

# Cristian Gallardo-Escárate

## List of Publications by Year in descending order

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165  
papers

3,049  
citations

159525

30  
h-index

254106

43  
g-index

172  
all docs

172  
docs citations

172  
times ranked

3354  
citing authors

#	ARTICLE	IF	CITATIONS
1	Single and repetitive microplastics exposures induce immune system modulation and homeostasis alteration in the edible mussel <i>Mytilus galloprovincialis</i> . <i>Fish and Shellfish Immunology</i> , 2018, 83, 52-60.	1.6	115
2	Functional Annotation of All Salmonid Genomes (FAASG): an international initiative supporting future salmonid research, conservation and aquaculture. <i>BMC Genomics</i> , 2017, 18, 484.	1.2	99
3	High-throughput transcriptome analysis of ISAV-infected Atlantic salmon <i>Salmo salar</i> unravels divergent immune responses associated to head-kidney, liver and gills tissues. <i>Fish and Shellfish Immunology</i> , 2015, 45, 367-377.	1.6	73
4	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 April 2010 – 31 May 2010. <i>Molecular Ecology Resources</i> , 2010, 10, 1098-1105.	2.2	71
5	Influences of thermal environment on fish growth. <i>Ecology and Evolution</i> , 2017, 7, 6814-6825.	0.8	69
6	RNA-Seq Analysis Using De Novo Transcriptome Assembly as a Reference for the Salmon Louse <i>Caligus rogercresseyi</i> . <i>PLoS ONE</i> , 2014, 9, e92239.	1.1	67
7	Polyethylene microbeads induce transcriptional responses with tissue-dependent patterns in the mussel <i>Mytilus galloprovincialis</i> . <i>Journal of Molluscan Studies</i> , 2017, 83, 220-225.	0.4	65
8	Novel insights into the response of Atlantic salmon ( <i>Salmo salar</i> ) to <i>Piscirickettsia salmonis</i> : Interplay of coding genes and lncRNAs during bacterial infection. <i>Fish and Shellfish Immunology</i> , 2016, 59, 427-438.	1.6	61
9	Long noncoding RNAs (lncRNAs) dynamics evidence immunomodulation during ISAV-Infected Atlantic salmon ( <i>Salmo salar</i> ). <i>Scientific Reports</i> , 2016, 6, 22698.	1.6	55
10	Authentication of commercialized crab-meat in Chile using DNA Barcoding. <i>Food Control</i> , 2012, 25, 239-244.	2.8	53
11	Dual RNA-Seq Uncovers Metabolic Amino Acids Dependency of the Intracellular Bacterium <i>Piscirickettsia salmonis</i> Infecting Atlantic Salmon. <i>Frontiers in Microbiology</i> , 2018, 9, 2877.	1.5	53
12	Intraspecies and interspecies hybrids in <i>Haliotis</i> : natural and experimental evidence and its impact on abalone aquaculture. <i>Reviews in Aquaculture</i> , 2011, 3, 74-99.	4.6	52
13	Microbiome dynamic modulation through functional diets based on pre- and probiotics (mannan-oligosaccharides and <i>Saccharomyces cerevisiae</i> ) in juvenile rainbow trout ( <i>Oncorhynchus mykiss</i> ). <i>Journal of Applied Microbiology</i> , 2017, 122, 1333-1347.	1.4	52
14	Metagenomic study of bacterial microbiota in persistent endodontic infections using Next-generation sequencing. <i>International Endodontic Journal</i> , 2018, 51, 1336-1348.	2.3	51
15	In the shadow: The emerging role of long non-coding RNAs in the immune response of Atlantic salmon. <i>Developmental and Comparative Immunology</i> , 2017, 73, 193-205.	1.0	49
16	Insulin-like growth factor-1 suppresses the Myostatin signaling pathway during myogenic differentiation. <i>Biochemical and Biophysical Research Communications</i> , 2015, 464, 596-602.	1.0	48
17	Comparative immunity of <i>Salmo salar</i> and <i>Oncorhynchus kisutch</i> during infestation with the sea louse <i>Caligus rogercresseyi</i> : An enrichment transcriptome analysis. <i>Fish and Shellfish Immunology</i> , 2016, 59, 276-287.	1.6	45
18	Molecular characterization and gene expression of ferritin in red abalone ( <i>Haliotis rufescens</i> ). <i>Fish and Shellfish Immunology</i> , 2011, 30, 430-433.	1.6	44

