

Matthew Lowell Baker, Ph.D.

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EXPERIENCE

2020-current Assistant Professor, Department of Biochemistry and Molecular Biology, The University of Texas Health Science Center at Houston

2020-current Adjunct Assistant Professor, Verna and Marrs McLean Department of Biochemistry and Molecular Biology, Baylor College of Medicine

2015-current Baylor Research Advocates for Student Scientists (BRASS) Faculty Liaison and Executive Committee member, Baylor College of Medicine

2015- current Brain Lab Faculty Director, Baylor College of Medicine

2015-2019 Faculty Senator, Baylor College of Medicine

2014-2020 Assistant Professor, Verna and Marrs McLean Department of Biochemistry and Molecular Biology, Baylor College of Medicine

2006-2013 Instructor, National Center for Macromolecular Imaging, Verna and Marrs McLean Department of Biochemistry and Molecular Biology, Baylor College of Medicine

2005-2006 Project Manager, Computational Center for Biomolecular Complexes, Baylor College of Medicine

2002-2006 Consultant, Institute for Defense Analyses

1999-2000 Teaching Assistant, Baylor College of Medicine

1995-1996 Laboratory Assistant, Purdue University

1995 Research Assistant, SMART Program, Baylor College of Medicine

1993-1996 Teaching Assistant, Purdue University

EDUCATION

- 2002-2005 Postdoctoral Associate, Department of Biochemistry and Molecular Biology, Baylor College of Medicine, Houston, TX
Advisor: Wah Chiu, Ph.D.
Funding: W.M. Keck Center for Computational Biology NLM Postdoctoral Fellowship (2002-2005)
- 1996-2002 Ph.D., Program in Structural and Computational Biology and Molecular Biophysics (SCBMB), Baylor College of Medicine, Houston, TX
Thesis title: Development and Application of Intermediate Resolution Structural Analysis Tools: Integrating Bioinformatics and Electron Cryo-microscopy
Advisor: Wah Chiu, Ph.D.
Funding: Predoctoral fellowships from The Welch Foundation (2000-2001), W.M. Keck Center for Computational Biology (1997-2000), Baylor Research Advocates of Student Scientists (1996-1997)
- 1992-1996 B.S. Biochemistry and Molecular Biology with a minor in Chemistry, Purdue University, W. Lafayette, IN

PUBLICATIONS

1. Wang, H.J., Lee, C.L., Yee, R.S.Z., Groom, L., Friedman, I., Babcock, L., Georgiou, D.K., Hong, J., Hanna, A.D., Recci, J., Choi, J.M., Dong, K., Romero, J., Sarkar, P., Voermans, N., Gaber, M.W., Jung, S.Y., **Baker, M.L.**, Pautler, R.G., Dirksen, R.T., Riazi, S., Hamilton, S.L. (Submitted) Adaptive thermogenesis sensitizes mice with a mutation in *Ryr1* to a life-threatening response to heat. Donovan, L.K., Delaidelli, A., Joseph, S.K., Bielimowicz, K., Fousek, K., Holgado, B.L., Manno, A., Srikanthan, D., Gad, A.Z., Van Ommeren, R., Przelicki, D., Richman, C., Ramaswamy, V., Daniels, C., Pallota, J.G., Douglas, T., Joynt, A.C.M., Haapasalo, J., Nor, C., Vladioiu, M.C., Kuzan-Fischer, C.M., Garzia, L., Mack, S.C., Varadharajan, S., **Baker, M.L.**, Hendrikse, L., Ly, M., Kharas, K., Balin, P., Wu, X., Qin, L., Huang, N., Stucklin, A.G., Morrissy, A.S., Cavalli, F.M.G., Luu, B., Suarez, R., De Antonellis, P., Michealraj, A., Rastan, A., Hegde, M., Komosa, M., Sirbu, O., Kumar, S.A., Abdullaev, Z., Faria, C.C., Yip, S., Hukin, J., Tabori, U., Hawkins, C., Aldape, K., Daugaard, M., Maris, J.M., Sorensen, P.H., Ahmed, N., Taylor, M.D. (2020) Locoregional delivery of CAR T cells to the cerebrospinal fluid for treatment of metastatic medulloblastoma and ependymoma. *Nat Med.* 26, 720-731.
2. Fousek, K., Watanabe, J., Joseph, S.K., George, A., An, X., Byrd, T.T., Morris, J.S., Luong, A., Martínez-Paniagua, M.A., Sanber, K., Navai, S.A., Gad, A.Z., Salsman, V.S., Mathew, P.R., Kim, H.N., Wagner, D.L., Brunetti, L., Jang, A., **Baker, M.L.**, Varadarajan, N., Hegde, M., Kim, Y.M., Heisterkamp, N., Abdel-Azim, H., Ahmed, N. (2020) CAR T-cells that target acute B-lineage leukemia irrespective of CD19 expression. *Leukemia*.

