



UNIVERSITI PUTRA MALAYSIA

***DIRECTED EVOLUTION OF RECOMBINANT C-TERMINAL TRUNCATED
LIPASE FROM *Staphylococcus epidermidis* AT2 FOR ENHANCED
THERMAL STABILITY***

JIIVITTHA VENO

FBSB 2018 8



**DIRECTED EVOLUTION OF RECOMBINANT C-TERMINAL TRUNCATED
LIPASE FROM *Staphylococcus epidermidis* AT2 FOR ENHANCED THERMAL
STABILITY**

By

JIIVITTHA VENO

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

June 2017

All material contained within the thesis, including without limitation text, logos, icons, photographs and all other artwork, is copyright material of Universiti Putra Malaysia unless otherwise stated. Use may be made of any material contained within the thesis for non-commercial purposes from the copyright holder. Commercial use of material may only be made with the express, prior, written permission of Universiti Putra Malaysia.

Copyright © Universiti Putra Malaysia



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

**DIRECTED EVOLUTION OF RECOMBINANT C-TERMINAL TRUNCATED
LIPASE FROM *Staphylococcus epidermidis* AT2 FOR ENHANCED THERMAL
STABILITY**

By

JIVITTHA VENO

June 2017

Chairman: Professor Raja Noor Zaliha Raja Abd Rahman, PhD
Faculty: Biotechnology and Biomolecular Sciences

Lipases specifically thermostable lipases which are origin from microbial are desirable commercially as they are resilient and robust. In the industrial processes, lipases are expected to operate at temperatures above 40°C and could retain activity in organic solvents. However, screening of organic tolerant lipases with increased thermal property from organisms is time consuming for high yield. Therefore, the objective of this study is to evolve rT-M386 lipase using error-prone PCR to achieve thermostability and to study the effect of mutation on biochemical properties and structural conformations of the lipase. In the first screening, approximately 1500 positive colonies were obtained. From these thousands of colonies, 900 colonies were analyzed quantitatively and resulted in seven mutant clones which exhibited higher activity when compared to rT-M386. Out of seven mutants, G210C lipase demonstrated a remarkable improvement of the activity by 5-fold when compared with rT-M386 at 50°C. rT-M386 and G210C were purified concurrently using GST-affinity chromatography with the yield of 92.25% and 92.17%, respectively. A distinct single band with a molecular weight of 69 kDa was observed on SDS-PAGE. The purified G210C lipase showed a 20°C increased of the optimum temperature. Apparently, rT-M386 could not maintain its stability for 30 min at temperatures above 20°C as its decreasing drastically. Meanwhile, G210C presented an exceptional thermal stability profile as it can sustain its stability at 50°C with 100% of relative activity. In addition, G210C lipase displayed more prolonged half-life in the range of 40-60°C as compared to rT-M386. Both lipases exhibited optimal activity and stability at pH 8. G210C exhibited the highest activity in the presence of diethyl ether, isopropanol, DMSO and methanol at 50°C compared to rT-M386. Structural analysis of rT-M386 and G210C lipases has demonstrated variations in structural conformation. CD spectral analysis revealed that G210C attained more structural stability compared to the

rT-M386 lipase and this supported the experimental findings. The structure was found more stable and compact as revealed by molecular dynamic simulation, suggesting its tolerance at elevated temperature. In conclusion, the results indicated that single residue substitution of G210C lipase contributes to the enhancement of thermal stability without adversely impacting the catalytic performance. rT-M386 lipase was successfully mutated via directed evolution strategy and the findings will be useful insight on the understanding of the structural-functional adaptation of thermostable lipases.



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

MUTASI SECARA RAWAK ATAS “RECOMBINANT C-TERMINAL TRUNCATED” LIPASE DARIPADA *Staphylococcus epidermidis* AT2 BAGI MENINGKATKAN KADAR STABILITI PADA SUHU TINGGI

Oleh

JIIVITTHA VENO

Jun 2017

Pengerusi: Professor Raja Noor Zaliha Raja Abd Rahman, PhD
Fakulti: Bioteknologi dan Sains Biomolekul

Lipase khususnya termostabil lipase yang berasal dari mikrob adalah diminati secara komersial kerana mereka adalah berdaya tahan dan teguh. Dalam proses perindustrian, lipase dijangka beroperasi pada suhu melebihi 40°C dan dapat mengekalkan aktiviti dalam pelarut organik. Walau bagaimanapun, penyaringan lipase yang stabil terhadap pelarut organik dengan peningkatan profil termal daripada organisma memerlukan lebih masa untuk hasil lipase yang tinggi. Maka, objektif kajian ini adalah untuk memutasikan rT-M386 lipase dengan menggunakan teknik Reaksi Berantai Polimer beralat untuk mencapai termostabiliti dan untuk mengkaji kesan mutasi dari segi sifat biokimia dan bentuk struktur lipase. Dalam pemeriksaan pertama, kira-kira 1000-1500 koloni positif telah diperolehi. Daripada ribuan koloni, 900 koloni telah dianalisis secara kuantitatif dan menghasilkan hanya 7 klon mutan yang menunjukkan aktiviti yang lebih tinggi jika dibandingkan dengan rT-M386. Mutan G210C menunjukkan peningkatan aktiviti sebanyak 5 kali ganda jika dibandingkan dengan rT-M386 pada 50°C. rT-M386 dan G210C telah ditulenkan menggunakan GST-afiniti kromatografi dengan hasil 92.25% dan 92.17% masing-masing. Satu jalur yang jelas dengan jisim molekul 69 kDa diperhatikan pada SDS-PAGE. G210C lipase yang ditulenkan menunjukkan peningkatan suhu optima sebanyak 20°C. rT-M386 tidak dapat mengekalkan kestabilan selama 30 minit pada suhu yang lebih tinggi daripada 20°C. Sementara itu, G210C menunjukkan profil kestabilan terma yang luar biasa kerana ia boleh mengekalkan kestabilan konformasi pada 50°C dengan 100% daripada aktiviti relatif. Di samping itu, G210C lipase menunjukkan separuh hayat yang lebih panjang dalam lingkungan 40-60°C berbanding dengan rT-M386. Kedua-dua lipase menunjukkan aktiviti optimum dan kestabilan pada pH 8. G210C menunjukkan aktiviti tertinggi dalam diethyl ether, isopropanol, DMSO dan metanol pada 50°C berbanding rT-M386. Analisis struktur

lipase rT-M386 dan G210C telah memaparkan variasi dalam konformasi struktur. Analisis CD spektrum mendedahkan bahawa G210C mencapai struktur yang lebih stabil berbanding dengan rT-M386 dan ini menyokong dapatan eksperimen. Struktur ini didapati lebih stabil dan padat seperti yang didedahkan oleh simulasi dinamik molekul, menunjukkan toleransi pada suhu tinggi. Kesimpulannya, keputusan menunjukkan bahawa satu penggantian residu G210C lipase menyumbang kepada peningkatan kestabilan haba tanpa memberi kesan negatif ke atas tahap pemangkinan. rT-M386 lipase telah berjaya bermutasi melalui strategi mutase secara rawak dan penemuan ini telah membolehkan pemahaman yang mendalam mengenai adaptasi struktur-fungsi lipase termostabil.

ACKNOWLEDGEMENT

I wish to express my foremost appreciation to my committee chair Professor Dr. Raja Noor Zaliha Raja Abdul Rahman and supervisory committee members, Associate Professor Mohd Shukuri Mohamad Ali and Dr. Nor Hafizah Ahmad Kamarudin for their invaluable guidance, encouragement, through the course of this thesis by enlightening me scientifically till the end this project. This thesis would not have been possible to submit at this present time without their strong support and selfless efforts to make the deadline.

My special thanks go to all my dear EMTech lab mates for their sincere help offers, cares, friendships, moral support, inspiration and for both productive and cheerful moments.

I am eternally grateful to my family and friends for their positive words, endless support and enormous encouragement throughout this project. Last but not least, MOM without you I would never be here and have succeeded in my academic endeavors.

This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfilment of the requirement for the degree of Master of Science. The members of the Supervisory Committee were as follows:

Raja Noor Zaliha Raja Abd. Rahman, PhD

Professor
Faculty of Biotechnology and Biomolecular Sciences
Universiti Putra Malaysia
(Chairman)

Mohd Shukuri Mohamad Ali, PhD

Associate Professor
Faculty of Biotechnology and Biomolecular Sciences
Universiti Putra Malaysia
(Member)

Nor Hafizah Ahmad Kamarudin, PhD

Senior lecturer
Centre of Foundation Studies for Agricultural Science
Universiti Putra Malaysia
(member)

ROBIAH BINTI YUNUS, PhD

Professor and Dean
School of Graduate Studies
Universiti Putra Malaysia

Date:

Declaration by graduate student

I hereby confirm that:

- this thesis is my original work;
- quotations, illustrations and citations have been duly referenced;
- this thesis has not been submitted previously or concurrently for any other degree at any other institutions;
- intellectual property from the thesis and copyright of thesis are fully-owned by Universiti Putra Malaysia, as according to the Universiti Putra Malaysia (Research) Rules 2012;
- written permission must be obtained from supervisor and the office of Deputy Vice-Chancellor (Research and Innovation) before thesis is published (in the form of written, printed or in electronic form) including books, journals, modules, proceedings, popular writings, seminar papers, manuscripts, posters, reports, lecture notes, learning modules or any other materials as stated in the Universiti Putra Malaysia (Research) Rules 2012;
- there is no plagiarism or data falsification/fabrication in the thesis, and scholarly integrity is upheld as according to the Universiti Putra Malaysia (Graduate Studies) Rules 2003 (Revision 2012-2013) and the Universiti Putra Malaysia (Research) Rules 2012. The thesis has undergone plagiarism detection software.

