Christiane Eichner

List of Publications by Year in descending order

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759233 794594 20 611 12 19 citations h-index g-index papers 23 23 23 460 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Roles of three putative salmon louse (Lepeophtheirus salmonis) prostaglandin E2 synthases in physiology and host–parasite interactions. Parasites and Vectors, 2021, 14, 206.	2.5	10
2	The FTZ-F1 gene encodes two functionally distinct nuclear receptor isoforms in the ectoparasitic copepod salmon louse (Lepeophtheirus salmonis). PLoS ONE, 2021, 16, e0251575.	2.5	6
3	The salmon louse genome: Copepod features and parasitic adaptations. Genomics, 2021, 113, 3666-3680.	2.9	17
4	A novel approach to co-expression network analysis identifies modules and genes relevant for moulting and development in the Atlantic salmon louse (Lepeophtheirus salmonis). BMC Genomics, 2021, 22, 832.	2.8	0
5	Identification of critical enzymes in the salmon louse chitin synthesis pathway as revealed by RNA interference-mediated abrogation of infectivity. International Journal for Parasitology, 2020, 50, 873-889.	3.1	10
6	Host gill attachment causes blood-feeding by the salmon louse (Lepeophtheirus salmonis) chalimus larvae and alters parasite development and transcriptome. Parasites and Vectors, 2020, 13, 225.	2.5	16
7	Heavy and light chain homologs of ferritin are essential for blood-feeding and egg production of the ectoparasitic copepod Lepeophtheirus salmonis. Molecular and Biochemical Parasitology, 2019, 232, 111197.	1.1	11
8	Airgun blasts used in marine seismic surveys have limited effects on mortality, and no sublethal effects on behaviour or gene expression, in the copepod Calanus finmarchicus. ICES Journal of Marine Science, 2019, 76, 2033-2044.	2.5	18
9	A scavenger receptor B (CD36)-like protein is a potential mediator of intestinal heme absorption in the hematophagous ectoparasite Lepeophtheirus salmonis. Scientific Reports, 2019, 9, 4218.	3.3	16
10	Chitin synthesis and degradation in Lepeophtheirus salmonis: Molecular characterization and gene expression profile during synthesis of a new exoskeleton. Comparative Biochemistry and Physiology Part A, Molecular & Ditterrative Physiology, 2019, 227, 123-133.	1.8	13
11	<scp>RNA</scp> sequencing reveals distinct gene expression patterns during the development of parasitic larval stages of the salmon louse (<i>Lepeophtheirus salmonis</i>). Journal of Fish Diseases, 2018, 41, 1005-1029.	1.9	23
12	Molecular characterization and functional analysis of a salmon louse (Lepeophtheirus salmonis,) Tj ETQq0 0 0 rg Biochemistry and Physiology Part A, Molecular & Dysiology, 2017, 206, 1-10.	BT /Overlo 1.8	ock 10 Tf 50 30 14
13	Molecular characterisation and functional analysis of LsChi2, a chitinase found in the salmon louse (Lepeophtheirus salmonis salmonis, KrĀ,yer 1838). Experimental Parasitology, 2015, 151-152, 39-48.	1.2	25
14	Characterization of a novel RXR receptor in the salmon louse (Lepeophtheirus salmonis, Copepoda) regulating growth and female reproduction. BMC Genomics, 2015, 16, 81.	2.8	18
15	Molecular characterization and knock-down of salmon louse (Lepeophtheirus salmonis) prostaglandin E synthase. Experimental Parasitology, 2015, 159, 79-93.	1.2	27
16	Instar growth and molt increments in Lepeophtheirus salmonis (Copepoda: Caligidae) chalimus larvae. Parasitology International, 2015, 64, 86-96.	1.3	28
17	A method for stable gene knock-down by RNA interference in larvae of the salmon louse (Lepeophtheirus salmonis). Experimental Parasitology, 2014, 140, 44-51.	1.2	43
18	The Salmon Louse Lepeophtheirus salmonis (Copepoda: Caligidae) Life Cycle Has Only Two Chalimus Stages. PLoS ONE, 2013, 8, e73539.	2.5	197

#	Article	IF	CITATIONS
19	Functional characterisation of the maternal yolk-associated protein (LsYAP) utilising systemic RNA interference in the salmon louse (Lepeophtheirus salmonis) (Crustacea: Copepoda). International Journal for Parasitology, 2009, 39, 1407-1415.	3.1	56
20	Salmon louse (Lepeophtheirus salmonis) transcriptomes during post molting maturation and egg production, revealed using EST-sequencing and microarray analysis. BMC Genomics, 2008, 9, 126.	2.8	61