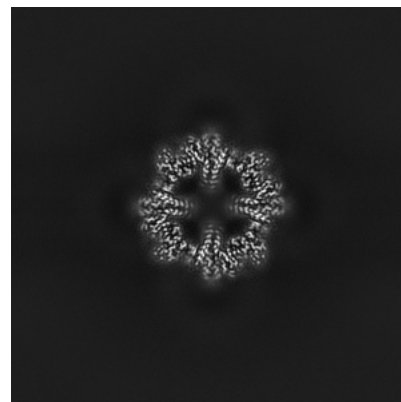
6.3.2 Raw map



X Index: 191



Y Index: 201

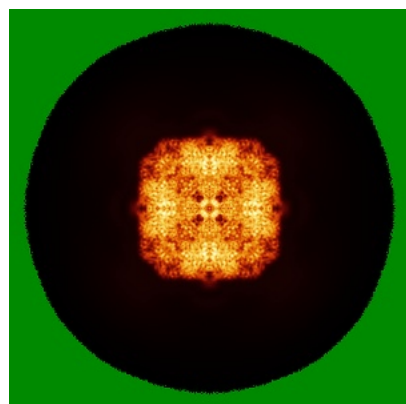


Z Index: 191

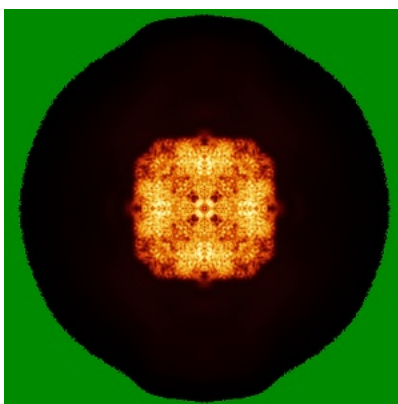
The images above show the largest variance slices of the map in three orthogonal directions.

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

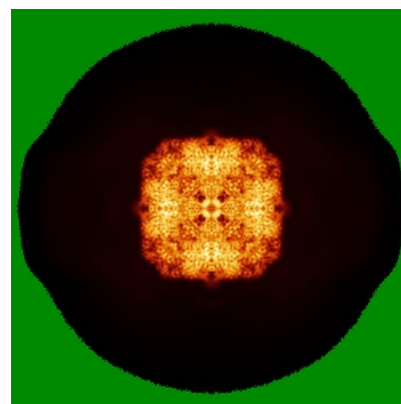
6.4.1 Primary map



X

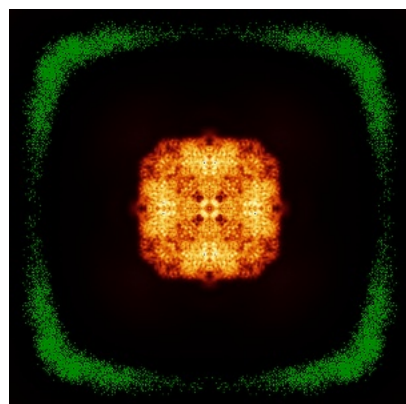


Y

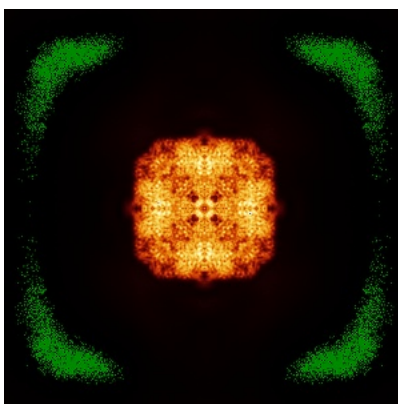


Z

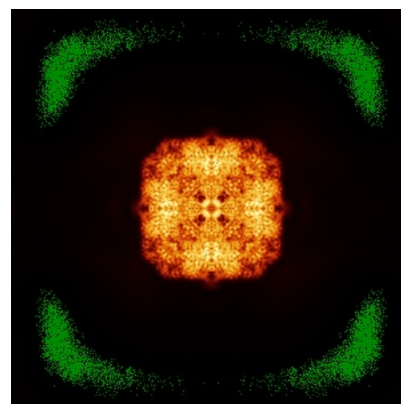
6.4.2 Raw map



X



Y

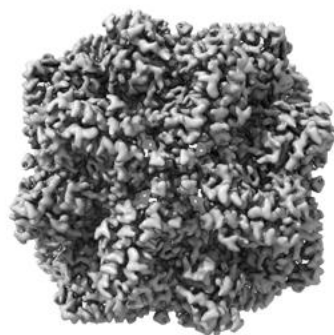


Z

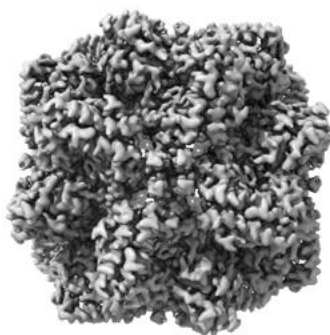
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

