

Gustavo D Parisi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1170006/publications.pdf>

Version: 2024-02-01

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	DisProt in 2022: improved quality and accessibility of protein intrinsic disorder annotation. <i>Nucleic Acids Research</i> , 2022, 50, D480-D487.	14.5	117
2	Impact of protein conformational diversity on AlphaFold predictions. <i>Bioinformatics</i> , 2022, 38, 2742-2748.	4.1	57
3	Structural and evolutionary analysis unveil functional adaptations in the promiscuous behavior of serum albumins. <i>Biochimie</i> , 2022, 197, 113-120.	2.6	2
4	CoDNAS-RNA: a database of conformational diversity in the native state of RNA. <i>Bioinformatics</i> , 2022, 38, 1745-1748.	4.1	1
5	MobiDB: intrinsically disordered proteins in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D361-D367.	14.5	183
6	Intrinsically Disordered Protein Ensembles Shape Evolutionary Rates Revealing Conformational Patterns. <i>Journal of Molecular Biology</i> , 2021, 433, 166751.	4.2	3
7	“Protein” no longer means what it used to. <i>Current Research in Structural Biology</i> , 2021, 3, 146-152.	2.2	3
8	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
9	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	14.5	141
10	Curating the gnomAD database: Report of novel variants in the globin-coding genes and bioinformatics analysis. <i>Human Mutation</i> , 2020, 41, 81-102.	2.5	8
11	Revenant: a database of resurrected proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	6
12	Exploring Conformational Space with Thermal Fluctuations Obtained by Normal-Mode Analysis. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 3068-3080.	5.4	4
13	Bovine serum albumin-catalysed cross aldol condensation: Influence of ketone structure. <i>Process Biochemistry</i> , 2019, 86, 50-57.	3.7	5
14	Network analysis of dynamically important residues in protein structures mediating ligand-binding conformational changes. <i>European Biophysics Journal</i> , 2019, 48, 559-568.	2.2	9
15	ProtMiscuity: a database of promiscuous proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	7
16	Ensembles from Ordered and Disordered Proteins Reveal Similar Structural Constraints during Evolution. <i>Journal of Molecular Biology</i> , 2019, 431, 1298-1307.	4.2	8
17	Bioinformatics calls the school: Use of smartphones to introduce Python for bioinformatics in high schools. <i>PLoS Computational Biology</i> , 2019, 15, e1006473.	3.2	2
18	Exploring Protein Conformational Diversity. <i>Methods in Molecular Biology</i> , 2019, 1851, 353-365.	0.9	2

#	ARTICLE	IF	CITATIONS
19	On the dynamical incompleteness of the Protein Data Bank. <i>Briefings in Bioinformatics</i> , 2019, 20, 356-359.	6.5	13
20	A Mild Procedure for Enone Preparation Catalysed by Bovine Serum Albumin in a Green and Easily Available Medium. <i>Catalysis Letters</i> , 2018, 148, 1750-1757.	2.6	6
21	Two novel unstable hemoglobin variants due to in-frame deletions of key amino acids in the β -globin chain. <i>European Journal of Haematology</i> , 2018, 100, 529-535.	2.2	3
22	Dynamics fingerprints of active conformers of epidermal growth factor receptor kinase. <i>Journal of Computational Chemistry</i> , 2018, 39, 2472-2480.	3.3	3
23	How is structural divergence related to evolutionary information?. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 859-866.	2.7	13
24	Large scale analysis of protein conformational transitions from aqueous to non-aqueous media. <i>BMC Bioinformatics</i> , 2018, 19, 27.	2.6	10
25	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. <i>Nucleic Acids Research</i> , 2018, 46, D471-D476.	14.5	190
26	Large-scale mapping of bioactive peptides in structural and sequence space. <i>PLoS ONE</i> , 2018, 13, e0191063.	2.5	18
27	Specificity traits consistent with legume-rhizobia coevolution displayed by <i>Ensifer meliloti</i> rhizosphere colonization. <i>Environmental Microbiology</i> , 2017, 19, 3423-3438.	3.8	33
28	Homology modeling in a dynamical world. <i>Protein Science</i> , 2017, 26, 2195-2206.	7.6	17
29	Evaluating the effect of mutations and ligand binding on transthyretin homotetramer dynamics. <i>PLoS ONE</i> , 2017, 12, e0181019.	2.5	9
30	Conformational diversity analysis reveals three functional mechanisms in proteins. <i>PLoS Computational Biology</i> , 2017, 13, e1005398.	3.2	46
31	Pockets as structural descriptors of EGFR kinase conformations. <i>PLoS ONE</i> , 2017, 12, e0189147.	2.5	15
32	Evolutionary Conserved Positions Define Protein Conformational Diversity. <i>PLoS Computational Biology</i> , 2016, 12, e1004775.	3.2	23
33	CoDNaS 2.0: a comprehensive database of protein conformational diversity in the native state. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw038.	3.0	60
34	Disorder transitions and conformational diversity cooperatively modulate biological function in proteins. <i>Protein Science</i> , 2016, 25, 1138-1146.	7.6	23
35	The tight-adhesion proteins TadGEF of <i>Bradyrhizobium diazoefficiens</i> USDA 110 are involved in cell adhesion and infectivity on soybean roots. <i>Microbiological Research</i> , 2016, 182, 80-88.	5.3	6
36	Outer membrane protein OmpQ of <i>Bordetella bronchiseptica</i> is required for mature biofilm formation. <i>Microbiology (United Kingdom)</i> , 2016, 162, 351-363.	1.8	8

