

Natalie K Goto

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9516198/publications.pdf>

Version: 2024-02-01

40
papers

2,567
citations

430874

18
h-index

302126

39
g-index

45
all docs

45
docs citations

45
times ranked

2899
citing authors

#	ARTICLE	IF	CITATIONS
1	A transient amphipathic helix in the prodomain of PCSK9 facilitates binding to low-density lipoprotein particles. <i>Journal of Biological Chemistry</i> , 2020, 295, 2285-2298.	3.4	15
2	Origin of conformational dynamics in a globular protein. <i>Communications Biology</i> , 2019, 2, 433.	4.4	11
3	Antimicrobial peptide LL-37 and its truncated forms, GI-20 and GF-17, exert spermicidal effects and microbicidal activity against <i>Neisseria gonorrhoeae</i> . <i>Human Reproduction</i> , 2018, 33, 2175-2183.	0.9	14
4	Dissecting the role of conformational change and membrane binding by the bacterial cell division regulator MinE in the stimulation of MinD ATPase activity. <i>Journal of Biological Chemistry</i> , 2017, 292, 20732-20743.	3.4	17
5	Rational design of proteins that exchange on functional timescales. <i>Nature Chemical Biology</i> , 2017, 13, 1280-1285.	8.0	76
6	Impact of Differential Detergent Interactions on Transmembrane Helix Dimerization Affinities. <i>ACS Omega</i> , 2016, 1, 277-285.	3.5	0
7	Activity-based profiling of the proteasome pathway during hepatitis C virus infection. <i>Proteomics</i> , 2015, 15, 3815-3825.	2.2	6
8	Prediction of Stable Globular Proteins Using Negative Design with Non-native Backbone Ensembles. <i>Structure</i> , 2015, 23, 2011-2021.	3.3	21
9	Profiling Kinase Activity during Hepatitis C Virus Replication Using a Wortmannin Probe. <i>ACS Infectious Diseases</i> , 2015, 1, 443-452.	3.8	7
10	Influence of hydrophobic mismatch on the catalytic activity of <i>Escherichia coli</i> GpG rhomboid protease. <i>Protein Science</i> , 2015, 24, 464-473.	7.6	15
11	The Importance of Intrinsic Order in a Disordered Protein Ligand. <i>Biophysical Journal</i> , 2014, 106, 1557-1558.	0.5	3
12	Micelle-Catalyzed Domain Swapping in the GlpG Rhomboid Protease Cytoplasmic Domain. <i>Biochemistry</i> , 2014, 53, 5907-5915.	2.5	8
13	A New Chemical Probe for Phosphatidylinositol Kinase Activity. <i>ChemBioChem</i> , 2014, 15, 1253-1256.	2.6	25
14	Activity-Based Protein Profiling of the <i>Escherichia coli</i> GlpG Rhomboid Protein Delineates the Catalytic Core. <i>Biochemistry</i> , 2012, 51, 7794-7803.	2.5	43
15	Contemporary Methods in Structure Determination of Membrane Proteins by Solution NMR. <i>Topics in Current Chemistry</i> , 2011, 326, 123-185.	4.0	19
16	Regulation of symmetric bacterial cell division by MinE. <i>Communicative and Integrative Biology</i> , 2011, 4, 101-103.	1.4	7
17	Regulation of symmetric bacterial cell division by MinE: What is the role of conformational dynamics?. <i>Communicative and Integrative Biology</i> , 2011, 4, 101-3.	1.4	4
18	¹ H, ¹³ C, ¹⁵ N chemical shift assignments for the <i>Neisseria gonorrhoeae</i> MinE regulator of cell division septum placement. <i>Biomolecular NMR Assignments</i> , 2010, 4, 227-229.	0.8	2

