Ferran Casals

List of Publications by Year in Descending Order

71 papers	9,531 citations	25 h-index	78 g-index
78 ext. papers	11,020 ext. citations	8.8 avg, IF	5.41 L-index

#	Paper	IF	Citations
71	A forensic population database in El Salvador: 58 STRs and 94 SNPs. *Forensic Science International: Genetics*, **2021**, 57, 102646	4.3	0
70	Assessment of the gene mosaicism burden in blood and its implications for immune disorders. *Scientific Reports*, **2021**, 11, 12940	4.9	0
69	Genome-wide postnatal changes in immunity following fetal inflammatory response. *FEBS Journal*, **2021**, 288, 2311-2331	5.7	
68	Second GHEP-ISFG exercise for DVI: "DNA-led" victimsUdentification in a simulated air crash. *Forensic Science International: Genetics*, **2021**, 53, 102527	4.3	1
67	Historical human remains identification through maternal and paternal genetic signatures in a founder population with extensive genealogical record. *American Journal of Physical Anthropology*, **2020**, 171, 645-658	2.5	2
66	FHLdb: A Comprehensive Database on the Molecular Basis of Familial Hemophagocytic Lymphohistiocytosis. *Frontiers in Immunology*, **2020**, 11, 107	8.4	3
65	The first GHEP-ISFG collaborative exercise on forensic applications of massively parallel sequencing. *Forensic Science International: Genetics*, **2020**, 49, 102391	4.3	2
64	Severe Autoinflammatory Manifestations and Antibody Deficiency Due to Novel Hypermorphic PLCG2 Mutations. *Journal of Clinical Immunology*, **2020**, 40, 987-1000	5.7	12
63	Genetic diagnosis of autoinflammatory disease patients using clinical exome sequencing. *European Journal of Medical Genetics*, **2020**, 63, 103920	2.6	9
62	Flow Sorting Enrichment and Nanopore Sequencing of Chromosome 1 From a Chinese Individual. *Frontiers in Genetics*, **2019**, 10, 1315	4.5	1
61	Genetic identification of Spanish civil war victims. The state of the art in Catalonia (Northeastern Spain). *Forensic Science International: Genetics Supplement Series*, **2019**, 7, 419-421	0.5	3
60	The BIOMEPOC Project: Personalized Biomarkers and Clinical Profiles in Chronic Obstructive Pulmonary Disease. *Archivos De Bronconeumologia*, **2019**, 55, 93-99	0.7	11
59	Unexpected relevant role of gene mosaicism in patients with primary immunodeficiency diseases. *Journal of Allergy and Clinical Immunology*, **2019**, 143, 359-368	11.5	29
58	The impact of endogenous content, replicates and pooling on genome capture from faecal samples. *Molecular Ecology Resources*, **2018**, 18, 319-333	8.4	24
57	Evaluating the Genetics of Common Variable Immunodeficiency: Monogenetic Model and Beyond. *Frontiers in Immunology*, **2018**, 9, 636	8.4	81
56	Genomes reveal marked differences in the adaptive evolution between orangutan species. *Genome Biology*, **2018**, 19, 193	18.3	5
55	Reply to UNo evidence for unknown archaic ancestry in South AsiaU *Nature Genetics*, **2018**, 50, 1637-1639	36.3	2

