

CURRICULUM VITAE

PERSONAL DATA

Name	<i>Eman Abdullah A Almuqri</i>
Nationality	Saudi
Position	Assistant Professor
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EDUCATION

Year	Academic Degree	Institution
<i>2016</i>	<i>PhD Degree of Genetics</i>	Huazhong University of Science and Technology
<i>2012</i>	<i>Master Degree of Genetics</i>	Central China Normal University
<i>2003</i>	<i>Bachelor Degree of Biology</i>	Science and Education College,

WORK EXPERIENCE

Period	Position	Address
<i>Lecturer, Since 2017, Until now</i>	Assistant Professor	<i>Al Imam Mohammad Ibn Saud Islamic University</i>

RESEARCH INTERESTS

Work in Molecular biology and cytogenetic Laboratories including (DNA Extraction, PCR Technique, Automated DNA Sequencing Technique and Agrose Gel Electro Phoresis, Gene Therapy).
Using molecular modelling and docking tools, and development of homology models for proteins aimed at structure based drug design.

PUBLICATIONS

1. Association of C161T and Pro12Ala Polymorphism in PPAR γ 2 with obesity in Chinese population Meta-analysis of 29 studies on non-Obesity individuals. (2014) Medical research
2. Eman Abdullah Almuqri, Mohammad Teimouri, Junaid Muhammad. Computational studies of C60-derivatives against IspE of Mycobacterium tuberculosis. International Journal of Life Sciences Research. 2016, Vol. 4, Issue 2, pp (152-158)
3. Eman Abdullah Almuqri, Mohammad Teimouri, Muhammad Junaid. In Silico identification of lead compounds for the inhibition of Mycobacterium tuberculosis IspE using complex based pharmacophore mapping, virtual screening and molecular dynamics simulation International Journal of Life Sciences Research. 2016, Vol. 4, Issue 2, pp: (253-262)
4. Muhammad Junaid#, Eman Abdullah Almuqri#, Junjun Liu, Houjin Zhang. Analyses of the Binding between Water Soluble C60 Derivatives and Potential Drug Targets through a Molecular Docking Approach. PLoS One. 2016, 11(2):e0147761.(# equal contribution)
5. Changqing Li, Muhammad Junaid, Eman Abdullah Almuqri, Shiguang Hao, Houjin Zhang. Structural analysis of a phosphonate hydroxylase with an access tunnel at the back of the active site. Acta Crystallogr F Struct Biol Commun. 2016, 72(Pt 5):362-8.
6. Kartikay Prasad, Suliman Yousef AlOmar, Eman Abdullah Almuqri, Hassan Ahmed Rudayni, Vijay Kumar. Genomics-guided identification of potential modulators of SARS-CoV-2 entry proteases, TMPRSS2 and Cathepsins B/L. PLoS One. 2021, 16(8): e0256141.