



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 13, 2024 – 01:06 AM EDT

PDB ID : 3P8L  
Title : Crystal structure of polyprenyl synthase from *Enterococcus faecalis* V583  
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Deposited on : 2010-10-14  
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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.

The types of validation reports are described at

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

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
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)	:	2.36.2

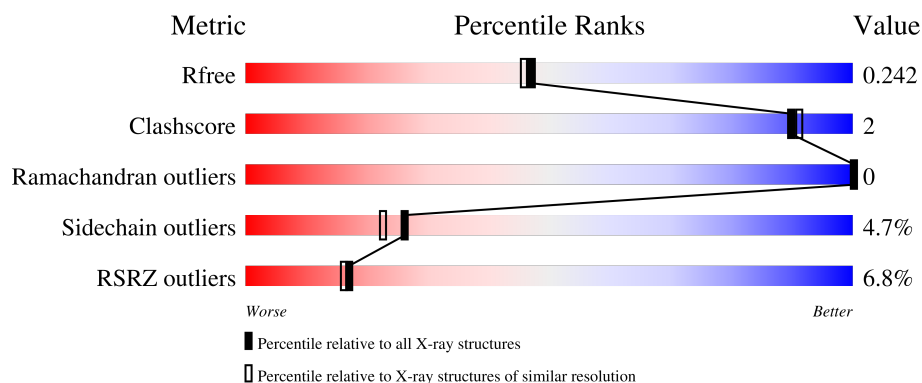
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	302	
1	B	302	

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 4498 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 Geranyltranstransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	283	Total	C	N	O	S	0	9	0
			2219	1408	378	424	9			
1	B	275	Total	C	N	O	S	0	3	0
			2111	1341	352	409	9			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	expression tag	UNP Q836W4
A	-7	ALA	-	expression tag	UNP Q836W4
A	-6	HIS	-	expression tag	UNP Q836W4
A	-5	HIS	-	expression tag	UNP Q836W4
A	-4	HIS	-	expression tag	UNP Q836W4
A	-3	HIS	-	expression tag	UNP Q836W4
A	-2	HIS	-	expression tag	UNP Q836W4
A	-1	HIS	-	expression tag	UNP Q836W4
A	0	SER	-	expression tag	UNP Q836W4
A	1	LEU	-	expression tag	UNP Q836W4
B	-8	MET	-	expression tag	UNP Q836W4
B	-7	ALA	-	expression tag	UNP Q836W4
B	-6	HIS	-	expression tag	UNP Q836W4
B	-5	HIS	-	expression tag	UNP Q836W4
B	-4	HIS	-	expression tag	UNP Q836W4
B	-3	HIS	-	expression tag	UNP Q836W4
B	-2	HIS	-	expression tag	UNP Q836W4
B	-1	HIS	-	expression tag	UNP Q836W4
B	0	SER	-	expression tag	UNP Q836W4
B	1	LEU	-	expression tag	UNP Q836W4

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	111	Total 111	O 111	0	0
2	B	57	Total 57	O 57	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	53.86Å 100.53Å 122.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.00 36.75 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.00-2.00) 99.1 (36.75-1.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.201 , 0.246 0.201 , 0.242	Depositor DCC
$R_{free}$ test set	1644 reflections (3.11%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.3	Xtriage
Anisotropy	0.477	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 45.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4498	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.99% 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

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	0.53	0/2280	0.61	0/3079
1	B	0.47	0/2149	0.58	0/2905
All	All	0.50	0/4429	0.60	0/5984

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	2219	0	2255	10	0
1	B	2111	0	2146	9	0
2	A	111	0	0	1	0
2	B	57	0	0	1	0
All	All	4498	0	4401	16	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 2.

