Marc C. Deller, D Phil

| Expert Structural Biologist | Structure-Based Drug Design | Crystallography & Cryo-EM | Driving Innovation Through Protein Science & Drug Discovery Excellence | Protein x AI |

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East Coast, United States, willing to relocate.

SUMMARY

Visionary biology leader transforming drug discovery through **20+ years** of protein science expertise. Co-founded biotech startup while delivering **400+ high-quality protein structures, including antibodies, kinases, receptors, ion channels, and GPCRs**, supporting over **6 FDA IND filings**, and increasing lab productivity by **67% using AI/ML and automation**. Built and managed **$8M+ structural biology platforms** across 2 state-of-the-art laboratories at Stanford and Incyte, leading **cross-functional teams of 10+** scientists to advance "undruggable" targets in oncology and immunology. **3 time patent holder** with **60+ publications** and a proven track record of translating structural information into business insights and therapeutic breakthroughs.

EXPERIENCE

CSO and Co-Founder (Pre-seed, Self-Employed)

Elora Therapeutics

2025 - Present Austin, United States (remote)
https://www.eloratherapeutics.com

- Co-founded biotech to address bioactive microplastic's threat to 2M patients.
- Preliminary design of engineered therapies, securing funding, and developed patent-pending enzyme tech.

Research Fellow (Director, Drug Discovery)

Incyte Pharmaceuticals, Structural Biology (2 Years, 10 months)

03/2022 - 12/2024 Wilmington, United States (on site)

- Accelerated structure-enabled drug discovery for complex oncology targets by delivering 100+ co-crystal structures across 10+ programs (CalR-Ab, ALK2i, CDKi, KRASi, FGFRi, JAKi, WRNi, VRK1i, USP-TPD), progressing over 6 FDA IND submissions and securing 3 patents including WRNi and CalR-Ab.
- Enhanced biology workflows by integrating automation, AI/ML, remote data, and cloud tech, increasing oncology drug discovery productivity by 4-fold.
- Shortened hit-to-lead timelines by collaborating with multidisciplinary teams to improve ADME/DMPK profiles, accelerating progression for "undruggable" targets including a novel KRAS-G12D inhibitor.
- Expanded Structure-Based Drug Design capabilities by designing innovative druggability workflows and robust screening strategies, guiding discovery for 5 new oncology targets leading to 3 med chem papers.
- Fostered seamless gene-to-structure workflows by leading network of 20+ CRO partners for structural biology, biophysics, and biochemistry projects, supporting target validation and assay creation.
- Established *in house* protein production and purification lab featuring *E.coli*, mammalian, Insect and cell-free expression systems and AKTA purification systems.

Associate Director (Group Lead, Drug Discovery)

Incyte Pharmaceuticals, Structural Biology (4 years, 1 month)

03/2018 - 03/2022 Wilmington, United States (on site)

- Established group and built comprehensive $8M automated structural biology platform from ground up by implementing X-ray crystallography liquid handling and imaging (Formulatrix) and Cryo-Electron Microscopy (TF-Glacios) systems, enhancing hit-to-lead progression.
- Eliminated bottlenecks in protein production and data collection by developing partnerships with 10+ external CROs and enhancing internal workflows, streamlining operations across therapeutic areas.
- Managed and mentored team of 5+ scientists across 10+ matrixed drug discovery programs by optimizing infrastructure and allocating $1.5M annual budget, improving project efficiency by 4-fold.
- Organised and ran weekly Biochemistry and Structural Biology Team meeting ensuring cross-functional alignment.

CORE COMPETENCIES

Technical Excellence

• Structure-Based Drug Design • X-Ray Crystallography • Cryo-EM • Construct Design • Protein Engineering • Protein Production • Protein Purification • AI/ML Integration • Gene-to-Structure Pipelines • Fragment-Based Drug Design • Protein-Ligand structure validation • Crystallization troubleshooting • AI/ML for protein design and business • Antibody structure • Kinase and Receptor Structure • Cytokine structure

Leadership & Strategy

• Communication & Adaptability • Team Leadership • Budget Management • CRO Partnerships • Process Optimization • Strategic Planning • Cross-Functional Collaboration • Mentoring • Data & Project Management • Human Skills & Decision Making

Business & Scientific Impact

• Patent Development • FDA IND Support • Revenue Generation • Productivity Enhancement • Risk Management • Regulatory Compliance

LEADERSHIP PHILOSOPHY

Curiosity: 20 years driving hands-on discovery through multidisciplinary approaches
Courage: 400+ structures determined, enabling breakthrough mechanistic insights
Creativity: 3 patents through innovative protein engineering and AI integration
Communication: 60+ publications translating structural data into actionable insights
Compassion: 6 IND filings supported while mentoring 20+ scientists across career
Collaboration: 2 state-of-the-art facilities built through global partnerships

