

Review

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Review

# The Neglected Sibling: NLRP2 Inflammasome in the Nervous System

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**Abstract:** While classical NOD-like receptor pyrin domain containing protein 1 (NLRP1) and NLRP3 inflammasomal proteins have been extensively investigated, the contribution of NLRP2 is still ill-defined in the nervous system. Given the putative significance of NLRP2 in orchestrating neuroinflammation, further inquiry is needed to gain a better understanding of its connectome, hence its specific targeting may hold a promising therapeutic implication. Therefore, bioinformatical approach for extracting information, specifically in the context of neuropathologies, is also undoubtedly preferred. To the best of our knowledge, there is no review study selectively targeting only NLRP2. Increasing, but still fragmentary evidence should encourage researchers to thoroughly investigate this inflammasome in various animal- and human models. Taken together, herein we aimed to review the current literature focusing on the role of NLRP2 inflammasome in the nervous system and more importantly, we provide an algorithm-based protein network of human NLRP2 for elucidating potentially valuable molecular partnerships.

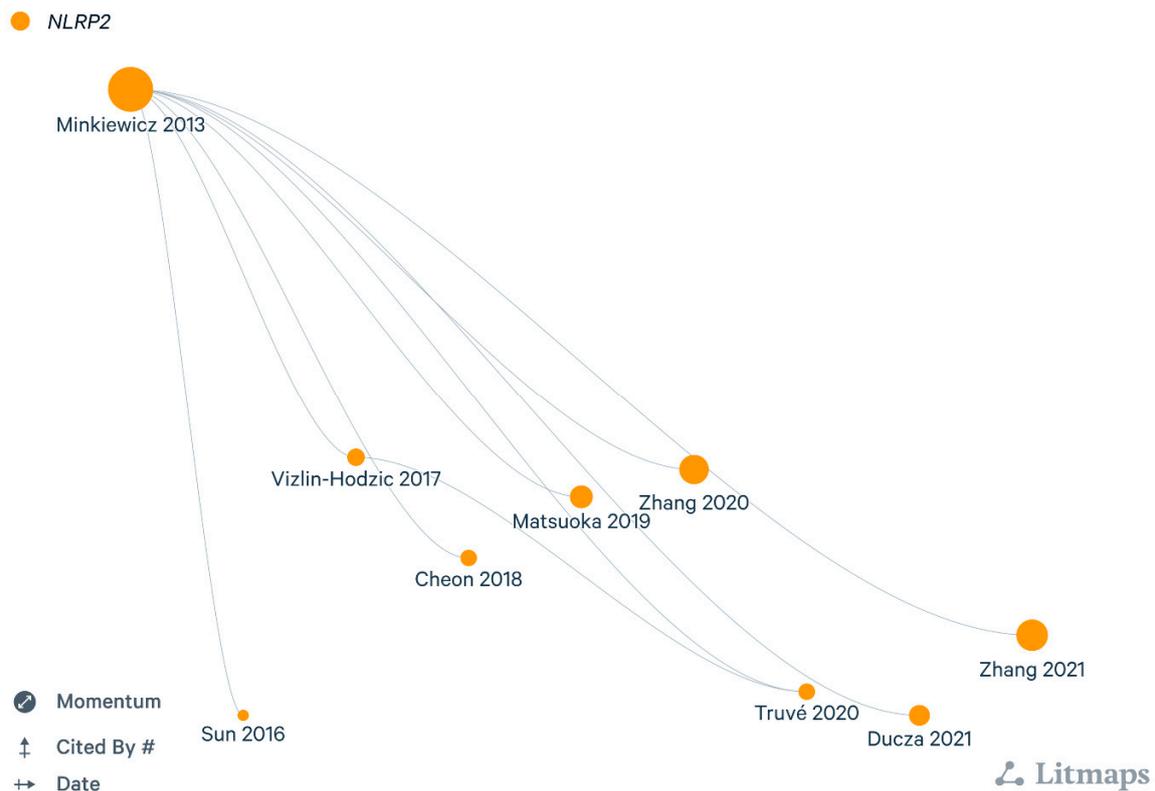
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## 1. Introduction

