

Dong Li

List of Publications by Year in descending order

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Version: 2024-02-01

124
papers

8,246
citations

101543

36
h-index

51608

86
g-index

133
all docs

133
docs citations

133
times ranked

14885
citing authors

#	ARTICLE	IF	CITATIONS
1	Treatment of severe Kaposiform lymphangiomatosis positive for NRAS mutation by MEK inhibition. <i>Pediatric Research</i> , 2023, 94, 1911-1915.	2.3	16
2	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. <i>Biological Psychiatry</i> , 2022, 91, 313-327.	1.3	114
3	Hypocalcemia as the Initial Presentation of Type 2 Bartter Syndrome: A Family Report. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, e1679-e1688.	3.6	2
4	Variants in ADD1 cause intellectual disability, corpus callosum dysgenesis, and ventriculomegaly in humans. <i>Genetics in Medicine</i> , 2022, 24, 319-331.	2.4	6
5	Analysis of histone variant constraint and tissue expression suggests five potential novel human disease genes: H2AFY2, H2AFZ, H2AFY, H2AFV, H1FO. <i>Human Genetics</i> , 2022, 141, 1409-1421.	3.8	3
6	Chromosome restructuring and number change during the evolution of <i>Morus notabilis</i> and <i>Morus alba</i> . <i>Horticulture Research</i> , 2022, 9, .	6.3	16
7	A novel unbalanced translocation between chromosomes 5p and 18q leading to dysmorphology and global developmental delay. <i>Molecular Genetics & Genomic Medicine</i> , 2022, , e1900.	1.2	1
8	Novel <i>PTH</i> Gene Mutations Causing Isolated Hypoparathyroidism. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, e2449-e2458.	3.6	2
9	Variants in PHF8 cause a spectrum of X-linked neurodevelopmental disorders and facial dysmorphology. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100102.	1.7	5
10	Expanding the phenotypic spectrum of ARCN1-related syndrome. <i>Genetics in Medicine</i> , 2022, 24, 1227-1237.	2.4	5
11	Exome and <i>RNA-Seq</i> analyses of an incomplete penetrance variant in <i>USP9X</i> in female-specific syndromic intellectual disability. <i>American Journal of Medical Genetics, Part A</i> , 2022, , .	1.2	1
12	Further supporting <i>SMARCC2</i> -related neurodevelopmental disorder through exome analysis and reanalysis in two patients. <i>American Journal of Medical Genetics, Part A</i> , 2022, 188, 878-882.	1.2	3
13	Contribution of Mendelian disorders in a population-based pediatric neurodegeneration cohort. <i>Journal of Pediatrics</i> , 2022, , .	1.8	0
14	Genetics etiologies and genotype phenotype correlations in a cohort of individuals with central conducting lymphatic anomaly. <i>European Journal of Human Genetics</i> , 2022, 30, 1022-1028.	2.8	9
15	Shared genetic risk between eating disorder and substance use-related phenotypes: Evidence from genome-wide association studies. <i>Addiction Biology</i> , 2021, 26, e12880.	2.6	28
16	De novo loss-of-function variants in X-linked MED12 are associated with Hardikar syndrome in females. <i>Genetics in Medicine</i> , 2021, 23, 637-644.	2.4	16
17	Expanded phenotypic spectrum of <i>JAG1</i> -associated diseases: Central conducting lymphatic anomaly with a pathogenic variant in <i>JAG1</i> . <i>Clinical Genetics</i> , 2021, 99, 742-743.	2.0	7
18	A novel heterotaxy gene: Expansion of the phenotype of TTC21B spectrum disease. <i>American Journal of Medical Genetics, Part A</i> , 2021, 185, 1266-1269.	1.2	5