DECLARATION

Signature: _____ Date: _____

Name and Matric No.: Jiivittha Venno, GS37107

TABLE OF CONTENTS

ABSTRACT	Page
ABSTRAK	i
ACKNOWLEDGEMENTS	iii
APPROVAL	v
DECLARATION	vi
LIST OF FIGURES	viii
LIST OF TABLES	xiii
LIST OF ABBREVIATIONS	xv
	xvi
CHAPTER	
1 INTRODUCTION	1
2 LITERATURE REVIEW	3
2.1 Lipases	3
2.2 Source of lipases	4
2.3 Bacterial Lipases	5
2.4 Staphylococcal lipases	6
2.5 Thermostable Lipase	7
2.6 Application of microbial lipases in industries	8
2.7 General structure of lipase	10
2.8 Protein Engineering	11
2.9 Directed evolution	12
2.10 Selection and screening techniques	12
2.11 Molecular dynamics simulation	12
3 MATERIALS AND METHODS	
3.1 Materials	15
3.2 Experimental design	15
3.3 Source of enzyme	16
3.4 Media preparation	16
3.4.1 Preparation of LB-tributylin agar	16
3.4.2 Preparation of LB-Rhodamine B agar	16
3.4.3 Preparation of Triolein agar	17
3.4.4 Preparation of LB broth	17
3.5 Preparation of glycerol stock culture	18
3.6 Preparation of competent cells	18
3.7 Plasmid extraction of rT-M386 and pGEX6p1 Vector	18
3.8 Generation of mutant library	18
3.8.1 Error-prone PCR	19
3.9 Purification of PCR product	19
3.10 Double digestion of purified PCR product and vector	19
3.11 Ligation of purified digested vector and PCR product	19
3.12 Heat shock transformation of <i>E. coli</i> strain BL21 (DE3) with ligated PCR product	20
3.13 Screening and selection of mutants	20

3.14	Expression of soluble proteins of mutants	20
3.15	Lipase activity assay	21
3.16	Protein Determination	21
3.16.1	Bovine Serum Albumin (BSA) standard curve	21
3.17	Sequencing and sequence analysis	21
3.18	SDS-PAGE analysis	22
3.19	Native PAGE analysis	22
3.20	Lipase activity staining	22
3.21	Purification of mutant and rT-M386 lipases	22
3.21.1	Preparation of crude extract	23
3.21.2	Glutathione-S-transferase (GST) affinity chromatography	23
3.22	Biochemical characterization of purified mutant and rT-M386 lipases	23
3.22.1	Effect of temperature on lipase activity	23
3.22.2	Effect of temperature on lipase stability	24
3.22.3	Effect of temperature on lipase thermal stability (half-life)	24
3.22.4	Effect of pH on lipase activity	24
3.22.5	Effect of pH on lipase stability	25
3.22.6	Effect of organic solvents on lipase activity	25
3.23	CD spectra analysis of purified mutant and rT-M386 lipases	25
3.23.1	Secondary structure analysis of purified mutant and rT-M386 lipases	25
3.23.2	Thermal denaturation of purified mutant and rT-M386 lipases	25
3.24	Computational analysis	25
3.24.1	3D structure prediction of mutant and rT-M386 lipases	25
3.24.2	Molecular Dynamic Simulations	26
3.25	Statistical analysis	27
4	RESULTS AND DISCUSSIONS	
4.1	Research background	28
4.2	Generation and of mutant library	28
4.2.1	Random mutagenesis by error-prone PCR (eP-PCR)	28
4.2.2	Cloning and transformation of competent <i>E. coli</i> cells with PCR product	31
4.3	Screening and selection of mutant clones	33
4.3.1	Quantitative analysis of mutant clones by lipase assay	34
4.3.2	Qualitative analysis of mutant 7 by plate assays	36
4.4	Analysis of the lipase gene in mutant 7 by double digestion and PCR	38
4.4.1	Sequence analysis of mutant 7 to identify mutation point	39
4.5	Expression of rT-M386 and G210C lipases	42
4.6	Purification of rT-M386 and G210C lipases by GST-affinity chromatography	43

4.6.1	Analysis of purification product rT-M386 and G210C lipases	46
4.7	Characterization of purified rT-M386 and G210C lipases	47
4.7.1	Effect of temperature on lipase activity and stability	48
4.7.2	Effect of mutation on lipase thermal stability (half-life)	51
4.7.3	Effect of pH on lipase activity and stability	54
4.7.4	Effect of organic solvents on lipase activity	58
4.8	CD spectra analysis of purified rT-M386 and G210C fusion lipases	60
4.8.1	Secondary structure analysis of purified rT-M386 and G210C fusion lipases	60
4.8.2	Thermal denaturation of purified rT-M386 and G210C lipases	62
4.9	Computational analysis	63
4.9.1	Template selection for homology modeling of rT-M386 and G210C lipases	63
4.9.2	Evaluation of the predicted rT-M386 and G210C lipases structures	64
4.9.3	Structural analysis of rT-M386 and G210C lipases	70
4.9.4	Molecular Dynamic Simulation of rT-M386 and G210C lipases	81
5	CONCLUSION	
5.1	Conclusion	97
5.2	Recommendations	98
	REFERENCES	99
	APPENDICES	120
	BIODATA OF THE STUDENT	127
	LIST OF PUBLICATIONS	128

LIST OF FIGURES

Figure		Page
1	Agarose gel 1% (w/v) electrophoresis of error-prone PCR and the purified PCR product.	28
2	Agarose gel 1% (w/v) electrophoresis of single and double digested pGEX6p1 vector and double digested PCR product.	29
3	Transformed cells spread on tributyrin solid media	30
4	Grid plates of mutant clones	31
5	Lipase activity of rT-M386 and mutant clones at 50°C	32
6	Qualitative screening for lipolytic activity	35
7	Agarose gel 1% (w/v) electrophoresis of recombinant plasmid extraction, double digestion and PCR	36
8	Sequence analysis of rT-M386 and mutant lipases.	38
9	SDS-PAGE analysis for small scale expression	41
10	GST-affinity chromatography profile.	42
11	SDS-PAGE analysis of purification	43
12	Analysis of purification product	45
13	Effect of temperature on lipase activity and stability	47
14	Effect of mutation on lipase thermal stability (half- life).	49
15	Effect of 55 and 60°C on G210C lipase thermal stability (half-life).	50
16	Effect of pH on lipase activity.	52
17	Effect of pH on lipase stability	54
18	Effect of organic solvents on lipase activity	56
19	Far-UV spectra of rT-M386 and G210C fusion lipases	58
20	Thermal denaturation curve of rT-M386 and G210C lipase	59
21	PSI-BLAST result of rT-M386 and G210C lipase.	60
22	Evaluation of predicted lipase structures with Ramachandran plot	62
23	Evaluation of predicted lipase structures with ERRAT	65
24	Predicted 3D structure of lipases	67
25	The predicted lid region of G210C lipase	68
26	Hydrogen bond interactions at mutation site	70
27	Calcium binding site of lipases	72
28	Zinc binding site of lipases	74
29	Schematic diagram of secondary structures	76
30	RMSD profile of the C α position for rT-M386 and G210C as per residue	79
31	RMSD profile for rT-M386 and G210C as per residue as per time	81
32	RMSF of the C α position as per residue for rT-M386 and G210C	83
33	SASA of rT-M386 and G210C as per time	85
34	Radius of Gyration of rT-M386 and G210C as per time	87
35	The 3D structure of rT-M386 lipase in time scale between 0, 10 and 20 ns simulation	89

36	The 3D structure of G210C lipase in time scale between 0, 10 and 20 ns simulation	90
37	Superposition of predicted structure of rT-M386 lipase and G210C lipase	92



LIST OF TABLES

Table		Page
1	Specific activity of rT-M386 and mutant 7 at 25°C	35
2	Specific activity of rT-M386 and mutant clones at 50°C	35
3	Purification table of lipases	46
4	Secondary structure composition of rT-M386 and G210C lipases	62



LIST OF ABBREVIATIONS

A280	Absorbance at 280 nm
A595	Absorbance at 595 nm
A600/ OD600	Absorbance/ optical density at 600 nm
A410	Absorbance at 410 nm
bp	base pair
xg	relative centrifugal force
g	gram
g/L	gram /Litre
h	hour
IPTG	isopropyl β -D- Thiogalactopyranoside
kDa	kilo Dalton
K	Kelvin
kB	kilo base pair
L	Liter
M	Molar
mA	mili ampere
mAU	mili absorbance unit
mM	millimolar
mdeg	mili degree
min	minute
ml	milliliter
mg/L	milligram/Liter
nm	nanometer
ns	nanosecond
OD	optical density
ps	picoseconds
rpm	rotation per minute
s	second
SDS	Sodium dodecyl sulphate
SDS-PAGE	Sodium dodecyl sulphate polyacrylamide gel electrophoresis
μ mole	micromole
μ L	microlitre
U/ mL	Unit per milliliter
U/ mg	Unit per milligram
v/ v	Volume per volume
w/ v	Weight per volume
V	Voltage

CHAPTER 1

INTRODUCTION

Lipases are versatile due to its capability to react in both aqueous and non-aqueous environments and as biocatalyst there are considerably economical compared to conventional chemical reactions. Thermostability of an enzyme is closely associated to its expression, folding, activities and functions, thereby thermal stability is fundamental property of an enzyme (Jemli, Ayadi-Zouari, Hlima, & Bejar, 2016). Thermostable lipases can be exploited in food processing, biopolymer; organic synthesis, biodiesel production, oleochemical and pulp industries (Andualema & Gessesse, 2012; Chakravorty, Parameswaran, Dubey, & Patra, 2011; Haki & Rakshit, 2003).

