



**UNIVERSITI PUTRA MALAYSIA**

***DIRECTED EVOLUTION OF AMS8 LIPASE TOWARDS ENHANCED  
ACTIVITY AND STABILITY AT LOW TEMPERATURE***

**PIREYA THARASENI A/P ARULU**

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ACTIVITY AND STABILITY AT LOW TEMPERATURE**

By

**PIREYA THARASENI A/P ARULU**

**Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in  
Fulfilment of the Requirements for the Degree of Master of Science**

**February 2017**

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Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfilment of the requirement for the degree of Master of Science

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**February 2017**

**Chairman : Mohd Shukuri Mohamad Ali, PhD**  
**Faculty: Biotechnology and Biomolecular Sciences**

Cold active lipases have huge biotechnological prospects due to their high catalytic activity at low temperature. Generally, cold active lipases demonstrate high specific activity at low temperature and rapidly denature in moderate range of temperature due to their thermosensitive nature. However, the factors that contribute to these cold adaptation properties are still vague. AMS8 lipase is a Family 1.3 lipase produced by Antarctic *Pseudomonas* sp. exhibits minimum activity at low temperature. The aim of this study is to evolve AMS8 lipase with enhanced activity and stability at low temperature and to study the effect of the amino acid substitution on the biochemical features of this lipase. The mutant library of AMS8 lipase was generated by error-prone PCR. Mutant M15 lipase was selected as it has the highest lipolytic activity at 20°C. M15 lipase was sequenced and two mutation points were identified which are R259C and V342E. *In silico* studies of this mutant have predicted that M15 lipase has increased structural flexibility compared to the native enzyme. Mutant M15 lipase was purified using gel filtration chromatography method. Biochemical characterization has revealed that M15 lipase has an optimum temperature at 20°C and is highly stable at 10°C. M15 lipase was optimally active at pH 6 and stable within a small range of pH, 6-10. The catalytic activity of the mutant was boosted in the presence of Ca<sup>2+</sup> and Na<sup>+</sup>. Moreover, M15 lipase was found to be tolerant towards hydrophobic organic solvents and demonstrated great specificity towards long-chain pNP esters and optimum activity was observed in pNP-laurate. Secondary structure analysis of M15 lipase revealed that the enzyme has attained more structural flexibility compared to the wild type. In conclusion, AMS8 lipase was successfully mutated via directed evolution strategy and the findings will be useful insight on the understanding of the cold active lipases properties.

Abstrak tesis yang dikemukakan kepada senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Master Sains

## **EVOLUSI TERARAH ATAS AMS8 LIPASE BAGI MENINGKATKAN KADAR AKTIVITI DAN STABILITI PADA SUHU RENDAH**

Oleh

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Lipase tahan sejuk merupakan enzim yang mempunyai kadar aktiviti pemangkin yang sangat tinggi pada suhu rendah dan oleh sebab itu, lipase tahan sejuk amat berpotensi dalam bidang industri bioteknologi. Enzim ini mempunyai kadar aktiviti degradasi yang tinggi pada suhu rendah tetapi dinyahaktifkan walaupun pada suhu yang sederhana. Bagaimanapun, faktor-faktor yang menyumbang kepada ciri-ciri penyesuaian dengan suhu rendah ini masih tidak jelas. AMS8 lipase yang dikategorikan dalam Family I.3 adalah disintesis oleh *Pseudomonas* Antartika, mempunyai kadar aktiviti pemangkin yang rendah pada suhu rendah. Eksperimen ini bertujuan untuk memutasikan AMS8 lipase supaya stabil dan bertindak pada kadar yang tinggi pada suhu rendah, dan untuk menganalisa kesan mutasi terhadap ciri-ciri biokimia enzim tersebut. Mutan-mutan AMS8 lipase dihasilkan dengan menggunakan teknik Reaksi Berantai Polimer berralat. Mutan M15 lipase telah dipilih kerana ia mempunyai kadar aktiviti yang tinggi pada suhu 20°C. Urutan amino asid mutan M15 lipase telah dikenalkan pasti dan didapati dua residue telah bermutasi iaitu R259C dan V342E. Analisa struktur mutan ini melalui perisian komputer telah menunjukkan bahawa struktur mutan mempunyai fleksibiliti yang lebih tinggi daripada struktur asal AMS8 lipase. Seterusnya, mutan M15 lipase telah dituliskan dan ciri-ciri biokimia enzim ini telah dikaji. Enzim ini berfungsi pada kadar optima pada suhu 20°C dan menunjukkan kestabilan yang sangat baik pada 10°C. M15 lipase juga aktif pada pH 6 dan stabil pada pH 6-8. Kadar aktiviti M15 lipase telah meningkat dalam kehadiran Ca<sup>2+</sup> dan Na<sup>+</sup>. Tambahan pula, M15 lipase menunjukkan kestabilan yang tinggi dalam pelarut organik hidrofobik dan juga menunjukkan kadar hidrolisis yang tinggi bagi substrat berantai panjang dan aktiviti maksima telah dilihat pada pNP-laurate. Struktur sekunder M15 lipase telah dianalisa dan didapati bahawa struktur M15 lipase adalah lebih fleksibel berbanding struktur AMS8 lipase. Kesimpulannya, AMS8 lipase telah berjaya dimutasi melalui teknik evolusi terarah. Penemuan kajian ini telah membolehkan pemahaman yang mendalam mengenai ciri-ciri lipase tahan sejuk.

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I certify that a Thesis Examination Committee has met on 14 February 2017 to conduct the final examination of Pireya Tharaseni a/p Arulu on her thesis entitled "Directed Evolution of AMS8 Lipase Towards Enhanced Activity and Stability at Low Temperature" in accordance with the Universities and University Colleges Act 1971 and the Constitution of the Universiti Putra Malaysia [P.U.(A) 106] 15 March 1998. The Committee recommends that the student be awarded the Master of Science.

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## TABLE OF CONTENTS

	Page
<b>ABSTRACT</b>	i
<b>ABSTRAK</b>	ii
<b>ACKNOWLEDGEMENT</b>	iii
<b>APPROVAL</b>	iv
<b>DECLARATION</b>	vi
<b>LIST OF TABLES</b>	xii
<b>LIST OF FIGURES</b>	xiii
<b>LIST OF ABBREVIATIONS</b>	xv
<b>CHAPTER</b>	
<b>1 INTRODUCTION</b>	<b>1</b>
<b>2 LITERATURE REVIEW</b>	<b>3</b>
2.1 Protein Engineering	3
2.2 Directed Evolution	3
2.2.1 Generation of mutant library	4
2.2.2 Screening and selection techniques	6
2.3 Evolution of enzyme functions	7
2.4 Lipase	8
2.4.1 Structural features of lipases	9
2.4.2 Source of lipases	10
2.4.3 Bacterial lipases	11
2.4.3.1 Classification of bacterial	11
2.5 Family I.3 lipases	12
2.6 Cold active lipases	13
2.6.1 Prospects of cold active lipases	14
2.7 <i>In silico</i> analysis of proteins	15
2.8 Circular dichroism spectrophotometer	16
<b>3 MATERIALS AND METHODS</b>	
3.1 Materials	17
3.2 Source of enzyme	17
3.3 Preparation of media	17
3.3.1 Preparation of selective media	17
3.3.2 Preparation of LB broth	17
3.4 Preparation of competent cells	17
3.5 Plasmid extraction	18
3.6 Generation of mutant library	18
3.6.1 Error-prone PCR	18
3.7 Purification of PCR product	18
3.8 Double digestion of purified PCR product and vector	19
3.9 Ligation of purified digested vector and PCR product	19
3.10 Heat shock transformation of <i>E.coli</i> strain BL21 (DE3) with ligated PCR product	19
3.11 Screening and selection of mutants	19

