Stefania Brocca

List of Publications by Year
in descending order

54 papers	2,534 citations	186209 28 h-index	197736 49 g-index
54 all docs	54 docs citations	54 times ranked	3084 citing authors

#	Article	IF	Citations
1	Shortâ€chain alcohols inactivate an immobilized industrial lipase through two different mechanisms. Biotechnology Journal, 2022, 17, e2100712.	1.8	16
2	Distribution of Charged Residues Affects the Average Size and Shape of Intrinsically Disordered Proteins. Biomolecules, 2022, 12, 561.	1.8	11
3	The coâ€existence of cold activity and thermal stability in an Antarctic GH42 Î²â€galactosidase relies on its hexameric quaternary arrangement. FEBS Journal, 2021, 288, 546-565.	2.2	31
4	The activity and stability of a cold-active acylaminoacyl peptidase rely on its dimerization by domain swapping. International Journal of Biological Macromolecules, 2021, 181, 263-274.	3.6	5
5	The â€œcold revolutionâ€. Present and future applications of cold-active enzymes and ice-binding proteins. New Biotechnology, 2020, 55, 5-11.	2.4	61
6	Liquidâ€"Liquid Phase Separation by Intrinsically Disordered Protein Regions of Viruses: Roles in Viral Life Cycle and Control of Virusâ€"Host Interactions. International Journal of Molecular Sciences, 2020, 21, 9045.	1.8	110
7	Relevance of Electrostatic Charges in Compactness, Aggregation, and Phase Separation of Intrinsically Disordered Proteins. International Journal of Molecular Sciences, 2020, 21, 6208.	1.8	61
8	Diverse effects of aqueous polar co-solvents on Candida antarctica lipase B. International Journal of Biological Macromolecules, 2020, 150, 930-940.	3.6	23
9	pH-Dependent Aggregation in Intrinsically Disordered Proteins Is Determined by Charge and Lipophilicity. Cells, 2020, 9, 145.	1.8	37
10	An arsenal of methods for the experimental characterization of intrinsically disordered proteins â€" How to choose and combine them?. Archives of Biochemistry and Biophysics, 2019, 676, 108055.	1.4	37
11	Depicting Conformational Ensembles of Î±-Synuclein by Single Molecule Force Spectroscopy and Native Mass Spectroscopy. International Journal of Molecular Sciences, 2019, 20, 5181.	1.8	7
12	Conformational Characterization and Classification of Intrinsically Disordered Proteins by Native Mass Spectrometry and Chargeâ€State Distribution Analysis. Proteomics, 2019, 19, 1800060.	1.3	34
13	Conformational properties of intrinsically disordered proteins bound to the surface of silica nanoparticles. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 1556-1564.	1.1	29
14	Conformational response to charge clustering in synthetic intrinsically disordered proteins. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 2204-2214.	1.1	16
15	Aggregation properties of a disordered protein are tunable by pH and depend on its net charge per residue. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 2543-2550.	1.1	29
16	Cryoâ€protective effect of an iceâ€binding protein derived from Antarctic bacteria. FEBS Journal, 2017, 284, 163-177.	2.2	64
17	Conformational effects in protein electrosprayâ€ionization mass spectrometry. Mass Spectrometry Reviews, 2016, 35, 111-122.	2.8	66
18	A bacterial acyl aminoacyl peptidase couples flexibility and stability as a result of cold adaptation. FEBS Journal, 2016, 283, 4310-4324.	2.2	19

