

Lisa N Kinch

List of Publications by Year in descending order

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Version: 2024-02-01

94
papers

8,592
citations

109321
35
h-index

54911
84
g-index

101
all docs

101
docs citations

101
times ranked

13200
citing authors

#	ARTICLE	IF	CITATIONS
1	Germline and sporadic mTOR pathway mutations in low-grade oncocytic tumor of the kidney. <i>Modern Pathology</i> , 2022, 35, 333-343.	5.5	34
2	Co-component signal transduction systems: Fast-evolving virulence regulation cassettes discovered in enteric bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	14
3	Enzymatic Specificity of Conserved Rho GTPase Deamidases Promotes Invasion of <i>Vibrio parahaemolyticus</i> at the Expense of Infection. <i>MBio</i> , 2022, 13, .	4.1	0
4	Role of Two Metacaspases in Development and Pathogenicity of the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>MBio</i> , 2021, 12, .	4.1	14
5	Manipulation of IRE1-Dependent MAPK Signaling by a <i>Vibrio</i> Agonist-Antagonist Effector Pair. <i>MSystems</i> , 2021, 6, .	3.8	3
6	A Fifth of the Protein World: Rossmann-like Proteins as an Evolutionarily Successful Structural unit. <i>Journal of Molecular Biology</i> , 2021, 433, 166788.	4.2	26
7	A combined RAD-Seq and WGS approach reveals the genomic basis of yellow color variation in bumble bee <i>Bombus terrestris</i> . <i>Scientific Reports</i> , 2021, 11, 7996.	3.3	7
8	Completeness and Consistency in Structural Domain Classifications. <i>ACS Omega</i> , 2021, 6, 15698-15707.	3.5	8
9	Accurate prediction of protein structures and interactions using a three-track neural network. <i>Science</i> , 2021, 373, 871-876.	12.6	2,843
10	Topology evaluation of models for difficult targets in the 14th round of the critical assessment of protein structure prediction (CASP14). <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1673-1686.	2.6	35
11	Target classification in the 14th <scp>round</scp> of the <scp>critical assessment of protein structure prediction</scp> (<scp>CASP14</scp>). <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1618-1632.	2.6	32
12	Assessment of domain interactions in the fourteenth round of the Critical Assessment of Structure Prediction (CASP14). <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1700-1710.	2.6	8
13	Genomics Reveals the Origins of Historical Specimens. <i>Molecular Biology and Evolution</i> , 2021, 38, 2166-2176.	8.9	24
14	RUVBL1/RUVBL2 ATPase Activity Drives PAQosome Maturation, DNA Replication and Radioresistance in Lung Cancer. <i>Cell Chemical Biology</i> , 2020, 27, 105-121.e14.	5.2	38
15	Structure, lipid scrambling activity and role in autophagosome formation of ATG9A. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 1194-1201.	8.2	196
16	Regulation of Beclin 1-Mediated Autophagy by Oncogenic Tyrosine Kinases. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9210.	4.1	27
17	Mutation severity spectrum of rare alleles in the human genome is predictive of disease type. <i>PLoS Computational Biology</i> , 2020, 16, e1007775.	3.2	11
18	Schnyder corneal dystrophy-associated UBIAD1 is defective in MK-4 synthesis and resists autophagy-mediated degradation. <i>Journal of Lipid Research</i> , 2020, 61, 746-757.	4.2	12

