## DESIGN AND SYNTHESIS OF A POTENTIAL INHIBITOR FOR DEN2 NS2B/NS3 SERINE PROTEASE

LEE YEAN KEE

FACULTY OF SCIENCE UNIVERSITY OF MALAYA KUALA LUMPUR

2011

## DESIGN AND SYNTHESIS OF A POTENTIAL INHIBITOR FOR DEN2 NS2B/NS3 SERINE PROTEASE

LEE YEAN KEE

### THESIS SUBMITTED IN FULFILLMENT OF THE REQUIREMENT FOR THE DEGREE OF DOCTOR OF PHILOSOPHY

DEPARTMENT OF CHEMISTRY FACULTY OF SCIENCE UNIVERSITY OF MALAYA KUALA LUMPUR

2011

### ABSTRACT

This work involves searching and designing of inhibitors for DEN2 NS2B/NS3 serine protease. It comprises three phases: modeling, synthesis and screening. Homology model construction of DEN2 NS2B/NS3 serine protease was carried out using HCV NS3/NS4A as a template. The model was then evaluated using server-based structural verification from UCLA-DOE Institute for Genomics and Proteomics server (http://nihserver.mbi.ucla.edu/SAVES/) and PROCHECK, VERIFY3D and ERRAT. The results revealed the homology model have reasonable protein fold compared to the crystal structure of DEN2 NS3 without the cofactor of NS2B bound within. The work then continued with *in silico* protein-ligand docking experiment using AUTODOCK 3.05, where the homology model was used as the macromolecule and the ligands were the competitive inhibitor (4-hydroxypanduratin A, panduratin A and ethyl 3-(4-(hydroxymethyl)-2-methoxy-5-nitrophenoxy)propanoate). The docking results suggested several putative binding informations for each of the ligand tested, when the detail binding interactions between the enzyme and the ligands were carried out. Based on these informations, a novel ligand was designed with better in silico binding energy. This ligand was then synthesised in convergent approach by employing 1,4dihydopyridine synthesis, Michael addition and Grignard reaction as the key steps. The screening was performed using the synthesised product on the DEN2 NS2B/NS3 serine protease recombinant and the result seemed to indicate the compound to exhibit uncompetitive inhibition mode.

### ABSTRAK

Kajian ini melibatkan pencarian dan rekaan inhibitor untuk enzim serine DEN2 NS2B/NS3. Ianva terdiri daripada tiga fasa: pemodelan, sintesis dan biocerakinan. Pembinaan model homologi enzim serine DEN2 NS2B/NS3 dilakukan dengan menggunakan struktur kristal HCV NS3/NS4A. Kemudian, model ini dinilai dengan menggunakan algoritma pengesahan struktur dari laman web UCLA-DOE Institut Genomik dan Proteomik (http://nihserver.mbi.ucla.edu/SAVES/, 16 April 2005). Dalam laman web ini, program PROCHECK, VERIFY3D dan ERRAT telah digunakan. Keputusan kajian menunjukkan model homologi yang dibina mempunyai struktur protein yang logikal berbanding dengan struktur kristal NS3 DEN2 tanpa kofaktor NS2B. Kajian ini dilanjutkan dengan in silico protein-ligand docking dengan menggunakan perisian AUTODOCK 3.05, di mana model homologi digunakan sebagai makromolekul ligan yang digunakan adalah inhibitor kompetitif (4dan hidroksipanduratin A, panduratin A dan etil-3-(4-(hidroksimetil)-2-metoksi-5nitrofinoksi)propanoat. Keputusan doking bagi kesemua ligan yang diuji memberi maklumat tentang mod interaksi antara enzim dan ligan. Berdasarkan maklumat tersebut, satu ligan baru direkacipta yang dijangka akan mempunyai keaktifan biologi vang lebih kuat akibat dari sudut tenaga pengikatannya yang lebih baik. Ligan ini kemudian disintesis cara konvergen dengan menggunakan langkah-langkah sintesis 1,4dihidropiridin, penambahan Michael dan tindakbalas Grignard sebagai langkah utama. Biocerakinan dilakukan ke atas enzim serin DEN2 NS2B/NS3 dengan menggunakan ligan yang telah disintesis tersebut. Keputusan menunjukkan ligan ini tidak mempamerkan mekanisme inhibisi kompetitif seperti yang dijangkakan.

