Malin M Young

List of Publications by Year
in descending order

27	1,607	361413 20	526287 27
papers	citations	h-index	g-index

27	27	27	1547
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structural model of the CopA copper ATPase of Enterococcus hirae based on chemical cross-linking. BioMetals, 2009, 22, 363-375.	4.1	25
2	Optimal bundling of transmembrane helices using sparse distance constraints. Protein Science, 2009, 13, 2613-2627.	7.6	36
3	Partial Acetylation of Lysine Residues Improves Intraprotein Cross-Linking. Analytical Chemistry, 2008, 80, 951-960.	6.5	34
4	The Collaboratory for MS3D: A New Cyberinfrastructure for the Structural Elucidation of Biological Macromolecules and Their Assemblies Using Mass Spectrometry-Based Approaches. Journal of Proteome Research, 2008, 7, 4848-4857.	3.7	29
5	Influence of crosslinker identity and position on gas-phase dissociation of lys-lys crosslinked peptides. Journal of the American Society for Mass Spectrometry, 2006, 17, 395-405.	2.8	29
6	"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
7	Structure and dynamics of dark-state bovine rhodopsin revealed by chemical cross-linking and high-resolution mass spectrometry. Protein Science, 2006, 15, 1303-1317.	7.6	50
8	Computational approaches for identification of conserved/unique binding pockets in the A chain of ricin. Bioinformatics, 2005, 21, 3089-3096.	4.1	6
9	PostDOCK:Â A Structural, Empirical Approach to Scoring Protein Ligand Complexes. Journal of Medicinal Chemistry, 2005, 48, 6821-6831.	6.4	36
10	Unambiguous Assignment of Intramolecular Chemical Cross-Links in Modified Mammalian Membrane Proteins by Fourier Transform-Tandem Mass Spectrometry. Analytical Chemistry, 2005, 77, 5101-5106.	6.5	40
11	Optimizing an Empirical Scoring Function for Transmembrane Protein Structure Determination. INFORMS Journal on Computing, 2004, 16, 406-418.	1.7	21
12	A Top-down method for the determination of residue-specific solvent accessibility in proteins. Journal of Mass Spectrometry, 2004, 39, 322-328.	1.6	61
13	Top-Down Characterization of Nucleic Acids Modified by Structural Probes Using High-Resolution Tandem Mass Spectrometry and Automated Data Interpretation. Analytical Chemistry, 2004, 76, 2438-2445.	6.5	75
14	Probing alpha-crystallin structure using chemical cross-linkers and mass spectrometry. Molecular Vision, 2004, 10, 857-66.	1.1	15
15	Exploring the conformational space of membrane protein folds matching distance constraints. Protein Science, 2003, 12, 1750-1761.	7.6	21
16	Isotopically labeled crosslinking reagents: resolution of mass degeneracy in the identification of crosslinked peptides. Bioorganic and Medicinal Chemistry Letters, 2003, 13, 4023-4026.	2.2	48
17	MS2Assign, automated assignment and nomenclature of tandem mass spectra of chemically crosslinked peptides. Journal of the American Society for Mass Spectrometry, 2003, 14, 834-850.	2.8	250
18	A top down approach to protein structural studies using chemical cross-linking and Fourier transform mass spectrometry. Rapid Communications in Mass Spectrometry, 2003, 17, 155-162.	1.5	117

#	Article	IF	Citations
19	A Top-Down Approach to Protein Structure Studies Using Chemical Cross-Linking and Fourier Transform Mass Spectrometry. European Journal of Mass Spectrometry, 2003, 9, 623-631.	1.0	46
20	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
21	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
22	Constrained walks and self-avoiding walks: implications for protein structure determination. Journal of Physics A, 2002, 35, 1-19.	1.6	9
23	Design, docking, and evaluation of multiple libraries against multiple targets. Proteins: Structure, Function and Bioinformatics, 2001, 42, 296-318.	2.6	66
24	High throughput protein fold identification by using experimental constraints derived from intramolecular cross-links and mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 5802-5806.	7.1	431
25	Predicting conformational switches in proteins. Protein Science, 1999, 8, 1752-1764.	7.6	74
26	Predicting allosteric switches in myosins. Protein Science, 1999, 8, 1806-1815.	7.6	23
27	A rapid method for exploring the protein structure universe. Proteins: Structure, Function and Bioinformatics, 1999, 34, 317-332.	2.6	15