

Andrew B Stergachis

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

5,335
citations

567281

15
h-index

677142

22
g-index

25
all docs

25
docs citations

25
times ranked

11462
citing authors

#	ARTICLE	IF	CITATIONS
1	Clinical utility of brain MRS imaging of patients with adult-onset non-cirrhotic hyperammonemia. <i>Molecular Genetics and Metabolism Reports</i> , 2021, 27, 100742.	1.1	1
2	Rewiring of human neurodevelopmental gene regulatory programs by human accelerated regions. <i>Neuron</i> , 2021, 109, 3239-3251.e7.	8.1	91
3	Single cell biologyâ€™a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2021, 1506, 74-97.	3.8	3
4	A retrospective study of adult patients with noncirrhotic hyperammonemia. <i>Journal of Inherited Metabolic Disease</i> , 2020, 43, 1165-1172.	3.6	12
5	Identification of an Identical de Novo SCAMP5 Missense Variant in Four Unrelated Patients With Seizures and Severe Neurodevelopmental Delay. <i>Frontiers in Pharmacology</i> , 2020, 11, 599191.	3.5	2
6	Biobanks could identify medically actionable findings relevant for COVID-19 clinical care. <i>Nature Medicine</i> , 2020, 26, 991-991.	30.7	9
7	Single-molecule regulatory architectures captured by chromatin fiber sequencing. <i>Science</i> , 2020, 368, 1449-1454.	12.6	106
8	Noncirrhotic hyperammonemia after deceased donor kidney transplantation: A case report. <i>American Journal of Transplantation</i> , 2019, 19, 3197-3201.	4.7	13
9	Recurrent SLC1A2 variants cause epilepsy via a dominant negative mechanism. <i>Annals of Neurology</i> , 2019, 85, 921-926.	5.3	23
10	Integrative Genomics Analysis Identifies ACVR1B as a Candidate Causal Gene of Emphysema Distribution. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019, 60, 388-398.	2.9	15
11	Using Data Independent Acquisition (DIA) to Model High-responding Peptides for Targeted Proteomics Experiments. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2331-2340.	3.8	47
12	Conservation of trans-acting circuitry during mammalian regulatory evolution. <i>Nature</i> , 2014, 515, 365-370.	27.8	211
13	Panorama: A Targeted Proteomics Knowledge Base. <i>Journal of Proteome Research</i> , 2014, 13, 4205-4210.	3.7	205
14	Developmental Fate and Cellular Maturity Encoded in Human Regulatory DNA Landscapes. <i>Cell</i> , 2013, 154, 888-903.	28.9	329
15	Exonic Transcription Factor Binding Directs Codon Choice and Affects Protein Evolution. <i>Science</i> , 2013, 342, 1367-1372.	12.6	267
16	DNase Iâ€™hypersensitive exons colocalize with promoters and distal regulatory elements. <i>Nature Genetics</i> , 2013, 45, 852-859.	21.4	112
17	Personal and population genomics of human regulatory variation. <i>Genome Research</i> , 2012, 22, 1689-1697.	5.5	98
18	An expansive human regulatory lexicon encoded in transcription factor footprints. <i>Nature</i> , 2012, 489, 83-90.	27.8	715

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19	Circuitry and Dynamics of Human Transcription Factor Regulatory Networks. <i>Cell</i> , 2012, 150, 1274-1286.	28.9	451
20	The accessible chromatin landscape of the human genome. <i>Nature</i> , 2012, 489, 75-82.	27.8	2,434
21	Rapid empirical discovery of optimal peptides for targeted proteomics. <i>Nature Methods</i> , 2011, 8, 1041-1043.	19.0	100
22	The SH2 Domain-Containing Proteins in 21 Species Establish the Provenance and Scope of Phosphotyrosine Signaling in Eukaryotes. <i>Science Signaling</i> , 2011, 4, ra83.	3.6	81
23	Long-Range Enhancement of β -Globin Gene Expression Is Dependent on Gt Motifs Residing in the HS3 Core Element of the Locus Control Region.. <i>Blood</i> , 2004, 104, 1222-1222.	1.4	0