

Giovanni Colonna

List of Publications by Year in descending order

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94
papers

2,988
citations

178989

28
h-index

190239

50
g-index

102
all docs

102
docs citations

102
times ranked

4116
citing authors

#	ARTICLE	IF	CITATIONS
1	System-Wide Pollution of Biomedical Data: Consequence of the Search for Hub Genes of Hepatocellular Carcinoma Without Spatiotemporal Consideration. <i>Molecular Diagnosis and Therapy</i> , 2021, 25, 9-27.	3.9	6
2	Besnoitiosis in donkeys: an emerging parasitic disease of equids in Italy. <i>Parasitology Research</i> , 2021, 120, 1811-1819.	1.6	3
3	Demographic transition and population ageing in Yogyakarta. <i>E3S Web of Conferences</i> , 2020, 200, 04002.	0.5	2
4	Did You Really Get the Message? Using Text Reminders to Stimulate Adoption of Agricultural Technologies. <i>Journal of Development Studies</i> , 2019, 55, 548-564.	2.1	54
5	¹ H-NMR metabolomic profiling of the crayfish <i>Astacus leptodactylus</i> subjected to polyphenol-enriched diets. <i>Aquaculture Nutrition</i> , 2018, 24, 524-538.	2.7	7
6	Combining doxorubicin with a phenolic extract from flaxseed oil: Evaluation of the effect on two breast cancer cell lines. <i>International Journal of Oncology</i> , 2017, 50, 468-476.	3.2	14
7	Comparison of the seleno-transcriptome expression between human non-cancerous mammary epithelial cells and two human breast cancer cell lines. <i>Oncology Letters</i> , 2017, 13, 2411-2417.	1.8	25
8	Conformational analysis of the human chemokine receptor CXCR3. <i>Molecular Immunology</i> , 2017, 92, 76-86.	2.4	1
9	Evaluating the associations between human circadian rhythms and dysregulated genes in liver cancer cells. <i>Oncology Letters</i> , 2017, 14, 7353-7359.	1.8	6
10	Serum Cytokine Profile Evaluation: A Tool to Define New Diagnostic and Prognostic Markers of Cancer Using Multiplexed Bead-Based Immunoassays. <i>Mediators of Inflammation</i> , 2016, 2016, 1-11.	3.1	30
11	Differential Response of Two Human Breast Cancer Cell Lines to the Phenolic Extract from Flaxseed Oil. <i>Molecules</i> , 2016, 21, 319.	3.9	16
12	A study on the structural features of SELK, an over-expressed protein in hepatocellular carcinoma, by molecular dynamics simulations in a lipid-water system. <i>Molecular BioSystems</i> , 2016, 12, 3209-3222.	2.8	13
13	Deducing the functional characteristics of the human selenoprotein SELK from the structural properties of its intrinsically disordered C-terminal domain. <i>Molecular BioSystems</i> , 2016, 12, 758-772.	2.8	11
14	Human MiR-544a Modulates SELK Expression in Hepatocarcinoma Cell Lines. <i>PLoS ONE</i> , 2016, 11, e0156908.	2.5	18
15	Conformational Ensembles Explored Dynamically from Disordered Peptides Targeting Chemokine Receptor CXCR4. <i>International Journal of Molecular Sciences</i> , 2015, 16, 12159-12173.	4.2	7
16	Evaluation of the Selenotranscriptome Expression in Two Hepatocellular Carcinoma Cell Lines. <i>Analytical Cellular Pathology</i> , 2015, 2015, 1-6.	1.5	28
17	Anti-Inflammatory Effects of a Methanol Extract from the Marine Sponge <i>Geodia cydonium</i> on the Human Breast Cancer MCF-7 Cell Line. <i>Mediators of Inflammation</i> , 2015, 2015, 1-9.	3.1	27
18	Structure-fluctuation-function relationships of seven pro-angiogenic isoforms of VEGFA, important mediators of tumorigenesis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 410-425.	2.3	14

