Enrico Di Cera

List of Publications by Year
in descending order

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		81900	98798
107	4,914	39	67
papers	citations	h-index	g-index

112	112	112	4149
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The active site region plays a critical role in Na+ binding to thrombin. Journal of Biological Chemistry, 2022, 298, 101458.	3.4	4
2	Cryo-EM structure of the prothrombin-prothrombinase complex. Blood, 2022, 139, 3463-3473.	1.4	19
3	Cryo-EM structures of human coagulation factors V and Va. Blood, 2021, 137, 3137-3144.	1.4	29
4	Role of sequence and position of the cleavage sites in prothrombin activation. Journal of Biological Chemistry, 2021, 297, 100955.	3.4	8
5	Zymogen and activated protein C have similar structural architecture. Journal of Biological Chemistry, 2020, 295, 15236-15244.	3.4	8
6	19F NMR reveals the conformational properties of free thrombin and its zymogen precursor prethrombin-2. Journal of Biological Chemistry, 2020, 295, 8227-8235.	3.4	7
7	Mechanisms of ligand binding. Biophysics Reviews, 2020, 1, 011303.	2.7	33
8	VE-1902â€"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
9	Role of the activation peptide in the mechanism of protein C activation. Scientific Reports, 2020, 10, 11079.	3.3	10
10	Residues W215, E217 and E192 control the allosteric E*-E equilibrium of thrombin. Scientific Reports, 2019, 9, 12304.	3.3	7
11	Probing prothrombin structure by limited proteolysis. Scientific Reports, 2019, 9, 6125.	3.3	7
12	Role of the I16-D194 ionic interaction in the trypsin fold. Scientific Reports, 2019, 9, 18035.	3.3	9
13	Structure of prothrombin in the closed form reveals new details on the mechanism of activation. Scientific Reports, 2018, 8, 2945.	3.3	28
14	Interplay between conformational selection and zymogen activation. Scientific Reports, 2018, 8, 4080.	3.3	22
15	Enhancing the anticoagulant profile of meizothrombin. Biomolecular Concepts, 2018, 9, 169-175.	2.2	10
16	Reversible covalent direct thrombin inhibitors. PLoS ONE, 2018, 13, e0201377.	2.5	13
17	Intrinsic thermodynamics of high affinity inhibitor binding to recombinant human carbonic anhydrase IV. European Biophysics Journal, 2018, 47, 271-290.	2.2	14
18	Induced Fit Is a Special Case of Conformational Selection. Biochemistry, 2017, 56, 2853-2859.	2.5	39

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19	Rational Design of Protein C Activators. Scientific Reports, 2017, 7, 44596.	3.3	6
20	Molecular Mechanisms of Enzyme Activation by Monovalent Cations. Journal of Biological Chemistry, 2016, 291, 20840-20848.	3.4	80
21	Thrombin Cleavage of Plasmodium falciparum Erythrocyte Membrane Protein 1 Inhibits Cytoadherence. MBio, 2016, 7, .	4.1	9
22	Structural Architecture of Prothrombin in Solution Revealed by Single Molecule Spectroscopy. Journal of Biological Chemistry, 2016, 291, 18107-18116.	3.4	26
23	Data publication with the structural biology data grid supports live analysis. Nature Communications, 2016, 7, 10882.	12.8	113
24	Loop Electrostatics Asymmetry Modulates the Preexisting Conformational Equilibrium in Thrombin. Biochemistry, 2016, 55, 3984-3994.	2.5	17
25	How the Linker Connecting the Two Kringles Influences Activation and Conformational Plasticity of Prothrombin. Journal of Biological Chemistry, 2016, 291, 6071-6082.	3.4	28
26	Potassium and the K+/H+ Exchanger Kha1p Promote Binding of Copper to ApoFet3p Multi-copper Ferroxidase. Journal of Biological Chemistry, 2016, 291, 9796-9806.	3.4	20
27	Why Ser and Not Thr Brokers Catalysis in the Trypsin Fold. Biochemistry, 2015, 54, 1457-1464.	2.5	12
28	John A. Schellman, 1924â€“2014. Biophysical Chemistry, 2015, 199, 51.	2.8	0
29	Kinetic Dissection of the Pre-existing Conformational Equilibrium in the Trypsin Fold. Journal of Biological Chemistry, 2015, 290, 22435-22445.	3.4	31
30	Prothrombin structure: unanticipated features and opportunities. Expert Review of Proteomics, 2014, 11, 653-655.	3.0	11
31	The linker connecting the two kringles plays a key role in prothrombin activation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7630-7635.	7.1	37
32	Essential role of conformational selection in ligand binding. Biophysical Chemistry, 2014, 186, 13-21.	2.8	92
33	Special issue on conformational selection. Biophysical Chemistry, 2014, 186, 1-2.	2.8	3
34	Conformational Selection Is a Dominant Mechanism of Ligand Binding. Biochemistry, 2013, 52, 5723-5729.	2.5	110
35	Crystal Structure of Prothrombin Reveals Conformational Flexibility and Mechanism of Activation. Journal of Biological Chemistry, 2013, 288, 22734-22744.	3.4	42
36	Rapid Interruption Of Occlusive Thrombus Formation By The Protein C Activator Enzyme EWE Thrombin (ProCase) In Primates. Blood, 2013, 122, 202-202.	1.4	0

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37	In vitro veritas: 90 years of biochemistry at Saint Louis University. Missouri Medicine, 2013, 110, 297-301.	0.3	0
38	Conformational Selection or Induced Fit? A Critical Appraisal of the Kinetic Mechanism. Biochemistry, 2012, 51, 5894-5902.	2.5	269
39	Conformational selection in trypsin-like proteases. Current Opinion in Structural Biology, 2012, 22, 421-431.	5.7	79
40	Exposure of R169 controls protein C activation and autoactivation. Blood, 2012, 120, 664-670.	1.4	23
41	Crystal Structures of Prethrombin-2 Reveal Alternative Conformations under Identical Solution Conditions and the Mechanism of Zymogen Activation. Biochemistry, 2011, 50, 10195-10202.	2.5	40
42	Crystallographic and Kinetic Evidence of Allostery in a Trypsin-like Protease. Biochemistry, 2011, 50, 6301-6307.	2.5	44
43	Allostery in trypsin-like proteases suggests new therapeutic strategies. Trends in Biotechnology, 2011, 29, 577-585.	9.3	80
44	Rigidification of the autolysis loop enhances Na+ binding to thrombin. Biophysical Chemistry, 2011, 159, 6-13.	2.8	21
45	Structural basis of thrombinâ€“proteaseâ€activated receptor interactions. IUBMB Life, 2011, 63, 375-382.	3.4	25
46	Introduction to mini-theme issue on â€œprotease-activated receptor signalingâ€• IUBMB Life, 2011, 63, 373-374.	3.4	0
47	Thrombin as an Anticoagulant. Progress in Molecular Biology and Translational Science, 2011, 99, 145-184.	1.7	17
48	Crystal structure of prethrombin-1. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 19278-19283.	7.1	37
49	Crystal Structure of Thrombin Bound to the Uncleaved Extracellular Fragment of PAR1. Journal of Biological Chemistry, 2010, 285, 15393-15398.	3.4	56
50	Engineering Thrombin for Selective Specificity toward Protein C and PAR1. Journal of Biological Chemistry, 2010, 285, 19145-19152.	3.4	38
51	Evidence of the E*â^'E Equilibrium from Rapid Kinetics of Na⁺ Binding to Activated Protein C and Factor Xa*. Journal of Physical Chemistry B, 2010, 114, 16125-16130.	2.6	20
52	Combinatorial Enzyme Design Probes Allostery and Cooperativity in the Trypsin Fold. Journal of Molecular Biology, 2010, 399, 306-319.	4.2	9
53	Mutant N143P Reveals How Na+ Activates Thrombin. Journal of Biological Chemistry, 2009, 284, 36175-36185.	3.4	31
54	Mechanism of the Anticoagulant Activity of Thrombin Mutant W215A/E217A. Journal of Biological Chemistry, 2009, 284, 24098-24105.	3.4	23

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55	Serine proteases. IUBMB Life, 2009, 61, 510-515.	3.4	306
56	Serine proteases. IUBMB Life, 2009, 61, spcone-spcone.	3.4	0
57	Kinetics of Allosteric Activation. Methods in Enzymology, 2009, 466, 259-271.	1.0	6
58	How I became a biochemist. IUBMB Life, 2008, 60, 859-861.	3.4	0
59	Thrombin. Molecular Aspects of Medicine, 2008, 29, 203-254.	6.4	282
60	Thrombin Mutant W215A/E217A Acts as a Platelet GPIb Antagonist. Arteriosclerosis, Thrombosis, and Vascular Biology, 2008, 28, 329-334.	2.4	41
61	Important Role of the Cys-191â€“Cys-220 Disulfide Bond in Thrombin Function and Allostery. Journal of Biological Chemistry, 2007, 282, 27165-27170.	3.4	29
62	Relative antithrombotic and antihemostatic effects of protein C activator versus low-molecular-weight heparin in primates. Blood, 2007, 109, 3733-3740.	1.4	49
63	Thrombin allostery. Physical Chemistry Chemical Physics, 2007, 9, 1291.	2.8	46
64	Mechanism of Na+ binding to thrombin resolved by ultra-rapid kinetics. Biophysical Chemistry, 2007, 131, 111-114.	2.8	26
65	Mutation of W215 Compromises Thrombin Cleavage of Fibrinogen, but Not of PAR1 or Protein C. Annals of the New York Academy of Sciences, 2006, 936, 456-458.	3.8	1
66	Thrombin: A paradigm for enzymes allosterically activated by monovalent cations. Rendiconti Lincei, 2006, 17, 97-113.	2.2	1
67	A Structural Perspective on Enzymes Activated by Monovalent Cations. Journal of Biological Chemistry, 2006, 281, 1305-1308.	3.4	115
68	Crystal Structure of Thrombin in a Self-inhibited Conformation. Journal of Biological Chemistry, 2006, 281, 32922-32928.	3.4	45
69	Rapid Kinetics of Na+ Binding to Thrombin. Journal of Biological Chemistry, 2006, 281, 40049-40056.	3.4	62
70	Safe Interruption of Ongoing Thrombosis by the Protein C Activator Thrombin Analog, W215A/E217A; a Comparison to Enoxaparin in Primates.. Blood, 2006, 108, 909-909.	1.4	2
71	Thrombomodulin-Dependent Protein C Activator Treatment Improves the Short-Term Outcome of Experimental Ischemic Stroke in Mice.. Blood, 2006, 108, 895-895.	1.4	0
72	Thrombomodulin Changes the Molecular Surface of Interaction and the Rate of Complex Formation between Thrombin and Protein C. Journal of Biological Chemistry, 2005, 280, 7956-7961.	3.4	46

