

Leszek Rychlewski

List of Publications by Year in descending order

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111
papers

7,707
citations

66250

44
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64407

83
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113
all docs

113
docs citations

113
times ranked

9862
citing authors

#	ARTICLE	IF	CITATIONS
1	High-density Peptide Arrays Help to Identify Linear Immunogenic B-cell Epitopes in Individuals Naturally Exposed to Malaria Infection. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 642-656.	2.5	29
2	FAM46 proteins are novel eukaryotic non-canonical poly(A) polymerases. <i>Nucleic Acids Research</i> , 2016, 44, 3534-3548.	6.5	60
3	Alphaherpesvirinae and Gammaherpesvirinae glycoprotein L and CMV UL130 originate from chemokines. <i>Virology Journal</i> , 2013, 10, 1.	1.4	135
4	Structural bioinformatics of the general transcription factor TFIID. <i>Biochimie</i> , 2013, 95, 680-691.	1.3	21
5	Sequence, structure and functional diversity of PD-(D/E)XK phosphodiesterase superfamily. <i>Nucleic Acids Research</i> , 2012, 40, 7016-7045.	6.5	122
6	Detailed Mechanism of Squalene Epoxidase Inhibition by Terbinafine. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 455-462.	2.5	88
7	VoteDock: Consensus docking method for prediction of protein-ligand interactions. <i>Journal of Computational Chemistry</i> , 2011, 32, 568-581.	1.5	82
8	Mapping the Substrate Binding Site of Phenylacetone Monooxygenase from <i>Thermobifida fusca</i> by Mutational Analysis. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5730-5738.	1.4	42
9	Squalene monooxygenase – a target for hypercholesterolemic therapy. <i>Biological Chemistry</i> , 2011, 392, 1053-1075.	1.2	40
10	Comprehensive Structural and Substrate Specificity Classification of the <i>Saccharomyces cerevisiae</i> Methyltransferome. <i>PLoS ONE</i> , 2011, 6, e23168.	1.1	50
11	Distant homologs of anti-apoptotic factor HAX1 encode parvalbumin-like calcium binding proteins. <i>BMC Research Notes</i> , 2010, 3, 197.	0.6	4
12	ELM: the status of the 2010 eukaryotic linear motif resource. <i>Nucleic Acids Research</i> , 2010, 38, D167-D180.	6.5	217
13	TOS1 is circularly permuted 1,3- β -glucanase. <i>Cell Cycle</i> , 2010, 9, 201-204.	1.3	13
14	Species Used for Drug Testing Reveal Different Inhibition Susceptibility for 17 β -Hydroxysteroid Dehydrogenase Type 1. <i>PLoS ONE</i> , 2010, 5, e10969.	1.1	17
15	Comprehensive classification of nucleotidyltransferase fold proteins: identification of novel families and their representatives in human. <i>Nucleic Acids Research</i> , 2009, 37, 7701-7714.	6.5	147
16	Molecular determinants archetypical to the phylum Nematoda. <i>BMC Genomics</i> , 2009, 10, 114.	1.2	11
17	Meta-basic estimates the size of druggable human genome. <i>Journal of Molecular Modeling</i> , 2009, 15, 695-699.	0.8	23
18	LiveBench-8: The large-scale, continuous assessment of automated protein structure prediction. <i>Protein Science</i> , 2009, 14, 240-245.	3.1	90

