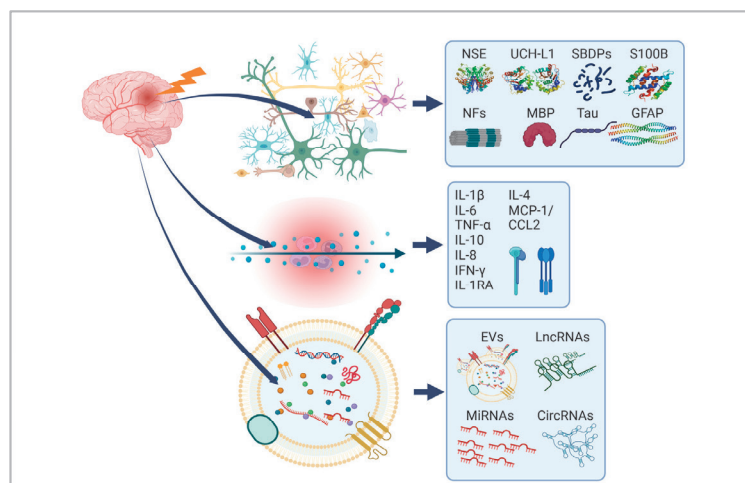


# Unveiling the predictive power of biomarkers in traumatic brain injury: A narrative review focused on clinical outcomes

Sitao Liang, Zihui Hu

Traumatic brain injury (TBI) has long-term consequences, including neurodegenerative disease risk. Current diagnostic tools are limited in detecting subtle brain damage. This review explores emerging biomarkers for TBI, including those related to neuronal injury, inflammation, EVs, and ncRNAs, evaluating their potential to predict clinical outcomes like mortality, recovery, and cognitive impairment. It addresses challenges and opportunities for implementing biomarkers in clinical practice, aiming to improve TBI diagnosis, prognosis, and treatment.

## BIOMARKERS IN TRAUMATIC BRAIN INJURY



This graphical abstract shows the diverse TBI biomarkers involved in key processes such as neuronal and glial injury, axonal damage, inflammation, and molecular signaling via extracellular vesicles and non-coding RNAs.

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## Graphical Abstract

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**Key words:** traumatic brain injury, biomarkers, extracellular vesicles, non-coding RNAs, clinical outcomes

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## INTRODUCTION

Traumatic brain injury (TBI) results from external forces impacting the brain, often involving direct trauma, acceleration/deceleration, or rotational forces. This complex interplay generates inertial forces that disrupt brain tissue and cells, leading to a cascade of neurological dysfunction<sup>1</sup>. TBI is a major public health concern, with the highest incidence among common neurological disorders, and poses a substantial global burden. Although traditionally seen as an acute condition, TBI is increasingly recognized for its chronic effects, including a higher risk of neurodegenerative diseases<sup>2</sup>. In 2019, there were 27.16

million new cases and 48.99 million prevalent cases of TBI, leading to 7.08 million years lived with disability (YLDs) (ref.<sup>3</sup>). Despite moderate-to-severe TBI often causing lasting functional impairment, outcomes vary widely among individuals with similar injuries, ranging from full recovery to severe disability or death<sup>4,5</sup>. This variability underscores the need for individualized treatment strategies, recognizing the unique patterns of impairments and their evolution over time<sup>5</sup>.

TBI is not a singular event but a complex cascade of pathological processes. The initial impact triggers a chain reaction of secondary injuries, characterized by molecular and cellular responses that persist long after the initial

trauma. These secondary injuries lead to neuronal and astroglial damage, axonal disruption, and inflammation, ultimately contributing to the long-term consequences of TBI. Understanding these intricate processes is crucial for developing effective neuroprotective and therapeutic interventions<sup>6</sup>. Currently, TBI diagnosis relies on the Glasgow Coma Scale (GCS), a clinical assessment tool that classifies TBI severity based on the patient's level of consciousness. The GCS categorizes injuries as severe (GCS 3–8), moderate (GCS 9–13), and mild (GCS 14–15) (ref.<sup>7</sup>). However, despite the use of advanced imaging techniques like CT and MRI, predicting long-term outcomes remains challenging. These methods often fail to detect diffuse axonal injury (DAI), a common TBI characterized by widespread shearing of nerve fibers, which significantly impacts long-term prognosis<sup>8</sup>. Biomarkers offer a promising avenue for improving TBI diagnosis, prognosis, and treatment monitoring. They can reveal injury-induced cellular, biochemical, and molecular changes, often detecting early microlesions that conventional imaging techniques miss<sup>9</sup>. By integrating biomarkers with clinical examination and imaging, clinicians can achieve more accurate severity assessment, predict outcomes more reliably, and evaluate treatment responses effectively<sup>10</sup>. The development of reliable biomarkers is crucial for early and accurate TBI diagnosis, paving the way for timely and effective interventions. The absence of such biomarkers currently limits our ability to provide optimal care for patients with TBI.

This narrative review aims to explore the predictive power of biomarkers in TBI, focusing on their ability to forecast clinical outcomes. We will examine the current landscape of biomarker research, analyzing biomarkers related to neuronal injury, inflammation, extracellular vesicles, and non-coding RNAs. We will critically evaluate the evidence on their predictive value for clinical outcomes, such as mortality, functional recovery, long-term disability, and cognitive impairment. Additionally, we will discuss the challenges and opportunities associated with biomarker use in clinical practice and provide recommendations for future research. By synthesizing current knowledge and highlighting future directions, this review seeks to illuminate the potential of biomarkers as valuable tools for improving TBI diagnosis, prognosis, and personalized treatment strategies.

## BIOMARKERS IN TRAUMATIC BRAIN INJURY: A DIVERSE LANDSCAPE

TBI can be classified as mild, moderate, or severe. Mild TBI (mTBI), often caused by head impacts resulting in rotational acceleration of the brain, can also occur without direct impact, such as in motor vehicle crashes with rapid head rotation. While mTBI typically does not produce visible brain damage, it can lead to rapid neurophysiological and neurological dysfunction that often resolves quickly. However, persistent cognitive dysfunction can occur in up to 15% of individuals<sup>11–13</sup>.