Organic tolerant lipases with increased thermal property are needed for industrial lipase-catalyzed reactions as they can increase the conversion rate of lipid substrates especially with the high melting point, resist the chemical modifications by elevated temperature and prevent contamination by microorganism (Bornscheuer & Pohl, 2001; S. Sharma & Kanwar, 2014). Lipases from *Candida antarctica* and *Burkholderia cepacia* are most well known in detergent and organic synthesis industrial applicants (Gunasekaran & Das, 2005). Although, many researches have characterized thermostable microbial lipases but there are only few lipases were reported to possess both thermostable and organic solvent-tolerant properties.

Up to now there are no studies described on thermostable lipases from *Staphylococcus* sp. and they are rarely exploited in the industrial processes because of their relatively lower catalytic activities and stabilities under conditions that required for industrial applications such as in high temperatures, non-aqueous solvents or extreme pH values (Cherif, Mnif, Hadrich, Abdelkafi, & Sayadi, n.d.). The highly produced staphylococcal lipases can be engineered to alter its properties for better performance in the practical applications in the aspect of quality and quantity (Horchani et al., 2012).

To expand the functionality of the lipase as well to explore the structure-function relationship, attempts had been made to evolve lipase that could overcome its limiting factors for industrial preference. Currently, recombinant DNA technology and protein engineering techniques have empowered lipases with wide enzymatic properties to compete with other well-established chemical technologies. Chemical compounds are environmentally hazardous unlike the harmless use of enzymes in the industry.

Over the years, researchers are intended to study the intrinsic stability of thermophilic proteins that render them to thermo-stabilization. The most commonly predicted factors are associated with their primary structure, hydrophobic interactions among the hydrophobic residues, formation of salt bridges due to the charged residues, hydrogen bonds between surrounding water molecules and the surface exposed hydrophilic

residues, packing efficiency, loop stabilization and defense against covalent destruction (Siddiqui, 2015; Trejo, 2013; Villeneuve, Muderhwa, Graille, & Haas, 2000).

Even though many thermostable lipases have been extensively studied on several aspects for years and commercialized, there are still numerous unresolved clear factors which influence the thermal stabilization of lipases correlating the role of sequence or amino acid compositions and structural conformations. Therefore, directed evolution which is leading to *in silico* comparison studies between thermostable and non-thermostable lipases could assist in the discovery of these factors. Eventually, this can bring out the effortless ways in protein engineering to produce lipases with remarkable characteristics based on industrial preferences. Recently, many enzymes were being engineered via directed evolution to own unique specificities and functionalities such thermostability, cold activity, gene expression, solubility, enantio-selectivity, substrate specificity, and solvent tolerance (Goomber, Kumar, Singh, Mishra, & Kaur, 2016; Sukumaran et al., 2015).

Previously, an organic tolerant AT2 lipase from *Staphylococcus epidermidis* had been truncated and designated as rT-M386 and in this study rT-M386 lipase was randomly mutated to enhance its thermal property. Therefore, this research aimed:

- a) To evolve rT-M386 lipase by directed evolution and identify the mutation point.
- b) To determine the biochemical and biophysical characteristics of selected purified mutant lipase (G210C).
- c) To analyze the effect of mutation on the structure of G210C lipase via *in silico* studies.

REFERENCES

- Abedi Karjiban, R., Lim, W. Z., Basri, M., & Abdul Rahman, M. B. (2014). Molecular dynamics of thermoenzymes at high temperature and pressure: A review. *Protein Journal*, 33(4), 369–376. <https://doi.org/10.1007/s10930-014-9568-8>
- Adamczak, M., & Krishna, S. H. (2004). Strategies for improving enzymes for efficient biocatalysis. *Food Technology and Biotechnology*, 42(4), 251–264.
- Adamczak, R., Porollo, A., & Meller, J. (2004). Accurate prediction of solvent accessibility using neural networks-based regression. *Proteins: Structure, Function, and Bioinformatics*, 56(4), 753–767. <https://doi.org/10.1002/prot.20176>
- Ahmed, E. H., Raghavendra, T., & Madamwar, D. (2010). An alkaline lipase from organic solvent tolerant *Acinetobacter* sp. EH28: Application for ethyl caprylate synthesis. *Bioresource Technology*, 101(10), 3628–3634. <https://doi.org/10.1016/j.biortech.2009.12.107>
- Akbulut, N., Tuzlakoglu Öztürk, M., Pijning, T., İşsever Öztürk, S., & Gümüşel, F. (2013). Improved activity and thermostability of *Bacillus pumilus* lipase by directed evolution. *Journal of Biotechnology*, 164(1), 123–129. <https://doi.org/10.1016/j.jbiotec.2012.12.016>
- Andualema, B., & Gessesse, A. (2012). Microbial Lipase and Their Industrial Applications: Review. *Biotechnology*. <https://doi.org/10.3923/biotech.2012.100.118>
- Angajala, G., Pavan, P., & Subashini, R. (2016). Lipases: An overview of its current challenges and prospectives in the revolution of biocatalysis. *Biocatalysis and Agricultural Biotechnology*, 7, 257–270. <https://doi.org/10.1016/j.bcab.2016.07.001>
- Angkawidjaja, C., & Kanaya, S. (2006). Family I.3 lipase: bacterial lipases secreted by the type I secretion system. *Cellular and Molecular Life Sciences*, 63(23), 2804–2817. <https://doi.org/10.1007/s00018-006-6172-x>
- Barriuso, J., Vaquero, M. E., Prieto, A., & Martínez, M. J. (2016). Structural traits and catalytic versatility of the lipases from the *Candida rugosa*-like family: A review. *Biotechnology Advances*, 34(5), 874–885. <https://doi.org/10.1016/j.biotechadv.2016.05.004>
- Bassegoda, A., Cesarini, S., & Diaz, P. (2012). LIPASE IMPROVEMENT: GOALS AND STRATEGIES. *Computational and Structural Biotechnology Journal*, 2(3). <https://doi.org/10.5936/csbj.201209005>

Bhattacharya, S., Lee, S., Grisshammer, R., Tate, C. G., & Vaidehi, N. (2014). Rapid computational prediction of thermostabilizing mutations for G protein-coupled receptors. *Journal of Chemical Theory and Computation*, 10(11), 5149–5160. <https://doi.org/10.1021/ct500616v>

Bisignano, P., & Moran, O. (2010). Molecular dynamics analysis of the wild type and dF508 mutant structures of the human CFTR nucleotide binding domain 1. *Biochimie*, 92(1), 51–57. <https://doi.org/10.1016/j.biochi.2009.09.007>

Bornscheuer, U. T., & Pohl, M. (2001). Improved biocatalysts by directed evolution and rational protein design. *Current Opinion in Chemical Biology*, 5(2), 137–143. [https://doi.org/10.1016/S1367-5931\(00\)00182-4](https://doi.org/10.1016/S1367-5931(00)00182-4)

Borrelli, G., & Trono, D. (2015). Recombinant Lipases and Phospholipases and Their Use as Biocatalysts for Industrial Applications. *International Journal of Molecular Sciences*, 16(9), 20774–20840. <https://doi.org/10.3390/ijms160920774>

Bradford, M. M. (1976). A rapid and sensitive method for the quantitation of microgram quantities of protein utilizing the principle of protein-dye binding. *Analytical Biochemistry*, 72(1–2), 248–254. [https://doi.org/10.1016/0003-2697\(76\)90527-3](https://doi.org/10.1016/0003-2697(76)90527-3)

Burgess, J. E., & Pletschke, B. I. (2008). Hydrolytic enzymes in sewage sludge treatment: A mini-review, 34(3), 27–46. Retrieved from <http://www.wrc.org.za>

Cadwell, R. C., & Joyce, G. F. (1992). Randomization of genes by PCR mutagenesis. *PCR Methods and Applications*, 2(1), 28–33. <https://doi.org/10.1101/GR.2.1.28>

Cao, H., Deng, L., Lei, M., Wang, F., & Tan, T. (2014). The role of temperature and solvent microenvironment on the activity of *Yarrowia lipolytica* Lipase 2: Insights from molecular dynamics simulation. *Journal of Molecular Catalysis B: Enzymatic*, 109, 101–108. <https://doi.org/10.1016/j.molcatb.2014.08.013>

Carugo, O., & Pongor, S. (2002). Protein fold similarity estimated by a probabilistic approach based on C (alpha) -C (alpha) distance comparison 1 Edited by B. Honig. *Journal of Molecular Biology*, 315(4), 887–898. <https://doi.org/10.1006/jmbi.2001.5250>

Cedrone, F., Ménez, A., & Quéméneur, E. (2000). Tailoring new enzyme functions by rational redesign. *Current Opinion in Structural Biology*, 10(4), 405–410. [https://doi.org/10.1016/S0959-440X\(00\)00106-8](https://doi.org/10.1016/S0959-440X(00)00106-8)

Chakravarty, S., Bhinge, A., & Varadarajan, R. (2002). A procedure for detection and quantitation of cavity volumes proteins. Application to measure the strength of the

hydrophobic driving force in protein folding. *The Journal of Biological Chemistry*, 277(35), 31345–53. <https://doi.org/10.1074/jbc.M201373200>

Chakravorty, D., Parameswaran, S., Dubey, V. K., & Patra, S. (2011). In silico characterization of thermostable lipases. *Extremophiles*, 15(1), 89–103. <https://doi.org/10.1007/s00792-010-0337-0>