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19	Comparative analysis of long non-coding RNAs in Atlantic and Coho salmon reveals divergent transcriptome responses associated with immunity and tissue repair during sea lice infestation. <i>Developmental and Comparative Immunology</i> , 2018, 87, 36-50.	1.0	40
20	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 December 2010â€“31 January 2011. <i>Molecular Ecology Resources</i> , 2011, 11, 586-589.	2.2	38
21	Comparative modulation of lncRNAs in wild-type and rag1-heterozygous mutant zebrafish exposed to immune challenge with spring viraemia of carp virus (SVCV). <i>Scientific Reports</i> , 2019, 9, 14174.	1.6	36
22	Transcriptome immunomodulation of in-feed additives in Atlantic salmon <i>Salmo salar</i> infested with sea lice <i>Caligus rogercresseyi</i> . <i>Fish and Shellfish Immunology</i> , 2015, 47, 450-460.	1.6	35
23	Uncovering the Complex Transcriptome Response of <i>Mytilus chilensis</i> against Saxitoxin: Implications of Harmful Algal Blooms on Mussel Populations. <i>PLoS ONE</i> , 2016, 11, e0165231.	1.1	35
24	High individual variability in the transcriptomic response of Mediterranean mussels to <i>Vibrio</i> reveals the involvement of myticins in tissue injury. <i>Scientific Reports</i> , 2019, 9, 3569.	1.6	34
25	MicroRNA-based transcriptomic responses of Atlantic salmon during infection by the intracellular bacterium <i>Piscirickettsia salmonis</i> . <i>Developmental and Comparative Immunology</i> , 2017, 77, 287-296.	1.0	33
26	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 August 2011â€“30 September 2011. <i>Molecular Ecology Resources</i> , 2012, 12, 185-189.	2.2	32
27	Discovery of sex-related genes through high-throughput transcriptome sequencing from the salmon louse <i>Caligus rogercresseyi</i> . <i>Marine Genomics</i> , 2014, 15, 85-93.	0.4	32
28	Ocean acidification and pathogen exposure modulate the immune response of the edible mussel <i>Mytilus chilensis</i> . <i>Fish and Shellfish Immunology</i> , 2017, 70, 149-155.	1.6	32
29	Iron metabolism modulation in Atlantic salmon infested with the sea lice <i>Lepeophtheirus salmonis</i> and <i>Caligus rogercresseyi</i> : A matter of nutritional immunity?. <i>Fish and Shellfish Immunology</i> , 2017, 60, 97-102.	1.6	32
30	The race between host and sea lice in the Chilean salmon farming: a genomic approach. <i>Reviews in Aquaculture</i> , 2019, 11, 325-339.	4.6	31
31	Transcriptional responses of <i>Mytilus chilensis</i> exposed in vivo to saxitoxin (STX). <i>Journal of Molluscan Studies</i> , 2013, 79, 323-331.	0.4	30
32	Immune response of apoptosis-related cysteine peptidases from the red abalone <i>Haliotis rufescens</i> (HrCas8 and HrCas3): Molecular characterization and transcription expression. <i>Fish and Shellfish Immunology</i> , 2014, 39, 90-98.	1.6	30
33	Saxitoxin Modulates Immunological Parameters and Gene Transcription in <i>Mytilus chilensis</i> Hemocytes. <i>International Journal of Molecular Sciences</i> , 2015, 16, 15235-15250.	1.8	30
34	mRNA-seq reveals skeletal muscle atrophy in response to handling stress in a marine teleost, the red cusk-eel ( <i>Genypterus chilensis</i> ). <i>BMC Genomics</i> , 2015, 16, 1024.	1.2	29
35	Uncovering iron regulation with species-specific transcriptome patterns in Atlantic and coho salmon during a <i>Caligus rogercresseyi</i> infestation. <i>Journal of Fish Diseases</i> , 2017, 40, 1169-1184.	0.9	29
36	Functional Diets Modulate lncRNA-Coding RNAs and Gene Interactions in the Intestine of Rainbow Trout <i>Oncorhynchus mykiss</i> . <i>Marine Biotechnology</i> , 2017, 19, 287-300.	1.1	29

