## Elisabetta Pizzi

## List of Publications by Year in descending order

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430874 395702 1,132 38 18 33 citations h-index g-index papers 38 38 38 1590 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Identification and preliminary characterization of Plasmodium falciparum proteins secreted upon gamete formation. Scientific Reports, 2022, $12$ , .	3.3	2
2	Structural organization of erythrocyte membrane microdomains and their relation with malaria susceptibility. Communications Biology, 2021, 4, 1375.	4.4	2
3	A Comprehensive Gender-related Secretome of Plasmodium berghei Sexual Stages. Molecular and Cellular Proteomics, 2020, 19, 1986-1997.	3.8	6
4	Caveolin-1 Endows Order in Cholesterol-Rich Detergent Resistant Membranes. Biomolecules, 2019, 9, 287.	4.0	12
5	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
6	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
7	Phylo_dCor: distance correlation as a novel metric for phylogenetic profiling. BMC Bioinformatics, 2017, 18, 396.	2.6	4
8	Global proteomic analysis of the oocyst/sporozoite of Toxoplasma gondiireveals commitment to a host-independent lifestyle. BMC Genomics, 2013, 14, 183.	2.8	54
9	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
10	Low Complexity Regions behave as tRNA sponges to help coâ€translational folding of plasmodial proteins. FEBS Letters, 2010, 584, 448-454.	2.8	32
11	A genomic glimpse of aminoacyl-tRNA synthetases in malaria parasite Plasmodium falciparum. BMC Genomics, 2009, 10, 644.	2.8	70
12	Revisiting the Plasmodium falciparum RIFIN family: from comparative genomics to 3D-model prediction. BMC Genomics, 2009, 10, 445.	2.8	20
13	<b><i>Plasmodium</i></b> 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
14	A novel series of compositionally biased substitution matrices for comparing Plasmodium proteins. BMC Bioinformatics, 2008, 9, 236.	2.6	18
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	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
17	A new parameter to study compositional properties of non-coding regions in eukaryotic genomes. Gene, 2006, 385, 75-82.	2.2	3
18	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

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19	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
20	Functional genomics, new tools in malaria research. Annali Dell'Istituto Superiore Di Sanita, 2005, 41, 469-77.	0.4	3
21	Dictionary-based methods for information extraction. Physica A: Statistical Mechanics and Its Applications, 2004, 342, 294-300.	2.6	6
22	A gene-family encoding small exported proteins is conserved across Plasmodium genus. Molecular and Biochemical Parasitology, 2003, 126, 209-218.	1.1	33
23	Pentamer vocabularies characterizing introns and intron-like intergenic tracts from Caenorhabditis elegans and Drosophila melanogaster. Gene, 2003, 304, 183-192.	2.2	26
24	Fine structure of Plasmodium falciparum subtelomeric sequences. Molecular and Biochemical Parasitology, 2001, 118, 253-258.	1.1	5
25	Low-Complexity Regions in <i>Plasmodium falciparum</i> Proteins. Genome Research, 2001, 11, 218-229.	5.5	50
26	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
27	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
28	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
29	Redesigning the substrate specificity of the hepatitis C virus NS3 protease. Folding & Design, 1996, 1, 35-42.	4.5	26
30	Mapping epitopes on protein surfaces. Biopolymers, 1995, 36, 675-680.	2.4	31
31	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
32	Variability within the Candida rugosa Upases family. Protein Engineering, Design and Selection, 1994, 7, 531-535.	2.1	97
33	Dynamics of telomere turnover inPlasmodium berghei. Molecular Biology Reports, 1994, 20, 27-33.	2.3	7
34	A database system for handling phage library-derived sequences. Gene, 1993, 128, 143-144.	2.2	2
35	A simple method for global sequence comparison. Nucleic Acids Research, 1992, 20, 131-136.	14.5	9
36	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

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37	Homology-derived three-dimensional structure prediction of Candida cylindracea lipase. Lipids and Lipid Metabolism, 1992, 1165, 129-133.	2.6	10
38	Detection of latent sequence periodicities. Nucleic Acids Research, 1990, 18, 3745-3752.	14.5	21