

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	Long read sequencing reveals novel isoforms and insights into splicing regulation during cell state changes. BMC Genomics, 2022, 23, 42.	2.8	11
2	Phase 2 of the Norwich COVID-19 testing initiative: an evaluation. Journal of Public Health, 2021, , .	1.8	1
3	MolluscDB: a genome and transcriptome database for molluscs. Philosophical Transactions of the Royal Society B: Biological Sciences, 2021, 376, 20200157.	4.0	17
4	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. PeerJ, 2021, 9, e10941.	2.0	79
5	Norwich COVID-19 testing initiative pilot: evaluating the feasibility of asymptomatic testing on a university campus. Journal of Public Health, 2021, 43, 82-88.	1.8	37
6	Benefits and pitfalls of captive conservation genetic management: Evaluating diversity in scimitar-horned oryx to support reintroduction planning. Biological Conservation, 2020, 241, 108244.	4.1	27
7	The Laboratory Domestication of Zebrafish: From Diverse Populations to Inbred Substrains. Molecular Biology and Evolution, 2020, 37, 1056-1069.	8.9	30
8	Deciphering mollusc shell production: the roles of genetic mechanisms through to ecology, aquaculture and biomimetics. Biological Reviews, 2020, 95, 1812-1837.	10.4	63
9	Field cricket genome reveals the footprint of recent, abrupt adaptation in the wild. Evolution Letters, 2020, 4, 19-33.	3.3	32
10	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
11	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. Evolutionary Applications, 2019, 12, 519-534.	3.1	39
12	A simple and robust real-time qPCR method for the detection of PIK3CA mutations. Scientific Reports, 2018, 8, 4290.	3.3	28
13	Deciphering the demographic history of allochronic differentiation in the pine processionary moth <i>Thaumetopoea pityocampa</i> . Molecular Ecology, 2018, 27, 264-278.	3.9	22
14	Maintaining their genetic distance: Little evidence for introgression between widely hybridizing species of <i>Geum</i> with contrasting mating systems. Molecular Ecology, 2018, 27, 1214-1228.	3.9	19
15	Preliminary insights into the genetics of bank vole tolerance to Puumala hantavirus in Sweden. Ecology and Evolution, 2018, 8, 11273-11292.	1.9	9
16	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
17	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
18	Inter and Intraspecific Genomic Divergence in <i>Drosophila montana</i> Shows Evidence for Cold Adaptation. Genome Biology and Evolution, 2018, 10, 2086-2101.	2.5	25

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19	The Genomic Basis of Color Pattern Polymorphism in the Harlequin Ladybird. <i>Current Biology</i> , 2018, 28, 3296-3302.e7.	3.9	92
20	Genotype Imputation To Improve the Cost-Efficiency of Genomic Selection in Farmed Atlantic Salmon. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1377-1383.	1.8	93
21	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
22	11 β -hydroxysteroid dehydrogenase-1 deficiency alters the gut microbiome response to Western diet. <i>Journal of Endocrinology</i> , 2017, 232, 273-283.	2.6	11
23	Development of a Medium Density Combined-Species SNP Array for Pacific and European Oysters (<i>Crassostrea gigas</i> and <i>Ostrea edulis</i>). <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2209-2218.	1.8	97
24	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
25	Targeted resequencing confirms the importance of chemosensory genes in aphid host race differentiation. <i>Molecular Ecology</i> , 2017, 26, 43-58.	3.9	27
26	Maternal inheritance of deltamethrin resistance in the salmon louse <i>Lepeophtheirus salmonis</i> (Kr�yer) is associated with unique mtDNA haplotypes. <i>PLoS ONE</i> , 2017, 12, e0180625.	2.5	27
27	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
28	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
29	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
30	Differential gene expression according to race and host plant in the pea aphid. <i>Molecular Ecology</i> , 2016, 25, 4197-4215.	3.9	59
31	Genomic prediction of host resistance to sea lice in farmed Atlantic salmon populations. <i>Genetics Selection Evolution</i> , 2016, 48, 47.	3.0	203
32	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
33	<sc>RAD</sc> mapping reveals an evolving, polymorphic and fuzzy boundary of a plant pseudoautosomal region. <i>Molecular Ecology</i> , 2016, 25, 414-430.	3.9	29
34	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
35	A new SNP-based vision of the genetics of sex determination in European sea bass (<i>Dicentrarchus</i>) Tj ETQq1 1 0.784314 rgBT /Overlook	3.0	103
36	Development and validation of a mixed-tissue oligonucleotide DNA microarray for Atlantic bluefin tuna, <i>Thunnus thynnus</i> (Linnaeus, 1758). <i>BMC Genomics</i> , 2015, 16, 1007.	2.8	8

