



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 25, 2023 – 09:12 PM EDT

PDB ID : 3FEM
Title : Structure of the synthase subunit Pdx1.1 (Snz1) of PLP synthase from *Saccharomyces cerevisiae*
Authors : Strohmeier, M.; Windeisen, V.; Sinning, I.; Tews, I.
Deposited on : 2008-11-30
Resolution : 3.02 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

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>.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.36
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

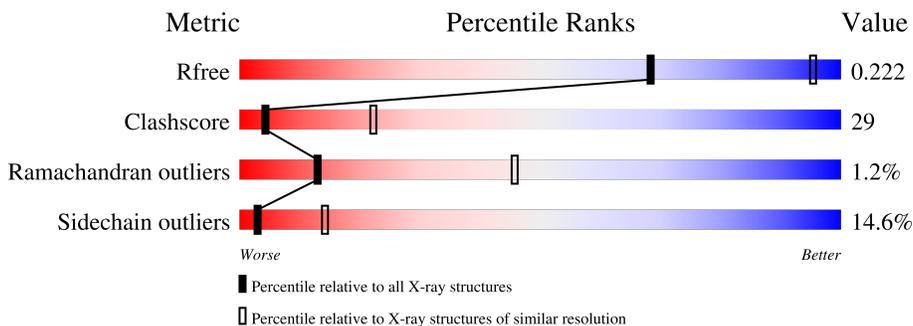
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.02 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	2399 (3.04-3.00)
Clashscore	141614	2734 (3.04-3.00)
Ramachandran outliers	138981	2640 (3.04-3.00)
Sidechain outliers	138945	2643 (3.04-3.00)

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 ≥ 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	297	49% 39% 6% • 5%
1	B	297	49% 39% 5% • 5%
1	C	297	52% 37% 6% • 5%
1	D	297	49% 39% 5% • 5%
1	E	297	50% 38% 5% • 5%
1	F	297	48% 39% 7% • 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12600 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 Pyridoxine biosynthesis protein SNZ1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	281	2099	1319	357	406	17	0	0	0
1	B	281	2099	1319	357	406	17	0	0	0
1	C	281	2099	1319	357	406	17	0	0	0
1	D	281	2099	1319	357	406	17	0	0	0
1	E	281	2099	1319	357	406	17	0	0	0
1	F	281	2099	1319	357	406	17	0	0	0

- Molecule 2 is water.

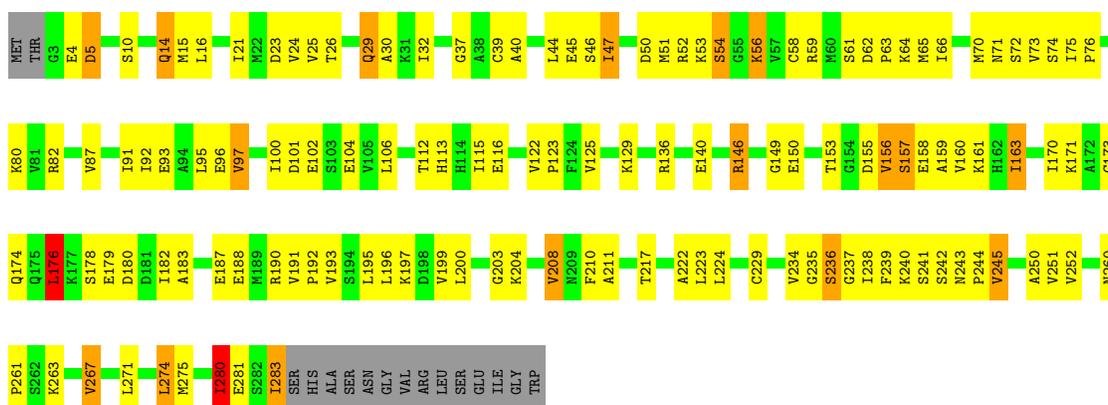
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	O 1	0	0
2	B	1	Total 1	O 1	0	0
2	C	1	Total 1	O 1	0	0
2	D	1	Total 1	O 1	0	0
2	E	1	Total 1	O 1	0	0
2	F	1	Total 1	O 1	0	0

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. 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. 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.

