James A Irving

List of Publications by Year in descending order

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79 papers	4,250 citations	147801 31 h-index	110387 64 g-index
85 all docs	85 docs citations	85 times ranked	4475 citing authors

#	Article	IF	Citations
1	The molecular species responsible for Î± 1 â€antitrypsin deficiency are suppressed by a small molecule chaperone. FEBS Journal, 2021, 288, 2222-2237.	4.7	8
2	Conversion of the death inhibitor ARC to a killer activates pancreatic Î² cell death in diabetes. Developmental Cell, 2021, 56, 747-760.e6.	7.0	8
3	The Importance of N186 in the Alpha-1-Antitrypsin Shutter Region Is Revealed by the Novel Bologna Deficiency Variant. International Journal of Molecular Sciences, 2021, 22, 5668.	4.1	5
4	Scaling Concepts in Serpin Polymer Physics. Materials, 2021, 14, 2577.	2.9	4
5	The development of highly potent and selective small molecule correctors of Z Î±1-antitrypsin misfolding. Bioorganic and Medicinal Chemistry Letters, 2021, 41, 127973.	2.2	9
6	Development of a small molecule that corrects misfolding and increases secretion of Z Î± ₁ â€antitrypsin. EMBO Molecular Medicine, 2021, 13, e13167.	6.9	33
7	The structural basis for Z Î± ₁ -antitrypsin polymerization in the liver. Science Advances, 2020, 6, .	10.3	26
8	High-resolution ex vivo NMR spectroscopy of human Z Î±1-antitrypsin. Nature Communications, 2020, 11, 6371.	12.8	15
9	Intrahepatic heteropolymerization of M and Z alpha-1-antitrypsin. JCI Insight, 2020, 5, .	5.0	16
10	Lanthanides compete with calcium for binding to cadherins and inhibit cadherin-mediated cell adhesion. Metallomics, 2019, 11, 914-924.	2.4	22
11	Characterisation of a type II functionally-deficient variant of alpha-1-antitrypsin discovered in the general population. PLoS ONE, 2019, 14, e0206955.	2.5	13
12	Serpinopathies. , 2019, , 6-26.		5
13	Probing the folding pathway of a consensus serpin using single tryptophan mutants. Scientific Reports, 2018, 8, 2121.	3.3	12
14	In Vitro Approaches for the Assessment of Serpin Polymerization. Methods in Molecular Biology, 2018, 1826, 87-107.	0.9	0
15	The pathological Trento variant of alphaâ€1â€antitrypsin (E75V) shows nonclassical behaviour during polymerization. FEBS Journal, 2017, 284, 2110-2126.	4.7	23
16	Electrophoresis- and FRET-Based Measures of Serpin Polymerization. Methods in Molecular Biology, 2017, 1639, 235-248.	0.9	1
17	Alpha1-Antitrypsin: Structure and Dynamics in Health, Disease and Drug Development. , 2017, , 49-80.		2
18	An antibody that prevents serpin polymerisation acts by inducing a novel allosteric behaviour. Biochemical Journal, 2016, 473, 3269-3290.	3.7	15

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19	Smoothing a rugged protein folding landscape by sequence-based redesign. Scientific Reports, 2016, 6, 33958.	3.3	22
20	Deficiency Mutations of Alpha-1 Antitrypsin. Effects on Folding, Function, and Polymerization. American Journal of Respiratory Cell and Molecular Biology, 2016, 54, 71-80.	2.9	31
21	An integrative approach combining ion mobility mass spectrometry, Xâ€ray crystallography, and nuclear magnetic resonance spectroscopy to study the conformational dynamics of Î±₁â€antitrypsin upon ligand binding. Protein Science, 2015, 24, 1301-1312.	7.6	37
22	Interactions between Nâ€linked glycosylation and polymerisation of neuroserpin within the endoplasmic reticulum. FEBS Journal, 2015, 282, 4565-4579.	4.7	19
23	Characterising the association of latency with Î±1-antitrypsin polymerisation using a novel monoclonal antibody. International Journal of Biochemistry and Cell Biology, 2015, 58, 81-91.	2.8	26
24	An antibody raised against a pathogenic serpin variant induces mutant-like behaviour in the wild-type protein. Biochemical Journal, 2015, 468, 99-108.	3.7	22
25	A singleâ€chain variable fragment intrabody prevents intracellular polymerization of Z Î± ₁ â€antitrypsin while allowing its antiproteinase activity. FASEB Journal, 2015, 29, 2667-2678.	0.5	44
26	Altered native stability is the dominant basis for susceptibility of Î±1-antitrypsin mutants to polymerization. Biochemical Journal, 2014, 460, 103-119.	3.7	25
27	Novel Mechanisms Of Immune Modulation By Alpha-1-Antitrypsin. Journal of Allergy and Clinical Immunology, 2014, 133, AB138.	2.9	0
28	Suppression of AÎ² toxicity by puromycin-sensitive aminopeptidase is independent of its proteolytic activity. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2013, 1832, 2115-2126.	3.8	16
29	A Molecular Switch Governs the Interaction between the Human Complement Protease C1s and Its Substrate, Complement C4. Journal of Biological Chemistry, 2013, 288, 15821-15829.	3.4	29
30	Reactive centre loop mutants of Î±-1-antitrypsin reveal position-specific effects on intermediate formation along the polymerization pathway. Bioscience Reports, 2013, 33, .	2.4	24
31	Defining The Mechanism Of Polymerisation That Underlies Î±1-Antitrypsin Deficiency. , 2012, , .		0
32	Phosphoproteins in Stress-Induced Disease. Progress in Molecular Biology and Translational Science, 2012, 106, 189-221.	1.7	41
33	Characterisation of serpin polymers in vitro and in vivo. Methods, 2011, 53, 255-266.	3.8	31
34	Unravelling the twists and turns of the serpinopathies. FEBS Journal, 2011, 278, 3859-3867.	4.7	42
35	The Serpinopathies. Methods in Enzymology, 2011, 501, 421-466.	1.0	35
36	P117 3D cryo-electron microscopic analysis of the disease mechanism of Â1-antitrypsin deficiency. Thorax, 2011, 66, A115-A115.	5.6	0

