

Aravind L Iyer

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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	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001 , 409, 860-921	50.4	17366
379	Conversion of 5-methylcytosine to 5-hydroxymethylcytosine in mammalian DNA by MLL partner TET1. <i>Science</i> , 2009 , 324, 930-5	33.3	4222
378	De-ubiquitination and ubiquitin ligase domains of A20 downregulate NF-kappaB signalling. <i>Nature</i> , 2004 , 430, 694-9	50.4	1453
377	AAA+: A class of chaperone-like ATPases associated with the assembly, operation, and disassembly of protein complexes. <i>Genome Research</i> , 1999 , 9, 27-43	9.7	1292
376	Genome sequence of an obligate intracellular pathogen of humans: <i>Chlamydia trachomatis</i> . <i>Science</i> , 1998 , 282, 754-9	33.3	1198
375	Bacterial rhodopsin: evidence for a new type of phototrophy in the sea. <i>Science</i> , 2000 , 289, 1902-6	33.3	1143
374	Impaired hydroxylation of 5-methylcytosine in myeloid cancers with mutant TET2. <i>Nature</i> , 2010 , 468, 839-43	50.4	1023
373	Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements. <i>Nucleic Acids Research</i> , 2001 , 29, 2994-3005	20.1	1013
372	AAA+: A Class of Chaperone-Like ATPases Associated with the Assembly, Operation, and Disassembly of Protein Complexes. <i>Genome Research</i> , 1999 , 9, 27-43	9.7	890
371	Classification and evolution of P-loop GTPases and related ATPases. <i>Journal of Molecular Biology</i> , 2002 , 317, 41-72	6.5	882
370	Horizontal gene transfer in prokaryotes: quantification and classification. <i>Annual Review of Microbiology</i> , 2001 , 55, 709-42	17.5	859
369	Role of Rpn11 metalloprotease in deubiquitination and degradation by the 26S proteasome. <i>Science</i> , 2002 , 298, 611-5	33.3	822
368	Genome sequence of the radioresistant bacterium <i>Deinococcus radiodurans</i> R1. <i>Science</i> , 1999 , 286, 1571-3	33.3	760
367	Complete genome sequence of the apicomplexan, <i>Cryptosporidium parvum</i> . <i>Science</i> , 2004 , 304, 441-5	33.3	757
366	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
365	Evolutionary history and higher order classification of AAA+ ATPases. <i>Journal of Structural Biology</i> , 2004 , 146, 11-31	3.4	622
364	Role of predicted metalloprotease motif of Jab1/Csn5 in cleavage of Nedd8 from Cul1. <i>Science</i> , 2002 , 298, 608-11	33.3	578

363	Structure and evolution of transcriptional regulatory networks. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 283-91	8.1	556
362	Genome of the extremely radiation-resistant bacterium <i>Deinococcus radiodurans</i> viewed from the perspective of comparative genomics. <i>Microbiology and Molecular Biology Reviews</i> , 2001 , 65, 44-79	13.2	512
361	The GAF domain: an evolutionary link between diverse phototransducing proteins. <i>Trends in Biochemical Sciences</i> , 1997 , 22, 458-9	10.3	489
360	Evolutionary genomics of nucleo-cytoplasmic large DNA viruses. <i>Virus Research</i> , 2006 , 117, 156-84	6.4	455
359	Conserved domains in DNA repair proteins and evolution of repair systems. <i>Nucleic Acids Research</i> , 1999 , 27, 1223-42	20.1	442
358	DNA Methylation on N6-Adenine in <i>C. elegans</i> . <i>Cell</i> , 2015 , 161, 868-78	56.2	424
357	Common origin of four diverse families of large eukaryotic DNA viruses. <i>Journal of Virology</i> , 2001 , 75, 11720-34	6.6	419
356	SAP - a putative DNA-binding motif involved in chromosomal organization. <i>Trends in Biochemical Sciences</i> , 2000 , 25, 112-4	10.3	409
355	Comparative genomics and evolution of proteins involved in RNA metabolism. <i>Nucleic Acids Research</i> , 2002 , 30, 1427-64	20.1	383
354	Gleaning non-trivial structural, functional and evolutionary information about proteins by iterative database searches. <i>Journal of Molecular Biology</i> , 1999 , 287, 1023-40	6.5	380
