

Elizabeth A Komives

List of Publications by Year in descending order

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152
papers

6,953
citations

53660

45
h-index

79541

73
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158
all docs

158
docs citations

158
times ranked

7024
citing authors

#	ARTICLE	IF	CITATIONS
1	How Thrombomodulin Enables W215A/E217A Thrombin to Cleave Protein C but Not Fibrinogen. <i>Biochemistry</i> , 2022, 61, 77-84.	1.2	1
2	Dimer dissociation is a key energetic event in the fold-switch pathway of KaiB. <i>Biophysical Journal</i> , 2022, 121, 943-955.	0.2	2
3	Allosteric couplings upon binding of RfaH to transcription elongation complexes. <i>Nucleic Acids Research</i> , 2022, 50, 6384-6397.	6.5	2
4	The Mechanism of NEDD8 Activation of CUL5 Ubiquitin E3 Ligases. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100019.	2.5	10
5	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2021, 49, 11211-11223.	6.5	7
6	Sequence and functional differences in the ATPase domains of CHD3 and SNF2H promise potential for selective regulability and drugability. <i>FEBS Journal</i> , 2021, 288, 4000-4023.	2.2	2
7	Serine protease dynamics revealed by NMR analysis of the thrombin-thrombomodulin complex. <i>Scientific Reports</i> , 2021, 11, 9354.	1.6	5
8	Hydrogen/Deuterium Exchange and Nuclear Magnetic Resonance Spectroscopy Reveal Dynamic Allostery on Multiple Time Scales in the Serine Protease Thrombin. <i>Biochemistry</i> , 2021, 60, 3441-3448.	1.2	15
9	Conformation and dynamics of the kinase domain drive subcellular location and activation of LRRK2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	35
10	Open, engage, bind, translocate: The multi-level dynamics of bacterial protein translocation. <i>Structure</i> , 2021, 29, 781-782.	1.6	2
11	Transcription factor NF- κ B unravels nucleosomes. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021, 1865, 129934.	1.1	13
12	Development of a Rapid and Sensitive CasRx-Based Diagnostic Assay for SARS-CoV-2. <i>ACS Sensors</i> , 2021, 6, 3957-3966.	4.0	35
13	Achieving a Realistic Native Protein Ensemble by HDX-MS and Computational Modeling. <i>Biophysical Journal</i> , 2021, 120, 5139-5140.	0.2	1
14	Differential Local Stability Governs the Metamorphic Fold Switch of Bacterial Virulence Factor RfaH. <i>Biophysical Journal</i> , 2020, 118, 96-104.	0.2	22
15	Surveying biomolecular frustration at atomic resolution. <i>Nature Communications</i> , 2020, 11, 5944.	5.8	40
16	Intrinsically Disordered Regions of the DNA-Binding Domain of Human FoxP1 Facilitate Domain Swapping. <i>Journal of Molecular Biology</i> , 2020, 432, 5411-5429.	2.0	12
17	Tuning of Conformational Dynamics Through Evolution-Based Design Modulates the Catalytic Adaptability of an Extremophilic Kinase. <i>ACS Catalysis</i> , 2020, 10, 10847-10857.	5.5	7
18	Complementarity of Hydrogen/Deuterium Exchange Mass Spectrometry and Cryo-Electron Microscopy. <i>Trends in Biochemical Sciences</i> , 2020, 45, 906-918.	3.7	31

