



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 10:41 AM UTC

PDB ID : 1PZ8 / pdb_00001pz8
Title : Modulation of agrin function by alternative splicing and Ca²⁺ binding
Authors : Stetefeld, J.; Alexandrescu, A.T.; Maciejewski, M.W.; Jenny, M.; Rathgeb-Szabo, K.; Schulthess, T.; Landwehr, R.; Frank, S.; Ruegg, M.A.; Kammerer, R.A.
Deposited on : 2003-07-10
Resolution : 2.35 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 : 4-5-2 with Phenix2.0
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

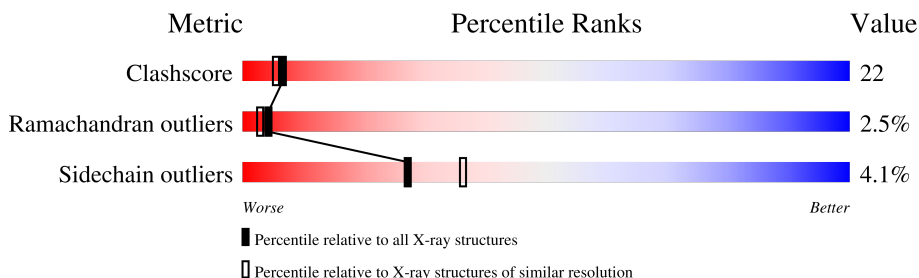
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	201	56% 30% • 12%
1	B	201	64% 19% 5% • 11%
1	C	201	65% 19% • 12%
1	D	201	63% 19% 5% • 12%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6058 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 Agrin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	176	Total	C	N	O	S	0	0	0
			1365	863	238	258	6			
1	B	179	Total	C	N	O	S	0	0	0
			1385	874	241	264	6			
1	C	176	Total	C	N	O	S	0	0	0
			1365	863	238	258	6			
1	D	177	Total	C	N	O	S	0	0	0
			1370	866	239	259	6			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	HIS	PRO	SEE REMARK 999	UNP P31696
A	34	LEU	ASP	SEE REMARK 999	UNP P31696
A	35	SER	ALA	SEE REMARK 999	UNP P31696
A	36	ASN	LEU	SEE REMARK 999	UNP P31696
A	37	GLU	ASP	SEE REMARK 999	UNP P31696
A	38	ILE	TYR	SEE REMARK 999	UNP P31696
A	42	-	PRO	SEE REMARK 999	UNP P31696
A	43	-	SER	SEE REMARK 999	UNP P31696
A	44	-	GLU	SEE REMARK 999	UNP P31696
B	33	HIS	PRO	SEE REMARK 999	UNP P31696
B	34	LEU	ASP	SEE REMARK 999	UNP P31696
B	35	SER	ALA	SEE REMARK 999	UNP P31696
B	36	ASN	LEU	SEE REMARK 999	UNP P31696
B	37	GLU	ASP	SEE REMARK 999	UNP P31696
B	38	ILE	TYR	SEE REMARK 999	UNP P31696
B	42	-	PRO	SEE REMARK 999	UNP P31696
B	43	-	SER	SEE REMARK 999	UNP P31696
B	44	-	GLU	SEE REMARK 999	UNP P31696
C	33	HIS	PRO	SEE REMARK 999	UNP P31696
C	34	LEU	ASP	SEE REMARK 999	UNP P31696
C	35	SER	ALA	SEE REMARK 999	UNP P31696

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Chain	Residue	Modelled	Actual	Comment	Reference
C	36	ASN	LEU	SEE REMARK 999	UNP P31696
C	37	GLU	ASP	SEE REMARK 999	UNP P31696
C	38	ILE	TYR	SEE REMARK 999	UNP P31696
C	42	-	PRO	SEE REMARK 999	UNP P31696
C	43	-	SER	SEE REMARK 999	UNP P31696
C	44	-	GLU	SEE REMARK 999	UNP P31696
D	33	HIS	PRO	SEE REMARK 999	UNP P31696
D	34	LEU	ASP	SEE REMARK 999	UNP P31696
D	35	SER	ALA	SEE REMARK 999	UNP P31696
D	36	ASN	LEU	SEE REMARK 999	UNP P31696
D	37	GLU	ASP	SEE REMARK 999	UNP P31696
D	38	ILE	TYR	SEE REMARK 999	UNP P31696
D	42	-	PRO	SEE REMARK 999	UNP P31696
D	43	-	SER	SEE REMARK 999	UNP P31696
D	44	-	GLU	SEE REMARK 999	UNP P31696

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	B	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0
2	D	1	Total Ca 1 1	0	0

- Molecule 3 is water.

