

Helen Piontkivska

List of Publications by Year in descending order

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71
papers

2,521
citations

201674

27
h-index

206112

48
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79
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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. <i>Nature Genetics</i> , 2020, 52, 1283-1293.	21.4	217
2	COVID-19 and emerging viral infections: The case for interferon lambda. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	177
3	Novel Protein Genes in Animal mtDNA: A New Sex Determination System in Freshwater Mussels (<i>Bivalvia: Unionoida</i>)?. <i>Molecular Biology and Evolution</i> , 2011, 28, 1645-1659.	8.9	156
4	Purifying selection and birth-and-death evolution in the ubiquitin gene family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 10866-10871.	7.1	137
5	Comparative Mitochondrial Genomics of Freshwater Mussels (<i>Bivalvia: Unionoida</i>) With Doubly Uniparental Inheritance of mtDNA: Gender-Specific Open Reading Frames and Putative Origins of Replication. <i>Genetics</i> , 2009, 183, 1575-1589.	2.9	114
6	Purifying Selection and Birth-and-death Evolution in the Histone H4 Gene Family. <i>Molecular Biology and Evolution</i> , 2002, 19, 689-697.	8.9	98
7	A Dominant Role for CD8 + -T-Lymphocyte Selection in Simian Immunodeficiency Virus Sequence Variation. <i>Journal of Virology</i> , 2004, 78, 14012-14022.	3.4	89
8	Molecular Evolution of the Nontandemly Repeated Genes of the Histone 3 Multigene Family. <i>Molecular Biology and Evolution</i> , 2002, 19, 68-75.	8.9	86
9	CD8+ T Cells from SIV Elite Controller Macaques Recognize Mamu-B*08-Bound Epitopes and Select for Widespread Viral Variation. <i>PLoS ONE</i> , 2007, 2, e1152.	2.5	75
10	Phylogeny of Trypanosomatidae and Bodonidae (Kinetoplastida) Based on 18S rRNA: Evidence for Paraphyly of Trypanosoma and Six Other Genera. <i>Molecular Biology and Evolution</i> , 2003, 20, 644-652.	8.9	73
11	Birth-and-Death Evolution in Primate MHC Class I Genes: Divergence Time Estimates. <i>Molecular Biology and Evolution</i> , 2003, 20, 601-609.	8.9	70
12	Functional diversification of the toll-like receptor gene family. <i>Immunogenetics</i> , 2008, 60, 249-256.	2.4	64
13	Analysis of gene expression in prostate cancer epithelial and interstitial stromal cells using laser capture microdissection. <i>BMC Cancer</i> , 2010, 10, 165.	2.6	57
14	Comprehensive Immunological Evaluation Reveals Surprisingly Few Differences between Elite Controller and Progressor Mamu-B*17-Positive Simian Immunodeficiency Virus-Infected Rhesus Macaques. <i>Journal of Virology</i> , 2008, 82, 5245-5254.	3.4	56
15	Evolutionary analysis of glycosyl hydrolase family 28 (GH28) suggests lineage-specific expansions in necrotrophic fungal pathogens. <i>Gene</i> , 2011, 479, 29-36.	2.2	56
16	Biom mineralization-related specialization of hemocytes and mantle tissues of the Pacific oysters <i>Crassostrea gigas</i> . <i>Journal of Experimental Biology</i> , 2017, 220, 3209-3221.	1.7	56
17	Aspartic Proteinase Phylogeny and the Origin of Pregnancy-Associated Glycoproteins. <i>Molecular Biology and Evolution</i> , 2003, 20, 1940-1945.	8.9	48
18	Molecular characterization and mRNA expression of two key enzymes of hypoxia-sensing pathways in eastern oysters <i>Crassostrea virginica</i> (Gmelin): Hypoxia-inducible factor 1 \pm (HIF-1 \pm) and HIF-prolyl hydroxylase (PHD). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2011, 6, 103-114.	1.0	44

