Hash Table-

1. GSNAP
2. Novoalign
3. mrFAST and mrsFAST
4. FANGS
5. MAQ
6. RMAP

Burrows-Wheeler Transform (BWT):

1. BWT
2. Bowtie
3. BWA
4. SOAP2

Benchmarking Methods (Features):

1. Quality Threshold
2. Number of mismatches
3. Seed length
4. Read length
5. Paired-end reads
6. Genome type
7. Gaped Alignment
8. SNP Awareness
9. Splicing awareness
10. Scalability
11. Accuracy evaluation
12. Rabema Evaluation



