

## Relationship between Type of Insert, Open/Closed, cDNA boundaries and Protein Translation

The Protein Translation function translates the DNA sequence within the defined cDNA boundaries according to the following rules:

Type Of Insert	Open/Closed	Translation Rule
cDNA with UTRs	n/a	Reports the longest Open Reading Frame (from start codon to stop codon) in any of the three forward frames
DNA Fragment	n/a	Does not translate. Non-coding can be selected as an Open/Closed value.
ORF	Closed with ATG	Translation occurs from the first ATG to an in frame stop codon
ORF	Closed, no ATG	Translation occurs from the nucleotide at the start of the cDNA boundary to an in frame stop codon
ORF	Open with ATG	Translation occurs from the first ATG to the end of the cDNA boundary
ORF	Open, no ATG	Translation occurs from the nucleotide at the start of the cDNA boundary to the end of the cDNA boundary
ORF Domain		same rules as ORF, ORF domain indicates that the construct codes for a modular domain (e.g., SH2)
ORF Subsequence		same rules as ORF, for a construct that is neither a full-length ORF nor an individual domain

Open/Closed is a mandatory feature for ORF, ORF domain, ORF subsequence

Open - no stop codon

Closed - stop codon

If the above rules are not satisfied, then translation does not occur