

Nir London

Curriculum Vitae



Personal details

Name: Nir London
Date of birth: 27.09.1982
E-mail: nir.london@weizmann.ac.il

Research appointments

- 2015-Current: Senior Scientist (Assistant professor)
Dept. of Organic Chemistry, The Weizmann Institute of Science, Rehovot, Israel.
- 2012-2015: EMBO Post-doctoral fellow
Dept. of pharmaceutical chemistry, University of California, San Francisco.
- Laboratory of Prof. Brian Shoichet
 - Topic: Development and application of a covalent probes discovery platform
 - Methods: Computational docking, Enzymology assays, Protein crystallography

Education

- 2007-2011: Ph.D. The Hebrew University, Jerusalem, Israel
Dept. of Microbiology & Molecular Genetics, Hadassah Medical School.
- Laboratory of Prof. Ora Schueler-Furman
 - Title: "Understanding, modeling and manipulating protein-peptide interactions".
- 2006-2007: M.Sc. The Hebrew University, Jerusalem, Israel.
The Integrated Program for Computer Sciences and Computational Biology
- Title: "Learning the energy landscapes of protein-protein interactions".
 - Avg.: 96.5, **direct PhD program**.
- 2003-2006: B.Sc. The Hebrew University, Jerusalem, Israel.
The Integrated Program for Computer Sciences and Computational Biology
- Avg.: 94.5, **magna cum laude**.

Awards and Scholarships

- 2013: Program for Breakthrough Biomedical Research post-doctoral Award (\$15,000)
- 2012-2014: EMBO long term post-doctoral fellowship (\$150,000)
- 2011: The International Dimitris N. Chorafas Foundation Award
- 2011: Chorev award. By the Israeli Chemical Society, Med. Chem. Section
- 2009-2011: Converging Technologies Fellowship for PhD studies
- 2010: Travel fellowship – The Hebrew University Research Authority
- 2009: 12th Israeli Bioinformatics Symp. - Outstanding student poster award
- 2006: Fellowship for ECCB'06 (sponsored by the Stein Donor)
- 2006-2007: Rector's Scholarship for M.Sc. students
- 2003, 2004: Dean's honor list

Participation at Conferences

Invited Talks:

- 2014: EMBO fellows meeting – USA
Covalent Docking of Large Libraries for the Discovery of Chemical Probes.
- 2014: Rosetta Conference – USA
Covalent Docking of Large Libraries for the Discovery of Chemical Probes.
- 2013: The joint Israeli/Polish/Ukrainian Biochemical Society conference – Israel
Covalent Docking of Large Libraries for the Discovery of Chemical Probes.
- 2013: Enzyme Function Initiative Meeting – USA
Computational approaches for HAD function prediction.
- 2011: The Israeli Society for Medicinal Chemistry Conference – Israel
Towards the computational design of peptide drugs.
- 2011: Pfizer, San Diego, USA
Computational modeling of peptide-protein interactions.
- 2010: Rosetta Conference – USA
Mapping the 'Farnesylome' - Structure-based Prediction of FTase Targets.
- 2009: Sudarsky Center for Computational Biology meeting – Israel
Paying the Entropic Cost, Peptides and Proteins In a Bind.
- 2008: Molecular Perspectives on Protein-Protein Interactions – Croatia
FunHunt - Model selection based on Rosetta energy landscape characteristics.
- 2008: Rosetta Conference – USA
OF rescuing MICE AND MEN: Structure-based computational design of superantigen inhibitors.
- 2007: Rosetta Conference – USA
New applications for "FunHunt" - the discriminator of energy funnels.

Posters:

- 2014: Biophysical Society meeting – USA
- 2013: Enzyme Function Initiative meeting – USA
- 2012: EMBO USA Fellows meeting – USA
- 2012: Enzyme Function Initiative meeting - USA
- 2010: 2nd Molecular Perspectives on Protein-Protein Interactions – Spain
- 2010: 13th Israeli Bioinformatics Symposium – Israel
- 2010: Capri Meeting – Spain
- 2010: Institute of Medical Research Israel-Canada meeting - Israel
- 2009: Rosetta Conference – USA
- 2009: 12th Israeli Bioinformatics Symposium – Israel
- 2008: EMBO practical docking workshop – Spain
- 2007: European Conference on Computational Biology – Israel
- 2006: 9th Israeli Bioinformatics Symposium – Israel
- 2006: Rosetta Conference – USA

Teaching

- 2009-2011: Teaching assistant. Computational Structural Biology Workshop. (A new course we constructed *de-novo*. Supervised 10 x 3h exercise sessions)
- 2014: Mentored rotation student at the Shoichet Lab: Norah Liang
- 2008-2011: Mentored rotation students at the Furman Lab: Michal Sperber, Lior Zimmerman, Avital Klein, Matan Kubovsky, Asya Frumkin

Military service

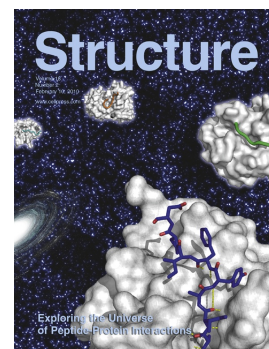
- 2000-2002: Intelligence corps.

