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(54) **NOVEL SH2CONTAINING INOSITOL 5'-PHOSPHATASE ISOFORM THAT PARTNERS WITH THE GRB2 ADAPTER PROTEIN**

(75) Inventors: **William G. Kerr**, Tampa, FL (US);
John M. Ninos, Tampa, FL (US)

Correspondence Address:
SALIWANCIK LLOYD & SALIWANCIK
A PROFESSIONAL ASSOCIATION
PO BOX 142950
GAINESVILLE, FL 32614-2950 (US)

(73) Assignee: **University of South Florida**, Tampa, FL

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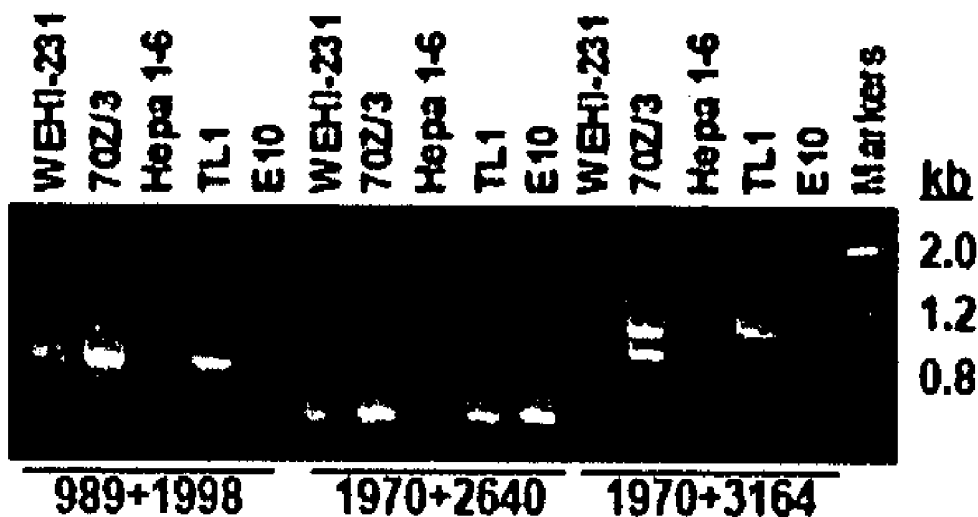
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435/461; 435/7.21; 536/23.1

(57) **ABSTRACT**

SH2 containing inositol 5'-phosphate (SHIP) modulates the activation of immune cells after recruitment to the membrane by Shc and the cytoplasmic tails of receptors. A novel SHIP isoform of approximately 104 kd expressed in primitive stem cell populations (s-SHIP) is described. It was found that s-SHIP is expressed in totipotent embryonic stem cells to the exclusion of the 145-kd SHIP isoform expressed in differentiated hematopoietic cells. s-SHIP is also expressed in primitive hematopoietic stem cells, but not in lineage-committed hematopoietic cells. In embryonic stem cells, s-SHIP partners with the adapter protein Grb2 without tyrosine phosphorylation and is present constitutively at the cell membrane. It is postulated that s-SHIP modulates the activation threshold of primitive stem cell populations.



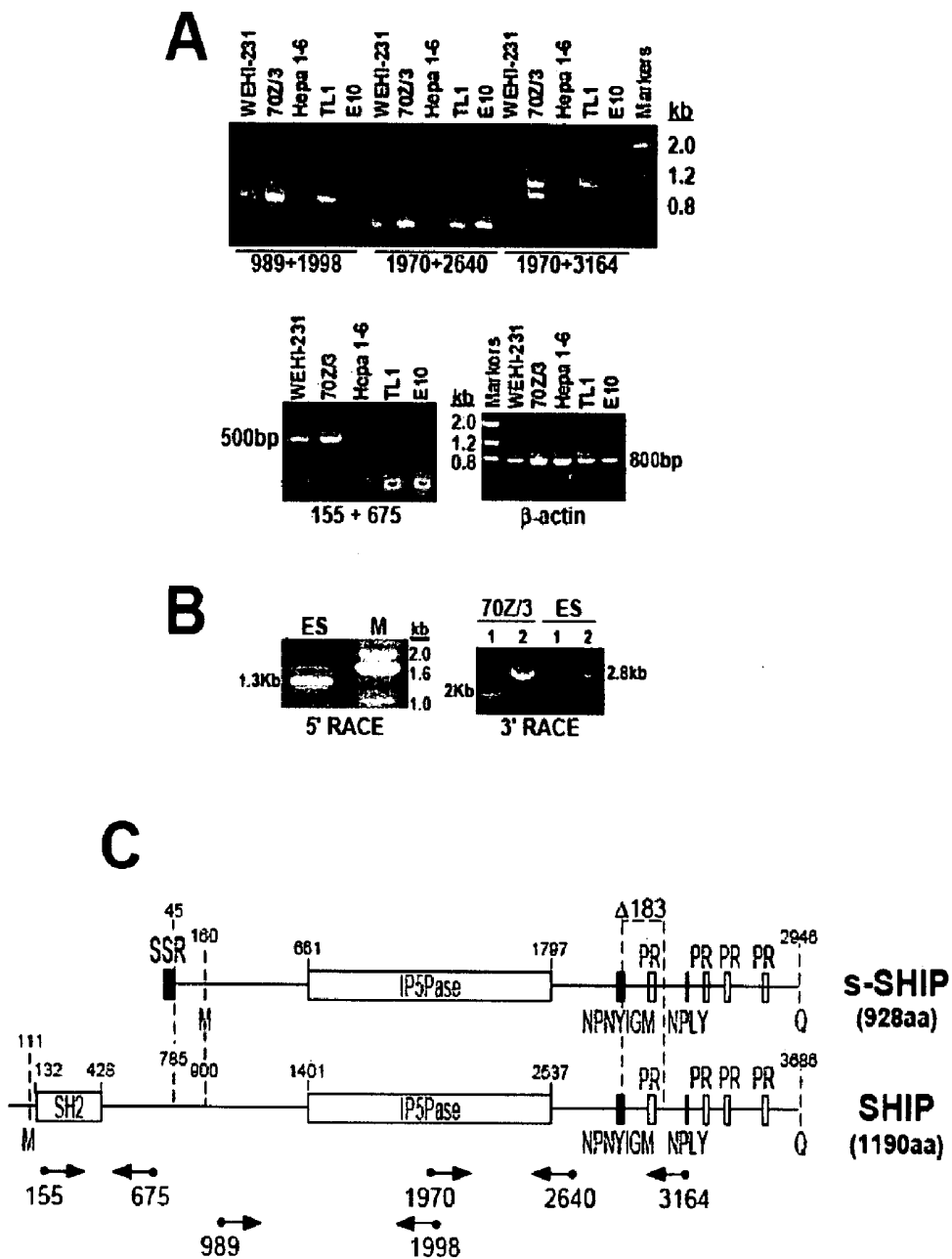


FIG. 1

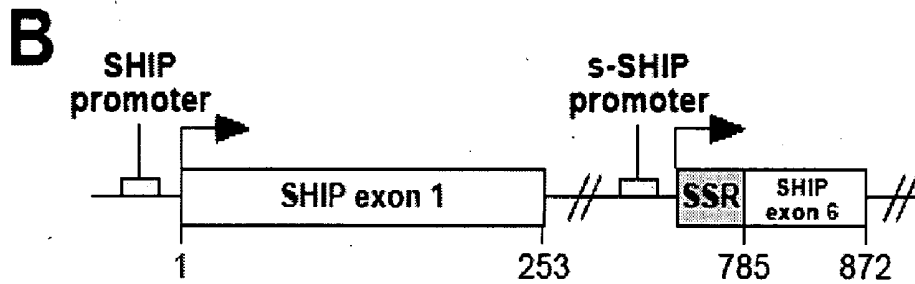
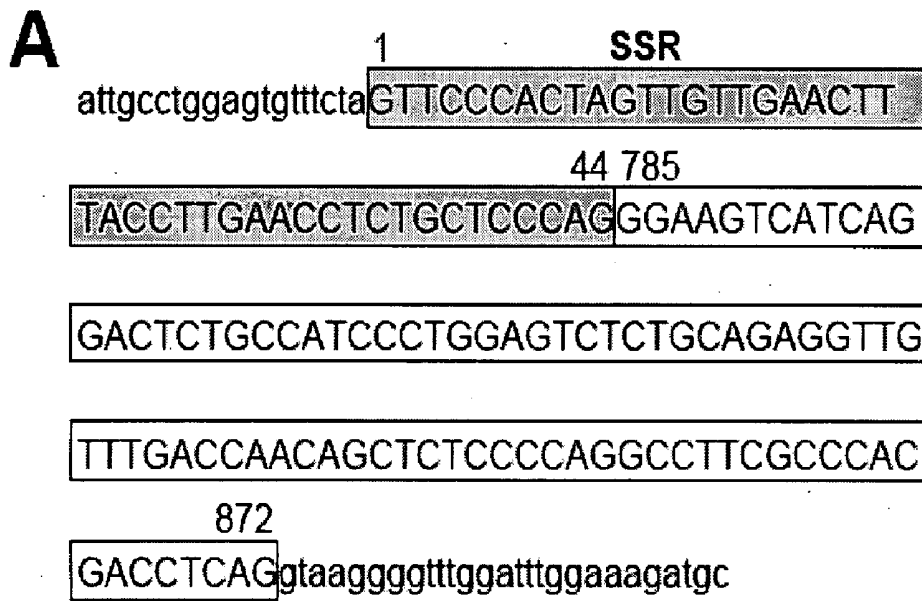


FIG. 3

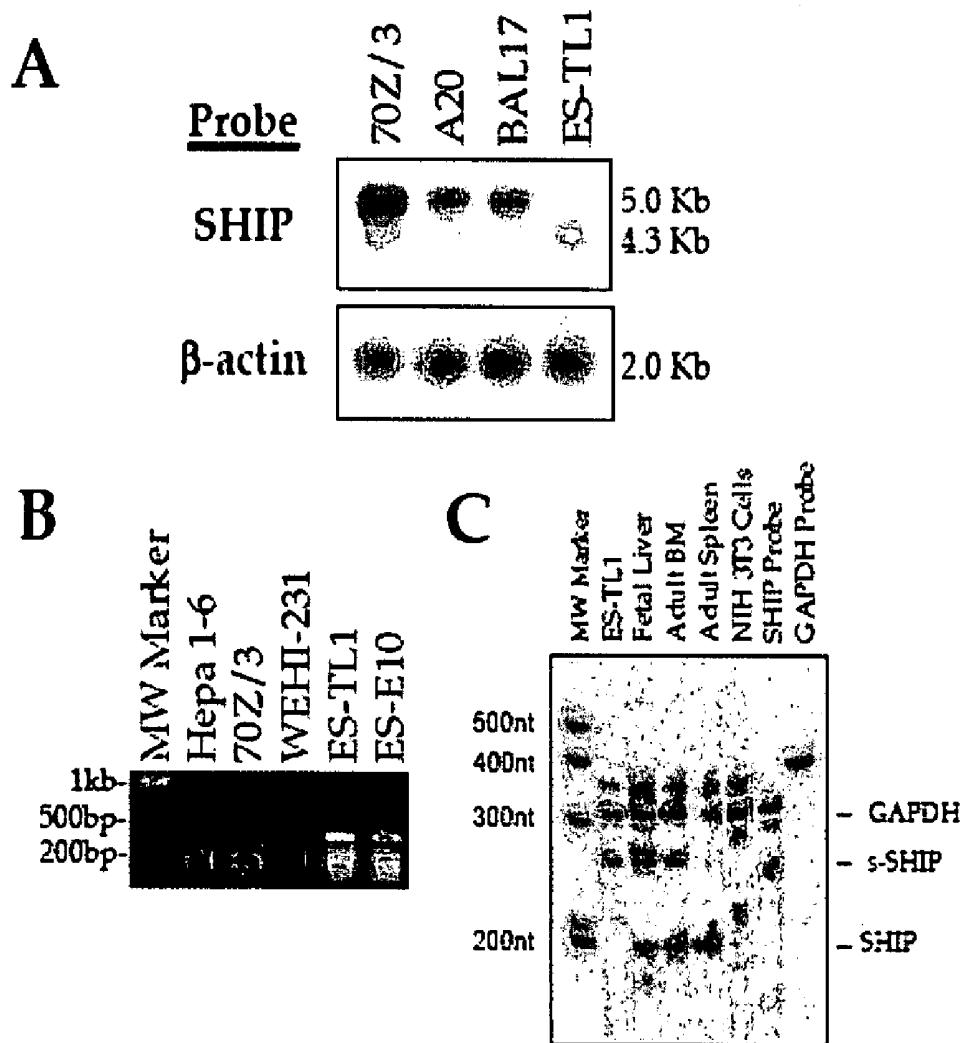


FIG. 4

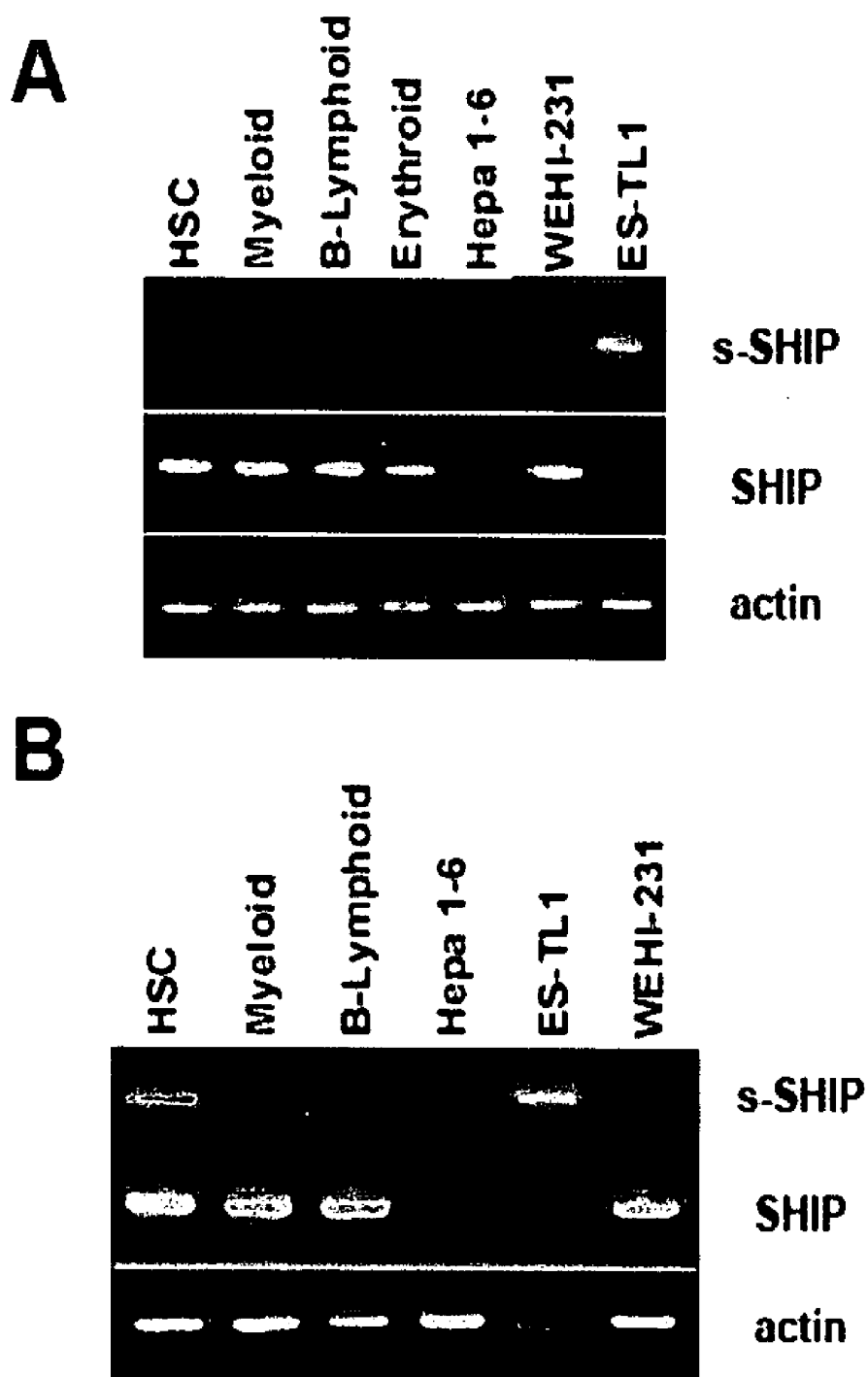


FIG. 5

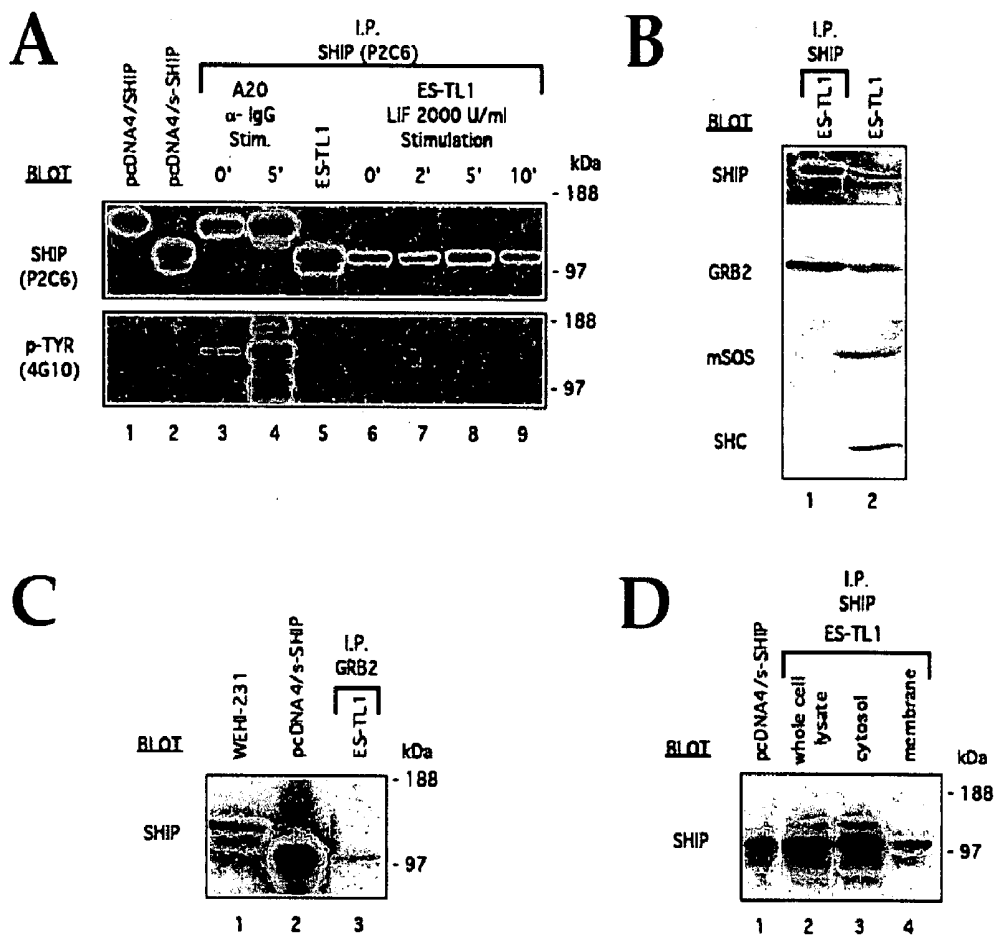


FIG. 6

A

1 SIP-110 SSR-like region

catggaagactctttccggT**GCCCCACTAATCCTTGATGTT**C

42 787

ACCTTGTCCCCT**GCCCCCAG**AGAAGTCATCCGGA

CCCTCCCATCCCTGGAGTCTCTGCAGAGGTTATT

TGACCAGCAGCTCTCCCCGGGCCTCCGTCCACG

874

TCCTCAGgtaaagggtcttgggggtgaaaaggtagattaatccc

B

SIP110.exon1	1	-	C	G	C	C	C	C	A	A	T	C	C	T	T	G	A	T	G	T	T	C	A	C	24	
s-SHIP.exon1	1	G	T	T	C	C	C	C	A	A	G	T	T	G	T	T	G	A	A	C	T	T	T	A	C	25

SIP110.exon1	25	C	T	T	G	T	-	C	C	C	C	T	G	C	C	C	C	A	G	A	A	G	A	A	G	T	48
s-SHIP.exon1	26	C	T	T	G	A	A	C	C	T	C	T	G	C	T	C	C	C	A	G	A	A	G	A	A	G	50

SIP110.exon1	49	C	A	T	C	C	G	G	A	C	C	T	C	C	C	A	T	C	C	C	T	G	G	A	G	73
s-SHIP.exon1	51	C	A	T	C	A	G	G	A	C	T	C	T	G	C	C	A	T	C	C	T	G	G	A	G	75

SIP110.exon1	74	T	C	T	C	T	G	C	A	G	A	G	G	T	T	A	T	T	T	G	A	C	C	A	G	C	98
s-SHIP.exon1	76	T	C	T	C	T	G	C	A	G	A	G	G	T	T	G	T	T	T	G	A	C	C	A	A	C	100

SIP110.exon1	99	A	G	C	T	C	T	C	C	C	C	G	G	G	C	C	T	C	C	G	T	C	C	A	C	G	123
s-SHIP.exon1	101	A	G	C	T	C	T	C	C	C	C	A	G	G	C	C	T	C	C	G	T	C	C	A	C	G	125

SIP110.exon1	124	T	C	C	T	C	A	G	130
s-SHIP.exon1	126	A	C	C	T	C	A	G	132

FIG. 7

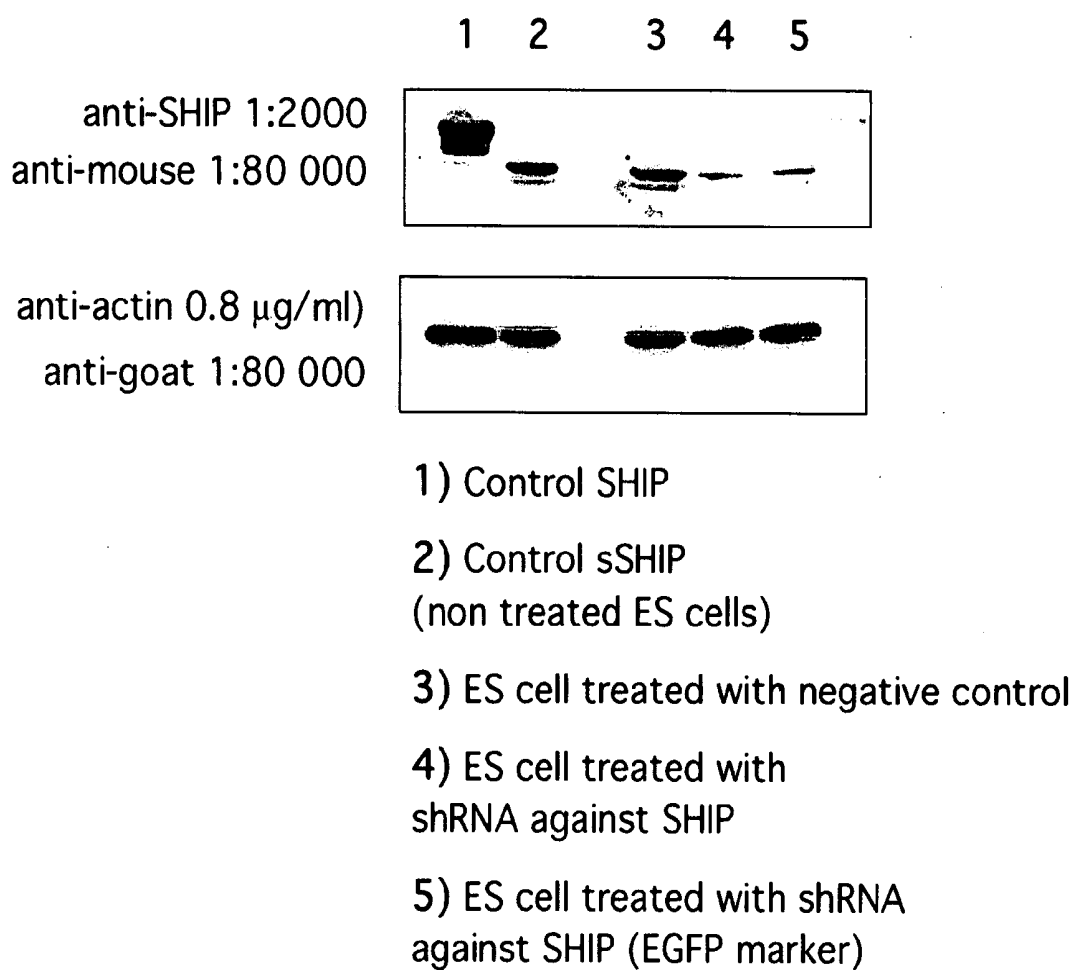


FIG. 8

**NOVEL SH2CONTAINING INOSITOL
5'-PHOSPHATASE ISOFORM THAT PARTNERS
WITH THE GRB2 ADAPTER PROTEIN**

CROSS REFERENCE TO RELATED
APPLICATIONS

[0001] This application claims priority to U.S. Provisional Patent Application Ser. No. 60/319,583 filed Sep. 30, 2002, the specification

FEDERAL RESEARCH STATEMENT

[0002] Federal Research Statement Paragraph] NIH/NIDDK RO1 DK54767

SUMMARY OF INVENTION

[0003] The present invention is a method of cloning a novel SHIP isoform, s-SHIP, and showing that it is expressed in murine embryonic stem cells and murine hematopoietic stem cells. Because of this it may be expressed in all stem cell types—ES, mesenchymal neural, hepatic, neural, muscle, and the like.

[0004] Its function has been partially characterized and it is recruited to the cell membrane even without an acute stimulation of ES cells, it can access its substrate and modulate PIPs levels that accumulate from P activation in response to basal level growth factor stimulation, even in resting stem cells—thus s-SHIP is likely to influence the proliferation and differentiation of stem cells.

[0005] Advantages of the present invention include: (1) human s-SHIP/SIP110 as a marker of stem cells an assay for expression of s-SHIP could be used determine whether a putative human ES cell line is really an ES cell by antibodies or RNA detection of s-SHIP or detection of its enzymatic activity; (2) pharmaceutical modulation of s-SHIP/SIP110 to control the growth and differentiation of human ES cells or other stem cell populations; (3) the human SIP110 cDNA—enforced expression, or inducible expression of s-SHIP could be used to keep human stem cells in an undifferentiated state; (4) the mouse s-SHIP cDNA if mouse cDNA can replace the human cDNA, then enforced expression, or inducible expression of murine s-SHIP, could be used to keep human stem cells in an undifferentiated state; and (5) fluorogenic assays with enzymatic substrates that can be carried out on viable cells to allow FACS sorting of primitive stem cell populations—either embryonic or tissue stem cells.

