

Sedigheh Zakeri

List of Publications by Year in descending order

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Version: 2024-02-01

122
papers

2,916
citations

201674

27
h-index

223800

46
g-index

124
all docs

124
docs citations

124
times ranked

3533
citing authors

#	ARTICLE	IF	CITATIONS
1	A Worldwide Map of <i>Plasmodium falciparum</i> K13-Propeller Polymorphisms. <i>New England Journal of Medicine</i> , 2016, 374, 2453-2464.	27.0	449
2	Multiple independent introductions of <i>Plasmodium falciparum</i> in South America. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 511-516.	7.1	100
3	Identification of the Midgut Microbiota of <i>An. stephensi</i> and <i>An. maculipennis</i> for Their Application as a Paratransgenic Tool against Malaria. <i>PLoS ONE</i> , 2011, 6, e28484.	2.5	91
4	Detection of malaria parasites by nested PCR in south-eastern, Iran: evidence of highly mixed infections in Chahbahar district. <i>Malaria Journal</i> , 2002, 1, 2.	2.3	78
5	In vitro and in vivo anti-malarial activity of <i>Boerhavia elegans</i> and <i>Solanum surattense</i> . <i>Malaria Journal</i> , 2010, 9, 124.	2.3	72
6	Molecular identification of Palearctic members of <i>Anopheles maculipennis</i> in northern Iran. <i>Malaria Journal</i> , 2007, 6, 6.	2.3	66
7	In vitro antiplasmodial and phytochemical study of five <i>Artemisia</i> species from Iran and in vivo activity of two species. <i>Parasitology Research</i> , 2010, 107, 593-599.	1.6	65
8	Survey for asymptomatic malaria cases in low transmission settings of Iran under elimination programme. <i>Malaria Journal</i> , 2012, 11, 126.	2.3	65
9	<i>Leptospira wolffii</i> , a potential new pathogenic <i>Leptospira</i> species detected in human, sheep and dog. <i>Infection, Genetics and Evolution</i> , 2010, 10, 273-277.	2.3	63
10	Mice Orally Immunized with a Transgenic Plant Expressing the Glycoprotein of Crimean-Congo Hemorrhagic Fever Virus. <i>Vaccine Journal</i> , 2011, 18, 2031-2037.	3.1	63
11	First Record of a New Member of <i>Anopheles</i> Hyrcanus Group From Iran: Molecular Identification, Diagnosis, Phylogeny, Status of <i>kdr</i> Resistance and <i>Plasmodium</i> Infection. <i>Journal of Medical Entomology</i> , 2009, 46, 1084-1093.	1.8	54
12	Circumsporozoite protein gene diversity among temperate and tropical <i>Plasmodium vivax</i> isolates from Iran. <i>Tropical Medicine and International Health</i> , 2006, 11, 729-737.	2.3	53
13	Genetic analysis of rDNA-ITS2 and RAPD loci in field populations of the malaria vector, <i>Anopheles stephensi</i> (Diptera: Culicidae): Implications for the control program in Iran. <i>Acta Tropica</i> , 2006, 97, 65-74.	2.0	48
14	Quinoline resistance associated polymorphisms in the <i>pfcr</i> , <i>pfmdr1</i> and <i>pfmrp</i> genes of <i>Plasmodium falciparum</i> in Iran. <i>Acta Tropica</i> , 2006, 97, 352-356.	2.0	47
15	Molecular characterization of <i>Plasmodium vivax</i> clinical isolates in Pakistan and Iran using <i>pvm</i> sp-1, <i>pvm</i> sp-3 and <i>pv</i> csp genes as molecular markers. <i>Parasitology International</i> , 2010, 59, 15-21.	1.3	47
16	Isolation and identification of <i>Asaia</i> sp. in <i>Anopheles</i> spp. mosquitoes collected from Iranian malaria settings: steps toward applying paratransgenic tools against malaria. <i>Parasites and Vectors</i> , 2018, 11, 367.	2.5	44
17	Merozoite surface protein-3 is a reliable marker for population genetic analysis of <i>Plasmodium vivax</i> . <i>Malaria Journal</i> , 2006, 5, 53.	2.3	41
18	POPULATION STRUCTURE ANALYSIS OF <i>PLASMODIUM VIVAX</i> IN AREAS OF IRAN WITH DIFFERENT MALARIA ENDEMICITY. <i>American Journal of Tropical Medicine and Hygiene</i> , 2006, 74, 394-400.	1.4	39