353	The HD domain defines a new superfamily of metal-dependent phosphohydrolases. <i>Trends in Biochemical Sciences</i> , 1998 , 23, 469-72	10.3	370
352	AT-hook motifs identified in a wide variety of DNA-binding proteins. <i>Nucleic Acids Research</i> , 1998 , 26, 4413-21	20.1	354
351	Chromosome 2 sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Science</i> , 1998 , 282, 1126-32	9.3	350
350	The domains of death: evolution of the apoptosis machinery. <i>Trends in Biochemical Sciences</i> , 1999 , 24, 47-53	10.3	347
349	Discovery of the principal specific transcription factors of Apicomplexa and their implication for the evolution of the AP2-integrase DNA binding domains. <i>Nucleic Acids Research</i> , 2005 , 33, 3994-4006	20.1	341
348	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
347	Comparison of the complete protein sets of worm and yeast: orthology and divergence. <i>Science</i> , 1998 , 282, 2022-8	33.3	339
346	The DNA-repair protein AlkB, EGL-9, and leprecan define new families of 2-oxoglutarate- and iron-dependent dioxygenases. <i>Genome Biology</i> , 2001 , 2, RESEARCH0007	18.3	337

345	START: a lipid-binding domain in StAR, HD-ZIP and signalling proteins. <i>Trends in Biochemical Sciences</i> , 1999 , 24, 130-2	10.3	337
344	The role of lineage-specific gene family expansion in the evolution of eukaryotes. <i>Genome Research</i> , 2002 , 12, 1048-59	9.7	332
343	STAND, a class of P-loop NTPases including animal and plant regulators of programmed cell death: multiple, complex domain architectures, unusual phyletic patterns, and evolution by horizontal gene transfer. <i>Journal of Molecular Biology</i> , 2004 , 343, 1-28	6.5	327
342	The cytoplasmic helical linker domain of receptor histidine kinase and methyl-accepting proteins is common to many prokaryotic signalling proteins. <i>FEMS Microbiology Letters</i> , 1999 , 176, 111-6	2.9	326
341	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
340	Origin and evolution of eukaryotic apoptosis: the bacterial connection. <i>Cell Death and Differentiation</i> , 2002 , 9, 394-404	12.7	323
339	Evolutionary genomics of the HAD superfamily: understanding the structural adaptations and catalytic diversity in a superfamily of phosphoesterases and allied enzymes. <i>Journal of Molecular Biology</i> , 2006 , 361, 1003-34	6.5	315
338	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
337	The U box is a modified RING finger - a common domain in ubiquitination. <i>Current Biology</i> , 2000 , 10, R137-4	7.4	309
336	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
335	Evolution of aminoacyl-tRNA synthetases--analysis of unique domain architectures and phylogenetic trees reveals a complex history of horizontal gene transfer events. <i>Genome Research</i> , 1999 , 9, 689-710	9.7	301
334	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
333	Evidence for massive gene exchange between archaeal and bacterial hyperthermophiles. <i>Trends in Genetics</i> , 1998 , 14, 442-4	8.5	294
332	Toprim--a conserved catalytic domain in type IA and II topoisomerases, DnaG-type primases, OLD family nucleases and RecR proteins. <i>Nucleic Acids Research</i> , 1998 , 26, 4205-13	20.1	290
331	Did DNA replication evolve twice independently?. <i>Nucleic Acids Research</i> , 1999 , 27, 3389-401	20.1	280
330	Eukaryotic signalling domain homologues in archaea and bacteria. Ancient ancestry and horizontal gene transfer. <i>Journal of Molecular Biology</i> , 1999 , 289, 729-45	6.5	280
329	Apoptotic molecular machinery: vastly increased complexity in vertebrates revealed by genome comparisons. <i>Science</i> , 2001 , 291, 1279-84	33.3	279
328	PAS: a multifunctional domain family comes to light. <i>Current Biology</i> , 1997 , 7, R674-7	6.3	278