[0006] The inventive method allows for identifying the presence, and delineation, of embryonic stem cells in a cell sample comprising a mixture of cells, the method comprising the steps of: adding to the sample M-MLV reverse transcriptase to primer pairs selected from the group consisting of s-SHIP, SHIP, and β -actin; and performing nested RT-PCR reactions wherein the presence of embryonic stem cells in the sample is indicated by cells that express s-SHIP mRNA. The method is applied to determine the presence of embryonic stem cells in the sample by the presence of s-SHIP enzymatic activity. Another indicator of the presence of the s-SHIP enzyme is achieved by adding anti-ship monoclonal antibody P2C6 to the sample under conditions, and for a time, suitable for antibody binding and detecting the presence of the antibodies bound to the cells in the

sample. Detection can be achieved by labeling the antibodies with a fluorochrome and testing by fluorescent activated cell sorting. The inventive method is also applicable for identifying the presence, and delineation, of hematopoietic stem cells in a cell sample comprising a mixture of cells, the method comprising substantially the same steps used for detection in embryonic stem cells. The method is also applicable to identifying subcellular signaling complexes involved in stem cell function co-localization by confocal immunofluorescent microscopy.

[0007] In addition to its diagnostic functionality, the method is also applicable therapeutically. Stem cells can be manipulated, due to s-SHIP's competition with mSos1, to either induce or retard cellular proliferation and differentiation. For example, one method of inhibiting differentiation of stem cells comprises the step of contacting the cells with s-SHIP enzyme whereby the accumulation of the s-SHIP enzyme prevents the accumulation of $PI^{3,4,5}P_3$. Generally, the stem cells are selected from a group consisting of hematopoietic progenitors of mature blood cells, hematopoietic progenitors of lymph cells, and embryonic stem progenitor cells.

[0008] The invention does not only consist of the s-SHIP enzyme, but includes a chemically inducible nucleic acid promoter fragment isolated from the 5' flanking region upstream of the coding region of the SHIP gene.

[0009] This promoter fragment is found in murine and human embryonic, as well as hematopoietic stem cells. By implanting a target cell population with cellular hosts of the nucleotide sequence, the vector cells can be used as a negative regulator of cell activation in populations such as B-Lymphoid, myeloid, and mast cells. Possible unicellular host cells could be a culture or tissue culture of cells selected from the group consisting of, a murine embryonic stem cell, a murine hematopoietic stem cell, a human embryonic stem cell, or a human hematopoietic stem cell.

[0010] The invention also consists of a method for inducing proliferation of stem cells by introducing anti-SHIP shRNA into the cell by electroporation. Additionally a means whereby identification stem cells in a cell sample is possible via detection of s-SHIP by immunofluorescence. This can be accomplished where the cell sample is a mixture of cells, in vivo, or in any situation where the presence of s-SHIP can be indicated. Also a method of identifying subcellular signaling complexes involved in stem cell function co-localization by confocal immunofluorescent microscopy is provided.

[0011] Proliferation of stem cells can also be induced by the introduction of an inhibitor of s-SHIP activity, such as a dominant negative mutant.

BRIEF DESCRIPTION OF DRAWINGS

[0012] For a fuller understanding of the nature and objects of the invention, reference should be made to the following detailed description, taken in connection with the accompanying drawings, in which:

[0013] FIG. 1 is an illustration of how ES cells express s-SHIP mRNA species different from that expressed in mature hematopoietic cells.

[0014] FIG. 2 indicates, graphically, the nucleotide sequence of s-SHIP cDNA and the predicted amino acid sequence of its major open reading frame (ORF).

[0015] FIG. 3 shows the organization of the first exon of s-SHIP.

[0016] FIG. 4 graphically indicates the analysis of s-SHIP and SHIP mRNA expression in ES cells and hematopoiesis.

[0017] FIG. 5 blot analysis revealing that HSCs express s-SHIP mRNA.

[0018] FIG. 6 illustrates that ES cells express the 8-SHIP protein isoform that associates with the Grb2 adapter protein.

[0019] FIG. 7 depicts the organization of the first axon of SIP-110, the human homolog of s-SHIP.

[0020] FIG. 8 demonstrates the decrease in s-SHIP expression after electroporation of embryonic stem cells with anti-SHIP shRNA.

BRIEF DESCRIPTION OF SEQUENCES

[0021] Sequence 1 is a mouse s-SHIP sequence of the SHIP isoform.

[0022] Sequence 2 is a mouse s-SHIP sequence of the SHIP isoform.

[0023] Sequence 3 is a human s-SHIP sequence of the SHIP isoform.

[0024] Sequences 4-8 are mouse s-SHIP promoter regions.

[0025] Sequences 9-10 are human s-SHIP promoter regions.

DETAILED DESCRIPTION

[0026] Cell Culture

[0027] The ES cell line, TLI, was obtained from Dr Patricia A. Labosky (University of Pennsylvania, Philadelphia) and was cultured in Dulbecco modified Eagle medium (Gibco-BRL, Grand Island, N.Y.) supplemented with 15% fetal bovine serum (FBS) (Summit Labs, Fort Collins, Colo.), 0.1 mM MEM nonessential amino acids, 2 mM L-glutamine, 50 μ M gentamicin, 50 μ M β -mercaptoethanol (β -ME), and 1000 U/mL leukemia inhibitory factor (LIF) (Gibco-BRL). The ES cell line, E10, was derived from TLI. WEHI-23 1, 70Z/3, A20, and BAL7 (B-cell lines) were maintained in RPMI 1640 medium (Mediatech, Herndon, Va.) with 10% FBS, 2 mM L-glutamine, 50 μ M β -ME (Gibco-BRL), and antibiotics. Hepa 1-6 and 293T cell lines were maintained in DMEM medium with the same supplements as described for the RPMI medium.

[0028] Reverse Transcription Polymerase Chain Reaction

[0029] Cells were washed once with ice-cold phosphate-buffered saline (PBS) and pelleted. Then cells were lysed, and total RNA was prepared using the RNeasy Mini Kit (Qiagen, Valencia, Calif.) according to the manufacturer's instructions. Reverse transcription (RT) of total cellular RNA and amplification of cDNA products for specific gene sequences was carried out using Ready-to-Go RT-PCR Beads (Ainarsham Pharmacia, Piscataway, N.J.) following the manufacturer's instructions. In this series of RT-polymerase chain reaction (PCR), 1- μ g total RNA and 1- μ each gene-specific primer (10 mM) were placed in a 50 μ L reaction volume. In general, PCR conditions were as follows: denaturation for 30 seconds at 94° C., annealing for 30

seconds at a temperature optimal for the primer pair (see below), and a 1-minute extension at 72° C. Nested RT-PCR assays to detect mRNAs expressed in sorted cells were carried out as described below.

[0030] Cell Sorts and Nested RT-PCR Assays

[0031] Femurs and tibias from adult (4- to 6-month-old) male C57BL/6 mice were isolated. Adult bone marrow (ABM) was flushed into chilled RPMI 1640 medium. Fetal livers (FLs) (day 14.5 of gestation) were isolated from pregnant female C57BL/6 mice. Cells were teased from the FLs into chilled RPMI. Cell clusters from the ABM and FL preparations were dispersed into single-cell suspensions with transfer pipettes and were passed over 70 μ m nylon cell strainers. Cell suspensions were pelleted, and red blood cells (RBCs) were lysed for 5 minutes at 4° C. in RBC lysis buffer (163 mM NH₄Cl, 10 mM KHCO₃, 0.13 mM EDTA). After RBC lysis, the cells were washed in PBS, passed over 70 μ m strainers, counted, and resuspended in staining media (PBS with 3% FBS and 10 mM HEPES) at 10⁷ cells/50 μ L. Cells were incubated in Fc Block (Pharmingen, San Diego, 10⁷ cells/50 μ L staining media and stained with the appropriate panel of fluorochrome-conjugated antimurine antibodies at 1 to 2 μ g/10⁷ cells/50 μ L staining media. Antibodies used were a lineage-fluorescein isothiocyanate panel of Mac-1 (Caltag Laboratories, Burlingame, Calif.), Gr-1, CD3, CD4 (GKI.5), CD8a (53-6.7) B220 (Pharmingen); B220-phycoerythrin (PE), Ter119-PE, c-kit-PE, and biotinylated Sca-1 (Pharmingen). Biotinylated Sca-1 was revealed with streptavidin-allophycocyanin (APC) (Pharmingen). After staining, the cells were washed and resuspended in staining media (50 μ L/10⁷ cells) plus propidium iodide (PI) at 1.0 μ M for dead cell exclusion. HSCs (Sca-1+c-kit+Lin-), B-lymphoid cells (B220+Gr-1-Mac-1-), myeloid cells (Gr-1+Mac-1+B220-), and erythroid cells (Ter119+Lin-) were sorted from ABM and FL using a FACStar flow cytometer (Becton Dickinson, San Jose, Calif.) equipped with an automatic cell deposition unit. ES cells (s-SHIP positive control), WEHI-231 cells (SHIP-positive control), and Hepa 1-6 cells (negative control) were also prepared in staining media and 10⁷ cells/50 μ L. Fifty viable cells of each population were deposited into separate wells of a 96-well PCR plate containing lysis buffer (0.4% Nonidet P-40, 60 μ M dNTP, 25 μ M dithiothreitol, 0.5 U/ μ L RNasin [Promega, Madison, Wis.]) and were lysed for 15 minutes on ice (adapted from Hu et al). RNA was reverse transcribed using multiple primer pairs for β -actin, s-SHIP, and SHIP and 48 U M-MLV reverse transcriptase per reaction in the buffer provided (Gibco-BRL). First-round PCR of 35 cycles was performed with addition of 40 μ M buffered RedTaq DNA polymerase (Sigma, St Louis, Mo.). One-microliter aliquots of the first-round PCR product were further amplified for 35 cycles using fully nested primers for each gene. Aliquots of second-round products were subjected to gel electrophoresis and visualized by ethidium bromide staining. cDNA and genomic cloning To determine the 5' and 3' termini of the s-SHIP cDNA, the inventors performed rapid amplification of cDNA ends (RACE) cloning using the Smart Race cDNA Amplification Kit (Clontech, Palo Alto, Calif.). Touch down PCR amplification conditions were used for 5' and 3' RACE reactions with the following cycling conditions: 30 seconds at 94° C. and 4 minutes at 72° C. for cycles 1 to 5; 30 seconds at 94° C., 30 seconds at 70° C., 4 minutes at 72° C. for cycles 6 to 10; 30 seconds at 94° C., 30 seconds at 68° C., 4 minutes at 72° C. for cycles 11 to 35. Smart Race

products were cloned using the TOPO TA cloning kit (Invitrogen, Carlsbad, Calif.). Sequences derived from the termini of the 5' and 3' RACE clones of s-SHIP were used to design primers that amplify the entire s-SHIP cDNA by RT-PCR. Full-length s-SHIP cDNAs were obtained by 2 separate RT-PCR amplifications of overlapping fragments that contained either 5' or 3' termini. These 2 fragments were cloned into the pcDNA3 vector (Invitrogen). Genomic sequences were isolated using a mouse GenomeWalker Kit (Clontech). Conditions for touchdown PCR amplification of genomic sequences were as described above. Sequencing of s-SHIP cDNAs and associated genomic clones were carried out at the DNA Sequencing Facility of the University of Pennsylvania Comprehensive Cancer Center.

[0032] Sequence Analysis

[0033] DNA and protein sequences were analyzed with MacVector 7.0 (Oxford Molecular, Madison, Wis.). Sequence alignments and comparisons were performed with the ClustalW algorithm. "The Celera Human Genome Unassembled Fragments database (<http://publicstion.celera.com>) (Celera Genomics, Rockville, Md.) was accessed to perform BlastN queries of the first 120 nucleotides of human 110-kD signaling inositol polyphosphate 5'-phosphatase (SIP-110) cDNA (GenBank accession number 050040).

[0034] Northern Blot Analysis and Ribonuclease Protection Assay

[0035] PolyA+RNA was prepared as described above. Northern blot analysis of SHIP mRNA expression was as described previously. For ribonuclease protection assay (RPA), the target sequence contained the 44-nucleotide SSR of s-SHIP mRNA and nucleotides 45-247 of s-SHIP (nucleotides 785-987 of SHIP). It was amplified using PCR with primers XHOESHIP1 (sense) and ASHIP987 (anti-sense). This PCR product was TA-cloned into pCR2.1-TOPO (Invitrogen) and then subcloned in a reverse orientation downstream of the T3 promoter of the pRRI-amp-18 vector (Ambion, Austin, Tex.). The vector was linearized for s-SHIP/SHIP probe synthesis. Anti-sense RNA probe was synthesized and labeled with 32 using the Maxiscript T7/T3 kit (Ambion) following the manufacturer's instructions. The probe for mouse GAPDH had 25 times lower specific activity than the s-SHIP/SHIP probe. The 100 nucleotide RNA markers were generated using templates provided by Ambion. RPA assay was performed on 10 µg total RNA for each sample and 20,000 cpm for each probe using the RPAIII kit (Ambion) according to the manufacturer's instructions. RPA products were visualized by running Quick Point precast gels (6% polyacrylamide denaturing gel; Novex, San Diego, Calif.) and then by autoradiography.

[0036] Transfections

[0037] SHIP cDNA was kindly provided by Dr Larry Rohrschneider. SHIP and s-SHIP cDNAs were cloned separately into the pcDNA4/HisMaxC expression vector (Invitrogen). These pcDNA4/SHIP and pcDNA4/s-SHIP plasmids were transfected into 293T kidney cells using the FuGENE 6 transfection reagent (Roche Molecular Biochemicals, Indianapolis, Ind.) according to the manufacturer's instructions.

[0038] Antibodies

[0039] Purified mouse antiSHIP monoclonal antibody, P2C6, was obtained from Drs David Lucas and Larry

Rohrschneider. It was used for immunoprecipitation at a concentration of 4 µg/1 mg total protein and for immunoblotting at a dilution of 1:1000. Rabbit antiGrb2 polyclonal antibody (sc-255; Santa Cruz Biotechnology, Santa Cruz, Calif.) was used for immunoprecipitation at a concentration of 2 µg/1 mg total protein and for immunoblotting at a dilution of 1:500. Rabbit antiShc polyclonal antibody (06-203; Upstate Biotechnology, Lake Placid, N.Y.) was used for immunoblotting at a concentration of 1 µg/mL. Rabbit antiSosl polyclonal antibody (06-246; Upstate Biotechnology) was used for immunoblotting at a concentration of 1 µg/mL. Mouse antiphosphotyrosine monoclonal antibody (4G1 0; 05-321; Upstate Biotechnology) was used for immunoblotting at a concentration of 1 µg/mL.

[0040] Immunoprecipitations and Immunoblots

[0041] Approximately 10⁷ cells were washed once with ice-cold PBS and pelleted. Cell pellets were then lysed in 0.5 to 1.0 mL modified RIPA buffer (1% Nonidet P-40, 50 mM Tris-HCl [pH 7.4], 0.25% Na-deoxycholate, 150 mM NaCl, 1 mM EDTA, 1 mM Na₃V0₄, 1 mM phenylmethylsulfonyl fluoride, 10 µg/mL leupeptin, 10 µg/mL pepstatin, 10 µg/mL aprotinin). Lysates were rocked for 30 minutes at 4° C., and cellular debris was removed by centrifugation at 14,000 g for 15 minutes. Total protein concentration of each lysate was determined by spectrophotometry using the BCA Protein Assay Kit (Pierce Chemical, Rockford, Ill.). Lysates were stored at 80° C. Whole cell lysates were subsequently mixed with NUPAGE 4× lithium dodecyl sulfate (LDS) sample buffer and lox sample reducing agent, heated for 10 minutes at 70° C., and loaded onto NuPAGE 10% or 4% to 12% Bis-Tria 1.0 mm gels (Invitrogen). For immunoprecipitations, equal concentrations of total protein (either 500 µg in 500 µL or 1 mg in 1 mL lysis buffer) were used for each individual experiment. Samples were precleared with 0.25 µg of the appropriate control IgG (normal mouse or rabbit IgG; Santa Cruz Biotechnology) together with 50 µL appropriate agarose bead conjugate (Protein G-Agarose, Fast Flow [immunoprecipitation (I.P.)]; Protein A-Agarose, Fast Flow [I.P.]; Upstate Biotechnology) for 1 hour at 4° C. Precleared samples were transferred to fresh tubes. Four microliters P2C6 antiSHIP monoclonal antibody or 2 µg antiGrb2 polyclonal antibody were added per milligram total protein and were incubated overnight with rocking at 4° C. Fifty microliters appropriate agarose bead conjugate was then added and rocked for 2 hours at 4° C. Agarose bead conjugates were pelleted (14000 g, 5 seconds), washed 3 times with cold PBS, and boiled in NuPAGE 4× LDS sample buffer with IOX sample reducing agent for 5 minutes at 100° C. Beads were pelleted and equal volumes of the immunoprecipitate supernatant were loaded onto NuPAGE 10% or 4% to 12% Bis-Tris gels. Proteins were separated for 50 minutes at 200 V using MOPS sodium dodecyl sulfate running buffer in an XCell II Mini-Cell unit (Protein molecular weights were compared using Novex MultiMark protein standards. Separated proteins were transferred to polyvinylidene difluoride (Bio-Rad Laboratories, Hercules, Calif.) or nitrocellulose [blots] (Millipore, Bedford, Mass.) membranes for 75 minutes at 30 V using the XCell II Blot Module. Immunoblotting was carried out using the enhanced chemiluminescence Western blotting analysis system following the manufacturer's instructions (Amersham Pharmacia).

[0042] Cell Stimulation

[0043] ES-TLI cells were split into 4 different 100-mm TC plates and grown overnight at 37° C. in ES media supplemented with 1000 U/mL LIF to approximate 80% confluence. LIF-supplemented media was removed, cells were washed twice with PBS, media without LIF was added, and cells were incubated for 5 hours. Cells were washed once with PBS and twice with Hanks balanced salt solution (HBSS; Mediatech). Then they were pre incubated in HBSS at 37° C. for 10 minutes. Cells were stimulated by the addition of HBSS containing 2000 U/ml. LIF and by incubation at 37° C. for either 2, 5, or 10 minutes. A control ES plate (0 minute) containing HBSS without LIF was incubated at 37° C. in parallel for 10 minutes. Stimulations were stopped by the removal of buffer and the addition of 10 μ L ice-cold PBS/1 mM Na PBSiNa was removed, and 10 μ L ice-cold modified RIPA buffer was added immediately. Cells were scraped, and cell lysates were processed as described above. A20 cells were grown in RPMI and were washed once with PBS and twice with HBSS. Then 2×10^7 cells were placed in separate 15-mL conicals and were pre-incubated in HBSS at 37° C. for 10 minutes. Cells were spun down, and HBSS was removed. After that, cells were stimulated with 1 mL HBSS containing 20 μ g/mL goat antimouse IgG (Southern Biotechnology Associates, Birmingham, Ala.) and were incubated at 37° C. for 5 minutes. Control A20 cells (0 minute) containing HESS without antimouse IgG were incubated in parallel. Stimulations were stopped by placing the conicals on ice and adding 2 mL ice-cold PBS/Na3VO4. Cells were pelleted, supernatant was removed, and 1 mL ice-cold modified RIPA buffer was added. Total protein (1.0 mg in 1 mL) of each preparation was used for subsequent immunoprecipitation experiments.

[0044] Membrane and Cytosol Fractionation

[0045] Two confluent 150 mm \times 25 mm plates of ES-TLI cells cultured in LIF were washed twice with chilled PBS, then collected with a chilled cell scraper. Cells were pelleted by centrifugation at 300 g and resuspended in 2 mL chilled sonication buffer (20 mM Tris-HCl, pH 8, 137 mM NaCl, 10% glycerol, 2 mM EDTA, 1 mM NaVO₄, 1 mM phenylmethylsulfonyl fluoride, 10 μ g/mL leupeptin, 10 μ g/mL pepstatin, and 10 μ g/mL aprotinin). This suspension was sonicated on ice for 20 seconds at 20% full output using a Fisher Model 60 Sonic Dismembrator equipped with a one-eighth inch diameter tip (Fisher Scientific, Pittsburgh, Pa.). Trypan blue dye exclusion and examination by phase-contrast microscopy confirmed that no intact cells remained. The suspension was centrifuged at 500 g for 5 minutes at 4° C. to remove the nuclear fraction. Postnuclear supernatant was centrifuged in Beckman 15 \times 31 mm polycarbonate tubes at 100 000 g for 20 minutes at 4° C. in a Beckman TL-100 centrifuge equipped with a TLA-100.3 rotor. The supernatant cytosol fraction was removed, and Triton X-100 was added to a final concentration of 1%. The membrane pellet was rinsed once with chilled sonication buffer and then resuspended in chilled sonication buffer plus 1% Triton X-100. Resuspension was achieved by needle probe sonication on ice for 30 seconds at 20% full output, and the resuspended membrane fraction was allowed to solubilize at 4° C. for 45 minutes with frequent gentle vortexing. Insoluble material was removed by centrifugation at 10 000 g for 15 minutes at 4° C. ES-TLI cells from a third 150 mm plate were collected in parallel with the cells

collected for fractionation in order to prepare an unfractionated whole cell lysate for comparison purposes. These cells were lysed in 1 mL of chilled sonication buffer/1% Triton X-100, rocked for 45 minutes at 4° C., and centrifuged at 10 000 g for 15 minutes at 4° C. to remove cellular debris. Total protein concentrations of the whole cell lysate, cytosol, and membrane fractions were determined by spectrophotometry using the BCA Protein Assay Kit. Whole cell lysate, cytosol, and membrane fractions were then diluted in sonication buffer/1% Triton X-100 to a final concentration of 1 mg/mL. Fractions were stored at -80° C. and 1 mg total protein (in 1 mL) of each preparation was used for subsequent immunoprecipitation experiments.

[0046] FIG. 1. illustrates how ES cells express e SHIP mRNA species different from that expressed in mature hematopoietic cells. (A) RT-PCR analysis of SHIP expression in ES cells and lineage-committed hematopoietic cell lines. All primers used in the RT-PCR assays were designed to amplify regions of SHIP mRNA encoded by separate exons; hence, the expected amplification products must arise from amplification of cDNA, not from contaminating genomic DNA. The following cell types were analyzed: B-lymphocyte cell lines 70Z/3 and WEHI-231, hepatoma cell line Hepa 1-6 (negative control), and ES cell lines TL1 and E10. Amplification of β -actin was included as a control for the RNA isolation and cDNA synthesis steps. PCR products were resolved on a 1% agarose gel and stained with ethidium bromide. (B) RACE cloning of s-SHIP mRNA. PCR products representing the 5' or 3' termini of the s-SHIP mRNA expressed in ES cells were generated by 5' and 3' RACE, respectively. For 3' RACE cloning of SHIP mRNA species in 70Z/3 and ES cells, the primers SHIP2766 (sense; lane 1) or SHIP1970 (sense; lane 2) were used. (C) Schematic depiction of the structure of the s-SHIP and SHIP cDNAs. Nucleotide numbering refers to GenBank accession numbers AF184912 and U52044, respectively. Functional domains and sequence motifs encoded in the s-SHIP and SHIP mRNAs are s-SHIP Region (SSR), Src-homology 2 domain (SH2), proline-rich motifs (PR), and NPXY and YIGM motifs. The internal M83 nucleotide deletion is illustrated. Initial methionine (M) and terminal glutamine (Q) amino acids for each mRNA are indicated, yielding proteins of 928 aa (s-SHIP) and 1191 aa (SHIP). Relative location and orientation of the primers used in the RT-PCR analysis or RACE cloning are indicated below the SHIP cDNA. Numbers below the primers (arrows) represent the 5' nucleotide in the primer based on its position in the SHIP cDNA sequence.

[0047] Results Identification and Characterization of s-SHIP mRNA

[0048] Previous analysis of SHIP expression indicated that its expression is restricted to cells of the hematopoietic system. However, while evaluating other cell types for expression of the SHIP gene, it was found that ES cells express SHIP mRNA. The inventors detected the presence of SHIP mRNA in polyA+RNA isolated from ES cells (TL1) using several different RT-PCR assays that amplify distinct regions of SHIP mRNA (FIG. 1A,C). However, primers that amplify the 5' portion of SHIP mRNA that encodes its SH2 domain failed to amplify the SHIP mRNA species expressed in ES cells, but they yielded the expected product when amplifying mRNA from B-lymphocyte cell lines (70Z/3, WEHI-231). Furthermore, we found that an ES cell line

(E10) with both SHIP alleles mutated by the insertion of a GFP transgene into exon 1 (J. Wang et al, unpublished data, September 1997) retains expression of SHIP mRNA as detected by several independent RT-PCR assays for SHIP expression (FIG. 1A,C). These results indicate that ES cells express a SHIP transcript, which the inventors designate s-SHIP, that differs at its 5' end from the SHIP mRNA previously described in differentiated hematopoietic cells.

[0049] To confirm the presence of a SHIP mRNA species with a different 5' end in ES cells and to determine its sequence, the inventors performed 5' Smart Race cDNA cloning using antisense primers complementary to the SHIP cDNA sequence. The inventors used primers from regions of SHIP that analysis in FIG. 1A indicated were also present in s-SHIP mRNA. Two separate 5' RACE reactions with primers ASHIP1998 and ASHIP1098 yielded a single product of either 1.3 kb (FIG. 1B) or 0.4 kb (data not shown), respectively. Sequence analysis of these 5' RACE products showed that the SHIP mRNA present in ES cells begins with a 44-nucleotide region not previously found in any murine SHIP cDNA identified to date (FIG. 2). The inventors designate this novel 44-nucleotide region the stem-SHIP region (SSR). The complete sequence of these 5' RACE products showed that the SSR forms the 5' end of the s-SHIP mRNA and is fused with the previously identified murine SHIP cDNA sequence beginning at nucleotide 785 and is identical up to nucleotide 1998 (GenBank accession number U52044).

[0050] To determine the sequence of the remainder of the s-SHIP transcript present in ES cells, the inventors performed 2 separate 3' RACE reactions (FIG. 1B) with sense strand specific primers (SHIP1970 and SHIP2766). Cloning and sequencing of these 3' RACE products indicated that s-SHIP mRNA is identical to SHIP mRNA from nucleotide 1970 through the end of the SHIP cDNA. To further confirm the sequence of the s-SHIP cDNA, the inventors obtained full-length s-SHIP cDNA by RT-PCR. Turning to FIG. 2, sequence analysis of the full-length s-SHIP cDNA confirmed that s-SHIP mRNA lacks the SH2 domain but has the 44-nucleotide SSR fused to nucleotide 785 of SHIP. However, like its hematopoietic counterpart, s-SHIP mRNA encodes an inositol 5'-phosphatase domain and several protein interaction motifs, including 2 NPXY motifs, a YIGM motif, and 4 proline-rich motifs (FIGS. 1C, 2). As Lucas and Rohrschneider found for SHIP mRNA in hematopoietic cells, s-SHIP mRNA is alternatively spliced to generate a form that lacks a 183-nucleotide region (nucleotides 2129-2311 of s-SHIP [accession number AF184912] corresponding to nucleotides 2869-3051 of SHIP). Forms of s-SHIP mRNA that contain or lack this 183-nucleotide region are present in ES cells, indicated by the RT-PCR reaction, with primers that span this expression arises from an internal promoter in the SHIP gene region (1970+3164 in FIG. 1A). Sequence analysis of these products confirmed that the alternative splice event that results in the Δ 83 s-SHIP mRNA (accession number AF184913) is identical to that described by Lucas and Rohrschneider for SHIP.