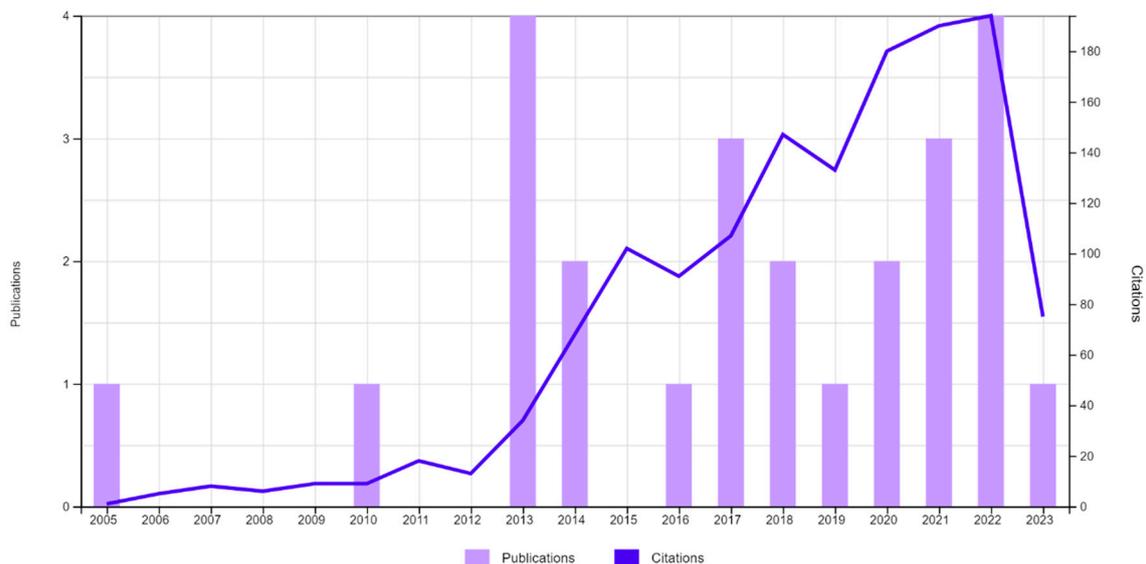
Acute inflammation is a physiological defense mechanism in response to pathogens and cell damages; chronic inflammation however, is considered as a dysregulated maladaptive clinical phenomenon without any recuperative benefits [1]. Chronic inflammation has been associated with many neurological disorders, [2] thus studying inflammasomes is of particular importance. Classically, the currently known canonical inflammasomes (NLRP1, NLRP2, NLRP3, NLRP6, NLRP7, NLRP9, NLRP12, absent in melanoma 2 and pyrin inflammasomes) recruit caspase-1 enzyme, cleaving the zymogen interleukin-1 $\beta$  (IL-1 $\beta$ ), IL-18 or IL-37 to induce lytic pyroptotic cell death and subsequent inflammatory downstream signaling [3–7]. NLRP2 (alternate names: NALP2, PYPAF2, NBS1, PAN1, CLR19.9) inflammasome is an intracellular multimer protein signaling hub assembled by three main elements: (i) a sensory component, termed NLRP, involved in the recognition of Pathogen-Associated Molecular patterns (PAMPs) and Damage-Associated Molecular Patterns (DAMPs), (ii) an adaptor unit, termed Apoptosis-associated Speck-like protein containing a caspase-activation and recruitment domain (ASC, CARD) as well as the (iii) effector caspase-1 enzyme [3,8–11]. NLRP2 activation recruits „function to find” (FIIND) and CARD-containing protein Cardinal that interacts with caspase-1 [12].

Of note, NLRP2 was earlier shown to govern inflammasome signaling by inhibiting nuclear factor kappa B (NF- $\kappa$ B) transcription factor [13,14]. Recent data have indicated that NLRP2 robustly increases the amount of NF- $\kappa$ B regulated cytokines in cystinosis [15]. Moreover, several lines of evidence support the critical regulator role of NLRP2 in the reproductive system, hence NLRP2 gene was reported as one of the mammalian maternal effect genes associated with murine embryogenesis, age-related maternal fertility and idiopathic recurrent miscarriage, respectively [16–18]. Besides, NLRP2 expression was also proven to associate with arsenic-induced skin lesion, chromosomal damages and respiratory disorders as well [19].

Intriguingly, despite the aforementioned past research on non-neural tissues, our gap of knowledge regarding NLRP2 and its connectome in neuropathological context has still yet to be improved (**Figures 1 and 2**). First, the present study focused on the experiments related to NLRP2 inflammasome in human and rodent models by providing a state-of-the-art of the literature. Secondly, a publicly available cutting-edge biomedical database called Search Tool for the Retrieval of Interacting Genes/Proteins (STRING, ver.11.5; string-db.org) [20] was employed to envisage potential protein interactions of NLRP2. Following the results of STRING analysis and Web of Science filtration we selected and described 15 proteins that are involved in neuropathologies, but not experimentally associated with NLRP2 inflammasome.



**Figure 1. Litmaps visualisation of original research articles targeting NLRP2 inflammasome in the nervous system** Articles are shown in display mode "Momentum". Calculation is based on "Cited By" count, weighed by recency.



