Ranad Shaheen

List of Publications by Year
in descending order

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Version: 2024-02-01

151 papers	8,462 citations	29994 54 h-index	56606 83 g-index
159 all docs	159 docs citations	159 times ranked	13248 citing authors

#	Article	IF	Citations
1	Mutations in phospholipase C eta-1 (PLCH1) are associated with holoprosencephaly. Journal of Medical Genetics, 2022, 59, 358-365.	1.5	3
2	Mitochondrial â€œdysmorphologyâ€• in variant classification. Human Genetics, 2022, 141, 55-64.	1.8	0
3	Clinicoâ€radiological features, molecular spectrum, and identification of prognostic factors in developmental and epileptic encephalopathy due to inosine triphosphate pyrophosphatase (ITPase) deficiency. Human Mutation, 2022, 43, 403-419.	1.1	9
4	THUMPD1 bi-allelic variants cause loss of tRNA acetylation and a syndromic neurodevelopmental disorder. American Journal of Human Genetics, 2022, 109, 587-600.	2.6	19
5	Hypomorphic GINS3 variants alter DNA replication and cause Meier-Gorlin syndrome. JCI Insight, 2022, 7, .	2.3	6
6	Survey of disorders of sex development in a large cohort of patients with diverse Mendelian phenotypes. American Journal of Medical Genetics, Part A, 2021, 185, 2789-2800.	0.7	7
7	Further delineation of <scp>MYO18B</scp>â€related autosomal recessive <scp>Klippelâ€Feil</scp> syndrome with myopathy and facial dysmorphism. American Journal of Medical Genetics, Part A, 2021, 185, 370-376.	0.7	4
8	Biallelic UBE4A loss-of-function variants cause intellectual disability and global developmental delay. Genetics in Medicine, 2021, 23, 661-668.	1.1	2
9	SCUBE3 loss-of-function causes a recognizable recessive developmental disorder due to defective bone morphogenetic protein signaling. American Journal of Human Genetics, 2021, 108, 115-133.	2.6	37
10	Further delineation of <scp>SMG9</scp>â€related heart and brain malformation syndrome. American Journal of Medical Genetics, Part A, 2021, 185, 1624-1630.	0.7	3
11	Transcriptome of CD8+ tumor-infiltrating T cells: a link between diabetes and colorectal cancer. Cancer Immunology, Immunotherapy, 2021, 70, 2625-2638.	2.0	3
12	Clinical, neuroimaging, and molecular spectrum of TECPR2 â€associated hereditary sensory and autonomic neuropathy with intellectual disability. Human Mutation, 2021, 42, 762-776.	1.1	18
13	Genetic testing results of children suspected to have Stickler syndrome type collagenopathy after ocular examination. Molecular Genetics & Genomic Medicine, 2021, 9, e1628.	0.6	3
14	Bi-allelic premature truncating variants in LTBP1 cause cutis laxa syndrome. American Journal of Human Genetics, 2021, 108, 1095-1114.	2.6	19
15	<scp>PLXNA2</scp> as a candidate gene in patients with intellectual disability. American Journal of Medical Genetics, Part A, 2021, 185, 3859-3865.	0.7	6
16	Missense NAA20 variantsimpairing the NatB protein N-terminal acetyltransferase cause autosomal recessivedevelopmental delay, intellectual disability, and microcephaly. Genetics in Medicine, 2021, 23, 2213-2218.	1.1	11
17	Lethal variants in humans: lessons learned from a large molecular autopsy cohort. Genome Medicine, 2021, 13, 161.	3.6	13
18	Biallelic Mutations in Tetratricopeptide Repeat Domain 26 (Intraflagellar Transport 56) Cause Severe Biliary Ciliopathy in Humans. Hepatology, 2020, 71, 2067-2079.	3.6	28

