

Elena Bosch

List of Publications by Year in descending order

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71
papers

4,368
citations

117625

34
h-index

110387

64
g-index

74
all docs

74
docs citations

74
times ranked

4897
citing authors

#	ARTICLE	IF	CITATIONS
1	Y-Chromosomal Diversity in Europe Is Clinal and Influenced Primarily by Geography, Rather than by Language. <i>American Journal of Human Genetics</i> , 2000, 67, 1526-1543.	6.2	519
2	Trading Genes along the Silk Road: mtDNA Sequences and the Origin of Central Asian Populations. <i>American Journal of Human Genetics</i> , 1998, 63, 1824-1838.	6.2	295
3	High-Resolution Analysis of Human Y-Chromosome Variation Shows a Sharp Discontinuity and Limited Gene Flow between Northwestern Africa and the Iberian Peninsula. <i>American Journal of Human Genetics</i> , 2001, 68, 1019-1029.	6.2	234
4	Online reference database of European Y-chromosomal short tandem repeat (STR) haplotypes. <i>Forensic Science International</i> , 2001, 118, 106-113.	2.2	198
5	The Genetic Legacy of Religious Diversity and Intolerance: Paternal Lineages of Christians, Jews, and Muslims in the Iberian Peninsula. <i>American Journal of Human Genetics</i> , 2008, 83, 725-736.	6.2	174
6	Balancing Selection Is the Main Force Shaping the Evolution of Innate Immunity Genes. <i>Journal of Immunology</i> , 2008, 181, 1315-1322.	0.8	173
7	Evaluating the Genetics of Common Variable Immunodeficiency: Monogenetic Model and Beyond. <i>Frontiers in Immunology</i> , 2018, 9, 636.	4.8	142
8	Recent Male-Mediated Gene Flow over a Linguistic Barrier in Iberia, Suggested by Analysis of a Y-Chromosomal DNA Polymorphism. <i>American Journal of Human Genetics</i> , 1999, 65, 1437-1448.	6.2	132
9	Identifying Genetic Traces of Historical Expansions: Phoenician Footprints in the Mediterranean. <i>American Journal of Human Genetics</i> , 2008, 83, 633-642.	6.2	127
10	Sex-Specific Migration Patterns in Central Asian Populations, Revealed by Analysis of Y-Chromosome Short Tandem Repeats and mtDNA. <i>American Journal of Human Genetics</i> , 1999, 65, 208-219.	6.2	119
11	Genetic and Demographic Implications of the Bantu Expansion: Insights from Human Paternal Lineages. <i>Molecular Biology and Evolution</i> , 2009, 26, 1581-1589.	8.9	114
12	Variation in Short Tandem Repeats Is Deeply Structured by Genetic Background on the Human Y Chromosome. <i>American Journal of Human Genetics</i> , 1999, 65, 1623-1638.	6.2	105
13	Genetic structure of north-west Africa revealed by STR analysis. <i>European Journal of Human Genetics</i> , 2000, 8, 360-366.	2.8	104
14	Paternal and maternal lineages in the Balkans show a homogeneous landscape over linguistic barriers, except for the isolated Aromuns. <i>Annals of Human Genetics</i> , 2006, 70, 459-487.	0.8	97
15	High resolution Y chromosome typing: 19 STRs amplified in three multiplex reactions. <i>Forensic Science International</i> , 2002, 125, 42-51.	2.2	93
16	Homogeneity and distinctiveness of Polish paternal lineages revealed by Y chromosome microsatellite haplotype analysis. <i>Human Genetics</i> , 2002, 110, 592-600.	3.8	91
17	Y Chromosomal Evidence for the Origins of Oceanic-Speaking Peoples. <i>Genetics</i> , 2002, 160, 289-303.	2.9	89
18	Population Genetics of Y-Chromosome Short Tandem Repeats in Humans. <i>Journal of Molecular Evolution</i> , 1997, 45, 265-270.	1.8	82

