

# Mikkel Heide Schierup

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4802811/publications.pdf>

Version: 2024-02-01

129  
papers

14,757  
citations

28242

55  
h-index

23514

111  
g-index

149  
all docs

149  
docs citations

149  
times ranked

20756  
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	6.0	1,583
2	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	2.6	1,098
3	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	13.7	768
4	RNA Exosome Depletion Reveals Transcription Upstream of Active Human Promoters. <i>Science</i> , 2008, 322, 1851-1854.	6.0	688
5	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012, 483, 169-175.	13.7	663
6	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	13.7	541
7	Consequences of Recombination on Traditional Phylogenetic Analysis. <i>Genetics</i> , 2000, 156, 879-891.	1.2	539
8	A high-coverage Neandertal genome from Vindija Cave in Croatia. <i>Science</i> , 2017, 358, 655-658.	6.0	501
9	The bonobo genome compared with the chimpanzee and human genomes. <i>Nature</i> , 2012, 486, 527-531.	13.7	445
10	A genomic history of Aboriginal Australia. <i>Nature</i> , 2016, 538, 207-214.	13.7	439
11	Pigs in sequence space: A 0.66X coverage pig genome survey based on shotgun sequencing. <i>BMC Genomics</i> , 2005, 6, 70.	1.2	283
12	Genomic Relationships and Speciation Times of Human, Chimpanzee, and Gorilla Inferred from a Coalescent Hidden Markov Model. <i>PLoS Genetics</i> , 2007, 3, e7.	1.5	281
13	Spider genomes provide insight into composition and evolution of venom and silk. <i>Nature Communications</i> , 2014, 5, 3765.	5.8	235
14	Recent speciation of <i>Capsella rubella</i> from <i>Capsella grandiflora</i> , associated with loss of self-incompatibility and an extreme bottleneck. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5246-5251.	3.3	204
15	Incomplete lineage sorting patterns among human, chimpanzee, and orangutan suggest recent orangutan speciation and widespread selection. <i>Genome Research</i> , 2011, 21, 349-356.	2.4	192
16	The making of a new pathogen: Insights from comparative population genomics of the domesticated wheat pathogen <i>Mycosphaerella graminicola</i> and its wild sister species. <i>Genome Research</i> , 2011, 21, 2157-2166.	2.4	191
17	The effect of subdivision on variation at multi-allelic loci under balancing selection. <i>Genetical Research</i> , 2000, 76, 51-62.	0.3	190
18	Fusion of two divergent fungal individuals led to the recent emergence of a unique widespread pathogen species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10954-10959.	3.3	171

#	ARTICLE	IF	CITATIONS
19	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. <i>Nature Communications</i> , 2015, 6, 5969.	5.8	164
20	Evolution and diversity of copy number variation in the great ape lineage. <i>Genome Research</i> , 2013, 23, 1373-1382.	2.4	161
21	The Transition to Self-Compatibility in <i>Arabidopsis thaliana</i> and Evolution within S-Haplotypes over 10 Myr. <i>Molecular Biology and Evolution</i> , 2006, 23, 1741-1750.	3.5	154
22	Repeated Adaptive Introgression at a Gene under Multiallelic Balancing Selection. <i>PLoS Genetics</i> , 2008, 4, e1000168.	1.5	151
23	Whole-Genome and Chromosome Evolution Associated with Host Adaptation and Speciation of the Wheat Pathogen <i>Mycosphaerella graminicola</i> . <i>PLoS Genetics</i> , 2010, 6, e1001189.	1.5	142
24	Identification and Characterization of a Polymorphic Receptor Kinase Gene Linked to the Self-Incompatibility Locus of <i>Arabidopsis lyrata</i> . <i>Genetics</i> , 2001, 158, 387-399.	1.2	142
25	Using biological networks to search for interacting loci in genome-wide association studies. <i>European Journal of Human Genetics</i> , 2009, 17, 1231-1240.	1.4	135
26	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , 2017, 548, 87-91.	13.7	130
27	Microsatellite analyses reveal fine-scale genetic structure in grey mouse lemurs ( <i>Microcebus</i> ). <i>Trends in Ecology and Evolution</i> , 2010, 25, 128-130.	2.0	128
28	Direct estimation of mutations in great apes reconciles phylogenetic dating. <i>Nature Ecology and Evolution</i> , 2019, 3, 286-292.	3.4	122
29	SOAPindel: Efficient identification of indels from short paired reads. <i>Genome Research</i> , 2013, 23, 195-200.	2.4	115
30	The comparative genomics and complex population history of <i>Papio</i> baboons. <i>Science Advances</i> , 2019, 5, eaau6947.	4.7	115
31	Recombination and the Molecular Clock. <i>Molecular Biology and Evolution</i> , 2000, 17, 1578-1579.	3.5	107
32	Estimating the number, frequency, and dominance of S-alleles in a natural population of <i>Arabidopsis lyrata</i> (Brassicaceae) with sporophytic control of self-incompatibility. <i>Heredity</i> , 2003, 90, 422-431.	1.2	107
33	Long-term stability and effective population size in North Sea and Baltic Sea cod ( <i>Gadus morhua</i> ). <i>Molecular Ecology</i> , 2005, 15, 321-331.	2.0	107
34	A New Isolation with Migration Model along Complete Genomes Infers Very Different Divergence Processes among Closely Related Great Ape Species. <i>PLoS Genetics</i> , 2012, 8, e1003125.	1.5	102
35	Inbreeding depression and outbreeding depression in plants. <i>Heredity</i> , 1996, 77, 461-468.	1.2	98
36	Genomic Determinants of Protein Evolution and Polymorphism in <i>Arabidopsis</i> . <i>Genome Biology and Evolution</i> , 2011, 3, 1210-1219.	1.1	98

