

# wwPDB X-ray Structure Validation Summary Report (i)

May 15, 2020 - 08:30 am BST

PDB ID : 1ZNN

Title : Structure of the synthase subunit of PLP synthase

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Deposited on : 2005-05-11

Resolution : 2.20 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 (i) symbol.

The following versions of software and data (see references (1)) 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 : 2.11

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)

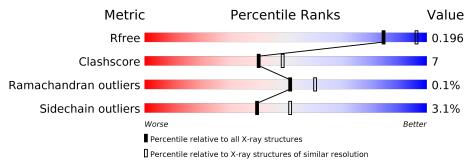
Validation Pipeline (wwPDB-VP) : 2.11

# 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 2.20 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
$R_{free}$	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)

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%

Mol	Chain	Length	Quality of chain				
1	A	325	64% 1	0%	•	25%	
1	В	325	65%	1%	•	25%	
1	С	325	65%	L0%		25%	
1	D	325	64% 1	0%	•	25%	
1	Е	325	66%	8%		25%	
1	F	325	66%	10%	)	25%	



# 2 Entry composition (i)

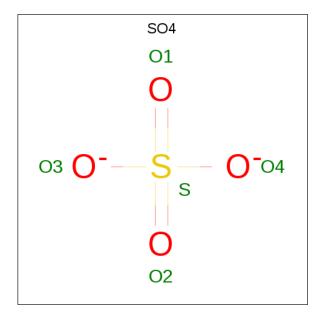
There are 4 unique types of molecules in this entry. The entry contains 12649 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PLP SYNTHASE.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	A	245	Total	С	N	О	S	0	0	0
1	Λ	240	1839	1153	325	349	12	U	0	
1	В	245	Total	С	N	О	S	0	0	0
1	Ъ	240	1839	1153	325	349	12	0	U	U
1	С	245	Total	С	N	О	S	0	0	0
1		240	1839	1153	325	349	12	0	U	
1	D	245	Total	С	N	О	S	0	0	0
1	ש	240	1839	1153	325	349	12	0	0	
1	Е	245	Total	С	N	О	S	0	0	0
1	12	240	1839	1153	325	349	12	U	0	
1	F	245	Total	С	N	О	S	0	0	0
1	L'	240	1839	1153	325	349	12	U	U	U

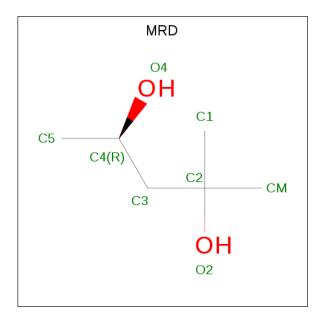
• Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	В	1	Total O S 5 4 1	0	0
2	В	1	Total O S 5 4 1	0	0
2	С	1	Total O S 5 4 1	0	0
2	С	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0
2	F	1	Total O S 5 4 1	0	0
2	F	1	Total O S 5 4 1	0	0

 $\bullet$  Molecule 3 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula:  $C_6H_{14}O_2).$ 





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 8 6 2	0	0
3	В	1	Total C O 8 6 2	0	0
3	С	1	Total C O 8 6 2	0	0
3	D	1	Total C O 8 6 2	0	0
3	Е	1	Total C O 8 6 2	0	0
3	F	1	Total C O 8 6 2	0	0

### • Molecule 4 is water.

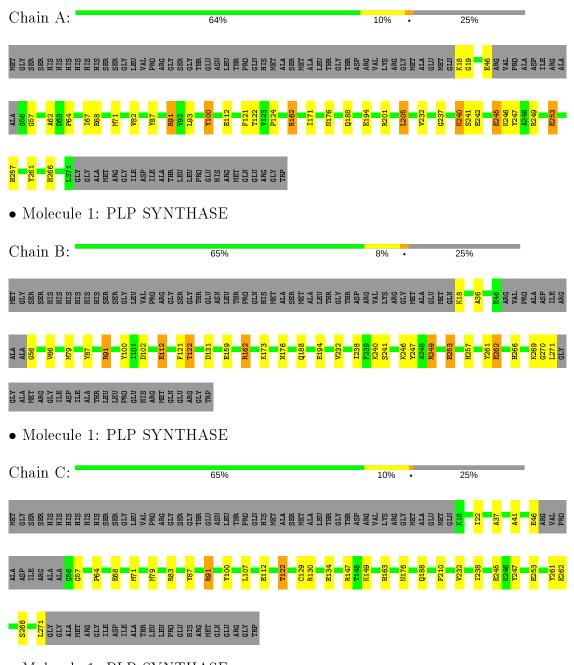
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	349	Total O 349 349	0	0
4	В	396	Total O 396 396	0	0
4	С	243	Total O 243 243	0	0
4	D	152	Total O 152 152	0	0
4	Е	162	Total O 162 162	0	0
4	F	205	Total O 205 205	0	0