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19	Structure and dynamics of the ASB9 CUL-RING E3 Ligase. <i>Nature Communications</i> , 2020, 11, 2866.	5.8	18
20	Structural basis for GPCR-independent activation of heterotrimeric Gi proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16394-16403.	3.3	43
21	Dynamics of ABC Transporter P-glycoprotein in Three Conformational States. <i>Scientific Reports</i> , 2019, 9, 15092.	1.6	26
22	Decoupling a tandem-repeat protein: Impact of multiple loop insertions on a modular scaffold. <i>Scientific Reports</i> , 2019, 9, 15439.	1.6	3
23	Cryo-EM structure of OSCA1.2 from <i>Oryza sativa</i> elucidates the mechanical basis of potential membrane hyperosmolality gating. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14309-14318.	3.3	71
24	Exclusivity and Compensation in NF κ B Dimer Distributions and I κ B Inhibition. <i>Biochemistry</i> , 2019, 58, 2555-2563.	1.2	14
25	DECA, A Comprehensive, Automatic Post-processing Program for HDX-MS Data*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2516-2523.	2.5	42
26	Accurate Prediction of Amide Exchange in the Fast Limit Reveals Thrombin Allostery. <i>Biophysical Journal</i> , 2019, 116, 49-56.	0.2	27
27	Hydrogen-deuterium exchange mass spectrometry reveals folding and allostery in protein-protein interactions. <i>Methods</i> , 2018, 144, 43-52.	1.9	29
28	Dynamic Consequences of Mutation of Tryptophan 215 in Thrombin. <i>Biochemistry</i> , 2018, 57, 2694-2703.	1.2	19
29	Conformational dynamics of the Hop1 HORMA domain reveal a common mechanism with the spindle checkpoint protein Mad2. <i>Nucleic Acids Research</i> , 2018, 46, 279-292.	6.5	68
30	Frustration, function and folding. <i>Current Opinion in Structural Biology</i> , 2018, 48, 68-73.	2.6	78
31	Deciphering and engineering chromodomain-methyllysine peptide recognition. <i>Science Advances</i> , 2018, 4, eaau1447.	4.7	15
32	Calcium sensing by the STIM1 ER-luminal domain. <i>Nature Communications</i> , 2018, 9, 4536.	5.8	51
33	RelA-Containing NF κ B Dimers Have Strikingly Different DNA-Binding Cavities in the Absence of DNA. <i>Journal of Molecular Biology</i> , 2018, 430, 1510-1520.	2.0	14
34	RNAs interact with BRD4 to promote enhanced chromatin engagement and transcription activation. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 687-697.	3.6	123
35	Prediction of the presence of a seventh ankyrin repeat in I κ B μ from homology modeling combined with hydrogen-deuterium exchange mass spectrometry (HDX-MS). <i>Protein Science</i> , 2018, 27, 1624-1635.	3.1	6
36	Ligand binding modulates the structural dynamics and activity of urokinase-type plasminogen activator: A possible mechanism of plasminogen activation. <i>PLoS ONE</i> , 2018, 13, e0192661.	1.1	3