**Figure 2. Number of publications and citations related to NLRP2 inflammasome in the nervous system (2005-2023)**

## 2. NLRP2 expression in the nervous system

### 2.1. Human NLRP2

For many years it remained elusive whether NLRP2 could be validated as a functional inflammasome in the human nervous system. The pioneering milestone was achieved by Julia Minkiewicz et al. in 2013 [7] by verifying the significance of NLRP2 inflammasome in human cortical astrocyte cultures. They proposed that NLRP2 interacted with ionotropic purinergic receptor X7 (P2X7) receptor and pannexin 1 (PNX1), hence mimicking inflammation with ATP stimulation rapidly resulted in caspase-1 activation and subsequent IL-1 $\beta$  release. Conversely, pharmacological blockade of astrocytic PNX1 and P2X7 receptor with probenecid and Brilliant Blue G (BBG) diminished the ATP-induced NLRP2 activation. In addition, siRNA-based silencing of NLRP2 was also found to disrupt caspase-1 activation, emphasizing its pivotal role in astrocyte immune responses. NLRP2 gene dysregulation was shown to be involved in human fetal brain development indicating a robust difference between cases of bipolar disorder and healthy individuals [21,22]. In line with this, Truvé et al. [23] in 2020 found considerable increase of NLRP2 expression in neural stem and mature cells of patients suffering from bipolar disorder.

### 2.2. Rodent NLRP2

To date, still more NLRP2 related experimental data are accessible from rodent models. Several rodent models are continuously used in drug development pipelines, but regrettably the limitations of these concepts are major hindrances to translation attempts from bench to bedside. Few years previously Sun et al. in 2016 [24] have already determined NLRP2 distribution at specific areas of the murine central nervous system. Low constitutive NLRP2 levels were observed in the cortex, hippocampus and striatum, which were significantly elevated following occlusion of middle cerebral artery mimicking ischemic stroke. Similar results were obtained in primary astrocyte cultures upon oxygen-glucose deprivation. These findings were further corroborated by Cheon et al. in 2018 [25], who searched the interaction of apoptosis signal-regulating kinase 1 (ASK1) protein with astroglial NLRP2 inflammasome after ischemic stroke. ASK1 inhibition effectively downregulated NLRP2, as well as proinflammatory cytokine release in murine model and cultured astrocytes. In former studies, NLRP1 and NLRP3 inflammasomes were recognised in neuropathic models and spinal injury [26–29], but only scanty data were provided about NLRP2 protein following peripheral inflammation. Matsuoka and his colleagues in their study [30] characterised NLRP2 inflammasome in NeuN- and peripherin positive dorsal root ganglia (DRG) cells of C-fibers implying its significant role in nociceptive processing. They found that both siRNA gene silencing of NLRP2 expression and pharmacological blockade of caspase-1 prevented nociceptive hypersensitivity, measured in two peripheral inflammatory models using either complete Freund adjuvant (CFA)- or ceramide. Their data did not support possible activation of matrix metalloproteinase enzyme 9 or other inflammasome types except NLRP2, therefore they hypothesized that caspase-1 enzyme in DRG neurons worked presumably in NLRP2-dependent manner. Enigmatically, inhibition of caspase-1 and siRNA silencing of NLRP2 attenuated mechanical, but not thermal hypersensitivity upon inflammation. This finding can be explained by the low NLRP2 level in thermal sensor transient receptor potential vanilloid subtype-1 positive neurons.

Our workgroup also investigated the putative changes of NLRP2 expression in CFA- induced inflammatory pain model within the spinal dorsal horn [31]. Although, NLRP1, NLRP2 and NLRP3 inflammasomes have been all detected in astrocytes of different brain areas [32], our results showed that dorsal horn astrocytes mainly expressed NLRP2, and colocalisation was entirely lacking between NLRP1 and astrocytes. With protein blot analysis we also verified a robust increase of NLRP2 protein in spinal cord tissue lysates upon CFA injection. Not unexpectedly, the role of astroglial NLRP2 has also been reported in chronic mild stress induced depression [33], where they introduced an

intraperitoneal injection of tryptophane derived metabolite kynurenine (Kyn), which upregulated NLRP2 in hippocampal primary astrocytes cultures. Simultaneously, Kyn treatment aided nuclear translocation of NF $\kappa$ B to promote NLRP2 transcription, eventually leading to inflammasome activation. These findings also illustrated that Kyn elicited depressive behaviour was eliminated following astrocytic NLRP2 knockdown, proposing a crucial role for NLRP2 in depressive behaviours.

Recently, the role of NLRP2 inflammasome has been elucidated in murine Alzheimer's disease [34]. In this study, glucagon-like peptide-1 (GLP-1) receptor agonist exenatide attenuated neuroinflammation in piriform cortex resulting in cognitive improvement of 5x FAD transgenic mice. Additionally, upon exendine-4 treatment of cultured astrocytes, lower amyloid  $\beta_{1-42}$  level was detected confirming the reduced inflammation and oxidative stress presumably via downregulation of NLRP2 inflammasome.