54	Phenotype, penetrance, and treatment of 133 cytotoxic T-lymphocyte antigen 4-insufficient subjects. *Journal of Allergy and Clinical Immunology*, **2018**, 142, 1932-1946	11.5	204
53	Y-chromosomal sequences of diverse Indian populations and the ancestry of the Andamanese. *Human Genetics*, **2017**, 136, 499-510	6.3	11
52	Length and repeat-sequence variation in 58 STRs and 94 SNPs in two Spanish populations. *Forensic Science International: Genetics*, **2017**, 30, 66-70	4.3	17
51	Morphometric, Behavioral, and Genomic Evidence for a New Orangutan Species. *Current Biology*, **2017**, 27, 3487-3498.e10	6.3	116
50	Detection of genomic rearrangements from targeted resequencing data in Parkinson's disease patients. *Movement Disorders*, **2017**, 32, 165-169	7	10
49	Genomic analysis of Andamanese provides insights into ancient human migration into Asia and adaptation. *Nature Genetics*, **2016**, 48, 1066-70	36.3	88
48	Chimpanzee genomic diversity reveals ancient admixture with bonobos. *Science*, **2016**, 354, 477-481	33.3	139
47	Natural Selection in the Great Apes. *Molecular Biology and Evolution*, **2016**, 33, 3268-3283	8.3	44
46	Genetic Load of Loss-of-Function Polymorphic Variants in Great Apes. *Genome Biology and Evolution*, **2016**, 8, 871-7	3.9	15
45	An assessment of a massively parallel sequencing approach for the identification of individuals from mass graves of the Spanish Civil War (1936-1939). *Electrophoresis*, **2016**, 37, 2841-2847	3.6	16
44	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, 6413-8	11.5	52
43	Mendelian genes for Parkinson's disease contribute to the sporadic forms of the disease. *Human Molecular Genetics*, **2015**, 24, 2023-34	5.6	20
42	Population and genomic lessons from genetic analysis of two Indian populations. *Human Genetics*, **2014**, 133, 1273-87	6.3	23
41	Selective constraint, background selection, and mutation accumulation variability within and between human populations. *BMC Genomics*, **2013**, 14, 495	4.5	13
40	Great ape genetic diversity and population history. *Nature*, **2013**, 499, 471-5	50.4	574
39	Exome sequencing identifies mutations in the gene TTC7A in French-Canadian cases with hereditary multiple intestinal atresia. *Journal of Medical Genetics*, **2013**, 50, 324-9	5.8	93
38	Rare allelic forms of PRDM9 associated with childhood leukemogenesis. *Genome Research*, **2013**, 23, 419-30	9.7	37
37	Whole-exome sequencing reveals a rapid change in the frequency of rare functional variants in a founding population of humans. *PLoS Genetics*, **2013**, 9, e1003815	6	52

36	Long-standing balancing selection in the THBS4 gene: influence on sex-specific brain expression and gray matter volumes in Alzheimer disease. *Human Mutation*, **2013**, 34, 743-53	4.7	6
35	Next-generation sequencing approaches for genetic mapping of complex diseases. *Journal of Neuroimmunology*, **2012**, 248, 10-22	3.5	15
34	Genetics. Human genetic variation, shared and private. *Science*, **2012**, 337, 39-40	33.3	27
33	Similarity in recombination rate estimates highly correlates with genetic differentiation in humans. *PLoS ONE*, **2011**, 6, e17913	3.7	13
32	Variation in genome-wide mutation rates within and between human families. *Nature Genetics*, **2011**, 43, 712-4	36.3	404
31	Genetic adaptation of the antibacterial human innate immunity network. *BMC Evolutionary Biology*, **2011**, 11, 202	3	20
30	Recent human evolution has shaped geographical differences in susceptibility to disease. *BMC Genomics*, **2011**, 12, 55	4.5	22
29	A population genetic approach to mapping neurological disorder genes using deep resequencing. *PLoS Genetics*, **2011**, 7, e1001318	6	72
28	A targeted association study of immunity genes and networks suggests novel associations with placental malaria infection. *PLoS ONE*, **2011**, 6, e24996	3.7	6
27	A map of human genome variation from population-scale sequencing. *Nature*, **2010**, 467, 1061-73	50.4	6142
26	Serotype-specific pneumococcal disease may be influenced by mannose-binding lectin deficiency. *European Respiratory Journal*, **2010**, 36, 856-63	13.6	11
25	Direct measure of the de novo mutation rate in autism and schizophrenia cohorts. *American Journal of Human Genetics*, **2010**, 87, 316-24	11	181
24	Human pseudogenes of the ABO family show a complex evolutionary dynamics and loss of function. *Glycobiology*, **2009**, 19, 583-91	5.8	12
23	Interrogating 11 fast-evolving genes for signatures of recent positive selection in worldwide human populations. *Molecular Biology and Evolution*, **2009**, 26, 2285-97	8.3	20
22	A variant in the gene FUT9 is associated with susceptibility to placental malaria infection. *Human Molecular Genetics*, **2009**, 18, 3136-44	5.6	9
21	A natural history of FUT2 polymorphism in humans. *Molecular Biology and Evolution*, **2009**, 26, 1993-2003	8.3	169
20	Decay of linkage disequilibrium within genes across HGDP-CEPH human samples: most population isolates do not show increased LD. *BMC Genomics*, **2009**, 10, 338	4.5	16
19	Genetic and structural analysis of MBL2 and MASP2 polymorphisms in south-eastern African children. *Tissue Antigens*, **2009**, 74, 298-307		14

