Roman A Zubarev

List of Publications by Citations

282 papers	15,682 citations	62 h-index	118 g-index
321 ext. papers	17,129 ext. citations	5.9 avg, IF	6.63 L-index

#	Paper	IF	Citations
282	Electron Capture Dissociation of Multiply Charged Protein Cations. A Nonergodic Process. *Journal of the American Chemical Society*, **1998**, 120, 3265-3266	16.4	1658
281	Electron capture dissociation for structural characterization of multiply charged protein cations. *Analytical Chemistry*, **2000**, 72, 563-73	7.8	852
280	Electron Capture Dissociation of Gaseous Multiply-Charged Proteins Is Favored at Disulfide Bonds and Other Sites of High Hydrogen Atom Affinity. *Journal of the American Chemical Society*, **1999**, 121, 2857-2862	16.4	512
279	Automated reduction and interpretation of high resolution electrospray mass spectra of large molecules. *Journal of the American Society for Mass Spectrometry*, **2000**, 11, 320-32	3.5	452
278	Reactions of polypeptide ions with electrons in the gas phase. *Mass Spectrometry Reviews*, **2003**, 22, 57-77	7.1	384
277	Localization of O-glycosylation sites in peptides by electron capture dissociation in a Fourier transform mass spectrometer. *Analytical Chemistry*, **1999**, 71, 4431-6	7.8	362
276	Localization of labile posttranslational modifications by electron capture dissociation: the case of gamma-carboxyglutamic acid. *Analytical Chemistry*, **1999**, 71, 4250-3	7.8	346
275	Orbitrap mass spectrometry. *Analytical Chemistry*, **2013**, 85, 5288-96	7.8	327
274	Electron capture dissociation of singly and multiply phosphorylated peptides. *Rapid Communications in Mass Spectrometry*, **2000**, 14, 1793-800	2.2	325
273	Electron-capture dissociation tandem mass spectrometry. *Current Opinion in Biotechnology*, **2004**, 15, 12-6	11.4	306
272	Low-mass ions observed in plasma desorption mass spectrometry of high explosives. *Journal of Mass Spectrometry*, **2000**, 35, 337-46	2.2	245
271	Automated de novo sequencing of proteins by tandem high-resolution mass spectrometry. *Proceedings of the National Academy of Sciences of the United States of America*, **2000**, 97, 10313-7	11.5	225
270	Towards An Understanding of the Mechanism of Electron-Capture Dissociation: A Historical Perspective and Modern Ideas. *European Journal of Mass Spectrometry*, **2002**, 8, 337-349	1.1	215
269	Electron detachment dissociation of peptide di-anions: an electron–hole recombination phenomenon. *Chemical Physics Letters*, **2001**, 342, 299-302	2.5	213
268	Electron capture dissociation of gaseous multiply charged ions by Fourier-transform ion cyclotron resonance. *Journal of the American Society for Mass Spectrometry*, **2001**, 12, 245-9	3.5	207
267	De novo peptide sequencing and identification with precision mass spectrometry. *Journal of Proteome Research*, **2007**, 6, 114-23	5.6	173
266	Techview: biochemistry. Biomolecule mass spectrometry. *Science*, **1999**, 284, 1289-90	33.3	168

265	Dissociative capture of hot (3–13 eV) electrons by polypeptide polycations: an efficient process accompanied by secondary fragmentation. *Chemical Physics Letters*, **2002**, 356, 201-206	2.5	165
264	ModifiComb, a new proteomic tool for mapping substoichiometric post-translational modifications, finding novel types of modifications, and fingerprinting complex protein mixtures. *Molecular and Cellular Proteomics*, **2006**, 5, 935-48	7.6	160
263	Electron capture dissociation proceeds with a low degree of intramolecular migration of peptide amide hydrogens. *Journal of the American Chemical Society*, **2008**, 130, 1341-9	16.4	149
262	Functional conservation of subfamilies of putative UDP-N-acetylgalactosamine:polypeptide N-acetylgalactosaminyltransferases in Drosophila, Caenorhabditis elegans, and mammals. One subfamily composed of l(2)35Aa is essential in Drosophila. *Journal of Biological Chemistry*, **2002**, 277, 22623-38	5.4	148
