

Help document

1. **iPtgxDB_insilico.jar**: In silico ORF predictor by Ulrich Omasits. Generates a GFF file of open reading frames for a given genomic sequence. Alternative start codons and minimal length are configurable.

Usage: java -jar iPtgxDB_insilico.jar [-alt <codon(s)>] [-extend <e>] [-laa] [-min <length>] [-out <file>] [-seq <file>] [-tab <output>]

-alt <codon(s)>	Alternative start codons (default: GTG TTG CTG)
-extend <e>	Get extension for all features 3' and 5' by <e> nucleotides in tabular output file
-laa	Take only longest alternative anchor for regions without a main start codon
-min <length>	The minimum protein length in aa (default: 10)
-out <file>	The output gff file
-seq <file>	The input sequence
-tab <output>	A tab-separated output file with sequences per entry

2. **iPtgxDB_convert.jar**: Genome Annotation Converter by Ulrich Omasits. Converts genome annotations from various formats to the GFF file format.

Usage: java -jar iPtgxDB_convert.jar [-all] [-broad <file>] [-chemgenome <file>] [-cmr <file>] [-ensembl <file>] [-extend <e>] [-genbank <file>] [-genoscope <file>] [-id <sequenceid>] [-out <output>] [-repseek <file>] [-seq <input>] [-short <file>] [-tab <output>]

-all	Convert exentsive, i.e. all features and attributes
-broad <file>	A BROAD genome summary per gene file
-chemgenome <file>	One or more fasta files generated by ChemGenome 2.0
-cmr <file>	A tab-separated tabular text file from CMR
-ensembl <file>	A plain-text Ensembl file
-extend <e>	Extend all features 3' by <e> nucleotides or automatically if e='auto'
-genbank <file>	A plain-text GenBank file
-genoscope <file>	A tab-separated tabular text file from Genoscope/MAGE
-id <sequenceid>	The sequence id for the GFF file [default: guessed from input file]
-out <output>	The output gff3 file
-repseek <file>	A repseek R-Table output file
-seq <input>	The genomic sequence
-short <file>	A tab-separated short ORF file
-tab <output>	A tab-separated output file with sequences per entry [requires seq]