### 3. Human NLRP2 connectome with STRING database

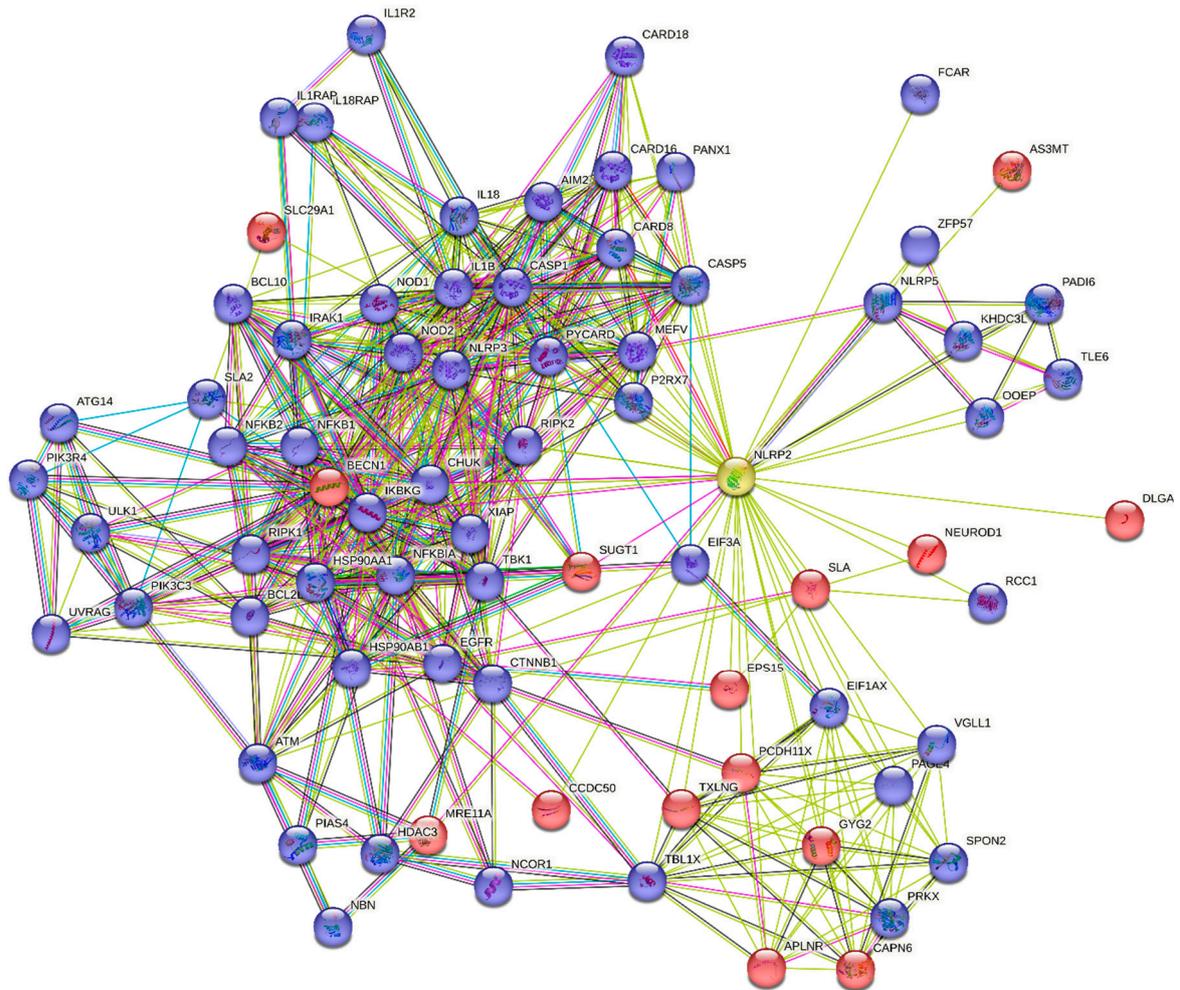
STRING (version 11.5; string-db.org) is a freely accessible online biological web resource. The query service of the platform was initiated with the following input: "NLRP2", species: "Homo sapiens". NLRP2 connectome was generated by our parameters that were as follows: full-STRING network (containing both functional and physical interactions), evidence-based network edges (types of interactions are shown with different line colors) with a cut-off interaction confidence score: 0.4. For data visualisation all the interaction sources were collected: textmining, experiments, databases, coexpression, neighbourhood, gene fusion, cooccurrence.

Based on our settings the network statistics of NLRP2 connectome involve 76 nodes (with an average node degree: 13.3), 504 edges, with a PPI enrichment p-value < 1.0e-16 (**Figure 3**). From the direct interactions of NLRP2 (45 nodes, **Table 1**), due to spatial limitations, possible functional partners with relevant role in neurological disorders (15 nodes), are introduced (in the order of their interaction score) in the **Supplementary information (3.1.-3.15, Table S1)**. Here, we focused on those items that were either not experimentally investigated earlier with NLRP2 protein or not reviewed here.

