



(19) **United States**

(12) **Patent Application Publication**  
VITALIANO et al.

(10) **Pub. No.: US 2016/0178652 A1**

(43) **Pub. Date: Jun. 23, 2016**

(54) **INTELLIGENT SENSOR PLATFORMS**

**Publication Classification**

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(51) **Int. Cl.**  
**G01N 35/00** (2006.01)  
**G06N 5/02** (2006.01)

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(52) **U.S. Cl.**  
CPC ..... **G01N 35/00722** (2013.01); **G06N 5/02** (2013.01)

(21) Appl. No.: **15/055,754**

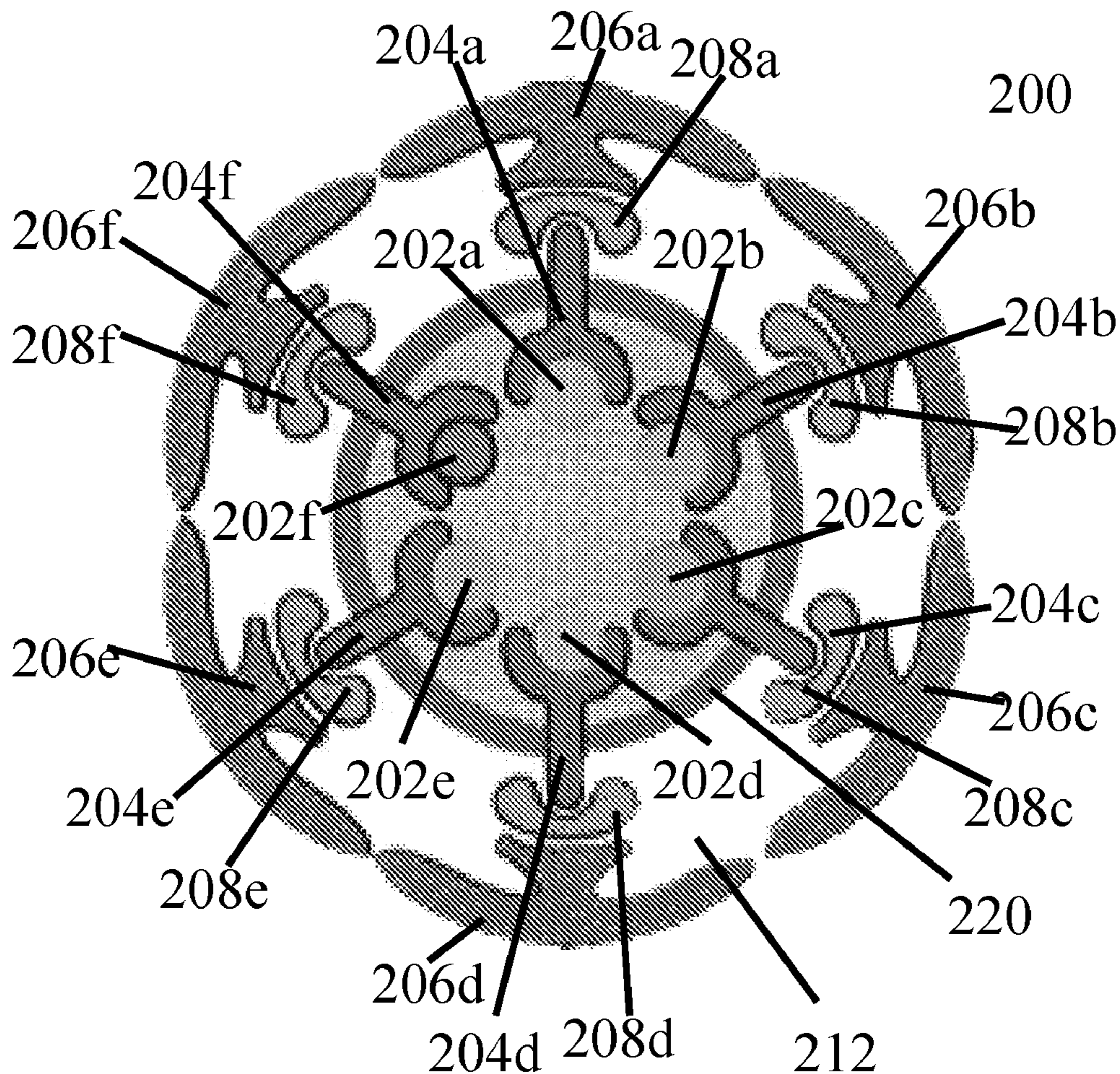
(22) Filed: **Feb. 29, 2016**

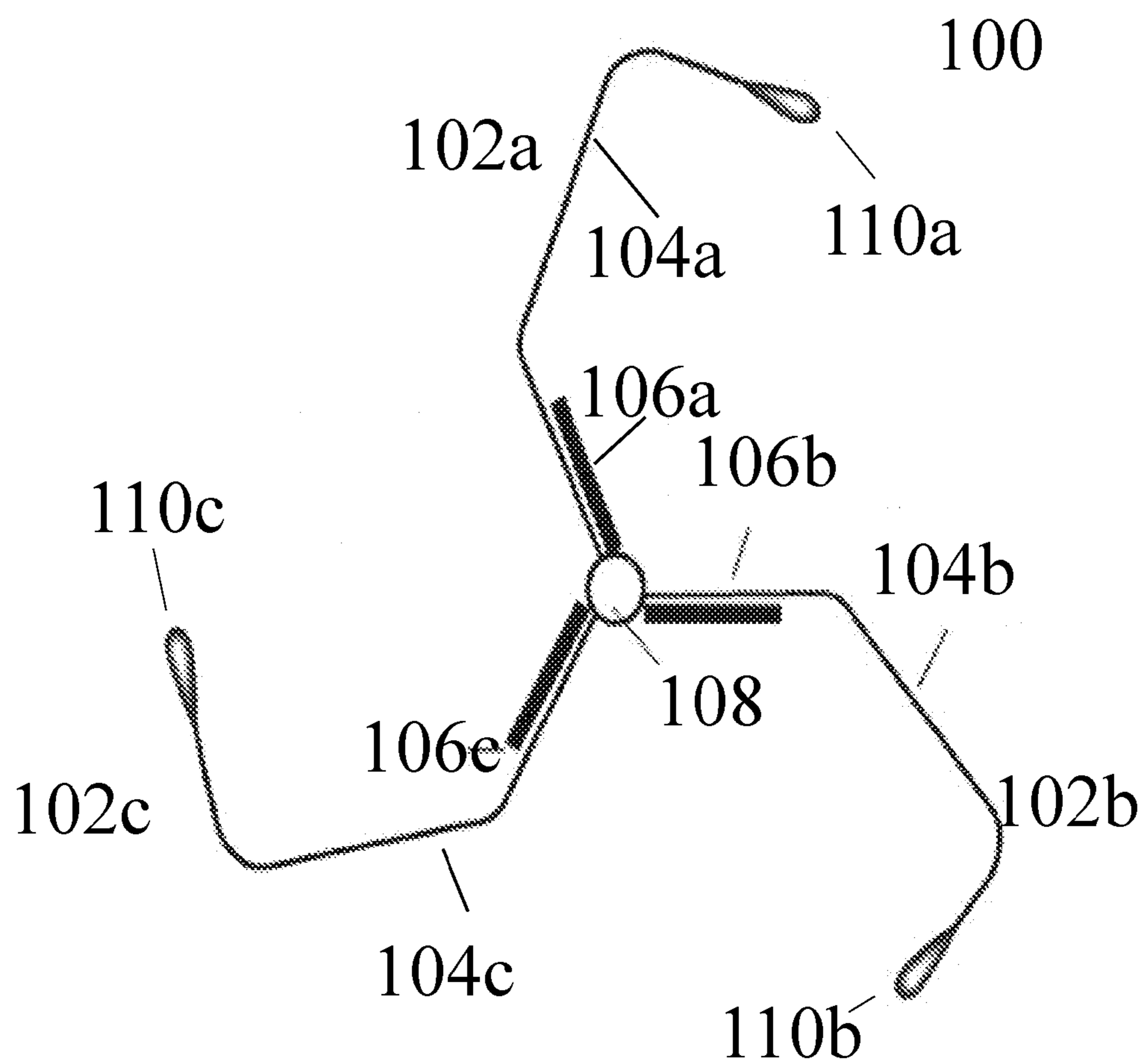
**Related U.S. Application Data**

(62) Division of application No. 12/399,906, filed on Mar. 6, 2009.

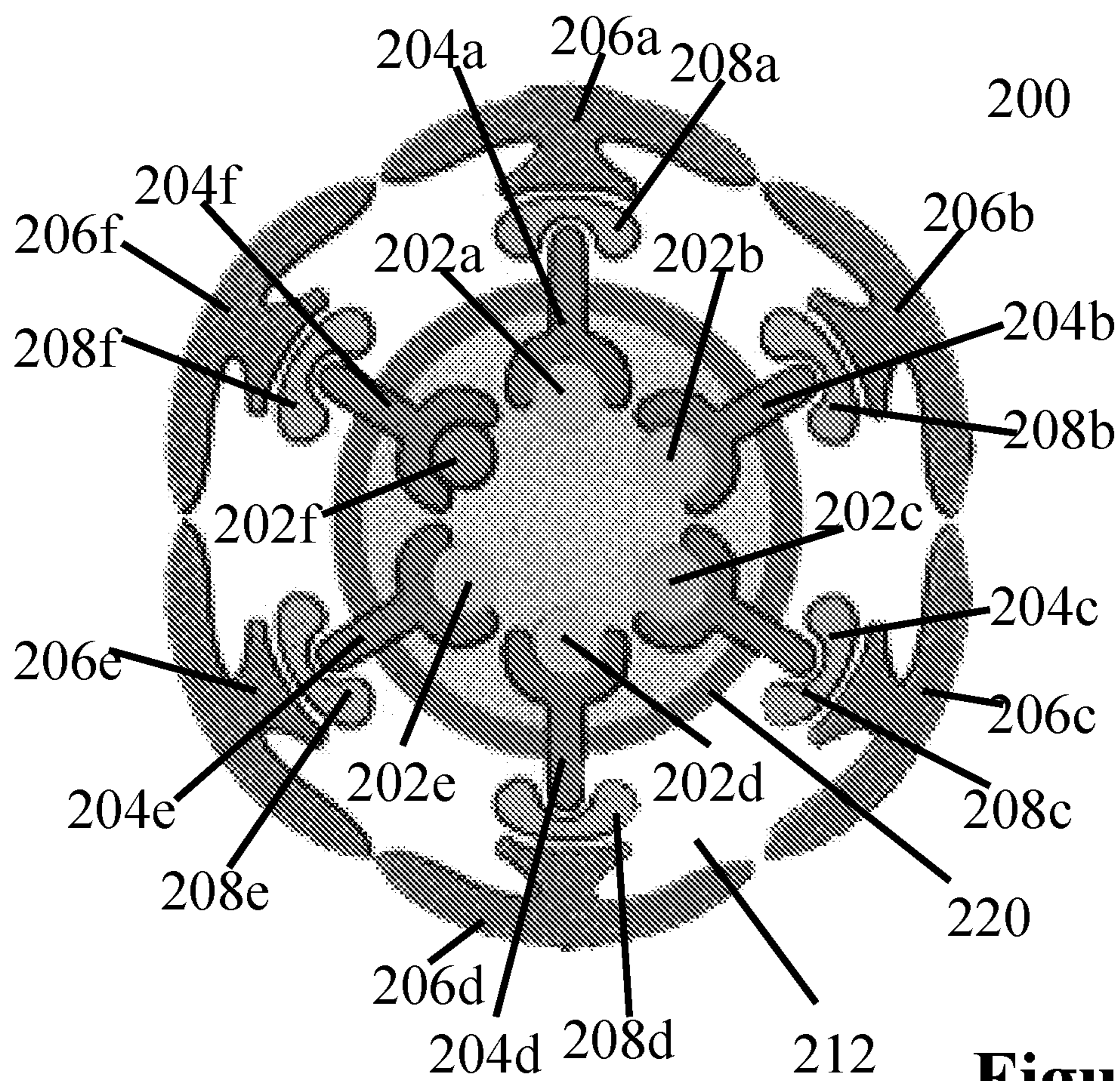
(57) **ABSTRACT**

The invention in suitable embodiments is directed to self-adapting, scalable, and communicating sensor platforms that are further capable of autonomous and/or cognitive action. In one aspect, the invention relates to a multifunction sensor platform, such as a biomedical sensor platform, bio-molecular sensor platform, electronics sensor platform, communications sensor platform, information processing sensor platform, and the like. In another invention embodiment, one or more sensors improve the efficacy of a healthcare element and/or its usage in treating and/or preventing a disease, condition, or disorder.

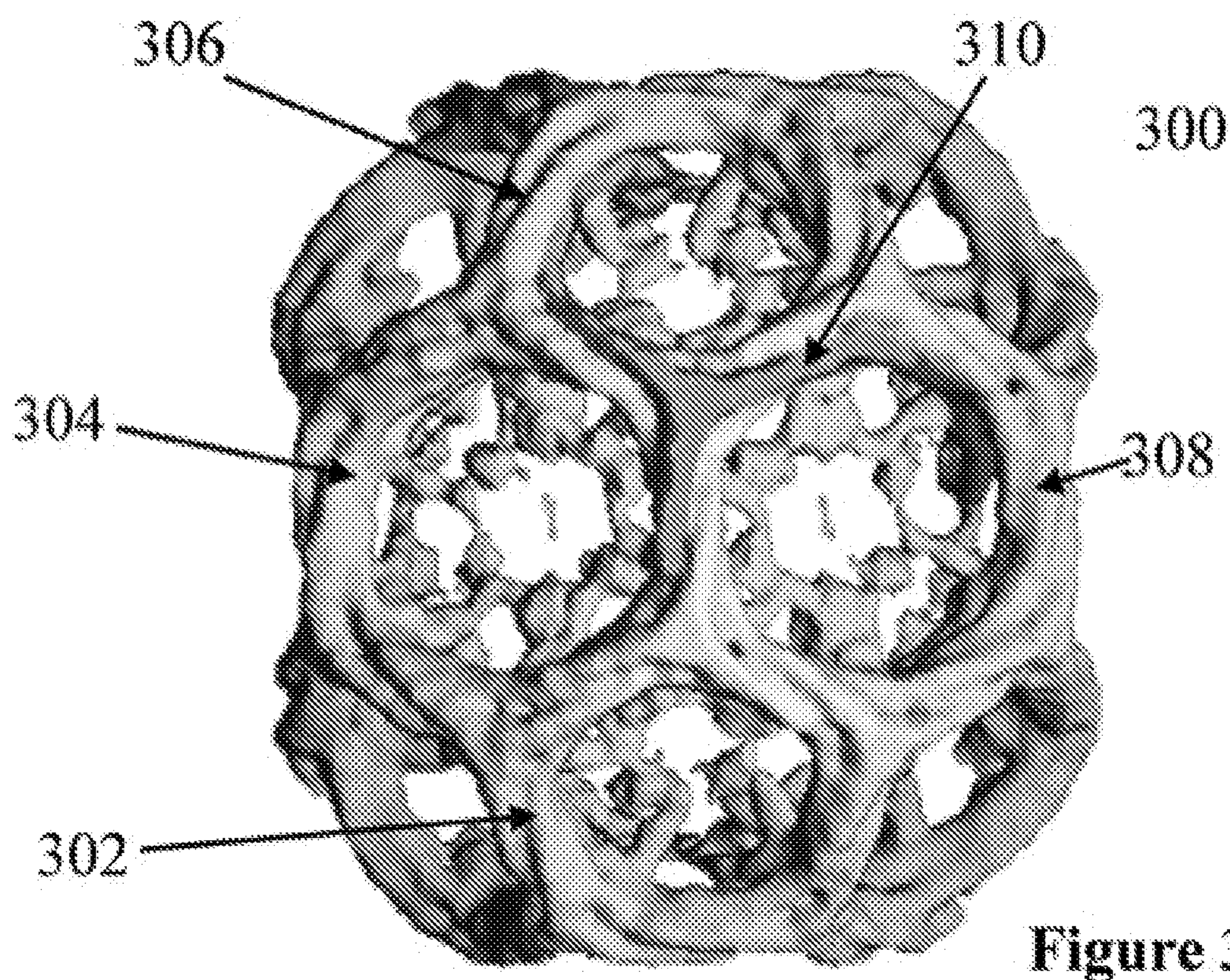




**Figure 1**



**Figure 2**



**Figure 3**

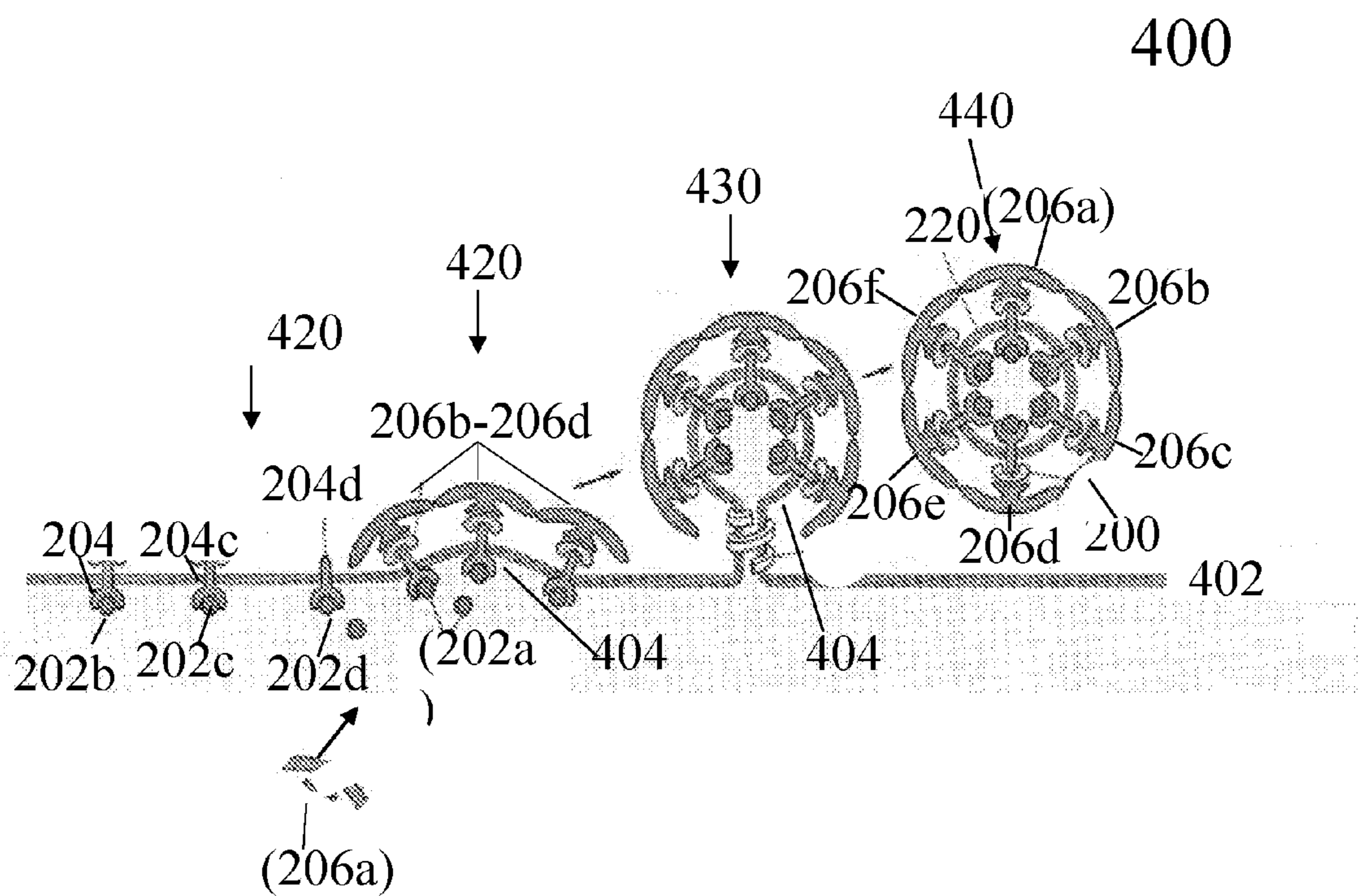


Figure 4

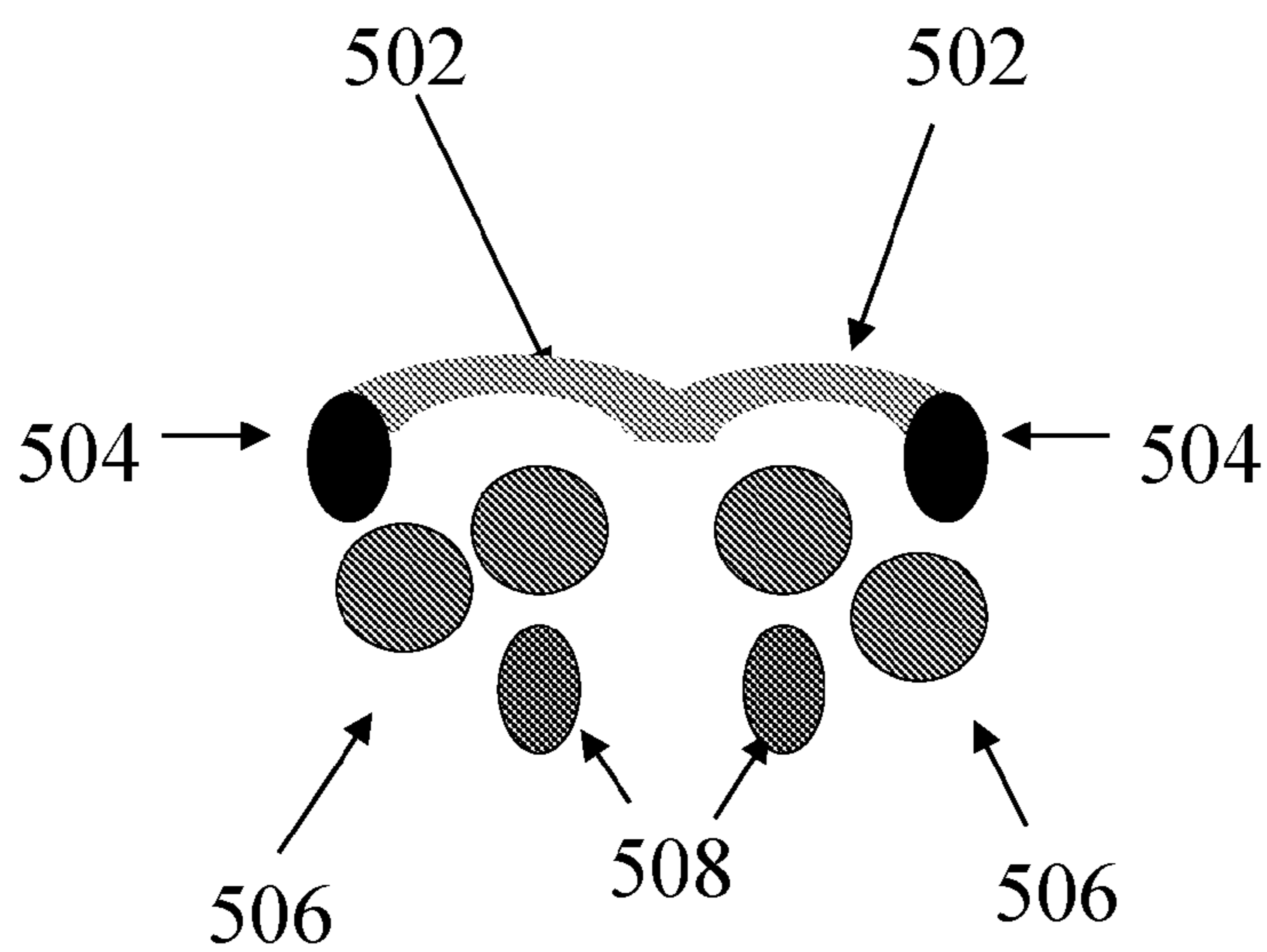


Figure 5

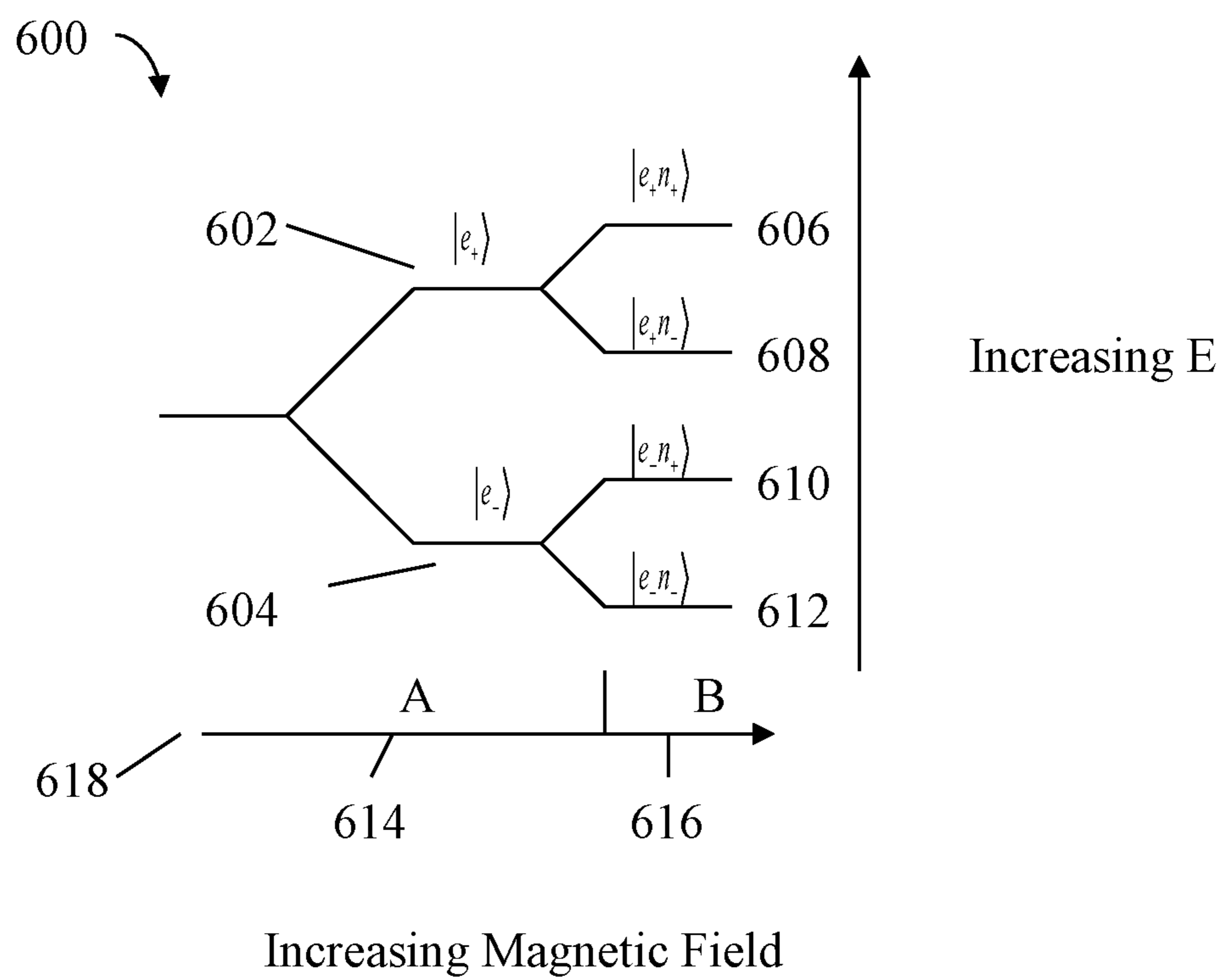


Figure 6

## INTELLIGENT SENSOR PLATFORMS

### FIELD OF THE INVENTION

**[0001]** This is a division of pending USPTO Utility application Ser. No. 12/399,906, with the title, "DYNAMIC BIOMANOPARTICLE ELEMENTS", originally filed on Mar. 6, 2009, and claims priority to that date. The invention relates generally to the field of intelligent, self-adapting, cognitive, autonomous, and scalable sensor platforms. In another invention embodiment, the invention relates to a multifunction sensor platform, such as a biomedical sensor platform, biomolecular sensor platform, electronics sensor platform, communications sensor platform, information processing sensor platform, and the like.

### BACKGROUND OF THE INVENTION

**[0002]** Structures at the nanoscale are sometimes referred to as nanoparticles. Some nanoparticles comprise cage elements that form cavities and or comprise vesicle elements; examples of which in the prior art teach elements such as nano-carbon endohedral cages (Fullerenes); capsids, the protein shell of a virus; liposomes; lipids; heat shock proteins; ferritins; vault ribonucleoprotein particles; Clathrin protein cages; and Coatomer I/II protein cages, among other various cage- or vesicle-forming elements. Additionally, prior art teaches that protein cage elements can coat vesicle elements; for example, Clathrin and Coatomer coated vesicles (CCV's). Additionally, prior art teaches that one or more types of cargo elements can be located internally with respect to a cage and vesicle element.

**[0003]** A cavity forming protein cage and a cage coated vesicle implementation is taught in issued U.S. Pat. No. 7,393,924 (Jul. 1, 2008, Vitaliano et al.) The cage and cage coated vesicle elements are formed in vitro from a plurality of isolated Clathrin/Coatomer protein subunits. As taught in U.S. Pat. No. 7,393,924, the enhanced functionalization capabilities of the isolated Clathrin and Coatomer I/II protein molecules enable a number of properties and features that make them superior to other cage and cage coated vesicle elements in the prior art.

**[0004]** But the instant invention teaches nanoscale element fabrication, assembly, operation, behavior and properties that are unique from prior protein art that encompasses various types of cavity-forming cage structures formed in vitro from a plurality of self-assembling subunits. For example, a fully formed Clathrin cage element as taught in U.S. Pat. No. 7,393,924, and generally speaking taught in other Clathrin art, is comprised of a plurality of 3-legged triskelia, each triskelion having 6 protein subunits; 3 Clathrin heavy chain and 3 Clathrin light chain subunits.

**[0005]** In marked contrast, the instant invention teaches that complete cages comprised of a plurality of 3-legged triskelia are not required to comprise one or more types of efficacious elements. Instead, in its most essential embodiment the instant invention teaches one or more nanoscale elements of one or more types formed from isolated, synthetic and or recombinant amino acid residues comprising in whole or in part one or more types of Clathrin and or Coatomer I/II proteins of one or more isoforms, including cloned isoforms. These isoforms with their differing amino acid sequences comprise (in this example, humans) the various types of Clathrin heavy chains, the various types of Clathrin light chains, encompass the distinct heavy chain and light chain

segments and domains, and in the case of Coatomer, comprise and encompass its domains and subunits, with different combinations of the latter known to exist within Coatomer complexes. Examples of amino acid sequences comprising Clathrin and Coatomer proteins, and their respective isoforms are listed in SEQ ID NO:1 to SEQ ID NO:30. Accordingly, one or more instant invention embodiments may also comprise minimalist, non-cage elements of one or more types. The minimalist element structure afforded by the instant invention affords a much broader and richer variety of element configurations and embodiments than those taught in prior Clathrin or other protein cage art.

**[0006]** For example, freed of the constraints of only forming cavity-forming protein cages in vitro, one or more non-cage invention elements may also form one or more other types of nanoscale elements and structures, enabling new classes and types of applications. Example non-cage embodiments include, but are not limited to, functionalized nanotubule structures; protein-based nano-dendrimers suitable for biomedical and bio-molecular applications; and self-assembling, stable, bioactive, protein-based, hydrogel nanoparticles (nanogels). In other embodiments, one or more nanoscale elements and structures may be additionally formed and comprised of one or more non-invention elements of one or more types. Such structural plasticity and flexible element functionality are not taught in prior protein cage art.

**[0007]** Prior art often teaches one or more types of protein cages that carry one or more types of additional elements, e.g., cargo, to enable overall functionality and produce efficacious results. However, unlike prior art, the instant invention teaches, in one embodiment, one or more non-cage or cage elements may carry no additional elements like cargo, yet still can comprise inherently efficacious elements of one or more types, like drug elements, but not limited to. In one embodiment, one or more invention elements operating alone and without any additional elements such as cargo and the like comprise unique new types of inherently efficacious agents and elements that are distinctly different in behavior and functionality from prior art, and their unique features correspondingly enable new types of applications.

**[0008]** In another embodiment, one or more elements and or their additional elements in whole or in part may require only minimal functionalization to be efficacious; e.g., they may not require PEGylation or other types of functionalization to operate effectively.

**[0009]** In another embodiment, one or more elements carry one or more types of cargo and the cargo acts as the efficacious element. In another embodiment, one or more elements together with cargo elements act in efficacious concert.

**[0010]** In another embodiment, one or more elements are penetrating elements that enter one or more cells and gain access to the cytosol and intracellular elements of one or more types, including one or more cell organelles. Such elements may, in one embodiment, require minimal functionalization. In another embodiment, one or more elements may comprise one or more membrane fusion elements. These various features are not taught in prior protein cage art. In one embodiment, using cell crossing techniques yield efficacious cancer treatments, gene therapy, and the like.

**[0011]** Further, in cage, cavity, and vesicle prior art, one or more types of additional elements, e.g., cargo, are often inserted into a complex, fully formed structure, a sometimes difficult and laborious process. But the invention, in one or more embodiments, teaches that using utilizing non-cage ele-



ments of one or more types makes the addition of one or more elements less difficult as there is no insertion process into a cage, cavity, or vesicle to contend with. In another embodiment, additional element functionalization is simplified by decorating just the external surface of a cage, a feature not taught in prior Clathrin art.

**[0012]** In another embodiment, one or more assay, diagnostic, therapeutic, and prosthetic applications and the like can be performed ensemble using the same bioengineered element.

**[0013]** These various functionalization capabilities enable a highly flexible nano-platform that features improved stability, rigidity, functionality and loading capacity relative to other nanoparticles, and being comprised of ubiquitous proteins, features low antigenicity in one or more embodiments. In one illustrative embodiment, one or more elements may be harmlessly dissolved, passed, and or excreted from the body.

**[0014]** In one embodiment, the current application teaches one or more elements comprising one or more types of hybrid elements and arrangements, which can produce efficacious results. In one embodiment, one or more invention elements are conjugated to natural biological/molecular elements, like cells, but not limited to, forming one or more types of hybrid elements in vitro and or in vivo. Such hybrid elements may operate alone or with additional elements, e.g., with cargo. In another embodiment, such hybrid elements may fuse in vitro and or in vivo with non-invention elements, such as those comprising natural elements in cells, but not limited to. This type of hybrid/fusion capability and flexibility is not taught in the prior art.

**[0015]** In another embodiment, the current application teaches one or more elements, functioning alone or with one or more additional elements, which comprise efficacious replacements for one or more elements of one or more types, including non-invention elements. In one embodiment, one or more elements may replace one or more types of naturally occurring cell elements, to efficacious effect. This replacement capability is not taught in the prior art.

**[0016]** In one embodiment, the instant invention teaches one or more elements, functioning alone or with one or more additional elements, which comprise one or more cellular repair elements, of one or more types; a capability not taught in the prior art. In another embodiment the elements are cellular regeneration elements.

**[0017]** Prior art also does not teach that cage, vesicle elements, or their various subunit elements efficaciously operate in the extra-cellular spaces, e.g., in the synaptic spaces between neurons. But the instant invention teaches one or more types of elements capable of such extracellular operation, including for the in situ remediation, removal and or sequestration of undesirable organic and or non-organic elements.

**[0018]** The invention further teaches a biological model that is consistent, not from the complete cage element level up, but from the minimalist, non-cage element level up, in vitro and in vivo, making drug discovery safer, more efficacious, more time and cost effective, and overall, a much more rapid process than prior art.

**[0019]** In another embodiment, one or more elements may comprise one or more types of minimalist, non-cage elements than that taught in prior art for doing clinical trials of one or more types of agents, including their targeted agent delivery, including high precision dosing.

**[0020]** In one embodiment, the instant invention teaches one or more elements that in whole or in part execute one or

more types of actions for creating, spawning, comprising, modifying, repairing, regenerating, reassembling, and or control and regulation of one or more cells, cellular elements, cell organelles, including like actions and behaviors involving cellular processes such as endocytosis, exocytosis, mitosis, trafficking and signaling, communication between cells, receptor upregulation and downregulation, other behaviors, and the like. Failures and defects in any of these cellular elements and processes can lead to diseases, for example, cancer. This type of efficacious behavior is not taught in prior art, including in protein cage art.

**[0021]** In one invention embodiment, one or more elements, with or without additional elements, and in some embodiments with minimal functionalization, enter the central nervous system, including passing the blood brain barrier (BBB) for efficacious effect. Although different protein cage types, e.g., viruses, have been investigated as MRI nano-probes, some types of these cages in prior art did not cross the BBB, and other types in prior art were shown to be immunogenic after crossing the BBB.

**[0022]** In one embodiment, the invention enables post administration delivery of one or more types of agents into the CNS in 30 minutes or less. In other embodiments, delivery of agents occurs in 30 minutes or more. In another embodiment, agents operate in the inter-neuronal spaces. Prior art does not teach such flexible CNS delivery arrangements.

**[0023]** The instant invention teaches self-directing, self-replicating, self-adapting, self-repairing, self-regulating, and or self-regenerating methods for one or more minimalist, non-cage elements, which can also perform on-the-fly target prioritization. Prior protein cage art does not teach such self-modifying methods at a minimalist, non-cage element level.

**[0024]** Prior art does not teach enabling and or utilizing quantum mechanical effects using just one or more minimalist, non-cage elements. But in one embodiment, the instant invention teaches enabling and utilizing such quantum mechanical effects.

**[0025]** The instant invention also teaches a plurality of elements of one or more types that can, in one illustrative embodiment, function as biomedical platform and the like, and in another example embodiment, function as a biomolecular component platform and the like, or as an information processing platform that can carry out algorithmically defined actions, and other types of platforms.

**[0026]** Thus, there exists a need for an improved bio-nano-structure element that overcomes the limitations in the prior art for various types of in vivo and in vitro applications.

#### SUMMARY OF THE INVENTION

**[0027]** The invention, in one aspect, remedies the deficiencies of the prior art by teaching modifiable, interactive, dynamic bio-nanoparticle elements, some of which may comprise minimalist, non-cage embodiments, with or without one or more additional elements of one or more types located on and or in one or more elements; whose applications, in one or more embodiments, focus on forming in whole or in part one or more nanoscale elements and structures of one or more types that execute one or more functions and or effect one or more ends in vivo and or in vitro.

**[0028]** In one illustrative embodiment, the invention is an improvement over other in vivo biodegradable polymer nanospheres, liposomes, lipids, capsids agent delivery systems, as

well as endohedral Fullerenes and other bio-nanoparticles in the prior art because the invention enables, among other unique features:

- [0029] Simplified nanoscale fabrication
- [0030] Simplified cargo and other element type attachment.
- [0031] Cell and organelle crossing, and or membrane fusion.
- [0032] Low antigenic, “green” nanotechnology.
- [0033] Interaction, control, and regulation of cellular processes, like endocytosis, exocytosis, mitosis, trafficking and signaling, communication between cells, receptor upregulation and downregulation, other cellular behaviors, and the like.
- [0034] Entering the CNS, including passing the blood brain barrier, and in some cases, in less than 30 minutes post administration.
- [0035] One or more elements that carry no additional elements, like cargo, and operating alone produce an efficacious effect, acting like a drug, for example.
- [0036] Hybrid invention elements comprised of one or more types of non-invention elements, e.g., natural cell elements.
- [0037] Self-modifying, orchestrated actions at a minimalist, non-cage level using natural control laws that govern biological elements.
- [0038] Methods and behaviors defined by algorithms.
- [0039] In one particular embodiment, one or more of self-assembling Clathrin and or Coatomer elements are functionalized, modified and or bioengineered using commercially available biotechnology tools and other tools and techniques known in the art, which makes the invention more versatile and cost-effective than the existing art.
- [0040] In another embodiment, one or more elements are also comprised of one or more non-invention elements, e.g., one or more invention elements are conjugated to natural biological/molecular elements, like cells, but not limited to, forming one or more types of hybrid elements in vitro and or in vivo.
- [0041] In one illustrative embodiment, one or more elements can be of any suitable size. According to an illustrative embodiment, one or more elements are nanoscale elements.
- [0042] The invention, in one embodiment, teaches one or more elements that dynamically and interactively respond to changing in vivo and or in vitro environments; e.g., change of pH, temperature, biochemical, or biological conditions, and the like.
- [0043] In one embodiment, one or more elements, in one or more configurations, utilize self-directing, self-adapting, self-assembling, self-repairing, self-regenerating, self-regulating, and or self-replicating methods.
- [0044] In one embodiment, one or more elements, in one or more configurations, utilize goal directed methods.
- [0045] In one embodiment, one or more elements utilize, respond to, and or exhibit one or more effects, such as quantum mechanical, mechanical, photonic, acoustic, electrical, biochemical and chemical, and the like.
- [0046] The invention, in one embodiment, provides one or more elements that maintain structural and or functional integrity long enough to do useful work, in vivo and or in vitro.
- [0047] According to one feature, one or more elements re-supply, repair, reassemble and or regenerate defective,

destroyed and or inoperable elements of one or more types, including non-invention elements, in vivo and or in vitro.

- [0048] In another embodiment, one or more types of elements, unlike other nanoparticles in the art; such as nano-carbon, virus capsids, as well as nano-coating elements like polysorbate; may exhibit no or limited immunogenic, toxic, and or environmental impact effects, and depending on cargo and other element type also may require little or no functionalization,
- [0049] In another embodiment, elements maintain structural integrity at room temperature in vitro and vivo, which eliminates the need for elaborate structure stabilizing mechanisms, like cooling systems.
- [0050] Another advantage of the invention is that its protein material does not exhibit extreme hydrophobicity.
- [0051] According to another feature, one or more elements are protected from the external environment, and the invention is stable with respect to dissociation and any element toxicity is sequestered from the surrounding in vivo and or in vitro environment.
- [0052] In some embodiments, bonding and or attachment methods of one or more types, e.g., covalent, non-covalent, and any other bond type that can be explained by quantum theory, are used to directly attach one or more elements, internally or externally to one or more other elements in an ordered arrangement.
- [0053] In one embodiment, one or more elements each may bond with one or more other elements, of one or more types, including invention and non-invention elements.
- [0054] In one embodiment, one or more elements may additionally have located on and or in them one or more cargo elements of one or more types, formed from one or more types of molecules.
- [0055] In another embodiment, the invention features precise, highly ordered placement of additional elements, like cargo elements, with minimal inter-element spacings on one or more elements and structures.
- [0056] In one embodiment, one or more cargo elements comprise natural, isolated, synthetic and or recombinant elements.
- [0057] In one embodiment, one or more cargo carrying elements include in whole or in part one or more non-invention elements of one or more types.
- [0058] In one embodiment, one or more cargo elements and or cargo carrying elements comprise hybrid elements of one or more types.
- [0059] In one embodiment, one or more elements of one or more types do not carry cargo elements.
- [0060] In one embodiment, nanoscale ensembles comprising one or more types of elements allow for a large variety and number of possible cargo element configurations.
- [0061] In one embodiment, one or more elements may additionally have located on and or in them one or more elements such as ligand elements, receptor elements, adaptor protein elements, and the like, formed from one or more types of molecules, which may also comprise one or more hybrid elements formed from one or more non-invention elements.
- [0062] In another embodiment, one or more elements may be comprised of one or more elements derived in part from one or more types of elements, for example, but not limited to, an amino acid sequence derived from a Clathrin or Coatomer protein.
- [0063] In another illustrative embodiment, one or more elements, in one or more configurations, are coated in whole

or in part with chemicals, metals, biomaterials, and or other substances, of one or more types.

**[0064]** In another illustrative embodiment, one or more elements, in one or more configurations, comprise one or more organic, inorganic, and or synthetic material elements, of one or more types, in one or more forms and or phases, in whole or in part

**[0065]** In one embodiment, one or more elements are radiation shielded, radio frequency (RF) shielded, thermally shielded, chemically shielded, and the like, in whole or in part, and in one or more configurations.

**[0066]** In various embodiments, one or more elements may be of more than one functionalization type, and or express more than one type of functionality.

**[0067]** In one embodiment, one or more elements in whole or in part may require minimal or no functionalization to be efficacious elements, like a drug and the like, but not limited to.

**[0068]** In another embodiment, one or more elements in whole or in part comprise one or more structures, of one or more types.

**[0069]** In another embodiment, one or more elements in whole or in part comprise a shape programmable and or shaped scaffolding system via which one or more elements of one or more types form one or more structures with one or more types of shapes and or functions.

**[0070]** In one embodiment, one or more elements act as one or more types of efficacious replacements for one or more other elements, including non-invention elements, in vitro and or in vivo, e.g., act as replacements for one or more natural elements commonly found in cells, but not limited to. This type of replacement functionality is not taught in prior art, including protein cage art.

**[0071]** According to one approach, various self-assembling and self-directed methods are employed. Elements and or their platforms can be formed from the bottom-up, one element at a time. Another advantage of bottom-up fabrication is that it reduces the amount of superfluous material that surrounds each cargo element, reducing the element's exposure to contaminant background radiation and thereby improving the functional effectiveness of the element.

**[0072]** In one embodiment, the instant application teaches one or more nanoscale elements of one or more types formed from isolated, synthetic and or recombinant amino acid residues comprising in whole or in part one or more types of Clathrin and or Coatomer I/II proteins of one or more isoforms, including cloned isoforms. The efficacious elements may comprise minimalist, non-cage forming elements in one or more embodiments. In other embodiments, one or more Clathrin or Coatomer cage elements comprise efficacious elements.

**[0073]** In one embodiment, one or more elements may additionally comprise a hybrid molecular element formed from one or more other types of molecules.

**[0074]** The instant invention teaches that in one or more non-cage element embodiments it features unique types of dynamic properties and capabilities not found in fully self-assembled, cavity-forming cage structures as taught in the prior art.

**[0075]** In one embodiment, an element is comprised of one or more 3-legged triskelia, each triskelion having 6 protein subunits; 3 Clathrin heavy and 3 light chain subunits. In another example embodiment, the instant invention teaches one or more configurations as being comprised of only 3

Clathrin heavy subunits or only 3 light chain subunits. In another illustrative embodiment, configurations comprised of less than 3 Clathrin heavy or 3 light chain subunits are enabled. In another embodiment, the invention teaches elements comprising in part one or more types of Clathrin and or Coatomer I/II proteins of one or more isoforms

**[0076]** Likewise, the invention teaches one or more highly flexible element embodiments formed from Coatomer I/II proteins. In one embodiment, one or more nanoscale elements of one or more types are formed from isolated, synthetic and or recombinant amino acid residues comprising in whole or in part one or more types of Coatomer I/II proteins of one or more isoforms, including cloned isoforms. Components of both COP1 and Clathrin-adaptor coats share the same structure and the same motif-based cargo recognition and accessory factor recruitment mechanisms, which leads to insights on conserved aspects of coat recruitment, polymerization and membrane deformation. These themes point to the way in which evolutionarily conserved features underpin these diverse cell pathways.

**[0077]** In one example embodiment, one or more elements comprised of Coatomer (COPI and COPII) proteins, which can efficaciously act alone or with additional elements, are used instead of Clathrin proteins, preferably in those applications where Coatomer characteristics would be more desirable than those of Clathrin. Coatomer I/II protein elements may, in one or more embodiments, be comprised of one or more alpha, beta, beta', gamma, delta, epsilon and or zeta subunits. Different combinations of these subunits are known to exist within Coatomer complexes. According to an illustrative embodiment, a Coatomer subunit is a nanoscale element. In one invention embodiment, Clathrin and Coatomer elements and one or more methods may be used together in one or more configurations, taking advantage of their respective capabilities.

**[0078]** Freed from the constraints of only assembling into cavity forming cages in vitro, one or more non-cage elements of one or more types may self-assemble into one or more other types of complex elements and or material forms, enabling new classes of applications. For example, but not limited to, using techniques known in the art, bioengineered strands of Clathrin and or Coatomer proteins form functionalized nano-tubules (Zhang, et al. 2007) for biomedical applications and bio-molecular components. In another bioengineered embodiment, invention elements comprise repeatedly branched, highly symmetrical structures, forming protein-based nano-dendrimers suitable for biomedical and bio-molecular applications. In another embodiment, self-assembling, stable, bioactive, protein-based, hydrogel nanoparticles (i.e., nanogels), some with tunable structural properties, are enabled. Generally, hydrogels are of interest to the biomedical field, e.g., for treating trauma, because the hydrated networks can provide a physiological environment where biological species can survive or grow. In other embodiments, one or more other types of non-cage forming structures, elements, and forms of materials comprised of invention elements are formed using techniques known in the art.

**[0079]** Unlike cage, cavity, and vesicle systems in the prior art where one or more additional elements, e.g., cargo, are inserted into a complex, fully formed structure; a sometimes difficult and laborious process; the invention, in one embodiment, teaches that it can be functionalized with one or more additional elements at a much more fundamental nano-ele-

ment level, e.g., by using non-cage elements of one or more types formed from amino acid residues of Clathrin or Coatmer proteins. Such functionalized, minimalist elements may further self-assemble in vitro into one or more nanoscale structure elements, including cages. This makes the addition of one or more elements easier and simpler as there is no insertion process into a completely formed cage, cavity, or vesicle. In another embodiment, additional element functionalization is simplified by decorating just the external surface of a cage.

**[0080]** According to one illustrative configuration, one or more types of elements, such as cargo elements, may interfere with the invention's overall operation if carried in the same element as other element types. Instead, the problematic elements are carried in a separate element that exclusively carries non-interfering elements, thereby inhibiting disruptive interference of invention operations. Such non-interfering elements may be functionally and or physically linked with other elements carrying other element types.

**[0081]** In one embodiment, one or more elements efficaciously operate alone and carry no additional elements, e.g., cargo. In one embodiment, such solo element functionality produces a unique new type of efficacious element, and its unique features correspondingly enable new types of applications.

**[0082]** Some embodiments include a molecule having an unpaired electron, a transition metal ion, which can be found in the active centers of many proteins (metalloproteins), or a material having any defect that produces an unpaired electron.

**[0083]** According to one in vivo application for enhanced medical imaging, paramagnetic lanthanide, transition metal ion complexes, and the like are cargo elements that modify the NMR relaxation times of nearby proton nuclei of H<sub>2</sub>O molecules, leading to brighter images and enhanced contrast between areas comprising the contrast agent and the surrounding tissues.

**[0084]** In another illustrative embodiment, one or more elements accept free radical molecules such as nitroxide molecule spin labels for electron paramagnetic resonance (EPR) based invention applications.

**[0085]** In another illustrative embodiment, one or more elements accept and or comprise one or more types of labels and assay strategies, and instruments for detection of one or more such labeled and or assay elements may include, but are not limited to: fluorescence and confocal microscopy, flow cytometry, laser scanning cytometry, fluorescence microplate analysis and biochips, immunoassay systems, nucleic acid-based diagnostics, and the like. In various embodiments, one or more elements meet and or surpass the requirements for label and assay sensitivity, accuracy and convenience.

**[0086]** In another embodiment, one or more types of elements such as comprising in whole or in part one or more large molecule elements, small molecule elements, cargo elements, agent elements, device elements, drug elements, and the like, enter the CNS, including passing the blood brain barrier, in 30 minutes or less and or in 30 minutes or more, post administration, and, depending on cargo and other element type, may require minimal functionalization for such element passage.

**[0087]** In some configurations, one or more elements comprise a cargo element, while in other configurations they comprise multiple elements, of one or more types. In some configurations, one or more or each of the elements and or

cargo elements is a metal, and or may include one or more metals. Alternatively, each of the elements and or cargo elements is or includes non-metal elements. In other embodiments, elements and or cargo elements are exclusively non-metal elements that may include gases, as well as other elements like biological elements, drugs, optics, polymers, etc. In another embodiment, one or more elements and or additional elements comprise one or more types of material forms, including a solid, gas, vapor, crystal, and the like. In another embodiment one or more invention and or non-invention elements, in one or more combinations, comprise one or more types of isolated, synthetic and or recombinant elements.

**[0088]** An invention element, in one functionalized configuration, includes receptor molecules; natural, isolated, synthetic and or recombinant, for capturing and ordering the placement of one or more elements, like cargo elements, on one or more elements.

**[0089]** An invention element, in another functionalized configuration, includes adapter molecules; natural, isolated, synthetic and or recombinant, disposed between the receptor molecules and one or more elements to couple the receptor molecules to another element, like to a cargo element.

**[0090]** An invention element, in one functionalized configuration features ligands, natural, isolated, synthetic and or recombinant, including drugs, of one more types attached to receptors and or adapter protein elements.

**[0091]** In one configuration, one or more elements, of one or more types, are attached to one or more types of amino acids on one or more elements.

**[0092]** In another configuration, biotin-avidin is used as a coupler of one or more elements, of one or more types, to one or more elements of one or more types.

**[0093]** In another configurations, PEGylation, a cross-linker, molecular bridge, molecular tether, and the like are used to attach one or more elements, of one or more types, to one or more elements of one or more types.

**[0094]** In one example, molecules of one or more types are attached to a short molecular tether to one or more elements via site directed substitution mutagenesis, followed by reaction of a unique amino acid group with a specific molecular label.

**[0095]** In another embodiment, free radicals, toxic elements, other types of undesirable elements and the like circulating within an in vivo environment are scavenged via molecular tethers, via other elements of one or more types attached to one or more invention elements, and or via direct binding to one or more elements.

**[0096]** In another embodiment, the invention takes full advantage of protein flexibility and plasticity to create elements of one or more types that are bonded, fastened, fused, and or affixed to one or more other elements, of one or more types.