261	Proteomics-grade de novo sequencing approach. *Journal of Proteome Research*, **2005**, 4, 2348-54	5.6	142
260	On the proper use of mass accuracy in proteomics. *Molecular and Cellular Proteomics*, **2007**, 6, 377-81	7.6	140
259	Heightened immune response to autocitrullinated Porphyromonas gingivalis peptidylarginine deiminase: a potential mechanism for breaching immunologic tolerance in rheumatoid arthritis. *Annals of the Rheumatic Diseases*, **2014**, 73, 263-9	2.4	134
258	Release of Active Peptidyl Arginine Deiminases by Neutrophils Can Explain Production of Extracellular Citrullinated Autoantigens in Rheumatoid Arthritis Synovial Fluid. *Arthritis and Rheumatology*, **2015**, 67, 3135-45	9.5	127
257	Mass spectrometric analysis of asparagine deamidation and aspartate isomerization in polypeptides. *Electrophoresis*, **2010**, 31, 1764-72	3.6	127
256	Electron capture/transfer versus collisionally activated/induced dissociations: solo or duet?. *Journal of the American Society for Mass Spectrometry*, **2008**, 19, 753-61	3.5	127
255	Improving protein identification using complementary fragmentation techniques in fourier transform mass spectrometry. *Molecular and Cellular Proteomics*, **2005**, 4, 835-45	7.6	123
254	Myeloid-derived suppressor cells express the death receptor Fas and apoptose in response to T cell-expressed FasL. *Blood*, **2011**, 117, 5381-90	2.2	120
253	Complete characterization of posttranslational modification sites in the bovine milk protein PP3 by tandem mass spectrometry with electron capture dissociation as the last stage. *Analytical Chemistry*, **2003**, 75, 2355-61	7.8	117
252	Distinguishing of Ile/Leu amino acid residues in the PP3 protein by (hot) electron capture dissociation in Fourier transform ion cyclotron resonance mass spectrometry. *Analytical Chemistry*, **2003**, 75, 1267-74	7.8	115
251	Fragmentation of peptides in MALDI in-source decay mediated by hydrogen radicals. *Analytical Chemistry*, **2005**, 77, 172-7	7.8	115
250	Hydrogen rearrangement to and from radical z fragments in electron capture dissociation of peptides. *Journal of the American Society for Mass Spectrometry*, **2007**, 18, 113-20	3.5	113
249	The challenge of the proteome dynamic range and its implications for in-depth proteomics. *Proteomics*, **2013**, 13, 723-6	4.8	112
248	Accuracy Requirements for Peptide Characterization by Monoisotopic Molecular Mass Measurements. *Analytical Chemistry*, **1996**, 68, 4060-4063	7.8	112

247	Rapid and deep human proteome analysis by single-dimension shotgun proteomics. *Molecular and Cellular Proteomics*, **2013**, 12, 3330-8	7.6	107
246	C alpha-C backbone fragmentation dominates in electron detachment dissociation of gas-phase polypeptide polyanions. *Chemistry - A European Journal*, **2005**, 11, 1803-12	4.8	106
245	Improved low-energy electron injection systems for high rate electron capture dissociation in Fourier transform ion cyclotron resonance mass spectrometry. *Rapid Communications in Mass Spectrometry*, **2001**, 15, 1849-54	2.2	106
244	Advantages of external accumulation for electron capture dissociation in Fourier transform mass spectrometry. *Analytical Chemistry*, **2001**, 73, 2998-3005	7.8	101
243	Facile disulfide bond cleavage in gaseous peptide and protein cations by ultraviolet photodissociation at 157 nm. *Angewandte Chemie - International Edition*, **2005**, 44, 6399-403	16.4	95
242	Electron capture dissociation distinguishes a single D-amino acid in a protein and probes the tertiary structure. *Journal of the American Society for Mass Spectrometry*, **2004**, 15, 1087-98	3.5	89
241	The SysteMHC Atlas project. *Nucleic Acids Research*, **2018**, 46, D1237-D1247	20.1	87
240	Optimizing heterologous protein production in the periplasm of E. coli by regulating gene expression levels. *Microbial Cell Factories*, **2013**, 12, 24	6.4	87
