



US 20110076696A1

(19) **United States**

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

(10) **Pub. No.: US 2011/0076696 A1**

(43) **Pub. Date: Mar. 31, 2011**

(54) **CARDIOVASCULAR SAFETY ASSAY**

application No. 10/483,617, filed on Jan. 13, 2004,  
now abandoned, filed as application No. PCT/EP2002/  
007364 on Jul. 2, 2002.

(75) Inventors: **GODELIEVE IRMA**  
**CHRISTINE MARIA HEYLEN,**  
**WESTMALLE (BE); CORNELUS**  
**GERARDUS MARIA JANSSEN,**  
**VOSSELAAR (BE); JURZAK**  
**MIREK, FRANKFIRT (DE);**  
**HENRICUS PETRUS**  
**MARTINUS MARIA VAN**  
**ASSOUW, JE OIRSCHOT (NL)**

(30) **Foreign Application Priority Data**

Jul. 13, 2001 (EP) ..... 01202689

**Publication Classification**

(51) **Int. Cl.**  
**G01N 33/567** (2006.01)  
**G01N 33/566** (2006.01)

(52) **U.S. Cl.** ..... **435/7.21; 436/504; 436/501**

(73) Assignee: **JANSSEN PHARMACEUTICA,**  
**N.V., BEERSE (BE)**

(57) **ABSTRACT**

(21) Appl. No.: **12/860,387**

The present invention provides assays and kits for the screening of test compounds for their capability to induce cardiotoxicity in a subject. Said assays and kits are based on the finding that the interaction of astemizole with the HERG potassium channel can be exploited to predict cardiotoxicity of compounds during the development of new therapeutics and other agents.

(22) Filed: **Aug. 20, 2010**

**Related U.S. Application Data**

(62) Division of application No. 11/593,399, filed on Nov. 6, 2006, now Pat. No. 7,820,453, which is a division of