**[0097]** In one illustrative embodiment, one or more elements and or bonded elements are coated in whole or in part with other elements, such as chemical, biological and or metallic materials, and the like. The coating elements may be or include organic, inorganic, and or synthetic materials, or a combination thereof.

**[0098]** In another invention embodiment, site directed mutagenesis is used to incorporate one or more elements, of one or more types, into one or more other elements, of one or more types.

**[0099]** In one embodiment site-directed mutagenesis using one or more types of primer; including its reverse complement; are used to insert one or more DNA sequences of one or more types into one or more coding regions of one or more elements.

**[0100]** In another embodiment, cloning is done of one or more genes encoding one or more elements. In another embodiment, one or more amino acids and or their encoder gene are controlled, regulated, modified, and the like, by one or more methods known in the art to produce an efficacious effect, in vivo and or in vitro.

**[0101]** In one embodiment, one or more elements of one or more types comprise targeted and or non-targeted drug elements, biological elements, other forms of healthcare elements, including cosmetic elements, in one or more configurations or combinations, for diagnosing, remedying, inhibiting, mitigating, curing, and or preventing one or more types of diseases, infections, physical or mental trauma, other forms of physical and mental afflictions, and the like, of one or more types, including types featuring minimal immunogenic and or toxic effects.

**[0102]** In one embodiment, one or more elements are used as a means for evaluating drug advancement and efficacy.

**[0103]** The invention teaches a biological model and or method that is consistent from a minimalist component level up, e.g., amino acid residues comprising in part one or more Clathrin and or Coatomer I/II proteins of one or more isoforms, making drug discovery safer, more efficacious, more time and cost effective, and overall, a much more rapid process.

**[0104]** In one personalized medicine embodiment, the invention reduces drug side effect profiles and or produces greater agent efficacy, as well as excludes agents that may have no efficacy in a particular individual. The invention, in one embodiment, provides for individual patient factors such as genotype, phenotype, age, gender, ethnicity etc., to be taken into account by one or more elements and factored into dosing and administration consideration.

**[0105]** In one embodiment, one or more elements comprise one or more types of pluripotent stem cells and or comprise one or more stem cell delivery methods.

**[0106]** According to one feature, one or more elements may be or include one or more research, therapeutic, diagnostic, vaccine, assay, and or prosthetic agents, in one or more configurations, and thereby constitute one or more types of biomedical elements. Such biomedical elements may be, for example, nano-structured and/or include chemical, biological and/or metallic materials. The biomedical elements may be or include organic, inorganic, and or synthetic materials, or a combination thereof.

**[0107]** Medical, biomedical, bioengineered, and or biological applications and platforms of the instant invention may include, but are not limited to, imaging; sensor; genetic and protein assay; diagnostic; drugs and drug delivery; prosthetic; inter- and extra-cellular tissue; whole organ; circulatory system; medical device; implantable defibrillator; pacemaker; coronary stents; angioplasty device; and other like applications.

**[0108]** In one embodiment, one or more elements comprise one or more applications that perform analysis, of one or more types, of disorders of complex inheritance.

**[0109]** In one embodiment, one or more elements comprise one or more applications that perform analysis, of one or more types, of pharmacologic therapy.

**[0110]** In one embodiment, one or more elements comprise one or more types of prognosis and therapy selection—“theragnostics”.

**[0111]** In one embodiment, one or more elements comprise one or more genomic applications of one or more types.

**[0112]** In one embodiment, one or more elements comprise one or more oncology applications of one or more types.

**[0113]** In one or more embodiments, one or more elements may use routes of administration comprising one or methods of one or more types, such as those defined by CDER Data Element Number C-DRG-00301 in the US FDA Data Standards manual. Routes of in vitro administration of one or more elements may also comprise one or more forms.

**[0114]** In one or more embodiments, one or more pharmaceutical and drug formulations of one or more types are used, in whole or in part, such as tablet, capsule, soft galantine capsule, topical, injections, eye drops, syrups and liquids, soap and cosmetics, birth control device, and the like, but not limited to, as well as one or more types of biologics, chemical compounds, water soluble compositions, and the like, but not limited to. In vitro formulations may also comprise one or more formulations of one or more types in one or more embodiments.

**[0115]** According to one feature, one or more elements respond to one or more external and/or internal stimuli, which can be, for example, mechanical, chemical, biochemical, biological, metabolic, covalent, non-covalent, photonic, sonic, acoustical, thermal, fluidic, electromagnetic, magnetic, radioactive, quantum mechanical, or electrical in nature. Examples of such a stimulus response is altering a cargo element carried by an element; the altering of the element itself; causing changes in cellular process like endocytosis, exocytosis, mitosis, trafficking and signaling, and the like, including other conformational changes.

**[0116]** In another embodiment, photonic energy impacting one or more elements produces electrical current, and or photonic energy, e.g., a laser.

**[0117]** In general, in another embodiment, one or more element and or platform are physically and/or functionally cooperative with other suitable types or forms of elements, agents, organisms, materials, substances, components, devices, and or systems, including non-invention elements, in vitro and/or in vivo.

**[0118]** The invention, in one embodiment, provides for a plurality of elements comprising aggregated, complex self-assembled nanoscale structures that dynamically bind together one or more types of endogenous, exogenous, homogeneous, and or heterogeneous elements into one or more complex elements, which also may have one or more payload types.

**[0119]** The invention, in one embodiment, provides a capability for in vivo and in vitro integration of one or more types of elements into other elements, devices and mechanisms, some of which may also be non-invention elements, that also may be linked together functionally or logically, including with other devices and or operators, locally or at a distance, significantly enhancing the overall capabilities of the invention.

**[0120]** In one embodiment, the invention provides for the ability of one or more elements to track, recognize, attack and or destroy multiple targets on the fly, in vivo and in vitro, using dynamic target prioritization for a single element type and or multiple element types.

**[0121]** In one application, one or more elements, including cargo elements, comprise one or more types of targeted agent delivery systems and or agents in vivo or in vitro, including high precision dosing, using, as appropriate, ligands, targeting moieties, and or other vectors. In one application, one or more targeted elements comprise one or more research, remedial, inhibitory, mitigation, preventive, prosthetic, assay, and or other type of bio-molecular agent or device, in one or more combinations, and may altogether comprise a unified element and or platform.

**[0122]** The invention, in one embodiment, provides for a method for targeted delivery systems that leverage and utilize biological control laws and that may act as self-directed systems.

**[0123]** According to another invention embodiment, one or more targeted elements may use molecular-imprint technology, which is used for the production of molecule-specific cavities that mimic the behavior of receptor binding sites, without the temperature sensitivity of natural systems.

**[0124]** According to another feature, biodegradable films may also be used as a pliable template for one or more targeted elements, which are pressed into a biodegradable film and then removed, leaving a physical mold of the element's shape. The film can then be hardened and used by an element to detect a particular element, which may be, but is not limited to, a particular receptor, protein, or cell, since its complex imprint shape on the film will bind only to that particular biological element.

**[0125]** In one embodiment, the invention provides for a targeting system using biodegradable nanocapsules for delivery of one or more elements in vivo or in vitro.

**[0126]** In another application, a nanoscale platform comprised of a plurality of elements performs molecular-level and or cellular-level target site loitering, monitoring, repair, construction and or dynamic, interactive control and regulation of biological systems, in vitro and in vivo.

**[0127]** In another embodiment, one or more elements, including in whole or in part one or more non-invention elements, operating alone or with one or more additional elements, comprise one or more types of membrane fusion elements. In one embodiment, the resulting biological processes and interactions from such fusion may lead to a series of controlled, regulated, extended, modulated, purposefully, and or self-directed methods and or behaviors of elements.

**[0128]** In one example embodiment, one or more elements in whole or in part execute one or more types of actions involving conformational changes, bonding, attachment, and or the fusion of one or more elements to a cell membrane, one or more of which actions may lead to changes in cellular processes, such as endocytosis, exocytosis, mitosis, trafficking and signaling, and the like, and or enable the precise dispatch and sequenced delivery of selected agents from an element to a target cell. Alternatively, a series of interlocking steps between a part of a cell membrane, and all, or a subset of the materials comprising an element may cause the cessation of one or more element's delivery to a target cell, and or enable delivery from other sources.

**[0129]** In another configuration, one or more elements dynamically respond to natural environmental conditions and manifest special functions. The various control laws that regulate biochemical reactions and physiological processes often display features that allow biomolecules or biological structures to perform more tasks than are reasonably expected from a simple mechanical device. In one embodiment, the

invention takes deliberate advantage of these biological control laws. Via the use of bio- and genetic engineering methods known in the art, the invention makes use of these control laws to dynamically regulate complex in vivo and in vitro biochemical reactions and physiological processes. An example of biological control laws at work is the automatic self-directed, self-assembly of in vitro and in vivo Clathrin and Coatomer proteins.

**[0130]** In one embodiment, intramolecular dynamics of biomolecules and the concerted and interlocking steps of conformational changes lead to deliberately purposeful actions. For example, one or more elements may fit spatially and each step in a process fits temporally (kinetically) with an element of anticipation of the purposeful outcome.

**[0131]** In another example case, the spatially and temporally defined events between the cell and one or more elements may cause the invention to release diagnostic and monitoring agents to determine the most appropriate course of therapeutic action. The calculated utilization of biological control laws by one or more elements may, for example, provide for a sophisticated drug delivery system that provides optimal dosing by altering its drug delivery behavior, as well as producing minimal side effect profiles.

**[0132]** A further advantage of the invention is that it provides elements that can be bio-engineered to prevent in vivo uptake by one or more types of organs, tissue, cells, and bone. In the converse, another advantage is that one or more elements can be bio-engineered for highly selective uptake by one or more types of targeted cells, tissue, organs, bone, as well as by other organic and inorganic matter. In another embodiment, one or more elements comprise a non-selective uptake, non-targeted drug delivery system.

**[0133]** In another embodiment, the invention provides for the ability of one or more elements to intelligently monitor, control and regulate, react, and further adjust biological processes after delivery of the payload, enabling high precision dosing.

**[0134]** Another advantage of the invention is that Clathrin can cross cell membranes including the blood brain barrier (Gragera et al 1993) and can move through the synaptic clefts (Granseth et al 2007). In one embodiment, bioengineered Clathrin actively transports substances in and out of cells including neurons and blood brain barrier cells.

**[0135]** In another embodiment, one or more elements, operating alone or with one or more additional elements, comprise one or more types of cell membrane crossing elements and gain access to the cytosol and intracellular elements of one or more types, including one or more cell organelles. Such elements may, in one embodiment, require minimal functionalization to cross the cell membrane and or enter a cell organelle.

**[0136]** In one embodiment, one or more elements, in whole or in part, in one or more combinations, take one or more actions to create, spawn, comprise, modify, regenerate, reassemble, and or control and regulate one or more cells, cellular elements and or cellular processes of one or more types.

**[0137]** In one embodiment, one or more elements, in whole or in part, in one or more combinations, take one or more actions to rectify and or repair failures and defects in cellular processes, such as, endocytosis, exocytosis, mitosis, trafficking and signaling, and the like. Such failures and defects can lead to diseases, for example, cancer.

**[0138]** In one embodiment, one or more elements comprise in situ in vivo elements for remediation, removal and or

sequestration of one or more types of contaminants, toxins, undesired organic or inorganic elements, and the like.

**[0139]** In one embodiment, one or more elements comprise in situ environmental elements for remediation, removal and or sequestration of one or more types of in vitro environmental contaminants and or toxins; for example, chlorinated solvents TCE, PCE, PCBs, c-DCE, DNAPL, heavy metals (chromium), biofilm, synthetic chemicals, and the like.

**[0140]** In one embodiment, some or all elements may also operate under the control and influence of other in vitro and or in vivo elements, including non-invention elements, and altogether may comprise a scalable, nanoscale platform.

**[0141]** In general, in another aspect, the invention is directed to a method of forming one or more types of scalable platforms, including the steps of providing one or more embodiments of the elements to deliberately carry out a series of tasks of one or more types, which tasks and or methods may be externally directed or internally self-directed, or a combination thereof. In other embodiments, one or more nanoscale platforms may be additionally comprised of one or more non-invention elements and platforms of one or more types.

**[0142]** One or more elements, in one platform embodiment, may also modify, process, manipulate, encode and decode, input, output, transmit, communicate, store and or read information using techniques and methods known in the art, in vivo and in vitro.

**[0143]** In one embodiment, scalable information processing platforms use some or all elements as bits that are programmable into a plurality of logical states. In another configuration, the invention features a scalable information-processing platform that may include one or more elements.

**[0144]** As a general characteristic, one or more elements may take any suitable form, and multiple embodiments may be used as elements, and or further combined in any suitable manner to create one or more cargo carrying and or non-cargo carrying nanoscale elements (“elements”), and or multifunction nanoscale platforms (“platforms”) of one or more types, operating in vitro and or in vivo, such as: multiple polypeptide elements and platforms; biological elements and platforms; large molecule elements and platforms; small molecule elements and platforms; biomedical elements and platforms; medical elements and platforms; diagnosis, cure, mitigation, treatment, prevention of disease or other type of drug elements and platforms; targeted and or non-targeted delivery elements and platforms; cell, cell organelles, or cell material crossing elements and platforms; personal medicine elements and platforms; elements and platforms that, post administration, in whole or in part enter the central nervous system, including passing the blood brain barrier in 30 minutes or less and or in 30 minutes or more; healthcare elements and platforms; reproductive health elements and platforms; substance abuse disorder treatment elements and platform; bioengineered elements and platforms; cosmetic elements and platforms; agricultural elements and platforms; sensor elements and platforms; research and development elements and platforms; scientific elements and platforms; crystal elements and platforms; electronic elements and platforms; photonic energy elements and platforms; information processing or storage elements and platforms; energy storage elements and platforms; in situ elements and platforms for remediation, removal and or sequestration of undesirable elements and platforms of one or more types; quantum mechanical elements and platforms; telecommunication elements and platforms; and the like; one or more of which nanoscale elements

and platforms may be additionally comprised of one or more non-invention elements and platforms of one or more types, and with or without one or more types of cargo elements located on and or in one or all or a subset of elements.

**[0145]** In general, in a further aspect, the invention is directed to a method of forming one or more formations of nanoscale elements formed in vitro from one or more elements of one or more types formed from isolated, synthetic and or recombinant amino acid residues comprising in whole or in part one or more types of Clathrin and or Coatomer I/II proteins of one or more isoforms, including cloned isoforms; with or without one or more additional elements of one or more types located on and or in one or more elements; forming in whole or in part one or more types of element carrying and or non-element carrying nanoscale elements and structures; one or more of which elements may also comprise one or more non-invention elements of one or more types, forming hybrid elements; wherein one or more elements, using one or more types of methods, executes one or more functions and or effects one or more ends in vivo and or in vitro.

#### BRIEF DESCRIPTION OF THE DRAWINGS

**[0146]** The foregoing and other aspects of the invention may be more fully understood from the following description, when read together with the accompanying drawings in which like reference numbers indicate like parts.

**[0147]** FIG. 1 is a conceptual diagram depicting a Clathrin triskelion comprised of one or more elements of one or more types employed in an illustrative embodiment of the invention.

**[0148]** FIG. 2 is a conceptual cross-sectional view of one or more Clathrin protein, receptor, adaptor protein, and cargo elements in an illustrative embodiment.

**[0149]** FIG. 3 is a computer generated frontal view of an actual Clathrin cage comprised of a plurality of Clathrin triskelia, and, in an illustrative embodiment, comprising one or more invention elements.

**[0150]** FIG. 4 is a flow diagram depicting conceptually the formation of individual Clathrin elements during endocytosis, which also serves to illustrate how the instant invention operates in one or more embodiments.

**[0151]** FIG. 5 is a conceptual diagram depicting Coatomer I/II protein comprised of one or more subunit and domain elements of the type employed in an illustrative embodiment of the invention.

**[0152]** FIG. 6 is an exemplary energy level diagram 600 illustrating the energy levels associated with a hyperfine interaction between electron and nuclear spin in the presence of magnetic fields.

#### DESCRIPTION OF THE ILLUSTRATIVE EMBODIMENTS

**[0153]** The instant invention is comprised of one or more formations of nanoscale elements formed in vitro from one or more elements of one or more types formed from isolated, synthetic and or recombinant amino acid residues comprising in whole or in part one or more types of Clathrin and or Coatomer I/II proteins of one or more isoforms, including cloned isoforms, and which operate in vitro and or in vivo. In one embodiment, one or more elements form one or more configurations of one or more types, described below.

**[0154]** FIG. 1 is a conceptual diagram illustrating the basic unit of Clathrin, a three-leg pinwheel protein structure, and

each complete leg is typically called a ‘monomer’. The arrangement of the monomers in the three-dimensional protein is the quaternary structure. Each Clathrin leg monomer is further comprised of two subunits, one 190 kDa subunit (“heavy chain”) and one 24-27 kDa subunit (“light chain”). Three, two-subunit Clathrin monomers self-assemble and combine to create triskelion element **100**. It is this triskelion morphology that allows Clathrin to form its unique polyhedral network.

[0155] In FIG. 1, the assembled triskelion element **100** is comprised of three monomer leg elements **102a-102c**. The three leg elements **102a-102c** extend radially from a hub section **108**. The filamentous portion of Clathrin triskelion legs **102a-102c** is formed by a continuous superhelix. A naturally occurring Clathrin leg is about 47.5 nm (475 Å) long. In the instant invention, Clathrin leg length and or molecular weights can be modified and or adjusted by using bioengineering techniques known in the art.

[0156] In the case of humans, there are two isoforms each of Clathrin heavy chain (CHC17 and CHC22) and light chain (LCA and LCB) subunits, all encoded by separate genes. CHC17 forms the ubiquitous Clathrin-coated vesicles that mediate membrane traffic. CHC22 is implicated in specialized membrane organization in skeletal muscle. CHC 17 is bound and regulated by LCA and LCB, whereas CHC22 does not functionally interact with either light chain.

[0157] In one embodiment, a Clathrin triskelion is composed of a trimer of heavy chains **104a-104c** each bound to a single light chain **106a-106c**, respectively. In the case of one isoform embodiment, CHC17 (SEQ ID NO:1), a Clathrin heavy chain element is comprised of a 1675 amino acid residue protein, which is encoded by a gene consisting of 32 exons. In the case of another isoform embodiment, CHC22, a Clathrin heavy chain element is comprised of a 1640 amino acid residue protein (SEQ ID NO:2).

[0158] In one or more invention embodiments, efficacious elements formed in part from Clathrin amino acid residues include, but are not limited to, a N-terminal globular domain **110a-110c** (residues 1-494) that interacts with adaptor proteins (e.g., AP-1, AP-2, b-arrestin), a light chain-binding region (residues 1074-1552), and a trimerization domain (residues 1550-1600) near the C-terminus.

[0159] One or more of the Clathrin heavy chain amino acid sequences as described in SEQ ID NO:1 and SEQ ID NO:2, but not limited to, and in whole or in part may be modified, altered, adapted or functionalized in one or more ways in one or more embodiments of the invention.

[0160] In the illustration, the three Clathrin monomer elements **102a-102c** are comprised of six subunit elements, three of which subunits are the heavy chain subunit elements **104a-104c**. The three heavy chain subunits are comprised of several distinct domains and segments, one or more of which may comprise one or more invention elements in one or more embodiments, and may be functionalized via one or more techniques known in the art.

[0161] In general, each heavy chain comprises eight repeated motifs (CHCR 0-7), which make up the proximal, knee, distal and ankle segments of a Clathrin leg. The heavy-chain amino terminus folds into the terminal domain (TD) and is attached to CHCR0 by a helical linker. (Brodsky, 2004). The three Clathrin heavy chains are joined at their C-termini (located within hub element **108**), extending into proximal and distal leg domains ending in globular N-terminal domain elements **110a-110c**, and which are responsible

for peptide binding. The Clathrin heavy chain terminal domains provide multiple interaction sites for a variety of adaptor proteins (AP) that can bind multiple receptors occupied by ligands. These sites prevent chemical interactions between cargo elements. The heavy chain N-terminal domain elements **110a-110c** are each comprised of a seven-bladed beta-propeller connected to a flexible physiological er region, respectively. This propeller domain interacts with a host of accessory proteins participating in receptor-mediated endocytosis such as adaptor proteins, non-visual arrestins and the uncoating ATPase, hsc70. The propeller domain is followed by a long filamentous segment, which is interrupted by a bent region between the distal and proximal domains, and ends in the trimerization domain at the C-terminus.

[0162] Besides harboring determinants important for driving the association of individual Clathrin molecules during lattice formation, each of the three heavy chain **104a-104c** proximal domains also include binding sites for attaching the three light chain subunit elements **106a-106c**, respectively, forming three complete Clathrin monomers. The three light chain subunits are also comprised of several distinct domains and segments, one or more of which may comprise one or more invention elements in one or more embodiments, and may be functionalized via one or more techniques known in the art.

[0163] Among other roles, Clathrin light chains prevent Clathrin heavy chains from interacting with each other. On the other hand, assembly proteins bind to light chains and cause a change in them such that they no longer prevent heavy chains from interacting. Clathrin light chains consist of what has been described as a linear array of domains: regions of protein discernable from the primary sequence or with distinct biochemical properties. These are an N-terminal segment, a region that is 100% conserved between light chains, a portion to which Hsc70 binds, a calcium binding domain, a region which binds the heavy chain, a site for neuronal-specific splice inserts and then finally a calmodulin-binding domain at the C-terminus domain (Royle, 2006). The light chain C-terminal residues are also important for enhancing the in vitro assembly of hub **108** at low pH.

[0164] One or more of the Clathrin light chain amino acid sequences as described in SEQ ID NO:12 and SEQ ID NO:13 but not limited to, and in whole or in part may be modified, altered, adapted or functionalized in one or more ways in one or more embodiments of the invention.

[0165] In one embodiment, each of the 3 heavy chain subunits **104a-104c** may each have 3 light chains subunits **106a-106c** attached, respectively, forming the typical, three-monomer Clathrin triskelion structure. But in another embodiment, each leg **102a-102c** may include only the 3 Clathrin heavy chain subunits **104a-104c**, respectively, which is distinctly unique from the classic Clathrin monomer configuration. In yet another unique embodiment, only 3, non-attached light chain subunits **106a-106c** are used.

[0166] In one distinctive embodiment of the invention, a 3-legged pinwheel configuration **100** is not enabled, and only partial pinwheel structures are used. In one embodiment, a partial pinwheel configuration of one or two legs (one or two Clathrin monomers) is comprised of one or two Clathrin heavy chains and one or two corresponding light chain subunits. In another embodiment, one or two elements comprised of only one or two Clathrin heavy chain subunits are used; e.g., subunits **102a**, or **102a-102b**. In one embodiment, only one or two unattached light chain subunits are used.



[0167] In another distinctive embodiment of the invention, one or more elements of one or more types are formed from isolated, synthetic and or recombinant amino acid residues comprising in part one or more types of Clathrin heavy chain and or light chain proteins of one or more isoforms as described in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:12 and SEQ ID NO:13, respectively.

[0168] In one embodiment, one or more N-terminal domain elements, e.g., 110a, 110b and or 110c are bioengineered to facilitate, modify, regulate or control peptide binding of one or more types, as well as interaction sites for one or more types of adaptor proteins.

[0169] In one embodiment, one or more domain elements of heavy chain subunits and or light chain subunits are bioengineered to facilitate, modify, regulate or control one or more Clathrin protein characteristics and or behaviors in vivo and or in vitro.

[0170] FIG. 2 is a conceptual cross-sectional view of a biological endohedral consisting of Clathrin protein elements. In this illustrative embodiment, one or more elements 102a-102c, 106a-106c, 104a-104c, 110a-110c, element 108, and or one or more types of elements formed from isolated, synthetic and or recombinant amino acid residues comprising in whole or in part one or more Clathrin proteins of one or more isoforms, and with or without one or more additional elements of one or more types, may comprise one or more multiple polypeptide elements of one more types. The latter are labeled in FIG. 2 as elements 206a, 204a, 202a, and 208a, which are formed in vitro, and also may operate in vitro and or in vivo. One or more of elements 206a, 204a, 202a, and or 208a may comprise one or more types of functionalization, include invention and non-invention elements, express one or more types of functionality, and or form one or more types of structures.

[0171] In one illustrative embodiment, but not limited to, one or more elements 206a may comprise one or more elements 102a-102c, 106a-106c, 104a-104c, 110a-110c, element 108, and or one or more types of elements formed from isolated, synthetic and or recombinant amino acid residues comprising in whole or in part one or more Clathrin proteins of one or more isoforms, and express one or more types of functionality in one or more embodiments.

[0172] In another embodiment, one or more elements 206a may be comprised of, and or help comprise one or more types of non-invention elements, such as a natural cell element in one embodiment, comprising one or more types of hybrid elements in one or more embodiments.

[0173] In another embodiment, one or more elements 206a may be comprised of, and or help comprise one or more types of isolated, synthetic, recombinant and or natural molecules in one or more embodiments.

[0174] In one illustrative embodiment, but not limited to, one or more elements 202a may comprise cargo elements of one or more types, including natural, isolated, synthetic and or recombinant, including natural and or synthetic ligands and or drugs, and may express more than one type of functionality. In one embodiment, one or more other elements, of one or more types, including invention and non-invention elements each may bond with one or more respective cargo elements 202a.

[0175] In one embodiment, one or more cargo elements 202a are cavity forming and are non-permeable, semi-permeable, and or permeable, and or can change from one permeable state to another. In one embodiment, the cavity forming

elements comprise one or more types of elements and or agents, including gas, vapor or fluid, with or without dopants. In one embodiment, one or more cargo cavities elements comprise one or more types of elements and or agents, including one or more types of metals.

[0176] In another illustrative embodiment, one or more efficacious cargo elements 202a carried on one or more elements may comprise the total functionality. In another embodiment, one or more other elements, of one or more types, including invention and non-invention elements may act in concert with one or more cargo elements 202a to achieve ensemble efficacy.

[0177] In one embodiment, but not limited to, one or more elements 204a may comprise attachment and or receptor elements for one or more elements 202a of one or more type, and or express more than one type of functionality. In one embodiment, one or more other elements, of one or more types, including invention and non-invention elements each may bond with one or more respective elements 204a. In another embodiment, receptor molecules 204a can be bioengineered to recognize and associate with specific molecules, which may also be synthetic and or natural ligands and or drugs. In another embodiment, receptor molecules 204a can be natural, isolated, synthetic and or recombinant.

[0178] In one embodiment, but not limited to, one or more elements 208a of the instant invention may comprise the major types of adaptor elements, like the heterotetrameric adaptor protein (AP) elements, and the monomeric GGA (Golgi-localizing, Gamma-adaptin ear domain homology, ARF-binding proteins) adaptors. In one illustrative embodiment, elements 208a comprise one or more small sigma subunits of various adaptins from different AP adaptor elements. The AP complex family has six members in mammals: AP-1A, AP-2, AP-3A and AP-4 are ubiquitously expressed. The other two members, AP-5 and AP-6, are cell-type specific isoforms of AP-1A and AP-3A: the epithelium-specific AP-1B and the neuron-restricted AP-3B. (Ohno, 2006). In another embodiment, AP180, like AP-2 and AP-3, binds to N-terminal domains 110a-110c of Clathrin. In one embodiment, one or more AP elements may be functionalized at one or more heavy chain terminal domain elements 110a-110c. In one embodiment, one or more other elements, of one or more types, including invention and non-invention elements each may bond with one or more respective elements 208a. In another embodiment, adapter molecules 208a are bioengineered to recognize specific receptor molecules and to couple the receptor molecules to Clathrin and or Coatomer protein elements. In another embodiment, adapter molecules 208a can be natural, isolated, synthetic and or recombinant.

[0179] In one embodiment, one or more elements 206a, 204a, and or 208a operate alone without cargo element 202a, and comprise one or more types of inherently efficacious solo acting elements.

[0180] In one embodiment, unlike prior Clathrin art, a plurality of elements 206a, 204a, and or 208a operate without cargo elements 202a, and comprise an inherently efficacious cage element 212 of one or more types, like a drug element, for example, which is unlike prior Clathrin art.

[0181] In one embodiment, also unlike prior Clathrin art, a plurality of elements 206a, with or without one or more additional other elements comprise cage element 212, and element 212 has one or more elements, of one or more types and affixed via one or methods, located on the outside part of cage element 212; that is, located outside the cavity formed by

cage **212**. In another embodiment, further unlike prior Clathrin art, a plurality of elements **206a**, with or without one or more additional other elements, comprise cage element **212**, and element **212** has one or more elements, of one or more types and affixed via one or methods, located on both the outside, and inside parts (i.e., located within the cage cavity), of cage element **212**.

[0182] According to one invention feature, cargo attachment element **204a** and or element **208a** shields cargo element **202a** in the same element **206a** from interacting. According to another feature, the shielding properties of element **206a** shields and inhibits chemical and molecular interactions between it and the external environment. According to a further feature, element **206a** protectively sequesters cargo elements **202a** from the external environment.

[0183] In another embodiment, one or more non-invention, “natural” Clathrin elements **206b-206f** (the term “natural” hereinafter generally refers to non-isolated, non-recombinant, and non-synthetic protein elements) join with one or more isolated, recombinant, and or synthetic elements; in this example, **206a**; to form a natural/invention hybrid Clathrin cage element **212**. In another embodiment, hybrid cage element **212** may also be comprised of natural cage element **220**, which is a vesicle, forming a hybrid Clathrin Coated Vesicle.

[0184] FIG. 3 is a computer generated frontal view of a Clathrin cage **300** comprised of a plurality of natural Clathrin triskelia elements **302-308**, respectively. In an illustrative embodiment, element **310** is an invention element, comprised of three heavy chain elements **104a-104c**—which may or may not include three respective light chain elements **106a-106c**—forming a hybrid or fused cage **300** comprised of natural elements and invention elements. In this role, element **310** comprises an efficacious replacement for a natural triskelia element.

[0185] FIG. 4 is a flow diagram **400** depicting, conceptually, the formation of a plurality of natural Clathrin elements **206b-206f**, and, in this example, along with invention element (**206a**) into cage **200**, which at step **440**, shows Clathrin coated vesicle **220**. The process by which natural Clathrin molecules **206b-206d** obtain natural cargo molecules **202b**, **202c**, and **202d** in this example is known as Clathrin mediated endocytosis (CME), a process wherein a cell takes in macromolecules by forming vesicles derived from the plasma membrane. Endocytosis is crucial to cellular function. Via CME, cells internalize cargo attachment elements, transmembrane channels, transporters and extracellular ligands such as hormones, growth factors and nutrients.

[0186] In one embodiment, one or more invention elements are biologically engineered to take or induce one or more types of actions, such as to create, spawn, comprise, modify, repair, regenerate, reassemble, and or control and regulate CME, as well as exocytosis, mitosis, trafficking, signaling processes, other behaviors, and the like. Defects and disorders in any of these critical cellular processes can lead to disease, and one or more types of these processes may be modified in one or more embodiments of the instant invention, for example, to achieve therapeutic effect.

[0187] In one embodiment, the instant invention takes or induces one or more efficacious actions involving receptor-mediated endocytosis that encompass nutrient uptake (LDL, transferrin, etc.), membrane recycling, membrane protein recycling, antigen uptake, synaptic vesicle recycling, and signaling receptor down-regulation.

[0188] In one or more embodiments, one or more invention elements comprise counterparts to natural Clathrin proteins that may inherently behave as a drug; e.g., one or more invention elements are functionalized for in vivo delivery and carry no additional elements, such as cargo. Such solo acting element embodiments would interact in one or more ways with natural cells and their processes, and by so doing diagnose, regulate and or cure one or more diseases and disorders relating to endocytosis.

[0189] An increase of a cellular component is called upregulation. Upregulation is an increase in the number of receptors, e.g., see elements **204b**, **204c**, and **204d** in FIG. 4, on the surface of target cells, making the cells more sensitive to a hormone or another agent. For example, there is an increase in uterine oxytocin receptors in the third trimester of pregnancy, promoting the contraction of the smooth muscle of the uterus. In one or more embodiments, one or more invention elements, either by acting alone and or in part with other elements of one or more types, including natural and or non-invention elements, efficaciously modify, control and regulate, interfere with, create, and or spawn elements, and or induce actions or behaviors that increase the upregulation of one or more types of receptors of the surfaces of target cells.

[0190] On the other hand there is downregulation, an example of which is the cellular decrease in the number of receptors to a molecule, such as a hormone or neurotransmitter, which reduces the cell’s sensitivity to the molecule. In the literature, downregulation is the process by which a cell decreases the quantity of a cellular component, such as RNA or protein, in response to an external variable. In one or more embodiments, one or more invention elements, either by acting alone and or in part with other elements of one or more types, including natural and or non-invention elements, efficaciously modify, control and regulate, interfere with, create, and or spawn elements, and or induce actions or behaviors that increase the downregulation of one or more types of receptors.

[0191] Exocytosis is the reverse process of endocytosis, whereby a cell directs secretory vesicles out of the cell membrane. These membrane-bound vesicles contain soluble proteins to be secreted to the extracellular environment as well as membrane proteins and lipids that are sent to become components of the cell membrane. Exocytotic vesicles are usually not Clathrin-coated; most of them have no coat at all. However, two observations suggest that Clathrin effectively ‘tracks’ vesicle proteins leaving a synapse. In one study (Granseth, et al, 2008) the amount of a Clathrin light chain (LC) tagged with the element mRFP leaving the synapse was proportional to the number of vesicles released by the stimulus, as assessed by the amplitude of a sypHy signal (sypHy is an improved fluorescent reporter of exocytosis). Second, in the same study the movement of LC-mRFP began without a significant delay and peaked with the sypHy signal. The movement of Clathrin out of the synapse together with synaptophysin and synaptobrevin is most easily explained as representing CME (Clathrin mediated endocytosis) of vesicles at sites removed from the active zone. This interpretation is consistent with studies showing that the machinery for CME is not at the active zone, but in the surrounding regions of membrane (Heuser & Reese, 1973; Ringstad et al. 1999; Qualmann et al. 2000; Teng & Wilkinson, 2000). Thus, Clathrin is naturally found in the extracellular space and may play a role in regulating exocytosis and or endocytosis. In one or more illustrative embodiment, one or more elements of one

or more types may efficaciously operate in inter- and or extracellular spaces of one or more types; for example, perform remediation, sequestration, or removal of one or more types of undesirable elements.

[0192] Membrane trafficking only occurs during interphase. As the cell enters mitosis, Clathrin-mediated membrane traffic is rapidly shut down and only resumes in late telophase. Clathrin may therefore have a separate function that is distinct from membrane trafficking, which operates during mitosis. Clathrin is thus a multifunction protein: during interphase its function is in membrane trafficking and during mitosis it has a role in stabilizing spindle fibers (Royle, 2006). In one invention embodiment, mitosis may be efficaciously controlled and regulated, modified, and or induced via one or more methods and instances of the instant invention.

[0193] In another embodiment, one or more elements are comprised of, but not limited to, one or more isolated, synthetic, and or recombinant adaptor protein molecules, tubulin protein molecules, dynamin protein molecules, epsin protein molecules, endophilin protein molecules, synaptotagmin protein molecules, and or other types of protein molecules associated with Clathrin and Coatamer proteins and processes, for efficacious effect.

[0194] In another embodiment, one or more natural adaptor protein molecules, tubulin protein molecules, dynamin protein molecules, epsin protein molecules, endophilin protein molecules, synaptotagmin protein molecules, and or other types of protein molecules involved with associated with Clathrin and Coatamer proteins and processes form efficacious hybrid elements when also comprised of one or more types of invention elements.

[0195] The CME process involves a dynamic interaction between Clathrin and a wide range of other protein molecules, and altering the compositions and behaviors of the various molecular parties involved. For example, the cell uses endocytosis to control and regulate the density of receptors on the cell surface and to acquire nutrients. Endocytosis of ligand-activated cargo attachment elements is essential for the proper attenuation of a variety of signal transduction processes, as well as for co-localization of activated cargo attachment elements with downstream signaling molecules. Endocytosis also counterbalances secretion, preventing continuous expansion of the plasma membrane. Endocytosis thus internalizes macromolecules and fluid, and after sorting, directs the internalized molecules for degradation or recycling.

[0196] The endocytosis process begins when proteins bound to cargo attachment elements accumulate in coated pits 404, which are specialized regions of the cell membrane 402 where it is indented and coated on its cytoplasmic side with a bristle-like coat composed of two natural proteins: Clathrin and protein adapters. Most, if not all, intracellular transport vesicles are encased in a proteinaceous coat, one class of which is Clathrin-coated vesicles (CCVs). CCVs also mediate the transport of lysosomal hydrolases from the trans-Golgi network, as well as the efficient internalization of extracellular solutes such as nutrients, hormones, growth factors, and immunoglobulins at the plasma membrane.

[0197] Clathrin also transports proteins from the Golgi to other organelles. In neurons, endocytosis is critical to allow rapid synaptic vesicle regeneration. Besides Clathrin, there are other coat-forming proteins, such as COP I and COP II, which mediate intracellular traffic and there are Clathrin-

independent endocytic pathways which mediate internalisation of a variety of cargo (Royle, 2006).

[0198] In one invention embodiment, the natural endocytosis process is transformed into a versatile therapeutic method to regulate the intensity, localization, half-life and function of signaling elements (signalosomes) that form in cells upon, for example, binding of growth factors, cytokines and morphogens to their cognate receptors. In one example embodiment, the invention rectifies breakdowns in the function of endocytic adaptors that might facilitate impairment of tissue homeostasis and consequent tumor development. In another illustrative embodiment, one or more invention elements, acting alone or not, interact with natural adaptor proteins required for appropriate receptor downregulation and which play distinct roles in oncogenesis. (Crosetto, et al. 2005) In another embodiment, CME elements might also comprise one or more invention cargo elements (202a in FIG. 4), which can be drugs, other ligands, and the like.

[0199] In one embodiment, referring to FIG. 4, a natural Clathrin coated vesicle 220 is desired to form to endocytose over-expressed natural receptor elements 204b and 204c that are initially located outside cell membrane 402. The appearance of one or more types of invention elements, such as element (206a) in the illustrative example, outside cell membrane 402 and or by crossing 402, dynamically begin to create, induce, spawn, mediate, control and regulate, regenerate, and or interact with one or more natural endocytosis processes and behaviors. With the prompting of one or more types of invention Clathrin elements, one or more biological processes acting on cell membrane 402 induce a Clathrin bud 404 to form at 420.

[0200] As shown at 430 and 440, after forming completely around bud 404, natural Clathrin elements 206b-206d pinch off (scission) from membrane 402 with the desired over expressed receptors 204b and 204c held inside vesicle 220. After excision, bud 404 has evolved into a plurality of natural Clathrin elements 206b-206f, some of which are attached to one or more types of over expressed receptor elements 204b and 204c, as well as attached to other receptor elements; which in this example are the normally expressed natural elements 204d.

[0201] In one illustrative embodiment, the otherwise all-natural plurality of Clathrin elements in FIG. 4 includes one or more non-cargo carrying; solo acting invention elements (206a), forming a "hybrid" CCV 440 with the desired efficacious properties and behavior. This hybrid CCV then follows normal pathways within the cell, causing downregulation of the desired over-expressed receptor elements, which may be associated with one or more types of neurotransmitters, viruses, cholesterol, as well as with other cargo types, restoring a cell to its normal, healthy state.

[0202] In another illustrative embodiment, natural Clathrin coated vesicle structure 440 in FIG. 4 is additionally comprised of one or more non-cargo carrying invention receptor element 204a and or adaptor element 208a (as illustrated in FIG. 2), forming a hybrid or fused Clathrin coated vesicle 440 in FIG. 4, with the desired efficacious properties and behavior. In another embodiment, one or more hybridized and or invention elements may enter the cell nucleus and or other organelles and cell elements.

[0203] The fusion and or participatory actions of one or more non-additional element carrying, solo acting invention elements 206a, 204a, and or 208a in FIG. 2 may yield a therapeutic effect, and are an example embodiment of inher-

ently efficacious invention elements in action. In another embodiment, natural or hybrid CCV **440** in FIG. **4** also includes one or more invention cargo molecules (**202a**) that may have been transported into the cell via their attachment to one or more natural and or invention receptor elements.

**[0204]** Referring again to FIG. **4**, in another example embodiment, a therapeutic effect is accomplished via one or more invention elements by regulating EGFR (epidermal growth factor receptor), which exists on the cell surface and is activated by binding of its specific ligands including epidermal growth factor and transforming growth factor  $\alpha$  (TGF $\alpha$ ).

**[0205]** When these natural cargo attachment elements are activated, cells rapidly clear them from the surface and destroy them. Control of EGF receptor signaling is performed by Clathrin-mediated endocytosis. Natural Clathrin coats also exist on endosomes and are involved in endosomal sorting of the EGFR. A defect in this overall process will likely lead to uninhibited growth of cells and tumors. EGFR expression, over-expression, or mutation is associated with cancer progression, advanced disease, drug resistance, aggressive disease, poor prognosis, and reduced survival. EGFR is considered one of the main proteins elevated in breast, lung, and prostate cancers, among others. Brain cancer is also implicated with over-expressed EGFR. Other work has shown that using monoclonal antibodies for EGFR, or anti-EGFR, has proven an effective strategy for getting nanoparticles to specifically attach themselves to cancer cells. Additional work has shown effectiveness of EGFR as the cancer-targeting pathway. In one embodiment, CME, cell fusion, cell penetrating, and or one or more types of other participatory actions of one or more solo operating, efficacious invention elements **206a**, **204a**, and or **208a** in FIG. **2** may yield a therapeutic effect in controlling, regulating, or mediating EGFR activity. In another example embodiment of modulating EGFR activity, cargo elements (**202a**) in FIG. **4** may comprise one or one or more types of cancer drugs or biologicals delivered directly into cells and organelles that are transported into the cell via their attachment to one or more natural and or invention receptor elements during CME, by cell fusion, by directly penetrating cell membrane **402**, and or by one or more types of other participatory actions. In another embodiment, invention cargo elements (**202a**) may comprise one or more diagnostic agents, or combine one or more diagnostic agents and therapeutic agents in the same payload. In one or more embodiments, one or more invention elements of one or more types may thus comprise an efficacious method for the diagnosis, treatment, remedying, curing, and or prevention of one or more types of cancers, including those cancer types that fall outside the scope of EGFR-related activity.

**[0206]** FIG. **5** is a conceptual diagram illustrating the basic units of Coatomer I and II proteins. COPII and Clathrin cages are both constructed from  $\alpha$ -solenoid and  $\beta$ -propeller building blocks (Fotin et al., 2004b; ter Haar et al., 1998; Ybe et al., 1999). In various embodiments of the invention, one or more elements of one or more types are formed from isolated, synthetic and or recombinant amino acid residues comprising in whole or in part one or more types of Coatomer proteins of one or more isoforms, including cloned isoforms. Examples of various Coatomer subunit amino sequences are listed in SEQ ID NO:15, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:29, and SEQ ID NO:30. In another embodiment, one or more Coatomer subunit amino

acid sequences may be modified, altered, adapted or functionalized in one or more ways in one or more embodiments of the invention.

**[0207]** In one embodiment, Coatomer is comprised of seven distinct subunits: alpha, beta, beta', gamma, delta, epsilon and zeta subunits, respectively.

**[0208]** In Clathrin, a triskelion assembly unit lies at each vertex, and the  $\alpha$ -solenoid legs of neighboring triskelia interdigitate extensively as they extend toward the adjacent vertices; the  $\beta$ -propeller is not part of the architectural core and instead projects in toward the membrane to interact with adaptor molecules (Fotin et al., 2004; Kirchhausen, 2000). In contrast, the COPII assembly unit is a rod that constitutes the edge of a cuboctahedron, and four rods converge to form the vertex with no interdigitation of assembly units.  $\alpha$ -solenoid domains form the core of the edge, but, unlike Clathrin, the COPII vertices are formed from  $\beta$ -propellers. In summary, the COPII and Clathrin lattices seem not to share common construction principles other than the use of  $\alpha$ -solenoid and  $\beta$ -propeller folds.

**[0209]** Crystallographic analysis of the Coatomer II assembly unit reveals a 28 nm long rod, element **502**, comprising a central solenoid dimer capped by two  $\beta$  propeller domains, elements **504**, at each end. GTPase, elements **508**, bind to adaptor elements **506**, which bind to elements **502**. In the illustration, element **502a** is an invention element that acts as an efficacious replacement element for one or more natural element **502**, forming a hybrid Coatomer element. The structural geometry and properties of COPI coats remain to be determined. However, by analogy to the COPII and Clathrin structural units, they probably involve a preassembled cage protein (CP) scaffold that is generated by the  $\beta$ -propeller-containing and  $\alpha$ -solenoid-containing subunits and an adaptor protein (AP) subcomplex. Together these could form an AP-CP heptaheteromeric functional unit in the cytosol. (Gurka, et al. 2006)

**[0210]** COPI and COPII play a major role in exocytosis, as also can their invention element counterparts. Clathrin can also play a role in exocytosis, but to a lesser extent than Coatomer. The exocytosis process refers to the fusion of intracellular vesicles with the plasma membrane. It occurs via two major processes, a constitutive pathway and a regulated pathway. These are the major ways that the cell secretes materials, wherein a cell secretes macromolecules (large molecules) by fusion of vesicles with the plasma membrane. Coatomer-coated vesicles, which are typically less than fifty nanometers in size, are also involved in vesicular transport between the Golgi apparatus, endoplasmic reticulum and plasma membrane. Coatomer I vesicles shuttle elements from the Golgi to the endoplasmic reticulum (ER). Coatomer II vesicles shuttle elements from the ER to the Golgi. Coat-protein I/II subunits (COPs) require ATP to assemble into a coat and unlike Clathrin coats, the Coatomer coat remains on the vesicle until docking occurs. In some instances, Coatomer proteins are also involved in endocytosis, but are unrelated to Clathrin. Thus, while Clathrin also mediates endocytic protein transport from the ER to the Golgi, Coatomers (COPI, COPII) primarily mediate intra-Golgi transport, as well as the reverse Golgi to ER transport of dilysine-tagged proteins. Coatomers reversibly associate with Golgi (non-Clathrin-coated) vesicles to mediate protein transport and for budding from Golgi membranes. In one or more embodiments, one or more COPI/COPII invention elements and or Clathrin invention elements, either by acting alone and or in part with other

elements of one or more types, including natural and or non-invention elements, efficaciously modify, control and regulate, interfere with, create, and or spawn elements and or induce actions or behaviors involving exocytosis.

**[0211]** Cells of the mammalian immune system undergo selective changes in protein glycosylation during differentiation, immune activation, and autoimmune disease. In many, if not most of these types of diseases endocytosis and cellular trafficking and signaling plays a role. Referring again to FIGS. 1, 2, 3, 4, (and 5, in some embodiments), but not limited to, in one embodiment, one or more invention elements of one or more types, in whole or in part selectively interfere with, fuse with, control and regulate, induce, and otherwise modify endocytosis, receptor-specific processing, trafficking and signaling, and other behaviors for efficacious effect in one or more types of autoimmune diseases, including, but not limited to, one or more types of diabetes, CNS autoimmune diseases, and other types of autoimmune diseases that effect the body.

**[0212]** Referring again to FIGS. 1, 2, 3, 4, (and 5 in some embodiments), but not limited to, in one embodiment, one or more invention elements of one or more types selectively interfere with, control and regulate, and or modify secretory products that participate in inflammation and immunoregulation; and also in other embodiments, whereby endocytosis mediated by specific receptors for immunoglobulin or by other opsonins is important in removal of damaged self or foreign particles. In another embodiment, defects in membrane receptor function, whether inherited or acquired, and the pathogenesis of immune diseases may be remedied, inhibited, mitigated, and or prevented.

**[0213]** Referring again to FIGS. 1, 2, 3, 4, and 5, in one embodiment, but not limited to, one or more invention elements of one or more types efficaciously fuse with and or functionally replace one or more natural elements commonly found in endocytosis, exocytosis, mitosis, trafficking and signaling, and the like, either by acting alone and or in part with other elements of one or more types, including natural and or non-invention elements.

**[0214]** Referring again to FIGS. 1, 2, 3, 4, and 5, but not limited to, in another embodiment, one or more invention elements of one or more types efficaciously cross over into a cell, its elements, and or its organelles, such as its nucleus, either by acting alone and or in part with other elements of one or more types, including natural and or non-invention elements.

**[0215]** Referring again to FIGS. 1, 2, 3, 4, and 5, in another embodiment, but not limited to, one or more invention elements efficaciously create, spawn, comprise, modify, repair, regenerate, reassemble, and or control and regulate one or more natural elements commonly found in endocytosis, exocytosis, mitosis, trafficking and signaling, other cellular behaviors, and the like, either by acting alone and or in part with other elements of one or more types, including natural and or non-invention elements.

**[0216]** Referring again to FIGS. 1, 2, 3, 4, and 5, in another embodiment, but not limited to, one or more invention elements efficaciously utilize natural and or genetically engineered elements to encode components of the intracellular sorting machinery that mediate the selective trafficking of lipids and proteins in the secretory and endocytic pathways, to efficacious effect.

**[0217]** Referring again to FIGS. 1, 2, 3, 4, and 5, in another embodiment, but not limited to, one or more invention ele-

ments efficaciously utilize genetic agents and elements, including, but not limited to, proteins; peptides; DNA and DNA variants; RNA and RNA variants such as mRNA, iRNA and siRNA; RNA-induced silencing complex (RISC), other genetic-modifying agents and methods, and the like.

**[0218]** In another embodiment, but not limited to, one or more invention elements efficaciously utilize one or more oligonucleotides in antisense therapy. These antisense DNA drugs work by binding to messenger RNAs from disease genes, so that the genetic code in the RNA cannot be read, stopping the production of the disease-causing protein.

**[0219]** In another illustrative embodiment, one or more elements may comprise one or more RNAi (RNA interference) elements and or RNAi variants such as small interfering RNA molecules (siRNA), but not limited to, that may collaborate with proteins in the cell and also may form a nanoscale element called a RISC (RNA-Induced Silencing Complex). RNAi and or RISCs may be used to head off a genetic disease before the first symptom appears, based on an analysis of an individual's predisposition to certain diseases. This methodology is a way of silencing a specific gene, for example, genes that direct cancer cells to proliferate or that create overproduction of proteins that cause rheumatoid arthritis. Basically, RNAi works by scanning RNA templates that may cause a disease and cleaving that RNA template, and enzymes then destroying the template before it can complete its actions on the offending DNA. One of the key barriers to successful RNAi therapy is their finding their way to a specific site in the body and then the RNAi not degrading rapidly before it can do useful work. In one illustrative embodiment, RNAi, siRNA, RISC elements and or other suitable methods may be targeted by an invention element such that one or more such RNA elements seek out and destroy potentially harmful genetic elements and or other genetic processes.

**[0220]** As noted in the literature, Clathrin heavy chain is known to be a cytosolic protein that functions as a vesicle transporter. However, the Clathrin heavy chain exists not only in cytosol but also in cell nuclei. The p53 gene, in which mutations have been found in >50% of human cancers, encodes a protein that plays an important role in preventing tumorigenesis. Clathrin heavy chain expression enhances p53-dependent transactivation, whereas the reduction of Clathrin heavy chain expression by RNA interference (RNAi) attenuates its transcriptional activity. Moreover, Clathrin heavy chain binds to the p53-responsive promoter in vivo and stabilizes p53-p300 interaction to promote p53-mediated transcription. Thus, nuclear Clathrin heavy chain is required for the transactivation of p53 target genes and plays a distinct role from Clathrin-mediated endocytosis (Enari, et al 2006). In one embodiment, p53 and or one or more other types of genes, their diseases and disorders, and or RNAi related activities may be efficaciously controlled and regulated, mitigated, prevented, and or modified via one or more embodiments of the instant invention.

**[0221]** Referring again to FIGS. 1, 2, 3, 4, and 5, in another embodiment, but not limited to, one or more elements, acting alone or not, would achieve therapeutic effect by deliberately controlling and regulating, or modifying faulty exocytosis and or endocytosis processes that produce disorders and diseases. This is a health critical situation, as the role of dopamine receptors and transporters; the excitability of dopaminergic neurons; and the regulation of extracellular dopamine levels in the brain, especially in relation to the diseased state, has proven to be imperative for a further understanding of

dopaminergic neurotransmission as a whole. For example, dopaminergic neurotransmission critically depends on exocytotic release and neuronal uptake of dopamine, as well as on diffusion away from the release site. Once target cells are reached, dopamine can bind to and activate dopamine receptors. The subsequent cellular response depends on the type of dopamine receptor that is activated and the signal transduction mechanisms that are coupled to these receptors. Disturbances in one or more of the above-mentioned aspects of dopaminergic transmission could lead to severe neurological and neuropsychiatric disorders such as Parkinson's disease, depression, addiction, schizophrenia, attention deficit hyperactivity disorder, restless legs syndrome, Tourette syndrome, and the like, and in or more invention embodiments, one or more such disorders may be efficaciously treated.

[0222] Referring again to FIGS. 1, 2, 3, 4, and 5, in another embodiment, but not limited to, one or more elements, during some operations may interact with, for example, an externally applied magnetic field, like during NMR. However, since invention protein elements are electrically neutral, only minimal (e.g., no) structural distortion of the elements occurs in the presence of the magnetic field. Therefore, using invention elements to capture other types of elements, which may be, for example, one or more NMR contrast agents for developmental imaging and diagnostic studies, and which contrast agents may also be capable of crossing cellular membranes, protects and extends the utility of the invention.

[0223] Referring again to FIGS. 1, 2, 3, 4, and 5, in another embodiment, but not limited to, one or more elements may comprise, for example, one or more metal ions including, but not limited to, the gadolinium (III) chelate compounds of DTPA, DO3A, DOTA and other variations of these linear and macrocyclic ligands that act as targeted and or non-targeted contrast agents.

