

Aravind L Iyer

List of Publications by Year in descending order

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Version: 2024-02-01

379
papers

87,622
citations

553

130
h-index

448

280
g-index

401
all docs

401
docs citations

401
times ranked

87337
citing authors

#	ARTICLE	IF	CITATIONS
1	Bacterial developmental checkpoint that directly monitors cell surface morphogenesis. <i>Developmental Cell</i> , 2022, 57, 344-360.e6.	3.1	10
2	Ribosome collisions induce mRNA cleavage and ribosome rescue in bacteria. <i>Nature</i> , 2022, 603, 503-508.	13.7	50
3	GATD3A, a mitochondrial deglycase with evolutionary origins from gammaproteobacteria, restricts the formation of advanced glycation end products. <i>BMC Biology</i> , 2022, 20, 68.	1.7	6
4	Discovering Biological Conflict Systems Through Genome Analysis: Evolutionary Principles and Biochemical Novelty. <i>Annual Review of Biomedical Data Science</i> , 2022, 5, 367-391.	2.8	15
5	Unification and extensive diversification of M/Orf3-related ion channel proteins in coronaviruses and other nidoviruses. <i>Virus Evolution</i> , 2021, 7, veab014.	2.2	17
6	Jumbo Phages: A Comparative Genomic Overview of Core Functions and Adaptions for Biological Conflicts. <i>Viruses</i> , 2021, 13, 63.	1.5	54
7	GREB1: An evolutionarily conserved protein with a glycosyltransferase domain links ER \pm glycosylation and stability to cancer. <i>Science Advances</i> , 2021, 7, .	4.7	19
8	Reformulation of an extant ATPase active site to mimic ancestral GTPase activity reveals a nucleotide base requirement for function. <i>ELife</i> , 2021, 10, .	2.8	12
9	Bacterial death and TRADD-N domains help define novel apoptosis and immunity mechanisms shared by prokaryotes and metazoans. <i>ELife</i> , 2021, 10, .	2.8	17
10	Babesia microti: Pathogen Genomics, Genetic Variability, Immunodominant Antigens, and Pathogenesis. <i>Frontiers in Microbiology</i> , 2021, 12, 697669.	1.5	26
11	Gene-teratogen interactions influence the penetrance of birth defects by altering Hedgehog signaling strength. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	4
12	HMCES Functions in the Alternative End-Joining Pathway of the DNA DSB Repair during Class Switch Recombination in B Cells. <i>Molecular Cell</i> , 2020, 77, 384-394.e4.	4.5	34
13	NONU-1 Encodes a Conserved Endonuclease Required for mRNA Translation Surveillance. <i>Cell Reports</i> , 2020, 30, 4321-4331.e4.	2.9	60
14	Identification of Uncharacterized Components of Prokaryotic Immune Systems and Their Diverse Eukaryotic Reformulations. <i>Journal of Bacteriology</i> , 2020, 202, .	1.0	49
15	A Membrane-Tethered Ubiquitination Pathway Regulates Hedgehog Signaling and Heart Development. <i>Developmental Cell</i> , 2020, 55, 432-449.e12.	3.1	21
16	Mycobacterium tuberculosis Rv0991c Is a Redox-Regulated Molecular Chaperone. <i>MBio</i> , 2020, 11, .	1.8	7
17	Comprehensive classification of ABC ATPases and their functional radiation in nucleoprotein dynamics and biological conflict systems. <i>Nucleic Acids Research</i> , 2020, 48, 10045-10075.	6.5	39
18	Evolutionarily ancient BAH ϵ -PHD protein mediates Polycomb silencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11614-11623.	3.3	30

