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The invention provides means and methods for producing compounds suitable for testing for the presence and/or identification of an immunogenic compound and/or a binding compound of interest. Immunogenic compounds and compositions are also herewith provided, as well as peptidomimetics of members of the cystine-knot family.

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(54) Title: BINDING COMPOUNDS, IMMUNOGENIC COMPOUNDS AND PEPTIDOMIMETICS

(57) Abstract: The invention provides means and methods for producing compounds suitable for testing for the presence and/or identification of an immunogenic compound and/or a binding compound of interest. Immunogenic compounds and compositions are also herewith provided, as well as peptidomimetics of members of the cystine-knot family.

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Binding compounds, immunogenic compounds and peptidomimetics of the beta-3 hairpin loop of cystine-knot growth factors

The invention relates to the field of biology. More specifically, the invention relates to
5 detection, identification and/or generation of binding molecules.

Interactions between binding molecules, which in general are biomolecules, and their
corresponding ligands are central to life. Cells often bear or contain receptor molecules that are
capable of specifically interacting or binding with another molecule such as for instance a
10 hormone, a peptide, a drug, an antigen, an effector molecule or with another receptor molecule;
enzymes bind with their substrate; antibody molecules and/or T cells bind with an antigen,
nucleic acid with protein, and so on. By “interacting or binding” it is meant that the binding
molecule and ligand approach each other within the range of molecular forces, and may
influence each others properties. This approach takes the binding molecule and its ligand through
15 various stages of molecular recognition comprising increasing degrees of intimacy and mutual
effect: they bind, albeit not always irreversibly.

Binding molecules have binding ability because they comprise distinct binding sites allowing for
the recognition of the ligand in question. The ligand, in turn, has a corresponding binding site,
and only when the two binding sites can interact by -- essentially spatial -- complementarity, the
20 two molecules can bind. Needless to say that, molecules having three dimensions, binding sites
are of a three dimensional nature, often one or more surface projections or protuberances of one
binding site correspond to one or more pockets or depressions in the other, forming a three-
dimensional lock-and-key arrangement, sometimes in an induced-fit variety. Sometimes, such a
protuberance comprises a single loop of the molecule in question, and it is only this protuberance
25 that essentially forms the binding site. In that case one often terms these binding sites as
comprising a linear or continuous binding site, wherein a mere linear part of the molecule in
question is in essence responsible for the binding interaction. This terminology is widely used to
describe for example antibody-antigen reactions wherein the antigen comprises part of a protein
sequence; a linear peptide. One then often speaks about a linear or continuous epitope, whereby
30 the binding site (epitope) of the antigenic molecule is formed by a loop of consecutively bound
amino acids. However, similar continuous binding sites (herein epitope and

binding site are use interchangeably) can be found with receptor-antigen interactions (such as with a T-cell receptor), with receptor-ligand interactions such as with hormone receptors and agonists or antagonists thereof, with receptor-cytokine interactions or with for example enzyme-substrate or receptor-drug interactions, whereby a linear part of a molecule is recognised as the binding site.

More often, however, such a protuberance or protuberances and depressions comprise various, distinct parts of the molecule in question, and it are the combined parts that essentially form the binding site. Commonly, one names such a binding site comprising distinct parts of the molecule in question a discontinuous or conformational binding site or epitope. For example, binding sites laying on proteins having not only a primary structure (the amino acid sequence of the protein molecule), but also secondary and tertiary structure (the folding of the molecule into alpha-helices or beta-sheets and its overall shape), and sometimes even quaternary structure (the interaction with other protein molecules) may comprise in their essential protuberances or depressions amino acids or short peptide sequences that lay far apart in the primary structure but are folded closely together in the binding site. In linear (continuous) binding sites the key amino acids mediating the contacts with the antibody are typically located within one part of the primary structure usually not greater than 15 amino acids in length. Peptides covering these sequences have affinities to the target proteins that are roughly within the range shown by the intact protein ligand. In conformational (discontinuous) binding sites however the key residues are in general distributed over two or more binding regions, which are often separated in the primary structure. Upon folding, these binding regions can be brought together on the protein surface to form a composite binding site. Even if the complete binding site mediates a high affinity interaction, peptides covering only one binding region, as synthesized in a linear scan of overlapping peptides, generally have very low affinities that often cannot be measured e.g. in normal ELISA or Biacore experiments.

Due to the central role binding molecules and their ligands play in life, there is an ever expanding interest in detection, identification and/or generation of binding molecules. Insight into the nature of binding sites for instance provides the possibility to design compounds capable of interfering with the binding between a binding

molecule and its ligand. Moreover, the generation of binding molecules mimicking binding sites of (complex) molecules is desired for a wide variety of applications. For instance, peptides mimicking a binding site of a proteinaceous molecule are suitable for diagnostic, therapeutic and/or prophylactic uses. Such peptides are for instance
5 suitable for use as an agonist or antagonist for a ligand-receptor pair.

Moreover, there is an ever expanding interest in detection, identification and/or generation of immunogenic compounds. Immunogenic compounds are particularly suitable for obtaining antibodies and/or T cells of interest. Moreover, such immunogenic compounds are suitable for evoking an immune response in a host,
10 which immune response preferably provides partial or full protection against subsequent challenge with said immunogenic compound and/or with an immunogen from which said immunogenic compound is derived. Preferably immunogenic compounds are generated that are capable of providing a partially or fully protective immune response in a host against subsequent challenge with a proteinaceous
15 molecule of interest. Such immunogenic compounds typically comprise a peptide sequence that is wholly or in part derived from said proteinaceous molecule of interest.

Methods for screening for a binding compound and/or immunogenic compound
20 of interest generally involve the production of a plurality of putative binding sites and/or immunogenic compounds and subsequent incubation with a molecule of interest (such as for instance a ligand, an antibody and/or a T cell) in order to find a compound capable of specifically binding said molecule of interest. An early work in the peptide field is WO 84/03564, related to a method of detecting or determining
25 antigenically active amino acid sequences or peptides in a protein. This work, providing the so-called Pepscan technology, involves the production of a plurality of different peptides after which the synthesised peptides are each tested with the binding molecule in question. This method allows detection of a continuous binding site and/or continuous epitope in a protein or peptide sequence. Pepscan technology
30 taken in a broad sense provides for the testing for or identification of (albeit linear) peptides essentially identical with, analogous to or mimicking binding sites, immunogenic sites or ligands of a various nature (mimotopes, Geyssen at al, Mol. Immunol. 23:709-715, 1986).

Pepscan technology allows identification of linear peptide sequences interacting with receptor molecules, enzymes, antibodies, and so on, in a rapid and straightforward fashion, allowing testing of a great many peptides for their reactivity with the binding molecule in question with relatively little effort.

5 However, the Pepscan technology is not suitable for testing of discontinuous or conformational binding sites. Moreover, the Pepscan technology is not suitable for obtaining peptides with a desired characteristic which peptides have an amino acid sequence that is not directly derived from the primary amino acid sequence of a given proteinaceous molecule.

10

 In WO 02/31510 a method for screening for discontinuous binding sites is disclosed. A molecular library is generated wherein a first segment is spotted in close proximity to a second segment in order to form a test entity. Various test entities comprising different segments are subsequently screened for the presence of a desired
15 binding site. This method is suitable for screening for the presence of a variety of binding sites present within a compound of interest. The segments that are spotted in close proximity to each other are either randomly synthesized or derived from a known amino acid sequence of a proteinaceous molecule. However, if the segments are randomly synthesized, a huge amount of test entities needs to be synthesized which is
20 laborious and time consuming. On the other hand, if the segments are directly derived from the primary sequence of a proteinaceous molecule of interest, a rather limited collection is obtained since peptides having an amino acid sequence that is not directly derived from said primary amino acid sequence of said proteinaceous molecule are not produced.

25

 The present invention provides a method for producing compounds that are suitable for screening for the presence of a binding site and/or immunogenic site of interest. A method of the invention provides compounds that on the one hand are at least in part based on a given proteinaceous molecule, but on the other hand do not
30 necessarily contain sequences that are exactly similar to (a part of) the primary sequence of said proteinaceous molecule. The invention provides a method wherein at least one sequence derived from the primary sequence of a proteinaceous molecule of interest is used in order to systematically generate and screen for binding compounds

and/or immunogenic compounds. The invention provides an efficient method for generating, selecting and/or identifying immunogenic compounds and/or binding compounds whose properties are comparable to, or even better than, a binding site and/or immunogenic site of an original proteinaceous molecule of interest. A preferred
5 embodiment of a method of the invention is particularly suitable for screening for desired binding characteristics and/or immunogenic characteristics because this embodiment provides peptides bound to a scaffold. The use of a scaffold more often results in peptides having a biologically relevant secondary structure, as compared to free, linear peptides. Moreover, if a preferred scaffold of the invention is used,
10 produced peptides need not be protected before they are attached to the scaffold, due to the fact that the formation of a first linkage between a peptide and a scaffold accelerates the formation of a second linkage between said peptide and said scaffold. Such preferred scaffold needs not be selectively functionalized. Hence, in a preferred embodiment an efficient method is provided wherein selected amino acid sequences
15 are incorporated into peptides, which peptides are coupled to a scaffold without the need of cumbersome protection and deprotection procedures. Said peptides are preferably coupled to said scaffold in solution, more preferably in an aqueous solution. The use of an aqueous solution provides various advantages. For instance, water is cheap, non-toxic and easy to remove by freeze drying (in comparison to for instance
20 DMF and DMSO). Moreover, (buffer) salts dissolve very well in water and water also has good solubility properties for most peptides (except for very hydrophobic ones).

Once a compound with a desired binding property and/or immunogenic property is selected with a method according to the invention, it is for instance
25 suitable for use as a peptidomimetic, an agonist, an antagonist, for preparing an immunogenic composition and/or for gaining more insight into the properties of a proteinaceous molecule of interest (such as for instance the secondary, tertiary and/or quaternary structure). While it is possible to identify a (discontinuous) binding site and/or epitope within a proteinaceous molecule of interest, it is preferred to provide a
30 compound with at least one improved characteristic, preferably at least one improved immunogenic and/or binding characteristic, as compared to a given proteinaceous molecule.

The invention in one aspect provides a method for producing a compound which is suitable for testing for the presence and/or identification of an immunogenic compound and/or a binding compound, the method comprising:

- selecting at least one amino acid residue within the primary sequence of at least one proteinaceous molecule, whereby said selected amino acid residue is preferably at least two amino acid residues located from other selected amino acid residues, if any;
- selecting at least one flanking sequence of at least one selected amino acid residue, which flanking sequence is located in the direction of the N-terminus and/or C-terminus of said at least one proteinaceous molecule, said flanking sequence having a length of between 2 and 48 amino acid residues; and
- producing a peptide comprising at least one of said flanking sequences, said peptide having a length of at least 4 and at most 50 amino acid residues.

In one embodiment said flanking sequence includes said selected amino acid residue. This is however not necessary.

15

A method according to the invention involves the production of at least one peptide – preferably a plurality of peptides – comprising sequences that are at least in part derived from a proteinaceous molecule of interest. A preferred embodiment involves systematic "shuffling" of flanking sequences (which flanking sequences are derived from a proteinaceous molecule of interest), resulting in a plurality of peptides which are preferably screened for the presence of a binding compound and/or immunogenic compound of interest. By varying the length, kind and/or amount of flanking sequences, a plurality of peptides is produced. The amount of peptides and the extent of differences between said peptides is chosen at will, depending on a particular application.

25

A method according to the present invention is particularly suitable for producing a plurality of compounds and screening said plurality of compounds for the presence of a compound with at least one desired characteristic. Said plurality of compounds preferably comprises at least 10, more preferably at least 100, most preferably at least 1000 compounds in order to enhance the chance that a compound with a desired characteristic is generated and selected. In a preferred embodiment said plurality of compounds is screened for the presence of a compound with a desired

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immunogenic characteristic. This is for instance done by incubating a plurality of compounds of the invention with a binding molecule such as an antibody and/or T cell and determining whether at least one compound is capable of specifically binding said binding molecule.

5 In a preferred embodiment a compound is selected which is capable of eliciting an immune response in a host. In this embodiment at least one compound of the invention is administered to a non-human animal and it is determined whether an immune response is elicited. Most preferably, a compound is selected which is capable of eliciting an immune response in a host, which immune response is directed against
10 a proteinaceous molecule of interest. Hence, a compound is preferably selected which is capable of eliciting an immune response in a host, such as a humoral and/or cellular response during which antibodies and/or T cells are produced, which antibodies and/or T cells are not only capable of specifically binding said compound, but which are also capable of specifically binding a proteinaceous molecule of interest. It was found that
15 a method of the present invention is particularly effective in generating and detecting such binding compounds and/or immunogenic compounds. In a preferred embodiment a compound is firstly selected during a first screening procedure using a binding molecule such as an antibody and/or T cell before it is administered to a non-human animal. Hence, according to this embodiment a two-step procedure is preferred
20 wherein peptides according to the invention are firstly screened *in vitro*, after which the immunogenic properties of promising candidate peptides are subsequently investigated *in vivo*.

A method of the invention is applicable to any given proteinaceous molecule of
25 interest whose primary sequence is at least partly known. If a method of the invention is performed in order to produce an immunogenic compound and/or binding compound, it is preferred to select at least one amino acid residue from a surface-exposed region of said proteinaceous molecule. This is of course only possible if the (secondary, tertiary and/or quaternary) structure of said proteinaceous molecule is at
30 least in part known. A method of the invention is however not restricted to proteinaceous molecules with an at least partially known structure. It is also possible to perform a method of the invention with a proteinaceous molecule with unknown (secondary, tertiary and/or quaternary) structure. In that case, of course, amino acid

residues of said proteinaceous molecule are selected at random. By selecting an amino acid residue is meant herein that an amino acid residue is taken into consideration. It need not be physically isolated or synthesized.

Once an amino acid residue is selected, at least one flanking sequence of said
5 amino acid residue is subsequently selected. A flanking sequence is defined as a number of consecutive amino acid residues which are located within five, preferably within three, amino acid residues from said selected amino acid residue in the primary sequence of said proteinaceous molecule of interest. Preferably, said flanking sequence is located directly adjacent to said selected amino acid residue. Hence, if an
10 amino acid residue at position n is selected, a flanking sequence located in the direction of the N-terminus preferably ends at amino acid position $n - 1$, while a flanking sequence located in the direction of the C-terminus preferably starts at amino acid position $n + 1$. In one embodiment a flanking sequence includes said selected amino acid residue. According to this embodiment, a flanking sequence
15 located in the direction of the N-terminus ends at amino acid position n , and/or a flanking sequence located in the direction of the C-terminus starts at amino acid position n . As used herein, a flanking sequence is called to "start" at its most N-terminal amino acid residue and a flanking sequence is called to "end" at its most C-terminal amino acid residue. The length of said flanking sequences is preferably
20 between 2 and 48 amino acid residues. Preferably, said length is between 4 and 30 amino acid residues, more preferably between 4 and 21 amino acid residues. The length of a flanking sequence of a selected amino acid residue that is located in the direction of the N-terminus need not necessarily to be the same as the length of a flanking sequence of the same selected amino acid residue that is located in the
25 direction of the C-terminus, although this is of course possible. Moreover, different flanking sequences of the same selected amino acid residue can be chosen, said flanking sequences being in the direction of the N-terminus and/or C-terminus, which flanking sequences are of different length. Hence, a method of the invention also comprises the selection of at least two flanking sequences of the same selected amino
30 acid residue, said at least two flanking sequences being in the same direction (of the N-terminus or C-terminus).

Once at least one flanking sequence is selected, a peptide is produced comprising at least one of said flanking sequences. A peptide is defined herein as a

compound comprising at least two consecutive amino acid residues that are linked to each other via a peptide bond. Besides natural amino acid residues, a peptide of the invention may comprise non-natural amino acid residues such as for instance D-amino acid residues. A peptide of the invention comprising at least one of said
5 flanking sequences is produced using any method known in the art, such as for instance solid-phase synthesis. The length of said peptide is between 4 and 50 amino acid residues. Preferably however, said peptide has a length of between 6 and 25 amino acid residues, since peptides with this length have been shown to provide optimal test results. Also provided is therefore a method according to the invention
10 wherein said peptide has a length of at most 25 amino acid residues. Preferably a plurality of peptides with different flanking sequences is synthesized, in order to efficiently screen for a desired binding compound and/or immunogenic compound.

A peptide of the invention is preferably coupled to a scaffold in order to obtain
15 a compound having a biologically relevant secondary structure. Moreover, scaffold-bound peptides are generally more stable as compared to peptides which are free in solution. One embodiment therefore provides a method according to the invention comprising contacting a produced peptide with a scaffold in order to form at least one linkage between said peptide and said scaffold. Preferably, at least two linkages
20 between said peptide and a scaffold are formed in order to obtain a constrained, biologically relevant structure. In a particularly preferred embodiment a peptide according to the invention is coupled to a scaffold, whereby the formation of a first linkage between said peptide and said scaffold accelerates the formation of a consecutive linkage. This provides the advantage that reactive side chains of said
25 peptide need not be protected by a protecting group during the coupling reaction between said peptide and said scaffold. Once a first linkage is formed, the second linkage is formed quickly enough in order to avoid the formation of too many unfavourable byproducts.

30 Therefore, the invention in one aspect provides a method for producing a compound which is suitable for testing for the presence and/or identification of an immunogenic compound and/or a binding compound, the method comprising:
- selecting at least one amino acid residue within the primary sequence of at least one

- proteinaceous molecule, whereby said selected amino acid residue is preferably at least two amino acid residues located from other selected amino acid residues, if any;
- selecting at least one flanking sequence of at least one selected amino acid residue, which flanking sequence is located in the direction of the N-terminus and/or
- 5 C-terminus of said at least one proteinaceous molecule, said flanking sequence having a length of between 2 and 48 amino acid residues;
- producing a peptide comprising at least one of said flanking sequences and at least two groups capable of reacting with a scaffold, said peptide having a length of at least 4 and at most 50 amino acid residues; and
- 10 - contacting said peptide with said scaffold in order to form at least two linkages between said peptide and said scaffold, whereby the formation of a linkage accelerates the formation of a consecutive linkage.

Produced peptides are preferably contacted with a scaffold in order to form at

15 least two linkages between said peptide and said scaffold, whereby the formation of a linkage between said peptide and said scaffold accelerates the formation of a consecutive linkage between said peptide and said scaffold. A scaffold is defined herein as any solid support capable of binding a peptide of the invention. Once a peptide is bound to a scaffold, its structure is preferably at least in part different from

20 the structure of said peptide when free in solution. The use of a scaffold results in a peptide of the invention with a biologically relevant secondary structure. Moreover, the resulting peptide-scaffold compound is generally more stable as compared to free peptides. It has been demonstrated that the fixed structure of a peptide bound to a scaffold is particularly suitable when said scaffold-bound peptide is to be used as an

25 immunogenic compound and/or a binding compound such as a ligand, agonist or antagonist. Preferably each peptide of a given plurality of peptides of the invention is coupled to essentially the same kind of scaffold, allowing for direct comparison between the individual peptides of said plurality of peptides. If the same kind of scaffold is used, differences between various compounds comprising said scaffold and

30 peptide are more likely to be attributable to the differences between the peptides. In a preferred embodiment an array is produced comprising a plurality of peptides of the invention, each peptide bound to a scaffold, allowing rapid selection of promising compounds from among many test compounds.

In one embodiment a method of the invention is provided wherein said at least two groups capable of reacting with a scaffold are identical. This provides the advantage that at least two linkages between the peptide and a scaffold are formed under the same reaction conditions. For ease of linkage, it is preferred that a peptide of the invention comprises at least one SH-functionality. In a more preferred embodiment said at least two groups capable of reacting with a scaffold are two SH-functionalities. An SH-functionality is defined herein as a part of a peptide (preferably an amino acid residue) comprising a sulfhydryl or thiol group (an SH group). However, other groups are possible. In a further preferred embodiment said at least one SH-functionality is a cysteine residue. In a most preferred embodiment a method of the invention is provided wherein said at least two groups capable of reacting with a scaffold are cysteine residues. In one embodiment, said groups capable of reacting with a scaffold are located at the first amino acid position of said peptide and at the last amino acid position of said peptide. In a further embodiment said groups capable of reacting with a scaffold which groups are located at the first amino acid position and at the last amino acid position of said peptide are cysteine residues. One embodiment therefore provides a method according to the invention comprising producing a peptide wherein the first and the last amino acid residues of said peptide are cysteines. In other embodiments at least one of said groups capable of reacting with a scaffold are located within the peptide sequence, as will be described in more detail throughout this application.

A peptide of the invention comprising at least one flanking sequence is coupled to a scaffold in order to obtain stable compounds with desired biological activities. In principle, any scaffold is suitable. Preferably however scaffold is used whereby the formation of a first linkage between a peptide of the invention and a scaffold accelerates the formation of a second linkage. In one preferred embodiment at least one linkage between a peptide of the invention and a scaffold comprises a thioether linkage. In a further preferred embodiment a peptide of the invention is coupled to a (hetero)aromatic compound, which (hetero)aromatic compound preferably comprises at least two benzylic halogen substituents, preferably a halomethylarene. In a preferred embodiment a peptide of the invention is coupled to a

bis(bromomethyl)benzene, a tris(bromomethyl)benzene, a tetra(bromomethyl)benzene or a derivative thereof. Most preferably a peptide according to the invention is coupled to meta-1,3-bis(bromomethyl)benzene (m-T2), ortho-1,2-bis(bromomethyl)benzene (o-T2), para-1,4-bis(bromomethyl)benzene (p-T2), meta-1,3-bis(bromomethyl)pyridine (m-P2), 2,4,6-tris(bromomethyl)mesitylene (T3) or meta-1,3-bis(bromomethyl)-5-azidobenzene (m-T3-N3).

In a particularly preferred embodiment, a nucleophilic substitution reaction according to WO 2004/077062 is performed in order to couple a peptide according to the invention to a scaffold. Such coupling reaction involves a nucleophilic substitution reaction wherein a molecule with a free nucleophilic functionality reacts with a scaffold. In a preferred embodiment said nucleophilic functionality comprises a thiol or sulfhydryl group. Thiols are effective nucleophiles for substitution at saturated carbon atoms. It is in general not difficult to provide a molecule with a nucleophilic functionality. For example, a peptide or peptidomimetic is easily functionalised with a thiol moiety by incorporating a cysteine residue in the peptide amino acid sequence.

Of course, various other nucleophilic functionalities, like amino acids with an alcohol (-OH) or an amine (-NH) moiety, can be similarly incorporated into a peptide of the invention. However, it should be emphasized that the chemistry required for the coupling reaction of an alcohol or amine in general does not allow to use unprotected peptides, in contrast to a method provided using SH-functionalized peptides. Therefore, a peptide of the invention preferably comprises at least two SH-functionalities, preferably at least two free cysteine sulfhydryl groups. A method according to the invention allows the use of an unprotected peptide wherein none of the amino acid side chains are protected or treated otherwise to prevent unwanted participation in the coupling reaction. Thus, a method according to the invention preferably comprises contacting an essentially unprotected peptide of the invention with a scaffold. Importantly, a method provided herein using an unprotected peptide saves costly time, effort and money because it does not require multistep protection/deprotection steps.

In a preferred embodiment, a peptide according to the invention is coupled to a scaffold by at least two nucleophilic substitution reactions wherein said peptide has at

least two free nucleophilic functionalities that form two bonds or linkages with a scaffold molecule. For instance, said peptide reacts with two, or more, saturated carbon atoms of a scaffold, said carbon atom being part of a reactive group. A nucleophilic substitution can also be an intermolecular process when the nucleophile and leaving group are part of a single molecule or molecular entity. In a preferred embodiment of the invention, a scaffold is provided with at least one molecule via at least one intramolecular nucleophilic substitution reaction. Intramolecular processes have a far more favourable entropy than the analogous intermolecular reactions because it is not necessary for two separate molecules to come together.

10 A common characteristic of a nucleophilic reaction that takes place on saturated carbon, is that the carbon atom is almost always bonded to a heteroatom, which is an atom other than carbon or hydrogen. Furthermore, the heteroatom is usually more electronegative than carbon and is also the so-called leaving group (L) in the substitution reaction. The leaving group departs with the electron pair by which it was originally bonded to the carbon atom. In a preferred embodiment, a scaffold is used which contains at least two leaving groups in order to facilitate the formation of at least two bonds with at least one peptide. The ease with which a leaving group departs can be related to the basicity of that group; weak bases are in general good leaving groups because they are able to accommodate the electron pair effectively. The reactivity of a reactive group is largely determined by the tendency of a leaving group to depart. Another factor which has some bearing on reactivity of a reactive group is the strength of the bond between the leaving group and the carbon atom, since this bond must break if substitution is to occur.

Thus, in a preferred embodiment, a scaffold comprising at least two good leaving groups is used in a method according to the present invention. Good leaving groups are in general the conjugate bases of strong acids. The most important leaving groups are conjugate bases of acids with pKa values below 5. Particularly interesting leaving groups include halide ions such as I-, Br-, and Cl-. A carbon-halogen (C-X) bond in an alkyl halide is polarised, with a partial positive charge on the carbon and a partial negative charge on the halogen. Thus, the carbon atom is susceptible to attack by a nucleophile (a reagent that brings a pair of electrons) and the halogen leaves as the halide ion (X-), taking on the two electrons from the C-X bond. In one embodiment, a reactive group comprises a carbon atom susceptible to attack by a nucleophile wherein

said reactive group comprises a carbon-halogen bond. In a preferred embodiment, a scaffold comprising at least two of such reactive groups is used to react with a di-SH functionalised peptide as nucleophile. Provided is a method according to the invention wherein a peptide of the invention is coupled to a scaffold comprising a

5 halogenoalkane. Halogenoalkanes (also known as haloalkanes or alkyl halides) are compounds containing a halogen atom (fluorine, chlorine, bromine or iodine) joined to one or more carbon atoms in a chain. Provided herein are dihaloscaffolds, comprising two halogen atoms, and tri- and tetrahaloscaffolds for the synthesis of conformationally constraint peptide constructs consisting of one or more looped
10 peptide segments. In general, a good leaving group is electronegative to polarize the carbon atom, it is stable with an extra pair of electrons once it has left, and is polarizable, to stabilize the transition state. With the exception of iodine, all of the halogens are more electronegative than carbon. Chlorine and bromine have fairly similar electronegativities and polarize the bond with the carbon fairly equally. When
15 ionized, both are very weak bases with Br⁻ being the weaker one of the two. Bromide ion is also more polarizable due to its larger size. Therefore, a method provided is advantageously practiced using a scaffold comprising at least two Cl atoms, more preferred using a scaffold comprising at least one Cl atom and at least one Br atom and even more preferred using a scaffold comprising at least two Br atoms.

20 In a preferred embodiment, a scaffold comprises an allylic system. In an allylic system, there are three carbon atoms, two of which are connected through a carbon-carbon double bond. In a preferred embodiment, the formation of a bond or linkage between a scaffold and a peptide according to the invention occurs via an allylic substitution reaction. An allylic substitution reaction refers to a substitution reaction
25 occurring at position 1 of an allylic system, the double bond being between positions 2 and 3. The incoming group is attached to the same atom 1 as the leaving group, or the incoming group becomes attached at the relative position 3, with movement of the double bond from 2/3 to 1/2. The reaction rate of allylic substitutions is very high, because the allyl cation reaction intermediate, a carbon atom bearing a positive
30 charge attached to a doubly-bonded carbon, is unusually stable. This is because an allylic cation is a resonance hybrid of two exactly equivalent structures. In either of the contributing structures, there is an empty p orbital with the pi cloud of the electron-deficient carbon. Overlap of this empty p orbital with the pi cloud of the

double bond results in delocalisation of the pi electrons, hereby providing electrons to the electron-deficient carbon and stabilizing the cation. Even more preferred is a scaffold comprising at least two allylic halogen atoms. Due to electron delocalisation, allyl halides tend to undergo ionization very readily to produce a carbocation and a
5 halide ion, such that breaking the carbon halide bond is rapid.

In a further embodiment of the invention, a carbon-oxygen double bond (i.e. a carbonyl group) is present in a scaffold. Similarly to the allylic system, resonance structures can be formed which contribute to stabilization of a carbocation. For example, a scaffold comprises two or more reactive groups comprising the structure -
10 C(O)-CH₂-halogen.

Furthermore, in a nucleophilic substitution reaction, the structure of the substrate plays just as important role as the nature of the leaving group. For example, if a nucleophile attacks the backside of the carbon, the reaction proceeds unhindered if the leaving group is bonded to a methyl, where the hydrogens leave
15 enough surface to attack the carbon. As that carbon becomes more substituted, larger groups hinder the path the nucleophile must take to displace the leaving group. For these reasons, it is also advantageous that a scaffold comprise at least two halomethyl groups.

In one embodiment, a scaffold comprises a conjugated polyene, also known as
20 aromatic compound, or arene, which is provided with at least two reactive groups. An aromatic compound is flat, with cyclic clouds of delocalised pi electrons above and below the plane of the molecule. Preferably, a molecular scaffold according to the invention comprises at least two benzylic halogen substituents, like for instance halomethyl groups. Suitable examples include, but are not limited, to
25 di(halomethyl)benzene, tri(halomethyl)benzene or tetra(halomethyl)benzene and derivatives thereof. The advantage of a benzylic halogen substituent is mainly to be sought in the special stability associated with the resonance of conjugated polyenes known as aromatic compounds; a benzylic halogen atom has an even stronger tendency to leave a carbon on which a nucleophilic substitution reaction takes place.

30 The embodiment involving reaction of a suitable peptide, such as SH-SH peptides, with halomethylbenzene derivatives is of very wide scope. The reaction runs successfully with a variety of aromatic compounds carrying at least two halomethyl

groups. These groups can be positioned in either *ortho*, *meta*, or *para* position. The intramolecular catalytic effect as described above is different for each mode of coupling because *para* and *meta*-cyclophanes are generally more strained than *ortho*-cyclophanes. Also provided are all other (hetero)aromatic compounds with at least two
5 halomethyl groups in *ortho*-, *meta*-, or *para*-position for the synthesis of a scaffold with at least one looped peptide structure.

Suitable molecular scaffolds for use in a method according to the invention also include polycyclic aromatic compounds with smaller or larger ring structures. However, a scaffold for use in a method according to the invention is not limited to
10 hydrocarbons. In contrast, a method provided is also suitably practiced using a heterocyclic aromatic scaffold – a cyclic molecule with at least one atom other than carbon in the ring structure, most commonly nitrogen, oxygen or sulfur. Examples include pyrrole, furan, thiophene, imidazole, oxazole, thiazole, pyrazole, -3-pyrroline, pyridine, pyrimidine and derivatives thereof. Preferred heterocyclic aromatic scaffold
15 include but are not limited to those comprising at least two halomethyl groups. A preferred scaffold is meta-dibromo-pyridine.

In another embodiment, a method provided comprises the use of a scaffold that is based on or which consists of multiple ring aromatic structures, such as fused-ring aromatic compounds. Two aromatic rings that share a carbon-carbon bond are said to
20 be fused. Suitable fused-ring aromatic scaffolds include for example naphthalene, anthracene or phenanthrene and derivatives thereof, provided that they contain at least two reactive groups. In a preferred embodiment, a fused-ring aromatic scaffold comprises at least two reactive groups wherein each group contains a highly reactive benzylic halogen atom, for example a halomethyl group.

25 Molecules comprising multiple aromatic or conjugated systems wherein the systems do not share a pair of carbon atoms are also useful as scaffold molecule. For example, a scaffold comprises a multi-ring or fused ring structure, for instance a scaffold wherein aromatic, e.g. benzene, rings are connected directly via a carbon-carbon bond can be tested. Alternatively, said rings are connected via a linker
30 comprising at least one atom. Examples of suitable scaffolds in a method of the invention are given in Figures 4, 5 and 6. A person skilled in the art will be able to select which versions of these molecules to use. From a commercial point of view, a scaffold according to the invention is preferably commercially available at a relatively

low cost and can be obtained in large quantities. For example, the dibromoscaffold 1,3-bis(bromomethyl)benzene is currently being sold for only around 5 euro per gram.

A method according to WO 2004/077062 thus allows for simple and
5 straightforward coupling of a peptide according to the invention to a scaffold wherein a first and second reactive group are used. The formation of a first linkage accelerates the formation of a consecutive linkage. Hence, the formation of a first linkage results in a cascade of reactions wherein the formation of a first linkage, also referred to as a (chemical) bond or connection, via a first reactive group increases the reactivity of a
10 second reactive group, and so on. Said chemical reactions involve changes at functional groups while the molecular skeleton of the scaffold remains essentially unchanged. An advantage of a method according to WO 2004/077062 is that essentially unprotected peptides can be coupled to a scaffold and the scaffold need not be selectively functionalized. Moreover, a method according to WO 2004/077062
15 allows coupling of a peptide according to the present invention in an aqueous solution, whereas other known coupling procedures are often performed in organic solvents via multiple protection-deprotection cycles. A preferred embodiment therefore provides a method according to the present invention wherein a peptide is coupled to a scaffold wherein the formation of a first linkage between said peptide and said scaffold
20 accelerates the formation of a second linkage between said peptide and said scaffold. A further preferred embodiment provides a method according to the invention wherein said peptide is coupled to a scaffold in solution. Most preferably, an aqueous solution is used.

25 Outlined below is a non-limiting schematic example of one embodiment according to the present invention. In this example two amino acid residues of a proteinaceous molecule of interest are selected. Said amino acid residues are preferably both selected from a surface-exposed region of said proteinaceous molecule. Said selected amino acid residues are preferably at least two amino acid residues
30 located from each other so that a flanking sequence of a first selected amino acid residue can be selected that does not comprise a second selected amino acid residue.

In this schematic example, the primary sequence of (part of) a proteinaceous molecule is represented by the sequence $X_1 - X_{24}$ (X stands for any amino acid residue):

Primary sequence

5 $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}X_{22}X_{23}X_{24}$

Subsequently, amino acid residues X_{10} and X_{15} are for instance selected.

Then, the following flanking sequences are for instance chosen:

10 Flanking sequences of X_{10} : $X_5X_6X_7X_8X_9$ and $X_{11}X_{12}$

Flanking sequences of X_{15} : $X_{13}X_{14}$ and $X_{16}X_{17}X_{18}X_{19}X_{20}$

Subsequently, peptides are produced comprising at least one of said flanking sequences and at least two groups capable of reacting with a scaffold. In this example, 15 said two groups capable of reacting with a scaffold are two cysteine residues, which are the first and last amino acid residues of said peptide. Of course, many alternative groups can be used and the positions of said groups within said peptide can be varied.

