

Kory R. Johnson, MS, Ph.D

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301-575-7504

SUMMARY I am a bioinformatics working professional with nearly 30 years of work experience in biotech and government.

Since 2006, I have worked at the National Institute of Neurological Disorders and Stroke (NINDS) at the National Institutes of Health (NIH).

Currently, I serve as Director of the NINDS Intramural Bioinformatics Core; overseeing both PhD bioinformatics analysts and bioinformatics application developers. Duties include, but are not limited to: assignment of work, scheduling of work, review of work, quality assurance of work, standardization and optimization of work-related methods, recruiting and retention of staff, representation of the Core in Institute-level and cross-Institute meetings, budget planning, budget adherence, and formal reporting to the Core steering committee. In addition to these duties, I first-hand perform on average 200 different omics-related analyses per year. While I also mentor/train research staff outside of the Core who choose to learn how to do bioinformatics analysis themselves.

In recognition of my accomplishments at NINDS, I have been awarded the Distinguished Performance Achievement Award seven times and the Merit Award for Excellence three times.

Former positions held have included those at the National Cancer Institute (NCI), Human Genome Sciences, and Gene Logic.

Notable career accomplishments to date include the co-founding of Gene Logic, the co-pioneering of predictive toxicogenomics, and the co-development of the NIH Stem Cell Data Management System.

To date, I have work published in over 100 manuscripts across 70 Journals. I also have been issued 5 patents in the field of predictive toxicogenomics and 1 patent in the field of stroke diagnosis.

Since 2009, I have taught graduate-level Bioinformatics as an adjunct professor for University of Maryland Global Campus (UMGC) and have been nominated for the Stanley J. Drazek Award for Teaching Excellence.

SKILLS

R, Next Generation Sequence Analysis (bulk RNA, sc/nRNA-Seq, TCR-Seq, BCR-Seq, Spatial-Seq, ChIP-Seq, ATAC-Seq, PhIP-Seq, DRiP-Seq, Pathogen-Seq, WGS, WXS), Microarray Analysis (RNA, miRNA, Methylation), classical sequence analysis, phylogenetics, protein structure modeling, serology analysis, Q-RT-PCR analysis, statistical analysis, machine learning, more.



EDUCATION

Ph.D., Bioinformatics and Computational Biology

George Mason University (2009)

Thesis: Genomic Profiling of Blood for Stroke Diagnosis

Elective Work: Identifying the molecular effects of Anthrax on Lung, Liver, and Kidney

MS, Bioinformatics

Johns Hopkins University (2003)

BS, Cell Biology and Molecular Genetics

University of Maryland (1995)

WORK EXPERIENCE

Director of Bioinformatics (5/2021 – Present)

**National Institute of Neurological Disorders and Stroke (NINDS),
National Institutes of Health (NIH),
Bethesda, Maryland**

Currently oversee PhD bioinformatics analyst and bioinformatics application developer staff working in the Bioinformatics Core. Duties include, but are not limited to: assignment of work, scheduling of work, review of work, quality assurance of work, standardization and optimization of work-related methods, recruiting and retention of staff, representation of the Core in Institute-level and cross-Institute meetings, budget planning, budget adherence, and formal reporting to the Core steering committee. While, in this capacity, I also first-hand perform ~200 ad-hoc omic analyses per year and mentor/train research staff outside of the Core who choose to learn how to do bioinformatics analysis themselves.

Bioinformatics Staff Scientist (9/2006 – 5/2021)

**National Institute of Neurological Disorders and Stroke (NINDS),
National Institutes of Health (NIH),
Bethesda, Maryland**

Served NINDS as the resident intramural bioinformatics subject matter expert. Duties included the performance of omic-based analysis support to all NINDS staff as needed. On average, I completed ~200 analyses per year; including those related to projects engaged with other Institutes at the NIH and those with external hospitals, universities, and agencies. For each analysis/project, I meet with the requestee(s) and discussed their goal(s). Where after, a list of requirements, including desired deliverables, was mutually mustered and a tentative action plan outlined and ultimately executed. I also served the Institute as a mentor in the recurring summer internship program each year; teaching visiting students how to perform different types of bioinformatics analysis.

WORK EXPERIENCE (continued)

Senior Biostatistician (1/2006 - 9/2006)

Gene Logic, Inc.