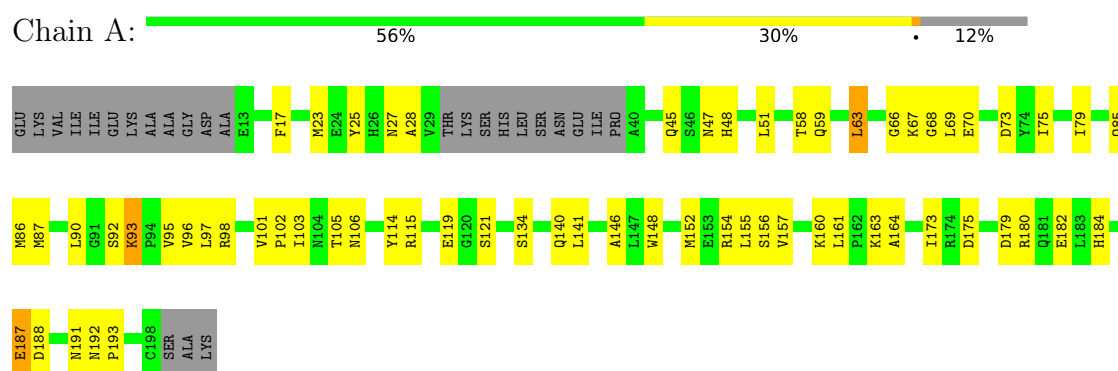
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	155	Total O 155 155	0	0
3	B	150	Total O 150 150	0	0
3	C	143	Total O 143 143	0	0
3	D	121	Total O 121 121	0	0

3 Residue-property plots [i](#)

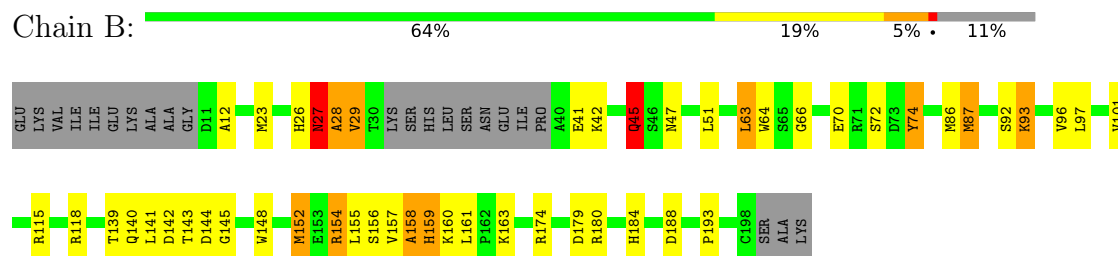
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS was not executed.

