

Full wwPDB X-ray Structure Validation Report (i)

Aug 9, 2020 – 01:02 PM BST

PDB ID	:	1Y75
Title	:	A new form of catalytically inactive phospholipase A2 with an unusual disul-
		phide bridge Cys 32- Cys 49 reveals recognition for N-acetylglucosmine
Authors	:	Jabeen, T.; Singh, N.; Jasti, J.; Singh, R.K.; Sharma, S.; Perbandt, M.; Betzel,
		C.; Kaur, P.; Srinivasan, A.; Singh, T.P.
Deposited on	:	2004-12-08
$\operatorname{Resolution}$:	2.30 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

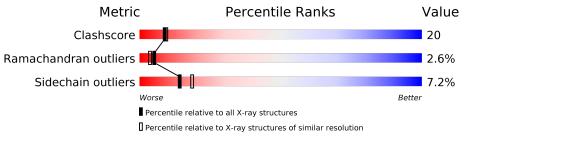
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
Clashscore	141614	$5643 \ (2.30-2.30)$
Ramachandran outliers	138981	5575(2.30-2.30)
Sidechain outliers	138945	5575(2.30-2.30)

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 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain		
1	А	118	70%	24%	6%
2	В	118	68%	28%	••



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2048 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.

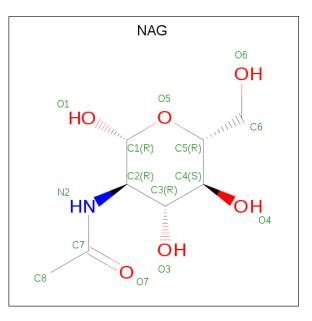
• Molecule 1 is a protein called phospholipase A2 isoform 5.

Mol	Chain	Residues		\mathbf{A}	toms			ZeroOcc	AltConf	Trace
1	Δ	118	Total	С	Ν	Ο	\mathbf{S}	0	0	0
	А	110	904	547	161	179	17			U

• Molecule 2 is a protein called phospholipase A2 isoform 6.

Mol	Chain	Residues		\mathbf{A}^{1}	toms			ZeroOcc	AltConf	Trace
2	В	118	Total 880	C 531	N 153	O 181	${ m S}$ 15	0	0	0

• Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 15	C 8	N 1	O 6	0	0

• Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	2	TotalZn22	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	132	Total O 132 132	0	0
5	В	115	Total O 115 115	0	0

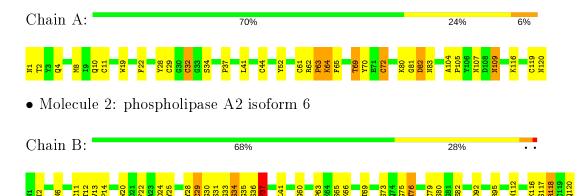


3 Residue-property plots (i)

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: phospholipase A2 isoform 5





4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants	77.66Å 77.66Å 68.42Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.95 - 2.30	Depositor
% Data completeness	99.0 (19.95-2.30)	Depositor
(in resolution range)	55.0 (15.55-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.216 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2048	wwPDB-VP
Average B, all atoms $(Å^2)$	49.0	wwPDB-VP



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: ZN, NAG

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).

Mal	Mol Chain		lengths	Bond angles		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.47	0/924	0.72	1/1250~(0.1%)	
2	В	0.43	0/898	0.66	0/1218	
All	All	0.46	0/1822	0.69	1/2468~(0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	A	63	PRO	CB-CA-C	5.03	124.57	112.00

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	А	904	0	804	42	0
2	В	880	0	783	28	0
3	А	15	0	15	5	0
4	А	2	0	0	0	0
5	А	132	0	0	4	0
5	В	115	0	0	6	0
All	All	2048	0	1602	69	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 20.

All (69) 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:28:TYR:HE2	1:A:37:PRO:HD3	1.27	0.97
2:B:60:GLY:HA2	5:B:222:HOH:O	1.66	0.94
1:A:28:TYR:CE2	1:A:37:PRO:HD3	2.17	0.78
1:A:52:TYR:CE2	1:A:64:LYS:HE2	2.19	0.78
1:A:62:ARG:HG3	1:A:62:ARG:HH11	1.52	0.75
2:B:36:SER:HB2	5:B:190:HOH:O	1.87	0.73
1:A:61:CYS:O	1:A:63:PRO:HD2	1.88	0.73
2:B:73:SER:O	2:B:76:THR:HG23	1.88	0.72
2:B:118:ARG:HB3	2:B:118:ARG:HH11	1.54	0.72
2:B:76:THR:HB	5:B:144:HOH:O	1.91	0.71
1:A:2:THR:CG2	3:A:301:NAG:H82	2.21	0.71
1:A:61:CYS:C	1:A:63:PRO:HD3	2.12	0.69
2:B:25:TYR:CZ	2:B:41:LEU:HD23	2.28	0.69
1:A:52:TYR:HE2	1:A:64:LYS:HE2	1.58	0.68
1:A:10:GLN:HA	5:A:528:HOH:O	1.95	0.66
1:A:61:CYS:O	1:A:63:PRO:CD	2.45	0.65
1:A:52:TYR:HE2	1:A:64:LYS:CE	2.11	0.64
2:B:30:GLY:HA3	5:B:206:HOH:O	1.97	0.63
2:B:79:CYS:HB2	5:B:223:HOH:O	1.99	0.62
1:A:34:SER:O	1:A:119:CYS:HB3	2.02	0.60
2:B:118:ARG:HB3	2:B:118:ARG:NH1	2.15	0.59
1:A:19:TRP:CZ3	3:A:301:NAG:H83	2.38	0.58
1:A:116:LYS:O	1:A:120:ASN:HB3	2.03	0.58
1:A:72:CYS:O	1:A:72:CYS:SG	2.60	0.58
1:A:41:LEU:O	1:A:44:CYS:HB2	2.05	0.57
2:B:69:THR:HG22	2:B:80:SER:HB2	1.86	0.57
1:A:2:THR:HG23	3:A:301:NAG:H82	1.87	0.56
1:A:62:ARG:HG3	1:A:62:ARG:NH1	2.19	0.56
1:A:61:CYS:C	1:A:63:PRO:CD	2.73	0.55
1:A:52:TYR:CD2	1:A:64:LYS:HE2	2.42	0.55
2:B:116:LYS:HG2	2:B:116:LYS:O	2.06	0.54
1:A:107:ASN:OD1	1:A:109:ASN:HB2	2.09	0.52
1:A:81:GLY:C	1:A:83:ASN:H	2.14	0.52
1:A:80:LYS:HB3	1:A:82:ASP:OD1	2.12	0.49
2:B:35:GLY:HA2	2:B:120:GLN:OXT	2.12	0.49
1:A:1:ASN:OD1	1:A:4:GLN:HG3	2.13	0.48
1:A:62:ARG:N	1:A:63:PRO:HD3	2.30	0.47

