Steven R Van Doren

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	MMP-7 marks severe pancreatic cancer and alters tumor cell signaling by proteolytic release of ectodomains. Biochemical Society Transactions, 2022, 50, 839-851.	3.4	6
2	Development of a Therapeutic Peptide for Cachexia Suggests a Platform Approach for Drug-like Peptides. ACS Pharmacology and Translational Science, 2022, 5, 344-361.	4.9	5
3	Fusion Peptide of SARS-CoV-2 Spike Rearranges into a Wedge Inserted in Bilayered Micelles. Journal of the American Chemical Society, 2021, 143, 13205-13211.	13.7	54
4	Docking of acetyl-CoA carboxylase to the plastid envelope membrane attenuates fatty acid production in plants. Nature Communications, 2020, 11, 6191.	12.8	23
5	The BADC and BCCP subunits of chloroplast acetyl-CoA carboxylase sense the pH changes of the light–dark cycle. Journal of Biological Chemistry, 2020, 295, 9901-9916.	3.4	20
6	NMR-based fragment screening and lead discovery accelerated by principal component analysis. Journal of Biomolecular NMR, 2019, 73, 675-685.	2.8	16
7	MT1-MMP Binds Membranes by Opposite Tips of Its β Propeller to Position It for Pericellular Proteolysis. Structure, 2019, 27, 281-292.e6.	3.3	15
8	Domain Gymnastics of an ABC Transporter. Structure, 2018, 26, 917-918.	3.3	1
9	Affinities and Comparisons of Enzyme States by Principal Component Analysis of NMR Spectra, Automated using TREND Software. Methods in Enzymology, 2018, 607, 217-240.	1.0	7
10	Tracking Equilibrium and Nonequilibrium Shifts inÂData with TREND. Biophysical Journal, 2017, 112, 224-233.	0.5	14
11	Peripheral membrane associations of matrix metalloproteinases. Biochimica Et Biophysica Acta - Molecular Cell Research, 2017, 1864, 1964-1973.	4.1	16
12	Mapping Lipid Bilayer Recognition Sites of Metalloproteinases and Other Prospective Peripheral Membrane Proteins. Methods in Molecular Biology, 2017, 1579, 61-86.	0.9	6
13	Multiple Ligand-Bound States of a Phosphohexomutase Revealed by Principal Component Analysis of NMR Peak Shifts. Scientific Reports, 2017, 7, 5343.	3.3	7
14	Phosphorylation-Dependent Effects on the Structural Flexibility of Phosphoglucosamine Mutase from <i>Bacillus anthracis</i> . ACS Omega, 2017, 2, 8445-8452.	3.5	4
15	Glycan Activation of a Sheddase: Electrostatic Recognition between Heparin and proMMP-7. Structure, 2017, 25, 1100-1110.e5.	3.3	11
16	Noninvasive Recognition and Biomarkers of Early Allergic Asthma in Cats Using Multivariate Statistical Analysis of NMR Spectra of Exhaled Breath Condensate. PLoS ONE, 2016, 11, e0164394.	2.5	7
17	Path to Collagenolysis. Journal of Biological Chemistry, 2016, 291, 7888-7901.	3.4	9
18	Binding Isotherms and Time Courses Readily from Magnetic Resonance. Analytical Chemistry, 2016, 88, 8172-8178.	6.5	19

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19	Transient Collagen Triple Helix Binding to a Key Metalloproteinase in Invasion and Development. Structure, 2015, 23, 257-269.	3.3	30
20	Phosphorylation in the Catalytic Cleft Stabilizes and Attracts Domains of a Phosphohexomutase. Biophysical Journal, 2015, 108, 325-337.	0.5	14
21	Matrix metalloproteinase interactions with collagen and elastin. Matrix Biology, 2015, 44-46, 224-231.	3.6	278
22	Charge-Triggered Membrane Insertion of Matrix Metalloproteinase-7, Supporter of Innate Immunity and Tumors. Structure, 2015, 23, 2099-2110.	3.3	24
23	Ambidextrous binding of cell and membrane bilayers by soluble matrix metalloproteinase-12. Nature Communications, 2014, 5, 5552.	12.8	44
24	Chemical shift assignments of domain 4 from the phosphohexomutase from Pseudomonas aeruginosa suggest that freeing perturbs its coevolved domain interface. Biomolecular NMR Assignments, 2014, 8, 329-333.	0.8	4
25	The Role of Collagen Charge Clusters in the Modulation of Matrix Metalloproteinase Activity. Journal of Biological Chemistry, 2014, 289, 1981-1992.	3.4	8
