

Summary

Independent Consultant: Antibody design & engineering, molecular modeling, bioinformatics, developability and immunogenicity prediction
Acknowledged as the Biogen expert on antibody sequence & design
Had an outsize impact – advancing >40 programs – all from part-time work
Combines deep technical expertise with collaboration skills

Experience

Mar 2025 - present individually & **Tope LLC** Billerica, MA
Independent Consultant

Twelve happy customers – biotech companies – as of Oct 2026...

2003-2026 **Biogen**, Molecular Discovery Cambridge, MA
Strategic Consultant (2026) / Senior Scientist (2022-2025) /
Scientist II (2017-2022) / Scientist I (2012-2017) / Consultant (2003-2012)

Designed antibodies (human, murine, rabbit, camelid) for affinity, stability, non-immunogenicity, developability, cross-reactivity, half-life extension

- Humanization (16 programs, all successful)
- Knowledge-/structure-based mutations/grafts (~30 programs, 5-30 designs each, with successes in ~90% of programs)
- Display library design (2 programs, both successful)
- Bispecific designs using common light chain (2, successful)

Stabilized a low-pH protein at pH 7 (6 of 20 designs worked)

Led a project team and contractors to evaluate and pilot structure-based AI/ML tools (e.g. AlphaFold and its peers, ImmuneBuilder, RFdiffusion), then host some on an internal server for wider use within the company

Advised VP and Business Development, informing corporate partnership decisions, with my evaluation of external antibody leads / technologies

Researched and implemented a new company approach to immunogenicity prediction. Licensed and adapted IEDB software tools. Mitigated risks for 14 programs (antibody and other), by ranking leads or redesigning.

Developed AbAnalyst, an automated user-friendly antibody sequence analysis program, served via web browser, in wide use within Biogen to:

- › align and characterize sequences based on germline and other databases
- › report unusual or problematic amino acids or covarying amino acid pairs
- › predict up/down CDR-H3 conformation for VHH “nanobodies”
- › predict Protein A binding of VH3 domains › etc.

Developed software to reverse-translate antibody sequences – to best match human germline and avoid undesired restriction enzyme sites – which became part of standard procedure, and improved yields

Created and applied software for several developability factors, e.g. asparagine deamidation rates, Spatial Aggregation Propensity for hydrophobic patches

	1997-2002 Mass. Institute of Technology Cambridge, MA Ph.D., Biological Physics, September 2002 Developed protein design method with more accurate electrostatic treatment of solvation. Wrote software licensed to Merck and Biogen. 1991-1995 U.S. Air Force Offutt AFB, NE Test Director / Test Physics Led a team of 5+ disciplines to design and direct flight and lab tests.
Education	1997-2002 Mass. Institute of Technology Cambridge, MA Ph.D., Biological Physics, September 2002 1995-1997 Auburn University Auburn, AL M.S., Physics 1987-1991 Tufts University Medford, MA B.S., Engineering Physics & Electrical Engineering, Summa cum laude
Skills	<u>Antibody design</u>: Humanization, stabilization, affinity maturation, cross-species affinity matching, developability, immunogenicity <u>Bioinformatics</u>: Antibody sequence analysis, custom tools and database curation (IMGT, vjdbase, NCBI, OAS, PDB, IEDB, clinical, PLaBdab), NGS <u>Molecular modeling</u>: PyMOL, MOE, Bioluminate, OpenMM, rotamers, patches <u>AI/ML structure-based tools</u>: AlphaFold, Boltz, Protenix, OpenFold, IgFold, ImmuneBuilder, MPNN's, RFdiffusion <u>Programming</u>: Python, Perl, C++, R, Mathematica, Matlab; Claude Code <u>Languages</u>: German (conversational), French (intermediate) <u>Collaboration & Leadership</u>: Cross-functional team leadership, autonomous project execution, software process integration & training
Publications & Patents	"Anti-transferrin receptor Antibodies...", WO2025207959 "Anti-[TfR] Antibodies...", US11827702B2 (2023) & US2024/0158494A1 "Anti-VLA-4 Antibodies... Reduced Effector...", US12037398B2 (2024). "Functional activity of anti-LINGO-1 antibody opicinumab requires target engagement at a secondary binding site", KJM Hanf et al., mAbs, 2020, 12:1. "Anti-GPIIB/IIIA Antibodies and Uses thereof", US10875924B2 (2020). "Humanized Anti-Alpha V Beta 5 Antibodies...", US2017/0362324A1. "Anti-CD154 Antibodies", US8961976B2 (2015); US8647625B2 (2014). "Antibody humanization by redesign of [CDR] residues proximate to the acceptor framework", KJM Hanf et al. <i>Methods</i>, 2014, 65 (1): 68-76. "Methods of humanizing immunoglobulin variable regions through rational modification of complementarity determining residues", U.S. Patents US8349324B2 (2013); US7678371B2 (2010). "Protein Design for Diversity of Sequences and Conformations Using Dead-end Elimination", KJM Hanf. In V Voynov, JA Caravella (eds.) <i>Therapeutic Proteins: Methods and Protocols</i>, Methods in Molecular Biology, 2012, 899, 127-144. "Structural understanding of stabilization patterns in engineered bispecific Ig-like antibody molecules", JL Jordan, JW Arndt, K Hanf, et al., <i>Proteins: Structure, Function, and Bioinformatics</i>, 2009, 77 (4), 832-41. "Anti-FN14 Antibodies and Uses Thereof", US2009/0324602A1. More at https://scholar.google.com/citations?euser=zyvk9wAAAAJ