

John D. Chodera



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New York, NY 10065

Education and positions

2019–	Associate Member, Memorial Sloan-Kettering Cancer Center
2019–	BIH Einstein Visiting Professor, Charité, Berlin
2013–	Faculty, Physiology, Biophysics, and Systems Biology Program, Weill Cornell Graduate School of Medical Sciences
2012–2019	Assistant Member, Memorial Sloan-Kettering Cancer Center
2008–2012	Independent Distinguished Postdoctoral Fellow, California Institute for Quantitative Biosciences (QB3), University of California, Berkeley
2007–2008	Independent research funding, sponsors Phillip L. Geissler and Susan Marqusee Postdoctoral researcher, Department of Chemistry, Stanford University
1999–2006	With Vijay S. Pande (head of Folding@Home distributed computing project) Ph.D. in Biophysics, University of California, San Francisco Committee: Ken A. Dill , Matthew P. Jacobson , Vijay S. Pande
1995–1999	B.S. in Biology, California Institute of Technology Undergraduate research with Paul H. Patterson (<i>molecular neurobiology</i>) and Jerry E. Solomon (<i>computational chemistry</i>)

Fellowships and awards

2022–2024	Einstein Visiting Fellowship
2019–2022	BIH Einstein Visiting Fellowship
2017	Silicon Therapeutics Open Science Fellowship
2013–2016	Louis V. Gerstner Young Investigator Award
2013–2014	Google Exacycle for External Faculty
2008–2012	QB3-Berkeley Distinguished Postdoctoral Fellowship, University of California, Berkeley
2005–2006	IBM Predoctoral Fellowship
2000–2005	Howard Hughes Medical Institute Predoctoral Fellowship

Research overview

My research aims to reimagine the way we develop small molecule drugs and pair therapeutics with individual patient tumors by bringing physical modeling and structure-informed machine learning into the cancer genomics era. By combining novel algorithmic advances to achieve orders-of-magnitude efficiency gains with powerful but inexpensive GPU hardware, machine learning, and distributed computing technologies, my lab is developing next-generation approaches and open source software for predicting small molecule binding affinities, designing small molecules with desired properties, predicting drug sensitivity or resistance of clinical mutations, and understanding the detailed structural mechanisms underlying oncogenic mutations. Using automated biophysical measurements, my laboratory collects new experimental data targeted to advance the quantitative accuracy of our methodologies and gather new insight into drug susceptibility and resistance in kinases and other cancer targets. My work makes extensive use of scalable Bayesian statistical inference, machine learning via probabilistic programming, and information theoretic principles for designing optimal experiments.

A major focus of the lab is the development of technologies required to enable fully autonomous decisionmaking in drug discovery. Such technologies empower medicinal chemists to manage a portfolio of correlated drug discovery programs without the need to make decisions about which molecules to synthesize, enabling them to focus on objectives and strategies instead. This includes the development of automated, modular decisionmaking frameworks inspired by reinforcement learning; integration of automated synthetic route planning; new architectures for fast structure-enabled machine learning; rearchitecting alchemical free energy calculations for differentiable machine learning frameworks to introduce learnability; and scalable Bayesian inference frameworks for automated experimental design and interpretation.

I am passionate about open science, disseminating scientific best practices, and maximizing research reproducibility.

I focus on training the next generation of interdisciplinary scientists equipped to tackle the most challenging problems in health and human disease for industrial drug discovery.

Major Research Collaborations



The COVID Moonshot (2020–) · <https://covid.postera.ai/covid>

I co-founded the **COVID Moonshot**, a global open science collaboration leveraging our free alchemical energy calculations on **Folding@home** to discovery a patent-free oral antiviral useful against COVID-19. Starting from an X-ray fragment screen, we produced SARS-CoV-2 main viral protease (Mpro) inhibitor preclinical candidates in just 18 months (*Nature Comment*). Together with the **Drugs for Neglected Diseases initiative (DNDi)**—the world's leading nonprofit developing new therapies for neglected diseases—we were awarded \$11M from the WHO Access to COVID Tools Accelerator (ACT-A) via the Wellcome Trust to carry out an accelerated preclinical program, with clinical trials expected in 2023. Our antiviral is expected to be free of the drug-drug interactions that present difficulties to widespread use of Paxlovid, and has differentiated resistance liabilities. We are working to partner with generics manufacturers to make our antiviral available for globally equitable and affordable access.



AI-driven Structure-enabled Antiviral Platform (ASAP) (2022–) · <https://asapdiscovery.org>

Together with **DNDi** and **PostEra**, I lead the **AI-driven Structure-enabled Antiviral Platform**, which uses artificial intelligence and computational chemistry to accelerate structure-based open science antiviral drug discovery and deliver oral antivirals for pandemics with the goal of global, equitable, and affordable access. I am the Contact PI on the **NIH NIAID Antiviral Drug Discover (AVIDD) Center** that currently funds ASAP, currently funded by a \$68M NIH award for the first three-year phase of a five-year \$110M grant.



Folding@home Consortium (2012–) · <http://foldingathome.org>

I am a founding member of the **Folding@home Consortium**, a worldwide network of laboratories that run the **Folding@home global distributed computing project** where hundreds of thousands of volunteers around the world (mostly gamers with GPUs) contribute idle computing cycles to enable us to study molecular mechanisms of disease and search for new potential therapeutics. As part of the COVID Moonshot effort, **Folding@home became the world's first exascale distributed computing platform in 2020**. Using our alchemical free energy methodologies on Folding@home, we accelerated lead optimization for preclinical candidates for the COVID Moonshot that are expected to enter clinical trials in 2023.



OpenMM molecular simulation framework (2006–) · <http://openmm.org>

I co-lead the **OpenMM Consortium**, which develops an open source GPU-accelerated molecular simulation package used both as a stand-alone tool for biomolecular simulation and as a library to enable other tools to use biomolecular simulation, such as **Isolde** and **AlphaFold2**. OpenMM is the fastest and most widely deployed GPU-accelerated biomolecular simulation package globally, and has been downloaded over 1.2 million times. OpenMM is currently funded by the NIH to effect a transformation in the biomolecular simulation community to enable the use of fast, accurate machine-learning force fields.



Open Force Field Initiative and Consortium (2019–) · <http://openforcefield.org>

I co-founded the **Open Force Field Initiative** (an NIH-funded collaboration) and related **Open Force Field Consortium** (funded by over a dozen industry partners), a scientific collaboration consisting of dozens of scientists around the world working to develop modern open source infrastructure for building and applying high-quality biomolecular force fields for accelerating drug discovery. These force fields and tools are used by pharma and academic labs around the world, and recently aided the discovery of a new preclinical candidate by the COVID Moonshot.



Statistical Assessment of the Modeling of Proteins and Ligands (SAMPL) (2012–) · <https://sAMPLchallenges.github.io>

I co-organize the **SAMPL Challenges**, which are iterative blind predictive modeling challenges for the computational chemistry community aimed at accelerating the generation of solutions to major obstacles limiting the progress of computer-aided drug discovery, focusing the community on solving these challenges, providing critical experimental data to computational researchers that lack access to data generation capabilities, and emphasizing knowledge sharing. The learnings from these challenges have been reported in over 14 special issues of the *Journal for Computer-Aided Molecular Design*. In some areas, we have managed to move computational methods for wide disagreement among methods to tightly-grouped predictions that can identify when the experimental data is wrong.



Critical Assessment of Computational Hit-finding Experiments (CACHE) (2022–) · <https://cache-challenge.org/>

I co-founded the **CACHE Challenge**, which aims to be the "CASP for hit-finding in drug discovery" by providing a new generation of AI- and physics-driven approaches to assess and refine their hit identification approaches against experimental data. Each CACHE Challenge focuses on identifying new chemical matter against an orphan target protein of pharmaceutical relevance, and all experimental data and compounds are disclosed into the public domain to accelerate drug discovery against these targets.



Open Molecular Software Foundation (OMSF) (2021–) · <http://openforcefield.org>

I work closely with the **Open Molecular Software Foundation (OMSF)**, a 501(c)3 nonprofit organization that aims to be thoughtful stewards for the biomolecular modeling and computer-aided drug discovery open source software communities. Using a funding mechanism I helped pioneer, OMSF can act as a fiscal sponsor that works with open source software communities in the biomolecular sciences to aid them in becoming self-governing organizations that serve the community with fiscally sustainable support from industrial, federal, and philanthropic sources. OMSF currently hosts the **Open Force Field Initiative and Consortium**, the **Open Free Energy Consortium**, and **OpenFold Consortium**.

Selected Significant Publications

Selected publications and preprints following promotion to Associate Member

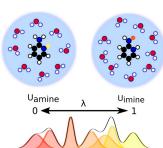


Preprint · [bioRxiv](#)

The COVID Moonshot Consortium, **Chodera JD** ‡, Lee A‡, London N‡, von Delft F‡

Open science discovery of oral non-covalent SARS-CoV-2 main protease inhibitors

We report the discovery of a new oral antiviral non-covalent SARS-CoV-2 main protease inhibitor developed by the COVID Moonshot, a global open science collaboration leveraging free energy calculations on Folding@home and ML-accelerated synthesis planning, now in accelerated preclinical studies funded by an \$11M grant from the WHO ACT-A program via the Wellcome Trust. We are currently in discussions with generics manufacturers about partnering with us throughout clinical trials (expected to begin in 2023) to ensure we can scale up production for global equitable and affordable access once approved by regulatory agencies.

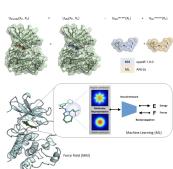


Preprint · [bioRxiv](#)

Wieder M, Fass J, and **Chodera JD**

Teaching free energy calculations to learn from experimental data

In this pioneering work, we show, for the first time, how we can use machine learning to systematically improve explicit solvent alchemical free energy calculations using fully machine learning force fields by fitting directly to experimental free energies. This is also the first work to show how to compute alchemical free energies in explicit solvent using fully machine learning force fields, and the first to show how this can also involve breaking and forming covalent bonds.

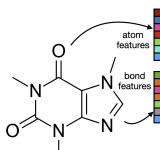


Preprint · [bioRxiv](#)

Rufa DA, Bruce Macdonald, HE, Fass J, Wieder M, Grinaway PB, Roitberg AE, Isayev O, and **Chodera JD**

Towards chemical accuracy for alchemical free energy calculations with hybrid physics-based machine learning / molecular mechanics potentials

In this first use of hybrid machine learning / molecular mechanics (ML/MM) potentials for alchemical free energy calculations, we demonstrate how the improved modeling of intramolecular ligand energetics offered by the quantum machine learning potential ANI-2x can significantly improve the accuracy in predicting kinase inhibitor binding free energy by reducing the error from 0.97 kcal/mol to 0.47 kcal/mol, which could drastically reduce the number of compounds that must be synthesized in lead optimization campaigns for minimal additional computational cost.

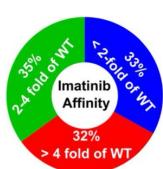


Chemical Science, in press · [DOI](#)

Wang Y, Fass J, and **Chodera JD**

End-to-end differentiable molecular mechanics force field construction

Molecular mechanics force fields have been a workhorse for computational chemistry and drug discovery. Here, we propose a new approach to force field parameterization in which graph convolutional networks are used to perceive chemical environments and assign molecular mechanics (MM) force field parameters. The entire process of chemical perception and parameter assignment is differentiable end-to-end with respect to model parameters, allowing new force fields to be easily constructed from MM or QM force fields, extended, and applied to arbitrary biomolecules.

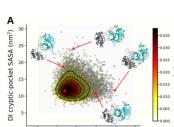


Proceedings of the National Academy of Sciences 118:e2111451118 · [DOI](#)

Lyczek A, Tilman-Berger B, Rangwala AM, Paung Y, Tom J, Philipose H, Guo J, Albanese SK, Robers MB, Knapp S, **Chodera JD**, Seeliger MA

Mutation in Abl kinase with altered drug binding kinetics indicates a novel mechanism of imatinib resistance

Here, we characterize the biophysical mechanisms underlying mutants of Abl kinase associated with clinical drug resistance to targeted cancer therapies. We uncover a surprising novel mechanism of mutational resistance to kinase inhibitor therapy in which the off-rate for inhibitor unbinding is increased without affecting inhibitor affinity.



Nature Chemistry 13:651, 2021 · [DOI](#)

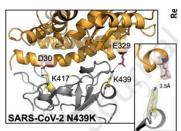
Zimmerman MI, Porter JR, Ward MD, Singh S, Vithani N, Meller A, Mallimadugula UL, Kuhn CE, Borowsky JH, Wiewiora RP, Hurley, MFD, Harbison AM, Fogarty CA, Coffland JE, Fadda E, Voelz VA, **Chodera JD**, Bowman GR

SARS-CoV-2 simulations go exascale to predict dramatic spike opening and cryptic pockets across the proteome

To accelerate a multitude of drug development activities to combat the global threat posed by COVID-19, over a million citizen scientists have banded together through the Folding@home distributed computing project to create the world's first Exascale computer and simulate protein dynamics. An unprecedented 0.1 seconds of simulation of the viral proteome reveal how the spike complex uses conformational masking to evade an immune response, conformational changes implicated in the function of other viral proteins, and cryptic pockets that are absent in experimental structures. These structures and mechanistic insights present new targets for the design of therapeutics.