26	Heparinoids Activate a Protease, Secreted by Mucosa and Tumors, via Tethering Supplemented by Allostery. ACS Chemical Biology, 2014, 9, 957-966.	3.4	12
27	Solution NMR of a 463-Residue Phosphohexomutase: Domain 4 Mobility, Substates, and Phosphoryl Transfer Defect. Biochemistry, 2012, 51, 807-819.	2.5	12
28	Remote Exosites of the Catalytic Domain of Matrix Metalloproteinase-12 Enhance Elastin Degradation. Biochemistry, 2011, 50, 9488-9499.	2.5	22
29	Solubilized elastin substrate for continuous fluorimetric assay of kinetics of elastases. Analytical Biochemistry, 2011, 408, 172-174.	2.4	7
30	Entropy Increases from Different Sources Support the High-affinity Binding of the N-terminal Inhibitory Domains of Tissue Inhibitors of Metalloproteinases to the Catalytic Domains of Matrix Metalloproteinases-1 and -3. Journal of Biological Chemistry, 2011, 286, 16891-16899.	3.4	8
31	Structural Basis of Extracellular Matrix Interactions with Matrix Metalloproteinases. , 2011, , 123-143.		2
32	Breaking the covalent connection: Chain connectivity and the catalytic reaction of PMM/PGM. Protein Science, 2010, 19, 1235-1242.	7.6	10
33	NMR and Bioinformatics Discovery of Exosites That Tune Metalloelastase Specificity for Solubilized Elastin and Collagen Triple Helices. Journal of Biological Chemistry, 2010, 285, 30918-30930.	3.4	22
34	An examination of the proteolytic activity for bovine pregnancy-associated glycoproteins 2 and 12. Biological Chemistry, 2010, 391, 259-270.	2.5	27
35	Apparent Tradeoff of Higher Activity in MMP-12 for Enhanced Stability and Flexibility in MMP-3. Biophysical Journal, 2010, 99, 273-283.	0.5	15
36	Nuclear magnetic resonance captures the elusive. F1000 Biology Reports, 2009, 1, 24.	4.0	0

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37	Inactivation of Nâ€TIMPâ€1 by Nâ€ŧerminal acetylation when expressed in bacteria. Biopolymers, 2008, 89, 960-968.	2.4	16
38	Mechanistic Insights into Phosphoprotein-Binding FHA Domains. Accounts of Chemical Research, 2008, 41, 991-999.	15.6	49
39	MMP-12 Catalytic Domain Recognizes Triple Helical Peptide Models of Collagen V with Exosites and High Activity. Journal of Biological Chemistry, 2008, 283, 21779-21788.	3.4	39
40	Solution Structure of Inhibitor-Free Human Metalloelastase (MMP-12) Indicates an Internal Conformational Adjustment. Journal of Molecular Biology, 2007, 374, 1333-1344.	4.2	20
41	Phosphoprotein and Phosphopeptide Interactions with the FHA Domain from Arabidopsis Kinase-Associated Protein Phosphataseâ€. Biochemistry, 2007, 46, 2684-2696.	2.5	48
42	Rapid determination of enzyme kinetics from fluorescence: Overcoming the inner filter effect. Analytical Biochemistry, 2007, 371, 43-51.	2.4	118
43	Hsc70 Contacts Helix III of the J Domain from Polyomavirus T Antigens:  Addressing a Dilemma in the Chaperone Hypothesis of How They Release E2F from pRb. Biochemistry, 2006, 45, 6917-6929.	2.5	35
44	Partially Unfolded Forms and Non-two-state Folding of a β-Sandwich: FHA Domain from Arabidopsis Receptor Kinase-associated Protein Phosphatase. Journal of Molecular Biology, 2006, 364, 225-240.	4.2	7
45	Eukaryotic cyclophilin as a molecular switch for effector activation. Molecular Microbiology, 2006, 61, 1485-1496.	2.5	64
46	1H, 13C, and 15N peak assignments and secondary structure of human macrophage metalloelastase (MMP-12) in its inhibitor-free state. Journal of Biomolecular NMR, 2006, 36, 55-55.	2.8	5
47	Solution Structure and Dynamics of Human MMPâ€12 (Metalloelastase) in its Inhibitorâ€Free State. FASEB Journal, 2006, 20, LB51.	0.5	0
48	FHA Domain of Kinase Associated Protein Phosphatase (KAPP): Interactions with PhosphoThr Peptides and a Receptor Kinase and Dynamics by NMR. FASEB Journal, 2006, 20, A465.	0.5	1