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37	TLR and IMD signaling pathways from <i>Caligus rogercresseyi</i> (Crustacea: Copepoda): In silico gene expression and SNPs discovery. <i>Fish and Shellfish Immunology</i> , 2014, 36, 428-434.	1.6	28
38	A galectin with quadruple-domain from red abalone <i>Haliotis rufescens</i> involved in the immune innate response against to <i>Vibrio anguillarum</i> . <i>Fish and Shellfish Immunology</i> , 2014, 40, 1-8.	1.6	25
39	Modulation of Atlantic salmon miRNome response to sea louse infestation. <i>Developmental and Comparative Immunology</i> , 2017, 76, 380-391.	1.0	25
40	Gene expression analysis in <i>Mytilus chilensis</i> populations reveals local patterns associated with ocean environmental conditions. <i>Journal of Experimental Marine Biology and Ecology</i> , 2012, 420-421, 56-64.	0.7	24
41	Nanopore sequencing of microbial communities reveals the potential role of sea lice as a reservoir for fish pathogens. <i>Scientific Reports</i> , 2020, 10, 2895.	1.6	24
42	The wastewater microbiome: A novel insight for COVID-19 surveillance. <i>Science of the Total Environment</i> , 2021, 764, 142867.	3.9	24
43	Characterization of the growth-related transcriptome in California red abalone ( <i>Haliotis rufescens</i> ) through RNA-Seq analysis. <i>Marine Genomics</i> , 2015, 24, 199-202.	0.4	23
44	Transcriptome analysis in <i>Concholepas concholepas</i> (Gastropoda, Muricidae): Mining and characterization of new genomic and molecular markers. <i>Marine Genomics</i> , 2011, 4, 197-205.	0.4	22
45	Characterization of the transcriptomes of <i>Haliotis rufescens</i> reproductive tissues. <i>Aquaculture Research</i> , 2014, 45, 1026-1040.	0.9	22
46	Deltamethrin (AlphaMax <sup>®</sup> , <sup>®</sup> ) reveals modulation of genes related to oxidative stress in the ectoparasite <i>Caligus rogercresseyi</i> : Implications on delousing drug effectiveness. <i>Aquaculture</i> , 2014, 433, 421-429.	1.7	22
47	Molecular cloning and expression of IRAK-4, IL-17 and I $\kappa$ B genes in <i>Haliotis rufescens</i> challenged with <i>Vibrio anguillarum</i> . <i>Fish and Shellfish Immunology</i> , 2014, 36, 503-509.	1.6	22
48	Intestinal transcriptome modulation by functional diets in rainbow trout: A high-throughput sequencing appraisal to highlight GALT immunomodulation. <i>Fish and Shellfish Immunology</i> , 2017, 64, 325-338.	1.6	22
49	Insights into the olfactory system of the ectoparasite <i>Caligus rogercresseyi</i> : Molecular characterization and gene transcription analysis of novel ionotropic receptors. <i>Experimental Parasitology</i> , 2014, 145, 99-109.	0.5	21
50	Identification of microRNAs associated with sexual maturity in rainbow trout brain and testis through small RNA deep sequencing. <i>Molecular Reproduction and Development</i> , 2015, 82, 651-662.	1.0	21
51	Fluorescence in situ hybridization of rDNA, telomeric (TTAGGG) <sub>n</sub> and (GATA) <sub>n</sub> repeats in the red abalone <i>Haliotis rufescens</i> (Archaeogastropoda: Haliotidae). <i>Hereditas</i> , 2006, 142, 73-79.	0.5	20
52	Identification of immune-related SNPs in the transcriptome of <i>Mytilus chilensis</i> through high-throughput sequencing. <i>Fish and Shellfish Immunology</i> , 2013, 35, 1899-1905.	1.6	20
53	Molecular characterization of two kazal-type serine proteinase inhibitor genes in the surf clam <i>Mesodesma donacium</i> exposed to <i>Vibrio anguillarum</i> . <i>Fish and Shellfish Immunology</i> , 2013, 34, 1448-1454.	1.6	20
54	Transcription expression of immune-related genes from <i>Caligus rogercresseyi</i> evidences host-dependent patterns on Atlantic and coho salmon. <i>Fish and Shellfish Immunology</i> , 2015, 47, 725-731.	1.6	20

