



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 13, 2024 – 07:17 AM EDT

PDB ID : 1P7O
Title : Crystal structure of phospholipase A2 (MIPLA4) from Micropechis ikaheka
Authors : Lok, S.M.; Swaminathan, K.
Deposited on : 2003-05-05
Resolution : 2.30 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	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

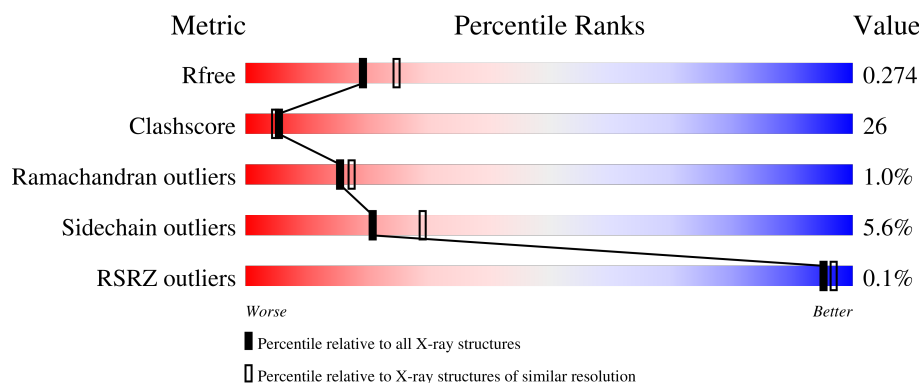
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (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 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	124	<div> <div>55%</div> <div>42%</div> <div>.</div> </div>
1	B	124	<div> <div>%</div> <div>71%</div> <div>25%</div> <div>.</div> </div>
1	C	124	<div> <div>69%</div> <div>26%</div> <div>5%</div> </div>
1	D	124	<div> <div>71%</div> <div>24%</div> <div>5%</div> </div>
1	E	124	<div> <div>64%</div> <div>34%</div> <div>.</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	124	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: green (59%), yellow (36%), and orange (5%). The percentages are labeled below the bar.

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6342 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	124	Total	C	N	O	S	0	0	0
			974	603	168	187	16			
1	B	124	Total	C	N	O	S	0	0	0
			974	603	168	187	16			
1	C	124	Total	C	N	O	S	0	0	0
			974	603	168	187	16			
1	D	124	Total	C	N	O	S	0	0	0
			974	603	168	187	16			
1	E	124	Total	C	N	O	S	0	0	0
			974	603	168	187	16			
1	F	124	Total	C	N	O	S	0	0	0
			974	603	168	187	16			

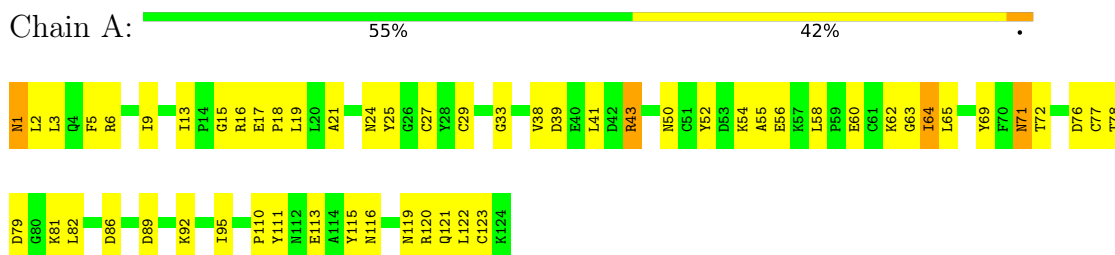
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	84	Total	O	0	0
			84	84		
2	B	84	Total	O	0	0
			84	84		
2	C	85	Total	O	0	0
			85	85		
2	D	78	Total	O	0	0
			78	78		
2	E	88	Total	O	0	0
			88	88		
2	F	79	Total	O	0	0
			79	79		

