

# Recommended Aligners by Application



	Read Length (nt)	RNA-Seq*	DNA Sequencing	smallRNA-Seq	ChIP-Seq	MeDIP-Seq	Bisulfite-Seq
Bowtie	<50	•*	•	•	•	•	
Bowtie2	50 - >200	•*	•	•	•	•	
Tophat / Tophat2	50bp - >200	•					
BWA	<50-100 or >200	•*	•	•	•	•	
BWA-SW	100 - >200		•		•	•	
TMAP (Ion Torrent)	<50 - >200	•*	•	•	•	•	
SHRiMP2	<50 - >200	•*	•	•	•	•	
STAR	50bp - >200	•					
GSNAP	<50 - >200	•	•		•	•	•

\*RNA-Seq alignment includes splicing/junction alignment except where stated otherwise

\*Applicable only for short reads (<50nt) which don't require splice junction aligners