Peer-reviewed research papers

1. **London N***, Miller RM*, Krishnan S*, Uchida K, Irwin JJ, Eidam O, Gibold L, Cimermančič P, Bonnet R, Shoichet BK, Taunton J (2014) Covalent docking of large libraries for the discovery of chemical probes. **Nature Chemical Biology**. 10(12):1066-72
doi:10.1038/nchembio.1666 [PMID: 25344815] *Featured on the cover.
2. **London N**, Farelli JD, Brown SD, Liu C, Huang H, Korczynska M, Al-Obaidi NF, Babbitt PC, Almo SC, Allen KN, Shoichet BK (2014) Covalent docking predicts substrates for Haloalkanoate Dehalogenase phosphatases. **Biochemistry**. DOI: 10.1021/bi501140k [PMID: 25513739]
3. Dong GQ, Calhoun S, Fan H, Kalyanaraman C, Branch MC, Mashiyama ST, **London N**, Jacobson MP, Babbitt PC, Shoichet BK, Armstrong RN, Sali A (2014) Prediction of substrates for glutathione transferases by covalent docking. **J Chem Inf Model**. 23;54(6):1687-99 [PMID: 24802635]
4. Gao M*, **London N***, Cheng K, Tamura R, Jin J, Schueler-Furman O, Yin H (2014) Rationally Designed Macrocyclic Peptides as Synergistic Agonists of LPS-Induced Inflammatory Response. **Tetrahedron**. DOI: 10.1016/j.tet.2014.07.026
5. Wexselblatt E, Oppenheimer-Shaanan Y, Kaspy I, **London N**, Schueler-Furman O, Yavin E, Glaser G, Katzhendler J, Ben-Yehuda S. (2012) Relacin, a novel antibacterial agent targeting the Stringent Response. **PLoS Pathog**. 8(9):e1002925 [PMID: 23028324]
6. **London N**, Gullá S, Keating AE, Schueler-Furman O. (2012) In Silico and in Vitro Elucidation of BH3 Binding Specificity toward Bcl-2. **Biochemistry**. 24;51(29):5841-50. [PMID: 22702834] *Highlighted on the journal's homepage.
7. Fleishman SJ, ... **London N**, ... (92 authors) ... Baker D. (2011) Community-wide assessment of protein-interface modeling suggests improvements to design methodology. **J Mol Biol**. 25;414(2):289-302. [PMID: 22001016]
8. **London N**, Hougland JL, Lamphear CL, Fierke CA and Schueler-Furman O (2011). Identification of a novel class of Farnesylation targets by structure-based modeling of binding specificity. **PLoS Comp. Biol**. 7(10):e1002170. [PMID: 21998565] *Selected post publication for oral presentation in ISMB 2012 (Long Beach, USA) Highlights track.
9. **London N**, Raveh B, Cohen E, Fathi G, Schueler-Furman O (2011). Rosetta FlexPepDock Web Server - High Resolution Modeling of Peptide-Protein Interactions. **NAR**. (Web Server issue):W249-53. [PMID: 21622962]
10. Raveh B, **London N**, Zimmerman L, Schueler-Furman O (2011). Rosetta FlexPepDock ab-initio: Simultaneous Folding, Docking and Refinement of Peptides onto their Receptors. **PLoS ONE**. 6(4):e18934 [PMID: 21572516]
11. Belitsky M, Avshalom H, Yelin I, **London N**, Shperber M, Schueler-Furman O, Engelberg-Kulka H (2010). The Escherichia coli Extracellular Death Factor EDF Induces The Endoribonucleolytic Activities of the toxins MazF and ChpBK. **Mol. Cell**. 41(6):625-35 [PMID: 21419338] *Featured in the "Preview" section.
12. Buch I, Fishelovitch D, **London N**, Raveh B, Wolfson HJ and Nussinov R (2010). Allosteric Regulation of Glycogen Synthase Kinase-3 β : A Theoretical Study. **Biochemistry**. 49(51):10890-901. [PMID: 21105670] *Highlighted on the journal's homepage.
13. Crawley SW, Gharaei MS, Ye Q, Yang Y, Raveh B, **London N**, Schueler-Furman O, Jia Z and Côté GP (2010). Autophosphorylation activates Dictyostelium MHCK A by providing a ligand for a phosphate-binding pocket in the α -kinase domain. **JBC**. 286(4):2607-16 [PMID: 21071445]
14. **London N***, Raveh B*, Movshovitz-Attias D and Schueler-Furman O (2010). Can Self-Inhibitory Peptides be Derived from the Interfaces of Globular Protein-Protein Interactions? **Proteins**. 78:3140-9. [PMID: 20607702]

