



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 12:28 am GMT

PDB ID : 1FXZ
Title : CRYSTAL STRUCTURE OF SOYBEAN PROGLYCININ A1AB1B HOMOTRIMER
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Deposited on : 2000-09-28
Resolution : 2.80 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

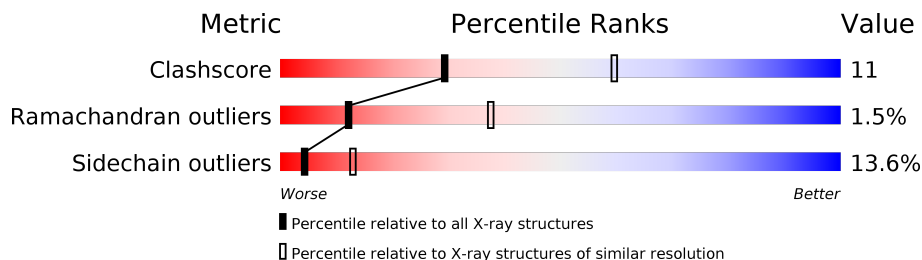
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	476	
1	B	476	
1	C	476	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8773 atoms, of which 0 are hydrogens and 0 are deuteriums.

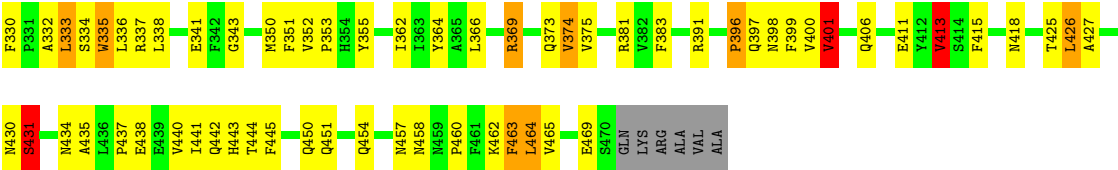
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called GLYCININ G1.

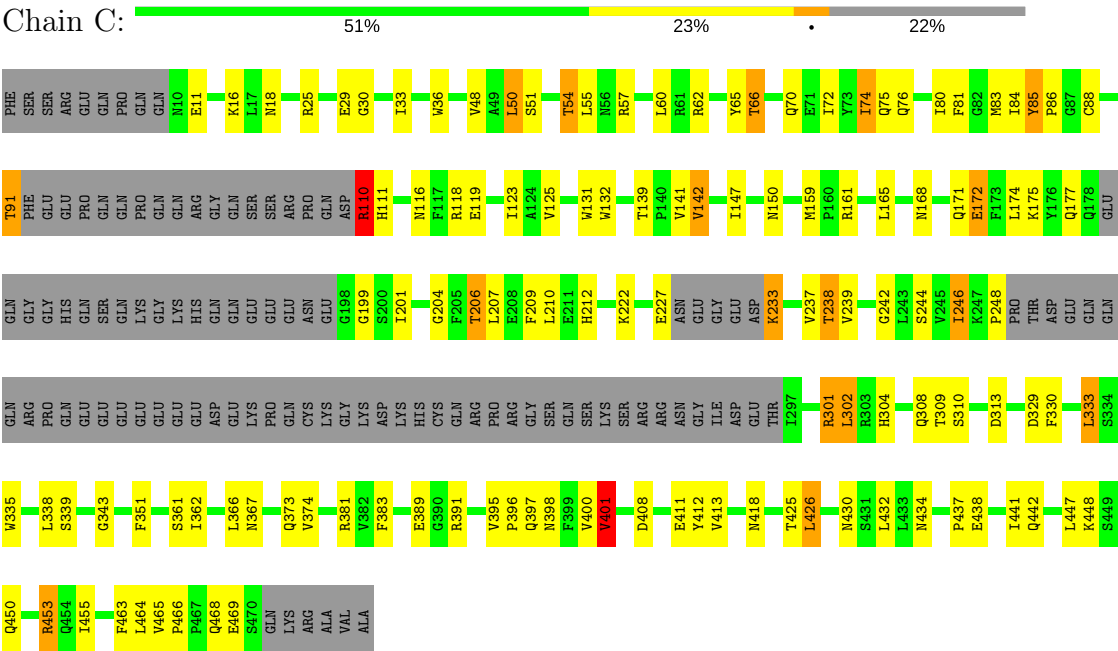
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	371	Total	C	N	O	S	0	0	0
			2913	1838	515	548	12			
1	B	371	Total	C	N	O	S	0	0	0
			2913	1838	515	548	12			
1	C	371	Total	C	N	O	S	0	0	0
			2913	1838	515	548	12			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	16	Total	O	0	0
			16	16		
2	B	6	Total	O	0	0
			6	6		
2	C	12	Total	O	0	0
			12	12		



● Molecule 1: GLYCININ G1



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	115.52Å 115.52Å 147.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.199 , 0.250	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8773	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.68	0/2971	1.37	32/4025 (0.8%)
1	B	0.68	0/2971	1.38	34/4025 (0.8%)
1	C	0.71	0/2971	1.40	34/4025 (0.8%)
All	All	0.69	0/8913	1.38	100/12075 (0.8%)

There are no bond length outliers.

The worst 5 of 100 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	61	ARG	NE-CZ-NH2	-9.69	115.45	120.30
1	A	61	ARG	NE-CZ-NH1	8.73	124.67	120.30
1	C	132	TRP	CD1-CG-CD2	8.63	113.21	106.30
1	B	132	TRP	CD1-CG-CD2	8.62	113.20	106.30
1	B	301	ARG	NE-CZ-NH2	-8.54	116.03	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	2913	0	2870	79	0
1	B	2913	0	2870	82	0
1	C	2913	0	2870	64	0
2	A	16	0	0	1	0
2	B	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	12	0	0	0	0
All	All	8773	0	8610	188	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 11.

The worst 5 of 188 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:33:ILE:HG21	1:A:172:GLU:HG2	1.63	0.81
1:B:65:TYR:HE1	1:C:398:ASN:HB3	1.47	0.80
1:A:65:TYR:HE1	1:B:398:ASN:HB3	1.49	0.78
1:A:398:ASN:HB3	1:C:65:TYR:HE1	1.54	0.72
1:A:168:ASN:HA	1:A:199:GLY:HA2	1.73	0.70

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	361/476 (76%)	333 (92%)	26 (7%)	2 (1%)	28	62
1	B	361/476 (76%)	333 (92%)	21 (6%)	7 (2%)	9	30
1	C	361/476 (76%)	327 (91%)	27 (8%)	7 (2%)	9	30
All	All	1083/1428 (76%)	993 (92%)	74 (7%)	16 (2%)	12	37

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	396	PRO
1	B	431	SER

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Mol	Chain	Res	Type
1	B	158	GLN
1	B	246	ILE
1	C	172	GLU

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	319/414 (77%)	274 (86%)	45 (14%)	4	12
1	B	319/414 (77%)	279 (88%)	40 (12%)	5	16
1	C	319/414 (77%)	274 (86%)	45 (14%)	4	12
All	All	957/1242 (77%)	827 (86%)	130 (14%)	4	13

5 of 130 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	150	ASN
1	B	337	ARG
1	C	426	LEU
1	B	158	GLN
1	B	225	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	171	GLN
1	B	367	ASN
1	C	367	ASN
1	B	348	ASN
1	B	378	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 carbohydrates 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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.