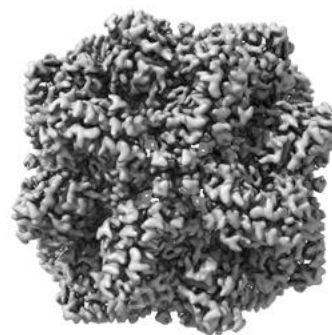
6.5.1 Primary map



X



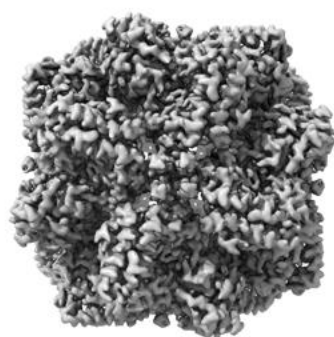
Y



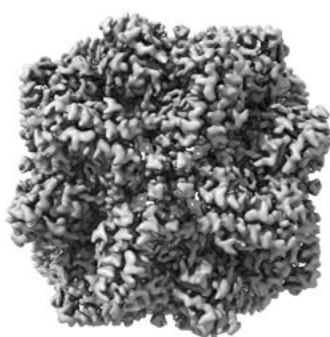
Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

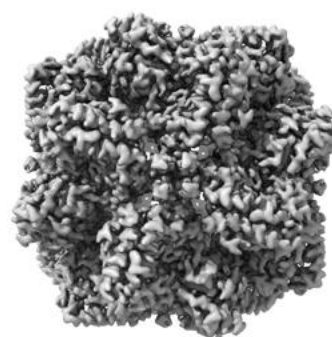
6.5.2 Raw map



X



Y



Z

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.

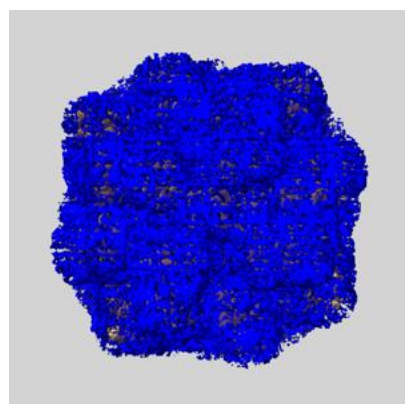
6.6 Mask visualisation [i](#)

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

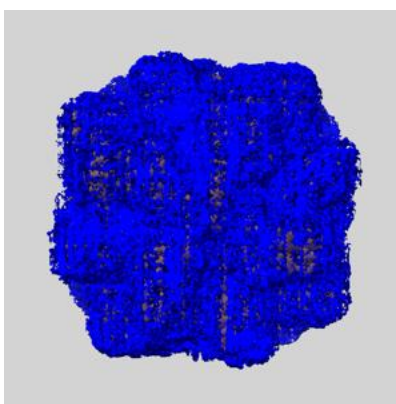
A mask typically either:

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

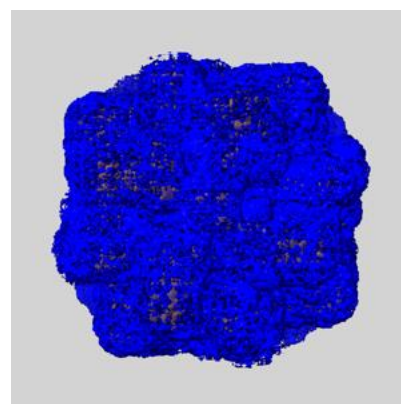
6.6.1 emd_46690_msk_1.map [i](#)



