Helen Piontkivska

List of Publications by Year in descending order

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71 2,521 papers citations

27 h-index 48 g-index

79 all docs 79 docs citations 79 times ranked 4581 citing authors

#	Article	IF	CITATIONS
1	Interferons and viruses induce a novel truncated ACE2 isoform and not the full-length SARS-CoV-2 receptor. Nature Genetics, 2020, 52, 1283-1293.	9.4	217
2	COVID-19 and emerging viral infections: The case for interferon lambda. Journal of Experimental Medicine, 2020, 217, .	4.2	177
3	Novel Protein Genes in Animal mtDNA: A New Sex Determination System in Freshwater Mussels (Bivalvia: Unionoida)?. Molecular Biology and Evolution, 2011, 28, 1645-1659.	3.5	156
4	Purifying selection and birth-and-death evolution in the ubiquitin gene family. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 10866-10871.	3.3	137
5	Comparative Mitochondrial Genomics of Freshwater Mussels (Bivalvia: Unionoida) With Doubly Uniparental Inheritance of mtDNA: Gender-Specific Open Reading Frames and Putative Origins of Replication. Genetics, 2009, 183, 1575-1589.	1.2	114
6	Purifying Selection and Birth-and-death Evolution in the Histone H4 Gene Family. Molecular Biology and Evolution, 2002, 19, 689-697.	3 . 5	98
7	A Dominant Role for CD8 + -T-Lymphocyte Selection in Simian Immunodeficiency Virus Sequence Variation. Journal of Virology, 2004, 78, 14012-14022.	1.5	89
8	Molecular Evolution of the Nontandemly Repeated Genes of the Histone 3 Multigene Family. Molecular Biology and Evolution, 2002, $19,68-75$.	3. 5	86
9	CD8+ T Cells from SIV Elite Controller Macaques Recognize Mamu-B*08-Bound Epitopes and Select for Widespread Viral Variation. PLoS ONE, 2007, 2, e1152.	1.1	75
10	Phylogeny of Trypanosomatidae and Bodonidae (Kinetoplastida) Based on 18S rRNA: Evidence for Paraphyly of Trypanosoma and Six Other Genera. Molecular Biology and Evolution, 2003, 20, 644-652.	3 . 5	73
11	Birth-and-Death Evolution in Primate MHC Class I Genes: Divergence Time Estimates. Molecular Biology and Evolution, 2003, 20, 601-609.	3.5	70
12	Functional diversification of the toll-like receptor gene family. Immunogenetics, 2008, 60, 249-256.	1.2	64
13	Analysis of gene expression in prostate cancer epithelial and interstitial stromal cells using laser capture microdissection. BMC Cancer, 2010, 10, 165.	1.1	57
14	Comprehensive Immunological Evaluation Reveals Surprisingly Few Differences between Elite Controller and Progressor <i>Mamu-B*17</i> -Positive Simian Immunodeficiency Virus-Infected Rhesus Macaques. Journal of Virology, 2008, 82, 5245-5254.	1.5	56
15	Evolutionary analysis of glycosyl hydrolase family 28 (GH28) suggests lineage-specific expansions in necrotrophic fungal pathogens. Gene, 2011, 479, 29-36.	1.0	56
16	Biomineralization-related specialization of hemocytes and mantle tissues of the Pacific oysters <i>Crassostrea gigas</i> . Journal of Experimental Biology, 2017, 220, 3209-3221.	0.8	56
17	Aspartic Proteinase Phylogeny and the Origin of Pregnancy-Associated Glycoproteins. Molecular Biology and Evolution, 2003, 20, 1940-1945.	3.5	48
18	Molecular characterization and mRNA expression of two key enzymes of hypoxia-sensing pathways in eastern oysters Crassostrea virginica (Gmelin): Hypoxia-inducible factor \hat{l}_{\pm} (HIF- \hat{l}_{\pm}) and HIF-prolyl hydroxylase (PHD). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2011, 6, 103-114.	0.4	44

