

# Karim Gharbi

## List of Publications by Year in descending order

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Version: 2024-02-01

84  
papers

7,629  
citations

61984

43  
h-index

58581

82  
g-index

92  
all docs

92  
docs citations

92  
times ranked

9501  
citing authors

#	ARTICLE	IF	CITATIONS
1	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 2012, 487, 94-98.	27.8	1,086
2	How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use?. <i>Rna</i> , 2016, 22, 839-851.	3.5	622
3	A Microsatellite Linkage Map of Rainbow Trout ( <i>Oncorhynchus mykiss</i> ) Characterized by Large Sex-Specific Differences in Recombination Rates. <i>Genetics</i> , 2000, 155, 1331-1345.	2.9	429
4	Special features of RAD Sequencing data: implications for genotyping. <i>Molecular Ecology</i> , 2013, 22, 3151-3164.	3.9	318
5	The effect of RAD allele dropout on the estimation of genetic variation within and between populations. <i>Molecular Ecology</i> , 2013, 22, 3165-3178.	3.9	259
6	Comparative Genome Analysis of the Primary Sex-Determining Locus in Salmonid Fishes. <i>Genome Research</i> , 2003, 13, 272-280.	5.5	228
7	Development and validation of a high density SNP genotyping array for Atlantic salmon ( <i>Salmo salar</i> ). <i>BMC Genomics</i> , 2014, 15, 90.	2.8	219
8	Genome wide association and genomic prediction for growth traits in juvenile farmed Atlantic salmon using a high density SNP array. <i>BMC Genomics</i> , 2015, 16, 969.	2.8	211
9	Genomic prediction of host resistance to sea lice in farmed Atlantic salmon populations. <i>Genetics Selection Evolution</i> , 2016, 48, 47.	3.0	203
10	Estimation of population allele frequencies from next-generation sequencing data: pool-based versus individual-based genotyping. <i>Molecular Ecology</i> , 2013, 22, 3766-3779.	3.9	195
11	Linkage maps of the Atlantic salmon ( <i>Salmo salar</i> ) genome derived from RAD sequencing. <i>BMC Genomics</i> , 2014, 15, 166.	2.8	151
12	A Linkage Map for Brown Trout ( <i>Salmo trutta</i> ): Chromosome Homeologies and Comparative Genome Organization With Other Salmonid Fish. <i>Genetics</i> , 2006, 172, 2405-2419.	2.9	147
13	Mapping and Validation of the Major Sex-Determining Region in Nile Tilapia ( <i>Oreochromis niloticus</i> L.) Using RAD Sequencing. <i>PLoS ONE</i> , 2013, 8, e68389.	2.5	144
14	Mapping the sex determination locus in the Atlantic halibut ( <i>Hippoglossus hippoglossus</i> ) using RAD sequencing. <i>BMC Genomics</i> , 2013, 14, 566.	2.8	133
15	A genetic linkage map for Arctic char ( <i>Salvelinus alpinus</i> ): evidence for higher recombination rates and segregation distortion in hybrid versus pure strain mapping parents. <i>Genome</i> , 2004, 47, 304-315.	2.0	124
16	A comparative analysis of the rainbow trout genome with 2 other species of fish (Arctic charr and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2005, 48, 1037-1051.	2.0	122
17	Rapid Convergent Evolution in Wild Crickets. <i>Current Biology</i> , 2014, 24, 1369-1374.	3.9	121
18	Characterisation of QTL-linked and genome-wide restriction site-associated DNA (RAD) markers in farmed Atlantic salmon. <i>BMC Genomics</i> , 2012, 13, 244.	2.8	120

