

Aravind L Iyer

List of Publications by Year in Descending Order

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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.

380
papers

72,278
citations

123
h-index

266
g-index

400
ext. papers

80,556
ext. citations

10.9
avg, IF

7.7
L-index

#	Paper	IF	Citations
380	Ribosome collisions induce mRNA cleavage and ribosome rescue in bacteria.. <i>Nature</i> , 2022 ,	50.4	4
379	GATD3A, a mitochondrial deglycase with evolutionary origins from gammaproteobacteria, restricts the formation of advanced glycation end products.. <i>BMC Biology</i> , 2022 , 20, 68	7.3	0
378	GREB1: An evolutionarily conserved protein with a glycosyltransferase domain links ER α glycosylation and stability to cancer. <i>Science Advances</i> , 2021 , 7,	14.3	4
377	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
376	Bacterial death and TRADD-N domains help define novel apoptosis and immunity mechanisms shared by prokaryotes and metazoans. <i>ELife</i> , 2021 , 10,	8.9	2
375	Unification and extensive diversification of M/Orf3-related ion channel proteins in coronaviruses and other nidoviruses. <i>Virus Evolution</i> , 2021 , 7, veab014	3.7	10
374	Jumbo Phages: A Comparative Genomic Overview of Core Functions and Adaptions for Biological Conflicts. <i>Viruses</i> , 2021 , 13,	6.2	14
373	: Pathogen Genomics, Genetic Variability, Immunodominant Antigens, and Pathogenesis. <i>Frontiers in Microbiology</i> , 2021 , 12, 697669	5.7	6
372	Gene-teratogen interactions influence the penetrance of birth defects by altering Hedgehog signaling strength. <i>Development (Cambridge)</i> , 2021 , 148,	6.6	3
371	Evolutionarily ancient BAH-PHD protein mediates Polycomb silencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 11614-11623	11.5	13
370	Novel Immunoglobulin Domain Proteins Provide Insights into Evolution and Pathogenesis of SARS-CoV-2-Related Viruses. <i>MBio</i> , 2020 , 11,	7.8	44
369	Antigen Discovery, Bioinformatics and Biological Characterization of Novel Immunodominant Babesia microti Antigens. <i>Scientific Reports</i> , 2020 , 10, 9598	4.9	5
368	Functional Innovation in the Evolution of the Calcium-Dependent System of the Eukaryotic Endoplasmic Reticulum. <i>Frontiers in Genetics</i> , 2020 , 11, 34	4.5	5
367	TET methylcytosine oxidases: new insights from a decade of research. <i>Journal of Biosciences</i> , 2020 , 45, 1	2.3	26
366	TET methylcytosine oxidases: new insights from a decade of research. <i>Journal of Biosciences</i> , 2020 , 45,	2.3	16
365	Highly regulated, diversifying NTP-dependent biological conflict systems with implications for the emergence of multicellularity. <i>ELife</i> , 2020 , 9,	8.9	11
364	An RNA Repair Operon Regulated by Damaged tRNAs. <i>Cell Reports</i> , 2020 , 33, 108527	10.6	7