[0224] Direct  $Gd^{3+}-OH_2$  chemical bonds, which exchange rapidly with other bulk  $H_2O$  molecules, produce the mechanism whereby unpaired electrons on  $Gd^{3+}$  relax the proton nuclei of many nearby  $H_2O$  molecules. Accordingly, the behavior of T1 contrast agents, such as those based on gadolinium requires good direct contact with tissue water molecules (spin-lattice relaxation mechanism) to be efficient. Thus, it is often preferable to bind them to the external surface of the carrier. (Hooker, et al. 2007) In one embodiment, one or more elements facilitate better contact to tissue water because one or more contrast agents of one or more types are not located in the interior part of a cage (in its cavity), but rather, located on much more exposed non-cage elements of one or more types. In one embodiment, one or more cage element 212 has one or more contrast agents of one or more types located on the outside part of cage element 212; or on both the inside and outside parts of element 212.

[0225] In another illustrative embodiment, one or more imaging or study elements comprise one or more treated manganese minerals, such as oxides, silicates, and carbonates for imaging and study enhancement.

[0226] Besides  $Gd^{3+}$  complexes, there is another important class of contrast agents for MRI that is based on polysaccharide coated iron oxide particles. Their peculiarity stems from the fact that their blood half-life and distribution to different organs of the reticuloendothelial system (RES) depend upon the particle size (Aime, et al 1998). In one embodiment, one or more elements comprise one or more of a wide range of lanthano-invention labeled derivatives for custom-designed contrast agents.

[0227] In another embodiment, one or more elements comprise one or more therapeutic agents in addition to one or more imaging contrast and diagnostic agents.

[0228] In another illustrative embodiment, targeted and or non-targeted in vivo delivery of one or more elements are internally and or externally monitored, directed, activated, deactivated and or regulated, locally and or at a remote distance by, for example, but not limited to, NMR, ESR, ultrasound, radio transmissions, and or biochemical reactions.

[0229] Additionally, in other embodiments, NMR is combined with other techniques, such as ENDOR, which combines the best aspects of ESR and NMR, to yield high sensitivity and nuclear selectivity, respectively, for in vivo and in vitro studies.

[0230] In one embodiment, one or more different sized, paramagnetic coated, quantum dots, and or photonic dots are used as one or more contrast markers in magnetic resonance imaging (Mulder, et al., 2009). In other embodiments, one or more different sized quantum dots, and or photonic dots may be used in positron emission tomography (PET) for in-vivo molecular imaging, or as fluorescent tracers in optical microscopy.

[0231] In another configuration, one or more types of elements comprise one or more radiodiagnostic agents for nuclear medicine.

[0232] Referring again to FIG. 2, in further illustrative embodiments, free-floating cargo may be carried in cavity forming cargo elements 202a that comprise a fluid, gas, or vapor; which free-floating cargo, for example, may be one or more molecular ensembles for enhanced medical imaging, and which cargo may also be carrying one or more therapeutic agents.

[0233] Referring again to FIGS. 1, 2, 3, 4, and 5, in another embodiment, but not limited to, one or more invention elements comprise one or more types of elements in whole or in part, such as one or more drug and pharmacological elements; biological elements; biomedical or medical elements; and the like, including healthcare elements; bioengineered elements; cosmetic elements; and the like.

[0234] Referring again to FIGS. 1, 2, 3, 4, and 5, but not limited to, in one embodiment, one or more elements of one or more types comprise targeted and or non-targeted drug delivery elements, including their high precision dosing, or other forms of healthcare elements for diagnosing, remedying, inhibiting, mitigating, curing, and or preventing one or more types of diseases, infections, physical or mental trauma, or other forms of physical and mental afflictions.

[0235] Referring again to FIGS. 1, 2, 3, 4, and 5, but not limited to, in one embodiment, one or more elements comprise an in vitro and or in vivo model and or system for research study, including a model, method, and or system for the research and development of new drugs, therapies, prosthetics, and drug delivery systems, including an accelerated drug discovery process.

[0236] Referring again to FIGS. 1, 2, 3, 4, and 5, in another embodiment, but not limited to, one or more elements, acting alone or not, are utilized for studying, discovering, preventing, curing, mitigating, and or healing one or more types of animal, tree, plant, grain, grass, agricultural, vegetable, and or fungal diseases, disorders, infestations, and or blights.

[0237] Referring again to FIGS. 1, 2, 3, 4, and 5, in another embodiment, but not limited to, one or more elements are used for studying, discovering, designing, and or enabling of genetically engineered elements, for example, one or more

types of genes, cells, and other biological elements and products in animals, trees, plants, grains, grasses, agriculture, vegetables and fungi.

**[0238]** In another illustrative embodiment, one or more elements comprise one or more methods for nourishing and or promoting healthy growth in one or more types of animals, trees, plants, grains, grasses, agriculture, vegetables and or fungi.

**[0239]** Referring again to FIGS. 2 and 4, in another embodiment, but not limited to, the heat shock cognate protein, hsc70, and its molecular co-chaperone auxilin, help to regulate the natural endocytosis aftermath of natural CCV uncoating and disassembly. Hsc70 also promotes uncoating and disassembly of Coatomer I and II vesicles. In cells over-expressing ATPase-deficient hsc70 mutants, uncoating of CCVs is inhibited in vivo. In one embodiment, bioengineered elements may be used to regulate under or over expression of hsc70 and or auxilin. In one example embodiment, using a monoclonal antibody or other agent type as cargo against hsc70 blocks the hsc70-mediated release of invention and or non-invention Clathrin from coated vesicles. In another example embodiment, or more auxilin elements comprise invention elements.

**[0240]** In one illustrative embodiment, one or more elements are stable with respect to dissociation, including one or more associated non-invention elements.

**[0241]** In another illustrative embodiment, disassembly and dissolution of one or more elements are deliberately inhibited and control and regulated, including one or more associated non-invention elements.

**[0242]** In one illustrative embodiment, one or more elements remain stable for a time certain or estimated time before the onset of dissociation, including one or more associated non-invention elements.

**[0243]** In one illustrative embodiment, dissociation of one or more elements may occur in whole or in part, including one or more associated non-invention elements.

**[0244]** In one illustrative embodiment, one or more cargo elements may comprise one or more uncoating and dissociation agents and or use one or more methods for controlled and regulated release of agents or cargo from one or more elements, including one or more associated non-invention elements.

**[0245]** In another embodiment, disassembly and dissolution of one or more elements, including one or more associated non-invention elements are inhibited, controlled and regulated, and or promoted by using one or more specific agents, stimuli, and or other methods.

**[0246]** In one embodiment, but not limited to, one or more invention elements of one or more types are formed in vitro via the following protocols, which may be modified and or substituted by one or more other types of protocols in one or more invention embodiments: (Adapted from Campbell, C et al., *Biochemistry* 23, 4420-4426 (1984), Pearse & Robinson, *EMBO J.* 9:1951-7 (1984), and Zhu, et. al., *Methods in Enzymology*, 328, 2001, Kedersh N, et al., *J. Cell Biology* 103, 1986.)

**[0247]** (Adapted from Campbell, C et al., *Biochemistry* 23, 4420-4426 (1984), Pearse & Robinson, *EMBO J.* 9:1951-7 (1984), and Zhu, et. al., *Methods in Enzymology*, 328, 2001, Kedersh N, et al., *J. Cell Biology* 103, 1986.)

Part I. Method of Differential Centrifugation.

**[0248]** 1. Make up 1 L of a buffer (buffer A) that comprises: 50 mM Mes pH 6.5, 100 mM NaCl, 1 mM EGTA, 0.5 mM MgCl<sub>2</sub>, 0.02% NaN<sub>3</sub>, 1 mM DTT a day prior to experiment and storage at 4° C.

**[0249]** 2. Add 1:100 PMSF proteases inhibitor to buffer A (200 ul/20 ml).

**[0250]** 3. Collect and wash 14 rat brains (~2.0 g) and livers (~20.0 g). Wash and place the brains in ice-cold buffer A. Perfuse the livers with ice-cold PBS and collect them in ice-cold buffer A.

**[0251]** 4. Mince and homogenize the brains in a Potter-Elvehjem grinder with 2 volume of ice-cold buffer A per total brain wet weight (~90 ml). Do the same with the livers (~400 ml).

**[0252]** 5. Centrifuge the homogenate at 23,000 g (11,900 rpm) in a Sorvall GSA or at 13,000 rpm in a Sorvall SS34 rotor for 45 min at 4° C.

**[0253]** 6. Collect the supernatant and centrifuge at 43,000 g (18,000 rpm) in a Sorvall SS34 rotor or at 20,000 rpm in a ti 45 Beckman rotor for 1 h at 4° C.

**[0254]** 7. Resuspend the pellet in 10 ml of ice-cold buffer A, use a loose-fitting Teflon-glass Dounce homogenizer.

**[0255]** 8. Collect homogenate in a 50 ml conical tube. Wash pestle and glass homogenizer with 5 ml of buffer A, and add this to homogenate until total volume is 15 ml. Add 1:100 PMSF

**[0256]** 9. Dilute the homogenate 1:1 with 15 ml of 12.5% Ficoll/12.5% sucrose (both in ice-cold buffer A), and mix by inversion to ensure homogeneity.

**[0257]** 10. Centrifuge at 43,000 g (18,000 rpm) in a Sorvall SS34 rotor or at 20,000 rpm in a ti 45 Beckman rotor for 30 min at 4° C.

**[0258]** 11. Collect the supernatant in a graduate cylinder and dilute it 1:5 in ice-cold buffer A. Add 1:100 PMSF

**[0259]** 12. Centrifuge the supernatant at 100,000 g (33,000 rpm) in a Beckman 70.1Ti rotor or at 31,100 rpm in a ti 45 Beckman rotor for 1 h at 4° C.

**[0260]** 13. Collect pellet and resuspend in 5-10 ml of ice-cold buffer A by using a loose-fitting Teflon-glass Dounce homogenizer. Add 1:100 PMSF

**[0261]** 14. Leave the homogenate on ice for about 30 min, and take an aliquot of 10 ul for EM, and dilute 1:10 for brain, 1:100 for liver.

Part II. Purification of CCVs Using Density Gradients (Zhu's CCVs and Clathrin Coat Preparation). Submit the Crude Clathrin-Coated Vesicles from Fresh Rat Brain to Discontinuous Sucrose Gradient for Remove Contaminating Vaults.

**[0262]** 1. CCVs resuspended in (5-10 ml) buffer A

**[0263]** 2. Preparer a discontinuous sucrose gradient in SW28 tubes by carefully layering 5 ml of 40%, 5 ml of 30%, 6 ml of 20%, 8.5 ml of 10%, and 8.5 of 5% sucrose solutions in buffer A from bottom to top.

**[0264]** 3. CCVs (5-10 ml) is laid on top of the gradient and centrifuged at 100,000 g (25,000 rpm) in a SW28 rotor for 1 hr at 4° C.

**[0265]** 4. Collect twenty-six 1.5 ml fractions from the top.

**[0266]** 5. Small aliquots from every other fraction are analyzed for CCVs using 10% SDS-PAGE. [Fractions comprising the CCVs (typically fractions 12-21 as numbered from the top of the gradient) are combined, diluted with 3 volumes of buffer A, and centrifuge at 112,000 g (31,100

rpm) in a ti 45 Beckman rotor for 1 h at 4° C. or at 33,000 rpm in a Beckman 70.1Ti rotor for 1 h at 4° C. Add 1:100 PMSF]

[0267] 6. Resuspend the pellet in ice-cold buffer A, do a protein assay to yield an approximate concentration. Usually add 1 to 2 ml of buffer A.

[0268] 7. Aliquot the homogenate in aliquots of 200 ul and store at -80° C. Take an aliquot of 10 ul each for EM and SDS-gel PAGE.

Part III. Isolation of Triskelia and APs from CCVs Using Keen's Method.

[0269] 1. Dialyze CCVs against 0.01M Tris buffer, Ph 8.5, 3 mM azide for 5 hours.

[0270] 2. Centrifuge at 240,000 g (51,200 rpm) for 20 min at 4° C. Because you are using low amount of sample; (IF we have less than 2 mL, Do not use the lid or close the centrifuge tubes of the 70.1 Ti rotor.) The soluble coat proteins comprising triskelial and APs are separated from the residual Clathrin-coat vesicle membranes.

[0271] 3. Collect the soluble fraction and do protein assay.

[0272] 4. Take an aliquot of 10 ul for EM and 50 ul for SDS-gel PAGE.

Part IV. Separation by FPLC of AP-1 from AP-2 with Hydroxyapatite Column

Solutions:

[0273]

Stocks:	1M NaH <sub>2</sub> PO <sub>4</sub> ; pH 7.1 5M NaCl 10% NaN <sub>3</sub>	(30 g/250 ml)
Low PO <sub>4</sub> buffer (500 ml):	10 mM NaH <sub>2</sub> PO <sub>4</sub> ; pH 7.1 100 mM NaCl 0.02% NaN <sub>3</sub> 0.1% beta-Mercaptoethanol	(5 ml of stock) (10 ml of stock) (1 ml of stock) (0.5 ml) (RT)
High PO <sub>4</sub> buffer (200 ml):	500 mM NaH <sub>2</sub> PO <sub>4</sub> ; pH 7.1 100 mM NaCl 0.02% NaN <sub>3</sub> 0.1% beta-Mercaptoethanol	(100 ml of stock) (4 ml of stock) (0.4 ml of stock) (0.2 ml) (RT)

[0274] Both buffers need to be filtered and degassed prior to use.

AP buffer:

100 mM MES, pH 7.0	39 g/2 l
150 mM NaCl	17.5 g/2 l
1 mM EDTA	4 ml of 500 mM solution/2 l
0.02% NaN <sub>3</sub>	4 ml of 10% solution/2 l
0.5 mM DTT	-> add just before use (4° C.)

[0275] Hydroxyapatite Column:

[0276] 5 ml Econo-Pac CHT-II from BioRad; the column is stored at 4° C. in low PO<sub>4</sub> buffer

Procedure:

[0277] Connect the hydroxyapatite column to the FPLC system via the BioRad adaptors. Put a 0.2μ syringe filter at the inlet of the column.

[0278] Use the following FPLC settings:

[0279] Sensitivity: 1

[0280] Flow: 1 ml/min

[0281] Chart Recorder speed: 0.5 cm/min

[0282] Make sure the fraction collector is set at "ml" and a volume of "1"

[0283] Pump A is used for the low PO<sub>4</sub> buffer; Pump B for the high PO<sub>4</sub> buffer. Wash the pumps with Valve 1 in position "3".

[0284] Once the FPLC system is set up, start washing the column with 20 ml of high PO<sub>4</sub> buffer (=20 min). Be sure to switch on UV-Lamp.

[0285] This is followed by equilibration of the column with low PO<sub>4</sub> buffer; i.e. until the baseline is stable. The back-pressure of the system should be approx. 0.1 MPa and must not exceed 0.35 Mpa.

[0286] During the equilibration phase (Valve 1 in position "1"="Load"), the 50 ml superloop is loaded with the AP sample (Pump C; 5 ml/min).

[0287] With the column equilibrated and the superloop loaded, switch Valve 1 into position "2"="Inject". The APs are injected over the column at a flow rate of 1 ml/min.

[0288] After the injection is completed, continue running low PO<sub>4</sub> buffer over the column until the baseline is stable. Don't forget to prepare 1.5 ml tubes for the fraction collector.

[0289] AP-1 and AP-2 are then eluted from the column using Method 6:

0.0	CONC % B	0.0
0.0	VALVE.POS	1.1
0.0	CM/ML	0.50
0.0	PORT.SET	6.1
40.0	CONC % B	0.0
40.0	ML/MIN	1.00
50.0	CONC % B	100

The elution profiles for AP-1 and AP-2 tend to vary considerably from one purification to another; AP-1 is eluted first.

[0290] AP-1 tends to be eluted from the column in three to four 1 ml fractions, usually starting at around #13. AP-2 is usually eluted in up to 15 fractions, starting at around #25. The fractions comprising the APs need to be verified by SDS-PAGE (two gels of 10% or 12%)

[0291] Wash column with low PO<sub>4</sub> buffer; store at 4° C.

[0292] Pooled AP-1 fractions and pooled AP-2 fractions are dialyzed against 1 liter of AP buffer overnight, and for a few more hours after exchanging the buffer (4° C.). The samples are then stored at 4° C.

[0293] Typically, the concentration for Clathrin (peak fractions) is approx. 0.5 mg/ml, for AP-1 and AP-2 between 0.3-0.5 mg/ml.

[0294] According to one illustrative embodiment, but is not limited to, recombinant Clathrin formation may be achieved in the following exemplar manner. Stoichiometric quantities of adaptor elements 208a comprising AP-1 and AP-2 are required for Clathrin self-assembly at physiological pH. However, in vitro Clathrin self-assembly occurs spontaneously below about pH 6.5. Recombinant terminal and distal domain fragments are produced and combined with recombinant-produced hub fragments in assembly buffer as described below in order to induce formation of one or more Clathrin elements, such as those comprising elements 206a, for use in the invention.

[0295] In one illustrative technique, bovine Clathrin heavy chain cDNA encoding heavy chain amino acids 1-1074 (SEQ ID NO: 1) is cloned into the pET23d vector (Novagen)



between the NcoI (234) and XhoI (158) sites. Expression of the cloned sequence results in a terminal and distal domain fragments having a C-terminal polyhistidine tag. Hub fragments corresponding to amino acids 1074-1675 (SEQ ID NO: 1) are cloned into vector pET15b (Novagen) between the BamHI (319) and XhoI (324) sites. Expression of the hub fragments produces the proximal leg domain and central trimerization domain of the Clathrin hub with an N-terminal polyhistidine tag. Vectors comprising the heavy chain and hub domains are expressed in *E. coli* by induction with 0.8 mM isopropyl-B-D-thiogalactopyranoside for 3 hours at 30 degrees Celsius. Expressed proteins are isolated, recombinant, and or synthetic from bacterial lysate in binding buffer (50 mM Tris-HCl (pH7.9), 0.5M NaCl, 5 mM imidazole) in a nickel affinity resin using the polyhistidine tag. Proteins are eluted with 206a mM EDTA and dialyzed against 50 mM Tris-HCl (pH7.9). Hub fragments are further isolated, recombinant, and or synthetic using size exclusion chromatography on a Superose 6 column (Pharmacia).

[0296] In another exemplar technique, Clathrin assembly reactions are performed using expressed heavy chain and hub fragments by overnight dialysis at 4 degrees Celsius in assembly buffer (100 mM 2-(N-morpholino)ethanesulfonic acid, pH 6.7, 0.5 mM MgCl<sub>2</sub>, 1 mM EGTA, 1 mM Tris(2-carboxyethyl)-phosphine hydrochloride, 3 mM CaCl<sub>2</sub>. Assembly reactions are centrifuged for 5 minutes at 12,000 rpm. The supernatant is then centrifuged for 45 minutes at 45,000 rpm (100,000×g). The pellets are resuspended in assembly buffer, and protein composition is determined on SDS-PAGE. The efficiency of element 206a formation can be determined by electron microscopy by diluting assembly reactions 1:5 in 10 mM Tris pH7.9, and placing aliquots on a glow-discharged carbon-coated grid, using 1% uranyl acetate as the stain.

[0297] According to another illustrative embodiment, but is not limited to, recombinant Clathrin formation may be achieved in the following exemplar manner, as described by Rapoport, et al. (MBC 2008): A cDNA encoding rat Clathrin heavy chain (Kirchhausen et al., 1987a) is used as a template to generate full-length (1675 HC), nested C-terminal truncations (1661 HC, 1643 HC, 1637 HC, 1630 HC, and 1596 HC), internal deletions (1675 PIVYGQ HC, 1643 PIVYGQ HC, and 1675 QLMLTA HC), and mutations (1643LML-AAA HC) of the heavy chain; each is then subcloned into the insect cell expression vector pFastBac1 (Invitrogen, Carlsbad, Calif.). A cDNA encoding rat liver Clathrin light chain LCa (Kirchhausen et al., 1987b) is used as the template to subclone the region encoding the full light chain (residues 1-256) into the insect cell expression vector pFastBacHTb. The final construct (rLCali) comprises at its N terminus a 6×-His-tag followed by a linker of 20 residues. Baculoviruses suitable for infection and expression are generated with the Bac-to-Bac system (BD Biosciences, San Jose, Calif.). Virus stocks are obtained after four rounds of amplification, and they are kept in the dark at 4° C. The open reading frame of rat brain Clathrin light chain LCal is also used as a template to subclone it into the bacterial expression vector pET28b (Novagen, Madison, Wis.) between the NcoI and EcoRI restriction sites so as to generate a native, nontagged light chain. All constructs are verified by DNA sequencing. Clathrin heavy chains together with light chain are expressed in Hi5 insect cells (1L, 1-1.5 206a cells/ml) grown for 2-3 d in spinner flasks at 27° C. in Excell 420 medium after coinfection with the appropriate viruses. Alternatively, Clathrin heavy chain only is expressed in a similar way. The cells are

centrifuged at 1000 rpm for 10 min at room temperature by using an H6000A rotor (Sorvall, Newton, Conn.), and the pellets are resuspended in 20 ml lysis buffer (50 mM Tris, pH 8.0, 300 mM NaCl, 1 mM EDTA, 3 mM mercaptoethanol, and half of a tablet of Complete Protease Inhibitor Cocktail [Roche Applied Science, Indianapolis, Ind.]). The resuspended pellets are sonicated for 1 min on ice (Flat tip at 20% power, Ultrasonic processor XL; Heat Systems, Farmingdale, N.Y.), cell debris is removed by centrifugation at 90,000 rpm for 20 min at 4° C. by using a TLA 100.4 rotor (Beckman Coulter, Fullerton, Calif.), and the supernatant (20 ml) is dialyzed at 4° C. for 12 h against 2×2 l of cage buffer (20 mM [2-(N-morpholino)ethanesulfonic acid] MES, pH 6.2, 2 mM CaCl<sub>2</sub>, 0.02% NaN<sub>3</sub>, and 0.5 mM dithiothreitol [DTT]). The sample is then centrifuged at 4° C., first at low speed (1000 rpm for 10 min) to remove large aggregates and then at high speed (54,000 rpm for 1 h) by using a Ti rotor (Beckman Coulter). The pellet, primarily comprising Clathrin (presumably assembled as cages) is resuspended in 6 ml of 100 mM MES, pH 6.5, 3 mM EDTA, 0.5 mM MgCl<sub>2</sub>, 0.02% NaN<sub>3</sub>, 0.5 mM DTT, and 0.5 mM phenylmethylsulfonyl fluoride followed by addition of 3 ml of 2.4M Tris, pH 7.4, 1 mM DTT, and incubation for 20 min at room temperature, a condition used to dissociate native Clathrin assemblies. The sample is centrifuged at 90,000 rpm for 20 min at 4° C. by using a TLA 100.4 rotor, and most of the Clathrin is recovered in the supernatant. The resulting sample is subjected to gel filtration chromatography (90 cm×Ø=3 cm column comprising Sephacryl-S 500 [GE Healthcare, Little Chalfont, Buckinghamshire, United Kingdom] in 0.5 M Tris, pH 7.4, 0.04% NaN<sub>3</sub>, and 0.5 mM DTT) at room temperature and with a flow of 2 ml/min. Fractions of 5.5 ml comprising the Clathrin peak (100 ml) are pooled and then subjected to adsorption chromatography (5 ml, hydroxyapatite, Econo-Pac CHT-II; Bio-Rad, Hercules, Calif.); the column is pre-equilibrated with low phosphate buffer (10 mM NaH<sub>2</sub>PO<sub>4</sub>, pH 7.1, 100 mM NaCl, 0.02% NaN<sub>3</sub>, and 0.5 mM DTT) and eluted with a linear gradient from low to high phosphate concentration (500 mM NaH<sub>2</sub>PO<sub>4</sub>, pH 7.1, 100 mM NaCl, 0.02% NaN<sub>3</sub>, and 0.5 mM DTT) at room temperature with a flow of 1 ml/min. Fractions (1 ml) are collected into microcentrifuge tubes comprising 21 of 0.5 M EDTA. Typical Clathrin yields are in the range of 3-40 mg per 1 l of cell culture. Western blot analysis is used to confirm the expression of Clathrin heavy and light chains. The rat Clathrin light chain rLCalb is expressed in *Escherichia coli* strain BL21 (DF3). The bacteria are grown in Luria-Bertani (LB) medium comprising 30 mg/l kanamycin at 37° C. with shaking (250 rpm) to an optical density of 0.5. Expression is induced by addition of isopropyl-d-thiogalactoside (IPTG) (final concentration, 0.6 mM). After 3 h, the cell are harvested by centrifugation at 5000 rpm for 10 min at 4° C. by using an H6000A rotor (Sorvall) and resuspended in ice-cold lysis buffer (20 mM Bis-Tris adjusted to pH 6.0 at room temperature, 0.5 mM dithiothreitol, 1 mM EDTA, and Complete Protease Inhibitor Cocktail) by using 20 ml of lysis buffer per 3.5 g of wet cell weight. The suspension is placed into a glass vessel, and the vessel is immersed in boiling water for 4 min and then chilled on ice. The boiled suspension is centrifuged at 54,000 rpm for 30 min at 4° C. by using a 60Ti rotor (Beckman Coulter) to remove the precipitated material. rLCalb is purified from the filtered supernatant (0.2-ml syringe filter) by anion exchange chromatography at 4° C. on a HiTrap MonoQ column equilibrated with buffer A (20 mM Bis-Tris, adjusted to pH 6.0 at room temperature, and

0.5 mM dithiothreitol) and eluted using a linear gradient from 0 to 32% buffer B (20 mM Bis-Tris, adjusted to pH 6.0 at room temperature, 0.5 mM dithiothreitol, and 1 M NaCl). For the in vitro reconstitution of Clathrin, recombinant heavy chain (expressed in insect cells without light chain) is mixed with excess rLCalb (expressed in bacteria) by using a weight ratio of 3:1 (equivalent to a molar ratio HC:LC of 1:2.4) just before cage or coat assembly for 40 min at room temperature.

#### [0298] Part V. Clathrin Coat Formation

##### Reagents

#### [0299] 1. Coat formation buffer

80 mM Mes hydrate pH 6.5	31.23 g/2 L
20 mM NaCl	2.34 g/2 L
2 mM EDTA	8 mL of 500 mM stock solution/2 L
0.4 mM DTT	1.6 mL of 500 mM stock solution/2 L

#### [0300] 2. Clathrin

#### [0301] 3. AP-2

##### Procedure

[0302] (1) Place a solution of clathrin and AP-2 into a dialysis chamber

[0303] clathrin: AP-2=3:1 to 4:1 (w/w)

[0304] (2) Dialyze over night against coat formation buffer; replace buffer and dialyze for an additional 3-4 h.

[0305] (3) Transfer to a centrifuge tube, centrifuge to remove larger aggregates

[0306] rotor: TLA-100.4, 12000 rpm, 4° C., 10 min

[0307] (4) Transfer supernatant to fresh centrifuge tube, centrifuge to collect coats

[0308] rotor: TLA-100.4, 65000 rpm, 4° C., 12 min

[0309] (5) Immediately withdraw supernatant with a 1 mL pipette.

[0310] (6) Wash carefully with buffer around the pellet.

[0311] (7) Resuspend the pellet by adding buffer, allowing to stand at room temperature for 10-15 min, then slowly wash buffer over the pellet to resuspend using a micropipettor (avoid foaming)

[0312] volume: 120-150 uL for a pellet of ~3 mm diameter

#### Part VI. Clathrin Cage Formation

##### Reagents

#### [0313] 1. Cage Formation Buffer:

[0314] 20 mM Mes, pH 6.2 (3.9 g/l) (7.8 g/2 l)

[0315] 2 mM CaCl<sub>2</sub> (2 ml of 1M/l) (4 ml of 1M/2 l)

[0316] 0.02% NaN<sub>3</sub> (2 ml of 10%/l) (4 ml of 10%/2 l)

[0317] 0.5 mM DTT (1 ml of 500 mM/l) (2 ml of 500mM/2 l)

#### [0318] 2. Clathrin

##### Procedure

[0319] (1) Place a solution of Clathrin (0.5-1 mg/mL) into a dialysis chamber

[0320] (2) Dialyze over night against cage formation buffer; replace buffer and dialyze for an additional 3-4 h.

[0321] (3) Transfer to a centrifuge tube, centrifuge to remove larger aggregates

[0322] rotor: TLA-100.4, 12000 rpm, 4° C., 10 min

[0323] (4) Transfer supernatant to fresh centrifuge tube, centrifuge to collect coats

[0324] rotor: TLA-100.4, 65000 rpm, 4° C., 12 min

[0325] (5) Immediately withdraw supernatant with a 1 mL pipette.

[0326] (6) Wash carefully with buffer around the pellet.

[0327] (7) Resuspend the pellet by adding buffer, allowing to stand at room temperature for 10-15 min, then slowly wash buffer over the pellet to resuspend using a micropipettor (avoid foaming)

#### [0328] Production of Recombinant Auxilin

[0329] A protein chimera of glutathione transferase (GST) with bovine auxilin (spanning residues 547-910) is generated by fusion in the vector pGEX4T-1 and then used for expression in *E. coli* BL21 (Fotin et al., 2004a). The bacteria are grown in LB medium supplemented with ampicillin to an OD<sub>600</sub> 0.5-0.6 at 37° C. Protein expression is induced by addition of 1 mM IPTG (final concentration) and the cells grown for another 4 h at 25° C. The cells (from 1 l of culture) are centrifuged at 5000 rpm for 15 min at 4° C., and the pellet is kept frozen overnight. The pellet is resuspended in 25 ml of pGEX lysis buffer (20 mM HEPES, pH 7.6, 100 mM KCl, 0.2 mM EDTA, 20% glycerol, 1 mM DTT, and half a tablet of Complete Protease Inhibitor Cocktail) and sonicated on ice using three consecutive sonication cycles of 60, 30, and 30 s (standard microtip, 20% power). The sample is centrifuged at 45,000 rpm for 1 h at 4° C. by using a 60Ti rotor, and the supernatant mixed with 0.5 ml of a 50% (vol/vol) slurry of glutathione-Sepharose 4 beads (GE Healthcare). After 2 h of end-over-end rotation at 4° C., the beads are poured into a propylene Econo-Column (Bio-Rad), washed with 15 ml of pGEX lysis buffer, and then washed with 15 ml of 25 mM HEPES, pH 7.0, 100 mM NaCl, and 0.1 mM EGTA. Elution of GST-auxilin (in 2 ml) is achieved by supplementing the solution with 50 mM glutathione, adjusted to pH 8. These steps are carried out at 4° C. Release of the GST portion is achieved by incubation of 1 mg of GST-auxilin with 1 U of thrombin at room temperature for 6 h. Proteolysis is ended by addition of 1 mg of Pefabloc SC (Roche Applied Science). The 40-Da auxilin fragment is further purified using a Mono S column (Pharmacia, Peapack, N.J.). The sample is first dialyzed overnight against MES buffer A (50 mM MES, pH 6.7, 1 mM EDTA, and 3 mM-mercaptoethanol), and then it is loaded onto the column (pre-equilibrated with MES buffer A) and eluted with a linear gradient of buffer A and with MES buffer B (50 mM MES, pH 6.7, 500 mM NaCl, 1 mM EDTA, and 3 mM-mercaptoethanol) at a flow of 1 ml/min. The auxilin sample is stored at 80° C. with 20% glycerol (final concentration).

#### [0330] Production of Recombinant Hsc70

[0331] N-terminal 6x-His-tagged bovine Hsc70 (full length) cloned into the pET21a vector is expressed in *E. coli* BL21. The bacteria are grown at 37° C. in LB supplemented with 0.1 mg/ml ampicillin to an OD<sub>600</sub> of 0.5, transferred to 28° C., and induced with 0.1 mM IPTG for 5 h. The cells are centrifuged at 5000 rpm for 15 min at 4° C., and the pellets from 1 l culture resuspended in 25 ml 50 mM Tris, pH 8.0, 300 mM NaCl, 1 mM ATP, 2 mM MgCl<sub>2</sub>, 10 mM-mercaptoethanol, and half a tablet of Complete Protease Inhibitor Cocktail without EDTA. The supernatant obtained after sonication and centrifugation (as with auxilin) is mixed with 1 ml of 50% (vol/vol) slurry of nickelnitrilotriacetic acid-agarose beads (QIAGEN, Valencia, Calif.) for 4 h by endover-end rotation at 4° C. The beads are placed into an Econo Pac column and then

washed with 30 ml of 50 mM Tris, pH 8.0, 300 mM NaCl, 10 mM-mercaptoethanol, 10 mM imidazole, 1 mM ATP, and 1 mM MgCl<sub>2</sub>). Hsc70 is then eluted at 4° C. with 5-6 ml of the same solution supplemented with 200 mM imidazole. Fractions of 1 ml are collected into microcentrifuge tubes comprising 40 l of 0.1 M EGTA. The samples comprising 20% glycerol (final concentration) are stored at 80° C.

**[0332]** According to another illustrative embodiment, Clathrin and or Coatamer I/II proteins are extracted and prepared from Clathrin and or Coatamer I/II coated vesicles obtained from non-rat, non-bovine organic tissue, including from human tissue, in whole or in part. In another embodiment, Clathrin and or Coatamer I/II coated proteins are extracted and prepared from Clathrin and or Coatamer I/II coated vesicles obtained by donor/recipient tissue matching using established techniques. In another embodiment, Clathrin and or Coatamer I/II proteins are prepared, in whole or in part, by using stem cells, cloning and or other genetic manipulation techniques known in the prior art to produce genetically matched tissue for a donor recipient.

**[0333]** According to one illustrative embodiment, the coat protein I (COPI) assembly process is carried out by preparing Coatamer subunits from cytosolic preparations, including methods, but are not limited to, as essentially described in Spang, et al., Proc. Natl. Acad. Sci. USA. 1998 Sep. 15; 95 (19): 11199-11204. Coatamer, a nanoscale element comprised of seven distinct subunits (alpha, beta, beta', gamma, delta, epsilon and zeta subunits, respectively) and ADP-ribosylation factor (ARF, an N-myristylated small GTP-binding protein) are the only cytoplasmic proteins needed.

**[0334]** In another illustrative embodiment, the coat protein I (COPI) assembly process is carried out by preparing Coatamer subunits from cytosolic preparations, including methods, but are not limited to, as essentially described in Sheff, et al, The Journal Of Biological Chemistry, Vol. 271, No. 12, Issue Of March 22, Pp. 7230-7236, 1996 "Purification of Rat Liver Coatamer (COPP)"—Purification of rat liver Coatamer is accomplished through a substantial modification of the method of Waters and Rothman (13). Unless otherwise noted, all operations are performed at 4° C. Approximately 250 g of fresh liver from 10-15 adult Sprague-Dawley rats (Harlan Sprague-Dawley) are homogenized in 2 volumes of buffer (25 mM Tris, pH 7.5, 320 mM sucrose, 500 mM KCl, 2 mM EDTA, 1 mM dithiothreitol) comprising protease inhibitors (2 mg/ml pepstatin A, antipain, and leupeptin; 1 mM phenylmethylsulfonyl fluoride) using a polytron homogenizer with 1.5-cm cutter assembly at maximum speed for three 1-min bursts on ice with 1-min rests. The lysate is cleared by sequential centrifugation at 9000 3 g for 15 min followed by centrifugation of the supernatant at 100,000 3 g for 1 h. This material (S100) is stored at 270° C. for up to 4 months. For a typical purification, 150 ml of S100 is diluted 6-fold with cytosol buffer (25 mM Tris, pH 7.5, 1 mM dithiothreitol, 1 mM EDTA plus protease inhibitors as above). Protein concentration is 5 mg/ml. Ammonium sulfate is added to 25% of saturation and stirred for 15 min on ice, and then precipitate is removed by centrifugation, and the supernatant is brought to ammonium sulfate at 45% of saturation with stirring on ice. The precipitate is collected by centrifugation and redissolved in 150 ml of cytosol buffer. An additional 120 ml of cytosol buffer is added and then 30 ml of 60% (w/v) polyethylene glycol 3350 in distilled H<sub>2</sub>O with gentle stirring. The mixture is incubated at 4° C. for 30 min, and the precipitate is collected by centrifugation at 10,000 3 g for 15

min. The precipitate is resuspended in 20 ml of G buffer (10 mM Tris, pH 7.5, 0.2 mM ATP, 0.2 mM CaCl<sub>2</sub>), the insoluble material is removed by centrifugation, and the supernatant is passed over a 20-ml column comprising 250 mg of DNase-I (Sigma) coupled to agarose (Affi-Gel-10, Bio-Rad, prepared according to the manufacturer's directions) to remove contaminating actin and actin binding proteins. Eluent is desalted into cytosol buffer using 10DG desalting columns (Bio-Rad) and applied to a 50-ml DEAE cellulose column (DE52, Whatman) equilibrated in cytosol buffer. COPI is eluted with a 100-400 mM KCl gradient over 200 ml, with the elution of COPI followed by spot blot on nitrocellulose using EAGE antibody. In a final step, peak COPI fractions are pooled, diluted 1:1 with cytosol buffer, and applied to a 1-ml Mono-Q column (Pharmacia) equilibrated in cytosol buffer and mounted on a fast protein liquid chromatography apparatus (Pharmacia). The column is swished with 300 mM NaCl and then eluted with a 350-400 mM NaCl gradient over 20 ml. COPI, as assayed by the presence of b-COP on a spot blot using EAGE antibody, eluted as a single peak. The presence and purity of COPI is confirmed by SDS-PAGE. An alternative final step is employed in preparing samples for two-dimensional dimensional gels. Here, DEAE eluent is concentrated in a Centricon-30 microconcentration (Amicon) to 400 ml and applied to a 24-ml Superose-6 (Pharmacia) column equilibrated in cytosol buffer with 50 mM KCl. As with Mono-Q, COPI eluted in a single peak. This final step produces a somewhat lower yield and comprises some contaminants between 30 and 100 KD by SDS-PAGE. For copurification of labeled CHO cytosol and rat liver COPI, all quantities are divided by 3, 1 ml of labeled cytosol is added to 50 ml of rat liver S100, and the Mono-Q column is used as the final step.

**[0335]** The increasing interest in the targeting of foreign moieties at sites in the body where their activity is required is addressed by the invention in one more embodiments. It is important that agents, like drugs, particularly those having undesirable side effects, are delivered to the site where they are supposed to act. Many molecular species require that they be delivered in a site specific manner, often to particular cells, for example, polynucleotides (anti-sense or ribozymes), metabolic co-factors or imaging agents. One such system has been described by Wu et al., J. Biol. Chem., 263, 14621-14624 and WO-A-9206180, in which a nucleic acid useful for gene therapy is conjugated with polylysine linked to galactose which is recognized by the asialoglycoprotein cargo attachment elements on the surface of cells to be targeted. However, there are many occasions, such as in the delivery of a cytotoxic drug, when it would not be satisfactory to use a delivery system in which the targeting and or masking moiety and or vector to be delivered is so exposed. This need is addressed by various delivery system embodiments of the invention that possess the flexibility to target a wide range of biologically active foreign moieties.

**[0336]** In one embodiment, the invention includes one or more elements having one or more suitable sites for subsequent attachment of a targeting and or masking moiety and or vector, and one or more elements having one or more surfaces and or protein coats to which one or more targeting and or masking moieties and or vectors have already been attached.

**[0337]** In one embodiment, one or more masking moieties are attached to the surface of one or more invention elements. These masking moieties prevent the recognition by a specific cell surface and instead allows for intravenous administration

applications. For example, the surface masking characteristics may be provided by poly (ethylene glycol) (PEG) by using various PEG-PLA and PLGA mixtures. PEG conjugation masks the protein's surface, reduces its renal filtration, prevents the approach of antibodies or antigen processing cells and reduces its degradation by proteolytic enzymes. In one embodiment, PEGylated elements significantly improve element stability and prevent leakage of agents from elements. Studies have shown that protein-based nanoparticles and liposomes without PEGs have a short circulation time due to rapid uptake by macrophages of the reticulo-endothelial system (RES), primarily in the liver and spleen. Finally, PEG conveys to molecules its physico-chemical properties and therefore modifies biodistribution and solubility of peptide and non-peptide nanoparticles. Thus, recent studies have used mostly nanoparticles with PEGs. The PEG coating is highly hydrated and this layer protects against interactions with molecular and biological components in the blood stream, as well as nonspecific binding to tissue. In one embodiment, one or more elements, in one or more configurations, are internally and or externally attached, coated, and treated, in whole or in part by using steric stabilizers including, but not limited to, steric stabilizers selected among dipalmitoyl phosphatidyl ethanolamine-PEG, PEG-stearate, the esters of the fatty acids from the myristic acid to the docosanoic acid with methyl ether PEG, the diacylphosphatidyl ethanolamines esterified with methyl ether PEG and the polylactates and the polyglycolactates esterified with methyl ether PEG. In one embodiment, one or more elements are not required to be PEGylated to efficaciously operate.

**[0338]** In another embodiment, one or more elements, and in one or more configurations are internally and or externally coated or treated in whole or in part with surfactants, including, but not limited to, surfactant agents selected among soybean phosphatidylcholine, dioleoyl phosphatidylcholine, dipalmitoyl phosphatidylcholine, hydrogenated soy-bean phosphatidylcholine, phosphatidylethanolamine and phosphatidylserine), and or with cosurfactants, including, but not limited to cosurfactant agents selected among ethanol, propanol, isopropanol, butanol, sodium taurocholate, sodium glycocholate, propylene glycol, butyric acid and benzoic acid.

**[0339]** In one or more embodiments, ligands can be of one or more efficacious types, such as drugs, and may be bioengineered, and or comprise isolated, recombinant, synthetic, and or cloned elements.

**[0340]** In one embodiment, one or more types of ligands may be functionalized and or attached in one or more ways to one or more elements.

**[0341]** In one embodiment, ligands are natural ligands of one or more types. In another embodiment, one or more types of natural ligands are modified and or functionalized. In another embodiment, invention element ligands and natural element ligands are combined to comprise one or more types of hybrid ligand elements.

**[0342]** In another embodiment, the course of a natural ligand and or invention ligand element during cellular signaling, trafficking, downregulation, upregulation, endocytosis, exocytosis, and other cellular entry or exit, cellular inter- and or intra-actions, and the like, may be efficaciously controlled, regulated, and or modified by one or more elements to yield one or more diagnosis, cure, mitigation, treatment, prevention of disease, or other types of efficacious effects, and the like.

**[0343]** Examples of some natural ligands, but not limited to, that may be subject to efficacious control, modification, and or regulation in one or more invention embodiments are listed below:

- [0344]** Toxins and lectins, e.g.,
- [0345]** Diphtheria Toxin
- [0346]** Pseudomonas toxin
- [0347]** Cholera toxin
- [0348]** Ricin
- [0349]** Concanavalin A
- [0350]** Viruses, e.g.,
- [0351]** Rous sarcoma virus
- [0352]** Semliki forest virus
- [0353]** Vesicular stomatitis virus
- [0354]** Adenovirus
- [0355]** Influenza
- [0356]** West Nile
- [0357]** Serum transport proteins and antibodies, e.g.,
- [0358]** Transferrin
- [0359]** Low density lipoprotein
- [0360]** Transcobalamin
- [0361]** Yolk proteins
- [0362]** IgE
- [0363]** Polymeric Ig
- [0364]** Maternal Ig
- [0365]** IgG, via Fc receptors
- [0366]** Hormones and Growth Factors, e.g.,
- [0367]** Insulin
- [0368]** Epidermal Growth Factor
- [0369]** Growth Hormone
- [0370]** Thyroid stimulating hormone
- [0371]** Nerve Growth Factor
- [0372]** Calcitonin
- [0373]** Glucagon
- [0374]** Prolactin
- [0375]** Luteinizing Hormone
- [0376]** Thyroid hormone
- [0377]** Platelet Derived Growth Factor
- [0378]** Interferon
- [0379]** Catecholamines
- [0380]** LDL
- [0381]** Neurotransmitters
- [0382]** Substance P
- [0383]** A neurotransmitter known to stimulate pain receptors
- [0384]** In one or more embodiments, one or more elements are conjugated (bonded) with one or more other elements (e.g., ligands), agents, materials, and or substances of one or more types, including those developed by 3<sup>rd</sup> parties, which may be used singly or mixed together in one or more configurations for medical and biological research, diagnosis, therapy, or prosthetic purposes. One or more biomedical elements such as ligands and other types of biomedical functionalization elements may be directly and or indirectly attached, bonded, fastened, cross-linked, and or affixed to and or incorporated into one or more invention elements, as well as one or more non-invention and or natural elements. In one embodiment, attachment is achieved via molecular tethers. In another embodiment, no molecular tether is involved. In one configuration, a free radical molecule may be attached directly to one or more invention elements. In another embodiment, one or more elements may be bonded, fastened, and or affixed to one or more elements by being included in a modified protein sequence of one or more elements or bonded elements; by

using a spacer; by covalent bonding; by site directed mutagenesis; by genetically engineered mutation and or modification; by peptides; by proteins; by DNA; by antibodies; by monoclonal antibodies; by recombinant elements; and via other bioengineering techniques and methods known in the art.

**[0385]** According to one embodiment, the protein amino acid sequence of one or more elements are modified to provide a site suitable for attachment thereto of an in vivo or in vitro targeting and or masking moiety. In one illustrative embodiment, one or more target-specific ligands and or targeting moieties are directly attached to one or more elements via one or more amino acid groups, and or attached via one or more short molecular tethers.

**[0386]** In another embodiment, one or more functionalization elements, of one or more types, comprise highly specific targeting agents, such as, but not limited to, antibodies, peptides or small molecules, large molecules, and other functional ligands, such as fluorophores and permeation enhancers, and the so functionalized nanoparticles may target receptors, transporter, enzymes and or intracellular processes in vivo with high affinity and specificity.

**[0387]** In one illustrative embodiment, one or more elements such as diagnostic, therapeutic, prosthetic, and or assay agents, but not limited to, are delivered to a target in vivo or in vitro using a variety of guidance techniques, including for example, optical (photonic), acoustic, electric, biological, chemical, mechanical reactions and forces, but not limited to, and one or more elements may be delivered singly and or in one or more configurations to one or more targets.

**[0388]** In another illustrative embodiment, one or more elements comprise one or more diagnostic agents like imaging contrast or radioactive agents to perform site designation, site specificity, and site retention for targeted in vivo delivery of therapeutics; the latter may also comprise part of the same diagnostic payload.

**[0389]** In one illustrative embodiment, the invention enables targeted agent delivery systems that retain their structural integrity and that may also loiter for a calculated period of time at the targeted area of concern after delivery of agent payload.

**[0390]** In one illustrative embodiment, one or more elements comprise molecules arranged in specific patterns. The pattern of elements precisely mirrors or mimics a spatial or physical pattern a target cell in a human or animal body expects to see and will recognize, and one or more elements are accepted by the target cell, which can be a cancer cell or HIV infected cell, for example.

**[0391]** In one embodiment, gold metal nanoparticle probes with sensor ligands and using electrical charges are bonded to one or more elements, and or attached to ligands, targeting moieties, and or vectors. The gold particles carry short strands of artificial DNA (oligonucleotides) tailored to match known segments of biological DNA that are implicated in, or linked to, disease.

**[0392]** Target-specific ligand binding and any subsequent changes within or to one or more elements may be a result of either covalent or non-covalent interactions—the latter including hydrogen bonding, ionic interactions, Van der Waals interactions, and hydrophobic bonds—depending on the application, system design, receptor design, cargo type and or the interaction/application environment.

**[0393]** In another illustrative embodiment, one or more elements, ligands, targeting moieties, vectors, and the like utilize the method of chirality.

**[0394]** In another illustrative embodiment, reactions and forces arise from one or more ligands and or targeting moieties binding to targets, including covalent and non-covalent interactions, which ligands are tethered and or directly attached to one or more invention elements. Ligand binding to one or more specific targets may produce one or more conformational changes sufficient to deform and or rupture one or one or more elements in whole or in part, thereby causing one or more elements to be released. The targeting moieties can be selected by one of ordinary skill in the art keeping in mind the specific cell surface to be targeted. For example, if one wishes to target the asialoglycoprotein receptor on the hepatocytes in the liver, an appropriate targeting moiety would be clustered trigalactosamine. Once a specific targeting moiety has been selected for a particular cell to target, the different targeting moieties can be attached either by covalent linkage directly onto the surface of one or more invention elements, or by indirect linkage via, for example, a biotin-avidin bridge. In another embodiment, depolymerization (e.g., by cytosolic Hsc 70) of the Clathrin and or Coatmer element exposes one or more transmembrane proteins (V-SNARE) that direct one or more elements to their destinations by binding to a specific T-SNARE protein on the target organelle. The fusion protein SNAP25 causes the one or more elements to fuse with the target membrane

**[0395]** In one embodiment, avidin is attached covalently to the surface of one or more elements and a biotinylated ligand attaches non-covalently to the avidin. In another embodiment, biotin is covalently attached to the surface of one or more invention elements, and then avidin is used as a bridge between the biotinylated polymer and the biotinylated ligand. Targeting agents may also include one or more biocompounds, or portions thereof, that interact specifically with individual cells, small groups of cells, or large categories of cells. Examples of useful targeting agents include, but are not limited to, low-density lipoproteins (LDL's), transferrin, asialoglycoproteins, gp120 envelope protein of the human immunodeficiency virus (HIV), and diphtheria toxin, antibodies, and carbohydrates. A variety of agents that direct compositions to particular cells are known in the prior art (see, for example, Cotten et al., *Methods Enzym*, 1993, 217, 618).

**[0396]** In another illustrative embodiment, one or more classical structural activity relationships (SARs) based drug discovery approaches are combined with one or more other techniques to form a specific case of targeted drug delivery, for example, but not limited to, one or more structural metabolism relationships (SMRs) that in combination with SARs are sometimes termed as retrometabolic drug design approaches. These active drugs are designed to undergo singular metabolic deactivation after they achieve their therapeutic roles, and may produce specific action at the site of application without affecting the rest of the body.

**[0397]** In another illustrative embodiment, one or more elements comprise one or more agent functionalities and or methods that produce targeting by changing molecular properties of an overall target molecule, as a result of enzymatic conversion, but also, for example, may involve one or more pharmacophores. These elements, sometimes referred to as the targetor (Tor) moiety, are converted by site-specific enzymes to active functions. In addition to the Tor moiety, one

or more other functions may be introduced into elements for in vivo use, which can be named as “protector functions” that serve as lipophilicity modifiers or protectors of certain functional groups in therapeutic agent molecules.

**[0398]** In other illustrative embodiments, one or more other types of targeting delivery systems and methods can be used, for example, but not limited to, in whole or in part in one or more configurations: surfactants (surface-active substances) and or cosurfactants; enzymatic physical-chemical-based targeting; site-specific enzyme-activated targeting; vectors, such as ligand-based, non-viral-based, and Protein/DNA polyplex vector targeting; receptor-based chemical targeting; organic and or inorganic synthetic elements; transmembrane proteins (V-SNARE); peptides, including peptides that cross cell membranes and home specifically to certain diseases; nanostructured dendrimers and hyperbranched polymers; molecular Trojan horses; adenovirus, herpes simplex virus, adeno-associated virus or other virus vectors for targeted delivery that do not cause toxicity; antibodies, including monoclonal antibodies; nanoparticles, including polymer nanoparticles like polymer, polybutylcyanoacrylate, and ethyl alcohol nanoparticles; immunotoxins; hormonal therapy; tissue-specific gene expression; gene therapy; pegylated immunoliposomes; anti-sense therapy; biological elements and or agents, including biological elements and agents conjugated with other agents, such as transferrin, but not limited to such; chemical elements and agents; devices, systems, and or mechanisms; liposomes, including liposomes conjugated with transferrin, but not limited to such; conformationally-constrained peptide drugs targeted at the blood-brain barrier; endogenous blood brain barrier and or blood tumor capillary transporters; inhibiting and or modulating blood brain barrier active efflux transporters; air and or other gas bubbles; blood brain barrier breaking and or disrupting elements and agents; blood brain barrier tight junction separating and or endocytoses elements and agents; vector-mediated delivery of opioid peptides to the brain; brain drug delivery of peptides and protein drugs via vector-mediated transport at the blood brain barrier, neurotrophic, neuroprotective, and various peptides and drugs, and the like.

**[0399]** In another illustrative embodiment, one or more elements cross various in vivo biological barriers, such as the transmucosal passage, and may also cross the blood-brain barrier (BBB) and the blood-cerebrospinal fluid (CSF) barrier for targeted and or non-targeted in vivo delivery of CNS agents and elements. In one embodiment, one or more BBB-passing elements comprise small and or large molecule drugs.

**[0400]** Natural Clathrin, and in particular its ability to ‘track’ vesicle proteins leaving a synapse into the extracellular space (Granseth, et al 2007) indicates that the protein is not immediately scavenged by phages and other “housecleaning” elements in the brain, and further, may move freely about CNS spaces. In one embodiment, one or more elements efficaciously move through the CNS spaces and comprise in situ elements for remediation, removal, and or sequestration of one or more types of contaminants, toxic elements, undesirable organic or inorganic elements, and the like.

**[0401]** In another embodiment, extensive modification and functionalization of agents and elements may not be required for CNS entrance and or BBB passage. Only minimal functionalization may be required, depending on cargo and element type.

**[0402]** In another embodiment, one or more CNS-entering and or BBB-passing elements of one or more types may

behave as a drug by themselves—i.e., they efficaciously operate alone without carrying additional elements, e.g., cargo elements. In another embodiment, one or more elements of one or more types carry one or more additional elements of one more types past the BBB.

