

Aravind L Iyer

List of Publications by Year in descending order

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380
papers

87,622
citations

466

130
h-index

357

283
g-index

401
all docs

401
docs citations

401
times ranked

78236
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	27.8	21,074
2	Conversion of 5-Methylcytosine to 5-Hydroxymethylcytosine in Mammalian DNA by MLL Partner TET1. <i>Science</i> , 2009, 324, 930-935.	12.6	4,989
3	De-ubiquitination and ubiquitin ligase domains of A20 downregulate NF- κ B signalling. <i>Nature</i> , 2004, 430, 694-699.	27.8	1,691
4	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.	5.5	1,549
5	Genome Sequence of an Obligate Intracellular Pathogen of Humans: <i>Chlamydia trachomatis</i> . <i>Science</i> , 1998, 282, 754-759.	12.6	1,449
6	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.	5.5	1,388
7	Bacterial Rhodopsin: Evidence for a New Type of Phototrophy in the Sea. <i>Science</i> , 2000, 289, 1902-1906.	12.6	1,357
8	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.	14.5	1,226
9	Impaired hydroxylation of 5-methylcytosine in myeloid cancers with mutant TET2. <i>Nature</i> , 2010, 468, 839-843.	27.8	1,160
10	Horizontal Gene Transfer in Prokaryotes: Quantification and Classification. <i>Annual Review of Microbiology</i> , 2001, 55, 709-742.	7.3	1,024
11	Classification and evolution of P-loop GTPases and related ATPases. <i>Journal of Molecular Biology</i> , 2002, 317, 41-72.	4.2	1,021
12	Role of Rpn11 Metalloprotease in Deubiquitination and Degradation by the 26S Proteasome. <i>Science</i> , 2002, 298, 611-615.	12.6	919
13	Genome Sequence of the Radioresistant Bacterium <i>Deinococcus radiodurans</i> R1. <i>Science</i> , 1999, 286, 1571-1577.	12.6	879
14	Complete Genome Sequence of the Apicomplexan, <i>Cryptosporidium parvum</i> . <i>Science</i> , 2004, 304, 441-445.	12.6	877
15	TETonic shift: biological roles of TET proteins in DNA demethylation and transcription. <i>Nature Reviews Molecular Cell Biology</i> , 2013, 14, 341-356.	37.0	733
16	Evolutionary history and higher order classification of AAA ⁺ ATPases. <i>Journal of Structural Biology</i> , 2004, 146, 11-31.	2.8	711
17	Structure and evolution of transcriptional regulatory networks. <i>Current Opinion in Structural Biology</i> , 2004, 14, 283-291.	5.7	683
18	Role of Predicted Metalloprotease Motif of Jab1/Csn5 in Cleavage of Nedd8 from Cul1. <i>Science</i> , 2002, 298, 608-611.	12.6	666