Gaithersburg, Maryland

Provided microarray analysis services for domestic and international clients. Predominantly used R, Ingenuity, and Genomatix. Analysis services included: Data Normalization (one-color, two-color), Exploratory Analysis (Tukey box plot, cov-based PCA, cor-based Heat), Outlier Analysis (z-score), Noise Modeling (CV~mean), Noise Filtering, Class Discovery (k-means, hierarchical), Statistical Testing (one sample, two sample, > two sample, paired, unpaired, parametric, non-parametric, equal variance, unequal variance, ordinal, continuous, count, ratio, categorical) +/- multiple comparison correction +/- bootstrap condition, Gene selection (Volcano plot), Confirmatory Analysis (cov-based PCA, cor-based Heat), Enrichment Analysis (Biological Functions, Canonical Pathways, Networks), Promoter Modeling, Power vs Sample-size Assessment, and Classification modeling.

Biostatistician (1/2003 - 1/2006)

Gene Logic, Inc.

Gaithersburg, Maryland

Researched and evaluated different modeling paradigms (e.g., PCR, DA, PLSR, SVM, RF, FS) using toxicogenomic microarray-based data. Per modeling, R was used. Goal was to generate predictive models for toxicity in different tissues that could be filed for patent protection and commercialized (see [PATENTS](#)).

Associate Biostatistician (1/2000 - 1/2003)

Gene Logic, Inc.

Gaithersburg, Maryland

Performed microarray analysis of 100's of toxicogenomic data sets representing different tissues (e.g., liver, kidney, heart) under different dose::time conditions. Per analysis, R was used. Goal was to identify markers of toxicity that could be filed for patent protection and commercialized (see [PATENTS](#)).

Bioinformatics Scientist (1/1999 - 1/2000)

Gene Logic, Inc.

Gaithersburg, Maryland

Developed and managed an automated sequence analysis pipeline for the characterization of differential expressed genes identified by RFLP. Per analysis, Perl was used. Automated steps included sequence trimming by Phred Score, repeat masking, and the performance of blast against refseq, est, and nr. Goal was to identify expressed genes under circumstances of disease and/or toxicity that could be filed for patent protection as markers and commercialized.

WORK EXPERIENCE (continued)

Research Scientist (1/1998 - 1/1999)

Gene Logic, Inc.

Gaithersburg, Maryland

Researched and developed branch DNA (bDNA) marker panels for use in High-throughput Screening (HITS).

Research Group Leader, Co-founder (5/1996 - 1/1998)

Gene Logic, Inc.

Gaithersburg, Maryland

Co-founded Gene Logic with funding provided by Oxford Bioscience Partners. Created and lead a 40-person lab responsible for Client tissue handling, RNA extraction, RNA isolation, cDNA synthesis, RFLP analysis, Band Recovery, Band Amplification, Band Purification and Sequencing (ABI). Additional responsibilities included staff recruitment, training, supervision and safety, budget adherence, LIMS design, reagent manufacturing and quality control, protocol development, capital equipment evaluation, purchase and maintenance.

Research Associate (5/1995 - 5/1996)

Human Genome Sciences, Inc.

Shady Grove, Maryland

Performed high-throughput Cloning, DNA extraction, DNA purification, and Sequencing (ABI) in the goal to first discover and patent genes in tissues of select species for patent protection and licensing.

Clinical Data Coordinator (5/1994 - 5/1995)

National Cancer Institute

Rockville, Maryland

Worked as a contractor (Battelle, Inc.) at the National Cancer Institute (NCI). Supervised group of 2-3 persons responsible for clinical trial data collection, data curation, database entry (Paradox), database validation/certification, and clinical code book compilation.

TEACHING EXPERIENCE

Adjunct Professor of Bioinformatics (2023 – Present)

Graduate School, Johns Hopkins university

Gene Expression Data Analysis and Visualization (AS.410.671)

TEACHING EXPERIENCE (continued)

Adjunct Professor of Bioinformatics (2009 – Present)

Graduate School, University of Maryland University College

Molecular Biology (BIOT601)

Introduction to Bioinformatics (BIOT630)

Adjunct Associate Professor of Bioinformatics (2009 – 2011)

Graduate School, George Mason University

Microarray Methodology (BINF636)

Gene Expression Analysis (BINF733)

Bioinformatics Instructor (2014 – 2019)

The Foundation for Advanced Education in the Sciences (FAES),

National Institutes of Health

RNA-Seq Analysis (BioTech 56)

PUBLISHED WORK (sorted by most recent date)

Iyer L, Johnson K, Collier S, Koretsky AP, Petrus E. Post-Critical Period **Transcriptional and Physiological Adaptations of Thalamocortical Connections after Sensory Loss**. bioRxiv [Preprint]. 2024 Nov 19:2024.11.19.624130. doi: 10.1101/2024.11.19.624130. PMID: 39876977; PMCID: PMC11774545.

