

Hafid Laayouni

List of Publications by Year in descending order

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52
papers

2,563
citations

304743

22
h-index

214800

47
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docs citations

57
times ranked

5247
citing authors

#	ARTICLE	IF	CITATIONS
1	Signatures of genetic variation in human microRNAs point to processes of positive selection and population-specific disease risks. <i>Human Genetics</i> , 2022, 141, 1673-1693.	3.8	3
2	Positive Selection in Human Populations: Practical Aspects and Current Knowledge. <i>Evolutionary Studies</i> , 2021, , 29-65.	0.1	1
3	Enhancers with tissue-specific activity are enriched in intronic regions. <i>Genome Research</i> , 2021, 31, 1325-1336.	5.5	21
4	Chromosome X-wide Analysis of Positive Selection in Human Populations: Common and Private Signals of Selection and its Impact on Inactivated Genes and Enhancers. <i>Frontiers in Genetics</i> , 2021, 12, 714491.	2.3	2
5	A fully integrated machine learning scan of selection in the chimpanzee genome. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa061.	3.2	1
6	The shaping of immunological responses through natural selection after the Roma Diaspora. <i>Scientific Reports</i> , 2020, 10, 16134.	3.3	2
7	Positive selection in admixed populations from Ethiopia. <i>BMC Genetics</i> , 2020, 21, 108.	2.7	6
8	Gene connectivity and enzyme evolution in the human metabolic network. <i>Biology Direct</i> , 2019, 14, 17.	4.6	11
9	Large multiple sequence alignments with a root-to-leaf regressive method. <i>Nature Biotechnology</i> , 2019, 37, 1466-1470.	17.5	25
10	Selection in the Introgressed Regions of the Chimpanzee Genome. <i>Genome Biology and Evolution</i> , 2018, 10, 1132-1138.	2.5	13
11	Influence of pathway topology and functional class on the molecular evolution of human metabolic genes. <i>PLoS ONE</i> , 2018, 13, e0208782.	2.5	3
12	Evaluating the Genetics of Common Variable Immunodeficiency: Monogenetic Model and Beyond. <i>Frontiers in Immunology</i> , 2018, 9, 636.	4.8	142
13	PopHuman: the human population genomics browser. <i>Nucleic Acids Research</i> , 2018, 46, D1003-D1010.	14.5	27
14	Y-chromosomal sequences of diverse Indian populations and the ancestry of the Andamanese. <i>Human Genetics</i> , 2017, 136, 499-510.	3.8	18
15	A 3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pan_tro_3.0). <i>GigaScience</i> , 2017, 6, 1-6.	6.4	17
16	MicroRNA Genetic Variation: From Population Analysis to Functional Implications of Three Allele Variants Associated with Cancer. <i>Human Mutation</i> , 2016, 37, 1060-1073.	2.5	15
17	Genomic analysis of Andamanese provides insights into ancient human migration into Asia and adaptation. <i>Nature Genetics</i> , 2016, 48, 1066-1070.	21.4	126
18	Natural Selection in the Great Apes. <i>Molecular Biology and Evolution</i> , 2016, 33, 3268-3283.	8.9	70

