



## RESEARCH ARTICLE

**REVISED** Common genetic signatures of Alzheimer's disease in Down Syndrome [version 2; peer review: 2 approved, 2 approved with reservations]Ayati Sharma<sup>1</sup>, Alisha Chunduri <sup>1,2</sup>, Asha Gopu<sup>1</sup>, Christine Shatrowsky<sup>1</sup>, Wim E. Crusio <sup>3,4</sup>, Anna Delprato <sup>1,3</sup><sup>1</sup>BioScience Project, PO Box 352, Wakefield, MA, 01880, USA<sup>2</sup>Department of Biotechnology, Chaitanya Bharathi Institute of Technology, Hyderabad, 500075, India<sup>3</sup>Institut de Neurosciences Cognitives et Intégratives d'Aquitaine, CNRS UMR 5287, Pessac, 33615, France<sup>4</sup>Institut de Neurosciences Cognitives et Intégratives d'Aquitaine, University of Bordeaux, Pessac, 33615, France**v2** First published: 05 Nov 2020, 9:1299  
<https://doi.org/10.12688/f1000research.27096.1>Latest published: 25 Oct 2021, 9:1299  
<https://doi.org/10.12688/f1000research.27096.2>**Abstract**

**Background:** People with Down Syndrome (DS) are born with an extra copy of Chromosome (Chr) 21 and many of these individuals develop Alzheimer's Disease (AD) when they age. This is due at least in part to the extra copy of the APP gene located on Chr 21. By 40 years, most people with DS have amyloid plaques which disrupt brain cell function and increase their risk for AD. About half of the people with DS develop AD and the associated dementia around 50 to 60 years of age, which is about the age at which the hereditary form of AD, early onset AD, manifests. In the absence of Chr 21 trisomy, duplication of APP alone is a cause of early onset Alzheimer's disease, making it likely that having three copies of APP is important in the development of AD and in DS.

**Methods:** We investigate the relationship between AD and DS through integrative analysis of genesets derived from a MeSH query of AD and DS associated beta amyloid peptides, Chr 21, GWAS identified AD risk factor genes, and differentially expressed genes in individuals with DS.

**Results:** Unique and shared aspects of each geneset were evaluated based on functional enrichment analysis, transcription factor profile and network interactions. Genes that may be important to both disorders in the context of direct association with APP processing, Tau post translational modification and network connectivity are ACSM1, APBA2, APLP1, BACE2, BCL2L, COL18A1, DYRK1A, IK, KLK6, METTL2B, MTOR, NFE2L2, NFKB1, PRSS1, QTRT1, RCAN1, RUNX1, SAP18 SOD1, SYNJ1, S100B.

**Conclusions:** Our findings confirm that oxidative stress, apoptosis, inflammation and immune system processes likely contribute to the pathogenesis of AD and DS which is consistent with other published

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report



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### Keywords

Alzheimer's Disease, Down Syndrome, Behavior, Memory, Learning

Any reports and responses or comments on the article can be found at the end of the article.

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**REVISED Amendments from Version 1**

In this version we have addressed each of the reviewer's concerns and recommendations which entailed minor edits to the text for clarification and correction. The data and findings reported in the original version have not changed.

**Any further responses from the reviewers can be found at the end of the article**

## Introduction

Amyloids are peptide or protein aggregates that form from the misfolding of normally soluble proteins, which then aggregate together due to their chemical properties and accumulate in extracellular compartments and organs<sup>4</sup>. Amyloids form fibrous structures and plaques that are highly insoluble, resistant to degradation, and are involved in several diseases such as Alzheimer's disease (AD), Down syndrome (DS), spongiform encephalopathies, and type II diabetes<sup>5,6</sup>. The amyloid plaques associated with AD are formed from peptides derived from the mis-processing of APP, a protein that is expressed in neurons where it is processed to A $\beta$  peptides, some of which are found in plaques<sup>5,7</sup>. The A $\beta$ 42 peptide is preferentially deposited in plaques. The toxic peptide fragments are called beta amyloids. In AD, the amyloid plaques deposit in brain tissue, destroy neuronal connectivity, disrupt signaling at synapses, and eventually result in nerve cell death, tissue loss, and a reduction in brain mass<sup>5</sup>. Oligomeric forms of the beta-amyloid and not the beta-pleated sheets in plaques themselves trigger the immune system and inflammatory processes<sup>8</sup>.

Early onset AD that runs in families is linked to the *APP* and *PSEN1/PSEN2* genes<sup>9</sup>. A mutation in one of these three genes may cause AD to develop early whereas the more general form of the disease, late onset, is typically linked to the *APOE* gene<sup>10</sup>. *PSEN1/PSEN2* are transmembrane proteins that are the catalytic subunit of gamma secretase, the enzyme responsible for cleaving APP. Mutations in the *PSEN* genes may result in the abnormal cleaving and processing of APP to smaller toxic beta amyloid fragments which aggregate and accumulate<sup>11,12</sup>.

People with Down Syndrome (DS) are born with an extra copy of chromosome 21 (Chr 21) and many of these individuals develop AD as they age<sup>13</sup>. This is due at least in part to the extra copy of the *APP* gene located on Chr 21. By the age of 40, most people with DS have amyloid plaques which disrupt brain cell function and increase their risk for AD<sup>6</sup>. At least half of the people with DS develop AD and the associated dementia around 50 to 60 years of age, which is about the age at which the hereditary form of AD, early onset AD, manifests<sup>1</sup>. Results from a longitudinal study report this number to be greater than 90%<sup>14</sup>.

Duplication of *APP* alone, in the absence of Chr 21 trisomy, is another cause of early onset AD<sup>15,16</sup> making it likely that having three copies of *APP* is important in the development of AD in DS. However, it is unclear whether the formation of

excess amyloids is biologically involved in Down Syndrome itself and not just AD in DS.

In both early and late onset AD the clinical symptoms include dementia, memory decline, and the inability to retain recent information or store new memories<sup>17</sup>. As the disease progresses, people with AD may exhibit problems with language, reasoning, decision making, executive function, mood swings, aggressive behavior, and apathy. Late stage symptoms of AD may result in seizures, hypertonia myoclonus, incontinence, and mutism<sup>18</sup>. **Death commonly occurs from general inanition, malnutrition, and pneumonia.**

Memory loss and forgetfulness, which is typical in individuals with AD, is less pronounced in people with both DS and AD. This may in part be a floor-effect due to the memory deficit already present in individuals with DS<sup>19-21</sup>. Studies report an impairment in verbal short-term memory (example: serial order of a list of words) relative to visuo-spatial memory (manual selection in serial order of locations) and deficits in explicit long-term memory<sup>22</sup>. Also in individuals with DS there is evidence of hippocampal dysfunction and deficits in prefrontal systems as compared with mental age-matched controls<sup>23</sup>. In people with DS, the hippocampal volume is reduced prior to the onset of dementia, and these reductions were found to relate to memory mainly due to the loss of neurons and neuronal volume as a result of neurofibrillary tangle formation<sup>24</sup>.

In this study we investigate the relationship between AD and DS through integrative geneset analysis of genes derived from peptides associated with amyloid plaques found in individuals with AD and DS, Chr 21 genes, AD risk factor genes, and differentially expressed genes (DEX) identified through a transcriptome analysis of people with DS for both the dorsal frontal cortex (DFC) and cerebellar cortex (CBC).

## Methods

### Geneset characteristics

All genesets used in this study are presented in *Extended data Workbook 1*<sup>25</sup>. The Chr 21 geneset was obtained from NCBI Gene. A total of **250 unique gene IDs** were obtained at the time of manuscript preparation (September 1st, 2020). The AD-DS geneset, consisting of 292 genes, was obtained from **GeneWeaver** using "Alzheimer's Down Syndrome" as the search term. The geneset was originally generated via **gene2mesh** v.1.1.1 (updated: 2019-01-07) from Medical Subject Headings (MESH Terms) GS236695 • [MeSH] Amyloid beta-Peptides: **D016229**. The AD risk factor geneset is comprised of 279 genes, many of which were identified and/or confirmed through a large scale GWAS of 71,880 clinically diagnosed AD and AD-by-proxy cases and 383,378 controls<sup>26</sup>.

The DEX genesets for the DFC (842) and CBC (570) were obtained from **The Down Syndrome Developmental Brain Transcriptome database**. Human Brain Transcriptome, Department of Neurobiology Yale University School of Medicine which is a publicly accessible database containing searchable differential gene expression information of transcriptome data in developing and adult DS versus control human brains.

