Close

Web of Science
Page 1 (Records 1 -- 1)

Print

[1]

Record 1 of 1

Title: First Comprehensive In Silico Analysis of the Functional and Structural Consequences of SNPs in Human GalNAc-T1 Gene

Author(s): Mohamoud, HSA (Mohamoud, Hussein Sheikh Ali); Hussain, MRM (Hussain, Muhammad Ramzan Manwar); El-Harouni, AA (El-Harouni, Ashraf A.); Shaik, NA (Shaik, Noor Ahmad); Qasmi, ZU (Qasmi, Zaheer Ulhaq); Merican, AF (Merican, Amir Feisal); Baig, M (Baig, Mukhtiar); Anwar, Y (Anwar, Yasir); Asfour, H (Asfour, Hani); Bondagji, N (Bondagji, Nabeel); Al-Aama, JY (Al-Aama, Jumana Yousuf)

Source: COMPUTATIONAL AND MATHEMATICAL METHODS IN MEDICINE **Article Number:** 904052 **DOI:** 10.1155/2014/904052 **Published:** 2014

Times Cited in Web of Science Core Collection: 7

Total Times Cited: 7

Usage Count (Last 180 days): 1

Usage Count (Since 2013): 7

Cited Reference Count: 48

Abstract: GalNAc-T1, a key candidate of GalNac-transferases genes family that is involved in mucin-type O-linked glycosylation pathway, is expressed in most biological tissues and cell types. Despite the reported association of GalNAc-T1 gene mutations with human disease susceptibility, the comprehensive computational analysis of coding, noncoding and regulatory SNPs, and their functional impacts on protein level, still remains unknown. Therefore, sequence-and structure-based computational tools were employed to screen the entire listed coding SNPs of GalNAc-T1 gene in order to identify and characterize them. Our concordant in silico analysis by SIFT, PolyPhen-2, PANTHER-cSNP, and SNPeffect tools, identified the potential nsSNPs (S143P, G258V, and Y414D variants) from 18 nsSNPs of GalNAc-T1. Additionally, 2 regulatory SNPs (rs72964406 and #x26; rs34304568) were also identified in GalNAc-T1 by using FastSNP tool. Using multiple computational approaches, we have systematically classified the functional mutations in regulatory and coding regions that can modify expression and function of GalNAc-T1 enzyme. These genetic variants can further assist in better understanding the wide range of disease susceptibility associated with the mucin-based cell signalling and pathogenic binding, and may help to develop novel therapeutic elements for associated diseases.

Accession Number: WOS:000332890200001

Language: English

Document Type: Article

KeyWords Plus: SINGLE NUCLEOTIDE POLYMORPHISMS; N-ACETYLGALACTOSAMINYLTRANSFERASE FAMILY; EPITHELIAL OVARIAN-CANCER; AMINO-ACID SUBSTITUTIONS; O-GLYCOSYLATION; LEUKOCYTE RECRUITMENT; PROTEIN-STRUCTURE; 3 MEMBERS; PREDICTION; MUTATIONS

Addresses: [Mohamoud, Hussein Sheikh Ali] SGUL, Div Biomed Sci BMS, Human Genet Res Ctr, London, England.
[Mohamoud, Hussein Sheikh Ali; Hussain, Muhammad Ramzan Manwar; El-Harouni, Ashraf A.; Shaik, Noor Ahmad; Asfour, Hani; Bondagji, Nabeel; Al-Aama, Jumana Yousuf] King Abdulaziz Univ, Princess Al Jawhara Al Ibrahim Ctr Excellence Res, Jeddah 21413, Saudi Arabia.
[El-Harouni, Ashraf A.; Shaik, Noor Ahmad; Al-Aama, Jumana Yousuf] King Abdulaziz Univ, Fac Med, Dept Med Genet, Jeddah 21413, Saudi Arabia.
[Qasmi, Zaheer Ulhaq] Univ Karachi, Dr Panjwani Ctr Mol Med & Drug Res, Int Ctr Chem & Biol Sci, Karachi 75270, Pakistan.
[Merican, Amir Feisal] Univ Malaya, Inst Biol Sci, Kuala Lumpur, Malaysia.
[Merican, Amir Feisal] Univ Malaya, Ctr Res Computat Sci & Informat Biol Bioind Envir, Kuala Lumpur, Malaysia.
[Baig, Mukhtiar] King Abdulaziz Univ, Fac Med, Rabigh, Saudi Arabia.
[Anwar, Yasir] King Abdulaziz Univ, Fac Sci, Dept Biol Sci, Jeddah, Saudi Arabia.
Reprint Address: Mohamoud, HSA (reprint author), SGUL, Div Biomed Sci BMS, Human Genet Res Ctr, London, England.
E-mail Addresses: husseinsheikh@live.co.uk
Author Identifiers:

Author	ResearcherID Number	ORCID Number
Baig, Mukhtiar	M-7274-2014	0000-0003-0058-2031
Mohamoud, Hussein	D-9796-2015	
shaik, noor	C-5509-2013	
Merican, Amir	B-3861-2010	0000-0001-6809-8815
Fac Sci, KAU, Biol Sci Dept	L-4228-2013	
Ul-Haq, Zaheer	E-3061-2010	0000-0002-8530-8711
Faculty of, Sciences, KAU	E-7305-2017	

Publisher: HINDAWI PUBLISHING CORPORATION
Publisher Address: 410 PARK AVENUE, 15TH FLOOR, #287 PMB, NEW YORK, NY 10022 USA
Web of Science Categories: Mathematical & Computational Biology
Research Areas: Mathematical & Computational Biology
IDS Number: AC9YG
ISSN: 1748-670X
eISSN: 1748-6718
29-char Source Abbrev.: COMPUT MATH METHOD M
ISO Source Abbrev.: Comput. Math. Method Med.
Source Item Page Count: 15
Open Access: gold
Output Date: 2017-08-10

Close

Web of Science
Page 1 (Records 1 -- 1)

Print

[1]