Gene name: **FCGR1A.**

External Ids for FCGR1A Gene: HGNC: 3613 NCBI Gene: 2209 Ensembl: ENSG00000150337 OMIM®: 146760 UniProtKB/Swiss-Prot: P12314

NCBI Gene Summary: This gene encodes a protein that plays an important role in the immune response. This protein is a high-affinity Fc-gamma receptor. The gene is one of three related gene family members located on chromosome 1.

GeneCards Summary: FCGR1A (Fc Gamma Receptor Ia) is a Protein Coding gene. Diseases associated with FCGR1A include Peritonitis and Pharyngitis. Among its related pathways are ADORA2B mediated anti-inflammatory cytokines production and Regulation of actin dynamics for phagocytic cup formation. Gene Ontology (GO) annotations related to this gene include *obsolete signal transducer activity, downstream of receptor* and *IgG binding*. An important paralog of this gene is FCRLB.

UniProtKB/Swiss-Prot Summary : High affinity receptor for the Fc region of immunoglobulins gamma. Functions in both innate and adaptive immune responses. Mediates IgG effector functions on monocytes triggering antibody-dependent cellular cytotoxicity (ADCC) of virus-infected cells.

Subcellular locations: Stabilized at the cell membrane through interaction with FCER1G.

The FCGR1A gene encodes the high-affinity immunoglobulin gamma Fc receptor I, commonly known as CD64. This receptor is predominantly expressed on immune cells such as monocytes, macrophages, and dendritic cells, playing a crucial role in both innate and adaptive immune responses. Its primary function involves binding the Fc region of immunoglobulin G (IgG) antibodies, facilitating processes like phagocytosis, antigen presentation, and the release of inflammatory mediators.

In the context of sepsis—a severe systemic inflammatory response to infection—FCGR1A is particularly significant. During infections, pro-inflammatory cytokines such as interferon-gamma (IFN-γ) stimulate an upregulation of CD64 expression on neutrophils. This increased expression enhances the immune system's capacity to recognize and eliminate pathogens. Notably, elevated levels of CD64 on neutrophils have been identified as a valuable biomarker for diagnosing bacterial infections and sepsis. The heightened expression of CD64 correlates with the activation status of neutrophils, providing clinicians with a diagnostic tool to assess the presence and severity of infection.

Furthermore, the interaction between CD64 and IgG complexes can amplify inflammatory responses. While this amplification is essential for effective pathogen clearance, it can also contribute to the excessive inflammation characteristic of sepsis. Therefore, understanding the regulation and function of FCGR1A is vital for developing therapeutic strategies aimed at modulating immune responses in septic patients, potentially improving outcomes by balancing pathogen elimination with the prevention of harmful inflammation.

Recent studies have further elucidated the diagnostic and prognostic significance of FCGR1A in sepsis:

- Diagnostic Role: Research has demonstrated that FCGR1A, along with other inflammation-related genes, holds diagnostic value for sepsis. Its expression levels can aid in distinguishing septic

patients from healthy individuals, thereby serving as a potential biomarker for early detection.

- Prognostic Role: Elevated expression of FCGR1A has been associated with patient survival in sepsis. Studies indicate that higher levels of FCGR1A correlate with improved survival rates, suggesting its potential as a prognostic biomarker to assess patient outcomes.

These findings underscore the importance of FCGR1A not only in the pathophysiology of sepsis but also in its potential utility in clinical settings for diagnosis and prognosis.

FCGR1A gamma receptor pathway: