# Curriculum Vitae and Bibliography
# Asha Nair, P.M.P., M.S.

## 1. PERSONAL INFORMATION

**Place of Birth** – Dubai, UAE

**Citizenship –** USA

## 2. PRESENT ACADEMIC RANK AND POSITION

**Informatics Specialist II** 07/2015 – Present
Division of Biomedical Statistics and Informatics (BSI),
Mayo Clinic, Rochester, MN

- Bioinformatics technical lead for messenger RNA (mRNA) and long intergenic non-coding RNA (lincRNA) Next Generation Sequencing (NGS) data
- Bioinformatics lead of microarray data from Affymetrix and Illumina platforms
- Technical and Project manager for both RNA-Seq and data integration projects for PI Dr. Raul Urrutia
- Continued support for development of RNA-Seq and lincRNA workflows to run in a High Performance Computing environment
- Work on a wide variety of projects for secondary and tertiary analyses on NGS mRNA and lincRNA, microarray, various diseases and cancer
- Work on the research and development of RNA sequencing best practices for clinical sequencing facility (DLMP)

Contribute to multiple concurrent research studies, grants, publications, posters and abstracts

## 3. EDUCATION

Rajiv Gandhi Institute of Technology, Kerala, India 2004
B.S., Electrical and Electronics Engineering

Project Management Institute, Inc., USA 2008
P.M.P., Project Management Professional

University of Minnesota Rochester, MN, USA 2012
MS, Biomedical Informatics and Computational Biology

University of Minnesota Rochester, MN, USA present
PhD, Biomedical Informatics and Computational Biology

## 4. BOARD CERTIFICATION(S)

**Project Management Institute, Inc. (PMI)**

Project Management Professional 2008 – Present

## 5. HONORS/AWARDS

Travel Fellowship Award 2014
ISMB 2014, Boston, MA

## 6. PREVIOUS PROFESSIONAL POSITIONS AND MAJOR APPOINTMENTS

**Engineering Apprentice** 2004
Dotsan Co. LLC, Sharjah, UAE

- Offered engineering assistance to senior estimation engineers, implemented cost estimation projects and created working models using designing software, AUTOCAD.

**Assistant Estimation Engineer** 2004 – 2008
Moeller Group (Felten & Guilleaume (F&G)), Dubai, UAE

- Offered technical assistance to senior electrical engineers and managing director, performed cost estimation and evaluation of estimation quotes from external clients, worked on the design of numerous projects and presented project outcomes to stakeholders.

**Graduate Intern** 2009 – 2010
University of Minnesota Rochester and Mayo Clinic, Rochester, MN

- Developed computational approaches to score prostate cases based on three antibody stains, assisted in discovering high grade regions and development of graphical interface for display of results.

**Informatics Associate** 2010 – 2012
Division of Biomedical Statistics and Informatics, Mayo Clinic,
Rochester, MN

- Worked with Informatics Specialists-I, II and lead on numerous NGS and microarray projects. Installed and evaluated various NGS tools for data analysis. Contributed to the development of NGS informatics applications such as exome and mRNA workflows, and presented the work at internal seminars and national conferences.

**Informatics Specialist** 2012 – 2015
Division of Biomedical Statistics and Informatics (BSI),
Mayo Clinic, Rochester, MN

- Bioinformatics analysis of messenger RNA (mRNA) and long intergenic non-coding RNA (lincRNA) Next Generation Sequencing (NGS) data
- Bioinformatics analysis of microarray data from Affymetrix and Illumina platforms
- Develop NGS secondary analysis workflows for mRNA and lincRNA to run in a High Performance Computing environment
- Work on a wide variety of projects for secondary and tertiary analyses on NGS mRNA and lincRNA, microarray, various diseases and cancer
- Work on the research and development of RNA sequencing best practices for clinical sequencing facility (DLMP)

Contribute to multiple concurrent research studies, grants, publications, posters and abstracts