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19	Rare Recurrent Variants in Noncoding Regions Impact Attention-Deficit Hyperactivity Disorder (ADHD) Gene Networks in Children of both African American and European American Ancestry. <i>Genes</i> , 2021, 12, 310.	2.4	10
20	The chromatin remodeler ISWI acts during <i>Drosophila</i> development to regulate adult sleep. <i>Science Advances</i> , 2021, 7, .	10.3	9
21	Expanding the genotypic and phenotypic spectrum in a diverse cohort of 104 individuals with Wiedemann-Steiner syndrome. <i>American Journal of Medical Genetics, Part A</i> , 2021, 185, 1649-1665.	1.2	34
22	<i>ALG13</i> linked intellectual disability: New variants, glycosylation analysis, and expanded phenotypes. <i>Journal of Inherited Metabolic Disease</i> , 2021, 44, 1001-1012.	3.6	9
23	Pathogenic variants in <i>CDH11</i> impair cell adhesion and cause Teebi hypertelorism syndrome. <i>Human Genetics</i> , 2021, 140, 1061-1076.	3.8	4
24	A DNA repair disorder caused by de novo monoallelic <i>DDB1</i> variants is associated with a neurodevelopmental syndrome. <i>American Journal of Human Genetics</i> , 2021, 108, 749-756.	6.2	6
25	Discovery of a neuromuscular syndrome caused by biallelic variants in <i>ASCC3</i> . <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100024.	1.7	1
26	A new syndrome of moyamoya disease, kidney dysplasia, aminotransferase elevation, and skin disease associated with de novo variants in <i>RNF213</i> . <i>American Journal of Medical Genetics, Part A</i> , 2021, 185, 2168-2174.	1.2	8
27	Pathogenic variants in <i>SMARCA5</i> , a chromatin remodeler, cause a range of syndromic neurodevelopmental features. <i>Science Advances</i> , 2021, 7, .	10.3	17
28	High-throughput Molecular Analysis of Pseudohypoparathyroidism 1b Patients Reveals Novel Genetic and Epigenetic Defects. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, e4603-e4620.	3.6	12
29	Cleft palate morphology, genetic etiology, and risk of mortality in infants with Robin sequence. <i>American Journal of Medical Genetics, Part A</i> , 2021, 185, 3694-3700.	1.2	1
30	Expanding the phenotype of <i>ASXL3</i> -related syndrome: A comprehensive description of 45 unpublished individuals with inherited and de novo pathogenic variants in <i>ASXL3</i> . <i>American Journal of Medical Genetics, Part A</i> , 2021, 185, 3446-3458.	1.2	12
31	Ciliopathies: Coloring outside of the lines. <i>American Journal of Medical Genetics, Part A</i> , 2021, 185, 687-694.	1.2	7
32	Chromosome 4q28.3q32.3 duplication in a patient with lymphatic malformations, craniosynostosis, and dysmorphic features. <i>Clinical Dysmorphology</i> , 2021, 30, 89-92.	0.3	2
33	De novo variants in <i>CACNA1E</i> found in patients with intellectual disability, developmental regression and social cognition deficit but no seizures. <i>Molecular Autism</i> , 2021, 12, 69.	4.9	12
34	Partial Loss of <i>USP9X</i> Function Leads to a Male Neurodevelopmental and Behavioral Disorder Converging on Transforming Growth Factor β Signaling. <i>Biological Psychiatry</i> , 2020, 87, 100-112.	1.3	42
35	Heterozygous de novo variants in <i>CSNK1G1</i> are associated with syndromic developmental delay and autism spectrum disorder. <i>Clinical Genetics</i> , 2020, 98, 571-576.	2.0	10
36	Clinical variability of <i>TUBB</i> -associated disorders: Diagnosis through reanalysis. <i>American Journal of Medical Genetics, Part A</i> , 2020, 182, 3035-3039.	1.2	7