Cell 184:1171, 2021 · DOI

Thompson EC, Rosen LE, Shepherd JG, Spreafico R, da Silva Filipe A, Wojcechowskyj JA, Davis C, Piccoli L, Pascall DJ, Dillen J, Lytras S, Czudnochowski N, Shah R, Meury M, Jesudason N, De Marco A, Li K, Bassi J, O'Toole A, Pinto D, Colquhoun RM, Culap K, Jackson B, Zatta F, Rambaut A, Jaconi S, Sreenu VB, Nix J, Zhang I, Jarrett RF, Glass WG, Beltrame M, Nomikou K, Pizzuto M, Tong L, Cameroni E, Cross TI, Johnson N, Di Julio J, Wickenhagen A, Ceschi A, Harbison AM, Mair D, Ferrari P, Smollett K, Sallusto F, Carmichael S, Garzoni C, Nichols J, Galli M, Hughes J, Riva A, Ho A, Schiuma M, Semple MG, Openshaw PJM, Fadda E, Baillie JK, Chodera JD, Rihm SJ, Lycet SJ, Virgin HW, Telenti A, Corti D, Robertson DL, Snell J, ISARIC4C Investigators



Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity

New mutations that enhance the affinity of SARS-CoV-2 spike protein for human ACE2—and potentially pose threats to antibody-based therapeutics and vaccines for COVID-19—are already emerging in the wild. We characterize and describe sentinel mutations of SARS-CoV-2 in the wild that herald challenges for combatting COVID-19, and use simulations of the RBD-ACE2 interface on Folding@home to biophysically characterize why these mutations can lead to enhanced affinity.

eLife 8:e45403, 2019 · DOI

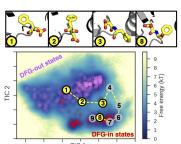
Rafal P. Wiewiora[†], Shi Chen[†], Fanwang Meng, Nicolas Babault, Anqi Ma, Wenyu Yu, Kun Qian, Hao Hu, Hua Zou, Junyi Wang, Shijie Fan, Gil Blum, Fabio Pittella-Silva, Kyle A. Beauchamp, Wolfram Tempel, Hualing Jiang, Kaixian Chen, Robert Skene, Y. George Zheng, Peter J. Brown, Jian Jin, **Chodera JD**[‡], and Minkui Luo[‡]



The dynamic conformational landscapes of the protein methyltransferase SETD8

In this work, we show how targeted X-ray crystallography using covalent inhibitors and depletion of native ligands to reveal structures of low-population hidden conformations can be combined with massively distributed molecular simulation to resolve the functional dynamic landscape of the protein methyltransferase SETD8 in unprecedented atomistic detail. Using an aggregate of six milliseconds of fully atomistic simulation from Foldinghome, we use Markov state models to illuminate the conformational dynamics of this important epigenetic protein.

Selected publications prior to promotion to Associate Member

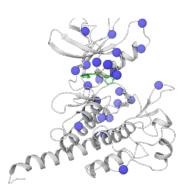


Cell Chemical Biology 26:390, 2019 · DOI

Hanson SM*, Georghiou G*, Miller WT, Rest JS, Chodera JD ‡, and Seeliger MA‡

What makes a kinase promiscuous for inhibitors?

Using a combination of chemogenomics, structural biology, and molecular simulation approaches, we identify a set of human kinases that are especially promiscuous binders of small molecule kinase inhibitors, and show that a prototypical member of this class, DDR1, achieves this promiscuity by virtue of its more stable Asp-DFG-out conformation.



Communications Biology 1:70, 2018 · DOI:

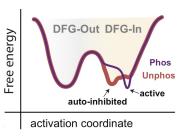
Hauser K, Negron C, Albanese SK, Ray S, Steinbrecher T, Abel R, and Chodera JD, and Wang L

Predicting resistance of clinical Abl mutations to targeted kinase inhibitors using alchemical free-energy calculations

The emergence of resistance mutations are a significant problem in precision cancer therapy. With cancer centers now routinely collecting tumor sequencing panels, it is apparent the vast majority of missense mutations in kinases—for which more than 36 small molecule inhibitors are available—are very rare, and no information will be available as to whether these mutations might reduce therapeutic efficacy for some inhibitors by inducing drug resistance. Here, we take the first steps toward using physical modeling to predict individualized therapeutic response, assessing how accurately the impact of clinical Abl mutations on inhibitor binding affinity can be predicted. Our results suggest free energy calculations are a promising tool for aiding therapeutic decisionmaking.

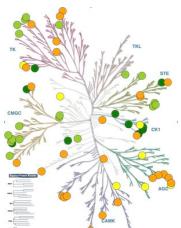
elife 7:e32766, 2018; DOI:

Ruff EF, Muretta JM, Thompson A, Lake E, Cyphers S, Albanese SK, Hanson SM, Behr JM, Thomas DT, Chodera JD, and Levinson NM



A dynamic mechanism for allosteric activation of Aurora kinase A by activation loop phosphorylation

Kinase phosphorylation is canonically believed to induce a conformational change of the DFG loop that borders the ATP binding site from out to in. Surprisingly, it seems that not all kinases behave this way. Through a combination of FRET, IR, and EPR labeling and large-scale molecular dynamics simulations, we show that phosphorylation activates Aurora kinase by a novel mechanism that does not simply correspond to a DFG-out to DFG-in population shift, but rather reorganization of DFG-in subpopulations. This paper follows our prior report in *Nature Chemical Biology* on the role of Tpx2 in activating a cellular subpopulation of Aurora by another surprising mechanism.



Biochemistry 57:4675–2018 • DOI

biochemistry 37:4073, 2018 • DOI: 10.1021/bi800333x

An open library of human kinase domain constructs for automated bacterial expression.

To establish a tractable experimental system for studying the biophysical determinants of selective kinase inhibitor resistance in clinical cancer mutations, we engineer a library of human kinase domains with useful bacterial expression with phosphatase coexpression. Over 350 requests have been made for these plasmids.

Scientific Advisory Board Memberships

One way I work to translate my research into impact is via participating in Scientific Advisory Boards (SABs) for companies using computational chemistry to accelerate drug discovery. Some of the SABs I have served on include:



Schrodinger (2013–2018) · <http://schrodinger.com>

I joined the Schrodinger SAB shortly after their first release of the FEP+ alchemical free energy calculation tool, aiming to ensure the first commercial turnkey product version of my field of alchemical free energy calculations had maximum impact for structure-enabled drug discovery. This effort was highly successful, with FEP+ near-universally used by industry to accelerate structure-enabled drug discovery efforts. I left in 2018 to focus my efforts on new, more scalable technologies and ways to use these tools for frontier problems in drug discovery.



OpenEye Scientific (2018–) · <https://www.eyesopen.com>

I joined the OpenEye SAB excited to help enable an ecosystem of open source computer-aided drug discovery tools and academic research that could rapidly be translated into impactful deployment within both industry and academia using their Orion cloud-based drug discovery platform. OpenEye was recently acquired by Cadence for \$500M.



Interline Therapeutics (2021–) · <https://www.interlinetx.com>

I am a founding SAB member and scientific cofounder of Interline Therapeutics, which has raised \$92M since its inception in 2021. Interline seeks to harness open source alchemical free energy methodologies that I developed to tackle problems in target and conformational selectivity to enable the design of small molecules that modulate protein communities.



Ventus Therapeutics (2021–) · <https://www.ventustx.com>

Ventus is a rapidly growing small molecule discovery company that has raised over \$300M in three funding rounds. In addition to featuring extraordinary medicinal chemistry talent, Ventus has developed a novel computational platform, ReSOLVE, to accelerate novel chemotype hit discovery for new targets. I joined the SAB to advise on the integration of structure-enabled open source computer-aided drug discovery workflows to accelerate hit-to-candidate progression.



Redesign Science (2020–) · <https://www.redesignscience.com>

Redesign Science is a NYC-based startup aiming to commercialize technologies I helped develop as a graduate student—the construction of Markov state models of coarse-grained biomolecular dynamics from distributed biomolecular simulations—to use as a platform to accelerate drug discovery.

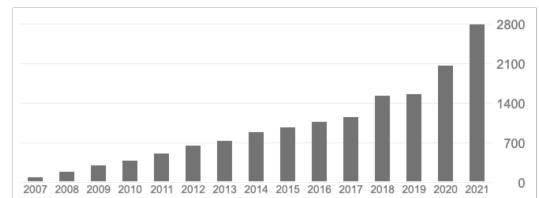
Open Source Software

All software developed by our lab can be found at <http://github.com/choderalab>

All software is licensed under permissive OSI-approved open source licenses and available on [GitHub](#)

All Publications

All publications: <http://choderalab.org/publications>
Google Scholar statistics: <http://goo.gl/qO0JW>
MyNCBI Bibliography: <http://goo.gl/e3kjgK>
bioRxiv preprints: <https://bit.ly/2LHGwxJ>
arXiv preprints: <https://bit.ly/2Rp2Y3T>
chemRxiv preprints: <https://chemrxiv.org/search?q=chodera>
Open source software: <http://github.com/choderalab>
Major datasets: <http://choderalab.org/data>
h-index: 56 / i10-index: 107 / citations: 17033 (6 Sep 2022)
* denotes co-first-authors
† denotes co-second-authors
‡ denotes co-corresponding authors



annual citation counts via Google Scholar (31 Dec 2021)

Submitted, Under Review, and Preprints

Open science antiviral discovery



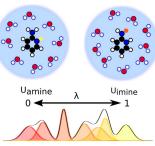
Preprint · [bioRxiv](#)

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Introducing learnability into biomolecular modeling for drug discovery

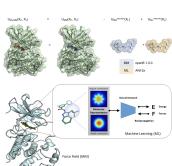


Preprint · [bioRxiv](#)

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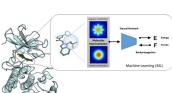


Preprint · [bioRxiv](#)

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Preprint · [arXiv](#)

Galvelis R, Varela-Rial A, Doerr S, Fino R, Eastman P, Markland TE, Chodera JD, and de Fabritiis G

NNP/MM: Fast molecular dynamics simulations with machine learning potentials and molecular mechanics

We demonstrate that a new generation of quantum machine learning (QML) potentials based on neural networks—which can achieve quantum chemical accuracy at a fraction of the cost—can be implemented efficiently in the OpenMM molecular dynamics simulation engine as part of hybrid machine learning / molecular mechanics (ML/MM) potentials that promise to deliver superior accuracy for modeling protein-ligand interactions.

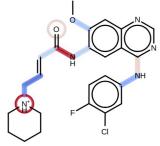
Force field parameterization

Preprint · [bioRxiv](#)

Stern CD, Bayly CI, Smith DGA, Fass J, Wang L-P, Mobley DL, and **Chodera JD**

Capturing non-local through-bond effects when fragmenting molecules for quantum chemical torsion scans

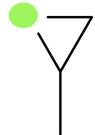
We show how the Wiberg Bond Order (WBO) can be used to construct small molecule fragmentation schemes that will avoid disrupting the chemical environment around torsions. The resulting fragmentation scheme powers the QCSubmit tool used to fragment and inject small molecule datasets into the QCFractal computation pipeline for deposition into the QCArchive quantum chemistry archive the Open Force Field Initiative uses for constructing force fields, as well as powering bespoke torsion refitting for individual molecules.



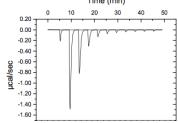
Preprint · [arXiv](#)

Wang Y, Fass J, Stern CD, and **Chodera JD**
Graph nets for partial charge prediction

Graph convolutional and message-passing networks can be a powerful tool for predicting physical properties of small molecules when coupled to a simple physical model that encodes the relevant invariances. Here, we show the ability of graph nets to predict partial atomic charges for use in molecular dynamics simulations and physical docking.



Experimental best practices

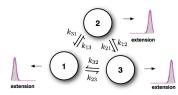


Preprint · [bioRxiv](#)

Boyce SE, Tellinghuisen JT, and **Chodera JD**

Avoiding accuracy-limiting pitfalls in the study of protein-ligand interactions with isothermal titration calorimetry

We demonstrate how to avoid accuracy-limiting problems in standard isothermal calorimetry experiments as well as capture the primary sources of uncertainty in thermodynamic parameters.

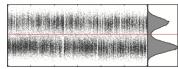


Preprint · [arXiv](#)

Chodera JD, Noé F, Hinrichs NS, Keller B, Elms PJ, Kaiser CM, Ewall-Wice A, Marqusee S, and Bustamante C

Bayesian hidden Markov model analysis of single-molecule biophysical experiments

We present a Bayesian hidden Markov model analysis scheme that allows biomolecular conformational dynamics—and the corresponding uncertainty due to limited data—to be inferred from single-molecule trajectories. This approach was developed for a single-molecule study examining folding dynamics of nascent proteins exiting the ribosome [Science 334:1723, 2011 · [DOI](#)].



Preprint · [arXiv](#)

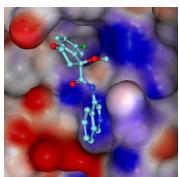
Chodera JD, Elms PJ, Swope WC, Prinz J-H, Marqusee S, Bustamante C, Noé F, and Pande VS

A robust approach to estimating rates from time-correlation functions

We present a simple, robust approach to estimating two-state rate constants from experimental or simulation data.

Reviews and Commentaries

Open science and globally equitable drug discovery



Nature 594:330, 2021 · DOI

von Delft F, Calmiano M, Chodera JD, Griffen E, Lee A, London N, Matviuk T, Perry B, Robinson M, and von Delft A

A white-knuckle ride of open COVID drug discovery

The COVID Moonshot is an open science effort to discover a direct-acting SARS-CoV-2 oral antiviral. Here, we share lessons from this effort, including the missed opportunity to develop a phase 2 ready drug more than a decade ago that could have halted the COVID-19 pandemic in its tracks.