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19	DNA repeat arrays in chicken and human genomes and the adaptive evolution of avian genome size. <i>BMC Evolutionary Biology</i> , 2005, 5, 12.	3.2	43
20	Identification of novel light-induced genes in the suprachiasmatic nucleus. <i>BMC Neuroscience</i> , 2007, 8, 98.	1.9	42
21	RNA editing by the host ADAR system affects the molecular evolution of the Zika virus. <i>Ecology and Evolution</i> , 2017, 7, 4475-4485.	1.9	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. <i>BMC Evolutionary Biology</i> , 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. <i>BMC Genomics</i> , 2004, 5, 31.	2.8	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> . <i>Journal of Experimental Biology</i> , 2020, 223, .	1.7	33
25	Machine Learning Maps Research Needs in COVID-19 Literature. <i>Patterns</i> , 2020, 1, 100123.	5.9	31
26	Molecular phylogenetics of Trypanosomatidae: contrasting results from 18S rRNA and protein phylogenies. <i>Parasites and Vectors</i> , 2003, 2, 15.	1.9	30
27	HIV type 1 tropism and inhibitors of viral entry: clinical implications. <i>AIDS Reviews</i> , 2006, 8, 60-77.	1.0	30
28	Effects of cadmium exposure and intermittent anoxia on nitric oxide metabolism in eastern oysters, <i>Crassostrea virginica</i> . <i>Journal of Experimental Biology</i> , 2010, 213, 433-444.	1.7	27
29	Cross-species mapping of bidirectional promoters enables prediction of unannotated 5' UTRs and identification of species-specific transcripts. <i>BMC Genomics</i> , 2009, 10, 189.	2.8	25
30	Efficiencies of maximum likelihood methods of phylogenetic inferences when different substitution models are used. <i>Molecular Phylogenetics and Evolution</i> , 2004, 31, 865-873.	2.7	24
31	Pyganodon (Bivalvia: Unionoida: Unionidae) phylogenetics: A male- and female-transmitted mitochondrial DNA perspective. <i>Molecular Phylogenetics and Evolution</i> , 2012, 63, 430-444.	2.7	23
32	Interactive effects of salinity variation and exposure to ZnO nanoparticles on the innate immune system of a sentinel marine bivalve, <i>Mytilus edulis</i> . <i>Science of the Total Environment</i> , 2020, 712, 136473.	8.0	23
33	ADAR Editing in Viruses: An Evolutionary Force to Reckon with. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	23
34	Nucleotide sequence polymorphism in circoviruses. <i>Infection, Genetics and Evolution</i> , 2008, 8, 130-138.	2.3	22
35	Evolutionary conservation of zinc finger transcription factor binding sites in promoters of genes co-expressed with WT1 in prostate cancer. <i>BMC Genomics</i> , 2008, 9, 337.	2.8	21
36	A secondary structure within a human piRNA modulates its functionality. <i>Biochimie</i> , 2019, 157, 72-80.	2.6	19

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37	Molecular Biomarkers of the Mitochondrial Quality Control Are Differently Affected by Hypoxia-Reoxygenation Stress in Marine Bivalves <i>Crassostrea gigas</i> and <i>Mytilus edulis</i> . <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	18
38	Stable G-quadruplex enabling sequences are selected against by the context-dependent codon bias. <i>Gene</i> , 2019, 696, 149-161.	2.2	17
39	Patterns of sequence evolution at epitopes for host antibodies and cytotoxic T-lymphocytes in human immunodeficiency virus type 1. <i>Virus Research</i> , 2006, 116, 98-105.	2.2	16
40	Evolutionary diversification of the avian fatty acid-binding proteins. <i>Gene</i> , 2011, 490, 1-5.	2.2	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. <i>Journal of Experimental Biology</i> , 2018, 221, .	1.7	15
42	Transcriptional response of key metabolic and stress response genes of a nuculanid bivalve, <i>Lembulus bicuspidatus</i> from an oxygen minimum zone exposed to hypoxia-reoxygenation. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2021, 256, 110617.	1.6	15
43	Within-host evolution of CD8+TL epitopes encoded by overlapping and non-overlapping reading frames of simian immunodeficiency virus. <i>Bioinformatics</i> , 2005, 21, iii39-iii44.	4.1	14
44	Frequent associations between CTL and T-Helper epitopes in HIV-1 genomes and implications for multi-epitope vaccine designs. <i>BMC Microbiology</i> , 2010, 10, 212.	3.3	14
45	Explaining Pathogenicity of Congenital Zika and Guillain-Barré Syndromes: Does Dysregulation of RNA Editing Play a Role?. <i>BioEssays</i> , 2019, 41, 1800239.	2.5	14
46	Between-Host Evolution of Cytotoxic T-Lymphocyte Epitopes in Human Immunodeficiency Virus Type 1: an Approach Based on Phylogenetically Independent Comparisons. <i>Journal of Virology</i> , 2004, 78, 11758-11765.	3.4	13
47	Role of Host-Driven Mutagenesis in Determining Genome Evolution of Sigma Virus (DMelSV); Tj ETQq1 1 0.784314, rgBT /Overlock 10	2.5	13
48	The Role of Reversible Protein Phosphorylation in Regulation of the Mitochondrial Electron Transport System During Hypoxia and Reoxygenation Stress in Marine Bivalves. <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	13
49	Evolution of Vertebrate Voltage-Gated Ion Channel α Chains by Sequential Gene Duplication. <i>Journal of Molecular Evolution</i> , 2003, 56, 277-285.	1.8	12
50	Lipid-protein interactions for ECA1 an N-ANTH domain protein involved in stress signaling in plants. <i>Chemistry and Physics of Lipids</i> , 2020, 231, 104919.	3.2	12
51	Environmental kinetoplastid-like 18S rRNA sequences and phylogenetic relationships among Trypanosomatidae: Paraphyly of the genus <i>Trypanosoma</i> . <i>Molecular and Biochemical Parasitology</i> , 2005, 144, 94-99.	1.1	11
52	Seasonality of birth defects in West Africa: could congenital Zika syndrome be to blame?. <i>F1000Research</i> , 2018, 7, 159.	1.6	10
53	Discovery of novel targets for multi-epitope vaccines: Screening of HIV-1 genomes using association rule mining. <i>Retrovirology</i> , 2009, 6, 62.	2.0	9
54	Molecular Trajectories Leading to the Alternative Fates of Duplicate Genes. <i>PLoS ONE</i> , 2012, 7, e38958.	2.5	8

