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(54) **METHOD OF SCREENING A SUBSTANCE INTERFERING IN THE ASSOCIATION OF DOCK2 AND ELMO**

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(57) **ABSTRACT**

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The present invention is related to provide a method for screening a substance interfering in the association of DOCK2 and ELMO1, a method for screening a substance interfering in the association of ELMO1 and Tiam1, and a method for searching a therapeutic agent for immune related diseases such as allergy, autoimmune diseases, GvH, graft rejection with the use of these searching methods, and so on. It was found that in DOCK2-mutant lacking 504 amino acid residues at the N terminus of DOCK2, Rac-activating ability was significantly decreased, and that actin polymerization could not be induced, and ELMO1 was identified as a molecule binding to this domain. It was found that DOCK2 was associated to ELMO1 via SH3 domain. Moreover, it was found that ELMO1 is bound with Tiam1 functioning as Rac-specific GDP/GTP exchange factor (GEF). It was found that DOCK2 activates Rac by recruiting Tiam1 via ELMO1.

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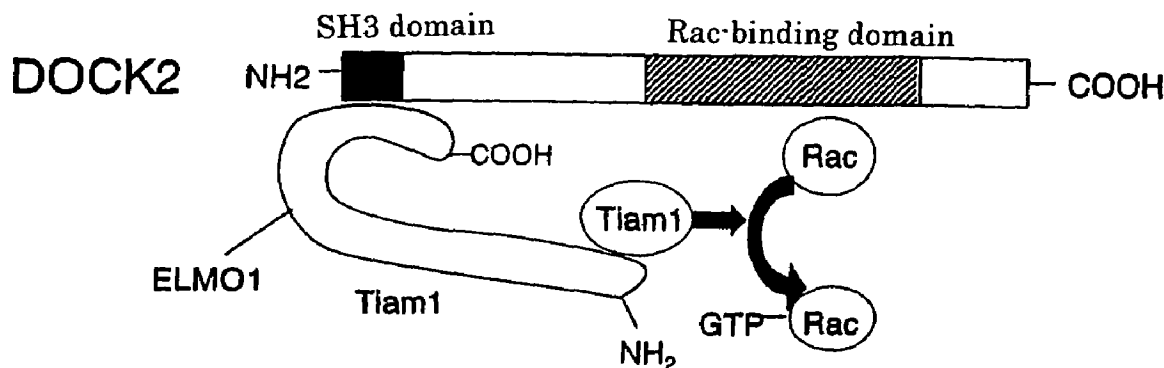
G01N 33/53 (2006.01)

(52) **U.S. Cl.** **435/7.1**

(58) **Field of Classification Search** None

See application file for complete search history.

7 Claims, 6 Drawing Sheets



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Fig. 1

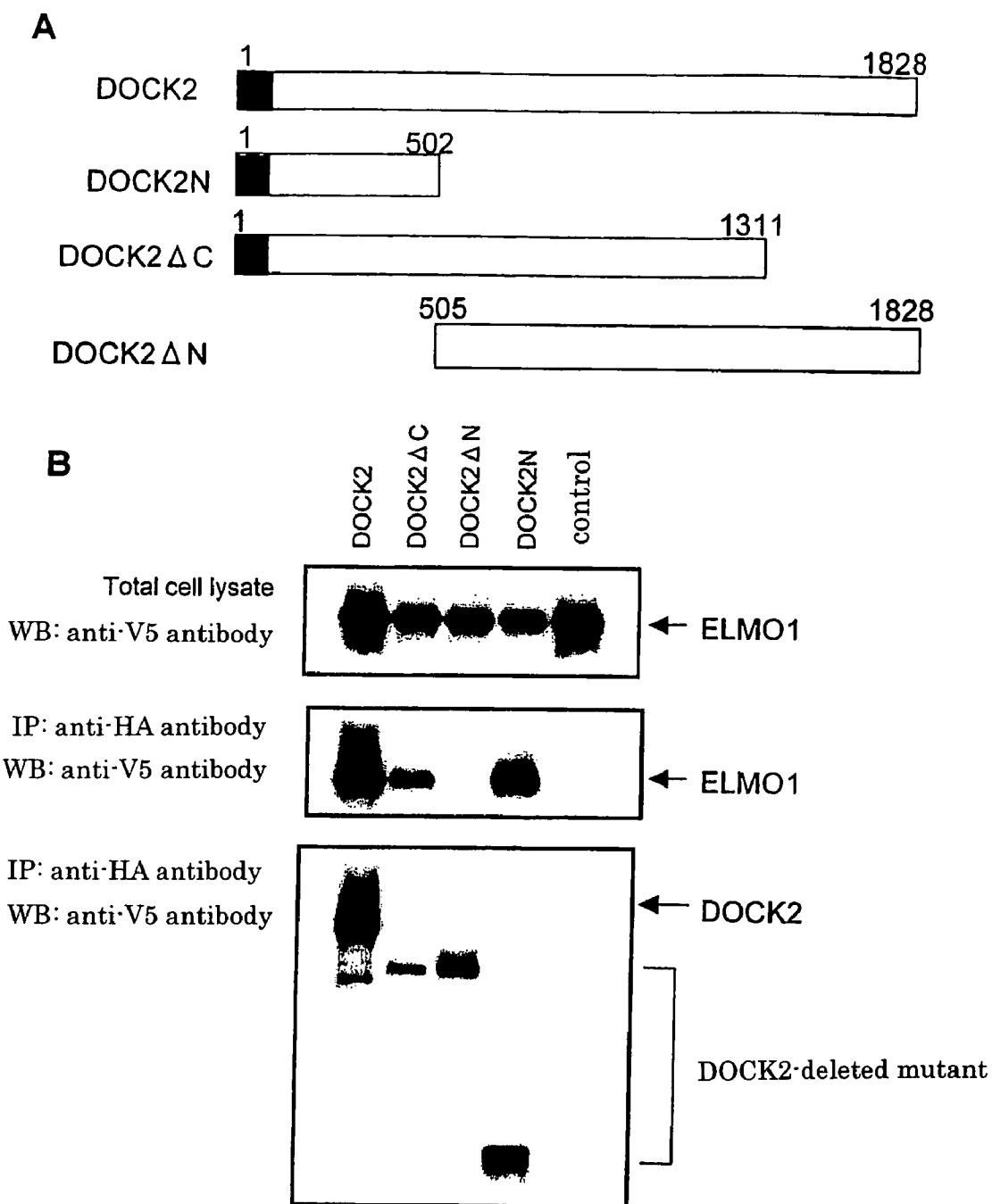


Fig. 2



Fig. 3

A

10 ERHGVAFYNF 20 FGGSEAQL 30 HLTLQIGDVVRI 40 QETGGDWYRGYL

50 IKHKLSQGIF 60 PTFIHLKEVT 70 VEKRRNIENI 80 IPAEIPLAQ

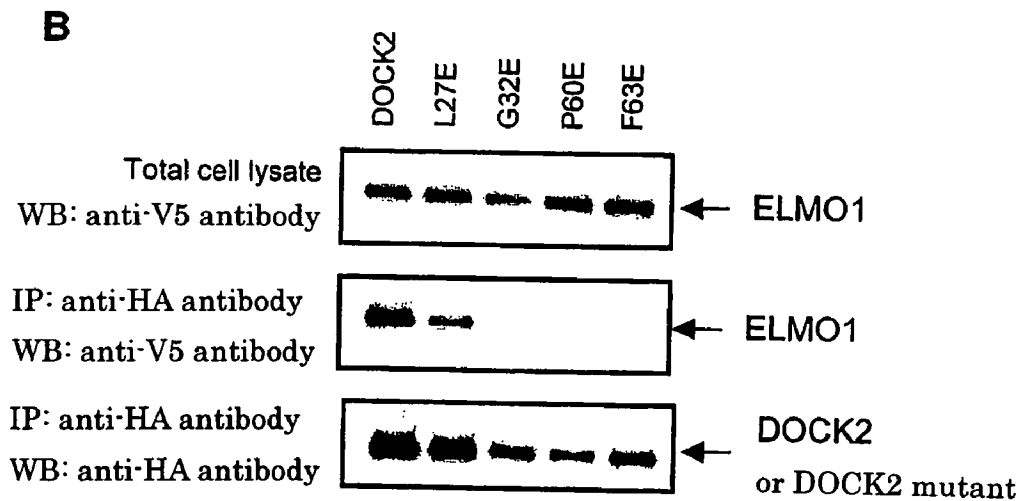


Fig. 4

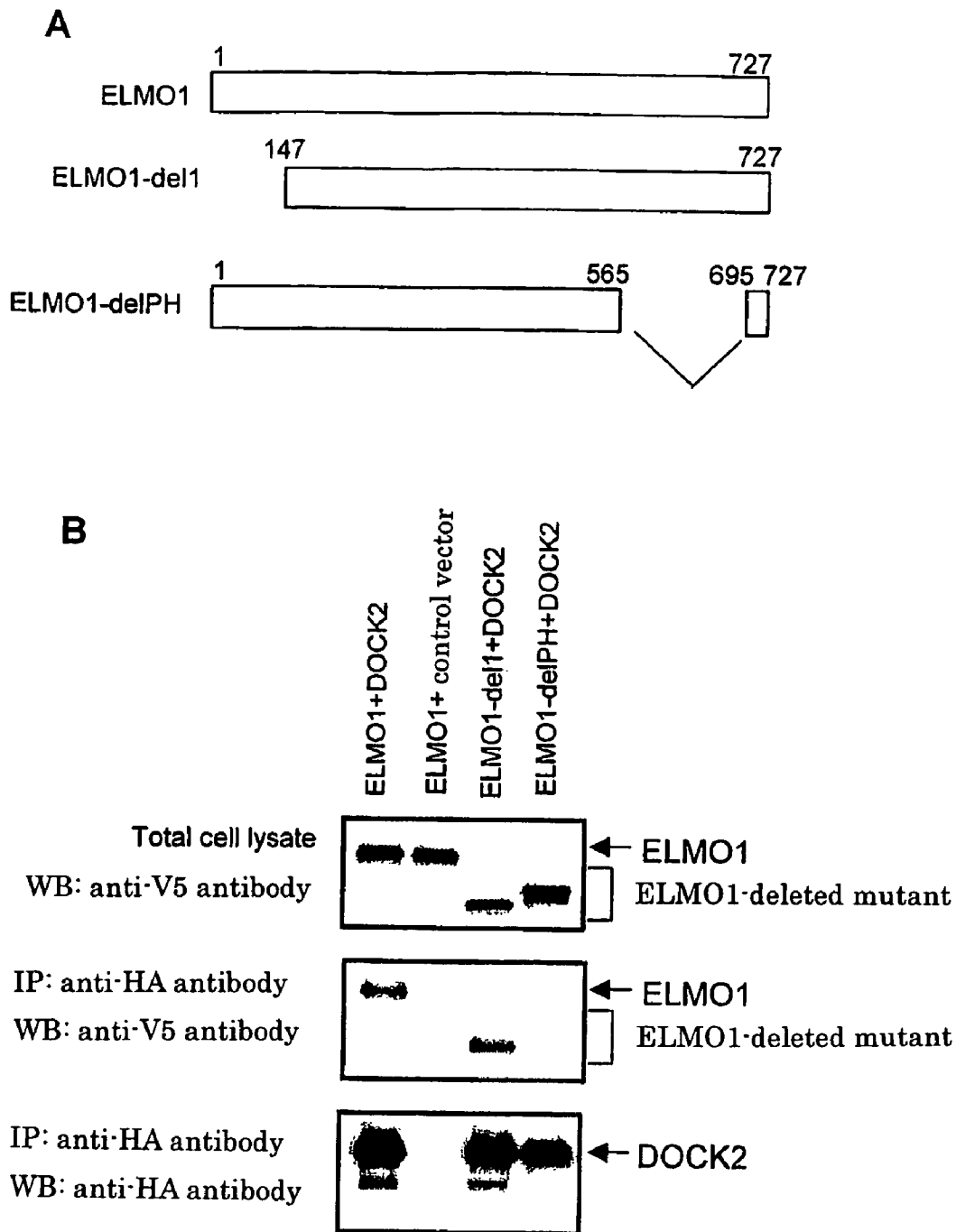


Fig. 5

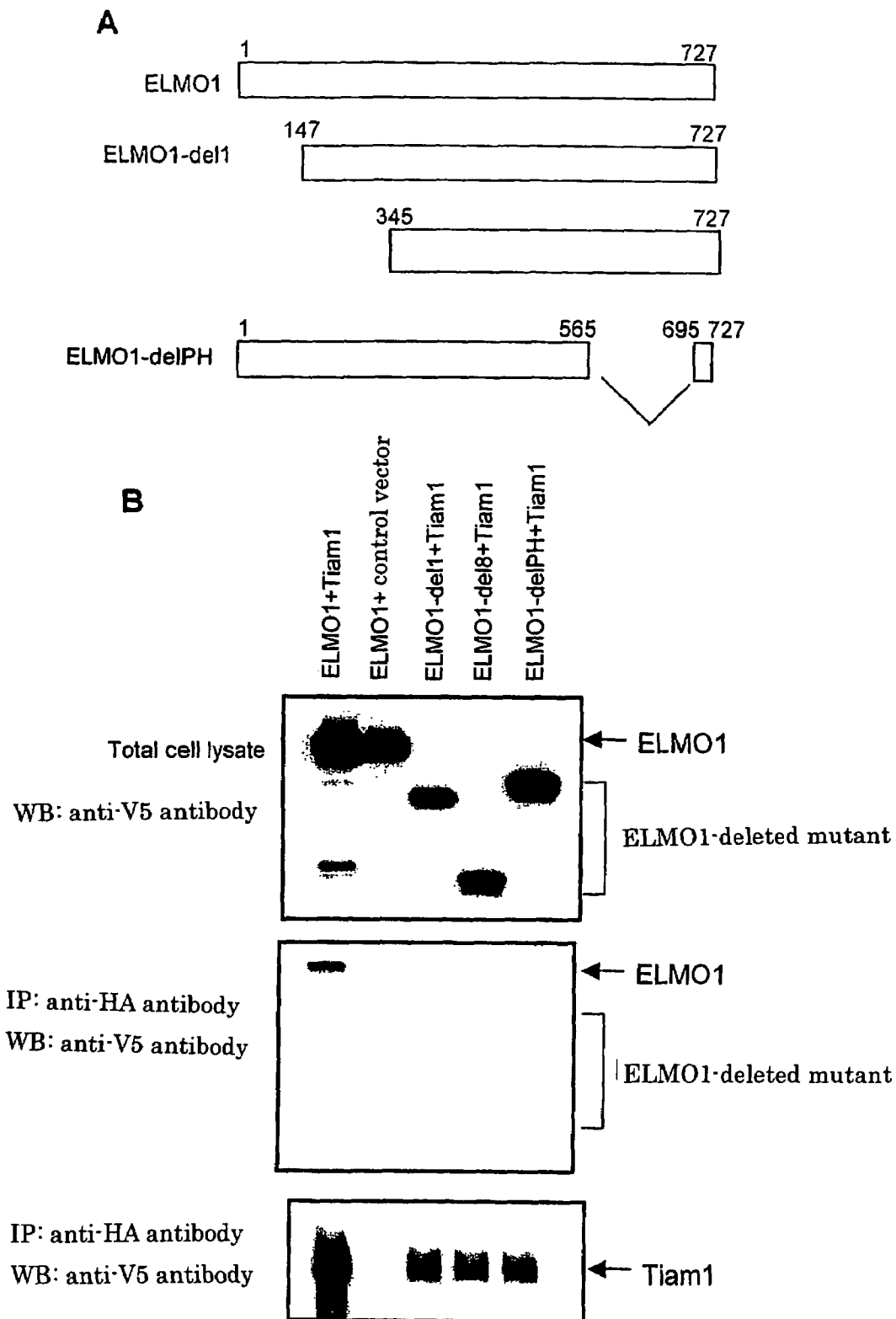
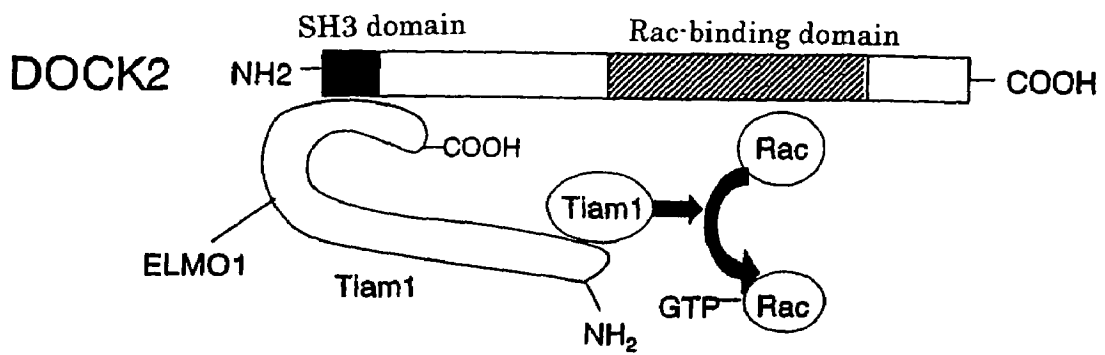


Fig. 6



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**METHOD OF SCREENING A SUBSTANCE
INTERFERING IN THE ASSOCIATION OF
DOCK2 AND ELMO**

TECHNICAL FIELD

The present invention relates to the identification of DOCK2 domain by using a deletion mutant, and a method for screening a substance interfering in the binding of DOCK 2 and SH3 domain of DOCK 2, particularly to a method for screening a substance interfering in the association of DOCK2 and ELMO, a method for screening a substance interfering in the association of ELMO and GDP/GTP exchange factor such as Tiam, or to a method for searching therapeutic agents for immune-related diseases, such as allergy, autoimmune diseases, GvH or graft rejection, with the use of these screening methods.