# 3 Residue-property plots (i)

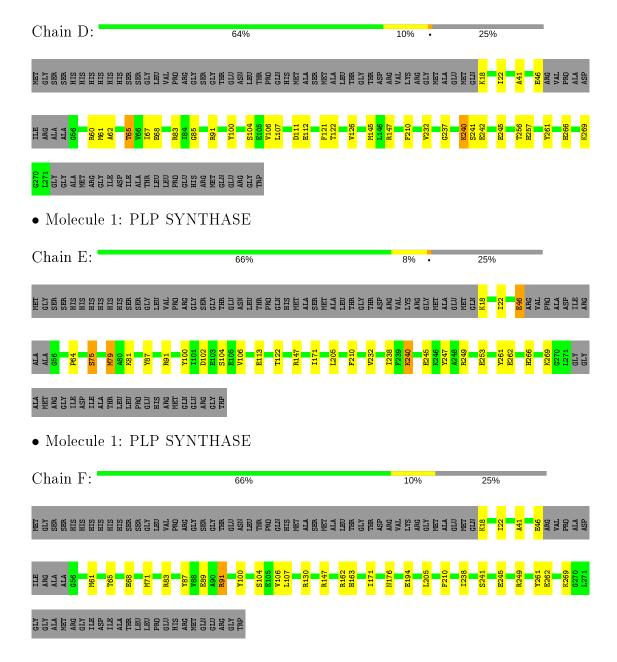
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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: PLP SYNTHASE



• Molecule 1: PLP SYNTHASE







# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 2	Depositor
Cell constants	162.53	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	49.94 - 2.20	Depositor
Resolution (A)	49.91 - 2.20	EDS
% Data completeness	99.9 (49.94-2.20)	Depositor
(in resolution range)	99.9 (49.91-2.20)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	3.13 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
D D.	0.159 , 0.198	Depositor
$R, R_{free}$	0.159 , $0.196$	DCC
$R_{free}$ test set	6320 reflections $(5.02%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.9	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.31 , 53.3	EDS
L-test for twinning <sup>2</sup>	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.019 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	12649	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.54% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities 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, 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	Mol Chain		ond lengths	В	ond angles	
IVIOI	Chain	RMSZ	RMSZ   $\# Z  > 5$		# Z >5	
1	A	0.98	4/1863~(0.2%)	0.86	5/2516 (0.2%)	
1	В	1.21	8/1863 (0.4%)	1.08	$10/2516 \ (0.4\%)$	
1	С	0.82	4/1863~(0.2%)	0.75	$1/2516 \ (0.0\%)$	
1	D	0.59	0/1863	0.65	0/2516	
1	E	0.65	1/1863~(0.1%)	0.67	0/2516	
1	F	0.67	0/1863	0.72	0/2516	
All	All	0.85	17/11178 (0.2%)	0.80	$16/15096 \ (0.1\%)$	

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(A)
1	В	253	GLU	CB-CG	16.29	1.83	1.52
1	В	253	GLU	CG-CD	15.50	1.75	1.51
1	A	253	GLU	CG-CD	12.68	1.71	1.51
1	A	253	GLU	CB-CG	12.67	1.76	1.52
1	В	253	GLU	CD-OE1	-11.49	1.13	1.25

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	${f Atoms}$	$\mathbf{Z}$	$\operatorname{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
1	В	253	GLU	OE1-CD-OE2	-22.16	96.70	123.30
1	В	91	ARG	NE-CZ-NH1	14.26	127.43	120.30
1	В	253	GLU	CG-CD-OE1	9.31	136.92	118.30
1	В	91	ARG	NE-CZ-NH2	-9.27	115.67	120.30
1	В	249	ARG	NE-CZ-NH1	6.59	123.60	120.30

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	1839	0	1864	37	1
1	В	1839	0	1864	40	7
1	С	1839	0	1864	23	0
1	D	1839	0	1864	26	0
1	E	1839	0	1864	22	1
1	F	1839	0	1864	21	0
2	A	10	0	0	0	0
2	В	10	0	0	0	0
2	С	10	0	0	0	0
2	D	10	0	0	0	0
2	E	10	0	0	0	0
2	F	10	0	0	0	0
3	A	8	0	14	0	0
3	В	8	0	14	0	0
3	С	8	0	14	2	0
3	D	8	0	14	0	0
3	E	8	0	14	0	0
3	F	8	0	14	0	0
4	A	349	0	0	20	4
4	В	396	0	0	24	1
4	С	243	0	0	12	0
4	D	152	0	0	12	0
4	Е	162	0	0	7	1
4	F	205	0	0	7	0
All	All	12649	0	11268	161	14

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 7.