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19	Strand-mediated interactions of protein domains. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1513-1527.	2.6	2
20	A lytic polysaccharide monooxygenase-like protein functions in fungal copper import and meningitis. Nature Chemical Biology, 2020, 16, 337-344.	8.0	61
21	Hyperactivation of TORC1 Drives Resistance to the Pan-HER Tyrosine Kinase Inhibitor Neratinib in HER2-Mutant Cancers. Cancer Cell, 2020, 37, 183-199.e5.	16.8	33
22	Recent advances suggest increased influence of selective pressure in allostery. Current Opinion in Structural Biology, 2020, 62, 183-188.	5.7	13
23	Assessing predictions on fitness effects of missense variants in calmodulin. Human Mutation, 2019, 40, 1463-1473.	2.5	8
24	CASP13 target classification into tertiary structure prediction categories. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1021-1036.	2.6	34
25	ECOD: identification of distant homology among multidomain and transmembrane domain proteins. BMC Molecular and Cell Biology, 2019, 20, 18.	2.0	12
26	The Legionella effector RavD binds phosphatidylinositol-3-phosphate and helps suppress endolysosomal maturation of the Legionella-containing vacuole. Journal of Biological Chemistry, 2019, 294, 6405-6415.	3.4	22
27	Identification of residues critical for topology inversion of the transmembrane protein TM4SF20 through regulated alternative translocation. Journal of Biological Chemistry, 2019, 294, 6054-6061.	3.4	5
28	Functional analysis of Rossmann-like domains reveals convergent evolution of topology and reaction pathways. PLoS Computational Biology, 2019, 15, e1007569.	3.2	45
29	Combined Blockade of Activating ERBB2 Mutations and ER Results in Synthetic Lethality of ER+/HER2 Mutant Breast Cancer. Clinical Cancer Research, 2019, 25, 277-289.	7.0	74
30	NK cell defects in X-linked pigmentary reticulate disorder. JCI Insight, 2019, 4, .	5.0	17
31	Functional and evolutionary analysis of viral proteins containing a Rossmann-like fold. Protein Science, 2018, 27, 1450-1463.	7.6	18
32	Definition and classification of evaluation units for tertiary structure prediction in CASP12 facilitated through semi-automated metrics. Proteins: Structure, Function and Bioinformatics, 2018, 86, 16-26.	2.6	12
33	Protein AMPylation by an Evolutionarily Conserved Pseudokinase. Cell, 2018, 175, 809-821.e19.	28.9	149
34	FlyXCDB: A Resource for Drosophila Cell Surface and Secreted Proteins and Their Extracellular Domains. Journal of Molecular Biology, 2018, 430, 3353-3411.	4.2	13
35	Acute Hepatopancreatic Necrosis Disease-Causing Vibrio parahaemolyticus Strains Maintain an Antibacterial Type VI Secretion System with Versatile Effector Repertoires. Applied and Environmental Microbiology, 2017, 83, .	3.1	88
36	Assessing predictions of fitness effects of missense mutations in SUMO-conjugating enzyme UBE2L. Human Mutation, 2017, 38, 1051-1063.	2.5	12

