

# 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	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
2	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
3	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
4	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
5	Integrating mutation data and structural analysis of the TP53 tumor-suppressor protein. <i>Human Mutation</i> , 2002, 19, 149-164.	2.5	122
6	A review on drug repurposing applicable to COVID-19. <i>Briefings in Bioinformatics</i> , 2021, 22, 726-741.	6.5	117
7	Identification of a $\beta$ -lactoglobulin lactosylation site. <i>BBA - Proteins and Proteomics</i> , 1998, 1388, 295-304.	2.1	88
8	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
9	Drug Design by Pharmacophore and Virtual Screening Approach. <i>Pharmaceuticals</i> , 2022, 15, 646.	3.8	68
10	The CD8 $\alpha$ 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
11	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
12	Transglutaminases and their substrates in biology and human diseases: 50 years of growing. <i>Amino Acids</i> , 2009, 36, 599-614.	2.7	55
13	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
14	Molecular cloning, differential expression and 3D structural analysis of the MHC class-II $\beta$ chain from sea bass ( <i>Dicentrarchus labrax</i> L.). <i>Fish and Shellfish Immunology</i> , 2007, 23, 853-866.	3.6	51
15	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
16	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
17	Modelling of fish interleukin-1 and its receptor. <i>Developmental and Comparative Immunology</i> , 2004, 28, 429-441.	2.3	45
18	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

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19	Molecular identification of ER $\alpha$ -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
20	Energy-based prediction of amino acid-nucleotide base recognition. <i>Journal of Computational Chemistry</i> , 2008, 29, 1955-1969.	3.3	44
21	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
22	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
23	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
24	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
25	Prediction of the protein structural class by specific peptide frequencies. <i>Biochimie</i> , 2009, 91, 226-229.	2.6	40
26	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
27	Diversity, Molecular Characterization and Expression of T Cell Receptor $\beta$ in a Teleost Fish, the Sea Bass ( <i>Dicentrarchus labrax</i> , L). <i>PLoS ONE</i> , 2012, 7, e47957.	2.5	40
28	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
29	Molecular modelling of miraculin: Structural analyses and functional hypotheses. <i>Biochemical and Biophysical Research Communications</i> , 2008, 367, 26-32.	2.1	36
30	Identification of proteins associated with ligand-activated estrogen receptor $\beta$ 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
31	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
32	Platelet-Derived Growth Factor-Receptor $\beta$ Strongly Inhibits Melanoma Growth In Vitro and In Vivo. <i>Neoplasia</i> , 2009, 11, 732-W7.	5.3	32
33	A theoretical study on predicted protein targets of apple polyphenols and possible mechanisms of chemoprevention in colorectal cancer. <i>Scientific Reports</i> , 2016, 6, 32516.	3.3	32
34	Predicting the stability of mutant proteins by computational approaches: an overview. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	32
35	New antimicrobial peptides against foodborne pathogens: From in silico design to experimental evidence. <i>Food Chemistry</i> , 2016, 211, 546-554.	8.2	31
36	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

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37	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
38	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
39	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
40	Interaction of human chymase with ginkgolides, terpene trilactones of Ginkgo biloba investigated by molecular docking simulations. <i>Biochemical and Biophysical Research Communications</i> , 2016, 473, 449-454.	2.1	27
41	PAX8 expression in high-grade serous ovarian cancer positively regulates attachment to ECM via Integrin $\alpha 3$ . <i>Cancer Cell International</i> , 2019, 19, 303.	4.1	27
42	Molecular Docking Simulations on Histone Deacetylases (HDAC)-1 and -2 to Investigate the Flavone Binding. <i>Biomedicines</i> , 2020, 8, 568.	3.2	27
43	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
44	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
45	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
46	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
47	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 uridylyltransferase (GALT) gene. <i>Gene</i> , 2015, 559, 112-118.	2.2	23
48	Geena 2, improved automated analysis of MALDI/TOF mass spectra. <i>BMC Bioinformatics</i> , 2016, 17, 61.	2.6	23
49	Searching for Chymase Inhibitors among Chamomile Compounds Using a Computational-Based Approach. <i>Biomolecules</i> , 2019, 9, 5.	4.0	23
50	Performance of Web tools for predicting changes in protein stability caused by mutations. <i>BMC Bioinformatics</i> , 2021, 22, 345.	2.6	23
51	PDGFR-alpha inhibits melanoma growth via CXCL10/IP-10: a multi-omics approach. <i>Oncotarget</i> , 2016, 7, 77257-77275.	1.8	22
52	<i>In silico</i> approach to find chymase inhibitors among biogenic compounds. <i>Future Medicinal Chemistry</i> , 2016, 8, 841-851.	2.3	22
53	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
54	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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55	Functional hypothesis on miraculin™ sweetness by a molecular dynamics approach. <i>Biochemical and Biophysical Research Communications</i> , 2010, 396, 726-730.	2.1	20
56	Comparing the modeled structures of PR-4 proteins from wheat. <i>Journal of Molecular Modeling</i> , 2003, 9, 9-15.	1.8	19
57	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
58	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
59	GALT Protein Database: Querying Structural and Functional Features of GALT Enzyme. <i>Human Mutation</i> , 2014, 35, 1060-1067.	2.5	19
60	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
61	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
62	Experimental Evidence and In Silico Identification of Tryptophan Decarboxylase in Citrus Genus. <i>Molecules</i> , 2017, 22, 272.	3.8	17
63	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
64	Tissue transglutaminase activity protects from cutaneous melanoma metastatic dissemination: an in vivo study. <i>Amino Acids</i> , 2013, 44, 53-61.	2.7	16
65	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
66	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
67	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. <i>Biomedicines</i> , 2021, 9, 1038.	3.2	15
68	Virtual Screening of Natural Compounds as Potential PI3K-AKT1 Signaling Pathway Inhibitors and Experimental Validation. <i>Molecules</i> , 2021, 26, 492.	3.8	15
69	The self-association of protein SV and its possible functional implications. <i>FEBS Journal</i> , 1999, 266, 1029-1035.	0.2	14
70	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
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	The evolution of a Web resource: The Galactosemia Proteins Database 2.0. <i>Human Mutation</i> , 2018, 39, 52-60.	2.5	13