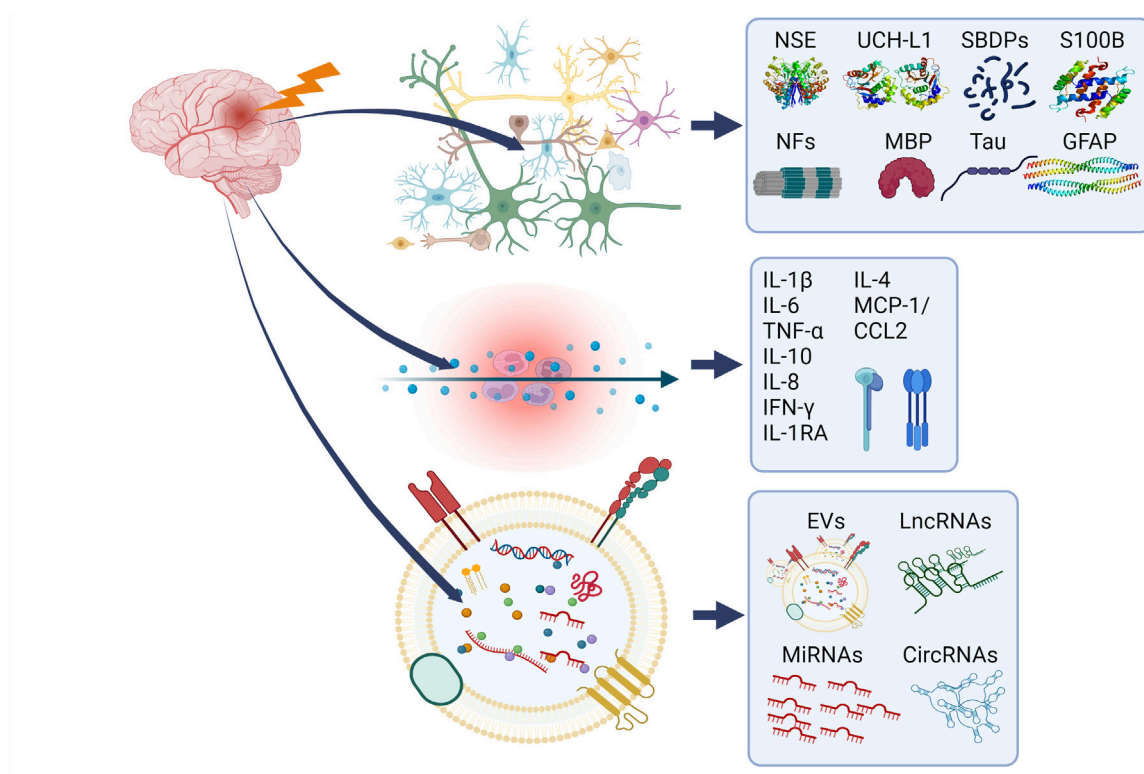
TBI pathogenesis involves two distinct phases: the primary injury, occurring immediately upon impact,

and the secondary injury, encompassing the body's attempts to limit and repair the damage<sup>14,15</sup>. The initial impact causes necrosis, tissue deformation, and shearing of neurons, axons, and glial cells, leading to excitotoxicity, oxidative damage, and cerebrovascular disturbances<sup>16</sup>. Complications include reduced mitochondrial respiration, lipid damage, activation of apoptotic and non-apoptotic cell death pathways, and initiation of inflammatory and protein degradation cascades<sup>17,18</sup>. The initial injury also disrupts the blood-brain barrier (BBB), increasing permeability and allowing further cellular damage and inflammation<sup>19,20</sup>. TBI-induced injury disrupts cerebral vascular autoregulation, leading to an imbalance between cerebral blood flow and metabolism, resulting in cerebral oxygen deprivation (ischemia). This triggers mitochondrial dysfunction, increased lactate levels, elevated intracellular calcium (Ca<sup>2+</sup>) ions, and reduced ATP production, contributing to the failure of ATP-dependent ion pumps and impaired glutamate uptake<sup>21</sup>. The initial injury sets off a cascade of secondary events, initiated by the release of glutamate from damaged neurons. Glutamate triggers edema, pro-inflammatory cytokine release, and further ischemia, perpetuating the cycle of damage<sup>1,16</sup>. TBI-induced metabolic changes affect amino acid, carbohydrate, and lipid metabolism, impacting both brain and other organ functions<sup>22</sup>. These complex processes manifest in a range of clinical symptoms, from motor deficits to debilitating neurocognitive and personality changes<sup>23</sup>.

An ideal and reliable fluid biomarker for TBI, as proposed by Wang et al.<sup>6</sup>, should possess several key characteristics to be truly effective. First, it should be released upon injury, meaning that head trauma triggers its release into readily accessible bodily fluids, allowing for non-invasive detection. Second, the biomarker should exhibit elevated levels in TBI patients compared to healthy individuals. Third, its concentration should correlate with the severity of the TBI, both quantitatively and qualitatively. Finally, the biomarker's levels should align with findings from other clinical diagnostic tools, such as the Glasgow Coma Scale (GCS), CT scans, and MRI. Fig. 1 provides an overview of diverse TBI biomarkers, each reflecting a specific aspect of the injury process. These biomarkers encompass markers of neuronal, axonal, myelin, and glial cell damage, inflammatory responses, extracellular vesicles, and a variety of non-coding RNA species.

## Neurological biomarkers in traumatic brain injury

A range of protein biomarkers have emerged as potential indicators of TBI, each reflecting damage to specific neurological structures. These include markers for dendrites (MAP2), neuron cell bodies (UCH-L1, NSE), axons (pNF-H, SBDPs, Tau protein), myelin (MBP), synapses (neurogranin, synaptogranin), astroglia (GFAP, S100B), and autoantibodies (anti-GFAP) (Table 1) (ref.<sup>6</sup>). The persistence of these biomarkers in blood and cerebrospinal fluid (CSF) varies. Some, like S-100B and GFAP, show acute elevations and typically return to baseline levels within days, while others, such as Tau protein, exhibit persistent aberrations correlating with long-term sequelae following TBI (ref.<sup>6,24</sup>). Tau, a microtubule-associated



**Fig. 1.** Summary of the different types of TBI biomarkers that denote many processes such as neuronal injury, glial injury, axonal injury, inflammation, extracellular vesicles, and various non-coding RNAs.

NSE, Neuron-specific enolase; UCH-L1, Ubiquitin C-terminal hydrolase-L1; SBDPs,  $\alpha$ -II-spectrin breakdown products; NFs, Neurofilament proteins; MBP, Myelin basic protein; GFAP, Glial fibrillary acidic protein; S100B, S100B calcium binding protein B; LncRNA, Long non-coding RNA; MiRNA, MicroRNA; CircRNA, Circular RNA; EV, extracellular vesicle.

protein encoded by the MAPT gene, plays a crucial role in maintaining microtubule stability within the axonal cytoskeleton<sup>25,26</sup>. Recent research has focused on total Tau and phosphorylated Tau, noting their elevated levels following TBI and their correlation with injury severity and long-term outcomes, particularly within six months post-injury<sup>27</sup>.