X



Y

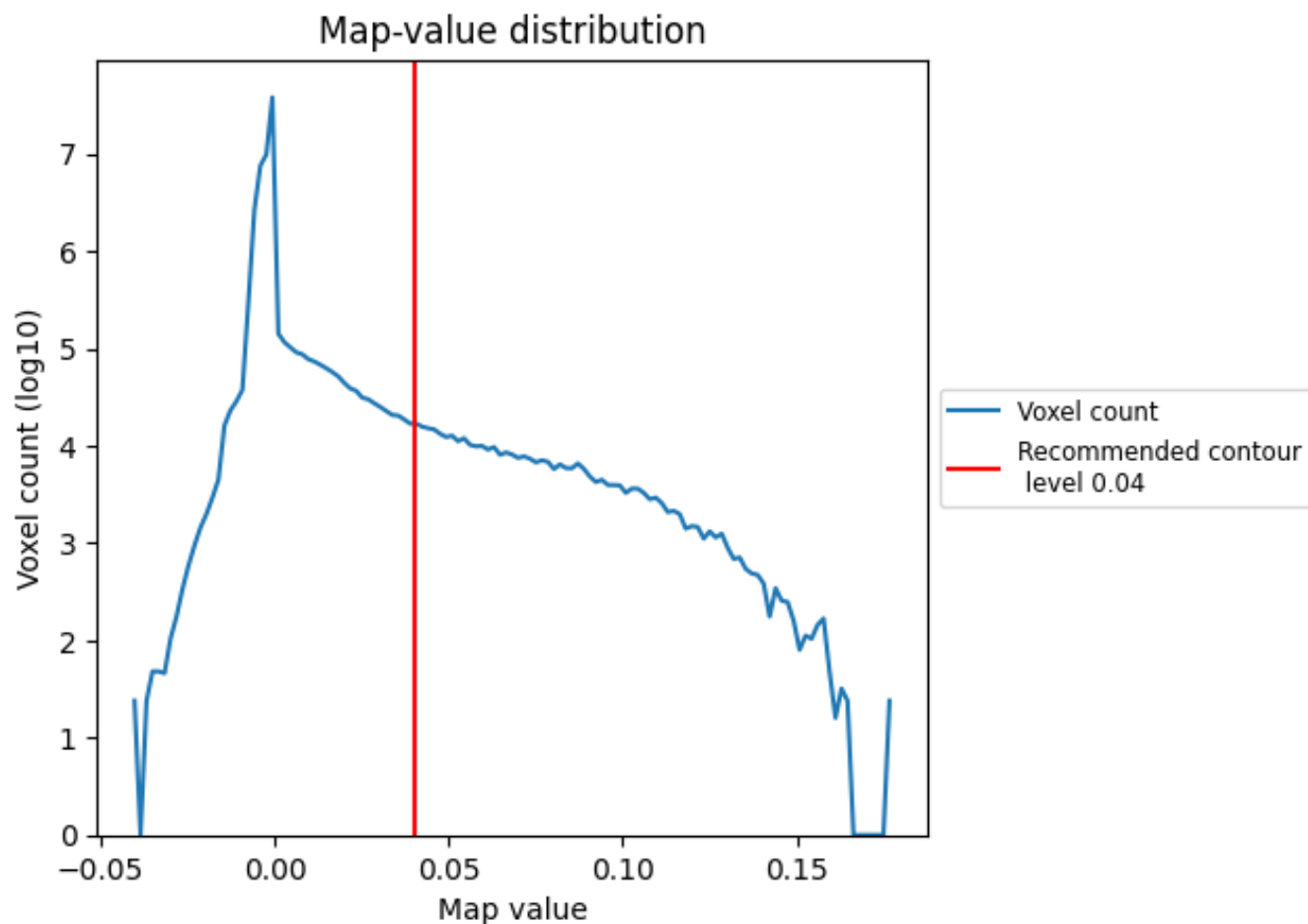


Z

7 Map analysis [i](#)