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37	Pet10p is a yeast perilipin that stabilizes lipid droplets and promotes their assembly. <i>Journal of Cell Biology</i> , 2017, 216, 3199-3217.	5.2	92
38	Relief of autoinhibition by conformational switch explains enzyme activation by a catalytically dead paralog. <i>ELife</i> , 2016, 5, .	6.0	19
39	Pyrimidine Salvage Enzymes Are Essential for De Novo Biosynthesis of Deoxypyrimidine Nucleotides in <i>Trypanosoma brucei</i> . <i>PLoS Pathogens</i> , 2016, 12, e1006010.	4.7	39
40	Assessment of CASP11 contact-assisted predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 164-180.	2.6	24
41	CASP 11 target classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 20-33.	2.6	31
42	Crystal structure of the human sterol transporter ABCG5/ABCG8. <i>Nature</i> , 2016, 533, 561-564.	27.8	233
43	Compact Structure Patterns in Proteins. <i>Journal of Molecular Biology</i> , 2016, 428, 4392-4412.	4.2	20
44	Proteomics Analysis Reveals Previously Uncharacterized Virulence Factors in <i>Vibrio proteolyticus</i> . <i>MBio</i> , 2016, 7, .	4.1	21
45	HP1BP3, a Chromatin Retention Factor for Co-transcriptional MicroRNA Processing. <i>Molecular Cell</i> , 2016, 63, 420-432.	9.7	32
46	Direct Demonstration That Loop1 of Scap Binds to Loop7. <i>Journal of Biological Chemistry</i> , 2016, 291, 12888-12896.	3.4	17
47	Classification of proteins with shared motifs and internal repeats in the <scp>ECOD</scp> database. <i>Protein Science</i> , 2016, 25, 1188-1203.	7.6	23
48	Evaluation of free modeling targets in CASP11 and ROLL. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 51-66.	2.6	70
49	Complete genome of <i>Pieris rapae</i> , a resilient alien, a cabbage pest, and a source of anti-cancer proteins. <i>F1000Research</i> , 2016, 5, 2631.	1.6	47
50	Bile salt receptor complex activates a pathogenic type III secretion system. <i>ELife</i> , 2016, 5, .	6.0	68
51	Structure of protein O-mannose kinase reveals a unique active site architecture. <i>ELife</i> , 2016, 5, .	6.0	33
52	Type VI Secretion System Toxins Horizontally Shared between Marine Bacteria. <i>PLoS Pathogens</i> , 2015, 11, e1005128.	4.7	71
53	Using homology relations within a database markedly boosts protein sequence similarity search. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7003-7008.	7.1	8
54	A Single Kinase Generates the Majority of the Secreted Phosphoproteome. <i>Cell</i> , 2015, 161, 1619-1632.	28.9	264

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55	<scp>ChSeq</scp>: A database of chameleon sequences. Protein Science, 2015, 24, 1075-1086.	7.6	47
56	The secretory pathway kinases. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 1687-1693.	2.3	31
57	Spectrum of diverse genomic alterations define nonâ€“clear cell renal carcinoma subtypes. Nature Genetics, 2015, 47, 13-21.	21.4	310
58	Large-scale determination of previously unsolved protein structures using evolutionary information. ELife, 2015, 4, e09248.	6.0	229
59	ECOD: An Evolutionary Classification of Protein Domains. PLoS Computational Biology, 2014, 10, e1003926.	3.2	321
60	Marker for type VI secretion system effectors. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9271-9276.	7.1	165
61	Vibrio Type III Effector VPA1380 Is Related to the Cysteine Protease Domain of Large Bacterial Toxins. PLoS ONE, 2014, 9, e104387.	2.5	22
62	Bioinformatics perspective on rhomboid intramembrane protease evolution and function. Biochimica Et Biophysica Acta - Biomembranes, 2013, 1828, 2937-2943.	2.6	26
63	Beclin 2 Functions in Autophagy, Degradation of G Protein-Coupled Receptors, and Metabolism. Cell, 2013, 154, 1085-1099.	28.9	130
64	Solution Structure of the WNK1 Autoinhibitory Domain, a WNK-Specific PF2 Domain. Journal of Molecular Biology, 2013, 425, 1245-1252.	4.2	13
65	Effectors of animal and plant pathogens use a common domain to bind host phosphoinositides. Nature Communications, 2013, 4, 2973.	12.8	62
66	A Novel Germline Mutation in <i>BAP1</i> Predisposes to Familial Clear-Cell Renal Cell Carcinoma. Molecular Cancer Research, 2013, 11, 1061-1071.	3.4	135
67	Autoinhibition and Salt Sensing are Linked in the WNK1 Kinase. FASEB Journal, 2012, 26, lb162.	0.5	0
68	Succination of Keap1 and Activation of Nrf2-Dependent Antioxidant Pathways in FH-Deficient Papillary Renal Cell Carcinoma Type 2. Cancer Cell, 2011, 20, 418-420.	16.8	92
69	CASP9 assessment of free modeling target predictions. Proteins: Structure, Function and Bioinformatics, 2011, 79, 59-73.	2.6	87
70	CASP9 target classification. Proteins: Structure, Function and Bioinformatics, 2011, 79, 21-36.	2.6	61
71	An automatic method for CASP9 free modeling structure prediction assessment. Bioinformatics, 2011, 27, 3371-3378.	4.1	24
72	Kinetic and Structural Insights into the Mechanism of AMPylation by VopS Fic Domain. Journal of Biological Chemistry, 2010, 285, 20155-20163.	3.4	77

