

# Carina M Schlebusch

## List of Publications by Year in descending order

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Version: 2024-02-01

53  
papers

2,351  
citations

304368

22  
h-index

233125

45  
g-index

61  
all docs

61  
docs citations

61  
times ranked

2804  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomics: Testing the limits of de-extinction. <i>Current Biology</i> , 2022, 32, R324-R327.	1.8	2
2	Human adaptation to arsenic in Bolivians living in the Andes. <i>Chemosphere</i> , 2022, 301, 134764.	4.2	7
3	Closing the Gaps in Genomic Research. <i>Trends in Genetics</i> , 2021, 37, 104-106.	2.9	4
4	Later Stone Age human hair from Vaalkrans Shelter, Cape Floristic Region of South Africa, reveals genetic affinity to Khoe groups. <i>American Journal of Physical Anthropology</i> , 2021, 174, 701-713.	2.1	3
5	Population collapse in Congo rainforest from 400 CE urges reassessment of the Bantu Expansion. <i>Science Advances</i> , 2021, 7, .	4.7	30
6	Evolutionary genomics in Africa. <i>Human Molecular Genetics</i> , 2021, 30, R1-R1.	1.4	5
7	The Genetic Variation of Lactase Persistence Alleles in Sudan and South Sudan. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	4
8	Multiple migrations to the Philippines during the last 50,000 years. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	50
9	Genetic substructure and complex demographic history of South African Bantu speakers. <i>Nature Communications</i> , 2021, 12, 2080.	5.8	47
10	Human origins in Southern African palaeo-wetlands? Strong claims from weak evidence. <i>Journal of Archaeological Science</i> , 2021, 130, 105374.	1.2	9
11	Philippine Ayta possess the highest level of Denisovan ancestry in the world. <i>Current Biology</i> , 2021, 31, 4219-4230.e10.	1.8	37
12	Comparison of sequencing data processing pipelines and application to underrepresented African human populations. <i>BMC Bioinformatics</i> , 2021, 22, 488.	1.2	5
13	The performance of common SNP arrays in assigning African mitochondrial haplogroups. <i>BMC Genomic Data</i> , 2021, 22, 43.	0.7	2
14	Bantu-speaker migration and admixture in southern Africa. <i>Human Molecular Genetics</i> , 2021, 30, R56-R63.	1.4	21
15	A reassessment of archaeological human remains recovered from rock shelters in Cathkin Peak, South Africa. <i>Azania</i> , 2021, 56, 508-538.	0.4	3
16	Male-biased migration from East Africa introduced pastoralism into southern Africa. <i>BMC Biology</i> , 2021, 19, 259.	1.7	4
17	Along the Indian Ocean Coast: Genomic Variation in Mozambique Provides New Insights into the Bantu Expansion. <i>Molecular Biology and Evolution</i> , 2020, 37, 406-416.	3.5	32
18	Y-Chromosome Variation in Southern African Khoe-San Populations Based on Whole-Genome Sequences. <i>Genome Biology and Evolution</i> , 2020, 12, 1031-1039.	1.1	6