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37	Functional profiling of endogenous SUMOylation sites. <i>FASEB Journal</i> , 2018, 32, 791.22.	0.2	0
38	NMR reveals a dynamic allosteric pathway in thrombin. <i>Scientific Reports</i> , 2017, 7, 39575.	1.6	21
39	Functional importance of stripping in NF κ B signaling revealed by a stripping-impaired I κ B μ mutant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1916-1921.	3.3	32
40	DNA and I κ B μ Both Induce Long-Range Conformational Changes in NF κ B. <i>Journal of Molecular Biology</i> , 2017, 429, 999-1008.	2.0	28
41	Unusual dimerization of a Bc Csp mutant leads to reduced conformational dynamics. <i>FEBS Journal</i> , 2017, 284, 1882-1896.	2.2	2
42	Discovery of a novel conformational equilibrium in urokinase-type plasminogen activator. <i>Scientific Reports</i> , 2017, 7, 3385.	1.6	27
43	Site-specific identification and quantitation of endogenous SUMO modifications under native conditions. <i>Nature Communications</i> , 2017, 8, 1171.	5.8	92
44	Monomeric ephrinB2 binding induces allosteric changes in Nipah virus G that precede its full activation. <i>Nature Communications</i> , 2017, 8, 781.	5.8	38
45	Resolving the NF κ B Heterodimer Binding Paradox: Strain and Frustration Guide the Binding of Dimeric Transcription Factors. <i>Journal of the American Chemical Society</i> , 2017, 139, 18558-18566.	6.6	27
46	Structural Basis for Shelterin Bridge Assembly. <i>Molecular Cell</i> , 2017, 68, 698-714.e5.	4.5	27
47	Model of the Ankyrin and SOCS Box Protein, ASB9, E3 Ligase Reveals a Mechanism for Dynamic Ubiquitin Transfer. <i>Structure</i> , 2016, 24, 1248-1256.	1.6	10
48	Structural characterization of the ternary complex that mediates termination of NF κ B signaling by I κ B μ . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6212-6217.	3.3	8
49	PEST Control of Molecular Stripping of NF κ B from DNA Transcription Sites. <i>Journal of Physical Chemistry B</i> , 2016, 120, 8532-8538.	1.2	20
50	Three-Dimensional Domain Swapping Changes the Folding Mechanism of the Forkhead Domain of FoxP1. <i>Biophysical Journal</i> , 2016, 110, 2349-2360.	0.2	29
51	Binding of NF κ B Appears to Twist the Ankyrin Repeat Domain of I κ B μ . <i>Biophysical Journal</i> , 2016, 110, 887-895.	0.2	10
52	Molecular stripping in the <i>NF- κ B/I κ B/DNA</i> genetic regulatory network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 110-115.	3.3	81
53	How the Ankyrin and SOCS Box Protein, ASB9, Binds to Creatine Kinase. <i>Biochemistry</i> , 2015, 54, 1673-1680.	1.2	11
54	The Folding Unit of Phosphofructokinase-2 as Defined by the Biophysical Properties of a Monomeric Mutant. <i>Biophysical Journal</i> , 2015, 108, 2350-2361.	0.2	8

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55	Thrombomodulin Binding Selects the Catalytically Active Form of Thrombin. <i>Biochemistry</i> , 2015, 54, 6650-6658.	1.2	17
56	Frustration in biomolecules. <i>Quarterly Reviews of Biophysics</i> , 2014, 47, 285-363.	2.4	253
57	The Phylogenetics of Dynamics in DNA Clamp Proteins. <i>Structure</i> , 2014, 22, 511-512.	1.6	0
58	Predicted disorder-to-order transition mutations in Î±BÎ± disrupt function. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 6480.	1.3	21
59	Expanding Proteome Coverage with Orthogonal-specificity Î±-Lytic Proteases. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 823-835.	2.5	54
60	Direct observation of a transient ternary complex during Î±BÎ±-mediated dissociation of NF-Î±B from DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 225-230.	3.3	40
61	Purification and characterization of the <i>Staphylococcus aureus</i> bacillithiol transferase BstA. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 2851-2861.	1.1	17
62	Long-Range Effects and Functional Consequences of Stabilizing Mutations in the Ankyrin Repeat Domain of Î±BÎ±. <i>Journal of Molecular Biology</i> , 2013, 425, 902-913.	2.0	10
63	Hydrogen-exchange mass spectrometry for the study of intrinsic disorder in proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1202-1209.	1.1	74
64	Single-Molecule FRET Reveals the Native-State Dynamics of the Î±BÎ± Ankyrin Repeat Domain. <i>Journal of Molecular Biology</i> , 2013, 425, 2578-2590.	2.0	25
65	Recognition of Methylated Peptides by <i>Drosophila melanogaster</i> Polycomb Chromodomain. <i>Journal of Proteome Research</i> , 2013, 12, 1467-1477.	1.8	5
66	Observation of Solvent Penetration during Cold Denaturation of E.â€coli Phosphofructokinase-2. <i>Biophysical Journal</i> , 2013, 104, 2254-2263.	0.2	11
67	Correlated Motions and Residual Frustration in Thrombin. <i>Journal of Physical Chemistry B</i> , 2013, 117, 12857-12863.	1.2	37
68	Identification of Methyllysine Peptides Binding to Chromobox Protein Homolog 6 Chromodomain in the Human Proteome. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2750-2760.	2.5	4
69	Allosteric networks in thrombin distinguish procoagulant vs. anticoagulant activities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21216-21222.	3.3	137
70	The Dynamic Structure of Thrombin in Solution. <i>Biophysical Journal</i> , 2012, 103, 79-88.	0.2	47
71	Role of disorder in Î±BÎ±-NFÎ±B interaction. <i>IUBMB Life</i> , 2012, 64, 499-505.	1.5	41
72	Consequences of Fuzziness in the NFÎ±B/Î±BÎ± Interaction. <i>Advances in Experimental Medicine and Biology</i> , 2012, 725, 74-85.	0.8	6

