

March 2021- Assistant Professor, Scripps Research,
Department of Integrative Structural and Computational Biology

EDUCATION

2020-2021 Basic Life Research Scientist
Advisor: Prof. Lucy Shapiro

2013-2019 Postdoctoral Fellow, Stanford University, USA
Advisor: Prof. Lucy Shapiro

2006–2013 Ph.D. in Computer Science
Tel-Aviv University, Israel
Thesis: "Structure Determination of Macromolecular Assemblies
by Data Integration, Application to the 26S Proteasome"
Advisors: Prof. Haim Wolfson, Tel Aviv University
Prof. Andrej Sali, University of California, San Francisco

2003-2005 M.Sc. in Computer Science (Summa Cum Laude)
Tel-Aviv University, Israel
Thesis: "Discovery of Protein Subunits in Cryo-EM Maps".
Advisors: Prof. Haim Wolfson, Tel Aviv University
Prof. Ruth Nussinov, Tel Aviv University

1996-2000 B.Sc. double major in Mathematics and Computer
Science (Magna Cum Laude), Tel-Aviv University, Israel

HONORS & AWARDS

2018 Finalist, Burroughs Wellcome Fund's Career Award at the Scientific Interface

2014-2015 Stanford Systems Biology Seed Grant Award

2013-2016 Life Sciences Research Foundation postdoctoral fellowship

2013 Weismann Institute of Science - National Postdoctoral
Award for Advancing Women in Science

2013 EMBO Long-Term Fellowship for Postdoctoral Research

2012 3DSig annual meeting, Best Paper Award

2009 Excellence Prize for Ph.D. Students, the School of Computer
Science, Tel Aviv University

2008-2011 Charles Clore Foundation Fellowship for Ph.D. Students

2007 RCSB PDB Poster Prize Award

2007 ISMB/ECCB 2007 Outstanding Poster Award

2007 Excellence Prize for Ph.D. Students, the School of Computer
Science, Tel Aviv University

2006-2007 Edmond J. Safra Scholarship for Bioinformatics Studies

PUBLICATIONS

Preprints

- **Lasker K***, Boeynaems S*, Vinson Lam , Emma Stainton , Maarten Jacquemyn , Dirk Daelemans , Elizabeth Villa , Alex Holehouse, Gitler A, Shapiro L. (2021) A modular platform for engineering function of natural and synthetic biomolecular condensates. doi: 10.1101/2021.02.03.429226
- Melfi MD, **Lasker K**, Zhou X, Shapiro L (2021). ATAC-seq reveals megabase-scale domains of a bacterial nucleoid. doi: 10.1101/2021.01.09.426053

