## Enrico Di Cera

## List of Publications by Year in descending order

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81900 98798 4,914 107 39 67 citations g-index h-index papers 112 112 112 4149 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Serine proteases. IUBMB Life, 2009, 61, 510-515.	3.4	306
2	Evolution of enzyme cascades from embryonic development to blood coagulation. Trends in Biochemical Sciences, 2002, 27, 67-74.	7.5	301
3	Thrombin. Molecular Aspects of Medicine, 2008, 29, 203-254.	6.4	282
4	Conformational Selection or Induced Fit? A Critical Appraisal of the Kinetic Mechanism. Biochemistry, 2012, 51, 5894-5902.	2.5	269
5	Thrombin is a sodium ion activated enzyme. Biochemistry, 1992, 31, 11721-11730.	2.5	247
6	Molecular Dissection of Na+ Binding to Thrombin. Journal of Biological Chemistry, 2004, 279, 31842-31853.	3.4	161
7	Thrombin Interactions. Chest, 2003, 124, 11S-17S.	0.8	115
8	A Structural Perspective on Enzymes Activated by Monovalent Cations. Journal of Biological Chemistry, 2006, 281, 1305-1308.	3.4	115
9	Data publication with the structural biology data grid supports live analysis. Nature Communications, 2016, 7, 10882.	12.8	113
10	Conformational Selection Is a Dominant Mechanism of Ligand Binding. Biochemistry, 2013, 52, 5723-5729.	2.5	110
11	Rational engineering of activity and specificity in a serine protease. Nature Biotechnology, 1997, 15, 146-149.	17.5	101
12	Molecular mapping of thrombin-receptor interactions. Proteins: Structure, Function and Bioinformatics, 2001, 45, 107-116.	2.6	99
13	Essential role of conformational selection in ligand binding. Biophysical Chemistry, 2014, 186, 13-21.	2.8	92
14	Release of Fibrinopeptides by the Slow and Fast Forms of Thrombinâ€. Biochemistry, 1996, 35, 4417-4426.	2.5	84
15	Site-Specific Thermodynamics:Â Understanding Cooperativity in Molecular Recognition. Chemical Reviews, 1998, 98, 1563-1592.	47.7	82
16	Allostery in trypsin-like proteases suggests new therapeutic strategies. Trends in Biotechnology, 2011, 29, 577-585.	9.3	80
17	Molecular Mechanisms of Enzyme Activation by Monovalent Cations. Journal of Biological Chemistry, 2016, 291, 20840-20848.	3.4	80
18	Conformational selection in trypsin-like proteases. Current Opinion in Structural Biology, 2012, 22, 421-431.	5.7	79

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19	Rational Design of a Potent Anticoagulant Thrombin. Journal of Biological Chemistry, 2000, 275, 39827-39830.	3.4	78
20	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
21	Energetics of Thrombinâ^'Thrombomodulin Interaction. Biochemistry, 1997, 36, 6674-6681.	2.5	66
22	Histoplasma acquisition of calcium and expression of CBP1 during intracellular parasitism. Molecular Microbiology, 1998, 27, 531-539.	2.5	65
23	Defining epitopes: It's not as easy as it seems. Nature Biotechnology, 1999, 17, 936-937.	17.5	64
24	Rapid Kinetics of Na+ Binding to Thrombin. Journal of Biological Chemistry, 2006, 281, 40049-40056.	3.4	62
25	Site-specific dissection of substrate recognition by thrombin. Nature Biotechnology, 1997, 15, 891-895.	17.5	60
26	Crystal Structure of Thrombin Bound to the Uncleaved Extracellular Fragment of PAR1. Journal of Biological Chemistry, 2010, 285, 15393-15398.	3.4	56
27	Mutation of W215 Compromises Thrombin Cleavage of Fibrinogen, but Not of PAR-1 or Protein Câ€. Biochemistry, 2000, 39, 8095-8101.	2.5	51
28	The Anticoagulant Thrombin Mutant W215A/E217A Has a Collapsed Primary Specificity Pocket. Journal of Biological Chemistry, 2004, 279, 39824-39828.	3.4	51
29	Kinetic Pathway for the Slow to Fast Transition of Thrombin. Journal of Biological Chemistry, 1997, 272, 30275-30282.	3.4	49
30	Relative antithrombotic and antihemostatic effects of protein C activator versus low-molecular-weight heparin in primates. Blood, 2007, 109, 3733-3740.	1,4	49
31	Stochastic linkage: Effect of random fluctuations on a twoâ€state process. Journal of Chemical Physics, 1991, 95, 5082-5086.	3.0	47
32	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
33	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
34	Thrombin allostery. Physical Chemistry Chemical Physics, 2007, 9, 1291.	2.8	46
35	Crystal Structure of Thrombin in a Self-inhibited Conformation. Journal of Biological Chemistry, 2006, 281, 32922-32928.	3.4	45
36	Site-Specific Analysis of Mutational Effects in Proteins. Advances in Protein Chemistry, 1998, 51, 59-119.	4.4	44