Ryan VH, Lawton S, Reyes JF, Hawrot J, Frankenfield AM, Seddighi S, Ramos DM, Faghri F, Johnson NL, Zou J, Kampmann M, Replogle J, Yuan H, Johnson KR, Maric D, Hao L, Nalls MA, Ward ME. **Maintenance of neuronal TDP-43 expression requires axonal lysosome transport**. bioRxiv [Preprint]. 2024 Oct 1:2024.09.30.615241. doi: 10.1101/2024.09.30.615241. PMID: 39803527; PMCID: PMC11722429.

Stephenson RA, Johnson KR, Cheng L, Yang LG, Root JT, Gopalakrishnan J, Shih HY, Narayan PS. **Triglyceride metabolism controls inflammation and APOE4-associated disease states in microglia**. bioRxiv [Preprint]. 2024 Apr 13:2024.04.11.589145. doi: 10.1101/2024.04.11.589145. PMID: 39803455; PMCID: PMC11722234.

Seetharam D, Chandar J, Ramsoomair CK, Desgraves JF, Medina AA, Hudson AJ, Amidei A, Castro JR, Govindarajan V, Wang S, Zhang Y, Sonabend AM, Valdez MJM, Maric D, Govindarajan V, Rivas SR, Lu VM, Tiwari R, Sharifi N, Thomas E, Alexander M, DeMarino C, Johnson K, De La Fuente MI, Nasany RA, Noviello TMR, Ivan ME, Komotar RJ, Iavarone A, Nath A, Heiss J, Ceccarelli M, Chiappinelli KB, Figueroa ME, Bayik D, Shah AH. **Targeting ZNF638 activates antiviral immune responses and potentiates immune checkpoint inhibition in glioblastoma**. bioRxiv [Preprint]. 2024 Oct 15:2024.10.13.618076. doi: 10.1101/2024.10.13.618076. PMID: 39464150; PMCID: PMC11507686.

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Saez-Atienzar S, Souza CDS, Chia R, Beal SN, Lorenzini I, Huang R, Levy J, Burciu C, Ding J, Gibbs JR, Jones A, Dewan R, Pensato V, Peverelli S, Corrado L, van Vugt JJFA, van Rheenen W, Tunca C, Bayraktar E, Xia M; International ALS Genomics Consortium; ITALSGEN Consortium; SLAGEN Consortium; Project MinE ALS Sequencing Consortium; Iacoangeli A, Shatunov A, Tiloca C, Ticozzi N, Verde F, Mazzini L, Kenna K, Al Khleifat A, Opie-Martin S, Raggi F, Filosto M, Piccinelli SC, Padovani A, Gagliardi S, Inghilleri M, Ferlini A, Vasta R, Calvo A, Moglia C, Canosa A, Manera U, Grassano M, Mandrioli J, Mora G, Lunetta C, Tanel R, Trojsi F, Cardinali P, Gallone S, Brunetti M, Galimberti D, Serpente M, Fenoglio C, Scarpini E, Comi GP, Corti S, Del Bo R, Ceroni M, Pinter GL, Taroni F, Bella ED, Bersano E, Curtis CJ, Lee SH, Chung R, Patel H, Morrison KE, Cooper-Knock J, Shaw PJ, Breen G, Dobson RJB, Dalgard CL; American Genome Center; Scholz SW, Al-Chalabi A, van den Berg LH, McLaughlin R, Hardiman O, Cereda C, Sorarù G, D'Alfonso S, Chandran S, Pal S, Ratti A, Gellera C, Johnson K, Doucet-O'Hare T, Pasternack N, Wang T, Nath A, Siciliano G, Silani V, Başak AN, Veldink JH, Camu W, Glass JD, Landers JE, Chiò A, Sattler R, Shaw CE, Ferraiuolo L, Fogh I, Traynor BJ. **Mechanism-free repurposing of drugs for C9orf72-related ALS/FTD using large-scale genomic data.** Cell Genom. 2024 Nov 13;4(11):100679. doi: 10.1016/j.xgen.2024.100679. Epub 2024 Oct 21. PMID: 39437787; PMCID: PMC11605688.

