

**Table S1. Key functionalities in various AGEs.**

Listed in the table below are four popular AGEs: BASys, ISGA, RAST and xBASE (listed non-alphabetically). For each engine, a selection of key features and functionalities (underlying tools) is indicated, as well as each AGE's most important underlying databases. The data was gathered from published literature and from online documentation.

| Engine Name      | Asgard | CodonW | CRITICA | Glimmer  | Alternative ORF Predictor Available? | HMMPFAM | HOMODELLER | MAST | PredictSPTM | PROSITE | PSIPRED | RNAmer | tRNAscan-SE | VADAR | Underlying Database ¶            |
|------------------|--------|--------|---------|----------|--------------------------------------|---------|------------|------|-------------|---------|---------|--------|-------------|-------|----------------------------------|
| ISGA (Ergatis)   | X      |        |         | X (v3)   | No                                   | X       |            | X    |             |         |         | X      | X           |       | RS, RT, GB, TF<br>CO, PF, SP, CC |
| RAST             |        |        |         | X (v3)   | Yes (RAST)                           |         |            |      |             |         |         |        | X           |       | PF, FF                           |
| BASys            |        |        | X       | X (v2.1) | No                                   |         | X          |      | X           | X       | X       |        |             | X     | RS, UP, P, KG<br>CC, PB, PF      |
| xBASE (coliBASE) |        | X      |         | X (v3)   | No                                   |         |            |      |             | X       |         | X      | X           |       | RS, UP, GB                       |

¶ COG: CO; CyberCellDB: CC; FIGfam: FF; Genbank: GB; PDB: PB; Pfam: PF; RegTransBase: RT; SwissProt: SP; TIGRFAM: TF; UniProt: UP; UniRef: UR; RefSeq (NCBI): RS. # Asgard: metabolic pathway reconstruction; CodonW: analysis of codon and amino acid usage; CRITICA: Coding Region Identification Tool Invoking Comparative Analysis; GLIMMER: ORF prediction; HMMER: profile hidden Markov models; HMMPFAM: HMM search against the PFAM database; HOMODELLER: predicts protein 3D structures; LipoP: predicts Gram-negative lipoprotein signal peptides, other signal peptides and n-terminal membrane helices; MAST: transcription factor binding site prediction; PredictSPTM: signal peptide prediction based on HMM alignments of SignalP predicted signal peptides; PROSITE: protein motif analysis; PSIPRED: protein structure prediction server; RNAmer: prediction of RNA-coding genes; tRNAscan-SE: tRNA prediction; VADAR: Volume Area Dihedral Angle Reporter; compilation of over 15 algorithms to assess peptide and protein structures from PDB data.