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37	Crystallographic and Kinetic Evidence of Allostery in a Trypsin-like Protease. Biochemistry, 2011, 50, 6301-6307.	2.5	44
38	Conserved water molecules in the specificity pocket of serine proteases and the molecular mechanism of Na+ binding., 1998, 30, 34-42.		42
39	Crystal Structure of Prothrombin Reveals Conformational Flexibility and Mechanism of Activation. Journal of Biological Chemistry, 2013, 288, 22734-22744.	3.4	42
40	Thrombin Mutant W215A/E217A Acts as a Platelet GPIb Antagonist. Arteriosclerosis, Thrombosis, and Vascular Biology, 2008, 28, 329-334.	2.4	41
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	Induced Fit Is a Special Case of Conformational Selection. Biochemistry, 2017, 56, 2853-2859.	2.5	39
43	Engineering Thrombin for Selective Specificity toward Protein C and PAR1. Journal of Biological Chemistry, 2010, 285, 19145-19152.	3.4	38
44	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
45	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
46	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
47	Mechanisms of ligand binding. Biophysics Reviews, 2020, 1, 011303.	2.7	33
48	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
49	Mutant N143P Reveals How Na+ Activates Thrombin. Journal of Biological Chemistry, 2009, 284, 36175-36185.	3.4	31
50	Kinetic Dissection of the Pre-existing Conformational Equilibrium in the Trypsin Fold. Journal of Biological Chemistry, 2015, 290, 22435-22445.	3.4	31
51	Dissecting substrate recognition by thrombin using the inactive mutant S195A. Biophysical Chemistry, 2002, 100, 315-323.	2.8	29
52	Thrombin: a paradigm for enzymes allosterically activated by monovalent cations. Comptes Rendus - Biologies, 2004, 327, 1065-1076.	0.2	29
53	Important Role of the Cys-191–Cys-220 Disulfide Bond in Thrombin Function and Allostery. Journal of Biological Chemistry, 2007, 282, 27165-27170.	3.4	29
54	Cryo-EM structures of human coagulation factors V and Va. Blood, 2021, 137, 3137-3144.	1.4	29

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55	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
56	Structure of prothrombin in the closed form reveals new details on the mechanism of activation. Scientific Reports, 2018, 8, 2945.	3.3	28
57	Determinants of Thrombin Specificity. Annals of the New York Academy of Sciences, 2001, 936, 133-146.	3.8	26
58	Mechanism of Na+ binding to thrombin resolved by ultra-rapid kinetics. Biophysical Chemistry, 2007, 131, 111-114.	2.8	26
59	Structural Architecture of Prothrombin in Solution Revealed by Single Molecule Spectroscopy. Journal of Biological Chemistry, 2016, 291, 18107-18116.	3.4	26
60	Structural basis of thrombin–proteaseâ€activated receptor interactions. IUBMB Life, 2011, 63, 375-382.	3.4	25
61	Mechanism of the Anticoagulant Activity of Thrombin Mutant W215A/E217A. Journal of Biological Chemistry, 2009, 284, 24098-24105.	3.4	23
62	Exposure of R169 controls protein C activation and autoactivation. Blood, 2012, 120, 664-670.	1.4	23
63	Interplay between conformational selection and zymogen activation. Scientific Reports, 2018, 8, 4080.	3.3	22
64	Rigidification of the autolysis loop enhances Na+ binding to thrombin. Biophysical Chemistry, 2011, 159, 6-13.	2.8	21
65	Role of P225 and the C136â€C201 disulfide bond in tissue plasminogen activator. Protein Science, 1998, 7, 1728-1737.	7.6	20
66	Evidence of the E*â^'E Equilibrium from Rapid Kinetics of Na <sup>+</sup> Binding to Activated Protein C and Factor Xa*. Journal of Physical Chemistry B, 2010, 114, 16125-16130.	2.6	20
67	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
68	Cryo-EM structure of the prothrombin-prothrombinase complex. Blood, 2022, 139, 3463-3473.	1.4	19
69	Thrombin as an Anticoagulant. Progress in Molecular Biology and Translational Science, 2011, 99, 145-184.	1.7	17
70	Loop Electrostatics Asymmetry Modulates the Preexisting Conformational Equilibrium in Thrombin. Biochemistry, 2016, 55, 3984-3994.	2.5	17
71	Intrinsic thermodynamics of high affinity inhibitor binding to recombinant human carbonic anhydrase IV. European Biophysics Journal, 2018, 47, 271-290.	2.2	14
72	Reversible covalent direct thrombin inhibitors. PLoS ONE, 2018, 13, e0201377.	2.5	13