363	Novel Immunoglobulin Domain Proteins Provide Insights into Evolution and Pathogenesis Mechanisms of SARS-Related Coronaviruses 2020 ,		7
362	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	17.6	17
361	NONU-1 Encodes a Conserved Endonuclease Required for mRNA Translation Surveillance. <i>Cell Reports</i> , 2020 , 30, 4321-4331.e4	10.6	21
360	Identification of Uncharacterized Components of Prokaryotic Immune Systems and Their Diverse Eukaryotic Reformulations. <i>Journal of Bacteriology</i> , 2020 , 202,	3.5	16
359	A Membrane-Tethered Ubiquitination Pathway Regulates Hedgehog Signaling and Heart Development. <i>Developmental Cell</i> , 2020 , 55, 432-449.e12	10.2	12
358	Mycobacterium tuberculosis Rv0991c Is a Redox-Regulated Molecular Chaperone. <i>MBio</i> , 2020 , 11,	7.8	3
357	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	20.1	9
356	Unusual Activity of a TET/JBP Family Enzyme. <i>Biochemistry</i> , 2019 , 58, 3627-3629	3.2	3
355	The catalytic core of DEMETER guides active DNA demethylation in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 17563-17571	11.5	12
354	Structural basis of HMCES interactions with abasic DNA and multivalent substrate recognition. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 607-612	17.6	22
353	Antimicrobial Peptides, Polymorphic Toxins, and Self-Nonself Recognition Systems in Archaea: an Untapped Armory for Intermicrobial Conflicts. <i>MBio</i> , 2019 , 10,	7.8	23
352	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	5.4	16
351	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,	6.3	20
350	Deciphering the Role of a SLOG Superfamily Protein YpsA in Gram-Positive Bacteria. <i>Frontiers in Microbiology</i> , 2019 , 10, 623	5.7	6
349	The Genes Reveal the Biosynthetic and Evolutionary Origins of the Group B Hemolytic Lipid, Granadaene. <i>Frontiers in Microbiology</i> , 2019 , 10, 3123	5.7	9
348	Identification of the mAm Methyltransferase PCIF1 Reveals the Location and Functions of mAm in the Transcriptome. <i>Molecular Cell</i> , 2019 , 75, 631-643.e8	17.6	95
347	Structure-function analysis of manganese exporter proteins across bacteria. <i>Journal of Biological Chemistry</i> , 2018 , 293, 5715-5730	5.4	16
346	Evolutionary convergence and divergence in archaeal chromosomal proteins and Chromo-like domains from bacteria and eukaryotes. <i>Scientific Reports</i> , 2018 , 8, 6196	4.9	12

345	Vms1 and ANKZF1 peptidyl-tRNA hydrolases release nascent chains from stalled ribosomes. <i>Nature</i> , 2018 , 557, 446-451	50.4	73
344	CRISPR Screens Uncover Genes that Regulate Target Cell Sensitivity to the Morphogen Sonic Hedgehog. <i>Developmental Cell</i> , 2018 , 44, 113-129.e8	10.2	61
343	A Nonhemolytic Group B Streptococcus Strain Exhibits Hypervirulence. <i>Journal of Infectious Diseases</i> , 2018 , 217, 983-987	7	12
342	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	11.5	15
341	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	11.5	36
340	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
339	TCR-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
338	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	6.1	4
337	Loss of the Spinocerebellar Ataxia type 3 disease protein ATXN3 alters transcription of multiple signal transduction pathways. <i>PLoS ONE</i> , 2018 , 13, e0204438	3.7	14
336	<i>Vibrio parahaemolyticus</i> RhsP represents a widespread group of pro-effectors for type VI secretion systems. <i>Nature Communications</i> , 2018 , 9, 3899	17.4	6
335	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	4.5	34
334	Inferring joint sequence-structural determinants of protein functional specificity. <i>ELife</i> , 2018 , 7,	8.9	10
333	THEMIS enhances TCR signaling and enables positive selection by selective inhibition of the phosphatase SHP-1. <i>Nature Immunology</i> , 2017 , 18, 433-441	19.1	43
332	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	4.7	9
331	Polyvalent Proteins, a Pervasive Theme in the Intergenomic Biological Conflicts of Bacteriophages and Conjugative Elements. <i>Journal of Bacteriology</i> , 2017 , 199,	3.5	19
330	A conserved NAD binding pocket that regulates protein-protein interactions during aging. <i>Science</i> , 2017 , 355, 1312-1317	33.3	102
329	Erasure of Tet-Oxidized 5-Methylcytosine by a SRAP Nuclease. <i>Cell Reports</i> , 2017 , 21, 482-494	10.6	19
328	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,	7.8	3

