

# David Comas

## List of Publications by Year in descending order

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87  
papers

10,894  
citations

71004

43  
h-index

60403

85  
g-index

91  
all docs

91  
docs citations

91  
times ranked

13425  
citing authors

#	ARTICLE	IF	CITATIONS
1	Population Histories and Genomic Diversity of South American Natives. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	10
2	Population history of North Africa based on modern and ancient genomes. <i>Human Molecular Genetics</i> , 2021, 30, R17-R23.	1.4	11
3	Deep genetic affinity between coastal Pacific and Amazonian natives evidenced by Australasian ancestry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	21
4	Genetic origins, singularity, and heterogeneity of Basques. <i>Current Biology</i> , 2021, 31, 2167-2177.e4.	1.8	11
5	Admixture Has Shaped Romani Genetic Diversity in Clinically Relevant Variants. <i>Frontiers in Genetics</i> , 2021, 12, 683880.	1.1	6
6	The Y Chromosome. <i>Evolutionary Studies</i> , 2021, , 121-136.	0.2	0
7	Whole-exome analysis in Tunisian Imazighen and Arabs shows the impact of demography in functional variation. <i>Scientific Reports</i> , 2021, 11, 21125.	1.6	4
8	The genetic scenario of Mercheros: an under-represented group within the Iberian Peninsula. <i>BMC Genomics</i> , 2021, 22, 897.	1.2	1
9	Recent Common Origin, Reduced Population Size, and Marked Admixture Have Shaped European Roma Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 3175-3187.	3.5	16
10	The place of metropolitan France in the European genomic landscape. <i>Human Genetics</i> , 2020, 139, 1091-1105.	1.8	1
11	Heterogeneity in Palaeolithic Population Continuity and Neolithic Expansion in North Africa. <i>Current Biology</i> , 2019, 29, 3953-3959.e4.	1.8	26
12	European Roma groups show complex West Eurasian admixture footprints and a common South Asian genetic origin. <i>PLoS Genetics</i> , 2019, 15, e1008417.	1.5	28
13	Spatially explicit analysis reveals complex human genetic gradients in the Iberian Peninsula. <i>Scientific Reports</i> , 2019, 9, 7825.	1.6	5
14	Dissecting human North African gene-flow into its western coastal surroundings. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190471.	1.2	13
15	Whole-genome sequence analysis of a Pan African set of samples reveals archaic gene flow from an extinct basal population of modern humans into sub-Saharan populations. <i>Genome Biology</i> , 2019, 20, 77.	3.8	50
16	People from Ibiza: an unexpected isolate in the Western Mediterranean. <i>European Journal of Human Genetics</i> , 2019, 27, 941-951.	1.4	25
17	The genetic landscape of Mediterranean North African populations through complete mtDNA sequences. <i>Annals of Human Biology</i> , 2018, 45, 98-104.	0.4	16
18	Sequence diversity of the Rh blood group system in Basques. <i>European Journal of Human Genetics</i> , 2018, 26, 1859-1866.	1.4	5

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19	Recent historical migrations have shaped the gene pool of Arabs and Berbers in North Africa. <i>Molecular Biology and Evolution</i> , 2017, 34, msw218.	3.5	56
20	Evaluating the Neolithic Expansion at Both Shores of the Mediterranean Sea. <i>Molecular Biology and Evolution</i> , 2017, 34, 3232-3242.	3.5	13
21	Whole Y-chromosome sequences reveal an extremely recent origin of the most common North African paternal lineage E-M183 (M81). <i>Scientific Reports</i> , 2017, 7, 15941.	1.6	24
22	Novel Mutations Causing C5 Deficiency in Three North-African Families. <i>Journal of Clinical Immunology</i> , 2016, 36, 388-396.	2.0	13
23	Demographic History of the Genus <i>Pan</i> Inferred from Whole Mitochondrial Genome Reconstructions. <i>Genome Biology and Evolution</i> , 2016, 8, 2020-2030.	1.1	19
24	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016, 538, 201-206.	13.7	1,216
25	Genomic insights into the origin of farming in the ancient Near East. <i>Nature</i> , 2016, 536, 419-424.	13.7	733
26	Genomic analysis of Andamanese provides insights into ancient human migration into Asia and adaptation. <i>Nature Genetics</i> , 2016, 48, 1066-1070.	9.4	126
27	Genetic evidence for an origin of the Armenians from Bronze Age mixing of multiple populations. <i>European Journal of Human Genetics</i> , 2016, 24, 931-936.	1.4	44
28	Reassessing the Evolutionary History of the 17q21 Inversion Polymorphism. <i>Genome Biology and Evolution</i> , 2015, 7, 3239-3248.	1.1	11
29	The genetics of East African populations: a Nilo-Saharan component in the African genetic landscape. <i>Scientific Reports</i> , 2015, 5, 9996.	1.6	25
30	Genetic Heterogeneity in Algerian Human Populations. <i>PLoS ONE</i> , 2015, 10, e0138453.	1.1	33
31	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.	3.3	75
32	Global diversity, population stratification, and selection of human copy-number variation. <i>Science</i> , 2015, 349, aab3761.	6.0	293
33	Tandem repeat variation in human and great ape populations and its impact on gene expression divergence. <i>Genome Research</i> , 2015, 25, 1591-1599.	2.4	69
34	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.	1.5	34
35	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413.	13.7	1,179
36	The influence of habitats on female mobility in Central and Western Africa inferred from human mitochondrial variation. <i>BMC Evolutionary Biology</i> , 2013, 13, 24.	3.2	9