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73	Discrete Kinetic Models from Funneled Energy Landscape Simulations. <i>PLoS ONE</i> , 2012, 7, e50635.	1.1	17
74	Protein Interactions among Fe65, the Low-Density Lipoprotein Receptor-Related Protein, and the Amyloid Precursor Protein. <i>Biochemistry</i> , 2011, 50, 6208-6216.	1.2	8
75	On the role of frustration in the energy landscapes of allosteric proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3499-3503.	3.3	165
76	Prediction of Native-State Hydrogen Exchange from Perfectly Funneled Energy Landscapes. <i>Journal of the American Chemical Society</i> , 2011, 133, 17463-17472.	6.6	68
77	The RelA Nuclear Localization Signal Folds upon Binding to $\mathbb{I}^{\circ}\mathbb{B}\mathbb{I}^{\pm}$. <i>Journal of Molecular Biology</i> , 2011, 405, 754-764.	2.0	29
78	Folding Kinetics of the Cooperatively Folded Subdomain of the $\mathbb{I}^{\circ}\mathbb{B}\mathbb{I}^{\pm}$ Ankyrin Repeat Domain. <i>Journal of Molecular Biology</i> , 2011, 408, 163-176.	2.0	24
79	Thermodynamic Compensation upon Binding to Exosite 1 and the Active Site of Thrombin. <i>Biochemistry</i> , 2011, 50, 4590-4596.	1.2	21
80	Detection of a ternary complex of NF- $\mathbb{I}^{\circ}\mathbb{B}$ and $\mathbb{I}^{\circ}\mathbb{B}\mathbb{I}^{\pm}$ with DNA provides insights into how $\mathbb{I}^{\circ}\mathbb{B}\mathbb{I}^{\pm}$ removes NF- $\mathbb{I}^{\circ}\mathbb{B}$ from transcription sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1367-1372.	3.3	26
81	Visualization of the nanospring dynamics of the $\mathbb{I}^{\circ}\mathbb{B}\mathbb{I}^{\pm}$ ankyrin repeat domain in real time. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10178-10183.	3.3	45
82	Consequences of IkappaB alpha hydroxylation by the factor inhibiting HIF (FIH). <i>FEBS Letters</i> , 2010, 584, 4725-4730.	1.3	19
83	Critical Salt Bridges Guide Capsid Assembly, Stability, and Maturation Behavior in Bacteriophage HK97. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1752-1763.	2.5	30
84	Flexible Regions within $\mathbb{I}^{\circ}\mathbb{B}\mathbb{I}^{\pm}$ Create the Ubiquitin-independent Degradation Signal. <i>Journal of Biological Chemistry</i> , 2010, 285, 32927-32936.	1.6	17
85	Molecular Mechanisms of System Control of NF- $\mathbb{I}^{\circ}\mathbb{B}$ Signaling by $\mathbb{I}^{\circ}\mathbb{B}\mathbb{I}^{\pm}$. <i>Biochemistry</i> , 2010, 49, 1560-1567.	1.2	134
86	HK97 Maturation Studied by Crystallography and H/2H Exchange Reveals the Structural Basis for Exothermic Particle Transitions. <i>Journal of Molecular Biology</i> , 2010, 397, 560-574.	2.0	27
87	Structure of the Minimal Interface Between ApoE and LRP. <i>Journal of Molecular Biology</i> , 2010, 398, 306-319.	2.0	53
88	Decoding of Lipoprotein Receptor Interactions: Properties of Ligand Binding Modules Governing Interactions with Apolipoprotein E. <i>Biochemistry</i> , 2010, 49, 1207-1216.	1.2	43
89	Kinetic enhancement of NF- $\mathbb{I}^{\circ}\mathbb{B}$ -DNA dissociation by $\mathbb{I}^{\circ}\mathbb{B}\mathbb{I}^{\pm}$. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19328-19333.	3.3	88
90	Interactions of the NPXY microdomains of the low density lipoprotein receptor-related protein 1. <i>Proteomics</i> , 2009, 9, 5016-5028.	1.3	59