3.11.1	Preparation of glycerol stock of mutants	20
3.12	Expression and harvesting of soluble proteins of mutants	20
3.13	Quantitative determination of lipase activity via colorimetric assay	20
3.13.1	Oleic acid standard curve	20
3.14	Sequencing and sequence analysis	21
3.15	PAGE electrophoresis	21
3.15.1	SDS PAGE	21
3.15.2	Native PAGE analysis	22
3.15.3	Activity staining	22
3.16	Expression and refolding of insoluble proteins of M15	22
3.17	Purification of mutant lipase via gel filtration chromatography	22
3.18	Characterization of purified M15 lipase	23
3.18.1	Biochemical characterization	23
3.18.1.1	Effect temperature of activity of M15 lipase	23
3.18.1.2	Effect temperature of stability of M15 lipase	23
3.18.1.3	Determination of half-life of M15 lipase	23
3.18.1.4	Effect of pH on activity of M15 lipase	23
3.18.1.5	Effect of pH on stability of M15 lipase	23
3.18.1.6	Effect of metal ions on activity of M15 lipase	24
3.18.1.7	Effect of organic solvents on M15 lipase	24
3.18.1.8	Substrates specificity of M15 lipase	24
3.18.2	Biophysical characterization	24
3.19	<i>In silico</i> studies	24
3.20	Statistical analysis	25

## 4

### RESULTS AND DISCUSSION

4.1	Introduction	26
4.2	Generation of mutant library	26
4.2.1	Error-prone PCR	26
4.2.2	Cloning and transformation of PCR product	27
4.3	Screening and selection of positive mutants	28
4.3.1	Quantitative analysis of mutant clones	28
4.4	Analysis of the mutation sites	30
4.5	Purification of M15	32
4.5.1	Gel filtration chromatography of M15 lipase	33
4.5.2	Analysis of purification product	34

4.6	Biochemical characterization of purified M15 lipase	36
4.6.1	Effect of temperature on activity and stability of M15 lipase	36
4.6.2	Effect pH on activity and stability of M15 lipase	38
4.6.3	Effect of metal ions on activity of M15 lipase	40
4.6.4	Effect of organic solvents on activity of M15 lipase	42
4.6.5	Effect of substrates on M15 lipase activity	44
4.7	<i>In silico</i> analysis	45
4.7.1	General structural analysis M15 lipase	45
4.7.2	Solvent accesible surface area (SASA)	49
4.7.3	B-factor	52
4.8	Circular dichroism spectrophotometer	52
4.8.1	Secondary structure analysis of M15 lipase	52
4.9	Overall comparison between M15 lipase and AMS8 lipase	55
<b>5</b>	<b>CONCLUSION AND RECOMMENDATIONS</b>	<b>58</b>
	<b>REFERENCES</b>	<b>60</b>
	<b>APPENDICES</b>	<b>76</b>
	<b>BIODATA OF STUDENT PUBLICATION</b>	<b>86</b>
		<b>87</b>

## LIST OF TABLES

Table		Page
1	Examples of lipase producing bacteria and their industrial application	11
2	Amount of oleic acid ( $\mu$ mole) used to plot the standard curve	21
3	Base pair substitutions and corresponding amino acid residues of mutants	32
4	Purification table of M15 lipase	34
5	Solvent Accessible Surface Area (SASA) of residues mapped close to the point of mutations in both AMS8 lipase And M15 lipase	50
6	B-factor of M15 lipase and AMS8 lipase at the mutation residues	52
7	Estimated secondary structure composition of AMS8 lipase and M15 lipase	55
8	comparison between AMS8 lipase and M15 lipase	56

## LIST OF FIGURES

Figure		Page
1	Basic steps of directed evolution	4
2	Broad range catalytic activity of lipases	9
3	$\alpha/\beta$ hydrolases fold of lipases	10
4	Agarose gel (1%) of purified error-prone PCR product	27
5	Agarose gel (1%) of double digested error-prone PCR and vector	27
6	Master plate containing mutants clones	28
7	Quantitative analysis of 20 variants and wild type at 20°C	29
8	Protein sequence alignment of variant M15 lipase and the wild type AMS8 lipase	31
9	Gel filtration chromatogram profile of M15 lipase	33
10	Analysis of purified M15 lipase	35
11	Effect of temperature on activity of M15 lipase	36
12	Effect of temperature on stability of M15 lipase	37
13	Half-life of m15 lipase at 10, 20 and 30°C for 960 min	38
14	Effect of pH on activity of M15 lipase	39
15	Effect of pH on stability of M15 lipase	40
16	Effect of metal ions on activity of M15 lipase	41
17	Effect of organic solvents on activity of M15 lipase	43
18	Effect of substrate on activity of M15 lipase	44
19	Predicted model of M15 lipase in linear ribbon diagram	46
20	Amino acid substitution and its interactions with adjacent residues	48
21	Structural differences of M15 lipase (brown) and AMS8 Lipase (Blue)	49
22	Far-UV spectra of M15 lipase and AMS8 lipase	54

## LIST OF ABBREVIATIONS

$A_{600}/O.D_{600}$	Absorbance/optical density at 600 nm
bp	Base pair
Da	Dalton
DMSO	Dimethyl sulfoxide
epPCR	Error-prone PCR
FFA	Free fatty acid
<i>g</i>	Relative centrifugal force
g	Gram
h	hour
IPTG	isopropyl $\beta$ -D- Thiogalactopyranoside
kDa	kilo Dalton
L	Liter
M	Molar
mM	Milimolar
mg	Miligram
mg/mL	Miligram per milliliter
min	Minute
nm	Nanometer
PCR	Polymerase chain reaction
ps	Picosecond
rpm	Rotation per minute
RTX	Repeat in toxin
s	Second
SDS	Sodium dodecyl sulphate
SDS-PAGE	Sodium dodecyl sulphate polyacrylamide gel electrophoresis



U	Unit
U/mL	Unit per milliliter
$\mu\text{L}$	microlitre
$\mu\text{mol}$	micromole
w/v	Weight per volume
v/v	Volume per volume
V	Voltage



## CHAPTER 1

### INTRODUCTION

The emergence of protein science is strikingly influenced by the discovery of the recombinant DNA and genetic engineering. Being a crucial part of the biotechnological advances, protein science embraces large scope of studies including molecular biology, genetics, cell biology, evolution, structural elucidation and functional properties of enzymes. Enormous attention and curiosity drawn towards this field of study has lead to invention of various techniques to alter and modify protein sequence, which can be distinctly categorized as directed evolution and rational design (Arnold, 1998).

Directed evolution is an established technique of protein engineering that generates astonishing range of genetic library with novel properties. Accumulation of beneficial mutants diversity followed by meticulously designed screening and selection strategies is requisite in isolating a mutant with desired properties (Tracewell and Arnold, 2009). Several techniques of generating a promising molecular library are widely demonstrated such as DNA shuffling, chemical mutagenesis, error-prone PCR and mutator strain (Aguinaldo and Arnold, 2002; Nannemann et al., 2011). Over the years, abundant number of enzymes are being engineered via directed evolution with unique functional properties and specificities. Among them, lipases are largely been evolved to boost their thermostability, cold activity, regio-, stereo- and enantioselectively, substrate specificity, and solvent tolerance (Bassegoda et al., 2012; Goomber et al., 2016).

