

Rainer Merkl

List of Publications by Year in descending order

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102
papers

4,332
citations

159585
30
h-index

118850
62
g-index

131
all docs

131
docs citations

131
times ranked

5753
citing authors

#	ARTICLE	IF	CITATIONS
1	Score-based prediction of genomic islands in prokaryotic genomes using hidden Markov models. BMC Bioinformatics, 2006, 7, 142.	2.6	349
2	The genome sequence of the extreme thermophile <i>Thermus thermophilus</i> . Nature Biotechnology, 2004, 22, 547-553.	17.5	345
3	The genome sequence of <i>Clostridium tetani</i> , the causative agent of tetanus disease. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1316-1321.	7.1	324
4	The Complete Genome Sequence of <i>Bacillus licheniformis</i> DSM13, an Organism with Great Industrial Potential. Journal of Molecular Microbiology and Biotechnology, 2004, 7, 204-211.	1.0	284
5	The genome of <i>Methanosarcina mazei</i> : evidence for lateral gene transfer between bacteria and archaea. Journal of Molecular Microbiology and Biotechnology, 2002, 4, 453-61.	1.0	266
6	Quantitative analysis of cell motility and chemotaxis in <i>Dictyostelium discoideum</i> by using an image processing system and a novel chemotaxis chamber providing stationary chemical gradients.. Journal of Cell Biology, 1989, 108, 973-984.	5.2	189
7	Gene Islands Integrated into tRNA ^{Gly} Genes Confer Genome Diversity on a <i>Pseudomonas aeruginosa</i> Clone. Journal of Bacteriology, 2002, 184, 6665-6680.	2.2	164
8	Ancestral protein reconstruction: techniques and applications. Biological Chemistry, 2016, 397, 1-21.	2.5	121
9	Identification and characterization of two novel primate-specific histone H3 variants, H3.X and H3.Y. Journal of Cell Biology, 2010, 190, 777-791.	5.2	106
10	Turning catalytically inactive human Argonaute proteins into active slicer enzymes. Nature Structural and Molecular Biology, 2013, 20, 814-817.	8.2	89
11	Comparative genomics and transcriptomics of lineages I, II, and III strains of <i>Listeria monocytogenes</i> . BMC Genomics, 2012, 13, 144.	2.8	88
12	YACOP: Enhanced gene prediction obtained by a combination of existing methods. In Silico Biology, 2003, 3, 441-51.	0.9	81
13	SIGI: score-based identification of genomic islands. BMC Bioinformatics, 2004, 5, 22.	2.6	76
14	The NHL domain of BRAT is an RNA-binding domain that directly contacts the <i>hunchback</i> mRNA for regulation. Genes and Development, 2014, 28, 749-764.	5.9	74
15	Stage-specific antigens reacting with monoclonal antibodies against contact site A, a cell-surface glycoprotein of <i>Dictyostelium discoideum</i> . Cell Differentiation, 1982, 11, 1-13.	0.4	72
16	Exploiting Protein Symmetry To Design Light-Controllable Enzyme Inhibitors. Angewandte Chemie - International Edition, 2014, 53, 595-598.	13.8	61
17	Nerve growth factor-mediated induction of choline acetyltransferase in PC12 cells: evaluation of the site of action of nerve growth factor and the involvement of lysosomal degradation products of nerve growth factor. Journal of Neuroscience, 1984, 4, 3039-3050.	3.6	56
18	Computational and Experimental Evidence for the Evolution of a (2±)8-Barrel Protein from an Ancestral Quarter-Barrel Stabilised by Disulfide Bonds. Journal of Molecular Biology, 2010, 398, 763-773.	4.2	54