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37	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	13.7	768
38	Genome-Wide Diversity in the Levant Reveals Recent Structuring by Culture. <i>PLoS Genetics</i> , 2013, 9, e1003316.	1.5	77
39	Gene flow from North Africa contributes to differential human genetic diversity in southern Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11791-11796.	3.3	174
40	Uniparental Markers in Italy Reveal a Sex-Biased Genetic Structure and Different Historical Strata. <i>PLoS ONE</i> , 2013, 8, e65441.	1.1	61
41	Genome-Wide and Paternal Diversity Reveal a Recent Origin of Human Populations in North Africa. <i>PLoS ONE</i> , 2013, 8, e80293.	1.1	39
42	Genomic Ancestry of North Africans Supports Back-to-Africa Migrations. <i>PLoS Genetics</i> , 2012, 8, e1002397.	1.5	275
43	Similarity in recombination rate and linkage disequilibrium at CYP2C and CYP2D cytochrome P450 gene regions among Europeans indicates signs of selection and no advantage of using tagSNPs in population isolates. <i>Pharmacogenetics and Genomics</i> , 2012, 22, 846-857.	0.7	12
44	Recombination Gives a New Insight in the Effective Population Size and the History of the Old World Human Populations. <i>Molecular Biology and Evolution</i> , 2012, 29, 25-30.	3.5	31
45	Evidence of Pre-Roman Tribal Genetic Structure in Basques from Uniparentally Inherited Markers. <i>Molecular Biology and Evolution</i> , 2012, 29, 2211-2222.	3.5	37
46	Reconstructing the Population History of European Romani from Genome-wide Data. <i>Current Biology</i> , 2012, 22, 2342-2349.	1.8	101
47	Recombination networks as genetic markers in a human variation study of the Old World. <i>Human Genetics</i> , 2012, 131, 601-613.	1.8	7
48	North African Jewish and non-Jewish populations form distinctive, orthogonal clusters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13865-13870.	3.3	49
49	The Basque Paradigm: Genetic Evidence of a Maternal Continuity in the Franco-Cantabrian Region since Pre-Neolithic Times. <i>American Journal of Human Genetics</i> , 2012, 90, 486-493.	2.6	58
50	North African Populations Carry the Signature of Admixture with Neandertals. <i>PLoS ONE</i> , 2012, 7, e47765.	1.1	67
51	Signatures of the Preagricultural Peopling Processes in Sub-Saharan Africa as Revealed by the Phylogeography of Early Y Chromosome Lineages. <i>Molecular Biology and Evolution</i> , 2011, 28, 2603-2613.	3.5	52
52	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.	1.4	35
53	Multiplex single-nucleotide polymorphism typing of the human Y chromosome using TaqMan probes. <i>Investigative Genetics</i> , 2011, 2, 13.	3.3	15
54	Mitochondrial DNA structure in North Africa reveals a genetic discontinuity in the Nile Valley. <i>American Journal of Physical Anthropology</i> , 2011, 145, 107-117.	2.1	40

