Biomarkers	Genes	Other gene names	Level	Stages	Sources	pathway	Other biomarkers	Sepsis related	Articles
1.PCT	CALCA	Calcitonin Related Polypeptide Alpha CGRP-Alpha Calcitonin CALC1 CGRP Calcitonin Gene-Related Peptide 1 Calcitonin Gene-Related Peptide I Alpha-Type CGRP Calcitonin 1 CGRP-I Calcitonin/Calcitonin-Related Polypeptide, Alpha Katacalcin CGRP-I PCT CT KC	Protein level	Diagnostic/Prognostic	Gram - bacterial infection	Neuroendocrine Pathways		Genecards/NO MalaCards/NO KEGG/NO UniProt/NO	1.The CALCA gene is not commonly used directly for sepsis diagnosis, as its product, PCT, is already well-established as a protein biomarker.
									2.Procalcitonin (PCT) is a reliable diagnostic and prognostic biomarker for sepsis and localized infections in burn ICU patients, outperforming traditional markers and aiding in monitoring treatment efficacy and outcomes.
									3.PCT is a valuable biomarker for sepsis management, aiding in: Early diagnosis. Differentiating bacterial infections from other inflammatory states. Guiding antibiotic therapy to reduce overuse and resistance. Monitoring treatment effectiveness through PCT kinetics.
									4.Diagnostic Value: PCT levels are significantly elevated in sepsis patients and are especially high in cases of G- bacterial infections. PCT can help distinguish between G- and G+ bacterial bloodstream infections. Prognostic Role: PCT levels correlate with disease severity and mortality, making it a valuable biomarker for sepsis prognosis.
									5.PCT is a moderate predictor of 30-day mortality in septic ED patients, with a high specificity but limited sensitivity. A threshold of 32.5 µg/L identifies patients at high risk of death but has limited utility in predicting ICU admissio
									6. Diagnostic Utility: PCT is a reliable early marker for differentiating sepsis from severe sepsis and septic shock, with high sensitivity and specificity for severe sepsis. PCT is superior to CRP, WBC, and AP-II in diagnosing sepsis severity. Prognostic Role: Higher PCT levels are associated with increased mortality and disease severity, making it a useful prognostic marker. Limitations: PCT's diagnostic utility for septic shock is limited compared to severe sepsis.
							IL-6 and IL-8		7. PCT as a Diagnostic Marker: PCT is one of the most reliable biomarkers for bacterial sepsis, with high diagnostic accuracy and rapid response kinetics. PCT in Prognosis: PCT levels predict disease severity and treatment response, aiding in patient risk stratification. Limitations: Elevated PCT can occur in non-infectious inflammatory states (e.g., trauma, surgery). Not a standalone marker; must be used in conjunction with clinical findings and other diagnostic tools.
							CRP		8.PCT as a Biomarker: PCT is a reliable marker for diagnosing bacterial sepsis and predicting outcomes in critically ill patients. It is superior to CRP and WBC but should be used alongside clinical judgment and other diagnostic tools.
									9. While PCT (protein) is a well-established marker for bacterial infections and sepsis, CALCA gene expression (mRNA) appears to lack sufficient sensitivity and specificity for clinical use in this study.
									10. PCT remains a robust biomarker for bacterial sepsis, and this assay enhances its clinical utility in rapid, bedside diagnostics. However, CALCA gene expression was not discussed as a diagnostic target in this study; the focus is on PCT protein levels.
									11. CALCA encodes Calcitonin Gene-Related Peptide 1, which was upregulated in AKI patients. However, its specific role as a diagnostic marker for sepsis alone (excluding AKI) remains unclear.
2.CRP	C-reactive protein	**C-Reactive Protein** **PTX1** **C-Reactive Protein, Pentraxin-Related** **Pentraxin 1**	Protein level	Diagnosis/Prognosis		Acute Phase Response Pathway	WBC	Genecards/Arthritis Septic MalaCards/1.Septic Arthritis- 2.Bacterial Sepsis- 3.Sepsis in Premature Infants UniProt/disease/YES	1.Protein Level: The study validated CRP as a diagnostic marker at the protein level using a turbidimetric assay, a standard wet-lab method. Gene Level: The study did not evaluate CRP gene expression (mRNA level). It focused exclusively on the protein concentrations in plasma.
									2.CRP is an acute-phase protein produced by the liver in response to inflammatory cytokines, particularly IL-6, TNF-α, and IL-1β. CRP is validated at the protein level through wet-lab methods like immunoturbidimetry and nephelometry, making it a robust diagnostic and prognostic tool for sepsis. While PCT rises earlier in response to bacterial infections, CRP is more cost-effective and widely available. Both markers complement each other in certain clinical scenarios.
									3.The study validates CRP as a protein-level marker for identifying individuals at risk of sepsis. It does not involve gene-level validation but emphasizes hsCRP's role in the inflammatory cascade, reinforcing its relevance in sepsis monitoring.
									4.CRP is a reliable indicator of sepsis resolution in ICU patients. A significant decrease in daily CRP levels provides clinicians with a valuable tool to evaluate the effectiveness of sepsis treatment and predict recovery, particularly in less severe cases.
							PCT, IL-6,		5.The review emphasizes that biomarkers like CRP are invaluable for early detection and monitoring at the protein level but should be used as part of a multi-modal diagnostic approach.
							PCT,IL-6, IL-8, IL-10,LBP,CD84, CD14,TREM-1		6.CRP remains a key biomarker for sepsis due to its availability and diagnostic utility, but its lack of specificity necessitates combination with other markers like PCT or cytokines for improved accuracy.
3.sTREM-1	TREM-1	**Triggering Receptor Expressed On Myeloid Cells 1** **TREM-1** **CD354** **Triggering Receptor Expressed On Monocytes 1** **CD354 Antigen**	protein biomarker	diagnostic/prognostic	infectious sepsis from non-infectious inflammatory	Inflammatory and Immune Pathways	TLR4	Genecards/Septic, septic shock MalaCards/Bacterial Sepsis KEGG/NO UniProt/septic shock	1. A cell-surface receptor expressed on neutrophils and monocytes/macrophages. Amplifies inflammation by promoting the release of pro-inflammatory cytokines like TNF-α, IL-6, and IL-1β. Activated during bacterial and fungal infections. TREM-1 is activated by both pathogen-associated molecular patterns (PAMPs) and damage-associated molecular patterns (DAMPs). Works synergistically with Toll-like receptors (TLRs), particularly TLR4, amplifying the inflammatory response. TREM-1, particularly its soluble form sTREM-1, is a promising biomarker and therapeutic target in sepsis. It offers potential for early diagnosis, prognosis, and personalized treatment strategies. Current research focuses on developing inhibitors and decoy receptors to modulate the TREM-1 pathway, aiming to balance immune response and reduce sepsis-related mortality.
									2. Expression of TREM-1 is significantly upregulated in septic conditions, particularly in neutrophils and monocytes infiltrating infected tissues. Activation of TREM-1 requires its interaction with the DAP12 adaptor protein. This signaling cascade enhances inflammatory cytokine secretion, chemokine production, and immune cell recruitment. The study highlights the potential of sTREM-1 as a diagnostic protein biomarker and TREM-1 inhibition as a therapeutic strategy, particularly in mitigating the hyperinflammatory phase of septic shock.
									3. Diagnostic Potential: TREM-1 and its soluble form (sTREM-1) are valuable biomarkers for distinguishing sepsis from non-infectious inflammatory conditions. Therapeutic Targeting: Complete inhibition of TREM-1 is detrimental in bacterial infections due to impaired immune clearance. Partial modulation could balance inflammation and bacterial control, reducing mortality in sepsis.
									4. the dynamic modulation of TREM-1 expression during sepsis and its dependence on infection type and pathogen. While sTREM-1 is a valuable diagnostic tool, surface TREM-1 expression provides deeper insights into imm
									5. Elevated sTREM-1 levels have shown specificity in identifying sepsis in critically ill patients compared to other markers like CRP and PCT. It is particularly effective in distinguishing bacterial infections from non-infectious inflammatory conditions.
							CRP, PCT		While sTREM-1 is a reliable biomarker, variability in expression levels may occur based on pathogen type and disease severity.
									6.Diagnostic Value of TREM-1 TREM-1 expression dynamics (gene and surface levels) are valuable for prognosis rather than initial diagnosis. TREM-1's role as a biomarker lies in identifying patients at higher risk of poor outcomes based on early immunosuppression.
									7. TREM1 as a Diagnostic and Prognostic Marker: Reduced TREM1 gene expression correlates with disease severity, making it a valuable marker for identifying critically ill patients and monitoring their recovery. Measurement of TREM1 mRNA levels could complement traditional biomarkers like CRP and PCT. TREM1 mRNA levels in PMNs reflect the severity of bacterial infections and can serve as a specific biomarker for diagnosing and monitoring sepsis progression.
							CRP, PCT		
							TNF-α, IL-6, IL-8, IL-10		8. TREM-1 Gene Expression No Significant Changes in Gene Expression: TREM-1 gene expression in monocytes did not increase with sepsis severity, unlike sTREM-1 levels in serum. Lack of correlation between serum sTREM-1 and monocyte TREM-1 gene expression. Cytokine Correlation Increased cytokines (TNF-α, IL-6, IL-8, IL-10) in serum correlated with disease severity. Cytokines showed stronger associations with mortality than sTREM-1 levels.
4.suPAR	PLAUR	Plasminogen Activator, Urokinase Receptor UPAR Urokinase Plasminogen Activator Surface Receptor URKR CD87 Urokinase-Type Plasminogen Activator (UPA) Receptor Monocyte Activation Antigen Mo3 U-PAR U-Plasminogen Activator Receptor Form 2 CD87 Antigen MO3	Protein biomarker	diagnostic/prognostic	not specific to a particular pathogen or infection type	Coagulation Pathways Vascular and Endothelial Inflammatory and Immune	CRP - PCT	Genecards/NO MalaCards/NO KEGG/NO UniProt/NO	1.Provides valuable prognostic information. Complements traditional biomarkers like CRP and PCT. Useful for triaging critically ill patients and identifying those at higher risk. While suPAR is not superior to CRP or PCT for diagnosing sepsis, its strength lies in prognostic value and its ability to reflect disease severity. suPAR could complement other biomarkers in managing sepsis but should not be u
							CRP - PCT		2.Diagnostic Use: suPAR complements existing sepsis biomarkers like CRP and PCT. Its high specificity makes it particularly useful in ruling out non-sepsis conditions. Prognostic Applications: suPAR levels can guide clinicians in assessing disease severity and risk of mortality. May help identify high-risk patients needing intensive care.
							CRP - PCT		3. suPAR is a valuable biomarker for risk stratification in septic patients, particularly for predicting 30-day mortality. While less effective for diagnosing sepsis compared to CRP and PCT, it plays a crucial role in long-term outcome prediction and complements other biomarkers in comprehensive sepsis management.
							CRP - PCT		4.suPAR is a useful biomarker for immune system activation and sepsis severity, showing promise as a complement to other markers like CRP and PCT. suPAR reflects immune system activation rather than direct inflammatory activity. Its correlation with SOFA scores indicates that it can serve as a marker of disease severity but not mortality.
							PCT		5.suPAR is a valuable biomarker for sepsis diagnosis and prognosis, particularly when combined with other markers like PCT and clinical scoring systems. uPAR lacks specificity for sepsis alone; its elevation reflects general immune activation.
5.LBP	LBP	Lipopolysaccharide Binding Protein Lipopolysaccharide-Binding Protein BPIFD2 BPI Fold Containing Family D, Member LPS-Binding Protein	Protein biomarker	Prognostic level	Gram - bacterial infection	Toll-like Receptor (TLR) Signaling Cytokine Storm Acute Phase Response Endothelial Dysfunction	LTR4	Genecards/ PUblication part MalaCards/Bacterial sepsis KEGG/NO UniProt/NO	1. LBP plays a central role in amplifying endotoxin-mediated inflammation and renal damage during sepsis. Targeting LBP, either through blood purification or pharmacological inhibitors, holds promise for preventing and managing sepsis-induced AKI. LBP levels could serve as a biomarker for detecting endotoxemia and predicting AKI risk in sepsis.

									2. Diagnostic and Prognostic Value: LBP reflects immune activation in response to bacterial endotoxins, particularly Gram-negative bacteria. Elevated levels correlate with sepsis severity and poor outcomes, supporting its use as a prognostic biomarker. Adding LBP to APACHE II or SOFA scores improves the accuracy of predicting mortality, highlighting the utility of multimodal assessment. It shows promise as a prognostic biomarker in the ED for early identification of high-risk patients
									3. Elevated LBP levels reflect the body's innate immune response and could serve as a valuable biomarker for sepsis diagnosis and prognosis. LPS levels predict worse outcomes, while lower LBP levels may indicate inadequate acute-phase response in critically ill patients. LBP could serve as a biomarker for monitoring sepsis progression and guiding interventions.
							LPS		4.LBP is an effective biomarker of systemic inflammation but is non-specific to the type of infection causing sepsis. While elevated levels indicate an acute-phase response, they do not correlate strongly with severity or mortality. LBP levels are elevated in response to systemic inflammation but do not reliably distinguish between Gram-negative, Gram-positive, or fungal infections.
							IL6		
							sCD14		5. LBP and sCD14 are valuable biomarkers for the early diagnosis of neonatal sepsis, showing strong correlation with cytokine levels and disease severity. LBP, in particular, offers a diagnostic advantage due to its persistence and sensitivity to immune activation. These findings support the potential integration of LBP and sCD14 into clinical practice for managing neonatal sepsis. The persistence of elevated LBP levels provides a larger diagnostic window for early-onset sepsis. sCD14 shows a stable pattern, reinforcing its value as a baseline marker of immune activation.
							CRP, IL6		6.Monitoring Sepsis: LBP alone is not a reliable biomarker for monitoring postoperative sepsis or predicting outcomes. CRP remains a more practical choice due to lower cost and established clinical use. Combination Strategies: Combining LBP with other biomarkers like procalcitonin (PCT) or IL-6 might improve diagnostic accuracy, though this requires further research.
							IL-6, IL-1β, IL-10, and CRP		7.LBP is a valuable biomarker for predicting disease progression in severe sepsis. An increase in LBP levels at 48 hours is strongly associated with the development of ARDS and higher mortality. No defined LBP cutoff to reliably identify survivors versus non-survivors.
							TNF-α		8.The F436L genetic variant of LBP alters its functional properties, leading to reduced binding to bacterial ligands and a dampened inflammatory response. This variant is associated with a more favorable clinical course in sepsis, suggesting potential protective effects against hyperinflammation.
							CRP,PCT		9. LBP is a valuable biomarker for monitoring disease progression and predicting outcomes in severe sepsis and septic shock. The dynamics of LBP levels, rather than single admission measurements, provide significant prognostic information and outperform CRP and PCT in specificity and predictive value.
