

## **HYDEN (HighLY DEgeNerate primers) - A Software for designing pairs of degenerate primers for a given set of DNA sequences (Ramot)**

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### Overview

HYDEN (HighLY DEgeNerate primers) is a program for designing pairs of degenerate primers for a given set of DNA sequences. HYDEN works well for large input sets of genomic sequences (e.g., hundreds of sequences of length 1Kbp).

HYDEN is a batch (i.e., command-line, as opposed to graphical interface) program, available for Windows XP (downloadable version) and Linux (upon request).

The HYDEN software is freely available for academic use.

It is also available for non-academic use under appropriate licensing. Please contact Ron Shamir (rshamir AT post.tau.ac.il) or Chaim Linhart (chaiml AT post.tau.ac.il) for further information.

### Degenerate Primers

A primer is degenerate if some of its positions admit more than one nucleotide. It is in fact a mixture of unique primers. For example, AAC{G,T}G{A,C,G}G is a 7-long degenerate primer, in which the fourth and sixth positions are degenerate. It corresponds to the primers AACGGAG, AACGGCG, AACGGGG, AACTGAG, AACTGCG, AACTGGG.

The degeneracy of a primer is the number of unique sequences it corresponds to (6 in the example above). Degenerate primers can be used in PCR reactions to amplify many related sequences from genomic DNA or from cDNA libraries. They can be used when some of the related genomic sequences are unknown, or known only in a related species.

In experiments, pairs of primers with combined degeneracies of up to 1010 were successfully used to amplify sequences from genomic background, with specificity over 99.5%.

Read more and download from here: <http://acgt.cs.tau.ac.il/hyden/HYDEN.htm>

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