**Workflow: DNA/RNA Sequence Optimization for Therapeutics**

* **Ensembl**
  + **Input:** Gene/variant ID, coordinates, or FASTA sequence
  + **Output:** Annotated genomic data (gene models, variants, regulatory elements, JSON/flat files)
* **Biopython**
  + **Input:** FASTA/GenBank/CSV/JSON sequence data, scripts in Python
  + **Output:** Parsed/manipulated biological sequences (FASTA, GenBank, PDB, etc. depending on task)
* **CD-HIT**
  + **Input:** FASTA sequence dataset (DNA/protein)
  + **Output:** Clustered sequences (representative clusters in FASTA, cluster reports in TXT)
* **DIAMOND**
  + **Input:** FASTA query (DNA/protein), reference database (BLAST-format)
  + **Output:** Alignment results (BLAST tabular, SAM, or binary DAA formats)
* **InterProScan**
  + **Input:** Protein sequence (FASTA)
  + **Output:** Domain/function annotation (TSV, XML, JSON, GFF3)
* **Rfam (with RNAcentral aggregation)**
  + **Input:** RNA sequence (FASTA) or accession number
  + **Output:** RNA family classification + secondary structure (Stockholm alignment, annotations)
* **mRNAid**
  + **Input:** Target protein coding sequence (FASTA/GenBank/JSON)
  + **Output:** Optimized mRNA sequence (FASTA/JSON, codon usage, structure predictions)
* **COOL**
  + **Input:** RNA sequence (FASTA) or structure constraints
  + **Output:** Optimized RNA constructs with predicted folding (FASTA/CT files)
* **oxDNA**
  + **Input:** DNA/RNA structure file (topology in TXT, sequence in FASTA)
  + **Output:** Molecular dynamics trajectory (trajectory files, JSON, XYZ formats)
* **ViennaRNA (RNAfold)**
  + **Input:** RNA sequence (FASTA)
  + **Output:** Secondary structure predictions (dot-bracket, CT, PostScript images, free energy values)
* **DNA Chisel**
  + **Input:** DNA sequence (FASTA/GenBank) + constraints/optimization rules (JSON/YAML)
  + **Output:** Optimized DNA sequence (FASTA/GenBank, with logs of applied changes)
* **IEDB Analysis Resource**
  + **Input:** Protein/peptide sequence (FASTA/RAW)
  + **Output:** Epitope predictions (CSV, TXT, JSON)
* **CRISPOR**
  + **Input:** Target DNA sequence or genomic coordinates (FASTA/GenBank)
  + **Output:** Guide RNA designs + scores (TSV, JSON, CSV)
* **RBS Calculator**
  + **Input:** DNA sequence containing ribosome binding site (FASTA/RAW)
  + **Output:** Translation initiation rate + optimized RBS (numeric values + FASTA/JSON)
* **KineFold**
  + **Input:** RNA sequence (FASTA/RAW)
  + **Output:** Kinetic folding pathways (dot-bracket trajectories, CT files, animated plots)
* **COPASI**
  + **Input:** Biochemical network model (SBML/XML/CSV)
  + **Output:** Simulation results (time-course data, steady-state analysis, plots, CSV)
* **Benchling**
  + **Input:** DNA/protein sequences (FASTA/GenBank), metadata, annotations
  + **Output:** Designed sequences, annotated plasmids, cloning maps (GenBank, FASTA, JSON exports)