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19	Genetic variation of TLR-4, TLR-9 and TIRAP genes in Iranian malaria patients. <i>Malaria Journal</i> , 2011, 10, 77.	2.3	38
20	Molecular Characterization of the Carboxypeptidase B1 of <i>Anopheles stephensi</i> and Its Evaluation as a Target for Transmission-Blocking Vaccines. <i>Infection and Immunity</i> , 2013, 81, 2206-2216.	2.2	36
21	Molecular characterization of antifolates resistance-associated genes, (dhfr and dhps) in <i>Plasmodium vivax</i> isolates from the Middle East. <i>Malaria Journal</i> , 2009, 8, 20.	2.3	34
22	Molecular Epidemiology of Leptospirosis in Northern Iran by Nested Polymerase Chain Reaction/Restriction Fragment Length Polymorphism and Sequencing Methods. <i>American Journal of Tropical Medicine and Hygiene</i> , 2010, 82, 899-903.	1.4	33
23	Genetic structure of <i>Plasmodium vivax</i> isolates from two malaria endemic areas in Afghanistan. <i>Acta Tropica</i> , 2010, 113, 12-19.	2.0	33
24	Association of pfcr1 But Not pfmdr1 Alleles with Chloroquine Resistance in Iranian Isolates of <i>Plasmodium falciparum</i> . <i>American Journal of Tropical Medicine and Hygiene</i> , 2008, 78, 633-640.	1.4	33
25	A simple and rapid nested polymerase chain reaction–restriction fragment length polymorphism technique for differentiation of pathogenic and nonpathogenic <i>Leptospira</i> spp.. <i>Diagnostic Microbiology and Infectious Disease</i> , 2009, 63, 251-256.	1.8	32
26	Population genetic structure and polymorphism analysis of gene encoding apical membrane antigen-1 (AMA-1) of Iranian <i>Plasmodium vivax</i> wild isolates. <i>Acta Tropica</i> , 2013, 126, 269-279.	2.0	31
27	Multiple genotypes of the merozoite surface proteins 1 and 2 in <i>Plasmodium falciparum</i> infections in a hypoendemic area in Iran. <i>Tropical Medicine and International Health</i> , 2005, 10, 1060-1064.	2.3	30
28	Chemical Composition and Antimicrobial Activities of Iranian Propolis. <i>Iranian Biomedical Journal</i> , 2018, 22, 50-65.	0.7	30
29	Genetic Mapping of the Duffy Binding Protein (DBP) Ligand Domain of <i>Plasmodium vivax</i> from Unstable Malaria Region in the Middle East. <i>American Journal of Tropical Medicine and Hygiene</i> , 2009, 80, 112-118.	1.4	30
30	Genetic diversity of transmission blocking vaccine candidate (Pvs25 and Pvs28) antigen in <i>Plasmodium vivax</i> clinical isolates from Iran. <i>Acta Tropica</i> , 2009, 109, 176-180.	2.0	26
31	IgG subclasses pattern and high-avidity antibody to the C-terminal region of merozoite surface protein 1 of <i>Plasmodium vivax</i> in an unstable hypoendemic region in Iran. <i>Acta Tropica</i> , 2009, 112, 1-7.	2.0	26
32	Human <i>Plasmodium vivax</i> diversity, population structure and evolutionary origin. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008072.	3.0	26
33	Measuring of IgG2c isotype instead of IgG2a in immunized C57BL/6 mice with <i>Plasmodium vivax</i> TRAP as a subunit vaccine candidate in order to correct interpretation of Th1 versus Th2 immune response. <i>Experimental Parasitology</i> , 2020, 216, 107944.	1.2	24
34	Detection of mixed <i>Plasmodium falciparum</i> & <i>P. vivax</i> infections by nested-PCR in Pakistan, Iran & Afghanistan. <i>Indian Journal of Medical Research</i> , 2010, 132, 31-5.	1.0	24
35	Antibody Responses and Avidity of Naturally Acquired Anti- <i>Plasmodium vivax</i> Duffy Binding Protein (PvDBP) Antibodies in Individuals from an Area with Unstable Malaria Transmission. <i>American Journal of Tropical Medicine and Hygiene</i> , 2011, 84, 944-950.	1.4	23
36	Spontaneous Mutations in the <i>Plasmodium falciparum</i> Sarcoplasmic/ Endoplasmic Reticulum Ca ²⁺ -ATPase (PfATP6) Gene among Geographically Widespread Parasite Populations Unexposed to Artemisinin-Based Combination Therapies. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 94-100.	3.2	23

