Elisabetta Pizzi

List of Publications by Year in descending order

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FLISARETTA DIZZI

#	Article	IF	CITATIONS
1	Genome-wide identification of genes upregulated at the onset of gametocytogenesis in Plasmodium falciparum. Molecular and Biochemical Parasitology, 2005, 143, 100-110.	1.1	135
2	Molecular model of the specificity pocket of the hepatitis C virus protease: implications for substrate recognition Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 888-892.	7.1	123
3	Acidic microenvironment plays a key role in human melanoma progression through a sustained exosome mediated transfer of clinically relevant metastatic molecules. Journal of Experimental and Clinical Cancer Research, 2018, 37, 245.	8.6	104
4	Variability within the Candida rugosa Upases family. Protein Engineering, Design and Selection, 1994, 7, 531-535.	2.1	97
5	A genomic glimpse of aminoacyl-tRNA synthetases in malaria parasite Plasmodium falciparum. BMC Genomics, 2009, 10, 644.	2.8	70
6	Global proteomic analysis of the oocyst/sporozoite of Toxoplasma gondiireveals commitment to a host-independent lifestyle. BMC Genomics, 2013, 14, 183.	2.8	54
7	Low-Complexity Regions in <i>Plasmodium falciparum</i> Proteins. Genome Research, 2001, 11, 218-229.	5.5	50
8	Set regulation in asexual and sexual Plasmodium parasites reveals a novel mechanism of stage-specific expression. Molecular Microbiology, 2006, 60, 870-882.	2.5	42
9	<i>Plasmodium</i> lipid rafts contain proteins implicated in vesicular trafficking and signalling as well as members of the PIR superfamily, potentially implicated in host immune system interactions. Proteomics, 2008, 8, 2500-2513.	2.2	37
10	A gene-family encoding small exported proteins is conserved across Plasmodium genus. Molecular and Biochemical Parasitology, 2003, 126, 209-218.	1.1	33
11	Low Complexity Regions behave as tRNA sponges to help coâ€ŧranslational folding of plasmodial proteins. FEBS Letters, 2010, 584, 448-454.	2.8	32
12	Mapping epitopes on protein surfaces. Biopolymers, 1995, 36, 675-680.	2.4	31
13	Redesigning the substrate specificity of the hepatitis C virus NS3 protease. Folding & Design, 1996, 1, 35-42.	4.5	26
14	Pentamer vocabularies characterizing introns and intron-like intergenic tracts from Caenorhabditis elegans and Drosophila melanogaster. Gene, 2003, 304, 183-192.	2.2	26
15	Core promoters are predicted by their distinct physicochemical properties in the genome of Plasmodium falciparum. Genome Biology, 2008, 9, R178.	9.6	26
16	Detection of latent sequence periodicities. Nucleic Acids Research, 1990, 18, 3745-3752.	14.5	21
17	Divergence of Noncoding Sequences and of Insertions Encoding Nonglobular Domains at a Genomic Region Well Conserved in Plasmodia. Journal of Molecular Evolution, 2000, 50, 474-480.	1.8	21
18	Revisiting the Plasmodium falciparum RIFIN family: from comparative genomics to 3D-model prediction. BMC Genomics, 2009, 10, 445.	2.8	20

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19	Proteomic Analysis of Detergent-resistant Membrane Microdomains in Trophozoite Blood Stage of the Human Malaria Parasite Plasmodium falciparum. Molecular and Cellular Proteomics, 2013, 12, 3948-3961.	3.8	20
20	Similarity in oligonucleotide usage in introns and intergenic regions contributes to long-range correlation in the Caenorhabditis elegans genome. Gene, 1999, 232, 87-95.	2.2	19
21	A novel series of compositionally biased substitution matrices for comparing Plasmodium proteins. BMC Bioinformatics, 2008, 9, 236.	2.6	18
22	Extensive turnover of telomeric DNA at aPlasmodium bergheichromosomal extremity marked by a rare recombinational event. Nucleic Acids Research, 1992, 20, 4491-4497.	14.5	14
23	The putative gene for the first enzyme of glutathione biosynthesis in Plasmodium berghei and Plasmodium falciparum. Molecular and Biochemical Parasitology, 1999, 99, 33-40.	1.1	14
24	The immunological selection of recombinant peptides from Cryptosporidium parvum reveals 14 proteins expressed at the sporozoite stage, 7 of which are conserved in other apicomplexaâ~†. Molecular and Biochemical Parasitology, 2007, 152, 159-169.	1.1	14
25	An Integrated Approach to Explore Composition and Dynamics of Cholesterol-rich Membrane Microdomains in Sexual Stages of Malaria Parasite. Molecular and Cellular Proteomics, 2017, 16, 1801-1814.	3.8	14
26	Caveolin-1 Endows Order in Cholesterol-Rich Detergent Resistant Membranes. Biomolecules, 2019, 9, 287.	4.0	12
27	Homology-derived three-dimensional structure prediction of Candida cylindracea lipase. Lipids and Lipid Metabolism, 1992, 1165, 129-133.	2.6	10
28	A simple method for global sequence comparison. Nucleic Acids Research, 1992, 20, 131-136.	14.5	9
29	Dynamics of telomere turnover inPlasmodium berghei. Molecular Biology Reports, 1994, 20, 27-33.	2.3	7
30	Dictionary-based methods for information extraction. Physica A: Statistical Mechanics and Its Applications, 2004, 342, 294-300.	2.6	6
31	A Comprehensive Gender-related Secretome of Plasmodium berghei Sexual Stages. Molecular and Cellular Proteomics, 2020, 19, 1986-1997.	3.8	6
32	Fine structure of Plasmodium falciparum subtelomeric sequences. Molecular and Biochemical Parasitology, 2001, 118, 253-258.	1.1	5
33	Phylo_dCor: distance correlation as a novel metric for phylogenetic profiling. BMC Bioinformatics, 2017, 18, 396.	2.6	4
34	A new parameter to study compositional properties of non-coding regions in eukaryotic genomes. Gene, 2006, 385, 75-82.	2.2	3
35	Functional genomics, new tools in malaria research. Annali Dell'Istituto Superiore Di Sanita, 2005, 41, 469-77.	0.4	3
36	A database system for handling phage library-derived sequences. Gene, 1993, 128, 143-144.	2.2	2

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37	Structural organization of erythrocyte membrane microdomains and their relation with malaria susceptibility. Communications Biology, 2021, 4, 1375.	4.4	2
38	Identification and preliminary characterization of Plasmodium falciparum proteins secreted upon gamete formation. Scientific Reports, 2022, 12, .	3.3	2