Genetic, transcriptome, proteomic and epidemiological evidence for blood brain barrier disruption

and polymicrobial brain invasion as determinant factors in Alzheimer's disease.

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Key words: virus, bacteria, fungi, microbes, Alzheimer's disease, immune system, inflammation,

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Running title: Alzheimer's disease relationship with multiple pathogens

Abstract

Multiple pathogens have been detected in Alzheimer's disease (AD) brains. A bioinformatics

approach was used to assess relationships between pathogens and AD genes (GWAS), the AD

hippocampal transcriptome and plaque or tangle proteins. Host/pathogen interactomes (C. albicans,

C. Neoformans, Bornavirus, B. Burgdorferri, cytomegalovirus, Ebola virus, HSV-1, HERV-W, HIV-1,

Epstein-Barr, hepatitis C, influenza, C. Pneumoniae, P. Gingivalis, H. Pylori, T. Gondii, T. Cruzi)

significantly overlap with misregulated AD hippocampal genes, with plaque and tangle proteins and,

except Bornavirus, Ebola and HERV-W, with AD genes. Upregulated AD hippocampal genes match

those upregulated by multiple bacteria, viruses, fungi or protozoa in immunocompetent blood cells.

AD genes are enriched in bone marrow and immune locations and in GWAS datasets reflecting

pathogen diversity, suggesting selection for pathogen resistance. The age of AD patients implies

resistance to infections afflicting the younger. APOE4 protects against malaria and hepatitis C, and

immune/inflammatory gain of function applies to APOE4, CR1, TREM2 and presentlin variants. 30/78

AD genes are expressed in the blood brain barrier (BBB), which is disrupted by AD risk factors

(ageing, alcohol, aluminium, concussion, cerebral hypoperfusion, diabetes, homocysteine,

hypercholesterolaemia, hypertension, obesity, pesticides, pollution, physical inactivity, sleep

disruption and smoking). The BBB and AD benefit from statins, NSAIDs, oestrogen, melatonin and the

[1]

Mediterranean diet. Polymicrobial involvement is supported by the upregulation of pathogen

sensors/defenders (bacterial, fungal, viral) in the AD brain, blood or CSF. Cerebral pathogen invasion permitted by BBB inadequacy, activating a hyper-efficient immune/inflammatory system, beta-amyloid and other antimicrobial defence may be responsible for AD which may respond to antibiotic, antifungal or antiviral therapy.

Introduction

Multiple pathogens have been implicated in Alzheimer's disease (AD) either via detection in the AD brain, or in epidemiological studies relating to serum antibodies. Pathological burden (cytomegalovirus, Herpes simplex (HSV-1), Borrelia burgdorferi, Chlamydia pneumoniae and Helicobacter pylori) rather than any individual pathogen may also be associated with AD [1]. Many pathogens are able to increase beta-amyloid deposition and tau phosphorylation in animal models, in vitro or in vivo and beta-amyloid itself is an antimicrobial peptide active against bacteria and fungi [2,3] and the influenza[4] and herpes simplex viruses [5,6]. These effects are summarised in Table 1 for a number of pathogens and for beta-amyloid.

Previous studies have shown that the life cycles of several pathogens implicated in AD relate to AD susceptibility genes [7]. The proteins found in AD plaques and tangles are also enriched in those used by HSV-1 during its life cycle [8] and the HSV-1 or *Toxoplasma Gondii* host interactomes are also enriched in AD susceptibility genes [9,10]

Similar studies have noted significant overlaps between the Epstein-Barr viral/host interactome and diseases in which the virus is implicated, including B cell lymphoma [11]or multiple sclerosis [12]. The interactomes of oncogenic viruses also relate to cancer genes [13] suggesting important gene/environment interactions that may condition disease susceptibility.

In this study, the host pathogen interactomes of 17 fungal, bacterial, viral and parasite pathogens were analysed in relation to 78 AD genes derived from genome-wide association studies (GWAS).

The anatomical location of these genes was also queried against proteomic /genomic datasets from multiple tissues.

The host genes of the pathogen interactomes were also compared with the combined up and down-regulated genes from a study of the AD hippocampus, post-mortem [14] and to the proteins found in plaques or neurofibrillary tangles. The upregulated genes from this AD hippocampal study were also

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compared with upregulated genes from numerous infection microarray datasets (viral, bacterial, fungal and protozoan) housed at the Molecular signatures database [15] or the Gene Expression Omnibus [16].

Pathogens have shaped human evolution, as the survivors of dangerous infections are endowed, via natural selection, with genes conveying resistance. The AD genes were also compared against a series of genome-wide association datasets related to general pathogen or protozoan diversity, viral diversity and the immune response to parasitic worms, across multiple human populations in different geographical locations. Such genes are likely to have been selected for pathogen resistance. [17-20].

The results show that host genes related to pathogens are enriched in all these AD parameters and that many AD susceptibility genes also relate to pathogens, but more likely to pathogen resistance than susceptibility. The anatomical data point to an immune function of many AD genes, while others are localised in the blood-brain barrier, which is disrupted by other environmental risk factors associated with AD.

Methods

The host/pathogen interactomes of two fungal species (*Candida albicans, Cryptococcus*Neoformans), the Borna virus, human cytomegalovirus, Ebola virus, Herpes simplex (HSV-1), human endogenous retroviruses HERV-W, the human immunodeficiency virus (HIV-1) (the latter from the HIV-1, human interaction database [21]

http://www.ncbi.nlm.nih.gov/genome/viruses/retroviruses/hiv-1/interactions, Epstein-Barr, hepatitis C and influenza A viruses, 3 bacterial species (*Chlamydia Pneumoniae, Porphyromonas Gingivalis, Helicobacter Pylori*) and 2 protozoans (*Toxoplasma Gondii* and *Trypanosoma Cruzi*) were obtained by literature survey and from extant databases. These referenced interactomes can be accessed at http://www.polygenicpathways.co.uk/HPI.htm.

Genes misregulated in the AD hippocampus are those reported from a post-mortem microarray study [14]. Up- and downregulated genes (N=2879) were combined for comparison with the pathogen interactomes. These interactomes contain multiple types of interaction (protein/protein, viral microRNA, and effects on transcription etc.) and it is not possible to compare like with like for this aspect.

The upregulated genes (N= 1690) from this AD hippocampal study contain the pathways relevant to pathogens and immune activation (inflammation, complement activation and the defence response) [14] and these were chosen for comparison with upregulated genes from infection datasets at the Molecular signatures database (MSigDB) http://software.broadinstitute.org/gsea/msigdb/index.jsp. MSigDB contains several thousand microarray gene sets which can be compared against the AD input [15]. Infection related datasets, and those related to Toll-like receptor ligands, were identified using search terms (e.g. infection, virus, bacteria, TLR1, lipopolysaccharide, etc.). Microarray viral infection datasets (upregulated gene sets) from the gene expression omnibus (GEO) [22] were also downloaded from the Harmonizome database http://amp.pharm.mssm.edu/Harmonizome/ from the Ma'ayan laboratory of computational systems. [23]. For the searched gene sets, most of the data outputs were restricted at source (by MSigDb or GEO) to the top upregulated genes (usually ~ 200-300).

The proteins found in plaques or neurofibrillary tangles are from two proteomics studies yielding 488 proteins in plaques [24] and 90 in tangles [25].

Seventy eight genes associated with Alzheimer's disease (Reported genes) were obtained from the NHGRI-EBI Catalog of published genome-wide association studies (GWAS) [26], Available at: www.ebi.ac.uk/gwas. Accessed January, 2016, version 1.0 using studies labelled as "Alzheimer's disease" or "Alzheimer's disease late-onset". These genes and their relationships with pathogens or the immune system are catalogued in Supplementary Table 1. These genes are highlighted in **bold** throughout the text.

Genes related to general pathogen diversity, protozoan and viral diversity and to the immune response to parasitic worms are from a series of papers concerning evolutionary selection pressure relevant to pathogen resistance [17-20].

The tissue and cellular distribution of the 78 AD genes were analysed using the functional enrichment analysis tool (FUNRICH) [27]. http://funrich.org/index.html. This tool derives proteomic and genomic distribution data from >1.5 million annotations. It provides the total number of genes in datasets from each region sampled and returns the significance of any enrichment for members of the uploaded AD genes, using the hypergeometric probability test, with p values corrected using the the Storey and Tibshirani method (Q values) [27]. AD gene enrichment was also analysed in a published blood brain barrier proteome dataset of mouse cerebral arteries (6620 proteins) [28].

The presence of the AD genes in exosomes, a means of transit through cells allowing intercellular communication[29,30], was assessed using ExoCarta (http://www.exocarta.org) a manually curated database of exosomal proteins, RNA and lipids [31]. The exosomal pathway is hijacked by several viruses, contributing to intercellular spread and immune evasion [32,33].

Assuming a human genome of 26846 coding genes and an interactome or other gene set of N genes one would expect N/26846 to exist in the comparator dataset. For example, when comparing 2879 misregulated AD hippocampal genes against any pathogen interactome one would expect 2879/26846 (10.7%) to figure in the pathogen interactome. This calculation was used to define expected values and the enrichment values (observed/expected) in relation to other datasets. Significance of the enrichment was calculated using the hypergeometric probability test. The resultant p values from each analysis series were corrected for false discovery (FDR) [34]. Nominally significant FDR corrected values are considered at P <0.05 and a corrected Bonferroni p value threshold is illustrated on each set of graphs. (Bonferroni P = 0.05/N, where N is the maximum number of possible comparisons for each situation (e.g. 78 AD genes or 1690 upregulated genes in the AD hippocampus).

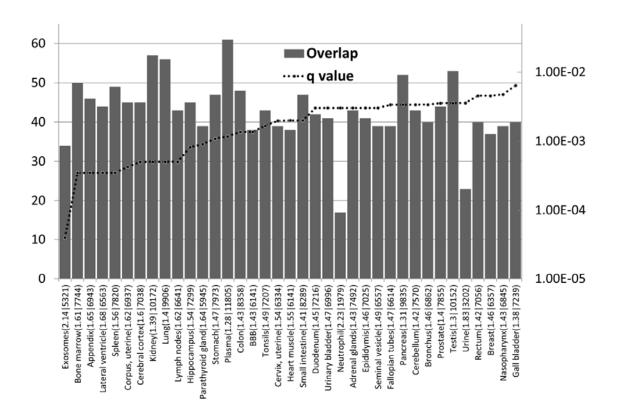
Results

The anatomical location of the AD genes (Fig 1)

Fig 1: The distribution and enrichment of 78 AD genes in diverse proteomic and genomic datasets (Funrich and Exocarta data). The bars indicate the number of genes (from 78) in each tissue and the dotted line the corrected p value (q value). The maximum on this axis is set to q = 0.05.

Observed/expected values, followed by the total number of genes expressed are appended after the identities of each sample. BBB refers to a separate blood brain barrier proteomics dataset. Cancer or cell line datasets are omitted and the data are limited to anatomical datasets containg more than 10 AD genes (Not all data are shown).

Figure 1



The AD genes are most significantly enriched in the exosome and bone marrow datasets. As noted above, exosomes are hijacked by many viruses for intercellular spread. Exosomes are prevalent in plasma [35](also enriched in AD genes) and are also the means by which intracellulary generated beta-amyloid is conveyed to the extracellular space [36]. In this context, and in relation to the antimicrobial effects of beta-amyloid, APP and gamma-secretase are highly expressed in the immune dendritic cells that scout for invading pathogens [7]. The bone marrow is the hematopoietic source of red and white blood cells and platelets [37]. B cells in the bone marrow rapidly respond to infection [38] and the bone marrow is also a source of angiogenic cells that are involved in vascular endothelial repair, a process that is disrupted in Alzheimer's disease [39,40]. The parathyroid gland expresses many AD genes and also plays a role in hematopoesis [41,42]. Other immune related areas enriched in AD genes include the appendix, spleen, tonsils, the lymph nodes and the bronchus and neutrophils. The appendix is an important component of mucosal immune function, particularly B cell-mediated immune responses and extrathymically derived T-lymphocytes [43]. The tonsils and nasopharynx, also enriched in AD genes, play an important role in the initial defence against respiratory pathogens [44].

AD genes are enriched in the lateral ventricle, a site of the choroid plexus [45]. This provides cerebrospinal fluid (CSF) and is the location of the blood-CSF barrier, which is exploited by pathogens to gain access to the brain. The choroid plexus plays an important role in pathogen defence [46]. Post-mortem gene expression studies of the choroid plexus epithelium in AD patients show changes indicative of increased permeability of the blood-cerebrospinal fluid barrierand a reduction of macrophage recruitment [47], factors that woud favour pathogen entry and reduce their phagocytosis by macrophages. The hippocampus bulges into the temporal horn of the lateral ventricle [48] and this area, a keystone of AD pathology, is thus in close proximity to a major site of

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cerebral pathogen entry. AD genes are also enriched in a separate BBB dataset from mouse cerebral arteries. This is discussed in greater detail below. Other barriers in intestinal and pulmonary tissues, also enriched in AD genes (Fig 1), might also be considered as potential sites of pathogen entry.

Immune systems play an important role at barrier interfaces [49].

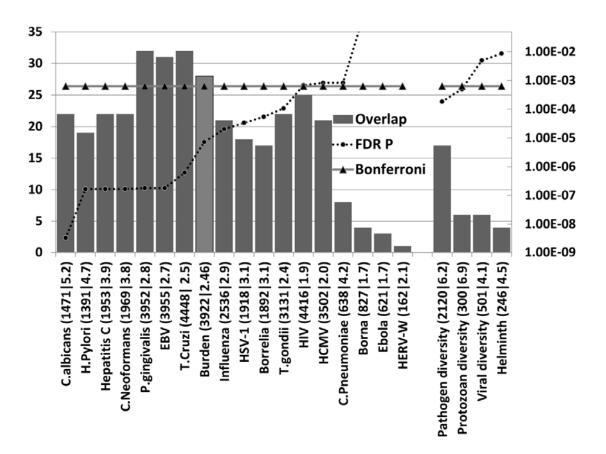
Although AD genes are expressed in other sites, the main focus, in terms of enrichment, relates to immune and barrier systems.

A number of the 78 AD genes (referenced in supplementary Table 1) are primarily concerned with immune function (HLA-DRB1, HLA-DRB5, HMHA1, IGH) while many others with diverse primary effects also possess relevant properties in relation to the immune system (ACE, ADAMTS20, AP2A2, BCL3, BIN1, CR1, CLU, CUGBP2, DISC1, EPHA1, GAB2, INPPSD, MEF2C. MS4A3, MS4A4A, RIN3, SCIMP, SPPL2A, STK24, TREM2, TREML2, ZNF224) or pathogen defence (e.g. phagocytosis or autophagy) (ABCA7, APOC1, APOE, BCAM, CD2AP, CD33, CDON, CELF1, PAX2, PTK2B, SASH1, SQSTM1). A number of the AD genes also act as primary receptors for pathogens. These include the poliovirus receptor PVR, the HSV-1 receptor PVRL2, and complement receptor (CR1), which binds to many opsonised pathogens but which may also act as an entry receptor for *Plasmodium falciparum*, *Legionella pneumophila and Mycobacterium tuberculosis*. CD33 binds to the HIV-1 gp120 protein and to diverse forms of sialic acid which coats many pathogens. Others bind bacterial lipopolysaccharides (APOC1 and TREM2) or the Escherichia coli cytotoxic necrotizing factor 1 (BCAM). Others (AP2A2, BIN1, CD2AP, and PICALM) are involved in endocytosis, an obligate requirement for pathogen entry following binding to cognate receptors (see supplementary Table 1 for references).

Host/pathogen interactomes are enriched in AD genes (Fig 2).

Fig 2. The number of AD genes (of 78) overlapping with diverse host/pathogen interactomes, or with those implicated in pathogen, protozoan or viral diversity or with the immune response to parasitic worms (Helminth) (Bars). The identities on the X-axis (e.g. *C. albicans* (1471|5.2) are appended with the total number of genes in each interactome (1471 in this case) or genetics dataset followed by the enrichment ratio (5.2 fold). The FDR-corrected p value for enrichment, derived from the hypergeometric distribution, is shown on the right hand axis (log scale) which is set to a maximum of 0.05. Invisible points are above this value. The Bonferroni cut-off level (p=0.05/78) is also shown. The Burden data (lighter shaded bar) correspond to the combined interactomes and AD gene overlaps of the human cytomegalovirus (HCMV), HSV-1, *Borrelia burgdorferi*, *Chlamydia pneumoniae* and *Helicobacter pylori*. EBV= Epstein-Barr virus.

Figure 2



All host/pathogen interactomes, with the exception of those of the Borna virus, Ebola virus and the HERV-W retrovirus were significantly enriched in AD genes (FDR p <0.05) with all but HIV-1, the cytomegalovirus and *C. pneumoniae* below the Bonferroni corrected value (P=6.41E-4). Pathogen burden (cytomegalovirus, HSV-1, *B. burgdorferi*, *C. Pneumoniae* and *H. Pylori*) has been associated with Alzheimer's disease [1] and the pooled interactomes of these five pathogens (3922 host genes) were significantly enriched in AD genes (p= 7.3E-6). Given the variety of pathogens reported in AD brains (Table 1) other cumulative effects might be expected for various permutations.

The most significant pathogens related to fungi (*C. albicans* and *C. Neoformans*), the gum disease pathogen *P. Gingivalis* and the Epstein-Barr and hepatitis C viruses. Numerous fungal species, including *C.albicans*, have been detected in the AD brain (Table 1), although *C. Neoformans* was not one of the species studied. Two case reports have demonstrated virtually complete recovery from long-term (3 years) mis-diagnosed dementia/Alzheimer's disease following antifungal treatment for *C. Neoformans* infection [50,51].

The Epstein-Barr virus has been associated with AD and hepatitis C associated with dementia (table 1). *In vivo* studies for the Epstein-Barr and Hepatitis C viruses are however limited by their inability to infect rats or mice. Several of these pathogens including *C. pneumoniae*, HSV-1, cytomegalovirus and the Epstein-Barr and hepatitis C viruses or *H. pylori* and *B. Burgdorferri* [52-59], periodontitis and P.Gingivalis [57]have also been associated wiith atherosclerosis, an important endophenotype in AD [60].

Apart from **APOE4** no AD genetic variants seem to have been studied in relation to effects on pathogens and it is impossible to note whether the variants favour or oppose their destructive potential. The apolipoprotein E (**APOE4**) variant protects against hepatitis C [61], but favours the cerebral entry of HSV-1 [62] and enhances the attachment of *C. pneumoniae* elementary bodies to host cells [63].

AD genes overlap with those implicated in pathogen, protozoan or viral diversity or with the immune response to parasitic worms (Fig 2).

The AD genes are enriched in a series of genome-wide and global-wide datasets related to general pathogen diversity, protozoan or viral diversity (the number of different pathogens in a geographic region) or with the immune response to parasitic worms, most significantly so for general pathogen and protozoan diversity (FDR p < 0.05). The overlaps in relation to viral diversity or the response to parasitic worms exceeded the Bonferroni cut-off.

In evolutionary terms, these pathogen-related genes likely reflect pathogen resistance rather than susceptibility [17-20].

It has also been noted that genes related to inflammatory diseases [64] or to the AD gene network [65] are subject to positive selection pressure. While many pathogens have been implicated in AD, the selection of AD genes for pathogen resistance rather than susceptibility seems logical in relation to several considerations, as already proposed [66,67]. Firstly, the old age of AD patients indicates survival from the many infectious diseases that are among the principal causes of death in adults and children. In the USA, the leading non-accidental causes of death in adults (2013 figures) include heart disease; cancers; chronic lower respiratory diseases; cerebrovascular diseases; Diabetes mellitus; Influenza and pneumonia; nephritis, nephrotic syndrome and nephrosis [68].

Certain viruses, helminths and bacteria are oncogenic and it has been estimated that 15-20% of cancers are due to infections [69]. The inverse association between the incidence of cancer and Alzheimer's disease [70] suggests that AD genes might well be cancer protective (but also that death due to cancer precludes AD). Inflammatory heart diseases [71] and atherosclerosis, cerebrovascular disorders and stroke have also been linked to infection [72,73]. Enteroviruses have been implicated in Type 1 diabetes mellitus [74].