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73	Simulation of conformational changes occurring when a protein interacts with its receptor. Computational Biology and Chemistry, 2007, 31, 196-206.	2.3	12
74	T cell receptor beta chain from sea bream ( <i>Sparus aurata</i> ): Molecular cloning, expression and modelling of the complexes with MHC class I. Molecular Immunology, 2008, 45, 2017-2027.	2.2	12
75	Wheat Subtilisin/Chymotrypsin Inhibitor (WSCI) as a scaffold for novel serine protease inhibitors with a given specificity. Molecular BioSystems, 2012, 8, 3335.	2.9	12
76	A New APEH Cluster with Antioxidant Functions in the Antarctic Hemoglobinless Icefish <i>Chionodraco hamatus</i> . PLoS ONE, 2015, 10, e0125594.	2.5	12
77	Probing the modelled structure of Wheatwin1 by controlled proteolysis and sequence analysis of unfractionated digestion mixtures. , 1999, 36, 192-204.		11
78	Evaluation of the structural quality of modeled proteins by using globularity criteria. BMC Structural Biology, 2007, 7, 9.	2.3	11
79	Pyrimidine-specific ribonucleoside hydrolase from the archaeon <i>Sulfolobus solfataricus</i> : biochemical characterization and homology modeling. FEBS Journal, 2008, 275, 1900-1914.	4.7	11
80	Molecular modelling of co-receptor CD8 $\alpha$ and its complex with MHC class I and T-cell receptor in sea bream ( <i>Sparus aurata</i> ). Fish and Shellfish Immunology, 2008, 25, 782-790.	3.6	11
81	Biochemical characterization and homology modeling of a purine-specific ribonucleoside hydrolase from the archaeon <i>Sulfolobus solfataricus</i> : Insights into mechanisms of protein stabilization. Archives of Biochemistry and Biophysics, 2009, 483, 55-65.	3.0	11
82	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
83	Transglutaminases and Their Substrates. , 2005, 38, 37-57.		10
84	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. Biological Chemistry, 2006, 387, 931-940.	2.5	10
85	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
86	An investigation into the molecular basis of cancer comorbidities in coronavirus infection. FEBS Open Bio, 2020, 10, 2363-2374.	2.3	10
87	Reply to Jakovac: About COVID-19 and vitamin D. American Journal of Physiology - Endocrinology and Metabolism, 2020, 318, E838-E838.	3.5	10
88	Alteration in the ubiquitin structure and function in the human lens: a possible mechanism of senile cataractogenesis. FEBS Letters, 2002, 531, 162-167.	2.8	9
89	Conformational Diseases and Structure-Toxicity Relationships: Lessons from Prion-Derived Peptides. Current Protein and Peptide Science, 2007, 8, 83-90.	1.4	9
90	Proteomic profile in familial breast cancer patients. Clinical Biochemistry, 2013, 46, 259-265.	1.9	8

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91	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
92	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
93	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
94	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
95	c-FLIP regulates autophagy by interacting with Beclin-1 and influencing its stability. <i>Cell Death and Disease</i> , 2021, 12, 686.	6.3	8
96	Investigating the Effects of Amino Acid Variations in Human Menin. <i>Molecules</i> , 2022, 27, 1747.	3.8	8
97	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
98	FASMA: A Service to Format and Analyze Sequences in Multiple Alignments. <i>Genomics, Proteomics and Bioinformatics</i> , 2007, 5, 253-255.	6.9	7
99	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
100	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
101	When it comes to homology, bad habits die hard. <i>Trends in Biochemical Sciences</i> , 2009, 34, 98-99.	7.5	6
102	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
103	Bioinformatics methodologies for coeliac disease and its comorbidities. <i>Briefings in Bioinformatics</i> , 2018, , .	6.5	6
104	Transamidation Down-Regulates Intestinal Immunity of Recombinant $\hat{\pm}$ -Gliadin in HLA-DQ8 Transgenic Mice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7019.	4.1	6
105	3D Modelling of Three Pro-Inflammatory Molecules in Selected Fish Species. <i>Current Pharmaceutical Design</i> , 2010, 16, 4203-4212.	1.9	5
106	Uncommon functional properties of the first piscine 26S proteasome from the Antarctic nototheniid <i>Trematomus bernacchii</i> . <i>Bioscience Reports</i> , 2016, 36, .	2.4	5
107	Structural properties of the protein SV-IV. <i>FEBS Journal</i> , 2004, 271, 263-271.	0.2	4
108	Structure and Ligands Interactions of Citrus Tryptophan Decarboxylase by Molecular Modeling and Docking Simulations. <i>Biomolecules</i> , 2019, 9, 117.	4.0	4