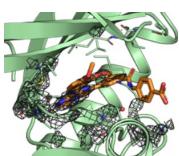
Knowable Magazine 09.27.2021 · web

Lee A, Chodera JD, von Delft F

Why we are developing a patent-free COVID antiviral therapy

In this Opinion, we present the case for a new open science driven model for drug discovery for pandemics.

Best practices for computer-aided drug discovery

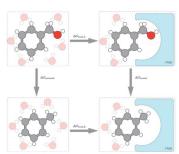


Living Journal of Computational Molecular Science 4:1497, 2022 · DOI

Hahn DF, Bayly CI, Boby ML, Bruce Macdonald HE, Chodera JD, Mey ASJS, Mobley DL, Perez Benito L, Schindler CEM, Tresadern G, Warren GL

Best practices for constructing, preparing, and evaluating protein-ligand binding affinity benchmarks

This living best practices paper for the Living Journal of Computational Molecular Sciences describes the current community consensus in how to curate experimental benchmark data for assessing predictive affinity models for drug discovery, how to prepare these systems for affinity calculations, and how to assess the results to compare performance.

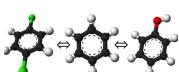


Living Journal of Computational Molecular Science 2:18378, 2020 · DOI

Mey ASJS[‡], Allen B, Bruce Macdonald HE, Chodera JD[‡], Kuhn M, Michel J, Mobley DL[‡], Naden LN, Prasad S, Rizzi A, Scheen J, Shirts MR[‡], Tresadern G, and Xu H

Best practices for alchemical free energy calculations

This living review for the Living Journal of Computational Molecular Sciences (LiveCoMS) covers the essential considerations for running alchemical free energy calculations for rational molecular design for drug discovery.

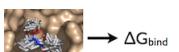


Current Opinion in Structural Biology 21:150, 2011 · DOI

Chodera JD, Mobley DL, Shirts MR, Dixon RW, Branson KM, and Pande VS

Free energy methods in drug discovery and design: Progress and challenges

A review of current opportunities and challenges for alchemical free energy calculations in drug discovery and design.



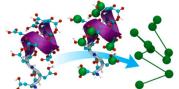
Annual Reports in Computational Chemistry 3:41, 2007 · DOI

Shirts MR, Mobley DL, Chodera JD

Alchemical free energy calculations: Ready for prime time?

A review of current alchemical free energy methodologies and their potential for use in drug discovery and ligand design.

Coarse-graining for biomolecular dynamics

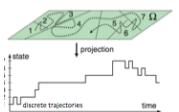


Journal of Chemical Theory and Computation 16:4757, 2020 · DOI

Gkeka P, Stoltz G, Farimani AB, Belkacemi Z, Ceriotti M, Chodera JD, Dinner AR, Ferguson A, Maillet JB, Minoux H, Peter C, Pietrucci F, Silveira A, Tkatchenko A, Trstanova Z, Wiewiora R, Leliévre T

Machine learning force fields and coarse-grained variables in molecular dynamics: application to materials and biological systems

We review the state of the art in applying machine learning to coarse grain force fields in space and time to study multiscale dynamics.

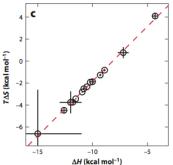


Current Opinion in Structural Biology 25:135, 2014 · DOI

Chodera JD and Noé F

Markov state models of biomolecular conformational dynamics

A review of exciting recent developments in the stochastic modeling of biomolecular dynamics using techniques I originally co-developed to study protein folding.

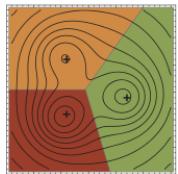


Annual Reviews in Biophysics 42:121, 2013 · DOI

Chodera JD and Mobley DL

Entropy-enthalpy compensation: Role and ramifications for rational ligand design

Entropy-enthalpy compensation is likely a universal phenomena, but not as severe as widely thought, and irrelevant for drug discovery and ligand design.

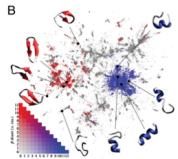


Journal of Chemical Physics 134:174105, 2011 · DOI

Prinz JH, Wu H, Sarich M, Keller B, Fischbach M, Held M, Chodera JD, Schütte, and Noé F

Markov models of molecular kinetics: Generation and validation

Current best practices for the generation and validation of Markov state models for describing the stochastic dynamics of biomolecular systems.



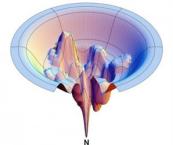
Proceedings of the National Academy of Sciences 108:12969, 2011 · DOI

Chodera JD and Pande VS

The Social Network (of protein conformations)

A new methodology for mapping protein conformational spaces is reminiscent of how we use two-dimensional maps to navigate a three-dimensional world.

Protein folding



Current Opinion in Structural Biology 17(3):342, 2007 · DOI

Dill KA, Ozkan SB, Weikl TR, Chodera JD, and Voelz VA

The protein folding problem: When will it be solved?

A review of the current state of the protein folding problem.

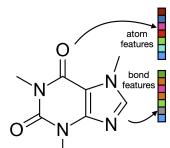
All Published and In Press Publications

New publications since promotion to Associate Member

Chemical Science, in press · DOI

Wang Y, Fass J, and Chodera JD

End-to-end differentiable molecular mechanics force field construction



Molecular mechanics force fields have been a workhorse for computational chemistry and drug discovery. Here, we propose a new approach to force field parameterization in which graph convolutional networks are used to perceive chemical environments and assign molecular mechanics (MM) force field parameters. The entire process of chemical perception and parameter assignment is differentiable end-to-end with respect to model parameters, allowing new force fields to be easily constructed from MM or QM force fields, extended, and applied to arbitrary biomolecules.



Journal of Chemical Theory and Computation 18:3566, 2022 · DOI

Boothroyd S, Wang L-P, Mobley DL, Chodera JD, and Shirts MR

The Open Force Field Evaluator: An automated, efficient, and scalable framework for the estimation of physical properties from molecular simulation

We describe a new software framework for automated evaluation of physical properties for the benchmarking and optimization of small molecule force fields according to best practices.



Journal of Chemical Theory and Computation 18:3577, 2022 · DOI

Boothroyd S, Madin OC, Mobley DL, Wang L-P, Chodera JD, and Shirts MR

Improving force field accuracy by training against condensed-phase mixture properties

We use a new automated framework for physical property evaluation and fitting to show how molecular mechanics force fields can be systematically improved by fitting to condensed phase properties.



Nature Reviews Chemistry, 6:287, 2022 · DOI

Ackloo S, Al-awar R, Amaro RE, Arrowsmith CH, Azevedo H, Batey RA, Bengio Y, Betz UAK, Bologa CG, Chodera JD, Cornell WD, Dunham I, Ecker GF, Edfeldt K, Edwards AM, Gilsom MK, Gordijo CR, Hessler G, Hillisch A, Hogner A, Irwin JJ, Jansen JM, Kuhn D, Leach AR, Lee AA, Lessel U, Moult J, Muegge I, Oprea TI, Perry BG, Riley, Singh Saikantendu K, Santhakumar V, Schapira M, Scholten C, Todd MH, Vedadi M, Volkamer A, and Wilson TM

CACHE (Critical Assessment of Computational Hit-finding Experiments): A public-private partnership benchmarking initiative to enable the development of computational methods for hit-finding

We describe CACHE: A new public-private partnership that aims to transform computer-aided drug discovery much the way that CASP transformed protein structure prediction into a reproducible, accurate engineering discipline.

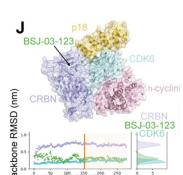


Journal of Computer-Aided Molecular Design 36:291, 2022 · DOI

Grosjean H, Isik M, Aimon A, Mobley D, Chodera JD, von Delft F, and Biggin PC

SAMPL7 protein-ligand challenge: A community-wide evaluation of computational methods against fragment screening and pose-prediction

We field a blind community challenge to assess how well state of the art computational chemistry methods can predict the binding modes of small druglike fragments to a protein target for which no chemical matter is known, PHIP2, using fragment screening at the Diamond Light Source.

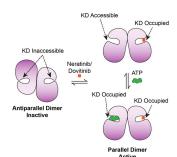


Cancer Discovery 12:356, 2022 · DOI

Li Q, Jiang B, Guo J, Shao H, Del Priore IS, Chang Q, Kudo R, Li Z, Razavi P, Liu B, Boghossian AS, Rees MG, Ronan MM, Roth JA, Donovan KA, Palafox M, Reis-Filho JS, de Stanchina E, Fischer ES, Rosen N, Serra V, Koff A, Chodera JD, Gray NS, and Chardardlapati S

INK4 tumor suppressor proteins mediate resistance to CDK4/6 kinase inhibitors

We demonstrate CDK6 causes drug resistance by binding INK4 proteins, and develop bifunctional degraders conjugating palbociclib with E3 ligands to overcome this mechanism of resistance.

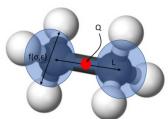


Nature Chemical Biology, 18:207, 2022 · DOI

Mellinghoff I, Tang CP, Clark O, Ferrarone J, Campos C, Lalani AS, Chodera JD, Intlekofer AM, and Elemento O

GCN2 kinase activation by ATP-competitive kinase inhibitors

We describe paradoxical activation of GCN2 kinase activity by the kinase inhibitor neratinib, and propose a model for how inhibitor-induced dimerization might cause this unusual activity.



Journal of Chemical Informatics and Modeling, 62:874, 2022 · DOI

Madin OC, Boothroyd S, Messerly RA, Chodera JD, Fass J, Shirts MR

Bayesian inference-driven model parameterization and model selection for 2CLJQ fluid models

Here, we show how Bayesian inference can be used to automatically perform model selection and fit parameters for a molecular mechanics force field.

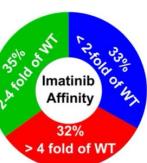


Journal of Chemical Theory and Computation, 17:6262, 2021 · DOI

Qiu Y, Smith DGA, Boothroyd B, Jang H, Wagner J, Bannan C, Gokey T, Lim VT, Stern CD, Rizzi A, Lucas X, Tjanaka B, Shirts MR[‡], Gilson MK[‡], Chodera JD[‡], Bayly CI[‡], Mobley DL[‡], Wang L-P[‡]

Development and benchmarking of Open Force Field v1.0.0, the Parsley small molecule force field

We present a new, modern small molecule force field for molecular design from the Open Force Field Initiative, a large industry-academic collaboration that focuses on open science, open data, and modern open source infrastructure.



Proceedings of the National Academy of Sciences 118:e2111451118 · DOI

Lyczek A, Tilman-Berger B, Rangwala AM, Paung Y, Tom J, Philipose H, Guo J, Albanese SK, Robers MB, Knapp S, Chodera JD, Seeliger MA

Mutation in Abl kinase with altered drug binding kinetics indicates a novel mechanism of imatinib resistance

Here, we characterize the biophysical mechanisms underlying mutants of Abl kinase associated with clinical drug resistance to targeted cancer therapies. We uncover a surprising novel mechanism of mutational resistance to kinase inhibitor therapy in which the off-rate for inhibitor unbinding is increased without affecting inhibitor affinity.

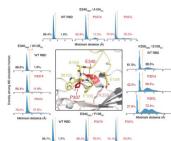


Journal of Chemical Physics 155:204801, 2021 · DOI

Smith DGA, Lolino AT, Glick ZL, Lee J, Alenaizan A, Barnes TA, Borca CH, Di Remigio R, Dotson DL, Ehlert S, Heide AG, Herbst MF, Hermann J, Hicks CB, Horton JT, Hurtado AG, Kraus P, Kruse P, Lee SJR, Misiewicz JP, Naden LN, Ramezanzehbarani F, Scheurer M, Shriber JB, Simmonett AC, Steinmetzer J, Wagner JR, Ward L, Welborn M, Altarawy D, Anwar J, Chodera JD, Dreuw A, Kulik HJ, Liu F, Martinez TJ, Matthews DA, Schaefer III HF, Sponer J, Turney JM, Wang L-P, De Silva N, King RA, Stanton JF, Gordon MS, Windus TL, Sherrill CD, Burns LA

Quantum chemistry common driver and databases (QCDB) and quantum chemistry engine (QCEngine): Automation and interoperability among computational chemistry programs

We describe a new community-wide approach to interoperability for quantum chemistry packages that will enable large-scale applications such as next-generation machine learning for chemistry and automated force field construction for drug discovery.

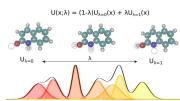


Nature 597:97, 2021 · DOI

Starr TN, Czudnochowski N, Zatta F, Park YJ, Liu Z, Addetia A, Pinto D, Beltramello M, Hernandez P, Greaney AJ, Marzi R, Glass WG, Zhang I, Dingens AS, Bowen JE, Wojciechowsky JA, De Marco A, Rosen LE, Zhou J, Montiel-Ruiz M, Kaiser H, Tucker H, Housley MP, di Julio J, Lombardo G, Agostini M, Sprugasci N, Culap K, Jaconi S, Meury M, Dellota E, Cameroni E, Croll TI, Nix JC, Havenar-Daughton C, Telenti A, Lempp FA, Pizzuto MS, Chodera JD, Hebner CM, Whelan SPJ, Virgin HW, Veesler D, Corti D, Bloom JD, Snell G

SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape

We comprehensively characterize escape, breadth, and potency across a panel of SARS-CoV-2 antibodies targeting the receptor binding domain, including the parent antibody of the recently approved Vir antibody drug (Sotrovimab), illuminating escape mutations with structural and dynamic insight into their mechanism of action.