239	Shared immunological targets in the lungs and joints of patients with rheumatoid arthritis: identification and validation. *Annals of the Rheumatic Diseases*, **2015**, 74, 1772-7	2.4	86
238	Prodynorphin mutations cause the neurodegenerative disorder spinocerebellar ataxia type 23. *American Journal of Human Genetics*, **2010**, 87, 593-603	11	86
237	The RBCC gene RFP2 (Leu5) encodes a novel transmembrane E3 ubiquitin ligase involved in ERAD. *Molecular Biology of the Cell*, **2007**, 18, 1670-82	3.5	86
236	Molecular profiling of prostate cancer derived exosomes may reveal a predictive signature for response to docetaxel. *Oncotarget*, **2015**, 6, 21740-54	3.3	84
235	Extent of modifications in human proteome samples and their effect on dynamic range of analysis in shotgun proteomics. *Molecular and Cellular Proteomics*, **2006**, 5, 2384-91	7.6	83
234	New data base-independent, sequence tag-based scoring of peptide MS/MS data validates Mowse scores, recovers below threshold data, singles out modified peptides, and assesses the quality of MS/MS techniques. *Molecular and Cellular Proteomics*, **2005**, 4, 1180-8	7.6	81
233	Electron capture dissociation of multiply charged peptide cations. *International Journal of Mass Spectrometry*, **1999**, 185-187, 787-793	1.9	81
232	Validation and development of MTH1 inhibitors for treatment of cancer. *Annals of Oncology*, **2016**, 27, 2275-2283	10.3	77
231	Complementary sequence preferences of electron-capture dissociation and vibrational excitation in fragmentation of polypeptide polycations. *Angewandte Chemie - International Edition*, **2006**, 45, 5301-3	16.4	77
230	Electron ionization dissociation of singly and multiply charged peptides. *Journal of the American Chemical Society*, **2009**, 131, 9977-85	16.4	74

229	Electron capture dissociation of polypeptides in a three-dimensional quadrupole ion trap: Implementation and first results. *Journal of the American Society for Mass Spectrometry*, **2005**, 16, 22-7	3.5	74
228	Applications of electron-ion dissociation reactions for analysis of polycationic chitooligosaccharides in Fourier transform mass spectrometry. *Analytical Chemistry*, **2003**, 75, 5994-6001	7.8	74
227	Electron capture versus energetic dissociation of protein ions. *International Journal of Mass Spectrometry*, **1999**, 182-183, 1-5	1.9	72
226	Small-molecule inhibitor of OGG1 suppresses proinflammatory gene expression and inflammation. *Science*, **2018**, 362, 834-839	33.3	71
225	Proteomic analysis of urinary biomarker candidates for nonmuscle invasive bladder cancer. *Proteomics*, **2012**, 12, 135-44	4.8	69
224	Liquid chromatography at critical conditions: comprehensive approach to sequence-dependent retention time prediction. *Analytical Chemistry*, **2006**, 78, 7770-7	7.8	68
223	Side-chain losses in electron capture dissociation to improve peptide identification. *Analytical Chemistry*, **2007**, 79, 2296-302	7.8	65
222	In silico instrumental response correction improves precision of label-free proteomics and accuracy of proteomics-based predictive models. *Molecular and Cellular Proteomics*, **2013**, 12, 2324-31	7.6	64
221	Distinguishing and quantifying peptides and proteins containing D-amino acids by tandem mass spectrometry. *Analytical Chemistry*, **2005**, 77, 4571-80	7.8	62
220	De novo sequencing of antimicrobial peptides isolated from the venom glands of the wolf spider Lycosa singoriensis. *Journal of Mass Spectrometry*, **2004**, 39, 193-201	2.2	62
219	Repurposing of auranofin: Thioredoxin reductase remains a primary target of the drug. *Biochimie*, **2019**, 162, 46-54	4.6	61
218	Tetrathiafulvaleno-Annelated Porphyrins. *Angewandte Chemie - International Edition*, **2001**, 40, 2497-2500	16.4	61
217	Electron capture dissociation of weakly bound polypeptide polycationic complexes. *Rapid Communications in Mass Spectrometry*, **2002**, 16, 2260-5	2.2	59