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19	Evidence for the Existence of Elaborate Enzyme Complexes in the Paleoarchean Era. <i>Journal of the American Chemical Society</i> , 2014, 136, 122-129.	13.7	51
20	Substrate preferences of Vsr DNA mismatch endonuclease and their consequences for the evolution of the <i>Escherichia coli</i> K-12 genome. <i>Journal of Molecular Biology</i> , 1995, 245, 1-7.	4.2	50
21	Post-translational glycosylation of the contact site A protein of <i>Dictyostelium discoideum</i> is important for stability but not for its function in cell adhesion. <i>EMBO Journal</i> , 1987, 6, 3663-3671.	7.8	49
22	Oligo kernels for datamining on biological sequences: a case study on prokaryotic translation initiation sites. <i>BMC Bioinformatics</i> , 2004, 5, 169.	2.6	47
23	The extended AT-hook is a novel RNA binding motif. <i>RNA Biology</i> , 2015, 12, 864-876.	3.1	47
24	Statistical evaluation and biological interpretation of non-random abundance in the <i>E. coli</i> K-12 genome of tetra- and pentanucleotide sequences related to VSP DNA mismatch repair. <i>Nucleic Acids Research</i> , 1992, 20, 1657-1662.	14.5	46
25	Oleic acid is a precursor of linoleic acid and the male sex pheromone in <i>Nasonia vitripennis</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2014, 51, 33-40.	2.7	45
26	Rosetta:MSF: a modular framework for multi-state computational protein design. <i>PLoS Computational Biology</i> , 2017, 13, e1005600.	3.2	43
27	Prescort: Predicting protein-protein interfaces utilizing four residue properties. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 154-168.	2.6	41
28	Characterizing the nuclease accessibility of DNA in human cells to map higher order structures of chromatin. <i>Nucleic Acids Research</i> , 2019, 47, 1239-1254.	14.5	40
29	Biased DNA repair. <i>Nature</i> , 1992, 355, 595-596.	27.8	39
30	The Arabidopsis THO/TREX component TEX1 functionally interacts with MOS11 and modulates mRNA export and alternative splicing events. <i>Plant Molecular Biology</i> , 2017, 93, 283-298.	3.9	39
31	Generation of catalytic human Ago4 identifies structural elements important for RNA cleavage. <i>Rna</i> , 2014, 20, 1532-1538.	3.5	31
32	Ancestral Tryptophan Synthase Reveals Functional Sophistication of Primordial Enzyme Complexes. <i>Cell Chemical Biology</i> , 2016, 23, 709-715.	5.2	31
33	Chapter 20 Cell Adhesion: Its Quantification, Assay of the Molecules Involved, and Selection of Defective Mutants in <i>Dictyostelium</i> and <i>Polysphondylium</i> . <i>Methods in Cell Biology</i> , 1987, 28, 359-385.	1.1	29
34	A Survey of Codon and Amino Acid Frequency Bias in Microbial Genomes Focusing on Translational Efficiency. <i>Journal of Molecular Evolution</i> , 2003, 57, 453-466.	1.8	29
35	The long non-coding RNA LINC00941 and SPRR5 are novel regulators of human epidermal homeostasis. <i>EMBO Reports</i> , 2019, 20, .	4.5	29
36	The Adaptor Protein ENY2 Is a Component of the Deubiquitination Module of the Arabidopsis SAGA Transcriptional Co-activator Complex but not of the TREX-2 Complex. <i>Journal of Molecular Biology</i> , 2018, 430, 1479-1494.	4.2	28

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37	Modelling the evolution of the archeal tryptophan synthase. BMC Evolutionary Biology, 2007, 7, 59.	3.2	27
38	Responses of amoebae to local stimulation by light. Cell Biology International Reports, 1983, 7, 611-616.	0.6	26
39	Monoclonal antibodies against Dictyostelium plasma membranes: their binding to simple sugars. Cell Differentiation, 1985, 17, 83-94.	0.4	26
40	Protein design on computers. Five new proteins: Shpilka, grendel, fingerclasp, leather, and aida. Proteins: Structure, Function and Bioinformatics, 1992, 12, 105-110.	2.6	26
41	Analysis of allosteric communication in a multienzyme complex by ancestral sequence reconstruction. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 346-354.	7.1	26
42	Light Regulation of Enzyme Allostery through Photo-responsive Unnatural Amino Acids. Cell Chemical Biology, 2019, 26, 1501-1514.e9.	5.2	25
43	Monoclonal anti-glycoprotein antibody that blocks cell adhesion in Polysphondylium pallidum. FEBS Journal, 1984, 140, 73-81.	0.2	24
44	Computational Design of Enzymes. Chemistry and Biology, 2008, 15, 421-423.	6.0	24
45	PROCOS: Computational analysis of protein-protein complexes. Journal of Computational Chemistry, 2011, 32, 2575-2586.	3.3	22
46	Reconstruction of ancestral enzymes. Perspectives in Science, 2016, 9, 17-23.	0.6	22
47	Evolutionary diversification of protein-protein interactions by interface add-ons. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8333-E8342.	7.1	22
48	DNA sequence encoded repression of rRNA gene transcription in chromatin. Nucleic Acids Research, 2010, 38, 5304-5314.	14.5	20
49	Artificial Light Regulation of an Allosteric Bienenzyme Complex by a Photosensitive Ligand. ChemBioChem, 2018, 19, 1750-1757.	2.6	19
50	Prediction of quaternary structure by analysis of hot spot residues in protein-protein interfaces: the case of anthranilate phosphoribosyltransferases. Proteins: Structure, Function and Bioinformatics, 2019, 87, 815-825.	2.6	18
51	Long-Term Persistence of Bi-functionality Contributes to the Robustness of Microbial Life through Exaptation. PLoS Genetics, 2016, 12, e1005836.	3.5	18
52	Plasmodium falciparum Nucleosomes Exhibit Reduced Stability and Lost Sequence Dependent Nucleosome Positioning. PLoS Pathogens, 2016, 12, e1006080.	4.7	18
53	Fast Quantitative Assay of Sequence-Specific Endonuclease Activity Based on DNA Sequencer Technology. Biological Chemistry Hoppe-Seyler, 1992, 373, 1223-1226.	1.4	17
54	Chorismate mutase of Thermus thermophilus is a monofunctional AroH class enzyme inhibited by tyrosine. Archives of Microbiology, 2004, 181, 195-203.	2.2	16