In this example the following peptides are for instance generated:

20

Peptides comprising 1 flanking sequence:

$CX_5X_6X_7X_8X_9C$

$CX_{11}X_{12}C$

$CX_{13}X_{14}C$

25

$CX_{16}X_{17}X_{18}X_{19}X_{20}C$

Peptides comprising 2 flanking sequences:

$CX_5X_6X_7X_8X_9X_5X_6X_7X_8X_9C$

$CX_5X_6X_7X_8X_9X_{11}X_{12}C$

30

$CX_5X_6X_7X_8X_9X_{13}X_{14}C$

$CX_5X_6X_7X_8X_9X_{16}X_{17}X_{18}X_{19}X_{20}C$

- 5 CX₁₁X₁₂X₅X₆X₇X₈X₉C
 CX₁₁X₁₂X₁₁X₁₂C
 CX₁₁X₁₂X₁₃X₁₄C
 CX₁₁X₁₂X₁₆X₁₇X₁₈X₁₉X₂₀C
- 10 CX₁₃X₁₄X₅X₆X₇X₈X₉C
 CX₁₃X₁₄X₁₁X₁₂C
 CX₁₃X₁₄X₁₃X₁₄C
 CX₁₃X₁₄X₁₆X₁₇X₁₈X₁₉X₂₀C
- 15 CX₁₆X₁₇X₁₈X₁₉X₂₀X₅X₆X₇X₈X₉C
 CX₁₆X₁₇X₁₈X₁₉X₂₀X₁₁X₁₂C
 CX₁₆X₁₇X₁₈X₁₉X₂₀X₁₃X₁₄C
 CX₁₆X₁₇X₁₈X₁₉X₂₀X₁₆X₁₇X₁₈X₁₉X₂₀C

Some possible peptides comprising 3 flanking sequences:

- 20 CX₅X₆X₇X₈X₉X₅X₆X₇X₈X₉X₅X₆X₇X₈X₉C
 CX₅X₆X₇X₈X₉X₅X₆X₇X₈X₉X₁₁X₁₂C
 CX₅X₆X₇X₈X₉X₅X₆X₇X₈X₉X₁₃X₁₄C
 CX₅X₆X₇X₈X₉X₅X₆X₇X₈X₉X₁₆X₁₇X₁₈X₁₉X₂₀C
- 25 CX₅X₆X₇X₈X₉X₁₁X₁₂X₅X₆X₇X₈X₉C
 CX₅X₆X₇X₈X₉X₁₁X₁₂X₁₁X₁₂C
 CX₅X₆X₇X₈X₉X₁₁X₁₂X₁₃X₁₄C
 CX₅X₆X₇X₈X₉X₁₁X₁₂X₁₆X₁₇X₁₈X₁₉X₂₀C
- CX₅X₆X₇X₈X₉X₁₃X₁₄X₅X₆X₇X₈X₉C
 CX₅X₆X₇X₈X₉X₁₃X₁₄X₁₁X₁₂C

CX₅X₆X₇X₈X₉X₁₃X₁₄X₁₃X₁₄C

CX₅X₆X₇X₈X₉X₁₃X₁₄X₁₆X₁₇X₁₈X₁₉X₂₀C

CX₅X₆X₇X₈X₉X₁₆X₁₇X₁₈X₁₉X₂₀X₅X₆X₇X₈X₉C

5 CX₅X₆X₇X₈X₉X₁₆X₁₇X₁₈X₁₉X₂₀X₁₁X₁₂C

CX₅X₆X₇X₈X₉X₁₆X₁₇X₁₈X₁₉X₂₀X₁₃X₁₄C

CX₅X₆X₇X₈X₉X₁₆X₁₇X₁₈X₁₉X₂₀X₁₆X₁₇X₁₈X₁₉X₂₀C

CX₁₁X₁₂X₅X₆X₇X₈X₉X₅X₆X₇X₈X₉C

10 CX₁₁X₁₂X₅X₆X₇X₈X₉X₁₁X₁₂C

CX₁₁X₁₂X₅X₆X₇X₈X₉X₁₃X₁₄C

CX₁₁X₁₂X₅X₆X₇X₈X₉X₁₆X₁₇X₁₈X₁₉X₂₀C

CX₁₁X₁₂X₁₁X₁₂X₅X₆X₇X₈X₉C

15 CX₁₁X₁₂X₁₁X₁₂X₁₁X₁₂C

CX₁₁X₁₂X₁₁X₁₂X₁₃X₁₄C

CX₁₁X₁₂X₁₁X₁₂X₁₆X₁₇X₁₈X₁₉X₂₀C

et cetera

20

Produced peptides are subsequently preferably coupled to a scaffold in order to generate a (test) compound according to the present invention. Preferably, a plurality of different peptides are coupled to scaffolds in order to produce a plurality of test compounds.

25

It will be evident that further combinations of three flanking sequences are possible in the above mentioned schematic example. Moreover, other peptides comprising more than three flanking sequences can be designed. However, the total length of the peptides does preferably not exceed 50 amino acid residues.

Furthermore, various embodiments of the invention involve the selection of flanking sequences of various different lengths. For instance, in the above mentioned schematic example the following flanking sequences of X_{10} are for instance selected:

$X_1X_2X_3X_4X_5X_6X_7X_8X_9$ and/or
 5 $X_2X_3X_4X_5X_6X_7X_8X_9$ and/or
 $X_3X_4X_5X_6X_7X_8X_9$ and/or
 $X_4X_5X_6X_7X_8X_9$ and/or
 $X_5X_6X_7X_8X_9$ and/or
 $X_6X_7X_8X_9$ and/or
 10 $X_7X_8X_9$ and/or
 X_8X_9 and/or
 X_9 and/or
 $X_{11}X_{12}X_{13}$ and/or
 $X_{11}X_{12}$ and/or
 15 X_{11}

By varying the kind, length and amount of flanking sequences, peptides of different kinds and/or lengths are produced. Preferably, peptides between 4-25 amino
 20 acid residues are generated.

The number of selected amino acid residues of a given proteinaceous molecule is variable and depends on a particular application. In one preferred embodiment at least two amino acid residues are selected. A method according to the invention is
 25 thus provided wherein at least two amino acid residues within the primary sequence of said at least one proteinaceous molecule are selected. In view of efficacy, at most five amino acid residues are preferably selected. Preferably, three or four amino acid residues are selected. In a particularly preferred embodiment two amino acid residues are selected.

30 It is of course also possible to perform a method of the invention with one selected amino acid residue of a proteinaceous molecule. In that case a peptide of the

invention comprises at least one flanking sequence of said one selected amino acid residue that is located in the direction of the N-terminus of said proteinaceous molecule and/or at least one flanking sequence of said one selected amino acid residue that is located in the direction of the C-terminus of said proteinaceous molecule. Of course, as outlined above, various flanking sequences of different length can be used.

The number and length of selected flanking sequences depends on a particular application. In one preferred embodiment a peptide is produced which comprises at least two flanking sequences. Said flanking sequences may be different from each other, or they may be the same. In one embodiment at least two flanking sequences of the same selected amino acid residue are incorporated into a peptide. In another embodiment however a peptide is produced which comprises a flanking sequence of a first selected amino acid residue and a flanking sequence of a second selected amino acid residue.

In a method according to the invention a peptide is produced which peptide comprises at least two groups capable of reacting with a scaffold. In a preferred embodiment said groups comprise at least one SH-group, preferably at least one cysteine residue, because a SH-group is particularly suitable for coupling a peptide to a scaffold comprising a (hetero)aromatic molecule. The use of a scaffold comprising a (hetero)aromatic molecule (preferably comprising at least one benzylic halogen substituent) is preferred, as already outlined above. If a group comprising at least one SH-group (for instance a cysteine residue) is used in a coupling reaction of a peptide with a scaffold, it is preferred that said peptide is at least in part devoid of other available cysteine residues. An available cysteine (residue) is defined as a cysteine whose SH-group is capable of reacting with another group. Hence, cysteine residues whose SH-group is not capable of reacting with another group, for instance because they are provided with a protecting group, are not covered by the term "available cysteine". If a peptide of the invention comprises other available cysteines, such other available cysteines could react with the scaffold instead of said at least one group that was intended to react with said scaffold. This way, unintended bonds between said peptide and said scaffold could be formed. Furthermore, said other available cysteines could form a disulfide bond with said group comprising an SH-group that was intended to react with said scaffold. In that case a coupling reaction between said

peptide and said scaffold could also be distorted. These problems are at least in part avoided when at least one cysteine residue present in a flanking region is replaced by a group that is incapable of forming a bond with other sulfhydrylgroup-containing moieties. In one embodiment this is performed with protecting groups or mimetics.

5 For instance, a cysteine that is protected with a removable protecting group, such as for instance a Cys(StBu) or, most preferably, a cysteine-(acetamidomethyl) group (Cys(Acm)), is used. Following attachment of a peptide of the invention to a scaffold to yield a compound of the invention, the protecting group is easily removed, for instance by reductive treatment. For instance, 1,4-DDT or ethane dithiol is used. It is also

10 possible to replace a cysteine residue of a flanking sequence by a bioisosteric unit. A bioisosteric unit is defined as a functionality having similar size and physicochemical properties.

Most preferably at least one cysteine in at least one of said flanking sequences is replaced by another amino acid residue that is unreactive with the scaffold, for

15 example an alanine residue. Provided is thus a method according to the invention wherein at least one cysteine in at least one of said flanking sequences is replaced by another amino acid residue. Most preferably all cysteines in all flanking sequences that are incorporated into a peptide are replaced by other amino acid residues that are unreactive with the scaffold that is used, in order to prevent attachment of said

20 peptide to the scaffold via a group other than the two groups having a SH group that are intended to bind to the scaffold.

In one preferred embodiment peptides of various different length are synthesised in order to provide a more diverse collection of potential binding

25 compounds and/or immunogenic compounds. Interactions between binding molecules and immunogenic interactions are often very specific. Hence, not only the sequence of a peptide of the invention but also its length is often relevant if a screen for a specific interaction is performed. Provided is therefore a method according to the invention comprising producing at least two peptides of different length. Most preferably, a

30 plurality of peptides with a length of between 6 and 25 amino acid residues is generated. If the secondary, tertiary and/or quaternary structure of a proteinaceous molecule of interest is known, it is furthermore preferred to select at least one amino acid residue from a surface-exposed region of said proteinaceous molecule.

If however the secondary, tertiary and/or quaternary structure of a proteinaceous molecule of interest is not, or only partly, known it is preferred to perform a preliminary screening. In that case a plurality of overlapping peptides is preferably synthesised which peptides have essentially the same length. Preferably 2, 3 or 4 sets of peptides are synthesised, wherein one set of peptides comprises peptides of about the same length. For instance, two sets of peptides are produced wherein one set comprises peptides with a length of about 8 amino acid residues and wherein the other set comprises peptides with a length of about 15 amino acid residues. According to this embodiment, said plurality of overlapping peptides (which is preferably coupled to a scaffold) is tested for a desired functionality (for instance their capability of binding to a binding compound of interest such as for example an antibody, T cell, ligand or receptor). If one or more peptides are found to be promising candidates, it is preferably determined from which region(s) of said proteinaceous molecule said promising candidates appear to be derived. Once said region(s) of said proteinaceous molecule is/are identified, a second procedure is preferably followed. In this second procedure a method of the invention is performed again. This time at least one amino acid residue is selected which is present in at least one of the above-mentioned region(s) identified in the first procedure.

In one embodiment a peptide which appears to be a promising candidate is combined with a second peptide (with formula $(X)_y$). Said second peptide is preferably at least in part derived from the same proteinaceous molecule. For instance, if two cysteine residues are used as groups that are capable of reacting with a scaffold, and if a promising peptide found during a screening is depicted as $(X)_x$, peptides with the formula $C(X)_xC(X)_y$ and/or $(X)_xC(X)_yC$ are preferably synthesised. In this formula C is a cysteine residue, $(X)_x$ represents at least one flanking sequence and $(X)_y$ represents any sequence derived from said at least one proteinaceous molecule. Preferably, $(X)_x$ and $(X)_y$ each represent at least one flanking sequence.

The resulting peptides are once again preferably coupled to a scaffold in order to produce stable test compounds according to the present invention. Said test compounds are preferably screened again for a desired functionality (for instance their capability of binding to a binding compound of interest such as for example an

antibody, T cell, ligand or receptor). Preferably, said test compounds are tested for the same functionality as compared to a first screening during which the promising peptide (X)_x was selected. This embodiment of the invention is particularly suitable for producing and/or identifying an immunogenic compound and/or a binding
5 compound that is at least in part derived from a proteinaceous molecule whose secondary, tertiary and/or quaternary structure is not, or only partly, known. According to one embodiment, 2, 3 or 4 sets of peptides are synthesised, wherein one set of peptides comprises peptides of about the same length, and the resulting peptides are subjected to a first screening assay using a binding molecule of interest.
10 Peptides which appear to be promising candidates are subsequently coupled to a second peptide which is also derived from said proteinaceous molecule whose secondary, tertiary and/or quaternary structure is not, or only partly, known in order to generate compounds with the formula C(X)_xC(X)_y and/or (X)_xC(X)_yC. The resulting peptides are subsequently screened again with a second screening assay using a
15 binding molecule of interest.

One embodiment thus provides a method according to the invention wherein a peptide is produced that comprises the format C(X)_xC(X)_y or C(X)_yC(X)_x and wherein C is a cysteine residue, (X)_x represents at least one of said flanking sequences and (X)_y represents any sequence derived from said at least one proteinaceous molecule.
20 Preferably, (X)_x and (X)_y each represent at least one of said flanking sequences.

Overlapping peptides are defined herein as peptides derived from a primary sequence of a proteinaceous molecule, wherein each peptide has at least one amino acid residue of said primary sequence in common with another peptide. For instance,
25 a plurality of peptides of length n are produced, wherein the first peptide starts at position 1 and ends at position n of the primary sequence of said proteinaceous molecule. The second peptide starts at position 2 and ends at position n+1 of the primary sequence of said proteinaceous molecule. The third peptide starts at position 3 and ends at position n+2 of the primary sequence of said proteinaceous molecule, et
30 cetera. Peptides which have essentially the same length are defined herein as peptides whose amounts of amino acid residues differ at most 5 amino acid residues

from each other. Preferably, said peptides have exactly the same amount of amino acid residues.

5 A peptide according to the invention preferably comprises at least two groups capable of reacting with a scaffold. If a peptide of the invention has two groups capable of reacting with a scaffold, a scaffold is preferably used which has two sites suitable for binding. The phrases "sites suitable for binding" and "binding sites" are used herein interchangeably and are defined as sites that are capable of binding a group capable of reacting with a scaffold, which group is present on a peptide
10 according to the invention. Said group is preferably a SH functionality, which is preferably used for a nucleophilic substitution reaction. An example of a suitable binding site of a scaffold is therefore a saturated carbon which is bonded to a heteroatom which heteroatom is more electronegative than carbon.

15 An example of a scaffold comprising two binding sites is an aromatic molecule comprising two halogen substituents. Preferably a bis(bromomethyl)benzene, a (bromomethyl)(chloromethyl)benzene or a bis(chloromethyl)benzene is used. Most preferably, meta-dibromoxylene (m-T2) is used.

In one embodiment a peptide according to the invention is produced which comprises at least three groups capable of reacting with a scaffold. This embodiment
20 provides the advantage that at least two loops are formed by a peptide of the invention which is bound to a scaffold at three sites. Each of said at least two loops is suitable for testing for the presence of a continuous binding site and/or immunogenic site. Preferably however at least two loops are tested together in order to search for the presence of a discontinuous binding site and/or immunogenic site. In a preferred
25 embodiment each loop comprises at least part of a flanking sequence, so that the characteristics of various (parts of) flanking sequences are tested simultaneously. Hence, a peptide of the invention preferably comprises at least two flanking sequences and at least three groups capable of reacting with a scaffold. Preferably said at least three groups capable of reacting with a scaffold are cysteine residues. A method
30 according to the invention is therefore provided wherein said peptide comprises at least three cysteine residues and at least two flanking sequences.

Of course, if a peptide of the invention contains three groups capable of reacting with a scaffold, a scaffold is preferably used which has (at least) three sites

suitable for binding. For instance an aromatic molecule comprising three halogen substituents is used. Said aromatic molecule preferably comprises a tris(bromomethyl)benzene, a bis(bromomethyl)(chloromethyl)benzene, a (bromomethyl)bis(chloromethyl)benzene or a tris(chloromethyl)benzene. Most
5 preferably, 2,4,6-tris(bromomethyl)mesitylene (T3) is used.

Likewise, if a peptide of the invention contains four groups capable of reacting with a scaffold, a scaffold is preferably used which has four sites suitable for binding. An aromatic molecule comprising four halogen substituents is preferably used. Said aromatic molecule preferably comprises a tetra(bromomethyl)benzene, a
10 tris(bromomethyl)(chloromethyl)benzene, a bis(bromomethyl)bis(chloromethyl)benzene, a (bromomethyl)tris(chloromethyl)benzene or a tetra (chloromethyl) benzene. Most preferably, 1,2,4,5 tetrabromodurene (T4) is used.

15 In one preferred embodiment a peptide with the formula $C(X)_x C(X)_y C$ or $C(X)_y C(X)_x C$ is produced. In this formula, C is a group capable of reacting with a scaffold, preferably a cysteine residue, $(X)_x$ represents at least one flanking sequence and $(X)_y$ represents any sequence derived from a proteinaceous molecule of interest. $(X)_y$ is preferably derived from the same proteinaceous molecule as $(X)_x$. Preferably,
20 $(X)_x$ and $(X)_y$ each represent at least one flanking sequence. In one embodiment the length of $(X)_x$ and $(X)_y$ is about the same, meaning that the difference between the amount of amino acid residues of $(X)_x$ and the amount of amino acid residues of $(X)_y$ is five or less. If such peptides are bound to a scaffold, two loops of essentially the same length are produced. This is however not necessary: in another embodiment the
25 length of $(X)_x$ and $(X)_y$ are significantly different from each other, meaning that the amount of amino acid residues of $(X)_x$ and the amount of amino acid residues of $(X)_y$ differ from each other by more than five amino acid residues. If such peptide is coupled to a scaffold, two loops of significantly different length is obtained.

30 A peptide with the above-mentioned formula, containing three groups capable of reacting with a scaffold, is preferably coupled to a scaffold with three binding sites.

Said peptide is preferably coupled to an aromatic molecule comprising three halogen substituents, more preferably to a tris(bromomethyl)benzene, most preferably to 2,4,6-tris(bromomethyl)mesitylene (T3). This for instance results in a structure as depicted in figure 7, which is particularly suitable for testing two peptide loops on one
5 scaffold.

A peptide with the formula $C(X)_x C(X)_y C$ or $C(X)_y C(X)_x C$ is produced in a variety of embodiments. In one embodiment various flanking sequences of a proteinaceous molecule of interest are selected, and said flanking sequences are
10 randomly combined in order to yield peptides with the formula $C(X)_x C(X)_y C$ or $C(X)_y C(X)_x C$ wherein $(X)_x$ and $(X)_y$ both comprise at least one flanking sequence. Said flanking sequences are preferably selected from at least one surface-exposed region of a proteinaceous molecule of interest. In another embodiment, a method of the invention is firstly performed in order to produce a plurality of peptides. Said
15 plurality of peptides is screened with a binding molecule of interest, such as for instance an antibody and/or T cell, in order to identify at least one promising candidate peptide of the formula $(X)_x$ with a desired immunogenic and/or binding property. Said promising candidate peptide is subsequently combined with another peptide with the formula $(X)_y$ in order to obtain a peptide with the formula
20 $C(X)_x C(X)_y C$ or $C(X)_y C(X)_x C$. Said peptide with the formula $(X)_y$ is preferably derived from the same proteinaceous molecule as said promising candidate peptide of the formula $(X)_x$. In one preferred embodiment a plurality of peptides with the formula $(X)_y$ is produced comprising overlapping peptides which are at least in part derived from the same proteinaceous molecule as said promising candidate peptide of the
25 formula $(X)_x$. Each peptide $(X)_y$ comprising an overlapping peptide is subsequently coupled to a promising candidate peptide of the formula $(X)_x$. The resulting peptides $C(X)_x C(X)_y C$ or $C(X)_y C(X)_x C$ are subsequently screened again, preferably in the same kind of screening assay during which promising candidate peptide of the formula $(X)_x$ was selected. If at least one peptide $C(X)_x C(X)_y C$ or $C(X)_y C(X)_x C$ appears to have a
30 desired immunogenic property and/or binding property, said peptide is selected.

If a peptide with the formula $C(X)_xC(X)_yC$ or $C(X)_yC(X)_xC$ is at least in part derived from a transmembrane protein, peptides $(X)_x$ and $(X)_y$ are preferably both derived from an extracellular loop domain of said transmembrane protein and/or from the free N-terminus. The free N-terminus of a transmembrane protein is defined
5 herein as the linear N-terminal part of said protein, starting at amino acid 1 and ending at the first amino acid residue of the first transmembrane domain (mostly a transmembrane helix). In one embodiment, a method of the invention is firstly performed wherein at least one amino acid residue present in an extracellular loop domain and/or the free N-terminus of a transmembrane protein is selected. According
10 to this embodiment, produced peptides comprising at least one flanking sequence present in said extracellular loop domain and/or in said free N-terminus are screened with a binding molecule of interest, such as for instance an antibody and/or T cell, in order to identify at least one promising candidate peptide of the formula $(X)_x$ with a desired immunogenic and/or binding property. Said promising candidate peptide is
15 subsequently combined with another peptide with the formula $(X)_y$ comprising at least one flanking sequence from an extracellular loop domain and/or the free N-terminus of said transmembrane protein in order to obtain a peptide with the formula $C(X)_xC(X)_yC$ or $C(X)_yC(X)_xC$. In one embodiment $(X)_x$ and $(X)_y$ comprise at least one flanking sequence derived from the same extracellular loop domain and/or
20 free N-terminus. Alternatively, or additionally, $(X)_x$ and $(X)_y$ comprise at least one flanking sequence derived from different domains of said transmembrane protein.

If a peptide with the formula $C(X)_xC(X)_yC$ or $C(X)_yC(X)_xC$ is at least in part derived from a proteinaceous molecule comprising at least two internal cystine bonds
25 between cysteine residues, such as a member of the cys-knot superfamily, peptides $(X)_x$ and $(X)_y$ preferably both comprise at least one flanking sequence of one or more cysteine residues of said proteinaceous molecule. Preferably, a method of the invention is performed wherein only cysteine residues of said proteinaceous molecule are selected. As a result, peptides are produced that comprise only (combinations of)
30 flanking sequences of at least one cysteine residue.

If the (secondary, tertiary and/or quaternary) structure of a proteinaceous molecule of interest is not known, a set of overlapping peptides is preferably generated. In one embodiment, three groups capable of reacting with a scaffold are placed at three sites within each overlapping peptide. The resulting peptide is

5 subsequently preferably coupled to a scaffold comprising (at least) three binding sites in order to provide a test compound according to the invention. In a preferred embodiment one group capable of reacting with a scaffold is placed at the first amino acid residue of an overlapping peptide, one group capable of reacting with a scaffold is placed at the last amino acid residue of said overlapping peptide and one group

10 capable of reacting with a scaffold is placed between said first and said last group capable of reacting with a scaffold. Since said groups capable of reacting with a scaffold are preferably cysteine residues, a peptide is preferably produced with the formula $C(X)_xC(X)_yC$ wherein $(X)_x$ and $(X)_y$ are preferably part of the same overlapping peptide. This peptide $C(X)_xC(X)_yC$ is preferably produced by replacing

15 the first amino acid residue of the sequence of an overlapping peptide, the last amino acid residue of the sequence of said overlapping peptide and one amino acid residue located in between said first and last amino acid residues by a cysteine. Alternatively, $(X)_x$ and $(X)_y$ each comprise an overlapping peptide. In one embodiment $(X)_x$ and $(X)_y$ contain about the same amount of amino acid residues. In that case, a set of

20 overlapping peptides consisting of n amino acid residues is preferably produced, wherein n is an odd number. Subsequently, amino acid residues 1, $(n+1)/2$ and n are replaced by cysteine. Other available cysteine residues are preferably either replaced by another amino acid residue or rendered inactive (for instance by a protective group) so that said other available cysteine residues do not interfere with the coupling

25 reaction between said peptide and a scaffold. The resulting peptides, $C(X)_xC(X)_yC$, are subsequently preferably coupled to a scaffold comprising (at least) three binding sites and subsequently tested for a desired characteristic.

In a further embodiment, a peptide with the formula $C(X)_xC(G)_nC(X)_yC$ or

30 $C(X)_yC(G)_nC(X)_xC$ is produced. In this formula, C represents a group capable of reacting with a scaffold, preferably a cysteine residue, $(G)_n$ represents a spacer, $(X)_x$

represents at least one flanking sequence and $(X)_y$ represents any sequence derived from at least one proteinaceous molecule. Preferably, $(X)_x$ and $(X)_y$ each represent at least one flanking sequence of the same proteinaceous molecule of interest.

Of course, it is also possible to replace the spacer by another flanking sequence
 5 $(X)_z$. In that case a peptide with formula $C(X)_xC(X)_zC(X)_yC$, $C(X)_xC(X)_yC(X)_zC$,
 $C(X)_yC(X)_zC(X)_xC$, $C(X)_yC(X)_xC(X)_zC$, $C(X)_zC(X)_xC(X)_yC$ and/or
 $C(X)_zC(X)_yC(X)_xC$ is produced.

Peptides with the above mentioned formulae are particularly suitable for
 coupling to a scaffold comprising (at least) four binding sites, or to two scaffolds
 10 wherein each scaffold comprises (at least) two binding sites. Non-limiting schematic
 examples of resulting compounds are depicted in figures 7 and 8.

If two scaffolds with at least two binding sites are used, such as for instance
 two separate m-P2 molecules, it is sometimes desired to regulate which cysteine
 15 residues are coupled to the first scaffold and which cysteine residues are coupled to
 the second scaffold. For instance, if a peptide with the formula
 $C_1(X)_xC_2(G)_nC_3(X)_yC_4$ is used, C_1 and C_2 are often intended to bind a first scaffold,
 whereas C_3 and C_4 are intended to bind a second scaffold. This is for instance
 performed by providing two cysteine residues that are intended to bind to a second
 20 scaffold (for instance C_3 and C_4) with a protecting group such as for instance
 methoxytrityl (Mmt) or trityl (Trt). In a first coupling reaction, a peptide comprising
 protected C_3 and C_4 is incubated with a first scaffold. Only C_1 and C_2 are now
 capable of binding the scaffold. Subsequently, C_3 and C_4 are deprotected. The
 resulting complex is now incubated with a second scaffold, which may be the same
 25 kind of scaffold as said first scaffold (although this is not necessary; said second
 scaffold and said first scaffold may as well be different from each other). This time, C_3
 and C_4 are capable of binding with said second scaffold. This way, C_1 and C_2 are
 bound to the first scaffold, and C_3 and C_4 are bound to the second scaffold. Of course,
 other combinations are possible.

If a peptide with the formula $C(X)_xC(G)_nC(X)_yC$, $C(X)_yC(G)_nC(X)_xC$,
 $C(X)_xC(X)_zC(X)_yC$, $C(X)_xC(X)_yC(X)_zC$, $C(X)_yC(X)_zC(X)_xC$, $C(X)_yC(X)_xC(X)_zC$,
 $C(X)_zC(X)_xC(X)_yC$ or $C(X)_zC(X)_yC(X)_xC$ is at least in part derived from a
transmembrane protein, peptides $(X)_x$ and $(X)_y$ and optionally $(X)_z$ are preferably
5 derived from an extracellular loop domain of said transmembrane protein and/or from
the free N-terminus. In one embodiment, a method of the invention is performed
wherein at least one promising peptide with the formula $(X)_x$ is selected during a first
screening method as described above, which peptide with the formula $(X)_x$ comprises
at least one flanking sequence derived from an extracellular loop domain and/or the
10 free N-terminus of a transmembrane protein. Said promising peptide of the formula
 $(X)_x$ is subsequently combined with another peptide with the formula $(X)_y$ and/or with
another peptide with the formula $(X)_z$ in order to obtain a peptide with a formula
selected from the group consisting of $C(X)_xC(G)_nC(X)_yC$, $C(X)_yC(G)_nC(X)_xC$,
 $C(X)_xC(X)_zC(X)_yC$, $C(X)_xC(X)_yC(X)_zC$, $C(X)_yC(X)_zC(X)_xC$, $C(X)_yC(X)_xC(X)_zC$,
15 $C(X)_zC(X)_xC(X)_yC$ and $C(X)_zC(X)_yC(X)_xC$. In one embodiment $(X)_x$ and $(X)_y$ and,
optionally, $(X)_z$ comprise at least one flanking sequence derived from the same
extracellular loop domain and/or from the free N-terminus. Alternatively, or
additionally, $(X)_x$ and $(X)_y$ and, optionally, $(X)_z$ comprise at least one flanking
sequence derived from a different domain of said transmembrane protein.

20

If a peptide with a formula selected from the group consisting of
 $C(X)_xC(G)_nC(X)_yC$, $C(X)_yC(G)_nC(X)_xC$, $C(X)_xC(X)_zC(X)_yC$, $C(X)_xC(X)_yC(X)_zC$,
 $C(X)_yC(X)_zC(X)_xC$, $C(X)_yC(X)_xC(X)_zC$, $C(X)_zC(X)_xC(X)_yC$ and $C(X)_zC(X)_yC(X)_xC$ is
at least in part derived from a proteinaceous molecule comprising at least two
25 internal cystine bonds between cysteine residues, such as for instance a member of
the cys-knot superfamily, peptides $(X)_x$ and $(X)_y$ and, optionally, $(X)_z$ preferably
comprise at least one flanking sequence of one or more cysteine residues of said
proteinaceous molecule. Preferably, a method of the invention is performed wherein
only cysteine residues of said proteinaceous molecule are selected. As a result,
30 peptides are produced that comprise only (combinations of) flanking sequences of at

least one cysteine residue. In one preferred embodiment peptides are generated which comprise at least one flanking sequence of at least two cysteine residues of said proteinaceous molecule. Most preferably peptides are generated which comprise at least two flanking sequences of at least two cysteine residues of said proteinaceous molecule.

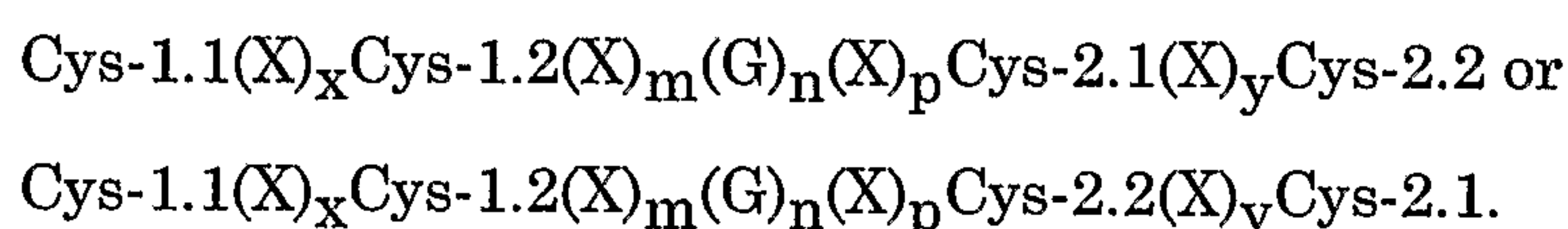
In one preferred embodiment a method according to the invention is performed as follows. A plurality of peptides is produced comprising a first cysteine Cys-1 of a SS-bridge of a proteinaceous molecule, a flanking sequence $(X)_x$ of said Cys-1 which flanking sequence is located in the direction of the C-terminus and has a length of x amino acid residues, followed by a second cysteine C, followed by n glycine residues $(G)_n$, followed by a third cysteine C, followed by a flanking sequence $(X)_y$ of the second cysteine residue Cys-2 of said SS-bridge which flanking sequence is located in the direction of the N-terminus and has a length of y amino acid residues, followed by the second cysteine Cys-2 of said SS-bridge. The resulting peptide contains the formula Cys-1 $(X)_xC(G)_nC(X)_y$ Cys-2. A plurality of different peptides is preferably synthesized wherein 0 is smaller than or equal to x, n, and y and wherein x, n, and y are smaller than or equal to 6. Additionally, $x+n+y$ is preferably smaller than or equal to 21, so that the resulting peptide is smaller than or equal to 25 amino acid residues. Produced peptides are subsequently preferably screened for a desired immunogenic characteristic and/or binding property. This is preferably performed after coupling of said peptide to a scaffold comprising (at least) four binding sites or to two scaffolds, each comprising (at least) two binding sites. Most preferably, said peptide is coupled to a T4 scaffold or to two T2 scaffolds. If two scaffolds are used, each scaffold comprising (at least) two binding sites, the two cysteine residues Cys-1 and Cys-2 are preferably coupled to the same scaffold in order to form a loop. The other two cysteine residues are preferably coupled to another scaffold in order to form a loop. As already explained hereinbefore, this is for instance accomplished by providing Cys-1 and Cys-2 with a protecting group while leaving the other two cysteine residues unprotected. In that case, the unprotected cysteine are coupled to a scaffold in order to form a loop. Subsequently, Cys-1 and Cys-2 are deprotected and coupled to another scaffold.

It is also possible to provide Cys-1 and Cys-2 with a first kind of protecting group, such as for instance Trt, and to provide the other two cysteine residues with a second kind of protecting group, such as for instance Mmt. Both kind of protecting groups are removed using different reagentia. This way, it is possible to determine
 5 what cysteine residues are capable of binding to a scaffold.

In a further embodiment a peptide with the formula $C(X)_x C(X)_m (G)_n (X)_p C(X)_y C$ is produced. In this formula, C represents a group capable of reacting with a scaffold, preferably a cysteine residue, $(G)_n$ represents a
 10 spacer, and $(X)_x$, $(X)_m$, $(X)_p$ and $(X)_y$ each represent at least one flanking sequence of a proteinaceous molecule of interest. This peptide is particularly suitable for coupling to two scaffolds, wherein each scaffold comprises (at least) two binding sites.