### Inflammatory biomarkers in traumatic brain injury

TBI triggers neuronal inflammation, leading to alterations in neuronal function<sup>72</sup>. This process involves the release of chemical mediators, including cytokines, which are produced by various cells<sup>73,74</sup>. Cytokine production often occurs in a cascade, where one cytokine stimulates target cells to produce additional cytokines, amplifying the inflammatory response<sup>75</sup>. As intercellular messengers, cytokines bind to receptors on target cells and initiate specific responses<sup>74</sup>. Inflammatory responses play a complex role in recovery following TBI. While essential for removing damaged neurons and initiating repair processes, prolonged inflammation can lead to excessive neuronal damage, contributing to long-term neurological deficits<sup>76,77</sup>. Understanding the balance between beneficial and detrimental aspects of inflammation is crucial for developing interventions that minimize unfavorable outcomes for TBI patients.

Biomarkers offer insights into the biological processes activated by TBI. Neuroinflammation, characterized by both beneficial and detrimental effects, is a primary

focus of biomarker research. Cytokines, primarily produced by immune cells like monocytes, lymphocytes, and macrophages, orchestrate the immune response and contribute to tissue repair<sup>78</sup>. They are categorized as pro-inflammatory (e.g., IL-1, IL-12, IL-18, IFN- $\gamma$ , TNF- $\alpha$ ) or anti-inflammatory (e.g., IL-4, IL-10, IL-13, IFN- $\alpha$ ) based on their role in immune regulation<sup>74</sup>. Despite advancements, a significant gap remains in understanding the relationship between inflammatory cytokines and long-term outcomes following TBI. The persistent release of pro-inflammatory cytokines contributes to neurodegenerative diseases<sup>79</sup>. Activated microglia, a type of immune cell in the brain, are a chronic source of neurotoxic factors, including TNF- $\alpha$ , nitric oxide (NO), IL-1 $\beta$ , and reactive oxygen species (ROS), leading to progressive neuronal damage. Chronic activation of microglia, whether by a single stimulus like lipopolysaccharide or multiple exposures, leads to cumulative neuronal loss over time, implicating them in neurodegenerative conditions<sup>80</sup>.

Previous research suggested a correlation between serum IL-1 $\beta$  levels and TBI severity, GCS score, and prognosis<sup>81</sup>. However, a recent meta-analysis of four studies involving 439 participants (263 with mTBI and 176 healthy controls) found no significant difference in blood IL-1 $\beta$  levels between cases and controls. Subgroup analysis revealed significantly elevated blood IL-1 $\beta$  levels in the acute phase (<7 days) after mTBI, indicating a role in the early inflammatory response. However, insufficient studies precluded a comprehensive analysis of chronic IL-

Table 1. Neuronal, axonal, myelin, and glial cell biomarkers in traumatic brain injury.

Biomarkers	Definition	Key features	Clinical Relevance	Ref.
Neuronal cell injury biomarkers				
NSE	A neuronal cytoplasmic enzyme involved in glycolysis.	<ul style="list-style-type: none"><li>- Predominantly found in neurons, released after acute neuronal damage; highly specific to the brain but limited by hemolysis interference</li></ul>	<ul style="list-style-type: none"><li>- Peaks within 12 hours post-TBI, declines within days.</li><li>- High levels indicate severe injury, associated with poor neurological outcomes and increased mortality.</li><li>- Limited utility due to potential false positives from hemolysis.</li></ul>	28–31
UCHL1	Ubiquitin-related enzyme in the cytoplasm of neurons.	<ul style="list-style-type: none"><li>- Plays a critical role in the ubiquitin-proteasome system, regulating protein degradation.</li><li>- Released into the bloodstream following TBI due to neuronal damage and blood-brain barrier disruption</li></ul>	<ul style="list-style-type: none"><li>- Levels increase within 6-24 hours post-TBI.</li><li>- Strongly correlates with injury severity, Glasgow Coma Scale (GCS) scores, and CT findings.</li><li>- Early high levels predict poor outcomes within three months.</li></ul>	32–40
Axonal and myelin-related injury biomarkers				
NFs (NF-L, NF-M, NF-H)	Structural proteins essential for neuronal cytoskeleton integrity.	<ul style="list-style-type: none"><li>- Released following axonal damage.</li><li>- Phosphorylation of NF-H enhances structural stability, making it a reliable marker of axonal injury.</li><li>- NF-L is more sensitive for detecting diffuse axonal injury.</li></ul>	<ul style="list-style-type: none"><li>- Elevated levels persist for an extended period post-TBI, indicating ongoing axonal damage.</li><li>- NF-L correlates with CT lesions and long-term neurological outcomes, particularly in sports-related concussions.</li><li>- NF-H is associated with white matter injury and predicts both chronic disability and mortality.</li></ul>	40–46
MBP	Major structural protein crucial for myelin sheath integrity.	<ul style="list-style-type: none"><li>- Holds myelin layers together, essential for proper nerve conduction.</li><li>- Released 1-3 days post-injury, reflecting delayed injury response.</li></ul>	<ul style="list-style-type: none"><li>- Elevated MBP levels correlate with severe outcomes, especially in cases of intracranial hemorrhage.</li><li>- Biomarker levels can remain high for up to two weeks, providing insight into ongoing myelin damage.</li><li>- Useful for assessing long-term prognosis but less effective for immediate diagnosis</li></ul>	29,47–52
Tau Protein	Microtubule-associated protein involved in stabilizing neuronal structure.	<ul style="list-style-type: none"><li>- Stabilizes microtubules in neurons; hyperphosphorylation leads to neurofibrillary tangles seen in neurodegenerative diseases. Released into CSF and blood post-TBI.</li></ul>	<ul style="list-style-type: none"><li>- Elevated CSF tau levels correlate with TBI severity and poor neurological outcomes.</li><li>- Serum tau may not always align with CT findings but is valuable for predicting long-term clinical outcomes and the risk of chronic traumatic encephalopathy (CTE).</li></ul>	53–57
SBDPs	Products of spectrin proteolysis by calpain and caspase.	<ul style="list-style-type: none"><li>- Serve as markers of necrosis (calpain) and apoptosis (caspase); specific to the central nervous system.</li><li>- SBDP 145, a 145 kDa fragment, is particularly noteworthy as a marker of necrotic cell death activation.</li></ul>	<ul style="list-style-type: none"><li>- Increase rapidly after TBI, reflecting the extent of neuronal damage.</li><li>- SBDP levels correlate with injury severity, lesion size on imaging, and are linked to outcomes like post-concussion syndrome and long-term cognitive impairment.</li></ul>	29,58–64



Table 1. (Continued)