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37	Population structure analysis of <i>Plasmodium vivax</i> in areas of Iran with different malaria endemicity. <i>American Journal of Tropical Medicine and Hygiene</i> , 2006, 74, 394-400.	1.4	23
38	Limited genetic diversity in the global <i>Plasmodium vivax</i> Cell traversal protein of Ookinetes and Sporozoites (CelTOS) sequences; implications for PvCelTOS-based vaccine development. <i>Infection, Genetics and Evolution</i> , 2017, 53, 239-247.	2.3	22
39	Molecular characterization of matrix metalloproteinase-1 (MMP-1) in <i>Lucilia sericata</i> larvae for potential therapeutic applications. <i>Electronic Journal of Biotechnology</i> , 2017, 29, 47-56.	2.2	22
40	High prevalence of the 437G mutation associated with sulfadoxine resistance among <i>Plasmodium falciparum</i> clinical isolates from Iran, three years after the introduction of sulfadoxine-pyrimethamine. <i>International Journal of Infectious Diseases</i> , 2010, 14, e123-e128.	3.3	21
41	Molecular surveillance of <i>Plasmodium vivax</i> dhfr and dhps mutations in isolates from Afghanistan. <i>Malaria Journal</i> , 2010, 9, 75.	2.3	20
42	<i>Plasmodium vivax</i> : Prevalence of mutations associated with sulfadoxine-pyrimethamine resistance in <i>Plasmodium vivax</i> clinical isolates from Pakistan. <i>Experimental Parasitology</i> , 2011, 127, 167-172.	1.2	20
43	Population genetics and natural selection in the gene encoding the Duffy binding protein II in Iranian <i>Plasmodium vivax</i> wild isolates. <i>Infection, Genetics and Evolution</i> , 2014, 21, 424-435.	2.3	20
44	Evolutionary analyses of the major variant surface antigen-encoding genes reveal population structure of <i>Plasmodium falciparum</i> within and between continents. <i>PLoS Genetics</i> , 2021, 17, e1009269.	3.5	20
45	Association of pfcrt but not pfmdr1 alleles with chloroquine resistance in Iranian isolates of <i>Plasmodium falciparum</i> . <i>American Journal of Tropical Medicine and Hygiene</i> , 2008, 78, 633-40.	1.4	20
46	Genetic mapping of the duffy binding protein (DBP) ligand domain of <i>Plasmodium vivax</i> from unstable malaria region in the Middle East. <i>American Journal of Tropical Medicine and Hygiene</i> , 2009, 80, 112-8.	1.4	20
47	Molecular monitoring of <i>Plasmodium falciparum</i> resistance to antimalarial drugs after adoption of sulfadoxine-pyrimethamine plus artesunate as the first line treatment in Iran. <i>Acta Tropica</i> , 2012, 121, 13-18.	2.0	19
48	New Insights Into Culturable and Unculturable Bacteria Across the Life History of Medicinal Maggots <i>Lucilia sericata</i> (Meigen) (Diptera: Calliphoridae). <i>Frontiers in Microbiology</i> , 2020, 11, 505.	3.5	19
49	Cell-traversal protein for ookinetes and sporozoites (CelTOS) formulated with potent TLR adjuvants induces high-affinity antibodies that inhibit <i>Plasmodium falciparum</i> infection in <i>Anopheles stephensi</i> . <i>Malaria Journal</i> , 2019, 18, 146.	2.3	18
50	<i>Plasmodium falciparum</i> : Sequence analysis of the gene encoding the C-terminus region of the merozoite surface protein-1, a potential malaria vaccine antigen, in Iranian clinical isolates. <i>Experimental Parasitology</i> , 2008, 118, 378-385.	1.2	17
51	Mutation analysis in pfmdr1 and pfmrp1 as potential candidate genes for artemisinin resistance in <i>Plasmodium falciparum</i> clinical isolates 4 years after implementation of artemisinin combination therapy in Iran. <i>Infection, Genetics and Evolution</i> , 2013, 14, 327-334.	2.3	17
52	Naturally acquired immune responses to thrombospondin-related adhesion protein (TRAP) of <i>Plasmodium vivax</i> in patients from areas of unstable malaria transmission. <i>Acta Tropica</i> , 2017, 173, 45-54.	2.0	17
53	High Prevalence of Double <i>Plasmodium falciparum</i> dhfr Mutations at Codons 108 and 59 in the Sistan-Baluchistan Province, Iran. <i>Journal of Infectious Diseases</i> , 2003, 187, 1828-1829.	4.0	16
54	Identification, Sequence Analysis, and Comparative Study on GSTe2 Insecticide Resistance Gene in Three Main World Malaria Vectors: <i>Anopheles stephensi</i> , <i>Anopheles culicifacies</i> , and <i>Anopheles fluviatilis</i> . <i>Journal of Medical Entomology</i> , 2006, 43, 1171-1177.	1.8	16