In a preferred embodiment, a peptide of this formula is synthesized using flanking sequences of a proteinaceous molecule of interest that comprises (at least)
 15 two SS-bridges, wherein in the primary sequence of said proteinaceous molecule the first cysteine of the second SS-bridge is located N-terminally from the second cysteine of the first SS-bridge, wherein said first cysteine of the second SS-bridge and said second cysteine from the first SS-bridge are preferably located within 6 amino acid residues from each other, and wherein the position of each cysteine of said SS-bridges
 20 within the primary sequence of said proteinaceous molecule is known. Hence, if the first cysteine of the second SS-bridge is located at position n, the second cysteine from the first SS-bridge is preferably located at position n+1, n+2, n+3, n+4, n+5 or n+6. According to this embodiment, a plurality of peptides is produced comprising the first cysteine Cys-1.1 of the first SS-bridge, a flanking sequence $(X)_x$ of said Cys-1.1 which
 25 flanking sequence is located in the direction of the C-terminus and has a length of x amino acid residues, followed by the first cysteine Cys-1.2 of the second SS-bridge, followed by a flanking sequence $(X)_m$ of said Cys-1.2 which flanking sequence is located in the direction of the C-terminus and has a length of m amino acid residues, followed by n glycine residues $(G)_n$, followed by a flanking sequence of the third
 30 cysteine residue present in said primary sequence – which may either be the second cysteine of the first SS-bridge (Cys-2.1) or the second cysteine of the second SS-bridge (Cys-2.2) – which flanking sequence is located in the direction of the N-terminus and

has a length of p amino acid residues, followed by said third cysteine residue, followed by a flanking sequence of the fourth cysteine residue present in said primary sequence which flanking sequence is located in the direction of the C-terminus and has a length of y amino acid residues, followed by the fourth cysteine residue present in said primary sequence, which may either be the second cysteine of the first SS-bridge (Cys-2.1) or the second cysteine of the second SS-bridge (Cys-2.2). The resulting peptide contains the formula



A plurality of different peptides is preferably synthesized wherein 0 is smaller than or equal to x, m, n, p and y and wherein x, m, n, p and y are smaller than or equal to 6. Additionally, x+m+n+p+y is preferably smaller than or equal to 21, so that the resulting peptides are smaller than or equal to 25 amino acid residues. Produced peptides are subsequently preferably screened for a desired immunogenic characteristic and/or binding property. This is preferably performed after coupling of said peptide to a scaffold comprising (at least) four binding sites or to two scaffolds, each comprising (at least) two binding sites. Most preferably, said peptide is coupled to a T4 scaffold or to two T2 scaffolds. If two scaffolds are used, each scaffold comprising (at least) two binding sites, the two cysteine residues of the first SS-bridge are preferably coupled to the same scaffold in order to form a loop. The two cysteine residues of the second SS-bridge are preferably coupled to another scaffold in order to form a loop. This is preferably performed as already explained hereinbefore. For instance, the two cysteine residues of the first SS-bridge are provided with a protecting group while the other two cysteine residues are kept unprotected. In that case, the unprotected cysteine are coupled to a scaffold in order to form a loop. Subsequently, the two cysteine residues of the first SS-bridge are deprotected and coupled to another scaffold.

It is also possible to provide the two cysteine residues of the first SS-bridge with a first kind of protecting group, such as for instance Trt, and to provide the other two cysteine residues with a second kind of protecting group, such as for instance Mmt. Both kind of protecting groups are removed using different reagentia. This way, it is possible to determine what cysteine residues are capable of binding to a scaffold.

In a further embodiment a peptide with the formula
 $C(X)_m(G)_n(X)_pC(X)_q(G)_r(X)_sC(X)_t(G)_u(X)_vC$ is produced. In this formula, C
represents a group capable of reacting with a scaffold, preferably a cysteine residue,
5 $(G)_n$, $(G)_r$ and $(G)_q$ represent a spacer and $(X)_m$, $(X)_p$, $(X)_q$, $(X)_s$, $(X)_t$ and $(X)_v$ each
represent at least one flanking sequence. This peptide is provided with three spacers,
allowing for flexible loops within said peptide. A peptide according to this formula is
also particularly suitable for coupling to two scaffolds, wherein each scaffold
comprises (at least) two binding sites.

10 In a preferred embodiment, a peptide according to this formula is synthesized
using flanking sequences of a proteinaceous molecule of interest that comprises (at
least) two SS-bridges, wherein the position of each cysteine of said SS-bridges within
the primary sequence of said proteinaceous molecule is not exactly known and
wherein in the primary sequence of said proteinaceous molecule two cysteine residues
15 are located within 6 amino acid residues from each other. In this case, one does not
know beforehand whether the first cysteine of a second SS-bridge is located
N-terminally or C-terminally from the second cysteine of a first SS-bridge. It is
therefore preferred to synthesize a plurality of molecules of the above mentioned
formula, said plurality of peptides comprising different combinations of cysteines and
20 flanking sequences, in order to screen for a peptide with a desired binding property
and/or immunogenic property. A method according to the present invention preferably
comprises selecting cysteine residues of SS-bridges, and flanking sequences thereof,
because an SS-bridge between cysteines of a proteinaceous molecule often results in
an internal loop. Such loop is regularly found to be involved in interaction between
25 said proteinaceous molecule and another compound. Hence, flanking sequences of
cysteine residues of SS-bridges have an increased chance of being involved with
binding events and/or immunity as compared to other sequences within a
proteinaceous molecule of interest.

30 In one preferred embodiment a plurality of peptides is produced comprising a
first cysteine (C_1) found in a primary sequence, a flanking sequence $(X)_m$ of said C_1
which flanking sequence is located in the direction of the C-terminus and has a length

of m amino acid residues, followed by n glycine residues (G)_n followed by a flanking sequence (X)_p of a third cysteine (C₃) found in a primary sequence, which flanking sequence is located in the direction of the N-terminus and has a length of p amino acid residues, followed by C₃, followed by a flanking sequence (X)_q of C₃, which

5 flanking sequence is located in the direction of the C-terminus and has a length of q amino acid residues, followed by r glycine residues (G)_r, followed by a flanking sequence of a second cysteine residue (C₂) present in said primary sequence which flanking sequence is located in the direction of the N-terminus and has a length of s amino acid residues, followed by C₂ – which may for instance be the second cysteine

10 of the first SS-bridge or the first cysteine of the second SS-bridge –, followed by a flanking sequence of C₂ present in said primary sequence which flanking sequence is located in the direction of the C-terminus and has a length of t amino acid residues, followed by u glycine residues (G)_u, followed a flanking sequence of the fourth cysteine residue present in said primary sequence (C₄) which flanking sequence is

15 located in the direction of the N-terminus and has a length of v amino acid residues, followed by the fourth cysteine residue (C₄). The resulting peptide is of the formula

$$C_1(X)_m(G)_n(X)_pC_3(X)_q(G)_r(X)_sC_2(X)_t(G)_u(X)_vC_4$$

A plurality of different peptides is preferably synthesized wherein 0 is smaller

20 than or equal to m, n, p, q, r, s, t, u and v and wherein m, n, p, q, r, s, t, u and v are smaller than or equal to 6. Additionally, m+n+p+q+r+s+t+u+v is preferably smaller than or equal to 21, so that the resulting peptides are smaller than or equal to 25 amino acid residues. Produced peptides are subsequently preferably screened for a desired immunogenic characteristic and/or binding property. This is preferably

25 performed after coupling of said peptide to a scaffold comprising (at least) four binding sites or to two scaffolds, each comprising (at least) two binding sites. Most preferably, said peptide is coupled to a T4 scaffold or to two T2 scaffolds. If two scaffolds are used, each scaffold comprising (at least) two binding sites, C₁ and C₃ are preferably coupled to the same scaffold in order to form a loop. C₂ and C₄ are

30 preferably coupled to another scaffold in order to form a loop. This is preferably

performed as already explained hereinbefore. For instance, C₁ and C₃ are provided with a protecting group while the other two cysteine residues are kept unprotected. In that case, the unprotected C₂ and C₄ are coupled to a scaffold in order to form a loop. Subsequently, C₁ and C₃ are deprotected and coupled to another scaffold.

5 It is also possible to provide C₁ and C₃ with a first kind of protecting group, such as for instance Trt, and to provide C₂ and C₄ with a second kind of protecting group, such as for instance Mmt. Both kind of protecting groups are removed using different reagentia. This way, it is possible to determine which cysteine residues are capable of binding to a scaffold.

10

It is of course also possible to generate other combinations. The above mentioned embodiment is for instance modified such that the positions of C₃, C₄ and their flanking sequences within the peptide are exchanged, for instance resulting in a peptide with the formula

15



A method according to the invention is in principle applicable to any
 20 proteinaceous molecule of which the primary sequence is known. In a preferred embodiment however a method according to the invention is provided wherein said proteinaceous molecule is selected from the group consisting of the cystine-knot family, transmembrane proteins, TNF-alpha, HGF-SF, FGF-beta, an interleukin, IL-5, a chemokine, a G-protein-coupled receptor, CCR4, CXCR5, IGF, LMF,
 25 endothelin-1, VIP, CGRP, PIF, EGF, TGF-alpha, the EGFR family, HER1, HER2/neu, HER3, HER4, p53, corticotrophin RF, ACTH, parathyroid hormone, CCK, substance P, NPY, GRP, neurotrophine, angiotensin-2, angiogenin, angiopoietin, neurotensine, SLCLC, SARS-derived protein, HIV-derived protein, papillomavirus-derived protein and FMDV. It has been found that a method of the
 30 invention is particularly suitable for generating immunogenic compounds and/or binding compounds that are at least partially derived from a member of said group.

If a method according to the invention involves selecting at least one amino acid residue from the primary sequence of a transmembrane protein, it is preferred to select at least one amino acid residue from an extracellular domain. However, according to the present invention optimal test results are obtained when a sequence
5 of a transmembrane protein is taken into consideration that consists of an extracellular domain as well as three amino acid residues located N-terminally and three amino acid residues located C-terminally of such extracellular domain. Provided is therefore a method according to the invention wherein said at least one amino acid residue is selected from a sequence of at least one transmembrane protein, said
10 sequence comprising an extracellular domain, three flanking amino acid residues located in the direction of the N-terminus of said at least one transmembrane protein, and three flanking amino acid residues located in the direction of the C-terminus of said at least one transmembrane protein.

15 In one particularly preferred embodiment a method of the invention is performed for producing a compound which is suitable for testing for the presence and/or identification of an immunogenic compound and/or binding compound that is at least partially derived from a member of the cystine-knot superfamily, preferably a member of the cystine-knot growth factor superfamily.

20 Growth factors represent a relatively large group of polypeptides which share the property of inducing cell multiplication both *in vivo* and *in vitro*. Although the level of sequence similarity between growth factors is not high, they can be classified into superfamilies based on their structural and functional similarities.

The crystal structures of four growth factors, nerve growth factor (NGF),
25 transforming growth factor-beta (TGF-beta), platelet-derived growth factor (PDGF), and human chorionic gonadotropin (hCG) from four separate superfamilies revealed that these proteins are structurally related and share a common overall topology. These proteins show very little sequence homology, but they all have an unusual arrangement of six cysteines linked to form a "cystine-knot" conformation. The active
30 forms of these proteins are dimers, either homo- or heterodimers. Because of their shape, there appears to be an intrinsic requirement for the cystine-knot growth factors to form dimers. This extra level of organization increases the variety of structures built around this simple structural motif.

In the crystal structures of transforming growth factor-beta 2 (TGF-beta2), platelet-derived growth factor (PDGF), nerve growth factor (NGF) and human chorionic gonadotropin (hCG), 6 conserved cysteine residues (CysI to CysVI in sequence order) form 3 disulphide bonds arranged in a knot-like topology. The two
 5 disulphide bonds between CysII and CysV ([CysII-V]) and between CysIII and CysVI ([CysIII-VI]) form a ring-like structure of 8 amino acids through which the remaining disulphide bond (between CysI and CysIV) penetrates (see Figure 1A). The sulfur (S) atoms of the conserved cysteines I to VI that are involved in the disulphide bonds are typically referred to as S1 to S6. Cystine knot domains with more than 6 cysteine
 10 residues can be found. The "extra" cysteine residues are normally used to create further disulphide bonds within the cystine knot domain or interchain disulphide bonds, during dimerisation. However, based on homology and topology it is always possible to indicate which cysteines represent the six conserved residues CysI to CysVI (see further below).

15 A similar knotted arrangement of disulphide bonds has been noted in the structures of some enzyme inhibitors and neurotoxins that bind to voltage-gated Ca^{2+} channels (McDonald et al.1993 ,Cell 73 421-424). In those sequences, however, the cystine topology differs: Cys[III-VI] penetrates a macrocyclic ring formed by Cys[I-IV] and Cys[II-V]. Thus, cystine-knot proteins fall into 2 structural classes: growth factor
 20 type and inhibitor-like cystine knots.

The cystine-knot growth factor superfamily is divided into subfamilies, which include the glycoprotein hormones (e.g. follicle stimulating hormone (FSH)), the transforming growth factor beta (TGF-beta) proteins (e.g. bone morphogenetic protein 4), the platelet-derived growth factor- like (PDGF-like) proteins (e.g. platelet derived
 25 growth factor A), nerve growth factors (NGF) (e.g. brain-derived neurotrophic factor) (see also Table 12).

All growth factor cystine knots structures have a similar topology, with 2 distorted beta-hairpin (beta-1 and beta-3) loops "above" the knot and a single (beta-2) loop "below" the knot. The beta-1 loop is formed by the stretch of amino acids between
 30 CysI and CysII ; the beta-2 loop is formed by the amino acids between CysIII and CysIV and the beta-3 loop is formed by the amino acids between CysIV and CysV (see Figure 1A). The sizes of the hairpin loops (i.e. the number of amino acids between the indicated cysteines) can vary significantly between family members.

There are three different "fingerprints" for the Cys-knot protein family: (1) GFCYSKNOT, (2) GLYCOHORMONE, en (3) NGF. These fingerprints differ from each other primarily in (1) the number and (2) the nature of the amino acids around the Cys-knot. A fingerprint comprises characteristic features of a given protein
 5 (sub)family and can thus be used to determine whether a given protein belongs to a given protein (sub) family.

For example, "NGF" is a 4-element fingerprint that provides a signature for the nerve growth factors. The fingerprint was derived from an initial alignment of 5 sequences: the motifs were drawn from conserved regions in the C-terminal portion
 10 of the alignment, each including at least one of the 6 Cys-residues involved in disulphide bond formation. Motifs 2 and 3 span the regions encoded by PROSITE pattern NGF (PS00248; [GSR]-CysII-[KRL]-G-[LIV]-[DE]-x(3)-[YW]-x-S-x-CysIII). Amino acid between brackets indicate the possible amino acids at that position. For example, the residue N-terminal to CysII can be either Gly, Ser or Arg. An x indicates
 15 any amino acid. Two iterations using the OWL22.1 algorithm were required to reach convergence, at which point a true set comprising 28 sequences was identified. An update of STPR37_9f identified a true set of 33 sequences."

"GLYHORMONE" is a 4-element fingerprint that provides a signature for the glycoprotein hormones. The fingerprint was derived from an initial alignment of 8
 20 sequences: the motifs were drawn from conserved regions spanning virtually the full alignment length, motifs 2 and 4 including regions encoded by PROSITE pattern GLY_HORMONE_ALPHA_1 (PS00779: CysII-x-G-C-CysIII-[FW]-S-[RQS]-A-[FY]-P-T-P), and GLY_HORMONE_ALPHA_2 (PS00780: N-H-T-x-CysV-x-CysVI-x-T-Cys-x(2)-H-K). Two iterations on OWL22.1 were required to reach convergence, at which
 25 point a true set comprising 23 sequences was identified. An update of STPR37_9f identified a true set of 34 sequences."

"GFCYSKNOT" is "a 2-element fingerprint that provides a signature for the growth factor cystine knot family. The fingerprint was derived from an initial alignment of 25 sequences - motif 1 spans the CysII-x-G-x-CysIII consensus (cf.
 30 PROSITE patterns PDGF (PS00249: P-[PSR]-Cys-V-x(3)-R-CysII-[GSTA]-G-Cys-CysIII), TGF_BETA (PS00250: [LIVM]-x(2)-P-x(2)-[FY]-x(4)-CysII-x-G-x-CysIII), GLY_HORMONE_BETA_1 (PS00261: CysII-[STAGM]-G-[HFYL]-CysIII-x-[ST]) and NGF (PS00248; [GSR]-CysII-[KRL]-G-[LIV]-[DE]-x(3)-[YW]-x-S-x-CysIII), motif 2

spans the CysV-x-CysVI pattern. Four iterations on OWL26.0 were required to reach convergence, at which point a true set comprising 192 sequences was identified.

Several false positives were also identified, most of which are highly biased (cysteine-rich) sequences (e.g. metallothioneins and keratins). An update of STPR37_9f

5 identified a true set of 198 sequences.

The present invention provides a method to design and produce mimics of each one of them, as well as of those family members to be discovered.

Mimicking binding sites of complex proteins, e.g. TNF-alpha, the CD
(cluster of differentiation antigen)-family, cytokines, antibodies or cell surface
10 receptors, by means of synthetic peptides is currently one of the most active areas in protein science and drug development. Many proteins exert their biological activity through interactions involving relatively small regions of their exposed surfaces. Molecules that mimic these surface epitopes are therefore of great interest, since they provide a means of mimicking the biological activity of the entire protein, for example
15 the ability of a protein to recognize certain physiological molecules, such as proteins and DNA, in a relatively small synthetic molecule. Short linear peptides are not ideal for this purpose, because of their inherent flexibility and susceptibility to proteolytic degradation. Instead, it is preferred to constrain linear peptide chains by cyclization into a looped peptide compound with biologically relevant secondary structure(s).

20 The present invention provides a rationalized strategy for the design of a looped peptide structure which is suitable as a peptidomimetic of a cystine-knot growth factor family member. The term 'peptidomimetic' as used herein refers to a (synthetic) peptide compound which mimics the ability of a Cys-knot family member to recognize certain physiological molecules. The invention furthermore provides a
25 method for producing compounds, at least partly derived from a proteinaceous molecule comprising at least one disulfide bond (for instance a member of the cystine-knot family), which compounds are suitable for testing for the presence and/or identification of an immunogenic compound and/or binding compound.

30 In one embodiment of the invention a proteinaceous molecule of interest comprises a disulfide bond between two cysteine residues, whereby said two cysteine residues are at least 3 and at most 21 amino acid residues located from each other in the primary sequence (meaning that the position of the first cysteine is x and the

position of the second cysteine is $x + n$, wherein $3 \leq n \leq 21$). In this embodiment, at least one peptide of the following formula is preferably synthesized: $(X)_m C_x (X)_{n-1} C_{x+n} (X)_p$ wherein C_x and C_{x+n} represent the cysteine residues at position x and position $x + n$, respectively, $(X)_m$ represents a flanking sequence of C_x that consists of m amino acid residues and that is located in the direction of the N-terminus, $(X)_p$ represents a flanking sequence of C_{x+n} that consists of p amino acid residues and that is located in the direction of the C-terminus, and $(X)_{n-1}$ represents the $n-1$ amino acid residues that are located between said first and said second cysteine residues in the primary sequence of said proteinaceous molecule. In one embodiment, at least one of said amino acid residues that are located between said first and said second cysteine residues is modified, but this is not necessary.

As already explained before, C_x and C_{x+n} are preferably the only cysteine residues present in said peptide. Other cysteine residues in the primary sequence of said proteinaceous molecule which are part of $(X)_m$, $(X)_{n-1}$ and/or $(X)_p$ are preferably changed into another amino acid residue such as for instance alanine, or rendered inactive, for instance using protecting groups, in order to avoid interaction between such "additional" cysteine residues and C_x and/or C_{x+n} . In a preferred embodiment a set of peptides of the formula $(X)_m C_x (X)_{n-1} C_{x+n} (X)_p$ is produced wherein the flanking sequences $(X)_m$ and $(X)_p$ are at least in part of different length. m and p preferably fulfil the formula $0 \leq m, p \leq 18$. Furthermore, $m+n+p$ are preferably less than, or equal to, 23 in order to produce a peptide with a length of 25 amino acid residues or less. Said at least one peptide is subsequently coupled to a scaffold.

In a further embodiment of the invention a proteinaceous molecule of interest comprises a disulfide bond between two cysteine residues, whereby said two cysteine residues are more than 21 amino acid residues located from each other in the primary sequence (meaning that the position of the first cysteine is x and the position of the second cysteine is $x + n$, wherein $n > 21$). In this embodiment, a part of the primary sequence of said proteinaceous molecule is preferably taken into consideration which starts at the amino acid residue at position $x + [(n-20)/2]$ and which ends at the amino acid residue at position $x + [(n+20)/2]$ within the primary sequence of said

proteinaceous molecule. A method of the invention is thus preferably performed with said part, meaning that at least one amino acid residue of said part is selected, at least one flanking sequence thereof is selected, et cetera. One embodiment therefore provides a method according to the invention wherein at least one amino acid residues
5 is selected from an SS-bridge sequence of said at least one proteinaceous molecule. Preferably, the two cysteines of said SS-bridge are located at position x and $(x + n)$, wherein $n > 21$, and said amino acid residue is preferably selected from a region of said SS-bridge sequence starting at amino acid position $x + [(n-20)/2]$ and ending at amino acid position $x + [(n+20)/2]$.

10

The following non-limiting example clarifies this embodiment. If two cysteine residues are located at position 1 and 31 of the primary sequence of a proteinaceous molecule, the following values are used: $x = 1$, $x+n = 31$, and $n=30$. Subsequently, a sequence between said two cysteine residues is considered, which starts at amino acid
15 position $1 + [(30-20)/2] = 6$ and which ends at amino acid position $1 + [(30+20)/2] = 26$. Thus, the sequence between position 6 and 26 within the primary sequence of said proteinaceous molecule is taken into consideration. At least one amino acid residue from said sequence between position 6 and 26 is selected, at least one flanking sequence of said at least one selected amino acid residue is selected, et cetera. Again,
20 preferably a plurality of peptides is generated, which peptides are preferably of different length and/or which peptides preferably comprise different flanking sequences.

If n is an odd number, the values $[(n-20)/2]$ and $[(n+20)/2]$ will not be integers. In that case the resulting value is round of. The first integer value is taken that is
25 either smaller or larger than said value. For instance, if $n=35$, the value of $[(n-20)/2]$ is 7.5. In that case, either the value 7 or 8 is chosen.

If a proteinaceous molecule of interest comprises more than one internal disulfide bond, wherein each disulfide bond is between two cysteine residues, a
30 method of the invention is preferably provided wherein at least one cysteine residue is selected. The invention therefore provides a method according to the invention wherein at least one of said selected amino acid residues within the primary sequence of said at least one proteinaceous molecule is a cysteine residue. More preferably each

selected amino acid residue is a cysteine residue of said proteinaceous molecule. As a consequence, in this more preferred embodiment, each selected flanking sequence is a flanking sequence of a cysteine residue. Peptides are produced comprising at least one flanking sequence of at least one cysteine residue. Preferably, different flanking
5 sequences are combined in one peptide. In a further preferred embodiment, a plurality of peptides comprising flanking sequences of different length are produced. This embodiment is particularly useful for screening for a binding compound and/or immunogenic compound, since the flanking sequences of cysteine residues that are usually bound to each other via disulfide bonds are often involved with interaction
10 events.

A member of the cystine-knot family comprises more than one disulfide bond. At least three disulfide bonds are present between three pairs of cysteine residues. Hence, a member of the cystine knot superfamily comprises at least six cysteine residues (CysI to CysVI in sequence order). If a member of the cystine knot family is
15 considered as a proteinaceous molecule of interest, preferably at least two of said cysteine residues are selected in a method according to the invention. Most preferably, CysIV and CysV are selected, because these cysteine residues and the amino acid residues between them naturally form the beta-3 hairpin (B3) loop within a proteinaceous molecule. Peptides mimicking said loop are found to be particularly
20 suitable as peptidomimetics of a member of the cystine-knot family.

Compounds that are designed and synthesized with a method according to the present invention are particularly suitable for screening for an immunogenic compound and/or binding compound of interest. In one embodiment a plurality of
25 peptides according to the present invention is synthesized and incubated with a binding molecule of interest, such as for instance an antibody or a functional part, derivative and/or analogue thereof, and/or a T cell or a functional part, derivative and/or analogue thereof. Bound peptides are selected and/or identified. One embodiment therefore provides a method for screening for the presence and/or
30 identity of an immunogenic compound and/or a binding compound of interest, the method comprising:

- producing a plurality of compounds comprising different peptides with a method according to the invention; and

- testing whether at least one of said compounds is capable of specifically binding an antibody or a functional part, derivative or analogue thereof specific for said at least one proteinaceous molecule, or a T cell or a functional part, derivative or analogue thereof specific for said at least one proteinaceous molecule. Said plurality of
5 compounds preferably comprises at least 10, more preferably at least 100, most preferably at least 1000 compounds in order to enhance the chance that a compound with a desired characteristic is present.

A functional part of an antibody or a T cell is defined as a part which has the
10 same immunogenic properties in kind, not necessarily in amount. By immunogenic properties is meant the capability to specifically bind an antigen. A derivative of an antibody or a T cell is defined as an antibody or a T cell which has been altered such that the immunogenic properties of the resulting derivative are essentially the same in kind, not necessarily in amount. A derivative can be provided in many ways, for
15 instance through conservative amino acid substitution.

A person skilled in the art is well able to generate analogous compounds of an antibody or a T cell. This is for instance done through screening of a peptide library. Such an analogue has essentially the same immunogenic properties of said antibody or T cell in kind, not necessarily in amount.

20

In one embodiment the immunogenic properties of a peptide of the invention are tested by providing a non-human animal with said compound and determining whether an immune response is elicited. Provided is therefore a method for screening for the presence and/or identity of an immunogenic compound, the method
25 comprising:

- producing a plurality of compounds comprising different peptides with a method according to the invention; and
- testing whether at least one of said compounds is capable of eliciting an immune response.

30

It is preferably tested whether a peptide of the invention is capable of eliciting an immune response against a proteinaceous molecule of interest. This is for instance performed by providing a non-human animal with a peptide of the invention, obtaining antibodies and/or T cells from said non-human animal, incubating said

antibodies and/or T cells with (an epitope of) a proteinaceous molecule of interest and determining whether said antibodies and/or T cells comprise an antibody and/or T cell which is capable of specifically binding said (epitope of said) proteinaceous molecule of interest.

5

If a compound of the invention appears to be an immunogenic compound and/or a binding compound of interest, it is preferably selected. A method according to the invention, further comprising selecting a compound comprising an immunogenic site or a binding site of interest is therefore also herewith provided. Said selected
10 compound is preferably identified.

In one embodiment a selected compound is directly used as an immunogenic compound and/or a binding compound. In an alternative embodiment, a selected compound is treated as a promising candidate compound. This means that further investigation is performed. In one embodiment said candidate compound is further
15 tested after a first round of screening. For instance, if a promising candidate compound is selected during an *in vitro* screening method, it is for instance further tested *in vivo* in a non-human animal. In one embodiment said promising candidate compound is modified and tested again for the presence of at least one improved characteristic. This is for instance performed with replacement net mapping, wherein
20 a plurality of peptides is synthesized. In each peptide at least one amino acid residue of the original promising peptide is replaced by another amino acid residue. The resulting peptides are tested again in order to determine whether at least one of the modified peptides comprises at least one improved characteristic.

In one embodiment a promising candidate peptide identified in a first
25 screening is combined with another peptide sequence in order to search for compounds with an improved immunogenic property and/or binding property.

A method of the invention is suitable for the production and/or identification of a compound according to the present invention comprising an immunogenic property and/or binding property of interest. An isolated, synthetic or recombinant compound
30 with a desired immunogenic property and/or binding property obtainable by a method according to the invention is therefore also herewith provided. Said compound preferably comprises a peptide according to the invention coupled to a scaffold. Said

scaffold preferably comprises a (hetero)aromatic molecule, more preferably a halomethylarene bis(bromomethyl)benzene, a tris(bromomethyl)benzene or a tetra(bromomethyl)benzene. Most preferably said scaffold comprises at least one meta-dibromoxylene (m-T2) scaffold, at least one 2,4,6-tris(bromomethyl)mesitylene
5 (T3) scaffold, and/or at least one 1,2,4,5 tetrabromodurene (T4) scaffold.

Compounds according to the invention are suitable for a wide variety of applications. For instance, a compound according to the invention is used for a therapeutic application. A compound according to the invention is for instance suitable for use as
10 an agonist or an antagonist for a receptor-ligand binding pair. In one embodiment a compound with a desired immunogenic property is synthesized and selected. The invention therefore provides an immunogenic compound obtainable by a method according to the invention. Said immunogenic compound for instance consists of an immunogenic peptide obtainable by a method of the invention. Preferably however an
15 immunogenic compound according to the invention comprises an immunogenic peptide bound to a scaffold in order to improve stability and biologic activity of said immunogenic peptide. In one embodiment an immunogenic peptide according to the invention is bound to a (hetero)aromatic molecule, preferably a halomethylarene, via at least two SH-functionalities since such coupling reactions are easily and rapidly
20 performed, even in aqueous solution, without the need of protecting amino acid residues of said immunogenic peptide (except for any additional cysteine residues). Moreover, the resulting immunogenic compound is stable and the peptide comprises a biologically significant structure. In a particularly preferred embodiment an immunogenic peptide according to the invention is coupled to a
25 bis(bromomethyl)benzene, a tris(bromomethyl)benzene or a tetra(bromomethyl)benzene. Most preferably an immunogenic compound is provided comprising an immunogenic peptide coupled to at least one meta-1,3-bis(bromomethyl)benzene (m-T2), ortho-1,2-bis(bromomethyl)benzene (o-T2), para-1,4-bis(bromomethyl)benzene (p-T2), meta-1,3-bis(bromomethyl)pyridine (m-P2),
30 2,4,6-tris(bromomethyl)mesitylene (T3), meta-1,3-bis(bromomethyl)-5-azidobenzene (m-T3-N3) and/or 1,2,4,5 tetrabromodurene (T4) scaffold.

The invention furthermore provides an immunogenic composition comprising an immunogenic compound obtainable by a method according to the invention. In one embodiment said immunogenic compound is coupled to a suitable carrier, for instance a saline solution and/or a protein carrier such as keyhole limpet haemocyanin (KLH), serum albumin (e.g. BSA or RSA), ovalbumin, Diphtheria Toxin (DT), virus-like particles, or any other suitable carrier well known in the art. However, the use of an immunogenic compound according to the present invention coupled to a scaffold often obviates the need to use a carrier. This provides the advantage that an immune response specifically directed against such additional carrier is avoided. One embodiment therefore provides an immunogenic composition comprising an immunogenic compound, which immunogenic compound comprises an immunogenic peptide bound to a scaffold, wherein said immunogenic composition is (essentially) devoid of an additional carrier. In one embodiment an immunogenic composition of the invention comprises a suitable adjuvant such as for instance Freund's Complete Adjuvant (FCA), Incomplete Freund Adjuvant (IFA), an oil in water or double oil in water emulsion or an Aluminum Salt Adjuvant, Montanide ISA, MF59, Aluminium Hydroxide, Titermax, RIBI, Saponins, and/or CoVaccine. An immunogenic composition according to the invention is preferably administered orally or by aerosol or it is preferably injected intramuscularly, subcutaneously or via high pressure needle-free transdermal injection. Dose ranges of (immunogenic) peptides and/or (immunogenic) compounds according to the invention to be used in a therapeutical and/or prophylactic application are designed on the basis of rising dose studies in the clinic in clinical trials for which rigorous protocol requirements exist and which do not need further explanation here. Typically, dosages of between 1 µg to 1 mg per kilogram of body weight are used.

A preferred embodiment provides an immunogenic composition according to the invention comprising at least two different immunogenic peptides according to the invention. Said at least two different immunogenic peptides are preferably capable of eliciting an immune response specifically directed against a proteinaceous molecule of interest. Most preferably said at least two different immunogenic peptides are capable of eliciting a protective immune response specifically directed against a proteinaceous molecule of interest in at least 50%, preferably at least 75%, more preferably at least

80%, most preferably at least 95% of the hosts. A protective immune response against a proteinaceous molecule is defined herein as an immune response that is capable of counteracting at least one property of said proteinaceous molecule.

5 In one embodiment each of said different peptides of the invention is capable of eliciting a protective immune response against said proteinaceous molecule in at least 50%, preferably at least 75%, more preferably at least 80%, most preferably at least 95% of the hosts. In one embodiment however each single peptide of the invention is by itself essentially not capable of inducing a protective immune response against a proteinaceous molecule of interest, whereas a combination of at least two peptides
10 according to the invention is capable of eliciting a protective immune response against said proteinaceous molecule in at least 50%, preferably at least 75%, more preferably at least 80%, most preferably at least 95% of the hosts. In this case an immunogenic composition comprising at least two immunogenic peptides according to the invention is particularly preferred. In one embodiment an immunogenic composition according
15 to the invention comprises at least three immunogenic peptides according to the invention.

An immunogenic composition of the invention comprising at least two immunogenic compounds according to the invention is particularly suitable for immunisation against a self-antigen. If an immune response against a self-antigen is
20 desired, a self-antigen is preferably used that is modified enough in order to be capable of eliciting an immune response, but which at the same time sufficiently resembles the original self-antigen so that an induced immune response is capable of recognizing self-antigens. Immunisation with such modified self-antigens regularly does not result in an effective immune response in view of the resemblance of the
25 modified self-antigens with unmodified self-antigens. A combination of at least two immunogenic peptides according to the invention however at least in part solves this problem because such combination is better capable of eliciting a protective immune response.

30 In one embodiment at least two different immunogenic peptides according to the invention are bound to the same scaffold. Immunogenicity is increased, for instance because peptides are fixed in another conformation, different three-dimensional orientations are obtained, and/or as a result of multivalence.

An immunogenic peptide and/or immunogenic compound obtainable by a method according to the present invention is for instance suitable for eliciting an immune response in a non-human animal. Subsequently, it is possible to isolate
5 antibodies and/or T cells capable of specifically binding said immunogenic peptide and/or immunogenic compound. Alternatively, or additionally, an antibody or T cell or functional part, derivative and/or analogue thereof, capable of specifically binding an immunogenic peptide and/or immunogenic compound of the invention, is generated *ex vivo*, for instance by incubating naive T cells with an antigen presenting cell which
10 has been pulsed with an immunogenic peptide according to the invention. One embodiment therefore provides a method according to the invention, further comprising selecting an immunogenic compound and/or a binding compound of interest, and producing an antibody or T cell or a functional part, derivative and/or analogue thereof capable of specifically binding said immunogenic compound. An
15 isolated or synthetic antibody or T cell, or a functional part, derivative and/or analogue thereof, capable of specifically binding an immunogenic peptide and/or an immunogenic compound obtainable by a method according to the present invention is therefore also herewith provided.

The invention furthermore provides an array comprising a binding compound
20 according to the invention. Such array is particularly suitable for screening a sample for the presence of specific molecules, such as a ligand or a receptor.

The invention furthermore provides an array comprising an immunogenic peptide and/or an immunogenic compound obtainable by a method according to the invention. Such array is particularly suitable for screening a sample for the presence
25 of antibodies and/or T cells capable of specifically binding said immunogenic peptide and/or immunogenic compound according to the invention. For instance, a sample obtained from an individual is screened with an array according to the invention in order to determine whether said individual comprises antibodies and/or T cells capable of specifically binding a proteinaceous molecule of interest. If such antibodies
30 and/or T cells appear to be present in said sample, it indicates that said individual is suffering from, or at risk of suffering from, a disorder involving the presence of said proteinaceous molecule of interest. Said (risk of) disorder is for instance caused by an

infection with a pathogen, by the presence of malignant cells, by an autoimmune disease, et cetera.

