



## Grigore Pintilie

Research Scientist

Bioengineering

### Bio

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#### BIO

York University, B.Sc. 1995-1999, Computer Science - Computer Graphics, HCI

University of Toronto, M.Sc. 1999-2001, Computer Science, Computer Graphics

Blueprint Initiative, 2001-2005 - Bioinformatics Research

MIT, Ph.D. 2005-2011 - Electrical Engineering and Computer Science, Biology - CryoEM map segmentation and fitting of atomic models

Baylor College of Medicine 2011-2017 - Scientific Programmer - Cryo-EM map analysis and atomic modeling

Stanford University 2017-present - Research Scientist - Cryo-EM map analysis and atomic modeling

#### ACADEMIC APPOINTMENTS

- Basic Life Science Research Associate, Bioengineering

#### LINKS

- <https://gregp.sites.stanford.edu/>: <https://gregp.sites.stanford.edu/>

### Publications

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#### PUBLICATIONS

- **Structural insights into the modulation of coronavirus spike tilting and infectivity by hinge glycans.** *Nature communications*  
Chmielewski, D., Wilson, E. A., Pintilie, G., Zhao, P., Chen, M., Schmid, M. F., Simmons, G., Wells, L., Jin, J., Singharoy, A., Chiu, W.  
2023; 14 (1): 7175
- **CryoEM structures of the human CLC-2 voltage gated chloride channel reveal a ball and chain gating mechanism.** *bioRxiv : the preprint server for biology*  
Xu, M., Neelands, T., Powers, A. S., Liu, Y., Miller, S. D., Pintilie, G., Du Bois, J., Dror, R. O., Chiu, W., Maduke, M.  
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- **Diagnosing and treating issues in cryo-EM map-derived models.** *Structure (London, England : 1993)*  
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- **Snapshots of the second-step self-splicing of Tetrahymena ribozyme revealed by cryo-EM.** *Nature communications*  
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- **Integrated analyses reveal a hinge glycan regulates coronavirus spike tilting and virus infectivity.** *Research square*  
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- **Snapshots of the first-step self-splicing of Tetrahymena ribozyme revealed by cryo-EM.** *Nucleic acids research*  
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- **Structural visualization of the tubulin folding pathway directed by human chaperonin TRiC/CCT.** *Cell*  
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- **Electron microscopy holdings of the Protein Data Bank: the impact of the resolution revolution, new validation tools, and implications for the future.** *Biophysical reviews*  
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- **Topological crossing in the misfolded Tetrahymena ribozyme resolved by cryo-EM.** *Proceedings of the National Academy of Sciences of the United States of America*  
Li, S., Palo, M. Z., Pintilie, G., Zhang, X., Su, Z., Kappel, K., Chiu, W., Zhang, K., Das, R.  
2022; 119 (37): e2209146119
- **Three-dimensional structure-guided evolution of a ribosome with tethered subunits.** *Nature chemical biology*  
Kim, D. S., Watkins, A., Bidstrup, E., Lee, J., Topkar, V., Kofman, C., Schwarz, K. J., Liu, Y., Pintilie, G., Roney, E., Das, R., Jewett, M. C.  
2022
- **Cryo-EM analysis of Ebola virus nucleocapsid-like assembly.** *STAR protocols*  
Wang, Y., Binning, J. M., Pintilie, G. D., Chiu, W., Amarasinghe, G. K., Leung, D. W., Su, Z.  
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- **Cryo-EM, Protein Engineering, and Simulation Enable the Development of Peptide Therapeutics against Acute Myeloid Leukemia.** *ACS central science*  
Zhang, K., Horikoshi, N., Li, S., Powers, A. S., Hameedi, M. A., Pintilie, G. D., Chae, H., Khan, Y. A., Suomivuori, C., Dror, R. O., Sakamoto, K. M., Chiu, W., Wakatsuki, et al  
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- **Cryo-ET of Toxoplasma parasites gives subnanometer insight into tubulin-based structures.** *Proceedings of the National Academy of Sciences of the United States of America*  
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- **Molecular basis for ATPase-powered substrate translocation by the Lon AAA+ protease.** *The Journal of biological chemistry*  
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- **The N-terminus of varicella-zoster virus glycoprotein B has a functional role in fusion.** *PLoS pathogens*  
Oliver, S. L., Xing, Y. n., Chen, D. H., Roh, S. H., Pintilie, G. D., Bushnell, D. A., Sommer, M. H., Yang, E. n., Carfi, A. n., Chiu, W. n., Arvin, A. M.  
2021; 17 (1): e1008961
- **Cryo-EM structures of full-length Tetrahymena ribozyme at 3.1 Å resolution.** *Nature*  
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- **Resolving individual atoms of protein complex by cryo-electron microscopy.** *Cell research*  
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- **Publisher Correction: A glycoprotein B-neutralizing antibody structure at 2.8 Å uncovers a critical domain for herpesvirus fusion initiation.** *Nature communications*  
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- **A 3.4-Å cryo-EM structure of the human coronavirus spike trimer computationally derived from vitrified NL63 virus particles.** *bioRxiv : the preprint server for biology*  
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- **A 3.4-Å cryo-electron microscopy structure of the human coronavirus spike trimer computationally derived from vitrified NL63 virus particles.** *QRB discovery*  
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- **Cryo-EM and MD infer water-mediated proton transport and autoinhibition mechanisms of Vo complex.** *Science advances*  
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- **Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures.** *Nature methods*  
Kappel, K. n., Zhang, K. n., Su, Z. n., Watkins, A. M., Kladwang, W. n., Li, S. n., Pintilie, G. n., Topkar, V. V., Rangan, R. n., Zheludev, I. N., Yesselman, J. D., Chiu, W. n., Das, et al  
2020; 17 (7): 699–707
- **Structural basis of amino acid surveillance by higher-order tRNA-mRNA interactions.** *Nature structural & molecular biology*  
Li, S., Su, Z., Lehmann, J., Stamatopoulou, V., Giarimoglou, N., Henderson, F. E., Fan, L., Pintilie, G. D., Zhang, K., Chen, M., Ludtke, S. J., Wang, Y., Stathopoulos, et al  
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- **Segmentation and Comparative Modeling in an 8.6-angstrom Cryo-EM Map of the Singapore Grouper Iridovirus** *STRUCTURE*  
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Kappel, K., Zhang, K., Su, Z., Pintilie, G., Chiu, W., Das, R.  
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- **The Chaperonin TRiC/CCT Associates with Prefoldin through a Conserved Electrostatic Interface Essential for Cellular Proteostasis** *CELL*  
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- **Cryo-EM structures of Helicobacter pylori vacuolating cytotoxin A oligomeric assemblies at near-atomic resolution** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Zhang, K., Zhang, H., Li, S., Pintilie, G. D., Mou, T., Gao, Y., Zhang, Q., van den Bedeme, H., Schmid, M. F., Au, S., Chiu, W.  
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- **Coupling of ssRNA cleavage with DNase activity in type III-A CRISPR-Csm revealed by cryo-EM and biochemistry** *CELL RESEARCH*  
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- **Cryo-EM structures of Helicobacter pylori vacuolating cytotoxin A oligomeric assemblies at near-atomic resolution.** *Proceedings of the National Academy of Sciences of the United States of America*  
Zhang, K., Zhang, H., Li, S., Pintilie, G. D., Mou, T., Gao, Y., Zhang, Q., van den Bedem, H., Schmid, M. F., Au, S. W., Chiu, W.  
2019
- **Structure of Calcarisporiella thermophila Hsp104 Disaggregase that Antagonizes Diverse Proteotoxic Misfolding Events** *STRUCTURE*  
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2019; 27 (3): 449-+
- **Coupling of ssRNA cleavage with DNase activity in type III-A CRISPR-Csm revealed by cryo-EM and biochemistry.** *Cell research*  
Guo, M., Zhang, K., Zhu, Y., Pintilie, G. D., Guan, X., Li, S., Schmid, M. F., Ma, Z., Chiu, W., Huang, Z.  
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- **Outcomes of the Cryo-EM Map and Model Challenges**  
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- **Evolving Data Standards for cryo Electron Microscopy**  
Lawson, C. L., Kryshchak, A., Pintilie, G., Berman, H. M., Chiu, W.  
INT UNION CRYSTALLOGRAPHY.2019: A68