Figure 1 A

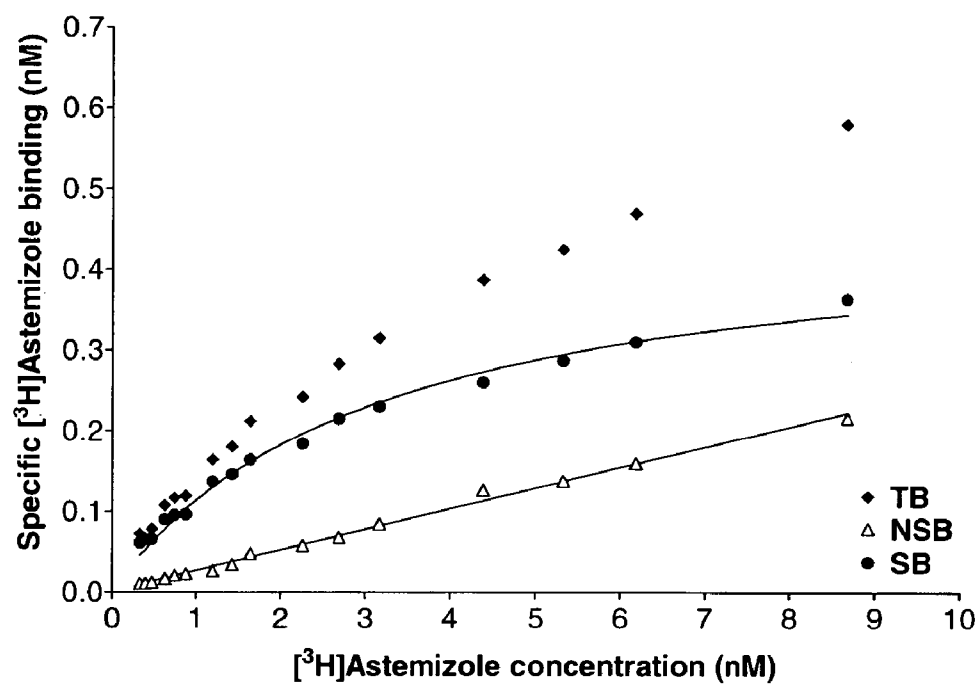


Figure 1 B

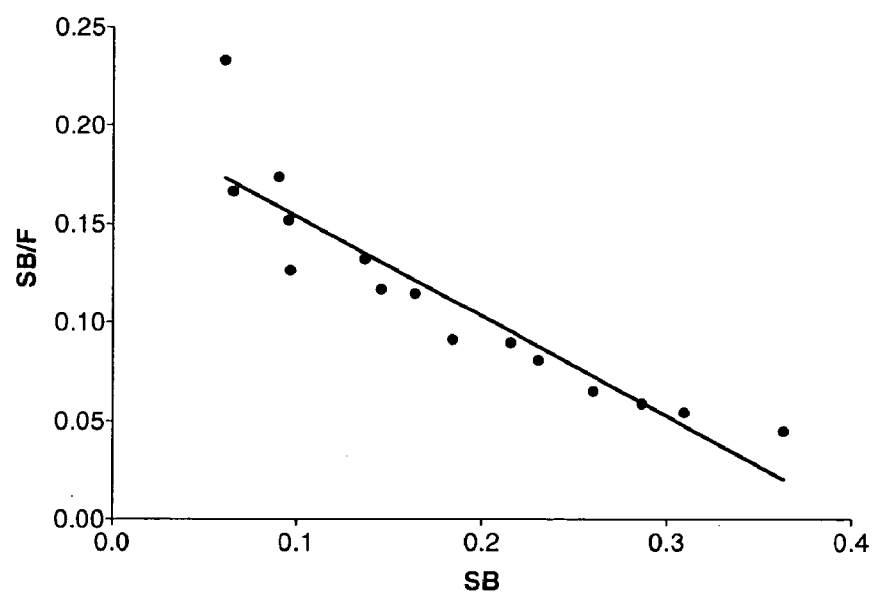
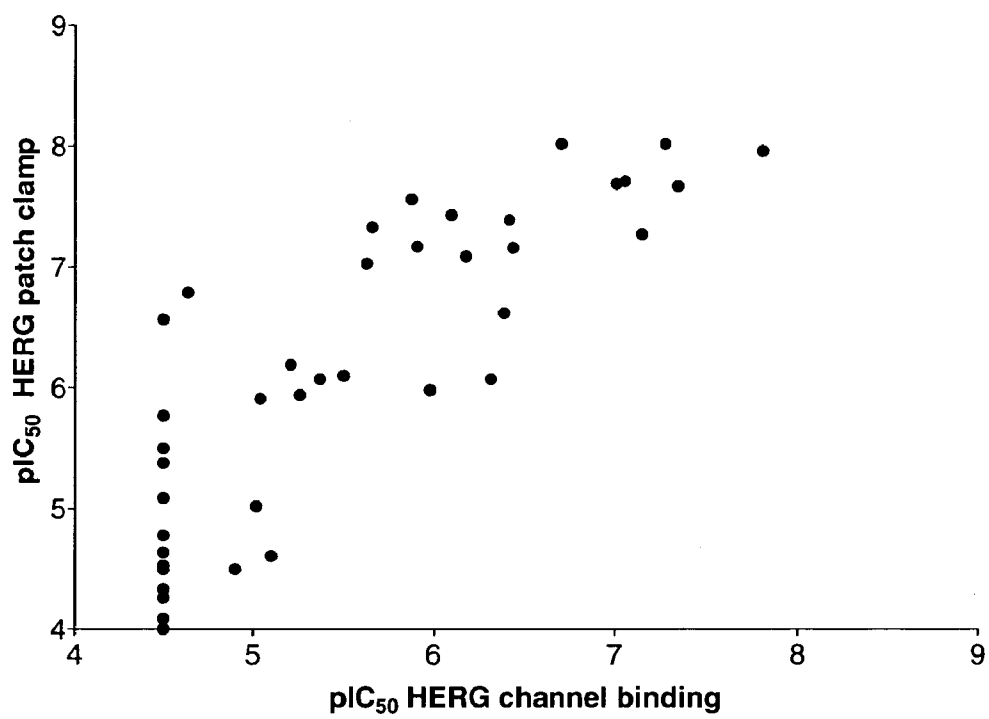


