

# Sherlock Holmes and the proteome – a detective s

FEBS Journal

274, 897-905

DOI: [10.1111/j.1742-4658.2007.05648.x](https://doi.org/10.1111/j.1742-4658.2007.05648.x)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Plasma/serum proteomics: pre-analytical issues. <i>Expert Review of Proteomics</i> , 2007, 4, 363-370.	3.0	52
2	Exploring the Platelet Proteome via Combinatorial, Hexapeptide Ligand Libraries. <i>Journal of Proteome Research</i> , 2007, 6, 4290-4303.	3.7	89
3	Contribution of solid-phase hexapeptide ligand libraries to the repertoire of human bile proteins. <i>Journal of Chromatography A</i> , 2007, 1176, 192-205.	3.7	51
4	Peptide enrichment and protein fractionation using selective electrophoresis. <i>Proteomics</i> , 2008, 8, 4197-4208.	2.2	22
5	Analysis of environmental stress response on the proteome level. <i>Mass Spectrometry Reviews</i> , 2008, 27, 556-574.	5.4	45
6	The ProteoMiner and the FortyNiners: Searching for gold nuggets in the proteomic arena. <i>Mass Spectrometry Reviews</i> , 2008, 27, 596-608.	5.4	125
7	Experimental and computational approaches to quantitative proteomics: Status quo and outlook. <i>Journal of Proteomics</i> , 2008, 71, 19-33.	2.4	108
8	The ProteoMiner in the proteomic arena: A non-depleting tool for discovering low-abundance species. <i>Journal of Proteomics</i> , 2008, 71, 255-264.	2.4	166
9	Affinity separation and enrichment methods in proteomic analysis. <i>Journal of Proteomics</i> , 2008, 71, 284-303.	2.4	136
10	Performance of Combinatorial Peptide Libraries in Capturing the Low-Abundance Proteome of Red Blood Cells. 2. Behavior of Resins Containing Individual Amino Acids. <i>Analytical Chemistry</i> , 2008, 80, 3557-3565.	6.5	40
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14	Chapter 6 A Proteomic Approach to the Analysis of RNA Degradosome Composition in <i>Escherichia coli</i> . <i>Methods in Enzymology</i> , 2008, 447, 99-117.	1.0	53
15	Extensive Analysis of the Cytoplasmic Proteome of Human Erythrocytes Using the Peptide Ligand Library Technology and Advanced Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2254-2269.	3.8	208
16	Hexapeptide combinatorial ligand libraries: the march for the detection of the low-abundance proteome continues. <i>BioTechniques</i> , 2008, 44, 663-665.	1.8	55
17	Liquid-phase-based separation systems for depletion, prefractionation and enrichment of proteins in biological fluids for in-depth proteomics analysis. <i>Electrophoresis</i> , 2009, 30, 249-261.	2.4	45
18	Combinatorial peptide ligand libraries for urine proteome analysis: Investigation of different elution systems. <i>Electrophoresis</i> , 2009, 30, 2405-2411.	2.4	95

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19	The art of observing rare protein species in proteomes with peptide ligand libraries. <i>Proteomics</i> , 2009, 9, 1492-1510.	2.2	141
20	Plant proteomics update (2007â€“2008): Second-generation proteomic techniques, an appropriate experimental design, and data analysis to fulfill MIAPE standards, increase plant proteome coverage and expand biological knowledge. <i>Journal of Proteomics</i> , 2009, 72, 285-314.	2.4	191
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24	Combinatorial peptide ligand libraries and plant proteomics: A winning strategy at a price. <i>Journal of Chromatography A</i> , 2009, 1216, 1215-1222.	3.7	59
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40	Combinatorial peptide ligand libraries: The conquest of the "hidden proteome"™ advances at great strides. <i>Electrophoresis</i> , 2011, 32, 960-966.	2.4	42
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52	Measurement of Organ-Specific and Acute-Phase Blood Protein Levels in Early Lyme Disease. <i>Journal of Proteome Research</i> , 2020, 19, 346-359.	3.7	14
53	Specific and Surrogate Cerebrospinal Fluid Markers in Creutzfeldt-Jakob Disease. <i>Advances in Neurobiology</i> , 2011, , 455-467.	1.8	4
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