The leading non-accidental causes of infant deaths were congenital malformations, deformations and chromosomal abnormalities; disorders related to short gestation and low birth weight, not elsewhere classified; newborn affected by maternal complications of pregnancy; sudden infant death syndrome; newborn affected by complications of placenta, cord and membranes; bacterial sepsis of newborn; respiratory distress of newborn; diseases of the circulatory system; and neonatal haemorrhage. Again, many of these relate to infections. In evolutionary terms, pandemics and infectious diseases have been, and in poorer countries still are, associated with high mortality.

In relation to Alzheimer's disease, the apolipoprotein E (APOE4) variant protects against malaria [75] and hepatitis C [61], although APOE4 favours cerebral entry of the herpes simplex virus [62] and enhances the attachment of Chlamydia pneumoniae elementary bodies to host cells [63]. Malaria and hepatitis C are both associated with high mortality [76,77] and the protective effects of APOE4 would encourage its maintenance in the population, to the detriment of infection by the less virulent agents.

The APOE4 variant is also associated with enhanced immune/inflammatory responses. For example, Toll-like receptor activation (TLR3, 4) in microglia induces cyclooxygenase-2 (PTGS2), microsomal prostaglandin E synthase (PTGES), and prostaglandin E2, an effect exaggerated in APOE4/APOE4 mice [78]. APOE4 is also associated with enhanced *in vivo* innate immune responses in human subjects. Whole blood from healthy APOE3/APOE4 volunteers induced higher cytokine levels on ex vivo stimulation with Toll-like receptor (TLR2, 4 or 5) ligands than blood from APOE3/APOE3 patients [79]. Gain of function also applies to AD variant forms of complement receptor CR1, which are better able to bind complement component C1q or C3B [80]. C1q and C3B are opsonins that interact with complement cell-surface receptors (C1qRp, CR1, CR3 and CR4) to promote phagocytosis (including that of infectious agents) and a local pro-inflammatory response [81]. TREM2 variants in AD are also associated with enhanced inflammatory responses (upregulation of proinflammatory cytokines) [82]. In presenilin (PSEN1) mutant knockin mice, microglial challenge with bacterial lipopolysaccharide

results in enhanced nitric oxide and inflammatory cytokine responses, relative to normal mice [83]. For these genes at least, this gain of immune/inflammatory function concords with selection for pathogen resistance.

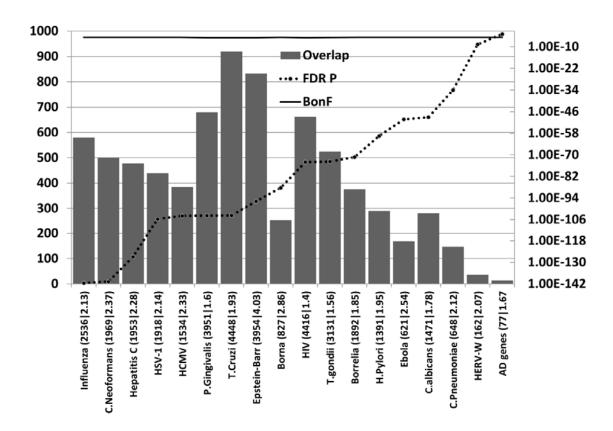
It has also been noted that unaffected offspring with a parental history of AD have an enhanced inflammatory response in lipopolysaccharide -stimulated whole blood samples, producing higher levels of interleukin 1beta, tumor necrosis factor alpha and interferon gamma in response to LPS. This effect was independent of the APOE4 variant [84] suggesting that other AD genes are also endowed with gain of function in relation to the immune/inflammatory system. Monocyte-derived dendritic cells from Alzheimer's disease patients also produce more interleukin 6 than those from healthy controls. AD monocytes stimulated with LPS also show a higher induced expression of the pro-inflammatory ICAM-1 adhesion molecule than controls [85]. Beta-amyloid also stimulates cytokine production in peripheral blood mononuclear cells (PBMC) and the production of the chemokines, RANTES, MIP-1beta, and eotaxin as well as that of CSF2 (colony stimulating factor 2 (granulocyte-macrophage)) and CSF3 (colony stimulating factor 3) is greater than controls in AD-derived PBMC stimulated with beta-amyloid [86].

Given the antimicrobial properties of beta-amyloid, any genetic variant that increase its production, at least in the periphery, might also be considered as desirable, in evolutionary terms, in relation to pathogen defence. A high percentage of AD GWAS genes are involved in APP processing [87]. The AD genetic variant of ABCA7 results in increased secretion of beta amyloid and raised beta-secretase activity in CHO- and HEK cells with the Swedish APP mutation [88], but the effects of late-onset AD variant genes on the beta-amyloid response to pathogens remain to be determined.

Host/pathogen interactome enrichment in misregulated genes of the Alzheimer's disease hippocampal transcriptome (Fig 3).

Fig 3. The number of genes misregulated (combined up and down) in a microarray study of the AD hippocampus overlapping with diverse host/pathogen interactomes. The identities on the X-axis (e.g.

C. albicans (1471|5.2) are appended with the total number of genes in each interactome (1471 in this case) or genetics dataset followed by the enrichment ratio (5.2 fold). The p value for enrichment, derived from the hypergeometric distribution, is shown on the right hand axis (log scale) which is set to a maximum of 0.05. The Bonferroni cut off (1.74E-05) is also shown.



All pathogen interactomes, most notably relating to influenza, *C. Neoformans* and Hepatitis C were highly enriched in genes relating to this microarray dataset (combined up and downregulated genes). The significance level of the interactome enrichment for most pathogens was several orders of magnitude below the Bonferroni cut off (p=1.74E-05) (Fig 3). 14/78 AD genes appear in this microarray dataset (FDR p = 0.001). Two case reports have demonstrated virtually complete recovery

from long-term (3 years) mis-diagnosed dementia/Alzheimer's disease following antifungal treatment for *C. Neoformans* infection [50,51]. Regarding the influenza data, bronchopneumonia, often caused by influenza, is a common final cause of death in dementia patients [89] and such recent infections close to death may well influence the data.

Regardless of the rank order, it is clear that many diverse pathogen interactomes affect several hundred genes of the 2879 misregulated in the AD hippocampus and/or that these misregulated AD genes represent a substantial percentage of the individual pathogens' interactomes (Fig 3).

Kegg pathway analysis of these misregulated hippocampal genes using the consensus path database [90] showed that many infection-related pathways were also significantly enriched (FDR p < 0.05). These included (pathogen with N genes followed by the FDR corrected p value): Epstein-Barr virus infection (74,5.5E-7); Salmonella infection (36,0.0001); Tuberculosis (57,0.0009); Epithelial cell signaling in Helicobacter pylori infection (28,0.00097); Shigellosis (27,0.001); Influenza A (54,0.003); Herpes simplex infection (56,0.0036); Vibrio cholerae infection (21,0.0089) ;HTLV-I infection (71,0.0096); Toxoplasmosis (37,0.013); Hepatitis B (43,0.018); Pathogenic Escherichia coli infection (20,0.02); Bacterial invasion of epithelial cells (26,0.02); Measles (38,0.04).

Upregulated genes in the AD hippocampus are enriched in genes upregulated by multiple viral, bacterial and fungal pathogens or Toll-like receptor ligands.

Numerous infection-related microarray datasets exist in the Molecular signatures database or in the Gene expression omnibus (see methods), using blood cells taken from infected patients, or cells or tissues infected under laboratory conditions.

Figure 4: The number of upregulated genes (bars) from the AD hippocampal transcriptome that overlap with upregulated genes in viral infection datasets from the Molecular signatures database or the Gene expression omnibus (see methods). The effects of the mimic poly(I:C) are also shown, as is the effect of interferon gamma on gene expression in microglial cells. For each datapoint, the name

of the virus is shown, followed by the cell type and the total number of upregulated genes in the viral datasets (limited by MSigDb or GEO). The significance of enrichment (right axis) represents the FDR corrected p value from the hypergeometric test. All values are below the Bonferroni corection (0.05/300 = 1.67E-04). Because the number of downloaded genes is mostly limited to 300, this is the maximum number of possible overlaps. The pale bar represents the microglial response to interferon gamma.

Tissue/cell abbreviations; A549= adenocarcinomic human alveolar basal epithelial cells; ABL = Akata Burkitt's lymphoma cells; B2B/16HBE, BE(2)C or BEAS-2B = human bronchial epithelial cells; BroLav = human bronchial lavage; Calu-3 = Cultured Human Airway Epithelial Cells; DC = dendritic cells; GRE = glioma cell line; HAE = human airway epithelial cells; HBEC = Human Bronchial Epithelial Cells; HEK = human embryonic kidney cells; HeLa = cervical cancer cell line; HuH-7 = hepatocarcinoma cell line; Macro = macrophage; Mgli = microglia; Mono =monocytes; NES = human nasal epithelial scrapings; NK = natural killer cells; PBMC = peripheral blood mononuclear cells; PLC/PRF/5 cells = human liver hepatoma cells; Trach epi = Tracheal epithelial cells

Viral abbreviations (Reading from the left): HIV= human immunodeficiency virus, Cox B3 =Coxsackie B3 virus; RSV = respiratory syncytial virus; LCMV= Lymphocytic Choriomeningitis Virus; HMPV= Human metapneumovirus; Ebola= Ebola virus; Influenza = Influenza A virus; Sendai = Sendai virus, HCoV = human coronavirus; IFNG = interferon gamma; SARS = severe acute respiratory syndrome coronavirus; HCMV = human cytomegalovirus; MCMV = mouse cytomegalovirus; Dhori = Dhori virus; EBV = Epstein-Barr virus; HepC = hepatitis C virus; KSHV= Kaposi's sarcoma-associated herpesvirus; HSV-1 = herpes simplex; Norwalk = Norwalk virus (Norovirus); Ad5 = adenovirus 5; SIV= Simian immunodeficiency virus; poly (I:C) = Polyinosinic:polycytidylic acid (a viral mimic stimulating Toll-like TLR3 receptors); NDV = Newcastle disease virus; WestEq = Western equine encephalomyelitis virus; LASV = Lassa virus; dsRNA = double stranded RNA; HEV = hepatitis E virus.

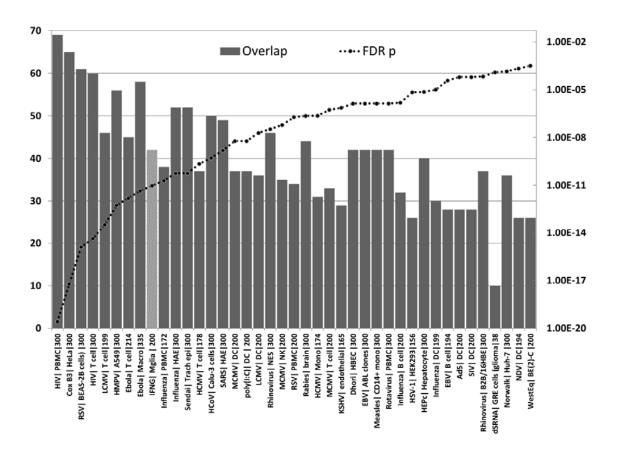


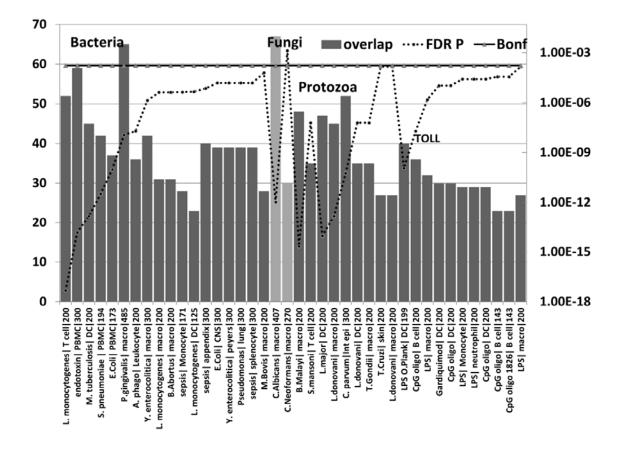
Fig 5

The number of upregulated genes (bars) from the AD hippocampal transcriptome that overlap with upregulated genes in bacterial (first batch), fungal (pale bar = C. albicans, C.Neoformans), nematode (B.Malayi) /trematode (S.Mansoni), or protozoan microarray datasets (see methods). The effects Lipopolysaccharides and other Toll receptor ligands are also shown.

For each datapoint, the name of the pathogen or ligand is shown, followed by the cell type and the total number of upregulated genes in the comparator datasets (limited by MSigDb or GEO). The significance of enrichment (right axis) represents the FDR corrected p value from the hypergeometric test. All values except for *C.Neoformans* are below the Bonferroni correction level.

Pathogen or ligand abbreviations (from left) *L. monocytogenes = Listeria monocytogenes*; endotoxin = gram-negative bacterial wall component; *S. pneumoniae = Streptococcus pneumoniae*; *E. Coli = Escherichia coli*; *P. gingivalis = Porphyromonas gingivalis*; *A. phago = Anaplasma phagocytophilum*; *Y. enterocolitica = Yersinia enterocolitica*; *M. Bovis = mycobacterium bovis*; *C. albicans = Candida albicans*, *C. Neoformans = Cryptococcus neoformans*, *B. Malayi = Brugia mala*yi (filarial parasite causing elephantiasis); *S. mansoni = Schistosoma mansoni*; *L. donovani = Leishmania donovani*; *C. parvum = Cryptosporidium parvum*; *L. Major = Leishmania major*; *T. Gondii = Toxoplasma Gondii*; *T. Cruzi = Trypanosoma Cruzi*; LPS = lipopolysaccharide; LPS O.Plank = Oscillatoria Planktothrix (cyanobacteria lipopolysaccharide) CpG oligo = CpG Oligodeoxynucleotide (TLR9 ligand);

Cell type abbreviations as for Fig 4. CNS = central nervous system; peyers = peyers patch; Int epi = intestinal epithelial cells;



The hippocampal genes upregulated in Alzheimer's disease were significantly enriched in upregulated genes in datasets from multiple viral species and to double stranded RNA and the viral mimic/TLR3 agonist, Polyinosinic:polycytidylic acid (poly I:C) (Fig 4). The viruses ranged from the benign (e.g. the rhinovirus that causes the common cold) to the highly malignant (e.g. the ebolavirus, rabies virus or HIV-1). They include common human infectious agents (e.g. adenovirus 5, influenza, Epstein-Barr virus, herpes simplex virus (HSV-1), measles or the Norwalk virus). Apart from HSV-1, the human cytomegalovirus, HIV-1 or hepatitis C (See Table 1) none of these have been implicated in Alzheimer's disease or dementia. Most microarray experiments related to immunocompetent blood cells (B cells, T cells, dendritic cells, monocytes and macrophages) or to cultured cell lines. No infection-related datasets were found for microglia, the brain resident immunocompetent cells, but significant enrichment of the AD upregulated genes was observed for genes upregulated by interferon gamma in microglial cells (Fig 4). Interferon gamma plays an important role in the response to viral, bacterial and parasitic infections [91].

The upregulated hippocampal genes in AD were also enriched in infection datasets for numerous bacteria as well as to fungal species (*C. albicans* and *C.neoformans*) and in those related to bacterial endotoxin or sepsis and to nematode/trematode or protozoan infection datasets (FDR p < 0.05) (Fig 5). This also applied to diverse lipopolysaccharide datasets and responses to Toll-like receptor ligands, CpG oligonucleotide (a ligand for TLR9, which mediates cellular response to unmethylated CpG dinucleotides in bacterial DNA (definition from Refseq)) and R848 (a ligand for TLR7/TLR8 both of which recognize RNA released from pathogens that enter the cell by endocytosis [92]) (Fig). With the exception of *H.Pylori, P.Gingivalis* and *Borrelia burgdorferi* and *C.albicans* or *C.Neoformans,* none have been implicated in AD.

Together these data suggest a significant parallel between the upregulated genes in the AD hippocampus and the responses to multiple and diverse infectious agents with little overall

discrimination between viral, bacterial, fungal or protozoan types of infection. Multiple pathogens

have been detected in the AD brain (see Table 1) and the diversity of these infection related overlaps

with the AD hippocampal transcriptome suggests that many other pathogens could induce similar

pathological transcriptome changes. Microbiome studies in the AD brain and periphery will help to

elucidate the role of multiple pathogens.

Pathogen interactomes are enriched in the proteins found in AD amyloid plaques and

neurofibrillary tangles (Fig 6).

Fig 6. Host pathogen interactome enrichment in a set of 488 proteins isolated from amyloid plaques

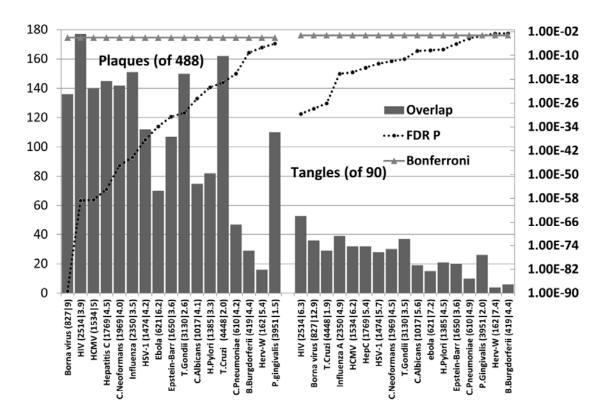
in the AD brain or from 90 proteins isolated from neurofibrillary tangles. The identities on the X-axis

are appended with the total number of genes in each interactome followed by the enrichment ratio.

The FDR p value for enrichment, derived from the hypergeometric distribution, is shown on the right

hand axis (log scale) which is set to a maximum of 0.05.

Figure 6



All pathogen interactomes were significantly enriched in proteins found in plaques and all except HERV-W and *B.Burgdorferi* interactomes significantly enriched in tangle proteins (below the Bonferroni cut-off level). The Borna virus and HIV-1 ranked highly in both cases. There is only one publication relating to Borna virus effects on beta-amyloid and none could be found for tangles. The microglial activation produced by the virus reduced brain parenchymal, but increased cerebral vascular beta-amyloid deposition, in APP transgenic mice [93]. The top agents relating to plaques were predominantly viral, while those relating to tangles were mostly viral, but included the parasites, *T. Cruzi* and *T.Gondii*.

Beta-amyloid is an antibacterial, antifungal and antiviral agent (Table 1). It has been shown that it

binds to *C.albicans* and *S.Typhimurium* [2] and presumably to other microbes. Such microbes may well have sequestered host proteins specific to their particular life cycles during their passage to the cell, and this would partly explain the interactome enrichment. In addition to the plaque proteins relating to pathogen life cycles (for example receptor binding, endocytosis and transport between intracellular compartments or nuclear entry and subsequent translation in the case of HSV-1), the proteins found in plaques and tangles contain many related to the immune system, inflammation and autophagy, all of which play a general role in pathogen defence [8,24,25] as does beta-amyloid. Viruses are transported via the microtubule network [94], which is also exploited by *C.Pneumoniae*, *T.Cruz*i and *T.Gondii* to reorganise cellular organelles to the pathogens' advantage [95,96]. Phosphorylated *tau* is a hallmark of neurofibrillary tangles and is induced by many pathogens (Table 1). Tau phosphorylation can also be induced by interferon gamma, an effect related to disinhibition of glycogen synthase kinase [97]. It is not clear whether or how such effects could influence the pathogens.

AD genes are localised in the Blood brain barrier

30/78 AD genes are expressed in the BBB proteome dataset of mouse cerebral arteries [28] (Fig 1).

The list below indicates the 30 BBB genes, annotated with the number of pathogen interactomes

with which they overlap. Most BBB expressed genes interact with none or few pathogens (5 or less of the 17 studied), suggesting a subdivision of mainly BBB and mainly pathogen related. This could of course be confounded by missing data, as several of these genes are poorly characterised in terms of function. These 30 genes (N interactomes in brackets) are:- PCNX (0), ABCA7 (1), ADAMTS20 (1), ATXN7L1 (1), TREML2 (1), AP2A2 (2), BCAM (2), CNTNAP2 (2), ECHDC3 (2), FRMD4A (2), GRIN3B (2), PAX2 (2), PICALM (2), DISC1 (3), LUZP2 (3), RELN (3), TTLL7 (3), FERMT2 (4), HMHA1 (4), MSRA (4), PPP1R3B (4), SASH1 (4), BIN1 (5), SORL1 (5), PVRL2 (7), MMP12 (8), CLU (9), PTK2B (10), BCL3 (13), SQSTM1 (13).