BACKGROUND ART

Immune response is a regulatory mechanism indispensable against infection for a living body, and immune cells are patrolling constantly in the living body, to respond rapidly to various sources of infection. Such characteristics that constitutive cells are moving continuously are not recognized in other complex living systems, and have been developed specifically in the immune system. Among the immune cells, cells such as neutrophils, macrophages are known to function during primary defense of infection, while T- and B-lymphocytes trigger antigen-specific immune response by recognizing external foreign substances via the antigen receptor. The above T- and B-lymphocytes differentiate in primary lymphoid organs such as thymus and bone marrow, and transfer to a particular compartment in second lymphoid organs such as spleen, lymph nodes, Payer's patch (lymphoid organs in the small intestine), and by recognizing antigens gathered there from various organs via the antigen receptor, induce specific immune response. At that time, the transfer of lymphocytes to a particular site of second lymphoid organ is very important for the formation of immune response. Heretofore, the transfer of the lymphocytes was known to be induced by protein called generally various chemokines, while the molecule mechanism that controls the mobility of the lymphocytes themselves remained unknown.

Change of cell polarization and cytoskeletal reorganization were indispensable for the cells movement (Cell 84, 359-369, 1996), and these were known to be controlled by G protein of low molecular weight such as Rho, Rac and Cdc42 (Proc. Natl. Acad. Sci. USA 92, 5027-5031, 1995; Science 279, 509-514, 1998; J. Cell Biol. 141, 1147-1157, 1998; Science 287, 1037-1040, 2000). Among these, Rac particularly provides driving force at the time of cell migration, by forming an actin-rich protrusion, called foliar protrusion (Science 279, 509-514, 1998; Cell 103, 227-238, 2000). On the other hand, molecules showing structural homology called CED5, DOCK 180 and Myoblast city (MBC) were identified in *Caenorhabditis elegans*, human and *Drosophila melanogaster*. These molecules are called CDM family molecules by their initials, and all of them are thought to be related to cytoskeletal reorganization by functioning upstream of Rac (Cell 84, 359-369, 1996; J. Cell Biol. 138, 589-603, 1997; Nature 392, 501-504, 1998; Genes Dev. 12, 3331-3336, 1998; Genes Dev. 12, 3337-3342, 1998; Nature Cell Biol. 2, 131-136, 2000). Although genetic analysis with the use of a deletion mutant has shown that the above CED-5 and Myoblast City are crucial for cell migration of particular types of cells, (J. Cell Biol. 138, 589-603, 1997; Nature 392, 501-504, 1998;

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Nature Cell Biol. 2, 131-136, 2000), physiological relevance of the CDM family proteins in mammals remained unknown.

It is known that DOCK2 (KIAA0209; DNA Res. 3, 321-329) encodes another member of the CDM family proteins, which is specifically expressed in human haematopoietic cells, and that the DOCK2 binds to activate Rac in 293T kidney cells (Biochem. Biophys. Acta 1452, 179-187, 1999). On the other hand, the present inventors isolated a new gene Hch belonging to the CDM family from mouse thymus cDNA library, and found that the gene product comprises 1828 amino acids, and encodes SH3 domain at the N terminus (Nature, 412, 826-831, 2001). Moreover, the present inventors confirmed by Northern Blot analysis using mouse organs that whereas DOCK180 was expressed in various organs, the expression of Hch was restricted to thymus and spleen. Further, by an analysis using cell lines they confirmed that Hch expression was observed in all T-, B- and macrophage cells, with the exception of two mutant T-cell lines. Furthermore, it has been revealed that a significant change in cell morphology and enhancement of adhesion were observed by introducing Hch into mutant T-cell line lacking Hch expression. Though 1677 of the 1828 amino acids encoded by Hch are identical to human DOCK2, and Hch was thought to be mouse DOCK2 homologue, the physiological function remained unknown.

The present inventors identified DOCK2 as a molecule belonging to the CDM family, expressing specifically in lymphocytes as mentioned above, and by generating the knockout mice, they revealed that the molecule was indispensable to lymphocyte migration (Nature, 412, 826-831, 2001). In DOCK2-deleted lymphocytes, active Rac is not detected by any of chemokine stimulation. Therefore, it can be thought that DOCK2 regulates lymphocyte migration via Rac activation. However, it remains unknown by which mechanism DOCK2 activates Rac. Rac functions as a molecule switch, and is activated by a GDP/GTP exchange factor (GEF). Though DOCK2 binds with Rac, it is hard from its structure, to think that it functions as GEF. Therefore, it is estimated that DOCK2 activates Rac by recruiting GEF via other molecules.

Recently, CED-12 being a molecule that associates with CED-5, which is one of the CDM family molecules, and that regulates cytoskeleton has been identified in *C. elegans*, and ELMO-1, -2 and -3 were reported as their mammalian homologues (Cell, 107, 27-41, 2001). Moreover, several dozens of GDP/GTP exchange factors (GEF) were known heretofore, and among these GEFs, as a molecule functioning as Rac-specific GEF, the following are known: Tiam-1 and -2 that determines the invasion to thymoma cell lines (Cell, 77, 537-549, 1994; Nature, 375, 338-340, 1995); Vav1 that regulates T cell receptor signal (Nature, 385, 169-172, 1997) besides Vav2, Vav3; Trio (J. Cell Science, 113, 729-739, 2000); STEF (J. Biol. Chem., 277, 2860-2868, 2002); and P-Rex1 (Cell, 108, 809-821, 2002). All these five molecules have a common domain, and comprise a function to provide GTP to Rac.

Autoimmune diseases and graft rejection are caused by the invasion of lymphocytes into the target organ. Therefore, it is thought that DOCK2 might be a suitable target molecule to treat or prevent such diseases or pathology. The object of the present invention is to identify the functional domain of DOCK2 by using a deletion mutant, to screen a substance interfering in the binding of DOCK2 and SH3 domain of DOCK2, particularly to provide a method for screening a substance interfering in the association of DOCK2 and ELMO, a method for screening a substance interfering in the association of ELMO and GDP/GTP exchange factor such as Tiam, or a method for searching therapeutic agents for

immune-related diseases, such as allergy, autoimmune diseases, GvH or graft rejection with the use of these screening methods, and the like.

DOCK2 is a molecule expressed specifically in lymphocytes, comprised of 1828 amino acid residues including SH3 domain, that activates Rac and regulates cytoskeleton to determine lymphocyte mobility. The present inventors have made a keen study to solve the above object, found that Rac-activating ability was significantly decreased in DOCK2 mutant lacking 504 amino acid residues in the N terminus including SH3 domain of DOCK 2, and that actin polymerization could not be induced, and they identified ELMO1 as a molecule binding to this domain. Moreover, as the binding of DOCK2 and ELMO1 was completely inhibited by the single amino acid mutation of SH3 domain, they have found that DOCK2 associates with ELMO1 via SH3 domain. Furthermore, they have found that ELMO1 binds with Tiam1 functioning as Rac-specific GDP/GTP exchange factor (GEF). In other words, they have found that DOCK2 activates Rac by recruiting Tiam1 via ELMO1. Therefore, they found that by inhibiting intermolecular interaction of SH3 domain of DOCK2, ELMO1 and Tiam1, the artificial control of lymphocyte migration was possible. The present invention has been thus completed with this knowledge.

DISCLOSURE OF THE INVENTION

In other words, the present invention relates to a method for screening a substance interfering in the association of DOCK2 and ELMO, comprising the steps of contacting DOCK2, ELMO and a test substance, and then estimating the level of formation of association of DOCK2 and ELMO ("1"); a method for screening a substance interfering in the association of DOCK2 and ELMO, comprising the steps of contacting SH3 domain of DOCK2, ELMO and a test substance, and then estimating the level of formation of association of SH3 domain of DOCK2 and ELMO ("2"); a method for screening a substance interfering in the association of DOCK2 and C terminus domain of ELMO, comprising the steps of contacting DOCK2, C terminus domain of ELMO and a test substance, and then estimating the level of formation of association of DOCK2 and C terminus domain of ELMO ("3"); a method for screening a substance interfering in the association of DOCK2 and ELMO, comprising the steps of contacting SH3 domain of DOCK2, C terminus domain of ELMO and a test substance, and then estimating the level of formation of association of SH3 domain of DOCK2 and C terminus domain of ELMO ("4"); the method for screening a substance interfering in the association of DOCK2 and ELMO according to any one of "1" to "4", wherein DOCK2 or its SH3 domain and/or ELMO or its C-terminus domain is bound with a marker protein and/or peptide tag ("5"); the method for screening a substance interfering in the association of DOCK2 and ELMO according to anyone of "1" to "5", wherein an antibody against ELMO or its C terminus domain is acted to DOCK2 or its SH3 domain fractionated by an antibody against DOCK2 or its SH3 domain, or an antibody against other peptides fused with DOCK2 or its SH3 domain, and the level of formation of association is estimated ("6"); the method for screening a substance interfering in the association of DOCK2 and ELMO according to any one of "1" to "6", wherein the level of formation of association is estimated by detecting GTP-binding form of activated-Rac ("7"); the method for screening a substance interfering in the association of DOCK2 and ELMO according to any one of "1" to "7", wherein the substance interfering in the association of DOCK2 and

ELMO is a substance promoting or suppressing the function of regulating lymphocyte migration ("8"); the method for screening a substance interfering in the association of DOCK2 and ELMO according to any one of "1" to "7", wherein the substance interfering in the association of DOCK2 and ELMO is a substance inhibiting the binding of DOCK2 and ELMO ("9"); the method for screening a substance interfering in the association of DOCK2 and ELMO according to any one of "1" to "9", wherein ELMO is ELMO1 ("10"); a method for searching a therapeutic agent for immune related diseases such as allergy, autoimmune diseases, GvH, and graft rejection wherein the method for screening a substance interfering in the association of DOCK2 and ELMO according to any one of "1" to "10" is used ("11"); and a method for searching a therapeutic agent for diseases caused by the suppression of lymphocyte migration, which promotes cytoskeletal reorganization by activating Rac, wherein the method for screening a substance interfering in the association of DOCK2 and ELMO according to any one of "1" to "10" is used ("12").

Moreover, the present invention is related to a method for screening a substance interfering in the association of ELMO and GDP/GTP exchange factor, comprising the steps of contacting ELMO, GDP/GTP exchange factor and a test substance, and then estimating the level of formation of association of ELMO and GDP/GTP exchange factor ("13"); a method for screening a substance interfering in the association of ELMO and GDP/GTP exchange factor, comprising the steps of contacting N terminus domain of ELMO, GDP/GTP exchange factor and a test substance, and then estimating the level of formation of association of N terminus domain of ELMO and GDP/GTP exchange factor ("14"); the method for screening a substance interfering in the association of ELMO and GDP/GTP exchange factor according to "13" or "14", wherein ELMO or its N terminus domain and/or GDP/GTP exchange factor is fused with another peptide ("15"); the method for screening a substance interfering in the association of ELMO and GDP/GTP exchange factor according to any one of "13" to "15", wherein an antibody against ELMO or its N terminus domain is acted to a GDP/GTP exchange factor fractionated by an antibody against GDP/GTP exchange factor or by an antibody against another peptide fused with GDP/GTP exchange factor, and the level of formation of association is estimated ("16"); the method for screening a substance interfering in the association of ELMO and GDP/GTP exchange factor according to any one of "13" to "16", wherein the level of formation of association is estimated by detecting GTP-binding form of activated-Rac ("17"); the method for screening a substance interfering in the association of ELMO and GDP/GTP exchange factor according to any one of "13" to "17", wherein the substance interfering in the association of ELMO and GDP/GTP exchange factor is a substance promoting or suppressing the function of regulating lymphocyte migration ("18"); the method for screening a substance interfering in the association of ELMO and GDP/GTP exchange factor according to any one of "13" to "17", wherein the substance interfering in the association of ELMO and GDP/GTP exchange factor is a substance inhibiting the binding of ELMO and GDP/GTP exchange factor ("19"); the method for screening a substance interfering in the association of ELMO and GDP/GTP exchange factor according to any one of "13" to "19", wherein ELMO is an ELMO bound with DOCK2 ("20"); the method for screening a substance interfering in the association of ELMO and GDP/GTP exchange factor according to any one of "13" to "20", wherein ELMO is ELMO1 ("21"); the method for screening a substance interfering in the association of ELMO

and GDP/GTP exchange factor according to any one of “13” to “21”, wherein the GDP/GTP exchange factor is a Rac-specific GDP/GTP exchange factor (“22”); the method for screening a substance interfering in the association of ELMO and GDP/GTP exchange factor according to “22”, wherein the Rac-specific GDP/GTP exchange factor is Tiam1 (“23”); a method for searching a therapeutic agent for immune related diseases such as allergy, autoimmune diseases, GvH, and graft rejection, wherein the method for screening a substance interfering in the association of ELMO and GDP/GTP exchange factor according to any one of “13” to “23” is used (“24”); and a method for searching a therapeutic agent for diseases caused by the suppression of lymphocyte migration, which promotes cytoskeletal reorganization by activating Rac, wherein the method for screening a substance interfering in the association of ELMO and GDP/GTP exchange factor according to any one of “13” to “23” is used (“25”).

Furthermore, the present invention relates to a method for screening a substance for promoting or suppressing Rac activation, comprising the steps of contacting DOCK2, ELMO, GDP/GTP exchange factor and a test substance, and then estimating the level of formation of association of DOCK2 and ELMO, or the level of formation of association of ELMO and GDP/GTP exchange factor (“26”); a method for screening a substance for promoting or suppressing Rac activation, comprising the steps of contacting SH3 domain of DOCK2, ELMO, GDP/GTP exchange factor and a test substance and then estimating the level of formation of association of SH3 domain of DOCK2 and ELMO, or the level of formation of association of ELMO and GDP/GTP exchange factor (“27”); the method for screening a substance for promoting or suppressing Rac activation according to “26” or “27”, wherein the level of formation of association is estimated by detecting GTP-binding form of activated-Rac (“28”); the method for screening a substance for promoting or suppressing Rac activation according to any one of “26” to “28”, wherein ELMO is an ELMO bound with DOCK2 (“29”); the method for screening a substance for promoting or suppressing Rac activation according to any one of “26” to “29”, wherein ELMO is ELMO1 (“30”); the method for screening a substance for promoting or suppressing Rac activation according to any one of “26” to “30”, wherein the GDP/GTP exchange factor is a Rac-specific GDP/GTP exchange factor (“31”); the method for screening a substance for promoting or suppressing Rac activation according to “31”, wherein the Rac-specific GDP/GTP exchange factor is Tiam1 (“32”); a method for searching a substance for promoting or suppressing the function of regulating lymphocyte migration, wherein the method for screening a substance promoting or suppressing Rac activation according to any one of “26” to “32” is used (“33”); a method for searching a therapeutic agent for immune related diseases such as allergy, autoimmune diseases, GvH, and graft rejection, wherein the method for screening a substance for promoting or suppressing Rac activation according to any one of “26” to “32” is used (“34”); and a method for searching a therapeutic agent for diseases caused by the suppression of lymphocyte migration, which promotes reconstruction of cytoskeleton by activating Rac, wherein the method for screening a substance for promoting or suppressing Rac activation according to any one of “26” to “32” is used (“35”); a therapeutic agent for immune related diseases such as allergy, autoimmune diseases, GvH and graft rejection, obtained by the searching method according to “11”, “24” or “34” (“36”); a therapeutic agent for diseases caused by the suppression of lymphocyte migration, promoting cytoskeletal reorganization by activating Rac, obtained by the searching method according to “12”, “25” or “35” (“37”); a method for screen-

ing a substance inhibiting DOCK2-function, by targeting N terminus domain of DOCK2 including SH3 domain, comprising the steps of contacting SH3 domain of DOCK2, the SH3 domain-binding protein and a test substance, and then estimating the level of formation of association of DOCK2 and SH3 domain-binding protein (“38”); and a method for screening a substance inhibiting DOCK2-function, by using a transgenic cell line expressing full-length DOCK2 and DOCK2-deleted mutants, comprising the steps of measuring and estimating the level of Rac activation in these cell lines, identifying the functional domain of DOCK2, searching a molecule associated with functional domain that associates with the functional domain, contacting the functional domain of DOCK2, the molecule associated with functional domain and a test substance, and estimating the level of formation of association of functional domain of DOCK2 and molecule associated with functional domain of DOCK2 (“39”).

BRIEF DESCRIPTION OF DRAWINGS

FIG. 1 is a figure showing that DOCK2 binds with ELMO1 at its N terminus domain.

A is a view showing a frame format of the structure of DOCK2 and DOCK2-deleted mutants. In the figure, the black-colored part is the SH3 domain.

B is a figure showing the analysis of the binding with ELMO1 by immunoprecipitation and Western Blot method, by transfecting genes encoding DOCK2 or DOCK2-deleted mutants to 293T cells with PcDNA ELMO1-V5 and by collecting the cells 48 hours later. Types of samples used for analysis, antibodies used for immunoprecipitation and Western Blot are shown on the left side.

FIG. 2 is a set of pictures showing that the Rac-activating ability is significantly decreased and that actin polymerization cannot be induced in DOCK2ΔN lacking N terminus domain essential for the binding with ELMO1.