A further embodiment provides an array comprising an antibody or T cell or functional part, derivative and/or analogue thereof according to the invention. Since
5 such antibody, T cell, functional part, derivative and/or analogue of the invention is capable of specifically binding an immunogenic compound of the invention, said array is for instance suitable for determining the presence of said immunogenic compound in a sample. Furthermore, if said immunogenic compound is a peptidomimetic of an immunogenic proteinaceous molecule of interest, said antibody, T cell, functional part,
10 derivative and/or analogue of the invention is also capable of specifically binding said proteinaceous molecule of interest. In that case said array is also suitable for determining the presence in a sample of said proteinaceous molecule of interest.

15 Detailed description

Investigation of various members of the cystine-knot growth factor family has revealed that peptides derived from the amino acid sequence of the beta-3 hairpin (B3) loop of a cystine-knot growth family member, which peptides have specific
20 characteristics, are particularly suitable for use as a peptidomimetic. Provided is therefore a peptidomimetic of a member of the cystine-knot growth factor family, comprising a polypeptide derived from the amino acid sequence of the beta-3 hairpin (B3) loop of said cystine-knot growth factor family member, wherein two amino acid residues have been replaced by a first and a second cysteine residue that are
25 covalently connected to each other via a scaffold, wherein a) said first scaffold-attached cysteine residue is located p residues C-terminal from the position that corresponds to amino acid CysIV in the wild-type B3-loop, indicated as position CysIV+ p, wherein $5 \leq p \leq 12$; b) said second scaffold-attached cysteine residue is located q residues N-terminal from the position that corresponds to amino acid CysV
30 in the wild-type B3-loop, indicated as position CysV - q, wherein $4 \leq q \leq 12$ and wherein $(p - q)$ is -3, -2, -1, 0, 1, 2 or 3; and c) the length of said polypeptide is from amino acid at position CysIV + x to amino acid at position CysV + y, wherein $-5 \leq x \leq 1$ and $1 \leq y \leq 6$ under the provision that $x + y = -1, 0, 1$ or 2. It was found that looped

peptide structures which meet these criteria are suitably used as mimics of Cys-knot family members, as evidenced among other by the ability to induce a specific antibody response in an animal.

Thus, to achieve a looped peptide structure which sufficiently resembles the native conformation of the B3-loop, there are a some general criteria which should be met with respect to the length of the polypeptide and the position of the cysteines residues within the polypeptide via which it is attached (cyclized) to the scaffold. The peptide length may also depend on the nature of the scaffold. These general criteria refer to the conserved residues CysIV and CysV which are positioned at the 'bottom' of the B3 loop in all members of the Cys-knot growth factor family members (see Figure 1B). It should be noted that, in the native protein, the B3-loop is formed as a result of the complex knot-structure and not by a disulphide bond between CysIV and CysV. In a peptidomimetic of the invention, a scaffold molecule physically constrains a polypeptide to induce a secondary structure which mimics the B3-loop. The scaffold is attached to cysteines within the polypeptide rather than at the ends of the polypeptide and the peptidomimetic can schematically be regarded as A-shaped molecule (see Figure 1C). A peptidomimetic of the invention is also referred to as a chemically linked peptide scaffold, abbreviated as CLIPS.

Identification of the B3-loop and of residues CysIV and CysV of a given Cys-knot protein family member can be done on the basis of sequence alignment of primary amino acid sequences. Table 13 shows such an alignment of various members of the Cys-knot growth factor family of different mammals. The B3 loop starts at the conserved residue CysIV and ends with the residue N-terminal to CysV, herein also referred to as residue CysV-1. Once the conserved CysIV and CysV residues have been identified, the suitable lengths of the polypeptide and the positions of the cysteines for attaching the polypeptide to the scaffold can be easily determined.

Tables 14A-E list the positions of the six conserved Cys residues (CysI to CysVI) for five different subfamilies of the Cys-knot growth factor family. For example, hCG-alpha contains ten cysteine residues (C-1 to C-10) at positions 7, 12, 28, 31, 32, 59, 60, 82, 84 and 87, respectively. Based on the sequence alignment, C-2 of hCG corresponds to CysI, C-3 to CysII, C-4 is an "extra" cysteine, C-5 corresponds to CysIII, etcetera. Thus, in case of hCG residue Cys60 corresponds to CysIV and residue Cys82 to CysV. As another example, in the GLHB subfamily member FSH-beta Cys51

corresponds to CysIV and Cys 82 to CysV. In a similar fashion, the CysIV and CysV residues can be readily identified for other Cys-knot family members.

The first and second criteria which have to be met define the positions at which the cysteines are to be introduced and via which the polypeptide is attached to the scaffold. The position of the first (i.e. N-terminal cysteine based on the sequence of the B3-loop) and second (i.e. C-terminal) cysteine are considered relevant for the ability of the scaffold to induce a secondary structure which optimally resembles the native protein. The first cysteine residue within said polypeptide is located C-terminal (or 'downstream') from the amino acid position that corresponds to amino acid CysIV in the B3-loop of wild-type protein. This position can be indicated as position CysIV+ p . The distance to said position CysIV should not be less than 5 residues and not more than 12 residues. In other words, the position of the first scaffold-attached cysteine corresponds to position CysIV+ p , wherein $5 \leq p \leq 12$. The second scaffold-attached cysteine residue is located N-terminal (or "upstream") from the amino acid position that corresponds to amino acid CysV in the B3-loop of wild-type protein. This position can be indicated as position CysV- q . The distance to said position CysV should not be less than 4 residues and not more than 12 residues. In other words, the position of the second scaffold-attached cysteine corresponds to position CysV- q , wherein $4 \leq q \leq 12$. Furthermore, to allow the binding of both cysteines to one scaffold without disturbing the formation of a hairpin, it is important that the cysteines are roughly positioned opposite of each other. For that reason it is required that $(p - q)$ is -3, -2, -1, 0, 1, 2 or 3. For example, the positions of the cysteines via which a polypeptide is attached to a scaffold correspond to amino acid position CysIV+12 and CysV-10, or to CysIV+11 and CysV-10, CysIV+10 and CysV-8, CysIV+9 and CysV-8, CysIV+8 and CysV-6, CysIV+7 and CysV-5, CysIV+7 and CysV-6, CysIV+7 and CysV-4, CysIV+5 and CysV-4 or CysIV+6 and CysV-4. Preferred positions for the cysteines are CysIV+10 and CysV-8, CysIV+7 and CysV-6 or CysIV+8 and CysV-6. Most preferably, a peptidomimetic according to the invention is provided wherein the position of said first and second cysteine correspond to positions CysIV+10 and CysV-8.

Preferably, the first and second cysteine are introduced at the positions of those amino acids which, in the crystal structure, are within a distance of up to 6 Å of each other and whose side chains are oriented in the same direction. Said side chains

are preferably not surface-exposed yet participate in the so-called hydrophobic core that keeps the B1- and B3-loops together.

The third criterium which should be met poses a restriction on the length of the peptide. According to this criterium, the length of the polypeptide is from amino acid at position CysIV + x to amino acid at position CysV + y, wherein $-5 \leq x \leq 1$; wherein $1 \leq y \leq 6$ and under the provision that $x + y = -1, 0, 1$ or 2 . In other words, the first residue of the polypeptide corresponds to residue CysIV+ x and the last residue to CysV+ y. The provision that $x + y = -1, 0, 1$ or 2 ensures that following attachment of the polypeptide to the scaffold the 'legs' of the A-shaped molecule (see Fig. 1C) are more or less of comparable length to ensure that the first and last residue of a polypeptide are 'neighbouring' residues in the hairpin structure. For example, the length of the peptide is from CysIV +1 to CysV + 1, from CysIV-5 to CysV +6, from CysIV-3 to CysV+4, from CysIV-5 to CysV+4 or from CysIV-2 to CysV+ 4. Preferably, the length of the polypeptide is from CysIV +1 to CysV + 1, from CysIV-2 to CysV+ 4 or from CysIV-5 to CysV+ 4. In case of FSHbeta, this means that the polypeptide for example corresponds to the stretch of from amino acid 52 (Cys51+1) to amino acid 83 (Cys82+1) or from amino acid 46 (Cys51-5) to amino acid 86 (Cys82+4).

The term 'derived from' is used to indicate that the polypeptide sequence does not have to be identical to the amino acid sequence found in the B3-loop of naturally occurring Cys-knot proteins. Rather, in most cases the polypeptide will, in addition to the two cysteine residues that have been introduced, differ in at least one amino acid from the sequence of the B3-loop in wild-type proteins of the Cys-knot family. As will be described below, it is preferred that any cysteine residue in the natural sequence other than the two cysteines at the two positions described above is changed into a residue that is not reactive with the scaffold in order to prevent attachment of the polypeptide to the scaffold via a residue other than said first and second cysteines.

Based on the above criteria the invention provides peptidomimetics of any known or yet to be identified member of the Cys-knot growth factor family, for example said member is a member of the glycoprotein hormone-beta (GLHB) family, the platelet-derived growth factor (PDGF) family, the transforming growth factor (TGF) family, the nerve growth factor (NGF) family or the glycoprotein hormone-alpha (GLHA) family.

As said, in a peptidomimetic provided herein a scaffold molecule physically constrains a polypeptide to induce a secondary structure which mimics the B3-loop. The Examples below demonstrate the relevance of the presence of a scaffold in a peptidomimetic as provided herein. When the first and second cysteine are connected
5 via a suitable scaffold, the resulting peptide appears a very effective immunogen. In contrast, when the first and second cysteine within one peptide molecule react with each other to form a disulphide bridge, the resulting looped peptide structure can not be used to induce a specific immune response in a test animal. It is conceivable that the physical constraint provided by the scaffold is important for the formation of a
10 hairpin structure that mimics the secondary structure of the B3-loop in naturally occurring Cys-knot family members.

Various types of scaffolds can be used in a looped peptide structure according to the invention. Suitable scaffolds are those capable of reacting with the first and second cysteine within the polypeptide to form a looped peptide structure. A
15 particular interesting scaffold molecule is a (hetero)aromatic compound, in particular those with at least two benzylic halogen substituents, such as a halomethylarene. These compounds are highly reactive towards thiol groups and rapidly form a covalent bond with peptides comprising a cysteine residue. In one embodiment, a scaffold is a bis(halomethyl)benzene or a tetra(halomethyl)benzene or a derivative thereof. In a
20 preferred embodiment, a scaffold is selected from the group consisting of ortho-, meta- and para- dihalomethylbenzene (also known as dihaloxylene) and 1,2,4,5 tetra halomethylbenzene (also known as 1,2,4,5-tetrahalodurene). More preferably, the scaffold is meta-dibromoxylene (m-T2) or 1,2,4,5 tetrabromodurene (T4). It should be noted that the term "scaffold" as used herein refers to the unreacted molecule that can
25 be used to prepare a peptidomimetic of the invention (e.g. meta-dibromobenzene) as well as to the scaffold moiety within the resulting peptidomimetic which has reacted with the cysteines and, in case of dibromobenzene, no longer contains the halogen atoms. Methods to construct a peptidomimetic with these scaffolds are discussed in WO2004077062.

30 Some combinations of scaffolds and peptides were observed that yielded very useful peptidomimetics. In one embodiment, a looped peptide structure comprises a polypeptide with a length from CysIV+1 to CysV+1 that is attached to a meta-dihaloxylylene scaffold, preferably meta-dibromoxylene. A preferred peptide

length for attachment to a tetrahalodurene scaffold, for example to 1,2,4,5
tetrabromodurene is from CysIV-2 to CysV+4.

Regarding the position of the cysteines through which a looped peptide
structure is formed onto a scaffold, particularly useful positions were identified for
5 different subfamilies of the Cys-knot superfamily of growth factors.

Preferred positions of the cysteines to obtain a mimic of a member of the
GLBH, the PDGF or the TGF subfamily are CysIV+10 in combination with CysV-8. In
case of FSH this corresponds to residues 61 and 74, in case of VEGF to residues 78
and 94 and in case of GDNF to residues 112 and 124. However, for GLBH family
10 members, positions CysIV+12 and CysV-10, CysIV+8 and CysV-6 or CysIV+7 and
CysV-5 also give good results. Likewise, positions CysIV+8 and CysV-6 or CysIV+12
and CysV-10 are suitably used for PDGF-family members and positions CysIV+10 and
CysV-10 or CysIV+7 and CysV-4 for TGF family members.

One preferred embodiment provides a VEGF peptidomimetic according to
15 the present invention, wherein the position of said first cysteine corresponds to amino
acid position CysIV+ 8 and wherein the position of said second cysteine corresponds to
position CysV-6 and wherein said polypeptide is derived from the B3-loop of a VEGF
protein.

Preferred positions for the cysteines to obtain a mimic of a member that
20 belongs to the NGF- family are CysIV+7 and CysV-6 (in case of NGF residues 87 and
102). Other useful combinations of cysteine positions for NGF family members include
CysIV+5 and CysV-4, CysIV+9 and CysV-8, and CysIV+11 and CysV-10.

Preferred positions for the cysteines to obtain a mimic of a member that
belongs to the GLHA- family are CysIV+8 and CysV-6 (in case of CG residues 68 and
25 76). Other useful combinations of cysteines positions for GLHA-family members
include CysIV+6 and CysV-4.

In one embodiment, the invention provides a mimic of a member of the
GLBH-, the PDGF- or the TGF-family wherein said mimic is a looped peptide
structure consisting of a polypeptide attached via two cysteines to a scaffold, said
30 polypeptide being derived from the amino acid sequence of the beta-3 hairpin loop of
said member, wherein the length of said polypeptide is from amino acid position
CysIV-5 to CysV+4 and wherein said polypeptide is attached via a first cysteine at
position CysIV+10 and a second cysteine at position CysV-8 to a tetrahalomethyl

benzene scaffold, preferably tetrabromodurene. In another embodiment, said polypeptide is attached via said cysteines to a bifunctionalized scaffold, for example a dibromobenzene, wherein the length of the peptide is somewhat shorter, for example from amino acid CysIV+1 to CysV+1.

5 In another embodiment, the invention provides a mimic of a member of the GLBH-, the PDGF- or the TGF-family wherein said mimic is a looped peptide structure consisting of a polypeptide attached via two cysteines to a scaffold, said polypeptide being derived from the amino acid sequence of the beta-3 hairpin loop of
10 said member, wherein the length of said polypeptide is from amino acid position CysIV-5 to CysV+4 and wherein said polypeptide is attached via a first cysteine at position CysIV+10 and a second cysteine at position CysV-8 to a tetrahalomethyl benzene scaffold, preferably tetrabromodurene. In another embodiment, said polypeptide is attached via said cysteines to a bifunctionalized scaffold, for example a dibromobenzene, wherein the length of the peptide is somewhat shorter, for example
15 from amino acid CysIV+1 to CysV+1.

 In yet another embodiment, the invention provides a mimic of a member of the GLBH-, the PDGF- or the TGF-family wherein said mimic is a looped peptide structure consisting of a polypeptide attached via two cysteines to a scaffold, said polypeptide being derived from the amino acid sequence of the beta-3 hairpin loop of
20 said member, wherein the length of said polypeptide is from amino acid position CysIV-5 to CysV+4 and wherein said polypeptide is attached via a first cysteine at position CysIV+10 and a second cysteine at position CysV-8 to a tetrahalomethyl benzene scaffold, preferably tetrabromodurene. In another embodiment, said polypeptide is attached via said cysteines to a bifunctionalized scaffold, for example a
25 dibromobenzene, wherein the length of the peptide is somewhat shorter, for example from amino acid CysIV+1 to CysV+1.

 In a further aspect, the invention provides a mimic of a member of the NGF-family wherein said mimic is a looped peptide structure consisting of a polypeptide attached via two cysteines to a scaffold, said polypeptide being derived
30 from the amino acid sequence of the beta-3 hairpin loop of said member, wherein the length of said polypeptide is from amino acid position CysIV-5 to CysV+4 and wherein said polypeptide is attached via a first cysteine at position CysIV+10 and a second cysteine at position CysV-8 to a tetrahalomethyl benzene scaffold, preferably

tetrabromodurene. In another embodiment, said polypeptide is attached via said cysteines to a bifunctionalized scaffold, for example a dibromobenzene, wherein the length of the peptide is somewhat shorter, for example from amino acid CysIV+1 to CysV+1.

5 In case the polypeptide length is such that it includes a CysIV and/or CysV residue this means that at least those cysteine(s) should not be present in the polypeptide to avoid a chemical reaction with the scaffold. They can for instance be changed into a residue that is unreactive with the scaffold, for example an alanine residue, to prevent attachment of the polypeptide to the scaffold via a cysteine other
10 than the two cysteines described above. Likewise, any other cysteine residue in the natural sequence is to be changed into a non-cysteine residue. For instance, the invention provides in a particular aspect a peptidomimetic of FSH consisting of a polypeptide derived from the B3-loop of FSH having the sequence
TFKELVYETCRVPGAAHHADSLCTYPVATQAH attached to meta-dibromobenzene
15 (see also Example 3). The polypeptide length corresponds to the stretch from CysIV+1 (Thr52) to CysV+1 (His52). The first C indicated in bold corresponds to position CysIV+10 (Val61 in FSH) and the second C to position CysV-8 (Tyr74 in FSH). Residue Cys66 in FSH is not present in the polypeptide to prevent unwanted interaction with the scaffold. In the polypeptide derived from FSH it is an alanine (the
20 first of the three alanine residues). The same amino acid changes with respect to the sequence of naturally occurring FSH can be found in another FSH peptidomimetic of the invention consisting of the polypeptide
KIQKTATFKELVYETCRVPGAAHHADSLCTYPVATQAHAGK (corresponding to CysIV-5 to CysV+4) attached to the scaffold 1,2,4,5 tetrabromodurene. However, in
25 this case also Cys84 in FSH (corresponding to CysVI) was changed into an alanine such that the last 5 residues are AHAGK instead of CHCGK as found in FSH.

It is also possible to use a polypeptide comprising a protected amino acid to avoid unwanted reactivity of said amino acid. In one embodiment, a polypeptide comprises in addition to the two cysteines intended for attachment to the scaffold a
30 cysteine residue (e.g. a residue corresponding to CysIV) that is protected with the removable protecting Cys(StBu) group. Following attachment to a scaffold to yield a peptidomimetic of the invention, the protecting group can easily be removed by reductive treatment, for example with 1,4-DDT or ethane dithiol.

In a further aspect, a peptidomimetic is prepared by attaching a polypeptide via two cysteines onto a scaffold wherein said polypeptide is derived from the B3-loop but wherein one or more amino acid residues are replaced by a bioisosteric unit. Bioisosteric replacement can be defined as the replacement of a functional group in a bioactive molecule by another functionality having similar size and physicochemical properties. Bioisosteric replacements are used in the pharma industry to optimize properties of drug candidates (activity, selectivity, transport), to remove unwanted side effects or to design molecules that are easier to synthesize. The bioisosteric replacement may be physicochemically or topologically based.

In still a further aspect, the invention provides a peptidomimetic for hCG consisting of the polypeptide VVANYRDVRFESCRLPGAPRGVNPVCSYAVALSQAAL attached to 1,2,4,5 tetrabromodurene as scaffold to form a looped structure that resembles the B3 loop of hCG. Two cysteines (indicated in bold) were introduced into the sequence at positions 61 (CysIV+10) and 74 (CysV-8). Cysteines at positions 51 (CysIV), 66, 82 (CysV) and 84 (CysVI) in the wild-type protein (see Table 13) were altered into alanine residues. The length of the polypeptide corresponds to the stretch from CysIV-2 (Val49) to CysV+4 (Leu86) in hCG. Also provided is a peptidomimetic comprising a polypeptide with the sequence NYRDVRFESCRLPGAPRGVNPVCSYAVALSAQ wherein the peptide is attached via the cysteines indicated in bold to the scaffold m-T2.

Also provided is an FSH peptidomimetic comprising a polypeptide with the sequence TFKCLVYETVRVPGAAHHADSLYTYPVACQAH attached to scaffold m-T2, an FSH peptidomimetic comprising a polypeptide with the sequence TFKELVYETCRVPGDAHHADSLCTYPVATQAH attached to scaffold m-T2, an FSH peptidomimetic comprising a polypeptide with the sequence TFKELVYETCRVPGAAHHADSLCTYPVATQAH attached to scaffold T3, an FSH peptidomimetic comprising a polypeptide with the sequence TFKELVYETCRVPGDAHHADKLCTYPVATQAH attached to scaffold m-T2, an FSH peptidomimetic comprising a polypeptide with the sequence TFKELVYETCRVPGDAHKADSLCTYPVATQAH attached to scaffold m-T2, a VEGF peptidomimetic comprising a polypeptide with the sequence ESNCTMQIMRIKPHQGQHIGEMSCQLQH attached to scaffold m-T2, a VEGF peptidomimetic comprising a polypeptide with the sequence

EESNCTMQIMRIKPHQGQHIGEMSCLQHN attached to scaffold m-T2 and a hCG peptidomimetic comprising a polypeptide with the sequence

NYRDVRFESCRLPGCPRGVNPVCSYAVALSAQ

5

S

S

NYRDVRFESCRLPGCPRGVNPVCSYAVALSAQ,

10 attached to two scaffolds m-T2. As is shown in the examples, these peptidomimetic are particularly suitable for eliciting FSH, hCG and VEGF-specific antisera.

Furthermore, the invention relates to a method for the preparation of a peptidomimetic of the invention. Provided is a method for preparing a looped peptide compound according to the invention, comprising the steps of providing the modified
 15 polypeptide and scaffold and contacting said polypeptide and scaffold under conditions that allow for the covalent attachment of said polypeptide to said scaffold, preferably wherein said contacting is performed in solution, more preferably in an aqueous solution. Said modified polypeptide has a sequence derived from the B3-loop of the protein of interest, wherein the length of the polypeptide meets the criteria mentioned
 20 above and wherein the polypeptide contains a first and a second cysteine residue at the positions as described in detail above. The polypeptide can be a synthetic peptide. Synthesis can be performed using standard solid phase peptide synthesis or any other way of producing polypeptides. The scaffold preferably comprises two reactive groups capable of forming a covalent bond with said first and second cysteine of the
 25 polypeptide, thereby inducing the formation of a looped peptide structure. The coupling reaction is preferably performed using a polypeptide with unprotected amino acid side chains. Preferably, the coupling reaction is performed in solution, more preferably in an aqueous solution. Detailed information regarding the synthesis of a looped peptide structure using halogen-functionalised scaffolds can be found in
 30 international patent application WO2004077062.

In another embodiment, a vaccine composition comprising a peptidomimetic according the invention is provided. Animal tests revealed that a composition comprising a peptidomimetic that satisfies the criteria disclosed herein

can induce the formation of a specific immune response. Example 3 shows that injection of the TFKELVYETCRVPGAAHHADSLCTYPVATQAH polypeptide derived from FSH (residues 52-83) cyclized onto a m-T2 scaffold in rats results in the production of antibodies that are reactive with native FSH. Good results were also
5 obtained with the FSH-derived peptide
KIQKTATFKELVYETCRVPGAAHHADSLCTYPVATQAHAGK (residues 49-86)
cyclized with T4 scaffold. The relevance of the polypeptide length as disclosed herein is demonstrated by the large reduction in antibody induction when a peptide is used having a sequence from the first cysteine (position CysIV+10) to the second cysteine
10 (position CysV-8). When attached to a scaffold, this peptide has a looped structure yet lacks the free ends representing the 'legs' of the characteristic A-shape
peptidomimetic of the invention.

The importance of peptide cyclization onto a suitable scaffold is apparent from Example 3 and Fig. 2 which demonstrate that the FSH-derived peptide
15 TFKELVYETCRVPGAAHHADSLCTYPVATQAH cyclized onto scaffold m-T2 yields a very high antibody titre whereas the serum of rats receiving only linear peptide or peptide that had been cyclized through a disulfide bridge between the two cysteines did not show significant recognition of FSH. In addition, for this particular peptide the meta-T2 scaffold is preferred over ortho- or para-T2 scaffolds.

20 Example 6 describes the results of a vaccination experiment performed in rats using various peptide compositions as peptide-based vaccine. Six weeks following peptide administration, the serum of the rats was tested for the ability to recognize hCG. For comparison, two commercially available antibodies against hCG were included. Rats that had been injected with a peptidomimetic according to the
25 invention showed a good hCG-specific antibody response whereas rats injected with the linear or SS-cyclized version of the same polypeptide did not show a significant response (Fig. 3).

The invention thus also provides for a vaccine comprising a looped peptide compound according to the invention. The immunogenic peptide compounds may be
30 used alone to induce cellular immunity. They may also be used, e.g. in a vaccine composition, in conjunction with other molecules in order to induce antibody production or a humoral response. The peptidomimetic can be coupled to a carrier, for example a protein carrier such as keyhole limpet haemocyanin (KLH), serum albumin

(e.g. BSA or RSA), Ovalbumin or other. Furthermore, an antibody specifically reactive with a looped peptide compound according to the invention is provided.

Also provided is the use of a vaccine comprising a Cys-knot peptidomimetic of the invention.

5 In one embodiment, a vaccine provided herein is used as birth control vaccine in mammals, preferably in humans. There are currently two major approaches to hormonal male contraception. One relies on testosterone (analogues) either alone or in combination with gonadotropin releasing hormone (GnRH) (analogues or immunizations), the other on immunizations against follicle-stimulating hormone
10 (FSH). Theoretically, the latter method will suppress spermatogenesis whilst not interfering with libido. In a preferred embodiment, the invention provides an anti-FSH vaccine for use in male contraception. Preferably, said anti-FSH vaccine does not include anti-luteinizing hormone (LH) antibodies (LH being responsible for the induction of testosterone which is necessary to maintain libido).

15 In another embodiment, the invention provides the use of a looped peptide compound as a therapeutic peptide in anti-cancer treatment. For example, a vaccine is provided that can be used in active immunotherapy. For example, said vaccine comprises a looped peptide compound that mimics hCG. The hCG hormone is naturally produced during pregnancy and is believed to stimulate growth and shield
20 the developing embryo from immune attack (i.e., rejection). hCG is a biochemical marker of malignancy associated with all the major types of cancer. The expression of hCG has been shown to correlate with tumor aggressiveness, i.e., the greater the hCG expression, the more aggressive the tumor. In both cases, hCG serves as a growth factor, encouraging rapid cell division. It promotes implantation and tissue invasion,
25 it fosters angiogenesis, the formulation of blood vessels and it facilitates immunosuppression, allowing the foetus or tumor to avoid rejection. Therefore, an immune response directed against hCG stimulates an immune attack against the tumor and neutralizes the hormonal benefits provided by hCG. As a result, an anti-hCG vaccine can be effective in blocking fertility, and therefore can also be effective in
30 treating cancer. Indeed, clinical studies using hCG vaccines in cancer indicate that an immune response to hCG plays a significant role in patient survival.

In a preferred embodiment, a vaccine is provided comprising a peptidomimetic of the invention that is capable of inducing a range of host immune

responses (humoral, cellular) against pro-angiogenic factors in tumor-bearing organisms. Of particular interest is a peptidomimetic of the VEGF-A/VEGFR-2 system, due to the critical role of this system in tumor angiogenesis (the formation of new blood vessels to the tumor).

5

The invention is exemplified by the Examples below. The Examples do not limit the scope of the invention in any way.

Brief description of the drawings

Figure 1: Schematic representation of the B3-loop of Cys-knot growth factor family members and peptidomimetics thereof. Panel A shows the general loop-structure of the various members of the Cys-knot protein family. Panel B shows the B3-loop including residues CysIV and CysV. Panel C shows the structural design of a peptidomimetic of the invention wherein two cysteines are introduced in the polypeptide such that covalent attachment of the polypeptide via these cysteines to a scaffold (indicated as T) induces the peptide to adopt a conformation which resembles the secondary structure of the B3-loop in the native protein

Figure 2: Results of a vaccination experiment using peptidomimetics of FSH. Serum of rats immunized with the peptide compound indicated at the X-axis was analysed using ELISA to determine whether the peptide can induce an immune response against native FSH. Four serial dilutions of the serum were tested (1/10, 1/30, 1/100, and 1/300). Polyclonal antibody 5215 (no. 15) and monoclonal antibody 6602 (no. 16) against FSH were used as positive control. Details are described in Example 3.

Figure 3: Results of a vaccination experiment using peptidomimetics of hCG. Serum of rats immunized with the peptide compound indicated at the X-axis (see Table 5 for the different peptides and scaffolds used) was analysed using ELISA to determine whether the peptide can induce an immune response against native hCG. Various serial dilutions of the serum were tested. Antibody hCG-B2 (no. 7) was used as positive control. Details are described in Example 6.

Figure 4: Aromatic scaffolds with ortho-, meta-, or para-positioning of two halomethyl groups. Hal refers to chlorine, bromo, or iodine atoms.

- 1,2-bis(halomethyl)benzene and other regioisomers
- 3,4-bis(halomethyl)pyridine (X=N) and other regioisomers
- 3,4-bis(halomethyl)pyridazine (X=N) and other regioisomers
- 4,5-bis(halomethyl)pyrimidine (X=N) and other regioisomers
- 4,5-bis(halomethyl)pyrazine (X=N) and other regioisomers

- 4,5-bis(halomethyl)-1,2,3-triazine (X=N) and other regioisomers
 5,6-bis(halomethyl)-1,2,4-triazine (X=N) and other regioisomers
 3,4-bis(halomethyl)pyrrole (X=N), -furan (X=O), -thiophene (X=S) and other regioisomers
- 5 4,5-bis(halomethyl)imidazole (X=N,N), -oxazole (X=N,O), -thiazol (X=S) and other regioisomers
 4,5-bis(halomethyl)-3H-pyrazole (X=N,N), -isooxazole (X=N,O), -isothiazol (X=S) and other regioisomers
 1,2-bis(bromomethylcarbonylamino)benzene (X₁=NH, X₂=O)
- 10 2,2'-bis(halomethyl)biphenylene
 2,2''-bis(halomethyl)terphenylene
 1,8-bis(halomethyl)naphthalene
 1,10-bis(halomethyl)anthracene
 Bis(2-halomethylphenyl)methane
- 15
- Figure 5: Aromatic scaffolds with ortho-, meta-, or para-positioning of three halomethyl groups:
- 1,2,3-tris(halomethyl)benzene and other regioisomers
 2,3,4-tris(halomethyl)pyridine (X=N) and other regioisomers
- 20 2,3,4-tris(halomethyl)pyridazine (X=N) and other regioisomers
 3,4,5-tris(halomethyl)pyrimidine (X=N) and other regioisomers
 4,5,6-tris(halomethyl)-1,2,3-triazine (X=N) and other regioisomers
 2,3,4-tris(halomethyl)pyrrole (X=N), -furan (X=O), -thiophene (X=S) and other regioisomers
- 25 2,4,5-bis(halomethyl)imidazole (X=N,N), -oxazole (X=N,O), -thiazol (X=S) and other regioisomers
 3,4,5-bis(halomethyl)-1H-pyrazole (X=N,N), -isooxazole (X=N,O), -isothiazol (X=S) and other regioisomers
 2,4,2'-tris(halomethyl)biphenylene
- 30 2,3',2''-tris(halomethyl)terphenylene
 1,3,8-tris(halomethyl)naphthalene
 1,3,10-tris(halomethyl)anthracene
 Bis(2-halomethylphenyl)methane

Figure 6: Aromatic scaffolds with ortho-, meta-, or para-positioning of four bromomethyl groups.

1,2,4,5-tetra(halomethyl)benzene and other regioisomers

5 1,2,4,5-tetra(halomethyl)pyridine (X=N) and other regioisomers

2,4,5,6-tetra(halomethyl)pyrimidine (X₁=X₂=N) and other regioisomers

2,3,4,5-tetra(halomethyl)pyrrole (X=NH), -furan (X=O), -thiophene (X=S) and other regioisomers

2,2',6,6'-tetra(halomethyl)biphenylene

10 2,2'',6,6''-tetra(halomethyl)terphenylene

2,3,5,6-tetra(halomethyl)naphthalene

2,3,7,8-tetra(halomethyl)anthracene

Bis(2,4-bis(halomethyl)phenyl)methane (X=CH₂)

15 Figure 7: Schematic representation of the one-step synthesis of single-, double-, and triple-loop peptide constructs.

Figure 8: Schematic representation of the stepwise synthesis of double-looped peptides via initial reaction of a partially Cys(Trt)-protected peptide with mP2,

20 followed by removal of the remaining Trt-protecting groups and subsequent reaction with a second equivalent of mP2.

Examples**Example 1: Design and preparation of immunogenic compounds based on CCR5**

5

Materials & MethodsSynthesis of Peptides on Microarrays and Reaction with m-P2 or T3-Scaffold

- 10 Grafting of the polypropylene support with polyacrylic acid was performed by irradiating the support in a 6% acrylic acid solution containing CuSO₄ using gamma radiation at a dose of 12 kGy. The grafted solid support containing carboxylic acid groups was subsequently reacted with t-butyloxycarbonyl-hexamethylenediamine (Boc-HMDA) using dicyclohexylcarbodiimide (DCC) with N-hydroxybenzotriazole
- 15 (HOBt) and subsequent cleavage of the Boc-groups using trifluoroacetic acid (TFA). The peptides were synthesized using standard Fmoc-chemistry and, after acylation, deprotected by reaction with TFA (15 ml/g resin) containing 13.3% (w) phenol, 5% (v) thioanisole, 2.5% (v) 1,2-ethanedithiol, and 5% (v) milliQ-H₂O^{*} for 2-4 hrs at RT. After washing 3x with H₂O, the peptide microarrays were treated with excess of a 1.0 mM
- 20 solution of either mP2 or T3 in 20 mM amm. bicarbonate (pH 7.8)/acetonitril (1:1 v/v) for 30-60 min. at room temperature, followed by 3x washing with 50% ACN/H₂O. Then, the microarrays were washed with excess of millipore H₂O and sonicated in disrupt-buffer (1% SDS/0.1% β-mercaptoethanol (BME) in phosphate buffered saline (PBS), pH 7.2) at 70 °C for 30 min. followed by sonication in millipore H₂O for another
- 25 45 min.

Synthese van Scaffolds:

The scaffolds are commercially available by Aldrich.

30 Screening of micro-arrays with antibodies

Microarrays were pretreated with PBS for 30 min. followed by precoating with incubation buffer (PBS containing 5% ovalbumin, 5% horse serum and 1% Tween-80)^{*}

^{*}Trade-mark

for 1 hour. Then, the microarrays were incubated with mAb (typically 1/1000, diluted in incubation buffer) overnight at 4 °C. After washing (3x10min.) with PBS/Tween-80 (0.05%), the peptides were incubated with peroxidase labeled rabbit anti-mouse antibody for 1 hr at 25 °C (rampo, 1/1000; Dako, Glostrup, Denmark) and
 5 subsequently, after washing again (3x10min.) with PBS/Tween-80 (0.05%), incubated with the peroxidase substrate 2,2'-azino-di-3-ethylbenzthiazoline sulfonate (ABTS; 50 mg in 100 ml 0.1M citric acid-sodium phosphate (McIlvaine) buffer (pH 4.0) containing 20 ul 30% H₂O₂). After 1h the absorbance (at 405 nm) was measured using a CCD-camera (XC-77RR, Sony, Japan). Bound mAb was removed by sonication in
 10 disrupt-buffer as described above. The micro-arrays were re-used for screening approximately 10-15 times.