327	GlcNAcylation destabilizes the active tetrameric PKM2 to promote the Warburg effect. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 13732-13737	11.5	54
326	Evolution and multiple roles of the Pancrustacea specific transcription factor zelda in insects. <i>PLoS Genetics</i> , 2017 , 13, e1006868	6	18
325	Transcription factors, chromatin proteins and the diversification of Hemiptera. <i>Insect Biochemistry and Molecular Biology</i> , 2016 , 69, 1-13	4.5	11
324	RNA damage in biological conflicts and the diversity of responding RNA repair systems. <i>Nucleic Acids Research</i> , 2016 , 44, 8525-8555	20.1	45
323	Molecular Markers of Radiation Induced Attenuation in Intrahepatic Plasmodium falciparum Parasites. <i>PLoS ONE</i> , 2016 , 11, e0166814	3.7	12
322	Transposons to toxins: the provenance, architecture and diversification of a widespread class of eukaryotic effectors. <i>Nucleic Acids Research</i> , 2016 , 44, 3513-33	20.1	30
321	The mechanism of force transmission at bacterial focal adhesion complexes. <i>Nature</i> , 2016 , 539, 530-535	50.4	78
320	Adenine methylation in eukaryotes: Apprehending the complex evolutionary history and functional potential of an epigenetic modification. <i>BioEssays</i> , 2016 , 38, 27-40	4.1	93
319	Proteasomal control of cytokinin synthesis protects Mycobacterium tuberculosis against nitric oxide. <i>Molecular Cell</i> , 2015 , 57, 984-994	17.6	81
318	Whole exome sequencing identifies the TNNI3K gene as a cause of familial conduction system disease and congenital junctional ectopic tachycardia. <i>International Journal of Cardiology</i> , 2015 , 185, 114-6	3.2	18
317	The eukaryotic translation initiation regulator CDC123 defines a divergent clade of ATP-grasp enzymes with a predicted role in novel protein modifications. <i>Biology Direct</i> , 2015 , 10, 21	7.2	6
316	DNA Methylation on N6-Adenine in <i>C. elegans</i> . <i>Cell</i> , 2015 , 161, 868-78	56.2	424
315	The ubiquitous yybP-ykoY riboswitch is a manganese-responsive regulatory element. <i>Molecular Cell</i> , 2015 , 57, 1099-1109	17.6	73
314	Expression, Purification, and Biological Characterization of Babesia microti Apical Membrane Antigen 1. <i>Infection and Immunity</i> , 2015 , 83, 3890-901	3.7	21
313	Comparative genomic analyses reveal a vast, novel network of nucleotide-centric systems in biological conflicts, immunity and signaling. <i>Nucleic Acids Research</i> , 2015 , 43, 10633-54	20.1	103
312	The natural history of ADP-ribosyltransferases and the ADP-ribosylation system. <i>Current Topics in Microbiology and Immunology</i> , 2015 , 384, 3-32	3.3	72
311	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. <i>BMC Bioinformatics</i> , 2015 , 16, 7	3.6	1
310	Genome of Rhodnius prolixus, an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 14936-41	11.5	220

309	CHAPTER 11: The TET/JBP Family of Nucleic Acid Base-Modifying 2-Oxoglutarate and Iron-Dependent Dioxygenases. <i>2-Oxoglutarate-Dependent Oxygenases</i> , 2015 , 289-308	1.8	4
308	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, 4801-4	16.4	37
307	Multiple enzymatic activities of ParB/Srx superfamily mediate sexual conflict among conjugative plasmids. <i>Nature Communications</i> , 2014 , 5, 5322	17.4	23
306	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, 14834-9	11.5	27
305	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, 14828-33	11.5	12
304	Resilience of biochemical activity in protein domains in the face of structural divergence. <i>Current Opinion in Structural Biology</i> , 2014 , 26, 92-103	8.1	33
303	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	10.2	20
302	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	3.6	1
301	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, 145-53	2.9	12
300	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. <i>Frontiers in Genetics</i> , 2014 , 5, 102	4.5	118
299	Lineage-specific expansions of TET/JBP 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, 1676-83	11.5	41
298	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, 360-72	4.8	18
297	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	4.5	16
296	The Knickkopf DOMON domain is essential for cuticle differentiation in <i>Drosophila melanogaster</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2014 , 86, 100-6	2.3	8
295	Simultaneous sequencing of oxidized methylcytosines produced by TET/JBP 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	11.5	21
294	New perspectives on the diversification of the RNA interference system: insights from comparative genomics and small RNA sequencing. <i>Wiley Interdisciplinary Reviews RNA</i> , 2014 , 5, 141-81	9.3	40
293	EFCAB7 and IQCE regulate hedgehog signaling by tethering the EVC-EVC2 complex to the base of primary cilia. <i>Developmental Cell</i> , 2014 , 28, 483-96	10.2	52
292	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