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19	Novel Immunoglobulin Domain Proteins Provide Insights into Evolution and Pathogenesis of SARS-CoV-2-Related Viruses. <i>MBio</i> , 2020, 11, .	1.8	81
20	Antigen Discovery, Bioinformatics and Biological Characterization of Novel Immunodominant Babesia microti Antigens. <i>Scientific Reports</i> , 2020, 10, 9598.	1.6	15
21	Functional Innovation in the Evolution of the Calcium-Dependent System of the Eukaryotic Endoplasmic Reticulum. <i>Frontiers in Genetics</i> , 2020, 11, 34.	1.1	9
22	TET methylcytosine oxidases: new insights from a decade of research. <i>Journal of Biosciences</i> , 2020, 45, 1.	0.5	49
23	An RNA Repair Operon Regulated by Damaged tRNAs. <i>Cell Reports</i> , 2020, 33, 108527.	2.9	33
24	Highly regulated, diversifying NTP-dependent biological conflict systems with implications for the emergence of multicellularity. <i>ELife</i> , 2020, 9, .	2.8	30
25	TET methylcytosine oxidases: new insights from a decade of research. <i>Journal of Biosciences</i> , 2020, 45, .	0.5	19
26	Identification of the m6Am Methyltransferase PCIF1 Reveals the Location and Functions of m6Am in the Transcriptome. <i>Molecular Cell</i> , 2019, 75, 631-643.e8.	4.5	183
27	Unusual Activity of a <i>Chlamydomonas</i> TET/JBP Family Enzyme. <i>Biochemistry</i> , 2019, 58, 3627-3629.	1.2	4
28	The catalytic core of DEMETER guides active DNA demethylation in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17563-17571.	3.3	23
29	Structural basis of HMCES interactions with abasic DNA and multivalent substrate recognition. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 607-612.	3.6	48
30	Antimicrobial Peptides, Polymorphic Toxins, and Self-Nonself Recognition Systems in Archaea: an Untapped Armory for Intermicrobial Conflicts. <i>MBio</i> , 2019, 10, .	1.8	41
31	Oxidative opening of the aromatic ring: Tracing the natural history of a large superfamily of dioxygenase domains and their relatives. <i>Journal of Biological Chemistry</i> , 2019, 294, 10211-10235.	1.6	24
32	The Origin and Evolution of Release Factors: Implications for Translation Termination, Ribosome Rescue, and Quality Control Pathways. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1981.	1.8	38
33	Deciphering the Role of a SLOG Superfamily Protein YpsA in Gram-Positive Bacteria. <i>Frontiers in Microbiology</i> , 2019, 10, 623.	1.5	15
34	The cyl Genes Reveal the Biosynthetic and Evolutionary Origins of the Group B Streptococcus Hemolytic Lipid, Granadaene. <i>Frontiers in Microbiology</i> , 2019, 10, 3123.	1.5	15
35	Structure–function analysis of manganese exporter proteins across bacteria. <i>Journal of Biological Chemistry</i> , 2018, 293, 5715-5730.	1.6	44
36	Evolutionary convergence and divergence in archaeal chromosomal proteins and Chromo-like domains from bacteria and eukaryotes. <i>Scientific Reports</i> , 2018, 8, 6196.	1.6	22

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37	Vms1 and ANKZF1 peptidyl-tRNA hydrolases release nascent chains from stalled ribosomes. <i>Nature</i> , 2018, 557, 446-451.	13.7	122
38	CRISPR Screens Uncover Genes that Regulate Target Cell Sensitivity to the Morphogen Sonic Hedgehog. <i>Developmental Cell</i> , 2018, 44, 113-129.e8.	3.1	95
39	A Nonhemolytic Group B Streptococcus Strain Exhibits Hypervirulence. <i>Journal of Infectious Diseases</i> , 2018, 217, 983-987.	1.9	18
40	Expansions, diversification, and interindividual copy number variations of AID/APOBEC family cytidine deaminase genes in lampreys. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3211-E3220.	3.3	23
41	Diversification of AID/APOBEC-like deaminases in metazoa: multiplicity of clades and widespread roles in immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3201-E3210.	3.3	56
42	Variations on a theme: evolution of the phage-shock-protein system in Actinobacteria. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 753-760.	0.7	7
43	Unexpected Evolution of Lesion-Recognition Modules in Eukaryotic NER and Kinetoplast DNA Dynamics Proteins from Bacterial Mobile Elements. <i>IScience</i> , 2018, 9, 192-208.	1.9	8
44	Loss of the Spinocerebellar Ataxia type 3 disease protein ATXN3 alters transcription of multiple signal transduction pathways. <i>PLoS ONE</i> , 2018, 13, e0204438.	1.1	23
45	"RETRACTED ARTICLE: <i>Vibrio parahaemolyticus</i> RhsP represents a widespread group of pro-effectors for type VI secretion systems. <i>Nature Communications</i> , 2018, 9, 3899.	5.8	8
46	Genome sequencing and assessment of plant growth-promoting properties of a <i>Serratia marcescens</i> strain isolated from vermicompost. <i>BMC Genomics</i> , 2018, 19, 750.	1.2	58
47	Inferring joint sequence-structural determinants of protein functional specificity. <i>ELife</i> , 2018, 7, .	2.8	14
48	TCR β -expressing macrophages induced by a pathogenic murine malaria correlate with parasite burden and enhanced phagocytic activity. <i>PLoS ONE</i> , 2018, 13, e0201043.	1.1	29
49	THEMIS enhances TCR signaling and enables positive selection by selective inhibition of the phosphatase SHP-1. <i>Nature Immunology</i> , 2017, 18, 433-441.	7.0	71
50	Novel clades of the HU/IHF superfamily point to unexpected roles in the eukaryotic centrosome, chromosome partitioning, and biologic conflicts. <i>Cell Cycle</i> , 2017, 16, 1093-1103.	1.3	14
51	Polyvalent Proteins, a Pervasive Theme in the Intergenomic Biological Conflicts of Bacteriophages and Conjugative Elements. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	33
52	A conserved NAD ⁺ binding pocket that regulates protein-protein interactions during aging. <i>Science</i> , 2017, 355, 1312-1317.	6.0	140
53	Erasure of Tet-Oxidized 5-Methylcytosine by a SRAP Nuclease. <i>Cell Reports</i> , 2017, 21, 482-494.	2.9	28
54	Multifunctional Involvement of a C2H2 Zinc Finger Protein (PbZfp) in Malaria Transmission, Histone Modification, and Susceptibility to DNA Damage Response. <i>MBio</i> , 2017, 8, .	1.8	5