[0051] FIG. 2 indicates the nucleotide sequence of s-SHIP cDNA and the predicted amino acid sequence of its major open reading frame (ORF). The first 784 nucleotides of the SHIP cDNA are provided for comparison above the bold arrow, s-SHIP cDNA sequence is indicated below the bold arrow, starting with the numeral 1 and continuing through

nucleotide 2946. Remaining a-SHIP cDNA sequence (nucleotides 2947-4125) is not shown because of size constraints, but it is identical to nucleotides 3687 to 4865 of the SHIP cDNA (data not shown). The number in parentheses (785) at nucleotide 45 of the s-SHIP cDNA indicates the nucleotide in the SHIP cDNA, where identity between the s-SHIP and SHIP cDNAs begins. ATG initiator codons for the SHIP and s-SHIP major ORFs are indicated in bold and underlined, and the termination codon shared by both isoforms is indicated by an asterisk. SH2 (dotted box), SSR (solid box), and Inositol 5 (dashed box) sequences are shown. The nucleotide sequence that encodes the Δ 183 nucleotide deletion is underlined. NPXY and proline-rich motifs are shaded black and gray, respectively.

[0052] FIG. 3 shows the organization of the first exon of s-SHIP. (A) Genomic sequence of the first exon of s-SHIP and adjacent intronic sequence. Uppercase letters represent the nucleotides in the first axon of s-SHIP, and lowercase letters represent the intronic sequence immediately flanking this axon. The 44 nucleotides enclosed in the shaded box indicate the SSR, and the 88 nucleotides in the clear box represent those found in both the s-SHIP and the 145-kd SHIP cDNAs, Numbers 785 and 872 indicate the position of each corresponding nucleotide in the murine 145-kd SHIP cDNA sequence (GenBank accession number U52044). (B) Schematic representation of the orientation of the predicted promoter regions and first axons of SHIP and s-SHIP relative to each other in the SHIP locus. Arrows indicate the transcriptional start points. The s-SHIP first axon consists of the 44-nucleotide SSR and the adjacent 88-nucleotide SHIP axon 6. Nucleotide numbering refers to the 145-kd SHIP cDNA sequence (accession number U52044).

[0053] Genomic Location of the s-SHIP First Exon Indicates its Expression Arises From an Internal Promoter in the SHIP Gene

[0054] To determine whether the 44-nucleotide SSR at the 5' end of the s-SHIP mRNA represents an independent exon or is a part of an existing exon in SHIP, the inventors isolated and sequenced the genomic DNA that spans this region. Sequence analysis of the genomic DNA revealed that the 44-nucleotide SSR is directly adjacent to a sequence that serves as exon 6 (nucleotides 785-872) in the SHIP isoform expressed in lineage-committed hematopoietic cells (FIG. 3). Thus, the 44-nucleotide SSR is not a discrete exon but is part of a larger 132-nucleotide region that serves as exon 1 in s-SHIP.

[0055] Furthermore, because the 132-nucleotide s-SHIP exon 1 is located at an internal site in the SHIP gene, s-SHIP expression must arise from an internal promoter that is 3' to the SH2-encoding exons and 5' to the exons that encode the inositol 5'-phosphatase domain (FIG. 3B). The location of s-SHIP exon 1 requires that its transcription initiate internally in the SHIP genomic locus in a region that serves as an intron for the SHIP mRNA expressed in differentiated hematopoietic cells.

[0056] Embryonic and Hematopoietic Stem Cells Express s-SHIP mRNA

[0057] RT-PCR analysis indicated that s-SHIP is the only SHIP transcript expressed in ES cells (FIG. 1). However, to determine whether s-SHIP is also expressed in the hematopoietic system along with its SH2-encoding counterpart, the

inventors analyzed total polyA+RNA isolated from ES cells and lineage-committed hematopoietic cell lines by Northern blot. This analysis showed that B-lymphocyte cell lines (70Z/3, A20, BAL17) express only the approximately 5 kb SHIP mRNA, whereas the ES cell line TLI expresses only the smaller, approximately 4.3 kb s-SHIP mRNA (FIG. 4A). In addition, an RT-PCR assay that is specific for s-SHIP expression showed that ES cells (TL1, E10) express s-SHIP, whereas B-lymphocyte cell lines (70Z/3, WEHI-231) do not (FIG. 4B). These results demonstrate that s-SHIP expression is silenced in differentiated hematopoietic cells.

[0058] FIG. 4. Analysis of s-SHIP and SHIP mRNA expression in ES cells and hematopoiesis. (A) Northern Blot analysis of SHIP mRNA species expressed by ES cells (TL1) and lineage-committed hematopoietic cell lines (70Z/3, A20, BAL17). A full-length SHIP cDNA clone was used to probe the filter. After initial hybridization with the SHIP probe, the filter was stripped and re-probed for β -actin to confirm that comparable amounts of RNA were loaded in each lane. (B) RT-PCR analysis of s-SHIP expression in ES cells (TL1, E10) and lineage-committed hematopoietic cell lines (70Z/3, WEHI-231). The primer pair ESHIP23 and ASHIP098 selectively amplifies s-SHIP mRNA and not SHIP mRNA. Analysis of the hepatoma cell line, Hepa 1-6, serves as a negative control for SHIP. (C) RPA analysis of s-SHIP and SHIP expression in ES cells and hematopoietic development. After annealing and RNase digestion, the s-SHIP/SHIP probe is protected for 247 nucleotides by s-SHIP mRNA and for 203 nucleotides by SHIP mRNA. Thus, a single probe is used to detect the relative abundance of the s-SHIP and SHIP mRNAs. Each RNA sample was incubated with a GAPDH probe as an internal control. Analysis of NIH3T3 cell RNA is provided as a negative control for both SHIP and s-SHIP mRNA expression.

[0059] To further assess the relative ratio of s-SHIP to SHIP mRNA expressed in different cell types and tissues, the inventors developed an RPA that simultaneously detects both s-SHIP and SHIP mRNAs (FIG. 4C). RPA analysis indicates that s-SHIP is expressed to the exclusion of SHIP in ES cells and that SHIP mRNA is the predominant form in adult spleen. However, in FL and ABM tissues that contain significant numbers of pluripotent HSC the inventors find coexpression of s-SHIP and SHIP mRNA. Interestingly, FL has significantly more s-SHIP than SHIP mRNA, whereas ABM has slightly less s-SHIP than SHIP mRNA. These results suggest that the relative abundance of s-SHIP mRNA in a tissue may correlate to the relative abundance of HSC activity in the tissue. For instance, FL is substantially enriched for primitive HSC activity relative to ABM, whereas the spleen is a poor source of HSC activity.

[0060] Focusing now on FIG. 5, HSCs express s-SHIP mRNA. HSCs and lineage-committed cells were sorted from ASM or day 14.5 FL and analyzed by nested RT-PCR assay for the expression of s-SHIP, SHIP, and β -actin mRNA. In both ABM and FL, s-SHIP mRNA was detected in HSCs (Sca-1+c-kit+Lin⁻) but not in the myeloid (Gr-1+/MAC-1+), B-lymphoid (B220+), or erythroid (Ter119+) lineages. Hepa 1-6 cells were sorted as the negative control for both s-SHIP and SHIP mRNA expression, and ES-TL1 and WEHI-231 cells were sorted as positive controls for s-SHIP and SHIP mRNA expression, respectively.

[0061] To directly assess the possibility that s-SHIP is expressed in HSC, the inventors developed a nested RT-PCR

procedure to detect the expression of s-SHIP and SHIP mRNAs. To define the s-SHIP expression pattern in vivo, the inventors sorted HSC (Sca-1+cKit+Lin⁻) as well as cells of the B-lymphoid (B220+), myeloid (Gr-1+Mac-1), and erythroid (Ter119 lineages from day 14.5 FL or ABM. Fifty cells of each population were deposited into single wells of a 96-well PCR plate containing lysis buffer and dNTPs. RNA was reverse transcribed by adding multiple primer pairs for s-SHIP, SHIP, and β -actin together with M-MLV reverse transcriptase. Nested RT-PCR reactions were performed (see "Materials and methods"). Representative RT-PCR results from multiple independent sorts of ABM and FL are shown in FIG. 5. The inventors detected s-SHIP mRNA in Sca-1+cKit+Lin⁻ HSC from both ABM and FL, but not in cells of the B-lymphoid, myeloid, or erythroid lineages. RT-PCR analysis of 50 sorted ES-TL1, WEHI-231, and Hepa 1-6 cells served as s-SHIP, SHIP, and negative controls. These results provide further support for the hypothesis that s-SHIP expression is restricted to primitive stem cell populations. The inventors also detected SHIP expression in HSC; thus, it remains to be determined whether the 2 isoforms are coexpressed in all HSC or whether they are discordantly expressed in distinct subsets of HSC.

[0062] Embryonic Stem Cells Express a Lower Molecular Weight Isoform of SHIP, Consistent with the Predicted Open-Reading Frame in the s-SHIP cDNA

[0063] FIG. 6 illustrates how ES cells express the 8-SHIP protein isoform that associates with the Grb2 adapter protein. (A) Immunoprecipitation and immunoblot detection of s-SHIP in ES cell lysates. Lysate from ES-TL1 cells cultured in LIF was immunoprecipitated with the P2C6 anti-SHIP monoclonal antibody, separated on gels, transferred to membranes, and probed with P2C6, revealing 104-kd and 97-kd proteins (lane 5). No tyrosine phosphorylation of these proteins was detected when they were probed with the 4G10 anti-phosphotyrosine antibody. For comparison, lysates from 293T cells transfected with SHIP cDNA (lane 1) and s-SHIP cDNA (lane 2) were included in the blots. To further assess the tyrosine phosphorylation status of s-SHIP, timed LIF stimulation studies were performed. ES-TL1 cells incubated for 5 hours without LIF were stimulated with 2000 U/mL LIF for 0, 2, 5, or 10 minutes and were rapidly lysed. Equal amounts of total protein were immunoprecipitated with the P2C6 antibody and probed separately with the P2C6 and 4G10 antibodies (lanes 6-9). No tyrosine phosphorylation of s-SHIP was detected at any time point with the 4G10 antibody. For comparison, A20 8-lymphoid cells were stimulated with antiIgG antibody for 0 or 5 minutes, lysed, immunoprecipitated with P2C6, and probed with P2C6 and 4G10 (lanes 3, 4), showing prominent tyrosine phosphorylation of SHIP at 5 minutes. Molecular mass standards are indicated on the right. (B) s-SHIP associates with Grb2 but not Shc in ES cells. ES-TL1 cell lysates were prepared and immunoprecipitated with the P2C8 anti-SHIP monoclonal antibody. Resolved immunoprecipitates were then blotted with antibodies specific for SHIP, Grb2, mSos1, or Shc (lane 1). Whole cell lysates from ES-TL1 cells were also included to confirm the expression of these proteins in ES cells (lane 2). (C) Grb2 associates with s-SHIP in ES cells. ES-TL1 cell lysate was prepared and immunoprecipitated with an antiGrb2 polyclonal antibody. Resolved immunoprecipitate was then blotted with the P2C6 anti-SHIP monoclonal antibody (lane 3). For comparison, whole cell lysate from WEHI-231 cells (lane 1) and 293T cells trans-

ected with s-SHIP cDNA (lane 2) were included. (D) Subcellular localization of s-SHIP protein in ES cells. Whole cell lysate, cytosol, and membrane fractions from ES-TLI cells were prepared as described. One milligram total protein from each fraction was immunoprecipitated with the P2C6 antiSHIP monoclonal antibody, and equal volumes of immunoprecipitate from each preparation were separated on gels, transferred, and blotted with the P2C6 antiSHIP monoclonal antibody (lanes 2-4). For comparison, whole cell lysate from 293T cells transfected with s-SHIP cDNA was included (lane 1). The major predicted open-reading frame (ORF) in s-SHIP mRNA begins with a Kozak consensus ATO that is 3' to the 44-nucleotide SSR (FIG. 2). This ATG and its associated ORF of 928 amino acids (aa) is predicted to yield a translated product of 104 kd. Immunoprecipitation and blotting with the antiSHIP monoclonal antibody P2C6, a kind gift of Drs. David Lucas and Larry Rohrschneider, revealed a SHIP protein in ES cell lysates with an apparent molecular weight (MW) of approximately 104 kd, consistent with the predicted MW (FIG. 6A). The P2C6 antibody reacts with a region of SHIP from aa-866 to aa-1020 that, based on the cDNA sequence, should also be present in the s-SHIP isoform. This smaller s-SHIP isoform is not detected in the B-lymphoid cell lines A20 and WEHI-231 (FIG. 6A-C). In addition, the endogenous s-SHIP protein immunoprecipitated from ES cells comigrated with the translated product of the s-SHIP cDNA when expressed after transfection of a non-ES cell line, 293T (FIG. 6A). Thus, this approximately 104-kd species represents the s-SHIP protein translated from the s-SHIP mRNA in ES cells, and not the COOH-terminal truncation product of SHIP with a similar MW identified by Damen et al. Furthermore, the inventors found that s-SHIP appeared as a doublet of approximately 104/97 kd in ES cells and in transfected 293T cells (FIG. 6A-D). This doublet presumably represents the translation products of 2 different s-SHIP mRNAs (928-aa and 867-aa [MW, 97.7 kd], respectively) generated by the alternative 183 nucleotide splice reaction identified in hematopoietic cells that also takes place in ES cells (FIG. 1A).

[0064] s-SHIP Forms a Complex with Grb2 and is Present Constitutively at the Membrane in Embryonic Stem Cells

[0065] The SHIP isoform expressed in mature hematopoietic cells is tyrosine phosphorylated on stimulation by growth factor, immune complexes, or BCR engagement. Phosphorylated SHIP is found associated with the adapter protein Shc, which facilitates SHIP recruitment to the plasma membrane, where it can then act on phosphatidylinositol substrates such as PIP3. However, the inventors found that s-SHIP is not tyrosine phosphorylated in either ES cells grown in LIF at steady state or ES cells deprived of LIF for 5 hours and subsequently stimulated with 2x LIF (FIG. 6A). Furthermore, s-SHIP in ES cells grown in LIF did not associate with Shc (FIG. 6B). Instead, immunoprecipitation of s-SHIP by the P2C6 anti-SHIP antibody coimmunoprecipitated the adapter protein Grb2. Similarly, immunoprecipitation with a poly clonal antibody specific for Grb2 coimmunoprecipitated s-SHIP (FIG. 6C). These results demonstrate an *in vivo* association between s-SHIP and the major adapter protein Grb2 in totipotent stem cells that does not require tyrosine phosphorylation of s-SHIP. s-SHIP does not appear to be associated with either Shc or mSos1 in ES cells, suggesting that it may have different preferences for partnering than the SHIP isoform (FIG. 6B). Immunoblot-

ting of ES cell lysates confirmed that Shc and mSos1 are expressed in ES cells. To further assess the potential for s-SHIP to play a signaling role in primitive stem cells, the inventors prepared cytosolic and membrane fractions of ES cells. Immunoprecipitation of s-SHIP from these subcellular fractions (FIG. 6D) demonstrates the presence of s-SHIP protein in the membrane fraction of ES cells. This membrane localization of s-SHIP and its association with a major adapter protein indicate a role for s-SHIP in signaling pathways active in primitive stem cells. s-SHIP demonstrates significant homology with the human 110-kd signaling inositol polyphosphate 5'-phosphatase

[0066] Clustal W Sequence Analysis revealed that s-SHIP and the human SHIP isoform SIP-110 (GenBank accession number U50040), described by Kavanaugh et al., share 78% nucleotide identity. Of note, Kavanaugh et al predicted a 976-aa protein (calculated MW, 109 kd) based on an ATG initiation codon at position 19 of GenBank accession number U50040. This ATG initiation site lacks strong Kozak consensus features. However, a second ATG initiation codon at position 160 displays a strong Kozak consensus sequence of CAnCATGG and would predict a translated protein of 929 aa (calculated MW, 104 kd). This shorter ORF of SIP-110 shares 88% amino acid identity with the s-SHIP ORF. Nucleotides 43-2786 of human SIP-110 cDNA are identical to nucleotides 787-3537 of human 145-kd SHIP cDNA (GenBank accession number U50041). Reminiscent of s-SHIP nucleotides 1-42 of SIP-110 are not found in the 145-kd SHIP cDNA. Kavanaugh et al put that SIP-110 is a splice variant of the 145-kd SHIP. However, the inventors hypothesized that SIP-110 may represent the human homologue of s-SHIP and may arise by alternative promoter use. To confirm this, the inventors conducted a BlastN query of the first 120 nucleotides of SIP-110 in the Celera Human Genome-Unassembled Fragments database. The inventors found 2 unassembled and uncharacterized genomic fragments (Celera accession numbers GA_x4N24A5JORM: 1 0.262 and GA_x4N24A6F9UD: 1.508) that span the first exon of SIP-110. These genomic fragments revealed that the first 42 nucleotides of SIP-110 are found in the SHIP intronic sequence and are followed directly by an 88-nucleotide sequence representing an internal SHIP exon corresponding to nucleotides 787-874 of 145-kd SHIP (FIG. 7A). Thus, analogous to s-SHIP, the first exon of SIP-110 is comprised of a 42-nucleotide SSR-like region unique to SIP-110 and an adjacent 88-nucleotide exon shared by both SIP-110 and 145-kd SHIP. The first exons of SIP-110 and s-SHIP show 82% nucleotide identity (FIG. 7B). These results establish that SIP-110 is the human homologue of s-SHIP.

[0067] Discussion

[0068] The SHIP protein is a key signaling component that participates in controlling the responses of several different hematopoietic cell types in the adult mouse, 1-3, 13, 16, 25. Results provide the first evidence that a SHIP isoform plays a specific role in the biologic composition of stem cell populations. Four lines of evidence support this hypothesis: (1) Totipotent ES cells express the s-SHIP isoform exclusively, (2) s-SHIP partners preferentially with Grb2 in ES cells, (3) s-SHIP is present constitutively in the membrane fraction of ES cells, and (4) s-SHIP expression within the hematopoietic compartment is restricted to fetal and adult hematopoietic stem cells. Results also suggest the evolution

of a transcription control mechanism that promotes the expression of s-SHIP in Stem cell populations.

[0069] The striking discordance between stem cells and mature hematopoietic cells in the expression of s-SHIP mRNA suggests a distinct signaling role for this SHIP isoform in stem cells. The SH2 domain of SHIP allows it to participate in signal transduction pathways in mature hematopoietic cells that involve partnering with Shc or binding to ITM motifs of receptors. The lack of an SH2 domain in s-SHIP may change its binding preferences and, therefore, the pathways with which it interacts. Consistent with this hypothesis, the inventors detected no association of s-SHIP with Shc in ES cells at steady state or after LIF stimulation. The inventors did find an association of s-SHIP with Grb2 in ES cells in the absence of tyrosine phosphorylation. Several groups have shown that SHIP can associate with Grb2 in stimulated hematopoietic cells through an interaction of the SH3 domain of Grb2 and the proline-rich motifs of SHIP. s-SHIP contains these same proline-rich motifs. In addition to SH3 domains, Grb2 contains an SH2 domain that enables its binding to other signal transduction components or receptors at the cell membrane. Grb2, through its SH2 domain, could recruit s-SHIP to tyrosine-phosphorylated receptors that are important in the biologic makeup of ES cells and HSCs. Thus, the absence of an SH2 domain may not preclude s-SHIP from acting at the cell membrane, but it may alter how it is recruited to the cell membrane and which signaling pathways it impacts.

[0070] Membrane recruitment of s-SHIP would enable its inositol 5"-phosphatase domain to access phosphatidylinositols such as PIP3 and to influence proliferation, differentiation, or apoptosis of stem cell populations. Because the association of s-SHIP with Grb2 does not appear to require tyrosine phosphorylation, this complex is likely to be present in quiescent stem cell populations. This preformed complex could rapidly associate with receptors that become tyrosine phosphorylated after basal level growth factor stimulation, enabling s-SHIP to prevent the accumulation of PIP3 to significant levels. In this way, s-SHIP could participate in the process of maintaining a stem cell population in a quiescent state. Furthermore, analogous to the proposal that SHIP interferes with the mSos1/Shc/Grb2 complex of the MAPK pathway in mature cells, one can envision a competition in stem cells between s-SHIP and mSos1 for Grb2. The outcome of this competition may influence the decision to remain quiescent or to activate the Ras/MAPK pathway that triggers proliferation and differentiation.

[0071] FIG. 7 depicts the organization of the first axon of SIP-110, the human homolog of s-SHIP. (A) Genomic sequence of the SIP-110 first exon and adjacent intronic sequence as compiled from the Celera Human Genome-Unassembled Fragments database (Celera accession numbers GA_x4N24A5.JORM: 1 0.262 and GA_x4N24A6F9UD:1.508). Uppercase letters represent the nucleotides in the SIP-110 first exon, and lowercase letters represent the intronic sequence immediately flanking this exon. The 42 nucleotides enclosed in the shaded box indicate the SSR-like region, and the 88 nucleotides in the clear box represent those nucleotides found in both the SIP-110 and the human 145-kd SHIP cDNAs. Based on the genomic fragment sequences, position 1 is listed as "T" rather than as the "C" assigned in the SIP-110 cDNA (GenBsnk accession number U50040). Numbers 787 and 874 indicate the posi-

tion of the corresponding nucleotide in the human 145-kd SHIP cDNA sequence (Gen Bank accession number U50041). (B) Clustal W alignment of the first exon sequences of human SIP-110 and murine s-SHIP. Matching nucleotides are shaded gray. Overall, the first axons of SIP-110 and s-SHIP show 82% nucleotide identity.

[0072] FIG. 8 demonstrates the decrease in s-SHIP expression after electroporation of embryonic stem cells with anti-SHIP shRNA. The electroporation conditions were as follows: 10 µg of protein were loaded into a 4-12% Bis-Tris gel (Invitrogen), 250V, 500 µF, 15 µg of plasmid, and sample was left to rest on ice, in cold PBS, for 30 minutes before being placed in a warm media.

[0073] The identification of a distinct SHIP isoform expressed from an internal site within the SHIP gene suggests the possibility that the recently reported SHIP-null mice may not be absolute nulls for expression from the SHIP locus. 1-3,25,48-50 The mutation strategy used by both groups involved the insertional mutation of the first exon that encodes a portion of the SH2 domain at the amino terminus of the SHIP isoform. This insertional mutation strategy clearly leads to the ablation of the SHIP isoform in mature hematopoietic cells. However, one would not predict that expression of the s-SHIP isoform in the embryo or in HSCs would be affected given that the s-SHIP first exon consists of the terminal 44 nucleotides of intron V, together with exon 6 of SHIP. This region is approximately 27 kb downstream of the 145-kd SHIP promoter. Nevertheless, ablation of SHIP expression by this strategy may lead to the dysregulation of s-SHIP expression by an unknown mechanism. In preliminary experiments, the inventors were unable to detect s-SHIP protein expression from total bone marrow of adult C57BL/6 mice in which the first exon of SHIP was insertionally mutated (data not shown). If it can be determined that s-SHIP expression during embryogenesis and hematopoietic development is intact in these SHIP-null strains, one might predict a novel phenotype in mice designed to be null for both s-SHIP and SHIP.

[0074] Kavanaugh et al" cloned and characterized the human SHIP isoform, SIP-110 that lacks an SH2 domain. They cloned SIP-110 cDNA (GenBank accession number U50040) from a human placenta cDNA expression library based on its affinity for a Grb2 SH3 domain in the absence of tyrosine phosphorylation. The overall structure of SIP-110 was similar to s-SHIP. However, SIP-110 was described as a 976-aa protein with an estimated molecular weight of 110 kd. Although the origin of the first 42 nucleotides of SIP-110 within the human SHIP gene was unknown, it was proposed that SIP-110 results from an alternative splice event. Analysis of the structure and the genomic location of the first exon of SIP-110 confirms that SIP-110 is the human homologue of s-SHIP. Furthermore, the structure and internal location of the SIP-110 first exon within the SHIP gene indicates that SIP-110 arises through alternative promoter use rather than as a splice variant, as was previously proposed. Although there are 2 potential ORFs for SIP-110 that predict proteins of 976 aa and 929 aa, the distal ATG initiation codon has Kozak consensus features that may favor translation of the 929-aa, 104-kd protein, which more closely resembles s-SHIP. Results demonstrate that s-SHIP is expressed in murine HSCs. Because cord blood within placenta is known to be enriched for HSCs, the inventors hypothesize that the SIP-110 cDNA isolated by Kavanaugh

et al" may have originated from cord blood HSC cDNA present in the placenta library.

[0075] In vitro studies with recombinant SIP-110 confirmed that it can bind Grb2, but its inositol 5"-phosphatase activity is unaffected by Grb2 binding." Furthermore, SIP-110 did not associate with Shc. These results can be extrapolated to s-SHIP, and they suggest that the purpose of Grb2 binding is not to alter s-SHIP enzymatic activity but rather to direct the subcellular localization of this activity.

[0076] Geier et al similarly found a 100-kd isoform of SHIP in both human and murine bone marrow using a polyclonal antibody to an amino acid sequence of murine SHIP (as 670 to as 868) that is also present in s-SHIP. Interestingly, they also found that a 100-kd isoform was the most prominent species in human peripheral blood mononuclear cells. Examination of the human ML-1 myeloblastic leukemia cell line revealed the presence of a 100-kd SHIP isoform and a 105-kd isoform and the absence of higher MW isoforms. When these ML-1 myeloblasts were induced to differentiate into monocytes in the presence of 12-O-tetradecanoylphorbol-13-acetate, higher MW isoforms (175 kd, 145 kd, and 130 kd) appeared, whereas the lower MW isoforms (105 kd, 100 kd) were no longer detectable. These results with ML-1 cells indicate that as human myeloid cells differentiate, human SHIP expression changes from the lower MW 105-kd and 100-kd isoforms to the higher MW isoforms. This is analogous to what the inventors found with s-SHIP and SHIP isoforms in murine hematopoietic cell development, and it suggests that the lower MW human isoforms characterized by Geier et al represent the SIP-110 identified by Kavanaugh et al." However, it is unclear why in their studies human peripheral blood displayed only the

lower MW 100-kd isoform. Wolf et al describe an additional 110-kd SHIP isoform, SHIP, which is the product of an out-of-frame splice event with a deletion of 167 nucleotides in the C-terminal region. This clearly represents a different isoform than s-SHIP. It remains to be determined which SHIP-related proteins, among these several isoforms encoding 100 kd to 110 kd, predominate during different stages of hematopoietic development.

[0077] Recently, Krause et al elegantly demonstrated that a single murine adult bone marrow stem cell can repopulate hematopoietic cells and a diverse array of nonhematopoietic epithelial tissues, including lung, liver, gastrointestinal tract, and skin. Given that s-SHIP is expressed in totipotent ES cells and at least a subset of bone marrow HSCs, this study raises the possibility that s-SHIP expression may serve to further characterize and delineate the pluripotent bone marrow stem cell capable of multi-organ engraftment that Krause et al identified.