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55	Relationship between DAPI-fluorescence fading and nuclear DNA content: An alternative method to DNA quantification?. <i>Biological Research</i> , 2007, 40, 29-40.	1.5	19
56	Transcriptomic insights on the ABC transporter gene family in the salmon louse <i>Caligus rogercresseyi</i> . <i>Parasites and Vectors</i> , 2015, 8, 209.	1.0	19
57	KARYOTYPE COMPOSITION IN THREE CALIFORNIA ABALONES AND THEIR RELATIONSHIP WITH GENOME SIZE. <i>Journal of Shellfish Research</i> , 2007, 26, 825-832.	0.3	18
58	RNA-seq analysis evidences multiple gene responses in <i>Caligus rogercresseyi</i> exposed to the anti-salmon lice drug azamethiphos. <i>Aquaculture</i> , 2015, 446, 156-166.	1.7	18
59	Whole-Genome Transcript Expression Profiling Reveals Novel Insights into Transposon Genes and Non-Coding RNAs during Atlantic Salmon Seawater Adaptation. <i>Biology</i> , 2022, 11, 1.	1.3	18
60	<i>Concholepas concholepas</i> Ferritin H-like subunit (CcFer): Molecular characterization and single nucleotide polymorphism associated to innate immune response. <i>Fish and Shellfish Immunology</i> , 2013, 35, 910-917.	1.6	17
61	Next-Generation Transcriptome Profiling of the Salmon Louse <i>Caligus rogercresseyi</i> Exposed to Deltamethrin (AlphaMaxâ,ç): Discovery of Relevant Genes and Sex-Related Differences. <i>Marine Biotechnology</i> , 2015, 17, 793-810.	1.1	17
62	<i>Caligus rogercresseyi</i> infestation is associated with <i>Piscirickettsia salmonis</i> -attributed mortalities in farmed salmonids in Chile. <i>Preventive Veterinary Medicine</i> , 2019, 171, 104771.	0.7	17
63	Chromosome-scale genome assembly of the sea louse <i>Caligus rogercresseyi</i> by SMRT sequencing and Hi-C analysis. <i>Scientific Data</i> , 2021, 8, 60.	2.4	17
64	Transcriptomic analysis of the hepatic response to stress in the red cusk-eel ( <i>Genypterus chilensis</i> ): Insights into lipid metabolism, oxidative stress and liver steatosis. <i>PLoS ONE</i> , 2017, 12, e0176447.	1.1	17
65	MicroRNA biogenesis pathway from the salmon louse ( <i>Caligus rogercresseyi</i> ): Emerging role in delousing drug response. <i>Gene</i> , 2015, 555, 231-241.	1.0	16
66	Lineage divergence, local adaptation across a biogeographic break, and artificial transport, shape the genetic structure in the ascidian <i>Pyura chilensis</i> . <i>Scientific Reports</i> , 2017, 7, 44559.	1.6	16
67	Inducedâ€œiron overdose modulate the immune response in Atlantic salmon increasing the susceptibility to <i>Piscirickettsia salmonis</i> infection. <i>Aquaculture</i> , 2020, 521, 735058.	1.7	16
68	SNP discovery and High Resolution Melting Analysis from massive transcriptome sequencing in the California red abalone <i>Haliotis rufescens</i> . <i>Marine Genomics</i> , 2013, 10, 11-16.	0.4	15
69	High-throughput SNP discovery and transcriptome expression profiles from the salmon louse <i>Caligus rogercresseyi</i> (Copepoda: Caligidae). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2014, 10, 9-21.	0.4	15
70	Antimicrobial peptides from Salmon <i>salar</i> skin induce frontal filament development and olfactory/cuticle-related genes in the sea louse <i>Caligus rogercresseyi</i> . <i>Aquaculture</i> , 2016, 464, 171-177.	1.7	15
71	<i>Caligus rogercresseyi</i> serine proteases: Transcriptomic analysis in response to delousing drugs treatments. <i>Aquaculture</i> , 2016, 465, 65-77.	1.7	15
72	From the viral perspective: Infectious salmon anemia virus (ISAV) transcriptome during the infective process in Atlantic salmon ( <i>Salmo salar</i> ). <i>Marine Genomics</i> , 2015, 20, 39-43.	0.4	14

