Gustavo D Parisi

List of Publications by Year in descending order

72 papers	2,567 citations	218677 26 h-index	223800 46 g-index
82 all docs	82 docs citations	82 times ranked	3079 citing authors

#	Article	IF	Citations
1	Characterization of a Nitric Oxide Synthase from the Plant Kingdom: NO Generation from the Green Alga <i>Ostreococcus tauri</i> Is Light Irradiance and Growth Phase Dependent Â. Plant Cell, 2010, 22, 3816-3830.	6.6	313
2	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. Nucleic Acids Research, 2018, 46, D471-D476.	14.5	190
3	MobiDB: intrinsically disordered proteins in 2021. Nucleic Acids Research, 2021, 49, D361-D367.	14.5	183
4	DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276.	14.5	141
5	Gamma carbonic anhydrases in plant mitochondria. Plant Molecular Biology, 2004, 55, 193-207.	3.9	124
6	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. Nucleic Acids Research, 2022, 50, D480-D487.	14.5	117
7	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. Nucleic Acids Research, 2021, 49, D404-D411.	14.5	95
8	Evolutionary Conservation of Protein Backbone Flexibility. Journal of Molecular Evolution, 2006, 63, 448-457.	1.8	83
9	Structural Constraints and Emergence of Sequence Patterns in Protein Evolution. Molecular Biology and Evolution, 2001, 18, 750-756.	8.9	82
10	Gamma carbonic anhydrase like complex interact with plant mitochondrial complex I. Plant Molecular Biology, 2004, 56, 947-957.	3.9	66
11	Role of the N-Terminal Starch-Binding Domains in the Kinetic Properties of Starch Synthase III from <i>Arabidopsis thaliana</i>. Biochemistry, 2008, 47, 3026-3032.	2.5	66
12	CoDNaS 2.0: a comprehensive database of protein conformational diversity in the native state. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw038.	3.0	60
13	Prediction of Sinorhizobium meliloti sRNA genes and experimental detection in strain 2011. BMC Genomics, 2008, 9, 416.	2.8	58
14	Impact of protein conformational diversity on AlphaFold predictions. Bioinformatics, 2022, 38, 2742-2748.	4.1	57
15	Conformational diversity analysis reveals three functional mechanisms in proteins. PLoS Computational Biology, 2017, 13, e1005398.	3.2	46
16	Analysis of Two Polyhydroxyalkanoate Synthases in Bradyrhizobium japonicum USDA 110. Journal of Bacteriology, 2013, 195, 3145-3155.	2.2	45
17	Functional and structural characterization of the catalytic domain of the starch synthase III from <i>Arabidopsis thaliana</i>. Proteins: Structure, Function and Bioinformatics, 2008, 70, 31-40.	2.6	42
18	Site-Specific Amino Acid Replacement Matrices from Structurally Constrained Protein Evolution Simulations. Molecular Biology and Evolution, 2002, 19, 352-356.	8.9	41

