Elena Bosch

List of Publications by Year
in descending order

71 papers	4,368 citations	117571 34 h-index	110317 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. American Journal of Human Genetics, 2000, 67, 1526-1543.	2.6	519
2	Trading Genes along the Silk Road: mtDNA Sequences and the Origin of Central Asian Populations. American Journal of Human Genetics, 1998, 63, 1824-1838.	2.6	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. American Journal of Human Genetics, 2001, 68, 1019-1029.	2.6	234
4	Online reference database of European Y-chromosomal short tandem repeat (STR) haplotypes. Forensic Science International, 2001, 118, 106-113.	1.3	198
5	The Genetic Legacy of Religious Diversity and Intolerance: Paternal Lineages of Christians, Jews, and Muslims in the Iberian Peninsula. American Journal of Human Genetics, 2008, 83, 725-736.	2.6	174
6	Balancing Selection Is the Main Force Shaping the Evolution of Innate Immunity Genes. Journal of Immunology, 2008, 181, 1315-1322.	0.4	173
7	Evaluating the Genetics of Common Variable Immunodeficiency: Monogenetic Model and Beyond. Frontiers in Immunology, 2018, 9, 636.	2.2	142
8	Recent Male-Mediated Gene Flow over a Linguistic Barrier in Iberia, Suggested by Analysis of a Y-Chromosomal DNA Polymorphism. American Journal of Human Genetics, 1999, 65, 1437-1448.	2.6	132
9	Identifying Genetic Traces of Historical Expansions: Phoenician Footprints in the Mediterranean. American Journal of Human Genetics, 2008, 83, 633-642.	2.6	127
10	Sex-Specific Migration Patterns in Central Asian Populations, Revealed by Analysis of Y-Chromosome Short Tandem Repeats and mtDNA. American Journal of Human Genetics, 1999, 65, 208-219.	2.6	119
11	Genetic and Demographic Implications of the Bantu Expansion: Insights from Human Paternal Lineages. Molecular Biology and Evolution, 2009, 26, 1581-1589.	3.5	114
12	Variation in Short Tandem Repeats Is Deeply Structured by Genetic Background on the Human Y Chromosome. American Journal of Human Genetics, 1999, 65, 1623-1638.	2.6	105
13	Genetic structure of north-west Africa revealed by STR analysis. European Journal of Human Genetics, 2000, 8, 360-366.	1.4	104
14	Paternal and maternal lineages in the Balkans show a homogeneous landscape over linguistic barriers, except for the isolated Aromuns. Annals of Human Genetics, 2006, 70, 459-487.	0.3	97
15	High resolution Y chromosome typing: 19 STRs amplified in three multiplex reactions. Forensic Science International, 2002, 125, 42-51.	1.3	93
16	Homogeneity and distinctiveness of Polish paternal lineages revealed by Y chromosome microsatellite haplotype analysis. Human Genetics, 2002, 110, 592-600.	1.8	91
17	Y Chromosomal Evidence for the Origins of Oceanic-Speaking Peoples. Genetics, 2002, 160, 289-303.	1.2	89
18	Population Genetics of Y-Chromosome Short Tandem Repeats in Humans. Journal of Molecular Evolution, 1997, 45, 265-270.	0.8	82