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91	An unexpected twist in viral capsid maturation. <i>Nature</i> , 2009, 458, 646-650.	13.7	120
92	Functional Dynamics of the Folded Ankyrin Repeats of I κ B Revealed by Nuclear Magnetic Resonance. <i>Biochemistry</i> , 2009, 48, 8023-8031.	1.2	22
93	Identification of high levels of phytochelatins, glutathione and cadmium in the phloem sap of <i>Brassica napus</i> . A role for thiol-peptides in the long-distance transport of cadmium and the effect of cadmium on iron translocation. <i>Plant Journal</i> , 2008, 54, 249-259.	2.8	311
94	Folding landscapes of ankyrin repeat proteins: experiments meet theory. <i>Current Opinion in Structural Biology</i> , 2008, 18, 27-34.	2.6	92
95	Rapid mass spectrometric analysis of ¹⁵ N-Leu incorporation fidelity during preparation of specifically labeled NMR samples. <i>Protein Science</i> , 2008, 17, 1636-1639.	3.1	7
96	The I κ B/NF κ B complex has two hot spots, one at either end of the interface. <i>Protein Science</i> , 2008, 17, 2051-2058.	3.1	48
97	Pre-folding I κ B Alters Control of NF- κ B Signaling. <i>Journal of Molecular Biology</i> , 2008, 380, 67-82.	2.0	58
98	Transfer of Flexibility between Ankyrin Repeats in I κ B upon Formation of the NF- κ B Complex. <i>Journal of Molecular Biology</i> , 2008, 380, 917-931.	2.0	61
99	Mutations in the Fourth EGF-like Domain Affect Thrombomodulin-Induced Changes in the Active Site of Thrombin. <i>Biochemistry</i> , 2008, 47, 10933-10939.	1.2	18
100	Structural and Functional Consequences of Tyrosine Phosphorylation in the LRP1 Cytoplasmic Domain. <i>Journal of Biological Chemistry</i> , 2008, 283, 15656-15664.	1.6	37
101	The Energy Landscapes of Repeat-Containing Proteins: Topology, Cooperativity, and the Folding Funnels of One-Dimensional Architectures. <i>PLoS Computational Biology</i> , 2008, 4, e1000070.	1.5	67
102	The plastic landscape of repeat proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7735-7736.	3.3	25
103	Localizing frustration in native proteins and protein assemblies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 19819-19824.	3.3	292
104	Stabilizing I κ B by Consensus-Design. <i>Journal of Molecular Biology</i> , 2007, 365, 1201-1216.	2.0	68
105	Induced Fit, Folding, and Recognition of the NF- κ B-Nuclear Localization Signals by I κ B and I κ B ² . <i>Journal of Molecular Biology</i> , 2007, 367, 262-274.	2.0	31
106	R-subunit Isoform Specificity in Protein Kinase A: Distinct Features of Protein Interfaces in PKA Types I and II by Amide H/2H Exchange Mass Spectrometry. <i>Journal of Molecular Biology</i> , 2007, 374, 487-499.	2.0	16
107	H/2H Exchange Mass Spectrometry of Protein Complexes. , 2007, , 169-187.		0
108	Amide H/2H Exchange Reveals a Mechanism of Thrombin Activation. <i>Biochemistry</i> , 2006, 45, 7724-7732.	1.2	15