3. Liebschner, D., Agonien, P.V., **Baker, M.L.**, Bunkoczi, G., Chen, V.B., Hintze, B., Hung, L.W., Jain, S., McCoy, A.J., Moriarty, N.W., Oeffner, R.D., Poon, B.K., Prisant, M.G., Read, R.J., Richardson, J.S., Richardson, D.C., Sammito, M.D., Sobolev, O.V., Stockwell, D.H., Terwilliger, T.C., Urzhumtsev, A.G., Videau, L.L., Williams, C.J., Admas, P.D. (2019) Macromolecular structure determination using X-rays, neutrons and electrons: Recent developments in Phenix. *Acta Cryst D*. 75, 861-877.
4. Fan, G., Baker, M.R., Wang, Z., Seryshev, B.A., Ludtke, S.J., **Baker, M.L.**, Serysheva, I.I. (2018) Cryo-EM reveals ligand induced allostery underlying InsP3R Channel gating. *Cell Res*. 12, 1158-1170.
5. Chen, M., **Baker, M.L.** (2018) Automation and assessment of *de novo* modeling with Pathwalking in near atomic resolution cryoEM density maps. *J Struct Biol*. S1047-8477(18), 30255-7.
6. Byrd, T.T., Fousek, K., Pignata, A., Szot, C., Samaha, H., Seaman, S., Dobrolecki, L., Salsman, V.S., Oo, H.Z., Bielamowicz, K., Landi, D., Rainusso, N., Hicks, J., Powell, S., **Baker, M.L.**, Wels, W.S., Koch, J., Sorensen, P.H., Deneen, B., Ellis, M.J., Lewis, M.T., Hegde, M., Fletcher, B.S., St Croix, B., Ahmed, N. (2018) TEM8/ANTXR1-Specific CAR T Cells as a Targeted Therapy for Triple-Negative Breast Cancer. *Cancer Res* 78, 489-500.
7. Dou, H., Burrows, D., **Baker, M.L.**, Ju, T. (2017) Flexible Fitting of Atomic Models into Cryo-EM Density Maps Guided by Helix Correspondences. *Biophys J* 112, 2479-2493.
8. Chen M., Baldwin P.R., Ludtke S.J., **Baker M.L.** (2016) De Novo modeling in cryo-EM density maps with Pathwalking. *J Struct Biol* 196, 289-298.
9. Hedge, M., Grada, Z., Pignata, A., Wakefield, A., Fousek, A., Bielamowicz, K., Chow, K., Brawley, V. S., Byrd, T., Krebs, S., Gottschalk, S., Mukherjee, M., **Baker, M. L.**, Dotti, G., Orange, J., Ahmed, N. (2016) A HER2/IL13R α 2-targeted CAR molecule enhances T cell activation through bifunctional immunological synapse formation and abrogates antigen escape in glioblastoma. *J Clin Invest* 126, 3036-3052.
10. Lawson C.L., Patwardhan A., **Baker M.L.**, Hryc C., Garcia E.S., Hudson B.P., Lagerstedt I., Ludtke S.J., Pintilie G., Sala R., Westbrook J.D., Berman H.M., Kleywegt G.J., Chiu W. (2016) EMDataBank unified data resource for 3DEM. *Nucleic Acids Res* 44(D1), 396-403.
11. Fan, G., **Baker, M. L.**, Wang, Z., Baker, M.R., Sinyaovsky, P. A., Chiu, W., Ludtke, S. J., and Serysheva, I. I. (2015) Gating Machinery of IP3R Channels Revealed by Cryo-EM. *Nature* 537, 336-341.
12. Dao, H., **Baker, M. L.**, Ju, T. (2015) Graph-based Deformable Matching of 3D Line Segments with Application in Protein Fitting. *The Visual Computer* 31, 961-977.
13. Zhang Z., He F., Constantine R., **Baker M. L.**, Baehr W., Schmid M. F., Wensel T. G., Agosto M. A. (2015) Domain organization and conformational plasticity of the G protein effector, PDE6. *J Biol Chem* 290,12833-43.

