

Laszlo Patthy

List of Publications by Citations

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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.

60
papers

3,397
citations

29
h-index

58
g-index

64
ext. papers

3,705
ext. citations

6
avg, IF

5.44
L-index

#	Paper	IF	Citations
60	Evolution of the proteases of blood coagulation and fibrinolysis by assembly from modules. <i>Cell</i> , 1985 , 41, 657-63	56.2	475
59	Genome evolution and the evolution of exon-shuffling--a review. <i>Gene</i> , 1999 , 238, 103-14	3.8	331
58	Intron-dependent evolution: preferred types of exons and introns. <i>FEBS Letters</i> , 1987 , 214, 1-7	3.8	247
57	Common evolutionary origin of the fibrin-binding structures of fibronectin and tissue-type plasminogen activator. <i>FEBS Letters</i> , 1983 , 163, 37-41	3.8	195
56	The implications of alternative splicing in the ENCODE protein complement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 5495-500	11.5	177
55	Modular exchange principles in proteins. <i>Current Opinion in Structural Biology</i> , 1991 , 1, 351-361	8.1	149
54	Detecting homology of distantly related proteins with consensus sequences. <i>Journal of Molecular Biology</i> , 1987 , 198, 567-77	6.5	141
53	A deletion in the myostatin gene causes the compact (Cmpt) hypermuscular mutation in mice. <i>Mammalian Genome</i> , 1998 , 9, 671-2	3.2	126
52	Modular Assembly of Genes and the Evolution of New Functions. <i>Genetica</i> , 2003 , 118, 217-231	1.5	112
51	Modules, multidomain proteins and organismic complexity. <i>FEBS Journal</i> , 2005 , 272, 5064-78	5.7	89
50	Refined solution structure and ligand-binding properties of PDC-109 domain b. A collagen-binding type II domain. <i>Journal of Molecular Biology</i> , 1992 , 223, 281-98	6.5	80
49	Exon shuffling and other ways of module exchange. <i>Matrix Biology</i> , 1996 , 15, 301-10; discussion 311-2	11.4	76
48	The LCCL module. <i>FEBS Journal</i> , 2000 , 267, 5751-7		73
47	Introns and exons. <i>Current Opinion in Structural Biology</i> , 1994 , 4, 383-392	8.1	72
46	Evidence for the involvement of type II domains in collagen binding by 72 kDa type IV procollagenase. <i>FEBS Letters</i> , 1991 , 282, 23-5	3.8	66
45	Modular assembly of genes and the evolution of new functions. <i>Genetica</i> , 2003 , 118, 217-31	1.5	64
44	Exons--original building blocks of proteins?. <i>BioEssays</i> , 1991 , 13, 187-92	4.1	63

43	Identifying protein-coding genes in genomic sequences. <i>Genome Biology</i> , 2009 , 10, 201	18.3	58
42	Identification and correction of abnormal, incomplete and mispredicted proteins in public databases. <i>BMC Bioinformatics</i> , 2008 , 9, 353	3.6	53
41	Both WFIKKN1 and WFIKKN2 have high affinity for growth and differentiation factors 8 and 11. <i>Journal of Biological Chemistry</i> , 2008 , 283, 23677-84	5.4	51
40	Gelatin-binding region of human matrix metalloproteinase-2: solution structure, dynamics, and function of the COL-23 two-domain construct. <i>Journal of Biological Chemistry</i> , 2001 , 276, 27613-21	5.4	50
39	The collagen-binding site of type-II units of bovine seminal fluid protein PDC-109 and fibronectin. <i>FEBS Journal</i> , 1990 , 193, 801-6		48
38	The second type II module from human matrix metalloproteinase 2: structure, function and dynamics. <i>Structure</i> , 1999 , 7, 1235-45	5.2	45
37	Analysis and identification of aromatic signals in the proton magnetic resonance spectrum of the kringle 4 fragment from human plasminogen. <i>Biochemistry</i> , 1985 , 24, 748-53	3.2	41
36	Sequence-specific ¹ H NMR assignments and structural characterization of bovine seminal fluid protein PDC-109 domain b. <i>Biochemistry</i> , 1991 , 30, 1663-72	3.2	40
35	NMR structure of the WIF domain of the human Wnt-inhibitory factor-1. <i>Journal of Molecular Biology</i> , 2006 , 357, 942-50	6.5	33
34	Peptide ligands for the fibronectin type II modules of matrix metalloproteinase 2 (MMP-2). <i>Journal of Biological Chemistry</i> , 2003 , 278, 12241-6	5.4	32
33	Distinct expression pattern of two related human proteins containing multiple types of protease-inhibitory modules. <i>Biological Chemistry</i> , 2002 , 383, 223-8	4.5	30
32	WFIKKN1 and WFIKKN2 bind growth factors TGF β , BMP2 and BMP4 but do not inhibit their signalling activity. <i>FEBS Journal</i> , 2010 , 277, 5040-50	5.7	29
31	Modular autonomy, ligand specificity, and functional cooperativity of the three in-tandem fibronectin type II repeats from human matrix metalloproteinase 2. <i>Journal of Biological Chemistry</i> , 2004 , 279, 46921-9	5.4	28
30	The col-1 module of human matrix metalloproteinase-2 (MMP-2): structural/functional relatedness between gelatin-binding fibronectin type II modules and lysine-binding kringle domains. <i>Biological Chemistry</i> , 2002 , 383, 137-48	4.5	23
29	Insertion of spliceosomal introns in proto-splice sites: the case of secretory signal peptides. <i>FEBS Letters</i> , 2004 , 575, 109-11	3.8	21
28	K153R polymorphism in myostatin gene increases the rate of promyostatin activation by furin. <i>FEBS Letters</i> , 2015 , 589, 295-301	3.8	19
27	Origin of fibronectin type II (FN2) modules: structural analyses of distantly-related members of the kringle family idey the kringle domain of neurotrypsin as a potential link between FN2 domains and kringles. <i>Protein Science</i> , 2001 , 10, 2114-22	6.3	19
26	Chemical modification and nuclear magnetic resonance studies on human plasminogen kringle 4. Assignment of tyrosine and histidine resonances to specific residues in the sequence. <i>FEBS Journal</i> , 1985 , 152, 439-46		19

