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CURRENT POSITIONS

2016 – present	Assistant Professor (tenure-track), Department of Pathology, University of California, San Francisco
2016 – present	Faculty member, UCSF Biomedical Sciences Graduate Program
2015 – present	Member, UCSF Helen Diller Family Comprehensive Cancer Center
2018 – present	Investigator, UCSF Brain Tumor Research Center
2016 – 2020	Director of Molecular Neuropathology, UCSF Clinical Cancer Genomics Laboratory
2020 – present	Director, UCSF Pathology Epigenomics Laboratory

EDUCATION

1998 – 2002	B.S. Molecular Cell Biology, Chemistry, College of William and Mary
2004 – 2012	MD, PhD, Georgetown University School of Medicine Thesis research completed in Tumor Biology Training Program
2012 – 2014	Anatomic Pathology Residency, University of California, San Francisco
2014 – 2016	Neuropathology Fellowship, University of California, San Francisco

LICENSURE

Physician and Surgeon License**,** Medical Board of California, A129659, 4/2/2014

Board certification in Anatomic Pathology and Neuropathology, American Board of Pathology, 9/18/2017

RESEARCH TRAINING

Defining the development of neural connections in *Xenopus laevis*
Mentor: Dr. Margaret Saha, Department of Biology, College of William and Mary
Undergraduate thesis research, January 1999 – June 2002

Regulation of oligodendrocyte differentiation and myelination
Mentor: Dr. Timothy Vartanian, Department of Neurology, Harvard University Medical School
Independent student research, Summer 2000, Winter 2000/2001, Summer 2001

Regulation of cell growth by the retinoblastoma tumor suppressor
Mentor: Dr. Erik Knudsen, Department of Cell Biology, University of Cincinnati College of Medicine
Summer Undergraduate Research Program in Molecular and Cell Biology, June – August 2002
Research Assistant, August 2002 – June 2004

Identification and therapeutic targeting of novel transforming pathways in glioblastoma multiforme
Mentor: Dr. Todd Waldman, Lombardi Cancer Center, Georgetown University School of Medicine
Graduate thesis research, July 2006 – June 2012

HONORS / AWARDS

1998	National Merit Scholar
1998-2002	William and Mary Monroe Scholar, College of William and Mary
2000-2002	Howard Hughes Medical Institute student research grants, College of William and Mary Undergraduate Science Education and Research Program
2004	Winning image, Cell of the Month Image Competition, displayed in the April 2004 issues of *Nature Cell Biology* and *Nature Reviews Molecular Cell Biology*
2004-2012	Strauss Physician-Scientist Training Fellowship, Georgetown University School of Medicine
2008-2010	Best poster presentation, Student Research Days, Georgetown University Biomedical Graduate Exposition
2008, 2011	Clifford C. Kaslow Research Achievement Award, Best basic science research by a student/resident, Research Day, Department of Medicine, Georgetown University Medical Center
2010, 2011	Robert Dickson Graduate Prize, recipient of inaugural award presented for excellence in a student publication, Lombardi Cancer Center, Georgetown University
2011	Best poster presentation, Lombardi Cancer Center Research Day, Georgetown University
2012	**Future Leaders in Basic Cancer Research**, one of four recipients of award presented at the 2012 American Association for Cancer Research Annual Meeting
2012	**Harold Weintraub Graduate Student Award**, one of twelve recipients of award presented at the 2012 Weintraub Memorial Symposium at the Fred Hutchinson Cancer Research Center
2013	Julius R. Krevans Award, recipient of annual award presented for clinical excellence to a UCSF intern in each specialty at San Francisco General Hospital
2013	Outstanding Resident Research Award, recipient of annual award from The Resident Research Training Program, University of California, San Francisco
2013, 2014	**Stowell-Orbison Award**, recipient of award presented at both the 2013 and 2014 U.S. & Canada Academy of Pathology Annual Meetings for best overall abstract presentation by a trainee
2014	International Society of Bone & Soft Tissue Pathology Young Investigator Award, best abstract presentation by a trainee at the 2014 U.S. & Canada Academy of Pathology Annual Meeting
2015	Hans Popper Hepatopathology Society Award, best abstract presentation by a trainee at the 2015 United States & Canada Academy of Pathology Annual Meeting
2015-2016	Career Development Research Award, UCSF Brain Tumor SPORE
2015-2020	**NIH Director's Early Independence Award**, sponsored by the NIH Common Fund's High-Risk, High-Reward Program to support early independence of exceptional early career scientists
2016-2021	UCSF Physician-Scientist Scholar Program, career development award sponsored by the University of California, San Francisco
2019	Lucien Rubinstein Award for best neuro-oncology abstract presented at the 2019 AANP annual meeting
2019-2021	Developmental Research Program Award, UCSF Brain Tumor SPORE
2020	**Ramzi S. Cotran Young Investigator Award**, from U.S. & Canada Academy of Pathology to recognize a body of investigative work which has contributed significantly to the diagnosis and understanding of human disease

PROFESSIONAL SERVICE

2014-2015	Ad hoc grant reviewer, Association for International Cancer Research, Leukaemia & Lymphoma Research, and the Marsden Fund of The Royal Society of New Zealand