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37	EP300 related Rubinstein-Taybi syndrome: Highlighted rare phenotypic findings and a genotype-phenotype meta-analysis of 74 patients. American Journal of Medical Genetics, Part A, 2020, 182, 2926-2938.	1.2	16
38	The variability of SMARCA4 related Coffin-Siris syndrome: Do nonsense candidate variants add to milder phenotypes?. American Journal of Medical Genetics, Part A, 2020, 182, 2058-2067.	1.2	14
39	Histone H3.3 beyond cancer: Germline mutations in Histone 3 Family 3A and 3B cause a previously unidentified neurodegenerative disorder in 46 patients. Science Advances, 2020, 6, .	10.3	43
40	Biliary-Atresia-Associated Mannosidase-1-Alpha-2 Gene Regulates Biliary and Ciliary Morphogenesis and Laterality. Frontiers in Physiology, 2020, 11, 538701.	2.8	13
41	Proteomic Profiling Reveals Roles of Stress Response, Ca ²⁺ Transient Dysregulation, and Novel Signaling Pathways in Alcohol-Induced Cardiotoxicity. Alcoholism: Clinical and Experimental Research, 2020, 44, 2187-2199.	2.4	6
42	Non-coding structural variation differentially impacts attention-deficit hyperactivity disorder (ADHD) gene networks in African American vs Caucasian children. Scientific Reports, 2020, 10, 15252.	3.3	5
43	Experiences with offering pro bono medical genetics services in the West Indies: Benefits to patients, physicians, and the community. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2020, 184, 1030-1041.	1.6	8
44	Further delineation of the clinical spectrum of KAT6B disorders and allelic series of pathogenic variants. Genetics in Medicine, 2020, 22, 1338-1347.	2.4	25
45	A second cohort of CHD3 patients expands the molecular mechanisms known to cause Snijders Blok-Campeau syndrome. European Journal of Human Genetics, 2020, 28, 1422-1431.	2.8	25
46	Activating variants in PDGFRB result in a spectrum of disorders responsive to imatinib monotherapy. American Journal of Medical Genetics, Part A, 2020, 182, 1576-1591.	1.2	21
47	Expanding the clinical and phenotypic heterogeneity associated with biallelic variants in ACO2. Annals of Clinical and Translational Neurology, 2020, 7, 1013-1028.	3.7	8
48	Application of exome sequencing to diagnose a novel presentation of the Cornelia de Lange syndrome in an Afro-Caribbean family. Molecular Genetics & Genomic Medicine, 2020, 8, e1318.	1.2	2
49	De Novo Variants in CNOT1, a Central Component of the CCR4-NOT Complex Involved in Gene Expression and RNA and Protein Stability, Cause Neurodevelopmental Delay. American Journal of Human Genetics, 2020, 107, 164-172.	6.2	37
50	MMHub, a database for the mulberry metabolome. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	14
51	Novel truncating mutations in CTNND1 cause a dominant craniofacial and cardiac syndrome. Human Molecular Genetics, 2020, 29, 1900-1921.	2.9	21
52	A homozygous truncating NALCN variant in two Afro-Caribbean siblings with hypotonia and dolichocephaly. American Journal of Medical Genetics, Part A, 2020, 182, 1877-1880.	1.2	3
53	Flavones Produced by Mulberry Flavone Synthase Type I Constitute a Defense Line against the Ultraviolet-B Stress. Plants, 2020, 9, 215.	3.5	21
54	Metabolic Profiling and Transcriptome Analysis of Mulberry Leaves Provide Insights into Flavonoid Biosynthesis. Journal of Agricultural and Food Chemistry, 2020, 68, 1494-1504.	5.2	45