**Table 1.** List of direct interactions of NLRP2

	Node protein hits	Full name	Interaction score
1	CASP1	Caspase-1	0.862
2	PYCARD	Apoptosis-associated speck-like protein containing a CARD	0.825
3	CASP5	Caspase-5	0.811
4	MEFV	Pyrin	0.798
5	CARD8	Caspase recruitment domain-containing protein 8	0.771
6	SLA	Src-like-adapter; Adapter protein	0.752
7	KHDC3L	KHDC3-like protein; KH domain containing 3 like, subcortical maternal complex member	0.739
8	BECN1	Beclin-1	0.664
9	AIM2	Interferon-inducible protein AIM2	0.645
10	P2RX7	P2X purinoceptor 7; Receptor	0.638
11	CARD16	Caspase recruitment domain-containing protein 16	0.629
12	PANX1	Pannexin-1	0.600
13	IL18	Interleukin-18	0.597

	<b>Node protein hits</b>	<b>Full name</b>	<b>Interaction score</b>
14	SLA2	Src-like-adaptor 2; Adapter protein	0.590
15	PAGE4	P antigen family member 4	0.575
16	EIF1AX	Eukaryotic translation initiation factor 1A	0.567
17	IL1B	Interleukin-1 beta	0.563
18	ZFP57	Krab domain-containing zinc finger protein	0.563
19	VGLL1	Transcription cofactor vestigial-like protein 1	0.562
20	CHUK	Inhibitor of nuclear factor kappa-B kinase subunit alpha	0.560
21	NLRP5	NACHT, LRR and PYD domains-containing protein 5	0.556
22	PCDH11X	Protocadherin-11 X-linked; Potential calcium-dependent cell-adhesion protein	0.547
23	GYG2	Glycogenin-2	0.515
24	OOEP	Oocyte-expressed protein homolog	0.514
25	MRE11A	Double-strand break repair protein MRE11	0.490
26	TLE6	Transducin-like enhancer protein 6	0.487
27	SUGT1	SGT1 homolog, MIS12 kinetochore complex assembly cochaperone	0.485
28	RIPK2	Receptor-interacting serine/threonine-protein kinase 2	0.473
29	SPON2	Spondin-2	0.471
30	IKBKG	NF-kappa-B essential modulator	0.470
31	EPS15	Epidermal growth factor receptor substrate 15	0.468
32	NEUROD1	Neurogenic differentiation factor 1	0.466
33	CAPN6	Calpain-6	0.462
34	PRKX	cAMP-dependent protein kinase catalytic subunit PRKX	0.456
35	TXLNG	Gamma-taxilin	0.455
36	DLGAP2	Disks large-associated protein 2	0.449
37	APLNR	Apelin receptor	0.445
38	SLC29A1	Solute carrier family 2	0.444
39	CARD18	Caspase recruitment domain-containing protein 18	0.437
40	AS3MT	Arsenite methyltransferase	0.423
41	CCDC50	Coiled-coil domain-containing protein 50	0.421
42	TBL1X	F-box-like/WD repeat-containing protein TBL1X	0.418
43	PADI6	Protein-arginine deiminase type-6	0.418
44	FCAR	Immunoglobulin alpha Fc receptor	0.408
45	RCC1	Regulator of chromosome condensation	0.400



**Figure 3.** The extended STRING connectome of NLRP2 protein. Color code is as follows: known interactions: light blue, from curated databases; magenta, experimentally determined; predicted interactions: green, gene neighbourhood; dark blue, gene co-occurrence; others: lime, text-mining; black, coexpression; purple, protein homology. Red colour indicates the selected 15 nodes potentially involved in neuropathologies.

#### 4. Discussion and future prospects

To date, neurodegenerative disorders lack effective therapeutic agents or programs to prevent, efficiently influence or at least decelerate disease progression. Moreover, the rise in absolute numbers of people afflicted far and wide proposes that management of main neurological disorders is globally inadequate and these people pose a significant socioeconomic burden owing to disability, illness and premature death [191,192].

Unquestionably, inflammasome signaling is affected in several neuroinflammation-based neurodegenerative disorders including AD, PD or HD that attract more increasing attention in studies investigating their place in clinical practice. Specifically, the NLRP3 inflammasome has been meticulously investigated in this context [193,194], but recently, role of other inflammasomes as pathological drivers in brain diseases was also conceptualised by Anna Chiarini et al [22]. This attempt markedly indicates that there is an urgent need to extend our comprehension regarding neurodegenerative mechanisms associated with inflammasomes other than NLRP3.

First, in this study we attempted to encompass the literature focusing on the expression and distribution of NLRP2 inflammasome in human and rodent neuropathological disorders (**Figure 4**). Taken together, in these models major NLRP2 expression was upregulated in primary astrocyte cultures [7,24,25,33,34], as well as in astrocytes of rodent spinal dorsal horn, respectively [31]. Beyond

the astrocytes the role of NLRP2 was also verified in NeuN- and peripherin positive mechanical, but not thermal sensor subsets of DRG cells by Matsuoka et al [30]. Furthermore, tissue distribution of NLRP2 protein was observed not only in adult cortex, hippocampus, striatum or spinal cord [24,31], but in neural stem cells as well [23].