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37	Targeting Serpins in High-Throughput and Structure-Based Drug Design. Methods in Enzymology, 2011, 501, 139-175.	1.0	15
38	Chapter 10. Structural Mechanisms of Inactivation in Proteolytically Inactive Serine Proteases from Sarcoptes scabiei. RSC Drug Discovery Series, 2011, , 229-241.	0.3	0
39	MUSTANG-MR Structural Sieving Server: Applications in Protein Structural Analysis and Crystallography. PLoS ONE, 2010, 5, e10048.	2.5	47
40	Structure of granzyme C reveals an unusual mechanism of protease autoinhibition. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5587-5592.	7.1	25
41	A major cathepsin B protease from the liver fluke Fasciola hepatica has atypical active site features and a potential role in the digestive tract of newly excysted juvenile parasites. International Journal of Biochemistry and Cell Biology, 2009, 41, 1601-1612.	2.8	39
42	Structural Mechanisms of Inactivation in Scabies Mite Serine Protease Paralogues. Journal of Molecular Biology, 2009, 390, 635-645.	4.2	33
43	Conformational Change in the Chromatin Remodelling Protein MENT. PLoS ONE, 2009, 4, e4727.	2.5	3
44	Epitope Mapping of FIX Inhibitors Identify Contact Residues in the Protease Domain.. Blood, 2009, 114, 3172-3172.	1.4	0
45	A serpin in the cellulosome of the anaerobic fungus Piromyces sp. strain E2. Mycological Research, 2008, 112, 999-1006.	2.5	34
46	Role of the Î±-Helix 163-170 in Factor Xa Catalytic Activity. Journal of Biological Chemistry, 2007, 282, 31569-31579.	3.4	23
47	DNA Accelerates the Inhibition of Human Cathepsin V by Serpins. Journal of Biological Chemistry, 2007, 282, 36980-36986.	3.4	40
48	Aeropin from the Extremophile Pyrobaculum aerophilum Bypasses the Serpin Misfolding Trap. Journal of Biological Chemistry, 2007, 282, 26802-26809.	3.4	20
49	The N terminus of the serpin, tengpin, functions to trap the metastable native state. EMBO Reports, 2007, 8, 658-663.	4.5	48
50	Peptide mimotopes selected with HIVâ€1â€blocking monoclonal antibodies against CCR5 represent motifs specific for HIVâ€1 entry. Immunology and Cell Biology, 2007, 85, 511-517.	2.3	8
51	Evolution and Classification of the Serpin Superfamily. , 2007, , 1-33.		4
52	Serpins in Prokaryotes. , 2007, , 131-162.		6
53	X-ray crystal structure of MENT: evidence for functional loopâ€“sheet polymers in chromatin condensation. EMBO Journal, 2006, 25, 3144-3155.	7.8	41
54	Requirement of multiple phage displayed peptide libraries for optimal mapping of a conformational antibody epitope on CCR5. Journal of Immunological Methods, 2005, 299, 21-35.	1.4	16