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19	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.	6.6	619
20	DNA Methylation on N6-Adenine in <i>C.Âelegans</i> . <i>Cell</i> , 2015, 161, 868-878.	28.9	602
21	Evolutionary genomics of nucleo-cytoplasmic large DNA viruses. <i>Virus Research</i> , 2006, 117, 156-184.	2.2	541
22	The GAF domain: an evolutionary link between diverse phototransducing proteins. <i>Trends in Biochemical Sciences</i> , 1997, 22, 458-459.	7.5	534
23	Conserved domains in DNA repair proteins and evolution of repair systems. <i>Nucleic Acids Research</i> , 1999, 27, 1223-1242.	14.5	501
24	Common Origin of Four Diverse Families of Large Eukaryotic DNA Viruses. <i>Journal of Virology</i> , 2001, 75, 11720-11734.	3.4	495
25	The many faces of the helix-turn-helix domain: Transcription regulation and beyond. <i>FEMS Microbiology Reviews</i> , 2005, 29, 231-262.	8.6	469
26	Comparative genomics and evolution of proteins involved in RNA metabolism. <i>Nucleic Acids Research</i> , 2002, 30, 1427-1464.	14.5	462
27	SAP â€“ a putative DNA-binding motif involved in chromosomal organization. <i>Trends in Biochemical Sciences</i> , 2000, 25, 112-114.	7.5	454
28	Polymorphic toxin systems: Comprehensive characterization of trafficking modes, processing, mechanisms of action, immunity and ecology using comparative genomics. <i>Biology Direct</i> , 2012, 7, 18.	4.6	440
29	The DNA-repair protein AlkB, EGL-9, and IpreCAN define new families of 2-oxoglutarate- and iron-dependent dioxygenases. <i>Genome Biology</i> , 2001, 2, research0007.1.	9.6	437
30	The HD domain defines a new superfamily of metal-dependent phosphohydrolases. <i>Trends in Biochemical Sciences</i> , 1998, 23, 469-472.	7.5	432
31	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.	14.5	426
32	Gleaning non-trivial structural, functional and evolutionary information about proteins by iterative database searches. <i>Journal of Molecular Biology</i> , 1999, 287, 1023-1040.	4.2	421
33	Chromosome Sequence of the Human Malaria Parasite <i>Plasmodium falciparum</i> . , 1998, 282, 1126-1132.		419
34	The Role of Lineage-Specific Gene Family Expansion in the Evolution of Eukaryotes. <i>Genome Research</i> , 2002, 12, 1048-1059.	5.5	416
35	AT-hook motifs identified in a wide variety of DNA-binding proteins. <i>Nucleic Acids Research</i> , 1998, 26, 4413-4421.	14.5	413
36	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.	4.2	407

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37	Comparison of the Complete Protein Sets of Worm and Yeast: Orthology and Divergence. , 1998, 282, 2022-2028.		404
38	The domains of death: evolution of the apoptosis machinery. Trends in Biochemical Sciences, 1999, 24, 47-53.	7.5	393
39	Origin and evolution of eukaryotic apoptosis: the bacterial connection. Cell Death and Differentiation, 2002, 9, 394-404.	11.2	380
40	Unification of Cas protein families and a simple scenario for the origin and evolution of CRISPR-Cas systems. Biology Direct, 2011, 6, 38.	4.6	379
41	Evolutionary Genomics of the HAD Superfamily: Understanding the Structural Adaptations and Catalytic Diversity in a Superfamily of Phosphoesterases and Allied Enzymes. Journal of Molecular Biology, 2006, 361, 1003-1034.	4.2	376
42	START: a lipid-binding domain in StAR, HD-ZIP and signalling proteins. Trends in Biochemical Sciences, 1999, 24, 130-132.	7.5	364
43	The U box is a modified RING finger " a common domain in ubiquitination. Current Biology, 2000, 10, R132-R134.	3.9	363
44	The cytoplasmic helical linker domain of receptor histidine kinase and methyl-accepting proteins is common to many prokaryotic signalling proteins. FEMS Microbiology Letters, 1999, 176, 111-116.	1.8	352
45	Evolution of Aminoacyl-tRNA Synthetases" Analysis of Unique Domain Architectures and Phylogenetic Trees Reveals a Complex History of Horizontal Gene Transfer Events. Genome Research, 1999, 9, 689-710.	5.5	346
46	Prediction of novel families of enzymes involved in oxidative and other complex modifications of bases in nucleic acids. Cell Cycle, 2009, 8, 1698-1710.	2.6	345
47	Toprim--a conserved catalytic domain in type IA and II topoisomerases, DnaG-type primases, OLD family nucleases and RecR proteins. Nucleic Acids Research, 1998, 26, 4205-4213.	14.5	338
48	Evidence for massive gene exchange between archaeal and bacterial hyperthermophiles. Trends in Genetics, 1998, 14, 442-444.	6.7	337
49	The many faces of the helix-turn-helix domain: Transcription regulation and beyond. FEMS Microbiology Reviews, 2005, 29, 231-262.	8.6	334
50	A DNA repair system specific for thermophilic Archaea and bacteria predicted by genomic context analysis. Nucleic Acids Research, 2002, 30, 482-496.	14.5	331
51	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.	7.1	329
52	Evolution of aminoacyl-tRNA synthetases--analysis of unique domain architectures and phylogenetic trees reveals a complex history of horizontal gene transfer events. Genome Research, 1999, 9, 689-710.	5.5	329
53	Modulation of TET2 expression and 5-methylcytosine oxidation by the CXXC domain protein IDAX. Nature, 2013, 497, 122-126.	27.8	323
54	PAS: a multifunctional domain family comes to light. Current Biology, 1997, 7, R674-R677.	3.9	319