15 CCR5

CCR5 is a cytokine co-receptor that is used by HIV for cellular entry. Antibodies specifically directed against CCR5 would therefore be suitable for counteracting cellular entry by HIV. However, immunization with whole CCR5 is problematic since
 20 CCR5 is a transmembrane protein. In order to be capable of eliciting CCR5-specific antibodies, immunogenic compounds based on CCR5 are therefore desired.

In order to design suitable test compounds, 4 CCR5 sequences were taken into account: one N-terminus domain (Nt) and three extracellular loop domains extended
 25 with about 1-6 adjacent amino acid residues of the transmembrane domains (N-terminally as well as C-terminally). These extracellular loop domains are called e1, e2 and e3. The primary sequences of the considered domains are as follows (starting N-terminally):

30 Nt: MDYQVSSPIYDINYTSEPCQKINVKQLA
 e1: PFWAHYAAAQWDFGNTMCQLLTGL
 e2: IFTRSQKEGLHYTCSSHFYPSQYQFWKNFQ
 e3: NTFQEFFGLNNCSSSNRLDQAM

The cysteine residues form native C-bridges in natural CCR5.

The extracellular domain at the N-terminal side of the Cys residue in e2 is called ECL2A whereas the extracellular domain at the C-terminal side of the Cys residue in
5 e2 is called ECL2B. Likewise, the extracellular domain at the N-terminal side of the Cys residue in e3 is called ECL3A whereas the extracellular domain at the C-terminal side of the Cys residue in e3 is called ECL3B.

ECL2A: TRSQKEGLHYT

10 ECL2B: SSHFPYSQYQFWK

ECL3A: QEFFGLNN

ECL3B: SSSNRLDQ

Subsequently, various amino acid residues are selected within the primary sequence
15 of Nt, e1, e2 and e3. Flanking sequences of these selected amino acids are selected and peptides are produced that comprise these flanking sequences. Cysteine residues are used as groups capable of reacting with a scaffold.

The following peptides were synthesized:

Peptides synthesized and screened

- 1 all 18 overlapping linear 21-mers covering MDYQVSSPIYDINYYTSEPCQKINVKQIA
- 2 all 9 overlapping linear 18-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
- 3 all 8 overlapping linear 19-mers covering Nt MDYQVSSPIYDINYYTSEPCQKINVK
- 4 all 7 overlapping linear 20-mers covering Nt MDYQVSSPIYDINYYTSEPCQKINVK
- 5 all 6 overlapping linear 21-mers covering Nt MDYQVSSPIYDINYYTSEPCQKINVK
- 6 all 7 overlapping linear 18-mers covering e1 PFWAHYAAQWDFGNTMCQLLTGL
- 7 all 6 overlapping linear 19-mers covering e1 PFWAHYAAQWDFGNTMCQLLTGL
- 8 all 5 overlapping linear 20-mers covering e1 PFWAHYAAQWDFGNTMCQLLTGL
- 9 all 4 overlapping linear 21-mers covering e1 PFWAHYAAQWDFGNTMCQLLTGL
- 10 all 13 overlapping linear 18-mers covering e2 IFTRSQKEGLHYTCSSHFPYSQYQFWKNFQ
- 11 all 12 overlapping linear 19-mers covering e2 IFTRSQKEGLHYTCSSHFPYSQYQFWKNFQ
- 12 all 11 overlapping linear 20-mers covering e2 IFTRSQKEGLHYTCSSHFPYSQYQFWKNFQ
- 13 all 10 overlapping linear 21-mers covering e2 IFTRSQKEGLHYTCSSHFPYSQYQFWKNFQ
- 14 all 5 overlapping linear 18-mers covering e3 NTFQEFFFGLNCCSSNRLLDQAM
- 15 all 4 overlapping linear 19-mers covering e3 NTFQEFFFGLNCCSSNRLLDQAM
- 16 all 3 overlapping linear 20-mers covering e3 NTFQEFFFGLNCCSSNRLLDQAM
- 17 all 2 overlapping linear 21-mers covering e3 NTFQEFFFGLNCCSSNRLLDQAM
- 18 all 23 overlapping T2 looped 6-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
- 19 all 22 overlapping T2 looped 7-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
- 20 all 21 overlapping T2 looped 8-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
- 21 all 20 overlapping T2 looped 9-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
- 22 all 19 overlapping T2 looped 10-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
- 23 all 18 overlapping T2 looped 11-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
- 24 all 17 overlapping T2 looped 12-mers covering MDYQVSSPIYDINYYTSEPCQKINVK

25 all 16 overlapping T2 looped 13-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
26 all 15 overlapping T2 looped 14-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
27 all 14 overlapping T2 looped 15-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
28 all 13 overlapping T2 looped 16-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
29 all 12 overlapping T2 looped 17-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
30 all 11 overlapping T2 looped 18-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
31 all 10 overlapping T2 looped 19-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
32 all 9 overlapping T2 looped 20-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
33 all 8 overlapping T2 looped 21-mers covering MDYQVSSPIYDINYYTSEPCQKINVK
34 all 8 overlapping T2 looped 6-mers covering e1 AAAQWDFGNTM
35 all 7 overlapping T2 looped 7-mers covering e1 AAAQWDFGNTM
36 all 6 overlapping T2 looped 8-mers covering e1 AAAQWDFGNTM
37 all 5 overlapping T2 looped 9-mers covering e1 AAAQWDFGNTM
38 all 4 overlapping T2 looped 10-mers covering e1 AAAQWDFGNTM
39 all 3 overlapping T2 looped 11-mers covering e1 AAAQWDFGNTM
40 all 2 overlapping T2 looped 12-mers covering e1 AAAQWDFGNTM
41 all 1 overlapping T2 looped 13-mers covering e1 AAAQWDFGNTM
42 all 7 overlapping T2 looped 6-mers covering e2a RSQKEGLHYT
43 all 6 overlapping T2 looped 7-mers covering e2a RSQKEGLHYT
44 all 5 overlapping T2 looped 8-mers covering e2a RSQKEGLHYT
45 all 4 overlapping T2 looped 9-mers covering e2a RSQKEGLHYT
46 all 3 overlapping T2 looped 10-mers covering e2a RSQKEGLHYT
47 all 2 overlapping T2 looped 11-mers covering e2a RSQKEGLHYT
48 all 1 overlapping T2 looped 12-mers covering e2a RSQKEGLHYT
49 all 10 overlapping T2 looped 6-mers covering e2b SSHFPYSQYQFWK
50 all 9 overlapping T2 looped 7-mers covering e2b SSHFPYSQYQFWK
51 all 8 overlapping T2 looped 8-mers covering e2b SSHFPYSQYQFWK

52 all 7 overlapping T2 looped 9-mers covering e2b SSHFPYSQYQFWK
53 all 6 overlapping T2 looped 10-mers covering e2b SSHFPYSQYQFWK
54 all 5 overlapping T2 looped 11-mers covering e2b SSHFPYSQYQFWK
55 all 4 overlapping T2 looped 12-mers covering e2b SSHFPYSQYQFWK
56 all 3 overlapping T2 looped 13-mers covering e2b SSHFPYSQYQFWK
57 all 2 overlapping T2 looped 14-mers covering e2b SSHFPYSQYQFWK
58 all 1 overlapping T2 looped 15-mers covering e2b SSHFPYSQYQFWK
59 all 13 overlapping T2 looped 6-mers covering e3 QEFFGLNNCSSSNRLD
60 all 12 overlapping T2 looped 7-mers covering e3 QEFFGLNNCSSSNRLD
61 all 11 overlapping T2 looped 8-mers covering e3 QEFFGLNNCSSSNRLD
62 all 10 overlapping T2 looped 9-mers covering e3 QEFFGLNNCSSSNRLD
63 all 9 overlapping T2 looped 10-mers covering e3 QEFFGLNNCSSSNRLD
64 all 8 overlapping T2 looped 11-mers covering e3 QEFFGLNNCSSSNRLD
65 all 7 overlapping T2 looped 12-mers covering e3 QEFFGLNNCSSSNRLD
66 all 6 overlapping T2 looped 13-mers covering e3 QEFFGLNNCSSSNRLD
67 all 5 overlapping T2 looped 14-mers covering e3 QEFFGLNNCSSSNRLD
68 all 4 overlapping T2 looped 15-mers covering e3 QEFFGLNNCSSSNRLD
69 all 3 overlapping T2 looped 16-mers covering e3 QEFFGLNNCSSSNRLD
70 all 2 overlapping T2 looped 17-mers covering e3 QEFFGLNNCSSSNRLD
71 all 1 overlapping T2 looped 18-mers covering e3 QEFFGLNNCSSSNRLD
72 all 11 overlapping T2 looped 18-mers covering Nt MDYQVSSPIYDINYYTSEPAQKINVK
73 all 10 overlapping T2 looped 19-mers covering Nt MDYQVSSPIYDINYYTSEPAQKINVK
74 all 9 overlapping T2 looped 20-mers covering Nt MDYQVSSPIYDINYYTSEPAQKINVK
75 all 8 overlapping T2 looped 21-mers covering Nt MDYQVSSPIYDINYYTSEPAQKINVK
76 all 13 overlapping T2 looped 18-mers covering Nt+e3 MDYQVSSPIYDINYYTSEPA-G-SSSNRLD
77 all 12 overlapping T2 looped 19-mers covering Nt+e3 MDYQVSSPIYDINYYTSEPA-G-SSSNRLD
78 all 11 overlapping T2 looped 20-mers covering Nt+e3 MDYQVSSPIYDINYYTSEPA-G-SSSNRLD

79 all 10 overlapping T2 looped 21-mers covering Nt+e3 MDYQVSSPIYDINYYTSEPA-G-SSSNRLD
80 all 4 overlapping T2 looped 18-mers covering Nt+e1 QKINVK-GG-AAQWDFGNTM
81 all 3 overlapping T2 looped 19-mers covering Nt+e1 QKINVK-GG-AAQWDFGNTM
82 all 2 overlapping T2 looped 20-mers covering Nt+e1 QKINVK-GG-AAQWDFGNTM
83 all 1 overlapping T2 looped 21-mers covering Nt+e1 QKINVK-GG-AAQWDFGNTM
84 all 2 overlapping T2 looped 18-mers covering Nt+ECL3A QKINVK-GG-QEFFGLNNC
85 all 1 overlapping T2 looped 19-mers covering Nt+ECL3A QKINVK-GG-QEFFGLNNC
86 all 10 overlapping T2 looped 18-mers covering e1+e2a AAAQWDFGNTM-GGG-RSQKEGLHYTC
87 all 9 overlapping T2 looped 19-mers covering e1+e2a AAAQWDFGNTM-GGG-RSQKEGLHYTC
88 all 8 overlapping T2 looped 20-mers covering e1+e2a AAAQWDFGNTM-GGG-RSQKEGLHYTC
89 all 7 overlapping T2 looped 21-mers covering e1+e2a AAAQWDFGNTM-GGG-RSQKEGLHYTC
90 all 12 overlapping T2 looped 18-mers covering e1+e2b AAAQWDFGNTM-GGG-SSHFPYSQYQFWK
91 all 11 overlapping T2 looped 19-mers covering e1+e2b AAAQWDFGNTM-GGG-SSHFPYSQYQFWK
92 all 10 overlapping T2 looped 20-mers covering e1+e2b AAAQWDFGNTM-GGG-SSHFPYSQYQFWK
93 all 9 overlapping T2 looped 21-mers covering e1+e2b AAAQWDFGNTM-GGG-SSHFPYSQYQFWK
94 all 9 overlapping T2 looped 18-mers covering e1+e3 AAAQWDFGNTM-GGGG-QEFFGLNNC
95 all 8 overlapping T2 looped 19-mers covering e1+e3 AAAQWDFGNTM-GGGG-QEFFGLNNC
96 all 7 overlapping T2 looped 20-mers covering e1+e3 AAAQWDFGNTM-GGGG-QEFFGLNNC
97 all 6 overlapping T2 looped 21-mers covering e1+e3 AAAQWDFGNTM-GGGG-QEFFGLNNC
98 all 9 overlapping T2 looped 18-mers covering e2a+e2b RSQKEGLHYT-A-SSHFPYSQYQFWK
99 all 8 overlapping T2 looped 19-mers covering e2a+e2b RSQKEGLHYT-A-SSHFPYSQYQFWK
100 all 7 overlapping T2 looped 20-mers covering e2a+e2b RSQKEGLHYT-A-SSHFPYSQYQFWK
101 all 6 overlapping T2 looped 21-mers covering e2a+e2b RSQKEGLHYT-A-SSHFPYSQYQFWK
102 all 14 overlapping T2 looped 18-mers covering e2b+e1 CSSHFPYSQYQFWK-GGG-AAQWDFGNTMC
103 all 13 overlapping T2 looped 19-mers covering e2b+e1 CSSHFPYSQYQFWK-GGG-AAQWDFGNTMC
104 all 12 overlapping T2 looped 20-mers covering e2b+e1 CSSHFPYSQYQFWK-GGG-AAQWDFGNTMC
105 all 11 overlapping T2 looped 21-mers covering e2b+e1 CSSHFPYSQYQFWK-GGG-AAQWDFGNTMC

1106 all 17 overlapping T2 looped 18-mers covering e2b+e3 CSSHFPYSQYQFWK-GG-QEFFGLNNASSSNRLD
 1107 all 16 overlapping T2 looped 19-mers covering e2b+e3 CSSHFPYSQYQFWK-GG-QEFFGLNNASSSNRLD
 1108 all 15 overlapping T2 looped 20-mers covering e2b+e3 CSSHFPYSQYQFWK-GG-QEFFGLNNASSSNRLD
 1109 all 14 overlapping T2 looped 21-mers covering e2b+e3 CSSHFPYSQYQFWK-GG-QEFFGLNNASSSNRLD
 1110 all 15 overlapping T2 looped 18-mers covering e3+e1 QEFFGLNNASSSNRLD-GGG-AAQWDFGNTM
 1111 all 14 overlapping T2 looped 19-mers covering e3+e1 QEFFGLNNASSSNRLD-GGG-AAQWDFGNTM
 1112 all 13 overlapping T2 looped 20-mers covering e3+e1 QEFFGLNNASSSNRLD-GGG-AAQWDFGNTM
 1113 all 12 overlapping T2 looped 21-mers covering e3+e1 QEFFGLNNASSSNRLD-GGG-AAQWDFGNTM
 1114 all 9 overlapping T2 looped 21-mers covering Nt+e3b MDYQVSSPIYDINYTSEC-G-CSSSNRLD
 1115 all 36 overlapping T2 looped 21-mers covering Nt+e3b DYQVSSPIYDINYTSEPC-G-CSSSNRLDQAMQ
 1116 T2 looped 19 to 21-mers covering Nt+e1 QKINVK-GG-CAAQWDFGNTMC
 1117 P2P2 looped 18 to 21-mers covering e1 AAAQWDFGNTM left and e2a SQKEGLHYT right C-----1-G-1-----C
 1118 P2P2 looped 21-mers covering e1 AQWDFGN left and e2a SSHFPYSQYQFWKN right C-----1-G-1-----C
 1119 P2P2 looped 21-mers covering e1 HYAAAQWDFGNTM left and e2a SSHFPYSQYQFWKN right C-----1-G-1-----C
 1120 P2P2 looped 21-mers covering Nt SEPCQKINVK left and e3 QEFFGLNNCSSN right C-----1-G-1-----C
 1121 T3 looped 16 to 20-mers peptides covering e1 AAAQWDFGNTM left and e2a RSQKEGLHYT right
 1122 T3 looped 20-mers peptides covering e1 AQWDFGNTM left and e2b SSHFPYSQYQFWKNF right
 1123 T3 looped 20-mers peptides covering e2b SSHFPYSQYQFWKNF left and e1 AAAQWDFGNTM right
 1124 T3 looped 20-mers peptides covering e2b SSHFPYSQYQFWKNF left and e3 QEFFGLNNASSSNRLDQ right
 1125 T3 looped 20-mers peptides covering e1 YAAAQWDFGNTM left and e3 QEFFGLNNASSSNRLDQ right, GCG in middle
 1126 T3 looped 20-mers peptides covering e3 QEFFGLNNASSSNRLDQ left and e1 YAAAQWDFGNTM right, GCG in middle
 1127 T3 looped 21-mers peptides covering e2 SLPGIIFTRSQKEGLHYTCSHFPYSQYQFWKNFQTL
 1128 T3 looped 21-mers peptides covering Nt DYQVSSPIYDINYTSEPCQKINVKQIAARLLPPLYS

In the first series of peptides (first row of the above Table), the C-terminal amino acids K, I, N, V, K, Q, I, and A of the Nt sequence were selected. Subsequently, N-terminal flanking sequences with a length of 21 amino acid residues were selected. Hence, MDYQVSSPIYDINYYTSEPCQ was a flanking sequence of K, DYQVSSPIYDINYYTSEPCQK was a flanking sequence of I, YQVSSPIYDINYYTSEPCQKI was a flanking sequence of N, et cetera. Subsequently, peptides were produced containing one of these flanking sequences.

Likewise, in the second series of peptides (second row of the above Table), the C-terminal amino acids P, C, Q, K, I, N, V and K of the Nt sequence were selected. Subsequently, N-terminal flanking sequences with a length of 18 amino acid residues were selected. Hence, MDYQVSSPIYDINYYTSE was a flanking sequence of P, DYQVSSPIYDINYYTSEP was a flanking sequence of C, YQVSSPIYDINYYTSEPC was a flanking sequence of Q, et cetera. Subsequently, peptides were produced containing one of these flanking sequences.

The peptides of the first 17 series of peptides (rows 1-17 of the above mentioned Table) were not bound to a scaffold and appeared to be less suitable as compared to scaffold-bound peptides.

In the 18th series of peptides all amino acids, except for the first 6 N-terminal amino acids, were selected and N-terminal flanking sequences with a length of 6 amino acids were selected. Subsequently, peptides were produced containing one of these flanking sequences and two cysteine residues. The peptides were coupled to a P2 scaffold via their two cysteine residues. Of note, if a flanking sequence comprised a cysteine residue that was not intended for coupling, the cysteine was replaced by alanine. The peptides of series 19-75 were produced similarly.

In series 76-116 flanking sequences derived from two different domains of CCR5 were combined. For instance, in series 76-79, flanking sequences derived from Nt were

combined with flanking sequences derived from e3. Likewise, in series 80-83, flanking sequences derived from Nt were combined with flanking sequences derived from e1, et cetera. The resulting peptides were coupled to P2 via two cysteine residues.

5

In series 117-120, two P2 scaffolds were used. Peptides were produced comprising two flanking sequences, wherein a flanking sequence derived from e1 was combined with a flanking sequence derived from E2A (rows 117-119 of the above Table) and a flanking sequence derived from Nt was combined with a flanking sequence derived from e3 (row 120 of the above Table). Cysteine residues were present at the start and the end of each flanking sequence (hence, there were four cysteines altogether). If a flanking sequence comprised a cysteine residue that was not intended for coupling, the cysteine was replaced by alanine. Subsequently, the peptides were coupled to two P2 scaffolds, using the above mentioned four cysteine residues. (The cysteine residues are depicted in the above Table as C and 1) The two cysteines depicted as C were both coupled to one T2 scaffold and the two cysteine residues depicted as 1 were both coupled to another scaffold.

In series 121-128, a T3 scaffold was used. Peptides were produced comprising two flanking sequences derived from different CCR5 domains. Three cysteine residues were incorporated into the peptides in order to couple them to a T3 scaffold.

Screening assay

The produced peptides were incubated with the commercially available anti-CCR5 antibody 2D7.

Results

30

Promising compounds that were capable of binding Ab 2D7 with a high affinity are depicted below.

		2D7 (1 µg/ml)	2D7 (10 µg/ml)	2D7 (0.1 µg/ml)
447	CQKEGLHYTC	2706	2943	261
443	CQKEGLHYC	2636	3090	148
449	CSQKEGLHYTC	2606	2889	99
1160	CWDFGNTMCQKEGLHYTC	2469	2765	315
450	CRSQKEGLHYTC	2364	2852	107
702	CNTMGGGRSQKEGLHYTC	1580	2787	68
1159	CQWDFGNTCQKEGLHYTC	1153	2636	213
719	CFGNTMGGGRSQKEGLHYT C	678	2819	113
1158	CAQWDFGNCQKEGLHYTC	416	2377	132

5

All compounds of the above Table comprise peptides bound to P2 or T3. All compounds were capable of binding antibody 2D7.

10 Conclusion: With this example we show that a method according to the invention is suitable for identifying mimics of CCR5, capable of binding 2D7, whereas linear peptides were not capable of binding 2D7.

Such peptides are further used in immunization experiments in order to elicit CCR5-specific antibodies capable of neutralizing HIV infection.

15

Example 2: Design and preparation of immunogenic compounds based on Interleukin 5

In order to design suitable test compounds, five series of compounds were generated.

- 5 The compounds were subsequently incubated with a commercially available antibody capable of specifically binding IL5 (Antibody 39D10):

Series 1

- 10 Overlapping 18-mer sequences of the entire IL5 sequence were generated. The peptides were not coupled to a scaffold. None of these peptides were capable of binding 39D10 with acceptable affinity.

Series 2

- 15 Overlapping 13-mer sequences of the entire IL5 sequence were generated. Peptides were produced containing one 13-mer sequence and a N-terminal and C-terminal cysteine residue. If a 13-mer comprised a cysteine residue that was not intended for coupling, the cysteine was replaced by alanine. Subsequently, the peptides were coupled to a P2 scaffold via their N-terminal and C-terminal cysteine residues. The resulting compounds were subsequently incubated with Ab 39D10. Some compounds
20 were capable of binding, but no favourable compound was found.

In series 3 – series 5, the following two interleukin 5 sequences were taken into account:

25

Part-1, KKKSGEERRRVNQFLDY
Part-2, LIANETLRIPVPVHKNH

- 30 Of note, the fourth amino acid residues of Part-1, serine, is a cysteine residue in natural human IL5. In order to avoid coupling of the scaffolds to this cysteine, the cysteine was replaced by serine.

Series 3

In this series, the first three amino acid sequences and the last three amino acid residues of Part-1 and Part-2 were selected. Subsequently, C-terminal and N-terminal flanking sequences with a length of between 14 and 16 amino acid residues were selected. Peptides were produced containing one flanking sequence and a N-terminal and C-terminal cysteine residue. Subsequently, the peptides were coupled to a P2 scaffold via their N-terminal and C-terminal cysteine residues. The resulting compounds were subsequently incubated with Ab 39D10. Some compounds comprising a flanking sequence of Part-1 were capable of binding Ab 39D10.

Series 4

In this series flanking sequences derived from Part-1 were combined with flanking sequences derived from Part-2. 21-mers were produced according to the following schematic sequences:

```

CXXXXXXXXXXCXXXXXXXXXXC
CXXXXXXXXXXCXXXXXXXXXXC
CXXXXXXXXXXCXXXXXXXXXXC
CXXXXXXCXXXXXXXXXXC
CXXXXXXCXXXXXXXXXXC
CXXXXXXCXXXXXXXXXXC
CXXXXXXCXXXXXXXXXXC
CXXXXXXCXXXXXXXXXXC
CXXXXXXCXXXXXXXXXXC
CXXXXXXCXXXXXXXXXXC
CXXXXXXCXXXXXXXXXXC
CXXXXXXCXXXXXXXXXXC
CXXXXXXCXXXXXXXXXXC
CXXXXXXCXXXXXXXXXXC
CXXXXXXCXXXXXXXXXXC

```

wherein the first stretch of X residues represents a flanking sequence derived from Part-1 and the second stretch of X residues represents a flanking sequence derived from Part-2. Hence, the lengths of the flanking sequences differ but the overall length of the resulting peptide is the same (21 amino acid residues). The peptides were coupled to a T3 scaffold. The resulting compounds were subsequently incubated with Ab 39D10. Various compounds were found with high binding affinity for Ab 39D10. These compounds are outlined below in more detail.

Series 5

Also in this series flanking sequences derived from Part-1 were combined with flanking sequences derived from Part-2. In this series the resulting peptides (containing a flanking sequence derived from Part-1 and a flanking sequence derived from Part-2) were of different length. The peptides were coupled to T3 via three cysteine residues and subsequently incubated with Ab 39D10. The results are outlined below in more detail.

Results

10

The following four peptides, coupled to T3, appear to have a high affinity for Ab 39D10:

15	1. Ac-CEERRRVCANETLRIPVPCGSC	(T3)	1:1500
	2. Ac-CSGEERRRVCANETLRIPCGSC	(T3)	1:1500
	3. Ac-CEERRRVNQCANETLRIPCGSC	(T3)	1:2000
	4. Ac- CGEERRRCIANETLRIPCGSC	(T3)	1:4000

All four peptides contain a partial sequence of Part-1 and a partial sequence of Part-2.

20

These four peptides were used in immunization experiments in order to test whether they are capable of eliciting antibodies against whole human IL5. The peptides, which are all derived from human IL5, appeared to be capable of eliciting antibodies that showed strong cross reaction with whole human IL5 with antibody titers of 1:1500, 1:2000 and 1:4000 (calculated according to OD values that were 50 % of the ODmax values).

25

Conclusion

Peptides comprising combinations of flanking sequences derived from different regions appear to most closely resemble a native IL5 epitope. These peptides were found with a screening method according to the invention.

30

EXAMPLE 3: Design and preparation of peptidomimetics of FSH and use thereof as peptide-vaccine.

In this experiment, polypeptides corresponding to the B3-loop of FSH were designed,
 5 wherein two amino acid residues have been replaced by a first and a second cysteine
 residue in the polypeptide which cysteines are attached to each other via a scaffold,
 wherein:

- said first scaffold-attached cysteine residue is introduced at position CysIV+ p
 located p residues C-terminal from the position that corresponds to amino acid CysIV
 10 in the wild-type B3-loop, wherein $5 \leq p \leq 12$;
- said second scaffold-attached cysteine residue is introduced at position CysV –
 q located q residues N-terminal from the position that corresponds to amino acid CysV
 in the wild-type B3-loop, wherein $4 \leq q \leq 12$ and wherein $(p - q)$ is -3, -2, -1, 0, 1, 2 or
 3; and
- 15 - the length of said polypeptide is from amino acid at position CysIV + x to
 amino acid at position CysV + y, wherein $-5 \leq x \leq 1$ and $1 \leq y \leq 6$ under the provision
 that $x + y = -1, 0, 1$ or 2.

Peptides were synthesized by solid-phase peptide synthesis using a 4-(2',4'-
 20 dimethoxyphenyl-Fmoc-aminomethyl)-phenoxy (RinkAmide) resin
 (BACHEM, Germany) on a Syro-synthesizer (MultiSynTech, Germany). All
 amino acids were purchased and used as N-alpha-(Fmoc) protected with
 side-chain functionalities protected as N-t-Boc (KW), O-t-Bu (DESTY),
 N-Trt (HNQ), S-Trt (C), or N-Pbf (R) groups. A coupling protocol using a
 25 6.5-fold excess of HBTU/HOBt/amino acid/DIPEA (1:1:1:2) in NMP with a 30
 min. activation time using double couplings was employed. Acetylated
 peptides were cleaved from the resin by reaction with TFA (15 mL/g
 resin) containing 13,3% (w) phenol, 5% (v) thioanisole, 2.5% (v)
 1,2-ethanediol, and 5% (v) milliQ-H₂O for 2-4h at room temperature, and
 30 subsequently precipitated with diethyl ether (at least 3x the volume of
 TFA). Crude peptides were purified by reversed-phase high performance
 liquid chromatography (RPC), either on a "DeltaPack" (25 or 40 x 100 mm
 inner diameter, 15 micrometer particle size, 100 A pore size; Waters, USA)

*

or on a "XTERRA" (50 x 4.6 mm inner diameter, 2.5 micrometer particle size Waters, USA) RP-18 preparative C18 column with a linear AB-gradient of 1-2% B/min where solvent A was 0.05% TFA in water and solvent B was 0.05% ACN. The correct primary ion molecular weight of the peptides was confirmed by electron-spray ionization mass spectrometry on a Micromass^{*} ZQ (Micromass, The Netherlands) or a VG Quattro II (VG Organic, UK) mass spectrometer. The polypeptides were either cyclized onto a T2 (1h reaction of peptide and 1.05 equivalent of T2 in 20% acetonitril (ACN)/80% ammonium bicarbonate (20 mM), pH 7.8 at room temperature), or T4 scaffold (1h reaction of peptide and 0.5 equivalent of T4 in 60% ACN/40% ammonium bicarbonate (20 mM), pH 7.8 at room temperature) or directly cyclized via SS-oxidation of the cysteines. The scaffolds were obtained from Sigma-Aldrich. In addition, a linear version of the polypeptide lacking the cysteines was prepared (see Table 4). Subsequently, female Wistar rats were immunized on day 0 with 400 uL of a ~2.5 mg/mL of the peptide or peptide-T-construct in PBS/CFA 1:1 (v/v) (PBS = Phosphate-Buffered Saline, CFA = Complete Freund's Adjuvance), followed by a booster (same quantity and concentration) at 4 weeks. Subsequently, the anti-peptide titers were determined after 6 weeks to check for immune response and finally the rats were bled after 8 weeks and the antisera collected. Antisera were analyzed in an FSH-binding ELISA (Greiner, PS; GDA-coating with 1 µg/mL of FSH (Biotrend)) using 2,2'-azine-di(ethylbenzthiazoline sulfonate) (ABTS) in combination with a peroxidase-labeled Goat-anti-rat serum as second antibody. Antibodies pAb 5215 (Biogenesis) and mAb 6602 (Medix Biochemicals) were included in the analysis as positive controls.

Table 4A

Sample no.	Polypeptide ^a	Scaffold ^b
1	*CRVPGDAHHAADSLC#	m-T2
2	*CRVPGDAHHAADSLC#	T4
3	*CVRVPGAAHHAADSLYC#	m-T2
4	*CVRVPGAAHHAADSLYC#	T4
5	*YETCRVPGDAHHAADSLCTYP#	m-T2

*Trade-mark

6	*YETCRVPGDAHHSLSCTYP#	T4
7	*TFKELVYETCRVPGAAHHSLSCTYPVATQAH#	m-T2
8	*KIQKTATFKELVYETCRVPGAAHHSLSCTYPVATQA HAGK#	T4
9	*CYTRDLVYKDPARPKIQKTC#	T4
10	*KIQKTATFKELVYETCRVPGAAHHSLSCTYPVATQA HAGK#	m-T2
11	*TQAHCGKADSDSTDC#	T4
12	*TFKELVYETCRVPGAAHHSLSCTYPVATQAH#	None; SS cyclized
13	*TFKELVYETCRVPGAAHHSLSCTYPVATQAH#	T4
14	*TFKELVYETVRVPGCAHHSLSLYTYPVATQAH#	None; linear

^a sequence of the polypeptide is given in one letter abbreviation. * denotes N-terminus and # denotes C-terminus.

^b m-T2 refers to meta-bis(bromomethyl)benzene and T4 refers to 1,2,4,5
5 tetrabromodurene.

The results shown in Figure 2 demonstrate the relevance of attaching a B3-derived polypeptide to a scaffold since neither the corresponding peptide cyclized via SS-oxidation nor the linear polypeptide are immunogenic by themselves.

Below, the same results are depicted with more detail in Tables 4B and 4C. Various values, such as the CLIPS positions p and q, are indicated.

Table 4B. Antibody responses from vaccination experiments with FSH-derived peptides of different length and surface region + corresponding neutralizing activities in FSH-stimulation assay.

No.	Peptide Sequence + CLIPS	CLIPS-positions (p, q)	AA's in FSH (x, y)	Ab-titre (10 wks) 2 rats ^b	Neutr. FSH-stimulat. assay ^c
1	* <u>C</u> RVPGDAHHSLS <u>C</u> # + m-T2	10, 8	10, -8	<1 (2x)	- (2x)

2	* <u>C</u> VRVPGAAHHADSL <u>C</u> # + <i>m</i> -T2	9, 7	9, -7	<1 (2x)	- (2x)
3	*YET <u>C</u> RVPGDAHHADSL <u>C</u> TYP# + <i>m</i> -T2	10, 8	7, -5	<1 (2x)	- (2x)
4	*TFKELVYET <u>C</u> RVPGAAHHADSL <u>C</u> TYPVATQ AH# + <i>m</i> -T2	10, 8	1, 1	<1; 4.0	- ; 1/64
5	*KIQKTATFKELVYET <u>C</u> RVPGAAHHADSL <u>C</u> TY PVATQAHAGK# <i>m</i> -T2	10, 8	-5, 4	<1 (2x)	- (2x)
6	* <u>C</u> RVPGDAHHADSL <u>C</u> # + T4	10, 8	10, -8	<1 (2x)	- (2x)
7	* <u>C</u> VRVPGAAHHADSL <u>C</u> # + T4	9, 7	9, -7	<1 (2x)	- (2x)
8	*YET <u>C</u> RVPGDAHHADSL <u>C</u> TYP# + T4	10, 8	7, -5	<1 (2x)	- (2x)
9	*KIQKTATFKELVYET <u>C</u> RVPGAAHHADSL <u>C</u> TY PVATQAHAGK# T4	10, 8	-5, 4	3.0; 2.5	1/16; -
10	* <u>C</u> YTRDLVYKDPAKPQKTC# + T4	-19, 31	-19, - 31	<1 (2x)	- (2x)
11	*TQAHC <u>G</u> KADSDSTDC# + T4	33, -12	29, - 12	<1 (2x)	- (2x)

^a Amino acids printed in bold are substituents for native Cys-residues at these positions, amino acids printed underlined indicate the Cys-residues at which the CLIPS are attached. ^bAntibody titres are given as ⁻¹⁰log values of the serum dilution at which the OD in the binding ELISA is still >3x the background-OD (1/10 dilution = 1, 1/100=2, 1/1000=3, 1/10 000=4, etc.). ^cgives the highest dilution of purified serum (protG-column) at which full blocking of the the FSH-induced bioactivity is still observed (at 6 ng/mL FSH cell-stimulation).

10 Table 4C. Antibody responses from vaccination experiments with FSH-β3 loop derived peptides icw. different CLIPS (at position CysIV+p, CysV-q; length: CysIV+x, CysV+y) and corresponding neutralizing activities in Y1-cell bioassay.