2014-present	Ad hoc reviewer, *Nature Communications*, *Cancer Cell, Cancer Research, JCO Precision Oncology*, *Acta Neuropathologica*, *Acta Neuropathologica Communications*, *Brain Pathology*, *Modern Pathology*, *Neuro-Oncology*, *Journal of Neuro-Oncology*, *Journal of Neuropathology and Experimental Neurology, American Journal of Medical Genetics*, *Journal of Translational Medicine*
2018-present	Editorial board, *Acta Neuropathologica*
2018	Ad hoc member, Special Emphasis Panel ZCA1 SRB-K (M2) for review of Provocative Question applications, National Cancer Institute, NIH
2017-2020	The Dr. L. Clarke, Jr. and Elaine F. Stout Award Selection Committee, United States & Canada Academy of Pathology
2019-present	Awards Committee, American Association of Neuropathologists
2020	Review committee, AACR Clinical/Translational Sarcoma Research Fellowship Award
2020-present	Senior Associate Editor, *Brain Pathology*

PROFESSIONAL MEMBERSHIPS

American Association for the Advancement of Science (AAAS), member 2002 – present

United States & Canada Academy of Pathology (USCAP), member 2013 – present

American Association of Neuropathologists (AANP), member 2015 – present

American Association for Cancer Research (AACR), member 2016 – present

American Society for Investigative Pathology (ASIP), member 2018 – present

Society for Neuro-Oncology (SNO), member 2018 – present

CONTRIBUTIONS TO SCIENCE

1. Deciphering the molecular pathogenesis of human brain tumors. Starting during my graduate training in Dr. Todd Waldman's lab at Georgetown University, a major focus of my research efforts has been determining the genetic alterations that drive tumorigenesis in the central nervous system. My initial work as a graduate student entailed the use of Affymetrix SNP copy number microarrays to perform genomic characterization on >100 glioblastoma tumor samples in the hopes of identifying novel gene amplifications and deletions that would point me towards new glioblastoma oncogenes and tumor suppressor genes. My data provided a high-resolution view of the amplifications and deletions that drive the pathogenesis of glioblastoma and identified several novel alterations that were present in multiple independent samples including homozygous deletions of the *CDKN2C* and *PTPRD* genes. I performed a variety of follow up experiments that clearly delineated these genes as novel glioblastoma tumor suppressors.[a,b] More recent genomic analysis of brain tumors and subsequent functional analysis in my independent laboratory at UCSF has delineated the genetic basis of several brain tumor subtypes, including chordoid glioma, astroblastoma, ganglioglioma, multinodular and vacuolating neuronal tumor, pleomorphic xanthoastrocytoma, myxoid glioneuronal tumor, spinal cord diffuse gliomas, pineal parenchymal tumors, and radiation-induced gliomas.[c-f]

a. **Solomon DA**, Kim JS, Jenkins S, Ressom H, Huang M, Coppa N, Mabanta L, Bigner D, Yan H, Jean W, Waldman T. Identification of $p18^{INK4c}$ as a tumor suppressor gene in glioblastoma multiforme. *Cancer Research* 2008, 68: 2564-9, PMID 18381405.
b. **Solomon DA**, Kim JS, Cronin JC, Sibenaller Z, Ryken T, Bigner D, Yan H, Rosenberg SA, Ressom H, Jean W, Samuels Y, Waldman T. Mutational inactivation of PTPRD in glioblastoma multiforme and malignant melanoma. *Cancer Research* 2008, 68: 10300-6, PMID 19074898.
c. Goode B, Mondal G, Hyun M, ..., **Solomon DA**. A recurrent kinase domain mutation in PRKCA defines chordoid glioma of the third ventricle. *Nature Communications* 2018, 9: 810, PMID 29476136.

d. Pekmezci M, Villanueva-Meyer JE, Goode B, ..., **Solomon DA**. The genetic landscape of ganglioglioma. *Acta Neuropathologica Communications* 2018, 6: 47, PMID 29880043.
e. Wood MD, Tihan T, Perry A, Chacko G, Turner C, Pu C, Payne C, Yu A, Bannykh SI, **Solomon DA**. Multimodal molecular analysis of astroblastoma enables reclassification of most cases into more specific molecular entities. *Brain Pathology* 2018, 28: 192-202, PMID 28960623.
f. Lopez GY, Van Ziffle J, Onodera C, ..., Perry A, **Solomon DA**. The genetic landscape of gliomas arising after therapeutic radiation. *Acta Neuropathologica* 2019, 137: 139-150, PMID: 30196423.