**[0403]** In another illustrative embodiment, one or more elements enter the CNS and or cross the blood brain barrier for targeted delivery of agents and elements, including, but not limited to, small and or large molecules, non-lipid-soluble micromolecules, macromolecules, light sources, hydrophilic and or hydrophobic agents, such as therapeutic, diagnostic, and prosthetic agents, and other structured cargo to specific cells and areas within the brain, and such agents and or cargo may comprise one or more sensor agents, assay agents, diagnostic agents, prosthetic agents, and also may comprise agents like central nervous system drugs, antibiotics, and antineoplastic agents of one or more types, but are not limited to such.

**[0404]** In another embodiment, one or more elements are capable of circumventing the fluid-brain barriers by intracellular routes related to three separate and distinct endocytic processes. The three endocytic processes from the least to the most specific are fluid- or bulk-phase endocytosis, adsorptive endocytosis, and receptor-mediated endocytosis.

**[0405]** There are several transport mechanisms and techniques known in the art to be involved in the uptake of nanoparticles by the brain across the BBB (Lockman et al. 2002, Begley, 2004, de Boer et al. 2007), one or more of which may be utilized in one or more invention embodiments. These mechanisms and techniques include: simple diffusion of lipophilic molecules, the BBB-specific influx transporters, including organic anion and cation transporters and transcytosis or endocytosis. In one embodiment, one or more elements are internalized at the BBB by one or two different endocytosis mechanisms: receptor-mediated endocytosis (RME) and adsorptive-mediated endocytosis (AME). AME is triggered by an electrostatic interaction between the positively charged moiety of the peptide and the negatively charged region of the plasma membrane. In contrast, RME is specific to certain peptides such as insulin and transferrin.

**[0406]** In one embodiment, delivery through the blood-brain barrier of one or more types of small or large molecule cargo elements, and or molecules with polar functional groups is accomplished via chimeric peptides. The latter are formed when a transportable vector, such as cationized albumin, lectins, or a receptor-specific monoclonal antibody, is conjugated to a therapeutic compound that is normally not transported through the BBB. In one embodiment, conjugation of drugs to transport vectors is facilitated by, but not limited to, the use of avidin-biotin technology. In another embodiment, chimeric peptides are not required to pass through the blood-brain barrier, depending on cargo and element types.

**[0407]** In another illustrative embodiment, one or more elements may be coated with one or more surfactants and or cosurfactants, including, but not limited to, polysorbate 20, 40, 60 and 80, and or with one or more other materials and substances to cross various biological barriers, such as the transmucosal passage, and also to overcome the blood-brain barrier (BBB), the transmucosal passage, and the blood-cerebrospinal fluid barrier (CSG) for targeted delivery of agents and elements nanoparticles. In another embodiment, surfactants and or cosurfactants are not required to achieve such BBB-passing functionality, depending on cargo and element

type. E.g., in the prior art, it has been shown that using such surfactants and co-surfactants can cause an immunogenic response.

**[0408]** In another illustrative embodiment, one or more elements may be cationized to facilitate blood brain barrier passage. In another embodiment, cationization is not required to achieve such functionality, depending on cargo and element type.

**[0409]** In another illustrative embodiment, one or more elements cross the blood brain barrier due to disruption of the barrier by acoustic techniques, such as by using ultrasound.

**[0410]** In another embodiment, zonula occludens toxin and its eukaryotic analogue, zonulin, (zot) are protein ligands attached to one or more invention elements. Zonulin, the natural ligand of the Zot target receptor, interacts with these cargo attachment elements at the blood brain barrier, unlocking the tight junctions (TJ) in the brain that regulate the blood-brain barrier at that receptor. TJ-unlocking allows passage of one or more elements through the BBB, and thereby enables delivery of small and large molecules, non-lipid-soluble micromolecules, macromolecules, light sources, and other structured cargo elements to the brain. In another embodiment, Zonulin is not required to pass through the blood-brain barrier, depending on cargo and element types.

**[0411]** Extracellular pathways circumventing the fluid-brain barriers in humans are comparable in the CNS of rodents and a subhuman primate. The most highly documented extracellular route is through the circumventricular organs (e.g., median eminence, organum vasculosum of the lamina terminalis, subfornical organ, and area postrema), all of which comprise fenestrated capillaries and, therefore, lie outside the BBB. In one embodiment, blood-borne macromolecules; specifically fluid-phase molecules released by the invention; escaping fenestrated vessels supplying the circumventricular organs move extracellularly into adjacent brain areas located behind the BBB.

**[0412]** The potential intracellular and extracellular pathways that blood-borne substances carried within one or more elements may follow in various embodiments for circumventing the fluid-brain barriers and entry to the CNS are therefore numerous, and various invention embodiments are used as appropriate. One invention embodiment, for example, uses the nasal cavity as a route for delivery of one or more types of drugs and other agents, especially for systemically acting drugs that are difficult to deliver via routes other than injection. Embodiments for the use of the nasal cavity for drug delivery also extend to circumventing the blood brain barrier. Drugs have been shown to reach the CNS from the nasal cavity by a direct transport across the olfactory region situated at the loft of the nasal cavity. It is the only site in the human body where the nervous system is in direct contact with the surrounding environment. In one embodiment, the nasal route would be important for rapid uptake of one or more types of drugs used in crisis treatments and management, such as for acute pain, epilepsy, psychic agitation, and for one or more other types of centrally acting drugs where the pathway from nose to brain provides a faster and more specific therapeutic effect. Furthermore, in another embodiment, the trigeminal nerve and, in animals, the vomeronasal organ also connects the nasal cavity with the brain tissue. One or more methods of nasal delivery to the CNS, which may also be used by the instant invention, but not limited to, are described in Dhuria, et al, 2008; Ma et al, 2007; and Thorne et al. 1995.

**[0413]** The nasal cavity has a relatively large absorptive surface area and the high vascularity of the nasal mucosa ensures that absorbed compounds are rapidly removed (Mainardes, et al 2006). In one embodiment, two routes, singly or in combination, are used via which one or more types of molecules are transported from the olfactory epithelium into the CNS and/or CSF. The first is the epithelial pathway, where one or more types of compounds pass paracellularly across the olfactory epithelium into the perineural spaces, crossing the cribriform plate and entering the subarachnoid space filled with CSF. From here the molecules can diffuse into the brain tissue or will be cleared by the CSF flow into the lymphatic vessels and subsequently into the systemic circulation. The second embodiment utilizes the olfactory nerve pathway, where compounds may be internalized into the olfactory neurones and pass inside the neuron through the cribriform plate into the olfactory bulb. In another embodiment, it is possible that further transport into the brain can occur by bridging the synapses between the neurons. After reaching the brain tissue, the drugs are cleared either via the CSF flow or via efflux pumps such as p-glycoprotein at the BBB into the systemic circulation. Despite the potential of the nasal route, there are some factors that limit the intranasal absorption of drugs. These barriers include the physical removal from the site of deposition in the nasal cavity by the mucociliary clearance mechanisms, enzymatic degradation in the mucus layer and nasal epithelium and the low permeability of the nasal epithelium removed (Mainardes, et al 2006). Colloidal carriers systems, such as nanoparticles and liposomes have demonstrated great efficacy in increasing drug bioavailability via the nasal route (Illum, 2002) In one invention embodiment, one or more elements comprise a colloidal carrier for enhanced nasal delivery of one or more elements, of one or more types.

**[0414]** Further, in one embodiment, it is possible to greatly improve the nasal absorption of one or more types of drugs and other elements by administering them in combination with an absorption enhancer that promotes the transport of the drug across the nasal membrane. Another invention embodiment comprises a nasal drug-delivery system that combines an absorption enhancing activity with a bioadhesive effect, which increases the residence time of the formulation in the nasal cavity. In one embodiment, this method can be even more effective for improving the nasal absorption of polar drugs. In one or more embodiments, a wide range of absorption enhancer systems can be utilized. In another embodiment, depending on cargo and element types, minimal functionalization may be required to take advantage of nasal absorption for efficacious passage to brain cells.

**[0415]** In another illustrative embodiment, one or more elements and in one or more configurations comprise in vivo and or in vitro sensor systems, assay systems, therapeutic drugs and other suitable methods to do genetic-based (trait-based) and or phenotype (state-based) drug dosing. In one embodiment, drugs are delivered at optimally effective and safe doses per each individual.

**[0416]** The invention, in one embodiment, provides for individual patient factors such as genotype, phenotype, age, gender, ethnicity etc., to be taken into account by one or more elements and factored into dosing and administration consideration. It has been demonstrated that inter-individual response variability can be 40-fold or more with practically all classes of psychotropic drugs. This makes it difficult to formulate rational guidelines for dosing and interpretation of

biological parameters (such as plasma or serum drug concentrations) that might be associated with a therapeutic response. Although much remains unknown, a number of factors have been characterized as important determinants of patient-to-patient variability. These encompass genetics, disease state, nutritional status, concurrent use of drugs, and other pharmacoeactive substances, including demographic factors such as age, gender, and ethnicity. Therefore, there is a requirement for in vivo systems that analyze many of these factors and dynamically adjust dosing accordingly.

**[0417]** In one embodiment, one or more elements comprise one or more personalized medicine elements, and which elements' efficacy may be increased, because responses arising from one or more individual variability factors; such as, but not limited to, genotype, phenotype, disease state, metabolic state, nutritional status, constant use of drugs, and other pharmacoeactive substances, and also demographic factors such as age, and ethnicity; are factored into the elements, pre-delivery and or post delivery. Side effect profiles may also be reduced via such personalized medicine embodiments.

**[0418]** In one embodiment, one or more elements comprise one or more patented drugs; drugs that are about to go off patent; have already gone off patent (generics); and or their active metabolites, and which drugs' efficacy may be beneficially altered and or enhanced by use of the invention. These beneficial changes in the status of an existing drug may be achieved by the invention in one or more embodiments, for example, but not limited to: the ability to target specific areas in the body; to pass the blood brain barrier; to cross over into cells and their organelles; to fuse with cell membranes; to gain access to the cytosol; to offer the benefits of low antigenicity or minimal immunogenic effects; to modify, regulate, and or control cellular processes; to more efficiently and efficaciously carry drugs; and or to dynamically and or statically adjust the drug's responses and dosages arising from inter-individual variability due to one or more factors, such as, but not limited to, genotype, phenotype, disease state, metabolic state, nutritional status, constant use of drugs, and other pharmacoeactive substances, and also demographic factors such as age, gender, and ethnicity of the patient. New patent filings for about to go off patent drugs and drugs already off patent may be enabled by one or more invention embodiments, such as affording increased drug efficacy, and or by enabling a better safety profile for the drug in question.

**[0419]** In various embodiments, the instant invention can carry one or more types of biomedical or healthcare elements, for example and without limitation: one or more therapeutic elements; pharmaceutical elements; diagnostic elements; assay elements; cosmetic elements; agents for treating one or more types of autoimmune diseases; agents for treating one or more types of infectious diseases; biological elements; radioactive agents or nuclear medicine agents; contrast agents; nano-scale biosensors; restorative agents; regenerative agents; cell, tissue, organ or circulatory repair elements; drug discovery agents; drug designer agents; drug research and development agents; drug fabrication agents; drug control and regulation agents; drug modifier agents; targeted drug delivery agents; clinical drug trial agents; antibiotics; antibacterials; vaccines; antiviral and anti-parasitic drugs; cytostatics; vitamins; proteins and peptides, including enzymes; hormones or other biological elements; prosthetic elements; intelligent nano-prostheses that supplement or enhance cell, tissue, or organ functioning; surgical elements; magnetic iron oxide nanoparticles; nano-scale biosensors; assays; diagnos-

tic systems or nano-devices for in vivo delivery of targeted therapy to combat diseases, such as cancer and HIV, and the like, including other types and forms of drug elements for the diagnosis, cure, mitigation, treatment, prevention of disease. Some or all such elements may operate under the control and influence of various other elements and or methods and comprise another type of invention platform.

**[0420]** In another illustrative embodiment, one or more elements in whole or in part, cure, mitigate, or treat one or more types of bodily injuries and insults, including traumatic injury, blood clots, and the like, but not limited to.

**[0421]** In one embodiment, nano-engineered scaffolds comprised of a plurality of elements are able to support and promote cellular differentiation and growth in injured or degenerated regions.

**[0422]** In one illustrative embodiment, one or more elements comprise one or more types of small and or large molecules and may utilize one or more methods to enter the CNS and or cross the blood brain barrier, in whole or in part, for delivery of one or more assay, diagnostic, therapeutic agents, and drugs, of one or more types, to cells and or targeted areas within the brain, like, for example: contrast agents; central nervous system drugs; antibiotics; antineoplastic agents, which may be used for treating malignant brain tumors (primary and or metastasized, of one or more types) or benign neoplasms; Parkinson's agents; Multiple Sclerosis agents; epilepsy agents; meningitis agents; Alzheimer's disease agents; HIV infection agents; memory agents; stroke agents; coma agents; and the like; or comprise one or more psychotropic agents or therapies of one or more types to study, diagnose, cure, mitigate, or treat of one or more types of mental health and illness, including, but not limited to, stress; anxiety; depression; mania; bipolar disorder; attention deficit (hyperactivity) disorder; panic attacks; phobias; addictions; anger; rage; suicidal thoughts and tendencies; substance abuse disorder; post traumatic stress disorder; psychoses; mental retardation; autism; delirium symptoms; schizophrenia; neuroses; and or enhancing memory; cognition; cognitive functioning; the effects of cognitive therapy, and the like; including other types and forms of drug elements for the diagnosis, cure, mitigation, treatment, or prevention of one or more types of CNS diseases. In another illustrative embodiment, one or more elements enter the CNS, including crossing the blood brain barrier, in whole or in part, to diagnose, cure, mitigate, or treat one or more types of CNS injuries and insults, including traumatic brain injury, blood clots, and the like, but not limited to.

**[0423]** In one embodiment, one or more elements promote neuroprotection by limiting the damaging effects of free radicals generated after head injury, a major factor contributing to neuropsychiatric degenerative disorders (e.g., Alzheimer's).

**[0424]** In one embodiment, nano-engineered scaffolds comprised of a plurality of elements are able to support and promote neuronal differentiation and growth in injured or degenerated brain regions.

**[0425]** In another illustrative embodiment, one or more elements comprise a light source, for use, for example, but not limited to, in a photodynamic therapy (PDT) system for age related macular degeneracy (AMD).

**[0426]** Compounds such as drugs, amino acids, carbohydrates, proteins, nucleotide bases, hormones, pesticides and co-enzymes have been successfully used in the prior art for the preparation of selective recognition matrices. A wide variety of print molecules have been used in various imprint-



ing protocols known in the art. Of all the imprinting strategies known in the art, it has become evident that the use of non-covalent interactions between the print molecule and the functional monomers is the more versatile. The apparent weakness of these interaction types, when considered individually, may be overcome by allowing a multitude of interaction points simultaneously. Together with the fast association and dissociation kinetics of these bond types, so that in a short time many possible combinations can be checked before the correct partners associate, this protocol has proven advantageous. Furthermore, the use of non-covalent interactions in the imprinting step closely resembles the recognition pattern observed in nature. Example invention molecular imprint embodiments in the art include, but are not limited to:

- [0427] Fragmented polymer monoliths
- [0428] Composite polymer beads
- [0429] Polymer beads from suspension, emulsion or dispersion polymerization
- [0430] In-situ polymerization
- [0431] Polymer particles bound in thin layers
- [0432] Polymer membranes
- [0433] Surface-imprinted polymer phases

[0434] In one illustrative embodiment, the invention uses molecular-imprint technology, wherein biodegradable films are used as a pliable template for elements, which elements are pressed into a film and then removed, leaving a physical mold of the element's shape. In one embodiment, this can facilitate catalysis of certain reactions and may also be used for shape selective separations. In other embodiments, imprinted polymers may facilitate the fabrication of elements to achieve selective diffusion; as chromatographic supports for the separation of enantiomers and oligonucleotides by invention elements; to provide the recognition element for an invention chemical sensor; and for the synthesis of polymeric materials that mimic biological cargo attachment elements and are targeted by invention elements, and or play a role in the design of new drugs. In one embodiment, this invention process provides for imprinted biodegradable capsule production with target or site-specific feature sizes at the molecular level. Other invention embodiments may utilize imprinted membranes and thin films that also function as an artificial cell wall for the selective transport of targeted drugs, peptides and biologically important molecules.

[0435] Surface imprinting involves the following steps: The print molecule, usually a large one, is first allowed to form adducts with functional monomers in solution and the formed elements are subsequently allowed to bind to an activated surface such as silica wafers or glass surfaces. Thus, with this technique, a designed imprinted (imaged) surface is obtained. This approach should potentially be valuable for creating specific cell binding surfaces. When preparing molecularly imprinted polymer monoliths against large imprint species, there is a risk of permanent entrapment of the template in the polymer after polymerization. When using thin polymeric layers or imprinted surfaces this drawback may be overcome.

[0436] In one embodiment, imprinted nanocapsules using techniques known in the art and as discussed above, one or more elements utilize and or constitute a nanocapsule with manifold, multi-tiered capabilities for in vivo administration and targeted delivery. The imprinted nanocapsule is delivered in vivo to detect and target a particular in vitro imprinted biological element, which may be, but is not limited to, a particular type of receptor, protein, or cell, since its imprint

shape on the nanocapsule will only bind in vivo to that particular biological element target. The molecular-level imprint process thereby provides for targeting one or more elements using biodegradable nanocapsules for in vivo agent delivery. In addition, vectors and targeting moieties, and blood brain barrier, transmucosal, and CSF barrier breaching elements, and other elements and substances may also be attached to the surface of the molecular imprint nanocapsule or otherwise be conjugated to it.

[0437] In another illustrative embodiment, one or more elements may be used in conjunction with molecularly imprinted polymers known in the art as recognition elements in biosensor-like devices. In one embodiment, imprinted polymer embodiments may be highly resistant sensing element alternatives.

[0438] In another illustrative embodiment, one or more elements are encapsulated in whole or in part in one or more biodegradable controlled-release polymers, which polymers may also be conjugated with other elements and agents. The polymer capsule, and or one or more elements may also be coated with one or more surfactants and or cosurfactants and or with other materials and substances. One or more targeting and or masking moieties and or other targeting vectors may also be attached on the polymer surface, and or on one or more elements.

[0439] In one embodiment, one or more elements are put into one or more biodegradable controlled-release polymeric capsules, and these elements transform "dumb" polymeric delivery capsules into "smart" systems.

[0440] In the instance of polymeric nanocapsules, which may be molecularly imprinted or not, illustrative controlled-release polymeric nanocapsule embodiments of the invention may include one or more of the following delivery systems, but not limited to, and in one or more configurations:

- [0441] 1. Diffusion-controlled systems
- [0442] 2. Water penetration-controlled delivery devices
- [0443] 3. Chemically controlled systems
- [0444] 4. Drugs covalently attached to polymer backbone systems, which delivery systems can be further subdivided into soluble systems and insoluble systems. Insoluble systems are used as a subcutaneous or intramuscular implant for the controlled release of the chemically tethered therapeutic agent. Soluble systems are used in targeting applications.
- [0445] 5. Drug release determined predominantly by erosion systems, whereby certain polymers can undergo a hydrolysis reaction at decreasing rates from the surface of a device inward, and under special circumstances the reaction can be largely confined to the outer layers of a solid device. Two such polymers are poly (ortho esters) and polyanhydrides, because the rates of hydrolysis of these polymers can be varied within very wide limits, considerable control over the rate of drug release can be achieved.
- [0446] 6. Poly (ortho esters) systems, which are highly hydrophobic polymers that comprise acid-sensitive linkages in the polymer backbone.
- [0447] 7. Polyanhydrides materials as bioerodible matrices for the controlled release of therapeutic agents. Aliphatic polyanhydrides hydrolyze very rapidly while aromatic polyanhydrides hydrolyze very slowly, and excellent control and regulate over the hydrolysis rate can be achieved by using copolymers of aliphatic and aromatic polyanhy-

drides. In this way, erosion rates over many days have been demonstrated, and erosion rates measured in years have been projected.

**[0448]** The form in which the foreign moiety, vector and or cargo are held within one or more elements will depend on the release properties and methods required. For release at the targeted site, it will be important to ensure that the right conditions prevail, for example, to permit cell localization and internalization via receptor mediated endocytosis.

**[0449]** In one illustrative embodiment, the invention enables one or more types of delivery systems that engage in an iterative, interactive, and dynamic dialog with one or more targets; follow a sequence of actions governed by biological control laws and methods; and or use behaviors and methods as defined by graphs and or an algebra, for example, a Lie algebra. In one illustrative example, one or more elements follow an algorithm expressed by the invention, such as in this illustrative embodiment:

**[0450]** 1) One or more elements, that may be with or without cargo elements, docks and or loiters on or near one or more cell membranes,

**[0451]** 2) One or more elements enter one or more target cells, while one or more other elements continue to loiter nearby or stay docked at the cell membrane.

**[0452]** 3) The docked and or loitering element elements wait for a time period,

**[0453]** 4) The targeted cell produces one or more reactions, for example, manufactures and or secretes an agent in response to the element's docking and or delivering its cargo,

**[0454]** 5) The docked element and or loitering elements analyze the new cell behavior and or its secretions,

**[0455]** 6) The docked element or loitering elements undergo a conformational change in response to the cell's new behavior,

**[0456]** 7) The docked element and or loitering elements self-adapt, producing yet another conformational change in the cell, and or releases another round of one or more agents that are taken up by the targeted cell, and,

**[0457]** 8) The foregoing process is repeated as required to achieve an efficacious effect.

**[0458]** In another embodiment, one or more light sources comprised of one or more elements operate in an intelligently staged sequence or orchestrated series of actions, which may be multiplexed or done in parallel by using one or more light and thermal energy emitting sources and methods. By using one or more light and or thermal energy emitting sources, optical and or thermal energies from one or more light sources operate on one or more photosensitive and or thermal sensitive elements comprising one or more elements that also comprise one or more entrapped agents. This method results in a staged series of overall actions that follow an intelligently ordered sequence of events. In an example embodiment, first a diagnostic agent from one or more elements is released by an optical and or thermal trigger, and the agent's positive finding of a disease, like cancer or HIV then causes one or more therapeutic agents to be released from the same and or other one or more other elements by one or more optical and or thermal triggers. Agent dosages are released in calculated amounts, and the dosages may be non-targeted or targeted.

**[0459]** In another illustrative embodiment, cavity-forming cargo elements have one or more compartments that in whole or in part are separated by one or more barriers, for example, but not limited to, one or more phospholipid membrane bar-

riers and or one or more barriers comprised of molecular-imprinted films. The barriers may exhibit structural transitions due to internal or external stimuli. In one embodiment, agents or cargo entrapped within one or more elements remain sequestered within their respective compartments until a change in barrier permeability state is triggered by contact, for example, by a ligand, with one or more specific targets or sites. The subsequent biochemical and or biological reactions cause the barriers to alter states into an opened state and release entrapped cargo and agents from one or more invention elements. In one example embodiment, binary mixtures of therapeutic and or diagnostic agents are mixed together as needed to dynamically and more efficaciously deal with a disease or disorder.

**[0460]** The invention, in one or more embodiments, comprises in whole or in part one or more elements, components, devices, systems, and the like, of one or more types, formed by using one or more engineering disciplines and related engineering technology disciplines of one or more types. Listed below are some such example invention embodiments, but are not limited to.

**[0461]** In one embodiment, the invention remedies the deficiencies of prior art by providing one or more elements of one or more types, a plurality of which may also comprise one or more nanoscale platforms of one or more types. A platform according to the invention may be used, for example, in biomedical, electronics, telecommunications, and information processing applications.

**[0462]** FIG. 6 is an exemplary energy level diagram 600 illustrating the energy levels associated with a hyperfine interaction between electron and nuclear spin in the presence of magnetic fields of the type used to do ESR spin label studies, which may be done in vivo and in vitro in one invention embodiment. The hyperfine interaction is a strictly quantum mechanical phenomenon. In an atom, the electron possesses an intrinsic quantum mechanical quantity known as spin. The nucleus of an atom also possesses spin. Intrinsic spin tends to generate a spin magnetic moment that is capable of interacting with other magnetic moments and fields. Generally, the spin magnetic moment of the nucleus does not interact with the spin magnetic moment of the electron. However, in the presence of a strong magnetic field, the spin magnetic moments of the electron and nucleus become coupled and interact.

**[0463]** In one illustrative embodiment, the electron is excited using pulses of electromagnetic radiation while maintaining its spin configuration. The source of the electromagnetic radiation may be, for example, an ordinary lamp, an LED, a time-varying magnetic field generator, a laser, or an electromagnetic field generator. A hyperfine interaction gives rise to electron nuclear double resonance (ENDOR) techniques. According to one illustrative embodiment of the invention, room temperature EPR and ENDOR techniques known in the art are used for performing in vivo spin probe studies.

**[0464]** In another embodiment, one or more elements comprise one or more diagnostic agents, and during the same NMR/MRI, or EPR, or ESR, or ESEEM, or ENDOR, or PET, or SPECT, or OCT operation, one or more elements use quantum information processing techniques known in the art can modify, process, manipulate, encode and decode, input, output, transmit, communicate, store and read information using one or more modulated signals, methodologies, or carrier signals of one or more types.

**[0465]** In one embodiment, one or more invention elements in one or more configurations, are bonded, tethered, or otherwise incorporated into one or more invention and or non-invention elements, comprising functionalized nanoscale elements, components, devices, systems, and or platforms such as, but not limited to, nano-lasers, quantum dots; photonic dots; nanoscale DNA chips; protein assay chips; assay elements; environmental, protein, phenotype, DNA, and or metabolic assay and analysis elements.

**[0466]** In another embodiment, one or more elements may comprise a bio-lasing structure, in vivo or in vitro.

**[0467]** In one embodiment, one or more elements in one or more configurations comprise nano-sensor elements; including, but not limited to, radioactivity sensors; chemical sensors; biological sensors; electromagnetic sensors; acoustic sensors; visible, infrared, and or ultraviolet wavelength sensors; tactile sensors; pressure sensors; volumetric sensors; flow sensors; and temperature sensors; and one or more of which sensors may constitute a bio-molecular device.

**[0468]** In one embodiment, one or more elements and or platforms utilize and or employ one or more types of transmitter and or receiver elements as sensors and or for transmission of information of one or more types in vivo and in vitro.

**[0469]** In another embodiment, one or more elements and in one or more configurations comprise one or more nanoscale elements, components, devices, systems, and or platforms that input, read out, process, analyze, output and report on information gathered by one or more types of diagnostic, test, label, tag, reporter, sensor, and or assay elements.

**[0470]** In one embodiment, quantum dots and or photonic dots are released in vivo or in vitro from one or more elements, and the quantum dots and or photonic dots are coated in whole or in part in one or more surfactants, cosurfactants, and other materials or sequestering substances.

**[0471]** In one embodiment, quantum dots are tagged to one or more elements. The specific wavelength glow of the quantum dots enables the identification of specific pathologies, disorders, metabolic states, proteins or DNA making it possible to diagnose various diseases.

**[0472]** In one embodiment, one or more nanoscale quantum dot assays using tiny permutations of color tag a million or more different proteins or genetic sequences in a process called multiplexing. In one embodiment, one or more quantum dots of various sizes are excited at the same wavelength but have different emission wavelengths, and act as probes in experiments where multiple fluorescent measurements need to be made simultaneously, such as flow cytometry or confocal microscopy.

**[0473]** In another illustrative embodiment, one or more elements are sufficient to implement in vivo or in vitro genetic and protein nanoscale optical biological assay systems and methods. In one illustrative configuration, one or more elements comprise one or more nano-scale DNA chips known in the art, and or one or more nano-scale DNA chips known in the art to detect DNA samples formed from bonding with the target DNA on a chip, and or reference DNA nano-chips.

**[0474]** In another illustrative configuration, one or more elements comprise one or more protein array techniques known in the art. The array surfaces are designed to bind to one or more hydrophobic, hydrophilic (cation or anion) or specific ligands, and also include a protein array reader known in the art.

**[0475]** In another illustrative embodiment, one or more elements are used in a multiplexed analysis system or method that provides a nanoscale replacement for DNA-chip technology and can be used for the analysis of genetic variance, proteomics, and gene expression.

**[0476]** In another embodiment, one or more elements produce specific light emissions and or thermal energies caused by their coming into contact with a particular metabolic state, medical disorder, disease pathology, genotype, phenotype and or other specific stimuli. One or more entrapped agents carried by one or more elements are thereby selectively triggered and released. In doing so, they form a targeted agent delivery system without exposing the entire body--or an indiscriminate area--to a similar dose of light, thermal energy, and or agents. The agents may be delivered in vivo by means known in the art.

**[0477]** In one illustrative embodiment, photonic energies from one or more elements thermally operate on one or more other elements that may have one or more entrapped materials, such as, but not limited to, therapeutic, diagnostic, and or therapeutic agents within an aqueous interior, and or that may have one or more entrapped nanoparticles such as liposomes, micelles, proteins, other biological and or bioengineered elements, including organic, inorganic, and synthetic materials, and or that may have one or more hydrophobic materials bound to a lipid bilayer membrane. The well-known permeability increase at the phase transition temperature provides a means to trigger release of an entrapped agent, like, for example release of a therapeutic agent in locally heated tissues. In one embodiment, efficient in vivo or in vitro release of entrapped agents at non-targeted and or targeted sites are triggered by light emitted by one or more light sources when the one or more elements comprise a photoisomerisable species.

**[0478]** In another embodiment, the method of one or more LuxR proteins and lux bioluminescence genes and or other luminescent causing genes known in the art are utilized and are bioengineered and incorporated into one or more elements, ligands, targeting moieties, and or vectors, which may also be conjugated with one or more other elements, materials, and substances. In one embodiment, luminescent causing genes provide optical pumping sufficient to excite one or more quantum dots and or photonic dots.

**[0479]** In an illustrative embodiment, in vivo release from one or more cargo elements comprised of one or more entrapped liposomal and or non-liposomal-entrapped agents are optically triggered by photons emitted by light sources of one or more types. In one illustrative embodiment, one or more light sources produce specific light wavelength emissions caused by their coming into contact with, for example, a specific disease at in vivo target site and causes diagnostic, therapeutic, and or prosthetic agents comprised in a photosensitive invention delivery system to be triggered and released from one or more invention elements, thereby forming a highly targeted drug delivery system. For example, in one embodiment, one or more cargo elements comprise an amphipathic lipid, such as a phospholipid, having two chains derived from fatty acid that allow the lipid to pack into a bilayer structure. One or more photosensitizers may be incorporated into the entrapped materials' cavity and or membranes.

**[0480]** In one illustrative embodiment, a phospholipid (1,2-(4'-n-butylphenylazo-4''(-phenylbutyroyl))-glycero-3-phosphocholine ('Bis-Azo PC'), is substituted with azobenzene

moieties in both acyl chains that can be photoisomerised by a fast nanolaser pulse. One or more other photoisomerisable species can be used in other embodiments. Agent release from one or more cargo elements occurs on the milliseconds timescale and photosensitised cargo elements thereby serve as light sensitive elements to allow for the triggered release of agents from one or more invention elements. In one embodiment, cholesterol additives may be used. The addition of cholesterol may have a marked effect on kinetics of agent release from cargo elements, and in some circumstances can result in substantial enhancement of light sensitivity in one or more photosensitised elements comprising one or more invention elements. In another embodiment, thermal and photosensitive activation systems acting together comprise one or more elements.

**[0481]** The invention, in one embodiment, comprises an in vitro and or in vivo nanoscale, biomolecular electronics element and or nano-electronics element, i.e., bio-molecular devices, which may be employed in a scalable, intelligent, biomolecular electronics device platform and or a nano-electronics device platform. The platform may also be comprised of one or more non-invention elements and devices, such as crystals, conductors, insulators, semiconductors, MEMS, and circuits, but not limited to such. And further, the platform may also be coated in one or more surfactants and or cosurfactants and or metals, elements, materials and substances.

**[0482]** In one embodiment, one or more elements and or platforms are used for biomolecular electronic and or nano-electronic devices. Biological molecules, particularly proteins and lipids are used to perform the basic properties necessary for the functioning of biomolecular electronic devices. These biological materials conduct and transfer molecules from one location to another, are capable of major color changes on application of an electric field or light and can produce cascades that can be used for amplification of an optical or an electronic signal. All these properties can be applied to electronic switches, gates, storage devices, biosensors, biological transistors, to name just a few. In general, the electrical properties of bilayer lipid membranes are easily measurable for signal generation and transduction. In one embodiment, hybrid elements comprising cells with intact plasma membranes can be considered to act as tiny capacitors under the influence of an electric field. Whereas sufficiently high field strength may increase the membrane potential past a critical point leading to the breakdown of the membrane, experimental care must be taken. (Dielectric breakdown of biological membrane occurs at about 1 volt across the membrane.) On the other hand, the use of electrostatic potentials around the lipid molecules is very attractive, because they are controllable.

**[0483]** In one embodiment, one or more elements comprise nanoscale elements, components, devices, systems and or platforms, in one or more configurations, which form connectors for carrying information from a storage, processing or communications element or device to another, of one or more types.

**[0484]** In one embodiment, one or more elements comprise one or more information processing elements, components, devices, systems and or platforms such as, for example, but not limited to, encoders and decoders, memory, logic gates, registers, circuits, wiring and connectors, input and output elements, analog to digital and digital to analog converters and system architectures known in the art.

**[0485]** In one embodiment, one or more invention elements comprise nanoscale elements, components, devices, systems and or platforms that modify, process, manipulate, encode and decode, input, output, transmit, communicate, store and read various forms and types of information using a variety of suitable techniques known in the art, in vivo and in vitro.

**[0486]** A scalable information-processing invention platform may also include an encoder, e.g., a predetermined or specific DNA sequence that deliberately encodes at least a subset of the elements to take the form of specified sequence, as well as a decoder for reading information from at least a subset of the protein-based information processing elements. Examples of such a bio-system decoder are, but not limited to, a dye-based protein assay, a quantum dot-based assay, or other protein assay methods known in the art. Another example of encoders/decoders is the use of NMR and ESR and other methods known in the art that can effect and discern protein behaviors and their physical characteristics. Another example of encoders/decoders is the use of photons of different wavelengths and photo detectors.

**[0487]** In one embodiment, one or more elements comprise in vitro and or in vivo nanoscale information processing elements, components, devices, systems and or platform, which may follow and execute algorithms of one or more types expressed by or use biological control and regulate laws, processes, and or methods, and or geometrically derived algorithms such as graphs and Lie algebras, including Clifford algebras, but not limited to.

**[0488]** In another embodiment, one or more elements comprise a cognitive information processing element, device, and or platform of one or more types that follow and execute algorithms expressed by or use biological control and regulate laws and or processes, and or geometrically derived algorithms such as graphs and Lie algebras, including Clifford algebras, but not limited to.

**[0489]** In another embodiment, one or more elements comprise a hybrid digital and analog information processing element, device, and or platform of one or more types, wherein enlisting the rich repertoire of biochemical reactions and adopting a nested hierarchical organization makes intermixing of digital and analog processing possible in bio-computing applications.

**[0490]** In one embodiment, one or more elements comprise one or more nanoscale information processing elements, components, devices, systems and or platform that utilize photons emitted by invention light sources of one or more types as the basis of computation and or transmission and communication.

**[0491]** According to one illustrative embodiment, one or more elements comprise one or more nano-computer elements, components, devices, systems and or platforms of one or more types that are programmable, and or autonomous acting, and or do cognitive processing, which bio-nano-computers may also utilize self-replicating, self-adapting, self-repairing, self-regulating, and or self-regenerating methods, and which are used for applications at the cellular, molecular, and nanoscale level that may include, but are not limited to, biomedical imaging, sensors, diagnostic systems, assay systems, therapeutic systems, drug delivery systems, prosthetic systems, cybernetic systems, cellular-level nano-fabrication systems, and inter- and intra-cellular imaging, repair, and engineering systems, the monitoring, sensing, imaging, diagnosing, repairing, constructing, fabricating, and or control and regulating of organic and or inorganic elements, and

which bio-nano-computer elements and or platforms also may utilize and leverage biological control and regulate laws and or methods, and or geometrically derived algorithms such as graphs and Lie algebras, including Clifford algebras, but not limited to, in the performance of their tasks.

**[0492]** In one illustrative embodiment, one or more element chains are created via a molecular bridge group. To align the elements with respect to one another and also with respect to an external magnetic or electrical field. In one embodiment, one or more elements and or platforms and in one or more configurations are embedded in another material, like liquid crystal.

**[0493]** In one embodiment, one or more elements and or platforms and in one or more configurations are coated completely and or partially in a metal.

**[0494]** In another embodiment, one or more elements and or platforms and in one or more configurations are coated completely and or partially in reflective and or non-reflective coatings.

**[0495]** In one embodiment, one or more elements and or platforms and in one or more configurations are used to coat completely and or partially metals, crystals, insulators, conductors, semiconductor components, wires, and devices.

**[0496]** In another illustrative embodiment, one or more elements and or platforms and in one or more configurations facilitate the externally and or mechanistically directed alignment of, for example, but not limited to, biological elements, various other non-invention nanoparticles, carbon nanotubes, crystals, conductors, semiconductors, insulators, and or other devices, materials and substances, which aligned assemblies may further be coated in one or more surfactants and or metals, elements, materials and substances.

**[0497]** In one embodiment, one or more elements in one or more configurations include other types of nanoparticle elements such as, but not limited to, polymer-based, polybutylcyanoacrylate-based, and cetyl alcohol-based nanoparticles, empty cage Fullerenes, endohedral Fullerenes, carbon nanotubes, cells, liposomes, capsids, dendrimers, micelles, and the like.

**[0498]** In another illustrative embodiment, one or more elements and or platforms of one or more types in whole or in part enable a shape programmable and or scaffolding system to which one or elements of one or more types, including natural and or non-invention elements are affixed and or further form more one or more structures of one more types

**[0499]** In one embodiment, one or more elements and or platforms in one or more configurations form and or include optical elements such as, but not limited to, optics; optoelectronic elements; photoelectric elements; photodetectors; and photosensitive elements, which optical elements may also be coated or treated in whole or in part with materials that affect their optical properties.

**[0500]** In one embodiment, one or more elements and or platforms and in one or more configurations form and or include imaging elements and sensors, such as, but not limited to, CCDs and CMOS optical elements.

**[0501]** In one embodiment, one or more elements and or platforms, in one or more configurations include and or comprise photonic to electrical energy conversion elements.

**[0502]** In one embodiment, one or more elements and or platforms form one or more electronic circuits, which circuit may also be comprised of one or more other elements such as empty Fullerenes, endohedral Fullerenes, nanotubes, crystals, insulators, conductors, semiconductors, and or other

materials, substances and devices, which circuits also may be coated in one or more surfactants and or cosurfactants and or other materials and substances.

**[0503]** In one embodiment, one or more elements and or platforms are switched on or off and or change states by applying an electric field, and may also comprise one or more transistors or devices in another embodiment.

**[0504]** In another embodiment, one or more elements and or platforms and in one or more configurations; self-assemble, and or are shape-programmed, and or use biological control and regulate laws, processes and methods, and or use geometrically derived algorithms such as graphs and Lie algebras, including Clifford algebras, but not limited to, and or are mechanically assembled via lithography, and or utilize other externally directed techniques and methods known the art, and or some combination thereof; form natural positions that are associated with electronic circuits and or information processing devices, such as atomic and molecular scale device design, their interconnection, nanofabrication and circuit architectures.

**[0505]** According to one illustrative embodiment, one or more elements and or platforms comprise one or more crystal structures and elements, of one or more types.

**[0506]** According to one illustrative embodiment, one or more elements and or platforms comprise one or more desiccated elements, of one or more types.

**[0507]** According to one illustrative embodiment, one or more invention comprise one or more hydrated and or rehydrated elements and or platforms, of one or more types.

**[0508]** According to one illustrative embodiment, one or more elements and or platforms comprise one or more rehydration elements and or platforms, of one or more types.

**[0509]** According to one illustrative embodiment, one or more elements and or platforms are embedded and or incorporated into one or more materials, substances, devices, agents, devices, systems, organisms, and or mechanisms of one or more types.

**[0510]** In another illustrative embodiment, one or more elements and or platforms comprise one or more magnetic nanoparticles of one or more types.

**[0511]** In one embodiment, one or more elements and or platforms are nanoscale recording memory media or components, which may incorporate metals, ferromagnetic materials, and or ferroelectric materials and elements, and or may form into magnetic rings, and or may form vertically polarized magnetic domains and or form magnetic domains on isolated islands of one or more types.

**[0512]** In one embodiment, one or more elements and or platforms are nanoscale photovoltaic cells or components of one or more types.

**[0513]** In one embodiment, one or more elements are nanoscale batteries or components of one or more type for storing electronic charge.

**[0514]** In one embodiment, one or more elements and or platforms comprise a nanoscale environmental hazard-screening device, and or comprise an in situ remediation, removal and or sequestration component or system of one or more types.

**[0515]** In one embodiment, one or more elements and or platforms comprise an opto-electronic device, system or component of one or more types.

**[0516]** In one illustrative embodiment, embodiment, one or more elements comprise one or more nanoscale passive and or active linear or nonlinear optic components, and or particle

detectors, and or other elements sufficient to implement in vivo or in vitro optical system arrays and methods.

**[0517]** In another embodiment, one or more elements comprise in vivo or in vitro detection, diagnostic and tracking agents for chemical, biological, and or nuclear elements and activities, but not limited to such.

**[0518]** In one embodiment, one or more elements and or platforms comprise a spin-based electronics element or system of one or more types.

**[0519]** In one embodiment, one or more elements and or platforms exploit the Coulomb blockade-like properties of self-assembled proteins, wherein a single particle at a time may move through a transmembrane protein-based channel.

**[0520]** In one embodiment, one or more elements and or platforms utilize and or exploit the Casimir effect, which is a small attractive force that acts between two closely parallel, uncharged conducting elements. It is due to quantum vacuum fluctuations of the electromagnetic field.

**[0521]** In some illustrative embodiments, one or more elements and or platforms and in one or more configurations are physically linked via molecular addends of one or more types, but are not limited to such addend types.

**[0522]** In other illustrative configurations, one or more elements and or platforms are functionally linked via photonic, chemical, electromagnetic, electrical and/or quantum (non-classical) interactions of one or more types, including the Internet, to work and cooperate locally and/or remotely.

**[0523]** One or more elements and or platforms of one or more types may be encapsulated, packaged, stored, incorporated, and or utilize one or more methods known in the art, including for example, but not limited to: catheters; injections, including intramuscular injections; syringes; droppers and bulbs; pills; intravenous means; oral means; anal means; capsules; nanocapsules; nanoparticles; nano-devices; prescriptions; hospital and medical supplies; dental supplies; non-prescriptions; medications; over the counter products and remedies; alternative medicine supplies, systems, products and devices; hair care products; splints, casts, walkers, crutches, canes, wheelchairs, and other ambulatory aids; natural foods; vitamin and mineral supplements; first aid products; emergency health care procedures, systems, devices, and products, including combat medicine; health care products; grafts; skin patches; bandages; adhesives; wraps; masks; markers; powders; granules; geriatric care products; pediatric care products; diagnostic devices, systems, and products; medical imaging devices, systems, and products; telemedicine devices, systems, and products; in vivo monitoring systems, products, systems, and devices; in vitro monitoring systems, products, systems, and devices; laundry products; chemical, nuclear and biological sensors;

sensors; bio-sensors; environmental sensors; combat systems, clothing, uniforms, and protective gear; food preparation products; food testing and safety devices, systems, and products; food storage wraps, systems, devices, and products; water treatment devices, systems and products; waste storage, management, and treatment systems and products; sewerage systems and products; plumbing systems and products; bed and bath products; animal care and veterinary products; animal feed; animal slaughter systems and products; cooking products; cookware; forensic devices, systems and products; home and office cleaning products; home products; office products; personal products; industrial products; home and office care products; paper products; personal hygiene products; sexual hygiene and safety products; sexual reproduction devices, systems, and products; sexual arousal products and devices; dental and dental care products; oral hygiene products, devices, and systems; robotic products, systems and devices; cybernetic devices; jewelry; novelties; solvents; agro-products; plants; animals; vehicles; biologicals; chemicals; cells; tissue; organs; proteins; liposomes; phages; micelles; peptides; antibodies; monoclonal antibodies; DNA; RNA; IRNA; siRNA; RISC; cloning; human contact; micro-electromechanical systems (MEMS) and other types of nano-systems; food utensils; tools; appliances; consumer electronics; paints and finishes; heating, ventilation and air conditioning systems; construction, building, home and office materials; water; milk; food and other edible or chewable substances and items; prostheses; food and drink additives and supplements; drinks; beverages; soaps; creams; ointments; salves; topical agents; cosmetics; beautifying agents; liquids; fluids; oils; gels; adhesives; aerosols; vapors; airborne methods; pumps; fragrances and perfumes; textiles; sporting and athletic goods and devices; physical work out and training systems, devices, and products; sports medicine systems, devices, and products; recreational products and gear; shoes, clothing, and apparel; eyewear; sprays; dyes; biological elements; organ; implants; stents; prosthetic devices; artificial skin, blood, limbs, joints, bones, cells, eyes, organs, and other artificial body parts and biological elements; subcutaneous means; incisions; surgical means; and in-patient and out-patient medical procedures.

**[0524]** The above-described embodiments have been set forth to describe more completely and concretely the present invention, and are not to be construed as limiting the invention. It is further intended that all matter and the description and drawings be interpreted as illustrative and not in a limiting sense. That is, while various embodiments of the invention have been described in detail, other alterations, which will be apparent to those skilled in the prior art, are intended to be embraced within the spirit and scope of the invention.

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<308> DATABASE ACCESSION NUMBER: UniProtKB/Q00610

<309> DATABASE ENTRY DATE: 2009-05-26

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	370					375					380				
Ala	Ser	Ala	Pro	Lys	Gly	Ile	Leu	Arg	Thr	Arg	Glu	Thr	Val	Gln	Lys
385					390					395				400	
Phe	Gln	Ser	Ile	Pro	Ala	Gln	Ser	Gly	Gln	Ala	Ser	Pro	Leu	Leu	Gln
				405					410					415	
Tyr	Phe	Gly	Ile	Leu	Leu	Asp	Gln	Gly	Gln	Leu	Asn	Lys	Leu	Glu	Ser
			420					425					430		
Leu	Glu	Leu	Cys	His	Leu	Val	Leu	Gln	Gln	Gly	Arg	Lys	Gln	Leu	Leu
	435						440					445			
Glu	Lys	Trp	Leu	Lys	Glu	Asp	Lys	Leu	Glu	Cys	Ser	Glu	Glu	Leu	Gly
	450					455					460				
Asp	Leu	Val	Lys	Thr	Thr	Asp	Pro	Met	Leu	Ala	Leu	Ser	Val	Tyr	Leu
465					470					475				480	
Arg	Ala	Asn	Val	Pro	Ser	Lys	Val	Ile	Gln	Cys	Phe	Ala	Glu	Thr	Gly
				485					490					495	
Gln	Phe	Gln	Lys	Ile	Val	Leu	Tyr	Ala	Lys	Lys	Val	Gly	Tyr	Thr	Pro
			500					505					510		
Asp	Trp	Ile	Phe	Leu	Leu	Arg	Gly	Val	Met	Lys	Ile	Ser	Pro	Glu	Gln
	515						520					525			
Gly	Leu	Gln	Phe	Ser	Arg	Met	Leu	Val	Gln	Asp	Glu	Glu	Pro	Leu	Ala
	530					535					540				
Asn	Ile	Ser	Gln	Ile	Val	Asp	Ile	Phe	Met	Glu	Asn	Ser	Leu	Ile	Gln
545					550					555				560	
Gln	Cys	Thr	Ser	Phe	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Asn	Arg	Pro	Ala
				565					570					575	
Glu	Gly	Leu	Leu	Gln	Thr	Trp	Leu	Leu	Glu	Met	Asn	Leu	Val	His	Ala
			580					585					590		
Pro	Gln	Val	Ala	Asp	Ala	Ile	Leu	Gly	Asn	Lys	Met	Phe	Thr	His	Tyr
		595					600					605			
Asp	Arg	Ala	His	Ile	Ala	Gln	Leu	Cys	Glu	Lys	Ala	Gly	Leu	Leu	Gln
	610					615					620				
Gln	Ala	Leu	Glu	His	Tyr	Thr	Asp	Leu	Tyr	Asp	Ile	Lys	Arg	Ala	Val
625					630					635				640	

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Val His Thr His Leu Leu Asn Pro Glu Trp Leu Val Asn Phe Phe Gly  
 645 650 655

Ser Leu Ser Val Glu Asp Ser Val Glu Cys Leu His Ala Met Leu Ser  
 660 665 670

Ala Asn Ile Arg Gln Asn Leu Gln Leu Cys Val Gln Val Ala Ser Lys  
 675 680 685

Tyr His Glu Gln Leu Gly Thr Gln Ala Leu Val Glu Leu Phe Glu Ser  
 690 695 700

Phe Lys Ser Tyr Lys Gly Leu Phe Tyr Phe Leu Gly Ser Ile Val Asn  
 705 710 715 720

Phe Ser Gln Asp Pro Asp Val His Leu Lys Tyr Ile Gln Ala Ala Cys  
 725 730 735

Lys Thr Gly Gln Ile Lys Glu Val Glu Arg Ile Cys Arg Glu Ser Ser  
 740 745 750

Cys Tyr Asn Pro Glu Arg Val Lys Asn Phe Leu Lys Glu Ala Lys Leu  
 755 760 765

Thr Asp Gln Leu Pro Leu Ile Ile Val Cys Asp Arg Phe Gly Phe Val  
 770 775 780

His Asp Leu Val Leu Tyr Leu Tyr Arg Asn Asn Leu Gln Arg Tyr Ile  
 785 790 795 800

Glu Ile Tyr Val Gln Lys Val Asn Pro Ser Arg Thr Pro Ala Val Ile  
 805 810 815

Gly Gly Leu Leu Asp Val Asp Cys Ser Glu Glu Val Ile Lys His Leu  
 820 825 830

Ile Met Ala Val Arg Gly Gln Phe Ser Thr Asp Glu Leu Val Ala Glu  
 835 840 845

Val Glu Lys Arg Asn Arg Leu Lys Leu Leu Leu Pro Trp Leu Glu Ser  
 850 855 860

Gln Ile Gln Glu Gly Cys Glu Glu Pro Ala Thr His Asn Ala Leu Ala  
 865 870 875 880

Lys Ile Tyr Ile Asp Ser Asn Asn Ser Pro Glu Cys Phe Leu Arg Glu  
 885 890 895

Asn Ala Tyr Tyr Asp Ser Ser Val Val Gly Arg Tyr Cys Glu Lys Arg  
 900 905 910

Asp Pro His Leu Ala Cys Val Ala Tyr Glu Arg Gly Gln Cys Asp Leu  
 915 920 925

Glu Leu Ile Lys Val Cys Asn Glu Asn Ser Leu Phe Lys Ser Glu Ala  
 930 935 940

Arg Tyr Leu Val Cys Arg Lys Asp Pro Glu Leu Trp Ala His Val Leu  
 945 950 955 960

Glu Glu Thr Asn Pro Ser Arg Arg Gln Leu Ile Asp Gln Val Val Gln  
 965 970 975

Thr Ala Leu Ser Glu Thr Arg Asp Pro Glu Glu Ile Ser Val Thr Val  
 980 985 990

Lys Ala Phe Met Thr Ala Asp Leu Pro Asn Glu Leu Ile Glu Leu Leu  
 995 1000 1005

Glu Lys Ile Val Leu Asp Asn Ser Val Phe Ser Glu His Arg Asn  
 1010 1015 1020

Leu Gln Asn Leu Leu Ile Leu Thr Ala Ile Lys Ala Asp Arg Thr  
 1025 1030 1035

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

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1415	1420	1425
Arg Leu Asp His Thr Trp Thr Val Ser Phe Phe Ser Lys Ala Gly		
1430	1435	1440
Gln Leu Pro Leu Val Lys Pro Tyr Leu Arg Ser Val Gln Ser His		
1445	1450	1455
Asn Asn Lys Ser Val Asn Glu Ala Leu Asn His Leu Leu Thr Glu		
1460	1465	1470
Glu Glu Asp Tyr Gln Gly Leu Arg Ala Ser Ile Asp Ala Tyr Asp		
1475	1480	1485
Asn Phe Asp Asn Ile Ser Leu Ala Gln Gln Leu Glu Lys His Gln		
1490	1495	1500
Leu Met Glu Phe Arg Cys Ile Ala Ala Tyr Leu Tyr Lys Gly Asn		
1505	1510	1515
Asn Trp Trp Ala Gln Ser Val Glu Leu Cys Lys Lys Asp His Leu		
1520	1525	1530
Tyr Lys Asp Ala Met Gln His Ala Ala Glu Ser Arg Asp Ala Glu		
1535	1540	1545
Leu Ala Gln Lys Leu Leu Gln Trp Phe Leu Glu Glu Gly Lys Arg		
1550	1555	1560
Glu Cys Phe Ala Ala Cys Leu Phe Thr Cys Tyr Asp Leu Leu Arg		
1565	1570	1575
Pro Asp Met Val Leu Glu Leu Ala Trp Arg His Asn Leu Val Asp		
1580	1585	1590
Leu Ala Met Pro Tyr Phe Ile Gln Val Met Arg Glu Tyr Leu Ser		
1595	1600	1605
Lys Val Asp Lys Leu Asp Ala Leu Glu Ser Leu Arg Lys Gln Glu		
1610	1615	1620
Glu His Val Thr Glu Pro Ala Pro Leu Val Phe Asp Phe Asp Gly		
1625	1630	1635
His Glu		
1640		

