

Angelo Facchiano

List of Publications by Year in descending order

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146
papers

3,291
citations

147801

31
h-index

189892

50
g-index

169
all docs

169
docs citations

169
times ranked

4344
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular Aspects of Spike-ACE2 Interaction. Encyclopedia, 2022, 2, 96-108.	4.5	4
2	Investigating the Effects of Amino Acid Variations in Human Menin. Molecules, 2022, 27, 1747.	3.8	8
3	Drug Design by Pharmacophore and Virtual Screening Approach. Pharmaceuticals, 2022, 15, 646.	3.8	68
4	Predicting the stability of mutant proteins by computational approaches: an overview. Briefings in Bioinformatics, 2021, 22, .	6.5	32
5	A review on drug repurposing applicable to COVID-19. Briefings in Bioinformatics, 2021, 22, 726-741.	6.5	117
6	GeenaR: A Web Tool for Reproducible MALDI-TOF Analysis. Frontiers in Genetics, 2021, 12, 635814.	2.3	4
7	A multiple network-based bioinformatics pipeline for the study of molecular mechanisms in oncological diseases for personalized medicine. Briefings in Bioinformatics, 2021, 22, .	6.5	4
8	A hypothesis on the capacity of plant odorant-binding proteins to bind volatile isoprenoids based on in silico evidences. ELife, 2021, 10, .	6.0	11
9	Transamidation Down-Regulates Intestinal Immunity of Recombinant β -Gliadin in HLA-DQ8 Transgenic Mice. International Journal of Molecular Sciences, 2021, 22, 7019.	4.1	6
10	c-FLIP regulates autophagy by interacting with Beclin-1 and influencing its stability. Cell Death and Disease, 2021, 12, 686.	6.3	8
11	Editorial: Computational Proteomics and Integration of Data Resources for Advanced Studies in Life Sciences. Frontiers in Genetics, 2021, 12, 729013.	2.3	0
12	Performance of Web tools for predicting changes in protein stability caused by mutations. BMC Bioinformatics, 2021, 22, 345.	2.6	23
13	Structural Dissection of Viral Spike-Protein Binding of SARS-CoV-2 and SARS-CoV-1 to the Human Angiotensin-Converting Enzyme 2 (ACE2) as Cellular Receptor. Biomedicines, 2021, 9, 1038.	3.2	15
14	STL1, a New AKT Inhibitor, Synergizes with Flavonoid Quercetin in Enhancing Cell Death in A Chronic Lymphocytic Leukemia Cell Line. Molecules, 2021, 26, 5810.	3.8	4
15	Virtual Screening of Natural Compounds as Potential PI3K-AKT1 Signaling Pathway Inhibitors and Experimental Validation. Molecules, 2021, 26, 492.	3.8	15
16	An investigation into the molecular basis of cancer comorbidities in coronavirus infection. FEBS Open Bio, 2020, 10, 2363-2374.	2.3	10
17	Molecular Docking Simulations on Histone Deacetylases (HDAC)-1 and -2 to Investigate the Flavone Binding. Biomedicines, 2020, 8, 568.	3.2	27
18	Reply to Jakovac: About COVID-19 and vitamin D. American Journal of Physiology - Endocrinology and Metabolism, 2020, 318, E838-E838.	3.5	10