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55	Digenic Heterozygous Mutations in SLC34A3 and SLC34A1 Cause Dominant Hypophosphatemic Rickets with Hypercalciuria. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, 2392-2400.	3.6	18
56	Kaposiform lymphangiomatosis effectively treated with MEK inhibition. <i>EMBO Molecular Medicine</i> , 2020, 12, e12324.	6.9	51
57	PRKACB variants in skeletal disease or adrenocortical hyperplasia: effects on protein kinase A. <i>Endocrine-Related Cancer</i> , 2020, 27, 647-656.	3.1	7
58	Intragenic Deletions of GNAS in Pseudohypoparathyroidism Type 1A Identify a New Region Affecting Methylation of Exon A/B. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, e3197-e3206.	3.6	6
59	Mutations in topoisomerase III β result in a B cell immunodeficiency. <i>Nature Communications</i> , 2019, 10, 3644.	12.8	37
60	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. <i>Nature Genetics</i> , 2019, 51, 1207-1214.	21.4	641
61	Generalized congenital epithelioid blue nevi (pigmented epithelioid melanocytomas) in an infant: Report of case and review of the literature. <i>Journal of Cutaneous Pathology</i> , 2019, 46, 954-959.	1.3	3
62	De Novo Heterozygous POLR2A Variants Cause a Neurodevelopmental Syndrome with Profound Infantile-Onset Hypotonia. <i>American Journal of Human Genetics</i> , 2019, 105, 283-301.	6.2	46
63	ARAF recurrent mutation causes central conducting lymphatic anomaly treatable with a MEK inhibitor. <i>Nature Medicine</i> , 2019, 25, 1116-1122.	30.7	136
64	Missense Mutations in NKAP Cause a Disorder of Transcriptional Regulation Characterized by Marfanoid Habitus and Cognitive Impairment. <i>American Journal of Human Genetics</i> , 2019, 105, 987-995.	6.2	11
65	Association of Rare Recurrent Copy Number Variants With Congenital Heart Defects Based on Next-Generation Sequencing Data From Family Trios. <i>Frontiers in Genetics</i> , 2019, 10, 819.	2.3	15
66	Gene domain-specific DNA methylation epigenatures highlight distinct molecular entities of ADNP syndrome. <i>Clinical Epigenetics</i> , 2019, 11, 64.	4.1	71
67	Isolated vocal cord paralysis in two siblings with compound heterozygous variants in MUSK: Expanding the phenotypic spectrum. <i>American Journal of Medical Genetics, Part A</i> , 2019, 179, 655-658.	1.2	7
68	Phenotypic spectrum associated with SPECC1L pathogenic variants: new families and critical review of the nosology of Teebi, Opitz GBBB, and Baraitser-Winter syndromes. <i>European Journal of Medical Genetics</i> , 2019, 62, 103588.	1.3	24
69	KAT6A Syndrome: genotype-phenotype correlation in 76 patients with pathogenic KAT6A variants. <i>Genetics in Medicine</i> , 2019, 21, 850-860.	2.4	68
70	De novo variants in Myelin regulatory factor (MYRF) as candidates of a new syndrome of cardiac and urogenital anomalies. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 969-972.	1.2	39
71	Heterozygous Deletion Impacting SMARCAD1 in the Original Kindred with Absent Dermatoglyphs and Associated Features (Baird, 1964). <i>Journal of Pediatrics</i> , 2018, 194, 248-252.e2.	1.8	6
72	Expanding the phenotypic spectrum of TP63-related disorders including the first set of monozygotic twins. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 75-81.	1.2	11

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73	Extension of the mutational and clinical spectrum of <i>SOX2</i> related disorders: Description of six new cases and a novel association with suprasellar teratoma. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 2710-2719.	1.2	7
74	Coronary Artery Calcium on Noncontrast Thoracic Computerized Tomography Scans and All-Cause Mortality. <i>Circulation</i> , 2018, 138, 2437-2438.	1.6	15
75	Heterozygous Mutations in <i>TBX1</i> as a Cause of Isolated Hypoparathyroidism. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 4023-4032.	3.6	15
76	HDL (High-Density Lipoprotein) Metrics and Atherosclerotic Risk in Women. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018, 38, 2236-2244.	2.4	52
77	Pathogenic variant in <i>EPHB4</i> results in central conducting lymphatic anomaly. <i>Human Molecular Genetics</i> , 2018, 27, 3233-3245.	2.9	73
78	<i>USMG5</i> Ashkenazi Jewish founder mutation impairs mitochondrial complex V dimerization and ATP synthesis. <i>Human Molecular Genetics</i> , 2018, 27, 3305-3312.	2.9	45
79	<i>CYP3A4</i> mutation causes vitamin D-dependent rickets type 3. <i>Journal of Clinical Investigation</i> , 2018, 128, 1913-1918.	8.2	77
80	Increasing diagnostic yield by RNA-Sequencing in rare disease—bypass hurdles of interpreting intronic or splice-altering variants. <i>Annals of Translational Medicine</i> , 2018, 6, 126-126.	1.7	9
81	Digenic Inheritance of <i>PROKR2</i> and <i>WDR11</i> Mutations in Pituitary Stalk Interruption Syndrome. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2017, 102, 2501-2507.	3.6	36
82	High-Quality Statin Trials Support the 2013 American College of Cardiology/American Heart Association Cholesterol Guidelines After the HOPE-3 Trial (Heart Outcomes Prevention Evaluation-3): MESA (The Multiethnic Study of Atherosclerosis). <i>Circulation</i> , 2017, 136, 1863-1865.	1.6	7
83	A genome-wide association study of anorexia nervosa suggests a risk locus implicated in dysregulated leptin signaling. <i>Scientific Reports</i> , 2017, 7, 3847.	3.3	23
84	Exome Sequencing Reveals Mutations in <i>AIRE</i> as a Cause of Isolated Hypoparathyroidism. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2017, 102, 1726-1733.	3.6	35
85	Short stature and hypoparathyroidism in a child with Kenny-Caffey syndrome type 2 due to a novel mutation in <i>FAM111A</i> gene. <i>International Journal of Pediatric Endocrinology (Springer)</i> , 2017, 2017, 1.	1.6	27
86	Late-onset hereditary hypophosphatemic rickets with hypercalciuria (HHRH) due to mutation of <i>SLC34A3/NPT2c</i> . <i>Bone</i> , 2017, 97, 15-19.	2.9	30
87	Safety and Effectiveness of JuvÃ©derm Ultra Plus Injectable Gel in Correcting Severe Nasolabial Folds in Chinese Subjects. <i>Plastic and Reconstructive Surgery - Global Open</i> , 2017, 5, e1133.	0.6	11
88	Monoallelic <i>BMP2</i> Variants Predicted to Result in Haploinsufficiency Cause Craniofacial, Skeletal, and Cardiac Features Overlapping Those of 20p12 Deletions. <i>American Journal of Human Genetics</i> , 2017, 101, 985-994.	6.2	44
89	<i>CYP3A4</i> Induction by Rifampin: An Alternative Pathway for Vitamin D Inactivation in Patients With <i>CYP24A1</i> Mutations. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2017, 102, 1440-1446.	3.6	72
90	Early Infantile Epileptic Encephalopathy in an <i>STXBP1</i> Patient with Lactic Acidemia and Normal Mitochondrial Respiratory Chain Function. <i>Case Reports in Genetics</i> , 2016, 2016, 1-5.	0.2	6