216	Prediction of NC□bond cleavage frequencies in electron capture dissociation of Trp-cage dications by force-field molecular dynamics simulations. *International Journal of Mass Spectrometry*, **2006**, 248, 124-135	1.9	58
215	Cerebrospinal fluid protein patterns in neurodegenerative disease revealed by liquid chromatography-Fourier transform ion cyclotron resonance mass spectrometry. *Proteomics*, **2004**, 4, 4010-8	4.8	58
214	Proteome Integral Solubility Alteration: A High-Throughput Proteomics Assay for Target Deconvolution. *Journal of Proteome Research*, **2019**, 18, 4027-4037	5.6	56
213	Proteomic pathway analysis reveals inflammation increases myeloid-derived suppressor cell resistance to apoptosis. *Molecular and Cellular Proteomics*, **2011**, 10, M110.002980	7.6	55
212	Urinary prognostic biomarkers and classification of IgA nephropathy by high resolution mass spectrometry coupled with liquid chromatography. *PLoS ONE*, **2013**, 8, e80830	3.7	54

211	Bifurcating fragmentation behavior of gas-phase tryptic peptide dications in collisional activation. *Journal of the American Society for Mass Spectrometry*, **2008**, 19, 1755-63	3.5	54
210	High levels of the adhesion molecule CD44 on leukemic cells generate acute myeloid leukemia relapse after withdrawal of the initial transforming event. *Leukemia*, **2011**, 25, 515-26	10.7	53
209	Blood plasma IgG Fc glycans are significantly altered in Alzheimer's disease and progressive mild cognitive impairment. *Journal of Alzheimer's Disease*, **2014**, 38, 567-79	4.3	52
208	Zwitterionic states in gas-phase polypeptide ions revealed by 157-nm ultra-violet photodissociation. *Chemistry - A European Journal*, **2006**, 12, 7920-8	4.8	52
207	Can the (M□X) Region in Electron Capture Dissociation Provide Reliable Information on Amino Acid Composition of Polypeptides?. *European Journal of Mass Spectrometry*, **2002**, 8, 461-469	1.1	52
206	MS analysis of rheumatoid arthritic synovial tissue identifies specific citrullination sites on fibrinogen. *Proteomics - Clinical Applications*, **2010**, 4, 511-8	3.1	51
205	DeMix-Q: Quantification-Centered Data Processing Workflow. *Molecular and Cellular Proteomics*, **2016**, 15, 1467-78	7.6	50
204	Intramolecular hydrogen atom transfer in hydrogen-deficient polypeptide radical cations. *Chemical Physics Letters*, **2000**, 330, 558-562	2.5	48
203	MH2+? ion production from protonated polypeptides by electron impact: observation and determination of ionization energies and a cross-section. *Chemical Physics Letters*, **2000**, 316, 19-23	2.5	48
202	Approaches and Limits for Accurate Mass Characterization of Large Biomolecules. *Analytical Chemistry*, **1995**, 67, 3793-3798	7.8	48
201	DeMix workflow for efficient identification of cofragmented peptides in high resolution data-dependent tandem mass spectrometry. *Molecular and Cellular Proteomics*, **2014**, 13, 3211-23	7.6	44
200	Sequence scrambling in shotgun proteomics is negligible. *Journal of the American Society for Mass Spectrometry*, **2011**, 22, 1121-4	3.5	44
199	Immunoaffinity enrichments followed by mass spectrometric detection for studying global protein tyrosine phosphorylation. *Journal of Proteome Research*, **2008**, 7, 2897-910	5.6	44
198	Cell line profiling to improve monoclonal antibody production. *Biotechnology and Bioengineering*, **2014**, 111, 748-60	4.9	43
197	Structural basis of SUFU-GLI interaction in human Hedgehog signalling regulation. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2563-79		42
196	A direct comparison of protein structure in the gas and solution phase: the Trp-cage. *Journal of Physical Chemistry B*, **2007**, 111, 13147-50	3.4	42
195	Binding of Pro-Gly-Pro at the active site of leukotriene A4 hydrolase/aminopeptidase and development of an epoxide hydrolase selective inhibitor. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 4227-32	11.5	41