#### ACKNOWLEDGEMENTS

First and foremost, I would like to express my deepest appreciation to my project supervisor, Prof. Dr. Noorsaadah Abd Rahman and co-supervisor, Prof. Dr. Rohana Yusof for their unfailing help, guidance and advice throughout the study. Many thanks were also extended to my supervisor during my research attachment in University of Bordeaux 1, Prof. Yannick Landais for his invaluable guidance.

I am also very grateful to the staffs of the Chemistry Department, University of Malaya, Mdm. Dara Fiona, Ms. Norzalida Zakaria, Mr. Fateh Ngaliman, Mr. Siew Yau Foo, Mr. Muhammad Akasah, Mdm. Nor Lela, for their co-operation and help during the study. My sincere thanks also extended to my labmates, Hwee Ying, Kim Tat, Chin Fei, Kheng Soo, Zaidul, Amanda, Choon Han, Marzieh Yaghoubi, Farah, Iskandar, and the other members of DDDRG (Drug Design and Development Research Group), as working partners throughout the project. Not forget to thank Dr. Mudiana for her help in the bioassay work done for the purpose of the compound evaluation. I am also very thankful to the financial sponsorship provided by MOSTI under the NSF Scheme.

Last but not least, I am indebted to my family and my friends who have always encouraged and supported me.

# CONTENTS

	Page
ABSTRACT	ii
ABSTRAK	iii
ACKNOWLEDGEMENTS	iv
CONTENTS	v
LIST OF FIGURES	X
LIST OF SCHEMES	xiii
LIST OF TABLES	XV
ABBREVIATIONS	xvi
APPENDICES	

CHA	PTER 1	INTRODUCTION	1-17
1.1	Deng	ae Fever (DF) and Dengue Haemorrhagic Fever (DHF)	1
	1.1.1	Symptoms and prevalence	1
	1.1.2	Diagnosis and treatment	2
1.2	Deng	ue Virus, the Genome and Lifecycles	3
	1.2.1	Transmission	3
	1.2.2	Polyprotein processing	4
1.3	Serine	e Proteases	8
	1.3.1	Dengue Virus NS2B/NS3 Serine Protease	8
	1.3.2	Mechanism of action	12
1.4	Appro	paches towards Dengue Virus Inhibition	13
	1.4.1	Attenuated vaccine	13
	1.4.2	Therapeutic agents: virus inhibitor	14

	1.4.3	Dengue Virus NS2B/NS3 Serine Protease inhibitor	14
1.5	Aims	and Objectives	17
СНА	PTER 2	2 HOMOLOGY, DOCKING AND NEW LIGAND DESIGN	18-60
		OF DEN2 NS2B/NS3 SERINE PROTEASE INHIBITION	
2.1	Molec	cular Modelling in Drug Design	18
2.2	Homo	ology Modelling	20
	2.2.1	Target-template selection	21
	2.2.2	Target-template alignment	22
	2.2.3	Model construction	23
	2.2.4	Model evaluations	23
2.3	Molec	cular Docking	25
	2.3.1	Introduction	25
	2.3.2	AUTODOCK	29
	2.3.3	Searching methods for AUTODOCK	30
	2.3.4	Scoring function of AUTODOCK	32
	2.3.5	Programs in AUTODOCK	33
2.4	Mater	ials and Methods	35
	2.4.1	Homology model of DEN2 NS2B/3 Serine Protease	35
	2.4.2	Comparison of the homology model with crystal structures of	36
		and DEN2 NS3 and HCV NS3/4A	
	2.4.3	Docking experiment using homology model	36
	2.4.4	Design of the new ligand from the docked bioactive molecules	39
2.5	Home	ology Model of DEN2 NS2B/NS3 Serine Protease	40
	2.5.1	Results	40
	2	2.5.1.1 Homology model building and model evaluation	40

