



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 5, 2021 – 03:06 pm BST

PDB ID : 6YSV  
Title : E. coli anaerobic trifunctional enzyme subunit-alpha  
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Deposited on : 2020-04-23  
Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.18  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.18

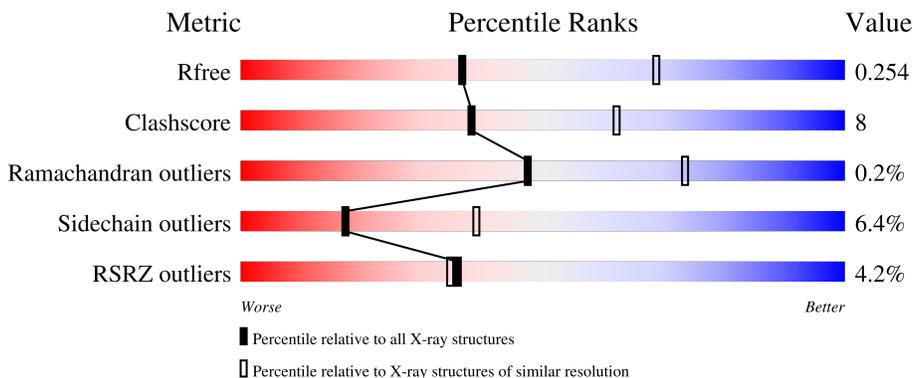
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	728	
1	B	728	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 10549 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Fatty acid oxidation complex subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	708	5303	3353	947	980	23	0	1	0
1	B	699	5167	3273	912	959	23	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

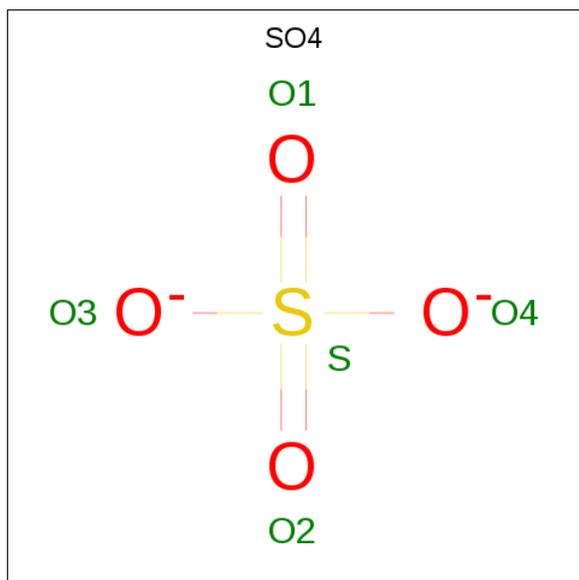
Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	initiating methionine	UNP P77399
A	-12	GLY	-	expression tag	UNP P77399
A	-11	SER	-	expression tag	UNP P77399
A	-10	SER	-	expression tag	UNP P77399
A	-9	HIS	-	expression tag	UNP P77399
A	-8	HIS	-	expression tag	UNP P77399
A	-7	HIS	-	expression tag	UNP P77399
A	-6	HIS	-	expression tag	UNP P77399
A	-5	HIS	-	expression tag	UNP P77399
A	-4	HIS	-	expression tag	UNP P77399
A	-3	SER	-	expression tag	UNP P77399
A	-2	GLN	-	expression tag	UNP P77399
A	-1	ASP	-	expression tag	UNP P77399
A	0	PRO	-	expression tag	UNP P77399
B	-13	MET	-	initiating methionine	UNP P77399
B	-12	GLY	-	expression tag	UNP P77399
B	-11	SER	-	expression tag	UNP P77399
B	-10	SER	-	expression tag	UNP P77399
B	-9	HIS	-	expression tag	UNP P77399
B	-8	HIS	-	expression tag	UNP P77399
B	-7	HIS	-	expression tag	UNP P77399
B	-6	HIS	-	expression tag	UNP P77399
B	-5	HIS	-	expression tag	UNP P77399
B	-4	HIS	-	expression tag	UNP P77399
B	-3	SER	-	expression tag	UNP P77399

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	GLN	-	expression tag	UNP P77399
B	-1	ASP	-	expression tag	UNP P77399
B	0	PRO	-	expression tag	UNP P77399

