## Emilia Huerta-SÃ;nchez

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3116746/publications.pdf

Version: 2024-02-01

32 papers 6,448 citations

279798 23 h-index 32 g-index

40 all docs

40 docs citations

times ranked

40

9979 citing authors

#	Article	IF	CITATIONS
1	Detection of Neanderthal Adaptively Introgressed Genetic Variants That Modulate Reporter Gene Expression in Human Immune Cells. Molecular Biology and Evolution, 2022, 39, .	8.9	24
2	Denisovans and Homo sapiens on the Tibetan Plateau: dispersals and adaptations. Trends in Ecology and Evolution, 2022, 37, 257-267.	8.7	17
3	Apportioning archaic variants among modern populations. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20200411.	4.0	11
4	ABO Genetic Variation in Neanderthals and Denisovans. Molecular Biology and Evolution, 2021, 38, 3373-3382.	8.9	7
5	The history and evolution of the Denisovan- <i>EPAS1</i> haplotype in Tibetans. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	48
6	The Impact of Recessive Deleterious Variation on Signals of Adaptive Introgression in Human Populations. Genetics, 2020, 215, 799-812.	2.9	30
7	Population genetics of wild <i>Macaca fascicularis</i> with lowâ€coverage shotgun sequencing of museum specimens. American Journal of Physical Anthropology, 2020, 173, 21-33.	2.1	11
8	Convergent evolution in human and domesticate adaptation to high-altitude environments. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180235.	4.0	90
9	Illuminating Women's Hidden Contribution to Historical Theoretical Population Genetics. Genetics, 2019, 211, 363-366.	2.9	32
10	Simultaneous Viral Exposure and Protection from Neanderthal Introgression. Cell, 2018, 175, 306-307.	28.9	1
10	Simultaneous Viral Exposure and Protection from Neanderthal Introgression. Cell, 2018, 175, 306-307.  Using Genomic Data to Infer Historic Population Dynamics of Nonmodel Organisms. Annual Review of Ecology, Evolution, and Systematics, 2018, 49, 433-456.	28.9	143
	Using Genomic Data to Infer Historic Population Dynamics of Nonmodel Organisms. Annual Review of		
11	Using Genomic Data to Infer Historic Population Dynamics of Nonmodel Organisms. Annual Review of Ecology, Evolution, and Systematics, 2018, 49, 433-456.  Archaic adaptive introgression in <i>TBX15/WARS2</i> i> Molecular Biology and Evolution, 2017, 34,	8.3	143
11 12	Using Genomic Data to Infer Historic Population Dynamics of Nonmodel Organisms. Annual Review of Ecology, Evolution, and Systematics, 2018, 49, 433-456.  Archaic adaptive introgression in <i>TBX15/WARS2</i> Molecular Biology and Evolution, 2017, 34, msw283.  Signatures of Archaic Adaptive Introgression in Present-Day Human Populations. Molecular Biology	8.3 8.9	143
11 12 13	Using Genomic Data to Infer Historic Population Dynamics of Nonmodel Organisms. Annual Review of Ecology, Evolution, and Systematics, 2018, 49, 433-456.  Archaic adaptive introgression in <i>TBX15/WARS2</i> Molecular Biology and Evolution, 2017, 34, msw283.  Signatures of Archaic Adaptive Introgression in Present-Day Human Populations. Molecular Biology and Evolution, 2017, 34, msw216. <i> Haplostrips</i> : revealing population structure through haplotype visualization. Methods in	8.3 8.9 8.9	143 101 146
11 12 13	Using Genomic Data to Infer Historic Population Dynamics of Nonmodel Organisms. Annual Review of Ecology, Evolution, and Systematics, 2018, 49, 433-456.  Archaic adaptive introgression in <i>TBX15/WARS2</i> Molecular Biology and Evolution, 2017, 34, msw283.  Signatures of Archaic Adaptive Introgression in Present-Day Human Populations. Molecular Biology and Evolution, 2017, 34, msw216. <i> Haplostrips  revealing population structure through haplotype visualization. Methods in Ecology and Evolution, 2017, 8, 1389-1392.  Leveraging Multiple Populations across Time Helps Define Accurate Models of Human Evolution: A</i>	8.3 8.9 8.9	143 101 146 49
11 12 13 14	Using Genomic Data to Infer Historic Population Dynamics of Nonmodel Organisms. Annual Review of Ecology, Evolution, and Systematics, 2018, 49, 433-456.  Archaic adaptive introgression in <i>TBX15/WARS2</i> . Molecular Biology and Evolution, 2017, 34, msw283.  Signatures of Archaic Adaptive Introgression in Present-Day Human Populations. Molecular Biology and Evolution, 2017, 34, msw216. <i> Haplostrips</i> .: revealing population structure through haplotype visualization. Methods in Ecology and Evolution, 2017, 8, 1389-1392.  Leveraging Multiple Populations across Time Helps Define Accurate Models of Human Evolution: A Reanalysis of the Lactase Persistence Adaptation. Human Biology, 2017, 89, 81.  A time transect of exomes from a Native American population before and after European contact.	8.3 8.9 8.9 5.2	143 101 146 49 8

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19	Greenlandic Inuit show genetic signatures of diet and climate adaptation. Science, 2015, 349, 1343-1347.	12.6	397
20	Selection on a Variant Associated with Improved Viral Clearance Drives Local, Adaptive Pseudogenization of Interferon Lambda 4 (IFNL4). PLoS Genetics, 2014, 10, e1004681.	3.5	87
21	Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. Nature, 2014, 512, 194-197.	27.8	904
22	Quantifying Population Genetic Differentiation from Next-Generation Sequencing Data. Genetics, 2013, 195, 979-992.	2.9	187
23	Robust Demographic Inference from Genomic and SNP Data. PLoS Genetics, 2013, 9, e1003905.	3.5	1,185
24	Genetic Signatures Reveal High-Altitude Adaptation in a Set of Ethiopian Populations. Molecular Biology and Evolution, 2013, 30, 1877-1888.	8.9	173
25	A Scan for Human-Specific Relaxation of Negative Selection Reveals Unexpected Polymorphism in Proteasome Genes. Molecular Biology and Evolution, 2013, 30, 1808-1815.	8.9	23
26	Distinguishing between Selective Sweeps from Standing Variation and from a De Novo Mutation. PLoS Genetics, 2012, 8, e1003011.	3.5	201
27	Natural Selection Affects Multiple Aspects of Genetic Variation at Putatively Neutral Sites across the Human Genome. PLoS Genetics, 2011, 7, e1002326.	3.5	146
28	Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude. Science, 2010, 329, 75-78.	12.6	1,339
29	Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. Nature Genetics, 2010, 42, 969-972.	21.4	297
30	Population Genetics of Polymorphism and Divergence Under Fluctuating Selection. Genetics, 2008, 178, 325-337.	2.9	59
31	Wagner's canalization model. Theoretical Population Biology, 2007, 71, 121-130.	1.1	28
32	Am I too fat? Bulimia as an epidemic. Journal of Mathematical Psychology, 2003, 47, 515-526.	1.8	56