Waqas Ahmed

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/10446150/publications.pdf

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11	171	1163117 8	1199594 12
papers	citations	h-index	g-index

12	12	12	428
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Association of ANRIL polymorphism (rs1333049:C>G) with myocardial infarction and its pharmacogenomic role in hypercholesterolemia. Gene, 2013, 515, 416-420.	2.2	29
2	Homozygosity Mapping and Targeted Sanger Sequencing Reveal Genetic Defects Underlying Inherited Retinal Disease in Families from Pakistan. PLoS ONE, 2015, 10, e0119806.	2.5	27
3	Clinical Utility of a Coronary Heart Disease Risk Prediction Gene Score in UK Healthy Middle Aged Men and in the Pakistani Population. PLoS ONE, 2015, 10, e0130754.	2.5	21
4	Role of tissue plasminogen activator and plasminogen activator inhibitor polymorphism in myocardial infarction. Molecular Biology Reports, 2011, 38, 2541-2548.	2.3	19
5	Identification of recurrent and novel mutations in TULP1 in Pakistani families with early-onset retinitis pigmentosa. Molecular Vision, 2012, 18, 1226-37.	1.1	17
6	Novel mutations in RDH5 cause fundus albipunctatus in two consanguineous Pakistani families. Molecular Vision, 2012, 18, 1558-71.	1.1	15
7	Identification of a recurrent insertion mutation in the LDLR gene in a Pakistani family with autosomal dominant hypercholesterolemia. Molecular Biology Reports, 2010, 37, 3869-3875.	2.3	14
8	The genetic spectrum of familial hypercholesterolemia in Pakistan. Clinica Chimica Acta, 2013, 421, 219-225.	1.1	12
9	A Novel Pathogenic Nonsense Triple-Nucleotide Mutation in the Low-Density Lipoprotein Receptor Gene and Its Clinical Correlation with Familial Hypercholesterolemia. Genetic Testing and Molecular Biomarkers, 2011, 15, 601-606.	0.7	5
10	Novel and recurrent LDLR gene mutations in Pakistani hypercholesterolemia patients. Molecular Biology Reports, 2012, 39, 7365-7372.	2.3	5
11	ANRIL polymorphism rs1333049, a novel genetic predictor for diabetic retinopathy complication. Meta Gene, 2017, 14, 33-37.	0.6	2