#	ARTICLE	IF	CITATIONS
37	Addressing the Role of Conformational Diversity in Protein Structure Prediction. PLoS ONE, 2016, 11, e0154923.	2.5	14
38	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
39	Conformational diversity and the emergence of sequence signatures during evolution. Current Opinion in Structural Biology, 2015, 32, 58-65.	5.7	35
40	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
41	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
42	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
43	Protein Conformational Diversity Correlates with Evolutionary Rate. Molecular Biology and Evolution, 2013, 30, 1500-1503.	8.9	36
44	BeEP Server: using evolutionary information for quality assessment of protein structure models. Nucleic Acids Research, 2013, 41, W398-W405.	14.5	5
45	Protein Conformational Diversity Modulates Sequence Divergence. Molecular Biology and Evolution, 2013, 30, 79-87.	8.9	31
46	Analysis of Two Polyhydroxyalkanoate Synthases in Bradyrhizobium japonicum USDA 110. Journal of Bacteriology, 2013, 195, 3145-3155.	2.2	45
47	CoDNAS: a database of conformational diversity in the native state of proteins. Bioinformatics, 2013, 29, 2512-2514.	4.1	31
48	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
49	Molecular cloning and characterization of procirsin, an active aspartic protease precursor from Cirsium vulgare (Asteraceae). Phytochemistry, 2012, 81, 7-18.	2.9	29
50	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
51	Identification of a new protective antigen of Bordetella pertussis. Vaccine, 2011, 29, 8731-8739.	3.8	26
52	PCDB: a database of protein conformational diversity. Nucleic Acids Research, 2011, 39, D475-D479.	14.5	25
53	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
54	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. Plant Cell, 2010, 22, 3816-3830.	6.6	313

#	ARTICLE	IF	CITATIONS
55	Functional and structural characterization of the catalytic domain of the starch synthase III from <i>Arabidopsis thaliana</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 31-40.	2.6	42
56	Teaching noncovalent interactions using protein molecular evolution. <i>Biochemistry and Molecular Biology Education</i> , 2008, 36, 284-286.	1.2	1
57	Prediction of <i>Sinorhizobium meliloti</i> sRNA genes and experimental detection in strain 2011. <i>BMC Genomics</i> , 2008, 9, 416.	2.8	58
58	Role of the N-Terminal Starch-Binding Domains in the Kinetic Properties of Starch Synthase III from <i>Arabidopsis thaliana</i> . <i>Biochemistry</i> , 2008, 47, 3026-3032.	2.5	66
59	Computational Biology in Argentina. <i>PLoS Computational Biology</i> , 2007, 3, e257.	3.2	6
60	Starch-synthase III family encodes a tandem of three starch-binding domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 27-31.	2.6	35
61	Rapid evolution of cytochrome c oxidase subunit II in camelids (Tylopoda, Camelidae). <i>Journal of Bioenergetics and Biomembranes</i> , 2006, 38, 293-297.	2.3	23
62	Evolutionary Conservation of Protein Backbone Flexibility. <i>Journal of Molecular Evolution</i> , 2006, 63, 448-457.	1.8	83
63	Quaternary Structure Constraints on Evolutionary Sequence Divergence. <i>Molecular Biology and Evolution</i> , 2006, 24, 349-351.	8.9	12
64	Generality of the Structurally Constrained Protein Evolution model: assessment on representatives of the four main fold classes. <i>Gene</i> , 2005, 345, 45-53.	2.2	24
65	The structurally constrained protein evolution model accounts for sequence patterns of the LbetaH superfamily. <i>BMC Evolutionary Biology</i> , 2004, 4, 41.	3.2	17
66	Gamma carbonic anhydrases in plant mitochondria. <i>Plant Molecular Biology</i> , 2004, 55, 193-207.	3.9	124
67	Gamma carbonic anhydrase like complex interact with plant mitochondrial complex I. <i>Plant Molecular Biology</i> , 2004, 56, 947-957.	3.9	66
68	Dynactins p25 and p27 are predicted to adopt the L ¹² H fold. <i>FEBS Letters</i> , 2004, 562, 1-4.	2.8	15
69	Site-Specific Amino Acid Replacement Matrices from Structurally Constrained Protein Evolution Simulations. <i>Molecular Biology and Evolution</i> , 2002, 19, 352-356.	8.9	41
70	Structural Constraints and Emergence of Sequence Patterns in Protein Evolution. <i>Molecular Biology and Evolution</i> , 2001, 18, 750-756.	8.9	82
71	Evolutionary Analysis of \hat{I}^3 -Carbonic Anhydrase and Structurally Related Proteins. <i>Molecular Phylogenetics and Evolution</i> , 2000, 14, 323-334.	2.7	17
72	Computational characterisation of potential RNA-binding sites in arenavirus nucleocapsid proteins. <i>Virus Genes</i> , 1996, 13, 247-254.	1.6	11