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Trends in Bioinformatics

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Signal peptide sequence analysis of selected protein sequences from *Cryptosporidium parvum* (Article) [\(Open Access\)](#)Barudin, M.A.^a, Isa, M.L.M.^{b,c}, Yusof, A.M.^{b,c} ^aDepartment of Biomedical Science, Kulliyah of Allied Health Sciences, International Islamic University Malaysia, Jalan Sultan Ahmad Shah, Bandar Indera Mahkota, Kuantan, Pahang 25200, Malaysia^bDepartment of Basic Medical Sciences, Kulliyah of Nursing, International Islamic University Malaysia, Jalan Sultan Ahmad Shah, Bandar Indera Mahkota, Kuantan, Pahang 25200, Malaysia^cIntegrated Cellular and Molecular Biology Cluster (iMolec), International Islamic University Malaysia, Jalan Sultan Ahmad Shah, Bandar Indera Mahkota, Kuantan, Pahang 25200, Malaysia

Abstract

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Background and Objective: Studies on signal peptides remain little and lacking to *Cryptosporidium*. This study represents the first attempt to investigate selected putative protein sequences of *Cryptosporidium parvum* in its established genome database for signal peptide. **Methodology:** Prediction analysis of protein sequences and identification of signal peptides on this parasite were analysed by SignalP 4.1 server. A total of 100 protein sequences were randomly selected and analysed, of which 6 (6%) corresponded to be predicted as signal peptide sequences. **Results:** Based on the comparison of sequences with database protein sequences in GenBank NCBI, almost all protein sequences were highly conserved with other protein sequences from different species of *Cryptosporidium*. Considering the secretory proteins in *Cryptosporidium*, several virulence protein sequences of this parasite may also show presence of N-terminal signal peptide or not. **Conclusion:** Hence, further studies need to be carried out for identification of N-terminal signal peptide function in *Cryptosporidium* for facilitating its virulence and pathogenesis pathway. © 2018 Mohd Aiman Barudin et al.

SciVal Topic Prominence Topic: [Proteins](#) | [Support Vector Machines](#) | [pseudo amino](#)Prominence percentile: 99.183 

Author keywords

[Cryptosporidium](#) [N-terminal](#) [Peptide](#) [Protein](#) [Signal](#)

Indexed keywords

EMTREE drug terms:

[ABC transporter](#) [acyltransferase](#) [adenosine triphosphatase](#) [aminopeptidase](#)
[casein kinase II](#) [cysteine proteinase](#) [diacylglycerol acyltransferase](#)
[DNA directed RNA polymerase III](#) [glycerol 3 phosphate acyltransferase](#) [glycoprotein](#)
[heat shock protein 70](#) [heat shock protein 90](#) [histone acetyltransferase](#)
[long chain fatty acid coenzyme A ligase](#) [membrane protein](#) [mucin](#) [nuclease S1](#) [peptidase](#)
[phospholipase C](#) [polyketide synthase](#) [protein p23](#) [ribonuclease inhibitor](#)
[serine proteinase](#) [signal peptide](#) [transcriptional regulator ATRX](#) [virulence factor](#)

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accuracy Agrobacterium tumefaciens amino acid composition amino acid sequence
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Komagataella pastoris Mycobacterium tuberculosis Neurospora crassa nonhuman
pathogenesis pathogenicity Pseudomonas syringae Ralstonia solanacearum
Saccharomyces cerevisiae Schistosoma mansoni sequence analysis

Chemicals and CAS Registry Numbers:

acyltransferase, 9012-30-0, 9054-54-0; adenosine triphosphatase, 37289-25-1, 9000-83-3; aminopeptidase, 9031-94-1; cysteine proteinase, 37353-41-6; diacylglycerol acyltransferase, 9029-98-5; DNA helicase; glycerol 3 phosphate acyltransferase, 9029-96-3; histone acetyltransferase, 9054-51-7; histone acetyltransferase KAT5; long chain fatty acid coenzyme A ligase, 9013-18-7; mucosa associated lymphoid tissue lymphoma translocation protein 1; nuclease S1, 37288-25-8; peptidase, 9013-14-3, 9031-96-3; phospholipase C, 9001-86-9; polyketide synthase, 79956-01-7; proprotein convertase 9; serine protease HTRAL1; serine proteinase, 37259-58-8; transcriptional regulator ATRX; Werner syndrome ATP dependent helicase

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