327	Construction and analysis of bacterial artificial chromosome libraries from a marine microbial assemblage. <i>Environmental Microbiology</i> , 2000 , 2, 516-29	5.2	277
326	A DNA repair system specific for thermophilic Archaea and bacteria predicted by genomic context analysis. <i>Nucleic Acids Research</i> , 2002 , 30, 482-96	20.1	273
325	Evolutionary history, structural features and biochemical diversity of the NlpC/P60 superfamily of enzymes. <i>Genome Biology</i> , 2003 , 4, R11	18.3	268
324	Modulation of TET2 expression and 5-methylcytosine oxidation by the CXXC domain protein IDAX. <i>Nature</i> , 2013 , 497, 122-6	50.4	265
323	Comparative genomics, evolution and origins of the nuclear envelope and nuclear pore complex. <i>Cell Cycle</i> , 2004 , 3, 1612-37	4.7	263
322	The complete genome of hyperthermophile <i>Methanopyrus kandleri</i> AV19 and monophyly of archaeal methanogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 4644-9	11.5	263
321	IMPALA: matching a protein sequence against a collection of PSI-BLAST-constructed position-specific score matrices. <i>Bioinformatics</i> , 1999 , 15, 1000-11	7.2	262
320	DNA polymerase beta-like nucleotidyltransferase superfamily: identification of three new families, classification and evolutionary history. <i>Nucleic Acids Research</i> , 1999 , 27, 1609-18	20.1	261
319	Plasmodium biology: genomic gleanings. <i>Cell</i> , 2003 , 115, 771-85	56.2	258
318	SURVEY AND SUMMARY: holliday junction resolvases and related nucleases: identification of new families, phyletic distribution and evolutionary trajectories. <i>Nucleic Acids Research</i> , 2000 , 28, 3417-32	20.1	257
317	The NACHT family - a new group of predicted NTPases implicated in apoptosis and MHC transcription activation. <i>Trends in Biochemical Sciences</i> , 2000 , 25, 223-4	10.3	256
316	Novel families of putative protein kinases in bacteria and archaea: evolution of the "eukaryotic" protein kinase superfamily. <i>Genome Research</i> , 1998 , 8, 1038-47	9.7	253
315	The catalytic domain of the P-type ATPase has the haloacid dehalogenase fold. <i>Trends in Biochemical Sciences</i> , 1998 , 23, 127-9	10.3	240
314	Lineage-specific loss and divergence of functionally linked genes in eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 11319-24	11.5	237
313	Comparative genomics of the FtsK-HerA superfamily of pumping ATPases: implications for the origins of chromosome segregation, cell division and viral capsid packaging. <i>Nucleic Acids Research</i> , 2004 , 32, 5260-79	20.1	234
312	Diversification and spectral tuning in marine proteorhodopsins. <i>EMBO Journal</i> , 2003 , 22, 1725-31	13	231
311	Evolution and diversification of lamprey antigen receptors: evidence for involvement of an AID-APOBEC family cytosine deaminase. <i>Nature Immunology</i> , 2007 , 8, 647-56	19.1	228
310	The impact of comparative genomics on our understanding of evolution. <i>Cell</i> , 2000 , 101, 573-6	56.2	227

309	A database of bacterial lipoproteins (DOLOP) with functional assignments to predicted lipoproteins. <i>Journal of Bacteriology</i> , 2006 , 188, 2761-73	3.5	225
308	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
307	Genome of <i>Rhodnius prolixus</i> , 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
306	Multiple transporters associated with malaria parasite responses to chloroquine and quinine. <i>Molecular Microbiology</i> , 2003 , 49, 977-89	4.1	219
305	The STAS domain - a link between anion transporters and antisigma-factor antagonists. <i>Current Biology</i> , 2000 , 10, R53-5	6.3	218
304	Evolutionary dynamics of prokaryotic transcriptional regulatory networks. <i>Journal of Molecular Biology</i> , 2006 , 358, 614-33	6.5	217
