

# Lisa N Kinch

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8636889/publications.pdf>

Version: 2024-02-01

94  
papers

8,592  
citations

109137

35  
h-index

54797

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.	2.9	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, .	3.3	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, .	1.8	0
4	Role of Two Metacaspases in Development and Pathogenicity of the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>MBio</i> , 2021, 12, .	1.8	14
5	Manipulation of IRE1-Dependent MAPK Signaling by a <i>Vibrio</i> Agonist-Antagonist Effector Pair. <i>MSystems</i> , 2021, 6, .	1.7	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.	2.0	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.	1.6	7
8	Completeness and Consistency in Structural Domain Classifications. <i>ACS Omega</i> , 2021, 6, 15698-15707.	1.6	8
9	Accurate prediction of protein structures and interactions using a three-track neural network. <i>Science</i> , 2021, 373, 871-876.	6.0	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.	1.5	35
11	Target classification in the 14th round of the critical assessment of protein structure prediction (CASP14). <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1618-1632.	1.5	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.	1.5	8
13	Genomics Reveals the Origins of Historical Specimens. <i>Molecular Biology and Evolution</i> , 2021, 38, 2166-2176.	3.5	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.	2.5	38
15	Structure, lipid scrambling activity and role in autophagosome formation of ATG9A. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 1194-1201.	3.6	196
16	Regulation of Beclin 1-Mediated Autophagy by Oncogenic Tyrosine Kinases. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9210.	1.8	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.	1.5	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.	2.0	12

#	ARTICLE	IF	CITATIONS
19	<sc>Î²-strand</sc>-mediated interactions of protein domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1513-1527.	1.5	2
20	A lytic polysaccharide monooxygenase-like protein functions in fungal copper import and meningitis. <i>Nature Chemical Biology</i> , 2020, 16, 337-344.	3.9	61
21	Hyperactivation of TORC1 Drives Resistance to the Pan-HER Tyrosine Kinase Inhibitor Neratinib in HER2-Mutant Cancers. <i>Cancer Cell</i> , 2020, 37, 183-199.e5.	7.7	33
22	Recent advances suggest increased influence of selective pressure in allostery. <i>Current Opinion in Structural Biology</i> , 2020, 62, 183-188.	2.6	13
23	Assessing predictions on fitness effects of missense variants in calmodulin. <i>Human Mutation</i> , 2019, 40, 1463-1473.	1.1	8
24	CASP13 target classification into tertiary structure prediction categories. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1021-1036.	1.5	34
25	ECOD: identification of distant homology among multidomain and transmembrane domain proteins. <i>BMC Molecular and Cell Biology</i> , 2019, 20, 18.	1.0	12
26	The Legionella effector RavD binds phosphatidylinositol-3-phosphate and helps suppress endolysosomal maturation of the Legionella-containing vacuole. <i>Journal of Biological Chemistry</i> , 2019, 294, 6405-6415.	1.6	22
27	Identification of residues critical for topology inversion of the transmembrane protein TM4SF20 through regulated alternative translocation. <i>Journal of Biological Chemistry</i> , 2019, 294, 6054-6061.	1.6	5
28	Functional analysis of Rossmann-like domains reveals convergent evolution of topology and reaction pathways. <i>PLoS Computational Biology</i> , 2019, 15, e1007569.	1.5	45
29	Combined Blockade of Activating ERBB2 Mutations and ER Results in Synthetic Lethality of ER+/HER2 Mutant Breast Cancer. <i>Clinical Cancer Research</i> , 2019, 25, 277-289.	3.2	74
30	NK cell defects in X-linked pigmentary reticulate disorder. <i>JCI Insight</i> , 2019, 4, .	2.3	17
31	Functional and evolutionary analysis of viral proteins containing a Rossmann-like fold. <i>Protein Science</i> , 2018, 27, 1450-1463.	3.1	18
32	Definition and classification of evaluation units for tertiary structure prediction in CASP12 facilitated through semi-automated metrics. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 16-26.	1.5	12
33	Protein AMPylation by an Evolutionarily Conserved Pseudokinase. <i>Cell</i> , 2018, 175, 809-821.e19.	13.5	149
34	FlyXCDB: A Resource for Drosophila Cell Surface and Secreted Proteins and Their Extracellular Domains. <i>Journal of Molecular Biology</i> , 2018, 430, 3353-3411.	2.0	13
35	Acute Hepatopancreatic Necrosis Disease-Causing <i>Vibrio parahaemolyticus</i> Strains Maintain an Antibacterial Type VI Secretion System with Versatile Effector Repertoires. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	88
36	Assessing predictions of fitness effects of missense mutations in SUMO-conjugating enzyme UBE2L. <i>Human Mutation</i> , 2017, 38, 1051-1063.	1.1	12

#	ARTICLE	IF	CITATIONS
37	Pet10p is a yeast perilipin that stabilizes lipid droplets and promotes their assembly. <i>Journal of Cell Biology</i> , 2017, 216, 3199-3217.	2.3	92
38	Relief of autoinhibition by conformational switch explains enzyme activation by a catalytically dead paralog. <i>ELife</i> , 2016, 5, .	2.8	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.	2.1	39
40	Assessment of CASP11 contact-assisted predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 164-180.	1.5	24
41	CASP 11 target classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 20-33.	1.5	31
42	Crystal structure of the human sterol transporter ABCG5/ABCG8. <i>Nature</i> , 2016, 533, 561-564.	13.7	233
43	Compact Structure Patterns in Proteins. <i>Journal of Molecular Biology</i> , 2016, 428, 4392-4412.	2.0	20
44	Proteomics Analysis Reveals Previously Uncharacterized Virulence Factors in <i>Vibrio proteolyticus</i> . <i>MBio</i> , 2016, 7, .	1.8	21
45	HP1BP3, a Chromatin Retention Factor for Co-transcriptional MicroRNA Processing. <i>Molecular Cell</i> , 2016, 63, 420-432.	4.5	32
46	Direct Demonstration That Loop1 of Scap Binds to Loop7. <i>Journal of Biological Chemistry</i> , 2016, 291, 12888-12896.	1.6	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.	3.1	23
48	Evaluation of free modeling targets in CASP11 and ROLL. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 51-66.	1.5	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.	0.8	47
50	Bile salt receptor complex activates a pathogenic type III secretion system. <i>ELife</i> , 2016, 5, .	2.8	68
51	Structure of protein O-mannose kinase reveals a unique active site architecture. <i>ELife</i> , 2016, 5, .	2.8	33
52	Type VI Secretion System Toxins Horizontally Shared between Marine Bacteria. <i>PLoS Pathogens</i> , 2015, 11, e1005128.	2.1	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.	3.3	8
54	A Single Kinase Generates the Majority of the Secreted Phosphoproteome. <i>Cell</i> , 2015, 161, 1619-1632.	13.5	264

#	ARTICLE	IF	CITATIONS
55	<scp>ChSeq</scp>: A database of chameleon sequences. <i>Protein Science</i> , 2015, 24, 1075-1086.	3.1	47
56	The secretory pathway kinases. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1687-1693.	1.1	31
57	Spectrum of diverse genomic alterations define non-“clear cell renal carcinoma subtypes. <i>Nature Genetics</i> , 2015, 47, 13-21.	9.4	310
58	Large-scale determination of previously unsolved protein structures using evolutionary information. <i>ELife</i> , 2015, 4, e09248.	2.8	229
59	ECOD: An Evolutionary Classification of Protein Domains. <i>PLoS Computational Biology</i> , 2014, 10, e1003926.	1.5	321
60	Marker for type VI secretion system effectors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9271-9276.	3.3	165
61	Vibrio Type III Effector VPA1380 Is Related to the Cysteine Protease Domain of Large Bacterial Toxins. <i>PLoS ONE</i> , 2014, 9, e104387.	1.1	22
62	Bioinformatics perspective on rhomboid intramembrane protease evolution and function. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 2937-2943.	1.4	26
63	Beclin 2 Functions in Autophagy, Degradation of G Protein-Coupled Receptors, and Metabolism. <i>Cell</i> , 2013, 154, 1085-1099.	13.5	130
64	Solution Structure of the WNK1 Autoinhibitory Domain, a WNK-Specific PF2 Domain. <i>Journal of Molecular Biology</i> , 2013, 425, 1245-1252.	2.0	13
65	Effectors of animal and plant pathogens use a common domain to bind host phosphoinositides. <i>Nature Communications</i> , 2013, 4, 2973.	5.8	62
66	A Novel Germline Mutation in <i>BAP1</i> Predisposes to Familial Clear-Cell Renal Cell Carcinoma. <i>Molecular Cancer Research</i> , 2013, 11, 1061-1071.	1.5	135
67	Autoinhibition and Salt Sensing are Linked in the WNK1 Kinase. <i>FASEB Journal</i> , 2012, 26, lb162.	0.2	0
68	Succination of Keap1 and Activation of Nrf2-Dependent Antioxidant Pathways in FH-Deficient Papillary Renal Cell Carcinoma Type 2. <i>Cancer Cell</i> , 2011, 20, 418-420.	7.7	92
69	CASP9 assessment of free modeling target predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 59-73.	1.5	87
70	CASP9 target classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 21-36.	1.5	61
71	An automatic method for CASP9 free modeling structure prediction assessment. <i>Bioinformatics</i> , 2011, 27, 3371-3378.	1.8	24
72	Kinetic and Structural Insights into the Mechanism of AMPylation by VopS Fic Domain. <i>Journal of Biological Chemistry</i> , 2010, 285, 20155-20163.	1.6	77

