

# Mikkel Heide Schierup

## List of Publications by Year in Descending Order

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**Version:** 2024-04-27

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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.

132  
papers

10,776  
citations

50  
h-index

103  
g-index

149  
ext. papers

13,276  
ext. citations

10.4  
avg, IF

5.73  
L-index

#	Paper	IF	Citations
132	The mutationathon highlights the importance of reaching standardization in estimates of pedigree-based germline mutation rates.. <i>ELife</i> , <b>2022</b> , 11,	8.9	2
131	losses in vertebrates are coupled to those of paralogs and .. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2022</b> , 119,	11.5	2
130	Incomplete lineage sorting and phenotypic evolution in marsupials.. <i>Cell</i> , <b>2022</b> ,	56.2	5
129	Studying mutation rate evolution in primates-a need for systematic comparison of computational pipelines. <i>GigaScience</i> , <b>2021</b> , 10,	7.6	1
128	Evolutionary and biomedical insights from a marmoset diploid genome assembly. <i>Nature</i> , <b>2021</b> , 594, 227-233	50.4	10
127	The germline mutational process in rhesus macaque and its implications for phylogenetic dating. <i>GigaScience</i> , <b>2021</b> , 10,	7.6	6
126	Small RNAs in Seminal Plasma as Novel Biomarkers for Germ Cell Tumors. <i>Cancers</i> , <b>2021</b> , 13,	6.6	5
125	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> , <b>2021</b> , 140, 183-201	6.3	16
124	Recombination Facilitates Adaptive Evolution in Rhizobial Soil Bacteria. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 5480-5490	8.3	2
123	Different historical generation intervals in human populations inferred from Neanderthal fragment lengths and mutation signatures. <i>Nature Communications</i> , <b>2021</b> , 12, 5317	17.4	4
122	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. <i>American Journal of Medical Genetics, Part C: Seminars in Medical Genetics</i> , <b>2020</b> , 184, 239-255	3.1	4
121	Extreme genetic signatures of local adaptation during <i>Lotus japonicus</i> colonization of Japan. <i>Nature Communications</i> , <b>2020</b> , 11, 253	17.4	14
120	Symbiosis genes show a unique pattern of introgression and selection within a species complex. <i>Microbial Genomics</i> , <b>2020</b> , 6,	4.4	15
119	The last pieces of a puzzling early meeting. <i>Science</i> , <b>2020</b> , 369, 1565-1566	33.3	0
118	The nature of Neanderthal introgression revealed by 27,566 Icelandic genomes. <i>Nature</i> , <b>2020</b> , 582, 78-83	30.4	33
117	Direct estimation of mutations in great apes reconciles phylogenetic dating. <i>Nature Ecology and Evolution</i> , <b>2019</b> , 3, 286-292	12.3	67
116	The comparative genomics and complex population history of baboons. <i>Science Advances</i> , <b>2019</b> , 5, eaau6947	6.47	69