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19	Editorial: Artificial Intelligence Bioinformatics: Development and Application of Tools for Omics and Inter-Omics Studies. <i>Frontiers in Genetics</i> , 2020, 11, 309.	2.3	8
20	Genomic diversity and novel genome-wide association with fruit morphology in <i>Capsicum</i> , from 746k polymorphic sites. <i>Scientific Reports</i> , 2019, 9, 10067.	3.3	53
21	Structure and Ligands Interactions of Citrus Tryptophan Decarboxylase by Molecular Modeling and Docking Simulations. <i>Biomolecules</i> , 2019, 9, 117.	4.0	4
22	Searching for Chymase Inhibitors among Chamomile Compounds Using a Computational-Based Approach. <i>Biomolecules</i> , 2019, 9, 5.	4.0	23
23	PAX8 expression in high-grade serous ovarian cancer positively regulates attachment to ECM via Integrin I α 3. <i>Cancer Cell International</i> , 2019, 19, 303.	4.1	27
24	Classification of microbial transglutaminases by evaluation of evolution trees, sequence motifs, secondary structure topology and conservation of potential catalytic residues. <i>Biochemical and Biophysical Research Communications</i> , 2019, 509, 506-513.	2.1	8
25	The evolution of a Web resource: The Galactosemia Proteins Database 2.0. <i>Human Mutation</i> , 2018, 39, 52-60.	2.5	13
26	Bioinformatics methodologies for coeliac disease and its comorbidities. <i>Briefings in Bioinformatics</i> , 2018, , .	6.5	6
27	Pre-Processing MALDI/TOF Mass Spectra by Using Geena 2. <i>Current Protocols in Bioinformatics</i> , 2018, 64, e59.	25.8	2
28	The genetic code is not an optimal code in a model taking into account both the biosynthetic relationships between amino acids and their physicochemical properties. <i>Journal of Theoretical Biology</i> , 2018, 459, 45-51.	1.7	8
29	Aryl hydrocarbon receptor, a tumor grade-associated marker of oral cancer, is directly downregulated by polydatin: A pilot study. <i>Oncology Reports</i> , 2018, 40, 1435-1442.	2.6	8
30	The role of chemical elements in melanoma. <i>European Journal of Molecular and Clinical Medicine</i> , 2017, 2, 73.	0.1	0
31	Bioinformatic resources for the investigation of proteins and proteomes. <i>Peptidomics</i> , 2017, 3, 1-10.	0.3	2
32	Immunoglobulin T from sea bass (<i>Dicentrarchus labrax</i> L.): molecular characterization, tissue localization and expression after nodavirus infection. <i>BMC Molecular Biology</i> , 2017, 18, 8.	3.0	37
33	Role of a shared epitope and other citrullination-sites in rheumatoid arthritis and in melanoma. <i>Expert Opinion on Therapeutic Targets</i> , 2017, 21, 993-994.	3.4	0
34	Binding of mycotoxins to proteins involved in neuronal plasticity: a combined in silico/wet investigation. <i>Scientific Reports</i> , 2017, 7, 15156.	3.3	14
35	Transglutaminase type 2 affects cell migration through post-translational modification of platelet-derived growth factor-BB. <i>Amino Acids</i> , 2017, 49, 473-481.	2.7	7
36	Experimental Evidence and In Silico Identification of Tryptophan Decarboxylase in Citrus Genus. <i>Molecules</i> , 2017, 22, 272.	3.8	17