Journal papers

- **Lasker K***, von Deizmann L*, Ahrens DG, Mann TH, Moerner WE, Shapiro L. (2020). Selective sequestration of signaling proteins in the PopZ membraneless organelle reinforces the spatial regulation of asymmetry in *Caulobacter crescentus*. Nat Microbiol. 5(3): 418-429.
- Watanabe R, Buschauer R, Böhning J, Audagnotto M, **Lasker K**, Boassa D, Taylor S, Villa E (2020). The in situ structure of a pathogenic mutant LRRK2 involved in Parkinson's Disease using cryo-electron tomography. Cell. 182(6):1508-1518.e16.
- Perez AM, Mann TH, **Lasker K**, Ahrens DG, Eckart MR, Shapiro L (2017). A localized complex of two protein oligomers controls the orientation of cell polarity. MBio. 8(1).
- **Lasker K***, Mann TH*, Shapiro L (2016). An intracellular compass spatially coordinates cell cycle modules in *Caulobacter crescentus*. Curr Opin Microbiol. 33:131-139.
- Ricci DP, Melfi MD, **Lasker K**, Dill DL, McAdams HH, Shapiro L (2016). Cell cycle progression in *Caulobacter* requires a nucleoid-associated protein with high AT sequence recognition. Proc Natl Acad Sci U S A. 113(40):E5952-5961.
- **Lasker K***, Schrader JM*, Men Y, Marshik T, Dill DL, McAdams HH, Shapiro L (2015). CauloBrowser: A systems biology resource of *Caulobacter crescentus*. Nucleic Acids Res. 44(D1):D640-5.
- Schmidt M, Rohou A, **Lasker K**, Yadav JK, Schiene-Fischer C, Fändrich M, Grigorieff N (2015). Peptide dimer structure in an A β (1-42) fibril visualized with cryo-EM. Proc Natl Acad Sci U S A. 12(38):11858-63.
- Villa E, **Lasker K** (2014). Finding the right fit: chiseling structures out of cryo-electron microscopy maps. Curr Opin Struct Biol. 25:118-125.
- Schrader JM, Zhou B, Li GW, **Lasker K**, Childers WS, Williams B, Long T, Crosson S, McAdams HH, Weissman JS, Shapiro L (2014). The coding and noncoding architecture of the *Caulobacter crescentus* genome. PLoS Genet. 10(7):e1004463.
- Politis A, Schmidt C, Tjioe E, Sandercock AM, **Lasker K**, Gordiyenko Y, Russel D, Sali A, Robinson CV (2015). Topological models of heteromeric protein assemblies from mass spectrometry: application to the yeast eIF3:eIF5 complex. Chem Biol. 22(1):117-128.

