

James A Huntington

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11824403/publications.pdf>

Version: 2024-02-01

76
papers

6,005
citations

71004

43
h-index

93651

72
g-index

76
all docs

76
docs citations

76
times ranked

5531
citing authors

#	ARTICLE	IF	CITATIONS
1	Z-Î± 1</sub> -antitrypsin polymers impose molecular filtration in the endoplasmic reticulum after undergoing phase transition to a solid state. <i>Science Advances</i> , 2022, 8, eabm2094.	4.7	15
2	Characterization of the neutralizing anti-Îµmizumab antibody in a patient with hemophilia A and inhibitor. <i>Journal of Thrombosis and Haemostasis</i> , 2021, 19, 711-718.	1.9	19
3	Ixodes ricinus Salivary Serpin Iripin-8 Inhibits the Intrinsic Pathway of Coagulation and Complement. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9480.	1.8	13
4	Addendum: KotÃ¡l et al. Ixodes ricinus Salivary Serpin Iripin-8 Inhibits the Intrinsic Pathway of Coagulation and Complement. <i>Int. J. Mol. Sci.</i> 2021, 22, 9480. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11271.	1.8	0
5	Linkage analysis combined with whole-exome sequencing identifies a novel prothrombin (<i>F2</i>) gene mutation in a Dutch Caucasian family with unexplained thrombosis. <i>Haematologica</i> , 2020, 105, e370-e372.	1.7	6
6	Discovery and characterisation of an antibody that selectively modulates the inhibitory activity of plasminogen activator inhibitor-1. <i>Scientific Reports</i> , 2019, 9, 1605.	1.6	20
7	Regulatory Mechanisms in Hemostasis. , 2018, , 1906-1911.		1
8	Identification of serpins specific for activated protein C using a lysate-based screening assay. <i>Scientific Reports</i> , 2018, 8, 8793.	1.6	14
9	Structural insights unravel the zymogenic mechanism of the virulence factor gingipain K from <i>Porphyromonas gingivalis</i> , a causative agent of gum disease from the human oral microbiome. <i>Journal of Biological Chemistry</i> , 2017, 292, 5724-5735.	1.6	8
10	Targeting activated protein C to treat hemophilia. <i>Current Opinion in Hematology</i> , 2017, 24, 446-452.	1.2	38
11	<i>SERPINC1</i> gene mutations in antithrombin deficiency. <i>British Journal of Haematology</i> , 2017, 178, 279-285.	1.2	36
12	Design and characterization of an APC-specific serpin for the treatment of hemophilia. <i>Blood</i> , 2017, 129, 105-113.	0.6	119
13	Whole-exome sequencing in evaluation of patients with venous thromboembolism. <i>Blood Advances</i> , 2017, 1, 1224-1237.	2.5	55
14	Structural transitions during prothrombin activation: On the importance of fragment 2. <i>Biochimie</i> , 2016, 122, 235-242.	1.3	17
15	Structure and Mechanism of Cysteine Peptidase Gingipain K (Kgp), a Major Virulence Factor of <i>Porphyromonas gingivalis</i> in Periodontitis. <i>Journal of Biological Chemistry</i> , 2014, 289, 32291-32302.	1.6	74
16	GpIbÎ± Interacts Exclusively with Exosite II of Thrombin. <i>Journal of Molecular Biology</i> , 2014, 426, 881-893.	2.0	35
17	The Shapes of Z-Î± 1 -Antitrypsin Polymers in Solution Support the C-Terminal Domain-Swap Mechanism of Polymerization. <i>Biophysical Journal</i> , 2014, 107, 1905-1912.	0.2	13
18	A hereditary bleeding disorder resulting from a premature stop codon in thrombomodulin (p.Cys537Stop). <i>Blood</i> , 2014, 124, 1951-1956.	0.6	45

