

Virtual Ribosome—a comprehensive DNA translation tool with support for integration of sequence feature annotation

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Received February 14, 2006; Revised March 1, 2006; Accepted March 20, 2006

ABSTRACT

Virtual Ribosome is a DNA translation tool with two areas of focus. (i) Providing a strong translation tool in its own right, with an integrated ORF finder, full support for the IUPAC degenerate DNA alphabet and all translation tables defined by the NCBI taxonomy group, including the use of alternative start codons. (ii) Integration of sequences feature annotation—in particular, native support for working with files containing intron/exon structure annotation. The software is available for both download and online use at <http://www.cbs.dtu.dk/services/VirtualRibosome/>.

INTRODUCTION

A large number of software packages for translating DNA sequences already exist, as services on the World Wide Web [e.g. the Expassy Translate Tool (<http://www.expassy.ch/tools/dna.html>)], as command-line tools [e.g. the GCG package (1)] and as user-friendly graphical applications [e.g. DNA strider (a personal favorite) (2) and ApE (<http://www.biology.utah.edu/jorgensen/wayned/ape/>)]. However, many of these fine tools do not support translating sequences containing degenerate nucleotides, have no or limited support for alternative translation tables (including alternative initiation codons) and in general have problems handling special case situations. The software described here aims at addressing these issues and providing a comprehensive solution for translation. The software is build on the experience gained from writing and maintaining the Rev-Trans server (3).

Another part of the rationale for creating Virtual Ribosome is to create an easy and consistent way to map the underlying intron/exon structure of a gene onto its protein product.

This makes it easy to build datasets that can be used for analyzing how the underlying exon structure is reflected in the protein [e.g. how exon modules maps onto the 3D structure of the protein, see the FeatureMap3D server (4) elsewhere in this issue].

SOFTWARE FEATURES

Support for the degenerate nucleotide alphabet

The software has full support for the IUPAC alphabet (Table 1) for degenerate nucleotides. For example, the codon TCN correctly translates to S (serine) and not X (unknown) as often seen in other translators.

Support for a wide range of translation tables

Full support for all translation tables defined by the NCBI taxonomy group (5) (see the list below). The command-line version of the software also has support for

Table 1. IUPAC alphabet of degenerate nucleotides

Letter	Description	Bases represented
A	Adenine	A
T	Thymine	T
G	Guanine	G
C	Cytosine	C
Y	pYrimidine	C T
R	puRine	A G
S	Strong	G C
W	Weak	A T
K	Keto	T G
M	aMino	A C
B	Not A	C G T
D	Not C	A G T
H	Not G	A C T
V	Not T/U	A C G
N	aNy	A C G T

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sequence for translation using the default parameters, without having to scroll through a page of obscure options. The options are grouped into logical sections further down the web page. For each option a short explanation is provided together with a link to a detailed description.

ACKNOWLEDGEMENTS

Special thanks to Ulrik de Lichtenberg for comments on the content and layout of the manuscript, and to Henrik Nielsen for inspiration for implementing the 'Intron phase' functionality. This work is supported by a grant from The Danish National Research Foundation and The Danish Research Agency. Funding to pay the Open Access publication charges for this article was provided by The Danish Research Agency.

Conflict of interest statement. None declared.

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