- Webb B, **Lasker K**, Velázquez-Muriel J, Schneidman-Duhovny D, Pellarin R, Bonomi M, Greenberg C, Raveh B, Tjioe E, Russel D, Sali A (2014). Modeling of proteins and their assemblies with the Integrative Modeling Platform. *Methods Mol Biol.* 1091:277-295.
- Pérez-Cano L, Eliahoo E, **Lasker K**, Wolfson HJ, Glaser F, Manor H, Bernadó P, Fernández-Recio J (2013). Conformational transitions in human translin enable nucleic acid binding. *Nucleic Acids Res*, 41, 9956-9966.
- Velazquez-Muriel JA, **Lasker K**, Russel D, Phillips J, Webb B, Schneidman-Duhovny D, Sali A (2012). Assembly of macromolecular complexes by satisfaction of spatial restraints from electron microscopy images. *Proc Natl Acad Sci USA*, 109, 18821-18826.
- Yang Z, **Lasker K**, Schneidman-Duhovny D, Webb B, Huang CC, Pettersen EF, Goddard TD, Meng EC, Sali A, Ferrin TE (2012). UCSF Chimera, MODELLER, and IMP: An integrated modeling system. *J Struct Biol*, 179, 269-78.
- **Lasker K***, Forster F*, Bohn S, Walzthoeni T, Villa E, Unverdorben P, Beck F, Aebersold R, Sali A, Baumeister W (2012). Molecular architecture of the 26S proteasome holocomplex determined by an integrative approach. *Proc Natl Acad Sci USA*, 109, 1380-87.
- Russel D, **Lasker K**, Webb B, Velazquez-Muriel JA, Scheidman-Duhovny D, Tjioe E, Sali A (2012). Putting the pieces together: integrative structure determination of macromolecular assemblies. *PLoS Biol*, 10, e1001244.
- Pathare GR, Nagy I, Bohn S, Unverdorben P, Hubert A, Körner R, Nickell S, **Lasker K**, Sali A, Tamura T, Nishioka T, Förster F, Baumeister W, Bracher A (2012). The proteasomal subunit Rpn6 is a molecular clamp holding the core and regulatory subcomplexes together. *Proc Natl Acad Sci USA*, 109, 149-54.
- Tjioe E*, **Lasker K***, Webb B, Wolfson HJ, Sali A (2011). MultiFit: a webserver of fitting multiple protein structures into their electron microscopy density map. *Nucleic Acids Res*, 39, W167-W170.
- **Lasker K**, Sali A, Wolfson HJ (2010). Determining macromolecular assembly structures by molecular docking and fitting into an electron density map. *Proteins:Struct Funct Bioinform*, 78, 3205-3211.
- **Lasker K**, Phillips JL, Russel D, Velázquez-Muriel J, Schneidman-Duhovny D, Tjioe E, Webb B, Schlessinger A, Sali A (2010). Integrative Structure Modeling of Macromolecular Assemblies from Proteomics Data. *Mol Cell Proteomics*, 9, 1689-1702.
- Förster F, **Lasker K**, Nickell S, Sali A, Baumeister W (2010). Towards an integrated structural model of the 26S proteasome. *Mol Cell Proteomics*, 9, 1666-1677.
- Förster F, **Lasker K**, Beck F, Nickell S, Sali A, Baumeister W (2009). An Atomic Model AAA-ATPase/20S core particle sub-complex of the 26S proteasome. *Biochem Biophys Res Commun* 388, 228-233.
- Nickell S, Beck F, Scheres SHW, Korinek A, Förster F, **Lasker K**, Mihalache O, Sun N, Nagy I, Sali A, Plitzko J, Carazo JM, Mann M, Baumeister W (2009). Molecular Architecture of the 26S Proteasome. *Proc Natl Acad Sci USA*, 29, 11943-11947.
- **Lasker K**, Topf M, Sali A, Wolfson HJ (2009). Inferential optimization for simultaneous fitting of multiple components into a cryoEM map of their assembly. *J Mol Biol*, 388, 180-194.
- Russel D, **Lasker K**, Phillips J, Schneidman-Duhovny D, Velazquez-Muriel JA, Sali A (2009). The structural dynamics of macromolecular complexes. *Curr Opin Cell Biol*, 21, 1-12.
- Topf M, **Lasker K**, Webb B, Wolfson HJ, Chiu W, Sali A (2008). Protein Structure Fitting and Refinement Guided by cryoEM Density. *Structure*, 16, 295-307.
- **Lasker K**, Dror O, Shatsky M, Nussinov R, Wolfson HJ (2007). EMatch: Discovery of high resolution structural homologues of protein domains in intermediate resolution cryo-EM maps, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4, 28-39 (cover paper).
- Dror O, **Lasker K**, Nussinov R, and Wolfson HJ (2007). EMatch: an efficient method for aligning atomic resolution subunits into intermediate-resolution cryo-EM maps of large macromolecular

assemblies. Acta Cryst, D63, 42-49.

Peer reviewed conference papers

- **Lasker K**, Dror O, Nussinov R, Wolfson HJ (2005). Discovery of Protein Substructures in EM Maps. Algorithms in Bioinformatics: 5th International Workshop, WABI 2005, Mallorca, Spain, October 3-6, 2005, Proceedings, edited by R. Casadio & G. Myers, vol. 3692 of Lecture Notes in Computer Science, 423-434.

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Book chapters

- **Lasker K**, Velazquez-Muriel J, Webb BM, Yang Z, Ferrin TE, Sali A (2012). Macromolecular assembly structures by comparative modeling and electron microscopy. Methods Mol Biol. 857,331-350.
- Webb B, **Lasker K**, Schneidman-Duhovny D, Tjioe E, Phillips J, Kim SJ, Velazquez-Muriel J, Russel D, Sali A (2011). Modeling of Proteins and their Assemblies with the Integrative Modeling Platform. Methods Mol Biol. 781, 377-397.