Regarding activatory stimuli, particular attention is given to purinergic signaling in human NLRP2 inflammasome activation, hence ATP is a well-known and adeptly characterised DAMP that facilitates inflammasome activation upon trauma [195]. Indeed, exogenous stimulation with ATP activates NLRP2 inflammasome resulting in caspase-1 mediated production of mature IL-1 $\beta$  [7]. According to all indications, ATP acts on P2X7 receptor that cooperates with PNX1, hence application of P2X7 receptor inhibitor BBG and PNX inhibitor probenecid diminishes NLRP2 activation. Nevertheless, it is important to underline that P2X4 receptor has been found to be functionally coupled with P2X7 receptor and pannexin-1 in NLRP3 inflammasome of gingival epithelial cells [196,197]. Overall, these observations are in accordance with findings reported by another group who found that heme, released following hemolysis or cell damage, activates NLRP3 inflammasome in macrophages via P2X7 and P2X4 signaling [198]. We speculate that this easily might be the case with NLRP2 inflammasome as well, however there are no experimental data that would confirm this hypothesis. In our earlier article we came up with the idea that overexpression of astroglial NLRP2 in spinal dorsal horn might be associated with their significant P2X4 upregulation as a consequence of intraplantar CFA injection [31,199]. Other triggering stimulus of NLRP2 activation is ischemic stroke, evoked experimentally by occlusion of middle cerebral artery mimicked in astrocyte cultures by oxygen-glucose deprivation [24]. Unsurprisingly, mounting evidence suggests that astrocyte-mediated inflammation may be potentially involved in the pathogenesis of mental disorders such as depression [200,201]. In their recent study, Zhang et al [33] found that tryptophan metabolite Kyn, that was deemed as a specific biomarker of depressive behaviours, upregulated NLRP2 inflammasome in astrocytes, which was supported by other observations also reporting significantly elevated levels of proinflammatory cytokines [202]. In bipolar disorder, neuroinflammatory biomarkers of cerebrospinal fluid were found to associate with cognitive decline. Moreover, persistent cognitive impairment is increasingly recognised in people suffering from bipolar disorder, suggesting a link between neuroinflammation, neurodegenerative states and mood abnormalities [203], which may be significantly modulated by NLRP2 inflammasome [21–23].

Secondly, the present study collects the connectome of NLRP2, envisaged with STRING platform. The obtained set of proteins were further filtered to 15 possible protein interactors involved in the disorders of the nervous system; their pathophysiological roles are discussed in details in **Supplementary Information, Table S1**. Many of these potential partnerships have not been earlier experimentally investigated. Beside, signaling of NLRP2 inflammasome also lacking from the collection of the Kyoto Encyclopedia of Genes and Genomes (KEGG) database **Figure S1**.

Concluding the revised literature and STRING based matches we hypothesize that the filtered NLRP2 connectome influences a plethora of molecular processes in neurons, such as glutamatergic excitotoxicity, apoptosis/ survival signaling and neuroinflammation.