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

Atom-1	Atom-2	$egin{aligned}  ext{Interatomic} \  ext{distance} \ ( ext{Å}) \end{aligned}$	$egin{aligned}  ext{Clash} \  ext{overlap } ( ext{Å}) \end{aligned}$
1:A:253:GLU:CG	1:A:253:GLU:CB	1.76	1.64
1:B:253:GLU:CB	1:B:253:GLU:CG	1.83	1.56
1:B:253:GLU:CG	1:B:253:GLU:CD	1.75	1.52

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Atom-1	Atom-2	$egin{array}{ll}  ext{Interatomic} \  ext{distance} \ ( ext{\AA}) \end{array}$	Clash overlap (Å)	
1:A:266:HIS:HE1	4:A:2889:HOH:O	1.28	1.16	
1:B:18:LYS:HG3	4:B:3130:HOH:O	1.53	1.06	

The worst 5 of 14 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	$egin{aligned} & & & & & & & & & & & & & & & & & & &$	Clash overlap (Å)
1:B:253:GLU:OE1	1:B:253:GLU:OE2[4_565]	1.02	1.18
1:B:253:GLU:CD	1:B:253:GLU:OE2[4_565]	1.20	1.00
1:B:253:GLU:OE1	1:B:253:GLU:OE1[4_565]	1.44	0.76
1:B:253:GLU:CD	1:B:253:GLU:OE1[4_565]	1.65	0.55
4:A:2937:HOH:O	4:A:2937:HOH:O[3_555]	1.65	0.55

# 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	Percei	ntiles
1	A	241/325 (74%)	237 (98%)	3 (1%)	1 (0%)	34	37
1	В	241/325 (74%)	240 (100%)	1 (0%)	0	100	100
1	С	241/325 (74%)	238 (99%)	2 (1%)	1 (0%)	34	37
1	D	241/325 (74%)	238 (99%)	3 (1%)	0	100	100
1	E	241/325 (74%)	233 (97%)	8 (3%)	0	100	100
1	F	241/325 (74%)	237 (98%)	4 (2%)	0	100	100
All	All	1446/1950 (74%)	1423 (98%)	21 (2%)	2 (0%)	51	60

#### All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	С	57	GLY
1	A	57	GLY



#### 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	Perce	ntiles
1	A	$189/251\ (75\%)$	183 (97%)	6 (3%)	39	50
1	В	189/251 (75%)	184 (97%)	5 (3%)	46	58
1	С	189/251 (75%)	183 (97%)	6 (3%)	39	50
1	D	189/251 (75%)	182 (96%)	7 (4%)	34	43
1	E	$189/251\ (75\%)$	181 (96%)	8 (4%)	30	38
1	F	189/251 (75%)	186 (98%)	3 (2%)	62	76
All	All	1134/1506 (75%)	1099 (97%)	35 (3%)	40	51

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	232	VAL
1	D	100	TYR
1	F	91	ARG
1	С	271	LEU
1	D	61	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	В	188	GLN
1	С	115	HIS
1	D	257	HIS
1	В	115	HIS
1	D	188	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)

18 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).

Mal	Т	Ch ain	Dag	T ! 1-	В	ond leng	$_{ m gths}$	В	ond ang	gles
Mol	Type	Chain	Res	Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	$\mid \# Z  > 2$
3	MRD	D	2891	-	7,7,7	0.25	0	9,10,10	0.55	0
2	SO4	E	2410	-	4,4,4	0.22	0	6,6,6	0.61	0
2	SO4	F	2411	-	4,4,4	0.27	0	6,6,6	0.58	0
2	SO4	E	2409	-	4,4,4	0.15	0	6,6,6	0.72	0
3	MRD	С	2890	-	7,7,7	0.41	0	9,10,10	0.29	0
2	SO4	В	2404	-	4,4,4	0.17	0	6,6,6	0.63	0
2	SO4	D	2407	-	4,4,4	0.37	0	6,6,6	1.15	0
2	SO4	D	2408	-	4,4,4	0.18	0	6,6,6	0.55	0
3	MRD	F	2893	-	7,7,7	0.39	0	9,10,10	0.42	0
3	MRD	A	2888	-	7,7,7	0.28	0	9,10,10	0.47	0
2	SO4	С	2405	-	4,4,4	0.50	0	6,6,6	0.86	0
2	SO4	A	2402	-	4,4,4	0.23	0	6,6,6	0.96	0
3	MRD	В	2889	-	7,7,7	0.42	0	9,10,10	0.65	0
2	SO4	В	2403	-	4,4,4	0.78	0	6,6,6	0.86	0
3	MRD	Е	2892	-	7,7,7	0.26	0	9,10,10	0.42	0
2	SO4	A	2401	-	4,4,4	0.55	0	6,6,6	0.50	0
2	SO4	С	2406	-	4,4,4	0.17	0	6,6,6	0.39	0
2	SO4	F	2412	-	4,4,4	0.13	0	6,6,6	0.36	0

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	nο	outliers	of tha	t kind	were	identifie	Ы
_	HIVAIII O	11()	OUULDID	$\mathbf{v}_{1}$ $\mathbf{v}_{11}a$	to KIIIU	WCLC		м.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MRD	D	2891	_	-	0/5/5/5	-
3	MRD	A	2888	-	-	0/5/5/5	-
3	MRD	F	2893	_	-	0/5/5/5	-
3	MRD	В	2889	-	-	0/5/5/5	-
3	MRD	E	2892	-	-	0/5/5/5	-
3	MRD	С	2890	-	-	0/5/5/5	-

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 2 short contacts:

Mol	Chain	$\operatorname{Res}$	Type	Clashes	Symm-Clashes
3	С	2890	MRD	2	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)

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

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

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

# 6.3 Carbohydrates (i)

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

# 6.4 Ligands (i)

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

## 6.5 Other polymers (i)

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