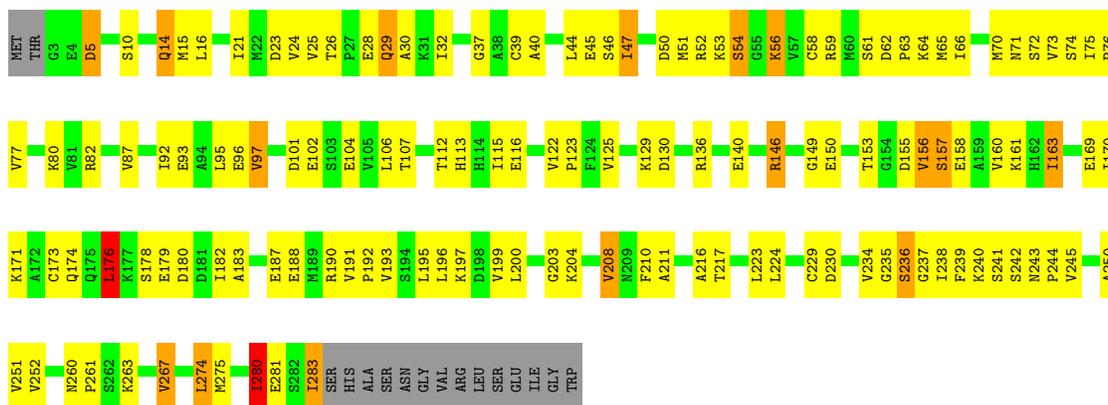
- Molecule 1: Pyridoxine biosynthesis protein SNZ1

Chain A: 



- Molecule 1: Pyridoxine biosynthesis protein SNZ1

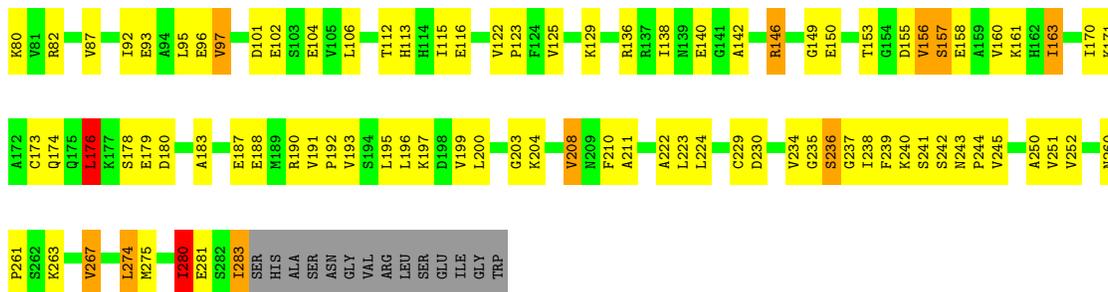
Chain B: 