Biomarkers	Definition	Key features	Clinical Relevance	Ref.
Glial cell injury biomarkers				
S100B Protein	Calcium-binding protein primarily found in astrocytes, Schwann cells, and myeloid-derived cells.	<ul style="list-style-type: none"><li>- Plays a key role in intracellular calcium homeostasis and astrocyte function. Released into the bloodstream following astrocytic injury.</li></ul>	<ul style="list-style-type: none"><li>- Elevated levels correlate with TBI severity, poor outcomes, and increased intracranial pressure.</li><li>- Widely used in early TBI management protocols in Scandinavia.</li><li>- However, its specificity is reduced due to possible extracranial sources of S100B, such as adipose tissue and muscles.</li></ul>	6,10,40, 65–68
GFAP	Intermediate filament protein specific to astrocytes.	<ul style="list-style-type: none"><li>- Supports the structural integrity and function of astrocytes.</li><li>- Highly specific to brain tissue and not typically found in blood.</li></ul>	<ul style="list-style-type: none"><li>- Levels rise significantly post-TBI, especially in moderate to severe cases.</li><li>- Useful for assessing TBI severity, guiding neuroimaging decisions, and predicting long-term cognitive and psychiatric outcomes.</li><li>- Elevated GFAP is also a strong predictor of poor neurological recovery.</li></ul>	10,40, 69–71

NSE, Neuron-specific enolase; mTBI, Mild Traumatic Brain Injury; UCHL1, Ubiquitin C-terminal hydrolase-L1; NFs, Neurofilament proteins; MBP, Myelin basic protein; GFAP, Glial fibrillary acidic protein; S100B, S100B calcium binding protein B; SBDPs,  $\alpha$ -II-spectrin breakdown products.

IL-1 $\beta$  levels<sup>82</sup>. Animal model studies have shown that early attenuation of IL-1 $\beta$ -dependent inflammatory signaling can prevent capillary damage by promoting pericyte coverage in the thalamus, highlighting the complex role of IL-1 $\beta$  in TBI recovery<sup>83</sup>. Further research is needed to fully understand the role of IL-1 $\beta$  and other cytokines in TBI progression and long-term outcomes.

IL-6 levels in the blood are elevated after TBI, potentially reflecting injury severity, though its predictive value for long-term outcomes remains unclear<sup>84</sup>. A recent meta-analysis by Malik et al.<sup>82</sup> indicated that a majority of studies (65%) showed significantly elevated IL-6 levels in mTBI patients compared to healthy controls<sup>82</sup>, though some studies showed reduced or no significant differences<sup>85-90</sup>. Elevated IL-2 and IL-6 levels in the acute phase suggest a role in the early inflammatory response<sup>91</sup>. Elevated IL-6 levels at 6 hours post-mTBI have also been associated with the duration of symptoms<sup>92-94</sup>. Other cytokines, including IL-8, IL-10, and TNF- $\alpha$ , are also produced in excess after TBI, but their correlation with injury severity and long-term outcomes requires further investigation<sup>10,84</sup>. High serum IL-8 levels have been associated with moderate and severe cerebral hypoperfusion in TBI patients<sup>95</sup>. A meta-analysis of IL-8 levels in mTBI found variable results, with some studies showing elevated levels, others showing reduced levels, and some reporting no significant differences<sup>82,96-98</sup>. Elevated levels of IL-1RA, IL-8, and IFN- $\gamma$  have been observed in mTBI patients, particularly within 24 hours, though the limited number of studies precluded a comprehensive meta-analysis<sup>82</sup>.

The rapid and dynamic nature of biofluid biomarkers following TBI presents a significant challenge in identifying reliable indicators of injury severity and prognosis. Adiponectin, a marker of inflammation, has been found elevated in the plasma of TBI patients and identified as an independent predictor of poor outcomes and mortality. Similarly, high-mobility group box 1 (HMGB1), a cytokine and marker of inflammation, has emerged as a significant predictor of one-year mortality in TBI patients. HMGB1 translocates from the nucleus to the cytoplasm in the early stages of injury, followed by uptake by phagocytic microglia, suggesting HMGB1 may serve as both a valuable biomarker and a potential therapeutic target for TBI patients<sup>40</sup>.

### Extracellular vesicles and non-coding RNAs in traumatic brain injury

Following a TBI, a complex cascade of secondary events unfolds, including excitotoxicity, free radical generation, and a neuroinflammatory response. These processes, which begin within minutes and can persist for months, contribute significantly to neuronal, glial, and vascular damage<sup>99</sup>. Secondary injuries, particularly neuroinflammation, are major determinants of TBI outcomes<sup>100</sup>. The initial injury triggers the release of damage-associated molecular patterns (DAMPs), activating immune responses and triggering the release of pro-inflammatory mediators. This, coupled with the activation of microglia and astrocytes and the infiltration of peripheral immune cells, intensifies the inflammatory response<sup>101</sup>. This pro-

inflammatory environment is strongly linked to tissue damage and poor neurological outcomes<sup>102</sup>.

### Extracellular vesicles

Extracellular vesicles (EVs), secreted by a variety of cells, are emerging as vital mediators of cell-to-cell communication, particularly in the central nervous system (CNS). Studies highlight their significant impact on neuronal differentiation, synaptic formation, glial interactions, and the regulation of homeostatic signaling and immune responses<sup>103-105</sup>. In the context of TBI, EVs play a crucial role in neuroimmune interactions, regulating neuroinflammation through their diverse cargo, which includes DNA fragments, RNA, lipids, and proteins<sup>106,107</sup>. Both the primary and secondary injuries following TBI influence the number and characteristics of EVs. For example, brain endothelial cells release EVs rich in occludin during vascular remodeling in response to mechanical injury<sup>108</sup>. Similarly, oxidative stress and reactive oxygen species (ROS) stimulate the release of EVs that regulate inflammation and vascular calcification<sup>109-111</sup>. Additionally, microglia activated by lipopolysaccharide (LPS), ATP, and pro-inflammatory cytokines (IL-1 $\beta$ , TNF- $\alpha$ , IFN- $\gamma$ ) release EVs with a distinct cargo profile, underscoring their critical role in neuroinflammation<sup>112-114</sup>.

TBI and subsequent neuroinflammation also trigger the release of astrocyte-derived EVs containing neurotoxic proteins and miRNAs, such as elevated levels of miR-21 in neuron-derived EVs. EVs are not only released locally but are also found in other biological fluids after TBI (ref.<sup>106</sup>). For instance, serum EV concentrations increase rapidly in TBI patients<sup>115,116</sup>, and cerebrovenous blood exhibits higher EV levels than arterial blood, suggesting an increased release from the brain<sup>117</sup>. In rodent studies, EVs positive for glial fibrillary acidic protein (GFAP+) and neuron-specific enolase (NSE+) peak at 3 hours post-TBI (ref.<sup>118</sup>), with GFAP+ EVs decreasing at 6 hours while NSE+ EVs remain elevated<sup>118</sup>.

