

Vivek Anantharaman

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

69
papers

6,610
citations

42
h-index

72
g-index

72
ext. papers

7,491
ext. citations

8.4
avg, IF

5.72
L-index

#	Paper	IF	Citations
69	Complete genome sequence of the apicomplexan, <i>Cryptosporidium parvum</i> . <i>Science</i> , 2004 , 304, 441-5	33.3	757
68	Comparative genomics and evolution of proteins involved in RNA metabolism. <i>Nucleic Acids Research</i> , 2002 , 30, 1427-64	20.1	383
67	The many faces of the helix-turn-helix domain: transcription regulation and beyond. <i>FEMS Microbiology Reviews</i> , 2005 , 29, 231-62	15.1	339
66	Polymorphic toxin systems: Comprehensive characterization of trafficking modes, processing, mechanisms of action, immunity and ecology using comparative genomics. <i>Biology Direct</i> , 2012 , 7, 18	7.2	309
65	The many faces of the helix-turn-helix domain: Transcription regulation and beyond. <i>FEMS Microbiology Reviews</i> , 2005 , 29, 231-262	15.1	300
64	Evolutionary history, structural features and biochemical diversity of the NlpC/P60 superfamily of enzymes. <i>Genome Biology</i> , 2003 , 4, R11	18.3	268
63	Comparative genomics, evolution and origins of the nuclear envelope and nuclear pore complex. <i>Cell Cycle</i> , 2004 , 3, 1612-37	4.7	263
62	Regulatory potential, phyletic distribution and evolution of ancient, intracellular small-molecule-binding domains. <i>Journal of Molecular Biology</i> , 2001 , 307, 1271-92	6.5	224
61	Comparative genomics of transcription factors and chromatin proteins in parasitic protists and other eukaryotes. <i>International Journal for Parasitology</i> , 2008 , 38, 1-31	4.3	206
60	Comparative Genomics, Evolution and Origins of the Nuclear Envelope and Nuclear Pore Complex. <i>Cell Cycle</i> , 2004 , 3, 1625-1650	4.7	206
59	New connections in the prokaryotic toxin-antitoxin network: relationship with the eukaryotic nonsense-mediated RNA decay system. <i>Genome Biology</i> , 2003 , 4, R81	18.3	199
58	Comprehensive analysis of the HEPN superfamily: identification of novel roles in intra-genomic conflicts, defense, pathogenesis and RNA processing. <i>Biology Direct</i> , 2013 , 8, 15	7.2	156
57	Comparative analysis of apicomplexa and genomic diversity in eukaryotes. <i>Genome Research</i> , 2004 , 14, 1686-95	9.7	149
56	Cache - a signaling domain common to animal Ca(2+)-channel subunits and a class of prokaryotic chemotaxis receptors. <i>Trends in Biochemical Sciences</i> , 2000 , 25, 535-7	10.3	149
55	Ancient conserved domains shared by animal soluble guanylyl cyclases and bacterial signaling proteins. <i>BMC Genomics</i> , 2003 , 4, 5	4.5	148
54	Emergence of diverse biochemical activities in evolutionarily conserved structural scaffolds of proteins. <i>Current Opinion in Chemical Biology</i> , 2003 , 7, 12-20	9.7	133
53	The CHASE domain: a predicted ligand-binding module in plant cytokinin receptors and other eukaryotic and bacterial receptors. <i>Trends in Biochemical Sciences</i> , 2001 , 26, 579-82	10.3	128

