

Prof. Dr. Philip M. Kim

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Professional Experience

University of Toronto, Terrence Donnelly Center for Cellular and Biomolecular Research, Department of Molecular Genetics and Department of Computer Science

Professor (July 2019 – present)
Associate Professor with Tenure (July 2014 – June 2019)
Assistant Professor, Tenure-stream (January 2009 – June 2014)

Yale University, Department of Molecular Biophysics & Biochemistry (December 2004 - November 2008)
Postdoctoral Associate / Associate Research Scientist. Advisor: Professor Mark B. Gerstein

McKinsey & Company (August 2003 - November 2004)
Associate. Management consulting of high-tech and pharmaceutical companies

Education

Massachusetts Institute of Technology (August 1998 - February 2003)
Ph.D., Artificial Intelligence Laboratory and Program in Physical Chemistry.

University of North Carolina at Chapel Hill (September 1997 - May 1998)
Research Exchange Student, Graduate Program in Cellular and Molecular Biophysics

University of Tuebingen (October 1994 - August 1997)
Vordiplom in Physics (German equivalent to B.S.)
Vordiplom in Biochemistry (German equivalent to B.S.)

Teaching Experience

University of Toronto, Department of Molecular Genetics, Professional Masters Program in Medical Genomics (September 2018-present)
Developed and taught new class: “Biological Statistics”. Novel course that teaches both statistical concepts as well as programming in R to students from non-quantitative backgrounds that will then go on to become practitioners in medical genomics.

University of Toronto, Department of Molecular Genetics (September 2010-December 2010, September 2011-December 2011, September 2012-January 2013, March 2014-May 2014, September 2016-September 2018)
Developed and taught new class: “A practical course in programming for biologists”. Novel course that teaches programming in R and Python to students from non-quantitative backgrounds.

University of Toronto, Department of Molecular Genetics (September 2011-May 2015)
Coordinated graduate class: “Student Seminar Series”

University of Toronto, Donnelly Centre (January 2009-present)
Mentored a cumulative total of 16 postdoctoral fellows, 14 graduate students and 30 undergraduate students

Massachusetts Institute of Technology, Department of Chemistry (September 2001 - January 2002)
Head Teaching Assistant, Class: “5.60 Thermodynamics and Kinetics”

Funding

Currently held

Canada Institute for Health Research, Project Grant, 2019-2024, \$720,000 *from Sep 2019*
National Institutes of Health (NHGRI), RO1 Grant (Co-PI, subcontract with NYU), 2019-2024, total award \$1,700,000 (\$400,000 to Kim) *from Sep 2019*
Canada Institute for Health Research, Project Grant, 2018-2023, \$900,000
Canada Institute for Health Research, Project Grant (Co-PI), 2018-2023, total award \$1,400,000 (\$500,000 to Kim)
Canada Institute for Health Research, Project Grant, 2017-2022, \$700,000
Natural Science and Engineering Research Council, 2017-2022, Discovery Grant, \$130,000
EMD Serono (Merck Group), Sponsored Research Agreement, 2016-2019, \$200,000
National Institutes of Health (NHGRI), RO1 Grant (Co-PI, subcontract with NYU), 2016-2021, total award \$2,000,000 (\$600,000 to Kim)

Previous

Canadian Cancer Society Research Institute, Innovation Grant, 2017-2019, \$200,000
Canadian Cancer Society Research Institute, Innovation Grant, 2014-2016, \$200,000
Human Frontiers Science Program, Young Investigator Grant (Lead PI), 2013-2016, total award \$1,050,000
Canadian Cancer Society Research Institute, Innovation Grant (subcontract), 2013-2015, total award \$200,000 (\$60,000 to Kim)
Canada Institute for Health Research, Operating Grant, 2012-2017, \$662,586
Ontario Genomics Institute, SPARK Grant, 2012, \$50,000
Genome Canada (subcontract), 2011-2013, total award \$10,000,000 (\$200,000 to Kim)
Natural Science and Engineering Research Council, 2010-2016, Discovery Grant, \$130,000
Ontario Research Fund, Global Leadership in Genomics 2 (subcontract), 2010-2014, total award \$2,200,000 (\$250,000 to Kim)
Canada Foundation for Innovation, Leadership Opportunity Fund, 2010-2015, \$230,000
Startup Funds, University of Toronto, from 2009, \$450,000

Honors/Awards

Ontario Research Fund Early Researcher Award (\$100,000) 2012
Genome Technology "PI of tomorrow" Award 2012
Connaught Award 2009
Boehringer Ingelheim Fonds Ph.D. Fellow 2001-2003
Merck Graduate Fellow in Bioinformatics 1999-2001
Howard Hughes Medical Institute Predoctoral Fellowship (Honorable Mention) 1999
Recipient of a study abroad fellowship from the University of Tuebingen 1997-1998
Award for the best Chemistry Student from the German Chemical Industry 1993
3rd West-German Champion in Judo 1993, Competitor in the State Judo League 1993-1994

Professional Activities

Co-founder, Resolute Bio, Biotechnology startup aiming to develop novel peptide-based therapeutics. Raised \$2M in seed funding and \$5M in pre-series A funding.
Scientific Advisory Board Member of ProteinQure
Submitted 5 invention disclosures and 1 patent application (currently pending)

