Andrew B Stergachis

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3017458/publications.pdf

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23	5,335	567281	677142
papers	citations	15 h-index	22 g-index

25	25	25	11462
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The accessible chromatin landscape of the human genome. Nature, 2012, 489, 75-82.	27.8	2,434
2	An expansive human regulatory lexicon encoded in transcription factor footprints. Nature, 2012, 489, 83-90.	27.8	715
3	Circuitry and Dynamics of Human Transcription Factor Regulatory Networks. Cell, 2012, 150, 1274-1286.	28.9	451
4	Developmental Fate and Cellular Maturity Encoded in Human Regulatory DNA Landscapes. Cell, 2013, 154, 888-903.	28.9	329
5	Exonic Transcription Factor Binding Directs Codon Choice and Affects Protein Evolution. Science, 2013, 342, 1367-1372.	12.6	267
6	Conservation of trans-acting circuitry during mammalian regulatory evolution. Nature, 2014, 515, 365-370.	27.8	211
7	Panorama: A Targeted Proteomics Knowledge Base. Journal of Proteome Research, 2014, 13, 4205-4210.	3.7	205
8	DNase Iâ€“hypersensitive exons colocalize with promoters and distal regulatory elements. Nature Genetics, 2013, 45, 852-859.	21.4	112
9	Single-molecule regulatory architectures captured by chromatin fiber sequencing. Science, 2020, 368, 1449-1454.	12.6	106
10	Rapid empirical discovery of optimal peptides for targeted proteomics. Nature Methods, 2011, 8, 1041-1043.	19.0	100
11	Personal and population genomics of human regulatory variation. Genome Research, 2012, 22, 1689-1697.	5.5	98
12	Rewiring of human neurodevelopmental gene regulatory programs by human accelerated regions. Neuron, 2021, 109, 3239-3251.e7.	8.1	91
13	The SH2 Domainâ€“Containing Proteins in 21 Species Establish the Provenance and Scope of Phosphotyrosine Signaling in Eukaryotes. Science Signaling, 2011, 4, ra83.	3.6	81
14	Using Data Independent Acquisition (DIA) to Model High-responding Peptides for Targeted Proteomics Experiments. Molecular and Cellular Proteomics, 2015, 14, 2331-2340.	3.8	47
15	Recurrent SLC1A2 variants cause epilepsy via a dominant negative mechanism. Annals of Neurology, 2019, 85, 921-926.	5.3	23
16	Integrative Genomics Analysis Identifies ACVR1B as a Candidate Causal Gene of Emphysema Distribution. American Journal of Respiratory Cell and Molecular Biology, 2019, 60, 388-398.	2.9	15
17	Noncirrhotic hyperammonemia after deceased donor kidney transplantation: A case report. American Journal of Transplantation, 2019, 19, 3197-3201.	4.7	13
18	A retrospective study of adult patients with noncirrhotic hyperammonemia. Journal of Inherited Metabolic Disease, 2020, 43, 1165-1172.	3.6	12

#	Article	IF	Citations
19	Biobanks could identify medically actionable findings relevant for COVID-19 clinical care. Nature Medicine, 2020, 26, 991-991.	30.7	9
20	Single cell biologyâ€"a Keystone Symposia report. Annals of the New York Academy of Sciences, 2021, 1506, 74-97.	3.8	3
21	Identification of an Identical de Novo SCAMP5 Missense Variant in Four Unrelated Patients With Seizures and Severe Neurodevelopmental Delay. Frontiers in Pharmacology, 2020, 11, 599191.	3.5	2
22	Clinical utility of brain MRS imaging of patients with adult-onset non-cirrhotic hyperammonemia. Molecular Genetics and Metabolism Reports, 2021, 27, 100742.	1.1	1
23	Long-Range Enhancement of Î²-Globin Gene Expression Is Dependent on Gt Motifs Residing in the HS3 Core Element of the Locus Control Region.. Blood, 2004, 104, 1222-1222.	1.4	0