The BBB location of a high proportion of AD genes indicates an important function in relation to AD. Several studies have reported that disruption of the blood brain barrier is an important feature of AD [98-101]. Cerebral microbleeds and cortical siderosis (an increase in blood-derived iron deposition) are a feature related to BBB disruption in AD patients [102-104]. Many bacteria depend upon the availability of free iron and such effects may contribute to their sucessful colonisation in AD [105].

Other environmental risk factors in AD disrupt the blood-brain barrier and BBB integrity is maintained by beneficial factors.

AD susceptibility genes might have been selected for pathogen resistance rather than susceptibility (see above). In which case, what are the factors, in the aged, that nevertheless permit the cerebral invasion of a large variety of pathogens? (See Table 1) Certain viruses (e.g. HSV-1) can enter the brain via the olfactory or other neural routes, exploiting an ability to use the axonal transport system [106]. Some parasites [107] and bacteria (e.g. *C. Pneumoniae* [108,109]) have also found ways to circumvent the barrier systems that usually protect the brain.

Aging itself leads to blood brain barrier dysfunction [110] and immunosenescence is also a feature of ageing and AD. However, while immunosenescence can increase susceptibility to pathogens due to immunodefficiency, it is also accompanied by an increase in the pro-inflammatory activity of monocytes and macrophages which can lead to chronic low grade inflammation, termed 'inflamm-

ageing"[111,112]. This increased inflammatory function also applies to microglia, the macrophage-like cells in the brain [113]. Certain AD gene variants are associated with enhanced pro-inflammatory responses (see above) and cerebral pathogen entry would thus be met with a doubly vigorous inflammatory response related to both immunosenescence and genetic variation. Persistently activated monocyte/macrophages have been observed in the blood of patients with early AD [114] and increased activation of microglia/macrophages, colocalized with the area of heavy beta-amyloid concentration, is also observed in the brains of AD patients [115].

Apart from pathogens, many other environmental risk factors have been reported in AD. These include diabetes, midlife hypertension or obesity, smoking and physical inactivity [116]. Other contributory factors include previous head injury [117], exposure to toxic metals (aluminium [118,119] or copper[120]), pesticides (organochlorine and organophosphate insecticides) [121,122], industrial chemicals (flame retardants) and air pollutants (particulate matter and ozone [123-126]). High levels of cholesterol or homocysteine [127-130] and low levels of folic acid [131,132] have also been associated with AD. In relation to cholesterol, atherosclerosis of the carotid arteries or of leptomeningeal vessels and in the circle of Willis has also been observed in AD. Such atherosclerotic effects can lead to chronic cerebral hypoperfusion [60,133,134]. Sleep disruption or obstructive sleep apnoea are also associated with AD risk [135,136].

Factors reported to be of benefit, or that reduce the incidence of AD include the use of non-steroidal anti-inflammatories (NSAIDs) [137,138], and the early use of statins [139-141] . Statins also have antimicrobial effects against oral microorganisms including *Aggregatibacter actinomycetemcomitans* and *P. Gingivalis*, and against most dental plaque bacteria, including *Streptococcus mutans*. They possess antiviral properties against the human cytomegalovirus, HSV-1, hepatitis B and C viruses, and antifungal properties against *Candida albicans*, *Aspergillus fumigatus*, and Zygomycetes species [142].

Beneficial dietary factors in AD include caffeine [130], chocolate (versus cognitive decline in the non-demented aged)[143]) and the Mediterranean diet [144-146]. Melatonin [147,148], estrogen [149-151] and memantine [152,153] also have reported benefits in AD.

The environmental risk factors associated with AD disrupt the BBB, and BBB integrity is maintained by the beneficial factors (Table 2). While infections are random uncontrollable events, many of the other environmental risk factors are modifiable by lifestyle changes, for example diet, obesity, smoking and exercise, and it has been estimated that addressing such modifiable risk factors might result in a significant reduction in the incidence of AD [116]. Amelioration of BBB disruption has already been proposed as a potential therapy in AD, and several drugs including angiotensin receptor blockers, etodolac (NSAID), granisetron (5HT3 serotonin receptor antagonist) or beclomethasone (corticosteroid) [154,155] as well as other NSAIDS, statins and other drugs referenced in Table 2 might be considered as suitable candidates.

Diverse pathogen sensors and defenders relating to bacteria, viruses, parasites and fungi are upregulated in the AD brain, blood or CSF.

We have evolved numerous pathogen detectors whose activation leads to stimulation of the immune system and to the production of defensive mechanisms, including inflammation and free radical attack. Multiple pattern recognition receptors including Toll-like receptors, C-type lectin receptors and nucleotide-binding oligomerization domain-like receptors (NOD-like) sense motifs in bacterial, viral, fungal and parasite proteins or other compounds or respond to foreign bacterial or viral DNA or RNA in cellular locations where host DNA or RNA should not exist [156-159].

Infection also activates inflammasomes, which trigger the maturation of proinflammatory cytokines, activating innate immune defences [160].

In addition to this, a large number of defensins and other antimicrobial peptides exist, targeting bacteria, fungi, parasites and viruses [161]. Beta-amyloid is one such [3].

EIF2AK2 (eukaryotic translation initiation factor 2 alpha kinase 2) better known as pkr, is activated by viral double stranded RNA and to bacterial RNA. This phosphorylates eif2alpha, leading to the arrest of the protein translation that is needed for viral replication. Pkr stimulation also leads to the production of interferon and to activation of the inflammasome [162-165]. Other viral RNA-sensors include RIG-I (coded by retinoic acid-inducible gene 1= DDX58), MDA5 (Melanoma Differentiation-Associated protein; coded by IFIH1) and LGP2 (coded by DEXH-box helicase 58= DHX58) [92].

Indoleamine 2,3-dioxygenase 1 (IDO1) diverts tryptophan metabolism to N-formyl-kynurenine, (away from serotonin production) .IDO1 upregulation is an important defence mechanism against pathogenic bacteria, many of which rely on host tryptophan. It is involved in antimicrobial defence and immune regulation, and its effects are not restricted to bacteria This IDO1 response is also deleterious to other pathogens and parasites, including T.Gondii, and to a number of viruses, including herpes simplex virus and other herpes viruses [166]. Kynurenine and kynurenic acid produced by IDO1 activation, are ligands for the aryl hydrocarbon receptor (AHR), which plays an important role in antimicrobial defence and immune regulation [167].

The function of these players with respect to the main pathogens studied above is reviewed in Supplementary Table 2, which also reports expression data in the Alzheimer's disease brain, blood or CSF. Data derived from this table are illustrated in Figs 7 (viral) and 8 (bacteria, fungi and parasites).

Fig 7 and 8. Viral (Fig 7) and fungal or bacterial (Fig 8) defenders and sensors and their expression (^

= upregulated; down = downregulated) in the brain, blood or cerebrospinal fluid of Alzheimer's disease patients. CP = choroid plexus; CSF= cerebrospinal fluid; GVS= granulovacuolar degeneration; HPC = hippocampus; lympho = lymphocytes; macro = macrophages; mcyt=monocytes; mgli = microglia; PBMC = peripheral blood mononuclear cells; Plaq = amyloid plaques; Ser = serum; tang = tangles;

 α defs or β defs= unspecified alpha or beta defensins: AGER= advanced glycosylation end productspecific receptor (also known as RAGE); APCS= amyloid P component, serum; CAMP = cathelicidin antimicrobial peptide (LL-37); Calpro= Calprotectin (\$100A8/\$100A9 dimer);CHI3L1 = chitinase 3 like

1 (aka YKL-40); C-type lectin = CLEC's; CRP = C-reactive protein; DEAD box proteins = DDX's;

Defensins = DEFA's, DEFB's: EIF2AK2 = eukaryotic translation initiation factor 2 alpha kinase 2 (pkr);

ELANE = elastase, neutrophil expressed; IAPP = islet amyloid polypeptide (Amylin); IDO1=
indoleamine 2,3-dioxygenase 1; Interferons = IFNA1, IFNA5, IFNB1, IFNG; LCN2 = lipocalin 2; LGALS3

= lectin, galactoside binding soluble 3; LTF = lactotransferrin; MAC = membrane attack complex

(complement components C5b-C9); MRC1 = mannose receptor, C type 1; NAIP = NLR family,

apoptosis inhibitory protein; NLRP1 and 3 = NLR family pyrin domain containing 1 and 3; NOD1 and

NOD2 = nucleotide binding oligomerization domain containing (1 and 2); RARRES2 and 3 = retinoic

acid receptor responder (2 and 3): \$100's=\$100 calcium binding protein; Toll-like receptors = TLR1

to 10; ZBP1 Z-DNA binding protein 1. Gene = gene related to the respective pathogen in association

studies or with Alzheimer's disease (Gene AD). mod sens = modified senstitivity; The strikethrough's

(e.g. TLR1) represent a pathogen's ability to inhibit or overcome the combative effects of the

defensive or sensor protein. ? = unknown

Borna = Borna virus; CMV = human cytomegalovirus; EBV = Epstein-Barr virus; HepC = Hepatitis C;

HSV-1= Herpes simplex; Influ= Influenza A virus; Borrel= Borrelia burgdorferi; C.Alb= Candida

albicans; C.Neo = Cryptococcus neoformans; C. Pneu = Chlamydia pneumoniae; H.Pyl= Helicobacter

pylori; P.Ging = Porphyrymonas gingivalis; T.Gon = Toxoplasma Gondii

Those shaded in black are those most implicated in Alzheimer's disease (Table 1)

Figure 7: Viruses:

Defenders Sensors β-amy-^ DDX21 ^ HPC DDX58 ^ brain, plasma EIF2AK2 ^ HPC, CSF, Borna lymph IFNA1 ^ microglia IFNA5 ^ HPC IFNB1 ? IFNG ^ PBMC ^ HPC TLR1 ^ HPC TLR2 ^ PBMC TLR4 ^ PBMC , brain TLR6 ? TLR7 ^brain TLR8 ^ mcyte/macro CMV B-amy ^ CRP ^ ser, CD163 ^ HPC, mgli/plaq EIF2AK2 ^ HPC, CSF, lympho plaq DDX39A ^ HPC IDO1 ^ HPC ,plaq/tang IFNG ^ PBMC ^ HPC TLR2 ^ PBMC TLR3 ? TLR4 ^ DEFB1 ^ CP, GVS (CMV gene) PBMC, plaq TLR5 ^ brain TLR9 ^ PBMC ZBP1 (AD gene) CHI3L1 ^ Brain CSF, **EBV** AGER ^ brain, plas CD163 ^ HPC, mgli /plaq CLEC2D ^ HPC DDX42 ^ HPC plasma, plaq CRP ^ ser, plaq EIF2AK2 ^ HPC, CSF, lympho IDO1 ^ HPC ,plag/tang LTF ^ brain NLRP3 ^ mcyte TLR2 ^ PBMC TLR3 ? TLR7 ^brain TLR8 ^ mcyte/macro TLR9 ^ mcyte DDX1 down HPC CLEC4M ^ HPC EIF2AK2 ^ HPC, CSF, lympho IDO1 HepC LTF ^ brain adefs ^ HPC plaq/tang NLRP3 ^ mcyte TLR2 ^ PBMC TLR4 ^ PBMC, brain TLR6? TLR7 ^brain HSV-1 β-amy ^ CRP ^ ser, plaq EIF2AK2 ^ HPC, CSF, lympho IDO1 ^ HPC ,plaq/tang DEFB1 ^ CP, GVS (HSV NLRP3 ^ mcvte TLR1 ^ HPC TLR2 ^ PBMC TLR3 ^ mcyte/macro TLR4 ^ PBMC, brain TLR6? gene) LGALS3 ^ serum LTF ^ TLR9 ^ mcyte ZBP1 (AD gene) brain MAC ^ brain/tang

β-amy ^ CAMP ? Influ
CRP ^ ser, plaq
DDX21 ^ HPC DDX39A ^ HPC
DEFA1 ^ blood
DEFB1 ^ CP, GVS
ELANE ^ brain LTF ^ brain

AGER ^brain, plas CLEC4M ^ HPC
DDX1 down HPC EIF2AK2 ^ HPC, CSF, lympho
IDO1 ^ HPC plaq/tang
NLRP3 ^ mcyte TLR2 ^ PBMC TLR6 ?
TLR7 ^brain TLR8 ^ mcyte/macro
TLR10 mod sens

General Viral detectors DDX1 DDX5 DDX47 down HPC DDX6 DDX21 DDX39A DDX42 ^ HPC DDX58 ^ brain, plasma DHX58 ^ brain EIF2AK2 ^ HPC, CSF, lympho IFNA1 ^ mgli IFNA5 ^ HPC IFNB1 ? IFNG ^ PBMC ^ HPC RARRES3 ^ HPC TLR3 ? TLR7 ^ brain TLR8 ^ mcyte/macrophages TLR9 ^ PBMC ZBP1 (AD gene)

Figure 8: Bacteria, fungi and T. Gondii

Defenders Sensors CAMP? DEFA1 ^ blood IDO1 ^ HPC plag/tang TLR1 ^ HPC Borrel DEFA1B ? ELANE ^ brain TLR2 ^ PBMC TLR4 ^ PBMC, plaq MAC ^ brain/tang TLR5 ^ brain TLR6 ? TLR7 ^ brain TLR8 ^ mcyte/macro TLR9 ^ PBMC β-amy ^ Calprot ^ brain, faecal CLEC7A ^ HPC IDO1 ^ HPC plaq/tang C.Alb CHI3L1 ^ Brain, CSF, plas, plag MRC1 ^ brain TLR2 ^ PBMC TLR4 ^ PBMC, plaq NLRP3 ^ mcyte CRP ^ ser, plaq DEFA4 ^ HPC DEFB4A ^ ser/CSF DEFB103A/B ? LGALS3 ^ ser LTF ^ brain MAC ^ brain/tang RARRES2 ^ HPC S100A12 ^ brain MRC1 ^ brain TLR1 ^ HPC TLR2 ^ PBMC C.Neo TLR3? TLR4 ^ PBMC, plaques Calpro ^ brain, faecal LTF ^ brain TLR9* ^ PBMC DEFB1 ^ CP, GVS APCS ^ plaques CRP ^ serum, IDO1 ^ HPC plaq/ tang C.Pneu plaques DEFB1 ^ CP, GVS NLRP3 ^ mcyte NOD1? LCN2 ^ brain ^ plasma down CSF NOD2 ? TLR2 ^ PBMC TLR4 ^ PBMC, plaq Calpro ^ brain, faecal CAMP? DEFA5/6? DEFB1 ^ CP, GVS DEFB4A ^ CD163 ^ HPC, mgli/plaq NLRP3 ^ H.Pvl ser, CSF DEFB103B ? LGALS3 ^ serum mcyte NOD1 ? NOD2 ? TLR1 ^ HPC LCN2 ^ brain ^ plasma down CSF LTF ^ TLR2 ^ PBMC TLR4 ^ PBMC, plaq brain MAC ^ brain/tang TLR6? TLR10? Calpro ^ brain, faecal CAMP? AGER ^ brain,plas CD163 ^ HPC, mgli/plag P.Ging CRP ^ ser, plaq DEFA1 ^ blood IDO1 ^ HPC plag/tang NLRP3 ^ mcyte DEFA1B ? DEFB4A ^ blood, CSF NOD1/NOD2 ? TLR1 ^ HPC TLR2 ^ PBMC TLR4 ^ PBMC , brain TLR6 ? TLR7 ^brain DEFB103B ? ELANE ^ brain LTF ^ brain MAC ^ brain/tang α,βdefs TLR8 \(^mcyte/macro TLR9 \(^mcyte) DEFA5? DEFB4A ^ blood, CSF IDO1 ^ HPC plaques/tang NLRP1 ^ mcyte T.Gon NLRP3 ^ mcyte TLR2 ^ PBMC TLR4 ^ LTF ^ brain PBMC, brain TLR5 hrain TLR9 hmcyte

General bacterial detectors IDO1 ^ HPC plaq/tang NAIP ^ HPC MAC ^ brain/tang NOD1 NOD2 ? TLR1 ^ HPC TLR2 ^ PBMC TLR4 ^ PBMC , brain TLR5 ^ brain TLR6 ? TLR7 ^ brain TLR8 ^ mcyte/macro TLR9* ^ PBMC TLR10 mod sens

These figures show that sensors and defenders relating to multiple pathogens are upregulated in the AD brain, blood or CSF. These involve reactions to many different classes (bacteria, viruses, fungi and parasites) and there appears to be no discrimination, or focus on any particular type. This would concord with the multiple and diverse pathogen species that have been detected in the AD brain (Table 1) and with the relationship between the AD genes or the hippocampal transcriptome with multiple pathogen species.

Caveats:

This analysis is based on overlapping gene symbols rather than on specific polymorphisms. There is thus no indication of the physiological weight or importance of any gene/pathogen interaction, some of which will be more important than others. Pathogen effects may also be strain-dependent, and the size of the interactomes also varies widely. Within any large interactome there will be deleterious, neutral and beneficial effects. While HSV-1 infection causes beta-amyloid deposition and neurodegeneration [168], in its latent form, the virus can have neuroprotective effects. For example the viral latency transcript inhibits apoptosis and promotes neurite sprouting in neuroblastoma cells [169], protects neuronal C1300 and Neuro2A cells from granzyme B-induced apoptosis and CD8 T-Cell killing [170] and also protects trigeminal neurones from apoptosis [171]. The Bornavirus is capable of promoting hippocampal degeneration in Man [172]. In rats Borna virus infection decreases choline acetyltransferase activity in the cerebral cortex, horizontal diagonal band of Broca , hippocampus and amygdala [173] a situation similar to that observed in Alzheimer's disease [174] but the inflammation and microglial activation it produces can also reduce beta-amyloid immunoreactivity in the brain parenchyma of Tg2576 mutant beta-amyloid mice [93]. Chronic, adult acquired T. Gondii infection causes neurologic and behavioural abnormalities secondary to inflammation and neuronal loss, in a strain-dependent manner [175]. T. Gondii infection in BALB/C mice induces neuroinflamation and learning and memory deficits. It also potentiates the toxic effects

of low doses of intracerebrally administered beta-amyloid[176], but chronic infection can also increase beta-amyloid phagocytosis and clearance by recruited monocytes [177].

Dementia or neurodegeneration, in the absence of amyloid plaques is, by current clinical definition, not considered as Alzheimer's disease, but as already noted, there is no inherent biological reason for this [178,179]. Such divergent effects might also be relevant to findings relating to the presence of amyloid plaques in the absence of dementia, as observed in the Nun study [180,181] or to diagnosed Alzheimer's disease in the absence of beta-amyloid. A recent report showed that ~15% of patients clinically diagnosed with AD do not have amyloid deposits as indexed by positron emission tomography [182]. While some amyloid-negative patients could be re-diagnosed (~50%), the clinical follow-up using other criteria in other amyloid-negative patients continued to support the definition of Alzheimer's disease.

There are also many inter-pathogen interactions relevant to this relatively small sample of the potential microbiome. For example HSV-1 infection activates replication of the Epstein-Barr virus, [183]. Gingipains or other proteases secreted by *P. Gingivalis* degrade multiple complement components [184] as well as alpha- and beta defensins [185], immunoglobulins, IgG1 and IgG3 [186] and interleukin-12, preventing its ability to stimulate interferon production [187]. Such effects enable the pathogen to counteract immune defence and would also impinge on the viability of many other pathogens.

HIV-1 is immunosuppressant and has been associated with many opportunistic pathogens including tuberculosis, toxoplasmosis, cytomegalovirus encephalitis and Cryptococcal brain invasion [188,189]. The human cytomegalovirus is also immunosuppressant via an ability to target MHC class I molecules for degradation [190]and to inhibit MHC class II antigen presentation [191]. Parasites, which maintain a long-term, if unwelcome presence in the host have also developed immunosuppressant and anti-defensive strategies[192,193]. In addition, the success of most pathogens depends upon their ability to subvert the defensive armoury of the host in some way.

The AD genes affect human processes relevant to the disease itself, but given that they are also part of pathogen interactomes, polymorphisms therein are also likely to affect pathogen life cycles or the ability of pathogens to promote diverse effects within the host. Apart from **APOE4** there are no studies relating to the effects of the AD gene variants on pathogens or their effects.

For these and many other reasons, it is perhaps unwise to rank the pathogens by order of importance in relation to their enrichment or p value in any of the data described above. Suffice it to say that diverse pathogens have been detected in the AD brain and all of the bioinformatics data presented above, whether related to genes, transcriptomes, plaques or tangles implicate multiple species of pathogens across viral, bacterial, fungal and protozoan classes.