							TNF-α, sCD14		10. This study highlights the dual role of LBP in sepsis: At low concentrations, it enhances immune recognition of LPS, amplifying inflammation. At high concentrations, it inhibits LPS activity, dampening excessive immune responses. Elevated LBP levels in severe sepsis serve as a protective mechanism to limit inflammation, making LBP a promising target for future therapeutic interventions.
6.IL6	IL6	Interleukin 6 IL-6 IFNB2 BSF2 HGF HSF B-Cell Stimulatory Factor 2 CTL Differentiation Factor Hybridoma Growth Factor Interferon Beta-2 Interleukin-6 IFN-Beta-2 BSF-2 CDF Interleukin 6 (Interferon, Beta 2) B-Cell Differentiation Factor Interferon, Beta 2 Interleukin BSF-2	Protein biomarker	Prognostic marker	various types of infections and distinguishing between specific conditions	Cytokine Storm and Inflammatory Signaling Acute Phase Response Pathway Vascular and Endothelial Pathways	TNF-α ,IL8 , HLA-DR, CD71	Genecards/NO MalaCards/Bscterial sepsis-septic Arthritis KEGG/NO UniProt/NO	1. IL-6 is a reliable biomarker for sepsis prognosis, with higher levels indicating worse outcomes. Its correlation with monocyte activation and cytokine production underscores its central role in sepsis pathophysiology. Monitoring IL-6 dynamics may aid in early risk stratification and personalized treatment of sepsis patients. IL-6 can serve as a rapid, bedside biomarker for identifying high-risk sepsis patients. Serial IL-6 measurements provide valuable information about disease progression and therapy effectiveness. Therapeutic Insights: Modulating IL-6 levels or targeting its downstream pathways may help balance immune hyperactivity and suppression in sepsis. Patients with high IL-6 had increased expression of: HLA-DR: Higher density, indicating activated monocytes. CD64 (FcγRI) and CD71 (transferrin receptor): Enhanced capacity for antigen presentation and metabolic activity.
									2. This study highlights the significant role of IL-6 genetic polymorphisms in determining the risk and severity of sepsis in children. The G-174C polymorphism in the IL-6 promoter region is particularly relevant, with the CC genotype predisposing to worse outcomes. These findings support the potential use of IL-6 genotyping as a prognostic tool in pediatric sepsis.
							CRP		3.IL-6 is a highly sensitive biomarker for the detection and monitoring of Gram-negative EOS in preterm newborns. Rapid changes in IL-6 levels correlate with sepsis severity and clinical outcomes, outperforming traditional markers like CRP. The findings highlight the importance of serial IL-6 measurements for early diagnosis and treatment monitoring in neonatal sepsis.
							PTX3 , PCT		4.Diagnostic Utility IL-6 was superior to PTX3, PCT, and CRP in diagnosing sepsis and septic shock. The dynamic range of IL-6 allowed it to discriminate between sepsis, septic shock, and non-septic conditions with high specificity. Prognostic Utility Persistent elevation of IL-6 in septic shock patients was strongly correlated with higher mortality. PTX3 served as a secondary biomarker for long-term outcomes but lacked the robust predictive power of IL-6. Combining IL-6 with PTX3 may enhance risk stratification in clinical practice.
									5. IL-6 as a Diagnostic Marker: IL-6 levels > 7 pg/mL can diagnose sepsis with high sensitivity and specificity. IL-6 > 75.7 pg/mL is indicative of Gram-negative bacterial sepsis. IL-6 as a Prognostic Marker: Rapid normalization of IL-6 levels signals treatment success. Persistent high levels suggest poor outcomes.
									6. Diagnostic and Prognostic Significance of IL-6 IL-6 serves as a sensitive biomarker for sepsis severity and early mortality risk: High plasma IL-6 levels (>3000 pg/mL) predict poor outcomes in WT mice. However, IL-6 absence (in IL-6KO mice) does not significantly improve survival, indicating that IL-6 is a marker rather than a mediator of sepsis-induced mortality. Physiological Roles of IL-6 Thermoregulation: IL-6 is essential for developing hypothermia during sepsis, which may reflect the body's response to inflammation.
7.HMGB1	HMGB1	High Mobility Group Box 1 SBP-1 HMG3 HMG1 High-Mobility Group (Nonhistone Chromosomal) Protein 1 Sulfoglucuronyl Carbohydrate Binding Protein High Mobility Group Protein B1 High Mobility Group Protein 1 DKFZp686A04236 Amphoterin HMG-1 High-Mobility Group Box 1	protein biomarker	prognostic marker	inflammation and immune system activation	Apoptosis and Cell Death Pathways Inflammatory and Immune Vascular and Endothelial		Genecards/High serum levels are found in several inflammatory events including sepsis MalaCards/Septic Arthritis-Bacterial sepsis KEGG/NO UniProt/NO	1.HMGB1 plays a significant role in the inflammatory processes of sepsis, making it a valuable therapeutic target. However, its reliability as a diagnostic biomarker is uncertain: Elevated HMGB1 levels are associated with sepsis severity, but they do not consistently correlate with survival or prognosis in patients.
							TNF, IL-1		2.Diagnostic Biomarker Potential: HMGB1 levels correlate with disease severity in sepsis and other inflammatory diseases. Elevated levels have been reported in septic patients, with higher levels linked to increased mortality. However, its delayed kinetics and variability among individuals make it less ideal as a standalone early diagnostic biomarker.
									3.HMGB1 in Severe Sepsis: HMGB1 levels were elevated in patients with severe sepsis compared to healthy controls. However, HMGB1 levels did not predict the severity of organ dysfunction or mortality in sepsis patients. Clinical Implications: While HMGB1 is a known mediator of inflammation in sepsis, its utility as a diagnostic or prognostic biomarker in clinical settings appears limited.
							CD4+ and CD8+ , CRP		4.HMGB1 in Sepsis: HMGB1 is highly expressed in sepsis patients, with levels increasing as disease severity progresses. It is closely associated with immune dysfunction, reflected by altered T-cell markers (CD4+ and CD8+). Prognostic Value: Elevated HMGB1 levels are indicative of worse prognosis, lower survival rates, and greater disease severity. HMGB1 could serve as a prognostic biomarker and potentially a therapeutic target for sepsis management.
							IFN-γ		5.Prognostic Value of HMGB1: Persistent and delayed HMGB1 release may indicate an ongoing hyperinflammatory state in sepsis, contributing to poor outcomes. Chronic diseases exacerbate this effect, suggesting a synergy between acute sepsis and underlying low-grade inflammation.
8.ELANE	ELANE	Elastase, Neutrophil Expressed HLE Neutrophil Elastase PMN Elastase Medullasin PMN-E ELA2 HNE NE Polymorphonuclear Leukocyte Elastase Bone Marrow Serine Protease Elastase 2, Neutrophil Leukocyte Elastase Elastase-2 Granulocyte-Derived Elastase Polymorphonuclear Elastase Human Leukocyte Elastase EC 3.4.21.37 EC 3.4.21 SCN1 GE	Protein biomarker gene biomarker in bioinformatics research	prognostic marker	where pyroptosis or excessive inflammation is involved. more closely linked to the host's immune response, particularly neutrophil activation	Cytokine Storm Vascular and Endothelial Coagulation Oxidative Stress		GeneCards/ Pathways by source for ELANE Gene MalaCards/NO KEGG/NO UniProt/NO	1.higher ELANE expression was linked to poorer outcomes. provide insights into potential biomarkers for sepsis prognosis and targets for therapeutic development.
									2.The analysis revealed that ELANE was significantly associated with sepsis severity, indicating its potential as a biomarker for diagnosing and prognosing sepsis. These findings suggest that monitoring ELANE expression could provide valuable insights into the severity of sepsis and that targeting NE may offer therapeutic benefits in managing the condition.
									Most of the studies were bioinformatics analysis
D-dimer	The genes indirectly involved in its formation and regulation include: FGA (Fibrinogen Alpha Chain) FGB (Fibrinogen Beta Chain) FGG (Fibrinogen Gamma Chain	D-dimer is a protein fragment, not a gene product directly. It is a degradation produc t of fibrin, which forms during the clotting process and is broken down by the enzyme plasmin during fibrinolysis.	protein biomarker	Prognostic marker					1.The study highlights D-dimer as a promising biomarker for predicting mortality in patients with suspected infection and sepsis.

9.IL8	**CXCL8**	C-X-C Motif Chemokine Ligand 8 MDNCF NAP-1 MONAP GCP-1 Monocyte-Derived Neutrophil Chemotactic Factor Monocyte-Derived Neutrophil-Activating Peptide Granulocyte Chemotactic Protein Chemokine (C-X-C Motif) Ligand 8 SCYB8 LYNAP LUCT LECT IL-8 GCP1 NAP1 NAF IL8 Beta Endothelial Cell-Derived Neutrophil Activating Peptide Lung Giant Cell Carcinoma-Derived Chemotactic Protein Lymphocyte Derived Neutrophil ActivatingPeptide Alveolar Macrophage Chemotactic Factor I Tumor Necrosis Factor-Induced Gene 1 Neutrophil-Activating Peptide 1 T-Cell Chemotactic Factor Interleukin 8 Interleukin-8 Emoctakin AMCF-I B-ENAP TSG-1 3-10C K60 Small Inducible Cytokine Subfamily B, Member 8 Beta-Thromboglobulin-Like Protein Neutrophil-Activating Protein C-X-C Motif Chemokine 8 Protein 3-10C	Protein biomarker	Prognostic marker		Inflammatory and Immune Vascular and Endothelial Coagulation	associated with increased levels of IL-1β, IL-6, IL-10, TNF-α, and CRP		1.IL-8 serves as a sensitive and specific biomarker for: Predicting infections and sepsis in burn patients with IL-8 levels above 234 pg/mL. Correlating with burn severity and MOF in patients with levels below 234 pg/mL. High IL-8 levels are indicative of severe inflammatory responses, leading to poor outcomes in burn patients. IL-8 measurement could guide early diagnosis and management of sepsis in burn patients. This biomarker provides clinicians with an early warning system to target timely therapeutic interventions.
							IL-1b, IL-6, IL-10, IL-12p70, TNF-a CRP and PCT CD64		2.IL-8: A potent chemoattractant that activates neutrophils. Levels increase with disease severity and are predictive of mortality. CD64: A marker of neutrophil activation, specific for bacterial infections. Rapidly measurable and reliable for assessing sepsis progression. Clinical Relevance: A single measurement of CD64 and IL-8 within 24 hours of sepsis onset is sufficient to: Differentiate stages of sepsis. Assess severity and organ dysfunction. Predict 28-day mortality.
									3. Increased Chemokine/Cytokine Levels: Five chemokines—CXCL8 (IL-8), CXCL10, CXCL12, CCL13, and CCL22—were significantly elevated in all three sepsis cases. Other chemokines, such as CXCL1, CXCL2, and CCL1, showed elevated levels in two of the three cases. No mRNA Changes: Despite increased protein levels of these chemokines, their corresponding mRNA expression levels were not altered, suggesting post-transcriptional regulation or accumulation of circulating proteins
							IL-6, IL-21, MCP-1 miR-3663-3p mRNA markers TDAG8 and TLR4		4.It emphasizes the role of miR-3663-3p as a potential biomarker for the rapid and reliable diagnosis of sepsis when combined with pro-inflammatory cytokines such as IL-6, IL-21, CXCL8, and MCP-1, along with mRNA markers TDAG8 and TLR4.
									5. The study highlights the significant elevation of IL-8 in sepsis, particularly in patients with shock. While IL-8 correlates with several clinical and inflammatory parameters, its prognostic value remains limited. IL-8 could serve as a biomarker for assessing shock severity and inflammatory activity in sepsis patients.
									6.Procalcitonin (PCT) is a highly effective biomarker for diagnosing sepsis and differentiating it from SIRS in critically ill patients. IL-6 and IL-8 are less reliable for diagnosis but may provide additional prognostic insights. IL-8, however, correlated with mortality risk in patients with sepsis.
							PCT, IL6		
							ICAM-1, VEGFR2, and urokinase IL-6, IL-10		7. The study highlights the potential of ICAM-1, VEGFR2, and urokinase as diagnostic tools for sepsis. Sepsis patients had significantly higher levels of: IL-6, IL-8, IL-10, ICAM-1, and urokinase compared to SIRS patients. These markers were also elevated compared to healthy controls. VEGFR2 levels were lower in sepsis patients compared to SIRS.
							CRP		8. Whole blood IL-8 outperforms plasma IL-8 and CRP in diagnosing sepsis in postoperative ICU patients. Its high diagnostic accuracy and practical advantages make it a promising biomarker for early sepsis detection
miRNA150	MIR150	MicroRNA 150 Hsa-MiR-150-5p Hsa-MiR-150-3p Hsa-Mir-150 MIRN150 Hsa-Mir-150_pre MIMAT0004610 MIMAT0000451 MI0000479 MiRNA150 Mir-150	gene biomarker	diagnostic/prognostic	general sepsis biomarker across diverse infection types	Inflammatory and Immune Cytokine Storm Regulates MYD88, CXCL8 Vascular and Endothelial Modulates VEGFA and ANGPT2 Apoptosis and Cell Death Controls FOXP1 and BCL2 Epigenetic Regulation	downregulation of ARG1, IL-6, and anti-inflammatory cytokines (TGF-β, IL-10).	Genecards/NO MalaCards/NO KEGG/NO UniProt/NO	1.MicroRNA-150 (miR-150): Central regulator downregulated in sepsis. ARG1 (Arginase-1): Key protein suppressed by miR-150, reducing MDSC-mediated immunosuppression. IL-6, IL-10, TGF-β: Cytokines influenced by miR-150 modulation.
							negatively correlated with pro-inflammatory cytokines (TNF-alpha, IL-1B) and the anti-inflammatory cytokine IL-10. miR-182 and miR-342-5p		2.This study highlights miR-150 as a candidate for non-invasive sepsis diagnostics and suggests its potential role in regulating immune responses during sepsis. Its expression levels in plasma and leukocytes can distinguish sepsis patients from healthy individuals. A proposed miR-150/IL-1B ratio could further refine severity assessment. miR-150 was significantly downregulated in both leukocytes and plasma of sepsis patients compared to controls. miR-182 and miR-342-5p were also altered but to a lesser extent.
									3. The study highlights the potential of combining miR-150 levels with the SOFA score to enhance prognostic accuracy in sepsis patients. miR-150 could serve as a valuable prognostic marker, reflecting underlying immune dysregulation in sepsis.
									4. The study highlights miR-150's potential as a prognostic biomarker in critically ill patients but suggests limited utility for sepsis diagnosis. Reduced miR-150 levels may indicate unfavorable outcomes and reflect immune dysregulation in critical illness. No significant difference was found in miR-150 levels between septic and non-septic critically ill patients. miR-150 levels were not correlated with common markers of inflammation or infection, such as C-reactive protein (CRP), procalcitonin (PCT), interleukin-6 (IL-6), interleukin-10 (IL-10), or tumor necrosis factor (TNF).
							miR-223: Associated with sepsis severity. miR-146a and miR-150: Correlated with survival and inflammatory regulation. miR-155 and miR-126: Implicated in endothelial function and sepsis progression.		5. miR-150: Downregulated in most studies, associated with immune modulation, anti-inflammatory effects, and endothelial integrity. miR-146a: Also downregulated, with anti-inflammatory and immune-regulating roles.