Grant review panel member, Canadian Cancer Research Society (CCSRI), Impact Panel, 2018
Grant review panel member, CCSRI, Innovation and Innovation to Impact Panel, 2018, 2019
Review panel member for Compute Canada Resource Allocation Competition 2018
Grant review panel member, for College of Medicine Research Awards, University of Saskatchewan 2018, 2019

Grant reviewer for *Natural Science and Engineering Research Council (Canada)*, *National Science Centre (Poland)*, *European Research Council*, *German Israeli Foundation*, *Canada Foundation for Innovation*, *Israeli Science Foundation*, *Fonds Wetenschappelijk Onderzoek (Flemish Science Foundation)*, *Agence Nationale de la Recherche (French National Research Agency)*, *Biotechnology and Biological Sciences Research Council*, *French National Research Agency (ANR)*, *Swiss National Fonds*, *Estonian Science Agency (ETIS)*, *National Science Centre (Poland)*

Editorial Board Member of *PLoS ONE*

Guest Editor for *PLoS Computational Biology*

Referee for *Nature Biotechnology*, *Nature Methods*, *Proceedings of the National Academy of Science*, *Genome Research*, *Genome Biology*, *Nucleic Acids Research*, *PLoS Computational Biology*, *Molecular Systems Biology*, *BMC Bioinformatics*, *Annual Review of Biochemistry*, *Pattern Recognition*, *Bioinformatics*, *Gene*, *Proteins*, *PLoS ONE*, *Protein Science*, *FEBS letters*, *Molecular and Cellular Proteomics*, *Molecular BioSystems*

Member of the Program Committee for BIOINFO 2019, ECCB 2016, ISMB/ECCB 2015, ECCB 2014, ISMB/ECCB 2013, ECCB 2012, ECCB 2010, ISMB/ECCB 2009, ISMB 2008, ISMB/ECCB 2007

Organizer of the PRD Specificity Prediction Challenge, DREAM4 2009

Publications (in press and published)

Strokach A, Corbi-Verge C, Kim PM. Predicting changes in protein stability caused by mutation using sequence- and structure-based methods in a CAG15 blind challenge. *Hum Mutat.* 2019 Jun 27. doi: 10.1002/humu.23852.

Savojarjo C, Petrosino M, Babbi G, Bovo S, **Corbi-Verge C**, Casadio R, Fariselli P, Folkman L, Garg A, Karimi M, Katsonis P, **Kim PM**, Lichtarge O, Martelli PL, Pasquo A, Pal D, Shen Y, **Strokach AV**, Turina P, Zhou Y, Andreoletti G, Brenner S, Chiaraluce R, Consalvi V, Capriotti E. Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAG15 challenge. *Hum Mutat.* 2019 Jun 17. doi: 10.1002/humu.23843.

Ichikawa DM, **Corbi-Verge C**, Shen MJ, Snider J, Wong V, Stagljjar I, **Kim PM#**, Noyes MB#. A Multireporter Bacterial 2-Hybrid Assay for the High-Throughput and Dynamic Assay of PDZ Domain-Peptide Interactions. *ACS Synth Biol.* 2019 Apr 18. doi: 10.1021/acssynbio.8b00499. [Epub ahead of print]

Garton M, Corbi-Verge C, Hu Y, **Nim S**, Tarasova N, Sherborne B, **Kim PM**. Rapid and accurate structure-based therapeutic peptide design using GPU accelerated thermodynamic integration. *Proteins.* 2019 Mar;87(3):236-244. doi:10.1002/prot.25644. Epub 2019 Jan 4.

Ben-David M, Huang H, **Sun MGF, Corbi-Verge C**, Petsalaki E, Liu K, Gfeller D, Garg P, Tempel W, Sochirca I, Shifman JM, Davidson A, Min J, **Kim PM**, Sidhu SS. Allosteric Modulation of Binding Specificity by Alternative Packing of Protein Cores. *J Mol Biol.* 2019 Jan 18;431(2):336-350. doi: 10.1016/j.jmb.2018.11.018. Epub 2018 Nov 22. PubMed PMID: 30471255.

Kataria M, Mouilleron S, **Seo MH, Corbi-Verge C, Kim PM**, Uhlmann F. A PxL motif promotes timely cell cycle substrate dephosphorylation by the Cdc14 phosphatase. *Nat Struct Mol Biol.* 2018 Dec;25(12):1093-1102. doi: 10.1038/s41594-018-0152-3.

Strokach A, Corbi-Verge C, Teyra J, Kim PM. Predicting the Effect of Mutations on Protein Folding and Protein-Protein Interactions. *Methods Mol Biol.* 2019;1851:1-17.

