

Martin Kollmar

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7069932/publications.pdf>

Version: 2024-02-01

53
papers

2,150
citations

218381

26
h-index

253896

43
g-index

61
all docs

61
docs citations

61
times ranked

3089
citing authors

#	ARTICLE	IF	CITATIONS
1	Drawing the tree of eukaryotic life based on the analysis of 2,269 manually annotated myosins from 328 species. <i>Genome Biology</i> , 2007, 8, R196.	13.9	313
2	Scipio: Using protein sequences to determine the precise exon/intron structures of genes and their orthologs in closely related species. <i>BMC Bioinformatics</i> , 2008, 9, 278.	1.2	137
3	Six Subgroups and Extensive Recent Duplications Characterize the Evolution of the Eukaryotic Tubulin Protein Family. <i>Genome Biology and Evolution</i> , 2014, 6, 2274-2288.	1.1	110
4	(Phosphanyloxazoline)palladium Complexes, Part I: (1-3-1,3-Dialkylallyl)(phosphanyloxazoline)palladium Complexes: X-Ray Crystallographic Studies, NMR Investigations, and Quantum-Chemical Calculations. <i>Chemistry - A European Journal</i> , 2001, 7, 4913-4927.	1.7	97
5	Crystal structure of the motor domain of a class-I myosin. <i>EMBO Journal</i> , 2002, 21, 2517-2525.	3.5	94
6	(1-3-Phenylallyl)(phosphanyloxazoline)palladium Complexes: X-Ray Crystallographic Studies, NMR Investigations, and Ab Initio/DFT Calculations (Phosphanyloxazoline)palladium Complexes, Part II. Part I see: ref. 5.. <i>Chemistry - A European Journal</i> , 2002, 8, 3103.	1.7	64
7	The nuclear F-actin interactome of <i>Xenopus</i> oocytes reveals an actin-bundling kinesin that is essential for meiotic cytokinesis. <i>EMBO Journal</i> , 2013, 32, 1886-1902.	3.5	62
8	Spaced words and kmacs: fast alignment-free sequence comparison based on inexact word matches. <i>Nucleic Acids Research</i> , 2014, 42, W7-W11.	6.5	61
9	A novel nuclear genetic code alteration in yeasts and the evolution of codon reassignment in eukaryotes. <i>Genome Research</i> , 2016, 26, 945-955.	2.4	61
10	Evolution of the eukaryotic ARP2/3 activators of the WASP family: WASP, WAVE, WASH, and WHAMM, and the proposed new family members WAWH and WAML. <i>BMC Research Notes</i> , 2012, 5, 88.	0.6	60
11	Waggawagga: comparative visualization of coiled-coil predictions and detection of stable single α -helices (SAH domains). <i>Bioinformatics</i> , 2015, 31, 767-769.	1.8	59
12	Fine-Tuning Motile Cilia and Flagella: Evolution of the Dynein Motor Proteins from Plants to Humans at High Resolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 3249-3267.	3.5	54
13	A holistic phylogeny of the coronin gene family reveals an ancient origin of the tandem-coronin, defines a new subfamily, and predicts protein function. <i>BMC Evolutionary Biology</i> , 2011, 11, 268.	3.2	53
14	The landscape of human mutually exclusive splicing. <i>Molecular Systems Biology</i> , 2017, 13, 959.	3.2	53
15	Coordinated recruitment of Spir actin nucleators and myosin V motors to Rab11 vesicle membranes. <i>ELife</i> , 2016, 5, .	2.8	53
16	Whole genome duplication events in plant evolution reconstructed and predicted using myosin motor proteins. <i>BMC Evolutionary Biology</i> , 2013, 13, 202.	3.2	51
17	Myosin repertoire expansion coincides with eukaryotic diversification in the Mesoproterozoic era. <i>BMC Evolutionary Biology</i> , 2017, 17, 211.	3.2	50
18	An (1-1-Allyl)palladium Complex of a Chiral Bidentate Ligand: X-Ray Crystallographic and NMR Studies on a (1-3,3-Diphenylallyl)(phosphinoxazoline)palladium Complex. <i>Organometallics</i> , 2002, 21, 4771-4775.	1.1	42