Chen, P. T., Chen, Y. C., Lin, Y. Y., & Su, H. H. (2015). Strategy for efficient production of recombinant *Staphylococcus epidermidis* lipase in *Bacillus subtilis*. *Biochemical Engineering Journal*, 103, 152–157. <https://doi.org/10.1016/j.bej.2015.07.008>

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. <https://doi.org/10.1002/bit.10407>

Cherif, S., Mnif, S., Hadrich, F., Abdelkafi, S., & Sayadi, S. (n.d.). A newly high alkaline lipase: an ideal choice for application in detergent formulations. <https://doi.org/10.1186/1476-511X-10-221>

Cherry, J. R., & Fidantsef, A. L. (2003). Directed evolution of industrial enzymes: An update. *Current Opinion in Biotechnology*, 14(4), 438–443. [https://doi.org/10.1016/S0958-1669\(03\)00099-5](https://doi.org/10.1016/S0958-1669(03)00099-5)

Choudhury, P., & Bhunia, B. (2015). Industrial Application of Lipase: a Review. *Biopharm Journal*, 1(2), 41–47. Retrieved from <http://www.biopharmj.com/journal/index.php/BIOPHARMJ/article/view/11>

Colovos, C., & Yeates, T. O. (1993). Verification of protein structures: Patterns of nonbonded atomic interactions. *Protein Science*, 2(9), 1511–1519. <https://doi.org/10.1002/pro.5560020916>

Contesini, F. J., Lopes, D. B., Macedo, G. A., Nascimento, M. da G., & Carvalho, P. de O. (2010). *Aspergillus* sp. lipase: Potential biocatalyst for industrial use. *Journal of Molecular Catalysis B: Enzymatic*, 67(3–4), 163–171. <https://doi.org/10.1016/j.molcatb.2010.07.021>

Craveur, P., Joseph, A. P., Rebehmed, J., & de Brevern, A. G. (2013). β -bulges: Extensive structural analyses of β -sheets irregularities. *Protein Science*, 22(10), n/a-n/a. <https://doi.org/10.1002/pro.2324>

de Pascale, D., Cusano, A. M., Autore, F., Parrilli, E., di Prisco, G., Marino, G., & Tutino, M. L. (2008). The cold-active Lip1 lipase from the Antarctic bacterium *Pseudoalteromonas haloplanktis* TAC125 is a member of a new bacterial lipolytic

enzyme family. *Extremophiles*, 12(3), 311–323. <https://doi.org/10.1007/s00792-008-0163-9>

De Simone, G., Galdiero, S., Manco, G., Lang, D., Rossi, M., & Pedone, C. (2000). A snapshot of a transition state analogue of a novel thermophilic esterase belonging to the subfamily of mammalian hormone-sensitive lipase 1. *Journal of Molecular Biology*, 303(5), 761–771. <https://doi.org/10.1006/jmbi.2000.4195>

Denard, C. A., Ren, H., & Zhao, H. (2015). Improving and repurposing biocatalysts via directed evolution. *Current Opinion in Chemical Biology*, 25, 55–64. <https://doi.org/10.1016/j.cbpa.2014.12.036>

Dheeman, D. S., Henahan, G. T. M., & Frías, J. M. (2011). Purification and properties of *Amycolatopsis mediterranei* DSM 43304 lipase and its potential in flavour ester synthesis. *Bioresource Technology*, 102(3), 3373–3379. <https://doi.org/10.1016/j.biortech.2010.11.074>

Edwardraja, S., Sriram, S., Govindan, R., Budisa, N., Lee, S.-G., Huber, R., ... Hansen, G. (2011). Enhancing the thermal stability of a single-chain Fv fragment by in vivo global fluorination of the proline residues. *Mol. Biosyst.*, 7(1), 258–265. <https://doi.org/10.1039/C0MB00154F>

Elumalai, P., Wu, J. W., & Liu, H.-L. (2010). Current advances in disulfide connectivity predictions. *Journal of the Taiwan Institute of Chemical Engineers*, 41(5), 525–539. <https://doi.org/10.1016/j.jtice.2010.05.011>

Ertuğrul, S., Dönmez, G., & Takaç, S. (2007). Isolation of lipase producing *Bacillus* sp. from olive mill wastewater and improving its enzyme activity. *Journal of Hazardous Materials*, 149(3), 720–724. <https://doi.org/10.1016/j.jhazmat.2007.04.034>

Fanaei Kahrani, Z., Emamzadeh, R., Nazari, M., & Rasa, S. M. M. (2017). Molecular basis of thermostability enhancement of Renilla luciferase at higher temperatures by insertion of a disulfide bridge into the structure. *Biochimica et Biophysica Acta - Proteins and Proteomics*, 1865(2), 252–259. <https://doi.org/10.1016/j.bbapap.2016.11.004>

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), 1033–1041. [https://doi.org/10.1016/S0300-9084\(00\)01188-3](https://doi.org/10.1016/S0300-9084(00)01188-3)

Friesner, R. A., Abel, R., Goldfeld, D. A., Miller, E. B., & Murrett, C. S. (2013). Computational methods for high resolution prediction and refinement of protein structures. *Current Opinion in Structural Biology*, 23(2), 177–184. <https://doi.org/10.1016/j.sbi.2013.01.010>

Frishman, D., & Argos, P. (1995). Knowledge-based protein secondary structure assignment. *Proteins: Structure, Function, and Genetics*, 23(4), 566–579. <https://doi.org/10.1002/prot.340230412>

Fukuchi, S., Yoshimune, K., Wakayama, M., Moriguchi, M., & Nishikawa, K. (2003). Unique amino acid composition of proteins in Halophilic Bacteria. *Journal of Molecular Biology*, 327(2), 347–357. [https://doi.org/10.1016/S0022-2836\(03\)00150-5](https://doi.org/10.1016/S0022-2836(03)00150-5)

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. <https://doi.org/10.1016/j.febslet.2008.05.037>

Geourjon, C., Combet, C., Blanchet, C., & Deléage, G. (2001). Identification of related proteins with weak sequence identity using secondary structure information. *Protein Science*, 10(4), 788–797. <https://doi.org/10.1110/ps.30001>

Gianese, G., Argos, P., & Pascarella, S. (2001). Structural adaptation of enzymes to low temperatures. *Protein Engineering Design and Selection*, 14(3), 141–148. <https://doi.org/10.1093/protein/14.3.141>

Goomber, S., Kumar, R., Singh, R., Mishra, N., & Kaur, J. (2016). Point mutation Gln121-Arg increased temperature optima of *Bacillus* lipase (1.4 subfamily) by fifteen degrees. *International Journal of Biological Macromolecules*, 88, 507–514. <https://doi.org/10.1016/j.ijbiomac.2016.04.022>

Gopinath, S. C. B., Anbu, P., Lakshmi priya, T., & Hilda, A. (2013). Strategies to characterize fungal lipases for applications in medicine and dairy industry. *BioMed Research International*, 2013, 154549. <https://doi.org/10.1155/2013/154549>

Grbavcic, S., Bezbradica, D., Izrael-zivkovic, L., Avramovic, N., Milosavic, N., Karadzic, I., & Knezevic-Jugovic, Z. (2011). Production of lipase and protease from an indigenous *Pseudomonas aeruginosa* strain and their evaluation as detergent additives: Compatibility study with detergent ingredients and washing performance. *Bioresource Technology*, 102(24), 11226–11233. <https://doi.org/10.1016/j.biortech.2011.09.076>

Grice, E. A., & Segre, J. A. (2011). The skin microbiome. *Nature Reviews Microbiology*, 9(4), 244–253. <https://doi.org/10.1038/nrmicro2537>

Gromiha, M. M., Oobatake, M., & Sarai, A. (1999). Important amino acid properties for enhanced thermostability from mesophilic to thermophilic proteins. *Biophysical Chemistry*, 82(1), 51–67. [https://doi.org/10.1016/S0301-4622\(99\)00103-9](https://doi.org/10.1016/S0301-4622(99)00103-9)

Gubbins, K. E., & Moore, J. D. (2010). Molecular Modeling of Matter: Impact and Prospects in Engineering. *Industrial & Engineering Chemistry Research*, 49(7), 3026–3046. <https://doi.org/10.1021/ie901909c>

Gunasekaran, V., & Das, D. (2005). Lipase fermentation: Progress and prospects. *Indian Journal of Biotechnology*, 4(4), 437–445.

Guncheva, M., & Zhiryakova, D. (2011). Catalytic properties and potential applications of *Bacillus* lipases. *Journal of Molecular Catalysis B: Enzymatic*, 68(1), 1–21. <https://doi.org/10.1016/j.molcatb.2010.09.002>

Gupta, R., Kumari, A., Syal, P., & Singh, Y. (2015). Molecular and functional diversity of yeast and fungal lipases: Their role in biotechnology and cellular physiology. *Progress in Lipid Research*, 57, 40–54. <https://doi.org/10.1016/j.plipres.2014.12.001>

Gupta, R., Rath, P., Gupta, N., & Bradoo, S. (2003). Lipase assays for conventional and molecular screening: an overview. *Biotechnology and Applied Biochemistry*, 37(1), 63. <https://doi.org/10.1042/BA20020059>

Haki, G. D., & Rakshit, S. K. (2003). Developments in industrially important thermostable enzymes: A review. *Bioresource Technology*, 89(1), 17–34. [https://doi.org/10.1016/S0960-8524\(03\)00033-6](https://doi.org/10.1016/S0960-8524(03)00033-6)

Harper, S., & Speicher, D. W. (2011). Purification of proteins fused to glutathione S-transferase. *Methods in Molecular Biology (Clifton, N.J.)*, 681, 259–80. https://doi.org/10.1007/978-1-60761-913-0_14

