

# 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	Design of typical genes for heterologous gene expression. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
2	Critical assessment of coiled-coil predictions based on protein structure data. <i>Scientific Reports</i> , 2021, 11, 12439.	1.6	14
3	Proteogenomics analysis of CUG codon translation in the human pathogen <i>Candida albicans</i> . <i>BMC Biology</i> , 2021, 19, 258.	1.7	2
4	The Proteinâ€Coding Human Genome: Annotating Highâ€Hanging Fruits. <i>BioEssays</i> , 2019, 41, e1900066.	1.2	17
5	Predicting Genes in Closely Related Species with Scipio and WebScipio. <i>Methods in Molecular Biology</i> , 2019, 1962, 193-206.	0.4	0
6	Waggawagga-CLI: A command-line tool for predicting stable single $\hat{\pm}$ -helices (SAH-domains), and the SAH-domain distribution across eukaryotes. <i>PLoS ONE</i> , 2018, 13, e0191924.	1.1	9
7	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
8	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
9	Nuclear codon reassignments in the genomics era and mechanisms behind their evolution. <i>BioEssays</i> , 2017, 39, 1600221.	1.2	35
10	The landscape of human mutually exclusive splicing. <i>Molecular Systems Biology</i> , 2017, 13, 959.	3.2	53
11	Distribution and evolution of stable single $\hat{\pm}$ -helices (SAH domains) in myosin motor proteins. <i>PLoS ONE</i> , 2017, 12, e0174639.	1.1	13
12	Myosin repertoire expansion coincides with eukaryotic diversification in the Mesoproterozoic era. <i>BMC Evolutionary Biology</i> , 2017, 17, 211.	3.2	50
13	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
14	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
15	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
16	Coordinated recruitment of Spir actin nucleators and myosin V motors to Rab11 vesicle membranes. <i>ELife</i> , 2016, 5, .	2.8	53
17	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
18	GenePainter v. 2.0 resolves the taxonomic distribution of intron positions. <i>Bioinformatics</i> , 2015, 31, 1302-1304.	1.8	9

#	ARTICLE	IF	CITATIONS
19	diArk – the database for eukaryotic genome and transcriptome assemblies in 2014. <i>Nucleic Acids Research</i> , 2015, 43, D1107-D1112.	6.5	7
20	Waggawagga: comparative visualization of coiled-coil predictions and detection of stable single $\pm$ -helices (SAH domains). <i>Bioinformatics</i> , 2015, 31, 767-769.	1.8	59
21	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
22	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
23	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
24	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
25	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
26	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
27	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
28	Expansion of the mutually exclusive spliced exome in <i>Drosophila</i> . <i>Nature Communications</i> , 2013, 4, 2460.	5.8	21
29	WebScipio: reconstructing alternative splice variants of eukaryotic proteins. <i>Nucleic Acids Research</i> , 2013, 41, W504-W509.	6.5	15
30	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
31	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
32	Evolution of the eukaryotic dynactin complex, the activator of cytoplasmic dynein. <i>BMC Evolutionary Biology</i> , 2012, 12, 95.	3.2	37
33	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
34	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
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	Predicting mutually exclusive spliced exons based on exon length, splice site and reading frame conservation, and exon sequence homology. BMC Bioinformatics, 2011, 12, 270.	1.2	23
38	A holistic phylogeny of the coronin gene family reveals an ancient origin of the tandem-coronin, defines a new subfamily, and predicts protein function. BMC Evolutionary Biology, 2011, 11, 268.	3.2	53
39	Reconstructing the phylogeny of 21 completely sequenced arthropod species based on their motor proteins. BMC Genomics, 2009, 10, 173.	1.2	23
40	Comparative genomic analysis of the arthropod muscle myosin heavy chain genes allows ancestral gene reconstruction and reveals a new type of 'partially' processed pseudogene. BMC Molecular Biology, 2008, 9, 21.	3.0	24
41	Scipio: Using protein sequences to determine the precise exon/intron structures of genes and their orthologs in closely related species. BMC Bioinformatics, 2008, 9, 278.	1.2	137
42	WebScipio: An online tool for the determination of gene structures using protein sequences. BMC Genomics, 2008, 9, 422.	1.2	30
43	Drawing the tree of eukaryotic life based on the analysis of 2,269 manually annotated myosins from 328 species. Genome Biology, 2007, 8, R196.	13.9	313
44	diArk – a resource for eukaryotic genome research. BMC Genomics, 2007, 8, 103.	1.2	19
45	Use of the myosin motor domain as large-affinity tag for the expression and purification of proteins in Dictyostelium discoideum. International Journal of Biological Macromolecules, 2006, 39, 37-44.	3.6	7
46	Thirteen is enough: the myosins of Dictyostelium discoideum and their light chains. BMC Genomics, 2006, 7, 183.	1.2	30
47	Pfarao: a web application for protein family analysis customized for cytoskeletal and motor proteins (CyMoBase). BMC Genomics, 2006, 7, 300.	1.2	28
48	Identification and phylogenetic analysis of Dictyostelium discoideum kinesin proteins. BMC Genomics, 2003, 4, 47.	1.2	31
49	An (1-Allyl)palladium Complex of a Chiral Bidentate Ligand: Crystallographic and NMR Studies on a (1-3,3-Diphenylallyl)(phosphinoxazoline)palladium Complex. Organometallics, 2002, 21, 4771-4775.	1.1	42
50	(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.. Chemistry - A European Journal, 2002, 8, 3103.	1.7	64
51	Crystal structure of the motor domain of a class-I myosin. EMBO Journal, 2002, 21, 2517-2525.	3.5	94
52	(Phosphanyloxazoline)palladium Complexes, Part I: (1-3-1,3-Dialkylallyl)(phosphanyloxazoline)palladium Complexes: X-Ray Crystallographic Studies, NMR Investigations, and Quantum-Chemical Calculations. Chemistry - A European Journal, 2001, 7, 4913-4927.	1.7	97
53	Predicting Tandemly Arrayed Gene Duplicates with WebScipio. , 0, , .		2