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19	Recessive, Deleterious Variants in SMG8 Expand the Role of Nonsense-Mediated Decay in Developmental Disorders in Humans. American Journal of Human Genetics, 2020, 107, 1178-1185.	2.6	20
20	Clinical, molecular, and biochemical delineation of asparagine synthetase deficiency in Saudi cohort. Genetics in Medicine, 2020, 22, 2071-2080.	1.1	7
21	YIF1B mutations cause a post-natal neurodevelopmental syndrome associated with Golgi and primary cilium alterations. Brain, 2020, 143, 2911-2928.	3.7	13
22	The natural history of infantile neuroaxonal dystrophy. Orphanet Journal of Rare Diseases, 2020, 15, 109.	1.2	11
23	An exome-first approach to aid in the diagnosis of primary ciliary dyskinesia. Human Genetics, 2020, 139, 1273-1283.	1.8	16
24	Expanding the clinical and phenotypic heterogeneity associated with biallelic variants in ACO2. Annals of Clinical and Translational Neurology, 2020, 7, 1013-1028.	1.7	8
25	Analysis of transcript-deleterious variants in Mendelian disorders: implications for RNA-based diagnostics. Genome Biology, 2020, 21, 145.	3.8	59
26	A genomics approach to females with infertility and recurrent pregnancy loss. Human Genetics, 2020, 139, 605-613.	1.8	59
27	The morbid genome of ciliopathies: an update. Genetics in Medicine, 2020, 22, 1051-1060.	1.1	68
28	Phenome-based approach identifies RIC1-linked Mendelian syndrome through zebrafish models, biobank associations and clinical studies. Nature Medicine, 2020, 26, 98-109.	15.2	32
29	Dysfunction of the ciliary ARMC9/TOGARAM1 protein module causes Joubert syndrome. Journal of Clinical Investigation, 2020, 130, 4423-4439.	3.9	43
30	Exploiting the Autozygome to Support Previously Published Mendelian Gene-Disease Associations: An Update. Frontiers in Genetics, 2020, 11, 580484.	1.1	13
31	Biallelic variants in CTU2 cause DREAMâ€PL syndrome and impair thiolation of tRNA wobble U34. Human Mutation, 2019, 40, 2108-2120.	1.1	25
32	MDH1 deficiency is a metabolic disorder of the malateâ€“aspartate shuttle associated with early onset severe encephalopathy. Human Genetics, 2019, 138, 1247-1257.	1.8	31
33	Perinatal distress in 1p36 deletion syndrome can mimic hypoxic ischemic encephalopathy. American Journal of Medical Genetics, Part A, 2019, 179, 1543-1546.	0.7	5
34	Bi-allelic Mutations in FAM149B1 Cause Abnormal Primary Cilium and a Range of Ciliopathy Phenotypes in Humans. American Journal of Human Genetics, 2019, 104, 731-737.	2.6	23
35	Biallelic novel missense HHAT variant causes syndromic microcephaly and cerebellarâ€vermis hypoplasia. American Journal of Medical Genetics, Part A, 2019, 179, 1053-1057.	0.7	15
36	PUS7 mutations impair pseudouridylation in humans and cause intellectual disability and microcephaly. Human Genetics, 2019, 138, 231-239.	1.8	53

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37	Genomic and phenotypic delineation of congenital microcephaly. Genetics in Medicine, 2019, 21, 545-552.	1.1	85
38	The many faces of peroxisomal disorders: Lessons from a large Arab cohort. Clinical Genetics, 2019, 95, 310-319.	1.0	12
39	Autozygome and high throughput confirmation of disease genes candidacy. Genetics in Medicine, 2019, 21, 736-742.	1.1	81
40	Congenital glaucoma and CYP1B1: an old story revisited. Human Genetics, 2019, 138, 1043-1049.	1.8	29
41	Expanding the phenome and variome of skeletal dysplasia. Genetics in Medicine, 2018, 20, 1609-1616.	1.1	46
42	Genetic investigation of 93 families with microphthalmia or posterior microphthalmos. Clinical Genetics, 2018, 93, 1210-1222.	1.0	38