	2.5.2	Discus	ssions	43
	2.5	5.2.1 C	omparison of the homology model with crystal structures	43
		of a	and DEN2 NS3 and HCV NS3/4A	
2.6	Molecul	lar Do	cking Studies	48
	2.6.1 R	Results		48
	2.0	6.1.1	Inhibition of bioactive compounds towards DEN2	48
			NS2B/NS3	
	2.0	6.1.2	Active site docking	49
	2.6.2 E	Discuss	sions	51
	2.0	6.2.1	Interactions between inhibitors and residues in DEN2	51
			NS2B/NS3	
	2.6	5.2.2	New ligand design strategy	57
	2.6	5.2.3	Virtual screening of newly designed ligand	59
СНА	PTER 3 S	SYNT	HESIS OF THE DESIGNED MOLECULE	61-97
<b>CHA</b> 3.1	PTER 3 S	<b>SYNT</b> inthetic	<b>HESIS OF THE DESIGNED MOLECULE</b> e Analysis	<b>61-97</b> 61
<b>CHA</b> 3.1 3.2	PTER 3 S Retrosy Chemist	SYNT nthetic try of l	<b>HESIS OF THE DESIGNED MOLECULE</b> c Analysis Pyridinyl, Dihydropyridinyl and Piperidinyl Ring	<b>61-97</b> 61 63
CHA 3.1 3.2	PTER 3 S Retrosy: Chemist Synthes	SYNT inthetic try of I sis: Syr	HESIS OF THE DESIGNED MOLECULE e Analysis Pyridinyl, Dihydropyridinyl and Piperidinyl Ring nthesis of Dihydropyridines	<b>61-97</b> 61 63
CHA 3.1 3.2 3.3	PTER 3 S Retrosy: Chemist Synthes 1, 4-Mio	SYNT Inthetic try of I sis: Syr chael A	HESIS OF THE DESIGNED MOLECULE c Analysis Pyridinyl, Dihydropyridinyl and Piperidinyl Ring nthesis of Dihydropyridines Addition	<b>61-97</b> 61 63 65
<ul> <li>CHA</li> <li>3.1</li> <li>3.2</li> <li>3.3</li> <li>3.4</li> </ul>	PTER 3 S Retrosy: Chemist Synthes 1, 4-Mid Weinreb	SYNT inthetic try of I sis: Syr chael A b Amic	HESIS OF THE DESIGNED MOLECULE e Analysis Pyridinyl, Dihydropyridinyl and Piperidinyl Ring nthesis of Dihydropyridines Addition de	<b>61-97</b> 61 63 65 67
<ul> <li>CHA</li> <li>3.1</li> <li>3.2</li> <li>3.3</li> <li>3.4</li> <li>3.5</li> </ul>	PTER 3 S Retrosy: Chemist Synthes 1, 4-Mid Weinret Materia	SYNT Inthetic try of I sis: Syr chael A b Amic ls and	HESIS OF THE DESIGNED MOLECULE e Analysis Pyridinyl, Dihydropyridinyl and Piperidinyl Ring othesis of Dihydropyridines Addition de Methods	<b>61-97</b> 61 63 65 67 69
<ul> <li>CHA</li> <li>3.1</li> <li>3.2</li> <li>3.3</li> <li>3.4</li> <li>3.5</li> </ul>	PTER 3 S Retrosy: Chemist Synthes 1, 4-Mid Weinret Materia 3.5.1 I	SYNT inthetic try of I sis: Syr chael A b Amic ls and Materia	HESIS OF THE DESIGNED MOLECULE 2 Analysis Pyridinyl, Dihydropyridinyl and Piperidinyl Ring athesis of Dihydropyridines Addition de Methods als and instruments used	<ul> <li>61-97</li> <li>61</li> <li>63</li> <li>65</li> <li>67</li> <li>69</li> <li>69</li> </ul>
<ul> <li>CHA</li> <li>3.1</li> <li>3.2</li> <li>3.3</li> <li>3.4</li> <li>3.5</li> </ul>	PTER 3 S Retrosy: Chemist Synthes 1, 4-Mic Weinret Materia 3.5.1 I 3.5.2 S	SYNT inthetic try of I sis: Syr chael A b Amic ls and Materi Synthe	HESIS OF THE DESIGNED MOLECULE e Analysis Pyridinyl, Dihydropyridinyl and Piperidinyl Ring athesis of Dihydropyridines Addition de Methods als and instruments used esis of Ethyl Nicotinate	<ul> <li>61-97</li> <li>61</li> <li>63</li> <li>65</li> <li>67</li> <li>69</li> <li>69</li> <li>72</li> </ul>
<ul> <li>CHA</li> <li>3.1</li> <li>3.2</li> <li>3.3</li> <li>3.4</li> <li>3.5</li> </ul>	PTER 3 S Retrosy: Chemist Synthes 1, 4-Mid Weinret Materia 3.5.1 I 3.5.2 S 3.5.3 S	SYNT inthetic try of I sis: Syr chael A b Amic ls and Materi Synthe Synthe	HESIS OF THE DESIGNED MOLECULE Analysis Pyridinyl, Dihydropyridinyl and Piperidinyl Ring thesis of Dihydropyridines Addition de Methods als and instruments used esis of Ethyl Nicotinate esis of diethyl 4-phenylpyridine-1,3(4H)-dicarboxylate	<ul> <li>61-97</li> <li>61</li> <li>63</li> <li>65</li> <li>67</li> <li>69</li> <li>69</li> <li>72</li> <li>73</li> </ul>
<ul> <li>CHA</li> <li>3.1</li> <li>3.2</li> <li>3.3</li> <li>3.4</li> <li>3.5</li> </ul>	PTER 3 S Retrosy: Chemist Synthes 1, 4-Mid Weinret Materia 3.5.1 I 3.5.2 S 3.5.3 S 3.5.3 S	SYNT inthetic try of I sis: Syr chael A b Amic ls and Materi Synthe Synthe Synthe	HESIS OF THE DESIGNED MOLECULE Analysis Pyridinyl, Dihydropyridinyl and Piperidinyl Ring thesis of Dihydropyridines Addition de Methods als and instruments used esis of Ethyl Nicotinate esis of diethyl 4-phenylpyridine-1,3(4H)-dicarboxylate esis of ethyl (1-phenoxycarbonyl-4-phenylpyridinyl)-	<ul> <li>61-97</li> <li>61</li> <li>63</li> <li>65</li> <li>67</li> <li>69</li> <li>69</li> <li>72</li> <li>73</li> <li>74</li> </ul>