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19	The genetics of East African populations: a Nilo-Saharan component in the African genetic landscape. <i>Scientific Reports</i> , 2015, 5, 9996.	3.3	25
20	Extreme selective sweeps independently targeted the X chromosomes of the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6413-6418.	7.1	75
21	Balancing immunity and tolerance: genetic footprint of natural selection in the transcriptional regulatory region of HLA-G. <i>Genes and Immunity</i> , 2015, 16, 57-70.	4.1	24
22	Recent Positive Selection Has Acted on Genes Encoding Proteins with More Interactions within the Whole Human Interactome. <i>Genome Biology and Evolution</i> , 2015, 7, 1141-1154.	2.5	59
23	Hierarchical boosting: a machine-learning framework to detect and classify hard selective sweeps in human populations. <i>Bioinformatics</i> , 2015, 31, 3946-3952.	4.1	85
24	VCF2Networks: applying genotype networks to single-nucleotide variants data. <i>Bioinformatics</i> , 2015, 31, 438-439.	4.1	5
25	1000 Genomes Selection Browser 1.0: a genome browser dedicated to signatures of natural selection in modern humans. <i>Nucleic Acids Research</i> , 2014, 42, D903-D909.	14.5	143
26	METABOLIC FLUX IS A DETERMINANT OF THE EVOLUTIONARY RATES OF ENZYME-ENCODING GENES. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 605-613.	2.3	16
27	Convergent evolution in European and Roma populations reveals pressure exerted by plague on Toll-like receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2668-2673.	7.1	88
28	Worldwide genetic variation at the 3' untranslated region of the HLA-G gene: balancing selection influencing genetic diversity. <i>Genes and Immunity</i> , 2014, 15, 95-106.	4.1	69
29	Population and genomic lessons from genetic analysis of two Indian populations. <i>Human Genetics</i> , 2014, 133, 1273-1287.	3.8	27
30	Human Genome Variation and the Concept of Genotype Networks. <i>PLoS ONE</i> , 2014, 9, e99424.	2.5	18
31	A system-level, molecular evolutionary analysis of mammalian phototransduction. <i>BMC Evolutionary Biology</i> , 2013, 13, 52.	3.2	21
32	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	27.8	768
33	Network-Level and Population Genetics Analysis of the Insulin/TOR Signal Transduction Pathway Across Human Populations. <i>Molecular Biology and Evolution</i> , 2012, 29, 1379-1392.	8.9	24
34	Distribution of events of positive selection and population differentiation in a metabolic pathway: the case of asparagine N-glycosylation. <i>BMC Evolutionary Biology</i> , 2012, 12, 98.	3.2	19
35	Molecular Evolution and Network-Level Analysis of the N-Glycosylation Metabolic Pathway Across Primates. <i>Molecular Biology and Evolution</i> , 2011, 28, 813-823.	8.9	30
36	Similarity in Recombination Rate Estimates Highly Correlates with Genetic Differentiation in Humans. <i>PLoS ONE</i> , 2011, 6, e17913.	2.5	18

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37	A genomic analysis identifies a novel component in the genetic structure of sub-Saharan African populations. <i>European Journal of Human Genetics</i> , 2011, 19, 84-88.	2.8	35
38	Genetic adaptation of the antibacterial human innate immunity network. <i>BMC Evolutionary Biology</i> , 2011, 11, 202.	3.2	23
39	The annotation of the asparagine N-linked glycosylation pathway in the Reactome database. <i>Glycobiology</i> , 2011, 21, 1395-1400.	2.5	7
40	Ten Simple Rules for Getting Help from Online Scientific Communities. <i>PLoS Computational Biology</i> , 2011, 7, e1002202.	3.2	12
41	A Targeted Association Study of Immunity Genes and Networks Suggests Novel Associations with Placental Malaria Infection. <i>PLoS ONE</i> , 2011, 6, e24996.	2.5	6
42	A genome-wide survey does not show the genetic distinctiveness of Basques. <i>Human Genetics</i> , 2010, 127, 455-458.	3.8	43
43	The annotation and the usage of scientific databases could be improved with public issue tracker software. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq035.	3.0	5
44	A variant in the gene FUT9 is associated with susceptibility to placental malaria infection. <i>Human Molecular Genetics</i> , 2009, 18, 3136-3144.	2.9	11
45	A Natural History of FUT2 Polymorphism in Humans. <i>Molecular Biology and Evolution</i> , 2009, 26, 1993-2003.	8.9	209
46	Decay of linkage disequilibrium within genes across HGDP-CEPH human samples: most population isolates do not show increased LD. <i>BMC Genomics</i> , 2009, 10, 338.	2.8	19
47	Isolated populations as treasure troves in genetic epidemiology: the case of the Basques. <i>European Journal of Human Genetics</i> , 2009, 17, 1490-1494.	2.8	17
48	From the detection of population structure to the reconstruction of population history: the historical reading of the human genome. <i>Heredity</i> , 2009, 103, 362-363.	2.6	2
49	Thermal evolution of gene expression profiles in <i>Drosophila subobscura</i> . <i>BMC Evolutionary Biology</i> , 2007, 7, 42.	3.2	58
50	Thermal evolution of pre-adult life history traits, geometric size and shape, and developmental stability in <i>Drosophila subobscura</i> . <i>Journal of Evolutionary Biology</i> , 2006, 19, 2006-2021.	1.7	35
51	The Evolutionary History of <i>Drosophila buzzatii</i> . XXXV. Inversion Polymorphism and Nucleotide Variability in Different Regions of the Second Chromosome. <i>Molecular Biology and Evolution</i> , 2003, 20, 931-944.	8.9	39
52	Toward a Physical Map of <i>Drosophila buzzatii</i> : Use of Randomly Amplified Polymorphic DNA Polymorphisms and Sequence-Tagged Site Landmarks. <i>Genetics</i> , 2000, 156, 1797-1816.	2.9	23