43	KIAA1109 Variants Are Associated with a Severe Disorder of Brain Development and Arthrogryposis. American Journal of Human Genetics, 2018, 102, 116-132.	2.6	46
44	GWAS signals revisited using human knockouts. Genetics in Medicine, 2018, 20, 64-68.	1.1	6
45	Molecular autopsy in maternalâ€“fetal medicine. Genetics in Medicine, 2018, 20, 420-427.	1.1	84
46	Mutations in multiple components of the nuclear pore complex cause nephrotic syndrome. Journal of Clinical Investigation, 2018, 128, 4313-4328.	3.9	89
47	ARL3 Mutations Cause Joubert Syndrome by Disrupting Ciliary Protein Composition. American Journal of Human Genetics, 2018, 103, 612-620.	2.6	70
48	Warsaw breakage syndrome: Further clinical and genetic delineation. American Journal of Medical Genetics, Part A, 2018, 176, 2404-2418.	0.7	16
49	Mutations in known disease genes account for the majority of autosomal recessive retinal dystrophies. Clinical Genetics, 2018, 94, 554-563.	1.0	12
50	Biallelic UFM1 and UFC1 mutations expand the essential role of ufmylation in brain development. Brain, 2018, 141, 1934-1945.	3.7	70
51	Mutations in DONSON disrupt replication fork stability and cause microcephalic dwarfism. Nature Genetics, 2017, 49, 537-549.	9.4	81
52	PLAA Mutations Cause a Lethal Infantile Epileptic Encephalopathy by Disrupting Ubiquitin-Mediated Endolysosomal Degradation of Synaptic Proteins. American Journal of Human Genetics, 2017, 100, 706-724.	2.6	37
53	GZF1 Mutations Expand the Genetic Heterogeneity of Larsen Syndrome. American Journal of Human Genetics, 2017, 100, 831-836.	2.6	14
54	Mutations in ARMC9, which Encodes a Basal Body Protein, Cause Joubert Syndrome in Humans and Ciliopathy Phenotypes in Zebrafish. American Journal of Human Genetics, 2017, 101, 23-36.	2.6	74

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55	The genetic landscape of familial congenital hydrocephalus. Annals of Neurology, 2017, 81, 890-897.	2.8	108
56	Autozygosity reveals recessive mutations and novel mechanisms in dominant genes: implications in variant interpretation. Genetics in Medicine, 2017, 19, 1144-1150.	1.1	77
57	Reply to â€œan extremely severe phenotype due to WDR81 nonsense mutationsâ€. Annals of Neurology, 2017, 82, 651-651.	2.8	1
58	A null mutation in MICU2 causes abnormal mitochondrial calcium homeostasis and a severe neurodevelopmental disorder. Brain, 2017, 140, 2806-2813.	3.7	38
59	Mutations of KIF14 cause primary microcephaly by impairing cytokinesis. Annals of Neurology, 2017, 82, 562-577.	2.8	62
60	Molecular and clinical spectra of FBXL4 deficiency. Human Mutation, 2017, 38, 1649-1659.	1.1	41
61	Expanding the genetic heterogeneity of intellectual disability. Human Genetics, 2017, 136, 1419-1429.	1.8	122
62	Computational Prediction of Position Effects of Apparently Balanced Human Chromosomal Rearrangements. American Journal of Human Genetics, 2017, 101, 206-217.	2.6	51
63	Expanding the allelic disorders linked to TCTN1 to include Varadi syndrome (Orofaciodigital) Tj ETQq1 1 0.784314 rgBT /Overlock	0.7	4
64	The genomic landscape of balanced cytogenetic abnormalities associated with human congenital anomalies. Nature Genetics, 2017, 49, 36-45.	9.4	251
65	Increasing the sensitivity of clinical exome sequencing through improved filtration strategy. Genetics in Medicine, 2017, 19, 593-598.	1.1	59