303	Evolution and classification of P-loop kinases and related proteins. <i>Journal of Molecular Biology</i> , 2003 , 333, 781-815	6.5	216
302	Prokaryotic homologs of the eukaryotic DNA-end-binding protein Ku, novel domains in the Ku protein and prediction of a prokaryotic double-strand break repair system. <i>Genome Research</i> , 2001 , 11, 1365-74	9.7	213
301	A novel superfamily of predicted cysteine proteases from eukaryotes, viruses and <i>Chlamydia pneumoniae</i> . <i>Trends in Biochemical Sciences</i> , 2000 , 25, 50-2	10.3	207
300	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
299	Comparative Genomics, Evolution and Origins of the Nuclear Envelope and Nuclear Pore Complex. <i>Cell Cycle</i> , 2004 , 3, 1625-1650	4.7	206
298	Prediction of the archaeal exosome and its connections with the proteasome and the translation and transcription machineries by a comparative-genomic approach. <i>Genome Research</i> , 2001 , 11, 240-52	9.7	204
297	Phosphoesterase domains associated with DNA polymerases of diverse origins. <i>Nucleic Acids Research</i> , 1998 , 26, 3746-52	20.1	203
296	Origin and evolution of the archaeo-eukaryotic primase superfamily and related palm-domain proteins: structural insights and new members. <i>Nucleic Acids Research</i> , 2005 , 33, 3875-96	20.1	201
295	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
294	Evolution of Aminoacyl-tRNA Synthetases: Analysis of Unique Domain Architectures and Phylogenetic Trees Reveals a Complex History of Horizontal Gene Transfer Events. <i>Genome Research</i> , 1999 , 9, 689-710	9.7	196
293	An antisense RNA controls synthesis of an SOS-induced toxin evolved from an antitoxin. <i>Molecular Microbiology</i> , 2007 , 64, 738-54	4.1	194
292	Adaptations of the helix-grip fold for ligand binding and catalysis in the START domain superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 43, 134-44	4.2	194

291	DNA-binding proteins and evolution of transcription regulation in the archaea. <i>Nucleic Acids Research</i> , 1999 , 27, 4658-70	20.1	192
290	Identification of the prokaryotic ligand-gated ion channels and their implications for the mechanisms and origins of animal Cys-loop ion channels. <i>Genome Biology</i> , 2005 , 6, R4	18.3	190
289	Comparative genomics of the Archaea (Euryarchaeota): evolution of conserved protein families, the stable core, and the variable shell. <i>Genome Research</i> , 1999 , 9, 608-28	9.7	189
288	Human and mouse homologs of Escherichia coli DinB (DNA polymerase IV), members of the UmuC/DinB superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 11922-7	11.5	188
287	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
286	Malaria parasite clag3 genes determine channel-mediated nutrient uptake by infected red blood cells. <i>Cell</i> , 2011 , 145, 665-77	56.2	181
285	Evolutionary connection between the catalytic subunits of DNA-dependent RNA polymerases and eukaryotic RNA-dependent RNA polymerases and the origin of RNA polymerases. <i>BMC Structural Biology</i> , 2003 , 3, 1	2.7	175
284	Comprehensive analysis of combinatorial regulation using the transcriptional regulatory network of yeast. <i>Journal of Molecular Biology</i> , 2006 , 360, 213-27	6.5	174
283	PFSETvs methylation of histone H3K36 represses virulence genes in Plasmodium falciparum. <i>Nature</i> , 2013 , 499, 223-7	50.4	171
282	Interplay between gene expression noise and regulatory network architecture. <i>Trends in Genetics</i> , 2012 , 28, 221-32	8.5	170
281	The HORMA domain: a common structural denominator in mitotic checkpoints, chromosome synapsis and DNA repair. <i>Trends in Biochemical Sciences</i> , 1998 , 23, 284-6	10.3	164
280	Evolution of cell-cell signaling in animals: did late horizontal gene transfer from bacteria have a role?. <i>Trends in Genetics</i> , 2004 , 20, 292-9	8.5	157
