

Igor Dolgalev

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## EDUCATION

**Master of Science:** Biotechnology and Entrepreneurship **2014**  
**New York University**, New York, NY.

**Bachelor of Arts:** Biological Sciences (Computational Biology Concentration) **2005**  
**Cornell University**, Ithaca, NY.

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## TECHNICAL SKILLS

**Programming:** Bash, Java, MATLAB, Perl, PHP, Python, R

**Databases:** Microsoft Access, MongoDB, MySQL, PostgreSQL

**NGS data analysis:** ABySS, ANNOVAR, bedtools, Bismark, Bowtie, BWA, Canu, CASAVA/bcl2fastq, Control-FREEC, CREST, DELLY, DESeq, DEXSeq, DiffBind, FusionCatcher, GATK, LoFreq, MACS, methylKit, MuTect, Picard, poretools, QIIME, rMATS, RSEM, samtools, SOAPdenovo, SomaticSniper, SPAdes, STAR, TopHat/Cufflinks, Velvet

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## PROFESSIONAL EXPERIENCE

**NYU Langone Medical Center**, New York, NY. **6/2013 - present**

**Senior Bioinformatics Programmer**, Genome Technology Center and Applied Bioinformatics Center  
Provided bioinformatics support related to Illumina MiSeq/HiSeq next-generation sequencing as well as gene expression microarray and NanoString nCounter technologies. Responsible for monitoring and managing projects, identifying and resolving problems that may impact the project results, maintaining research software and hardware, and working with departmental leadership on developing and implementing data management policies. Created and operated the pipelines for processing DNA-Seq (somatic and germline SNVs, indels, structural variants, de novo assembly), RNA-Seq (differential expression, alternative splicing, gene fusions), and ChIP-Seq (peak calling, differential binding) data. Trained new bioinformaticians. Assisted GTC users with interpreting the results and performed custom additional analysis to address specific project needs.

**Memorial Sloan Kettering Cancer Center**, New York, NY. **10/2007 - 6/2013**

**Bioinformatics Engineer III**, Geoffrey Beene Translational Oncology Core Facility

**Senior Bioinformatician**, Geoffrey Beene Translational Oncology Core Facility

**Bioinformatician Technician**, Geoffrey Beene Translational Oncology Core Facility

Provided bioinformatics support relating to the genomics-based approaches utilized by the core, primarily for high-throughput PCR, Sanger and next-generation sequencing (Illumina MiSeq/HiSeq), and mutation detection. Participated in the establishment, management, and maintenance of the relational database for projects, sequencing quality data, biological samples, primers, mutations, and other data. Performed quality analysis of the generated sequencing data and developed solutions for enhancing future performance. Operated the pipeline for genomic data processing, variant detection, and genomic consequence calculation. Also directly and indirectly assisted the core users in analyzing biomedical data and addressing scientific problems with computational techniques and tools.

**Weill Cornell Medical College**, New York, NY. **9/2005 - 9/2007**

**Research Technician II**, Laboratory of Dr. Ronald Crystal, Dept. of Genetic Medicine

**Research Technician I**, Laboratory of Dr. Ronald Crystal, Dept. of Genetic Medicine

Worked on uncovering the genetic basis of various pulmonary disorders. My primary responsibility was analysis of gene expression microarray data using established methods as well as investigation of additional analytical tools. The process entailed sample management, array image quality assessment, statistical analysis of the expression data, and annotation retrieval from biological databases. Also involved in training other researchers on the use of analysis software, working with genotyping/SNP data, and performing real-time RT-PCR.

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## PUBLICATIONS

Calorie restriction suppresses age-dependent hippocampal transcriptional signatures.

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Schafer MJ, [Dolgalev I](#), Alldred MJ, Heguy A, Ginsberg SD.  
*PLOS ONE*. 2015 Jul 29;10(7):e0133923.

Functional Genomic Analysis Identifies Indoxyl Sulfate as a Major, Poorly Dialyzable Uremic Toxin in End-Stage Renal Disease.

Jhavar S, Singh P, Torres D, Ramirez-Valle F, Kassem H, Banerjee T, [Dolgalev I](#), Heguy A, Zavadil J, Lowenstein J.

*PLOS ONE*. 2015 Mar 26;10(3):e0118703.

Whole exome sequencing reveals frequent genetic alterations in BAP1, NF2, CDKN2A and CUL1 in malignant pleural mesothelioma.

Guo G, Chmielecki J, Goparaju C, Heguy A, [Dolgalev I](#), Carbone M, Seepo S, Meyerson M, Pass HI.  
*Cancer Research*, 2015, 75(2): 264-9.

Targeted mutational profiling of peripheral T-cell lymphoma not otherwise specified highlights new mechanisms in a heterogeneous pathogenesis.

Schatz JH, Horwitz SM, Teruya-Feldstein J, Lunning MA, Viale A, Huberman K, Socci ND, Lailier N, Heguy A, [Dolgalev I](#), Migliacci JC, Pirun M, Palomba ML, Weinstock DM, Wendel HG.

*Leukemia*, 2015, 29(1): 237-41.

Control of Embryonic Stem Cell Identity by BRD4-Dependent Transcriptional Elongation of Super-Enhancer-Associated Pluripotency Genes.

Di Micco R, Fontanals-Cirera B, Low V, Ntziachristos P, Yuen SK, Lovell CD, [Dolgalev I](#), Yonekubo Y, Zhang G, Rusinova E, Gerona-Navarro G, Canamero M, Ohlmeyer M, Aifantis I, Zhou MM, Tsigros A, Hernando E.