In the CSF, EVs concentrations double following brain injury<sup>119</sup>. TBI also induces inflammatory changes in salivary-derived EVs, which could play a role in intercellular communication. The ability of EVs to cross the BBB and their presence in both CSF and peripheral blood make them promising biomarkers for TBI, drawing significant research interest<sup>120</sup>. EVs carry information from their parent cells, which can be used to identify specific disease signatures. For example, elevated levels of Tau, amyloid-beta (Ab) 42, and IL-10 have been found in the EVs of military personnel with mild TBI, suggesting a link to chronic postconcussive symptoms and neuroinflammation<sup>86</sup>. Increased levels of phosphorylated Tau (p-Tau), neurofilament light (NfL), IL-6, and TNF- $\alpha$  in CNS-enriched EVs of older veterans correlate with cognitive impairment and inflammatory processes<sup>121</sup>. The molecular composition of circulating EVs changes significantly in individuals with mild TBI. Specific microRNAs (miRNAs) associated with inflammation and CNS disorders, such as hsa-miR-139-5p and hsa-miR-18a-5p, show marked differences<sup>122</sup>. Additionally, TBI alters the protein composition of EVs in the CSF, with elevated levels of  $\alpha$ II-spectrin

breakdown products (BDPs), GFAP, and synaptophysin detectable in CSF-derived EVs (ref.<sup>119</sup>).

Research indicates that flotillin-1, associated with neuroregeneration, is uniquely present in the CSF after TBI. Moreover, the downregulation of ADP-ribosylation factor 6 (Arf6) and the delayed upregulation of Ras-related protein Rab7a (Rab7a) in the CSF post-TBI are linked to poor outcomes<sup>123</sup>. TBI-induced changes in gene expression within salivary-derived EVs also suggest their potential as biomarkers for assessing TBI severity<sup>124</sup>. These findings underscore the significant changes in EVs and their molecular cargo in response to TBI, both in the CNS and peripheral circulation. The presence of altered EVs in biological fluids holds great promise as a diagnostic and assessment tool for TBI.

### *non-coding RNAs*

Diagnosing and predicting outcomes for TBI is challenging due to the varied nature of injuries and individual patient differences. Traditional diagnostic methods often fall short in addressing this complexity. Advances in EVs proteomics have shown promise in cancer research, particularly through liquid biopsies, and similar potential exists for TBI diagnostics<sup>36,125</sup>. However, a standardized and reliable evaluation system for this application is still needed.

Extracellular non-coding RNAs (ncRNAs) are notably resistant to degradation, making them promising candidates for stable and specific disease biomarkers<sup>126</sup>. Correlating these biomarkers with clinical parameters can provide valuable insights into TBI and recovery, enhancing diagnostic accuracy, risk stratification, treatment evaluation, prognostic prediction, and the development of personalized treatment strategies<sup>126,127</sup>. Extracellular microRNAs (miRNAs) are particularly appealing as TBI biomarkers due to their stability and ease of detection. Harrison et al.<sup>106</sup> showed that miR-21, miR-146, miR-7a, and miR-7b were upregulated, while miR-212 was downregulated in the brains of TBI model mice. Building on this, Ko et al.<sup>128</sup> developed a diagnostic method based on miRNA expression profiles (miR-129-5p, miR-212-5p, miR-9-5p, miR-152-5p, miR-21, miR-374b-5p, miR-664-3p), achieving 99% accuracy in distinguishing TBI from controls. Further research by Ko et al.<sup>129</sup> highlighted substantial overlap between miRNA biomarkers in pre-clinical models and clinical samples, validating their utility. Puffer et al.<sup>130</sup> identified 11 differentially expressed miRNAs in the plasma of TBI patients, linking these miRNAs to pathways related to injury and development. Additionally, extracellular circular RNAs (circRNAs) have been implicated in TBI, with studies showing significant differential expression in brain cells post-injury, with 155 upregulated and 76 downregulated circRNAs<sup>131</sup>. A controlled cortical impact (CCI) model in mice identified 191 differentially expressed circRNAs in the cortex, associated with inflammation, cell death, and repair<sup>132</sup>. While extracellular long non-coding RNAs (lncRNAs) are recognized as promising diagnostic markers in neuro-oncology, their potential in TBI diagnosis is still being explored<sup>133</sup>. Studies have indicated significant changes in

lncRNA expression following TBI. For instance, Zhong et al.<sup>134</sup> reported significant alterations in the expression of 823 lncRNAs in the mouse cortex after CCI, with 667 upregulated and 156 downregulated. Similarly, Wang et al.<sup>135</sup> found 271 differentially expressed lncRNAs in the hippocampus of TBI rats. Functional analyses revealed that these lncRNAs are significantly enriched in categories related to inflammation, transcription, apoptosis, and necrosis. These findings suggest that extracellularly enriched lncRNAs and circRNAs hold significant potential as diagnostic biomarkers for TBI. Further exploration into their diagnostic utility is warranted<sup>136</sup>.

Among ncRNAs, miRNAs are particularly significant in TBI pathogenesis<sup>137,138</sup>. Numerous studies have highlighted significant changes in miRNA expression post-TBI. Table 2 provides a detailed summary of these alterations in miRNA expression patterns, their functional roles, and potential mechanisms in TBI pathophysiology. MiRNAs have gained increasing research interest as novel mediators of neuroinflammation in brain trauma contexts<sup>139,140</sup>. During the acute phase of TBI, neuroinflammation is triggered in the brain, exacerbating damage and leading to neurological deficits<sup>141</sup>. It is widely recognized that curbing neuroinflammation can improve TBI prognosis. Several miRNAs have demonstrated potential in reducing neuroinflammation and improving outcomes for TBI patients<sup>142,143</sup>. For example, miR-873a-5p, which is upregulated in the brain lesion areas of TBI patients, has been shown to reduce microglia-mediated neuroinflammation by inhibiting ERK and NF- $\kappa$ B phosphorylation. Treatment of a TBI mouse model with miR-873a-5p resulted in reduced brain damage and edema<sup>144</sup>. Another study demonstrated that increasing miR-23a expression suppressed the secretion of inflammatory factors such as IL-6, IL-1 $\beta$ , and TNF- $\alpha$ , in a TBI cell model. In a mouse model, elevated miR-23a expression reactivated the PTEN/AKT/mTOR signaling pathway, improving prognosis in the injured brain<sup>145</sup>.