279	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
278	The WWE domain: a common interaction module in protein ubiquitination and ADP ribosylation. <i>Trends in Biochemical Sciences</i> , 2001 , 26, 273-5	10.3	155
277	Comparative analysis of apicomplexa and genomic diversity in eukaryotes. <i>Genome Research</i> , 2004 , 14, 1686-95	9.7	149
276	Comparative genomic analysis of archaeal genotypic variants in a single population and in two different oceanic provinces. <i>Applied and Environmental Microbiology</i> , 2002 , 68, 335-45	4.8	149
275	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
274	Novel predicted RNA-binding domains associated with the translation machinery. <i>Journal of Molecular Evolution</i> , 1999 , 48, 291-302	3.1	149

273	Classification of the caspase-hemoglobinase fold: detection of new families and implications for the origin of the eukaryotic separins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 46, 355-67	4.2	148
272	Ancient conserved domains shared by animal soluble guanylyl cyclases and bacterial signaling proteins. <i>BMC Genomics</i> , 2003 , 4, 5	4.5	148
271	The bacterial replicative helicase DnaB evolved from a RecA duplication. <i>Genome Research</i> , 2000 , 10, 5-16	9.7	148
270	Fold prediction and evolutionary analysis of the POZ domain: structural and evolutionary relationship with the potassium channel tetramerization domain. <i>Journal of Molecular Biology</i> , 1999 , 285, 1353-61	6.5	146
269	Natural history of eukaryotic DNA methylation systems. <i>Progress in Molecular Biology and Translational Science</i> , 2011 , 101, 25-104	4	144
268	A superfamily of archaeal, bacterial, and eukaryotic proteins homologous to animal transglutaminases. <i>Protein Science</i> , 1999 , 8, 1714-9	6.3	142
267	Classification and evolutionary history of the single-strand annealing proteins, RecT, Redbeta, ERF and RAD52. <i>BMC Genomics</i> , 2002 , 3, 8	4.5	136
266	An evolutionary classification of the metallo-beta-lactamase fold proteins. <i>In Silico Biology</i> , 1999 , 1, 69-91		136
265	A novel family of predicted phosphoesterases includes Drosophila prune protein and bacterial RecJ exonuclease. <i>Trends in Biochemical Sciences</i> , 1998 , 23, 17-9	10.3	134
264	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
263	G-patch: a new conserved domain in eukaryotic RNA-processing proteins and type D retroviral polyproteins. <i>Trends in Biochemical Sciences</i> , 1999 , 24, 342-4	10.3	131
262	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
261	The natural history of the WRKY-GCM1 zinc fingers and the relationship between transcription factors and transposons. <i>Nucleic Acids Research</i> , 2006 , 34, 6505-20	20.1	130
260	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
259	Guilt by association: contextual information in genome analysis. <i>Genome Research</i> , 2000 , 10, 1074-7	9.7	125
258	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
257	The prokaryotic antecedents of the ubiquitin-signaling system and the early evolution of ubiquitin-like beta-grasp domains. <i>Genome Biology</i> , 2006 , 7, R60	18.3	122
256	Trends in protein evolution inferred from sequence and structure analysis. <i>Current Opinion in Structural Biology</i> , 2002 , 12, 392-9	8.1	122

255	Comparative Genomics of the Archaea (Euryarchaeota): Evolution of Conserved Protein Families, the Stable Core, and the Variable Shell. <i>Genome Research</i> , 1999 , 9, 608-628	9.7	119
254	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. <i>Frontiers in Genetics</i> , 2014 , 5, 102	4.5	118
253	The BED finger, a novel DNA-binding domain in chromatin-boundary-element-binding proteins and transposases. <i>Trends in Biochemical Sciences</i> , 2000 , 25, 421-3	10.3	118
