

Table 2 A subset of short read aligners available for histone modification ChIP-seq alignment

Software tool	Web address
Seed and extend strategy	
MAQ	http://maq.sourceforge.net/
SOAP	http://soap.genomics.org.cn/index.html
SHRiMP	http://compbio.cs.toronto.edu/shrimp/
ZOOM	http://www.bioinform.com/zoom
BFAST	http://sourceforge.net/projects/bfast/
Using a hash table or more recently a suffix array generated from Burrows–Wheeler transform	
BOWTIE	http://bowtie-bio.sourceforge.net
BWA	http://bio-bwa.sourceforge.net
SOAP2	http://soap.genomics.org.cn/index.html
