

**Table 1.** Algorithms and software for spliced-sequence alignments that are commonly used to infer primary transcript structures from cDNAs or ESTs. One can install and run all algorithms locally, while web-based software tools are also available, for e.g. ASPIC, GENESEQER, MGALIN, and SIM4.

### Algorithms for spliced-sequence alignments

ASPIC	<a href="http://t.caspur.it/ASPIC/">http://t.caspur.it/ASPIC/</a>
DDS/GAP2	<a href="http://www.tigr.org/software/alignment.shtml">http://www.tigr.org/software/alignment.shtml</a>
EST_GENOME	<a href="http://www.well.ox.ac.uk/~rmott/ESTGENOME/est_genome.shtml">http://www.well.ox.ac.uk/~rmott/ESTGENOME/est_genome.shtml</a>
EXALIN	<a href="http://blast.wustl.edu/exalin">http://blast.wustl.edu/exalin</a>
GENEQER	<a href="http://deepc2.psi.iastate.edu/cgi-bin/gc.cgi">http://deepc2.psi.iastate.edu/cgi-bin/gc.cgi</a>
GMAP	<a href="http://www.gene.com/share/gmap">http://www.gene.com/share/gmap</a>
MGALIGN	<a href="http://origin.bic.nus.edu.sg/mgalign/">http://origin.bic.nus.edu.sg/mgalign/</a>
MRNAVSGEN	<a href="http://genes.mit.edu/genoa">http://genes.mit.edu/genoa</a>
SIM4	<a href="http://globin.cse.psu.edu/html/docs/sim4.html">http://globin.cse.psu.edu/html/docs/sim4.html</a>
SPA	<a href="http://www.biozentrum.unibas.ch/~nimwegen/cgi-bin/spa.cgi">http://www.biozentrum.unibas.ch/~nimwegen/cgi-bin/spa.cgi</a>
SPIDEY	<a href="http://www.ncbi.nlm.nih.gov/spidey">http://www.ncbi.nlm.nih.gov/spidey</a>
WABA	<a href="http://hgwdev-hiram.cse.ucsc.edu/IntronWS120/index.html">http://hgwdev-hiram.cse.ucsc.edu/IntronWS120/index.html</a>