<210> SEQ ID NO 3  
 <211> LENGTH: 1583  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <300> PUBLICATION INFORMATION:  
 <308> DATABASE ACCESSION NUMBER: NCBI/EAX03047  
 <309> DATABASE ENTRY DATE: 2006-12-18  
 <313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(1583)

<400> SEQUENCE: 3

Met Ala Gln Ile Leu Pro Val Arg Phe Gln Glu His Phe Gln Leu Gln		
1	5	10 15
Asn Leu Gly Ile Asn Pro Ala Asn Ile Gly Phe Ser Thr Leu Thr Met		
	20	25 30
Glu Ser Asp Lys Phe Ile Cys Ile Arg Glu Lys Val Gly Glu Gln Ala		
	35	40 45
Gln Val Thr Ile Ile Asp Met Ser Asp Pro Met Ala Pro Ile Arg Arg		
	50	55 60
Pro Ile Ser Ala Glu Ser Ala Ile Met Asn Pro Ala Ser Lys Val Ile		
	65	70 75 80
Ala Leu Lys Ala Gly Lys Thr Leu Gln Ile Phe Asn Ile Glu Met Lys		
	85	90 95

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Ser Lys Met Lys Ala His Thr Met Ala Glu Glu Val Ile Phe Trp Lys  
 100 105 110

Trp Val Ser Val Asn Thr Val Ala Leu Val Thr Glu Thr Ala Val Tyr  
 115 120 125

His Trp Ser Met Glu Gly Asp Ser Gln Pro Met Lys Met Phe Asp Arg  
 130 135 140

His Thr Ser Leu Val Gly Cys Gln Val Ile His Tyr Arg Thr Asp Glu  
 145 150 155 160

Tyr Gln Lys Trp Leu Leu Leu Val Gly Ile Ser Ala Gln Gln Asn Arg  
 165 170 175

Val Val Gly Ala Met Gln Leu Tyr Ser Val Asp Arg Lys Val Ser Gln  
 180 185 190

Pro Ile Glu Gly His Ala Ala Ala Phe Ala Glu Phe Lys Met Glu Gly  
 195 200 205

Asn Ala Lys Pro Ala Thr Leu Phe Cys Phe Ala Val Arg Asn Pro Thr  
 210 215 220

Gly Gly Lys Leu His Ile Ile Glu Val Gly Gln Pro Ala Ala Gly Asn  
 225 230 235 240

Gln Pro Phe Val Lys Lys Ala Val Asp Val Phe Phe Pro Pro Glu Ala  
 245 250 255

Gln Asn Asp Phe Pro Val Ala Met Gln Ile Gly Ala Lys His Gly Val  
 260 265 270

Ile Tyr Leu Ile Thr Lys Tyr Gly Tyr Leu His Leu Tyr Asp Leu Glu  
 275 280 285

Ser Gly Val Cys Ile Cys Met Asn Arg Ile Ser Ala Asp Thr Ile Phe  
 290 295 300

Val Thr Ala Pro His Lys Pro Thr Ser Gly Ile Ile Gly Val Asn Lys  
 305 310 315 320

Lys Gly Gln Val Leu Ser Val Cys Val Glu Glu Asp Asn Ile Val Asn  
 325 330 335

Tyr Ala Thr Asn Val Leu Gln Asn Pro Asp Leu Gly Leu Arg Leu Ala  
 340 345 350

Val Arg Ser Asn Leu Ala Gly Ala Glu Lys Leu Phe Val Arg Lys Phe  
 355 360 365

Asn Thr Leu Phe Ala Gln Gly Ser Tyr Ala Glu Ala Ala Lys Val Ala  
 370 375 380

Ala Ser Ala Pro Lys Gly Ile Leu Arg Thr Arg Glu Thr Val Gln Lys  
 385 390 395 400

Phe Gln Ser Ile Pro Ala Gln Ser Gly Gln Ala Ser Pro Leu Leu Gln  
 405 410 415

Tyr Phe Gly Ile Leu Leu Asp Gln Gly Gln Leu Asn Lys Leu Glu Ser  
 420 425 430

Leu Glu Leu Cys His Leu Val Leu Gln Gln Gly Arg Lys Gln Leu Leu  
 435 440 445

Glu Lys Trp Leu Lys Glu Asp Lys Leu Glu Cys Ser Glu Glu Leu Gly  
 450 455 460

Asp Leu Val Lys Thr Thr Asp Pro Met Leu Ala Leu Ser Val Tyr Leu  
 465 470 475 480

Arg Ala Asn Val Pro Ser Lys Val Ile Gln Cys Phe Ala Glu Thr Gly  
 485 490 495



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Gln	Phe	Gln	Lys	Ile	Val	Leu	Tyr	Ala	Lys	Lys	Val	Gly	Tyr	Thr	Pro
			500					505					510		
Asp	Trp	Ile	Phe	Leu	Leu	Arg	Gly	Val	Met	Lys	Ile	Ser	Pro	Glu	Gln
		515					520					525			
Gly	Leu	Gln	Phe	Ser	Arg	Met	Leu	Val	Gln	Asp	Glu	Glu	Pro	Leu	Ala
	530					535					540				
Asn	Ile	Ser	Gln	Ile	Val	Asp	Ile	Phe	Met	Glu	Asn	Ser	Leu	Ile	Gln
545					550					555					560
Gln	Cys	Thr	Ser	Phe	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Asn	Arg	Pro	Ala
				565					570					575	
Glu	Gly	Leu	Leu	Gln	Thr	Trp	Leu	Leu	Glu	Met	Asn	Leu	Val	His	Ala
				580					585				590		
Pro	Gln	Val	Ala	Asp	Ala	Ile	Leu	Gly	Asn	Lys	Met	Phe	Thr	His	Tyr
		595					600						605		
Asp	Arg	Ala	His	Ile	Ala	Gln	Leu	Cys	Glu	Lys	Ala	Gly	Leu	Leu	Gln
	610					615					620				
Gln	Ala	Leu	Glu	His	Tyr	Thr	Asp	Leu	Tyr	Asp	Ile	Lys	Arg	Ala	Val
625					630					635					640
Val	His	Thr	His	Leu	Leu	Asn	Pro	Glu	Trp	Leu	Val	Asn	Phe	Phe	Gly
				645					650					655	
Ser	Leu	Ser	Val	Glu	Asp	Ser	Val	Glu	Cys	Leu	His	Ala	Met	Leu	Ser
			660					665					670		
Ala	Asn	Ile	Arg	Gln	Asn	Leu	Gln	Leu	Cys	Val	Gln	Val	Ala	Ser	Lys
		675					680					685			
Tyr	His	Glu	Gln	Leu	Gly	Thr	Gln	Ala	Leu	Val	Glu	Leu	Phe	Glu	Ser
	690					695					700				
Phe	Lys	Ser	Tyr	Lys	Gly	Leu	Phe	Tyr	Phe	Leu	Gly	Ser	Ile	Val	Asn
705					710					715					720
Phe	Ser	Gln	Asp	Pro	Asp	Val	His	Leu	Lys	Tyr	Ile	Gln	Ala	Ala	Cys
				725					730					735	
Lys	Thr	Gly	Gln	Ile	Lys	Glu	Val	Glu	Arg	Ile	Cys	Arg	Glu	Ser	Ser
			740					745					750		
Cys	Tyr	Asn	Pro	Glu	Arg	Val	Lys	Asn	Phe	Leu	Lys	Glu	Ala	Lys	Leu
		755					760					765			
Thr	Asp	Gln	Leu	Pro	Leu	Ile	Ile	Val	Cys	Asp	Arg	Phe	Gly	Phe	Val
	770					775					780				
His	Asp	Leu	Val	Leu	Tyr	Leu	Tyr	Arg	Asn	Asn	Leu	Gln	Arg	Tyr	Ile
785					790					795					800
Glu	Ile	Tyr	Val	Gln	Lys	Val	Asn	Pro	Ser	Arg	Thr	Pro	Ala	Val	Ile
				805					810					815	
Gly	Gly	Leu	Leu	Asp	Val	Asp	Cys	Ser	Glu	Glu	Val	Ile	Lys	His	Leu
			820					825					830		
Ile	Met	Ala	Val	Arg	Gly	Gln	Phe	Ser	Thr	Asp	Glu	Leu	Val	Ala	Glu
		835					840						845		
Val	Glu	Lys	Arg	Asn	Arg	Leu	Lys	Leu	Leu	Leu	Pro	Trp	Leu	Glu	Ser
		850				855					860				
Gln	Ile	Gln	Glu	Gly	Cys	Glu	Glu	Pro	Ala	Thr	His	Asn	Ala	Leu	Ala
865					870					875					880
Lys	Ile	Tyr	Ile	Asp	Ser	Asn	Asn	Ser	Pro	Glu	Cys	Phe	Leu	Arg	Glu
				885					890					895	
Asn	Ala	Tyr	Tyr	Asp	Ser	Ser	Val	Val	Gly	Arg	Tyr	Cys	Glu	Lys	Arg

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900	905	910
Asp Pro His Leu Ala Cys Val Ala Tyr Glu Arg Gly Gln Cys Asp Leu 915 920 925		
Glu Leu Ile Lys Val Cys Asn Glu Asn Ser Leu Phe Lys Ser Glu Ala 930 935 940		
Arg Tyr Leu Val Cys Arg Lys Asp Pro Glu Leu Trp Ala His Val Leu 945 950 955 960		
Glu Glu Thr Asn Pro Ser Arg Arg Gln Leu Ile Asp Gln Val Val Gln 965 970 975		
Thr Ala Leu Ser Glu Thr Arg Asp Pro Glu Glu Ile Ser Val Thr Val 980 985 990		
Lys Ala Phe Met Thr Ala Asp Leu Pro Asn Glu Leu Ile Glu Leu Leu 995 1000 1005		
Glu Lys Ile Val Leu Asp Asn Ser Val Phe Ser Glu His Arg Asn 1010 1015 1020		
Leu Gln Asn Leu Leu Ile Leu Thr Ala Ile Lys Ala Asp Arg Thr 1025 1030 1035		
Arg Val Met Glu Tyr Ile Ser Arg Leu Asp Asn Tyr Asp Ala Leu 1040 1045 1050		
Asp Ile Ala Ser Ile Ala Val Ser Ser Ala Leu Tyr Glu Glu Ala 1055 1060 1065		
Phe Thr Val Phe His Lys Phe Asp Met Asn Ala Ser Ala Ile Gln 1070 1075 1080		
Val Leu Ile Glu His Ile Gly Asn Leu Asp Arg Ala Tyr Glu Phe 1085 1090 1095		
Ala Glu Arg Cys Asn Glu Pro Ala Val Trp Ser Gln Leu Ala Gln 1100 1105 1110		
Ala Gln Leu Gln Lys Asp Leu Val Lys Glu Ala Ile Asn Ser Tyr 1115 1120 1125		
Ile Arg Gly Asp Asp Pro Ser Ser Tyr Leu Glu Val Val Gln Ser 1130 1135 1140		
Ala Ser Arg Ser Asn Asn Trp Glu Asp Leu Val Lys Phe Leu Gln 1145 1150 1155		
Met Ala Arg Lys Lys Gly Arg Glu Ser Tyr Ile Glu Thr Glu Leu 1160 1165 1170		
Ile Phe Ala Leu Ala Lys Thr Ser Arg Val Ser Glu Leu Glu Asp 1175 1180 1185		
Phe Ile Asn Gly Pro Asn Asn Ala His Ile Gln Gln Val Gly Asp 1190 1195 1200		
Arg Cys Tyr Glu Glu Gly Met Tyr Glu Ala Ala Lys Leu Leu Tyr 1205 1210 1215		
Ser Asn Val Ser Asn Phe Ala Arg Leu Ala Ser Thr Leu Val His 1220 1225 1230		
Leu Gly Glu Tyr Gln Ala Ala Val Asp Asn Ser Arg Lys Ala Ser 1235 1240 1245		
Ser Thr Arg Thr Trp Lys Glu Val Cys Phe Ala Cys Met Asp Gly 1250 1255 1260		
Gln Glu Phe Arg Phe Ala Gln Leu Cys Gly Leu His Ile Val Ile 1265 1270 1275		
His Ala Asp Glu Leu Glu Glu Leu Met Cys Tyr Tyr Gln Asp Arg 1280 1285 1290		

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Gly Tyr Phe Glu Glu Leu Ile Leu Leu Leu Glu Ala Ala Leu Gly  
 1295 1300 1305  
 Leu Glu Arg Ala His Met Gly Met Phe Thr Glu Leu Ala Ile Leu  
 1310 1315 1320  
 Tyr Ser Lys Phe Lys Pro Gln Lys Met Leu Glu His Leu Glu Leu  
 1325 1330 1335  
 Phe Trp Ser Arg Val Asn Ile Pro Lys Val Leu Arg Ala Ala Glu  
 1340 1345 1350  
 Gln Ala His Leu Trp Ala Glu Leu Val Phe Leu Tyr Asp Lys Tyr  
 1355 1360 1365  
 Glu Glu Tyr Asp Asn Ala Val Leu Thr Met Met Ser His Pro Thr  
 1370 1375 1380  
 Glu Ala Trp Lys Glu Gly Gln Phe Lys Asp Ile Ile Thr Lys Val  
 1385 1390 1395  
 Ala Asn Val Glu Leu Cys Tyr Arg Ala Leu Gln Phe Tyr Leu Asp  
 1400 1405 1410  
 Tyr Lys Pro Leu Leu Ile Asn Asp Leu Leu Leu Val Leu Ser Pro  
 1415 1420 1425  
 Arg Leu Asp His Thr Trp Thr Val Ser Phe Phe Ser Lys Ala Gly  
 1430 1435 1440  
 Gln Leu Pro Leu Val Lys Pro Tyr Leu Arg Ser Val Gln Ser His  
 1445 1450 1455  
 Asn Asn Lys Ser Val Asn Glu Ala Leu Asn His Leu Leu Thr Glu  
 1460 1465 1470  
 Glu Glu Asp Tyr Gln Asp Ala Met Gln His Ala Ala Glu Ser Arg  
 1475 1480 1485  
 Asp Ala Glu Leu Ala Gln Lys Leu Leu Gln Trp Phe Leu Glu Glu  
 1490 1495 1500  
 Gly Lys Arg Glu Cys Phe Ala Ala Cys Leu Phe Thr Cys Tyr Asp  
 1505 1510 1515  
 Leu Leu Arg Pro Asp Met Val Leu Glu Leu Ala Trp Arg His Asn  
 1520 1525 1530  
 Leu Val Asp Leu Ala Met Pro Tyr Phe Ile Gln Val Met Arg Glu  
 1535 1540 1545  
 Tyr Leu Ser Lys Val Asp Lys Leu Asp Ala Leu Glu Ser Leu Arg  
 1550 1555 1560  
 Lys Gln Glu Glu His Val Thr Glu Pro Ala Pro Leu Val Phe Asp  
 1565 1570 1575  
 Phe Asp Gly His Glu  
 1580

<210> SEQ ID NO 4  
 <211> LENGTH: 1685  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <300> PUBLICATION INFORMATION:  
 <308> DATABASE ACCESSION NUMBER: NCBI/BAA04801  
 <309> DATABASE ENTRY DATE: 2004-01-10  
 <313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(1685)

<400> SEQUENCE: 4

Gln Glu Glu Thr Ile Thr Pro Asp Ser Ala Met Ala Gln Ile Leu Pro  
 1 5 10 15

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Ile	Arg	Phe	Gln	Glu	His	Leu	Gln	Leu	Gln	Asn	Leu	Gly	Ile	Asn	Pro
			20					25					30		
Ala	Asn	Ile	Gly	Phe	Ser	Thr	Leu	Thr	Met	Glu	Ser	Asp	Lys	Phe	Ile
		35					40					45			
Cys	Ile	Arg	Glu	Lys	Val	Gly	Glu	Gln	Ala	Gln	Val	Val	Ile	Ile	Asp
	50					55					60				
Met	Asn	Asp	Pro	Ser	Asn	Pro	Ile	Arg	Arg	Pro	Ile	Ser	Ala	Asp	Ser
	65				70					75					80
Ala	Ile	Met	Asn	Pro	Ala	Ser	Lys	Val	Ile	Ala	Leu	Lys	Ala	Gly	Lys
			85						90					95	
Thr	Leu	Gln	Ile	Phe	Asn	Ile	Glu	Met	Lys	Ser	Lys	Met	Lys	Ala	His
		100						105						110	
Thr	Met	Thr	Asp	Asp	Val	Thr	Phe	Trp	Lys	Trp	Ile	Ser	Leu	Asn	Thr
		115					120						125		
Val	Ala	Leu	Val	Thr	Asp	Asn	Ala	Val	Tyr	His	Trp	Ser	Met	Glu	Gly
	130					135					140				
Glu	Ser	Gln	Pro	Val	Lys	Met	Phe	Asp	Arg	His	Ser	Ser	Leu	Ala	Gly
	145				150					155					160
Cys	Gln	Ile	Ile	Asn	Tyr	Arg	Thr	Asp	Ala	Lys	Gln	Lys	Trp	Leu	Leu
				165					170					175	
Leu	Thr	Gly	Ile	Ser	Ala	Gln	Gln	Asn	Arg	Val	Val	Gly	Ala	Met	Gln
		180						185					190		
Leu	Tyr	Ser	Val	Asp	Arg	Lys	Val	Ser	Gln	Pro	Ile	Glu	Gly	His	Ala
	195						200					205			
Ala	Ser	Phe	Ala	Gln	Phe	Lys	Met	Glu	Gly	Asn	Ala	Glu	Glu	Ser	Thr
	210					215					220				
Leu	Phe	Cys	Phe	Ala	Val	Arg	Gly	Gln	Ala	Gly	Gly	Lys	Leu	His	Ile
	225				230					235					240
Ile	Glu	Val	Gly	Thr	Pro	Pro	Thr	Gly	Asn	Gln	Pro	Phe	Pro	Lys	Lys
				245					250					255	
Ala	Val	Asp	Val	Phe	Phe	Pro	Pro	Glu	Ala	Gln	Asn	Asp	Phe	Pro	Val
			260					265					270		
Ala	Met	Gln	Ile	Ser	Glu	Lys	His	Asp	Val	Val	Phe	Leu	Ile	Thr	Lys
		275					280					285			
Tyr	Gly	Tyr	Ile	His	Leu	Tyr	Asp	Leu	Glu	Thr	Gly	Thr	Cys	Ile	Tyr
	290					295					300				
Met	Asn	Arg	Ile	Ser	Gly	Glu	Thr	Ile	Phe	Val	Thr	Ala	Pro	His	Glu
	305				310					315					320
Ala	Thr	Ala	Gly	Ile	Ile	Gly	Val	Asn	Arg	Lys	Gly	Gln	Val	Leu	Ser
				325					330					335	
Val	Cys	Val	Glu	Glu	Glu	Asn	Ile	Ile	Pro	Tyr	Ile	Thr	Asn	Val	Leu
			340					345					350		
Gln	Asn	Pro	Asp	Leu	Ala	Leu	Arg	Met	Ala	Val	Arg	Asn	Asn	Leu	Ala
		355					360					365			
Gly	Ala	Glu	Glu	Leu	Phe	Ala	Arg	Lys	Phe	Asn	Ala	Leu	Phe	Ala	Gln
				370		375					380				
Gly	Asn	Tyr	Ser	Glu	Ala	Ala	Lys	Val	Ala	Ala	Asn	Ala	Pro	Lys	Gly
	385				390					395					400
Ile	Leu	Arg	Thr	Pro	Asp	Thr	Ile	Arg	Arg	Phe	Gln	Ser	Val	Pro	Ala
				405					410					415	
Gln	Pro	Gly	Gln	Thr	Ser	Pro	Leu	Leu	Gln	Tyr	Phe	Gly	Ile	Leu	Leu

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420					425					430					
Asp	Gln	Gly	Gln	Leu	Asn	Lys	Tyr	Glu	Ser	Leu	Glu	Leu	Cys	Arg	Pro
		435					440					445			
Val	Leu	Gln	Gln	Gly	Arg	Lys	Gln	Leu	Leu	Glu	Lys	Trp	Leu	Lys	Glu
		450					455					460			
Asp	Lys	Leu	Glu	Cys	Ser	Glu	Glu	Leu	Gly	Asp	Leu	Val	Lys	Ser	Val
		465					470					475			480
Asp	Pro	Thr	Leu	Ala	Leu	Ser	Val	Tyr	Leu	Arg	Ala	Asn	Val	Pro	Asn
				485					490					495	
Lys	Val	Ile	Gln	Cys	Phe	Ala	Glu	Thr	Gly	Gln	Val	Gln	Lys	Ile	Val
			500					505					510		
Leu	Tyr	Ala	Lys	Lys	Val	Gly	Tyr	Thr	Pro	Asp	Trp	Ile	Phe	Leu	Leu
		515					520					525			
Arg	Asn	Val	Met	Arg	Ile	Ser	Pro	Asp	Gln	Gly	Gln	Gln	Phe	Ala	Gln
		530					535					540			
Met	Leu	Val	Gln	Asp	Glu	Glu	Pro	Leu	Ala	Asp	Ile	Thr	Gln	Ile	Val
		545					550					555			560
Asp	Val	Phe	Met	Glu	Tyr	Asn	Leu	Ile	Gln	Gln	Cys	Thr	Ala	Phe	Leu
				565					570						575
Leu	Asp	Ala	Leu	Lys	Asn	Asn	Arg	Pro	Ser	Glu	Gly	Pro	Leu	Gln	Thr
			580					585						590	
Arg	Leu	Leu	Glu	Met	Asn	Leu	Met	His	Ala	Pro	Gln	Val	Ala	Asp	Ala
		595					600					605			
Ile	Leu	Gly	Asn	Gln	Met	Phe	Thr	His	Tyr	Asp	Arg	Ala	His	Ile	Ala
		610					615					620			
Gln	Leu	Cys	Glu	Lys	Ala	Gly	Leu	Leu	Gln	Arg	Ala	Leu	Glu	His	Phe
		625					630					635			640
Thr	Asp	Leu	Tyr	Asp	Ile	Lys	Arg	Ala	Val	Val	His	Thr	His	Leu	Leu
				645					650					655	
Asn	Pro	Glu	Trp	Leu	Val	Asn	Tyr	Phe	Gly	Ser	Leu	Ser	Val	Glu	Asp
			660					665						670	
Ser	Leu	Glu	Cys	Leu	Arg	Ala	Met	Leu	Ser	Ala	Asn	Ile	Arg	Gln	Asn
		675					680					685			
Leu	Gln	Ile	Cys	Val	Gln	Val	Ala	Ser	Lys	Tyr	His	Glu	Gln	Leu	Ser
		690					695					700			
Thr	Gln	Ser	Leu	Ile	Glu	Leu	Phe	Glu	Ser	Phe	Lys	Ser	Phe	Glu	Gly
		705					710					715			720
Leu	Phe	Tyr	Phe	Leu	Gly	Ser	Ile	Val	Asn	Phe	Ser	Gln	Asp	Pro	Asp
				725					730					735	
Val	His	Phe	Lys	Tyr	Ile	Gln	Ala	Ala	Cys	Lys	Thr	Gly	Gln	Ile	Lys
			740					745					750		
Glu	Val	Glu	Arg	Ile	Cys	Arg	Glu	Ser	Asn	Cys	Tyr	Asp	Pro	Glu	Arg
		755					760					765			
Val	Lys	Asn	Phe	Leu	Lys	Glu	Ala	Lys	Leu	Thr	Asp	Gln	Leu	Pro	Leu
		770					775					780			
Ile	Ile	Val	Cys	Asp	Arg	Phe	Asp	Phe	Val	His	Asp	Leu	Val	Leu	Tyr
		785					790					795			800
Leu	Tyr	Arg	Asn	Asn	Leu	Gln	Lys	Tyr	Ile	Glu	Ile	Tyr	Val	Gln	Lys
			805						810					815	
Val	Asn	Pro	Ser	Arg	Leu	Pro	Val	Val	Ile	Gly	Gly	Leu	Leu	Asp	Val
			820					825						830	

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Asp Cys Ser Glu Asp Val Ile Lys Asn Leu Ile Leu Val Val Arg Gly  
 835 840 845

Gln Phe Ser Thr Asp Glu Leu Val Ala Glu Val Glu Lys Arg Asn Arg  
 850 855 860

Leu Lys Leu Leu Leu Pro Trp Leu Glu Ala Arg Ile His Glu Gly Cys  
 865 870 875 880

Glu Glu Pro Ala Thr His Asn Ala Leu Ala Lys Ile Tyr Ile Asp Ser  
 885 890 895

Asn Asn Asn Pro Glu Arg Phe Leu Arg Glu Asn Pro Tyr Tyr Asp Ser  
 900 905 910

Arg Val Val Gly Lys Tyr Cys Glu Lys Arg Asp Pro His Leu Ala Cys  
 915 920 925

Val Ala Tyr Glu Arg Gly Gln Cys Asp Leu Glu Leu Ile Asn Val Cys  
 930 935 940

Asn Glu Asn Ser Leu Phe Lys Ser Leu Ser Arg Tyr Leu Val Arg Arg  
 945 950 955 960

Lys Asp Pro Glu Leu Trp Gly Ser Val Leu Leu Glu Ser Asn Pro Tyr  
 965 970 975

Arg Arg Pro Leu Ile Asp Gln Val Val Gln Thr Ala Leu Ser Glu Thr  
 980 985 990

Gln Asp Pro Glu Glu Val Ser Val Thr Val Lys Ala Phe Met Thr Ala  
 995 1000 1005

Asp Leu Pro Asn Glu Leu Ile Glu Leu Leu Glu Lys Ile Val Leu  
 1010 1015 1020

Asp Asn Ser Val Phe Ser Glu His Arg Asn Leu Gln Asn Leu Leu  
 1025 1030 1035

Ile Leu Thr Ala Ile Lys Ala Asp Arg Thr Arg Val Met Glu Tyr  
 1040 1045 1050

Ile Asn Arg Leu Asp Asn Tyr Asp Ala Pro Asp Ile Ala Asn Ile  
 1055 1060 1065

Ala Ile Ser Asn Glu Leu Phe Glu Glu Ala Phe Ala Ile Phe Arg  
 1070 1075 1080

Lys Phe Asp Val Asn Thr Ser Ala Val Gln Val Leu Ile Glu His  
 1085 1090 1095

Ile Gly Asn Leu Asp Arg Ala Tyr Glu Phe Ala Glu Arg Cys Asn  
 1100 1105 1110

Glu Pro Ala Val Trp Ser Gln Leu Ala Lys Ala Gln Leu Gln Lys  
 1115 1120 1125

Gly Met Val Lys Glu Ala Ile Asp Ser Tyr Ile Lys Ala Asp Asp  
 1130 1135 1140

Pro Ser Ser Tyr Met Glu Val Val Gln Ala Ala Asn Thr Ser Gly  
 1145 1150 1155

Asn Trp Glu Glu Leu Val Lys Tyr Leu Gln Met Ala Arg Lys Lys  
 1160 1165 1170

Ala Arg Glu Ser Tyr Val Glu Thr Glu Leu Ile Phe Ala Leu Ala  
 1175 1180 1185

Lys Thr Asn Arg Leu Ala Glu Leu Glu Glu Phe Ile Asn Gly Pro  
 1190 1195 1200

Asn Asn Ala His Ile Gln Gln Val Gly Asp Arg Cys Tyr Asp Glu  
 1205 1210 1215

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

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1595                    1600                    1605  
 Phe Ile Gln Val Met Lys Glu Tyr Leu Thr Lys Val Asp Lys Leu  
   1610                    1615                    1620  
 Asp Ala Ser Glu Ser Leu Arg Lys Glu Glu Glu Gln Ala Thr Glu  
   1625                    1630                    1635  
 Thr Gln Pro Ile Val Tyr Gly Gln Pro Gln Leu Met Leu Thr Ala  
   1640                    1645                    1650  
 Gly Pro Ser Val Ala Val Pro Pro Gln Ala Pro Phe Gly Tyr Gly  
   1655                    1660                    1665  
 Tyr Thr Ala Pro Pro Tyr Gly Gln Pro Gln Pro Gly Phe Gly Tyr  
   1670                    1675                    1680  
 Ser Met  
   1685

<210> SEQ ID NO 5  
 <211> LENGTH: 1682  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <300> PUBLICATION INFORMATION:  
 <308> DATABASE ACCESSION NUMBER: NCBI/EAW94395  
 <309> DATABASE ENTRY DATE: 2006-12-18  
 <313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(1682)

<400> SEQUENCE: 5

Met Ala Gln Ile Leu Pro Ile Arg Phe Gln Glu His Leu Gln Leu Gln  
   1                    5                    10                    15  
 Asn Leu Gly Ile Asn Pro Ala Asn Ile Gly Phe Ser Thr Leu Thr Met  
                   20                    25                    30  
 Glu Ser Asp Lys Phe Ile Cys Ile Arg Glu Lys Val Gly Glu Gln Ala  
                   35                    40                    45  
 Gln Val Val Ile Ile Asp Met Asn Asp Pro Ser Asn Pro Ile Arg Arg  
   50                    55                    60  
 Pro Ile Ser Ala Asp Ser Ala Ile Met Asn Pro Ala Ser Lys Val Ile  
   65                    70                    75                    80  
 Ala Leu Lys Ala Gly Lys Thr Leu Gln Ile Phe Asn Ile Glu Met Lys  
                   85                    90                    95  
 Ser Lys Met Lys Ala His Thr Met Thr Asp Asp Val Thr Phe Trp Lys  
                   100                    105                    110  
 Trp Ile Ser Leu Asn Thr Val Ala Leu Val Thr Asp Asn Ala Val Tyr  
                   115                    120                    125  
 His Trp Ser Met Glu Gly Glu Ser Gln Pro Val Lys Met Phe Asp Arg  
   130                    135                    140  
 His Ser Ser Leu Ala Gly Cys Gln Ile Ile Asn Tyr Arg Thr Asp Ala  
   145                    150                    155                    160  
 Lys Gln Lys Trp Leu Leu Leu Thr Gly Ile Ser Ala Gln Gln Asn Arg  
                   165                    170                    175  
 Val Val Gly Ala Met Gln Leu Tyr Ser Val Asp Arg Lys Val Ser Gln  
                   180                    185                    190  
 Pro Ile Glu Gly His Ala Ala Ser Phe Ala Gln Phe Lys Met Glu Gly  
                   195                    200                    205  
 Asn Ala Glu Glu Ser Thr Leu Phe Cys Phe Ala Val Arg Gly Gln Ala  
   210                    215                    220  
 Gly Gly Lys Leu His Ile Ile Glu Val Gly Thr Pro Pro Thr Gly Asn  
   225                    230                    235                    240



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Gln Pro Phe Pro Lys Lys Ala Val Asp Val Phe Phe Pro Pro Glu Ala  
 245 250 255

Gln Asn Asp Phe Pro Val Ala Met Gln Ile Ser Glu Lys His Asp Val  
 260 265 270

Val Phe Leu Ile Thr Lys Tyr Gly Tyr Ile His Leu Tyr Asp Leu Glu  
 275 280 285

Thr Gly Thr Cys Ile Tyr Met Asn Arg Ile Ser Gly Glu Thr Ile Phe  
 290 295 300

Val Thr Ala Pro His Glu Ala Thr Ala Gly Ile Ile Gly Val Asn Arg  
 305 310 315 320

Lys Gly Gln Val Leu Ser Val Cys Val Glu Glu Glu Asn Ile Ile Pro  
 325 330 335

Tyr Ile Thr Asn Val Leu Gln Asn Pro Asp Leu Ala Leu Arg Met Ala  
 340 345 350

Val Arg Asn Asn Leu Ala Gly Ala Glu Glu Leu Phe Ala Arg Lys Phe  
 355 360 365

Asn Ala Leu Phe Ala Gln Gly Asn Tyr Ser Glu Ala Ala Lys Val Ala  
 370 375 380

Ala Asn Ala Pro Lys Gly Ile Leu Arg Thr Pro Asp Thr Ile Arg Arg  
 385 390 395 400

Phe Gln Ser Val Pro Ala Gln Pro Gly Gln Thr Ser Pro Leu Leu Gln  
 405 410 415

Tyr Phe Gly Ile Leu Leu Asp Gln Gly Gln Leu Asn Lys Tyr Glu Ser  
 420 425 430

Leu Glu Leu Cys Arg Pro Val Leu Gln Gln Gly Arg Lys Gln Leu Leu  
 435 440 445

Glu Lys Trp Leu Lys Glu Asp Lys Leu Glu Cys Ser Glu Glu Leu Gly  
 450 455 460

Asp Leu Val Lys Ser Val Asp Pro Thr Leu Ala Leu Ser Val Tyr Leu  
 465 470 475 480

Arg Ala Asn Val Pro Asn Lys Val Ile Gln Cys Phe Ala Glu Thr Gly  
 485 490 495

Gln Val Gln Lys Ile Val Leu Tyr Ala Lys Lys Val Gly Tyr Thr Pro  
 500 505 510

Asp Trp Ile Phe Leu Leu Arg Asn Val Met Arg Ile Ser Pro Asp Gln  
 515 520 525

Gly Gln Gln Phe Ala Gln Met Leu Val Gln Asp Glu Glu Pro Leu Ala  
 530 535 540

Asp Ile Thr Gln Ile Val Asp Val Phe Met Glu Tyr Asn Leu Ile Gln  
 545 550 555 560

Gln Cys Thr Ala Phe Leu Leu Asp Ala Leu Lys Asn Asn Arg Pro Ser  
 565 570 575

Glu Gly Pro Leu Gln Thr Arg Leu Leu Glu Met Asn Leu Met His Ala  
 580 585 590

Pro Gln Val Ala Asp Ala Ile Leu Gly Asn Gln Met Phe Thr His Tyr  
 595 600 605

Asp Arg Ala His Ile Ala Gln Leu Cys Glu Lys Ala Gly Leu Leu Gln  
 610 615 620

Arg Ala Leu Glu His Phe Thr Asp Leu Tyr Asp Ile Lys Arg Ala Val  
 625 630 635 640

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Val	His	Thr	His	Leu	Leu	Asn	Pro	Glu	Trp	Leu	Val	Asn	Tyr	Phe	Gly
				645					650					655	
Ser	Leu	Ser	Val	Glu	Asp	Ser	Leu	Glu	Cys	Leu	Arg	Ala	Met	Leu	Ser
			660					665					670		
Ala	Asn	Ile	Arg	Gln	Asn	Leu	Gln	Ile	Cys	Val	Gln	Val	Ala	Ser	Lys
		675					680					685			
Tyr	His	Glu	Gln	Leu	Ser	Thr	Gln	Ser	Leu	Ile	Glu	Leu	Phe	Glu	Ser
	690					695					700				
Phe	Lys	Ser	Phe	Glu	Gly	Leu	Phe	Tyr	Phe	Leu	Gly	Ser	Ile	Val	Asn
705					710					715					720
Phe	Ser	Gln	Asp	Pro	Asp	Val	His	Phe	Lys	Tyr	Ile	Gln	Ala	Ala	Cys
				725					730					735	
Lys	Thr	Gly	Gln	Ile	Lys	Glu	Val	Glu	Arg	Ile	Cys	Arg	Glu	Ser	Asn
			740					745					750		
Cys	Tyr	Asp	Pro	Glu	Arg	Val	Lys	Asn	Phe	Leu	Lys	Glu	Ala	Lys	Leu
		755						760				765			
Thr	Asp	Gln	Leu	Pro	Leu	Ile	Ile	Val	Cys	Asp	Arg	Phe	Asp	Phe	Val
	770					775					780				
His	Asp	Leu	Val	Leu	Tyr	Leu	Tyr	Arg	Asn	Asn	Leu	Gln	Lys	Tyr	Ile
785					790					795					800
Glu	Ile	Tyr	Val	Gln	Lys	Val	Asn	Pro	Ser	Arg	Leu	Pro	Val	Val	Ile
				805					810					815	
Gly	Gly	Leu	Leu	Asp	Val	Asp	Cys	Ser	Glu	Asp	Val	Ile	Lys	Asn	Leu
			820					825					830		
Ile	Leu	Val	Val	Arg	Gly	Gln	Phe	Ser	Thr	Asp	Glu	Leu	Val	Ala	Glu
		835					840					845			
Val	Glu	Lys	Arg	Asn	Arg	Leu	Lys	Leu	Leu	Leu	Pro	Trp	Leu	Glu	Ala
	850					855					860				
Arg	Ile	His	Glu	Gly	Cys	Glu	Glu	Pro	Ala	Thr	His	Asn	Ala	Leu	Ala
865					870					875					880
Lys	Ile	Tyr	Ile	Asp	Ser	Asn	Asn	Asn	Pro	Glu	Arg	Phe	Leu	Arg	Glu
				885					890					895	
Asn	Pro	Tyr	Tyr	Asp	Ser	Arg	Val	Val	Gly	Lys	Tyr	Cys	Glu	Lys	Arg
		900						905					910		
Asp	Pro	His	Leu	Ala	Cys	Val	Ala	Tyr	Glu	Arg	Gly	Gln	Cys	Asp	Leu
		915					920					925			
Glu	Leu	Ile	Asn	Val	Cys	Asn	Glu	Asn	Ser	Leu	Phe	Lys	Ser	Leu	Ser
	930						935				940				
Arg	Tyr	Leu	Val	Arg	Arg	Lys	Asp	Pro	Glu	Leu	Trp	Gly	Ser	Val	Leu
945						950				955					960
Leu	Glu	Ser	Asn	Pro	Tyr	Arg	Arg	Pro	Leu	Ile	Asp	Gln	Val	Val	Gln
				965					970					975	
Thr	Ala	Leu	Ser	Glu	Thr	Gln	Asp	Pro	Glu	Glu	Val	Ser	Val	Thr	Val
			980					985						990	
Lys	Ala	Phe	Met	Thr	Ala	Asp	Leu	Pro	Asn	Glu	Leu	Ile	Glu	Leu	Leu
		995					1000					1005			
Glu	Lys	Ile	Val	Leu	Asp	Asn	Ser	Val	Phe	Ser	Glu	His	Arg	Asn	
	1010						1015				1020				
Leu	Gln	Asn	Leu	Leu	Ile	Leu	Thr	Ala	Ile	Lys	Ala	Asp	Arg	Thr	
	1025						1030				1035				
Arg	Val	Met	Glu	Tyr	Ile	Asn	Arg	Leu	Asp	Asn	Tyr	Asp	Ala	Pro	



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Arg Leu Asp His Thr Arg Ala Val Asn Tyr Phe Ser Lys Val Lys  
 1430 1435 1440  
 Gln Leu Pro Leu Val Lys Pro Tyr Leu Arg Ser Val Gln Asn His  
 1445 1450 1455  
 Asn Asn Lys Ser Val Asn Glu Ser Leu Asn Asn Leu Phe Ile Thr  
 1460 1465 1470  
 Glu Glu Asp Tyr Gln Ala Leu Arg Thr Ser Ile Asp Ala Tyr Asp  
 1475 1480 1485  
 Asn Phe Asp Asn Ile Ser Leu Ala Gln Arg Leu Glu Lys His Glu  
 1490 1495 1500  
 Leu Ile Glu Phe Arg Arg Ile Ala Ala Tyr Leu Phe Lys Gly Asn  
 1505 1510 1515  
 Asn Arg Trp Lys Gln Ser Val Glu Leu Cys Lys Lys Asp Ser Leu  
 1520 1525 1530  
 Tyr Lys Asp Ala Met Gln Tyr Ala Ser Glu Ser Lys Asp Thr Glu  
 1535 1540 1545  
 Leu Ala Glu Glu Leu Leu Gln Trp Phe Leu Gln Glu Glu Lys Arg  
 1550 1555 1560  
 Glu Cys Phe Gly Ala Cys Leu Phe Thr Cys Tyr Asp Leu Leu Arg  
 1565 1570 1575  
 Pro Asp Val Val Leu Glu Thr Ala Trp Arg His Asn Ile Met Asp  
 1580 1585 1590  
 Phe Ala Met Pro Tyr Phe Ile Gln Val Met Lys Glu Tyr Leu Thr  
 1595 1600 1605  
 Lys Val Asp Ala Ile Lys Glu Lys Val Asp Lys Leu Asp Ala Ser  
 1610 1615 1620  
 Glu Ser Leu Arg Lys Glu Glu Glu Gln Ala Thr Glu Thr Gln Pro  
 1625 1630 1635  
 Ile Val Tyr Gly Gln Pro Gln Leu Met Leu Thr Ala Gly Pro Ser  
 1640 1645 1650  
 Val Ala Val Pro Pro Gln Ala Pro Phe Gly Tyr Gly Tyr Thr Ala  
 1655 1660 1665  
 Pro Pro Tyr Gly Gln Pro Gln Pro Gly Phe Gly Tyr Ser Met  
 1670 1675 1680

<210> SEQ ID NO 6  
 <211> LENGTH: 1675  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <300> PUBLICATION INFORMATION:  
 <308> DATABASE ACCESSION NUMBER: NCBI/EAW94399  
 <309> DATABASE ENTRY DATE: 2006-12-18  
 <313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(1675)

<400> SEQUENCE: 6

Met Ala Gln Ile Leu Pro Ile Arg Phe Gln Glu His Leu Gln Leu Gln  
 1 5 10 15  
 Asn Leu Gly Ile Asn Pro Ala Asn Ile Gly Phe Ser Thr Leu Thr Met  
 20 25 30  
 Glu Ser Asp Lys Phe Ile Cys Ile Arg Glu Lys Val Gly Glu Gln Ala  
 35 40 45  
 Gln Val Val Ile Ile Asp Met Asn Asp Pro Ser Asn Pro Ile Arg Arg  
 50 55 60



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465				470					475					480	
Arg	Ala	Asn	Val	Pro	Asn	Lys	Val	Ile	Gln	Cys	Phe	Ala	Glu	Thr	Gly
				485					490					495	
Gln	Val	Gln	Lys	Ile	Val	Leu	Tyr	Ala	Lys	Lys	Val	Gly	Tyr	Thr	Pro
			500					505					510		
Asp	Trp	Ile	Phe	Leu	Leu	Arg	Asn	Val	Met	Arg	Ile	Ser	Pro	Asp	Gln
		515					520					525			
Gly	Gln	Gln	Phe	Ala	Gln	Met	Leu	Val	Gln	Asp	Glu	Glu	Pro	Leu	Ala
	530					535					540				
Asp	Ile	Thr	Gln	Ile	Val	Asp	Val	Phe	Met	Glu	Tyr	Asn	Leu	Ile	Gln
545					550					555					560
Gln	Cys	Thr	Ala	Phe	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Asn	Arg	Pro	Ser
				565					570					575	
Glu	Gly	Pro	Leu	Gln	Thr	Arg	Leu	Leu	Glu	Met	Asn	Leu	Met	His	Ala
			580					585					590		
Pro	Gln	Val	Ala	Asp	Ala	Ile	Leu	Gly	Asn	Gln	Met	Phe	Thr	His	Tyr
		595					600					605			
Asp	Arg	Ala	His	Ile	Ala	Gln	Leu	Cys	Glu	Lys	Ala	Gly	Leu	Leu	Gln
	610					615					620				
Arg	Ala	Leu	Glu	His	Phe	Thr	Asp	Leu	Tyr	Asp	Ile	Lys	Arg	Ala	Val
625					630					635					640
Val	His	Thr	His	Leu	Leu	Asn	Pro	Glu	Trp	Leu	Val	Asn	Tyr	Phe	Gly
				645					650					655	
Ser	Leu	Ser	Val	Glu	Asp	Ser	Leu	Glu	Cys	Leu	Arg	Ala	Met	Leu	Ser
			660					665					670		
Ala	Asn	Ile	Arg	Gln	Asn	Leu	Gln	Ile	Cys	Val	Gln	Val	Ala	Ser	Lys
		675					680					685			
Tyr	His	Glu	Gln	Leu	Ser	Thr	Gln	Ser	Leu	Ile	Glu	Leu	Phe	Glu	Ser
	690					695					700				
Phe	Lys	Ser	Phe	Glu	Gly	Leu	Phe	Tyr	Phe	Leu	Gly	Ser	Ile	Val	Asn
705					710					715					720
Phe	Ser	Gln	Asp	Pro	Asp	Val	His	Phe	Lys	Tyr	Ile	Gln	Ala	Ala	Cys
				725					730					735	
Lys	Thr	Gly	Gln	Ile	Lys	Glu	Val	Glu	Arg	Ile	Cys	Arg	Glu	Ser	Asn
			740					745					750		
Cys	Tyr	Asp	Pro	Glu	Arg	Val	Lys	Asn	Phe	Leu	Lys	Glu	Ala	Lys	Leu
		755					760					765			
Thr	Asp	Gln	Leu	Pro	Leu	Ile	Ile	Val	Cys	Asp	Arg	Phe	Asp	Phe	Val
	770					775					780				
His	Asp	Leu	Val	Leu	Tyr	Leu	Tyr	Arg	Asn	Asn	Leu	Gln	Lys	Tyr	Ile
785					790					795					800
Glu	Ile	Tyr	Val	Gln	Lys	Val	Asn	Pro	Ser	Arg	Leu	Pro	Val	Val	Ile
				805					810					815	
Gly	Gly	Leu	Leu	Asp	Val	Asp	Cys	Ser	Glu	Asp	Val	Ile	Lys	Asn	Leu
			820					825					830		
Ile	Leu	Val	Val	Arg	Gly	Gln	Phe	Ser	Thr	Asp	Glu	Leu	Val	Ala	Glu
		835					840					845			
Val	Glu	Lys	Arg	Asn	Arg	Leu	Lys	Leu	Leu	Leu	Pro	Trp	Leu	Glu	Ala
	850					855					860				
Arg	Ile	His	Glu	Gly	Cys	Glu	Glu	Pro	Ala	Thr	His	Asn	Ala	Leu	Ala
865					870					875					880

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Lys Ile Tyr Ile Asp Ser Asn Asn Asn Pro Glu Arg Phe Leu Arg Glu  
885 890 895  
Asn Pro Tyr Tyr Asp Ser Arg Val Val Gly Lys Tyr Cys Glu Lys Arg  
900 905 910  
Asp Pro His Leu Ala Cys Val Ala Tyr Glu Arg Gly Gln Cys Asp Leu  
915 920 925  
Glu Leu Ile Asn Val Cys Asn Glu Asn Ser Leu Phe Lys Ser Leu Ser  
930 935 940  
Arg Tyr Leu Val Arg Arg Lys Asp Pro Glu Leu Trp Gly Ser Val Leu  
945 950 955 960  
Leu Glu Ser Asn Pro Tyr Arg Arg Pro Leu Ile Asp Gln Val Val Gln  
965 970 975  
Thr Ala Leu Ser Glu Thr Gln Asp Pro Glu Glu Val Ser Val Thr Val  
980 985 990  
Lys Ala Phe Met Thr Ala Asp Leu Pro Asn Glu Leu Ile Glu Leu Leu  
995 1000 1005  
Glu Lys Ile Val Leu Asp Asn Ser Val Phe Ser Glu His Arg Asn  
1010 1015 1020  
Leu Gln Asn Leu Leu Ile Leu Thr Ala Ile Lys Ala Asp Arg Thr  
1025 1030 1035  
Arg Val Met Glu Tyr Ile Asn Arg Leu Asp Asn Tyr Asp Ala Pro  
1040 1045 1050  
Asp Ile Ala Asn Ile Ala Ile Ser Asn Glu Leu Phe Glu Glu Ala  
1055 1060 1065  
Phe Ala Ile Phe Arg Lys Phe Asp Val Asn Thr Ser Ala Val Gln  
1070 1075 1080  
Val Leu Ile Glu His Ile Gly Asn Leu Asp Arg Ala Tyr Glu Phe  
1085 1090 1095  
Ala Glu Arg Cys Asn Glu Pro Ala Val Trp Ser Gln Leu Ala Lys  
1100 1105 1110  
Ala Gln Leu Gln Lys Gly Met Val Lys Glu Ala Ile Asp Ser Tyr  
1115 1120 1125  
Ile Lys Ala Asp Asp Pro Ser Ser Tyr Met Glu Val Val Gln Ala  
1130 1135 1140  
Ala Asn Thr Ser Gly Asn Trp Glu Glu Leu Val Lys Tyr Leu Gln  
1145 1150 1155  
Met Ala Arg Lys Lys Ala Arg Glu Ser Tyr Val Glu Thr Glu Leu  
1160 1165 1170  
Ile Phe Ala Leu Ala Lys Thr Asn Arg Leu Ala Glu Leu Glu Glu  
1175 1180 1185  
Phe Ile Asn Gly Pro Asn Asn Ala His Ile Gln Gln Val Gly Asp  
1190 1195 1200  
Arg Cys Tyr Asp Glu Lys Met Tyr Asp Ala Ala Lys Leu Leu Tyr  
1205 1210 1215  
Asn Asn Val Ser Asn Phe Gly Arg Leu Ala Ser Thr Leu Val His  
1220 1225 1230  
Leu Gly Glu Tyr Gln Ala Ala Val Asp Gly Ala Arg Lys Ala Asn  
1235 1240 1245  
Ser Thr Arg Thr Trp Lys Glu Val Cys Phe Ala Cys Val Asp Gly  
1250 1255 1260

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Lys	Glu	Phe	Arg	Leu	Ala	Gln	Met	Cys	Gly	Leu	His	Ile	Val	Val
1265						1270					1275			
His	Ala	Asp	Glu	Leu	Glu	Glu	Leu	Ile	Asn	Tyr	Tyr	Gln	Asp	Arg
1280						1285					1290			
Gly	Tyr	Phe	Glu	Glu	Leu	Ile	Thr	Met	Leu	Glu	Ala	Ala	Leu	Gly
1295						1300					1305			
Leu	Glu	Arg	Ala	His	Met	Gly	Met	Phe	Thr	Glu	Leu	Ala	Ile	Leu
1310						1315					1320			
Tyr	Ser	Lys	Phe	Lys	Pro	Gln	Lys	Met	Arg	Glu	His	Leu	Glu	Leu
1325						1330					1335			
Phe	Trp	Ser	Arg	Val	Asn	Ile	Pro	Lys	Val	Leu	Arg	Ala	Ala	Glu
1340						1345					1350			
Gln	Ala	His	Leu	Trp	Ala	Glu	Leu	Val	Phe	Leu	Tyr	Asp	Lys	Tyr
1355						1360					1365			
Glu	Glu	Tyr	Asp	Asn	Ala	Ile	Ile	Thr	Met	Met	Asn	His	Pro	Thr
1370						1375					1380			
Asp	Ala	Trp	Lys	Glu	Gly	Gln	Phe	Lys	Asp	Ile	Ile	Thr	Lys	Val
1385						1390					1395			
Ala	Asn	Val	Glu	Leu	Tyr	Tyr	Arg	Ala	Ile	Gln	Phe	Tyr	Leu	Glu
1400						1405					1410			
Phe	Lys	Pro	Leu	Leu	Leu	Asn	Asp	Leu	Leu	Met	Val	Leu	Ser	Pro
1415						1420					1425			
Arg	Leu	Asp	His	Thr	Arg	Ala	Val	Asn	Tyr	Phe	Ser	Lys	Val	Lys
1430						1435					1440			
Gln	Leu	Pro	Leu	Val	Lys	Pro	Tyr	Leu	Arg	Ser	Val	Gln	Asn	His
1445						1450					1455			
Asn	Asn	Lys	Ser	Val	Asn	Glu	Ser	Leu	Asn	Asn	Leu	Phe	Ile	Thr
1460						1465					1470			
Glu	Glu	Asp	Tyr	Gln	Ala	Leu	Arg	Thr	Ser	Ile	Asp	Ala	Tyr	Asp
1475						1480					1485			
Asn	Phe	Asp	Asn	Ile	Ser	Leu	Ala	Gln	Arg	Leu	Glu	Lys	His	Glu
1490						1495					1500			
Leu	Ile	Glu	Phe	Arg	Arg	Ile	Ala	Ala	Tyr	Leu	Phe	Lys	Gly	Asn
1505						1510					1515			
Asn	Arg	Trp	Lys	Gln	Ser	Val	Glu	Leu	Cys	Lys	Lys	Asp	Ser	Leu
1520						1525					1530			
Tyr	Lys	Asp	Ala	Met	Gln	Tyr	Ala	Ser	Glu	Ser	Lys	Asp	Thr	Glu
1535						1540					1545			
Leu	Ala	Glu	Glu	Leu	Leu	Gln	Trp	Phe	Leu	Gln	Glu	Glu	Lys	Arg
1550						1555					1560			
Glu	Cys	Phe	Gly	Ala	Cys	Leu	Phe	Thr	Cys	Tyr	Asp	Leu	Leu	Arg
1565						1570					1575			
Pro	Asp	Val	Val	Leu	Glu	Thr	Ala	Trp	Arg	His	Asn	Ile	Met	Asp
1580						1585					1590			
Phe	Ala	Met	Pro	Tyr	Phe	Ile	Gln	Val	Met	Lys	Glu	Tyr	Leu	Thr
1595						1600					1605			
Lys	Val	Asp	Lys	Leu	Asp	Ala	Ser	Glu	Ser	Leu	Arg	Lys	Glu	Glu
1610						1615					1620			
Glu	Gln	Ala	Thr	Glu	Thr	Gln	Pro	Ile	Val	Tyr	Gly	Gln	Pro	Gln
1625						1630					1635			
Leu	Met	Leu	Thr	Ala	Gly	Pro	Ser	Val	Ala	Val	Pro	Pro	Gln	Ala



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1640          1645          1650
Pro Phe Gly Tyr Gly Tyr Thr Ala Pro Pro Tyr Gly Gln Pro Gln
1655          1660          1665

Pro Gly Phe Gly Tyr Ser Met
1670          1675

<210> SEQ ID NO 7
<211> LENGTH: 1679
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<300> PUBLICATION INFORMATION:
<308> DATABASE ACCESSION NUMBER: NCBI/EAW94397
<309> DATABASE ENTRY DATE: 2006-12-18
<313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(1679)