No.	Peptide Sequence + CLIPS	CLIPS-positions (p, q)	AA's in FSH (x, y)	Ab-titre (10 wks) 2 rats ^b	Neutr. FSH-stimulat. assay ^c
1	*TFKELVYET <u>C</u> RVPGAAHHADSL <u>C</u> TYPVATQ	10, 8	10, -8	3.0; <1	1/16; -

	AH# + m-T2				
2	*TFKELVYET <u>CR</u> VPGAHHADSL <u>CT</u> YPVATQ AH# + SS	10, 8	10, -8	<1 (2x)	- (2x)
3	*TFKELVYET <u>CR</u> VPGAHHADSL <u>CT</u> YPVATQ AH# + T4	10, 8	10, -8	<1 (2x)	- (2x)
4	*TFKELVYET <u>YR</u> VPGCAHHADSLYTPVATQ AH#	n.a.	10, -8	<1 (2x)	- (2x)

^a Amino acids printed in bold are substituents for native Cys-residues at these positions, amino acids printed underlined indicate the Cys-residues at which the CLIPS are attached. ^bAntibody titres are given as $^{-10}\log$ values of the serum dilution at which the OD in the binding ELISA is still >3x the background-OD (1/10 dilution = 1, 1/100=2, 1/1000=3, 1/10 000=4, etc.). ^cgives the highest dilution of purified serum (protG-column) at which full blocking of the the FSH-induced bioactivity is still observed (at 6 ng/mL FSH cell-stimulation).

10 The results clearly demonstrate that it is possible to generate immunogenic compounds derived from the beta3 loop of FSH (see compounds 4 and 9 in Table 4B and compound 1 in Table 4C). The immunogenic compounds give rise to the production of FSH-specific antibodies.

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EXAMPLE 4: Design and preparation of peptidomimetics of FSH and use thereof as peptide-vaccine.

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In this experiment, a set of polypeptides corresponding to the β 3-loop of FSH, differing in length and chiral configuration of the cysteine residues for CLIPS-attachment, were designed and synthesized as described above. The polypeptides were cyclized onto an *m*-T2 (1h reaction of peptide and 1.05 equivalent of *m*-T2 in 20% acetonitril /80% ammonium bicarbonate (20 mM), pH 7.8 at room temperature). Subsequently, female Wistar rats were immunized on day 0 with 400 μ L of a ~2.5 mg/mL of the peptide or peptide-T-construct in PBS/CFA 1:1 (v/v) (PBS = Phosphate-Buffered

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Saline, CFA = Complete Freund's Adjuvance), followed by a booster (same quantity and concentration) at 4 weeks. Subsequently, the anti-peptide titers were determined after 6 weeks to check for immune response and finally the rats were bled after 10 weeks and the antisera collected. Antisera were analyzed in an FSH-binding ELISA (Greiner, PS; GDA-coating with 1 μ g/mL of FSH (Biotrend)) using 2,2'-azine-di(ethylbenzthiazoline sulfonate) (ABTS) in combination with a peroxidase-labeled Goat-anti-rat serum as second antibody. Antibodies pAb 5215 (Biogenesis) and mAb 6602 (Medix Biochemicals) were included in the analysis as positive controls.

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Table 7. Antibody responses from vaccination experiments with various FSH- β 3 loop *m*-T2 CLIPS-peptides (fixed CLIPS-position at CysIV+p, CysV-q) of variable length (CysIV+x, CysV+y) and corresponding neutralizing activities in Y1-cell bioassay.

No.	Peptide Sequence + CLIPS	CLIPS-positions (p, q)	AA's in FSH (x, y)	Ab-titre (10 wks) 2 rats ^b	Neutr. FSH-stimulat. assay ^c
1	*TFKELVYET <u>CR</u> VPGDAH <u>HADSLCT</u> YPVAT QAH# + <i>m</i>-T2	10, 8	1, 1	3.0; 4.0	1/250; 1/500
6	*TFKELVYET <u>CR</u> VPGAAH <u>HADSLCT</u> YPVAT QAH# + T3/DTT	10, 8	1, 1	3.5; <1	1/125; -

^a Amino acids printed in bold are substituents for native Cys-residues at these positions, amino acids printed underlined indicate the Cys-residues at which the CLIPS are attached. ^bAntibody titres are given as ⁻¹⁰log values of the serum dilution at which the OD in the binding ELISA is still >3x the background-OD (1/10 dilution = 1, 1/100=2, 1/1000=3, 1/10 000=4, etc.). ^cgives the highest dilution of purified serum (protG-column) at which full blocking of the the FSH-induced bioactivity is still observed (at 6 ng/mL FSH cell-stimulation).

From Table 7 it is concluded that a compound comprising peptide
TFKELVYETCRVPGDAHHADSLCTYPVATQAH bound to scaffold T2 is preferred.

Moreover, a compound comprising peptide

TFKELVYETCRVPGAAHHADSLCTYPVATQAH bound to scaffold T3 is preferred.

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EXAMPLE 5: Design and preparation of structurally optimized peptidomimetics of FSH and use thereof as peptide-vaccine.

In this experiment, a set of polypeptides corresponding to the β 3-loop of FSH were
 10 structurally optimized using Ab-binding data from a replacement analysis study
 screened with the mAb's 5828 and 6602. The polypeptides were cyclized onto an *m*-T2
 (1h reaction of peptide and 1.05 equivalent of *m*-T2 in 20% acetonitril/80%
 ammonium bicarbonate (20 mM), pH 7.8 at room temperature). Subsequently, female
 Wistar rats were immunized on day 0 with 400 μ L of a $\sim$ 2.5 mg/mL of the CLIPS-
 15 peptide construct in PBS/CFA 1:1 (v/v) (PBS = Phosphate-Buffered Saline, CFA =
 Complete Freund's Adjuvance), followed by a booster (same quantity and
 concentration) at 4 weeks. Subsequently, the anti-peptide titers were determined
 after 6 weeks to check for immune response and finally the rats were bled after 10
 weeks and the antisera collected. Antisera were analyzed in an FSH-binding ELISA
 20 (Greiner, PS; GDA-coating with 1 μ g/mL of FSH (Biotrend)) using 2,2'-azine-
 di(ethylbenzthiazoline sulfonate) (ABTS) in combination with a peroxidase-labeled
 Goat-anti-rat serum as second antibody. Antibodies pAb 5215 (Biogenesis) and mAb
 6602 (Medix Biochemicals) were included in the analysis as positive controls.

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Table 8. Antibody responses from vaccination experiments with FSH- β 3 loop *m*-T2 CLIPS-peptides + corresponding neutralizing activities in Y1-cell bioassay.

No.	Peptide Sequence + CLIPS	CLIPS-positions (p, q)	AA's in FSH (x, y)	Ab-titre (10 wks) 2 rats ^b	Neutr. FSH- stimulat. assay ^c
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1	*TFKELVYET <u>CR</u> VPGDAH <u>HAD</u> SL <u>CT</u> YPVAT QAH# + m-T2	10, 8	1, 1	1.5; 3.0	1/2; 1/4
2	*TFKELVYET <u>CR</u> VPGDAH <u>HAD</u> KL <u>CT</u> YPVAT QAH# + m-T2	10, 8	1, 1	3.5; 2.0	1/64; 1/2
3	*TFKELVYET <u>CR</u> VPGDAH <u>KAD</u> SL <u>CT</u> YPVAT QAH# + m-T2	10, 8	1, 1	>4.5; <1	1/1000; -

^a Amino acids printed in bold are substituents for native Cys-residues at these positions, amino acids printed underlined indicate the Cys-residues at which the CLIPS are attached. ^bAntibody titres are given as ⁻¹⁰log values of the serum dilution at which the OD in the binding ELISA is still >3x the background-OD (1/10 dilution = 1, 1/100=2, 1/1000=3, 1/10 000=4, etc.). ^cgives the highest dilution of purified serum (protG-column) at which full blocking of the the FSH-induced bioactivity is still observed (at 6 ng/mL FSH cell-stimulation).

10 From Table 8 it is concluded that a compound comprising peptide TFKELVYETCRVPGDAHHADKLCTYPVATQAH bound to scaffold T2 is preferred. Moreover, a compound comprising peptide TFKELVYETCRVPGDAHKADSLCTYPVATQAH bound to scaffold T2 is preferred.

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EXAMPLE 6: Design and preparation of peptidomimetics of h-CG and use thereof as peptide-vaccine.

20 In this experiment, polypeptides corresponding to the B3-loop of hCG were designed and synthesized as described above. The polypeptides were either cyclized onto a T2 (1h reaction of peptide and 1.05 equiv of T2 in 20% ACN/80% amm. bicarb (20 mM), pH 7.8 at room temperature), or T4 scaffold (1h reaction of peptide and 0.5 equiv. of T4 in 60% ACN/40% amm. bicarb (20 mM), pH 7.8 at room temperature) or directly
25 cyclized via SS-oxidation of the cysteines. In addition, a linear version of the polypeptide lacking cysteines was prepared (see Table 5). Rats were immunized with the various peptides or peptide-constructs as described for the FSH-peptide mimics in Example 1. Commercial antibody CG-B2 against hCG (obtained from Imgen) were

included in the analysis as positive controls in order to validate the coating of hCG (obtained from Biotrend) on the ELISA-surface.

Table 9A

Sample no.	Polypeptide ^a	Scaffold ^b
1	*NYRDVRFESCRLPGAPRGVNPVCSYAVALSQAQ#	m-T2
2	*NYRDVRFESCRLPGAPRGVNPVCSYAVALSQAQ#	None; SS-cyclized
3	*NYRDVRFESCRLPGAPRGVNPVCSYAVALSQAQ#	T4
4	*NYRDVRFESIRLPGAPRGVNPVVS YAVALSQAQ#	None; linear
5	*VVANYRDVRFESCRLPGAPRGVNPVCSYAVALSQAQAAL#	m-T2
6	*VVANYRDVRFESCRLPGAPRGVNPVCSYAVALSQAQAAL#	T4

^a sequence of the polypeptide is given in one letter abbreviation. * denotes N-terminus and # denotes C-terminus.

^b m-T2 refers to meta-dibromobenzene; T4 refers to 1,2,4,5 tetrabromodurene.

The results shown in Figure 3 demonstrate the relevance of attaching a B3-derived polypeptide to a scaffold since neither the corresponding peptide cyclized via SS-oxidation nor the linear polypeptide are immunogenic by themselves.

Below, the same results are depicted with more detail in Table 9B. Various values, such as the CLIPS positions p and q, are indicated.

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Table 9B. Antibody responses from vaccination experiments with hCG-β3 loop derived peptides icw. different CLIPS + corresponding neutralizing activities in hCG bioassay.

No.	Peptide Sequence + CLIPS	CLIPS-positions (p, q)	AA's in hCG (x, y)	Ab-titre (10 wks) 2 rats ^b	Neutr. hCG-stimulat. assay
2	*NYRDVRFESCRLPGAPRGVNPVC	10, 8	1, 1	4.0; <1	- (2x)

	SYAVALSAQ# + m-T2				
4	*NYRDVRFESCRLPGAPRGVNPVC SYAVALSAQ# + SS	10, 8	1, 1	<1; 1.0	- (2x)
5	*NYRDVRFESCRLPGAPRGVNPVC SYAVALSAQ# + T4	10, 8	1, 1	<1 (2x)	- (2x)
6	*NYRDVRFESIRLPGAPRGVNPVVS YAVALSAQ#	n.a.	1, 1	<1 (2x)	- (2x)
7	*VVANYRDVRFESCRLPGAPRGVN PVC SYAVALSAQAAL# + m-T2	10, 8	1, 1	<1 (2x)	- (2x)
8	*VVANYRDVRFESCRLPGAPRGVN PVC SYAVALSAQAAL# + T4	10, 8	1, 1	3.0; <1	- (2x)

^a Amino acids printed in bold are substituents for native Cys-residues at these positions, amino acids printed underlined indicate the Cys-residues at which the CLIPS are attached. ^bAntibody titres are given as ⁻¹⁰log values of the serum dilution at which the OD in the binding ELISA is still >3x the background-OD (1/10 dilution = 1, 1/100=2, 1/1000=3, 1/10 000=4, etc.). ^c "+" means that 10-fold diluted serum is able to block hCG-induced cell-stimulation (1 and 5 ng/mL hCG); "-" means that no hCG-blocking effect was observed.

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EXAMPLE 7: Design and preparation of peptidomimetics of hCG and use thereof as peptide-vaccine.

In this experiment, a set of polypeptides corresponding to the β 3-loop of hCG, differing in length and positions of the cysteine residues for CLIPS-attachment, were designed and synthesized as described above. The polypeptides were cyclized onto an m-T2 (1h reaction of peptide and 1.05 equivalent of T2 in 20% acetonitril /80% ammonium bicarbonate (20 mM), pH 7.8 at room temperature). Subsequently, female Wistar rats were immunized on day 0 with 400 μ L of a ~2.5 mg/mL of the peptide or peptide-T-construct in PBS/CFA 1:1 (v/v) (PBS = Phosphate-Buffered Saline, CFA = Complete Freund's Adjuvance), followed by a booster (same quantity and concentration) at 4 weeks. Subsequently, the anti-peptide titers were determined after 6 weeks to check

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for immune response and finally the rats were bled after 10 weeks and the antisera collected. Antisera were analyzed in an FSH-binding ELISA (Greiner, PS; GDA-coating with 1 μ g/mL of hCG (Biotrend)) using 2,2'-azine-di(ethylbenzthiazoline sulfonate) (ABTS) in combination with a peroxidase-labeled Goat-anti-rat serum as second antibody. Antibody B2 was included in the analysis as positive control.

Table 10. Antibody responses from vaccination experiments with hCG- β 3 loop *m-T2* CLIPS-peptides (CLIPS at CysIV+p, CysV-q) of different peptide length (CysIV+x, CysV+y) and corresponding neutralizing activities in hCG-bioassay.

No.	Peptide Sequence + CLIPS	CLI PS- pos itio ns (p, q)	AA's in hCG (x, y)	Ab- titre (9 wks) 2 rats ^b	Neutr. hCG- stimul at.ass ay ^c
5	*NYRDVRFESCRLPGAPRGVNPVCSYAVAVALSAQ# + m-T2	8, 6	1, 1	1.9 (2x)	- (2x)
6	*ANYRDVRFESCRLPGAPRGVNPVCSYAVAVALSAQA# + m-T2	8, 6	0, 2	<1 (2x)	- (2x)
7	*VANYRDVRFESCRLPGAPRGVNPVCSYAVAVALSAQAA# + m-T2	8, 6	-1, 3	<1; 1.9	- (2x)
8	*NYRDVRFESCRLPGDPRGVNPVCSYAVAVALSAQ# + m-T2	8, 6	1, 1	<1 (2x)	- (2x)
8	*NYRDVRFESCRLPGCPRGVNPVCSYAVAVALSAQ# + m-T2 S S *NYRDVRFESCRLPGCPRGVNPVCSYAVAVALSAQ# + m-T2	8, 6 8, 6	1, 1 1, 1	2.9; 1.8	+ , -

^a Amino acids printed in bold are substituents for native Cys-residues at these positions, amino acids printed underlined indicate the Cys-residues at which the CLIPS are attached. ^bAntibody titres are given as $^{-10}\log$ values of the serum dilution at which the OD in the binding ELISA is still >3x the background-OD (1/10 dilution = 1, 1/100=2, 1/1000=3, 1/10 000=4, etc.). ^c "+" means that 10-fold diluted serum is able

to block hCG-induced cell-stimulation (1 and 5 ng/mL hCG); "-" means that no hCG-blocking effect was observed.

5 From Table 10 it is concluded that a compound comprising peptide

*NYRDVRFESCRLPGCPRGVNPVCSYAVALSAQ# + m-T2

S

S

*NYRDVRFESCRLPGCPRGVNPVCSYAVALSAQ# + m-T2

10

bound to scaffold T2 is preferred.

15 **EXAMPLE 8: Design and preparation of peptidomimetics of VEGF-A and use thereof as peptide-vaccine.**

In this experiment, a set of polypeptides corresponding to the $\beta 5$ -turn- $\beta 6$ loop of VEGF-A (corresponding to $\square 3$ -loop of FSH en hCG), differing in length and positions
 20 of the cysteine residues for CLIPS-attachment, were designed and synthesized as described above. The polypeptides were cyclized onto an *m*-T2 (1h reaction of peptide and 1.05 equivalent of T2 in 20% acetonitril /80% ammonium bicarbonate (20 mM), pH 7.8 at room temperature). Subsequently, female Wistar rats were immunized on day 0 with 400 μ L of a ~ 2.5 mg/mL of the peptide or CLIPS-peptide-construct in
 25 PBS/CFA 1:1 (v/v) (PBS = Phosphate-Buffered Saline, CFA = Complete Freund's Adjuvance), followed by a booster (same quantity and concentration) at 4 weeks. Subsequently, the anti-peptide titers were determined after 6 weeks to check for immune response and finally the rats were bled after 9 weeks and the antisera collected. Antisera were analyzed in an VEGF-binding ELISA (Greiner, PS; GDA-coating with 0.1 μ g/mL of VEGF-A using 2,2'-azine-di(ethylbenzthiazoline sulfonate) (ABTS) in combination with a peroxidase-labeled Goat-anti-rat serum as second
 30 antibody. mAb 293 was included in the analysis as positive control.

Table 11. Antibody responses from vaccination experiments with VEGF-A β 5-turn- β 6 loop *m*-T2 CLIPS-peptides with different CLIPS-position (CysIV+p, CysV-q) and different peptide length (CysIV+x, CysV+y, and corresponding neutralizing activities in VEGF-proliferation assay.

No.	Peptide Sequence + CLIPS ^a	CLIPS-positions (p, q)	AA's in VEGF (x, y)	Ab-titre (9 wks) 2 rats ^b	Neutr. VEGF-prolif. assay ^c
1	*ESNITMQIMRIKPHQGQHIGEMSFLQH# + <i>m</i> -T2	n.a.	5, -3	>1.8 (2x)	- (2x)
2	*ESNCTMQIMRIKPHQGQHIGEMSCLQH# + <i>m</i> -T2	8, 6	5, -3	>2.8 (2x)	+ (2x)
3	*ESNITCQIMRIKPHQGQHIGECFLQH# + <i>m</i> -T2	10, 8	5, -3	>2.8 (2x)	+, -
4	*ESNITMQCMRIKPHQGQHICEMSFLQH# + <i>m</i> -T2	12, 10	5, -3	>2.8;<1.8	+, -
5	*ESNITMQICRIKPHQGQHICGEMSFLQH# + <i>m</i> -T2	13, 11	5, -3	>1.8;<1.8	nd
6	*EESNITMQIMRIKPHQGQHIGEMSFLQHN#	n.a.	4, -2	>2.8;<1.8	- (2x)
7	*EESNCTMQIMRIKPHQGQHIGEMSCLQHN# + <i>m</i> -T2	8, 6	4, -2	>2.8 (2x)	+, -
8	*EESNITCQIMRIKPHQGQHIGECFLQHN# + <i>m</i> -T2	10, 8	4, -2	>2.8;<1.8	+, -
9	*EESNITMQCMRIKPHQGQHICEMSFLQHN# + <i>m</i> -T2	12, 10	4, -2	>1.8;<1.8	nd
10	*EESNITMQICRIKPHQGQHICGEMSFLQHN# + <i>m</i> -T2	13, 11	4, -2	<1.8 (2x)	nd

^bAntibody titres are given as number of 10-fold dilutions for which the OD (mAb-

binding ELISA) > 3x times OD-background. ^c "+" means that 10-fold diluted serum is able to block cell-proliferation induced by addition of 20 ng/mL VEGF; "-" means that

no cell-proliferation inhibition was observed at 20 ng/mL VEGF.

From Table 11 it is concluded that a compound comprising peptide
ESNCTMQIMRIKPHQGQHIGEMSCLQH bound to scaffold T2 is preferred.

Moreover, a compound comprising peptide

EESNCTMQIMRIKPHQGQHIGEMSCLQHN bound to scaffold T2 is preferred.

5

Conclusion: CLIPS positions 8, 6 (p=8 and q = 6) en 10,8 (p=10 and q=8) are preferred.

Table 12: Overview of Cys-knot Protein Sub-Families

	<i>Glycoprotein Hormone-α Family</i>
5	Glycoprotein Hormone (or gonadotropin)- α 1,2(GLHA-1,2)
	<i>Glycoprotein Hormone-β Family</i>
	Choriogonadotropin- β (β -CG)
	Gonadotropin- β 1,2 (GTH-I,II)
10	Follicle Stimulating Hormone (or follotropin)- β (FSH- β)
	Luteinizing Hormone- β (or lutropin)- β (β -LH)
	Thyroid Stimulating Hormone (or thyrotropin)- β (TSH)
	Contactin-Associated Protein-like 2 precursor (CTA-2)
	Glycoprotein Hormone beta-5 precursor (GPB-5)
15	
	<i>Nerve Growth Factor Family</i>
	Nerve Growth Factor (NGF)
	Neurotrophin-3,4,5,7 (NT-3,4,5,7; HDNF)
	Brain-derived Neurotropic Factor (BDNF)
20	
	<i>PDGF-family</i>
	Platelet-derived Growth FactorA,B-1,2 (PDGF-A,B-1,2)
	PDGF-related transforming protein sis (TSIS,_SMSAV, P28SIS)Placenta Growth Factor (PLGF)
25	Vascular Endothelial Growth Factor A,B,C,D,H (VEGF-A,B,C,D,H)
	Vascular Endothelial Growth Factor Toxin (TXVE, SVVEGF, ICPP)
	<i>Transforming Growth Factor Superfamily</i>
	Transforming Growth Factor-beta 1-5 (TGF β 1-5)
30	Activin- β (Inhibin- β)
	ATP-dependent CLP-protease ATP-binding subunit CLPX (CLPX)
	Bone Morphogenetic protein 2-8,10,15 (BMP 2-8,10,15)
	60A Protein Precursor (Glass Bottom Boat Protein, 60A)
	CET-1 Caenorhabditis Elegans
35	Decapentaplegic Protein Precursor (DECA)
	DVR1-Protein Precursor (Vegital Hemisphere VG1 Protein)
	Dorsalin-1 Precursor (DSL1)
	XNR-1,2,4 (Xenopus Laevis)
	ZNR-1 Brachydanio Rerio (Zebrafish)
40	VG1-Gallus Gallus (Chicken)
	Placental Bone Morphogenetic proteinNodal precursor (NODA)
	Norrie Disease Protein (NDP)
	Prostate Differentiation Factor (PDF)
	(Embryonic) Growth Differentiation Factor 1-9 (GDF-1-9)
45	Glial Cell Line-derived Neurotrophic Factor Precursor (GDNF)
	Left-right determining factor-b precursor (lefty-b protein, LFTB)
	Megakaryocyte Stimulating Factor (MSF)
	Mucin-2 precursor (Intestinal Mucin-2)
	Muellerian Inhibiting Factor (MIS)
50	Neurturin Precursor (NRTN)
	Persephin Precursor (PSPN)

Sclerostin (SOST)
Screw Protein Precursor (SCW)
Univin Precursor (UNIV)

5

Table 14 : Position of conserved cysteines in various members of the Cys-knot protein family. The numbers between brackets refer to the Pfam databases of multiple alignments of protein domains or conserved protein regions. The first column lists all cysteines residues found within the protein. The second column gives the designation of the six conserved cysteines residues (CysI to CysVI). The other columns indicates the corresponding amino acid position (starting from the N-terminus) for individual subfamily members.

15

Table 14A : Glycoprotein Hormone-Alpha Subfamily (PF00236)

			hCG-a
C-1			7
C-2	CysI		10
C-3	CysII		28
C-4			31
C-5	CysIII		32
C-6			59
C-7	CysIV		60
C-8	CysV		82
C-9	CysVI		84
C-10			87

Table 14B : Glycoprotein Hormone-Beta Subfamily (PS00689/PS00261)

		hCG-beta	FSH-beta
C-1	CysI	9	3
C-2		23	17
C-3		26	20
C-4	CysII	34	28
C-5	CysIII	38	32
C-6	CysIV	57	51
C-7		72	66
C-8	CysV	88	82
C-9	CysVI	90	84
C-10		93	87
C-11		100	94

C-12		110	104
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Table 14C: NGF-subfamily (PF00243)

		NGF	BDNF
C-1	CysI	15	13
C-2	CysII	58	58
C-3	CysIII	68	68
C-4	CysIV	80	80
C-5	CysV	108	109
C-6	CysVI	110	111

Table 14D: PDGF-subfamily (PF00341)

		PDGF	PLGF	VEGF-A
C-1	CysI	16	35	26
C-2		43	60	51
C-3	CysII	49	66	57
C-4		52	69	60
C-5	CysIII	53	70	61
C-6	CysIV	60	77	68
C-7	CysV	97	111	102
C-8	CysVI	99	113	104

5

Table 14E: TGF-subfamily

		TGF-B2	BMP2	BMP7	GDNF	GDF-15
C-1		7	-	-	-	9
C-2	CysI	15	14	38	42	16
C-3		16	-	-	-	17
C-4	CysII	44	43	67	69	46
C-5	CysIII	48	47	71	73	50
C-6		77	78	103	102	79
C-7	CysIV	78	79	104	103	80
C-8	CysV	109	111	136	132	111
C-9	CysVI	111	113	138	134	113

CLAIMS:

1. A peptidomimetic of a member of the cystine-knot growth factor family, comprising a polypeptide derived from the amino acid sequence of the beta-3 hairpin (B3) loop of said cystine-knot growth factor family member, wherein two amino acid residues have been replaced by a first and a second cysteine residue in the polypeptide, which cysteines are attached to each other via a scaffold and wherein any cysteine residue in the natural sequence is changed into a residue that is not reactive with the scaffold, wherein:
 - said scaffold is an aromatic molecule;
 - said first scaffold-attached cysteine residue is introduced at position CysIV+ p located p residues C-terminal from the position that corresponds to amino acid CysIV in the wild-type B3-loop, wherein $5 \leq p \leq 12$;
 - said second scaffold-attached cysteine residue is introduced at position CysV - q located q residues N-terminal from the position that corresponds to amino acid CysV in the wild-type B3-loop, wherein $4 \leq q \leq 12$ and wherein $(p - q)$ is -3, -2, -1, 0, 1, 2 or 3;
 - the polypeptide extends from amino acid at position CysIV + x to amino acid at position CysV + y, wherein $-5 \leq x \leq 1$ and $1 \leq y \leq 6$ under the provision that $x + y = -1, 0, 1$ or 2; and
 - the position of said first and second cysteine correspond to positions CysIV+10 and CysV-8, CysIV+9 and CysV-8, CysIV+8 and CysV-6, CysIV+7 and CysV-5, CysIV+7 and CysV-6, CysIV+7 and CysV-4, CysIV+5 and CysV-4, or CysIV+6 and CysV-4.
2. The peptidomimetic of claim 1, wherein the aromatic molecule is a heteroaromatic molecule.

3. The peptidomimetic according to claim 1 or 2, wherein the length of the polypeptide is from CysIV +1 to CysV + 1, from CysIV-5 to CysV +6, from CysIV-3 to CysV+4, from CysIV-5 to CysV+4, or from CysIV-2 to CysV+ 4.
4. The peptidomimetic according to any one of claims 1 to 3, wherein the length of the polypeptide is from CysIV +1 to CysV + 1, from CysIV-2 to CysV+ 4, or from CysIV-5 to CysV+ 4.
5. The peptidomimetic according to any one of claims 1 to 4, wherein the positions of said first and second cysteine correspond to position CysIV+10 and CysV-8, CysIV+7 and CysV-6, or CysIV+8 and CysV-6.
6. The peptidomimetic according to any one of claims 1 to 5, wherein the positions of said first and second cysteine correspond to positions CysIV+10 and CysV-8.
7. The peptidomimetic according to any one of claims 1 to 6, wherein the scaffold used to prepare said peptidomimetic is an aromatic molecule comprising a benzyl wherein the benzyl is at least di-halogenated.
8. The peptidomimetic according to claim 7, wherein the aromatic molecule is a heteroaromatic molecule.
9. The peptidomimetic according to claim 7 or 8, wherein said scaffold is a halomethylarene.
10. The peptidomimetic according to claim 7 or 8, wherein said scaffold is selected from the group consisting of ortho-, meta- and para-dihaloxylene and 1,2,4,5 tetra halodurene.

11. The peptidomimetic according to claim 7 or 8, wherein said scaffold is meta-dibromoxylene (m-T2) or 1,2,4,5 tetrabromodurene (T4).
12. The peptidomimetic according to claim 7, wherein the polypeptide length is from CysIV+1 to CysV + 1 and wherein said scaffold is meta-dihaloxylene.
13. The peptidomimetic according to claim 7, wherein the polypeptide length extends from CysIV+1 to CysV + 1 and wherein said scaffold is meta-dibromoxylene.
14. The peptidomimetic according to claim 7, wherein the polypeptide length is from CysIV -2 to CysV + 4 and wherein said scaffold is 1,2,4,5 tetrahalodurene.
15. The peptidomimetic according to claim 7, wherein the polypeptide length is from CysIV -2 to CysV + 4 and wherein said scaffold is 1,2,4,5 tetrabromodurene.
16. The peptidomimetic according to any one of claims 1 to 15, wherein said member of the cystine-knot growth factor family is a member of the glycoprotein hormone-beta (GLHB) subfamily, the platelet-derived growth factor (PDGF) subfamily, the transforming growth factor (TGF) subfamily, the nerve growth factor (NGF) subfamily, or the glycoprotein hormone-alpha (GLHA) subfamily.
17. The peptidomimetic according to any one of claims 1 to 15, wherein the position of said first cysteine corresponds to amino acid position CysIV+ 10 and wherein the position of said second cysteine corresponds to position CysV-8.
18. The peptidomimetic according to claim 17, wherein said polypeptide is derived from the B3-loop of a member of the GLHB subfamily, the PDGF subfamily, or the TGF subfamily.

19. The peptidomimetic according to any one of claims 1 to 15, wherein the position of said first cysteine corresponds to amino acid position CysIV+ 8 and wherein the position of said second cysteine corresponds to position CysV-6.

20. The peptidomimetic according to claim 19, wherein said polypeptide is derived from the B3-loop of a member of the GLHA subfamily.

21. The peptidomimetic according to any one of claims 1 to 15, wherein the position of said first cysteine corresponds to amino acid position CysIV+ 7 and wherein the position of said second cysteine corresponds to position CysV-6.

22. The peptidomimetic according to claim 21, wherein said polypeptide is derived from the B3-loop of a member of the nerve growth factor (NGF)- subfamily.

23. The peptidomimetic according to any one of claims 1 to 15, wherein the position of said first cysteine corresponds to amino acid position CysIV+ 8 and wherein the position of said second cysteine corresponds to position CysV-6 and wherein said polypeptide is derived from the B3-loop of a vascular endothelial growth factor (VEGF) protein.

24. A peptidomimetic selected from the group consisting of:

the polypeptide TFKELVYETCRVPGAAHHADSLCTYPVATQAH attached to scaffold meta-1,3-bis(bromomethyl)benzene (m-T2),

the polypeptide KIQKTATFKELVYETCRVPGAAHHADSLCTYPVATQAHAGK attached to scaffold 1,2,4,5 tetrabromodurene (T4),

the polypeptide TFKCLVYETVRVPGAAHHADSLYTYPVACQAH attached to scaffold m-T2,

the polypeptide TFKELVYETCRVPGDAHHADSLCTYPVATQAH attached to scaffold m-T2,

the polypeptide TFKELVYETCRVPGAAHHADSLCTYPVATQAH attached to scaffold 2,4,6-tris(bromomethyl)mesitylene (T3),

the polypeptide NYRDVRFESCRLPGAPRGVNPVCSYAVALSQAQ attached to scaffold m-T2, and

the polypeptide VVANYRDVRFESCRLPGAPRGVNPVCSYAVALSQAQAAL attached to scaffold m-T2.

25. A method for preparing a peptidomimetic according to any one of claims 1 to 21, comprising the steps of providing a polypeptide and a scaffold and contacting said polypeptide and scaffold under conditions that allow for the covalent attachment of said polypeptide to said scaffold, wherein the scaffold used to prepare said peptidomimetic is an aromatic molecule comprising at least two benzylic halogen substituents.

26. The method according to claim 25, wherein the aromatic molecule is a heteroaromatic molecule.

27. The method according to claim 25, wherein said contacting is performed in solution.

28. The method according to claim 25, wherein said contacting is performed in an aqueous solution.

29. A vaccine composition comprising the peptidomimetic according to any one of claims 1 to 24, and a pharmaceutically acceptable excipient.