A is a picture showing the analysis of the expression of DOCK2 or DOCK2ΔN in BEα16-3, N3-5, and transgenic cell lines (17-11, 84-3) by Western Blot with the use of polyclonal antibody against DOCK2. In the figures, NS means non-specific band.

B is a picture that activated Rac is detected by pulling-down cell extract of 84-3, 17-11, BEα16-3 with GST fusion protein of PAK1 Rac-binding domain, and by staining with anti-Rac antibody.

C is a picture showing the investigation of cell polarization and actin polymerization by staining BEα16-3, 17-11, 84-3 with propidium iodide and phalloidin.

FIG. 3 is a picture showing that DOCK 2 associates with ELMO1 via its SH3 domain.

A is a figure showing the amino acid sequence 10-89 including DOCK2 SH3 domain SEQ ID NO: 8). Amino acid residues substituted to glutamic acid are shown in bold letter.

B is a figure showing the analysis of the binding of DOCK2 with ELMO1 by immunoprecipitation and Western Blot method, by transfecting genes encoding DOCK2 or DOCK2 SH3-deleted mutants to 293T cells with PcDNA ELMO1-V5 and by collecting the cells 48 hours later. Types of samples used for analysis, antibodies used for immunoprecipitation and Western Blot are shown on the left side.

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FIG. 4 is a figure showing that ELMO1 is bound with DOCK2 at its C terminus domain.

A is a view showing a frame format of the structure of ELMO1 and of ELMO1-deleted mutants used in this experiment.

B is a figure showing the analysis of the binding of ELMO1 with DOCK2 by immunoprecipitation and Western Blot method, by transfecting genes encoding ELMO1 or ELMO1-deleted mutants to 293T cells with PcDNA DOCK2-HA or a control vector and by collecting the cells 48 hours later. Types of samples used for analysis, antibodies used for immunoprecipitation and Western Blot are shown on the left side.

FIG. 5 is a figure showing that ELMO1 is bound to Tiam1 at its N terminus domain.

A is a view showing a frame format of the structure of ELMO1 and of ELMO1-deleted mutants used in this experiment.

B is a figure showing the analysis of the binding with Tiam1 by immunoprecipitation and Western Blot method, by transfecting genes encoding ELMO1 or ELMO1-deleted mutants to 293T cells with PCI Tiam1-HA or a control vector and by collecting the cells 48 hours later. Types of samples used for analysis, antibodies used for immunoprecipitation and Western Blot are shown on the left side.

FIG. 6 is a schematical view of the Rac-activating mechanism by DOCK2.

It is a figure showing that DOCK2 activates Rac via ELMO1 by recruiting Tiam1 functioning as GEF of Rac.

BEST MODE OF CARRYING OUT THE INVENTION

As for the method for screening a substance interfering in the association of DOCK2 and ELMO of the present invention, there is no specific limitation as long as it is a method comprising the steps of contacting DOCK2, ELMO and a test substance, and then estimating the level of formation of the association of DOCK2 and ELMO; a method comprising the steps of contacting SH3 domain of DOCK2, ELMO and a test substance, and then estimating the level of formation of the association of SH3 domain of DOCK2 and ELMO; a method comprising the steps of contacting DOCK2, C terminus domain of ELMO and a test substance, and then estimating the level of formation of the association of DOCK2, C terminus domain of ELMO; a method comprising the steps of contacting SH3 domain of DOCK2, C terminus domain of ELMO, and a test substance, and then estimating the level of formation of the association of SH3 domain of DOCK2, C terminus of ELMO. Moreover, as for the above-mentioned DOCK2 or its SH3 domain and/or ELMO or its C terminus domain, a fusion protein or a fusion peptide wherein these and marker protein and/or peptide tag are bound can be used. Moreover, as for the above ELMO, ELMO1, ELMO2, ELMO3 can be specifically exemplified, and ELMO1 can be preferably exemplified.

As for the above SH3 domain of DOCK2, a DOCK2 mutant having a function to associate with ELMO, and that is a peptide containing a whole or a part of SH3 domain of DOCK2 can be exemplified, and specific examples include DOCK2N comprising amino acid residue 1-502 of DOCK2 and DOCK2ΔC comprising amino acid residue 1-1311 of DOCK2. Furthermore, as for the above C terminus domain of ELMO, a mutant of ELMO having the function to associate with SH3 domain of DOCK2, and that is a peptide containing a whole or a part of C terminus domain of ELMO can be exemplified, and specific examples include ELMO1-del1

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comprising amino acid residue 147-727 of ELMO1, and ELMO1-del8 comprising amino acid residue 345-727 of ELMO1. Hereinafter, DOCK2 and the above SH3 domain of DOCK2 can be referred together to as "DOCK2 and the like", and ELMO such as ELMO1 and the above C terminus domain of ELMO can be referred together to as "ELMO and the like".

The above DOCK2 mutant or ELMO mutant can be prepared by modifying DOCK2 genes or ELMO genes according to a common procedure. As for DOCK2 genes, Hch (mouse DOCK2) genes (GenBank Accession No. AY027438; Nature, Vol 412, 23 August, 826-831, 2001) and human DOCK2 genes (XM_047961; DNA Res. 3, 321-329) can be specifically exemplified, but the origin of DOCK2 genes is not limited to mouse, human and the like. Moreover, as for ELMO genes such as ELMO1, besides mouse ELMO1 genes (AF398883; Cell, Vol. 107 (1), 27-41, 2001) and human ELMO1 genes (AF398885; Cell, Vol. 107(1) 27-41, 2001), ELMO2 genes (human AF398886, mouse AF398884), ELMO3 genes (human NM_024712) can be specifically exemplified. However, the origin of DOCK2 and ELMO genes is not limited to mouse, human and the like. Additionally, the amino acid sequence of mouse DOCK2, human DOCK2, mouse ELMO1, and human ELMO1 are shown as Seq. ID Nos. 1, 2, 3 and 4, respectively.

As for a marker protein in a fusion protein or fusion peptide wherein the above DOCK2 and the like or ELMO and the like are bound with a marker protein and/or peptide tag, there is no specific limitation as long as it is a marker protein conventionally known, and alkaline phosphatase, Fc domain of an antibody, HRP, and GFP can be exemplified. Moreover, as for a peptide tag, examples include peptide tags conventionally known, including epitope tags such as HA, FLAG and Myc; affinity tag such as GST, maltose-binding protein, biotinylated peptide and oligo-histidine. The fusion protein or fusion peptide can be prepared by a common procedure, and can separate/fractionate fusion protein or fusion peptide with DOCK2 and the like, ELMO1 and the like and HA-tag, by using specific antibody against HA tag.

In the method for screening a substance interfering in the association of DOCK2 and ELMO such as ELMO1, as for a method for contacting DOCK2 and the like, ELMO and the like, and a test substance, there is no specific limitation as long as it is a contacting method that can evaluate the level of the formation of the association of DOCK2 and the like and ELMO and the like, and examples include a method for contacting DOCK2 and the like and ELMO and the like, in the presence of a test substance in a cell-free system; a method for introducing an expression vector integrated with ELMO and the like or genes encoding ELMO and the like, in a cell expressing DOCK2 and the like together with a test substance; a method for introducing an expression vector integrated with DOCK2 and the like or genes encoding DOCK2 and the like, in a cell expressing ELMO and the like together with a test substance; or a method for introducing an expression vector integrated with DOCK2 and the like or genes encoding DOCK2 and the like, an expression vector integrated with ELMO and the like or genes encoding ELMO and the like, and a test substance, in a cell not expressing DOCK2 and the like nor ELMO and the like.

As for cells used for contacting with the above test substance, bacterial prokaryotic cells such as *E. Coli*, *streptomyces*, *Bacillus subtilis*, *Streptococcus* and *Staphylococcus*; eukaryotic cells such as yeast and *Aspergillus*; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9; plant and animal cells such as L cells, CHO cells, COS cells, HeLa cells, C127 cells and BALB/c3T3 cells (including mutant strain lacking dihydrofolate reductase or thymidine kinase), BHK21 cells,

HEK293 cells, Bowes melanoma cells and oocytes can be exemplified, and animal cells are preferable. Moreover, as for the method for introducing DOCK2 and the like or ELMO and the like in these cells, besides the above methods for introducing genes, a noncytotoxic reagent such as Chariot (Active Motif) that can form a non-covalent binding with an enormous molecule, change the structure of an enormous molecule such as protein, and that can deliver the enormous molecule such as protein into the cells, can be used.

As for the above expression vector, expression vector for animal cells are preferable, and examples of the expression vector for animal cells include: expression system derived from chromosome, episome, and virus; for example vectors derived from bacterial plasmid, yeast plasmid, papovavirus such as SV40, vaccinia virus, adenovirus, fowl poxvirus, pseudorabies virus, lentivirus, and retrovirus; vectors derived from bacteriophage, transposon, or from combination thereof, for example those derived from plasmid and bacteriophage elements, such as cosmids and phagemids. These expression systems can include regulatory sequences that not only induce expression but also regulate expression. Moreover, liposome can be used in place of expression vectors for animal cells. Further, the introduction of the expression vectors for animal cells into cells can be performed by a method described in various standard laboratory manuals such as Davis et al. (BASIC METHODS IN MOLECULAR BIOLOGY, 1986) and Sambrook et al. (MOLECULAR CLONING: A LABORATORY MANUAL, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and examples include calcium phosphate transfection, DEAE-dextran mediated transfection, transfection, microinjection, cationic lipid mediated transfection, electroporation, transduction, scrape loading, ballistic introduction, and infection.

In the method for screening a substance interfering the association of DOCK2 and ELMO such as ELMO1 of the present invention, as for the method for estimating the level of formation of the association of DOCK2 and the like and ELMO and the like, a method for measuring/estimating immunochemically the level of formation of the association of DOCK2 and the like and ELMO and the like, by acting an antibody against ELMO and the like to DOCK2 and the like being separated/fractionated, or by acting an antibody against DOCK2 and the like to ELMO and the like being separated/fractionated, can be exemplified. To separate/fractionate DOCK2 and the like or ELMO and the like, specific antibodies against DOCK2 and the like or ELMO and the like or tag-specific antibodies can be used. Moreover, yeast two hybrid system that can detect protein-protein interaction by using a minute amount of protein and without labeling; or a biosensor using the surface plasmon resonance reaction that can observe at real time as a surface plasmon resonance signal; or a method for measuring/estimating the level of formation of the association by using NMR method that can detect the change of tertiary structure, can be also exemplified. Moreover, publicly known methods for searching interacting protein, such as far western method using *E. coli* expression system and a method using affinity chromatography can be exemplified.

In the method for screening a substance interfering in the association of DOCK2 and ELMO of the present invention, as another method to estimate the level of formation of the association of DOCK2 and the like and ELMO and the like, an estimation method by detecting a GTP-binding form of activated Rac can be exemplified. To detect activated Rac, a pull-down method using GST fusion protein of PAK1 Rac-binding domain can be used.

As for samples to be tested in the method for screening a substance interfering in the association of DOCK2 and ELMO of the present invention, for example, peptides, proteins, synthesized compounds, microbial fermented materials, marine organism extracts, plant extracts, prokaryotic cells extract, eukaryotic unicellular extract, animal cells extract or library thereof can be exemplified. Furthermore, in the method for screening a substance interfering in the association of DOCK2 and ELMO of the present invention, control experiment can be carried out simultaneously. As for control, negative control that does not affect the formation of association of DOCK2 and the like and ELMO and the like, and/or positive control that affect the formation of association of DOCK2 and the like and ELMO and the like can be used.

As for the above substances interfering in the association of DOCK2 and ELMO, substances promoting or suppressing the function of regulating lymphocyte migration, particularly a substance suppressing the function of regulating lymphocyte migration such as substances inhibiting the binding of DOCK2 and ELMO. As for the function of regulating lymphocyte migration, there is no specific limitation as long as it is a function regulating the mobility of lymphocytes based on the expression of DOCK2 genes. Examples include a function promoting cytoskeletal reorganization, in particular actin polymerization in lymphocytes by activating Rac and making a Rac-GTP binding; a function of migrating lymphocytes in response to stimulation of chemokines such as SLC, SDF-1, and BLC; homing function to a secondary lymphoid organ such as spleen, lymph nodes, Payer's notch and the like; function of transferring mature thymus T cells to peripheral blood in response to ELC chemokine stimulation; or a function of migrating CD4⁺CD8⁺ immature thymus cells in response to SDF-1 chemokine stimulation.

The present invention relates also to a method for screening a substance interfering in the association of ELMO and GDP/GTP exchange factor (GEF), or to a method for screening a substance promoting or suppressing Rac activation. As for the method for screening a substance interfering in the association of ELMO and GEF, there is no specific limitation as long as it is a method comprising the steps of contacting ELMO, GEF, and a test substance, and then estimating the level of formation of association of ELMO and GEF; or a method comprising the steps of contacting N terminus domain of ELMO, GEF and a test substance, and then estimating the level of formation of association of N terminus domain of ELMO and GEF. Moreover, as for the method for screening a substance promoting or suppressing Rac activation, there is no specific limitation as long as it is a method comprising the steps of contacting DOCK2, ELMO, GEF and a test substance, or by contacting SH3 domain of DOCK2, ELMO, GEF and a test substance, and then estimating the level of formation of association of DOCK2 and ELMO, or the level of formation of association of ELMO and GEF. Further, as for the above ELMO, ELMO bound with DOCK2 can be used.

As for the above ELMO, examples include ELMO1, ELMO2, ELMO3, and among these, ELMO1 can be preferably exemplified. Moreover, as for the above GEF, Rac-specific GDP/GTP exchange factors such as Tiam1, Tiam2, Vav1, Vav2, Vav3, Trio, STEF, P-Rex1 are preferable, and among these, Tiam1 can be preferably exemplified. As for the above Tiam1 gene, mouse Tiam1 gene (NM_009384; Cell Vol. 77(4), 537-549, 1994), human Tiam1 gene (NM_003253; Oncogene Vol. 10(7), 1371-1376, 1995) can be exemplified, but the origin of Tiam1 gene is not limited to mouse, human and the like. Amino acid sequences of mouse Tiam1, human Tiam1 are shown in Seq. ID. Nos. 5 and 6, respectively.

Methods used for the above method for screening a substance interfering in the association of DOCK2 and ELMO, including the above method for screening a substance interfering in the association of ELMO and GEF, or a method for estimating the level of formation of association of ELMO and GEF, a method for estimating the level of formation of association of DOCK2 and ELMO, a method of using ELMO fused with other peptides, or its N terminus, and GEF, in the method for screening a substance for promoting or suppressing Rac activity, can be applied accordingly.

By using the method for screening a substance interfering in the association of DOCK2, ELMO such as ELMO1, the method for screening a substance interfering in the association of ELMO and GEF, the method for screening a substance promoting or suppressing Rac activation of the present invention, particularly the method for screening a substance promoting or suppressing the function of regulating lymphocyte migration, screening of preventive/therapeutic agents of immune related diseases such as allergy, autoimmune diseases, GvH, graft rejection targeting DOCK2 can be possible. As it can be anticipated that substances suppressing the function of regulating lymphocyte migration obtained by the method for screening a substance promoting or suppressing the function of regulating lymphocyte migration, such as anti-DOCK2 SH3 domain antibody, DOCK2 SH3 domain-binding molecule (including low molecular compounds), antisense strand of DOCK2 gene, antibodies recognizing specifically the DOCK2 SH3 domain-binding site of C terminus domain of ELMO such as ELMO1, molecules binding to the DOCK2 SH2 domain-binding site of C terminus domain of ELMO such as ELMO1 (including low molecular compounds), antibodies recognizing specifically GEF-binding site such as Tiam1 of N terminus domain of ELMO such as ELMO1, molecules binding to GEF-binding site such as Tiam1 of N terminus domain of ELMO such as ELMO1 (including low molecular compound), or antisense strand of ELMO such as ELMO1, can suppress artificially lymphocyte mobility, the possibility for these suppressive substances to be a therapeutic agent against immune-related diseases such as allergy, autoimmune diseases, GvH, graft rejection is high. When the therapeutic agent is used as drugs, various prescribed compounds such as pharmaceutically acceptable normal carrier, bonding agent, stabilizing agent, excipient, diluent, pH buffer agent, disintegrator, solubilizer, dissolving adjuvant, isotonic agent can be added, and can be administered by an administration form used generally, for example orally in formulation form such as powder, granule, capsule, syrup, and suspending agent, or parenterally in form of injection those formulated in form of solution, emulsion, suspending solution and the like.

Moreover, when using the method for screening a substance interfering in the association of DOCK2 and ELMO1, the method for screening a substance interfering in the association of ELMO1 and Tiam1, the method for screening a substance promoting or suppressing Rac activity of the present invention, in particular the method for screening a substance promoting the function of regulating lymphocyte migration, cytoskeletal reorganization is promoted by activating Rac, and thus, screening of preventive/therapeutic agents against diseases caused by suppression of lymphocyte migration, such as various cancers, or immunodeficiency caused by drugs/irradiation, can be possible.

