



# wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 01:44 PM GMT

PDB ID : 1LPB  
Title : THE 2.46 ANGSTROMS RESOLUTION STRUCTURE OF THE PANCRE-  
ATIC LIPASE COLIPASE COMPLEX INHIBITED BY A C11 ALKYL  
PHOSPHONATE  
Authors : Egloff, M.-P.; Van Tilbeurgh, H.; Cambillau, C.  
Deposited on : 1994-08-19  
Resolution : 2.46 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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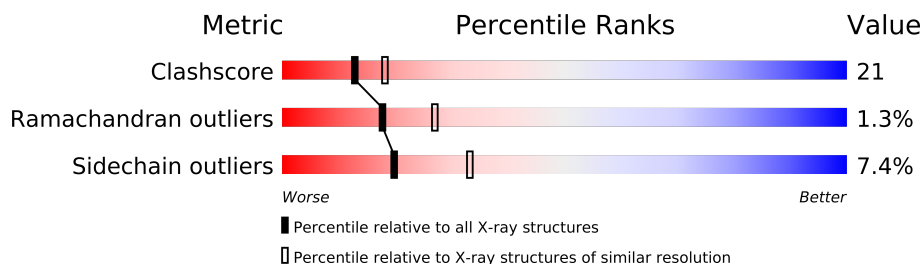
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 21963  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.46 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))
Clashscore	79885	4471 (2.50-2.42)
Ramachandran outliers	78287	4383 (2.50-2.42)
Sidechain outliers	78261	4385 (2.50-2.42)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	95	
2	B	449	

## 2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 6110 atoms, of which 1525 are hydrogens and 0 are deuterium.

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.

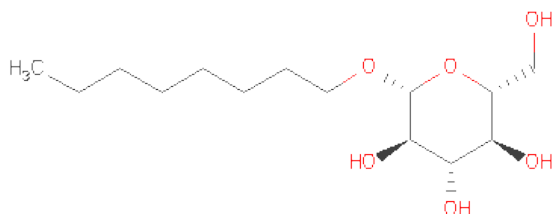
- Molecule 1 is a protein called COLIPASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	85	Total	C	H	N	O	S	0	0	0
			786	389	148	111	128	10			

- Molecule 2 is a protein called LIPASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	449	Total	C	H	N	O	S	0	0	0
			4270	2212	779	600	661	18			

- Molecule 3 is SUGAR (B-OCTYLGLUCOSIDE) (three-letter code: BOG) (formula: C<sub>14</sub>H<sub>28</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	H	O	4	0
			24	14	4	6		
3	A	1	Total	C	H	O	4	0
			24	14	4	6		

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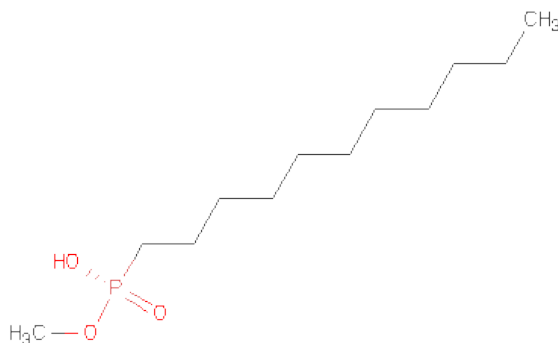
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	4	0
			24	14	4	6		
3	B	1	Total	C	H	O	8	1
			48	28	8	12		
3	B	1	Total	C	H	O	8	1
			48	28	8	12		

- 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		

- Molecule 5 is METHOXYUNDECYLPHOSPHINICACID (three-letter code: MUP) (formula:  $C_{12}H_{27}O_3P$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	O	P	0	1
			30	24	4	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	44	Total	H	O	0	0
			132	88	44		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	241	Total	H	O	0	0
			723	482	241		



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	133.70Å 133.70Å 93.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.46	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-2.46)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.183 , 0.285	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6110	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, MUP, BOG

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	0.54	0/645	0.84	1/869 (0.1%)
2	B	0.58	0/3583	0.84	1/4864 (0.0%)
All	All	0.58	0/4228	0.84	2/5733 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	25	SER	N-CA-C	-5.76	95.46	111.00
2	B	334	ASN	N-CA-CB	5.55	120.59	110.60

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	638	148	462	38	0
2	B	3491	779	2571	135	0
3	A	40	8	43	14	0
3	B	100	20	109	25	0
4	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	30	0	52	3	0
6	A	44	88	0	6	0
6	B	241	482	0	31	0
All	All	4585	1525	3237	176	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 21.