Figure 2



**CARDIOVASCULAR SAFETY ASSAY****CROSS-REFERENCE TO RELATED APPLICATIONS**

**[0001]** This application is a divisional of U.S. application Ser. No. 11/593,399, filed Nov. 6, 2006, which is a divisional of U.S. application Ser. No. 10/483,617, filed Jan. 13, 2004, now abandoned, which is a 371 of PCT/EP2002/07364, filed Jul. 2, 2002, which claims priority to European Patent Application No. 01202689, filed Jul. 13, 2001, all of which are incorporated by reference in their entirety.

**FIELD OF INVENTION**

**[0002]** The present invention relates to the field of cardiovascular safety assays and provides assays and kits for the screening of test compounds for their capability to induce cardiotoxicity in a subject. Said assays and kits are based on the finding that the interaction of astemizole with the HERG potassium channel can be exploited to predict potential cardiotoxicity of compounds during the development of new therapeutics and other agents. The present invention finds particularly advantageous use in high throughput screening of chemical compound libraries.

**BACKGROUND OF THE INVENTION**

**[0003]** Evidence has accrued that several drugs may prolong cardiac repolarisation (hence, "measured as" the QT interval of the surface electrocardiogram) to such a degree that potentially life-threatening ventricular arrhythmias e.g. torsades de pointes (TdP) may occur, especially in case of overdosage or pharmacokinetic interaction.

**[0004]** The number of drugs reported to induce QT interval prolongation with or without TdP continues to increase (W. Haverkamp et al. (2000) Cardiovascular Research 47, 219-233). As many as 50 clinically available or still investigational non-cardiovascular drugs and cardiovascular non-anti-arrhythmic drugs have been implicated. A number of drugs, both old and new, have either been withdrawn from the market or have had their sale restricted. Of concern is the interval, usually measured in years, from the marketing of these drugs to initial recognition of their association with QT interval prolongation and/or TdP. It would therefore be beneficial to investigate any new chemical entity for this potential side effect before its first use in man at an early stage of the development of new therapeutics and/or other agents.

**[0005]** A key component in the present development of new therapeutic agents consists of High Throughput Screening (HTS) of chemical compound libraries. Pharmaceutical companies have established large collections of structurally distinct compounds, which act as the starting point for drug target lead identification programs. A typical corporate compound collection now comprises between 100,000 and 1,000,000 discrete chemical entities. While a few years ago a throughput of a few thousand compounds a day and per assay was considered to be sufficient, pharmaceutical companies nowadays aim at ultra high throughput screening techniques with several hundreds of thousands of compounds tested per week. In a typical HTS related screen format, assays are performed in multi-well microplates, such as 96, 384 or 1536 well plates. The use of these plates facilitates automation such as the use of automated reagent dispensers and robotic pipetting instrumentation. Further, to reduce the cycle time, the costs and the resources for biochemicals such as recombinant proteins, HTS related screens are preferably performed at room temperature with a single measurement for each of the compounds tested in the assay.

**[0006]** A decisive criterion in the lead evaluation process will be an early recognition of their potential association with QT prolongation and/or TdP. However, there are currently no reliable, fast, easy screening methods available to assess cardiotoxicity, which can cope with the number of compounds identified in the currently deployed HTS techniques. It is an object of this invention to solve this problem in the art by providing assays and kits which are based on the finding that the interaction of astemizole with the HERG potassium channel can be exploited to predict cardiotoxicity of compounds during the development of new therapeutics and other agents.

