

Giovanni Minervini

List of Publications by Year in descending order

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Version: 2024-02-01

70
papers

2,678
citations

236925

25
h-index

206112

48
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79
all docs

79
docs citations

79
times ranked

4079
citing authors

#	ARTICLE	IF	CITATIONS
1	The RING 2.0 web server for high quality residue interaction networks. <i>Nucleic Acids Research</i> , 2016, 44, W367-W374.	14.5	369
2	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017, 45, D219-D227.	14.5	242
3	Critical assessment of protein intrinsic disorder prediction. <i>Nature Methods</i> , 2021, 18, 472-481.	19.0	187
4	Ca ²⁺ binding to F ₁ ATP synthase \hat{I}^2 subunit triggers the mitochondrial permeability transition. <i>EMBO Reports</i> , 2017, 18, 1065-1076.	4.5	170
5	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	14.5	141
6	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.	14.5	117
7	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021, 49, D404-D411.	14.5	95
8	Heterozygous Reelin Mutations Cause Autosomal-Dominant Lateral Temporal Epilepsy. <i>American Journal of Human Genetics</i> , 2015, 96, 992-1000.	6.2	94
9	Human haptoglobin structure and function – a molecular modelling study. <i>FEBS Journal</i> , 2008, 275, 5648-5656.	4.7	78
10	RING 3.0: fast generation of probabilistic residue interaction networks from structural ensembles. <i>Nucleic Acids Research</i> , 2022, 50, W651-W656.	14.5	75
11	Blues server: electrostatic properties of wild-type and mutated protein structures. <i>Bioinformatics</i> , 2012, 28, 2189-2190.	4.1	72
12	FELLS: fast estimator of latent local structure. <i>Bioinformatics</i> , 2017, 33, 1889-1891.	4.1	72
13	High-Conductance Channel Formation in Yeast Mitochondria is Mediated by F-ATP Synthase e and g Subunits. <i>Cellular Physiology and Biochemistry</i> , 2018, 50, 1840-1855.	1.6	57
14	RepeatsDB: a database of tandem repeat protein structures. <i>Nucleic Acids Research</i> , 2014, 42, D352-D357.	14.5	53
15	Lys300 Plays a Major Role in the Catalytic Mechanism of Maize Polyamine Oxidase. <i>Biochemistry</i> , 2005, 44, 16108-16120.	2.5	48
16	Arginine 107 of yeast ATP synthase subunit g mediates sensitivity of the mitochondrial permeability transition to phenylglyoxal. <i>Journal of Biological Chemistry</i> , 2018, 293, 14632-14645.	3.4	40
17	Whole-Exome Sequencing Identifies Pathogenic Variants in <i>TJP1</i> Gene Associated With Arrhythmogenic Cardiomyopathy. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002123.	3.6	38
18	VHLdb: A database of von Hippel-Lindau protein interactors and mutations. <i>Scientific Reports</i> , 2016, 6, 31128.	3.3	36