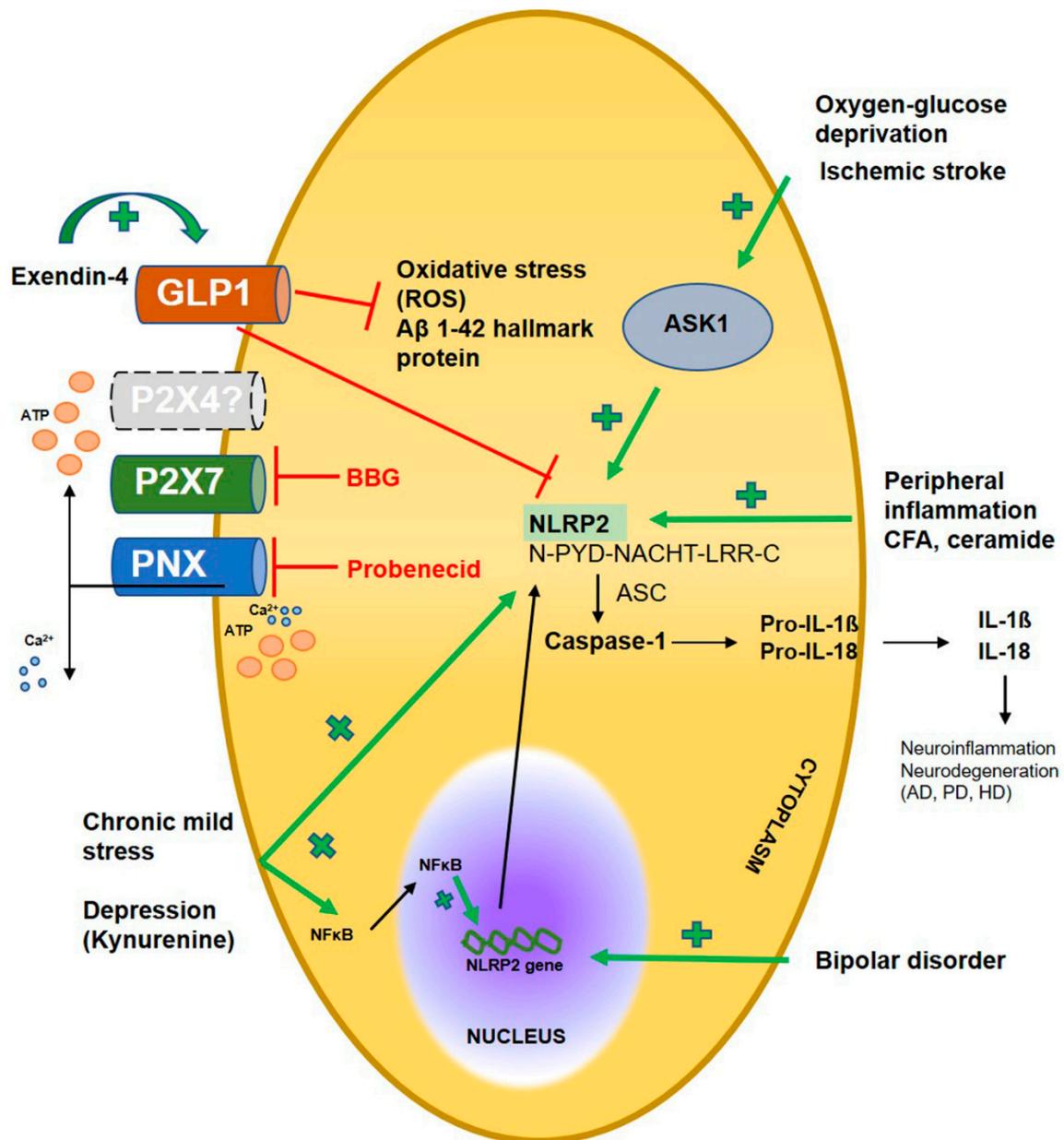
**Glutamatergic excitotoxicity** - The integrity of glutamatergic signaling is essential for preserving neuronal homeostasis and evade neurodegeneration. SLA1 prevents glutamatergic excitotoxicity by degrading excessive NMDA receptors [35]. As a synergist, apelin also disrupts NMDA receptor-mediated excitotoxicity in rat hippocampus through survival kinases AKT and Raf/ERK-1/2 [143]. Furthermore, the role of DLGAPs is to anchor glutamate receptors in the postsynaptic membrane and to link them with other proteins including other glutamate receptors, signaling- and cytoskeletal factors while regulating both ionotropic and metabotropic glutamate receptors via synaptic scaling [119–122]. Low DLGAP2 expression was detected in age-related cognitive decline and AD [131], which may relate to other findings, such as low spine density or reduced excitatory postsynaptic current, revealed in orbitofrontal cortex of DLGAP2 knockout mice [126,128]. Directed expression bHLH transcription factor NEUROD1 stimulates neuronal maturation and integration as well as ameliorates deficits of dendritic spine density in hippocampal neurons of APPxPS1 model of AD [95]. Besides, ENT1 inhibitor J4 mitigates the damages of long-term

potentiation, excitatory synaptic expression as well as GSK-3 $\beta$  or PKA signaling of neuronal plasticity and alleviate memory deficits in APP/PS1 model of AD [165].

**Apoptosis/survival signaling-** It is of particular importance to gain a better understanding on the signaling of neuronal apoptosis/survival in neurodegenerative states. Impairment of autophagy via reduction of BECN1 level results in overproduction of microglial IL-1 $\beta$  and IL-18 proinflammatory cytokines in AD patients. Deficits of BECN1 mediated phagocytosis causes dysfunctional recruitment of phagocytic receptors CD36 and Trem2 that may associate with extracellular accumulation of A $\beta$  plaques and other cellular debris. Recently, in early phase of HD BECN1 administration has successfully cleared mutant HTT accumulation and reversed progrediation [42–46]. Apelin exerts positive impacts on redox homeostasis and prevents mitochondrial cytochrome c release and caspase-3 activation in cultured murine cortical neurons [142]. Furthermore, EPS15 participates in the EGF-AKT pathway mediated pro-survival cell signaling reduced in dopaminergic neurodegeneration [82,83]. CCDC50 autophagy receptor inhibits inflammatory responses by disrupting NLRP3 [186,187] and prevents EGFR downregulation as well as regulate NF- $\kappa$ B, Fas and interferon signaling. As exposure, in contrast, triggers apoptosis of cerebellar neurons via activation of JNK and p38MAPK signaling [171] as well as upregulates Bax and decreases Bcl-2 factor [181]. A rescue factor SUGT1, functioning as a chaperone protein/heat shock protein, was also recognised to counteract pathological aggregation of  $\alpha$ -synuclein and neurotoxicity in PD. SUGT1 mRNA was highly elevated in fronto-temporal cortex in human PD [74,75]. Its significance has been earlier described in AD, hence decreased SUGT1 immunopositivity was found in degenerating neurons of AD patients [76].