194	Ionization energies of multiply protonated polypeptides obtained by tandem ionization in Fourier transform mass spectrometers. *Journal of Mass Spectrometry*, **2002**, 37, 1141-4	2.2	41

193	Analytical utility of small neutral losses from reduced species in electron capture dissociation studied using SwedECD database. *Analytical Chemistry*, **2008**, 80, 8089-94	7.8	40
192	De novo sequencing of peptides secreted by the skin glands of the Caucasian Green Frog Rana ridibunda. *Rapid Communications in Mass Spectrometry*, **2008**, 22, 3517-25	2.2	39
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190	Dissociation of peptide ions by fast atom bombardment in a quadrupole ion trap. *Rapid Communications in Mass Spectrometry*, **2005**, 19, 2163-71	2.2	39
189	Toward proteome-scale identification and quantification of isoaspartyl residues in biological samples. *Journal of Proteome Research*, **2009**, 8, 4615-21	5.6	37
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186	Covariation of Peptide Abundances Accurately Reflects Protein Concentration Differences. *Molecular and Cellular Proteomics*, **2017**, 16, 936-948	7.6	36
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183	Prognostic polypeptide blood plasma biomarkers of Alzheimer's disease progression. *Journal of Alzheimer's Disease*, **2014**, 40, 659-66	4.3	35
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181	Letter: the diagnostic value of amino acid side-chain losses in electron capture dissociation of polypeptides. Comment on: "Can the (M(.)-X) region in electron capture dissociation provide reliable information on amino acid composition of polypeptides?", Eur. J. Mass Spectrom. 8, 461-469 (2002). *European Journal of Mass Spectrometry*, **2003**, 9, 221-2	1.1	34
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179	Approach for Identifying Human Leukocyte Antigen (HLA)-DR Bound Peptides from Scarce Clinical Samples. *Molecular and Cellular Proteomics*, **2016**, 15, 3017-29	7.6	33
178	C57BL/6 mice need MHC class II Aq to develop collagen-induced arthritis dependent on autoreactive T cells. *Annals of the Rheumatic Diseases*, **2013**, 72, 1225-32	2.4	32
177	Impact of temperature dependent sampling procedures in proteomics and peptidomics--a characterization of the liver and pancreas post mortem degradome. *Molecular and Cellular Proteomics*, **2011**, 10, M900229MCP200	7.6	32
176	On studying protein phosphorylation patterns using bottom-up LC-MS/MS: the case of human alpha-casein. *Analyst, The*, **2007**, 132, 768-76	5	32

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174	Cationic gold nanoparticles elicit mitochondrial dysfunction: a multi-omics study. *Scientific Reports*, **2019**, 9, 4366	4.9	31
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172	The exosome associates cotranscriptionally with the nascent pre-mRNP through interactions with heterogeneous nuclear ribonucleoproteins. *Molecular Biology of the Cell*, **2009**, 20, 3459-70	3.5	31
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163	Probing solution- and gas-phase structures of Trp-cage cations by chiral substitution and spectroscopic techniques. *International Journal of Mass Spectrometry*, **2006**, 253, 263-273	1.9	29
162	Cytotoxic and Proinflammatory Effects of Metal-Based Nanoparticles on THP-1 Monocytes Characterized by Combined Proteomics Approaches. *Journal of Proteome Research*, **2017**, 16, 689-697	5.6	28
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160	IgG antibodies to cyclic citrullinated peptides exhibit profiles specific in terms of IgG subclasses, Fc-glycans and a fab-Peptide sequence. *PLoS ONE*, **2014**, 9, e113924	3.7	27
159	SwedCAD, a database of annotated high-mass accuracy MS/MS spectra of tryptic peptides. *Journal of Proteome Research*, **2007**, 6, 4063-7	5.6	27
158	Tandem MALDI/EI ionization for tandem Fourier transform ion cyclotron resonance mass spectrometry of polypeptides. *International Journal of Mass Spectrometry*, **2003**, 226, 181-187	1.9	27

