

# Ferran Casals

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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 map of human genome variation from population-scale sequencing. <i>Nature</i> , <b>2010</b> , 467, 1061-73	50.4	6142
70	Great ape genetic diversity and population history. <i>Nature</i> , <b>2013</b> , 499, 471-5	50.4	574
69	Variation in genome-wide mutation rates within and between human families. <i>Nature Genetics</i> , <b>2011</b> , 43, 712-4	36.3	404
68	Phenotype, penetrance, and treatment of 133 cytotoxic T-lymphocyte antigen 4-insufficient subjects. <i>Journal of Allergy and Clinical Immunology</i> , <b>2018</b> , 142, 1932-1946	11.5	204
67	Direct measure of the de novo mutation rate in autism and schizophrenia cohorts. <i>American Journal of Human Genetics</i> , <b>2010</b> , 87, 316-24	11	181
66	A natural history of FUT2 polymorphism in humans. <i>Molecular Biology and Evolution</i> , <b>2009</b> , 26, 1993-2003	3.3	169
65	Balancing selection is the main force shaping the evolution of innate immunity genes. <i>Journal of Immunology</i> , <b>2008</b> , 181, 1315-22	5.3	150
64	Chimpanzee genomic diversity reveals ancient admixture with bonobos. <i>Science</i> , <b>2016</b> , 354, 477-481	33.3	139
63	How malleable is the eukaryotic genome? Extreme rate of chromosomal rearrangement in the genus <i>Drosophila</i> . <i>Genome Research</i> , <b>2001</b> , 11, 230-9	9.7	129
62	Morphometric, Behavioral, and Genomic Evidence for a New Orangutan Species. <i>Current Biology</i> , <b>2017</b> , 27, 3487-3498.e10	6.3	116
61	Exome sequencing identifies mutations in the gene <i>TTC7A</i> in French-Canadian cases with hereditary multiple intestinal atresia. <i>Journal of Medical Genetics</i> , <b>2013</b> , 50, 324-9	5.8	93
60	Genomic analysis of Andamanese provides insights into ancient human migration into Asia and adaptation. <i>Nature Genetics</i> , <b>2016</b> , 48, 1066-70	36.3	88
59	Evaluating the Genetics of Common Variable Immunodeficiency: Monogenetic Model and Beyond. <i>Frontiers in Immunology</i> , <b>2018</b> , 9, 636	8.4	81
58	A population genetic approach to mapping neurological disorder genes using deep resequencing. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1001318	6	72
57	The foldback-like transposon <i>Galileo</i> is involved in the generation of two different natural chromosomal inversions of <i>Drosophila buzzatii</i> . <i>Molecular Biology and Evolution</i> , <b>2003</b> , 20, 674-85	8.3	64
56	SNP analysis to results (SNPator): a web-based environment oriented to statistical genomics analyses upon SNP data. <i>Bioinformatics</i> , <b>2008</b> , 24, 1643-4	7.2	57
55	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> , <b>2015</b> , 112, 6413-8	11.5	52