While there are statistical limitations to this type of analysis, correction for false discovery followed by the Bonferroni correction has been conservatively applied. The relationship of AD to pathogens is supported by experimental observation (Table 1) and by the antimicrobial effects of beta-amyloid. This study also relies on multiple and diverse *in silico* bioinformatic analyses linking AD GWAS genes, plaques and tangles as well as the hippocampal transcriptome to multiple pathogen interactomes, and the upregulated AD hippocampal genes to multiple infection datasets from diverse pathogen species. Polymicrobial involvement is also supported by the diversity of bacterial, viral and fungal sensors and defenders that are upregulated in the AD brain, blood or CSF. Each comparison relates to single pathogens but given the diversity of pathogens detected in AD such effects are likely to be cumulative.

Discussion

Multiple and diverse pathogens (bacteria, viruses, fungi and spirochetes) have been detected in the AD brain and many cause neurodegeneration, increase beta-amyloid deposition and tau phosphorylation or are killed/incapacitated by beta-amyloid, an antimicrobial peptide that is part of the innate immune defence system. Representatives of these pathogens target multiple AD GWAS genes, and their interactomes are enriched in genes related to the AD hippocampal transcriptome

and to the proteins found in AD plaques and tangles. The upregulated genes of the AD hippocampal transcriptome also correspond to those upregulated by multiple species of viral, bacterial, fungal and protozoan pathogens or by interferon gamma and Toll-like receptor ligands.

The AD genes are preferentially localised in the bone marrow and other immunocompetent tissues, and in exosomes that are hijacked by pathogens for intercellular spread. They are also localised in the lateral ventricle and the hippocampus which abuts this area, a prime site of pathogen invasion via the choroid plexus and the blood/csf barrier.

The AD genes are enriched in global GWAS datasets relating to pathogen diversity, suggesting that some have been selected for pathogen resistance rather that susceptibility. This is supported by the old age of AD patients, indicating survival from the many infections that contribute to mortality in the younger population. APOE4 variants protect against malaria and hepatitis C, and immune/inflammatory gain of function applies to APOE4, CR1, TREM2 and presentilin variants, supporting this contention. Logically, any gene variant increasing the production of the antimicrobial peptide beta-amyloid in response to pathogens might also be considered as beneficial in these evolutionary terms. Apart from APOE4, there is however little data examining the effects of AD gene variants on pathogen life cycles or that relate specifically to pathogen responses.

Many AD genes are also localised in the blood brain barrier. This should provide an effective shield against many infections but it is disrupted by multiple environmental risk factors implicated in Alzheimer's disease and protected by several factors reported to be beneficial in relation to Alzheimer's disease, including NSAIDs, statins, oestrogen, memantine, melatonin, and components of the Mediterranean diet.

The relationship between pathogens and Alzheimer's disease has a long history coupled with a degree of scepticism, perhaps related to an inability to fulfil Koch's postulate. For example, the same pathogen is not always found in all AD brains, or in different laboratories. Laboratory confirmation in animal models may be impossible for certain pathogens, for example the Epstein-Barr or hepatitis C

virus, that do not infect rodents. Nevertheless, the diversity of pathogens able to promote neurodegeneration, beta-amyloid deposition or to mimic the effects observed in the hippocampal AD transcriptome suggests that many candidates, alone or severally, could be involved in the pathogenesis of AD. A polymicrobial involvement seems likely given the multiple species detected in the AD brain. Evidently, this could be assessed by microbiome studies in the periphery or in postmortem brains.

Recent work suggests that the production of the antimicrobial/antiviral peptide beta-amyloid is an expected consequence of infection in general [2,3]. In the context of the amyloid hypothesis [194], this places pathogens upstream of the production of this toxic peptide, and logically as causal, both in terms of beta-amyloid production and in relation to Alzheimer's disease.

Two separate case reports have shown remission from dementia or mis-diagnosed Alzheimer's disease in patients subsequently diagnosed with and treated for *Cryptococcus neoformans* infection [50,51].

In a Greek study, *H. Pylori*-infected AD patients receiving the triple eradication regime (omeprazole, clarithromycin and amoxicillin) showed improved cognitive and functional status parameters where bacterial eradication was successful [195]. *H. Pylori* eradication in AD patients with peptic ulcer was also associated with a decreased risk of AD progression in a Taiwanese study [196].

Taking all of the above into consideration the combined data suggest that polymicrobial brain invasion, enabled by environmentally-induced blood-brain barrier defects may be responsible for Alzheimer's disease. This could essentially be mediated via activation of a hyper-efficient inflammatory network, including the call-up of beta-amyloid that, as a consequence, causes massive neuronal destruction in a tissue incapable of regeneration. The role of the innate immune system and the inflammatory response in neurotoxicity has recently been reviewed, and innate surveillance mediated cell death has been suggested as a plausible common pathogenic pathway responsible for many neurodegenerative diseases, including AD [197].

It is therefore not unreasonable to suggest that antibiotic, antifungal and antiviral agents, possibly in combination, tailored to the individual, might be able to halt, delay or perhaps even provide remission in patients with Alzheimer's disease.

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Table 1: The effects of diverse pathogens on beta-amyloid deposition, tau phosphorylation and their relationships with Alzheimer's disease.

	Effects on beta-	Presence in Alzheimer's disease	Antibodies in
	amyloid	brain	Alzheimer's disease
	deposition or		blood and other
	Tau		analyses
	phosphorylation		
Viruses			
Borna virus	In transgenic mice	?	Associates with a
	expressing an APP		rare form of
	mutant (Tg2576)		hippocampal
	infection of cortical		degeneration but
	and limbic brain		not specifically with
	areas is		Alzheimer's disease
	characterized by		[172]
	T-cell infiltrates,		
	high cytokine		
	expression and a		
	massive microglial		
	activation in the		
	hippocampus and		
	neocortex.The		
	inflammatory		
	effects and		
	microglial		

	activation were		
	linked to a		
	decrease of		
	parenchymal beta-		
	amyloid deposits		
	but an increase of		
	beta-amyloid		
	deposits in the		
	walls of cerebral		
	vessels [93].		
Epstein-Barr virus:	No reports	The virus has been detected in a	Viral IgG levels are
human		small percentage of AD brains (6%).	increased in
herpesvirus 4		In aged individuals followed for 5	Alzheimer's patients
		years EBV-positive or HHV-6-positive	with the IRF7 GG
		peripheral blood leukocytes	genotype (interferon
		increased in those who developed	regulatory factor7)
		clinical AD [198]	[199]
HSV-1 (herpes	HSV-1 induces	Numerous studies have reported the presence of HSV-1 in	
simplex)	beta-amyloid and	Alzheimer's disease brains or an association with HSV-1	
	tau	seropositivity (reviewed in [200]).	
	phosphorylation in		
	cell culture or in		
	mice, effects that		
	can be attenuated		
	by acyclovir in cell		

	culture [200]		
HSV-2 Herpes	Increases beta-	Present at relatively low frequency in	?
simplex virus 2	amyloid deposition	brains of both control (20%) and	
	and tau	Alzheimer's patients (13%) [202]	
	phosphorylation in		
	human SK-N-MC		
	neuroblastoma		
	cells[201]		
Human	Beta-amyloid	?	Seropositivity
cytomegalovirus :	production is		associated with
human	increased by		Azheimer's disease
herpesvirus-5	cytomegalovirus		and with cognitive
	infection in human		decline in the aged
	foreskin fibroblasts		[204]. Infectious
	: Seropositivity		burden consisting of
	associated with the		cytomegalovirus,
	presence of brain		HSV-1, <i>B</i> .
	neurofibrillary		burgdorferi, C.
	tangles in post-		Pneumoniae and H.
	mortem human		Pylori is associated
	brain [203]		with Alzheimer's
			disease [1]
HHV-6 Human	No reports found	Present in a higher proportion of the	Viral DNA detected
herpesvirus 6		AD than of age-matched normal	in a higher
		brain(70 vs 40%) [202]	proportion of

Influenza A	No reports found	?	No association
			between past
			infections and
			Alzheimer's disease
			in a large study
			[207] Previous
			vaccination against
			influenza,
			diphtheria, tetanus
			or the poliovirus
			has been associated
			with a lower risk for
			Alzheimer's disease
			[208]. A particular
			strain
			(A/Vietnam/1203/04
			H5N1 virus) can
			enter the mouse
			brain from the
			periphery, causing
			neurodegeneration
			and alpha-synuclein
			(SNCA)
			accumulation: Cell
			death primarily

HIV-1: human	Amyloid plaques fou	nd in the brains of HIV-1 patients and	As treatment for
immunodeficiency	beta-amyloid deposition predicts neurocognitive disorders		AIDS has improved
virus	in HIV-1 infected APOE4 carriers [210,211].CSF beta-		dementia associated
	amyloid and tau leve	els correlate with AIDS associated	with AIDS
	dementia[212]		(NeuroAIDS) has
			increased in the
			ageing population
			[213,214]
Bacteria			
Chlamydia	C. Pneumoniae	Detected in the Alzheimer's brain in	Meta-analysis :
pneumoniae	infection produces	apposition to plaques and tangles	Evidence for <i>C.</i>
	beta-amyloid	[217-222]	Pneumoniae
	deposition in the		infection (Odds ratio
	brains of BALB/C		= 5.66) [223]
	mice which		
	resolves as the		
	bacterial antibody		
	titre decreases		
	[215,216].		
Helicobacter	H. pylori infection	?	A recent meta-
pylori	in rats increases		analysis has
	cerebral beta-		reported a
	amyloid deposition		significant
	via upregulation of		association between

	presenilin 2 , and		H. Pylori infection
	impairs learning		and dementia (Odds
	and memory [224]		ratio= 1.71) [226] .
	and increases tau		Cognitive function
	phosphorylation in		and survival rates
	cell culture (mouse		have been reported
	neuroblastoma		to be improved
	N2a cells) or in vivo		following H. Pylori
	(rats) via glycogen		eradication in
	synthase kinase		Alzheimer's disease
	beta[225].		patients [195,227].
			Progression of
			dementia has also
			been reported to be
			reduced in
			Alzheimer's patients
			with peptic ulcer
			following H. Pylori
			eradication [196]
Propionibacterium	?	Propionibacterium acnes was	
acnes		identified in frontal cortex biopsy	
		specimens in three of four AD	
		patients. The bacterium was	
		cultivated from frontal cortical	
		biopsy specimens [228,229].	

Spirochetes				
Borrelia	Beta-amyloid	Detected in the Alzheimer's disease	Meta-analysis :	
burgdorferi	deposition and tau	brain[231].	Evidence for	
	phosphorylation	Detected in 14 AD brains and not in	Spirochetal infection	
	induced by the	any of 13 control brains. Spirochetes	associated with	
	spirochete in	were also found in AD blood and CSF	Alzheimer's disease	
	cocultured	[232]. Beta-amyloid and bacterial	(Odds ratio = 10.61)	
	mammalian	DNA are components of pure	[223]	
	glial/neuronal cells	bacterial biofilms and of senile		
	[230]	plaques in AD [233,234]		
Fungal/yeast speci	es detected in the AD	brain include: - Saccharomyces cerevisia	e; Malassezia globosa;	
Malassezia restricta; Penicillium Phoma, Candida albicans, Candida ortholopsis, Candida tropicalis,				
Cladosporium, Neosartorya hiratsukae, Sclerotinia borealis [235,236]. Filamentous micro-organisms,				
possibly relating to actinomycetes have been found in control and AD brains with a four to five-fold				
higher frequency ir	n Alzheimer's disease [2	237]. C. famata, C. albicans or C. glabrat	a antigens have been	
found in AD cerebr	ospinal fluid[238].			
Antibodies to Cand	lida famata, Candida a	lbicans. Syncephalastrum racemosum ar	nd <i>Phoma betae</i> stain	
corpora amylacea in the brains of Alzheimer's disease patients [239].				
Two case reports indicated virtually complete recovery from long-term (3 years) mis-diagnosed				
dementia/Alzheimer's disease following antifungal treatment for <i>C. Neoformans</i> infection [50,51].				
Periodontal pathogens: Periodontitis has been associated with Alzheimer's disease and with cognitive				
decline in AD patients [240-242]. Periodontal disease has been associated with increased beta-amyloid				
load in patients in vivo [243].				
Actinomyces	?	?	Serum IgG levels	
naeslundii			associated with	

			increased risk of AD
			[244]
Porphyromonas	?	P. Gingivalis lipopolysaccharide	?
gingivalis		detected in 4/10 Alzheimer's brains	
		post-mortem [245]	
Fusobacterium	?	?	Antibody levels to F.
nucleatum			nucleatum and P.
Prevotella	?	?	intermedia
intermedia			increased in
			Alzheimer's disease
			serum [246]
Treponemes (oral pathogens) detected in the brains of AD patients using species specific PCR			
T. pectinovorum, T. amylovorum, T. lecithinolyticum, T. maltophilum, T. medium, T. socranskii, T.			
denticola, T. vincenti [234,247].			
Treponema pallidum causes syphilis. Syphilitic dementia is associated with the pathological features of			
AD [248]			
Parasites			

Toxoplasma	T. Gondii infection ?	A high
gondii	has been reported	seroprevalence for
	to inhibit	the Toxoplasma
	neurodegeneration	gondii parasite has
	in transgenic mice	also been reported
	(Tg2576)	in one study of
	expressing the	Alzheimer's disease
	Swedish APP	patients [250], but
	mutation [249] and	not confirmed in
	to reduce amyloid	others [251,252]
	plaque deposition	
	in 5xFAD mice,	
	effects attributed	
	to immune	
	activation, via	
	recruitment of	
	Ly6C(hi)	
	monocytes and by	
	enhancement of	
	phagocytosis and	
	degradation of	
	soluble beta-	
	amyloid [177].	
	Chronic infection in	
	mice does produce	
	neuroinflammation	
	and neuronal	
	[80] injury , including	

Leishmania	Increased tau	Î)	?
amazonensis	phosphorylation in			
	the brains of			
	infected mice			
	[253].			
Trypanosoma	?	?		Isolated cases of
Cruzi (causes				central nervous
Chagas disease)				system involvement
				can include
				dementia,
				confusion, chronic
				encephalopathy and
				sensory and motor
				deficits [254]
Plasmodium	Cerebral			Not applicable
berghei (causes	accumulation of			
malaria in	beta-amyloid in			
rodents)	infected malaria-			
	susceptible mice			
	(CBA/J and			
	C57BL/6) [255].			

Beta-amyloid:

Antimicrobial effects of beta-amyloid have been noted against *Candida albicans, Escherichia coli;*Staphylococcus epidermidis; Streptococcus pneumoniae; Staphylococcus aureus; Listeria

monocytogenes ;Enterococcus faecalis ; Streptococcus agalactia . It also protects against Salmonella

typhinurim meningitis in transgenic (5XFAD) mice expressing human beta-amyloid and in nematodes (C.

elegans). Beta-amyloid binds to C. albicans and S. typhimurium. In transgenic (5XFAD) mice, S.

typhimurium infection increases beta-amyloid deposition and bacteria are embedded within betaamyloid deposits in the brain [2,3]. Beta-amyloid has antiviral effects against the influenza[4] and
herpes simplex [5,6]viruses.

However, beta-amyloid can stimulate the infection of target cells expressing CD4 and an appropriate coreceptor by HIV-1, not allowing infection in cells lacking these receptors. It also stimulated infection by amphotrophic Moloney leukemia virus, herpes simplex virus, and vesicular stomatitis virus, a phenomenon also observed with other synthetic fibril-forming peptides [256].

Table 2. The effects of Alzheimer's disease environmental risk factors and beneficial agents on blood brain barrier function.

Alzheimer's disease risk factor	Effects on blood brain barrier
Ageing	Aging leads to barrier dysfunction and vascular
	hyperpermeability in peripheral and blood-brain barriers [110]
Air pollution	Long-term air pollution disrupts the BBB in children and young
	adults and causes neuroinflammation, an altered brain innate
	immune response, and accumulation of beta-amyloid and alpha-
	synuclein starting in childhood [123]
Alcohol abuse	Alcohol(ism) has deleterious effects on the BBB[257,257,258]
Aluminium	Aluminium increases BBB permeability in rats [259]
Beta-amyloid	Beta-amyloid disrupts BBB integrity in mice [260]
Brain trauma (concussion)	Mild traumatic brain injury produces early disruption of the BBB
	in animal models and in Man [261,262].
Cerebral	Cerebral hypoperfusion reduces oxygen, glucose and other
hypoperfusion/ischaemia	nutrient supply to the brain, damaging parenchymal cells, and
(carotid/leptomeningeal.circle of	the blood-brain barrier [263].
Willis atherosclerosis)	
Copper/aluminium	Nanoparticles from aluminium, silver or copper increase spinal
	cord pathology after trauma, an effect correlated with
	breakdown of the blood-spinal cord barrier [264]
Diabetes mellitus	BBB dysfunction plays a role in diabetes-associated neurological
	complications (stroke, vascular dementia and cognitive deficits)
	[265]
Homocysteine	Hyperhomocysteinemia increases permeability of the blood-

	brain barrier via N-methyl-D-aspartate (NMDA) receptor
	activation [266]
Hypercholesterolaemia	High cholesterol disrupts the blood brain barrier, an effect
	blocked by simvastatin [267]
Hypertension	Hypertension causes blood-brain barrier breakdown via
	mechanisms involving inflammation, oxidative stress, and
	vasoactive circulating molecules [268]
Obesity	Obesity induces systemic inflammation and blood-brain barrier
	disruption in mice, an effect augmented by age [269]
Pesticides	Several pesticides are able to disrupt the BBB in animal models
	[270-272]
Physical inactivity	Exercise in animal models of cerebral ischaemia/stroke,
	diabetes, and brain metastasis has been shown to improve BBB
	function [273]. Physical activity counters the negative influence
	of PICALM, BIN1, and CLU risk alleles on episodic memory
	functioning in a dementia-free population [274](all of these are
	expressed in the BBB proteome dataset)[275-277]
Poor sleep	Sleep disruption or sleep apnoea are both associated with
	impaired blood-brain barrier function [278,279].
Smoking	Nicotine and smoking disrupt brain microvasculature and the
	blood brain barrier[280]
Viruses capable of disrupting the	Viruses infecting humans known to cause disruption of the BBB
blood brain barrier	or endothelial junctions include HIV-1, human T-cell leukemia
	virus, lymphocytic choriomeningitis virus and the West Nile virus
	[281]. Bacterial lipopolysaccharide is disruptive in BBB models

	[282].
Beneficial effects	
Anti-inflammatories	Aspirin and celecoxib prevent disruption of the BBB in Vesicular
	Stomatitis Virus-infected mice [283]. Dexamethasone and
	methylprednisolone as well as NSAID's (ibuprofen and
	indomethacin) reduce vascular permeability in a rat glioma
	model [284]. Nimesulide (a selective cyclooxygenase-2 inhibitor)
	attenuates blood-brain barrier disruption in animal models of
	cerebral ischaemia [285]
Caffeine	Caffeine is effective against BBB disruption in animal models of
	Alzheimer's or Parkinson's disease [286].
Chocolate (caffeine,	Theobromine is a phosphodiesterase inhibitor and
theobromine and resveratrol)	downregulates PDE4 in a glioma cell line [287]. PDE4 inhibition
	(rolipram) reduces BBB damage in ischaemic stroke in mice
	[288]. Caffeine and theobromine are adenosine receptor
	antagonists [289]. Extracellular adenosine increases BBB
	permeability and adenosine receptor antagonism blocks the
	entry of inflammatory cells and soluble factors into the brain
	[290].
Folic acid	Vitamin B12-B6-folate treatment improves BBB function in
	patients with hyperhomocysteinaemia and mild cognitive
	impairment [291] . Folic acid decreases BBB leakage and reactive
	astrogliosis following seizures in pregnant and prepubertal rats
	[292].
Melatonin	Melatonin protects BBB integrity by downregulating matrix

	metalloprotease activity (MMP9) [293]
Memantine	Memantine (approved for use in dementia patients) [152] blocks
	the deleterious effects of homocysteine on the blood-brain
	barrier [266].
Oestrogen	Oestrogen protects against BBB breakdown in animal models of
	stroke or following lipopolysaccharide challenge and maintains
	barrier integrity [294-297]
Components of the	Omega-3 fatty acids reduce BBB disruption in hypoxic/ischaemic
Mediterranean diet	brain injury [298]. Fish oil reduces BBB disruption in a rat model
	of juvenile traumatic brain injury [299]. Virgin olive oil reduces
	BBB permeability following middle cerebral artery occlusion in
	rats [300]. Aged garlic extract protects against BBB disruption
	caused by a high saturated fatty acid diet in mice [301] .
	Resveratrol, a component of grape and red fruit skins, and red
	wine[302], maintains the integrity of the BBB after cerebral
	ischemia reperfusion in rats [303].
Statins	Statins have been reported to ameliorate BBB dysfunction
	produced by high cholesterol [267] , oxidised low-density
	lipoprotein [304], sepsis, intracerebral haemorrhage [305,306] or
	cerebral malaria [307]

87

[88]

89

Supplementary table 1:

Definitions of the Alzheimer's disease susceptibility genes studied. While many other functions are recognised, for example relating to beta-amyloid, cholesterol, lipid and glucose metabolism or diabetes, *inter alia* [1-4], the properties isolated in this table focus specifically on immune and pathogen-related effects. The relationship between AD genes, the immune system and inflammation has also previously emphasised [5] and in a recent study from the Alzheimer's Disease Neuroimaging Initiative, another subset of Alzheimer's disease genes showed genetic overlap between Alzheimer's disease and immune-mediated diseases [6].

