

Mutation Miner

Submitted by [witte](#) [1] on Sat, 2011-01-01 09:11

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Title	Mutation Miner
Publication Type	Conference Paper
Year of Publication	2005
Refereed Designation	Refereed
Authors	Baker, C. J. O. [5], R. Witte [6], A. B. Gurpur [7], and V. Ryzhikov [8]
Conference Name	5th International Conference of the Canadian Proteomics Initiative (CPI 2005)
Date Published	May 13–14
Conference Location	Toronto, Ontario, Canada
Type of Work	Poster
Abstract	Biological researchers today have access to vast amounts of exponentially growing research data in a structured form within several publicly accessible databases. A large proportion of salient information is however still hidden within individual research papers, since costly manual database curation efforts are overwhelmed by the scale of new information being generated. In the domain of protein engineering, critical units of information required from the literature include: the identity of the mutated protein, the identity and position of wild type residues that are mutated, the identity of the resulting mutant residues and the impacts of the mutations on functional properties of the proteins. Mutation Miner is a system designed to automate the extraction of mutations and textual annotations describing the impacts of mutations on protein properties (mutation annotations) from full text scientific literature. Furthermore, the system retrieves and carries out bioinformatic analyses on mutated sequences providing the mapped coordinates of mutants on a selected structure. Integration of multiple formatted mutation annotations with associated residue coordinates facilitates their rendering with structure visualization tools. We describe the architecture and tools that support Mutation Miner (Text mining-NLP, Sequence Analysis, Structure Visualization) and present performance evaluations that demonstrate the feasibility of this approach.
Notes	This poster was also presented at the Knowledge-based Bioinformatics Workshop (KBB), September 21st-23rd, 2005, Montréal, Québec, Canada.
Attachment	Size
CPI2005-poster.png [9]	397.65 KB



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