All (16) 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:289[A]:GLN:HA	1:A:289[A]:GLN:OE1	1.90	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:HIS:HD2	2:A:307:HOH:O	1.85	0.59
1:A:285[A]:ASN:OD1	1:A:289[A]:GLN:NE2	2.38	0.56
1:B:173:HIS:CD2	1:B:214:GLN:HG2	2.48	0.48
1:A:137[A]:MET:HE3	1:B:137[A]:MET:SD	2.54	0.47
1:B:219:LEU:HD13	1:B:292:LEU:HD11	1.97	0.47
1:A:289[A]:GLN:OE1	1:A:289[A]:GLN:CA	2.59	0.45
1:A:182[B]:GLU:HG3	1:A:203:THR:HG23	1.98	0.45
1:B:173:HIS:CG	1:B:214:GLN:HG2	2.53	0.43
1:B:185:LEU:HG	1:B:206:ALA:HB2	1.99	0.43
1:A:244:TYR:CB	1:A:245:PRO:CD	2.98	0.42
1:A:137[A]:MET:HB3	1:B:137[A]:MET:HE1	2.02	0.41
1:B:121:GLN:NE2	2:B:333:HOH:O	2.52	0.41
1:A:116:LEU:HD23	1:B:116:LEU:HD23	2.02	0.41
1:A:244:TYR:CB	1:A:245:PRO:HD3	2.51	0.41
1:B:245:PRO:HB3	1:B:250:ILE:HD13	2.03	0.41

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	288/302 (95%)	282 (98%)	6 (2%)	0	100	100
1	B	274/302 (91%)	270 (98%)	4 (2%)	0	100	100
All	All	562/604 (93%)	552 (98%)	10 (2%)	0	100	100

There are no Ramachandran outliers to report.

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

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	238/244 (98%)	226 (95%)	12 (5%)	24	20
1	B	225/244 (92%)	216 (96%)	9 (4%)	31	29
All	All	463/488 (95%)	442 (96%)	21 (4%)	26	24

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	77	TYR
1	A	94	ARG
1	A	127	GLN
1	A	161	LYS
1	A	193	ASN
1	A	197	GLU
1	A	214	GLN
1	A	216	ARG
1	A	242	SER
1	A	281	GLU
1	A	287	LEU
1	B	77	TYR
1	B	161	LYS
1	B	163	SER
1	B	216	ARG
1	B	217	ASP
1	B	221	ASP
1	B	223	THR
1	B	281	GLU
1	B	291	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	147	GLN
1	B	121	GLN
1	B	127	GLN
1	B	277	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

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

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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	283/302 (93%)	0.28	24 (8%) 10 10	29, 47, 91, 128	0
1	B	275/302 (91%)	0.24	14 (5%) 28 27	31, 53, 88, 104	0
All	All	558/604 (92%)	0.26	38 (6%) 17 16	29, 51, 91, 128	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	293	ARG	8.1
1	A	223	THR	6.5
1	A	222	ALA	6.1
1	A	224	SER	5.2
1	B	163	SER	4.0
1	A	161	LYS	3.7
1	B	162	VAL	3.6
1	A	-4	HIS	3.6
1	A	221	ASP	3.5
1	A	-5	HIS	3.1
1	A	220	LEU	3.1
1	B	276	PRO	3.1
1	A	292	LEU	3.1
1	A	164	LEU	2.8
1	A	219	LEU	2.8
1	A	117	THR	2.7
1	B	117	THR	2.7
1	B	246	ALA	2.6
1	A	74	ILE	2.5
1	B	116	LEU	2.5
1	A	116	LEU	2.4
1	A	180	LEU	2.4
1	A	248	LEU	2.4
1	A	247	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	144	ALA	2.3
1	A	71	LEU	2.3
1	B	161	LYS	2.3
1	B	197	GLU	2.2
1	B	3	ASN	2.2
1	B	180	LEU	2.2
1	B	247	LEU	2.2
1	A	162	VAL	2.1
1	A	250	ILE	2.1
1	A	-6	HIS	2.1
1	A	149	MET	2.1
1	B	38	HIS	2.1
1	B	196	GLU	2.0
1	B	275	VAL	2.0

## 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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.