Chris Cotsapas PhD
CURRICULUM VITAE – June 13, 2017

Education

ARCS	Imperial College, London UK (Biochemistry) 2000
BSc	Imperial College, London UK (Biochemistry) 2000
PhD	University of New South Wales, Sydney, Australia (Biochemistry & Molecular Genetics) 2007

Career/Academic Appointments:

2005-2007	Research Associate, Center for Human Genetics Research, MGH (Boston, MA)
2007-2010	Research Fellow, Center for Human Genetics Research, MGH (Boston, MA)
2005-present	Research Affiliate, Broad Institute of MIT and Harvard (Cambridge, MA)
2010-present	Visiting Faculty, Analytical/Translational Genetics Unit, MGH (Boston, MA)
2010-2016	Assistant Professor, Dept. of Neurology, Yale School of Medicine (New Haven, CT)
2011-2016	Assistant Professor, Dept. of Genetics, Yale School of Medicine (New Haven, CT)
2011-present	Research Affiliate, Stanley Center for Psychiatric Research (Boston, MA)
2016-present	Associate Professor, Dept. of Neurology, Yale School of Medicine (New Haven, CT)
2016-present	Associate Professor, Dept. of Genetics, Yale School of Medicine (New Haven, CT)

Funding Record
Current Grants

Agency: NIH/NIAID
I.D.# R01 AI122220
Title: "Genomics of NFkB-mediated gene regulation in multiple sclerosis"
P.I.: Chris Cotsapas PhD
Percent effort: 12%
Total costs for project period: $1,827,500
Project period: 09/01/2015 – 08/31/2020

Agency: European Commission (Horizon 2020 program)
I.D.#: 733161
Title: "MultipleMS: Multiple manifestations of genetic and non-genetic factors in multiple sclerosis disentangled with a multi-omics approach to accelerate personalized medicine"
P.I.: Ingrid Kockum PhD and Maja Jagodic PhD
Role on project: work package leader, responsible for all genetic analyses across the project. Executive board member.
Percent effort: 30%
Total costs for project period: $1,679,324
Project period: 01/01/2017 – 12/31/2021

Agency: NIH/NIAID
I.D.# U01 AI089859
Title: "Determining the Genetic Basis of Vaccine Response"
P.I.: Chris Cotsapas, PhD
Role on project: PI on component project to perform a multi-center GWAS on vaccine response
Percent Effort: 20%
Direct costs per year: $305,024
Total costs for project period: $398,522
Project period: 12/01/2011 – 06/30/2017 No Cost Extension

Agency: NIH/NIAID
I.D.# U19 AI056363
Title: "Autoimmune Centers of Excellence pilot: T and B cell responses across autoimmune diseases"
P.I.: Chris Cotsapas PhD
Role on project: Site PI for independent, integrative pilot to recruit new onset patients
Percent Effort: 20%
Direct costs per year: $110,300
Total costs for project period: $375,683 (of $1,200,000 awarded to Dr Cotsapas across 6 sites)
Project period: 05/01/2011 – 04/30/2017 No Cost Extension

Agency: Rasmussen's Encephalitis Children's Project
I.D.#: RE-03
Title: "Unraveling the genetic architecture of RE by exome sequencing 30 RE trios"
P.I.: Chris Cotsapas PhD
Percent effort: 5%
Total costs for project period: $75,000
Project period: 03/01/2013-02/28/2017

Agency: NIH/NIAID
I.D.#: P01 AI039671
Title: "Costimulatory Mechanisms of Autoimmunity"
P.I.: David Hafler MD
Role on project: key personnel in functional analysis of low-frequency variation in CD155
Percent effort: 10%
Total costs for project period: $11,329,354
Project period: 10/01/2015 – 09/30/2020

Agency: National MS Society
I.D.# RG 5016A20/1
Title: "Can a High Salt Diet Drive Induction of Pathogenic T Cells in Humans?"
P.I.: David Hafler, MD, PhD
Role on project: key personnel for genetic and genomic analysis of salt responses in T cells
Percent effort: 10%
Total costs for project period: $545,398
Project period: 07/01/2014 – 06/30/2017