54	Whole-exome sequencing reveals a rapid change in the frequency of rare functional variants in a founding population of humans. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003815	6	52
53	Natural Selection in the Great Apes. <i>Molecular Biology and Evolution</i> , <b>2016</b> , 33, 3268-3283	8.3	44
52	Low occurrence of gene transposition events during the evolution of the genus <i>Drosophila</i> . <i>Evolution; International Journal of Organic Evolution</i> , <b>2003</b> , 57, 1325-35	3.8	39
51	Rare allelic forms of PRDM9 associated with childhood leukemogenesis. <i>Genome Research</i> , <b>2013</b> , 23, 419-30	9.7	37
50	A new split of the Hox gene complex in <i>Drosophila</i> : relocation and evolution of the gene labial. <i>Molecular Biology and Evolution</i> , <b>2003</b> , 20, 2042-54	8.3	36
49	Unexpected relevant role of gene mosaicism in patients with primary immunodeficiency diseases. <i>Journal of Allergy and Clinical Immunology</i> , <b>2019</b> , 143, 359-368	11.5	29
48	Genetics. Human genetic variation, shared and private. <i>Science</i> , <b>2012</b> , 337, 39-40	33.3	27
47	The impact of endogenous content, replicates and pooling on genome capture from faecal samples. <i>Molecular Ecology Resources</i> , <b>2018</b> , 18, 319-333	8.4	24
46	Signatures of selection in the human olfactory receptor OR511 gene. <i>Molecular Biology and Evolution</i> , <b>2008</b> , 25, 144-54	8.3	24
45	Population and genomic lessons from genetic analysis of two Indian populations. <i>Human Genetics</i> , <b>2014</b> , 133, 1273-87	6.3	23
44	Molecular characterization and chromosomal distribution of Galileo, Kepler and Newton, three foldback transposable elements of the <i>Drosophila buzzatii</i> species complex. <i>Genetics</i> , <b>2005</b> , 169, 2047-54	5.4	23
43	Recent human evolution has shaped geographical differences in susceptibility to disease. <i>BMC Genomics</i> , <b>2011</b> , 12, 55	4.5	22
42	Testing chromosomal phylogenies and inversion breakpoint reuse in <i>Drosophila</i> . <i>Genetics</i> , <b>2007</b> , 175, 167-77	4	22
41	Mendelian genes for Parkinson's disease contribute to the sporadic forms of the disease. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 2023-34	5.6	20
40	Genetic adaptation of the antibacterial human innate immunity network. <i>BMC Evolutionary Biology</i> , <b>2011</b> , 11, 202	3	20
39	Interrogating 11 fast-evolving genes for signatures of recent positive selection in worldwide human populations. <i>Molecular Biology and Evolution</i> , <b>2009</b> , 26, 2285-97	8.3	20
38	Extreme individual marker $F_{ST}$ values do not imply population-specific selection in humans: the NRG1 example. <i>Human Genetics</i> , <b>2007</b> , 121, 759-62	6.3	20
37	A BAC-based physical map of the <i>Drosophila buzzatii</i> genome. <i>Genome Research</i> , <b>2005</b> , 15, 885-92	9.7	20

36	Length and repeat-sequence variation in 58 STRs and 94 SNPs in two Spanish populations. <i>Forensic Science International: Genetics</i> , <b>2017</b> , 30, 66-70	4.3	17
35	Decay of linkage disequilibrium within genes across HGDP-CEPH human samples: most population isolates do not show increased LD. <i>BMC Genomics</i> , <b>2009</b> , 10, 338	4.5	16
34	An assessment of a massively parallel sequencing approach for the identification of individuals from mass graves of the Spanish Civil War (1936-1939). <i>Electrophoresis</i> , <b>2016</b> , 37, 2841-2847	3.6	16
33	Next-generation sequencing approaches for genetic mapping of complex diseases. <i>Journal of Neuroimmunology</i> , <b>2012</b> , 248, 10-22	3.5	15
32	Abundance and chromosomal distribution of six <i>Drosophila buzzatii</i> transposons: BuT1, BuT2, BuT3, BuT4, BuT5, and BuT6. <i>Chromosoma</i> , <b>2006</b> , 115, 403-12	2.8	15
31	Genetic Load of Loss-of-Function Polymorphic Variants in Great Apes. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 871-7	3.9	15
30	Genetic and structural analysis of MBL2 and MASP2 polymorphisms in south-eastern African children. <i>Tissue Antigens</i> , <b>2009</b> , 74, 298-307		14
29	Selective constraint, background selection, and mutation accumulation variability within and between human populations. <i>BMC Genomics</i> , <b>2013</b> , 14, 495	4.5	13
28	Similarity in recombination rate estimates highly correlates with genetic differentiation in humans. <i>PLoS ONE</i> , <b>2011</b> , 6, e17913	3.7	13
27	Human pseudogenes of the ABO family show a complex evolutionary dynamics and loss of function. <i>Glycobiology</i> , <b>2009</b> , 19, 583-91	5.8	12
26	Duplicative and conservative transpositions of larval serum protein 1 genes in the genus <i>Drosophila</i> . <i>Genetics</i> , <b>2004</b> , 168, 253-64	4	12
25	Severe Autoinflammatory Manifestations and Antibody Deficiency Due to Novel Hyperomorphic PLCG2 Mutations. <i>Journal of Clinical Immunology</i> , <b>2020</b> , 40, 987-1000	5.7	12
24	Y-chromosomal sequences of diverse Indian populations and the ancestry of the Andamanese. <i>Human Genetics</i> , <b>2017</b> , 136, 499-510	6.3	11
23	Serotype-specific pneumococcal disease may be influenced by mannose-binding lectin deficiency. <i>European Respiratory Journal</i> , <b>2010</b> , 36, 856-63	13.6	11
22	The BIOMEPOC Project: Personalized Biomarkers and Clinical Profiles in Chronic Obstructive Pulmonary Disease. <i>Archivos De Bronconeumologia</i> , <b>2019</b> , 55, 93-99	0.7	11
21	Detection of genomic rearrangements from targeted resequencing data in Parkinson's disease patients. <i>Movement Disorders</i> , <b>2017</b> , 32, 165-169	7	10
20	LOW OCCURRENCE OF GENE TRANSPOSITION EVENTS DURING THE EVOLUTION OF THE GENUS <i>DROSOPHILA</i> . <i>Evolution; International Journal of Organic Evolution</i> , <b>2003</b> , 57, 1325	3.8	10
19	A variant in the gene FUT9 is associated with susceptibility to placental malaria infection. <i>Human Molecular Genetics</i> , <b>2009</b> , 18, 3136-44	5.6	9

