

**Q\*cert – CoqTheoremProver[CTP]/OCaml as Bio-informatics Platform in the Context of Understanding Protein Folding Mechanisms Based on General Purpose Libraries – A Simple Interesting Insight Into the Promising, Challenging & Interesting World of Protein Engineering and Applications.**

**D.N.T.Kumar**

**Current Member : ante Inst,UTD,Dallas,TX,USA.**

**email id : [hmfg2014@gmail.com](mailto:hmfg2014@gmail.com)**

**[I] Introduction & Inspiration :**

“Coq is a formal proof management system. It provides a formal language to write mathematical definitions, executable algorithms and theorems together with an environment for semi-interactive development of machine-checked proofs. Typical applications include the [certification of properties of programming languages](#)(e.g. the [CompCert](#) compiler certification project, or the [Bedrock](#) verified low-level programming library), the [formalization of mathematics](#)(e.g. the full formalization of the [Feit-Thompson theorem](#) or [homotopy type theory](#)) and [teaching](#). “

**[Source : <https://coq.inria.fr/>] && [ [https://en.wikipedia.org/wiki/Lattice\\_protein](https://en.wikipedia.org/wiki/Lattice_protein)]**

**[Source : <https://ocaml.org/>] &&**

**[Source : <http://dimacs.rutgers.edu/~alantha/papers2/alantha-bill-bc.pdf>]**

**[Source : <https://discuss.ocaml.org/t/ocaml-for-data-science/1878>]**

**[Source : <https://github.com/TheButlah/BatlCaml>] – For Future AI Applications.**

“We present Q\*cert, a platform for the specification, verification, and implementation of query compilers written using the Coq proof assistant. The Q\*cert platform is open source and includes some support for SQL and OQL, and for code generation to Spark and Cloudant. “

***(PDF) Q\*cert: A Platform for Implementing and Verifying Query Compilers. Available from:***

**Source :** “S. Auerbach, Joshua & Hirzel, Martin & Mandel, Louis & Shinnar, Avraham & Siméon, Jérôme. (2017). Q\*cert: A Platform for Implementing and Verifying Query Compilers. 1703-1706. 10.1145/3035918.3056447. “ - Very much inspirational.

**[Source : [https://researcher.watson.ibm.com/researcher/view\\_group.php?id=8299](https://researcher.watson.ibm.com/researcher/view_group.php?id=8299)]**

**[Source : <https://ncatlab.org/nlab/show/Coq>]**

**[Source : <https://querycert.github.io/doc.html>]**

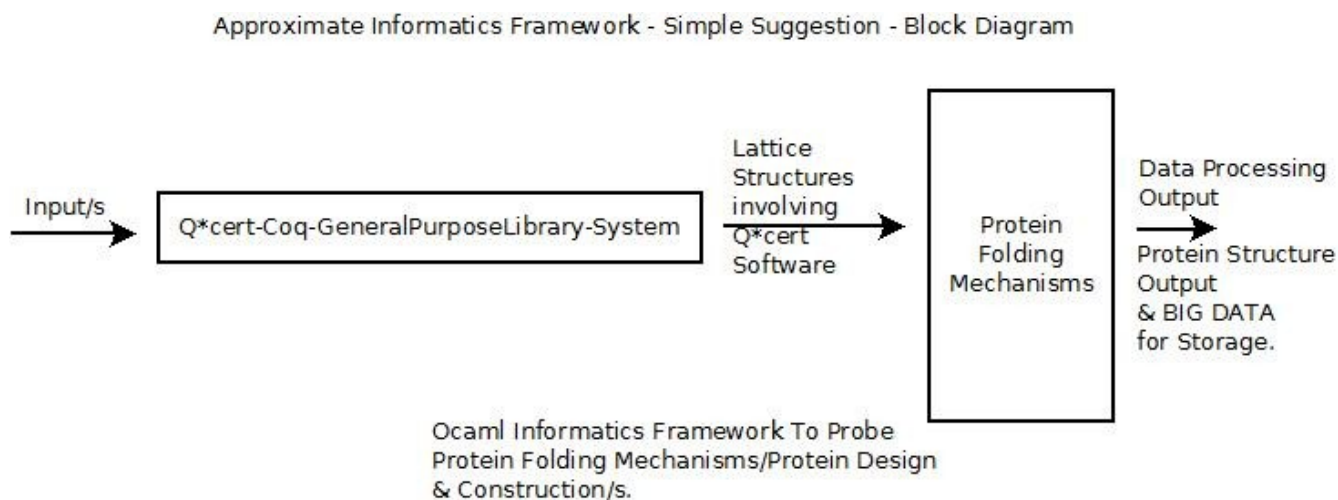
**[Source : <https://www.irif.fr/~sozeau/repos/coq/order/>] - Excellent information.**

AI Based Catalysis Informatics Framework Using JI Prolog/jCompound Mapper/JikesRVM/IoT Computing Environments – A Novel Insight into the Chemical Informatics World of Catalysis. [Source : <http://vixra.org/abs/1805.0120>]

Schur Group Theory Software Interfacing with Ruby Language in the Context of Ruby Based Machine Learning - An Interesting Insight into the Informatics World of Group Theory and its Nano-Bio Applications. [Source : <http://vixra.org/abs/1806.0075>]

[Source - [http://vixra.org/author/nirmal\\_tej\\_kumar](http://vixra.org/author/nirmal_tej_kumar) [ 29-31]]

## [II] Q\*cert/General Purpose Libraries Based Protein Folding Informatics & Data Processing Framework :



[ Figure I – Approximate Protein Folding Informatics Framework ]

\*\*\*[Source : The Knaster-Tarski theorem on complete lattices ]\*\*\*

[[http://en.wikipedia.org/wiki/Knaster-Tarski\\_theorem](http://en.wikipedia.org/wiki/Knaster-Tarski_theorem)]

[<https://www.irif.fr/~sozeau/repos/coq/order/Lattice.v>]

[<https://www.quora.com/Do-you-think-there-are-any-niches-in-AI-ML-for-which-Functional-Programming-is-a-good-fit>] – **Future Trends Using AI/ML/DL in Ocaml.**

[<http://users.umiacs.umd.edu/~hal/software.html>]

### **[III] Conclusion/s With Future Perspectives :**

A simple but powerful informatics platform was/is presented to the readers to probe the frontiers of Protein Folding Mechanisms based on Q\*cert/Coq/Ocaml – Software. To the best of our knowledge, this is one of the pioneering R&D attempts from us. Hope our readers will certainly consider our technical short notes and take this R&D one more step forward.

**”Lattice proteins are highly simplified computer models of proteins which are used to investigate Protein Folding “ - Wiki.**

### **[IV] Acknowledgment/s :**

Pure Academic R&D Only. Special thanks to all who made this happen.  
[ Non-Profit R&D]  
**THE END**