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55	Eukaryotic Signalling Domain Homologues in Archaea and Bacteria. Ancient Ancestry and Horizontal Gene Transfer. <i>Journal of Molecular Biology</i> , 1999, 289, 729-745.	4.2	318
56	Construction and analysis of bacterial artificial chromosome libraries from a marine microbial assemblage. <i>Environmental Microbiology</i> , 2000, 2, 516-529.	3.8	313
57	Did DNA replication evolve twice independently?. <i>Nucleic Acids Research</i> , 1999, 27, 3389-3401.	14.5	312
58	Evolutionary history, structural features and biochemical diversity of the NlpC/P60 superfamily of enzymes. <i>Genome Biology</i> , 2003, 4, R11.	9.6	312
59	Apoptotic Molecular Machinery: Vastly Increased Complexity in Vertebrates Revealed by Genome Comparisons. <i>Science</i> , 2001, 291, 1279-1284.	12.6	309
60	Plasmodium Biology. <i>Cell</i> , 2003, 115, 771-785.	28.9	291
61	Novel Families of Putative Protein Kinases in Bacteria and Archaea: Evolution of the "Eukaryotic" Protein Kinase Superfamily. <i>Genome Research</i> , 1998, 8, 1038-1047.	5.5	290
62	IMPALA: matching a protein sequence against a collection of PSI-BLAST-constructed position-specific score matrices. <i>Bioinformatics</i> , 1999, 15, 1000-1011.	4.1	288
63	Ufd2, a Novel Autoantigen in Scleroderma, Regulates Sister Chromatid Separation. <i>Cell Cycle</i> , 2004, 3, 1612-1618.	2.6	287
64	The NACHT family " a new group of predicted NTPases implicated in apoptosis and MHC transcription activation. <i>Trends in Biochemical Sciences</i> , 2000, 25, 223-224.	7.5	286
65	DNA polymerase beta-like nucleotidyltransferase superfamily: identification of three new families, classification and evolutionary history. <i>Nucleic Acids Research</i> , 1999, 27, 1609-1618.	14.5	285
66	Diversification and spectral tuning in marine proteorhodopsins. <i>EMBO Journal</i> , 2003, 22, 1725-1731.	7.8	284
67	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, 5260-5279.	14.5	284
68	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, 4644-4649.	7.1	283
69	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, 3417-3432.	14.5	279
70	The Impact of Comparative Genomics on Our Understanding of Evolution. <i>Cell</i> , 2000, 101, 573-576.	28.9	273
71	Evolution and Classification of P-loop Kinases and Related Proteins. <i>Journal of Molecular Biology</i> , 2003, 333, 781-815.	4.2	271
72	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, 11319-11324.	7.1	268