49	PhosphoThr Peptide Binding Clobally Rigidifies Much of the FHA Domain from Arabidopsis Receptor Kinase-Associated Protein Phosphatase,. Biochemistry, 2005, 44, 10119-10134.	2.5	23
50	1H, 13C and 15N resonance assignments of the kinase-interacting FHA domain of Arabidopsis thaliana kinase-associated protein phosphatase. Journal of Biomolecular NMR, 2003, 25, 253-254.	2.8	5
51	Global Orientation of Bound MMP-3 and N-TIMP-1 in Solution via Residual Dipolar Couplings,. Biochemistry, 2003, 42, 7950-7958.	2.5	20
52	Structural Basis for a Lethal Mutation in U6 RNAâ€,‡. Biochemistry, 2003, 42, 1470-1477.	2.5	30
53	Increased Backbone Mobility in β-Barrel Enhances Entropy Gain Driving Binding of N-TIMP-1 to MMP-3. Journal of Molecular Biology, 2003, 327, 719-734.	4.2	78
54	NMR structure of the forkhead-associated domain from the Arabidopsis receptor kinase-associated protein phosphatase. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 11261-11266.	7.1	43

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55	Hsc70-interacting HPD Loop of the J Domain of Polyomavirus T Antigens Fluctuates in ps to ns and μs to ms. Journal of Molecular Biology, 2002, 321, 503-516.	4.2	15
56	Structure of the UGAGAU hexaloop that braces Bacillus RNase P for action. Nature Structural Biology, 2002, 9, 397-403.	9.7	15
57	NMR Structure of the N-terminal J Domain of Murine Polyomavirus T Antigens. Journal of Biological Chemistry, 2000, 275, 36094-36103.	3.4	35
58	NMR structure of tissue inhibitor of metalloproteinases-1 implicates localized induced fit in recognition of matrix metalloproteinases. Journal of Molecular Biology, 2000, 295, 257-268.	4.2	40
59	Tissue inhibitor of metalloproteinases-1 undergoes microsecond to millisecond motions at sites of matrix metalloproteinase-induced fit 1 1Edited by P. E. Wright. Journal of Molecular Biology, 2000, 301, 537-552.	4.2	24
60	1H, 13C and 15N resonance assignments and secondary structure of the N-terminal domain of human tissue inhibitor of metalloproteinases-1. Journal of Biomolecular NMR, 1999, 14, 289-290.	2.8	5
61	TIMP-1 Contact Sites and Perturbations of Stromelysin 1 Mapped by NMR and a Paramagnetic Surface Probeâ€. Biochemistry, 1998, 37, 9650-9657.	2.5	52
62	Folding and characterization of the amino-terminal domain of human tissue inhibitor of metalloproteinases-1 (TIMP-1) expressed at high yield inE. coli. FEBS Letters, 1996, 384, 155-161.	2.8	99
63	Solution structure of the catalytic domain of human stromelysin complexed with a hydrophobic inhibitor. Protein Science, 1995, 4, 2487-2498.	7.6	80
64	Modern multidimensional protein NMR spectroscopy. TrAC - Trends in Analytical Chemistry, 1994, 13, 24-36.	11.4	3
65	An Auxiliary RF Channel with Convenient Phase Control for NMR Spectrometers. Journal of Magnetic Resonance Series A, 1993, 104, 222-225.	1.6	2
66	Thebc 1 complexes ofRhodobacter sphaeroides andRhodobacter capsulatus. Journal of Bioenergetics and Biomembranes, 1993, 25, 195-209.	2.3	152
67	Modern NMR spectroscopy of proteins and peptides in solution and its relevance to drug design. Journal of Computer - Aided Molecular Design, 1993, 1, 391-417.	1.0	4
68	Assembly of the Rieske iron-sulfur subunit of the cytochrome bc1 complex in the Escherichia coli and Rhodobacter sphaeroides membranes independent of the cytochrome b and c1 subunits. Biochemistry, 1993, 32, 628-636.	2.5	42
69	Assignments for the main-chain nuclear magnetic resonances and delineation of the secondary structure of the catalytic domain of human stromelysin-1 as obtained from triple-resonance 3D NMR experiments. Biochemistry, 1993, 32, 13109-13122.	2.5	39
70	Phenotypic and genetic characterization of cytochrome c2-deficient mutants of Rhodobacter sphaeroides. Biochemistry, 1988, 27, 1918-1925.	2.5	121
71	Catalytic Sites for Reduction and Oxidation of Quinones. , 1987, , 617-624.		72