Lipases are ubiquitous enzyme that are widely acclaimed for their broad range of catalytic activity (Borrelli and Trono, 2015). Lipases are naturally synthesized by plants, animals and microorganisms, especially bacteria, yeasts and fungi (Treichel et al., 2010). Owing to their versatility and broad prospective in biotechnological industries, bacterial lipases are one of the largely studied group of lipases (Hasan et al., 2006). Each bacterial lipases are basically distinct in their adaptation features and functional properties. One of this kind is the cold active lipases. Cold active lipase are kinetically unique from other type of lipases as they exhibit excellent catalytic efficiency at low temperature. Their nature of being highly thermoliable is one of the key factors drawing this enzyme to be largely used in industrial application (Feller, 2013). However, factors that contribute to this unique properties of cold active lipases are still being experimented and varies in different type of lipases.

Therefore, AMS8 lipase, which was previously isolated from *Pseudomonas* sp bacteria was engineered via directed evolution to enhance the activity and stability of the enzyme at low temperature. The objectives are as follows:

- a) To evolve AMS8 lipase by error-prone PCR
- b) To identify the mutation points and purify the mutated AMS8 lipase
- c) To analyze the mutant biochemically, biophysically and via *in silico* approaches



## REFERENCES

- Aguinaldo, A. M., & Arnold, F. (2002). Staggered extension process (StEP) *in vitro* recombination. In B. -Y. Chen & H.W. Janes (Eds.), *Methods in Molecular Biology: PCR Cloning Protocols* (pp. 235-239). New Jersey, Totowa: Humana Press Inc.
- Ali, M. S. M., Fuzi, S. F. M., Ganasen, M., Rahman, R. N. Z. R. A., Basri, M. & Salleh, A. B. (2013a). Structural adaptation of cold-adapted RTX lipase from *Pseudomonas* sp. Strain AMS8 revealed via homology molecular dynamics simulation approaches. *Biomed Research International*, 1-9.
- Ali, M. S. M., Ganasen, M., Rahman, R. N. Z. R., Chor, A. L., Salleh, A. B & Basri, M., (2013b). Cold-adapted RTX lipase from Antarctic *Pseudomonas* sp. Strain AMS8 isolation, molecular modelling and heterologous expression. *Protein Journal*, 317-325.
- Allen, M. P. (2004). Introduction to molecular dynamics simulation. *Computational Soft Matter*, 23, 1–28.
- Alves, R., Chaleil, R. A. G. & Sternberg, M. J. E. (2002). Evolution of enzymes in metabolism: A network perspective. *Journal of Molecular Biology*, 320, 751-770.
- Amada, K., Haruki, M., Imanaka, T., Morikawa, M. & Kanaya, S. (2000). Overproduction in *Escherichia coli*, purification and characterization of a family I.3 lipase from *Pseudomonas* sp. MIS38. *Biochimica et Biophysica Acta*, 1478, 201-210.
- Amada, K., Kwon, H., Haruki, M., Morikawa, M. & Kanaya, S. (2001). Ca<sup>2+</sup> induced folding of a family I.3 lipase with repetitive Ca<sup>2+</sup> binding motifs at the C-terminus. *FEBS letters*, 509, 17-21.
- Andualema, B. & Gessesse, A. (2013). Microbial lipases and their industrial applications: review. *Biotechnology*, 11(3), 100-118.
- Angkawidjaja, C. & Kanaya, S. (2006). Family I.3 lipase: bacterial lipases secreted by the type I secretion system. *Cellular and Molecular Life Sciences*, 63, 2804-2817.
- Angkawidjaja, C., Matsumura, H., Koga, Y., Takano, K. & Kanaya, S. (2010). X-ray crystallographic and MD simulation studies on the mechanism of interfacial activation of a family I.3 lipase with two lids. *Journal of Molecular Biology*, 400, 82-95.
- Angkawidjaja, C., Paul, A., Koga, Y., Takano, K. & Kanaya, S. (2005). Importance of a repetitive nine-residue sequence motif for intracellular stability and functional structure of a family I.3 lipase. *FEBS Letters*, 579, 4707–4712.

- Angkawidjaja, C., You, D. J., Matsumura, H., Koga, Y., Takano, K. & Kanaya, S (2007). Extracellular overproduction and preliminary crystallographic analysis of a family 1.3 lipase. *Acta Crystallographica Section F: Structural Biology and Crystallization Communication*, 63, 187-189.
- Alquati, C., De Gioia, L., Santarossa, G., Alberghina, L., Fantucci, P. & Lotti, M. (2002). The cold-active lipase of *Pseudomonas fragi*: Heterologous expression, biochemical characterization and molecular modeling. *European Journal of Biochemistry*, 269, 3321-3328.
- Aravindan, R., Anbumathi, P. & Viruthagiri, T. (2007). Lipase applications in food industry. *Indian Journal of Biotechnological*, 6, 141-148.
- Arnold, F. (1990). Engineering enzymes for non-aqueous solvents. *Trends in Biotechnology*, 8, 244-249.
- Arnold, F. (1998). Engineering Proteins for non-natural environments. *Accounts of Chemical Research*, 31, 125-131.
- Arnold, F. H., Wintrode, P.L., Miyazaki, K. & Gershenson, A. (2001). How enzymes adapt: Lessons from directed evolution. *TRENDS in Biochemical Sciences*, 26(2), 100-106.
- Arpigny, J. L. & Jaeger, K. E. (1999). Bacterial lipolytic enzymes: Classification and properties. *The Biochemical Journal*, 343(1), 177-183.
- Arpigny, J. L., Lamotte, J. & Gerday, Ch. (1997). Molecular adaptation to cold of an Antarctic bacterial lipase. *Journal of Molecular Catalysis B: Enzymatic*, 3, 29-35.
- Balan, A., Ibrahim, D., Abdul Rahim, R. & Ahmad Rashid, F. A. (2012). Purification and characterization of a thermostable lipase from *Geobacillus thermodenitrificans* IBRL-nra. *Enzyme Research*, 1-7.
- Bassalo, M. C., Liu, R. & Gill, R. T. (2016). Directed evolution and synthetic biology applications to microbial systems. *Current Opinion in Biotechnology*, 39, 126-133.
- Bassegoda, A., Cesarini, S. & Diaz, P. (2012). Lipase improvement: Goals and strategies. *Computational and Structural Biotechnology Journal*, 2(3), 1-8.
- Bessler, C., Schmitt, J., Maurer, K. & Schmid, R. D. (2003). Directed evolution of bacterial  $\alpha$ -amylase: Toward enhanced pH-performance and higher specific activity. *Protein Science*, 12, 2141-2149.
- Berg, J. M., Tymoczko, J. L. & Stryer, L. (2002). *Biochemistry*. New York: W H Freeman and Company.
- Bisignano, P. and Moran, O. (2009). Molecular dynamics analysis of the wild type and dF508 mutant structures of the human CFTR-nucleotide binding domain 1. *Biochimie*, 92(1), 51-57.

