



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 04:39 pm GMT

PDB ID : 1E0Y  
Title : STRUCTURE OF THE D170S/T457E DOUBLE MUTANT OF VANILLYL-ALCOHOL OXIDASE  
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Deposited on : 2000-04-11  
Resolution : 2.75 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

<http://wwpdb.org/validation/2016/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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

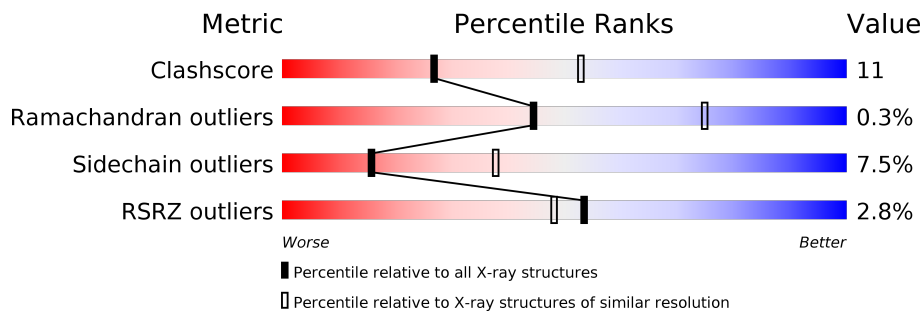
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.75 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))
Clashscore	112137	4174 (2.80-2.72)
Ramachandran outliers	110173	4103 (2.80-2.72)
Sidechain outliers	110143	4106 (2.80-2.72)
RSRZ outliers	101464	3697 (2.80-2.72)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	560	
1	B	560	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	FCR	B	601	-	-	-	X

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8753 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.

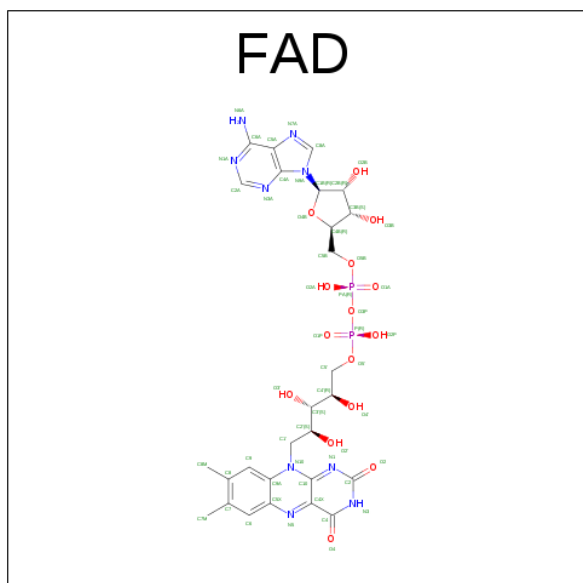
- Molecule 1 is a protein called VANILLYL-ALCOHOL OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	550	Total	C	N	O	S	3	0	0
			4287	2753	730	781	23			
1	B	550	Total	C	N	O	S	0	0	0
			4269	2740	726	780	23			

There are 6 discrepancies between the modelled and reference sequences:

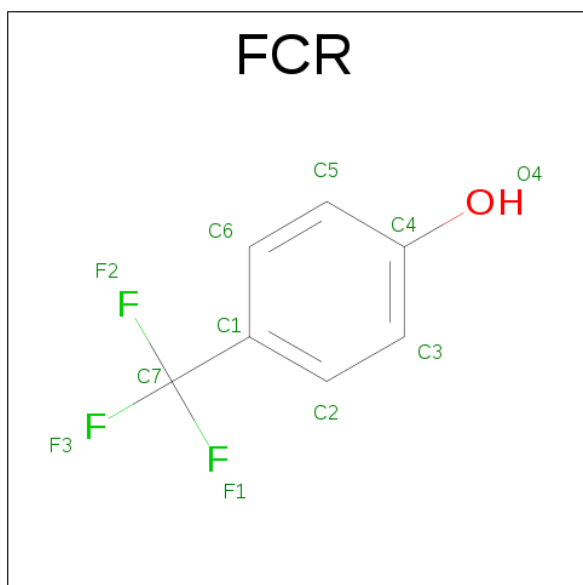
Chain	Residue	Modelled	Actual	Comment	Reference
A	274	GLY	ARG	CONFLICT	UNP P56216
A	457	GLU	THR	ENGINEERED MUTATION	UNP P56216
A	170	SER	ASP	ENGINEERED MUTATION	UNP P56216
B	274	GLY	ARG	CONFLICT	UNP P56216
B	457	GLU	THR	ENGINEERED MUTATION	UNP P56216
B	170	SER	ASP	ENGINEERED MUTATION	UNP P56216

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is ALPHA,ALPHA,ALPHA-TRIFLUORO-P-CRESOL (three-letter code: FCR) (formula: C<sub>7</sub>H<sub>5</sub>F<sub>3</sub>O).