14. Wang, Z., Hryc, C.F., Bamme, B., Afonine, P.V., Jakana, J., Chen, D.C., Liu, X., **Baker, M.L.**, Kao, C., Ludtke, S.J., Schmid, M.F., Adams, P.A., and Chiu, W. (2014) An atomic model of BMV using direct electron detection and real-space optimization. *Nat Commun* 5, 4808.
15. Gipson, P., **Baker, M.L.**, Raytcheva, D., Haase, C., Pret, J., King, J.A., and Chiu, W. (2014) Protruding knob-like proteins violate all local symmetries in an icosahedral marine virus. *Nat Commun* 5, 4278.
16. Rizzo, A.A., Suhanovsky, M.M., **Baker, M.L.**, Fraser, L.C.R., Jones, L.M., Rempel, D.L., Gross, M.L., Chiu, W., Alexandrescu, A.T., and Teschke, C.M. (2014) Multiple functional roles of the accessory I-Domain of bacteriophage P22 coat protein revealed by NMR structure and cryoEM Modeling. *Structure* 22, 830-41.
17. Grada, Z., Hegde, M., Byrd, T., Shaffer, D. R., Ghazi, A., Brawley, V. S., Corder, A., Schönfeld, K., Koch, J., Dotti, G., Heslop, H. E., Gottschalk, S., Wels, W. S., **Baker, M. L.**, and Ahmed, N. (2013). TanCAR: A novel bispecific chimeric antigen receptor for cancer immunotherapy. *Mol Ther Nucleic Acids* 2, e105.
18. **Baker, M. L.**, Hryc, C. F., Zhang, Q., Wu, W., Jakana, J., Haase-Pettingell, C., Afonine, P. V., Adams, P. D., King, J. A., Jiang, W., and Chiu, W. (2013). Validated near-atomic resolution structure of bacteriophage epsilon15 derived from cryo-EM and modeling. *Proc Natl Acad Sci U S A* 110, 12301-6.
19. Chang, J., Liu, X., Rochat, R. H., **Baker, M. L.**, and Chiu, W. (2012). Reconstructing virus structures from nanometer to near-atomic resolutions with cryo-electron microscopy and tomography. *Adv Exp Med Biol* 726, 49-90.
20. **Baker, M. L.**, Baker, M. R., Hryc, C. F., Ju, T., and Chiu, W. (2012). Gorgon and pathwalking: macromolecular modeling tools for subnanometer resolution density maps. *Biopolymers* 97, 655-68.
21. **Baker, M. L.**, Baker, M. R., and Cong, Y. (2012). Computational Methods for Interpretation of EM Maps at Subnanometer Resolution. In *eLS* (Chichester, UK: John Wiley & Sons, Ltd).
22. Henderson, R., Sali, A., **Baker, M. L.**, Carragher, B., Devkota, B., Downing, K. H., Egelman, E. H., Feng, Z., Frank, J., Grigorieff, N., Jiang, W., Ludtke, S. J., Medalia, O., Penczek, P. A., Rosenthal, P. B., Rossmann, M. G., Schmid, M. F., Schröder, G. F., Steven, A. C., Stokes, D. L., et al. (2012). Outcome of the first electron microscopy validation task force meeting. *Structure* 20, 205-14.
23. Baker, M. R., Rees, I., Ludtke, S. J., Chiu, W., and **Baker, M. L.** (2012). Constructing and validating initial Ca models from subnanometer resolution density maps with pathwalking. *Structure* 20, 450-63.
24. Zhang, R., Hryc, C. F., Cong, Y., Liu, X., Jakana, J., Gorchakov, R., **Baker, M. L.**, Weaver, S. C., and Chiu, W. (2011). 4.4 Å cryo-EM structure of an enveloped alphavirus Venezuelan equine encephalitis virus. *EMBO J* 30, 3854-63.

