



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 8Z6P / pdb_00008z6p
Title : Crystal structure of Procerain-B from *Calotropis gigantea*
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Deposited on : 2024-04-19
Resolution : 1.50 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

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
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

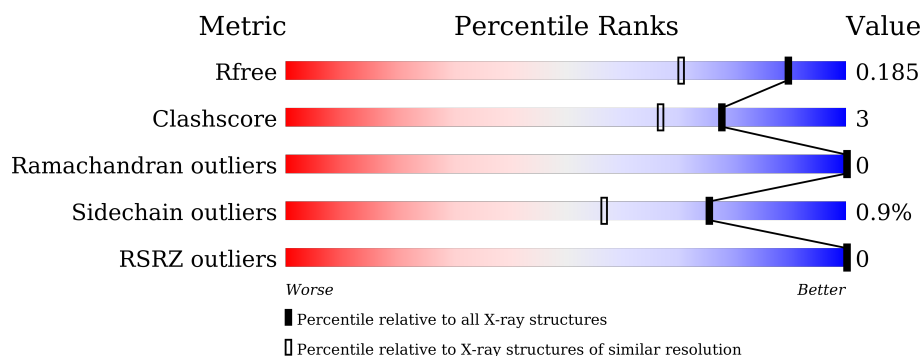
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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}	164625	3717 (1.50-1.50)
Clashscore	180529	4048 (1.50-1.50)
Ramachandran outliers	177936	3970 (1.50-1.50)
Sidechain outliers	177891	3967 (1.50-1.50)
RSRZ outliers	164620	3718 (1.50-1.50)

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 $\leq 5\%$. 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	339	<div> <div>59%</div> <div>37%</div> </div>
1	B	339	<div> <div>56%</div> <div>6%</div> <div>39%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3658 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 Procerain B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	212	Total	C	N	O	S	0	2	0
			1696	1066	302	318	10			
1	B	208	Total	C	N	O	S	0	2	0
			1662	1050	294	308	10			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	176	Total	O	0	1
			177	177		
2	B	123	Total	O	0	0
			123	123		

- Molecule 1: Procerain B

- Molecule 1: Procerain B

Chain B:

Sequence logo for Chain B. The y-axis lists amino acids: MET, ARG, LEU, GLN, GLU, GLY, ALA, ILE, LEU, L128, K137, F141, I166, M172, K191, Y201, K206, Y213, V229, K239, N240, V272, N286, E293, V296, R302, R316, I317, N320, SER, ASN, GLN, SER, G325, I330, Y339. The x-axis shows three regions: 56%, 6%, and 39%. The 56% region is dominated by MET. The 6% region shows a mix of amino acids. The 39% region is dominated by ARG.

Amino Acid	56%	6%	39%
MET	High	Low	Low
ARG	Low	Low	High
LEU	Low	Low	Low
GLN	Low	Low	Low
GLU	Low	Low	Low
GLY	Low	Low	Low
ALA	Low	Low	Low
ILE	Low	Low	Low
L128	Low	Low	Low
K137	Low	Low	Low
F141	Low	Low	Low
I166	Low	Low	Low
M172	Low	Low	Low
K191	Low	Low	Low
Y201	Low	Low	Low
K206	Low	Low	Low
Y213	Low	Low	Low
V229	Low	Low	Low
K239	Low	Low	Low
N240	Low	Low	Low
V272	Low	Low	Low
N286	Low	Low	Low
E293	Low	Low	Low
V296	Low	Low	Low
R302	Low	Low	Low
R316	Low	Low	Low
I317	Low	Low	Low
N320	Low	Low	Low
SER	Low	Low	Low
ASN	Low	Low	Low
GLN	Low	Low	Low
SER	Low	Low	Low
G325	Low	Low	Low
I330	Low	Low	Low
Y339	Low	Low	Low