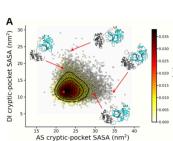


Chemical Science 12:11364, 2021 · DOI

Wieder M, Fass J, and Chodera JD

Fitting quantum machine learning potentials to experimental free energy data: Predicting tautomer ratios in solution

We demonstrate, for the first time, how alchemical free energy calculations can be performed on systems simulated entirely with quantum machine learning potentials and how these potentials can be retrained on experimental free energies to generalize to new molecules from limited training data. We apply this approach to a difficult problem in small molecule drug discovery: Predicting accurate tautomer ratios in solution.

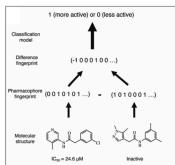


Nature Chemistry 13:651, 2021 · DOI

Zimmerman MI, Porter JR, Ward MD, Singh S, Vithani N, Meller A, Mallimadugula UL, Kuhn CE, Borowsky JH, Wiewiora RP, Hurley, MFD, Harbison AM, Fogarty CA, Coffland JE, Fadda E, Voelz VA, Chodera JD, Bowman GR

SARS-CoV-2 simulations go exascale to predict dramatic spike opening and cryptic pockets across the proteome

To accelerate a multitude of drug development activities to combat the global threat posed by COVID-19, over a million citizen scientists have banded together through the Folding@home distributed computing project to create the world's first Exascale computer and simulate protein dynamics. An unprecedented 0.1 seconds of simulation of the viral proteome reveal how the spike complex uses conformational masking to evade an immune response, conformational changes implicated in the function of other viral proteins, and cryptic pockets that are absent in experimental structures. These structures and mechanistic insights present new targets for the design of therapeutics.

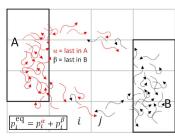


Chemical Communications 57:5909, 2021 · DOI

Morris A, McCorkindale W, the COVID Moonshot Consortium, Drayman N, Chodera JD, Tay S, London N, Lee AA

Discovery of SARS-CoV-2 main protease inhibitors using a synthesis-directed de novo design model

We show how a machine learning models of ligand affinity can be coupled to synthetic enumeration models to rapidly generate potent inhibitors of the SARS-CoV-2 main viral protease.



Journal of Chemical Theory and Computation 17:3119, 2021 · DOI

Suárez E, Wiewiora RP, Wehmeyer C, Noé F, Chodera JD[‡], Zuckerman DM[‡]

What Markov State Models can and cannot do: Correlation versus path-based observables in protein-folding models

Markov state models are now well-established for describing the long-time conformational dynamics of proteins. Here, we take a critical look of what properties can reliably be extracted from these coarse-grained models.

Cell 184:1171, 2021 · DOI

Thompson EC, Rosen LE, Shepherd JG, Spreafico R, da Silva Filipe A, Wojciechowsky JA, Davis C, Piccoli L, Pascall DJ, Dillen J, Lytras S, Czudnochowski N, Shah R, Meury M, Jesudason N, De Marco A, Li K, Bassi J, O'Toole A, Pinto D, Colquhoun RM, Culap K, Jackson B, Zatta F, Rambaut A, Jaconi S, Sreenu VB, Nix J, Zhang I, Jarrett RF, Glass WG, Beltramello M, Nomikou K, Pizzuto M, Tong L, Cameroni E, Cross TI, Johnson N, Di Julio J, Wickenhagen A, Ceschi A, Harbison AM, Mair D, Ferrari P, Smollett K, Sallusto F, Carmichael S, Garzoni C, Nichols J, Galli M, Hughes J, Riva A, Ho A, Schiuma M, Semple MG, Openshaw PJM, Fadda E, Baillie JK, Chodera JD, Rihm SJ, Lycet SJ, Virgin HW, Telenti A, Corti D, Robertson DL, Snell J, ISARIC4C Investigators

Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity

New mutations that enhance the affinity of SARS-CoV-2 spike protein for human ACE2—and potentially pose threats to antibody-based therapeutics and vaccines for COVID-19—are already emerging in the wild. We characterize and describe sentinel mutations of SARS-CoV-2 in the wild that herald challenges for combatting COVID-19, and use simulations of the RBD-ACE2 interface on Folding@home to biophysically characterize why these mutations can lead to enhanced affinity.

Nature Chemistry 12:581, 2020 · DOI

Chodera JD[‡], Lee AA[‡], London N[‡], and von Delft F[‡]

Crowdsourcing drug discovery for pandemics

The COVID-19 pandemic has left the world scrambling to find effective therapies to stem the tidal wave of death and put an end to the worldwide disruption caused by SARS-CoV-2. In this Correspondence, we argue for the need for a new open, collaborative drug discovery model (exemplified by our COVID Moonshot collaboration) that breaks free of the limitations of industry-led competitive drug discovery efforts that necessarily restrict information flow and hinder rapid progress by prioritizing profits and patent protection over human lives.



Journal of Computer Aided Molecular Design 35:131, 2021 · DOI

Isik M, Rustenburg AS, Gunner MR, Mobley DL, Chodera JD

Overview of the SAMPL6 pKa challenge: evaluating small molecule microscopic and macroscopic pKa predictions

The SAMPL6 pKa challenge assessed the ability of the computational chemistry community to predict macroscopic and microscopic pKas for a set of druglike molecules resembling kinase inhibitors. This paper reports on the overall performance and lessons learned, including the surprising finding that many tools predict reasonably accurate macroscopic pKas corresponding to the wrong microscopic protonation sites.

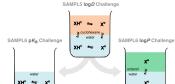


Journal of Computer Aided Molecular Design 34:335, 2020 · DOI

Isik M, Bergazin TD, Fox T, Rizzi A, Chodera JD, and Mobley DL

Assessing the accuracy of octanol-water partition coefficient predictions in the SAMPL6 Part II log P Challenge

We report the performance assessment of the 91 methods that were submitted to the SAMPL6 blind challenge for predicting octanol-water partition coefficient ($\log P$) measurements. The average RMSE of the most accurate five MM-based, QM-based, empirical, and mixed approach methods based on RMSE were 0.92 ± 0.13 , 0.48 ± 0.06 , 0.47 ± 0.05 , and 0.50 ± 0.06 , respectively.

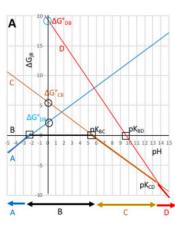


Journal of Computer Aided Molecular Design 34:561, 2020 · DOI

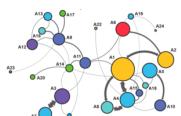
Gunner MR, Murakami T, Rustenburg AS, Isik M, Chodera JD

Standard state free energies, not pK_a 's, are ideal for describing small molecule protonation and tautomeric states

Here, we demonstrate how the physical nature of protonation and tautomeric state effects means that the standard state free energies of each microscopic protonation/tautomeric state at a single pH is sufficient to describe the complete pH-dependent microscopic and macroscopic populations. We introduce a new kind of diagram that uses this concept to illustrate a variety of pH-dependent phenomena, and show how it can be used to identify common issues with protonation state prediction algorithms. As a result, we recommend future blind prediction challenges utilize microstate free energies at a single reference pH as the minimal sufficient information for assessing prediction accuracy and utility.



eLife 8:e45403, 2019 · DOI



Rafal P. Wiewiora[†], Shi Chen[†], Fanwang Meng, Nicolas Babault, Anqi Ma, Wenyu Yu, Kun Qian, Hao Hu, Hua Zou, Junyi Wang, Shijie Fan, Gil Blum, Fabio Pittella-Silva, Kyle A. Beauchamp, Wolfram Tempel, Hualing Jiang, Kaixian Chen, Robert Skene, Y. George Zheng, Peter J. Brown, Jian Jin, Chodera JD[‡], and Minkui Luo[‡]

The dynamic conformational landscapes of the protein methyltransferase SETD8

In this work, we show how targeted X-ray crystallography using covalent inhibitors and depletion of native ligands to reveal structures of low-population hidden conformations can be combined with massively distributed molecular simulation to resolve the functional dynamic landscape of the protein methyltransferase SETD8 in unprecedented atomistic detail. Using an aggregate of six milliseconds of fully atomistic simulation from Foldinghome, we use Markov state models to illuminate the conformational dynamics of this important epigenetic protein.



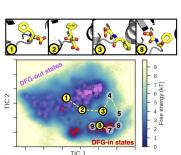
Nature Communications 10:2691, 2019 · DOI

Minuesa G, Albanese SK, Chow A, Schurer A, Park SM, Rotsides CZ, Taggart J, Rizzi A, Naden LN, Chou T, Gourkanti S, Cappel D, Passarelli MC, Fairchild L, Adura C, Glickman FJ, Schulman J, Famulare C, Patel M, Eibl JK, Ross GM, Tan DS, Leslie CS, Beeming T, Golgur Y, Chodera JD, and Kharas MG.

Small-molecule targeting of MUSASHI RNA-binding activity in acute myeloid leukemia

We use absolute alchemical free energy calculations to identify the likely interaction site for a small hydrophobic ligand that shows activity against MUSASHI in AML.

Publications prior to promotion to Associate Member



Cell Chemical Biology 26:390, 2019 · DOI

Hanson SM*, Georghiou G*, Miller WT, Rest JS, Chodera JD[‡], and Seeliger MA[‡]

What makes a kinase promiscuous for inhibitors?

Using a combination of chemogenomics, structural biology, and molecular simulation approaches, we identify a set of human kinases that are especially promiscuous binders of small molecule kinase inhibitors, and show that a prototypical member of this class, DDR1, achieves this promiscuity by virtue of its more stable Asp-DFG-out conformation.

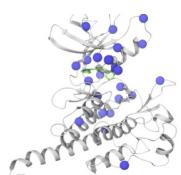


Journal of Chemical Theory and Computation 15:402, 2019 · DOI

Zanette C, Bannan CC, Bayly CI, Fass J, Gilson MK, Shirts MR, Chodera JD, Mobley DL

Toward learned chemical perception of force field typing rules

We show how machine learning can learn typing rules for molecular mechanics force fields within a Bayesian statistical framework.

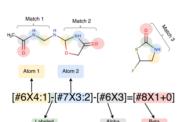


Communications Biology 1:70, 2018 · DOI

Hauser K, Negron C, Albanese SK, Ray S, Steinbrecher T, Abel R, and Chodera JD, and Wang L

Predicting resistance of clinical Abl mutations to targeted kinase inhibitors using alchemical free-energy calculations

We show how alchemical free energy calculations can be used to predict whether clinical point mutations in human kinase domains confer resistance or susceptibility to targeted kinase inhibitors.



Journal of Chemical Theory and Computation 14:6076, 2018 · DOI

Mobley DL[‡], Bannan CC, Rizzi A, Bayly CI, Chodera JD, Lim VT, Lim NM, Beauchamp KA, Shirts MR, Gilson MK, and Eastman PK

Escaping atom types using direct chemical perception with SMIRNOFF v0.1

We describe the philosophy behind a modern approach to molecular mechanics forcefield parameterization, and present initial results for the first SMIRNOFF-encoded forcefield: SMIRNOFF99Frosst.



Journal of Chemical Theory and Computation 15:813, 2019 · DOI

Swenson DWH, Prinz JH, Noé F, Chodera JD, and Bolhuis PG

OpenPathSampling: A Python framework for path sampling simulations. I. Basics

To make powerful path sampling techniques broadly accessible and efficient, we have produced a new Python framework for easily implementing path sampling strategies (such as transition path and interface sampling) in Python. This first publication describes some of the theory and capabilities behind the approach.

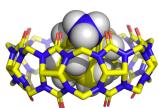


Journal of Chemical Theory and Computation 15:837, 2019 · DOI

Swenson DWH, Prinz JH, Noé F, Chodera JD, and Bolhuis PG

OpenPathSampling: A Python framework for path sampling simulations. II. Building and customizing path ensembles and sample schemes

To make powerful path sampling techniques broadly accessible and efficient, we have produced a new Python framework for easily implementing path sampling strategies (such as transition path and interface sampling) in Python. This second publication describes advanced aspects of the theory and details of how to customize path ensembles.



Journal of Computer Aided Molecular Design 32:937, 2018 · DOI

Rizzi A, Murkli S, McNeill J, Yao W, Sullivan M, Gilson MK, Chiu MW, Isaacs L, Gibb BC, Mobley DL‡, and Chodera JD ‡

Overview of the SAMPL6 host-guest binding affinity prediction challenge

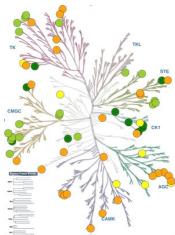
We present an overview of the host-guest systems and participant performance for the SAMPL6 host-guest blind affinity prediction challenges, assessing how well various physical modeling approaches were able to predict ligand binding affinities for simple ligand recognition problems where receptor sampling and protonation state effects are eliminated due to the simplicity of supramolecular hosts. We find that progress is now stagnated likely due to force field limitations.