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19	Antagonistic pleiotropy and mutation accumulation influence human senescence and disease. <i>Nature Ecology and Evolution</i> , 2017, 1, 55.	7.8	82
20	HLA class I and class II DNA typing and the origin of Basques. <i>Tissue Antigens</i> , 1998, 51, 30-40.	1.0	76
21	Human mitochondrial DNA sequence variation in the Moroccan population of the Souss area. <i>Annals of Human Biology</i> , 2001, 28, 295-307.	1.0	76
22	Duplications of the AZFa region of the human Y chromosome are mediated by homologous recombination between HERVs and are compatible with male fertility. <i>Human Molecular Genetics</i> , 2003, 12, 341-347.	2.9	74
23	Population history of north Africa: evidence from classical genetic markers. <i>Human Biology</i> , 1997, 69, 295-311.	0.2	71
24	Dynamics of a Human Interparalog Gene Conversion Hotspot. <i>Genome Research</i> , 2004, 14, 835-844.	5.5	70
25	High level of male-biased Scandinavian admixture in Greenlandic Inuit shown by Y-chromosomal analysis. <i>Human Genetics</i> , 2003, 112, 353-363.	3.8	66
26	Copy number variation analysis in the great apes reveals species-specific patterns of structural variation. <i>Genome Research</i> , 2011, 21, 1626-1639.	5.5	66
27	Mitochondrial DNA variation and the origin of the Europeans. <i>Human Genetics</i> , 1997, 99, 443-449.	3.8	61
28	SNP analysis to results (SNPator): a web-based environment oriented to statistical genomics analyses upon SNP data. <i>Bioinformatics</i> , 2008, 24, 1643-1644.	4.1	61
29	Allele Frequencies for 20 Microsatellites in a Worldwide Population Survey. <i>Human Heredity</i> , 1997, 47, 189-196.	0.8	47
30	Macrophage-specific MHCII expression is regulated by a remote <i>Ciita</i> enhancer controlled by NFAT5. <i>Journal of Experimental Medicine</i> , 2018, 215, 2901-2918.	8.5	47
31	Mendelian genes for Parkinson's disease contribute to the sporadic forms of the disease. <i>Human Molecular Genetics</i> , 2015, 24, 2023-2034.	2.9	45
32	Allele frequencies of 13 short tandem repeats in population samples from the Iberian Peninsula and Northern Africa. <i>International Journal of Legal Medicine</i> , 2000, 113, 208-214.	2.2	42
33	Low Exchangeability of Selenocysteine, the 21st Amino Acid, in Vertebrate Proteins. <i>Molecular Biology and Evolution</i> , 2009, 26, 2031-2040.	8.9	38
34	Properties of human disease genes and the role of genes linked to Mendelian disorders in complex disease aetiology. <i>Human Molecular Genetics</i> , 2017, 26, ddw405.	2.9	38
35	Native American Y Chromosomes in Polynesia: The Genetic Impact of the Polynesian Slave Trade. <i>American Journal of Human Genetics</i> , 2003, 72, 1282-1287.	6.2	36
36	The case of the unreliable SNP: Recurrent back-mutation of Y-chromosomal marker P25 through gene conversion. <i>Forensic Science International</i> , 2006, 159, 14-20.	2.2	36

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37	Extreme Population Differences in the Human Zinc Transporter ZIP4 (SLC39A4) Are Explained by Positive Selection in Sub-Saharan Africa. <i>PLoS Genetics</i> , 2014, 10, e1004128.	3.5	34
38	Y chromosome STR haplotypes in four populations from northwest Africa. <i>International Journal of Legal Medicine</i> , 2000, 114, 36-40.	2.2	33
39	Recent human evolution has shaped geographical differences in susceptibility to disease. <i>BMC Genomics</i> , 2011, 12, 55.	2.8	27
40	Signatures of Selection in the Human Olfactory Receptor OR511 Gene. <i>Molecular Biology and Evolution</i> , 2007, 25, 144-154.	8.9	26
41	Signatures of Evolutionary Adaptation in Quantitative Trait Loci Influencing Trace Element Homeostasis in Liver. <i>Molecular Biology and Evolution</i> , 2016, 33, 738-754.	8.9	26
42	Extreme individual marker FST values do not imply population-specific selection in humans: the NRG1 example. <i>Human Genetics</i> , 2007, 121, 759-762.	3.8	23
43	Interrogating 11 Fast-Evolving Genes for Signatures of Recent Positive Selection in Worldwide Human Populations. <i>Molecular Biology and Evolution</i> , 2009, 26, 2285-2297.	8.9	20
44	Evolutionary and Functional Evidence for Positive Selection at the Human CD5 Immune Receptor Gene. <i>Molecular Biology and Evolution</i> , 2012, 29, 811-823.	8.9	20
45	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
46	Detection of genomic rearrangements from targeted resequencing data in Parkinson's disease patients. <i>Movement Disorders</i> , 2017, 32, 165-169.	3.9	19
47	Similarity in Recombination Rate Estimates Highly Correlates with Genetic Differentiation in Humans. <i>PLoS ONE</i> , 2011, 6, e17913.	2.5	18
48	STR data for 21 loci in northwestern Africa. <i>Forensic Science International</i> , 2001, 116, 41-51.	2.2	16
49	The shared genetic architecture of schizophrenia, bipolar disorder and lifespan. <i>Human Genetics</i> , 2021, 140, 441-455.	3.8	16
50	Analysis of Ancestral and Functionally Relevant CD5 Variants in Systemic Lupus Erythematosus Patients. <i>PLoS ONE</i> , 2014, 9, e113090.	2.5	15
51	The Counteracting Effects of Demography on Functional Genomic Variation: The Roma Paradigm. <i>Molecular Biology and Evolution</i> , 2021, 38, 2804-2817.	8.9	14
52	Inadvertent diagnosis of male infertility through genealogical DNA testing. <i>Journal of Medical Genetics</i> , 2005, 42, 366-368.	3.2	13
53	Patterns of genetic structure and adaptive positive selection in the Lithuanian population from high-density SNP data. <i>Scientific Reports</i> , 2019, 9, 9163.	3.3	13
54	Admixture and sexual bias in the population settlement of La R�union Island (Indian Ocean). <i>American Journal of Physical Anthropology</i> , 2008, 136, 100-107.	2.1	11

