

Muhammad Ansar

List of Publications by Year in descending order

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119
papers

4,087
citations

159358

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123
docs citations

123
times ranked

6989
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping the NPHP-JBTS-MKS Protein Network Reveals Ciliopathy Disease Genes and Pathways. <i>Cell</i> , 2011, 145, 513-528.	13.5	531
2	WDR62 is associated with the spindle pole and is mutated in human microcephaly. <i>Nature Genetics</i> , 2010, 42, 1010-1014.	9.4	255
3	Alterations of the CIB2 calcium- and integrin-binding protein cause Usher syndrome type 1J and nonsyndromic deafness DFNB48. <i>Nature Genetics</i> , 2012, 44, 1265-1271.	9.4	217
4	Mutation in NSUN2, which Encodes an RNA Methyltransferase, Causes Autosomal-Recessive Intellectual Disability. <i>American Journal of Human Genetics</i> , 2012, 90, 856-863.	2.6	189
5	Mapping autosomal recessive intellectual disability: combined microarray and exome sequencing identifies 26 novel candidate genes in 192 consanguineous families. <i>Molecular Psychiatry</i> , 2018, 23, 973-984.	4.1	147
6	Homozygous and heterozygous disruptions of ANK3: at the crossroads of neurodevelopmental and psychiatric disorders. <i>Human Molecular Genetics</i> , 2013, 22, 1960-1970.	1.4	137
7	Mutations of ESRRB Encoding Estrogen-Related Receptor Beta Cause Autosomal-Recessive Nonsyndromic Hearing Impairment DFNB35. <i>American Journal of Human Genetics</i> , 2008, 82, 125-138.	2.6	127
8	Noncoding Mutations of HGF Are Associated with Nonsyndromic Hearing Loss, DFNB39. <i>American Journal of Human Genetics</i> , 2009, 85, 25-39.	2.6	119
9	Loss-of-Function Mutations of ILDR1 Cause Autosomal-Recessive Hearing Impairment DFNB42. <i>American Journal of Human Genetics</i> , 2011, 88, 127-137.	2.6	108
10	Functional Null Mutations of MSRB3 Encoding Methionine Sulfoxide Reductase Are Associated with Human Deafness DFNB74. <i>American Journal of Human Genetics</i> , 2011, 88, 19-29.	2.6	107
11	Mutations in the Alpha 1,2-Mannosidase Gene, MAN1B1, Cause Autosomal-Recessive Intellectual Disability. <i>American Journal of Human Genetics</i> , 2011, 89, 176-182.	2.6	73
12	Mutation of ATF6 causes autosomal recessive achromatopsia. <i>Human Genetics</i> , 2015, 134, 941-950.	1.8	69
13	Reduced Euchromatin histone methyltransferase 1 causes developmental delay, hypotonia, and cranial abnormalities associated with increased bone gene expression in Kleefstra syndrome mice. <i>Developmental Biology</i> , 2014, 386, 395-407.	0.9	65
14	A missense mutation in the PISA domain of HsSAS-6 causes autosomal recessive primary microcephaly in a large consanguineous Pakistani family. <i>Human Molecular Genetics</i> , 2014, 23, 5940-5949.	1.4	63
15	Biallelic Truncating Mutations in FMN2, Encoding the Actin-Regulatory Protein Formin 2, Cause Nonsyndromic Autosomal-Recessive Intellectual Disability. <i>American Journal of Human Genetics</i> , 2014, 95, 721-728.	2.6	62
16	Homozygosity Mapping Reveals Mutations of GRXCR1 as a Cause of Autosomal-Recessive Nonsyndromic Hearing Impairment. <i>American Journal of Human Genetics</i> , 2010, 86, 138-147.	2.6	58
17	Delineation of a Human Mendelian Disorder of the DNA Demethylation Machinery: TET3 Deficiency. <i>American Journal of Human Genetics</i> , 2020, 106, 234-245.	2.6	56
18	Genetic studies of autosomal recessive primary microcephaly in 33 Pakistani families: novel sequence variants in ASPM gene. <i>Neurogenetics</i> , 2006, 7, 105-110.	0.7	55

