

Vivek Anantharaman

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/1626459/vivek-anantharaman-publications-by-year.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	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
68	Jumbo Phages: A Comparative Genomic Overview of Core Functions and Adaptions for Biological Conflicts. <i>Viruses</i> , 2021 , 13,	6.2	14
67	Antigen Discovery, Bioinformatics and Biological Characterization of Novel Immunodominant Babesia microti Antigens. <i>Scientific Reports</i> , 2020 , 10, 9598	4.9	5
66	Structure-function analysis of manganese exporter proteins across bacteria. <i>Journal of Biological Chemistry</i> , 2018 , 293, 5715-5730	5.4	16
65	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
64	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
63	Molecular Markers of Radiation Induced Attenuation in Intrahepatic Plasmodium falciparum Parasites. <i>PLoS ONE</i> , 2016 , 11, e0166814	3.7	12
62	The mechanism of force transmission at bacterial focal adhesion complexes. <i>Nature</i> , 2016 , 539, 530-535	50.4	78
61	The ubiquitous yybP-ykoY riboswitch is a manganese-responsive regulatory element. <i>Molecular Cell</i> , 2015 , 57, 1099-1109	17.6	73
60	Expression, Purification, and Biological Characterization of Babesia microti Apical Membrane Antigen 1. <i>Infection and Immunity</i> , 2015 , 83, 3890-901	3.7	21
59	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
58	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. <i>Frontiers in Genetics</i> , 2014 , 5, 102	4.5	118
57	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
56	Evolution of Eukaryotic Chromatin Proteins and Transcription Factors 2013 , 421-502		1
55	Radiation-induced cellular and molecular alterations in asexual intraerythrocytic Plasmodium falciparum. <i>Journal of Infectious Diseases</i> , 2013 , 207, 164-74	7	15
54	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
53	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

52	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
51	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
50	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
49	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
48	Comparative genomics uncovers novel structural and functional features of the heterotrimeric GTPase signaling system. <i>Gene</i> , 2011 , 475, 63-78	3.8	43
47	Molecular correlates of experimental cerebral malaria detectable in whole blood. <i>Infection and Immunity</i> , 2011 , 79, 1244-53	3.7	14
46	Novel eukaryotic enzymes modifying cell-surface biopolymers. <i>Biology Direct</i> , 2010 , 5, 1	7.2	49
45	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
44	OST-HTH: a novel predicted RNA-binding domain. <i>Biology Direct</i> , 2010 , 5, 13	7.2	59
43	Pathogenic roles of CD14, galectin-3, and OX40 during experimental cerebral malaria in mice. <i>PLoS ONE</i> , 2009 , 4, e6793	3.7	30
42	Apprehending multicellularity: regulatory networks, genomics, and evolution. <i>Birth Defects Research Part C: Embryo Today Reviews</i> , 2009 , 87, 143-64		13
41	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
40	AMIN domains have a predicted role in localization of diverse periplasmic protein complexes. <i>Bioinformatics</i> , 2008 , 24, 2423-6	7.2	12
39	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
38	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
37	The DOMON domains are involved in heme and sugar recognition. <i>Bioinformatics</i> , 2007 , 23, 2660-4	7.2	50
36	Molecular factors and biochemical pathways induced by febrile temperature in intraerythrocytic <i>Plasmodium falciparum</i> parasites. <i>Infection and Immunity</i> , 2007 , 75, 2012-25	3.7	111
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		46

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 NYN domains: novel predicted RNases with a PIN domain-like fold. <i>RNA Biology</i> , 2006 , 3, 18-27	4.8	97
32	The signaling helix: a common functional theme in diverse signaling proteins. <i>Biology Direct</i> , 2006 , 1, 25	7.2	101
31	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
30	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
29	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
28	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
27	Comparative Genomics, Evolution and Origins of the Nuclear Envelope and Nuclear Pore Complex. <i>Cell Cycle</i> , 2004 , 3, 1625-1650	4.7	206
26	Comparative analysis of apicomplexa and genomic diversity in eukaryotes. <i>Genome Research</i> , 2004 , 14, 1686-95	9.7	149
25	Comparative genomics, evolution and origins of the nuclear envelope and nuclear pore complex. <i>Cell Cycle</i> , 2004 , 3, 1612-37	4.7	263
24	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
23	The SHS2 module is a common structural theme in functionally diverse protein groups, like Rpb7p, FtsA, Gyrl, and MTH1598/TM1083 superfamilies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 795-807	4.2	21
22	Complete genome sequence of the apicomplexan, <i>Cryptosporidium parvum</i> . <i>Science</i> , 2004 , 304, 441-5	33.3	757
21	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
20	Ancient conserved domains shared by animal soluble guanylyl cyclases and bacterial signaling proteins. <i>BMC Genomics</i> , 2003 , 4, 5	4.5	148
19	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
18	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
17	Evolutionary connections between bacterial and eukaryotic signaling systems: a genomic perspective. <i>Current Opinion in Microbiology</i> , 2003 , 6, 490-7	7.9	47

16	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
15	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
14	Evolutionary history, structural features and biochemical diversity of the NlpC/P60 superfamily of enzymes. <i>Genome Biology</i> , 2003 , 4, R11	18.3	268
13	Monophyly of class I aminoacyl tRNA synthetase, USPA, ETPP, 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
12	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
11	Comparative genomics and evolution of proteins involved in RNA metabolism. <i>Nucleic Acids Research</i> , 2002 , 30, 1427-64	20.1	383
10	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
9	The GOLD domain, a novel protein module involved in Golgi function and secretion. <i>Genome Biology</i> , 2002 , 3, research0023	18.3	80
8	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
7	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
6	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
5	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
4	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
3	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
2	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
1	The Phage-shock-protein (PSP) Envelope Stress Response: Discovery of Novel Partners and Evolutionary History		1