Pending Grants

Agency: NIH/NINDS
I.D.#: pending
Title: "Shared Genetics and Risk Factors Between Epilepsy and Psychiatric Disease"
P.I.: Chris Cotsapas PhD
Total costs for project period: $2,549,522
Project period: 04/01/2018 – 03/31/2023

Past Grants

Agency: Doris Duke Charitable Foundation
Title: "Regulating Dendritic Cell Migration During Vaccination"
P.I.: Stephanie E Eisenbarth MD PhD
Role on project: key personnel for genetic analysis of variation in dendritic cell function
Percent effort: 5%
Total costs for project period: $450,000
Project period: 07/01/2013 – 06/30/2016

Agency: Progressive MS Alliance
I.D.# PA-1501-02906
Title: "An International Network to Decipher Function and Impact of CNS-relevant Risk Variants for MS"
P.I.: David Hafler, MD
Role on project: Overall coordination; PI on component project to identify CNS-relevant MS risk variants
Percent Effort: 4%
Direct costs per year: $75,000
Total costs for project period: $75,000
Project period: 05/01/2015-04/30/2016

Agency: MGH Fund for Medical Discovery Post-doctoral Fellowship
I.D.#: ECOR-2008-011
Title: "Discovering Genetic Contributors to Drug Metabolism in Mice and Humans"
P.I.: Chris Cotsapas PhD
Percent effort: 100%
Total costs for project period: $75,000
Project period: 07/01/2008-06/30/2009

Agency: NIH/NIAID
I.D.# U19 AI089992
Title: "Novel Technologies to define molecular signatures of individual immune responses"
P.I.: David Hafler MD
Role on project: PI of flow cytometry and genetics analysis core (Years 4 and 5)
Percent Effort: 10%
Direct costs per year: $1,921,328
Total costs for project period: $11,358,701
Project period: 07/12/2010 – 06/30/2015

Agency: NIH/NINDS
I.D.# R01 NS049477
Title: "A Haplotype Map for Multiple Sclerosis"
P.I.: Steven Hauser MD
Role on project: key personnel to lead genetic analysis of multiple sclerosis risk
Percent Effort: 15%
Direct costs per year: $33,033
Total costs for project period: $453,399
Project period: 09/01/2010 – 05/31/2015

Agency: Broad Institute SPARC award
I.D.#: SPARC-2007-0025
Title: "Identifying the genetic components of toxic drug response using a mouse model"
P.I.: Mark J Daly PhD
Role on project: project leader, analyst
Percent effort: 50%
Total costs for project period: $200,000
Project period: 03/01/2007-02/28/2010