#	Article	IF	Citations
19	Protein Conformational Diversity Correlates with Evolutionary Rate. Molecular Biology and Evolution, 2013, 30, 1500-1503.	8.9	36
20	Starch-synthase III family encodes a tandem of three starch-binding domains. Proteins: Structure, Function and Bioinformatics, 2006, 65, 27-31.	2.6	35
21	On the effect of protein conformation diversity in discriminating among neutral and disease related single amino acid substitutions. BMC Genomics, 2012, 13, S5.	2.8	35
22	Conformational diversity and the emergence of sequence signatures during evolution. Current Opinion in Structural Biology, 2015, 32, 58-65.	5.7	35
23	Specificity traits consistent with legumeâ€rhizobia coevolution displayed by <i>Ensifer meliloti</i> rhizosphere colonization. Environmental Microbiology, 2017, 19, 3423-3438.	3.8	33
24	Protein Conformational Diversity Modulates Sequence Divergence. Molecular Biology and Evolution, 2013, 30, 79-87.	8.9	31
25	CoDNaS: a database of conformational diversity in the native state of proteins. Bioinformatics, 2013, 29, 2512-2514.	4.1	31
26	Molecular cloning and characterization of procirsin, an active aspartic protease precursor from Cirsium vulgare (Asteraceae). Phytochemistry, 2012, 81, 7-18.	2.9	29
27	Identification of a new protective antigen of Bordetella pertussis. Vaccine, 2011, 29, 8731-8739.	3.8	26
28	PCDB: a database of protein conformational diversity. Nucleic Acids Research, 2011, 39, D475-D479.	14.5	25
29	Generality of the Structurally Constrained Protein Evolution model: assessment on representatives of the four main fold classes. Gene, 2005, 345, 45-53.	2.2	24
30	Rapid evolution of cytochrome c oxidase subunit II in camelids (Tylopoda, Camelidae). Journal of Bioenergetics and Biomembranes, 2006, 38, 293-297.	2.3	23
31	Evolutionary Conserved Positions Define Protein Conformational Diversity. PLoS Computational Biology, 2016, 12, e1004775.	3.2	23
32	Disorder transitions and conformational diversity cooperatively modulate biological function in proteins. Protein Science, 2016, 25, 1138-1146.	7.6	23
33	Targeting a Cross-Reactive Gly m 5 Soy Peptide as Responsible for Hypersensitivity Reactions in a Milk Allergy Mouse Model. PLoS ONE, 2014, 9, e82341.	2.5	22
34	Large-scale mapping of bioactive peptides in structural and sequence space. PLoS ONE, 2018, 13, e0191063.	2.5	18
35	Evolutionary Analysis of Î³-Carbonic Anhydrase and Structurally Related Proteins. Molecular Phylogenetics and Evolution, 2000, 14, 323-334.	2.7	17
36	The structurally constrained protein evolution model accounts for sequence patterns of the LbetaH superfamily. BMC Evolutionary Biology, 2004, 4, 41.	3.2	17

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37	Homology modeling in a dynamical world. Protein Science, 2017, 26, 2195-2206.	7.6	17
38	Mutations in Two Putative Phosphorylation Motifs in the Tomato Pollen Receptor Kinase LePRK2 Show Antagonistic Effects on Pollen Tube Length. Journal of Biological Chemistry, 2011, 286, 4882-4891.	3.4	16
39	Dynactins p25 and p27 are predicted to adopt the LβH fold. FEBS Letters, 2004, 562, 1-4.	2.8	15
40	Pockets as structural descriptors of EGFR kinase conformations. PLoS ONE, 2017, 12, e0189147.	2.5	15
41	Addressing the Role of Conformational Diversity in Protein Structure Prediction. PLoS ONE, 2016, 11, e0154923.	2.5	14
42	How is structural divergence related to evolutionary information?. Molecular Phylogenetics and Evolution, 2018, 127, 859-866.	2.7	13
43	On the dynamical incompleteness of the Protein Data Bank. Briefings in Bioinformatics, 2019, 20, 356-359.	6.5	13
44	Quaternary Structure Constraints on Evolutionary Sequence Divergence. Molecular Biology and Evolution, 2006, 24, 349-351.	8.9	12
45	Computational characterisation of potential RNA-binding sites in arenavirus nucleocapsid proteins. Virus Genes, 1996, 13, 247-254.	1.6	11
46	Large scale analysis of protein conformational transitions from aqueous to non-aqueous media. BMC Bioinformatics, 2018, 19, 27.	2.6	10
47	Evaluating the effect of mutations and ligand binding on transthyretin homotetramer dynamics. PLoS ONE, 2017, 12, e0181019.	2.5	9
48	Network analysis of dynamically important residues in protein structures mediating ligand-binding conformational changes. European Biophysics Journal, 2019, 48, 559-568.	2.2	9
49	Distribution of Mosquitoes in the South East of Argentina and First Report on the Analysis Based on 18S rDNA and COI Sequences. PLoS ONE, 2013, 8, e75516.	2.5	9
50	Ensembles from Ordered and Disordered Proteins Reveal Similar Structural Constraints during Evolution. Journal of Molecular Biology, 2019, 431, 1298-1307.	4.2	8
51	Curating the gnomAD database: Report of novel variants in the globin‐coding genes and bioinformatics analysis. Human Mutation, 2020, 41, 81-102.	2.5	8
52	Outer membrane protein OmpQ of Bordetella bronchiseptica is required for mature biofilm formation. Microbiology (United Kingdom), 2016, 162, 351-363.	1.8	8
53	ProtMiscuity: a database of promiscuous proteins. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	7
54	Computational Biology in Argentina. PLoS Computational Biology, 2007, 3, e257.	3.2	6