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37	Unusual Antioxidant Properties of 26S Proteasome Isolated from Cold-Adapted Organisms. International Journal of Molecular Sciences, 2017, 18, 1605.	4.1	0
38	Bioinformatic resources for the investigation of proteins and proteomes. Peptidomics, 2016, 2, .	0.3	1
39	PDGFR-alpha inhibits melanoma growth via CXCL10/IP-10: a multi-omics approach. Oncotarget, 2016, 7, 77257-77275.	1.8	22
40	New antimicrobial peptides against foodborne pathogens: From in silico design to experimental evidence. Food Chemistry, 2016, 211, 546-554.	8.2	31
41	Uncommon functional properties of the first piscine 26S proteasome from the Antarctic nototheniid <i>Trematomus bernacchii</i> . Bioscience Reports, 2016, 36, .	2.4	5
42	The fluorescent monomeric protein Kusabira Orange. Pressure effect on its structure and stability. Biochemistry and Biophysics Reports, 2016, 7, 138-143.	1.3	1
43	Polymorphism of the phosphoserine phosphatase gene in <i>Streptococcus thermophilus</i> and its potential use for typing and monitoring of population diversity. International Journal of Food Microbiology, 2016, 236, 138-147.	4.7	10
44	NMR and computational data of two novel antimicrobial peptides. Data in Brief, 2016, 8, 562-569.	1.0	3
45	A theoretical study on predicted protein targets of apple polyphenols and possible mechanisms of chemoprevention in colorectal cancer. Scientific Reports, 2016, 6, 32516.	3.3	32
46	Geena 2, improved automated analysis of MALDI/TOF mass spectra. BMC Bioinformatics, 2016, 17, 61.	2.6	23
47	<i>In silico</i> approach to find chymase inhibitors among biogenic compounds. Future Medicinal Chemistry, 2016, 8, 841-851.	2.3	22
48	Interaction of human chymase with ginkgolides, terpene trilactones of <i>Ginkgo biloba</i> investigated by molecular docking simulations. Biochemical and Biophysical Research Communications, 2016, 473, 449-454.	2.1	27
49	Comparative Analysis of MALDI-TOF Mass Spectrometric Data in Proteomics: A Case Study. Lecture Notes in Computer Science, 2016, , 154-164.	1.3	0
50	Preface: BITS2014, the annual meeting of the Italian Society of Bioinformatics. BMC Bioinformatics, 2015, 16, S1.	2.6	0
51	Clinical and molecular spectra in galactosemic patients from neonatal screening in northeastern Italy: Structural and functional characterization of new variations in the galactose-1-phosphate uridyltransferase (GALT) gene. Gene, 2015, 559, 112-118.	2.2	23
52	A New APEH Cluster with Antioxidant Functions in the Antarctic Hemoglobinless Icefish <i>Chionodraco hamatus</i> . PLoS ONE, 2015, 10, e0125594.	2.5	12
53	Statistical Analysis of Protein Structural Features: Relationships and PCA Grouping. Lecture Notes in Computer Science, 2015, , 33-43.	1.3	1
54	GALT Protein Database: Querying Structural and Functional Features of GALT Enzyme. Human Mutation, 2014, 35, 1060-1067.	2.5	19

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55	A novel class of bifunctional acylpeptide hydrolases—potential role in the antioxidant defense systems of the Antarctic fish <i>Trematomus bernacchii</i> . <i>FEBS Journal</i> , 2014, 281, 401-415.	4.7	18
56	Rapid peptidomic profiling of peritoneal fluid by MALDI-TOF mass spectrometry for the identification of biomarkers of endometriosis. <i>Gynecological Endocrinology</i> , 2014, 30, 872-876.	1.7	25
57	Molecular characterization, gene structure and antibacterial activity of a g-type lysozyme from the European sea bass (<i>Dicentrarchus labrax</i> L.). <i>Molecular Immunology</i> , 2014, 62, 10-18.	2.2	45
58	Bioinformatics in Italy: BITS2012, the ninth annual meeting of the Italian Society of Bioinformatics. <i>BMC Bioinformatics</i> , 2013, 14, S1.	2.6	1
59	Proteomic profile in familial breast cancer patients. <i>Clinical Biochemistry</i> , 2013, 46, 259-265.	1.9	8
60	Complement C3f serum levels may predict breast cancer risk in women with gross cystic disease of the breast. <i>Journal of Proteomics</i> , 2013, 85, 44-52.	2.4	19
61	Tissue transglutaminase activity protects from cutaneous melanoma metastatic dissemination: an in vivo study. <i>Amino Acids</i> , 2013, 44, 53-61.	2.7	16
62	Mutation spectrum in the French cohort of galactosemic patients and structural simulation of 27 novel missense variations. <i>Molecular Genetics and Metabolism</i> , 2012, 107, 438-447.	1.1	25
63	Wheat Subtilisin/Chymotrypsin Inhibitor (WSCI) as a scaffold for novel serine protease inhibitors with a given specificity. <i>Molecular BioSystems</i> , 2012, 8, 3335.	2.9	12
64	Diversity, Molecular Characterization and Expression of T Cell Receptor $\hat{\beta}$ in a Teleost Fish, the Sea Bass (<i>Dicentrarchus labrax</i> , L). <i>PLoS ONE</i> , 2012, 7, e47957.	2.5	40
65	Correlation assessment among clinical phenotypes, expression analysis and molecular modeling of 14 novel variations in the human galactose-1-phosphate uridylyltransferase gene. <i>Human Mutation</i> , 2012, 33, 1107-1115.	2.5	25
66	Solving Biclustering with a GRASP-Like Metaheuristic: Two Case-Studies on Gene Expression Analysis. <i>Lecture Notes in Computer Science</i> , 2012, , 253-267.	1.3	1
67	Human aryl-hydrocarbon receptor and its interaction with dioxin and physiological ligands investigated by molecular modelling and docking simulations. <i>Biochemical and Biophysical Research Communications</i> , 2011, 413, 176-181.	2.1	18
68	The application of atmospheric pressure matrix-assisted laser desorption/ionization to the analysis of long-term cryopreserved serum peptidome. <i>Analytical Biochemistry</i> , 2011, 417, 174-181.	2.4	21
69	Identification of proteins associated with ligand-activated estrogen receptor $\hat{\alpha}$ in human breast cancer cell nuclei by tandem affinity purification and nano LC-MS/MS. <i>Proteomics</i> , 2011, 11, 172-179.	2.2	35
70	3D Modelling of Three Pro-Inflammatory Molecules in Selected Fish Species. <i>Current Pharmaceutical Design</i> , 2010, 16, 4203-4212.	1.9	5
71	Transglutaminase participates in the blockade of neurotransmitter release by tetanus toxin: evidence for a novel biological function. <i>Amino Acids</i> , 2010, 39, 257-269.	2.7	13
72	Standardized sample preparation phases for a quantitative measurement of plasma peptidome profiling by MALDI-TOF. <i>Journal of Proteomics</i> , 2010, 73, 1355-1367.	2.4	20