The data was generated from 15 sets of a DS and a matched control brain each. The specimens ranged from embryonic development to adulthood<sup>27</sup>.

### Geneset overlap

Common genes among the AD-DS, Chr 21, DEX DFC, DEX CBC and AD risk factor genesets were assessed using venn diagram analysis (<http://www.interactivenn.net/>) and visualized with the UpSet Library in RStudio, R Version 4.0.2.

### Keyword categories

Keyword categories were used to evaluate the genesets. The keyword categories were chosen based on the major phenotypes associated with AD and DS. The terms used were: aging, Alzheimer’s disease, amyloid; apoptosis, behavior cholesterol, circadian, cognition; Down Syndrome, face, fibril, immune, inflammation, insulin, learning, leptin, memory, muscle, myelin; obesity, sleep, speech, and tau.

### Functional analyses

Gene ontology characterization of the genesets was performed in both DAVID and the Gene Ontology database for Biological Process (BP). The Benjamini corrected P-value was used to determine enrichment significance. Functional information based on GO annotations for the genes associated with a keyword search term related to AD and DS were identified and noted.

Gene Ontology pathway enrichment was used to further characterize the AD-DS and Chr21 genesets in order to obtain a

broader overview of collective gene function. The Benjamini-corrected P-value was used to determine significance.

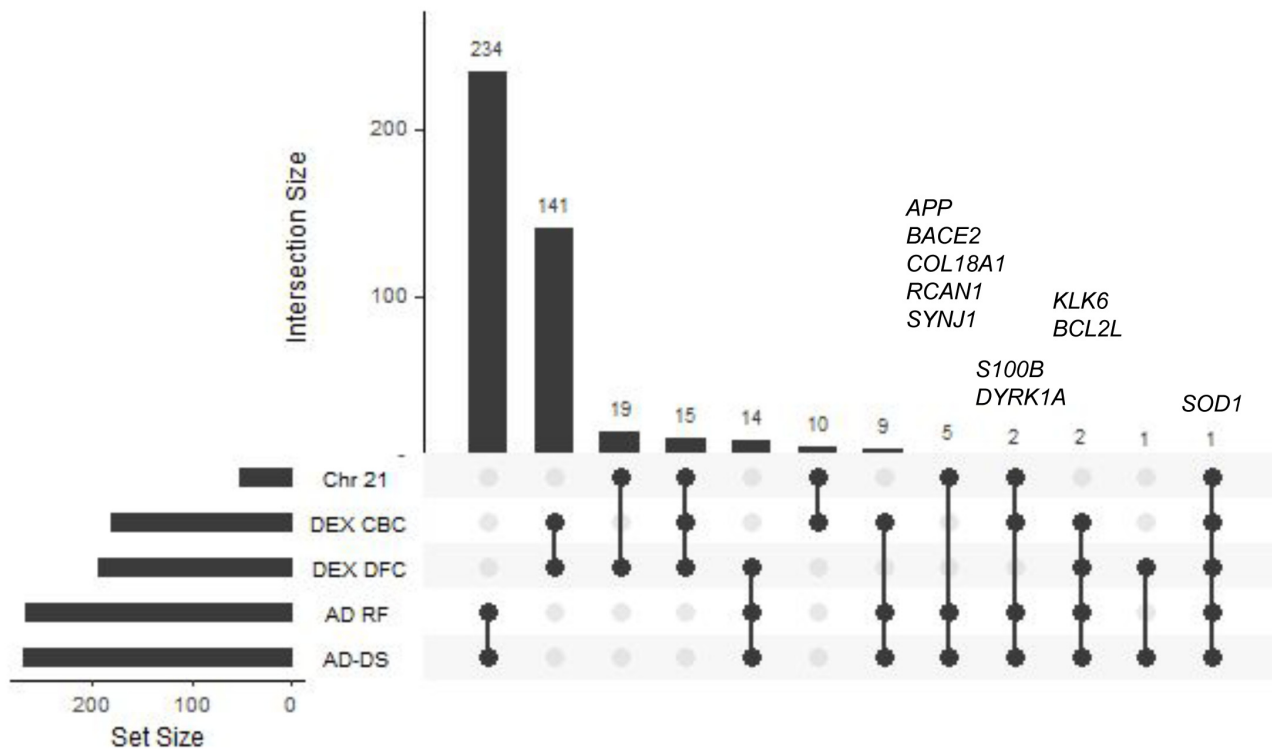
### APP protein interaction network

The APP protein-protein interaction network was built in STRING (version 11.0), based on experimentally validated interactions. The combined scores for the interactions are computed by combining the probabilities from the different evidence channels and corrected for the probability of randomly observing an interaction. First and 2nd shell interactions are included in the network. The network was exported from STRING and analyzed in Cytoscape (version 3.7). Network bottlenecks and clusters were identified with Cytoscape plugins CytoHubba (version 0.1) and MCODE (version 1.6.1), respectively.

## Results

### Geneset overlap

The number of common genes among all of the 5 genesets (AD-DS, Chr 21, AD risk factors, DEX DFC, and DEX CBC) along with the gene names and Gene Ontology classifiers are shown in Figure 1 and Extended data Workbook 2<sup>28</sup>. The AD-DS, Chr 21 and AD risk factor genesets overlap by eight genes: *APP*, *BACE2*, *COL18A1*, *DYRK1A*, *RCAN1*, *SOD1*, *SYNJ1*, and *S100B* (Figure 1). *BACE2* encodes an integral membrane glycoprotein that cleaves the APP protein into amyloid-β, a critical step in the cause of AD and DS. *COL18A1* encodes the alpha chain of type XVIII collagen. It is associated with vascular deposits and senile plaques in AD brains<sup>29</sup>. The *DYRK1A* gene product can phosphorylate APP and alter the protein’s stability



**Figure 1. GeneSet overlap.** UpSet plot showing geneset overlap highlighting gene content similarity between the AD-DS, Chr21, AD risk factors DEX DFC, and DEX CBC genes.

and the formation of amyloid- $\beta$ <sup>30,31</sup>. Increased *RCAN1* expression is associated with neuronal death and Tau hyperphosphorylation, as well as neurofibrillary tangle formation in individuals with DS and AD<sup>32</sup>.

*SOD1* is the only gene present in all of the genesets. *SOD1* is associated with apoptosis and oxidative stress<sup>33</sup>. The extra copy of *SOD* on Chr 21 results in increased gene expression and increased production of H<sub>2</sub>O<sub>2</sub> which is believed to underlie many of the DS-related pathologies<sup>33</sup>. *SOD1* is also associated with neurodegeneration in amyotrophic lateral sclerosis and AD<sup>34,35</sup>. *SYNJ1* encodes a lipid phosphatase that is involved in autophagosomal/endosomal trafficking and synaptic vesicle recycling. Its dysfunction has been linked to several neurodegenerative diseases, including AD and DS<sup>36</sup>. *S100 $\beta$*  belongs to a family of cytokines that are strongly associated with activity underlying AD related pathologies such as APP processing, protein inclusion formation, and Tau post-translational modifications. *S100 $\beta$*  is also linked to DS. *S100 $\beta$*  levels are increased in neuronal progenitor cells of DS patients<sup>37</sup> and in human induced pluripotent stem cells derived from DS patients<sup>38</sup>. Two additional genes, *KLK6* and *BCL2L*, are shared among the AD-DS, AD risk factors, DEX DFC and DEX CBC genesets. *KLK6* has been proposed as a biomarker for AD<sup>39</sup>. *BCL2L* is located on the outer mitochondrial membrane and is a negative regulator of apoptosis<sup>40</sup>.