[0078] It will be seen that the objects set forth above, and those made apparent from the foregoing description, are efficiently attained and since certain changes may be made in the above construction without departing from the scope of the invention, it is intended that all matters contained in the foregoing description or shown in the accompanying drawings shall be interpreted as illustrative and not in a limiting sense.

[0079] It is also to be understood that the following claims are intended to cover all of the generic and specific features of the invention herein described, and all statements of the scope of the invention which, as a matter of language, might be the to fall therebetween. Now that the invention has been described,

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Cys 3035	Cys	Thr	Cys	Cys	Thr	Gly 3040	Cys	Thr	Ala	Gly	Cys 3045	Thr	Cys	Thr
Thr 3050	Cys	Thr	Thr	Gly	Cys	Cys 3055	Thr	Ala	Gly	Cys	Thr 3060	Thr	Cys	Ala
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Thr 3110	Gly	Thr	Gly	Gly	Thr	Cys 3115	Cys	Ala	Ala	Gly	Ala 3120	Ala	Gly	Thr
Gly 3125	Thr	Gly	Cys	Thr	Gly	Cys 3130	Thr	Gly	Gly	Cys	Thr 3135	Gly	Cys	Cys
Ala 3140	Cys	Ala	Cys	Thr	Gly	Thr 3145	Gly	Cys	Gly	Gly	Cys 3150	Ala	Gly	Ala
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Ala 3185	Cys	Ala	Gly	Ala	Cys	Ala 3190	Gly	Cys	Ala	Gly	Ala 3195	Cys	Ala	Gly
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Ala 3290	Ala	Gly	Ala	Thr	Ala	Thr 3295	Ala	Ala	Ala	Thr	Ala 3300	Ala	Thr	Ala
Ala 3305	Thr	Ala	Thr	Thr	Ala	Thr 3310	Thr	Ala	Ala	Thr	Ala 3315	Ala	Thr	Ala
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Thr Gly Thr Gly Thr Cys 3965	Cys Thr Thr Gly Gly 3970	Thr Thr Ala Cys 3975

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 4070 4075 4080
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 <213> ORGANISM: Mus musculus
 <400> SEQUENCE: 2

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225				230					235						240
Gly	Ala	Ala	Thr	Cys	Thr	Ala	Cys	Cys	Ala	Ala	Cys	Ala	Gly	Gly	Cys
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Gly	Thr	Thr	Gly	Ala	Gly	Thr	Cys	Thr	Gly	Gly	Gly	Ala	Ala	Ala	Cys
			340					345						350	
Thr	Gly	Ala	Thr	Cys	Gly	Thr	Thr	Ala	Ala	Gly	Ala	Ala	Gly	Thr	Cys
		355					360						365		
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Thr	Gly	Gly	Thr	Gly	Ala	Thr	Thr	Thr	Thr	Gly	Gly	Thr	Gly	Gly	Ala
	450					455					460				
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465					470					475					480
Ala	Thr	Cys	Cys	Thr	Gly	Ala	Gly	Gly	Ala	Ala	Gly	Gly	Ala	Ala	Thr
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			500					505					510		
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			565						570					575	
Gly	Ala	Gly	Cys	Cys	Thr	Gly	Ala	Cys	Ala	Thr	Gly	Ala	Thr	Cys	Ala
		580						585					590		
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 645 650 655

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Cys Cys Ala Gly Ala Gly Cys Ala Thr Gly Ala Gly Ala Ala Thr Cys
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Cys Cys Thr Cys Cys Thr Thr Gly Gly Gly Gly Thr Thr Cys Gly Thr
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Cys Ala	Ala Ala Ala Cys	Thr	Ala Thr Ala Thr	Gly	Ala Ala Cys
1040		1045		1050	
Ala Thr	Cys Cys Thr Gly	Cys	Gly Gly Thr Thr	Cys	Cys Thr Gly
1055		1060		1065	
Gly Cys	Cys Cys Thr Gly	Gly	Gly Ala Gly Ala	Cys	Ala Ala Gly
1070		1075		1080	
Ala Ala	Gly Cys Thr Ala	Ala	Gly Cys Cys Cys	Ala	Thr Thr Thr
1085		1090		1095	
Ala Ala	Cys Ala Thr Cys	Ala	Cys Cys Cys Ala	Cys	Cys Gly Cys
1100		1105		1110	
Thr Thr	Cys Ala Cys Cys	Cys	Ala Cys Cys Thr	Cys	Thr Thr Cys
1115		1120		1125	
Thr Gly	Gly Cys Thr Thr	Gly	Gly Gly Gly Ala	Thr	Cys Thr Cys
1130		1135		1140	
Ala Ala	Cys Thr Ala Cys	Cys	Gly Cys Gly Thr	Gly	Gly Ala Gly
1145		1150		1155	
Cys Thr	Gly Cys Cys Cys	Ala	Cys Thr Thr Gly	Gly	Gly Ala Gly
1160		1165		1170	
Gly Cys	Ala Gly Ala Gly	Gly	Cys Cys Ala Thr	Cys	Ala Thr Cys
1175		1180		1185	
Cys Ala	Gly Ala Ala Gly	Ala	Thr Cys Ala Ala	Gly	Cys Ala Ala
1190		1195		1200	
Cys Ala	Gly Cys Ala Gly	Thr	Ala Thr Thr Cys	Ala	Gly Ala Cys
1205		1210		1215	
Cys Thr	Thr Cys Thr Gly	Gly	Cys Cys Cys Ala	Cys	Gly Ala Cys
1220		1225		1230	
Cys Ala	Ala Cys Thr Gly	Cys	Thr Cys Cys Thr	Gly	Gly Ala Gly
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1340		1345		1350	
Cys Ala	Gly Ala Ala Ala	Gly	Cys Ala Ala Cys	Ala	Gly Gly Gly
1355		1360		1365	
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Ala Gly Thr Gly Ala Cys 1475	Cys Ala Cys Ala Gly Cys 1480	Cys Cys Thr 1485
Gly Thr Cys Thr Thr Thr 1490	Gly Cys Cys Ala Cys Gly 1495	Thr Thr Thr 1500
Gly Ala Ala Gly Cys Gly 1505	Gly Gly Ala Gly Thr Cys 1510	Ala Cys Ala 1515
Thr Cys Thr Cys Ala Ala 1520	Thr Thr Cys Gly Thr Cys 1525	Thr Cys Cys 1530
Ala Ala Gly Ala Ala Thr 1535	Gly Gly Thr Cys Cys Thr 1540	Gly Gly Cys 1545
Ala Cys Thr Gly Thr Ala 1550	Gly Ala Thr Ala Gly Cys 1555	Cys Ala Ala 1560
Gly Gly Gly Cys Ala Gly 1565	Ala Thr Cys Gly Ala Gly 1570	Thr Thr Thr 1575
Cys Thr Thr Gly Cys Ala 1580	Thr Gly Cys Thr Ala Cys 1585	Gly Cys Cys 1590
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1790						1795						1800		
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1850						1855						1860		
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1865						1870						1875		
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1880						1885						1890		
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1895						1900						1905		
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1910						1915						1920		
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1925						1930						1935		
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2000						2005						2010		
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2030						2035						2040		
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2075						2080						2085		
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2090						2095						2100		
Gly	Ala	Gly	Ala	Thr	Gly	Ala	Thr	Cys	Ala	Ala	Thr	Cys	Cys	Ala
2105						2110						2115		
Ala	Ala	Cys	Thr	Ala	Cys	Ala	Thr	Thr	Gly	Cys	Cys	Ala	Ala	Cys
2120						2125						2130		
Cys	Gly	Ala	Gly	Gly	Thr	Cys	Cys	Cys	Thr	Gly	Cys	Cys	Cys	Cys
2135						2140						2145		

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Gly 2180	Gly	Ala	Ala	Ala	Gly	Gly 2185	Thr	Gly	Gly	Ala	Ala 2190	Gly	Cys	Thr
Cys 2195	Thr	Gly	Cys	Thr	Cys	Cys 2200	Ala	Gly	Gly	Ala	Gly 2205	Gly	Ala	Cys
Cys 2210	Thr	Gly	Cys	Thr	Gly	Cys 2215	Thr	Gly	Ala	Cys	Gly 2220	Ala	Ala	Gly
Cys 2225	Cys	Cys	Gly	Ala	Gly	Ala 2230	Thr	Gly	Thr	Thr	Thr 2235	Gly	Ala	Gly
Ala 2240	Ala	Cys	Cys	Cys	Ala	Cys 2245	Thr	Gly	Thr	Ala	Thr 2250	Gly	Gly	Ala
Thr 2255	Cys	Cys	Gly	Thr	Gly	Ala 2260	Gly	Thr	Thr	Cys	Cys 2265	Thr	Thr	Cys
Cys 2270	Cys	Thr	Ala	Ala	Gly	Cys 2275	Thr	Gly	Gly	Thr	Gly 2280	Cys	Cys	Cys
Ala 2285	Gly	Gly	Ala	Ala	Ala	Gly 2290	Ala	Gly	Cys	Ala	Gly 2295	Gly	Ala	Gly
Thr 2300	Cys	Thr	Cys	Cys	Cys	Ala 2305	Ala	Gly	Ala	Thr	Gly 2310	Cys	Thr	Gly
Cys 2315	Gly	Gly	Ala	Ala	Gly	Gly 2320	Ala	Gly	Cys	Cys	Cys 2325	Cys	Cys	Gly
Cys 2330	Cys	Cys	Thr	Gly	Thr	Cys 2335	Cys	Ala	Gly	Ala	Cys 2340	Cys	Cys	Ala
Gly 2345	Gly	Ala	Ala	Thr	Cys	Thr 2350	Cys	Ala	Thr	Cys	Ala 2355	Cys	Cys	Cys
Ala 2360	Gly	Cys	Ala	Thr	Cys	Gly 2365	Thr	Gly	Cys	Thr	Cys 2370	Cys	Cys	Cys
Ala 2375	Ala	Ala	Gly	Cys	Cys	Cys 2380	Ala	Ala	Gly	Ala	Gly 2385	Gly	Thr	Gly
Gly 2390	Ala	Gly	Ala	Gly	Thr	Gly 2395	Thr	Cys	Ala	Ala	Gly 2400	Gly	Gly	Gly
Ala 2405	Cys	Ala	Ala	Gly	Cys	Ala 2410	Ala	Ala	Cys	Ala	Gly 2415	Gly	Cys	Cys
Cys 2420	Cys	Thr	Gly	Thr	Gly	Cys 2425	Cys	Thr	Gly	Thr	Cys 2430	Cys	Thr	Thr
Gly 2435	Gly	Cys	Cys	Cys	Cys	Ala 2440	Cys	Ala	Cys	Cys	Cys 2445	Cys	Gly	Gly
Ala 2450	Thr	Cys	Cys	Gly	Cys	Thr 2455	Cys	Cys	Thr	Thr	Thr 2460	Ala	Cys	Cys
Thr 2465	Gly	Thr	Thr	Cys	Thr	Thr 2470	Cys	Thr	Thr	Cys	Thr 2475	Gly	Cys	Thr
Gly 2480	Ala	Gly	Gly	Gly	Cys	Ala 2485	Gly	Ala	Ala	Thr	Gly 2490	Ala	Cys	Cys
Ala 2495	Gly	Thr	Gly	Gly	Gly	Gly 2500	Ala	Cys	Ala	Ala	Gly 2505	Ala	Gly	Cys
Cys 2510	Ala	Ala	Gly	Gly	Gly	Ala 2515	Ala	Gly	Cys	Cys	Cys 2520	Ala	Ala	Gly
Gly	Cys	Cys	Thr	Cys	Ala	Gly	Cys	Cys	Ala	Gly	Thr	Thr	Cys	Cys

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2525	2530	2535
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Gly Thr 2555	Cys Ala Ala Gly 2560	Ala Gly Gly Cys Cys Thr 2565
Ala Ala 2570	Gly Cys Cys Thr 2575	Thr Cys Cys Ala Gly Gly 2580
Gly Ala 2585	Ala Ala Thr Gly 2590	Ala Gly Cys Cys Ala Gly 2595
Ala Cys 2600	Ala Ala Cys Ala 2605	Cys Cys Cys Ala Thr Cys 2610
Gly Cys 2615	Thr Cys Cys Ala 2620	Cys Gly Gly Cys Cys Ala 2625
Cys Thr 2630	Gly Cys Cys Ala 2635	Gly Thr Cys Ala Ala Gly 2640
Cys Cys 2645	Thr Gly Cys Thr 2650	Gly Thr Cys Cys Thr Gly 2655
Cys Thr 2660	Gly Cys Ala Ala 2665	Cys Ala Thr Thr Cys Cys 2670
Gly Gly 2675	Cys Ala Gly Ala 2680	Ala Cys Thr Ala Cys 2685
Gly Ala 2690	Cys Ala Ala Cys 2695	Ala Cys Ala Gly Ala Ala 2700
Cys Cys 2705	Cys Cys Ala Cys 2710	Cys Ala Thr Gly Gly Cys 2715
Cys Ala 2720	Cys Cys Gly Cys 2725	Cys Ala Ala Gly Ala Gly 2730
Gly Gly 2735	Gly Cys Thr Gly 2740	Cys Thr Thr Gly Gly Cys 2745
Ala Cys 2750	Thr Gly Cys Cys 2755	Ala Thr Gly Cys Ala Gly 2760
Gly Cys 2765	Thr Gly Cys Thr 2770	Gly Gly Thr Gly Ala Thr 2775
Ala Gly 2780	Cys Cys Thr Gly 2785	Ala Gly Gly Ala Ala 2790
Cys Ala 2795	Cys Ala Ala Ala 2800	Gly Cys Ala Gly Ala Cys 2805
Cys Gly 2810	Cys Cys Thr Cys 2815	Thr Cys Thr Cys Ala Gly 2820
Gly Cys 2825	Cys Thr Cys Thr 2830	Cys Thr Cys Ala Gly Gly 2835
Cys Cys 2840	Thr Cys Thr Thr 2845	Gly Gly Ala Gly Gly Ala 2850
Cys Cys 2855	Thr Gly Cys Thr 2860	Ala Gly Cys Thr Cys Thr 2865
Thr Gly 2870	Cys Cys Thr Ala 2875	Gly Cys Thr Thr Cys Ala 2880
Cys Cys 2885	Cys Ala Gly Gly 2890	Cys Thr Gly Thr Gly Thr 2895
Thr Thr 2900	Thr Thr Thr Thr 2905	Cys Ala Gly Gly Ala Ala 2910

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Gly	Cys	Cys	Thr	Cys	Ala	Cys	Thr	Thr	Cys	Thr	Cys	Thr	Gly	Thr
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2930						2935					2940			
Cys	Thr	Gly	Cys	Thr	Gly	Gly	Cys	Thr	Gly	Cys	Cys	Ala	Cys	Ala
2945						2950					2955			
Cys	Thr	Gly	Thr	Gly	Cys	Gly	Gly	Cys	Ala	Gly	Ala	Thr	Gly	Cys
2960						2965					2970			
Thr	Ala	Ala	Ala	Gly	Cys	Thr	Gly	Gly	Ala	Thr	Gly	Ala	Cys	Ala
2975						2980					2985			
Ala	Ala	Cys	Gly	Cys	Ala	Cys	Gly	Cys	Cys	Ala	Thr	Ala	Cys	Ala
2990						2995					3000			
Gly	Ala	Cys	Ala	Gly	Cys	Ala	Gly	Ala	Cys	Ala	Gly	Cys	Gly	Gly
3005						3010					3015			
Cys	Ala	Cys	Thr	Gly	Gly	Gly	Thr	Cys	Thr	Cys	Ala	Gly	Ala	Ala
3020						3025					3030			
Cys	Thr	Thr	Gly	Gly	Ala	Thr	Thr	Cys	Cys	Thr	Gly	Gly	Gly	Cys
3035						3040					3045			
Cys	Thr	Thr	Cys	Thr	Thr	Cys	Cys	Ala	Gly	Thr	Cys	Gly	Cys	Cys
3050						3055					3060			
Gly	Thr	Thr	Thr	Thr	Ala	Ala	Ala	Gly	Ala	Ala	Ala	Gly	Gly	Ala
3065						3070					3075			
Ala	Cys	Thr	Ala	Ala	Cys	Gly	Gly	Ala	Gly	Cys	Thr	Gly	Cys	Thr
3080						3085					3090			
Cys	Ala	Thr	Cys	Cys	Gly	Ala	Gly	Gly	Gly	Thr	Gly	Ala	Ala	Gly
3095						3100					3105			
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3110						3115					3120			
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3125						3130					3135			
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3140						3145					3150			
Gly	Thr	Gly	Cys	Thr	Gly	Thr	Gly	Thr	Thr	Ala	Ala	Gly	Thr	Gly
3155						3160					3165			
Cys	Thr	Thr	Thr	Ala	Thr	Gly	Ala	Ala	Cys	Ala	Thr	Thr	Thr	Gly
3170						3175					3180			
Thr	Cys	Gly	Gly	Gly	Cys	Thr	Gly	Gly	Cys	Cys	Thr	Cys	Cys	Ala
3185						3190					3195			
Gly	Thr	Gly	Cys	Thr	Gly	Ala	Gly	Gly	Thr	Gly	Cys	Cys	Ala	Gly
3200						3205					3210			
Thr	Cys	Ala	Gly	Cys	Cys	Thr	Gly	Ala	Ala	Cys	Cys	Cys	Thr	Ala
3215						3220					3225			
Thr	Gly	Cys	Cys	Cys	Ala	Gly	Gly	Cys	Cys	Cys	Ala	Cys	Thr	Ala
3230						3235					3240			
Ala	Thr	Cys	Cys	Cys	Ala	Ala	Ala	Thr	Gly	Gly	Thr	Gly	Gly	Gly
3245						3250					3255			
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3260						3265					3270			
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3305						3310					3315			
Gly	Gly	Gly	Cys	Thr	Cys	Thr	Ala	Cys	Thr	Gly	Cys	Ala	Gly	Gly
3320						3325					3330			
Gly	Ala	Cys	Cys	Cys	Gly	Ala	Ala	Cys	Ala	Gly	Thr	Cys	Thr	Gly
3335						3340					3345			
Cys	Ala	Thr	Gly	Gly	Cys	Thr	Ala	Ala	Gly	Thr	Gly	Gly	Cys	Ala
3350						3355					3360			
Cys	Ala	Ala	Gly	Gly	Ala	Gly	Cys	Cys	Thr	Gly	Gly	Cys	Cys	Cys
3365						3370					3375			
Thr	Gly	Thr	Cys	Cys	Ala	Gly	Cys	Thr	Thr	Cys	Ala	Gly	Ala	Gly
3380						3385					3390			
Ala	Thr	Cys	Cys	Ala	Ala	Gly	Cys	Thr	Gly	Cys	Thr	Thr	Thr	Thr
3395						3400					3405			
Thr	Gly	Cys	Thr	Gly	Gly	Gly	Gly	Thr	Thr	Cys	Thr	Gly	Thr	Cys
3410						3415					3420			
Ala	Cys	Ala	Gly	Gly	Cys	Cys	Thr	Gly	Ala	Thr	Cys	Cys	Thr	Cys
3425						3430					3435			
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3440						3445					3450			
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3455						3460					3465			
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3470						3475					3480			
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3485						3490					3495			
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3500						3505					3510			
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3515						3520					3525			
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3530						3535					3540			
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3545						3550					3555			
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3560						3565					3570			
Cys	Ala	Cys	Thr	Gly	Gly	Ala	Gly	Gly	Thr	Gly	Gly	Gly	Cys	Ala
3575						3580					3585			
Gly	Cys	Thr	Ala	Thr	Cys	Ala	Cys	Cys	Ala	Thr	Ala	Cys	Cys	Cys
3590						3595					3600			
Thr	Gly	Ala	Gly	Thr	Thr	Gly	Gly	Gly	Cys	Cys	Ala	Ala	Gly	Cys
3605						3610					3615			
Cys	Cys	Ala	Cys	Cys	Cys	Cys	Ala	Cys	Cys	Cys	Cys	Thr	Ala	Cys
3620						3625					3630			
Cys	Cys	Thr	Gly	Cys	Ala	Ala	Cys	Ala	Thr	Thr	Thr	Cys	Thr	Gly
3635						3640					3645			
Ala	Thr	Gly	Thr	Trp	Cys	Thr	Gly	Ala	Gly	Gly	Ala	Ala	Gly	Ala
3650						3655					3660			
Gly	Thr	Cys	Thr	Cys	Cys	Ala	Cys	Cys	Ala	Thr	Ala	Gly	Thr	Cys

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3665	3670	3675
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3680	3685	3690
Cys Thr Cys Cys Ala Gly	Cys Cys Thr Gly Cys	Thr Ala Thr Cys
3695	3700	3705
Ala Gly Gly Gly Ala Ala	Gly Gly Thr Gly Ala	Gly Cys Ala Thr
3710	3715	3720
Thr Gly Gly Thr Cys Cys	Cys Ala Gly Gly Cys	Thr Cys Thr Cys
3725	3730	3735
Ala Ala Ala Ala Thr Ala	Gly Thr Gly Cys Ala	Gly Cys Cys Thr
3740	3745	3750
Cys Thr Thr Cys Thr Thr	Cys Cys Cys Ala Ala	Gly Cys Thr Cys
3755	3760	3765
Thr Gly Gly Gly Gly Thr	Gly Cys Ala Cys Cys	Cys Thr Gly Thr
3770	3775	3780
Gly Thr Cys Cys Thr Thr	Gly Gly Thr Thr Ala	Cys Cys Ala Gly
3785	3790	3795
Gly Ala Gly Ala Cys Thr	Ala Gly Gly Gly Thr	Thr Gly Thr Gly
3800	3805	3810
Ala Thr Ala Thr Cys Thr	Thr Thr Thr Cys Thr	Thr Gly Thr Cys
3815	3820	3825
Thr Thr Gly Cys Thr Thr	Thr Thr Thr Gly Ala	Thr Ala Thr Ala
3830	3835	3840
Thr Cys Ala Gly Gly Ala	Thr Thr Ala Ala Thr	Gly Thr Ala Gly
3845	3850	3855
Gly Ala Ala Ala Cys Cys	Ala Gly Ala Cys Cys	Thr Ala Gly Ala
3860	3865	3870
Thr Thr Ala Thr Thr Cys	Ala Gly Gly Ala Gly	Ala Gly Thr Ala
3875	3880	3885
Gly Gly Thr Ala Thr Ala	Thr Cys Cys Cys Cys	Thr Gly Thr Gly
3890	3895	3900
Thr Thr Thr Cys Cys Cys	Ala Gly Thr Cys Thr	Gly Ala Gly Thr
3905	3910	3915
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Gly Cys Cys Thr Thr Thr	Cys Thr Ala	
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 <211> LENGTH: 4147
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

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Ala Thr Gly Thr Thr Cys Ala Cys Cys Thr Thr Gly Thr Cys Cys Cys
20 25 30
Cys Thr Gly Cys Cys Cys Cys Cys Ala Gly Ala Gly Ala Ala Gly Thr
35 40 45
Cys Ala Thr Cys Cys Gly Gly Ala Cys Cys Cys Thr Cys Cys Cys Ala
50 55 60

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Thr Cys Cys Cys Thr Gly Gly Ala Gly Thr Cys Thr Cys Thr Gly Cys
 65 70 75 80
 Ala Gly Ala Gly Gly Thr Thr Ala Thr Thr Thr Gly Ala Cys Cys Ala
 85 90 95
 Gly Cys Ala Gly Cys Thr Cys Thr Cys Cys Cys Cys Gly Gly Gly Cys
 100 105 110
 Cys Thr Cys Cys Gly Thr Cys Cys Ala Cys Gly Thr Cys Cys Thr Cys
 115 120 125
 Ala Gly Gly Thr Thr Cys Cys Thr Gly Gly Thr Gly Ala Gly Gly Cys
 130 135 140
 Cys Ala Ala Thr Cys Cys Cys Ala Thr Cys Ala Ala Cys Ala Thr Gly
 145 150 155 160
 Gly Thr Gly Thr Cys Cys Ala Ala Gly Cys Thr Cys Ala Gly Cys Cys
 165 170 175
 Ala Ala Cys Thr Gly Ala Cys Ala Ala Gly Cys Cys Thr Gly Thr Thr
 180 185 190
 Gly Thr Cys Ala Thr Cys Cys Ala Thr Thr Gly Ala Ala Gly Ala Cys
 195 200 205
 Ala Ala Gly Gly Thr Cys Ala Ala Gly Gly Cys Cys Thr Thr Gly Cys
 210 215 220
 Thr Gly Cys Ala Cys Gly Ala Gly Gly Thr Cys Cys Thr Gly Ala
 225 230 235 240
 Gly Thr Cys Thr Cys Cys Gly Cys Ala Cys Cys Gly Gly Cys Cys Cys
 245 250 255
 Thr Cys Cys Cys Thr Thr Ala Thr Cys Cys Cys Thr Cys Cys Ala Gly
 260 265 270
 Thr Cys Ala Cys Cys Thr Thr Thr Gly Ala Gly Gly Thr Gly Ala Ala
 275 280 285
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 290 295 300
 Ala Thr Thr Cys Cys Thr Cys Ala Gly Ala Ala Ala Thr Gly Cys
 305 310 315 320
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 340 345 350
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 370 375 380
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 385 390 395 400
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 405 410 415
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 420 425 430
 Ala Thr Thr Thr Cys Thr Gly Ala Ala Thr Ala Ala Gly Thr Thr Gly
 435 440 445
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 Cys Ala Gly Ala Gly Ala Ala Gly Gly Ala Gly Ala Ala Gly Ala Thr

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Ala Thr Cys Ala Gly Cys Cys Ala Cys Ala Thr Cys Thr Gly Thr Ala
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Cys Thr Gly Ala Cys Ala Ala Cys Gly Thr Gly Ala Ala Gly Ala Cys
900 905 910