Gene	Name	Immune or pathogen related properties
Symbol		
ABCA7	ATP-binding cassette, sub-family A	Plays a prominent role in phagocytosis
	(ABC1), member 7	by macrophages (demonstrated with
		Staphylococcus aureus). This is an
		important line of general host defence
		against pathogens [7]. Overexpression
		of ABCA7 in HeLa cells resulted
		increases intracellular and cell surface
		ceramide and intracellular
		phosphatidylserine levels [8].
		Ceramide reactivates the herpes
		simplex virus from latency [9] and is
		also incorporated into C.Pneumoniae
		inclusions [10]. APOA1 and APOE are
		substrates for ABCA7, and in cultured

HEK-293 cells, plasma membrane-
situated ABCA7 increases the efflux of
phosphatidylcholine and
sphingomyelin efflux to APOA1 and
APOE, with no effect on cholesterol
efflux[11] . Sphingomyelin is enriched
in extracellular herpes simplex viral
membranes [12] . It is a receptor for the
Helicobacter toxin VacA [13] and is
also incorporated into inclusion bodies
in C.Pneumoniae infected cells [14].
Phosphatidylcholine plays an important
role in the fusion of herpes simplex
glycoproteins B and H with the host
cell lipid membrane, a process used in
viral entry [15]. Phosphatidylcholine is
also able to trigger capsular
enlargement in C.Neoformans infection
[16].
Cholesterol efflux to lipid-laden
APOE, but not to lipid free APOE, is
increased by ABCA7 expression in
HEK-293 cells [17].
11LX-2/3 cens [1/].
Modifies the C termini of peptides for

angiotensin I converting enzyme

ACE

		presentation by major
		histocompatibility complex class I
		molecules, which increases the
		efficiency of antigen-specific CD8+ T
		cell priming [18].
ADAMTS20	ADAM metallopeptidase with	Cleaves the chondroitin sulfate
	thrombospondin type 1 motif, 20	proteoglycan, versican[19] which
		interacts with myeloid and lymphoid
		cells promoting their adhesion and the
		production of inflammatory cytokines:
		Inflammatory agents, such as double-
		stranded viral RNA mimetics, stimulate
		stromal cells, smooth muscle cells and
		fibroblasts, to produce fibrillar
		extracellular matrices enriched in
		versican and hyaluronan that promote
		the adhesion of leukocytes [20]
AP2A2	adaptor-related protein complex 2,	Induces the renewal and maintenance
111 2112	alpha 2 subunit	
	aipna 2 suvunu	of hematopoietic stem cells [21].
		Required for binding of human
		immunodeficiency virus type 1 Nef and
		cooperative assembly of a CD4-Nef-

		AP-2 complex [22].
A DOC1	l' d' OI	A POCKET LINE IN THE INTERPRETATION OF THE INTERPRETATION OFT THE INTERPRETATION OF THE
APOC1	apolipoprotein C-I	APOC1 binds to lipopolysaccharide
		(LPS), an outer-membrane component
		of gram-negative bacteria and is
		involved in the presentation of LPS to
		macrophages. This improves the
		inflammatory response, thus protecting
		against infection [23]. APOC1 is a
		component of high density lipoprotein:
		Herpes simplex is present in all
		lipoprotein blood fractions in blood
		(VLDL, LDL and HDL) and the lipid
		component of these lipoproteins binds
		to viral glycoprotein B [24]
APOE	apolipoprotein E	APOE4 favours cerebral access of
		HSV-1 in mice [25] and enhances
		C.pneumoniae adherence to host cells
		[26] and HIV-1 cell entry in vitro [27],
		but is protective against chronic
		hepatitis C virus infection [28]. The
		allele relates to increased viral load in
		HHV-6 infected epilepsy patients [29].
		Hepatitis B pathology has a more
		benign course in ApoE2-E4 carriers

		[30].
ATXN7L1	ataxin 7-like 1	None found
BCAM	basal cell adhesion molecule	Adhesion molecule involved in red
	(Lutheran blood group)	blood cell adhesion to the vascular
		endothelium [31] Also plays a role in
		abnormal red blood cell adhesion in
		sickle cell disease (c.f. malaria) [32].
		Acts as a receptor for Escherichia coli
		cytotoxic necrotizing factor 1, a toxin
		found in E.coli strains causing
		meningitis [33]
BCL3	B-cell CLL/lymphoma 3	BCL3 is essential for the development,
		survival and activity of adaptive
		immune cells. BCL3-deficient mice are
		more susceptible to bacterial and
		parasitic infection [34].
BIN1	bridging integrator 1	BIN1 negatively controls the
		expression of indoleamine 2,3-
		dioxygenase IDO1 in cancer cells [35].
		IDO1 activation diverts tryptophan
		metabolism to N-formyl-kynurenine,
		(away from serotonin production)
		.IDO1 upregulation is an important

defence mechanism against pathogenic bacteria, many of which rely on host tryptophan. It is involved in antimicrobial defence and immune regulation, and its effects are not restricted to bacteria This IDO1 response is also deleterious to other pathogens and parasites, including T.Gondii, and to a number of viruses, including herpes simplex virus and other herpes viruses [166]. Kynurenine and kynurenic acid produced by IDO1 activation, are ligands for the aryl hydrocarbon receptor (AHR), which plays an important role in antimicrobial defence and immune regulation [167]. A BIN1isoform is required for macrophage phagocytosis, a key mechanism in the destruction of many pathogens [36] One of a member of scaffold proteins are regulated by and mediating cell attachment, growth factor, and chemokine signalling [37]

Cas scaffolding protein family

member 4

CASS4

CD2AP	CD2-associated protein	CD2AP and other endocytosis-
		associated proteins play a role in
		enteropathogenic Escherichia coli
		pedestal formation [38]: Also required
		for late endosomal trafficking of the H.
		pylori VacA toxin [39]. Clathrin and
		related proteins including CD2AP are
		involved in the recruitment of proteins
		that promote actin polymerization at
		the interface of T cells and antigen
		presenting cells [40]. Decreased
		CD2AP expression enhances the
		production of type I interferons in
		human plasmacytoid dendritic cells
		which secrete type I interferons in
		response to microbial stimuli [41]
CD33	CD33 molecule	A member of the sialic acid binding
		Immunoglobulin g-like lectin
		(SIGLEC) family. CD33-related
		SIGLEC's regulate adaptive immune
		responses and are also important as
		macrophage pattern recognition
		receptors for sialylated pathogens,
		including enveloped viruses [42].

	CD33 binds to alpha 2-3- or alpha 2-6-
	linked sialic acids (N-acetyl neuranimic
	acid) [43]. These residues bind to the
	influenza virus and the reovirus [44]
	and these particular sialic acids are
	expressed on the surface envelope
	glycoproteins (B, D and H) of the
	herpes simplex virion, and are required
	for viral entry into cells [45]. N-acetyl
	neuranimic acid is expressed by
	C.Neoformans and is involved in
	fungal adhesion to macrophages [46]
	and is also a component of the cell wall
	of <i>B.Burgdorferi</i> [47] while
	Helicobacter pylori adhesins also bind
	to this particular form of sialic acid
	[48,49] as does <i>P.Gingivalis</i> [50]. CD33
	binds to sialic acid acquired by P.
	aeruginosa and to the HIV-1 gp120
	protein [51].
call adhesion associated oncogene	A gang associated with the acquisition
cell adhesion associated, oncogene	A gene associated with the acquisition
regulated	of Staphylococcus aureus bacteraemia
	[52]
carcinoembryonic antigen-related	The CEACAM family are docking sites

CDON

CEACAM16

	cell adhesion molecule 16	for pathogenic bacteria [53] but this
		particular protein has not been
		characterised in relation to this effect
CELF1	CUGBP, Elav-like family member 1	A downstream effector of interferon
		beta signalling in macrophages [54].
CLU	clusterin	Inhibits the membrane attack complex,
		composed of complement components
		C5 to C9. This is deposed on the
		bacterial surface forming channels that
		cause bacterial lysis [55,56].
CNTNAP2	contactin associated protein-like 2	None found
CR1	complement component (3b/4b)	Many pathogens are recognised by the
	receptor 1 (Knops blood group)	complement system and coated with
		complement components C1q, C3b and
		iC3b. This "opsonisation" prepares the
		microbe for phagocytosis via binding
		of the complement components to
		complement receptors, including CR1
		[57]. Receptor for the malaria pathogen
		Plasmodium falciparum [58],
		Legionella pneumophila [59],
		Mycobacterium tuberculosis[60] and
		Cryptococcus neoformans

CUGBP2	CUGBP, Elav-like family member 2	CUGBP2 silences the expression of
(changed to		cyclo-oxygenase 2 (PTGS2), thus
CELF2)		regulating inflammatory processes [61]
		CUGBP2 is regulated in response to T-
		cell signalling and increased CELF2
		expression drives a network of
		activation-induced alternative splicing
		events in Jurkat cells [62].
DISC1	disrupted in schizophrenia 1	DISC1 has many functions relevant to
DISCI	disrupted in schizophrenia 1	•
		the psychiatric diseases in which it is
		implicated, among which is control of
		the intracellular traffic of mRNAs,
		neurotransmitter receptors, vesicles and
		mitochondria along the microtubule
		network [63,64] . Although DISC1 has
		not been related to any particular virus
		or pathogen, the microtubule network
		provides a set of railway tracks used by
		many viruses during their life cycles
		[65-67]. Such traffic is also important
		in the regulation of the immunological
		synapse and in the building of
		functional phagosomes [68]
ECHDC3	enoyl CoA hydratase domain	Expressed in whole blood cells and

	containing 3	platelets, but no functional data
		available [69,70] .One of several genes
		downregulated by Trypanosoma Cruzi
		in mouse macrophages [71]
EPHA1	EPH receptor A1	Suppresses T cell activation and Th2
		cytokine expression, while preventing
		activation-induced cell death in the
		lung [72]. Upregulated in dendritic
		antigen-presenting cells in response to
		the human papillomavirus E7 peptide
		[73] . Mice infected with M.
		tuberculosis displayed higher
		expression of EPHA1 and EPHA2 in
		monocytes as well as ephrinA1[74]
EXOC3L2	exocyst complex component 3-like	None found
	2	
FAM113B	chromosome 5 open reading frame	This locus is considered non-coding by
(now	64	other groups due to a lack of
C5orf64)		experimental support for the protein,
		but NCBI annotates the protein because
		it meets minimal RefSeq quality
		criteria for representation. The coding
		status remains uncertain. [19 Nov

		2014](Refseq)
FANCD2OS	FANCD2 opposite strand	No functional publications
FERMT2	fermitin family member 2	None found
FLJ37543	chromosome 5 open reading frame	None found
(now	64	
C5orf64)		
FRMD4A	FERM domain containing 4A	None found
GAB2	GRB2-associated binding protein 2	An adaptor protein involved in multiple
		receptor tyrosine kinase signalling
		pathways: phosphorylated by
		stimulation with growth factors-,
		cytokines-, Immunoglobulin Fc- and
		antigen receptors [75] Gab2 knockout
		mice show reduced inflammatory
		cytokine levels in, and are relatively
		protected against Mycobacterium
		tuberculosis infection[76].
GRIN3B	glutamate receptor, ionotropic, N-	None found
	methyl-D-aspartate 3B	
HLA-DRB1	major histocompatibility complex,	Bind to pathogen antigens and present
	class II, DR beta 1	them to T-cells [77].

HLA-DRB5	major histocompatibility complex,	
	class II, DR beta 5	
HMHA1	histocompatibility (minor) HA-1	When HA-1 peptide was added to
		mixtures of plasmacytoid DC dendritic
		cells and T cells, bystander suppression
		of the response to a colocalized recall
		Epstein-barr viral antigen occurred
		primarily via indolamine-2,3-
		dioxygenase (IDO1) production.
		Bystander suppression is a process
		whereby Antigen-specific (adaptive) T
		regulatory cells inhibit the T effector
		cell response both to specific antigen
		and to a colocalized third-party antigen
		[78]: minor histocompatibility antigens
		refer to immunogenic peptides which,
		when complexed with MHC, can
		generate an immune response after
		recognition by specific T-cells. The
		peptides are derived from polymorphic
		intracellular proteins, which are
		cleaved by normal pathways of antigen
		processing (Definition from Uniprot).
HS3ST1	heparan sulfate (glucosamine) 3-O-	Heparan sulfate biosynthetic enzymes

	sulfotransferase 1	are key components in generating a
		myriad of distinct heparan sulfate fine
		structures that carry out multiple
		biologic activities. The enzyme
		encoded by this gene is a member of
		the heparan sulfate biosynthetic
		enzyme family. It possesses both
		heparan sulfate glucosaminyl 3-O-
		sulfotransferase activity, anticoagulant
		heparan sulfate conversion activity, and
		is a rate limiting enzyme for synthesis
		of anticoagulant heparan. This enzyme
		is an intraluminal Golgi resident
		protein. [provided by RefSeq, Jul
		2008]. Heparan sulphates act as
		attachment sites for many viruses
		[79,80]
IGH	immunoglobulin heavy locus	Forms the heavy chain of multiple
		antibodies [77].
INPP5D	inositol polyphosphate-5-	Phosphatidylinositol (PtdIns)
	phosphatase, 145kDa	phosphatase that specifically
		hydrolyses the 5-phosphate of
		phosphatidylinositol-3,4,5-
		trisphosphate (PtdIns(3,4,5)P3) to
	<u>I</u>	

produce PtdIns(3,4)P2, thereby negatively regulating the PI3K (phosphoinositide 3-kinase) pathways. Acts as a negative regulator of B-cell antigen receptor signalling. Mediates signalling from the FC-gamma-RIIB receptor (FCGR2B), playing a central role in terminating signal transduction from activating immune/hematopoietic cell receptor systems. Acts as a negative regulator of myeloid cell proliferation/survival and chemotaxis, mast cell degranulation, immune cells homeostasis, integrin alpha-IIb/beta-3 signalling in platelets and JNK signalling in B-cells. Regulates proliferation of osteoclast precursors, macrophage programming, phagocytosis and activation and is required for endotoxin tolerance. Involved in the control of cell-cell junctions, CD32a signalling in neutrophils and modulation of EGFinduced phospholipase C activity. Key regulator of neutrophil migration, by

		governing the formation of the leading
		edge and polarization required for
		chemotaxis. Modulates FCGR3/CD16-
		mediated cytotoxicity in NK cells.
		Mediates the activin/TGF-beta-induced
		apoptosis through its Smad-dependent
		expression. May also hydrolyse
		PtdIns(1,3,4,5)P4, and could thus affect
		the levels of the higher inositol
		polyphosphates like InsP6.2 (Definition
		from Uniprot)
LUZP2	leucine zipper protein 2	None found
MEF2C	myocyte enhancer factor 2C	MEF2C orchestrates early B-cell
		development [81] and is also involved
		in the activation induced cell death of
		macrophages after priming with
		Salmonella typhimurium, type 5
		adenovirus or Interferon-gamma [82].
		Also a risk gene for periodontitis [83],
		a known risk factor for Alzheimer's
		disease [84]
MMP12	matrix metallopeptidase 12	Degrades elastin, a matrikine derived
	(macrophage elastase)	from extracellular matrix proteins:
	` 1 & ,	_

		immune responses, organ development,
		minute responses, organ development,
		wound repair, angiogenesis,
		atherosclerosis, tumor progression and
		metastasis due to their ability to alter
		cellular migration, chemotaxis, and
		mitogenesis.[85] . Aging and various
		inflammatory diseases such as
		atherosclerosis, abdominal aortic
		aneurysms, chronic obstructive
		pulmonary diseases, cancer and type 2
		diabetes are characterized by the
		destruction of elastin fibres [86]
MMP3	matrix metallopeptidase 3	PolyI:C treatment (viral DNA mimic)
	(stromelysin 1, progelatinase)	increases the expression levels of
		Mmp3 mRNA and protein in
		astrocytes, but not microglia [87].
MPZL1	myelin protein zero-like 1	Present in CD133(+) precursors
		(CD133= hematopoietic precursor
		antigen) and endothelial cells, and
		mainly in mesenchymal and
		committed myelomonocytic progenitor
		cells, and in erythroid precursor cell
		lines [88].

MS4A3	membrane-spanning 4-domains,	Modulates cell cycle progression in
	subfamily A, member 3	hematopoietic cells [89]
	(hematopoietic cell-specific)	
MS4A4A	membrane-spanning 4-domains, subfamily A, member 4A	Localised in Hematopoietic cells [89]: Expressed in lung mast cells Silencing MS4A4 promotes mast cell proliferation and migration. Mast cells express Toll receptors and play an important role in pathogen recognition and in acquired immunity against parasitic infections [90,91].
MS4A4E	membrane-spanning 4-domains, subfamily A, member 4E	None found
MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	Localised in Lymphoid tissues, Kidney Colon and Wilm's tumor cells [89]
MSRA	methionine sulfoxide reductase A Catalyses two reactions (from KEGG) (1) peptide-L-methionine + thioredoxin disulfide + H2O = peptide-L-methionine (S)-S-oxide + thioredoxin;	Could have an important function as a repair enzyme for proteins that have been inactivated by oxidation. Catalyzes the reversible oxidation-reduction of methionine sulfoxide in proteins to methionine (From Uniprot).

	(2) L-methionine + thioredoxin	
	disulfide + H2O = L-methionine	
	(S)-S-oxide + thioredoxin	
MTHFD1L	methylenetetrahydrofolate	The protein encoded by this gene is
	dehydrogenase (NADP+ dependent)	involved in the synthesis of
	1-like Catalyses the reaction	tetrahydrofolate (THF) in the
	(KEGG)	mitochondrion. THF is important in the
	ATP + formate + tetrahydrofolate =	de novo synthesis of purines and
	ADP + phosphate + 10-	thymidylate and in the regeneration of
	formyltetrahydrofolate	methionine from homocysteine
		(Refseq)
NDUFAF6	NADH dehydrogenase (ubiquinone) complex I, assembly factor 6	None found
NME8	NME/NM23 family member 8	The NME8 locus has been associated
		in a genome-wide study with the
		bacterial disease periodontitis [92] also
		a known risk factor for Alzheimer's
		disease [84].
PAX2	paired box 2	PAX2 negatively regulates beta
		defensin-1, an antimicrobial peptide
		implicated in the resistance of
		epithelial surfaces to microbial
		colonization [93].