Journal of Computer Aided Molecular Design 32:1117, 2018 · DOI

Isik M, Levorse D, Rustenburg AS, Ndukwie IE, Wang H, Reibarkh M, Martin GE, Makarov AA, Mobley DL, Rhodes T‡, and Chodera JD ‡

pKa measurements for the SAMPL6 prediction challenge for a set of kinase inhibitor-like fragments

The SAMPL5 blind challenge exercises identified neglect of protonation state effects as a major accuracy-limiting factor in physical modeling of biomolecular interactions. In this study, we report the experimental measurements behind a SAMPL6 blind challenges in which we assess the ability of community codes to predict small molecule pKas for small molecule resembling fragments of selective kinase inhibitors.

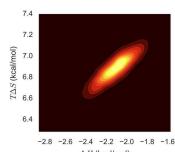


Biochemistry 57:4675, 2018 · DOI

Albanese SK*, Parton DL*, Isik M†, Rodríguez-Laureano L†, Hanson SM, Gradia S, Jeans C, Levinson NM, Seeliger M, and Chodera JD

An open library of human kinase domain constructs for automated bacterial expression

To establish a tractable experimental system for studying the biophysical determinants of selective kinase inhibitor resistance in clinical cancer mutations, we engineer a library of human kinase domains with useful bacterial expression with phosphatase coexpression. Over 350 requests have been made for these plasmids.

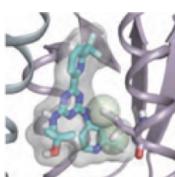


PLOS ONE 3(9): e0203224, 2018 · DOI

Nguyen TH, Rustenburg AS, Krimmer SG, Zhang H, Clark JD, Novick PA, Branson K, Pande VS, Chodera JD ‡, MinH DDL‡

Bayesian analysis of isothermal titration calorimetry for binding thermodynamics

We show how Bayesian inference can produce greatly improved estimates of statistical uncertainty from isothermal titration calorimetry (ITC) experiments, allowing the joint distribution of thermodynamic parameter uncertainties to be inferred.

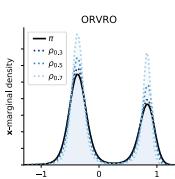


Nature 559:125, 2018 · DOI

Intlekofer AM*, Shih AH*, Wang B, Nazir A, Rustenburg AS, Albanese SK, Patel M, Famulare C, Correa FM, Arcila ME, Taylor J, Tallman MS, Roshal M, Petsko GA, Chodera JD, Thompson CB‡, Levine RL‡, Stein, EM‡

Acquired resistance to IDH inhibition through trans or cis dimer-interface mutations

Clinical double mutations acting in trans in cancer patients receiving IDH2 inhibitors act through a novel biophysical mechanism.

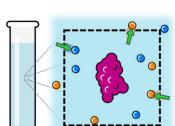


Entropy 20:318, 2018 · DOI

Fass J, Sivak DA, Crooks GE, Beauchamp KA, Leimkuhler B, and Chodera JD

Quantifying configuration-sampling error in Langevin simulations of complex molecular systems

We address a fundamental question regarding why molecular dynamics simulation works despite the fact that the use of finite timesteps leads to error in the sampled probability densities and populations, demonstrating how to measure configuration-space sampling error for an important class of Langevin integrators widely used in biomolecular simulation.



Journal of Physical Chemistry B 122:5466, 2018 · DOI

Ross GA, Rustenburg AS, Grinaway PB, Fass J, and Chodera JD

Biomolecular simulations under realistic salt conditions

We show how NCMC can be used to implement an efficient osmostat in molecular dynamics simulations to model realistic fluctuations in ion environments around biomolecules, and illustrate how the local salt environment around biological macromolecules can differ substantially from bulk.

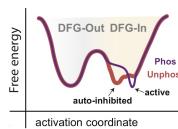


Journal of Physical Chemistry 122:5579, 2018 · DOI

Gill SC, Lim NM, Grinaway PB, Rustenburg AS, Fass J, Ross GA, Chodera JD, and Mobley DL

Binding Modes of Ligands Using Enhanced Sampling (BLUES): Rapid Decorrelation of Ligand Binding Modes Using Nonequilibrium Candidate Monte Carlo

Nonequilibrium candidate Monte Carlo can be used to accelerate the sampling of ligand binding modes by orders of magnitude over instantaneous Monte Carlo.

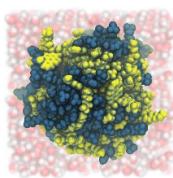


eLife 7:e32766, 2018 · DOI

Ruff EF, Muretta JM, Thompson A, Lake E, Cyphers S, Albanese SK, Hanson SM, Behr JM, Thomas DT, Chodera JD, and Levinson NM

A dynamic mechanism for allosteric activation of Aurora kinase A by activation loop phosphorylation

Through a combination of FRET, IR, and EPR labeling and large-scale molecular dynamics simulations, we show that phosphorylation activates Aurora kinase by a novel mechanism that does not simply correspond to a DFG-out to DFG-in population shift, but rather reorganization of DFG-in subpopulations.

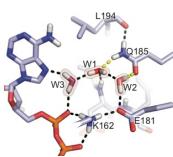


Nature Materials 17:361, 2018 · DOI

Shamay Y, Shah J, Tschaharganeh DF, Roxbury D, Budhathoki-Uprety J, Ijsik M, Mizrahi A, Nawaly K, Sugarman JL, Baut E, Neiman MR, Johnson DC, Sridharan R, Chu KL, Rajasekhar VK, Chodera JD, Lowe SW, and Heller DA

Quantitative self-assembly prediction yields targeted nanoparticles

A decision tree based on predicted physical properties and molecular descriptors is capable of predicting the assembly of drug/dye nanoparticles that can be used in tumor-targeted selective kinase inhibitor therapy to minimize on- and off-pathway toxicity.



Nature Chemical Biology 13:402, 2017 · DOI

Cyphers S, Ruff E, Behr JM, Chodera JD, and Levinson NM

A conserved water-mediated hydrogen bond network governs allosteric activation in Aurora kinase A

Over 50 microseconds of aggregate simulation data on Folding@home reveal a surprisingly stable hydrogen bond network underlies allosteric activation by Tpx2.

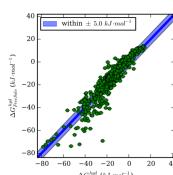


Nature Chemical Biology 13:494, 2017 · DOI

Intlekofer A, Wang B, Liu H, Shah H, Carmona-Fontaine C, Rustenburg AS, Salah S, Gunner MR, Chodera JD, Cross JR, and Thompson CB

Acidification enhances production of L-2-hydroxyglutarate through alternative substrate use by dehydrogenase enzymes

At low pH, metabolic enzymes lactate dehydrogenase and malate dehydrogenase undergo shifts in substrate utilization that have high relevance to cancer metabolism due to surprisingly simple protonation state effects.



Journal of Chemical & Engineering Data 62:1559, 2017 · DOI

Matos GDR, Kyu DY, Loeffler HH, Chodera JD, Shirts MR, and Mobley DL

Approaches for calculating solvation free energies and enthalpies demonstrated with an update of the FreeSolv database

We review alchemical approaches to computing solvation free energies and update FreeSolv—the most popular database of hydration free energies of neutral molecules—with more computed and experimental properties.

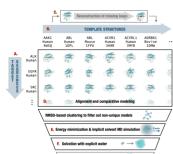


PLoS Computational Biology 13:e1005659, 2017 · DOI

Eastman P, Swails J, Chodera JD, McGibbon RT, Zhao Y, Beauchamp KA, Wang LP, Simmonett AC, Harrigan MP, Brooks BR, and Pande VS

OpenMM 7: Rapid development of high performance algorithms for molecular dynamics

The latest version of the GPU-accelerated molecular simulation OpenMM features a variety of incredibly flexible but fast tools for rapidly prototyping, evaluating, and deploying new simulation algorithms.



PLoS Computational Biology 12:e1004728, 2016 · DOI

Parton DL, Grinaway PB, Hanson SM, Beauchamp KA, and Chodera JD

Ensembler: Enabling high-throughput molecular simulations at the superfamily scale

We demonstrate a new tool that enables—for the first time—massively parallel molecular simulation studies of biomolecular dynamics at the superfamily scale, illustrating its application to protein tyrosine kinases, an important class of drug targets in cancer.

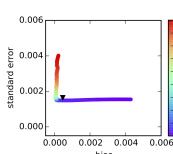


Journal of Clinical Investigation 126:3529, 2016 · DOI

Xu J, Pham CG, Albanese SK, Dong Y, Oyama T, Lee CH, Rodrik-Outmezguine V, Yao Z, Han S, Chen D, Parton DL, Chodera JD, Rosen N, Cheng EH, and Hsieh JJ

Mechanistically distinct cancer-associated mTOR activation clusters predict sensitivity to rapamycin

We use massively parallel distributed molecular simulations on Folding@home to probe the mechanism activating mutations of the mTOR kinase identified in clinical populations.



Journal of Chemical Theory and Computation 12:1799, 2016 · DOI

Chodera JD

A simple method for automated equilibration detection in molecular simulations

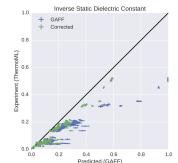
We present a simple approach to automatically determining the equilibrated region of a molecular simulation, a longstanding challenge formerly without a good solution.

Journal of Computer Aided Molecular Design, 30:945, 2016 · DOI

Rustenburg AS, Dancer J, Lin B, Ortwinne D, Mobley DL, and Chodera JD

Measuring cyclohexane-water distribution coefficients for the SAMPL5 challenge

To test the accuracy of physical modeling techniques in predicting free energies of transfer between aqueous and nonpolar solvents, we worked with Genentech to develop a new protocol to measure cyclohexane-water distribution coefficients for 53 druglike compounds at pH 7.4, fielding a blind community challenge as part of the [SAMPL5 exercise](#). A special issue of JCAMD was published with 16 papers describing various approaches used by participants to predict this data and understand their failures.

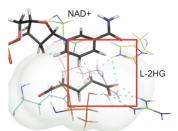


Journal of Physical Chemistry B 119:12912, 2015 · DOI

Beauchamp KA, Behr JM, Rustenburg AS, Bayly CI, Kroenlein K, and Chodera JD

Towards automated benchmarking of atomistic forcefields: Neat liquid densities and static dielectric constants from the ThermoML data archive

Molecular mechanics forcefields are critical to computer-guide drug design, but the benchmarking and improvement of these forcefields has been hindered by the lack of high-quality machine-readable physical property datasets. We show how the NIST-curated ThermoML Archive, which stores physical property data in an IUPAC-standard XML format, can eliminate these roadblocks and reveal issues with current generation forcefields.

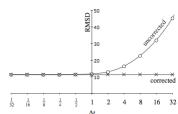


Cell Metabolism 22:1–8, 2015 · DOI

Intlekofer AM, Dematteo RG, Venetti S, Finley LWS, Lu Chao, Judkins AR, Rutenburg AS, Grinaway PB, Chodera JD, Cross JR, and Thompson CB

Hypoxia introduces production of L-2-Hydroxyglutarate

Molecular docking is used to demonstrate the potential for alternative substrate usage by isocitrate dehydrogenases under hypoxic conditions in cancer.

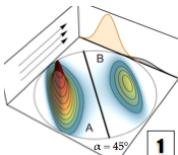


Journal of Physical Chemistry B, 118:6466–6474, 2014. William C. Swope Festschrift · DOI

Sivak DA, Chodera JD, and Crooks GE

Time step rescaling recovers continuous-time dynamical properties for discrete-time Langevin integration of nonequilibrium systems

We derive a simple, easy-to-implement Langevin integrator that has universally useful properties in molecular simulations.

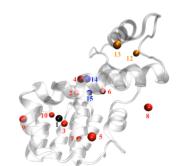


Physical Review X 4:011020, 2014 · DOI

Prinz J-H, Chodera JD, and Noé F

Spectral rate theory for two-state kinetics

We present a new mathematical framework for unifying various two-state rate theories presented in the physical chemistry literature over many decades, and provide a quantitative way to measure reaction coordinate quality.

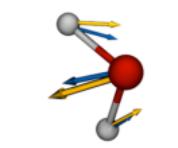


Journal of Computer Aided Molecular Design 27:989–1007, 2013 · DOI

Wang K, Chodera JD, Yang Y, and Shirts MR

Identifying ligand binding sites and poses using GPU-accelerated Hamiltonian replica exchange molecular dynamics

We show how bound ligand poses can be identified even when the location of the binding sites are unknown using the machinery of alchemical modern free energy calculations on graphics processors.



Journal of Physical Chemistry B 117:9956–9972, 2013 · DOI

Wang L-P, Head-Gordon TL, Ponder JW, Ren P, Chodera JD, Eastman PK, Martinez TJ, and Pande VS

Systematic improvement of a classical molecular model of water

Water is the most important molecule in biology, and accurate treatment of its interactions is critical to accurate modeling for drug discovery. While polarizable models of water can achieve very high accuracies, they are both difficult to parameterize and expensive to employ. Here, we show how a high quality inexpensive polarizable model of liquid water can be derived using an automated parameterization engine.



Physical Review X 3:011007, 2013 · DOI

Sivak DA, Chodera JD, and Crooks GE

Using nonequilibrium fluctuation theorems to understand and correct errors in equilibrium and nonequilibrium discrete Langevin dynamics simulations

All molecular dynamics simulations introduce error into the sampled distribution by virtue of the finite timestep used to integrate the equations of motion on a digital computer. While traditional approaches to analyzing this error are extremely complicated, we show how interpreting finite-timestep integrators as a form of nonequilibrium driving leads to simple, straightforward schemes for assessing the impact of these errors, as well as correcting for them.