## 7. PROFESSIONAL & COMMUNITY MEMBERSHIPS, SOCIETIES AND SERVICES

Project Management Institute, Inc. (PMI) 2008 – Present
Member

International Society for Computational Biology (ISCB) 2011 – Present
Member

## 8. EDUCATIONAL ACTIVITIES

### A. Curriculum/Course Development

Development of BSI Education Modules 07/2013 - Present
Mayo Clinic, Rochester, Minnesota

- Arranging content together for the RNA Sequencing education modules

## B. Teaching

### Seminars

XGen Congress and Exposition Highlights 2011
Bioinformatics PI Support Meeting
Rochester, MN

RNA-Seq differential expression analysis using edgeR 2012 & 2013
Bioinformatics PI Support Meeting, and
Formal Training to new Informatics Specialists
Rochester, MN

IPA Ingenuity for Pathway analysis 2013
Bioinformatics PI Support Meeting
Rochester, MN

ISMB 2014 Highlights 2014
Bioinformatics PI Support Meeting
Rochester, MN

Tophat Fusion Post processing and filters 2014
Bioinformatics PI Support Meeting
Rochester, MN

RNA-Skim for gene expression quantification 2014
RNA Technical Orientation Group Meeting
Rochester, MN

Effect of RNA degradation on gene expression 2014
Bioinformatics Technical Meeting
Rochester, MN

Fusion annotation and visualization for RNA-Seq data 2016
Bioinformatics PI Support Meeting
Rochester, MN

LincRNAs in normal prostate samples 2017
Allied Health Staff Meeting
Rochester, MN

## E. Honors and Awards for Education

First prize for poster competition held at UMR Symposium January 2016

Poster title: Differential frequency of miRNA binding sites for
Triple Negative breast cancer

## 9. INSTITUTIONAL/DEPARTMENTAL ADMINISTRATIVE RESPONSIBILITIES, COMMITTEE MEMBERSHIPS AND OTHER ACTIVITIES

### Mayo Clinic in Rochester

Microarray Technology Oriented Group (TOG), Co-Lead 2011 - Present

- I offer as a one of the primary contacts for microarray projects
- I manage microarray projects and assign to Informatics Specialists that are trained in this technology
- I am responsible for training, assigning projects, designing appropriate analysis plans, and providing consultation to Mayo and external investigators

mRNA Technology Oriented Group (TOG), Member and co-developer 2012 – Present

- I offer as a one of the primary contacts for mRNA-Seq projects
- I actively work on the testing and development of the workflow
- I am responsible for training, designing appropriate analysis plans, and providing consultation to Mayo and external investigators

lincRNA Technology Oriented Group (TOG), Lead 2012 - Present

- I developed and continue to improve the lincRNA analysis workflow
- I am responsible for training Informatics Specialists for this workflow
- I also assign and manage the projects involving the analysis of lincRNA NGS data

## 10. PRESENTATIONS

### International

-

### National

- *TREAT – A comprehensive open framework for targeted re-sequencing analysis* 3/2011
  Poster Presentation, Cambridge Healthtech Institute’s XGen Congress and Exposition
  San Diego, CA, USA

- *Optimizing sequence yield and interpreting data quality for RNA Sequencing* 07/2012
  Poster Presentation, Intelligent Systems for Molecular Biology (ISMB)
  Long Beach, CA, USA

- *MAP-RSeq – Mayo Analysis Pipeline for RNA Sequencing* 10/2013
  Poster Presentation, American Society for Human Genetics (ASHG)
  Boston, MA, USA

- *Identification of circular RNAs and their potential regulation in Breast Cancer Subtypes* 07/2014
  Poster Presentation, Intelligent Systems for Molecular Biology (ISMB)
  Boston, MA, US

**Regional**

- *Identification of expressed long intergenic non-coding RNA (lincRNA) using Whole Transcriptome Sequencing technology* 10/2013
  Poster Presentation, Center for Individualized Medicine (CIM)
  Mayo Clinic, Rochester, MN, USA

