

# James A Huntington

## List of Publications by Year in descending order

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76  
papers

6,005  
citations

61984

43  
h-index

82547

72  
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76  
all docs

76  
docs citations

76  
times ranked

5034  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of a serpinâ€“protease complex shows inhibition by deformation. <i>Nature</i> , 2000, 407, 923-926.	27.8	1,022
2	Structure of the antithrombinâ€“thrombinâ€“heparin ternary complex reveals the antithrombotic mechanism of heparin. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 857-862.	8.2	345
3	Directing thrombin. <i>Blood</i> , 2005, 106, 2605-2612.	1.4	298
4	Structure and properties of ovalbumin. <i>Biomedical Applications</i> , 2001, 756, 189-198.	1.7	283
5	Crystal structure of a stable dimer reveals the molecular basis of serpin polymerization. <i>Nature</i> , 2008, 455, 1255-1258.	27.8	236
6	How vitronectin binds PAI-1 to modulate fibrinolysis and cell migration. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 541-544.	8.2	217
7	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.	7.1	188
8	Antithrombinâ€“S195A factor Xa-heparin structure reveals the allosteric mechanism of antithrombin activation. <i>EMBO Journal</i> , 2006, 25, 2029-2037.	7.8	163
9	Molecular basis of $\alpha_1$ -antitrypsin deficiency revealed by the structure of a domainâ€“swapped trimer. <i>EMBO Reports</i> , 2011, 12, 1011-1017.	4.5	142
10	Shape-shifting serpins â€“ advantages of a mobile mechanism. <i>Trends in Biochemical Sciences</i> , 2006, 31, 427-435.	7.5	136
11	Crystal Structure of Thrombin Bound to Heparin. <i>Journal of Biological Chemistry</i> , 2005, 280, 2745-2749.	3.4	133
12	Serpins Flex Their Muscle. <i>Journal of Biological Chemistry</i> , 2010, 285, 24299-24305.	3.4	128
13	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.	3.4	121
14	Design and characterization of an APC-specific serpin for the treatment of hemophilia. <i>Blood</i> , 2017, 129, 105-113.	1.4	119
15	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.	4.2	116
16	Serpins Flex Their Muscle. <i>Journal of Biological Chemistry</i> , 2010, 285, 24307-24312.	3.4	97
17	Thrombin-Cofactor Interactions. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2006, 26, 1738-1745.	2.4	90
18	How Small Peptides Block and Reverse Serpin Polymerisation. <i>Journal of Molecular Biology</i> , 2004, 342, 931-941.	4.2	82

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19	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.	7.1	78
20	Formation of the Antithrombin Heterodimer In Vivo and the Onset of Thrombosis. <i>Blood</i> , 1999, 94, 3388-3396.	1.4	76
21	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.	3.4	74
22	The Molecular Basis of Thrombin Allostery Revealed by a 1.8 Å Structure of the "Slow" Form. <i>Structure</i> , 2003, 11, 469-479.	3.3	69
23	Crystal Structure of Antithrombin in a Heparin-Bound Intermediate State. <i>Biochemistry</i> , 2003, 42, 8712-8719.	2.5	68
24	Targeting thrombin " rational drug design from natural mechanisms. <i>Trends in Pharmacological Sciences</i> , 2003, 24, 589-595.	8.7	66
25	How Na <sup>+</sup> activates thrombin " a review of the functional and structural data. <i>Biological Chemistry</i> , 2008, 389, 1025-1035.	2.5	64
26	Serpin Conformational Change in Ovalbumin. Enhanced Reactive Center Loop Insertion through Hinge Region Mutations. <i>Biochemistry</i> , 1997, 36, 5432-5440.	2.5	62
27	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.	3.4	62
28	Crystal structure of the prothrombinase complex from the venom of <i>Pseudonaja textilis</i> . <i>Blood</i> , 2013, 122, 2777-2783.	1.4	62
29	Crystal Structure of Monomeric Native Antithrombin Reveals a Novel Reactive Center Loop Conformation. <i>Journal of Biological Chemistry</i> , 2006, 281, 35478-35486.	3.4	59
30	Molecular basis of thrombin recognition by protein C inhibitor revealed by the 1.6-Å structure of the heparin-bridged complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4661-4666.	7.1	59
31	Whole-exome sequencing in evaluation of patients with venous thromboembolism. <i>Blood Advances</i> , 2017, 1, 1224-1237.	5.2	55
32	Crystal structure of wild-type human thrombin in the Na <sup>+</sup> -free state. <i>Biochemical Journal</i> , 2005, 392, 21-28.	3.7	54
33	The Heparin Binding Properties of Heparin Cofactor II Suggest an Antithrombin-like Activation Mechanism. <i>Journal of Biological Chemistry</i> , 2004, 279, 50267-50273.	3.4	53
34	Crystal Structure of Anticoagulant Thrombin Variant E217K Provides Insights into Thrombin Allostery. <i>Journal of Biological Chemistry</i> , 2004, 279, 26387-26394.	3.4	52
35	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.	4.2	51
36	Antithrombin~Heparin Affinity Reduced by Fucosylation of Carbohydrate at Asparagine 155. <i>Biochemistry</i> , 1996, 35, 8881-8889.	2.5	50