Invited Speaking Engagements, Presentations, Symposia & Workshops

2017: HKU/Pasteur Immunology course (Hong Kong, China), "Systems approaches to quantitative regulatory changes in immune cell function leading to autoimmune disease risk"
2017: ACTRIMS (Orlando FL), "Update on multiple sclerosis genetics and genomics studies"
2016: ENCODE Annual User's Meeting (Stanford, CA), "Identifying risk-mediating regulatory regions"
2016: FOCiS (Boston, MA), "Low-frequency variation in multiple sclerosis risk"
2016: University of Pennsylvania (Philadelphia PA), "Regulatory variation in autoimmune disease"
2016: Brigham and Women's Hospital (Boston MA), "A fraction of eQTLs mediate GWAS risk effects"
2016: Broad Institute (Cambridge MA), "Genetic mapping of non-coding effects on disease risk"
2016: Type 1 diabetes TrialNet (Seattle WA) "Precision medicine in T1D guided by genetics"
2016: Banff early career scientist workshop (Banff, AB) "Pathogenic gene regulatory effects in autoimmune disease"
2015: ENCODE Annual User's Meeting (Washington, DC), "Systematic dissection of changes gene regulatory programs driving autoimmune disease risk"
2015: Department of Antiquities (Nicosia, Cyprus) "A proposal for establishing the origins of early Neolithic Cypriots from sequencing of ancient DNA"
2015: Sex-dependent Neurodiscovery and CNS Therapeutics, Radcliffe Institute for Advanced Study at Harvard University (Boston, MA), "*in silico* CHiP-seq approaches for inferring sex-specific genetic effects in psychiatric and autoimmune disease".
2015: Computational Biology Symposium, UC Berkeley (Berkeley, CA), "Harnessing genetics and genomics to answer the unsolved question of pathogenesis"
2015: Department of Genome Sciences, University of Washington (Seattle, WA), "Using disease co-morbidity to understand pathogenesis"
2015: Keysone Symposium on Autoimmunity and Tolerance (Keystone, CO), "Genetics to systems biology of immune disease"
2014: Singapore Centre on Environmental Life Sciences Engineering (Singapore), "Dissecting genetic associations to uncover pathogenesis"
2014: Consortium of Multiple Sclerosis Centers/Americas Committee for Treatment and Research in Multiple Sclerosis (Dallas TX), "Uncovering MS Susceptibility Pathways from Large-Scale Genetic Studies"
2014: ECTRIMS Summer School on the genetics of MS (Talinn, Estonia), "Shared effects across autoimmune and inflammatory diseases"
2014: Brain Recovery Project meeting (Los Angeles, CA), "Genetic causes of Rasmussen's Encephalitis"
2014: Rasmussen's Encephalitis Children's Project (Los Angeles CA), "Exome sequencing in Rasmussen's Encephalitis families".
2014: Center for Computational Molecular Biology, Brown University (Providence RA), "Systematic approaches to uncover mechanisms underlying complex immune-mediated diseases"
2013: International Multiple Sclerosis Genetics Consortium (Paris, France). "Low-frequency variation in multiple sclerosis".
2013: HudsonAlpha Institute (Huntsville AL). "Large-scale trans-eQTLs mediate patterns of transcriptional co-regulation"
2012: Neuroimmunology Seminar, Johns Hopkins School of Medicine. "Inferring the pathogenesis of multiple sclerosis from large-scale genetic studies".
2012: Montreal Heart Institute (Montreal Canada). "Genetic insights into autoimmune disease".
2012: Strategy conference, Euroepinomics Consortium. "Genetic studies in common, complex epilepsies".
2011: National Genomics Institute of Mexico and Slim Health Institute. (Mexico City, Mexico): organizer and head instructor, 3-day workshop on complex trait genetic methods.
2011: Joint meeting of the International Congress of Human Genetics/American Society of Human Genetics (Montreal, Canada): "Targeted resequencing of multiple sclerosis candidate genes".
2011: Genentech Inc (San Francisco CA). "Shared genetic influences in autoimmune disease".

2011: Royal Netherlands Society for Arts and Sciences. "Genetics to pathogenesis in autoimmune disease".
2010: Dept of Computer Science Columbia University (New York NY). "Assembling the parts list of pathogenesis with genetics and genomics"
2008: Federation of Clinical Immunology Societies (Boston, MA,). "Pervasive sharing of genetic effects across autoimmune diseases"
2007: Lund University Medical School (Malmo, Sweden): organizer and head instructor, 3-day workshop on complex trait genetic methods.
2007: Wellcome Trust Center for Human Genetics (Oxford, UK), "The use of shared controls in genome-wide association studies".