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19	AutoMotif Server for prediction of phosphorylation sites in proteins using support vector machine: 2007 update. <i>Journal of Molecular Modeling</i> , 2008, 14, 69-76.	0.8	32
20	Pcons: A neural-network-based consensus predictor that improves fold recognition. <i>Protein Science</i> , 2008, 10, 2354-2362.	3.1	285
21	The mitotic entry regulator NIPA is a prototypic BIR domain protein. <i>Cell Cycle</i> , 2008, 7, 2073-2075.	1.3	7
22	Uncharacterized DUF1574 leptospira proteins are SGNH hydrolases. <i>Cell Cycle</i> , 2008, 7, 542-544.	1.3	7
23	The fold recognition of CP2 transcription factors gives new insights into the function and evolution of tumor suppressor protein p53. <i>Cell Cycle</i> , 2008, 7, 2907-2915.	1.3	39
24	HSV-1 UL45 encodes a carbohydrate binding C-type lectin protein. <i>Cell Cycle</i> , 2008, 7, 269-271.	1.3	5
25	3D-Fun: predicting enzyme function from structure. <i>Nucleic Acids Research</i> , 2008, 36, W303-W307.	6.5	10
26	XtalPred: a web server for prediction of protein crystallizability. <i>Bioinformatics</i> , 2007, 23, 3403-3405.	1.8	269
27	ProteinSplit: splitting of multi-domain proteins using prediction of ordered and disordered regions in protein sequences for virtual structural genomics. <i>Journal of Physics Condensed Matter</i> , 2007, 19, 285222.	0.7	5
28	Target Specific Compound Identification Using a Support Vector Machine. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2007, 10, 189-196.	0.6	32
29	Identification of IL-18RAP mRNA truncated splice variants in human testis and the other human tissues. <i>Cytokine</i> , 2007, 39, 178-183.	1.4	19
30	eHiTS-to-VMD Interface Application. The Search for Tyrosine ^α -tRNA Ligase Inhibitors. <i>Journal of Chemical Information and Modeling</i> , 2007, 47, 695-702.	2.5	6
31	The RPSP: Web server for prediction of signal peptides. <i>Polymer</i> , 2007, 48, 5493-5496.	1.8	18
32	Realm of PD-(D/E)XK nuclease superfamily revisited: detection of novel families with modified transitive meta profile searches. <i>BMC Structural Biology</i> , 2007, 7, 40.	2.3	57
33	Evaluation of 3D-Jury on CASP7 models. <i>BMC Bioinformatics</i> , 2007, 8, 304.	1.2	33
34	Herpes glycoprotein gL is distantly related to chemokine receptor ligands. <i>Antiviral Research</i> , 2007, 75, 83-86.	1.9	12
35	Identification of Herpes TATT-binding protein. <i>Antiviral Research</i> , 2007, 75, 167-172.	1.9	53
36	The challenge of protein structure determination ^α —lessons from structural genomics. <i>Protein Science</i> , 2007, 16, 2472-2482.	3.1	135

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37	LigProf: A simple tool for in silico prediction of ligand-binding sites. <i>Journal of Molecular Modeling</i> , 2007, 13, 445-455.	0.8	9
38	Analysis of structure and function of tenascin-C. <i>International Journal of Biochemistry and Cell Biology</i> , 2006, 38, 1594-1602.	1.2	41
39	Three dimensional model of severe acute respiratory syndrome coronavirus helicase ATPase catalytic domain and molecular design of severe acute respiratory syndrome coronavirus helicase inhibitors. <i>Journal of Computer-Aided Molecular Design</i> , 2006, 20, 305-319.	1.3	14
40	Support-vector-machine classification of linear functional motifs in proteins. <i>Journal of Molecular Modeling</i> , 2006, 12, 453-461.	0.8	6
41	PDB-LF: database of predicted enzymatic functions for unannotated protein structures from structural genomics. <i>BMC Bioinformatics</i> , 2006, 7, 53.	1.2	31
42	Eukaryotic Domain of Unknown Function DUF738 Belongs to Gcn5-related N-acetyltransferase Superfamily. <i>Cell Cycle</i> , 2006, 5, 2927-2930.	1.3	16
43	Human Herpesvirus 1 UL24 Gene Encodes a Potential PD-(D/E)XK Endonuclease. <i>Journal of Virology</i> , 2006, 80, 2575-2577.	1.5	35
44	Novel SARS Unique AdoMet-Dependent Methyltransferase. <i>Cell Cycle</i> , 2006, 5, 2414-2416.	1.3	6
45	Molecular modeling of phosphorylation sites in proteins using a database of local structure segments. <i>Journal of Molecular Modeling</i> , 2005, 11, 431-438.	0.8	10
46	Protein domain of unknown function DUF1023 is an $\hat{1}\pm/\hat{1}^2$ hydrolase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 1-6.	1.5	4
47	AutoMotif server: prediction of single residue post-translational modifications in proteins. <i>Bioinformatics</i> , 2005, 21, 2525-2527.	1.8	61
48	Identification of novel restriction endonuclease-like fold families among hypothetical proteins. <i>Nucleic Acids Research</i> , 2005, 33, 3598-3605.	6.5	83
49	FFAS03: a server for profile-profile sequence alignments. <i>Nucleic Acids Research</i> , 2005, 33, W284-W288.	6.5	522
50	Practical lessons from protein structure prediction. <i>Nucleic Acids Research</i> , 2005, 33, 1874-1891.	6.5	109
51	A support vector machine approach to the identification of phosphorylation sites. <i>Cellular and Molecular Biology Letters</i> , 2005, 10, 73-89.	2.7	18
52	Predicting Protein Structures Accurately. <i>Science</i> , 2004, 304, 1597b-1599b.	6.0	6
53	Detecting distant homology with Meta-BASIC. <i>Nucleic Acids Research</i> , 2004, 32, W576-W581.	6.5	92
54	Novel Physiological Modulation of the Pu Promoter of TOL Plasmid. <i>Journal of Biological Chemistry</i> , 2004, 279, 7777-7784.	1.6	46