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55	Prevalence of mutations associated with antimalarial drugs in <i>Plasmodium falciparum</i> isolates prior to the introduction of sulphadoxine-pyrimethamine as first-line treatment in Iran. <i>Malaria Journal</i> , 2007, 6, 148.	2.3	16
56	Immune responses elicited by co-immunization of <i>Plasmodium vivax</i> and <i>P. falciparum</i> MSP-1 using prime-boost immunization strategies. <i>Parasite Immunology</i> , 2011, 33, 594-608.	1.5	16
57	Molecular genetic analysis of <i>Plasmodium vivax</i> isolates from Eastern and Central Sudan using <i>pvcsp</i> and <i>pvmsp-3</i> genes as molecular markers. <i>Infection, Genetics and Evolution</i> , 2015, 32, 12-22.	2.3	16
58	Absence of asymptomatic malaria infection in endemic area of bashagard district, hormozgan province, iran. <i>Iranian Journal of Parasitology</i> , 2012, 7, 36-44.	0.6	16
59	Sequence heterogeneity of the merozoite surface protein-1 gene (MSP-1) of <i>Plasmodium vivax</i> wild isolates in southeastern Iran. <i>Acta Tropica</i> , 2003, 88, 91-97.	2.0	15
60	Co-occurrence of pederin-producing and <i>Wolbachia</i> endobacteria in <i>Paederus fuscipes</i> Curtis, 1840 (Coleoptera: Staphilinidae) and its evolutionary consequences. <i>MicrobiologyOpen</i> , 2019, 8, e777.	3.0	15
61	Non-variant specific antibody responses to the C-terminal region of merozoite surface protein-1 of <i>Plasmodium falciparum</i> (PfMSP-119) in Iranians exposed to unstable malaria transmission. <i>Malaria Journal</i> , 2010, 9, 257.	2.3	14
62	Molecular assessment of <i>atpase6</i> mutations associated with artemisinin resistance among unexposed and exposed <i>Plasmodium falciparum</i> clinical isolates to artemisinin-based combination therapy. <i>Malaria Journal</i> , 2012, 11, 373.	2.3	14
63	Combining Monophosphoryl Lipid A (MPL), CpG Oligodeoxynucleotide (ODN), and QS-21 Adjuvants Induces Strong and Persistent Functional Antibodies and T Cell Responses against Cell-Traversal Protein for Ookinetes and Sporozoites (CelTOS) of <i>Plasmodium falciparum</i> in BALB/c Mice. <i>Infection and Immunity</i> , 2019, 87, .	2.2	14
64	RESTRICTED T-CELL EPITOPE DIVERSITY IN THE CIRCUMSPOROZOITE PROTEIN FROM <i>PLASMODIUM FALCIPARUM</i> POPULATIONS PREVALENT IN IRAN. <i>American Journal of Tropical Medicine and Hygiene</i> , 2007, 76, 1046-1051.	1.4	14
65	Molecular evidence of mixed <i>P. vivax</i> and <i>P. falciparum</i> infections in northern Islamic Republic of Iran. <i>Eastern Mediterranean Health Journal</i> , 2004, 10, 336-342.	0.8	14
66	Anti-Plasmodial Assessment of Four Different Iranian Propolis Extracts. <i>Archives of Iranian Medicine</i> , 2017, 20, 270-281.	0.6	14
67	Molecular assessment of <i>dhfr/dhps</i> mutations among <i>Plasmodium vivax</i> clinical isolates after introduction of sulfadoxine/pyrimethamine in combination with artesunate in Iran. <i>Infection, Genetics and Evolution</i> , 2012, 12, 38-44.	2.3	13
68	Population genetics, sequence diversity and selection in the gene encoding the <i>Plasmodium falciparum</i> apical membrane antigen 1 in clinical isolates from the south-east of Iran. <i>Infection, Genetics and Evolution</i> , 2013, 17, 51-61.	2.3	13
69	Morphological and Molecular Characteristic of <i>Megaselia scalaris</i> (Diptera: Phoridae) Larvae as the Cause of Urinary Myiasis. <i>Journal of Medical Entomology</i> , 2017, 54, 781-784.	1.8	13
70	Molecular evidence of mixed <i>P. vivax</i> and <i>P. falciparum</i> infections in northern Islamic Republic of Iran. <i>Eastern Mediterranean Health Journal</i> , 2004, 10, 336-42.	0.8	13
71	Comparative analysis of the profiles of IgG subclass-specific responses to <i>Plasmodium falciparum</i> apical membrane antigen-1 and merozoite surface protein-1 in naturally exposed individuals living in malaria hypoendemic settings, Iran. <i>Malaria Journal</i> , 2015, 14, 58.	2.3	12
72	IgG subclass antibodies to three variants of <i>Plasmodium falciparum</i> merozoite surface protein-1 (PfMSP-119) in an area with unstable malaria transmission in Iran. <i>Acta Tropica</i> , 2011, 119, 84-90.	2.0	11

