

# Full wwPDB X-ray Structure Validation Report (i)

#### Aug 15, 2023 – 04:11 PM EDT

PDB ID : 1SQZ

Title: Design of specific inhibitors of Phopholipase A2: Crystal structure of the com-

plex formed between Group II Phopholipase A2 and a designed peptide Dehy

dro-Ile-Ala-Arg-Ser at 1.2A resolution

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Deposited on : 2004-03-22

Resolution : 1.20 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) 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)

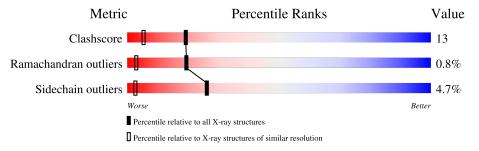
Validation Pipeline (wwPDB-VP) : 2.35

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY\ DIFFRACTION$ 

The reported resolution of this entry is 1.20 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
Clashscore	141614	1286 (1.22-1.18)
Ramachandran outliers	138981	1240 (1.22-1.18)
Sidechain outliers	138945	1239 (1.22-1.18)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain					
1	A	121	81%		16%	•		
2	В	5	60%	20%	20%			



## 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 1300 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.

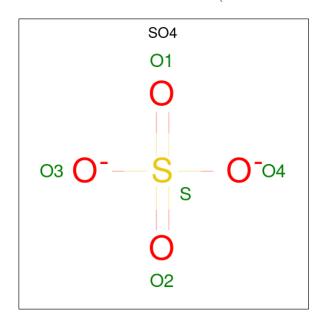
• Molecule 1 is a protein called Phospholipase A2.

$\mathbf{Mol}$	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	121	Total 975	C 607	N 167	O 185	S 16	0	4	0

• Molecule 2 is a protein called synthetic peptide.

Mol	Chain	Residues	A	Atoms		ZeroOcc	AltConf	Trace	
2	В	5	Total 40	C 26	N 7	O 7	0	0	0

• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0

### • Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	270	Total O 270 270	0	0

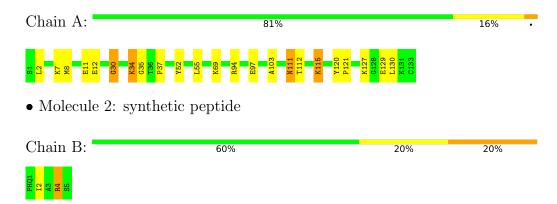


# 3 Residue-property plots (i)

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





# 4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 43	Depositor
Cell constants	52.55Å 52.55Å 47.83Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	17.68 - 1.20	Depositor
% Data completeness	100.0 (17.68-1.20)	Depositor
(in resolution range)	100.0 (17.00 1.20)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
Refinement program	REFMAC 5.0	Depositor
$R, R_{free}$	0.209 , 0.217	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1300	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	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: PHQ, SO4

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		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.54	0/995	0.69	0/1333	
2	В	0.66	0/29	1.26	0/37	
All	All	0.54	0/1024	0.71	0/1370	

There are no bond length outliers.

There are no bond angle outliers.

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	975	0	932	25	0
2	В	40	0	40	5	0
3	A	15	0	0	1	0
4	A	270	0	0	9	0
All	All	1300	0	972	26	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 13.

All (26) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



A + 1	A4 2	Interatomic	Clash
Atom-1	Atom-2	${\rm distance} \ ({\rm \AA})$	$overlap (\AA)$
1:A:2:LEU:HD13	2:B:2:ILE:HG23	1.54	0.89
1:A:2:LEU:CD1	2:B:2:ILE:HG23	2.16	0.76
1:A:8:MET:HE1	4:A:546:HOH:O	1.93	0.68
1:A:115:LYS:HE3	3:A:302:SO4:O3	2.02	0.59
1:A:115:LYS:HG2	4:A:493:HOH:O	2.08	0.54
1:A:2:LEU:C	1:A:2:LEU:HD23	2.30	0.52
1:A:2:LEU:HD21	4:A:462:HOH:O	2.09	0.52
1:A:97:GLU:HG2	4:A:381:HOH:O	2.09	0.52
1:A:127:LYS:HG2	4:A:523:HOH:O	2.08	0.52
1:A:34:LYS:CG	4:A:438:HOH:O	2.58	0.51
1:A:12:GLU:HG3	1:A:103:ALA:HB1	1.92	0.50
1:A:34:LYS:HG3	4:A:438:HOH:O	2.11	0.50
1:A:111:ASN:N	1:A:111:ASN:HD22	2.11	0.49
1:A:7:LYS:O	1:A:11:GLU:HG3	2.13	0.49
2:B:2:ILE:HD12	2:B:2:ILE:N	2.29	0.47
1:A:37:PRO:HD3	1:A:130:LEU:HD12	1.96	0.46
1:A:30:GLY:HA2	2:B:4:ARG:O	2.15	0.45
1:A:69:LYS:HD3	1:A:69:LYS:HA	1.72	0.45
1:A:2:LEU:HD13	2:B:2:ILE:CG2	2.36	0.45
1:A:35:GLY:HA2	1:A:127:LYS:O	2.17	0.45
1:A:52:TYR:CE2	1:A:69:LYS:NZ	2.85	0.45
1:A:52:TYR:HE2	1:A:69:LYS:HZ1	1.63	0.44
1:A:69:LYS:HD3	4:A:567:HOH:O	2.18	0.43
1:A:55:LEU:HD22	1:A:94[B]:ARG:HD2	2.02	0.42
1:A:120:TYR:HA	1:A:121:PRO:HD3	1.95	0.41
1:A:112:THR:HG23	4:A:315:HOH:O	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	123/121 (102%)	117 (95%)	5 (4%)	1 (1%)	19 3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
2	В	2/5~(40%)	1 (50%)	1 (50%)	0	100	100
All	All	125/126~(99%)	118 (94%)	6 (5%)	1 (1%)	19	3

#### All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	30	GLY

#### 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	108/104 (104%)	104 (96%)	4 (4%)	34 4		
2	В	3/3 (100%)	2 (67%)	1 (33%)	0 0		
All	All	111/107 (104%)	106 (96%)	5 (4%)	26 3		

#### All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	LYS
1	A	111	ASN
1	A	115	LYS
1	A	129	GLU
2	В	4	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	ASN
1	A	111	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 monosaccharides in this entry.

### 5.6 Ligand geometry (i)

3 ligands are modelled in this entry.

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			
MIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	SO4	A	302	-	4,4,4	0.18	0	6,6,6	0.16	0
3	SO4	A	301	-	4,4,4	0.14	0	6,6,6	0.20	0
3	SO4	A	303	-	4,4,4	0.10	0	6,6,6	0.24	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	302	SO4	1	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.