HIGHLIGHTS

KRAS G12D Inhibitor IND, 2025

https://marcdeller.click/kras

WRN Inhibitor Patent Filing, 2025

www.marcdeller.click/wrn1

Co-Founding of Elora Therapeutics, 2025

www.eloratherapeutics.com

EXPERIENCE

Director (Head of Research Core Facility)

Stanford University, Macromolecular Structure Knowledge Center (2 years, 10 months)

06/2015 - 03/2018 California, United States (on site)

- Founded new structural biology service center by overseeing $1M operational budget and streamlining facility access for 50+ SSRL/SLAC users, gaining 20+ new users within first year.
- Enhanced high-throughput protein production capabilities by mentoring 2 scientists and equipping 50+ researchers with advanced characterization techniques, driving platform adoption, and synchrotron access.
- Generated $60,000 annual lab revenue by producing 6 novel protein structures, contributing to 3 publications (including structure of novel PKS module), and facilitating 3 NIH-SBIR grant submissions.

Senior Scientist (Antibody Structure & Proteomics)

Scripps Research Institute, Joint Center for Structural Genomics (8 years, 11 months)

08/2006 - 06/2015 San Diego, United States (on site)

- Executed structural genomics throughput by 10% by optimizing crystallography workflows for NIH Protein Structure Initiative, deploying automation and mentoring 3 scientists.
- Determined 70+ novel protein structures for therapeutically relevant targets (including: ion channels, cellulases, and HCV/HIV-env neutralizing antibodies) through process optimization and salvage strategies.
- Authored 40+ peer-reviewed manuscripts by solving complex structural challenges and establishing thought leadership in structural biology field.
- Trained beam line scientists in SSRL-SMB group with priority access to SSRL beam line 7-1.

Principal Scientist (Drug Discovery)

Pfizer, Structural Biology (4 years, 6 months)

08/2001 - 01/2006 San Diego, United States (on site)

- Advanced pharmaceutical research by solving 200+ protein structures and leading hit-to-lead initiatives across global Pfizer laboratories, supporting 3+ FDA IND applications including VEGFRi.
- Delivered improved drug candidates (VEGFRi, ERKi, cMETi, HIV-TOPOi/PROi) by optimizing sample preparation and data collection protocols for high-quality protein co-complex structures.
- Aligned cross-functional teams in chemistry, computation, data science, and clinical research by leading global structure-enabled drug discovery pipelines, ensuring seamless project execution.

Postdoctoral Research Fellow (Protein Structure)

Yale University School of Medicine

08/1999 - 08/2001 New Haven, United States (on site)

- Led JAK kinase research in cloning, expression, purification, and biochemical analyses.

EDUCATION

D Phil (PhD equivalent, Protein Structure)

University of Oxford, Laboratory of Molecular Biophysics

08/1995 - 08/1999 Oxford, United Kingdom

- Dissertation: Structural, Functional, Biochemical, and Biophysical Studies of Cytokines and Cytokine Receptors.
- Solved first Oncostatin-M structure (PDB ID: 1EVS).

B.Sc. (Including 1 year Industrial Placement)

University of Leeds, Biochemistry and Molecular Biology

08/1991 - 08/1995 Leeds, United Kingdom

- First Class Honors (US equivalent: **A or 70-100%**).

HIGHLIGHTS

Candidates in Clinical Trials, 2025

KRAS-G12D (INCB161734):
https://www.clinicaltrials.gov/study/NCT06179160
JAK2-V617F (INCB160058):
https://www.clinicaltrials.gov/study/NCT06213818
CALR-AB (INCA033989):
https://www.clinicaltrials.gov/study/NCT05936359
CDK2 (INCB123667):
https://www.clinicaltrials.gov/study/NCT07023627

PROJECTS AND LINKS

Resume Chatbot, ask about my leadership style?
www.marcdeller.click/chat

Elora Therapeutics
www.eloratherapeutics.com

Personal Blog
www.marcdeller.com

LinkedIn
www.linkedin.com/in/marccdeller

Google Scholar
www.marcdeller.click/scholar

Protein Structures
www.marcdeller.click/proteins

Mentored Lemelson-MIT Student Prize
www.marcdeller.click/lyseia

Your one-stop shop for producing, crystallizing biomolecules
www.marcdeller.click/mskc

Top articles in structural biology (Spring 2020)
www.marcdeller.click/special

TECHNICAL SKILLS

Structural Biology Expertise

X-ray Crystallography, Cryo-EM, NMR, Protein Crystallization, EM Grid Prep, Protein Expression (E.coli, Mammalian, Insect, Cell-free), Protein Purification, Construct Design, Protein Engineering, Model Building, Data Processing, Ligand Fitting, MR, Protein Structure Validation, Protein AI/ML, Homology modeling.

