Massimo Domenico Sammito, PhD

AI Product Director · Drug Discovery & Biologics · Agentic AI

Cambridge, UK | +44 7753 400788 | massimo.sammito@gmail.com | linkedin.com/in/massimosammito | Google Scholar | ORCID

PROFILE

AI product director who turns frontier AI into drug-discovery products that scientists adopt, with 10+ years across computational structural biology, biologics discovery and R&D platforms. At Recursion, sets the vision and roadmap for an integrated agentic AI ecosystem across the design-make-test-learn cycle and leads a team of 4 Product Managers. At AstraZeneca, led a ~20-person product organisation (8 direct reports) owning the Biologics Discovery Platform for 200+ scientists, shipping an SVP Award-winning developability product and GenAI workflows that cut antibody design time by 30%. PhD scientist (25+ papers, h-index 21, first-author Nature Methods) experienced in AI governance, alliances and vendor strategy in regulated R&D.

Core strengths: AI product strategy & portfolio roadmaps · leading product teams · drug discovery (biologics & small molecules) · agentic AI & LLM products · protein & antibody design · AI governance in regulated R&D · alliances & vendor negotiation · scientific & executive stakeholder management

PROFESSIONAL EXPERIENCE

Recursion | UK Mar 2026 – Present

Associate Director, Product

- **Product leadership:** Lead a team of 4 Product Managers, each owning a portfolio of AI and agentic products across different stages of the drug-discovery pipeline.
- **Agentic DMTL ecosystem:** Set the vision and roadmap for an integrated agentic AI ecosystem across the design-make-test-learn (DMTL) cycle; own the Design layer and lead, through indirect PM reports, the implementation of Test and Learn.
- **Hit-ID & Design:** Own the Hit Identification & Design product area, with 2–3 agentic AI products in pilot with computational scientists.
- **Research to product:** Partner with Valence Labs, Recursion's AI research unit, to bring advanced models in transcriptomics, genomics and de novo design into products for discovery teams.

AstraZeneca | Cambridge, UK Oct 2024 – Jan 2026

Director, R&D IT – Data, Analytics & AI (Product Management, Biologics Discovery Platform)

- **Team leadership:** Led a product organisation of ~20 with 8 direct reports (Product Owners, AI Scientists, Engineers), building an agile, science-first delivery culture.
- **Platform ownership:** Owned product vision and roadmap for the Biologics Discovery Platform, serving 200+ scientists globally.
- **Shipped AI products:** Delivered a developability-prediction product that won the internal SVP Award, and GenAI workflows that reduced overall antibody design time by 30%.
- **AI governance:** Set up and chaired the AI risk-governance framework; 100% of deployed models and data products met internal regulatory and safety standards.
- **Vendor strategy:** Moved Seqera (Nextflow) from user-based to usage-based licensing to scale cost-effectively; worked with Schrödinger on token optimisation for a 15% efficiency gain.
- **AI ecosystem:** Set up collaborations with NVIDIA (model fine-tuning) and Rhino Health (federated learning) to open new AI capabilities for the R&D pipeline.
- **Scientific velocity:** Identified the bottleneck in screening campaigns and delivered on-demand AWS EC2 sandbox environments, speeding up scientific delivery by 50%.

AstraZeneca | Cambridge, UK Aug 2022 – Oct 2024

Associate Principal Scientist – Strategic AI Lead, Antibody Discovery

- **AI-designed antibodies:** Led AI-driven antibody discovery for 3+ campaigns that produced experimentally validated, high-affinity lead candidates.
- **Hybrid modelling:** Drove the shift to hybrid physics-based + deep-learning workflows, improving prediction accuracy by 15% over legacy methods.

- **Data strategy:** Defined the data strategy for large-scale model training, curating 1.4M antibody sequences (OAS) and 7k structures (SAbDab) into a proprietary training asset.
- **Alliances:** Managed partnerships with AI biotechs Nabla Bio and Absci: joint discovery programmes across 4 targets.
- **Bridge role:** Led the liaison between wet-lab and computational teams, turning biological needs into executable technical roadmaps.

PhoreMost | Cambridge, UK Jun 2021 – Aug 2022
Senior Computational Scientist II

- Designed AI/ML pipelines for peptide-library engineering that fed directly into R&D decisions; replaced manual analysis with automated workflows and introduced agile practices to the science team.

University of Cambridge | Cambridge, UK May 2018 – Jun 2021
Marie Skłodowska-Curie Individual Fellow

- Secured competitive EU funding and managed the end-to-end lifecycle of scientific software development, delivering tools for X-ray crystallographic data phasing.
- Developed reproducible methodologies for structural biology, disseminated through high-impact publications, including early validation of AlphaFold/CASP14 models for structure solution (Proteins, 2021).

C.S.I.C. | Spain Jan 2017 – May 2018
Postdoctoral Fellow

- Developed computational methods for X-ray crystallography and data clustering; supported research delivery and reproducibility.
- Supervised and mentored PhD students in research projects.

Georg-August-Universität Göttingen | Germany Sep 2015 – May 2016
Postdoctoral Researcher

- Conducted computational research in structural biology focused on algorithm development.

C.S.I.C. | Spain Jan 2011 – Sep 2015
Bioinformatics Computer Scientist (PhD Student)

- Developed computational algorithms for crystallography and applied machine learning to structural bioinformatics.
- Published peer-reviewed work in computational biology and structure determination.

AI FLUENCY & PROTOTYPING

- **Agentic prototyping:** Build functional prototypes with Claude Code and Codex using a spec-first workflow (design doc → technical spec → agent implementation), plus a local multimodal model stack.
- **Architecture literacy:** Understand agentic architectures, multi-agent workflows and software-engineering practice well enough to shape technical direction with engineering and research teams.

EDUCATION

PhD, Biotechnology (Computational Crystallography) – Universitat de Barcelona, 2015

MSc, Bioinformatics (dual degree) – Universitat Pompeu Fabra & Università di Bologna, 2011

BSc, Computer Science – Università di Catania, 2009

SELECTED PUBLICATIONS

Author of 25+ peer-reviewed publications with an h-index of 21. Full list on Google Scholar / ORCID.

- Proteins (2021): Assessing the utility of CASP14 models for molecular replacement. Validating AlphaFold performance.
- Acta Crystallographica D (2020): ALEPH: a network-oriented approach for the generation of fragment-based libraries and for structure interpretation. Corresponding author.
- Acta Crystallographica D (2019): Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix.

- Nature Methods (2013): Exploiting tertiary structure through local folds for crystallographic phasing. First author.

SKILLS & TOOLS

AI & science: LLM/agentic products, protein & antibody design models, developability prediction, federated learning, model evaluation

Technical: Python, PyTorch, SQL, Java, C++; AWS (Bedrock, S3, EC2), Kubernetes, Nextflow

Product: Portfolio prioritisation, roadmapping, product discovery, OKRs, Agile; Airfocus, JIRA, Confluence, Smartsheet, Miro; Claude Code, Codex, Cursor, Gemini

Languages: Italian (native), English (full professional), Spanish (full professional), French (intermediate)