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19	Novel sequence variants in the TMC1 gene in Pakistani families with autosomal recessive hearing impairment. <i>Human Mutation</i> , 2005, 26, 396-396.	1.1	52
20	Adenylate cyclase 1 (ADCY1) mutations cause recessive hearing impairment in humans and defects in hair cell function and hearing in zebrafish. <i>Human Molecular Genetics</i> , 2014, 23, 3289-3298.	1.4	48
21	Global genetic insight contributed by consanguineous Pakistani families segregating hearing loss. <i>Human Mutation</i> , 2019, 40, 53-72.	1.1	48
22	Genetic mapping of an autosomal recessive postaxial polydactyly type A to chromosome 13q13.3-q21.2 and screening of the candidate genes. <i>Human Genetics</i> , 2012, 131, 415-422.	1.8	44
23	Autosomal-Recessive Hearing Impairment Due to Rare Missense Variants within S1PR2. <i>American Journal of Human Genetics</i> , 2016, 98, 331-338.	2.6	43
24	Novel candidate genes and variants underlying autosomal recessive neurodevelopmental disorders with intellectual disability. <i>Human Genetics</i> , 2018, 137, 735-752.	1.8	42
25	A Recurrent Intragenic Deletion Mutation in DSG4 Gene in Three Pakistani Families with Autosomal Recessive Hypotrichosis. <i>Journal of Investigative Dermatology</i> , 2004, 123, 247-248.	0.3	41
26	A novel homozygous missense mutation in <i>WNT10B</i> in familial split-hand/foot malformation. <i>Clinical Genetics</i> , 2012, 82, 48-55.	1.0	38
27	Challenges and solutions for gene identification in the presence of familial locus heterogeneity. <i>European Journal of Human Genetics</i> , 2015, 23, 1207-1215.	1.4	35
28	A novel deletion mutation in the TUSC3 gene in a consanguineous Pakistani family with autosomal recessive nonsyndromic intellectual disability. <i>BMC Medical Genetics</i> , 2011, 12, 56.	2.1	33
29	A novel autosomal recessive non-syndromic deafness locus (DFNB35) maps to 14q24.1-q24.3 in large consanguineous kindred from Pakistan. <i>European Journal of Human Genetics</i> , 2003, 11, 77-80.	1.4	32
30	A novel insertion mutation in the cartilage-derived morphogenetic protein-1 (CDMP1) gene underlies Grebe-type chondrodysplasia in a consanguineous Pakistani family. <i>BMC Medical Genetics</i> , 2008, 9, 102.	2.1	32
31	Identification of CACNA1D variants associated with sinoatrial node dysfunction and deafness in additional Pakistani families reveals a clinical significance. <i>Journal of Human Genetics</i> , 2019, 64, 153-160.	1.1	32
32	A locus for hereditary hypotrichosis localized to human chromosome 18q21.1. <i>European Journal of Human Genetics</i> , 2003, 11, 623-628.	1.4	30
33	RNAi as a new therapeutic strategy against HCV. <i>Biotechnology Advances</i> , 2010, 28, 27-34.	6.0	30
34	Biallelic variants in PSMB1 encoding the proteasome subunit $\beta 26$ cause impairment of proteasome function, microcephaly, intellectual disability, developmental delay and short stature. <i>Human Molecular Genetics</i> , 2020, 29, 1132-1143.	1.4	30
35	Novel mutations in the keratin-74 (KRT74) gene underlie autosomal dominant woolly hair/hypotrichosis in Pakistani families. <i>Human Genetics</i> , 2011, 129, 419-424.	1.8	29
36	Bi-allelic Loss-of-Function Variants in DNMBP Cause Infantile Cataracts. <i>American Journal of Human Genetics</i> , 2018, 103, 568-578.	2.6	29