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73	The catalytic domain of the P-type ATPase has the haloacid dehalogenase fold. Trends in Biochemical Sciences, 1998, 23, 127-129.	7.5	263
74	Evolution and diversification of lamprey antigen receptors: evidence for involvement of an AID-APOBEC family cytosine deaminase. Nature Immunology, 2007, 8, 647-656.	14.5	263
75	A Database of Bacterial Lipoproteins (DOLOP) with Functional Assignments to Predicted Lipoproteins. Journal of Bacteriology, 2006, 188, 2761-2773.	2.2	255
76	Comparative Genomics, Evolution and Origins of the Nuclear Envelope and Nuclear Pore Complex. Cell Cycle, 2004, 3, 1625-1650.	2.6	254
77	Evolutionary Dynamics of Prokaryotic Transcriptional Regulatory Networks. Journal of Molecular Biology, 2006, 358, 614-633.	4.2	254
78	A novel superfamily of predicted cysteine proteases from eukaryotes, viruses and Chlamydia pneumoniae. Trends in Biochemical Sciences, 2000, 25, 50-52.	7.5	249
79	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. Genome Research, 2001, 11, 1365-1374.	5.5	246
80	Origin and evolution of the archaeo-eukaryotic primase superfamily and related palm-domain proteins: structural insights and new members. Nucleic Acids Research, 2005, 33, 3875-3896.	14.5	246
81	Regulatory potential, phyletic distribution and evolution of ancient, intracellular small-molecule-binding domains ¹¹ Edited by F. Cohen. Journal of Molecular Biology, 2001, 307, 1271-1292.	4.2	243
82	Phosphoesterase domains associated with DNA polymerases of diverse origins. Nucleic Acids Research, 1998, 26, 3746-3752.	14.5	242
83	The STAS domain "a link between anion transporters and antisigma-factor antagonists. Current Biology, 2000, 10, R53-R55.	3.9	239
84	Multiple transporters associated with malaria parasite responses to chloroquine and quinine. Molecular Microbiology, 2003, 49, 977-989.	2.5	237
85	Interplay between gene expression noise and regulatory network architecture. Trends in Genetics, 2012, 28, 221-232.	6.7	235
86	An antisense RNA controls synthesis of an SOS-induced toxin evolved from an antitoxin. Molecular Microbiology, 2007, 64, 738-754.	2.5	234
87	Malaria Parasite clag3 Genes Determine Channel-Mediated Nutrient Uptake by Infected Red Blood Cells. Cell, 2011, 145, 665-677.	28.9	228
88	Comparative genomics of transcription factors and chromatin proteins in parasitic protists and other eukaryotes. International Journal for Parasitology, 2008, 38, 1-31.	3.1	226
89	Comprehensive analysis of the HEPN superfamily: identification of novel roles in intra-genomic conflicts, defense, pathogenesis and RNA processing. Biology Direct, 2013, 8, 15.	4.6	221
90	Discovery of Novel DENN Proteins: Implications for the Evolution of Eukaryotic Intracellular Membrane Structures and Human Disease. Frontiers in Genetics, 2012, 3, 283.	2.3	220

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91	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, 240-252.	5.5	219
92	PfSETVs methylation of histone H3K36 represses virulence genes in <i>Plasmodium falciparum</i> . <i>Nature</i> , 2013, 499, 223-227.	27.8	219
93	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.	5.5	219
94	DNA-binding proteins and evolution of transcription regulation in the archaea. <i>Nucleic Acids Research</i> , 1999, 27, 4658-4670.	14.5	218
95	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, 134-144.	2.6	218
96	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.	2.3	218
97	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> , 2004, 6, R4.	9.6	218
98	New connections in the prokaryotic toxin-antitoxin network: relationship with the eukaryotic nonsense-mediated RNA decay system. <i>Genome Biology</i> , 2003, 4, R81.	9.6	213
99	Comprehensive Analysis of Combinatorial Regulation using the Transcriptional Regulatory Network of Yeast. <i>Journal of Molecular Biology</i> , 2006, 360, 213-227.	4.2	207
100	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.	5.5	202
101	Human and mouse homologs of <i>Escherichia coli</i> 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, 11922-11927.	7.1	200
102	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, 10633-10654.	14.5	200
103	The WWE domain: a common interaction module in protein ubiquitination and ADP ribosylation. <i>Trends in Biochemical Sciences</i> , 2001, 26, 273-275.	7.5	194
104	Evolution of cell-cell signaling in animals: did late horizontal gene transfer from bacteria have a role?. <i>Trends in Genetics</i> , 2004, 20, 292-299.	6.7	189
105	Natural History of Eukaryotic DNA Methylation Systems. <i>Progress in Molecular Biology and Translational Science</i> , 2011, 101, 25-104.	1.7	187
106	The HORMA domain: a common structural denominator in mitotic checkpoints, chromosome synapsis and DNA repair. <i>Trends in Biochemical Sciences</i> , 1998, 23, 284-286.	7.5	186
107	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.	14.5	184
108	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.	9.7	183

