



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 02:04 pm GMT

PDB ID : 2FF3
Title : Crystal structure of Gelsolin domain 1:N-wasp V2 motif hybrid in complex with actin
Authors : Xue, B.; Aguda, A.H.; Robinson, R.C.
Deposited on : 2005-12-19
Resolution : 2.00 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

<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
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

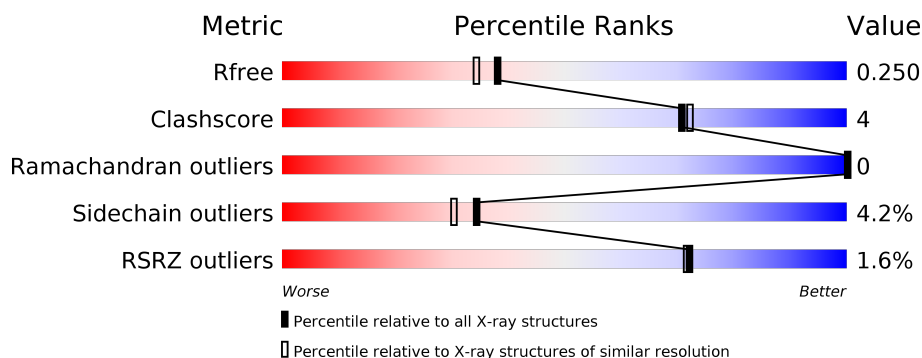
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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 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.

Mol	Chain	Length	Quality of chain
1	A	150	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 6%, green 75%, grey 17%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 75% 6% 17% </div> </div>
2	C	15	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 7%, orange 20%, green 80%, grey 80%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 7% 20% 80% </div> </div>
3	B	375	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 13%, green 82%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 82% 13% 5% </div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4192 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 Gelsolin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	125	Total	C	N	O	S	0	0	0
			1000	647	168	184	1			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	MET	-	EXPRESSION TAG	UNP P06396
A	4	LYS	-	EXPRESSION TAG	UNP P06396
A	5	HIS	-	EXPRESSION TAG	UNP P06396
A	6	HIS	-	EXPRESSION TAG	UNP P06396
A	7	HIS	-	EXPRESSION TAG	UNP P06396
A	8	HIS	-	EXPRESSION TAG	UNP P06396
A	9	HIS	-	EXPRESSION TAG	UNP P06396
A	10	HIS	-	EXPRESSION TAG	UNP P06396
A	11	HIS	-	EXPRESSION TAG	UNP P06396
A	12	HIS	-	EXPRESSION TAG	UNP P06396
A	13	GLY	-	EXPRESSION TAG	UNP P06396
A	14	GLY	-	EXPRESSION TAG	UNP P06396
A	15	LEU	-	EXPRESSION TAG	UNP P06396
A	16	VAL	-	EXPRESSION TAG	UNP P06396
A	17	PRO	-	EXPRESSION TAG	UNP P06396
A	18	ARG	-	EXPRESSION TAG	UNP P06396
A	19	GLY	-	EXPRESSION TAG	UNP P06396
A	20	SER	-	EXPRESSION TAG	UNP P06396
A	21	HIS	-	EXPRESSION TAG	UNP P06396
A	22	GLY	-	EXPRESSION TAG	UNP P06396
A	23	GLY	-	EXPRESSION TAG	UNP P06396
A	24	SER	-	EXPRESSION TAG	UNP P06396

- Molecule 2 is a protein called Neural Wiskott-Aldrich syndrome protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			17	9	3	5			

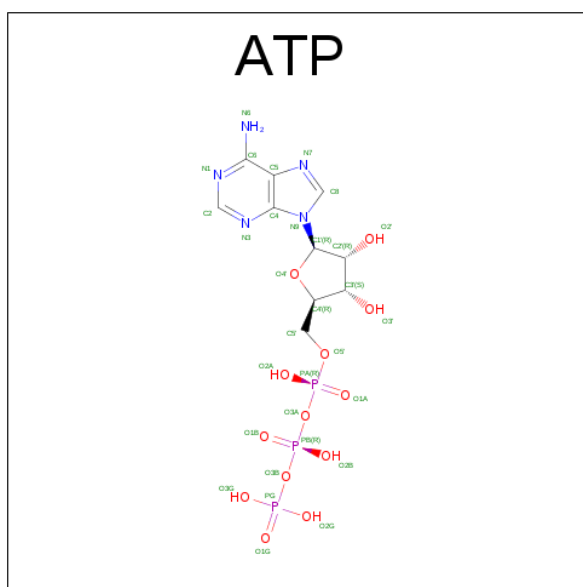
- Molecule 3 is a protein called Actin, alpha skeletal muscle.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	358	Total	C	N	O	S	0	0	0
			2802	1778	468	537	19			