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73	Population genetics structure of <i>Plasmodium vivax</i> circumsporozoite protein during the elimination process in low and unstable malaria transmission areas, southeast of Iran. <i>Acta Tropica</i> , 2016, 160, 23-34.	2.0	11
74	Detection of arboviruses in mosquitoes: Evidence of circulation of chikungunya virus in Iran. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008135.	3.0	11
75	Dynamics of prevalence and distribution pattern of avian <i>Plasmodium</i> species and its vectors in diverse zoogeographical areas - A review. <i>Infection, Genetics and Evolution</i> , 2020, 81, 104244.	2.3	11
76	Identification, Sequence Analysis, and Comparative Study on GSTe2 Insecticide Resistance Gene in Three Main World Malaria Vectors: <i>Anopheles stephensi</i> , <i>Anopheles culicifacies</i> , and <i>Anopheles fluviatilis</i> . <i>Journal of Medical Entomology</i> , 2006, 43, 1171-1177.	1.8	10
77	Non-allele specific antibody responses to genetically distinct variant forms of <i>Plasmodium vivax</i> Duffy binding protein (PvDBP-II) in Iranians exposed to seasonal malaria transmission. <i>Acta Tropica</i> , 2014, 136, 89-100.	2.0	10
78	High prevalence of pfdhfrâ€“pfdhps triple mutations associated with anti-malarial drugs resistance in <i>Plasmodium falciparum</i> isolates seven years after the adoption of sulfadoxineâ€“pyrimethamine in combination with artesunate as first-line treatment in Iran. <i>Infection, Genetics and Evolution</i> , 2015, 31, 183-189.	2.3	10
79	Analysis of genetic diversity and population structure of gene encoding cell-traversal protein for ookinetes and sporozoites (CelTOS) vaccine candidate antigen in global <i>Plasmodium falciparum</i> populations. <i>Infection, Genetics and Evolution</i> , 2018, 59, 113-125.	2.3	10
80	Poly(I:C) adjuvant strongly enhances parasite-inhibitory antibodies and Th1 response against <i>Plasmodium falciparum</i> merozoite surface protein-1 (42-kDa fragment) in BALB/c mice. <i>Medical Microbiology and Immunology</i> , 2018, 207, 151-166.	4.8	10
81	Gene copy number and function of the APL1 immune factor changed during <i>Anopheles</i> evolution. <i>Parasites and Vectors</i> , 2020, 13, 18.	2.5	10
82	Biological, immunological and functional properties of two novel multi-variant chimeric recombinant proteins of CSP antigens for vaccine development against <i>Plasmodium vivax</i> infection. <i>Molecular Immunology</i> , 2017, 90, 158-171.	2.2	9
83	Genetic variability of CYP2B6 polymorphisms in southeast Iranian population: implications for malaria and HIV/AIDS treatment. <i>Archives of Iranian Medicine</i> , 2014, 17, 685-91.	0.6	9
84	Anti-malarial seroprevalence assessment during an elimination programme in Chabahar District, south-eastern Iran. <i>Malaria Journal</i> , 2016, 15, 382.	2.3	8
85	Th1 immune response to <i>Plasmodium falciparum</i> recombinant thrombospondinâ€“related adhesive protein (TRAP) antigen is enhanced by TLR3â€“specific adjuvant, poly(I:C) in <i>BALB/c</i> mice. <i>Parasite Immunology</i> , 2018, 40, e12538.	1.5	8
86	Immunological evaluation of two novel engineered <i>Plasmodium vivax</i> circumsporozoite proteins formulated with different human-compatible vaccine adjuvants in C57BL/6 mice. <i>Medical Microbiology and Immunology</i> , 2019, 208, 731-745.	4.8	8
87	Heterogeneity in the acquisition of naturally acquired antibodies to cell-traversal protein for ookinetes and sporozoites (CelTOS) and thrombospondin-related adhesion protein (TRAP) of <i>Plasmodium falciparum</i> in naturally infected patients from unstable malaria areas in Iran. <i>Acta Tropica</i> , 2019, 190, 365-374.	2.0	8
88	A review of combination adjuvants for malaria vaccines: a promising approach for vaccine development. <i>International Journal for Parasitology</i> , 2021, 51, 699-717.	3.1	8
89	Restricted T-cell epitope diversity in the circumsporozoite protein from <i>Plasmodium falciparum</i> populations prevalent in Iran. <i>American Journal of Tropical Medicine and Hygiene</i> , 2007, 76, 1046-51.	1.4	8
90	Analysis of von Willebrand factor A domain-related protein (WARP) polymorphism in temperate and tropical <i>Plasmodium vivax</i> field isolates. <i>Malaria Journal</i> , 2009, 8, 137.	2.3	7