3.5.5	Synthesis of ethyl (1-tert-butoxycarbonyl-4-phenylpyridinyl)-	75
	3(4H)-carboxylate	
3.5.6	Synthesis of ethyl (1-tert-butoxycarbonyl-2-butyl-4-phenyl)-	76
	3,4-dihydropyridinyl-3-carboxylate	
3.5.7	Synthesis of ethyl (1-tert-butoxycarbonyl-2-butyl-4-phenyl)-	77
	piperidinyl-3-carboxylate	
3.5.8	Synthesis of (1-tert-butoxycarbonyl-2-butyl-4-phenyl)-	78
	piperidinyl-3-carboxylic acid	
3.5.9	Synthesis of 1-tert-butoxycarbonyl-2-butyl-3-	79
	(methoxy(methyl)carbamoyl)-4-phenylpiperidine	
3.5.10	Synthesis of 1-tert-butoxycarbonyl-2-butyl-3-(benzo-1,3-	80
	dioxol-4-carbonyl)-4-phenylpiperidine	
3.5.11	Synthesis of 1-tert-butoxycarbonyl-2-butyl-3-hydroxymethyl-4-	81
	phenylpiperidine	
3.5.12	Synthesis of 1-tert-butoxycarbonyl-2-butyl-3-formyl-4-	82
	phenylpiperidine	
3.5.13	Synthesis of 1-tert-butoxycarbonyl-3-(benzo-1,3-dioxol-4-	83
	carbonyl)-2-butyl-4-phenylpiperidine	
3.5.14	Synthesis of (2-butyl-4-phenylpiperidin-3-yl)(2,3-	84
	dihydroxyphenyl)methanone	
Results	s and Discussions	86
3.6.1	Synthesis setup for the designed ligand: (2-butyl-4-	86
	phenylpiperidin-3-yl)(2,3-dihydroxyphenyl)methanone	
3.6.2	Stereochemical Control of the Proposed Synthesis	96

