

Analysis of Meta-genomics Information w.r.t XML Files from KMAP* + BaseX [DB System] + HOL-Isabelle Theorem Prover -> A Novel & Simple Suggestion to develop ::-> Next Generation Bio-informatics R&D Platforms.

[Exploring : KAUST Meta-genomic Analysis Platform (KMAP*) + XML based Bio-informatics]

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[I] Main Idea + Inspiration + Introduction :

KAUST Metagenomic Analysis Platform (KMAP), enabling access to massive analytics of re-annotated metagenomic data
[Source -> <https://www.cbrc.kaust.edu.sa/aamg/kmap.start/#>]

[II] R&D Informatics Framework :

*Design your own R&D Algorithms based on our TITLE.Rigorous Testing in Progress @ the TIME of Submission.Keep Testing Novel Algorithms.
Thanks for understanding.*

[III] Important Reference/s :

[a] <https://www.cbrc.kaust.edu.sa/aamg/kmap.start/> ;

[b] <https://basex.org/basex/gui/>;

[c] <https://www.ebi.ac.uk/biosamples/graph/search> ;

[d] <https://homepages.inf.ed.ac.uk/jcheney/projects/XQuery/> ;

[e] <https://isabelle.in.tum.de/nominal/> ; <https://isabelle.in.tum.de/> ;

[IV] Acknowledgment/s : Non-Profit R&D ; Inspire Others Always ; Sincere Thanks to all WHO made this happen in my LIFE.

[V] Conclusion/s + Future Perspective/s : One of the pioneering R&D Efforts in this highly challenging domain of S&T.

[THE END]