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55	How Unique Is the Rice Transcriptome?. <i>Science</i> , 2004, 303, 168b-168.	6.0	4
56	Protein structure prediction for the male-specific region of the human Y chromosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2305-2310.	3.3	46
57	The PDB-Preview database: a repository of in-silico models of 'on-hold' PDB entries. <i>Bioinformatics</i> , 2004, 20, 2482-2484.	1.8	2
58	DCC proteins: a novel family of thiol-disulfide oxidoreductases. <i>Trends in Biochemical Sciences</i> , 2004, 29, 339-342.	3.7	7
59	BTLCP proteins: a novel family of bacterial transglutaminase-like cysteine proteinases. <i>Trends in Biochemical Sciences</i> , 2004, 29, 392-395.	3.7	29
60	Integrated web service for improving alignment quality based on segments comparison. <i>BMC Bioinformatics</i> , 2004, 5, 98.	1.2	9
61	BOF: a novel family of bacterial OB-fold proteins. <i>FEBS Letters</i> , 2004, 567, 297-301.	1.3	36
62	Structure prediction, evolution and ligand interaction of CHASE domain. <i>FEBS Letters</i> , 2004, 576, 287-290.	1.3	28
63	Ligand.Info Small-Molecule Meta-Database. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2004, 7, 757-761.	0.6	50
64	LiveBench-6: Large-scale automated evaluation of protein structure prediction servers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 542-547.	1.5	61
65	CAFASP3: The third critical assessment of fully automated structure prediction methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 503-516.	1.5	108
66	Application of 3D-Jury, GRDB, and Verify3D in fold recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 418-423.	1.5	53
67	Protein structure prediction of CASP5 comparative modeling and fold recognition targets using consensus alignment approach and 3D assessment. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 410-417.	1.5	72
68	mRNA Cap-1 Methyltransferase in the SARS Genome. <i>Cell</i> , 2003, 113, 701-702.	13.5	119
69	3D-Jury: a simple approach to improve protein structure predictions. <i>Bioinformatics</i> , 2003, 19, 1015-1018.	1.8	689
70	The 2002 Olympic Games of Protein Structure Prediction. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 157-160.	1.0	13
71	Detection of reliable and unexpected protein fold predictions using 3D-Jury. <i>Nucleic Acids Research</i> , 2003, 31, 3291-3292.	6.5	61
72	ELM server: a new resource for investigating short functional sites in modular eukaryotic proteins. <i>Nucleic Acids Research</i> , 2003, 31, 3625-3630.	6.5	555

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73	Ligand-Info, searching for similar small compounds using index profiles. <i>Bioinformatics</i> , 2003, 19, 1041-1042.	1.8	40
74	ORFeus: detection of distant homology using sequence profiles and predicted secondary structure. <i>Nucleic Acids Research</i> , 2003, 31, 3804-3807.	6.5	118
75	Ab Initio SERVER PROTOTYPE FOR PREDICTION OF PHOSPHORYLATION SITES IN PROTEINS*. <i>Computational Methods in Science and Technology</i> , 2003, 9, 93-100.	0.3	2
76	In silico identification, structure prediction and phylogenetic analysis of the 2â€²-O-ribose (cap 1) methyltransferase domain in the large structural protein of ssRNA negative-strand viruses. <i>Protein Engineering, Design and Selection</i> , 2002, 15, 101-108.	1.0	69
77	Fold-recognition detects an error in the Protein Data Bank. <i>Bioinformatics</i> , 2002, 18, 1391-1395.	1.8	20
78	Errors in theD. radioduranslarge ribosomal subunit structure detected by protein fold-recognition and structure validation tools. <i>FEBS Letters</i> , 2002, 525, 174-175.	1.3	9
79	Fold-recognition analysis predicts that the Tag protein family shares a common domain with the helix-hairpin-helix DNA glycosylases. <i>DNA Repair</i> , 2002, 1, 391-395.	1.3	6
80	RNA:(guanine-N2) methyltransferases RsmC/RsmD and their homologs revisited--bioinformatic analysis and prediction of the active site based on the uncharacterized Mj0882 protein structure. <i>BMC Bioinformatics</i> , 2002, 3, 10.	1.2	30
81	Sequence analysis and structure prediction of 23S rRNA:m1C methyltransferases reveals a conserved core augmented with a putative Zn-binding domain in the N-terminus and family-specific elaborations in the C-terminus. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2002, 4, 93-9.	1.0	8
82	3D-Hit: fast structural comparison of proteins. <i>Applied Bioinformatics</i> , 2002, 1, 223-5.	1.7	18
83	Unusual evolutionary history of the tRNA splicing endonuclease EndA: Relationship to the LAGLIDAG and PD-(D/E)XK deoxyribonucleases. <i>Protein Science</i> , 2001, 10, 656-660.	3.1	17
84	Reassignment of specificities of two cap methyltransferase domains in the reovirus lambda 2 protein. <i>Genome Biology</i> , 2001, 2, research0038.1.	13.9	47
85	Fold Predictions for Bacterial Genomes. <i>Journal of Structural Biology</i> , 2001, 134, 219-231.	1.3	25
86	Identification of a PD-(D/E)XK-like domain with a novel configuration of the endonuclease active site in the methyl-directed restriction enzyme Mrr and its homologs. <i>Gene</i> , 2001, 267, 183-191.	1.0	34
87	CAFASP2: The second critical assessment of fully automated structure prediction methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 171-183.	1.5	130
88	LiveBench-2: Large-scale automated evaluation of protein structure prediction servers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 184-191.	1.5	67
89	The herpesvirus alkaline exonuclease belongs to the restriction endonuclease PD-(D/E)XK superfamily: insight from molecular modeling and phylogenetic analysis. , 2001, 22, 219-230.		36
90	LiveBench-1: Continuous benchmarking of protein structure prediction servers. <i>Protein Science</i> , 2001, 10, 352-361.	3.1	135