MacDonald M, Fonseca PAS, Johnson KR, Murray EM, Kember RL, Kranzler HR, Mayfield RD, da Silva D. **Divergent gene expression patterns in alcohol and opioid use disorders lead to consistent alterations in functional networks within the dorsolateral prefrontal cortex.** Transl Psychiatry. 2024 Oct 14;14(1):437. doi: 10.1038/s41398-024-03143-z. PMID: 39402051; PMCID: PMC11473550.

Lin HP, Petersen JD, Gilsrud AJ, Madruga A, D'Silva TM, Huang X, Shammas MK, Randolph NP, Johnson KR, Li Y, Jones DR, Pacold ME, Narendra DP. **DELE1 maintains muscle proteostasis to promote growth and survival in mitochondrial myopathy.** EMBO J. 2024 Nov;43(22):5548-5585. doi: 10.1038/s44318-024-00242-x. Epub 2024 Oct 8. PMID: 39379554; PMCID: PMC11574132.

Rajebhosale P, Jone A, Johnson KR, Hofland R, Palarpalar C, Khan S, Role LW, Talmage DA. **Neuregulin1 Nuclear Signaling Influences Adult Neurogenesis and Regulates a Schizophrenia Susceptibility Gene Network within the Mouse Dentate Gyrus.** J Neurosci. 2024 Oct 23;44(43):e0063242024. doi: 10.1523/JNEUROSCI.0063-24.2024. PMID: 39214704; PMCID: PMC11502234.

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Bolduc V, Sizov K, Brull A, Esposito E, Chen GS, Uapinyoying P, Sarathy A, Johnson KR, Bönemann CG. **Allele-specific CRISPR-Cas9 editing inactivates a single nucleotide variant associated with collagen VI muscular dystrophy.** Mol Ther Nucleic Acids. 2024 Jul 16;35(3):102269. doi: 10.1016/j.omtn.2024.102269. PMID: 39171142; PMCID: PMC11338111.

Mortazavi A, Khan AU, Nieblas-Bedolla E, Boddeti U, Bachani M, Ksendzovsky A, Johnson K, Zaghloul KA. **Differential gene expression underlying epileptogenicity in patients with gliomas.** Neurooncol Adv. 2024 Jun 21;6(1):vdae103. doi: 10.1093/noajnl/vdae103. PMID: 39022648; PMCID: PMC11252565.

Pasternack N, Doucet-O'Hare T, Johnson K; NYGC Consortium; Paulsen O, Nath A. **Endogenous retroviruses are dysregulated in ALS.** iScience. 2024 May 28;27(7):110147. doi: 10.1016/j.isci.2024.110147. PMID: 38989463; PMCID: PMC11233923.

Snyder A, Ryan VH, Hawrot J, Lawton S, Ramos DM, Qi YA, Johnson KR, Reed X, Johnson NL, Kollasch AW, Duffy MF, VandeVrede L, Cochran JN, Miller BL, Toro C, Bielekova B, Marks DS, Yokoyama JS, Kwan JY, Cookson MR, Ward ME. **An ANXA11 P93S variant dysregulates TDP-43 and causes corticobasal syndrome.** Alzheimers Dement. 2024 Aug;20(8):5220-5235. doi: 10.1002/alz.13915. Epub 2024 Jun 26. PMID: 38923692; PMCID: PMC11350008.

MacDonald M, Fonseca PAS, Johnson K, Murray EM, Kember RL, Kranzler H, Mayfield D, da Silva D. **Divergent gene expression patterns in alcohol and opioid use disorders lead to consistent alterations in functional networks within the Dorsolateral Prefrontal Cortex.** bioRxiv [Preprint]. 2024 May 1:2024.04.29.591734. doi: 10.1101/2024.04.29.591734. Update in: Transl Psychiatry. 2024 Oct 14;14(1):437. doi: 10.1038/s41398-024-03143-z. PMID: 38746311; PMCID: PMC11092658.