*Cell Reports*, 2014, 9(1): 234-47.

SPOP mutations in prostate cancer across demographically diverse patient cohorts.

Blattner M, Lee DJ, O'Reilly C, Park K, MacDonald TY, Khani F, Turner KR, Chiu YL, Wild PJ, [Dolgalev I](#), Heguy A, Sboner A, Ramazangolu S, Hieronymus H, Sawyers C, Tewari AK, Moch H, Yoon GS, Known YC, Andr n O, Fall K, Demichelis F, Mosquera JM, Robinson BD, Barbieri CE, Rubin MA.

*Neoplasia*, 2014, 16(1): 14-20.

The integrated landscape of driver genomic alterations in glioblastoma.

Frattini V, Trifonov V, Chan JM, Castano A, Lia M, Abate F, Keir ST, Ji AX, Zoppoli P, Niola F, Danussi C, [Dolgalev I](#), Porrati P, Pellegatta S, Heguy A, Gupta G, Pisapia DJ, Canoll P, Bruce JN, McLendon RE, Yan H, Aldape K, Finocchiaro G, Mikkelsen T, Priv  GG, Bigner DD, Lasorella A, Rabadan R, Iavarone A.

*Nature Genetics*, 2013, 45(10): 1141-1149.

The mutational landscape of adenoid cystic carcinoma.

Ho AS, Kannan K, Roy DM, Morris LG, Ganly I, Katabi N, Ramaswami D, Walsh LA, Eng S, Huse JT, Zhang J, [Dolgalev I](#), Huberman K, Heguy A, Viale A, Drobnjak M, Leversha MA, Rice CE, Singh B, Iyer NG, Leemans CR, Bloemena E, Ferris RL, Seethala RR, Gross BE, Liang Y, Sinha R, Peng L, Raphael BJ, Turcan S, Gong Y, Schultz N, Kim S, Chiosea S, Shah JP, Sander C, Lee W, Chan TA.

*Nature Genetics*, 2013, 45(7): 791-798.

Prognostic Relevance of Integrated Genetic Profiling in Acute Myeloid Leukemia.

Patel JP, Gonen M, Figueroa ME, Fernandez H, Sun Z, Racevskis J, Van Vlierberghe P, [Dolgalev I](#), Thomas S, Aminova O, Huberman K, Cheng J, Viale A, Socci ND, Heguy A, Cherry A, Vance G, Higgins RR, Ketterling RP, Gallagher RE, Litzow M, van den Brink MRM, Lazarus HM, Rowe JM, Luger S, Ferrando A, Paietta E, Tallman MS, Melnick A, Abdel-Wahab O, Levine RL.

*The New England Journal of Medicine*, 2012, 366(12): 1079-1089.

Concurrent Loss of the PTEN and RB1 Tumor Suppressors Attenuates RAF Dependence in Melanomas Harboring (V600E) BRAF.

Xing F, Persaud Y, Pratilas CA, Taylor BS, Janakiraman M, She QB, Gallardo H, Liu C, Merghoub T, Hefter B, [Dolgalev I](#), Viale A, Heguy A, De Stanchina E, Cobrinik D, Bollag G, Wolchok J, Houghton A,

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Solit DB.

*Oncogene*, 2012, 31(4): 446-457.

Mutations in GNA11 in Uveal Melanoma.

Van Raamsdonk CD, Griewank KG, Crosby MB, Garrido MC, Vemula S, Wiesner T, Obenauf AC, Wackernagel W, Green G, Bouvier N, Sozen MM, Baimukanova G, Roy R, Heguy A, Dolgalev I, Khanin R, Busam K, Speicher MR, O'Brien J, Bastian BC.

*The New England Journal of Medicine*, 2010, 363(23): 2191-2199.

Integrative Genomic Profiling of Human Prostate Cancer.

Taylor BS, Schultz N, Hieronymus H, Gopalan A, Xiao Y, Carver BS, Arora VK, Kaushik P, Cerami E, Reva B, Antipin Y, Mitsiades N, Landers T, Dolgalev I, Major JE, Wilson M, Socci ND, Lash AE, Heguy A, Eastham JA, Scher HI, Reuter VE, Scardino PT, Sander C, Sawyers CL, Gerald WL.

*Cancer Cell*, 2010, 18(1): 11-22.

Genetic Characterization of TET1, TET2, and TET3 Alterations in Myeloid Malignancies.

Abdel-Wahab O, Mullally A, Hedvat C, Garcia-Manero G, Patel J, Wadleigh M, Malinge S, Yao J, Kilpivaara O, Bhat R, Huberman K, Thomas S, Dolgalev I, Heguy A, Paietta E, Le Beau MM, Beran M, Tallman MS, Ebert BL, Kantarjian HM, Stone RM, Gilliland DG, Crispino JD, Levine RL.

*Blood*, 2009, 114(1): 144-147.

Variability in Small Airway Epithelial Gene Expression Among Normal Smokers.

Ammous Z, Hackett NR, Butler MW, Raman T, Dolgalev I, O'Connor TP, Harvey BG, Crystal RG.

*Chest*, 2008, 133(6): 1344-1353.

Responses of the Human Airway Epithelium Transcriptome to In Vivo Injury.

Heguy, A, Harvey BG, Leopold PL, Dolgalev I, Raman T, Crystal RG.

*Physiological Genomics*, 2007, 29(2): 139-148.