Peer-Reviewed Presentations & Symposia

2016: CSHL Biology of Genomes meeting (Cold Spring Harbor NY). "Identifying the Gene Regulatory Effects of Autoimmune Disease Risk Alleles".
2015: CSHL Biology of Genomes meeting (Cold Spring Harbor NY). "Immune-mediated disease GWAS risk variants are not consistent with eQTL data".
2014: American Society of Human Genetics (San Diego CA). "Low-frequency coding variation in PRF1 and GALC mediate multiple sclerosis risk."
2014: American Society of Human Genetics (San Diego CA). "Characterizing the Local Ancestry of Established Multiple Sclerosis Risk Loci in Hispanics."
2014: American Society of Human Genetics (San Diego CA). "Effect Fine Mapping: a method to identify association-driving variants in large genomic datasets."
2014: CSHL Biology of Genomes meeting (Cold Spring Harbor NY). "Large-scale trans-eQTLs in HapMap populations affect hundreds of genes and mediate patterns of transcriptional coregulation"
2013: American Society of Human Genetics (Boston MA). "A computational framework for identifying genes perturbed by MS associated variants through regulatory element disruption."
2013: American Society of Human Genetics (Boston MA). "Uncovering the genetic architecture of complex traits using network approaches."
2013: American Society of Human Genetics (Boston MA). "Exome array analysis of rare and low-frequency variation in multiple sclerosis."
2012: American Society of Human Genetics (San Francisco, CA). "A novel spatial mapping method identifies shared genetic effects across immune-mediated diseases."
2012: Wellcome Trust/Nature Genetics Genomics of Common Diseases (Washington, DC). "Spatial mapping across inflammatory disease suggests many new shared loci".
2012: CSHL Biology of Genomes meeting (Cold Spring Harbor NY). "The transcriptional regulation of a perturbed regulatory T-cell"
2011: CSHL Biology of Genomes meeting (Cold Spring Harbor NY). "Pervasive sharing of genetic effects in autoimmune disease".
2010: American Society of Human Genetics (Washington DC). "Estimating the Contextual Likelihood of SNP Incidence Genome-Wide and Negative Selection in the Exome via Whole Genome Sequencing of a Human Population."
2010: American Society of Human Genetics (Washington DC). "Inferring pathogenic mechanisms from genome-wide association studies in autoimmune disease."
2010: CSHL Biology of Genomes meeting (Cold Spring Harbor NY). "DAPPLE: a network method for identifying causal genes in GWAS loci".
2009: American Society of Human Genetics (Honolulu, HI). "Validating a novel hepatocyte culture platform for in vitro pharmacogenomics."
2009: American Society of Human Genetics (Honolulu, HI). "The genetic architecture of autoimmunity."
2009: Gordon Research Conference on Quantitative Genetics and Genomics (Biddeford, ME). "Inferring shared pathways from genetic studies in autoimmune disease"
2009: CSHL Biology of Genomes (Cold Spring Harbor NY). "Inter-chromosomal LD in the human genome".
2008: American Society of Human Genetics (Philadelphia, PA). "in silico fine mapping: The example of gene expression traits in Mouse Liver."
2008: American Society of Human Genetics (Philadelphia, PA). "The shared genetic architecture of

common autoimmune diseases."

2008: CSHL Biology of Genomes meeting (Cold Spring Harbor NY). "Genome-wide association identifies risk variants for SLE at 6q23 near TNFAIP3".

2007: CSHL Biology of Genomes meeting (Cold Spring Harbor NY)."Genome-wide association in rheumatoid arthritis identifies a risk locus at 6q23".

2006: American Society of Human Genetics (New Orleans, LA). "A genome-wide scan for variation in the polyadenylation signal and correlation to expression levels."

2005: CSHL Biology of Genomes meeting (Cold Spring Harbor NY). "Genetic dissection of gene regulation in multiple mouse tissues".

2004: CSHL Biology of Genomes meeting (Cold Spring Harbor NY). "Identifying genetic determinants of gene expression in the mouse".

Professional Service

Peer Review Groups/Grant Study Sections

2017: Member, NIH/NINDS ZNS1 SRB-M (02)

2016: Member, NIH/NINDS NST-2 study section

2016: Member, NIH special emphasis UM1 panels *Limited Competition: Knockout Mouse Production and Phenotyping Project* and *Limited Competition: Knockout Mouse Phenotyping Project Database*

2014: Member, review panel for investigator-initiated research grants, Singapore Medical Research Council.