Seo MH, Kim PM. The present and the future of motif-mediated protein-protein interactions. *Curr Opin Struct Biol.* 2018 Jun;50:162-170. doi: 10.1016/j.sbi.2018.04.005

Garton M, Nim S, Stone T, Wang K, Deber C, **Kim PM**. A method to generate highly stable D-amino acid analogs of bioactive helical peptides using a mirror image of the entire PDB. *Proc Natl Acad Sci* 2018 Feb 13;115(7):1505-1510

Park SJ, Song S, Yang GS, **Kim PM**, Yoon S, Kim JH, Sung J. The Chemical Fluctuation Theorem governing gene expression. *Nat Commun*. 2018 Jan 19;9(1):297. doi: 10.1038/s41467-017-02737-0

Teyra J, Huang H, Jain S, Guan X, Dong A, Liu Y, Tempel W, Min J, Tong Y, **Kim PM**, Bader GD, Sidhu SS. Comprehensive Analysis of the Human SH3 Domain Family Reveals a Wide Variety of Non-canonical Specificities. *Structure*. 2017 Oct 3;25(10):1598-1610.e3. doi: 10.1016/j.str.2017.07.017. Epub 2017 Sep 7.

Garton M, **Sayadi M**, **Kim PM**. A computational approach for designing D-proteins with non-canonical amino acid optimised binding affinity. *PLoS One*. 2017 Nov 6;12(11):e0187524

Najafabadi HS, **Garton M**, Weirauch MT, Mnaimneh S, Yang A, **Kim PM**, Hughes TR. Non-base-contacting residues enable kaleidoscopic evolution of metazoan C2H2 zinc finger DNA binding. *Genome Biol*. 2017 Sep 6;18(1):167. doi: 10.1186/s13059-017-1287-y.

Sun MGF, **Kim PM**. Data driven flexible backbone protein design. *PLoS Comput Biol*. 2017 Aug 24;13(8):e1005722. doi: 10.1371/journal.pcbi.1005722.

Davey NE, **Seo MH**, Yadav VK, **Jeon J**, **Nim S**, Krystkowiak I, Blikstad C, **Dong D**, Markova N, **Kim PM***, Ivarsson Y*. Discovery of short linear motif-mediated interactions through phage display of intrinsically disordered regions of the human proteome. *FEBS J*. 2017 Feb;284(3):485-498. doi: 10.1111/febs.13995.

Seo MH, **Nim S**, **Jeon J**, **Kim PM**. Large-Scale Interaction Profiling of Protein Domains Through Proteomic Peptide-Phage Display Using Custom Peptidomes. *Methods Mol Biol*. 2017;1518:213-226.

Corbi-Verge C, **Garton M**, **Nim S**, **Kim PM**. Strategies to Develop Inhibitors of Motif-Mediated Protein-Protein Interactions as Drug Leads. *Annu Rev Pharmacol Toxicol*. 2017 Jan 6;57:39-60.

Sun MGF*, **Seo MH***, **Nim S**, **Corbi-Verge C**, **Kim PM**. Protein Engineering by Highly Parallel Screening of Computationally Designed Variants. *Science Advances* 2016 Vol. 2, no. 7, e1600692

Corbi-Verge C, **Kim PM**. Motif mediated protein-protein interactions as drug targets. *Cell Commun Signal*. 2016 Mar 2;14(1):8.

Nim S*, **Jeon CJ***, **Corbi C**, **Seo MH**, **Ivarsson Y**, Tarasova N, **Kim PM**. Highly parallel intracellular inhibition of protein-protein interactions identifies novel cancer drug leads. *Nature Chem Biol* 2016 Feb 22. doi: 10.1038/nchembio.2026

Na H, Laver JD, **Jeon J**, **Singh F**, Ancevicus K, Fan Y, Cao WX, Nie K, Yang Z, Luo H, Wang M, Rissland O, Westwood JT, **Kim PM**, Smibert CA, Lipshitz HD, Sidhu SS. A high-throughput pipeline for the production of synthetic antibodies for analysis of ribonucleoprotein complexes. *RNA*. 2016 Feb 4.

Garrido-Urbani S, Garg P, Ghossoub R, **Arnold R**, Lembo F, Sundell GN, **Kim PM**, Lopez M, Zimmermann P, Sidhu SS, Ivarsson Y. Proteomic peptide phage display uncovers novel interactions of the PDZ1-2 supramodule of syntenin. *FEBS Lett*. 2016 Jan;590(1):3-12. doi: 10.1002/1873-3468.12037

Witvliet D, **Strokach A**, **Giraldo AF**, **Teyra J**, **Colak RA**, **Kim PM**. ELASPIC web-server: proteome-wide structure based prediction of mutation effects on protein stability and binding affinity. *Bioinformatics* 2016 Jan 21. pii: btw031

Colak RA, **Kim TH**, Kazan H, **Oh Y**, Cruz M, Valladares A, Peralta J, Escobedo J, Parra E, **Kim PM***, Goldenberg A#. JBASE: Joint Bayesian Analysis of Sub-phenotypes and Epistasis. *Bioinformatics* 2016 Jan 15;32(2):203-10

Garton M, Najafabadi HS, Schmitges FW, Radovani E, Hughes TR, **Kim PM**. Breaking the C2H2 recognition code enigma: a structural approach reveals the influence of neighbor context on DNA binding specificity. *Nucleic Acids Res* 2015 Oct 30;43(19):9147-57

Jeon CJ, Singh F, Braun T, Arnold R, Teyra J, Kim PM. PAT: predictor for structured units and its application for the optimization of target molecules for the generation of synthetic antibodies. *BMC Bioinformatics* 2016 Apr 1;17:150

Hao Y*, Colak R*, Teyra J*, Corbi-Verge C, Ignatchenko A, Hahne H, Wilhelm M, Kuster B, Braun P, Kaida D, Kislinger T, **Kim PM.** Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. *Cell Rep.* 2015 Jul 14;12(2):183-9. doi: 10.1016/j.celrep.2015.06.031.