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19	Parentage assignment using microsatellites in turbot ( <i>Scophthalmus maximus</i> ) and rainbow trout ( <i>Oncorhynchus mykiss</i> ) hatchery populations. Canadian Journal of Fisheries and Aquatic Sciences, 1998, 55, 715-723.	1.4	118
20	Glucocorticoids promote structural and functional maturation of foetal cardiomyocytes: a role for PGC-1 $\alpha$ . Cell Death and Differentiation, 2015, 22, 1106-1116.	11.2	109
21	Distribution of ancestral proto-Actinopterygian chromosome arms within the genomes of 4R-derivative salmonid fishes (Rainbow trout and Atlantic salmon). BMC Genomics, 2008, 9, 557.	2.8	107
22	A new SNP-based vision of the genetics of sex determination in European sea bass ( <i>Dicentrarchus</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	3.0	103
23	A novel sex-determining QTL in Nile tilapia ( <i>Oreochromis niloticus</i> ). BMC Genomics, 2015, 16, 171.	2.8	102
24	Development of a Medium Density Combined-Species SNP Array for Pacific and European Oysters ( <i>Crassostrea gigas</i> and <i>Ostrea edulis</i> ). G3: Genes, Genomes, Genetics, 2017, 7, 2209-2218.	1.8	97
25	Genotype Imputation To Improve the Cost-Efficiency of Genomic Selection in Farmed Atlantic Salmon. G3: Genes, Genomes, Genetics, 2017, 7, 1377-1383.	1.8	93
26	The Genomic Basis of Color Pattern Polymorphism in the Harlequin Ladybird. Current Biology, 2018, 28, 3296-3302.e7.	3.9	92
27	poRe: an R package for the visualization and analysis of nanopore sequencing data. Bioinformatics, 2015, 31, 114-115.	4.1	85
28	Gene conversion rapidly generates major histocompatibility complex diversity in recently founded bird populations. Molecular Ecology, 2011, 20, 5213-5225.	3.9	84
29	Sturgeon conservation genomics: <i>scp</i> SNP discovery and validation using <i>scp</i> RAD sequencing. Molecular Ecology, 2013, 22, 3112-3123.	3.9	79
30	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. PeerJ, 2021, 9, e10941.	2.0	79
31	Statistical models for RNA-seq data derived from a two-condition 48-replicate experiment. Bioinformatics, 2015, 31, 3625-3630.	4.1	76
32	Quality control of next-generation sequencing data without a reference. Frontiers in Genetics, 2014, 5, 111.	2.3	75
33	Determination of Quantitative Trait Loci (QTL) for Early Maturation in Rainbow Trout ( <i>Oncorhynchus</i> ) Tj ETQq1 1 0,784314 rgBT/Overlock 73	2.4	73
34	Gene mapping in fishes: a means to an end. Genetica, 2001, 111, 3-23.	1.1	71
35	Identification of a Sex-Linked SNP Marker in the Salmon Louse ( <i>Lepeophtheirus salmonis</i> ) Using RAD Sequencing. PLoS ONE, 2013, 8, e77832.	2.5	63
36	Deciphering mollusc shell production: the roles of genetic mechanisms through to ecology, aquaculture and biomimetics. Biological Reviews, 2020, 95, 1812-1837.	10.4	63