#	ARTICLE	IF	CITATIONS
19	A Phylogenetic Analysis of the Brassicales Clade Based on an Alignment-Free Sequence Comparison Method. <i>Frontiers in Plant Science</i> , 2012, 3, 192.	1.7	41
20	Polyphyly of nuclear lamin genes indicates an early eukaryotic origin of the metazoan-type intermediate filament proteins. <i>Scientific Reports</i> , 2015, 5, 10652.	1.6	39
21	Cross-species protein sequence and gene structure prediction with fine-tuned WebScipio 2.0 and Scipio. <i>BMC Research Notes</i> , 2011, 4, 265.	0.6	38
22	Evolution of the eukaryotic dynactin complex, the activator of cytoplasmic dynein. <i>BMC Evolutionary Biology</i> , 2012, 12, 95.	3.2	37
23	Nuclear codon reassignments in the genomics era and mechanisms behind their evolution. <i>BioEssays</i> , 2017, 39, 1600221.	1.2	35
24	Molecular Phylogeny of Sequenced Saccharomycetes Reveals Polyphyly of the Alternative Yeast Codon Usage. <i>Genome Biology and Evolution</i> , 2014, 6, 3222-3237.	1.1	34
25	Identification and phylogenetic analysis of Dictyostelium discoideum kinesin proteins. <i>BMC Genomics</i> , 2003, 4, 47.	1.2	31
26	Thirteen is enough: the myosins of Dictyostelium discoideum and their light chains. <i>BMC Genomics</i> , 2006, 7, 183.	1.2	30
27	WebScipio: An online tool for the determination of gene structures using protein sequences. <i>BMC Genomics</i> , 2008, 9, 422.	1.2	30
28	Pfarao: a web application for protein family analysis customized for cytoskeletal and motor proteins (CyMoBase). <i>BMC Genomics</i> , 2006, 7, 300.	1.2	28
29	Comparative genomic analysis of the arthropod muscle myosin heavy chain genes allows ancestral gene reconstruction and reveals a new type of 'partially' processed pseudogene. <i>BMC Molecular Biology</i> , 2008, 9, 21.	3.0	24
30	GenePainter: a fast tool for aligning gene structures of eukaryotic protein families, visualizing the alignments and mapping gene structures onto protein structures. <i>BMC Bioinformatics</i> , 2013, 14, 77.	1.2	24
31	Reconstructing the phylogeny of 21 completely sequenced arthropod species based on their motor proteins. <i>BMC Genomics</i> , 2009, 10, 173.	1.2	23
32	Predicting mutually exclusive spliced exons based on exon length, splice site and reading frame conservation, and exon sequence homology. <i>BMC Bioinformatics</i> , 2011, 12, 270.	1.2	23
33	Endogenous Stochastic Decoding of the CUG Codon by Competing Ser- and Leu-tRNAs in <i>Ascoidea asiatica</i> . <i>Current Biology</i> , 2018, 28, 2046-2057.e5.	1.8	22
34	Expansion of the mutually exclusive spliced exome in <i>Drosophila</i> . <i>Nature Communications</i> , 2013, 4, 2460.	5.8	21
35	diArk – a resource for eukaryotic genome research. <i>BMC Genomics</i> , 2007, 8, 103.	1.2	19
36	The Protein-coding Human Genome: Annotating High-Hanging Fruits. <i>BioEssays</i> , 2019, 41, e1900066.	1.2	17

#	ARTICLE	IF	CITATIONS
37	WebScipio: reconstructing alternative splice variants of eukaryotic proteins. <i>Nucleic Acids Research</i> , 2013, 41, W504-W509.	6.5	15
38	Kassiopeia: a database and web application for the analysis of mutually exclusive exomes of eukaryotes. <i>BMC Genomics</i> , 2014, 15, 115.	1.2	14
39	Critical assessment of coiled-coil predictions based on protein structure data. <i>Scientific Reports</i> , 2021, 11, 12439.	1.6	14
40	Axonopathy in the Central Nervous System Is the Hallmark of Mice with a Novel Intragenic Null Mutation of <i>Dystonin</i> . <i>Genetics</i> , 2016, 204, 191-203.	1.2	13
41	How tRNAs dictate nuclear codon reassignments: Only a few can capture non-cognate codons. <i>RNA Biology</i> , 2017, 14, 293-299.	1.5	13
42	Distribution and evolution of stable single α -helices (SAH domains) in myosin motor proteins. <i>PLoS ONE</i> , 2017, 12, e0174639.	1.1	13
43	diArk 2.0 provides detailed analyses of the ever increasing eukaryotic genome sequencing data. <i>BMC Research Notes</i> , 2011, 4, 338.	0.6	12
44	Shared Gene Structures and Clusters of Mutually Exclusive Spliced Exons within the Metazoan Muscle Myosin Heavy Chain Genes. <i>PLoS ONE</i> , 2014, 9, e88111.	1.1	12
45	GenePainter v. 2.0 resolves the taxonomic distribution of intron positions. <i>Bioinformatics</i> , 2015, 31, 1302-1304.	1.8	9
46	Waggawagga-CLI: A command-line tool for predicting stable single α -helices (SAH-domains), and the SAH-domain distribution across eukaryotes. <i>PLoS ONE</i> , 2018, 13, e0191924.	1.1	9
47	Use of the myosin motor domain as large-affinity tag for the expression and purification of proteins in <i>Dictyostelium discoideum</i> . <i>International Journal of Biological Macromolecules</i> , 2006, 39, 37-44.	3.6	7
48	diArk – the database for eukaryotic genome and transcriptome assemblies in 2014. <i>Nucleic Acids Research</i> , 2015, 43, D1107-D1112.	6.5	7
49	Predicting Tandemly Arrayed Gene Duplicates with WebScipio. , 0, , .		2
50	Conservation and divergence between cytoplasmic and muscle-specific actin capping proteins: insights from the crystal structure of cytoplasmic Cap32/34 from <i>Dictyostelium discoideum</i> . <i>BMC Structural Biology</i> , 2012, 12, 12.	2.3	2
51	Proteogenomics analysis of CUG codon translation in the human pathogen <i>Candida albicans</i> . <i>BMC Biology</i> , 2021, 19, 258.	1.7	2
52	Predicting Genes in Closely Related Species with Scipio and WebScipio. <i>Methods in Molecular Biology</i> , 2019, 1962, 193-206.	0.4	0
53	Design of typical genes for heterologous gene expression. <i>Scientific Reports</i> , 2022, 12, .	1.6	0