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19	DNA repeat arrays in chicken and human genomes and the adaptive evolution of avian genome size. BMC Evolutionary Biology, 2005, 5, 12.	3.2	43
20	Identification of novel light-induced genes in the suprachiasmatic nucleus. BMC Neuroscience, 2007, 8, 98.	0.8	42
21	RNA editing by the host ADAR system affects the molecular evolution of the Zika virus. Ecology and Evolution, 2017, 7, 4475-4485.	0.8	39
22	Extreme primary and secondary protein structure variability in the chimeric male-transmitted cytochrome c oxidase subunit II protein in freshwater mussels: Evidence for an elevated amino acid substitution rate in the face of domain-specific purifying selection. BMC Evolutionary Biology, 2008, 8, 165.	3.2	37
23	Multi-species sequence comparison reveals dynamic evolution of the elastin gene that has involved purifying selection and lineage-specific insertions/deletions. BMC Genomics, 2004, 5, 31.	1.2	35
24	Effects of intermittent hypoxia on the cell survival and inflammatory responses in the intertidal marine bivalves <i>Mytilus edulis</i> and <i>Crassostrea gigas</i> . Journal of Experimental Biology, 2020, 223, .	0.8	33
25	Machine Learning Maps Research Needs in COVID-19 Literature. Patterns, 2020, 1, 100123.	3.1	31
26	Molecular phylogenetics of Trypanosomatidae: contrasting results from 18S rRNA and protein phylogenies. Parasites and Vectors, 2003, 2, 15.	1.9	30
27	HIV type 1 tropism and inhibitors of viral entry: clinical implications. AIDS Reviews, 2006, 8, 60-77.	0.5	30
28	Effects of cadmium exposure and intermittent anoxia on nitric oxide metabolism in eastern oysters, <i>Crassostrea virginica </i> Ournal of Experimental Biology, 2010, 213, 433-444.	0.8	27
29	Cross-species mapping of bidirectional promoters enables prediction of unannotated 5' UTRs and identification of species-specific transcripts. BMC Genomics, 2009, 10, 189.	1.2	25
30	Efficiencies of maximum likelihood methods of phylogenetic inferences when different substitution models are used. Molecular Phylogenetics and Evolution, 2004, 31, 865-873.	1.2	24
31	Pyganodon (Bivalvia: Unionoida: Unionidae) phylogenetics: A male- and female-transmitted mitochondrial DNA perspective. Molecular Phylogenetics and Evolution, 2012, 63, 430-444.	1.2	23
32	Interactive effects of salinity variation and exposure to ZnO nanoparticles on the innate immune system of a sentinel marine bivalve, Mytilus edulis. Science of the Total Environment, 2020, 712, 136473.	3.9	23
33	ADAR Editing in Viruses: An Evolutionary Force to Reckon with. Genome Biology and Evolution, 2021, 13, .	1.1	23
34	Nucleotide sequence polymorphism in circoviruses. Infection, Genetics and Evolution, 2008, 8, 130-138.	1.0	22
35	Evolutionary conservation of zinc finger transcription factor binding sites in promoters of genes co-expressed with WT1 in prostate cancer. BMC Genomics, 2008, 9, 337.	1.2	21
36	A secondary structure within a human piRNA modulates its functionality. Biochimie, 2019, 157, 72-80.	1.3	19

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37	Molecular Biomarkers of the Mitochondrial Quality Control Are Differently Affected by Hypoxia-Reoxygenation Stress in Marine Bivalves Crassostrea gigas and Mytilus edulis. Frontiers in Marine Science, 2020, 7, .	1.2	18
38	Stable G-quadruplex enabling sequences are selected against by the context-dependent codon bias. Gene, 2019, 696, 149-161.	1.0	17
39	Patterns of sequence evolution at epitopes for host antibodies and cytotoxic T-lymphocytes in human immunodeficiency virus type 1. Virus Research, 2006, 116, 98-105.	1.1	16
40	Evolutionary diversification of the avian fatty acid-binding proteins. Gene, 2011, 490, 1-5.	1.0	16
41	Potential trade-offs between biomineralization and immunity revealed by shell properties and gene expression profiles of two closely related <i>Crassostrea</i> species. Journal of Experimental Biology, 2018, 221, .	0.8	15
42	Transcriptional response of key metabolic and stress response genes of a nuculanid bivalve, Lembulus bicuspidatus from an oxygen minimum zone exposed to hypoxia-reoxygenation. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2021, 256, 110617.	0.7	15
43	Within-host evolution of CD8+-TL epitopes encoded by overlapping and non-overlapping reading frames of simian immunodeficiency virus. Bioinformatics, 2005, 21, iii39-iii44.	1.8	14
44	Frequent associations between CTL and T-Helper epitopes in HIV-1 genomes and implications for multi-epitope vaccine designs. BMC Microbiology, 2010, 10, 212.	1.3	14
45	Explaining Pathogenicity of Congenital Zika and Guillain–Barré Syndromes: Does Dysregulation of RNA Editing Play a Role?. BioEssays, 2019, 41, 1800239.	1.2	14
46	Between-Host Evolution of Cytotoxic T-Lymphocyte Epitopes in Human Immunodeficiency Virus Type 1: an Approach Based on Phylogenetically Independent Comparisons. Journal of Virology, 2004, 78, 11758-11765.	1.5	13
47	Role of Host-Driven Mutagenesis in Determining Genome Evolution of Sigma Virus (DMelSV;) Tj ETQq1 1 0.7843	14 _{1.} FBT /C	Overlock 107
48	The Role of Reversible Protein Phosphorylation in Regulation of the Mitochondrial Electron Transport System During Hypoxia and Reoxygenation Stress in Marine Bivalves. Frontiers in Marine Science, 2020, 7, .	1.2	13
49	Evolution of Vertebrate Voltage-Gated Ion Channel α Chains by Sequential Gene Duplication. Journal of Molecular Evolution, 2003, 56, 277-285.	0.8	12
50	Lipidâ^'protein interactions for ECA1 an N-ANTH domain protein involved in stress signaling in plants. Chemistry and Physics of Lipids, 2020, 231, 104919.	1.5	12
51	Environmental kinetoplastid-like 18S rRNA sequences and phylogenetic relationships among Trypanosomatidae: Paraphyly of the genus Trypanosoma. Molecular and Biochemical Parasitology, 2005, 144, 94-99.	0.5	11
52	Seasonality of birth defects in West Africa: could congenital Zika syndrome be to blame?. F1000Research, 2018, 7, 159.	0.8	10
53	Discovery of novel targets for multi-epitope vaccines: Screening of HIV-1 genomes using association rule mining. Retrovirology, 2009, 6, 62.	0.9	9
54	Molecular Trajectories Leading to the Alternative Fates of Duplicate Genes. PLoS ONE, 2012, 7, e38958.	1.1	8