2012: Member, review panel for junior investigator *Veni* prizes, Dutch Medical Council

2012: Member, review panel for investigator-initiated research grants Arthritis Research UK

2012: External reviewer, faculty search, Department of Biochemistry and Molecular Medicine, UCD

2011: Member, review panel for Framework VII applications, European Research Council

2011: Member, review panel for investigator-initiated research grants Dutch Arthritis Association

2010: Discussant, Workshop on genetics of human epilepsy, National Institute of Neurological Disease/Stroke

Advisory Boards

2013 Member, genetics scientific advisory board, Biogen Idec Inc.

2012-present Member, scientific advisory board, Rasmussen's Encephalitis Kids Project

2010-2011 Member, genetics scientific advisory panel, Illumina Inc.

Journal Service

2013-present Associate editor, PLoS Genetics.

2010-present Reviewer for Nature, Science, Nature Genetics, Nature Immunology, Nature Biotechnology, Nature Medicine, Nature Reviews Genetics, Genes and Immunity, Arthritis and Rheumatism, Trends in Genetics, Trends in Immunology, American Journal of Human Genetics, Diabetes, Epilepsia, Diabetologia, Bioinformatics, Human Molecular Genetics, Genome Research, European Journal of Human Genetics, PLoS Genetics, PLoS ONE, Mammalian Genome.

Consortium activities

2015-present Founding member, Epi25 Consortium (epilepsy)

2011-2014 Member, steering committee, ImmunoChip Consortium

2010-present Member, analysis committee, International Multiple Sclerosis Genetics Consortium

2013-present Chair, exome chip working group, International Multiple Sclerosis Genetics Consortium

Yale University Service

2013-2016 Chair, dissertation committee, Jiaqi Jin, Department of Genetics.

2013-2016 Member, dissertation committee, Andrew Smith, Department of Psychiatry.

2014-2017 Member, faculty search committee, Department of Genetics.

2015-2016 Member, faculty search committees for Depts of Immunobiology, Psychiatry

2015-present Member, dissertation committee, Saige Pompura, Department of Neurology.

2016-present Member, dissertation committees, Daniel Burkhardt and Weilai Dong, Department of Genetics.

2016-present Member, dissertation committee, Megan Cahill, School of Public Health.

Public Service

2015-2016 Improbable Research (Boston MA) podcast series

2014 Department of Antiquities (Nicosia, Cyprus) "Where did the first Cypriots come from?"

2014 Amathus Rotary Club (Limassol, Cyprus) "If dogs come from wolves, why do wolves still exist?"

2010 Amathus Rotary Club (Limassol, Cyprus) "I don't have summers off, either"

Bibliography (Cotsapas is †first, or ‡ corresponding author; 5747 citations, h-index 23)

†1. Cotsapas, C., Chan, E., Kirk, M., Tanaka, M. & Little, P. Genetic variation and the control of transcription. *Cold Spring Harb. Symp. Quant. Biol.* **68,** 109–114 (2003).

2. Plenge, R. M. *et al.* Whole genome association study using a 100K SNP array in rheumatoid arthritis. **54,** S400–S400 (2006).

†3. Williams, R. B. H. *et al.* Normalization procedures and detection of linkage signal in genetical-genomics experiments. *Nature Genetics* **38,** 855–6; author reply 856–9 (2006).

†4. Cotsapas, C. *et al.* Genetic dissection of gene regulation in multiple mouse tissues. *Mamm. Genome* **17,** 490–495 (2006).

5. Nott, D. J. *et al.* Hierarchical Bayes variable selection and microarray experiments. *Journal of Multivariate Analysis* **98,** 852–872 (2007).

6. Plenge, R. M. *et al.* Two independent alleles at 6q23 associated with risk of rheumatoid arthritis. *Nature Genetics* **39,** 1477–1482 (2007).

7. Pomati, F., Cotsapas, C., Castiglioni, S., Zuccato, E. & Calamari, D. Gene expression profiles in zebrafish (Danio rerio) liver cells exposed to a mixture of pharmaceuticals at environmentally relevant concentrations. *Chemosphere* **70,** 65–73 (2007).