#	ARTICLE	IF	CITATIONS
37	Ancestral Population Genomics: The Coalescent Hidden Markov Model Approach. <i>Genetics</i> , 2009, 183, 259-274.	1.2	96
38	Characterization of the 2'-5'-oligoadenylate synthetase ubiquitin-like family. <i>Nucleic Acids Research</i> , 2003, 31, 3166-3173.	6.5	91
39	Selective single molecule sequencing and assembly of a human Y chromosome of African origin. <i>Nature Communications</i> , 2019, 10, 4.	5.8	90
40	Haplotype Structure of the Stigmatic Self-Incompatibility Gene in Natural Populations of <i>Arabidopsis lyrata</i> . <i>Molecular Biology and Evolution</i> , 2003, 20, 1741-1753.	3.5	89
41	Breaking Free: The Genomics of Allopolyploidy-Facilitated Niche Expansion in White Clover. <i>Plant Cell</i> , 2019, 31, 1466-1487.	3.1	89
42	Evolutionary Dynamics of Sporophytic Self-Incompatibility Alleles in Plants. <i>Genetics</i> , 1997, 147, 835-846.	1.2	84
43	The Number of Self-Incompatibility Alleles in a Finite, Subdivided Population. <i>Genetics</i> , 1998, 149, 1153-1162.	1.2	81
44	MATE AVAILABILITY AND FECUNDITY SELECTION IN MULTI-ALLELIC SELF-INCOMPATIBILITY SYSTEMS IN PLANTS. <i>Evolution; International Journal of Organic Evolution</i> , 1998, 52, 19-29.	1.1	79
45	Extensive X-linked adaptive evolution in central chimpanzees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2054-2059.	3.3	79
46	Estimating Divergence Time and Ancestral Effective Population Size of Bornean and Sumatran Orangutan Subspecies Using a Coalescent Hidden Markov Model. <i>PLoS Genetics</i> , 2011, 7, e1001319.	1.5	79
47	Detecting archaic introgression using an unadmixed outgroup. <i>PLoS Genetics</i> , 2018, 14, e1007641.	1.5	78
48	Relative roles of mutation and recombination in generating allelic polymorphism at an MHC class II locus in <i>Peromyscus maniculatus</i> . <i>Genetical Research</i> , 2003, 82, 89-99.	0.3	75
49	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
50	Expression of Distinct Self-Incompatibility Specificities in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2009, 182, 1313-1321.	1.2	72
51	The nature of Neanderthal introgression revealed by 27,566 Icelandic genomes. <i>Nature</i> , 2020, 582, 78-83.	13.7	71
52	Recombination, Balancing Selection and Phylogenies in MHC and Self-Incompatibility Genes. <i>Genetics</i> , 2001, 159, 1833-1844.	1.2	70
53	Diversity and Linkage of Genes in the Self-Incompatibility Gene Family in <i>Arabidopsis lyrata</i> . <i>Genetics</i> , 2003, 164, 1519-1535.	1.2	67
54	Comparative analysis of protein coding sequences from human, mouse and the domesticated pig. <i>BMC Biology</i> , 2005, 3, 2.	1.7	65