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37	Taurine treatment of retinal degeneration and cardiomyopathy in a consanguineous family with SLC6A6 taurine transporter deficiency. <i>Human Molecular Genetics</i> , 2020, 29, 618-623.	1.4	29
38	Novel <i>CLDN14</i> mutations in Pakistani families with autosomal recessive non-syndromic hearing loss. <i>American Journal of Medical Genetics, Part A</i> , 2012, 158A, 315-321.	0.7	28
39	Homozygosity mapping reveals novel and known mutations in Pakistani families with inherited retinal dystrophies. <i>Scientific Reports</i> , 2015, 5, 9965.	1.6	28
40	FAM92A Underlies Nonsyndromic Postaxial Polydactyly in Humans and an Abnormal Limb and Digit Skeletal Phenotype in Mice. <i>Journal of Bone and Mineral Research</i> , 2019, 34, 375-386.	3.1	27
41	Mutations in <i>WDR62</i> gene in Pakistani families with autosomal recessive primary microcephaly. <i>BMC Neurology</i> , 2011, 11, 119.	0.8	26
42	Genetic heterogeneity of synpolydactyly: a novel locus <i>SPD3</i> maps to chromosome 14q11.2-q12. <i>Clinical Genetics</i> , 2006, 69, 518-524.	1.0	23
43	Novel <i>VPS13B</i> Mutations in Three Large Pakistani Cohen Syndrome Families Suggests a Baloch Variant with Autistic-Like Features. <i>BMC Medical Genetics</i> , 2015, 16, 41.	2.1	23
44	A homozygous missense variant in type I keratin <i>KRT25</i> causes autosomal recessive woolly hair. <i>Journal of Medical Genetics</i> , 2015, 52, 676-680.	1.5	23
45	Bi-allelic Variants in <i>IQSEC1</i> Cause Intellectual Disability, Developmental Delay, and Short Stature. <i>American Journal of Human Genetics</i> , 2019, 105, 907-920.	2.6	22
46	Genetic analysis of consanguineous families presenting with congenital ocular defects. <i>Experimental Eye Research</i> , 2016, 146, 163-171.	1.2	21
47	Biallelic variants in <i>LINGO1</i> are associated with autosomal recessive intellectual disability, microcephaly, speech and motor delay. <i>Genetics in Medicine</i> , 2018, 20, 778-784.	1.1	21
48	Visual impairment and progressive phthisis bulbi caused by recessive pathogenic variant in <i>MARK3</i> . <i>Human Molecular Genetics</i> , 2018, 27, 2703-2711.	1.4	21
49	A novel autosomal recessive nonsyndromic hearing impairment locus (<i>DFNB42</i>) maps to chromosome 3q13.31-q22.3. <i>American Journal of Medical Genetics, Part A</i> , 2005, 133A, 18-22.	0.7	20
50	Recurrent intragenic deletion mutation in desmoglein 4 gene underlies autosomal recessive hypotrichosis in two Pakistani families of Balochi and Sindhi origins. <i>Archives of Dermatological Research</i> , 2006, 298, 135-137.	1.1	20
51	Intragenic deletions in the <i>dystrophin</i> gene in 211 Pakistani Duchenne muscular dystrophy patients. <i>Pediatrics International</i> , 2008, 50, 162-166.	0.2	20
52	Expansion of the spectrum of <i>ITGB6</i> -related disorders to adolescent alopecia, dentogingival abnormalities and intellectual disability. <i>European Journal of Human Genetics</i> , 2016, 24, 1223-1227.	1.4	20
53	Novel homozygous sequence variants in the <i>GDF5</i> gene underlie acromesomelic dysplasia type Grebe in consanguineous families. <i>Congenital Anomalies (discontinued)</i> , 2017, 57, 45-51.	0.3	20
54	Sequence variants in genes causing nonsyndromic hearing loss in a Pakistani cohort. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e917.	0.6	20