66	Clinical genomics expands the morbid genome of intellectual disability and offers a high diagnostic yield. Molecular Psychiatry, 2017, 22, 615-624.	4.1	187
67	Novel phenotypes and loci identified through clinical genomics approaches to pediatric cataract. Human Genetics, 2017, 136, 205-225.	1.8	73
68	A novel mechanism for variable phenotypic expressivity in Mendelian diseases uncovered by an AU-rich element (ARE)-creating mutation. Genome Biology, 2017, 18, 144.	3.8	19
69	Gonadal mosaicism for ACTA1 gene masquerading as autosomal recessive nemaline myopathy. American Journal of Medical Genetics, Part A, 2016, 170, 2219-2221.	0.7	8
70	ADAT3â€related intellectual disability: Further delineation of the phenotype. American Journal of Medical Genetics, Part A, 2016, 170, 1142-1147.	0.7	32
71	Epileptic encephalopathy with continuous spike-and-wave during sleep maps to a homozygous truncating mutation in AMPA receptor component FRRS1L. Clinical Genetics, 2016, 90, 282-283.	1.0	16
72	Novel copy number variants and major limb reduction malformation: Report of three cases. American Journal of Medical Genetics, Part A, 2016, 170, 1245-1250.	0.7	8

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73	Characterizing the morbid genome of ciliopathies. Genome Biology, 2016, 17, 242.	3.8	118
74	Hyperekplexia, microcephaly and simplified gyral pattern caused by novel ASNS mutations, case report. BMC Neurology, 2016, 16, 105.	0.8	32
75	Expanding the clinical and genetic heterogeneity of hereditary disorders of connective tissue. Human Genetics, 2016, 135, 525-540.	1.8	89
76	On the phenotypic spectrum of serine biosynthesis defects. Journal of Inherited Metabolic Disease, 2016, 39, 373-381.	1.7	45
77	A homozygous truncating mutation in PUS3 expands the role of tRNA modification in normal cognition. Human Genetics, 2016, 135, 707-713.	1.8	112
78	Clinical genomics can facilitate countrywide estimation of autosomal recessive disease burden. Genetics in Medicine, 2016, 18, 1244-1249.	1.1	82
79	Cell-Intrinsic Adaptation Arising from Chronic Ablation of a Key Rho GTPase Regulator. Developmental Cell, 2016, 39, 28-43.	3.1	40
80	Mutations in CIT, encoding citron rho-interacting serine/threonine kinase, cause severe primary microcephaly in humans. Human Genetics, 2016, 135, 1191-1197.	1.8	30
81	A lethal phenotype associated with tissue plasminogen deficiency in humans. Human Genetics, 2016, 135, 1209-1211.	1.8	2
82	The syndrome dysmorphic facies, renal agenesis, ambiguous genitalia, microcephaly, polydactyly and lissencephaly (DREAMâ€PL): Report of two additional patients. American Journal of Medical Genetics, Part A, 2016, 170, 3222-3226.	0.7	17
83	Homozygous KCNMA1 mutation as a cause of cerebellar atrophy, developmental delay and seizures. Human Genetics, 2016, 135, 1295-1298.	1.8	65
84	Phenotype variability of infantile-onset multisystem neurologic, endocrine, and pancreatic disease IMNEPD. Orphanet Journal of Rare Diseases, 2016, 11, 52.	1.2	13
85	FBXO32, encoding a member of the SCF complex, is mutated in dilated cardiomyopathy. Genome Biology, 2016, 17, 2.	3.8	35
86	Accelerating matchmaking of novel dysmorphology syndromes through clinical and genomic characterization of a large cohort. Genetics in Medicine, 2016, 18, 686-695.	1.1	55
87	Mutations in SMG9, Encoding an Essential Component of Nonsense-Mediated Decay Machinery, Cause a Multiple Congenital Anomaly Syndrome in Humans and Mice. American Journal of Human Genetics, 2016, 98, 643-652.	2.6	51