PCDH11X	protocadherin 11 X-linked	None found
PCNX1	pecanex homolog (Drosophila)	None found
PICALM	phosphatidylinositol binding	Involved in clathrin-mediated
	clathrin assembly protein	endocytosis, a process used by many
		viruses to gain entry to the cell [94]
		(AP2A2 and BIN1 are also involved in
		this process)see KEGG pathway (red
		text genes)
		http://www.genome.jp/kegg-
		bin/show pathway?hsa04144+274+161
POLN	polymerase (DNA directed) nu	POLN can perform translesion
		synthesis past thymine glycol, a
		common endogenous and radiation-
		induced product of reactive oxygen
		species damage to DNA. Thymine
		glycol blocks DNA synthesis by most
		DNA polymerases, but POLN was
		particularly adept at efficient and
		accurate translesion synthesis past a
		5S-thymine glycol [95].
PPP1R37	protein phosphatase 1, regulatory	No publications
	subunit 37	

protein phosphatase 1, regulatory	None found
subunit 3B	
protein tyrosine kinase 2 beta	Involved in Toll-like receptor
	signalling (pathogen recognition
	receptors)(TLR2, TLR4) in
	macrophages [96]. Involved in the
	natural killer cell cytotoxic pathway
	[97] and in the microglial production of
	nitric oxide produced by
	lipopolysaccharide and interferon
	gamma [98]
noliovirus recentor	Mediates entry of the poliovirus and
ponovinus receptor	
	binds to NECTIN1 (a receptor for
	HSV-1 and 2) [99] and NECTIN3 (a
	receptor for HSV-1) [100] [101,102]
poliovirus receptor-related 2	Entry receptor for HSV-1 [103].
(herpesvirus entry mediator B)	
reelin	Reelin plays a prominent role in the
	brain but also in the intestine where the
	reeler mutation down-regulates genes
	related to the immune response,
	inflammation, and tumor development
	[104] . Reelin deposits in the
	poliovirus receptor poliovirus receptor-related 2 (herpesvirus entry mediator B)

		hippocampus are a conserved
		neuropathological feature of aging, and
		such deposits are accelerated in adult
		wild-type mice prenatally exposed to a
		viral-like infection [105].
RFC3	replication factor C (activator 1) 3,	The elongation of primed DNA
	38kDa	templates by DNA polymerase delta
		and DNA polymerase epsilon requires
		the accessory proteins proliferating cell
		nuclear antigen (PCNA) and replication
		factor C (RFC).RFC3 is one of 5
		subunits of this complex (Refseq). Host
		nuclear DNA processing factors are
		also recruited to viral genomes, RFC3
		is one of many recruited to the HSV-1
		viral genome [106]
RIN3	Ras and Rab interactor 3	RIN 3 inhibits mast cell migration
		toward stem cell factor, which recruits
		mast cells to sites of infection or injury,
		where they release pro-inflammatory
		substances [107].
SASH1	SAM and SH3 domain containing 1	Scaffold molecule involved in Toll
		receptor (TLR4) signalling, a receptor
		involved in the recognition of bacterial

		lipopolysaccharides[108].
SCIMP	SLP adaptor and CSK interacting	SCIMP is expressed in B cells and
SCHVII		
	membrane protein	other antigen-presenting cells and is
		involved in major histocompatibility
		complex class II signalling [109].
SLC24A4	solute carrier family 24	None found
	(sodium/potassium/calcium	
	exchanger), member 4	
SLC4A1AP	solute carrier family 4 (anion	None found
	exchanger), member 1, adaptor	
	protein	
SORL1	sortilin-related receptor, L(DLR	None found
	class) A repeats containing	
SPPL2A	signal peptide peptidase like 2A	SPPL2A is a protease that cleaves
		CD74, the invariant chain of the
		MHCII complex, and an important
		chaperone regulating antigen
		presentation for the immune response.
		[110].
SQSTM1	sequestosome 1	Autophagy can either promote or
		restrict viral replication. SQSTM1is an
		autophagy receptor involved in the life

		cycles of the Chikungunya virus[111],
		Coxsackievirus[112], Dengue virus
		[113], the encephalomyocarditis virus
		[114], enterovirus 71[115], hepatitis B
		[116], HIV-1[117], Herpes simplex
		(HSV-1) [118], Kaposi's sarcoma virus
		[119], measles [120], Varicella zoster
		[121] and the West Nile virus [122]
STK24	serine/threonine kinase 24	Important regulator of neutrophil
		degranulation which results in the
		releases of proteases and other
		cytotoxic agents, including matrix
		metalloproteinases and
		myeloperoxidase These granule
		contents are antimicrobial, but can also
		cause tissue damage [123]
TOMM40	translocase of outer mitochondrial	The influenza viral protein PB1-F2
	membrane 40 homolog (yeast)	translocates into mitochondria via
		TOMM40 channels and impairs innate
		immunity [124]. TOMM40 is required
		for replication of the African swine
		fever virus [125]
TREM2	triggering receptor expressed on	A receptor for bacterial
		lipopolysaccharide that acts as a

	myeloid cells 2	phagocytic receptor for bacteria. It also inhibits the production of inflammatory cytokines induced by Toll like
		receptors [126-128].
TREML2	triggering receptor expressed on	TREML2 (Triggering receptor
	myeloid cells-like 2	expressed on myeloid cells (TREM)-
		like transcript 2) is expressed on T cells
		and regulates interleukin-2 and
		interferon-gamma production [129].
TRIP4	thyroid hormone receptor interactor	None found: This protein is localized in
	4:	the nucleus and contains an E1A-type
		zinc finger domain, which mediates
		interaction with transcriptional
		coactivators and ligand-bound nuclear
		receptors, such as thyroid hormone
		receptor and retinoid X receptor alpha,
		but not glucocorticoid receptor
		(Refseq).
TTLL7	tubulin tyrosine ligase-like family,	None found
	member 7	
ZCWPW1	zinc finger, CW type with PWWP	None found
	domain 1	

ZNF224	zina fingar protain 224	Wilms turns 1 (WT1) respects 7NEOO4
ZNF224	zinc finger protein 224	Wilms tumor 1 (WT1) recruits ZNF224
		to the interferon regulatory factor 8
		(IRF8) promoter [130]
		The IRF family proteins bind to the
		IFN-stimulated response element
		(ISRE) and regulate expression of
		genes stimulated by type I IFNs,
		namely IFN-alpha and IFN-beta. IRF
		family proteins also control expression
		of IFN-alpha and IFN-beta-regulated
		genes that are induced by viral
		infection. [provided by RefSeq, Jul
		2008]

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Supplementary Table 2: A survey of the roles of diverse microbial sensors and defensive proteins. Their expression levels in the Alzheimer's disease brain, blood, cerebrospinal fluid or other defined cells etc. are also reviewed.

Gene	Function	Alzheimer's disease
AGER advanced	Recognizes advanced	Increases in protein levels

glycosylation end productglycosylation end products, and in the percentage of specific receptor (more members of the S100 protein AGER expressing microglia commonly known as RAGE) family, beta-amyloid and in the Alzheimer's disease amyloid fibrils, HMGB1, and brain linked with disease β-integrin macrophage 1 severity[10].Plasma protein antigen (Mac-1) [1]. levels increased in Receptor for S100B, Alzheimer's disease [11] but S100A4, 6,11,12,13, S100P decreased levels of a soluble [2], Expressed on endothelial isoform [12,13] cells macrophages, neutrophils, dendritic cells, T cells, B cells, alveolar type II cells and alveolar epithelial cells[3]. AGER(-/-) mice were relatively protected from influenza virus induced mortality showing improved viral clearance, enhanced cellular T cell response and activation of neutrophils [4]. AGER activation enhances the ability of neutrophils to eradicate bacteria (E.Coli) in vitro and in vivo via activation of NADPH

oxidase[5].	
Involved in the adhesion of	
Helicobacter pylori to gastric	
epithelial cells [6]. P.	
gingivalis infection enhances	
AGER expression in Murine	
aortic endothelial cells [7].	
Bacteria produce, metabolize	
and accumulate AGEs	
.Escherichia coli cells secret	
AGEs [8]. Influenza A viral	
pneumonia is associated with	
enhanced AGER expression	
on endothelium and de novo	
expression on bronchial	
epithelium in mice[4]. The	
Epstein Barr viral protein	
LMP1 binds to the AGER	
promoter [9]	
Antimicrobial peptide with	Key component of amyloid
broad spectrum activity	plaques
against bacterial	
(Enterococci, E.Coli,	
streptococci, staphylococci,	
pseudomonas, listeria) and	

βAmyloid

fungal (Candida albicans)	
species {Soscia, Kirby, et al.	
2010 1912 /id} . It also has	
antiviral effects against	
Herpes simplex (HSV-1)	
{Bourgade, Le Page, et al.	
2016 10595 /id}{Bourgade,	
Garneau, et al. 2015 10596	
/id} and the influenza virus	
{White, Kandel, et al. 2014	
8740 /id}. Borna virus	
infection induced microglial	
activation can reduce plaque	
formation in Tg2576 APP	
mutant transgenic mice [14]	
Binds to several bacterial	Protein levels elevated in the
lipopolysaccharides (S.	AD brain and associated with
pyrogens and rough strains of	plaques, but low levels in
E. coli) preventing	plaques were seen in
complement activation[15].	individuals with AD
Increased levels of APCS in	pathology without dementia
the atherotic plaques of	[18].
C.Pneumoniae infected mice	
fed an atherogenic diet [16].	
Binds avidly to C. Albicans	

APCS amyloid P component,

serum (commonly known as

SAP)

	when amyloid is formed in	
	fungal cell walls [17]	
CAMP cathelicidin	In addition to its	None found
antimicrobial peptide (LL-	antibacterial, antifungal, and	
37)	antiviral activities, the	
	encoded protein functions in	
	cell chemotaxis, immune	
	mediator induction, and	
	inflammatory response	
	regulation. [provided by	
	RefSeq, Sep 2014].	
	[19]Antiviral versus	
	influenza	
	Kills P.Gingivalis [20] but	
	degraded by a P.gingivalis	
	secreted protease (gingipain)	
	[21]. DEFB1 and CAMP	
	(cathelicidin/LL-37) kill	
	H.pylori [22]. Borrelia	
	burgdorferi is killed by	
	human polymorphonuclear	
	leukocyte granule	
	components (elastase	
	ELANE, CAMP,	
	bactericidal/permeability-	

	increasing protein (BPI), and	
	human neutrophil peptide-	
	1)[23].	
CD163 CD163 molecule	Functions as an acute phase-	Upregulated in the AD
	regulated receptor involved	hippocampus [29].
	in the clearance and	Parenchymal microglia were
	endocytosis of	immunoreactive for CD163
	hemoglobin/haptoglobin	in all of 31 AD cases often
	complexes by macrophages,	associated with amyloid
	and may thereby protect	plaques [30]
	tissues from free	
	hemoglobin-mediated	
	oxidative damage. This	
	protein may also function as	
	an innate immune sensor for	
	bacteria and inducer of local	
	inflammation. [provided by	
	RefSeq, Aug 2011]	
	Upregulated in the gastric	
	mucosa of H. pylori infected	
	children [24]. Upregulated by	
	P.Gingivalis in periodontal	
	ligament cells [25]. Kupffer	
	cell/macrophage activation	
	indicated by increased	

	CD163 is found in the livers	
	of hepatitis C infected	
	patients [26]. The	
	cytomegalovirus encoded	
	IL10 chemokine mimic	
	upregulates CD163 in	
	macrophages [27]. serum	
	levels of soluble CD163 in	
	Epstein-Barr virus positive	
	children positively correlate	
	with EBV-DNA copies [28]	
CHI3L1 chitinase 3 like 1	Chitinases catalyze the	CSF levels of CHI3L1 are
(aka YKL-40)	hydrolysis of chitin, which is	associated with Alzheimer's
	an abundant glycopolymer	disease [33-35]. Plasma
	found in insect exoskeletons	levels are also increased and
	and fungal cell walls. The	the protein is found in
	protein lacks chitinase	astrocytes near a subset of
	activity and is secreted by	amyloid plaques
	activated macrophages,	(immunohistochemistry) [36]
	chondrocytes, neutrophils	
	and synovial cells. The	
	protein is thought to play a	
	role in the process of	
	inflammation and tissue	
	remodeling. [provided by	

	RefSeq, Sep 2009]	
	CHI3L1 is induced by fungal	
	infection (Candida albicans)	
	and induces the	
	antimicrobial peptides beta-	
	defensin 3 and cathelicidin	
	(CAMP) [31]. In transgenic	
	mice expressing the Epstein-	
	Barr virus LMP1 protein	
	CHI3L1is induced in the	
	epidermis and is secreted and	
	autoantibodies to CHI3L1 are	
	generated [32]	
CLEC2B C-type lectin	CLEC-2 is a HIV-1	Upregulated in the AD
domain family 2 member B	attachment factor and	hippocampus [29]
	platelets capture and transfer	
	infectious HIV-1 via DC-	
	SIGN and CLEC-2 [37].	
	Expression induced by	
	infection of Akata cells [38]	
CLEC2D C-type lectin	Expression upregulated by	Upregulated in the AD
domain family 2 member D	respiratory syncytial virus	hippocampus [29]
	(RSV) infection, in the	
	BEAS-2B respiratory	
	epithelial cell line and	
domain family 2 member B CLEC2D C-type lectin	attachment factor and platelets capture and transfer infectious HIV-1 via DC- SIGN and CLEC-2 [37]. Expression induced by infection of Akata cells [38] Expression upregulated by respiratory syncytial virus (RSV) infection, in the BEAS-2B respiratory	hippocampus [29] Upregulated in the AD

	primary human bronchial	
	epithelial cells [39].	
	Expression is induced in B	
	cells and inflamed tonsils	
	following viral infection (
	Epstein-Barr virus or HIV	
	infection) and in inflamed	
	tonsils [40].	
CLEC4M C-type lectin	recognizes	Upregulated in the AD
domain family 4 member M	numerous evolutionarily	hippocampus [29]
(L-SIGN)	divergent pathogens ranging	
	from parasites to viruses,	
	with a large impact on public	
	health[provided by	
	RefSeq, Feb 2009] CD209	
	(DC-SIGN) and CLEC4M	
	(L-SIGN) are endocytic	
	receptors for influenza A	
	virus entry and infection,	
	and for the Hepatitis C virus,	
	HIV-1, Sindbis virus, and	
	act as cofactors for cellular	
	entry by Ebola virus.	
	CLEC4M also a receptor for	
	Mycobacterium tuberculosis,	

	Schistosomes and	
	Leishmania infant [41-46]	
CLEC7A C-type lectin	Functions as a pattern-	Upregulated in the AD
domain family 7 member A	recognition receptor that	hippocampus [29]
(Dectin 1)	recognizes a variety of beta-	
	1,3-linked and beta-1,6-	
	linked glucans from fungi	
	and plants, and in this way	
	plays a role in innate immune	
	response[provided	
	by RefSeq, Jul	
	2008].Activated by	
	C.albicans, and	
	Mycobacterium bovis [47]	
CRP C-reactive protein,	Involved in several host	High serum levels associated
pentraxin-related	defence related functions	with AD (dependent on
	based on its ability to	methodology) [54], but levels
	recognize foreign pathogens	of CRP in a mild and
	and damaged cells of the host	moderate dementia subgroup
	and to initiate their	were significantly lower than
	elimination by interacting	that in the control group [55].
	with humoral and cellular	A recently developed high-
	effector systems in the blood.	sensitivity (Hs) test reported
	Consequently, the level of	high serum levels of Hs-CRP

this protein in plasma in AD patients[56]. CRP increases greatly during acute staining of the hippocampal phase response to tissue CA1/2 region correlates with injury, infection, or other $A\beta$ staining in the AD brain inflammatory stimuli. [57]. [provided by RefSeq, Sep 2009]. Chlamydial lipopolysaccharide serum levels in coronary syndrome correlate with CRP levels [48].High CRP levels observed in H.Pylori and C.Pneumoniae infection [49]. High antibody response to multiple pathogens (cytomegalovirus, herpes simplex virus-1, Hepatitis A virus, Helicobacter pylori and Chlamydia pneumoniae) associated with CRP in atherosclerosis patients [50]. Antibodies to P. gingivalis associate with high levels of SAA and high concentrations of CRP in periodontitis

	patients[51]. Serum CRP	
	elevated in fungal esophagitis	
	or enterocolitis due to	
	C.albicans [52]. High serum	
	levels of CRP found in	
	numerous bacterial or viral	
	infections: (Dengue virus,	
	Cytomegalovirus , Epstein	
	Barr virus, Parvovirus B19,	
	HSV-1 and -2 and Influenza	
	A and B: [53]	
DDX1 DEAD/H-box	DDX1, DDX21, and DHX36	Down regulated in the AD
helicase 1	helicases form a complex	hippocampus [29]
	with the adaptor molecule	
	TRIF to sense double	
	stranded viral RNA,	
	including Influenza and Poly-	
	IC in dendritic cells	
	[58].Binds to hepatitis C	
	biotinylated RNA [59]	
DDX18 DEAD-box helicase	Few publications	Upregulated in the AD
18		hippocampus [29]
DDX21 DEAD-box helicase	DDX1, DDX21, and DHX36	Upregulated in the AD
21	helicases form a complex	hippocampus [29]

	with the adaptor molecule	
	TRIF to sense double	
	stranded viral RNA a in	
	dendritic cells [58]. DDX21	
	inhibits replication of the	
	influenza virus [60].Interacts	
	with a Borna virus protein	
	[61]	
DDX27 DEAD-box helicase	?	Upregulated in the AD
27		hippocampus [29]
DDX39A DEAD-box	Needed for the expression of	Upregulated in the AD
helicase 39A	Kaposi sarcoma-associated	hippocampus [29]
	herpesvirus ORF57 [62]. The	
	UL69 gene product of the	
	human cytomegalovirus	
	belongs to a family of	
	regulatory proteins conserved	
	among all herpesviruses and	
	binds to DDX39A [63]. Mx	
	proteins exert their antiviral	
	activity against the influenza	
	virus by interfering with the	
	function of the RNA	
	helicases DDX39B and	
	DDX39A [64] .	

DDX42 DEAD-box helicase	The expression of N-terminal	Upregulated in the AD
42	DDX42 binds to the NS4A	hippocampus [29]
	protein of the Japanese	
	encephalitis virus and	
	DDX42 is able to overcome	
	antagonism of interferon	
	responses by the virus [65].	
	Also a potential target of an	
	Epstein-Barr viral	
	microRNA [66] . The	
	Japanese encephalitis virus	
	encodes for interferon	
	antagonist proteins, one of	
	which, NS4A, binds to	
	DDX42 [65]	
DDX47 DEAD-box helicase	Interacts with the E1E4	Down regulated in the AD
47	protein of human	hippocampus [29]
	papillomavirus type 16 [67]	
DDX5 DEAD-box helicase 5	This gene encodes a DEAD	Down regulated in the AD
	box protein, which is a RNA-	hippocampus [29]
	dependent ATPase, and also	
	a proliferation-associated	
	nuclear antigen, specifically	
	reacting with the simian virus	
	40 tumor antigen	

	[provided by RefSeq, Feb	
	2016] DDX3,5 and 6 play a	
	role in hepatitis C viral	
	•	
	replication [68]. DDX5	
	interacts with the SARS	
	coronavirus [69]	
DDX58 DEXD/H-box	DEAD box proteins,	Expression increased in the
helicase 58 ()commonly	characterized by the	temporal cortex and plasma
known as RIG-1)	conserved motif Asp-Glu-	of mild cognitive impairment
	Ala-Asp (DEAD), are	patients with pathologic
	putative RNA helicases	evidence of senile plaques
	which are implicated in a	and neurofibrillary tangles
	number of cellular processes	[71]
	involving RNA binding and	
	alteration of RNA secondary	
	structure. This gene encodes	
	a protein containing RNA	
	helicase-DEAD box protein	
	motifs and a caspase	
	recruitment domain (CARD).	
	It is involved in viral double-	
	stranded (ds) RNA	
	recognition and the	
	regulation of immune	
	response. [provided by	

	RefSeq, Jul 2008] The	
	DDX58 -activating 5'	
	triphosphate group is	
	removed post-	
	transcriptionally by a viral	
	function and modified	
	DDX58 does not bind the	
	RNAs of Hantaan virus,	
	Crimean-Congo hemorrhagic	
	fever virus or the Borna	
	disease virus [70].	
DDX6 DEAD-box helicase 6	The protein is an RNA	Upregulated in the AD
	helicase found in P-bodies	hippocampus [29]
	and stress granules, and	
	functions in translation	
	suppression and mRNA	
	degradation. It is required for	
	microRNA-induced gene	
	silencing. Multiple	
	alternatively spliced variants,	
	encoding the same protein,	
	have been identified.	
	[provided by RefSeq, Mar	
	2012]. It also controls gene	
	expression in RNA viruses	

	[72]. DDX3,5 and 6 play a role in hepatitis C viral replication [68]. Binds to a Dengue virus RNA [73]	
DEFA1 defensin alpha 1	Found in the microbicidal granules of neutrophils and likely plays a role in phagocyte-mediated host defence. (from Refseq) Defends against S. aureus, E. coli and E. aerogenes [74] anthrax toxin, C,Difficile toxin B, diphtheria toxin, and Pseudomonas exotoxin A [75-77] and also inhibit the adenovirus, BK polyoma virus and HIV-1 [78-80]. Binds to P.Gingivalis [81].	Defensins alpha1 and 2 (now coded only by DEFA1) are upregulated in Alzheimer's disease blood cells [84]; DEFA1/DEFA1B, DEFA3 and DEFB4A increased in sera and CSF of AD patients [85]