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91	Screening urinalysis in dogs with urinary shedding of leptospires. <i>Comparative Clinical Pathology</i> , 2010, 19, 271-274.	0.7	7
92	Cloning, expression and transmission-blocking activity of anti-PvWARP, malaria vaccine candidate, in <i>Anopheles stephensi</i> mysorensis. <i>Malaria Journal</i> , 2010, 9, 158.	2.3	7
93	Prevalence of mutations in the antifolates resistance-associated genes (dhfr and dhps) in <i>Plasmodium vivax</i> parasites from Eastern and Central Sudan. <i>Infection, Genetics and Evolution</i> , 2014, 26, 153-159.	2.3	7
94	Vaccine adjuvants CpG (oligodeoxynucleotides ODNs), MPL (3-O-deacylated monophosphoryl lipid A) and naloxone-enhanced Th1 immune response to the <i>Plasmodium vivax</i> recombinant thrombospondin-related adhesive protein (TRAP) in mice. <i>Medical Microbiology and Immunology</i> , 2018, 207, 271-286.	4.8	7
95	Polar <i>Plasmodium falciparum</i> lipids induce lipogenesis in rat adipocytes in vitro. <i>Microbes and Infection</i> , 2000, 2, 1789-1798.	1.9	6
96	Single nucleotide polymorphisms in <i>Plasmodium falciparum</i> V type H+ pyrophosphatase gene (pfvp2) and their associations with pfcr1 and pfmdr1 polymorphisms. <i>Infection, Genetics and Evolution</i> , 2014, 24, 111-115.	2.3	6
97	Administration of naloxone in combination with recombinant <i>Plasmodium vivax</i> AMA-1 in BALB/c mice induces mixed Th1/Th2 immune responses. <i>Parasite Immunology</i> , 2015, 37, 521-532.	1.5	6
98	Natural acquired inhibitory antibodies to <i>Plasmodium vivax</i> Duffy binding protein (PvDBP-II) equally block erythrocyte binding of homologous and heterologous expressed PvDBP-II on the surface of COS-7 cells. <i>Medical Microbiology and Immunology</i> , 2016, 205, 85-95.	4.8	6
99	Mosquito-borne viral diseases and potential transmission blocking vaccine candidates. <i>Infection, Genetics and Evolution</i> , 2018, 63, 195-203.	2.3	6
100	How can we develop an effective subunit vaccine to achieve successful malaria eradication?. <i>Microbial Pathogenesis</i> , 2021, 160, 105203.	2.9	6
101	Monitoring pyrethroid insecticide resistance in major malaria vector <i>Anopheles culicifacies</i> : comparison of molecular tools and conventional susceptibility test. <i>Iranian Biomedical Journal</i> , 2007, 11, 169-176.	0.7	6
102	A comparative study on worldwide genetic diversity and population structure analysis of <i>Plasmodium vivax</i> thrombospondin-related adhesive protein (PvTRAP) and its implications for the vivax vaccine design. <i>Infection, Genetics and Evolution</i> , 2015, 36, 410-423.	2.3	5
103	Multiple Genotypes of the Commonly Co-Segregating Toll-Like Receptor 4 Asp299Gly and Thr399Ile in Baluchi Malaria Patients from Iran. <i>Cell Journal</i> , 2013, 15, 182-9.	0.2	5
104	Genotyping <i>Plasmodium vivax</i> isolates infecting <i>Anopheles stephensi</i> , an Asian main malaria vector. <i>Experimental Parasitology</i> , 2013, 134, 48-51.	1.2	4
105	Identification, molecular characterization and expression of aminopeptidase N-1 (APN-1) from <i>Anopheles stephensi</i> in SF9 cell line as a candidate molecule for developing a vaccine that interrupt malaria transmission. <i>Malaria Journal</i> , 2020, 19, 79.	2.3	4
106	Population genetic structure analysis of thrombospondin-related adhesive protein (TRAP) as a vaccine candidate antigen in worldwide <i>Plasmodium falciparum</i> isolates. <i>Infection, Genetics and Evolution</i> , 2020, 80, 104197.	2.3	4
107	Serological evidence of West Nile virus infection among birds and horses in some geographical locations of Iran. <i>Veterinary Medicine and Science</i> , 2021, 7, 204-209.	1.6	4
108	Absence of Asymptomatic Malaria Infection in a Cross-sectional Study in Iranshahr District, Iran under Elimination Programmes. <i>Iranian Journal of Parasitology</i> , 2017, 12, 90-100.	0.6	4