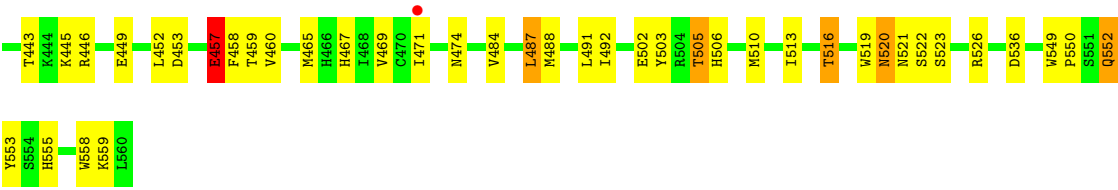


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	F	O	0	0
			11	7	3	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	42	Total	O	0	0
			42	42		
4	B	38	Total	O	0	0
			38	38		





## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	131.28Å 131.28Å 134.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.75 24.04 – 2.75	Depositor EDS
% Data completeness (in resolution range)	97.3 (20.00-2.75) 97.1 (24.04-2.75)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.02 (at 2.76Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.225 , 0.287 0.217 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	52.6	Xtriage
Anisotropy	0.383	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 46.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.006 for l,-k,h 0.017 for -l,-k,-h 0.025 for -h,-l,-k 0.006 for -h,l,k 0.038 for -h,k,-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	8753	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% 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

### 5.1 Standard geometry

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

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	0.52	1/4406 (0.0%)	1.52	58/5997 (1.0%)
1	B	0.49	0/4387	1.52	50/5972 (0.8%)
All	All	0.51	1/8793 (0.0%)	1.52	108/11969 (0.9%)

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	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	221	LYS	CG-CD	9.88	1.86	1.52

The worst 5 of 108 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	211	ARG	CD-NE-CZ	20.72	152.61	123.60
1	A	211	ARG	CD-NE-CZ	18.02	148.83	123.60
1	B	398	ARG	NE-CZ-NH1	15.28	127.94	120.30
1	B	211	ARG	CA-CB-CG	13.88	143.93	113.40
1	A	211	ARG	CA-CB-CG	13.79	143.75	113.40

There are no chirality outliers.

All (1) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	A	37	VAL	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	4287	0	4166	103	2
1	B	4269	0	4136	104	1
2	A	53	0	29	3	0
2	B	53	0	29	1	0
3	B	11	0	5	0	0
4	A	42	0	0	1	0
4	B	38	0	0	2	0
All	All	8753	0	8365	195	2

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 11.

The worst 5 of 195 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:B:297:ARG:HB3	1:B:298:PRO:HD3	1.56	0.86
1:A:349:GLY:H	1:A:352:ASN:HD21	1.27	0.83
1:A:550:PRO:HB2	1:A:552:GLN:NE2	1.94	0.82
1:B:397:VAL:HG13	1:B:407:THR:HG21	1.66	0.78
1:A:57:THR:HG22	1:A:74:ILE:HD11	1.64	0.77

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:LYS:NZ	1:A:489:ARG:CD[4_565]	1.98	0.22
1:A:37:VAL:O	1:B:391:GLU:OE2[6_655]	2.00	0.20

## 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 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	546/560 (98%)	512 (94%)	33 (6%)	1 (0%)	51	81
1	B	546/560 (98%)	512 (94%)	32 (6%)	2 (0%)	38	69
All	All	1092/1120 (98%)	1024 (94%)	65 (6%)	3 (0%)	44	75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	418	PRO
1	B	418	PRO
1	B	371	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 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	455/481 (95%)	420 (92%)	35 (8%)	15	36
1	B	452/481 (94%)	419 (93%)	33 (7%)	16	39
All	All	907/962 (94%)	839 (92%)	68 (8%)	16	38

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	503	TYR
1	B	95	PHE
1	B	503	TYR

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Mol	Chain	Res	Type
1	A	505	THR
1	A	554	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	79	ASN
1	B	128	ASN
1	B	467	HIS
1	A	552	GLN
1	B	485	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 carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

3 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	FAD	A	600	1	51,58,58	1.49	11 (21%)	54,89,89	1.73	10 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	FAD	B	600	1	51,58,58	1.43	9 (17%)	54,89,89	1.68	10 (18%)
3	FCR	B	601	-	11,11,11	0.93	0	16,16,16	1.48	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FAD	A	600	1	-	0/28/50/50	0/6/6/6
2	FAD	B	600	1	-	0/28/50/50	0/6/6/6
3	FCR	B	601	-	-	0/6/6/6	0/1/1/1

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	600	FAD	PA-O2A	-3.93	1.35	1.55
2	B	600	FAD	PA-O2A	-3.81	1.36	1.55
2	A	600	FAD	P-O2P	-2.68	1.41	1.55
2	B	600	FAD	C2-N1	-2.67	1.32	1.38
2	B	600	FAD	P-O2P	-2.65	1.41	1.55

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	600	FAD	C4X-C4-N3	-5.14	116.16	123.48
2	A	600	FAD	C4X-C4-N3	-4.29	117.37	123.48
2	A	600	FAD	N3A-C2A-N1A	-3.68	125.65	128.86
2	A	600	FAD	O5B-PA-O1A	-3.55	94.93	109.25
2	B	600	FAD	O5B-PA-O1A	-3.44	95.38	109.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600	FAD	3	0
2	B	600	FAD	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	550/560 (98%)	-0.01	12 (2%) 62 57	32, 49, 73, 88	1 (0%)
1	B	550/560 (98%)	0.05	19 (3%) 44 38	33, 49, 73, 86	0
All	All	1100/1120 (98%)	0.02	31 (2%) 53 48	32, 49, 73, 88	1 (0%)

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	330	ARG	3.5
1	B	62	HIS	3.4
1	B	7	PHE	3.3
1	A	325	ARG	3.3
1	B	57	THR	3.2

### 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	FCR	B	601	11/11	0.72	0.34	4.44	72,74,78,78	0
2	FAD	A	600	53/53	0.94	0.15	-0.57	46,49,53,54	0
2	FAD	B	600	53/53	0.95	0.14	-0.89	46,49,53,54	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.