115	Breaking Free: The Genomics of Allopolyploidy-Facilitated Niche Expansion in White Clover. <i>Plant Cell</i> , <b>2019</b> , 31, 1466-1487	11.6	37
114	Evidence for Faster X Chromosome Evolution in Spiders. <i>Molecular Biology and Evolution</i> , <b>2019</b> , 36, 12818-12938	13.9	8
113	Selective single molecule sequencing and assembly of a human Y chromosome of African origin. <i>Nature Communications</i> , <b>2019</b> , 10, 4	17.4	47
112	Transcriptome profiling of fetal Klinefelter testis tissue reveals a possible involvement of long non-coding RNAs in gonocyte maturation. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 430-439	5.6	28
111	Detecting archaic introgression using an unadmixed outgroup. <i>PLoS Genetics</i> , <b>2018</b> , 14, e1007641	6	42
110	Dynamic Copy Number Evolution of X- and Y-Linked Ampliconic Genes in Human Populations. <i>Genetics</i> , <b>2018</b> , 209, 907-920	4	19
109	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> , <b>2018</b> , 9, 586	9.8	17
108	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> , <b>2017</b> , 114, 1613-1618	11.5	32
107	Evidence for Adaptive Introgression of Disease Resistance Genes Among Closely Related Species. <i>G3: Genes, Genomes, Genetics</i> , <b>2017</b> , 7, 2677-2683	3.2	11
106	A high-coverage Neandertal genome from Vindija Cave in Croatia. <i>Science</i> , <b>2017</b> , 358, 655-658	33.3	312
105	Long-chain n-3 and n-6 polyunsaturated fatty acids and risk of atrial fibrillation: Results from a Danish cohort study. <i>PLoS ONE</i> , <b>2017</b> , 12, e0190262	3.7	9
104	Transcriptome analysis of the response of Burmese python to digestion. <i>GigaScience</i> , <b>2017</b> , 6, 1-18	7.6	10
103	Assembly and analysis of 100 full MHC haplotypes from the Danish population. <i>Genome Research</i> , <b>2017</b> , 27, 1597-1607	9.7	10
102	Analysis of 62 hybrid assembled human Y chromosomes exposes rapid structural changes and high rates of gene conversion. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006834	6	23
101	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. <i>Nature</i> , <b>2017</b> , 548, 87-91	50.4	87
100	Demographic History of the Genus Pan Inferred from Whole Mitochondrial Genome Reconstructions. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 2020-30	3.9	18
99	Nationwide Genomic Study in Denmark Reveals Remarkable Population Homogeneity. <i>Genetics</i> , <b>2016</b> , 204, 711-722	4	40
98	A genomic history of Aboriginal Australia. <i>Nature</i> , <b>2016</b> , 538, 207-214	50.4	268

97	Spitting for Science: Danish High School Students Commit to a Large-Scale Self-Reported Genetic Study. <i>PLoS ONE</i> , <b>2016</b> , 11, e0161822	3.7	4
96	High-resolution genetic maps of <i>Lotus japonicus</i> and <i>L. burttii</i> based on re-sequencing of recombinant inbred lines. <i>DNA Research</i> , <b>2016</b> , 23, 487-494	4.5	5
95	Selective Sweeps across Twenty Millions Years of Primate Evolution. <i>Molecular Biology and Evolution</i> , <b>2016</b> , 33, 3065-3074	8.3	18
94	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. <i>Nature Communications</i> , <b>2015</b> , 6, 5969	17.4	119
93	Inference of purifying and positive selection in three subspecies of chimpanzees ( <i>Pan troglodytes</i> ) from exome sequencing. <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 1122-32	3.9	25
92	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , <b>2015</b> , 97, 576-92	11	649
91	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
90	Strong Selective Sweeps on the X Chromosome in the Human-Chimpanzee Ancestor Explain Its Low Divergence. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005451	6	39
89	Spider genomes provide insight into composition and evolution of venom and silk. <i>Nature Communications</i> , <b>2014</b> , 5, 3765	17.4	169
88	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> , <b>2014</b> , 24, 467-74	9.7	27
87	Identifying disease associated genes by network propagation. <i>BMC Systems Biology</i> , <b>2014</b> , 8 Suppl 1, S6	3.5	20
86	Unraveling recombination rate evolution using ancestral recombination maps. <i>BioEssays</i> , <b>2014</b> , 36, 892-900	4	4
85	Lineage sorting in apes. <i>Annual Review of Genetics</i> , <b>2014</b> , 48, 519-35	14.5	26
84	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , <b>2014</b> , 346, 1320-31	33.3	1182
83	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> , <b>2014</b> , 22, 1040-5	5.3	23
82	Rates and patterns of great ape retrotransposition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 13457-62	11.5	46
81	Great ape genetic diversity and population history. <i>Nature</i> , <b>2013</b> , 499, 471-5	50.4	574
80	Evolution and diversity of copy number variation in the great ape lineage. <i>Genome Research</i> , <b>2013</b> , 23, 1373-82	9.7	119