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73	The misuse of terms in scientific literature. <i>Bioinformatics</i> , 2010, 26, 2498-2498.	4.1	0
74	Analysis of galactosemia-linked mutations of GALT enzyme using a computational biology approach. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 103-113.	2.1	40
75	Functional hypothesis on miraculin™ sweetness by a molecular dynamics approach. <i>Biochemical and Biophysical Research Communications</i> , 2010, 396, 726-730.	2.1	20
76	Molecular and structural characterisation of a macrophage migration inhibitory factor from sea bass (<i>Dicentrarchus labrax</i> L.). <i>Veterinary Immunology and Immunopathology</i> , 2010, 136, 297-304.	1.2	16
77	Critical Assessment of Side Chain Conformation Prediction in Modelling of Single Point Amino Acid Mutation. <i>Advances in Experimental Medicine and Biology</i> , 2010, 680, 283-289.	1.6	2
78	Evolution of cell-mediated immune defences: Cloning and structural characterisation of the T cell receptor beta chain from the icefish <i>Chionodraco hamatus</i> (Perciformes: Channichthyidae). <i>Italian Journal of Zoology</i> , 2009, 76, 258-268.	0.6	3
79	Intestinal T Cell Responses to Gluten Peptides Are Largely Heterogeneous: Implications for a Peptide-Based Therapy in Celiac Disease. <i>Journal of Immunology</i> , 2009, 182, 4158-4166.	0.8	158
80	When it comes to homology, bad habits die hard. <i>Trends in Biochemical Sciences</i> , 2009, 34, 98-99.	7.5	6
81	A scale space approach for unsupervised feature selection in mass spectra classification for ovarian cancer detection. <i>BMC Bioinformatics</i> , 2009, 10, S9.	2.6	6
82	Transglutaminases and their substrates in biology and human diseases: 50 years of growing. <i>Amino Acids</i> , 2009, 36, 599-614.	2.7	55
83	Prediction of the protein structural class by specific peptide frequencies. <i>Biochimie</i> , 2009, 91, 226-229.	2.6	40
84	Redesigning the reactive site loop of the wheat subtilisin/chymotrypsin inhibitor (WSCI) by site-directed mutagenesis. A protein-protein interaction study by affinity chromatography and molecular modeling. <i>Biochimie</i> , 2009, 91, 1112-1122.	2.6	3
85	Molecular characterisation and structural analysis of an interferon homologue in sea bass (<i>Dicentrarchus labrax</i> L.). <i>Molecular Immunology</i> , 2009, 46, 943-952.	2.2	47
86	Biochemical characterization and homology modeling of a purine-specific ribonucleoside hydrolase from the archaeon <i>Sulfolobus solfataricus</i> : Insights into mechanisms of protein stabilization. <i>Archives of Biochemistry and Biophysics</i> , 2009, 483, 55-65.	3.0	11
87	GALT Protein Database, a Bioinformatics Resource for the Management and Analysis of Structural Features of a Galactosemia-related Protein and Its Mutants. <i>Genomics, Proteomics and Bioinformatics</i> , 2009, 7, 71-76.	6.9	19
88	Platelet-Derived Growth Factor-Receptor \pm Strongly Inhibits Melanoma Growth In Vitro and In Vivo. <i>Neoplasia</i> , 2009, 11, 732-737.	5.3	32
89	Human Prion Protein Helices: Studying Their Stability by Molecular Dynamics Simulations (SUPPLEMENTARY MATERIAL). <i>Protein and Peptide Letters</i> , 2009, 16, 1057-1062.	0.9	3
90	A Machine Learning Approach to Mass Spectra Classification with Unsupervised Feature Selection. <i>Lecture Notes in Computer Science</i> , 2009, , 242-252.	1.3	1