88	Exome-based caseâ€“control association study using extreme phenotype design reveals novel candidates with protective effect in diabetic retinopathy. Human Genetics, 2016, 135, 193-200.	1.8	45
89	Expanding the clinical, allelic, and locus heterogeneity of retinal dystrophies. Genetics in Medicine, 2016, 18, 554-562.	1.1	89
90	Matching Two Independent Cohorts ValidatesDPH1as a Gene Responsible for Autosomal Recessive Intellectual Disability with Short Stature, Craniofacial, and Ectodermal Anomalies. Human Mutation, 2015, 36, 1015-1019.	1.1	32

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91	Identification of embryonic lethal genes in humans by autozygosity mapping and exome sequencing in consanguineous families. Genome Biology, 2015, 16, 116.	3.8	91
92	A founder CEP120 mutation in Jeune asphyxiating thoracic dystrophy expands the role of centriolar proteins in skeletal ciliopathies. Human Molecular Genetics, 2015, 24, 1410-1419.	1.4	70
93	Mutation in WDR4 impairs tRNA m7G46 methylation and causes a distinct form of microcephalic primordial dwarfism. Genome Biology, 2015, 16, 210.	3.8	132
94	Accelerating Novel Candidate Gene Discovery in Neurogenetic Disorders via Whole-Exome Sequencing of Prescreened Multiplex Consanguineous Families. Cell Reports, 2015, 10, 148-161.	2.9	375
95	Revisiting disease genes based on whole-exome sequencing in consanguineous populations. Human Genetics, 2015, 134, 1029-1034.	1.8	17
96	Positional mapping ofPRKD1,NRP1andPRDM1as novel candidate disease genes in truncus arteriosus. Journal of Medical Genetics, 2015, 52, 322-329.	1.5	30
97	The clinical utility of molecular karyotyping for neurocognitive phenotypes in a consanguineous population. Genetics in Medicine, 2015, 17, 719-725.	1.1	19
98	T (brachyury) is linked to a Mendelian form of neural tube defects in humans. Human Genetics, 2015, 134, 1139-1141.	1.8	13
99	Intrafamilial clinical heterogeneity of CSPP1â€related ciliopathy. American Journal of Medical Genetics, Part A, 2015, 167, 2478-2480.	0.7	9
100	Identification of a novel MKS locus defined byTMEM107mutation. Human Molecular Genetics, 2015, 24, 5211-5218.	1.4	42
101	Variable phenotypic expression of COG6 mutations. Journal of Medical Genetics, 2014, 51, 425.2-426.	1.5	2
102	Mutation inPLK4, encoding a master regulator of centriole formation, defines a novel locus for primordial dwarfism. Journal of Medical Genetics, 2014, 51, 814-816.	1.5	35
103	Genomic analysis of primordial dwarfism reveals novel disease genes. Genome Research, 2014, 24, 291-299.	2.4	142
104	Mutations in CSPP1, Encoding a Core Centrosomal Protein, Cause a Range of Ciliopathy Phenotypes in Humans. American Journal of Human Genetics, 2014, 94, 73-79.	2.6	77
105	Identification of three novel <scp>ECEL1</scp> mutations in three families with distal arthrogryposis type <scp>5D</scp>. Clinical Genetics, 2014, 85, 568-572.	1.0	29
106	The ECEL1-related strabismus phenotype is consistent with congenital cranial dysinnervation disorder. Journal of AAPOS, 2014, 18, 362-367.	0.2	22
107	CC2D1A Regulates Human Intellectual and Social Function as well as NF-ÎºB Signaling Homeostasis. Cell Reports, 2014, 8, 647-655.	2.9	60
108	Neu-Laxova Syndrome, an Inborn Error of Serine Metabolism, Is Caused by Mutations in PHGDH. American Journal of Human Genetics, 2014, 94, 898-904.	2.6	93

