**LIST OF POTENTIAL RECOMMENDERS**

1. **[**Joshua W Knowles, MD**]**

[Assistant Professor of Medicine]

[Stanford University Medical Center]

[https://profiles.stanford.edu/joshua-knowles?tab=bio]

1. **How does this recommender know me**?

[dependent recommender] We collaborated in two papers : “[Predictive network modeling in human induced pluripotent stem cells identifies key driver genes for insulin responsiveness](javascript:void(0))” and “[Analysis of transcriptional variability in a large human iPSC library reveals genetic and non-genetic determinants of heterogeneity](https://www.sciencedirect.com/science/article/pii/S1934590916304015)”.

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Two papers:

1.[Predictive network modeling in human induced pluripotent stem cells identifies key driver genes for insulin responsiveness](javascript:void(0)) [Cell Stem Cell] [2017] [This is the 2nd project in summary of contribution]

2. [Analysis of transcriptional variability in a large human iPSC library reveals genetic and non-genetic determinants of heterogeneity](https://www.sciencedirect.com/science/article/pii/S1934590916304015).[PLOS Computational Biology] [2020]

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2. Andrew Pieper, MD, PhD

[**Director, Neurotherapeutic**]

[Boston University]

[https://www.uhhospitals.org/-/media/Files/HDI/Harrington-Investigators/andrew-pieper-cv-full.pdf]

[https://clevelandadrc.org/about-us/meet-the-team/andrew-pieper-md-phd/]

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[**independent** recommender].

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[Project 4] The human brainome: network analysis identifies HSPA2 as a novel Alzheimer’s disease target

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In their review paper, it mentioned our work in multi-omics section: “Petyuk et al.[221](https://onlinelibrary.wiley.com/doi/full/10.1002/med.21709?casa_token=Khe2AXyD5OcAAAAA%3AXW4uuVcjbNqCiEPSCG-nrH-BmVFOCt3ZQcsMc7_TKK_9HJTdd8h_2OSTrRdGirr0VXlkVya6PtnZkA#med21709-bib-0221) integrated DNA variation, RNA expression, and proteome profiles to prioritize key targets in LOAD. An integrative analysis showed that heat shock protein family A member 2 (HSPA2) played a key role, validated in two cell lines.[221](https://onlinelibrary.wiley.com/doi/full/10.1002/med.21709?casa_token=Khe2AXyD5OcAAAAA%3AXW4uuVcjbNqCiEPSCG-nrH-BmVFOCt3ZQcsMc7_TKK_9HJTdd8h_2OSTrRdGirr0VXlkVya6PtnZkA#med21709-bib-0221)”

It emphasizes our work as one of the representative works applying Multi-omics data integration, using multiple molecular layers to describe AD pathogenesis.

1. GIUSEPPE LUPO

[Associate professor, Dept. of Chemistry, Sapienza University of Rome]

[Sapienza University of Rome]

[https://phd.uniroma1.it/web/GIUSEPPE-LUPO\_nC1517\_EN.aspx]

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[Project 4] Metabolic network failures in Alzheimer's disease: A biochemical road map

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### In their review paper, it mentioned our work in section “Harnessing High-Throughput Human Brain Datasets to Identify Candidate Regulatory Pathways of Cognitive Decline”.

In the paper it goes like : “Moreover, increased levels of HSPB2 were shown to be associated with cognitive impairment by proteomic assays in DLPFC samples [[20](https://link.springer.com/article/10.1007/s13311-019-00743-2#ref-CR20)]. Remarkably, a different study also disclosed a heat shock protein, HSPA2, as a candidate key driver of AD-related neuropathology [[22](https://link.springer.com/article/10.1007/s13311-019-00743-2#ref-CR22)].”