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37	Helix D Elongation and Allosteric Activation of Antithrombin. Journal of Biological Chemistry, 2002, 277, 8551-8558.	3.4	50
38	The Serpins: Nature's Molecular Mousetraps. Science Progress, 2001, 84, 125-136.	1.9	47
39	Natural inhibitors of thrombin. Thrombosis and Haemostasis, 2014, 111, 583-589.	3.4	47
40	A hereditary bleeding disorder resulting from a premature stop codon in thrombomodulin (p.Cys537Stop). Blood, 2014, 124, 1951-1956.	1.4	45
41	Thrombin plasticity. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 246-252.	2.3	44
42	Crystal Structure of Protein C Inhibitor Provides Insights into Hormone Binding and Heparin Activation. Structure, 2003, 11, 205-215.	3.3	43
43	Homozygous Deficiency of Heparin Cofactor II. Circulation, 2004, 110, 1303-1307.	1.6	43
44	The P6âˆ²P2 Region of Serpins Is Critical for Proteinase Inhibition and Complex Stability. Biochemistry, 1997, 36, 9562-9570.	2.5	40
45	Targeting activated protein C to treat hemophilia. Current Opinion in Hematology, 2017, 24, 446-452.	2.5	38
46	<i>SERPINC1</i> gene mutations in antithrombin deficiency. British Journal of Haematology, 2017, 178, 279-285.	2.5	36
47	Heparin-induced substrate behavior of antithrombin Cambridge II. Blood, 2003, 102, 4028-4034.	1.4	35
48	Structure of Native Protein C Inhibitor Provides Insight into Its Multiple Functions. Journal of Biological Chemistry, 2007, 282, 13759-13768.	3.4	35
49	Gplb± Interacts Exclusively with Exosite II of Thrombin. Journal of Molecular Biology, 2014, 426, 881-893.	4.2	35
50	Role of Arginine 132 and Lysine 133 in Heparin Binding to and Activation of Antithrombin. Journal of Biological Chemistry, 1996, 271, 29353-29358.	3.4	34
51	Sugar and alcohol molecules provide a therapeutic strategy for the serpinopathies that cause dementia and cirrhosis. FEBS Journal, 2006, 273, 2450-2552.	4.7	34
52	Allosteric Activation of Antithrombin Critically Depends upon Hinge Region Extension. Journal of Biological Chemistry, 2004, 279, 47288-47297.	3.4	32
53	The Heparin Binding Site of Protein C Inhibitor Is Protease-dependent. Journal of Biological Chemistry, 2008, 283, 36039-36045.	3.4	31
54	Crystal structures of protease nexin-1 in complex with heparin and thrombin suggest a 2-step recognition mechanism. Blood, 2012, 120, 459-467.	1.4	31

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55	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.	0.8	28
56	Loop-Sheet Mechanism of Serpin Polymerization Tested by Reactive Center Loop Mutations*. <i>Journal of Biological Chemistry</i> , 2010, 285, 30752-30758.	3.4	27
57	Thrombin Inhibition by Serpins Disrupts Exosite II. <i>Journal of Biological Chemistry</i> , 2010, 285, 38621-38629.	3.4	21
58	Discovery and characterisation of an antibody that selectively modulates the inhibitory activity of plasminogen activator inhibitor-1. <i>Scientific Reports</i> , 2019, 9, 1605.	3.3	20
59	Characterization of the neutralizing anti-emicizumab antibody in a patient with hemophilia A and inhibitor. <i>Journal of Thrombosis and Haemostasis</i> , 2021, 19, 711-718.	3.8	19
60	The Influence of Hinge Region Residue Glu-381 on Antithrombin Allosterity and Metastability. <i>Journal of Biological Chemistry</i> , 2004, 279, 4913-4921.	3.4	18
61	Structural transitions during prothrombin activation: On the importance of fragment 2. <i>Biochimie</i> , 2016, 122, 235-242.	2.6	17
62	Z- $\hat{1}$ -antitrypsin polymers impose molecular filtration in the endoplasmic reticulum after undergoing phase transition to a solid state. <i>Science Advances</i> , 2022, 8, eabm2094.	10.3	15
63	Molecular contortionism “on the physical limits of serpin “loop-sheet” polymers. <i>Biological Chemistry</i> , 2010, 391, 973-82.	2.5	14
64	Identification of serpins specific for activated protein C using a lysate-based screening assay. <i>Scientific Reports</i> , 2018, 8, 8793.	3.3	14
65	The Shapes of Z- $\hat{1}$ -Antitrypsin Polymers in Solution Support the C-Terminal Domain-Swap Mechanism of Polymerization. <i>Biophysical Journal</i> , 2014, 107, 1905-1912.	0.5	13
66	Ixodes ricinus Salivary Serpin Iripin-8 Inhibits the Intrinsic Pathway of Coagulation and Complement. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9480.	4.1	13
67	Heparin Activation of Serpins. , 2005, , 367-398.		12
68	New insight into serpin polymerization and aggregation. <i>Prion</i> , 2009, 3, 12-14.	1.8	12
69	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.	3.4	8
70	Serpin Polymerization In Vitro. <i>Methods in Enzymology</i> , 2011, 501, 379-420.	1.0	6
71	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.	3.5	6
72	Allosteric activation of antithrombin is independent of charge neutralization or reversal in the heparin binding site. <i>FEBS Letters</i> , 2006, 580, 4709-4712.	2.8	5

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73	Structural Insights into the Life History of Thrombin. , 2008, , 80-106.		4
74	Slow thrombin in solution. Biochemical Journal, 2005, 390, e1-3.	3.7	2
75	Regulatory Mechanisms in Hemostasis. , 2018, , 1906-1911.		1
76	Addendum: KotÅil et al. Ixodes ricinus Salivary Serpin Iripin-8 Inhibits the Intrinsic Pathway of Coagulation and Complement. Int. J. Mol. Sci. 2021, 22, 9480. International Journal of Molecular Sciences, 2021, 22, 11271.	4.1	0