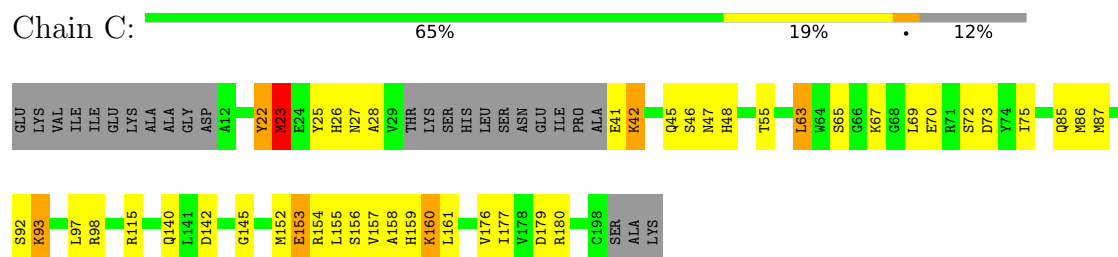
• Molecule 1: Agrin



• Molecule 1: Agrin

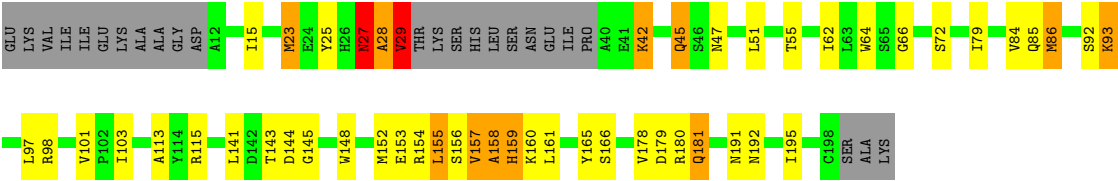


• Molecule 1: Agrin



• Molecule 1: Agrin





4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	76.85Å 56.56Å 84.59Å 90.00° 99.75° 90.00°	Depositor
Resolution (Å)	20.00 – 2.35	Depositor
% Data completeness (in resolution range)	100.0 (20.00-2.35)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.218 , 0.260	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6058	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.84	1/1392 (0.1%)	0.99	1/1888 (0.1%)
1	B	0.96	1/1412 (0.1%)	1.02	5/1916 (0.3%)
1	C	1.00	2/1392 (0.1%)	1.04	5/1888 (0.3%)
1	D	1.02	3/1397 (0.2%)	1.10	5/1895 (0.3%)
All	All	0.96	7/5593 (0.1%)	1.04	16/7587 (0.2%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	87	MET	SD-CE	-10.80	1.52	1.79
1	C	87	MET	SD-CE	-9.72	1.55	1.79
1	D	64	TRP	C-O	-6.88	1.16	1.24
1	C	23	MET	SD-CE	-6.52	1.63	1.79
1	D	86	MET	SD-CE	-5.62	1.65	1.79

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	27	ASN	N-CA-C	8.43	128.76	110.80
1	B	101	VAL	N-CA-C	6.68	114.50	107.76
1	D	29	VAL	N-CA-CB	-5.74	101.74	111.50
1	D	72	SER	N-CA-C	5.52	118.29	110.50
1	C	156	SER	N-CA-C	-5.47	103.38	111.81

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	1365	0	1349	67	0
1	B	1385	0	1365	49	0
1	C	1365	0	1349	58	0
1	D	1370	0	1354	63	0
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
3	A	155	0	0	14	0
3	B	150	0	0	9	0
3	C	143	0	0	13	0
3	D	121	0	0	4	0
All	All	6058	0	5417	236	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 22.

The worst 5 of 236 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:D:29:VAL:CG1	1:D:181:GLN:HB3	1.62	1.28
1:D:29:VAL:HG22	1:D:181:GLN:CG	1.64	1.26
1:D:29:VAL:HG13	1:D:181:GLN:CB	1.79	1.12
1:D:27:ASN:OD1	1:D:145:GLY:HA3	1.58	1.01
1:D:29:VAL:HG22	1:D:181:GLN:HG2	1.00	1.00

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	172/201 (86%)	157 (91%)	12 (7%)	3 (2%)	7	6
1	B	175/201 (87%)	158 (90%)	11 (6%)	6 (3%)	3	1
1	C	172/201 (86%)	160 (93%)	10 (6%)	2 (1%)	10	9
1	D	173/201 (86%)	159 (92%)	8 (5%)	6 (4%)	3	1
All	All	692/804 (86%)	634 (92%)	41 (6%)	17 (2%)	4	3

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	28	ALA
1	B	29	VAL
1	B	159	HIS
1	D	27	ASN
1	D	28	ALA

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	146/166 (88%)	142 (97%)	4 (3%)	39	52
1	B	148/166 (89%)	142 (96%)	6 (4%)	27	36
1	C	146/166 (88%)	141 (97%)	5 (3%)	32	43
1	D	146/166 (88%)	137 (94%)	9 (6%)	16	19
All	All	586/664 (88%)	562 (96%)	24 (4%)	27	36

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	160	LYS
1	D	42	LYS
1	D	29	VAL

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Mol	Chain	Res	Type
1	D	45	GLN
1	B	45	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	45	GLN
1	D	47	ASN
1	D	181	GLN
1	B	85	GLN
1	B	59	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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.