HSP stands for heat shock protein and there are multiple of them. While previous work found the connection of HSPB2 to cognitive impairment, our study found HSPA2 as a candidate key driver of Alzheimer’s disease (AD)

1. Eugenia Trushina

[Professor of Neurology]

[Mayo Clinic]

[https://www.mayo.edu/research/faculty/trushina-eugenia-ph-d/bio-00027310]

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[Project 1] Metabolic network failures in Alzheimer's disease: A biochemical road map

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Paper1: Application of Metabolomics in Alzheimer’s Disease [https://www.frontiersin.org/articles/10.3389/fneur.2017.00719/full]

“This suggests that metabolism could play an essential role in early AD mechanisms. Depending on the stage of AD and individual traits (e.g., age, sex, race, etc.), treatment options may vary and most likely will require combinatorial therapy ([17](https://www.frontiersin.org/articles/10.3389/fneur.2017.00719/full#B17), [18](https://www.frontiersin.org/articles/10.3389/fneur.2017.00719/full#B18)). ”

This paper mentioned the subtle different role of metabolism play in early Alzheimer’s disease. Given a different individual traits group (e.g., age, sex, race, etc), our study showed we should use different panel of metabolites for early diagnosis and disease prediction and it is this idea, personalized medicine, lay the foundation of this paper.

# Paper 2: Sex and *APOE* ε4 genotype modify the Alzheimer’s disease serum metabolome

https://www.nature.com/articles/s41467-020-14959-w

“In one of the largest blood-based metabolomics studies of AD, we identified metabolic alterations in various stages across the trajectory of the disease. For instance, higher levels of SMs and PCs were observed in early stages of AD as defined by abnormal cerebrospinal fluid (CSF) Aβ1–42 levels, whereas intermediate changes, measured by CSF total tau, were correlated with increased levels of SMs and long-chain acylcarnitines[45](https://www.nature.com/articles/s41467-020-14959-w#ref-CR45).”

“Metabolomics data processing followed published protocols[45](https://www.nature.com/articles/s41467-020-14959-w#ref-CR45),[71](https://www.nature.com/articles/s41467-020-14959-w#ref-CR71) with a few adjustments.”

“ Sample extraction, metabolite measurement, identification, quantification, and primary quality control (QC) followed standard procedures[45](https://www.nature.com/articles/s41467-020-14959-w#ref-CR45),[71](https://www.nature.com/articles/s41467-020-14959-w#ref-CR71).”

This paper cited our work multiple times. The first time is about the discovery of our work. (I also mentioned the detail in summary of contribution). The last two citation is about adopting the computational method, protocols used in our study to process and analyze metabolite data in Alzheimer’s disease context.

# Paper 3: A comprehensive protocol for multiplatform metabolomics analysis in patient-derived skin fibroblasts

[https://link.springer.com/article/10.1007/s11306-019-1544-z]

“Affected metabolic pathways in MCI and AD patients included the TCA cycle, amino acid metabolism, and lipid metabolism (Trushina et al. [2013](https://link.springer.com/article/10.1007/s11306-019-1544-z#ref-CR32)) where later studies also identified changes in acylcarnitines (Toledo et al. [2017](https://link.springer.com/article/10.1007/s11306-019-1544-z#ref-CR31))”

It mentioned our study as one of the supportive evidences for this sentence: “metabolite changes became more pronounced in CSF and plasma from AD patients supporting the hypothesis that alterations in mitochondrial function underlie early disease mechanisms”

1. Jun Ye, PhD

## [**President and CEO at Sentieon Inc**]

## [**Sentieon Inc]**

1. **How does this recommender know me**?

[**independent** recommender, asking me some technical detail questions after reading the computational part of the paper].

[Project 2] Analysis of transcriptional variability in a large human iPSC library reveals genetic and non-genetic determinants of heterogeneity

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Jun Ye is willing to talk to the computational perspective/algorithm for all my projects. He likes to talk about the Bayesian Network for disease modeling, causal inference.

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Jun Ye appreciated the biological network modeling as its explanatory could demystify the causal relationship among genes. As a CEO of bioinformatics company served to improve the quality of gene expression data, which is related to the upstream of the whole bioinformatics analysis pipeline, who he would like to expand his company’s business by vertically adopting the network modeling pipeline as downstream analysis.