- Molecule 1: Pyridoxine biosynthesis protein SNZ1

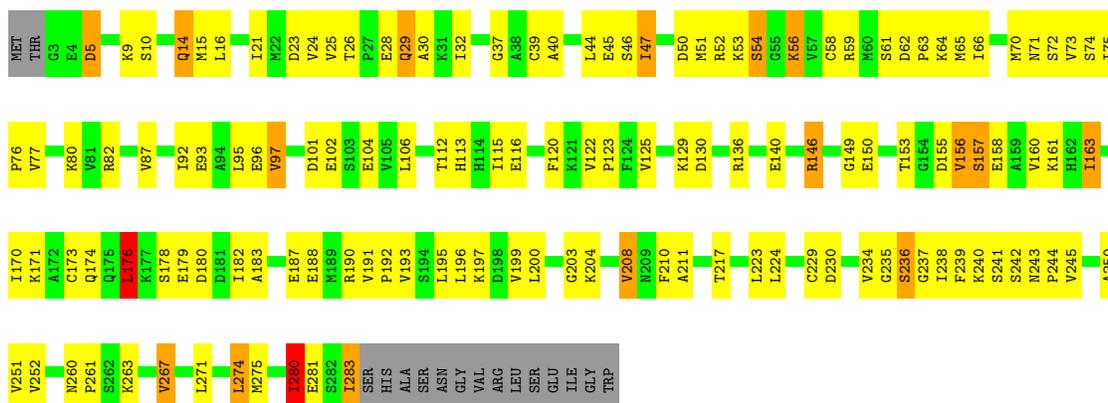
Chain C: 





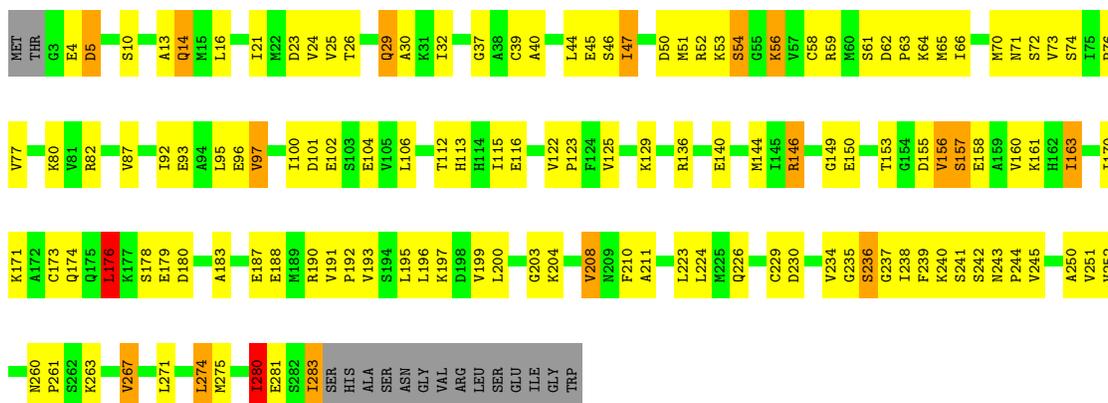
- Molecule 1: Pyridoxine biosynthesis protein SNZ1