30. The vaccine composition according to claim 29, wherein said peptidomimetic is coupled to a carrier.

31. The vaccine composition according to claim 30, wherein the carrier is keyhole limpet haemocyanin (KLH).

Table 13. Alignment of various members of the cys-knot protein family

	N-terminus	Cysl (B1-loop)	CysII	CysIII (B2-loop)	CysIV (B3-loop)	CysV	CysVI + C-terminus	
hGLHA	PDVQDCPE	CTLQENPFFSQPGAPILQ	CMGC	CFSRAYPTPLRSKKTMLVQKNVTSESTC	CVAKSYNRVTVMGGFKVENHTA	CH	OSTCYVYHKS	
hFSH-β	S	CELTNITIAIEKEECRFQISINTTW	CAGY	CYTRDLVYKDPARPKIKT	CTFKELVETVRVPGCAHHADSLVTPVATQ	CH	CGKCDSDSDCTVIRGLGPSYCSFGEMKE	
hCG-β	SKEPLRPR	CRPINATLAVEKEGCPVCTVNTTI	CAGY	CPTMTRVLQGVLPALPQW	CNYRDVRFESIRLPGCPRGVPVWSYAVALS	CQ	CALCRRSTTDCGGFKDHP LTCDDPRFQDSSSSKAPPPSLPSPSRLLPGPSDTPILPQ	
hTSH-β	F	CIPTeyTMHIERRECAVCLTINTTI	CAGY	CMTRDINGKLFIPKYALSQDV	CTYRDFYRTVEIPGCP LHVHPYFSYPVALS	CK	CGKONTDYSDCIHEAKTNYCTKPKQKSYLVGFVS	
hLH-β	SREPLRPW	CHPINALAVEKEGCPVCTVNTTI	CAGY	CPTMMRVLQAVLPPLPQW	CTYRDVRFESIRLPGCPRGVPVWSFPVALS	CR	CGPCRRSTSDCGGPKDHP LTCDHPQLSGLLFL	
hNGF	SSSHPIFHIRGEFSV	CDSVSVWVGDKTTATDIKGEVMVLGEVINNINSVFKQYFFETK	CRDPNPVD SG		CRGIDSKHWNSY			
hBDNF	HSDPARRGELSV	CDSISEWTAADKKTAVDMSGGTVTVLEKVPVSKGQLKQFYETK	CNPMGYTKEG		CRGIDKRHWNSQ			
	N-terminus	Cysl (B1-loop)	CysII	CysIII (B2-loop)	CysIV (B3-loop)	CysV	CysVI	
hVEGF-a	APMAEGGGQNHEWKFMDVYQRSY	CHIETLVDIFQEYDPDEIEYIFKPSCVPLMR	CGGC	CNDEGLE	CVPTESNITMQIMRIKPHQGGHIGEMSFLQH NK	CE	CRPKKDR	
hPLGF	SEVEVWPFQEVWGRSY	CRALERLVDVWSEYPSVEVEHMFSPSCVSLLR	CTGC	CGDENLH	CVPVETANVTMQLLKIRSGDRPSYVELTFSQHVR	CE	CRPLREK	
hPDGF-a	SIEEAVPAV	CKTRTVIIEIPRSQVDPTSANFLWPPPCVEV KR	CTGC	CNTSSVK	CQPSRVHHRSVKAKVEYVRKKPKLKEVQVRLEE HLE	CA	CATTSLN	
hPDGF-b	SLGSLTIAEPAMIAE	CKTRTEVFEISRRLIDRTNANFLVWPPCVEVQR	CSGC	CNNRN VQ	CRPTQVQLRPVQVRKIEIVRKPIFKKATVTL EDHLA	CK	CETVAAA	
	N-terminus	Cysl (B1-loop)	CysII	CysIII (B2-loop)	CysIV (B3-loop)	CysV	CysVI	
hTGFB-1	ALDTNYCFSSSTEKN	CCVRQLYIDFRKDLGWKWIHEPKGYHANF	CLGP	CPYIWSLDTQYSKVLALYNQHNPGASAAPC	CVPOALEPLPIVYVYVGRPKPKEQLSNMIVRS	CK	CS	
hBMP-2	QAKHKQRKRLKSS	CKRHPLYVDFSDVGWNDWIVAPPGYHAFY	CHGE	CPFPLADHLNSTNHAIVQTLVNSVNSKIPKAC	CVPTELSAISM LYL DENEKAVLKNYQDMVVEG	CG	CR	
hBMP-7	STGSKQRSQNRSKTPKNQEALRMANVAENSSSDQRQA	CKKHELYVSFRDLGWQDWIAPPEGYAAAY	CEGE	CAPFLNSYMNATNHAIVQTLVHFINPETVPKPC	CAPTQLNAISVL YFDDSSNWILKKYRNMMVRA	CG	CH	
hBMP-10	NAKGNY	CKRTPLYIDFKEIGWDSWIAPPGYEAYE	CRGV	CNYPLAEHLTPTKHAIQALVHLKNSQKASKAC	CVPTKLEPISILYLDKGWVTKFYKGYEGMAVSE	CG	CR	
hGDNF	SPDKQMAVLPRRERNRQAAAANPENSRGKGRRGQRGKNRG	CVLTAILNLVTDLGLGYETKEELIFRY	CSGS	CDAAEITTYDKILKNLSRNRLVSDKVGQAC	CRPIAFDDDL SFLDDNLVYHILRKHS AKR	CG	CI	
hGDF-5	APLATRQGKRPSKNL KAR	CSRKALHVNFKDMGWDDWIAPLEYEAFH	CEGL	CEFFPLRSHLEPTNHAIVQTLMNSMDPESTPPTC	CVPTRLSPISILFIDSANNVWYKQYEDMVVES	CG	CR	
hGDF-15	ARARNGDHCPLGPGR	CCRLHTVRASLEDLGWADWWLSPREVQVTM	CIGA	CPSQFRAANMHAQIKTSLHRLKPDVTVPAPC	CVPASYNPMWLIQKTDITGVS LQTYDDLAKD	CH	CI	

2/9

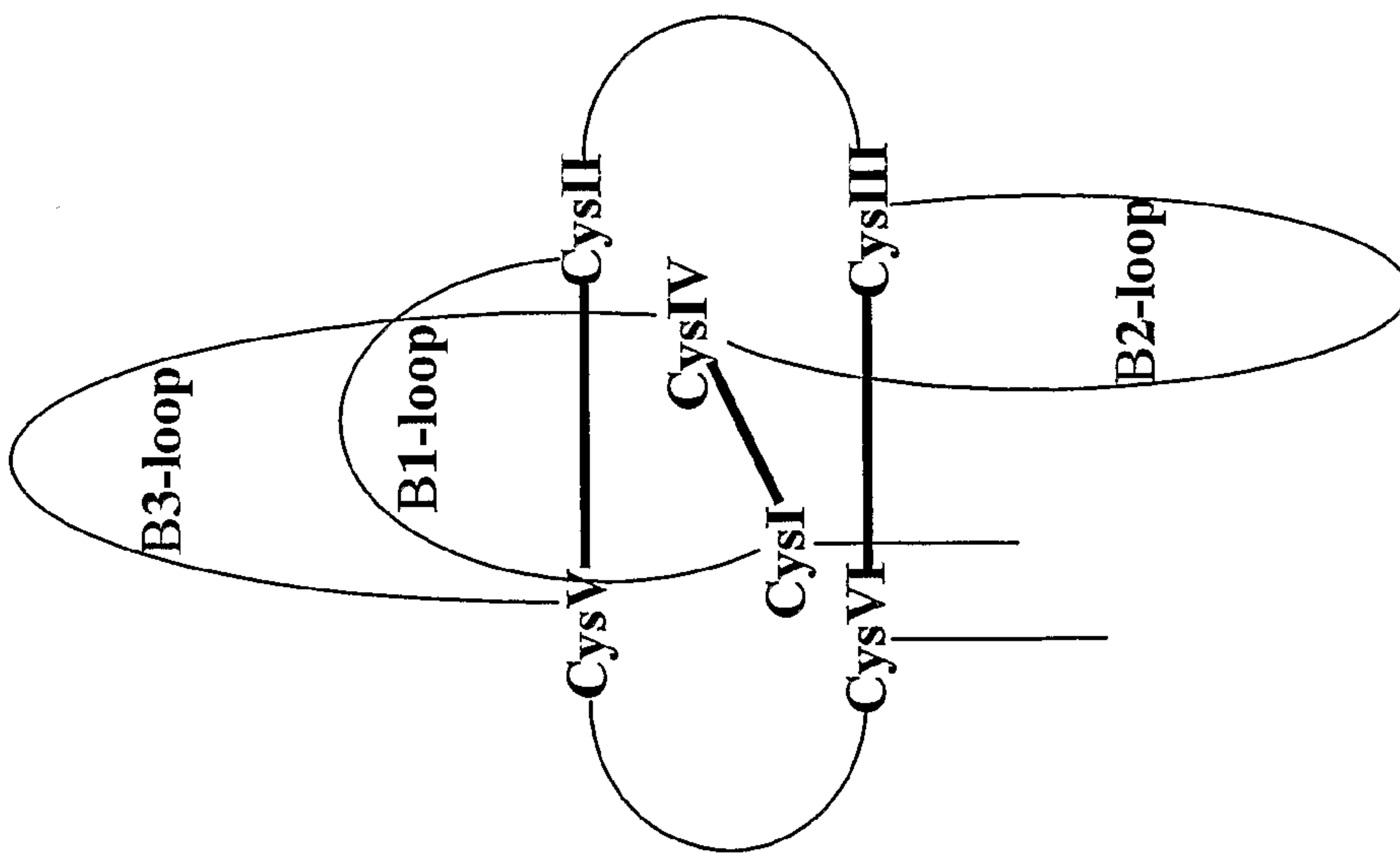


Fig. 1A

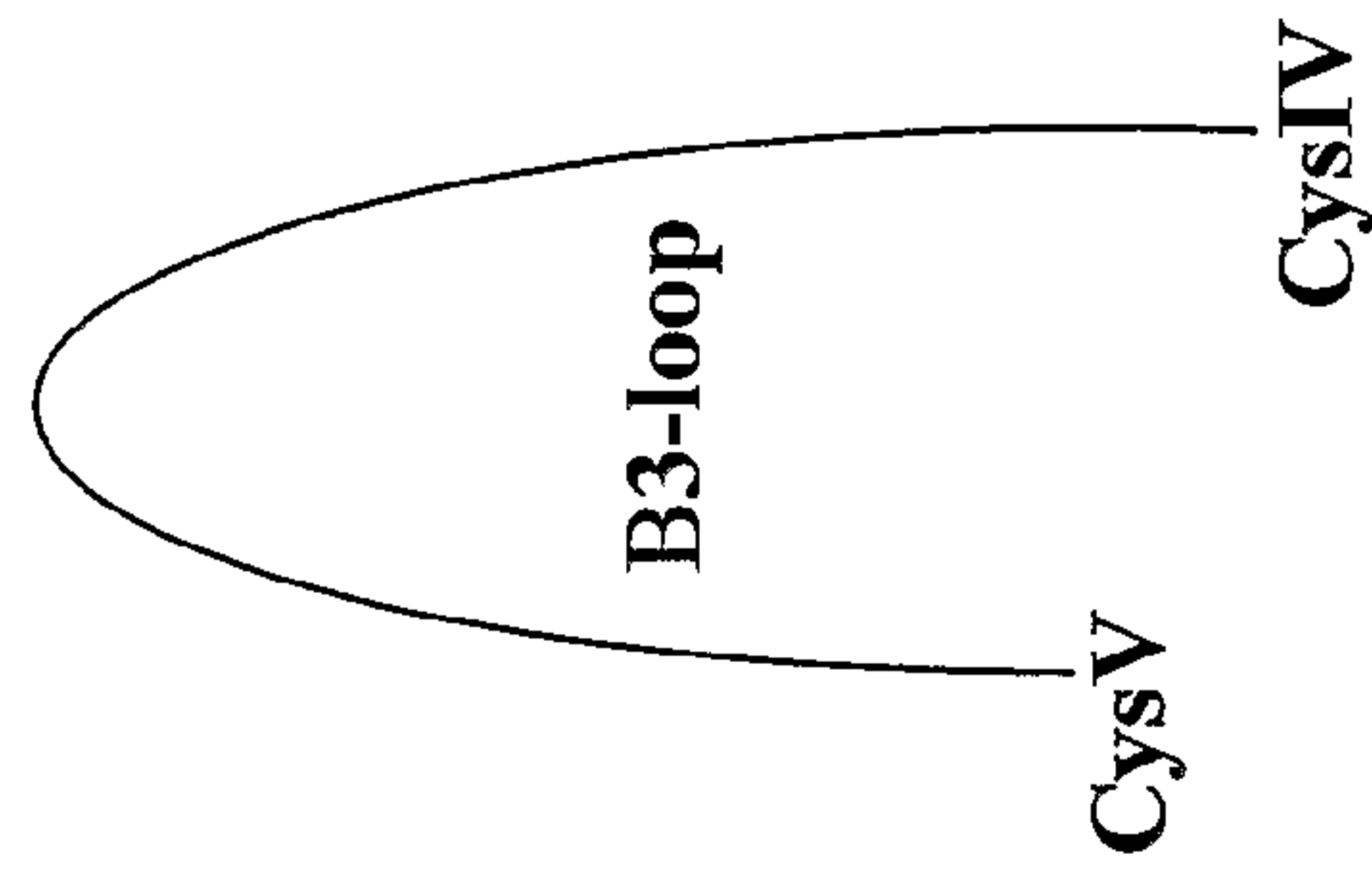


Fig. 1B

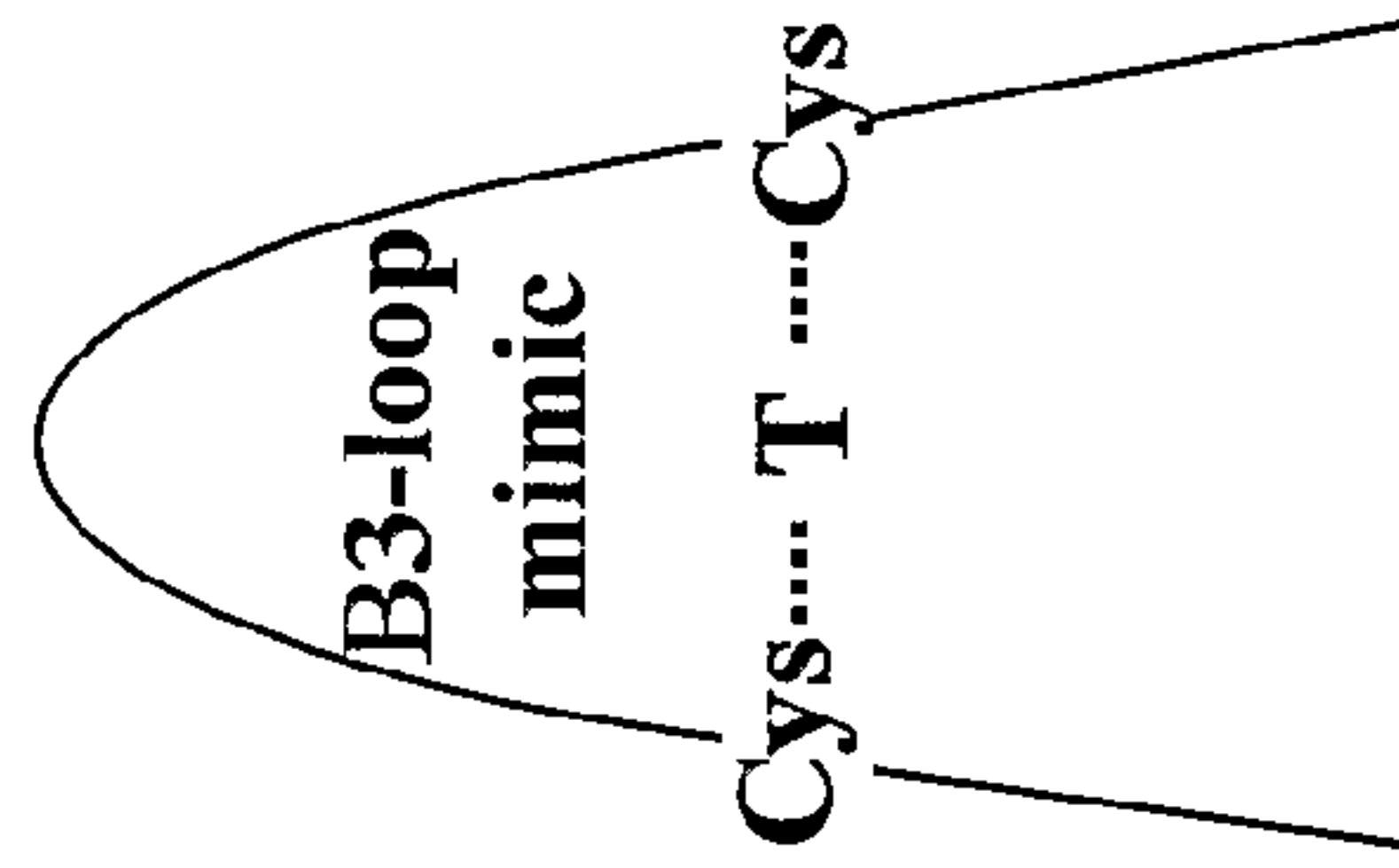


Fig. 1C

3/9

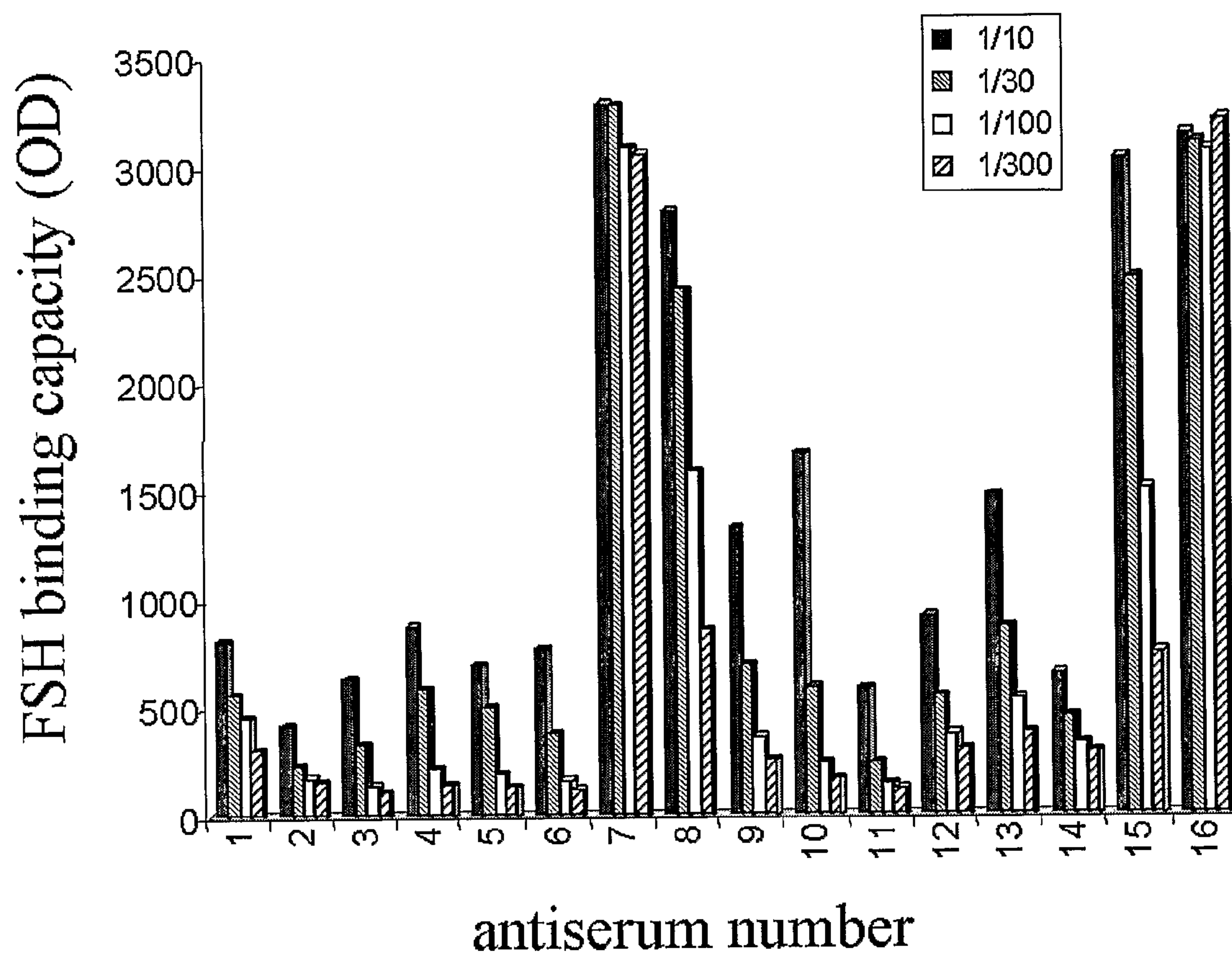


Fig. 2

4/9

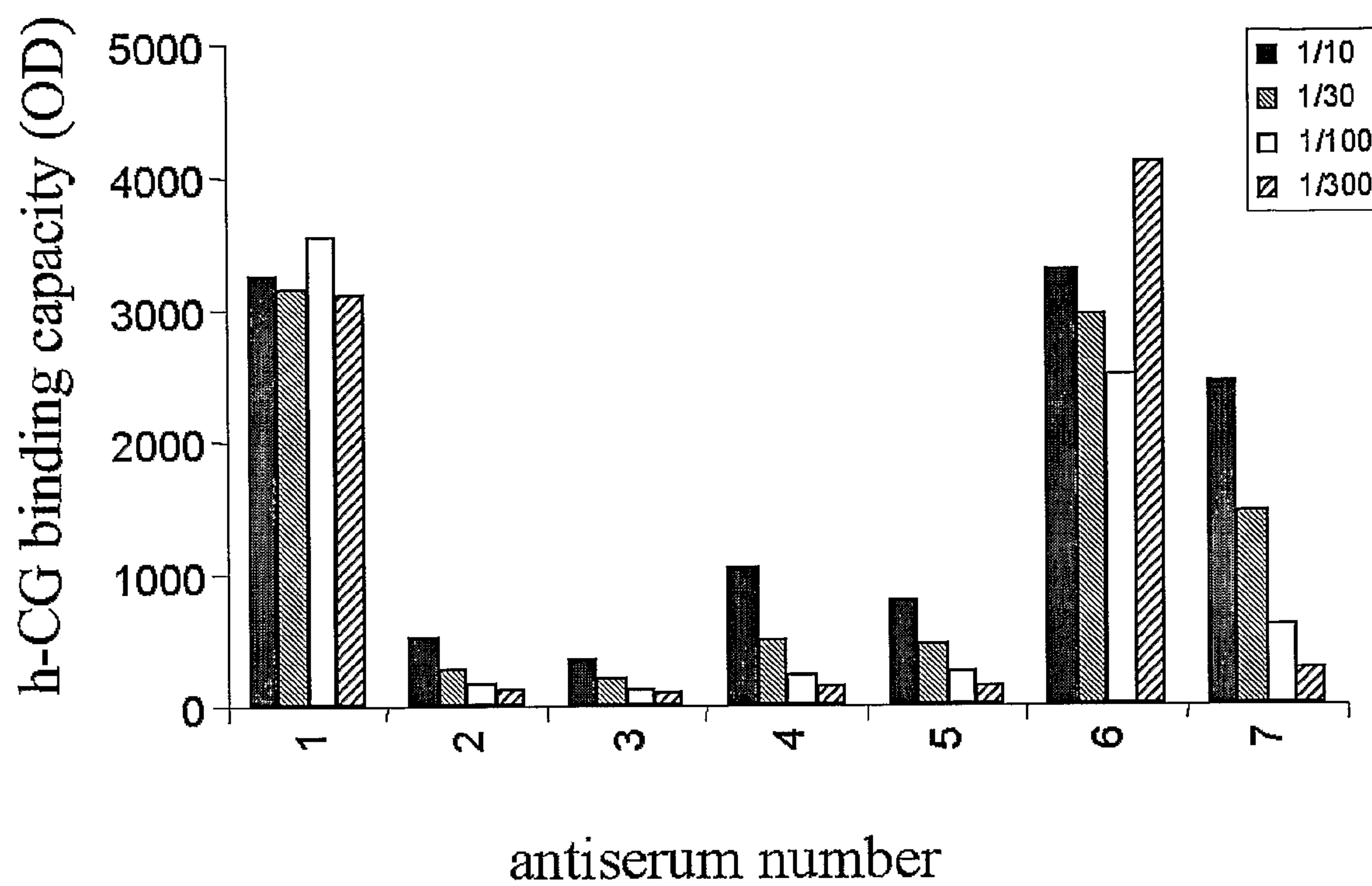
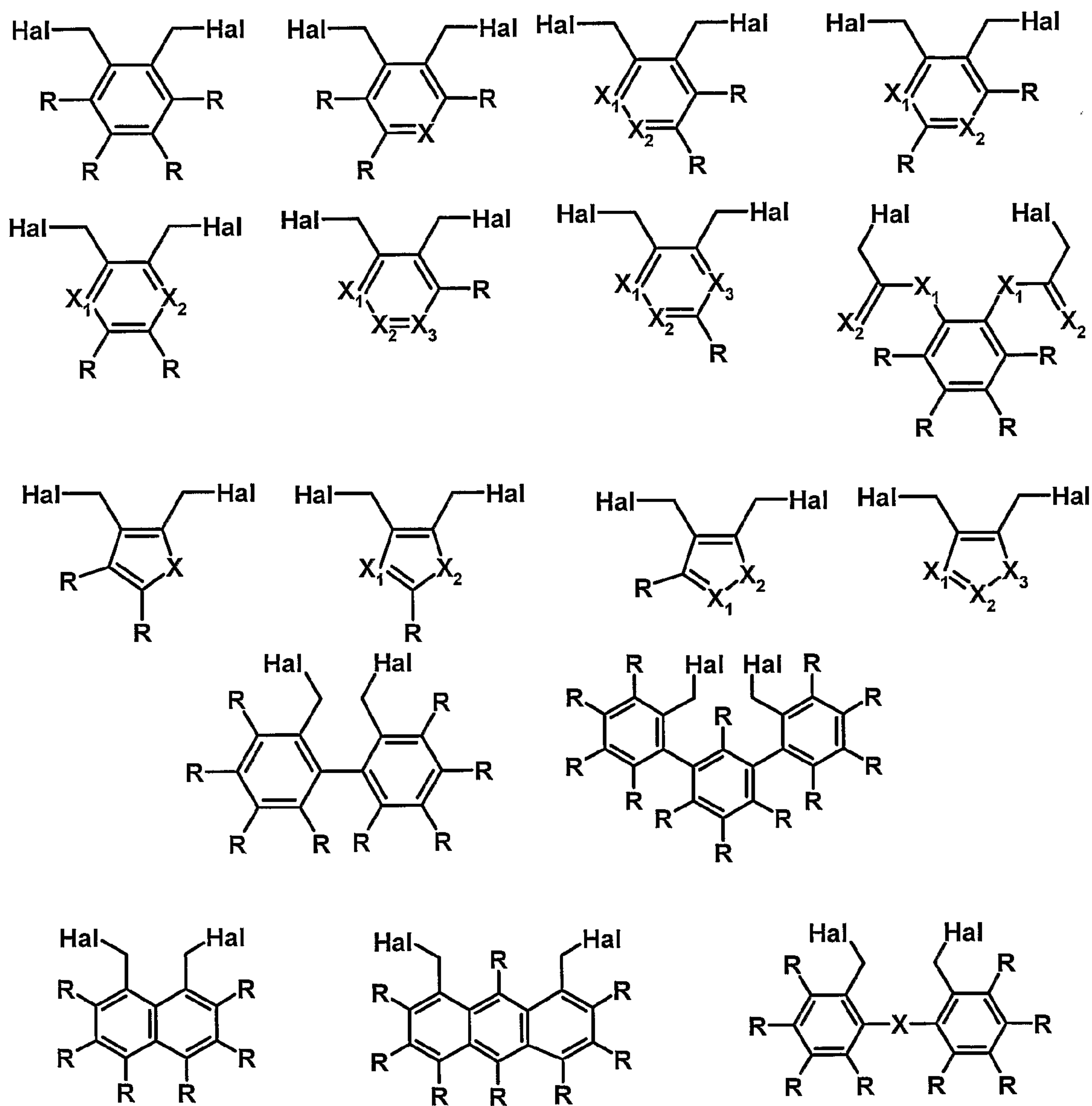


