

Ainnocence Achieves New Milestone with Protein Foundation Models

Proprietary sequence-first model rivals and in key areas surpasses the leading ProteinGym sequence-only baselines

SAN FRANCISCO, CA, UNITED STATES, August 23, 2025 /EINPresswire.com/ -- [Ainnocence](#), a pioneer in generative AI for biotechnology, today announced the successful internal benchmarking of its protein language model, AINN-P1, trained on UniRef sequences with up to 167 million parameters.

Comparative performance on the ProteinGym zero-shot leaderboard

Model (Input Modality)	Avg. ρ	Activity	Binding	Expression	Stability
AINN-P1 (Single seq.)	0.441	0.358	0.390	0.391	0.625
Progen2 M (Single seq.)	0.380	0.393	0.295	0.433	0.396
ESM2 (150 M) (Single seq.)	0.387	0.391	0.326	0.402	0.510
xTrimoPGLM-1B-MLM (Single seq.)	0.379	0.390	0.298	0.406	0.445
Wavenet (MSA)	0.373	0.379	0.325	0.350	0.449
xTrimoPGLM-100B-int4 (Single seq.)	0.364	0.378	0.259	0.380	0.450

The baseline numbers are from the July 2025 ProteinGym zero-shot leaderboard; Ainnocence values are few-shot results reported below.

AINN-P1 is Ainnocence's protein language foundation model, built to understand protein sequence patterns to power next-generation drug discovery. The new model posts state-of-the-art Spearman correlation scores across four core protein-fitness tasks, reinforcing Ainnocence's sequence-first drug-discovery platform and underscoring its competitiveness against much larger transformer models from Meta and BioMap.

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Sequence is the new paradigm”

Dr. Lurong Pan

Highlights:

- Top overall sequence-only score: With an average $\rho = 0.441$, AINN-P1 edges past ProSST (0.438) while using orders-of-magnitude fewer parameters than 100 B-scale transformers.
- Best-in-class stability prediction: A $\rho = 0.625$ on stability is the highest of any published sequence-first model, providing critical accuracy for manufacturability screens.
- Closing the binding gap: AINN-P1's binding $\rho = 0.390$ exceeds ESM2-150M by 0.064 points, narrowing the historic advantage of structure-aware models.

Detailed benchmark results

Recent in-house evaluations of the AINN-P1 performed in a few-shot embedding regime for efficiency, produced the following Spearman correlations: Activity 0.3581, Binding 0.3901, Expression 0.3913, Stability 0.6251. These metrics match or exceed many transformer-based

benchmarks, demonstrating that smart architecture and curated data can beat brute-force scale.

Crucially, these benchmarks were achieved without expensive full fine-tuning. Instead, fixed AINN-P1 embeddings feed lightweight regressors – a strategy that slashes compute costs while preserving accuracy, and aligns with emerging best practices when only limited experimental data are available.

Context within the protein-AI landscape

Meta's ESM family and BioMap's 100 B-parameter xTrimo model have advanced the field dramatically, yet their training budgets remain prohibitive for most labs. Ainnocence's leaner AINN-P1 delivers comparable accuracy without billion-scale parameters or MSAs, validating a sequence-only paradigm for broad adoption.

"Sequence is the new paradigm," said [Dr. Lurong Pan, CEO](#). "By learning the language of proteins, we predict complex properties without relying on structures or wet-lab screens. These results rival Big Tech's best while remaining cost-efficient."

Integration & impact on [Ainnocence's platform](#)

The upgraded model is now being rolled into SentinusAI® (antibody engineering), CarbonAI® (small-molecule & PROTAC design) and CellulaAI® (cell-therapy optimization). Higher-fidelity predictions of stability and expression accelerate antibody lead-opt studies, while enhanced activity/binding scores improve small-molecule hit selection – compressing discovery timelines from years to weeks.

Ainnocence invites research groups and biopharma partners to leverage its sequence-first AI platform for protein engineering, vaccine work and hard-to-drug targets. Contact service@ainnocence.com or visit www.ainnocence.com for collaboration details.

About Ainnocence

Founded in 2021, Ainnocence is a next-generation biotech company whose self-evolving AI platform can virtually screen 10^{10} protein sequences or small-molecule candidates for multitarget and multi-objective optimization, optimizing multiple properties simultaneously to deliver high-probability leads with unprecedented speed and cost efficiency.

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