Ala Gly Gly Cys Ala Thr Thr Gly Cys Ala Ala Ala Cys Ala Cys Ala
915 920 925

Cys Thr Gly Gly Gly Gly Ala Ala Cys Ala Ala Gly Gly Gly Ala Gly
930 935 940

Cys Cys Gly Thr Gly Gly Gly Gly Gly Thr Gly Thr Cys Gly Thr Thr
945 950 955 960

Cys Ala Thr Gly Thr Thr Cys Ala Ala Thr Gly Gly Ala Ala Cys Cys
965 970 975

Thr Cys Cys Thr Thr Ala Gly Gly Gly Thr Thr Cys Gly Thr Cys Ala
980 985 990

Ala Cys Ala Gly Cys Cys Ala Cys Thr Thr Gly Ala Cys Thr Thr Cys
995 1000 1005

Ala Gly Gly Ala Ala Gly Thr Gly Ala Ala Ala Ala Gly Ala Ala
1010 1015 1020

Ala Cys Thr Cys Ala Gly Gly Cys Gly Ala Ala Ala Cys Cys Ala
1025 1030 1035

Ala Ala Ala Cys Thr Ala Thr Ala Thr Gly Ala Ala Cys Ala Thr
1040 1045 1050

Thr Cys Thr Cys Cys Gly Gly Thr Thr Cys Cys Thr Gly Gly Cys
1055 1060 1065

Cys Cys Thr Gly Gly Gly Cys Gly Ala Cys Ala Ala Gly Ala Ala
1070 1075 1080

Gly Cys Thr Gly Ala Gly Thr Cys Cys Cys Thr Thr Thr Ala Ala
1085 1090 1095

Cys Ala Thr Cys Ala Cys Thr Cys Ala Cys Cys Gly Cys Thr Thr
1100 1105 1110

Cys Ala Cys Gly Cys Ala Cys Cys Thr Cys Thr Thr Cys Thr Gly
1115 1120 1125

Gly Thr Thr Thr Gly Gly Gly Gly Ala Thr Cys Thr Thr Ala Ala
1130 1135 1140

Cys Thr Ala Cys Cys Gly Thr Gly Thr Gly Gly Ala Thr Cys Thr
1145 1150 1155

Gly Cys Cys Thr Ala Cys Cys Thr Gly Gly Gly Ala Gly Gly Cys
1160 1165 1170

Ala Gly Ala Ala Ala Cys Cys Ala Thr Cys Ala Thr Cys Cys Ala
1175 1180 1185

Gly Ala Ala Ala Ala Thr Cys Ala Ala Gly Cys Ala Gly Cys Ala
1190 1195 1200

Gly Cys Ala Gly Thr Ala Cys Gly Cys Ala Gly Ala Cys Cys Thr
1205 1210 1215

Cys Cys Thr Gly Thr Cys Cys Cys Ala Cys Gly Ala Cys Cys Ala
1220 1225 1230

Gly Cys Thr Gly Cys Thr Cys Ala Cys Ala Gly Ala Gly Ala Gly
1235 1240 1245

Gly Ala Gly Gly Gly Ala Gly Cys Ala Gly Ala Ala Gly Gly Thr
1250 1255 1260

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Cys	Thr	Thr	Cys	Cys	Thr	Ala	Cys	Ala	Cys	Thr	Thr	Cys	Gly	Ala
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1280					1285							1290		
Gly	Thr	Thr	Thr	Gly	Cys	Cys	Cys	Cys	Ala	Ala	Cys	Cys	Thr	Ala
1295					1300							1305		
Cys	Cys	Gly	Thr	Thr	Thr	Thr	Gly	Ala	Gly	Ala	Gly	Ala	Cys	Thr
1310						1315						1320		
Gly	Ala	Cys	Thr	Cys	Gly	Gly	Gly	Ala	Cys	Ala	Ala	Ala	Thr	Ala
1325					1330							1335		
Cys	Gly	Cys	Cys	Thr	Ala	Cys	Ala	Cys	Cys	Ala	Ala	Gly	Cys	Ala
1340						1345						1350		
Gly	Ala	Ala	Ala	Gly	Cys	Gly	Ala	Cys	Ala	Gly	Gly	Gly	Ala	Thr
1355						1360						1365		
Gly	Ala	Ala	Gly	Thr	Ala	Cys	Ala	Ala	Cys	Thr	Thr	Gly	Cys	Cys
1370						1375						1380		
Thr	Thr	Cys	Cys	Thr	Gly	Gly	Thr	Gly	Thr	Gly	Ala	Cys	Cys	Gly
1385						1390						1395		
Ala	Gly	Thr	Cys	Cys	Thr	Cys	Thr	Gly	Gly	Ala	Ala	Gly	Thr	Cys
1400						1405						1410		
Thr	Thr	Ala	Thr	Cys	Cys	Cys	Cys	Thr	Gly	Gly	Thr	Gly	Cys	Ala
1415						1420						1425		
Cys	Gly	Thr	Gly	Gly	Thr	Gly	Thr	Gly	Thr	Cys	Ala	Gly	Thr	Cys
1430						1435						1440		
Thr	Thr	Ala	Thr	Gly	Gly	Cys	Ala	Gly	Thr	Ala	Cys	Cys	Ala	Gly
1445						1450						1455		
Cys	Gly	Ala	Cys	Ala	Thr	Cys	Ala	Thr	Gly	Ala	Cys	Gly	Ala	Gly
1460						1465						1470		
Thr	Gly	Ala	Cys	Cys	Ala	Cys	Ala	Gly	Cys	Cys	Cys	Thr	Gly	Thr
1475						1480						1485		
Cys	Thr	Thr	Thr	Gly	Cys	Cys	Ala	Cys	Ala	Thr	Thr	Thr	Gly	Ala
1490						1495						1500		
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1505						1510						1515		
Cys	Cys	Ala	Gly	Thr	Thr	Thr	Gly	Thr	Cys	Thr	Cys	Cys	Ala	Ala
1520						1525						1530		
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1535						1540						1545		
Thr	Gly	Thr	Thr	Gly	Ala	Cys	Ala	Gly	Cys	Cys	Ala	Ala	Gly	Gly
1550						1555						1560		
Ala	Cys	Ala	Gly	Ala	Thr	Thr	Gly	Ala	Gly	Thr	Thr	Thr	Cys	Thr
1565						1570						1575		
Cys	Ala	Gly	Gly	Thr	Gly	Cys	Thr	Ala	Thr	Gly	Cys	Cys	Ala	Cys
1580						1585						1590		
Ala	Thr	Thr	Gly	Ala	Ala	Gly	Ala	Cys	Cys	Ala	Ala	Gly	Thr	Cys
1595						1600						1605		
Cys	Cys	Ala	Gly	Ala	Cys	Cys	Ala	Ala	Ala	Thr	Thr	Cys	Thr	Ala
1610						1615						1620		
Cys	Cys	Thr	Gly	Gly	Ala	Gly	Thr	Thr	Cys	Cys	Ala	Cys	Thr	Cys
1625						1630						1635		
Gly	Ala	Gly	Cys	Thr	Gly	Cys	Thr	Thr	Gly	Gly	Ala	Gly	Ala	Gly

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1640	1645	1650
Thr Thr Thr Thr Gly Thr	Cys Ala Ala Gly Ala Gly	Thr Cys Ala
1655	1660	1665
Gly Gly Ala Ala Gly Gly	Ala Gly Ala Ala Ala Ala	Thr Gly Ala
1670	1675	1680
Ala Gly Ala Ala Gly Gly	Ala Ala Gly Thr Gly Ala	Gly Gly Gly
1685	1690	1695
Gly Gly Ala Gly Cys Thr	Gly Gly Thr Gly Gly Thr	Gly Ala Ala
1700	1705	1710
Gly Thr Thr Thr Gly Gly	Thr Gly Ala Gly Ala Cys	Thr Cys Thr
1715	1720	1725
Thr Cys Cys Ala Ala Ala	Gly Cys Thr Gly Ala Ala	Gly Cys Cys
1730	1735	1740
Cys Ala Thr Thr Ala Thr	Cys Thr Cys Thr Gly Ala	Cys Cys Cys
1745	1750	1755
Thr Gly Ala Gly Thr Ala	Cys Cys Thr Gly Cys Thr	Ala Gly Ala
1760	1765	1770
Cys Cys Ala Gly Cys Ala	Cys Ala Thr Cys Cys Thr	Cys Ala Thr
1775	1780	1785
Cys Ala Gly Cys Ala Thr	Cys Ala Ala Gly Thr Cys	Cys Thr Cys
1790	1795	1800
Thr Gly Ala Cys Ala Gly	Cys Gly Ala Cys Gly Ala	Ala Thr Cys
1805	1810	1815
Cys Thr Ala Thr Gly Gly	Cys Gly Ala Gly Gly Gly	Cys Thr Gly
1820	1825	1830
Cys Ala Thr Thr Gly Cys	Cys Cys Thr Thr Cys Gly	Gly Thr Thr
1835	1840	1845
Ala Gly Ala Gly Gly Cys	Cys Ala Cys Ala Gly Ala	Ala Ala Cys
1850	1855	1860
Gly Cys Ala Gly Cys Thr	Gly Cys Cys Cys Ala Thr	Cys Thr Ala
1865	1870	1875
Cys Ala Cys Gly Cys Cys	Thr Cys Thr Cys Ala Cys	Cys Cys Ala
1880	1885	1890
Cys Cys Ala Thr Gly Gly	Gly Gly Ala Gly Thr Thr	Gly Ala Cys
1895	1900	1905
Ala Gly Gly Cys Cys Ala	Cys Thr Thr Cys Cys Ala	Gly Gly Gly
1910	1915	1920
Gly Gly Ala Gly Ala Thr	Cys Ala Ala Gly Cys Thr	Gly Cys Ala
1925	1930	1935
Gly Ala Cys Cys Thr Cys	Thr Cys Ala Gly Gly Gly	Cys Ala Ala
1940	1945	1950
Gly Ala Cys Gly Ala Gly	Gly Gly Ala Gly Ala Ala	Gly Cys Thr
1955	1960	1965
Cys Thr Ala Thr Gly Ala	Cys Thr Thr Thr Gly Thr	Gly Ala Ala
1970	1975	1980
Gly Ala Cys Gly Gly Ala	Gly Cys Gly Thr Gly Ala	Thr Gly Ala
1985	1990	1995
Ala Thr Cys Cys Ala Gly	Thr Gly Gly Gly Cys Cys	Ala Ala Ala
2000	2005	2010
Gly Ala Cys Cys Cys Thr	Gly Ala Ala Gly Ala Gly	Cys Cys Thr
2015	2020	2025

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Cys Ala	Cys Cys Ala Gly	Cys	Cys Ala Cys Gly	Ala	Cys Cys Cys
2030		2035		2040	
Cys Ala	Thr Gly Ala Ala	Gly	Cys Ala Gly Thr	Gly	Gly Gly Ala
2045		2050		2055	
Ala Gly	Thr Cys Ala Cys	Thr	Ala Gly Cys Ala	Gly	Gly Gly Cys
2060		2065		2070	
Cys Cys	Cys Thr Cys Cys	Gly	Thr Gly Cys Ala	Gly	Thr Gly Gly
2075		2080		2085	
Cys Thr	Cys Cys Ala Gly	Cys	Ala Thr Cys Ala	Cys	Thr Gly Ala
2090		2095		2100	
Ala Ala	Thr Cys Ala Thr	Cys	Ala Ala Cys Cys	Cys	Cys Ala Ala
2105		2110		2115	
Cys Thr	Ala Cys Ala Thr	Gly	Gly Gly Ala Gly	Thr	Gly Gly Gly
2120		2125		2130	
Gly Cys	Cys Cys Thr Thr	Thr	Gly Gly Gly Cys	Cys	Ala Cys Cys
2135		2140		2145	
Ala Ala	Thr Gly Cys Cys	Cys	Cys Thr Gly Cys	Ala	Cys Gly Thr
2150		2155		2160	
Gly Ala	Ala Gly Cys Ala	Gly	Ala Cys Cys Thr	Thr	Gly Thr Cys
2165		2170		2175	
Cys Cys	Cys Thr Gly Ala	Cys	Cys Ala Gly Cys	Ala	Gly Cys Cys
2180		2185		2190	
Cys Ala	Cys Ala Gly Cys	Cys	Thr Gly Gly Ala	Gly	Cys Thr Ala
2195		2200		2205	
Cys Gly	Ala Cys Cys Ala	Gly	Cys Cys Gly Cys	Cys	Cys Ala Ala
2210		2215		2220	
Gly Gly	Ala Cys Thr Cys	Cys	Cys Cys Gly Cys	Thr	Gly Gly Gly
2225		2230		2235	
Gly Cys	Cys Cys Thr Gly	Cys	Ala Gly Gly Gly	Gly	Ala Gly Ala
2240		2245		2250	
Ala Ala	Gly Thr Cys Cys	Thr	Cys Cys Gly Ala	Cys	Ala Cys Cys
2255		2260		2265	
Thr Cys	Cys Cys Gly Gly	Cys	Cys Ala Gly Cys	Cys	Gly Cys Cys
2270		2275		2280	
Cys Ala	Thr Ala Thr Cys	Ala	Cys Cys Cys Ala	Ala	Gly Ala Ala
2285		2290		2295	
Gly Thr	Thr Thr Thr Thr	Ala	Cys Cys Cys Thr	Cys	Ala Ala Cys
2300		2305		2310	
Ala Gly	Cys Ala Ala Ala	Cys	Cys Gly Gly Gly	Gly	Thr Cys Thr
2315		2320		2325	
Cys Cys	Cys Thr Cys Cys	Cys	Ala Gly Gly Ala	Cys	Ala Cys Ala
2330		2335		2340	
Gly Gly	Ala Gly Thr Cys	Ala	Ala Gly Gly Cys	Cys	Cys Ala Gly
2345		2350		2355	
Thr Gly	Ala Cys Cys Thr	Gly	Gly Gly Gly Ala	Ala	Gly Ala Ala
2360		2365		2370	
Cys Gly	Cys Ala Gly Gly	Gly	Gly Ala Cys Ala	Cys	Gly Cys Thr
2375		2380		2385	
Gly Cys	Cys Thr Cys Ala	Gly	Gly Ala Gly Gly	Ala	Cys Cys Thr
2390		2395		2400	

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Gly 2405	Cys	Cys	Gly	Cys	Thr	Gly 2410	Ala	Cys	Gly	Ala	Ala 2415	Gly	Cys	Cys
Cys 2420	Gly	Ala	Gly	Ala	Thr	Gly 2425	Thr	Thr	Thr	Gly	Ala 2430	Gly	Ala	Ala
Cys 2435	Cys	Cys	Cys	Cys	Thr	Gly 2440	Thr	Ala	Thr	Gly	Gly 2445	Gly	Thr	Cys
Cys 2450	Cys	Thr	Gly	Ala	Gly	Thr 2455	Thr	Cys	Cys	Thr	Thr 2460	Cys	Cys	Cys
Thr 2465	Ala	Ala	Gly	Cys	Cys	Thr 2470	Gly	Cys	Thr	Cys	Cys 2475	Cys	Ala	Gly
Gly 2480	Ala	Ala	Gly	Gly	Ala	Cys 2485	Cys	Ala	Gly	Gly	Ala 2490	Ala	Thr	Cys
Cys 2495	Cys	Cys	Cys	Ala	Ala	Ala 2500	Ala	Thr	Gly	Cys	Cys 2505	Gly	Cys	Gly
Gly 2510	Ala	Ala	Gly	Gly	Ala	Ala 2515	Cys	Cys	Cys	Cys	Cys 2520	Gly	Cys	Cys
Cys 2525	Thr	Gly	Cys	Cys	Cys	Gly 2530	Gly	Ala	Ala	Cys	Cys 2535	Cys	Gly	Gly
Cys 2540	Ala	Thr	Cys	Thr	Thr	Gly 2545	Thr	Cys	Gly	Cys	Cys 2550	Cys	Ala	Gly
Cys 2555	Ala	Thr	Cys	Gly	Thr	Gly 2560	Cys	Thr	Cys	Ala	Cys 2565	Cys	Ala	Ala
Ala 2570	Gly	Cys	Cys	Cys	Ala	Gly 2575	Gly	Ala	Gly	Gly	Cys 2580	Thr	Gly	Ala
Thr 2585	Cys	Gly	Cys	Gly	Gly	Cys 2590	Gly	Ala	Gly	Gly	Gly 2595	Gly	Cys	Cys
Cys 2600	Gly	Gly	Cys	Ala	Ala	Gly 2605	Cys	Ala	Gly	Gly	Thr 2610	Gly	Cys	Cys
Cys 2615	Gly	Cys	Gly	Cys	Cys	Cys 2620	Cys	Gly	Gly	Cys	Thr 2625	Gly	Cys	Gly
Cys 2630	Thr	Cys	Cys	Thr	Thr	Cys 2635	Ala	Cys	Gly	Thr	Gly 2640	Cys	Thr	Cys
Ala 2645	Thr	Cys	Cys	Thr	Cys	Thr 2650	Gly	Cys	Cys	Gly	Ala 2655	Gly	Gly	Gly
Cys 2660	Ala	Gly	Gly	Gly	Cys	Gly 2665	Gly	Cys	Cys	Gly	Gly 2670	Cys	Gly	Gly
Gly 2675	Gly	Ala	Cys	Ala	Ala	Gly 2680	Ala	Gly	Cys	Cys	Ala 2685	Ala	Gly	Gly
Gly 2690	Ala	Ala	Gly	Cys	Cys	Cys 2695	Ala	Ala	Gly	Ala	Cys 2700	Cys	Cys	Cys
Gly 2705	Gly	Thr	Cys	Ala	Gly	Cys 2710	Thr	Cys	Cys	Cys	Ala 2715	Gly	Gly	Cys
Cys 2720	Cys	Cys	Gly	Gly	Thr	Gly 2725	Cys	Cys	Gly	Gly	Cys 2730	Cys	Ala	Ala
Gly 2735	Ala	Gly	Gly	Cys	Cys	Cys 2740	Ala	Thr	Cys	Ala	Ala 2745	Gly	Cys	Cys
Thr 2750	Thr	Cys	Cys	Ala	Gly	Ala 2755	Thr	Cys	Gly	Gly	Ala 2760	Ala	Ala	Thr
Cys 2765	Ala	Ala	Cys	Cys	Ala	Gly 2770	Cys	Ala	Gly	Ala	Cys 2775	Cys	Cys	Cys
Gly	Cys	Cys	Cys	Ala	Cys	Cys	Cys	Cys	Gly	Ala	Cys	Gly	Cys	Cys

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2780	2785	2790
Gly Cys 2795	Gly Gly Cys Cys 2800	Gly Cys Cys Gly Cys Thr 2805
Ala Gly 2810	Thr Cys Ala Ala 2815	Gly Ala Gly Cys Cys Cys 2820
Gly Gly 2825	Thr Gly Cys Thr 2830	Gly Cys Ala Cys Cys Thr 2835
Gly Cys 2840	Ala Cys Thr Cys 2845	Cys Ala Ala Gly Gly Gly 2850
Cys Gly 2855	Ala Cys Thr Ala 2860	Cys Gly Cys Gly Ala 2865
Cys Ala 2870	Cys Cys Gly Ala 2875	Gly Cys Thr Cys Cys Cys 2880
Thr Cys 2885	Ala Cys Gly Gly 2890	Cys Ala Ala Gly Cys Ala 2895
Gly Cys 2900	Cys Gly Gly Ala 2905	Gly Gly Ala Gly Gly Gly 2910
Ala Cys 2915	Cys Ala Gly Gly 2920	Gly Cys Cys Thr Cys Thr 2925
Cys Ala 2930	Gly Gly Ala Cys 2935	Thr Gly Cys Cys Ala Thr 2940
Gly Thr 2945	Gly Ala Ala Gly 2950	Cys Cys Thr Cys Ala 2955
Ala Gly 2960	Cys Thr Gly Cys 2965	Cys Ala Cys Thr Gly Ala 2970
Gly Gly 2975	Gly Ala Gly Cys 2980	Cys Cys Ala Gly Ala Gly 2985
Cys Gly 2990	Gly Cys Gly Thr 2995	Gly Ala Ala Gly Cys Cys 3000
Gly Gly 3005	Ala Cys Cys Cys 3010	Thr Cys Thr Cys Cys Cys 3015
Ala Cys 3020	Cys Thr Cys Cys 3025	Thr Gly Cys Thr Gly Gly 3030
Cys Thr 3035	Cys Cys Thr Gly 3040	Cys Cys Ala Gly Cys 3045
Cys Thr 3050	Ala Thr Gly Cys 3055	Ala Ala Gly Gly Cys Thr 3060
Thr Gly 3065	Thr Thr Thr Thr 3070	Cys Ala Gly Gly Ala Ala 3075
Gly Cys 3080	Cys Thr Ala Gly 3085	Thr Thr Cys Thr Gly 3090
Gly Gly 3095	Cys Cys Cys Ala 3100	Cys Ala Gly Ala Gly Thr 3105
Cys Thr 3110	Gly Cys Cys Thr 3115	Thr Gly Ala Gly Ala 3120
Ala Gly 3125	Cys Ala Cys Cys 3130	Ala Ala Gly Thr Gly Cys 3135
Gly Gly 3140	Cys Thr Gly Gly 3145	Ala Ala Gly Ala Ala Ala 3150
Gly Cys 3155	Ala Cys Ala Cys 3160	Cys Ala Gly Ala Cys Gly 3165

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Ala Ala Cys Ala Ala Ala Cys Ala Gly Thr Cys Thr Gly Gly Gly	3170	3175	3180
Thr Cys Cys Cys Cys Ala Gly Cys Thr Cys Gly Cys Thr Cys Thr	3185	3190	3195
Thr Gly Gly Thr Ala Cys Thr Thr Gly Gly Gly Ala Cys Cys Cys	3200	3205	3210
Cys Ala Gly Thr Gly Cys Cys Thr Cys Gly Thr Thr Gly Ala Gly	3215	3220	3225
Gly Gly Cys Gly Cys Cys Ala Thr Thr Cys Thr Gly Ala Ala Gly	3230	3235	3240
Ala Ala Ala Gly Gly Ala Ala Cys Thr Gly Cys Ala Gly Cys Gly	3245	3250	3255
Cys Cys Gly Ala Thr Thr Thr Gly Ala Gly Gly Gly Thr Gly Gly	3260	3265	3270
Ala Gly Ala Thr Ala Thr Ala Gly Ala Thr Ala Ala Thr Ala Ala	3275	3280	3285
Thr Ala Ala Thr Ala Thr Thr Ala Ala Thr Ala Ala Thr Ala Ala	3290	3295	3300
Thr Ala Ala Thr Gly Gly Cys Cys Ala Cys Ala Thr Gly Gly Ala	3305	3310	3315
Thr Cys Gly Ala Ala Cys Ala Cys Thr Cys Ala Thr Gly Ala Thr	3320	3325	3330
Gly Thr Gly Cys Cys Ala Ala Ala Thr Gly Cys Thr Gly Thr Gly	3335	3340	3345
Cys Thr Ala Ala Gly Thr Gly Cys Thr Thr Thr Ala Cys Gly Ala	3350	3355	3360
Ala Cys Ala Thr Thr Cys Gly Thr Cys Ala Thr Ala Thr Cys Ala	3365	3370	3375
Gly Gly Ala Thr Gly Ala Cys Cys Thr Cys Gly Ala Gly Ala Gly	3380	3385	3390
Cys Thr Gly Ala Gly Gly Cys Thr Cys Thr Ala Gly Cys Ala Cys	3395	3400	3405
Cys Thr Ala Ala Ala Ala Cys Cys Ala Cys Gly Thr Gly Cys Cys	3410	3415	3420
Cys Ala Ala Ala Cys Cys Cys Ala Cys Cys Ala Gly Thr Thr Thr	3425	3430	3435
Ala Ala Ala Ala Cys Gly Gly Thr Gly Thr Gly Thr Gly Thr Thr	3440	3445	3450
Cys Gly Gly Ala Gly Gly Gly Gly Thr Gly Ala Ala Ala Gly Cys	3455	3460	3465
Ala Thr Thr Ala Ala Gly Ala Ala Gly Cys Cys Cys Ala Gly Thr	3470	3475	3480
Gly Cys Cys Cys Thr Cys Cys Thr Gly Gly Ala Gly Thr Gly Ala	3485	3490	3495
Gly Ala Cys Ala Ala Gly Gly Gly Cys Thr Cys Gly Gly Cys Cys	3500	3505	3510
Thr Thr Ala Ala Gly Gly Ala Gly Cys Thr Gly Ala Ala Gly Ala	3515	3520	3525
Gly Thr Cys Thr Gly Gly Gly Thr Ala Gly Cys Thr Thr Gly Thr	3530	3535	3540

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Thr	Thr	Ala	Gly	Gly	Gly	Thr	Ala	Cys	Ala	Ala	Gly	Ala	Ala	Gly
3545						3550					3555			
Cys	Cys	Thr	Gly	Thr	Thr	Cys	Thr	Gly	Thr	Cys	Cys	Ala	Gly	Cys
3560						3565					3570			
Thr	Thr	Cys	Ala	Gly	Thr	Gly	Ala	Cys	Ala	Cys	Ala	Ala	Gly	Cys
3575						3580					3585			
Thr	Gly	Cys	Thr	Thr	Thr	Ala	Gly	Cys	Thr	Ala	Ala	Ala	Gly	Thr
3590						3595					3600			
Cys	Cys	Cys	Gly	Cys	Gly	Gly	Gly	Thr	Thr	Cys	Cys	Gly	Gly	Cys
3605						3610					3615			
Ala	Thr	Gly	Gly	Cys	Thr	Ala	Gly	Gly	Cys	Thr	Gly	Ala	Gly	Ala
3620						3625					3630			
Gly	Cys	Ala	Gly	Gly	Gly	Ala	Thr	Cys	Thr	Ala	Cys	Cys	Thr	Gly
3635						3640					3645			
Gly	Cys	Thr	Thr	Cys	Thr	Cys	Ala	Gly	Thr	Thr	Cys	Thr	Thr	Thr
3650						3655					3660			
Gly	Gly	Thr	Thr	Gly	Gly	Ala	Ala	Gly	Gly	Ala	Gly	Cys	Ala	Gly
3665						3670					3675			
Gly	Ala	Ala	Ala	Thr	Cys	Ala	Gly	Cys	Thr	Cys	Cys	Thr	Ala	Thr
3680						3685					3690			
Thr	Cys	Thr	Cys	Cys	Ala	Gly	Thr	Gly	Gly	Ala	Gly	Ala	Gly	Ala
3695						3700					3705			
Thr	Cys	Thr	Gly	Gly	Cys	Cys	Thr	Cys	Ala	Gly	Cys	Thr	Thr	Gly
3710						3715					3720			
Gly	Gly	Cys	Thr	Ala	Gly	Ala	Gly	Ala	Thr	Gly	Cys	Cys	Ala	Ala
3725						3730					3735			
Gly	Gly	Cys	Cys	Thr	Gly	Thr	Gly	Cys	Cys	Ala	Gly	Gly	Thr	Thr
3740						3745					3750			
Cys	Cys	Cys	Thr	Gly	Thr	Gly	Cys	Cys	Cys	Thr	Cys	Cys	Thr	Cys
3755						3760					3765			
Gly	Ala	Gly	Gly	Thr	Gly	Gly	Gly	Cys	Ala	Gly	Cys	Cys	Ala	Thr
3770						3775					3780			
Cys	Ala	Cys	Cys	Ala	Gly	Cys	Cys	Ala	Cys	Ala	Gly	Thr	Thr	Ala
3785						3790					3795			
Ala	Gly	Cys	Cys	Ala	Ala	Gly	Cys	Cys	Cys	Cys	Cys	Cys	Ala	Ala
3800						3805					3810			
Cys	Ala	Thr	Gly	Thr	Ala	Thr	Thr	Cys	Cys	Ala	Thr	Cys	Gly	Thr
3815						3820					3825			
Gly	Cys	Thr	Gly	Gly	Thr	Ala	Gly	Ala	Ala	Gly	Ala	Gly	Thr	Cys
3830						3835					3840			
Thr	Thr	Thr	Gly	Cys	Thr	Gly	Thr	Thr	Gly	Cys	Thr	Cys	Cys	Cys
3845						3850					3855			
Gly	Ala	Ala	Ala	Gly	Cys	Cys	Gly	Thr	Gly	Cys	Thr	Cys	Thr	Cys
3860						3865					3870			
Cys	Ala	Gly	Cys	Cys	Thr	Gly	Gly	Cys	Thr	Gly	Cys	Cys	Ala	Gly
3875						3880					3885			
Gly	Gly	Ala	Gly	Gly	Gly	Thr	Gly	Gly	Gly	Cys	Cys	Thr	Cys	Thr
3890						3895					3900			
Thr	Gly	Gly	Thr	Thr	Cys	Cys	Ala	Gly	Gly	Cys	Thr	Cys	Thr	Thr
3905						3910					3915			
Gly	Ala	Ala	Ala	Thr	Ala	Gly	Thr	Gly	Cys	Ala	Gly	Cys	Cys	Thr