52	Monophyly of class I aminoacyl tRNA synthetase, USPA, ETFP, photolyase, and PP-ATPase nucleotide-binding domains: implications for protein evolution in the RNA. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 48, 1-14	4.2	123
51	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. <i>Frontiers in Genetics</i> , 2014 , 5, 102	4.5	118
50	The two faces of Alba: the evolutionary connection between proteins participating in chromatin structure and RNA metabolism. <i>Genome Biology</i> , 2003 , 4, R64	18.3	114
49	Molecular factors and biochemical pathways induced by febrile temperature in intraerythrocytic Plasmodium falciparum parasites. <i>Infection and Immunity</i> , 2007 , 75, 2012-25	3.7	111
48	The signaling helix: a common functional theme in diverse signaling proteins. <i>Biology Direct</i> , 2006 , 1, 25	7.2	101
47	The NYN domains: novel predicted RNAses with a PIN domain-like fold. <i>RNA Biology</i> , 2006 , 3, 18-27	4.8	97
46	SPOUT: a class of methyltransferases that includes spoU and trmD RNA methylase superfamilies, and novel superfamilies of predicted prokaryotic RNA methylases. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2002 , 4, 71-5	0.9	90
45	Live virus-free or die: coupling of antiviral immunity and programmed suicide or dormancy in prokaryotes. <i>Biology Direct</i> , 2012 , 7, 40	7.2	86
44	The GOLD domain, a novel protein module involved in Golgi function and secretion. <i>Genome Biology</i> , 2002 , 3, research0023	18.3	80
43	The mechanism of force transmission at bacterial focal adhesion complexes. <i>Nature</i> , 2016 , 539, 530-535	50.4	78
42	The ubiquitous yybP-ykoY riboswitch is a manganese-responsive regulatory element. <i>Molecular Cell</i> , 2015 , 57, 1099-1109	17.6	73
41	Application of comparative genomics in the identification and analysis of novel families of membrane-associated receptors in bacteria. <i>BMC Genomics</i> , 2003 , 4, 34	4.5	67
40	Novel conserved domains in proteins with predicted roles in eukaryotic cell-cycle regulation, decapping and RNA stability. <i>BMC Genomics</i> , 2004 , 5, 45	4.5	66
39	Ter-dependent stress response systems: novel pathways related to metal sensing, production of a nucleoside-like metabolite, and DNA-processing. <i>Molecular BioSystems</i> , 2012 , 8, 3142-65		61
38	MOSC domains: ancient, predicted sulfur-carrier domains, present in diverse metal-sulfur cluster biosynthesis proteins including Molybdenum cofactor sulfurases. <i>FEMS Microbiology Letters</i> , 2002 , 207, 55-61	2.9	61
37	OST-HTH: a novel predicted RNA-binding domain. <i>Biology Direct</i> , 2010 , 5, 13	7.2	59
36	TRAM, a predicted RNA-binding domain, common to tRNA uracil methylation and adenine thiolation enzymes. <i>FEMS Microbiology Letters</i> , 2001 , 197, 215-21	2.9	57
35	Gene flow and biological conflict systems in the origin and evolution of eukaryotes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012 , 2, 89	5.9	53

34	Comparative genomics of protists: new insights into the evolution of eukaryotic signal transduction and gene regulation. <i>Annual Review of Microbiology</i> , 2007 , 61, 453-75	17.5	52
33	The DOMON domains are involved in heme and sugar recognition. <i>Bioinformatics</i> , 2007 , 23, 2660-4	7.2	50
32	Novel eukaryotic enzymes modifying cell-surface biopolymers. <i>Biology Direct</i> , 2010 , 5, 1	7.2	49
31	Evolutionary connections between bacterial and eukaryotic signaling systems: a genomic perspective. <i>Current Opinion in Microbiology</i> , 2003 , 6, 490-7	7.9	47
30	Adhesion molecules and other secreted host-interaction determinants in Apicomplexa: insights from comparative genomics. <i>International Review of Cytology</i> , 2007 , 262, 1-74		46
29	HutC/FarR-like bacterial transcription factors of the GntR family contain a small molecule-binding domain of the chorismate lyase fold. <i>FEMS Microbiology Letters</i> , 2003 , 222, 17-23	2.9	45
28	Comparative genomics uncovers novel structural and functional features of the heterotrimeric GTPase signaling system. <i>Gene</i> , 2011 , 475, 63-78	3.8	43
27	Peptide-N-glycanases and DNA repair proteins, Xp-C/Rad4, are, respectively, active and inactivated enzymes sharing a common transglutaminase fold. <i>Human Molecular Genetics</i> , 2001 , 10, 1627-30	5.6	40
26	Analysis of DBC1 and its homologs suggests a potential mechanism for regulation of sirtuin domain deacetylases by NAD metabolites. <i>Cell Cycle</i> , 2008 , 7, 1467-72	4.7	36
25	Presence of a classical RRM-fold palm domain in Thg1-type 3U5U nucleic acid polymerases and the origin of the GGDEF and CRISPR polymerase domains. <i>Biology Direct</i> , 2010 , 5, 43	7.2	33
24	Heterogeneous nuclear ribonucleoprotein L-like (hnRNPLL) and elongation factor, RNA polymerase II, 2 (ELL2) are regulators of mRNA processing in plasma cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 16252-7	11.5	32
23	Pathogenic roles of CD14, galectin-3, and OX40 during experimental cerebral malaria in mice. <i>PLoS ONE</i> , 2009 , 4, e6793	3.7	30
22	ATP hydrolysis by a domain related to translation factor GTPases drives polymerization of a static bacterial morphogenetic protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E151-60	11.5	29
21	The PRC-barrel: a widespread, conserved domain shared by photosynthetic reaction center subunits and proteins of RNA metabolism. <i>Genome Biology</i> , 2002 , 3, RESEARCH0061	18.3	28
20	Host biomarkers and biological pathways that are associated with the expression of experimental cerebral malaria in mice. <i>Infection and Immunity</i> , 2008 , 76, 4518-29	3.7	26
19	Expression, Purification, and Biological Characterization of Babesia microti Apical Membrane Antigen 1. <i>Infection and Immunity</i> , 2015 , 83, 3890-901	3.7	21
18	The SHS2 module is a common structural theme in functionally diverse protein groups, like Rpb7p, FtsA, GyrI, and MTH1598/TM1083 superfamilies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 795-807	4.2	21
17	MEDS and PocR are novel domains with a predicted role in sensing simple hydrocarbon derivatives in prokaryotic signal transduction systems. <i>Bioinformatics</i> , 2005 , 21, 2805-11	7.2	20