25	Expression, purification and characterization of the second Kunitz-type protease inhibitor domain of the human WFIKKN protein. <i>FEBS Journal</i> , 2003 , 270, 2101-7		18
24	The aromatic ¹ H-NMR spectrum of plasminogen kringle 4. A comparative study of human, porcine and bovine homologs. <i>FEBS Journal</i> , 1986 , 159, 581-95		18
23	Both LCCL-domains of human CRISPLD2 have high affinity for lipid A. <i>Biochimie</i> , 2014 , 97, 66-71	4.6	16
22	Latent myostatin has significant activity and this activity is controlled more efficiently by WFIKKN1 than by WFIKKN2. <i>FEBS Journal</i> , 2013 , 280, 3822-39	5.7	16
21	Reassessing domain architecture evolution of metazoan proteins: major impact of gene prediction errors. <i>Genes</i> , 2011 , 2, 449-501	4.2	16
20	MisPred: a resource for identification of erroneous protein sequences in public databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat053	5	15
19	Characterization of a Wnt-binding site of the WIF-domain of Wnt inhibitory factor-1. <i>FEBS Letters</i> , 2012 , 586, 3122-6	3.8	14
18	Reassessing domain architecture evolution of metazoan proteins: the contribution of different evolutionary mechanisms. <i>Genes</i> , 2011 , 2, 578-98	4.2	14
17	Biological functions of the WAP domain-containing multidomain proteins WFIKKN1 and WFIKKN2. <i>Biochemical Society Transactions</i> , 2011 , 39, 1416-20	5.1	13
16	Analysis of the aliphatic ¹ H-NMR spectrum of plasminogen kringle 4. A comparative study of human, porcine, bovine and chicken homologs. <i>FEBS Journal</i> , 1988 , 170, 549-63		12
15	Wnts grasp the WIF domain of Wnt Inhibitory Factor 1 at two distinct binding sites. <i>FEBS Letters</i> , 2015 , 589, 3044-51	3.8	10
14	Reassessing domain architecture evolution of metazoan proteins: major impact of errors caused by confusing paralogs and epaktologs. <i>Genes</i> , 2011 , 2, 516-61	4.2	10
13	Structure, function and disease relevance of Wnt inhibitory factor 1, a secreted protein controlling the Wnt and hedgehog pathways. <i>Growth Factors</i> , 2019 , 37, 29-52	1.6	8
12	Putative extremely high rate of proteome innovation in lancelets might be explained by high rate of gene prediction errors. <i>Scientific Reports</i> , 2016 , 6, 30700	4.9	8
11	NMR solution structure of the neurotrypsin Kringle domain. <i>Biochemistry</i> , 2008 , 47, 12290-8	3.2	8
10	FixPred: a resource for correction of erroneous protein sequences. <i>Database: the Journal of Biological Databases and Curation</i> , 2014 , 2014, bau032	5	7
9	Exon skipping-rich transcriptomes of animals reflect the significance of exon-shuffling in metazoan proteome evolution. <i>Biology Direct</i> , 2019 , 14, 2	7.2	6
8	Use of signals of positive and negative selection to distinguish cancer genes and passenger genes. <i>ELife</i> , 2021 , 10,	8.9	3

7	Influence of WFIKKN1 on BMP1-mediated activation of latent myostatin. <i>FEBS Journal</i> , 2016 , 283, 4515-4527	3.7	2
6	Alternative Splicing: Evolution 2008 ,		2
5	Exon Shuffling Played a Decisive Role in the Evolution of the Genetic Toolkit for the Multicellular Body Plan of Metazoa. <i>Genes</i> , 2021 , 12,	4.2	2
4	Morphological Stasis and Proteome Innovation in Cephalochordates. <i>Genes</i> , 2018 , 9,	4.2	1
3	Fold class and evolutionary mobility of protein modules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 22652	11.5	1
2	Identification and Correction of Erroneous Protein Sequences in Public Databases. <i>Methods in Molecular Biology</i> , 2016 , 1415, 179-92	1.4	1
1	Miguel Llin̄ and the Structure of the Kringle Fold. <i>Protein Journal</i> , 2021 , 40, 450-453	3.9	