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73	In-feed additives modulate ionotropic receptor genes from the sea louse <i>Caligus rogercresseyi</i> : A comparative analysis in two host salmonid species. <i>Aquaculture</i> , 2016, 451, 99-105.	1.7	14
74	In silico transcriptome analysis of cuticle-related genes associated with delousing drug responses in the sea louse <i>Caligus rogercresseyi</i> . <i>Aquaculture</i> , 2016, 450, 123-135.	1.7	14
75	Catching the complexity of salmon-lice interactions. <i>Fish and Shellfish Immunology</i> , 2019, 90, 199-209.	1.6	14
76	Cathepsin Gene Family Reveals Transcriptome Patterns Related to the Infective Stages of the Salmon Louse <i>Caligus rogercresseyi</i> . <i>PLoS ONE</i> , 2015, 10, e0123954.	1.1	13
77	The Atlantic salmon ( <i>Salmo salar</i> ) antimicrobial peptide cathelicidin-2 is a molecular host-associated cue for the salmon louse ( <i>Lepeophtheirus salmonis</i> ). <i>Scientific Reports</i> , 2018, 8, 13738.	1.6	13
78	Potential Involvement of lncRNAs in the Modulation of the Transcriptome Response to Nodavirus Challenge in European Sea Bass ( <i>Dicentrarchus labrax</i> L.). <i>Biology</i> , 2020, 9, 165.	1.3	13
79	Genetic Analysis of an Artificially Produced Hybrid Abalone ( <i>Haliotis rufescens</i> — <i>Haliotis</i> ) Tj ETQq1 1 0.784314 rgBT/Overl	0.3	12
80	Hybridization between <i>Haliotis rufescens</i> and <i>Haliotis discus hannai</i> : evaluation of fertilization, larval development, growth and thermal tolerance. <i>Aquaculture Research</i> , 2013, 44, 1206-1220.	0.9	12
81	The myostatin gene of <i>Mytilus chilensis</i> evidences a high level of polymorphism and ubiquitous transcript expression. <i>Gene</i> , 2014, 536, 207-212.	1.0	12
82	Sequencing and de novo assembly of the red cusk-eel ( <i>Genypterus chilensis</i> ) transcriptome. <i>Marine Genomics</i> , 2014, 18, 105-107.	0.4	12
83	Transcriptome survey of the lipid metabolic pathways involved in energy production and ecdysteroid synthesis in the salmon louse <i>Caligus rogercresseyi</i> (Crustacea: Copepoda). <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2014, 176, 9-17.	0.7	12
84	Selection of reference genes as internal controls for gene expression in tissues of red abalone <i>Haliotis rufescens</i> (Mollusca, Vetigastropoda; Swainson, 1822). <i>Gene</i> , 2014, 549, 258-265.	1.0	12
85	The <i>Caligus rogercresseyi</i> miRNome: Discovery and transcriptome profiling during the sea lice ontogeny. <i>Agri Gene</i> , 2017, 4, 8-22.	1.9	12
86	RNA-Seq analysis of European sea bass ( <i>Dicentrarchus labrax</i> L.) infected with nodavirus reveals powerful modulation of the stress response. <i>Veterinary Research</i> , 2020, 51, 64.	1.1	12
87	Low-density culture of red abalone juveniles, <i>Haliotis rufescens</i> Swainson 1822, recirculating aquaculture system and flow-through system. <i>Aquaculture Research</i> , 2011, 42, 161-168.	0.9	11
88	Sex-dependent transcriptome analysis and single nucleotide polymorphism (SNP) discovery in the brine shrimp <i>Artemia franciscana</i> . <i>Marine Genomics</i> , 2014, 18, 151-154.	0.4	11
89	Increasing transcriptome response of serpins during the ontogenetic stages in the salmon louse <i>Caligus rogercresseyi</i> (Copepoda: Caligidae). <i>Marine Genomics</i> , 2014, 15, 55-64.	0.4	11
90	First report of the sea louse <i>Caligus rogercresseyi</i> found in farmed Atlantic salmon in the Magallanes region, Chile. <i>Aquaculture</i> , 2019, 512, 734386.	1.7	11