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109	Synthesis and antiplasmodial activity of novel phenanthroline derivatives: An study. Iranian Journal of Basic Medical Sciences, 2018, 21, 202-211.	1.0	4
110	Evaluation of Naturally Acquired Antibody Responses to Two Variant Forms of Plasmodium vivax Apical Membrane Antigen-1 in Individuals Living in Areas of Low and Unstable Malaria Transmission of Iran. Archives of Iranian Medicine, 2015, 18, 834-43.	0.6	4
111	Identification and typing of Cameroonian isolates of P. malariae using monoclonal antibodies against P. brasilianum. Acta Tropica, 2006, 99, 97-101.	2.0	3
112	Limited genetic diversity and purifying selection in Iranian Plasmodium falciparum Generative Cell Specific 1 (PfGCS1), a potential target for transmission-blocking vaccine. Infection, Genetics and Evolution, 2014, 22, 150-156.	2.3	3
113	Worldwide population genetic analysis and natural selection in the Plasmodium vivax Generative Cell Specific 1 (PvGCS1) as a transmission-blocking vaccine candidate. Infection, Genetics and Evolution, 2016, 43, 50-57.	2.3	3
114	High Transmission Potential of West Nile Virus Lineage 1 for Cx. pipiens s.l. of Iran. Viruses, 2020, 12, 397.	3.3	3
115	Expression of a New Recombinant Collagenase Protein of in SF9 Insect Cell as a Potential Method for Wound Healing. Iranian Journal of Biotechnology, 2019, 17, e2429.	0.3	3
116	Analysis of Fcγ receptor IIa (cd32) gene polymorphism and anti-malarial IgG subclass antibodies to asexual blood-stage antigen of Plasmodium falciparum in an unstable malaria endemic area of Iran. Experimental Parasitology, 2013, 134, 115-121.	1.2	2
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