1. **Record Nr.**   UNINA9910714875503321

   Autore   Doyle Charles

   Titolo   IMPEACHMENT GROUNDS . PART 3 HAMILTON, WILSON AND STORY (98-895) / / Charles Doyle

   Pubbl/distr/stampa Washington DC : , : [publisher not identified], , 1998

   Edizione   [[Library of Congress public edition].]

   Descrizione fisica 1 online resource

   Collana   Report / Congressional Research Service ; ; 98-895

   Disciplina   342.73062

   Soggetti   Impeachments - United States

   Lingua di pubblicazione Inglese

   Formato   Materiale a stampa

   Livello bibliografico Monografia

   Note generali   The CRS report home page provides access to all versions published since 2018 in accordance with P.L. 115-141; earliest version dated 1998.

   Sommario/riassunto This is a collection of selected background materials pertinent to the issue of what constitutes impeachable misconduct for purposes of Article II, section 4 of the United States Constitution quoted below. It includes excerpts from No.65 of the Federalist Papers by Alexander Hamilton, and from the writings of his contemporaries Supreme Court Justices James Wilson and Joseph Story. It is the third of six segments that together with footnotes comprise, Impeachment Grounds: A Collection of Selected Materials, CRS Report 98-882(pdf) . The President, Vice President and all Civil Officers of the United States, shall be removed from Office on impeachment for, and Conviction of, Treason, Bribery, or other high Crimes and Misdemeanors. U.S.Const. Art. II, ¿4.

2.	Record Nr.	UNINA9910591037703321
	Autore	Saeed Fahad
	Titolo	High-Performance Algorithms for Mass Spectrometry-Based Omics / / by Fahad Saeed, Muhammad Haseeb
	Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2022
	ISBN	9783031019609 3031019601
	Edizione	[1st ed. 2022.]
	Descrizione fisica	1 online resource (146 pages)
	Collana	Computational Biology, , 2662-2432
	Disciplina	005.1
	Soggetti	Bioinformatics Mass spectrometry Computer science Computational and Systems Biology Mass Spectrometry Theory and Algorithms for Application Domains Computer Science
	Lingua di pubblicazione	Inglese
	Formato	Materiale a stampa
	Livello bibliografico	Monografia
	Nota di bibliografia	Includes bibliographical references and index.
	Nota di contenuto	1. Need for High Performance Computing for Big MS Data -- 2. Introduction to Mass Spectrometry Data -- 3. A Review of Spectral Pre-processing -- 4. MS-REDUCE: An Ultra Data Reduction Algorithm -- 5. GPU-DAEMON: A Template to Support Development of GPU Algorithms -- 6. GPU-ArraySort: GPU Based Array Sorting Technique -- 7. G-MSR: A GPU Based Dimensionality Reduction Algorithm -- 8. Simulator Driven Proteomics -- 9. Future and Proposed Work.
	Sommario/riassunto	To date, processing of high-throughput Mass Spectrometry (MS) data is accomplished using serial algorithms. Developing new methods to process MS data is an active area of research but there is no single strategy that focuses on scalability of MS based methods. Mass spectrometry is a diverse and versatile technology for high-throughput functional characterization of proteins, small molecules and metabolites in complex biological mixtures. In the recent years the technology has rapidly evolved and is now capable of generating

increasingly large (multiple tera-bytes per experiment) and complex (multiple species/microbiome/high-dimensional) data sets. This rapid advance in MS instrumentation must be matched by equally fast and rapid evolution of scalable methods developed for analysis of these complex data sets. Ideally, the new methods should leverage the rich heterogeneous computational resources available in a ubiquitous fashion in the form of multicore, manycore, CPU-GPU, CPU-FPGA, and IntelPhi architectures. The absence of these high-performance computing algorithms now hinders scientific advancements for mass spectrometry research. In this book we illustrate the need for high-performance computing algorithms for MS based proteomics, and proteogenomics and showcase our progress in developing these high-performance algorithms.