25. Srinivasan, S., Vyas, N. K., **Baker, M. L.**, and Quiocho, F. A. (2011). Crystal structure of the cytoplasmic N-terminal domain of subunit I, a homolog of subunit a, of V-ATPase. *J Mol Biol* 412, 14-21.
26. **Baker, M. L.**, Abeysinghe, S. S., Schuh, S., Coleman, R. A., Abrams, A., Marsh, M. P., Hryc, C. F., Ruths, T., Chiu, W., and Ju, T. (2011). Modeling protein structure at near atomic resolutions with Gorgon. *J Struct Biol* 174, 360-73.
27. Lawson, C. L., **Baker, M. L.**, Best, C., Bi, C., Dougherty, M., Feng, P., van Ginkel, G., Devkota, B., Lagerstedt, I., Ludtke, S. J., Newman, R. H., Oldfield, T. J., Rees, I., Sahni, G., Sala, R., Velankar, S., Warren, J., Westbrook, J. D., Henrick, K., Kleywegt, G. J., et al. (2011). EMDataBank.org: unified data resource for CryoEM. *Nucleic Acids Res* 39, D456-64.
28. Chen, D. H., **Baker, M. L.**, Hryc, C. F., DiMaio, F., Jakana, J., Wu, W., Dougherty, M., Haase-Pettingell, C., Schmid, M. F., Jiang, W., Baker, D., King, J. A., and Chiu, W. (2011). Structural basis for scaffolding-mediated assembly and maturation of a dsDNA virus. *Proc Natl Acad Sci U S A* 108, 1355-60.
29. **Baker, M.**, and Prasad, B. V. (2010). Rotavirus cell entry. *Curr Top Microbiol Immunol* 343, 121-48.
30. **Baker, M. L.**, Marsh, M. P., and Chiu, W. (2010). Electron Cryomicroscopy of Molecular Nanomachines and Cells. In *Nanotechnology* (Wiley-VCH Verlag GmbH & Co.), p. 89-111.
31. Haspel, N., Moll, M., **Baker, M. L.**, Chiu, W., and Kavraki, L. E. (2010). Tracing conformational changes in proteins. *BMC Struct Biol* 10 Suppl 1, S1.
32. Abeysinghe, S., **Baker, M. L.**, Chiu, W., and Ju, T. (2010). Semi-isometric registration of line features for flexible fitting of protein structures. *Comput Graph Forum* 29, 2243-2252.
33. **Baker, M. L.**, Baker, M. R., Hryc, C. F., and Dimaio, F. (2010). Analyses of subnanometer resolution cryo-EM density maps. *Methods Enzymol* 483, 1-29.
34. **Baker, M. L.**, Zhang, J., Ludtke, S. J., and Chiu, W. (2010). Cryo-EM of macromolecular assemblies at near-atomic resolution. *Nat Protoc* 5, 1697-708.
35. Liu, X., Zhang, Q., Murata, K., **Baker, M. L.**, Sullivan, M. B., Fu, C., Dougherty, M. T., Schmid, M. F., Osburne, M. S., Chisholm, S. W., and Chiu, W. (2010). Structural changes in a marine podovirus associated with release of its genome into *Prochlorococcus*. *Nat Struct Mol Biol* 17, 830-6.
36. Zhang, J., **Baker, M. L.**, Schröder, G. F., Douglas, N. R., Reissmann, S., Jakana, J., Dougherty, M., Fu, C. J., Levitt, M., Ludtke, S. J., Frydman, J., and Chiu, W. (2010). Mechanism of folding chamber closure in a group II chaperonin. *Nature* 463, 379-83.
37. Cong, Y., **Baker, M. L.**, Jakana, J., Woolford, D., Miller, E. J., Reissmann, S., Kumar, R. N., Redding-Johanson, A. M., Batth, T. S., Mukhopadhyay, A., Ludtke, S. J., Frydman, J., and Chiu, W. (2010). 4.0-Å resolution cryo-EM structure of the mammalian chaperonin TRiC/CCT reveals its unique subunit arrangement. *Proc Natl Acad Sci U S A* 107, 4967-72.