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37	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
38	poRe: an R package for the visualization and analysis of nanopore sequencing data. <i>Bioinformatics</i> , 2015, 31, 114-115.	4.1	85
39	Statistical models for RNA-seq data derived from a two-condition 48-replicate experiment. <i>Bioinformatics</i> , 2015, 31, 3625-3630.	4.1	76
40	Glucocorticoids promote structural and functional maturation of foetal cardiomyocytes: a role for PGC-1 α . <i>Cell Death and Differentiation</i> , 2015, 22, 1106-1116.	11.2	109
41	A novel sex-determining QTL in Nile tilapia (<i>Oreochromis niloticus</i>). <i>BMC Genomics</i> , 2015, 16, 171.	2.8	102
42	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
43	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
44	A Survey of the ATP-Binding Cassette (ABC) Gene Superfamily in the Salmon Louse (<i>Lepeophtheirus</i>) Tj ETQq 0 0 rgBT /Overlock 10 Tf 5	2.5	19
45	Quality control of next-generation sequencing data without a reference. <i>Frontiers in Genetics</i> , 2014, 5, 111.	2.3	75
46	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
47	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
48	Rapid Convergent Evolution in Wild Crickets. <i>Current Biology</i> , 2014, 24, 1369-1374.	3.9	121
49	Transcriptome analyses of <i>Anguillicola crassus</i> from native and novel hosts. <i>PeerJ</i> , 2014, 2, e684.	2.0	7
50	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
51	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
52	Sturgeon conservation genomics: SNP discovery and validation using RAD sequencing. <i>Molecular Ecology</i> , 2013, 22, 3112-3123.	3.9	79
53	Estimation of population allele frequencies from next-generation sequencing data: pool versus individual-based genotyping. <i>Molecular Ecology</i> , 2013, 22, 3766-3779.	3.9	195
54	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

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55	Special features of RAD Sequencing data: implications for genotyping. <i>Molecular Ecology</i> , 2013, 22, 3151-3164.	3.9	318
56	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
57	Identification of a Sex-Linked SNP Marker in the Salmon Louse (<i>Lepeophtheirus salmonis</i>) Using RAD Sequencing. <i>PLoS ONE</i> , 2013, 8, e77832.	2.5	63
58	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
59	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
60	Genome Sequence of <i>Stenotrophomonas maltophilia</i> PML168, Which Displays Baeyer-Villiger Monooxygenase Activity. <i>Journal of Bacteriology</i> , 2012, 194, 4753-4754.	2.2	6
61	Microsatellites Cross-Species Amplification across Some African Cichlids. <i>International Journal of Evolutionary Biology</i> , 2012, 2012, 1-7.	1.0	11
62	Analysis of the Meiotic Segregation in Intergeneric Hybrids of Tilapias. <i>International Journal of Evolutionary Biology</i> , 2012, 2012, 1-10.	1.0	5
63	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
64	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 2012, 487, 94-98.	27.8	1,086
65	Gene conversion rapidly generates major histocompatibility complex diversity in recently founded bird populations. <i>Molecular Ecology</i> , 2011, 20, 5213-5225.	3.9	84
66	Genetic dissection of MHC-associated susceptibility to <i>Lepeophtheirus salmonis</i> in Atlantic salmon. <i>BMC Genetics</i> , 2009, 10, 20.	2.7	30
67	Determination of Quantitative Trait Loci (QTL) for Early Maturation in Rainbow Trout (<i>Oncorhynchus</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 100	2.4	73
68	Distribution of ancestral proto-Actinopterygian chromosome arms within the genomes of 4R-derivative salmonid fishes (Rainbow trout and Atlantic salmon). <i>BMC Genomics</i> , 2008, 9, 557.	2.8	107
69	Genome organization of glutamine synthetase genes in rainbow trout & (Oncorhynchus) Tj ETQq1 1 0.784314 rgBT / Overlock 100	1.1	6
70	Na ⁺ /K ⁺ /2Cl ⁻ 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
71	Characterization of transferrin-linked microsatellites in brown trout (<i>Salmo trutta</i>) and Atlantic salmon (<i>Salmo salar</i>). <i>Molecular Ecology Notes</i> , 2006, 6, 547-549.	1.7	8
72	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

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73	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
74	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
75	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
76	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
77	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
78	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
79	Comparative Genome Analysis of the Primary Sex-Determining Locus in Salmonid Fishes. <i>Genome Research</i> , 2003, 13, 272-280.	5.5	228
80	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
81	Gene mapping in fishes: a means to an end. <i>Genetica</i> , 2001, 111, 3-23.	1.1	71
82	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
83	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
84	Parentage assignment using microsatellites in turbot (<i>Scophthalmus maximus</i>) and rainbow trout (<i>Oncorhynchus mykiss</i>) hatchery populations. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 1998, 55, 715-723.	1.4	118