**[0007]** The currently available in vitro models comprise heterologous expression systems, disaggregated cells, isolated tissues and the isolated intact (Langendorf-perfused) heart. In all models the effect of potassium current blockade is assessed by measurement of either ionic currents using two-electrode voltage clamp recordings (Dascal N. (1987) Crit. Rev. Biochem 22, 341-356) or patch-clamp recordings (Zhou Z. et al., (1998) Biophysical Journal 74, 230-241), of membrane potentials using microelectrodes or confocal microscopy (Dall'Asta V. et al. (1997) Exp. Cell Research 231, 260-268). None of the aforementioned methods can be used in an HTS screen in view of the complexity of the experimental procedures, the slow cycling times, the nature of the source materials (i.e. isolated tissues and disaggregated cells thereof) and the reliability of the test results.

**[0008]** The present inventors surprisingly found that a binding assay using labeled astemizole as a specific ligand for the HERG channel can be used to predict the potential association of compounds with QT prolongation and/or TdP. This binding assay solves the aforementioned problems and can be deployed in an HTS related screen format.

**[0009]** A similar assay has been described by Chadwick C. et al. (Chadwick C. et al., (1993) Circulation Research 72, 707-714) wherein [<sup>3</sup>H]-dofetilide has been identified as a specific radioligand for the cardiac delayed rectifier K<sup>+</sup> channel. This article further demonstrates a good correlation between dofetilide displacement and potassium channel blocking activity of a number of antiarrhythmic compounds. This binding assay facilitates the characterization of drug-channel interactions at the molecular level.

**[0010]** In this assay labeled dofetilide has been prepared from the dibromo precursor by <sup>3</sup>H-exchange yielding the incorporation of two <sup>3</sup>H-labels per molecule. There is a direct correlation between the number of <sup>3</sup>H-labels per molecule and the sensitivity of the binding assay. The present invention provides an improved binding assay over the above, as the use of a desmethylastemizole precursor in a reaction with [<sup>3</sup>H]-methyl iodide resulted in the incorporation of three <sup>3</sup>H-labels per molecule astemizole. The specific activity of the thus obtained radioligand is 1.5-2 times higher than the specific activity of [<sup>3</sup>H]-dofetilide.

**[0011]** Further, the dofetilide assay could not be used in an HTS related screen format since the ventricular myocytes isolated from adult male guinea pigs had to be used within 6 hours of isolation. In addition only 36% of the isolated cells were viable and could be used in the binding assay. In order to be used in an HTS related screen, the starting material should be readily available and in sufficient amounts. The present invention solves this problem as membrane preparations of HEK293 cells, stably expressing the HERG potassium channel, are used. Said cells can be maintained in culture in sufficient amount avoiding the need and supply of animal models and as cell membranes are used in the binding assay, the latter can be stored in binding assay ready aliquots at -80° C. for later use. A further drawback of the dofetilide binding assay described by Chadwick et al. has to do with the incubation

protocol. As viable myocytes are used, the incubation has to be performed at the physiological temperature of 34° C. The latter undoubtedly increases the costs, possible cycle time and complexity of the assay if to be performed in an HTS related screen format. The present invention solves this problem as it was surprisingly demonstrated that the membrane preparations could be incubated at room temperature. Especially in light of a study by Zhou Z. et al. Zhou Z. et al., (1998) Biophysical Journal 74, 230-241) which concluded that the kinetic properties measured for HERG are markedly dependent on temperature and that differences observed in several reports, are diminished when studies are performed at physiological temperatures, i.e. 35° C.

[0012] This and other aspects of the invention will be described herein below.

#### SUMMARY OF THE INVENTION

[0013] The present invention provides an assay for screening test compounds for their capability to induce cardiotoxicity in a subject, the method comprising incubating a source containing HERG or a fragment thereof with a reference compound and the test compound, for a time sufficient to allow binding of the reference compound and of the test compound with the HERG polypeptide channel and measuring the effect of the test compound on the amount of reference compound bound to HERG.