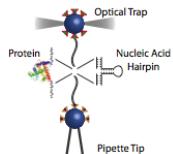


Journal of Chemical Theory and Computation 9:461, 2012 · DOI

Eastman P, Friedrichs MS, Chodera JD, Radmer RJ, Bruns CM, Ku JP, Beauchamp KA, Lane TJ, Wang L, Shukla D, Tye T, Houston M, Stich T, Klein C, Shirts MR, and Pande VS

OpenMM 4: A reusable, extensible, hardware independent library for high performance molecular simulation

Inexpensive consumer GPUs promise a 100-fold increase in simulation power by problems that can effectively exploit their highly specialized structure. Here, we describe the latest advances in an extremely high performance, open-source, extensible GPU-accelerated library and toolkit for molecular simulation.

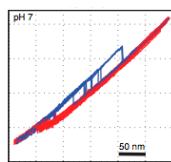


Biophysical Journal 103:1490, 2012 · DOI

Elms PJ, Chodera JD, Bustamante CJ, Marqusee S

The limitations of constant-force-feedback experiments

Popular constant-force-feedback single-molecule experiments can cause severe artifacts in single-molecule force spectroscopy data. We demonstrate a simple alternative that eliminates these artifacts.



Proceedings of the National Academy of Sciences 109:3796, 2012 · DOI

Elms PJ, Chodera JD, Bustamante C, Marqusee S

The molten globule state is unusually deformable under mechanical force

We measure the physical properties of the molten globule state of apo-myoglobin, and show that it is unusually deformable compared to typical protein native states.

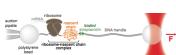
$$f_{\text{exp}} = \int d\vec{r} f(\vec{r}) p_1(\vec{r})$$

Journal of Chemical Theory and Computation 8:3445, 2012 · DOI

Pitera JW and Chodera JD

On the use of experimental observations to bias simulated ensembles

We show how the concept of maximum entropy can be used to recover unbiased conformational distributions from experimental data, and how this concept relates to the popular ‘ensemble refinement’ schemes for NMR data analysis.

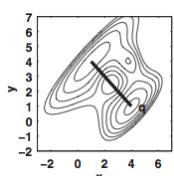


Science 334:1723, 2011 · DOI

Kaiser CM, Goldman DH, Chodera JD, Tinoco I, Jr., and Bustamante C

The ribosome modulates nascent protein folding

Using single-molecule force spectroscopy, we show how the ribosome itself modulates the folding dynamics of nascent protein chains emerging from the exit tunnel.

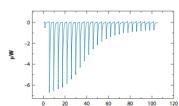


Physical Review Letters 107:098102, 2011 · DOI

Chodera JD and Pande VS

Splitting probabilities as a test of reaction coordinate choice in single-molecule experiments

We demonstrate a simple test for identifying poor reaction coordinates in single-molecule experiments.

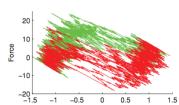


Analytical Biochemistry 414:297, 2011 · DOI

Tellinghuisen JT and Chodera JD

Systematic errors in isothermal titration calorimetry: Concentrations and baselines

A word of caution about large errors in isothermal titration calorimetry measurements arising from ligand concentration errors.

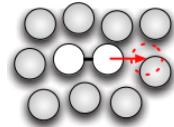


Journal of Chemical Physics 134:024111, 2011 · DOI

Minh DDL, Chodera JD

Estimating equilibrium ensemble averages using multiple time slices from driven nonequilibrium processes: Theory and application to free energies, moments, and thermodynamic length in single-molecule pulling experiments

We derive a new estimator for estimating equilibrium expectations from nonequilibrium experiments, and show how it can be used to estimate a variety of useful quantities in simulated single-molecule force spectroscopy experiments.

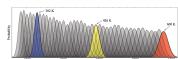


Proceedings of the National Academy of Sciences 108:E1009, 2011 · DOI

Nilmeier JP, Crooks GE, Minh DDL, and Chodera JD

Nonequilibrium candidate Monte Carlo is an efficient tool for equilibrium simulation

We present a significant generalization of Monte Carlo methods that provide an enormously useful tool for enhancing the efficiency of molecular simulations and enabling molecular design.

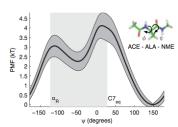


Journal of Chemical Physics 134:244108, 2011 · DOI

Prinz J-H, Chodera JD, Pande VS, Smith JC, and Noé F

Optimal use of data in parallel tempering simulations for the construction of discrete-state Markov models of biomolecular dynamics

We demonstrate how multitemperature data from parallel tempering simulations can be used to construct fully temperature-dependent models of the dynamics of biomolecular systems.

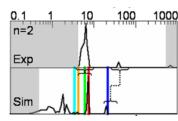


Journal of Chemical Physics 134:244107, 2011 · DOI

Chodera JD, Swope WC, Noé F, Prinz J-H, Shirts MR, and Pande VS

Dynamical reweighting: Improved estimates for dynamical properties from simulations at multiple temperatures

We describe how reweighing techniques can provide optimal estimates of temperature-dependent dynamical properties from simulations conducted at multiple temperatures.

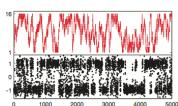


Proceedings of the National Academy of Sciences 108:4822, 2011 · DOI

Noé F, Doose S, Daidone I, Löllmann M, Sauer M, Chodera JD, and Smith JC

Dynamical fingerprints: A theoretical framework for understanding biomolecular processes by combination of simulation and kinetic experiments

We present a new framework for comparing essential features of the dynamics between experiment and simulation to identify the kinetics processes contributing to individual relaxation timescales in perturbation-response or correlation spectroscopy experiments.



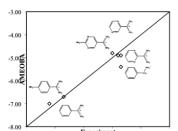
Journal of Chemical Physics 135:194110, 2011 · DOI

Chodera JD and Shirts MR

Replica exchange and expanded ensemble simulations as Gibbs sampling:

Simple improvements for enhanced mixing

We show how a simple change to the way exchanges are handled in the popular replica-exchange simulation methodology can astronomically increase efficiency at no increase in computational cost.

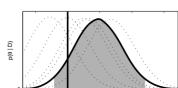


Journal of Physical Chemistry B 114:2549, 2010 · DOI

Ponder JW, Wu C, Ren P, Pande VS, Chodera JD, Mobley DL, Schnieders MJ, Haque I, Lambrecht DS, DiStasio RA Jr., Head-Gordon M, Clark GN, Johnson ME, and Head-Gordon T

Current status of the AMOEBA polarizable force field

The AMOEBA polarizable force field is able to reproduce a diverse set of physical chemical phenomenon to high accuracy.



Journal of Chemical Physics 133:105102, 2010 · DOI

Chodera JD and Noé F

Probability distributions of molecular observables computed from Markov models.

II. Uncertainties in observables and their time-evolution

A simple Bayesian approach for the modeling of statistical uncertainties in kinetic and equilibrium quantities computed from Markov state models of biomolecular dynamics.

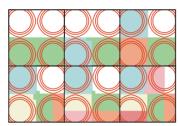


Biophysical Journal 98:3062, 2010 · DOI

Adelman JL, Chodera JD, Kuo IW, Miller TF, and Barsky D

The mechanical properties of PCNA: Implications for the loading and function of a DNA sliding clamp

Molecular simulations of the PCNA clamp responsible for DNA polymerase processivity show a surprisingly small energetic penalty for the deformation required for clamp loading. Featured on issue cover.

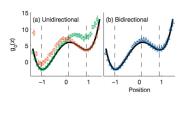


Journal of Chemical Physics 131:045106, 2009 · DOI

Bacallado S, Chodera JD, and Pande VS

Bayesian comparison of Markov models of molecular dynamics with detailed balance constraint

A Bayesian scheme for comparing state space decompositions for Markov state models of biomolecular dynamics that incorporates the fact that physical systems must obey detailed balance. This paper utilizes recent results from Markov chain theory on edge-reinforced random walks.



Journal of Chemical Physics 131:134110, 2009 · DOI

Minh DDL, Chodera JD

Optimal estimators and asymptotic variances for nonequilibrium path-ensemble averages

We derive an optimal estimator and corresponding statistical uncertainties for inferring expectations of bidirectional nonequilibrium processes. These estimators have widespread applicability in single-molecule biophysical force-spectroscopy experiments and nonequilibrium molecular simulations.

Journal of Chemical Physics 129:124105, 2008 · DOI

Shirts MR, Chodera JD

Statistically optimal analysis of samples from multiple equilibrium states

We present a highly general, statistically optimal approach for producing estimates of free energies and equilibrium expectations from multiple simulations that provably extracts all useful information from the data.



Journal of Medicinal Chemistry 51:769, 2008 · DOI

Nicholls A*, Mobley DL*, Guthrie JP, Chodera JD, and Pande VS

Predicting small-molecule solvation free energies: A blind challenge test for computational chemistry

A blind evaluation of the accuracy of alchemical free energy methods for computing gas-to-water transfer free energies (solvation free energies) of small molecules demonstrates that modern forcefields are likely sufficiently accurate to be useful in drug design.

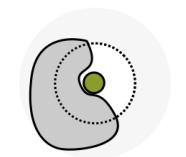


Journal of Physical Chemistry B 112:938, 2008 · DOI

Mobley DL, Dill KA, and Chodera JD

Treating entropy and conformational changes in implicit solvent simulations of small molecules

An quantitative examination of how much conformational entropy contributes to hydration free energies of small molecules, with implications for ligand binding.

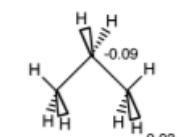


Journal of Physical Chemistry B 111:13052, 2007 · DOI

Shirts MR*, Mobley DL*, Chodera JD, and Pande VS

Accurate and efficient corrections for missing dispersion interactions in molecular simulations

We identify a major source of systematic error in absolute alchemical free energy calculations of ligand binding and show how a simple procedure can inexpensively and accurately eliminate it.

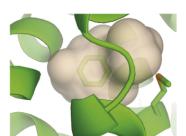


Journal of Physical Chem B 111:2242, 2007 · DOI

Mobley DL, Dumont E, Chodera JD, Bayly CI, Cooper MD, and Dill KA

Comparison of charge models for fixed-charge force fields: Small-molecule hydration free energies in explicit solvent

We compare a number of popular methods for deriving charge models for small molecules, deriving lessons about best practices for accurate simulations.

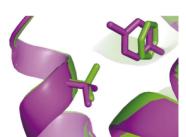


Journal of Molecular Biology 371:1118, 2007 · DOI

Mobley DL, Graves AP, Chodera JD, McReynolds AC, Shoichet BK, and Dill KA

Predicting absolute ligand binding free energies to a simple model site

We show how alchemical free energy calculations are capable of accurate blind prediction of small-molecule binding affinities to a simple model protein binding site.



Journal of Chemical and Theoretical Computation 3:1231, 2007 · DOI

Mobley DL, Chodera JD, and Dill KA

Confine-and-release method: Obtaining correct binding free energies in the presence of protein conformational change

We present a general scheme for obtaining correct ligand binding affinities when protein conformational change is implicated in ligand binding.



Journal of Chemical Physics 126:155101, 2007 · DOI

Chodera JD*, Singhal N*, Swope WC, Pitera JW, Pande VS, and Dill KA

Automatic discovery of metastable states for the construction of Markov models of macromolecular conformational dynamics

Proposing one of the first automated algorithms for discovering kinetically metastable states of biomolecules from molecular simulations, this paper shows how many biomolecules can possess numerous distinct long-lived conformational states even though the equilibrium populations of these states may too small for standard structural biology techniques to detect.

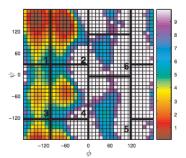


Proceedings of the National Academy of Sciences 104:11987, 2007 · DOI

Ozkan SB, Wu GA, Chodera JD, and Dill KA

Protein Folding by Zipping and Assembly

A review of the utility of the proposed zipping and assembly mechanism for the concomitant formation of secondary and tertiary structure in protein folding for predicting folding pathways and native structures.

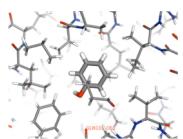


Journal of Chemical Theory and Computation 3:26, 2007 · DOI

Chodera JD, W. C. Swope, J. W. Pitera, C. Seok, and K. A. Dill

Use of the weighted histogram analysis method for the analysis of simulated and parallel tempering simulations

The weighted histogram analysis method (WHAM), a mainstay of molecular dynamics simulation analysis, is thoroughly explained and modernized for the analysis of simulated and parallel tempering simulation data.

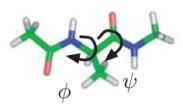


Journal of Chemical Physics 125:084902, 2006 · DOI

Mobley DL, Chodera JD, and Dill KA

On the use of orientational restraints and symmetry corrections in alchemical free energy calculations

We illustrate how orientational restraints can be used to greatly reduce the computational effort in alchemical calculations of ligand binding free energies, and clarify how symmetry corrections are necessary when molecules contain symmetric or pseudosymmetric substituents.

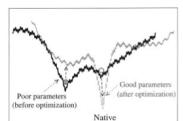


Multiscale Modeling and Simulation 5:1214, 2006 · DOI

Chodera JD, Swope WC, Pitera JW, and Dill KA

Long-time protein folding dynamics from short-time molecular dynamics simulations

We show how the long-time dynamics of biomolecular systems can be recapitulated from statistics collected from short molecular simulations sampling transitions between kinetically metastable states.