									6. Prognostic Potential: miR-150 can serve as a biomarker to assess sepsis progression and predict outcomes.(yellow article) Levels of white blood cells (WBC), IL-6, CRP, and TNF-α were significantly elevated in sepsis rats compared to controls. Downregulated in Sepsis: miR-150 levels were significantly reduced in sepsis rats compared to both sham operation and control groups. Time-Dependent Decline: Levels of miR-150 progressively decreased over time (6 hours, 12 hours, and 24 hours post-operation).
							miR-25 demonstrated superior diagnostic accuracy Upregulated: miR-25, miR-122, miR-133a, miR-150, miR-223 Downregulated: miR-146a		7. Several miRNAs were highlighted as upregulated or downregulated in sepsis: Upregulated: miR-25, miR-122, miR-133a, miR-150, miR-223 Downregulated: miR-146a These miRNAs correlate with disease severity, prognosis, and stages of sepsis. Notably, miR-150 and miR-223 were linked with disease severity and patient survival. miRNAs like miR-25 demonstrated superior diagnostic accuracy compared to CRP and PCT. miR-150 and miR-133a levels were strongly associated with mortality in critically ill patients.
							miRNA-223 and miRNA-146a miRNA-133a, miRNA-574-5p, and miRNA-16 miRNA-122 miRNA-4772 miRNA-181b		8. miRNA-150: Low levels are associated with poor prognosis in critically ill patients. miRNA-223 and miRNA-146a: Downregulated in sepsis patients. miRNA-133a, miRNA-574-5p, and miRNA-16: Upregulated in sepsis patients. miRNA-122: Shows significant expression differences between septic and healthy patients. miRNA-4772 family (e.g., miRNA-4772-3p): Upregulated in sepsis. miRNA-181b: Downregulated in sepsis patients.
miRNA155	miRNA155	MicroRNA 155 Hsa-MiR-155-5p Hsa-Mir-155 Hsa-MiR-155-3p MIRN155 Hsa-Mir-155_pre MIMAT0000646 MIMAT0004658 MI0000681 MiRNA155 Mir-155	gene biomarker	diagnostic/prognostic	blend of source-dependent specificity pathogen or inflammatory stimulus general immune system functions	Inflammatory and Immune Pathways/ Amplifies TNF-α, IL-6, and IL-1β/ Promotes Th1/Th17 Vascular and Endothelial Pathways/ Epigenetic and Transcriptomic Regulation/ Targets SOCS1, SHIP1, and VEGFA		GeneCards/ miRNA role in immune response in sepsis MalaCards/ NO	1. Diagnostic Use: miR-155 helps identify sepsis early, offering a marker for timely intervention. Prognostic Use: It indicates disease severity, progression, and likely outcomes, aiding in treatment decisions and risk stratification.
									2.Diagnostic Value: miR-155 levels distinguish between healthy individuals and sepsis patients. Prognostic Value: High miR-155 levels predict disease severity and poor survival outcomes. Mechanism: miR-155 drives immunosuppression by promoting the proliferation of CD39+ Tregs, which exacerbates disease progression. The percentage of CD39+ Tregs was higher in sepsis patients, with the highest levels in septic shock cases.
									3.Diagnostic Role: miR-155 is a promising marker for early diagnosis of ALI/ARDS in septic patients, with high sensitivity and specificity. Prognostic Insights: Elevated miR-155 levels indicate more severe lung injury and poorer pulmonary function.

									4.miR-155 plays a critical role in septic shock by driving myocardial and vascular dysfunction through multiple mechanisms, including: Amplification of NO/cGMP signaling. Suppression of Ang II reactivity via AT1R downregulation. Dysregulation of the CD47-thrombospondin-1 axis. Therapeutic Potential: Genetic deletion or pharmacologic inhibition of miR-155 improved survival and cardiovascular outcomes in septic shock models.
							miR-146a		5. The study reports that miR-155 was reduced (downregulated) in the peripheral blood mononuclear cells (PBMCs) of sepsis patients compared to healthy controls. Dysregulated miRNAs, particularly miR-146a, play a critical role in balancing pro-inflammatory and anti-inflammatory responses in sepsis. miRNAs like miR-146a may serve as potential biomarkers for disease severity and targets for therapeutic interventions.
miRNA146a	miRNA146a	MicroRNA 146a Hsa-MIR-146a-3p Hsa-MIR-146a-5p Hsa-Mir-146a Hsa-Mir-146 MIRN146A MIRN146 Hsa-Mir-146-P4_pre MicroRNA 146 2 MIMAT0000449 MIMAT0004608 MIRNA146A MI0000477 MiR-146a	gene biomarker	diagnostic/prognostic			miR-223	GeneCards/ NO MalaCards/ Bacterial Sepsis Septic Arthritis	1.miR-146a and miR-223 have strong potential as novel biomarkers for the early diagnosis of sepsis, offering better specificity and sensitivity than traditional markers. In this study, miR-155 showed no significant changes in expression levels across the three groups, suggesting it does not serve as a useful biomarker in this context. miR-223 emerged as the most reliable biomarker due to its distinct reduction in sepsis compared to SIRS.
							miR-146b		2. Both miR-146a and miR-146b are elevated in sepsis patients and associated with increased disease severity and systemic inflammation. miR-146b is a more reliable biomarker than miR-146a for: Diagnosing sepsis. Predicting mortality risk and overall prognosis. miR-146b showed stronger correlations than miR-146a with: CRP (r = 0.494 vs. 0.283). TNF-α (r = 0.368 vs. 0.181). IL-6 (r = 0.408 vs. 0.188).
									3. Plasma miR-146a levels are lower in sepsis patients compared to non-sepsis-SIRS patients, suggesting its potential as a biomarker for distinguishing these conditions.
									4.Role of miR-146a: miR-146a acts as a critical anti-inflammatory regulator by targeting TLR/NF-κB pathways. Its upregulation reduces cytokine production and improves survival in septic mice.
									5. miR-146a stands out as a strong candidate biomarker for diagnosing and monitoring sepsis severity. Dysregulated microRNAs, including miR-223 and miR-155, play significant roles in sepsis pathophysiology but require further study for clinical application.
							miR-150, miR-223		6. Extracellular miRNAs, particularly miR-150, miR-223, and miR-146a, hold significant potential as diagnostic and prognostic biomarkers for sepsis. Intracellular miRNAs play critical regulatory roles in inflammatory pathways, highlighting their dual importance as both biomarkers and therapeutic targets.
miRNA223	miRNA223	MIR223 MicroRNA 223 Hsa-MIR-223-5p Hsa-MIR-223-3p Hsa-Mir-223 MIRN223 Hsa-Mir-223_pre MIMAT0000280 MIMAT0004570 MI0000300 MiRNA223 Mir-223	gene biomarker	diagnostic/prognostic		inflammatory pathways		GeneCards/ NO MalaCards/ NO	1. miR-223 could serve as a prognostic biomarker, with higher levels indicating improved survival. It may also be a potential therapeutic target for immunomodulation in sepsis.
									2. Diagnostic Role: miR-223 is a promising biomarker for sepsis, with the ability to distinguish it from SIRS and provide insights into disease progression. Therapeutic Potential: Targeting miR-223 could offer a novel approach to controlling inflammation in sepsis and other inflammatory diseases.
									3. Circulating miRNAs show high diagnostic accuracy for sepsis, outperforming traditional markers like PCT and CRP. miR-223 stands out as a strong diagnostic candidate due to its correlation with disease severity and specificity for sepsis.
							miR-7110-5p		4. miR-223-3p is a promising biomarker for diagnosing sepsis secondary to pneumonia with high sensitivity and specificity. miR-7110-5p also shows potential but requires further validation.
10.IL10	IL10	Interleukin 10 IL-10 CSIF Cytokine Synthesis Inhibitory Factor IL10A TGIF T-Cell Growth Inhibitory Factor Interleukin-10 GVHDS	protein biomarker	prognostic marker	universal immune regulatory cytokine	Inflammatory and Immune Pathways Endothelial Protection Metabolic Pathways Apoptosis		GeneCards/ NO MalaCards/ Bacterial Sepsis Septic Arthritis	1. While IL-10 is not directly useful as a diagnostic marker, it holds value in understanding the immune dynamics of sepsis and could complement other biomarkers in prognostic assessments
									2.The study demonstrates that IL-10 is a key mediator of immune suppression during polymicrobial sepsis. Delayed neutralization of IL-10 restores immune function and improves survival, highlighting the potential for phase-specific therapeutic interventions targeting IL-10 in sepsis management.
									3. IL-10 levels at admission showed potential as a prognostic marker for sepsis outcomes. Combining IL-10 with other markers, such as IL-6, improved predictive accuracy for mortality and MOF.
									4. L-10 is a key mediator of sepsis-induced immunosuppression, inhibiting pro-inflammatory cytokines (e.g., TNF-α) and antigen presentation (via reduced HLA-DR). Elevated IL-10 levels may serve as a marker of immunosuppression in septic shock.
							IL17 , PCT		5.IL-10 and IL-17 offer early diagnostic value by reflecting the immune and inflammatory responses in sepsis. PCT enhances diagnostic precision for bacterial infections and sepsis severity.
									6. Timely administration of IL-10 can delay shock onset, providing a critical window for surgical or medical intervention.
									7. The study demonstrates that PCT and IL-10 are effective biomarkers for diagnosing severe sepsis and predicting patient outcomes. Their combined use improves accuracy, offering a promising approach for early and tailored interventions in sepsis management.
			gene marker	giagnostic marker					polymorphism in gene make prediction about sepsis.
11.IL1B	IL1b								
12.S100A8	S100A8	S100 Calcium Binding Protein A8 MRP8 P8 Migration Inhibitory Factor-Related Protein 8 Leukocyte L1 Complex Light Chain Calprotectin L1L Subunit Cystic Fibrosis Antigen S100-A8 60B8AG MRP-8 CGLA CAGA CFAG Urinary Stone Protein Band A Protein S100-A8 Calgranulin A S100 Calcium-Binding Protein A8 Calgranulin-A CP-10 MA387 L1Ag MIF NIF	Protein marker/ some studies mRNA level	diagnostic/prognostic	universal role in the inflammatory response	Inflammatory and Immune Pathways/Cytokine Storm/ Neutrophil Recruitment and Activation Endothelial Dysfunction Act as DAMPs, amplifying pro-inflammatory cytokines Promote chemotaxis and NET formation Drive ROS release, contributing to tissue damage.		GeneCards/ NO MalaCards/ Septic Arthritis	1. the study emphasizes the prognostic value of S100A8/S100A9 in identifying septic shock patients at higher risk of mortality. Elevated S100A8/S100A9 levels reflect severe inflammation and cellular damage in septic shock. The identified proteoforms (e.g., oxidized S100A8) may serve as specific biomarkers for prognosis.
							S100A9		2. Findings suggest S100A8/A9 mRNA levels could serve as surrogate biomarkers for endotoxin tolerance and sepsis-induced immune dysfunctions. Elevated S100A8/A9 levels reflect immune dysfunction in sepsis and may predict hospital-acquired infections or poor outcomes. IL-10 appears to mediate the induction of S100A8/A9 during immune reprogramming, while IFNγ can reverse these changes. 100A8/A9 mRNA levels could guide patient stratification for personalized treatments targeting immune restoration (e.g., IFNγ therapy).
							S100A9		3. the study highlights the diagnostic value of serum S100A8/A9 levels in distinguishing SIC patients and predicting disease severity. demonstrates that S100A8/A9 contributes to SIC development via the ERK1/2-Drp1 signaling pathway, leading to mitochondrial dysfunction. It highlights the potential of targeting S100A8/A9 as a therapeutic strategy and its use as a biomarker for SIC diagnosis and prognosis.
							(PCT) and (CRP), S100A9		4.S100A8/A9 is a reliable biomarker for identifying sepsis severity and associated organ injuries. Early detection using S100A8/A9 levels can improve prognosis and guide treatment strategies. Elevated serum levels correlate with sepsis severity and mortality. Performs better than traditional biomarkers like procalcitonin (PCT) and C-reactive protein (CRP) in predicting ICU admission and mortality.
							S100A9		5. The study identifies S100A8/A9hi neutrophils as key drivers of mitochondrial dysfunction and endothelial cell death in sepsis. the study highlights the diagnostic and prognostic value of S100A8/A9 in identifying severe endothelial damage and predicting poor outcomes in sepsis. Monitoring S100A8/A9 levels could help identify sepsis patients at high risk for severe endothelial damage and poor outcomes.
							S100A9		6.The article discusses the significant diagnostic value of S100A8/A9 in identifying and monitoring inflammation in sepsis and other inflammatory conditions. Elevated levels of S100A8/A9 are associated with diseases such as sepsis, rheumatoid arthritis, and inflammatory bowel disease. S100A8/A9 is more sensitive than conventional markers like CRP in monitoring inflammation.
									7. The study highlights S100A8 as both a diagnostic biomarker and a potential therapeutic target for sepsis. Elevated levels are indicative of severe sepsis, but S100A8 supplementation offers a protective mechanism by mitigating cytokine storm and systemic inflammation. S100A8 reduced inflammatory cytokine levels (e.g., TNF-α, IL-6, IL-1β) and attenuated cytokine storm severity. S100A8 suppressed TLR4-MyD88 signaling in peritoneal macrophages, reducing cytokine production and systemic inflammation.

							S100A9		8. S100a8/a9 gene expression in blood was significantly elevated in septic arthritis mice compared to non-arthritic mice as early as day 2 post-infection. Elevated gene expression correlated positively with bone erosion severity on day 10. Plasma S100a8/a9 protein levels were upregulated in all infected mice but did not differentiate between arthritic and non-arthritic groups. S100a8/a9 gene expression shows promise as an early biomarker for septic arthritis, enabling timely intervention. It plays a critical role in the inflammatory response and joint damage, especially in Staphylococcus aureus-induced infections.
							S100A9, S10012		9. S100A8/S100A9 and S100A12 are valuable biomarkers for assessing mortality risk in septic shock patients, particularly in the early phase. highlights the diagnostic and prognostic value of S100A8/S100A9 and S100A12, demonstrating their potential to predict mortality and complement clinical scoring systems.