38. DiMaio, F., Tyka, M. D., **Baker, M. L.**, Chiu, W., and Baker, D. (2009). Refinement of protein structures into low-resolution density maps using rosetta. *J Mol Biol* 392, 181-90.
39. Li, Z., **Baker, M. L.**, Jiang, W., Estes, M. K., and Prasad, B. V. (2009). Rotavirus architecture at subnanometer resolution. *J Virol* 83, 1754-66.
40. Abeysinghe, S. S., **Baker, M. L.**, Wah Chiu, and Tao Ju (2008). Segmentation-free skeletonization of grayscale volumes for shape understanding. 2008 IEEE International Conference on Shape Modeling and Applications, 63-71.
41. Abeysinghe, S., Ju, T., **Baker, M. L.**, and Chiu, W. (2008). Shape modeling and matching in identifying 3D protein structures. *Computer-Aided Design* 40, 708 - 720.
42. Jiang, W., **Baker, M. L.**, Jakana, J., Weigele, P. R., King, J., and Chiu, W. (2008). Backbone structure of the infectious epsilon15 virus capsid revealed by electron cryomicroscopy. *Nature* 451, 1130-4.
43. Serysheva, I. I., Ludtke, S. J., **Baker, M. L.**, Cong, Y., Topf, M., Eramian, D., Sali, A., Hamilton, S. L., and Chiu, W. (2008). Subnanometer-resolution electron cryomicroscopy-based domain models for the cytoplasmic region of skeletal muscle RyR channel. *Proc Natl Acad Sci U S A* 105, 9610-5.
44. **Baker, M. L.**, Zhou, Z. H., and Chiu, W. (2008). Structure of Phytoreovirus. In *Segmented Double-stranded RNA Viruses: Structure and Molecular Biology*, J. T. Patton, ed. (Caister Academic Press), p. 89-103.
45. Ludtke, S. J., **Baker, M. L.**, Chen, D. H., Song, J. L., Chuang, D. T., and Chiu, W. (2008). De novo backbone trace of GroEL from single particle electron cryomicroscopy. *Structure* 16, 441-8.
46. Ju, T., **Baker, M. L.**, and Chiu, W. (2007). Computing a family of skeletons of volumetric models for shape description. *Comput Aided Des* 39, 352-360.
47. **Baker, M. L.**, Ju, T., and Chiu, W. (2007). Identification of secondary structure elements in intermediate-resolution density maps. *Structure* 15, 7-19.
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50. Marsh, M. P., Campos, S. K., **Baker, M. L.**, Chen, C. Y., Chiu, W., and Barry, M. A. (2006). Cryoelectron microscopy of protein IX-modified adenoviruses suggests a new position for the C terminus of protein IX. *J Virol* 80, 11881-6.
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55. Chiu, W., **Baker, M. L.**, Jiang, W., Dougherty, M., and Schmid, M. F. (2005). Electron cryomicroscopy of biological machines at subnanometer resolution. *Structure* 13, 363-72.
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65. Zhou, Z. H., **Baker, M. L.**, Jiang, W., Dougherty, M., Jakana, J., Dong, G., Lu, G., and Chiu, W. (2001). Electron cryomicroscopy and bioinformatics suggest protein fold models for rice dwarf virus. *Nat Struct Biol* 8, 868-73.

66. Petrosino, J. F., **Baker, M.**, and Palzkill, T. (1999). Susceptibility of beta-lactamase to core amino acid substitutions. *Protein Eng* 12, 761-9.
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GRANTS - ACTIVE

1P01GM063210 - "PHENIX: Integrated Algorithms For High Quality Models"

National Institutes of Health 25% effort (7/1/2018-6/30/2022)

Role: Co-Investigator (Adams, PI)

Aims: This grant seeks to develop new modeling and analysis tools for X-ray crystallographic and cryo-EM data in an effort to produce high quality models. With the growing number of cryo-EM data sets at near-atomic resolutions, this work seeks to establish new tools for map analysis and model building for cryo-EM maps in the 2-5Å resolution range. Dr. Baker's role is to lead the cryo-EM map analysis and model building portion of the grant.

1U54CA232568-01 - "Discovery And Development Of Optimal Immunotherapeutic Strategies For Childhood Cancers"

National Institutes of Health 10% effort (9/1/2018-6/30/2023)

Role: Co-Investigator (Marris and Mackall, PI)

Aims: CAR T cells are synthetic receptors that can be engineered modularly and are therefore amenable to multivalent targeting. Investigators in this project pioneered the development of bivalent and trivalent CAR T cells and are conducting the first-in-human testing of a T cells expressing a bivalent CAR. Emerging technologies are now available to endow individual T cells with quad-CAR specificities and potentially multivalent CAR T cells. This project will optimize platform(s) for generating multivalent CAR T cells and by incorporating data generated in Projects 1 and 3 of this U54, create specific lead candidate multi-specific CARs for targeting pediatric AML, and high risk pediatric solid/brain tumors and brain tumors.

1P01GM121203-01A1 - "An Automated Pipeline for Macromolecular Structure Discovery in Cellular Electron Cryo-Tomography"

National Institutes of Health 25% effort (salary only) (9/1/2018-7/31/2023)

Role: Investigator (Volkman, PI)

Aims: EMAN2 is software for analysis of electron microscopy images in 3D. It is used in a wide range of health related areas, such as learning how drugs interact with target molecules, how viruses interact with cells and developing a physical understanding the biochemistry of the cell. This grant continues the development and support of EMAN2, with a particular focus on validation and interoperability.

R01GM080139 - "Support and Development of EMAN for Electron Microscopy Image Processing"

National Institutes of Health 25% effort (salary only) (06/01/2006-08/31/2023)

Role: Co-PI (Ludtke, PI)

Aims: EMAN2 is software for analysis of electron microscopy images in 3D. It is used in a wide range of health related areas, such as learning how drugs interact with target molecules, how viruses interact with cells and developing a physical understanding the biochemistry of the cell. This grant continues the development and support of EMAN2, with a particular focus on validation and interoperability.