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55	Identification of Surface Epitopes Associated with Protection against Highly Immune-Evasive VIsE-Expressing Lyme Disease Spirochetes. Infection and Immunity, 2018, 86, .	1.0	8
56	Evolutionary Relationships Of Popenaias popeii and the Early Evolution Of Lampsiline Bivalves (Unionidae): Phylogenetic Analyses Of Dna and Amino Acid Sequences From F and M Mitochondrial Genomes. Malacologia, 2008, 50, 303-318.	0.2	7
57	Seasonality of birth defects in West Africa: could congenital Zika syndrome be to blame?. F1000Research, 2018, 7, 159.	0.8	7
58	Rapid fixation of a distinctive sequence motif in the $3\hat{a}\in^2$ noncoding region of the clade of West Nile virus invading North America. Gene, 2007, 399, 152-161.	1.0	6
59	Molecular characterization and expression of a novel homolog of uncoupling protein 5 (UCP5) from the eastern oyster Crassostrea virginica (Bivalvia: Ostreidae). Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2009, 4, 121-127.	0.4	5
60	Delineating Surface Epitopes of Lyme Disease Pathogen Targeted by Highly Protective Antibodies of New Zealand White Rabbits. Infection and Immunity, 2019, 87, .	1.0	5
61	Proteome Dynamics and Bioinformatics Reveal Major Alterations in the Turnover Rate of Functionally Related Cardiac and Plasma Proteins in a Dog Model of Congestive Heart Failure. Journal of Cardiac Failure, 2022, 28, 588-600.	0.7	4
62	Shedding light on lipid metabolism in Kinetoplastida: A phylogenetic analysis of phospholipase D protein homologs. Gene, 2018, 656, 95-105.	1.0	3
63	Retained duplications and deletions of CYP2C genes among primates. Molecular Phylogenetics and Evolution, 2018, 125, 204-212.	1.2	3
64	The Role of the Vascular Endothelial Growth Factor (VEGF) Signaling in Biomineralization of the Oyster Crassostrea gigas. Frontiers in Marine Science, $2018, 5, \ldots$	1.2	3
65	Automated Isoform Diversity Detector (AIDD): a pipeline for investigating transcriptome diversity of RNA-seq data. BMC Bioinformatics, 2020, 21, 578.	1.2	3
66	Expanding Inclusivity with Learner-Generated Study Aids in Three Different Science Courses. Journal of Chemical Education, 2021, 98, 3379-3383.	1.1	2
67	Matchmaking in Bioinformatics. F1000Research, 2018, 7, 171.	0.8	2
68	Diversifying selection detected in only a minority of xenobiotic-metabolizing <i>CYP1-3</i> genes among primate species. Xenobiotica, 2020, 50, 1406-1412.	0.5	1
69	Coevolutionary Analysis Identifies Protein–Protein Interaction Sites between HIV-1 Reverse Transcriptase and Integrase. Virus Evolution, 2016, 2, vew002.	2.2	0
70	Identification Of Candidate Genes Contributing To Exercise Performance Phenotype Using Bioinformatics Analysis. Medicine and Science in Sports and Exercise, 2016, 48, 729.	0.2	0
71	ADARâ€editing Landscapes Predict Biomarkers for Neuropsychiatric Disorders. FASEB Journal, 2020, 34, 1-1.	0.2	0