#	ARTICLE	IF	CITATIONS
19	Natural inhibitors of thrombin. <i>Thrombosis and Haemostasis</i> , 2014, 111, 583-589.	1.8	47
20	Crystal structure of the prothrombinase complex from the venom of <i>Pseudonaja textilis</i> . <i>Blood</i> , 2013, 122, 2777-2783.	0.6	62
21	Crystal structures of protease nexin-1 in complex with heparin and thrombin suggest a 2-step recognition mechanism. <i>Blood</i> , 2012, 120, 459-467.	0.6	31
22	Identification of a Catalytic Exosite for Complement Component C4 on the Serine Protease Domain of C1s. <i>Journal of Immunology</i> , 2012, 189, 2365-2373.	0.4	28
23	Thrombin plasticity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 246-252.	1.1	44
24	Molecular basis of α_1 -antitrypsin deficiency revealed by the structure of a domain-swapped trimer. <i>EMBO Reports</i> , 2011, 12, 1011-1017.	2.0	142
25	Serpin Polymerization In Vitro. <i>Methods in Enzymology</i> , 2011, 501, 379-420.	0.4	6
26	Loop-Sheet Mechanism of Serpin Polymerization Tested by Reactive Center Loop Mutations*. <i>Journal of Biological Chemistry</i> , 2010, 285, 30752-30758.	1.6	27
27	Molecular basis of factor IXa recognition by heparin-activated antithrombin revealed by a 1.7-Å structure of the ternary complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 645-650.	3.3	78
28	Serpins Flex Their Muscle. <i>Journal of Biological Chemistry</i> , 2010, 285, 24307-24312.	1.6	97
29	Thrombin Inhibition by Serpins Disrupts Exosite II. <i>Journal of Biological Chemistry</i> , 2010, 285, 38621-38629.	1.6	21
30	Serpins Flex Their Muscle. <i>Journal of Biological Chemistry</i> , 2010, 285, 24299-24305.	1.6	128
31	Molecular contortionism on the physical limits of serpin loop-sheet polymers. <i>Biological Chemistry</i> , 2010, 391, 973-82.	1.2	14
32	New insight into serpin polymerization and aggregation. <i>Prion</i> , 2009, 3, 12-14.	0.9	12
33	The Critical Role of Hinge-Region Expulsion in the Induced-Fit Heparin Binding Mechanism of Antithrombin. <i>Journal of Molecular Biology</i> , 2009, 386, 1278-1289.	2.0	51
34	Crystal structure of a stable dimer reveals the molecular basis of serpin polymerization. <i>Nature</i> , 2008, 455, 1255-1258.	13.7	236
35	How Na ⁺ activates thrombin a review of the functional and structural data. <i>Biological Chemistry</i> , 2008, 389, 1025-1035.	1.2	64
36	The Heparin Binding Site of Protein C Inhibitor Is Protease-dependent. <i>Journal of Biological Chemistry</i> , 2008, 283, 36039-36045.	1.6	31

#	ARTICLE	IF	CITATIONS
37	Molecular basis of thrombin recognition by protein C inhibitor revealed by the 1.6-Å structure of the heparin-bridged complex. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4661-4666.	3.3	59
38	Structural Insights into the Life History of Thrombin. , 2008, , 80-106.		4
39	Structure of Native Protein C Inhibitor Provides Insight into Its Multiple Functions. Journal of Biological Chemistry, 2007, 282, 13759-13768.	1.6	35
40	Sugar and alcohol molecules provide a therapeutic strategy for the serpinopathies that cause dementia and cirrhosis. FEBS Journal, 2006, 273, 2450-2552.	2.2	34
41	Thrombin-Cofactor Interactions. Arteriosclerosis, Thrombosis, and Vascular Biology, 2006, 26, 1738-1745.	1.1	90
42	Allosteric activation of antithrombin is independent of charge neutralization or reversal in the heparin binding site. FEBS Letters, 2006, 580, 4709-4712.	1.3	5
43	Antithrombinâ€™S195A factor Xa-heparin structure reveals the allosteric mechanism of antithrombin activation. EMBO Journal, 2006, 25, 2029-2037.	3.5	163
44	Shape-shifting serpins â€™ advantages of a mobile mechanism. Trends in Biochemical Sciences, 2006, 31, 427-435.	3.7	136
45	Crystal Structure of Monomeric Native Antithrombin Reveals a Novel Reactive Center Loop Conformation. Journal of Biological Chemistry, 2006, 281, 35478-35486.	1.6	59
46	Slow thrombin in solution. Biochemical Journal, 2005, 390, e1-3.	1.7	2
47	Heparin Activation of Serpins. , 2005, , 367-398.		12
48	Crystal Structure of Thrombin Bound to Heparin. Journal of Biological Chemistry, 2005, 280, 2745-2749.	1.6	133
49	Directing thrombin. Blood, 2005, 106, 2605-2612.	0.6	298
50	Crystal structure of wild-type human thrombin in the Na ⁺ -free state. Biochemical Journal, 2005, 392, 21-28.	1.7	54
51	Homozygous Deficiency of Heparin Cofactor II. Circulation, 2004, 110, 1303-1307.	1.6	43
52	The Influence of Hinge Region Residue Glu-381 on Antithrombin Allostery and Metastability. Journal of Biological Chemistry, 2004, 279, 4913-4921.	1.6	18
53	The Heparin Binding Properties of Heparin Cofactor II Suggest an Antithrombin-like Activation Mechanism. Journal of Biological Chemistry, 2004, 279, 50267-50273.	1.6	53
54	Allosteric Activation of Antithrombin Critically Depends upon Hinge Region Extension. Journal of Biological Chemistry, 2004, 279, 47288-47297.	1.6	32