- *A catalog of identified circular RNAs in Breast Cancer Subtypes* 10/2014
  Poster Presentation, Center for Individualized Medicine (CIM)
  Mayo Clinic, Rochester, MN, USA

## 11. RESEARCH INTERESTS

My research interests include the following:

- Use Bioinformatics Methods and tools to analyze Next Generation Sequencing data, both genomic and whole transcriptomic data types

- Use Bioinformatics Methods and tools to analyze Microarray data for both Affymetrix and Illumina platforms

- Develop methods to identify, quantify, annotate and further detect differential expressed genes for mRNA, lincRNA and circular RNA (circRNA) types

- Develop methods to integrate mRNA-microRNA, mRNA-ChIP-Seq, mRNA-miRNA-circRNA-lincRNA interactions in the whole transcriptome landscape

- Identify tumor-normal differences in terms of gene expression and regulation in various cancer types using mRNA, miRNA, circRNA and lincRNA datasets

## 12. BIBLIOGRAPHY

### Full length, peer-reviewed, original articles

1. Graham RP, **Nair AA**, Davila JI, Jin L, Jen J, Sukov WR, Wu TT, Appelman HD, Torres-Mora J, Perry KD, Zhang L, Kloft-Nelson SM, Knudson RA, Greipp PT, Folpe AL. Mod Pathol. 2017 Jul 21. doi: 10.1038/modpathol.2017.68. PMID: 28731043

2. Sarmento OF, Svingen PA, Xiong Y, Sun Z, Bamidele AO, Mathison AJ, Smyrk TC, **Nair AA**, Gonzalez MM, Sagstetter MR, Baheti S, McGovern DP, Friton JJ, Papadakis KA, Gautam G, Xavier RJ, Urrutia RA, Faubion WA. J Biol Chem. 2017 Jan 13;292(2):706-722. doi: 10.1074/jbc.M116.749663. Epub 2016 Dec 1. PMID: 27909059

3. **Nair AA**, Niu N, Tang X, Thompson KJ, Wang L, Kocher JP, Subramanian S, Kalari KR. Oncotarget. 2016 Dec 6;7(49):80967-80979. doi: 10.18632/oncotarget.13134. PMID: 27829232

4. Davila JI, Fadra NM, Wang X, McDonald AM, **Nair AA**, Crusan BR, Wu X, Blommel JH, Jen J, Rumilla KM, Jenkins RB, Aypar U, Klee EW, Kipp BR, Halling KC. BMC Genomics. 2016 Oct 20;17(1):814. PMID: 27765019

5. Kalari KR, Thompson KJ, **Nair AA**, Tang X, Bockol MA, Jhawar N, Swaminathan SK, Lowe VJ, Kandimalla KK. Front Neurosci. 2016 Mar 1;10:71. doi: 10.3389/fnins.2016.00071. eCollection 2016. PMID: 26973449

6. Kitange GJ, Mladek AC, Schroeder MA, Pokorny JC, Carlson BL, Zhang Y, **Nair AA**, Lee JH, Yan H, Decker PA, Zhang Z, Sarkaria JN. Cell Rep. 2016 Mar 22;14(11):2587-98. doi: 10.1016/j.celrep.2016.02.045. Epub 2016 Mar 10. PMID: 26972001

7. Iankov ID, Kurokawa CB, D'Assoro AB, Ingle JN, Domingo-Musibay E, Allen C, Crosby CM, **Nair AA**, Liu MC, Aderca I, Federspiel MJ, Galanis E. Cancer Gene Ther. 2015 Sep;22(9):438-44. doi: 10.1038/cgt.2015.36. Epub 2015 Aug 14. PMID: 26272026

8. Larson NB, McDonnell S, French AJ, Fogarty Z, Cheville J, Middha S, Riska S, Baheti S, **Nair AA**, Wang L, Schaid DJ, Thibodeau SN. Am J Hum Genet. 2015 Jun 4;96(6):869-82. doi: 10.1016/j.ajhg.2015.04.015. Epub 2015 May 14. PMID: 25983244

9. Thalji NM, Hagler MA, Zhang H, Casaclang-Verzosa G, **Nair AA**, Suri RM, Miller JD. Non-Biased Molecular Screening Identifies Novel Molecular Regulators of Fibrogenic and Proliferative Signaling in Myxomatous Mitral Valve Disease. Circ Cardiovasc Genet. 2015 Mar 26. pii: CIRCGENETICS.114.000921. PubMed PMID: 25814644.

10. Zhang Y, Tao C, Jiang G, **Nair AA**, Su J, Chute CG, Liu H. Network-based analysis reveals distinct association patterns in a semantic MEDLINE-based drug-disease-gene network. J Biomed Semantics. 2014 Aug 6;5:33. doi:10.1186/2041-1480-5-33. eCollection 2014. PubMed PMID: 25170419; PubMed CentralPMCID: PMC4137727.

11. Kalari KR, **Nair AA**, Bhavsar JD, O'Brien DR, Davila JI, Bockol MA, Nie J, Tang X, Baheti S, Doughty JB, Middha S, Sicotte H, Thompson AE, Asmann YW, Kocher JP. MAP-RSeq: Mayo Analysis Pipeline for RNA sequencing. BMC Bioinformatics. 2014 Jun27;15:224. doi: 10.1186/1471-2105-15-224. PubMed PMID: 24972667; PubMed CentralPMCID: PMC4228501.

12. Dudakovic A, Camilleri E, Riester SM, Lewallen EA, Kvasha S, Chen X, Radel DJ,Anderson JM, **Nair AA**, Evans JM, Krych AJ, Smith J, Deyle DR, Stein JL, Stein GS, Im HJ, Cool SM, Westendorf JJ, Kakar S, Dietz AB, van Wijnen AJ. High-resolution molecular validation of self-renewal and spontaneous differentiation in clinical-grade adipose-tissue derived human mesenchymal stem cells. J CellBiochem. 2014 Oct;115(10):1816-28. doi: 10.1002/jcb.24852. PubMed PMID: 24905804; PubMed Central PMCID: PMC4225070.

13. Camilleri M, Carlson P, Acosta A, Busciglio I, **Nair AA**, Gibbons SJ, FarrugiaG, Klee EW. RNA sequencing shows transcriptomic changes in rectosigmoid mucosa inpatients with irritable bowel syndrome-diarrhea: a pilot case-control study. Am JPhysiol Gastrointest Liver Physiol. 2014 Jun 15;306(12):G1089-98. doi:10.1152/ajpgi.00068.2014. Epub 2014 Apr 24. PubMed PMID: 24763552; PubMed CentralPMCID: PMC4059976.

14. Sun Z, Asmann YW, **Nair A**, Zhang Y, Wang L, Kalari KR, Bhagwate AV, Baker TR, Carr JM, Kocher JP, Perez EA, Thompson EA. Impact of library preparation on downstream analysis and interpretation of RNA-Seq data: comparison between Illumina PolyA and NuGEN Ovation protocol. PLoS One. 2013 Aug 19;8(8):e71745. doi: 10.1371/journal.pone.0071745. eCollection 2013. PubMed PMID: 23977132; PubMed Central PMCID: PMC3747248.

15. Borad MJ, Champion MD, Egan JB, Liang WS, Fonseca R, Bryce AH, McCullough AE, Barrett MT, Hunt K, Patel MD, Young SW, Collins JM, Silva AC, Condjella RM, BlockM, McWilliams RR, Lazaridis KN, Klee EW, Bible KC, Harris P, Oliver GR, BhavsarJD, **Nair AA**, Middha S, Asmann Y, Kocher JP, Schahl K, Kipp BR, Barr Fritcher EG, Baker A, Aldrich J, Kurdoglu A, Izatt T, Christoforides A, Cherni I, Nasser S, Reiman R, Phillips L, McDonald J, Adkins J, Mastrian SD, Placek P, Watanabe AT,Lobello J, Han H, Von Hoff D, Craig DW, Stewart AK, Carpten JD. Integratedgenomic characterization reveals novel, therapeutically relevant drug targets in FGFR and EGFR pathways in sporadic intrahepatic cholangiocarcinoma. PLoS Genet.2014 Feb 13;10(2):e1004135. doi: 10.1371/journal.pgen.1004135. eCollection 2014Feb. PubMed PMID: 24550739; PubMed Central PMCID: PMC3923676.