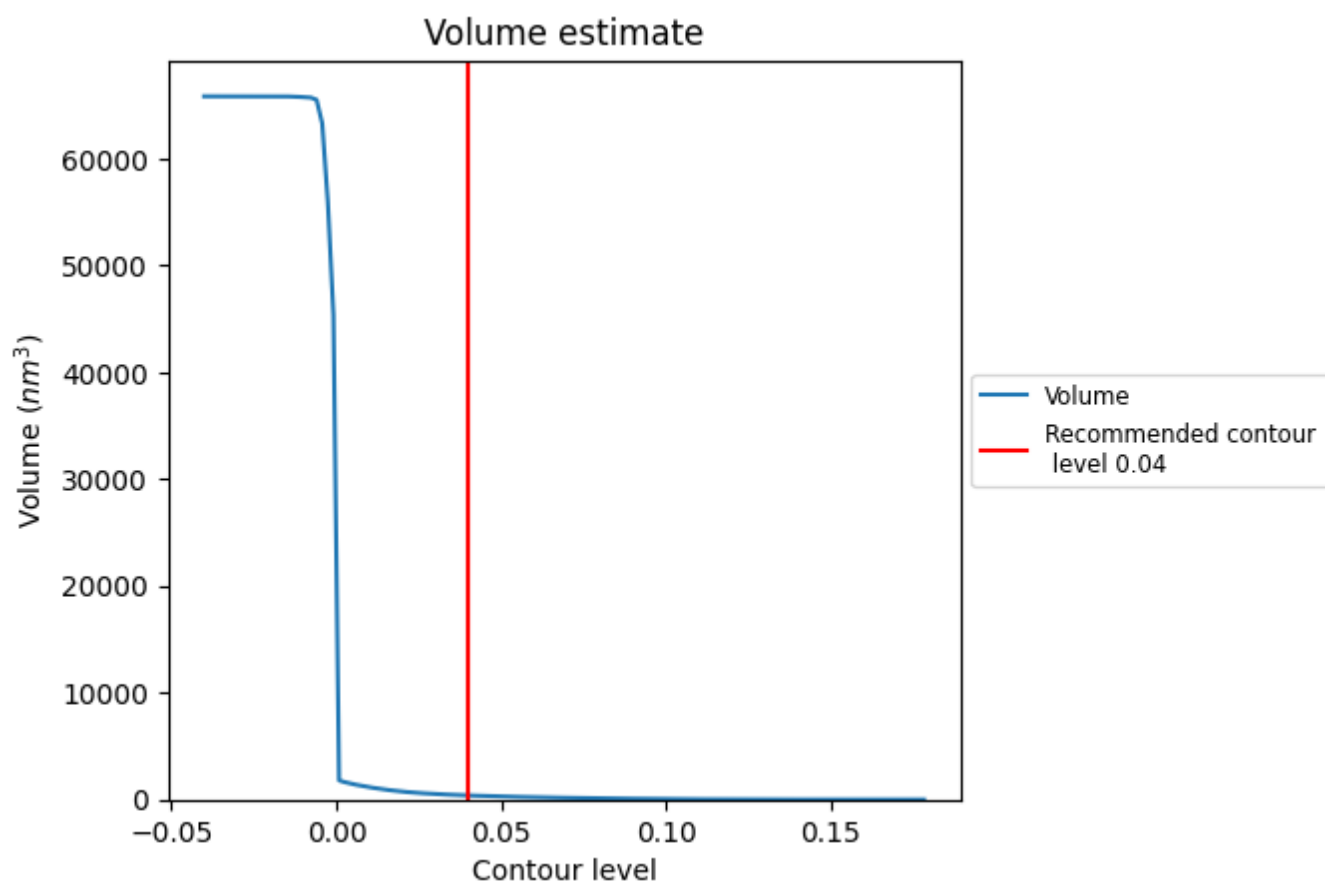
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