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155	Apoptotic, regenerative, and immune-related signaling in human islets from type 2 diabetes individuals. *Journal of Proteome Research*, **2009**, 8, 5650-6	5.6	26
154	Calibration function for the Orbitrap FTMS accounting for the space charge effect. *Journal of the American Society for Mass Spectrometry*, **2010**, 21, 1846-51	3.5	26
153	IgG Fc galactosylation predicts response to methotrexate in early rheumatoid arthritis. *Arthritis Research and Therapy*, **2017**, 19, 182	5.7	25
152	Isotope depletion of large biomolecules: Implications for molecular mass measurements. *Journal of the American Society for Mass Spectrometry*, **1998**, 9, 149-156	3.5	25
151	Backbone carbonyl group basicities are related to gas-phase fragmentation of peptides and protein folding. *Angewandte Chemie - International Edition*, **2007**, 46, 1481-4	16.4	25
150	IgM antibodies against phosphorylcholine promote polarization of T regulatory cells from patients with atherosclerotic plaques, systemic lupus erythematosus and healthy donors. *Atherosclerosis*, **2018**, 268, 36-48	3.1	24
149	Two dimensional mass mapping as a general method of data representation in comprehensive analysis of complex molecular mixtures. *Analytical Chemistry*, **2009**, 81, 3738-45	7.8	23
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145	Predictive urinary biomarkers for steroid-resistant and steroid-sensitive focal segmental glomerulosclerosis using high resolution mass spectrometry and multivariate statistical analysis. *BMC Nephrology*, **2014**, 15, 141	2.7	21
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139	Fragmentation of positively-charged biological ions activated with a beam of high-energy cations. *Analytical Chemistry*, **2014**, 86, 372-9	7.8	20
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137	Relative specificities of water and ammonia losses from backbone fragments in collision-activated dissociation. *Journal of Proteome Research*, **2007**, 6, 2669-73	5.6	20
136	Physicochemical properties determining the detection probability of tryptic peptides in Fourier transform mass spectrometry. A correlation study. *Analytical Chemistry*, **2004**, 76, 5872-7	7.8	20
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134	The PredictAD project: development of novel biomarkers and analysis software for early diagnosis of the Alzheimer's disease. *Interface Focus*, **2013**, 3, 20120072	3.9	19
133	Alzheimer's disease and mild cognitive impairment are associated with elevated levels of isoaspartyl residues in blood plasma proteins. *Journal of Alzheimer's Disease*, **2011**, 27, 113-8	4.3	19
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129	Toward a comprehensive characterization of the phosphotyrosine proteome. *Cellular Signalling*, **2011**, 23, 1387-95	4.9	18
128	Heme binding in gas-phase holo-myoglobin cations: distal becomes proximal?. *Journal of the American Society for Mass Spectrometry*, **2011**, 22, 1763-70	3.5	18
127	Proteomics and pathway analysis identifies JNK signaling as critical for high linear energy transfer radiation-induced apoptosis in non-small lung cancer cells. *Molecular and Cellular Proteomics*, **2009**, 8, 1117-29	7.6	18
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1	Tetrathiafulvaleno-Annelated Porphyrins We gratefully acknowledge financial support from Carlsbergfondet and Bengt Lundquists Minnesfond for a post-doctoral position to T. B., the University of Odense for a Ph.D. scholarship to J. O. J. and the French Embassy Copenhagen for a travel grant to J. B. We thank HASYLAB at DESY, Hamburg for beam time at beam line BW1 and DANSYNC for financial support. The gift of Jan Skov Peterson's FORTRAN program LSQREFL is gratefully acknowledged. Finally, we thank Prof. K. S. *Angewandte Chemie - International Edition*, **2001**, 40, 2497-2500	16.4	