Furthermore, as for the method for screening a substance inhibiting DOCK2 function of the present invention, examples include a method making the N terminus domain of DOCK2 including SH3 domain as target, comprising the steps of contacting SH3 domain of DOCK2 and the SH3

domain-binding protein and a test substance, and then estimating the level of formation of association of DOCK2 and SH3 domain-binding protein; and a method by using transgenic cell line expressing full length DOCK2 and DOCK2-deleted mutant, measuring/estimating the level of Rac activation in these cell lines, identifying the functional domain of DOCK2, searching a molecule associated with functional domain that associates with the functional domain, contacting the functional domain of DOCK2, the molecule associated with functional domain and a test substance, and estimating the level of formation of association of functional domain of DOCK2 and molecule associated with the functional domain. As for the method for contacting with a test substance, the method for estimating the level of formation of association, or the method for measuring the level of Rac activation, the methods mentioned above can be used. As for the method for identifying the functional domain of DOCK2, or for the preparation of transgenic cell line expressing full length DOCK2 and DOCK2-deleted mutant, methods described in the following examples can be used.

In the following, the present invention will be explained in detail by reference to the examples, while the technical scope of the present invention is not limited to these examples.

EXAMPLE 1

Binding of N Terminus Domain of DOCK2 and ELMO 1

Recently, CED-12 has been identified as a molecule that associates with CED-5 and regulates cytoskeleton in nematodes, and ELMO1 has been reported as its mammal homologue (Cell 107, 27-41, 2001). Therefore, in order to investigate whether DOCK2 binds with ELMO1 or not, by using PcDNA/His max vector (Invitrogen), gene constructs encoding full length DOCK2 or various DOCK2-deleted mutants in which HA tag (YPYDVPDYA: Seq. ID No. 7) is introduced at the C terminus (PcDNA DOCK2-HA, PcDNA DOCK2 N-HA, PcDNA DOCK2ΔC-HA, PcDNA DOCK2ΔN-HA), were constructed. Then, the gene constructs were introduced into 293T cells (provided by Dr. Shinji Hatakeyama, Kyushu University) together with a gene in which ELMO1 cDNA is introduced into PcDNA V5-His vector (Invitrogen) (PcDNA ELMO1-V5). DOCK2 construct was prepared from genes isolated by the present inventors (Nature, 412, 826-831, 2001), and ELMO1 construct was prepared from mouse tissue cDNA by PCR according to a common method. The genes encoding the used DOCK2-deleted mutant are as follows, and they are shown schematically in FIG. 1.

- 1) PcDNA DOCK2 N-HA; genes encoding amino acid residue 1-502 of DOCK2
- 2) PcDNA DOCK2ΔC-HA; genes encoding amino acid residue 1-1311 of DOCK2
- 3) PcDNA DOCK2ΔN-HA; genes encoding amino acid residue 505-1828 of DOCK2

The cells were collected 48 hours after gene introduction, dissolved with Lysis buffer (Cell signaling), and analysed by Western Blot method using anti-V5 antibody (Invitrogen) to immunoprecipitants by total cell lysate and anti-HA antibody (Roche). For each of total cell lysate, a band of approximately 100-KD corresponding to ELMO1 was detected for anti-V5 antibody (FIG. 1B; top). However, for the immunoprecipitants, a band corresponding to ELMO1 was detected, when genes encoding full length DOCK2, DOCK2ΔC and DOCK2 N, while no band was detected when DOCK2ΔN lacking amino acid residues from N terminus to 504 of DOCK2 (FIG. 1B; lower figure of the middle line). From these results, it has

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been clarified that DOCK2 associates with ELMO1 in the domain of amino acid residues from its N terminus to 502.

EXAMPLE 2

Rac Activation in DOCK2ΔN Lacking the N Terminus Domain

To clarify the influence of the association with ELMO1 to the function of DOCK 2, gene constructs encoding full length DOCK2 and a mutant lacking 504 amino acid residues of the N terminus of DOCK2 (DOCK2ΔN) were constructed by using PBJ1 vector. Then, a stable transgenic cell strain was established by introducing the gene constructs into the T cell strain, BEα16-3 (provided from National Jewish Center, Dr. Philppa Marrack), wherein the expression of DOCK 2 gene is deleted. N3-5 is a wild-type T cell strain expressing DOCK2, and 17-11 (Nature, 412, 826-831, 2001) and 84-3 are transgenic cell strains expressing full length DOCK2 and DOCK2ΔN, respectively, that the present inventors have established. In the Western Blot analysis using anti-DOCK2 polyclonal antibody that the present inventors have prepared, the expression of DOCK2 and DOCK2ΔN was approximately the same in 17-11 and 84-3 (FIG. 2A). Therefore, by targeting to 17-11 and 84-3, Rac activity in these cell strains was compared and analyzed by pull-down method using GST fusion protein of PAK1 Rac binding domain. In 17-11 expressing full length DOCK2, GTP-binding form of activated Rac was easily detected, whereas in 84-3 expressing DOCK2ΔN lacking the binding site with ELMO 1, Rac activating ability was significantly decreased (FIG. 2B). From the nuclear stain of 17-11 and 84-3 with PI (propidium iodide), it has been revealed that in any case, the nucleus is eccentrically located, in other words, that cell polarization is performed, which is different from BEα16-3, the parent cell strain (FIG. 2C; top). On the contrary, when these cells are stained with phalloidin, which is a probe for F-actin, actin polymerization was observed only for 17-11, and not in 84-3, as in the case of BEα16-3, wherein the DOCK2 expression is deleted (FIG. 2C; bottom). From these results, the association of DOCK2 and ELMO1 has been suggested to be extremely crucial to the full activation of Rac as well as to cytoskeletal reorganization, relating thereof. From the above, it has been clarified that in DOCK2ΔN, lacking N terminus domain being essential for the binding with ELMO1, the Rac-activating ability is significantly decreased, and that actin polymerization cannot be induced.

EXAMPLE 3

Association with ELMO1, via SH3 Domain of DOCK2

SH (Src-homology)3 domain known to be related with the protein-protein interaction is encoded at the N-terminus of DOCK2. As it was found that 502 amino acid residues at the N terminus of DOCK2 are crucial for the association with ELMO1, it was investigated if it is mediated by SH3 domain. Amino acid residues commonly conserved exist in the SH3 domain. Therefore, gene constructs encoding various DOCK2 SH3 mutants wherein HA tag is introduced into C terminus by using PcDNA/His max vector, were constructed. Then, these were introduced into 293T cells with PcDNA ELMO1-V5, and were analyzed in the same manner as in FIG. 1B. Genes encoding DOCK2 SH3 mutant are as follows: 1) PcDNA L27E-HA; gene encoding mutant wherein leucine at the 27 position of DOCK2 is substituted to glutamic acid

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- 2) PcDNA G32E-HA; gene encoding mutant wherein glycine at the 32 position of DOCK2 is substituted to glutamic acid
- 3) PcDNA P60E-HA; gene encoding mutant wherein poline at the 60 position of DOCK2 is substituted to glutamic acid
- 4) PcDNA F63E-HA; gene encoding mutant wherein phenylalanine at the 63 position of DOCK2 is substituted to glutamic acid

Amino acid sequence from 10-89 including DOCK2 SH3 domain is shown in FIG. 3A. For each of total cell lysate, an approximately 100-KD band corresponding to ELMO1 for anti-V5 antibody was detected (FIG. 3B; top). However, when targeting to immunoprecipitants using anti-HA antibody, the band corresponding to ELMO1 was not detected except for those introduced with PcDNA DOCK2-HA and PcDNA L27E-HA (FIG. 3B; middle). On the other hand, when any one of the genes has been introduced, DOCK2 and DOCK2 SH3 mutant expressions were almost of the same level (FIG. 3B; lower). The above results show that the association of DOCK2 and ELMO1 is completely inhibited by substituting a single amino acid of SH3 domain. Therefore, it has been clarified that DOCK2 is bound to ELMO1 via its SH3 domain.

EXAMPLE 4

Binding of C Terminus Domain of ELMO1 and DOCK2

Next, to identify the functional domain of ELMO1 binding with DOCK2, gene constructs encoding various ELMO1-deleted mutants were constructed by using PcDNA V5His vector, and were analyzed by introducing these into 293T cells with PcDNA DOCK2-HA. Genes herein used, encoding ELMO1-deleted mutants are as follows, which are shown schematically in FIG. 4A.

- 1) PcDNA ELMO1-del1-V5; gene encoding amino acid residues at the position 147-727 of ELMO1
- 2) PcDNA ELMO1-del8-V5; gene encoding amino acid residues at the position 345-727 of ELMO1
- 3) PcDNA ELMO1-del10-V5; gene encoding amino acid residues at the position 1-613 of ELMO1

For each of the total cell lysate, band corresponding to ELMO1 or its deleted mutant was detected with anti-V5 antibody (FIG. 4B; top). However, as for immunoprecipitants with anti-HA antibody, bands reacting to anti-V5 antibody were observed when genes encoding full length ELMO1, ELMO1-del1 and ELMO1-del8 were introduced, but not when PcDNA ELMO1-del10 lacking amino acid residues at the position 614-727 of ELMO1, was expressed (FIG. 4B; middle, bottom). From these, C terminus domain including amino acid residues at the position 614-727 of ELMO1 was revealed to be crucial for the association of DOCK2 SH3 domain. From these results, it has been clarified that ELMO1 was bound with DOCK2 in its C terminus domain.

EXAMPLE 5

Binding of N Terminus Domain of ELMO1 and Tiam1

Tiam 1 has been identified as a molecule that determines the invasion of thymoma cell lines, and is known to function as Rac-specific GDP/GTP exchange factor (GEF) (Cell 77, 537-549, 1994; Nature 375, 338-340, 1995). As the association of DOCK2 and ELMO1 is necessary for the full activation of Rac, it has been estimated that DOCK2 might recruit Tiam1 via ELMO1. To investigate this assumption, from a

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Tiam1 gene amplified by PCR method from cDNA derived from mouse organs, a construct encoding Tiam1 wherein HA tag was introduced at its C terminus (PCI Tiam1-HA) was constructed with the use of PCI vector (Promega), introduced into 293T cells with genes encoding full length or various ELMO1-deleted mutants (PcDNA ELMO1-V5, PcDNA ELMO1-delPH-V5, PcDNA ELMO1-del8-V5, PcDNA ELMO1-del1), and was then analyzed. PcDNA ELMO1-delPH-V5 is a gene encoding amino acid residues at the position 1-565 and 695-727 of ELMO1. ELMO1-deleted mutants herein used are shown schematically in FIG. 5A. For each of the total cell lysate, a band corresponding to ELMO1 or its deleted mutant was detected with anti-V5 antibody (FIG. 5B; top). In immunoprecipitants with anti-HA antibody, when PcDNA ELMO1-V5 and PcDNA ELMO1-delPH-V5 were introduced, bands reacting to anti-V5 antibody were detected (FIG. 5B; middle, bottom). This shows that Tiam1 binds with ELMO1. However, as for mutants lacking amino acid residues from N terminus to 146, or to 344, of ELMO1, such binding was not observed (FIG. 5B; middle, bottom). From these results, it has been revealed that ELMO1 is associated with Tiam1 at its N terminus.

From the above, the following has been revealed:

- 1) DOCK2 binds to the C terminus domain of ELMO1 via SH3 domain
- 2) ELMO1 binds with Tiam1 via its N terminus domain

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3) Rac-activating ability is significantly decreased in DOCK2 mutants that cannot bind with ELMO1.

Therefore, it has been shown that DOCK2 activates Rac by recruiting Tiam1 that functions as GEF of Rac, via ELMO1 (FIG. 6).

As autoimmune diseases and graft rejection are induced when lymphocytes invade into the target tissues, DOCK2 signaling should be the excellent target to treat or prevent these diseases or pathologic conditions. The finding of the invention shows that interaction between molecules such as DOCK2, ELMO1 and Tiam1 regulate Rac activation that is essential for cell mobility. Therefore, it can be thought that by blocking the intermolecular interaction, the invasion of lymphocytes can be inhibited. Therefore, these intermolecular interactions are anticipated to be the target of drug discovery heading to the development of method for treating or preventing autoimmune diseases or graft rejection.

INDUSTRIAL APPLICABILITY

According to the present invention, it is possible to elucidate the interaction between molecules of DOCK2, and to provide a substance controlling lymphocyte migration and a method to regulate lymphocyte migration targeting DOCK2. Moreover, according to the present invention, it is possible to provide preventive or therapeutic agents of autoimmune diseases or graft rejections after implantation.

SEQUENCE LISTING

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Asp Val Val Arg Ile Gln Glu Thr Cys Gly Asp Trp Tyr Arg Gly Tyr
 35           40           45
Leu Ile Lys His Lys Leu Ser Gln Gly Ile Phe Pro Thr Ser Phe Ile
 50           55           60
His Leu Lys Glu Val Thr Val Glu Lys Arg Arg Asn Ile Glu Asn Ile
 65           70           75           80
Ile Pro Ala Glu Ile Pro Leu Ala Gln Glu Val Thr Thr Thr Leu Trp
 85           90           95
Glu Trp Gly Ser Ile Trp Lys Gln Leu Tyr Val Ala Ser Lys Lys Glu
100          105          110
Arg Phe Leu Gln Val Gln Ser Met Met Tyr Asp Leu Met Glu Trp Arg
115          120          125
Ser Gln Leu Leu Ser Gly Thr Leu Pro Lys Asp Glu Leu Lys Glu Leu
130          135          140
Lys Gln Lys Val Thr Ser Lys Ile Asp Tyr Gly Asn Lys Ile Leu Glu
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Leu Asp Leu Ile Val Arg Asp Glu Asp Gly Asn Ile Leu Asp Pro Asp
165          170          175

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-continued

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Lys	Ile	Thr	Glu	Arg	Ile	Lys	Glu	Glu	Met	Ser	Lys	Asp	Gln	Pro	Asp
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Tyr	Leu	Val	Arg	Trp	Gly	Ser	Lys	Gly	Phe	Pro	Lys	Glu	Ile	Glu	Met
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Leu	Asn	Asn	Leu	Lys	Val	Val	Phe	Thr	Asp	Leu	Gly	Asn	Lys	Asp	Leu
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Arg	Pro	Phe	Gly	Val	Ala	Val	Met	Asp	Ile	Thr	Asp	Ile	Ile	Lys	Gly
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Lys	Ala	Glu	Ser	Asp	Glu	Glu	Lys	Gln	His	Phe	Ile	Pro	Phe	His	Pro
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Ala	Ser	Lys	Gly	Asp	Ser	Gly	Gly	Gln	Gly	Leu	Trp	Val	Thr	Met	Lys
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Ile	Met	Cys	Val	Cys	Thr	Glu	Asp	Gly	Lys	Val	Leu	Pro	Asn	Ala	Ile
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Tyr	Tyr	Gln	Val	Lys	Gln	Pro	Arg	Trp	Met	Glu	Thr	Val	Lys	Val	Ala
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			500					505					510		
His	Arg	Ser	Ser	Leu	Glu	Ser	Lys	Asp	Lys	Gly	Glu	Lys	Asn	Phe	Ala
		515					520					525			
Met	Ser	Tyr	Val	Lys	Leu	Met	Lys	Glu	Asp	Gly	Thr	Thr	Leu	His	Asp
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Gly	Tyr	His	Glu	Leu	Val	Val	Leu	Lys	Gly	Asp	Ser	Lys	Lys	Met	Glu
545					550					555					560
Asp	Ala	Ser	Ala	Tyr	Leu	Thr	Leu	Pro	Ser	Tyr	Arg	His	Pro	Val	Glu
			565						570					575	
Asn	Lys	Gly	Ala	Thr	Leu	Ser	Arg	Ser	Ser	Ser	Ser	Val	Gly	Gly	Leu
			580					585					590		
Ser	Val	Ser	Ser	Arg	Asp	Val	Phe	Ser	Ile	Ser	Thr	Leu	Val	Cys	Ser