- Bisswanger, H. (2002). *Enzyme Kinetics: Principles and Methods*. Germany: Weinheim.
- Bloom, J. D. & Arnold, F. H. (2009). In the light of directed evolution: Pathways of adaptive protein evolution. *Proceedings of the National Academy of Sciences*, 106, 9995–10000.
- Borders, C. L., Broadwater, J. A., Bekeny, P. A., Salmon, J. E., Lee, A. N., Eldridge, A. M. & Pett, V. B. (1994). A structural role for arginine in proteins: Multiple hydrogen bonds to backbone carbonyl oxygens. *Protein Science*, 3, 541-548.
- Bordoli, L., Kiefer, F., Arnold, K., Benkert, P., Battey, J & Schwede, T. (2009). Protein structure homology modeling using SWISS-MODEL workspace. *Nature*, 4(1), 1-13.
- Borrelli, G. M. & Trono, D. (2015). Recombinant lipases and phospholipases and their use as biocatalysts for industrial applications. *International Journal of Molecular Sciences*, 1(9), 20774-20840.
- Bradford, M. M. (1976). A rapid and sensitive method for the quantification of microgram quantities of protein using the principle of protein-dye binding. *Analytical Biochemistry* 72, 248-254.
- Cadwell, R. C. & Joyce, G. F. (1992). Randomization of genes by PCR mutagenesis. *Genome Research*, 2(1), 28-33.
- Carugo, O. & Pongor, S. (2001). A normalized root-mean-square distance for comparing protein three-dimensional structures. *Protein Science*, 10(7), 1470-1473.
- Casas-Godoy, L., Duquesne, S., Bordes, F., Sandoval, G. & Marty, A. (2012). Lipases: An overview. In Sandoval, G (Ed.), *Lipases and Phospholipases: Methods and Protocols, Methods in Molecular Biology* (pp. 3-30). Germany: Springer Science+Business Media New York.
- Cavicchioli, R., Siddiqui, K. S., Andrews, D. & Sowers, K. R. (2002). Low-temperature extremophiles and their applications. *Current Opinion in Biotechnology*, 13, 253–261.
- Chen, K & Arnold, F.H. (1993). Turning the activity of an enzyme for unusual environments: Sequential random mutagenesis of subtilisin E for catalysis in dimethylformamide. *Biochemistry Communicated* , 90, 5618–5622.
- Chen, W. & Georgiou, G. (2002). Cell-surface display of heterologous proteins: From high-throughput screening to environmental applications. *Biotechnology and Bioengineering*, 79 (5), 496-503.
- Cheng, M., Angkawidjaja, C., Kogal, Y & Kanaya, K. (2014). Calcium-independent opening of lid1 of a family I.3 lipase by a single Asp to Arg mutation at the calcium-binding site. *Protein Engineering, Design & Selection*, 27, 169–176.

- Cheng, Y. Y., Qian, Y. K., Feng, Z., Wu, Z. H., Liu, H. & Li, Z. L. (2011). A novel cold-adapted lipase from *Sorangium cellulosum* strain So0157-2: Gene cloning, expression and enzymatic characterization. *International Journal of Molecular Sciences*, 12, 6765-6780.
- Cherry, J. R. & Fidantsef, A. L. (2003). Directed evolution of industrial enzymes: An update. *Current Opinion in Biotechnology*, 14, 438-443.
- Choo, D.-W., Kurihara, T., Suzuki, T., Soda, K. & Esaki, N. (1998). A cold-adapted lipase of an Alaskan *Psychrotroph*, *Pseudomonas* sp. Strain B11-1: Gene cloning and enzyme purification and characterization. *Applied and Environmental Microbiology*, 64(2), 486-491.
- Cirino, P. C., Mayer, K. M. & Umeno, D. (2003). Generating mutant libraries using error-prone PCR. In F. H. Arnold & G. Gerogiou (Eds.), *Methods in Molecular Biology* (pp. 3-9). New Jersey, Totowa: Humana Press Inc.
- Cobb, R. E., Si, T. & Zhao, H. (2012). Directed evolution: An evolving and enabling synthetic biology tool. *Current Opinion in Chemical Biology*, 59(5), 1432-1440.
- Cowan, J. A. (2002). Structural and catalytic chemistry of magnesium-dependent enzymes. *BioMetals*, 15, 225-235.
- Dalby, P. A. (2011). Strategy and success for the directed evolution of enzymes. *Current Opinion in Structural Biology*, 21, 473-480.
- Cui, S. S., Lin, X. Z. & Shen, J.H. (2011). Effects of co-expression of molecular chaperones on heterologous soluble expression of the cold-active lipase *Lip-948*. *Protein Expression and Purification*, 77, 166-172.
- Delepelaire, P. (2004). Type I secretion in gram-negative bacteria. *Biochimica et Biophysica Acta - Molecular Cell Research*, 149-161.
- Dey, A., Chattopadhyay, A., Mukhopadhyay, S. K., Saha, P., Chatterjee, S., Maiti, T. K. & Roy, P. (2014). Production, partial purification and characterization of an extracellular psychrotrophic lipase from *Pseudomonas* sp. ADT3, *Journal of Bioremediation and Biodegradation*, 5, 1-8.
- Durham, E., Dorr, B., Woetzel, N., Staritzbichler, R. & Meiler, J. (2009). Solvent accessible surface area approximations for rapid and accurate protein structure prediction. *Journal of Molecular Modeling*, 15(9), 1080-1093.
- Durrant, J.D. & McCammon, J.A. (2011). Molecular dynamics simulations and drug discovery. *BioMed Center Biology*, 9(71), 2-9.
- Eijsink, V. G. H., Gåseidnes, S., Borchert, T. V. & Burg, B. (2005). Directed evolution of enzyme stability. *Biomolecular Engineering*, 22(13), 21-30.
- Elias, M., Wieczorek, G., Rosenne, S. & Tawfik, D. S. (2014). The universality of

- enzymatic rate-temperature dependency. *Trends in Biochemical Sciences*, 39(1), 1-7.
- Engström, K., Nyhlén, J., Sandström, A. G. & Bäckvall, J. E. (2010). Directed evolution of an enantioselective lipase with broad substrate scope for hydrolysis of  $\alpha$ -substituted esters. *Journal of the American Chemical Society*, 132(20), 7038-7042.
- Ericsson, D.J., Kasrayan, A., Johansson, P., Bergfors, T., Sandstrom, A.G., Backvall, J. & Mowbray, S.L. (2007). X-ray structure of *Candida antarctica* Lipase A shows a novel lid structure and a likely mode of interfacial activation. *Journal of Molecular Biology*, 376, 109-119.
- Eriksen, D. T., Chiun, P., Hsieh, H., Lynn, P. & Zhao, H. (2013). Directed evolution of a cellobiose utilization pathway in *Saccharomyces cerevisiae* by simultaneously engineering multiple proteins. *Microbial Cell Factories*, 12(16), 2-11.
- Feller, G. (2013). Psychrophilic enzymes: From folding to function and biotechnology. *Scientifica*, 2-28.
- Feller, G. & Gerday, C. (1997). Psychrophilic enzymes: molecular basis of cold adaptation. *Cellular and Molecular Life Sciences*, 53, 830-841.
- Fernandez-Gacio, A., Uguen, M. & Fastrez, J. (2003). Phage display as a tool for the directed evolution of enzymes. *Trends in Biotechnology*, 21(1), 408-414.
- Fojan, P., Jonson, P. H., Petersen, M. T. N. & Petersen, S. B. (2000). What distinguishes an esterase from a lipase: A novel structural approach. *Biochimie*, 82(11), 1033-1044.
- Francis, J. C. & Hansche, P. E. (1973). Directed evolution of metabolic pathways in microbial populations II. a repeatable adaptation in *Saccharomyces Cerevisiae*. *Genetics*, 74(2), 259-265.
- Fromant, M., Blanquet, S. & Plateau, P. (1995). Direct random mutagenesis of gene-sized DNA fragments using polymerase chain reaction. *Analytical Biochemistry*, 224, 347-353.
- Ganasen, M., Yaacob, N., Rahman, R. N. Z. R. A., Leow, A. T. C., Basri, M., Salleh, A. B. & Ali, M. S. M. (2016). Cold-adapted organic solvent tolerant alkalophilic family I.3 lipase from an Antarctica *Pseudomonas*. *International Journal of Biological Macromolecules*, 92, 1266-1276.
- Gatti-Lafranconi, P., Caldarazzo, S. M., Villa, A., Alberghina, L. & Lotti, M. (2008). Unscrambling thermal stability and temperature adaptation in evolved variants of a cold-active lipase. *FEBS Letters*, 582(15), 2313-2318.
- Gaur, R., Gupta, A. & Khare, S. K. (2008). Purification and characterization of lipase from solvent tolerant *Pseudomonas aeruginosa* PseA. *Process Biochemistry*, 43,



1040-1046.