2. Advancing targeted therapy for neuro-oncology patients. Based on my genomic findings in glioblastoma tumor samples including recurrent *CDKN2A/B* and *CDKN2C* deletions as well as amplifications of *CDK4* or *CDK6*, it became clear that targeting this pathway represented a new rational therapeutic strategy for this uniformly lethal brain cancer. In order to test this, I worked with Pfizer to obtain access to their new first-in-class CDK4/6 small molecule inhibitor, PD-0332991 (now called palbociclib and FDA-approved for the treatment of breast cancer). This drug demonstrated remarkable efficacy in arresting the growth of *CDKN2A*/*B* and *CDKN2C* deficient glioblastomas, both in vitro and in an orthotopic xenograft model.[a] This work led to initiation of "A phase II study of PD-0332991 in patients with recurrent Rb positive glioblastoma" at UCSF starting September 2010 (ClinicalTrials ID NCT01227434). I have also significantly contributed to other preclinical studies demonstrating efficacy of targeting gliomas harboring *BRAF* V600E mutation and histone H3 K27M mutation using targeted therapeutics.[b,c] As the Director of Molecular Neuropathology at UCSF, I have been leading the implementation of both next-generation sequencing and genome-wide DNA methylation profiling for improving the diagnosis, identifying pathogenic germline alterations, and directing targeted therapy for neuro-oncology patients.[d] The targeted NGS panel that I have developed at UCSF is currently being utilized as the genomic testing platform for an ongoing nationwide precision medicine clinical trial for pediatric high-grade gliomas by the Pediatric Neuro-Oncology Consortium (trial PNOC008). Most recently, we have identified that bithalamic glioma, an unresectable and uniformly lethal brain tumor of childhood, is genetically defined by oncogenic *EGFR* exon 20 insertions occurring in the absence of *EGFR* gene amplification or histone H3 mutation which cause sensitivity to specific small molecule tyrosine kinase inhibitors that we have found to prolong survival for affected children.[e]

a. Michaud K[*], **Solomon DA**[*], Oermann E, Kim JS, Zhong WZ, Prados MD, Ozawa T, James CD, Waldman T. *contributed equally. Pharmacologic inhibition of cyclin-dependent kinases 4 and 6 arrests the growth of glioblastoma multiforme intracranial xenografts. *Cancer Research* 2010, 70: 3228-38, PMID 20354191.
b. Nicolaides TP, Li H, **Solomon DA**, Hariono S, Hashizume R, Barkovich K, Baker SJ, Paugh BS, Jones C, Forshew T, Hindley GF, Hodgson JG, Kim JS, Rowitch DH, Weiss WA, Waldman T, James CD. Targeted therapy for $BRAF^{V600E}$ malignant astrocytoma. *Clinical Cancer Research* 2011, 17: 7595-604, PMID 22038996.
c. Hashizume R, Andor N, Ihara Y, Lerner R, Gan H, Chen X, Fang D, Huang X, Tom MW, Ngo V, **Solomon D**, Mueller S, Paris P, Zhang Z, Petritsch C, Gupta N, Waldman T, James CD. Pharmacologic inhibition of histone demethylation as a therapy for pediatric brainstem glioma. *Nature Medicine* 2014, 20: 1394-6, PMID 25401693.
d. Kline CN, Joseph NM, Grenert JP, ..., Perry A, Nicolaides T, **Solomon DA**. Targeted next-generation sequencing of pediatric neuro-oncology patients improves diagnosis, identifies pathogenic germline mutations, and directs targeted therapy. *Neuro-Oncology* 2017, 19: 699-709, PMID 28453743.
e. Mondal G, Lee JC, ..., Perry A, Orr BA, **Solomon DA**. Pediatric bithalamic gliomas have a distinct epigenetic signature and frequent EGFR exon 20 insertions resulting in potential sensitivity to targeted kinase inhibition. *Acta Neuropathologica* 2020, 139: 1071-1088, PMID 32303840.

3. Discovery of cohesin gene mutations in human cancer. During my graduate training, I made an important discovery in the field of cancer biology by identifying mutational inactivation of the *STAG2* gene as one of the first common genetic causes of aneuploidy in human cancer.[a] Subsequently during my pathology residency training at UCSF, I identified frequent truncating mutations of this cohesin complex gene *STAG2* in urothelial bladder carcinoma and Ewing sarcoma which define molecular subgroups of these tumors with distinct clinical outcomes.[b,c] The Cancer Genome Atlas has identified *STAG2* as one of only twelve genes that are significantly mutated in four or more human cancer types, although the precise function of *STAG2* inactivation during tumorigenesis remains unknown. A major focus of the ongoing research efforts in my laboratory is determining the function of *STAG2* during development and tumorigenesis and identifying therapeutic vulnerabilities in the many cancers harboring cohesin gene alterations.[d]

a. **Solomon DA**, Kim T, Diaz-Martinez LA, Fair J, Elkahloun AG, Harris BT, Toretsky J, Rosenberg SA, Samuels Y, Shukla N, Ladanyi M, James CD, Yu H, Kim JS, Waldman T. Mutational inactivation of STAG2 causes aneuploidy in human cancer. *Science* 2011, 333: 1039-43, PMID 25052185. Featured in 'This week in *Science*'.
b. **Solomon DA**, Kim JS, Bondaruk J, Shariat SF, Wang ZF, Elkahloun AG, Ozawa T, Gerard J, Zhuang D, Zhang S, Navai N, Siefker-Radtke A, Phillips JJ, Robinson BD, Rubin MA, Volkmer B, Hautmann R, Kufer R, Hogendoorn PCW, Netto G, Theodorescu D, James CD, Czerniak B, Miettinen M, Waldman T. Frequent truncating mutations of STAG2 in bladder cancer. *Nature Genetics* 2013, 45: 1428-30, PMID 24121789.
c. Brohl AS, **Solomon DA**, Chang W, Wang J, Song YK, Sindiri S, Patidar R, Hurd L, Chen L, Shern JF, Gerard J, Kim JS, Lopez Guerrero JA, Machado I, Wai DH, Picci P, Triche TJ, Horvai AE, Miettinen M, Wei JS, Catchpoole D, Llombart-Bosch A, Waldman T, Khan J. The genomic landscape of the Ewing sarcoma family of tumors reveals recurrent STAG2 mutation. *PLoS Genetics* 2014, 10: e1004475, PMID 25010205.
d. Mondal G, Stevers M, Goode B, Ashworth A, **Solomon DA**. A requirement for *STAG2* in DNA replication fork progression creates a targetable synthetic lethality in cohesin-mutant cancers. *Nature Communications* 2019, 10: 1686, PMID 30975996.

