



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 2FH2 / pdb_00002fh2
Title : C-terminal half of gelsolin soaked in EGTA at pH 4.5
Authors : Chumnarnsilpa, S.; Loonchanta, A.; Xue, B.; Choe, H.; Urosev, D.; Wang, H.;
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Deposited on : 2005-12-23
Resolution : 2.50 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

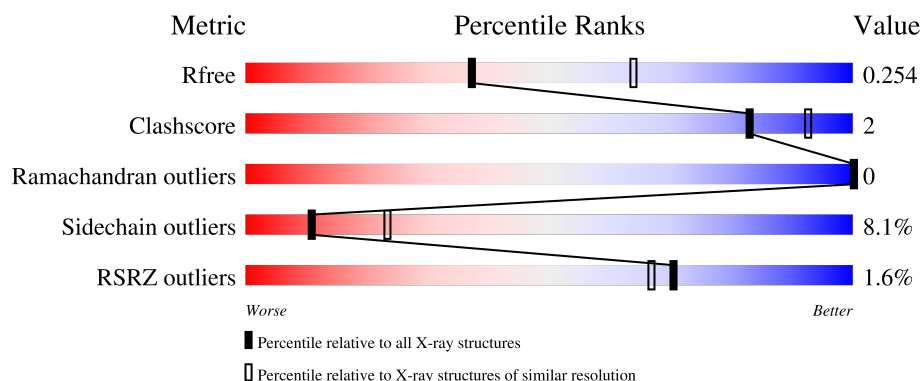
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	344	% 81% 10% • 7%
1	B	344	2% 82% 11% • 6%
1	C	344	% 87% 6% • 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7835 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	321	Total	C	N	O	S	0	0	0
			2485	1571	425	482	7			
1	B	324	Total	C	N	O	S	0	0	0
			2515	1587	433	489	6			
1	C	322	Total	C	N	O	S	0	0	0
			2495	1576	427	486	6			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Ca	0	0
			3	3		
2	B	3	Total	Ca	0	0
			3	3		
2	C	2	Total	Ca	0	0
			2	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	134	Total	O	0	0
			134	134		
3	B	125	Total	O	0	0
			125	125		
3	C	73	Total	O	0	0
			73	73		

- 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	85.29Å 90.93Å 157.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.92 – 2.50 19.92 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.5 (19.92-2.50) 99.2 (19.92-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.75 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.204 , 0.255 0.208 , 0.254	Depositor DCC
R_{free} test set	2165 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	39.2	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 22.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7835	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.74	2/2542 (0.1%)	0.86	0/3447
1	B	0.72	0/2573	0.88	0/3493
1	C	0.68	0/2553	0.86	1/3467 (0.0%)
All	All	0.71	2/7668 (0.0%)	0.87	1/10407 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	517	MET	SD-CE	-6.47	1.63	1.79
1	A	662	MET	SD-CE	-5.37	1.66	1.79

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	639	PRO	O-C-N	5.66	123.81	121.15

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	2485	0	2405	14	0
1	B	2515	0	2437	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2495	0	2416	8	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	2	0	0	0	0
3	A	134	0	0	2	0
3	B	125	0	0	2	0
3	C	73	0	0	0	0
All	All	7835	0	7258	35	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 2.

All (35) 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:B:647:ASN:HD22	1:B:647:ASN:C	1.98	0.71
1:B:465:ASN:ND2	1:B:479:SER:OG	2.32	0.63
1:A:715:THR:N	3:A:234:HOH:O	2.32	0.61
1:A:647:ASN:C	1:A:647:ASN:HD22	2.12	0.57
1:B:647:ASN:ND2	3:B:5072:HOH:O	2.38	0.57
1:A:662:MET:CE	1:A:734:LEU:HB3	2.37	0.55
1:B:493:THR:N	1:B:494:PRO:CD	2.72	0.52
1:B:647:ASN:C	1:B:647:ASN:ND2	2.68	0.52
1:A:483:THR:HG22	1:A:496:GLN:HE22	1.76	0.50
1:B:662:MET:HB3	1:B:664:GLU:OE1	2.12	0.50
1:C:647:ASN:C	1:C:647:ASN:HD22	2.20	0.50
1:A:504:GLU:CD	1:A:517:MET:HE1	2.38	0.49
1:B:507:HIS:HA	3:B:108:HOH:O	2.13	0.49
1:B:610:GLU:HG3	1:B:615:TRP:CZ2	2.48	0.48
1:C:571:THR:HG23	1:C:572:PRO:HD2	1.96	0.48
1:B:564:ASN:HD21	1:B:635:MET:HE1	1.79	0.47
1:A:640:PRO:HG2	1:A:732:TRP:CZ3	2.51	0.46
1:C:571:THR:CG2	1:C:572:PRO:HD2	2.45	0.46
1:A:539:PHE:CE2	1:A:553:GLU:HB2	2.51	0.45
1:A:493:THR:N	1:A:494:PRO:CD	2.79	0.45
1:B:571:THR:HB	1:B:572:PRO:CD	2.46	0.45
1:B:436:ALA:HB2	1:C:527:GLU:HB3	1.99	0.45
1:C:664:GLU:HG2	1:C:740:TYR:OH	2.17	0.44
1:B:664:GLU:CD	1:B:664:GLU:H	2.26	0.44
1:C:507:HIS:O	1:C:511:LEU:HD13	2.19	0.43
1:B:640:PRO:HG3	1:B:732:TRP:CE3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:473:GLN:HB3	3:A:140:HOH:O	2.19	0.42
1:A:451:TYR:CE2	1:A:453:TYR:HB3	2.53	0.42
1:A:647:ASN:C	1:A:647:ASN:ND2	2.75	0.42
1:C:465:ASN:ND2	1:C:483:THR:OG1	2.37	0.42
1:A:512:PHE:O	1:A:515:LYS:HB2	2.20	0.41
1:C:493:THR:N	1:C:494:PRO:CD	2.82	0.41
1:A:640:PRO:HG2	1:A:732:TRP:CE3	2.56	0.41
1:B:452:ASN:ND2	1:B:461:GLN:HG2	2.36	0.40
1:A:594:LEU:HD22	1:A:598:LEU:HD22	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	315/344 (92%)	310 (98%)	5 (2%)	0	100	100
1	B	320/344 (93%)	313 (98%)	7 (2%)	0	100	100
1	C	318/344 (92%)	307 (96%)	11 (4%)	0	100	100
All	All	953/1032 (92%)	930 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	257/274 (94%)	233 (91%)	24 (9%)	8	18
1	B	260/274 (95%)	235 (90%)	25 (10%)	8	17
1	C	258/274 (94%)	244 (95%)	14 (5%)	20	41
All	All	775/822 (94%)	712 (92%)	63 (8%)	11	23