Hasan, F., Shah, A. A., & Hameed, A. (2006). Industrial applications of microbial lipases. *Enzyme and Microbial Technology*, 39(2), 235–251. <https://doi.org/10.1016/j.enzmictec.2005.10.016>

Hasan, F., Shah, A. A., & Hameed, A. (2009). Methods for detection and characterization of lipases: A comprehensive review. *Biotechnology Advances*, 27(6), 782–798. <https://doi.org/10.1016/j.biotechadv.2009.06.001>

Henzler-Wildman, K. A., Lei, M., Thai, V., Kerns, S. J., Karplus, M., & Kern, D. (2007). A hierarchy of timescales in protein dynamics is linked to enzyme catalysis. *Nature*, 450(7171), 913–916. <https://doi.org/10.1038/nature06407>

Hermann, V. M., Cutfield, J. F., & Hubbard, M. J. (2005). Biophysical characterization of ERp29. Evidence for a key structural role of cysteine 125. *The Journal of Biological Chemistry*, 280(14), 13529–37. <https://doi.org/10.1074/jbc.M410889200>

Herminia González-Navarro, M. Carmen Bañó, and, & Abad*, C. (2001). The Closed/Open Model for Lipase Activation. Addressing Intermediate Active Forms of Fungal Enzymes by Trapping of Conformers in Water-Restricted Environments†. <https://doi.org/10.1021/BI002202D>

Higgins, D. G., Thompson, J. D., & Gibson, T. J. (1996). [22] Using CLUSTAL for multiple sequence alignments (pp. 383–402). [https://doi.org/10.1016/S0076-6879\(96\)66024-8](https://doi.org/10.1016/S0076-6879(96)66024-8)

Holtje, H. D., Folkers, G., & Luzar, A. (1998). Molecular Modeling, Basic Principles and Applications. *Computers in Physics*, 12(1), 41. <https://doi.org/10.1063/1.168645>

Horchani, H., Aissa, I., Ouertani, S., Zarai, Z., Gargouri, Y., & Sayari, A. (2012). Staphylococcal lipases: Biotechnological applications. *Journal of Molecular Catalysis B: Enzymatic*, 76, 125–132. <https://doi.org/10.1016/j.molcatb.2011.11.018>

Horchani, H., Mosbah, H., Salem, N. Ben, Gargouri, Y., & Sayari, A. (2009). Biochemical and molecular characterisation of a thermoactive, alkaline and detergent-stable lipase from a newly isolated *Staphylococcus aureus* strain. *Journal of Molecular Catalysis B: Enzymatic*, 56(4), 237–245. <https://doi.org/10.1016/j.molcatb.2008.05.011>

Hummer, G., Garde, S., Garca, A. E., Paulaitis, M. E., Pratt, L. R., & Wolynes, P. G. (1998). The pressure dependence of hydrophobic interactions is consistent with the observed pressure denaturation of proteins (protein foldingprotein folding kineticshydrophobic effectactivation volumesprotein unfolding). *Biophysics*, 95, 1552–1555. Retrieved from <http://www.pnas.org/content/95/4/1552.full.pdf>

Imai, K., & Mitaku, S. (2005). Mechanisms of secondary structure breakers in soluble proteins. *BIOPHYSICS*, 1, 55–65. <https://doi.org/10.2142/biophysics.1.55>

Jaeger, K. E., & Eggert, T. (2002). Lipases for biotechnology. *Current Opinion in Biotechnology*, 13(4), 390–397. [https://doi.org/10.1016/S0958-1669\(02\)00341-5](https://doi.org/10.1016/S0958-1669(02)00341-5)

Jaeger, K. E., & Reetz, M. T. (1998). Microbial lipases form versatile tools for biotechnology. *Trends in Biotechnology*, 16(9), 396–403. [https://doi.org/10.1016/S0167-7799\(98\)01195-0](https://doi.org/10.1016/S0167-7799(98)01195-0)

Jaenicke, R., & Bohm, G. (1998). The stability of proteins in extreme environments. *Current Opinion in Structural Biology*, 8(6), 738–748. [https://doi.org/10.1016/S0959-440X\(98\)80094-8](https://doi.org/10.1016/S0959-440X(98)80094-8)

Jemli, S., Ayadi-Zouari, D., Hlima, H. Ben, & Bejar, S. (2016). Biocatalysts: application and engineering for industrial purposes. *Critical Reviews in Biotechnology*, 36(2), 246–258. <https://doi.org/10.3109/07388551.2014.950550>

Jeong, S. T., Kim, H. K., Kim, S. J., Chi, S. W., Pan, J. G., Oh, T. K., & Ryu, S. E. (2002). Novel zinc-binding center and a temperature switch in the *Bacillus stearothermophilus* L1 lipase. *Journal of Biological Chemistry*, 277(19), 17041–17047. <https://doi.org/10.1074/jbc.M200640200>

Joseph, B., Ramteke, P. W., Thomas, G., & Shrivastava, N. (2006). *Biotechnology and molecular biology reviews. Biotechnology and Molecular Biology Reviews* (Vol. 2). Academic Journals. Retrieved from <http://www.academicjournals.org/journal/BMBR/article-abstract/8B5C9F410944>

Kamal, M. Z., Ahmad, S., Molugu, T. R., Vijayalakshmi, A., Deshmukh, M. V., Sankaranarayanan, R., & Rao, N. M. (2011). In vitro evolved non-aggregating and thermostable lipase: Structural and thermodynamic investigation. *Journal of Molecular Biology*, 413(3), 726–741. <https://doi.org/10.1016/j.jmb.2011.09.002>

Karshikoff, A., Nilsson, L., & Ladenstein, R. (2015). Rigidity versus flexibility: the dilemma of understanding protein thermal stability. *FEBS Journal*, 282(20), 3899–3917. <https://doi.org/10.1111/febs.13343>

Katava, M., Kalimeri, M., Stirnemann, G., & Sterpone, F. (2016). Stability and Function at High Temperature. What Makes a Thermophilic GTPase Different from Its Mesophilic Homologue. *The Journal of Physical Chemistry B*, 120(10), 2721–2730. <https://doi.org/10.1021/acs.jpcc.6b00306>

Khaleghinejad, S. H., Motalleb, G., Karkhane, A. A., Aminzadeh, S., & Yakhchali, B. (2016). Study the effect of F17S mutation on the chimeric *Bacillus thermocatenulatus* lipase. *Journal of Genetic Engineering and Biotechnology*, 14(1), 83–89. <https://doi.org/10.1016/j.jgeb.2016.08.002>

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 surface. *Molecular Biology Reports*, 38(5), 2919–2926. <https://doi.org/10.1007/s11033-010-9954-z>

Kihara, D. (2005). The effect of long-range interactions on the secondary structure formation of proteins. *Protein Science*, 14(8), 1955–1963. <https://doi.org/10.1110/ps.051479505>

Kim, H.-K., Park, S.-Y., Lee, J.-K., & Oh, T.-K. (1998). Gene Cloning and Characterization of Thermostable Lipase from *Bacillus stearothermophilus* L1. *Bioscience, Biotechnology, and Biochemistry*, 62(1), 66–71. <https://doi.org/10.1271/bbb.62.66>

Kirti, S. (2013). *Characterization of thermostable and alkalophilic lipase enzyme from endophytic fungus Leptosphaerulina sp.* THAPAR UNIVERSITY. Retrieved from <http://dspace.thapar.edu:8080/jspui/handle/10266/2541>

Klibanov, A. M. (1997). Why are enzymes less active in organic solvents than in water? *Trends in Biotechnology*, 15(3), 97–101. [https://doi.org/10.1016/S0167-7799\(97\)01013-5](https://doi.org/10.1016/S0167-7799(97)01013-5)

Kory, N., Grond, S., Kamat, S. S., Li, Z., Krahmer, N., Chitraju, C., ... Walther, T. C. (2017). Mice lacking lipid droplet-associated hydrolase, a gene linked to human prostate cancer, have normal cholesterol ester metabolism. *Journal of Lipid Research*, 58(1), 226–235. <https://doi.org/10.1194/jlr.M072538>

Kotzia, G. A., & Labrou, N. E. (2011). Engineering substrate specificity of *E. carotovora* l-asparaginase for the development of biosensor. *Journal of Molecular Catalysis B: Enzymatic*, 72(3–4), 95–101. <https://doi.org/10.1016/j.molcatb.2011.05.003>

Kourist, R., Jochens, H., Bartsch, S., Kuipers, R., Padhi, S. K., Gall, M., ... Bornscheuer, U. T. (2010). The α/β -Hydrolase Fold 3DM Database (ABHDB) as a Tool for Protein Engineering. *ChemBioChem*, 11(12), 1635–1643. <https://doi.org/10.1002/cbic.201000213>

Krieger, E., Joo, K., Lee, J., Lee, J., Raman, S., Thompson, J., ... Karplus, K. (2009). Improving physical realism, stereochemistry, and side-chain accuracy in homology modeling: Four approaches that performed well in CASP8. *Proteins: Structure, Function, and Bioinformatics*, 77(S9), 114–122. <https://doi.org/10.1002/prot.22570>

Krishnaveni, M. (2013). Characterization of lipase producing *Staphylococcus aureus* MTCC 10787 from soil sample at Salem, Tamil Nadu, India. *Journal of Pharmacy Research*, 6(2), 304–308. <https://doi.org/10.1016/j.jopr.2013.02.005>

Kronqvist, N. (2009). *Staphylococcal surface display in directed evolution*. Skolan för bioteknologi, Kungliga Tekniska högskolan.