4. Deciphering the molecular pathogenesis of mesothelial neoplasia. I have led the discovery of the molecular basis of the four distinct subtypes of mesothelial neoplasms that occur in the peritoneal cavity. We found that malignant mesothelioma harbors frequent *BAP1*, *SETD2*, *DDX3X*, and *NF2* mutations.[a] In contrast, well-differentiated papillary mesothelioma lacks alterations in these genes and instead is defined by mutually exclusive mutations in *TRAF7* or *CDC42*.[b] We also identified that adenomatoid tumor of the genital tract, the most common neoplasm of the epididymis, is defined by *TRAF7* mutations, indicating a shared molecular pathogenesis with well-differentiated papillary mesothelioma.[c] Our genetic analysis of the fourth type of mesothelial neoplasm, multicystic mesothelioma, is currently in progress. We have begun functional studies to identify how *TRAF7* mutations that are frequent in mesothelial neoplasms, as well as meningiomas and perineuriomas, cause tumorigenesis in these specific tumor types, with preliminary results demonstrating that they cause activation of NF-kB pathway signaling.[c]

a. Joseph NM, Chen YY, Nasr A, Yeh I, Talevich E, Onodera C, Bastian BC, Rabban JT, Garg K, Zaloudek C, **Solomon DA**. Genomic profiling of malignant peritoneal mesothelioma reveals recurrent alterations in epigenetic regulatory genes BAP1, SETD2, and DDX3X. *Modern Pathology* 2017, 30: 246-254, PMID 27813512.
b. Stevers M, Rabban JT, Garg K, Van Ziffle J, Onodera C, Grenert JP, Yeh I, Bastian BC, Zaloudek C, **Solomon DA**. Well-differentiated papillary mesothelioma of the peritoneum is genetically defined by mutually exclusive mutations in TRAF7 and CDC42. *Modern Pathology* 2019, 32: 88-99, PMID 30171198.
c. Goode B, Joseph NM, Stevers M, Van Ziffle J, Onodera C, Talevich E, Grenert JP, Yeh I, Bastian BC, Phillips JJ, Garg K, Rabban JT, Zaloudek C, **Solomon DA**. Adenomatoid tumors of the

male and female genital tract are defined by TRAF7 mutations that drive aberrant NF-kB pathway activation. *Modern Pathology* 2018, 31: 660-673, PMID 29148537.

5. Identification of a novel cyclin D1 splice variant and other new mechanisms of cell cycle regulation. During my two years of post-baccalaureate research in the lab of Dr. Erik Knudsen at the University of Cincinnati College of Medicine, I investigated the mechanisms by which the retinoblastoma tumor suppressor protein controls cell cycle transitions. We identified how cooperation with histone deacetylases and the Swi/Snf chromatin remodeling complex regulate the dynamic interaction of RB with target gene promoters to block uncontrolled cell cycle progression.[a,b] I also discovered a novel oncogenic splice variant of cyclin D1 that we termed cyclin D1b, which lacks a critical C-terminal phosphorylation site resulting in constitutive nuclear localization and oncogenic activity.[c] I also discovered that components of the DNA replication machinery localize into discrete subnuclear foci after DNA damage where they dynamically exchange with distinct kinetics, supporting a model in which DNA repair occurs at a limited number of stationary repair foci within the cell nucleus with which lesional DNA dynamically associates.[d]

a. Angus SP[*], **Solomon DA[*]**, Kuschel L, Hennigan RF, Knudsen ES. *contributed equally. Retinoblastoma tumor suppressor: analyses of dynamic behavior in living cells reveal multiple modes of regulation. *Molecular and Cellular Biology* 2003, 23: 8172-88, PMID 14855976.
b. Siddiqui H[*], **Solomon DA[*]**, Gunawardena RW, Wang Y, Knudsen ES. *contributed equally. Histone deacetylation of RB-responsive promoters: requisite for specific gene repression but dispensable for cell cycle inhibition. *Molecular and Cellular Biology* 2003, 23: 7719-31, PMID 14560017.
c. **Solomon DA**, Wang Y, Fox SR, Lambeck TC, Giesting S, Lan Z, Senderowicz AM, Conti CJ, Knudsen ES. Cyclin D1 splice variants: differential effects on localization, RB phosphorylation, and cellular transformation. *Journal of Biological Chemistry* 2003, 278: 30339-47, PMID 12746453.
d. **Solomon DA**, Cardoso MC, Knudsen ES. Dynamic targeting of the replication machinery to sites of DNA damage. *Journal of Cell Biology* 2004, 166: 455-63, PMID 15314062.