291	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	7.2	26
290	Two Pfam protein families characterized by a crystal structure of protein lpg2210 from <i>Legionella pneumophila</i> . <i>BMC Bioinformatics</i> , 2013 , 14, 265	3.6	3
289	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	7.2	39
288	A hemolytic pigment of Group B <i>Streptococcus</i> allows bacterial penetration of human placenta. <i>Journal of Experimental Medicine</i> , 2013 , 210, 1265-81	16.6	116
287	Modulation of TET2 expression and 5-methylcytosine oxidation by the CXXC domain protein IDAX. <i>Nature</i> , 2013 , 497, 122-6	50.4	265
286	TETonic shift: biological roles of TET proteins in DNA demethylation and transcription. <i>Nature Reviews Molecular Cell Biology</i> , 2013 , 14, 341-56	48.7	627
285	PFSETvs methylation of histone H3K36 represses virulence genes in <i>Plasmodium falciparum</i> . <i>Nature</i> , 2013 , 499, 223-7	50.4	171
284	Filling out the structural map of the NTF2-like superfamily. <i>BMC Bioinformatics</i> , 2013 , 14, 327	3.6	40
283	LUD, a new protein domain associated with lactate utilization. <i>BMC Bioinformatics</i> , 2013 , 14, 341	3.6	6
282	Evolution of Eukaryotic Chromatin Proteins and Transcription Factors 2013 , 421-502		1
281	Radiation-induced cellular and molecular alterations in asexual intraerythrocytic <i>Plasmodium falciparum</i> . <i>Journal of Infectious Diseases</i> , 2013 , 207, 164-74	7	15
280	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
279	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, 7635-55	20.1	83
278	Interplay between gene expression noise and regulatory network architecture. <i>Trends in Genetics</i> , 2012 , 28, 221-32	8.5	170
277	Insights from the architecture of the bacterial transcription apparatus. <i>Journal of Structural Biology</i> , 2012 , 179, 299-319	3.4	36
276	MORC2 signaling integrates phosphorylation-dependent, ATPase-coupled chromatin remodeling during the DNA damage response. <i>Cell Reports</i> , 2012 , 2, 1657-69	10.6	85
275	Novel transglutaminase-like peptidase and C2 domains elucidate the structure, biogenesis and evolution of the ciliary compartment. <i>Cell Cycle</i> , 2012 , 11, 3861-75	4.7	36
274	Bacterial GRAS domain proteins throw new light on gibberellic acid response mechanisms. <i>Bioinformatics</i> , 2012 , 28, 2407-11	7.2	59

273	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
272	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
271	ALOG 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	7.2	29
270	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
269	Identification of novel components of NAD-utilizing metabolic pathways and prediction of their biochemical functions. <i>Molecular BioSystems</i> , 2012 , 8, 1661-77		46
268	Evolutionary and Biochemical Aspects of Chemical Stress Resistance in <i>Saccharomyces cerevisiae</i> . <i>Frontiers in Genetics</i> , 2012 , 3, 47	4.5	7
267	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	4.5	187
266	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
265	The natural history of ubiquitin and ubiquitin-related domains. <i>Frontiers in Bioscience - Landmark</i> , 2012 , 17, 1433-60	2.8	36
264	The HARE-HTH and associated domains: novel modules in the coordination of epigenetic DNA and protein modifications. <i>Cell Cycle</i> , 2012 , 11, 119-31	4.7	60
263	Structure of the Plasmodium 6-cysteine s48/45 domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 6692-7	11.5	51
262	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
261	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	8.8	48
260	Structure and evolution of ubiquitin and ubiquitin-related domains. <i>Methods in Molecular Biology</i> , 2012 , 832, 15-63	1.4	33
259	Natural history of the eukaryotic chromatin protein methylation system. <i>Progress in Molecular Biology and Translational Science</i> , 2011 , 101, 105-76	4	50
258	Natural history of eukaryotic DNA methylation systems. <i>Progress in Molecular Biology and Translational Science</i> , 2011 , 101, 25-104	4	144
257	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, 4532-52	20.1	130
256	Malaria parasite clag3 genes determine channel-mediated nutrient uptake by infected red blood cells. <i>Cell</i> , 2011 , 145, 665-77	56.2	181