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55	H2r: Identification of evolutionary important residues by means of an entropy based analysis of multiple sequence alignments. BMC Bioinformatics, 2008, 9, 151.	2.6	16
56	CLIPS-1D: analysis of multiple sequence alignments to deduce for residue-positions a role in catalysis, ligand-binding, or protein structure. BMC Bioinformatics, 2012, 13, 55.	2.6	16
57	Maize EMBRYO SAC family peptides interact differentially with pollen tubes and fungal cells. Journal of Experimental Botany, 2015, 66, 5205-5216.	4.8	16
58	Development of photoswitchable inhibitors for β -galactosidase. Organic and Biomolecular Chemistry, 2018, 16, 7430-7437.	2.8	16
59	Functional characterisation of two Δ^{12} -desaturases demonstrates targeted production of linoleic acid as pheromone precursor in <i>Nasonia</i> . Journal of Experimental Biology, 2019, 222, .	1.7	16
60	A Comparative Categorization of Protein Function Encoded in Bacterial or Archeal Genomic Islands. Journal of Molecular Evolution, 2006, 62, 1-14.	1.8	15
61	Gene silencing pathways found in the green alga <i>Volvox carteri</i> reveal insights into evolution and origins of small RNA systems in plants. BMC Genomics, 2016, 17, 853.	2.8	15
62	Efficient and flexible access to fully protected trinucleotides suitable for DNA synthesis by automated phosphoramidite chemistry. Chemical Communications, 1996, , 2677.	4.1	14
63	Conversion of Anthranilate Synthase into Isochorismate Synthase: Implications for the Evolution of Chorismate-Utilizing Enzymes. Angewandte Chemie - International Edition, 2015, 54, 11270-11274.	13.8	14
64	Improving thermal and detergent stability of <i>Bacillus stearothermophilus</i> neopullulanase by rational enzyme design. Protein Engineering, Design and Selection, 2015, 28, 147-151.	2.1	14
65	Combining ancestral sequence reconstruction with protein design to identify an interface hotspot in a key metabolic enzyme complex. Proteins: Structure, Function and Bioinformatics, 2017, 85, 312-321.	2.6	14
66	Pathomechanism of mutated and secreted retinoschisin in X-linked juvenile retinoschisis. Experimental Eye Research, 2018, 177, 23-34.	2.6	14
67	A comparative categorization of gene flux in diverse microbial species. Genomics, 2005, 86, 462-475.	2.9	13
68	Identification of the retinoschisin-binding site on the retinal Na/K-ATPase. PLoS ONE, 2019, 14, e0216320.	2.5	13
69	Experimental Assessment of the Importance of Amino Acid Positions Identified by an Entropy-Based Correlation Analysis of Multiple-Sequence Alignments. Biochemistry, 2012, 51, 5633-5641.	2.5	12
70	Relationship of Catalysis and Active Site Loop Dynamics in the β -Barrel Enzyme Indole-3-glycerol Phosphate Synthase. Biochemistry, 2018, 57, 3265-3277.	2.5	12
71	Rosetta design with co-evolutionary information retains protein function. PLoS Computational Biology, 2021, 17, e1008568.	3.2	12
72	Focus on Molecules: Norrin. Experimental Eye Research, 2012, 102, 109-110.	2.6	11