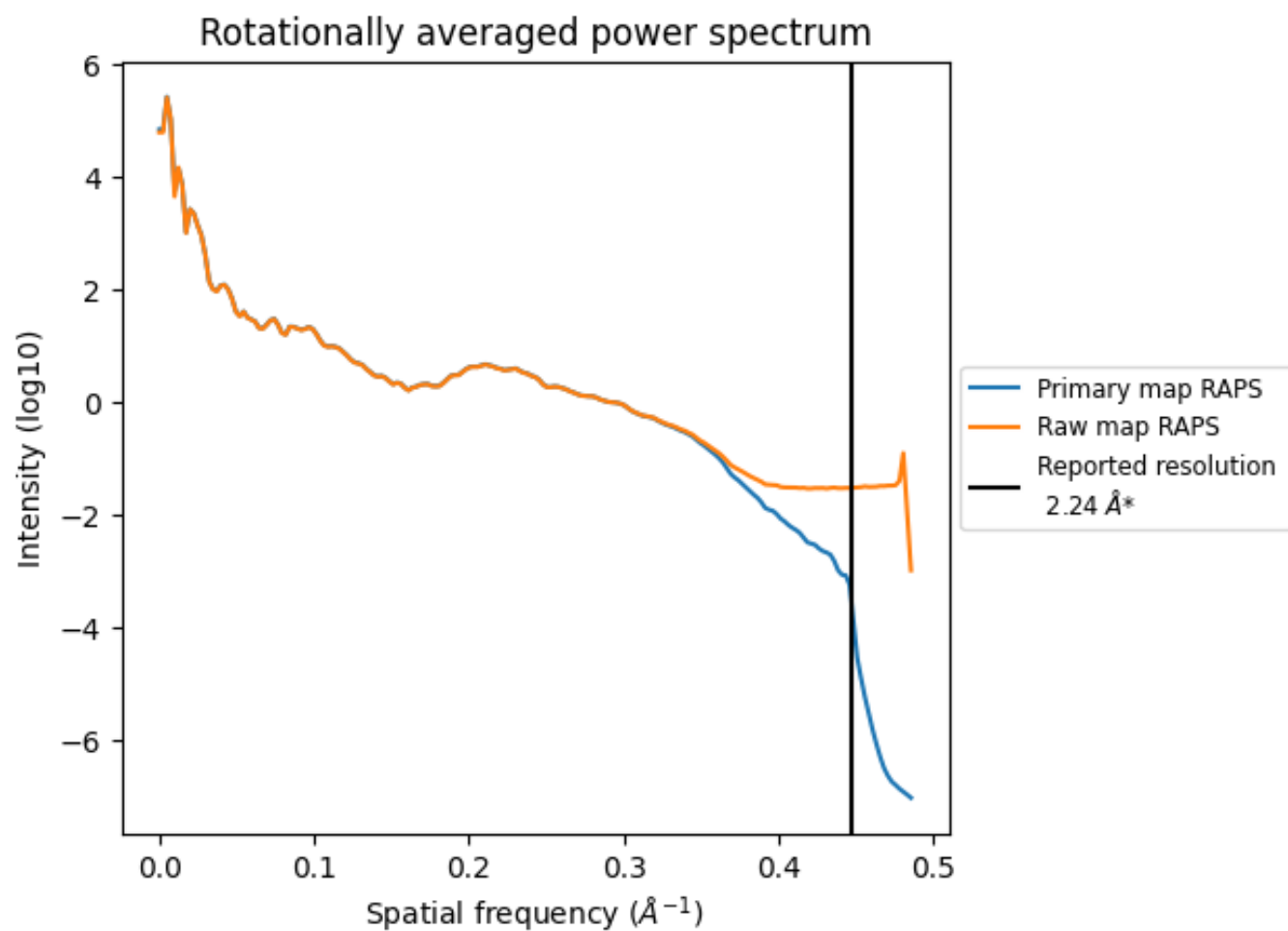
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 386 nm^3 ; this corresponds to an approximate mass of 349 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 ⓘ