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109	GeenaR: A Web Tool for Reproducible MALDI-TOF Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 635814.	2.3	4
110	A multiple network-based bioinformatics pipeline for the study of molecular mechanisms in oncological diseases for personalized medicine. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	4
111	STL1, a New AKT Inhibitor, Synergizes with Flavonoid Quercetin in Enhancing Cell Death in A Chronic Lymphocytic Leukemia Cell Line. <i>Molecules</i> , 2021, 26, 5810.	3.8	4
112	Molecular Aspects of Spike-ACE2 Interaction. <i>Encyclopedia</i> , 2022, 2, 96-108.	4.5	4
113	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
114	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
115	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
116	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
117	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
118	NMR and computational data of two novel antimicrobial peptides. <i>Data in Brief</i> , 2016, 8, 562-569.	1.0	3
119	FAST (Flexible Analysis by Software Tool) and CHAMP (CHemico-physical AMinoacidic Parameter data) Tj ETQq1 1 0,784314 rgBT /Overl 4.1 2		
120	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
121	New computational strategy to analyze the interactions of ER <sup>1±</sup> and ER <sup>1²</sup> with different ERE sequences. <i>Journal of Computational Chemistry</i> , 2007, 28, 1031-1041.	3.3	2
122	Effect of positive charge in VIP16 <sup>13</sup> -glutamyl diamino derivatives on hVPAC1 and hVPAC2 receptor function. <i>Journal of Peptide Science</i> , 2008, 14, 102-109.	1.4	2
123	Bioinformatic resources for the investigation of proteins and proteomes. <i>Peptidomics</i> , 2017, 3, 1-10.	0.3	2
124	Pre-Processing MALDI/TOF Mass Spectra by Using Geena 2. <i>Current Protocols in Bioinformatics</i> , 2018, 64, e59.	25.8	2
125	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
126	New graphic representation of structural parameters of proteins. <i>Bioinformatics</i> , 1988, 4, 303-305.	4.1	1



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127	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
128	Bioinformatics in Italy: BITS2012, the ninth annual meeting of the Italian Society of Bioinformatics. <i>BMC Bioinformatics</i> , 2013, 14, S1.	2.6	1
129	Bioinformatic resources for the investigation of proteins and proteomes. <i>Peptidomics</i> , 2016, 2, .	0.3	1
130	The fluorescent monomeric protein Kusabira Orange. Pressure effect on its structure and stability. <i>Biochemistry and Biophysics Reports</i> , 2016, 7, 138-143.	1.3	1
131	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
132	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
133	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
134	Statistical Analysis of Protein Structural Features: Relationships and PCA Grouping. <i>Lecture Notes in Computer Science</i> , 2015, , 33-43.	1.3	1
135	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
136	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
137	Erratum to "Molecular properties of glutamate dehydrogenase from the extreme thermophilic archaeobacterium <i>Sulfolobus solfataricus</i> " [Biochimica et Biophysica Acta 1251 (1995) 170-176]. <i>BBA - Proteins and Proteomics</i> , 1996, 1292, 207.	2.1	0
138	Prion Protein Misfolding: Conformational Stability of the $\beta$ -2-Helix. , 2006, , 575-576.		0
139	The N-terminal 1-16 peptide derived in vivo from protein seminal vesicle protein IV modulates $\beta$ -thrombin activity: potential clinical implications. <i>Experimental and Molecular Medicine</i> , 2008, 40, 541.	7.7	0
140	The misuse of terms in scientific literature. <i>Bioinformatics</i> , 2010, 26, 2498-2498.	4.1	0
141	Preface: BITS2014, the annual meeting of the Italian Society of Bioinformatics. <i>BMC Bioinformatics</i> , 2015, 16, S1.	2.6	0
142	The role of chemical elements in melanoma. <i>European Journal of Molecular and Clinical Medicine</i> , 2017, 2, 73.	0.1	0
143	Role of "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
144	Unusual Antioxidant Properties of 26S Proteasome Isolated from Cold-Adapted Organisms. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1605.	4.1	0

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145	Editorial: Computational Proteomics and Integration of Data Resources for Advanced Studies in Life Sciences. <i>Frontiers in Genetics</i> , 2021, 12, 729013.	2.3	0
146	Comparative Analysis of MALDI-TOF Mass Spectrometric Data in Proteomics: A Case Study. <i>Lecture Notes in Computer Science</i> , 2016, , 154-164.	1.3	0