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109	Thermodynamics Reveal that Helix Four in the NLS of NF- κ B p65 Anchors κ B, Forming a Very Stable Complex. <i>Journal of Molecular Biology</i> , 2006, 360, 421-434.	2.0	69
110	Automated extraction of backbone deuteration levels from amide H/2H mass spectrometry experiments. <i>Protein Science</i> , 2006, 15, 583-601.	3.1	70
111	Solvent accessibility of protein surfaces by amide H/2H exchange MALDI-TOF mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2006, 17, 1490-1497.	1.2	57
112	Ligand-induced Conformational Changes in the Acetylcholine-binding Protein Analyzed by Hydrogen-Deuterium Exchange Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2006, 281, 12170-12177.	1.6	46
113	An Improved Grafting Technique for Mature Arabidopsis Plants Demonstrates Long-Distance Shoot-to-Root Transport of Phytochelatin in Arabidopsis. <i>Plant Physiology</i> , 2006, 141, 108-120.	2.3	144
114	Regions of I κ B that are critical for its inhibition of NF- κ B{middle dot}DNA interaction fold upon binding to NF- κ B. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18951-18956.	3.3	82
115	Protein-protein interaction dynamics by amide H/2H exchange mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2005, 240, 285-290.	0.7	24
116	Structural and functional consequences of methionine oxidation in thrombomodulin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1703, 141-147.	1.1	27
117	Measurement of Solvent Accessibility at Protein-Protein Interfaces. , 2005, 305, 065-080.		20
118	Thrombomodulin Tightens the Thrombin Active Site Loops To Promote Protein C Activation. <i>Biochemistry</i> , 2005, 44, 14784-14791.	1.2	35
119	The Energy Landscape of Modular Repeat Proteins: Topology Determines Folding Mechanism in the Ankyrin Family. <i>Journal of Molecular Biology</i> , 2005, 354, 679-692.	2.0	91
120	Dynamics of the Fragment of Thrombomodulin Containing the Fourth and Fifth Epidermal Growth Factor-like Domains Correlate with Function. <i>Biochemistry</i> , 2005, 44, 1225-1233.	1.2	10
121	Application of Amide Proton Exchange Mass Spectrometry for the Study of Protein-Protein Interactions. <i>Current Protocols in Protein Science</i> , 2005, 40, Unit20.9.	2.8	9
122	Biophysical characterization of the free κ B ankyrin repeat domain in solution. <i>Protein Science</i> , 2004, 13, 1767-1777.	3.1	101
123	Two Apolipoprotein E Mimetic Peptides, ApoE(130~149) and ApoE(141~155) ₂ , Bind to LRP1. <i>Biochemistry</i> , 2004, 43, 7328-7335.	1.2	78
124	Allosteric Changes in Solvent Accessibility Observed in Thrombin upon Active Site Occupation. <i>Biochemistry</i> , 2004, 43, 5246-5255.	1.2	40
125	Two different proteins that compete for binding to thrombin have opposite kinetic and thermodynamic profiles. <i>Protein Science</i> , 2004, 13, 166-176.	3.1	45
126	NMR Structures Reveal How Oxidation Inactivates Thrombomodulin. <i>Biochemistry</i> , 2003, 42, 11932-11942.	1.2	27