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55	Identification of Surface Epitopes Associated with Protection against Highly Immune-Evasive VlsE-Expressing Lyme Disease Spirochetes. <i>Infection and Immunity</i> , 2018, 86, .	2.2	8
56	Evolutionary Relationships Of <i>Popenaias popeii</i> and the Early Evolution Of Lampsiline Bivalves (Unionidae): Phylogenetic Analyses Of Dna and Amino Acid Sequences From F and M Mitochondrial Genomes. <i>Malacologia</i> , 2008, 50, 303-318.	0.4	7
57	Seasonality of birth defects in West Africa: could congenital Zika syndrome be to blame?. <i>F1000Research</i> , 2018, 7, 159.	1.6	7
58	Rapid fixation of a distinctive sequence motif in the 3' noncoding region of the clade of West Nile virus invading North America. <i>Gene</i> , 2007, 399, 152-161.	2.2	6
59	Molecular characterization and expression of a novel homolog of uncoupling protein 5 (UCP5) from the eastern oyster <i>Crassostrea virginica</i> (Bivalvia: Ostreidae). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2009, 4, 121-127.	1.0	5
60	Delineating Surface Epitopes of Lyme Disease Pathogen Targeted by Highly Protective Antibodies of New Zealand White Rabbits. <i>Infection and Immunity</i> , 2019, 87, .	2.2	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. <i>Journal of Cardiac Failure</i> , 2022, 28, 588-600.	1.7	4
62	Shedding light on lipid metabolism in Kinetoplastida: A phylogenetic analysis of phospholipase D protein homologs. <i>Gene</i> , 2018, 656, 95-105.	2.2	3
63	Retained duplications and deletions of CYP2C genes among primates. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 204-212.	2.7	3
64	The Role of the Vascular Endothelial Growth Factor (VEGF) Signaling in Biomineralization of the Oyster <i>Crassostrea gigas</i> . <i>Frontiers in Marine Science</i> , 2018, 5, .	2.5	3
65	Automated Isoform Diversity Detector (AIDD): a pipeline for investigating transcriptome diversity of RNA-seq data. <i>BMC Bioinformatics</i> , 2020, 21, 578.	2.6	3
66	Expanding Inclusivity with Learner-Generated Study Aids in Three Different Science Courses. <i>Journal of Chemical Education</i> , 2021, 98, 3379-3383.	2.3	2
67	Matchmaking in Bioinformatics. <i>F1000Research</i> , 2018, 7, 171.	1.6	2
68	Diversifying selection detected in only a minority of xenobiotic-metabolizing <i>CYP1-3</i> genes among primate species. <i>Xenobiotica</i> , 2020, 50, 1406-1412.	1.1	1
69	Coevolutionary Analysis Identifies Protein-Protein Interaction Sites between HIV-1 Reverse Transcriptase and Integrase. <i>Virus Evolution</i> , 2016, 2, vew002.	4.9	0
70	Identification Of Candidate Genes Contributing To Exercise Performance Phenotype Using Bioinformatics Analysis. <i>Medicine and Science in Sports and Exercise</i> , 2016, 48, 729.	0.4	0
71	ADAR Editing Landscapes Predict Biomarkers for Neuropsychiatric Disorders. <i>FASEB Journal</i> , 2020, 34, 1-1.	0.5	0