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3920	3925	3930
Thr Thr Thr Cys Thr Thr	Cys Cys Thr Ala Thr	Cys Thr Cys Thr
3935	3940	3945
Gly Thr Gly Gly Cys Thr	Thr Thr Cys Ala Gly Cys	Thr Cys Thr
3950	3955	3960
Gly Cys Thr Thr Cys Cys	Thr Thr Gly Gly Thr Thr	Ala Thr Thr
3965	3970	3975
Ala Gly Gly Ala Gly Ala	Ala Thr Ala Gly Ala Thr	Gly Gly Gly
3980	3985	3990
Thr Gly Ala Thr Gly Thr	Cys Thr Thr Thr Cys Cys	Thr Thr Ala
3995	4000	4005
Thr Gly Thr Thr Gly Cys	Thr Thr Thr Thr Cys	Ala Ala Cys
4010	4015	4020
Ala Thr Ala Gly Cys Ala	Gly Ala Ala Thr Thr Ala	Ala Thr Gly
4025	4030	4035
Thr Ala Gly Gly Gly Ala	Gly Cys Thr Ala Ala Ala	Thr Cys Cys
4040	4045	4050
Ala Gly Thr Gly Gly Thr	Gly Thr Gly Thr Gly Thr	Gly Ala Ala
4055	4060	4065
Thr Gly Cys Ala Gly Ala	Ala Gly Gly Gly Ala Ala	Thr Gly Cys
4070	4075	4080
Ala Cys Cys Cys Cys Ala	Cys Ala Thr Thr Cys Cys	Cys Ala Thr
4085	4090	4095
Gly Ala Thr Gly Gly Ala	Ala Gly Thr Cys Thr Gly	Cys Gly Thr
4100	4105	4110
Ala Ala Cys Cys Ala Ala	Thr Ala Ala Ala Thr Thr	Gly Thr Gly
4115	4120	4125
Cys Cys Thr Thr Thr Cys	Thr Cys Ala Cys Thr Cys	Ala Ala Ala
4130	4135	4140
Ala Cys Cys Cys		
4145		

<210> SEQ ID NO 4
 <211> LENGTH: 457
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 4

Ala Ala Gly Cys Thr Gly Ala Thr Gly Thr Cys Ala Cys Thr Gly Cys
1 5 10 15
Thr Cys Thr Gly Cys Ala Ala Gly Gly Ala Gly Cys Thr Cys Cys Ala
20 25 30
Thr Gly Gly Gly Thr Ala Ala Cys Gly Gly Ala Gly Ala Gly Cys Cys
35 40 45
Cys Thr Gly Ala Gly Ala Gly Ala Gly Gly Gly Thr Gly Gly Gly
50 55 60
Gly Gly Ala Gly Cys Thr Thr Cys Ala Thr Gly Gly Gly Thr Ala Ala
65 70 75 80
Thr Gly Gly Gly Ala Gly Cys Cys Cys Cys Thr Ala Cys Cys Cys Ala
85 90 95
Cys Cys Cys Ala Gly Gly Ala Gly Gly Ala Thr Gly Gly Cys Cys Ala
100 105 110

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Cys Ala Gly Cys Ala Ala Gly Ala Gly Ala Ala Ala Gly Thr Gly Cys
 115 120 125

Thr Cys Ala Thr Thr Ala Gly Ala Gly Thr Gly Ala Cys Cys Cys Thr
 130 135 140

Gly Gly Gly Thr Cys Thr Cys Cys Thr Cys Thr Cys Thr Gly Thr Cys
 145 150 155 160

Cys Ala Gly Ala Thr Gly Thr Cys Thr Cys Thr Gly Cys Ala Gly Cys
 165 170 175

Ala Cys Thr Cys Ala Cys Ala Gly Thr Ala Ala Thr Thr Gly Gly Cys
 180 185 190

Cys Cys Ala Gly Gly Thr Gly Gly Ala Gly Thr Cys Thr Gly Gly Ala
 195 200 205

Ala Thr Gly Thr Thr Cys Cys Ala Gly Gly Cys Thr Thr Gly Thr Thr
 210 215 220

Gly Gly Ala Ala Gly Cys Thr Cys Thr Thr Gly Cys Thr Cys Thr Cys
 225 230 235 240

Ala Thr Ala Gly Ala Ala Thr Cys Thr Gly Ala Gly Cys Thr Cys Thr
 245 250 255

Ala Ala Cys Thr Gly Ala Gly Cys Thr Gly Gly Gly Ala Ala Ala Gly
 260 265 270

Thr Thr Gly Ala Thr Cys Ala Thr Thr Thr Gly Thr Thr Thr Ala Thr
 275 280 285

Thr Cys Cys Thr Thr Thr Thr Ala Gly Gly Gly Thr Ala Thr Thr Gly
 290 295 300

Gly Gly Gly Gly Gly Gly Cys Ala Cys Gly Gly Ala Thr Gly Thr Ala
 305 310 315 320

Thr Gly Cys Ala Thr Gly Cys Thr Gly Gly Thr Ala Thr Gly Thr Ala
 325 330 335

Thr Gly Cys Ala Thr Gly Cys Thr Gly Gly Gly Gly Ala Thr Gly Thr
 340 345 350

Ala Gly Gly Gly Cys Cys Thr Cys Ala Thr Gly Thr Gly Thr Gly Cys
 355 360 365

Thr Ala Ala Ala Thr Ala Cys Ala Thr Gly Thr Gly Cys Cys Thr Ala
 370 375 380

Thr Thr Cys Thr Gly Thr Ala Ala Thr Gly Thr Thr Thr Thr Cys Thr
 385 390 395 400

Thr Gly Thr Thr Thr Gly Thr Thr Thr Thr Thr Ala Ala Cys Thr Cys
 405 410 415

Ala Ala Ala Thr Thr Ala Ala Thr Thr Ala Gly Ala Gly Gly Cys Ala
 420 425 430

Gly Thr Thr Thr Cys Thr Cys Thr Gly Thr Thr Thr Ala Cys Cys Ala
 435 440 445

Gly Cys Cys Cys Gly Gly Gly Cys Cys
 450 455

<210> SEQ ID NO 5
 <211> LENGTH: 938
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <400> SEQUENCE: 5

Ala Ala Ala Thr Cys Ala Cys Cys Ala Cys Ala Cys Gly Gly Cys Cys
 1 5 10 15

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Ala Ala Thr Ala Cys Thr Cys Cys Cys Cys Cys Cys Ala Ala Cys
20 25 30

Thr Cys Cys Thr Cys Cys Cys Ala Ala Ala Thr Cys Cys Cys Thr
35 40 45

Cys Thr Ala Cys Cys Cys Ala Cys Thr Cys Ala Ala Ala Thr Thr Cys
50 55 60

Thr Thr Ala Thr Cys Thr Thr Gly Thr Ala Thr Thr Cys Thr Thr Thr
65 70 75 80

Ala Thr Cys Ala Thr Thr Ala Thr Thr Ala Thr Ala Cys Ala Thr Ala
85 90 95

Thr Gly Thr Gly Thr Ala Thr Ala Thr Ala Thr Gly Thr Gly Thr Gly
100 105 110

Thr Gly Thr Gly Thr Ala Thr Ala Thr Ala Thr Ala Thr Ala Thr Ala
115 120 125

Thr Ala Cys Thr Ala Thr Ala Thr Ala Cys Thr Gly Cys Thr Ala Ala
130 135 140

Thr Gly Ala Gly Thr Ala Ala Cys Ala Thr Thr Thr Ala Gly Thr Gly
145 150 155 160

Thr Thr Ala Thr Thr Cys Ala Thr Thr Gly Asn Thr Gly Cys Asn Thr
165 170 175

Gly Thr Thr Thr Asn Cys Ala Ala Thr Gly Asn Gly Cys Thr Thr Thr
180 185 190

Cys Cys Ala Gly Gly Asn Gly Gly Cys Thr Gly Gly Gly Gly Gly Gly
195 200 205

Ala Asn Gly Gly Cys Thr Cys Ala Gly Asn Gly Gly Gly Cys Ala Ala
210 215 220

Ala Ala Thr Thr Cys Thr Ala Gly Cys Thr Gly Cys Ala Cys Ala Ala
225 230 235 240

Gly Cys Cys Thr Ala Ala Gly Gly Ala Cys Cys Ala Gly Gly Gly Thr
245 250 255

Thr Cys Ala Gly Ala Thr Cys Cys Cys Cys Ala Ala Thr Ala Thr Ala
260 265 270

Ala Ala Gly Gly Cys Thr Gly Gly Cys Thr Gly Gly Ala Cys Ala Thr
275 280 285

Gly Gly Gly Gly Gly Cys Thr Thr Gly Cys Cys Thr Ala Thr Gly Ala
290 295 300

Thr Ala Cys Thr Ala Gly Cys Ala Thr Gly Cys Thr Thr Gly Cys Thr
305 310 315 320

Gly Gly Ala Ala Gly Cys Ala Ala Ala Gly Ala Cys Ala Gly Gly Gly
325 330 335

Ala Ala Thr Cys Cys Cys Thr Gly Gly Ala Gly Ala Cys Thr Thr Ala
340 345 350

Asn Ala Ala Thr Cys Thr Cys Ala Asn Ala Ala Gly Thr Gly Ala Thr
355 360 365

Cys Thr Gly Gly Gly Cys Thr Gly Gly Ala Cys Ala Gly Ala Cys Thr
370 375 380

Ala Gly Cys Thr Gly Ala Ala Cys Thr Gly Gly Cys Cys Ala Gly Cys
385 390 395 400

Thr Cys Thr Gly Gly Gly Thr Thr Cys Ala Thr Asn Ala Ala Asn Ala
405 410 415

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Ala Ala Cys Cys Cys Thr Asn Cys Cys Thr Cys Cys Ala Thr Ala Ala
420 425 430

Cys Ala Thr Ala Ala Ala Gly Thr Gly Thr Gly Ala Asn Gly Gly Ala
435 440 445

Asn Ala Ala Ala Gly Gly Cys Ala Cys Cys Thr Ala Ala Thr Gly Thr
450 455 460

Cys Ala Ala Cys Cys Thr Cys Ala Ala Ala Cys Cys Cys Cys Thr Ala
465 470 475 480

Cys Cys Thr Gly Cys Ala Thr Gly Thr Gly Cys Ala Cys Ala Cys Ala
485 490 495

Cys Ala Thr Ala Cys Ala Thr Cys Cys Ala Cys Ala Cys Cys Ala Cys
500 505 510

Ala Cys Ala Cys Ala Cys Ala Cys Gly Cys Ala Cys Ala Cys Ala Cys
515 520 525

Ala Cys Ala Cys Ala Cys Ala Cys Ala Cys Cys Ala Cys Ala Cys Ala
530 535 540

Cys Ala Cys Ala Cys Ala Cys Ala Cys Ala Cys Ala Cys Ala Ala Ala Thr Ala
545 550 555 560

Ala Ala Thr Ala Ala Gly Thr Ala Ala Ala Thr Ala Ala Ala Thr Ala
565 570 575

Ala Ala Ala Thr Ala Thr Thr Thr Ala Gly Cys Thr Cys Thr Cys Cys
580 585 590

Ala Gly Ala Cys Cys Ala Ala Ala Thr Cys Thr Thr Gly Gly Thr Gly
595 600 605

Ala Ala Ala Cys Cys Cys Ala Thr Gly Cys Ala Thr Thr Thr Gly Cys
610 615 620

Ala Thr Thr Thr Gly Thr Gly Thr Gly Thr Gly Thr Cys Cys Thr Ala
625 630 635 640

Cys Ala Ala Ala Cys Ala Cys Thr Gly Ala Ala Gly Gly Thr Thr Ala
645 650 655

Ala Gly Ala Ala Gly Cys Ala Thr Gly Cys Thr Cys Cys Thr Thr Ala
660 665 670

Gly Thr Ala Ala Thr Thr Thr Thr Ala Thr Ala Gly Cys Ala Gly Thr
675 680 685

Thr Thr Gly Cys Gly Thr Thr Thr Cys Cys Ala Gly Ala Thr Thr Gly
690 695 700

Ala Ala Ala Ala Cys Ala Gly Ala Thr Thr Cys Thr Ala Thr Ala Gly
705 710 715 720

Gly Cys Thr Ala Cys Ala Cys Ala Gly Thr Gly Cys Thr Ala Ala Ala
725 730 735

Thr Gly Gly Ala Thr Thr Ala Thr Gly Cys Thr Cys Ala Gly Ala Thr
740 745 750

Ala Cys Ala Gly Ala Thr Thr Gly Ala Ala Ala Ala Gly Gly Ala Thr
755 760 765

Ala Cys Ala Gly Ala Thr Thr Gly Ala Ala Ala Ala Gly Gly Gly Thr
770 775 780

Cys Gly Gly Gly Gly Thr Cys Thr Gly Gly Gly Cys Cys Ala Gly Gly
785 790 795 800

Ala Thr Gly Ala Cys Gly Gly Gly Cys Cys Ala Ala Cys Thr Ala Thr
805 810 815

Cys Thr Thr Thr Gly Cys Cys Cys Gly Gly Gly Cys Thr Thr Gly Thr

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	820							825										830
Cys	Cys	Thr	Thr	Cys	Ala	Gly	Gly	Gly	Ala	Ala	Gly	Gly	Gly	Thr	Thr			
	835						840					845						
Ala	Cys	Ala	Gly	Gly	Ala	Thr	Thr	Cys	Ala	Cys	Cys	Ala	Cys	Thr	Gly			
	850						855					860						
Gly	Gly	Gly	Thr	Gly	Thr	Gly	Gly	Cys	Cys	Thr	Ala	Thr	Cys	Thr	Gly			
	865					870				875					880			
Cys	Thr	Gly	Thr	Thr	Ala	Gly	Gly	Ala	Cys	Cys	Thr	Gly	Ala	Ala	Thr			
				885					890						895			
Thr	Gly	Cys	Cys	Thr	Gly	Gly	Ala	Gly	Thr	Gly	Thr	Thr	Thr	Cys	Thr			
				900				905							910			
Ala	Gly	Thr	Thr	Cys	Cys	Cys	Ala	Cys	Thr	Ala	Gly	Thr	Thr	Gly	Thr			
		915					920							925				
Thr	Gly	Ala	Ala	Cys	Thr	Thr	Thr	Ala	Cys									
	930						935											

<210> SEQ ID NO 6
 <211> LENGTH: 986
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 6

Gly	Cys	Ala	Asn	Thr	Cys	Thr	Gly	Ala	Gly	Gly	Ala	Cys	Thr	Cys	Thr
1			5						10					15	
Gly	Cys	Cys	Ala	Thr	Cys	Cys	Thr	Gly	Gly	Ala	Gly	Thr	Cys	Thr	Cys
			20					25					30		
Thr	Gly	Cys	Ala	Gly	Ala	Gly	Gly	Thr	Thr	Gly	Thr	Thr	Thr	Gly	Ala
			35				40						45		
Cys	Cys	Ala	Ala	Cys	Ala	Gly	Cys	Thr	Cys	Thr	Cys	Cys	Cys	Cys	Ala
		50				55					60				
Gly	Gly	Cys	Cys	Thr	Thr	Cys	Gly	Cys	Cys	Cys	Ala	Cys	Gly	Ala	Cys
				70						75					80
Cys	Thr	Cys	Ala	Gly	Gly	Thr	Ala	Ala	Gly	Gly	Gly	Gly	Thr	Thr	Thr
				85					90						95
Gly	Gly	Ala	Thr	Thr	Thr	Gly	Gly	Ala	Ala	Ala	Gly	Ala	Thr	Gly	Cys
			100					105					110		
Ala	Ala	Thr	Thr	Gly	Cys	Thr	Ala	Thr	Ala	Gly	Gly	Ala	Gly	Gly	Gly
			115				120						125		
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 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 8

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 35 40 45

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 50 55 60

Ala Gly Gly Ala Gly Gly Ala Thr Gly Gly Cys Cys Ala Cys Ala Gly
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Cys Ala Ala Gly Ala Gly Ala Ala Ala Gly Thr Gly Cys Thr Cys Ala
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Gly Thr	Thr Ala Ala Ala	Ala	Gly Cys Thr Thr Cys	Cys Ala Thr
1955		1960		1965
Cys Thr	Cys Thr Cys Thr	Cys	Thr Thr Thr Gly Cys	Thr Gly Ala
1970		1975		1980
Ala Thr	Ala Ala Thr Gly	Ala	Ala Cys Cys Thr Cys	Ala Gly Gly
1985		1990		1995
Thr Thr	Gly Thr Thr Cys	Ala	Ala Gly Ala Gly Ala	Cys Cys Gly
2000		2005		2010
Gly Ala	Ala Thr Gly Thr	Thr	Cys Thr Thr Cys Ala	Cys Cys Thr
2015		2020		2025
Gly Cys	Cys Thr Gly Cys	Ala	Cys Ala Cys Ala Thr	Cys Thr Cys
2030		2035		2040
Thr Thr	Cys Ala Cys Thr	Thr	Thr Cys Thr Thr Thr	Thr Ala Thr
2045		2050		2055
Ala Gly	Ala Thr Cys Ala	Gly	Gly Thr Ala Gly Gly	Gly Ala Cys
2060		2065		2070
Thr Gly	Gly Gly Cys Gly	Thr	Gly Thr Ala Gly Ala	Thr Gly Gly
2075		2080		2085
Ala Ala	Cys Ala Ala Ala	Cys	Thr Gly Thr Thr Thr	Thr Cys Cys
2090		2095		2100
Gly Thr	Thr Cys Cys Cys	Cys	Ala Gly Cys Cys Ala	Thr Cys Thr
2105		2110		2115
Cys Thr	Gly Cys Ala Gly	Gly	Thr Gly Cys Ala Cys	Thr Cys Cys
2120		2125		2130

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Ala Cys 2135	Ala Thr Ala Ala 2140	Ala Thr Cys Ala Ala 2145	Gly Thr Gly Thr 2150
Thr Ala 2150	Ala Ala Ala Gly 2155	Thr Gly Cys Thr Thr 2160	Thr Gly Ala Thr 2165
Thr Ala 2165	Ala Ala Cys Ala 2170	Gly Gly Ala Cys Ala 2175	Gly Cys Gly 2180
Cys Gly 2180	Thr Thr Cys Thr 2185	Thr Gly Ala Gly Thr 2190	Cys Ala Thr 2195
Cys Thr 2195	Gly Thr Thr Cys 2200	Ala Cys Ala Thr Ala 2205	Cys Thr Gly Thr 2210
Cys Thr 2210	Gly Gly Cys Ala 2215	Ala Gly Cys Gly Cys 2220	Thr Gly Ala Cys 2225
Thr Gly 2225	Ala Gly Gly Gly 2230	Thr Cys Thr Cys Cys 2235	Cys Thr Gly 2240
Thr Ala 2240	Cys Cys Cys Thr 2245	Gly Thr Thr Cys Thr 2250	Ala Gly Ala 2255
Ala Cys 2255	Thr Ala Ala Cys 2260	Ala Ala Ala Ala Gly 2265	Cys Gly Ala 2270
Ala Thr 2270	Cys Ala Ala Cys 2275	Ala Thr Ala Cys Ala 2280	Gly Ala Ala Ala 2285
Ala Cys 2285	Thr Gly Thr Thr 2290	Ala Thr Thr Thr Ala 2295	Gly Thr Gly Ala 2300
Cys Thr 2300	Gly Ala Thr Thr 2305	Ala Ala Ala Cys Thr 2310	Ala Cys Gly 2315
Ala Ala 2315	Gly Gly Cys Ala 2320	Thr Gly Gly Gly Cys 2325	Thr Gly Ala 2330
Gly Ala 2330	Ala Ala Thr Ala 2335	Ala Cys Thr Cys Ala 2340	Cys Ala Gly 2345
Thr Thr 2345	Ala Ala Gly Ala 2350	Ala Cys Ala Thr Thr 2355	Thr Gly Cys Thr 2360
Gly Ala 2360	Thr Cys Thr Thr 2365	Gly Cys Ala Gly Ala 2370	Gly Ala Cys 2375
Cys Thr 2375	Gly Gly Gly Thr 2380	Thr Gly Gly Gly Thr 2385	Cys Cys Thr 2390
Ala Gly 2390	Cys Ala Cys Ala 2395	Cys Ala Cys Ala Gly 2400	Gly Ala Cys 2405
Ala Gly 2405	Thr Thr Cys Cys 2410	Ala Gly Thr Cys Cys 2415	Cys Gly Gly Thr 2420
Gly Thr 2420	Gly Thr Cys Cys 2425	Thr Thr Thr Thr 2430	Cys Ala Cys 2435
Thr Thr 2435	Cys Thr Gly Thr 2440	Gly Gly Ala Cys Ala 2445	Cys Ala Ala Gly 2450
Thr Thr 2450	Thr Thr Ala Cys 2455	Ala Cys Ala Thr Ala 2460	Gly Thr Gly Cys 2465
Ala Cys 2465	Ala Cys Ala Cys 2470	Ala Thr Ala Cys Ala 2475	Thr Cys Ala 2480
Cys Ala 2480	Thr Ala Thr Ala 2485	Ala Ala Ala Ala 2490	Cys Ala Gly Ala 2495
Ala Cys 2495	Ala Thr Thr Thr 2500	Ala Ala Ala Gly Thr 2505	Ala Thr Gly 2510
Thr Thr 2510	Thr Ala Ala Ala 2515	Ala Ala Cys Gly Gly 2520	Ala Ala Thr 2525

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2510	2515	2520
Cys Ala Thr Thr Thr Ala 2525	Thr Ala Thr Ala Gly 2530	Gly Gly Thr Thr Thr 2535
Thr Cys Ala Thr Thr Thr 2540	Ala Cys Ala Thr Ala 2545	Gly Gly Thr Ala 2550
Ala Ala Thr Ala Gly Gly 2555	Cys Ala Ala Ala Ala 2560	Ala Thr Cys Thr 2565
Gly Cys Ala Thr Thr Thr 2570	Thr Ala Thr Thr Gly 2575	Thr Thr Thr Cys 2580
Thr Ala Ala Gly Thr Thr 2585	Thr Thr Ala Ala Thr 2590	Thr Thr Ala Thr 2595
Thr Thr Thr Thr Cys Thr 2600	Cys Thr Gly Thr Gly 2605	Thr Gly Thr Ala 2610
Cys Ala Thr Ala Cys Gly 2615	Cys Ala Thr Gly Cys 2620	Cys Thr Cys Cys 2625
Thr Thr Ala Thr Cys Thr 2630	Gly Thr Ala Thr Gly 2635	Thr Gly Thr Ala 2640
Thr Gly Cys Ala Cys Thr 2645	Gly Thr Gly Thr Gly 2650	Cys Ala Thr Gly 2655
Cys Ala Thr Gly Ala Ala 2660	Cys Cys Cys Ala Cys 2665	Ala Gly Ala Gly 2670
Ala Cys Cys Ala Gly Ala 2675	Ala Gly Ala Gly Thr 2680	Ala Cys Cys Ala 2685
Cys Ala Gly Ala Thr Thr 2690	Cys Thr Cys Thr Gly 2695	Gly Ala Gly Cys 2700
Thr Gly Gly Ala Gly Thr 2705	Gly Ala Thr Thr Gly 2710	Ala Thr Ala Gly 2715
Gly Cys Thr Gly Thr Thr 2720	Gly Gly Gly Ala Gly 2725	Cys Cys Ala Cys 2730
Thr Cys Cys Ala Cys Ala 2735	Thr Gly Gly Gly Gly 2740	Ala Thr Thr Cys 2745
Ala Gly Ala Gly Thr Thr 2750	Gly Ala Ala Cys Thr 2755	Thr Thr Cys Gly 2760
Thr Cys Thr Cys Thr Gly 2765	Cys Ala Ala Gly Ala 2770	Ala Cys Ala Gly 2775
Cys Cys Ala Gly Cys Thr 2780	Cys Thr Thr Ala Ala 2785	Cys Thr Gly Ala 2790
Thr Gly Gly Cys Thr Thr 2795	Thr Thr Ala Cys Cys 2800	Thr Cys Cys Ala 2805
Gly Cys Cys Ala Cys Cys 2810	Thr Thr Thr Thr Cys 2815	Cys Cys Thr Cys 2820
Thr Thr Thr Thr Thr Ala 2825	Ala Ala Ala Thr Thr 2830	Thr Cys Cys Thr 2835
Thr Cys Cys Thr Thr Cys 2840	Cys Thr Thr Thr Thr 2845	Thr Gly Ala Gly 2850
Ala Cys Ala Gly Gly Gly 2855	Thr Cys Thr Cys Ala 2860	Ala Thr Ala Cys 2865
Thr Thr Ala Gly Cys Thr 2870	Cys Ala Thr Cys Cys 2875	Cys Ala Ala Cys 2880
Thr Thr Gly Ala Cys Cys 2885	Cys Cys Ala Cys Thr 2890	Cys Thr Thr Cys 2895

