Identification of De Novo peptide and motif prediction on Hypothyroidism protein (FOXE1) using insilico tools

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Abstract
Internationally about one billion people are estimated to be iodine deficient; however, it is unknown how often this results in hypothyroidism. In this present research investigation, we focus on the potential motif sequence for the mutated gene coded protein related to hypothyroidism disorder. The FOXE1 peptide sequence modeling is based on the Helix-Turn-Helix (HTH) motif sequence. We used advanced peptide modeling server for methodology studies. The final results of our project clearly explain that the identified motif –peptide sequence and the 3D peptide structure are potential candidates for drug docking studies and also act as novel molecular markers useful for pharmacoinformitcs and clinical endocrinology studies.

Keywords: Motif prediction, FOXE1 and Peptide modeling

INTRODUCTION
Globally, about one billion people are estimated to be iodine deficient; however, it is unknown how often this results in hypothyroidism [1]. In large population-based studies in Western countries with sufficient dietary iodine, 0.3–0.4% of the population have overt hypothyroidism. A larger proportion, 4.3–8.5%, has subclinical hypothyroidism. Of people with subclinical hypothyroidism, 80% have a TSH level below the 10 mIU/l mark regarded as the threshold for treatment. Children with subclinical hypothyroidism often return to normal thyroid function, and a small proportion develops overt hypothyroidism (as predicted by evolving antibody and TSH levels, the presence of celiac disease, and the presence of a goiter) [2]. In population-based studies, women were seven times more likely than men to have TSH levels above 10 mU/l. 2–4% of people with subclinical hypothyroidism will progress to overt hypothyroidism each year. The risk is higher in those with antibodies against thyroid peroxidase. Subclinical hypothyroidism is estimated to affect approximately 2% of children; in the adults subclinical hypothyroidism is more common in the elderly, and in Caucasians. There is a much higher rate of thyroid disorders, the most common of which is hypothyroidism, in individuals with Down syndrome and Turner syndrome [3].

Methodology
In this investigation, 3 major steps are involved, namely:
- Literature studies
- Motif identification
- Peptide modeling

As part of literature studies, OMIM, NCBI Map viewer and PMC literature database were used. The potential mutation gene (FOXE1) coded protein sequence is retrieved from UNIPORT database in FASTA format. The retrieved sequence was applied into gym motif server in order to identify the Helix-Turn-Helix (HTH) motif sequence. We used advanced peptide modeling server for methodology studies. The final results of our project clearly explain that the identified motif –peptide sequence and the 3D peptide structure are potential candidates for drug docking studies and also act as novel molecular markers useful for pharmacoinformitcs and clinical endocrinology studies.

RESULTS AND DISCUSSION
FOXE1 belongs to a large family of forkhead box (FOX) transcription factors with a conserved winged-helix DNA-binding domain [6]. Thyroid gland organogenesis involves the dorso-caudal migration of a median endodermal bud that
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originates from the posterior region of the pharyngeal floor. The thyroid primordium migrates to the area located between the fourth pharyngeal pouches and eventually fuses with them. The adult thyroid gland is composed of cells derived from all 3 germ layers, but thyroid follicular cells (TFCs), which are responsible for thyroid hormone biosynthesis, appear to derive primarily from the median primordium, though a contribution from the endoderm of the pharyngeal pouches has also been proposed [7]. The (FOXE1) which is present in 9th chromosome Fig (1). The identified protein sequence length is 370 aa (Fig 2) and 177-201aa peptide was found using GYM motif tool Fig (3). The identified motif sequence was modeled using PEP-FOLD server. In Fig: 4. the 3D structure of the peptide sequence is shown in ca wire frame model [8].
CONCLUSION
The identification of target protein is a challenge for structure based drug designing. SHBG target protein is a molecule involved in the disorders of the PCOs and Hypothyroidism in females. We modelled the amino acids sequences of the SHBG which were converted to 3 dimensional structures. The 3D structure clearly explains the drug molecular binding sites which helps in future drug designing and drug docking studies.

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CONFLICT OF INTEREST
No conflict of interest.

REFERENCES