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91	Effect of positive charge in VIP16 ³ -glutamyl diamino derivatives on hVPAC1 and hVPAC2 receptor function. <i>Journal of Peptide Science</i> , 2008, 14, 102-109.	1.4	2
92	Energy-based prediction of amino acid-nucleotide base recognition. <i>Journal of Computational Chemistry</i> , 2008, 29, 1955-1969.	3.3	44
93	Understanding the role of the topology in protein folding by computational inverse folding experiments. <i>Computational Biology and Chemistry</i> , 2008, 32, 233-239.	2.3	3
94	Pyrimidine-specific ribonucleoside hydrolase from the archaeon <i>Sulfolobus solfataricus</i> : biochemical characterization and homology modeling. <i>FEBS Journal</i> , 2008, 275, 1900-1914.	4.7	11
95	Time-course analysis of genome-wide gene expression data from hormone-responsive human breast cancer cells. <i>BMC Bioinformatics</i> , 2008, 9, S12.	2.6	27
96	T cell receptor beta chain from sea bream (<i>Sparus aurata</i>): Molecular cloning, expression and modelling of the complexes with MHC class I. <i>Molecular Immunology</i> , 2008, 45, 2017-2027.	2.2	12
97	A CD4 homologue in sea bass (<i>Dicentrarchus labrax</i>): Molecular characterization and structural analysis. <i>Molecular Immunology</i> , 2008, 45, 3168-3177.	2.2	57
98	Molecular modelling of miraculin: Structural analyses and functional hypotheses. <i>Biochemical and Biophysical Research Communications</i> , 2008, 367, 26-32.	2.1	36
99	Molecular modelling of co-receptor CD8 α and its complex with MHC class I and T-cell receptor in sea bream (<i>Sparus aurata</i>). <i>Fish and Shellfish Immunology</i> , 2008, 25, 782-790.	3.6	11
100	The N-terminal 1-16 peptide derived in vivo from protein seminal vesicle protein IV modulates α -thrombin activity: potential clinical implications. <i>Experimental and Molecular Medicine</i> , 2008, 40, 541.	7.7	0
101	Conformational Diseases and Structure-Toxicity Relationships: Lessons from Prion-Derived Peptides. <i>Current Protein and Peptide Science</i> , 2007, 8, 83-90.	1.4	9
102	Identification of a novel point mutation in the ligand-binding domain of the human glucocorticoid receptor (hGR) in a patient with glucocorticoid resistance. <i>International Journal on Disability and Human Development</i> , 2007, 6, .	0.2	2
103	Interleukin-10 expression by real-time PCR and homology modelling analysis in the European sea bass (<i>Dicentrarchus Labrax</i> L.). <i>Aquaculture</i> , 2007, 270, 512-522.	3.5	42
104	Molecular cloning, differential expression and 3D structural analysis of the MHC class-II β chain from sea bass (<i>Dicentrarchus labrax</i> L.). <i>Fish and Shellfish Immunology</i> , 2007, 23, 853-866.	3.6	51
105	FASMA: A Service to Format and Analyze Sequences in Multiple Alignments. <i>Genomics, Proteomics and Bioinformatics</i> , 2007, 5, 253-255.	6.9	7
106	Transamidation of Wheat Flour Inhibits the Response to Gliadin of Intestinal T Cells in Celiac Disease. <i>Gastroenterology</i> , 2007, 133, 780-789.	1.3	160
107	New computational strategy to analyze the interactions of ER α and ER β with different ERE sequences. <i>Journal of Computational Chemistry</i> , 2007, 28, 1031-1041.	3.3	2
108	Simulation of conformational changes occurring when a protein interacts with its receptor. <i>Computational Biology and Chemistry</i> , 2007, 31, 196-206.	2.3	12