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

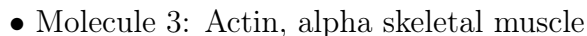
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Ca	0	0
			1	1		
4	A	2	Total	Ca	0	0
			2	2		

- Molecule 5 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	107	Total 107	O 107	0	0
6	B	230	Total 230	O 230	0	0
6	C	2	Total 2	O 2	0	0

- Molecule 1: Gelsolin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.00Å 69.35Å 179.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.88 – 2.00 89.93 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.0 (54.88-2.00) 97.0 (89.93-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.67 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.210 , 0.250 0.211 , 0.250	Depositor DCC
R_{free} test set	2419 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	22.4	Xtriage
Anisotropy	0.273	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4192	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.07% 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: CA, ATP

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	0.40	0/1027	0.68	2/1388 (0.1%)
2	C	0.29	0/16	1.20	0/20
3	B	0.36	0/2863	0.70	13/3880 (0.3%)
All	All	0.37	0/3906	0.70	15/5288 (0.3%)

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	154	ASP	CB-CG-OD2	6.97	124.57	118.30
3	B	244	ASP	CB-CG-OD2	6.68	124.31	118.30
3	B	292	ASP	CB-CG-OD2	6.32	123.99	118.30
3	B	288	ASP	CB-CG-OD2	6.22	123.89	118.30
3	B	311	ASP	CB-CG-OD2	5.98	123.69	118.30
1	A	66	ASP	CB-CG-OD2	5.96	123.67	118.30
3	B	184	ASP	CB-CG-OD2	5.59	123.33	118.30
3	B	11	ASP	CB-CG-OD2	5.50	123.25	118.30
3	B	179	ASP	CB-CG-OD2	5.44	123.20	118.30
3	B	51	ASP	CB-CG-OD2	5.38	123.14	118.30
3	B	56	ASP	CB-CG-OD2	5.36	123.13	118.30
3	B	211	ASP	CB-CG-OD2	5.35	123.11	118.30
3	B	363	ASP	CB-CG-OD2	5.33	123.10	118.30
3	B	81	ASP	CB-CG-OD2	5.29	123.06	118.30
1	A	84	ASP	CB-CG-OD2	5.06	122.86	118.30

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	1000	0	963	10	0
2	C	17	0	11	0	0
3	B	2802	0	2769	21	0
4	A	2	0	0	0	0
4	B	1	0	0	0	0
5	B	31	0	12	0	0
6	A	107	0	0	3	0
6	B	230	0	0	1	0
6	C	2	0	0	0	0
All	All	4192	0	3755	31	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 4.