									10
13.S100A9	S100A9	S100 Calcium Binding Protein A9 MRP-14 MRP14 P14 Migration Inhibitory Factor-Related Protein 14 Leukocyte L1 Complex Heavy Chain Calprotectin L1H Subunit S100-A9 MAC387 60B8AG LIAG CGLB CAGB CFAG MIF NIF Protein S100-A9 Calgranulin B S100 Calcium-Binding Protein A9 (Calgranulin B) S100 Calcium-Binding Protein A9 Calgranulin-B L1AG	Protein marker/ gene	diagnostic/prognostic	universal role in the inflammatory response	Inflammatory and Immune Pathways/Cytokine Storm/ Neutrophil Recruitment and Activation Endothelial Dysfunction Act as DAMPs, amplifying pro-inflammatory cytokines Promote chemotaxis and NET formation Drive ROS release, contributing to tissue damage.		GeneCards/ NO MalaCards/ Bacterial Sepsis	1.study primarily evaluates the therapeutic role of targeting S100A9, the significant elevation of S100A9 levels in plasma and lungs during sepsis suggests potential diagnostic value as a biomarker for inflammation severity.
									2.This study identifies S100A9 as a critical mediator of inflammation and pyroptosis in sepsis-associated acute kidney injury. It highlights S100A9 as both a potential diagnostic biomarker and a therapeutic target for mitigating kidney injury in sepsis patients.
									3. Elevated plasma S100A9 levels suggest it could serve as a biomarker for sepsis diagnosis. Deficiency of S100A9 mitigates these effects, suggesting therapeutic potential for targeting S100A8/A9 in sepsis.
14.S100A12	S100A12	S100A12 S100 Calcium Binding Protein A12 CAAF1 CGRP CAGC P6 Extracellular Newly Identified RAGE-Binding Protein Migration Inhibitory Factor-Related Protein 6 Calcium-Binding Protein In Amniotic Fluid 1 Neutrophil S100 Protein ENRAGE MRP6 Protein S100-A12 Calgranulin C EN-RAGE MRP-6 S100 Calcium-Binding Protein A12 (Calgranulin C) S100 Calcium-Binding Protein A12 Calgranulin-C Calcitermin	protein marker/ gene	diagnostic marker	universal role in the inflammatory response	Inflammatory and Immune Pathways/Cytokine Storm/ Neutrophil Recruitment and Activation Endothelial Dysfunction Act as DAMPs, amplifying pro-inflammatory cytokines Promote chemotaxis and NET formation Drive ROS release, contributing to tissue damage.		GeneCards/ NO MalaCards/ NO	1. Monitoring S100A12 levels could help in diagnosing sepsis and assessing its severity. This study identifies S100A12 as a proinflammatory amplifier of innate immunity, particularly through TLR4-mediated monocyte activation. It has potential diagnostic value in sepsis and may serve as a therapeutic target to modulate excessive inflammatory responses.
									2.S100A12 is a promising biomarker for systemic inflammation in severe sepsis, with significant elevation across all infection types. The high local levels during peritonitis suggest that S100A12 is released predominantly at the site of infection. S100A12 has diagnostic value for identifying systemic inflammation and sepsis, but its lack of correlation with disease severity limits its prognostic utility.
									3. S100A12 demonstrated high diagnostic value for sepsis (AUC = 0.997) and moderate value for AF (AUC = 0.632). S100A12 expression was significantly elevated in sepsis and AF, correlating with immune and inflammatory pathways. S100A12 upregulation in serum and atrial tissue was associated with inflammation, reduced heart rate, and increased susceptibility to AF in septic mice. The study initially identified S100A12 at the gene level using bioinformatics and MR methods. It validated these findings at the protein level in experimental mouse models, demonstrating functional and therapeutic relevance.
							S100A9, CHPT1, CPEB4, DNAJC3, MAFG, NARF, SNX3, METTL9		4.This study is a combination of in silico (bioinformatics) and wet lab (experimental validation) approaches The identified genes, particularly S100A12 and S100A9, demonstrate strong potential as diagnostic biomarkers for sepsis. Nine key dysregulated genes were identified: CHPT1, CPEB4, DNAJC3, MAFG, NARF, SNX3, S100A9, S100A12, and METTL9. These genes were progressively upregulated in sepsis and demonstrated strong predictive potential with AUC values of 0.957 (logistic regression) and 0.987 (random forest).
15.sCD14-ST/ CD14	CD14	CD14 Molecule Myeloid Cell-Specific Leucine-Rich Glycoprotein Monocyte Differentiation Antigen CD14 CD14 Antigen My23 Antigen	protein marker	diagnostic/prognostic	universal pattern recognition receptor pathogen-associated molecular patterns (PAMPs)	Inflammatory and Immune Pathways/Toll-like Receptor (TLR) Signaling/ Cytokine Storm/ Endothelial Dysfunction Acute Phase Response/ Systemic Inflammation		GeneCards/ NO MalaCards/ Bacterial Sepsis Septic Arthritis	1. CD14: The decreased mCD14 and elevated sCD14 levels in sepsis patients suggest its diagnostic utility for distinguishing sepsis severity. mCD14: Reduced levels on cell surfaces may reflect immune cell dysfunction, a hallmark of immune suppression in severe sepsis or septic shock. sCD14: Elevated levels in the bloodstream indicate a systemic inflammatory response, often proportional to the disease's severity.
									2. Elevated TLR2, TLR4, and CD14 protein level expression distinguishes sepsis patients from healthy individuals. Decreased expression of TLR2 and CD14 on monocytes at admission correlates with higher mortality, indicating potential as prognostic biomarkers.
									3. Diagnostic Value: Elevated protein levels of sCD14-ST in plasma were specific to sepsis and distinguished it from SIRS and healthy controls. sCD14-ST is a sensitive biomarker for early and rapid diagnosis of sepsis. Prognostic Value: sCD14-ST levels correlate with sepsis severity, as indicated by SOFA scores, and track the response to treatment. This makes sCD14-ST a potential prognostic marker for monitoring sepsis progression and therapeutic efficacy.
									4. Diagnostic Role: Elevated protein levels of Presepsin in plasma make it a reliable diagnostic biomarker for distinguishing sepsis from SIRS and other conditions. Faster and more accurate than traditional markers. Prognostic Role: Presepsin levels correlate with the severity of sepsis and predict mortality, supporting its use as a prognostic biomarker.
									5. sCD14-ST (Presepsin) production is tightly linked to bacterial infections, making it a specific diagnostic biomarker for sepsis. Unlike general inflammatory markers, its production depends on bacterial phagocytosis, enhancing specificity for sepsis.
							PCT, CRP		6.Diagnostic Value: Presepsin shows higher specificity for bacterial infections than other markers such as CRP and procalcitonin (PCT). Levels rise significantly in the early stages of sepsis, making it an early diagnostic biomarker. Prognostic Value: Levels correlate with the severity of infection and systemic inflammatory response. Elevated presepsin levels are linked to poor outcomes, including mortality.
16.CD64	FCGR1A	Fc Gamma Receptor Ia FcgammaRIa FCGR1 FCG1 FcgammaRI CD64A CD64 Fc Fragment Of IgG, High Affinity Ia, Receptor For (CD64) Fc Fragment Of IgG, High Affinity Ia, Receptor (CD64) High Affinity Immunoglobulin Gamma Fc Receptor I Fc Fragment Of IgG Receptor Ia IgG Fc Receptor I Fc-Gamma RIA Fc-Gamma RI IGFR1 Fc-Gamma Receptor I A1 CD64 Antigen Fc Gamma RI FCRI FcRI	protein marker	diagnostic/prognostic	bacterial infections	Inflammatory and Immune/ Cytokine Storm Pathogen Recognition and Phagocytosis Oxidative Stress/ ROS production Acute Phase Response/ Immune activation	IL-8	GeneCards /NO MalaCards/ Bacterial Sepsis Septic Arthritis	1. Diagnostic: CD64 and IL-8 distinguished sepsis severity stages effectively. Prognostic: Both markers predicted 28-day mortality with high sensitivity and specificity.
							PCT, CRP, WBC		2. The CD64 index is identified as the most reliable biomarker among those tested for the diagnosis of severe systemic bacterial infection and sepsis in critically ill patients. Its high diagnostic accuracy supports its use as a diagnostic marker rather than focusing on prognostic implications. Prognostic Value: While the primary focus was diagnostic, the CD64 index also provided insights into the severity of systemic bacterial infections and sepsis progression, potentially aiding early therapeutic decisions.
									3.Diagnostic: nCD64 protein expression is highly sensitive and specific for diagnosing sepsis at ICU admission. Adding nCD64 to CRP improves diagnostic accuracy. Prognostic: nCD64 levels correlate with treatment appropriateness and can monitor response to antibiotics. Persistently elevated levels after three days suggest inappropriate antibiotic therapy.
									4. Prognostic Value: CD64 expression showed limited ability to predict mortality the diagnostic value of CD64 protein expression on neutrophils for identifying sepsis in ICU patients.
							BCL2A1 gene		5. BCL2A1 and FCGR1A showed strong potential as diagnostic biomarkers for sepsis. BCL2A1 emerged as a novel candidate with clinical relevance, validated across multiple independent datasets. highlights BCL2A1 as a novel gene-level biomarker with significant diagnostic and prognostic value for sepsis, validated by both bulk RNA-seq and scRNA-seq data

17.CD11b, ITGAM	ITGAM, CD11b	Integrin Subunit Alpha M MAC-1 CD11b CR3A Integrin, Alpha M (Complement Component 3 Receptor 3 Subunit) Cell Surface Glycoprotein MAC-1 Subunit Alpha Complement Component 3 Receptor 3 Subunit Macrophage-1 Antigen Alpha Subunit CD11 Antigen-Like Family Member B Leukocyte Adhesion Receptor MO1 Integrin Alpha-M CR-3 Alpha Chain Integrin, Alpha M (Complement Component Receptor 3, Alpha ; Also Known As CD11b (P170), Macrophage Antigen Alpha Polypeptide) Neutrophil Adherence Receptor Alpha-M Subunit Macrophage Antigen Alpha Polypeptide Neutrophil Adherence Receptor Antigen CD11b (P170) CD11b Antigen MAC1A SLEB6 CD11B MO1A	protein marker	diagnostic/prognostic	universal immune receptor	Inflammatory and Immune/ Pathogen Recognition and Phagocytosis Leukocyte Adhesion and Migration Vascular and Endothelial/ Endothelial Dysfunction Oxidative Stress/ ROS Production Acute Phase Response/ Immune Activation	CD14	GeneCards/ NO MalaCards/ Bacterial Sepsis	1. sCD14 levels can serve as a potential biomarker for detecting sepsis and stratifying disease severity. The dynamic regulation of CD11b and cytokine profiles may help in identifying stages of sepsis.
							CD64		2.The study highlights neutrophil CD64 as a superior diagnostic biomarker for severe sepsis, with excellent sensitivity and specificity. CD11b also provides additional diagnostic value but is less effective than CD64. Both markers show potential prognostic relevance for monitoring immune recovery in sepsis survivors.
							CRP		3.introduces the CRP/CD11b ratio as a novel and effective diagnostic parameter for identifying gram-positive sepsis
							CXCR2		4. CD11b: Significantly increased on neutrophils of septic patients compared to healthy controls over the 5-day study period. CXCR2: Significantly reduced in septic patients compared to controls ($p < 0.02$). CXCR1: No significant changes or correlations were observed with disease severity or oxygenation. focusing on protein-level markers like CD11b and CXCR2. These changes correlate with disease severity, highlighting their potential as both diagnostic and prognostic markers in septic shock.
18.C3AR1/C5aR	C3AR1	Complement C3a Receptor 1 C3AR AZ3B C3a Anaphylatoxin Chemotactic Receptor Complement Component 3a Receptor 1 HNFAG09 Complement Component 3 Receptor 1 C3a-R C3R1 /	protein/gene marker	diagnostic/prognostic	universal / level of activation may vary based on: The type of pathogen	Inflammatory and Immune/ Cytokine Storm Neutrophil Recruitment and Activation Vascular and Endothelial/ Endothelial Dysfunction Oxidative Stress/ ROS production		GeneCards/NO MalaCards/ NO	1. CD63 and C3AR1 are identified as key diagnostic markers for septic shock due to their significant differential gene expression and involvement in immune and inflammatory pathways./gene
		Complement C5a Receptor 1 C5AR 2 3 4 5 CD88 C5R1 C5A C5a Anaphylatoxin Chemotactic Receptor 1 Complement Component 5a Receptor 1 C5a-R Complement Component 5 Receptor 1 (C5a Ligand) C5a Anaphylatoxin Chemotactic Receptor C5a Anaphylatoxin Receptor CD88 Antigen C5a Ligand C5aR					ITGAM, CD44, IL2Rg		2.Single-Cell RNA Sequencing:/gene ITGAM and C3AR1 were predominantly expressed in macrophage clusters. CD44 and IL2RG were expressed across various immune cell types, reflecting their widespread involvement in immune modulation. Diagnostic: The core genes (ITGAM, CD44, C3AR1, IL2RG) provide potential biomarkers for distinguishing sepsis from SIRS and tracking disease progression. Prognostic: The expression levels of ITGAM and C3AR1 in macrophages correlate with inflammatory responses, suggesting their use as markers for immune dysregulation severity.
							C5a		3.Diagnostic:/protein Elevated levels of C3a and C5a in plasma could indicate the degree of complement system activation and immune dysregulation in sepsis. Prognostic: The balance between C3a and C5a activity could serve as a marker of disease severity and guide therapeutic strategies.
							caspase-5		4. identifies C3aR1 and caspase-5 as potential biomarkers for diagnosing and understanding the severity of sepsis/gene
									5. Diagnostic: Elevated protein C3a, C5a, Bb, and M-ficolin levels could serve as early biomarkers of sepsis.
									6. Diagnostic Value: Increased expression of C5aR at both the mRNA and protein levels during sepsis suggests it could serve as a biomarker for disease severity. Prognostic Value: High levels of C5aR correlate with poor outcomes. Blocking C5aR reduces cytokine levels and bacterial load, improving survival, which highlights its potential as a therapeutic target.
									7.This study demonstrates that C3aR and C5aR are upregulated during lung inflammation caused by sepsis./gene These receptors could serve as both diagnostic markers and therapeutic targets in sepsis and other inflammatory lung conditions.
									8. The C5a–C5aR axis holds both diagnostic and prognostic significance in sepsis./protein Measuring C5a and C5aR levels could help stratify patients based on disease severity and predict clinical outcomes
									9. Diagnostic and Prognostic Relevance:/protein Diagnostic: Reduced C5aR expression on neutrophils reliably differentiated septic shock patients from healthy controls with high sensitivity and specificity. Prognostic: Lower C5aR expression and higher cC5aR levels were associated with worse outcomes, making them potential prognostic markers.
20.LCN2	LCN2	LCN2 Lipocalin NGAL Neutrophil Gelatinase-Associated Lipocalin Oncogene 24p3 24p3 25 KDa Alpha-2-Microglobulin-Related Subunit Of MMP-9 Siderocalin P25 Migration-Stimulating Factor Inhibitor Lipocalin 2 (Oncogene 24p3) Siderocalin LCN2 Lipocalin-2 MSFI HNL	protein/gene marker	diagnostic/prognostic	Not Pathogen-Dependent	Inflammatory and Immune/ Nutritional Immunity/ Cytokine Storm Vascular and Endothelial/ Endothelial Dysfunction Oxidative Stress/ Iron regulation Organ-Specific Pathways/ Acute Kidney Injury (AKI)		Genecards/ Pathways & Interactions for LCN2 Gene MalaCards/ NO	1. Diagnostic Role:/gene/protein Elevated plasma LCN-2 serves as a biomarker for SIC and correlates with myocardial injury severity. Prognostic Role: High LCN-2 levels are associated with worse cardiac function, suggesting its potential as a prognostic indicator for SIC outcomes.
