

配列解析チーム

ポール・ホートン



研究テーマ

- 配列アラインメント
 - ・塩基配列とアミノ酸配列の類似配列検索 (LAST)
 - ・ゲノム・アラインメント・スコアの統計モデル
- 繰り返し配列同定法の改良
- タンパク質立体構造予測 (FORTE)
- 次世代シーケンサーの誤読修正 (RECOUNT)
- タンパク質の細胞内局在予測 (WoLF PSORT)
 - ・ミトコンドリア外膜のプロテオーム解析

Sequence Analysis Software

LAST

last.cbrc.jp — effectively aligns genomes and proteomes

seq.cbrc.jp/recount

— correct tag count bias from sequencer error

FORTE

www.cbrc.jp/htbin/

forte.cgi/forte_form.pl — protein structure from sequence

WoLF PSORT

wolfpsort.org — prediction of protein subcellular localization

Bioinformatics Research

BMC Structural Biology

Research article
Protein-segment universe exhibiting transitions at intermediate segment length in conformational subspaces
Kazuyoshi Suzuki^{1,2}, Takamasa Hirokawa¹, Junichi Higo^{1,2,3} and Kentaro Tomii^{1,2,3}
Published online 17 January 2009

Incorporating sequence quality data into alignment improves DNA read mapping
Martin C. Frith¹, Raymond Wan and Paul Horton

Improved Prediction of Transcription Binding Sites from Chromatin Modification Data

Kengo Sato¹, Tom Whittaker², Timothy L. Bailey and Paul Horton
Proceedings of CBRC 2010 Montreal, Canada, May 2010

Cell

Leading Edge
Correspondence

Mitochondrial β -Barrel Proteins, an Exclusive Club?

Article at BMC Bioinformatics 2010, 11:40

doi:10.1186/1471-2109-11-40

RESEARCH ARTICLE
Parameters for accurate genome alignment

Martin C. Frith¹, Hitoshi Hamada², Paul Horton¹

Methodology
HAMSTER: visualizing microarray experiments as a set of minimum spanning trees
Raymond Wan^{1,2}, Larisa Kiseleva², Hajime Harada², Hiromichi Mamitsuka² and Paul Horton²

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