- Georlette, D., Blaise, V., Collins, T., D'Amico, S., Gratia, E., Hoyoux, A., Marx, J.-C., Sonan, G., Feller, G. & Gerday, C. (2004). Some like it cold: Biocatalysis at low temperatures. *FEMS Microbiology Reviews*, 28, 25-48.
- Gerday, C., Aittaleb, M., Bentahir, M., Chessa, J. P., Claverie, P., D'Amico, S., Dumont, J., Garsoux, G., Georlette, D., Hoyoux, A., Lonhienne, T., Meuwis, M.A. and Feller, G. (2000). Cold-adapted enzymes: from fundamentals to biotechnology. *Trends in Biotechnology*, 18, 103-107.
- Gilham, D. & Lehner, R. (2005). Techniques to measure lipase and esterase activity *in vitro*. *Methods*, 36, 139-147.
- Glogauer, A., Martini, V. P., Faoro, H., Couto, G. H., Müller-Santos, M., Monteiro, R. A., Mitchell, D.A., de Souza, E.M., Pedrosal, F.O. & Krieger, Nadia. (2011). Identification and characterization of a new true lipase isolated through metagenomic approach. *FEMS Microbiology Cell Factories*, 10(54), 2-15.
- Goomber, S., Kumar, A. & Kaur, J. (2016). Disruption of N terminus long range non covalent interactions shifted temp. opt 25 °C to cold: Evolution of point mutant *Bacillus* lipase by error prone PCR. *Gene*, 576, 237–243.
- Green, M. R. & Sambrook, J. (2012). *Molecular Cloning*. New York: Cold Spring Harbor.
- Greenfield, N. J. (2006). Using circular dichroism spectra to estimate protein secondary structure. *Nature Protocols*, 1(6), 2876–2890.
- Gunasekaran, V. & Das, D. (2005). Lipase fermentation: Progress and prospects. *Indian Journal of Biotechnology*, 4, 437-445.
- Gupta, N. G., Khare, S.K. & Prakash, V. (2015). Cold active lipase from psychrophile and their industrial application. In Sinha, A., Srivastava, S. & Kumar, R. (Eds.), *Microbial Biodiversity: A boon for Agriculture Sustainability* (pp. 211-224). New Delhi: Biotech Books.
- Gupta, R., Gupta, N. & Rathi, P. (2004). Bacterial lipases: An overview of production, purification and biochemical properties. *Applied Microbiology and Biotechnology*, 64(6), 763-81.
- Gupta, R., Rathi, P., Gupta, N. & Bradoo, S. (2003). Lipase assays for conventional and molecular screening: an overview. *Biotechnological Applied Biochemistry*, 37, 63-71.
- Hanahan, D. (1983). Studies on transformation of *Escherichia coli* with plasmids. *Journal of Molecular Biology*, 166(4), 557-580.
- Hasan, F., Shah, A. A. & Hameed, A. (2006). Industrial applications of microbial lipases. *Enzyme and Microbial Technology*, 39, 235-251.

- Hasan, F., Shah, A. A. & Hameed, A. (2009). Methods for detection and characterization of lipases: A comprehensive review. *Biotechnology Advances*, 27(6), 82-98.
- Hasson, T., Oostenbrink, C. & van Gunsteren, W.F. (2002). Molecular dynamics simulations. *Current Opinion in Structural Biology*, 12, 190-196.
- Hedstrom, L. (2001). Enzyme specificity and selectivity. *Encyclopedia of Life Sciences*, 1-7.
- Hethley, J., Lai, J., Loutet, S., Martin, M. & Tang, V. (2002). Effect of Tricine, glycine and Tris buffers on alkaline phosphatase activity. *Journal of Experimental Microbiology and Immunology*, 2, 33-38.
- Hogg, P. J. (2003). Disulfide bonds as switches for protein function. *TRENDS in Biochemical Sciences*, 28(1), 210-214.
- Holland, B., Schmitt, L. & Youn, J. (2005). Type 1 protein secretion in bacteria, the ABC-transporter dependent pathway. *Molecular Membrane Biology*, 22, 29-39.
- Houde, A., Kademi, A. & Leblanc, D. (2004). Lipases and their industrial applications an overview. *Applied Biochemistry and Biotechnology*, 118, 155-170.
- Jäckel, C., Kast, P. & Hilvert, D. (2008). Protein design by directed evolution. *Annual Reviews of Biophysics*, 37, 153-73.
- Jaeger, K.E., Dijkstra, B.W. & Reetz, M.T. (1999). Bacterial biocatalysts: Molecular biology, three-dimensional structures, and biotechnological applications of lipases. *Annual Reviews of Microbiology*, 53, 315-351.
- James, J. J., Lakshmi, S. B., Raviprasad, V., Ananth, J. M., Kanguene, P. & Gautam, P. (2003). Insights from molecular dynamics simulations into pH-dependent enantioselective hydrolysis of ibuprofen esters by *Candida rugosa* lipase. *Protein Engineering*, 16(12), 1017-1024.
- Jeon, J. H., Kim, J. T., Kim, Y. J., Kim, H. K., Lee, H. S., Kang, S. G., Kim, S-J. & Lee, J. H. (2009). Cloning and characterization of a new cold-active lipase from a deep-sea sediment metagenome. *Applied Microbiology and Biotechnology*, 81, 865-874.
- Jing, R., Wang, Y., Wu, Y., Hua, Y., Dai, X., & Li, M. (2014). Theoretical & computational science a research of predicting the B-factor base on the protein sequence. *Journal of Theoretical and Computational Science*, 1(3), 2-7.
- Jinwei, Z., Lin, S. & Zeng, R. (2007). Cloning, expression, and characterization of a cold-adapted lipase gene from an Antarctic deep-sea psychrotrophic bacterium, *Psychrobacter* sp. 7195. *Biotechnology*, 17(4), 604-610.