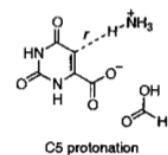


Journal of Computational Chemistry 24:89, 2003 · DOI

Seok C, Rosen JB, Chodera JD, Dill KA

MOPED: Method for optimizing physical energy parameters using decoys

We propose a new way to optimize parameters for a physical energy function using decoy structures for protein folding studies.



Journal of the American Chemical Society 123:12837, 2001 · DOI

Lee TS*, Chong LT*, Chodera JD, and Kollman PA

An alternative explanation for the catalytic proficiency of orotidine 5'-phosphate decarboxylase

A combined QM and MD analysis of potential plausible mechanisms to explain the enormous catalytic acceleration of one of the most proficient enzymes known.

Peer reviewer for scientific journals

Bioinformatics, Biopolymers, Chemical Physics, Computation, Drug Discovery Today, European Biophysics Journal, Entropy, International Journal of Molecular Sciences, Journal of the American Chemical Society, Journal of Chemical Theory and Computation, Journal of Computer-Aided Molecular Design, Journal of Computational Chemistry, Journal of Computational Physics, Journal of Physical Chemistry, Journal of Physical Chemistry Letters, Molecular Physics, Multiscale Modeling & Simulation, Nature Chemistry, Nature Communications, Nature Physics, Pacific Symposium in Biocomputing, PLoS Computational Biology, PLoS One, Proceedings of the National Academy of Sciences, Science, Scientific Reports, Structure

Graduate Programs

2013- Program in Physiology, Biophysics, and Systems Biology (PBSB)

2013- Tri-Institutional PhD Program in Chemical Biology (TPCB)

2013- Tri-Institutional Program in Computational Biology and Medicine (CBM)

2015- Gerstner Sloan Kettering Graduate Program (GSK)

Teaching

Virginia Tech
Summer 2017

MolSSI Software Summer School Instructor

Molecular Software Sciences Institute

Tri-I
2015-2018

CBM Journal Club Moderator

Tri-I Computational Biology and Medicine Program

WCMC
2018-

BCMB Biochemistry

WCMC Graduate School of Medical Sciences (statistical mechanics and thermodynamics unit, 3.0 lecture hours)

Grant Reviews and Study Sections

NIH

Macromolecular Structure and Function B [MSFB] (*early career reviewer*)

NSF

Ad hoc reviewer and virtual panel member for Chemical Theory, Models, and Computational Methods (CTMC)

Conferences organized

2020-	Pause due to COVID-19 pandemic
London, UK Sep 2019	CompBioMed 2019
Berlin, Germany May 2019	IET London
Göttingen, Germany May 2019	MolKin 2019: Molecular Kinetics: Sampling, Design and Machine Learning Freie Universität Berlin, Germany
Boston, MA May 2018	Alchemical Free Energy Methods Workshop Novartis, Cambridge, MA
San Francisco, CA Sep 2017	Free Energy Methods and Molecular Kinetics in Drug Design Workshop Novartis, Cambridge, MA
Berkeley, CA Jan 2017	MolSSI Workshop on Workflows in Biomolecular Simulation Autodesk
Boston, MA May 2016	SMML//2017: Statistical Mechanics // Machine Learning University of California, Berkeley
Cambridge, MA May 2016	Free Energy Methods in Drug Design Workshop Vertex Pharmaceuticals, Boston, MA
Berlin, Germany Sep 2015	Markov State Models in Drug Design Workshop Novartis, Cambridge, MA
Boston, MA May 2014	World Molecular Kinetics Workshop 2015 Freie Universität Berlin, Germany
Berlin, Germany Sep 2013	Free Energy Methods in Drug Design Workshop Vertex Pharmaceuticals, Boston, MA
Cambridge, MA May 2012	World Molecular Kinetics Workshop 2013 Freie Universität Berlin, Germany
Berlin, Germany Sep 2011	Free Energy Methods in Drug Design Workshop Vertex Pharmaceuticals, Cambridge, MA
Cambridge, MA May 2010	World Molecular Kinetics Workshop 2011 Freie Universität Berlin, Germany
Berlin, Germany May 2009	Free Energy Methods in Drug Design Workshop Vertex Pharmaceuticals, Cambridge, MA
	World Molecular Kinetics Workshop 2009 Freie Universität Berlin, Germany

Funding

All funding sources are publicly available online at <http://choderalab.org/funding>

Active

Single-Investigator Grants

Vir Biosciences Sponsored Research Agreement SK2019-0582

Development of alchemical free energy methods for predicting the impact of point mutations

The goal of this project is to develop alchemical free energy methods for predicting the impact of point mutations on antibody:antigen affinities.

8/1/2019 – 7/31/2023

\$55,556 annual direct costs

Relay Therapeutics Collaboration SK2018-0162

Development of efficient open source cloud-enabled free energy based lead optimization algorithms and integrative Bayesian model of experimental biophysical and molecular simulation data

The goal of this project is to develop open source scalable cloud workflows for lead optimization using relative alchemical free energy calculations, as well as Bayesian integrative modeling techniques for experimental biophysical data and molecular simulations.

4/5/2018 – 4/4/2023

\$124,828 annual direct costs

Interline Therapeutics Sponsored Research Agreement SK2020-0898

Identification of key biophysical interactions in ligase-substrate recognition

The goal of this project is to identify key biophysical interactions necessary for ligase-substrate recognition and developing quantitative accurate open source tools for predicting changes in affinity associated with point mutations in either ubiquitin ligases or their substrate peptides.

1/15/2021 – 1/14/2023

\$187,998 direct costs

Collaborative Grants

NIH NIAID U19 1U19AI171399-01 (MPI: Chodera [Contact PI]; Alpha Lee, Potera; Ben Perry, DNDI)

AI-driven Structure-enabled Antiviral Platform (ASAP) co-Is: Karla Kirkegaard (Stanford), Matt Bogyo (Stanford), Jesse Bloom (Fred Hutch), Frank von Delft (Diamond Light Source), Martin Walsh (Diamond Light Source), Alpha Lee (PostEra), Nir London (Weizmann), Ed Griffen (MedChemica), Laurent Fraisse (DNDI), Haim Barr (Weizmann), Daren Fearon (Diamond Light Source), Kris White (Mount Sinai), Adolfo García-Sastre (Mount Sinai), Randy Albrecht (Mount Sinai)

05/16/2022 – 04/30/2025

The goal of this antiviral drug discovery (AViDD) Center is to use an AI-accelerated structure-enabled discovery platform to build a pipeline of novel oral antivirals against coronaviruses, flaviviruses, and picornaviruses using an open science, IP-free discovery paradigm to act as a nexus for global antiviral discovery.

Total federal funds awarded: \$67,662,387

Total direct costs: \$49,000,085

Total F&A for MSKCC: \$18,662,302 Eligible for non-competitive renewal for two more years for an additional \$42M.

NSF CHI 1904822 (PI: David Minh, IIT)

Collaborative Research: CDS&E: Elucidating Binding using Bayesian Inference to Integrate Multiple Data Sources

The goal of this project is to develop a scalable approach to Bayesian inference from biophysical experiments

9/1/2019 – 8/31/2023

\$47,327 annual direct costs to the Chodera lab

NIH R01 1R01GM132386 (MPI: John Chodera; Michael Shirts, University of Colorado [Contact PI])

Open data-driven infrastructure for building biomolecular force fields for predictive biophysics and drug design

co-Is: David Mobley (UCI), Lee-Ping Wang (UC Davis), Michael Gilson (UCSD)

The goal of this project is to develop a modern open infrastructure for building fully consistent biopolymer and small molecule force fields for drug design and predictive biophysical modeling.

6/1/2019 – 5/30/2023

\$20,684 annual direct costs to the Chodera lab

Note: Chodera was a PI of this multi-PI/PD grant for the first year, but moved to co-I status in subsequent years due to NIGMS limit two active GMS PI grants.

NIH R01 GM124270 (PI: David Mobley, UCI)

Advancing predictive physical modeling through focused development of model systems

to drive new modeling innovations

The goal of this project is to enable blind community challenges that drive progress toward quantitative accuracy in the field of computational physical modeling of drug-receptor interactions.

9/10/2018 – 8/31/2023

\$42,711 annual direct costs to the Chodera lab

NIH 1R01GM140090 (PI: Tom Markland, Stanford University)

OpenMM: Scalable biomolecular modeling, simulation, and machine learning

co-I: Gianni de Fabritiis (Universitat de Pompeu Fabra, Barcelona)

The goal of this project is to support continued development of OpenMM, transition to a community governance and distributed development model, and extension to integrate physical and machine learning models to enable genomic-scale biomolecular modeling, simulation, and prediction.

7/1/2021 – 3/31/2025

\$36,685 annual direct costs to the Chodera lab

BIH Einstein Visiting Professorship at the Charité Berlin

Computational polypharmacology: A new paradigm for selectively promiscuous kinase inhibitors

The goal of this project is to develop structure-informed machine learning approaches to predicting kinase inhibitor polypharmacology for computer-guided small molecule design.

1/1/2019 – 12/31/2024

EUR150,000 annual direct costs to Chodera (via Charité) for Berlin working group (with six-month no-cost extension)

NIH 3R01GM132386-02S1 (PI: Michael Shirts, University of Colorado Boulder)

Supplement to: Open data-driven infrastructure for building biomolecular force fields for predictive biophysics and drug design

co-Is: David Mobley (UCI), Lee-Ping Wang (UC Davis), Michael Gilson (UCSD)

The goal of this project is to support continued development of OpenMM, transition to a community governance and distributed development model, and extension to integrate physical and machine learning models to enable genomic-scale biomolecular modeling, simulation, and prediction.

3/1/2021 – 2/28/2022

\$132,694 annual direct costs for this supplement

JDC wrote this proposal to secure additional funding for a critical community resource (QCArchive/QCFractal) he will help direct.

Fellowships

Sukrit Singh // Postdoctoral Fellow

Damon Runyon Quantitative Biology Fellowship

5/1/2022 – 4/30/2025

\$240,000 stipend support

Pending

Single-Investigator Grants and Contracts

I plan to consolidate my NIH NIGMS funding ending 2022–2023 into an R35 (MIRA) for the Jan 2023 deadline.

Collaborative Grants

NIH NCI R01 GM145739-01 (MPI: Chiosis/Gewirth)

4/1/2022 – 3/31/2027

Mechanistic investigations into Glyc62GRP94 epichaperones

The role of the Chodera lab in this project is to use MD simulations to uncover the effect of the N-glycan on GRP94 structure and ligand binding.

\$50,000 annual direct costs to the Chodera lab

NIH 1P01 CA262136-01A1 (PI: Li)

7/1/2022 -- 6/30/2027

GRP94 in Cancer Biology and Immuno-oncology (Project 1; Project leader: Chiosis)

The role of the Chodera lab in this project is to use MD simulations to discover improved inhibitors that target this cancer-specific GRP94 variant.

\$50,000 annual direct costs to the Chodera lab

Fellowships

None

Completed

Single-Investigator Grants and Contracts

NIH R01 GM121505

The role of reorganization energy in achieving selective kinase inhibition

The goal of this project is to probe the role of protein reorganization energy in achieving selectivity in targeted kinase inhibition with small molecules.

9/1/2017 – 8/31/2022

\$196,250 annual direct costs to the Chodera lab

Bayer Sponsored Research Agreement SK2019-1289

Development of a combined machine learning / alchemical free energy approach to predict the impact of mutations on small molecule kinase inhibitor binding

The goal of this project is to develop open source scalable free energy and machine learning workflows in collaboration with the Volkamer lab (Charité Berlin) to predict kinase mutations small molecule therapeutics may be effective against.

3/1/2020 – 4/30/2022

\$117,105 annual direct costs to the Chodera lab

NSF RAPID CHE2033426

RAPID: Identifying Biophysical Determinants of Binding to the SARS-CoV-2 Main Viral Protease

The goal of this proposal is to assess the accuracy of large-scale alchemical free energy calculations in identifying potent inhibitors of the SARS-CoV-2 main viral protease (Mpro) with the COVID Moonshot.

7/1/2020 – 6/30/2021

\$112,994 direct costs to Chodera lab

Entasis Therapeutics Sponsored Research Agreement SK2018-0163

Development of efficient equilibrium and nonequilibrium algorithms for predicting small molecule porin permeation with potential of mean force methods

The goal of this project is to develop algorithms and open source tools for efficient equilibrium and nonequilibrium potential of mean force calculations for bacterial porins.

4/5/2018 – 4/5/2019

\$74,074 annual direct costs to the Chodera lab

Parker Institute for Cancer Immunotherapy Pilot Grant

Physics-based computational prediction of cancer-associated mutant MHC class II epitopes

The goal of this project is to develop algorithms and open source tools for efficient computation of MHC class II epitope binding affinities.

4/2/2018 – 4/1/2019

\$75,000 annual direct costs to the Chodera lab

NSF D3SC EAGER CTMC

A probabilistic framework for automated forcefield parameterization from experimental datasets

The goal of this project is to develop a scalable Bayesian inference infrastructure to parameterize molecular mechanics forcefields using experimental datasets.

9/1/2017 – 8/31/2019

\$52,030 annual direct costs to the Chodera lab

Silicon Therapeutics Sponsored Research Agreement

Development of efficient open source free energy based lead optimization algorithms

The goal of this project is to develop open source scalable parallel workflows for lead optimization using relative alchemical free energy calculations.

5/17/2017 – 11/17/2018

\$48,655 annual direct costs to the Chodera lab

Merck KGaA Sponsored Research Agreement

Developing automated workflows for absolute alchemical free energy calculations

The goal of this project is to develop open source automated workflows using absolute alchemical free energy calculations for use in prioritizing compounds for synthesis in drug discovery applications.