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19	Intrinsically disordered amphiphilic peptides as potential targets in drug delivery vehicles. <i>Molecular BioSystems</i> , 2015, 11, 2925-2932.	2.8	6
20	The gene expression profiling of hepatocellular carcinoma by a network analysis approach shows a dominance of intrinsically disordered proteins (IDPs) between hub nodes. <i>Molecular BioSystems</i> , 2015, 11, 2933-2945.	2.8	5
21	The Cytokine Profile in Patients with Hepatocellular Carcinoma and Type 2 Diabetes. <i>PLoS ONE</i> , 2015, 10, e0134594.	2.5	22
22	Synergistic Antitumor Effect of Doxorubicin and Tacrolimus (FK506) on Hepatocellular Carcinoma Cell Lines. <i>Scientific World Journal</i> , The, 2014, 2014, 1-9.	2.2	15
23	An overview of the sequence features of N- and C-terminal segments of the human chemokine receptors. <i>Cytokine</i> , 2014, 70, 141-150.	3.2	15
24	Structure–function relationship and evolutionary history of the human selenoprotein M (SelM) found over-expressed in hepatocellular carcinoma. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 447-456.	2.3	17
25	Peptides targeting chemokine receptor CXCR4: structural behavior and biological binding studies. <i>Journal of Peptide Science</i> , 2014, 20, 270-278.	1.5	8
26	Vitamin C Effect on Mitoxantrone-Induced Cytotoxicity in Human Breast Cancer Cell Lines. <i>PLoS ONE</i> , 2014, 9, e115287.	2.5	40
27	Randomized Controlled Trial of the Shang Ring Versus Conventional Surgical Techniques for Adult Male Circumcision. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2014, 65, 447-455.	2.2	43
28	A Holistic Approach to Study the Effects of Natural Antioxidants on Inflammation and Liver Cancer. <i>Cancer Treatment and Research</i> , 2014, 159, 311-323.	0.0	12
29	Ascorbic Acid: Its Role in Immune System and Chronic Inflammation Diseases. <i>Mini-Reviews in Medicinal Chemistry</i> , 2014, 14, 444-452.	2.6	161
30	Peptide Folding Problem: A Molecular Dynamics Study on Polyalanines Using Different Force Fields. <i>International Journal of Peptide Research and Therapeutics</i> , 2013, 19, 117-123.	1.9	14
31	Genealogy of an ancient protein family: the Sirtuins, a family of disordered members. <i>BMC Evolutionary Biology</i> , 2013, 13, 60.	3.1	47
32	Evaluation of Selenite Effects on Selenoproteins and Cytokine in Human Hepatoma Cell Lines. <i>Molecules</i> , 2013, 18, 2549-2562.	3.9	30
33	Dissimilar cytokine patterns in different human liver and colon cancer cell lines. <i>Cytokine</i> , 2013, 64, 584-589.	3.2	4
34	Common structural interactions between the receptors CXCR3, CXCR4 and CXCR7 complexed with their natural ligands, CXCL11 and CXCL12, by a modeling approach. <i>Cytokine</i> , 2013, 64, 316-321.	3.2	23
35	The protein–protein interaction network of the human Sirtuin family. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1998-2009.	2.3	28
36	Cancer biomarker profiling in patients with chronic hepatitis C virus, liver cirrhosis and hepatocellular carcinoma. <i>Oncology Reports</i> , 2013, 29, 2163-2168.	2.6	18

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37	Cysteinyll-glycine reduces mucosal pro-inflammatory cytokine response to fMLP in a piglet model of intestinal atrophy. <i>FASEB Journal</i> , 2013, 27, 356.6.	0.5	0
38	Loss of Gnas Imprinting Differentially Affects REM/NREM Sleep and Cognition in Mice. <i>PLoS Genetics</i> , 2012, 8, e1002706.	3.4	54
39	Cytokine Profile of Patients with Type 2 Diabetes and/or Chronic Hepatitis C Infection. <i>PLoS ONE</i> , 2012, 7, e39486.	2.5	27
40	Selective Endothelial Overexpression of Arginase II Induces Endothelial Dysfunction and Hypertension and Enhances Atherosclerosis in Mice. <i>PLoS ONE</i> , 2012, 7, e39487.	2.5	28
41	The N-terminal Region of CXCL11 as Structural Template for CXCR3 Molecular Recognition: Synthesis, Conformational Analysis, and Binding Studies. <i>Chemical Biology and Drug Design</i> , 2012, 80, 254-265.	3.4	14
42	A possible predictive marker of progression for hepatocellular carcinoma. <i>Oncology Letters</i> , 2011, 2, 1247-1251.	1.8	22
43	Structural and functional studies of the human selenium binding protein-1 and its involvement in hepatocellular carcinoma. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011, 1814, 513-522.	2.3	51
44	Structural and Functional Similarities between Osmotin from <i>Nicotiana Tabacum</i> Seeds and Human Adiponectin. <i>PLoS ONE</i> , 2011, 6, e16690.	2.5	37
45	CytReD: A database collecting human cytokinome information. <i>Bioinformatics</i> , 2011, 6, 207-208.	0.5	3
46	Functional hypothesis on miraculin™ sweetness by a molecular dynamics approach. <i>Biochemical and Biophysical Research Communications</i> , 2010, 396, 726-730.	2.2	20
47	Human Cytokinome: a new challenge for systems biology. <i>Bioinformatics</i> , 2010, 5, 166-167.	0.5	29
48	Modeling of the Bacterial Mechanism of Methicillin-Resistance by a Systems Biology Approach. <i>PLoS ONE</i> , 2009, 4, e6226.	2.5	20
49	Human Sirt-1: Molecular Modeling and Structure-Function Relationships of an Unordered Protein. <i>PLoS ONE</i> , 2009, 4, e7350.	2.5	58
50	CytokineDB: a database collecting biological information. <i>Bioinformatics</i> , 2009, 4, 92-93.	0.5	3
51	Understanding the role of the topology in protein folding by computational inverse folding experiments. <i>Computational Biology and Chemistry</i> , 2008, 32, 233-239.	2.4	3
52	Molecular modelling of miraculin: Structural analyses and functional hypotheses. <i>Biochemical and Biophysical Research Communications</i> , 2008, 367, 26-32.	2.2	36
53	ESBRI: A web server for evaluating salt bridges in proteins. <i>Bioinformatics</i> , 2008, 3, 137-138.	0.5	144
54	On new challenge for the Bioinformatics. <i>Bioinformatics</i> , 2008, 3, 238-239.	0.5	7