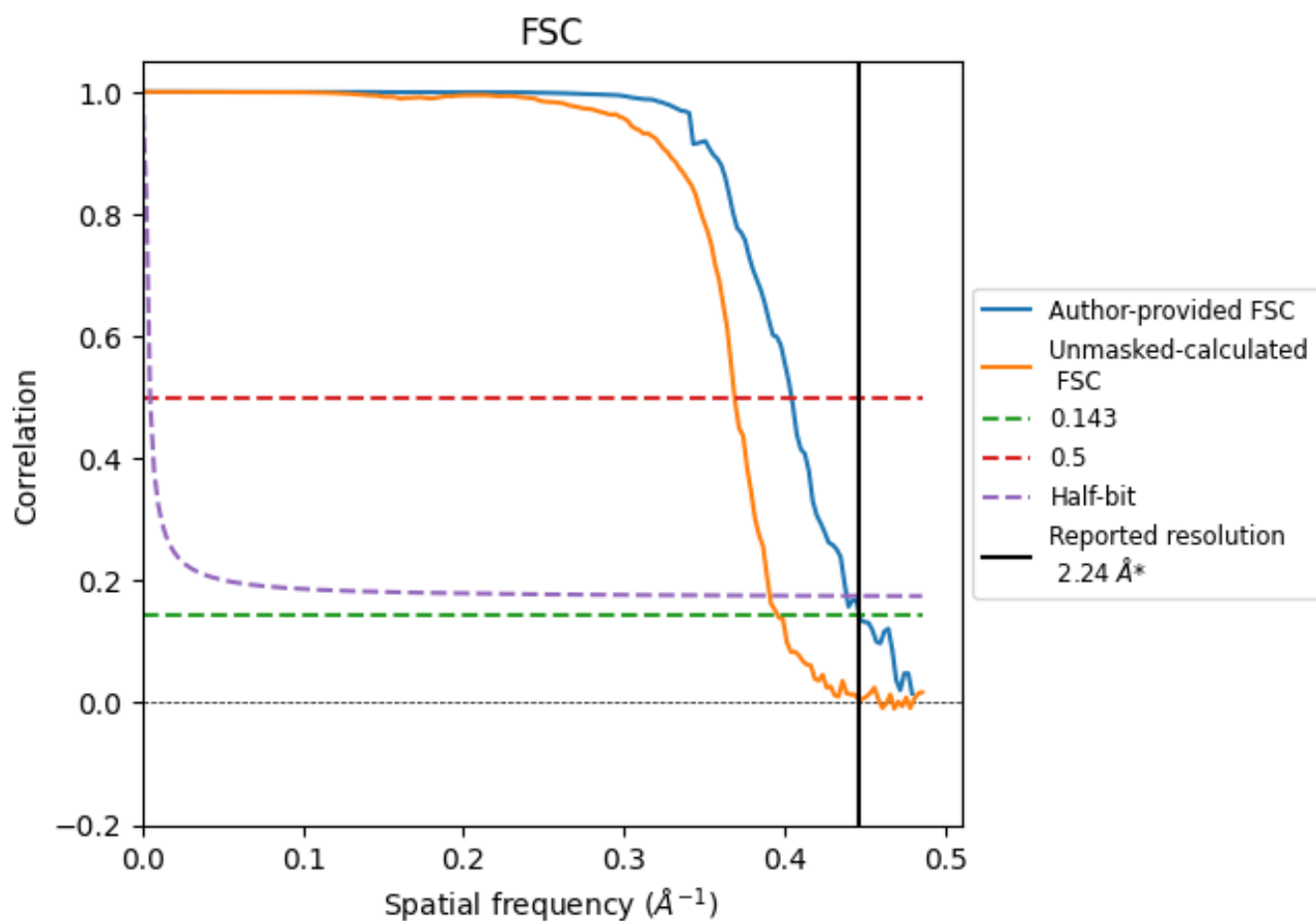


*Reported resolution corresponds to spatial frequency of 0.446 Å⁻¹

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 0.446 \AA^{-1}

8.2 Resolution estimates [i](#)

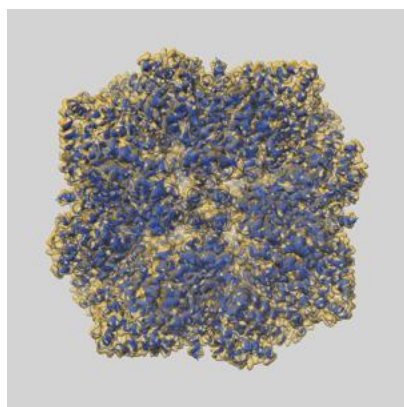
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.24	-	-
Author-provided FSC curve	2.24	2.47	2.28
Unmasked-calculated*	2.53	2.71	2.56

*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 2.53 differs from the reported value 2.24 by more than 10 %

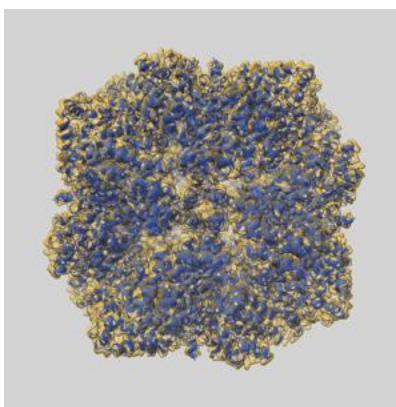
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-46690 and PDB model 9DAE. Per-residue inclusion information can be found in section 3 on page 15.