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	31.39Å 91.36Å 64.48Å 90.00° 89.98° 90.00°	Depositor
Resolution (Å)	30.40 – 1.50 30.40 – 1.50	Depositor EDS
% Data completeness (in resolution range)	99.0 (30.40-1.50) 99.0 (30.40-1.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 1.50Å)	Xtriage
Refinement program	PHENIX 1.21_5207	Depositor
R, R_{free}	0.149 , 0.181 0.150 , 0.185	Depositor DCC
R_{free} test set	2821 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	15.7	Xtriage
Anisotropy	0.286	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 32.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.387 for h,-k,-l	Xtriage
Reported twinning fraction	0.360 for h,-k,-l	Depositor
Outliers	0 of 57503 reflections	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	3658	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.51% 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

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

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	0.34	0/1725	0.60	0/2325
1	B	0.33	0/1693	0.59	0/2280
All	All	0.34	0/3418	0.60	0/4605

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	1696	0	1640	8	0
1	B	1662	0	1614	10	0
2	A	177	0	0	0	0
2	B	123	0	0	2	0
All	All	3658	0	3254	18	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 3.

All (18) 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:239:LYS:HG2	1:A:240:ASN:ND2	2.14	0.63
1:A:243:LYS:HE2	1:A:243:LYS:H	1.71	0.55
1:B:137:LYS:NZ	2:B:401:HOH:O	2.40	0.54
1:A:240:ASN:ND2	1:A:325:GLY:HA2	2.27	0.50
1:A:152:OCS:OD3	1:A:283:HIS:HA	2.12	0.49
1:B:201:TYR:CE2	1:B:205:LYS:HD2	2.47	0.48
1:B:141:PHE:CE2	1:B:172[B]:MET:HG3	2.49	0.48
1:B:191:LYS:HD3	2:B:520:HOH:O	2.13	0.48
1:A:248:VAL:O	1:A:251:GLN:HG2	2.14	0.46
1:B:165:ILE:HG13	1:B:229:VAL:HG21	1.98	0.46
1:B:293:GLU:CD	1:B:316:ARG:HH12	2.20	0.45
1:A:240:ASN:HD22	1:A:325:GLY:HA2	1.83	0.44
1:B:286:ASN:HB2	1:B:302:ARG:HB3	1.99	0.44
1:B:239:LYS:HG2	1:B:240:ASN:OD1	2.18	0.43
1:A:141:PHE:CE2	1:A:172[B]:MET:HE3	2.54	0.43
1:B:317:ILE:HG21	1:B:330:ILE:HD12	2.02	0.41
1:A:243:LYS:H	1:A:243:LYS:CE	2.34	0.40
1:B:272:VAL:HG11	1:B:296:VAL:HG11	2.03	0.40

There are no symmetry-related clashes.

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	211/339 (62%)	206 (98%)	5 (2%)	0	100	100
1	B	205/339 (60%)	200 (98%)	5 (2%)	0	100	100
All	All	416/678 (61%)	406 (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	178/294 (60%)	176 (99%)	2 (1%)	70	48
1	B	173/294 (59%)	172 (99%)	1 (1%)	84	70
All	All	351/588 (60%)	348 (99%)	3 (1%)	75	57

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	213	TYR
1	A	280	ARG
1	B	213	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	221	GLN
1	A	240	ASN
1	B	251	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](#)

2 non-standard protein/DNA/RNA residues 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
1	OCS	A	152	1	7,8,9	0.86	0	6,11,13	0.78	0
1	OCS	B	152	1	7,8,9	0.88	0	6,11,13	0.75	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 no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OCS	A	152	1	-	1/4/7/9	-
1	OCS	B	152	1	-	1/4/7/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	152	OCS	N-CA-CB-SG
1	B	152	OCS	N-CA-CB-SG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	152	OCS	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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 ⓘ

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, 95th 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 ²)	Q<0.9
1	A	211/339 (62%)	-1.23	0 100 100	7, 15, 23, 33	2 (0%)
1	B	207/339 (61%)	-1.03	0 100 100	11, 18, 31, 45	2 (0%)
All	All	418/678 (61%)	-1.13	0 100 100	7, 16, 28, 45	4 (0%)

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [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, 95th 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	B-factors(Å ²)	Q<0.9
1	OCS	A	152	9/10	0.99	0.03	9,12,16,16	0
1	OCS	B	152	9/10	0.99	0.04	12,15,20,25	0

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.