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73	Mapping the Allosteric Communication Network of Aminodeoxychorismate Synthase. Journal of Molecular Biology, 2019, 431, 2718-2728.	4.2	11
74	Conserved genomic neighborhood is a strong but no perfect indicator for a direct interaction of microbial gene products. BMC Bioinformatics, 2020, 21, 5.	2.6	11
75	Towards Photochromic Azobenzene-Based Inhibitors for Tryptophan Synthase. Chemistry - A European Journal, 2021, 27, 2439-2451.	3.3	11
76	A Fast and Precise Approach for Computational Saturation Mutagenesis and its Experimental Validation by Using an Artificial (Î² ₈)-Barrel Protein. ChemBioChem, 2011, 12, 1544-1550.	2.6	10
77	Hexamerization of Geranylgeranylglycerol Phosphate Synthase Ensures Structural Integrity and Catalytic Activity at High Temperatures. Biochemistry, 2018, 57, 2335-2348.	2.5	10
78	A Fold-Independent Interface Residue Is Crucial for Complex Formation and Allosteric Signaling in Class I Glutamine Amidotransferases. Biochemistry, 2019, 58, 2584-2588.	2.5	10
79	H2rs: Deducing evolutionary and functionally important residue positions by means of an entropy and similarity based analysis of multiple sequence alignments. BMC Bioinformatics, 2014, 15, 118.	2.6	9
80	TransCent: Computational enzyme design by transferring active sites and considering constraints relevant for catalysis. BMC Bioinformatics, 2009, 10, 54.	2.6	8
81	CLIPS-4D: a classifier that distinguishes structurally and functionally important residue-positions based on sequence and 3D data. Bioinformatics, 2013, 29, 3029-3035.	4.1	8
82	Light-Regulation of Tryptophan Synthase by Combining Protein Design and Enzymology. International Journal of Molecular Sciences, 2019, 20, 5106.	4.1	8
83	Statistical evidence for a biochemical pathway of natural, sequence- targeted G/C to C/G transversion mutagenesis in Haemophilus influenzae Rd. Nucleic Acids Research, 1996, 24, 4146-4151.	14.5	7
84	Genes optimized by evolution for accurate and fast translation encode in Archaea and Bacteria a broad and characteristic spectrum of protein functions. BMC Genomics, 2010, 11, 617.	2.8	7
85	AGeNNT: annotation of enzyme families by means of refined neighborhood networks. BMC Bioinformatics, 2017, 18, 274.	2.6	7
86	Dimerization Determines Substrate Specificity of a Bacterial Prenyltransferase. ChemBioChem, 2012, 13, 1297-1303.	2.6	6
87	TrpB2 Enzymes are <i>O</i> -Phospho-serine Dependent Tryptophan Synthases. Biochemistry, 2014, 53, 6078-6083.	2.5	6
88	Elucidation of the functional roles of the Q and I motifs in the human chromatin-remodeling enzyme BRG1. Journal of Biological Chemistry, 2019, 294, 3294-3310.	3.4	6
89	Versatile controlling system for cryopreparation techniques in electron microscopy. Journal of Electron Microscopy Technique, 1991, 17, 450-455.	1.1	4
90	GO4genome: A Prokaryotic Phylogeny Based on Genome Organization. Journal of Molecular Evolution, 2009, 68, 550-562.	1.8	4

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91	Sequence selection by FitSS4ASR alleviates ancestral sequence reconstruction as exemplified for geranylgeranylgeranyl glycerol phosphate synthase. <i>Biological Chemistry</i> , 2019, 400, 367-381.	2.5	4
92	Ancestral Sequence Reconstruction as a Tool for the Elucidation of a Stepwise Evolutionary Adaptation. <i>Methods in Molecular Biology</i> , 2019, 1851, 171-182.	0.9	4
93	An assessment of catalytic residue 3D ensembles for the prediction of enzyme function. <i>BMC Bioinformatics</i> , 2015, 16, 359.	2.6	3
94	Assessing in silico the recruitment and functional spectrum of bacterial enzymes from secondary metabolism. <i>BMC Evolutionary Biology</i> , 2017, 17, 36.	3.2	3
95	Key2Ann: a tool to process sequence sets by replacing database identifiers with a human-readable annotation. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 35-46.	1.5	2
96	Reprogramming the Specificity of a Protein Interface by Computational and Data-Driven Design. <i>Structure</i> , 2021, 29, 292-304.e3.	3.3	2
97	Sequence and functional differences in the ATPase domains of CHD3 and SNF2H promise potential for selective regulability and drugability. <i>FEBS Journal</i> , 2021, 288, 4000-4023.	4.7	2
98	Evidence for the preferential reuse of subdomain motifs in primordial protein folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1167-1179.	2.6	2
99	Key2Ann: a tool to process sequence sets by replacing database identifiers with a human-readable annotation. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, .	1.5	2
100	Rosetta:MSF:NN: Boosting performance of multi-state computational protein design with a neural network. <i>PLoS ONE</i> , 2021, 16, e0256691.	2.5	1
101	AMIGOS: a method for the inspection of genomic organisation or structure and its application to characterise conserved gene arrangements. <i>In Silico Biology</i> , 2006, 6, 281-306.	0.9	1
102	secureBLAST. <i>In Silico Biology</i> , 2003, 3, 405-9.	0.9	0