3.6

CHAPTER 4 INHIBITION STUDY OF THE DESIGNED AND

98-118

### SYNTHESISED COMPOUND AGAINST DEN2

### NS2B/NS3 SERINE PROTEASE

4.1	Introd	luction	98
4.2	Cell Cytopathic Effect		
4.3	Analysis of Enzyme Kinetics Data		
4.4	Mater	ials and Methods	105
	4.4.1	Materials	105
	4.4.2	Instrument used for Analysis and Bioassay	105
	4.4.3	Expression and Purification of DEN2 NS2B/NS3 serine	105
		protease complex	
	4.4.4	DEN2 NS2B/NS3 Inhibition assay using fluorogenic peptides	108
	4.4.5	Determination of K <sub>i</sub> for the synthesised compound	109
4.5	Resul	ts	110
	4.5.1	Cytopathic effect study of the compound 14	110
	4.5.2	In vitro kinetic assay of CP14	112
	4.5.3	Lineweaver-Burk plot of the inhibition assays	114
	4.5.4	Effect of CP14 against DEN2 Viral Replication	115
4.6	Discu	assions	116
CHA	PTER :	5 GENERAL DISCUSSIONS	119-122
CHA	PTER (	6 CONCLUSIONS	123
REFERENCES			124-134

# LIST OF FIGURES

Figures		Page
1.1	World distribution of Dengue in year 2008	2
1.2	Structural and non-structural polyprotein assembly of DEN2 virus	5
1.3	Proteolytic process at the catalytic triad of serine proteas	13
1.4	Small peptide substrate	15
1.5	Structures of the compounds with terminal guanidinyl group that	16
	have potential inhibition activity against DEN2 NS2B-NS3 serine	
	protease	
2.1	Structure of Taxol®	18
2.2	The protocol of Lamarckian Genetic Algorithm (LGA) search	32
	method	
2.3	Work flow of homology model construction for 3D structure of	36
	DEN2 NS2B/NS3 serine protease	
2.4	Workflow of performing docking experiment using AUTODOCK	38
	3.05	
2.5	Ramachandran plot of built homology model of DEN2 NS2B/NS3	41
	complex	
2.6	VERIFY 3D plot of DEN2 NS2B/NS3 homology model	42
2.7	ERRAT analysis of DEN2 NS2B/NS3 homology model	43
2.8	Structures of flavivirus serine proteases	46
2.9	Spatial arrangement of catalytic triad	47
2.10	Structure of the selected competitive inhibitors	49
2.11	Connolly surface representations of the active site of DEN2	50
	NS2B/NS3 protease with the bound ligands	

2.12	Hydrogen bond analysis of the docked ligands	52
2.13	Van der Waals interactions and hydrophobic interactions between	54
	the docked ligands (1, 2 and 3) and the DEN2 NS2B/NS3 serine	
	protease protein model	
2.14	Molecular orientation of the docked ligand at the catalytic triad of	56
	DEN2 NS2B/NS3	
2.15	Superimposition of the best docked conformer of the three	58
	competitive inhibitor	
2.16	Superimposition of the best docked conformer of the three	59
	competitive inhibitor ligands	
2.17	Binding interactions illustration between the newly designed	60
	ligand and the homology model of DEN2 NS2B/NS3 serine	
	protease	
4.1	Lineweaver-Burk plot of 1/v versus 1/[S] to evaluate $K_{m}$ and $V_{max}$	102
4.2	Lineweaver-Burk plot of different inhibitor	104
4.3	Workflow of harvesting and purification of DEN2 NS2B/NS3	107
	serine protease complex	
4.4	HepG2 cell morphology	110
4.5	Percent inhibition of CP14 on various DEN2 virus titre in HepG2	111
	cells	
4.6	Plot of intensity versus concentration of fluorogenic moiety of the	112
	peptide substrate, AMC	
4.7	Curves with different concentration of CP14, [I], of enzyme	113
	velocity versus substrate concentrations	
4.8	Lineweaver-Burk plot of CP14 with the different concentration of	114
	inhibitor	

4.9	RT-PCR of DENV2 serine protease from HepG2 cell in the	
	presence of CP14	
4.10	Plausible bindings suggested by AUTODOCK3.05	118