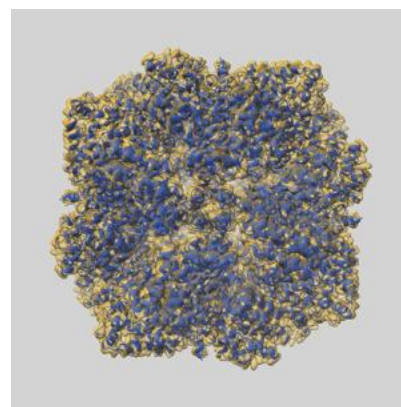
9.1 Map-model overlay [i](#)



X



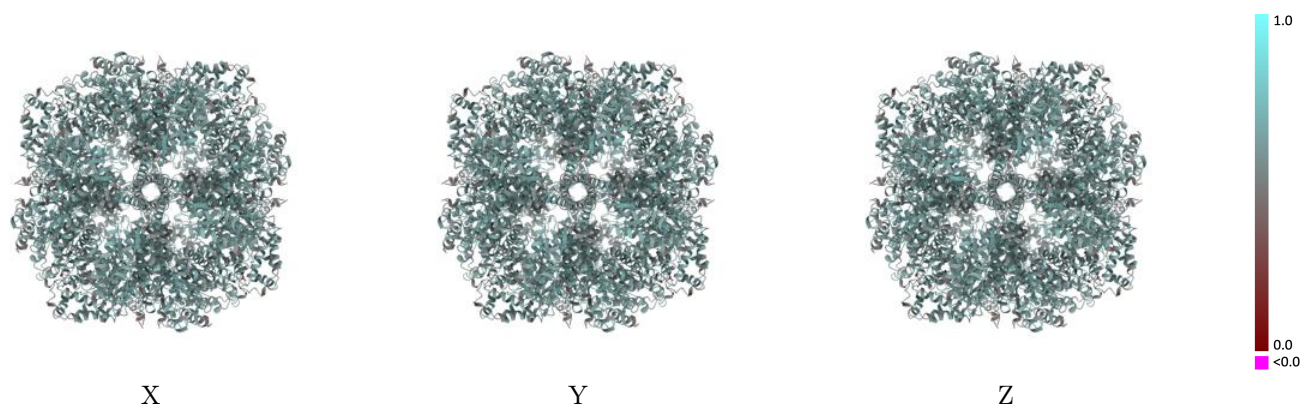
Y



Z

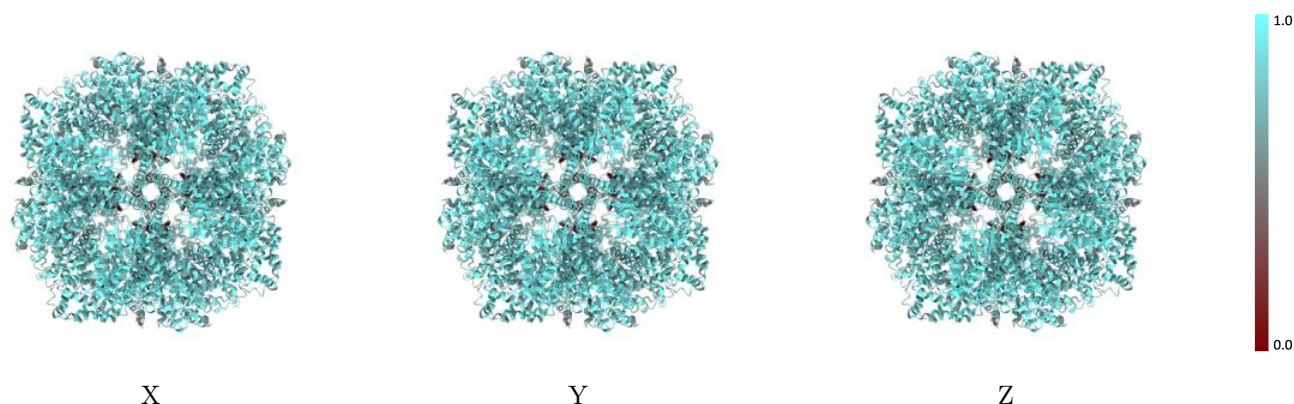
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