	Antiviral versus Influenza A	
	[82].Alpha-defensin	
	transcription activated by the	
	hepatitis C core protein	
	(specific gene symbol not	
	possible) [83]	
DEFA1B defensin alpha 1B	The protein encoded by this	DEFA1/DEFA1B, DEFA3
	gene, defensin, alpha 1, is	and DEFB4A increased in
	found in the microbicidal	sera and CSF of AD patients
	granules of neutrophils and	[85]
	likely plays a role in	
	phagocyte-mediated host	
	defense. Several alpha	
	defensin genes are clustered	
	on chromosome 8. This gene	
	differs from defensin, alpha 3	
	by only one amino acid (from	
	Refseq). Binds to	
	P.Gingivalis [81]. Release	
	induced by H.Pylori [86].	
	Borrelia burgdorferi is killed	
	by human	
	polymorphonuclear	
	leukocyte granule	
	components (elastase	

	ELANE, CAMP,	
	bactericidal/permeability-	
	increasing protein (BPI), and	
	human neutrophil peptide-	
	1(DEFA1))[23]	
DEFA3 defensin alpha 3	Found in the microbicidal	DEFA1/DEFA3/ DEFB4A
	granules of neutrophils and	elevated in the serum and
	likely plays a role in	cerebrospinal fluid of AD
	phagocyte-mediated host	patients [84]
	defense. (from Refseq)	
	Defends (relatively weakly)	
	against S. aureus, E. coli and	
	E. aerogenes [74]	
DEFA4 defensin alpha 4	Found in neutrophils; it	Upregulated in the
	exhibits corticostatic activity	hippocampus [29]
	and inhibits corticotropin	
	stimulated corticosterone	
	production. [provided by	
	RefSeq, Oct 2014]. Potent	
	killer of Escherichia coli,	
	Streptococcus faecalis, and	
	Candida albicans [87].	
DEFA5 defensin alpha 5	The protein encoded by this	?
_	gene, defensin, alpha 5, is	
	highly expressed in the	

	secretory granules of Paneth	
	cells of the ileum. [provided	
	by RefSeq, Oct 2014]Kills	
	H.Pylori [88]. Unmethylated	
	CpG motifs in Toxoplasma	
	gondii DNA induce TLR9-	
	and IFN-β-dependent	
	expression of DEFA5 in	
	intestinal epithelial cells.[89]	
DEFA6 defensin alpha 6	The protein encoded by this	?
	gene, defensin, alpha 6, is	
	highly expressed in the	
	secretory granules of Paneth	
	cells of the small intestine,	
	and likely plays a role in host	
	defense of human bowel.	
	[provided by RefSeq, Oct	
	2014] Kills H.Pylori [88]	
DEFB1 defensin beta 1	A gene associated with HSV-	Upregulated in the
	1 and cytomegalovirus	Alzheimer's disease choroid
	seropositivity in children	plexus and in
	with acute lymphoblastic	granulovacuolar degeneration
	leukaemia [90] ,as well as	structures [95]
	with <i>H.Pylori</i> or chlamydial	
	infections [91,92], also	

	endowed with antimicrobial
	activity against
	C.Neoformans and other
	pathogens [93].DEFB1 and
	CAMP (cathelicidin/LL-37)
	kill H.pylori [22]. Protects
	mice from influenza
	pathogenesis with a
	mechanism other than
	inhibition of viral replication.
	plasmacytoid dendritic cells
	and monocytes increased
	production of DEFB1 peptide
	and mRNA as early as 2 h
	following infection of
	purified cells and peripheral
	blood mononuclear cells with
	influenza, HSV-1, and
	Sendai virus[94].
DEFB103A defensin beta	An antibiotic peptide which
103A	is induced by bacteria and
	interferon gamma, and which
	displays antimicrobial
	activity against S. aureus, S.
	pyogenes, P. aeruginosa, E.

	coli, and C. albicans.	
	[provided by RefSeq, Oct	
	2014] .	
DEFB103B defensin beta	This gene encodes defensin,	?
103B	beta 103, which has broad	
	spectrum antimicrobial	
	activity and may play an	
	important role in innate	
	epithelial defense. [provided	
	by RefSeq, Oct 2014]Kills	
	H.Pylori [96].Binds to	
	P.Gingivalis [81]. Antiviral	
	versus Influenza A [97]	
DEFB4A defensin beta 4A	This gene encodes defensin,	DEFA1/DEFA3/ DEFB4A
	beta 4, an antibiotic peptide	elevated in the serum and
	which is locally regulated by	cerebrospinal fluid of AD
	inflammation. [provided by	patients [84]
	RefSeq, Jul 2008]. Has	
	potent antimicrobial activity	
	against Gram-negative	
	bacteria and Candida, but not	
	Gram-positive	
	Staphylococcus aureus	
	[98].kills H.Pylori [99] Also	
	involved in defence against	

	Varicella zoster, human	
	respiratory syncytial virus,	
	HIV-1 and the Human	
	papillomavirus [100-103].	
	Binds to P.Gingivalis [81].	
	slow-replicating type II and	
	III T.Gonidii induce high	
	levels of DEFB4A gene	
	expression in human	
	intestinal epithelial cells	
	[104]	
Defensins	A large number of antimicrobia	al pentides (almost 2000
Belefishis	animal derived peptides, 112 fr	
		-
	bacteria, parasites, fungi or viru	•
	be considered as one such [106	ין
	•	
DHX58 DEXH-box helicase	Detects double stranded viral	Upregulated in total brain
58	RNA and activates antiviral	and frontal lobe of AD
	reponses [107,108].	patients [109]
EIF2AK2 eukaryotic	Several stimuli including	Upregulated in the AD
translation initiation factor 2	TNF and other cytokines,	hippocampus [29] and CSF
alpha kinase 2 (commonly	double stranded viral RNA	[121] and activated in AD
known as PKR)	or bacterial ligands acting via	lymphocytes [122]
	Toll receptors activate	
	EIF2AK2 resulting in the	

inhibition of protein synthesis necessary for viral replication. Activation also results in the production of interferons alpha and beta [110]. Activated by lipopolysaccharide or bacterial RNA or by the mycotoxin deoxynivalenol, shiga toxin, and ricin [111-115]. Activated by HCMV, but the virus possesses proteins able to antagonise EIF2AK2 [116]. Activated by HSV-1 which is also able to evade EIF2AK2 activation [117] and by hepatitis C and influenza viruses [118]. Epstein-Barr virus-encoded small RNAs bind the protein PKR and inhibit its activation [119]. Not activated by the Borna virus, suggesting an evasive strategy to abolish antiviral activities [120]

ELANE elastase, neutrophil Following activation, this Increased expression in the expressed protease hydrolyzes proteins vessel wall of leptomeningeal within specialized neutrophil vessels in AD . Arterial lysosomes, called azurophil elastin degradation was granules, as well as proteins observed from Braak stage of the extracellular matrix. III onward and correlated The enzyme may play a role with Braak tau pathology in degenerative and [126]. inflammatory diseases In the brain parenchyma through proteolysis of elastase immunoreactivity is collagen-IV and elastin. This restricted to neurons and is protein also degrades the markedly elevated in a outer membrane protein A proportion of neurofibrillary (OmpA) of E. coli as well as tangle-bearing neurons [127]. the virulence factors of such bacteria as Shigella, Salmonella and Yersinia. [provided by RefSeq, Jan 2016] . Kills Borrelia burgdorferi [23]. H. pylori extract-activated human neutrophils result in endothelial cell detachment from human umbilical vein endothelial cells monolayers

	which can be blocked by an	
	which can be blocked by an	
	elastase antibody. The	
	bacterium also inhibits	
	elastase [123]. Elevated	
	serum levels in patients with	
	influenza virus-associated	
	encephalopathy [124].	
	Periodontain, a protease	
	secreted by P.Gingivalis,	
	inactivates the human serpin,	
	alpha1-proteinase inhibitor,	
	the primary endogenous	
	regulator of human	
	neutrophil elastase, which	
	may be responsible for	
	increased elastase activity in	
	periodontitis [125].	
Gamma-secretase	Localised in dendritic cells that	t scout for invading
	pathogens. Cleaves receptors for	or many pathogens including
	those for adenoviruses, C.Neof	Formans, cytomegalovirus,
	Epstein-Barr virus, Hendra virus	us, hepatitis C, HHV-6, HIV-1,
	HSV-1, influenza, rhinovirus,	measles, Nipah virus,
	Papilloma virus, P.Gingivalis,	rabies, S.Aureus and
	streptococci, Vaccinia and othe	er pox viruses [128].
IAPP islet amyloid	Commonly found in	Accumulates intraneuronally

polypeptide (Amylin)	pancreatic islets of patients	in brains of Alzheimer's
	suffering diabetes mellitus	disease patients, particularly
	type II, or harboring an	in those with type-2 diabetes
	insulinoma. Studies suggest	[130].See review for
	that this protein, like the	common links between
	related beta-amyloid (Abeta)	bacteria, diabetes and
	associated with Alzheimer's	Alzheimer's disease [131]
	disease, can induce apoptotic	
	cell-death in particular	
	cultured cells, an effect that	
	may be relevant to the	
	development of type II	
	diabetes. This protein also	
	exhibits a bactericidal,	
	antimicrobial activity.	
	[provided by RefSeq, Sep	
	2014]. Inhibits the growth of	
	Staphylococcus aureus and	
	Escherichia coli [129]	
IDO1 indoleamine 2,3-	Catalyses the production of	IDO1 expression is increased
dioxygenase 1	N-formylkynurenine from	in the AD hippocampus and
	tryptophan. Expression is	is associated with amyloid
	stimulated by interferon	plaques and neurofibrillary
	gamma and other	tangles. Quinolinic acid
	inflammatory cytokines.	immunoreactivity is localised

This diverts tryptophan in microglial and astrocytic metabolism away from cells around amyloid plaques serotonin production, and in the vicinity of neurofibrillary tangles [145towards kynurenines and can lead to overproduction of the 147]. kynurenic acid and quinolinic acid, N-methyl-D-aspartate receptor antagonist and agonist respectively. The subsequent depletion of tryptophan is deleterious to many microbes that depend upon this metabolite [132]. Diversion to the kynurenine pathway also produces metabolites activating the aryl hydrocarbon receptor which also plays a role in antimicrobial defence and immune activation. This pathway is relevant to antibacterial and antiviral effects[133]. Involed in C.albicans defence [134] and in the response to B.

	Burgdorferi [135].Restricts	
	C.Pneumoniae replication in	
	dendritic cells [136].Induced	
	by HSV-1 [137], Influenza	
	and hepatitis C infection	
	[138,139] . Induced by	
	C.Albicans at sites of	
	infection and in dendritic	
	cells and effector neutrophils	
	[140]. IDO1 activation	
	restricts HCMV replication,	
	but the virus is able to	
	counteract this block [141].	
	Expression increased by a	
	DPG3 strain of P.Gingivalis	
	[142] . Activated by T.Gondii	
	infection in the mouse spleen	
	[143] . Indiced by the	
	Epstein-Barr virus in human	
	macrophages [144]	
IFNA1 interferon, alpha 1	The protein encoded by this	The NK cell activity induced
	gene is produced by	by either interferon-alpha
	macrophages and has	(IFN-alpha) or interleukin-2
	antiviral activity. This gene is	(IL-2) in DAT was also
	intronless and the encoded	significantly lower than in

protein is secreted. [provided	the normal controls [148]
by RefSeq, Sep 2011]	white matter microglia were
Orthologs	intensely labeled for alpha-
a	IFN [149]
The protein encoded by this	Increased cytotoxic response
gene belongs to the type I	by NK cells to IL-2 (mean
class of interferons, which	increase +102%) and IFN-
are important for defense	beta (mean increase +132%)
against viral infections. In	in SDAT patients [151].
addition, type I interferons	
are involved in cell	
differentiation and anti-tumor	
defenses. Following secretion	
in response to a pathogen,	
type I interferons bind a	
homologous receptor	
complex and induce	
transcription of genes such as	
those encoding inflammatory	
cytokines and chemokines.	
Overactivation of type I	
interferon secretion is linked	
to autoimmune diseases.	
Mice deficient for this gene	
display several phenotypes	
	by RefSeq, Sep 2011] Orthologs a The protein encoded by this gene belongs to the type I class of interferons, which are important for defense against viral infections. In addition, type I interferons are involved in cell differentiation and anti-tumor defenses. Following secretion in response to a pathogen, type I interferons bind a homologous receptor complex and induce transcription of genes such as those encoding inflammatory cytokines and chemokines. Overactivation of type I interferon secretion is linked to autoimmune diseases. Mice deficient for this gene

	including defects in B cell	
	maturation and increased	
	susceptibility to viral	
	infection. [provided by	
	RefSeq, Sep 2015]The Borna	
	virus nucleoprotein inhibits	
	type I IFN expression by	
	interfering with the IRF7	
	pathway [150] .	
IFNG Interferon Gamma	The active protein is a	Increased spontaneous and
	homodimer that binds to the	IL-2-induced release of IFN-
	interferon gamma receptor	gamma and TNF-alpha from
	which triggers a cellular	NK cells were found in DAT
	response to viral and	patients compared to healthy
	microbial infections.	subjects. [154]: IFN-γ and
	Mutations in this gene are	TNF-α levels, in peripheral
	associated with an increased	blood mononuclear cells,
	susceptibility to viral,	assessed in patients with AD
	bacterial and parasitic	in mild and severe stages,
	infections and to several	respectively, are higher than
	autoimmune diseases.	those observed in patients
	[provided by RefSeq, Dec	with moderate stage and MCI
	2015]. A P.Gingivalis	[155]. Increased IL2 and
	protease, (gingipain) cleaves	IFNG secretion from
	interleukin-12, reducing its	mononuclear cells observed

ability to stimulate IFNG in AD patients in the production [152]. moderately severe stage of Upregulated in the brains of the disease [156]: IFNG Borna virus infected cats levels increased in peripheral blood mononuclear cells [153]. [157]. No increase in plasma [158] or CSF levels [159]: higher levels of IL-1beta (interleukin 1beta) (P < .001), IL-1beta to IL-1ra ratio (P < .001), tumor necrosis factor alpha (P = .008), IL-6 (P = .04), and interferon gamma (P = .01) in the non-afflicted offspring of patients with AD [160]. All participants with Apo $\varepsilon 3/\varepsilon 4$ or $\varepsilon 4/\varepsilon 4$ alleles showed a distinct biochemical profile characterized by low Creactive protein and ApoE levels and by high cortisol, interleukin 13, apolipoprotein B, and gamma interferon

		levels[161] . CSF interferon γ
		was only detected in
		cytomegalovirus seropositive
		subjects and was
		significantly associated with
		neurofibrillary tangles [162].
		Higher levels of IL-6 and
		IFN-γ were found more in
		the cultured T lymphocytes
		of the AD patients [163].
		IFNA5 and IFNG
		upregulated in the AD
		hippocampus [29]. Infectious
		burden and IFNG levels
		associated with AD (HCMV,
		HSV-1, B. burgdorferi, C.
		pneumoniae and H. pylori)
		[164]
LCN2 lipocalin 2	This gene encodes a protein	Lcn2 levels are decreased in
	that belongs to the lipocalin	CSF of patients with mild
	family. Members of this	cognitive impairment and
	family transport small	AD and increased in brain
	hydrophobic molecules such	regions associated with AD
	as lipids, steroid hormones	pathology in human
	and retinoids. The protein	postmortem brain tissue

encoded by this gene is a	[167] .Plasma levels are
neutrophil gelatinase-	increased in mild cognitive
associated lipocalin and plays	impairment [168].
a role in innate immunity by	
limiting bacterial growth as a	
result of sequestering iron-	
containing siderophores.	
Mice lacking this gene are	
more susceptible to bacterial	
infection than wild type	
mice. [provided by RefSeq,	
Sep 2015] involved in host	
defence against	
C.Pneumoniae possibly by	
limiting the availability of	
iron to the pathogen [165].	
Upregulated in the gastric	
mucosa of H.Pylori infected	
patients [166]	
The protein exhibits	Serum levels increased in
antimicrobial activity against	AD [172]
bacteria and fungi[provided	
by RefSeq, Oct 2014}	
LGALS3 knockout mice are	
more susceptible to	
	neutrophil gelatinase- associated lipocalin and plays a role in innate immunity by limiting bacterial growth as a result of sequestering iron- containing siderophores. Mice lacking this gene are more susceptible to bacterial infection than wild type mice. [provided by RefSeq, Sep 2015] involved in host defence against C.Pneumoniae possibly by limiting the availability of iron to the pathogen [165]. Upregulated in the gastric mucosa of H.Pylori infected patients [166] The protein exhibits antimicrobial activity against bacteria and fungi[provided by RefSeq, Oct 2014} LGALS3 knockout mice are

	C.Albicans infection [169].	
	Plays an important role in	
	innate immunity to infection	
	and colonization of H. pylori	
	[170]. HSV-1 infection	
	increases the carbohydrate	
	binding activity and the	
	secretion of cellular LGALS3	
	[171]	
LTF lactotransferrin	Antimicrobial, antiviral,	expression up-regulated in
	antifungal and antiparasitic	both neurons and glia in
	activity has been found for	affected AD tissue [181]
	this protein and its peptides.	
	Alternatively spliced	
	transcript variants encoding	
	different isoforms have been	
	found for this gene.	
	[provided by RefSeq, Sep	
	2014]. Kills T.Gondii and	
	C.Albicans [173].	
	lactoferricin is generated by	
	gastric pepsin cleavage of	
	lactoferrin and kills albicans,	
	C. tropicalis and C.	
	neoformans[174].Neutralises	