79	SOAPindel: efficient identification of indels from short paired reads. <i>Genome Research</i> , <b>2013</b> , 23, 195-200.	0.7	92
78	Orthologous genes identified by transcriptome sequencing in the spider genus <i>Stegodyphus</i> . <i>BMC Genomics</i> , <b>2012</b> , 13, 70	4.5	31
77	Association mapping and disease: evolutionary perspectives. <i>Methods in Molecular Biology</i> , <b>2012</b> , 856, 275-91	1.4	2
76	DNA Topoisomerases maintain promoters in a state competent for transcriptional activation in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , <b>2012</b> , 8, e1003128	6	29
75	The bonobo genome compared with the chimpanzee and human genomes. <i>Nature</i> , <b>2012</b> , 486, 527-31	50.4	350
74	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , <b>2012</b> , 483, 169-75	50.4	517
73	A new isolation with migration model along complete genomes infers very different divergence processes among closely related great ape species. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1003125	6	83
72	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> , <b>2012</b> , 109, 10954-9	11.5	133
71	Extensive X-linked adaptive evolution in central chimpanzees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 2054-9	11.5	66
70	An effort to use human-based exome capture methods to analyze chimpanzee and macaque exomes. <i>PLoS ONE</i> , <b>2012</b> , 7, e40637	3.7	24
69	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , <b>2011</b> , 469, 529-33	50.4	431
68	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> , <b>2011</b> , 21, 2157-66	9.7	150
67	Incomplete lineage sorting patterns among human, chimpanzee, and orangutan suggest recent orangutan speciation and widespread selection. <i>Genome Research</i> , <b>2011</b> , 21, 349-56	9.7	152
66	Genomic determinants of protein evolution and polymorphism in <i>Arabidopsis</i> . <i>Genome Biology and Evolution</i> , <b>2011</b> , 3, 1210-9	3.9	71
65	Estimating divergence time and ancestral effective population size of Bornean and Sumatran orangutan subspecies using a coalescent hidden Markov model. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1001319	6	69
64	The Coalescent of Bacterial Populations <b>2010</b> , 1-18		4
63	Molecular evolution within and between self-incompatibility specificities. <i>Molecular Biology and Evolution</i> , <b>2010</b> , 27, 11-20	8.3	22
62	Whole-genome and chromosome evolution associated with host adaptation and speciation of the wheat pathogen <i>Mycosphaerella graminicola</i> . <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001189	6	106

61	Insertion and deletion processes in recent human history. <i>PLoS ONE</i> , <b>2010</b> , 5, e8650	3.7	22
60	Ancestral population genomics: the coalescent hidden Markov model approach. <i>Genetics</i> , <b>2009</b> , 183, 259-74	4	80
59	Local phylogeny mapping of quantitative traits: higher accuracy and better ranking than single-marker association in genomewide scans. <i>Genetics</i> , <b>2009</b> , 181, 747-53	4	12
58	Expression of distinct self-incompatibility specificities in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , <b>2009</b> , 182, 1313-21	4.1	39
57	Increased rate of human mutations where DNA and RNA polymerases collide. <i>Trends in Genetics</i> , <b>2009</b> , 25, 523-7	8.5	6
56	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> , <b>2009</b> , 10, 20	2.1	14
55	Using biological networks to search for interacting loci in genome-wide association studies. <i>European Journal of Human Genetics</i> , <b>2009</b> , 17, 1231-40	5.3	117
54	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> , <b>2009</b> , 106, 5246-51	11.5	170
53	RNA polymerase plays both sides: Vivid and bidirectional transcription around and upstream of active promoters. <i>Cell Cycle</i> , <b>2009</b> , 8, 1105-1111	4.7	12
52	Transmission ratio distortion in <i>Arabidopsis lyrata</i> : effects of population divergence and the S-locus. <i>Heredity</i> , <b>2008</b> , 100, 71-8	3.6	13
51	Genomic consequences of selection on self-incompatibility genes. <i>Current Opinion in Plant Biology</i> , <b>2008</b> , 11, 116-22	9.9	26
50	When gametophytic self-incompatibility meets gynodioecy. <i>Genetical Research</i> , <b>2008</b> , 90, 27-35	1.1	12
49	Selection at work in self-incompatible <i>Arabidopsis lyrata</i> . II. Spatial distribution of S haplotypes in Iceland. <i>Genetics</i> , <b>2008</b> , 180, 1051-9	4	23
48	RNA exosome depletion reveals transcription upstream of active human promoters. <i>Science</i> , <b>2008</b> , 322, 1851-4	33.3	584
47	Repeated adaptive introgression at a gene under multiallelic balancing selection. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000168	6	105
46	Genetic structure, lack of sex-biased dispersal and behavioral flexibility in the pair-living fat-tailed dwarf lemur, <i>Cheirogaleus medius</i> . <i>Behavioral Ecology and Sociobiology</i> , <b>2007</b> , 61, 943-954	2.5	10
45	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> , <b>2007</b> , 24, 611-9	8.3	18
44	Genomic relationships and speciation times of human, chimpanzee, and gorilla inferred from a coalescent hidden Markov model. <i>PLoS Genetics</i> , <b>2007</b> , 3, e7	6	235