CURRENT RESEARCH SUPPORT

NIH Director's Early Independence Award (DP5 OD021403) Solomon (PI) 09/01/2015 – 09/30/2020
Cohesin gene mutations in tumorigenesis NCE through 09/30/2021
Aim: Determine the function of the cohesin complex gene *STAG2* during mammalian development and tumorigenesis and identify therapeutic vulnerabilities in the many cancers harboring cohesin gene mutations.

UCSF Glioblastoma Precision Medicine Program Solomon (PI) 07/01/2018 – 06/30/2023
Project #1: A comprehensive genomic-based treatment program for glioblastoma at UCSF
Aim for Project #1 on which I am the lead PI: To establish a precision medicine program for the diagnosis and treatment of glioblastoma.

UCSF Glioblastoma Precision Medicine Program Solomon (co-PI) 07/01/2019 – 06/30/2021
Project #6: Genomic, epigenomic, and transcriptomic analysis of paired initial and recurrent glioblastoma
Aim for Project #6 on which I am the co-PI: To determine the genetic, epigenetic, and transcriptional evolution of glioblastoma that drives recurrence and resistance to therapy.

Developmental Research Award, UCSF Brain Tumor SPORE Solomon (PI) 09/01/2019 – 08/31/2021
Improving brain tumor diagnostics: integrating methylation and mutation profiles
Aim: Development and clinical implementation of genome-wide methylation profiling as an ancillary diagnostic tool for accurate classification and subtyping of CNS tumors at UCSF Medical Center.

COMPLETED RESEARCH SUPPORT

UCSF Wolfe Meningioma Program Project Award Solomon (PI) 01/01/2019 – 12/31/2019
Functional assessment of *TRAF7* mutations in meningioma development
Aim: Determine the functional mechanism by which the frequent *TRAF7* mutations drive tumorigenesis of meningiomas.

UCSF Physician-Scientist Scholar Program Solomon (PI) 07/01/2016 – 06/30/2017
Cohesin gene mutations in tumorigenesis
Aim: Determine the function of the cohesin complex gene *STAG2* during mammalian development and tumorigenesis and identify therapeutic vulnerabilities in the many cancers harboring cohesin gene mutations.

Career Development Award, UCSF Brain Tumor SPORE Solomon (PI) 09/01/2015 – 08/30/2016
Genomic analysis of pineal parenchymal tumors
Aim: Determine the genetic alterations that drive pineocytoma, pineal parenchymal tumor of intermediate differentiation, and pineoblastoma to identify better prognostic markers and new molecular targets for developing novel targeted therapeutics.

UCSF500 Cancer Gene Panel Pilot Program Award Solomon (PI) 01/12/2015 – 01/11/2016
Genomic analysis of choroid plexus tumors
Aim: Determine the genetic alterations that drive choroid plexus papillomas and carcinomas to identify better prognostic markers and new molecular targets for developing novel targeted therapeutics.

Howard Hughes Medical Institute student research grants, College of William and Mary Undergraduate Science Education and Research Program, Spring 2002, Fall 2001, Spring 2000.

PEER-REVIEWED SCIENTIFIC PUBLICATIONS

Cohesin gene mutations in tumorigenesis

1. Mondal G, Stevers M, Goode B, Ashworth A, **Solomon DA**. A requirement for *STAG2* in DNA replication fork progression creates a targetable synthetic lethality in cohesin-mutant cancers. *Nature Communications* 2019, 10: 1686, PMID 30975996

2. Lelo A, Prip F, Harris BT, **Solomon D**, Berry DL, Chaldekas K, Kumar A, Simko J, Jensen JB, Bhattacharyya P, Mannion C, Kim JS, Philips G, Dyrskjøt L, Waldman T. STAG2 is a biomarker for prediction of recurrence and progression in papillary non-muscle-invasive bladder cancer. *Clinical Cancer Research* 2018, 24: 4145-4153, PMID 29954776

3. Ding S, Diep J, Feng N, Ren L, Li B, Ooi YS, Wang X, Brulois KF, Yasukawa LL, Li X, Kuo CJ, **Solomon DA**, Carette JE, Greenberg HB. STAG2 deficiency induces interferon responses via cGAS-STING pathway and restricts virus infection. *Nature Communications* 2018, 9: 1485, PMID 29662124

4. Brohl AS, **Solomon DA**, Chang W, Wang, J, Song YK, Sindiri S, Patidar R, Hurd L, Chen L, Shern JF, Gerard J, Kim JS, Lopez Guerrero JA, Machado I, Wai DH, Picci P, Triche TJ, Horvai AE, Miettinen M, Wei JS, Catchpoole D, Llombart-Bosch A, Waldman T, Khan J. The genomic landscape of the Ewing sarcoma family of tumors reveals recurrent STAG2 mutation. *PLoS Genetics* 2014, 10: e1004475, PMID 25010205

5. Bailey ML, O'Neil NJ, van Pel DM, **Solomon DA**, Waldman T, Hieter P. Glioblastoma cells containing mutations in the cohesin component, STAG2, are sensitive to PARP inhibition. *Molecular Cancer Therapeutics* 2014, 13: 724-732, PMID 24356817