**Keyword enrichment**

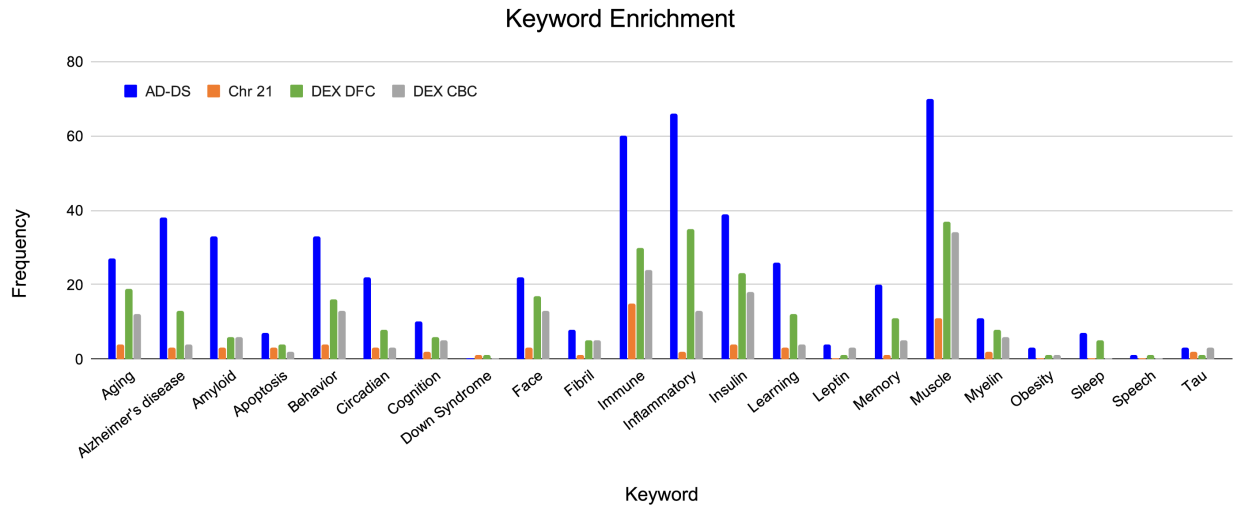
Each of the genesets were evaluated for association with AD and DS related phenotypes (Figure 2 and Extended data, Workbook 3<sup>41</sup>). The keyword categories shared among all genesets are muscle, immune, insulin, glucose, behavior, oxidation and heart. The AD-DS geneset has a high frequency of genes associated with most of the keyword categories. The largest represented categories are: AD, muscle, inflammation/immune system, insulin, amyloid, behavior, aging, learning/memory, circadian processes and face/facial features. There were no genes

directly associated with DS. For the Chr 21 geneset, unlike the AD-DS geneset, there were very few genes associated with the keyword categories. The highest frequency categories are immune, muscle, aging, behavior and insulin. Three genes are connected to AD (*NDUFV3*, *APP* and *BACE2*) and one with DS (*DSCAM*).

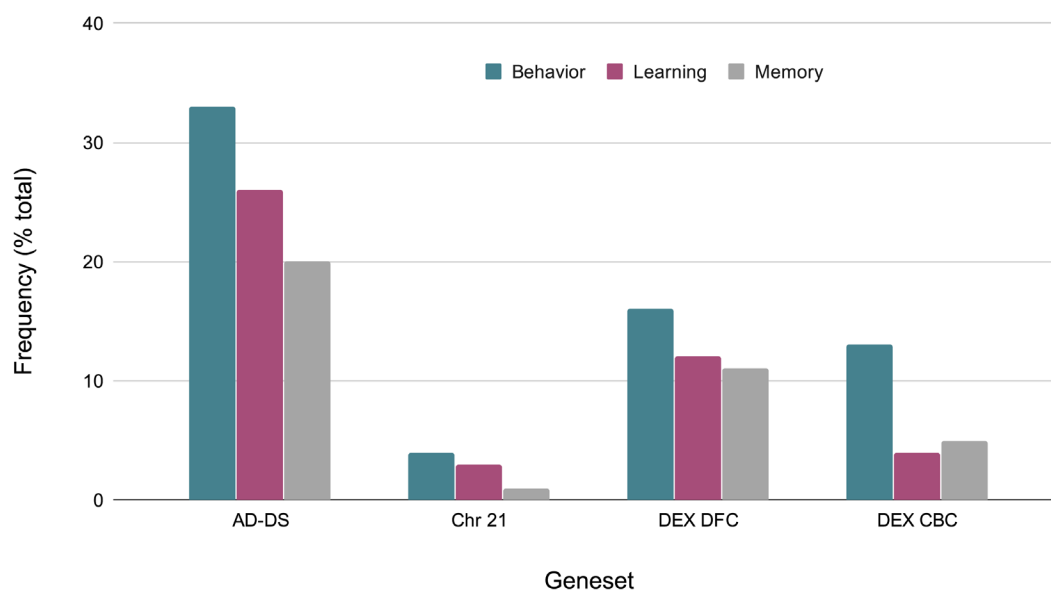
The enriched keyword categories for the DEX DFC are very similar to the results obtained for the AD-DS geneset: muscle, inflammation/immune system, insulin, aging, face/facial features, behavior, AD, and learning/memory. There are 13 genes directly associated with AD (*NDUFS2*, *APAF1*, *BACE1*, *CACNA1F*, *COX5B*, *COX6A2*, *GRIN1*, *GRIN2A*, *LPL*, *PLD3*, *PSEN1*, *RYR3*, *UQCRC1*) and one gene associated with DS (*DSCR9*). For the DEX CBC geneset the most representative categories are again similar to the AD-DS geneset as well as the DEX DFC geneset: muscle, immune/inflammation, insulin, behavior, face/facial features, aging and amyloid. There are four genes directly linked to AD (*ATP5H*, *APOE*, *APAF1*, *RYR3*). There are no genes directly associated with DS.

**Behavior-related genes**

Given that behavioral phenotypes are highly shared between AD and DS, the specific types of behaviors identified from the keyword enrichment were evaluated more in depth. The AD-DS geneset has a large number of behavior related genes and genes related to learning and memory: (Behavior 33, Learning 26, Memory 21). This observation is based on the GO results obtained for three random genesets of the same size: Behavior 7,2,1; Learning 0,1,1; Memory: 0,0,1. The behavior gene categories are diverse and include fear, locomotion, eating and feeding, addiction related (nicotine, cocaine, ethanol), social, and others such as circadian, mating, and response to pain. The learning categories include visual learning, associative learning, and also olfactory, motor, and nonassociative learning. The memory related categories are short-term and long-term memory, and in one instance, susceptibility to memory impairment (Figure 3).



**Figure 2. Keyword enrichment.** Identification of genes associated with terms relating to AD and DS based on gene ontology term classification. AD-DS genes: blue, Chr 21 genes: orange, DEX DFC genes: green, DEX CBC genes: gray, X-axis, keyword categories; Y-axis, frequency of occurrence in the geneset.



**Figure 3. Evaluation of GO classification terms based on behavioral, memory, and learning categories.** Comparison of frequencies of behavior related genes in the AD-DS, Chr 21, DEX DFC, and DEX CBC genesets. X-axis, geneset; Y-axis, frequency of occurrence (percentage of total genes) in the geneset.

### Functional analyses

Many of the significant BP enrichment classifiers for the AD-DS geneset are associated with cell death ( $P=3.01E-83$ ), apoptosis ( $P=1.30E-70$ ) and inflammation/immune system ( $P=1.65E-36$ ). For the Chr21 geneset, the significant BP enriched terms are linked to keratin (keratinization,  $P=1.04E-37$ ), skin (skin development ( $P=2.83E-29$ ) and epithelium processes ( $P=3.19E-15$ ) as well as tissue ( $P=3.56E-14$ ), organ ( $P=3.40E-09$ ) and anatomical structure development ( $P=8.66E-09$ ). The significant pathways associated with the AD-DS geneset are related to neurodegenerative disorders (AD  $P=3.1E-23$ , Parkinson's disease ( $P=1.39E-04$ ) and Huntington's disease  $P=1.36E-07$ ) as well as many signaling pathways linked to insulin ( $P=1.86E-09$ ) and inflammation (Jak/Stat  $P=9.49E-04$ ), Toll receptor ( $P=4.04E-10$ ), Interferon-gamma signaling ( $P=8.90E-06$ ). There were no significant pathways associated with Chr 21. All pathways are listed in *Extended data* Workbook 4<sup>42</sup>.

### Transcriptional profile

The transcription profiles of the AD-DS and Chr 21 genesets were evaluated here and compared with the DEX genesets which were previously evaluated by Olmos-Serrano *et al.*<sup>27</sup> (*Extended data*, Workbook 5<sup>43</sup>). There are 64 transcription factors and genes known to impact transcription present in the AD-DS geneset. Several of these are directly associated with AD (*GSK3B*, *IL1B*, *MAPK3/8/10/14*, *WNT1*, *WNT3A*, *KAT5*, *NOTCH1* and *TNF*), Tau (*GSK3B* and *CLU*) and amyloid (*CD36*, *NLRP3*, *CLU*, *FOXO3*, *PARP1*, *PRNP*). Of these, many are related to mitochondria processes (*AKT1*, *CLU*, *GSK3B*, *HIF1A*, *MAPK3,8,10,14*, *MTOR*, *NFKB1*, *PPARGCIA*, *PARP1*, *PRNP*, *PRKCA*, *SIRT1*, *STAT3*, *SREBF2*, *UBB*) and also inflammation, oxidative stress, and aging (*TP53*, *STAT1/3*, *NFKB1*, *HIF1A*, and *NEF2L2*).