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55	<i>O</i> -GlcNAcylation destabilizes the active tetrameric PKM2 to promote the Warburg effect. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 13732-13737.	3.3	105
56	Evolution and multiple roles of the Pancrustacea specific transcription factor zelda in insects. PLoS Genetics, 2017, 13, e1006868.	1.5	24
57	Molecular Markers of Radiation Induced Attenuation in Intrahepatic Plasmodium falciparum Parasites. PLoS ONE, 2016, 11, e0166814.	1.1	13
58	Transposons to toxins: the provenance, architecture and diversification of a widespread class of eukaryotic effectors. Nucleic Acids Research, 2016, 44, 3513-3533.	6.5	54
59	The mechanism of force transmission at bacterial focal adhesion complexes. Nature, 2016, 539, 530-535.	13.7	120
60	Editorial overview: Sequences and topology: Protein function - synthesizing information from sequence, structure and disorder. Current Opinion in Structural Biology, 2016, 38, vii-ix.	2.6	0
61	Adenine methylation in eukaryotes: Apprehending the complex evolutionary history and functional potential of an epigenetic modification. BioEssays, 2016, 38, 27-40.	1.2	132
62	RNA damage in biological conflicts and the diversity of responding RNA repair systems. Nucleic Acids Research, 2016, 44, 8525-8555.	6.5	64
63	Transcription factors, chromatin proteins and the diversification of Hemiptera. Insect Biochemistry and Molecular Biology, 2016, 69, 1-13.	1.2	14
64	Structure and sequence analyses of Bacteroides proteins BVU_4064 and BF1687 reveal presence of two novel predominantly-beta domains, predicted to be involved in lipid and cell surface interactions. BMC Bioinformatics, 2015, 16, 7.	1.2	8
65	Genome of <i>Rhodnius prolixus</i> , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14936-14941.	3.3	329
66	Proteasomal Control of Cytokinin Synthesis Protects Mycobacterium tuberculosis against Nitric Oxide. Molecular Cell, 2015, 57, 984-994.	4.5	101
67	Whole exome sequencing identifies the TNNI3K gene as a cause of familial conduction system disease and congenital junctional ectopic tachycardia. International Journal of Cardiology, 2015, 185, 114-116.	0.8	29
68	The eukaryotic translation initiation regulator CDC123 defines a divergent clade of ATP-grasp enzymes with a predicted role in novel protein modifications. Biology Direct, 2015, 10, 21.	1.9	9
69	DNA Methylation on N6-Adenine in C.Âelegans. Cell, 2015, 161, 868-878.	13.5	602
70	The Ubiquitous yybP-ykoY Riboswitch Is a Manganese-Responsive Regulatory Element. Molecular Cell, 2015, 57, 1099-1109.	4.5	120
71	Expression, Purification, and Biological Characterization of Babesia microti Apical Membrane Antigen 1. Infection and Immunity, 2015, 83, 3890-3901.	1.0	28
72	Comparative genomic analyses reveal a vast, novel network of nucleotide-centric systems in biological conflicts, immunity and signaling. Nucleic Acids Research, 2015, 43, 10633-10654.	6.5	200