6. **Solomon DA**, Kim JS, Bondaruk J, Shariat SF, Wang ZF, Elkahloun AG, Ozawa T, Gerard J, Zhuang D, Zhang S, Navai N, Siefker-Radtke A, Phillips JJ, Robinson BD, Rubin MA, Volkmer B, Hautmann R, Kufer R, Hogendoorn PCW, Netto G, Theodorescu D, James CD, Czerniak B, Miettinen M, Waldman T. Frequent truncating mutations of STAG2 in bladder cancer. *Nature Genetics* 2013, 45: 1428-1430, PMID 24121789

7. **Solomon DA**, Kim T, Diaz-Martinez LA, Fair J, Elkahloun AG, Harris BT, Toretsky J, Rosenberg SA, Samuels Y, Shukla N, Ladanyi M, James CD, Yu H, Kim JS, Waldman T. Mutational inactivation of STAG2 causes aneuploidy in human cancer. *Science* 2011, 333: 1039-1043, PMID 21852505, featured in 'This week in *Science*'

Brain tumor molecular pathogenesis and targeted therapy

8. Sloan EA, Chiang J, Alexandrescu S, Eschbacher JM, Wang W, Mafra M, Uddin N, Carr-Boyd E, Watson M, Punsoni M, Oviedo A, Kleinschmidt-DeMasters BK, Dylan J. Coss DJ, M. Beatriz Lopes MB, Raffel C, Berger MS, Chang S, Reddy A, Ramani B, Ferris SP, Lee JC, Hofmann JW, Cho SJ, Horvai AE, Pekmezci M, Tihan T, Bollen AW, Rodriguez F, Ellison D, Perry A, **Solomon DA**. Intracranial mesenchymal tumor with EWS-CREB

fusion – a unifying diagnosis for the spectrum of intracranial myxoid mesenchymal tumors and angiomatoid fibrous histiocytoma-like neoplasms. *Brain Pathology* 2020 Epub Nov 3, PMID 33141488

9. Schulte JD, Buerki RA, La Pointe SL, Molinaro AM, Zhang Y, Villanueva-Meyer JE, Perry A, Phillips JJ, Tihan T, Bollen AW, Pekmezci M, Butowski N, Oberheim-Bush NA, Taylor JW, Chang S, Theodosopoulos P, Aghi MK, Hervey-Jumper SL, Berger MS, **Solomon DA**, Clarke JL. Clinical, radiologic, and genetic characteristics of histone H3 K27M-mutant diffuse midline glioma in adults. *Neuro-Oncology Advances* 2020 Epub Oct 22, PMID pending

10. Sievers P, Sill M, Schrimpf D, Stichel D, Reuss DE, Sturm D, Hench J, Frank S, Krskova L, Vicha A, Zapotocky M, Bison B, Castel D, Grill J, Debily MA, Harter PN, Snuderl M, Kramm CM, Reifenberger G, Korshunov A, Jabado N, Wesseling P, Wick W, **Solomon DA**, Perry A, Jacques TS, Jones C, Witt O, Pfister SM, von Deimling A, Jones DTW, Sahm F. A subset of pediatric-type thalamic gliomas share a distinct DNA methylation profile, H3K27me3 loss and frequent alteration of EGFR. *Neuro-Oncology* 2020 Epub Nov 1, PMID 33130881

11. Ramani B, Gupta R, Wu J, Barreto J, Bollen AW, Tihan T, Mummaneni PV, Ames C, Clark A, Oberheim Bush NA, Butowski N, Phillips D, King BE, Bator SM, Treynor EC, Zherebitskiy V, Quinn PS, Walker JB, Pekmezci M, Sullivan DV, Hofmann JW, Sloan EA, M Chang S, Berger MS, **Solomon DA**, Perry A. The immunohistochemical, DNA methylation, and chromosomal copy number profile of cauda equina paraganglioma is distinct from extra-spinal paraganglioma. *Acta Neuropathologica* 2020, 140: 907-917, PMID 32892244

12. Chen WC, Vasudevan HN, Choudhury A, Pekmezci M, Lucas CG, Phillips J, Magill ST, Susko MS, Braunstein SE, Oberheim Bush NA, Boreta L, Nakamura JL, Villanueva-Meyer JE, Sneed PK, Perry A, McDermott MW, **Solomon DA**, Theodosopoulos PV, Raleigh DR. A prognostic gene-expression signature and risk score for meningioma recurrence after resection. *Neurosurgery* 2020 Epub Aug 29, PMID 32860417

13. Lucas CG, Gupta R, Doo P, Lee JC, Cadwell CR, Ramani B, Hofmann JW, Sloan EA, Kleinschmidt-DeMasters BK, Lee HS, Wood MD, Grafe M, Born D, Vogel H, Salamat S, Puccetti D, Scharnhorst D, Samuel D, Cooney T, Cham E, Jin LW, Khatib Z, Maher O, Chamyan G, Brathwaite C, Bannykh S, Mueller S, Kline CN, Banerjee A, Reddy A, Taylor JW, Clarke JL, Oberheim Bush NA, Butowski N, Gupta N, Auguste KI, Sun PP, Roland JL, Raffel C, Aghi MK, Theodosopoulos P, Chang E, Hervey-Jumper S, Phillips JJ, Pekmezci M, Bollen AW, Tihan T, Chang S, Berger MS, Perry A, **Solomon DA**. Comprehensive analysis of diverse low-grade neuroepithelial tumors with FGFR1 alterations reveals a distinct molecular signature of rosette-forming glioneuronal tumor. *Acta Neuropathologica Communications* 2020, 8: 151, PMID 32859279