For the Chr 21 geneset, 18 transcription factors were identified. *RUNX1* which is associated with ossification<sup>44</sup> and nervous system development<sup>45</sup> observed comparable expression in a study comparing AD and DS brains. Gene variants of *RUNX1* are associated with both AD and DS<sup>46</sup>. The *OLIG1/OLIG2* transcription factors regulate oligodendroglial differentiation and myelination and neuron fate commitment<sup>47</sup>. In DS, due to the gene triplication, *OLIG1/OLIG2* causes alterations in brain development<sup>48</sup>. *OLIG2* is associated with the psychotic symptoms of AD and also schizophrenia<sup>49</sup>. Of the Chr 21 transcription factors, only one is associated with mitochondria—*GABPA*— which is involved in the activation of cytochrome oxidase expression and nuclear control of mitochondrial function<sup>50</sup>.

There is one common transcription factor between the AD-DS and DEX-DFC genesets: *NFE2L2* (also known as *NRF2*), which is associated with the oxidative stress response with aging, spatial learning, memory, and neuro-inflammation via regulation of antioxidant response elements<sup>51,52</sup>. *NFE2L2/NRF2* regulates *BACE1*, the rate-limiting enzyme for amyloid- $\beta$  peptide ( $A\beta$ ) generation. *NRF2* activation decreases production of *BACE1* and *BACE1* antisense RNA (*BACE1-AS*) transcripts and  $A\beta$  production and ameliorates cognitive deficits in animal models of AD<sup>53</sup>. Depletion of *NFE2L2/NRF2* increases *BACE1* and *BACE1-AS* expression and  $A\beta$  production and worsens cognitive deficits<sup>54</sup>.

There are two transcription factors common between the AD-DS and DEX-CBC genesets. *MTOR* has been identified as a key target for therapeutic intervention in AD because of its regulation of several key signaling pathways: phosphoinositide 3-kinase (PI3-K)/protein kinase B (Akt),

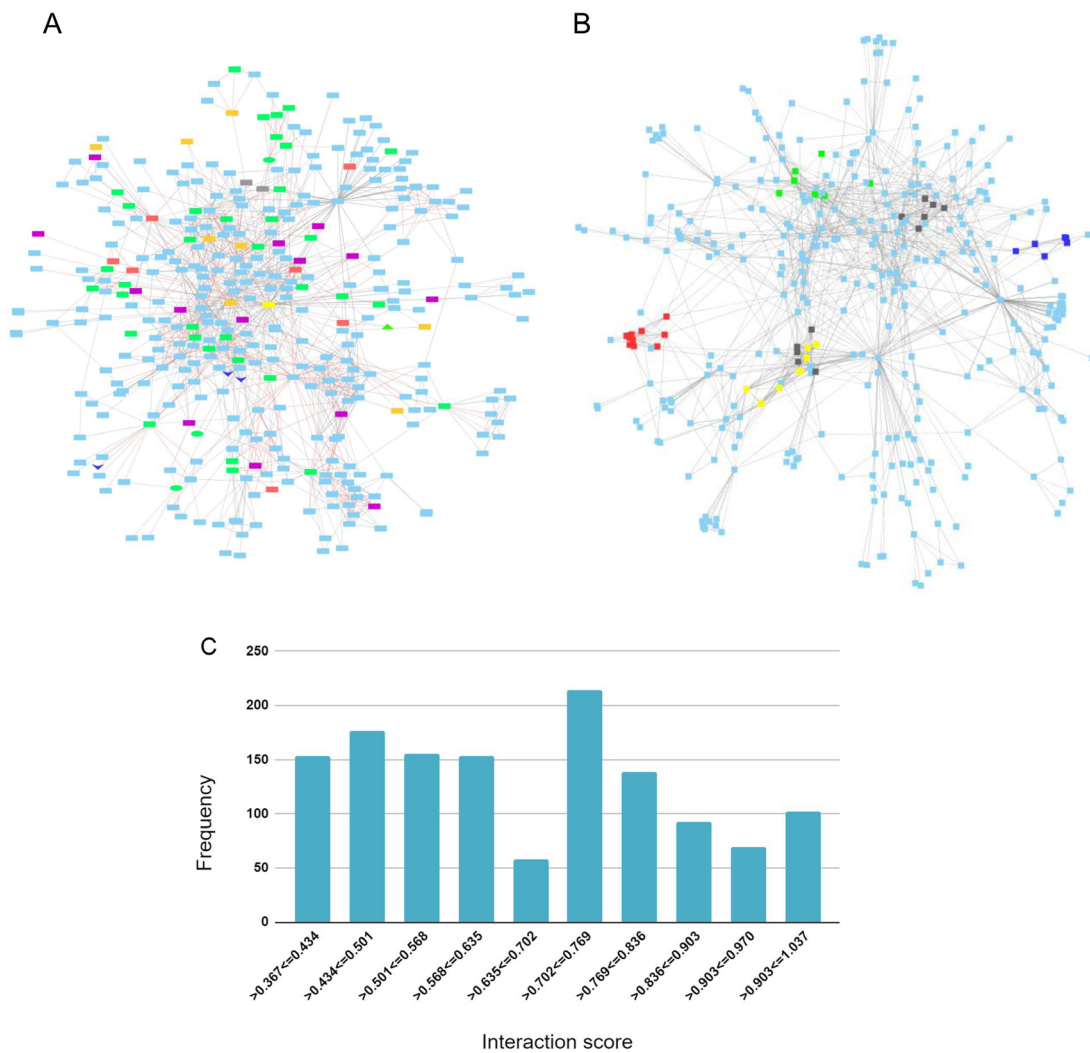
glycogen synthase kinase 3 [GSK-3], AMP-activated protein kinase (AMPK), and insulin/insulin-like growth factor 1 (IGF-1)<sup>55</sup>. Both upstream and downstream components of mTOR signaling are associated with AD progression and pathogenesis. *MTOR* inhibits autophagic processes and contributes to amyloid  $\beta$ -peptide generation and/or clearance<sup>56</sup>. *MTOR* activation also contributes to aberrant hyperphosphorylated tau<sup>57</sup>. The other common TF is *NFKB1* which is a key regulator of innate immunity and strongly associated with the inflammatory response involving cytokines and chemokines<sup>58</sup>. *NFKB1* is also linked to aging and AD<sup>59,60</sup>.

### APP protein-protein interaction network

An *APP* protein-protein interaction network was created to identify genes from the genesets evaluated in this study that are

connected to *APP* through 1st and 2nd shell interactions. A total of 362 proteins make up the network (*Extended data Workbook 6*<sup>61</sup>).

The *APP* protein interaction network overlaps by 48 genes with the AD-DS geneset, 41 with the AD risk factor geneset, 21 with the DEX DFC, 12 with the DEX CBC geneset and four with the Chr 21 geneset. The shared genes are highlighted in the network to visualize and forecast additional genes that are potentially involved in *APP* signaling and that are relevant to both AD and DS (*Figure 4A*). The top proteins that bridge (bottlenecks) the different sections of the network and that may signify information flow are: *APP*, *ENSG00000259680* (a novel protein coding gene with similarity to immunoglobulin heavy chain variable region.), *SHC1*, *DLG4*, *STUB1*, *KLC1*, *GFA1*, *CENPJ*, and *GNO1*.



**Figure 4. APP protein-protein interaction network. (A)** Geneset overlap between 1<sup>st</sup> and 2<sup>nd</sup> shell interactions and the AD-DS, Chr 21, DEX DFC, and DEX CBC genesets. AD-DS genes unique: red; Chr 21 genes unique: gray; DEX DFC genes unique: purple; CBC genes unique: orange; AD risk factors (RF) and AD-DS genes shared: green; DEX DFC genes shared with RF & AD-DS genes: green oval; CBC and DFC shared genes: dark blue V; CBC genes shared with RF: green triangle; *APP*: yellow rectangle. **(B)** Interaction network gene clusters. Cluster 1: red – COP subunits, signalosome complex, development; Ubiquitin, Cluster 2: yellow – Tubulin, microtubules, motors, intracellular transport; Cluster 3: green – apoptosis, insulin signaling, ubiquitin, VEGFR growth factor signaling; Cluster 4: blue – Ubiquitin, autophagy; and Cluster 5: black – *APP* processing (PSEN, gamma secretase complex). **(C)** Distribution frequency for interaction score.