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595					600					605					
Thr	Lys	Leu	Thr	Gln	Asn	Val	Gly	Leu	Leu	Gly	Leu	Leu	Lys	Trp	Arg
610						615					620				
Met	Lys	Pro	Gln	Leu	Leu	Gln	Glu	Asn	Leu	Glu	Lys	Leu	Lys	Ile	Val
625					630					635					640
Asp	Gly	Glu	Glu	Val	Val	Lys	Phe	Leu	Gln	Asp	Thr	Leu	Asp	Ala	Leu
				645					650					655	
Phe	Asn	Ile	Met	Met	Glu	His	Ser	Gln	Ser	Asn	Glu	Tyr	Asp	Ile	Leu
			660					665					670		
Val	Phe	Asp	Ala	Leu	Ile	Tyr	Ile	Ile	Gly	Leu	Ile	Ala	Asp	Arg	Lys
		675					680					685			
Phe	Gln	His	Phe	Asn	Thr	Val	Leu	Glu	Ala	Tyr	Ile	Gln	Gln	His	Phe
	690					695					700				
Ser	Ala	Thr	Leu	Ala	Tyr	Lys	Lys	Leu	Met	Thr	Val	Leu	Lys	Thr	Tyr
705					710					715					720
Leu	Asp	Thr	Ser	Ser	Arg	Gly	Glu	Gln	Cys	Glu	Pro	Ile	Leu	Arg	Thr
				725					730					735	
Leu	Lys	Ala	Leu	Glu	Tyr	Val	Phe	Lys	Phe	Ile	Val	Arg	Ser	Arg	Thr
		740						745					750		
Leu	Phe	Ser	Gln	Leu	Tyr	Glu	Gly	Lys	Glu	Gln	Met	Glu	Phe	Glu	Glu
		755					760					765			
Ser	Met	Arg	Arg	Leu	Phe	Glu	Ser	Ile	Asn	Asn	Leu	Met	Lys	Ser	Gln
	770					775					780				
Tyr	Lys	Thr	Thr	Ile	Leu	Leu	Gln	Val	Ala	Ala	Leu	Lys	Tyr	Ile	Pro
785				790					795						800
Ser	Val	Leu	His	Asp	Val	Glu	Thr	Val	Phe	Asp	Ala	Lys	Leu	Leu	Ser
			805						810					815	
Gln	Leu	Leu	Tyr	Glu	Phe	Tyr	Thr	Cys	Ile	Pro	Pro	Val	Lys	Leu	Gln
			820					825					830		
Lys	Gln	Lys	Val	Gln	Ser	Met	Asn	Glu	Ile	Val	Gln	Ser	Asn	Leu	Phe
		835					840					845			
Lys	Lys	Gln	Glu	Cys	Arg	Asp	Ile	Leu	Leu	Pro	Val	Ile	Thr	Lys	Glu
		850				855					860				
Leu	Lys	Glu	Leu	Leu	Glu	Gln	Arg	Asp	Asp	Gly	Gln	His	Gln	Ala	Glu
865					870					875					880
Lys	Lys	His	Cys	Val	Glu	Leu	Leu	Asn	Ser	Ile	Leu	Glu	Val	Leu	Ser
			885						890					895	
Cys	Gln	Asp	Ala	Ala	Phe	Thr	Tyr	Asp	His	Ile	Gln	Glu	Ile	Met	Val
			900					905					910		
Gln	Leu	Leu	Arg	Thr	Val	Asn	Arg	Thr	Val	Ile	Thr	Met	Gly	Arg	Asp
		915					920						925		
His	Ala	Leu	Ile	Ser	His	Phe	Glu	Ala	Cys	Met	Thr	Ala	Ile	Leu	Asp
	930					935					940				
Gln	Met	Gly	Asp	Gln	His	Tyr	Ser	Phe	Tyr	Ile	Glu	Thr	Phe	Gln	Thr
945					950					955					960
Ser	Ser	Asp	Leu	Val	Asp	Phe	Leu	Met	Glu	Thr	Phe	Ile	Met	Phe	Lys
			965						970					975	
Asp	Leu	Ile	Gly	Lys	Asn	Val	Tyr	Pro	Gly	Asp	Trp	Met	Ala	Met	Ser
			980					985					990		
Met	Val	Gln	Asn	Arg	Val	Phe	Leu	Arg	Ala	Ile	Asn	Lys	Phe	Ala	Glu
		995					1000					1005			
Thr	Met	Asn	Gln	Lys	Phe	Leu	Glu	His	Thr	Ser	Phe	Glu	Phe	Gln	Leu
1010						1015						1020			

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Trp Asn Asn Tyr Phe His Leu Ala Val Ala Phe Ile Thr Gln Asp Ser
 1025 1030 1035 1040
 Leu Gln Leu Glu Gln Phe Thr His Ala Lys Tyr Asn Lys Ile Leu Asn
 1045 1050 1055
 Lys Tyr Gly Asp Met Arg Arg Leu Ile Gly Phe Ser Ile Arg Asp Met
 1060 1065 1070
 Trp Tyr Lys Leu Gly Gln Asn Lys Ile Cys Phe Ile Pro Gly Met Val
 1075 1080 1085
 Gly Pro Ile Leu Glu Met Thr Leu Ile Pro Glu Ala Glu Leu Arg Lys
 1090 1095 1100
 Ala Thr Ile Pro Ile Phe Phe Asp Met Met Leu Cys Glu Tyr Gln Arg
 1105 1110 1115 1120
 Thr Gly Ala Phe Lys Lys Phe Glu Asn Glu Ile Ile Leu Lys Leu Asp
 1125 1130 1135
 His Glu Val Glu Gly Gly Arg Gly Asp Glu Gln Tyr Met Gln Leu Leu
 1140 1145 1150
 Glu Ser Ile Leu Met Glu Cys Thr Ala Glu His Pro Thr Ile Ala Lys
 1155 1160 1165
 Ser Val Glu Asn Phe Val Ser Leu Val Lys Gly Leu Leu Glu Lys Leu
 1170 1175 1180
 Leu Asp Tyr Arg Gly Val Met Thr Asp Glu Ser Lys Asp Asn Arg Met
 1185 1190 1195 1200
 Ser Cys Thr Val Asn Leu Leu Asn Phe Tyr Lys Asp Asn Asn Arg Glu
 1205 1210 1215
 Glu Met Tyr Ile Arg Tyr Leu Tyr Lys Leu Arg Asp Leu His Leu Asp
 1220 1225 1230
 Cys Glu Asn Tyr Thr Glu Ala Ala Tyr Thr Leu Leu Leu His Thr Trp
 1235 1240 1245
 Leu Leu Lys Trp Ser Asp Glu Gln Cys Ala Ser Gln Val Met Gln Thr
 1250 1255 1260
 Gly Gln Gln His Pro Gln Thr His Arg Gln Leu Lys Glu Thr Leu Tyr
 1265 1270 1275 1280
 Glu Thr Ile Ile Gly Tyr Phe Asp Lys Gly Lys Met Trp Glu Glu Ala
 1285 1290 1295
 Ile Ser Leu Cys Lys Glu Leu Ala Glu Gln Tyr Glu Met Glu Ile Phe
 1300 1305 1310
 Asp Tyr Glu Leu Leu Ser Gln Asn Leu Thr Gln Gln Ala Lys Phe Tyr
 1315 1320 1325
 Glu Asn Ile Met Lys Ile Leu Arg Thr Lys Pro Asp Tyr Phe Ala Val
 1330 1335 1340
 Gly Tyr Tyr Gly Gln Gly Phe Pro Ser Phe Leu Arg Asn Lys Val Phe
 1345 1350 1355 1360
 Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp Phe Gln Met Gln
 1365 1370 1375
 Leu Leu Ser Gln Phe Pro Asn Ala Glu Lys Met Asn Thr Thr Ser Ala
 1380 1385 1390
 Pro Gly Asp Asp Val Arg Asn Ala Pro Gly Gln Tyr Ile Gln Cys Phe
 1395 1400 1405
 Thr Val Gln Pro Val Leu Asp Glu His Pro Arg Phe Lys Asn Lys Pro
 1410 1415 1420
 Val Pro Asp Gln Ile Ile Asn Phe Tyr Lys Ser Asn Tyr Val Gln Lys
 1425 1430 1435 1440

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Phe His Tyr Ser Arg Pro Val Arg Arg Gly Lys Val Asp Pro Glu Asn
 1445 1450 1455
 Glu Phe Ala Ser Met Trp Ile Glu Arg Thr Ser Phe Leu Thr Ala Tyr
 1460 1465 1470
 Lys Leu Pro Gly Ile Leu Arg Trp Phe Glu Val Val His Met Ser Gln
 1475 1480 1485
 Thr Thr Ile Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr Val
 1490 1495 1500
 Asn Glu Lys Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu Ser
 1505 1510 1515 1520
 Leu Pro Ile Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro
 1525 1530 1535
 Ala Val Met Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu
 1540 1545 1550
 Glu Tyr Ser Arg Glu His Pro Glu Asp Gln Asp Lys Leu Ser His Leu
 1555 1560 1565
 Lys Asp Leu Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys
 1570 1575 1580
 Ile His Glu Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp Arg
 1585 1590 1595 1600
 Met Glu Glu Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu Tyr
 1605 1610 1615
 Gly Val Arg Glu Met Pro Asp Phe Glu Asp Arg Arg Val Gly Arg Pro
 1620 1625 1630
 Arg Ser Met Leu Arg Ser Tyr Arg Gln Met Ser Val Ile Ser Leu Ala
 1635 1640 1645
 Ser Met His Ser Asp Cys Ser Thr Pro Ser Lys Val Pro Ala Glu Ser
 1650 1655 1660
 Phe Asp Leu Glu Ser Ala Pro Pro Lys Thr Pro Lys Val Glu Glu Glu
 1665 1670 1675 1680
 Pro Ile Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg Arg Ser
 1685 1690 1695
 Lys Lys Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu Lys Ala
 1700 1705 1710
 Ala Thr Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys Gln Glu Phe Met
 1715 1720 1725
 Ser Asp Thr Asn Leu Ser Glu His Ala Ala Ile Pro Ala Arg Val Ser
 1730 1735 1740
 Ile Leu Ser Gln Met Ser Phe Ala Ser Gln Ser Met Pro Thr Ile Pro
 1745 1750 1755 1760
 Ala Leu Thr Leu Ser Val Ala Gly Val Pro Gly Leu Asp Glu Ala Asn
 1765 1770 1775
 Thr Ser Pro Arg Leu Ser Gln Thr Phe Phe Gln Val Ser Asp Gly Asp
 1780 1785 1790
 Lys Lys Thr Leu Lys Lys Lys Lys Val Asn Gln Phe Phe Lys Thr Met
 1795 1800 1805
 Leu Ala Ser Lys Ser Ser Glu Glu Ser Lys Gln Ile Pro Asp Phe Leu
 1810 1815 1820
 Ser Thr Asn Met
 1825

<210> SEQ ID NO 2
 <211> LENGTH: 1830
 <212> TYPE: PRT

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

Met Ala Pro Trp Arg Lys Ala Asp Lys Glu Arg His Gly Val Ala Ile
1 5 10 15
Tyr Asn Phe Gln Gly Ser Gly Ala Pro Gln Leu Ser Leu Gln Ile Gly
20 25 30
Asp Val Val Arg Ile Gln Glu Thr Cys Gly Asp Trp Tyr Arg Gly Tyr
35 40 45
Leu Ile Lys His Lys Met Leu Gln Gly Ile Phe Pro Lys Ser Phe Ile
50 55 60
His Ile Lys Glu Val Thr Val Glu Lys Arg Arg Asn Thr Glu Asn Ile
65 70 75 80
Ile Pro Ala Glu Ile Pro Leu Ala Gln Glu Val Thr Thr Thr Leu Trp
85 90 95
Glu Trp Gly Ser Ile Trp Lys Gln Leu Tyr Val Ala Ser Lys Lys Glu
100 105 110
Arg Phe Leu Gln Val Gln Ser Met Met Tyr Asp Leu Met Glu Trp Arg
115 120 125
Ser Gln Leu Leu Ser Gly Thr Leu Pro Lys Asp Glu Leu Lys Glu Leu
130 135 140
Lys Gln Lys Val Thr Ser Lys Ile Asp Tyr Gly Asn Lys Ile Leu Glu
145 150 155 160
Leu Asp Leu Ile Val Arg Asp Glu Asp Gly Asn Ile Leu Asp Pro Asp
165 170 175
Asn Thr Ser Val Ile Ser Leu Phe His Ala His Glu Glu Ala Thr Asp
180 185 190
Lys Ile Thr Glu Arg Ile Lys Glu Glu Met Ser Lys Asp Gln Pro Asp
195 200 205
Tyr Ala Met Tyr Ser Arg Ile Ser Ser Ser Pro Thr His Ser Leu Tyr
210 215 220
Val Phe Val Arg Asn Phe Val Cys Arg Ile Gly Glu Asp Ala Glu Leu
225 230 235 240
Phe Met Ser Leu Tyr Asp Pro Asn Lys Gln Thr Val Ile Ser Glu Asn
245 250 255
Tyr Leu Val Arg Trp Gly Ser Arg Gly Phe Pro Lys Glu Ile Glu Met
260 265 270
Leu Asn Asn Leu Lys Val Val Phe Thr Asp Leu Gly Asn Lys Asp Leu
275 280 285
Asn Arg Asp Lys Ile Tyr Leu Ile Cys Gln Ile Val Arg Val Gly Lys
290 295 300
Met Asp Leu Lys Asp Thr Gly Ala Lys Lys Cys Thr Gln Gly Leu Arg
305 310 315 320
Arg Pro Phe Gly Val Ala Val Met Asp Ile Thr Asp Ile Ile Lys Gly
325 330 335
Lys Ala Glu Ser Asp Glu Glu Lys Gln His Phe Ile Pro Phe His Pro
340 345 350
Val Thr Ala Glu Asn Asp Phe Leu His Ser Leu Leu Gly Lys Val Ile
355 360 365
Ala Ser Lys Gly Asp Ser Gly Gly Gln Gly Leu Trp Val Thr Met Lys
370 375 380
Met Leu Val Gly Asp Ile Ile Gln Ile Arg Lys Asp Tyr Pro His Leu
385 390 395 400

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Val	Asp	Arg	Thr	Thr	Val	Val	Ala	Arg	Lys	Leu	Gly	Phe	Pro	Glu	Ile
				405					410					415	
Ile	Met	Pro	Gly	Asp	Val	Arg	Asn	Asp	Ile	Tyr	Ile	Thr	Leu	Leu	Gln
			420					425					430		
Gly	Asp	Phe	Asp	Lys	Tyr	Asn	Lys	Thr	Thr	Gln	Arg	Asn	Val	Glu	Val
		435					440					445			
Ile	Met	Cys	Val	Cys	Ala	Glu	Asp	Gly	Lys	Thr	Leu	Pro	Asn	Ala	Ile
	450					455					460				
Cys	Val	Gly	Ala	Gly	Asp	Lys	Pro	Met	Asn	Glu	Tyr	Arg	Ser	Val	Val
465					470					475					480
Tyr	Tyr	Gln	Val	Lys	Gln	Pro	Arg	Trp	Met	Glu	Thr	Val	Lys	Val	Ala
				485					490					495	
Val	Pro	Ile	Glu	Asp	Met	Gln	Arg	Ile	His	Leu	Arg	Phe	Met	Phe	Arg
			500					505					510		
His	Arg	Ser	Ser	Leu	Glu	Ser	Lys	Asp	Lys	Gly	Glu	Lys	Asn	Phe	Ala
		515					520					525			
Met	Ser	Tyr	Val	Lys	Leu	Met	Lys	Glu	Asp	Gly	Thr	Thr	Leu	His	Asp
	530					535					540				
Gly	Phe	His	Asp	Leu	Val	Val	Leu	Lys	Gly	Asp	Ser	Lys	Lys	Met	Glu
545				550						555					560
Asp	Ala	Ser	Ala	Tyr	Leu	Thr	Leu	Pro	Ser	Tyr	Arg	His	His	Val	Glu
				565					570					575	
Asn	Lys	Gly	Ala	Thr	Leu	Ser	Arg	Ser	Ser	Ser	Ser	Val	Gly	Gly	Leu
			580					585					590		
Ser	Val	Ser	Ser	Arg	Asp	Val	Phe	Ser	Ile	Ser	Thr	Leu	Val	Cys	Ser
		595					600					605			
Thr	Lys	Leu	Thr	Gln	Asn	Val	Gly	Leu	Leu	Gly	Leu	Leu	Lys	Trp	Arg
	610					615					620				
Met	Lys	Pro	Gln	Leu	Leu	Gln	Glu	Asn	Leu	Glu	Lys	Leu	Lys	Ile	Val
625				630						635					640
Asp	Gly	Glu	Glu	Val	Val	Lys	Phe	Leu	Gln	Asp	Thr	Leu	Asp	Ala	Leu
				645					650					655	
Phe	Asn	Ile	Met	Met	Glu	His	Ser	Gln	Ser	Asp	Glu	Tyr	Asp	Ile	Leu
			660					665					670		
Val	Phe	Asp	Ala	Leu	Ile	Tyr	Ile	Ile	Gly	Leu	Ile	Ala	Asp	Arg	Lys
		675					680					685			
Phe	Gln	His	Phe	Asn	Thr	Val	Leu	Glu	Ala	Tyr	Ile	Gln	Gln	His	Phe
	690					695					700				
Ser	Ala	Thr	Leu	Ala	Tyr	Lys	Lys	Leu	Met	Thr	Val	Leu	Lys	Thr	Tyr
705					710					715					720
Leu	Asp	Thr	Ser	Ser	Arg	Gly	Glu	Gln	Cys	Glu	Pro	Ile	Leu	Arg	Thr
			725						730					735	
Leu	Lys	Ala	Leu	Glu	Tyr	Val	Phe	Lys	Phe	Ile	Val	Arg	Ser	Arg	Thr
			740					745					750		
Leu	Phe	Ser	Gln	Leu	Tyr	Glu	Gly	Lys	Glu	Gln	Met	Glu	Phe	Glu	Glu
		755					760					765			
Ser	Met	Arg	Arg	Leu	Phe	Glu	Ser	Ile	Asn	Asn	Leu	Met	Lys	Ser	Gln
	770					775					780				
Tyr	Lys	Thr	Thr	Ile	Leu	Leu	Gln	Val	Ala	Ala	Leu	Lys	Tyr	Ile	Pro
785					790					795					800
Ser	Val	Leu	His	Asp	Val	Glu	Met	Val	Phe	Asp	Ala	Lys	Leu	Leu	Ser
			805						810					815	
Gln	Leu	Leu	Tyr	Glu	Phe	Tyr	Thr	Cys	Ile	Pro	Pro	Val	Lys	Leu	Gln