16	Diversification of catalytic activities and ligand interactions in the protein fold shared by the sugar isomerases, eIF2B, DeoR transcription factors, acyl-CoA transferases and methenyltetrahydrofolate synthetase. <i>Journal of Molecular Biology</i> , 2006 , 356, 823-42	6.5	17
15	Structure-function analysis of manganese exporter proteins across bacteria. <i>Journal of Biological Chemistry</i> , 2018 , 293, 5715-5730	5.4	16
14	Radiation-induced cellular and molecular alterations in asexual intraerythrocytic Plasmodium falciparum. <i>Journal of Infectious Diseases</i> , 2013 , 207, 164-74	7	15
13	Molecular correlates of experimental cerebral malaria detectable in whole blood. <i>Infection and Immunity</i> , 2011 , 79, 1244-53	3.7	14
12	Jumbo Phages: A Comparative Genomic Overview of Core Functions and Adaptions for Biological Conflicts. <i>Viruses</i> , 2021 , 13,	6.2	14
11	Apprehending multicellularity: regulatory networks, genomics, and evolution. <i>Birth Defects Research Part C: Embryo Today Reviews</i> , 2009 , 87, 143-64		13
10	An autoinhibitory conformation of the Bacillus subtilis spore coat protein SpoIVA prevents its premature ATP-independent aggregation. <i>FEMS Microbiology Letters</i> , 2014 , 358, 145-53	2.9	12
9	AMIN domains have a predicted role in localization of diverse periplasmic protein complexes. <i>Bioinformatics</i> , 2008 , 24, 2423-6	7.2	12
8	Molecular Markers of Radiation Induced Attenuation in Intrahepatic Plasmodium falciparum Parasites. <i>PLoS ONE</i> , 2016 , 11, e0166814	3.7	12
7	TCR α -expressing macrophages induced by a pathogenic murine malaria correlate with parasite burden and enhanced phagocytic activity. <i>PLoS ONE</i> , 2018 , 13, e0201043	3.7	10
6	Antigen Discovery, Bioinformatics and Biological Characterization of Novel Immunodominant Babesia microti Antigens. <i>Scientific Reports</i> , 2020 , 10, 9598	4.9	5
5	Variations on a theme: evolution of the phage-shock-protein system in Actinobacteria. <i>Antonie Van Leeuwenhoek</i> , 2018 , 111, 753-760	2.1	3
4	Effects of Nucleoside Analogs on Native and Site-Directed Mutants of HTLV Type 1 Reverse Transcriptase. <i>Bioorganic Chemistry</i> , 2000 , 28, 293-305	5.1	3
3	Evolution of Eukaryotic Chromatin Proteins and Transcription Factors 2013 , 421-502		1
2	The Phage-shock-protein (PSP) Envelope Stress Response: Discovery of Novel Partners and Evolutionary History		1
1	Reformulation of an extant ATPase active site to mimic ancestral GTPase activity reveals a nucleotide base requirement for function. <i>ELife</i> , 2021 , 10,	8.9	1