							OLFM4		2. Diagnostic Role:/gene Early expression of LCN2, OLFM4, and other neutrophil-related genes could help identify patients at risk of ARDS. Prognostic Role: The association of these genes with disease severity and outcomes suggests their potential for stratifying risk and tailoring interventions.
									3.Lcn2 functions as a diagnostic marker on both the protein and gene levels, with protein-level validation providing stronger support for its utility in clinical settings.Sustained Lcn2 Expression: Liver: Lcn2 mRNA levels were rapidly induced 3 hours post-CLP and remained elevated for 30 hours. This persistent expression was confirmed at the protein level. Lung: Lcn2 mRNA levels were higher at baseline compared to the liver and showed similar rapid and sustained elevation post-CLP.
							VEGFA		4. miRNA and mRNA changes (LCN2, VEGFA) correlate with organ dysfunction, making them potential diagnostic markers for specific SOFA components.
							MPO, MMP9, TLR2		5. study highlights the potential of hub genes as biomarkers and therapeutic targets for sepsis and COVID-19./gene MPO, MMP9, TLR2, and LCN2 emerge as key diagnostic candidates, while CD247, CD2, and CD40LG may help in prognostic assessments.
							IL10, LCN2, IL7R, CD40LG, CD28		6.Diagnostic Role: The identified hub genes (IL10, LCN2, IL7R, CD40LG, CD28) serve as reliable diagnostic markers for sepsis. Prognostic Role: LCN2 showed significant differences between shock and non-shock patients, suggesting a role in predicting sepsis severity.
									7. Diagnostic Role:/protein Elevated serum Lcn-2 is an early biomarker for sepsis-induced kidney injury. Prognostic Role: MΦ-derived iron-bound Lcn-2 predicts renal recovery during sepsis.
							Resistin, and IL-8		8. NGAL (Neutrophil Gelatinase-Associated Lipocalin), Resistin, and IL-8 are identified as protein biomarkers differentiate severe sepsis/shock from uncomplicated sepsis.. No Temporal Changes in mRNA: mRNA expression of target genes remained stable over time, indicating that transcriptional changes occurred early in the disease course.

21.CXCL10 IP-10	CXCL10	C-X-C Motif Chemokine Ligand 10 IP-10 GIP-10 SCYB10 IFI10 Crg-2 Mob-1 INP10 C7 Small Inducible Cytokine Subfamily B (Cys-X-Cys), Member 10 10 KDa Interferon Gamma-Induced Protein Small-Inducible Cytokine B10 C-X-C Motif Chemokine 10 Protein 10 From Interferon (Gamma)-Induced Cell Line Interferon-Inducible Cytokine IP-10 Chemokine (C-X-C Motif) Ligand 10 Gamma IP10 Gamma-IP10	protein/gene marker	diagnostic/prognostic	not pathogen-dependent.	Inflammatory and Immune Pathways/ Cytokine Storm/ T-cell and NK Cell Recruitment Vascular and Endothelial/ Endothelial Dysfunction Immune Dysregulation/ Immune Exhaustion		Genecards/ NO Malacards / Bacterial Sepsis Septic Arthritis	1.Diagnostic and Prognostic Relevance:/protein(yellow) Diagnostic Value: MMP-1, MMP-2, MMP-7, MMP-13, and soluble E-selectin are effective in differentiating SIRS from sepsis. IL-1α, IP-10, sTNF-R2, and sFas are indicative of sepsis severity. Prognostic Value: Elevated levels of MMP-3, MMP-10, IL-1α, IP-10, and sTNF-R2 correlate with higher mortality risk.
									2. Diagnostic Role:/protein IL-1β, IL-7, IL-12, RANTES, MIP-1β, and IP-10 show strong diagnostic potential to distinguish sepsis from malaria and febrile controls.
									3. CXCL10 is Elevated During Septic Shock: High concentrations of CXCL10 were observed in plasma and peritoneal lavage fluid during CLP-induced sepsis, peaking 8 hours after the procedure. CXCL10 levels correlated with hypothermia, increased cytokine production, and poor survival. Elevated CXCL10 levels in plasma can serve as an indicator of sepsis severity.
									4. Elevated synovial fluid CXCL10 levels make it a promising diagnostic marker and therapeutic target in septic arthritis./protein
									5. The identified genes (TNFAIP6, GBP1, CXCL10, CXCL5, FCN1, PID1) can stratify septic patients and identify those who might benefit from IFN-γ therapy.
22.IFN-γ	IFNG	Interferon Gamma Immune Interferon IFN-Gamma IMD69 IFG IFI	protein marker	therapeutic role	IFN-gamma production is largely infection-dependent, bacterial/virus	Inflammatory and Immune Pathways/ Cytokine Storm/ T-cell and Macrophage Activation Vascular and Endothelial Pathways/ Endothelial Dysfunction Immune Dysregulation Pathways/ Immune Exhaustion		GeneCards/NO MalaCards/ bacterial sepsis Septic Arthritis	1. study demonstrates that IFN-γ effectively restores immune function in sepsis by reducing T-cell apoptosis, modulating cytokine responses, and downregulating regulatory T cells. /protein These findings highlight IFN-γ as a promising therapeutic candidate for targeted immune enhancement in sepsis.
									2. The findings suggest that therapeutic modulation of the type I IFN pathway could improve outcomes in sepsis by balancing immune activation and inflammation./protein
							TLR4		3.Diagnostic Value:/protein Altered TLR4 expression on NK cells may help differentiate sepsis from SIRS. Impaired IFN-γ production could serve as a biomarker of immune dysfunction in sepsis. Prognostic Value: Reduced NK cell counts and function (e.g., diminished IFN-γ production) may indicate worse immune status and poorer outcomes in sepsis.
									4
23.IFN-α	IFNA1	Interferon Alpha 1 IFN-Alpha0 IFN-ALPHA IFNA13 IFNA@ IFL IFN Interferon Alpha-1/13 Interferon Alpha 1b Interferon Alpha-D IFN-Alpha-1/13 LeIF D Interferon-Alpha1 IFN-Alpha 1b	protein marker	Therapeutic role	More virus infection	Inflammatory and Immune Pathways/ cytokine storm/ Antiviral Defense/Immune Dysregulation Vascular and Endothelial/ Endothelial Dysfunction Oxidative Stress/ ROS Production		Genecards/ No MalaCards/ No	
24.IFN-β	IFNB1	Interferon Beta 1 IFB IFNB IFF Interferon, Beta 1, Fibroblast Fibroblast Interferon Interferon Beta IFN-Beta Interferon-Beta	protein marker	therapeutic role	viral, bacterial, or parasitic infections	Inflammatory and Immune Pathways/cytokine storm/ Antiviral Defense/Immune Dysregulation Vascular and Endothelial/ Endothelial Dysfunction Oxidative Stress/ROS Production		Genecards/ No MalaCards/ No	4. IFN-β restored immune function, indicating potential as a prognostic marker for therapeutic response and survival improvement. study demonstrates that IFN-β effectively restores alveolar macrophage function, enhances neutrophil recruitment, and reduces lung injury, thereby improving survival in a murine model of sepsis-induced ARDS. These findings suggest IFN-β as a potential therapeutic strategy for sepsis-related immune suppression and ARDS.
									5.Prognostic Value: IFN-β expression levels correlate with survival outcomes in experimental sepsis models, suggesting potential as a prognostic biomarker.
									6. Type I IFNs, particularly IFN-β, are central mediators of inflammation in sepsis. While they play essential roles in host defense, their overproduction during sepsis can exacerbate inflammation and tissue damage, making them a potential therapeutic target.
25.CCL19	CCL19	C-C Motif Chemokine Ligand 19 ELC CK Beta-11 Exodus-3 MIP-3b SCYA19 Ckb11 Small Inducible Cytokine Subfamily A (Cys-Cys), Member 19 Epstein-Barr Virus-Induced Molecule 1 Ligand Chemokine Macrophage Inflammatory Protein 3-Beta	protein marker	more prognostic	not pathogen-dependent	Inflammatory and Immune/ Cytokine Storm/ Immune Dysregulation Adaptive Immune/ T-cell Activation and Trafficking	CCL28, and VEGF-A	GeneCards/ NO malaCards/ No	1.Elevated levels of CCL19, CCL28, and VEGF-A could serve as biomarkers for sepsis susceptibility and severity./protein
26.CCL25	CCL25	C-C Motif Chemokine Ligand 25 TECK SCYA25 Ckb15 Small Inducible Cytokine Subfamily A (Cys-Cys), Member 25 Chemokine (C-C Motif) Ligand 25 Small-Inducible Cytokine A25 Thymus Expressed Chemokine C-C Motif Chemokine 25 Chemokine TECK Ck Beta-15 TECKvar Thymus-Expressed Chemokine	protein/gene marker	Therapeutic	not pathogen-dependent primarily expressed in the thymus and intestinal mucosa	Inflammatory and Immune/ Immune Dysregulation Gut Barrier and Mucosal Immunity/ Gut Barrier Integrity Adaptive Immune/ T-cell Trafficking		GeneCards/ NO malaCards/ No	Diagnostic and Prognostic Relevance: Elevated serum levels of CCL25 were associated with sepsis and could serve as a biomarker for inflammation and endothelial dysfunction in ALI. Therapeutic Potential: Neutralizing CCL25 showed promise as a therapeutic strategy to reduce inflammation, improve endothelial barrier function, and mitigate sepsis-induced ALI.
27.CX3CR1	CX3CR1	C-X3-C Motif Chemokine Receptor 1 V28 CMKBRL1 CMKDR1 CCRL1 GPR13 Chemokine (C-X3-C Motif) Receptor 1 Beta Chemokine Receptor-Like 1 Chemokine (C-X3-C) Receptor 1 G-Protein Coupled Receptor 13 CX3C Chemokine Receptor 1 Fractalkine Receptor C-X3-C CKR-1 CMK-BRL-1 CMK-BRL1 Chemokine (C-C) Receptor-Like 1 GPRV28	protein/gene marker	more prognostic than diagnostic	not pathogen-dependent	Inflammatory and Immune Pathways/ cytokine storm/ Monocyte and Macrophage Recruitment Vascular and Endothelial Pathways/. Endothelial Dysfunction Immune Dysregulation/ Immune Exhaustion Oxidative Stress/ ROS production		GeneCards/ NO malaCards/ NO	1. mRNA Level: CX3CR1 mRNA expression was significantly downregulated in septic shock patients compared to healthy controls. Nonsurvivors showed persistently lower CX3CR1 mRNA levels than survivors. Protein Level: CX3CR1 protein expression on monocytes was similarly reduced. The downregulation was more pronounced in nonsurvivors. Soluble CX3CL1 Levels: Elevated sCX3CL1 levels in septic patients' serum correlated with disease severity and poor outcomes. Diagnostic Value: The significant reduction in CX3CR1 mRNA and protein levels in septic patients suggests its potential as a diagnostic marker for immune dysfunction in septic shock. Prognostic Value: CX3CR1 mRNA levels predicted patient survival with: Sensitivity: 88% Specificity: 78% (threshold: 0.00135). Persistent CX3CR1 downregulation correlated with poor outcomes and higher mortality rates.
									2. The study suggests potential therapeutic manipulation of CX3CR1-mediated signals to enhance bacterial clearance and reduce mortality in sepsis./gene While the focus was on the mechanistic roles, it hints at diagnostic implications for CX3CR1 expression or function in sepsis susceptibility.
									3.CX3CR1 mRNA and protein levels were downregulated in the same tissues post-CLP. highlights the regulatory relationship between fractalkine and CX3CR1 in sepsis, suggesting that targeting NF-κB could modulate these interactions and potentially improve outcomes.
									4. Fractalkine could serve as a biomarker for sepsis severity and mortality. /protein(yellow) Blocking Fractalkine or its receptor CX3CR1 may represent a therapeutic strategy for reducing inflammation and improving outcomes in sepsis.
									5. CX3CR1 Expression:/gene/protein CX3CR1 mRNA and protein levels were significantly decreased in monocytes from septic shock patients compared to healthy controls. Non-survivors exhibited a more pronounced and persistent downregulation than survivors. sCX3CL1 Levels: Serum levels of soluble fractalkine were elevated in septic shock patients, particularly in non-survivors, suggesting increased cleavage of membrane-bound CX3CL1 The study highlights the potential of CX3CR1 as a prognostic biomarker for mortality in septic shock. Persistent downregulation of CX3CR1 on monocytes is associated with poor outcomes, underscoring its role in sepsis-induced immunosuppression.
									6.Survival Analysis: Patients with CX3CR1 expression above the threshold showed significantly better survival rates at both D7 and D28 compared to those below the threshold. highlights CX3CR1 mRNA as a reliable, early biomarker of mortality in ICU patients, potentially useful for risk stratification and immunomonitoring. Its role in identifying high-risk patients for tailored interventions is emphasized.

28.P2X7	P2RX7	P2RX7 Purinergic Receptor P2X 7 P2X7 P2X Purinoceptor 7 ATP Receptor P2Z Receptor MGC20089 Purinergic Receptor P2X, Ligand-Gated Ion Channel, 7 Purinergic Receptor P2X, Ligand-Gated Ion Channel, 7 Pumergic Receptor P2X 7 Purinergic Receptor P2X7 Receptor External Ids for P2RX7 Gene	protein/gene marker	more prognostic then diagnostic	not pathogen-dependent	Inflammatory and Immune Pathways/ Cytokine Storm/ Immune Cell Activation Vascular and Endothelial Pathways/Endothelial Dysfunction Apoptosis and Cell Death Pathways/Pyroptosis Oxidative Stress/ ROS production	NLRP3	GeneCards/ NO malaCards/ NO	1. Diagnostic:/protein P2X7 receptor expression and mitochondrial dysfunction could serve as biomarkers for immune paralysis in sepsis. Prognostic: Early NLRP3 inflammasome dysfunction strongly correlated with mortality, suggesting its potential as a prognostic marker. The study identifies the P2X7 receptor as a critical regulator of mitochondrial function and immune suppression in sepsis, offering a potential target for therapeutic intervention. Restoring NLRP3 inflammasome activation could improve outcomes in septic patients.
							CD39		2.study highlights P2X7 and CD39 as potential therapeutic and diagnostic targets for managing SAE and its associated cognitive impairments in sepsis.gene/protein P2X7 receptor mRNA expression was significantly increased in the hippocampus of septic mice 24 hours after sepsis induction (CLP group) compared to the sham-operated group. This suggests an upregulation of P2X7 as part of the inflammatory response in this brain region. Cerebral Cortex: No significant change in P2X7 receptor mRNA expression was observed in the cerebral cortex of septic mice. This indicates regional specificity in the brain's inflammatory response to sepsis.