The APP network contains six major clusters (Figure 4B). Cluster 1: COP subunits, signalosome complex, development, ubiquitin; Cluster 2: TUBULIN, microtubules, motors, intracellular transport; Cluster 3: apoptosis, insulin signaling, ubiquitin, VEGFR growth factor signaling; Cluster 4: UBIQUITIN, autophagy; Cluster 5: APP processing (PSEN, gamma secretase complex); and Cluster 6: TUBULIN, microtubules.

The AD risk factor genes, Chr 21, and AD-DS genes are mostly dispersed throughout the network but a couple of areas in the network contain several connected AD risk factor genes. Predicted genes of interest based on their connectivity to these areas are *METTL2B* (tRNA methylation), *IK* (immune response), *SAPI8* (RNA splicing), *QRT1* (tRNA modification), *APLP1* (Prion pathway), *PRSSI* (proteolysis, extracellular matrix digestion), *ACSM1* (lipid metabolism), *APBA2* (binds beta amyloid, synaptic transmission, and nervous system development). The validity of all of the interaction scores range from 0.4–1.00 and, for the most part, are uniformly distributed with 695 of the interactions falling in the low to mid-range of 0.4 and 0.7 and 617 falling in the mid to high-range of 0.7 and 1.0 (Figure 4C).

## Conclusion

Genesets associated with AD, DS, and Chr 21 were evaluated to identify genes, transcription factors, and pathways that may shed light on the relationship between AD and DS. Genes common to multiple genesets are either directly involved in APP processing or in TAU post translational modification. Many of the genes associated with the amyloid plaques in AD and DS function in learning and memory. A network analysis of APP protein-protein interactions was used to analyze the topology and connectivity of the genesets and, based on interactions with common AD-DS genes and AD risk factor genes, provide the foundation to predict potential genes of interest. Genes that connect the network and represent information flow as well as regions of high interconnectivity are also of interest for follow up studies. Given the central role of APP related processes in the pathology of AD and DS, all of the proteins in the APP interaction network are either potential risk factors for AD or may contribute to disease progression in both

AD and DS. Taken together, our findings confirm that oxidative stress, apoptosis, inflammation and immune system processes likely contribute to the pathogenesis of AD and DS which is consistent with other published reports<sup>1-3</sup>.

## Data availability

### Underlying data

All data underlying the results are available as part of the article and no additional source data are required.

### Extended data

Figshare: Extended Data Workbook 1. Genesets: AD-DS, Chr 21, AD risk factors, DEX DFC and CBC, <https://doi.org/10.6084/m9.figshare.13106693.v1><sup>25</sup>.

Figshare: Extended Data Workbook 2. Common Genes: Gene overlap between the AD-DS, Chr 21, AD risk factors, DEX DFC and CBC genesets, <https://doi.org/10.6084/m9.figshare.13106741.v1><sup>28</sup>.

Figshare: Extended Data Workbook 3. Keyword Gene Enrichment: Enrichment of the AD-DS, Chr 21, AD risk factors, DEX DFC and CBC genesets, <https://doi.org/10.6084/m9.figshare.13106750.v1><sup>41</sup>.

Figshare: Extended Data Workbook 4. GO Terms and Pathways: Gene Ontology Biological Process terms and pathways associated with the AD-DS and Chr 21 genesets, <https://doi.org/10.6084/m9.figshare.13106762.v1><sup>42</sup>.

Figshare: Extended Data Workbook 5. Transcription Factors: TFs present in the AD-DS, Chr 21 genesets, <https://doi.org/10.6084/m9.figshare.13106774.v1><sup>43</sup>.

Figshare: Extended Data Workbook 6. APP Network File: APP protein-protein interaction network, <https://doi.org/10.6084/m9.figshare.13106777.v1><sup>61</sup>.

Data are available under the terms of the [Creative Commons Attribution 4.0 International license \(CC-BY 4.0\)](https://creativecommons.org/licenses/by/4.0/).

## References

- Lott IT, Head E: **Dementia in Down syndrome: unique insights for Alzheimer disease research.** *Nat Rev Neurol.* 2019; **15**(3): 135–47. [PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- Wiseman FK, Al-Janabi T, Hardy J, et al.: **A genetic cause of Alzheimer disease: mechanistic insights from Down syndrome.** *Nat Rev Neurosci.* 2015; **16**(9): 564–74. [PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- Hartley D, Blumenthal T, Carrillo M, et al.: **Down syndrome and Alzheimer's disease: Common pathways, common goals.** *Alzheimers Dement.* 2015; **11**(6): 700–9. [PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- Rambaran RN, Serpell LC: **Amyloid fibrils: abnormal protein assembly.** *Prion.* 2008; **2**(3): 112–7. [PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- Gouras GK, Olsson TT, Hansson O:  **$\beta$ -Amyloid peptides and amyloid plaques in Alzheimer's disease.** *Neurotherapeutics.* 2015; **12**(1): 3–11. [PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- Annus T, Wilson LR, Hong YT, et al.: **The pattern of amyloid accumulation in the brains of adults with Down syndrome.** *Alzheimers Dement.* 2016; **12**(5): 538–45. [PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
- Gu L, Guo Z: **Alzheimer's A $\beta$ 42 and A $\beta$ 40 peptides form interlaced amyloid**