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127	All Three LDL Receptor Homology Regions of the LDL Receptor-Related Protein Bind Multiple Ligands. <i>Biochemistry</i> , 2003, 42, 13049-13057.	1.2	37
128	Identification of the protein kinase A regulatory RIÎ-catalytic subunit interface by amide H/2H exchange and protein docking. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13264-13269.	3.3	88
129	Amide H/2H Exchange Reveals Communication Between the cAMP and Catalytic Subunit-binding Sites in the RIÎ± Subunit of Protein Kinase A. <i>Journal of Molecular Biology</i> , 2002, 323, 377-386.	2.0	95
130	Solvent Exposed Non-contacting Amino Acids Play a Critical Role in NF-Î²B/Î²BÎ± Complex Formation. <i>Journal of Molecular Biology</i> , 2002, 324, 587-597.	2.0	31
131	Epitope mapping of a monoclonal antibody against human thrombin by H/D-exchange mass spectrometry reveals selection of a diverse sequence in a highly conserved protein. <i>Protein Science</i> , 2002, 11, 1300-1308.	3.1	112
132	Solvent accessibility of the thrombin-thrombomodulin interface. Edited by M. F. Moody. <i>Journal of Molecular Biology</i> , 2001, 306, 575-589.	2.0	106
133	Phosphorylation causes subtle changes in solvent accessibility at the interdomain interface of methylesterase CheB 1. Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2001, 307, 967-976.	2.0	60
134	Structural Evaluation of Phospholipid Bicelles for Solution-State Studies of Membrane-Associated Biomolecules. <i>Biophysical Journal</i> , 2001, 81, 2163-2171.	0.2	265
135	Orientation and Effects of Mastoparan X on Phospholipid Bicelles. <i>Biophysical Journal</i> , 2001, 80, 280-293.	0.2	120
136	Disulfide bond plasticity in epidermal growth factor. , 2000, 40, 168-174.		21
137	Solution structure of the smallest cofactor-active fragment of thrombomodulin. <i>Nature Structural Biology</i> , 2000, 7, 200-204.	9.7	42
138	Electrostatic dependence of the thrombin-thrombomodulin interaction 1. Edited by J. A. Wells. <i>Journal of Molecular Biology</i> , 2000, 296, 651-658.	2.0	61
139	Production of large quantities of isotopically labeled protein in <i>Pichia pastoris</i> by fermentation. , 1999, 13, 149-159.		102
140	Measurement of Amide Hydrogen Exchange by MALDI-TOF Mass Spectrometry. <i>Analytical Chemistry</i> , 1998, 70, 3987-3995.	3.2	198
141	Energetics of Thrombin~Thrombomodulin Interaction. <i>Biochemistry</i> , 1997, 36, 6674-6681.	1.2	66
142	Structure of the fifth EGF-like domain of thrombomodulin: an EGF-like domain with a novel disulfide-bonding pattern 1. Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1997, 273, 913-926.	2.0	35
143	The Structural Basis for Pseudoreversion of the H95N Lesion by the Secondary S96P Mutation in Triosephosphate Isomerase. <i>Biochemistry</i> , 1996, 35, 15474-15484.	1.2	15
144	Continuous Production of Thrombomodulin from a <i>Pichia pastoris</i> Fermentation. <i>Journal of Chemical Technology and Biotechnology</i> , 1996, 67, 143-148.	1.6	13

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145	Structural resiliency of an EGF-like subdomain bound to its target protein, thrombin. <i>Protein Science</i> , 1996, 5, 195-203.	3.1	16
146	Synthesis, activity, and preliminary structure of the fourth EGF-like domain of thrombomodulin. <i>Protein Science</i> , 1995, 4, 1683-1695.	3.1	27
147	Thrombin-binding affinities of different disulfide-bonded isomers of the fifth EGF-like domain of thrombomodulin. <i>Protein Science</i> , 1995, 4, 2129-2137.	3.1	23
148	Three reviewer rule. <i>Bio/technology</i> , 1995, 13, 1030-1031.	1.9	0
149	Large-scale expression, purification and characterization of small fragments of thrombomodulin: the roles of the sixth domain and of methionine 388. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 1177-1187.	1.0	66
150	Thrombin inhibition by cyclic peptides from thrombomodulin. <i>Protein Science</i> , 1995, 4, 773-780.	3.1	17
151	Thrombin-bound structure of an EGF subdomain from human thrombomodulin determined by transferred nuclear Overhauser effects. <i>Biochemistry</i> , 1994, 33, 13553-13560.	1.2	26
152	Target binding triggers hierarchical phosphorylation of human Argonaute-2 to promote target release. <i>ELife</i> , 0, 11, .	2.8	11