TALKS

- 2021 Emergent Simplicity in Biophysical Dynamics. Telluride, CO (Upcoming).
- 2021 Plasticity in Biological Organization. Telluride, CO (Upcoming).
- 2020 Biology seminar series, The Catholic University of America, virtual.
- 2020 IDPSeminars, virtual.
- 2020 Special seminar, The Scripps Research Institute in San Diego, CA.
- 2020 Special seminar, Developmental Biology, Stanford University, CA.
- 2020 Special seminar, Computer Science, Tel Aviv University, Israel.
- 2019 American Society of Cell Biology Annual Meeting. Washington, DC.
- 2019 Stanford Developmental Biology Annual Retreat. Monterey, CA .
- 2019 Prokaryotic Data and journal club seminar series. Stanford University, CA.
- 2019 Biophysical Society Annual Meeting, Baltimore, MD.
- 2019 Bacterial locomotion and signal transduction (BLAST). New Orleans, LA.
- 2018 Intrinsically Disordered Proteins, Special Interest Group, Stanford University, CA.
- 2017 5th Annual iHuman Forum. ShanghaiTech, China.
- 2017 Stanford Developmental Biology Annual Retreat. Monterey, CA
- 2016 American Society of Cell Biology Annual Meeting. San Francisco, CA.
- 2016 University of California San Diego Bioinformatics Seminar Series. San Diego, CA.
- 2015 American Society of Cell Biology Annual Meeting. San Diego, CA.
- 2015 Optogenetics Keystone Symposia. Denver, CO.
- 2015 Winter q-bio Meeting, Maui, HI.
- 2015 Stanford Developmental Biology Annual Retreat. Monterey, CA.
- 2012 A Satellite Meeting of the Annual Conference of the International Society for Computational Biology (3Dsig12). Long Beach, CA.
- 2012 20th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), Highlights Track. Long Beach, CA.
- 2011 Three Dimensional Electron Microscopy, Gordon Research Conference. Colby-Sawyer College, NH.
- 2011 Molecular Structural Biology Annual Retreat. Max Planck Institute of Biochemistry, Munich, Germany.

2011 Pacific Symposium on Biocomputing. Big Island of Hawaii, HI.
 2010 A Satellite Meeting of the Annual Conference of the International Society for Computational Biology (3Dsig10). Boston, MA.
 2010 Boston Area CryoEM Meeting. Brandeis University, MA.
 2009 Protein Folding Machinery 4th Annual Meeting. Thomas Fogarty Winery, CA.
 2009 Bay Area CryoEM Meeting, Stanford University, CA.
 2009 17th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), Highlights Track. Stockholm, Sweden.
 2008 Protein Folding machinery 3rd annual meeting. University of California, San Francisco, CA.
 2007 A Satellite Meeting of the Annual Conference of the International Society for Computational Biology (3Dsig07). Vienna, Austria.
 2007 CryoEM Structure Mining Workshop. National Center for Molecular Imaging, Houston, TX.
 2007 Protein Folding Machinery 2th Annual Meeting. Stanford University, CA.
 2007 Biophysical Society 51th Annual Meeting, Baltimore, MD.
 2005 Algorithms in Bioinformatics: 5th International Workshop (WABI05). Mallorca, Spain.

TUTORIALS

2010 Modeling of cryoEM maps workshop, University of Houston, USA.

PEER REVIEWS

Peer Reviewed manuscripts for PNAS, Journal of Cell Biology, Structure, Journal of Structural Biology, Biophysical journal, Bioinformatics, BMC structural biology, Scientific Reports, and IEEE/ACM Transactions on Computational Biology and Bioinformatics.

COMMITTEES

2020-2021 Application evaluator for the Paris Region Fellowship Programme
 2019-2021 IDPSIG: Intrinsically Disordered Proteins, Special Interest Group
 2017-2021 Proceedings Program Committee for the annual international conference on Intelligent Systems for Molecular Biology (ISMB)
 2015-2016 Remote expert evaluator, Horizon 2020

INDUSTRY EXPERIENCE

2002-2005 Intelligence, IDF: Programming officer, team leader and project manager. Overall responsibility for development of the main research supporting infrastructure platform in the army intelligence unit. Direct responsibility for 3 software projects in geographic information processing, knowledge sharing and expert systems.