#	ARTICLE	IF	CITATIONS
55	Crystal Structure of Anticoagulant Thrombin Variant E217K Provides Insights into Thrombin Allostery. <i>Journal of Biological Chemistry</i> , 2004, 279, 26387-26394.	1.6	52
56	Structure of the antithrombin-thrombin-heparin ternary complex reveals the antithrombotic mechanism of heparin. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 857-862.	3.6	345
57	How Small Peptides Block and Reverse Serpin Polymerisation. <i>Journal of Molecular Biology</i> , 2004, 342, 931-941.	2.0	82
58	Crystal Structure of Protein C Inhibitor Provides Insights into Hormone Binding and Heparin Activation. <i>Structure</i> , 2003, 11, 205-215.	1.6	43
59	The Molecular Basis of Thrombin Allostery Revealed by a 1.8 Å... Structure of the "Slow" Form. <i>Structure</i> , 2003, 11, 469-479.	1.6	69
60	How vitronectin binds PAI-1 to modulate fibrinolysis and cell migration. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 541-544.	3.6	217
61	Crystal Structure of Antithrombin in a Heparin-Bound Intermediate State. <i>Biochemistry</i> , 2003, 42, 8712-8719.	1.2	68
62	Targeting thrombin - rational drug design from natural mechanisms. <i>Trends in Pharmacological Sciences</i> , 2003, 24, 589-595.	4.0	66
63	Serpin Polymerization Is Prevented by a Hydrogen Bond Network That Is Centered on His-334 and Stabilized by Glycerol. <i>Journal of Biological Chemistry</i> , 2003, 278, 15116-15122.	1.6	62
64	Heparin-induced substrate behavior of antithrombin Cambridge II. <i>Blood</i> , 2003, 102, 4028-4034.	0.6	35
65	Helix D Elongation and Allosteric Activation of Antithrombin. <i>Journal of Biological Chemistry</i> , 2002, 277, 8551-8558.	1.6	50
66	Crystal structures of native and thrombin-complexed heparin cofactor II reveal a multistep allosteric mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11079-11084.	3.3	188
67	Structure and properties of ovalbumin. <i>Biomedical Applications</i> , 2001, 756, 189-198.	1.7	283
68	The Serpin Inhibitory Mechanism Is Critically Dependent on the Length of the Reactive Center Loop. <i>Journal of Biological Chemistry</i> , 2001, 276, 27541-27547.	1.6	121
69	The Serpins: Nature's Molecular Mousetraps. <i>Science Progress</i> , 2001, 84, 125-136.	1.0	47
70	Structure of a serpin-protease complex shows inhibition by deformation. <i>Nature</i> , 2000, 407, 923-926.	13.7	1,022
71	Formation of the Antithrombin Heterodimer In Vivo and the Onset of Thrombosis. <i>Blood</i> , 1999, 94, 3388-3396.	0.6	76
72	A 2.6 Å structure of a serpin polymer and implications for conformational disease 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 293, 449-455.	2.0	116

#	ARTICLE	IF	CITATIONS
73	Serpin Conformational Change in Ovalbumin. Enhanced Reactive Center Loop Insertion through Hinge Region Mutations. <i>Biochemistry</i> , 1997, 36, 5432-5440.	1.2	62
74	The P6-P2 Region of Serpins Is Critical for Proteinase Inhibition and Complex Stability. <i>Biochemistry</i> , 1997, 36, 9562-9570.	1.2	40
75	Antithrombin-Heparin Affinity Reduced by Fucosylation of Carbohydrate at Asparagine 155. <i>Biochemistry</i> , 1996, 35, 8881-8889.	1.2	50
76	Role of Arginine 132 and Lysine 133 in Heparin Binding to and Activation of Antithrombin. <i>Journal of Biological Chemistry</i> , 1996, 271, 29353-29358.	1.6	34