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91	<i>SMARCE1</i> , a rare cause of Coffin–Siris Syndrome: Clinical description of three additional cases. <i>American Journal of Medical Genetics, Part A</i> , 2016, 170, 1967-1973.	1.2	18
92	Enhanced B Cell Alloantigen Presentation and Its Epigenetic Dysregulation in Liver Transplant Rejection. <i>American Journal of Transplantation</i> , 2016, 16, 497-508.	4.7	17
93	Aortic coarctation and carotid artery aneurysm in a patient with hardikar syndrome: Cardiovascular implications for affected individuals. <i>American Journal of Medical Genetics, Part A</i> , 2016, 170, 482-486.	1.2	1
94	Association of a rare NOTCH4 coding variant with systemic sclerosis: a family-based whole exome sequencing study. <i>BMC Musculoskeletal Disorders</i> , 2016, 17, 462.	1.9	12
95	Mutation in IRF2BP2 is responsible for a familial form of common variable immunodeficiency disorder. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 138, 544-550.e4.	2.9	54
96	Mutations in TBCK, Encoding TBC1-Domain-Containing Kinase, Lead to a Recognizable Syndrome of Intellectual Disability and Hypotonia. <i>American Journal of Human Genetics</i> , 2016, 98, 782-788.	6.2	50
97	Association of Mutations in SLC12A1 Encoding the NKCC2 Cotransporter With Neonatal Primary Hyperparathyroidism. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2016, 101, 2196-2200.	3.6	25
98	GRIN2D Recurrent De Novo Dominant Mutation Causes a Severe Epileptic Encephalopathy Treatable with NMDA Receptor Channel Blockers. <i>American Journal of Human Genetics</i> , 2016, 99, 802-816.	6.2	138
99	Expanding the <i>SPECC1L</i> mutation phenotypic spectrum to include Teebi hypertelorism syndrome. <i>American Journal of Medical Genetics, Part A</i> , 2015, 167, 2497-2502.	1.2	26
100	Mitochondrial Disease Sequence Data Resource (MSeqDR): A global grass-roots consortium to facilitate deposition, curation, annotation, and integrated analysis of genomic data for the mitochondrial disease clinical and research communities. <i>Molecular Genetics and Metabolism</i> , 2015, 114, 388-396.	1.1	76
101	Mutations in <i>SPECC1L</i> , encoding sperm antigen with calponin homology and coiled-coil domains 1-like, are found in some cases of autosomal dominant Opitz G/BBB syndrome. <i>Journal of Medical Genetics</i> , 2015, 52, 104-110.	3.2	40
102	Value of whole exome sequencing for syndromic retinal dystrophy diagnosis in young patients. <i>Clinical and Experimental Ophthalmology</i> , 2015, 43, 132-138.	2.6	7
103	Delayed diagnosis of congenital myasthenia due to associated mitochondrial enzyme defect. <i>Neuromuscular Disorders</i> , 2015, 25, 257-261.	0.6	16
104	Genetic sharing and heritability of paediatric age of onset autoimmune diseases. <i>Nature Communications</i> , 2015, 6, 8442.	12.8	58
105	Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. <i>Nature Medicine</i> , 2015, 21, 1018-1027.	30.7	212
106	Exome sequencing reveals a nonsense mutation in MMP13 as a new cause of autosomal recessive metaphyseal anadysplasia. <i>European Journal of Human Genetics</i> , 2015, 23, 264-266.	2.8	13
107	Autosomal Dominant Hypoparathyroidism Caused by Germline Mutation in <i>GNA11</i> : Phenotypic and Molecular Characterization. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2014, 99, E1774-E1783.	3.6	79
108	AGC1 Deficiency Causes Infantile Epilepsy, Abnormal Myelination, and Reduced N-Acetylaspartate. <i>JIMD Reports</i> , 2014, 14, 77-85.	1.5	57