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

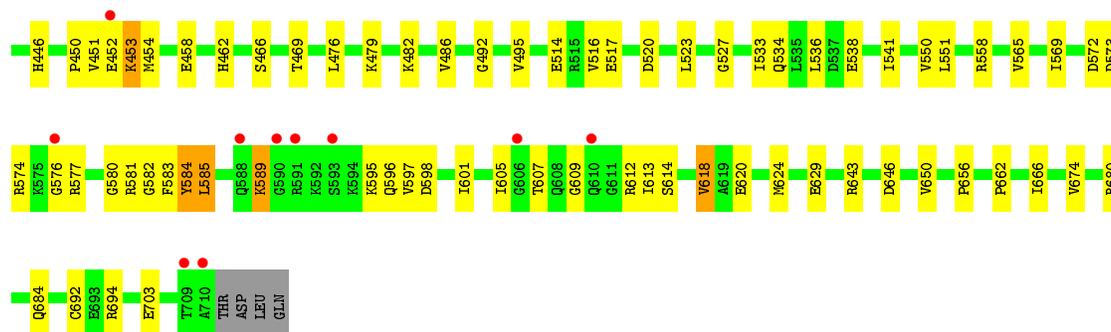
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	34	Total	O	0	0
			34	34		

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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	B	10	Total	O	0	0
			10	10		





## 4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	128.58Å 90.75Å 172.91Å 90.00° 96.11° 90.00°	Depositor
Resolution (Å)	54.51 – 2.70 54.51 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.6 (54.51-2.70) 97.6 (54.51-2.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.20 (at 2.69Å)	Xtrriage
Refinement program	PHENIX 1.16 3549	Depositor
R, $R_{free}$	0.224 , 0.255 0.224 , 0.254	Depositor DCC
$R_{free}$ test set	2749 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	85.7	Xtrriage
Anisotropy	0.222	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 64.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	10549	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	107.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.24	0/5397	0.41	0/7314
1	B	0.24	0/5252	0.42	0/7121
All	All	0.24	0/10649	0.42	0/14435

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 [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5303	0	5389	65	0
1	B	5167	0	5207	97	0
2	A	25	0	0	1	0
2	B	10	0	0	0	0
3	A	34	0	0	2	0
3	B	10	0	0	0	0
All	All	10549	0	10596	161	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 8.

The worst 5 of 161 close contacts within the same asymmetric unit are listed below, sorted by

their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:GLY:H	1:A:134:THR:HG22	1.43	0.83
1:B:584:TYR:HB3	1:B:597:VAL:HA	1.61	0.82
1:B:577:ARG:HA	1:B:585:LEU:HD11	1.62	0.81
1:A:558:ARG:NH1	1:A:629:GLU:OE2	2.15	0.80
1:B:175:ARG:HE	1:B:362:ARG:HH22	1.29	0.78

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 X-ray entries followed by that with respect to entries of similar resolution.

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	707/728 (97%)	677 (96%)	29 (4%)	1 (0%)	51	78
1	B	695/728 (96%)	660 (95%)	33 (5%)	2 (0%)	41	66
All	All	1402/1456 (96%)	1337 (95%)	62 (4%)	3 (0%)	47	73

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	222	PRO
1	A	363	ARG
1	B	573	ASP

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

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	548/583 (94%)	525 (96%)	23 (4%)	30	58
1	B	524/583 (90%)	478 (91%)	46 (9%)	10	23
All	All	1072/1166 (92%)	1003 (94%)	69 (6%)	17	39

5 of 69 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	536	LEU
1	B	585	LEU
1	B	618	VAL
1	B	19	ILE
1	B	16	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	153	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

7 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	SO4	B	802	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	B	801	-	4,4,4	0.14	0	6,6,6	0.04	0
2	SO4	A	805	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	A	804	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	A	802	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	A	801	-	4,4,4	0.14	0	6,6,6	0.05	0
2	SO4	A	803	-	4,4,4	0.14	0	6,6,6	0.05	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	804	SO4	1	0

## 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 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å <sup>2</sup> )	Q < 0.9
1	A	708/728 (97%)	0.23	20 (2%) 53 54	60, 90, 158, 218	0
1	B	699/728 (96%)	0.38	39 (5%) 24 23	64, 110, 177, 220	0
All	All	1407/1456 (96%)	0.31	59 (4%) 36 35	60, 100, 171, 220	0

The worst 5 of 59 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3	MET	10.4
1	B	709	THR	7.8
1	B	710	ALA	7.3
1	B	105	ILE	6.2
1	B	104	VAL	5.3

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	B	801	5/5	0.77	0.25	164,166,166,167	0
2	SO4	B	802	5/5	0.77	0.23	164,164,165,165	0
2	SO4	A	803	5/5	0.78	0.27	149,150,151,152	0
2	SO4	A	802	5/5	0.82	0.25	178,179,179,180	0
2	SO4	A	801	5/5	0.88	0.48	147,147,149,151	0
2	SO4	A	805	5/5	0.95	0.25	216,218,219,219	5
2	SO4	A	804	5/5	0.98	0.25	124,128,128,128	5

## 6.5 Other polymers [i](#)

There are no such residues in this entry.