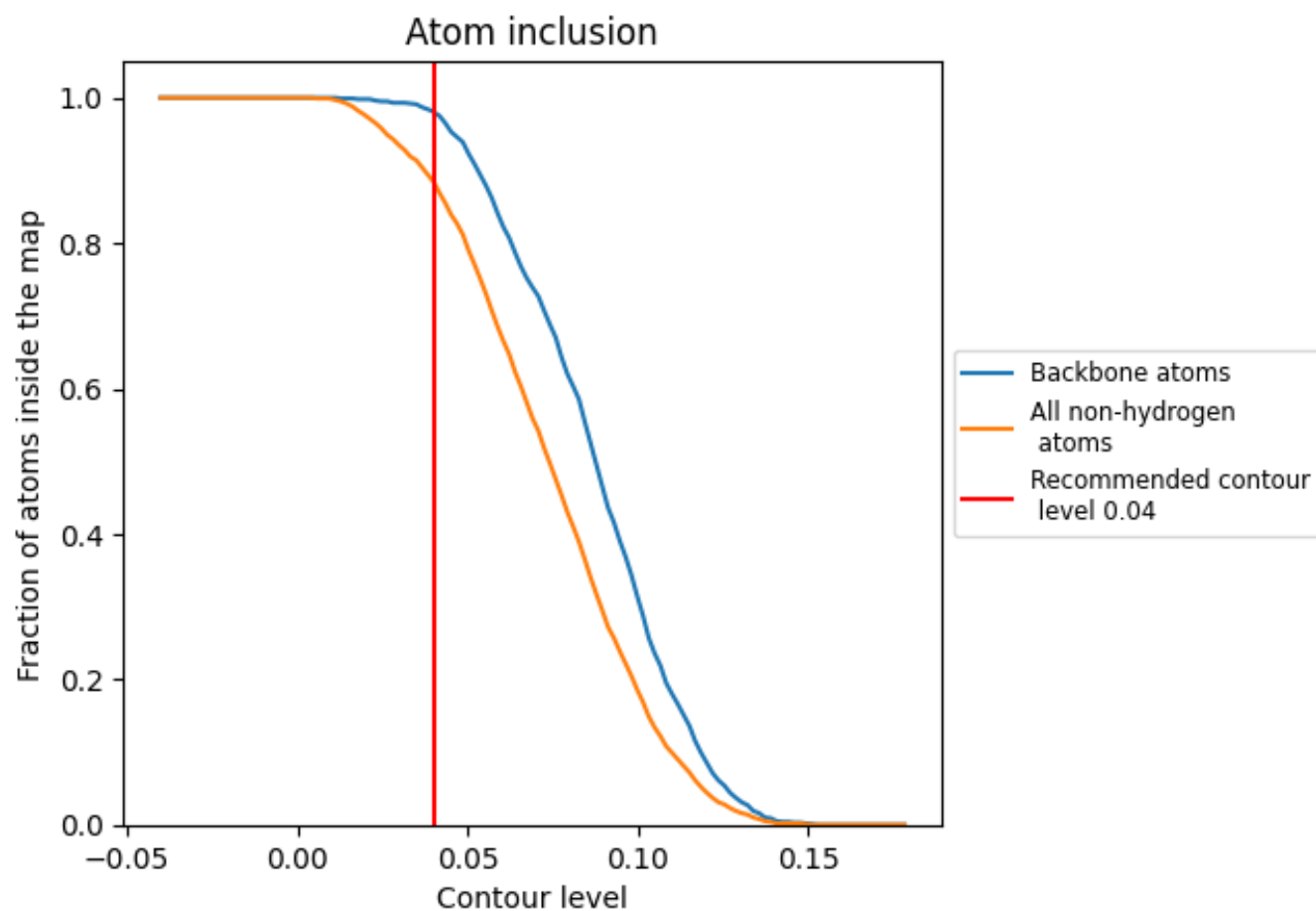
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).



















































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 88% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8840	 0.5950
A	 0.8820	 0.5960
BA	 0.8860	 0.5950
C	 0.8830	 0.5950
DA	 0.8860	 0.5940
E	 0.8820	 0.5950
FA	 0.8830	 0.5950
G	 0.8860	 0.5950
HA	 0.8820	 0.5940
I	 0.8860	 0.5930
JA	 0.8820	 0.5950
K	 0.8820	 0.5950
LA	 0.8830	 0.5960
M	 0.8830	 0.5940
NA	 0.8820	 0.5950
O	 0.8830	 0.5950
PA	 0.8830	 0.5940
Q	 0.8860	 0.5960
RA	 0.8820	 0.5960
S	 0.8820	 0.5950
TA	 0.8860	 0.5950
V	 0.8860	 0.5960
VA	 0.8830	 0.5950
X	 0.8830	 0.5950
Z	 0.8860	 0.5940