Chain D: 49% 39% 5% • 5%



- Molecule 1: Pyridoxine biosynthesis protein SNZ1

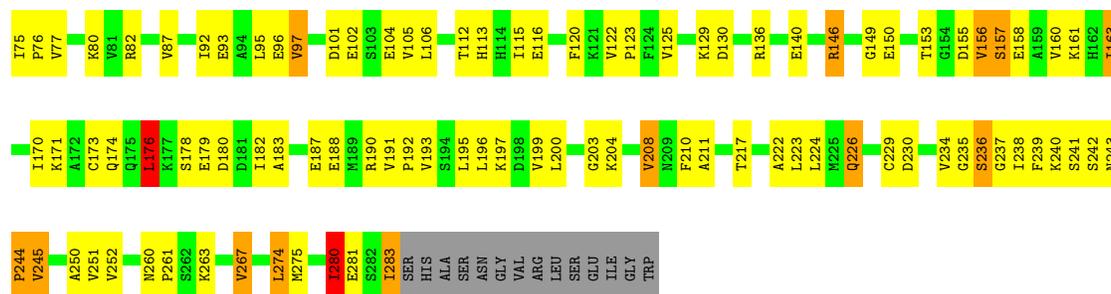
Chain E: 50% 38% 5% • 5%



- Molecule 1: Pyridoxine biosynthesis protein SNZ1

Chain F: 48% 39% 7% • 5%





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	154.07Å 154.22Å 154.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.02 19.79 – 3.03	Depositor EDS
% Data completeness (in resolution range)	99.7 (20.00-3.02) 99.2 (19.79-3.03)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.07 (at 3.04Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.162 , 0.181 0.224 , 0.222	Depositor DCC
R_{free} test set	2009 reflections (2.81%)	wwPDB-VP
Wilson B-factor (Å ²)	71.4	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 23.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.34$, $\langle L^2 \rangle = 0.17$	Xtriage
Estimated twinning fraction	0.149 for -h,l,k 0.149 for -l,-k,-h 0.149 for k,h,-l 0.348 for k,l,h 0.348 for l,h,k	Xtriage
Reported twinning fraction	0.470 for H,K,L 0.298 for K,-L,-H 0.231 for -L,-H,K	Depositor
Outliers	0 of 71521 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	12600	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.06% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.51	0/2125	0.67	0/2861
1	B	0.53	0/2125	0.69	0/2861
1	C	0.51	0/2125	0.68	0/2861
1	D	0.53	0/2125	0.69	0/2861
1	E	0.51	0/2125	0.68	0/2861
1	F	0.53	0/2125	0.69	0/2861
All	All	0.52	0/12750	0.68	0/17166

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
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
All	All	0	6

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	176	LEU	Peptide
1	B	176	LEU	Peptide
1	C	176	LEU	Peptide
1	D	176	LEU	Peptide

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Mol	Chain	Res	Type	Group
1	E	176	LEU	Peptide

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	2099	0	2162	130	0
1	B	2099	0	2162	132	1
1	C	2099	0	2162	122	0
1	D	2099	0	2162	129	0
1	E	2099	0	2162	129	0
1	F	2099	0	2162	129	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
All	All	12600	0	12972	747	1

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 29.

The worst 5 of 747 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:173:CYS:O	1:B:176:LEU:HD22	1.29	1.32
1:F:173:CYS:O	1:F:176:LEU:HD22	1.31	1.29
1:D:173:CYS:O	1:D:176:LEU:HD22	1.28	1.26
1:A:173:CYS:O	1:A:176:LEU:HD22	1.31	1.25
1:C:173:CYS:O	1:C:176:LEU:HD22	1.29	1.23

All (1) 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:B:76:PRO:CD	1:F:35:LYS:NZ[3_655]	2.05	0.15

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	279/297 (94%)	242 (87%)	33 (12%)	4 (1%)	11	41
1	B	279/297 (94%)	239 (86%)	37 (13%)	3 (1%)	14	48
1	C	279/297 (94%)	241 (86%)	35 (12%)	3 (1%)	14	48
1	D	279/297 (94%)	242 (87%)	34 (12%)	3 (1%)	14	48
1	E	279/297 (94%)	238 (85%)	38 (14%)	3 (1%)	14	48
1	F	279/297 (94%)	240 (86%)	35 (12%)	4 (1%)	11	41
All	All	1674/1782 (94%)	1442 (86%)	212 (13%)	20 (1%)	13	46

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	236	SER
1	B	236	SER
1	C	236	SER
1	D	236	SER
1	E	236	SER

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	229/242 (95%)	195 (85%)	34 (15%)	3	13
1	B	229/242 (95%)	196 (86%)	33 (14%)	3	14
1	C	229/242 (95%)	196 (86%)	33 (14%)	3	14
1	D	229/242 (95%)	196 (86%)	33 (14%)	3	14
1	E	229/242 (95%)	196 (86%)	33 (14%)	3	14
1	F	229/242 (95%)	195 (85%)	34 (15%)	3	13
All	All	1374/1452 (95%)	1174 (85%)	200 (15%)	3	14

5 of 200 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	156	VAL
1	E	74	SER
1	F	283	ILE
1	D	176	LEU
1	D	275	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	90	GLN
1	E	14	GLN
1	F	243	ASN
1	D	243	ASN
1	E	90	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](#)

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.