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820					825					830					
Lys	Gln	Lys	Val	Gln	Ser	Met	Asn	Glu	Ile	Val	Gln	Ser	Asn	Leu	Phe
		835						840					845		
Lys	Lys	Gln	Glu	Cys	Arg	Asp	Ile	Leu	Leu	Pro	Val	Ile	Thr	Lys	Glu
	850					855					860				
Leu	Lys	Glu	Leu	Leu	Glu	Gln	Lys	Asp	Asp	Met	Gln	His	Gln	Val	Leu
865					870					875					880
Glu	Arg	Lys	Tyr	Cys	Val	Glu	Leu	Leu	Asn	Ser	Ile	Leu	Glu	Val	Leu
				885						890					895
Ser	Tyr	Gln	Asp	Ala	Ala	Phe	Thr	Tyr	His	His	Ile	Gln	Glu	Ile	Met
			900						905					910	
Val	Gln	Leu	Leu	Arg	Thr	Val	Asn	Arg	Thr	Val	Ile	Thr	Met	Gly	Arg
		915						920						925	
Asp	His	Ile	Leu	Ile	Ser	His	Phe	Val	Ala	Cys	Met	Thr	Ala	Ile	Leu
	930					935					940				
Asn	Gln	Met	Gly	Asp	Gln	His	Tyr	Ser	Phe	Tyr	Ile	Glu	Thr	Phe	Gln
945					950						955				960
Thr	Ser	Ser	Glu	Leu	Val	Asp	Phe	Leu	Met	Glu	Thr	Phe	Ile	Met	Phe
				965						970					975
Lys	Asp	Leu	Ile	Gly	Lys	Asn	Val	Tyr	Pro	Gly	Asp	Trp	Met	Ala	Met
			980						985					990	
Ser	Met	Val	Gln	Asn	Arg	Val	Phe	Leu	Arg	Ala	Ile	Asn	Lys	Phe	Ala
		995					1000							1005	
Glu	Thr	Met	Asn	Gln	Lys	Phe	Leu	Glu	His	Thr	Asn	Phe	Glu	Phe	Gln
	1010					1015					1020				
Leu	Trp	Asn	Asn	Tyr	Phe	His	Leu	Ala	Val	Ala	Phe	Ile	Thr	Gln	Asp
1025					1030					1035					1040
Ser	Leu	Gln	Leu	Glu	Gln	Phe	Ser	His	Ala	Lys	Tyr	Asn	Lys	Ile	Leu
				1045						1050					1055
Asn	Lys	Tyr	Gly	Asp	Met	Arg	Arg	Leu	Ile	Gly	Phe	Ser	Ile	Arg	Asp
			1060						1065					1070	
Met	Trp	Tyr	Lys	Leu	Gly	Gln	Asn	Lys	Ile	Cys	Phe	Ile	Pro	Gly	Met
		1075					1080							1085	
Val	Gly	Pro	Ile	Leu	Glu	Met	Thr	Leu	Ile	Pro	Glu	Ala	Glu	Leu	Arg
	1090					1095						1100			
Lys	Ala	Thr	Ile	Pro	Ile	Phe	Phe	Asp	Met	Met	Leu	Cys	Glu	Tyr	Gln
1105					1110					1115					1120
Arg	Ser	Gly	Asp	Phe	Lys	Lys	Phe	Glu	Asn	Glu	Ile	Ile	Leu	Lys	Leu
				1125						1130					1135
Asp	His	Glu	Val	Glu	Gly	Gly	Arg	Gly	Asp	Glu	Gln	Tyr	Met	Gln	Leu
			1140						1145					1150	
Leu	Glu	Ser	Ile	Leu	Met	Glu	Cys	Ala	Ala	Glu	His	Pro	Thr	Ile	Ala
		1155						1160						1165	
Lys	Ser	Val	Glu	Asn	Phe	Val	Asn	Leu	Val	Lys	Gly	Leu	Leu	Glu	Lys
		1170					1175					1180			
Leu	Leu	Asp	Tyr	Arg	Gly	Val	Met	Thr	Asp	Glu	Ser	Lys	Asp	Asn	Arg
1185					1190					1195					1200
Met	Ser	Cys	Thr	Val	Asn	Leu	Leu	Asn	Phe	Tyr	Lys	Asp	Asn	Asn	Arg
				1205						1210					1215
Glu	Glu	Met	Tyr	Ile	Arg	Tyr	Leu	Tyr	Lys	Leu	Arg	Asp	Leu	His	Leu
			1220						1225					1230	
Asp	Cys	Asp	Asn	Tyr	Thr	Glu	Ala	Ala	Tyr	Thr	Leu	Leu	Leu	His	Thr
		1235						1240						1245	

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Trp Leu Leu Lys Trp Ser Asp Glu Gln Cys Ala Ser Gln Val Met Gln
 1250 1255 1260

Thr Gly Gln Gln His Pro Gln Thr His Arg Gln Leu Lys Glu Thr Leu
 1265 1270 1275 1280

Tyr Glu Thr Ile Ile Gly Tyr Phe Asp Lys Gly Lys Met Trp Glu Glu
 1285 1290 1295

Ala Ile Ser Leu Cys Lys Glu Leu Ala Glu Gln Tyr Glu Met Glu Ile
 1300 1305 1310

Phe Asp Tyr Glu Leu Leu Ser Gln Asn Leu Ile Gln Gln Ala Lys Phe
 1315 1320 1325

Tyr Glu Ser Ile Met Lys Ile Leu Arg Pro Lys Pro Asp Tyr Phe Ala
 1330 1335 1340

Val Gly Tyr Tyr Gly Gln Gly Phe Pro Ser Phe Leu Arg Asn Lys Val
 1345 1350 1355 1360

Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp Phe Gln Met
 1365 1370 1375

Gln Leu Met Thr Gln Phe Pro Asn Ala Glu Lys Met Asn Thr Thr Ser
 1380 1385 1390

Ala Pro Gly Asp Asp Val Lys Asn Ala Pro Gly Gln Tyr Ile Gln Cys
 1395 1400 1405

Phe Thr Val Gln Pro Val Leu Asp Glu His Pro Arg Phe Lys Asn Lys
 1410 1415 1420

Pro Val Pro Asp Gln Ile Ile Asn Phe Tyr Lys Ser Asn Tyr Val Gln
 1425 1430 1435 1440

Arg Phe His Tyr Ser Arg Pro Val Arg Arg Gly Thr Val Asp Pro Glu
 1445 1450 1455

Asn Glu Phe Ala Ser Met Trp Ile Glu Arg Thr Ser Phe Val Thr Ala
 1460 1465 1470

Tyr Lys Leu Pro Gly Ile Leu Arg Trp Phe Glu Val Val His Met Ser
 1475 1480 1485

Gln Thr Thr Ile Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr
 1490 1495 1500

Ala Asn Glu Lys Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu
 1505 1510 1515 1520

Thr Leu Pro Ile Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp
 1525 1530 1535

Pro Ala Val Met Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr
 1540 1545 1550

Glu Glu Tyr Val Arg Asp His Pro Glu Asp Gln Asp Lys Leu Thr His
 1555 1560 1565

Leu Lys Asp Leu Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile
 1570 1575 1580

Lys Ile His Glu Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp
 1585 1590 1595 1600

Arg Met Glu Glu Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu
 1605 1610 1615

Tyr Gly Val Arg Glu Met Pro Asp Phe Asp Asp Arg Arg Val Gly Arg
 1620 1625 1630

Pro Arg Ser Met Leu Arg Ser Tyr Arg Gln Met Ser Ile Ile Ser Leu
 1635 1640 1645

Ala Ser Met Asn Ser Asp Cys Ser Thr Pro Ser Lys Pro Thr Ser Glu
 1650 1655 1660

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Ser Phe Asp Leu Glu Leu Ala Ser Pro Lys Thr Pro Arg Val Glu Gln
 1665 1670 1675 1680

Glu Glu Pro Ile Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg
 1685 1690 1695

Arg Ser Lys Lys Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu
 1700 1705 1710

Lys Ala Ala Ala Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys His Glu
 1715 1720 1725

Phe Met Ser Asp Thr Asn Leu Ser Glu His Ala Ala Ile Pro Leu Lys
 1730 1735 1740

Ala Ser Val Leu Ser Gln Met Ser Phe Ala Ser Gln Ser Met Pro Thr
 1745 1750 1755 1760

Ile Pro Ala Leu Ala Leu Ser Val Ala Gly Ile Pro Gly Leu Asp Glu
 1765 1770 1775

Ala Asn Thr Ser Pro Arg Leu Ser Gln Thr Phe Leu Gln Leu Ser Asp
 1780 1785 1790

Gly Asp Lys Lys Thr Leu Thr Arg Lys Lys Val Asn Gln Phe Phe Lys
 1795 1800 1805

Thr Met Leu Ala Ser Lys Ser Ala Glu Glu Gly Lys Gln Ile Pro Asp
 1810 1815 1820

Ser Leu Ser Thr Asp Leu
 1825 1830

<210> SEQ ID NO 3
 <211> LENGTH: 727
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 3

Met Pro Pro Pro Ser Asp Ile Val Lys Val Ala Ile Glu Trp Pro Gly
 1 5 10 15

Ala Tyr Pro Lys Leu Met Glu Ile Asp Gln Lys Lys Pro Leu Ser Ala
 20 25 30

Ile Ile Lys Glu Val Cys Asp Gly Trp Ser Leu Ala Asn His Glu Tyr
 35 40 45

Phe Ala Leu Gln His Ala Asp Ser Ser Asn Phe Tyr Ile Thr Glu Lys
 50 55 60

Asn Arg Asn Glu Ile Lys Asn Gly Thr Ile Leu Arg Leu Thr Thr Ser
 65 70 75 80

Pro Ala Gln Asn Ala Gln Gln Leu His Glu Arg Ile Gln Ser Ser Ser
 85 90 95

Met Asp Ala Lys Leu Glu Ala Leu Lys Asp Leu Ala Ser Leu Ser Arg
 100 105 110

Asp Val Thr Phe Ala Gln Glu Phe Ile Asn Leu Asp Gly Ile Ser Leu
 115 120 125

Leu Thr Gln Met Val Glu Ser Gly Thr Glu Arg Tyr Gln Lys Leu Gln
 130 135 140

Lys Ile Met Lys Pro Cys Phe Gly Asp Met Leu Ser Phe Thr Leu Thr
 145 150 155 160

Ala Phe Val Glu Leu Met Asp His Gly Ile Val Ser Trp Asp Thr Phe
 165 170 175

Ser Val Ala Phe Ile Lys Lys Ile Ala Ser Phe Val Asn Lys Ser Ala
 180 185 190

Ile Asp Ile Ser Ile Leu Gln Arg Ser Leu Ala Ile Leu Glu Ser Met
 195 200 205

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Val Leu Asn Ser His Asp Leu Tyr Gln Lys Val Ala Gln Glu Ile Thr
 210 215 220
 Ile Gly Gln Leu Ile Pro His Leu Gln Gly Thr Asp Gln Glu Ile Gln
 225 230 235 240
 Thr Tyr Thr Ile Ala Val Ile Asn Ala Leu Phe Leu Lys Ala Pro Asp
 245 250 255
 Glu Arg Arg Gln Glu Met Ala Asn Ile Leu Ala Gln Lys Gln Leu Arg
 260 265 270
 Tyr Ile Ile Leu Thr His Val Ile Arg Ala Gln Arg Ala Ile Asn Asn
 275 280 285
 Glu Met Ala His Gln Leu Tyr Val Leu Gln Val Leu Thr Phe Asn Leu
 290 295 300
 Leu Glu Asp Arg Met Met Thr Lys Met Asp Pro Gln Asp Gln Ala Gln
 305 310 315 320
 Arg Asp Ile Ile Phe Glu Leu Arg Arg Ile Ala Phe Asp Ala Glu Ser
 325 330 335
 Glu Pro Asn Asn Ser Ser Gly Ser Met Glu Lys Arg Lys Ser Met Tyr
 340 345 350
 Thr Arg Asp Tyr Lys Lys Leu Gly Phe Ile Asn His Val Asn Pro Ala
 355 360 365
 Met Asp Phe Thr Gln Thr Pro Pro Gly Met Leu Ala Leu Asp Asn Met
 370 375 380
 Leu Tyr Phe Ala Lys His His Gln Asp Ala Tyr Ile Arg Ile Val Leu
 385 390 395 400
 Glu Asn Ser Ser Arg Glu Asp Lys His Glu Cys Pro Phe Gly Arg Ser
 405 410 415
 Ser Ile Glu Leu Thr Lys Met Leu Cys Glu Ile Leu Lys Val Gly Glu
 420 425 430
 Leu Pro Ser Glu Thr Cys Asn Asp Phe His Pro Met Phe Phe Thr His
 435 440 445
 Asp Arg Ser Phe Glu Glu Phe Phe Cys Ile Cys Ile Gln Leu Leu Asn
 450 455 460
 Lys Thr Trp Lys Glu Met Arg Ala Thr Ser Glu Asp Phe Asn Lys Val
 465 470 475 480
 Met Gln Val Val Lys Glu Gln Val Met Arg Ala Leu Thr Thr Lys Pro
 485 490 495
 Ser Ser Leu Asp Gln Phe Lys Ser Lys Leu Gln Asn Leu Ser Tyr Thr
 500 505 510
 Glu Ile Leu Lys Ile Arg Gln Ser Glu Arg Met Asn Gln Glu Asp Phe
 515 520 525
 Gln Ser Arg Pro Ile Leu Glu Leu Lys Glu Lys Ile Gln Pro Glu Ile
 530 535 540
 Leu Glu Leu Ile Lys Gln Gln Arg Leu Asn Arg Leu Val Glu Gly Thr
 545 550 555 560
 Cys Phe Arg Lys Leu Asn Ala Arg Arg Arg Gln Asp Lys Phe Trp Tyr
 565 570 575
 Cys Arg Leu Ser Pro Asn His Lys Val Leu His Tyr Gly Asp Leu Glu
 580 585 590
 Glu Ser Pro Gln Gly Glu Val Pro His Asp Ser Leu Gln Asp Lys Leu
 595 600 605
 Pro Val Ala Asp Ile Lys Ala Val Val Thr Gly Lys Asp Cys Pro His
 610 615 620

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Met Lys Glu Lys Gly Ala Leu Lys Gln Asn Lys Glu Val Leu Glu Leu
625                630                635                640

Ala Phe Ser Ile Leu Tyr Asp Ser Asn Cys Gln Leu Asn Phe Ile Ala
        645                650                655

Pro Asp Lys His Glu Tyr Cys Ile Trp Thr Asp Gly Leu Asn Ala Leu
        660                665                670

Leu Gly Lys Asp Met Met Ser Asp Leu Thr Arg Asn Asp Leu Asp Thr
        675                680                685

Leu Leu Ser Met Glu Ile Lys Leu Arg Leu Leu Asp Leu Glu Asn Ile
        690                695                700

Gln Ile Pro Asp Ala Pro Pro Pro Ile Pro Lys Glu Pro Ser Asn Tyr
705                710                715                720

Asp Phe Val Tyr Asp Cys Asn
        725

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<210> SEQ ID NO 4

<211> LENGTH: 727

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

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Met Pro Pro Pro Ala Asp Ile Val Lys Val Ala Ile Glu Trp Pro Gly
  1                5                10                15

Ala Tyr Pro Lys Leu Met Glu Ile Asp Gln Lys Lys Pro Leu Ser Ala
        20                25                30

Ile Ile Lys Glu Val Cys Asp Gly Trp Ser Leu Ala Asn His Glu Tyr
        35                40                45

Phe Ala Leu Gln His Ala Asp Ser Ser Asn Phe Tyr Ile Thr Glu Lys
        50                55                60

Asn Arg Asn Glu Ile Lys Asn Gly Thr Ile Leu Arg Leu Thr Thr Ser
        65                70                75                80

Pro Ala Gln Asn Ala Gln Gln Leu His Glu Arg Ile Gln Ser Ser Ser
        85                90                95

Met Asp Ala Lys Leu Glu Ala Leu Lys Asp Leu Ala Ser Leu Ser Arg
        100                105                110

Asp Val Thr Phe Ala Gln Glu Phe Ile Asn Leu Asp Gly Ile Ser Leu
        115                120                125

Leu Thr Gln Met Val Glu Ser Gly Thr Glu Arg Tyr Gln Lys Leu Gln
        130                135                140

Lys Ile Met Lys Pro Cys Phe Gly Asp Met Leu Ser Phe Thr Leu Thr
        145                150                155                160

Ala Phe Val Glu Leu Met Asp His Gly Ile Val Ser Trp Asp Thr Phe
        165                170                175

Ser Val Ala Phe Ile Lys Lys Ile Ala Ser Phe Val Asn Lys Ser Ala
        180                185                190

Ile Asp Ile Ser Ile Leu Gln Arg Ser Leu Ala Ile Leu Glu Ser Met
        195                200                205

Val Leu Asn Ser His Asp Leu Tyr Gln Lys Val Ala Gln Glu Ile Thr
        210                215                220

Ile Gly Gln Leu Ile Pro His Leu Gln Gly Ser Asp Gln Glu Ile Gln
        225                230                235                240

Thr Tyr Thr Ile Ala Val Ile Asn Ala Leu Phe Leu Lys Ala Pro Asp
        245                250                255

Glu Arg Arg Gln Glu Met Ala Asn Ile Leu Ala Gln Lys Gln Leu Arg
        260                265                270

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Ser Ile Ile Leu Thr His Val Ile Arg Ala Gln Arg Ala Ile Asn Asn
 275 280 285

