

wwPDB X-ray Structure Validation Summary Report (i)

Jun 14, 2020 – 06:40 pm BST

PDB ID : 2YAH

> Title : X-ray induced reduction of laccase from Thermus thermophilus HB27 (25. 0-

> > 37.5 percent dose)

: Serrano-Posada, H.; Rudino-Pinera, E. Authors

2011-02-22 Deposited on

1.80 Å(reported) Resolution

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 A user guide is available at

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity 4.02b-467

> 1.8.5 (274361), CSD as541be (2020) Mogul

Xtriage (Phenix) 1.13 EDS 2.11

Percentile statistics 20191225.v01 (using entries in the PDB archive December 25th 2019)

> Refmac 5.8.0158

7.0.044 (Gargrove) CCP4 Engh & Huber (2001)

Ideal geometry (proteins) Ideal geometry (DNA, RNA) Parkinson et al. (1996)

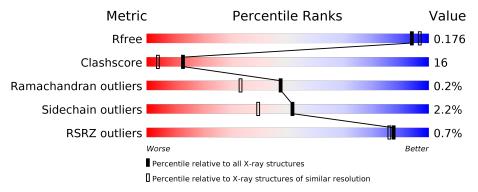
Validation Pipeline (wwPDB-VP) 2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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.



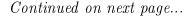
Metric	$\begin{array}{c} \textbf{Whole archive} \\ (\# \textbf{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
R_{free}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 >=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 <=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					
			<mark>%</mark>					
1	A	439	82%	17%	•			

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	MPD	A	1472	-	-	X	-
4	MRD	A	1479	-	-	X	-





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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MRD	A	1480	-	-	X	-
5	ОН	A	1481	-	-	X	-



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 4412 atoms, of which 1 is hydrogen 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 LACCASE.

Mol	Chain	Residues	${f Atoms}$			ZeroOcc	AltConf	Trace		
1	Λ	439	Total	С	N	О	S	0	27	0
1	A	439	3770	2421	680	653	16	0	37	U

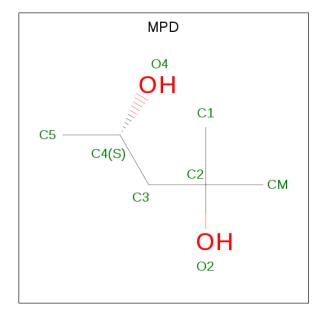
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Modelled Actual C		Reference
Α	53	ILE	LEU	SEE REMARK 999	UNP Q72HW2

• Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

\mathbf{Mol}	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
2	A	3	Total Cu 3 3	0	0

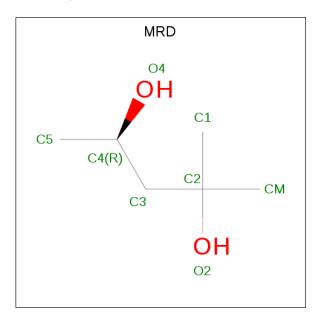
• Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 8 6 2	0	0
3	A	1	Total C O 8 6 2	0	0
3	A	1	Total C O 8 6 2	0	0
3	A	1	Total C O 8 6 2	0	0
3	A	1	Total C O 8 6 2	0	0
3	A	1	Total C O 8 6 2	0	0
3	A	1	Total C O 8 6 2	0	0
3	A	1	Total C O 8 6 2	0	0
3	A	1	Total C O 8 6 2	0	0
3	A	1	Total C O 8 6 2	0	0

• Molecule 4 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula: $C_6H_{14}O_2$).



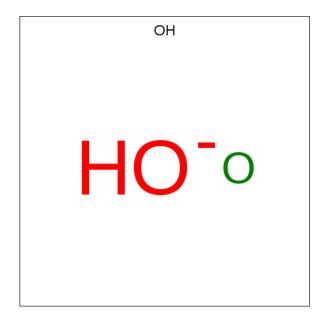
Mol	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
4	A	1	Total C O 8 6 2	0	0



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 8 6 2	0	0
4	A	1	Total C O 8 6 2	0	0
4	A	1	Total C O 8 6 2	0	0
4	A	1	Total C O 8 6 2	0	0
4	A	1	Total C O 8 6 2	0	0

• Molecule 5 is HYDROXIDE ION (three-letter code: OH) (formula: HO).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 2	H 1	O 1	0	0

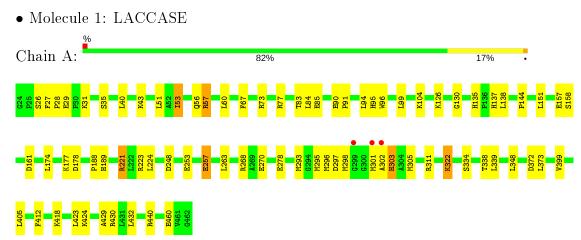
• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	509	Total O 509 509	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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 electron 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 dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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.