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19	Probing mammalian spermine oxidase enzymeâ€“substrate complex through molecular modeling, site-directed mutagenesis and biochemical characterization. <i>Amino Acids</i> , 2011, 40, 1115-1126.	2.7	35
20	Arg-8 of yeast subunit e contributes to the stability of F-ATP synthase dimers and to the generation of the full-conductance mitochondrial megachannel. <i>Journal of Biological Chemistry</i> , 2019, 294, 10987-10997.	3.4	32
21	BOOGIE: Predicting Blood Groups from High Throughput Sequencing Data. <i>PLoS ONE</i> , 2015, 10, e0124579.	2.5	31
22	The role of mitochondrial ATP synthase in cancer. <i>Biological Chemistry</i> , 2020, 401, 1199-1214.	2.5	29
23	RAPHAEL: recognition, periodicity and insertion assignment of solenoid protein structures. <i>Bioinformatics</i> , 2012, 28, 3257-3264.	4.1	27
24	Assessment of phenolic herbicide toxicity and mode of action by different assays. <i>Environmental Science and Pollution Research</i> , 2016, 23, 7398-7408.	5.3	27
25	The lipoprotein <sc>HP1454</sc> of <i>Helicobacter pylori</i> regulates <sc>T</sc>â€“cell response by shaping <sc>T</sc>â€“cell receptor signalling. <i>Cellular Microbiology</i> , 2019, 21, e13006.	2.1	27
26	Isoform-specific interactions of the von Hippel-Lindau tumor suppressor protein. <i>Scientific Reports</i> , 2015, 5, 12605.	3.3	26
27	The invasive Manila clam <i>Ruditapes philippinarum</i> (Adams and Reeve, 1850) in Northern Adriatic Sea: Population genetics assessed by an integrated molecular approach. <i>Fisheries Research</i> , 2011, 110, 259-267.	1.7	25
28	Do Natural Proteins Differ from Random Sequences Polypeptides? Natural vs. Random Proteins Classification Using an Evolutionary Neural Network. <i>PLoS ONE</i> , 2012, 7, e36634.	2.5	25
29	SARSâ€“CoVâ€“2 variants preferentially emerge at intrinsically disordered protein sites helping immune evasion. <i>FEBS Journal</i> , 2022, 289, 4240-4250.	4.7	25
30	Genotype-phenotype relations of the von Hippel-Lindau tumor suppressor inferred from a large-scale analysis of disease mutations and interactors. <i>PLoS Computational Biology</i> , 2019, 15, e1006478.	3.2	24
31	The f subunit of human ATP synthase is essential for normal mitochondrial morphology and permeability transition. <i>Cell Reports</i> , 2021, 35, 109111.	6.4	22
32	Mapping pathogenic mutations suggests an innovative structural model for the pendrin (SLC26A4) transmembrane domain. <i>Biochimie</i> , 2017, 132, 109-120.	2.6	19
33	Design and Analysis of a Petri Net Model of the Von Hippel-Lindau (VHL) Tumor Suppressor Interaction Network. <i>PLoS ONE</i> , 2014, 9, e96986.	2.5	18
34	<i>CDKN2A</i> Unclassified Variants in Familial Malignant Melanoma: Combining Functional and Computational Approaches for Their Assessment. <i>Human Mutation</i> , 2014, 35, 828-840.	2.5	17
35	Insights into the proline hydroxylase (PHD) family, molecular evolution and its impact on human health. <i>Biochimie</i> , 2015, 116, 114-124.	2.6	17
36	HIF1â€“dependent induction of the mitochondrial chaperone TRAP1 regulates bioenergetic adaptations to hypoxia. <i>Cell Death and Disease</i> , 2021, 12, 434.	6.3	17

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37	Calmodulin Enhances Cryptochrome Binding to INAD in Drosophila Photoreceptors. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 280.	2.9	15
38	A targeted next-generation gene panel reveals a novel heterozygous nonsense variant in the TP63 gene in patients with arrhythmogenic cardiomyopathy. <i>Heart Rhythm</i> , 2019, 16, 773-780.	0.7	15
39	The clinical spectrum of CASQ1-related myopathy. <i>Neurology</i> , 2018, 91, e1629-e1641.	1.1	14
40	The pVHL neglected functions, a tale of hypoxia-dependent and -independent regulations in cancer. <i>Open Biology</i> , 2020, 10, 200109.	3.6	14
41	Massive non-natural proteins structure prediction using grid technologies. <i>BMC Bioinformatics</i> , 2009, 10, S22.	2.6	13
42	Evaluation of the steric impact of flavin adenine dinucleotide in Drosophila melanogaster cryptochrome function. <i>Biochemical and Biophysical Research Communications</i> , 2014, 450, 1606-1611.	2.1	13
43	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. <i>Human Mutation</i> , 2017, 38, 1042-1050.	2.5	13
44	In silico investigation of PHD3 specific HIF1α proline 567 hydroxylation: A new player in the VHL/HIF1α interaction pathway?. <i>FEBS Letters</i> , 2013, 587, 2996-3001.	2.8	11
45	Structural in silico dissection of the collagen V interactome to identify genotype-phenotype correlations in classic Ehlers-Danlos Syndrome (EDS). <i>FEBS Letters</i> , 2015, 589, 3871-3878.	2.8	11
46	<i>In silico</i> Structural Study of Random Amino Acid Sequence Proteins Not Present in Nature. <i>Chemistry and Biodiversity</i> , 2009, 6, 2311-2336.	2.1	10
47	Assessing predictors for new post translational modification sites: A case study on hydroxylation. <i>PLoS Computational Biology</i> , 2020, 16, e1007967.	3.2	10
48	Selection Dynamic of <i>Escherichia coli</i> Host in M13 Combinatorial Peptide Phage Display Libraries. <i>Bioscience, Biotechnology and Biochemistry</i> , 2011, 75, 812-815.	1.3	8
49	Computational analysis of prolyl hydroxylase domain-containing protein 2 (PHD2) mutations promoting polycythemia insurgence in humans. <i>Scientific Reports</i> , 2016, 6, 18716.	3.3	8
50	Naïve Bayes ant colony optimization for designing high dimensional experiments. <i>Applied Soft Computing Journal</i> , 2016, 49, 259-268.	7.2	6
51	Novel interactions of the von Hippel-Lindau (pVHL) tumor suppressor with the CDKN1 family of cell cycle inhibitors. <i>Scientific Reports</i> , 2017, 7, 46562.	3.3	6
52	Novel Missense Variant in <i>MYL2</i> Gene Associated With Hypertrophic Cardiomyopathy Showing High Incidence of Restrictive Physiology. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002824.	3.6	6
53	Never born proteins as a test case for ab initio protein structures prediction. <i>Bioinformatics</i> , 2008, 3, 177-179.	0.5	6
54	Neurocognitive assessment and DNA sequencing expand the phenotype and genotype spectrum of Alström syndrome. <i>American Journal of Medical Genetics, Part A</i> , 2021, 185, 732-742.	1.2	5

