In silico DESIGNING OF A PROSPECTIVE DRUG AGAINST HUMAN HERPES VIRUS GROUP

By:

RABIYA NISAR

ID: 15001254012

SUPERVISOR:

DR. NOUMAN RASOOL

Department ofLife Sciences
School of Science
University of Managementand Technology, Lahore, Pakistan

2018

In silico DESIGNING OF A PROSPECTIVE DRUG AGAINST HUMAN HERPES VIRUS GROUP

Submitted to University of Management and Technology Lahore

In partial fulfilment of the requirements

For the award of degree of

MASTER OF SCIENCE
IN
BIOTECHNOLOGY

BY

RABIYA NISAR

ID

1	5	0	0	1	2	5	4	0	1	2

SESSION: 2015-2017

DEPARTMENT OF LIFE SCIENCES
SCHOOL OF SCIENCE
UNIVERSITY OF MANAGEMENT AND TECHNOLOGY,
LAHORE, PAKISTAN.

DECLARATION

I **Rabiya Nisar** d/o **Rana Nisar Ahmed**ID: **15001254012**, Session 2015-2017 hereby declare that the matter printed in the thesis titled "***In silico* Designingof a Prospective Drug Against Human Herpes Virus Group**" is my own work and has not yet been printed, published and submitted as research work, thesis or publication in any form in any university, research institution etc. in Pakistan or abroad.

Dated: **Rabiya Nisar**

DEDICATION

I dedicate this thesis

to

my Parents, my Brothers Zubair NisarRana, Talha Nisar Rana and my Sister Dr. Nida Nisar Rana

without their prayers

I would never be able

to

work hard and gain this achivement.

ACKNOWLEDGEMENT

All praise to **Almighty Allah**, most tolerant and most humane who empowered me and has given me capacities to do some examination work and to add to honourable field of learning. This thesis depicts the examination work embraced at School of Science, University of Management and Technology, Lahore under the supervision of Professor **Dr. Nouman Rasool** to whom I am very obligated for supervision, proposing the subject, entire time consolation, direction, support and recommendations. His recommendations, talks, directions and remarks were dependably wellspring of inspiration and enthusiasm for me. He is constantly decent, kind, constantly prepared to help understudies for information and explore and took torment all through my exploration. I am very obliged to him for his observation, persistence, gigantic learning and valuable time. I could not have envisioned having a superior chief and guide for my exploration work and postulation.

In conclusion, I feel feeble and insufficient in vocabulary to discover appropriate words to express my emotions with weepy eyes for my cherishing **Parents** who showed me to venture out, talk the main word and roused me all through of my life, whose hands are constantly raised for petitions which made me effective in each field of my life. They upheld me to accomplish sources in my scholastic undertakings and different circles of life. Their day and night supplications empower me to join higher thoughts of life, taking care of all of issues and helped my good to achieve my objectives.

Rabiya Nisar

Abstract

The infection associated with Human Herpes Virus Group leads to long term effects in terms of various diseases, specifically neurological ones. The Herpes infection is an emerging threat and no clinically approved antiviral treatment is discovered yet to cure the disease. Computational approaches for drug development are proven to be effective and time efficient as these are not based on costly and hectic laborious works. In drug discovery, the molecular dynamics simulations help in the study of the motions of biological macromolecules such as proteins and nucleic acids. Computational mechanisms of biological targets and their related small-molecule ligands are useful in drug discovery; these include identifying the binding sites, virtual screening of numerous compounds libraries and estimation of ligand binding energies. The binding process of the tegument proteins with the inhibitorsilluminates the process of inhibition with efficiency and specificity of that inhibitor. It was aim of the present study to identify potential inhibitors of the virus replication and the tegument proteins were targeted in this study using 2053 plant derived compounds. The successfully docked compounds with high binding affinity and reactivity are reported against the proteins. These are all effective drug like compounds. Due to higher affinities and reactivity of these compounds against the tegument proteins, these compounds can be further analysed using *in vitro* and i*n vivo* approach to elucidate their inhibitory mechanism against HHV.

TABLE OF CONTENTS

TITLE **Page No.**

Chapter -3

Chapter -4

Chapter -5

Chapter -6

List of Tables

List of Figures

Sr. No. **Title** **Page No.**

1. Introduction

Herpesviridae family consists of the three sub-families which include (1) Alphaherpesvirinae, (2) Betaherpesvirinae and (3) Gammaherpesvirinae, their individuals taint a wide scope of creature species which includewarm-blooded creatures, reptiles and winged animals (Davison *et al*., 2009). As of not long ago, in excess of 130 herpes-infections are found, from thoseeight are known ashuman pathogens. These include the Alphaherpesvirinae members varicella zoster infection (VZV), herpes simplex infection compose 1 (HSV-1) and herpes simplex infection write 2 (HSV-2). Betaherpesvirinae individuals human herpesvirus compose 6 (HHV-6) and human herpesvirus write 7 (HHV-7) andhuman cytomegalovirus (HCMV).Gammaherpesvirinae individualsKaposi's sarcoma-related herpesvirus (KSHV) and Epstein-Barr infection (EBV). The HSV causes most ordinarily mucocutaneous diseases, bringing about repetitive or genital sores (Roizman *et al*., 2007). HCMV contamination is in charge of around 8% of irresistible mononuclear-sister cases and is additionally connected with inflammatory ailments (Söderberg-Nauclér, 2006; Steininger, 2007). KSHV and EBV are related to a few malignancies, for example, Kaposi's sarcoma andBurkitt's lymphoma (Chang *et al*., 1994; Kutok and Wang, 2006).