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73	The TET/JP Family of Nucleic Acid Base-Modifying 2-Oxoglutarate and Iron-Dependent Dioxygenases. 2-Oxoglutarate-Dependent Oxygenases, 2015, , 289-308.	0.8	4
74	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. <i>Frontiers in Genetics</i> , 2014, 5, 102.	1.1	164
75	Lineage-specific expansions of TET/JP genes and a new class of DNA transposons shape fungal genomic and epigenetic landscapes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1676-1683.	3.3	51
76	A highly conserved family of domains related to the DNA-glycosylase fold helps predict multiple novel pathways for RNA modifications. <i>RNA Biology</i> , 2014, 11, 360-372.	1.5	35
77	Editorial overview: Sequences and topology: sequences, structures, genomes and populations. <i>Current Opinion in Structural Biology</i> , 2014, 26, vii-viii.	2.6	0
78	Analysis of two domains with novel RNA-processing activities throws light on the complex evolution of ribosomal RNA biogenesis. <i>Frontiers in Genetics</i> , 2014, 5, 424.	1.1	21
79	THE KNICKKOPF DOMON DOMAIN IS ESSENTIAL FOR CUTICLE DIFFERENTIATION IN <i>Drosophila melanogaster</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2014, 86, 100-106.	0.6	8
80	Simultaneous sequencing of oxidized methylcytosines produced by TET/JP dioxygenases in <i>Coprinopsis cinerea</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5149-58.	3.3	25
81	New perspectives on the diversification of the <i>RNA</i> interference system: insights from comparative genomics and small <i>RNA</i> sequencing. <i>Wiley Interdisciplinary Reviews RNA</i> , 2014, 5, 141-181.	3.2	62
82	EFCAB7 and IQCE Regulate Hedgehog Signaling by Tethering the EVC-EVC2 Complex to the Base of Primary Cilia. <i>Developmental Cell</i> , 2014, 28, 483-496.	3.1	76
83	A TET Homologue Protein from <i>Coprinopsis cinerea</i> (CcTET) That Biochemically Converts 5-Methylcytosine to 5-Hydroxymethylcytosine, 5-Formylcytosine, and 5-Carboxylcytosine. <i>Journal of the American Chemical Society</i> , 2014, 136, 4801-4804.	6.6	56
84	Multiple enzymatic activities of ParB/Srx superfamily mediate sexual conflict among conjugative plasmids. <i>Nature Communications</i> , 2014, 5, 5322.	5.8	28
85	Selection of the lamprey VLRC antigen receptor repertoire. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14834-14839.	3.3	30
86	Genomic donor cassette sharing during VLRA and VLRC assembly in jawless vertebrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14828-14833.	3.3	18
87	The Natural History of ADP-Ribosyltransferases and the ADP-Ribosylation System. <i>Current Topics in Microbiology and Immunology</i> , 2014, 384, 3-32.	0.7	99
88	Resilience of biochemical activity in protein domains in the face of structural divergence. <i>Current Opinion in Structural Biology</i> , 2014, 26, 92-103.	2.6	39
89	Protein and DNA Modifications: Evolutionary Imprints of Bacterial Biochemical Diversification and Geochemistry on the Provenance of Eukaryotic Epigenetics. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a016063-a016063.	2.3	26
90	Structure and computational analysis of a novel protein with metallopeptidase-like and circularly permuted winged-helix-turn-helix domains reveals a possible role in modified polysaccharide biosynthesis. <i>BMC Bioinformatics</i> , 2014, 15, 75.	1.2	1