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109	PreSSAPro: A software for the prediction of secondary structure by amino acid properties. <i>Computational Biology and Chemistry</i> , 2007, 31, 389-392.	2.3	15
110	Evaluation of the structural quality of modeled proteins by using globularity criteria. <i>BMC Structural Biology</i> , 2007, 7, 9.	2.3	11
111	Amino acid propensities for secondary structures are influenced by the protein structural class. <i>Biochemical and Biophysical Research Communications</i> , 2006, 342, 441-451.	2.1	132
112	The CD8 β from sea bass (<i>Dicentrarchus labrax</i> L.): Cloning, expression and 3D modelling. <i>Fish and Shellfish Immunology</i> , 2006, 20, 637-646.	3.6	57
113	Prion Protein Misfolding: Conformational Stability of the β -Helix. , 2006, , 575-576.		0
114	Assessment of the conformational features of vasoactive intestinal peptide in solution by limited proteolysis experiments. <i>Biopolymers</i> , 2006, 81, 110-119.	2.4	7
115	Comparative gene expression profiling reveals partially overlapping but distinct genomic actions of different antiestrogens in human breast cancer cells. <i>Journal of Cellular Biochemistry</i> , 2006, 98, 1163-1184.	2.6	43
116	Modeling the 3D structure of wheat subtilisin/chymotrypsin inhibitor (WSCI). Probing the reactive site with two susceptible proteinases by time-course analysis and molecular dynamics simulations. <i>Biological Chemistry</i> , 2006, 387, 931-940.	2.5	10
117	Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry for the Discrimination of Food-Borne Microorganisms. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1180-1189.	3.1	134
118	Modelling of HLA-DQ2 and its interaction with gluten peptides to explain molecular recognition in celiac disease. <i>Journal of Molecular Graphics and Modelling</i> , 2005, 23, 419-431.	2.4	33
119	Structure/function of KRAB repression domains: Structural properties of KRAB modules inferred from hydrodynamic, circular dichroism, and FTIR spectroscopic analyses. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 604-616.	2.6	15
120	Transglutaminases and Their Substrates. , 2005, 38, 37-57.		10
121	Homology Modeling Studies on Human Galactose-1-phosphate Uridyltransferase and on Its Galactosemia-Related Mutant Q188R Provide an Explanation of Molecular Effects of the Mutation on Homo- and Heterodimers. <i>Journal of Medicinal Chemistry</i> , 2005, 48, 773-779.	6.4	43
122	A genomic view of estrogen actions in human breast cancer cells by expression profiling of the hormone-responsive transcriptome. <i>Journal of Molecular Endocrinology</i> , 2004, 32, 719-775.	2.5	80
123	Structural properties of the protein SV-IV. <i>FEBS Journal</i> , 2004, 271, 263-271.	0.2	4
124	Molecular identification of ER α -positive breast cancer cells by the expression profile of an intrinsic set of estrogen regulated genes. <i>Journal of Cellular Physiology</i> , 2004, 200, 440-450.	4.1	44
125	Modelling of fish interleukin-1 and its receptor. <i>Developmental and Comparative Immunology</i> , 2004, 28, 429-441.	2.3	45
126	Theoretical model of the three-dimensional structure of a sugar-binding protein from <i>Pyrococcus horikoshii</i> : structural analysis and sugar-binding simulations. <i>Biochemical Journal</i> , 2004, 380, 677-684.	3.7	25