Dysregulation of aforementioned GSK-3 signaling, inhibited by PDK1/AKT kinase [204,205], contributes to the hyperphosphorylation of tau protein as well as A $\beta$ -induced cell death in AD pathogenesis. Abundant GSK-3 level was found in postmortem brain of AD patients, moreover large body of evidence support that GSK-3 activator lysophosphatidic acid associates with AD biomarkers A $\beta$ , total tau and phospho-tau [56,58]. In contrast, GSK-3 inhibits ER stress sensor  $\gamma$ -TXLN, promoting apoptosis- and autophagy emphasized by the fact that blockade of  $\gamma$ -TXLN alone may lead to tau hyperphosphorylation in AD [116].

**Neuroinflammation-** Several key mechanisms have been identified in neurodegenerative diseases as summarized above, also including neuroinflammation, which evokes a great challenge to clinical practice. Neuroinflammation has been recognised in dementia and is typically linked to cognitive decline with elevated levels of proinflammatory markers (IL-1, IL-6, IL-8, C-reactive protein) in patients suffering from dementia [206–208]. However, recent data suggest that inflammatory proteins may express both pro- and anti-inflammatory actions making the interpretation even more difficult in complex neurodegenerative states [209]. In fact, the versatility of postmortem samples as well as challenges of appropriate resolution in detection of cytokines taken from patient samples may all lead to controversial conclusions [210,211]. Indeed, neuroinflammation is still regarded as one of the crucial molecular processes of dementia, but we still do not know whether this mechanism is consequential or causative, in regards of neurodegenerative progrediation. Of note, it receives growing evidence that neuroinflammation may appear as an early temporal red flag event that may link to other mechanisms in contributing to neuropathologies [212–214].



**Figure 4. State-of-the-art in relation to NLRP2 protein in neuropathologies.** ASC: Apoptosis-associated Speck-like protein containing a caspase-activation and recruitment domain, **ASK1**: Apoptosis signal-regulating kinase 1, **BBG**: Brilliant Blue G, **GLP-1**: Glucagon-like peptide-1, **NFκB**: Nuclear factor kappa B, **P2X4**, **P2X7**- P2X purinoreceptor X4,7, **PNX1**-Pannexin-1, **ROS**-reactive oxygen species

In fact, neuroinflammation and generally the therapeutic potential of targeting inflammasomes has been increasingly recognised in neurodegenerative conditions since 2013, when Heneka et al. [215] proved the significance of NLRP3 inflammasome with *nlrp3*<sup>-/-</sup> mice in AD. Since then many efforts have been made to seek selective and potent NLRP3 inhibitors, because the currently US Food and Drug Administration (FDA) approved inhibitors of multiple inflammatory diseases include only canakinumab, anakinra and riloncept. Nevertheless, these inhibitors do not cross efficiently the blood-brain barrier and lack proper pharmacokinetic properties [216,217].

A great achievement was reached when a potent diarylsulfonylurea compound MCC950 (also termed as CRID3, CP-456773), endowed with NLRP3 selectivity, showed therapeutic improvement in several preclinical models such as experimental autoimmune encephalomyelitis, AD and PD, respectively [218–221]. In the search for new inhibitors Stavudine (d4T), acting as an inhibitor of

nucleoside reverse transcriptase, has been published recently to downregulate NLRP3 activation in AD also suppressing caspase-1 activity [222]. Furthermore, Gastaldi et al. [223] by applying the pharmacophore-hybridization method synthesised and screened several benzo[d]imidazole-2-one derivatives to test their inhibitory effect on NLRP3 evoked pyroptosis and IL-1 $\beta$  production.

However, it is increasingly becoming clear that NLRP3 is not the only inflammasome involved in neurodegenerative states. Notably, Kaushal et al. [224] has already reported elevated mRNA level of NLRP1 and highlighted the causative role of NLRP1-caspase 1-caspase-6 signaling in the accumulation of A $\beta$ <sub>42</sub> deposits in AD.

In contrast, as NLRP3 and NLRP1 “steal” the show from NLRP2 although it has already been justified in human neuropathologies, till today no effective and specific pharmacological blockers have been designed. Hopefully, in the coming years focus will be also placed on the development of NLRP2 inhibitors by the representatives of industry and academia.

## 5. Conclusions

Taken together, NLRP2 inflammasome based on STRING analysis may cooperate with at least 15 proteins earlier described in neurological disorders, which are associated with the derangement of excitotoxicity, cellular apoptosis/survival and neuroinflammation. Thus, the context of this filtered connectome in the nervous system requires an experimental approach both in rodent and human models. In the future, complete understanding of inflammasome signaling including NLRP2 mediated processes may open up new prospects for efficient inhibitors and/or therapeutic agents, which are currently lacking from our armamentarium.

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**Author Contributions:** Conceptualization: LD Manuscript writing, data visualisation, editing and supervision: LD, BG. All authors have read and agreed to the published version of the manuscript.

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