

One subgroup of cytokines, the hematopoietins, regulates hematopoietic stem cell differentiation to maintain the proper number and proportions of each blood cell type. For example, the production of erythrocytes is stimulated by the release of erythropoietin from the kidneys in response to decreased blood oxygen levels. Similarly, thrombopoietin stimulates the proliferation and differentiation of megakaryocytes, leading to increased platelet production. Another cytokine subgroup, the chemokines, is secreted by cells of the immune system, and act to coordinate the immune response to an invading antigen. This is a large and diverse class of proteins, and includes RANTES, eotaxin, lymphotactin, MIP-1, and the interleukins. Many of these polypeptides have uses in the diagnosis and treatment of immunological disorders and infection (Holldack, J. et al., *Med Ped Oncol Suppl* 2:2-9; Chapter 23, *Immunology*, edited by Elgert, K.).

Carrier Proteins

[0009] A number of soluble proteins found in blood function as carriers of other molecules such as nutrients and waste products. Carrier proteins can also bind exogenously delivered drugs and influence pharmacokinetic properties such as serum half-life and tissue adsorption. Serum albumin, comprising about half of the protein found in blood plasma, regulates osmotic pressure of blood, as well as binds many bioactive molecules. Transferrin is a blood carrier protein that regulates iron levels, while ceruloplasmin regulates copper levels. Thus there exists a clear need for novel polynucleotides and polypeptides (as well as antibodies, agonists, and antagonists) useful in diagnostic and therapeutic methods for detecting, preventing, diagnosing, prognosticating, treating, and/or ameliorating hematopoietic and hematologic diseases and disorders; such as, for example, leukemias, lymphomas, hemophilias, anemias, immunodeficiency disorders (including AIDS), amongst many other conditions. See, e.g., "Blood Related Disorders" and "Immune Activity" sections, *infra*.

SUMMARY OF THE INVENTION

[0010] The present invention encompasses human secreted proteins/polypeptides, and isolated nucleic acid molecules encoding said proteins/polypeptides, useful for detecting, preventing, diagnosing, prognosticating, treating, and/or ameliorating hematopoietic and hematologic disorders and diseases. Antibodies that bind these polypeptides are also encompassed by the present invention; as are vectors, host cells, and recombinant and synthetic methods for producing said polynucleotides, polypeptides, and/or antibodies. The invention further encompasses screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention also encompasses methods and compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

DETAILED DESCRIPTION

Polynucleotides and Polypeptides of the Invention

Description of Table 1A

[0011] Table 1A summarizes information concerning certain polynucleotides and polypeptides of the invention. The first column provides the gene number in the application for

each clone identifier. The second column provides a unique clone identifier, "Clone ID:," for a cDNA clone related to each contig sequence disclosed in Table 1A. Third column, the cDNA Clones identified in the second column were deposited as indicated in the third column (i.e. by ATCC Deposit No:Z and deposit date). Some of the deposits contain multiple different clones corresponding to the same gene. In the fourth column, "Vector" refers to the type of vector contained in the corresponding cDNA Clone identified in the second column. In the fifth column, the nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the corresponding cDNA clone identified in the second column and, in some cases, from additional related cDNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X. In the sixth column, "Total NT Seq." refers to the total number of nucleotides in the contig sequence identified as SEQ ID NO:X." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." (seventh column) and the "3' NT of Clone Seq." (eighth column) of SEQ ID NO:X. In the ninth column, the nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, in column ten, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep." In the eleventh column, the translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be routinely translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

[0012] In the twelfth and thirteenth columns of Table 1A, the first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." In the fourteenth column, the predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion". The amino acid position of SEQ ID NO:Y of the last amino acid encoded by the open reading frame is identified in the fifteenth column as "Last AA of ORF".

[0013] SEQ ID NO:X (where X may be any of the polynucleotide sequences disclosed in the sequence listing) and the translated SEQ ID NO:Y (where Y may be any of the polypeptide sequences disclosed in the sequence listing) are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used, for example, to generate antibodies which bind specifically to proteins containing the polypeptides and the secreted proteins encoded by the cDNA clones identified in Table 1A and/or elsewhere herein.