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73	Efficient Barrier Protective Signaling by Activated Protein C Is Mechanistically Linked to Protein C Activation on Endothelial Cells.. Blood, 2005, 106, 28-28.	1.4	1
74	The Conformation of the Activation Peptide of Protein C Is Influenced by Ca2+ and Na+ Binding. Journal of Biological Chemistry, 2004, 279, 38519-38524.	3.4	32
75	Molecular Dissection of Na+ Binding to Thrombin. Journal of Biological Chemistry, 2004, 279, 31842-31853.	3.4	161
76	The Anticoagulant Thrombin Mutant W215A/E217A Has a Collapsed Primary Specificity Pocket. Journal of Biological Chemistry, 2004, 279, 39824-39828.	3.4	51
77	Thrombin: a paradigm for enzymes allosterically activated by monovalent cations. Comptes Rendus - Biologies, 2004, 327, 1065-1076.	0.2	29
78	Sustained Pharmacological Activation of Protein C (PC) in Baboons.. Blood, 2004, 104, 3499-3499.	1.4	0
79	Thrombin Interactions. Chest, 2003, 124, 11S-17S.	0.8	115
80	The Thrombin Mutant W215A/E217A Shows Safe and Potent Anticoagulant and Antithrombotic Effects in Vivo. Journal of Biological Chemistry, 2002, 277, 27581-27584.	3.4	71
81	Evolution of enzyme cascades from embryonic development to blood coagulation. Trends in Biochemical Sciences, 2002, 27, 67-74.	7.5	301
82	Dissecting substrate recognition by thrombin using the inactive mutant S195A. Biophysical Chemistry, 2002, 100, 315-323.	2.8	29
83	Replacement of thrombin residue G184 with Lys or Arg fails to mimic Na+ binding. Proteins: Structure, Function and Bioinformatics, 2001, 43, 315-318.	2.6	7
84	Molecular mapping of thrombin-receptor interactions. Proteins: Structure, Function and Bioinformatics, 2001, 45, 107-116.	2.6	99
85	Determinants of Thrombin Specificity. Annals of the New York Academy of Sciences, 2001, 936, 133-146.	3.8	26
86	A simple method for the determination of individual rate constants for substrate hydrolysis by serine proteases. Protein Science, 2000, 9, 1589-1593.	7.6	47
87	Rational Design of a Potent Anticoagulant Thrombin. Journal of Biological Chemistry, 2000, 275, 39827-39830.	3.4	78
88	Mutation of W215 Compromises Thrombin Cleavage of Fibrinogen, but Not of PAR-1 or Protein Câ€. Biochemistry, 2000, 39, 8095-8101.	2.5	51
89	Role of residue Y99 in tissue plasminogen activator. Protein Science, 2000, 9, 619-622.	7.6	6
90	Defining epitopes: It's not as easy as it seems. Nature Biotechnology, 1999, 17, 936-937.	17.5	64

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91	Conserved water molecules in the specificity pocket of serine proteases and the molecular mechanism of Na+ binding. , 1998, 30, 34-42.		42
92	Role of P225 and the C136â€€201 disulfide bond in tissue plasminogen activator. Protein Science, 1998, 7, 1728-1737.	7.6	20
93	Histoplasma acquisition of calcium and expression of CBP1 during intracellular parasitism. Molecular Microbiology, 1998, 27, 531-539.	2.5	65
94	Synthesis and Characterization of More Potent Analogues of Hirudin Fragment 1â˜47 Containing Non-Natural Amino Acids,. Biochemistry, 1998, 37, 13507-13515.	2.5	35
95	Site-Specific Thermodynamics:Â Understanding Cooperativity in Molecular Recognition. Chemical Reviews, 1998, 98, 1563-1592.	47.7	82
96	Site-Specific Analysis of Mutational Effects in Proteins. Advances in Protein Chemistry, 1998, 51, 59-119.	4.4	44
97	Kinetic Pathway for the Slow to Fast Transition of Thrombin. Journal of Biological Chemistry, 1997, 272, 30275-30282.	3.4	49
98	Energetics of Thrombinâ˜Thrombomodulin Interaction. Biochemistry, 1997, 36, 6674-6681.	2.5	66
99	Site-specific dissection of substrate recognition by thrombin. Nature Biotechnology, 1997, 15, 891-895.	17.5	60
100	Rational engineering of activity and specificity in a serine protease. Nature Biotechnology, 1997, 15, 146-149.	17.5	101
101	Release of Fibrinopeptides by the Slow and Fast Forms of Thrombinâ€. Biochemistry, 1996, 35, 4417-4426.	2.5	84
102	Site-Specific thermodynamics of ising networks: A theorem for linearly connected subsystems. Biopolymers, 1994, 34, 673-678.	2.4	5
103	Thermodynamic basis of site-specific cooperativity. Biopolymers, 1994, 34, 1001-1005.	2.4	2
104	Looking at Fokker-Planck dynamics with a noisy instrument. Journal of Statistical Physics, 1993, 71, 1179-1190.	1.2	2
105	Meanâ€field treatment of local binding processes. Journal of Chemical Physics, 1992, 96, 6515-6522.	3.0	9
106	Thrombin is a sodium ion activated enzyme. Biochemistry, 1992, 31, 11721-11730.	2.5	247
107	Stochastic linkage: Effect of random fluctuations on a twoâ€state process. Journal of Chemical Physics, 1991, 95, 5082-5086.	3.0	47