<400> SEQUENCE: 7

Met Ala Gln Ile Leu Pro Ile Arg Phe Gln Glu His Leu Gln Leu Gln
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Asn Leu Gly Ile Asn Pro Ala Asn Ile Gly Phe Ser Thr Leu Thr Met
20          25          30

Glu Ser Asp Lys Phe Ile Cys Ile Arg Glu Lys Val Gly Glu Gln Ala
35          40          45

Gln Val Val Ile Ile Asp Met Asn Asp Pro Ser Asn Pro Ile Arg Arg
50          55          60

Pro Ile Ser Ala Asp Ser Ala Ile Met Asn Pro Ala Ser Lys Val Ile
65          70          75          80

Ala Leu Lys Gly Ile Lys Glu Ser Gly Lys Thr Leu Gln Ile Phe Asn
85          90          95

Ile Glu Met Lys Ser Lys Met Lys Ala His Thr Met Thr Asp Asp Val
100         105         110

Thr Phe Trp Lys Trp Ile Ser Leu Asn Thr Val Ala Leu Val Thr Asp
115        120        125

Asn Ala Val Tyr His Trp Ser Met Glu Gly Glu Ser Gln Pro Val Lys
130        135        140

Met Phe Asp Arg His Ser Ser Leu Ala Gly Cys Gln Ile Ile Asn Tyr
145        150        155        160

Arg Thr Asp Ala Lys Gln Lys Trp Leu Leu Leu Thr Gly Ile Ser Ala
165        170        175

Gln Gln Asn Arg Val Val Gly Ala Met Gln Leu Tyr Ser Val Asp Arg
180        185        190

Lys Val Ser Gln Pro Ile Glu Gly His Ala Ala Ser Phe Ala Gln Phe
195        200        205

Lys Met Glu Gly Asn Ala Glu Glu Ser Thr Leu Phe Cys Phe Ala Val
210        215        220

Arg Gly Gln Ala Gly Gly Lys Leu His Ile Ile Glu Val Gly Thr Pro
225        230        235        240

Pro Thr Gly Asn Gln Pro Phe Pro Lys Lys Ala Val Asp Val Phe Phe
245        250        255

Pro Pro Glu Ala Gln Asn Asp Phe Pro Val Ala Met Gln Ile Ser Glu
260        265        270

Lys His Asp Val Val Phe Leu Ile Thr Lys Tyr Gly Tyr Ile His Leu
275        280        285

Tyr Asp Leu Glu Thr Gly Thr Cys Ile Tyr Met Asn Arg Ile Ser Gly
290        295        300

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Glu Thr Ile Phe Val Thr Ala Pro His Glu Ala Thr Ala Gly Ile Ile  
 305 310 315 320  
 Gly Val Asn Arg Lys Gly Gln Val Leu Ser Val Cys Val Glu Glu Glu  
 325 330 335  
 Asn Ile Ile Pro Tyr Ile Thr Asn Val Leu Gln Asn Pro Asp Leu Ala  
 340 345 350  
 Leu Arg Met Ala Val Arg Asn Asn Leu Ala Gly Ala Glu Glu Leu Phe  
 355 360 365  
 Ala Arg Lys Phe Asn Ala Leu Phe Ala Gln Gly Asn Tyr Ser Glu Ala  
 370 375 380  
 Ala Lys Val Ala Ala Asn Ala Pro Lys Gly Ile Leu Arg Thr Pro Asp  
 385 390 395 400  
 Thr Ile Arg Arg Phe Gln Ser Val Pro Ala Gln Pro Gly Gln Thr Ser  
 405 410 415  
 Pro Leu Leu Gln Tyr Phe Gly Ile Leu Leu Asp Gln Gly Gln Leu Asn  
 420 425 430  
 Lys Tyr Glu Ser Leu Glu Leu Cys Arg Pro Val Leu Gln Gln Gly Arg  
 435 440 445  
 Lys Gln Leu Leu Glu Lys Trp Leu Lys Glu Asp Lys Leu Glu Cys Ser  
 450 455 460  
 Glu Glu Leu Gly Asp Leu Val Lys Ser Val Asp Pro Thr Leu Ala Leu  
 465 470 475 480  
 Ser Val Tyr Leu Arg Ala Asn Val Pro Asn Lys Val Ile Gln Cys Phe  
 485 490 495  
 Ala Glu Thr Gly Gln Val Gln Lys Ile Val Leu Tyr Ala Lys Lys Val  
 500 505 510  
 Gly Tyr Thr Pro Asp Trp Ile Phe Leu Leu Arg Asn Val Met Arg Ile  
 515 520 525  
 Ser Pro Asp Gln Gly Gln Gln Phe Ala Gln Met Leu Val Gln Asp Glu  
 530 535 540  
 Glu Pro Leu Ala Asp Ile Thr Gln Ile Val Asp Val Phe Met Glu Tyr  
 545 550 555 560  
 Asn Leu Ile Gln Gln Cys Thr Ala Phe Leu Leu Asp Ala Leu Lys Asn  
 565 570 575  
 Asn Arg Pro Ser Glu Gly Pro Leu Gln Thr Arg Leu Leu Glu Met Asn  
 580 585 590  
 Leu Met His Ala Pro Gln Val Ala Asp Ala Ile Leu Gly Asn Gln Met  
 595 600 605  
 Phe Thr His Tyr Asp Arg Ala His Ile Ala Gln Leu Cys Glu Lys Ala  
 610 615 620  
 Gly Leu Leu Gln Arg Ala Leu Glu His Phe Thr Asp Leu Tyr Asp Ile  
 625 630 635 640  
 Lys Arg Ala Val Val His Thr His Leu Leu Asn Pro Glu Trp Leu Val  
 645 650 655  
 Asn Tyr Phe Gly Ser Leu Ser Val Glu Asp Ser Leu Glu Cys Leu Arg  
 660 665 670  
 Ala Met Leu Ser Ala Asn Ile Arg Gln Asn Leu Gln Ile Cys Val Gln  
 675 680 685  
 Val Ala Ser Lys Tyr His Glu Gln Leu Ser Thr Gln Ser Leu Ile Glu  
 690 695 700

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Leu Phe Glu Ser Phe Lys Ser Phe Glu Gly Leu Phe Tyr Phe Leu Gly  
 705 710 715 720  
 Ser Ile Val Asn Phe Ser Gln Asp Pro Asp Val His Phe Lys Tyr Ile  
 725 730 735  
 Gln Ala Ala Cys Lys Thr Gly Gln Ile Lys Glu Val Glu Arg Ile Cys  
 740 745 750  
 Arg Glu Ser Asn Cys Tyr Asp Pro Glu Arg Val Lys Asn Phe Leu Lys  
 755 760 765  
 Glu Ala Lys Leu Thr Asp Gln Leu Pro Leu Ile Ile Val Cys Asp Arg  
 770 775 780  
 Phe Asp Phe Val His Asp Leu Val Leu Tyr Leu Tyr Arg Asn Asn Leu  
 785 790 795 800  
 Gln Lys Tyr Ile Glu Ile Tyr Val Gln Lys Val Asn Pro Ser Arg Leu  
 805 810 815  
 Pro Val Val Ile Gly Gly Leu Leu Asp Val Asp Cys Ser Glu Asp Val  
 820 825 830  
 Ile Lys Asn Leu Ile Leu Val Val Arg Gly Gln Phe Ser Thr Asp Glu  
 835 840 845  
 Leu Val Ala Glu Val Glu Lys Arg Asn Arg Leu Lys Leu Leu Leu Pro  
 850 855 860  
 Trp Leu Glu Ala Arg Ile His Glu Gly Cys Glu Glu Pro Ala Thr His  
 865 870 875 880  
 Asn Ala Leu Ala Lys Ile Tyr Ile Asp Ser Asn Asn Asn Pro Glu Arg  
 885 890 895  
 Phe Leu Arg Glu Asn Pro Tyr Tyr Asp Ser Arg Val Val Gly Lys Tyr  
 900 905 910  
 Cys Glu Lys Arg Asp Pro His Leu Ala Cys Val Ala Tyr Glu Arg Gly  
 915 920 925  
 Gln Cys Asp Leu Glu Leu Ile Asn Val Cys Asn Glu Asn Ser Leu Phe  
 930 935 940  
 Lys Ser Leu Ser Arg Tyr Leu Val Arg Arg Lys Asp Pro Glu Leu Trp  
 945 950 955 960  
 Gly Ser Val Leu Leu Glu Ser Asn Pro Tyr Arg Arg Pro Leu Ile Asp  
 965 970 975  
 Gln Val Val Gln Thr Ala Leu Ser Glu Thr Gln Asp Pro Glu Glu Val  
 980 985 990  
 Ser Val Thr Val Lys Ala Phe Met Thr Ala Asp Leu Pro Asn Glu Leu  
 995 1000 1005  
 Ile Glu Leu Leu Glu Lys Ile Val Leu Asp Asn Ser Val Phe Ser  
 1010 1015 1020  
 Glu His Arg Asn Leu Gln Asn Leu Leu Ile Leu Thr Ala Ile Lys  
 1025 1030 1035  
 Ala Asp Arg Thr Arg Val Met Glu Tyr Ile Asn Arg Leu Asp Asn  
 1040 1045 1050  
 Tyr Asp Ala Pro Asp Ile Ala Asn Ile Ala Ile Ser Asn Glu Leu  
 1055 1060 1065  
 Phe Glu Glu Ala Phe Ala Ile Phe Arg Lys Phe Asp Val Asn Thr  
 1070 1075 1080  
 Ser Ala Val Gln Val Leu Ile Glu His Ile Gly Asn Leu Asp Arg  
 1085 1090 1095  
 Ala Tyr Glu Phe Ala Glu Arg Cys Asn Glu Pro Ala Val Trp Ser

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1100	1105	1110
Gln Leu Ala Lys Ala Gln Leu Gln Lys Gly Met Val Lys Glu Ala 1115 1120 1125		
Ile Asp Ser Tyr Ile Lys Ala Asp Asp Pro Ser Ser Tyr Met Glu 1130 1135 1140		
Val Val Gln Ala Ala Asn Thr Ser Gly Asn Trp Glu Glu Leu Val 1145 1150 1155		
Lys Tyr Leu Gln Met Ala Arg Lys Lys Ala Arg Glu Ser Tyr Val 1160 1165 1170		
Glu Thr Glu Leu Ile Phe Ala Leu Ala Lys Thr Asn Arg Leu Ala 1175 1180 1185		
Glu Leu Glu Glu Phe Ile Asn Gly Pro Asn Asn Ala His Ile Gln 1190 1195 1200		
Gln Val Gly Asp Arg Cys Tyr Asp Glu Lys Met Tyr Asp Ala Ala 1205 1210 1215		
Lys Leu Leu Tyr Asn Asn Val Ser Asn Phe Gly Arg Leu Ala Ser 1220 1225 1230		
Thr Leu Val His Leu Gly Glu Tyr Gln Ala Ala Val Asp Gly Ala 1235 1240 1245		
Arg Lys Ala Asn Ser Thr Arg Thr Trp Lys Glu Val Cys Phe Ala 1250 1255 1260		
Cys Val Asp Gly Lys Glu Phe Arg Leu Ala Gln Met Cys Gly Leu 1265 1270 1275		
His Ile Val Val His Ala Asp Glu Leu Glu Glu Leu Ile Asn Tyr 1280 1285 1290		
Tyr Gln Asp Arg Gly Tyr Phe Glu Glu Leu Ile Thr Met Leu Glu 1295 1300 1305		
Ala Ala Leu Gly Leu Glu Arg Ala His Met Gly Met Phe Thr Glu 1310 1315 1320		
Leu Ala Ile Leu Tyr Ser Lys Phe Lys Pro Gln Lys Met Arg Glu 1325 1330 1335		
His Leu Glu Leu Phe Trp Ser Arg Val Asn Ile Pro Lys Val Leu 1340 1345 1350		
Arg Ala Ala Glu Gln Ala His Leu Trp Ala Glu Leu Val Phe Leu 1355 1360 1365		
Tyr Asp Lys Tyr Glu Glu Tyr Asp Asn Ala Ile Ile Thr Met Met 1370 1375 1380		
Asn His Pro Thr Asp Ala Trp Lys Glu Gly Gln Phe Lys Asp Ile 1385 1390 1395		
Ile Thr Lys Val Ala Asn Val Glu Leu Tyr Tyr Arg Ala Ile Gln 1400 1405 1410		
Phe Tyr Leu Glu Phe Lys Pro Leu Leu Leu Asn Asp Leu Leu Met 1415 1420 1425		
Val Leu Ser Pro Arg Leu Asp His Thr Arg Ala Val Asn Tyr Phe 1430 1435 1440		
Ser Lys Val Lys Gln Leu Pro Leu Val Lys Pro Tyr Leu Arg Ser 1445 1450 1455		
Val Gln Asn His Asn Asn Lys Ser Val Asn Glu Ser Leu Asn Asn 1460 1465 1470		
Leu Phe Ile Thr Glu Glu Asp Tyr Gln Ala Leu Arg Thr Ser Ile 1475 1480 1485		

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Asp Ala Tyr Asp Asn Phe Asp Asn Ile Ser Leu Ala Gln Arg Leu  
 1490 1495 1500  
 Glu Lys His Glu Leu Ile Glu Phe Arg Arg Ile Ala Ala Tyr Leu  
 1505 1510 1515  
 Phe Lys Gly Asn Asn Arg Trp Lys Gln Ser Val Glu Leu Cys Lys  
 1520 1525 1530  
 Lys Asp Ser Leu Tyr Lys Asp Ala Met Gln Tyr Ala Ser Glu Ser  
 1535 1540 1545  
 Lys Asp Thr Glu Leu Ala Glu Glu Leu Leu Gln Trp Phe Leu Gln  
 1550 1555 1560  
 Glu Glu Lys Arg Glu Cys Phe Gly Ala Cys Leu Phe Thr Cys Tyr  
 1565 1570 1575  
 Asp Leu Leu Arg Pro Asp Val Val Leu Glu Thr Ala Trp Arg His  
 1580 1585 1590  
 Asn Ile Met Asp Phe Ala Met Pro Tyr Phe Ile Gln Val Met Lys  
 1595 1600 1605  
 Glu Tyr Leu Thr Lys Val Asp Lys Leu Asp Ala Ser Glu Ser Leu  
 1610 1615 1620  
 Arg Lys Glu Glu Glu Gln Ala Thr Glu Thr Gln Pro Ile Val Tyr  
 1625 1630 1635  
 Gly Gln Pro Gln Leu Met Leu Thr Ala Gly Pro Ser Val Ala Val  
 1640 1645 1650  
 Pro Pro Gln Ala Pro Phe Gly Tyr Gly Tyr Thr Ala Pro Pro Tyr  
 1655 1660 1665  
 Gly Gln Pro Gln Pro Gly Phe Gly Tyr Ser Met  
 1670 1675

<210> SEQ ID NO 8  
 <211> LENGTH: 1569  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <300> PUBLICATION INFORMATION:  
 <308> DATABASE ACCESSION NUMBER: NCBI/AAB40909  
 <309> DATABASE ENTRY DATE: 1997-01-15  
 <313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(1569)

<400> SEQUENCE: 8

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 20 25 30  
 Glu Ser Asp Lys Phe Ile Cys Ile Arg Glu Lys Val Gly Glu Gln Ala  
 35 40 45  
 Gln Val Thr Ile Ile Asp Met Ser Asp Pro Met Ala Pro Ile Arg Arg  
 50 55 60  
 Pro Ile Ser Ala Glu Ser Ala Ile Met Asn Pro Ala Ser Lys Val Ile  
 65 70 75 80  
 Ala Leu Lys Ala Gly Lys Thr Leu Gln Ile Phe Asn Ile Glu Met Lys  
 85 90 95  
 Ser Lys Met Lys Ala His Thr Met Ala Glu Glu Val Ile Phe Trp Lys  
 100 105 110  
 Trp Val Ser Val Asn Thr Val Ala Leu Val Thr Glu Thr Ala Val Tyr  
 115 120 125

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His	Trp	Ser	Met	Glu	Gly	Asp	Ser	Gln	Pro	Met	Lys	Met	Phe	Asp	Arg
130						135					140				
His	Thr	Ser	Leu	Val	Gly	Cys	Gln	Val	Ile	His	Tyr	Arg	Thr	Asp	Glu
145					150					155					160
Tyr	Gln	Lys	Trp	Leu	Leu	Leu	Val	Gly	Ile	Ser	Ala	Gln	Gln	Asn	Arg
				165					170					175	
Val	Val	Gly	Ala	Met	Gln	Leu	Tyr	Ser	Val	Asp	Arg	Lys	Val	Ser	Gln
			180					185					190		
Pro	Ile	Glu	Gly	His	Ala	Ala	Ala	Phe	Ala	Glu	Phe	Lys	Met	Glu	Gly
		195					200					205			
Asn	Ala	Lys	Pro	Ala	Thr	Leu	Phe	Cys	Phe	Ala	Val	Arg	Asn	Pro	Thr
210						215					220				
Gly	Gly	Lys	Leu	His	Ile	Ile	Glu	Val	Gly	Gln	Pro	Ala	Ala	Gly	Asn
225					230					235					240
Gln	Pro	Phe	Val	Lys	Lys	Ala	Val	Asp	Val	Phe	Phe	Pro	Pro	Glu	Ala
				245					250					255	
Gln	Asn	Asp	Phe	Pro	Val	Ala	Met	Gln	Ile	Gly	Ala	Lys	His	Gly	Val
			260					265					270		
Ile	Tyr	Leu	Ile	Thr	Lys	Tyr	Gly	Tyr	Leu	His	Leu	Tyr	Asp	Leu	Glu
		275					280					285			
Ser	Gly	Val	Cys	Ile	Cys	Met	Asn	Arg	Ile	Ser	Ala	Asp	Thr	Ile	Phe
290						295					300				
Val	Thr	Ala	Pro	His	Lys	Pro	Thr	Ser	Gly	Ile	Ile	Gly	Val	Asn	Lys
305					310					315					320
Lys	Gly	Gln	Val	Leu	Ser	Val	Cys	Val	Glu	Glu	Asp	Asn	Ile	Val	Asn
				325					330					335	
Tyr	Ala	Thr	Asn	Val	Leu	Gln	Asn	Pro	Asp	Leu	Gly	Leu	Arg	Leu	Ala
			340					345					350		
Val	Arg	Ser	Asn	Leu	Ala	Gly	Ala	Glu	Lys	Leu	Phe	Val	Arg	Lys	Phe
		355					360					365			
Asn	Thr	Leu	Phe	Ala	Gln	Gly	Ser	Tyr	Ala	Glu	Ala	Ala	Lys	Val	Ala
370						375					380				
Ala	Ser	Ala	Pro	Lys	Gly	Ile	Leu	Arg	Thr	Arg	Glu	Thr	Val	Gln	Lys
385					390					395					400
Phe	Gln	Ser	Ile	Pro	Ala	Gln	Ser	Gly	Gln	Ala	Ser	Pro	Leu	Leu	Gln
				405					410					415	
Tyr	Phe	Gly	Ile	Leu	Leu	Asp	Gln	Gly	Gln	Leu	Asn	Lys	Leu	Glu	Ser
			420					425					430		
Leu	Glu	Leu	Cys	His	Leu	Val	Leu	Gln	Gln	Gly	Arg	Lys	Gln	Leu	Leu
		435					440					445			
Glu	Lys	Trp	Leu	Lys	Glu	Asp	Lys	Leu	Glu	Cys	Ser	Glu	Glu	Leu	Gly
		450				455					460				
Asp	Leu	Val	Lys	Thr	Thr	Asp	Pro	Met	Leu	Ala	Leu	Ser	Val	Tyr	Leu
465					470					475					480
Arg	Ala	Asn	Val	Pro	Ser	Lys	Val	Ile	Gln	Cys	Phe	Ala	Glu	Thr	Gly
				485					490					495	
Gln	Phe	Gln	Lys	Ile	Val	Leu	Tyr	Ala	Lys	Lys	Val	Gly	Tyr	Thr	Pro
			500					505					510		
Asp	Trp	Ile	Phe	Leu	Leu	Arg	Gly	Val	Met	Lys	Ile	Ser	Pro	Glu	Gln
		515					520					525			
Gly	Leu	Gln	Phe	Ser	Arg	Met	Leu	Val	Gln	Asp	Glu	Glu	Pro	Leu	Ala



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Arg Tyr Leu Val Cys Arg Lys Asp Pro Glu Leu Trp Ala His Val Leu  
 945 950 955 960

Glu Glu Thr Asn Pro Ser Arg Arg Gln Leu Ile Asp Gln Val Val Gln  
 965 970 975

Thr Ala Leu Ser Glu Thr Arg Asp Pro Glu Glu Ile Ser Val Thr Val  
 980 985 990

Lys Ala Phe Met Thr Ala Asp Leu Pro Asn Glu Leu Ile Glu Leu Leu  
 995 1000 1005

Glu Lys Ile Val Leu Asp Asn Ser Val Phe Ser Glu His Arg Asn  
 1010 1015 1020

Leu Gln Asn Leu Leu Ile Leu Thr Ala Ile Lys Ala Asp Arg Thr  
 1025 1030 1035

Arg Val Met Glu Tyr Ile Ser Arg Leu Asp Asn Tyr Asp Ala Leu  
 1040 1045 1050

Asp Ile Ala Ser Ile Ala Val Ser Ser Ala Leu Tyr Glu Glu Ala  
 1055 1060 1065

Phe Thr Val Phe His Lys Phe Asp Met Asn Ala Ser Ala Ile Gln  
 1070 1075 1080

Val Leu Ile Glu His Ile Gly Asn Leu Asp Arg Ala Tyr Glu Phe  
 1085 1090 1095

Ala Glu Arg Cys Asn Glu Pro Ala Val Trp Ser Gln Leu Ala Gln  
 1100 1105 1110

Ala Gln Leu Gln Lys Asp Leu Val Lys Glu Ala Ile Asn Ser Tyr  
 1115 1120 1125

Ile Arg Gly Asp Asp Pro Ser Ser Tyr Leu Glu Val Val Gln Ser  
 1130 1135 1140

Ala Ser Arg Ser Asn Asn Trp Glu Asp Leu Val Lys Phe Leu Gln  
 1145 1150 1155

Met Ala Arg Lys Lys Gly Arg Glu Ser Tyr Ile Glu Thr Glu Leu  
 1160 1165 1170

Ile Phe Ala Leu Ala Lys Thr Ser Arg Val Ser Glu Leu Glu Asp  
 1175 1180 1185

Phe Ile Asn Gly Pro Asn Asn Ala His Ile Gln Gln Val Gly Asp  
 1190 1195 1200

Arg Cys Tyr Glu Glu Gly Met Tyr Glu Ala Ala Lys Leu Leu Tyr  
 1205 1210 1215

Ser Asn Val Ser Asn Phe Ala Arg Leu Ala Ser Thr Leu Val His  
 1220 1225 1230

Leu Gly Glu Tyr Gln Ala Ala Val Asp Asn Ser Arg Lys Ala Ser  
 1235 1240 1245

Ser Thr Arg Thr Trp Lys Glu Val Cys Phe Ala Cys Met Asp Gly  
 1250 1255 1260

Gln Glu Phe Arg Phe Ala Gln Leu Cys Gly Leu His Ile Val Ile  
 1265 1270 1275

His Ala Asp Glu Leu Glu Glu Leu Met Cys Tyr Tyr Gln Asp Arg  
 1280 1285 1290

Gly Tyr Phe Glu Glu Leu Ile Leu Leu Leu Glu Ala Ala Leu Gly  
 1295 1300 1305

Leu Glu Arg Ala His Met Gly Met Phe Thr Glu Leu Ala Ile Leu  
 1310 1315 1320



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Tyr Ser Lys Phe Lys Pro Gln Lys Met Leu Glu His Leu Glu Leu  
 1325 1330 1335  
 Phe Trp Ser Arg Val Asn Ile Pro Lys Val Leu Arg Ala Ala Glu  
 1340 1345 1350  
 Gln Ala His Leu Trp Ala Glu Leu Val Phe Leu Tyr Asp Lys Tyr  
 1355 1360 1365  
 Glu Glu Tyr Asp Asn Ala Val Leu Thr Met Met Ser His Pro Thr  
 1370 1375 1380  
 Glu Ala Trp Lys Glu Gly Gln Phe Lys Asp Ile Ile Thr Lys Val  
 1385 1390 1395  
 Ala Asn Val Glu Leu Cys Tyr Arg Ala Leu Gln Phe Tyr Leu Asp  
 1400 1405 1410  
 Tyr Lys Pro Leu Leu Ile Asn Asp Leu Leu Leu Val Leu Ser Pro  
 1415 1420 1425  
 Arg Leu Asp His Thr Trp Thr Val Ser Phe Phe Ser Lys Ala Gly  
 1430 1435 1440  
 Gln Leu Pro Leu Val Lys Pro Tyr Leu Arg Ser Val Gln Ser His  
 1445 1450 1455  
 Asn Asn Lys Ser Val Asn Glu Ala Leu Asn His Leu Leu Thr Glu  
 1460 1465 1470  
 Lys Glu Asp Tyr Gln Asp Ala Met Gln His Ala Ala Glu Ser Arg  
 1475 1480 1485  
 Asp Ala Glu Leu Ala Gln Lys Leu Leu Gln Trp Phe Leu Glu Glu  
 1490 1495 1500  
 Gly Lys Arg Glu Cys Phe Ala Ala Cys Leu Phe Thr Cys Tyr Asp  
 1505 1510 1515  
 Leu Leu Arg Pro Asp Met Val Leu Glu Leu Ala Trp Arg His Asn  
 1520 1525 1530  
 Leu Val Asp Leu Ala Met Pro Tyr Phe Ile Gln Val Met Arg Glu  
 1535 1540 1545  
 Tyr Leu Ser Lys Val Asp Lys Leu Asp Ala Leu Glu Ser Leu Pro  
 1550 1555 1560  
 Pro Ser Lys Arg Ser Met  
 1565

<210> SEQ ID NO 9  
 <211> LENGTH: 1639  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <300> PUBLICATION INFORMATION:  
 <308> DATABASE ACCESSION NUMBER: NCBI/AAH51800  
 <309> DATABASE ENTRY DATE: 2006-10-06  
 <313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(1639)

<400> SEQUENCE: 9

Met Ala Gln Ile Leu Pro Ile Arg Phe Gln Glu His Leu Gln Leu Gln  
 1 5 10 15  
 Asn Leu Gly Ile Asn Pro Ala Asn Ile Gly Phe Ser Thr Leu Thr Met  
 20 25 30  
 Glu Ser Asp Lys Phe Ile Cys Ile Arg Glu Lys Val Gly Glu Gln Ala  
 35 40 45  
 Gln Val Val Ile Ile Asp Met Asn Asp Pro Ser Asn Pro Ile Arg Arg  
 50 55 60  
 Pro Ile Ser Ala Asp Ser Ala Ile Met Asn Pro Ala Ser Lys Val Ile

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65	70	75	80
Ala Leu Lys Ala Gly Lys Thr Leu Gln Ile Phe Asn Ile Glu Met Lys	85	90	95
Ser Lys Met Lys Ala His Thr Met Thr Asp Asp Val Thr Phe Trp Lys	100	105	110
Trp Ile Ser Leu Asn Thr Val Ala Leu Val Thr Asp Asn Ala Val Tyr	115	120	125
His Trp Ser Met Glu Gly Glu Ser Gln Pro Val Lys Met Phe Asp Arg	130	135	140
His Ser Ser Leu Ala Gly Cys Gln Ile Ile Asn Tyr Arg Thr Asp Ala	145	150	155
Lys Gln Lys Trp Leu Leu Leu Thr Gly Ile Ser Ala Gln Gln Asn Arg	165	170	175
Val Val Gly Ala Met Gln Leu Tyr Ser Val Asp Arg Lys Val Ser Gln	180	185	190
Pro Ile Glu Gly His Ala Ala Ser Phe Ala Gln Phe Lys Met Glu Gly	195	200	205
Asn Ala Glu Glu Ser Thr Leu Phe Cys Phe Ala Val Arg Gly Gln Ala	210	215	220
Gly Gly Lys Leu His Ile Ile Glu Val Gly Thr Pro Pro Thr Gly Asn	225	230	235
Gln Pro Phe Pro Lys Lys Ala Val Asp Val Phe Phe Pro Pro Glu Ala	245	250	255
Gln Asn Asp Phe Pro Val Ala Met Gln Ile Ser Glu Lys His Asp Val	260	265	270
Val Phe Leu Ile Thr Lys Tyr Gly Tyr Ile His Leu Tyr Asp Leu Glu	275	280	285
Thr Gly Thr Cys Ile Tyr Met Asn Arg Ile Ser Gly Glu Thr Ile Phe	290	295	300
Val Thr Ala Pro His Glu Ala Thr Ala Gly Ile Ile Gly Val Asn Arg	305	310	315
Lys Gly Gln Val Leu Ser Val Cys Val Glu Glu Glu Asn Ile Ile Pro	325	330	335
Tyr Ile Thr Asn Val Leu Gln Asn Pro Asp Leu Ala Leu Arg Met Ala	340	345	350
Val Arg Asn Asn Leu Ala Gly Ala Glu Glu Leu Phe Ala Arg Lys Phe	355	360	365
Asn Ala Leu Phe Ala Gln Gly Asn Tyr Ser Glu Ala Ala Lys Val Ala	370	375	380
Ala Asn Ala Pro Lys Gly Ile Leu Arg Thr Pro Asp Thr Ile Arg Arg	385	390	395
Phe Gln Ser Val Pro Ala Gln Pro Gly Gln Thr Ser Pro Leu Leu Gln	405	410	415
Tyr Phe Gly Ile Leu Leu Asp Gln Gly Gln Leu Asn Lys Tyr Glu Ser	420	425	430
Leu Glu Leu Cys Arg Pro Val Leu Gln Gln Gly Arg Lys Gln Leu Leu	435	440	445
Glu Lys Trp Leu Lys Glu Asp Lys Leu Glu Cys Ser Glu Glu Leu Gly	450	455	460
Asp Leu Val Lys Ser Val Asp Pro Thr Leu Ala Leu Ser Val Tyr Leu	465	470	475
			480

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Arg	Ala	Asn	Val	Pro	Asn	Lys	Val	Ile	Gln	Cys	Phe	Ala	Glu	Thr	Gly
			485						490					495	
Gln	Val	Gln	Lys	Ile	Val	Leu	Tyr	Ala	Lys	Lys	Val	Gly	Tyr	Thr	Pro
			500					505					510		
Asp	Trp	Ile	Phe	Leu	Leu	Arg	Asn	Val	Met	Arg	Ile	Ser	Pro	Asp	Gln
		515					520					525			
Gly	Gln	Gln	Phe	Ala	Gln	Met	Leu	Val	Gln	Asp	Glu	Glu	Pro	Leu	Ala
	530					535					540				
Asp	Ile	Thr	Gln	Ile	Val	Asp	Val	Phe	Met	Glu	Tyr	Asn	Leu	Ile	Gln
545					550					555					560
Gln	Cys	Thr	Ala	Phe	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Asn	Arg	Pro	Ser
				565					570					575	
Glu	Gly	Pro	Leu	Gln	Thr	Arg	Leu	Leu	Glu	Met	Asn	Leu	Met	His	Ala
			580					585					590		
Pro	Gln	Val	Ala	Asp	Ala	Ile	Leu	Gly	Asn	Gln	Met	Phe	Thr	His	Tyr
		595					600					605			
Asp	Arg	Ala	His	Ile	Ala	Gln	Leu	Cys	Glu	Lys	Ala	Gly	Leu	Leu	Gln
	610					615					620				
Arg	Ala	Leu	Glu	His	Phe	Thr	Asp	Leu	Tyr	Asp	Ile	Lys	Arg	Ala	Val
625					630					635					640
Val	His	Thr	His	Leu	Leu	Asn	Pro	Glu	Trp	Leu	Val	Asn	Tyr	Phe	Gly
				645					650					655	
Ser	Leu	Ser	Val	Glu	Asp	Ser	Leu	Glu	Cys	Leu	Arg	Ala	Met	Leu	Ser
			660					665					670		
Ala	Asn	Ile	Arg	Gln	Asn	Leu	Gln	Ile	Cys	Val	Gln	Val	Ala	Ser	Lys
		675					680					685			
Tyr	His	Glu	Gln	Leu	Ser	Thr	Gln	Ser	Leu	Ile	Glu	Leu	Phe	Glu	Ser
	690					695					700				
Phe	Lys	Ser	Phe	Glu	Gly	Leu	Phe	Tyr	Phe	Leu	Gly	Ser	Ile	Val	Asn
705					710					715					720
Phe	Ser	Gln	Asp	Pro	Asp	Val	His	Phe	Lys	Tyr	Ile	Gln	Ala	Ala	Cys
				725					730					735	
Lys	Thr	Gly	Gln	Ile	Lys	Glu	Val	Glu	Arg	Ile	Cys	Arg	Glu	Ser	Asn
			740					745					750		
Cys	Tyr	Asp	Pro	Glu	Arg	Val	Lys	Asn	Phe	Leu	Lys	Glu	Ala	Lys	Leu
		755					760					765			
Thr	Asp	Gln	Leu	Pro	Leu	Ile	Ile	Val	Cys	Asp	Arg	Phe	Asp	Phe	Val
	770					775					780				
His	Asp	Leu	Val	Leu	Tyr	Leu	Tyr	Arg	Asn	Asn	Leu	Gln	Lys	Tyr	Ile
785					790					795					800
Glu	Ile	Tyr	Val	Gln	Lys	Val	Asn	Pro	Ser	Arg	Leu	Pro	Val	Val	Ile
				805					810					815	
Gly	Gly	Leu	Leu	Asp	Val	Asp	Cys	Ser	Glu	Asp	Val	Ile	Lys	Asn	Leu
			820					825					830		
Ile	Leu	Val	Val	Arg	Gly	Gln	Phe	Ser	Thr	Asp	Glu	Leu	Val	Ala	Glu
		835					840					845			
Val	Glu	Lys	Arg	Asn	Arg	Leu	Lys	Leu	Leu	Leu	Pro	Trp	Leu	Glu	Ala
	850					855					860				
Arg	Ile	His	Glu	Gly	Cys	Glu	Glu	Pro	Ala	Thr	His	Asn	Ala	Leu	Ala
865					870					875					880

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Lys Ile Tyr Ile Asp Ser Asn Asn Asn Pro Glu Arg Phe Leu Arg Glu  
885 890 895

Asn Pro Tyr Tyr Asp Ser Arg Val Val Gly Lys Tyr Cys Glu Lys Arg  
900 905 910

Asp Pro His Leu Ala Cys Val Ala Tyr Glu Arg Gly Gln Cys Asp Leu  
915 920 925

Glu Leu Ile Asn Val Cys Asn Glu Asn Ser Leu Phe Lys Ser Leu Ser  
930 935 940

Arg Tyr Leu Val Arg Arg Lys Asp Pro Glu Leu Trp Gly Ser Val Leu  
945 950 955 960

Leu Glu Ser Asn Pro Tyr Arg Arg Pro Leu Ile Asp Gln Val Val Gln  
965 970 975

Thr Ala Leu Ser Glu Thr Gln Asp Pro Glu Glu Val Ser Val Thr Val  
980 985 990

Lys Ala Phe Met Thr Ala Asp Leu Pro Asn Glu Leu Ile Glu Leu Leu  
995 1000 1005

Glu Lys Ile Val Leu Asp Asn Ser Val Phe Ser Glu His Arg Asn  
1010 1015 1020

Leu Gln Asn Leu Leu Ile Leu Thr Ala Ile Lys Ala Asp Arg Thr  
1025 1030 1035

Arg Val Met Glu Tyr Ile Asn Arg Leu Asp Asn Tyr Asp Ala Pro  
1040 1045 1050

Asp Ile Ala Asn Ile Ala Ile Ser Asn Glu Leu Phe Glu Glu Ala  
1055 1060 1065

Phe Ala Ile Phe Arg Lys Phe Asp Val Asn Thr Ser Ala Val Gln  
1070 1075 1080

Val Leu Ile Glu His Ile Gly Asn Leu Asp Arg Ala Tyr Glu Phe  
1085 1090 1095

Ala Glu Arg Cys Asn Glu Pro Ala Val Trp Ser Gln Leu Ala Lys  
1100 1105 1110

Ala Gln Leu Gln Lys Gly Met Val Lys Glu Ala Ile Asp Ser Tyr  
1115 1120 1125

Ile Lys Ala Asp Asp Pro Ser Ser Tyr Met Glu Val Val Gln Ala  
1130 1135 1140

Ala Asn Thr Ser Gly Asn Trp Glu Glu Leu Val Lys Tyr Leu Gln  
1145 1150 1155

Met Ala Arg Lys Lys Ala Arg Glu Ser Tyr Val Glu Thr Glu Leu  
1160 1165 1170

Ile Phe Ala Leu Ala Lys Thr Asn Arg Leu Ala Glu Leu Glu Glu  
1175 1180 1185

Phe Ile Asn Gly Pro Asn Asn Ala His Ile Gln Gln Val Gly Asp  
1190 1195 1200

Arg Cys Tyr Asp Glu Lys Met Tyr Asp Ala Ala Lys Leu Leu Tyr  
1205 1210 1215

Asn Asn Val Ser Asn Phe Gly Arg Leu Ala Ser Thr Leu Val His  
1220 1225 1230

Leu Gly Glu Tyr Gln Ala Ala Val Asp Gly Ala Arg Lys Ala Asn  
1235 1240 1245

Ser Thr Arg Thr Trp Lys Glu Val Cys Phe Ala Cys Val Asp Gly  
1250 1255 1260

Lys Glu Phe Arg Leu Ala Gln Met Cys Gly Leu His Ile Val Val

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1265	1270	1275
His Ala Asp Glu Leu Glu Glu	Leu Ile Asn Tyr Tyr	Gln Asp Arg
1280	1285	1290
Gly Tyr Phe Glu Glu Leu Ile	Thr Met Leu Glu Ala	Ala Leu Gly
1295	1300	1305
Leu Glu Arg Ala His Met Gly	Met Phe Thr Glu Leu	Ala Ile Leu
1310	1315	1320
Tyr Ser Lys Phe Lys Pro Gln	Lys Met Arg Glu His	Leu Glu Leu
1325	1330	1335
Phe Trp Ser Arg Val Asn Ile	Pro Lys Val Leu Arg	Ala Ala Glu
1340	1345	1350
Gln Ala His Leu Trp Ala Glu	Leu Val Phe Leu Tyr	Asp Lys Tyr
1355	1360	1365
Glu Glu Tyr Asp Asn Ala Ile	Ile Thr Met Met Asn	His Pro Thr
1370	1375	1380
Asp Ala Trp Lys Glu Gly Gln	Phe Lys Asp Ile Ile	Thr Lys Val
1385	1390	1395
Ala Asn Val Glu Leu Tyr Tyr	Arg Ala Ile Gln Phe	Tyr Leu Glu
1400	1405	1410
Phe Lys Pro Leu Leu Leu Asn	Asp Leu Leu Met Val	Leu Ser Pro
1415	1420	1425
Arg Leu Asp His Thr Arg Ala	Val Asn Tyr Phe Ser	Lys Val Lys
1430	1435	1440
Gln Leu Pro Leu Val Lys Pro	Tyr Leu Arg Ser Val	Gln Asn His
1445	1450	1455
Asn Asn Lys Ser Val Asn Glu	Ser Leu Asn Asn Leu	Phe Ile Thr
1460	1465	1470
Glu Glu Asp Tyr Gln Ala Leu	Arg Thr Ser Ile Asp	Ala Tyr Asp
1475	1480	1485
Asn Phe Asp Asn Ile Ser Leu	Ala Gln Arg Leu Glu	Lys His Glu
1490	1495	1500
Leu Ile Glu Phe Arg Arg Ile	Ala Ala Tyr Leu Phe	Lys Gly Asn
1505	1510	1515
Asn Arg Trp Lys Gln Ser Val	Glu Leu Cys Lys Lys	Asp Ser Leu
1520	1525	1530
Tyr Lys Asp Ala Met Gln Tyr	Ala Ser Glu Ser Lys	Asp Thr Glu
1535	1540	1545
Leu Ala Glu Glu Leu Leu Gln	Trp Phe Leu Gln Glu	Glu Lys Arg
1550	1555	1560
Glu Cys Phe Gly Ala Cys Leu	Phe Thr Cys Tyr Asp	Leu Leu Arg
1565	1570	1575
Pro Asp Val Val Leu Glu Thr	Ala Trp Arg His Asn	Ile Met Asp
1580	1585	1590
Phe Ala Met Pro Tyr Phe Ile	Gln Val Met Lys Glu	Tyr Leu Thr
1595	1600	1605
Lys Val Asp Lys Leu Asp Ala	Ser Glu Ser Leu Arg	Lys Glu Glu
1610	1615	1620
Glu Gln Ala Thr Glu Thr Gln	Pro Ile Val Tyr Gly	Asn Leu Ser
1625	1630	1635

Leu

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<210> SEQ ID NO 10
<211> LENGTH: 1626
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<300> PUBLICATION INFORMATION:
<308> DATABASE ACCESSION NUMBER: NCBI/AAB40908
<309> DATABASE ENTRY DATE: 1997-01-15
<313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(1626)

<400> SEQUENCE: 10

Met Ala Gln Ile Leu Pro Val Arg Phe Gln Glu His Phe Gln Leu Gln
1          5          10          15

Asn Leu Gly Ile Asn Pro Ala Asn Ile Gly Phe Ser Thr Leu Thr Met
20          25          30

Glu Ser Asp Lys Phe Ile Cys Ile Arg Glu Lys Val Gly Glu Gln Ala
35          40          45

Gln Val Thr Ile Ile Asp Met Ser Asp Pro Met Ala Pro Ile Arg Arg
50          55          60

Pro Ile Ser Ala Glu Ser Ala Ile Met Asn Pro Ala Ser Lys Val Ile
65          70          75          80

Ala Leu Lys Ala Gly Lys Thr Leu Gln Ile Phe Asn Ile Glu Met Lys
85          90          95

Ser Lys Met Lys Ala His Thr Met Ala Glu Glu Val Ile Phe Trp Lys
100         105         110

Trp Val Ser Val Asn Thr Val Ala Leu Val Thr Glu Thr Ala Val Tyr
115         120         125

His Trp Ser Met Glu Gly Asp Ser Gln Pro Met Lys Met Phe Asp Arg
130         135         140

His Thr Ser Leu Val Gly Cys Gln Val Ile His Tyr Arg Thr Asp Glu
145         150         155         160

Tyr Gln Lys Trp Leu Leu Leu Val Gly Ile Ser Ala Gln Gln Asn Arg
165         170         175

Val Val Gly Ala Met Gln Leu Tyr Ser Val Asp Arg Lys Val Ser Gln
180         185         190

Pro Ile Glu Gly His Ala Ala Ala Phe Ala Glu Phe Lys Met Glu Gly
195         200         205

Asn Ala Lys Pro Ala Thr Leu Phe Cys Phe Ala Val Arg Asn Pro Thr
210         215         220

Gly Gly Lys Leu His Ile Ile Glu Val Gly Gln Pro Ala Ala Gly Asn
225         230         235         240

Gln Pro Phe Val Lys Lys Ala Val Asp Val Phe Phe Pro Pro Glu Ala
245         250         255

Gln Asn Asp Phe Pro Val Ala Met Gln Ile Gly Ala Lys His Gly Val
260         265         270

Ile Tyr Leu Ile Thr Lys Tyr Gly Tyr Leu His Leu Tyr Asp Leu Glu
275         280         285

Ser Gly Val Cys Ile Cys Met Asn Arg Ile Ser Ala Asp Thr Ile Phe
290         295         300

Val Thr Ala Pro His Lys Pro Thr Ser Gly Ile Ile Gly Val Asn Lys
305         310         315         320

Lys Gly Gln Val Leu Ser Val Cys Val Glu Glu Asp Asn Ile Val Asn
325         330         335

Tyr Ala Thr Asn Val Leu Gln Asn Pro Asp Leu Gly Leu Arg Leu Ala

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340					345					350					
Val	Arg	Ser	Asn	Leu	Ala	Gly	Ala	Glu	Lys	Leu	Phe	Val	Arg	Lys	Phe
		355					360					365			
Asn	Thr	Leu	Phe	Ala	Gln	Gly	Ser	Tyr	Ala	Glu	Ala	Ala	Lys	Val	Ala
	370					375					380				
Ala	Ser	Ala	Pro	Lys	Gly	Ile	Leu	Arg	Thr	Arg	Glu	Thr	Val	Gln	Lys
385					390					395					400
Phe	Gln	Ser	Ile	Pro	Ala	Gln	Ser	Gly	Gln	Ala	Ser	Pro	Leu	Leu	Gln
				405					410					415	
Tyr	Phe	Gly	Ile	Leu	Leu	Asp	Gln	Gly	Gln	Leu	Asn	Lys	Leu	Glu	Ser
			420					425					430		
Leu	Glu	Leu	Cys	His	Leu	Val	Leu	Gln	Gln	Gly	Arg	Lys	Gln	Leu	Leu
		435					440					445			
Glu	Lys	Trp	Leu	Lys	Glu	Asp	Lys	Leu	Glu	Cys	Ser	Glu	Glu	Leu	Gly
	450					455					460				
Asp	Leu	Val	Lys	Thr	Thr	Asp	Pro	Met	Leu	Ala	Leu	Ser	Val	Tyr	Leu
465					470					475					480
Arg	Ala	Asn	Val	Pro	Ser	Lys	Val	Ile	Gln	Cys	Phe	Ala	Glu	Thr	Gly
				485					490					495	
Gln	Phe	Gln	Lys	Ile	Val	Leu	Tyr	Ala	Lys	Lys	Val	Gly	Tyr	Thr	Pro
			500					505					510		
Asp	Trp	Ile	Phe	Leu	Leu	Arg	Gly	Val	Met	Lys	Ile	Ser	Pro	Glu	Gln
	515						520					525			
Gly	Leu	Gln	Phe	Ser	Arg	Met	Leu	Val	Gln	Asp	Glu	Glu	Pro	Leu	Ala
	530					535					540				
Asn	Ile	Ser	Gln	Ile	Val	Asp	Ile	Phe	Met	Glu	Asn	Ser	Leu	Ile	Gln
545					550					555					560
Gln	Cys	Thr	Ser	Phe	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Asn	Arg	Pro	Ala
				565					570					575	
Glu	Gly	Leu	Leu	Gln	Thr	Trp	Leu	Leu	Glu	Met	Asn	Leu	Val	His	Ala
			580					585					590		
Pro	Gln	Val	Ala	Asp	Ala	Ile	Leu	Gly	Asn	Lys	Met	Phe	Thr	His	Tyr
		595					600					605			
Asp	Arg	Ala	His	Ile	Ala	Gln	Leu	Cys	Glu	Lys	Ala	Gly	Leu	Leu	Gln
	610					615					620				
Gln	Ala	Leu	Glu	His	Tyr	Thr	Asp	Leu	Tyr	Asp	Ile	Lys	Arg	Ala	Val
625					630					635					640
Val	His	Thr	His	Leu	Leu	Asn	Pro	Glu	Trp	Leu	Val	Asn	Phe	Phe	Gly
				645					650					655	
Ser	Leu	Ser	Val	Glu	Asp	Ser	Val	Glu	Cys	Leu	His	Ala	Met	Leu	Ser
			660					665					670		
Ala	Asn	Ile	Arg	Gln	Asn	Leu	Gln	Leu	Cys	Val	Gln	Val	Ala	Ser	Lys
		675					680					685			
Tyr	His	Lys	Gln	Leu	Gly	Thr	Gln	Ala	Leu	Val	Glu	Leu	Phe	Glu	Ser
	690					695					700				
Phe	Lys	Ser	Tyr	Lys	Gly	Leu	Phe	Tyr	Phe	Leu	Gly	Ser	Ile	Val	Asn
705					710					715					720
Phe	Ser	Gln	Asp	Pro	Asp	Val	His	Leu	Lys	Tyr	Ile	Gln	Ala	Ala	Cys
				725					730					735	
Lys	Thr	Gly	Gln	Ile	Lys	Glu	Val	Glu	Arg	Ile	Cys	Arg	Glu	Ser	Ser
			740					745					750		





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Ala	Ser	Arg	Ser	Asn	Asn	Trp	Glu	Asp	Leu	Val	Lys	Phe	Leu	Gln
1145						1150					1155			
Met	Ala	Arg	Lys	Lys	Gly	Arg	Glu	Ser	Tyr	Ile	Glu	Thr	Glu	Leu
1160						1165					1170			
Ile	Phe	Ala	Leu	Ala	Lys	Thr	Ser	Arg	Val	Ser	Glu	Leu	Glu	Asp
1175						1180					1185			
Phe	Ile	Asn	Gly	Pro	Asn	Asn	Ala	His	Ile	Gln	Gln	Val	Gly	Asp
1190						1195					1200			
Arg	Cys	Tyr	Glu	Glu	Gly	Met	Tyr	Glu	Ala	Ala	Lys	Leu	Leu	Tyr
1205						1210					1215			
Ser	Asn	Val	Ser	Asn	Phe	Ala	Arg	Leu	Ala	Ser	Thr	Leu	Val	His
1220						1225					1230			
Leu	Gly	Glu	Tyr	Gln	Ala	Ala	Val	Asp	Asn	Ser	Arg	Lys	Ala	Ser
1235						1240					1245			
Ser	Thr	Arg	Thr	Trp	Lys	Glu	Val	Cys	Phe	Ala	Cys	Met	Asp	Gly
1250						1255					1260			
Gln	Glu	Phe	Arg	Phe	Ala	Gln	Leu	Cys	Gly	Leu	His	Ile	Val	Ile
1265						1270					1275			
His	Ala	Asp	Glu	Leu	Glu	Glu	Leu	Met	Cys	Tyr	Tyr	Gln	Asp	Arg
1280						1285					1290			
Gly	Tyr	Phe	Glu	Glu	Leu	Ile	Leu	Leu	Leu	Glu	Ala	Ala	Leu	Gly
1295						1300					1305			
Leu	Glu	Arg	Ala	His	Met	Gly	Met	Phe	Thr	Glu	Leu	Ala	Ile	Leu
1310						1315					1320			
Tyr	Ser	Lys	Phe	Lys	Pro	Gln	Lys	Met	Leu	Glu	His	Leu	Glu	Leu
1325						1330					1335			
Phe	Trp	Ser	Arg	Val	Asn	Ile	Pro	Lys	Val	Leu	Arg	Ala	Ala	Glu
1340						1345					1350			
Gln	Ala	His	Leu	Trp	Ala	Glu	Leu	Val	Phe	Leu	Tyr	Asp	Lys	Tyr
1355						1360					1365			
Glu	Glu	Tyr	Asp	Asn	Ala	Val	Leu	Thr	Met	Met	Ser	His	Pro	Thr
1370						1375					1380			
Glu	Ala	Trp	Lys	Glu	Gly	Gln	Phe	Lys	Asp	Ile	Ile	Thr	Lys	Val
1385						1390					1395			
Ala	Asn	Val	Glu	Leu	Cys	Tyr	Arg	Ala	Leu	Gln	Phe	Tyr	Leu	Asp
1400						1405					1410			
Tyr	Lys	Pro	Leu	Leu	Ile	Asn	Asp	Leu	Leu	Leu	Val	Leu	Ser	Pro
1415						1420					1425			
Arg	Leu	Asp	His	Thr	Trp	Thr	Val	Ser	Phe	Phe	Ser	Lys	Ala	Gly
1430						1435					1440			
Gln	Leu	Pro	Leu	Val	Lys	Pro	Tyr	Leu	Arg	Ser	Val	Gln	Ser	His
1445						1450					1455			
Asn	Asn	Lys	Ser	Val	Asn	Glu	Ala	Leu	Asn	His	Leu	Leu	Thr	Glu
1460						1465					1470			
Lys	Glu	Asp	Tyr	Gln	Gly	Leu	Arg	Ala	Ser	Ile	Asp	Ala	Tyr	Asp
1475						1480					1485			
Asn	Phe	Asp	Asn	Ile	Ser	Leu	Ala	Gln	Gln	Leu	Glu	Lys	His	Gln
1490						1495					1500			
Leu	Met	Glu	Phe	Arg	Cys	Ile	Ala	Ala	Tyr	Leu	Tyr	Lys	Gly	Asn
1505						1510					1515			
Asn	Trp	Trp	Ala	Gln	Ser	Val	Glu	Leu	Cys	Lys	Lys	Asp	His	Leu

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1520	1525	1530
Tyr Lys Asp Ala Met Gln His Ala Ala Glu Ser Arg Asp Ala Glu		
1535	1540	1545
Leu Ala Gln Lys Leu Leu Gln Trp Phe Leu Glu Glu Gly Lys Arg		
1550	1555	1560
Glu Cys Phe Ala Ala Cys Leu Phe Thr Cys Tyr Asp Leu Leu Arg		
1565	1570	1575
Pro Asp Met Val Leu Glu Leu Ala Trp Arg His Asn Leu Val Asp		
1580	1585	1590
Leu Ala Met Pro Tyr Phe Ile Gln Val Met Arg Glu Tyr Leu Ser		
1595	1600	1605
Lys Val Asp Lys Leu Asp Ala Leu Glu Ser Leu Pro Pro Ser Lys		
1610	1615	1620
Arg Ser Met		
1625		

<210> SEQ ID NO 11  
 <211> LENGTH: 1639  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <300> PUBLICATION INFORMATION:  
 <308> DATABASE ACCESSION NUMBER: NCBI/EAW94398  
 <309> DATABASE ENTRY DATE: 2006-12-18  
 <313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(1639)

