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Novel algorithms for protein sequence analysis

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STELLINGEN

behorende bij het proefschrift

Novel algorithms for protein sequence analysis

1. G protein-coupled receptors are very successful drug targets since 30-45% of current drugs interact with this class of proteins.

Hopkins AL and Groom CR. Nat Rev Drug Discov. 2002 1:727-730

2. Conserved residues are important; very conserved residues are very important.

Prof. G. Vriend

3. Conserved residues are important; divergent residues may also be important because they are conserved in subgroups.

This thesis

4. Motif discovery is often conducted via sequence alignments. However it is equally feasible to identify motifs directly from unaligned sequences.

This thesis

5. If you don't ask big questions, you won't get big answers. The crystallization of G protein-coupled receptors seems feasible now.

Science DOI: 10.1126/science.1164772; Rasmussen SG et al. Nature 2007 450:383-387; Rosenbaum DM et al. Science 2007 318:1266-1273

6. Many receptor models used in drug design may not be useful after all.

Science DOI: 10.1126/science.1164772; <http://www.sciencedaily.com/releases/2008/10/081002204433.htm>

7. 96% of the human genome was considered as junk. But the junk may very well be the crown jewels, the stuff that orchestrates the coding sequences in biologically meaningful activities.

Berg P. Am J Hum Genet. 2006 4: 603-605

8. Despite decades of research on biological sequences, there is perhaps more hidden information in these than we know and novel methodology is certainly welcomed.

9. Give us tools and we will finish the job.

Winston Churchill (1941)

10. It is never too late to learn new skills.

11. The taste of the food served in Chinese restaurants in the Netherlands is a perfect example of how an evolving entity with inherited recipes adapts to a new environment.

12. Everything that has a beginning has an end.

The Matrix