16. Allen M, Zou F, Chai HS, Younkin CS, Crook J, Pankratz VS, Carrasquillo MM,Rowley CN, **Nair AA**, Middha S, Maharjan S, Nguyen T, Ma L, Malphrus KG, Palusak R,Lincoln S, Bisceglio G, Georgescu C, Schultz D, Rakhshan F, Kolbert CP, Jen J,Haines JL, Mayeux R, Pericak-Vance MA, Farrer LA, Schellenberg GD; Alzheimer's Disease Genetics Consortium, Petersen RC, Graff-Radford NR, Dickson DW, YounkinSG, Ertekin-Taner N. Novel late-onset Alzheimer disease loci variants associate with brain gene expression. Neurology. 2012 Jul 17;79(3):221-8. doi:10.1212/WNL.0b013e3182605801. Epub 2012 Jun 20. PubMed PMID: 22722634; PubMedCentral PMCID: PMC3398432.

17. Zou F, Chai HS, Younkin CS, Allen M, Crook J, Pankratz VS, Carrasquillo MM, Rowley CN, **Nair AA**, Middha S, Maharjan S, Nguyen T, Ma L, Malphrus KG, Palusak R,Lincoln S, Bisceglio G, Georgescu C, Kouri N, Kolbert CP, Jen J, Haines JL,Mayeux R, Pericak-Vance MA, Farrer LA, Schellenberg GD; Alzheimer's Disease Genetics Consortium, Petersen RC, Graff-Radford NR, Dickson DW, Younkin SG, Ertekin-Taner N. Brain expression genome-wide association study (eGWAS) identifies human disease-associated variants. PLoS Genet. 2012;8(6):e1002707.doi: 10.1371/journal.pgen.1002707. Epub 2012 Jun 7. PubMed PMID: 22685416; PubMedCentral PMCID: PMC3369937.

18. Allen M, Zou F, Chai HS, Younkin CS, Miles R, **Nair AA**, Crook JE, Pankratz VS, Carrasquillo MM, Rowley CN, Nguyen T, Ma L, Malphrus KG, Bisceglio G, OrtolazaAI, Palusak R, Middha S, Maharjan S, Georgescu C, Schultz D, Rakhshan F, Kolbert CP, Jen J, Sando SB, Aasly JO, Barcikowska M, Uitti RJ, Wszolek ZK, Ross OA, Petersen RC, Graff-Radford NR, Dickson DW, Younkin SG, Ertekin-Taner N.Glutathione S-transferase omega genes in Alzheimer and Parkinson disease risk, age-at-diagnosis and brain gene expression: an association study with mechanistic implications. Mol Neurodegener. 2012 Apr 11;7:13. doi: 10.1186/1750-1326-7-13.PubMed PMID: 22494505; PubMed Central PMCID: PMC3393625.

19. Kalari KR, Rossell D, Necela BM, Asmann YW, **Nair A**, Baheti S, Kachergus JM,Younkin CS, Baker T, Carr JM, Tang X, Walsh MP, Chai HS, Sun Z, Hart SN,Leontovich AA, Hossain A, Kocher JP, Perez EA, Reisman DN, Fields AP, ThompsonEA. Deep Sequence Analysis of Non-Small Cell Lung Cancer: Integrated Analysis of Gene Expression, Alternative Splicing, and Single Nucleotide Variations in Lung Adenocarcinomas with and without Oncogenic KRAS Mutations. Front Oncol. 2012 Feb 10;2:12. doi: 10.3389/fonc.2012.00012. eCollection 2012. PubMed PMID: 22655260;PubMed Central PMCID: PMC3356053.