[0014] In a preferred embodiment of this invention, the assay consists of incubating membrane preparations of cells, preferably HEK293 cells, expressing on the surface thereof the HERG polypeptide channel comprising the amino acid sequence of SEQ ID NO:2 or a fragment thereof; with a labeled reference compound. Wherein said labeled reference compound is a drug capable to induce cardiac arrhythmia in a subject, preferably said labeled reference compound is [<sup>3</sup>H]-astemizole. Incubating the above together with the test compound and measure the effect of the test compound on the amount of reference compound bound to the HERG polypeptide channel. In a further embodiment the means of measurement consist of separating means to remove the excess of unbound labeled reference compound from the incubation mixture and of means for detection of the labeled reference compound wherein the latter preferably consists of radiolabeled measurement using scintillation counting.

[0015] The invention further provides a high-throughput assay for screening compounds for their capability to induce cardiotoxicity in a subject, the assay comprising:

[0016] a) contacting membrane preparations of cells expressing on the surface thereof HERG polypeptide channels having an amino acid sequence that is at least 80% identical to that of SEQ ID NO:2 or fragments thereof, with a labeled reference compound for a time sufficient to allow binding of the reference compound with the HERG polypeptide channel;

[0017] b) contacting membrane preparations of cells expressing on the surface thereof HERG polypeptide channels having an amino acid sequence that is at least 80% identical to that of SEQ ID NO:2 or fragments thereof, with the labeled reference compound of step a) together with the test compound for a time sufficient to allow binding of the reference compound and of the test compound with the HERG polypeptide channel;

[0018] c) measuring the amount of labeled reference compound bound to the HERG channel in step a);

[0019] d) measuring the amount of labeled reference compound bound to the HERG channel in step b); and

[0020] e) compare the amount of labeled reference compound bound to the HERG channel measured in step a) with the amount of labeled reference compound bound to the HERG polypeptide channel measured in step b).

In a preferred embodiment of the high-throughput screening assay, the membrane preparations are derived from cells, preferably HEK293 cells, expressing on the surface thereof HERG polypeptide channels encoded by the amino acid sequence consisting of SEQ ID NO:2. In a further embodiment of the high-throughput screening assay the labeled reference compound is astemizole, preferably [<sup>3</sup>H]-astemizole.

[0021] The present invention also encompasses kits for screening compounds for their capability to induce cardiotoxicity in a subject as well as the use of reagents, including polynucleotides, polypeptides and suitable reference compounds in the assays of the present invention.

#### BRIEF DESCRIPTION OF THE DRAWING

[0022] FIG. 1A shows the saturation binding of [<sup>3</sup>H]-astemizole to cell membrane preparations of HEK293 cells stably transfected with the HERG channel cDNA. TB represents Total Binding measured, NSB represents Non Specific Binding measured and SB represents Specific Binding measured.

[0023] FIG. 1B shows the Scatchard plot for the saturation binding experiments. From the fitted line a  $K_D$  of  $3.07 \pm 2.26$  nM (n=11) could be determined with a  $B_{max}$  (Maximal Binding) of  $3260 \pm 900$  fmol/mg protein (n=11).

[0024] FIG. 2 shows the binding affinities of 42 reference compounds compared to the electrophysiological patch clamp data. A Spearman rank correlation coefficient of 0.87 could be obtained.

#### DETAILED DESCRIPTION

[0025] The present invention relates to the field of cardiovascular safety assays and provides assays and kits for the screening of test compounds for their capability to induce cardiotoxicity in a subject. Said assays and kits are based on the finding that the interaction of astemizole with the HERG potassium channel can be exploited to predict cardiotoxicity of compounds during the development of new therapeutics and other agents. The present invention finds particularly advantageous use in high throughput screening of chemical compound libraries.

[0026] In one embodiment of the present invention, the assay for screening test compounds comprises: a) incubating a source containing HERG or a fragment thereof with i) a reference compound, ii) the test compound; and b) measuring the effect of the test compound on the amount of reference compound bound to HERG.

[0027] In a specific embodiment of the present invention the assays are used to assess the capability of the test compounds to induce cardiac arrhythmia in a subject.