Najafabadi HS, Mnaimneh S, Schmitges FW, **Garton M,** Lam KN, Yang A, Albu M, Weirauch MT, Radovani E, **Kim PM,** Greenblatt J, Frey BJ, Hughes TR. C2H2 zinc finger proteins greatly expand the human regulatory lexicon. *Nature Biotechnol.* 2015 May;33(5):555-62.

Berliner N*, Teyra J*, Colak R*, Garcia Lopez S, Kim PM. Combining structural modeling with ensemble machine learning to accurately predict stability effects of mutations on protein stability and protein-protein interactions. *PLoS ONE* 2014 Sep 22;9(9):e107353.

Jeon J, Nim S, Teyra J, Datti A, Wrana JL, Sidhu SS, Moffat J, **Kim PM.** Integrated prediction and in vivo validation of novel cancer drug targets. *Genome Medicine* 2014 Jul 30;6(7):57

Babu M*, **Arnold R***, Bundalovic-Torma C, Gagarinova A, Wong KS, Phanse S, Kumar A, Wagih O, Krunal L, Samanfar B, Stewart G, Graham C, Aoki H, Brown E, Golshani A, **Kim P,** Moreno-Hagelsieb G, Greenblatt J, Houry WA, Parkinson J, Emili A. Quantitative genome-wide genetic interaction screens reveal the global functional organization of soluble protein complexes in *Escherichia coli*. *PLoS Genetics* 2014 Feb 20;10(2):e1004120

van der Lee R, Buljan M, Daughdrill G, Dunker K, Fuxreiter M, Gough J, Gsponer J, Jones D, **Kim PM,** Kriwacki R, Lang B, Pappu R, Tompa P, Uversky V, Wright P, Babu MM. Classification of Intrinsically Disordered Regions and Proteins. *Chemical Reviews* 2014 Jul 9;114(13):6589-631.

Abu-Odeh M, Bar-Mag T, Huang H, **Kim T,** Salah Z, Abdeen SK, Sudol M, Reichmann D, Sidhu S, **Kim PM,** Aqeilan RI. Characterizing WW Domain Interactions of Tumor Suppressor WWOX Reveals its Association with Multiprotein Networks. *J Biol Chem.* 2014 Mar 28;289(13):8865-80

Ivarsson Y, Arnold R, McLaughlin M, **Nim S,** Joshi R, Ray D, Liu B, **Teyra J,** Pawson T, Moffat J, Li S, Sidhu SS, **Kim PM.** Proteomic peptide phage display: large scale interaction profiling using human and viral phage peptidomes. *Proc Natl Acad Sci.* 2014 Feb 18;111(7):2542-7

Chen C, Ha BH, Thévenin AF, Lou HJ, Zhang R, Yip KY, Peterson JR, Gerstein M, **Kim PM,** Filippakopoulos P, Knapp S, Boggon TJ, Turk BE. Identification of a major determinant for serine-threonine kinase phosphoacceptor specificity. *Mol Cell.* 2014 Jan 9;53(1):140-7

Vizeacoumar FJ, **Arnold R,** Vizeacoumar FS, Chandrashekar M, Buzina A, Young JT, Kwan JH, Sayad A, Mero P, Lawo S, Tanaka H, Brown KR, Baryshnikova A, Mak AB, Fedyshyn Y, Wang Y, Brito GC, Kasimer D, Makhnevych T, Ketela T, Datti A, Babu M, Emili A, Pelletier L, Wrana J, Wainberg Z, **Kim PM,** Rottapel R, O'Brien CA, Andrews B, Boone C, Moffat J. A negative genetic interaction map in isogenic cancer cell lines reveals cancer cell vulnerabilities. *Mol Syst Biol.* 2013 Oct 8;9:696. doi: 10.1038/msb.2013.54.

Colak R*, Kim T*, Michaut M, **Sun MFG,** Irimia M, Bellay J, Myers CL, Blencowe BJ, **Kim PM.** Distinct types of disorder in the human proteome: functional implications for alternative splicing. *PLoS Comp Biol* 2013 Apr;9(4):e1003030

Teyra J, Kim PM. Interpreting protein networks with three-dimensional structures. *Nat Methods.* 2013 Jan;10(1):43-4.