20. Theis JL, Sharpe KM, Matsumoto ME, Chai HS, **Nair AA**, Theis JD, de Andrade M,Wieben ED, Michels VV, Olson TM. Homozygosity mapping and exome sequencing revealGATAD1 mutation in autosomal recessive dilated cardiomyopathy. Circ Cardiovasc Genet. 2011 Dec;4(6):585-94. doi: 10.1161/CIRCGENETICS.111.961052. Epub 2011 Sep 30. PubMed PMID: 21965549; PubMed Central PMCID: PMC3248690.

21. Asmann YW, Middha S, Hossain A, Baheti S, Li Y, Chai HS, Sun Z, Duffy PH, Hadad AA, **Nair A**, Liu X, Zhang Y, Klee EW, Kalari KR, Kocher JP. TREAT: a bioinformatics tool for variant annotations and visualizations in targeted and exome sequencing data. Bioinformatics. 2012 Jan 15;28(2):277-8. doi: 10.1093/bioinformatics/btr612. Epub 2011 Nov 15. PubMed PMID: 22088845; PubMed Central PMCID: PMC3259432.

22. Karnes RJ, Cheville JC, Ida CM, Sebo TJ, **Nair AA**, Tang H, Munz JM, Kosari F, Vasmatzis G. The ability of biomarkers to predict systemic progression in men with high-risk prostate cancer treated surgically is dependent on ERG status. Cancer Res. 2010 Nov 15;70(22):8994-9002. doi: 10.1158/0008-5472.CAN-10-1358.Epub 2010 Nov 9. PubMed PMID: 21062978.

## Book Chapters

1. Li X, **Nair A**, Wang S, Wang L. Quality control of RNA-seq experiments. Methods Mol Biol. 2015;1269:137-46. doi: 10.1007/978-1-4939-2291-8_8. PubMed PMID:25577376

## Abstracts

1. **Asha Nair**, Yan W. Asmann, Sumit Middha, Asif Hossain, Saurabh Baheti, High-Seng Chai, Zhifu Sun, Patrick H. Duffy, Ahmed A. Hadad, Ying Li, Xiaoyu Liu, Yuji Zhang, Eric W. Klee, and Jean-Pierre A. Kocher. TREAT: A comprehensive open framework for targeted re-sequencing analysis [abstract]. XGen Congress & Exposition; 2011 March 14-16; San Diego, California, USA;

2. **Asha Nair**, Steven Hart, Hugues Sicotte, Terry M. Therneau, Eric W. Klee, Jason Sinnwell, Yuji Zhang, Ying Li, Chen Wang, Ann L. Oberg, Sumit Middha, and Jean-Pierre A. Kocher. Optimizing sequence yield & interpreting data quality for RNA-Seq [abstract]. Intelligent systems for Molecular Biology; 2012 July 15-17; Long Beach, California, USA;

3. **Nair A. Asha**, Kalari R. Krishna, Bhavsar Jaysheel, Tang Xiaojia, Davila Jaime, Nie Jinfu, O’Brien R. Daniel, Kocher Jean-Pierre. MAP-RSeq - Mayo Analysis Pipeline for RNA Seq: A comprehensive workflow for RNA-Sequencing data analysis [abstract]. American Society of Human Genetics; 2013 October 22-26; Boston, Massachusetts, USA;

4. Jinfu Jeff Nie, Krishna R. Kalari, Jaysheel Bhavsar, **Asha A. Nair**, Xiaojia Tang, Jaime Davila, Daniel R. O’Brien, Jean-Pierre Kocher. MAP-RSeq - Mayo Analysis Pipeline for RNA Seq: A comprehensive workflow for RNA-Sequencing data analysis [abstract]. Individualizing Medicine Conference; 2013 Sep 30-Oct 3; Mayo Civic Center, Rochester, Minnesota, USA;