Fig. 3

5/9

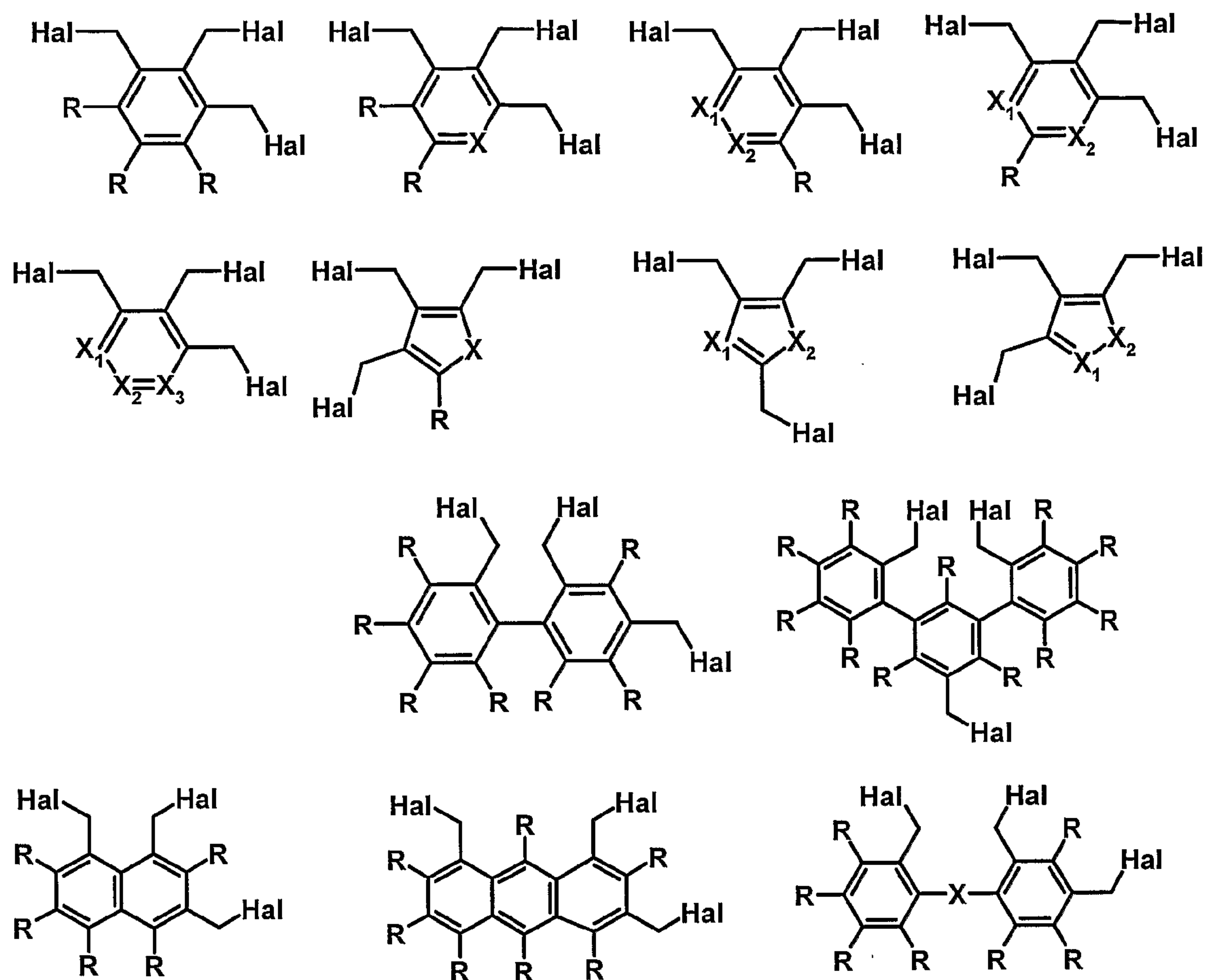


$X_{1,2,3} = \text{N(H)}, \text{O}, \text{S}$

also all other ortho, meta, and para derivatives of the compounds depicted

Fig. 4

6/9

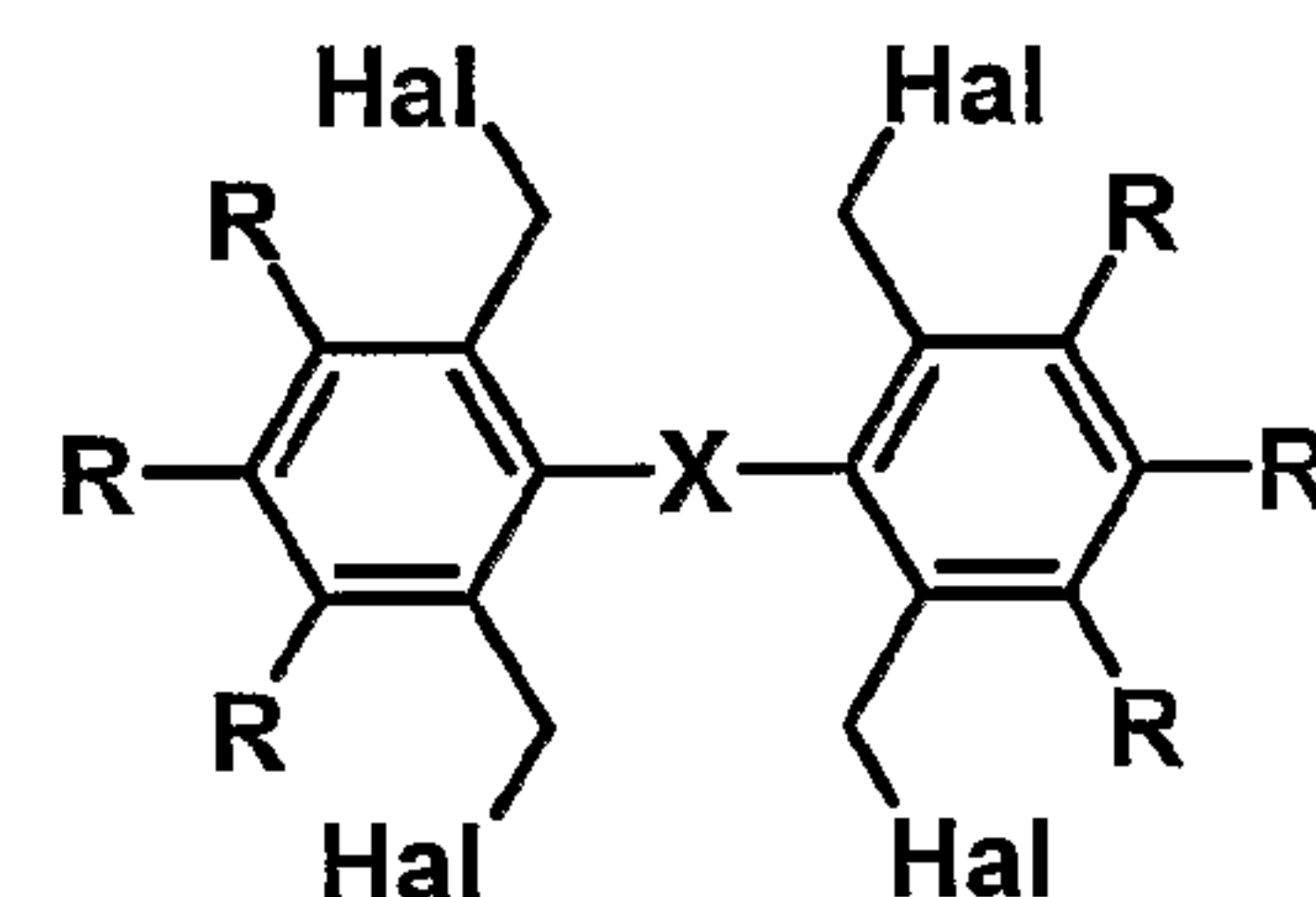
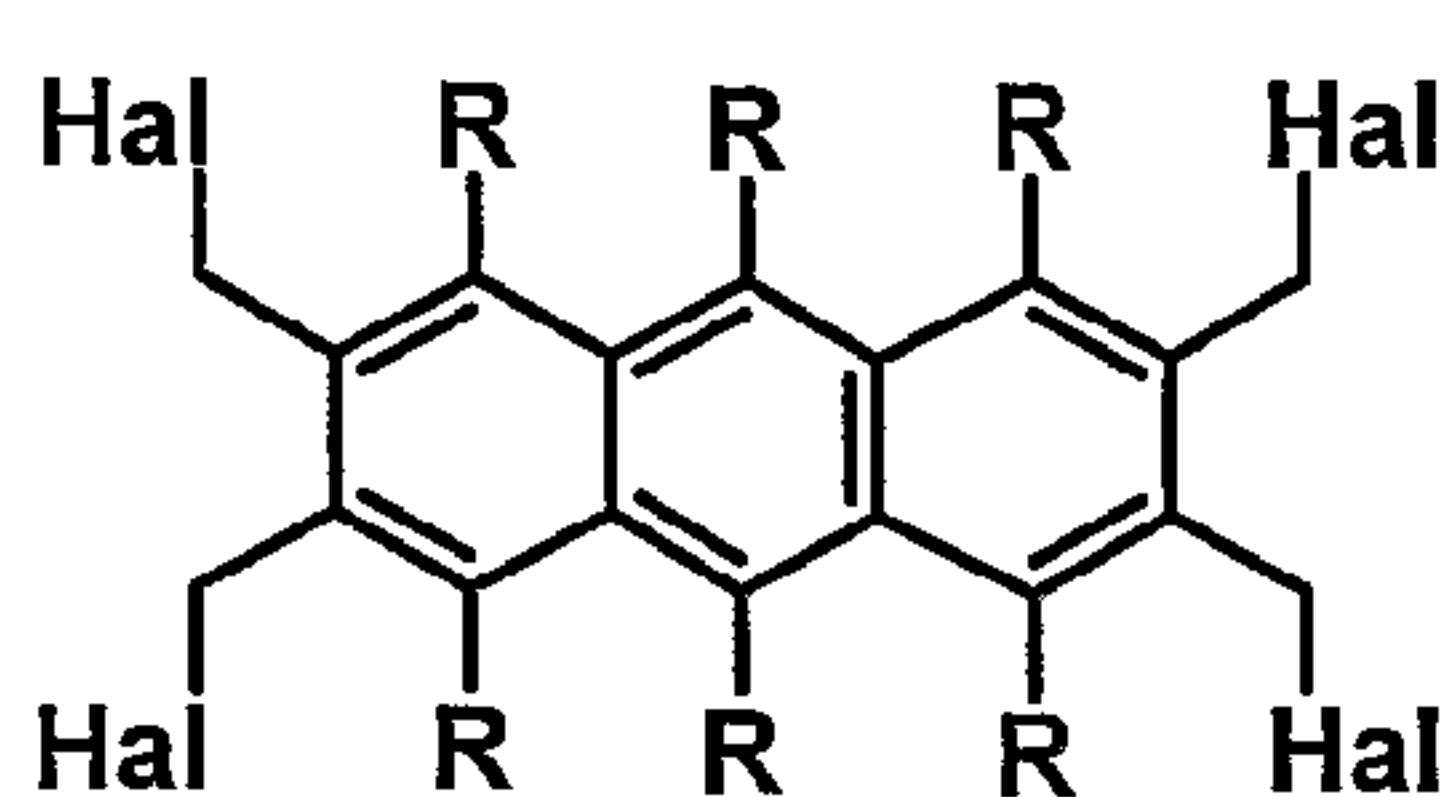
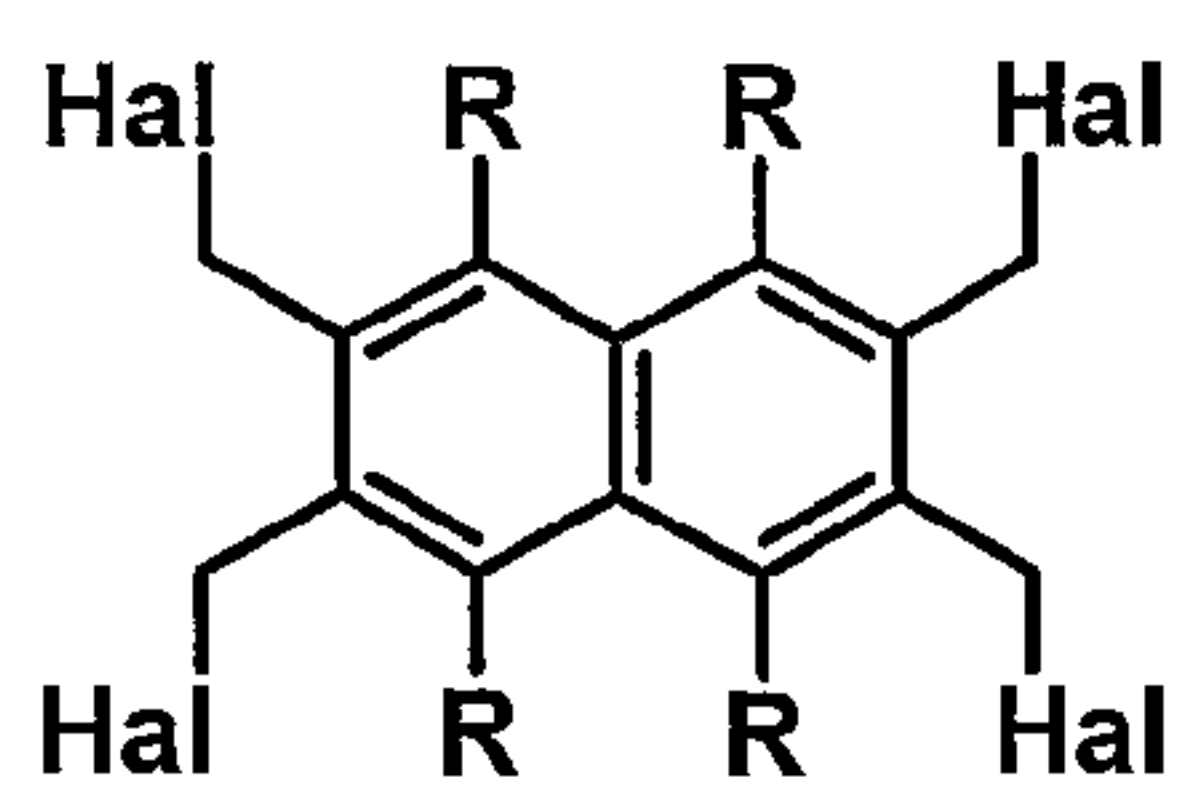
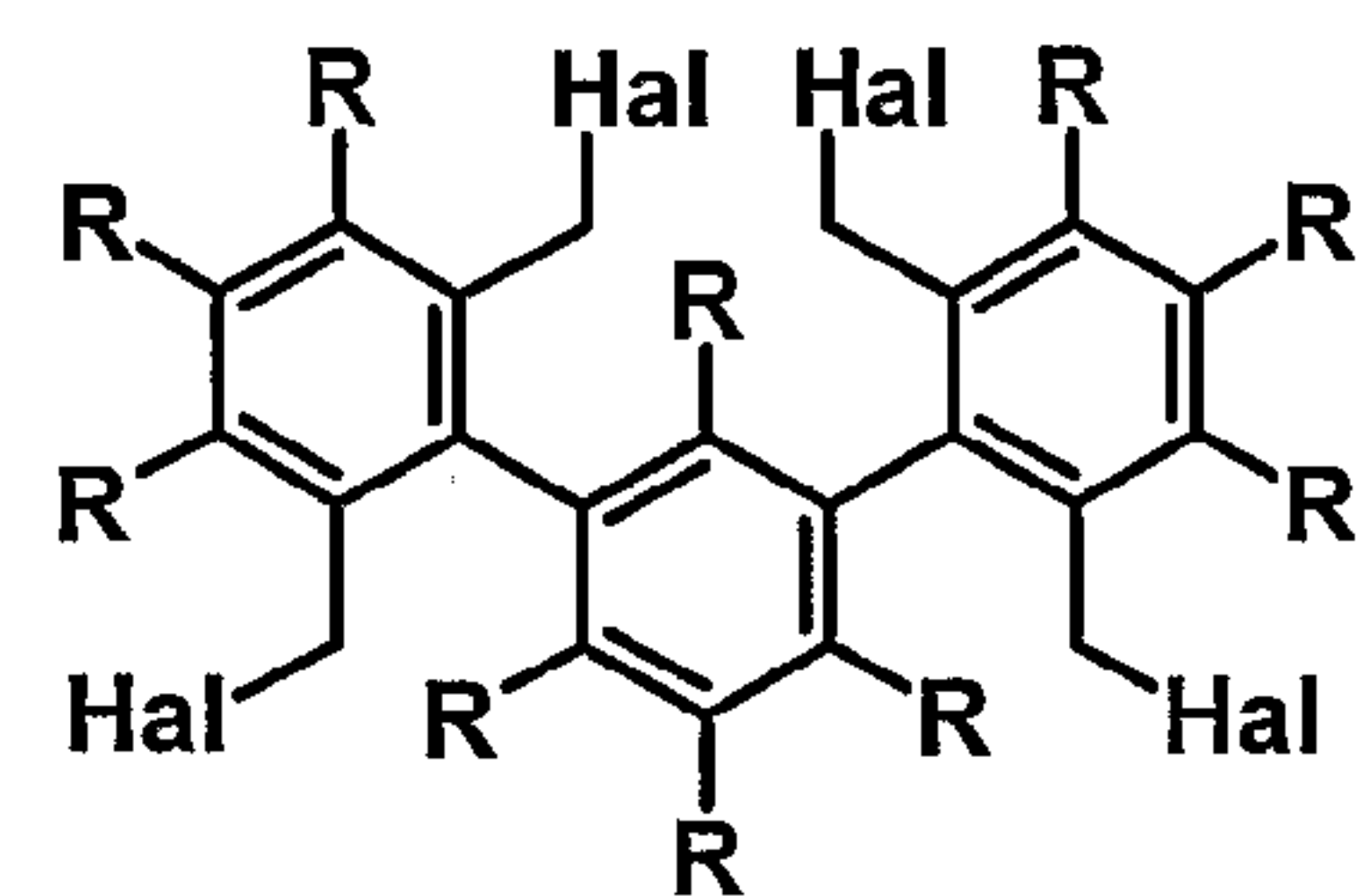
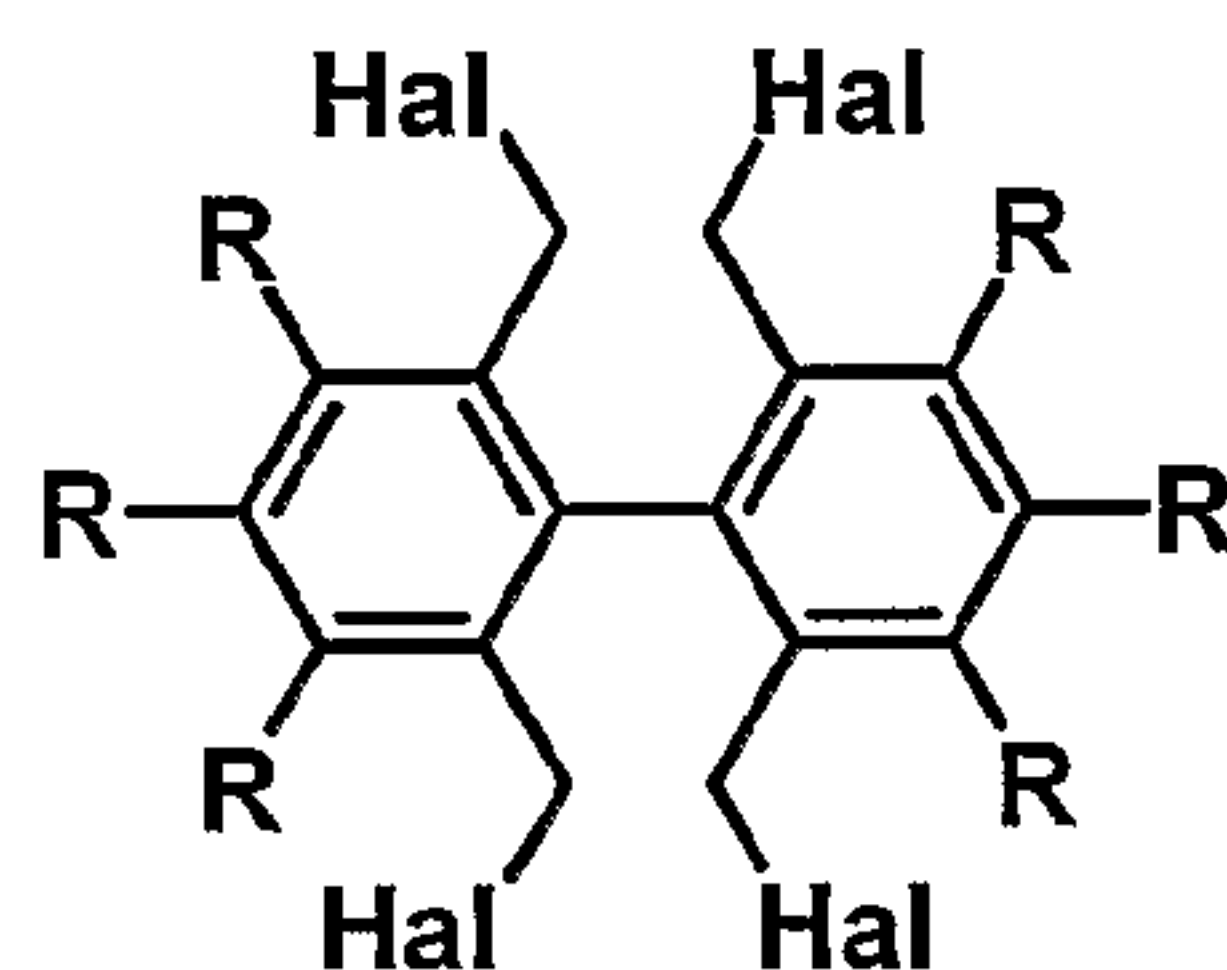
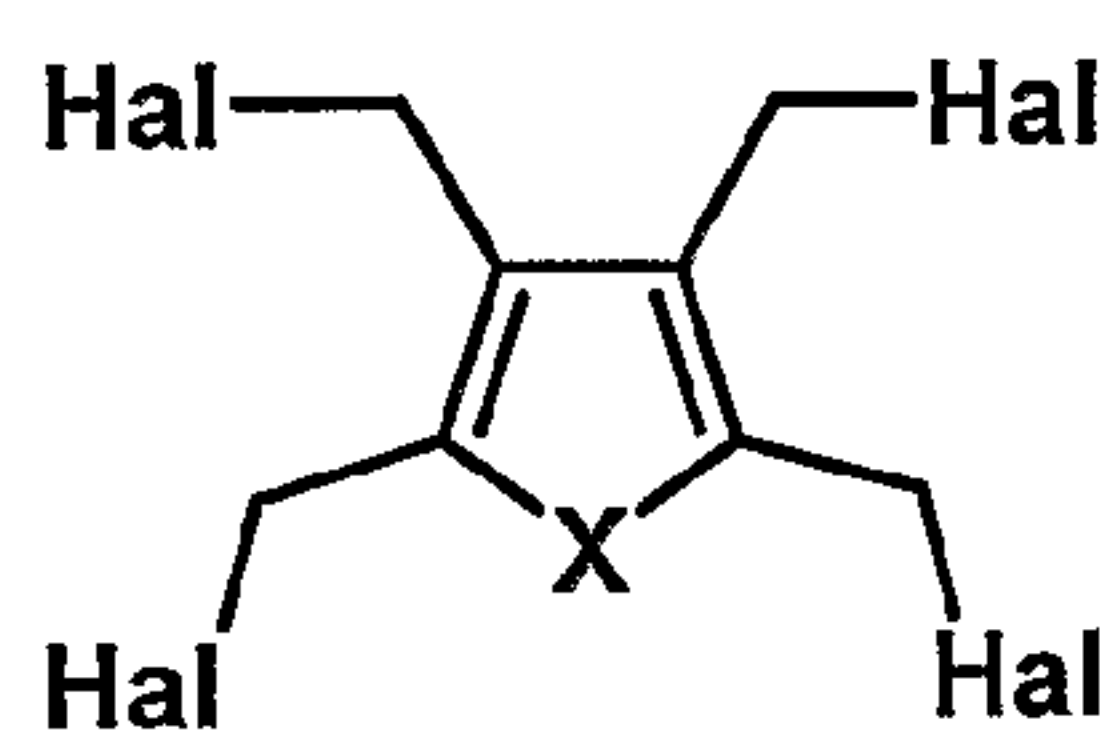
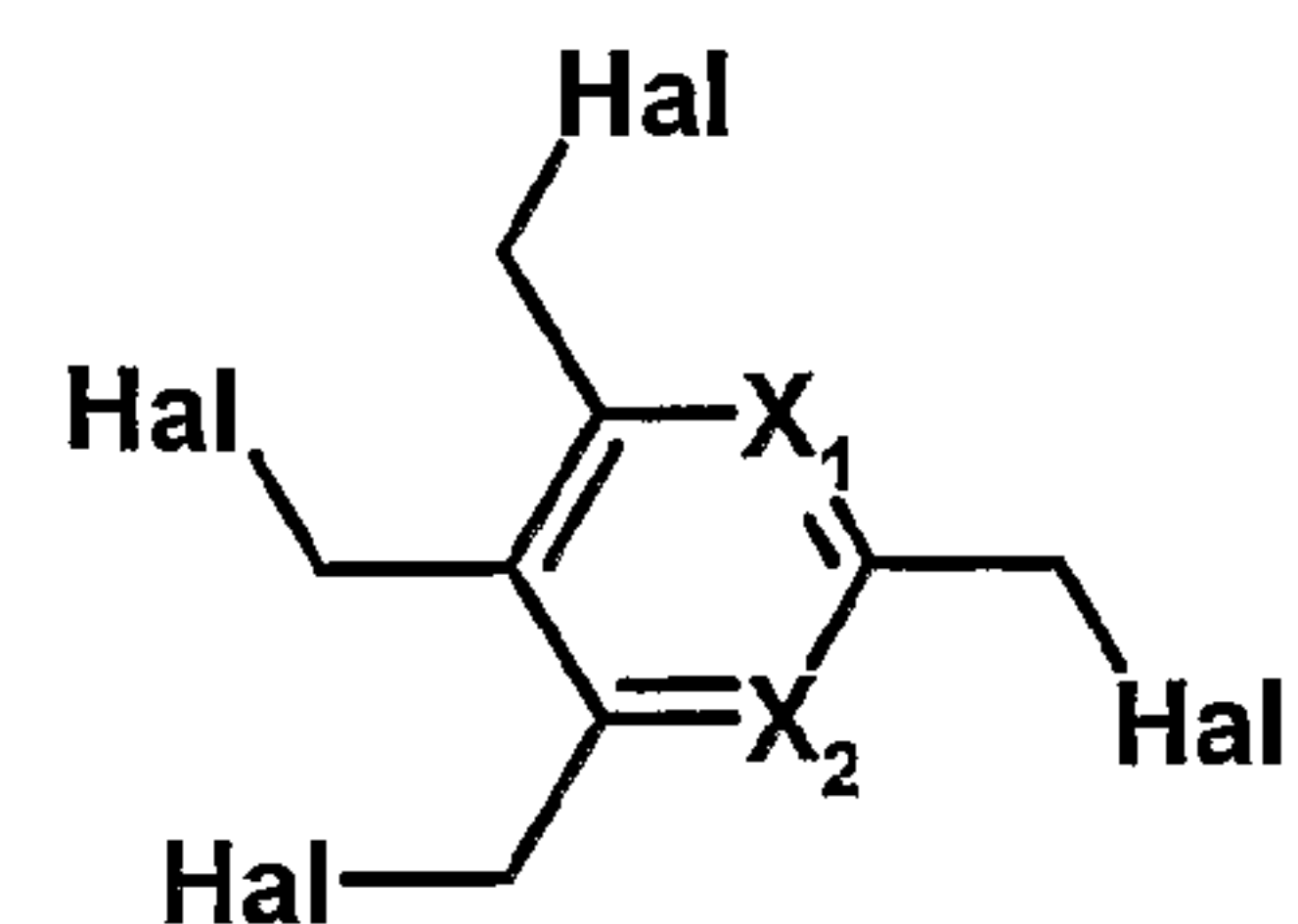
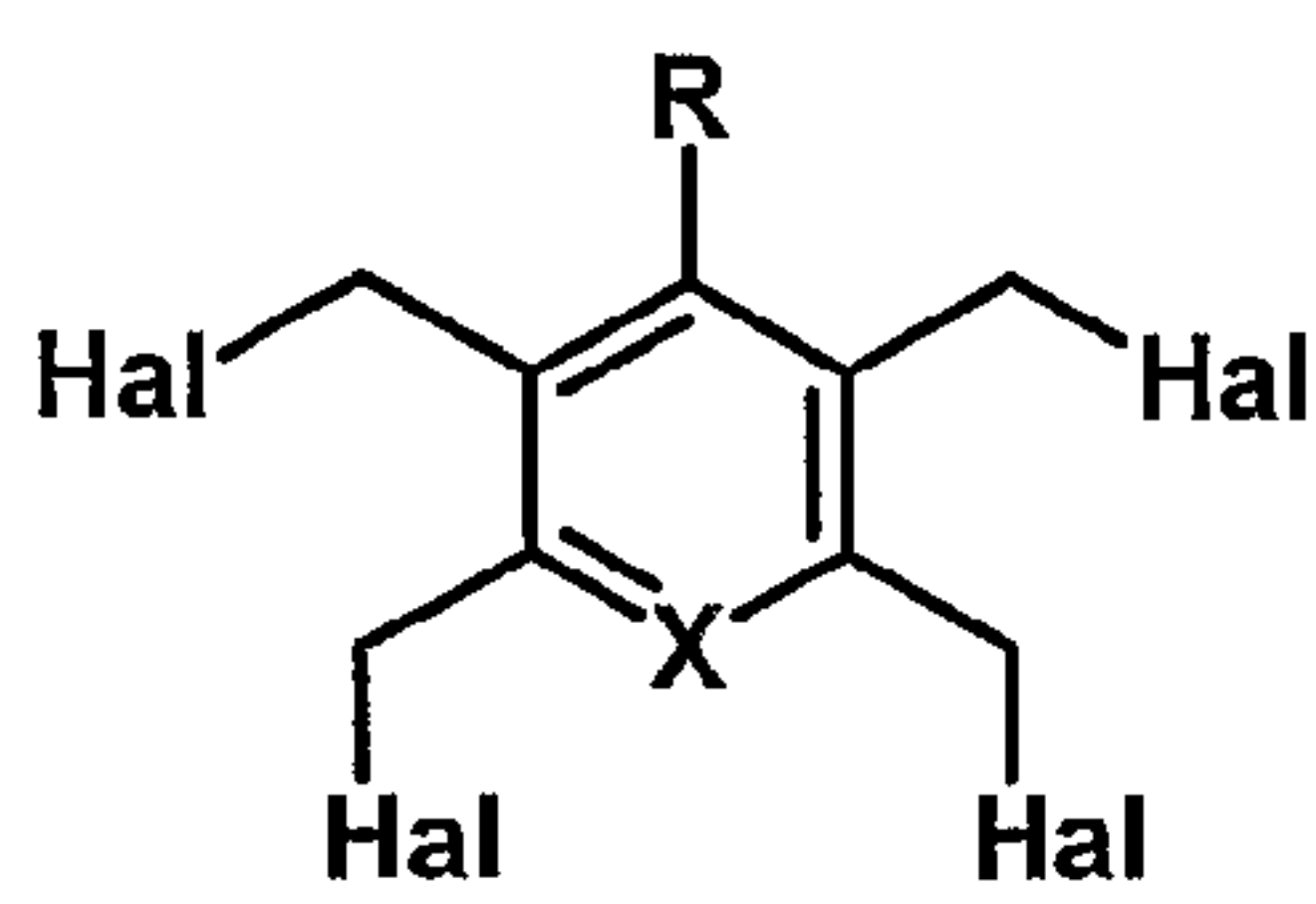
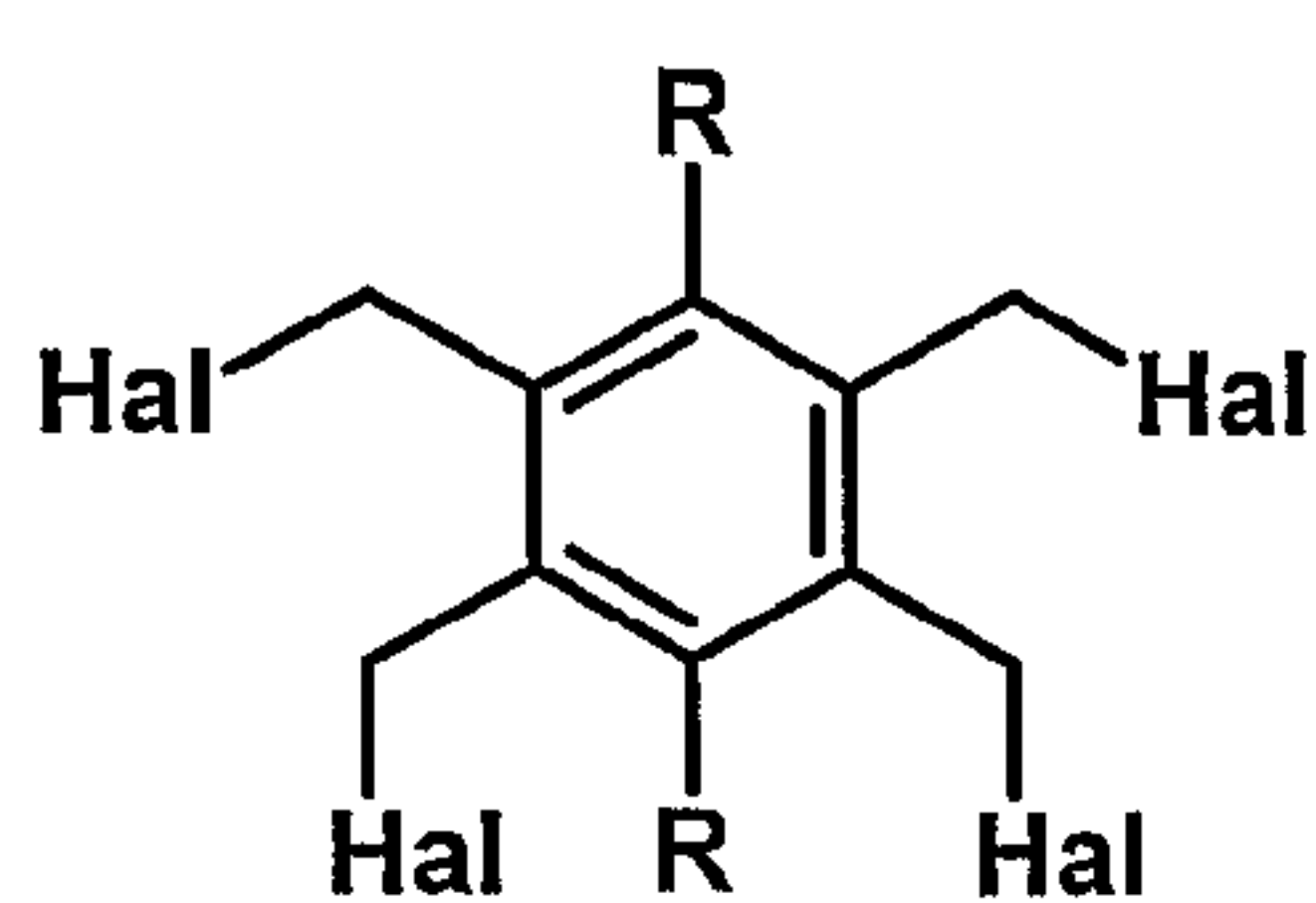


$\text{X}_{1,2,3} = \text{N(H)}, \text{O}, \text{S}$

also all other ortho, meta, and para derivatives of the compounds depicted

Fig. 5

7/9



$X_{1,2} = \text{N(H)}, \text{O}, \text{S}$

also all other possible ortho, meta, and para derivatives of the compounds depicted

Fig. 6

8/9

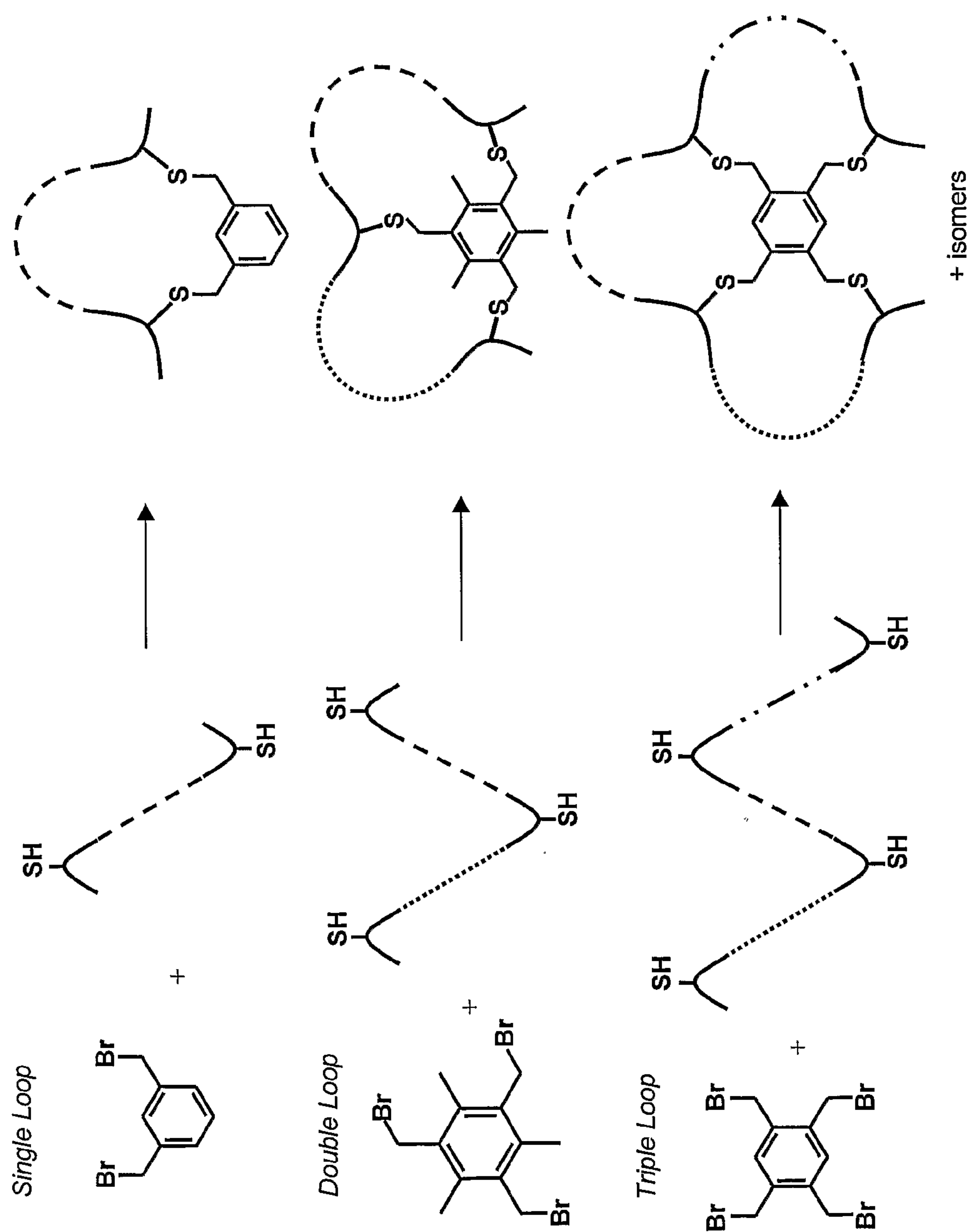


Fig. 7

9/9

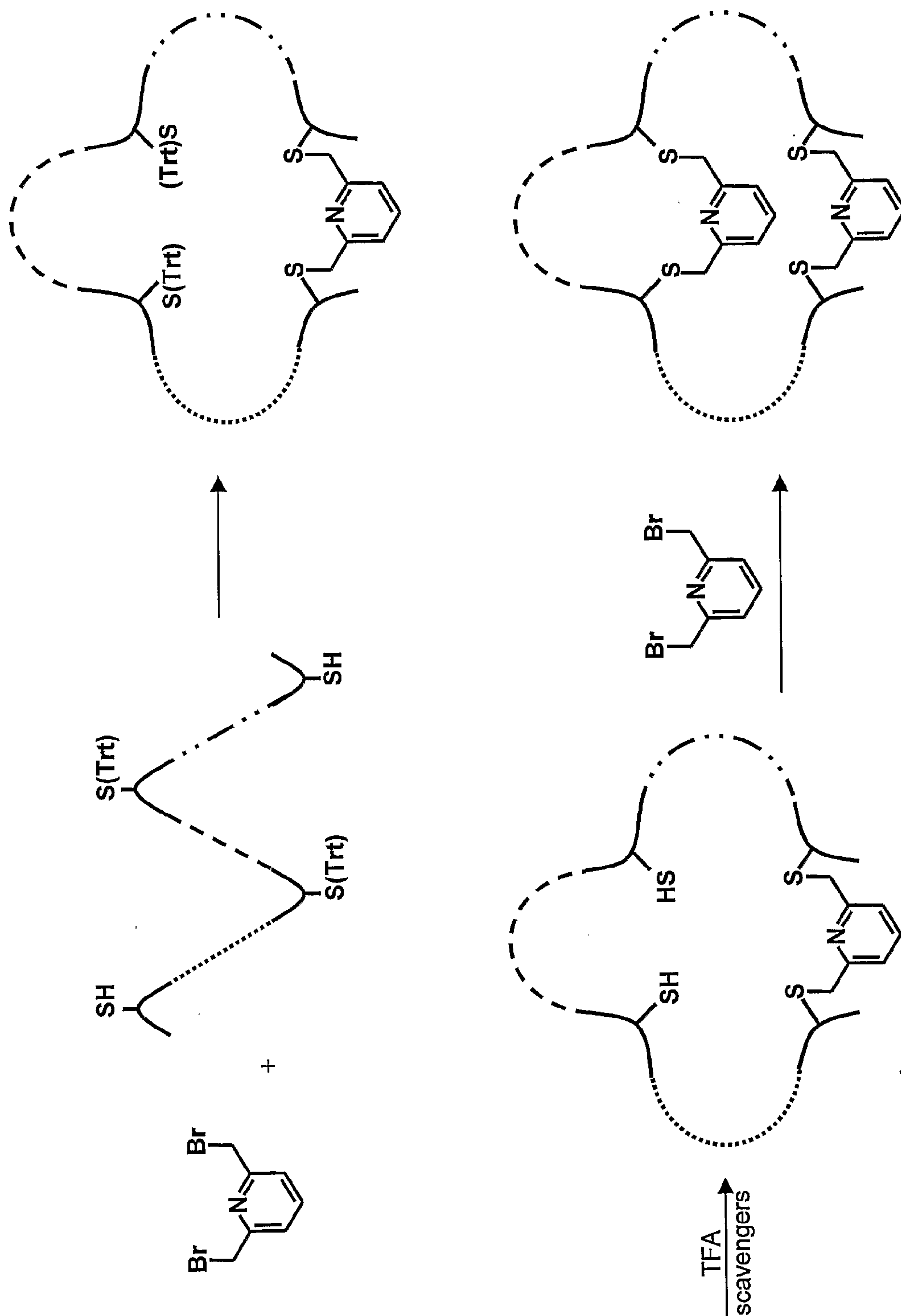


Fig. 8