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19	Antagonistic pleiotropy and mutation accumulation influence human senescence and disease. Nature Ecology and Evolution, 2017, 1, 55.	3.4	82
20	HLA class I and class II DNA typing and the origin of Basques. Tissue Antigens, 1998, 51, 30-40.	1.0	76
21	Human mitochondrial DNA sequence variation in the Moroccan population of the Souss area. Annals of Human Biology, 2001, 28, 295-307.	0.4	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. Human Molecular Genetics, 2003, 12, 341-347.	1.4	74
23	Population history of north Africa: evidence from classical genetic markers. Human Biology, 1997, 69, 295-311.	0.4	71
24	Dynamics of a Human Interparalog Gene Conversion Hotspot. Genome Research, 2004, 14, 835-844.	2.4	70
25	High level of male-biased Scandinavian admixture in Greenlandic Inuit shown by Y-chromosomal analysis. Human Genetics, 2003, 112, 353-363.	1.8	66
26	Copy number variation analysis in the great apes reveals species-specific patterns of structural variation. Genome Research, 2011, 21, 1626-1639.	2.4	66
27	Mitochondrial DNA variation and the origin of the Europeans. Human Genetics, 1997, 99, 443-449.	1.8	61
28	SNP analysis to results (SNPator): a web-based environment oriented to statistical genomics analyses upon SNP data. Bioinformatics, 2008, 24, 1643-1644.	1.8	61
29	Allele Frequencies for 20 Microsatellites in a Worldwide Population Survey. Human Heredity, 1997, 47, 189-196.	0.4	47
30	Macrophage-specific MHCII expression is regulated by a remote Ciita enhancer controlled by NFAT5. Journal of Experimental Medicine, 2018, 215, 2901-2918.	4.2	47
31	Mendelian genes for Parkinson's disease contribute to the sporadic forms of the diseaseâ€. Human Molecular Genetics, 2015, 24, 2023-2034.	1.4	45
32	Allele frequencies of 13 short tandem repeats in population samples from the Iberian Peninsula and Northern Africa. International Journal of Legal Medicine, 2000, 113, 208-214.	1.2	42
33	Low Exchangeability of Selenocysteine, the 21st Amino Acid, in Vertebrate Proteins. Molecular Biology and Evolution, 2009, 26, 2031-2040.	3.5	38
34	Properties of human disease genes and the role of genes linked to Mendelian disorders in complex disease aetiology. Human Molecular Genetics, 2017, 26, ddw405.	1.4	38
35	Native American Y Chromosomes in Polynesia: The Genetic Impact of the Polynesian Slave Trade. American Journal of Human Genetics, 2003, 72, 1282-1287.	2.6	36
36	The case of the unreliable SNP: Recurrent back-mutation of Y-chromosomal marker P25 through gene conversion. Forensic Science International, 2006, 159, 14-20.	1.3	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. PLoS Genetics, 2014, 10, e1004128.	1.5	34
38	Y chromosome STR haplotypes in four populations from northwest Africa. International Journal of Legal Medicine, 2000, 114, 36-40.	1.2	33
39	Recent human evolution has shaped geographical differences in susceptibility to disease. BMC Genomics, 2011, 12, 55.	1.2	27
40	Signatures of Selection in the Human Olfactory Receptor OR5I1 Gene. Molecular Biology and Evolution, 2007, 25, 144-154.	3.5	26
41	Signatures of Evolutionary Adaptation in Quantitative Trait Loci Influencing Trace Element Homeostasis in Liver. Molecular Biology and Evolution, 2016, 33, 738-754.	3.5	26
42	Extreme individual marker FST values do not imply population-specific selection in humans: the NRG1 example. Human Genetics, 2007, 121, 759-762.	1.8	23
43	Interrogating 11 Fast-Evolving Genes for Signatures of Recent Positive Selection in Worldwide Human Populations. Molecular Biology and Evolution, 2009, 26, 2285-2297.	3.5	20
44	Evolutionary and Functional Evidence for Positive Selection at the Human CD5 Immune Receptor Gene. Molecular Biology and Evolution, 2012, 29, 811-823.	3.5	20
45	Decay of linkage disequilibrium within genes across HGDP-CEPH human samples: most population isolates do not show increased LD. BMC Genomics, 2009, 10, 338.	1.2	19
46	Detection of genomic rearrangements from targeted resequencing data in Parkinson's disease patients. Movement Disorders, 2017, 32, 165-169.	2.2	19
47	Similarity in Recombination Rate Estimates Highly Correlates with Genetic Differentiation in Humans. PLoS ONE, 2011, 6, e17913.	1.1	18
48	STR data for 21 loci in northwestern Africa. Forensic Science International, 2001, 116, 41-51.	1.3	16
49	The shared genetic architecture of schizophrenia, bipolar disorder and lifespan. Human Genetics, 2021, 140, 441-455.	1.8	16
50	Analysis of Ancestral and Functionally Relevant CD5 Variants in Systemic Lupus Erythematosus Patients. PLoS ONE, 2014, 9, e113090.	1.1	15
51	The Counteracting Effects of Demography on Functional Genomic Variation: The Roma Paradigm. Molecular Biology and Evolution, 2021, 38, 2804-2817.	3.5	14
52	Inadvertent diagnosis of male infertility through genealogical DNA testing. Journal of Medical Genetics, 2005, 42, 366-368.	1.5	13
53	Patterns of genetic structure and adaptive positive selection in the Lithuanian population from high-density SNP data. Scientific Reports, 2019, 9, 9163.	1.6	13
54	Admixture and sexual bias in the population settlement of La RÃ©union Island (Indian Ocean). American Journal of Physical Anthropology, 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. Electrophoresis, 2007, 28, 3201-3206.	1.3	10
56	Y-chromosomal STR haplotypes in Inuit and Danish population samples. Forensic Science International, 2003, 132, 228-232.	1.3	9
57	Impact of the functional CD5 polymorphism A471V on the response of chronic lymphocytic leukaemia to conventional chemotherapy regimens. British Journal of Haematology, 2017, 177, 147-150.	1.2	8
58	African signatures of recent positive selection in human FOXI1. BMC Evolutionary Biology, 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. International Journal of Molecular Sciences, 2021, 22, 5315.	1.8	6
60	Y-chromosome diversity in Bantu and Pygmy populations from Central Africa. International Congress Series, 2006, 1288, 234-236.	0.2	5
61	Draft Genome Sequence of Aeromonas molluscorum Strain 848T ^T , Isolated from Bivalve Molluscs. Genome Announcements, 2013, 1, .	0.8	5
62	Sequence diversity of the Rh blood group system in Basques. European Journal of Human Genetics, 2018, 26, 1859-1866.	1.4	5
63	A New Risk Variant for Multiple Sclerosis at 11q23.3 Locus Is Associated with Expansion of CXCR5+ Circulating Regulatory T Cells. Journal of Clinical Medicine, 2020, 9, 625.	1.0	5
64	Draft Genome Sequence of the Aeromonas diversa Type Strain. Genome Announcements, 2013, 1, .	0.8	4
65	Reply to: Retesting the influences of mutation accumulation and antagonistic pleiotropy on human senescence and disease. Nature Ecology and Evolution, 2019, 3, 994-995.	3.4	4
66	DDR1methylation is associated with bipolar disorder and the isoform expression and methylation of myelin genes. Epigenomics, 2021, 13, 845-858.	1.0	4
67	The shaping of immunological responses through natural selection after the Roma Diaspora. Scientific Reports, 2020, 10, 16134.	1.6	2
68	Adaptive selection drives TRPP3 loss-of-function in an Ethiopian population. Scientific Reports, 2020, 10, 20999.	1.6	2
69	Paternal and maternal lineages in the Balkans show a homogeneous landscape over linguistic barriers, except for the isolated Aromuns. Annals of Human Genetics, 2006, .	0.3	2
70	Understanding signatures of positive natural selection in human zinc transporter genes. Scientific Reports, 2022, 12, 4320.	1.6	2
71	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.	1.1	1