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109	A truncating mutation in B3GNT1 causes severe Walkerâ€“Warburg syndrome. Neurogenetics, 2013, 14, 243-245.	0.7	31
110	Mutations in EOGT Confirm the Genetic Heterogeneity of Autosomal-Recessive Adams-Oliver Syndrome. American Journal of Human Genetics, 2013, 92, 598-604.	2.6	114
111	Identification of KLHL41 Mutations Implicates BTB-Kelch-Mediated Ubiquitination as an Alternate Pathway to Myofibrillar Disruption in Nemaline Myopathy. American Journal of Human Genetics, 2013, 93, 1108-1117.	2.6	147
112	Mutations in DDX59 Implicate RNA Helicase in the Pathogenesis of Orofaciodigital Syndrome. American Journal of Human Genetics, 2013, 93, 555-560.	2.6	45
113	Mutation inADAT3, encoding adenosine deaminase acting on transfer RNA, causes intellectual disability and strabismus. Journal of Medical Genetics, 2013, 50, 425-430.	1.5	91
114	Genomic analysis of Meckelâ€“Gruber syndrome in Arabs reveals marked genetic heterogeneity and novel candidate genes. European Journal of Human Genetics, 2013, 21, 762-768.	1.4	56
115	Mutations inTMEM231cause Meckelâ€“Gruber syndrome. Journal of Medical Genetics, 2013, 50, 160-162.	1.5	34
116	A novel syndrome of hypohidrosis and intellectual disability is linked to COG6 deficiency. Journal of Medical Genetics, 2013, 50, 431-436.	1.5	40
117	Autozygome-guided exome sequencing in retinal dystrophy patients reveals pathogenetic mutations and novel candidate disease genes. Genome Research, 2013, 23, 236-247.	2.4	226
118	WNT1 mutation with recessive osteogenesis imperfecta and profound neurological phenotype. Journal of Medical Genetics, 2013, 50, 491-492.	1.5	45
119	Autozygome maps dispensable DNA and reveals potential selective bias against nullizygosity. Genetics in Medicine, 2012, 14, 515-519.	1.1	10
120	Genomic analysis of mitochondrial diseases in a consanguineous population reveals novel candidate disease genes. Journal of Medical Genetics, 2012, 49, 234-241.	1.5	164
121	Study of autosomal recessive osteogenesis imperfecta in Arabia reveals a novel locus defined byTMEM38Bmutation. Journal of Medical Genetics, 2012, 49, 630-635.	1.5	124
122	In search of triallelism in Bardetâ€“Biedl syndrome. European Journal of Human Genetics, 2012, 20, 420-427.	1.4	111
123	Vanishing white matter disease caused by EIF2B2 mutation with the presentation of an adrenoleukodystrophy phenotype. Gene, 2012, 496, 141-143.	1.0	5
124	POC1A Truncation Mutation Causes a Ciliopathy in Humans Characterized by Primordial Dwarfism. American Journal of Human Genetics, 2012, 91, 330-336.	2.6	70
125	3M Syndrome: An Easily Recognizable yet Underdiagnosed Cause of Proportionate Short Stature. Journal of Pediatrics, 2012, 161, 139-145.e1.	0.9	27
126	Congenital disorder of glycosylation IIa: The trouble with diagnosing a dysmorphic inborn error of metabolism. American Journal of Medical Genetics, Part A, 2012, 158A, 245-246.	0.7	12

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127	Clinical, biochemical and molecular characterization of peroxisomal diseases in Arabs. Clinical Genetics, 2011, 79, 60-70.	1.0	18
128	Human Mutations in NDE1 Cause Extreme Microcephaly with Lissencephaly. American Journal of Human Genetics, 2011, 88, 536-547.	2.6	196
129	Human Mutations in NDE1 Cause Extreme Microcephaly with Lissencephaly. American Journal of Human Genetics, 2011, 88, 677.	2.6	3