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91	Transcriptome Profiling of Long Non-coding RNAs During the Atlantic Salmon Smoltification Process. <i>Marine Biotechnology</i> , 2021, 23, 308-320.	1.1	11
92	Individual Identification of Decapod Crustaceans I: Color Patterns in Rock Shrimp ( <i>Rhynchocinetes</i> ) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	0.3	10
93	<i>Cordyceps cuncunae</i> (Ascomycota, Hypocreales), a new pleoanamorphic species from temperate rainforest in southern Chile. <i>Mycological Progress</i> , 2012, 11, 733-739.	0.5	10
94	Long non-coding RNAs are associated with spatiotemporal gene expression profiles in the marine gastropod <i>Tegula atra</i> . <i>Marine Genomics</i> , 2017, 33, 39-45.	0.4	10
95	RNA-Seq analysis reveals that spring viraemia of carp virus induces a broad spectrum of PIM kinases in zebrafish kidney that promote viral entry. <i>Fish and Shellfish Immunology</i> , 2020, 99, 86-98.	1.6	10
96	Karyotype analysis of interspecific hybrids between <i>Haliotis rufescens</i> and <i>Haliotis discus HANNAL</i> . <i>Aquaculture Research</i> , 2011, 42, 1460-1466.	0.9	9
97	SNP discovery in the marine gastropod <i>Concholepas concholepas</i> by high-throughput transcriptome sequencing. <i>Conservation Genetics Resources</i> , 2013, 5, 1053-1054.	0.4	9
98	Modulation of insulin-like receptor gene (MdlR) in response to feeding in the surf clam <i>Mesodesma donacium</i> (Lamarck, 1818). <i>Journal of Molluscan Studies</i> , 2015, 81, 37-43.	0.4	9
99	Prohibitin-2 gene reveals sex-related differences in the salmon louse <i>Caligus rogercresseyi</i> . <i>Gene</i> , 2015, 564, 73-80.	1.0	9
100	Identification and expression of antioxidant and immune defense genes in the surf clam <i>Mesodesma donacium</i> challenged with <i>Vibrio anguillarum</i> . <i>Marine Genomics</i> , 2015, 19, 65-73.	0.4	9
101	Molecular characterization of collagen IV evidences early transcription expression related to the immune response against bacterial infection in the red abalone ( <i>Haliotis rufescens</i> ). <i>Fish and Shellfish Immunology</i> , 2015, 42, 241-248.	1.6	9
102	Density-dependent effects of <i>Caligus rogercresseyi</i> infestation on the immune responses of <i>Salmo salar</i> . <i>Fish and Shellfish Immunology</i> , 2016, 59, 365-374.	1.6	9
103	Silencing of ionotropic receptor 25a decreases chemosensory activity in the salmon louse <i>Lepeophtheirus salmonis</i> during the infective stage. <i>Gene</i> , 2019, 697, 35-39.	1.0	9
104	GENOME SIZE ESTIMATION IN TWO POPULATIONS OF THE NORTHERN CHILEAN SCALLOP, <i>ARGOPECTEN PURPURATUS</i> , USING FLUORESCENCE IMAGE ANALYSIS. <i>Journal of Shellfish Research</i> , 2005, 24, 55-60.	0.3	8
105	Ubiquitin-conjugating enzyme E2-like gene associated to pathogen response in <i>Concholepas concholepas</i> : SNP identification and transcription expression. <i>Fish and Shellfish Immunology</i> , 2012, 33, 1065-1068.	1.6	8
106	Transcriptome analysis of the couch potato (CPO) protein reveals an expression pattern associated with early development in the salmon louse <i>Caligus rogercresseyi</i> . <i>Gene</i> , 2014, 536, 1-8.	1.0	8
107	Parentage assignment in hybrid abalones ( <i>Haliotis rufescens</i> × <i>Haliotis discus hannaï</i> ) based on microsatellite DNA markers. <i>Aquaculture Research</i> , 2015, 46, 216-225.	0.9	8
108	Two novel male-associated peroxinectin genes are downregulated by exposure to delousing drugs in <i>Caligus rogercresseyi</i> . <i>Gene</i> , 2015, 557, 98-102.	1.0	8