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91	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.	0.7	17
92	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.	1.9	221
93	Two novel PIWI families: roles in inter-genomic conflicts in bacteria and Mediator-dependent modulation of transcription in eukaryotes. <i>Biology Direct</i> , 2013, 8, 13.	1.9	45
94	Two Pfam protein families characterized by a crystal structure of protein lpg2210 from <i>Legionella pneumophila</i> . <i>BMC Bioinformatics</i> , 2013, 14, 265.	1.2	3
95	Novel autoproteolytic and DNA-damage sensing components in the bacterial SOS response and oxidized methylcytosine-induced eukaryotic DNA demethylation systems. <i>Biology Direct</i> , 2013, 8, 20.	1.9	59
96	A hemolytic pigment of Group B <i>Streptococcus</i> allows bacterial penetration of human placenta. <i>Journal of Experimental Medicine</i> , 2013, 210, 1265-1281.	4.2	147
97	Modulation of TET2 expression and 5-methylcytosine oxidation by the CXXC domain protein IDAX. <i>Nature</i> , 2013, 497, 122-126.	13.7	323
98	TETonic shift: biological roles of TET proteins in DNA demethylation and transcription. <i>Nature Reviews Molecular Cell Biology</i> , 2013, 14, 341-356.	16.1	733
99	PfSETvs methylation of histone H3K36 represses virulence genes in <i>Plasmodium falciparum</i> . <i>Nature</i> , 2013, 499, 223-227.	13.7	219
100	Filling out the structural map of the NTF2-like superfamily. <i>BMC Bioinformatics</i> , 2013, 14, 327.	1.2	74
101	LUD, a new protein domain associated with lactate utilization. <i>BMC Bioinformatics</i> , 2013, 14, 341.	1.2	8
102	Radiation-Induced Cellular and Molecular Alterations in Asexual Intraerythrocytic <i>Plasmodium falciparum</i> . <i>Journal of Infectious Diseases</i> , 2013, 207, 164-174.	1.9	21
103	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.	3.3	40
104	Computational identification of novel biochemical systems involved in oxidation, glycosylation and other complex modifications of bases in DNA. <i>Nucleic Acids Research</i> , 2013, 41, 7635-7655.	6.5	115
105	The HARE-HTH and associated domains. <i>Cell Cycle</i> , 2012, 11, 119-131.	1.3	81
106	Structure of the <i>Plasmodium</i> 6-cysteine s48/45 domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6692-6697.	3.3	69
107	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.	3.3	35
108	The Scaffolding Protein Synapse-Associated Protein 97 Is Required for Enhanced Signaling Through Isotype-Switched IgG Memory B Cell Receptors. <i>Science Signaling</i> , 2012, 5, ra54.	1.6	54

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109	Insights from the architecture of the bacterial transcription apparatus. <i>Journal of Structural Biology</i> , 2012, 179, 299-319.	1.3	46
110	MORC2 Signaling Integrates Phosphorylation-Dependent, ATPase-Coupled Chromatin Remodeling during the DNA Damage Response. <i>Cell Reports</i> , 2012, 2, 1657-1669.	2.9	110
111	Novel transglutaminase-like peptidase and C2 domains elucidate the structure, biogenesis and evolution of the ciliary compartment. <i>Cell Cycle</i> , 2012, 11, 3861-3875.	1.3	46
112	Bacterial GRAS domain proteins throw new light on gibberellic acid response mechanisms. <i>Bioinformatics</i> , 2012, 28, 2407-2411.	1.8	93
113	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
114	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.	1.9	440
115	ALOC domains: provenance of plant homeotic and developmental regulators from the DNA-binding domain of a novel class of DIRS1-type retroposons. <i>Biology Direct</i> , 2012, 7, 39.	1.9	41
116	Live virus-free or die: coupling of antiviral immunity and programmed suicide or dormancy in prokaryotes. <i>Biology Direct</i> , 2012, 7, 40.	1.9	119
117	Identification of novel components of NAD-utilizing metabolic pathways and prediction of their biochemical functions. <i>Molecular BioSystems</i> , 2012, 8, 1661.	2.9	63
118	Evolutionary and Biochemical Aspects of Chemical Stress Resistance in <i>Saccharomyces cerevisiae</i> . <i>Frontiers in Genetics</i> , 2012, 3, 47.	1.1	7
119	Discovery of Novel DENN Proteins: Implications for the Evolution of Eukaryotic Intracellular Membrane Structures and Human Disease. <i>Frontiers in Genetics</i> , 2012, 3, 283.	1.1	220
120	Gene flow and biological conflict systems in the origin and evolution of eukaryotes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 89.	1.8	67
121	The natural history of ubiquitin and ubiquitin-related domains. <i>Frontiers in Bioscience - Landmark</i> , 2012, 17, 1433.	3.0	44
122	Interplay between gene expression noise and regulatory network architecture. <i>Trends in Genetics</i> , 2012, 28, 221-232.	2.9	235
123	Structure and Evolution of Ubiquitin and Ubiquitin-Related Domains. <i>Methods in Molecular Biology</i> , 2012, 832, 15-63.	0.4	37
124	Functional diversification of the RING finger and other binuclear treble clef domains in prokaryotes and the early evolution of the ubiquitin system. <i>Molecular BioSystems</i> , 2011, 7, 2261.	2.9	55
125	Natural History of the Eukaryotic Chromatin Protein Methylation System. <i>Progress in Molecular Biology and Translational Science</i> , 2011, 101, 105-176.	0.9	65
126	Natural History of Eukaryotic DNA Methylation Systems. <i>Progress in Molecular Biology and Translational Science</i> , 2011, 101, 25-104.	0.9	187

