

Protein structure prediction on the Web: a case study u

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Comparative Protein Structure Modeling Using Modeller. Current Protocols in Bioinformatics, 2006, 15, Unit-5.6.	25.8	2,858
3	Bioinformatic identification of novel methyltransferases. Epigenomics, 2009, 1, 163-175.	2.1	47
4	Integrase-directed recovery of functional genes from genomic libraries. Nucleic Acids Research, 2009, 37, e118-e118.	14.5	12
5	A 3D structure model of the melibiose permease of Escherichia coli represents a distinctive fold for Na ⁺ symporters. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15291-15296.	7.1	34
6	A Periplasmic Thioredoxin-Like Protein Plays a Role in Defense against Oxidative Stress in <i>Neisseria gonorrhoeae</i> . Infection and Immunity, 2009, 77, 4934-4939.	2.2	27
7	Pattern of Expression and Substrate Specificity of Chloroplast Ferredoxins from <i>Chlamydomonas reinhardtii</i> . Journal of Biological Chemistry, 2009, 284, 25867-25878.	3.4	122
8	Single-Residue Changes in the C-Terminal Disulfide-Bonded Loop of the <i>Pseudomonas aeruginosa</i> Type IV Pilin Influence Pilus Assembly and Twitching Motility. Journal of Bacteriology, 2009, 191, 6513-6524.	2.2	48
9	Comparative analysis of plant genomes allows the definition of the "Phytolongins": a novel non-SNARE longin domain protein family. BMC Genomics, 2009, 10, 510.	2.8	23
10	Cloning and characterization of a glucosyltransferase from <i>Crocus sativus</i> stigmas involved in flavonoid glucosylation. BMC Plant Biology, 2009, 9, 109.	3.6	36
11	The F-BAR Protein Syp1 Negatively Regulates WASp-Arp2/3 Complex Activity during Endocytic Patch Formation. Current Biology, 2009, 19, 1979-1987.	3.9	64
12	Loop residues of the receptor binding domain of <i>Bacillus thuringiensis</i> Cry11Ba toxin are important for mosquitocidal activity. FEBS Letters, 2009, 583, 2021-2030.	2.8	22
13	Key role of a PtdIns-4,5P2 micro domain in ionic regulation of the mammalian heart Na ⁺ /Ca ²⁺ exchanger. Cell Calcium, 2009, 45, 546-553.	2.4	12
14	Perlecan domain I-conjugated, hyaluronic acid-based hydrogel particles for enhanced chondrogenic differentiation via BMP-2 release. Biomaterials, 2009, 30, 6964-6975.	11.4	100
15	I-TASSER: Fully automated protein structure prediction in CASP8. Proteins: Structure, Function and Bioinformatics, 2009, 77, 100-113.	2.6	384
16	Genome-wide association study identifies variants in TMPRSS6 associated with hemoglobin levels. Nature Genetics, 2009, 41, 1170-1172.	21.4	217
17	Four newly isolated fuselloviruses from extreme geothermal environments reveal unusual morphologies and a possible interviral recombination mechanism. Environmental Microbiology, 2009, 11, 2849-2862.	3.8	85
18	β -Glycosyl Azides as Substrates for β -Glycosynthases: Preparation of Efficient β -L-Fucosynthases. Chemistry and Biology, 2009, 16, 1097-1108.	6.0	65
19	Identification of Functional LsrB-Like Autoinducer-2 Receptors. Journal of Bacteriology, 2009, 191, 6975-6987.	2.2	86

