

Vivek Anantharaman

List of Publications by Year in descending order

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69
papers

8,103
citations

61984

43
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91884

69
g-index

73
all docs

73
docs citations

73
times ranked

9612
citing authors

#	ARTICLE	IF	CITATIONS
1	Bacterial developmental checkpoint that directly monitors cell surface morphogenesis. <i>Developmental Cell</i> , 2022, 57, 344-360.e6.	7.0	10
2	Jumbo Phages: A Comparative Genomic Overview of Core Functions and Adaptions for Biological Conflicts. <i>Viruses</i> , 2021, 13, 63.	3.3	54
3	Reformulation of an extant ATPase active site to mimic ancestral GTPase activity reveals a nucleotide base requirement for function. <i>ELife</i> , 2021, 10, .	6.0	12
4	Antigen Discovery, Bioinformatics and Biological Characterization of Novel Immunodominant Babesia microti Antigens. <i>Scientific Reports</i> , 2020, 10, 9598.	3.3	15
5	Structure–function analysis of manganese exporter proteins across bacteria. <i>Journal of Biological Chemistry</i> , 2018, 293, 5715-5730.	3.4	44
6	Variations on a theme: evolution of the phage-shock-protein system in Actinobacteria. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 753-760.	1.7	7
7	TCR ^{hi} -expressing macrophages induced by a pathogenic murine malaria correlate with parasite burden and enhanced phagocytic activity. <i>PLoS ONE</i> , 2018, 13, e0201043.	2.5	29
8	Molecular Markers of Radiation Induced Attenuation in Intrahepatic Plasmodium falciparum Parasites. <i>PLoS ONE</i> , 2016, 11, e0166814.	2.5	13
9	The mechanism of force transmission at bacterial focal adhesion complexes. <i>Nature</i> , 2016, 539, 530-535.	27.8	120
10	The Ubiquitous yyb-ykoY Riboswitch Is a Manganese-Responsive Regulatory Element. <i>Molecular Cell</i> , 2015, 57, 1099-1109.	9.7	120
11	Expression, Purification, and Biological Characterization of Babesia microti Apical Membrane Antigen 1. <i>Infection and Immunity</i> , 2015, 83, 3890-3901.	2.2	28
12	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. <i>Frontiers in Genetics</i> , 2014, 5, 102.	2.3	164
13	An autoinhibitory conformation of the <i>Bacillus subtilis</i> spore coat protein SpoIVA prevents its premature ATP-independent aggregation. <i>FEMS Microbiology Letters</i> , 2014, 358, 145-153.	1.8	17
14	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.	4.6	221
15	Radiation-Induced Cellular and Molecular Alterations in Asexual Intraerythrocytic Plasmodium falciparum. <i>Journal of Infectious Diseases</i> , 2013, 207, 164-174.	4.0	21
16	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.	7.1	40
17	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, 16252-16257.	7.1	35
18	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.	2.9	88

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19	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.	4.6	440
20	Live virus-free or die: coupling of antiviral immunity and programmed suicide or dormancy in prokaryotes. <i>Biology Direct</i> , 2012, 7, 40.	4.6	119
21	Gene flow and biological conflict systems in the origin and evolution of eukaryotes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 89.	3.9	67
22	Comparative genomics uncovers novel structural and functional features of the heterotrimeric GTPase signaling system. <i>Gene</i> , 2011, 475, 63-78.	2.2	57
23	Molecular Correlates of Experimental Cerebral Malaria Detectable in Whole Blood. <i>Infection and Immunity</i> , 2011, 79, 1244-1253.	2.2	19
24	Novel eukaryotic enzymes modifying cell-surface biopolymers. <i>Biology Direct</i> , 2010, 5, 1.	4.6	77
25	Presence of a classical RRM-fold palm domain in Thg1-type 3'-5' nucleic acid polymerases and the origin of the GGDEF and CRISPR polymerase domains. <i>Biology Direct</i> , 2010, 5, 43.	4.6	40
26	OST-HTH: a novel predicted RNA-binding domain. <i>Biology Direct</i> , 2010, 5, 13.	4.6	67
27	Pathogenic Roles of CD14, Galectin-3, and OX40 during Experimental Cerebral Malaria in Mice. <i>PLoS ONE</i> , 2009, 4, e6793.	2.5	34
28	Apprehending multicellularity: Regulatory networks, genomics, and evolution. <i>Birth Defects Research Part C: Embryo Today Reviews</i> , 2009, 87, 143-164.	3.6	15
29	Comparative genomics of transcription factors and chromatin proteins in parasitic protists and other eukaryotes. <i>International Journal for Parasitology</i> , 2008, 38, 1-31.	3.1	226
30	AMIN domains have a predicted role in localization of diverse periplasmic protein complexes. <i>Bioinformatics</i> , 2008, 24, 2423-2426.	4.1	16
31	Host Biomarkers and Biological Pathways That Are Associated with the Expression of Experimental Cerebral Malaria in Mice. <i>Infection and Immunity</i> , 2008, 76, 4518-4529.	2.2	31
32	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, 1467-1472.	2.6	42
33	The DOMON domains are involved in heme and sugar recognition. <i>Bioinformatics</i> , 2007, 23, 2660-2664.	4.1	63
34	Molecular Factors and Biochemical Pathways Induced by Febrile Temperature in Intraerythrocytic <i>Plasmodium falciparum</i> Parasites. <i>Infection and Immunity</i> , 2007, 75, 2012-2025.	2.2	132
35	Adhesion Molecules and Other Secreted Host-Interaction Determinants in Apicomplexa: Insights from Comparative Genomics. <i>International Review of Cytology</i> , 2007, 262, 1-74.	6.2	51
36	Comparative Genomics of Protists: New Insights into the Evolution of Eukaryotic Signal Transduction and Gene Regulation. <i>Annual Review of Microbiology</i> , 2007, 61, 453-475.	7.3	55

