

Aligner	publication	Indexing	Pairwise alignment	Max. read length (bp)
BWA	2009	BWT-FM	Semi-Global	125
Bowtie	2009	BWT-FM	HD	76

CloudBurst	2009	Hashing	Landau-Vishkin	36
GNUMAP	2009	Hashing	NW	36
Blast	1990	Hashing	Heuristic	1000

Samtools	2009	BWT-FM	Local	500
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Table 1: Table of Genome *Aligners* with breakable setting.