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55	Genetic structure of Tunisian ethnic groups revealed by paternal lineages. <i>American Journal of Physical Anthropology</i> , 2011, 146, 271-280.	2.1	43
56	Insights into the Demographic History of African Pygmies from Complete Mitochondrial Genomes. <i>Molecular Biology and Evolution</i> , 2011, 28, 1099-1110.	3.5	105
57	Hunter-gatherer genomic diversity suggests a southern African origin for modern humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5154-5162.	3.3	394
58	Reconstructing the Indian Origin and Dispersal of the European Roma: A Maternal Genetic Perspective. <i>PLoS ONE</i> , 2011, 6, e15988.	1.1	61
59	The Distribution and Most Recent Common Ancestor of the 17q21 Inversion in Humans. <i>American Journal of Human Genetics</i> , 2010, 86, 161-171.	2.6	59
60	The genome-wide structure of the Jewish people. <i>Nature</i> , 2010, 466, 238-242.	13.7	369
61	Genetic and Demographic Implications of the Bantu Expansion: Insights from Human Paternal Lineages. <i>Molecular Biology and Evolution</i> , 2009, 26, 1581-1589.	3.5	114
62	Linguistic and maternal genetic diversity are not correlated in Native Mexicans. <i>Human Genetics</i> , 2009, 126, 521-531.	1.8	40
63	An evaluation of the genetic-matched pair study design using genome-wide SNP data from the European population. <i>European Journal of Human Genetics</i> , 2009, 17, 967-975.	1.4	8
64	Admixture and sexual bias in the population settlement of La Réunion Island (Indian Ocean). <i>American Journal of Physical Anthropology</i> , 2008, 136, 100-107.	2.1	11
65	Identifying Genetic Traces of Historical Expansions: Phoenician Footprints in the Mediterranean. <i>American Journal of Human Genetics</i> , 2008, 83, 633-642.	2.6	127
66	Northwest Siberian Khanty and Mansi in the junction of West and East Eurasian gene pools as revealed by uniparental markers. <i>European Journal of Human Genetics</i> , 2008, 16, 1254-1264.	1.4	53
67	Correlation between Genetic and Geographic Structure in Europe. <i>Current Biology</i> , 2008, 18, 1241-1248.	1.8	449
68	Independent Introduction of Two Lactase-Persistence Alleles into Human Populations Reflects Different History of Adaptation to Milk Culture. <i>American Journal of Human Genetics</i> , 2008, 82, 57-72.	2.6	301
69	The Dawn of Human Matrilineal Diversity. <i>American Journal of Human Genetics</i> , 2008, 82, 1130-1140.	2.6	392
70	Maternal traces of deep common ancestry and asymmetric gene flow between Pygmy hunter-gatherers and Bantu-speaking farmers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1596-1601.	3.3	157
71	The Genographic Project Public Participation Mitochondrial DNA Database. <i>PLoS Genetics</i> , 2007, 3, e104.	1.5	99
72	Evidence of Still-Ongoing Convergence Evolution of the Lactase Persistence T-13910 Alleles in Humans. <i>American Journal of Human Genetics</i> , 2007, 81, 615-625.	2.6	135

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73	SNPlexing the human Y-chromosome: A single-assay system for major haplogroup screening. <i>Electrophoresis</i> , 2007, 28, 3201-3206.	1.3	10
74	Phylogeography of the human mitochondrial L1c haplogroup: Genetic signatures of the prehistory of Central Africa. <i>Molecular Phylogenetics and Evolution</i> , 2007, 43, 635-644.	1.2	56
75	The portability of tagSNPs across populations: A worldwide survey. <i>Genome Research</i> , 2006, 16, 323-330.	2.4	82
76	Brief communication: mtDNA variation in North Cameroon: Lack of asian lineages and implications for back migration from Asia to sub-Saharan Africa. <i>American Journal of Physical Anthropology</i> , 2005, 128, 678-681.	2.1	43
77	Admixture, migrations, and dispersals in Central Asia: evidence from maternal DNA lineages. <i>European Journal of Human Genetics</i> , 2004, 12, 495-504.	1.4	145
78	Insights into the western Bantu dispersal: mtDNA lineage analysis in Angola. <i>Human Genetics</i> , 2004, 115, 439-47.	1.8	70
79	A Global Perspective on Genetic Variation at the ADH Genes Reveals Unusual Patterns of Linkage Disequilibrium and Diversity. <i>American Journal of Human Genetics</i> , 2002, 71, 84-99.	2.6	261
80	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.	2.6	234
81	Georgian and Kurd mtDNA sequence analysis shows a lack of correlation between languages and female genetic lineages. , 2000, 112, 5-16.		60
82	Genetic structure of north-west Africa revealed by STR analysis. <i>European Journal of Human Genetics</i> , 2000, 8, 360-366.	1.4	104
83	Alu insertion polymorphisms in NW Africa and the Iberian Peninsula: evidence for a strong genetic boundary through the Gibraltar Straits. <i>Human Genetics</i> , 2000, 107, 312-319.	1.8	124
84	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.	2.6	119
85	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.	2.6	105
86	mtDNA analysis of the Galician population: a genetic edge of European variation. <i>European Journal of Human Genetics</i> , 1998, 6, 365-375.	1.4	141
87	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.	2.6	295