#	ARTICLE	IF	CITATIONS
55	CoaSim: a flexible environment for simulating genetic data under coalescent models. <i>BMC Bioinformatics</i> , 2005, 6, 252.	1.2	64
56	The effect of hitch-hiking on genes linked to a balanced polymorphism in a subdivided population. <i>Genetical Research</i> , 2000, 76, 63-73.	0.3	63
57	Allelic Genealogies in Sporophytic Self-Incompatibility Systems in Plants. <i>Genetics</i> , 1998, 150, 1187-1198.	1.2	60
58	Mate Availability and Fecundity Selection in Multi-Allelic Self- Incompatibility Systems in Plants. <i>Evolution; International Journal of Organic Evolution</i> , 1998, 52, 19.	1.1	59
59	Population-level Studies of Multiallelic Self-incompatibility Loci, with Particular Reference to Brassicaceae. <i>Annals of Botany</i> , 2000, 85, 227-239.	1.4	58
60	Rates and patterns of great ape retrotransposition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13457-13462.	3.3	57
61	Strong Selective Sweeps on the X Chromosome in the Human-Chimpanzee Ancestor Explain Its Low Divergence. <i>PLoS Genetics</i> , 2015, 11, e1005451.	1.5	56
62	Uneven segregation of sporophytic self-incompatibility alleles in <i>Arabidopsis lyrata</i> . <i>Journal of Evolutionary Biology</i> , 2004, 17, 554-561.	0.8	54
63	Nationwide Genomic Study in Denmark Reveals Remarkable Population Homogeneity. <i>Genetics</i> , 2016, 204, 711-722.	1.2	54
64	Lineage Sorting in Apes. <i>Annual Review of Genetics</i> , 2014, 48, 519-535.	3.2	48
65	Molecular Evolution within and between Self-Incompatibility Specificities. <i>Molecular Biology and Evolution</i> , 2010, 27, 11-20.	3.5	47
66	Selection at Work in Self-Incompatible <i>Arabidopsis lyrata</i> : Mating Patterns in a Natural Population. <i>Genetics</i> , 2006, 172, 477-484.	1.2	46
67	Incomplete lineage sorting and phenotypic evolution in marsupials. <i>Cell</i> , 2022, 185, 1646-1660.e18.	13.5	43
68	Transcriptome profiling of fetal Klinefelter testis tissue reveals a possible involvement of long non-coding RNAs in gonocyte maturation. <i>Human Molecular Genetics</i> , 2018, 27, 430-439.	1.4	42
69	Evolutionary and biomedical insights from a marmoset diploid genome assembly. <i>Nature</i> , 2021, 594, 227-233.	13.7	42
70	Analysis of 62 hybrid assembled human Y chromosomes exposes rapid structural changes and high rates of gene conversion. <i>PLoS Genetics</i> , 2017, 13, e1006834.	1.5	42
71	Whole genome association mapping by incompatibilities and local perfect phylogenies. <i>BMC Bioinformatics</i> , 2006, 7, 454.	1.2	41
72	DNA Topoisomerases Maintain Promoters in a State Competent for Transcriptional Activation in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2012, 8, e1003128.	1.5	40