Drug Discovery Skills

Structure-Based Drug Design, Fragment-Based Drug Design, Hit-to-Lead, ADME/DMPK, Biochemical Assay Development, HTS, Biophysical Characterization (SPR, ITC, DLS, MS).

PATENTS

Tricyclic Compounds as Inhibitors of WRN, 2025
www.marcdeller.click/wrn1

Bicyclic Compounds as Inhibitors of WRN, 2024
www.marcdeller.click/wrn2

Anti-mutant Calreticulin (CALR) Antibodies and uses thereof, 2022
www.marcdeller.click/calr

DEL-based Inhibitors of VRK1
Pending

CONTINUOUS LEARNING

2025 - Google: Foundations of Project Management
https://marcdeller.click/project

2025 - IBM: Introduction to Artificial Intelligence
https://marcdeller.click/ai

2025 - AWS: Serverless Architectures
https://marcdeller.click/aws

2024 - Google: Foundations: Data, Data, Everywhere
https://marcdeller.click/data

2024 - Coursera: Introduction to R: Basic R syntax
https://marcdeller.click/R

2024 - Coursera: Dashboard Development with Shiny: GenAI for Retail Analysis
https://marcdeller.click/shiny

2024 - LinkedIn: Amplify Your Communication Skills with Generative AI
https://marcdeller.click/amplify

LATEST PUBLICATIONS (60 TOTAL)

Full List at Google Scholar

https://marcdeller.click/scholar

Discovery of INCB159020, an Orally Bioavailable KRAS G12D Inhibitor

J. Med. Chem.

Qinda et al.

2025 https://pubs.acs.org/doi/abs/10.1021/acs.jmedchem.4c02662

Support for KRASi FDA IND filing: Discovered an oral inhibitor for the KRAS G12D mutation, aiming to balance potency and ADME properties. This could expand treatment options beyond KRAS G12C lung cancer therapies.

Discovery of (4-pyrazolyl)-2-aminopyrimidines as potent and selective Inhibitors of cyclin-dependent kinase 2

J. Med. Chem.

JR Hummel et al.

2024 https://pubs.acs.org/doi/abs/10.1021/acs.jmedchem.3c02287

Support for CDK2i FDA IND filing: Design of a highly selective CDK2 inhibitor from a novel chemical class with antitumor activity, overcoming toxicity and selectivity issues of previous therapies.

TECHNICAL SKILLS

Technology & Automation Knowledge

AI/ML, Linux, Cloud Computing, Laboratory Automation, Crystallization Robotics, Data Analysis, Computational Chemistry, Globus, AWS, Google Cloud, SLURM, LIMS, ELN, DOE.

Software Proficiency

PyMOL, Chimera, COOT, Schrödinger, GROMACS, PHENIX, CCP4, R/Shiny, Python, MATLAB, AWS, Rockmaker, HKL2000/3000, CCG, PSILO, MOE, ALPHAFOLD, RFDiffusion, ProteinMPNN, RELION, CryoSPARC, ChemCart, Benchling, Word, PowerPoint, Access, Excel, Canva, Adobe, JIRA, Confluence, Smartsheet.

Data Analysis and ML/AI Skills

R/Shiny, Spotfire, GraphPad, Prism, MATLAB, Python, RDKit, PANDAS, Nanome, LLAMA, PERPLEXITY, ChatGTP, GEMINI.

MOST CITED PUBLICATIONS

Crystal structure of a soluble cleaved HIV-1 envelope trimer

Science, 979 citations

JP Julien, A Cupo, D Sok, RL Stanfield, D Lyumkis, MC Deller et al.

2013
www.science.org/doi/abs/10.1126/science.1245625

Exciting paper: High-resolution structure of cleaved HIV-1 envelope trimer with neutralizing antibody reveals key details for infection and vaccine design.

Supersite of immune vulnerability on the glycosylated face of HIV-1 envelope glycoprotein gp120

Nature structural & molecular biology, 420 citations

Leopold Kong et al.

2013 www.nature.com/articles/nsmb.2594

This study reveals: The HIV-1 glycan shield's Asn332120 can be penetrated by antibodies like PGT 135, which use elongated CDR loops to bypass glycans and target vulnerable protein areas. This offers a blueprint for vaccine design.

Protein stability: a crystallographer's perspective

Structural Biology and Crystallization Communications, 370 citations

Marc C Deller, Leopold Kong, Bernhard Rupp

2016
https://journals.iucr.org/f/issues/2016/02/00/en5571/index.html

Featured as a "Top article in structural biology (Spring 2020)": Practical discussion on protein stability, vital for optimizing expression, purification, formulation, storage, and structural studies in biotech, pharma, and academia.