- fibrils. *J Neurochem.* 2013; **126**(4): 305–11.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)**
8. Gasic-Milenkovic J, Dukic-Stefanovic S, Deuther-Conrad W, et al.: **Beta-amyloid peptide potentiates inflammatory responses induced by lipopolysaccharide, interferon-gamma and advanced glycation endproducts in a murine microglia cell line.** *Eur J Neurosci.* 2003; **17**(4): 813–21.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  9. Bekris LM, Yu CE, Bird TD, et al.: **Genetics of Alzheimer disease.** *J Geriatr Psychiatry Neurol.* 2010; **23**(4): 213–27.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  10. Lanoiselée HM, Nicolas G, Wallon D, et al.: **APP, PSEN1, and PSEN2 mutations in early-onset Alzheimer disease: A genetic screening study of familial and sporadic cases.** *PLoS Med.* 2017; **14**(3): e1002270.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  11. Cai Y, An SS, Kim S: **Mutations in presenilin 2 and its implications in Alzheimer's disease and other dementia-associated disorders.** *Clin Interv Aging.* 2015; **10**: 1163–72.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  12. Kelleher RJ 3rd, Shen J: **Presenilin-1 mutations and Alzheimer's disease.** *Proc Natl Acad Sci U S A.* 2017; **114**(4): 629–31.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  13. Nixon DW: **Down syndrome, obesity, alzheimer's disease, and cancer: A brief review and hypothesis.** *Brain Sci.* 2018; **8**(4): 53.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  14. McCarron M, McCallion P, Reilly E, et al.: **A prospective 14-year longitudinal follow-up of dementia in persons with Down syndrome.** *J Intellect Disabil Res.* 2014; **58**(1): 61–70.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  15. Rovelet-Lecrux A, Hannequin D, Raux G, et al.: **APP locus duplication causes autosomal dominant early-onset Alzheimer disease with cerebral amyloid angiopathy.** *Nat Genet.* 2006; **38**(1): 24–6.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  16. Sleegers K, Brouwers N, Gijssels I, et al.: **APP duplication is sufficient to cause early onset Alzheimer's dementia with cerebral amyloid angiopathy.** *Brain.* 2006; **129**(Pt 11): 2977–83.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  17. Jahn H: **Memory loss in Alzheimer's disease.** *Dialogues Clin Neurosci.* 2013; **15**(4): 445–54.  
[PubMed Abstract](#) | [Free Full Text](#)
  18. Li XL, Hu N, Tan MS, et al.: **Behavioral and psychological symptoms in Alzheimer's disease.** *Biomed Res Int.* 2014; **2014**: 927804.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  19. Jarrold C, Baddeley AD, Hewes AK: **Verbal short-term memory deficits in Down syndrome: a consequence of problems in rehearsal?** *J Child Psychol Psychiatry.* 2000; **41**(2): 233–44.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  20. **Memory and neuropsychology in Down syndrome.** 2020; [cited 2020 Feb 20]. [Reference Source](#)
  21. Godfrey M, Lee NR: **Memory profiles in Down syndrome across development: a review of memory abilities through the lifespan.** *J Neurodev Disord.* 2018; **10**(1): 5.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  22. Nadel L: **Down's syndrome: a genetic disorder in biobehavioral perspective.** *Genes Brain Behav.* 2003; **2**(3): 156–66.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  23. Pennington BF, Moon J, Edgin J, et al.: **The neuropsychology of Down syndrome: evidence for hippocampal dysfunction.** *Child Dev.* 2003; **74**(1): 75–93.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  24. Salehi A, Ashford JW, Mufson EJ: **The Link between Alzheimer's Disease and Down Syndrome. A Historical Perspective.** *Curr Alzheimer Res.* 2016; **13**(1): 2–6.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  25. Delprato A: **Extended Data Workbook 1. Genesets: AD-DS, Chr 21, AD risk factors, DEX DFC and CBC.** *figshare.* Dataset. 2020.  
<http://www.doi.org/10.6084/m9.figshare.13106693.v1>
  26. Jansen IE, Savage JE, Watanabe K, et al.: **Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimer's disease risk.** *Nat Genet.* 2019; **51**(3): 404–13.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  27. Olmos-Serrano JL, Kang HJ, Tyler WA, et al.: **Down syndrome developmental brain transcriptome reveals defective oligodendrocyte differentiation and myelination.** *Neuron.* 2016; **89**(6): 1208–22.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  28. Delprato A: **Extended Data Workbook 2. Common Genes: Gene overlap between the AD-DS, Chr 21, AD risk factors, DEX DFC and CBC genesets.** *figshare.* Dataset. 2020.  
<http://www.doi.org/10.6084/m9.figshare.13106741.v1>
  29. van Horssen J, Wilhelmus MM, Heljasvaara R, et al.: **Collagen XVIII: a novel heparan sulfate proteoglycan associated with vascular amyloid depositions and senile plaques in Alzheimer's disease brains.** *Brain Pathol.* 2002; **12**(4): 456–62.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  30. Ryo SR, Jeong HK, Radnaabazar C, et al.: **DYRK1A-mediated hyperphosphorylation of Tau. A functional link between Down syndrome and Alzheimer disease.** *J Biol Chem.* 2007; **282**(48): 34850–7.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  31. García-Cerro S, Rueda N, Vidal V, et al.: **Normalizing the gene dosage of Dyrk1A in a mouse model of Down syndrome rescues several Alzheimer's disease phenotypes.** *Neurobiol Dis.* 2017; **106**: 76–88.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  32. Lloret A, Badia MC, Giraldo E, et al.: **Amyloid- $\beta$  toxicity and tau hyperphosphorylation are linked via RCAN1 in Alzheimer's disease.** *J Alzheimers Dis.* 2011; **27**(4): 701–9.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  33. Perluigi M, Butterfield DA: **Oxidative Stress and Down Syndrome: A Route toward Alzheimer-Like Dementia.** *Curr Gerontol Geriatr Res.* 2012; **2012**: 724904.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  34. Yoon EJ, Park HJ, Kim GY, et al.: **Intracellular amyloid beta interacts with SOD1 and impairs the enzymatic activity of SOD1: implications for the pathogenesis of amyotrophic lateral sclerosis.** *Exp Mol Med.* 2009; **41**(9): 611–7.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  35. Beckman JS, Estévez AG, Crow JP, et al.: **Superoxide dismutase and the death of motoneurons in ALS.** *Trends Neurosci.* 2001; **24**(11 Suppl): S15–20.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  36. Drouet V, Lesage S: **Synaptojanin 1 mutation in Parkinson's disease brings further insight into the neuropathological mechanisms.** *Biomed Res Int.* 2014; **2014**: 289728.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  37. Esposito G, Imitola J, Lu J, et al.: **Genomic and functional profiling of human Down syndrome neural progenitors implicates S100B and aquaporin 4 in cell injury.** *Hum Mol Genet.* 2008; **17**(3): 440–57.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  38. Chen C, Jiang P, Xue H, et al.: **Role of astroglia in Down's syndrome revealed by patient-derived human-induced pluripotent stem cells.** *Nat Commun.* 2014; **5**: 4430.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  39. Diamandis EP, Yousef GM, Petraki C, et al.: **Human kallikrein 6 as a biomarker of alzheimer's disease.** *Clin Biochem.* 2000; **33**(8): 663–7.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  40. Martínez-Serrano A, Castillo CG, Courtois ET, et al.: **Modulation of the generation of dopaminergic neurons from human neural stem cells by Bcl-X(L): mechanisms of action.** *Vitam Horm.* 2011; **87**: 175–205.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  41. Delprato A: **Extended Data Workbook 3. Keyword Gene Enrichment: Enrichment of the AD-DS, Chr 21, AD risk factors, DEX DFC and CBC genesets.** *figshare.* Dataset. 2020.  
<http://www.doi.org/10.6084/m9.figshare.13106750.v1>
  42. Delprato A: **Extended Data Workbook 4. GO Terms and Pathways: Gene Ontology Biological Process terms and pathways associated with the AD-DS and Chr 21 genesets.** *figshare.* Dataset. 2020.  
<http://www.doi.org/10.6084/m9.figshare.13106762.v1>
  43. Delprato A: **Extended Data Workbook 5. Transcription Factors: TFs present in the AD-DS, Chr 21 genesets.** *figshare.* Dataset. 2020.  
<http://www.doi.org/10.6084/m9.figshare.13106774.v1>
  44. Qin X, Jiang Q, Matsuo Y, et al.: **Cbfb regulates bone development by stabilizing Runx family proteins.** *J Bone Miner Res.* 2015; **30**(4): 706–14.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  45. Wang JW, Stifani S: **Roles of Runx Genes in Nervous System Development.** *Adv Exp Med Biol.* 2017; **962**: 103–16.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  46. Patel A, Rees SD, Kelly MA, et al.: **Association of variants within APOE, SORL1, RUNX1, BACE1 and ALDH18A1 with dementia in Alzheimer's disease in subjects with Down syndrome.** *Neurosci Lett.* 2011; **487**(2): 144–8.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  47. Emery B, Lu QR: **Transcriptional and Epigenetic Regulation of Oligodendrocyte Development and Myelination in the Central Nervous System.** *Cold Spring Harb Perspect Biol.* 2015; **7**(9): a020461.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  48. Chakrabarti L, Best TK, Cramer NP, et al.: **Olig1 and Olig2 triplication causes developmental brain defects in Down syndrome.** *Nat Neurosci.* 2010; **13**(8): 927–34.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  49. Sims R, Hollingworth P, Moskvina V, et al.: **Evidence that variation in the oligodendrocyte lineage transcription factor 2 (OLIG2) gene is associated with psychosis in Alzheimer's disease.** *Neurosci Lett.* 2009; **461**(1): 54–9.  
[PubMed Abstract](#) | [Publisher Full Text](#)
  50. Yang ZF, Drumea K, Mott S, et al.: **GABP transcription factor (nuclear respiratory factor 2) is required for mitochondrial biogenesis.** *Mol Cell Biol.* 2014; **34**(17): 3194–201.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  51. Zamponi E, Zamponi N, Coskun P, et al.: **Nrf2 stabilization prevents critical oxidative damage in Down syndrome cells.** *Aging Cell.* 2018; **17**(5): e12812.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
  52. Branca C, Ferreira E, Nguyen TV, et al.: **Genetic reduction of Nrf2 exacerbates**

- cognitive deficits in a mouse model of Alzheimer's disease.** *Hum Mol Genet.* 2017; **26**(24): 4823–35.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
53. Rojo AI, Pajares M, Rada P, *et al.*: **NRF2 deficiency replicates transcriptomic changes in Alzheimer's patients and worsens APP and TAU pathology.** *Redox Biol.* 2017; **13**: 444–51.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
54. Bahn G, Park JS, Yun UJ, *et al.*: **NRF2/ARE pathway negatively regulates BACE1 expression and ameliorates cognitive deficits in mouse Alzheimer's models.** *Proc Natl Acad Sci USA.* 2019; **116**(25): 12516–23.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
55. Wang C, Yu JT, Miao D, *et al.*: **Targeting the mTOR signaling network for Alzheimer's disease therapy.** *Mol Neurobiol.* 2014; **49**(1): 120–35.  
[PubMed Abstract](#) | [Publisher Full Text](#)
56. Cai Z, Chen G, He W, *et al.*: **Activation of mTOR: a culprit of Alzheimer's disease?** *Neuropsychiatr Dis Treat.* 2015; **11**: 1015–30.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
57. Tang Z, Bereczki E, Zhang H, *et al.*: **Mammalian target of rapamycin (mTor) mediates tau protein dyshomeostasis: implication for Alzheimer disease.** *J Biol Chem.* 2013; **288**(22): 15556–70.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
58. Granic I, Dolga AM, Nijholt IM, *et al.*: **Inflammation and NF-kappaB in Alzheimer's disease and diabetes.** *J Alzheimers Dis.* 2009; **16**(4): 809–21.  
[PubMed Abstract](#) | [Publisher Full Text](#)
59. Kitamura Y, Shimohama S, Ota T, *et al.*: **Alteration of transcription factors NF-kappaB and STAT1 in Alzheimer's disease brains.** *Neurosci Lett.* 1997; **237**(1): 17–20.  
[PubMed Abstract](#) | [Publisher Full Text](#)
60. Jones SV, Kounatidis I: **Nuclear Factor-Kappa B and Alzheimer Disease, Unifying Genetic and Environmental Risk Factors from Cell to Humans.** *Front Immunol.* 2017; **8**: 1805.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
61. Delprato A: **Extended Data Workbook 6. APP Network File: APP protein-protein interaction network.** *figshare.* Dataset. 2020.  
<http://www.doi.org/10.6084/m9.figshare.13106777.v1>