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127	Comparing the modeled structures of PR-4 proteins from wheat. <i>Journal of Molecular Modeling</i> , 2003, 9, 9-15.	1.8	19
128	Identification of a Novel Domain of Fibroblast Growth Factor 2 Controlling Its Angiogenic Properties. <i>Journal of Biological Chemistry</i> , 2003, 278, 8751-8760.	3.4	40
129	Active Sequences Collection (ASC) database: a new tool to assign functions to protein sequences. <i>Nucleic Acids Research</i> , 2003, 31, 379-382.	14.5	28
130	Platelet-derived Growth Factor-BB and Basic Fibroblast Growth Factor Directly Interact in Vitro with High Affinity. <i>Journal of Biological Chemistry</i> , 2002, 277, 1284-1291.	3.4	27
131	Alteration in the ubiquitin structure and function in the human lens: a possible mechanism of senile cataractogenesis. <i>FEBS Letters</i> , 2002, 531, 162-167.	2.8	9
132	Integrating mutation data and structural analysis of the TP53 tumor-suppressor protein. <i>Human Mutation</i> , 2002, 19, 149-164.	2.5	122
133	Transglutaminase-mediated polyamination of vasoactive intestinal peptide (VIP) Gln16 residue modulates VIP/PACAP receptor activity. <i>FEBS Journal</i> , 2002, 269, 3211-3219.	0.2	6
134	Primary structure of alpha-globin chains from river buffalo (<i>Bubalus bubalis</i> L.) hemoglobins. <i>The Protein Journal</i> , 2001, 20, 171-179.	1.1	3
135	In vitro phosphorylation of high molecular weight glutenin subunits from wheat endosperm. <i>Plant Physiology and Biochemistry</i> , 1999, 37, 931-938.	5.8	1
136	The self-association of protein SV40 and its possible functional implications. <i>FEBS Journal</i> , 1999, 266, 1029-1035.	0.2	14
137	Probing the modelled structure of Wheatwin1 by controlled proteolysis and sequence analysis of unfractionated digestion mixtures. , 1999, 36, 192-204.		11
138	Probing the modelled structure of Wheatwin1 by controlled proteolysis and sequence analysis of unfractionated digestion mixtures. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 36, 192-204.	2.6	1
139	Identification of a β -lactoglobulin lactosylation site. <i>BBA - Proteins and Proteomics</i> , 1998, 1388, 295-304.	2.1	88
140	Effect of a Weak Electrolyte on the Critical Micellar Concentration of Sodium Dodecyl Sulfate. <i>Journal of Colloid and Interface Science</i> , 1998, 200, 310-312.	9.4	47
141	Erratum to "Molecular properties of glutamate dehydrogenase from the extreme thermophilic archaeobacterium <i>Sulfolobus solfataricus</i> " [<i>Biochimica et Biophysica Acta</i> 1251 (1995) 170-176]. <i>BBA - Proteins and Proteomics</i> , 1996, 1292, 207.	2.1	0
142	Molecular properties of glutamate dehydrogenase from the extreme thermophilic archaeobacterium <i>Sulfolobus solfataricus</i> . <i>BBA - Proteins and Proteomics</i> , 1995, 1251, 170-176.	2.1	0
143	The amino acid sequence of a protein from wheat kernel closely related to proteins involved in the mechanisms of plant defence. <i>The Protein Journal</i> , 1993, 12, 379-386.	1.1	29
144	Converter: a program to convert crystallographic coordinates among different molecular graphics standards on PC-IBM platforms. <i>Bioinformatics</i> , 1991, 7, 395-396.	4.1	0

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145	FAST (Flexible Analysis by Software Tool) and CHAMP (CHemico-physical AMinoacidic Parameter data) Tj ETQq1 1 0,784314 rgBT /Overl 4.1	4.1	1
146	New graphic representation of structural parameters of proteins. Bioinformatics, 1988, 4, 303-305.	4.1	1