255	Comparative genomics uncovers novel structural and functional features of the heterotrimeric GTPase signaling system. <i>Gene</i> , 2011 , 475, 63-78	3.8	43
254	Clinical and molecular aspects of malaria fever. <i>Trends in Parasitology</i> , 2011 , 27, 442-9	6.4	43
253	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	7.2	324
252	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, 2261-77		49
251	Molecular correlates of experimental cerebral malaria detectable in whole blood. <i>Infection and Immunity</i> , 2011 , 79, 1244-53	3.7	14
250	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, 9473-97	20.1	102
249	Impaired hydroxylation of 5-methylcytosine in myeloid cancers with mutant TET2. <i>Nature</i> , 2010 , 468, 839-43	50.4	1023
248	UMA and MABP domains throw light on receptor endocytosis and selection of endosomal cargoes. <i>Bioinformatics</i> , 2010 , 26, 1477-80	7.2	17
247	Origin and evolution of peptide-modifying dioxygenases and identification of the wybutosine hydroxylase/hydroperoxidase. <i>Nucleic Acids Research</i> , 2010 , 38, 5261-79	20.1	44
246	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, 13408-13	11.5	58
245	CYSTM, a novel cysteine-rich transmembrane module with a role in stress tolerance across eukaryotes. <i>Bioinformatics</i> , 2010 , 26, 149-52	7.2	33
244	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, 8675-86	5.4	55
243	Structural basis of oligomerization in septin-like GTPase of immunity-associated protein 2 (GIMAP2). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 20299-304	11.5	37
242	The bridge-region of the Ku superfamily is an atypical zinc ribbon domain. <i>Journal of Structural Biology</i> , 2010 , 172, 294-9	3.4	13
241	Identification of novel families and classification of the C2 domain superfamily elucidate the origin and evolution of membrane targeting activities in eukaryotes. <i>Gene</i> , 2010 , 469, 18-30	3.8	93
240	Diversity and evolution of chromatin proteins encoded by DNA viruses. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2010 , 1799, 302-18	6	50
239	Robustness and evolvability in natural chemical resistance: identification of novel systems properties, biochemical mechanisms and regulatory interactions. <i>Molecular BioSystems</i> , 2010 , 6, 1475-91		10
238	High-confidence mapping of chemical compounds and protein complexes reveals novel aspects of chemical stress response in yeast. <i>Molecular BioSystems</i> , 2010 , 6, 175-81		12

237	Novel eukaryotic enzymes modifying cell-surface biopolymers. <i>Biology Direct</i> , 2010 , 5, 1	7.2	49
236	Presence of a classical RRM-fold palm domain in Thg1-type 3P 5R nucleic acid polymerases and the origin of the GGDEF and CRISPR polymerase domains. <i>Biology Direct</i> , 2010 , 5, 43	7.2	33
235	Predicted class-I aminoacyl tRNA synthetase-like proteins in non-ribosomal peptide synthesis. <i>Biology Direct</i> , 2010 , 5, 48	7.2	41
234	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, 1160-6		15
233	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, 1167-73		3
232	OST-HTH: a novel predicted RNA-binding domain. <i>Biology Direct</i> , 2010 , 5, 13	7.2	59
231	MicroRNA targeting in mammalian genomes: genes and mechanisms. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010 , 2, 148-161	6.6	28
230	Impaired Hydroxylation of 5-Methylcytosine In TET2 mutated Patients with Myeloid Malignancies. <i>Blood</i> , 2010 , 116, 1-1	2.2	1
229	Pathogenic roles of CD14, galectin-3, and OX40 during experimental cerebral malaria in mice. <i>PLoS ONE</i> , 2009 , 4, e6793	3.7	30
228	Genomic analysis reveals a tight link between transcription factor dynamics and regulatory network architecture. <i>Molecular Systems Biology</i> , 2009 , 5, 294	12.2	116
227	Prediction of novel families of enzymes involved in oxidative and other complex modifications of bases in nucleic acids. <i>Cell Cycle</i> , 2009 , 8, 1698-710	4.7	303
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- 3 A ubiquitin-based mechanism for the oligogenic inheritance of heterotaxy and heart defects 1
- 2 Discovery of the role of a SLOG superfamily biological conflict systems associated protein IodA (YpsA) in oxidative stress protection and cell division inhibition in Gram-positive bacteria 1
- 1 NONU-1 encodes a conserved endonuclease required for mRNA translation surveillance 4