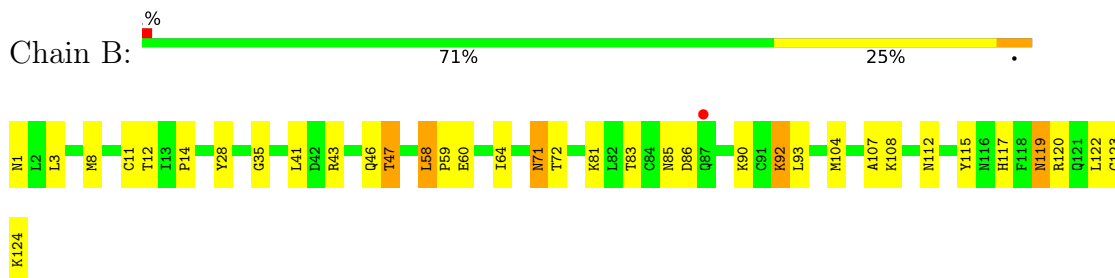
3 Residue-property plots

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

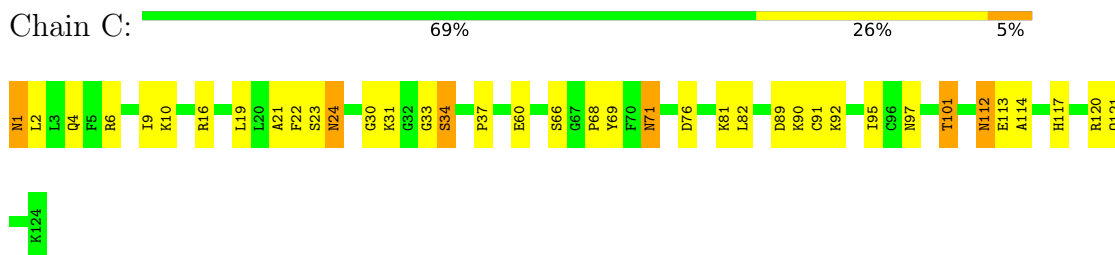
• Molecule 1: PHOSPHOLIPASE A2



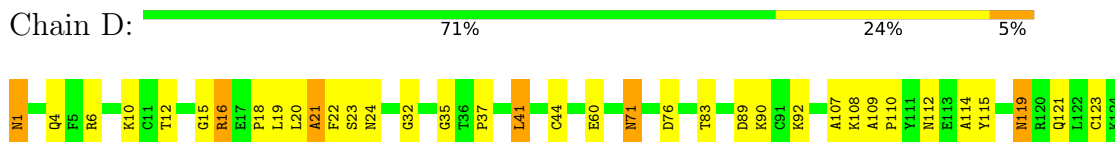
• Molecule 1: PHOSPHOLIPASE A2



• Molecule 1: PHOSPHOLIPASE A2



• Molecule 1: PHOSPHOLIPASE A2



• Molecule 1: PHOSPHOLIPASE A2

N1	L2
L3	F118
O4	N119
F5	R120
R6	Q121
N7	L122
H8	C123
I9	K124
K10	
A16	
E17	
A21	
K31	
G32	
G35	
D39	
E40	
L41	
D42	
R43	
N50	
D53	
K57	
L58	
P59	
E60	
G67	
P68	
N71	
K81	
M85	
D86	
O87	
M88	
D89	
K90	
L93	
F94	
I95	
R100	
V111	
N112	
E113	
F114	

F94	F95	C96	N97	K108	M112	E113	A114	Y115	M116	H117	F118	M119	R120	Q121	L122	C123	K124																																						
N1	L2	L3	O4	F5	R6		I9	K10	P18	L19	S23	G30	K31	G32		T36	D39	F40	L41	D42	R43	N50		D53		E56	K57		E60	G61	K62	G63	I64	L65		M71	T72		D76	C77	T78		K81	L82	T83	C84			Q87	A88	D89	K90	C91	K92	L93

4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, α , β , γ	88.04Å 88.04Å 262.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	7.99 – 2.30 19.79 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.4 (7.99-2.30) 87.6 (19.79-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.58 (at 2.01Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.220 , 0.274 0.220 , 0.274	Depositor DCC
R_{free} test set	5389 reflections (9.15%)	wwPDB-VP
Wilson B-factor (Å ²)	32.6	Xtriage
Anisotropy	0.186	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 42.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.489 for -h,k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6342	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% 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](#)