#	ARTICLE	IF	CITATIONS
73	Fido, a Novel AMPylation Domain Common to Fic, Doc, and AvrB. PLoS ONE, 2009, 4, e5818.	1.1	116
74	A Database of Domain Definitions for Proteins with Complex Interdomain Geometry. PLoS ONE, 2009, 4, e5084.	1.1	19
75	Analysis of CASP8 targets, predictions and assessment methods. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap003-bap003.	1.4	29
76	AMPylation of Rho GTPases by <i>Vibrio</i> VopS Disrupts Effector Binding and Downstream Signaling. Science, 2009, 323, 269-272.	6.0	343
77	Structure prediction for CASP8 with all-atom refinement using Rosetta. Proteins: Structure, Function and Bioinformatics, 2009, 77, 89-99.	1.5	425
78	The human Ago2 MC region does not contain an eIF4E-like mRNA cap binding motif. Biology Direct, 2009, 4, 2.	1.9	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.	3.1	97
81	Longin-like folds identified in CHiPS and DUF254 proteins: Vesicle trafficking complexes conserved in eukaryotic evolution. Protein Science, 2006, 15, 2669-2674.	3.1	32
82	Human Herpesvirus 1 UL24 Gene Encodes a Potential PD-(D/E)XK Endonuclease. Journal of Virology, 2006, 80, 2575-2577.	1.5	35
83	Identification of novel restriction endonuclease-like fold families among hypothetical proteins. Nucleic Acids Research, 2005, 33, 3598-3605.	6.5	83
84	EDD, a novel phosphotransferase domain common to mannose transporter EIIA, dihydroxyacetone kinase, and DegV. Protein Science, 2005, 14, 360-367.	3.1	16
85	DCC proteins: a novel family of thiol-disulfide oxidoreductases. Trends in Biochemical Sciences, 2004, 29, 339-342.	3.7	7
86	BTLCP proteins: a novel family of bacterial transglutaminase-like cysteine proteinases. Trends in Biochemical Sciences, 2004, 29, 392-395.	3.7	29
87	BOF: a novel family of bacterial OB-fold proteins. FEBS Letters, 2004, 567, 297-301.	1.3	36
88	Deciphering a novel thioredoxin-like fold family. Proteins: Structure, Function and Bioinformatics, 2003, 52, 323-331.	1.5	13
89	CASP5 target classification. Proteins: Structure, Function and Bioinformatics, 2003, 53, 340-351.	1.5	20
90	CASP5 assessment of fold recognition target predictions. Proteins: Structure, Function and Bioinformatics, 2003, 53, 395-409.	1.5	91

#	ARTICLE	IF	CITATIONS
91	Sec61 is a component of the archaeal protein secretory system. Trends in Biochemical Sciences, 2002, 27, 170-171.	3.7	49
92	Evolution of protein structures and functions. Current Opinion in Structural Biology, 2002, 12, 400-408.	2.6	144
93	Expanding the nitrogen regulatory protein superfamily: Homology detection at below random sequence identity. Proteins: Structure, Function and Bioinformatics, 2002, 48, 75-84.	1.5	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