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91	Polyphyletic evolution of type II restriction enzymes revisited: two independent sources of second-hand folds revealed. <i>Trends in Biochemical Sciences</i> , 2001, 26, 9-11.	3.7	64
92	mRNA:guanine-N7 cap methyltransferases: identification of novel members of the family, evolutionary analysis, homology modeling, and analysis of sequence-structure-function relationships. <i>BMC Bioinformatics</i> , 2001, 2, 2.	1.2	25
93	A study of quality measures for protein threading models. <i>BMC Bioinformatics</i> , 2001, 2, 5.	1.2	174
94	Three-dimensional modeling of the I-TevI homing endonuclease catalytic domain, a GIYâ€“YIG superfamily member, using NMR restraints and Monte Carlo dynamics. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 717-721.	1.0	16
95	Structure prediction meta server. <i>Bioinformatics</i> , 2001, 17, 750-751.	1.8	219
96	ATP-activated oligomerization as a mechanism for apoptosis regulation: Fold and mechanism prediction for CED-4. , 2000, 39, 197-203.		30
97	Atomic model of the 5-methylcytosine-specific restriction enzyme McrA reveals an atypical zinc finger and structural similarity to betabetaalphaMe endonucleases. <i>Molecular Microbiology</i> , 2000, 37, 1280-1281.	1.2	24
98	From fold to function predictions: an apoptosis regulator protein BID. <i>Computers & Chemistry</i> , 2000, 24, 511-517.	1.2	2
99	Improving the quality of twilightâ€“zone alignments. <i>Protein Science</i> , 2000, 9, 1487-1496.	3.1	120
100	The 2000 Olympic Games of protein structure prediction; fully automated programs are being evaluated vis-Ã-vis human teams in the protein structure prediction experiment CAFASP2. <i>Protein Engineering, Design and Selection</i> , 2000, 13, 667-670.	1.0	17
101	Prediction of a common fold for all four subunits of the yeast tRNA splicing endonuclease: implications for the evolution of the EndA/Sen family. <i>FEBS Letters</i> , 2000, 486, 328-329.	1.3	14
102	Comparison of sequence profiles. Strategies for structural predictions using sequence information. <i>Protein Science</i> , 2000, 9, 232-241.	3.1	431
103	From fold predictions to function predictions: Automation of functional site conservation analysis for functional genome predictions. <i>Protein Science</i> , 1999, 8, 1104-1115.	3.1	59
104	CAFASP-1: Critical assessment of fully automated structure prediction methods. , 1999, 37, 209-217.		110
105	The <i>Helicobacter pylori</i> genome: From sequence analysis to structural and functional predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 36, 20-30.	1.5	18
106	Functional insights from structural predictions: Analysis of the <i>Escherichia coli</i> genome. <i>Protein Science</i> , 1999, 8, 614-624.	3.1	38
107	CAFASP-1: critical assessment of fully automated structure prediction methods. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, Suppl 3, 209-17.	1.5	60
108	The <i>Helicobacter pylori</i> genome: From sequence analysis to structural and functional predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 36, 20-30.	1.5	1

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109	Fold prediction by a hierarchy of sequence, threading, and modeling methods. <i>Protein Science</i> , 1998, 7, 1431-1440.	3.1	91
110	Fold and function predictions for <i>Mycoplasma genitalium</i> proteins. <i>Folding & Design</i> , 1998, 3, 229-238.	4.5	94
111	Similarities and differences between nonhomologous proteins with similar folds: evaluation of threading strategies. <i>Folding & Design</i> , 1997, 2, 307-317.	4.5	23