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37	The control of sea lice in Atlantic salmon by selective breeding. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150574.	3.4	61
38	Differential gene expression according to race and host plant in the pea aphid. <i>Molecular Ecology</i> , 2016, 25, 4197-4215.	3.9	59
39	Dynamics of Copy Number Variation in Host Races of the Pea Aphid. <i>Molecular Biology and Evolution</i> , 2015, 32, 63-80.	8.9	55
40	Comparative mapping of expressed sequence tags containing microsatellites in rainbow trout ( <i>Oncorhynchus mykiss</i> ). <i>BMC Genomics</i> , 2005, 6, 54.	2.8	54
41	High levels of interspecific gene flow in an endemic cichlid fish adaptive radiation from an extreme lake environment. <i>Molecular Ecology</i> , 2015, 24, 3421-3440.	3.9	53
42	Salmon lice ( <i>Lepeophtheirus salmonis</i> ) showing varying emamectin benzoate susceptibilities differ in neuronal acetylcholine receptor and GABA-gated chloride channel mRNA expression. <i>BMC Genomics</i> , 2013, 14, 408.	2.8	49
43	Characterization of the mantle transcriptome in bivalves: <i>Pecten maximus</i> , <i>Mytilus edulis</i> and <i>Crassostrea gigas</i> . <i>Marine Genomics</i> , 2016, 27, 9-15.	1.1	46
44	Characterization and comparison of microsatellites derived from repeat-enriched libraries and expressed sequence tags. <i>Animal Genetics</i> , 2005, 36, 309-315.	1.7	41
45	The challenges of detecting subtle population structure and its importance for the conservation of emperor penguins. <i>Molecular Ecology</i> , 2017, 26, 3883-3897.	3.9	41
46	Reference-free SNP discovery for the Eurasian beaver from restriction site-associated DNA paired-end data. <i>Molecular Ecology</i> , 2013, 22, 3141-3150.	3.9	40
47	Detailed insights into pan-European population structure and inbreeding in wild and hatchery Pacific oysters ( <i>Crassostrea gigas</i> ) revealed by genome-wide SNP data. <i>Evolutionary Applications</i> , 2019, 12, 519-534.	3.1	39
48	Norwich COVID-19 testing initiative pilot: evaluating the feasibility of asymptomatic testing on a university campus. <i>Journal of Public Health</i> , 2021, 43, 82-88.	1.8	37
49	Field cricket genome reveals the footprint of recent, abrupt adaptation in the wild. <i>Evolution Letters</i> , 2020, 4, 19-33.	3.3	32
50	Juxtaposed microsatellite systems as diagnostic markers for admixture: an empirical evaluation with brown trout ( <i>Salmo trutta</i> ) as model organism. <i>Molecular Ecology</i> , 2000, 9, 1873-1886.	3.9	30
51	Genetic dissection of MHC-associated susceptibility to <i>Lepeophtheirus salmonis</i> in Atlantic salmon. <i>BMC Genetics</i> , 2009, 10, 20.	2.7	30
52	Dispersal in the sub-Antarctic: king penguins show remarkably little population genetic differentiation across their range. <i>BMC Evolutionary Biology</i> , 2016, 16, 211.	3.2	30
53	The Laboratory Domestication of Zebrafish: From Diverse Populations to Inbred Substrains. <i>Molecular Biology and Evolution</i> , 2020, 37, 1056-1069.	8.9	30
54	RAD mapping reveals an evolving, polymorphic and fuzzy boundary of a plant pseudoautosomal region. <i>Molecular Ecology</i> , 2016, 25, 414-430.	3.9	29

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55	Characterization of Na, K-ATPase genes in Atlantic salmon ( <i>Salmo salar</i> ) and comparative genomic organization with rainbow trout ( <i>Oncorhynchus mykiss</i> ). <i>Molecular Genetics and Genomics</i> , 2005, 273, 474-483.	2.1	28
56	A simple and robust real-time qPCR method for the detection of PIK3CA mutations. <i>Scientific Reports</i> , 2018, 8, 4290.	3.3	28
57	Targeted resequencing confirms the importance of chemosensory genes in aphid host race differentiation. <i>Molecular Ecology</i> , 2017, 26, 43-58.	3.9	27
58	Benefits and pitfalls of captive conservation genetic management: Evaluating diversity in scimitar-horned oryx to support reintroduction planning. <i>Biological Conservation</i> , 2020, 241, 108244.	4.1	27
59	Maternal inheritance of deltamethrin resistance in the salmon louse <i>Lepeophtheirus salmonis</i> (KrÅyer) is associated with unique mtDNA haplotypes. <i>PLoS ONE</i> , 2017, 12, e0180625.	2.5	27
60	Inter and Intraspecific Genomic Divergence in <i>Drosophila montana</i> Shows Evidence for Cold Adaptation. <i>Genome Biology and Evolution</i> , 2018, 10, 2086-2101.	2.5	25
61	Deciphering the demographic history of allochronic differentiation in the pine processionary moth <i>Thaumetopoea pityocampa</i> . <i>Molecular Ecology</i> , 2018, 27, 264-278.	3.9	22
62	The CCAP KnowledgeBase: linking protistan and cyanobacterial biological resources with taxonomic and molecular data. <i>Systematics and Biodiversity</i> , 2013, 11, 407-413.	1.2	20
63	Na <sup>+</sup> /K <sup>+</sup> /2Cl <sup>-</sup> cotransporter and CFTR gill expression after seawater transfer in smolts (0+) of different Atlantic salmon ( <i>Salmo salar</i> ) families. <i>Aquaculture</i> , 2007, 272, 625-635.	3.5	19
64	Maintaining their genetic distance: Little evidence for introgression between widely hybridizing species of <i>Geum</i> with contrasting mating systems. <i>Molecular Ecology</i> , 2018, 27, 1214-1228.	3.9	19
65	A Survey of the ATP-Binding Cassette (ABC) Gene Superfamily in the Salmon Louse ( <i>Lepeophtheirus</i> )	2.5	19
66	MolluscDB: a genome and transcriptome database for molluscs. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2021, 376, 20200157.	4.0	17
67	Evidence of Gene Conversion Events Between Paralogous Sequences Produced by Tetraploidization in Salmoninae Fish. <i>Journal of Molecular Evolution</i> , 2002, 54, 501-510.	1.8	16
68	Linkage arrangement of Na,K-ATPase genes in the tetraploid-derived genome of the rainbow trout ( <i>Oncorhynchus mykiss</i> ). <i>Animal Genetics</i> , 2004, 35, 321-325.	1.7	16
69	Significant Synteny and Colocalization of Ecologically Relevant Quantitative Trait Loci Within and Across Species of Salmonid Fishes. <i>Genetics</i> , 2017, 207, 741-754.	2.9	15
70	Assessing genotype-phenotype associations in three dorsal colour morphs in the meadow spittlebug <i>Philaenus spumarius</i> (L.) (Hemiptera: Aphrophoridae) using genomic and transcriptomic resources. <i>BMC Genetics</i> , 2016, 17, 144.	2.7	14
71	Microsatellites Cross-Species Amplification across Some African Cichlids. <i>International Journal of Evolutionary Biology</i> , 2012, 2012, 1-7.	1.0	11
72	11 $\beta$ -hydroxysteroid dehydrogenase-1 deficiency alters the gut microbiome response to Western diet. <i>Journal of Endocrinology</i> , 2017, 232, 273-283.	2.6	11