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20	Comprehensive Molecular Structure of the Eukaryotic Ribosome. <i>Structure</i> , 2009, 17, 1591-1604.	3.3	140
22	The Akt C-Terminal Modulator Protein Is an Acyl-CoA Thioesterase of the Hotdog-Fold Family. <i>Biochemistry</i> , 2009, 48, 5507-5509.	2.5	17
23	Assessing computational methods for predicting protein stability upon mutation: good on average but not in the details. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 553-560.	2.1	325
24	Purification, characterization and sequencing of the major β -1,3-glucanase from the midgut of <i>Tenebrio molitor</i> larvae. <i>Insect Biochemistry and Molecular Biology</i> , 2009, 39, 861-874.	2.7	53
25	Crystal Structure of the HEAT Domain from the Pre-mRNA Processing Factor Symplekin. <i>Journal of Molecular Biology</i> , 2009, 392, 115-128.	4.2	19
26	Periplasmic Domains of <i>Pseudomonas aeruginosa</i> PilN and PilO Form a Stable Heterodimeric Complex. <i>Journal of Molecular Biology</i> , 2009, 394, 143-159.	4.2	72
27	Structural genomics approach to drug discovery for <i>Mycobacterium tuberculosis</i> . <i>Current Opinion in Microbiology</i> , 2009, 12, 318-325.	5.1	31
28	The Human Asparaginase-like Protein 1 hASRGL1 Is an Ntn Hydrolase with β -Aspartyl Peptidase Activity. <i>Biochemistry</i> , 2009, 48, 11026-11031.	2.5	73
29	Evidence of Mineralization Activity and Supramolecular Assembly by the N-Terminal Sequence of ACCBP, a Biom mineralization Protein That Is Homologous to the Acetylcholine Binding Protein Family. <i>Biomacromolecules</i> , 2009, 10, 3298-3305.	5.4	13
30	Dissection of USP catalytic domains reveals five common insertion points. <i>Molecular BioSystems</i> , 2009, 5, 1797.	2.9	135
31	P.2.b.005 Magnetisation imaging in major depressive disorder. <i>European Neuropsychopharmacology</i> , 2009, 19, S393-S394.	0.7	0
32	Functional analysis of the Bunyamwera orthobunyavirus Gc glycoprotein. <i>Journal of General Virology</i> , 2009, 90, 2483-2492.	2.9	48
33	Biochemical Characterization of the RNase II Family of Exoribonucleases from the Human Pathogens <i>Salmonella typhimurium</i> and <i>Streptococcus pneumoniae</i> . <i>Biochemistry</i> , 2009, 48, 11848-11857.	2.5	21
34	Chapter 10 Protein Import in Chloroplasts. <i>Advances in Botanical Research</i> , 2009, , 277-332.	1.1	5
35	Thiol isomerases negatively regulate the cellular shedding activity of ADAM17. <i>Biochemical Journal</i> , 2010, 428, 439-450.	3.7	149
36	Identification and characterization of a strict and a promiscuous <i>N</i> -acetylglucosamine-1-P uridylyltransferase in <i>Arabidopsis</i> . <i>Biochemical Journal</i> , 2010, 430, 275-284.	3.7	34
37	Basic protein structure prediction for the biologist: A review. <i>Archives of Biological Sciences</i> , 2010, 62, 857-871.	0.5	27
38	Dominant-Negative Mutations in β -II Spectrin Cause West Syndrome with Severe Cerebral Hypomyelination, Spastic Quadriplegia, and Developmental Delay. <i>American Journal of Human Genetics</i> , 2010, 86, 881-891.	6.2	131

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39	Mutations in HPSE2 Cause Urofacial Syndrome. American Journal of Human Genetics, 2010, 86, 963-969.	6.2	88
40	In silico analysis of antibody triggering biofilm associated protein in <i>Acinetobacter baumannii</i> . Journal of Theoretical Biology, 2010, 266, 275-290.	1.7	45
41	The annotation of full zinc proteomes. Journal of Biological Inorganic Chemistry, 2010, 15, 1071-1078.	2.6	27
42	Savicalin, a lipocalin from hemocytes of the soft tick, <i>Ornithodoros savignyi</i> . Experimental and Applied Acarology, 2010, 52, 313-326.	1.6	13
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49	Refolded dengue virus type 2 NS1 protein expressed in <i>Escherichia coli</i> preserves structural and immunological properties of the native protein. Journal of Virological Methods, 2010, 167, 186-192.	2.1	47
50	Structural Insights into the COP9 Signalosome and Its Common Architecture with the 26S Proteasome Lid and eIF3. Structure, 2010, 18, 518-527.	3.3	68
51	Structures of Get3, Get4, and Get5 Provide New Models for TA Membrane Protein Targeting. Structure, 2010, 18, 897-902.	3.3	34
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62	Characterization of aryl hydrocarbon receptor interacting protein (AIP) mutations in familial isolated pituitary adenoma families. Human Mutation, 2010, 31, 950-960.	2.5	154
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87	SLEEPLESS, a Ly-6/neurotoxin family member, regulates the levels, localization and activity of Shaker. Nature Neuroscience, 2010, 13, 69-75.	14.8	99
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95	Biosynthesis of a New UDP-sugar, UDP-2-acetamido-2-deoxyxylose, in the Human Pathogen <i>Bacillus cereus</i> Subspecies <i>cytotoxicus</i> NVH 391-98. Journal of Biological Chemistry, 2010, 285, 24825-24833.	3.4	16
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127	Epstein-Barr Virus LF2 Protein Regulates Viral Replication by Altering Rta Subcellular Localization. Journal of Virology, 2010, 84, 9920-9931.	3.4	28
128	Characterization of the haem-uptake system of the equine pathogen <i>Streptococcus equi</i> subsp. <i>equi</i> . Microbiology (United Kingdom), 2010, 156, 1824-1835.	1.8	12
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