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73	Fido, a Novel AMPylation Domain Common to Fic, Doc, and AvrB. PLoS ONE, 2009, 4, e5818.	2.5	116
74	A Database of Domain Definitions for Proteins with Complex Interdomain Geometry. PLoS ONE, 2009, 4, e5084.	2.5	19
75	Analysis of CASP8 targets, predictions and assessment methods. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap003-bap003.	3.0	29
76	AMPylation of Rho GTPases by <i>Vibrio</i> VopS Disrupts Effector Binding and Downstream Signaling. Science, 2009, 323, 269-272.	12.6	343
77	Structure prediction for CASP8 with all-atom refinement using Rosetta. Proteins: Structure, Function and Bioinformatics, 2009, 77, 89-99.	2.6	425
78	The human Ago2 MC region does not contain an eIF4E-like mRNA cap binding motif. Biology Direct, 2009, 4, 2.	4.6	29
79	Realm of PD-(D/E)XK nuclease superfamily revisited: detection of novel families with modified transitive meta profile searches. BMC Structural Biology, 2007, 7, 40.	2.3	57
80	Site-2 protease regulated intramembrane proteolysis: Sequence homologs suggest an ancient signaling cascade. Protein Science, 2006, 15, 84-93.	7.6	97
81	Longin-like folds identified in CHiPS and DUF254 proteins: Vesicle trafficking complexes conserved in eukaryotic evolution. Protein Science, 2006, 15, 2669-2674.	7.6	32
82	Human Herpesvirus 1 <i>UL24</i> Gene Encodes a Potential PD-(D/E)XK Endonuclease. Journal of Virology, 2006, 80, 2575-2577.	3.4	35
83	Identification of novel restriction endonuclease-like fold families among hypothetical proteins. Nucleic Acids Research, 2005, 33, 3598-3605.	14.5	83
84	EDD, a novel phosphotransferase domain common to mannose transporter EIIA, dihydroxyacetone kinase, and DegV. Protein Science, 2005, 14, 360-367.	7.6	16
85	DCC proteins: a novel family of thiol-disulfide oxidoreductases. Trends in Biochemical Sciences, 2004, 29, 339-342.	7.5	7
86	BTLCF proteins: a novel family of bacterial transglutaminase-like cysteine proteinases. Trends in Biochemical Sciences, 2004, 29, 392-395.	7.5	29
87	BOF: a novel family of bacterial OB-fold proteins. FEBS Letters, 2004, 567, 297-301.	2.8	36
88	Deciphering a novel thioredoxin-like fold family. Proteins: Structure, Function and Bioinformatics, 2003, 52, 323-331.	2.6	13
89	CASP5 target classification. Proteins: Structure, Function and Bioinformatics, 2003, 53, 340-351.	2.6	20
90	CASP5 assessment of fold recognition target predictions. Proteins: Structure, Function and Bioinformatics, 2003, 53, 395-409.	2.6	91

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91	Sec61 ¹² is a component of the archaeal protein secretory system. Trends in Biochemical Sciences, 2002, 27, 170-171.	7.5	49
92	Evolution of protein structures and functions. Current Opinion in Structural Biology, 2002, 12, 400-408.	5.7	144
93	Expanding the nitrogen regulatory protein superfamily: Homology detection at below random sequence identity. Proteins: Structure, Function and Bioinformatics, 2002, 48, 75-84.	2.6	16
94	Hyperactivation of Torc1 Drives Resistance to the Pan-Her Tyrosine Kinase Inhibitor Neratinib in Her2-Mutant Cancers. SSRN Electronic Journal, 0, , .	0.4	0