UNIVERSITI TEKNOLOGI MARA (UiTM)

COMPUTATIONAL PREDICTION OF EIGHT E2F TRANSCRIPTION FACTORS (E2F1-E2F8) IN *Homo sapiens*

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TABLE OF CONTENTS

ABSTRACT

The family members of *Homo sapiens* E2F proteins are the transcription factors responsible for the regulation of genes interplay in cell cycle routines. Presently, there are eight members of E2F proteins with few of them represent multiple isomers. The relatedness and interconnection of their regulatory principle has strong grounding basis with the protein sequences. In this study, the amino acid similarity comparison of the eight E2F proteins generated predicted similarity as high as 74 percent (E2F4 and E2F5) with most of them within the range of 30 – 40 percent. Phylogenetic classification presented the E2F transcription factors to be classified into three major subgroups comprising E2F1-3 in subgroup 1, E2F4, 5, 7, and 8 in subgroup 2, and E2F6 solely in subgroup 3. In characterization of transmembrane helices, only four of them predicted to have transmembrane domain (E2F1, one TM; E2F3, two TM; E2F7, three TM; and E2F8, three TM). The E2F proteins also predicted to localise in nuclear of the cell except for E2F3 (in extracellular) and E2F8 (in cytoplasmic). Amino acid similarity comparison between the E2F proteins with protein data bank (PDB) resulted in similarity as high as 100 percent (E2F4 with ICF7) with other comparison generated similarities higher than 39 percent. These prediction analyses demonstrated significant findings on the molecular similarity relationship between the eight E2F transcription factors. The similarities and deviation among the eight members would provide in deep idea documenting their functionality.

CHAPTER ONE

INTRODUCTION

1.1 Computational prediction

Computational prediction in bioinformatics fields is a significant task of systems biology and mathematical biology. Computational systems biology aims to develop and use efficient algorithms, data structures, visualization, and communication tools to orchestrate the integration of large quantities of biological data with the goal of computer modeling. It involves the use of computer simulations of biological systems like cellular subsystems (such as the networks of metabolites and enzymes which comprise metabolism, signal transduction pathways and gene regulatory networks) to both analyze and visualize the complex connections of these cellular processes (Kitano, 2002).

A computer simulation is a computer program or network of computers that attempts to simulate an abstract model of a particular system. Computer simulations have become a useful part of mathematical modeling of many natural systems in physics (computational physics), astrophysics, chemistry and biology, human systems in economics, psychology, and social science and in the process of engineering new technology, to gain insight into the operation of those (Strogatz, 2007).