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127	A novel immunity system for bacterial nucleic acid degrading toxins and its recruitment in various eukaryotic and DNA viral systems. <i>Nucleic Acids Research</i> , 2011, 39, 4532-4552.	6.5	184
128	Malaria Parasite <i>clag3</i> Genes Determine Channel-Mediated Nutrient Uptake by Infected Red Blood Cells. <i>Cell</i> , 2011, 145, 665-677.	13.5	228
129	Comparative genomics uncovers novel structural and functional features of the heterotrimeric GTPase signaling system. <i>Gene</i> , 2011, 475, 63-78.	1.0	57
130	Clinical and molecular aspects of malaria fever. <i>Trends in Parasitology</i> , 2011, 27, 442-449.	1.5	66
131	Unification of Cas protein families and a simple scenario for the origin and evolution of CRISPR-Cas systems. <i>Biology Direct</i> , 2011, 6, 38.	1.9	379
132	Molecular Correlates of Experimental Cerebral Malaria Detectable in Whole Blood. <i>Infection and Immunity</i> , 2011, 79, 1244-1253.	1.0	19
133	Evolution of the deaminase fold and multiple origins of eukaryotic editing and mutagenic nucleic acid deaminases from bacterial toxin systems. <i>Nucleic Acids Research</i> , 2011, 39, 9473-9497.	6.5	154
134	Novel eukaryotic enzymes modifying cell-surface biopolymers. <i>Biology Direct</i> , 2010, 5, 1.	1.9	77
135	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.	1.9	40
136	Predicted class-I aminoacyl tRNA synthetase-like proteins in non-ribosomal peptide synthesis. <i>Biology Direct</i> , 2010, 5, 48.	1.9	45
137	The structure of SSO2064, the first representative of Pfam family PF01796, reveals a novel two-domain zinc-ribbon OB-fold architecture with a potential acyl-CoA-binding role. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1160-1166.	0.7	20
138	Structure of the first representative of Pfam family PF04016 (DUF364) reveals enolase and Rossmann-like folds that combine to form a unique active site with a possible role in heavy-metal chelation. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1167-1173.	0.7	3
139	OST-HTH: a novel predicted RNA-binding domain. <i>Biology Direct</i> , 2010, 5, 13.	1.9	67
140	MicroRNA targeting in mammalian genomes: genes and mechanisms. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 148-161.	6.6	33
141	Impaired hydroxylation of 5-methylcytosine in myeloid cancers with mutant TET2. <i>Nature</i> , 2010, 468, 839-843.	13.7	1,160
142	UMA and MABP domains throw light on receptor endocytosis and selection of endosomal cargoes. <i>Bioinformatics</i> , 2010, 26, 1477-1480.	1.8	23
143	Origin and evolution of peptide-modifying dioxygenases and identification of the wybutosine hydroxylase/hydroperoxidase. <i>Nucleic Acids Research</i> , 2010, 38, 5261-5279.	6.5	46
144	A structural basis for antigen recognition by the T cell-like lymphocytes of sea lamprey. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 13408-13413.	3.3	66

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145	CYSTM, a novel cysteine-rich transmembrane module with a role in stress tolerance across eukaryotes. <i>Bioinformatics</i> , 2010, 26, 149-152.	1.8	47
146	Myosin 1G Is an Abundant Class I Myosin in Lymphocytes Whose Localization at the Plasma Membrane Depends on Its Ancient Divergent Pleckstrin Homology (PH) Domain (Myo1PH). <i>Journal of Biological Chemistry</i> , 2010, 285, 8675-8686.	1.6	58
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