[0028] As used herein the term "test compound" refers to a chemically defined molecule whose cardiac arrhythmia inducing capability is assessed in an assay according to the invention. Test compounds include, but are not limited to, drugs, ligands (natural or synthetic), polypeptides, peptides, peptide mimics, polysaccharides, saccharides, glycoproteins, nucleic acids, polynucleotides and small organic molecules. In one embodiment test compounds comprise an existing library of compounds. In another embodiment, test compounds comprise a novel library of compounds.

[0029] As used herein the term "reference compound" refers to a drug capable to induce cardiotoxicity in a subject.

Reference compounds include, but are not limited to, astemizole, terfenadine, erythromycin, sparfloxacin, probucol, terodiline and sertindole.

**[0030]** As used herein the term “HERG” refers to the Human Ether-a-go-go-Related Gene channel. It is a delayed rectifier potassium channel that plays a role in the control of action potential repolarization in many cell types. HERG was originally cloned from human hippocampus and it is strongly expressed in the heart. The HERG polypeptides according to the invention include isolated and purified proteins having an amino acid sequence that is at least 80% identical to that of SEQ ID NO:2 or a fragment thereof. In a further embodiment the HERG polypeptide channel according to the invention has an amino acid sequence comprising the amino acid sequence of SEQ ID NO:2. In a preferred embodiment the HERG polypeptide according to the invention consists of SEQ ID NO:2.

**[0031]** Variants of the defined sequence and fragments also form part of the invention. Variants include those that vary from the parent sequence by conservative amino acid changes, wherein “conservative amino acid changes” refers to the replacement of one or more amino acid residue(s) in the parent sequence without affecting the biological activity of the parent molecule based on the art recognized substitutability of certain amino acids (See e.g. M. Dayhoff, *In Atlas of Protein Sequence and Structure*, Vol. 5, Supp. 3, pgs 345-352, 1987). Further variants are variants in which several, 5-10, 1-5, or 1-2 amino acids are substituted, deleted or added in any combination.

**[0032]** Methods for comparing the identity and similarity of two or more sequences are well known in the art. Thus for instance, programs available in the Winconsin Sequence Analysis Package, version 9.1 (Devreux J. et al, *Nucleic Acid Res.*, 12, 387-395, 1984), for example the programs BESTFIT and GAP, may be used to determine the % identity between two polynucleotides and the % identity and the % similarity between two polypeptide sequences. BESTFIT uses the “local homology” algorithm of Smith and Waterman (*J. Mol. Biol.*, 147, 195-197, 1981) and finds the best single region of similarity between two sequences. BESTFIT is more suited to compare two polynucleotide or two polypeptide sequences that are dissimilar in length, the program assuming that the shorter sequence represents a portion of the longer. In comparison, GAP aligns two sequences, finding a “maximum similarity”, according to the algorithm of Needleman and Wunsch (*J. Mol. Biol.*, 48, 443-453, 1970). GAP is more suited to compare sequences that are approximately the same length and an alignment is expected over the entire length. Preferably, the parameters “Gap Weight” and “Length Weight” used in each program are 50 and 3 for polynucleotide sequences, and 12 and 4 for polypeptide sequences, respectively. Preferably, % identities and similarities are determined when the two sequences being compared are optimally aligned. Other programs for determining identity and/or similarity between sequences are also known in the art, for instance the BLAST family of programs (Altschul S F et al, *Nucleic Acids Res.*, 25:3389-3402, 1997).

**[0033]** Those skilled in the art will recognize that the polypeptides according to the invention, i.e. the HERG polypeptide channel, could be obtained by a plurality of recombinant DNA techniques including, for example, hybridization, polymerase chain reaction (PCR) amplification, or de novo DNA synthesis (See e.g., T. Maniatis et al. *Molecular Cloning: A Laboratory Manual*, 2d Ed. Chap. 14 (1989)). Thus, in a further embodiment the present invention provides the use of the isolated and purified polynucleotides encoding the HERG polypeptide or a fragment thereof, in an

assay or kit according to the invention. In another embodiment the present invention provides the use of the isolated and purified polynucleotide encoding the HERG polypeptide channel or a fragment thereof comprising the polynucleotide sequence of SEQ ID NO:1. In a preferred embodiment the present invention provides the use of the isolated and purified polynucleotide encoding the HERG polypeptide channel consisting of the polynucleotide sequence of SEQ ID NO:1.