Further research has demonstrated that the miRNA let-7 family member, let-7c-5p, is downregulated in mice with TBI. Overexpression of miR-let-7c-5p has been shown to mitigate neuroinflammation, decrease microglia/macrophage activation, reduce brain edema, and improve neurological function<sup>146</sup>. Additionally, let-7c-5p mimic treatments have been found to inhibit the release of inflammatory mediators in primary microglia exposed to oxygen-glucose deprivation. Another study identified elevated levels of miR-142 and miR-155 in immune and glial cells following TBI, indicating their involvement in astrocyte activation and the promotion of neuroinflammation in both human and rat models<sup>147</sup>. In a different TBI mouse model, increased levels of miR-146a were observed in the brain and serum. Overexpression of miR-146a through mimics was shown to inhibit the JNK and NF- $\kappa$ B pathways, thereby reducing neuroinflammation<sup>148</sup>. Furthermore, miR-21, which has been previously reported to be upregulated following TBI, plays a complex role in TBI pathology<sup>149</sup>. MiR-21 is secreted from neurons near the injury site and contributes to neuroinflammation by activating microglia<sup>150</sup>. These findings highlight the

**Table 2.** Non-coding RNAs involved in traumatic brain injury.

Non-coding RNA	Functions and associated mechanisms in brain injury	Ref.
<b>LncRNAs</b>		
lncRNA MALAT1	<ul style="list-style-type: none"> <li>- Modulates inflammation targets in hASC-derived exosomes.</li> <li>- Downregulated in TBI models; correlates with edema.</li> <li>- Overexpression reduces edema and inflammatory markers.</li> <li>- Exosomes with MALAT1 lessen cortical damage and activate MAPK.</li> <li>- Inhibition suppresses angiogenesis by affecting endothelial health.</li> <li>- Regulates angiogenesis via EZH2/NOTCH1.</li> <li>- Knockdown increases NR2B levels, causing damage under OGD/R.</li> <li>- Binds and inhibits miR-125b-5p, promoting neuroinflammation.</li> </ul>	151–157
lncRNA Meg3	<ul style="list-style-type: none"> <li>- Decreased in TBI patients; negatively correlates with cytokines.</li> <li>- Regulates microglial inflammation via miR-7a-5p/Nlrp3.</li> </ul>	158, 159
lncRNA Gm4419	<ul style="list-style-type: none"> <li>- Promotes astrocyte apoptosis during TBI.</li> <li>- Acts as a sponge for miR-4661, upregulating TNF-<math>\alpha</math>.</li> </ul>	160
lncRNA HOTAIR	<ul style="list-style-type: none"> <li>- Involved in microglial activation and inflammation.</li> <li>- Regulates MYD88 ubiquitination.</li> </ul>	161
lncRNA Neat1	<ul style="list-style-type: none"> <li>- Aggravates motor/cognitive functions post-TBI.</li> <li>- Inhibits apoptosis/inflammation in TBI cortex.</li> <li>- Knockdown elevates NR2B levels, causing OGD/R damage.</li> </ul>	156,162
lncRNA Snhg1	<ul style="list-style-type: none"> <li>- Its inhibition increases apoptosis.</li> <li>- Reduces HIF-1<math>\alpha</math>/VEGF-A by binding miR-338.</li> </ul>	163
lncRNA NKILA	<ul style="list-style-type: none"> <li>- Decreases proliferation and inhibits apoptosis.</li> <li>- Binds to miR-195 and upregulates NLRX1 levels.</li> </ul>	164
lncRNA ZFAS1	<ul style="list-style-type: none"> <li>- Its inhibition reduces inflammation, apoptosis; recovers function.</li> </ul>	165
lncRNA KCNQ1OT1	<ul style="list-style-type: none"> <li>- Its downregulation has neuroprotective effects including the damage of brain microvascular and neuron loss in TBI mice.</li> <li>- Modulates the miR-873-5p-TRAF6-p38/NF-<math>\kappa</math>B axis.</li> </ul>	166
lncRNA PRR34-AS1	<ul style="list-style-type: none"> <li>- Its downregulation has neuroprotective effects including reducing brain microvascular damage and neuron loss.</li> <li>- Targets miR-498.</li> </ul>	167
lncRNA 4933431K23Rik	<ul style="list-style-type: none"> <li>- Regulates microglial-induced neuroinflammation.</li> <li>- Inhibits microglial activation by elevating Smad7 expression.</li> </ul>	168
lncRNA GAS5	<ul style="list-style-type: none"> <li>- Levels are related to injury severity and inflammation.</li> <li>- Contributes to neuronal apoptosis during TBI.</li> <li>- Modulates the miR-335/Rasa1 axis.</li> </ul>	169, 170
lncRNA VLDLR-AS1	<ul style="list-style-type: none"> <li>- Levels lower in rmTBI vs. controls.</li> <li>- Correlates with depression symptoms.</li> </ul>	171
lncRNA H19	<ul style="list-style-type: none"> <li>- Increased in perilesional tissue after TBI; reverts over time.</li> <li>- Its knockdown aids recovery, preserves neuronal integrity.</li> <li>- Facilitates anti-inflammatory microglial/macrophage phenotypes.</li> <li>- Promotes activation of the Nrf2/HO-1 axis.</li> </ul>	172
lncRNA TUBB6	<ul style="list-style-type: none"> <li>- Key role in neuroprotection via TUBB6/Nrf2 pathway.</li> </ul>	173
<b>CircRNAs</b>		
circMETTL9	<ul style="list-style-type: none"> <li>- Downregulation improves neurological deficits and apoptosis.</li> <li>- Activates SND1 in astrocytes.</li> </ul>	174
circScmh1	<ul style="list-style-type: none"> <li>- Exosomes reduce hippocampal nerve damage.</li> <li>- Promotes microglial M2 polarization.</li> </ul>	175
circIgfbp2	<ul style="list-style-type: none"> <li>- Its inhibition relieves mitochondrial dysfunction.</li> <li>- Modulates miR-370-3p/BACH1/HO-1 axis.</li> </ul>	176
circPtpn14	<ul style="list-style-type: none"> <li>- Important for brain protection by melatonin.</li> <li>- Controls 5-LOX expression involved in ferroptosis.</li> </ul>	177
circLphn3	<ul style="list-style-type: none"> <li>- Improves BBB permeability upon TBI.</li> <li>- Regulates tight junction protein expression after TBI.</li> </ul>	178
circ0116449	<ul style="list-style-type: none"> <li>- Methylation-related; reduces neuronal loss.</li> <li>- Modulates miR-142-3p-NR1D2 axis as a miRNA sponge.</li> </ul>	179
circRNA_009194	<ul style="list-style-type: none"> <li>- Improves outcomes in rats with TBI.</li> <li>- Regulates the voltage-gated sodium channel Nav1.3 in TBI.</li> </ul>	180