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55	The tight-adhesion proteins TadGEF of Bradyrhizobium diazoefficiens USDA 110 are involved in cell adhesion and infectivity on soybean roots. Microbiological Research, 2016, 182, 80-88.	5.3	6
56	A Mild Procedure for Enone Preparation Catalysed by Bovine Serum Albumin in a Green and Easily Available Medium. Catalysis Letters, 2018, 148, 1750-1757.	2.6	6
57	Revenant: a database of resurrected proteins. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	6
58	BeEP Server: using evolutionary information for quality assessment of protein structure models. Nucleic Acids Research, 2013, 41, W398-W405.	14.5	5
59	Bovine serum albumin-catalysed cross aldol condensation: Influence of ketone structure. Process Biochemistry, 2019, 86, 50-57.	3.7	5
60	On the analysis and comparison of conformer-specific essential dynamics upon ligand binding to a protein. Journal of Chemical Physics, 2015, 142, 245101.	3.0	4
61	Hb Wilde and Hb Patagonia: two novel elongated betaâ€globin variants causing dominant betaâ€thalassemia. European Journal of Haematology, 2015, 94, 498-503.	2.2	4
62	Exploring Conformational Space with Thermal Fluctuations Obtained by Normal-Mode Analysis. Journal of Chemical Information and Modeling, 2020, 60, 3068-3080.	5.4	4
63	Two novel unstable hemoglobin variants due to inâ€frame deletions of key amino acids in the Î²â€globin chain. European Journal of Haematology, 2018, 100, 529-535.	2.2	3
64	Dynamics fingerprints of active conformers of epidermal growth factor receptor kinase. Journal of Computational Chemistry, 2018, 39, 2472-2480.	3.3	3
65	Intrinsically Disordered Protein Ensembles Shape Evolutionary Rates Revealing Conformational Patterns. Journal of Molecular Biology, 2021, 433, 166751.	4.2	3
66	â€œProteinâ€•no longer means what it used to. Current Research in Structural Biology, 2021, 3, 146-152.	2.2	3
67	Twentyâ€One Novel EGFR Kinase Domain variants in Patients with Nonsmall Cell Lung Cancer. Annals of Human Genetics, 2015, 79, 385-393.	0.8	2
68	Bioinformatics calls the school: Use of smartphones to introduce Python for bioinformatics in high schools. PLoS Computational Biology, 2019, 15, e1006473.	3.2	2
69	Exploring Protein Conformational Diversity. Methods in Molecular Biology, 2019, 1851, 353-365.	0.9	2
70	Structural and evolutionary analysis unveil functional adaptations in the promiscuous behavior of serum albumins. Biochimie, 2022, 197, 113-120.	2.6	2
71	Teaching noncovalent interactions using protein molecular evolution. Biochemistry and Molecular Biology Education, 2008, 36, 284-286.	1.2	1
72	CoDNaS-RNA: a database of conformational diversity in the native state of RNA. Bioinformatics, 2022, 38, 1745-1748.	4.1	1