8. Sabeti, P. C. *et al.* Genome-wide detection and characterization of positive selection in human populations. *Nature* **449,** 913–918 (2007).

9. Choy, E. *et al.* Genetic analysis of human traits in vitro: drug response and gene expression in lymphoblastoid cell lines. *PLoS Genetics* **4,** e1000287 (2008).

†10. Graham, R. R. *et al.* Genetic variants near TNFAIP3 on 6q23 are associated with systemic lupus erythematosus. *Nature Genetics* **40,** 1059–1061 (2008).

‡11. Cotsapas, C. Identifying genetic components of drug response in mice. *Pharmacogenomics*, **9**, 1323–1330 (2008).

12. Cowley, M. J. *et al.* Intra- and inter-individual genetic differences in gene expression. *Mamm. Genome* **20,** 281–295 (2009).

†13. Cotsapas, C. *et al.* Common body mass index-associated variants confer risk of extreme obesity. *Hum. Mol. Genet.* **18,** 3502–3507 (2009).

14. Rossin, E. *et al.* The Use of Protein-protein Interaction in Loci Associated to Crohn's and Rheumatoid Arthritis Reveals Evidence of Risk Spread Across Functional Networks. *Clinical Immunology* **135,** S119 (2010).

15. Kirby, A. *et al.* Fine mapping in 94 inbred mouse strains using a high-density haplotype resource. *Genetics* **185,** 1081–1095 (2010).

†16. Cotsapas, C. *et al.* Expression analysis of loci associated with type 2 diabetes in human tissues. *Diabetologia* **53,** 2334–2339 (2010).

†17. Cotsapas, C. *et al.* Pervasive sharing of genetic effects in autoimmune disease. *PLoS Genetics* **7,** e1002254 (2011).

‡18. Rossin, E. J. *et al.* Proteins encoded in genomic regions associated with immune-mediated disease physically interact and suggest underlying biology. *PLoS Genetics* **7,** e1001273 (2011).

19. Hatoum, I. J. *et al.* Heritability of the weight loss response to gastric bypass surgery. *J. Clin. Endocrinol. Metab.* **96,** E1630–3 (2011).

20. Maurano, M. T. *et al.* Systematic Localization of Common Disease-Associated Variation in Regulatory DNA. *Science* **337,** 1190–1195 (2012).

21. Morris, D. L. *et al.* Unraveling multiple MHC gene associations with systemic lupus erythematosus: model choice indicates a role for HLA alleles and non-HLA genes in Europeans. *Am. J. Hum. Genet.* **91,** 778–793 (2012).

‡22. Voight, B. F. & Cotsapas, C. Human genetics offers an emerging picture of common pathways and mechanisms in autoimmunity. *Current Opinion in Immunology* **24,** 552–557 (2012).

‡23. Cotsapas, C. & Hafler, D. A. Immune-mediated disease genetics: the shared basis of pathogenesis. *Trends Immunol.* **34,** 22–26 (2013).

24. International Multiple Sclerosis Genetics Consortium (IMSGC). Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. *Nature Genetics* **45,** 1353–1360 (2013).

25. Hatoum, I. J. *et al.* Weight loss after gastric bypass is associated with a variant at 15q26.1. *Am. J. Hum. Genet.* **92,** 827–834 (2013).