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109	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, 355-367.	2.6	178
110	Comparative Analysis of Apicomplexa and Genomic Diversity in Eukaryotes. <i>Genome Research</i> , 2004, 14, 1686-1695.	5.5	172
111	Novel Predicted RNA-Binding Domains Associated with the Translation Machinery. <i>Journal of Molecular Evolution</i> , 1999, 48, 291-302.	1.8	170
112	The bacterial replicative helicase DnaB evolved from a RecA duplication. <i>Genome Research</i> , 2000, 10, 5-16.	5.5	167
113	Cache â€“ a signaling domain common to animal Ca ²⁺ -channel subunits and a class of prokaryotic chemotaxis receptors. <i>Trends in Biochemical Sciences</i> , 2000, 25, 535-537.	7.5	166
114	Guilt by Association: Contextual Information in Genome Analysis. <i>Genome Research</i> , 2000, 10, 1074-1077.	5.5	164
115	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, 335-345.	3.1	164
116	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. <i>Frontiers in Genetics</i> , 2014, 5, 102.	2.3	164
117	A superfamily of archaeal, bacterial, and eukaryotic proteins homologous to animal transglutaminases. <i>Protein Science</i> , 1999, 8, 1714-1719.	7.6	161
118	Ancient conserved domains shared by animal soluble guanylyl cyclases and bacterial signaling proteins. <i>BMC Genomics</i> , 2003, 4, 5.	2.8	160
119	G-patch: a new conserved domain in eukaryotic RNA-processing proteins and type D retroviral polyproteins. <i>Trends in Biochemical Sciences</i> , 1999, 24, 342-344.	7.5	159
120	Fold prediction and evolutionary analysis of the POZ domain: structural and evolutionary relationship with the potassium channel tetramerization domain 1 Edited by F. Cohen. <i>Journal of Molecular Biology</i> , 1999, 285, 1353-1361.	4.2	158
121	Classification and evolutionary history of the single-strand annealing proteins, RecT, Red ¹ , ERF and RAD52. <i>BMC Genomics</i> , 2002, 3, 8.	2.8	158
122	The natural history of the WRKYâ€“GCM1 zinc fingers and the relationship between transcription factors and transposons. <i>Nucleic Acids Research</i> , 2006, 34, 6505-6520.	14.5	157
123	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.	14.5	154
124	The CHASE domain: a predicted ligand-binding module in plant cytokinin receptors and other eukaryotic and bacterial receptors. <i>Trends in Biochemical Sciences</i> , 2001, 26, 579-582.	7.5	150
125	A novel family of predicted phosphoesterases includes <i>Drosophila</i> prune protein and bacterial recJ exonuclease. <i>Trends in Biochemical Sciences</i> , 1998, 23, 17-19.	7.5	149
126	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.	9.6	148