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37	The signaling helix: a common functional theme in diverse signaling proteins. <i>Biology Direct</i> , 2006, 1, 25.	4.6	117
38	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, 823-842.	4.2	20
39	The NYN Domains: Novel Predicted RNAses with a PIN Domain-Like Fold. <i>RNA Biology</i> , 2006, 3, 18-27.	3.1	124
40	The many faces of the helix-turn-helix domain: Transcription regulation and beyond. <i>FEMS Microbiology Reviews</i> , 2005, 29, 231-262.	8.6	334
41	The many faces of the helix-turn-helix domain: Transcription regulation and beyond. <i>FEMS Microbiology Reviews</i> , 2005, 29, 231-262.	8.6	469
42	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, 2805-2811.	4.1	24
43	Comparative Genomics, Evolution and Origins of the Nuclear Envelope and Nuclear Pore Complex. <i>Cell Cycle</i> , 2004, 3, 1625-1650.	2.6	254
44	Comparative Analysis of Apicomplexa and Genomic Diversity in Eukaryotes. <i>Genome Research</i> , 2004, 14, 1686-1695.	5.5	172
45	Ufd2, a Novel Autoantigen in Scleroderma, Regulates Sister Chromatid Separation. <i>Cell Cycle</i> , 2004, 3, 1612-1618.	2.6	287
46	Novel conserved domains in proteins with predicted roles in eukaryotic cell-cycle regulation, decapping and RNA stability. <i>BMC Genomics</i> , 2004, 5, 45.	2.8	72
47	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.	2.6	27
48	Complete Genome Sequence of the Apicomplexan, <i>Cryptosporidium parvum</i> . <i>Science</i> , 2004, 304, 441-445.	12.6	877
49	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.	2.8	83
50	Ancient conserved domains shared by animal soluble guanylyl cyclases and bacterial signaling proteins. <i>BMC Genomics</i> , 2003, 4, 5.	2.8	160
51	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.	1.8	52
52	Emergence of diverse biochemical activities in evolutionarily conserved structural scaffolds of proteins. <i>Current Opinion in Chemical Biology</i> , 2003, 7, 12-20.	6.1	147
53	Evolutionary connections between bacterial and eukaryotic signaling systems: a genomic perspective. <i>Current Opinion in Microbiology</i> , 2003, 6, 490-497.	5.1	51
54	New connections in the prokaryotic toxin-antitoxin network: relationship with the eukaryotic nonsense-mediated RNA decay system. <i>Genome Biology</i> , 2003, 4, R81.	9.6	213

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55	The two faces of Alba: the evolutionary connection between proteins participating in chromatin structure and RNA metabolism. <i>Genome Biology</i> , 2003, 4, R64.	9.6	138
56	Evolutionary history, structural features and biochemical diversity of the NlpC/P60 superfamily of enzymes. <i>Genome Biology</i> , 2003, 4, R11.	9.6	312
57	Comparative genomics and evolution of proteins involved in RNA metabolism. <i>Nucleic Acids Research</i> , 2002, 30, 1427-1464.	14.5	462
58	The PRC-barrel: a widespread, conserved domain shared by photosynthetic reaction center subunits and proteins of RNA metabolism. <i>Genome Biology</i> , 2002, 3, research0061.1.	9.6	35
59	The GOLD domain, a novel protein module involved in Golgi function and secretion. <i>Genome Biology</i> , 2002, 3, research0023.1.	9.6	106
60	Monophyly of class I aminoacyl tRNA synthetase, USPA, ETPF, photolyase, and PP-ATPase nucleotide-binding domains: implications for protein evolution in the RNA world. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 1-14.	2.6	142
61	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.	1.8	64
62	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.	1.0	91
63	Regulatory potential, phyletic distribution and evolution of ancient, intracellular small-molecule-binding domains ¹¹ Edited by F. Cohen. <i>Journal of Molecular Biology</i> , 2001, 307, 1271-1292.	4.2	243
64	TRAM, a predicted RNA-binding domain, common to tRNA uracil methylation and adenine thiolation enzymes. <i>FEMS Microbiology Letters</i> , 2001, 197, 215-221.	1.8	64
65	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, 579-582.	7.5	150
66	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, 1627-1630.	2.9	45
67	TRAM, a predicted RNA-binding domain, common to tRNA uracil methylation and adenine thiolation enzymes. <i>FEMS Microbiology Letters</i> , 2001, 197, 215-221.	1.8	4
68	Effects of Nucleoside Analogs on Native and Site-Directed Mutants of HTLV Type 1 Reverse Transcriptase. <i>Bioorganic Chemistry</i> , 2000, 28, 293-305.	4.1	3
69	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, 535-537.	7.5	166