14. Carter-Febres M, Schneller N, Fair D, **Solomon D**, Perry A, Roy A, Linscott L, Alashari M, Kestle JR, Bruggers CS. Adjuvant maintenance larotrectinib therapy in 2 children with NTRK fusion-positive high-grade cancers. *Journal of Pediatric Hematology and Oncology* 2020 Epub Oct 21, PMID 33093355

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BOOK CHAPTERS

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REVIEWS AND OTHER PUBLICATIONS

1. Louis DN, Wesseling P, Aldape K, Brat DJ, Capper D, Cree IA, Eberhart C, Figarella-Branger D, Fouladi M, Fuller GN, Giannini C, Haberler C, Hawkins C, Komori T, Kros JM, Ng HK, Orr BA, Park SH, Paulus W, Perry A, Pietsch T, Reifenberger G, Rosenblum M, Rous B, Sahm F, Sarkar C, **Solomon DA**, Tabori U, van den Bent MJ, von Deimling A, Weller M, White VA, Ellison DW. cIMPACT-NOW update 6: new entity and diagnostic

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4. Kline CN, Packer RJ, Hwang EI, Raleigh DR, Braunstein S, Raffel C, Bandopadhayay P, **Solomon DA**, Aboian M, Cha S, Mueller S. Case-based review: pediatric medulloblastoma. *Neuro-Oncology Practice* 2017, 4: 138-150, PMID 29692919

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THESES

Identification and therapeutic targeting of novel transforming pathways in human glioblastoma multiforme
Solomon DA and Waldman T
Thesis submitted in partial fulfillment of the requirements for the degree of Doctor of Philosophy in Biomedical Sciences – Tumor Biology from Georgetown University Graduate School of Arts & Sciences, April 2010

Developmental characterization of the GABA neurotransmitter system in *Xenopus laevis*
Solomon DA and Saha MS
Thesis submitted in partial fulfillment of the requirements for the degree of Bachelor of Science with Honors in Interdisciplinary Studies – Molecular Cell Biology from the College of William and Mary, May 2002

INVITED TALKS

Comprehensive analysis of diverse low-grade neuroepithelial tumors with FGFR1 alterations reveals a distinct molecular signature of rosette-forming glioneuronal tumor
Annual meeting of the Society for Neuro-Oncology, November 2020

The role of STAG2 and the cohesin complex during development and tumorigenesis
Familial tumor syndromes with CNS manifestations
Neuropathology Day, University of Toronto, November 2020

Transforming neuropathology from a microscopic impression to an exact science
Neurosurgery Grand Rounds, National Cancer Institute, NIH, October 2020

Neuropathology Evening Specialty Conference: The Stars Come Out at Night
Annual meeting of the United States & Canada Academy of Pathology, Los Angeles, March 2020

Clinicopathologic features of new molecularly defined tumors of the central nervous system
50th Annual Plecnik Memorial Symposium, Faculty of Medicine, University of Ljubljana, Slovenia, Dec 2019

Next-generation sequencing for glioma integrated diagnosis and treatment: where does imaging fit in?
Neuroradiology Series: Brain Tumors, annual meeting of the Radiological Society of North America, Chicago, December 2019

The genomic landscape and targeted therapy for pediatric bithalamic gliomas
Annual meeting of the American Association of Neuropathologists, Atlanta, June 2019

The role of STAG2 and the cohesin complex during development and tumorigenesis
Molecular Pathology Seminar Series, Johns Hopkins Medical Center, Baltimore, January 2019

Deciphering the molecular pathogenesis of human brain tumors
International Academy of Pathology Congress, Dead Sea, Amman, Jordan, October 2018

The genetic landscape of ganglioglioma
Annual meeting of the American Association of Neuropathologists, Louisville, June 2018

Targeted NGS of paired tumor and normal DNA reveals frequent cancer predisposing germline alterations in neuro-oncology patients
Annual meeting of the Brain Tumor Epidemiology Consortium, Banff, June 2017

Targeted next-generation sequencing of neuro-oncology patients improves diagnosis, identifies pathogenic germline alterations, and directs targeted therapy
Inaugural University of California, San Francisco & Koc University School of Medicine Surgical Pathology Workshop, Istanbul, Turkey, May 2017

Targeted NGS of paired tumor and normal DNA reveals frequent cancer predisposing germline alterations in neuro-oncology patients
Annual meeting of the American Association of Neuropathologists, Orange County, June 2017

Next-generation sequencing: an ancillary diagnostic tool for CNS tumors
Special Course on Genetics, Genomics, and Epigenomics in Clinical Neuropathology Practice, annual meeting of the American Association of Neuropathologists, Orange County, June 2017

Genomic analysis of chordoid glioma of the third ventricle identifies a defining oncogenic driver
Annual meeting of the United States & Canada Academy of Pathology, San Antonio, March 2017