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	93.63Å 110.29Å 96.27Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.67 - 1.80	Depositor
Resolution (A)	28.67 - 1.80	EDS
% Data completeness	96.0 (28.67-1.80)	Depositor
(in resolution range)	95.6 (28.67-1.80)	EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.96 (at 1.79Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
P. P.	0.148 , 0.179	Depositor
R, R_{free}	0.144 , 0.176	DCC
R_{free} test set	2264 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	11.2	Xtriage
Anisotropy	0.093	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.32, 55.6	EDS
L-test for twinning ²	$ < L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4412	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.71% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities estimated from amplitudes.

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: MRD, MPD, CU, OH

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 Ch	Chain	Boı	nd lengths	Bond angles		
	Chain	RMSZ	# Z > 5	RMSZ	# Z >5	
1	A	0.46	$2/3869 \ (0.1\%)$	0.56	0/5262	

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(ext{\AA})$
1	A	257[A]	GLU	CD-OE1	-6.96	1.18	1.25
1	A	257[B]	GLU	CD-OE1	-6.96	1.18	1.25

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	3770	0	3845	103	0
2	A	3	0	0	0	0
3	A	80	0	140	19	0
4	A	48	0	82	35	0
5	A	1	1	0	2	0
6	A	509	0	0	28	3
All	All	4411	1	4067	132	3

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 16.

The worst 5 of 132 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} & ext{Interatomic} \ & ext{distance} \ & ext{(Å)} \end{aligned}$	Clash overlap (Å)
4:A:1474:MRD:H3C1	6:A:2087:HOH:O	1.19	1.31
4:A:1479:MRD:H1C1	4:A:1479:MRD:H5C3	1.22	1.15
4:A:1468:MRD:H5C2	4:A:1468:MRD:HMC1	1.10	1.10
1:A:189:HIS:HB2	4:A:1480:MRD:H1C1	1.30	1.08
4:A:1468:MRD:C5	4:A:1468:MRD:HMC1	1.87	1.04

All (3) 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	$egin{aligned} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{aligned}$	Clash overlap (Å)
6:A:2125:HOH:O	6:A:2414:HOH:O[6_444]	1.67	0.53
6:A:2188:HOH:O	6:A:2488:HOH:O[8_445]	1.89	0.31
6:A:2135:HOH:O	6:A:2135:HOH:O[4_545]	1.97	0.23

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	Favoured Allowed		Percentiles	
1	A	476/439 (108%)	464 (98%)	11 (2%)	1 (0%)	47	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	\mathbf{Type}	
1	A	399	VAL	



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	406/367 (111%)	396 (98%)	10 (2%)	47 34	

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	221[B]	ARG
1	A	268	ARG
1	A	311	ARG
1	A	221[A]	ARG
1	A	303	HIS

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

Mol	Chain	Res	Type
1	A	36	GLN
1	A	229	ASN
1	A	307	GLN
1	A	388	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)

Of 20 ligands modelled in this entry, 1 is modelled with single atom and 3 are monoatomic - leaving 16 for Mogul analysis.

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	Trens	Chain	Res	Link	В	ond leng	$_{ m gths}$	В	gles	
MIOI	Type	Chain	nes	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MRD	A	1467	_	7,7,7	0.79	0	9,10,10	1.03	1 (11%)
4	MRD	A	1468	-	7,7,7	0.78	0	9,10,10	0.69	0
3	MPD	A	1470	-	7,7,7	0.86	0	9,10,10	0.94	0
3	MPD	A	1471	_	7,7,7	0.88	0	9,10,10	1.34	1 (11%)
4	MRD	A	1479	-	7,7,7	0.79	0	9,10,10	1.07	0
3	MPD	A	1475	-	7,7,7	0.46	0	9,10,10	1.05	0
3	MPD	A	1478	_	7,7,7	0.83	0	9,10,10	0.89	0
3	MPD	A	1476	_	7,7,7	0.42	0	9,10,10	1.02	0
3	MPD	A	1472	_	7,7,7	0.67	0	9,10,10	1.94	2 (22%)
4	MRD	A	1480	-	7,7,7	1.10	0	9,10,10	1.35	2 (22%)
3	MPD	A	1469	-	7,7,7	0.49	0	9,10,10	0.59	0
3	MPD	A	1465	-	7,7,7	0.71	0	9,10,10	0.46	0
4	MRD	A	1466	_	7,7,7	1.19	0	9,10,10	0.77	0
3	MPD	A	1473		7,7,7	0.86	0	9,10,10	1.30	2 (22%)
3	MPD	A	1477	-	7,7,7	0.74	0	9,10,10	0.95	0
4	MRD	A	1474	-	7,7,7	0.50	0	9,10,10	1.67	2 (22%)

