

# Ardit Mishra

## AI Engineer & Builder • Agents, Evaluation & Computational Biology

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### PROFESSIONAL SUMMARY

AI engineer and builder with a bioinformatics degree. A confident answer isn't the same as a correct one, so I build systems that check AI's work: a multi-agent build system that runs on free models and accepts work only when a test passes, and science tools whose every claim cites its source. I evaluate models under leakage-aware splits and publish the unflattering numbers, build the Python pipelines and APIs underneath, and work daily with Claude Code and Codex, with AI review and the test suite as the gate.

### ENGINEERING & RESEARCH PROJECTS

**Tri-AI — Multi-Agent Build System** • Founder & Systems Architect Sep 2026 – Present  
**Live:** [tri-ai.arditmishra.com](https://tri-ai.arditmishra.com) • Python, SQLite, Hermes agents, Telegram, Ollama, multi-provider routing, Windows services

- Built a multi-agent system: a request arrives on Telegram, a planner splits it into steps, free and local models build each, a reviewer model approves, and one preview link comes back. A step is accepted only when its verification command **exits 0**, never on its own report: one free model deleted 387 of 389 lines and reported success.
- Made that guarantee hold under failure: leased claims, heartbeats that require **observable progress**, process-tree kills, stash-based revert and stuck-agent detection. Router, gateway, workers and dashboard self-heal under a watchdog, verified by killing all four.
- **Verified routing instead of configuring it:** called all 574 models a router advertised; 20 answered as themselves and 22 served a different model at HTTP 200. Paid models are opt-in, so a build costs **\$0**. ~2,500 tests gate every deploy.

**Genclarus — Grounded Gene & Variant Explainer** • Founder & AI Engineer Jul – Sep 2026  
**Live:** [genclarus.com](https://genclarus.com) • Next.js, TypeScript, NVIDIA NIM, Vercel

- Built a web app that turns a gene symbol or variant rsID into a plain-language, cited explanation. Every sentence renders deterministically from typed facts in **ClinVar**, **dbSNP**, **gnomAD**, **UniProt**, **MyGene** and **MyVariant**, each bound to its source field.
- No language model writes factual content, and a fail-closed validator rejects whatever it cannot ground. Added hybrid **BM25 + embedding retrieval** over a 173-record corpus at **Recall@10 0.950**, **MRR 0.775**. 343 tests gate every merge.

**Peptide-MHC Class I Binding Predictor** • Independent Research Feb – May 2026  
**Live:** [peptide.arditmishra.com](https://peptide.arditmishra.com) • XGBoost, PyTorch, TypeScript, MHCflurry data

- Built a browser-local workbench that scores 8–11 residue peptides against human HLA class I alleles; the model runs entirely in the browser, so no sequence leaves the reader's machine.
- Evaluated **15 approaches** (CNN, BiLSTM, Transformer, frozen ESM-2) on 120,000 measurements across 129 alleles with **peptide-grouped splits**; shipped the baseline at **ROC-AUC 0.9188**, **PR-AUC 0.8085**, with a published split-difficulty ladder and Python↔TypeScript parity to 7.5e-08.

**BioStudio — Variant Control Bench** • Independent Nov 2025 – Feb 2026  
**Live:** [biostudio.arditmishra.com](https://biostudio.arditmishra.com) • JavaScript, Three.js, React, Node, Python, XGBoost, RDKit

- Built a pre-order check for synthetic DNA: a separate verifier re-derives the requested edits from the exported sequence and the **GRCh38 reference alone**, and the order is held until it can — verify(fasta, reference) has no parameter through which the request could arrive.
- Attacked it with 22 mutation operators whose ground truth comes from the file: **19,823 attempts, 0 false pass, 0 false hold**. Closed 32 defects from **four independent adversarial reviews**, each kept as a regression.

**GenomeSight — Sequence Analysis Workbench** • Independent Aug – Dec 2025  
**Live:** [genomesight.arditmishra.com](https://genomesight.arditmishra.com) • React, FastAPI, Cython, Docker, Render

- Built a deterministic workbench for GC content, k-mer profiling, six-frame ORFs, IUPAC motif and restriction-site search, codon usage and alignment; each result names its method. Optional **Cython accelerator at 5.3×–11.0×** and 67 backend tests.

**RNA-seq: Multiple Sclerosis & Sephin1** • Loyola University Chicago, four-person team Jan – May 2023  
EAE mouse-model transcriptomics across three arms — **FastQC**, **Kallisto** pseudoalignment, **Sleuth** differential expression, **WebGestalt** enrichment, **Snakemake**-orchestrated in R/Bioconductor.

### EXPERIENCE

**Proprietary Futures Trader** • Independent / Proprietary Trading Firms Dec 2020 – Present  
• Trade NQ, ES and Gold under defined drawdown and position-sizing limits; built Python/Pandas tooling over execution history.

**Data Manager** • 4225 Giddings Inc., Chicago, IL Aug 2018 – Nov 2021  
• Automated Clover POS extraction and reporting in Python, cutting 8–10 weekly hours; added k-means customer segments.

### EDUCATION

**Loyola University Chicago** • B.S. Bioinformatics Aug 2018 – Dec 2024

### TECHNICAL SKILLS

**Languages:** Python, R, SQL, TypeScript, JavaScript, Bash, Cython • **AI Systems & Tooling:** multi-agent orchestration, Claude Code, Codex, MCP, Ollama, Hermes agents, multi-provider routing, hybrid retrieval (BM25 + embeddings), NVIDIA NIM • **ML:** PyTorch, scikit-learn, XGBoost, SHAP, CNN/BiLSTM/Transformer, ESM-2, Hugging Face • **Evaluation & Testing:** leakage-aware splits, ROC-AUC/PR-AUC, calibration, retrieval evals (Recall@k, MRR), adversarial fuzzing, pytest, Vitest, Playwright • **Backend, Web & Infra:** FastAPI, Next.js, React, Node, Tailwind, Three.js, PostgreSQL, Docker, GitHub Actions, AWS, GCP, Vercel, Render • **Bioinformatics:** Biopython, RDKit, Kallisto, Sleuth, GRCh38, ClinVar, gnomAD, Open Targets, ChEMBL, MHCflurry, AlphaFold, AlphaMissense