**Table 2.** (Continued)

Non-coding RNA	Functions and associated mechanisms in brain injury	Ref.
circHtra1	- Promotes neuronal loss and immune deficiency. - Controls miR-3960/GRB10 axis.	181
circLrp1b	- Inhibition reduces inflammation and autophagy in TBI. - Regulates miR-27a-3p/Dram2 signaling pathway.	182
circRNA-chr8	- Plays a pro-inflammatory role in TBI. - Involved in sequestering mmu-let-7a-5p.	183
Hsa_circ_0018401	- Potential biomarker; binds miR-127-5p, correlates with TBI severity.	184
<b>MiRNAs</b>		
miR-212-5p	- Protects against neuron death from iron toxicity. - Negatively regulates Ptg2, impacts ferroptosis.	185
miR-212, miR-132	- Its overexpression in BMEC decreases barrier properties. - Potential targets: Cldn1, Jam3, Tjap1.	186
miR-132	- Its overexpression improves repair and clinical symptoms post-TBI. - Accelerates neurogenesis and tissue repair. - Enhances neuroblast migration, reduces microglia accumulation.	187
miR-146a	- Improves TBI outcomes, downregulates inflammatory cytokines. - MiR-146a inhibits the JNK and NF-κB signaling pathways.	148
miR-155	- Inhibition decreases neuroinflammation, enhances recovery. - Regulates NADPH oxidase 2 in microglia/macrophages. - Substantial decrease in TBI model; increased BACH1 expression.	188,189
miR-429	- Inhibition reduces inflammation, brain damage. - Targets DUSP1, inhibits pro-inflammatory release.	190
miR-124-3p	- Microglial exosomes improve cognition, reduce degeneration. - Targets the Rela/ApoE signaling pathway. - Elevated in blood and plasma at 2 d post-TBI vs. controls. - Higher levels correlate with larger chronic lesion areas. - Exosomes with high miR-124-3p levels reduce apoptosis and ER stress. - Binds to IRE1α, reducing its expression and inhibiting ER stress. - Transferred from microglia-derived exosomes to injured neurons, providing neuroprotection.	191–195
miR-93, miR-191, miR-499	- Elevated in TBI patients; higher in severe cases. - Strong predictive power for trauma cases.	196
miR-21-3p	- Increased in BMVECs post-TBI is detrimental to BBB restoration. - Its downregulation may aid BBB recovery.	197
miR-21	- Upregulation improves outcomes, reduces microvascular injury. - Overexpression of miR-21 activates the axis of Ang-1/Tie-2.	198–200
miR-21, miR-92, miR-16	- High predictive power for trauma diagnosis. - Potential biomarkers for survival.	201
miR-21, miR-92a, miR-874	- Involved in protective effects of exercise post-TBI.	202
miR-21, miR-124a, miR-107	- Increased at various times post-injury. - Linked to inflammatory proteins; inverse relationship with miRNA levels.	203
miR-107	- Participates in GRN expression regulation.	204
miR-23a	- Its overexpression inhibits neuroinflammation, aids prognosis. - Reactivates PTEN/AKT/mTOR pathway inhibited by TBI.	145
miR-23b	- Its overexpression has neuroprotective impact post-TBI. - Targets ATG12 to inhibit autophagy.	205
miR-27a	- Overexpression protects brain, suppresses neuroinflammation. - Targets FoxO3a, inhibiting its expression.	206
miR-136-3p, miR-9-3p	- Elevated levels distinguish mTBI from naïve rats. - Plasma levels higher in sTBI patients.	207
miR-219a-5p	- Discriminates sTBI/mTBI patients, regulates apoptosis. - Inhibits CCNA2 and CACUL1, affecting apoptotic pathways.	208
miR-145-3p	- Maintains Th17/Treg balance, reduces inflammation via the miR-145-3p/NFATc2/NF-κB axis.	209
miR-193a	- Its inhibition suppresses the NLRP3 expression and brain injury and neuroinflammation post-TBI.	210

**Table 2.** (Continued)

Non-coding RNA	Functions and associated mechanisms in brain injury	Ref.
miR-34b	- Trauma-induced anxiety was reduced by miR-34b, which targets CRHR1 to decrease HPA axis hyperactivity.	211
miR-433	- miR-433 expression was lower in patients with tibial fracture and craniocerebral injury compared to controls. - miR-433 regulates SPP1 mRNA and protein by binding to its 3'-UTR.	212
miR-711	- miR-711 levels increased in the cortex post-TBI and in vitro, due to rapid transcription (pri-miR-711) rather than catabolism. - Increases correlated with downregulation of Akt, activating FoxO3, GSK3 $\alpha/\beta$ , pro-apoptotic PUMA, Bim, and mitochondrial release of cytochrome c and AIF. - Administration of miR-711 inhibitor post-TBI increased Akt, reduced apoptosis, and decreased cortical lesion volume and neuronal loss.	213
miR-302	- Pulsatile shear stress suppressed miR-302; exogenous miR-302 inhibited ERK1/2 and connexin43 phosphorylation. - Elevated miR-302 improved cognitive function and reduced brain damage by decreasing edema and contusion volume.	214
miR let-7c-5p	- Its overexpression suppresses inflammatory factor release and microglial activation. - Inhibits caspase-3 expression.	146
miR-9-5p	- Contributes to neurological recovery, reduces microvascular damage and neuroinflammation. - Activates the Hedgehog pathway and inhibits the NF- $\kappa$ B/MMP-9 pathway.	215
miR-17-92 cluster	- Exosomes enriched with miR-17-92 reduce neuroinflammation and enhance angiogenesis and neurogenesis, improving TBI recovery.	216
miR-22	- Provides neuroprotection by reducing damage and apoptosis in neuronal cells post-TBI.	217
miR-31	- Regulates apoptosis factors (BCL2, p-AKT1, BAX) and the PTEN/AKT signaling pathway. - Overexpression inhibits neuronal cell apoptosis in TBI in vitro.	218
miR-141-3p	- Regulates the HIF-1A/VEGFA axis to reduce neuronal cell death. - Ursolic acid regulates miR-141-3p to reduce TBI-induced apoptosis, oxidative damage, and inflammation. - In TBI mice, ursolic acid activates the PI3K/AKT pathway via miR-141-3p regulation.	219
miR-223-3p	- Influences sex-specific neuroinflammation post-TBI and inhibits neurite elongation. - Targets Armex1 and is negatively correlated with its expression.	220, 221
miR-330-5p	- Reduces inflammatory cytokines and restores motor function in TBI rats. - Promotes anti-inflammatory microglia polarization via Ehmt2-mediated CXCL14 transcription.	222
miR-15a/16-1	- Intranasal delivery of the antagomir mimicked the protective effects of genetic deletion, improving sensorimotor and cognitive outcomes, enhancing white/gray matter integrity, and reducing inflammation compared to control antagomir-treated mice post-TBI.	223
miR-9a-5p	- Poorly expressed in the brain tissue of rats with TBI. - ELAVL1 is a downstream target of miR-9a-5p, negatively regulating its expression. - Increased miR-9a-5p expression protects against brain tissue damage in TBI rats by targeting ELAVL1.	224
miR-9-5p	- Expression decreased in biperiden-treated patients compared to placebo group. - Regulates stress response genes related to axonogenesis and neuronal death, relevant to PTE and TBI. - Biperiden may alter miR-9-5p expression in serum EVs, potentially aiding TBI resolution.	225
miR-206, miR-549a-3p	- Serum exosomes show good predictive value as biomarkers of TBI. - Correlate well with BDNF, NSE, and S100 $\beta$ , indicating potential as biomarkers in TBI patients.	226
miR-148a-3p	- MiR-148a-3p was highly expressed in TBI. - Significantly improved neurological scores and reduced brain injury in a rat TBI model by promoting microglial M1 to M2 transition. - Alleviated TBI by inhibiting the NF- $\kappa$ B pathway.	227
miR-127-5p	- Downregulated in patients with TBI. - Negative correlation with miR-423-3p confirmed binding to hsa_circ_0018401 via dual luciferase assay. - hsa_circ_0018401 and miR-127-5p, alone or in combination, have clinical value for TBI diagnosis, stratification, and outcome prediction.	184

critical role of miRNAs as key regulators of neuroinflammation in TBI, emphasizing their potential as therapeutic targets for managing this complex condition.