<400> SEQUENCE: 11

Met Ala Gln Ile Leu Pro Ile Arg Phe Gln Glu His Leu Gln Leu Gln		
1	5	10 15
Asn Leu Gly Ile Asn Pro Ala Asn Ile Gly Phe Ser Thr Leu Thr Met		
	20	25 30
Glu Ser Asp Lys Phe Ile Cys Ile Arg Glu Lys Val Gly Glu Gln Ala		
	35	40 45
Gln Val Val Ile Ile Asp Met Asn Asp Pro Ser Asn Pro Ile Arg Arg		
	50	55 60
Pro Ile Ser Ala Asp Ser Ala Ile Met Asn Pro Ala Ser Lys Val Ile		
	65	70 75 80
Ala Leu Lys Ala Gly Lys Thr Leu Gln Ile Phe Asn Ile Glu Met Lys		
	85	90 95
Ser Lys Met Lys Ala His Thr Met Thr Asp Asp Val Thr Phe Trp Lys		
	100	105 110
Trp Ile Ser Leu Asn Thr Val Ala Leu Val Thr Asp Asn Ala Val Tyr		
	115	120 125
His Trp Ser Met Glu Gly Glu Ser Gln Pro Val Lys Met Phe Asp Arg		
	130	135 140
His Ser Ser Leu Ala Gly Cys Gln Ile Ile Asn Tyr Arg Thr Asp Ala		
	145	150 155 160
Lys Gln Lys Trp Leu Leu Leu Thr Gly Ile Ser Ala Gln Gln Asn Arg		
	165	170 175
Val Val Gly Ala Met Gln Leu Tyr Ser Val Asp Arg Lys Val Ser Gln		
	180	185 190
Pro Ile Glu Gly His Ala Ala Ser Phe Ala Gln Phe Lys Met Glu Gly		
	195	200 205
Asn Ala Glu Glu Ser Thr Leu Phe Cys Phe Ala Val Arg Gly Gln Ala		
	210	215 220

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

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

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

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Phe Lys Pro Leu Leu Leu Asn Asp Leu Leu Met Val Leu Ser Pro  
 1415 1420 1425  
 Arg Leu Asp His Thr Arg Ala Val Asn Tyr Phe Ser Lys Val Lys  
 1430 1435 1440  
 Gln Leu Pro Leu Val Lys Pro Tyr Leu Arg Ser Val Gln Asn His  
 1445 1450 1455  
 Asn Asn Lys Ser Val Asn Glu Ser Leu Asn Asn Leu Phe Ile Thr  
 1460 1465 1470  
 Glu Glu Asp Tyr Gln Ala Leu Arg Thr Ser Ile Asp Ala Tyr Asp  
 1475 1480 1485  
 Asn Phe Asp Asn Ile Ser Leu Ala Gln Arg Leu Glu Lys His Glu  
 1490 1495 1500  
 Leu Ile Glu Phe Arg Arg Ile Ala Ala Tyr Leu Phe Lys Gly Asn  
 1505 1510 1515  
 Asn Arg Trp Lys Gln Ser Val Glu Leu Cys Lys Lys Asp Ser Leu  
 1520 1525 1530  
 Tyr Lys Asp Ala Met Gln Tyr Ala Ser Glu Ser Lys Asp Thr Glu  
 1535 1540 1545  
 Leu Ala Glu Glu Leu Leu Gln Trp Phe Leu Gln Glu Glu Lys Arg  
 1550 1555 1560  
 Glu Cys Phe Gly Ala Cys Leu Phe Thr Cys Tyr Asp Leu Leu Arg  
 1565 1570 1575  
 Pro Asp Val Val Leu Glu Thr Ala Trp Arg His Asn Ile Met Asp  
 1580 1585 1590  
 Phe Ala Met Pro Tyr Phe Ile Gln Val Met Lys Glu Tyr Leu Thr  
 1595 1600 1605  
 Lys Val Asp Lys Leu Asp Ala Ser Glu Ser Leu Arg Lys Glu Glu  
 1610 1615 1620  
 Glu Gln Ala Thr Glu Thr Gln Pro Ile Val Tyr Gly Asn Leu Ser  
 1625 1630 1635

Leu

<210> SEQ ID NO 12  
 <211> LENGTH: 248  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <300> PUBLICATION INFORMATION:  
 <308> DATABASE ACCESSION NUMBER: UniProtKB/P09496  
 <309> DATABASE ENTRY DATE: 2009-05-26  
 <313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(248)

&lt;400&gt; SEQUENCE: 12

Met Ala Glu Leu Asp Pro Phe Gly Ala Pro Ala Gly Ala Pro Gly Gly  
 1 5 10 15  
 Pro Ala Leu Gly Asn Gly Val Ala Gly Ala Gly Glu Glu Asp Pro Ala  
 20 25 30  
 Ala Ala Phe Leu Ala Gln Gln Glu Ser Glu Ile Ala Gly Ile Glu Asn  
 35 40 45  
 Asp Glu Ala Phe Ala Ile Leu Asp Gly Gly Ala Pro Gly Pro Gln Pro  
 50 55 60  
 His Gly Glu Pro Pro Gly Gly Pro Asp Ala Val Asp Gly Val Met Asn  
 65 70 75 80  
 Gly Glu Tyr Tyr Gln Glu Ser Asn Gly Pro Thr Asp Ser Tyr Ala Ala

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85					90					95					
Ile	Ser	Gln	Val	Asp	Arg	Leu	Gln	Ser	Glu	Pro	Glu	Ser	Ile	Arg	Lys
			100					105						110	
Trp	Arg	Glu	Glu	Gln	Met	Glu	Arg	Leu	Glu	Ala	Leu	Asp	Ala	Asn	Ser
		115						120				125			
Arg	Lys	Gln	Glu	Ala	Glu	Trp	Lys	Glu	Lys	Ala	Ile	Lys	Glu	Leu	Glu
		130					135				140				
Glu	Trp	Tyr	Ala	Arg	Gln	Asp	Glu	Gln	Leu	Gln	Lys	Thr	Lys	Ala	Asn
145					150					155					160
Asn	Arg	Val	Ala	Asp	Glu	Ala	Phe	Tyr	Lys	Gln	Pro	Phe	Ala	Asp	Val
				165					170					175	
Ile	Gly	Tyr	Val	Thr	Asn	Ile	Asn	His	Pro	Cys	Tyr	Ser	Leu	Glu	Gln
			180					185						190	
Ala	Ala	Glu	Glu	Ala	Phe	Val	Asn	Asp	Ile	Asp	Glu	Ser	Ser	Pro	Gly
		195					200					205			
Thr	Glu	Trp	Glu	Arg	Val	Ala	Arg	Leu	Cys	Asp	Phe	Asn	Pro	Lys	Ser
		210				215					220				
Ser	Lys	Gln	Ala	Lys	Asp	Val	Ser	Arg	Met	Arg	Ser	Val	Leu	Ile	Ser
225					230					235					240
Leu	Lys	Gln	Ala	Pro	Leu	Val	His								
				245											

&lt;210&gt; SEQ ID NO 13

&lt;211&gt; LENGTH: 229

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;300&gt; PUBLICATION INFORMATION:

&lt;308&gt; DATABASE ACCESSION NUMBER: UniProtKB/P09497

&lt;309&gt; DATABASE ENTRY DATE: 2009-05-26

&lt;313&gt; RELEVANT RESIDUES IN SEQ ID NO: (1)..(229)

&lt;400&gt; SEQUENCE: 13

Met	Ala	Asp	Asp	Phe	Gly	Phe	Phe	Ser	Ser	Ser	Glu	Ser	Gly	Ala	Pro
1				5					10					15	
Glu	Ala	Ala	Glu	Glu	Asp	Pro	Ala	Ala	Ala	Phe	Leu	Ala	Gln	Gln	Glu
			20					25					30		
Ser	Glu	Ile	Ala	Gly	Ile	Glu	Asn	Asp	Glu	Gly	Phe	Gly	Ala	Pro	Ala
		35					40					45			
Gly	Ser	His	Ala	Ala	Pro	Ala	Gln	Pro	Gly	Pro	Thr	Ser	Gly	Ala	Gly
		50				55					60				
Ser	Glu	Asp	Met	Gly	Thr	Thr	Val	Asn	Gly	Asp	Val	Phe	Gln	Glu	Ala
65					70					75					80
Asn	Gly	Pro	Ala	Asp	Gly	Tyr	Ala	Ala	Ile	Ala	Gln	Ala	Asp	Arg	Leu
				85					90					95	
Thr	Gln	Glu	Pro	Glu	Ser	Ile	Arg	Lys	Trp	Arg	Glu	Glu	Gln	Arg	Lys
			100					105						110	
Arg	Leu	Gln	Glu	Leu	Asp	Ala	Ala	Ser	Lys	Val	Thr	Glu	Gln	Glu	Trp
			115					120						125	
Arg	Glu	Lys	Ala	Lys	Lys	Asp	Leu	Glu	Glu	Trp	Asn	Gln	Arg	Gln	Ser
			130			135					140				
Glu	Gln	Val	Glu	Lys	Asn	Lys	Ile	Asn	Asn	Arg	Ile	Ala	Asp	Lys	Ala
145					150					155					160
Phe	Tyr	Gln	Gln	Pro	Asp	Ala	Asp	Ile	Ile	Gly	Tyr	Val	Ala	Ser	Glu
				165					170						175

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Glu Ala Phe Val Lys Glu Ser Lys Glu Glu Thr Pro Gly Thr Glu Trp  
 180 185 190

Glu Lys Val Ala Gln Leu Cys Asp Phe Asn Pro Lys Ser Ser Lys Gln  
 195 200 205

Cys Lys Asp Val Ser Arg Leu Arg Ser Val Leu Met Ser Leu Lys Gln  
 210 215 220

Thr Pro Leu Ser Arg  
 225

<210> SEQ ID NO 14  
 <211> LENGTH: 236  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <300> PUBLICATION INFORMATION:  
 <308> DATABASE ACCESSION NUMBER: NCBI/NP\_001070145  
 <309> DATABASE ENTRY DATE: 2008-05-01  
 <313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(236)

<400> SEQUENCE: 14

Met Ala Glu Leu Asp Pro Phe Gly Ala Pro Ala Gly Ala Pro Gly Gly  
 1 5 10 15

Pro Ala Leu Gly Asn Gly Val Ala Gly Ala Gly Glu Glu Asp Pro Ala  
 20 25 30

Ala Ala Phe Leu Ala Gln Gln Glu Ser Glu Ile Ala Gly Ile Glu Asn  
 35 40 45

Asp Glu Ala Phe Ala Ile Leu Asp Gly Gly Ala Pro Gly Pro Gln Pro  
 50 55 60

His Gly Glu Pro Pro Gly Gly Pro Asp Ala Val Asp Gly Val Met Asn  
 65 70 75 80

Gly Glu Tyr Tyr Gln Glu Ser Asn Gly Pro Thr Asp Ser Tyr Ala Ala  
 85 90 95

Ile Ser Gln Val Asp Arg Leu Gln Ser Glu Pro Glu Ser Ile Arg Lys  
 100 105 110

Trp Arg Glu Glu Gln Met Glu Arg Leu Glu Ala Leu Asp Ala Asn Ser  
 115 120 125

Arg Lys Gln Glu Ala Glu Trp Lys Glu Lys Ala Ile Lys Glu Leu Glu  
 130 135 140

Glu Trp Tyr Ala Arg Gln Asp Glu Gln Leu Gln Lys Thr Lys Ala Asn  
 145 150 155 160

Asn Arg Val Ala Asp Glu Ala Phe Tyr Lys Gln Pro Phe Ala Asp Val  
 165 170 175

Ile Gly Tyr Val Ala Ala Glu Glu Ala Phe Val Asn Asp Ile Asp Glu  
 180 185 190

Ser Ser Pro Gly Thr Glu Trp Glu Arg Val Ala Arg Leu Cys Asp Phe  
 195 200 205

Asn Pro Lys Ser Ser Lys Gln Ala Lys Asp Val Ser Arg Met Arg Ser  
 210 215 220

Val Leu Ile Ser Leu Lys Gln Ala Pro Leu Val His  
 225 230 235

<210> SEQ ID NO 15  
 <211> LENGTH: 1224  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <300> PUBLICATION INFORMATION:



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<308> DATABASE ACCESSION NUMBER: UniProtKB/P53621

<309> DATABASE ENTRY DATE: 2009-05-26

<313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(1224)

<400> SEQUENCE: 15

Met Leu Thr Lys Phe Glu Thr Lys Ser Ala Arg Val Lys Gly Leu Ser  
1 5 10 15

Phe His Pro Lys Arg Pro Trp Ile Leu Thr Ser Leu His Asn Gly Val  
20 25 30

Ile Gln Leu Trp Asp Tyr Arg Met Cys Thr Leu Ile Asp Lys Phe Asp  
35 40 45

Glu His Asp Gly Pro Val Arg Gly Ile Asp Phe His Lys Gln Gln Pro  
50 55 60

Leu Phe Val Ser Gly Gly Asp Asp Tyr Lys Ile Lys Val Trp Asn Tyr  
65 70 75 80

Lys Leu Arg Arg Cys Leu Phe Thr Leu Leu Gly His Leu Asp Tyr Ile  
85 90 95

Arg Thr Thr Phe Phe His His Glu Tyr Pro Trp Ile Leu Ser Ala Ser  
100 105 110

Asp Asp Gln Thr Ile Arg Val Trp Asn Trp Gln Ser Arg Thr Cys Val  
115 120 125

Cys Val Leu Thr Gly His Asn His Tyr Val Met Cys Ala Gln Phe His  
130 135 140

Pro Thr Glu Asp Leu Val Val Ser Ala Ser Leu Asp Gln Thr Val Arg  
145 150 155 160

Val Trp Asp Ile Ser Gly Leu Arg Lys Lys Asn Leu Ser Pro Gly Ala  
165 170 175

Val Glu Ser Asp Val Arg Gly Ile Thr Gly Val Asp Leu Phe Gly Thr  
180 185 190

Thr Asp Ala Val Val Lys His Val Leu Glu Gly His Asp Arg Gly Val  
195 200 205

Asn Trp Ala Ala Phe His Pro Thr Met Pro Leu Ile Val Ser Gly Ala  
210 215 220

Asp Asp Arg Gln Val Lys Ile Trp Arg Met Asn Glu Ser Lys Ala Trp  
225 230 235 240

Glu Val Asp Thr Cys Arg Gly His Tyr Asn Asn Val Ser Cys Ala Val  
245 250 255

Phe His Pro Arg Gln Glu Leu Ile Leu Ser Asn Ser Glu Asp Lys Ser  
260 265 270

Ile Arg Val Trp Asp Met Ser Lys Arg Thr Gly Val Gln Thr Phe Arg  
275 280 285

Arg Asp His Asp Arg Phe Trp Val Leu Ala Ala His Pro Asn Leu Asn  
290 295 300

Leu Phe Ala Ala Gly His Asp Gly Gly Met Ile Val Phe Lys Leu Glu  
305 310 315 320

Arg Glu Arg Pro Ala Tyr Ala Val His Gly Asn Met Leu His Tyr Val  
325 330 335

Lys Asp Arg Phe Leu Arg Gln Leu Asp Phe Asn Ser Ser Lys Asp Val  
340 345 350

Ala Val Met Gln Leu Arg Ser Gly Ser Lys Phe Pro Val Phe Asn Met  
355 360 365

Ser Tyr Asn Pro Ala Glu Asn Ala Val Leu Leu Cys Thr Arg Ala Ser

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

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Ile Pro Asp Ile Asp Pro Asn Ala Lys Leu Leu Gln Pro Pro Ala Pro  
 785 790 795 800

Ile Met Pro Leu Asp Thr Asn Trp Pro Leu Leu Thr Val Ser Lys Gly  
 805 810 815

Phe Phe Glu Gly Thr Ile Ala Ser Lys Gly Lys Gly Gly Ala Leu Ala  
 820 825 830

Ala Asp Ile Asp Ile Asp Thr Val Gly Thr Glu Gly Trp Gly Glu Asp  
 835 840 845

Ala Glu Leu Gln Leu Asp Glu Asp Gly Phe Val Glu Ala Thr Glu Gly  
 850 855 860

Leu Gly Asp Asp Ala Leu Gly Lys Gly Gln Glu Glu Gly Gly Gly Trp  
 865 870 875 880

Asp Val Glu Glu Asp Leu Glu Leu Pro Pro Glu Leu Asp Ile Ser Pro  
 885 890 895

Gly Ala Ala Gly Gly Ala Glu Asp Gly Phe Phe Val Pro Pro Thr Lys  
 900 905 910

Gly Thr Ser Pro Thr Gln Ile Trp Cys Asn Asn Ser Gln Leu Pro Val  
 915 920 925

Asp His Ile Leu Ala Gly Ser Phe Glu Thr Ala Met Arg Leu Leu His  
 930 935 940

Asp Gln Val Gly Val Ile Gln Phe Gly Pro Tyr Lys Gln Leu Phe Leu  
 945 950 955 960

Gln Thr Tyr Ala Arg Gly Arg Thr Thr Tyr Gln Ala Leu Pro Cys Leu  
 965 970 975

Pro Ser Met Tyr Gly Tyr Pro Asn Arg Asn Trp Lys Asp Ala Gly Leu  
 980 985 990

Lys Asn Gly Val Pro Ala Val Gly Leu Lys Leu Asn Asp Leu Ile Gln  
 995 1000 1005

Arg Leu Gln Leu Cys Tyr Gln Leu Thr Thr Val Gly Lys Phe Glu  
 1010 1015 1020

Glu Ala Val Glu Lys Phe Arg Ser Ile Leu Leu Ser Val Pro Leu  
 1025 1030 1035

Leu Val Val Asp Asn Lys Gln Glu Ile Ala Glu Ala Gln Gln Leu  
 1040 1045 1050

Ile Thr Ile Cys Arg Glu Tyr Ile Val Gly Leu Ser Val Glu Thr  
 1055 1060 1065

Glu Arg Lys Lys Leu Pro Lys Glu Thr Leu Glu Gln Gln Lys Arg  
 1070 1075 1080

Ile Cys Glu Met Ala Ala Tyr Phe Thr His Ser Asn Leu Gln Pro  
 1085 1090 1095

Val His Met Ile Leu Val Leu Arg Thr Ala Leu Asn Leu Phe Phe  
 1100 1105 1110

Lys Leu Lys Asn Phe Lys Thr Ala Ala Thr Phe Ala Arg Arg Leu  
 1115 1120 1125

Leu Glu Leu Gly Pro Lys Pro Glu Val Ala Gln Gln Thr Arg Lys  
 1130 1135 1140

Ile Leu Ser Ala Cys Glu Lys Asn Pro Thr Asp Ala Tyr Gln Leu  
 1145 1150 1155

Asn Tyr Asp Met His Asn Pro Phe Asp Ile Cys Ala Ala Ser Tyr  
 1160 1165 1170

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Arg Pro Ile Tyr Arg Gly Lys Pro Val Glu Lys Cys Pro Leu Ser  
 1175 1180 1185

Gly Ala Cys Tyr Ser Pro Glu Phe Lys Gly Gln Ile Cys Arg Val  
 1190 1195 1200

Thr Thr Val Thr Glu Ile Gly Lys Asp Val Ile Gly Leu Arg Ile  
 1205 1210 1215

Ser Pro Leu Gln Phe Arg  
 1220

<210> SEQ ID NO 16  
 <211> LENGTH: 1224  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <300> PUBLICATION INFORMATION:  
 <308> DATABASE ACCESSION NUMBER: NCBI/NP\_004362  
 <309> DATABASE ENTRY DATE: 2008-05-11  
 <313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(1224)

<400> SEQUENCE: 16

Met Leu Thr Lys Phe Glu Thr Lys Ser Ala Arg Val Lys Gly Leu Ser  
 1 5 10 15

Phe His Pro Lys Arg Pro Trp Ile Leu Thr Ser Leu His Asn Gly Val  
 20 25 30

Ile Gln Leu Trp Asp Tyr Arg Met Cys Thr Leu Ile Asp Lys Phe Asp  
 35 40 45

Glu His Asp Gly Pro Val Arg Gly Ile Asp Phe His Lys Gln Gln Pro  
 50 55 60

Leu Phe Val Ser Gly Gly Asp Asp Tyr Lys Ile Lys Val Trp Asn Tyr  
 65 70 75 80

Lys Leu Arg Arg Cys Leu Phe Thr Leu Leu Gly His Leu Asp Tyr Ile  
 85 90 95

Arg Thr Thr Phe Phe His His Glu Tyr Pro Trp Ile Leu Ser Ala Ser  
 100 105 110

Asp Asp Gln Thr Ile Arg Val Trp Asn Trp Gln Ser Arg Thr Cys Val  
 115 120 125

Cys Val Leu Thr Gly His Asn His Tyr Val Met Cys Ala Gln Phe His  
 130 135 140

Pro Thr Glu Asp Leu Val Val Ser Ala Ser Leu Asp Gln Thr Val Arg  
 145 150 155 160

Val Trp Asp Ile Ser Gly Leu Arg Lys Lys Asn Leu Ser Pro Gly Ala  
 165 170 175

Val Glu Ser Asp Val Arg Gly Ile Thr Gly Val Asp Leu Phe Gly Thr  
 180 185 190

Thr Asp Ala Val Val Lys His Val Leu Glu Gly His Asp Arg Gly Val  
 195 200 205

Asn Trp Ala Ala Phe His Pro Thr Met Pro Leu Ile Val Ser Gly Ala  
 210 215 220

Asp Asp Arg Gln Val Lys Ile Trp Arg Met Asn Glu Ser Lys Ala Trp  
 225 230 235 240

Glu Val Asp Thr Cys Arg Gly His Tyr Asn Asn Val Ser Cys Ala Val  
 245 250 255

Phe His Pro Arg Gln Glu Leu Ile Leu Ser Asn Ser Glu Asp Lys Ser  
 260 265 270

Ile Arg Val Trp Asp Met Ser Lys Arg Thr Gly Val Gln Thr Phe Arg

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275					280					285					
Arg	Asp	His	Asp	Arg	Phe	Trp	Val	Leu	Ala	Ala	His	Pro	Asn	Leu	Asn
290					295					300					
Leu	Phe	Ala	Ala	Gly	His	Asp	Gly	Gly	Met	Ile	Val	Phe	Lys	Leu	Glu
305					310					315					320
Arg	Glu	Arg	Pro	Ala	Tyr	Ala	Val	His	Gly	Asn	Met	Leu	His	Tyr	Val
325					330					335					
Lys	Asp	Arg	Phe	Leu	Arg	Gln	Leu	Asp	Phe	Asn	Ser	Ser	Lys	Asp	Val
340					345					350					
Ala	Val	Met	Gln	Leu	Arg	Ser	Gly	Ser	Lys	Phe	Pro	Val	Phe	Asn	Met
355					360					365					
Ser	Tyr	Asn	Pro	Ala	Glu	Asn	Ala	Val	Leu	Leu	Cys	Thr	Arg	Ala	Ser
370					375					380					
Asn	Leu	Glu	Asn	Ser	Thr	Tyr	Asp	Leu	Tyr	Thr	Ile	Pro	Lys	Asp	Ala
385					390					395					400
Asp	Ser	Gln	Asn	Pro	Asp	Ala	Pro	Glu	Gly	Lys	Arg	Ser	Ser	Gly	Leu
405					410					415					
Thr	Ala	Val	Trp	Val	Ala	Arg	Asn	Arg	Phe	Ala	Val	Leu	Asp	Arg	Met
420					425					430					
His	Ser	Leu	Leu	Ile	Lys	Asn	Leu	Lys	Asn	Glu	Ile	Thr	Lys	Lys	Val
435					440					445					
Gln	Val	Pro	Asn	Cys	Asp	Glu	Ile	Phe	Tyr	Ala	Gly	Thr	Gly	Asn	Leu
450					455					460					
Leu	Leu	Arg	Asp	Ala	Asp	Ser	Ile	Thr	Leu	Phe	Asp	Val	Gln	Gln	Lys
465					470					475					480
Arg	Thr	Leu	Ala	Ser	Val	Lys	Ile	Ser	Lys	Val	Lys	Tyr	Val	Ile	Trp
485					490					495					
Ser	Ala	Asp	Met	Ser	His	Val	Ala	Leu	Leu	Ala	Lys	His	Ala	Ile	Val
500					505					510					
Ile	Cys	Asn	Arg	Lys	Leu	Asp	Ala	Leu	Cys	Asn	Ile	His	Glu	Asn	Ile
515					520					525					
Arg	Val	Lys	Ser	Gly	Ala	Trp	Asp	Glu	Ser	Gly	Val	Phe	Ile	Tyr	Thr
530					535					540					
Thr	Ser	Asn	His	Ile	Lys	Tyr	Ala	Val	Thr	Thr	Gly	Asp	His	Gly	Ile
545					550					555					560
Ile	Arg	Thr	Leu	Asp	Leu	Pro	Ile	Tyr	Val	Thr	Arg	Val	Lys	Gly	Asn
565					570					575					
Asn	Val	Tyr	Cys	Leu	Asp	Arg	Glu	Cys	Arg	Pro	Arg	Val	Leu	Thr	Ile
580					585					590					
Asp	Pro	Thr	Glu	Phe	Lys	Phe	Lys	Leu	Ala	Leu	Ile	Asn	Arg	Lys	Tyr
595					600					605					
Asp	Glu	Val	Leu	His	Met	Val	Arg	Asn	Ala	Lys	Leu	Val	Gly	Gln	Ser
610					615					620					
Ile	Ile	Ala	Tyr	Leu	Gln	Lys	Lys	Gly	Tyr	Pro	Glu	Val	Ala	Leu	His
625					630					635					640
Phe	Val	Lys	Asp	Glu	Lys	Thr	Arg	Phe	Ser	Leu	Ala	Leu	Glu	Cys	Gly
645					650					655					
Asn	Ile	Glu	Ile	Ala	Leu	Glu	Ala	Ala	Lys	Ala	Leu	Asp	Asp	Lys	Asn
660					665					670					
Cys	Trp	Glu	Lys	Leu	Gly	Glu	Val	Ala	Leu	Leu	Gln	Gly	Asn	His	Gln
675					680					685					

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Ile Val Glu Met Cys Tyr Gln Arg Thr Lys Asn Phe Asp Lys Leu Ser  
 690 695 700

Phe Leu Tyr Leu Ile Thr Gly Asn Leu Glu Lys Leu Arg Lys Met Met  
 705 710 715 720

Lys Ile Ala Glu Ile Arg Lys Asp Met Ser Gly His Tyr Gln Asn Ala  
 725 730 735

Leu Tyr Leu Gly Asp Val Ser Glu Arg Val Arg Ile Leu Lys Asn Cys  
 740 745 750

Gly Gln Lys Ser Leu Ala Tyr Leu Thr Ala Ala Thr His Gly Leu Asp  
 755 760 765

Glu Glu Ala Glu Ser Leu Lys Glu Thr Phe Asp Pro Glu Lys Glu Thr  
 770 775 780

Ile Pro Asp Ile Asp Pro Asn Ala Lys Leu Leu Gln Pro Pro Ala Pro  
 785 790 795 800

Ile Met Pro Leu Asp Thr Asn Trp Pro Leu Leu Thr Val Ser Lys Gly  
 805 810 815

Phe Phe Glu Gly Thr Ile Ala Ser Lys Gly Lys Gly Gly Ala Leu Ala  
 820 825 830

Ala Asp Ile Asp Ile Asp Thr Val Gly Thr Glu Gly Trp Gly Glu Asp  
 835 840 845

Ala Glu Leu Gln Leu Asp Glu Asp Gly Phe Val Glu Ala Thr Glu Gly  
 850 855 860

Leu Gly Asp Asp Ala Leu Gly Lys Gly Gln Glu Glu Gly Gly Gly Trp  
 865 870 875 880

Asp Val Glu Glu Asp Leu Glu Leu Pro Pro Glu Leu Asp Ile Ser Pro  
 885 890 895

Gly Ala Ala Gly Gly Ala Glu Asp Gly Phe Phe Val Pro Pro Thr Lys  
 900 905 910

Gly Thr Ser Pro Thr Gln Ile Trp Cys Asn Asn Ser Gln Leu Pro Val  
 915 920 925

Asp His Ile Leu Ala Gly Ser Phe Glu Thr Ala Met Arg Leu Leu His  
 930 935 940

Asp Gln Val Gly Val Ile Gln Phe Gly Pro Tyr Lys Gln Leu Phe Leu  
 945 950 955 960

Gln Thr Tyr Ala Arg Gly Arg Thr Thr Tyr Gln Ala Leu Pro Cys Leu  
 965 970 975

Pro Ser Met Tyr Gly Tyr Pro Asn Arg Asn Trp Lys Asp Ala Gly Leu  
 980 985 990

Lys Asn Gly Val Pro Ala Val Gly Leu Lys Leu Asn Asp Leu Ile Gln  
 995 1000 1005

Arg Leu Gln Leu Cys Tyr Gln Leu Thr Thr Val Gly Lys Phe Glu  
 1010 1015 1020

Glu Ala Val Glu Lys Phe Arg Ser Ile Leu Leu Ser Val Pro Leu  
 1025 1030 1035

Leu Val Val Asp Asn Lys Gln Glu Ile Ala Glu Ala Gln Gln Leu  
 1040 1045 1050

Ile Thr Ile Cys Arg Glu Tyr Ile Val Gly Leu Ser Val Glu Thr  
 1055 1060 1065

Glu Arg Lys Lys Leu Pro Lys Glu Thr Leu Glu Gln Gln Lys Arg  
 1070 1075 1080

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Ile Cys Glu Met Ala Ala Tyr Phe Thr His Ser Asn Leu Gln Pro
 1085                               1090           1095

Val His Met Ile Leu Val Leu Arg Thr Ala Leu Asn Leu Phe Phe
 1100                               1105           1110

Lys Leu Lys Asn Phe Lys Thr Ala Ala Thr Phe Ala Arg Arg Leu
 1115                               1120           1125

Leu Glu Leu Gly Pro Lys Pro Glu Val Ala Gln Gln Thr Arg Lys
 1130                               1135           1140

Ile Leu Ser Ala Cys Glu Lys Asn Pro Thr Asp Ala Tyr Gln Leu
 1145                               1150           1155

Asn Tyr Asp Met His Asn Pro Phe Asp Ile Cys Ala Ala Ser Tyr
 1160                               1165           1170

Arg Pro Ile Tyr Arg Gly Lys Pro Val Glu Lys Cys Pro Leu Ser
 1175                               1180           1185

Gly Ala Cys Tyr Ser Pro Glu Phe Lys Gly Gln Ile Cys Arg Val
 1190                               1195           1200

Thr Thr Val Thr Glu Ile Gly Lys Asp Val Ile Gly Leu Arg Ile
 1205                               1210           1215

Ser Pro Leu Gln Phe Arg
 1220

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<210> SEQ ID NO 17
<211> LENGTH: 1233
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<300> PUBLICATION INFORMATION:
<308> DATABASE ACCESSION NUMBER: NCBI/NP_001091868
<309> DATABASE ENTRY DATE: 2008-05-11
<313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(1233)

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<400> SEQUENCE: 17

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Met Leu Thr Lys Phe Glu Thr Lys Ser Ala Arg Val Lys Gly Leu Ser
 1                               5           10           15

Phe His Pro Lys Arg Pro Trp Ile Leu Thr Ser Leu His Asn Gly Val
                               20           25           30

Ile Gln Leu Trp Asp Tyr Arg Met Cys Thr Leu Ile Asp Lys Phe Asp
 35                               40           45

Glu His Asp Gly Pro Val Arg Gly Ile Asp Phe His Lys Gln Gln Pro
 50                               55           60

Leu Phe Val Ser Gly Gly Asp Asp Tyr Lys Ile Lys Val Trp Asn Tyr
 65                               70           75           80

Lys Leu Arg Arg Cys Leu Phe Thr Leu Leu Gly His Leu Asp Tyr Ile
                               85           90           95

Arg Thr Thr Phe Phe His His Glu Tyr Pro Trp Ile Leu Ser Ala Ser
 100                              105           110

Asp Asp Gln Thr Ile Arg Val Trp Asn Trp Gln Ser Arg Thr Cys Val
 115                              120           125

Cys Val Leu Thr Gly His Asn His Tyr Val Met Cys Ala Gln Phe His
 130                              135           140

Pro Thr Glu Asp Leu Val Val Ser Ala Ser Leu Asp Gln Thr Val Arg
 145                              150           155           160

Val Trp Asp Ile Ser Gly Leu Arg Lys Lys Asn Leu Ser Pro Gly Ala
 165                              170           175

Val Glu Ser Asp Val Arg Gly Ile Thr Gly Val Asp Leu Phe Gly Thr

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180				185				190							
Thr	Asp	Ala	Val	Val	Lys	His	Val	Leu	Glu	Gly	His	Asp	Arg	Gly	Val
195				200				205							
Asn	Trp	Ala	Ala	Phe	His	Pro	Thr	Met	Pro	Leu	Ile	Val	Ser	Gly	Ala
210				215				220							
Asp	Asp	Arg	Gln	Val	Lys	Ile	Trp	Arg	Met	Asn	Glu	Ser	Lys	Ala	Trp
225				230				235							
Glu	Val	Asp	Thr	Cys	Arg	Gly	His	Tyr	Asn	Asn	Val	Ser	Cys	Ala	Val
245				250				255							
Phe	His	Pro	Arg	Gln	Glu	Leu	Ile	Leu	Ser	Asn	Ser	Glu	Asp	Lys	Ser
260				265				270							
Ile	Arg	Val	Trp	Asp	Met	Ser	Lys	Arg	Thr	Gly	Val	Gln	Thr	Phe	Arg
275				280				285							
Arg	Asp	His	Asp	Arg	Phe	Trp	Val	Leu	Ala	Ala	His	Pro	Asn	Leu	Asn
290				295				300							
Leu	Phe	Ala	Ala	Gly	His	Asp	Gly	Gly	Met	Ile	Val	Phe	Lys	Leu	Glu
305				310				315							
Arg	Glu	Arg	Pro	Ala	Tyr	Ala	Val	His	Gly	Asn	Met	Leu	His	Tyr	Val
325				330				335							
Lys	Asp	Arg	Phe	Leu	Arg	Gln	Leu	Asp	Phe	Asn	Ser	Ser	Lys	Asp	Val
340				345				350							
Ala	Val	Met	Gln	Leu	Arg	Ser	Gly	Ser	Lys	Phe	Pro	Val	Phe	Asn	Met
355				360				365							
Ser	Tyr	Asn	Pro	Ala	Glu	Asn	Ala	Val	Leu	Leu	Cys	Thr	Arg	Ala	Ser
370				375				380							
Asn	Leu	Glu	Asn	Ser	Thr	Tyr	Asp	Leu	Tyr	Thr	Ile	Pro	Lys	Asp	Ala
385				390				395							
Asp	Ser	Gln	Asn	Pro	Asp	Ala	Pro	Glu	Gly	Lys	Arg	Ser	Ser	Gly	Leu
405				410				415							
Thr	Ala	Val	Trp	Val	Ala	Arg	Asn	Arg	Phe	Ala	Val	Leu	Asp	Arg	Met
420				425				430							
His	Ser	Leu	Leu	Ile	Lys	Asn	Leu	Lys	Asn	Glu	Ile	Thr	Lys	Lys	Val
435				440				445							
Gln	Val	Pro	Asn	Cys	Asp	Glu	Ile	Phe	Tyr	Ala	Gly	Thr	Gly	Asn	Leu
450				455				460							
Leu	Leu	Arg	Asp	Ala	Asp	Ser	Ile	Thr	Leu	Phe	Asp	Val	Gln	Gln	Lys
465				470				475							
Arg	Thr	Leu	Ala	Ser	Val	Lys	Ile	Ser	Lys	Val	Lys	Tyr	Val	Ile	Trp
485				490				495							
Ser	Ala	Asp	Met	Ser	His	Val	Ala	Leu	Leu	Ala	Lys	His	Glu	His	Ser
500				505				510							
Cys	Pro	Leu	Pro	Leu	Thr	Ala	Ile	Val	Ile	Cys	Asn	Arg	Lys	Leu	Asp
515				520				525							
Ala	Leu	Cys	Asn	Ile	His	Glu	Asn	Ile	Arg	Val	Lys	Ser	Gly	Ala	Trp
530				535				540							
Asp	Glu	Ser	Gly	Val	Phe	Ile	Tyr	Thr	Thr	Ser	Asn	His	Ile	Lys	Tyr
545				550				555							
Ala	Val	Thr	Thr	Gly	Asp	His	Gly	Ile	Ile	Arg	Thr	Leu	Asp	Leu	Pro
565				570				575							
Ile	Tyr	Val	Thr	Arg	Val	Lys	Gly	Asn	Asn	Val	Tyr	Cys	Leu	Asp	Arg
580				585				590							



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

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Asn Arg Asn Trp Lys Asp Ala Gly Leu Lys Asn Gly Val Pro Ala Val
      995                1000                1005

Gly Leu Lys Leu Asn Asp Leu Ile Gln Arg Leu Gln Leu Cys Tyr
  1010                1015                1020

Gln Leu Thr Thr Val Gly Lys Phe Glu Glu Ala Val Glu Lys Phe
  1025                1030                1035

Arg Ser Ile Leu Leu Ser Val Pro Leu Leu Val Val Asp Asn Lys
  1040                1045                1050

Gln Glu Ile Ala Glu Ala Gln Gln Leu Ile Thr Ile Cys Arg Glu
  1055                1060                1065

Tyr Ile Val Gly Leu Ser Val Glu Thr Glu Arg Lys Lys Leu Pro
  1070                1075                1080

Lys Glu Thr Leu Glu Gln Gln Lys Arg Ile Cys Glu Met Ala Ala
  1085                1090                1095

Tyr Phe Thr His Ser Asn Leu Gln Pro Val His Met Ile Leu Val
  1100                1105                1110

Leu Arg Thr Ala Leu Asn Leu Phe Phe Lys Leu Lys Asn Phe Lys
  1115                1120                1125

Thr Ala Ala Thr Phe Ala Arg Arg Leu Leu Glu Leu Gly Pro Lys
  1130                1135                1140

Pro Glu Val Ala Gln Gln Thr Arg Lys Ile Leu Ser Ala Cys Glu
  1145                1150                1155

Lys Asn Pro Thr Asp Ala Tyr Gln Leu Asn Tyr Asp Met His Asn
  1160                1165                1170

Pro Phe Asp Ile Cys Ala Ala Ser Tyr Arg Pro Ile Tyr Arg Gly
  1175                1180                1185

Lys Pro Val Glu Lys Cys Pro Leu Ser Gly Ala Cys Tyr Ser Pro
  1190                1195                1200

Glu Phe Lys Gly Gln Ile Cys Arg Val Thr Thr Val Thr Glu Ile
  1205                1210                1215

Gly Lys Asp Val Ile Gly Leu Arg Ile Ser Pro Leu Gln Phe Arg
  1220                1225                1230

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&lt;210&gt; SEQ ID NO 18

&lt;211&gt; LENGTH: 953

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;300&gt; PUBLICATION INFORMATION:

&lt;308&gt; DATABASE ACCESSION NUMBER: UniProtKB/P53618

&lt;309&gt; DATABASE ENTRY DATE: 2009-05-05

&lt;313&gt; RELEVANT RESIDUES IN SEQ ID NO: (1)..(953)

&lt;400&gt; SEQUENCE: 18

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Met Thr Ala Ala Glu Asn Val Cys Tyr Thr Leu Ile Asn Val Pro Met
1                5                10                15

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Asp Ser Glu Pro Pro Ser Glu Ile Ser Leu Lys Asn Asp Leu Glu Lys
      20                25                30

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Gly Asp Val Lys Ser Lys Thr Glu Ala Leu Lys Lys Val Ile Ile Met
      35                40                45

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Ile Leu Asn Gly Glu Lys Leu Pro Gly Leu Leu Met Thr Ile Ile Arg
      50                55                60

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Phe Val Leu Pro Leu Gln Asp His Thr Ile Lys Lys Leu Leu Leu Val
      65                70                75                80

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Phe Trp Glu Ile Val Pro Lys Thr Thr Pro Asp Gly Arg Leu Leu His

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85					90					95					
Glu	Met	Ile	Leu	Val	Cys	Asp	Ala	Tyr	Arg	Lys	Asp	Leu	Gln	His	Pro
			100						105				110		
Asn	Glu	Phe	Ile	Arg	Gly	Ser	Thr	Leu	Arg	Phe	Leu	Cys	Lys	Leu	Lys
		115					120					125			
Glu	Ala	Glu	Leu	Leu	Glu	Pro	Leu	Met	Pro	Ala	Ile	Arg	Ala	Cys	Leu
	130					135					140				
Glu	His	Arg	His	Ser	Tyr	Val	Arg	Arg	Asn	Ala	Val	Leu	Ala	Ile	Tyr
145					150					155					160
Thr	Ile	Tyr	Arg	Asn	Phe	Glu	His	Leu	Ile	Pro	Asp	Ala	Pro	Glu	Leu
				165					170					175	
Ile	His	Asp	Phe	Leu	Val	Asn	Glu	Lys	Asp	Ala	Ser	Cys	Lys	Arg	Asn
			180					185					190		
Ala	Phe	Met	Met	Leu	Ile	His	Ala	Asp	Gln	Asp	Arg	Ala	Leu	Asp	Tyr
		195					200					205			
Leu	Ser	Thr	Cys	Ile	Asp	Gln	Val	Gln	Thr	Phe	Gly	Asp	Ile	Leu	Gln
	210					215					220				
Leu	Val	Ile	Val	Glu	Leu	Ile	Tyr	Lys	Val	Cys	His	Ala	Asn	Pro	Ser
225					230					235					240
Glu	Arg	Ala	Arg	Phe	Ile	Arg	Cys	Ile	Tyr	Asn	Leu	Leu	Gln	Ser	Ser
				245						250				255	
Ser	Pro	Ala	Val	Lys	Tyr	Glu	Ala	Ala	Gly	Thr	Leu	Val	Thr	Leu	Ser
			260					265					270		
Ser	Ala	Pro	Thr	Ala	Ile	Lys	Ala	Ala	Ala	Gln	Cys	Tyr	Ile	Asp	Leu
		275					280					285			
Ile	Ile	Lys	Glu	Ser	Asp	Asn	Asn	Val	Lys	Leu	Ile	Val	Leu	Asp	Arg
290						295					300				
Leu	Ile	Glu	Leu	Lys	Glu	His	Pro	Ala	His	Glu	Arg	Val	Leu	Gln	Asp
305					310					315					320
Leu	Val	Met	Asp	Ile	Leu	Arg	Val	Leu	Ser	Thr	Pro	Asp	Leu	Glu	Val
				325					330					335	
Arg	Lys	Lys	Thr	Leu	Gln	Leu	Ala	Leu	Asp	Leu	Val	Ser	Ser	Arg	Asn
			340					345						350	
Val	Glu	Glu	Leu	Val	Ile	Val	Leu	Lys	Lys	Glu	Val	Ile	Lys	Thr	Asn
			355				360					365			
Asn	Val	Ser	Glu	His	Glu	Asp	Thr	Asp	Lys	Tyr	Arg	Gln	Leu	Leu	Val
						375					380				
Arg	Thr	Leu	His	Ser	Cys	Ser	Val	Arg	Phe	Pro	Asp	Met	Ala	Ala	Asn
385					390					395					400
Val	Ile	Pro	Val	Leu	Met	Glu	Phe	Leu	Ser	Asp	Asn	Asn	Glu	Ala	Ala
				405					410					415	
Ala	Ala	Asp	Val	Leu	Glu	Phe	Val	Arg	Glu	Ala	Ile	Gln	Arg	Phe	Asp
			420					425					430		
Asn	Leu	Arg	Met	Leu	Ile	Val	Glu	Lys	Met	Leu	Glu	Val	Phe	His	Ala
			435				440					445			
Ile	Lys	Ser	Val	Lys	Ile	Tyr	Arg	Gly	Ala	Leu	Trp	Ile	Leu	Gly	Glu
						455					460				
Tyr	Cys	Ser	Thr	Lys	Glu	Asp	Ile	Gln	Ser	Val	Met	Thr	Glu	Ile	Arg
465					470					475					480
Arg	Ser	Leu	Gly	Glu	Ile	Pro	Ile	Val	Glu	Ser	Glu	Ile	Lys	Lys	Glu
				485					490					495	

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Ala Gly Glu Leu Lys Pro Glu Glu Glu Ile Thr Val Gly Pro Val Gln  
500 505 510

Lys Leu Val Thr Glu Met Gly Thr Tyr Ala Thr Gln Ser Ala Leu Ser  
515 520 525

Ser Ser Arg Pro Thr Lys Lys Glu Glu Asp Arg Pro Pro Leu Arg Gly  
530 535 540

Phe Leu Leu Asp Gly Asp Phe Phe Val Ala Ala Ser Leu Ala Thr Thr  
545 550 555 560

Leu Thr Lys Ile Ala Leu Arg Tyr Val Ala Leu Val Gln Glu Lys Lys  
565 570 575

Lys Gln Asn Ser Phe Val Ala Glu Ala Met Leu Leu Met Ala Thr Ile  
580 585 590

Leu His Leu Gly Lys Ser Ser Leu Pro Lys Lys Pro Ile Thr Asp Asp  
595 600 605

Asp Val Asp Arg Ile Ser Leu Cys Leu Lys Val Leu Ser Glu Cys Ser  
610 615 620

Pro Leu Met Asn Asp Ile Phe Asn Lys Glu Cys Arg Gln Ser Leu Ser  
625 630 635 640

His Met Leu Ser Ala Lys Leu Glu Glu Glu Lys Leu Ser Gln Lys Lys  
645 650 655

Glu Ser Glu Lys Arg Asn Val Thr Val Gln Pro Asp Asp Pro Ile Ser  
660 665 670

Phe Met Gln Leu Thr Ala Lys Asn Glu Met Asn Cys Lys Glu Asp Gln  
675 680 685

Phe Gln Leu Ser Leu Leu Ala Ala Met Gly Asn Thr Gln Arg Lys Glu  
690 695 700

Ala Ala Asp Pro Leu Ala Ser Lys Leu Asn Lys Val Thr Gln Leu Thr  
705 710 715 720

Gly Phe Ser Asp Pro Val Tyr Ala Glu Ala Tyr Val His Val Asn Gln  
725 730 735

Tyr Asp Ile Val Leu Asp Val Leu Val Val Asn Gln Thr Ser Asp Thr  
740 745 750

Leu Gln Asn Cys Thr Leu Glu Leu Ala Thr Leu Gly Asp Leu Lys Leu  
755 760 765

Val Glu Lys Pro Ser Pro Leu Thr Leu Ala Pro His Asp Phe Ala Asn  
770 775 780

Ile Lys Ala Asn Val Lys Val Ala Ser Thr Glu Asn Gly Ile Ile Phe  
785 790 795 800

Gly Asn Ile Val Tyr Asp Val Ser Gly Ala Ala Ser Asp Arg Asn Cys  
805 810 815

Val Val Leu Ser Asp Ile His Ile Asp Ile Met Asp Tyr Ile Gln Pro  
820 825 830

Ala Thr Cys Thr Asp Ala Glu Phe Arg Gln Met Trp Ala Glu Phe Glu  
835 840 845

Trp Glu Asn Lys Val Thr Val Asn Thr Asn Met Val Asp Leu Asn Asp  
850 855 860

Tyr Leu Gln His Ile Leu Lys Ser Thr Asn Met Lys Cys Leu Thr Pro  
865 870 875 880

Glu Lys Ala Leu Ser Gly Tyr Cys Gly Phe Met Ala Ala Asn Leu Tyr  
885 890 895

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Ala Arg Ser Ile Phe Gly Glu Asp Ala Leu Ala Asn Val Ser Ile Glu  
                   900                  905                  910

Lys Pro Ile His Gln Gly Pro Asp Ala Ala Val Thr Gly His Ile Arg  
                   915                  920                  925

Ile Arg Ala Lys Ser Gln Gly Met Ala Leu Ser Leu Gly Asp Lys Ile  
           930                  935                  940

Asn Leu Ser Gln Lys Lys Thr Ser Ile  
 945                  950

<210> SEQ ID NO 19  
 <211> LENGTH: 906  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <300> PUBLICATION INFORMATION:  
 <308> DATABASE ACCESSION NUMBER: UniProtKB/P35606  
 <309> DATABASE ENTRY DATE: 2009-05-05  
 <313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(906)

<400> SEQUENCE: 19

Met Pro Leu Arg Leu Asp Ile Lys Arg Lys Leu Thr Ala Arg Ser Asp  
 1                  5                  10                  15

Arg Val Lys Ser Val Asp Leu His Pro Thr Glu Pro Trp Met Leu Ala  
                   20                  25                  30

Ser Leu Tyr Asn Gly Ser Val Cys Val Trp Asn His Glu Thr Gln Thr  
           35                  40                  45

Leu Val Lys Thr Phe Glu Val Cys Asp Leu Pro Val Arg Ala Ala Lys  
   50                  55                  60

Phe Val Ala Arg Lys Asn Trp Val Val Thr Gly Ala Asp Asp Met Gln  
 65                  70                  75                  80

Ile Arg Val Phe Asn Tyr Asn Thr Leu Glu Arg Val His Met Phe Glu  
                   85                  90                  95

Ala His Ser Asp Tyr Ile Arg Cys Ile Ala Val His Pro Thr Gln Pro  
           100                  105                  110

Phe Ile Leu Thr Ser Ser Asp Asp Met Leu Ile Lys Leu Trp Asp Trp  
   115                  120                  125

Asp Lys Lys Trp Ser Cys Ser Gln Val Phe Glu Gly His Thr His Tyr  
   130                  135                  140

Val Met Gln Ile Val Ile Asn Pro Lys Asp Asn Asn Gln Phe Ala Ser  
 145                  150                  155                  160

Ala Ser Leu Asp Arg Thr Ile Lys Val Trp Gln Leu Gly Ser Ser Ser  
           165                  170                  175

Pro Asn Phe Thr Leu Glu Gly His Glu Lys Gly Val Asn Cys Ile Asp  
           180                  185                  190

Tyr Tyr Ser Gly Gly Asp Lys Pro Tyr Leu Ile Ser Gly Ala Asp Asp  
   195                  200                  205

Arg Leu Val Lys Ile Trp Asp Tyr Gln Asn Lys Thr Cys Val Gln Thr  
   210                  215                  220

Leu Glu Gly His Ala Gln Asn Val Ser Cys Ala Ser Phe His Pro Glu  
 225                  230                  235                  240

Leu Pro Ile Ile Ile Thr Gly Ser Glu Asp Gly Thr Val Arg Ile Trp  
           245                  250                  255

His Ser Ser Thr Tyr Arg Leu Glu Ser Thr Leu Asn Tyr Gly Met Glu  
           260                  265                  270

Arg Val Trp Cys Val Ala Ser Leu Arg Gly Ser Asn Asn Val Ala Leu

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275					280					285					
Gly	Tyr	Asp	Glu	Gly	Ser	Ile	Ile	Val	Lys	Leu	Gly	Arg	Glu	Glu	Pro
290					295					300					
Ala	Met	Ser	Met	Asp	Ala	Asn	Gly	Lys	Ile	Ile	Trp	Ala	Lys	His	Ser
305					310					315					320
Glu	Val	Gln	Gln	Ala	Asn	Leu	Lys	Ala	Met	Gly	Asp	Ala	Glu	Ile	Lys
				325					330					335	
Asp	Gly	Glu	Arg	Leu	Pro	Leu	Ala	Val	Lys	Asp	Met	Gly	Ser	Cys	Glu
			340					345						350	
Ile	Tyr	Pro	Gln	Thr	Ile	Gln	His	Asn	Pro	Asn	Gly	Arg	Phe	Val	Val
		355					360					365			
Val	Cys	Gly	Asp	Gly	Glu	Tyr	Ile	Ile	Tyr	Thr	Ala	Met	Ala	Leu	Arg
	370					375					380				
Asn	Lys	Ser	Phe	Gly	Ser	Ala	Gln	Glu	Phe	Ala	Trp	Ala	His	Asp	Ser
385					390					395					400
Ser	Glu	Tyr	Ala	Ile	Arg	Glu	Ser	Asn	Ser	Ile	Val	Lys	Ile	Phe	Lys
			405						410					415	
Asn	Phe	Lys	Glu	Lys	Lys	Ser	Phe	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ser
			420					425					430		
Ile	Tyr	Gly	Gly	Phe	Leu	Leu	Gly	Val	Arg	Ser	Val	Asn	Gly	Leu	Ala
		435					440					445			
Phe	Tyr	Asp	Trp	Asp	Asn	Thr	Glu	Leu	Ile	Arg	Arg	Ile	Glu	Ile	Gln
		450				455					460				
Pro	Lys	His	Ile	Phe	Trp	Ser	Asp	Ser	Gly	Glu	Leu	Val	Cys	Ile	Ala
465					470					475					480
Thr	Glu	Glu	Ser	Phe	Phe	Ile	Leu	Lys	Tyr	Leu	Ser	Glu	Lys	Val	Leu
				485					490					495	
Ala	Ala	Gln	Glu	Thr	His	Glu	Gly	Val	Thr	Glu	Asp	Gly	Ile	Glu	Asp
			500					505					510		
Ala	Phe	Glu	Val	Leu	Gly	Glu	Ile	Gln	Glu	Ile	Val	Lys	Thr	Gly	Leu
		515					520					525			
Trp	Val	Gly	Asp	Cys	Phe	Ile	Tyr	Thr	Ser	Ser	Val	Asn	Arg	Leu	Asn
	530					535					540				
Tyr	Tyr	Val	Gly	Gly	Glu	Ile	Val	Thr	Ile	Ala	His	Leu	Asp	Arg	Thr
545					550					555					560
Met	Tyr	Leu	Leu	Gly	Tyr	Ile	Pro	Lys	Asp	Asn	Arg	Leu	Tyr	Leu	Gly
				565					570					575	
Asp	Lys	Glu	Leu	Asn	Ile	Ile	Ser	Tyr	Ser	Leu	Leu	Val	Ser	Val	Leu
			580					585					590		
Glu	Tyr	Gln	Thr	Ala	Val	Met	Arg	Arg	Asp	Phe	Ser	Met	Ala	Asp	Lys
		595					600					605			
Val	Leu	Pro	Thr	Ile	Pro	Lys	Glu	Gln	Arg	Thr	Arg	Val	Ala	His	Phe
	610					615					620				
Leu	Glu	Lys	Gln	Gly	Phe	Lys	Gln	Gln	Ala	Leu	Thr	Val	Ser	Thr	Asp
625					630					635					640
Pro	Glu	His	Arg	Phe	Glu	Leu	Ala	Leu	Gln	Leu	Gly	Glu	Leu	Lys	Ile
				645					650					655	
Ala	Tyr	Gln	Leu	Ala	Val	Glu	Ala	Glu	Ser	Glu	Gln	Lys	Trp	Lys	Gln
			660					665					670		
Leu	Ala	Glu	Leu	Ala	Ile	Ser	Lys	Cys	Gln	Phe	Gly	Leu	Ala	Gln	Glu
		675					680					685			