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Continued from pre Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}~({ m \AA})$	overlap (Å)
1:A:81:GLY:O	1:A:83:ASN:N	2.48	0.47
1:A:69:THR:HB	1:A:80:LYS:HB2	1.96	0.46
2:B:33:GLY:O	2:B:34:SER:CB	2.64	0.46
2:B:69:THR:CG2	2:B:80:SER:HB2	2.44	0.46
2:B:13:VAL:N	2:B:14:PRO:HD3	2.31	0.45
2:B:22:PHE:O	2:B:29:CYS:HB3	2.16	0.45
1:A:52:TYR:HE2	1:A:64:LYS:CD	2.30	0.44
2:B:69:THR:HG22	2:B:80:SER:CB	2.47	0.44
1:A:29:CYS:HA	3:A:301:NAG:H61	1.99	0.44
1:A:62:ARG:N	1:A:63:PRO:CD	2.79	0.44
1:A:104:ALA:HA	1:A:105:PRO:HD3	1.89	0.44
1:A:64:LYS:HD3	1:A:64:LYS:HA	1.72	0.44
1:A:120:ASN:HB2	2:B:20:TRP:CE2	2.53	0.44
2:B:6:ASN:N	2:B:6:ASN:HD22	2.16	0.43
2:B:92:ASP:OD1	2:B:95:ARG:NH1	2.52	0.43
2:B:25:TYR:CE2	2:B:41:LEU:HD23	2.54	0.43
1:A:64:LYS:HD2	5:A:431:HOH:O	2.20	0.42
1:A:109:ASN:HA	1:A:109:ASN:HD22	1.65	0.42
2:B:12:THR:C	2:B:14:PRO:HD3	2.40	0.42
1:A:116:LYS:NZ	5:A:452:HOH:O	2.50	0.42
1:A:52:TYR:CE2	1:A:64:LYS:CE	2.90	0.42
1:A:65:PHE:HB3	5:A:516:HOH:O	2.20	0.42
2:B:25:TYR:CE1	2:B:41:LEU:HD23	2.56	0.41
1:A:8:MET:HE3	1:A:70:TYR:CD2	2.55	0.41
1:A:22:PHE:HE1	1:A:41:LEU:HD21	1.86	0.41
2:B:14:PRO:HD2	5:B:134:HOH:O	2.21	0.41
1:A:32:CYS:SG	3:A:301:NAG:H62	2.62	0.40
2:B:24:ASP:OD2	2:B:112:ASN:HA	2.21	0.40
1:A:69:THR:HG22	1:A:80:LYS:HD2	2.03	0.40
2:B:28:TYR:O	2:B:30:GLY:N	2.55	0.40
2:B:36:SER:O	2:B:37:PRO:C	2.59	0.40
2:B:11:CYS:O	2:B:75:GLY:HA2	2.21	0.40

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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	А	116/118~(98%)	109 (94%)	5(4%)	2(2%)	9 8
2	В	116/118~(98%)	102 (88%)	10 (9%)	4(3%)	3 2
All	All	232/236~(98%)	211 (91%)	15~(6%)	6 (3%)	5 4

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	82	ASP
2	В	34	SER
1	А	32	CYS
2	В	29	CYS
2	В	31	SER
2	В	37	PRO

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	А	98/98~(100%)	93~(95%)	5 (5%)	24 33
2	В	96/96~(100%)	87~(91%)	9 (9%)	8 10
All	All	194/194~(100%)	180~(93%)	14 (7%)	14 18

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	\mathbf{Res}	Type
1	А	11	CYS
1	А	64	LYS
1	А	69	THR
1	А	72	CYS
1	А	109	ASN
2	В	2	ILE

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Mol	Chain	\mathbf{Res}	Type
2	В	37	PRO
2	В	63	PRO
2	В	65	SER
2	В	66	LYS
2	В	76	THR
2	В	82	GLU
2	В	117	SER
2	В	118	ARG

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Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	\mathbf{Res}	Type
1	А	54	GLN
1	А	109	ASN
2	В	6	ASN
2	В	110	ASN
2	В	112	ASN
2	В	120	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 2 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 lengths Bond ang		les	
	туре	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	А	301	-	15, 15, 15	0.43	0	21,21,21	1.29	1 (4%)

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.

\mathbf{M}	ol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3		NAG	А	301	-	-	2/6/26/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	301	NAG	O6-C6-C5	5.20	129.12	111.29

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	301	NAG	C1-C2-N2-C7
3	А	301	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	А	301	NAG	5	0

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.