#	ARTICLE	IF	CITATIONS
19	Appropriation of the MinD protein-interaction motif by the dimeric interface of the bacterial cell division regulator MinE. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 18416-18421.	7.1	40
20	Insights into the effect of detergents on the full-length rhomboid protease from <i>Pseudomonas aeruginosa</i> and its cytosolic domain. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2009, 1788, 2444-2453.	2.6	18
21	Subtilisin Kexin Isozyme-1 (SKI-1): Production, purification, inhibitor design and biochemical applications. <i>Advances in Experimental Medicine and Biology</i> , 2009, 611, 83-84.	1.6	3
22	Investigation of the utility of selective methyl protonation for determination of membrane protein structures. <i>Journal of Biomolecular NMR</i> , 2008, 42, 49-58.	2.8	7
23	Probing the structure of the Ff bacteriophage major coat protein transmembrane helix dimer by solution NMR. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007, 1768, 3206-3215.	2.6	10
24	Inhibition of siRNA Binding to a p19 Viral Suppressor of RNA Silencing by Cysteine Alkylation. <i>Angewandte Chemie - International Edition</i> , 2007, 46, 2005-2009.	13.8	19
25	Stabilized recombinant suppressors of RNA silencing: Functional effects of linking monomers of Carnation Italian Ringspot virus p19. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007, 1774, 1528-1535.	2.3	14
26	Conformation of the Cell Division Regulator MinE: Evidence for Interactions between the Topological Specificity and Anti-MinCD Domains. <i>Biochemistry</i> , 2006, 45, 4593-4601.	2.5	18
27	Structural Basis for Cooperative Transcription Factor Binding to the CBP Coactivator. <i>Journal of Molecular Biology</i> , 2006, 355, 1005-1013.	4.2	166
28	Structural Characterization of Unfolded States of Apomyoglobin using Residual Dipolar Couplings. <i>Journal of Molecular Biology</i> , 2004, 340, 1131-1142.	4.2	165
29	Polar residue tagging of transmembrane peptides. <i>Biopolymers</i> , 2003, 71, 675-685.	2.4	86
30	The hydrophobicity threshold for peptide insertion into membranes. <i>Current Topics in Membranes</i> , 2002, 52, 465-479.	0.9	9
31	Cooperativity in Transcription Factor Binding to the Coactivator CREB-binding Protein (CBP). <i>Journal of Biological Chemistry</i> , 2002, 277, 43168-43174.	3.4	166
32	What is the average conformation of bacteriophage T4 lysozyme in solution? a domain orientation study using dipolar couplings measured by solution NMR. Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2001, 308, 745-764.	4.2	90
33	Ligand-induced structural changes to maltodextrin-binding protein as studied by solution NMR spectroscopy. <i>Journal of Molecular Biology</i> , 2001, 309, 961-974.	4.2	126
34	New developments in isotope labeling strategies for protein solution NMR spectroscopy. <i>Current Opinion in Structural Biology</i> , 2000, 10, 585-592.	5.7	222
35	Orienting domains in proteins using dipolar couplings measured by liquid-state NMR: differences in solution and crystal forms of maltodextrin binding protein loaded with ¹² C-cyclodextrin. <i>Journal of Molecular Biology</i> , 2000, 295, 1265-1273.	4.2	197
36	A robust and cost-effective method for the production of Val, Leu, Ile (delta 1) methyl-protonated ¹⁵ N-, ¹³ C-, ² H-labeled proteins. <i>Journal of Biomolecular NMR</i> , 1999, 13, 369-374.	2.8	461

#	ARTICLE	IF	CITATIONS
37	An HNCQ-based Pulse Scheme for the Measurement of ^{13}C - ^1H One-bond Dipolar couplings in ^{15}N , ^{13}C Labeled Proteins. Journal of Biomolecular NMR, 1998, 12, 325-332.	2.8	54
38	Threshold hydrophobicity dictates helical conformations of peptides in membrane environments. , 1998, 39, 465-470.		68
39	Alpha-helical, but not beta-sheet, propensity of proline is determined by peptide environment.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 6676-6681.	7.1	278
40	Folding proteins into membranes. Nature Structural and Molecular Biology, 1996, 3, 815-818.	8.2	56