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55	Identification of Rare LRP5 Variants in a Cohort of Males with Impaired Bone Mass. International Journal of Molecular Sciences, 2021, 22, 10834.	4.1	5
56	Insights into the molecular features of the von Hippelâ€Lindau-like protein. Amino Acids, 2019, 51, 1461-1474.	2.7	4
57	Structural protein reorganization and fold emergence investigated through amino acid sequence permutations. Amino Acids, 2015, 47, 147-152.	2.7	3
58	Validation of a new tool for seafood safety and traceability: the case of Manila clam Ruditapes philippinarum. Economia Agro-Alimentare, 2011, , 503-507.	0.5	3
59	Expanding the clinical-pathological and genetic spectrum of RYR1-related congenital myopathies with cores and minicores: an Italian population study. Acta Neuropathologica Communications, 2022, 10, 54.	5.2	3
60	The E3 ubiquitin-protein ligase MDM2 is a novel interactor of the von Hippelâ€Lindau tumor suppressor. Scientific Reports, 2020, 10, 15850.	3.3	2
61	A Model Based Ant Colony Design for the Protein Engineering Problem. Lecture Notes in Computer Science, 2010, , 352-359.	1.3	2
62	Design and dynamic simulation of minimal metallo-proteins. Journal of Molecular Modeling, 2011, 17, 2919-2925.	1.8	1
63	The Ca 2+ regulatory site of the permeability transition pore is within the catalytic core of F-ATP synthase. Biochimica Et Biophysica Acta - Bioenergetics, 2016, 1857, e65-e66.	1.0	1
64	Characterization of the pVHL Interactome in Human Testis Using High-Throughput Library Screening. Cancers, 2022, 14, 1009.	3.7	1
65	Health state of mollusc productive sites: Biochemical, physiological and molecular markers. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2010, 157, S38.	1.8	0
66	<i>In silico</i> study of the structure and function of <i>Streptococcus mutans</i> plasmidic proteins. Bio-Algorithms and Med-Systems, 2017, 13, 51-61.	2.4	0
67	Pore formation by yeast mitochondrial ATP synthase involves subunits e, g and b. Biochimica Et Biophysica Acta - Bioenergetics, 2018, 1859, e16-e17.	1.0	0
68	Role of F-ATP synthase f subunit in dimer formation and PTP modulation. Biochimica Et Biophysica Acta - Bioenergetics, 2018, 1859, e110.	1.0	0
69	Porting Biological Applications in Grid: An Experience within the EUChinaGRID Framework. , 2009, , 67-71.		0
70	Molecular Effects of Mutations in Human Genetic Diseases. International Journal of Molecular Sciences, 2022, 23, 6408.	4.1	0