5. **Nair Asha**, Zhang Yuji, Bhavsar Jaysheel, Middha Sumit, Kocher Jean-Pierre.Identification of expressed long intergenic non-coding RNA (lincRNA) using Whole Transcriptome RNA Sequencing technology [abstract]. Individualizing Medicine Conference; 2013 Sep 30-Oct 3; Mayo Civic Center, Rochester, Minnesota, USA;

6. **Nair A. Asha**, Thompson J. Kevin, Tang Xiaojia, Kocher Jean-Pierre, Subramanian Subayya, Kalari R. Krishna. Identification of circular RNAs (circRNAs) and their potential regulation in Breast Cancer Subtypes [abstract]. Intelligent systems for Molecular Biology; 2014 July 11-15; Boston, Massachusetts, USA;

7. **Nair Asha**, Kocher Jean-Pierre, Subbaya Subramanian, Krishna Kalari. A catalog of identified circular RNAs in Breast Cancer Subtypes [abstract]. Individualizing Medicine Conference; 2014 October 6-8; Mayo Civic Center, Rochester, Minnesota, USA;

8. Yuji Zhang, **Asha Nair**, Yan W. Asmann, Lewis R. Roberts, Tushar C. Patel. Systematic Identification of Long Intergenic Non-coding RNAs Regulated in Hepatocellular Carcinoma [abstract]. American Association for the Study of Liver Diseases; 2014 Nov 7-11; Boston, Massachusetts, USA;

9. Yuji Zhang Y, Amy J. French, **Asha A. Nair**, Shannon McDonnel, Sumit Middha, Shaun Riska, Zachary Fogarty, Daniel Schaid, Stephen N. Thibodeau, Patel T. Systematic Identification of tissue-specific Long Intergenic Non-coding RNAs in Liver Hepatocellular Carcinoma [abstract]. National Relocation Conference; 2014 May 7-9; Orlando, Florida, USA;

10. Michaela Kachadoorian, Mariet Allen, Sarah Lincoln, Aditya Karhade, Lester Manly, Fanggeng Zou, High Seng Chai, Curtis S. Younkin, Julia Crook, V. Shane Pankratz, Minerva M. Carrasquillo, **Asha A. Nair**, Sumit Middha, Sooraj Maharjan, Thuy Nguyen, Li Ma, Kimberly G. Malphrus, Gina Bisceglio, Ronald C. Petersen, Neill R. Graff-Radford, Dennis W. Dickson, Steven G. Younkin, Nilufer Ertekin-Taner. Transcriptional regulation of genes at the Alzheimer's disease risk loci [abstract]. Alzheimer's Association International Conference; 2014 July 12 - 17; Copenhagen, Denmark;

11. Michaela Kachadoorian, Mariet Allen, Aditya Karhade, Lester Manly, Fanggeng Zou, High Seng Chai, Curtis S. Younkin, Julia Crook, V. Shane Pankratz, Minerva M. Carrasquillo, **Asha A. Nair**, Sumit Middha, Sooraj Maharjan, Thuy Nguyen, Li Ma, Kimberly G. Malphrus, Sarah Lincoln, Gina Bisceglio, Christopher P. Kolbert, Jin Jen, Ronald C. Petersen, Neill R. Graff-Radford, Steven G. Younkin, Dennis W. Dickson, Nilufer Ertekin-Taner. Investigation of transcriptional regulation at the Alzheimer's disease risk loci. American Academy of Neurology [abstract]. 2014 April 26 - May 3; Philadelphia, PA, USA;

12. Molly Bisbee, **Asha Nair**, Paula Carlson, Chris Kolbert, Cheryl Bernard, Purna Kashyap, Gianrico Farrugia, Michael Camilleri, Madhusudan Grover. Transcriptomic changes in colonic mucosa in patients with Campylobacter jejuni post infectious irritable bowel syndrome [abstract]. Digestive Disease Week; 2015 May 16-19; Washington, District of Columbia, USA;