Targeted next-generation sequencing of pediatric neuro-oncology patients improves diagnosis, identifies pathogenic germline alterations, and directs targeted therapy
Annual Meeting of the American Association of Neuropathologists, Baltimore, June 2016

Cohesin gene mutations in tumorigenesis: from discovery to clinical significance
Educational session on Cohesin and cancer, annual meeting of the American Association of Cancer Research, New Orleans, April 2016

Diffuse midline gliomas with histone H3-K27M mutation: the spectrum of morphologic variation and associated genetic alterations
Annual meeting of the American Association of Neuropathologists, Denver, June 2015

Sample type bias in the analysis of cancer genomes: the impact of intratumoral heterogeneity, admixed normal cells, and ex vivo growth on cancer genomics analyses
Molecular Medicine Tri-Conference, session on Biospecimen Science & Sample Prep, San Francisco, Feb 2014

Hydrophilic polymer emboli: A not so unusual cause of lower extremity gangrene
South Bay Pathology Society, Palo Alto, December 2013

Frequent truncating mutations of the cohesin complex gene STAG2 in bladder cancer
University of California, San Francisco Resident Research Symposium, May 2013

Identification of a genetic cause of aneuploidy in human cancer
Michael Smith Genome Sciences Centre, British Columbia Cancer Agency, Vancouver, Canada, May 2012

Mutational inactivation of STAG2 causes aneuploidy in human cancer

Harold M. Weintraub Memorial Symposium, Fred Hutchinson Cancer Research Center, Seattle, WA, May 2012

Identification of a genetic cause of aneuploidy in human cancer
Plenary session of 1st annual George M. Kober Research Day, Georgetown School of Medicine, May 2012

Mutational inactivation of STAG2 causes aneuploidy in human cancer
Future Leaders in Basic Cancer Research Special Symposium, 2012 American Association for Cancer Research Annual Meeting, Chicago, IL, April 2012

Identification and therapeutic targeting of novel transforming pathways in glioblastoma multiforme
Departments of Medicine & Oncology Grand Rounds, Virginia Hospital Center, May 2011

Mutational inactivation of STAG2 causes aneuploidy in human cancer
Department of Medicine Grand Rounds, Georgetown University Medical Center, May 2011

Pharmacologic inhibition of CDK4/6 suppresses the growth of glioblastoma multiforme intracranial xenografts
Neuro Tumor Club Dinner Meeting, Society for Neuro-Oncology, 2010 American Association for Cancer Research Annual Meeting, Washington, DC, April 2010

Copy number analysis of human tumors identifies new cancer genes including CDKN2C and PTPRD
Sidney Kimmel Cancer Center, Johns Hopkins University School of Medicine, November 2008

Identification of $p18^{INK4c}$ as a tumor suppressor gene in glioblastoma multiforme
Department of Medicine Grand Rounds, Georgetown University Medical Center, May 2008

EXTRAMURAL POSTER PRESENTATIONS

Pediatric bithalamic diffuse gliomas are distinguished from their unilateral counterparts by frequent EGFR exon 20 insertions and rare histone H3 mutations
Annual meeting of the Pediatric Society for Neuro-Oncology, San Francisco, May 2019

Well-differentiated papillary mesothelioma of the peritoneum is genetically defined by mutually exclusive mutations in TRAF7 and CDC42
Annual meeting of the United States & Canada Academy of Pathology, Washington, DC, March 2019

Adenomatoid tumors of the male and female genital tract are defined by TRAF7 mutations that drive aberrant NF-kB pathway activation
Annual meeting of the United States & Canada Academy of Pathology, Vancouver, March 2018

Inactivating BAP1 mutations causing loss of nuclear expression define the majority of malignant peritoneal mesotheliomas
Annual meeting of the United States & Canada Academy of Pathology, Seattle, March 2016

Molecular analysis of the Ras-Raf-MAPK pathway in Langerhans cell histiocytosis
Annual meeting of the United States & Canada Academy of Pathology, Boston, March 2015

Frequent inactivating mutations of the cohesin complex gene STAG2 in Ewing's sarcoma associated with TP53 mutations and poor outcome
Annual meeting of the United States & Canada Academy of Pathology, San Diego, March 2014
*selected for Stowell-Orbison award and young investigator award from the International Society of Bone & Soft Tissue Pathology

Frequent truncating mutations of the cohesin complex gene STAG2 in bladder cancer
American Society for Clinical Oncology Genitourinary Cancers Symposium, San Francisco, January 2014

Frequent truncating mutations of the cohesin complex gene STAG2 in bladder cancer
Annual meeting of the United States & Canada Academy of Pathology, Baltimore, March 2013
*selected for Stowell-Orbison award

Mutational inactivation of STAG2 causes aneuploidy in human cancer
Annual meeting of the American Association for Cancer Research, Chicago, April 2012
*named a "Highly rated poster" in the top 2.5% of abstracts presented at the meeting

Sample type bias in the analysis of cancer genomes
Biospecimen Research Network Symposium, National Cancer Institute, NIH, March 2009

Deregulated localization - a novel mechanism for D-type cyclins in promoting tumorigenesis
Genes, Environment & Disease conference sponsored by NIEHS, Harvard Medical School, June 2003