## LIST OF SCHEMES

Scheme		Page
3.1	Retrosynthesis analysis of the targeted compound	62
3.2	Hantzsch dihydropyridine synthesis	63
3.3	Hilgeroth's synthesis of dihydropyridine as the precursor of cubanes	64
3.4	Synthesis of inhibitors of 2,3-oxidosqualene-lanosterol cycliase	66
	using 1,4-Michael addition as a key step	
3.5	Proposed reaction using 1,4-Michael addition as the key step to	67
	incorporate the butyl moiety to the dihydropyridine	
3.6	General example of ketone synthesis from Weinreb amide using	67
	Grignard reagent	
3.7	Structure of the target compound	86
3.8	Esterification of nicotinic acid	86
3.9	1,4-nuceophilic addition of the phenyl moiety to ethyl nicotinate	87
	activated by ethyl chloroformate	
3.10	Proposed reaction mechanism related to the deprotection of the	88
	dihydropyridine 4 and the rearomatisation	
3.11	1,4-nuceophilic addition of the phenyl moiety to ethyl nicotinate	89
	activated by phenyl chloroformate	
3.12	Functional group interconversion from phenyl carbamate to t-butyl	89
	carbamate followed by 1,4-Michael addition of butyl moiety	
	insertion	
3.13	Reduction of 6 using 10% palladium on activated carbon	90
3.14	Partial synthesis of designed ligand, with 3 moieties attached	91
3.15	Functional group interconversions from ethyl ester to Weinreb	92

xiii

amide

3.16	Reaction of Weinreb amide to make ketone by Grignard reagent	92
3.17	Revised route from Weinreb amide 9 to furnish the targeted product	93
3.18	Revised route to synthesise aldehyde 12 from ester 7	94
3.19	Different routes to synthesise target molecule 14	95
3.20	NOE on the compound 6	97

# LIST OF TABLES

Table		Page
2.1	Structural verification (PROCHECK, VERIFY3D, ERRAT) and	47
	comparison between structure of HCV NS3/NS4A crystal, homology	
	model of DEN2 NS2B/NS3 and DEN2 NS3 crystal	
2.2	K <sub>i</sub> values of the found competitive inhibitors	49
2.3	Energies (in kcal/mol) calculated using AUTODOCK 3.05	51
2.4	Residues in the active site of DEN2 NS2B/NS3 that are involved in	53
	hydrogen bonding with the various ligands	
2.5	Residues in the active site of DEN2 NS2B/NS3 that are involved in	55
	Van der Waals interaction	
3.1	List of molecules that were used and synthesised in this work	69
3.2	Percent yield of the targeted product from 3 different route of	96
	synthesis	
4.1	Comparison of the binding site, $V_{\text{max}}$ and $K_{\text{m}}$ among different type of	103
	inhibitor	

## ABBREVIATIONS

%	Percent
φ	Psi
φ	Phi
π	Pi
[E]	Enzyme Concentration
[ES]	Enzyme-Substrate Concentration
[I]	Inhibitor Concentration
[P]	Product Concentration
[S]	Substrate Concentration
μg	Microgram
μl	Microlitre
<sup>13</sup> C	Carbon 13
1d	One Dimentional
$^{1}\mathrm{H}$	Proton
3d	Three Dimentional
Å	Angstrom
Ala	Alanine
AMBER	Assisted Model Building with Energy Refinement
AMC	Aminomethylcoumrin
Arg	Arginine
Asn	Asparagine
Asp	Aspartic Acid
BCl <sub>3</sub>	Boron Trichloride

ВНК	Baby Hamster Kidney Fibroblast cells
BOC	Butoxycarbonyl
bp	Base Pair
brd	Broad Doublet
brs	Broad Singlet
С	Capsid
C6/36	Larval Tissue
CaH <sub>2</sub>	Calcium Hydride
CH <sub>2</sub> Cl <sub>2</sub>	Dichloromethane
CHARMM	Chemistry at Harvard Molecular Mechanics
cm <sup>3</sup>	Cubic Centimetre
CuCN	Copper(I) Cyanide
CuI	Copper(I) Iodide
d	Doublet
dd	Doublet of Doublet
dddd	Doublet of Doublet of Doublet of Doublet
DEN2	Dengue Virus Type 2
DENV	Dengue Virus
DF	Dengue Fever
DHF	Dengue Haemorragic Fever
DMAP	1,4-Dimethylaminopyridine
DME	Dimethyl Ether
DMP	Dess-Martin Periodinane
DSS	Dengue Shock Syndrome
dt	Doublet of Triplet
Е	Envelope

eg	Examples
EI	Electron Impact
eqv.	Equivalent
ER	Endoplasmic Reticulum
et al.	And Others
Et <sub>2</sub> O	Diethyl Ether
EtOAc	Ethyl Acetate
EtOCOCl	Ethyl Chloroformate
EtOH	Ethanol
EtOH	Ethanol
g	Gram
GA	Genetic Algorithm
GI	Gastrointestinal
Gln	Glutamine
Glu	Glutamic Acid
Gly	Glycine
H <sub>2</sub>	Hydrogen
H <sub>2</sub> O	Water
H <sub>2</sub> SO <sub>4</sub>	Sulphuric Acid
HCl	Hydrochloric Acid
HCV	Hepatitis C Virus
HeLa	Henrietta Lacks
HepG2	Liver Hepatocellular Cells
hex	Hexane
His	Histidine