18	Genetic diagnosis of autoinflammatory disease patients using clinical exome sequencing. <i>European Journal of Medical Genetics</i> , <b>2020</b> , 63, 103920	2.6	9
17	Long-standing balancing selection in the THBS4 gene: influence on sex-specific brain expression and gray matter volumes in Alzheimer disease. <i>Human Mutation</i> , <b>2013</b> , 34, 743-53	4.7	6
16	Evolutionary analysis of genes of two pathways involved in placental malaria infection. <i>Human Genetics</i> , <b>2008</b> , 123, 343-57	6.3	6
15	A targeted association study of immunity genes and networks suggests novel associations with placental malaria infection. <i>PLoS ONE</i> , <b>2011</b> , 6, e24996	3.7	6
14	Genomes reveal marked differences in the adaptive evolution between orangutan species. <i>Genome Biology</i> , <b>2018</b> , 19, 193	18.3	5
13	FHLdb: A Comprehensive Database on the Molecular Basis of Familial Hemophagocytic Lymphohistiocytosis. <i>Frontiers in Immunology</i> , <b>2020</b> , 11, 107	8.4	3
12	Genetic identification of Spanish civil war victims. The state of the art in Catalonia (Northeastern Spain). <i>Forensic Science International: Genetics Supplement Series</i> , <b>2019</b> , 7, 419-421	0.5	3
11	Historical human remains identification through maternal and paternal genetic signatures in a founder population with extensive genealogical record. <i>American Journal of Physical Anthropology</i> , <b>2020</b> , 171, 645-658	2.5	2
10	Is there selection for the pace of successive inactivation of the arpAT gene in primates?. <i>Journal of Molecular Evolution</i> , <b>2008</b> , 67, 23-8	3.1	2
9	Further confirmation for unknown archaic ancestry in Andaman and South Asia		2
8	The first GHEP-ISFG collaborative exercise on forensic applications of massively parallel sequencing. <i>Forensic Science International: Genetics</i> , <b>2020</b> , 49, 102391	4.3	2
7	Reply to <del>U</del> No evidence for unknown archaic ancestry in South AsiaUNature <i>Genetics</i> , <b>2018</b> , 50, 1637-1639	36.3	2
6	Flow Sorting Enrichment and Nanopore Sequencing of Chromosome 1 From a Chinese Individual. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 1315	4.5	1
5	Second GHEP-ISFG exercise for DVI: "DNA-led" victimsUidentification in a simulated air crash. <i>Forensic Science International: Genetics</i> , <b>2021</b> , 53, 102527	4.3	1
4	A forensic population database in El Salvador: 58 STRs and 94 SNPs. <i>Forensic Science International: Genetics</i> , <b>2021</b> , 57, 102646	4.3	0
3	Assessment of the gene mosaicism burden in blood and its implications for immune disorders. <i>Scientific Reports</i> , <b>2021</b> , 11, 12940	4.9	0
2	Next-generation sequencing for rare diseases231-242		
1	Genome-wide postnatal changes in immunity following fetal inflammatory response. <i>FEBS Journal</i> , <b>2021</b> , 288, 2311-2331	5.7	