LATEST PUBLICATIONS (60 TOTAL)

Discovery of potent and selective inhibitors of wild-type and gatekeeper mutant fibroblast growth factor receptor (FGFR) 2/3

J. Med. Chem.

Artem Shvartsbart et al.

2022 https://pubs.acs.org/doi/abs/10.1021/acs.jmedchem.2c01366

Support for FGFR2/3i FDA IND filing: Discovery of new FGFR2/3 inhibitors that overcome resistance and reduce side effects like hyperphosphatemia, offering promise for cancers such as cholangiocarcinoma and bladder cancer.

Structure–function analysis of the extended conformation of a polyketide synthase module

Journal of the American Chemical Society

Xiuyuan Li, et al.

2018 https://pubs.acs.org/doi/abs/10.1021/jacs.8b02100

Groundbreaking study: Resolves a debate in PKS biology by showing that the extended module conformation is functionally active for chain elongation and modification, providing key insights for engineered antibiotics.

Validation of Protein–Ligand Crystal Structure Models: Small Molecule and Peptide Ligands

Protein Crystallography: Methods and Protocols

Edwin Pozharski, Marc C Deller, Bernhard Rupp

2017 https://link.springer.com/protocol/10.1007/978-1-4939-7000-1_25

Emphasizes need for high-quality protein structures in the age of predictive AI: Emphasizes the need for validating protein-ligand models vital for drug discovery, focusing on criteria like electron density, stereochemistry, and binding plausibility, and suggests tools to aid researchers facing limited ligand data.

Lipid interactions and angle of approach to the HIV-1 viral membrane of broadly neutralizing antibody 10E8: Insights for vaccine and therapeutic design

PLoS pathogens

Adriana Irimia et al.

2017

https://journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1006212

Landmark study: Redefining HIV-1 neutralization this study indicates that the broadly protective 10E8 antibody targets a hybrid epitope comprising gp41 MPER and viral lipids. Its light chain interacts with lipids, positioning MPER perpendicular to the membrane, providing key insights for lipid-based HIV vaccine design.

Key gp120 glycans pose roadblocks to the rapid development of VRC01-class antibodies in an HIV-1-infected Chinese donor

Immunity

Leopold Kong et al.

2016 https://www.cell.com/immunity/fulltext/S1074-7613(16)30095-4

Pivotal study: Bridges gaps in HIV vaccine design by showing how early VRC01-class antibody precursors overcome glycan obstacles through light-chain changes, highlighting roadblocks like N276/V5 glycan clashes and a quick maturation pathway for broad neutralization to inform next-gen immunogens targeting the CD4-binding site.

REFERENCES

Dr. Adam Lee, Head of Data Logistics, Incyte

alee@incyte.com

Dr. Guofeng Zhang, Head of Biochemistry and Structural Biology, Incyte

guzhang@incyte.com

MOST CITED PUBLICATIONS

The Role of the Secondary Coordination Sphere in a Fungal Polysaccharide Monooxygenase

ACS chemical biology, 130 citations

Elise A Span, Daniel LM Suess, Marc C Deller, R David Britt, Michael A Marletta

2017

https://pubs.acs.org/doi/abs/10.1021/acschembio.7b00016

This study elucidates: Critical hydrogen-bonding networks in fungal PMOs that control oxygen activation and proton transfer are key to improving enzymatic cellulose breakdown, benefiting biofuel production and biomass use.

Models of protein–ligand crystal structures: trust, but verify

Journal of computer-aided molecular design, 113 citations

Marc C Deller, Bernhard Rupp

2015

https://link.springer.com/article/10.1007/s10822-015-9833-8

This paper establishes: X-ray crystallography is the gold standard for precise protein-ligand models, crucial for drug design and biology, but rigorous validation is needed to prevent overinterpretation.

PUBLICATIONS (MISC)

2017

- Crystallisation of Proteins and Macromolecular Complexes: Past, Present and Future
  MC Deller, B Rupp
  eLS

2015

- Crystal structure of a two-subunit TrkA octameric gating ring assembly
  MC Deller, HA Johnson, MD Miller, G Spraggon, MA Elsliger, IA Wilson.
  Plos one 10 (3), e0122512

2014

- Approaches to automated protein crystal harvesting
  MC Deller, B Rupp
  Structural Biology and Crystallization Communications 70 (2), 133-155

2000

- Crystal structure and functional dissection of the cytostatic cytokine oncostatin M
  MC Deller, KR Hudson, S Ikemizu, J Bravo, EY Jones, JK Heath
  Structure 8 (8), 863-874

2000

- Cell surface receptors
  MC Deller, EY Jones
  Current opinion in structural biology 10 (2), 213-219