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55	Biallelic missense variants in ZBTB11 can cause intellectual disability in humans. <i>Human Molecular Genetics</i> , 2018, 27, 3177-3188.	1.4	19
56	Bi-allelic Variants in DYNC1I2 Cause Syndromic Microcephaly with Intellectual Disability, Cerebral Malformations, and Dysmorphic Facial Features. <i>American Journal of Human Genetics</i> , 2019, 104, 1073-1087.	2.6	19
57	Mutation Analysis of the <i>ASPM</i> Gene in 18 Pakistani Families With Autosomal Recessive Primary Microcephaly. <i>Journal of Child Neurology</i> , 2010, 25, 715-720.	0.7	18
58	Mapping of three novel loci for non-syndromic autosomal recessive mental retardation (NS-ARMR) in consanguineous families from Pakistan. <i>Clinical Genetics</i> , 2010, 78, 478-483.	1.0	17
59	Inhibition of full length Hepatitis C Virus particles of 1a genotype through small interference RNA. <i>Virology Journal</i> , 2011, 8, 203.	1.4	17
60	Biallelic variants in FBXL3 cause intellectual disability, delayed motor development and short stature. <i>Human Molecular Genetics</i> , 2019, 28, 972-979.	1.4	17
61	Novel missense mutations in lipase H (LIPH) gene causing autosomal recessive hypotrichosis (LAH2). <i>Journal of Dermatological Science</i> , 2009, 54, 12-16.	1.0	16
62	A Novel Deletion Mutation in Proteoglycan-4 Underlies Camptodactyly-Arthropathy-Coxa-Vara-Pericarditis Syndrome in a Consanguineous Pakistani Family. <i>Archives of Medical Research</i> , 2011, 42, 110-114.	1.5	16
63	Genetic analysis of four Pakistani families with achromatopsia and a novel S4 motif mutation of CNGA3. <i>Japanese Journal of Ophthalmology</i> , 2011, 55, 676-680.	0.9	16
64	A novel WDR62 mutation causes primary microcephaly in a Pakistani family. <i>Molecular Biology Reports</i> , 2013, 40, 591-595.	1.0	16
65	Confirmation of the Role of <i>DHX38</i> in the Etiology of Early-Onset Retinitis Pigmentosa. , 2018, 59, 4552.		16
66	Variants in KIAA0825 underlie autosomal recessive postaxial polydactyly. <i>Human Genetics</i> , 2019, 138, 593-600.	1.8	16
67	Recurrent mutations in functionally-related EDA and EDAR genes underlie X-linked isolated hypodontia and autosomal recessive hypohidrotic ectodermal dysplasia. <i>Archives of Dermatological Research</i> , 2009, 301, 625-629.	1.1	15
68	Mutations in the gene phospholipase C, delta-1 (PLCD1) underlying hereditary leukonychia. <i>European Journal of Dermatology</i> , 2012, 22, 736-739.	0.3	15
69	Novel mutations in the gene <i>HOXC13</i> underlying pure hair and nail ectodermal dysplasia in consanguineous families. <i>British Journal of Dermatology</i> , 2013, 169, 478-480.	1.4	15
70	DFNB39, a recessive form of sensorineural hearing impairment, maps to chromosome 7q11.22-q21.12. <i>European Journal of Human Genetics</i> , 2003, 11, 812-815.	1.4	14
71	Novel <i>TMPRSS3</i> variants in Pakistani families with autosomal recessive non-syndromic hearing impairment. <i>Clinical Genetics</i> , 2012, 82, 56-63.	1.0	14
72	Localization of A Novel Autosomal Recessive Non-Syndromic Hearing Impairment Locus (DFNB38) to 6q26-q27 in a Consanguineous Kindred from Pakistan. <i>Human Heredity</i> , 2003, 55, 71-74.	0.4	13