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127	Emergence of diverse biochemical activities in evolutionarily conserved structural scaffolds of proteins. <i>Current Opinion in Chemical Biology</i> , 2003, 7, 12-20.	6.1	147
128	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.	8.5	147
129	Genomic analysis reveals a tight link between transcription factor dynamics and regulatory network architecture. <i>Molecular Systems Biology</i> , 2009, 5, 294.	7.2	146
130	An evolutionary classification of the metallo-beta-lactamase fold proteins. <i>In Silico Biology</i> , 1999, 1, 69-91.	0.9	145
131	The BED finger, a novel DNA-binding domain in chromatin-boundary-element-binding proteins and transposases. <i>Trends in Biochemical Sciences</i> , 2000, 25, 421-423.	7.5	142
132	Monophyly of class I aminoacyl tRNA synthetase, USPA, ETPF, photolyase, and PP-ATPase nucleotide-binding domains: implications for protein evolution in the RNA world. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 1-14.	2.6	142
133	A conserved NAD ⁺ binding pocket that regulates protein-protein interactions during aging. <i>Science</i> , 2017, 355, 1312-1317.	12.6	140
134	Trends in protein evolution inferred from sequence and structure analysis. <i>Current Opinion in Structural Biology</i> , 2002, 12, 392-399.	5.7	139
135	The two faces of Alba: the evolutionary connection between proteins participating in chromatin structure and RNA metabolism. <i>Genome Biology</i> , 2003, 4, R64.	9.6	138
136	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, 51-56.	7.1	135
137	Detection of novel members, structure-function analysis and evolutionary classification of the 2H phosphoesterase superfamily. <i>Nucleic Acids Research</i> , 2002, 30, 5229-5243.	14.5	133
138	Prune cAMP phosphodiesterase binds nm23-H1 and promotes cancer metastasis. <i>Cancer Cell</i> , 2004, 5, 137-149.	16.8	132
139	Molecular Factors and Biochemical Pathways Induced by Febrile Temperature in Intraerythrocytic <i>Plasmodium falciparum</i> Parasites. <i>Infection and Immunity</i> , 2007, 75, 2012-2025.	2.2	132
140	Adenine methylation in eukaryotes: Apprehending the complex evolutionary history and functional potential of an epigenetic modification. <i>BioEssays</i> , 2016, 38, 27-40.	2.5	132
141	Small but versatile: the extraordinary functional and structural diversity of the $\hat{1}^2$ -grasp fold. <i>Biology Direct</i> , 2007, 2, 18.	4.6	127
142	The alpha/beta fold uracil DNA glycosylases: a common origin with diverse fates. <i>Genome Biology</i> , 2000, 1, research0007.1.	9.6	126
143	Rickettsiae and Chlamydiae: evidence of horizontal gene transfer and gene exchange. <i>Trends in Genetics</i> , 1999, 15, 173-175.	6.7	124
144	The NYN Domains: Novel Predicted RNAses with a PIN Domain-Like Fold. <i>RNA Biology</i> , 2006, 3, 18-27.	3.1	124

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145	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.	2.2	124
146	Homologues of 26S proteasome subunits are regulators of transcription and translation. <i>Protein Science</i> , 1998, 7, 1250-1254.	7.6	123
147	Vms1 and ANKZF1 peptidyl-tRNA hydrolases release nascent chains from stalled ribosomes. <i>Nature</i> , 2018, 557, 446-451.	27.8	122
148	The Ubiquitous yybP-ykoY Riboswitch Is a Manganese-Responsive Regulatory Element. <i>Molecular Cell</i> , 2015, 57, 1099-1109.	9.7	120
149	The mechanism of force transmission at bacterial focal adhesion complexes. <i>Nature</i> , 2016, 539, 530-535.	27.8	120
150	Live virus-free or die: coupling of antiviral immunity and programmed suicide or dormancy in prokaryotes. <i>Biology Direct</i> , 2012, 7, 40.	4.6	119
151	A Multidomain Adhesion Protein Family Expressed in <i>Plasmodium falciparum</i> Is Essential for Transmission to the Mosquito. <i>Journal of Experimental Medicine</i> , 2004, 199, 1533-1544.	8.5	118
152	The signaling helix: a common functional theme in diverse signaling proteins. <i>Biology Direct</i> , 2006, 1, 25.	4.6	117
153	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.	14.5	115
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155	MORC2 Signaling Integrates Phosphorylation-Dependent, ATPase-Coupled Chromatin Remodeling during the DNA Damage Response. <i>Cell Reports</i> , 2012, 2, 1657-1669.	6.4	110
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