Table S12

Software	Analysis	Reference
Alien Hunter	Detection of local compositional biases using variable-order motif distributions method to identify horizontally acquired (HGT) DNA regions	[92]
Artemis	Genome viewer and annotation tool	[117]
Artemis Comparison Tool (ACT)	Genome sequence multiple alignment and comparison viewer	[118]
BLASTCLUST	Clustering of proteomes	[119]
BioLayout Express[3D]	Network analysis of microarray expression data	[74,75]
BLAST	Homology prediction	[119]
GLIMMER, RBS finder & TransTermHP	Automated detection of potential coding sequences (CDSs), Shine-Dalgarno sequences and rho-independent transcription terminators	[120]
Pathway Tools	Metabolic pathway reconstruction	[121]
PFAM database	Domain-based identification of protein families	[122]
PROSITE	Prediction of lipoproteins and proteins recognized by sortases	[123]
Reciprocal best-match BLASTP/FASTA	Determination of orthologous gene sets	[119]
REPuter	Sequence repeats	[124]
RFAM database	Stable non-coding RNAs	[125]
SignalP	Secreted proteins	[126]
TMHMM	Membrane/transmembrane proteins	[127]