

References

- Altschul, S. F., Gish, W., Miller, W., Myers, E. W. and Lipman, D. J. (1990) Basic local alignment search tool. J. Mol. Biol. 215, 403-410.
- Bairoch, A. (1992) *PROSITE: a dictionary of sites and patterns in proteins*. Nucleic Acids Res. 20 (Supplement), 2013-2018.
- Brendel, V., Bucher, P., Nourbakhsh, I. R., Blaisdell, B. E. and Karlin, S. (1992) *Methods and algorithms for statistical analysis of protein sequences*. Proc. Natl. Acad. Sci. USA 89, 2002-2006.
- Claverie, J.M. and Daulmerie, C. (1991) *Smoothing profiles with sliding windows: better to wear a hat!* CABIOS 7, 113-115.
- Claverie, J.M., Sauvaget, I. and Bougueleret, L. (1990) *k-Tuple frequency analysis: from intron/exon discrimination to T-cell epitope mapping*. Meth. Enzymol. 183, 237-252.
- Cockwell, K. Y. and Giles, I. G. (1989) *Software tools for motif and pattern scanning: program descriptions including a universal sequence reading algorithm*. CABIOS 5, 227-232.
- Eguchi, Y. and Seto, Y. (1992) *Prediction of the functional sites on amino acid sequences*. Genome Informatics Workshop III, 14.-15. December 1992, Yokohama.
- Fuchs, R. (1991) *MacPattern: protein pattern searching on the Apple Macintosh*. CABIOS 7, 105-106.
- Fuchs, R. (1993a) *Block searches on VAX and Alpha computer systems*. CABIOS, in press.
- Fuchs, R. (1993b) *Fast protein block searches*. CABIOS, in press.
- Gabrielian, A.E., Ivanov, V.S. and Kozhich, A.T. (1990) *On searching for the active sites in protein and peptide hormones*. CABIOS 6, 1-2.
- Ghosh, D. (1990) *A relational database of transcription factors*. Nucleic Acids Res. 18, 1749-1756.
- Henikoff, S., Wallace, J. C. and Brown, J. P. (1990) *Finding protein similarities with nucleotide sequence databases*. Methods Enzymol. 183, 111-132.
- Henikoff, S. (1991) *Playing with blocks: some pitfalls of forcing multiple alignments*. New Biol. 3, 1148-1154.
- Henikoff, S. and Henikoff, J. G. (1991) *Automated assembly of protein blocks for database searching*. Nucleic Acids Res. 19, 6565-6572.

Karlin, S., Morris, M., Ghandour, G. and Leung, M. Y. (1988) Efficient algorithms for molecular sequence analysis. *Proc. Natl. Acad. Sci. USA* 85, 841-845.

Karlin, S. and Altschul, S. F. (1990) Methods for assessing the statistical significance of molecular sequence features by using general scoring schemes. *Proc. Natl. Acad. Sci. USA* 87, 2264-2268.

Karlin, S., Blaisdell, B. E. and Brendel, V. (1990) Identification of significant sequence patterns in proteins. *Meth. Enzymol.* 183, 388-402.

Karlin, S., Bucher, P. and Brendel, V. (1991) Statistical methods and insights for protein and DNA sequences. *Annu. Rev. Biophys. Biophys. Chem.* 20, 175-203.

Karlin, S. and Brendel, V. (1992) Chance and statistical significance in protein and DNA sequence analysis. *Science* 257, 39-49.

Prestridge, D. S. (1991) SIGNAL SCAN: a computer program that scans DNA sequences for eukaryotic transcriptional elements. *CABIOS* 7, 203-206.

Sibbald, P. R., Sommerfeld, H. and Argos, P. (1991) Automated protein sequence pattern handling and PROSITE searching. *CABIOS* 7, 535-536.

Sibbald, P. R., Sommerfeldt, H. and Argos, P. (1992) Overseer: a nucleotide sequence searching tool. *CABIOS* 8, 45-48.

Smith, H.O., Annau, T.M. and Chandrasegaran, S. (1990) Finding sequence motifs in groups of functionally related proteins. *Proc. Natl. Acad. Sci. USA* 87, 826-830.

Smith, R. F. and Smith, T. F. (1990) Automatic generation of primary sequence patterns from sets of related protein sequences. *Proc. Natl. Acad. Sci. USA* 87, 118-122.

Sternberg, M. J. E. (1991) PROMOT: a FORTRAN program to scan protein sequences against a library of known motifs. CABIOS 7, 257-260.

Wallace, J. C. and Henikoff, S. (1992) PATMAT: a searching and extraction program for sequence, pattern and block queries and databases. *CABIOS* 8, 249-254.