Glu Met Ala His Gln Leu Tyr Val Leu Gln Val Leu Thr Phe Asn Leu
 290 295 300

Leu Glu Asp Arg Met Met Thr Lys Met Asp Pro Gln Asp Gln Ala Gln
 305 310 315 320

Arg Asp Ile Ile Phe Glu Leu Arg Arg Ile Ala Phe Asp Ala Glu Ser
 325 330 335

Glu Pro Asn Asn Ser Ser Gly Ser Met Glu Lys Arg Lys Ser Met Tyr
 340 345 350

Thr Arg Asp Tyr Lys Lys Leu Gly Phe Ile Asn His Val Asn Pro Ala
 355 360 365

Met Asp Phe Thr Gln Thr Pro Pro Gly Met Leu Ala Leu Asp Asn Met
 370 375 380

Leu Tyr Phe Ala Lys His His Gln Asp Ala Tyr Ile Arg Ile Val Leu
 385 390 395 400

Glu Asn Ser Ser Arg Glu Asp Lys His Glu Cys Pro Phe Gly Arg Ser
 405 410 415

Ser Ile Glu Leu Thr Lys Met Leu Cys Glu Ile Leu Lys Val Gly Glu
 420 425 430

Leu Pro Ser Glu Thr Cys Asn Asp Phe His Pro Met Phe Phe Thr His
 435 440 445

Asp Arg Ser Phe Glu Glu Phe Phe Cys Ile Cys Ile Gln Leu Leu Asn
 450 455 460

Lys Thr Trp Lys Glu Met Arg Ala Thr Ser Glu Asp Phe Asn Lys Val
 465 470 475 480

Met Gln Val Val Lys Glu Gln Val Met Arg Ala Leu Thr Thr Lys Pro
 485 490 495

Ser Ser Leu Asp Gln Phe Lys Ser Lys Leu Gln Asn Leu Ser Tyr Thr
 500 505 510

Glu Ile Leu Lys Ile Arg Gln Ser Glu Arg Met Asn Gln Glu Asp Phe
 515 520 525

Gln Ser Arg Pro Ile Leu Glu Leu Lys Glu Lys Ile Gln Pro Glu Ile
 530 535 540

Leu Glu Leu Ile Lys Gln Gln Arg Leu Asn Arg Leu Val Glu Gly Thr
 545 550 555 560

Cys Phe Arg Lys Leu Asn Ala Arg Arg Arg Gln Asp Lys Phe Trp Tyr
 565 570 575

Cys Arg Leu Ser Pro Asn His Lys Val Leu His Tyr Gly Asp Leu Glu
 580 585 590

Glu Ser Pro Gln Gly Glu Val Pro His Asp Ser Leu Gln Asp Lys Leu
 595 600 605

Pro Val Ala Asp Ile Lys Ala Val Val Thr Gly Lys Asp Cys Pro His
 610 615 620

Met Lys Glu Lys Gly Ala Leu Lys Gln Asn Lys Glu Val Leu Glu Leu
 625 630 635 640

Ala Phe Ser Ile Leu Tyr Asp Ser Asn Cys Gln Leu Asn Phe Ile Ala
 645 650 655

Pro Asp Lys His Glu Tyr Cys Ile Trp Thr Asp Gly Leu Asn Ala Leu
 660 665 670

Leu Gly Lys Asp Met Met Ser Asp Leu Thr Arg Asn Asp Leu Asp Thr
 675 680 685

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Leu Leu Ser Met Glu Ile Lys Leu Arg Leu Leu Asp Leu Glu Asn Ile
 690 695 700

Gln Ile Pro Asp Ala Pro Pro Pro Ile Pro Lys Glu Pro Ser Asn Tyr
 705 710 715 720

Asp Phe Val Tyr Asp Cys Asn
 725

<210> SEQ ID NO 5
 <211> LENGTH: 1591
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 5

Met Gly Asn Ala Glu Ser Gln Asn Val Asp His Glu Phe Tyr Gly Glu
 1 5 10 15

Lys His Ala Ser Leu Gly Arg Lys His Thr Ser Arg Ser Leu Arg Leu
 20 25 30

Ser His Lys Thr Arg Arg Thr Arg His Ala Ser Ser Gly Lys Ala Ile
 35 40 45

His Arg Asn Ser Glu Val Ser Thr Arg Ser Ser Ser Thr Pro Ser Ile
 50 55 60

Pro Gln Ser Leu Ala Glu Asn Gly Leu Glu Pro Phe Ser Gln Glu Gly
 65 70 75 80

Ala Leu Asp Asp Phe Gly Asp Pro Ile Trp Val Asp Arg Val Asp Met
 85 90 95

Gly Leu Arg Pro Val Ser Tyr Thr Asp Ser Ser Val Thr Pro Ser Val
 100 105 110

Asp Gly Ser Ile Val Leu Thr Ala Ala Ser Val Gln Ser Met Pro Asp
 115 120 125

Ser Glu Glu Ser Arg Leu Tyr Gly Asp Asp Ala Thr Tyr Leu Ala Glu
 130 135 140

Gly Gly Arg Arg Gln Cys Pro Tyr Thr Ser Asn Gly Pro Thr Phe Met
 145 150 155 160

Glu Thr Ala Ser Phe Lys Lys Lys Arg Ser Lys Ser Ala Asp Ile Trp
 165 170 175

Arg Glu Asp Ser Leu Glu Phe Ser Leu Ser Asp Leu Ser Gln Glu His
 180 185 190

Leu Thr Ser Asn Glu Glu Ile Leu Gly Ser Ala Glu Glu Lys Asp Cys
 195 200 205

Glu Glu Ala Arg Gly Met Glu Thr Glu Ala Ser Pro Arg Gln Leu Ser
 210 215 220

Thr Cys Gln Arg Ala Asn Ser Leu Gly Asp Leu Tyr Ala Gln Lys Asn
 225 230 235 240

Ser Gly Val Lys Ala Asn Gly Gly Pro Arg Asn Arg Phe Ser Ser Tyr
 245 250 255

Cys Arg Asn Leu Val Ser Asp Ile Pro Asp Leu Ala Lys His Lys Met
 260 265 270

Pro Pro Ala Ala Ala Glu Glu Thr Pro Pro Tyr Ser Asn Tyr Asn Thr
 275 280 285

Leu Pro Cys Arg Lys Ser His Cys Leu Ser Glu Gly Ala Thr Asn Pro
 290 295 300

Gln Ile Ser Leu Ser Lys Ser Met Gln Gly Arg Arg Ala Lys Thr Thr
 305 310 315 320

Gln Asp Val Asn Thr Gly Glu Gly Ser Glu Phe Ala Asp Ser Gly Ile
 325 330 335

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Glu Gly Ala Thr Thr Asp Thr Asp Leu Leu Ser Arg Arg Ser Asn Ala
 340 345 350
 Thr Asn Ser Ser Tyr Ser Pro Pro Thr Gly Arg Ala Phe Val Gly Ser
 355 360 365
 Asp Ser Gly Ser Ser Ser Thr Gly Asp Arg Ala Arg Gln Gly Val Tyr
 370 375 380
 Glu Asn Phe Arg Arg Glu Leu Glu Met Ser Thr Thr Asn Ser Glu Ser
 385 390 395
 Leu Glu Glu Ala Gly Ser Ala His Ser Asp Glu Gln Ser Ser Gly Thr
 405 410 415
 Leu Ser Ser Pro Gly Gln Ser Asp Ile Leu Leu Thr Ala Ala Gln Gly
 420 425 430
 Thr Val Arg Lys Ala Gly Ala Leu Ala Val Lys Asn Phe Leu Val His
 435 440 445
 Lys Lys Asn Lys Lys Val Glu Ser Ala Thr Arg Arg Lys Trp Lys His
 450 455 460
 Tyr Trp Val Ser Leu Lys Gly Cys Thr Leu Phe Phe Tyr Glu Thr Asp
 465 470 475 480
 Gly Arg Ser Gly Ile Asp His Asn Ser Val Pro Lys His Ala Val Trp
 485 490 495
 Val Glu Asn Ser Ile Val Gln Ala Val Pro Glu His Pro Lys Lys Asp
 500 505 510
 Phe Val Phe Cys Leu Ser Asn Ser Leu Gly Asp Ala Phe Leu Phe Gln
 515 520 525
 Thr Thr Ser Gln Thr Glu Leu Glu Asn Trp Ile Thr Ala Ile His Ser
 530 535 540
 Ala Cys Ala Ala Ala Val Ala Arg His His His Lys Glu Asp Thr Leu
 545 550 555 560
 Arg Leu Leu Lys Ser Glu Ile Lys Lys Leu Glu Gln Lys Ile Asp Met
 565 570 575
 Asp Glu Lys Met Lys Lys Met Gly Glu Met Gln Leu Ser Ser Val Thr
 580 585 590
 Asp Ser Lys Lys Lys Lys Thr Ile Leu Asp Gln Ile Phe Val Trp Glu
 595 600 605
 Gln Asn Leu Glu Gln Phe Gln Met Asp Leu Phe Arg Phe Arg Cys Tyr
 610 615 620
 Leu Ala Ser Leu Gln Gly Gly Glu Leu Pro Asn Pro Lys Arg Leu Leu
 625 630 635 640
 Ala Phe Ala Ser Arg Pro Thr Lys Val Ala Met Gly Arg Leu Gly Ile
 645 650 655
 Phe Ser Val Ser Ser Phe His Ala Leu Val Ala Ala Arg Thr Gly Glu
 660 665 670
 Ile Gly Val Arg Arg Arg Thr Gln Ala Met Ser Arg Ser Ala Ser Lys
 675 680 685
 Arg Arg Ser Arg Phe Ser Ser Leu Trp Gly Leu Asp Thr Thr Ser Lys
 690 695 700
 Lys Lys Gln Gly Arg Pro Thr Ile Asn Gln Val Phe Gly Glu Gly Thr
 705 710 715 720
 Asp Ala Val Lys Arg Ser Leu Glu Gly Ile Phe Asp Asp Thr Val Pro
 725 730 735
 Asp Gly Lys Arg Glu Lys Glu Val Val Leu Pro Ser Val His Gln His
 740 745 750

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Asn	Pro	Asp	Cys	Asp	Ile	Trp	Val	His	Glu	Tyr	Phe	Thr	Pro	Ser	Trp
		755					760					765			
Phe	Cys	Leu	Pro	Asn	Asn	Gln	Pro	Ala	Leu	Thr	Val	Val	Arg	Pro	Gly
	770					775					780				
Asp	Thr	Ala	Arg	Asp	Thr	Leu	Glu	Leu	Ile	Cys	Lys	Thr	His	Gln	Leu
785					790					795					800
Asp	His	Ser	Ala	His	Tyr	Leu	Arg	Leu	Lys	Phe	Leu	Met	Glu	Asn	Arg
				805					810						815
Val	Gln	Phe	Tyr	Ile	Pro	Gln	Pro	Glu	Glu	Asp	Ile	Tyr	Glu	Leu	Leu
			820					825					830		
Tyr	Lys	Glu	Ile	Glu	Ile	Cys	Pro	Lys	Val	Thr	Gln	Asn	Ile	His	Ile
		835					840					845			
Glu	Lys	Ser	Asp	Ala	Ala	Ala	Asp	Asn	Tyr	Gly	Phe	Leu	Leu	Ser	Ser
	850					855					860				
Val	Asp	Glu	Asp	Gly	Ile	Arg	Arg	Leu	Tyr	Val	Asn	Ser	Val	Lys	Glu
865					870					875					880
Thr	Gly	Leu	Ala	Ser	Lys	Lys	Gly	Leu	Lys	Ala	Gly	Asp	Glu	Ile	Leu
				885					890						895
Glu	Ile	Asn	Asn	Arg	Ala	Ala	Gly	Thr	Leu	Asn	Ser	Ser	Met	Leu	Lys
			900					905						910	
Asp	Phe	Leu	Ser	Gln	Pro	Ser	Leu	Gly	Leu	Leu	Val	Arg	Thr	Tyr	Pro
		915					920						925		
Glu	Pro	Glu	Gly	Gly	Val	Glu	Leu	Leu	Glu	Asn	Pro	Pro	His	Arg	Val
	930					935					940				
Asp	Gly	Pro	Val	Asp	Leu	Gly	Glu	Ser	Pro	Leu	Ala	Phe	Leu	Thr	Ser
945					950					955					960
Asn	Pro	Gly	His	Ser	Leu	Ser	Ser	Glu	Gln	Gly	Ser	Ser	Ala	Glu	Thr
				965					970						975
Ala	Pro	Glu	Glu	Gly	Glu	Gly	Pro	Asp	Leu	Glu	Ser	Ser	Asp	Glu	Thr
			980					985						990	
Asp	His	Ser	Ser	Lys	Ser	Thr	Glu	Gln	Val	Ala	Ala	Phe	Cys	Arg	Ser
		995					1000						1005		
Leu	His	Glu	Met	Ser	Pro	Ser	Asp	Ser	Ser	Pro	Ser	Pro	Gln	Asp	Ala
	1010					1015					1020				
Thr	Ser	Pro	Gln	Leu	Ala	Thr	Thr	Arg	Gln	Leu	Ser	Asp	Ala	Asp	Lys
1025				1030						1035					1040
Leu	Arg	Lys	Val	Ile	Cys	Glu	Leu	Leu	Glu	Thr	Glu	Arg	Thr	Tyr	Val
				1045						1050					1055
Lys	Asp	Leu	Asn	Cys	Leu	Met	Glu	Arg	Tyr	Leu	Lys	Pro	Leu	Gln	Lys
		1060						1065					1070		
Glu	Thr	Phe	Leu	Thr	Gln	Asp	Glu	Leu	Asp	Val	Leu	Phe	Gly	Asn	Leu
	1075						1080						1085		
Thr	Glu	Met	Val	Glu	Phe	Gln	Val	Glu	Phe	Leu	Lys	Thr	Leu	Glu	Asp
	1090					1095						1100			
Gly	Val	Arg	Leu	Val	Pro	Asp	Leu	Glu	Lys	Leu	Glu	Lys	Val	Asp	Gln
1105					1110					1115					1120
Phe	Lys	Lys	Val	Leu	Phe	Ser	Leu	Gly	Gly	Ser	Phe	Leu	Tyr	Tyr	Ala
				1125						1130					1135
Asp	Arg	Phe	Lys	Leu	Tyr	Ser	Ala	Phe	Cys	Ala	Ser	His	Thr	Lys	Val
			1140					1145					1150		
Pro	Lys	Val	Leu	Val	Lys	Ala	Lys	Thr	Asp	Thr	Ala	Phe	Lys	Ala	Phe
	1155						1160						1165		
Leu	Asp	Ala	Gln	Asn	Pro	Arg	Gln	Gln	His	Ser	Ser	Thr	Leu	Glu	Ser

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1170	1175	1180
Tyr Leu Ile Lys Pro Ile Gln Arg Val Leu Lys Tyr Pro Leu Leu Leu 1185 1190 1195 1200		
Arg Glu Leu Phe Ala Leu Thr Asp Ala Glu Ser Glu Glu His Tyr His 1205 1210 1215		
Leu Asp Val Ala Ile Lys Thr Met Asn Lys Val Ala Ser His Ile Asn 1220 1225 1230		
Glu Met Gln Lys Ile His Glu Glu Phe Gly Ala Val Phe Asp Gln Leu 1235 1240 1245		
Ile Ala Glu Gln Thr Gly Glu Lys Lys Glu Val Ala Asp Leu Ser Met 1250 1255 1260		
Gly Asp Leu Leu Leu His Thr Ser Val Ile Trp Leu Asn Pro Pro Ala 1265 1270 1275 1280		
Ser Leu Gly Lys Trp Lys Lys Glu Pro Glu Leu Ala Ala Phe Val Phe 1285 1290 1295		
Lys Thr Ala Val Val Leu Val Tyr Lys Asp Gly Ser Lys Gln Lys Lys 1300 1305 1310		
Lys Leu Val Gly Ser His Arg Leu Ser Ile Tyr Glu Glu Trp Asp Pro 1315 1320 1325		
Phe Arg Phe Arg His Met Ile Pro Thr Glu Ala Leu Gln Val Arg Ala 1330 1335 1340		
Leu Pro Ser Ala Asp Ala Glu Ala Asn Ala Val Cys Glu Ile Val His 1345 1350 1355 1360		
Val Lys Ser Glu Ser Glu Gly Arg Pro Glu Arg Val Phe His Leu Cys 1365 1370 1375		
Cys Ser Ser Pro Glu Ser Arg Lys Asp Phe Leu Lys Ser Val His Ser 1380 1385 1390		
Ile Leu Arg Asp Lys His Arg Arg Gln Leu Leu Lys Thr Glu Ser Leu 1395 1400 1405		
Pro Ser Ala Gln Gln Tyr Val Pro Phe Gly Gly Lys Arg Leu Cys Ala 1410 1415 1420		
Leu Lys Gly Ala Arg Pro Ala Met Ser Arg Ala Val Ser Ala Pro Ser 1425 1430 1435 1440		
Lys Ser Leu Gly Arg Arg Arg Arg Arg Leu Ala Arg Asn Arg Phe Thr 1445 1450 1455		
Ile Asp Ser Asp Ala Ile Ser Ala Ser Ser Pro Glu Lys Glu Pro Gln 1460 1465 1470		
Gln Pro Ala Gly Gly Gly Asp Thr Asp Arg Trp Val Glu Glu Gln Phe 1475 1480 1485		
Asp Leu Ala Gln Tyr Glu Glu Gln Asp Asp Ile Lys Glu Thr Asp Ile 1490 1495 1500		
Leu Ser Asp Asp Asp Glu Phe Cys Glu Ser Leu Lys Gly Ala Ser Val 1505 1510 1515 1520		
Asp Arg Asp Leu Gln Glu Gln Leu Gln Ala Ala Ser Ile Ser Gln Arg 1525 1530 1535		
Ala Arg Gly Arg Arg Thr Leu Asp Ser His Ala Ser Arg Met Thr Gln 1540 1545 1550		
Leu Lys Lys Gln Ala Ala Leu Ser Gly Ile Asn Gly Gly Leu Glu Ser 1555 1560 1565		
Ala Ser Glu Glu Val Ile Trp Val Arg Arg Glu Asp Phe Ala Pro Ser 1570 1575 1580		
Arg Lys Leu Asn Thr Glu Ile 1585 1590		