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109	A genome-wide association study of anorexia nervosa. <i>Molecular Psychiatry</i> , 2014, 19, 1085-1094.	7.9	282
110	Molecular footprints of domestication and improvement in soybean revealed by whole genome re-sequencing. <i>BMC Genomics</i> , 2013, 14, 579.	2.8	186
111	Mutations in PDGFRB Cause Autosomal-Dominant Infantile Myofibromatosis. <i>American Journal of Human Genetics</i> , 2013, 92, 1001-1007.	6.2	174
112	Draft genome of the wheat A-genome progenitor <i>Triticum urartu</i> . <i>Nature</i> , 2013, 496, 87-90.	27.8	700
113	<i>Aegilops tauschii</i> draft genome sequence reveals a gene repertoire for wheat adaptation. <i>Nature</i> , 2013, 496, 91-95.	27.8	714
114	Whole-genome sequencing of giant pandas provides insights into demographic history and local adaptation. <i>Nature Genetics</i> , 2013, 45, 67-71.	21.4	303
115	Draft genome sequence of the mulberry tree <i>Morus notabilis</i> . <i>Nature Communications</i> , 2013, 4, 2445.	12.8	277
116	Identification and characterization of Sox genes in the silkworm, <i>Bombyx mori</i> . <i>Molecular Biology Reports</i> , 2011, 38, 3573-3584.	2.3	23
117	Genetic diversity, molecular phylogeny and selection evidence of the silkworm mitochondria implicated by complete resequencing of 41 genomes. <i>BMC Evolutionary Biology</i> , 2010, 10, 81.	3.2	40
118	MicroRNAs of <i>Bombyx mori</i> identified by Solexa sequencing. <i>BMC Genomics</i> , 2010, 11, 148.	2.8	107
119	Single base-resolution methylome of the silkworm reveals a sparse epigenomic map. <i>Nature Biotechnology</i> , 2010, 28, 516-520.	17.5	349
120	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , 2010, 42, 1027-1030.	21.4	439
121	BmSE, a SINE family with 3' ends of (ATTT) repeats in domesticated silkworm (<i>Bombyx mori</i>). <i>Journal of Genetics and Genomics</i> , 2010, 37, 125-135.	3.9	7
122	Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm (<i>Bombyx mori</i>). <i>PLoS ONE</i> , 2010, 5, 1-10.	12.6	342
123	BmHrp28 is a RNA-binding protein that binds to the female-specific exon 4 of <i>Bombyx mori dsx</i> pre-mRNA. <i>Insect Molecular Biology</i> , 2009, 18, 795-803.	2.0	3
124	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008, 456, 60-65.	27.8	834