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19	Evaluation of the Conformational Stability of Recombinant Desulfurizing Enzymes from a Newly Isolated Rhodococcus sp.. Molecular Biotechnology, 2016, 58, 1-11.	1.3	5
20	Structural investigation of the cold-adapted acylaminoacyl peptidase from Sporosarcina psychrophila by atomistic simulations and biophysical methods. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 2203-2213.	1.1	25
21	Effects of methanol on a methanol-tolerant bacterial lipase. Applied Microbiology and Biotechnology, 2013, 97, 8609-8618.	1.7	35
22	Extracting structural information from charge-state distributions of intrinsically disordered proteins by non-denaturing electrospray-ionization mass spectrometry. Intrinsically Disordered Proteins, 2013, 1, e25068.	1.9	33
23	A comparative study of Whi5 and retinoblastoma proteins: from sequence and structure analysis to intracellular networks. Frontiers in Physiology, 2013, 4, 315.	1.3	17
24	Reciprocal Influence of Protein Domains in the Cold-Adapted Acyl Aminoacyl Peptidase from Sporosarcina psychrophila. PLoS ONE, 2013, 8, e56254.	1.1	12
25	Intramolecular interactions stabilizing compact conformations of the intrinsically disordered kinase-inhibitor domain of Sic1: a molecular dynamics investigation. Frontiers in Physiology, 2012, 3, 435.	1.3	25
26	Amplification of the CUP1 gene is associated with evolution of copper tolerance in Saccharomyces cerevisiae. Microbiology (United Kingdom), 2012, 158, 2325-2335.	0.7	47
27	Laboratory evolution of copper tolerant yeast strains. Microbial Cell Factories, 2012, 11, 1.	1.9	189
28	Lengthâ€dependent compaction of intrinsically disordered proteins. FEBS Letters, 2012, 586, 70-73.	1.3	26
29	Charge-Surface Correlation in Electrospray Ionization of Folded and Unfolded Proteins. Analytical Chemistry, 2011, 83, 6459-6463.	3.2	119
30	Compaction Properties of an Intrinsically Disordered Protein: Sic1 and Its Kinase-Inhibitor Domain. Biophysical Journal, 2011, 100, 2243-2252.	0.2	62
31	Electrospray ionizationâ€mass spectrometry conformational analysis of isolated domains of an intrinsically disordered protein. Biotechnology Journal, 2011, 6, 96-100.	1.8	22
32	Defining Structural Domains of an Intrinsically Disordered Protein: Sic1, the Cyclin-Dependent Kinase Inhibitor of Saccharomyces cerevisiae. Molecular Biotechnology, 2011, 47, 34-42.	1.3	10
33	Recombinant lipase from<i>Candida rugosa</i>for regioselective hydrolysis of peracetylated nucleosides. A comparison with commercial non-recombinant lipases. Biocatalysis and Biotransformation, 2010, 28, 108-116.	1.1	13
34	Order propensity of an intrinsically disordered protein, the cyclinâ€dependentâ€kinase inhibitor Sic1. Proteins: Structure, Function and Bioinformatics, 2009, 76, 731-746.	1.5	64
35	Electrosprayâ€ionization mass spectrometry as a tool for fast screening of protein structural properties. Biotechnology Journal, 2009, 4, 73-87.	1.8	28
36	Sequence of the lid affects activity and specificity of Candida rugosa lipase isoenzymes. Protein Science, 2009, 12, 2312-2319.	3.1	119

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37	The lid is a structural and functional determinant of lipase activity and selectivity. Journal of Molecular Catalysis B: Enzymatic, 2006, 39, 166-170.	1.8	110
38	Comparison of bovine and porcine Î2-lactoglobulin: a mass spectrometric analysis. Journal of Mass Spectrometry, 2006, 41, 717-727.	0.7	31
39	Secondary structure, conformational stability and glycosylation of a recombinant Candida rugosa lipase studied by Fourier-transform infrared spectroscopy. Biochemical Journal, 2005, 385, 511-517.	1.7	167
40	Activity and enantioselectivity of wildtype and lid mutatedCandida rugosa lipase isoform 1 in organic solvents. Biotechnology and Bioengineering, 2004, 86, 236-240.	1.7	30
41	Heterologous expression of bovine and porcine Î2-lactoglobulins in Pichia pastoris: towards a comparative functional characterisation. Journal of Biotechnology, 2004, 109, 169-178.	1.9	8
42	Monitoring the transport of recombinantCandida rugosalipase by a green fluorescent protein-lipase fusion. Biotechnology Letters, 2003, 25, 1945-1948.	1.1	9
43	Blocking the tunnel: engineering of Candida rugosa lipase mutants with short chain length specificity. Protein Engineering, Design and Selection, 2002, 15, 595-601.	1.0	100
44	High lipase production by Candida rugosa is associated with G1 cells. A flow cytometry study. Biotechnology Letters, 2001, 23, 1803-1808.	1.1	4
45	Mutants provide evidence of the importance of glycosydic chains in the activation of lipase 1 from <i>Candida rugosa</i>. Protein Science, 2000, 9, 985-990.	3.1	34
46	Characterization of the Candida rugosa lipase system and overexpression of the lip1 isoenzyme in a non-conventional yeast. Chemistry and Physics of Lipids, 1998, 93, 47-55.	1.5	23
47	Physiological control on the expression and secretion of Candida rugosa lipase. Chemistry and Physics of Lipids, 1998, 93, 143-148.	1.5	71
48	Design, total synthesis, and functional overexpression of the Candida rugosa lipl gene coding for a major industrial lipase. Protein Science, 1998, 7, 1415-1422.	3.1	114
49	Title is missing!. Biotechnology Letters, 1997, 11, 689-695.	0.5	31
50	Effect of the leader sequence on the expression of recombinant C. rugosa lipase by S. cerevisiae cells. Biotechnology Letters, 1996, 18, 281.	1.1	16
51	Localization of lipase genes on Candida rugosa chromosomes. Current Genetics, 1995, 28, 454-457.	0.8	32
52	Variability within the Candida rugosa Upases family. Protein Engineering, Design and Selection, 1994, 7, 531-535.	1.0	97
53	Cloning and analysis of Candida cylindracea lipase sequences. Gene, 1993, 124, 45-55.	1.0	131
54	A homozygous missense arginine to histidine substitution at position 482 of the ?-galactosidase in an Italian infantile GM1-gangliosidosis patient. Human Genetics, 1992, 90, 247-50.	1.8	19