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55	FASMA: A Service to Format and Analyze Sequences in Multiple Alignments. <i>Genomics, Proteomics and Bioinformatics</i> , 2007, 5, 253-255.	7.5	7
56	PreSSAPro: A software for the prediction of secondary structure by amino acid properties. <i>Computational Biology and Chemistry</i> , 2007, 31, 389-392.	2.4	16
57	Evaluation of the structural quality of modeled proteins by using globularity criteria. <i>BMC Structural Biology</i> , 2007, 7, 9.	2.2	11
58	Invariant Ser211 is involved in the catalysis of PD-L4, type I RIP from <i>Phytolacca dioica</i> leaves. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 209-218.	3.2	31
59	Characterization and kinetics studies of water buffalo (<i>Bubalus bubalis</i>) myoglobin. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2006, 145, 230-238.	1.7	55
60	Amino acid propensities for secondary structures are influenced by the protein structural class. <i>Biochemical and Biophysical Research Communications</i> , 2006, 342, 441-451.	2.2	134
61	Modelling of fish interleukin-1 and its receptor. <i>Developmental and Comparative Immunology</i> , 2004, 28, 429-441.	2.3	45
62	Anti-thrombin action of low-dose acetylsalicylic acid. <i>European Journal of Pharmacology</i> , 2003, 460, 59-62.	3.6	10
63	Homology modelling of the human eukaryotic initiation factor 5A (eIF-5A). <i>Protein Engineering, Design and Selection</i> , 2001, 14, 881-890.	2.4	44
64	Inhibition of antithrombin by protein SV-IV normalizes the coagulation of hemophilic blood. <i>European Journal of Pharmacology</i> , 2000, 391, 1-9.	3.6	9
65	Second codon positions of genes and the secondary structures of proteins. Relationships and implications for the origin of the genetic code. <i>Gene</i> , 2000, 261, 63-69.	2.3	81
66	Cautionary note: complex (dys)function of the serotonin transporter. <i>Biological Psychiatry</i> , 2000, 48, 334-335.	1.3	1
67	Probing the modelled structure of <i>Wheatwin1</i> by controlled proteolysis and sequence analysis of unfractionated digestion mixtures. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 36, 192-204.	3.2	12
68	Correlations of nucleotide substitution rates and base composition of mammalian coding sequences with protein structure. <i>Gene</i> , 1999, 238, 23-31.	2.3	28
69	Water transfer energetics and solid-like packing of globular proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996, 24, 388-393.	3.2	8
70	Enthalpy convergence temperatures: proteins and model compounds. <i>Thermochimica Acta</i> , 1995, 251, 371-377.	2.7	7
71	Molecular properties of glutamate dehydrogenase from the extreme thermophilic archaebacterium <i>Sulfolobus solfataricus</i> . <i>BBA - Proteins and Proteomics</i> , 1995, 1251, 170-176.	2.0	0
72	Do Globular Proteins Require Some Structural Peculiarity To Best Function at High Temperatures?. <i>Journal of the American Chemical Society</i> , 1995, 117, 16-20.	14.6	28