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Thr Cys	Thr Thr Gly Cys	Cys	Thr Thr Ala Gly	Thr	Cys Ala Cys
2900		2905		2910	
Cys Ala	Cys Ala Ala Thr	Gly	Thr Thr Thr Ala Gly	Thr Thr Thr	
2915		2920		2925	
Ala Thr	Ala Ala Gly Cys	Ala	Thr Gly Cys Gly Thr	Cys Ala Cys	
2930		2935		2940	
Thr Ala	Thr Gly Cys Cys	Cys	Gly Gly Cys Thr Thr	Thr Ala Ala	
2945		2950		2955	
Ala Thr	Ala Ala Ala Cys	Thr	Cys Ala Cys Cys Cys	Ala Thr Ala	
2960		2965		2970	
Ala Thr	Cys Cys Cys Ala	Gly	Cys Ala Cys Thr Gly	Ala Ala Gly	
2975		2980		2985	
Thr Ala	Gly Ala Cys Ala	Ala	Ala Ala Gly Gly Gly	Ala Gly Gly	
2990		2995		3000	
Ala Thr	Cys Gly Ala Thr	Gly	Gly Gly Gly Cys Thr	Gly Ala Cys	
3005		3010		3015	
Thr Gly	Gly Cys Cys Ala	Cys	Ala Ala Gly Cys Cys	Gly Thr Gly	
3020		3025		3030	
Cys Thr	Thr Cys Ala Ala	Gly	Thr Thr Cys Ala Ala	Thr Gly Ala	
3035		3040		3045	
Ala Gly	Ala Cys Cys Cys	Thr	Gly Thr Cys Thr Cys	Ala Ala Gly	
3050		3055		3060	
Gly Gly	Ala Ala Thr Ala	Ala	Gly Gly Cys Ala Cys	Ala Gly Ala	
3065		3070		3075	
Gly Gly	Ala Thr Ala Gly	Ala	Gly Cys Cys Ala Thr	Ala Cys Gly	
3080		3085		3090	
Cys Cys	Thr Gly Ala Cys	Cys	Thr Cys Cys Thr Cys	Cys Thr Cys	
3095		3100		3105	
Thr Gly	Gly Cys Cys Thr	Cys	Thr Ala Cys Cys Cys	Ala Gly Gly	
3110		3115		3120	
Cys Ala	Cys Ala Thr Gly	Thr	Gly Cys Ala Thr Ala	Cys Ala Cys	
3125		3130		3135	
Ala Cys	Ala Cys Cys Ala	Cys	Ala Cys Ala Cys Ala	Cys Ala Cys	
3140		3145		3150	
Ala Cys	Ala Cys Ala Cys	Ala	Cys Ala Cys Ala Cys	Ala Cys Ala	
3155		3160		3165	
Cys Ala	Cys Ala Cys Ala	Cys	Ala Gly Ala Gly Ala	Gly Ala Gly	
3170		3175		3180	
Ala Gly	Ala Gly Ala Gly	Ala	Gly Ala Gly Ala Gly	Ala Gly Ala	
3185		3190		3195	
Gly Ala	Gly Ala Gly Ala	Gly	Ala Gly Ala Gly Ala	Gly Ala Gly	
3200		3205		3210	
Ala Gly	Ala Gly Ala Gly	Ala	Gly Ala Ala Ala Cys	Thr Thr Thr	
3215		3220		3225	
Thr Thr	Cys Cys Thr Cys	Thr	Thr Thr Thr Thr Thr	Thr Thr Thr	
3230		3235		3240	
Ala Ala	Ala Ala Ala Thr	Ala	Thr Thr Ala Thr Thr	Thr Ala Thr	
3245		3250		3255	
Thr Thr	Cys Ala Thr Gly	Thr	Ala Thr Ala Thr Gly	Ala Gly Thr	
3260		3265		3270	

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Ala Cys 3275	Ala Cys Thr Gly 3280	Thr Thr Gly Cys Thr Gly 3285	Thr Cys Thr 3290	Ala Gly Ala Cys 3295	Ala Cys Cys Cys Cys 3300	Ala Ala Ala 3305	Ala Gly Gly Cys 3310	Ala Thr Cys Ala Gly Ala 3315	Thr Cys Cys 3320	Thr Thr Gly Ala Cys 3325	Ala Ala Ala Thr Gly 3330	Gly Thr Thr 3335	Gly Thr Thr Gly Cys 3340	Ala Cys Cys Ala Thr 3345	Gly Thr Gly 3350	Thr Gly Cys Thr 3355	Ala Cys Cys Thr Cys 3370	Ala Thr Gly Gly 3375	Ala Ala Ala Gly Cys 3385	Ala Gly Thr Cys Ala Gly 3390	Thr Thr Thr Ala Ala 3395	Cys Cys Ala Thr Cys 3405	Thr Thr Thr 3410	Ala Cys Thr Thr Thr Thr 3425	Ala Ala Thr Gly Ala Gly 3430	Cys Ala Ala 3435	Ala Thr Ala Ala Thr Thr 3440	Gly Cys Thr Thr Cys Cys 3445	Ala Ala Gly 3450	Thr Ala Ala Ala Thr Ala 3455	Cys Thr Ala Cys Thr Ala 3460	Ala Thr Ala 3465	Thr Ala Thr Thr Thr Cys 3470	Thr Ala Ala Cys Cys Ala 3475	Thr Ala Cys 3480	Thr Ala Thr Ala Cys Ala 3485	Ala Gly Gly Ala Ala Thr 3490	Thr Ala Thr 3495	Thr Ala Ala Ala Thr Thr 3500	Ala Cys Gly Gly Ala Thr 3505	Ala Ala Thr 3510	Ala Gly Gly Ala Gly Ala 3515	Ala Thr Ala Ala Ala Ala 3520	Ala Ala Thr 3525	Thr Ala Thr Ala Ala Gly 3530	Thr Cys Ala Cys Thr Thr 3535	Thr Ala Thr 3540	Ala Ala Thr Gly Cys Thr 3545	Ala Thr Cys Thr Ala Ala 3550	Thr Cys Cys 3555	Ala Thr Cys Thr Ala Gly 3560	Ala Ala Cys Ala Ala Ala 3565	Ala Ala Cys 3570	Ala Cys Thr Gly Thr Ala 3575	Ala Thr Ala Ala Thr Gly 3580	Cys Ala Ala 3585	Ala Ala Gly Ala Gly Cys 3590	Gly Cys Ala Gly Thr Gly 3595	Cys Cys Thr 3600	Ala Gly Ala Thr Thr Ala 3605	Ala Ala Thr Ala Ala Ala 3610	Thr Ala Ala 3615	Ala Ala Thr Gly Cys Ala 3620	Gly Ala Cys Cys Ala Ala 3625	Thr Ala Ala 3630	Gly Thr Ala Ala Ala Cys 3635	Thr Thr Ala Thr Ala 3640	Gly Cys Ala 3645	Gly Cys Ala Thr Gly 3650	Gly Ala Ala Ala Thr 3655	Gly Ala Cys 3660
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3650	3655	3660
Gly Ala Ala Ala Thr Thr 3665	Cys Cys Thr Ala Ala 3670	Cys Ala Ala Ala 3675
Ala Ala Gly Cys Thr Cys 3680	Ala Ala Gly Ala Thr 3685	Gly Gly Gly Cys 3690
Ala Gly Thr Thr Thr Ala 3695	Thr Thr Thr Ala Ala 3700	Ala Gly Thr Gly 3705
Ala Ala Ala Thr Ala Cys 3710	Ala Gly Gly Ala Gly 3715	Ala Ala Thr 3720
Ala Ala Ala Gly Cys Ala 3725	Cys Ala Gly Ala Ala 3730	Gly Ala Thr 3735
Ala Cys Thr Cys Ala Ala 3740	Ala Gly Gly Cys Ala 3745	Thr Ala Gly Ala 3750
Ala Gly Thr Thr Ala Ala 3755	Cys Ala Thr Ala Gly 3760	Gly Gly Gly 3765
Gly Cys Thr Gly Gly Cys 3770	Gly Ala Gly Ala Thr 3775	Gly Gly Cys Thr 3780
Cys Thr Ala Cys Ala Gly 3785	Gly Thr Ala Ala Gly 3790	Ala Gly Cys Ala 3795
Cys Cys Cys Gly Ala Cys 3800	Thr Gly Cys Thr Cys 3805	Thr Thr Cys Cys 3810
Ala Ala Ala Gly Gly Thr 3815	Cys Cys Thr Gly Ala 3820	Gly Thr Thr Cys 3825
Ala Ala Ala Thr Cys Cys 3830	Cys Ala Gly Cys Ala 3835	Ala Cys Cys Ala 3840
Cys Ala Thr Gly Gly Thr 3845	Gly Gly Cys Thr Cys 3850	Ala Cys Ala Ala 3855
Cys Cys Ala Thr Cys Cys 3860	Gly Thr Ala Ala Thr 3865	Gly Ala Gly Ala 3870
Thr Thr Thr Gly Ala Cys 3875	Thr Cys Cys Cys Thr 3880	Cys Thr Thr Cys 3885
Thr Gly Gly Thr Gly Thr 3890	Gly Thr Cys Thr Gly 3895	Ala Ala Gly Ala 3900
Cys Ala Gly Cys Thr Ala 3905	Cys Ala Gly Thr Gly 3910	Thr Ala Cys Thr 3915
Thr Ala Ala Cys Ala Thr 3920	Ala Thr Ala Ala Thr 3925	Ala Ala Thr 3930
Ala Ala Ala Thr Ala Ala 3935	Ala Ala Cys Thr Thr 3940	Thr Ala Ala Ala 3945
Ala Ala Ala Ala Ala Ala 3950	Ala Thr Thr Ala Ala 3955	Ala Gly Ala Ala 3960
Gly Thr Thr Ala Ala Cys 3965	Ala Thr Ala Gly Ala 3970	Ala Gly Cys Cys 3975
Cys Ala Cys Thr Cys Ala 3980	Gly Gly Ala Cys Cys 3985	Cys Cys Ala Cys 3990
Thr Cys Ala Gly Thr Cys 3995	Cys Thr Ala Gly Ala 4000	Gly Thr Ala Thr 4005
Gly Ala Cys Ala Thr Thr 4010	Ala Thr Thr Ala Thr 4015	Gly Gly Ala Cys 4020
Ala Thr Thr Ala Ala Ala 4025	Ala Ala Gly Ala Gly 4030	Ala Ala Ala 4035

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Thr Thr Cys Ala Gly Cys Ala Gly Thr Ala Gly Thr Gly Thr Gly	4040	4045	4050
Cys Ala Thr Gly Cys Ala Cys Thr Gly Cys Ala Thr Ala Thr Ala	4055	4060	4065
Thr Ala Cys Ala Cys Ala Ala Ala Thr Cys Cys Thr Thr Gly Ala	4070	4075	4080
Gly Thr Thr Thr Cys Ala Thr Ala Cys Cys Ala Ala Ala Thr Gly	4085	4090	4095
Cys Cys Thr Thr Thr Ala Gly Ala Cys Cys Ala Cys Thr Thr Gly	4100	4105	4110
Thr Gly Gly Cys Thr Cys Thr Gly Cys Ala Ala Ala Cys Cys Thr	4115	4120	4125
Gly Thr Ala Ala Thr Cys Cys Thr Ala Gly Cys Ala Cys Thr Thr	4130	4135	4140
Gly Thr Gly Ala Ala Ala Ala Gly Gly Thr Cys Ala Gly Cys Thr	4145	4150	4155
Cys Ala Gly Gly Ala Ala Cys Thr Thr Thr Gly Gly Gly Ala Ala	4160	4165	4170
Gly Gly Thr Cys Ala Thr Gly Ala Ala Ala Cys Thr Cys Thr Thr	4175	4180	4185
Gly Cys Cys Cys Cys Thr Cys Cys Ala Gly Ala Ala Gly Gly Gly	4190	4195	4200
Ala Gly Ala Gly Gly Cys Thr Ala Ala Thr Thr Ala Ala Cys Ala	4205	4210	4215
Thr Thr Thr Cys Thr Cys Ala Gly Ala Cys Cys Ala Cys Ala Gly	4220	4225	4230
Gly Gly Cys Gly Gly Gly Ala Ala Cys Cys Gly Ala Cys Cys Thr	4235	4240	4245
Gly Cys Gly Gly Gly Thr Gly Gly Gly Gly Ala Cys Ala Gly Ala	4250	4255	4260
Cys Thr Gly Thr Thr Gly Cys Cys Cys Ala Thr Thr Thr Cys Cys	4265	4270	4275
Ala Gly Ala Cys Thr Ala Gly Gly Gly Ala Ala Gly Thr Cys Cys	4280	4285	4290
Thr Thr Gly Thr Cys Ala Cys Cys Thr Cys Ala Thr Thr Cys Cys	4295	4300	4305
Cys Thr Ala Ala Ala Gly Ala Cys Cys Ala Ala Thr Cys Ala Ala	4310	4315	4320
Thr Thr Thr Ala Ala Ala Gly Gly Gly Thr Gly Cys Ala Cys Thr	4325	4330	4335
Gly Thr Thr Cys Cys Gly Cys Cys Ala Ala Thr Cys Ala Thr Ala	4340	4345	4350
Thr Thr Gly Thr Gly Cys Cys Thr Ala Gly Thr Thr Gly Cys Thr	4355	4360	4365
Gly Ala Thr Gly Cys Thr Cys Thr Ala Thr Thr Cys Thr Gly Cys	4370	4375	4380
Cys Cys Thr Thr Ala Gly Ala Ala Ala Cys Cys Gly Thr Ala Thr	4385	4390	4395
Ala Ala Ala Ala Ala Cys Thr Ala Gly Cys Gly Ala Ala Gly Gly	4400	4405	4410

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Gly	Gly	Thr	Ala	Cys	Cys	Ala	Gly	Gly	Gly	Gly	Thr	Ala	Ala	Cys
4415						4420					4425			
Cys	Cys	Cys	Cys	Thr	Cys	Thr	Cys	Cys	Thr	Thr	Cys	Ala	Gly	Gly
4430						4435					4440			
Thr	Cys	Thr	Gly	Gly	Gly	Ala	Cys	Ala	Ala	Thr	Cys	Cys	Cys	Ala
4445						4450					4455			
Cys	Thr	Ala	Cys	Ala	Cys	Thr	Gly	Gly	Ala	Ala	Cys	Ala	Ala	Thr
4460						4465					4470			
Ala	Ala	Thr	Thr	Thr	Cys	Cys	Thr	Cys	Thr	Gly	Gly	Cys	Thr	Thr
4475						4480					4485			
Thr	Thr	Thr	Gly	Cys	Ala	Thr	Thr	Gly	Ala	Thr	Cys	Ala	Cys	Ala
4490						4495					4500			
Gly	Cys	Thr	Cys	Cys	Ala	Cys	Thr	Thr	Cys	Gly	Thr	Gly	Gly	Thr
4505						4510					4515			
Ala	Ala	Gly	Thr	Thr	Ala	Ala	Gly	Ala	Cys	Thr	Cys	Cys	Cys	Thr
4520						4525					4530			
Gly	Gly	Ala	Gly	Thr	Cys	Thr	Thr	Ala	Cys	Ala	Thr	Thr	Gly	Gly
4535						4540					4545			
Cys	Ala	Ala	Ala	Thr	Gly	Cys	Ala	Gly	Gly	Cys	Ala	Ala	Ala	Ala
4550						4555					4560			
Gly	Ala	Ala	Thr	Cys	Cys	Gly	Ala	Ala	Ala	Cys	Thr	Cys	Ala	Ala
4565						4570					4575			
Gly	Gly	Thr	Cys	Ala	Thr	Cys	Thr	Ala	Ala	Ala	Ala	Cys	Thr	Ala
4580						4585					4590			
Cys	Ala	Thr	Ala	Gly	Cys	Ala	Ala	Gly	Cys	Ala	Thr	Gly	Cys	Thr
4595						4600					4605			
Gly	Cys	Thr	Ala	Gly	Cys	Cys	Thr	Gly	Gly	Gly	Cys	Thr	Cys	Cys
4610						4615					4620			
Ala	Thr	Gly	Ala	Gly	Ala	Cys	Cys	Cys	Thr	Gly	Gly	Gly	Gly	Gly
4625						4630					4635			
Ala	Gly	Gly	Gly	Gly	Cys	Ala	Gly	Ala	Gly	Gly	Gly	Ala	Gly	Ala
4640						4645					4650			
Cys	Cys	Gly	Thr	Thr	Cys	Ala	Gly	Ala	Ala	Gly	Ala	Cys	Ala	Gly
4655						4660					4665			
Thr	Cys	Ala	Ala	Gly	Ala	Thr	Gly	Thr	Thr	Gly	Cys	Ala	Gly	Cys
4670						4675					4680			
Ala	Gly	Cys	Ala	Cys	Ala	Gly	Gly	Cys	Ala	Gly	Cys	Cys	Thr	Gly
4685						4690					4695			
Gly	Cys	Cys	Ala	Cys	Cys	Ala	Gly	Thr	Gly	Cys	Thr	Gly	Thr	Cys
4700						4705					4710			
Ala	Cys	Cys	Ala	Gly	Ala	Cys	Ala	Thr	Gly	Thr	Thr	Ala	Ala	Thr
4715						4720					4725			
Gly	Thr	Thr	Gly	Gly	Ala	Ala	Thr	Ala	Ala	Ala	Gly	Cys	Cys	Thr
4730						4735					4740			
Cys	Ala	Ala	Thr	Cys	Ala	Thr	Gly	Ala	Cys	Thr	Cys	Thr	Cys	Cys
4745						4750					4755			
Cys	Ala	Gly	Thr	Thr	Thr	Thr	Ala	Thr	Ala	Ala	Thr	Thr	Gly	Gly
4760						4765					4770			
Ala	Ala	Ala	Thr	Ala	Ala	Gly	Ala	Ala	Ala	Gly	Gly	Ala	Ala	Ala
4775						4780					4785			
Gly	Ala	Cys	Thr	Ala	Thr	Ala	Gly	Gly	Ala	Ala	Cys	Ala	Ala	Cys

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4790	4795	4800
Thr Gly 4805	Thr Gly Thr Thr 4810	Cys Ala Gly Ala Ala Cys Ala Cys Thr 4815
Ala Thr 4820	Thr Thr Ala Thr 4825	Ala Ala Thr Ala Gly Cys Ala Ala Ala 4830
Gly Ala 4835	Thr Cys Thr Cys 4840	Ala Gly Ala Gly Thr Ala Ala Cys Cys 4845
Cys Ala 4850	Ala Ala Cys Thr Thr 4855	Cys Thr Ala Gly Ala Cys Ala Thr 4860
Thr Gly 4865	Ala Thr Thr Thr 4870	Gly Gly Ala Ala Gly Ala Thr Cys 4875
Thr Cys 4880	Thr Thr Gly Gly 4885	Cys Ala Gly Cys Thr Thr Ala Thr Thr 4890
Thr Thr 4895	Gly Ala Ala Ala 4900	Ala Cys Thr Thr Thr Ala Cys Ala Ala 4905
Thr Gly 4910	Thr Thr Ala Ala 4915	Ala Thr Ala Thr Gly Thr Ala Ala Ala 4920
Ala Ala 4925	Cys Ala Ala Gly 4930	Gly Ala Cys Ala Gly Thr Thr Thr Thr 4935
Gly Thr 4940	Thr Thr Thr Thr 4945	Thr Gly Thr Thr Thr Thr Gly Thr Thr 4950
Thr Thr 4955	Gly Thr Thr Thr 4960	Thr Gly Thr Thr Thr Thr Ala Gly Gly 4965
Gly Ala 4970	Thr Ala Thr Ala 4975	Thr Ala Thr Thr Cys Ala Thr Ala Thr 4980
Ala Thr 4985	Gly Thr Ala Thr 4990	Ala Thr Gly Ala Ala Thr Gly Ala Ala 4995
Ala Ala 5000	Cys Cys Cys Ala 5005	Ala Ala Cys Thr Thr Ala Ala Ala Ala 5010
Thr Thr 5015	Cys Cys Cys Cys 5020	Ala Cys Thr Ala Thr Gly Cys Thr Thr 5025
Thr Ala 5030	Ala Ala Gly Gly 5035	Cys Thr Thr Thr Cys Thr Gly Ala Cys 5040
Ala Ala 5045	Thr Ala Ala Cys 5050	Ala Gly Ala Ala Ala Gly Ala Gly Ala 5055
Ala Ala 5060	Thr Ala Gly Ala 5065	Gly Ala Ala Thr Cys Cys Ala Thr Ala 5070
Ala Ala 5075	Ala Ala Cys Thr 5080	Ala Gly Thr Thr Cys Thr Gly Ala Ala 5085
Ala Cys 5090	Thr Ala Thr Cys 5095	Ala Ala Thr Ala Gly Gly Cys Thr Thr 5100
Gly Ala 5105	Cys Ala Cys Thr 5110	Cys Thr Thr Thr Ala Gly Cys Thr Gly 5115
Cys Cys 5120	Ala Gly Gly Ala 5125	Gly Ala Gly Cys Thr Gly Ala Ala Thr 5130
Cys Thr 5135	Gly Ala Ala Cys 5140	Ala Cys Ala Gly Gly Gly Ala Ala Cys 5145
Cys Cys 5150	Cys Ala Cys Cys 5155	Cys Ala Gly Cys Ala Cys Cys Cys Cys 5160
Ala Ala 5165	Ala Thr Thr Thr 5170	Gly Gly Ala Thr Thr Ala Thr Thr Gly 5175

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Thr Thr	Thr Thr Ala Thr	Thr Thr Thr Ala Thr	Cys Thr Thr Thr	5180	5185	5190
Cys Cys	Cys Cys Thr Ala	Cys Cys Cys Cys Cys	Ala Ala Gly Ala	5195	5200	5205
Cys Ala	Gly Gly Gly Thr	Thr Thr Cys Thr Cys	Thr Gly Cys Gly	5210	5215	5220
Thr Gly	Gly Thr Cys Cys	Thr Gly Gly Cys Thr	Gly Thr Cys Cys	5225	5230	5235
Thr Gly	Gly Ala Ala Cys	Thr Cys Gly Gly Ala	Gly Ala Thr Cys	5240	5245	5250
Cys Thr	Cys Thr Gly Cys	Cys Thr Cys Thr Cys	Thr Gly Cys Cys	5255	5260	5265
Thr Cys	Thr Cys Thr Gly	Cys Cys Thr Cys Thr	Cys Thr Cys Thr	5270	5275	5280
Cys Thr	Cys Thr Cys Thr	Gly Cys Cys Thr Cys	Thr Cys Thr Cys	5285	5290	5295
Thr Gly	Cys Cys Thr Cys	Thr Cys Thr Cys Thr	Cys Thr Cys Thr	5300	5305	5310
Cys Thr	Cys Thr Cys Thr	Cys Thr Gly Cys Cys	Thr Cys Thr Cys	5315	5320	5325
Thr Cys	Thr Cys Thr Cys	Thr Cys Thr Cys Thr	Gly Cys Cys Cys	5330	5335	5340
Cys Thr	Cys Gly Cys Thr	Gly Cys Cys Thr Cys	Thr Cys Thr Cys	5345	5350	5355
Thr Gly	Cys Cys Thr Cys	Thr Cys Thr Cys Thr	Gly Cys Cys Cys	5360	5365	5370
Cys Thr	Cys Thr Cys Thr	Gly Cys Cys Cys Cys	Thr Cys Thr Cys	5375	5380	5385
Thr Gly	Cys Cys Cys Cys	Thr Cys Thr Cys Thr	Cys Thr Thr Cys	5390	5395	5400
Cys Cys	Cys Thr Cys Thr	Cys Thr Gly Cys Cys	Thr Cys Thr Cys	5405	5410	5415
Thr Cys	Thr Cys Thr Gly	Cys Cys Cys Thr Cys	Thr Cys Thr	5420	5425	5430
Gly Cys	Cys Thr Cys Thr	Cys Thr Gly Cys Cys	Thr Cys Thr Gly	5435	5440	5445
Cys Cys	Thr Cys Cys Thr	Gly Ala Gly Thr Gly	Cys Thr Gly Gly	5450	5455	5460
Gly Ala	Thr Thr Thr Ala	Ala Ala Gly Gly Cys	Ala Thr Cys Ala	5465	5470	5475
Gly Cys	Cys Ala Thr Cys	Ala Cys Thr Thr Cys	Cys Ala Gly Cys	5480	5485	5490
Thr Thr	Cys Cys Thr Thr	Thr Ala Thr Cys Ala	Thr Thr Thr Thr	5495	5500	5505
Ala Ala	Ala Ala Ala Gly	Ala Ala Thr Thr Thr	Cys Cys Thr Ala	5510	5515	5520
Thr Gly	Thr Gly Ala Cys	Thr Ala Cys Thr Gly	Thr Ala Thr Thr	5525	5530	5535
Thr Ala	Ala Ala Thr Cys	Ala Cys Cys Ala Cys	Ala Cys Gly Gly	5540	5545	5550

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Cys	Cys	Ala	Ala	Thr	Ala	Cys	Thr	Cys	Cys	Cys	Cys	Cys	Cys	Cys
5555						5560					5565			
Ala	Ala	Cys	Thr	Cys	Cys	Thr	Cys	Cys	Cys	Ala	Ala	Ala	Thr	Cys
5570						5575					5580			
Cys	Cys	Cys	Thr	Cys	Thr	Ala	Cys	Cys	Cys	Ala	Cys	Thr	Cys	Ala
5585						5590					5595			
Ala	Ala	Thr	Thr	Cys	Thr	Thr	Ala	Thr	Cys	Thr	Thr	Gly	Thr	Ala
5600						5605					5610			
Thr	Thr	Cys	Thr	Thr	Thr	Ala	Thr	Cys	Ala	Thr	Thr	Ala	Thr	Thr
5615						5620					5625			
Ala	Thr	Ala	Cys	Ala	Thr	Ala	Thr	Gly	Thr	Gly	Thr	Ala	Thr	Ala
5630						5635					5640			
Thr	Ala	Thr	Gly	Thr	Gly	Thr	Gly	Thr	Gly	Thr	Gly	Thr	Ala	Thr
5645						5650					5655			
Ala	Thr	Ala	Thr	Ala	Thr	Ala	Thr	Ala	Thr	Ala	Cys	Thr	Ala	Thr
5660						5665					5670			
Ala	Thr	Ala	Cys	Thr	Gly	Cys	Thr	Ala	Ala	Thr	Gly	Ala	Gly	Thr
5675						5680					5685			
Ala	Ala	Cys	Ala	Thr	Thr	Thr	Ala	Gly	Thr	Gly	Thr	Thr	Ala	Thr
5690						5695					5700			
Thr	Cys	Ala	Thr	Thr	Gly	Thr	Thr	Gly	Cys	Ala	Thr	Gly	Thr	Thr
5705						5710					5715			
Thr	Thr	Cys	Ala	Ala	Thr	Gly	Thr	Gly	Cys	Thr	Thr	Thr	Cys	Cys
5720						5725					5730			
Ala	Gly	Gly	Ala	Gly	Gly	Cys	Thr	Gly	Gly	Gly	Gly	Gly	Gly	Ala
5735						5740					5745			
Thr	Gly	Gly	Cys	Thr	Cys	Ala	Gly	Thr	Gly	Gly	Gly	Cys	Ala	Ala
5750						5755					5760			
Ala	Ala	Thr	Thr	Cys	Thr	Ala	Gly	Cys	Thr	Gly	Cys	Ala	Cys	Ala
5765						5770					5775			
Ala	Gly	Cys	Cys	Thr	Ala	Ala	Gly	Gly	Ala	Cys	Cys	Ala	Gly	Gly
5780						5785					5790			
Gly	Thr	Thr	Cys	Ala	Gly	Ala	Thr	Cys	Cys	Cys	Cys	Ala	Ala	Thr
5795						5800					5805			
Ala	Thr	Ala	Ala	Ala	Gly	Gly	Cys	Thr	Gly	Gly	Cys	Thr	Gly	Gly
5810						5815					5820			
Ala	Cys	Ala	Thr	Gly	Gly	Thr	Gly	Gly	Cys	Thr	Thr	Gly	Cys	Cys
5825						5830					5835			
Thr	Ala	Thr	Gly	Ala	Thr	Ala	Cys	Thr	Ala	Gly	Cys	Ala	Thr	Gly
5840						5845					5850			
Cys	Thr	Thr	Gly	Cys	Thr	Gly	Gly	Ala	Ala	Gly	Cys	Ala	Ala	Ala
5855						5860					5865			
Gly	Ala	Cys	Ala	Gly	Gly	Gly	Ala	Ala	Thr	Cys	Cys	Cys	Thr	Gly
5870						5875					5880			
Gly	Ala	Gly	Ala	Cys	Thr	Thr	Ala	Gly	Ala	Ala	Thr	Cys	Thr	Cys
5885						5890					5895			
Ala	Gly	Ala	Ala	Gly	Thr	Gly	Ala	Thr	Cys	Thr	Gly	Gly	Gly	Cys
5900						5905					5910			
Thr	Gly	Gly	Ala	Cys	Ala	Gly	Ala	Cys	Thr	Ala	Gly	Cys	Thr	Gly
5915						5920					5925			
Ala	Ala	Cys	Thr	Gly	Gly	Cys	Cys	Ala	Gly	Cys	Thr	Cys	Thr	Gly

