Natalie A Twine

List of Publications by Year
in descending order

35	1,768	516710 16	454955 30
papers	citations	h-index	g-index

40	40	40	3820
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Data-driven platform for identifying variants of interest in COVID-19 virus. Computational and Structural Biotechnology Journal, 2022, 20, 2942-2950.	4.1	2
2	Evidence for polygenic and oligogenic basis of Australian sporadic amyotrophic lateral sclerosis. Journal of Medical Genetics, 2021, 58, 87-95.	3.2	48
3	Genetic analysis of GLT8D1 and ARPP21 in Australian familial and sporadic amyotrophic lateral sclerosis. Neurobiology of Aging, 2021, 101, 297.e9-297.e11.	3.1	6
4	Genetic Analysis of Tryptophan Metabolism Genes in Sporadic Amyotrophic Lateral Sclerosis. Frontiers in Immunology, 2021, 12, 701550.	4.8	8
5	Fast and accurate exhaustive higher-order epistasis search with BitEpi. Scientific Reports, 2021, 11, 15923.	3.3	11
6	VariantSpark: Cloud-based machine learning for association study of complex phenotype and large-scale genomic data. GigaScience, 2020, 9, .	6.4	10
7	Identity by descent analysis identifies founder events and links SOD1 familial and sporadic ALS cases. Npj Genomic Medicine, 2020, 5, 32.	3.8	20
8	Genetic and immunopathological analysis of CHCHD10 in Australian amyotrophic lateral sclerosis and frontotemporal dementia and transgenic TDP-43 mice. Journal of Neurology, Neurosurgery and Psychiatry, 2020, 91, 162-171.	1.9	8
9	Artificial Intelligence and Machine Learning in Bioinformatics. , 2019, , 272-286.		11
10	Monozygotic twins and triplets discordant for amyotrophic lateral sclerosis display differential methylation and gene expression. Scientific Reports, 2019, 9, 8254.	3.3	36
11	Molecular Phenotyping of Telomerized Human Bone Marrow Skeletal Stem Cells Reveals a Genetic Program of Enhanced Proliferation and Maintenance of Differentiation Responses. JBMR Plus, 2018, 2, 257-267.	2.7	21
12	Genome-wide Analyses Identify KIF5A as a Novel ALS Gene. Neuron, 2018, 97, 1268-1283.e6.	8.1	517
13	Transcription factor ZNF25 is associated with osteoblast differentiation of human skeletal stem cells. BMC Genomics, 2016, 17, 872.	2.8	10
14	Molecular characterisation of stromal populations derived from human embryonic stem cells: Similarities to immortalised bone marrow derived stromal stem cells. Bone Reports, 2015, 3, 32-39.	0.4	1
15	Proteomic Validation of Transcript Isoforms, Including Those Assembled from RNA-Seq Data. Journal of Proteome Research, 2015, 14, 3541-3554.	3.7	13
16	RNA-Seq analysis of the toxicant-induced transcriptome of the marine diatom, Ceratoneis closterium. Marine Genomics, 2014, 16, 45-53.	1.1	20
17	Tools to Covisualize and Coanalyze Proteomic Data with Genomes and Transcriptomes: Validation of Genes and Alternative mRNA Splicing. Journal of Proteome Research, 2014, 13, 84-98.	3.7	40
18	Next generation sequence analysis of the transcriptome of Sydney rock oysters (Saccostrea) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62 Tc	1.1	7

#	Article	IF	Citations
19	Identification of differentiation-stage specific markers that define the ex vivo osteoblastic phenotype. Bone, 2014, 67, 23-32.	2.9	62
20	454 pyrosequencing-based analysis of gene expression profiles in the amphipod Melita plumulosa: Transcriptome assembly and toxicant induced changes. Aquatic Toxicology, 2014, 153, 73-88.	4.0	38
21	Sequencing of hippocampal and cerebellar transcriptomes provides new insights into the complexity of gene regulation in the human brain. Neuroscience Letters, 2013, 541, 263-268.	2.1	8
22	Generation of Mice Deficient in both KLF3/BKLF and KLF8 Reveals a Genetic Interaction and a Role for These Factors in Embryonic Globin Gene Silencing. Molecular and Cellular Biology, 2013, 33, 2976-2987.	2.3	38
23	The CACCC-Binding Protein KLF3/BKLF Represses a Subset of KLF1/EKLF Target Genes and Is Required for Proper Erythroid Maturation In Vivo. Molecular and Cellular Biology, 2012, 32, 3281-3292.	2.3	37
24	Whole Transcriptome Sequencing Reveals Gene Expression and Splicing Differences in Brain Regions Affected by Alzheimer's Disease. PLoS ONE, 2011, 6, e16266.	2.5	266
25	Epigenetics of human T cells during the G₀â†'G₁ transition. Genome Research, 2009, 19, 1325-1337.	5.5	19
26	Inhibitors of poly ADP-ribose polymerase (PARP) induce apoptosis of myeloid leukemic cells: potential for therapy of myeloid leukemia and myelodysplastic syndromes. Haematologica, 2009, 94, 638-646.	3.5	78
27	High Resolution Molecular Analysis of 5q- Syndrome Patients at Diagnosis and Following Lenalidomide Therapy. Blood, 2008, 112, 225-225.	1.4	0
28	High Resolution Genomic Mapping of Breast Cancer Derived T-MDS/TAML. Blood, 2008, 112, 2692-2692.	1.4	0
29	MicroRNA Expression Profiling of High and Low Risk MDS. Blood, 2008, 112, 3645-3645.	1.4	1
30	Prevalence and prognostic significance of allelic imbalance by single-nucleotide polymorphism analysis in low-risk myelodysplastic syndromes. Blood, 2007, 110, 3365-3373.	1.4	190
31	The JAK2 V617F mutation identifies a subgroup of MDS patients with isolated deletion 5q and a proliferative bone marrow. Leukemia, 2006, 20, 1319-1321.	7.2	92
32	Kinesin Family Member 20A (KIF20A) Is Specifically down Regulated in 5q- CD34+ and CD61+ Cells and Uniparental Disomy Is Not a Feature of 5q- Syndrome.. Blood, 2006, 108, 2611-2611.	1.4	0
33	The JAK2 V617F Mutation Identifies Specific Subgroups of Myelodysplastic Syndrome (MDS).. Blood, 2006, 108, 2610-2610.	1.4	0
34	Tapasin gene polymorphism in systemic onset juvenile rheumatoid arthritis: a family-based case-control study. Arthritis Research, 2005, 7, R285.	2.0	13
35	The ?174G allele of the interleukin-6 gene confers susceptibility to systemic arthritis in children: A multicenter study using simplex and multiplex juvenile idiopathic arthritis families. Arthritis and Rheumatism, 2003, 48, 3202-3206.	6.7	123