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73	Spectrin Anastasia ($\hat{I} \pm \sup>1/78</sup>$): a new spectrin variant ($\hat{I} \pm 45$ Arg Thr) with moderate elliptocytogenic potential. <i>British Journal of Haematology</i> , 1995, 89, 933-936.	2.7	10
74	Determination of hydrophobic hydration in protein unfolding by an intrinsic reference state. <i>BBA - Proteins and Proteomics</i> , 1994, 1208, 15-21.	2.0	4
75	Rat protein SV-IV (seminal vesicle protein No. 4) accelerates human blood coagulation in vitro by selective inhibition of antithrombin III. <i>Biochemical Pharmacology</i> , 1994, 48, 345-352.	4.6	15
76	The Role of Conditional Hydration on the Thermodynamics of Protein Folding. <i>Journal of the American Chemical Society</i> , 1994, 116, 2677-2678.	14.6	15
77	<i>In vitro</i> cross-linking of calf lens $\hat{I} \pm$ crystallin by malondialdehyde. <i>International Journal of Peptide and Protein Research</i> , 1994, 44, 342-347.	0.1	21
78	Inhibition of interleukin-1 release and activity by the rat seminal vesicle protein SV-IV. <i>Journal of Leukocyte Biology</i> , 1993, 53, 214-222.	3.3	19
79	Structural organization and stability of a thermoresistant domain generated by in vivo hydrolysis of the α -crystallin B chain from calf lens. <i>Biochemistry</i> , 1992, 31, 9279-9287.	2.6	6
80	The molecular localization of non-tryptophan chromophores in calf lens crystallins. <i>BBA - Proteins and Proteomics</i> , 1989, 995, 64-69.	2.0	4
81	Unfolding pathway of myoglobin: effect of denaturants on solvent accessibility to tyrosyl residues detected by second-derivative spectroscopy. <i>Biochemistry</i> , 1987, 26, 2130-2134.	2.6	31
82	Dynamic aspects of the heme-binding site in phylogenetically distant myoglobins. <i>BBA - Proteins and Proteomics</i> , 1987, 913, 150-154.	2.0	13
83	Unfolding pathway of myoglobin: Molecular properties of intermediate forms. <i>Archives of Biochemistry and Biophysics</i> , 1986, 244, 459-469.	3.2	94
84	RESOLUTION OF OVERLAPPING BANDS IN THE NEAR-UV ABSORPTION SPECTRUM OF INDOLE DERIVATIVES. <i>Photochemistry and Photobiology</i> , 1985, 42, 505-508.	2.6	11
85	Myoglobin structure and regulation of solvent accessibility of heme pocket. <i>International Journal of Peptide and Protein Research</i> , 1985, 26, 195-207.	0.1	21
86	Determination of tyrosine exposure in proteins by second-derivative spectroscopy. <i>Biochemistry</i> , 1984, 23, 1871-1875.	2.6	270
87	Structural and functional aspects of the heart ventricle myoglobin of bluefin tuna. <i>Comparative Biochemistry and Physiology A, Comparative Physiology</i> , 1983, 76, 481-485.	0.6	19
88	Unfolding pathway of myoglobin. Evidence for a multistate process. <i>Biochemistry</i> , 1983, 22, 4165-4170.	2.6	65
89	Heme and cysteine microenvironments of tuna apomyoglobin. Evidence of two independent unfolding regions. <i>Biochemistry</i> , 1982, 21, 212-215.	2.6	35
90	Simultaneous determination of tyrosine and tryptophan residues in proteins by second-derivative spectroscopy. <i>Analytical Biochemistry</i> , 1982, 126, 251-257.	2.5	92

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91	Tryptophanyl fluorescence heterogeneity of apomyoglobins. Correlation with the presence of two distinct structural domains. <i>Biochemistry</i> , 1981, 20, 792-799.	2.6	68
92	Second-derivative spectroscopy of proteins: Studies on tyrosyl residues. <i>Analytical Biochemistry</i> , 1980, 106, 49-54.	2.5	49
93	The effect of evolution on homologous proteins. <i>Biochimica Et Biophysica Acta (BBA) - Protein Structure</i> , 1978, 532, 354-367.	1.5	19
94	Amino acid sequence around a reactive cysteine of yeast alcohol dehydrogenase. <i>Biochemical and Biophysical Research Communications</i> , 1975, 66, 900-906.	2.2	5