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Gly Gly Thr Thr Cys Ala	Thr Cys Ala Ala Gly Ala	Ala Ala Cys
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Cys Cys Thr Ala Cys Cys	Thr Cys Cys Ala Thr	Ala Cys Ala
5960	5965	5970
Thr Ala Ala Ala Gly Thr	Gly Thr Gly Ala Thr	Gly Ala Gly
5975	5980	5985
Ala Ala Ala Gly Gly Cys	Ala Cys Cys Thr Ala	Ala Thr Gly Thr
5990	5995	6000
Cys Ala Ala Cys Cys Thr	Cys Ala Ala Ala Cys	Cys Cys Thr
6005	6010	6015
Ala Cys Cys Thr Gly Cys	Ala Thr Gly Thr Gly	Cys Ala Cys Ala
6020	6025	6030
Cys Ala Cys Ala Thr Ala	Cys Ala Thr Cys Cys	Ala Cys Ala Cys
6035	6040	6045
Cys Ala Cys Ala Cys Ala	Cys Ala Cys Ala Cys	Ala Cys Ala Cys
6050	6055	6060
Ala Cys Ala Cys Ala Cys	Ala Cys Ala Cys Ala	Cys Ala Cys Ala
6065	6070	6075
Cys Cys Ala Cys Ala Cys	Ala Cys Ala Cys Ala	Cys Ala Cys Ala
6080	6085	6090
Cys Ala Cys Ala Ala Ala	Thr Ala Ala Ala Thr	Ala Ala Gly Thr
6095	6100	6105
Ala Ala Ala Thr Ala Ala	Ala Thr Ala Ala Ala	Ala Thr Ala Thr
6110	6115	6120
Thr Thr Ala Gly Cys Thr	Cys Thr Cys Cys Ala	Gly Ala Cys Cys
6125	6130	6135
Ala Ala Ala Thr Cys Thr	Thr Gly Gly Thr Gly	Ala Ala Cys
6140	6145	6150
Cys Cys Ala Thr Gly Cys	Ala Thr Thr Thr Gly	Cys Ala Thr Thr
6155	6160	6165
Thr Gly Thr Gly Thr Gly	Thr Gly Thr Cys Cys	Thr Ala Cys Ala
6170	6175	6180
Ala Ala Cys Ala Cys Thr	Gly Ala Ala Gly Gly	Thr Thr Ala Ala
6185	6190	6195
Gly Ala Ala Gly Cys Ala	Thr Gly Cys Thr Cys	Cys Thr Thr Ala
6200	6205	6210
Gly Thr Ala Ala Thr Thr	Thr Thr Ala Thr Ala	Gly Cys Ala Gly
6215	6220	6225
Thr Thr Thr Gly Cys Gly	Thr Thr Cys Cys Ala	Gly Ala Thr
6230	6235	6240
Thr Gly Ala Ala Ala Ala	Cys Ala Gly Ala Thr	Thr Cys Thr Ala
6245	6250	6255
Thr Ala Gly Gly Cys Thr	Ala Cys Ala Cys Ala	Gly Thr Gly Cys
6260	6265	6270
Thr Ala Ala Ala Thr Gly	Gly Ala Thr Thr Ala	Thr Gly Cys Thr
6275	6280	6285
Cys Ala Gly Ala Thr Ala	Cys Ala Gly Ala Thr	Thr Gly Ala Ala
6290	6295	6300
Ala Ala Gly Gly Ala Thr	Ala Cys Ala Gly Ala	Thr Thr Gly Ala
6305	6310	6315

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Ala Ala Ala Gly Gly Gly Thr Cys Gly Gly Gly Gly Thr Cys Thr
 6320 6325 6330

Gly Gly Gly Cys Cys Ala Gly Gly Ala Thr Gly Ala Cys Gly Gly
 6335 6340 6345

Gly Cys Cys Ala Ala Cys Thr Ala Thr Cys Thr Thr Thr Gly Cys
 6350 6355 6360

Cys Cys Gly Gly Gly Cys Thr Thr Gly Thr Cys Cys Thr Thr Cys
 6365 6370 6375

Ala Gly Gly Gly Ala Ala Gly Gly Gly Thr Thr Ala Cys Ala Gly
 6380 6385 6390

Gly Ala Thr Thr Cys Ala Cys Cys Ala Cys Thr Gly Gly Gly Gly
 6395 6400 6405

Thr Gly Thr Gly Gly Cys Cys Thr Ala Thr Cys Thr Gly Cys Thr
 6410 6415 6420

Gly Thr Thr Ala Gly Gly Ala Cys Cys Thr Gly Ala Ala Thr Thr
 6425 6430 6435

Gly Cys Cys Thr Gly Gly Ala Gly Thr Gly Thr Thr Thr Cys Thr
 6440 6445 6450

Ala Gly Thr Thr Cys Cys Cys Ala Cys Thr Ala Gly Thr Thr Gly
 6455 6460 6465

Thr Thr Gly Ala Ala Cys Thr Thr Thr Ala Cys Cys Thr Thr Gly
 6470 6475 6480

Ala Ala Cys Cys Thr Cys Thr Gly Cys Thr Cys Cys Cys Ala Gly
 6485 6490 6495

<210> SEQ ID NO 9
 <211> LENGTH: 361
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

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Thr Ala Gly Ala Gly Thr Gly Cys Ala Gly Thr Thr Thr Gly Gly Cys
 20 25 30

Thr Ala Ala Ala Gly Cys Ala Ala Ala Ala Cys Cys Thr Ala Gly Gly
 35 40 45

Thr Ala Cys Ala Gly Thr Cys Ala Gly Gly Gly Ala Cys Thr Ala Cys
 50 55 60

Ala Cys Ala Ala Thr Thr Cys Cys Ala Gly Thr Thr Cys Gly Cys Thr
 65 70 75 80

Gly Thr Gly Gly Gly Thr Thr Gly Gly Gly Ala Ala Gly Gly Gly Ala
 85 90 95

Thr Gly Gly Gly Thr Gly Gly Gly Cys Cys Ala Gly Thr Gly Cys Thr
 100 105 110

Gly Gly Cys Ala Ala Gly Cys Cys Thr Thr Gly Ala Thr Cys Thr Thr
 115 120 125

Thr Gly Cys Cys Cys Gly Gly Gly Cys Thr Thr Gly Thr Cys Cys Thr
 130 135 140

Thr Cys Thr Gly Gly Gly Gly Ala Gly Ala Ala Thr Thr Ala Cys Cys
 145 150 155 160

Thr Gly Cys Thr Thr Cys Thr Gly Cys Thr Gly Gly Ala Cys Thr Gly

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Gly Gly Ala Gly Gly Thr Cys Thr Thr Gly Thr Thr Ala Thr Cys Ala
 165 170 175

Thr Gly Gly Ala Ala Thr Thr Thr Gly Ala Ala Cys Ala Gly Thr Ala
 180 185 190

Gly Cys Thr Thr Gly Thr Gly Thr Gly Thr Gly Cys Thr Gly Cys Ala
 195 200 205

Gly Cys Thr Thr Thr Thr Thr Ala Cys Ala Ala Cys Thr Ala Ala Ala
 210 215 220

Gly Thr Thr Ala Ala Thr Thr Gly Gly Ala Gly Gly Cys Cys Ala Gly
 225 230 235 240

Thr Thr Gly Cys Thr Cys Thr Gly Gly Gly Ala Ala Gly Cys Gly Gly
 245 250 255

Ala Thr Gly Gly Gly Gly Thr Gly Gly Gly Ala Gly Gly Ala Cys Ala
 260 265 270

Thr Gly Gly Cys Cys Ala Gly
 275

<210> SEQ ID NO 11
 <211> LENGTH: 784
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(784)
 <223> OTHER INFORMATION: SHIP cDNA

<400> SEQUENCE: 11

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ggcaatttct gagaggcaac aggcggcagg tctcagccta gagagggccc tgaactactt    60
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tggtcctcctgg gtggaacctat ggcaacatca cccgctccaa ggcagaggag ctactttcca    180
gagccggcaa ggacgggagc ttccttgctc gtgccagcga gtccatcccc cgggcctacg    240
cactctgcgt gctgttccgg aattgtgttt acacttacag gattotgccc aatgaggacg    300
ataaattcac tgttcaggca tccgaagggt tccccatgag gttcttcacg aagctggacc    360
agctcatcga cttttacaag aaggaaaaca tggggctggt gaccacctg cagtaccccg    420
tgcccctgga ggaggaggat gctattgatg aggctgagga ggacactgta gaaagtgtca    480
tgtcaccacc tgagctgcct cccagaaaca ttctatgctc tgccgggccc agcgaggcca    540
aggaccttcc tcttgcaaca gagaaccccc gagcccctga ggtcaccgg ctgagtctct    600
ccgagacact gtttcagcgt ctacagagca tggataccag tggggttccc gaggagcacc    660
tgaaagccat ccaggattat ctgagcactc agctcctcct ggattccgac tttttgaaga    720
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atgg                                                    784
    
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<210> SEQ ID NO 12
 <211> LENGTH: 225
 <212> TYPE: PRT
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 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(225)
 <223> OTHER INFORMATION: SHIP amino acid sequence

<400> SEQUENCE: 12

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 Lys Ala Glu Glu Leu Leu Ser Arg Ala Gly Lys Asp Gly Ser Phe Leu
 20 25 30
 Val Arg Ala Ser Glu Ser Ile Pro Arg Ala Tyr Ala Leu Cys Val Leu
 35 40 45
 Phe Arg Asn Cys Val Tyr Thr Tyr Arg Ile Leu Pro Asn Glu Asp Asp
 50 55 60
 Lys Phe Thr Val Gln Ala Ser Glu Gly Val Pro Met Arg Phe Phe Thr
 65 70 75 80
 Lys Leu Asp Gln Leu Ile Asp Phe Tyr Lys Lys Glu Asn Met Gly Leu
 85 90 95
 Val Thr His Leu Gln Tyr Pro Val Pro Leu Glu Glu Glu Asp Ala Ile
 100 105 110
 Asp Glu Ala Glu Glu Asp Thr Val Glu Ser Val Met Ser Pro Pro Glu
 115 120 125
 Leu Pro Pro Arg Asn Ile Pro Met Ser Ala Gly Pro Ser Glu Ala Lys
 130 135 140
 Asp Leu Pro Leu Ala Thr Glu Asn Pro Arg Ala Pro Glu Val Thr Arg
 145 150 155 160
 Leu Ser Leu Ser Glu Thr Leu Phe Gln Arg Leu Gln Ser Met Asp Thr
 165 170 175
 Ser Gly Leu Pro Glu Glu His Leu Lys Ala Ile Gln Asp Tyr Leu Ser
 180 185 190
 Thr Gln Leu Leu Leu Asp Ser Asp Phe Leu Lys Thr Gly Ser Ser Asn
 195 200 205
 Leu Pro His Leu Lys Lys Leu Met Ser Leu Leu Cys Lys Glu Leu His
 210 215 220
 Gly
 225

<210> SEQ ID NO 13
 <211> LENGTH: 2946
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(2946)
 <223> OTHER INFORMATION: s-SHIP cDNA (partial)

<400> SEQUENCE: 13

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ccacgacctc aggtgccccg agaggccagt cccatcacca tgggtgccaa actcagccaa    180
ttgacaagtc tgctgtcttc cattgaagat aaggccaagt ccttgctgca cgagggtc    240
gaatctacca acaggcgctt ccttatccct cgggtcacct ttgaggtgaa gtcagagtc    300
ctgggcattc ctcagaaaa gcactctcaa gtggacgttg agtctgggaa actgatcgtt    360
aagaagtcca aggatggttc tgaggacaag ttctacagcc acaaaaaaat cctgcagctc    420
attaagtccc agaagtttct aaacaagttg gtgattttgg tggagacgga gaaggagaaa    480
atcctgagga aggaatatgt ttttgctgac tctaagaaaa gagaaggctt ctgtcaactc    540
ctgcagcaga tgaagaacaa gcattcggag cagccagagc ctgacatgat caccatcttc    600
    
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attggcactt ggaacatggg taatgcaccc cctcccaaga agatcacgtc ctggtttctc	660
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gtgattggca cccaggagga tccccttggg gagaaggagt ggctggagct actcaggcac	780
tccctgcaag aagtcaccag catgacattt aaaacagttg ccatccacac cctctggaac	840
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gacaacgtga agacaggcat cgccaacacc ctgggaaaca agggagcagt gggagtgtcc	960
ttcatgttca atggaacctc cttggggttc gtcaacagcc acttgacttc tggaaagcga	1020
aaaaagctca ggagaatca aaactatatg aacatcctgc ggttctggc cctgggagac	1080
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caacagcagt attcagacct tctggcccac gaccaactgc tctggagag gaaggaccag	1260
aaggtcttcc tgcactttga ggaggaagag atcaccttcg ccccccacta tctgattgaa	1320
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caagggcaga tctgagtttt tgcattgctac gccacactga agaccaagtc ccagactaag	1620
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aagccatta tctctgacct cgagtactta ctggaccagc atatcctgat cagcattaaa	1800
tcctctgaca gtgacgagtc ctatggtgaa ggctgcaatt ccctctgctt ggagaccaca	1860
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aggggagaga ttaagctgca gacctcccag ggcaaatga gggagaagct ctatgacttt	1980
gtgaagacag agcgggatga atccagtga atgaaatgct tgaagaacct caccagccat	2040
gacctatga ggcaatggga gccttctggc aggtccctg catgtggtgt ctccagcctc	2100
aatgagatga tcaatccaaa ctacattggt atggggcctt ttggacagcc cctgcatggg	2160
aatcaaccc tgtcccaga tcagcaactc acagcttggg gttatgacca gctacccaaa	2220
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ctgtcgccaa agaagttttc atcttcaca gccaacagag gtccctgccc cagggtgcaa	2340
gaggcaagac ctggggatct gggaaagggt gaagctctgc tccaggagga cctgctgctg	2400
acgaagccc agatgtttga gaacctctg tatggatccg tgagttcctt ccctaagctg	2460
gtgcccagga aagagcagga gtctcccaag atgctgcgga aggagcccc gcctgtcca	2520
gaccagggaa tctcatcacc cagcatcgtg ctcccaag cccaagaggt ggagagtgtc	2580
aaggggacaa gcaaacagcg ccctgtgctt gtccttggcc ccacacccc gatccgctcc	2640
tttacctggt cttcttctgc tgagggcaga atgaccagtg gggacaagag ccaagggag	2700
cccaaggcct cagccagttc ccaagcccca gtgccagtca agaggcctgt caagccttcc	2760
aggtcagaaa tgagccagca gacaacaccc atcccagctc cacggccacc cctgccagtc	2820
aagagtctct ctgtctgca gctgcaacat tccaaaggca gagactaccg tgacaacaca	2880

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gaactccccc accatggcaa gcaccgcaaa gaggaggggc tgcttgccag gactgccatg 2940
cagtga 2946

<210> SEQ ID NO 14
<211> LENGTH: 928
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(928)
<223> OTHER INFORMATION: s-SHIP amino acid sequence (partial)

<400> SEQUENCE: 14

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Arg Ser Leu Ile Pro Pro Val Thr Phe Glu Val Lys Ser Glu Ser Leu
35 40 45
Gly Ile Pro Gln Lys Met His Leu Lys Val Asp Val Glu Ser Gly Lys
50 55 60
Leu Ile Val Lys Lys Ser Lys Asp Gly Ser Glu Asp Lys Phe Tyr Ser
65 70 75 80
His Lys Lys Ile Leu Gln Leu Ile Lys Ser Gln Lys Phe Leu Asn Lys
85 90 95
Leu Val Ile Leu Val Glu Thr Glu Lys Glu Lys Ile Leu Arg Lys Glu
100 105 110
Tyr Val Phe Ala Asp Ser Lys Lys Arg Glu Gly Phe Cys Gln Leu Leu
115 120 125
Gln Gln Met Lys Asn Lys His Ser Glu Gln Pro Glu Pro Asp Met Ile
130 135 140
Thr Ile Phe Ile Gly Thr Trp Asn Met Gly Asn Ala Pro Pro Pro Lys
145 150 155 160
Lys Ile Thr Ser Trp Phe Leu Ser Lys Gly Gln Gly Lys Thr Arg Asp
165 170 175
Asp Ser Ala Asp Tyr Ile Pro His Asp Ile Tyr Val Ile Gly Thr Gln
180 185 190
Glu Asp Pro Leu Gly Glu Lys Glu Trp Leu Glu Leu Leu Arg His Ser
195 200 205
Leu Gln Glu Val Thr Ser Met Thr Phe Lys Thr Val Ala Ile His Thr
210 215 220
Leu Trp Asn Ile Arg Ile Val Val Leu Ala Lys Pro Glu His Glu Asn
225 230 235 240
Arg Ile Ser His Ile Cys Thr Asp Asn Val Lys Thr Gly Ile Ala Asn
245 250 255
Thr Leu Gly Asn Lys Gly Ala Val Gly Val Ser Phe Met Phe Asn Gly
260 265 270
Thr Ser Leu Gly Phe Val Asn Ser His Leu Thr Ser Gly Ser Glu Lys
275 280 285
Lys Leu Arg Arg Asn Gln Asn Tyr Met Asn Ile Leu Arg Phe Leu Ala
290 295 300
Leu Gly Asp Lys Lys Leu Ser Pro Phe Asn Ile Thr His Arg Phe Thr
305 310 315 320

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His Leu Phe Trp Leu Gly Asp Leu Asn Tyr Arg Val Glu Leu Pro Thr
 325 330 335

Trp Glu Ala Glu Ala Ile Ile Gln Lys Ile Lys Gln Gln Gln Tyr Ser
 340 345 350

Asp Leu Leu Ala His Asp Gln Leu Leu Leu Glu Arg Lys Asp Gln Lys
 355 360 365

Val Phe Leu His Phe Glu Glu Glu Glu Ile Thr Phe Ala Pro Thr Tyr
 370 375 380

Arg Phe Glu Arg Leu Thr Arg Asp Lys Tyr Ala Tyr Thr Lys Gln Lys
 385 390 395 400

Ala Thr Gly Met Lys Tyr Asn Leu Pro Ser Trp Cys Asp Arg Val Leu
 405 410 415

Trp Lys Ser Tyr Pro Leu Val His Val Val Cys Gln Ser Tyr Gly Ser
 420 425 430

Thr Ser Asp Ile Met Thr Ser Asp His Ser Pro Val Phe Ala Thr Phe
 435 440 445

Glu Ala Gly Val Thr Ser Gln Phe Val Ser Lys Asn Gly Pro Gly Thr
 450 455 460

Val Asp Ser Gln Gly Gln Ile Glu Phe Leu Ala Cys Tyr Ala Thr Leu
 465 470 475 480

Lys Thr Lys Ser Gln Thr Lys Phe Tyr Leu Glu Phe His Ser Ser Cys
 485 490 495

Leu Glu Ser Phe Val Lys Ser Gln Glu Gly Glu Asn Glu Glu Gly Ser
 500 505 510

Glu Gly Glu Leu Val Val Arg Phe Gly Glu Thr Leu Pro Lys Leu Lys
 515 520 525

Pro Ile Ile Ser Asp Pro Glu Tyr Leu Leu Asp Gln His Ile Leu Ile
 530 535 540

Ser Ile Lys Ser Ser Asp Ser Asp Glu Ser Tyr Gly Glu Gly Cys Ile
 545 550 555 560

Ala Leu Arg Leu Glu Thr Thr Glu Ala Gln His Pro Ile Tyr Thr Pro
 565 570 575

Leu Thr His His Gly Glu Met Thr Gly His Phe Arg Gly Glu Ile Lys
 580 585 590

Leu Gln Thr Ser Gln Gly Lys Met Arg Glu Lys Leu Tyr Asp Phe Val
 595 600 605

Lys Thr Glu Arg Asp Glu Ser Ser Gly Met Lys Cys Leu Lys Asn Leu
 610 615 620

Thr Ser His Asp Pro Met Arg Gln Trp Glu Pro Ser Gly Arg Val Pro
 625 630 635 640

Ala Cys Gly Val Ser Ser Leu Asn Glu Met Ile Asn Pro Asn Tyr Ile
 645 650 655

Gly Met Gly Pro Phe Gly Gln Pro Leu His Gly Lys Ser Thr Leu Ser
 660 665 670

Pro Asp Gln Gln Leu Thr Ala Trp Ser Tyr Asp Gln Leu Pro Lys Asp
 675 680 685

Ser Ser Leu Gly Pro Gly Arg Gly Glu Gly Pro Pro Thr Pro Pro Ser
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Gln Pro Pro Leu Ser Pro Lys Lys Phe Ser Ser Ser Thr Ala Asn Arg
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(130)
<223> OTHER INFORMATION: first exon of SIP-110

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cccacccctg gagtctctgc agaggttatt tgaccagcag ctctcccgg gcctccgtcc   120
acgtcctcag                                     130

<210> SEQ ID NO 18
<211> LENGTH: 132
<212> TYPE: DNA
<213> ORGANISM: Mus musculus
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(132)
<223> OTHER INFORMATION: first exon of s-SHIP

<400> SEQUENCE: 18

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ccacgacctc ag                                     132

```

We claim:

1. A method for identifying the presence of stem cells in a cell sample, comprising detecting the presence of cells expressing s-SHIP RNA within the cell sample.

2. The method of claim 1, wherein the presence of stem cells in the sample is indicated by the presence of s-SHIP enzymatic activity.

3. The method of claim 1, wherein said detecting comprises adding anti-SHIP monoclonal antibody P2C6 or P1C1 to the sample under conditions, and for a time, suitable for antibody binding; and detecting the presence of the antibodies bound to the cells in the sample, wherein the presence of stem cells in the sample is indicated by cells that express the s-SHIP isoform.

4. The method of claim 3, wherein the antibodies are labeled with a fluorochrome.

5. The method of claim 4, wherein the detection of antibodies is by fluorescence activated cell sorting.

6. The method of claim 1, wherein the stem cells are embryonic stem cells.

7. The method of claim 1, wherein the stem cells are tissue-specific stem cells.

8. The method of claim 7, wherein then stem cells are hematopoietic stem cells.

9. The method of claim 3, wherein the stem cells are hematopoietic stem cells and the monoclonal antibody is P2C6.

10. A method for inhibiting proliferation of stem cells, comprising contacting the cells with s-SHIP thereby increasing competition with mSos1 for Grb2 in the stem cells.

11. The method of claim 10, wherein the stem cells are selected from the group consisting of hematopoietic progenitors of mature blood cells, hematopoietic progenitors of lymph cells, and embryonic stem cells.

12. A method of inhibiting differentiation of stem cells, comprising contacting the stem cells with s-SHIP enzyme whereby the accumulation of the s-SHIP enzyme prevents the accumulation of $PI^3,4,5,P_3$, or other signaling pathways and intermediates influenced by s-SHIP activity.

13. The method of claim 12, wherein the stem cells are selected from the group consisting of hematopoietic progenitors of mature blood cells and hematopoietic progenitors of lymphoid cells.

14. A recombinant nucleic acid promoter fragment isolated from an internal region of the SHIP gene where s-SHIP transcription is controlled, wherein the promoter fragment comprises a nucleotide fragment internal to the SHIP gene.

15. The recombinant nucleotide promoter fragment of claim 14, wherein the amino acid sequence is selected from the group consisting of SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, and SEQ ID NO: 10.

16. The recombinant nucleotide promoter fragment of claim 14, wherein the fragment is found in stem cells selected from the group consisting of: murine embryonic

stem cells, murine hematopoietic stem cells, human embryonic stem cells, and human hematopoietic stem cells.

17. A method for inducing proliferation of stem cells, comprising introducing anti-SHIP shRNA into the cell by electroporation.

18. The method of claim 17, wherein the stem cells are selected from the group consisting of hematopoietic progenitors of mature blood cells, hematopoietic progenitors of lymph cells, and embryonic stem cells.

19. A method for identifying stem cells in a cell sample, comprising detecting s-SHIP by immunofluorescence.

20. The method of claim 19, wherein the cell sample is a complex mixture of cells.

21. The method of claim 20, wherein the cell sample is in vivo.

22. The method of claim 20, wherein the presence of stem cells is indicated by the presence of the s-SHIP isoform.

23. A method for inducing proliferation in stem cells, comprising introducing an inhibitor of s-SHIP activity.

24. The method of claim 23, wherein the inhibitor of s-SHIP is a dominant negative mutant.

25. The method of claim 23, wherein the inhibitor of s-SHIP is shRNA.

26. The method of claim 23, wherein the stem cells are selected from the group consisting of hematopoietic progenitors of mature blood cells, hematopoietic progenitors of lymph cells, and embryonic stem cells.

27. The method of claim 23, wherein the stem cells are induced to differentiate.

28. A method for identifying stem cell-specific signaling components, comprising contacting the signaling component with s-SHIP.

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专利名称(译)	含有肌醇5'-磷酸酶同种型的新型SH2与Grb2衔接蛋白结合		
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[标]申请(专利权)人(译)	南佛罗里达大学		
申请(专利权)人(译)	南佛罗里达大学		
当前申请(专利权)人(译)	南佛罗里达大学		
[标]发明人	KERR WILLIAM G NINOS JOHN M		
发明人	KERR, WILLIAM G. NINOS, JOHN M.		
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摘要(译)

含有肌醇5'-磷酸 (SHIP) 的SH2在通过Shc和受体的细胞质尾部募集到膜后调节免疫细胞的活化。描述了在原始干细胞群 (s-SHIP) 中表达的约104kd的新型SHIP同种型。发现s-SHIP在全能胚胎干细胞中表达，排除在分化的造血细胞中表达的145-kd SHIP同种型。s-SHIP也在原始造血干细胞中表达，但在谱系定型的造血细胞中不表达。在胚胎干细胞中，s-SHIP与衔接蛋白Grb2结合而没有酪氨酸磷酸化，并且组成性地存在于细胞膜上。据推测，s-SHIP调节原始干细胞群的激活阈值。