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
4	MRD	A	1467	-	-	0/5/5/5	-
4	MRD	A	1468	-	-	1/5/5/5	-
3	MPD	A	1470	-	-	2/5/5/5	-
3	MPD	A	1471	-	=	1/5/5/5	-
4	MRD	A	1479	_	-	1/5/5/5	-
3	MPD	A	1475	-	=	1/5/5/5	-



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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MPD	A	1478	-	-	5/5/5/5	-
3	MPD	A	1476	-	-	4/5/5/5	-
3	MPD	A	1472	-	=	1/5/5/5	-
4	MRD	A	1480	-	-	2/5/5/5	-
3	MPD	A	1469	-	-	0/5/5/5	-
3	MPD	A	1465	-	=	0/5/5/5	-
4	MRD	A	1466	-	-	0/5/5/5	-
3	MPD	A	1473	-	-	1/5/5/5	-
3	MPD	A	1477	-	=	1/5/5/5	-
4	MRD	A	1474	-	=	0/5/5/5	-

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	ype Atoms		$Observed(^o)$	$\operatorname{Ideal}({}^o)$
3	A	1472	MPD	CM-C2-C1	-4.65	100.89	110.57
3	A	1471	MPD	CM-C2-C1	3.28	117.41	110.57
4	A	1474	MRD	C5-C4-C3	-3.25	96.38	111.69
4	A	1474	MRD	O4-C4-C3	2.57	121.73	111.36
3	A	1473	MPD	CM-C2-C1	-2.56	105.23	110.57

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1468	MRD	C2-C3-C4-C5
3	A	1478	MPD	O2-C2-C3-C4
3	A	1478	MPD	C2-C3-C4-O4
3	A	1478	MPD	C2-C3-C4-C5
3	A	1476	MPD	C1-C2-C3-C4

There are no ring outliers.

12 monomers are involved in 54 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1467	MRD	2	0
4	A	1468	MRD	4	0
3	A	1471	MPD	4	0
4	A	1479	MRD	7	0
3	A	1478	MPD	2	0



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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1476	MPD	4	0
3	A	1472	MPD	6	0
4	A	1480	MRD	17	0
3	A	1465	MPD	1	0
3	A	1473	MPD	1	0
3	A	1477	MPD	1	0
4	A	1474	MRD	5	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^{th} 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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q < 0.9
1	A	439/439 (100%)	-0.48	3 (0%) 87 86	3, 10, 26, 70	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	301	MET	3.7
1	A	302	ALA	2.4
1	A	299	GLY	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 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. The B-factors column lists the minimum, median, 95^{th} 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	${f B-factors}({f \AA}^2)$	Q<0.9
3	MPD	A	1476	8/8	0.70	0.26	27,40,41,49	8
4	MRD	A	1479	8/8	0.72	0.25	38,41,44,47	8
5	ОН	A	1481	1/1	0.78	0.38	36,36,36,44	2
3	MPD	A	1475	8/8	0.81	0.23	17,26,35,36	8



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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
4	MRD	A	1480	8/8	0.83	0.39	12,23,29,31	8
4	MRD	A	1474	8/8	0.83	0.21	16,34,41,44	8
3	MPD	A	1473	8/8	0.84	0.17	19,24,29,30	8
3	MPD	A	1478	8/8	0.85	0.19	36,41,43,45	8
3	MPD	A	1471	8/8	0.86	0.21	$15,\!33,\!50,\!50$	0
3	MPD	A	1472	8/8	0.89	0.17	28,36,37,38	0
3	MPD	A	1477	8/8	0.90	0.14	31,39,50,56	0
3	MPD	A	1469	8/8	0.91	0.19	15,36,47,49	0
4	MRD	A	1468	8/8	0.92	0.12	26,33,35,36	0
3	MPD	A	1470	8/8	0.94	0.12	16,21,24,25	8
4	MRD	A	1467	8/8	0.95	0.12	28,31,35,36	0
3	MPD	A	1465	8/8	0.96	0.09	9,11,15,18	0
4	MRD	A	1466	8/8	0.96	0.08	11,18,23,26	0
2	CU	A	1464	1/1	0.99	0.06	18,18,18,18	1
2	CU	A	1462	1/1	1.00	0.04	10,10,10,10	0
2	CU	A	1463	1/1	1.00	0.02	9,9,9,9	0

6.5 Other polymers (i)

There are no such residues in this entry.