Barbosa-Morais NL, Irimia M, Pan Q, Xiong HY, Gueroussov S, Lee LJ, Slobodeniuc V, Kutter C, Watt S, **Colak R**, **Kim T**, Misquitta-Ali CM, Wilson MD, **Kim PM**, Odom DT, Frey BJ, Blencowe BJ. The evolutionary landscape of alternative splicing in vertebrate species. *Science*. 2012 Dec 21;338(6114):1587-93

Arnold R, **Boonen K**, **Sun MG**, **Kim PM**. Computational analysis of interactomes: current and future perspectives for bioinformatics approaches to model the host-pathogen interaction space. *Methods*. 2012 Aug;57(4):508-18

Ellis JD*, Barrios-Rodiles M*, **Colak R***, Irimia M, **Kim TH**, Calarco JA, Wang X, Pan Q, O'hanlon D, **Kim PM#**, Wrana JL#, Blencowe BJ#. Tissue-specific alternative splicing remodels protein-protein interaction networks. *Mol Cell* 2012 Jun 29;46(6):884-92

Arnold R, **Boonen K**, **Sun MFG**, **Kim PM**. Computational analysis of interactomes: Current and future perspectives for bioinformatics approaches to model the host-pathogen interaction space. *Methods* 2012 Aug;57(4):508-18

Teyra J, **Sidhu SS**, **Kim PM**. Elucidation of the binding preferences of peptide recognition modules: SH3 and PDZ domains. **FEBS Lett**. 2012 Jun 9. [Epub ahead of print]

Hooda Y, **Kim PM**. Computational structural analysis of protein interactions and networks. **Proteomics**. 2012 May;12(10):1697-705. doi: 10.1002/pmic.201100597.

Sun MFG*, **Sikora M***, Costanzo M, Boone C, **Kim PM**. Network Evolution: Rewiring and Signatures of Conservation in Signaling. *PLoS Comp. Biol.* 2012 Mar;8(3):e1002411

Bellay J, **Michaut M**, **Kim TH**, **Han S**, **Colak R**, Myers CL, **Kim PM**. An Omics Perspective on Protein Disorder. *Molecular Biosystems* 2012 Jan 1;8(1): 185-93

Kim TH, **Tyndel M**, Bader GD, Gfeller D#, **Kim PM#**. MUSI: An integrated system to identify multiple specificity in large peptide or nucleotide data sets. *Nucleic Acids Research* 2011 Dec 30

Yip KY*, **Utz L***, **Sitwell S**, Turk BE, Gerstein MB#, **Kim PM#**. Identification of Specificity Determining Residues in Peptide Recognition Domains using an Information Theoretic Approach Applied to Large-Scale Binding Maps. *BMC Biology* 2011, 9:53

Sun MFG, **Kim PM**. Evolution of Biological Networks. *Genome Biology* 2011 Dec 28;12(12):235

Gfeller D, Butty F, Wierzbicka M, Verschueren E, Vanhee P, Huang H, Ernst A, **Dar N**, Stagljar I, Serrano L, Sidhu SS, Bader GD, **Kim PM**. The multiple-specificity landscape of modular peptide recognition domains. *Mol Syst Biol*. 2011 Apr 26;7:484.

Bellay J, Atluri G, Sing TL, Toufighi K, Costanzo M, Ribeiro PS, Pandey G, Baller J, Vandersluis B, Michaut M, Han S, **Kim P**, Brown GW, Andrews BJ, Boone C, Kumar V, Myers CL. Putting genetic interactions in context through a global modular decomposition. *Genome Res*. 2011 Aug;21(8):1375-87.

Fasolo J, Sboner A, **Sun MG**, Yu H, Chen R, Sharon D, **Kim PM**, Gerstein M, Snyder M. Diverse protein kinase interactions identified by protein microarrays reveal novel connections between cellular processes. *Genes Dev*. 2011 Apr 1;25(7):767-78.

Bellay J, **Han S**, Michaut M, **Kim T**, Costanzo M, Andrews BJ, Boone C, Bader GD, Myers CL, **Kim PM**. Bringing order to protein disorder through comparative genomics and genetic interactions. *Genome Biol*. 2011 Feb 16;12(2):R14.

Shou C, Bhardwaj N, Lam HY, Yan KK, **Kim PM**, Snyder M, Gerstein MB. Measuring the evolutionary rewiring of biological networks. *PLoS Comput Biol*. 2011 Jan 6;7(1):e1001050.

Bhardwaj N, **Kim PM**#, Gerstein MB#. Rewiring of transcriptional regulatory networks: hierarchy, rather than connectivity, better reflects the importance of regulators. *Sci Signal*. 2010 Nov 2;3(146):ra79. [# joint corresponding author]

Ernst A, Gfeller D, Kan Z, Seshagiri S, **Kim PM**, Bader GD, Sidhu SS. Coevolution of PDZ domain-ligand interactions analyzed by high-throughput phage display and deep sequencing. *Mol Biosyst*. 2010 Oct;6(10):1782-90.

Lam HY, **Kim PM**, Mok J, Tonikian R, Sidhu SS, Turk BE, Snyder M, Gerstein MB. MOTIPS: automated motif analysis for predicting targets of modular protein domains. *BMC Bioinformatics*. 2010 May 11;11:243.

Mok J, **Kim PM**, Lam HYK, Piccirillo S, Zhou X, Jeschke GR, Sheridan DL, Parker SA, Desai V, Jwa M, Camerone E, Niu H, Good M, Remenyi A, Ma JLN, Sheu YJ, Sassi HE, Sopko R, Chan CSM, De Virgilio C, Hollingsworth NM, Lim WA, Stern DF, Stillman B, Andrews BJ, Gerstein MB, Snyder M, Turk B. Deciphering protein kinase specificity through large-scale analysis of yeast phosphorylation motifs. *Sci. Signaling* (2010) Feb 16;3(109):ra12.