							CD14		3.Elevated plasma CD14 and P2X7 expression in septic patients could serve as biomarkers of sepsis severity./protein Prognostic: The ability of CD14 to modulate bacterial clearance and inflammation suggests a potential role in predicting sepsis outcomes.
							ATP, ADP		4.P2X7 Receptor: Expression in Septic Patients: Similar to P2Y2, P2X7 mRNA levels did not show significant differences between septic patients and the control groups. This indicates that transcriptional changes in P2X7 are not prominent in sepsis or are potentially regulated post-transcriptionally. dysregulated ATPergic signaling is a feature of early sepsis and identifies ATP, ADP, and related enzymatic activities as promising diagnostic biomarkers. Elevated A2a receptor expression in neutrophils and monocytes highlights its role in sepsis-related immune dysfunction and potential as a therapeutic target.
									5. systemic blockade of P2X7R protects against sepsis-induced intestinal barrier dysfunction. /protein This protective effect is mediated through the suppression of pro-inflammatory cytokines, reduced M1 macrophage activation, and maintenance of tight junction integrity via ER6/NF-κB signaling pathways.
29.PTX3	PTX3	PTX3 Pentraxin 3 TSG-14 Tumor Necrosis Factor-Inducible Gene 14 Protein TNFAIP5 Tumor Necrosis Factor Alpha-Induced Protein 5 Pentraxin-Related Protein PTX3 TNF Alpha-Induced Protein 5 Long Pentraxin 3 Pentraxin-Related Gene, Rapidly Induced By IL-1 Beta Pentaxin-Related Gene, Rapidly Induced By IL-1 Beta Tumor Necrosis Factor, Alpha-Induced Protein 5 Tumor Necrosis Factor-Inducible Protein TSG-14 Pentaxin-Related Protein PTX3 Pentraxin 3, Long 2 TSG14	protein/gene marker	prognostic more than diagnostic	not pathogen-dependent	Inflammatory and Immune Pathways/ Acute Phase Response / Pathogen Recognition and Clearance/ Complement Activation and Regulation Vascular and Endothelial/ Endothelial Dysfunction Coagulation/ Coagulation and Fibrinolysis Immune Regulation/ Resolution of Inflammation			1. Studies confirm PTX3 as an early and independent predictor of mortality in septic patients. Elevated PTX3 levels predict disease severity in bacterial (e.g., pneumonia), fungal (e.g., aspergillosis), and viral infections (e.g., dengue). PTX3 levels decrease with effective treatment, making it a marker for therapeutic response. PTX3 is a robust biomarker for diagnosing and monitoring sepsis. Its rapid response to infection and strong correlation with disease severity and outcomes make it a valuable tool in clinical settings. PTX3's role as a diagnostic and prognostic marker is based on its protein levels in the bloodstream, which correlate with disease severity, organ dysfunction, and patient outcomes.
									2. Elevated PTX3 in Septic Patients:/protein/gene PTX3 levels were significantly higher in septic patients (median: 22,031 pg/mL) compared to healthy volunteers (median: 438 pg/mL). Non-survivors had higher PTX3 levels (median: 204,879 pg/mL) than survivors (median: 14,893 pg/mL), correlating with disease severity. In septic shock patients and HV, PTX3 mRNA peaked 2 hours post-LPS stimulation, while protein levels increased continuously and peaked at 24 hours. PTX3 protein stability was significantly higher than TNF-α, contributing to sustained circulating levels. PTX3 mRNA expression was maintained in septic patients, with slower decay compared to pro-inflammatory cytokines like TNF-α. PTX3 transcription was less susceptible to endotoxin tolerance, indicating its robust gene-level regulation.
							PCT, CRP		3.PTX3 is a reliable biomarker for the early identification of severe sepsis and prediction /protein of mortality in emergency room patients with suspected infections. Its rapid response to inflammation and strong correlation with sepsis severity make it superior to CRP and comparable to PCT.
									4. PTX3's oligomerization state serves as a novel biomarker for resolving inflammation and predicting survival in sepsis/protein . The dynamic shift from octameric to monomeric PTX3 by day 2 post-ICU admission correlates with better outcomes, making it a potential tool for monitoring treatment responses and disease progression.
							PCT,CRP		5. Elevated PTX3 levels are associated with disease severity and mortality in sepsis and infections like pneumonia, tuberculosis, and fungal diseases./protein Persistently high PTX3 levels in sepsis correlate with poor outcomes, organ dysfunction, and coagulation abnormalities. PTX3 outperforms CRP and PCT in predicting mortality and disease severity in septic patients.
							PCT,CRP		6.PTX3 is a robust protein biomarker for diagnosing sepsis and septic shock, with excellent correlation to disease severity and outcomes./protein Its superior diagnostic performance compared to CRP and PCT makes it a valuable tool for early ICU risk stratification and clinical decision-making.
									7. PTX3 protects against sepsis-induced myocardial injury by downregulating apoptosis and autophagy through/protein the inhibition of the PI3K/AKT/mTOR signaling pathway. This suggests PTX3 as a potential therapeutic target for managing sepsis-related cardiac complications.
30.TRAIL	TNFSF10	TNFSF10 TNF Superfamily Member 10 Apo-2L TRAIL CD253 TANCR TL2 Tumor Necrosis Factor (Ligand) Superfamily, Member 10 Tumor Necrosis Factor Ligand Superfamily Member 10 Apo-2 Ligand APO2L Chemokine Tumor Necrosis Factor Ligand Superfamily Memb Tumor Necrosis Factor (Ligand) Family, Member 10 TNF-Related Apoptosis Inducing Ligand TRAIL Tumor Necrosis Factor Superfamily Member 10 TNF-Related Apoptosis-Inducing Ligand Tumor Necrosis Factor Ligand 6A Protein TRAIL CD253 Antigen TNLG6A	protein marker	diagnostic/prognostic	triggered by inflammatory signals rather than specific pathogens	Apoptosis and Cell Death Pathways/ immune Cell Apoptosis/Endothelial Cell Apoptosis Inflammatory and Immune Pathways/. Immune Dysregulation/ Cytokine Storm Vascular and Endothelial/ Endothelial Dysfunction		GeneCards / NO MalaCards/ NO	1. identifies TRAIL as a key mediator of immune suppression during sepsis, /protein contributing to impaired bacterial clearance and reduced CD8 T-cell responses. Targeting the TRAIL pathway may have therapeutic potential to restore immunity and reduce mortality associated with secondary infections in septic patients.
									2. TRAIL Levels and Organ Dysfunction:/protein Lower TRAIL levels (<28.5 pg/mL) were associated with: Increased organ dysfunction (higher SOFA scores). Greater incidence of septic shock in all cohorts. Lower TRAIL levels were associated with higher lactate levels and greater vasopressor use, reflecting hemodynamic instability. Diagnostic: TRAIL differentiates septic shock from sepsis and non-infectious critical illness. Potential use as a marker of immune dysfunction in septic patients. Prognostic: Low TRAIL levels predict higher mortality and severe organ dysfunction, making it a candidate for risk stratification.
									3. TRAIL Levels and Sepsis Severity:/protein Plasma TRAIL levels were significantly lower in septic and septic shock patients compared to controls TRAIL levels were associated with sepsis severity and could serve as a biomarker for distinguishing sepsis and septic shock from non-septic critically ill patients.
							FASL, Caspase 3		4. Downregulated Genes (Pro-Apoptotic Pathways):/gene/ptotein TRAIL (TNF-related apoptosis-inducing ligand): Reduced expression (0.82-fold) in LPS-tolerant macrophages. TRAIL is involved in apoptosis induction, and its downregulation correlates with increased macrophage survival. FASL (Fas ligand): Downregulated to 0.67-fold. FASL plays a role in extrinsic apoptotic signaling, and its suppression helps protect macrophages. Caspase 3: Downregulated (0.65-fold). Caspase 3 is a key executor of apoptosis, and its reduced expression decreases apoptotic activity in macrophages.
									5. Mean plasma sTRAIL levels were significantly lower in septic patients compared to healthy controls (16.9 ± 8.3 vs. 68.3 ± 8.6 pg/mL, $p < 0.01$). Severe sepsis and septic shock patients had lower sTRAIL levels than patients with milder sepsis ($p < 0.05$). Diagnostic: sTRAIL levels differentiated septic patients from healthy controls and distinguished sepsis severity (sepsis, severe sepsis, septic shock). Prognostic: Lower sTRAIL levels were associated with worse outcomes, including higher APACHE II scores and mortality, suggesting its potential as a prognostic biomarker. sTRAIL could serve as a biomarker for assessing immune status and guiding treatment decisions in sepsis
									6. Elevated TRAIL levels and increased T-cell apoptosis could serve as early markers of trauma-induced immunosuppression./protein
									7. TRAIL and IP-10 were particularly useful in distinguishing viral infections, while CRP, IL-6, and PCT were more indicative of bacterial infections./protein
31.MMP8	MMP8	MMP8 Matrix Metallopeptidase 8 CLG1 Matrix Metalloproteinase 8 (Neutrophil Collagenase) Matrix Metalloproteinase-8 Neutrophil Collagenase PMNL Collagenase PMNL-CL MMP-8 PMN Leukocyte Collagenase Collagenase 2 EC 3.4.24.34 EC 3.4.24.47 HNC	protein/gene	diagnostic/prognostic	not pathogen-dependent	Inflammatory and Immune/ Cytokine Storm/ Neutrophil Activation Vascular and Endothelial/ Endothelial Dysfunction Extracellular Matrix/ ECM Degradation and Remodeling		GeneCards/ NO MalaCards/ NO	1. Serum levels of MMP-8, MMP-9, and TIMP-1 were significantly higher in sepsis patients compared to healthy controls:/protein Elevated MMP-8 and TIMP-1 levels upon ICU admission are associated with poor outcomes, indicating their potential utility as prognostic biomarkers. The findings support the role of MMP-8 in the inflammatory response during sepsis and its excessive upregulation in severe cases. High MMP-8 and TIMP-1 levels are associated with increased mortality in severe sepsis and septic shock, highlighting their potential as prognostic biomarkers.
									2. This study identifies MMP-8 as a key player in the inflammatory response to sepsis and a potential therapeutic target./protein/gene MMP-8 Gene: Expression increased in pediatric septic shock patients; higher levels correlate with worse outcomes. Elevated MMP-8 levels in blood correlate with increased disease severity, organ failure, and mortality, suggesting its use as a biomarker for risk stratification in sepsis.

									3. Diagnostic:/protein/gene Elevated MMP8 levels distinguish sepsis patients from healthy controls. Prognostic: High MMP8 expression is associated with increased mortality, making it a potential prognostic biomarker.
							TIMP-1		4. TIMP-1 and MMP-8 may serve as biomarkers for distinguishing patients with overt DIC in the early stages of sepsis./protein Elevated TIMP-1 levels in the early phase were associated with the severity of coagulopathy and the presence of overt DIC. MMP-8, while elevated, had a less direct association with coagulation outcomes.
									5. highlights the significant elevation of MMP-2 and MMP-8 in severe sepsis and their correlation with disease severity./protein Elevated MMP-2 and MMP-8 levels could serve as markers of sepsis severity. Prognostic: Higher MMP-2 levels in skin blister fluid were associated with non-survivors, suggesting a potential prognostic role in severe sepsis.
									6. MMP8 plays a critical role in bacterial clearance and immune regulation in juvenile sepsis./protein While its inhibition improves outcomes in adults, this study underscores its protective role in younger hosts, emphasizing the need for age-specific therapeutic approaches.
							MMP9		7. Diagnostic:/protein High MMP-8 and low MMP-9 levels were useful biomarkers for identifying sepsis in ICU patients. MMP-2 and MMP-9 levels were associated with survival, with lower MMP-2 levels predicting poorer outcomes.
									8. Prognostic:/gene/protein MMP8's role in driving immune tolerance and its association with sepsis outcomes suggest it could serve as a prognostic marker, though further studies are needed. MMP8 was identified as the most upregulated MMP gene in DCs from septic mice through microarray and RT-PCR analysis.
32.MMP9	MMP9	Matrix Metallopeptidase 9 CLG4B Matrix Metalloproteinase 9 (Gelatinase B, 92kDa Gelatinase, 92kDa Type IV Collagenase) Matrix Metalloproteinase-9 EC 3.4.24.35 MMP-9 GELB Matrix Metallopeptidase 9 (Gelatinase B, 92kDa Gelatinase, 92kDa Type IV Collagenase) 92 KDa Type IV Collagenase Macrophage Gelatinase Type V Collagenase 92 KDa Gelatinase Gelatinase B EC 3.4.24 MANDP	protein/gene	diagnostic/prognostic	not pathogen-dependent	Extracellular Matrix Pathways/ ECM Degradation and Remodeling Inflammatory and Immune/ Cytokine Storm/ Neutrophil Recruitment and Activation Vascular and Endothelial/ Endothelial Dysfunction		GeneCards/NO MalaCards/ Septic Arthritis	1. Gene Level:/gene/protein MMP-9 mRNA levels were quantified using RT-PCR, showing increased expression during infection. Elevated MMP-9 levels during sepsis indicate its potential role as a biomarker for inflammatory responses in bacterial infections. Reduced MMP-9 activity was associated with impaired bacterial clearance and increased tissue damage, suggesting its importance in determining infection outcomes.
									2. MMP-9 expression (mRNA and protein levels) was significantly elevated in lung tissues of CLP-induced septic mice. MMP-9 protects against sepsis-induced ALI by promoting sRAGE release, which mitigates the harmful effects of RAGE/NF-κB activation. Targeting the MMP-9/sRAGE axis may represent a therapeutic strategy for sepsis-related lung injury.
									3. Elevated MMP-2 and MMP-9 activity could serve as biomarkers for BBB(blood-brain barrier) dysfunction in sepsis./protein Prognostic: Persistent MMP-9 activity might indicate the severity of BBB disruption and related outcomes.
									4. Diagnostic:/protein The study demonstrated the utility of MMP-9 as a biomarker for the early detection of sepsis, with the biosensor enabling rapid identification.
									5. Plasma MMP-9 levels were highest on ICU Day 1 and decreased over time during recovery./protein Elevated MMPs (e.g., MMP-9, MMP-8) could serve as markers of severe sepsis.
							IL-8, and C5aR IFNγ, IL-12, and TLR4		6. Upregulated genes, such as MMP9, IL-8, and C5aR, reflect immune activation and may serve as biomarkers for sepsis severity./gene The expression of certain genes (IFNγ, IL-12, and TLR4) correlated with patient outcomes, suggesting potential prognostic utility.
							CD44, and EGR1		7. Upregulated expression of MMP9, CD44, and EGR1 in sepsis highlights their potential as biomarkers. These genes could also serve as therapeutic targets given their central roles in sepsis pathogenesis.