# Open Peer Review

Current Peer Review Status:    

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Version 1

Reviewer Report 09 March 2021

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? **Joseph H. Lee** 

Gertrude.H. Sergievsky Center and Taub Institute for Research on Alzheimer's Disease and the Aging Brain, College of Physicians and Surgeons, Columbia University, New York City, NY, USA

**Nicole Schupf**

Columbia University Medical Center, New York, NY, USA

This paper by Delprato, Sharma, and colleagues examined genetic and transcriptomic factors that may explain Alzheimer's disease in Down syndrome by putting together five genesets: genes on chromosome 21; genes identified from the search term "Alzheimer's Down syndrome" using GeneWeaver; genes identified from a large-scale genome-wide association study (GWAS); genes identified from the differential gene expression study of the dorsal frontal cortex (DFC) and cerebellar cortex (CBC) using the Down Syndrome Developmental Brain Transcriptome database. Subsequently, they performed a series of bioinformatic analyses to generate associated genes and concluded that oxidative stress, apoptosis, and inflammation/immune system processes were important biological processes in AD in DS. This paper is timely as an increasing number of genomic and transcriptomic studies are being carried out to better understand the biology of AD in adults with DS and the non-DS population. However, there are a few points that need to be clarified:

- The title, "[Common genetic signatures of Alzheimer's disease in Down Syndrome](#)," suggests that this paper deals with genes that are likely to be involved in the neurodegenerative disease process in adults with Down syndrome. However, it is stated that the differential gene expression geneset was obtained from the Down Syndrome Developmental Brain Transcriptome Database, which included 15 sets of DS brains and matched control brains, where some of the brain specimens in the database were in embryonic stages. It is unclear how well these DS brain samples from embryonic stages would represent the neurodegenerative processes associated with AD in DS. It would be informative to repeat the analysis after excluding tissues that were from embryonic stages, if the sample size is sufficient.
- In the Introduction (page 3, lines 4-8), it is stated that "Amyloids form fibrous structures and plaques ... are involved in several diseases, such as Alzheimer's disease (AD), [Down Syndrome](#)

(DS), ...." Most would agree that adults with DS have a high risk of developing AD. However, it is unclear whether the formation of excess amyloids is biologically involved in the Down Syndrome itself, not just AD in DS. It should be clarified whether the wide range of DS phenotypes shown in Figure 2 can be attributed to the amyloid form fibrous structure and plaques.

- Comparisons of the genes identified from AD-DS vs. DEX DFC and AD-DS vs. DEX CBC were interesting. It would be equally interesting to present DEX DFC vs. DEX CBC comparisons as they may represent genes involved in cognitive vs. motor processes.

**Is the work clearly and accurately presented and does it cite the current literature?**

Yes

**Is the study design appropriate and is the work technically sound?**

Yes

**Are sufficient details of methods and analysis provided to allow replication by others?**

Yes

**If applicable, is the statistical analysis and its interpretation appropriate?**

Yes

**Are all the source data underlying the results available to ensure full reproducibility?**

Yes

**Are the conclusions drawn adequately supported by the results?**

Partly

**Competing Interests:** No competing interests were disclosed.

**Reviewer Expertise:** Human genetics, Genetic epidemiology, Alzheimer's disease, Down syndrome, Autosomal dominant forms of Alzheimer's disease.

**We confirm that we have read this submission and believe that we have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however we have significant reservations, as outlined above.**

Reviewer Report 15 February 2021

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**Ann-Charlotte Granholm**

1

Knoebel Institute for Healthy Aging and the Department of Biology, University of Denver, Denver, CO, USA

<sup>2</sup> Karolinska Institutet, Stockholm, Sweden

This is an excellent genetic study of comparisons between AD and DS-related AD by Delprato and collaborators. Overall, this is an interesting and timely publication. The GeneSet overlay in Figure 1 is an excellent demonstration of the findings. There are only a few comments to be made and these are listed below.

1. In the abstract, last sentence, the authors state that “Our findings indicate that oxidative stress, apoptosis, and inflammation/immune system processes likely underlie the pathogenesis of AD and DS”. However, these contributors to AD in DS have already been known for quite some time, albeit maybe not at the genetic level. It would be better to reformulate this sentence to something like this: “Our findings confirm that oxidative stress, apoptosis, and inflammation/immune system processes likely contribute to AD in DS – these processes have been investigated in animal models and post mortem human tissues previously but not at the human genetic level”. Or something like that.
2. Introduction, first sentence: “stick together” should be replaced with “aggregate”.
3. First paragraph of Introduction: “a protein that typically resides around nerve cells” should be replaced with “an integral membrane protein that is concentrated in synapses of neurons”.  
Introduction first paragraph: “Smaller aggregates of beta-amyloid and not the plaques themselves...” This could be more specific. For example “Oligomeric forms of the beta-amyloid, and not the beta-pleated sheets in plaques” or something like that.
4. Second paragraph of Introduction: “About half of the people with DS develop AD and the associated dementia around 50 to 60 years of age”. It is actually thought by most people now that 90% or more of those with DS developed AD – this should be referenced and corrected.
5. Throughout the text, “AD individuals” or “DS individuals” should be replaced with “people or individuals with AD or DS” – those who have either condition do not wish to be defined by their disease. This is very important.
6. Generally, people refer to DS-related AD as DS-AD and not AD-DS, since the DS condition came first.
7. Last sentence of Conclusions: it would not hurt to follow this statement with some literature citations that, indeed, confirm that these same processes have been proposed by others using both post mortem human tissue and animal models for DS. This would place these findings in the light of previous literature and acknowledge that these processes have been proposed by others and are here confirmed by gene expression studies.

**Is the work clearly and accurately presented and does it cite the current literature?**

Partly

**Is the study design appropriate and is the work technically sound?**

Yes

**Are sufficient details of methods and analysis provided to allow replication by others?**

Yes

**If applicable, is the statistical analysis and its interpretation appropriate?**

Yes

**Are all the source data underlying the results available to ensure full reproducibility?**

Yes

**Are the conclusions drawn adequately supported by the results?**

Yes

**Competing Interests:** No competing interests were disclosed.

**Reviewer Expertise:** Down syndrome and Alzheimer's disease.

**I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.**

Author Response 19 Oct 2021

**Anna Delprato**, PO Box 352, Wakefield, USA

Reviewer 3:

This is an excellent genetic study of comparisons between AD and DS-related AD by Delprato and collaborators. Overall, this is an interesting and timely publication. The GeneSet overlay in Figure 1 is an excellent demonstration of the findings. There are only a few comments to be made and these are listed below.

- In the abstract, last sentence, the authors state that "Our findings indicate that oxidative stress, apoptosis, and inflammation/immune system processes likely underlie the pathogenesis of AD and DS". However, these contributors to AD in DS have already been known for quite some time, albeit maybe not at the genetic level. It would be better to reformulate this sentence to something like this: "Our findings confirm that oxidative stress, apoptosis, and inflammation/immune system processes likely contribute to AD in DS – these processes have been investigated in animal models and post mortem human tissues previously but not at the human genetic level". Or something like that.

Response:

Done.

- Introduction, first sentence: "stick together" should be replaced with "aggregate".

Response:

Done.

- First paragraph of Introduction: “a protein that typically resides around nerve cells” should be replaced with “an integral membrane protein that is concentrated in synapses of neurons”.

Response:

Done.

Introduction first paragraph: “Smaller aggregates of beta-amyloid and not the plaques themselves...” This could be more specific. For example “Oligomeric forms of the beta-amyloid, and not the beta-pleated sheets in plaques” or something like that.

Response:

Done.

- Second paragraph of Introduction: “About half of the people with DS develop AD and the associated dementia around 50 to 60 years of age”. It is actually thought by most people now that 90% or more of those with DS developed AD –this should be referenced and corrected.

