Gabriel Santpere BarÃ³

List of Publications by Year in descending order

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56 6,824 32 57
papers citations h-index g-index

66 66 12419
all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	Phylogenomic analyses of the genus <i>Drosophila</i> reveals genomic signals of climate adaptation. Molecular Ecology Resources, 2022, 22, 1559-1581.	4.8	15
2	Transcriptomic taxonomy and neurogenic trajectories of adult human, macaque, and pig hippocampal and entorhinal cells. Neuron, 2022, 110, 452-469.e14.	8.1	142
3	Human herpesvirus diversity is altered in HLA class I binding peptides. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2123248119.	7.1	3
4	Spatial and cell type transcriptional landscape of human cerebellar development. Nature Neuroscience, 2021, 24, 1163-1175.	14.8	98
5	Disruption of NEUROD2 causes a neurodevelopmental syndrome with autistic features via cell-autonomous defects in forebrain glutamatergic neurons. Molecular Psychiatry, 2021, 26, 6125-6148.	7.9	21
6	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. Nature Communications, 2021, 12, 3968.	12.8	48
7	Mechanisms of Binding Specificity among bHLH Transcription Factors. International Journal of Molecular Sciences, 2021, 22, 9150.	4.1	45
8	Molecular topography of an entire nervous system. Cell, 2021, 184, 4329-4347.e23.	28.9	328
9	Regulation of prefrontal patterning and connectivity by retinoic acid. Nature, 2021, 598, 483-488.	27.8	59
10	The Presence of Human Herpesvirus 6 in the Brain in Health and Disease. Biomolecules, 2020, 10, 1520.	4.0	24
	The Presence of Human Herpesvirus 6 in the Brain in Health and Disease. Biomolecules, 2020, 10, 1520. Transcriptional priming as a conserved mechanism of lineage diversification in the developing mouse and human neocortex. Science Advances, 2020, 6, .	4.0	24
10	Transcriptional priming as a conserved mechanism of lineage diversification in the developing mouse		
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10 11 12	Transcriptional priming as a conserved mechanism of lineage diversification in the developing mouse and human neocortex. Science Advances, 2020, 6, . Expanding the Geographic Characterisation of Epstein–Barr Virus Variation through Gene-Based Approaches. Microorganisms, 2020, 8, 1686. Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the	3.6	10
10 11 12 13	Transcriptional priming as a conserved mechanism of lineage diversification in the developing mouse and human neocortex. Science Advances, 2020, 6, . Expanding the Geographic Characterisation of Epstein–Barr Virus Variation through Gene-Based Approaches. Microorganisms, 2020, 8, 1686. Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. Cell Reports, 2020, 31, 107489. Whole-genome sequence analysis of a Pan African set of samples reveals archaic gene flow from an extinct basal population of modern humans into sub-Saharan populations. Genome Biology, 2019, 20,	10.3 3.6 6.4	43 10 91
10 11 12 13	Transcriptional priming as a conserved mechanism of lineage diversification in the developing mouse and human neocortex. Science Advances, 2020, 6, . Expanding the Geographic Characterisation of Epstein–Barr Virus Variation through Gene-Based Approaches. Microorganisms, 2020, 8, 1686. Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. Cell Reports, 2020, 31, 107489. Whole-genome sequence analysis of a Pan African set of samples reveals archaic gene flow from an extinct basal population of modern humans into sub-Saharan populations. Genome Biology, 2019, 20, 77.	10.3 3.6 6.4 8.8	43 10 91 50
10 11 12 13 14	Transcriptional priming as a conserved mechanism of lineage diversification in the developing mouse and human neocortex. Science Advances, 2020, 6, . Expanding the Geographic Characterisation of Epstein–Barr Virus Variation through Gene-Based Approaches. Microorganisms, 2020, 8, 1686. Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. Cell Reports, 2020, 31, 107489. Whole-genome sequence analysis of a Pan African set of samples reveals archaic gene flow from an extinct basal population of modern humans into sub-Saharan populations. Genome Biology, 2019, 20, 77. Modeling the Evolution of Human Brain Development Using Organoids. Cell, 2019, 179, 1250-1253. Whole genome diversity of inherited chromosomally integrated HHV-6 derived from healthy	10.3 3.6 6.4 8.8 28.9	43 10 91 50 23