43	Whole genome association mapping by incompatibilities and local perfect phylogenies. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 454	3.6	31
42	The transition to self-compatibility in <i>Arabidopsis thaliana</i> and evolution within S-haplotypes over 10 Myr. <i>Molecular Biology and Evolution</i> , <b>2006</b> , 23, 1741-50	8.3	119
41	GeneRecon--a coalescent based tool for fine-scale association mapping. <i>Bioinformatics</i> , <b>2006</b> , 22, 2317-87.2		8
40	Selection at work in self-incompatible <i>Arabidopsis lyrata</i> : mating patterns in a natural population. <i>Genetics</i> , <b>2006</b> , 172, 477-84	4	40
39	The effective size of the Icelandic population and the prospects for LD mapping: inference from unphased microsatellite markers. <i>European Journal of Human Genetics</i> , <b>2006</b> , 14, 1044-53	5.3	8
38	Long-term stability and effective population size in North Sea and Baltic Sea cod ( <i>Gadus morhua</i> ). <i>Molecular Ecology</i> , <b>2006</b> , 15, 321-31	5.7	96
37	Microsatellite analyses reveal fine-scale genetic structure in grey mouse lemurs ( <i>Microcebus murinus</i> ). <i>Molecular Ecology</i> , <b>2005</b> , 14, 2363-72	5.7	115
36	CoaSim: a flexible environment for simulating genetic data under coalescent models. <i>BMC Bioinformatics</i> , <b>2005</b> , 6, 252	3.6	57
35	Evidence of recombination among early-vaccination era measles virus strains. <i>BMC Evolutionary Biology</i> , <b>2005</b> , 5, 52	3	28
34	Pigs in sequence space: a 0.66X coverage pig genome survey based on shotgun sequencing. <i>BMC Genomics</i> , <b>2005</b> , 6, 70	4.5	221
33	Comparative analysis of protein coding sequences from human, mouse and the domesticated pig. <i>BMC Biology</i> , <b>2005</b> , 3, 2	7.3	54
32	Uneven segregation of sporophytic self-incompatibility alleles in <i>Arabidopsis lyrata</i> . <i>Journal of Evolutionary Biology</i> , <b>2004</b> , 17, 554-61	2.3	48
31	The Icelandic Cancer Project--a population-wide approach to studying cancer. <i>Nature Reviews Cancer</i> , <b>2004</b> , 4, 488-92	31.3	12
30	The Effect of Enzyme Heterozygosity on Growth in a Strictly Outcrossing Species, the Self-Incompatible <i>Arabis Petraea</i> (Brassicaceae). <i>Hereditas</i> , <b>2004</b> , 128, 21-31	2.4	28
29	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> , <b>2003</b> , 90, 422-31	3.6	79
28	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> , <b>2003</b> , 82, 89-99	1.1	74
27	Haplotype structure of the stigmatic self-incompatibility gene in natural populations of <i>Arabidopsis lyrata</i> . <i>Molecular Biology and Evolution</i> , <b>2003</b> , 20, 1741-53	8.3	69
26	Characterization of the 2U5Uoligoadenylate synthetase ubiquitin-like family. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3166-73	20.1	75



