

Nicola Pozzi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8286813/publications.pdf>

Version: 2024-02-01

59
papers

1,562
citations

304743

22
h-index

345221

36
g-index

63
all docs

63
docs citations

63
times ranked

2048
citing authors

#	ARTICLE	IF	CITATIONS
1	Anti-Phospholipid Antibodies in COVID-19 Are Different From Those Detectable in the Anti-Phospholipid Syndrome. <i>Frontiers in Immunology</i> , 2020, 11, 584241.	4.8	137
2	Endocrine Disruption of Androgenic Activity by Perfluoroalkyl Substances: Clinical and Experimental Evidence. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019, 104, 1259-1271.	3.6	102
3	Essential role of conformational selection in ligand binding. <i>Biophysical Chemistry</i> , 2014, 186, 13-21.	2.8	92
4	Conformational selection in trypsin-like proteases. <i>Current Opinion in Structural Biology</i> , 2012, 22, 421-431.	5.7	79
5	Antibodies to Domain I of β_2 Glycoprotein I are in close relation to patients risk categories in Antiphospholipid Syndrome (APS). <i>Thrombosis Research</i> , 2011, 128, 583-586.	1.7	68
6	Histone H4 Promotes Prothrombin Autoactivation. <i>Journal of Biological Chemistry</i> , 2013, 288, 35749-35757.	3.4	57
7	Formation of methionine sulfoxide by peroxynitrite at position 1606 of von Willebrand factor inhibits its cleavage by ADAMTS-13: A new prothrombotic mechanism in diseases associated with oxidative stress. <i>Free Radical Biology and Medicine</i> , 2010, 48, 446-456.	2.9	56
8	Lupus anticoagulant identifies two distinct groups of patients with different antibody patterns. <i>Thrombosis Research</i> , 2018, 172, 172-178.	1.7	49
9	Crystallographic and Kinetic Evidence of Allostery in a Trypsin-like Protease. <i>Biochemistry</i> , 2011, 50, 6301-6307.	2.5	44
10	Multiple-Organ Complement Deposition on Vascular Endothelium in COVID-19 Patients. <i>Biomedicines</i> , 2021, 9, 1003.	3.2	44
11	Crystal Structure of Prothrombin Reveals Conformational Flexibility and Mechanism of Activation. <i>Journal of Biological Chemistry</i> , 2013, 288, 22734-22744.	3.4	42
12	Crystal Structures of Prethrombin-2 Reveal Alternative Conformations under Identical Solution Conditions and the Mechanism of Zymogen Activation. <i>Biochemistry</i> , 2011, 50, 10195-10202.	2.5	40
13	Apolipoprotein L1 confers pH-switchable ion permeability to phospholipid vesicles. <i>Journal of Biological Chemistry</i> , 2017, 292, 18344-18353.	3.4	39
14	Autoactivation of Thrombin Precursors. <i>Journal of Biological Chemistry</i> , 2013, 288, 11601-11610.	3.4	37
15	The linker connecting the two kringles plays a key role in prothrombin activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7630-7635.	7.1	37
16	Fibrinogen-elongated β_3 Chain Inhibits Thrombin-induced Platelet Response, Hindering the Interaction with Different Receptors. <i>Journal of Biological Chemistry</i> , 2008, 283, 30193-30204.	3.4	34
17	How the Linker Connecting the Two Kringles Influences Activation and Conformational Plasticity of Prothrombin. <i>Journal of Biological Chemistry</i> , 2016, 291, 6071-6082.	3.4	28
18	Structure of prothrombin in the closed form reveals new details on the mechanism of activation. <i>Scientific Reports</i> , 2018, 8, 2945.	3.3	28

#	ARTICLE	IF	CITATIONS
19	Î2-Glycoprotein I binds to thrombin and selectively inhibits the enzyme procoagulant functions. <i>Journal of Thrombosis and Haemostasis</i> , 2013, 11, 1093-1102.	3.8	27
20	Structure of Coagulation Factor II: Molecular Mechanism of Thrombin Generation and Development of Next-Generation Anticoagulants. <i>Frontiers in Medicine</i> , 2018, 5, 281.	2.6	27
21	Structural Architecture of Prothrombin in Solution Revealed by Single Molecule Spectroscopy. <i>Journal of Biological Chemistry</i> , 2016, 291, 18107-18116.	3.4	26
22	Redesigning allosteric activation in an enzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5221-5225.	7.1	25
23	Chemical synthesis and characterization of wild-type and biotinylated N-terminal domain 1-64 of Î2-glycoprotein I. <i>Protein Science</i> , 2010, 19, 1065-1078.	7.6	23
24	Exposure of R169 controls protein C activation and autoactivation. <i>Blood</i> , 2012, 120, 664-670.	1.4	23
25	Thrombin Inhibition by Serpins Disrupts Exosite II. <i>Journal of Biological Chemistry</i> , 2010, 285, 38621-38629.	3.4	21
26	Rigidification of the autolysis loop enhances Na ⁺ binding to thrombin. <i>Biophysical Chemistry</i> , 2011, 159, 6-13.	2.8	21
27	Discovery and characterization of 2 novel subpopulations of aPS/PT antibodies in patients at high risk of thrombosis. <i>Blood Advances</i> , 2019, 3, 1738-1749.	5.2	20
28	The J-elongated conformation of Î2-glycoprotein I predominates in solution: implications for our understanding of antiphospholipid syndrome. <i>Journal of Biological Chemistry</i> , 2020, 295, 10794-10806.	3.4	20
29	Oxidation of Met1606 in von Willebrand factor is a risk factor for thrombotic and septic complications in chronic renal failure. <i>Biochemical Journal</i> , 2012, 442, 423-432.	3.7	18
30	Oxidized von Willebrand factor is efficiently cleaved by serine proteases from primary granules of leukocytes: divergence from ADAMTS-13. <i>Journal of Thrombosis and Haemostasis</i> , 2011, 9, 1620-1627.	3.8	17
31	Loop Electrostatics Asymmetry Modulates the Preexisting Conformational Equilibrium in Thrombin. <i>Biochemistry</i> , 2016, 55, 3984-3994.	2.5	17
32	Molecular mapping of Î±-thrombin (Î±T)/Î2-glycoprotein I (Î2Gpl) interaction reveals how Î2Gpl affects Î±T functions. <i>Biochemical Journal</i> , 2016, 473, 4629-4650.	3.7	16
33	Complement Activation and Thrombin Generation by MBL Bound to Î2-Glycoprotein I. <i>Journal of Immunology</i> , 2020, 205, 1385-1392.	0.8	16
34	RNase A oligomerization through 3D domain swapping is favoured by a residue located far from the swapping domains. <i>Biochimie</i> , 2011, 93, 1846-1857.	2.6	14
35	A Multimodality Approach to Assessing Factor I Genetic Variants in Atypical Hemolytic Uremic Syndrome. <i>Kidney International Reports</i> , 2019, 4, 1007-1017.	0.8	14
36	Bioorthogonal Chemistry Enables Single-Molecule FRET Measurements of Catalytically Active Protein Disulfide Isomerase. <i>ChemBioChem</i> , 2021, 22, 134-138.	2.6	14

#	ARTICLE	IF	CITATIONS
37	Reversible covalent direct thrombin inhibitors. PLoS ONE, 2018, 13, e0201377.	2.5	13
38	Why Ser and Not Thr Brokers Catalysis in the Trypsin Fold. Biochemistry, 2015, 54, 1457-1464.	2.5	12
39	Development of Nanosilicate-Hydrogel Composites for Sustained Delivery of Charged Biopharmaceutics. ACS Applied Materials & Interfaces, 2021, 13, 27880-27894.	8.0	12
40	Conformational and biochemical characterization of a biologically active rat recombinant Protease Nexin-1 expressed in E. coli. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 602-614.	2.3	11
41	Prothrombin structure: unanticipated features and opportunities. Expert Review of Proteomics, 2014, 11, 653-655.	3.0	11
42	Peptide ligand-based ELISA reagents for antibody detection. Analytical Biochemistry, 2018, 559, 55-61.	2.4	11
43	Enhancing the anticoagulant profile of meizothrombin. Biomolecular Concepts, 2018, 9, 169-175.	2.2	10
44	An allosteric redox switch in domain V of Î²2-glycoprotein I controls membrane binding and anti-domain I autoantibody recognition. Journal of Biological Chemistry, 2021, 297, 100890.	3.4	10
45	Reduction of protein disulfide isomerase results in open conformations and stimulates dynamic exchange between structural ensembles. Journal of Biological Chemistry, 2022, 298, 102217.	3.4	10
46	VE-1902-A direct thrombin inhibitor with reversible covalent mechanism of action shows efficacy with reduced bleeding in rodent models of thrombosis. Thrombosis Research, 2020, 190, 112-121.	1.7	8
47	Granzyme A Produced by Î³Î² T Cells Activates ER Stress Responses and ATP Production, and Protects Against Intracellular Mycobacterial Replication Independent of Enzymatic Activity. Frontiers in Immunology, 2021, 12, 712678.	4.8	8
48	Modeling ADAMTS13-von Willebrand Factor interaction: Implications for oxidative stress-related cardiovascular diseases and type 2A von Willebrand Disease. Biophysical Chemistry, 2012, 160, 1-11.	2.8	7
49	Costimulatory Effects of an Immunodominant Parasite Antigen Paradoxically Prevent Induction of Optimal CD8 T Cell Protective Immunity. PLoS Pathogens, 2016, 12, e1005896.	4.7	7
50	Rational Design of Protein C Activators. Scientific Reports, 2017, 7, 44596.	3.3	6
51	A Novel ELISA Assay for the Detection of Anti-Prothrombin Antibodies in Antiphospholipid Syndrome Patients at High Risk of Thrombosis. Frontiers in Immunology, 2021, 12, 741589.	4.8	6
52	WEDGE: an anticoagulant thrombin mutant produced by autoactivation. Journal of Thrombosis and Haemostasis, 2015, 13, 111-114.	3.8	5
53	Dual effect of histone H4 on prothrombin activation. Journal of Thrombosis and Haemostasis, 2016, 14, 1814-1818.	3.8	5
54	Post-Transplant Thrombotic Microangiopathy due to a Pathogenic Mutation in Complement Factor I in a Patient With Membranous Nephropathy: Case Report and Review of Literature. Frontiers in Immunology, 0, 13, .	4.8	5

#	ARTICLE	IF	CITATIONS
55	Protein engineering by chemical methods: Incorporation of nonnatural amino acids as a tool for studying protein folding, stability, and function. <i>Peptide Science</i> , 2018, 110, e24090.	1.8	4
56	Alpha-hydroxytropolones are noncompetitive inhibitors of human RNase H1 that bind to the active site and modulate substrate binding. <i>Journal of Biological Chemistry</i> , 2022, 298, 101790.	3.4	1
57	The Fibrinogen Elongated Î³-Chain Inhibits Thrombin-Induced Platelet Response, Hindering the Interaction with Different Receptors.. <i>Blood</i> , 2008, 112, 2023-2023.	1.4	0
58	X-Ray Crystallographic and Single-Molecule Fluorescence Studies of Beta-2 Glycoprotein I Reveal an Alternative Mechanism of Autoantibody Recognition. <i>Blood</i> , 2019, 134, 91-91.	1.4	0
59	Î±-hydroxytropolones Inhibit RNase H1 Noncompetitively Despite Binding in the Active Site. <i>FASEB Journal</i> , 2022, 36, .	0.5	0