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19	Khoe-San Genomes Reveal Unique Variation and Confirm the Deepest Population Divergence in Homo sapiens. <i>Molecular Biology and Evolution</i> , 2020, 37, 2944-2954.	3.5	60
20	Sahelian pastoralism from the perspective of variants associated with lactase persistence. <i>American Journal of Physical Anthropology</i> , 2020, 173, 423-436.	2.1	13
21	African population history: an ancient DNA perspective. <i>Current Opinion in Genetics and Development</i> , 2020, 62, 8-15.	1.5	29
22	Patterns of African and Asian admixture in the Afrikaner population of South Africa. <i>BMC Biology</i> , 2020, 18, 16.	1.7	12
23	DNA is the key to unlocking our ancient African past. <i>Biochemist</i> , 2020, 42, 12-17.	0.2	2
24	Genetic Affinities among Southern Africa Hunter-Gatherers and the Impact of Admixing Farmer and Herder Populations. <i>Molecular Biology and Evolution</i> , 2019, 36, 1849-1861.	3.5	21
25	Unraveling African diversity from a cross-disciplinary perspective. <i>Evolutionary Anthropology</i> , 2019, 28, 288-292.	1.7	1
26	Genetic data and radiocarbon dating question Plovers Lake as a Middle Stone Age hominin-bearing site. <i>Journal of Human Evolution</i> , 2019, 131, 203-209.	1.3	4
27	Population history and genetic adaptation of the Fulani nomads: inferences from genome-wide data and the lactase persistence trait. <i>BMC Genomics</i> , 2019, 20, 915.	1.2	36
28	Tales of Human Migration, Admixture, and Selection in Africa. <i>Annual Review of Genomics and Human Genetics</i> , 2018, 19, 405-428.	2.5	78
29	Ancient human DNA: How sequencing the genome of a boy from Ballito Bay changed human history. <i>South African Journal of Science</i> , 2018, 114, 3.	0.3	5
30	Patterns of variation in cis-regulatory regions: examining evidence of purifying selection. <i>BMC Genomics</i> , 2018, 19, 95.	1.2	8
31	Adaptation to infectious disease exposure in indigenous Southern African populations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170226.	1.2	13
32	Southern African ancient genomes estimate modern human divergence to 350,000 to 260,000 years ago. <i>Science</i> , 2017, 358, 652-655.	6.0	351
33	Northeast African genomic variation shaped by the continuity of indigenous groups and Eurasian migrations. <i>PLoS Genetics</i> , 2017, 13, e1006976.	1.5	45
34	The disappearing San of southeastern Africa and their genetic affinities. <i>Human Genetics</i> , 2016, 135, 1365-1373.	1.8	22
35	Selenium metabolism to the trimethylselenonium ion (TMSe) varies markedly because of polymorphisms in the indolethylamine N-methyltransferase gene. <i>American Journal of Clinical Nutrition</i> , 2015, 102, 1406-1415.	2.2	40
36	Human Adaptation to Arsenic-Rich Environments. <i>Molecular Biology and Evolution</i> , 2015, 32, 1544-1555.	3.5	113

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37	Genetic variation reveals large-scale population expansion and migration during the expansion of Bantu-speaking peoples. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20141448.	1.2	92
38	Lactase Persistence Alleles Reveal Partial East African Ancestry of Southern African Khoe Pastoralists. <i>Current Biology</i> , 2014, 24, 852-858.	1.8	111
39	MtDNA control region variation affirms diversity and deep sub-structure in populations from southern Africa. <i>BMC Evolutionary Biology</i> , 2013, 13, 56.	3.2	67
40	Stronger signal of recent selection for lactase persistence in Maasai than in Europeans. <i>European Journal of Human Genetics</i> , 2013, 21, 550-553.	1.4	34
41	Bridging disciplines to better elucidate the evolution of early Homo sapiens in southern Africa. <i>South African Journal of Science</i> , 2013, 109, 8.	0.3	15
42	Possible Positive Selection for an Arsenic-Protective Haplotype in Humans. <i>Environmental Health Perspectives</i> , 2013, 121, 53-58.	2.8	44
43	Age of the Association between <i>Helicobacter pylori</i> and Man. <i>PLoS Pathogens</i> , 2012, 8, e1002693.	2.1	271
44	Genetic variation of 15 autosomal STR loci in various populations from southern Africa. <i>Forensic Science International: Genetics</i> , 2012, 6, e20-e21.	1.6	6
45	Extensive Population Structure in San, Khoe, and Mixed Ancestry Populations from Southern Africa Revealed by 44 Short 5-SNP Haplotypes. <i>Human Biology</i> , 2012, 84, 695-724.	0.4	13
46	Genomic Variation in Seven Khoe-San Groups Reveals Adaptation and Complex African History. <i>Science</i> , 2012, 338, 374-379.	6.0	364
47	. The Genetic Landscape of Sub-Saharan African Populations. , 2012, , 369-381.		1
48	Genetic variation and population structure of Sudanese populations as indicated by 15 Identifier sequence-tagged repeat (STR) loci. <i>Investigative Genetics</i> , 2011, 2, 12.	3.3	33
49	Different contributions of ancient mitochondrial and Y-chromosomal lineages in "Karretjie people"™ of the Great Karoo in South Africa. <i>Journal of Human Genetics</i> , 2011, 56, 623-630.	1.1	40
50	Development of a single base extension method to resolve Y chromosome haplogroups in sub-Saharan African populations. <i>Investigative Genetics</i> , 2010, 1, 6.	3.3	42
51	Issues raised by use of ethnic-group names in genome study. <i>Nature</i> , 2010, 464, 487-487.	13.7	21
52	SNaPshot minisequencing to resolve mitochondrial macrohaplogroups found in Africa. <i>Electrophoresis</i> , 2009, 30, 3657-3664.	1.3	48
53	Revisiting the demographic history of Central African populations from a genetic perspective. , 0, , 1-29.		1