130	Recessive Mutations in DOCK6, Encoding the Guanidine Nucleotide Exchange Factor DOCK6, Lead to Abnormal Actin Cytoskeleton Organization and Adams-Oliver Syndrome. American Journal of Human Genetics, 2011, 89, 328-333.	2.6	115
131	Mutations in FKBP10 cause both Bruck syndrome and isolated osteogenesis imperfecta in humans. American Journal of Medical Genetics, Part A, 2011, 155, 1448-1452.	0.7	63
132	A TCTN2 mutation defines a novel Meckel Gruber syndrome locus. Human Mutation, 2011, 32, 573-578.	1.1	72
133	Loss-of-function variant in DNASE1L3 causes a familial form of systemic lupus erythematosus. Nature Genetics, 2011, 43, 1186-1188.	9.4	366
134	Molecular Characterization of Newborn Glaucoma Including a Distinct Aniridic Phenotype. Ophthalmic Genetics, 2011, 32, 138-142.	0.5	40
135	FKBP10 and Bruck Syndrome: Phenotypic Heterogeneity or Call for Reclassification?. American Journal of Human Genetics, 2010, 87, 306-307.	2.6	47
136	FKBP10 and Bruck Syndrome: Phenotypic Heterogeneity or Call for Reclassification?. American Journal of Human Genetics, 2010, 87, 571.	2.6	3
137	Persistence strategies of Bacillus cereus spores isolated from dairy silo tanks. Food Microbiology, 2010, 27, 347-355.	2.1	113
138	Clinical and molecular characterisation of Bardet-Biedl syndrome in consanguineous populations: the power of homozygosity mapping. Journal of Medical Genetics, 2010, 47, 236-241.	1.5	76
139	Novel CENPJ mutation causes Seckel syndrome. Journal of Medical Genetics, 2010, 47, 411-414.	1.5	149
140	Allelic heterogeneity in inbred populations: The Saudi experience with AlstrÃ¶m syndrome as an illustrative example. American Journal of Medical Genetics, Part A, 2009, 149A, 662-665.	0.7	48
141	Zellweger syndrome caused by PEX13 deficiency: Report of two novel mutations. American Journal of Medical Genetics, Part A, 2009, 149A, 1219-1223.	0.7	13
142	FREM1 Mutations Cause Bifid Nose, Renal Agenesis, and Anorectal Malformations Syndrome. American Journal of Human Genetics, 2009, 85, 414-418.	2.6	86
143	FREM1 Mutations Cause Bifid Nose, Renal Agenesis, and Anorectal Malformations Syndrome. American Journal of Human Genetics, 2009, 85, 756.	2.6	1
144	Molecular characterization of retinitis pigmentosa in Saudi Arabia. Molecular Vision, 2009, 15, 2464-9.	1.1	61

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145	Environment driven cereulide production by emetic strains of Bacillus cereus. International Journal of Food Microbiology, 2008, 127, 60-67.	2.1	27
146	Occurrence of emetic toxin producing Bacillus cereus in the dairy production chain. International Dairy Journal, 2006, 16, 740-749.	1.5	69
147	Potential of selected infant food formulas for production of Bacillus cereus emetic toxin, cereulide. International Journal of Food Microbiology, 2006, 107, 287-294.	2.1	60
148	Emetic toxin-producing strains of Bacillus cereus show distinct characteristics within the Bacillus cereus group. International Journal of Food Microbiology, 2006, 109, 132-138.	2.1	141
149	Cereulide-producing strains of Bacillus cereus show diversity. Archives of Microbiology, 2005, 184, 141-151.	1.0	46
150	Identification and Partial Characterization of the Nonribosomal Peptide Synthetase Gene Responsible for Cereulide Production in Emetic Bacillus cereus. Applied and Environmental Microbiology, 2005, 71, 105-113.	1.4	249
151	Sperm bioassay for rapid detection of cereulide-producing Bacillus cereus in food and related environments. International Journal of Food Microbiology, 2004, 94, 175-183.	2.1	88