Han SJ, Kim PM. Chaperonin activity modulates codon adaptation. *Mol. Syst. Biol.* (2010);6:342. Epub 2010 Jan 19

Costanzo M*, Baryshnikova A*, Bellay J, Kim Y, Spear ED, Sevier SD, Ding H, Koh JLY, Toufighi K, Mostafavi S, **Prinz J**, St. Onge R, Vandersluis B, Alizadeh S, Bahr S, Brost RL, Chen Y, Cokol M, Deshpande R, Li Z, Li ZY, Liang W, Marback M, Paw J, San Luis BJ, Shuteriqi E, Hin A, Tong AHY, van Dyk N, Wallace IM, Whitney JA, Weirauch MT, Zhong G, Zhu H, Houry W, Brudno M, Ragibizadeh S, Papp B, Roth FP, Giaever G, Nislow C, Troyanskaya OG, Bussey H, Bader GD, Gingras AC, Morris QD, **Kim PM**, Kaiser CK, Myers CM, Andrews B, Boone C. The Genetic Landscape of the Cell. *Science* (2010) Jan 22;327(5964):425-31.

Lam HYK*, Mu XJ*, Tanzer A, Stuetz A, Snyder M, **Kim PM**, Korbel JO, Gerstein MB. BreakSeq: Mining a breakpoint library rapidly identifies structural variants in personal genomes and reveals biases in their formation. *Nature Biotech.* (2010) Jan;28(1):47-55. Epub 2009 Dec 27

Tonikian R*, Xin X*, Toret CP*, Gfeller D, Landgraf C, Panni S, Paoluzi S, Castagnoli L, Currell B, Seshagiri S, Yu H, Winsor B, Vidal M, Gerstein MB, Bader GD, Volkmer R#, Cesareni G#, Drubin DG#, **Kim PM**#, Sidhu SS#, Boone C#. Bayesian modeling of the yeast SH3 domain interactome predicts spatiotemporal dynamics of endocytosis proteins. *PLoS Biology* 2009 Oct;7(10):e1000218. [#joint corresponding author]

Yip KY, **Kim PM**, McDermott D, Gerstein MB. Multi-level Learning: Improving the Prediction of Protein, Domain and Residue Interactions by Allowing Information Flow between Levels. *BMC Bioinformatics* 2009 Aug 5;10:241.

Alexander RP, **Kim PM**, Emonet T, Gerstein MB. Understanding modularity in molecular networks requires dynamics. *Science Signal*. 2009 Jul 28;2(81):pe44.

Kim PM*, Lam HY*, Urban AE, Korbel JO, Affourtit J, Grubert F, Chen X, Weissman S, Snyder M, Gerstein MB. Analysis of copy number variants and segmental duplications in the human genome: Evidence for a change in the process of formation in recent evolutionary history. *Genome Res*. 2008 18(12):1865-74.

Hasin Y, Olender T, Khen M, Gonzaga-Jauregui C, **Kim PM**, Urban AE, Snyder M, Gerstein MB, Lancet D, Korbel JO. High-resolution copy-number variation map reflects human olfactory receptor diversity and evolution. *PLoS Genet*. 2008 Nov;4(11):e1000249.

Korbel JO*, **Kim PM***, Chen X, Urban AE, Weissman S, Snyder M, Gerstein MB. The current excitement about copy-number variation: how it relates to gene duplications and protein families. *Curr Opin Struct Biol*. 2008 Jun;18(3):366-74.

Kim PM*, Sboner A*, Xia Y, Gerstein M. The role of disorder in interaction networks: a structural analysis. *Mol Syst Biol*. 2008;4:179.

Kim PM*, Korbel JO*, Gerstein MB. Positive selection at the protein network periphery: evaluation in terms of structural constraints and cellular context. *Proc Natl Acad Sci U S A*. 2007 Dec 18;104(51):20274-9.

Yip KY, Patel P, **Kim PM**, Engelman DM, McDermott D, Gerstein M. An integrated system for studying residue coevolution in proteins. *Bioinformatics*. 2008 Jan15;24(2):290-2.

Korbel JO, Urban AE, Affourtit JP, Godwin B, Grubert F, Simons JF, **Kim PM**, Palejev D, Carriero NJ, Du L, Taillon BE, Chen Z, Tanzer A, Saunders AC, Chi J, Yang F, Carter NP, Hurles ME, Weissman SM, Harkins TT, Gerstein MB, Egholm M, Snyder M. Paired-end mapping reveals extensive structural variation in the human genome. *Science*. 2007 Oct 19;318(5849):420-6.

Lu LJ, Sboner A, Huang YJ, Lu HX, Gianoulis TA, Yip KY, **Kim PM**, Montelione GT, Gerstein MB. Comparing classical pathways and modern networks: towards the development of an edge ontology. *Trends Biochem Sci*. 2007 Jul;32(7):320-31.

Yu H*, **Kim PM***, Sprecher E, Trifonov V, Gerstein M. The importance of bottlenecks in protein networks: correlation with gene essentiality and expression dynamics. *PLoS Comput Biol*. 2007 Apr 20;3(4):e59.