Kumar, R., Singh, R., & Kaur, J. (2013). Characterization and molecular modelling of an engineered organic solvent tolerant, thermostable lipase with enhanced enzyme activity. *Journal of Molecular Catalysis B: Enzymatic*, 97, 243–251. <https://doi.org/10.1016/j.molcatb.2013.09.001>

Laemmli, U. K. (1970). Cleavage of Structural Proteins during the Assembly of the Head of Bacteriophage T4. *Nature*, 227(5259), 680–685. <https://doi.org/10.1038/227680a0>

Leader, D. P., & Milner-White, E. (2012). Structure Motivator: A tool for exploring small three-dimensional elements in proteins. *BMC Structural Biology*, 12(1), 26. <https://doi.org/10.1186/1472-6807-12-26>

Lee, D.-W., Kim, H.-W., Lee, K.-W., Kim, B.-C., Choe, E.-A., Seung Lee, H.-, ... Pyun, Y.-R. (2001). Purification and characterization of two distinct thermostable lipases from the gram-positive thermophilic bacterium *Bacillus thermoleovorans* ID-1. *Enzyme and Microbial Technology*, 29(6–7), 363–371. [https://doi.org/10.1016/S0141-0229\(01\)00408-2](https://doi.org/10.1016/S0141-0229(01)00408-2)

Leemhuis, H., Kelly, R. M., & Dijkhuizen, L. (2009). Directed evolution of enzymes: Library screening strategies. *IUBMB Life*, 61(3), 222–228. <https://doi.org/10.1002/iub.165>

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. <https://doi.org/10.1007/s00792-007-0069-y>

Lindahl, E. (2015). Molecular Dynamics Simulations (pp. 3–26). https://doi.org/10.1007/978-1-4939-1465-4_1

Linko, Y.-Y., Lämä, M., Wu, X., Uosukainen, E., Seppälä, J., & Linko, P. (1998). Biodegradable products by lipase biocatalysis. *Journal of Biotechnology*, 66(1), 41–50. [https://doi.org/10.1016/S0168-1656\(98\)00155-2](https://doi.org/10.1016/S0168-1656(98)00155-2)

Lopez-Lopez, O., Cerdan, M., & Siso, M. (2014). New Extremophilic Lipases and Esterases from Metagenomics. *Current Protein & Peptide Science*, 15(5), 445–455. <https://doi.org/10.2174/1389203715666140228153801>

Madan, B., & Mishra, P. (2014). Directed evolution of *Bacillus licheniformis* lipase for improvement of thermostability. *Biochemical Engineering Journal*, 91, 276–282. <https://doi.org/10.1016/j.bej.2014.08.022>

Magyar, C., Gromiha, M. M., Sávolgy, Z., & Simon, I. (2016). The role of stabilization centers in protein thermal stability. *Biochemical and Biophysical Research Communications*, 471(1), 57–62. <https://doi.org/10.1016/j.bbrc.2016.01.181>

Manco, G., Camardella, L., Febbraio, F., Adamo, G., Carratore, V., & Rossi, M. (2000). Homology modeling and identification of serine 160 as nucleophile of the active site in a thermostable carboxylesterase from the archaeon *Archaeoglobus fulgidus*. *Protein*

Engineering Design and Selection, 13(3), 197–200.
<https://doi.org/10.1093/protein/13.3.197>

Mansfeld, J., & Ulbrich-Hofmann, R. (2007). The stability of engineered thermostable neutral proteases from *Bacillus stearothermophilus* in organic solvents and detergents. *Biotechnology and Bioengineering*, 97(4), 672–679. <https://doi.org/10.1002/bit.21292>

Martinez-Martinez, M., Golyshin, P. N., & Ferrer, M. (2017). Functional Screening of Metagenomic Libraries: Enzymes Acting on Greasy Molecules as Study Case (pp. 13–36). https://doi.org/10.1007/8623_2015_104

Martinez, R., Schwaneberg, U., & Roccatano, D. (2011). Temperature effects on structure and dynamics of the psychrophilic protease subtilisin S41 and its thermostable mutants in solution. *Protein Engineering Design and Selection*, 24(7), 533–544. <https://doi.org/10.1093/protein/gzr014>

Masomian, M., Rahman, R. N. Z. R. A., Salleh, A. B., Basri, M., Baker, P., & Sedelnikova, S. (2016). Analysis of Comparative Sequence and Genomic Data to Verify Phylogenetic Relationship and Explore a New Subfamily of Bacterial Lipases. *PLOS ONE*, 11(3), e0149851. <https://doi.org/10.1371/journal.pone.0149851>

Matak, M. Y., & Moghaddam, M. E. (2009). The role of short-range Cys171?Cys178 disulfide bond in maintaining cutinase active site integrity: A molecular dynamics simulation. *Biochemical and Biophysical Research Communications*, 390(2), 201–204. <https://doi.org/10.1016/j.bbrc.2009.09.073>

Metzger, J. O., & Bornscheuer, U. (2006). Lipids as renewable resources: current state of chemical and biotechnological conversion and diversification. *Applied Microbiology and Biotechnology*, 71(1), 13–22. <https://doi.org/10.1007/s00253-006-0335-4>

Mittermaier, A., & Kay, L. E. (2006). New Tools Provide New Insights in NMR Studies of Protein Dynamics. *Science*, 312(5771). Retrieved from <http://science.sciencemag.org/content/312/5771/224>

Mnisi, S. M. (2005). Cloning, properties and expression of a novel esterase from *Bacillus coagulans* strain 18-11. Retrieved from <http://www.repository.up.ac.za/handle/2263/24613>

Momen-Roknabadi, A., Sadeghi, M., Pezeshk, H., & Marashi, S.-A. (2008). Impact of residue accessible surface area on the prediction of protein secondary structures. *BMC Bioinformatics*, 9(1), 357. <https://doi.org/10.1186/1471-2105-9-357>

Morley, K. L., & Kazlauskas, R. J. (2005). Improving enzyme properties: when are closer mutations better? *Trends in Biotechnology*, 23(5), 231–237. <https://doi.org/10.1016/j.tibtech.2005.03.005>

Moroni, L., Gellini, C., & Remigio Salvi, P. (2015). Thermal Denaturation of Proteins and Chemical Equilibrium. *World Journal of Chemical Education*, 3(3), 59–63. <https://doi.org/10.12691/wjce-3-3-1>

Nagano, N., Ota, M., & Nishikawa, K. (1999). Strong hydrophobic nature of cysteine residues in proteins. *FEBS Letters*, 458(1), 69–71. [https://doi.org/10.1016/S0014-5793\(99\)01122-9](https://doi.org/10.1016/S0014-5793(99)01122-9)

Navarro López, E., Robles Medina, A., González Moreno, P. A., Esteban Cerdán, L., & Molina Grima, E. (2016). Extraction of microalgal lipids and the influence of polar lipids on biodiesel production by lipase-catalyzed transesterification. *Bioresource Technology*, 216, 904–913. <https://doi.org/10.1016/j.biortech.2016.06.035>

Nawani, N., & Kaur, J. (2000). Purification, characterization and thermostability of lipase from a thermophilic *Bacillus* sp. J33. *Molecular and Cellular Biochemistry*, 206(1–2), 91–6. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/10839198>

Noble, M. E. M., Cleasby, A., Johnson, L. N., Egmond, M. R., & Frenken, L. G. J. (1993). The crystal structure of triacylglycerol lipase from *Pseudomonas glumae* reveals a partially redundant catalytic aspartate. *FEBS Letters*, 331(1–2), 123–128. [https://doi.org/10.1016/0014-5793\(93\)80310-Q](https://doi.org/10.1016/0014-5793(93)80310-Q)

Oh, B.-C., Kim, H.-K., Lee, J.-K., Kang, S.-C., & Oh, T.-K. (1999). *Staphylococcus haemolyticus* lipase: biochemical properties, substrate specificity and gene cloning. *FEMS Microbiology Letters*, 179(2), 385–392. <https://doi.org/10.1111/j.1574-6968.1999.tb08753.x>

Okumura, H. (2012). Temperature and pressure denaturation of chignolin: Folding and unfolding simulation by multibaric-multithermal molecular dynamics method. *Proteins: Structure, Function, and Bioinformatics*, 80(10), 2397–2416. <https://doi.org/10.1002/prot.24125>

Orengo, C. A., Brown, N. P., & Taylor, W. R. (1992). Fast structure alignment for protein databank searching. *Proteins: Structure, Function, and Genetics*, 14(2), 139–167. <https://doi.org/10.1002/prot.340140203>

Osredkar, J., & Sustar, N. (2011). Copper and zinc, biological role and significance of copper/zinc imbalance. *Journal of Clinical Toxicology*, 3(2161), 495. Retrieved from https://www.researchgate.net/profile/Josko_Osredkar/publication/232279169_Special_

Issue_Title_Heavy_Metal_Toxicity_Handling_Editors/links/0912f508107cb41c1a000000.pdf

Pace, N., & Weerapana, E. (2014). Zinc-binding cysteines: Diverse functions and structural motifs. *Biomolecules*, 4(2), 419–434. <https://doi.org/10.3390/biom4020419>

Packer, M. S., & Liu, D. R. (2015). Methods for the directed evolution of proteins. *Nature Publishing Group*, 3927, :1-16. <https://doi.org/10.1038/nrg3927>

Pal, D., & Chakrabarti, P. (1999). Estimates of the Loss of Main-Chain Conformational, 339(December 1998), 332–339.

Patel, M., Mistry, J., Desai, S., Patel, S., & Desai, S. (2016). Isolation and Characterization of Lipase producing Bacteria from Vegetable Oil Spillage Site. *International Journal of Current Microbiology and Applied Sciences.*, 5(8), 214–232.