GRANTS - PENDING

Renewal of "Structure-Function of IP3R Channels" (reviewed 12/2019 - 14th percentile)

National Institutes of Health 25% effort

Role: Investigator (Serysheva, PI)

Aims: The maintenance of Ca²⁺ homeostasis in the human body is largely dependent upon the function of inositol 1,4,5-trisphosphate receptors (IP3Rs). The goal of this research program is to establish a detailed understanding of the mechanisms of IP3R gating and modulation using cryoEM, biochemistry and computational modeling.

GRANTS - COMPLETED

DBI-1408887 - "Collaborative Research: ABI Innovations: Algorithms And Tools For Modeling Macromolecular Assemblies"

National Science Foundation

(9/1/2014-12/31/2017)

Role: Principal Investigator

Aims: Building on our established Gorgon modeling software, this proposal seeks to develop and maintain a more comprehensive and extensible modeling toolkit for subnanometer resolution density maps. This projects combines both software and modeling innovation, as well as leveraging currently available modeling software, in a a single integrated user-environment.

R039378-I - "Immunogenomics to Create New Therapies for High-Risk Childhood Cancers"

St. Baldrick's Foundation and Stand Up To Cancer (SU2C)

(7/1/2013-6/30/2017)

Role: Co-Investigator (Harris, PI)

Aims: This cancer "Dream Team" from seven institutions aims to establish genomics-based immunotherapy as the second revolution in childhood cancer. Our multidisciplinary team focuses on the discovery of cell surface molecules on pediatric cancers that can be targeted using antibody-derived binding proteins and develop new therapeutics based upon this targeting element. The team consists of investigators across seven institutions.

5R01GM079429 - "Unified Data Resource for Large Complexes Determined by Cryo-Electron Microscopy"

National Institutes of Health

(6/1/2013-5/31/2017)

Role: Investigator (Chiu, PI)

Aims: A collaboration between NCMI, PDB and EBI, this grants seeks to build a public repository site for cryoEM density maps with associated meta-data and portal for various

software useful for annotators and biological end-users. The recently funded renewal extends our development by building upon community based recommendations to develop best practice standards for cryo-EM imaging and modeling, as well as implement new standards for data validation.

1R21GM100229 - "Atomic Resolution Cryo-EM using Model-Based Constraints"

National Institutes of Health

(8/1/2013-7/31/2015)

Role: Principal Investigator

Aims: This proposal utilizes a novel "sequence-free" method to rapidly build de novo models for individual proteins from cryo-EM density maps. When combined with our proposed cryo-EM density map refinement and reconstruction techniques, it will be possible to produce atomic resolution models of an entire macromolecular assembly.

IIS-0705474 - "Integrated Modeling of Biomolecular Nanomachines"

(8/1/2007-7/31/2010)

National Science Foundation

Role: Principal Investigator

Aims: This proposal looks to develop modeling tools for macromolecular machines through an integrated approach centered on integrating computational techniques with cryo-EM. This multi-PI proposal combines modeling expertise at Baylor College of Medicine, UCSF, University of Washington and Washington University in St. Louis.

PATENTS

Pending, "Chimeric Antigen Receptor For Bispecific Activation And Targeting Of T-Lymphocytes", Nabil M. Ahmed, Zakaria Grada, Meenakshi Hegde, **Matthew L. Baker**, And Donald R. Shaffer

SOFTWARE DEVELOPMENT

Pathwalking - project lead, software for fully automated model building from near atomic resolution cryo-EM density maps; C/C++ and python

Gorgon - project lead, interactive model building software for sub nanometer resolution cryo-EM density maps; C/C++ and python, development and distribution through GitHub and Anaconda

EMAN - developer, image processing software suite for cryo-EM (developer); C/C++ and python

Phenix - developer, software suite for automated structure determination in X-ray crystallography; C/C++ and python

Chimera - developer, software for visualization of macromolecular structure; UI development and python

INVITED TALKS

2019

"Model Metrics Evaluations and Outcomes: Pathwalking", Model Metrics Challenge Workshop, Palo Alto, CA

"Automation and Validation in CryoEM Modeling", Spring 2019 ACS National Meeting and Exposition, Orlando, FL

"The Structure of a Transcribing Reovirus: Insights into Capsid Stabilization, Replication and Genome Organization of a DsDNA Virus", Joint Structure Group Meeting, Houston, TX

2018

"Molecular Mechanisms of Ion Channel Gating", SMART Program Student Seminar, Baylor College of Medicine, Houston TX

"Cryo-EM Model Building and Refinement", American Crystallography Association Annual Meeting, Toronto, Canada.