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	412	MET
1	A	413	ASP
1	A	419	GLN
1	A	458	ARG
1	A	473	GLN
1	A	527	GLU
1	A	537	ARG
1	A	555	LEU
1	A	569	LEU
1	A	592	GLN
1	A	594	LEU
1	A	598	LEU
1	A	601	GLN
1	A	632	ASP
1	A	634	LYS
1	A	635	MET
1	A	647	ASN
1	A	648	LYS
1	A	651	ARG
1	A	664	GLU
1	A	674	LEU
1	A	686	LYS
1	A	690	GLU
1	A	702	ARG
1	B	425	ILE
1	B	470	GLN
1	B	490	LEU
1	B	498	ARG
1	B	500	VAL
1	B	511	LEU
1	B	521	LYS
1	B	536	THR
1	B	555	LEU
1	B	569	LEU

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Mol	Chain	Res	Type
1	B	570	LYS
1	B	594	LEU
1	B	598	LEU
1	B	599	ARG
1	B	610	GLU
1	B	638	HIS
1	B	647	ASN
1	B	648	LYS
1	B	651	ARG
1	B	662	MET
1	B	674	LEU
1	B	695	GLU
1	B	713	ARG
1	B	721	LYS
1	B	725	GLU
1	C	490	LEU
1	C	527	GLU
1	C	555	LEU
1	C	570	LYS
1	C	592	GLN
1	C	603	VAL
1	C	610	GLU
1	C	634	LYS
1	C	647	ASN
1	C	648	LYS
1	C	664	GLU
1	C	674	LEU
1	C	713	ARG
1	C	714	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	419	GLN
1	A	440	GLN
1	A	452	ASN
1	A	461	GLN
1	A	473	GLN
1	A	496	GLN
1	A	647	ASN
1	B	452	ASN
1	B	465	ASN

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Mol	Chain	Res	Type
1	B	470	GLN
1	B	473	GLN
1	B	485	GLN
1	B	496	GLN
1	B	592	GLN
1	B	647	ASN
1	C	421	GLN
1	C	452	ASN
1	C	465	ASN
1	C	470	GLN
1	C	496	GLN
1	C	507	HIS
1	C	647	ASN
1	C	679	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 8 ligands modelled in this entry, 8 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](#)

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	321/344 (93%)	-0.26	3 (0%) 81 78	26, 35, 52, 81	0
1	B	324/344 (94%)	-0.20	7 (2%) 62 58	24, 36, 57, 76	0
1	C	322/344 (93%)	-0.00	5 (1%) 70 67	31, 43, 58, 73	0
All	All	967/1032 (93%)	-0.15	15 (1%) 70 67	24, 39, 57, 81	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	635	MET	3.5
1	B	635	MET	3.3
1	B	459	GLN	3.1
1	B	454	ARG	3.1
1	B	636	ASP	2.9
1	C	635	MET	2.9
1	C	636	ASP	2.6
1	C	453	TYR	2.6
1	A	691	GLU	2.5
1	B	741	TRP	2.3
1	C	689	GLN	2.3
1	B	453	TYR	2.3
1	B	637	ALA	2.2
1	C	712	ASP	2.1
1	A	638	HIS	2.1

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 oligosaccharides 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. 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($\text{\AA}^2$)	Q<0.9
2	CA	B	2003	1/1	0.96	0.07	35,35,35,35	0
2	CA	B	2001	1/1	0.99	0.02	27,27,27,27	0
2	CA	B	2002	1/1	0.99	0.03	25,25,25,25	0
2	CA	A	1003	1/1	0.99	0.06	26,26,26,26	0
2	CA	C	3001	1/1	0.99	0.04	31,31,31,31	0
2	CA	A	1002	1/1	1.00	0.02	26,26,26,26	0
2	CA	A	1001	1/1	1.00	0.08	27,27,27,27	0
2	CA	C	3002	1/1	1.00	0.08	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.