252	Detection of novel members, structure-function analysis and evolutionary classification of the 2H phosphoesterase superfamily. <i>Nucleic Acids Research</i> , 2002 , 30, 5229-43	20.1	117
251	Rickettsiae and Chlamydiae: evidence of horizontal gene transfer and gene exchange. <i>Trends in Genetics</i> , 1999 , 15, 173-5	8.5	117
250	A hemolytic pigment of Group B Streptococcus allows bacterial penetration of human placenta. <i>Journal of Experimental Medicine</i> , 2013 , 210, 1265-81	16.6	116
249	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
248	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
247	Homologues of 26S proteasome subunits are regulators of transcription and translation. <i>Protein Science</i> , 1998 , 7, 1250-4	6.3	113
246	Molecular cloning, expression, and structural prediction of deoxyhypusine hydroxylase: a HEAT-repeat-containing metalloenzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 51-6	11.5	113
245	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
244	Small but versatile: the extraordinary functional and structural diversity of the beta-grasp fold. <i>Biology Direct</i> , 2007 , 2, 18	7.2	110
243	Prune cAMP phosphodiesterase binds nm23-H1 and promotes cancer metastasis. <i>Cancer Cell</i> , 2004 , 5, 137-49	24.3	110
242	The alpha/beta fold uracil DNA glycosylases: a common origin with diverse fates. <i>Genome Biology</i> , 2000 , 1, RESEARCH0007	18.3	107
241	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
240	A conserved NAD binding pocket that regulates protein-protein interactions during aging. <i>Science</i> , 2017 , 355, 1312-1317	33.3	102
239	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
238	The signaling helix: a common functional theme in diverse signaling proteins. <i>Biology Direct</i> , 2006 , 1, 25	7.2	101

237	Saccharomyces cerevisiae SMT4 encodes an evolutionarily conserved protease with a role in chromosome condensation regulation. <i>Genetics</i> , 2001 , 158, 95-107	4	100
236	The NYN domains: novel predicted RNases with a PIN domain-like fold. <i>RNA Biology</i> , 2006 , 3, 18-27	4.8	97
235	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
234	Evolution of bacterial RNA polymerase: implications for large-scale bacterial phylogeny, domain accretion, and horizontal gene transfer. <i>Gene</i> , 2004 , 335, 73-88	3.8	95
233	A multidomain adhesion protein family expressed in Plasmodium falciparum is essential for transmission to the mosquito. <i>Journal of Experimental Medicine</i> , 2004 , 199, 1533-44	16.6	94
232	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
231	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
230	Structure of a lamprey variable lymphocyte receptor in complex with a protein antigen. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 725-30	17.6	91
229	Chitinases of the avian malaria parasite Plasmodium gallinaceum, a class of enzymes necessary for parasite invasion of the mosquito midgut. <i>Journal of Biological Chemistry</i> , 2000 , 275, 10331-41	5.4	91
228	Novel predicted peptidases with a potential role in the ubiquitin signaling pathway. <i>Cell Cycle</i> , 2004 , 3, 1440-50	4.7	89
227	MutL homologs in restriction-modification systems and the origin of eukaryotic MORC ATPases. <i>Biology Direct</i> , 2008 , 3, 8	7.2	88
226	Extensive domain shuffling in transcription regulators of DNA viruses and implications for the origin of fungal APSES transcription factors. <i>Genome Biology</i> , 2002 , 3, RESEARCH0012	18.3	88
225	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
224	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
223	Unraveling the biochemistry and provenance of pupylation: a prokaryotic analog of ubiquitination. <i>Biology Direct</i> , 2008 , 3, 45	7.2	84
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