HIV	Human Immunodeficiency Virus
HIV-1	Human Immunodeficiency Virus Type 1
HOAc	Acetic Acid
HRMS	High Resolution Mass Spectrometry
id	Identity
Ile	Isoleucine
Inc.	Incorporated
<i>i</i> -PrMgCl	Isopropyl Magnesium Chloride
IUPAC	International Union of Pure and Applied Chemistry
kcal	kilo Calorie
kD	kilo Dalton
K <sub>i</sub>	Inhibition Constant
K <sub>m</sub>	Michaelis-Menten Constant
LGA	Larmackian Genetic Algorithm
LiAlH <sub>4</sub>	Lithium Aluminium Hydride
LRMS	Low Resolution Mass Spectrometry
LS	Local Search
Lys	Lysine
М	Molar
m	Multiplet
m/z	Mass-to-charge Ratio
MCA	4-methyl-coumaryl-7-amides
МеОН	Methanol
МеОН	Methanol
Mg	Magnesium
MgSO <sub>4</sub>	Magnesium Sulphate

min	Minute
ml	Millilitre
mm	Millimetre
mm <sup>3</sup>	Cubic millimitre
mM	Millimolar
mmol	Millmole
MNTD	Minimum Non-Toxic Dose
mol	Mole
Na <sub>2</sub> CO <sub>3</sub>	Sodium Carbonate
$Na_2S_2O_3$	Sodium Thiosulphate
Na <sub>2</sub> SO <sub>4</sub>	Sodium Sulphate
NaOH	Sodium Hydroxide
n-BuLi	n-Buthyllithium
NH <sub>3</sub>	Ammonia
NH <sub>3</sub>	Ammonia
NH <sub>4</sub> Cl	Ammonium Chloride
NHMe(OMe).HCl	N,O-dimethylhydroxylamine hydrochloride
Ni <sup>2+</sup>	Nickel (II) ion
nm	Nanometre
NMR	Nuclear Magnetic Resonance
NOE	Nuclear Overhauser Effect
NTA	Nitrilotriacetic Acid
NTPase	Nucleoside Triphosphatase
°C	Celsius
OD	Optical Density

OPLS	Optimized Potentials for Liquid Simulations
ORF	Open Reading Frame
PAGE	Polyacrylamide Gel Electrophoresis
Pd	Palladium
Pd/C	Palladium on Activated Carbon
pdb	Protein Data Bank
Phe	Phenylalanine
PhMgCl	Phenyl Magnesium Chloride
PhOCOCl	Phenyl Chloroformate
Pro	Proline
PyBrOP	Bromo-tris-pyrrolidino-phosphonium hexafluorophosphate
q	Quartet
ref.	Reference
RMSD	Root Mean Square Deviation
RNA	Ribonucleic Acid
rpm	Rotation Per Minute
rt	Room Temperature
RT-PCR	Reverse Transcriptase-Polymerase Chain Reaction
S	Singlet
SA	Simulated Annealing
SAR	Structure-Activity Relationship
SBDD	Structural-Based Drug Design
SDS	Sodium Dodecyl Sulfate
Ser	Serine
t	Triplet
TBE	Tick-Borne Encephalitis

t-BOC	tert-Butoxycarbonyl
t-BuOK	Potassium tert-Butoxide
TCID	Tissue Culture Infective Dose
TCID	Tissue Culture Infective Dose
THF	Tetrahydrofuran
Thr	Threonine
TLC	Thin Layer Chromatography
TMEDA	Tetramethylethylenediamine
Tris	Tris(hydroxymethyl)aminomethane
Tyr	Tyrosine
UCLA	University of California, Los Angeles
US	United States
UV	Ultraviolet
v	Enzyme Velocity
Val	Valine
V <sub>max</sub>	Maximum Enzyme Velocity
WHO	World Health Organisation
ZnSO <sub>4</sub>	Zinc(II) Sulphate
α	Alpha
β	Beta
γ	Gamma
μm	Micrometer
μΜ	Micromolar