7/26/2016 – 1/25/2019

\$90,273 annual direct costs to the Chodera lab

Astra-Zeneca iMed Sponsored Research Agreement

Evaluating the potential for Markov state models of conformational dynamics to advance quantitative prediction of thermodynamics and kinetics of selective kinase inhibitors

The goal of this project is to evaluate the potential for Markov state models of conformational dynamics to quantitatively

predict the thermodynamics and kinetics of selective kinase inhibitors to CK2 and SYK.

7/30/2015 – 1/30/2017

\$117,505 annual direct costs to the Chodera lab

Gerstner Family Foundation

Louis V. Gerstner, Jr. Young Investigator Award

Dates: 2/1/2013 – 1/30/2016

\$75,000 annual direct costs

MSKCC Functional Genomics Initiative (FGI) Rapid Response Grant

Biophysical characterization of clinically-identified kinase mutations

The goal of this project is to quantify the impact of clinically-identified kinase domain mutations on FDA-approved selective kinase inhibitor binding.

4/1/2016 – 3/31/2016

\$25,000 annual direct costs

MSKCC Functional Genomics Initiative (FGI) Rapid Response Grant

Biophysical characterization of clinically-identified K-Ras mutants

The goal of this project is to biophysically characterize clinically-identified K-Ras mutants.

7/1/2016 – 6/30/2016

\$25,000 annual direct costs

Fellowships

Dominic Rufa // TPCB Graduate Student

MolSSI Seed Software Fellowship

1/1/2022 – 6/30/2022

\$20,000 stipend support

Yuanqing Wang // PBSB Graduate Student

Anagenex Open Science Fellowship

9/1/2021 – 2/28/2022

\$21,750 stipend support

Karmen Čondić-Jurkić, Postdoctoral Research Fellow

Open Force Field Consortium Postdoctoral Fellowship

4/1/2020 – 3/31/2021

\$88,864.10 stipend, supplies, and travel support

Ivy Zhang CBM Graduate Student

MolSSI COVID-19 Seed Software Fellowship

7/1/2020 – 12/31/2020

\$20,000/year stipend support

Hannah Bruce Macdonald, Postdoctoral Fellow

MolSSI Investment Software Fellowship

7/1/2019 – 12/31/2020

\$50,000/year stipend support

Marcus Wieder, Postdoctoral Research Fellow

Austrian Schrödinger Stipendium

10/1/2018 – 9/30/2019

Fellowship recipient direct paid

Simon Boothroyd, Postdoctoral Research Fellow

XtalPi / Open Force Field Consortium Distinguished Postdoctoral Fellowship

10/1/2018 – 9/30/2019

Fellowship recipient direct paid

Andrea Rizzi, CBM Graduate Student

MolSSI Open Force Field Predoctoral Fellowship

1/1/2019 – 6/30/2019

\$20,000/six months stipend support

Rafal P. Wiewiora, TPCB Graduate Student

DOD Peer-Reviewed Cancer Research Program Award

8/15/2017 – 8/14/2019

\$75,000/year for stipend and supplies

Karmen Čondić-Jurkić, Postdoctoral Research Fellow
Open Force Field Consortium Postdoctoral Fellowship

1/1/2019 – 6/30/2019

\$60,628 stipend and travel support

Chaya Stern, TPCB Graduate Student

MolSSI Phase II Fellowship

7/1/2018 – 12/31/2018

\$40,000/year stipend support

Chaya Stern, TPCB Graduate Student

MolSSI Phase I Fellowship

7/1/2018 – 12/31/2018

\$40,000/year stipend

Chaya Stern, TPCB Graduate Student

NSF Graduate Research Fellowship

8/1/2015 – 7/30/2018

\$32,000/year stipend support

Mehtap Isik, TPCB Graduate Student

Doris J. Hutchison Fellowship

7/1/2017 – 6/30/2018

\$38,668/year stipend support

Gregory A. Ross, Postdoctoral Fellow

Molecular Software Sciences Institute (MolSSI) Graduate Research Fellowship

\$50,000/year stipend support

Steven Albanese, GSK Graduate Student

Summer Internship, Schrödinger

Summer 2017

Ariën S. Rustenburg, PBSB Graduate Student

Summer Internship, Genentech

Summer 2015

Andrea Rizzi, CBM Graduate Student

Tri-I CBM Student Stipend Assistance

\$13,500/year stipend support

Collaborative Grants

Chan Zuckerberg Initiative – Essential Open Source Software for Science (PI: Tom Markland, Stanford University)

co-I: Gianni de Fabritiis (Universitat de Pompeu Fabra, Barcelona)

OpenMM: Key infrastructure for biomolecular modeling and simulation

The goal of this project is to support continued development of OpenMM, transition to a community governance and distributed development model, and extension to integrate physical and machine learning models to enable genomic-scale biomolecular modeling, simulation, and prediction.

9/1/2020 – 4/1/2021

JDC wrote this proposal to secure funding for a key community infrastructure project that his lab depends upon.

\$180,000 total direct costs to support this project

Functional Genomics Initiative (FGI)

Integrated Approaches Annotate Functions of Cancer-associated H3K36 Methyltransferases

The goal of this project is to develop approaches for using large-scale physical modeling and biochemical experiments to annotate the functions of clinical cancer mutations.

1/1/2019 – 12/31/2020

co-PI: Minkui Luo

\$125,000 annual direct costs to the Chodera lab

2014 Functional Genomics Initiative (PI: James Hsieh, MSKCC)

Characterization of Cancer-derived mTOR Mutations for Precision Therapeutics

The goal of this project is to understand the mechanism underlying clinically-identified mTOR activating mutants and evaluate the potential for rapalog therapy to aid the 2% of cancer patients harboring mTOR mutations.

5/1/2015 – 4/30/2017

\$118,000

2014 STARR Cancer Consortium (PI: Minkui Luo, MSKCC)

Designing sinefungin scaffolds as specific protein methyltransferase inhibitors

The goal of this project is to use computational techniques that explicitly incorporate protein flexibility to design selective inhibitors for protein lysine methyltransferases.

1/1/2015 – 6/30/2017

\$125,000

Personnel

Current members

Postdocs

- Sukrit Singh, PhD Washington University St. Louis (6/1/2021–)
Damon Runyon Quantitative Biology Fellow
Selective inhibition and drug resistance in clinical kinase inhibitors

Graduate Students

- Ivy Zhang (8/1/2018–)
Program in Physiology, Biophysics, and Systems Biology (PBSB)
Scalable free energy calculations for predicting the impact of mutations on protein-protein interactions
- Yuanqing Wang (7/1/2018–)
Program in Physiology, Biophysics, and Systems Biology (PBSB)
Machine learning of physics for drug discovery
- Dominic Rufa (4/1/2019–)
Tri-Institutional Program in Computational Biology and Medicine (CBM)
Machine learning for alchemical free energy calculations
- Talia Kimber (4/1/2019–) [co-supervised with Andrea Volkamer, Charité Berlin]
Charité Universitätmedizin (supervisor: Andrea Volkamer)
Freie Universität Berlin, Computer Science PhD program (supervisor: Frank Noé)
Machine learning for optimizing affinity/selectivity and predicting resistance
- Alexander Payne (8/1/2020–) [co-supervised with Rich Hite, MSKCC Structural Biology Program]
Program in Physiology, Biophysics, and Systems Biology (PBSB)
Combining cryo-EM with Markov state models, virtual screening, and free energy calculations for drug discovery
- Viktor Belay (8/1/2020–) [co-supervised with Rich Hite, MSKCC Structural Biology Program]
Program in Physiology, Biophysics, and Systems Biology (PBSB)
Combining cryo-EM with Markov state models, virtual screening, and free energy calculations for drug discovery
- Michael Retchin (7/1/2021–)
Tri-Institutional Program in Computational Biology and Medicine (CBM)
New technologies for autonomous drug discovery
- Benjamin Kaminow (1/1/2022–)
Tri-Institutional Program in Computational Biology and Medicine (CBM)
Structure-enabled machine learning for drug discovery

Software Scientists

- Iván Pulido (7/1/2021–)
Alchemical free energy calculation software infrastructure; software infrastructure support for ASAP

Research Associates

- Erica Goldberger (7/1/2019–)
Lab manager; Automated measurements of small molecule binding affinities to model drug targets for improving quantitative predictions for drug discovery

Past trainees

My lab trains interdisciplinary scientists to tackle the most challenging problems in drug discovery.

Postdocs

- David Schaller, PhD Freie Universität Berlin (7/1/2020–7/31/2022) (**Berlin group**)
Current position: *Associate Scientist*, [Nuvisan](#)
- Ana Silveira, PhD Federal University of Rio de Janeiro (8/1/2018–7/31/2019)
Current position: *Senior Investigator*, [Rovant Sciences](#)
- Jiaye Guo, PhD Stony Brook University (10/1/2018–5/31/2021)
Current position: *Senior Scientist I*, [Schrodinger](#)
- Simon Boothroyd, PhD Lancaster University (11/1/2018–10/31/2019)
Current position: *Senior Researcher, Scientific Programmer*, [Rovant Sciences](#)
- William Glass, PhD Southampton (5/1/2020–7/31/2021)
Current position: *Molecular Dynamics Research Scientist*, [Exscientia](#)
- Jaime Rodríguez-Guerra Pedregal, PhD Autonomous University of Barcelona (4/1/2019–5/31/2021) (**Berlin group**)
Current position: *Software Engineer*, [Quansight](#)
- Karmen Čondić-Jurkić, PhD Friedrich Alexander University, Erlangen (4/6/2019–)
Current position: *Executive Director and Co-Founder*, [Open Molecular Software Foundation](#)
- Hannah Bruce Macdonald, PhD University of Southampton (10/1/2018–9/30/2020)
Current position: *Senior Scientist I*, [Merck Sharp & Dohme \(MSD\)](#)
- Marcus Wieder, PhD University of Vienna (9/1/2018–4/16/2020)
Current position: *Faculty*, [University of Vienna](#)
- Levi N. Naden (until 8/10/2018)
Current position: *Software Scientist* at the NSF [Molecular Sciences Software Institute \(MolSSI\)](#)
- Sonya M. Hanson (until 6/30/2017)
Next position: *Postdoctoral Researcher with Joachim Frank*, [Columbia University](#)
Current position: Group Leader and Research Scientist, Center for Computational Biology, [Flatiron Institute](#), Simons Foundation, NYC
- Gregory Ross (until 6/30/2017)
Current position: *Principal Scientist*, [Schrödinger](#)
- David W. H. Swenson (until 12/30/2015)
Current position: *Software Scientist*, [Open Free Energy Consortium](#)
- Daniel L. Parton (until 8/31/2015)
Current position: *Lead Data Scientist*, [Bardess Group](#)
- Kyle A. Beauchamp (until 6/12/2015)
Current position: *Senior Director of Data Science*, [Tempus](#)
- Jan-Hendrik Prinz (until 1/30/2015)
Current position: *Digital Solutions Architect*, [Keylight GmbH](#)
- Sarah E. Boyce (until 10/31/2013)
Current position: *Director*, [Schrödinger](#)

Graduate Students

- Joshua Fass (9/1/2015–11/9/2020)
Tri-Institutional Program in Computational Biology and Medicine (CBM)
Current position: *Scientist*, [Relay Therapeutics](#)
- Mehtap Isik (6/1/2015–9/11/2020 anticipated)
Tri-Institutional Program in Chemical Biology (TPCB)
Current position: *Scientist, Computational Chemistry*, [Moderna](#)
- Rafal Wiewiora (6/1/2015–8/31/2020)
Tri-Institutional Training Program in Chemical Biology (TPCB)
Current position: *Scientist*, [Rovant Sciences](#)
- Ariën Sebastian Rustenburg (10/1/2013–10/19/2018)
Program in Physiology, Biophysics, and Systems Biology (PBSB)
Current position: *DevOps Engineer, Software for Chemistry & Materials*, [SCM](#)

- Andrea Rizzi (9/1/2015–12/31/2019)
Tri-Institutional Program in Computational Biology and Medicine (CBM)
Current position: *Postdoctoral Fellow, Michele Parrinello Group, ETH Zürich*
- Chaya Stern (4/01/2014–6/30/2020)
Tri-Institutional Training Program in Chemical Biology (TPCB)
Current position: *Senior Principal Scientist, Odyssey Therapeutics*
- Steven Albanese (6/1/2015–3/31/2019)
Gerstner Graduate Program (GSK)
Current position: *Principal Scientist II, Schrödinger*
- Patrick B. Grinaway (7/1/2013–12/31/2018)
Program in Physiology, Biophysics, and Systems Biology (PPSB)
Current position: *Scientist, Onai*
- Julie M. Behr (1/10/2014–12/31/2016)
Tri-Institutional Program in Computational Biology and Medicine (CBM)
Current position: *Transferred to Imielinski lab after publishing three papers with the Chodera lab*

Technicians

- Liza Casella (1/19/2021–11/6/2021)
Current position: *Research Associate, Kingdom Supercultures*
- Binisha Karki (8/1/2019–8/28/2020)
Current position: *Research Associate, BioNTech*
- Lucelenie Rodriguez (7/1/2015–12/31/2016; 12/4/2017–7/20/2018)
Current position: *Medical student, NYU School of Medicine*
- Erin Grundy (6/1/18–7/31/2019)
Current position: *Graduate student, George Washington University*