

David Comas

List of Publications by Year in descending order

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87
papers

10,894
citations

61984

43
h-index

53230

85
g-index

91
all docs

91
docs citations

91
times ranked

12087
citing authors

#	ARTICLE	IF	CITATIONS
1	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016, 538, 201-206.	27.8	1,216
2	Ancient human genomes suggest three ancestral populations for present-day Europeans. <i>Nature</i> , 2014, 513, 409-413.	27.8	1,179
3	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	27.8	768
4	Genomic insights into the origin of farming in the ancient Near East. <i>Nature</i> , 2016, 536, 419-424.	27.8	733
5	Correlation between Genetic and Geographic Structure in Europe. <i>Current Biology</i> , 2008, 18, 1241-1248.	3.9	449
6	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.	7.1	394
7	The Dawn of Human Matrilineal Diversity. <i>American Journal of Human Genetics</i> , 2008, 82, 1130-1140.	6.2	392
8	The genome-wide structure of the Jewish people. <i>Nature</i> , 2010, 466, 238-242.	27.8	369
9	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.	6.2	301
10	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
11	Global diversity, population stratification, and selection of human copy-number variation. <i>Science</i> , 2015, 349, aab3761.	12.6	293
12	Genomic Ancestry of North Africans Supports Back-to-Africa Migrations. <i>PLoS Genetics</i> , 2012, 8, e1002397.	3.5	275
13	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.	6.2	261
14	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
15	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.	7.1	174
16	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.	7.1	157
17	Admixture, migrations, and dispersals in Central Asia: evidence from maternal DNA lineages. <i>European Journal of Human Genetics</i> , 2004, 12, 495-504.	2.8	145
18	mtDNA analysis of the Galician population: a genetic edge of European variation. <i>European Journal of Human Genetics</i> , 1998, 6, 365-375.	2.8	141

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19	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.	6.2	135
20	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
21	Genomic analysis of Andamanese provides insights into ancient human migration into Asia and adaptation. <i>Nature Genetics</i> , 2016, 48, 1066-1070.	21.4	126
22	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.	3.8	124
23	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
24	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
25	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
26	Insights into the Demographic History of African Pygmies from Complete Mitochondrial Genomes. <i>Molecular Biology and Evolution</i> , 2011, 28, 1099-1110.	8.9	105
27	Genetic structure of north-west Africa revealed by STR analysis. <i>European Journal of Human Genetics</i> , 2000, 8, 360-366.	2.8	104
28	Reconstructing the Population History of European Romani from Genome-wide Data. <i>Current Biology</i> , 2012, 22, 2342-2349.	3.9	101
29	The Genographic Project Public Participation Mitochondrial DNA Database. <i>PLoS Genetics</i> , 2007, 3, e104.	3.5	99
30	The portability of tagSNPs across populations: A worldwide survey. <i>Genome Research</i> , 2006, 16, 323-330.	5.5	82
31	Genome-Wide Diversity in the Levant Reveals Recent Structuring by Culture. <i>PLoS Genetics</i> , 2013, 9, e1003316.	3.5	77
32	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.	7.1	75
33	Insights into the western Bantu dispersal: mtDNA lineage analysis in Angola. <i>Human Genetics</i> , 2004, 115, 439-47.	3.8	70
34	Tandem repeat variation in human and great ape populations and its impact on gene expression divergence. <i>Genome Research</i> , 2015, 25, 1591-1599.	5.5	69
35	North African Populations Carry the Signature of Admixture with Neandertals. <i>PLoS ONE</i> , 2012, 7, e47765.	2.5	67
36	Uniparental Markers in Italy Reveal a Sex-Biased Genetic Structure and Different Historical Strata. <i>PLoS ONE</i> , 2013, 8, e65441.	2.5	61

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37	Reconstructing the Indian Origin and Dispersal of the European Roma: A Maternal Genetic Perspective. PLoS ONE, 2011, 6, e15988.	2.5	61
38	Georgian and Kurd mtDNA sequence analysis shows a lack of correlation between languages and female genetic lineages. , 2000, 112, 5-16.		60
39	The Distribution and Most Recent Common Ancestor of the 17q21 Inversion in Humans. American Journal of Human Genetics, 2010, 86, 161-171.	6.2	59
40	The Basque Paradigm: Genetic Evidence of a Maternal Continuity in the Franco-Cantabrian Region since Pre-Neolithic Times. American Journal of Human Genetics, 2012, 90, 486-493.	6.2	58
41	Phylogeography of the human mitochondrial L1c haplogroup: Genetic signatures of the prehistory of Central Africa. Molecular Phylogenetics and Evolution, 2007, 43, 635-644.	2.7	56
42	Recent historical migrations have shaped the gene pool of Arabs and Berbers in North Africa. Molecular Biology and Evolution, 2017, 34, msw218.	8.9	56
43	Northwest Siberian Khanty and Mansi in the junction of West and East Eurasian gene pools as revealed by uniparental markers. European Journal of Human Genetics, 2008, 16, 1254-1264.	2.8	53
44	Signatures of the Preagricultural Peopling Processes in Sub-Saharan Africa as Revealed by the Phylogeography of Early Y Chromosome Lineages. Molecular Biology and Evolution, 2011, 28, 2603-2613.	8.9	52
45	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. Genome Biology, 2019, 20, 77.	8.8	50
46	North African Jewish and non-Jewish populations form distinctive, orthogonal clusters. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13865-13870.	7.1	49
47	Genetic evidence for an origin of the Armenians from Bronze Age mixing of multiple populations. European Journal of Human Genetics, 2016, 24, 931-936.	2.8	44
48	Brief communication: mtDNA variation in North Cameroon: Lack of asian lineages and implications for back migration from Asia to sub-Saharan Africa. American Journal of Physical Anthropology, 2005, 128, 678-681.	2.1	43
49	Genetic structure of Tunisian ethnic groups revealed by paternal lineages. American Journal of Physical Anthropology, 2011, 146, 271-280.	2.1	43
50	Linguistic and maternal genetic diversity are not correlated in Native Mexicans. Human Genetics, 2009, 126, 521-531.	3.8	40
51	Mitochondrial DNA structure in North Africa reveals a genetic discontinuity in the Nile Valley. American Journal of Physical Anthropology, 2011, 145, 107-117.	2.1	40
52	Genome-Wide and Paternal Diversity Reveal a Recent Origin of Human Populations in North Africa. PLoS ONE, 2013, 8, e80293.	2.5	39
53	Evidence of Pre-Roman Tribal Genetic Structure in Basques from Uniparentally Inherited Markers. Molecular Biology and Evolution, 2012, 29, 2211-2222.	8.9	37
54	A genomic analysis identifies a novel component in the genetic structure of sub-Saharan African populations. European Journal of Human Genetics, 2011, 19, 84-88.	2.8	35