2017

"Modeling Structure and Function in Ion Channel Gating", Schrodinger, New York, NY

"Structural and Computational Approaches in Cancer Biology", SMART Program Student Seminar, Baylor College of Medicine, Houston TX

"Automating de novo model building with Pathwalker", CryoEM Map and Model Challenge Assessment Meeting, Palo Alto, CA

"Advancements in Cryo-EM Model Building", Phenix Developers Meeting, Berkley, CA.

2016

"Building and Validating Atomic Models for EM Density Maps", Microscopy and Microanalysis Annual Conference 2015, Columbus, OH

"Modeling Macromolecular Structure and Function", SMART Program Student Seminar, Baylor College of Medicine, Houston TX

"Modeling Structure and Function of an Ion Channel", CIBR Short Talks, Baylor College of Medicine, Houston TX

2015

"Modeling Macromolecular Structure and Function with CryoEM", Advanced Structural and Chemical Imaging Symposium, Pullman, WA

"Modeling Macromolecular Structure and Function", Workshop on Single Particle Reconstruction, Structural Variability and Modeling, Baylor College of Medicine, Houston TX

"Cryo-EM of Macromolecular Assemblies", SMART Program Student Seminar, Baylor College of Medicine, Houston TX

"Modeling the Structure and Function of an Ion Channel", Microscopy and Microanalysis Annual Conference 2015, Portland, OR

2014

"Modeling Macromolecular Assemblies with Gorgon", SBGrid Webinar

"Modeling Macromolecular Assemblies", SMART Program Student Seminar, Baylor College of Medicine, Houston TX

"Deciphering Macromolecular structure and function through integrating cryo-EM and computational modeling", The University of Texas Health Science Center, Houston, TX

2013

"Computational approaches in cryo-EM modeling", SMART Program Student Seminar, Baylor College of Medicine, Houston TX

2012

"Macromolecular modeling at non-atomic resolutions", SMART Program Student Seminar, Baylor College of Medicine, Houston TX

2011

"Modeling protein structure at near-atomic resolutions", The University of Texas Health Science Center, Houston, TX

"Modeling at near-atomic resolutions with Gorgon and Pathwalker", NCMI Workshop on Single Particle Reconstruction, Validation and Analysis. Houston, TX

"Modeling with cryo-EM density maps at near-atomic resolutions", Pacific Symposium on Biocomputing 2011. Kohala Coast, HI

2010

"Model validation with near-atomic resolution cryo-EM density maps", EM Validation Task Force Meeting, Rutgers University, New Brunswick, NJ

"SSEHunter and de novo modeling from cryo-EM density maps", Modeling of Cryo-EM Density Maps, Baylor College of Medicine, Houston, TX

2009

"Building structural models from cryo-EM density maps", 2009 Annual Meeting of the American Crystallography Association, Toronto, CA

"Protein structure modeling in cryo-EM", SMART Program Student Seminar, Baylor College of Medicine, Houston TX

"Building structural models from cryo-EM density maps", Department of Pathology, The University of Texas Health Science Center, Houston, TX

"Modeling protein structure at near-atomic resolutions with Gorgon", Bioimage Informatics, Ashburn, VA

2008

"Building structural models from cryo-EM density maps", Supercomputing 2008, Austin, TX

"Modeling macromolecular structure directly from cryo-EM density maps", The 9th Asia-Pacific Microscopy Conference, Jeju, Korea

"Building structural models directly from cryo-EM density maps", Gordon Research Conference on Three-Dimensional Electron Microscopy, Barga, Italy

2007

"Building structural models in subnanometer resolution cryo-EM density maps", AAAS-SWARM Annual Meeting, Clear Lake, TX

"Ab initio modeling of a herpes simplex virus capsid protein assessed by cryo-EM density", Biophysical Society 51st Annual Meeting, Baltimore, MD

"Building structural models in cryo-EM density maps", Barcelona Supercomputing Center, Barcelona, Spain

"Building structural models in subnanometer resolution cryo-EM density maps", Protein Assembly, Dynamics and Function Meeting, Institut des Hautes Etudes Scientifiques, Bures-sur-Yvette, France

2006

"Building structural models in cryo-EM density maps", Critical Assessment of Structure Prediction 7, Asilomar, CA

"Building models from subnanometer resolution cryo-EM density maps", Southwest Regional American Chemical Society, Houston, TX

"Building structural models in subnanometer resolution cryo-EM density maps", Centro Nacional de Biotecnologia, Madrid, Spain

"Building structural models in subnanometer resolution cryo-EM density maps", Gordon Research Conference on Three-Dimensional Electron Microscopy, Barga, Italy