- Jiewei, T., Zuchao, L., Peng, Q., Lei, W. & Yongiang, T. (2014). Purification and characterization of a cold-adapted lipase from *Oceanobacillus* strain PT-11. *PLOS ONE*, 9(7), 1-7.
- Joseph, B. & Ramteke, P. W. (2013). Extracellular solvent stable cold-active lipase from psychrotrophic *Bacillus sphaericus* MTCC 7526: Partial purification and characterization. *Annals of Microbiology*, 63(1), 363-370.
- Joseph, B., Ramteke, P. W. & Thomas, G. (2008). Cold active microbial lipases: Some hot issues and recent developments. *Biotechnology Advances*, 26(5), 457-470.
- Joseph, B., Ramteke, P. W., Thomas, G. & Shrivastava, N. (2007). Standard review cold-active microbial lipases: a versatile tool for industrial applications. *Biotechnology and Molecular Biology Review*, 2(2), 39-48.
- Joseph, B., Shrivastava, N. & Ramteke, P.W. (2012). Extracellular cold-active lipase of *Microbacterium luteolum* isolated from Gangotri glacier, western Himalaya: Isolation, partial purification and characterization. *Journal of Genetic Engineering and Biotechnology*, 10(1), 137-144.
- Kang, H. Y., Kim, J. F., Kim, M. H., Park, S. H., Oh, T. K. & Hur, C. G. (2006). MELDB: A database for microbial esterases and lipases. *FEBS Letters*, 580, 2736-2740.
- Karadzic, I., Masui, A., Zivkovic, L. I., & Fujiwara, N. (2006). Purification and characterization of an alkaline lipase from *Pseudomonas aeruginosa* isolated from putrid mineral cutting oil as component of metalworking fluid. *Journal of Bioscience and Bioengineering*, 102(2), 82-89.
- Karplus, M. (2002). Molecular dynamics simulations of biomolecules. *Accounts of Chemical Research*, 35(6), 321-323.
- Kavitha, M. (2016). Cold active lipases-an update. *Frontiers in life science*, 9(3), 226-238.
- Kelly, S. M., Jess, T. J. & Price, N. C. (2005). How to study proteins by circular dichroism. *Biochimica et Biophysica Acta - Proteins and Proteomics*, 1751, 119-139.
- Khurana, J., Singh, R. & Kaur, J. (2011). Engineering of *Bacillus* lipase by directed evolution for enhanced thermal stability: effect of isoleucine to threonine mutation at protein structure. *Molecular Biology Reports*, 38, 2919-2926.
- Kim, Y. O., Khosasih, V., Nam, B. H., Lee, S. J., Suwanto, A. & Kim, H. K. (2012). Gene cloning and catalytic characterization of cold-adapted lipase of *Photobacterium* sp. MA1-3 isolated from blood clam. *Journal of Bioscience and Bioengineering*, 114 (6), 589-595.
- Kim, K. R., Kwon, D. Y., Yoon, S. H., Kim, W. Y. & Kim, K. H. (2005). Purification, refolding, and characterization of recombinant *Pseudomonas fluorescens* lipase.

*Protein Expression and Purification*, 39(1), 124-129.

- Kim, Y. W., Lee, S. S., Warren, R. A. J. & Withers, S. G. (2004). Directed evolution of a glycosynthase from *Agrobacterium* sp. increases its catalytic activity dramatically and expands its substrate repertoire. *Journal of Biological Chemistry*, 114(6), 589-595.
- Korman, T. P. & Bowie, J. U. (2012). Crystal structure of *Proteus mirabilis* lipase, a novel lipase from the proteus/psychrophilic subfamily of lipase family I.1. *PLoS ONE*, 7(12), 1-8.
- Kronqvist, N. (2009). Staphylococcal surface display in directed evolution. Royal Institute of Technology, Sweden.
- Kumar, S., Kikon, K., Upadhyay, A., Kanwar, S.S. & Gupta, R. (2005). Production, purification, and characterization of lipase from thermophilic and alkaliphilic *Bacillus coagulans* BTS-3. *Protein Expression & Purification*, 41, 38-44.
- Kumar, T. M., Singh, R., Kumar Singh, R., Kim, I.-W. & Lee, J.-K. (2012). Computational approaches for rational design of proteins with novel functionalities. *Computational and Structural Biotechnology*, 2, 1-13.
- Kuwahara, K., Angkawidjaja, C., Matsumura, H., Kogal, Y., Takano, K. & Kanaya, S. (2008). Importance of the Ca<sup>2+</sup>-binding sites in the N-catalytic domain of a family I.3 lipase for activity and stability. *Protein Engineering, Design & Selection*, 21(12), 737-744.
- Kwon, D. Y. & Rhee, J. S. (1986). A simple and rapid colorimetric method for determination of free fatty acids for lipase assay. *JAACS*, 63(1), 86-92.
- Kwon, H. J., Haruki, M., Morikawa, M., Omori, K. & Kanaya, S. (2002). Role of repetitive nine-residue sequence motifs in secretion, enzymatic activity, and protein conformation of a family I.3 lipase. *Journal of Bioscience and Bioengineering*, 93(2), 157-164.
- Laane, C., Boeren, S., Vos, K. & Veeger, C. (1987.) Rules for optimization of biocatalysis in organic solvents. *Biotechnological Bioengineering*, 30(1), 81-87.
- Laemmli, U. K. (1970). Cleavage of structure protein during assembly of the head of bacteriophage T4. *Nature*, 227, 680-685.
- Lane, M. D. & Seelig, B. (2014). Advances in the directed evolution of proteins. *Current Opinion in Chemical Biology*, 129-136.
- Leemhuis, H., Kelly, R. M. & Dijkhuizen, L. (2009). Directed evolution of enzymes: Library screening strategies. *IUBMB Life*, 61(3), 222-228.
- Leow, T. C., Rahman, R. N. Z. R. A., Basri, M. & Salleh, A. B. (2007). A thermoalkaliphilic lipase of *Geobacillus* sp. T1. *Extremophiles*, 11(3), 527-535.

- Li, S., Pang, H., Lin, K., Xu, J., Zhao, J. & Fan, L. (2011). Refolding, purification and characterization of an organic solvent-tolerant lipase from *Serratia marcescens* ECU1010. *Journal of Molecular Catalysis B: Enzymatic*, 148, 114-120.
- Liebeton, K., Zonta, A., Schimossek, K., Nardini, M., Lang, D., Dijkstra, B. W. & Jaeger, K. E. (2000). Directed evolution of an enantioselective lipase. *Chemistry & Biology*, 7(9), 709-718.
- Linhartová, I., Bumba, L., Mašín, J., Basler, M., Osička, R., Kamanová, J., Procházková, K., Adrinks, I., Hejnova –Holubova, J., Sadilkova, L., Morova, J. & Sebo, Peter., (2010). RTX proteins: a highly diverse family secreted by a common mechanism. *FEMS Microbiology Reviews*, 34, 1076-1112.
- Lipovsek, D., Antipov, E., Armstrong, K. A., Olsen, M. J., Klibanov, A. M., Tidor, B. & Wittrup, K. D. (2007). Selection of horseradish peroxidase variants with enhanced enantioselectivity by yeast surface display. *Chemistry and Biology*, 14, 1176-1185.
- Maharana, A. & Ray, P. (2015). A novel cold-active lipase from psychrotolerant *Pseudomonas* sp. AKM-L5 showed organic solvent resistant and suitable for detergent formulation. *Journal of Molecular Catalysis. B, Enzymatic*, 120, 173-178.
- Maiangwa, J., Ali, M. S. M., Salleh, A. B., Rahman, R. N. Z. R. A., Shariff, F. M. & Leow, T. C. (2015). Adaptational properties and applications of cold-active lipases from psychrophilic bacteria. *Extremophiles*, 9(2), 235-247.
- Mala, J.G.S. & Takeuchi, S. (2008). Understanding structural features of microbial lipases- An overview. *Analytical Chemistry Insights*, 3, 9-19.
- Maraitea, A., Hoyos, P., Carballeira, J.S., Cabrerac, A.C., Ansorge-Schumacher, M.B. & Alcantara, A. R. (2013). Lipase from *Pseudomonasstutzeri*: Purification, homology modelling and rational explanation of the substrate binding mode. *Journal of Molecular Catalysis B: Enzymatic*, 87, 88-97.
- Maruyama, T., Nakajima, M., Ichikawa, S., Nabetani, H., Furusoki, S. & Seki, M. (2000). Oil-water interfacial activation of lipase for interesterification of triglyceride and fatty acid. *Journal of American Oil Chemists' Society*, 77(11), 1121-1126.
- Masdro, N., Shukor, M.S.A., Khan, A., Halmi, M.I.E., Abdullah, S.R.S., Shamaan, N.P. & Shukor, M. Y. (2015). Isolation and characterization of a molybdenum-reducing and SDS-degrading *Klebsiella oxytoca* strain Aft-7 and its bioremediation application in the environment. *Bioversitas*, 16(2), 238-246.
- Mayeer, D.P., Anderson, D., Cary, C. & Cowan, D.A. (2014). Some like it cold: Understanding the survival strategies of psychrophiles. *EMBO Reports*, 17(6), 781-927.
- McCabe, R. W., Rodger, A. & Taylor, A. (2005). A study of the secondary structure of

*Candida antarctica* lipase B using synchrotron radiation circular dichroism measurements. *Enzyme and Microbial Technology*, 36, 70–74.