- **Cryo-EM structure of a 40 kDa SAM-IV riboswitch RNA at 3.7 Å resolution.** *Nature communications*  
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- **Structure of Calcarisporiella thermophila Hsp104 Disaggregase that Antagonizes Diverse Proteotoxic Misfolding Events.** *Structure (London, England : 1993)*  
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- **Comparison of Crystal and Cryoem Structures of Hsp104 and ClpB Disaggregases**  
Joachimiak, A., Michalska, K., Zhang, K., March, Z., Hatzos-Skintges, C., Pintilie, G., Bigelow, L., Castellano, L., Miles, L., Jackrel, M., Chuang, E., Jedrzejczak, R., Shorter, et al  
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- **The 3.5-Å CryoEM Structure of Nanodisc-Reconstituted Yeast Vacuolar ATPase Vo Proton Channel** *The 3.5-Å CryoEM Structure of Nanodisc-Reconstituted Yeast Vacuolar ATPase Vo Proton Channel*  
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- **Electron Cryo-microscopy Structure of Ebola Virus Nucleoprotein Reveals a Mechanism for Nucleocapsid-like Assembly** *Cell*  
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- **Resolution and Probabilistic Models of Components in CryoEM Maps of Mature P22 Bacteriophage** *BIOPHYSICAL JOURNAL*  
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