

# Margareta Ramström

## List of Publications by Year in descending order

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35  
papers

1,306  
citations

394421

19  
h-index

361022

35  
g-index

36  
all docs

36  
docs citations

36  
times ranked

1923  
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of MS-based methods for identification and quantification of proteins altered during early pregnancy in dogs. <i>Journal of Proteomics</i> , 2019, 192, 223-232.	2.4	8
2	Development of a Parallel Reaction Monitoring-MS Method To Quantify IGF Proteins in Dogs and a Case of Nonislet Cell Tumor Hypoglycemia. <i>Journal of Proteome Research</i> , 2019, 18, 18-29.	3.7	5
3	Effect of insulin treatment on circulating insulin-like growth factor I and IGF-binding proteins in cats with diabetes mellitus. <i>Journal of Veterinary Internal Medicine</i> , 2018, 32, 1579-1590.	1.6	7
4	Insufficient antibody validation challenges oestrogen receptor beta research. <i>Nature Communications</i> , 2017, 8, 15840.	12.8	170
5	Quantitative and Selective Analysis of Feline Growth Related Proteins Using Parallel Reaction Monitoring High Resolution Mass Spectrometry. <i>PLoS ONE</i> , 2016, 11, e0167138.	2.5	7
6	The H3 chaperone function of NASP is conserved in Arabidopsis. <i>Plant Journal</i> , 2016, 88, 425-436.	5.7	19
7	Functionalized silk assembled from a recombinant spider silk fusion protein (Zê4RepCT) produced in the methylotrophic yeast <i>Pichia pastoris</i> . <i>Biotechnology Journal</i> , 2016, 11, 687-699.	3.5	26
8	The WD40 Domain Protein MSI1 Functions in a Histone Deacetylase Complex to Fine-Tune Abscisic Acid Signaling. <i>Plant Cell</i> , 2016, 28, 42-54.	6.6	116
9	High-abundant protein depletion strategies applied on dog cerebrospinal fluid and evaluated by high-resolution mass spectrometry. <i>Biochemistry and Biophysics Reports</i> , 2015, 3, 68-75.	1.3	4
10	The Eph Tyrosine Kinase Receptors EphB2 and EphA2 Are Novel Proteolytic Substrates of Tissue Factor/Coagulation Factor VIIa. <i>Journal of Biological Chemistry</i> , 2014, 289, 32379-32391.	3.4	18
11	An automated mass spectrometry-based screening method for analysis of sulfated glycosaminoglycans. <i>Biochemical and Biophysical Research Communications</i> , 2014, 450, 598-603.	2.1	8
12	Characterisation of the post-translational modifications of a novel, human cell line-derived recombinant human factor VIII. <i>Thrombosis Research</i> , 2013, 131, 78-88.	1.7	108
13	Characterization of $\hat{1}^3$ -Carboxylated Tryptic Peptides by Collision-Induced Dissociation and Electron Transfer Dissociation Mass Spectrometry. <i>European Journal of Mass Spectrometry</i> , 2011, 17, 497-506.	1.0	8
14	Targeted protein pullout from human tissue samples using competitive elution. <i>Biotechnology Journal</i> , 2011, 6, 28-37.	3.5	3
15	Automated sample preparation method for mass spectrometry analysis on recombinant proteins. <i>Journal of Chromatography A</i> , 2009, 1216, 4457-4464.	3.7	2
16	Generation of an affinity matrix useful in the purification of natural inhibitors of plasmeprin II, an antimalarial drug target. <i>Biotechnology and Applied Biochemistry</i> , 2009, 52, 149-157.	3.1	31
17	Characterization of heat-labile uracil-DNA glycosylase from <i>Psychrobacter</i> sp. HJ147 and its application to the polymerase chain reaction. <i>Biotechnology and Applied Biochemistry</i> , 2009, 52, 167.	3.1	9
18	Affibody-mediated transferrin depletion for proteomics applications. <i>Biotechnology Journal</i> , 2007, 2, 1389-1398.	3.5	42

#	ARTICLE	IF	CITATIONS
19	Approaches for systematic proteome exploration. <i>New Biotechnology</i> , 2007, 24, 155-168.	2.7	24
20	Proteomics of Human Cerebrospinal Fluid. , 2007, , 269-284.		0
21	A simplified multidimensional approach for analysis of complex biological samples: on-line LC-CE-MS. <i>Analyst</i> , 2006, 131, 791-798.	3.5	26
22	Depletion of High-Abundant Proteins in Body Fluids Prior to Liquid Chromatography Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Journal of Proteome Research</i> , 2005, 4, 410-416.	3.7	68
23	Reproducibility of Tryptic Digestion Investigated by Quantitative Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Journal of Proteome Research</i> , 2005, 4, 394-399.	3.7	7
24	Cerebrospinal fluid protein patterns in neurodegenerative disease revealed by liquid chromatographyâ€Fourier transform ion cyclotron resonance mass spectrometry. <i>Proteomics</i> , 2004, 4, 4010-4018.	2.2	64
25	Peptide and protein characterization by high-rate electron capture dissociation Fourier transform ion cyclotron resonance mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2004, 39, 719-729.	1.6	42
26	Protein identification by liquid chromatographyâ€mass spectrometry using retention time prediction. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2004, 803, 131-135.	2.3	48
27	Quantitative Analysis of Tryptic Protein Mixtures Using Electrospray Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Journal of Proteome Research</i> , 2004, 3, 587-594.	3.7	9
28	Explorative Study of the Protein Composition of Amniotic Fluid by Liquid Chromatography Electrospray Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Journal of Proteome Research</i> , 2004, 3, 884-889.	3.7	43
29	Miniaturized proteomics and peptidomics using capillary liquid separation and high resolution mass spectrometry. <i>FEBS Letters</i> , 2004, 567, 92-95.	2.8	26
30	Localized changes in the structural stability of myoglobin upon adsorption onto silica particles, as studied with hydrogen/deuterium exchange mass spectrometry. <i>Journal of Colloid and Interface Science</i> , 2003, 263, 441-448.	9.4	48
31	A novel mass spectrometric approach to the analysis of hormonal peptides in extracts of mouse pancreatic islets. <i>FEBS Journal</i> , 2003, 270, 3146-3152.	0.2	15
32	Protein identification in cerebrospinal fluid using packed capillary liquid chromatography Fourier transform ion cyclotron resonance mass spectrometry. <i>Proteomics</i> , 2003, 3, 184-190.	2.2	35
33	Evaluation of Shotgun Sequencing for Proteomic Analysis of Human Plasma Using HPLC Coupled with Either Ion Trap or Fourier Transform Mass Spectrometry. <i>Journal of Proteome Research</i> , 2003, 2, 383-393.	3.7	71
34	Prediction of Chromatographic Retention and Protein Identification in Liquid Chromatography/Mass Spectrometry. <i>Analytical Chemistry</i> , 2002, 74, 5826-5830.	6.5	136
35	Liquid chromatography and electron-capture dissociation in Fourier transform ion cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2002, 16, 988-992.	1.5	52