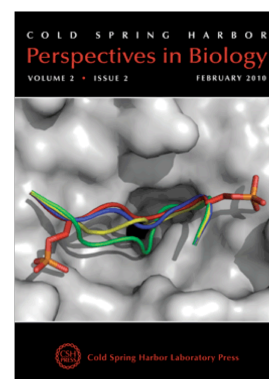


15. Raveh B*, **London N***, and Schueler-Furman O (2010). Sub-angstrom modeling of complexes between flexible peptides and globular proteins. **Proteins**. 78:2029-40. [PMID: 20455260]
16. Movshovitz-Attias D, **London N**, and Schueler-Furman O (2010). On the use of structural templates for high-resolution docking. **Proteins**. 78:1939-49. [PMID: 20408170]
17. **London N**, and Schueler-Furman O (2010). The Structural Basis of Peptide-Protein Binding Strategies. **Structure**. 18:188-199. [PMID: 20159464] **Featured on the cover.*
18. Dassa B, **London N**, Stoddard B, Schueler-Furman O and Pietrokovsky S (2009). Fractured genes: A novel genomic arrangement involving new split inteins and homing endonuclease family. **NAR**. 37:2560-73 [PMID: 19264795]
19. **London N**, Schueler-Furman O (2008) FunHunt: Model selection based on energy landscape characteristics. **Biochem Soc T**. 36:1418-1421 [PMID: 19021567]
20. **London N**, Schueler-Furman O (2008) Funnel hunting in a rough terrain: learning and discriminating native energy funnels. **Structure**. 16:269-79. [PMID: 18275818]
21. **London N**, Schueler-Furman O (2007) Assessing the energy landscape of CAPRI targets by FunHunt. **Proteins**. 69:809-15 [PMID: 17803233]
22. Wang C, Schueler-Furman O, Andre I, **London N**, Fleishman SJ, Bradley P, Qian B, Baker D (2007) RosettaDock in CAPRI rounds 6-12. **Proteins**. 69:758-63 [PMID: 17671979]



Reviews and Book chapters

1. **London N**, Raveh B and Schueler-Furman O (2013) Druggable protein-protein interactions - from hot spots to hot segments. **Curr. Opin. Chem. Biol.** 17(6):952-9. doi: 10.1016/j.cbpa.2013.10.011. [PMID: 24183815]
2. **London N***, Raveh B* and Schueler-Furman O (2013) Peptide docking and structure-based characterization of peptide binding: from knowledge to know-how. **Curr. Opin. Struct. Biol.** 23(6):894-902. doi: 10.1016/j.sbi.2013.07.006 [PMID: 24138780]
3. **London N**[§], Ambroggio X[§] (2013) An accurate binding interaction model in de novo computational protein design of interactions: If you build it, they will bind. **J. Struct. Biol.** S1047-8477(13)00083-X [PMID: 23558036] [§]*Corresponding author*
4. Al-Quadani T, Price CT, **London N**, Schueler-Furman O, AbuKwaik Y. (2011) Anchoring of bacterial effectors to host membranes through host-mediated lipidation by prenylation: a common paradigm. **Trends Microbiol.** 19(12):573-9. [PMID: 21983544]
5. **London N**, Raveh B and Schueler-Furman O (2012) Modeling peptide-protein interactions. **Methods Mol Biol.** 2012;857:375-98. In "Homology Modeling" Edited by Orry A & Abagyan R. [PMID: 22323231]
6. Kanarek N, **London N**, Schueler-Furman O and Ben-Neriah, Y (2010) Ubiquitination and Degradation of the Inhibitors of NF-kB. **Cold Spring Harbor Perspectives in Biology** 2(2):a000166 [PMID: 20182612] **Featured on the cover.*
7. **London N** and Schueler-Furman O (2009) High resolution protein-protein docking. In "**Protein-protein complexes: Analysis, modeling and drug design**" Edited by Zacharias M. Published by Imperial Press.



Patents

Inhibitors of UDP-Galactopyranose Mutase, Kiessling et al., P140379US01, USSN: 62/007355

Miscellaneous

- 2014: Member of the "Biophysical Society"
- 2006-Present: Served as reviewer for the following journals: Proteins, PLoS Computational Biology, Journal of Computer-Aided Molecular Design, PLoS ONE, PeerJ, Biopolymers
- 2008-Present: Founder and editor in chief of the "Macromolecular Modeling Blog" (With over 700 subscribers worldwide)
- 2011: Program committee for AFP/CAFA – computational function prediction meeting.
- 2009-2011: Coordinator of the Israeli academic "Protein engineering seminar" a bi-monthly joint meeting of Israeli academic groups to discuss research and advancement in the field of protein engineering.
- 2006-2011: Participant in rounds 9-21 of the CAPRI international contest for the prediction of protein complex structures.
- 2008-2009: Volunteer at "Halon" foundation - tutoring children with learning disabilities.