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109	Pesticides Drive Stochastic Changes in the Chemoreception and Neurotransmission System of Marine Ectoparasites. <i>International Journal of Molecular Sciences</i> , 2016, 17, 700.	1.8	8
110	RNA interference in <i>Haliotis rufescens</i> myostatin evidences upregulation of insulin signaling pathway. <i>Agri Gene</i> , 2016, 1, 93-99.	1.9	8
111	Functional diets modulate the acute phase protein response in <i>Oncorhynchus mykiss</i> subjected to chronic stress and challenged with <i>Vibrio anguillarum</i> . <i>Fish and Shellfish Immunology</i> , 2017, 66, 62-70.	1.6	8
112	De novo transcriptome analysis of the red seaweed <i>Gracilaria chilensis</i> and identification of linkers associated with phycobilisomes. <i>Marine Genomics</i> , 2017, 31, 17-19.	0.4	8
113	Transcriptomic response of rainbow trout ( <i>Oncorhynchus mykiss</i> ) skeletal muscle to <i>Flavobacterium psychrophilum</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 31, 100596.	0.4	8
114	First report of the reduction in treatment efficacy of the organophosphate azamethiphos against the sea lice <i>Caligus rogercresseyi</i> (Boxshall & Bravo, 2000). <i>Aquaculture Research</i> , 2020, 51, 436-439.	0.9	8
115	Genetic Variability of Cultured Populations of Red Abalone in Chile: An Approach Based on Heterologous Microsatellites. <i>Journal of Shellfish Research</i> , 2010, 29, 709-715.	0.3	7
116	Effect of triploidy in the expression of immune-related genes in coho salmon <i>Oncorhynchus kisutch</i> (Walbaum) infected with <i>Piscirickettsia salmonis</i> . <i>Aquaculture Research</i> , 2015, 46, 59-63.	0.9	7
117	Aquaporin family genes exhibit developmentally-regulated and host-dependent transcription patterns in the sea louse <i>Caligus rogercresseyi</i> . <i>Gene</i> , 2016, 585, 119-127.	1.0	7
118	Long noncoding RNAs: Unexplored players in the drug response of the sea louse <i>Caligus rogercresseyi</i> . <i>Agri Gene</i> , 2017, 4, 1-7.	1.9	7
119	Long-term serial culture of <i>Piscirickettsia salmonis</i> leads to a genomic and transcriptomic reorganization affecting bacterial virulence. <i>Aquaculture</i> , 2020, 529, 735634.	1.7	7
120	Adaptive Differences in Gene Expression in Farm-Impacted Seedbeds of the Native Blue Mussel <i>Mytilus chilensis</i> . <i>Frontiers in Genetics</i> , 2021, 12, 666539.	1.1	7
121	Adaptive mitochondrial genome functioning in ecologically different farm-impacted natural seedbeds of the endemic blue mussel <i>Mytilus chilensis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2022, 42, 100955.	0.4	7
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125	Hydrogen peroxide modulates antioxidant system transcription, evidencing sex-dependent responses in <i>Caligus rogercresseyi</i> . <i>Aquaculture Research</i> , 2017, 48, 969-978.	0.9	6
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146	Phylogenetic and mycogeographical aspects of <i>Lactarius</i> and <i>Rhizopogon</i> associated with <i>Pinus radiata</i> in south-central Chile. <i>Phytotaxa</i> , 2015, 226, 177.	0.1	3
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155	Comparative modulation of lncRNAs in wild-type and RAG1 heterozygous mutant zebrafish exposed to an immune challenge with Spring Viremia of Carp Virus (SVCV). <i>Fish and Shellfish Immunology</i> , 2019, 91, 416.	1.6	2
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