The worst 5 of 176 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:333:SER:HB3	3:B:452[A]:BOG:H3'1	1.30	1.11
2:B:258:PHE:O	3:B:451[B]:BOG:H2	1.51	1.07
1:A:31:ASP:H	3:A:97:BOG:H6'2	1.32	0.93
2:B:307:MET:HE3	2:B:327:LEU:HD21	1.52	0.90
2:B:121:ILE:HD12	2:B:157:ALA:HB2	1.52	0.90

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	83/95 (87%)	78 (94%)	3 (4%)	2 (2%)	9	12
2	B	447/449 (100%)	417 (93%)	25 (6%)	5 (1%)	21	32
All	All	530/544 (97%)	495 (93%)	28 (5%)	7 (1%)	18	27

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	78	ILE
1	A	8	ILE
2	B	248	ILE
2	B	334	ASN
1	A	7	ILE

### 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	74/83 (89%)	66 (89%)	8 (11%)	9	15
2	B	383/383 (100%)	357 (93%)	26 (7%)	22	37
All	All	457/466 (98%)	423 (93%)	34 (7%)	20	33

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	132	VAL
2	B	190	ARG
2	B	436	GLU
2	B	153	LEU
1	A	89	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	151	HIS
2	B	425	ASN
2	B	289	ASN
2	B	88	ASN
2	B	244	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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$
3	BOG	A	96	-	20,20,20	0.83	1 (5%)	25,25,25	1.33	3 (12%)
3	BOG	A	97	-	20,20,20	0.83	1 (5%)	25,25,25	1.90	6 (24%)
3	BOG	B	450	-	20,20,20	0.69	0	25,25,25	1.54	6 (24%)
3	BOG	B	451[A]	-	20,20,20	0.91	1 (5%)	25,25,25	1.80	7 (28%)
3	BOG	B	451[B]	-	20,20,20	1.33	3 (15%)	25,25,25	3.11	7 (28%)
3	BOG	B	452[A]	-	20,20,20	1.04	1 (5%)	25,25,25	2.43	9 (36%)
3	BOG	B	452[B]	-	20,20,20	0.58	0	25,25,25	1.70	3 (12%)
5	MUP	B	901[A]	2	13,14,15	43.91	2 (15%)	11,14,17	1.25	1 (9%)
5	MUP	B	901[B]	2	13,14,15	46.76	1 (7%)	11,14,17	1.46	2 (18%)

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
3	BOG	A	96	-	-	0/11/31/31	0/1/1/1
3	BOG	A	97	-	-	0/11/31/31	0/1/1/1
3	BOG	B	450	-	-	0/11/31/31	0/1/1/1
3	BOG	B	451[A]	-	1/1/5/5	0/11/31/31	0/1/1/1
3	BOG	B	451[B]	-	-	0/11/31/31	0/1/1/1
3	BOG	B	452[A]	-	-	0/11/31/31	0/1/1/1
3	BOG	B	452[B]	-	-	1/11/31/31	0/1/1/1
5	MUP	B	901[A]	2	-	0/9/13/15	0/0/0/0
5	MUP	B	901[B]	2	-	0/9/13/15	0/0/0/0

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	901[B]	MUP	P-C1	-168.58	1.64	1.84
5	B	901[A]	MUP	P-C1	-158.28	1.65	1.84
3	B	451[B]	BOG	C4-C5	3.29	1.60	1.53
5	B	901[A]	MUP	P-O2P	3.23	1.67	1.60
3	B	451[B]	BOG	O1-C1	3.18	1.46	1.40

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	451[B]	BOG	O1-C1-C2	8.60	119.13	108.18
3	B	451[B]	BOG	C1'-O1-C1	8.18	128.69	113.96
3	B	452[B]	BOG	C1'-O1-C1	6.97	126.50	113.96
3	B	451[B]	BOG	O4-C4-C3	-5.97	96.97	110.35
3	B	452[A]	BOG	C1'-O1-C1	5.79	124.37	113.96

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	451[A]	BOG	C1

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	452[B]	BOG	C1'-O1-C1-O5

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.