"Deciphering macromolecular structure", 3rd International Symposium on Structural Analysis of Supermolecular Assemblies by Hybrid Methods, Lake Tahoe, CA

2005

"The cryo-EM definitions project", 3DEM Developers Workshop, Hinxton, UK

"Computational approaches to the structural analysis of intermediate resolution structures", Institute for Defense Analyses, Alexandria, VA

"Computational approaches to biological complexes", Gordon Research Conference on Three-Dimensional Electron Microscopy, New London, NH

"Tools for visualization of macromolecular machines", Visualization of Large Biomolecular Complexes, La Jolla, CA

"Analysis of Macromolecular Assemblies", Workshop on Structural and Computational Proteomics of Biological Complexes. Houston, TX

2004

"Analysis of intermediate resolution structures", 12th International Conference on Intelligent Systems for Molecular Biology 3DSIG, Glasgow, UK

2003

"Structural feature extraction in intermediate resolution macromolecular assemblies", Visualization of Biological Complexes, Emeryville, CA

"Subnanometer Resolution Structure of Rotavirus", 4th International virus assembly symposium, Sardinia, Italy

2002

"Structural analysis of intermediate resolution structures", 15th International Congress on Electron Microscopy, Durbin, South Africa

"Fold discovery in macromolecular machines through electron cryomicroscopy and bioinformatics", National Library of Medicine Annual Trainee Meeting, Salt Lake City, UT

2001

"Identification of an N-terminal redox sensor in RYR1", Biophysical Society 45th Annual Meeting, Boston, MA

"Subnanometer resolution structure of Rice Dwarf Virus by Cryo-EM", XVII Biennial Conference on Phage/Virus Assembly, Helsinki, Finland.

1998

"Structure of the double shelled rice dwarf virus", American Society for Virology 17th Annual Meeting, Vancouver, Canada

AWARDS

2018 Diana Brown Memorial BCM/BRASS Mentor of the Year

2008 Poster award, 3DEM GRC

2006 Dunn award, W.M. Keck Center

2006 Poster award, 3DEM GRC

2005 Poster award, 3DEM GRC

2001 Travel award, XVII Biennial Conference on Phage/Virus Assembly

2000 Dunn award, W.M. Keck Center Retreat

1999	Dunn award, W.M. Keck Center Retreat
1998	Travel award, American Society of Virology
1997	Dunn award, W.M. Keck Center Retreat
1996-1997	Baylor Research Advocates for Student Scientists (BRASS) scholar

TEACHING

2019	Instructor, Sealy Center for Structural Biology/UTMB Workshop on CryoEM Data Processing
2019	Instructor, Electron Cryo-Microscopy, Baylor College of Medicine
2016-current	Instructor, Current Topics in CIBR, Baylor College of Medicine
2014-current	Instructor, Applications to Biology of Computation, Baylor College of Medicine
2015	Instructor, Symposium on CryoEM
2009	Instructor, Modeling Cryo-EM Density Maps Workshop
2009	Instructor, Cryo-EM Modeling Workshop
2008	Instructor, Cryo-EM Format Standards Workshop
2007	Instructor, Cryo-EM Mining Workshop
2002-2015	Instructor, Annual NCMI Workshop on Cryo-EM, Visualization and Modeling
1999	Teaching assistant, Structure of Macromolecules, Baylor College of Medicine
1995-1996	Teaching assistant for Biology I, Purdue University
1994-1996	Teaching assistant for Biostatistics, Purdue University

TRAINING

Corey Hryc, SMART Student (2009), lab technician (2009-2011), postdoctoral fellow (2020-current)

Ryan Rochat, M.D., Ph.D., Scholarship Oversight Committee member (2018-current)

Reed Corum, Rice Undergraduate student (2015-current)

Hang Dou, Ph.D. Thesis committee (2015-2017), Washington University in St. Louis

Tunay Durmaz, Ph.D., Postdoctoral advisor (2015-2017)

Shoba Navai, M.D., Scholarship Oversight Committee member (2015-2017)

Daniel Landi, M.D., Scholarship Oversight Committee member (2014-2017)

Muyuan Chen, Graduate student co-mentor (2013-2018)

Derek Burrows, Ph.D. Thesis committee (2012-2014), Washington University in St. Louis

Mariah Baker, Ph.D., Postdoctoral Fellow (2009-2012)

Muthu Alagappan, SMART Student (2009)

Michael Marsh, Ph.D., Postdoctoral advisor (2008-2010)

Sasakthi Abeysingh, Ph.D., Thesis committee (2007-2010)