18	Balancing selection is the main force shaping the evolution of innate immunity genes. *Journal of Immunology*, **2008**, 181, 1315-22	5.3	150
17	SNP analysis to results (SNPator): a web-based environment oriented to statistical genomics analyses upon SNP data. *Bioinformatics*, **2008**, 24, 1643-4	7.2	57
16	Is there selection for the pace of successive inactivation of the arpAT gene in primates?. *Journal of Molecular Evolution*, **2008**, 67, 23-8	3.1	2
15	Evolutionary analysis of genes of two pathways involved in placental malaria infection. *Human Genetics*, **2008**, 123, 343-57	6.3	6
14	Signatures of selection in the human olfactory receptor OR5I1 gene. *Molecular Biology and Evolution*, **2008**, 25, 144-54	8.3	24
13	Extreme individual marker F(ST)values do not imply population-specific selection in humans: the NRG1 example. *Human Genetics*, **2007**, 121, 759-62	6.3	20
12	Testing chromosomal phylogenies and inversion breakpoint reuse in Drosophila. *Genetics*, **2007**, 175, 167-77	4	22
11	Abundance and chromosomal distribution of six Drosophila buzzatii transposons: BuT1, BuT2, BuT3, BuT4, BuT5, and BuT6. *Chromosoma*, **2006**, 115, 403-12	2.8	15
10	A BAC-based physical map of the Drosophila buzzatii genome. *Genome Research*, **2005**, 15, 885-92	9.7	20
9	Molecular characterization and chromosomal distribution of Galileo, Kepler and Newton, three foldback transposable elements of the Drosophila buzzatii species complex. *Genetics*, **2005**, 169, 2047-59	4	23
8	Duplicative and conservative transpositions of larval serum protein 1 genes in the genus Drosophila. *Genetics*, **2004**, 168, 253-64	4	12
7	The foldback-like transposon Galileo is involved in the generation of two different natural chromosomal inversions of Drosophila buzzatii. *Molecular Biology and Evolution*, **2003**, 20, 674-85	8.3	64
6	A new split of the Hox gene complex in Drosophila: relocation and evolution of the gene labial. *Molecular Biology and Evolution*, **2003**, 20, 2042-54	8.3	36
5	Low occurrence of gene transposition events during the evolution of the genus Drosophila. *Evolution; International Journal of Organic Evolution*, **2003**, 57, 1325-35	3.8	39
4	LOW OCCURRENCE OF GENE TRANSPOSITION EVENTS DURING THE EVOLUTION OF THE GENUS DROSOPHILA. *Evolution; International Journal of Organic Evolution*, **2003**, 57, 1325	3.8	10
3	How malleable is the eukaryotic genome? Extreme rate of chromosomal rearrangement in the genus Drosophila. *Genome Research*, **2001**, 11, 230-9	9.7	129
2	Further confirmation for unknown archaic ancestry in Andaman and South Asia		2
1	Next-generation sequencing for rare diseases231-242		