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73	Why Ser and Not Thr Brokers Catalysis in the Trypsin Fold. Biochemistry, 2015, 54, 1457-1464.	2.5	12
74	Prothrombin structure: unanticipated features and opportunities. Expert Review of Proteomics, 2014, $11,653-655$ .	3.0	11
75	Enhancing the anticoagulant profile of meizothrombin. Biomolecular Concepts, 2018, 9, 169-175.	2.2	10
76	Role of the activation peptide in the mechanism of protein C activation. Scientific Reports, 2020, 10, 11079.	3.3	10
77	Meanâ€field treatment of local binding processes. Journal of Chemical Physics, 1992, 96, 6515-6522.	3.0	9
78	Combinatorial Enzyme Design Probes Allostery and Cooperativity in the Trypsin Fold. Journal of Molecular Biology, 2010, 399, 306-319.	4.2	9
79	Thrombin Cleavage of Plasmodium falciparum Erythrocyte Membrane Protein 1 Inhibits Cytoadherence. MBio, 2016, 7, .	4.1	9
80	Role of the I16-D194 ionic interaction in the trypsin fold. Scientific Reports, 2019, 9, 18035.	3.3	9
81	Zymogen and activated protein C have similar structural architecture. Journal of Biological Chemistry, 2020, 295, 15236-15244.	3.4	8
82	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
83	Role of sequence and position of the cleavage sites in prothrombin activation. Journal of Biological Chemistry, 2021, 297, 100955.	3.4	8
84	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
85	Residues W215, E217 and E192 control the allosteric E*-E equilibrium of thrombin. Scientific Reports, 2019, 9, 12304.	3.3	7
86	Probing prothrombin structure by limited proteolysis. Scientific Reports, 2019, 9, 6125.	3.3	7
87	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
88	Role of residue Y99 in tissue plasminogen activator. Protein Science, 2000, 9, 619-622.	7.6	6
89	Kinetics of Allosteric Activation. Methods in Enzymology, 2009, 466, 259-271.	1.0	6
90	Rational Design of Protein C Activators. Scientific Reports, 2017, 7, 44596.	3.3	6

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91	Site-Specific thermodynamics of ising networks: A theorem for linearly connected subsystems. Biopolymers, 1994, 34, 673-678.	2.4	5
92	The active site region plays a critical role in Na+ binding to thrombin. Journal of Biological Chemistry, 2022, 298, 101458.	3.4	4
93	Special issue on conformational selection. Biophysical Chemistry, 2014, 186, 1-2.	2.8	3
94	Looking at Fokker-Planck dynamics with a noisy instrument. Journal of Statistical Physics, 1993, 71, 1179-1190.	1.2	2
95	Thermodynamic basis of site-specific cooperativity. Biopolymers, 1994, 34, 1001-1005.	2.4	2
96	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
97	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
98	Thrombin: A paradigm for enzymes allosterically activated by monovalent cations. Rendiconti Lincei, 2006, 17, 97-113.	2.2	1
99	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
100	How I became a biochemist. IUBMB Life, 2008, 60, 859-861.	3.4	0
101	Serine proteases. IUBMB Life, 2009, 61, spcone-spcone.	3.4	O
102	Introduction to mini-theme issue on "protease-activated receptor signaling― IUBMB Life, 2011, 63, 373-374.	3.4	0
103	John A. Schellman, 1924–2014. Biophysical Chemistry, 2015, 199, 51.	2.8	0
104	Sustained Pharmacological Activation of Protein C (PC) in Baboons Blood, 2004, 104, 3499-3499.	1.4	0
105	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
106	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
107	In vitro veritas: 90 years of biochemistry at Saint Louis University. Missouri Medicine, 2013, 110, 297-301.	0.3	0