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	0.38	0/995	0.63	0/1339
1	B	0.38	0/995	0.72	4/1339 (0.3%)
1	C	0.38	0/995	0.62	0/1339
1	D	0.36	0/995	0.61	0/1339
1	E	0.39	0/995	0.71	2/1339 (0.1%)
1	F	0.39	0/995	0.59	0/1339
All	All	0.38	0/5970	0.65	6/8034 (0.1%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	92	LYS	CA-CB-CG	7.57	130.06	113.40
1	E	32	GLY	N-CA-C	-6.46	96.96	113.10
1	B	92	LYS	N-CA-CB	-5.96	99.87	110.60
1	B	92	LYS	CB-CA-C	5.72	121.83	110.40
1	B	92	LYS	CB-CG-CD	-5.61	97.02	111.60

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	974	0	911	63	0
1	B	974	0	911	45	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	974	0	911	43	0
1	D	974	0	911	46	0
1	E	974	0	911	48	0
1	F	974	0	911	59	0
2	A	84	0	0	27	0
2	B	84	0	0	13	0
2	C	85	0	0	10	0
2	D	78	0	0	7	0
2	E	88	0	0	18	0
2	F	79	0	0	19	0
All	All	6342	0	5466	294	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 26.

The worst 5 of 294 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:64:ILE:HD12	1:A:64:ILE:H	1.12	1.09
1:F:71:ASN:HD21	1:F:92:LYS:HE3	1.22	1.03
1:E:112:ASN:HB2	2:E:212:HOH:O	1.62	0.98
1:A:13:ILE:HG22	2:A:146:HOH:O	1.65	0.97
1:D:112:ASN:HD21	1:D:114:ALA:HB3	1.29	0.97

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	122/124 (98%)	115 (94%)	7 (6%)	0	100	100
1	B	122/124 (98%)	116 (95%)	6 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	122/124 (98%)	114 (93%)	7 (6%)	1 (1%)	19	23
1	D	122/124 (98%)	112 (92%)	7 (6%)	3 (2%)	5	4
1	E	122/124 (98%)	118 (97%)	3 (2%)	1 (1%)	19	23
1	F	122/124 (98%)	117 (96%)	3 (2%)	2 (2%)	9	9
All	All	732/744 (98%)	692 (94%)	33 (4%)	7 (1%)	15	17

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	34	SER
1	F	32	GLY
1	D	16	ARG
1	D	21	ALA
1	D	32	GLY

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	108/108 (100%)	100 (93%)	8 (7%)	13	17
1	B	108/108 (100%)	102 (94%)	6 (6%)	21	29
1	C	108/108 (100%)	103 (95%)	5 (5%)	27	38
1	D	108/108 (100%)	103 (95%)	5 (5%)	27	38
1	E	108/108 (100%)	104 (96%)	4 (4%)	34	48
1	F	108/108 (100%)	100 (93%)	8 (7%)	13	17
All	All	648/648 (100%)	612 (94%)	36 (6%)	21	29

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	1	ASN
1	F	119	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	36	THR
1	F	71	ASN
1	B	112	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	71	ASN
1	E	1	ASN
1	F	119	ASN
1	D	119	ASN
1	E	50	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](#)

There are no ligands in this entry.

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	124/124 (100%)	-0.14	0 100 100	26, 39, 53, 66	0
1	B	124/124 (100%)	-0.20	1 (0%) 86 89	24, 36, 53, 65	0
1	C	124/124 (100%)	-0.21	0 100 100	23, 35, 48, 61	0
1	D	124/124 (100%)	-0.24	0 100 100	22, 35, 49, 59	0
1	E	124/124 (100%)	-0.17	0 100 100	24, 36, 55, 66	0
1	F	124/124 (100%)	-0.22	0 100 100	27, 39, 53, 61	0
All	All	744/744 (100%)	-0.20	1 (0%) 95 97	22, 37, 53, 66	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	87	GLN	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 monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.