All (31) 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:78:ASN:HB3	6:A:797:HOH:O	1.62	0.97
3:B:220:ALA:HB1	3:B:226:GLU:HG3	1.68	0.74
3:B:299:MET:CE	3:B:313:MET:HG3	2.18	0.73
1:A:76:LEU:HB3	1:A:78:ASN:ND2	2.10	0.66
3:B:372:ARG:NH2	6:B:1121:HOH:O	2.32	0.62
3:B:313:MET:HE3	3:B:317:ILE:HD11	1.82	0.61
1:A:29:HIS:HD2	1:A:31:GLU:H	1.49	0.59
3:B:313:MET:CE	3:B:317:ILE:HD11	2.34	0.57
1:A:138:LEU:HD21	1:A:140:TYR:CE2	2.39	0.57
3:B:117:GLU:OE2	3:B:371:HIS:HE1	1.89	0.56
3:B:220:ALA:CB	3:B:226:GLU:HG3	2.36	0.55
3:B:335:ARG:HA	3:B:338:SER:OG	2.06	0.54
3:B:186:THR:HG22	3:B:190:MET:CE	2.37	0.54
1:A:129:THR:HG23	6:A:715:HOH:O	2.08	0.53
3:B:178:LEU:HD22	3:B:180:LEU:HB3	1.90	0.52
3:B:124:PHE:CE2	3:B:132:MET:HG2	2.46	0.50
1:A:29:HIS:CD2	1:A:31:GLU:H	2.29	0.50
3:B:299:MET:HE1	3:B:313:MET:HG3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:313:MET:HE3	3:B:317:ILE:CD1	2.43	0.49
3:B:190:MET:HE1	3:B:206:ARG:HA	1.96	0.47
3:B:186:THR:HG22	3:B:190:MET:HE3	1.97	0.46
1:A:78:ASN:HD22	1:A:78:ASN:C	2.19	0.46
3:B:190:MET:HG3	3:B:209:VAL:HG21	1.97	0.45
1:A:78:ASN:ND2	1:A:80:ASN:H	2.16	0.44
3:B:272:ALA:HB1	3:B:276:GLU:HB3	2.00	0.43
3:B:37:ARG:HH21	3:B:84:LYS:HE2	1.83	0.43
3:B:172:PRO:HA	3:B:175:ILE:HD12	2.00	0.43
3:B:106:THR:HB	3:B:137:GLN:HG3	2.01	0.43
1:A:80:ASN:HB3	6:A:703:HOH:O	2.19	0.42
1:A:78:ASN:HD21	1:A:80:ASN:HB2	1.86	0.41
3:B:218:TYR:O	3:B:255:PHE:HA	2.21	0.40

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	123/150 (82%)	121 (98%)	2 (2%)	0	100	100
2	C	1/15 (7%)	0	1 (100%)	0	100	100
3	B	354/375 (94%)	349 (99%)	5 (1%)	0	100	100
All	All	478/540 (88%)	470 (98%)	8 (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	103/123 (84%)	98 (95%)	5 (5%)	29	24
2	C	1/12 (8%)	1 (100%)	0	100	100
3	B	304/318 (96%)	292 (96%)	12 (4%)	37	34
All	All	408/453 (90%)	391 (96%)	17 (4%)	34	30

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	LEU
1	A	76	LEU
1	A	78	ASN
1	A	138	LEU
1	A	139	LYS
3	B	56	ASP
3	B	65	LEU
3	B	66	THR
3	B	100	GLU
3	B	132	MET
3	B	177	ARG
3	B	178	LEU
3	B	193	LEU
3	B	216	LEU
3	B	236	LEU
3	B	293	LEU
3	B	353	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	HIS
1	A	78	ASN
1	A	118	GLN
3	B	87	HIS
3	B	92	ASN
3	B	225	ASN
3	B	280	ASN
3	B	371	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

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$
5	ATP	B	900	4	27,33,33	1.07	2 (7%)	25,52,52	1.67	2 (8%)

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
5	ATP	B	900	4	-	0/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	900	ATP	PG-O3B	2.08	1.63	1.60
5	B	900	ATP	C5-C4	3.01	1.47	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
5	B	900	ATP	N3-C2-N1	-6.56	123.14	128.86
5	B	900	ATP	C4-C5-N7	-2.62	106.88	109.41

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](#)

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	125/150 (83%)	-0.07	2 (1%) 72 71	10, 21, 30, 34	0
2	C	3/15 (20%)	1.62	1 (33%) 0 1	34, 34, 39, 40	0
3	B	358/375 (95%)	0.09	5 (1%) 75 75	10, 23, 42, 47	0
All	All	486/540 (90%)	0.06	8 (1%) 72 71	10, 23, 41, 47	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	68	TYR	3.1
3	B	51	ASP	3.1
2	C	155	GLY	2.9
3	B	250	ILE	2.6
3	B	231	ALA	2.4
3	B	270	GLU	2.3
1	A	80	ASN	2.1
3	B	62	ARG	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [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. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
4	CA	A	702	1/1	1.00	0.12	1.30	15,15,15,15	0
5	ATP	B	900	31/31	0.98	0.12	-0.16	12,18,19,19	0
4	CA	A	701	1/1	0.99	0.12	-0.24	14,14,14,14	0
4	CA	B	700	1/1	0.99	0.13	-	15,15,15,15	0

6.5 Other polymers

There are no such residues in this entry.