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73	Long read sequencing reveals novel isoforms and insights into splicing regulation during cell state changes. BMC Genomics, 2022, 23, 42.	2.8	11
74	Preliminary insights into the genetics of bank vole tolerance to Puumala hantavirus in Sweden. Ecology and Evolution, 2018, 8, 11273-11292.	1.9	9
75	Characterization of transferrin-linked microsatellites in brown trout ( <i>Salmo trutta</i> ) and Atlantic salmon ( <i>Salmo salar</i> ). Molecular Ecology Notes, 2006, 6, 547-549.	1.7	8
76	Development and validation of a mixed-tissue oligonucleotide DNA microarray for Atlantic bluefin tuna, <i>Thunnus thynnus</i> (Linnaeus, 1758). BMC Genomics, 2015, 16, 1007.	2.8	8
77	Transcriptome analyses of <i>Anguillicola crassus</i> from native and novel hosts. PeerJ, 2014, 2, e684.	2.0	7
78	Genome organization of glutamine synthetase genes in rainbow trout & (Oncorhynchus Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 54	1.1	6
79	Genome Sequence of <i>Stenotrophomonas maltophilia</i> PML168, Which Displays Baeyer-Villiger Monooxygenase Activity. Journal of Bacteriology, 2012, 194, 4753-4754.	2.2	6
80	A first genetic map in the genus <i>Streptocarpus</i> generated with RAD sequencing based SNP markers. South African Journal of Botany, 2018, 117, 158-168.	2.5	6
81	A newly developed genetic sex marker and its application to understanding chemically induced feminisation in roach ( <i>Rutilus rutilus</i> ). Molecular Ecology Resources, 2020, 20, 1007-1022.	4.8	6
82	Analysis of the Meiotic Segregation in Intergeneric Hybrids of Tilapias. International Journal of Evolutionary Biology, 2012, 2012, 1-10.	1.0	5
83	Identifying the larva of the fan mussel, <i>Atrina fragilis</i> (Pennant, 1777) (Pinnidae). Journal of Molluscan Studies, 2018, 84, 247-258.	1.2	2
84	Phase 2 of the Norwich COVID-19 testing initiative: an evaluation. Journal of Public Health, 2021, . .	1.8	1