33.HLA-DR	HLA-DR	HLA-DRB1 Major Histocompatibility Complex, Class II, DR Beta 1 HLA-DR1B Major Histocompatibility Complex, Class II, DR Beta 1 HLA Class II Histocompatibility Antigen, DR-1 Beta Chain HLA Class II Histocompatibility Antigen, DRB1 Beta Chain MHC Class II HLA-DR Beta 1 Chain Human Leucocyte Antigen DRB1 Human Leukocyte Antigen DRB1 Lymphocyte Antigen DRB1 HLA-DRB DRB1 SS1	ptotein / gene marker	prognostic/diagnostic	not pathogen-dependent	Adaptive Immune/ Antigen Presentation and T-cell Activation Inflammatory and Immune/ Immune Dysregulation Cytokine Storm and Resolution/ Immune Regulation		GeneCards/ NO MalaCards/ Bacterial Sepsis Septic Arthritis	1. Low HLA-DR expression on T cells or monocytes, along with reduced soluble HLA-DR, were early markers for sepsis susceptibility./protein The findings suggest that monitoring these markers can predict severe sepsis and guide early interventions. These markers can potentially enhance early diagnosis and stratification of patients, enabling timely therapeutic interventions.
									2. Low HLA-DRA mRNA expression and reduced TNFα response are markers of sepsis-induced immunosuppression.protein/gene HLA-DRA expression and the TNFα:HLA-DRA ratio correlate with disease severity (SOFA score), indicating potential prognostic utility. HLA-DRA mRNA levels as a diagnostic and prognostic tool in sepsis management
									3.Reduced mHLA-DR expression is a sensitive and specific marker for sepsis-induced immunosuppression./gene/protein Helps differentiate between septic and non-septic inflammatory conditions. Prognostic: Dynamic changes in mHLA-DR levels, particularly the recovery slope, predict sepsis outcomes, including survival and infection risks.
									4. This study validates HLA-DRA mRNA expression as a viable biomarker for sepsis-induced immunosuppression./ protein/gene The strong correlation between HLA-DRA mRNA and mHLA-DR protein levels suggests that qRT-PCR offers a practical, scalable alternative to flow cytometry for monitoring immune status in sepsis. Lower HLA-DRA and mHLA-DR levels were associated with more severe sepsis and poorer outcomes.
									5. HLA-DRA mRNA downregulation is a sensitive indicator of sepsis-induced immunosuppression. Persistently low HLA-DRA mRNA levels correlate with severe sepsis, organ failure (SOFA), and poor outcomes. measurement of HLA-DRA mRNA is a reliable and reproducible method for assessing immunosuppression in sepsis.
									6. Low CD74 mRNA levels indicate severe immune dysfunction and identify patients at risk for poor outcomes after septic shock./protein /gene CD74 mRNA serves as a robust prognostic biomarker, correlating with 28-day mortality, even after adjusting for clinical confounders. mHLA-DR also predicted mortality:
									7.Reduced mHLA-DR expression on days 3–4 identified patients at risk for developing sepsis./protein The slope of mHLA-DR recovery provided early warning of immune dysfunction. A lack of mHLA-DR recovery between days 1–4 serves as an independent predictor of sepsis. The findings suggest the utility of mHLA-DR monitoring in tailoring interventions to prevent infections in high-risk patients.
									8. Reduced monocyte HLA-DR expression identified patients at risk of infection after trauma./protein Persistently low HLA-DR levels and impaired T-cell recovery were associated with poor clinical outcomes.
34.TNF-α	TNF	TNF Tumor Necrosis Factor TNF-Alpha TNFSF2 TNFA DIF Tumor Necrosis Factor Ligand Superfamily Member 2 TNF-A Tumor Necrosis Factor (TNF Superfamily, Member 2) Tumor Necrosis Factor Ligand 1F Tumor Necrosis Factor-Alpha Tumor Necrotic Factor Alpha TNF Superfamily, Member 2 TNF, Macrophage-Derived TNF, Monocyte-Derived APC1 Protein Cachectin TNLG1F	protein/gene		not pathogen-dependent	Inflammatory and Immune/ ctokine storm/ Immune Cell Recruitment Vascular and Endothelial/ Endothelial Dysfunction Coagulation/ Coagulation Cascade Activation Apoptosis and Cell Death/ mmune and Endothelial Cell Death		GeneCards/ septic- septic shock MalaCards/ Bacterial Sepsis septin Arthritis-	TNF has a dual role in sepsis, functioning both as a pro-inflammatory mediator that contributes to tissue damage and as a necessary component for immune defense. This complexity makes it difficult to establish a straightforward diagnostic or prognostic application. TNF expression levels rise sharply during the early phase of sepsis but decline quickly, making it a transient marker that may not consistently reflect disease progression or outcomes. TNF levels in blood can vary greatly among patients due to genetic differences (e.g., polymorphisms like -308G/A or TNFB1/TNFB2) and the heterogeneity of sepsis itself (source of infection, timing, comorbidities). Many studies, including those reviewed, emphasize the association of TNF polymorphisms (e.g., rs1800629, rs361525) with susceptibility to sepsis or immune response modulation. This highlights a preference for exploring its predispositional role rather than its clinical utility as a marker.
35.MYD88	MYD88	MYD88 MYD88 Innate Immune Signal Transduction Adaptor Myeloid Differentiation Primary Response Protein MyD88 Myeloid Differentiation Primary Response Gene (88) Myeloid Differentiation Primary Response 88 TLR Adaptor MYD88 Mutant Myeloid Differentiation Primary Response 88 MYD88D IMD68 WM1	protein/gene	more prognostic	Not pathogen-dependent	Inflammatory and Immune/ cytokine storm/Pathogen Recognition and Immune Activation Oxidative Stress/ ROS and NO Production Immune Dysregulation/ Late-Stage Immunosuppression	TLR2/4	GeneCards/ NO MalaCards/ Bacterial Sepsis	1.MyD88 is a key adapter molecule: It mediates the inflammatory cascade in sepsis by interacting with TLR2 and TLR4./gene Protective effects of knockouts: Deficiency in TLR2, TLR4, or MyD88 significantly reduces inflammation, hypoxia, and apoptosis, with MyD88-/- mice demonstrating the most robust protection.
									2. While MyD88-/- mice were protected from lymphocyte death, they failed to mount effective immune responses, leading to increased mortality during sepsis./gene Highlights the delicate balance between limiting apoptosis and enabling pathogen clearance
									3. Polymicrobial Sepsis: MyD88 is the dominant pathway mediating systemic inflammation, cardiac dysfunction, and mortality. Trif plays a negligible role./gene
36.NLRP3	NLRP3	NLR Family Pyrin Domain Containing 3 PYPAF1 CLR1.1 NALP3 Cryopyrin AGTAVPRL C1orf7 CIAS1 FCAS All AVP FCU MWS Nucleotide-Binding Oligomerization Domain, Leucine Rich Repeat And Pyrin Domain Containing 3	protein/gene marker	diagnostic/prognostic	Not pathogen-dependent	Inflammatory and Immune/ Pyroptosis and Inflammatory Cell Death/ cytokine storm Oxidative Stress/ ROS Production and Mitochondrial Dysfunction Immune Dysregulation/ Late-Stage Immunosuppression			1. NLRP3 Expression:/gene Sepsis Patients: Showed significantly higher NLRP3 mRNA and protein expression than healthy controls. Genotype Effect: GG/GC genotypes were associated with higher NLRP3 expression and increased cytokine production (TNF-α, IL-1β) compared to CC genotype.

									2. For diagnosing sepsis:/protein NLRP3 had an AUC (Area Under the Curve) of 0.980, with 95.2% sensitivity and 90% specificity at a cutoff of 125.73 pg/mL. For septic shock: AUC was 0.992, with 97.4% sensitivity and 98.6% specificity at a cutoff of 231.87 pg/mL. NLRP3 is a reliable biomarker for identifying high-risk septic patients, particularly for differentiating septic shock. Prognostic Value: Elevated NLRP3 levels are associated with higher 30-day mortality, highlighting its utility in risk stratification.
									3. findings suggest that NLRP3 expression levels could correlate with liver injury severity and treatment efficacy./gene NLRP3 Overexpression: Drives excessive inflammasome activation, resulting in: Increased IL-1β and IL-18 gene expression. Disruption of bile acid transporters (Mrp2, Bsep) and compensatory upregulation of Mrp3, Mrp4. Inflammatory Cascade: Elevated cytokines lead to hepatocyte damage and mitochondrial dysfunction, further impairing bile acid metabolism.
									4. The study identifies LXB4 and NLRP3-related pathways as potential biomarkers for monitoring the progression and resolution of sepsis./gene
							IL31, IL1BETA		5. Diagnostic and Prognostic Value:/protein/gene IL-31, IL-1β, and NLRP3 can differentiate between SIRS and sepsis and predict septic shock. The biomarker panel outperforms individual biomarkers in sensitivity and specificity.
							HCAR1		6. NLRP3 mRNA expression is a highly sensitive and specific biomarker for sepsis./gene/protein(yellow) HCAR1 shows potential for early detection and immune modulation in sepsis.
37.TLR2	TLR2	Toll Like Receptor 2 TIL4 Toll-Like Receptor 2 CD282 Toll/Interleukin-1 Receptor-Like Protein 4 CD282 Antigen	protein/gene marker	diagnostic/prognostic	Gram-positive bacteria	Inflammatory and Immune/ Pathogen Recognition and Immune Activation/Cytokine Storm Oxidative Stress/ ROS Production Immune Dysregulation/Late-Stage Immunosuppression	TF,	GeneCards/ NO MalaCards/ Bacterial Sepsis septic Arthritis	1. At the gene level, TLR2 plays a pivotal role in:/gene Upregulating TF (F3 gene) expression, linking innate immune activation to coagulation in sepsis. Amplifying pro-inflammatory gene expression (e.g., IL-6, TNF-α), exacerbating SIC.
									2. TLR2 and TLR4:/protein No significant differences in expression levels among the sepsis, severe sepsis, septic shock, and healthy groups. TLR2 and TLR4 levels were not directly associated with cytokine production in severe cases. CD11b: Expression was higher in early sepsis but did not show significant differences in severe sepsis or septic shock.
									3. TLR-2 mRNA and protein levels are significantly elevated in sepsis, particularly in Gram-positive and Gram-negative infections./gene/protein TLR-4 mRNA is upregulated in Gram-positive sepsis, but no corresponding increase in protein levels was observed.
									4. TLR-2 and TLR-4 levels were significantly higher on leukocytes from sepsis patients compared to healthy controls./protein
38.TLR4	TLR4	Toll Like Receptor 4 HTG8 Toll-Like Receptor 4 ARMD10 CD284 TLR-4 Toll Like Receptor 4 Protein Homolog Of Drosophila Toll CD284 Antigen TOLL	protein/gene marker	diagnostic/prognostic	Gram-negative bacteria	Inflammatory and Immune/ Pathogen Recognition and Immune Activation/Cytokine Storm Oxidative Stress/ ROS Production Immune Dysregulation/Late-Stage Immunosuppression		GeneCards/ NO MalaCards/ Bacterial Sepsis septic Arthritis	1. TLR4 is crucial for detecting lipopolysaccharide (LPS) from gram-negative bacteria and initiating the immune response./gene Excessive TLR4 activation leads to hyperinflammation, contributing to systemic inflammatory response syndrome (SIRS) and multi-organ dysfunction. Targeting TLR4 or its downstream pathways may mitigate immune overactivation and reduce sepsis severity.
									2. TLR4 modulation remains a promising target for managing sepsis and inflammatory diseases./gene/protein Biomarkers like cytokines (IL-6, TNF-α) could help identify TLR4 overactivation in patients.
									3.The study highlights the utility of TLR gene expression as a predictive tool for sepsis, offering earlier diagnosis than current clinical and laboratory methods./gene Early upregulation of TLRs suggests their role in the host's recognition of infection and the initiation of immune responses. mRNA expression levels of TLR-1, TLR-2, TLR-4, TLR-5, and TLR-9
							DLL1		3.Notch as a Diagnostic Tool:/protein/gene Soluble DLL1 and Notch1 receptor levels could serve as biomarkers for sepsis progression and organ dysfunction. 3. Therapeutic Potential: Modulating Notch signaling offers a promising strategy for controlling inflammation and preventing organ failure in sepsis.
39.NOTCH1						Inflammatory and Immune Pathways/ cytokine storm/ Immune Dysregulation Vascular and Endothelial Pathways/ Endothelial Dysfunction and Angiogenesis Tissue Injury and Repair/Tissue Repair and Regeneration		GeneCards/ NO MalaCards/ NO	1. Soluble DLL1 and Notch signaling markers show potential for early sepsis detection./protein Therapeutic Potential: Modulating Notch signaling may reduce inflammation, preserve endothelial function, and improve sepsis outcomes.
									2. Notch pathway inhibition may reverse immunosuppression, offering a novel approach to sepsis treatment.(yellow) Findings at the Gene Level:/gene Increased Jagged1 and Hes1 mRNA levels indicate upregulation of the Notch signaling pathway in sepsis patients. Elevated PD-1 and IL-10 mRNA levels suggest immune tolerance and T cell exhaustion. Findings at the Protein Level:/protein Septic patients had higher PD-1 and PD-L1 protein levels compared to healthy controls. Protein-level measurements correlate with immune suppression and disease severity.
									3. Diagnostic Implications: Elevated Notch1 mRNA in PBMCs could serve as a biomarker for immune dysfunction in sepsis and septic shock. Other Notch Receptors: No significant differences in the mRNA levels of Notch2, Notch3, or Notch4.
									4. otch1 Signaling Pathway:/ptotein/gene Activation: Involves cleavage of the Notch1 receptor, releasing the NICD, which translocates to the nucleus to regulate target gene expression (e.g., Hes1). Decreased NICD levels indicate endothelial dysfunction in sepsis.
40.BCL2	BCL2	BCL2 Apoptosis Regulator 2 PPP1R50 Bcl-2 Protein Phosphatase 1, Regulatory Subunit 50 Apoptosis Regulator Bcl-2 B-Cell CLL/Lymphoma 2 BCL2, Apoptosis Regulator	protein/gene			Apoptosis and Cell Death/ Lymphocyte Apoptosis/ Mitochondrial Integrity Immune Dysregulation/ Late-Stage Immunosuppression Oxidative Stress/ Protection Against Oxidative Damage	Bim, Bcl-xl, Bid	Genecards/NO MalaCards/ Septic Arthritis	1. Gene Expression Changes in Severe Sepsis:/gene Increased expression of pro-apoptotic genes (Bim, Bid, Bak) and decreased expression of anti-apoptotic genes (Bcl-2, Bcl-xl) suggest heightened apoptosis susceptibility in sepsis. Bim (BH3-Only): mRNA: Upregulated by more than 50-fold compared to healthy controls. Bid (BH3-Only): mRNA: Increased 12-fold in sepsis patients. Bcl-2 protein levels are significantly reduced in lymphocytes of septic patients, contributing to the immune dysfunction observed in severe sepsis. This complements the upregulation of pro-apoptotic genes and proteins like Bim, Bid, and Bak, tipping the balance towards apoptosis and lymphocyte depletion.
							caspase-3, sFasL		2. Diagnostic Relevance:/protein Caspase-3 and sFasL levels were highlighted as robust biomarkers for sepsis diagnosis. Prognostic Relevance: Decreased Bcl-2 levels correlated with the progression to MOF, providing prognostic insights into patient outcomes.