Mohassel P, Rooney J, Zou Y, Johnson K, Norato G, Hearn H, Nalls MA, Yun P, Ogata T, Silverstein S, Sleboda DA, Roberts TJ, Rifkin DB, Bönemann CG. **Collagen type VI regulates TGF β bioavailability in skeletal muscle.** bioRxiv [Preprint]. 2023 Jun 24:2023.06.22.545964. doi: 10.1101/2023.06.22.545964. PMID: 38586035; PMCID: PMC10996771.

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Bolduc V, Sizov K, Brull A, Esposito E, Chen GS, Uapinyoying P, Sarathy A, Johnson K, Bönemann CG. **Allele-specific CRISPR/Cas9 editing inactivates a single nucleotide variant associated with collagen VI muscular dystrophy.** bioRxiv [Preprint]. 2024 Mar 22:2024.03.22.586265. doi: 10.1101/2024.03.22.586265. Update in: Mol Ther Nucleic Acids. 2024 Jul 16;35(3):102269. doi: 10.1016/j.omtn.2024.102269. PMID: 38585815; PMCID: PMC10996683.

Donkervoort S, van de Locht M, Ronchi D, Reunert J, McLean CA, Zaki M, Orbach R, de Winter JM, Conijn S, Hoomoedt D, Neto OLA, Magri F, Viaene AN, Foley AR, Gorokhova S, Bolduc V, Hu Y, Acquaye N, Napoli L, Park JH, Immadisetty K, Miles LB, Essawi M, McModie S, Ferreira LF, Zanotti S, Neuhaus SB, Medne L, ElBagoury N, Johnson KR, Zhang Y, Laing NG, Davis MR, Bryson-Richardson RJ, Hwee DT, Hartman JJ, Malik FI, Kekenos-Huskey PM, Comi GP, Sharaf-Eldin W, Marquardt T, Ravenscroft G, Bönemann CG, Ottenheim CAC. **Pathogenic TNNI1 variants disrupt sarcomere contractility resulting in hypo- and hypercontractile muscle disease.** Sci Transl Med. 2024 Apr 3;16(741):eadg2841. doi: 10.1126/scitranslmed.adg2841. Epub 2024 Apr 3. PMID: 38569017.

Chen KG, Park K, Maric D, Johnson KR, Robey PG, Mallon BS. **Metabolic Quadrivalency in RSeT Human Embryonic Stem Cells.** bioRxiv [Preprint]. 2024 Feb 22:2024.02.21.581486. doi: 10.1101/2024.02.21.581486. PMID: 38496581; PMCID: PMC10942463.

Chen KG, Johnson KR, Park K, Maric D, Yang F, Liu WF, Fann YC, Mallon BS, Robey PG. **Resistance to Naïve and Formative Pluripotency Conversion in RSeT Human Embryonic Stem Cells.** bioRxiv [Preprint]. 2024 Apr 12:2024.02.16.580778. doi: 10.1101/2024.02.16.580778. PMID: 38410444; PMCID: PMC10896352.

Walitt B, Singh K, LaMunion SR, Hallett M, Jacobson S, Chen K, Enose-Akahata Y, Apps R, Barb JJ, Bedard P, Brychta RJ, Buckley AW, Burbelo PD, Calco B, Cathay B, Chen L, Chigurupati S, Chen J, Cheung F, Chin LMK, Coleman BW, Courville AB, Deming MS, Drinkard B, Feng LR, Ferrucci L, Gabel SA, Gavin A, Goldstein DS, Hassanzadeh S, Horan SC, Horovitz SG, Johnson KR, Govan AJ, Knutson KM, Kreskow JD, Levin M, Lyons JJ, Madian N, Malik N, Mammen AL, McCulloch JA, McGurkin PM, Milner JD, Moaddel R, Mueller GA, Mukherjee A, Muñoz-Braceras S, Norato G, Pak K, Pinal-Fernandez I, Popa T, Reoma LB, Sack MN, Safavi F, Saligan LN, Sellers BA, Sinclair S, Smith B, Snow J, Solin S, Stussman BJ, Trinchieri G, Turner SA, Vetter CS, Vial F, Vizioli C, Williams A, Yang SB; Center for Human Immunology, Autoimmunity, and Inflammation (CHI) Consortium; Nath A. **Deep phenotyping of post-infectious myalgic encephalomyelitis/chronic fatigue syndrome.** Nat Commun. 2024 Feb 21;15(1):907. doi: 10.1038/s41467-024-45107-3. PMID: 38383456; PMCID: PMC10881493.