Response:

We have added this information to the introduction.

- Throughout the text, “AD individuals” or “DS individuals” should be replaced with “people or individuals with AD or DS” – those who have either condition do not wish to be defined by their disease. This is very important.

Response:

Thank you for the correction. We have edited the text accordingly.

- Generally, people refer to DS-related AD as DS-AD and not AD-DS, since the DS condition came first.

Response:

To the best of our knowledge each instance of the “AD-DS” designation refers to the datasets and figures generated in the study and not the condition of AD in people with DS.

- Last sentence of Conclusions: it would not hurt to follow this statement with some literature citations that, indeed, confirm that these same processes have been proposed by others using both post mortem human tissue and animal models for DS. This would place these findings in the light of previous literature and acknowledge that these processes have been proposed by others and are here confirmed by gene expression studies.

Response:

The Conclusion section has been modified and references have been added.

**Competing Interests:** No competing interests were disclosed.

Reviewer Report 08 February 2021

<https://doi.org/10.5256/f1000research.29930.r76772>

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### William C. Mobley

Department of Neurosciences, University of California San Diego School of Medicine, La Jolla, CA, USA

Sharma and colleagues have examined data for genetic contributions to the emergence of Alzheimer's disease (AD) in those with Down syndrome (DS). Their methods include the creation and/or mining of various genesets, including one for AD and DS derived from a MeSH query, as well as genesets representing Chromosome 21, AD risk factors from GWAS data, and differentially expressed genes in the DS cortex and cerebellum. Overlaps between genesets were examined to identify genes of interest, including tissues and biological processes, functional analyses, behavior and transcription as well as an APP protein-protein interaction network. Overall, the findings confirm some expected associations and point to possible novel associations that may prove useful to those exploring the biology of AD in DS (AD-DS).

Having stated the positives, additional comments may prove useful to enhance the appreciation of the work. First, it should be clarified that *APP* is expressed in neurons wherein it is processed to A $\beta$  peptides, some of which are found in plaques. It is not true that A $\beta$  peptides are due to misprocessing of APP but instead that one of its products the A $\beta$ 42 peptide is preferentially deposited in plaques. An increase in the relative levels of A $\beta$ 42 to shorter A $\beta$  species is cited as playing a role in pathogenesis, as well it might, but A $\beta$ 42 is nevertheless a normal product of APP. Note, however, also, that A $\beta$ 42 and other A $\beta$  species are present in toxic oligomeric complexes that are now viewed as more significant for pathogenesis than are the amyloid plaques. A second comment concerns the section examining transcriptional profiles wherein a listing of differentially regulated genes is given. While the corresponding RNA levels corresponding to these genes differ in AD-DS versus controls only some of the genes listed encode transcription factors. I suspect the authors meant to convey that the products of these genes may impact transcription.

In the end, this paper will be important to the extent that it drives the testing of specific hypotheses. The large amount of data that comes from such analyses may not readily suggest follow-on studies. Given the extensive work invested here, the authors might choose to highlight a small subset of findings and predict relationships that, if further supported, would more incisively speak to the biology of AD in DS.

**Is the work clearly and accurately presented and does it cite the current literature?**

Yes

**Is the study design appropriate and is the work technically sound?**

Yes



**Are sufficient details of methods and analysis provided to allow replication by others?**

Yes

**If applicable, is the statistical analysis and its interpretation appropriate?**

I cannot comment. A qualified statistician is required.

**Are all the source data underlying the results available to ensure full reproducibility?**

Yes

**Are the conclusions drawn adequately supported by the results?**

Yes

**Competing Interests:** No competing interests were disclosed.

**Reviewer Expertise:** Studies on the pathogenesis of AD in DS.

**I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.**

Author Response 19 Oct 2021

**Anna Delprato**, PO Box 352, Wakefield, USA

Reviewer 2:

Sharma and colleagues have examined data for genetic contributions to the emergence of Alzheimer's disease (AD) in those with Down syndrome (DS). Their methods include the creation and/or mining of various genesets, including one for AD and DS derived from a MeSH query, as well as genesets representing Chromosome 21, AD risk factors from GWAS data, and differentially expressed genes in the DS cortex and cerebellum. Overlaps between genesets were examined to identify genes of interest, including tissues and biological processes, functional analyses, behavior and transcription as well as an APP protein-protein interaction network. Overall, the findings confirm some expected associations and point to possible novel associations that may prove useful to those exploring the biology of AD in DS (AD-DS).

Having stated the positives, additional comments may prove useful to enhance the appreciation of the work.

First, it should be clarified that APP is expressed in neurons wherein it is processed to A $\beta$  peptides, some of which are found in plaques. It is not true that A $\beta$  peptides are due to misprocessing of APP but instead that one of its products the A $\beta$ 42 peptide is preferentially deposited in plaques. An increase in the relative levels of A $\beta$ 42 to shorter A $\beta$  species is cited as playing a role in pathogenesis, as well it might, but A $\beta$ 42 is nevertheless a normal product of APP. Note, however, also, that A $\beta$ 42 and other A $\beta$  species are present in toxic oligomeric complexes that are now viewed as more significant for pathogenesis than are the amyloid plaques.

Response:

We thank the reviewer for the clarification concerning the processing of A $\beta$  peptides. We

have included this information in the introduction of the revised manuscript.

A second comment concerns the section examining transcriptional profiles wherein a listing of differentially regulated genes is given. While the corresponding RNA levels corresponding to these genes differ in AD-DS versus controls, only some of the genes listed encode transcription factors. I suspect the authors meant to convey that the products of these genes may impact transcription.

Response:

We have clarified this point in the revised manuscript.

In the end, this paper will be important to the extent that it drives the testing of specific hypotheses. The large amount of data that comes from such analyses may not readily suggest follow-on studies. Given the extensive work invested here, the authors might choose to highlight a small subset of findings and predict relationships that, if further supported, would more incisively speak to the biology of AD in DS.

Response:

There is a subset of findings highlighted in the Results section of the abstract. We have added more context to emphasize the significance of these findings.

**Competing Interests:** No competing interests were disclosed.

Reviewer Report 24 November 2020

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**Daniel W. Nixon**

<sup>1</sup> Cancer Treatment Centers of America, Southeastern Regional Medical Center, Newnan, GA, USA

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This is a well-written paper that adds useful information to the literature. The connection between Down syndrome and Alzheimer's disease is clinically well established and is currently not preventable, leading to increased difficulty in Down syndrome management. Genetic examination as in this paper should stimulate further molecular research in Down syndrome including the genetic influences on obesity, common in Down syndrome and a risk factor in Alzheimer's disease. I suggest further research by this group in adipokines such as leptin and adiponectin as well as interactions between Wnt, BACE, Notch, BCL and DYRK. This could lead to better understanding of the relationships between Down syndrome, Alzheimer's disease, leukemia and solid tumors. Down syndrome is associated with an increased risk of leukemia and a decreased risk for solid tumors while Alzheimer's disease is associated with a decreased risk for various solid tumors.

**Is the work clearly and accurately presented and does it cite the current literature?**

Yes

**Is the study design appropriate and is the work technically sound?**

Yes

**Are sufficient details of methods and analysis provided to allow replication by others?**

Yes

**If applicable, is the statistical analysis and its interpretation appropriate?**

Yes

**Are all the source data underlying the results available to ensure full reproducibility?**

Yes

**Are the conclusions drawn adequately supported by the results?**

Yes

**Competing Interests:** No competing interests were disclosed.

**I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.**

Author Response 19 Oct 2021

**Anna Delprato**, PO Box 352, Wakefield, USA

Reviewer 1:

This is a well-written paper that adds useful information to the literature. The connection between Down syndrome and Alzheimer's disease is clinically well established and is currently not preventable, leading to increased difficulty in Down syndrome management. Genetic examination as in this paper should stimulate further molecular research in Down syndrome including the genetic influences on obesity, common in Down syndrome and a risk factor in Alzheimer's disease. I suggest further research by this group in adipokines such as leptin and adiponectin as well as interactions between Wnt, BACE, Notch, BCL and DYRK. This could lead to better understanding of the relationships between Down syndrome, Alzheimer's disease, leukemia and solid tumors. Down syndrome is associated with an increased risk of leukemia and a decreased risk for solid tumors while Alzheimer's disease is associated with a decreased risk for various solid tumors.

Response:

Thank you for the encouraging review and the information pertaining to cancer and solid tumor formation in the context of AD and DS. We will keep this in mind for future studies.

**Competing Interests:** No competing interests were disclosed.

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