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73	Genetic mapping of a novel hypotrichosis locus to chromosome 7p21.3â€“p22.3 in a Pakistani family and screening of the candidate genes. <i>Human Genetics</i> , 2010, 128, 213-220.	1.8	13
74	Exome sequencing discloses KALRN homozygous variant as likely cause of intellectual disability and short stature in a consanguineous pedigree. <i>Human Genomics</i> , 2016, 10, 26.	1.4	13
75	Post-transcriptional inhibition of hepatitis C virus replication through small interference RNA. <i>Virology Journal</i> , 2011, 8, 112.	1.4	12
76	DFNB44, a Novel Autosomal Recessive Non-Syndromic Hearing Impairment Locus, Maps to Chromosome 7p14.1-q11.22. <i>Human Heredity</i> , 2004, 57, 195-199.	0.4	11
77	DFNB89, a novel autosomal recessive nonsyndromic hearing impairment locus on chromosome 16q21-q23.2. <i>Human Genetics</i> , 2011, 129, 379-385.	1.8	11
78	Recessive progressive symmetric erythrokeratoderma results from a homozygous loss-of-function mutation of <i>KRT83</i> and is allelic with dominant monilethrix. <i>Journal of Medical Genetics</i> , 2017, 54, 186-189.	1.5	11
79	A novel pathogenic missense variant in <i>CNNM4</i> underlying Jalili syndrome: Insights from molecular dynamics simulations. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e902.	0.6	11
80	Deficiency of TET3 leads to a genome-wide DNA hypermethylation epismature in human whole blood. <i>Npj Genomic Medicine</i> , 2021, 6, 92.	1.7	11
81	Mutations in the lipase <i>H</i> gene causing autosomal recessive hypotrichosis and woolly hair. <i>Australasian Journal of Dermatology</i> , 2015, 56, e66-70.	0.4	10
82	Novel C8orf37 mutations cause retinitis pigmentosa in consanguineous families of Pakistani origin. <i>Molecular Vision</i> , 2015, 21, 236-43.	1.1	10
83	A novel autosomal recessive non-syndromic hearing impairment locus (DFNB47) maps to chromosome 2p25.1-p24.3. <i>Human Genetics</i> , 2006, 118, 605-610.	1.8	9
84	Mutations in Lipase H Gene Underlie Autosomal Recessive Hypotrichosis in Five Pakistani Families. <i>Acta Dermato-Venereologica</i> , 2010, 90, 93-94.	0.6	9
85	NS4A protein as a marker of HCV history suggests that different HCV genotypes originally evolved from genotype 1b. <i>Virology Journal</i> , 2011, 8, 317.	1.4	9
86	Two Cases of Recessive Intellectual Disability Caused by NDST1 and METTL23 Variants. <i>Genes</i> , 2020, 11, 1021.	1.0	9
87	A Novel <i>ESRRB</i> Deletion Is a Rare Cause of Autosomal Recessive Nonsyndromic Hearing Impairment among Pakistani Families. <i>Genetics Research International</i> , 2011, 2011, 1-4.	2.0	8
88	Application of Short Tandem Repeat markers in diagnosis of chromosomal aneuploidies and forensic DNA investigation in Pakistan. <i>Gene</i> , 2014, 548, 217-222.	1.0	8
89	Segregation of Incomplete Achromatopsia and Alopecia Due to PDE6H and LPAR6 Variants in a Consanguineous Family from Pakistan. <i>Genes</i> , 2016, 7, 41.	1.0	8
90	Stable Huh-7 cell lines expressing non-structural proteins of genotype 1a of hepatitis C virus. <i>Journal of Virological Methods</i> , 2013, 189, 65-69.	1.0	7

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91	Whole-exome sequencing revealed a nonsense mutation in <i>STKLD1</i> causing non-syndromic pre-axial polydactyly type A affecting only upper limb. <i>Clinical Genetics</i> , 2019, 96, 134-139.	1.0	7
92	Novel autosomal recessive non-syndromic hearing impairment locus (DFNB71) maps to chromosome 8p22-q21.3. <i>Journal of Human Genetics</i> , 2009, 54, 141-144.	1.1	6
93	Novel mutations in the genes <i>TGM1</i> and <i>ALOXE3</i> underlying autosomal recessive congenital ichthyosis. <i>International Journal of Dermatology</i> , 2016, 55, 524-530.	0.5	6
94	Sequence variants in nine different genes underlying rare skin disorders in 10 consanguineous families. <i>International Journal of Dermatology</i> , 2017, 56, 1406-1413.	0.5	6
95	Dominant monoallelic variant in the <i>PAK2</i> gene causes Knobloch syndrome type 2. <i>Human Molecular Genetics</i> , 2021, 31, 1-9.	1.4	6
96	<i>ADAMTS1</i> , <i>MPDZ</i> , <i>MVD</i> , and <i>SEZ6</i> : candidate genes for autosomal recessive nonsyndromic hearing impairment. <i>European Journal of Human Genetics</i> , 2021, , .	1.4	6
97	Localization of a novel locus for hereditary nail dysplasia to chromosome 17q25.1-17q25.3. <i>Clinical Genetics</i> , 2004, 66, 73-78.	1.0	5
98	A new autosomal recessive nonsyndromic hearing impairment locus DFNB96 on chromosome 1p36.31-q36.13. <i>Journal of Human Genetics</i> , 2011, 56, 866-868.	1.1	5
99	Mitral regurgitation as a phenotypic manifestation of nonphotosensitive trichothiodystrophy due to a splice variant in <i>MPLKIP</i> . <i>BMC Medical Genetics</i> , 2016, 17, 13.	2.1	5
100	Exome sequencing identifies novel and known mutations in families with intellectual disability. <i>BMC Medical Genomics</i> , 2021, 14, 211.	0.7	5
101	Novel Autosomal Recessive Nonsyndromic Hearing Impairment Locus DFNB90 Maps to 7p22.1-p15.3. <i>Human Heredity</i> , 2011, 71, 106-112.	0.4	4
102	Wolfram-like syndrome with bicuspid aortic valve due to a homozygous missense variant in <i>CDK13</i> . <i>Journal of Human Genetics</i> , 2021, 66, 1009-1018.	1.1	4
103	A Novel Homozygous Nonsense Mutation p.Cys366* in the <i>WNT10B</i> Gene Underlying Split-Hand/Split-Foot Malformation in a Consanguineous Pakistani Family. <i>Frontiers in Pediatrics</i> , 2019, 7, 526.	0.9	4
104	Mapping of a novel autosomal recessive nonsyndromic deafness locus (DFNB46) to chromosome 18p11.32-p11.31. <i>American Journal of Medical Genetics, Part A</i> , 2005, 133A, 23-26.	0.7	3
105	Genetic analysis of Xp22.3 micro-deletions in seventeen families segregating isolated form of X-linked ichthyosis. <i>Journal of Dermatological Science</i> , 2015, 80, 214-217.	1.0	3
106	Inability of the most commonly used forensic genetic markers to distinguish between samples belonging to different ethnicities of Pakistan with diverse genetic background. <i>Forensic Science International: Genetics</i> , 2016, 22, e7-e8.	1.6	3
107	Novel missense and 5'-UTR splice site variants in <i>LHFPL5</i> cause autosomal recessive nonsyndromic hearing impairment. <i>Journal of Human Genetics</i> , 2018, 63, 1099-1107.	1.1	3
108	Cohen Syndrome-Associated Cataract Is Explained by <i>VPS13B</i> Functions in Lens Homeostasis and Is Modified by Additional Genetic Factors. , 2020, 61, 18.		3