#	ARTICLE	IF	CITATIONS
73	Evidence that the rate of strong selective sweeps increases with population size in the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1613-1618.	3.3	40
74	The Mutationathon highlights the importance of reaching standardization in estimates of pedigree-based germline mutation rates. <i>ELife</i> , 2022, 11, .	2.8	38
75	A fine-scale recombination map of the human-chimpanzee ancestor reveals faster change in humans than in chimpanzees and a strong impact of GC-biased gene conversion. <i>Genome Research</i> , 2014, 24, 467-474.	2.4	37
76	Orthologous genes identified by transcriptome sequencing in the spider genus <i>Stegodyphus</i> . <i>BMC Genomics</i> , 2012, 13, 70.	1.2	34
77	Intrahaplotype Polymorphism at the Brassica S Locus. <i>Genetics</i> , 2001, 159, 811-822.	1.2	34
78	Identifying disease associated genes by network propagation. <i>BMC Systems Biology</i> , 2014, 8, S6.	3.0	33
79	Inference of Purifying and Positive Selection in Three Subspecies of Chimpanzees ( <i>Pan troglodytes</i> ) from Exome Sequencing. <i>Genome Biology and Evolution</i> , 2015, 7, 1122-1132.	1.1	33
80	Transcriptome analysis of the adult human Klinefelter testis and cellularity-matched controls reveals disturbed differentiation of Sertoli- and Leydig cells. <i>Cell Death and Disease</i> , 2018, 9, 586.	2.7	33
81	Dynamic Copy Number Evolution of X- and Y-Linked Ampliconic Genes in Human Populations. <i>Genetics</i> , 2018, 209, 907-920.	1.2	32
82	The Effect of Enzyme Heterozygosity on Growth in a Strictly Outcrossing Species, the Self-Incompatible <i>Arabis Petraea</i> (Brassicaceae). <i>Hereditas</i> , 2004, 128, 21-31.	0.5	31
83	Evidence for Adaptive Introgression of Disease Resistance Genes Among Closely Related <i>Arabidopsis</i> Species. <i>C3: Genes, Genomes, Genetics</i> , 2017, 7, 2677-2683.	0.8	31
84	Symbiosis genes show a unique pattern of introgression and selection within a <i>Rhizobium leguminosarum</i> species complex. <i>Microbial Genomics</i> , 2020, 6, .	1.0	31
85	Extreme genetic signatures of local adaptation during <i>Lotus japonicus</i> colonization of Japan. <i>Nature Communications</i> , 2020, 11, 253.	5.8	30
86	Evidence of recombination among early-vaccination era measles virus strains. <i>BMC Evolutionary Biology</i> , 2005, 5, 52.	3.2	29
87	Genomic consequences of selection on self-incompatibility genes. <i>Current Opinion in Plant Biology</i> , 2008, 11, 116-122.	3.5	29
88	Evaluating genetic causes of azoospermia: What can we learn from a complex cellular structure and single-cell transcriptomics of the human testis?. <i>Human Genetics</i> , 2021, 140, 183-201.	1.8	29
89	Insertion and Deletion Processes in Recent Human History. <i>PLoS ONE</i> , 2010, 5, e8650.	1.1	29
90	Heterogeneity in Regional GC Content and Differential Usage of Codons and Amino Acids in GC-Poor and GC-Rich Regions of the Genome of <i>Apis mellifera</i> . <i>Molecular Biology and Evolution</i> , 2006, 24, 611-619.	3.5	28

#	ARTICLE	IF	CITATIONS
91	Selective Sweeps across Twenty Millions Years of Primate Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 3065-3074.	3.5	28
92	An Effort to Use Human-Based Exome Capture Methods to Analyze Chimpanzee and Macaque Exomes. <i>PLoS ONE</i> , 2012, 7, e40637.	1.1	28
93	Selection at Work in Self-Incompatible <i>Arabidopsis lyrata</i> . II. Spatial Distribution of S Haplotypes in Iceland. <i>Genetics</i> , 2008, 180, 1051-1059.	1.2	27
94	Variation and association to diabetes in 2000 full mtDNA sequences mined from an exome study in a Danish population. <i>European Journal of Human Genetics</i> , 2014, 22, 1040-1045.	1.4	26
95	The germline mutational process in rhesus macaque and its implications for phylogenetic dating. <i>GigaScience</i> , 2021, 10, .	3.3	26
96	Evidence for Faster X Chromosome Evolution in Spiders. <i>Molecular Biology and Evolution</i> , 2019, 36, 1281-1293.	3.5	25
97	<i>PRDM9</i> losses in vertebrates are coupled to those of paralogs <i>ZCWPW1</i> and <i>ZCWPW2</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	24
98	Different historical generation intervals in human populations inferred from Neanderthal fragment lengths and mutation signatures. <i>Nature Communications</i> , 2021, 12, 5317.	5.8	23
99	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
100	Transmission ratio distortion in <i>Arabidopsis lyrata</i> : effects of population divergence and the S-locus. <i>Heredity</i> , 2008, 100, 71-78.	1.2	18
101	Transcriptome analysis of the response of Burmese python to digestion. <i>GigaScience</i> , 2017, 6, 1-18.	3.3	17
102	Recombination in <i>Mycoplasma hominis</i> . <i>Infection, Genetics and Evolution</i> , 2002, 1, 277-285.	1.0	16
103	Haplotype frequencies in a sub-region of chromosome 19q13.3, related to risk and prognosis of cancer, differ dramatically between ethnic groups. <i>BMC Medical Genetics</i> , 2009, 10, 20.	2.1	16
104	The Icelandic Cancer Project – a population-wide approach to studying cancer. <i>Nature Reviews Cancer</i> , 2004, 4, 488-492.	12.8	15
105	Local Phylogeny Mapping of Quantitative Traits: Higher Accuracy and Better Ranking Than Single-Marker Association in Genomewide Scans. <i>Genetics</i> , 2009, 181, 747-753.	1.2	15
106	Assembly and analysis of 100 full MHC haplotypes from the Danish population. <i>Genome Research</i> , 2017, 27, 1597-1607.	2.4	15
107	When gametophytic self-incompatibility meets gynodioecy. <i>Genetical Research</i> , 2008, 90, 27-35.	0.3	14
108	RNA polymerase plays both sides: Vivid and bidirectional transcription around and upstream of active promoters. <i>Cell Cycle</i> , 2009, 8, 1105-1111.	1.3	13

#	ARTICLE	IF	CITATIONS
109	Long-chain n-3 and n-6 polyunsaturated fatty acids and risk of atrial fibrillation: Results from a Danish cohort study. PLoS ONE, 2017, 12, e0190262.	1.1	13
110	The effective size of the Icelandic population and the prospects for LD mapping: inference from unphased microsatellite markers. European Journal of Human Genetics, 2006, 14, 1044-1053.	1.4	11
111	Genetic structure, lack of sex-biased dispersal and behavioral flexibility in the pair-living fat-tailed dwarf lemur, Cheirogaleus medius. Behavioral Ecology and Sociobiology, 2007, 61, 943-954.	0.6	11
112	Integration and reanalysis of transcriptomics and methylomics data derived from blood and testis tissue of men with 47, XXY Klinefelter syndrome indicates the primary involvement of Sertoli cells in the testicular pathogenesis. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2020, 184, 239-255.	0.7	11
113	GeneRecon—a coalescent based tool for fine-scale association mapping. Bioinformatics, 2006, 22, 2317-2318.	1.8	8
114	High-resolution genetic maps of Lotus japonicus and L. burttii based on re-sequencing of recombinant inbred lines. DNA Research, 2016, 23, 487-494.	1.5	8
115	Increased rate of human mutations where DNA and RNA polymerases collide. Trends in Genetics, 2009, 25, 523-527.	2.9	7
116	Population dynamics of GC-changing mutations in humans and great apes. Genetics, 2021, 218, .	1.2	7
117	Recombination Facilitates Adaptive Evolution in Rhizobial Soil Bacteria. Molecular Biology and Evolution, 2021, 38, 5480-5490.	3.5	7
118	Sequence analysis of measles virus strains collected during the pre- and early-vaccination era in Denmark reveals a considerable diversity of ancient strains. Apmis, 2002, 110, 113-122.	0.9	6
119	Small RNAs in Seminal Plasma as Novel Biomarkers for Germ Cell Tumors. Cancers, 2021, 13, 2346.	1.7	6
120	Unraveling recombination rate evolution using ancestral recombination maps. BioEssays, 2014, 36, 892-900.	1.2	5
121	Spitting for Science: Danish High School Students Commit to a Large-Scale Self-Reported Genetic Study. PLoS ONE, 2016, 11, e0161822.	1.1	5
122	Association Mapping and Disease: Evolutionary Perspectives. Methods in Molecular Biology, 2012, 856, 275-291.	0.4	2
123	The last pieces of a puzzling early meeting. Science, 2020, 369, 1565-1566.	6.0	2
124	Synopsis of subcategories and recommended methods. , 1997, , 49-81.		1
125	Studying mutation rate evolution in primates—a need for systematic comparison of computational pipelines. GigaScience, 2021, 10, .	3.3	1
126	Gene Genealogies, Variation and Evolution: A Primer in Coalescent Theory. By Jotun Hein, Mikkel Heide Schierup, and Carsten Wiuf. Oxford and New York: Oxford University Press. \$124.50 (hardcover); \$59.50 (paper). xiii + 276 p; ill.; index. ISBN: 0-19-852995-3 (hc); 0-19-852996-1 (pb). 2005.. Quarterly Review of Biology, 2005, 80, 473-474.	0.0	0



#	ARTICLE	IF	CITATIONS
127	Biological networks and epistasis in genome-wide association studies. Nature Precedings, 2007, , .	0.1	0
128	Genomic relationships and speciation times of human, chimpanzee and gorilla inferred from a coalescent Hidden Markov Model. PLoS Genetics, 2005, preprint, e7.	1.5	0
129	List of methods and their description. , 1997, , 83-194.		0