Kim PM, Lu LJ, Xia Y, Gerstein MB. Relating three-dimensional structures to protein networks provides evolutionary insights. *Science*. 2006 Dec 22;314(5807):1938-41.

Yip KY, Yu H, **Kim PM**, Schultz M, Gerstein M. The tYNA platform for comparative interactomics: a web tool for managing, comparing and mining multiple networks. *Bioinformatics*. 2006 Dec 1;22(23):2968-70.

Kim PM, Tidor B. Limitations of quantitative gene regulation models: a case study. *Genome Res*. 2003 Nov;13(11):2391-5.

Kim PM, Tidor B. Subsystem identification through dimensionality reduction of large-scale gene expression data. *Genome Res*. 2003 Jul;13(7):1706-18.

Invited and Refereed Talks

American Peptide Symposium, Monterey, CA, USA, June 2019

Alchemical Free Energy Workshop*, Goettingen, Germany, May 2019

Yale University, Department of Pharmacology, New Haven, CT, USA, April 2019

Protein Engineering Summit, Boston, MA, USA, April 2019

Winter Quantitative Biology*, Ko Olina, HI, USA, February 2019

Workshop on Single Cell and Massively Parallel Approaches, Holetown, Barbados, January 2019

International Peptide Symposium*, Kyoto, Japan, December 2018

Keynote, Protein Engineering Summit Europe, Lisbon, Portugal, November 2018

Boulder Peptide Symposium, Boulder*, CO, USA, September 2018

EMBO Workshop on Modularity of Signaling Proteins and Networks*, Seefeld, Austria, September 2018

Basic and Life Sciences, Cavtat, Croatia, June 2018

Protein Engineering Canada, Vancouver, BC, Canada, June 2018

Helmholtz Zentrum Seminar, Munich, Germany, May 2018

Seoul Forum on Systems and Synthetic Biology of ARS, Seoul, Korea, May 2018

UCLA Structural Biology Seminar / Octant Bio, Los Angeles, CA, USA, May 2018

Winter Quantitative Biology*, Wailea, HI, USA, February 2018

Keynote, PepTalk: the Protein Science Week, San Diego, CA, USA, January 2018

Canadian Cancer Research Conference, Vancouver, BC, Canada, November 2017

University of Toronto, Cell and Systems Biology, September 2017

Advances in Biomedical Research, Medils, Split, Croatia, July 2017

Merck Research Laboratories, Kenilworth, NJ, USA, May 2017

Winter Quantitative Biology*, Kauai, HI, USA, February 2017

Technical University of Munich, Munich, Germany, December 2016

Computational Drug Development, Boston, MA, USA, December 2016

Canceromatics Conference, CNIO (Spanish National Cancer Centre), Madrid, Spain, November 2016
Rockefeller University, Center for Physics and Biology, New York, NY, USA, October 2016
EMBO Seefeld Workshop on Modules*, Seefeld in Tirol, Austria, September 2016
KCS Symposium, Busan, Korea, July 2016
RWTH Aachen, Aachen, Germany, April 2016
McGill Barbados Workshop on Cellular Adaptation, Holetown, Barbados, April 2016
Bioprocess International Conference, Oakland, CA, USA, March 2016
Universität Köln, Köln, Germany, February 2016
Keynote, PepTalk: the Protein Science Week, San Diego, CA, USA, January 2016
International Conference on Systems Biology, Singapore, November 2015
Yonsei University, Department of Biotechnology, Seoul, Korea, November 2015
Keynote, BIOINFO 2015, Seoul, Korea, October 2015
Chung-Ang University, Department of Chemistry, Seoul, Korea, October 2015
Daegu Gyeongbuk Institute of Science and Technology, Daegu, Korea, October 2015
Chinese University of Hong Kong, Hong Kong SAR, China, September 2015
Ludwig Maximilians Universität München, München, Germany, September 2015
Seoul National University, Department of Chemistry, Seoul, Korea, September 2015
Merrimack Pharmaceuticals, Cambridge, MA, USA, May 2015
Protein Engineering and Antibody Summit, Boston, MA, USA, May 2015
Meeting on Systems Biology: Networks, Cold Spring Harbor Laboratory, New York, USA, March 2015
Centre for Integrative Genomics, Universite Lausanne, Lausanne, Switzerland, February 2015
Max-Delbrueck Centrum Berlin, Berlin, Germany, January 2015
Charite Berlin Comprehensive Cancer Center, Berlin, Germany, January 2015
Universitaet Duesseldorf, Institut fuer Neuropathologie, Duesseldorf, Germany, January 2015
Artificial Intelligence in Medicine Retreat, Toronto, ON, Canada, November 2014
GTC Protein Summit, Boston, MA, October 2014
BPS Conference on Disordered Motifs, Dublin, Ireland, October 2014
SUNY Stony Brook, Stony Brook, NY, USA, Laufer Center for Systems Biology, September 2014
Uppsala Universitet, Uppsala, Sweden, BMC Department of Chemistry, September 2014
Gordon Research Conference on Intrinsically Disordered Proteins, Easton, MA, July 2014
Society for Molecular Biology and Evolution Annual Conference, San Juan, Puerto Rico, June 2014
University of Munich, Munich, Germany, February 2014
GTC Protein Summit, San Diego, CA, USA, October 2013
Shanghai Tech University, Shanghai, China, October 2013
Conference of the Society for Bioinformatics of the Nordic Countries, Torun, Poland, June 2013
Keynote, Symposium on Cellular Dynamics of Macromolecular Complexes, Montreal, Quebec, June 2013
International Workshop on Complexity in Quantitative Biology, Pohang, South Korea, February 2013
Immunotherapy Conference 2012, Havana, Cuba, November 2012
NGS Bioinformatics Conference, Chennai, India, November 2012
ECCB 2012 Highlight Talk*, Basel, Switzerland, September, 2012
University of California at San Francisco, Department of Bioengineering, San Francisco, CA, July 2012
Biomathematics and Statistics Symposium, University of Guelph, June 2012
Indiana University Purdue University, Center for Computational Biology and Bioinformatics, March 2012
Universite Libre Brussels, Department of Computer Science, February 2012
Gene Regulation Workshop, Holetown, Barbados, January 2012
GIW / KSSB 2012, Busan, Korea, December 2011
Yonsei University, Department of Biotechnology, Seoul, Korea, December 2011
New York University, Center for Genomics and Systems Biology, New York, NY, October 2011
FEBS Workshop on Modular Protein Domains and Networks in Disease*, Seefeld, Austria, September 2011
ISMB/ECCB 2011 Highlight Talk*, Vienna, Austria, July 2011
University of Vienna, Department of Computational Systems Biology, Vienna, Austria, July 2011
Winter School in Computational Biology, Brisbane, Queensland, Australia, June 2011
ESF-EMBO Conference on Protein Interactions*, Costa Brava, Spain, November 2010
Systems Biology and New Sequencing Tech, Center for Genomic Regulation, Barcelona, Spain, May 2010
Dialogue on Reverse Engineering Assessment and Methods (DREAM 4), Broad Institute of MIT and Harvard, Cambridge, MA, December 2009