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109	Phenotype Expansion for Atypical Gaucher Disease Due to Homozygous Missense PSAP Variant in a Large Consanguineous Pakistani Family. <i>Genes</i> , 2022, 13, 662.	1.0	3
110	Genetic analysis of a consanguineous Pakistani family with Leber congenital amaurosis identifies a novel mutation in GUCY2D gene. <i>Journal of Genetics</i> , 2014, 93, 527-530.	0.4	2
111	A Novel Locus for Ectodermal Dysplasia of Hair, Nail and Skin Pigmentation Anomalies Maps to Chromosome 18p11.32-p11.31. <i>PLoS ONE</i> , 2015, 10, e0129811.	1.1	2
112	Role of alternative phosphorylation and O-glycosylation of erythropoietin receptor in modulating its function: an in silico study. <i>Turkish Journal of Biology</i> , 2017, 41, 816-825.	2.1	1
113	Transient central diabetes insipidus during prolonged sinus surgery: case report and literature review. <i>Otolaryngology Case Reports</i> , 2020, 14, 100139.	0.0	1
114	A novel homozygous frameshift variant in the C3orf52 gene underlying isolated hair loss in a consanguineous family. <i>European Journal of Dermatology</i> , 2021, 31, 409-411.	0.3	1
115	Loss of Function Variants in the XPC Causes Severe Xeroderma Pigmentosum in Three Large Consanguineous Families. <i>Klinische Padiatrie</i> , 2022, 234, 123-129.	0.2	1
116	Genetic Analysis of Consanguineous Pakistani Families with Congenital Stationary Night Blindness. <i>Ophthalmic Research</i> , 2022, 65, 104-110.	1.0	1
117	Lapachol-Induced Upregulation of Sirt1/Sirt3 is linked with Improved Skin Wound Healing in Alloxan-induced Diabetic Mice.. <i>Iranian Journal of Pharmaceutical Research</i> , 2021, 20, 419-430.	0.3	1
118	Intragenic deletion mutation in the gene desmoglein 4 underlies autosomal recessive hypotrichosis in six consanguineous families. <i>Journal of Taibah University Medical Sciences</i> , 2016, 11, 203-210.	0.5	0
119	Naphthoquinones from promote skin wound healing through Sirt3 regulation. <i>Iranian Journal of Basic Medical Sciences</i> , 2020, 23, 1139-1145.	1.0	0