									3. Improved survival in Bcl-2 transgenic mice supports the hypothesis that targeting apoptosis pathways could improve outcomes in septic patients./protein
									4. Early and severe down-expression of Bcl-2 in CMNC serves as a strong predictor of mortality in severe sepsis./gene A clear cutoff value for Bcl-2 expression was identified, suggesting its utility as a biomarker for risk stratification.
							Bid, FAS		5. Day 1–2: BCL-2 mRNA expression was slightly decreased in septic shock patients compared to healthy controls./gene Day 3–5: Expression levels returned to normal, suggesting a transient downregulation during the early phase of septic shock. BID and FAS mRNA levels emerged as potential biomarkers for routine apoptosis monitoring in septic shock. Elevated pro-apoptotic gene expression suggests a possible correlation with disease severity and immune suppression, though further studies are needed for validation.
									6. Higher Bcl-2 expression in survivors suggests its potential as a biomarker for better outcomes in severe sepsis./protein
							HLA-DR,PD-1		7. Diagnostic Utility:/protein/gene Biomarkers like HLA-DR, PD-1, and cytokine levels can help diagnose sepsis-induced immunosuppression and stratify patient risk. Prognostic Potential: Low Bcl-2 expression and high levels of immune checkpoint molecules are associated with worse outcomes. Downregulation of Bcl-2 in immune cells correlates with increased apoptosis and immunosuppression.
41.PD-1	PDCD1	PDCD1 Programmed Cell Death 1 PD1 CD279 HSLE1 PD-1 Systemic Lupus Erythematosus Susceptibility 2 Programmed Cell Death Protein 1 Protein PD-1 SLEB2 HPD-1 Programmed Cell Death 1 Protein CD279 Antigen HPD-L	prorein marker	more prognostic		Immune Dysregulation Pathways/ Late-Stage Immunosuppression Adaptive Immune Pathways/ T-cell Exhaustion and Regulation Inflammatory and Immune Pathways/ cytokine regulation	PD-L1	GeneCards/ Malacards/ Bacterial Sepsis	1. sPD-L1 serves as a reliable biomarker to differentiate septic patients from those with non-septic infections and inflammatory diseases./protein(yellow) Higher sPD-L1 levels reflect immune dysregulation and may help assess sepsis severity.
							PD-L1		2.High PD-1 and PD-L1 levels are markers of immune dysfunction and are associated with poor outcomes in sepsis./protein
									3.PD-L1 and sPD-L1 levels serve as biomarkers for stratifying immune-compromised septic patients./protein Elevated PD-L1/sPD-L1 levels and low SaO_2 are associated with poorer outcomes, higher reinfection rates, and increased mortality.
									4. Combining PD-1, HLA-DR, and nCD64 achieved high sensitivity and specificity for diagnosing sepsis, /protein(yellow) outperforming individual biomarkers or clinical scoring systems A panel integrating PD-1, HLA-DR, and CD64 provides a reliable diagnostic and prognostic tool for sepsis management.
									5. Co-expression of PD-1 and LAG3 on T cells is a potential biomarker for severe immune dysfunction in sepsis./protein
									6. PD-1 expression on CD4+ T cells was significantly elevated in septic shock patients compared to controls, particularly in non-survivors./protein Survivors showed normalization of PD-1 expression by day 7. Persistent PD-1 overexpression and lack of TCR diversity recovery correlate strongly with mortality.

42.CCL2									
43.ARG1	ARG1	ARG1 Arginase 1 Arginase-1 Liver-Type Arginase Arginase, Liver Type I Arginase EC 3.5.3.1	protein/gene	diagnostic/prognostic			IL1R2, ELANE, MPO, MMP9	GeneCrads/NO MalaCards/ Bacterial Sepsis	1. ARG1, IL1R2, ELANE, MPO, MMP9./gene Associated with immune dysregulation and oxidative stress during sepsis.
							IL10		2.Elevated IL-10 expression suggests a biomarker for immunosuppressive phases in sepsis./gene Ratios of iNOS (M1) and ARG1 (M2) could be diagnostic markers for macrophage polarization states.
									3. ARG1 emerges as a multifunctional biomarker in sepsis for:(yellow)/gene Diagnosis: Differentiating sepsis severity and related conditions. Prognosis: Predicting treatment response and survival outcomes.
44.IL1R2	IL1R2	IL1R2 Interleukin 1 Receptor Type 2 CD121b IL1RB CD121 Antigen-Like Family Member B Interleukin-1 Receptor Type II Interleukin-1 Receptor Type 2 Interleukin-1 Receptor Beta IL-1 Type II Receptor IL-1R-Beta IL-1RT-2 CDw121b IL-1R-2 IL-1RT2 Type II Interleukin-1 Receptor, Beta Interleukin 1 Receptor, Type II Antigen CDw121b CD121b Antigen IL1R2c	protein/gene marker	diagnostic/prognostic	distinguished sepsis from bacterial infections			GeneCards/ NO MalaCards/ Bacterial Sepsis	1. IL1R2 offers a non-invasive, rapid diagnostic tool for sepsis and pathogen identification. /gene/protein It could improve early diagnosis, guide antibiotic selection, and enhance sepsis management.
									2. In sepsis, IL1R2 transcription was significantly increased in monocytes, aligning with the higher plasma sIL-1R2 levels./gene/protein sIL-1R2 distinguished sepsis from bacterial infections and could differentiate sepsis based on the Sepsis-2 and Sepsis-3 criteria.
							IGHG1, LCN2, LTF, MMP8, OLFM4		3. ifferentially expressed genes included: Upregulated in septic shock: IGHG1, IL1R2, LCN2, LTF, MMP8, OLFM4. These genes showed significant ability to distinguish septic shock from non-septic shock based on ROC analysis.
IL1B	IL1B	Interleukin 1 Beta IL1F2 IL1-BETA Interleukin-1 Beta IL-1 Beta Catabolin IL-1B Pro-Interleukin-1-Beta Preinterleukin 1 Beta Interleukin 1beta IL1beta IL-1	protein gene marker	diagnostic/prognoatic			IL-6, TNF-α	GeneCards/ Septic Shock MalaCards/ Bacterial Sepsis	1. The findings indicate potential biomarkers of immune dysfunction in late sepsis (IL-1β, IL-6, TNF-α)./gene These genes may reflect the extent of immunosuppression during sepsis.
							IL-1R2		2. PMNs from sepsis patients exhibited a marked reduction in IL-1β mRNA and protein synthesis in response to endotoxin stimulation compared to controls./gene Elevated IL-1R2 expression on PMNs and tolerance to endotoxin-induced IL-1β expression may serve as markers for sepsis.
45.CD177	CD177	CD177 Molecule PRV1 NB1 CD177 Antigen HNA2A Polycythemia Rubra Vera Protein Human Neutrophil Alloantigen 2a NB1 Glycoprotein HNA-2a NB1 GP PRV-1 Polycythemia Rubra Vera 1 Cell Surface Receptor	protein/gene marker	diagnostic/prognostic				GeneCards/ NO MalaCards/ NO	1. CD177 proposed as a marker for sepsis, reflecting changes in neutrophil function during the disease./gene(yellow) The study investigates both gene-level (CD177 mRNA expression) and protein-level (CD177 surface expression) changes, providing a comprehensive view of the biomarker's potential
46.OLFM4		Olfactomedin 4 GW112 OIB GC1 G-CSF-Stimulated Clone 1 Protein Antiapoptotic Protein GW112 Olfactomedin-4 Olfactomedin Tiarin HGC-1 HOLID PDP4 OLM4 BA209J19.1 UNQ362	protein/gene marker	more prognostic marker				GeneCards/ NO MalaCards/ NO	1. OLFM4+ neutrophil percentage is strongly linked to mortality and could serve as a prognostic biomarker for sepsis severity and outcomes.
							CD177, MAPK14		2.Diagnostic Value: OLFM4 is a promising biomarker for distinguishing between severe and mild infectious diseases, including sepsis and ARDS./protein/gene Prognostic Value: Higher OLFM4 expression indicates poor prognosis in sepsis and other diseases.
									3. Plasma Olfm4 is elevated in septic shock but lacks specificity as a diagnostic marker./protein
47.MAPK14	MAPK14	Mitogen-Activated Protein Kinase 14 PRKM14 PRKM15 CSBP1 CSBP2 CSPB1 Mxi2 P38 Mitogen-Activated Protein Kinase P38 Alpha MAX-Interacting Protein CSAID-Binding Protein MAP Kinase P38 Alpha P38 MAP Kinase 2 MAP Kinase 14 EC 2.7.11.24 4 SAPK2A 3 CSBP Cytokine Suppressive Anti-Inflammatory Drug Binding Protein P38 Mitogen Activated Protein Kinase Stress-Activated Protein Kinase 2A Stress-Activated Protein Kinase 2a MAP Kinase Mxi2 MAP Kinase MXI2 P38alpha Exip EC 2.7.11 P38ALPHA MAPK 14 SAPK2a EXIP MXI2 RK	gene marker	diagnostic/prognostic		Epigenetic and Transcriptomic Regulation Pathways/Immune Gene Transcription Hypoxia and Metabolic Pathways/ Metabolic Shift	PID1, CS, CYP1B1, FLVCR1, IFIT2	GeneCards/ NO MalaCards/ NO	1. Diagnostic Biomarkers: PID1, CS, CYP1B1, FLVCR1, IFIT2, MAPK14 were identified as diagnostic genes for sepsis. Validation: These genes demonstrated high sensitivity and specificity for diagnosing sepsis across datasets and experimental models.
48.VCAM1/ ICAM1	VCAP1/ICAM1	Vascular Cell Adhesion Molecule 1 CD106 Vascular Cell Adhesion Protein 1 CD106 Antigen INCAM-100 V-CAM 1 VCAM-1/ Intercellular Adhesion Molecule 1 CD54 BB2 Major Group Rhinovirus Receptor ICAM-1 Intercellular Adhesion Molecule 1 (CD54), Human Rhinovirus Receptor Epididymis Secretory Sperm Binding Protein Cell Surface Glycoprotein P3.58 Human Rhinovirus Receptor CD54 Antigen P3.58	protein/gene marker	more prognostic		Vascular and Endothelial Pathways/ Endothelial Activation	VCAM1+ EC-EVs	GeneCards/NO MiaCards/Bacterial sepsis Septic Arthritis	1. Diagnostic: Elevated levels of VCAM1+ EC-EVs can serve as a biomarker for sepsis-related ARDS. Prognostic: VCAM1+ EC-EVs could potentially predict the severity and progression of lung injury in septic patients.

50.SOCS3	OCS3	Suppressor Of Cytokine Signaling 3 SOCS-3 SSI-3 CIS3 Cish3 Cytokine-Inducible SH2 Protein 3 STAT-Induced STAT Inhibitor 3 SSI3 ATOD4 CIS-3				Epigenetic and Transcriptomic Regulation Pathways/ Gene Expression Modulation Inflammatory and Immune Pathways/ Anti-inflammatory Signals		GeneCards/ NO Malacards/ Septic Arthritis	
51.GATA3	GATA3	GATA Binding Protein 3 HDR Trans-Acting T-Cell-Specific Transcription Factor GATA-3 GATA-Binding Factor 3 GATA-Binding Protein 3 HDRS				Inflammatory and Immune Pathways/ Immune Cell Recruitment Adaptive Immune Pathways/ T-cell Activation/Regulation of Differentiation		GeneCards/ NO MalaCards/ Bacterial sepsis	
52.CCR7/8	CCR7	C-C Motif Chemokine Receptor 7 CDw197 BLR2 CMKBR7 CD197 EBI1 Epstein-Barr Virus-Induced G-Protein Coupled Receptor 1 Chemokine (C-C Motif) Receptor 7 C-C Chemokine Receptor Type 7 MIP-3 Beta Receptor CC-CKR-7 CCR-7 Lymphocyte-Specific G Protein-Coupled Peptide Receptor EBV-Induced G Protein-Coupled Receptor 1 EBV-Induced G-Protein Coupled Receptor 1 Epstein-Barr Virus Induced Gene 1 Burkitt'S Lymphoma Receptor CC Chemokine Receptor 7 CD197 Antigen C-C CKR-7 EVI1	protein/ gene marker	diagnostic/prognostic		Adaptive Immune Pathways/ Regulation of Differentiation Inflammatory and Immune Pathways/ Immune Cell Recruitment		GeneCards/ NO MalaCrads/ Bactreial sepsis	
53.CCR2	CCR2	C-C Motif Chemokine Receptor 2 CC-CKR-2 MCP-1-R CMKBR2 CD192 CKR2 Monocyte Chemoattractant Protein 1 Receptor Chemokine (C-C Motif) Receptor 2 C-C Chemokine Receptor Type 2 FLJ78302 CCR-2 Monocyte Chemotactic Protein 1 Receptor MCP-1 Receptor CD192 Antigen C-C CKR-2 CCR2A CCR2B CKR2A CKR2B PCLUD	protein/gene marker	diagnostic/prognostic		Inflammatory and Immune Pathways/ Immune Cell Recruitment		GeneCards/ NO MalaCards/ No	
54.HIF1a	HIF1A	Hypoxia Inducible Factor 1 Subunit Alpha BHLHe78 PASD8 MOP1 Class E Basic Helix-Loop-Helix Protein 78 PAS Domain-Containing Protein 8 Member Of PAS Protein HIF-1alpha HIF1 Hypoxia Inducible Factor 1, Alpha Subunit (Basic Helix-Loop-Helix Transcription Factor) Basic-Helix-Loop-Helix-PAS Protein MOP1 Hypoxia-Inducible Factor 1-Alpha HIF-1-Alpha Hypoxia Inducible Factor 1 Alpha Subunit Hypoxia-Inducible Factor1alpha Member Of PAS Superfamily 1 ARNT Interacting Protein ARNT-Interacting Protein HIF1-ALPHA HIF1-Alpha BHLHE78 HIF-1A	protein/ gene marker	diagnostic/prognostic		Vascular and Endothelial Pathways/ Vascular Integrity Hypoxia and Metabolic Pathways/ Metabolic Shift Epigenetic and Transcriptomic Regulation Pathways/ Gene Expression Modulation		GeneCards/ NO MalaCards/NO	1. Diagnostic Biomarker: HIF-1α alone and as part of a composite measure was effective in distinguishing septic from non-septic patients./gene/protein Prognostic Biomarker: HIF-1α levels were predictive of ICU mortality and disease severity.
									2. HIF-1α mRNA levels in leukocytes show potential as a diagnostic biomarker for sepsis severity./gene
IKZF1									