26. Querol, L. *et al.* Protein array-based profiling of CSF identifies RBPJ as an autoantigen in multiple sclerosis.

Neurology **81,** 956–963 (2013).
27. Solovieff, N., Cotsapas, C., Lee, P. H., Purcell, S. M. & Smoller, J. W. Pleiotropy in complex traits: challenges and strategies. *Nature Reviews Genetics* **14,** 483–495 (2013).
28. Damotte, V. *et al.* A gene pathway analysis highlights the role of cellular adhesion molecules in multiple sclerosis susceptibility. *Genes Immun* **15,** 126–132 (2014).
29. Morris, D. L. *et al.* MHC associations with clinical and autoantibody manifestations in European SLE. *Genes Immun* **15,** 210–217 (2014).
30. Winsvold, B. S. *et al.* Genetic analysis for a shared biological basis between migraine and coronary artery disease. *Neurol Genet* **1,** e10 (2015).
31. Housley, W. J. *et al.* Genetic variants associated with autoimmunity drive NFκB signaling and responses to inflammatory stimuli. *Science Translational Medicine* **7,** 291-93 (2015).
32. Moutsianas, L. *et al.* Class II HLA interactions modulate genetic risk for multiple sclerosis. *Nature Genetics* **47,** 1107–1113 (2015).
33. Malik, R. *et al.* Shared genetic basis for migraine and ischemic stroke: A genome-wide analysis of common variants. *Neurology* **84,** 2132–2145 (2015).
‡34. Choi, J., Shooshtari, P., Samocha, K. E., Daly, M. J. & Cotsapas, C. Network analysis of genome-wide selective constraint reveals a gene network active in early fetal brain intolerant of mutation. *PLoS Genetics* **12,** e1006121 (2016).
35. Garyu, J. W., Meffre, E., Cotsapas, C. & Herold, K. C. Progress and challenges for treating Type 1 diabetes. *Journal of Autoimmunity* **71,** 1–9 (2016).
‡36. Cotsapas C. NR1H3 p.Arg415Gln Is Not Associated to Multiple Sclerosis Risk. *Neuron* **92,** 333–335 (2016).
37. Tooley, J. E. *et al.* Changes in T- cell subsets identify responders to FcR- nonbinding anti- CD3 mAb (teplizumab) in patients with type 1 diabetes. *Eur. J. Immunol.* **46,** 230–241 (2016).
38. Raj, P. *et al.* Regulatory polymorphisms modulate the expression of HLA class II molecules and promote autoimmunity. *Elife* **5,** e12089 (2016).
39. Barrera, L. A. *et al.* Survey of variation in human transcription factors reveals prevalent DNA binding changes. *Science* **351,** 1450–1454 (2016).
40. Roden C, Gaillard J, Kanoria S, Rennie W, Barish S, Cheng J, Pan W, Liu J, Cotsapas C, Ding Y, Lu J. Novel determinants of mammalian primary microRNA processing revealed by systematic evaluation of hairpin-containing transcripts and human genetic variation. *Genome Research* **27**(3): 374-384 (2017).
‡41. Chun, S. *et al.* Limited statistical evidence for shared genetic effects of eQTLs and autoimmune-disease-associated loci in three major immune-cell types. *Nature Genetics* **45,** 1353 (2017).
‡42. Brynedal, B. *et al.* Large-Scale trans-eQTLs Affect Hundreds of Transcripts and Mediate Patterns of Transcriptional Co-regulation. *AJHG* **100**, 581-591 (2017) [Featured in Clyde, Nature Reviews Genetics 2017]
‡43. Singh A and Cotsapas C. Genetic mapping of human immune system function. In Human Innate Immunity, World Scientific Press, 2017.

Scholarship in press

‡1. Shooshtari P, Huang H and Cotsapas C. Integrative genetic and epigenetic analysis uncovers regulatory mechanisms of autoimmune disease. *American Journal of Human Genetics*, to appear. Preprint at http://biorxiv.org/content/early/2016/05/19/054361
2. Anttila V *et al*. Analysis of shared heritability in common disorders of the brain. http://biorxiv.org/content/early/2016/04/16/048991
‡3. Mitrovic M, Hafler DA, Cotsapas C. Multiple Sclerosis. In Neurogenetics, Geschwind D, ed. Elsevier, to appear
4. Patsopoulos N, *et al*, on behalf of the International MS Genetics Consortium. The Multiple Sclerosis Genomic Map: Role of peripheral immune cells and resident microglia in susceptibility. Preprint at http://www.biorxiv.org/content/early/2017/07/13/143933