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<210> SEQ ID NO 6
<211> LENGTH: 1591
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6
Met Gly Asn Ala Glu Ser Gln His Val Glu His Glu Phe Tyr Gly Glu
  1          5          10          15
Lys His Ala Ser Leu Gly Arg Asn Asp Thr Ser Arg Ser Leu Arg Leu
  20          25          30
Ser His Lys Thr Arg Arg Thr Arg His Ala Ser Ser Gly Lys Val Ile
  35          40          45
His Arg Asn Ser Glu Val Ser Thr Arg Ser Ser Ser Thr Pro Ser Ile
  50          55          60
Pro Gln Ser Leu Ala Glu Asn Gly Leu Glu Pro Phe Ser Gln Asp Gly
  65          70          75          80
Thr Leu Glu Asp Phe Gly Ser Pro Ile Trp Val Asp Arg Val Asp Met
  85          90          95
Gly Leu Arg Pro Val Ser Tyr Thr Asp Ser Ser Val Thr Pro Ser Val
  100         105         110
Asp Ser Ser Ile Val Leu Thr Ala Ala Ser Val Gln Ser Met Pro Asp
  115         120         125
Thr Glu Glu Ser Arg Leu Tyr Gly Asp Asp Ala Thr Tyr Leu Ala Glu
  130         135         140
Gly Gly Arg Arg Gln His Ser Tyr Thr Ser Asn Gly Pro Thr Phe Met
  145         150         155         160
Glu Thr Ala Ser Phe Lys Lys Lys Arg Ser Lys Ser Ala Asp Ile Trp
  165         170         175
Arg Glu Asp Ser Leu Glu Phe Ser Leu Ser Asp Leu Ser Gln Glu His
  180         185         190
Leu Thr Ser Asn Glu Glu Ile Leu Gly Ser Ala Glu Glu Lys Asp Cys
  195         200         205
Glu Glu Ala Arg Gly Met Glu Thr Arg Ala Ser Pro Arg Gln Leu Ser
  210         215         220
Thr Cys Gln Arg Ala Asn Ser Leu Gly Asp Leu Tyr Ala Gln Lys Asn
  225         230         235         240
Ser Gly Val Thr Ala Asn Met Gly Pro Gly Ser Lys Phe Ala Gly Tyr
  245         250         255
Cys Arg Asn Leu Val Ser Asp Ile Pro Asn Leu Ala Asn His Lys Met
  260         265         270
Pro Pro Ala Ala Ala Glu Glu Thr Pro Pro Tyr Ser Asn Tyr Asn Thr
  275         280         285
Leu Pro Cys Arg Lys Ser His Cys Leu Ser Glu Gly Ala Thr Asn Pro
  290         295         300
Gln Ile Ser His Ser Asn Ser Met Gln Gly Arg Arg Ala Lys Thr Thr
  305         310         315         320
Gln Asp Val Asn Ala Gly Glu Gly Ser Glu Phe Ala Asp Ser Gly Ile
  325         330         335
Glu Gly Ala Thr Thr Asp Thr Asp Leu Leu Ser Arg Arg Ser Asn Ala
  340         345         350
Thr Asn Ser Ser Tyr Ser Pro Thr Thr Gly Arg Ala Phe Val Gly Ser
  355         360         365
Asp Ser Gly Ser Ser Ser Thr Gly Asp Ala Ala Arg Gln Gly Val Tyr

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370					375					380					
Glu	Asn	Phe	Arg	Arg	Glu	Leu	Glu	Met	Ser	Thr	Thr	Asn	Ser	Glu	Ser
385					390						395				400
Leu	Glu	Glu	Ala	Gly	Ser	Ala	His	Ser	Asp	Glu	Gln	Ser	Ser	Gly	Thr
				405					410					415	
Leu	Ser	Ser	Pro	Gly	Gln	Ser	Asp	Ile	Leu	Leu	Thr	Ala	Ala	Gln	Gly
			420					425						430	
Thr	Val	Arg	Lys	Ala	Gly	Ala	Leu	Ala	Val	Lys	Asn	Phe	Leu	Val	His
		435					440					445			
Lys	Lys	Asn	Lys	Lys	Val	Glu	Ser	Ala	Thr	Arg	Arg	Lys	Trp	Lys	His
	450					455					460				
Tyr	Trp	Val	Ser	Leu	Lys	Gly	Cys	Thr	Leu	Phe	Phe	Tyr	Glu	Ser	Asp
465					470					475					480
Gly	Arg	Ser	Gly	Ile	Asp	His	Asn	Ser	Ile	Pro	Lys	His	Ala	Val	Trp
				485					490						495
Val	Glu	Asn	Ser	Ile	Val	Gln	Ala	Val	Pro	Glu	His	Pro	Lys	Lys	Asp
			500					505					510		
Phe	Val	Phe	Cys	Leu	Ser	Asn	Ser	Leu	Gly	Asp	Ala	Phe	Leu	Phe	Gln
		515						520				525			
Thr	Thr	Ser	Gln	Thr	Glu	Leu	Glu	Asn	Trp	Ile	Thr	Ala	Ile	His	Ser
	530					535					540				
Ala	Cys	Ala	Thr	Ala	Val	Ala	Arg	His	His	His	Lys	Glu	Asp	Thr	Leu
545					550					555					560
Arg	Leu	Leu	Lys	Ser	Glu	Ile	Lys	Lys	Leu	Glu	Gln	Lys	Ile	Asp	Met
				565					570						575
Asp	Glu	Lys	Met	Lys	Lys	Met	Gly	Glu	Met	Gln	Leu	Ser	Ser	Val	Thr
			580					585						590	
Asp	Ser	Lys	Lys	Lys	Lys	Thr	Ile	Leu	Asp	Gln	Ile	Phe	Val	Trp	Glu
		595					600					605			
Gln	Asn	Leu	Glu	Gln	Phe	Gln	Met	Asp	Leu	Phe	Arg	Phe	Arg	Cys	Tyr
	610					615					620				
Leu	Ala	Ser	Leu	Gln	Gly	Gly	Glu	Leu	Pro	Asn	Pro	Lys	Arg	Leu	Leu
625					630					635					640
Ala	Phe	Ala	Ser	Arg	Pro	Thr	Lys	Val	Ala	Met	Gly	Arg	Leu	Gly	Ile
				645					650						655
Phe	Ser	Val	Ser	Ser	Phe	His	Ala	Leu	Val	Ala	Ala	Arg	Thr	Gly	Glu
			660					665					670		
Thr	Gly	Val	Arg	Arg	Arg	Thr	Gln	Ala	Met	Ser	Arg	Ser	Ala	Ser	Lys
		675					680						685		
Arg	Arg	Ser	Arg	Phe	Ser	Ser	Leu	Trp	Gly	Leu	Asp	Thr	Thr	Ser	Lys
	690					695					700				
Lys	Lys	Gln	Gly	Arg	Pro	Ser	Ile	Asn	Gln	Val	Phe	Gly	Glu	Gly	Thr
705					710					715					720
Glu	Ala	Val	Lys	Lys	Ser	Leu	Glu	Gly	Ile	Phe	Asp	Asp	Ile	Val	Pro
				725					730					735	
Asp	Gly	Lys	Arg	Glu	Lys	Glu	Val	Val	Leu	Pro	Asn	Val	His	Gln	His
			740					745					750		
Asn	Pro	Asp	Cys	Asp	Ile	Trp	Val	His	Glu	Tyr	Phe	Thr	Pro	Ser	Trp
		755					760						765		
Phe	Cys	Leu	Pro	Asn	Asn	Gln	Pro	Ala	Leu	Thr	Val	Val	Arg	Pro	Gly
	770					775					780				
Asp	Thr	Ala	Arg	Asp	Thr	Leu	Glu	Leu	Ile	Cys	Lys	Thr	His	Gln	Leu
785					790					795					800

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Asp His Ser Ala His Tyr Leu Arg Leu Lys Phe Leu Ile Glu Asn Lys
 805 810 815

Met Gln Leu Tyr Val Pro Gln Pro Glu Glu Asp Ile Tyr Glu Leu Leu
 820 825 830

Tyr Lys Glu Ile Glu Ile Cys Pro Lys Val Thr His Ser Ile His Ile
 835 840 845

Glu Lys Ser Asp Thr Ala Ala Asp Thr Tyr Gly Phe Ser Leu Ser Ser
 850 855 860

Val Glu Glu Asp Gly Ile Arg Arg Leu Tyr Val Asn Ser Val Lys Glu
 865 870 875 880

Thr Gly Leu Ala Ser Lys Lys Gly Leu Lys Ala Gly Asp Glu Ile Leu
 885 890 895

Glu Ile Asn Asn Arg Ala Ala Asp Ala Leu Asn Ser Ser Met Leu Lys
 900 905 910

Asp Phe Leu Ser Gln Pro Ser Leu Gly Leu Leu Val Arg Thr Tyr Pro
 915 920 925

Glu Leu Glu Glu Gly Val Glu Leu Leu Glu Ser Pro Pro His Arg Val
 930 935 940

Asp Gly Pro Ala Asp Leu Asp Glu Ser Pro Leu Ala Phe Leu Thr Ser
 945 950 955 960

Asn Pro Gly His Ser Leu Cys Ser Glu Gln Gly Ser Ser Ala Glu Thr
 965 970 975

Ala Pro Glu Glu Thr Glu Gly Pro Asp Leu Glu Ser Ser Asp Glu Thr
 980 985 990

Asp His Ser Ser Lys Ser Thr Glu Gln Val Ala Ala Phe Cys Arg Ser
 995 1000 1005

Leu His Glu Met Asn Pro Ser Asp Gln Asn Pro Ser Pro Gln Asp Ser
 1010 1015 1020

Thr Gly Pro Gln Leu Ala Thr Met Arg Gln Leu Ser Asp Ala Asp Asn
 1025 1030 1035 1040

Val Arg Lys Val Ile Cys Glu Leu Leu Glu Thr Glu Arg Thr Tyr Val
 1045 1050 1055

Lys Asp Leu Asn Cys Leu Met Glu Arg Tyr Leu Lys Pro Leu Gln Lys
 1060 1065 1070

Glu Thr Phe Leu Thr Gln Asp Glu Leu Asp Val Leu Phe Gly Asn Leu
 1075 1080 1085

Thr Glu Met Val Glu Phe Gln Val Glu Phe Leu Lys Thr Leu Glu Asp
 1090 1095 1100

Gly Val Arg Leu Val Pro Asp Leu Glu Lys Leu Glu Lys Val Asp Gln
 1105 1110 1115 1120

Phe Lys Lys Val Leu Phe Ser Leu Gly Gly Ser Phe Leu Tyr Tyr Ala
 1125 1130 1135

Asp Arg Phe Lys Leu Tyr Ser Ala Phe Cys Ala Ile His Thr Lys Val
 1140 1145 1150

Pro Lys Val Leu Val Lys Ala Lys Thr Asp Thr Ala Phe Lys Ala Phe
 1155 1160 1165

Leu Asp Ala Gln Asn Pro Lys Gln Gln His Ser Ser Thr Leu Glu Ser
 1170 1175 1180

Tyr Leu Ile Lys Pro Ile Gln Arg Ile Leu Lys Tyr Pro Leu Leu Leu
 1185 1190 1195 1200

Arg Glu Leu Phe Ala Leu Thr Asp Ala Glu Ser Glu Glu His Tyr His
 1205 1210 1215

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Leu Asp Val Ala Ile Lys Thr Met Asn Lys Val Ala Ser His Ile Asn
    1220                                1225                    1230

Glu Met Gln Lys Ile His Glu Glu Phe Gly Ala Val Phe Asp Gln Leu
    1235                                1240                    1245

Ile Ala Glu Gln Thr Gly Glu Lys Lys Glu Val Ala Asp Leu Ser Met
    1250                                1255                    1260

Gly Asp Leu Leu Leu His Thr Thr Val Ile Trp Leu Asn Pro Pro Ala
    1265                                1270                    1275                    1280

Ser Leu Gly Lys Trp Lys Lys Glu Pro Glu Leu Ala Ala Phe Val Phe
    1285                                1290                    1295

Lys Thr Ala Val Val Leu Val Tyr Lys Asp Gly Ser Lys Gln Lys Lys
    1300                                1305                    1310

Lys Leu Val Gly Ser His Arg Leu Ser Ile Tyr Glu Asp Trp Asp Pro
    1315                                1320                    1325

Phe Arg Phe Arg His Met Ile Pro Thr Glu Ala Leu Gln Val Arg Ala
    1330                                1335                    1340

Leu Ala Ser Ala Asp Ala Glu Ala Asn Ala Val Cys Glu Ile Val His
    1345                                1350                    1355                    1360

Val Lys Ser Glu Ser Glu Gly Arg Pro Glu Arg Val Phe His Leu Cys
    1365                                1370                    1375

Cys Ser Ser Pro Glu Ser Arg Lys Asp Phe Leu Lys Ala Val His Ser
    1380                                1385                    1390

Ile Leu Arg Asp Lys His Arg Arg Gln Leu Leu Lys Thr Glu Ser Leu
    1395                                1400                    1405

Pro Ser Ser Gln Gln Tyr Val Pro Phe Gly Gly Lys Arg Leu Cys Ala
    1410                                1415                    1420

Leu Lys Gly Ala Arg Pro Ala Met Ser Arg Ala Val Ser Ala Pro Ser
    1425                                1430                    1435                    1440

Lys Ser Leu Gly Arg Arg Arg Arg Arg Leu Ala Arg Asn Arg Phe Thr
    1445                                1450                    1455

Ile Asp Ser Asp Ala Val Ser Ala Ser Ser Pro Glu Lys Glu Ser Gln
    1460                                1465                    1470

Gln Pro Pro Gly Gly Gly Asp Thr Asp Arg Trp Val Glu Glu Gln Phe
    1475                                1480                    1485

Asp Leu Ala Gln Tyr Glu Glu Gln Asp Asp Ile Lys Glu Thr Asp Ile
    1490                                1495                    1500

Leu Ser Asp Asp Asp Glu Phe Cys Glu Ser Val Lys Gly Ala Ser Val
    1505                                1510                    1515                    1520

Asp Arg Asp Leu Gln Glu Arg Leu Gln Ala Thr Ser Ile Ser Gln Arg
    1525                                1530                    1535

Glu Arg Gly Arg Lys Thr Leu Asp Ser His Ala Ser Arg Met Ala Gln
    1540                                1545                    1550

Leu Lys Lys Gln Ala Ala Leu Ser Gly Ile Asn Gly Gly Leu Glu Ser
    1555                                1560                    1565

Ala Ser Glu Glu Val Ile Trp Val Arg Arg Glu Asp Phe Ala Pro Ser
    1570                                1575                    1580

Arg Lys Leu Asn Thr Glu Ile
    1585                                1590

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<210> SEQ ID NO 7

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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HA-tag sequence

<400> SEQUENCE: 7

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
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<210> SEQ ID NO 8
 <211> LENGTH: 80
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 8

Glu Arg His Gly Val Ala Phe Tyr Asn Phe Gly Gly Ser Glu Ala Gln
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His Leu Thr Leu Gln Ile Gly Asp Val Val Arg Ile Gln Glu Thr Gly
 20 25 30

Gly Asp Trp Tyr Arg Gly Tyr Leu Ile Lys His Lys Leu Ser Gln Gly
 35 40 45

Ile Phe Pro Thr Ser Phe Ile His Leu Lys Glu Val Thr Val Glu Lys
 50 55 60

Arg Arg Asn Ile Glu Asn Ile Ile Pro Ala Glu Ile Pro Leu Ala Gln
 65 70 75 80

The invention claimed is:

1. A method for screening a substance interfering in the association of DOCK2 and ELMO, comprising the steps of contacting DOCK2, ELMO and a test substance, and then estimating the level of interference of association of DOCK2 and ELMO by detecting a GTP-binding form of activated-Rac.

2. The method for screening a substance interfering in the association of DOCK2 and ELMO according to claim 1, wherein the substance interfering in the association of DOCK2 and ELMO is a substance promoting or suppressing the function of regulating lymphocyte migration.

3. The method for screening a substance interfering in the association of DOCK2 and ELMO according to claim 1, wherein the substance interfering in the association of DOCK2 and ELMO is a substance inhibiting the binding of DOCK2 and ELMO.

4. The method for screening a substance interfering in the association of DOCK2 and ELMO according to claim 1, wherein ELMO is ELMO1.

5. A method for screening a substance interfering in the association of DOCK2 and ELMO, comprising the steps of contacting an SH3 domain of DOCK2, ELMO and a test substance, and then estimating the level of interference of association of the SH3 domain of DOCK2 and ELMO by detecting a GTP-binding form of activated-Rac.

6. A method for screening a substance interfering in the association of DOCK2 and the C terminus domain of ELMO, comprising the steps of contacting DOCK2, the C terminus domain of ELMO and a test substance, and then estimating the level of interference of association of DOCK2 and the C terminus domain of ELMO by detecting a GTP-binding form of activated-Rac.

7. A method for screening a substance interfering in the association of DOCK2 and ELMO, comprising the steps of contacting an SH3 domain of DOCK2, the C terminus domain of ELMO and a test substance, and then estimating the level of interference of association of the SH3 domain of DOCK2 and the C terminus domain of ELMO by detecting a GTP-binding form of activated-Rac.

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