25	Diversity and linkage of genes in the self-incompatibility gene family in <i>Arabidopsis lyrata</i> . <i>Genetics</i> , <b>2003</b> , 164, 1519-35	4	47
24	Sequence analysis of measles virus strains collected during the pre- and early-vaccination era in Denmark reveals a considerable diversity of ancient strains. <i>Apmis</i> , <b>2002</b> , 110, 113-22	3-4	5
23	Recombination in <i>Mycoplasma hominis</i> . <i>Infection, Genetics and Evolution</i> , <b>2002</b> , 1, 277-85	4-5	13
22	Identification and characterization of a polymorphic receptor kinase gene linked to the self-incompatibility locus of <i>Arabidopsis lyrata</i> . <i>Genetics</i> , <b>2001</b> , 158, 387-99	4	104
21	Intrahaplotype polymorphism at the Brassica S locus. <i>Genetics</i> , <b>2001</b> , 159, 811-22	4	31
20	Recombination, balancing selection and phylogenies in MHC and self-incompatibility genes. <i>Genetics</i> , <b>2001</b> , 159, 1833-44	4	56
19	Recombination and the molecular clock. <i>Molecular Biology and Evolution</i> , <b>2000</b> , 17, 1578-9	8.3	95
18	The effect of subdivision on variation at multi-allelic loci under balancing selection. <i>Genetical Research</i> , <b>2000</b> , 76, 51-62	1.1	166
17	The effect of hitch-hiking on genes linked to a balanced polymorphism in a subdivided population. <i>Genetical Research</i> , <b>2000</b> , 76, 63-73	1.1	52
16	Population-level Studies of Multiallelic Self-incompatibility Loci, with Particular Reference to Brassicaceae. <i>Annals of Botany</i> , <b>2000</b> , 85, 227-239	4.1	36
15	Consequences of recombination on traditional phylogenetic analysis. <i>Genetics</i> , <b>2000</b> , 156, 879-91	4	415
14	Mate Availability and Fecundity Selection in Multi-Allelic Self- Incompatibility Systems in Plants. <i>Evolution; International Journal of Organic Evolution</i> , <b>1998</b> , 52, 19	3.8	44
13	MATE AVAILABILITY AND FECUNDITY SELECTION IN MULTI-ALLELIC SELF-INCOMPATIBILITY SYSTEMS IN PLANTS. <i>Evolution; International Journal of Organic Evolution</i> , <b>1998</b> , 52, 19-29	3.8	71
12	The number of self-incompatibility alleles in a finite, subdivided population. <i>Genetics</i> , <b>1998</b> , 149, 1153-62		68
11	Allelic genealogies in sporophytic self-incompatibility systems in plants. <i>Genetics</i> , <b>1998</b> , 150, 1187-98	4	36
10	Evolutionary dynamics of sporophytic self-incompatibility alleles in plants. <i>Genetics</i> , <b>1997</b> , 147, 835-46	4	62
9	Inbreeding depression and outbreeding depression in plants. <i>Heredity</i> , <b>1996</b> , 77, 461-468	3.6	75
8	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores		13



7	The germline mutational process in rhesus macaque and its implications for phylogenetic dating	3
6	Detecting archaic introgression without archaic reference genomes	1
5	Direct estimation of mutations in great apes reveals significant recent human slowdown in the yearly mutation rate	3
4	Selective single molecule sequencing and assembly of a human Y chromosome of African origin	1
3	The genomic architecture of introgression among sibling species of bacteria	4
2	Different historical generation intervals in human populations inferred from Neanderthal fragment lengths and patterns of mutation accumulation	1
1	Inferring the Process of Human-Chimpanzee Speciation	1