- McCullum, E. O., Williams, B. A. R., Zhang, J. & Chaput, J. C. (2010). Random mutagenesis by error-prone PCR. In Braman, J (Ed.), *Methods in Molecular Biology: In vitro Mutagenesis Protocols* (pp.103-109). New York: Springer Science + Business Media.
- McLachlan, M.J., Sullivan, R.P. and Zhao, H. (2009). Directed enzyme evolution and high throughput screening. In Tao, J., Lin, G., Liese, A. (Eds.), *Biocatalysis for the Pharmaceutical Industry-Discovery, Development and Manufacturing* (pp. 45-64). Singapore: John Wiley and Sons.
- Medyantseva, E.P., Vertlib, M G. & Budnikov, G. K. (1998). Metal ions as enzyme effectors. *Russian Chemical Reviews*, 67(3), 225-232.
- Mierlo, C.P.M., de Jongh, H. H. J. & Visser, A. J. W. G. (2007). Circular dichroism of proteins in solution and at interfaces. *Applied Spectroscopy Reviews*, 35(4), 277-313.
- Miyazaki, K., Wintrode, P. L., Grayling, R. A., Rubingh, D. N. & Arnold, F. H. (2000). Directed evolution study of temperature adaptation in a psychrophilic enzyme. *Journal of Molecular Biology*, 297(4), 1015-1026.
- Moyer, C. L. & Morita, R. Y. (2007). Psychrophiles and psychrotrophs. *Encyclopedia of Life Sciences*, 1-6.
- Mrabet, N. T., Broeck, X. A. V., Brande, I. V., Stanssens, P., Lambeir, A. M., Matthijssens, G., Jenkins, J., Chiadmi, M., Tilbeurgh, H. V., Rey, F., Janin, J., Quax, W. J., Lasters, I., Maeyer, M. D. & Wodak, S. J. (1992). Arginine residues as stabilizing elements in proteins. *Biochemistry*, 31, 2239-2253.
- Naik, S., Basu, A., Saikia, R., Madan, B., Paul, P., Chatterjee, R., Brask, J. & Svendsen, A. (2010). Lipases for use in industrial biocatalysis: Specificity of selected structural groups of lipases. *Journal of Molecular Catalysis B: Enzymatic*, 65, 18-23.
- Nannemann, D. P., Birmingham, W. R., Scism, R. A. & Bachmann, B. O. (2011). Assessing directed evolution methods for the generation of biosynthetic enzymes with potential in drug biosynthesis. *Future Medicinal Chemistry*, 3(7), 809-819.
- Narasu, M. L., Sirisha, E., Rajasekar, N. & Lakshmi Narasu, M. (2010). Isolation and optimization of lipase producing bacteria from oil contaminated soils. *Advances in Biological Research*, 4(5), 249–252.
- Nawani, N. & Kaur, J. (2000). Purification, characterization and thermostability of lipase from a thermophilic *Bacillus* sp. J33. *Molecular and Cellular Biochemistry*, 206, 91–96.
- Packer, M. S. & Liu, D. R. (2015). Over many generations, iterated mutation and

natural selection during biological evolution provide solutions for challenges that organisms face in the natural world. *Nature Publishing Group*, 3927, 1-16.

- Pal, D. & Chakrabarti, P. (1998). Different types of interaction involving cysteine sulfhydryl group in proteins. *Journal of Biomolecular Structure & Dynamics*, 15(6), 1059-1072.
- Pandey, A., Benjamin, S., Soccol, C. R., Nigam, P., Krieger, N. & Soccol, V. T. (1999). The realm of microbial lipases in biotechnology. *Biotechnology and Applied Biochemistry*, 29 (2), 119–131.
- Petrounia, I. P. & Arnold, F. H. (2000). Designed evolution of enzymatic properties. *Current Opinion in Biotechnology*, 11, 325-330.
- Panizza, P., Syfantou, N., Pastor, F. I. J., Rodriguez, S. & Diaz, P. (2012). Acidic lipase Lip 1.3 from *Pseudomonas fluorescens*-like strain displays unusual properties and shows activity on secondary alcohols. *Journal of Applied Microbiology*, 114, 722-732.
- Petsko, G. A. & Ringe, C. (2004) *Protein structure and function*. United States: New Science Press.
- Pouderoyen, G., Eggert, T., Jaeger, K.E. & Dijkstra, B. (2001). The crystal structure of *Bacillus subtilis* lipase: A minimal  $\alpha/\beta$  hydrolase fold enzyme. *Journal of Molecular Biology*, 309, 215-226.
- Pritchard, L., Corne, D., Kell, D., Rowland, J. & Winson, M. (2005). A general model of error-prone PCR. *Journal of Theoretical Biology*, 234, 497-509.
- Rashid, N., Shimada, Y., Ezaki, S., Atomi, H., & Imanaka, T. (2001). Low-temperature lipase from psychrotrophic *Pseudomonas* sp. strain KB700A. *Applied and Environmental Microbiology*, 67(9), 4064-4069.
- Reetz, M. T., Soni, P., Fernandez, L., Gumulya, Y. & Carballeira, J. D. (2010). Increasing the stability of an enzyme toward hostile organic solvents by directed evolution based on iterative saturation mutagenesis using the B-FIT method. *The Royal Society of Chemistry*, 46, 8657-8658.
- Rehm, S., Trodler, P. & Pleiss, J. (2010). Solvent-induced lid opening in lipases: A molecular dynamics study. *Protein Science*, 19 (11), 2122-30.
- Riordan, J. F. (1977). The role of metals in enzyme activity. *Annals of Clinical and Laboratory Science*, 7(2), 119-129.
- Rosenberg, J. M. (1991). Structure and function of restriction endonucleases. *Current Opinion in Structural Biology*, 1, 104–113.
- Rubin-Pitela, S.B., Chob, C. M-H., Chenb, W. & Zhaoa, H. (2006). Directed evolution tools in bioproduct and bioprocess development. In Chang-Tian,Y (Ed.),

*Bioprocessing for Value-Added Products from Renewable Resources* (pp. 49-72). Netherlands: Elsevier Science.