FEBS Workshop on Modular Protein Domains in Disease*, Seefeld, Austria, September 2009
Genome Biology and Bioinformatics Retreat, Toronto, ON, May 2009
University of Toronto, Department of Molecular Genetics, Toronto, ON, March 2009
Korean Conference on Systems Biology and Bioinformatics, Cheongju, Korea, November 2008
University of Cambridge, Department of Biochemistry, Cambridge, UK, July 2008
National University of Singapore, Department of Biochemistry, Singapore, May 2008
University of Toronto, Terrence Donnelly Centre for Cellular and Biomolecular Research, Toronto, ON, May 2008
University of California Davis, Department of Computer Science, Davis, CA, May 2008
Spanish National Cancer Research Center (CNIO), Madrid, Spain, April 2008
Scripps Research Institute, San Diego, CA, April 2008
Fred Hutchinson Cancer Research Center, Seattle, WA, March 2008
Carnegie-Mellon University, Lane Center for Computational Biology, Pittsburgh, PA, March 2008
University of California Irvine, Department of Computer Science, Irvine, CA, March 2008
University of Maryland, Department of Bioengineering, College Park, MD, February 2008
Universitaet Duesseldorf, Fakultae fuer Informatik, Duesseldorf, Germany, February 2008
Wellcome Trust Sanger Institute, Hinxton, Cambridge, UK, February 2008
EMBL-EBI, Hinxton, Cambridge, UK, February 2008
Max Planck Institutes Selection Symposium, Berlin, Germany, February 2008
University of California Davis, Genome Center, Davis, CA, January 2008
Georgia Institute of Technology, School of Biology, Atlanta, GA, January 2008
EMBL/CRG, Systems Biology Unit, Barcelona, Spain, January 2008
University of Pennsylvania, Department of Biology, Philadelphia, PA, January 2008
Institute for Molecular Bioscience, University of Queensland, Brisbane, Australia, December 2007
Munich Information Center for Protein Sequences (MIPS), Munich, Germany, November 2007
University of Munich, Fakultae fuer Informatik, Mathematik und Statistik, Munich, Germany, November 2007
Memorial Sloan-Kettering Cancer Center, Computational Biology Seminar, New York, NY, November 2007
FEBS Workshop on Modular Protein Domains*, Seefeld, Austria, September 2007
ISMB/ECCB 2007 Highlight Talk*, Vienna Austria, July 2007
Biopathways SiG (ISMB 2007), Vienna, Austria, July 2007
ZBSA Research Seminar, Freiburg, Germany, July 2007
Boehringer Ingelheim Fonds Meeting, Woods Hole, MA, September 2006
German Conference on Bioinformatics, Tuebingen, Germany, September 2006
NSF Workshop on Mechanisms of Cellular Networks, Telluride, CO, August 2006
Yeast Genetics and Molecular Biology Meeting*, Princeton, NJ, July 2006
Yale Center for Structural Biology Seminar, New Haven, CT, February 2006
ERATO Kitano Center for Systems Biology, Tokyo, Japan, August 2004
SONY Computer Science Laboratories, Tokyo, Japan, August 2004
Institut Pasteur, Paris, France, August 2004

*denotes refereed talk