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Cys Leu His His Ala Gln Asp Tyr Gly Gly Leu Leu Leu Leu Ala Thr  
 690 695 700  
 Ala Ser Gly Asn Ala Asn Met Val Asn Lys Leu Ala Glu Gly Ala Glu  
 705 710 715 720  
 Arg Asp Gly Lys Asn Asn Val Ala Phe Met Ser Tyr Phe Leu Gln Gly  
 725 730 735  
 Lys Val Asp Ala Cys Leu Glu Leu Leu Ile Arg Thr Gly Arg Leu Pro  
 740 745 750  
 Glu Ala Ala Phe Leu Ala Arg Thr Tyr Leu Pro Ser Gln Val Ser Arg  
 755 760 765  
 Val Val Lys Leu Trp Arg Glu Asn Leu Ser Lys Val Asn Gln Lys Ala  
 770 775 780  
 Ala Glu Ser Leu Ala Asp Pro Thr Glu Tyr Glu Asn Leu Phe Pro Gly  
 785 790 795 800  
 Leu Lys Glu Ala Phe Val Val Glu Glu Trp Val Lys Glu Thr His Ala  
 805 810 815  
 Asp Leu Trp Pro Ala Lys Gln Tyr Pro Leu Val Thr Pro Asn Glu Glu  
 820 825 830  
 Arg Asn Val Met Glu Glu Gly Lys Asp Phe Gln Pro Ser Arg Ser Thr  
 835 840 845  
 Ala Gln Gln Glu Leu Asp Gly Lys Pro Ala Ser Pro Thr Pro Val Ile  
 850 855 860  
 Val Ala Ser His Thr Ala Asn Lys Glu Glu Lys Ser Leu Leu Glu Leu  
 865 870 875 880  
 Glu Val Asp Leu Asp Asn Leu Glu Leu Glu Asp Ile Asp Thr Thr Asp  
 885 890 895  
 Ile Asn Leu Asp Glu Asp Ile Leu Asp Asp  
 900 905

<210> SEQ ID NO 20  
 <211> LENGTH: 877  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <300> PUBLICATION INFORMATION:  
 <308> DATABASE ACCESSION NUMBER: NCBI/EAW79040  
 <309> DATABASE ENTRY DATE: 2006-12-18  
 <313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(877)

<400> SEQUENCE: 20

Met Leu Ala Ser Leu Tyr Asn Gly Ser Val Cys Val Trp Asn His Glu  
 1 5 10 15  
 Thr Gln Thr Leu Val Lys Thr Phe Glu Val Cys Asp Leu Pro Val Arg  
 20 25 30  
 Ala Ala Lys Phe Val Ala Arg Lys Asn Trp Val Val Thr Gly Ala Asp  
 35 40 45  
 Asp Met Gln Ile Arg Val Phe Asn Tyr Asn Thr Leu Glu Arg Val His  
 50 55 60  
 Met Phe Glu Ala His Ser Asp Tyr Ile Arg Cys Ile Ala Val His Pro  
 65 70 75 80  
 Thr Gln Pro Phe Ile Leu Thr Ser Ser Asp Asp Met Leu Ile Lys Leu  
 85 90 95  
 Trp Asp Trp Asp Lys Lys Trp Ser Cys Ser Gln Val Phe Glu Gly His  
 100 105 110

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Thr	His	Tyr	Val	Met	Gln	Ile	Val	Ile	Asn	Pro	Lys	Asp	Asn	Asn	Gln
		115					120					125			
Phe	Ala	Ser	Ala	Ser	Leu	Asp	Arg	Thr	Ile	Lys	Val	Trp	Gln	Leu	Gly
	130					135					140				
Ser	Ser	Ser	Pro	Asn	Phe	Thr	Leu	Glu	Gly	His	Glu	Lys	Gly	Val	Asn
145					150					155					160
Cys	Ile	Asp	Tyr	Tyr	Ser	Gly	Gly	Asp	Lys	Pro	Tyr	Leu	Ile	Ser	Gly
				165					170					175	
Ala	Asp	Asp	Arg	Leu	Val	Lys	Ile	Trp	Asp	Tyr	Gln	Asn	Lys	Thr	Cys
			180						185				190		
Val	Gln	Thr	Leu	Glu	Gly	His	Ala	Gln	Asn	Val	Ser	Cys	Ala	Ser	Phe
		195					200					205			
His	Pro	Glu	Leu	Pro	Ile	Ile	Ile	Thr	Gly	Ser	Glu	Asp	Gly	Thr	Val
	210					215					220				
Arg	Ile	Trp	His	Ser	Ser	Thr	Tyr	Arg	Leu	Glu	Ser	Thr	Leu	Asn	Tyr
225					230					235					240
Gly	Met	Glu	Arg	Val	Trp	Cys	Val	Ala	Ser	Leu	Arg	Gly	Ser	Asn	Asn
				245					250					255	
Val	Ala	Leu	Gly	Tyr	Asp	Glu	Gly	Ser	Ile	Ile	Val	Lys	Leu	Gly	Arg
			260					265					270		
Glu	Glu	Pro	Ala	Met	Ser	Met	Asp	Ala	Asn	Gly	Lys	Ile	Ile	Trp	Ala
		275					280					285			
Lys	His	Ser	Glu	Val	Gln	Gln	Ala	Asn	Leu	Lys	Ala	Met	Gly	Asp	Ala
	290					295					300				
Glu	Ile	Lys	Asp	Gly	Glu	Arg	Leu	Pro	Leu	Ala	Val	Lys	Asp	Met	Gly
305					310					315					320
Ser	Cys	Glu	Ile	Tyr	Pro	Gln	Thr	Ile	Gln	His	Asn	Pro	Asn	Gly	Arg
				325					330					335	
Phe	Val	Val	Val	Cys	Gly	Asp	Gly	Glu	Tyr	Ile	Ile	Tyr	Thr	Ala	Met
			340					345					350		
Ala	Leu	Arg	Asn	Lys	Ser	Phe	Gly	Ser	Ala	Gln	Glu	Phe	Ala	Trp	Ala
		355					360					365			
His	Asp	Ser	Ser	Glu	Tyr	Ala	Ile	Arg	Glu	Ser	Asn	Ser	Ile	Val	Lys
	370					375					380				
Ile	Phe	Lys	Asn	Phe	Lys	Glu	Lys	Lys	Ser	Phe	Lys	Pro	Asp	Phe	Gly
385					390					395					400
Ala	Glu	Ser	Ile	Tyr	Gly	Gly	Phe	Leu	Leu	Gly	Val	Arg	Ser	Val	Asn
				405					410					415	
Gly	Leu	Ala	Phe	Tyr	Asp	Trp	Asp	Asn	Thr	Glu	Leu	Ile	Arg	Arg	Ile
			420					425					430		
Glu	Ile	Gln	Pro	Lys	His	Ile	Phe	Trp	Ser	Asp	Ser	Gly	Glu	Leu	Val
		435					440					445			
Cys	Ile	Ala	Thr	Glu	Glu	Ser	Phe	Phe	Ile	Leu	Lys	Tyr	Leu	Ser	Glu
	450					455					460				
Lys	Val	Leu	Ala	Ala	Gln	Glu	Thr	His	Glu	Gly	Val	Thr	Glu	Asp	Gly
465					470					475					480
Ile	Glu	Asp	Ala	Phe	Glu	Val	Leu	Gly	Glu	Ile	Gln	Glu	Ile	Val	Lys
				485					490					495	
Thr	Gly	Leu	Trp	Val	Gly	Asp	Cys	Phe	Ile	Tyr	Thr	Ser	Ser	Val	Asn
			500					505					510		
Arg	Leu	Asn	Tyr	Tyr	Val	Gly	Gly	Glu	Ile	Val	Thr	Ile	Ala	His	Leu



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Asp	Arg	Thr	Met	Tyr	Leu	Leu	Gly	Tyr	Ile	Pro	Lys	Asp	Asn	Arg	Leu
	530					535					540				
Tyr	Leu	Gly	Asp	Lys	Glu	Leu	Asn	Ile	Ile	Ser	Tyr	Ser	Leu	Leu	Val
545					550					555					560
Ser	Val	Leu	Glu	Tyr	Gln	Thr	Ala	Val	Met	Arg	Arg	Asp	Phe	Ser	Met
				565					570					575	
Ala	Asp	Lys	Val	Leu	Pro	Thr	Ile	Pro	Lys	Glu	Gln	Arg	Thr	Arg	Val
			580					585					590		
Ala	His	Phe	Leu	Glu	Lys	Gln	Gly	Phe	Lys	Gln	Gln	Ala	Leu	Thr	Val
		595					600					605			
Ser	Thr	Asp	Pro	Glu	His	Arg	Phe	Glu	Leu	Ala	Leu	Gln	Leu	Gly	Glu
	610					615						620			
Leu	Lys	Ile	Ala	Tyr	Gln	Leu	Ala	Val	Glu	Ala	Glu	Ser	Glu	Gln	Lys
625					630					635					640
Trp	Lys	Gln	Leu	Ala	Glu	Leu	Ala	Ile	Ser	Lys	Cys	Gln	Phe	Gly	Leu
				645					650					655	
Ala	Gln	Glu	Cys	Leu	His	His	Ala	Gln	Asp	Tyr	Gly	Gly	Leu	Leu	Leu
			660					665					670		
Leu	Ala	Thr	Ala	Ser	Gly	Asn	Ala	Asn	Met	Val	Asn	Lys	Leu	Ala	Glu
		675					680					685			
Gly	Ala	Glu	Arg	Asp	Gly	Lys	Asn	Asn	Val	Ala	Phe	Met	Ser	Tyr	Phe
	690					695					700				
Leu	Gln	Gly	Lys	Val	Asp	Ala	Cys	Leu	Glu	Leu	Leu	Ile	Arg	Thr	Gly
705					710					715					720
Arg	Leu	Pro	Glu	Ala	Ala	Phe	Leu	Ala	Arg	Thr	Tyr	Leu	Pro	Ser	Gln
				725					730					735	
Val	Ser	Arg	Val	Val	Lys	Leu	Trp	Arg	Glu	Asn	Leu	Ser	Lys	Val	Asn
			740					745					750		
Gln	Lys	Ala	Ala	Glu	Ser	Leu	Ala	Asp	Pro	Thr	Glu	Tyr	Glu	Asn	Leu
		755					760					765			
Phe	Pro	Gly	Leu	Lys	Glu	Ala	Phe	Val	Val	Glu	Glu	Trp	Val	Lys	Glu
	770					775					780				
Thr	His	Ala	Asp	Leu	Trp	Pro	Ala	Lys	Gln	Tyr	Pro	Leu	Val	Thr	Pro
785					790					795					800
Asn	Glu	Glu	Arg	Asn	Val	Met	Glu	Glu	Gly	Lys	Asp	Phe	Gln	Pro	Ser
				805					810					815	
Arg	Ser	Thr	Ala	Gln	Gln	Glu	Leu	Asp	Gly	Lys	Pro	Ala	Ser	Pro	Thr
			820					825					830		
Pro	Val	Ile	Val	Ala	Ser	His	Thr	Ala	Asn	Lys	Glu	Glu	Lys	Ser	Leu
		835					840					845			
Leu	Glu	Leu	Glu	Val	Asp	Leu	Asp	Asn	Leu	Glu	Leu	Glu	Asp	Ile	Asp
	850					855					860				
Thr	Thr	Asp	Ile	Asn	Leu	Asp	Glu	Asp	Ile	Leu	Asp	Asp			
865					870					875					

&lt;210&gt; SEQ ID NO 21

&lt;211&gt; LENGTH: 511

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;300&gt; PUBLICATION INFORMATION:

&lt;308&gt; DATABASE ACCESSION NUMBER: UniProtKB/ P48444

&lt;309&gt; DATABASE ENTRY DATE: 2009-05-26

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&lt;313&gt; RELEVANT RESIDUES IN SEQ ID NO: (1)..(511)

&lt;400&gt; SEQUENCE: 21

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

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Ser Gly Asn Gly Cys Asp Val Asn Ile Glu Tyr Glu Leu Gln Glu Asp
385                               390                       395                   400

Asn Leu Glu Leu Asn Asp Val Val Ile Thr Ile Pro Leu Pro Ser Gly
                               405                       410                   415

Val Gly Ala Pro Val Ile Gly Glu Ile Asp Gly Glu Tyr Arg His Asp
                               420                       425                   430

Ser Arg Arg Asn Thr Leu Glu Trp Cys Leu Pro Val Ile Asp Ala Lys
                               435                       440                   445

Asn Lys Ser Gly Ser Leu Glu Phe Ser Ile Ala Gly Gln Pro Asn Asp
450                               455                       460

Phe Phe Pro Val Gln Val Ser Phe Val Ser Lys Lys Asn Tyr Cys Asn
465                               470                       475                   480

Ile Gln Val Thr Lys Val Thr Gln Val Asp Gly Asn Ser Pro Val Arg
                               485                       490                   495

Phe Ser Thr Glu Thr Thr Phe Leu Val Asp Lys Tyr Glu Ile Leu
                               500                       505                   510

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<210> SEQ ID NO 22
<211> LENGTH: 552
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<300> PUBLICATION INFORMATION:
<308> DATABASE ACCESSION NUMBER: NCBI/ACA05944
<309> DATABASE ENTRY DATE: 2008-02-20
<313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(552)

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<400> SEQUENCE: 22

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Met Ala Glu Cys Asn Leu Val Ala Ile Leu Ile Ser Ser Ile Asp Asn
1                               5                       10                   15

Pro Leu Asp Lys Asn Leu Asp Asn Gly Gly Asn Ser Cys Leu Asp Phe
                               20                       25                   30

Arg Pro Leu Asn Ser Phe Ser Gln Pro Gln Val Leu Leu Ala Ala Ala
35                               40                       45

Val Cys Thr Lys Ala Gly Lys Ala Ile Val Ser Arg Gln Phe Val Glu
50                               55                       60

Met Thr Arg Thr Arg Ile Glu Gly Leu Leu Ala Ala Phe Pro Lys Leu
65                               70                       75                   80

Met Asn Thr Gly Lys Gln His Thr Phe Val Glu Thr Glu Ser Val Arg
85                               90                       95

Tyr Val Tyr Gln Pro Met Glu Lys Leu Tyr Met Val Leu Ile Thr Thr
100                              105                       110

Lys Asn Ser Asn Ile Leu Glu Asp Leu Glu Thr Leu Arg Leu Phe Ser
115                              120                       125

Arg Val Ile Pro Glu Tyr Cys Arg Ala Leu Glu Glu Asn Glu Ile Ser
130                              135                       140

Glu His Cys Phe Asp Leu Ile Phe Ala Phe Asp Glu Ile Val Ala Leu
145                              150                       155                   160

Gly Tyr Arg Glu Asn Val Asn Leu Ala Gln Ile Arg Thr Phe Thr Glu
165                              170                       175

Met Asp Ser His Glu Glu Lys Val Phe Arg Ala Val Arg Glu Thr Gln
180                              185                       190

Glu Arg Glu Ala Lys Ala Glu Met Arg Arg Lys Ala Lys Glu Leu Gln
195                              200                       205

Gln Ala Arg Arg Asp Ala Glu Arg Gln Gly Lys Lys Ala Pro Gly Phe

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

<210> SEQ ID NO 23  
 <211> LENGTH: 308  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <300> PUBLICATION INFORMATION:  
 <308> DATABASE ACCESSION NUMBER: UniProtKB/O14579  
 <309> DATABASE ENTRY DATE: 2009-05-05  
 <313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(308)  
 <400> SEQUENCE: 23

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

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<210> SEQ ID NO 24
<211> LENGTH: 256
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<300> PUBLICATION INFORMATION:
<308> DATABASE ACCESSION NUMBER: NCBI/NP_955476
<309> DATABASE ENTRY DATE: 2008-09-28
<313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(256)

<400> SEQUENCE: 24

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Met Ala Pro Pro Ala Pro Gly Pro Ala Ser Gly Gly Ser Gly Glu Val
1          5          10          15

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Asp Glu Leu Phe Asp Val Lys Asn Ala Phe Tyr Ile Gly Ser Tyr Gln
      20                               25                 30

Gln Cys Ile Asn Glu Ala Gln Arg Val Lys Leu Ser Ser Pro Glu Arg
      35                               40                 45

Asp Val Glu Arg Asp Val Phe Leu Tyr Arg Ala Tyr Leu Ala Gln Arg
      50                               55                 60

Lys Phe Gly Val Val Leu Asp Glu Ile Lys Pro Ser Ser Ala Pro Glu
      65                               70                 75                 80

Leu Gln Ala Val Arg Met Phe Ala Asp Tyr Leu Ala His Glu Ser Arg
      85                               90                 95

Arg Asp Ser Ile Val Ala Glu Leu Asp Arg Glu Met Ser Arg Ser Val
      100                              105                 110

Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala Ala Ser Ile Tyr Leu
      115                              120                 125

His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala Leu His Gln Gly Asp
      130                              135                 140

Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile Leu Leu Lys Leu Asp
      145                              150                 155                 160

Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg Met Gln Asp Leu Asp
      165                              170                 175

Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala Trp Val Ser Leu Ala
      180                              185                 190

Thr Asp Ser Gly Tyr Pro Glu Thr Leu Val Asn Leu Ile Val Leu Ser
      195                              200                 205

Gln His Leu Gly Lys Pro Pro Glu Val Thr Asn Arg Tyr Leu Ser Gln
      210                              215                 220

Leu Lys Asp Ala His Arg Ser His Pro Phe Ile Lys Glu Tyr Gln Ala
      225                              230                 235                 240

Lys Glu Asn Asp Phe Asp Arg Leu Val Leu Gln Tyr Ala Pro Ser Ala
      245                              250                 255

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&lt;210&gt; SEQ ID NO 25

&lt;211&gt; LENGTH: 257

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;300&gt; PUBLICATION INFORMATION:

&lt;308&gt; DATABASE ACCESSION NUMBER: NCBI/NP\_955474

&lt;309&gt; DATABASE ENTRY DATE: 2008-09-28

&lt;313&gt; RELEVANT RESIDUES IN SEQ ID NO: (1)..(257)

&lt;400&gt; SEQUENCE: 25

```

Met Ala Pro Pro Ala Pro Gly Pro Ala Ser Gly Gly Ser Gly Glu Val
  1                               5                 10                 15

Asp Glu Leu Phe Asp Val Lys Asn Ala Phe Tyr Ile Gly Ser Tyr Gln
      20                               25                 30

Gln Cys Ile Asn Glu Ala Gln Arg Val Lys Leu Ser Ser Pro Glu Arg
      35                               40                 45

Asp Val Glu Arg Asp Val Phe Leu Tyr Arg Ala Tyr Leu Ala Gln Arg
      50                               55                 60

Lys Phe Gly Val Val Leu Asp Glu Ile Lys Pro Ser Ser Ala Pro Glu
      65                               70                 75                 80

Leu Gln Ala Val Arg Met Phe Ala Asp Tyr Leu Ala His Glu Ser Arg
      85                               90                 95

Ser Thr Ala Met Thr Val Gln Ile Leu Leu Lys Leu Asp Arg Leu Asp

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	100		105		110	
Leu	Ala Arg Lys Glu Leu Lys Arg Met Gln Asp Leu Asp Glu Asp Ala					
	115		120		125	
Thr	Leu Thr Gln Leu Ala Thr Ala Trp Val Ser Leu Ala Thr Gly Gly					
	130		135		140	
Glu	Lys Leu Gln Asp Ala Tyr Tyr Ile Phe Gln Glu Met Ala Asp Lys					
	145		150		155	160
Cys	Ser Pro Thr Leu Leu Leu Leu Asn Gly Gln Ala Ala Cys His Met					
		165		170		175
Ala	Gln Gly Arg Trp Glu Ala Ala Glu Gly Leu Leu Gln Glu Ala Leu					
		180		185		190
Asp	Lys Asp Ser Gly Tyr Pro Glu Thr Leu Val Asn Leu Ile Val Leu					
		195		200		205
Ser	Gln His Leu Gly Lys Pro Pro Glu Val Thr Asn Arg Tyr Leu Ser					
		210		215		220
Gln	Leu Lys Asp Ala His Arg Ser His Pro Phe Ile Lys Glu Tyr Gln					
		225		230		235
Ala	Lys Glu Asn Asp Phe Asp Arg Leu Val Leu Gln Tyr Ala Pro Ser					
		245		250		255

Ala

&lt;210&gt; SEQ ID NO 26

&lt;211&gt; LENGTH: 874

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;300&gt; PUBLICATION INFORMATION:

&lt;308&gt; DATABASE ACCESSION NUMBER: UniProtKB/ Q9Y678

&lt;309&gt; DATABASE ENTRY DATE: 2009-04-14

&lt;313&gt; RELEVANT RESIDUES IN SEQ ID NO: (1)..(874)

&lt;400&gt; SEQUENCE: 26

Met	Leu Lys Lys Phe Asp Lys Lys Asp Glu Glu Ser Gly Gly Gly Ser					
1		5		10		15
Asn	Pro Phe Gln His Leu Glu Lys Ser Ala Val Leu Gln Glu Ala Arg					
		20		25		30
Val	Phe Asn Glu Thr Pro Ile Asn Pro Arg Lys Cys Ala His Ile Leu					
		35		40		45
Thr	Lys Ile Leu Tyr Leu Ile Asn Gln Gly Glu His Leu Gly Thr Thr					
		50		55		60
Glu	Ala Thr Glu Ala Phe Phe Ala Met Thr Lys Leu Phe Gln Ser Asn					
		65		70		75
Asp	Pro Thr Leu Arg Arg Met Cys Tyr Leu Thr Ile Lys Glu Met Ser					
		85		90		95
Cys	Ile Ala Glu Asp Val Ile Ile Val Thr Ser Ser Leu Thr Lys Asp					
		100		105		110
Met	Thr Gly Lys Glu Asp Asn Tyr Arg Gly Pro Ala Val Arg Ala Leu					
		115		120		125
Cys	Gln Ile Thr Asp Ser Thr Met Leu Gln Ala Ile Glu Arg Tyr Met					
		130		135		140
Lys	Gln Ala Ile Val Asp Lys Val Pro Ser Val Ser Ser Ser Ala Leu					
		145		150		155
Val	Ser Ser Leu His Leu Leu Lys Cys Ser Phe Asp Val Val Lys Arg					
		165		170		175

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Trp	Val	Asn	Glu	Ala	Gln	Glu	Ala	Ala	Ser	Ser	Asp	Asn	Ile	Met	Val
		180						185					190		
Gln	Tyr	His	Ala	Leu	Gly	Leu	Leu	Tyr	His	Val	Arg	Lys	Asn	Asp	Arg
		195					200					205			
Leu	Ala	Val	Asn	Lys	Met	Ile	Ser	Lys	Val	Thr	Arg	His	Gly	Leu	Lys
	210					215					220				
Ser	Pro	Phe	Ala	Tyr	Cys	Met	Met	Ile	Arg	Val	Ala	Ser	Lys	Gln	Leu
225					230					235					240
Glu	Glu	Glu	Asp	Gly	Ser	Arg	Asp	Ser	Pro	Leu	Phe	Asp	Phe	Ile	Glu
				245					250					255	
Ser	Cys	Leu	Arg	Asn	Lys	His	Glu	Met	Val	Val	Tyr	Glu	Ala	Ala	Ser
			260					265					270		
Ala	Ile	Val	Asn	Leu	Pro	Gly	Cys	Ser	Ala	Lys	Glu	Leu	Ala	Pro	Ala
		275					280					285			
Val	Ser	Val	Leu	Gln	Leu	Phe	Cys	Ser	Ser	Pro	Lys	Ala	Ala	Leu	Arg
	290					295					300				
Tyr	Ala	Ala	Val	Arg	Thr	Leu	Asn	Lys	Val	Ala	Met	Lys	His	Pro	Ser
305					310					315					320
Ala	Val	Thr	Ala	Cys	Asn	Leu	Asp	Leu	Glu	Asn	Leu	Val	Thr	Asp	Ser
				325					330					335	
Asn	Arg	Ser	Ile	Ala	Thr	Leu	Ala	Ile	Thr	Thr	Leu	Leu	Lys	Thr	Gly
			340					345					350		
Ser	Glu	Ser	Ser	Ile	Asp	Arg	Leu	Met	Lys	Gln	Ile	Ser	Ser	Phe	Met
	355						360					365			
Ser	Glu	Ile	Ser	Asp	Glu	Phe	Lys	Val	Val	Val	Val	Gln	Ala	Ile	Ser
	370					375					380				
Ala	Leu	Cys	Gln	Lys	Tyr	Pro	Arg	Lys	His	Ala	Val	Leu	Met	Asn	Phe
385					390					395					400
Leu	Phe	Thr	Met	Leu	Arg	Glu	Glu	Gly	Gly	Phe	Glu	Tyr	Lys	Arg	Ala
				405					410					415	
Ile	Val	Asp	Cys	Ile	Ile	Ser	Ile	Ile	Glu	Glu	Asn	Ser	Glu	Ser	Lys
			420					425					430		
Glu	Thr	Gly	Leu	Ser	His	Leu	Cys	Glu	Phe	Ile	Glu	Asp	Cys	Glu	Phe
		435					440					445			
Thr	Val	Leu	Ala	Thr	Arg	Ile	Leu	His	Leu	Leu	Gly	Gln	Glu	Gly	Pro
	450					455						460			
Lys	Thr	Thr	Asn	Pro	Ser	Lys	Tyr	Ile	Arg	Phe	Ile	Tyr	Asn	Arg	Val
465					470					475					480
Val	Leu	Glu	His	Glu	Glu	Val	Arg	Ala	Gly	Ala	Val	Ser	Ala	Leu	Ala
				485					490					495	
Lys	Phe	Gly	Ala	Gln	Asn	Glu	Glu	Met	Leu	Pro	Ser	Ile	Leu	Val	Leu
			500					505					510		
Leu	Lys	Arg	Cys	Val	Met	Asp	Asp	Asp	Asn	Glu	Val	Arg	Asp	Arg	Ala
		515					520						525		
Thr	Phe	Tyr	Leu	Asn	Val	Leu	Glu	Gln	Lys	Gln	Lys	Ala	Leu	Asn	Ala
	530					535						540			
Gly	Tyr	Ile	Leu	Asn	Gly	Leu	Thr	Val	Ser	Ile	Pro	Gly	Leu	Glu	Arg
545					550					555					560
Ala	Leu	Gln	Gln	Tyr	Thr	Leu	Glu	Pro	Ser	Glu	Lys	Pro	Phe	Asp	Leu
				565					570					575	
Lys	Ser	Val	Pro	Leu	Ala	Thr	Ala	Pro	Met	Ala	Glu	Gln	Arg	Thr	Glu



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580				585				590							
Ser	Thr	Pro	Ile	Thr	Ala	Val	Lys	Gln	Pro	Glu	Lys	Val	Ala	Ala	Thr
		595					600					605			
Arg	Gln	Glu	Ile	Phe	Gln	Glu	Gln	Leu	Ala	Ala	Val	Pro	Glu	Phe	Arg
	610					615					620				
Gly	Leu	Gly	Pro	Leu	Phe	Lys	Ser	Ser	Pro	Glu	Pro	Val	Ala	Leu	Thr
625					630					635					640
Glu	Ser	Glu	Thr	Glu	Tyr	Val	Ile	Arg	Cys	Thr	Lys	His	Thr	Phe	Thr
				645					650					655	
Asn	His	Met	Val	Phe	Gln	Phe	Asp	Cys	Thr	Asn	Thr	Leu	Asn	Asp	Gln
			660					665					670		
Thr	Leu	Glu	Asn	Val	Thr	Val	Gln	Met	Glu	Pro	Thr	Glu	Ala	Tyr	Glu
		675					680					685			
Val	Leu	Cys	Tyr	Val	Pro	Ala	Arg	Ser	Leu	Pro	Tyr	Asn	Gln	Pro	Gly
	690					695					700				
Thr	Cys	Tyr	Thr	Leu	Val	Ala	Leu	Pro	Lys	Glu	Asp	Pro	Thr	Ala	Val
705					710					715					720
Ala	Cys	Thr	Phe	Ser	Cys	Met	Met	Lys	Phe	Thr	Val	Lys	Asp	Cys	Asp
				725					730					735	
Pro	Thr	Thr	Gly	Glu	Thr	Asp	Asp	Glu	Gly	Tyr	Glu	Asp	Glu	Tyr	Val
			740					745					750		
Leu	Glu	Asp	Leu	Glu	Val	Thr	Val	Ala	Asp	His	Ile	Gln	Lys	Val	Met
		755					760					765			
Lys	Leu	Asn	Phe	Glu	Ala	Ala	Trp	Asp	Glu	Val	Gly	Asp	Glu	Phe	Glu
	770					775					780				
Lys	Glu	Glu	Thr	Phe	Thr	Leu	Ser	Thr	Ile	Lys	Thr	Leu	Glu	Glu	Ala
785					790					795					800
Val	Gly	Asn	Ile	Val	Lys	Phe	Leu	Gly	Met	His	Pro	Cys	Glu	Arg	Ser
				805					810					815	
Asp	Lys	Val	Pro	Asp	Asn	Lys	Asn	Thr	His	Thr	Leu	Leu	Leu	Ala	Gly
			820					825					830		
Val	Phe	Arg	Gly	Gly	His	Asp	Ile	Leu	Val	Arg	Ser	Arg	Leu	Leu	Leu
		835					840					845			
Leu	Asp	Thr	Val	Thr	Met	Gln	Val	Thr	Ala	Arg	Ser	Leu	Glu	Glu	Leu
	850					855					860				
Pro	Val	Asp	Ile	Ile	Leu	Ala	Ser	Val	Gly						
865					870										

&lt;210&gt; SEQ ID NO 27

&lt;211&gt; LENGTH: 871

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;300&gt; PUBLICATION INFORMATION:

&lt;308&gt; DATABASE ACCESSION NUMBER: NCBI/NP\_036265

&lt;309&gt; DATABASE ENTRY DATE: 2008-08-20

&lt;313&gt; RELEVANT RESIDUES IN SEQ ID NO: (1)..(871)

&lt;400&gt; SEQUENCE: 27

Met	Ile	Lys	Lys	Phe	Asp	Lys	Lys	Asp	Glu	Glu	Ser	Gly	Ser	Gly	Ser
1				5					10					15	
Asn	Pro	Phe	Gln	His	Leu	Glu	Lys	Ser	Ala	Val	Leu	Gln	Glu	Ala	Arg
			20					25					30		
Ile	Phe	Asn	Glu	Thr	Pro	Ile	Asn	Pro	Arg	Arg	Cys	Leu	His	Ile	Leu
		35					40					45			

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Thr Lys Ile Leu Tyr Leu Leu Asn Gln Gly Glu His Phe Gly Thr Thr  
 50 55 60

Glu Ala Thr Glu Ala Phe Phe Ala Met Thr Arg Leu Phe Gln Ser Asn  
 65 70 75 80

Asp Gln Thr Leu Arg Arg Met Cys Tyr Leu Thr Ile Lys Glu Met Ala  
 85 90 95

Thr Ile Ser Glu Asp Val Ile Ile Val Thr Ser Ser Leu Thr Lys Asp  
 100 105 110

Met Thr Gly Lys Glu Asp Val Tyr Arg Gly Pro Ala Ile Arg Ala Leu  
 115 120 125

Cys Arg Ile Thr Asp Gly Thr Met Leu Gln Ala Ile Glu Arg Tyr Met  
 130 135 140

Lys Gln Ala Ile Val Asp Lys Val Ser Ser Val Ser Ser Ser Ala Leu  
 145 150 155 160

Val Ser Ser Leu His Met Met Lys Ile Ser Tyr Asp Val Val Lys Arg  
 165 170 175

Trp Ile Asn Glu Ala Gln Glu Ala Ala Ser Ser Asp Asn Ile Met Val  
 180 185 190

Gln Tyr His Ala Leu Gly Val Leu Tyr His Leu Arg Lys Asn Asp Arg  
 195 200 205

Leu Ala Val Ser Lys Met Leu Asn Lys Phe Thr Lys Ser Gly Leu Lys  
 210 215 220

Ser Gln Phe Ala Tyr Cys Met Leu Ile Arg Ile Ala Ser Arg Leu Leu  
 225 230 235 240

Lys Glu Thr Glu Asp Gly His Glu Ser Pro Leu Phe Asp Phe Ile Glu  
 245 250 255

Ser Cys Leu Arg Asn Lys His Glu Met Val Ile Tyr Glu Ala Ala Ser  
 260 265 270

Ala Ile Ile His Leu Pro Asn Cys Thr Ala Arg Glu Leu Ala Pro Ala  
 275 280 285

Val Ser Val Leu Gln Leu Phe Cys Ser Ser Pro Lys Pro Ala Leu Arg  
 290 295 300

Tyr Ala Ala Val Arg Thr Leu Asn Lys Val Ala Met Lys His Pro Ser  
 305 310 315 320

Ala Val Thr Ala Cys Asn Leu Asp Leu Glu Asn Leu Ile Thr Asp Ser  
 325 330 335

Asn Arg Ser Ile Ala Thr Leu Ala Ile Thr Thr Leu Leu Lys Thr Gly  
 340 345 350

Ser Glu Ser Ser Val Asp Arg Leu Met Lys Gln Ile Ser Ser Phe Val  
 355 360 365

Ser Glu Ile Ser Asp Glu Phe Lys Val Val Val Val Gln Ala Ile Ser  
 370 375 380

Ala Leu Cys Gln Lys Tyr Pro Arg Lys His Ser Val Met Met Thr Phe  
 385 390 395 400

Leu Ser Asn Met Leu Arg Asp Asp Gly Gly Phe Glu Tyr Lys Arg Ala  
 405 410 415

Ile Val Asp Cys Ile Ile Ser Ile Val Glu Glu Asn Pro Glu Ser Lys  
 420 425 430

Glu Ala Gly Leu Ala His Leu Cys Glu Phe Ile Glu Asp Cys Glu His  
 435 440 445

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Thr	Val	Leu	Ala	Thr	Lys	Ile	Leu	His	Leu	Leu	Gly	Lys	Glu	Gly	Pro	450	455	460	
Arg	Thr	Pro	Val	Pro	Ser	Lys	Tyr	Ile	Arg	Phe	Ile	Phe	Asn	Arg	Val	465	470	475	480
Val	Leu	Glu	Asn	Glu	Ala	Val	Arg	Ala	Ala	Ala	Val	Ser	Ala	Leu	Ala	485	490	495	
Lys	Phe	Gly	Ala	Gln	Asn	Glu	Ser	Leu	Leu	Pro	Ser	Ile	Leu	Val	Leu	500	505	510	
Leu	Gln	Arg	Cys	Met	Met	Asp	Thr	Asp	Asp	Glu	Val	Arg	Asp	Arg	Ala	515	520	525	
Thr	Phe	Tyr	Leu	Asn	Val	Leu	Gln	Gln	Arg	Gln	Met	Ala	Leu	Asn	Ala	530	535	540	
Thr	Tyr	Ile	Phe	Asn	Gly	Leu	Thr	Val	Ser	Val	Pro	Gly	Met	Glu	Lys	545	550	555	560
Ala	Leu	His	Gln	Tyr	Thr	Leu	Glu	Pro	Ser	Glu	Lys	Pro	Phe	Asp	Met	565	570	575	
Lys	Ser	Ile	Pro	Leu	Ala	Met	Ala	Pro	Val	Phe	Glu	Gln	Lys	Ala	Glu	580	585	590	
Ile	Thr	Leu	Val	Ala	Thr	Lys	Pro	Glu	Lys	Leu	Ala	Pro	Ser	Arg	Gln	595	600	605	
Asp	Ile	Phe	Gln	Glu	Gln	Leu	Ala	Ala	Ile	Pro	Glu	Phe	Leu	Asn	Ile	610	615	620	
Gly	Pro	Leu	Phe	Lys	Ser	Ser	Glu	Pro	Val	Gln	Leu	Thr	Glu	Ala	Glu	625	630	635	640
Thr	Glu	Tyr	Phe	Val	Arg	Cys	Ile	Lys	His	Met	Phe	Thr	Asn	His	Ile	645	650	655	
Val	Phe	Gln	Phe	Asp	Cys	Thr	Asn	Thr	Leu	Asn	Asp	Gln	Leu	Leu	Glu	660	665	670	
Lys	Val	Thr	Val	Gln	Met	Glu	Pro	Ser	Asp	Ser	Tyr	Glu	Val	Leu	Ser	675	680	685	
Cys	Ile	Pro	Ala	Pro	Ser	Leu	Pro	Tyr	Asn	Gln	Pro	Gly	Ile	Cys	Tyr	690	695	700	
Thr	Leu	Val	Arg	Leu	Pro	Asp	Asp	Asp	Pro	Thr	Ala	Val	Ala	Gly	Ser	705	710	715	720
Phe	Ser	Cys	Thr	Met	Lys	Phe	Thr	Val	Arg	Asp	Cys	Asp	Pro	Asn	Thr	725	730	735	
Gly	Val	Pro	Asp	Glu	Asp	Gly	Tyr	Asp	Asp	Glu	Tyr	Val	Leu	Glu	Asp	740	745	750	
Leu	Glu	Val	Thr	Val	Ser	Asp	His	Ile	Gln	Lys	Val	Leu	Lys	Pro	Asn	755	760	765	
Phe	Ala	Ala	Ala	Trp	Glu	Glu	Val	Gly	Asp	Thr	Phe	Glu	Lys	Glu	Glu	770	775	780	
Thr	Phe	Ala	Leu	Ser	Ser	Thr	Lys	Thr	Leu	Glu	Glu	Ala	Val	Asn	Asn	785	790	795	800
Ile	Ile	Thr	Phe	Leu	Gly	Met	Gln	Pro	Cys	Glu	Arg	Ser	Asp	Lys	Val	805	810	815	
Pro	Glu	Asn	Lys	Asn	Ser	His	Ser	Leu	Tyr	Leu	Ala	Gly	Ile	Phe	Arg	820	825	830	
Gly	Gly	Tyr	Asp	Leu	Leu	Val	Arg	Ser	Arg	Leu	Ala	Leu	Ala	Asp	Gly	835	840	845	
Val	Thr	Met	Gln	Val	Thr	Val	Arg	Ser	Lys	Glu	Arg	Thr	Pro	Val	Asp				

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850                      855                      860

Val Ile Leu Ala Ser Val Gly  
865                      870

<210> SEQ ID NO 28  
 <211> LENGTH: 768  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens  
 <300> PUBLICATION INFORMATION:  
 <308> DATABASE ACCESSION NUMBER: NCBI/EAW79270  
 <309> DATABASE ENTRY DATE: 2006-12-18  
 <313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(768)

<400> SEQUENCE: 28

Met Ile Leu Thr Lys Asp Met Thr Gly Lys Glu Asp Asn Tyr Arg Gly  
1                      5                      10                      15

Pro Ala Val Arg Ala Leu Cys Gln Ile Thr Asp Ser Thr Met Leu Gln  
                    20                      25                      30

Ala Ile Glu Arg Tyr Met Lys Gln Ala Ile Val Asp Lys Val Pro Ser  
                    35                      40                      45

Val Ser Ser Ser Ala Leu Val Ser Ser Leu His Leu Leu Lys Cys Ser  
50                      55                      60

Phe Asp Val Val Lys Arg Trp Val Asn Glu Ala Gln Glu Ala Ala Ser  
65                      70                      75                      80

Ser Asp Asn Ile Met Val Gln Tyr His Ala Leu Gly Leu Leu Tyr His  
                    85                      90                      95

Val Arg Lys Asn Asp Arg Leu Ala Val Asn Lys Met Ile Ser Lys Val  
                    100                      105                      110

Thr Arg His Gly Leu Lys Ser Pro Phe Ala Tyr Cys Met Met Ile Arg  
115                      120                      125

Val Ala Ser Lys Gln Leu Glu Glu Glu Asp Gly Ser Arg Asp Ser Pro  
130                      135                      140

Leu Phe Asp Phe Ile Glu Ser Cys Leu Arg Asn Lys His Glu Met Val  
145                      150                      155                      160

Val Tyr Glu Ala Ala Ser Ala Ile Val Asn Leu Pro Gly Cys Ser Ala  
                    165                      170                      175

Lys Glu Leu Ala Pro Ala Val Ser Val Leu Gln Leu Phe Cys Ser Ser  
180                      185                      190

Pro Lys Ala Ala Leu Arg Tyr Ala Ala Val Arg Thr Leu Asn Lys Val  
195                      200                      205

Ala Met Lys His Pro Ser Ala Val Thr Ala Cys Asn Leu Asp Leu Glu  
210                      215                      220

Asn Leu Val Thr Asp Ser Asn Arg Ser Ile Ala Thr Leu Ala Ile Thr  
225                      230                      235                      240

Thr Leu Leu Lys Thr Gly Ser Glu Ser Ser Ile Asp Arg Leu Met Lys  
245                      250                      255

Gln Ile Ser Ser Phe Met Ser Glu Ile Ser Asp Glu Phe Lys Val Val  
260                      265                      270

Val Val Gln Ala Ile Ser Ala Leu Cys Gln Lys Tyr Pro Arg Lys His  
275                      280                      285

Ala Val Leu Met Asn Phe Leu Phe Thr Met Leu Arg Glu Glu Gly Gly  
290                      295                      300

Phe Glu Tyr Lys Arg Ala Ile Val Asp Cys Ile Ile Ser Ile Ile Glu  
305                      310                      315                      320

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Glu Asn Ser Glu Ser Lys Glu Thr Gly Leu Ser His Leu Cys Glu Phe  
                           325  330  335

Ile Glu Asp Cys Glu Phe Thr Val Leu Ala Thr Arg Ile Leu His Leu  
                           340  345  350

Leu Gly Gln Glu Gly Pro Lys Thr Thr Asn Pro Ser Lys Tyr Ile Arg  
                           355  360  365

Phe Ile Tyr Asn Arg Val Val Leu Glu His Glu Glu Val Arg Ala Gly  
                           370  375  380

Ala Val Ser Ala Leu Ala Lys Phe Gly Ala Gln Asn Glu Glu Met Leu  
                           385  390  395  400

Pro Ser Ile Leu Val Leu Leu Lys Arg Cys Val Met Asp Asp Asp Asn  
                           405  410  415

Glu Val Arg Asp Arg Ala Thr Phe Tyr Leu Asn Val Leu Glu Gln Lys  
                           420  425  430

Gln Lys Ala Leu Asn Ala Gly Tyr Ile Leu Asn Gly Leu Thr Val Ser  
                           435  440  445

Ile Pro Gly Leu Glu Arg Ala Leu Gln Gln Tyr Thr Leu Glu Pro Ser  
                           450  455  460

Glu Lys Pro Phe Asp Leu Lys Ser Val Pro Leu Ala Thr Ala Pro Met  
                           465  470  475  480

Ala Glu Gln Arg Thr Glu Ser Thr Pro Ile Thr Ala Val Lys Gln Pro  
                           485  490  495

Glu Lys Val Ala Ala Thr Arg Gln Glu Ile Phe Gln Glu Gln Leu Ala  
                           500  505  510

Ala Val Pro Glu Phe Arg Gly Leu Gly Pro Leu Phe Lys Ser Ser Pro  
                           515  520  525

Glu Pro Val Ala Leu Thr Glu Ser Glu Thr Glu Tyr Val Ile Arg Cys  
                           530  535  540

Thr Lys His Thr Phe Thr Asn His Met Val Phe Gln Phe Asp Cys Thr  
                           545  550  555  560

Asn Thr Leu Asn Asp Gln Thr Leu Glu Asn Val Thr Val Gln Met Glu  
                           565  570  575

Pro Thr Glu Ala Tyr Glu Val Leu Cys Tyr Val Pro Ala Arg Ser Leu  
                           580  585  590

Pro Tyr Asn Gln Pro Gly Thr Cys Tyr Thr Leu Val Ala Leu Pro Lys  
                           595  600  605

Glu Asp Pro Thr Ala Val Ala Cys Thr Phe Ser Cys Met Met Lys Phe  
                           610  615  620

Thr Val Lys Asp Cys Asp Pro Thr Thr Gly Glu Thr Asp Asp Glu Gly  
                           625  630  635  640

Tyr Glu Asp Glu Tyr Val Leu Glu Asp Leu Glu Val Thr Val Ala Asp  
                           645  650  655

His Ile Gln Lys Val Met Lys Leu Asn Phe Glu Ala Ala Trp Asp Glu  
                           660  665  670

Val Gly Asp Glu Phe Glu Lys Glu Glu Thr Phe Thr Leu Ser Thr Ile  
                           675  680  685

Lys Thr Leu Glu Glu Ala Val Gly Asn Ile Val Lys Phe Leu Gly Met  
                           690  695  700

His Pro Cys Glu Arg Ser Asp Lys Val Pro Asp Asn Lys Asn Thr His  
                           705  710  715  720

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Thr Leu Leu Leu Ala Gly Val Phe Arg Gly Gly His Asp Ile Leu Val
      725                      730                      735

Arg Ser Arg Leu Leu Leu Leu Asp Thr Val Thr Met Gln Val Thr Ala
      740                      745                      750

Arg Ser Leu Glu Glu Leu Pro Val Asp Ile Ile Leu Ala Ser Val Gly
      755                      760                      765

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<210> SEQ ID NO 29
<211> LENGTH: 177
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<300> PUBLICATION INFORMATION:
<308> DATABASE ACCESSION NUMBER: UniProtKB/P61923
<309> DATABASE ENTRY DATE: 2009-05-05
<313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(177)

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<400> SEQUENCE: 29

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Met Glu Ala Leu Ile Leu Glu Pro Ser Leu Tyr Thr Val Lys Ala Ile
1          5          10          15

Leu Ile Leu Asp Asn Asp Gly Asp Arg Leu Phe Ala Lys Tyr Tyr Asp
20          25          30

Asp Thr Tyr Pro Ser Val Lys Glu Gln Lys Ala Phe Glu Lys Asn Ile
35          40          45

Phe Asn Lys Thr His Arg Thr Asp Ser Glu Ile Ala Leu Leu Glu Gly
50          55          60

Leu Thr Val Val Tyr Lys Ser Ser Ile Asp Leu Tyr Phe Tyr Val Ile
65          70          75          80

Gly Ser Ser Tyr Glu Asn Glu Leu Met Leu Met Ala Val Leu Asn Cys
85          90          95

Leu Phe Asp Ser Leu Ser Gln Met Leu Arg Lys Asn Val Glu Lys Arg
100         105         110

Ala Leu Leu Glu Asn Met Glu Gly Leu Phe Leu Ala Val Asp Glu Ile
115         120         125

Val Asp Gly Gly Val Ile Leu Glu Ser Asp Pro Gln Gln Val Val His
130         135         140

Arg Val Ala Leu Arg Gly Glu Asp Val Pro Leu Thr Glu Gln Thr Val
145         150         155         160

Ser Gln Val Leu Gln Ser Ala Lys Glu Gln Ile Lys Trp Ser Leu Leu
165         170         175

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Arg

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<210> SEQ ID NO 30
<211> LENGTH: 210
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<300> PUBLICATION INFORMATION:
<308> DATABASE ACCESSION NUMBER: NCBI/NP_057513
<309> DATABASE ENTRY DATE: 2009-03-29
<313> RELEVANT RESIDUES IN SEQ ID NO: (1)..(210)

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<400> SEQUENCE: 30

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Met Gln Arg Pro Glu Ala Trp Pro Arg Pro His Pro Gly Glu Gly Ala
1          5          10          15

Ala Ala Ala Gln Ala Gly Gly Pro Ala Pro Pro Ala Arg Ala Gly Glu
20          25          30

Pro Ser Gly Leu Arg Leu Gln Glu Pro Ser Leu Tyr Thr Ile Lys Ala
35          40          45

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

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In view of the foregoing, what is claimed is:

**1.** An intelligent sensor platform comprising: (a) more than one sensor element capable of executing or following a self-adaptive algorithm and including a capability for an autonomous and/or a cognitive action, (b) a selected sensor function, (c) a bi-directional communications link and data and/or instructions to or from the sensor element are communicated over the link, wherein a scalable, distributed and intelligent platform comprising more than one interconnected sensor is enabled.

**2.** The intelligent sensor platform of claim 1, wherein the self-adaptive algorithm includes one or more algorithms including, but not limited to, biological control law, graph, Lie algebra, Clifford algebra algorithms, or a combination thereof.

**3.** The intelligent sensor platform of claim 1, wherein the autonomous and/or cognitive action includes one or more actions including, but not limited to, self-adapting, self-directing, self-insight, self-reasoning, self-repairing, self-regulating, self-regenerating action, self-replicating, perceiving, knowledge acquisition actions, or a combination thereof.

**4.** The intelligent sensor platform of claim 1, wherein the sensor function is selected from an activation, adjustment, command, control, classifying, cybernetic, storage, deactivation, diagnosing, directing, identifying, processing, monitoring, programmable, prosthetic, receiving, sensing, targeting, transmitting function.

**5.** The intelligent sensor platform of claim 1, wherein the sensor element is further capable of following and/or executing non-self adaptive algorithms.

**6.** The intelligent sensor platform of claim 1, wherein the sensor element is one or more sensor element type suitable for executing or following an algorithm.

**7.** The intelligent sensor platform of claim 1, wherein the sensor element and/or the link is physically linked to a local or remote element, device, user, operator.

**8.** The intelligent sensor platform of claim 1, wherein the sensor element and/or the link is functionally or logically linked to a local or remote element, device, user, operator.

**9.** The intelligent sensor platform of claim 1, wherein the link is a biochemical, biological, chemical, electrical, electromagnetic, wired network, Internet, intra-molecular, kinetic, mechanical, metabolic, wireless network, optical, photonic, physiological, or a quantum mechanical link, or a combination thereof.

**10.** The intelligent sensor platform of claim 1, wherein the sensor is further capable of being incorporated into an agent, device, material, mechanism, organism, substance, or a system of one or more type.

**11.** The intelligent sensor platform of claim 1, wherein the sensor element is further capable of sensing and/or responding to an internal or external stimulus.

**12.** The intelligent sensor platform of claim 11, wherein the stimulus includes one or more stimuli including, but not limited to, an acoustical, chemical, biochemical, biological, fluidic, metabolic, covalent, non-covalent, ionic, disorder, disease, electrical, electromagnetic, genotype, magnetic, mechanical, phenotype, photonic, toxin, temperature, pH, pathogen, pathology, quantum mechanical, radioactive, radiological, sonic stimuli, or a combination thereof.

**13.** The intelligent sensor platform of claim 1, wherein the sensor element is further capable of absorbing energy, receiving energy, storing energy, emitting energy, controlling energy, transforming energy, or transmitting energy, or a combination thereof.

**14.** The intelligent sensor platform of claim **13**, wherein the energy is acoustical, biochemical, bioluminescent, biological, Casimir, chemical, Coulomb blockade, laser, electron, electrical, electrical field, electromagnetic, enzyme, ESR, light emitting diode, luminescent, magnetic field, mechanical, metabolic, NMR, pH, ordinary light, photoisomerisable species, OCT, optoelectronic, PET, photodetector, photoelectric, photonic, photosensitive, photovoltaic, quantum dot, quantum mechanical, radio transmission, sonic, SPECT, spin-electron, or thermal energy, or a combination thereof.

**15.** The intelligent sensor platform of claim **13**, wherein the energy further enables in whole or in part the sensor to perform an action.

**16.** The intelligent sensor platform of claim **1**, wherein the sensor platform comprises multiple sensor elements, selected functions, communication links.

**17.** The intelligent sensor platform of claim **1**, wherein the sensor is further capable of being formulated for in vivo or in vitro use in human or animals.

**18.** The intelligent sensor platform of claim **17**, wherein the sensor is capable of improving the efficacy of a healthcare element and/or usage thereof in treating or preventing a disease, condition, or disorder.

**19.** The intelligent sensor platform of claim **17**, wherein a formulation comprised of purified or synthetic clathrin coatomer or non-clathrin coatomer protein molecules is further capable of comprising the intelligent sensor for in vivo or in vitro use.

**20.** A method for an intelligent sensor platform comprising: (a) forming more than one sensor element capable of executing or following a self-adaptive algorithm and including a capability for an autonomous and/or a cognitive action, (b) a selected sensor function, (c) a bi-directional communications link and data and/or instructions to or from the sensor element are communicated over the link, wherein a scalable, distributed and intelligent platform comprising more than one interconnected sensor is enabled.

\* \* \* \* \*