- Rubingh, D.N and Grayling, R.A. (2012). Protein Engineering. In S. Lutz and U.T. Bornscheuer (Ed.), *Biotechnology* (pp. 140-164). USA: The Procter and Gamble Company.
- Sangeetha, R., Arulpandi, I., & Geetha, A. (2011). Bacterial lipases as potential industrial biocatalysts: An overview. *Research Journal of Microbiology*, 6(1), 1-24.
- Sangster, J. (1989). Octanol-water partition coefficients of simple organics compounds. *Journal of Physical and Chemical Reference Data*, 18 (3), 1111- 1227.
- Selifonova, O., Valle, F. & Schellenberger, V. (2001). Rapid evaluation of novel traits in microorganisms. *Applied and Environmental Microbiology*, 67, 3645-3649.
- Sharma, R., Chistib, Y & Banerjee, U. C. (2001). Production, purification, characterization, and applications of lipases. *Biotechnology Advances*, 19, 627-662.
- Shuo-Shuo, C., Xue-Zheng, L. & Ji-Hong, S. (2011). Effects of co-expression of molecular chaperones on heterologous soluble expression of the cold-active lipase Lip-948. *Protein Expression and Purification*, 77(2), 166-172.
- Siddiqui, K. S. & Cavicchioli, R. (2006). Cold-adapted enzymes. *Annual Reviews of Biochemistry*, 75, 403–433.
- Silver, P.A., Way, J.C., Arnold, F.H. & Meyerowitz, J. T. (2014). Synthetic biology: engineering explored. *Nature*, 509, 166–167.
- Sirisha, E., Rajasekar, N. & Narasu, M. L. (2010). Isolation and optimization of lipase producing bacteria from oil contaminated soils. *Advances in Biological Research*, 4(5), 249-252.
- Sissi, C. & Palumbo, M. (2009). Effects of magnesium and related divalent metal ions in topoisomerase structure and function. *Nucleic Acids Research*, 37(3), 702-711.
- Smalas, A. O., Leiros, H. K. S., Os, V. & Willassen, N. P. (2000). Cold adapted enzymes. *Biotechnology Annual Review*, 6, 1-57.
- Sriprapundh, D., Vieille, C. & Zeikus, G. J. (2003). Directed evolution of *Thermotoga neapolitana* xylose isomerase: High activity on glucose at low temperature and low pH. *Protein Engineering*, 16(9), 683-690.
- Steapnkova, V., Bidmanova, S., Koudelakova, T., Prokop, Z., Chaloupkova, R. & Damborsky, J. (2013). Strategies for stabilization of enzymes in organic solvents. *ACS Catalysis*, 3(12), 2823–2836.



- Svedsen, A. (2000). Lipase protein engineering. *Biochimica et Biophysica Acta*, 223-238.
- Sverdlov, E. & Azhikina, T. (2005). Primer Walking. *Encyclopedia of Life Sciences*, 1-3.
- Suzuki, T., Nakayama, T., Kurihara, T., Nishini, T. & Esaki, N. Cold-active lipolytic activity of psychrotrophic *Acinetobacter* sp. Strain No. 6. *Journal of Bioscience and Bioengineering*, 92(2), 144-148.
- Tao, H. & Cornish, V.W. (2002). Milestones in directed enzyme evolution. *Current Opinion in Chemical Biology*, 6, 858-864.
- Taylor, J. L., Price, J. E. & Toney, M. D. (2015). Directed evolution of the substrate specificity of dialkylglycine decarboxylase. *Biochimica et Biophysica Acta - Proteins and Proteomics*. 1854(2), 146-155.
- Tetin, S. Y., Prendergast, F. G. & Yu Venyaminov, S. (2003). Accuracy of protein secondary structure determination from circular dichroism spectra based on immunoglobulin. *Analytical Biochemistry*, 321(2), 183-187.
- Tiwari, M.K., Singh, R., Singh, R.K, Kim, I-W. & Lee, J-K. (2012). Computational approaches for rational design of proteins with novel functionalities. *Computational and Structural Biotechnological Journal*, 2, 1-13.
- Tracewell, C. A. & Arnold, F. H. (2009). Directed enzyme evolution: climbing fitness peaks one amino acid at a time. *Current Opinion in Chemical Biology*, 13, 3-9.
- Treichel, H., de Oliveira, D., Mazutti, M. A., Di Luccio, M. & Oliveira, J. V. (2010). A review on microbial lipases production. *Food and Bioprocess Technology*, 3, 182-196.
- Tutino, M. L., di Prisco, G., Marino, G & de Pascale, D. (2009). Cold-adapted esterases and lipases: From fundamentals to application. *Protein & Peptide letters*, 16, 1172-1180.
- Turanli-Yildiz, B., Alkim, C. & Petek Cakar, Z. (2012). Protein Engineering Methods and Applications. In P.Kaumaya (Ed.), *Protein Engineering* (pp. 33-56).Croatia: INTECH.
- Turner, N.A., Needs, E.C., Khan, J.A. & Vulfson, E.V. (2000). Analysis of conformational states of *Candida rugosa* lipase in solution: Implications for mechanism of interfacial activation and separation of open and closed forms. *Biotechnology and Bioengineering*, 72(1), 108-118.
- Vallejo, L. F. & Rinas, U. (2004). Microbial cell factories strategies for the recovery of active proteins through refolding of bacterial inclusion body proteins. *Microbial Cell Factories*, 3(11), 1-12.
- Verma N, Thakur, S. & Bhatt A. K. (2012). Microbial Lipases: Industrial applications

- and properties (A Review). *International Research Journal of Biological Sciences*, 1(8), 2278–3202.
- Wang, D., Zhao, C., Cheng, R. & Sun, F. (2000). Estimation of the mutation rate during error-prone Polymerase Chain Reaction. *Journal of Computational Biology*, 7(12), 143–158.
- Werkman, J. R., Pattanaik, S. & Yuan, L. (2011). Directed evolution through DNA shuffling for the improvement and understanding of genes and promoters. *Methods in Molecular Biology*, 754, 325-342.
- Whitmore, L. & Wallace, B. A. (2004). DICHROWEB, an online server for protein secondary analyses from circular dichroism spectroscopic data. *Nucleic Acids Research*, 32, 668-673.
- Wintrode, P. L., Miyazaki, K. & Arnold, F.H. (2000). Cold adaptation of a mesophilic subtilisin-like protease by laboratory evolution. *The Journal of Biological Chemistry*, 275(41), 31625-31640.
- Wu, D. Y. & Wallace, R. B. (1989). Specificity of the nick-closing activity of bacteriophage T4 DNA ligase. *Gene*, 76(2), 245-54.
- Xiao, H., Bao, Z. & Zhao, H. (2015). High throughput screening and selection methods for directed enzyme evolution. *Industrial & Engineering Chemistry Research*, 54, 4011-4020.
- Yan, Q., Duan, X., Liu, Y., Jiang, Z. & Yang, S. (2016). Expression and characterization of a novel 1,3-regioselective cold-adapted lipase from *Rhizomucor endophyticus* suitable for biodiesel synthesis. *Biotechnology for Biofuels*, 9(86), 1-13.
- Yano, T., Oue, S. & Kagamiyama, H. (1998). Directed evolution of an aspartate aminotransferase with new substrate specificities. *Biochemistry*, 95, 5511–5515.
- Yuan, Z., Bailey, T. L. & Teasdale, R. D. (2005). Prediction of protein B-factor profiles. *Proteins: Structure, Function and Genetics*, 58(4), 905-912.
- Zhang, P. Y-H., Himmel, M.E. & Mielenz, J.R. (2006). Outlook for cellulase improvement: Screening and selection strategies. *Biotechnology Advances*, 24, 452-481.
- Zhang, J.W. & Zeng, R.Y. (2008). Molecular cloning and expression of a cold-adapted lipase gene from an Antarctic deep sea psychrotrophic bacterium *Pseudomonas* sp. 7323. *Marine Biotechnology*, 10, 612–621.
- Zhao, H. (2004). Staggered extension process in vitro DNA recombination. *Methods in Enzymology*, 338, 42-49.

Zhaor, J. & Winkler, M. E. (2000). Reduction of GC to TA transversion mutation by overexpression of MutS in *Escherichia coli* K-12. *Journal of Bacteriology*, 182 (17), 5025-5028.

Zheng, X., Chu, X., Zhang, W., Wu, N. & Fan, Y. (2011). A novel cold-adapted lipase from *Acinetobacter* sp. XMZ-26: gene cloning and characterization. *Applied Microbiology and Biotechnology*, 90, 971-990.