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55	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
56	Genetic Heterogeneity in Algerian Human Populations. <i>PLoS ONE</i> , 2015, 10, e0138453.	2.5	33
57	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.	8.9	31
58	European Roma groups show complex West Eurasian admixture footprints and a common South Asian genetic origin. <i>PLoS Genetics</i> , 2019, 15, e1008417.	3.5	28
59	Heterogeneity in Palaeolithic Population Continuity and Neolithic Expansion in North Africa. <i>Current Biology</i> , 2019, 29, 3953-3959.e4.	3.9	26
60	The genetics of East African populations: a Nilo-Saharan component in the African genetic landscape. <i>Scientific Reports</i> , 2015, 5, 9996.	3.3	25
61	People from Ibiza: an unexpected isolate in the Western Mediterranean. <i>European Journal of Human Genetics</i> , 2019, 27, 941-951.	2.8	25
62	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.	3.3	24
63	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, .	7.1	21
64	Demographic History of the Genus <i>Pan</i> Inferred from Whole Mitochondrial Genome Reconstructions. <i>Genome Biology and Evolution</i> , 2016, 8, 2020-2030.	2.5	19
65	The genetic landscape of Mediterranean North African populations through complete mtDNA sequences. <i>Annals of Human Biology</i> , 2018, 45, 98-104.	1.0	16
66	Recent Common Origin, Reduced Population Size, and Marked Admixture Have Shaped European Roma Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 3175-3187.	8.9	16
67	Multiplex single-nucleotide polymorphism typing of the human Y chromosome using TaqMan probes. <i>Investigative Genetics</i> , 2011, 2, 13.	3.3	15
68	Novel Mutations Causing C5 Deficiency in Three North-African Families. <i>Journal of Clinical Immunology</i> , 2016, 36, 388-396.	3.8	13
69	Evaluating the Neolithic Expansion at Both Shores of the Mediterranean Sea. <i>Molecular Biology and Evolution</i> , 2017, 34, 3232-3242.	8.9	13
70	Dissecting human North African gene-flow into its western coastal surroundings. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190471.	2.6	13
71	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.	1.5	12
72	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

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73	Reassessing the Evolutionary History of the 17q21 Inversion Polymorphism. <i>Genome Biology and Evolution</i> , 2015, 7, 3239-3248.	2.5	11
74	Population history of North Africa based on modern and ancient genomes. <i>Human Molecular Genetics</i> , 2021, 30, R17-R23.	2.9	11
75	Genetic origins, singularity, and heterogeneity of Basques. <i>Current Biology</i> , 2021, 31, 2167-2177.e4.	3.9	11
76	SNPlexing the human Y-chromosome: A single-assay system for major haplogroup screening. <i>Electrophoresis</i> , 2007, 28, 3201-3206.	2.4	10
77	Population Histories and Genomic Diversity of South American Natives. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	10
78	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
79	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.	2.8	8
80	Recombination networks as genetic markers in a human variation study of the Old World. <i>Human Genetics</i> , 2012, 131, 601-613.	3.8	7
81	Admixture Has Shaped Romani Genetic Diversity in Clinically Relevant Variants. <i>Frontiers in Genetics</i> , 2021, 12, 683880.	2.3	6
82	Sequence diversity of the Rh blood group system in Basques. <i>European Journal of Human Genetics</i> , 2018, 26, 1859-1866.	2.8	5
83	Spatially explicit analysis reveals complex human genetic gradients in the Iberian Peninsula. <i>Scientific Reports</i> , 2019, 9, 7825.	3.3	5
84	Whole-exome analysis in Tunisian Imazighen and Arabs shows the impact of demography in functional variation. <i>Scientific Reports</i> , 2021, 11, 21125.	3.3	4
85	The place of metropolitan France in the European genomic landscape. <i>Human Genetics</i> , 2020, 139, 1091-1105.	3.8	1
86	The genetic scenario of Mercheros: an under-represented group within the Iberian Peninsula. <i>BMC Genomics</i> , 2021, 22, 897.	2.8	1
87	The Y Chromosome. <i>Evolutionary Studies</i> , 2021, , 121-136.	0.1	0