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55	Functional insights from the distribution and role of homopeptide repeat-containing proteins. Genome Research, 2005, 15, 537-551.	5.5	189
56	The High Resolution Crystal Structure of the Human Tumor Suppressor Maspin Reveals a Novel Conformational Switch in the G-helix. Journal of Biological Chemistry, 2005, 280, 22356-22364.	3.4	69
57	The High Resolution Crystal Structure of a Native Thermostable Serpin Reveals the Complex Mechanism Underpinning the Stressed to Relaxed Transition. Journal of Biological Chemistry, 2005, 280, 8435-8442.	3.4	29
58	The Murine Orthologue of Human Antichymotrypsin. Journal of Biological Chemistry, 2005, 280, 43168-43178.	3.4	97
59	Human clade B serpins (ov-serpins) belong to a cohort of evolutionarily dispersed intracellular proteinase inhibitor clades that protect cells from promiscuous proteolysis. Cellular and Molecular Life Sciences, 2004, 61, 301-325.	5.4	159
60	Computational analysis of evolution and conservation in a protein superfamily. Methods, 2004, 32, 73-92.	3.8	11
61	The Evolution of Enzyme Specificity in Fasciola spp.. Journal of Molecular Evolution, 2003, 57, 1-15.	1.8	106
62	The 1.5 Ã... Crystal Structure of a Prokaryote Serpin. Structure, 2003, 11, 387-397.	3.3	44
63	Hurpin Is a Selective Inhibitor of Lysosomal Cathepsin L and Protects Keratinocytes from Ultraviolet-Induced Apoptosis. Biochemistry, 2003, 42, 7381-7389.	2.5	72
64	Cloning and Expression of the Major SecretedCathepsin B-Like Protein from Juvenile Fasciola hepatica andAnalysis of Immunogenicity following Liver FlukeInfection. Infection and Immunity, 2003, 71, 6921-6932.	2.2	88
65	Inhibitory Activity of a Heterochromatin-associated Serpin (MENT) against Papain-like Cysteine Proteinases Affects Chromatin Structure and Blocks Cell Proliferation. Journal of Biological Chemistry, 2002, 277, 13192-13201.	3.4	77
66	Serpins in Prokaryotes. Molecular Biology and Evolution, 2002, 19, 1881-1890.	8.9	112
67	The Serpin SQN-5 Is a Dual Mechanistic-Class Inhibitor of Serine and Cysteine Proteinases. Biochemistry, 2002, 41, 3189-3199.	2.5	61
68	Evidence That Serpin Architecture Intrinsically Supports Papain-like Cysteine Protease Inhibition:â€‰Engineering Î±1-Antitrypsin To Inhibit Cathepsin Proteases. Biochemistry, 2002, 41, 4998-5004.	2.5	71
69	Serpins: Finely Balanced Conformational Traps. IUBMB Life, 2002, 54, 1-7.	3.4	38
70	Sequence, Organization, Chromosomal Localization, and Alternative Splicing of the Human Serine Protease Inhibitor Gene Hurpin (PI13) Which Is Upregulated in Psoriasis. DNA and Cell Biology, 2001, 20, 123-131.	1.9	8
71	Protein structural alignments and functional genomics. Proteins: Structure, Function and Bioinformatics, 2001, 42, 378-382.	2.6	76
72	The Serpins Are an Expanding Superfamily of Structurally Similar but Functionally Diverse Proteins. Journal of Biological Chemistry, 2001, 276, 33293-33296.	3.4	1,069

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73	Phylogeny of the Serpin Superfamily: Implications of Patterns of Amino Acid Conservation for Structure and Function. Genome Research, 2000, 10, 1845-1864.	5.5	488
74	For the record: A single amino acid substitution affects substrate specificity in cysteine proteinases from Fasciola hepatica. Protein Science, 2000, 9, 2567-2572.	7.6	59
75	Simple Modifications of the Serpin Reactive Site Loop Convert SCCA2 into a Cysteine Proteinase Inhibitor:Â A Critical Role for the P3â€˜ Proline in Facilitating RSL Cleavageâ€. Biochemistry, 2000, 39, 7081-7091.	2.5	47
76	Phylogeny of the Serpin Superfamily: Implications of Patterns of Amino Acid Conservation for Structure and Function. Genome Research, 2000, 10, 1845-1864.	5.5	145
77	Serpins in theCaenorhabditis elegans genome. , 1999, 36, 31-41.		18
78	Human Ovalbumin Serpin Evolution: Phylogenic Analysis, Gene Organization, and Identification of New PI8-Related Genes Suggest That Two Interchromosomal and Several Intrachromosomal Duplications Generated the Gene Clusters at 18q21â€“q23 and 6p25. Genomics, 1999, 62, 490-499.	2.9	43
79	Serpins in the Caenorhabditis elegans genome. Proteins: Structure, Function and Bioinformatics, 1999, 36, 31-41.	2.6	8