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19	Transcriptome and epigenome landscape of human cortical development modeled in organoids. Science, 2018, 362, .	12.6	220
20	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	12.6	516
21	Spatiotemporal transcriptomic divergence across human and macaque brain development. Science, 2018, 362, .	12.6	279
22	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. Science, 2018, 362, .	12.6	805
23	Comprehensive functional genomic resource and integrative model for the human brain. Science, 2018, 362, .	12.6	618
24	Transcriptome evolution from breast epithelial cells to basal-like tumors. Oncotarget, 2018, 9, 453-463.	1.8	11
25	Gene Expression Profile in Frontal Cortex in Sporadic Frontotemporal Lobar Degeneration-TDP. Journal of Neuropathology and Experimental Neurology, 2018, 77, 608-627.	1.7	15
26	Interhemispheric gene expression differences in the cerebral cortex of humans and macaque monkeys. Brain Structure and Function, 2017, 222, 3241-3254.	2.3	16
27	Evolution of the Human Nervous System Function, Structure, and Development. Cell, 2017, 170, 226-247.	28.9	316
28	Similar genomic proportions of copy number variation within gray wolves and modern dog breeds inferred from whole genome sequencing. BMC Genomics, 2017, 18, 977.	2.8	24
29	Genetic factors affecting EBV copy number in lymphoblastoid cell lines derived from the 1000 Genome Project samples. PLoS ONE, 2017, 12, e0179446.	2.5	22
30	Differences in molecular evolutionary rates among microRNAs in the human and chimpanzee genomes. BMC Genomics, 2016, 17, 528.	2.8	13
31	Natural Selection in the Great Apes. Molecular Biology and Evolution, 2016, 33, 3268-3283.	8.9	70
32	Extreme selective sweeps independently targeted the X chromosomes of the great apes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6413-6418.	7.1	75
33	Genome data from a sixteenth century pig illuminate modern breed relationships. Heredity, 2015, 114, 175-184.	2.6	39
34	Analysis of Five Gene Sets in Chimpanzees Suggests Decoupling between the Action of Selection on Protein-Coding and on Noncoding Elements. Genome Biology and Evolution, 2015, 7, 1490-1505.	2.5	1
35	Genome-Wide Analysis of Wild-Type Epstein–Barr Virus Genomes Derived from Healthy Individuals of the 1000 Genomes Project. Genome Biology and Evolution, 2014, 6, 846-860.	2.5	74
36	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. Nature, 2014, 507, 225-228.	27.8	328

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37	Accelerated exon evolution within primate segmental duplications. Genome Biology, 2013, 14, R9.	9.6	19
38	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	27.8	768
39	Enhanced Botrytis cinerea Resistance of Arabidopsis Plants Grown in Compost May Be Explained by Increased Expression of Defense-Related Genes, as Revealed by Microarray Analysis. PLoS ONE, 2013, 8, e56075.	2.5	31
40	Evidence for Premature Lipid Raft Aging in APP/PS1 Double-Transgenic Mice, a Model of Familial Alzheimer Disease. Journal of Neuropathology and Experimental Neurology, 2012, 71, 868-881.	1.7	69
41	Breeding system and ecological traits of the critically endangered endemic plant Limonium barceloi (Gil and Llorens) (Plumbaginaceae). Plant Systematics and Evolution, 2012, 298, 1101-1110.	0.9	10
42	Severe Alterations in Lipid Composition of Frontal Cortex Lipid Rafts from Parkinson's Disease and Incidental Parkinson's Disease. Molecular Medicine, 2011, 17, 1107-1118.	4.4	308
43	Altered Distribution of RhoA in Alzheimer's Disease and A \hat{I}^2 PP Overexpressing Mice. Journal of Alzheimer's Disease, 2010, 19, 37-56.	2.6	67
44	Lipid Alterations in Lipid Rafts from Alzheimer's Disease Human Brain Cortex. Journal of Alzheimer's Disease, 2010, 19, 489-502.	2.6	235
45	LRRK2 and neurodegeneration. Acta Neuropathologica, 2009, 117, 227-246.	7.7	62
46	Morphological alterations to neurons of the amygdala and impaired fear conditioning in a transgenic mouse model of Alzheimer's disease. Journal of Pathology, 2009, 219, 41-51.	4.5	54
47	Delineation of Early Changes in Cases with Progressive Supranuclear Palsyâ€Like Pathology. Astrocytes in Striatum are Primary Targets of Tau Phosphorylation and GFAP Oxidation. Brain Pathology, 2009, 19, 177-187.	4.1	44
48	VDAC and $\mathrm{ER\hat{l}}\pm$ interaction in caveolae from human cortex is altered in Alzheimer's disease. Molecular and Cellular Neurosciences, 2009, 42, 172-183.	2.2	83
49	Argyrophilic grain disease. Brain, 2008, 131, 1416-1432.	7.6	183
50	Coenzyme Q Induces Tau Aggregation, Tau Filaments, and Hirano Bodies. Journal of Neuropathology and Experimental Neurology, 2008, 67, 428-434.	1.7	13
51	Brain Protein Preservation Largely Depends on the Postmortem Storage Temperature. Journal of Neuropathology and Experimental Neurology, 2007, 66, 35-46.	1.7	151
52	C-Terminal end and aminoacid Lys48 in HMG-CoA lyase are involved in substrate binding and enzyme activity. Molecular Genetics and Metabolism, 2007, 91, 120-127.	1.1	10
53	Abnormal Sp1 transcription factor expression in Alzheimer disease and tauopathies. Neuroscience Letters, 2006, 397, 30-34.	2.1	62
54	Low molecular weight species of tau in Alzheimer's disease are dependent on tau phosphorylation sites but not on delayed post-mortem delay in tissue processing. Neuroscience Letters, 2006, 399, 106-110.	2.1	18

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55	Expression of transcription factors c-Fos, c-Jun, CREB-1 and ATF-2, and caspase-3 in relation with abnormal tau deposits in Pick's disease. Acta Neuropathologica, 2006, 111, 341-350.	7.7	4
56	Immediate Early Genes, Inducible Transcription Factors and Stress Kinases in Alzheimer's Disease. , 2006, , 243-260.		1