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55	SNPlexing the human Y-chromosome: A single-assay system for major haplogroup screening. <i>Electrophoresis</i> , 2007, 28, 3201-3206.	2.4	10
56	Y-chromosomal STR haplotypes in Inuit and Danish population samples. <i>Forensic Science International</i> , 2003, 132, 228-232.	2.2	9
57	Impact of the functional CD5 polymorphism A471V on the response of chronic lymphocytic leukaemia to conventional chemotherapy regimens. <i>British Journal of Haematology</i> , 2017, 177, 147-150.	2.5	8
58	African signatures of recent positive selection in human FOXP1. <i>BMC Evolutionary Biology</i> , 2010, 10, 267.	3.2	6
59	Contribution of Evolutionary Selected Immune Gene Polymorphism to Immune-Related Disorders: The Case of Lymphocyte Scavenger Receptors CD5 and CD6. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5315.	4.1	6
60	Y-chromosome diversity in Bantu and Pygmy populations from Central Africa. <i>International Congress Series</i> , 2006, 1288, 234-236.	0.2	5
61	Draft Genome Sequence of <i>Aeromonas molluscorum</i> Strain 848T ^T , Isolated from Bivalve Molluscs. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
62	Sequence diversity of the Rh blood group system in Basques. <i>European Journal of Human Genetics</i> , 2018, 26, 1859-1866.	2.8	5
63	A New Risk Variant for Multiple Sclerosis at 11q23.3 Locus Is Associated with Expansion of CXCR5+ Circulating Regulatory T Cells. <i>Journal of Clinical Medicine</i> , 2020, 9, 625.	2.4	5
64	Draft Genome Sequence of the <i>Aeromonas diversa</i> Type Strain. <i>Genome Announcements</i> , 2013, 1, .	0.8	4
65	Reply to: Retesting the influences of mutation accumulation and antagonistic pleiotropy on human senescence and disease. <i>Nature Ecology and Evolution</i> , 2019, 3, 994-995.	7.8	4
66	<i>DDR1</i> methylation is associated with bipolar disorder and the isoform expression and methylation of myelin genes. <i>Epigenomics</i> , 2021, 13, 845-858.	2.1	4
67	The shaping of immunological responses through natural selection after the Roma Diaspora. <i>Scientific Reports</i> , 2020, 10, 16134.	3.3	2
68	Adaptive selection drives TRPP3 loss-of-function in an Ethiopian population. <i>Scientific Reports</i> , 2020, 10, 20999.	3.3	2
69	Paternal and maternal lineages in the Balkans show a homogeneous landscape over linguistic barriers, except for the isolated Aromuns. <i>Annals of Human Genetics</i> , 2006, .	0.8	2
70	Understanding signatures of positive natural selection in human zinc transporter genes. <i>Scientific Reports</i> , 2022, 12, 4320.	3.3	2
71	Analysis of Five Gene Sets in Chimpanzees Suggests Decoupling between the Action of Selection on Protein-Coding and on Noncoding Elements. <i>Genome Biology and Evolution</i> , 2015, 7, 1490-1505.	2.5	1