Patkar, S., Vind, J., Kelstrup, E., Christensen, M. ., Svendsen, A., Borch, K., & Kirk, O. (1998). Effect of mutations in *Candida antarctica* B lipase. *Chemistry and Physics of Lipids*, 93(1), 95–101. [https://doi.org/10.1016/S0009-3084\(98\)00032-2](https://doi.org/10.1016/S0009-3084(98)00032-2)

Pentony, M. M., Ward, J., & Jones, D. T. (2010). Computational resources for the prediction and analysis of native disorder in proteins (pp. 369–393). https://doi.org/10.1007/978-1-60761-444-9_25

Persson, M., Mladenoska, I., Wehtje, E., & Adlercreutz, P. (2002). Preparation of lipases for use in organic solvents. *Enzyme and Microbial Technology*, 31(6), 833–841. [https://doi.org/10.1016/S0141-0229\(02\)00184-9](https://doi.org/10.1016/S0141-0229(02)00184-9)

Perticaroli, S., Nickels, J. D., Ehlers, G., & Sokolov, A. P. (2014). Rigidity, Secondary Structure, and the Universality of the Boson Peak in Proteins. *Biophysical Journal*, 106(12), 2667–2674. <https://doi.org/10.1016/j.bpj.2014.05.009>

Petrounia, I. P., & Arnold, F. H. (2000). Designed evolution of enzymatic properties. *Current Opinion in Biotechnology*, 11(4), 325–330. [https://doi.org/10.1016/S0958-1669\(00\)00107-5](https://doi.org/10.1016/S0958-1669(00)00107-5)

Pio, T. F., & Macedo, G. A. (2009). Chapter 4 Cutinases: (pp. 77–95). [https://doi.org/10.1016/S0065-2164\(08\)00804-6](https://doi.org/10.1016/S0065-2164(08)00804-6)

Rahman, I. A., Rahman, R. N. Z. R. A., Salleh, A. B., & Basri, M. (2013). Formulation and Evaluation of an Automatic Dishwashing Detergent Containing T1 Lipase. *Journal*

of *Surfactants and Detergents*, 16(3), 427–434. <https://doi.org/10.1007/s11743-012-1398-0>

Ramakrishnan, K., Krishna, V., Kumar Ks, V., Bs, L., Anishetty, S., & Gautam, P. (2008). Molecular dynamics simulations of lipases. *International Journal of Integrative Biology*, 2(3), 204–213. Retrieved from [http://www.ugcfrp.ac.in/images/userfiles/6376-md review.pdf](http://www.ugcfrp.ac.in/images/userfiles/6376-md%20review.pdf)

Ramnath, L., Sithole, B., & Govinden, R. (2017). Classification of Lipolytic Enzymes and their Biotechnological Applications in the Pulping Industry. *Canadian Journal of Microbiology*, 63(October 2016), 1–14. <https://doi.org/10.1139/cjm-2016-0447>

Rasila, T. S., Pajunen, M. I., & Savilahti, H. (2009). Critical evaluation of random mutagenesis by error-prone polymerase chain reaction protocols, *Escherichia coli* mutator strain, and hydroxylamine treatment. *Analytical Biochemistry*, 388(1), 71–80. <https://doi.org/10.1016/j.ab.2009.02.008>

Rathi, P. C., Jaeger, K. E., & Gohlke, H. (2015). Structural rigidity and protein thermostability in variants of lipase a from *Bacillus subtilis*. *PLoS ONE*, 10(7), 1–24. <https://doi.org/10.1371/journal.pone.0130289>

Rosenstein, R., & Götz, F. (2000). Staphylococcal lipases: Biochemical and molecular characterization. *Biochimie*, 82(11), 1005–1014. [https://doi.org/10.1016/S0300-9084\(00\)01180-9](https://doi.org/10.1016/S0300-9084(00)01180-9)

Samad, M. Y. A., Razak, C. N. A., Salleh, A. B., Zin Wan Yunus, W. M., Ampon, K., & Basri, M. (1989). A plate assay for primary screening of lipase activity. *Journal of Microbiological Methods*, 9(1), 51–56. [https://doi.org/10.1016/0167-7012\(89\)90030-4](https://doi.org/10.1016/0167-7012(89)90030-4)

Sambrook, J., Fritsch, E. F., & Maniatis, T. (1989). Molecular cloning: a laboratory manual. *Molecular Cloning: A Laboratory Manual*, (Ed. 2). Retrieved from <https://www.cabdirect.org/cabdirect/abstract/19901616061>

Sammond, D. W., Kastelowitz, N., Himmel, M. E., Yin, H., Crowley, M. F., & Bomble, Y. J. (2016). Comparing Residue Clusters from Thermophilic and Mesophilic Enzymes Reveals Adaptive Mechanisms. *PLOS ONE*, 11(1), e0145848. <https://doi.org/10.1371/journal.pone.0145848>

Sangeetha, R., Arulpandi, I., & Geetha, A. (2011). Bacterial Lipases as Potential Industrial Biocatalysts: An Overview. *Research Journal of Microbiology*, 6(1), 1–24.

Santini, S., Crowet, J. M., Thomas, A., Paquot, M., Vandenbol, M., Thonart, P., ... Charlotiaux, B. (2009). Study of *Thermomyces lanuginosa* Lipase in the Presence of

Tributyrilglycerol and Water. *Biophysical Journal*, 96(12), 4814–4825. <https://doi.org/10.1016/j.bpj.2009.03.040>

Sarupria, S., Ghosh, T., García, A. E., & Garde, S. (2010). Studying pressure denaturation of a protein by molecular dynamics simulations. *Proteins: Structure, Function, and Bioinformatics*, 78(7), NA-NA. <https://doi.org/10.1002/prot.22680>

Schallmeyer, M., Singh, A., & Ward, O. P. (2004). Developments in the use of *Bacillus* species for industrial production. *Canadian Journal of Microbiology*, 50(1), 1–17. <https://doi.org/10.1139/w03-076>

Secundo, F., Carrea, G., Tarabiono, C., Gatti-Lafranconi, P., Brocca, S., Lotti, M., ... Eggert, T. (2006). The lid is a structural and functional determinant of lipase activity and selectivity. *Journal of Molecular Catalysis B: Enzymatic*, 39(1–4), 166–170. <https://doi.org/10.1016/j.molcatb.2006.01.018>

Shanmugam, S. (2009). *Enzyme Technology*. IK International Pvt Ltd. Retrieved from https://books.google.com.my/books?hl=en&lr=&id=KrGn_obcy6QC&oi=fnd&pg=PA1&dq=Shanmugam+Enzyme++technology.++&ots=WYHkEJPfn9&sig=bVcBvuEH3yBX3Pa-4Ou4MVQwrb0&redir_esc=y#v=onepage&q=ShanmugamEnzyme technology.&f=false

Sharma, A. K., Sharma, V., & Saxena, J. (2016). A short review on extracellular lipase producing microorganisms. *Advance Pharmaceutical Journal*, 1(3), 59–65.

Sharma, R., Chisti, Y., Chand, U., & Banerjee, U. C. (2001). Production, purification, characterization, and applications of lipases. *Biotechnology Advances*, 19(8), 627–662. [https://doi.org/10.1016/S0734-9750\(01\)00086-6](https://doi.org/10.1016/S0734-9750(01)00086-6)

Sharma, S., & Kanwar, S. S. (2014). Organic solvent tolerant lipases and applications. *TheScientificWorldJournal*, 2014, 625258. <https://doi.org/10.1155/2014/625258>

Sheldon, R. A., Pereira, P. C., Liese, A., Bornscheuer, U. T., Stolz, A., Sheldon, R. A., ... Hughes, G. J. (2017). Biocatalysis engineering: the big picture. *Chem. Soc. Rev.*, 46(10), 2678–2691. <https://doi.org/10.1039/C6CS00854B>

Siddiqui, K. S. (2015). Some like it hot, some like it cold: Temperature dependent biotechnological applications and improvements in extremophilic enzymes. *Biotechnology Advances*, 33(8), 1912–1922. <https://doi.org/10.1016/j.biotechadv.2015.11.001>

Siloto, R. M. P., & Weselake, R. J. (2012). Site saturation mutagenesis: Methods and applications in protein engineering. *Biocatalysis and Agricultural Biotechnology*, 1(3), 181–189. <https://doi.org/10.1016/j.bcab.2012.03.010>

Silver, P. A., Way, J. C., Arnold, F. H., & Meyerowitz, J. T. (2014). Synthetic biology: Engineering explored. *Nature*, 509(7499), 166–167. <https://doi.org/10.1038/509166a>

Simons, J. W. F. A., Götz, F., Egmond, M. R., & Verheij, H. M. (1998). Biochemical properties of staphylococcal (phospho)lipases. *Chemistry and Physics of Lipids*, 93(1–2), 27–37. [https://doi.org/10.1016/S0009-3084\(98\)00026-7](https://doi.org/10.1016/S0009-3084(98)00026-7)

Singh, R., Tiwari, M., Singh, R., & Lee, J.-K. (2013). From Protein Engineering to Immobilization: Promising Strategies for the Upgrade of Industrial Enzymes. *International Journal of Molecular Sciences*, 14(1), 1232–1277. <https://doi.org/10.3390/ijms14011232>

Sivashanmugam, A., Murray, V., Cui, C., Zhang, Y., Wang, J., & Li, Q. (2009). Practical protocols for production of very high yields of recombinant proteins using *Escherichia coli*. *Protein Science: A Publication of the Protein Society*, 18(5), 936–48. <https://doi.org/10.1002/pro.102>

Smyth, D. R., Mrozkiewicz, M. K., McGrath, W. J., Listwan, P., & Kobe, B. (2003). Crystal structures of fusion proteins with large-affinity tags. *Protein Science*, 12(7), 1313–1322. <https://doi.org/10.1110/ps.0243403>

Sommer, P., Bormann, C., & Götz, F. (1997). Genetic and biochemical characterization of a new extracellular lipase from *Streptomyces cinnamomeus*. *Applied and Environmental Microbiology*, 63(9), 3553–60. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/9293006>

Stanger, H. E., Syud, F. A., Espinosa, J. F., Giriat, I., Muir, T., & Gellman, S. H. (2001). Length-dependent stability and strand length limits in antiparallel beta -sheet secondary structure. *Proceedings of the National Academy of Sciences of the United States of America*, 98(21), 12015–20. <https://doi.org/10.1073/pnas.211536998>

Stemmer, W. P. (1994). DNA shuffling by random fragmentation and reassembly: In vitro recombination for molecular evolution. *Proceedings of the National Academy of Sciences*, 91(22), 10747–10751.