	HSV-1 amd prevents	
	replication [175]. Inhibits	
	P.Gingivalis proteases [176].	
	Effective versus H.Pylori	
	[177]. Inhibits influenza virus	
	hemagglutination [178].	
	Antiviral versus hepatitis C	
	[179].Inhibits Epstein Barr	
	virus infection [180]	
MAC: Membrane attack	Activated by C.Albicans but	The complement system is
complex: A complex	secreted fungal proteases	activated in the AD brain and
composed of complement	degrade C5 and can inhibit	MAC is abundantly present
components C5b to C9 that	MAC formation [183,184].	and associated with
attaches to bacteria, creating	Activated by P.Gingivalis	neurofibrillary tangles, in the
pores that kill by lysis [182].	which is also able to degrade	neuronal cytoplasm,
	C5 [185,186].Kills H.Pylori	lipofuscin granules,
	in vitro but the pathogen	lysosomes, dystrophic
	evades MAC by binding to	neurites within neuritic
	CD59, and inhibitor of MAC	plaques, and neuropil threads
	formation [187]. Attacks	[190-192]
	Borrelia burgdorferi, which	
	retaliates via a protein	
	(CspA) which binds C7 and	
	C9 and blocks MAC	
	assembly and membrane	

	insertion [188]. HSV-1	
	infected neuronal or skin	
	cells activate complement	
	and though initially resistant	
	to MAC deposition the skin	
	cells eventually succumb to	
	MAC deposition. Neuronal	
	Paju cells are more resistant	
	but MAC is deposited on	
	~10% of these [189].	
MRC1 mannose receptor, C	The protein encoded by this	mRNAs for TNF, AGI,
type 1	gene is a type I membrane	MRC1 and CHI3L1; CHI3L2
	receptor that mediates the	were significantly increased
	endocytosis of glycoproteins	in the AD brain [195]
	by macrophages. The protein	
	has been shown to bind high-	
	mannose structures on the	
	surface of potentially	
	pathogenic viruses, bacteria,	
	and fungi so that they can be	
	neutralized by phagocytic	
	engulfment.[provided by	
	RefSeq, Sep 2015].	
	Recognises C.Albicans	
	[193]. Higher fungal burdens	

	for C.Neoformans in MRC1	
	knockout mice [194]	
NAIP NLR family, apoptosis	Senses bacterial flagellin	Upregulated in the AD
inhibitory protein	[196] and type III secretion	hippocampus [29]
	system needle proteins from	
	several bacterial pathogens,	
	including Salmonella	
	typhimurium,	
	enterohemorrhagic	
	Escherichia coli, Shigella	
	flexneri, and Burkholderia	
	species [197]. Inhibits	
	Legionella pneumophila	
	infection [198].	
NLRP1 NLR family pyrin	Activated by Bacillus	Monocyte expression of
domain containing 1	anthracis lethal toxin,	NLRP1, NLRP3, PYCARD,
	Toxoplasma gondii, muramyl	caspases 1, 5 and 8) and
	dipeptide (a constituent of	downstream effectors (IL-1β,
	both Gram-positive and	IL-18) up-regulated in severe
	Gram-negative bacteria)	and mild AD [201]
	[199]. NLRP1 and NLRP3	
	both activated by T.Gondii	
	[200]	
NLRP3 NLR family pyrin	Activated by Staphylococcus	The NLRP1 and NLRP3
domain containing 3	aureus, Candida albicans and	inflammasomes are both

	the influenza virus as well as	activated in AD monocytes
	beta-amyloid [202].Activated	[201]
	by C.Neoformans [203],	
	C.Pneumoniae [204],	
	H.Pylori [205] and by	
	P.Gingivalis LPS [206] but	
	also subject to proteolysis by	
	the bacterium [207].	
	Activated and subsequently	
	inhibited by HSV-1	
	[208].Activated by the	
	Hepatitis C virus [209] and	
	by the Influenza a virus in	
	dendritic cells [210]. An	
	Epstein-Barr virus micro	
	RNA can be secreted from	
	infected B cells via exosomes	
	to inhibit the NLRP3	
	inflammasome [211]	
NOD1 nucleotide binding	This protein is an	
oligomerization domain	intracellular pattern-	
containing 1	recognition receptor (PRR)	
	that initiates inflammation in	
	response to a subset of	
	bacteria through the detection	

	of bacterial diaminopimelic
	acid. Multiple alternatively
	spliced transcript variants
	differring in the 5' UTR have
	been described, but the full-
	length nature of these
	variants has not been
	determined. [provided by
	RefSeq, Oct 2009].
	P. gingivalis outer membrane
	vesicles induce strong TLR2
	and TLR4-specific responses
	and moderate responses in
	TLR7, TLR8, TLR9, NOD1
	and NOD2 expressing-HEK-
	Blue cells [212]. Nod1(-/-)
	and Nod2(-/-) mice show
	delayed bacterial clearance of
	C. pneumoniae [213]. H.
	pylori activates the
	intracellular NOD1, NOD2,
	and NLRP3 [214]
NOD2 nucleotide binding	The protein is primarily
oligomerization domain	expressed in the peripheral
containing 2	blood leukocytes. It plays a

	role in the immune response	
	to intracellular bacterial	
	lipopolysaccharides (LPS) by	
	recognizing the muramyl	
	dipeptide (MDP) derived	
	from them and activating the	
	NFKB protein. Mutations in	
	this gene have been	
	associated with Crohn	
	disease and Blau syndrome.	
	Alternatively spliced	
	transcript variants encoding	
	distinct isoforms have been	
	found for this gene.	
	[provided by RefSeq, Jun	
	2014]	
	P. gingivalis outer membrane	
	vesicles induce strong TLR2	
	and TLR4-specific responses	
	and moderate responses in	
	TLR7, TLR8, TLR9, NOD1	
	and NOD2 expressing-HEK-	
	Blue cells [212]	
RARRES2 retinoic acid	The active protein has several	Upregulated in the
receptor responder 2:	roles, including that as an	hippocampus [29]
	<u> </u>	

i de la companya de		
	antimicrobial protein with	
	activity against bacteria and	
	fungi. [provided by RefSeq,	
	Nov 2014]	
	_	
	_	
RARRES3 retinoic acid	Viral RNA detector [216-	Upregulated in the
receptor responder 3	220]	hippocampus [29]
S100A4 S100 calcium	Dimerises with S100A9 and	Upregulated in the
binding protein A4	stimulates AGER and TLR4	hippocampus [29]
	[221]	
Calprotectin =	TLR4 agonist that is secreted	Faecal levels increased in
S100A8+S100A9	during the stress response of	AD patients [227] . S100B,
	phagocytes. Involved in	S100A9 and S100A12, but
	promoting the inflammatory	not S100A8, were
	response to infections and a	consistently associated with
	potent amplifier of	the neuropathological
	inflammation [222].	hallmarks of AD in post-
	Cytoplasmic calprotectin	mortem brains [228]
	inhibits C.Neoformans	
	growth [223]. Restricts	
	H.Pylori growth [224]. Kills	
S100A4 S100 calcium binding protein A4 Calprotectin =	Dimerises with S100A9 and stimulates AGER and TLR4 [221] TLR4 agonist that is secreted during the stress response of phagocytes. Involved in promoting the inflammatory response to infections and a potent amplifier of inflammation [222]. Cytoplasmic calprotectin inhibits C.Neoformans growth [223]. Restricts	Upregulated in the hippocampus [29] Faecal levels increased in AD patients [227] . S100B, S100A9 and S100A12, but not S100A8, were consistently associated with the neuropathological hallmarks of AD in post-

	Candida Spp Escherichia	
	coli, Klebsiella spp,	
	Staphylococcus aureus, and	
	Staphylococcus epidermidis	
	[225]. Confers resistance to	
	P.Gingivalis [226].	
S100A8 S100 calcium	See Calprotectin	S100B, S100A9 and
binding protein A8		S100A12, but not S100A8,
		were consistently associated
		with the neuropathological
		hallmarks of AD in post-
		mortem brains [228]
S100A9 S100 calcium	See Calprotectin	Low CSF S100A9 and beta-
binding protein A9	S100A9 is also required for	amyloid levels in AD
	the maturation of TLR3,	correlate with each other
	which recognises viral	[230]
	double standed RNA in the	
	endosomal compartment of	
	macrophages [229].	
S100A11 S100 calcium	Expression increased in the	Upregulated in the
binding protein A11	blood of infectious	hippocampus [29]
	myocarditis patients	
	(staphylococcal IE and	
	streptococcal) [2,231]	
S100A12 S100 calcium	S100A12 has antifungal	S100B, S100A9 and

1: 1:		G100 A 12 1 G100 A 0
binding protein A12	activity against Candida	S100A12, but not S100A8,
	albicans, C. krusei, C.	were consistently associated
	glabrata and C. tropicalis and	with the neuropathological
	Listeria monocytogenes but	hallmarks of AD in post-
	not Escherichia coli K-12 or	mortem brains [228]
	Pseudomonas	Upregulated in the
	aeruginosa[232]. Induced in	hippocampus [29].
	response to H. pylori	
	infection and inhibits	
	bacterial growth by binding	
	nutrient zinc [224].	
S100B S100 calcium binding	Pathogenic bacteria increase	Low serum S100B levels in
protein B	S100B expression in human	AD patients [237].
	enteric glial cells where	S100B, S100A9 and
	S100B integrates bacteria-	S100A12, but not S100A8,
	induced Toll-like receptor	were consistently associated
	signalling [233]. Forms	with the neuropathological
	complexes with TLR2	hallmarks of AD in post-
	ligands, particularly fungal	mortem brains [228]
	RNA and inhibits TLR2 via	
	AGER (advanced	
	glycosylation end product-	
	specific receptor), dampening	
	pathogen-induced	
	inflammation. In addition,	

upon binding to nucleic	
acids, S100B activates	
intracellular toll receptors	
which feedback to inhibit	
S100B transcription [234].	
Low blood levels of S100B	
are a marker for invasive	
aspergillosis [235]. S100B	
expression is reduced in	
Borna virus-infected brains	
and no upregulation of the	
expression of S100B, or	
RAGE, was observed in the	
persistently infected brains	
even when incited with	
several inflammatory stimuli,	
including lipopolysaccharide	
[236].	
Recognises peptidoglycan, a	Upregulated in the
component of bacterial cell	hippocampus [29]
walls and acylated	
lipoproteins	
as a heterodimer with	
TLR2[238,239].	
cotransfection of TLR2-	

TLR1 toll like receptor 1

TLR1 or TLR2-TLR6 required for the activation induced by H. pylori LPS preparations [240]. agonists of TLR1/2, TLR3, TLR4 and TLR9 increase the phagocytosis of encapsulated Cryptococcus neoformans [241].P.Gingivalis fimbriae use TLR1 or TLR6 for cooperative TLR2-dependent activation of transfected cell lines while the bacterial lipopolysaccharide prefers TLR1 [242].TLR1/TLR2 dimers recognise Borrelia burgdorferi [243]. Borna disease virus nucleoproteins and host NFKB1 share a common ankyrin-like motif. When THP1-CD14 cells were pre-treated with the viral nucleoprotein, NFKB1 activation by Toll-like receptor ligands was

	suppressed (for TLR1/2;	
	TLR4; TLR2/6; TLR2;	
	TLR7/8). [244].	
TLR10 toll like receptor 10	Involved in the response to	Upon Aβ stimulation, AD
	influenza infection [245]. A	PBMCs generally down-
	TLR2/TLR10 heterodimer	regulated TLR ratios,
	functions in H. pylori	whereas control PBMCs up-
	lipopolysaccharide and	regulated TLR ratios. TLR3,
	Listeria monocytogenes	TLR4, TLR5, TLR7, TLR8,
	recognition[246,247].	TLR9, and TLR10 ratios
		exhibited the greatest
		difference between patients
		and control subjects [248]
TLR2 toll like receptor 2	TLR2 and TLR4, acting via	TLR2 and TLR4 expression
	the adapter protein MyD88,	are increased in AD
	signal responses to	peripheral blood
	Cryptococcus neoformans,	mononuclear cells [266]
	Aspergillus fumigatus and	
	Candida albicans [249].	
	TLR2 and TLR4 are	
	activated by H.Pylori [250].	
	Activated by herpes simplex	
	(HSV-1) and Listeria	
	monocytogenes in microglial	
	cells [251,252] Activated by	

Porphyromonas gingivalis [253]. Stimulated by the hepatitis C core protein [254]. TLR2 is induced by Haemophilus influenza (bacterium) [255] . TLR2 and TLR9 synergistically stimulate innate antiviral activities, thereby protecting against HSV infection in the brain[256]: TLR2 TLR4 and TLR9 ligands promote the microglial uptake of betaamyloid [257] . Amyloids from bacterial curli fibrils (from E. coli, Salmonella, and some Enterobacteriales)activate TLR2 [258]: TLR2 recognizes many microbial components. including lipoproteins/lipopeptides from various pathogens, peptidoglycan and lipoteichoic acid from Grampositive bacteria,

lipoarabinomannan from mycobacteria, glycosylphosphatidylinositol anchors from Trypanosoma cruzi, modulin from Staphylococcus epidermis, zymosan from fungi and glycolipids from Treponema maltophilum, and lipopolysaccharides preparations from Leptospira interrogans, Porphyromonas gingivalis and Helicobacter pylori [259]. HSV-1 glycoprotein B activates NFκB activation through TLR2/TLR6 but not with TLR1 although it coimmunoprecipitates with TLR1,2 and 6[260] Activated by C.Pneumoniae which also activates TLR4 but to a lesser extent [261,262]. the production of tumor necrosis factor (TNF) α by

	macrophages in response to	
	Toxoplasma gondii	
	glycosylphosphatidylinositols	
	require the expression of both	
	Toll-like receptors TLR2 and	
	TLR4 [263]. Recognises	
	HCMV [264]. Epstein-Barr	
	virus activates TLRs,	
	including TLR2, TLR3, and	
	TLR9 [265].	
TLR3 toll like receptor 3	Recognises double stranded	TRL3- and TLR8-expressing
	viral RNA [267]. Antiviral	Monocytes/macrophages are
	against HSV-1 and	increased in Alzheimer's
	upregulated by the virus in	disease patients and in mild
	neural stem cells, resulting in	cognitive impairment [272]
	beta-interferon induction	
	[268]. TLR3 and TLR4	
	activate cholesterol-25-	
	hydroxylase producing 25-	
	hydroxycholesterol [269],	
	which along with 27-	
	hydroxycholesterol inhibits	
	the replication of enveloped	
	and non-enveloped viruses	
	[270]. TLR3 and TLR9	
	<u> </u>	

	recognise HCMV [271]	
TLR4 toll like receptor 4	Lipopolysaccharide [273]	TLR2 and TLR4 expression
	leptospiral LPS	are increased in AD
	Campylobacter jejuni [274]	peripheral blood
	Helicobacter pylori [250]	mononuclear cells [266].
	C.Neoformans	TLR4 expression increased
	glucuronoxylomannan [275]	in the Alzheimer's disease
		brain in regions of beta-
	TLR2 and TLR4 activation	amyloid deposition[283]
	reduce Hepatitis B infection	
	[276]	
	TLR4 896 A>G increased	
	risk for all parasitic	
	infections (ORG 1.59;	
	95%CI 1.05-2.42), malaria	
	(1.31; 95%CI 1.04-1.66),	
	brucellosis (2.66; 95%CI	
	1.66-4.27), cutaneous	
	leishmaniasis (7.22; 95%CI	
	1.91-27.29),	
	neurocysticercosis (4.39;	
	95%CI 2.53-7.61),	
	Streptococcus pyogenes	
	tonsillar disease (2.93;	
	95%CI 1.24-6.93), typhoid	

fever (2.51; 95%CI 1.18-5.34) and adult urinary tract infections (1.98; 95%CI 1.04-3.98), but was protective for leprosy (0.36; 95%CI 0.22-0.60). TLR4 1196 C>T effects were similar to TLR4 896 A>G for brucellosis, cutaneous leishmaniasis, leprosy, typhoid fever and S. pyogenes tonsillar disease, and was protective for bacterial vaginosis in pregnancy (0.55; 95%CI 0.31-0.98) and Haemophilus influenzae tonsillar disease (0.42; 95%CI 0.17-1.00). The majority of significant associations were among predominantly Asian populations and significant associations were rare among European populations. Hepatitis C viral protein

NS5A downmodulates NKG2D on natural killer cells via the TLR4 pathway [254]. TLR2 and TLR4 activated by HSV-1 in astrocytes [277].P. gingivalis GroEL protein may contribute to cardiovascular disorders by increasing TLR4 expression [278]. P. gingivalis outer membrane vesicles induce strong TLR2 and TLR4-specific responses and moderate responses in TLR7, TLR8, TLR9, NOD1 and NOD2 expressing-HEK-Blue cells [212]. Senses the C.Pneumoniae heat shock protein [279] and a bacterial phospholipase D [280]. Phagocytosis of B. burgdorferi by microglia increases expression of TLR1, -2, 4 and 5 [281]. Induced by HCMV [282]

TLR5 toll like receptor 5	Recognises bacterial flagellin	Upregulated relative to aged
TERES ton fixe receptor 5		
	[284]. Microglia and	controls in the AD
	astrocytes respond to B.	hippocampus and superior
	burgdorferi through TLR1/2	frontal gyrus [287]
	and TLR5. Phagocytosis of	
	B. burgdorferi by microglia	
	increases expression of	
	TLR1, -2, 4 and 5 [281].	
	Toxoplasma gondii- derived	
	profilin triggers human	
	TLR5-dependent cytokine	
	production [285]. HCMV	
	infection potentiates TLR5	
	ligand-stimulated cytokine	
	production [286].	
TLR6 toll like receptor 6	TLR2/TLR6 dimers	NF
	recognise bacterial	
	lipoproteins (from Refseq)	
	but are also activated in	
	response to viral infection	
	(Dengue virus, hepatitis C,	
	HIV-1, influenza, inter alia)	
	[288-291]. HSV-1	
	glycoprotein B activates NF-	
	кВ activation through	

	TLR2/TLR6 but not with	
	TLR1 although it	
	coimmunoprecipitates with	
	TLR1,2 and 6[260].	
	P.Gingivalis fimbriae use	
	TLR1 or TLR6 for	
	cooperative TLR2-dependent	
	activation of transfected cell	
	lines [242]. Involved in	
	responses to B .Burgdorferi	
	outer surface protein A	
	lipoprotein[292].	
TLR7 toll like receptor 7	Senses single stranded RNA	Upregulated relative to aged
	viruses in endosomes [293].	controls in the AD superior
	TLR7 and TLR8 act as	frontal gyrus [287]
	endosomal recognition	
	receptors for a number of	
	ssRNA viruses including	
	influenza, HIV-1, VSV,	
	Sendai virus, coxsackie B	
	virus, coronaviruses (mouse	
	hepatitis virus and severe	
	acute repiratory syndrome	
	coronavirus), and flaviviruses	
	(HCV, dengue virus and	
TLR7 toll like receptor 7	lipoprotein[292]. Senses single stranded RNA viruses in endosomes [293]. TLR7 and TLR8 act as endosomal recognition receptors for a number of ssRNA viruses including influenza, HIV-1, VSV, Sendai virus, coxsackie B virus, coronaviruses (mouse hepatitis virus and severe acute repiratory syndrome coronavirus), and flaviviruses	controls in the AD superior

West Nile virus) [294]. P. gingivalis outer membrane vesicles induce strong TLR2 and TLR4-specific responses and moderate responses in TLR7, TLR8, TLR9, NOD1 and NOD2 expressing-HEK-Blue cells [212]. Borrelia burgdorferi induces the production of type I interferons by human dendritic cells via TLR7 and TLR9. Indoleamine 2,3dioxygenase (IDO1) induction and kynurenine production were mediated by the same TLR7-dependent recognition process [135]. TLR7 stimulates the expression of Epstein-Barr virus latent membrane protein 1in infected cells [295].Epstein-Barr virus inhibits the stimulatory effect of TLR7/8 and TLR9

	agonists in human B	
	lymphocytes enabling	
	evasion of the immune	
	system [296]	
TLR8 toll like receptor 8	An endosomal receptor that	TRL3- and TLR8-expressing
	recognizes single stranded	Monocytes/macrophages are
	RNA viruses such as	increased in Alzheimer's
	Influenza, Sendai, and	disease patients and in mild
	Coxsackie B viruses. Also	cognitive impairment [272]
	recognises bacterial RNA	
	from streptococci [297] and	
	Staphylococcus aureus [298].	
	P. gingivalis outer membrane	
	vesicles induce strong TLR2	
	and TLR4-specific responses	
	and moderate responses in	
	TLR7, TLR8, TLR9, NOD1	
	and NOD2 expressing-HEK-	
	Blue cells [212]. TLR8 is	
	activated by Borrelia	
	burgdorferi RNA in the	
	phagosome of human	
	monocytes[299].	
TLR9 toll like receptor 9	This gene is preferentially	The rs187084 variant
	expressed in immune cell	homozygote GG was

rich tissues, such as spleen, significantly associated with lymph node, bone marrow a decreased AD risk in a and peripheral blood Chinese study. This leukocytes. Studies in mice protective variant related to and human indicate that this increased TLR9 expression receptor mediates cellular in peripheral blood response to unmethylated monocytes [301]. CpG dinucleotides in Transcription of TLR3, bacterial DNA to mount an TLR4, TLR5, TLR7, TLR8, innate immune response. TLR9, and TLR10 following [provided by RefSeq, Jul beta-amyloid stimulation is 2008]. TLR3, TLR7, TLR8, depressed in mononuclear and TLR9 also detect distinct cells of AD patients [248] forms of viral nucleic acids [294].TLR2 and TLR9 protect against HSV-1 infection in the mouse brain [256] P. gingivalis outer membrane vesicles induce strong TLR2 and TLR4specific responses and moderate responses in TLR7, TLR8, TLR9, NOD1 and NOD2 expressing-HEK-Blue cells [212]. Unmethylated

	CpG motifs in Toxoplasma	
	gondii DNA induce TLR9-	
	and IFN-β-dependent	
	expression of DEFA5 in	
	intestinal epithelial	
	cells.[89].Upregulated in	
	dendritic cells by	
	C.Pneumoniae nasal	
	infection [300]	
ZBP1 Z-DNA binding	This gene encodes a Z-DNA	ZBP1 was identified as an
protein 1	binding protein. The encoded	Alzheimer's disease
	protein plays a role in the	susceptibility gene using
	innate immune response by	hippocampal atrophy as a
	binding to foreign DNA and	quantitative Trait [304]
	inducing type-I interferon	
	production. Alternatively	
	spliced transcript variants	
	encoding multiple isoforms	
	have been observed for this	
	gene. [provided by RefSeq,	
	Dec 2011]. ZBP1 recognises	
	foreign DNA in the cytosol	
	and inhibits HSV-1	
	replication[302].HCMV	
	induces the interferon	

response via ZBP1[303].	

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