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Hasan S, Fernandopulle MS, Humble SW, Frankenfield AM, Li H, Prestil R, Johnson KR, Ryan BJ, Wade-Martins R, Ward ME, Hao L. **Multi-modal proteomic characterization of lysosomal function and proteostasis in progranulin-deficient neurons.** Mol Neurodegener. 2023 Dec 18;18(1):96. doi: 10.1186/s13024-023-00696-3. Erratum for: Mol Neurodegener. 2023 Nov 16;18(1):87. doi: 10.1186/s13024-023-00673-w. PMID: 38111033; PMCID: PMC10729419.

Snyder A, Ryan VH, Hawrot J, Lawton S, Ramos DM, Qi YA, Johnson K, Reed X, Johnson NL, Kollasch AW, Duffy M, VandeVrede L, Cochran JN, Miller BL, Toro C, Bielekova B, Yokoyama JS, Marks DS, Kwan JY, Cookson MR, Ward ME. **An ANXA11 P93S variant dysregulates TDP-43 and causes corticobasal syndrome.** Res Sq [Preprint]. 2023 Oct 19:rs.3.rs-3462973. doi: 10.21203/rs.3.rs-3462973/v1. Update in: Alzheimers Dement. 2024 Aug;20(8):5220-5235. doi: 10.1002/alz.13915. PMID: 37886540; PMCID: PMC10602153.

Shah AH, Rivas SR, Doucet-O'Hare TT, Govindarajan V, DeMarino C, Wang T, Ampie L, Zhang Y, Banasavadi-Siddegowda YK, Walbridge S, Maric D, Garcia-Montojo M, Suter RK, Lee MH, Zaghoul KA, Steiner J, Elkahoul AG, Chandar J, Seetharam D, Desgraves J, Li W, Johnson K, Ivan ME, Komotar RJ, Gilbert MR, Heiss JD, Nath A. **Human endogenous retrovirus K contributes to a stem cell niche in glioblastoma.** J Clin Invest. 2023 Jul 3;133(13):e167929. doi: 10.1172/JCI167929. PMID: 37395282; PMCID: PMC10313366.

Choi BR, Johnson KR, Maric D, McGavern DB. **Monocyte-derived IL-6 programs microglia to rebuild damaged brain vasculature.** Nat Immunol. 2023 Jul;24(7):1110-1123. doi: 10.1038/s41590-023-01521-1. Epub 2023 May 29. PMID: 37248420; PMCID: PMC11531796.

Kim B, Kim D, Schulmann A, Patel Y, Caban-Rivera C, Kim P, Jambhale A, Johnson KR, Feng N, Xu Q, Kang SJ, Mandal A, Kelly M, Akula N, McMahon FJ, Lipska B, Marenco S, Auluck PK. **Cellular Diversity in Human Subgenual Anterior Cingulate and Dorsolateral Prefrontal Cortex by Single-Nucleus RNA-Sequencing.** J Neurosci. 2023 May 10;43(19):3582-3597. doi: 10.1523/JNEUROSCI.0830-22.2023. Epub 2023 Apr 10. PMID: 37037607; PMCID: PMC10184745.

Spagnolo PA, Johnson K, Hodgkinson C, Goldman D, Hallett M. **Methylome changes associated with functional movement/conversion disorder: Influence of biological sex and childhood abuse exposure.** Prog Neuropsychopharmacol Biol Psychiatry. 2023 Jul 13;125:110756. doi: 10.1016/j.pnpbp.2023.110756. Epub 2023 Mar 21. PMID: 36958667; PMCID: PMC10205664.

PUBLISHED WORK (continued)

Wang Z, Li Q, Kolls BJ, Mace B, Yu S, Li X, Liu W, Chaparro E, Shen Y, Dang L, Del Águila Á, Bernstock JD, Johnson KR, Yao J, Wetsel WC, Moore SD, Turner DA, Yang W. **Sustained overexpression of spliced X-box-binding protein-1 in neurons leads to spontaneous seizures and sudden death in mice.** Commun Biol. 2023 Mar 9;6(1):252. doi: 10.1038/s42003-023-04594-8. PMID: 36894627; PMCID: PMC9998612.