Sukumaran, R. K., Sankar, V., Madhavan, A., S., M., Satheesh, V., Idris, A. S. O., & Beevi, U. S. (2015). Enzyme Technologies: Current and Emerging Technologies for Development of Novel Enzyme Catalysts. In *Enzymes in Food and Beverage Processing*, 39–66. <https://doi.org/10.1021/bk-1977-0047>

Sulaiman, S., You, D.-J., Kanaya, E., Koga, Y., & Kanaya, S. (2014). Crystal Structure and Thermodynamic and Kinetic Stability of Metagenome-Derived LC-Cutinase. *Biochemistry*, 53(11), 1858–1869. <https://doi.org/10.1021/bi401561p>

Sulong, M. R., Zaliha Raja Abd. Rahman, R. N., Salleh, A. B., & Basri, M. (2006). A novel organic solvent tolerant lipase from *Bacillus sphaericus* 205y: Extracellular expression of a novel OST-lipase gene. *Protein Expression and Purification*, 49(2), 190–195. <https://doi.org/10.1016/j.pep.2006.04.015>

Tanaka, T., Masunari, S., Ishii, J., Wakamura, K., Segawa, M., Fukuda, H., & Kondo, A. (2010). Displaying non-natural, functional molecules on yeast surfaces via biotin streptavidin interaction. *Journal of Biotechnology*, 145(1), 79–83. <https://doi.org/10.1016/j.jbiotec.2009.10.011>

Tee, K. L., & Wong, T. S. (2013). Polishing the craft of genetic diversity creation in directed evolution. *Biotechnology Advances*, 31(8), 1707–1721. <https://doi.org/10.1016/j.biotechadv.2013.08.021>

Tello-Solis, S. R., & Romero-Garcia, B. (2001). Thermal denaturation of porcine pepsin: a study by circular dichroism. *International Journal of Biological Macromolecules*, 28(2), 129–133. [https://doi.org/10.1016/S0141-8130\(00\)00154-9](https://doi.org/10.1016/S0141-8130(00)00154-9)

Terpe, K. (2013). Overview of thermostable DNA polymerases for classical PCR applications: from molecular and biochemical fundamentals to commercial systems. *Applied Microbiology and Biotechnology*, 97(24), 10243–10254. <https://doi.org/10.1007/s00253-013-5290-2>

Thakur, S. (2012). Lipases, Its sources, Properties and Applications: A Review. *International Journal of Scientific & Engineering Research*, 3(7), 1–29.

Tian, J., Wu, N., Chu, X., & Fan, Y. (2010). Predicting changes in protein thermostability brought about by single- or multi-site mutations. *BMC Bioinformatics*, 11(1), 370. <https://doi.org/10.1186/1471-2105-11-370>

Tiesinga, J. J. W., Pouderoyen, G. van, Nardini, M., Ransac, S., & Dijkstra, B. W. (2007). Structural Basis of Phospholipase Activity of *Staphylococcus hyicus* lipase. *Journal of Molecular Biology*, 371(2), 447–456. <https://doi.org/10.1016/j.jmb.2007.05.041>

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 Biotechnology Journal*, 2(3). <https://doi.org/10.5936/csbj.201209002>

Tolia, N. H., & Joshua-Tor, L. (2006). Strategies for protein coexpression in *Escherichia coli*. *Nature Methods*, 3(1), 55–64. <https://doi.org/10.1038/nmeth0106-55>

Tompa, D. R., Gromiha, M. M., & Saraboji, K. (2016). Contribution of main chain and side chain atoms and their locations to the stability of thermophilic proteins. *Journal of Molecular Graphics and Modelling*, 64, 85–93. <https://doi.org/10.1016/j.jmgm.2016.01.001>

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(2), 182–196. <https://doi.org/10.1007/s11947-009-0202-2>

Trejo, E. S. U. (2013). Protein adaptations in archaeal extremophiles. *Archaea*, 2013. <https://doi.org/10.1155/2013/373275>

Turanli-yildiz, B., Alkim, C., & Cakar, Z. P. (2012). Protein Engineering Methods and Applications. *Protein Engineering*, (June 2017), 33–58. <https://doi.org/10.5772/27306>

Tyndall, J. D. A., Sinchaikul, S., Fothergill-Gilmore, L. A., Taylor, P., & Walkinshaw, M. D. (2002). Crystal structure of a thermostable lipase from *Bacillus stearothermophilus* P1. *Journal of Molecular Biology*, 323(5), 859–869. [https://doi.org/10.1016/S0022-2836\(02\)01004-5](https://doi.org/10.1016/S0022-2836(02)01004-5)

Undurraga, D., Markovits, A., & Erazo, S. (2001). Cocoa butter equivalent through enzymic interesterification of palm oil midfraction. *Process Biochemistry*, 36(10), 933–939. [https://doi.org/10.1016/S0032-9592\(00\)00260-0](https://doi.org/10.1016/S0032-9592(00)00260-0)

Unsworth, L. D., van der Oost, J., & Koutsopoulos, S. (2007). Hyperthermophilic enzymes stability, activity and implementation strategies for high temperature applications. *FEBS Journal*, 274(16), 4044–4056. <https://doi.org/10.1111/j.1742-4658.2007.05954.x>

Vermelho, A. B., Noronha, E. F., Filho, E. X. F., Ferrara, M. A., & Bon, E. P. S. (2013). Diversity and Biotechnological Applications of Prokaryotic Enzymes. In *The Prokaryotes* (pp. 213–240). Berlin, Heidelberg: Springer Berlin Heidelberg. https://doi.org/10.1007/978-3-642-31331-8_112

Vieille, C., & Zeikus, G. J. (2001). Hyperthermophilic enzymes: sources, uses, and molecular mechanisms for thermostability. *Microbiology and Molecular Biology Reviews* : MMBR, 65(1), 1–43. <https://doi.org/10.1128/MMBR.65.1.1-43.2001>

Villeneuve, P., Muderhwa, J. M., Graille, J., & Haas, M. J. (2000). Customizing lipases for biocatalysis: A survey of chemical, physical and molecular biological approaches.

Journal of Molecular Catalysis - B Enzymatic, 9(4–6), 113–148.
[https://doi.org/10.1016/S1381-1177\(99\)00107-1](https://doi.org/10.1016/S1381-1177(99)00107-1)

Wang, Y., Srivastava, K. C., Shen, G.-J., & Wang, H. Y. (1995). Thermostable alkaline lipase from a newly isolated thermophilic *Bacillus*, strain A30-1 (ATCC 53841). *Journal of Fermentation and Bioengineering*, 79(5), 433–438. [https://doi.org/10.1016/0922-338X\(95\)91257-6](https://doi.org/10.1016/0922-338X(95)91257-6)

Wen, S., Tan, T., & Zhao, H. (2013). Improving the thermostability of lipase Lip2 from *Yarrowia lipolytica*. *Journal of Biotechnology*, 164(2), 248–253. <https://doi.org/10.1016/j.jbiotec.2012.08.023>

Xiao, H., Bao, Z., & Zhao, H. (2015). High Throughput Screening and Selection Methods for Directed Enzyme Evolution. *Industrial & Engineering Chemistry Research*, 54(16), 4011–4020. <https://doi.org/10.1021/ie503060a>

Xiao, P.-J., Lentz, T. B., & Samulski, R. J. (2012). Recombinant adeno-associated virus: clinical application and development as a gene-therapy vector. *Therapeutic Delivery*, 3(7), 835–856. <https://doi.org/10.4155/tde.12.63>

Yang, H., Liu, L., Li, J., Chen, J., & Du, G. (2015a). Rational Design to Improve Protein Thermostability: Recent Advances and Prospects. *ChemBioEng Reviews*, 2(2), 87–94. <https://doi.org/10.1002/cben.201400032>

Yang, H., Liu, L., Li, J., Chen, J., & Du, G. (2015b). Rational Design to Improve Protein Thermostability: Recent Advances and Prospects. *ChemBioEng Reviews*, 2(2), 87–94. <https://doi.org/10.1002/cben.201400032>

Zhang, N., Suen, W.-C., Windsor, W., Xiao, L., Madison, V., & Zaks, A. (2003). Improving tolerance of *Candida antarctica* lipase B towards irreversible thermal inactivation through directed evolution. *Protein Engineering Design and Selection*, 16(8), 599–605. <https://doi.org/10.1093/protein/gzg074>

Zhao, H., & Arnold, F. H. (1997). Combinatorial protein design: Strategies for screening protein libraries. *Current Opinion in Structural Biology*, 7(4), 480–485. [https://doi.org/10.1016/S0959-440X\(97\)80110-8](https://doi.org/10.1016/S0959-440X(97)80110-8)

Zhu, P., Hu, Y., Ma, T., & Wang, H. (2010). Study of AFM-based nanometric cutting process using molecular dynamics. *Applied Surface Science*, 256(23), 7160–7165. <https://doi.org/10.1016/j.apsusc.2010.05.044>