## FUTURE PROSPECTIVE AND RECOMMENDATIONS

To enhance the clinical utility of inflammatory markers in diagnosing mTBI, addressing the significant variability in current study designs, analyses, and reporting is crucial. Improving the quality of evidence for these markers will involve enrolling representative and diverse study cohorts. Large-scale, multicenter initiatives like the CENTER-TBI and TRACK-TBI studies present an excellent opportunity to achieve this goal. By including participants from varied populations, these studies can generate findings that are more broadly applicable to mTBI cases<sup>228</sup>. The substantial sample sizes provided by such multicenter studies allow for more accurate statistical analysis, accounting for various confounding factors such as age, gender, previous head injuries, and extent of extracranial damage. These methodological advancements will contribute to a more reliable understanding of how inflammatory markers can be used in mTBI diagnosis and treatment.

A key challenge is distinguishing neuroinflammation from systemic inflammation due to extracranial injuries. Several strategies are being explored to tackle this issue: (I) Statistical Corrections and Control Groups: Using statistical methods to adjust for extracranial injuries or including patients with orthopedic injuries alongside healthy controls can help isolate neuroinflammation<sup>229,230</sup>. (II) Cranial EVs: Analyzing inflammatory markers within cranially derived EVs may offer a direct measure of the cranial inflammatory response, potentially providing a clearer indication of neuroinflammation<sup>130,231</sup>. (III) MicroRNA Analysis: Assessing microRNAs as biochemical markers of inflammation could help identify signals specific to neuroinflammation<sup>230,232</sup>. (IV) Proteomic Techniques: Employing proteomics might uncover biomarkers uniquely associated with the neuroinflammatory response<sup>233</sup>.

Looking ahead, there is a shift expected from traditional analytical methods, such as ELISA Immunoplex, and SIMOA, to Point-of-Care (POC) platforms that use electrochemical biosensors<sup>234,235</sup>. POC platforms offer the advantage of quickly identifying biomarker concentrations at the site of injury or in emergency settings without the need for extensive laboratory processing<sup>236</sup>. Recent developments show that POC tests combining UCH-L1 and GFAP can match the sensitivity of traditional lab-based methods. Given that some inflammatory markers rise rapidly after injury, integrating them into POC platforms could be beneficial for early mTBI assessment. However, solid evidence is needed before incorporating these markers into routine clinical practice.

Research involving EVs in TBI faces several hurdles, such as the need for standardized isolation protocols and dealing with the inherent heterogeneity of EVs<sup>237</sup>. This variability in size, shape, and content, along with the

diverse origins of EVs, complicates the use of a single profiling approach<sup>237</sup>. Moreover, exosome toxicity adds another layer of complexity, highlighting the need for further research to develop safe and effective exosome-based treatments for TBI. Establishing standardized methods for EV isolation and analysis will be crucial for ensuring consistent and comparable results across studies<sup>238</sup>. The application of machine learning to analyze EV cargo data shows promise for developing predictive models for disease diagnosis and treatment. By integrating various omics data types, machine learning can identify patterns and relationships, leading to personalized treatment recommendations based on individual patient profiles<sup>239,240</sup>.

Emerging research indicates that mTBI may elevate the risk of neurodegenerative diseases if proper recovery time is not allowed<sup>241</sup>. Such injuries are common among athletes and military personnel but are often underreported. Therefore, finding objective markers that go beyond traditional assessments – like symptom evaluations, cognitive tests, and balance assessments – is critical<sup>242,243</sup>. Exosomal biomarkers, acting as a "liquid biopsy," could provide valuable insights into brain-specific changes following Mtb (ref.<sup>244</sup>). Further research on these biomarkers could illuminate the long-term effects of mTBI, including the potential development of conditions like Alzheimer's disease or chronic traumatic encephalopathy. Expanding testing protocols and further investigating exosomal biomarkers will be essential for improving long-term outcomes for individuals with mTBI (ref.<sup>238</sup>). Building a strong interdisciplinary research community will be key to advancing TBI management and prevention<sup>238</sup>.

## CONCLUSIONS

The diverse etiology, pathology, and clinical progression of TBI present substantial challenges for the use of traditional biomarkers in both clinical practice and research. Neuroimaging methods such as CT and MRI are effective for detecting major head injuries but fall short in identifying subtle neural damage or structural changes, and their high costs restrict their widespread application. Fluid biomarkers, although potentially useful for correlating with neuronal, axonal, or glial cell injuries, often suffer from low abundance and require highly sensitive assays, which can result in undetectable levels. EVs and non-coding RNAs, particularly miRNAs, offer promising alternatives. Elevated levels of these biomarkers in TBI patients compared to healthy individuals have been observed. Research indicates that EVs and miRNAs can provide high diagnostic accuracy for TBI, especially in cases with diffuse injuries, where increased levels of exosomal GFAP and neurofilament light chains are noted. Moreover, miRNA profiles in CSF and serum plasma show distinct variations following TBI, reflecting injury severity and aiding in both diagnosis and severity assessment. Despite the advantages of isolating exosomes and miRNAs over traditional fluid proteins, challenges remain due to the variability in miRNA expression among in-

dividuals, particularly those with altered consciousness. Identifying the most effective miRNAs and establishing reliable cutoff values for TBI diagnosis and prognosis continue to be complex issues that need to be addressed.

### Search strategy and selection criteria

The search strategy for this review involved systematically querying electronic databases, including PubMed, Scopus, and Web of Science, for articles published up to August 1, 2024. Keywords such as “traumatic brain injury,” “biomarkers,” “extracellular vesicles,” “non-coding RNAs,” and “clinical outcomes” were used in various combinations. Selection criteria included peer-reviewed original research or review articles focusing on biomarker applications in TBI prognosis or diagnosis. Exclusion criteria encompassed studies with insufficient methodological details or non-human data. References were screened based on relevance, quality, and recency to ensure comprehensive coverage of the topic.

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