Hasan S, Fernandopulle MS, Humble SW, Frankenfield AM, Li H, Prestil R, Johnson KR, Ryan BJ, Wade-Martins R, Ward ME, Hao L. **Multi-modal Proteomic Characterization of Lysosomal Function and Proteostasis in Progranulin-Deficient Neurons.** bioRxiv [Preprint]. 2023 Feb 24:2023.02.24.529955. doi: 10.1101/2023.02.24.529955. Update in: Mol Neurodegener. 2023 Nov 16;18(1):87. doi: 10.1186/s13024-023-00673-w. PMID: 36865171; PMCID: PMC9980118.

Enose-Akahata Y, Wang L, Almsned F, Johnson KR, Mina Y, Ohayon J, Wang XW, Jacobson S. **The repertoire of CSF antiviral antibodies in patients with neuroinflammatory diseases.** Sci Adv. 2023 Jan 4;9(1):eabq6978. doi: 10.1126/sciadv.abq6978. Epub 2023 Jan 4. PMID: 36598996; PMCID: PMC9812372.

Garcia-Montojo M, Simula ER, Fathi S, McMahan C, Ghosal A, Berry JD, Cudkowicz M, Elkahloun A, Johnson K, Norato G, Jensen P, James T, Sechi LA, Nath A. **Antibody Response to HML-2 May Be Protective in Amyotrophic Lateral Sclerosis.** Ann Neurol. 2022 Nov;92(5):782-792. doi: 10.1002/ana.26466. Epub 2022 Aug 24. PMID: 36053951; PMCID: PMC9805205.

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Gur D, Bain EJ, Johnson KR, Aman AJ, Pasolli HA, Flynn JD, Allen MC, Deheyn DD, Lee JC, Lippincott-Schwartz J, Parichy DM. **In situ differentiation of iridophore crystalloypes underlies zebrafish stripe patterning.** Nat Commun. 2022 Jul 26;13(1):4330. doi: 10.1038/s41467-022-32152-z. Erratum for: Nat Commun. 2020 Dec 15;11(1):6391. doi: 10.1038/s41467-020-20088-1. PMID: 35882864; PMCID: PMC9325738.

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Differential expression of molecules associated with intra-cerebral hemorrhage.
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Molecular toxicology modeling methods.
Issued Patent: US-7,415,358

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Molecular toxicology modeling – liver.

Issued Patent: US-7,590,493

Molecular toxicology modeling – kidney.

Issued Patent: US-7,426,441

Molecular toxicology modeling - primary hepatocytes.

Issued Patent: US-7,469,185

AWARDS

Distinguished Performance Achievement Award

National Institute of Neurological Disorders and Stroke (NINDS)

Division of Intramural Research (DIR)

National Institutes of Health (NIH)

Received: 2011, 2012, 2013, 2014, 2015, 2016, 2021

Merit Award for Excellence

National Institute of Neurological Disorders and Stroke (NINDS)

Division of Intramural Research (DIR)

Received: 2008, 2012, 2015

Stanley J. Drazek Teaching Excellence Award

University of Maryland University College

Nominated: 2011, 2012

Service Award, 3yrs

SRA International, Inc.

Received: 2009

Service Award, 10yrs

Gene Logic, Inc.

Received: 2006

Service Award, 7yrs

Gene Logic, Inc.

Received: 2003

Service Award, 3yrs

Gene Logic, Inc.

Received: 1999

INVITED TALKS

Bioinformatics at NINDS: Who We Are and What We Do.

Neuroscience Data Symposium (Annual, 2006-Present)
National Institute of Neurological Disorders & Stroke (NINDS)

Differential HERV expression in developing Neurons by RNA-Seq.

Special Interest Seminar (2016)
National Institute of Neurological Disorders & Stroke (NINDS)

RNA-Seq Analysis of the Rat SON.

RNA-Seq Analysis Workshop (2015)
National Institutes of Health (NIH)

Quantitative Profiling of the TCR repertoire using barcoding.

National Heart Lung and Blood (NHLBI) Conference Series (2014)
National Institutes of Health (NIH)

Standardization of JCV Serology data for PML risk.

PML Consortium (2014)
New York Academy of Sciences, New York

HERV-K expression in ALS.

Biomedical Computing Interest Group (2014)
National Institutes of Health (NIH)

MEMBERSHIPS

American Statistical Association
International Society of Computational Biology
North America Scholar Consortium
The Science Advisory Board
Virginia Academy of Sciences
Washington Statistical Society

FEDERAL CLEARANCE

Public trust.

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Available upon request.