

Malin M Young

List of Publications by Year in descending order

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27
papers

1,607
citations

361413

20
h-index

526287

27
g-index

27
all docs

27
docs citations

27
times ranked

1547
citing authors

#	ARTICLE	IF	CITATIONS
1	High throughput protein fold identification by using experimental constraints derived from intramolecular cross-links and mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 5802-5806.	7.1	431
2	MS2Assign, automated assignment and nomenclature of tandem mass spectra of chemically crosslinked peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2003, 14, 834-850.	2.8	250
3	A top down approach to protein structural studies using chemical cross-linking and Fourier transform mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2003, 17, 155-162.	1.5	117
4	Top-Down Characterization of Nucleic Acids Modified by Structural Probes Using High-Resolution Tandem Mass Spectrometry and Automated Data Interpretation. <i>Analytical Chemistry</i> , 2004, 76, 2438-2445.	6.5	75
5	Predicting conformational switches in proteins. <i>Protein Science</i> , 1999, 8, 1752-1764.	7.6	74
6	Design, docking, and evaluation of multiple libraries against multiple targets. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 42, 296-318.	2.6	66
7	A Top-down method for the determination of residue-specific solvent accessibility in proteins. <i>Journal of Mass Spectrometry</i> , 2004, 39, 322-328.	1.6	61
8	Structure and dynamics of dark-state bovine rhodopsin revealed by chemical cross-linking and high-resolution mass spectrometry. <i>Protein Science</i> , 2006, 15, 1303-1317.	7.6	50
9	Isotopically labeled crosslinking reagents: resolution of mass degeneracy in the identification of crosslinked peptides. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2003, 13, 4023-4026.	2.2	48
10	A Top-Down Approach to Protein Structure Studies Using Chemical Cross-Linking and Fourier Transform Mass Spectrometry. <i>European Journal of Mass Spectrometry</i> , 2003, 9, 623-631.	1.0	46
11	Unambiguous Assignment of Intramolecular Chemical Cross-Links in Modified Mammalian Membrane Proteins by Fourier Transform-Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2005, 77, 5101-5106.	6.5	40
12	PostDOCK: A Structural, Empirical Approach to Scoring Protein Ligand Complexes. <i>Journal of Medicinal Chemistry</i> , 2005, 48, 6821-6831.	6.4	36
13	Optimal bundling of transmembrane helices using sparse distance constraints. <i>Protein Science</i> , 2009, 13, 2613-2627.	7.6	36
14	Partial Acetylation of Lysine Residues Improves Intraprotein Cross-Linking. <i>Analytical Chemistry</i> , 2008, 80, 951-960.	6.5	34
15	Influence of crosslinker identity and position on gas-phase dissociation of lys-lys crosslinked peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2006, 17, 395-405.	2.8	29
16	The Collaboratory for MS3D: A New Cyberinfrastructure for the Structural Elucidation of Biological Macromolecules and Their Assemblies Using Mass Spectrometry-Based Approaches. <i>Journal of Proteome Research</i> , 2008, 7, 4848-4857.	3.7	29
17	Structural model of the CopA copper ATPase of <i>Enterococcus hirae</i> based on chemical cross-linking. <i>BioMetals</i> , 2009, 22, 363-375.	4.1	25
18	Predicting allosteric switches in myosins. <i>Protein Science</i> , 1999, 8, 1806-1815.	7.6	23

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19	"Zero-length" cross-linking in solid state as an approach for analysis of protein-protein interactions. Protein Science, 2006, 15, 429-440.	7.6	23
20	Exploring the conformational space of membrane protein folds matching distance constraints. Protein Science, 2003, 12, 1750-1761.	7.6	21
21	Optimizing an Empirical Scoring Function for Transmembrane Protein Structure Determination. INFORMS Journal on Computing, 2004, 16, 406-418.	1.7	21
22	Computer-assisted Mutagenesis of Ecotin to Engineer Its Secondary Binding Site for Urokinase Inhibition. Journal of Biological Chemistry, 2002, 277, 26623-26631.	3.4	20
23	A rapid method for exploring the protein structure universe. Proteins: Structure, Function and Bioinformatics, 1999, 34, 317-332.	2.6	15
24	Probing alpha-crystallin structure using chemical cross-linkers and mass spectrometry. Molecular Vision, 2004, 10, 857-66.	1.1	15
25	Constrained walks and self-avoiding walks: implications for protein structure determination. Journal of Physics A, 2002, 35, 1-19.	1.6	9
26	Genomes to Life "Center for Molecular and Cellular Systems": A Research Program for Identification and Characterization of Protein Complexes. OMICS A Journal of Integrative Biology, 2002, 6, 287-303.	2.0	7
27	Computational approaches for identification of conserved/unique binding pockets in the A chain of ricin. Bioinformatics, 2005, 21, 3089-3096.	4.1	6