**[0034]** The term “fragments thereof” describes a piece, or sub-region of protein or polynucleotide molecule whose sequence is disclosed herein, such that said fragment comprises 5 or more amino acids that are contiguous in the parent protein, or such that said fragment comprises 15 or more nucleic acids that are contiguous in the parent polynucleotide. The term “fragments thereof” is intended to include “functional fragments” wherein the isolated fragment, piece or sub-region comprises a functionally distinct region such as an active site, a binding site or a phosphorylation site of the receptor protein. Functional fragments may be produced by cloning technology, or as the natural products of alternative splicing techniques.

**[0035]** As used herein, “isolated” refers to the fact that the polynucleotides, proteins and polypeptides, or respective fragments thereof in question, have been removed from its in vivo environment so that it can be manipulated by the skilled artisan, such as but not limited to sequencing, restriction digestion, site-directed mutagenesis, and subcloning into expression vectors for a nucleic acid fragment as well as obtaining the protein or protein fragments in quantities that afford the opportunity to generate polyclonal antibodies, monoclonal antibodies, amino acid sequencing, and peptide digestion. Therefore, the nucleic acids as described herein can be present in whole cells or in cell lysates or in a partially, substantially or wholly purified form.

**[0036]** A polypeptide is considered “purified” when it is purified away from environmental contaminants. Thus a polypeptide isolated from cells is considered to be substantially purified when purified from cellular components by standard methods while a chemically synthesized polypeptide sequence is considered to be substantially purified when purified from its chemical precursors. A “substantially pure” protein or nucleic acid will typically comprise at least 85% of a sample with greater percentages being preferred. One method for determining the purity of a protein or nucleic acid molecule, is by electrophoresing a preparation in a matrix such as polyacrylamide or agarose. Purity is evidenced by the appearance of a single band after staining. Other methods for assessing purity include chromatography and analytical centrifugation.

**[0037]** The term “time sufficient to allow binding” as used herein refers to the time needed to generate a detectable amount of labeled reference compound bound to the HERG polypeptide channel. The time needed to generate this detectable amount will vary depending on the assay system. One of skill in the art will know the amount of time sufficient to generate a detectable amount of labeled reference compound bound to the HERG polypeptide channel based upon the assay system.

#### Assays

**[0038]** Assays of the present invention can be designed in many formats generally known in the art of screening compounds for binding polypeptide channels.

**[0039]** The assays of the present invention advantageously exploit the fact that the interaction of astemizole with the

HERG potassium channel can be exploited to predict cardiotoxicity of compounds during the development of new therapeutics and other agents.

Therefore, the present invention provides an assay for screening test compounds, the assay comprising a) incubating a source containing HERG or a fragment thereof with; i) a reference compound, ii) the test compound; and b) measuring the effect of the test compound on the amount of reference compound bound to HERG.

**[0040]** In a first embodiment of this invention the source containing HERG is an isolated and purified protein which encodes HERG having an amino acid sequence that is at least 80% identical to that of SEQ ID NO:2 or a fragment thereof.

**[0041]** In a second embodiment of this invention the source containing HERG is an isolated and purified protein which encodes HERG comprising the amino acid sequence of SEQ ID NO: 2 or a fragment thereof.

**[0042]** In a further embodiment of this invention the source containing HERG are cells expressing on the surface thereof the HERG polypeptide channel or a fragment thereof.

**[0043]** In another embodiment of this invention the source containing HERG are membrane preparations of cells expressing on the surface thereof the HERG polypeptide channel or a fragment thereof.

**[0044]** In an alternative embodiment of this invention, the reference compound is a compound capable to induce cardiotoxicity in a subject, preferably selected from the group consisting of astemizole, terfenadine, erythromycin, sparfloxacin, probucol, terodiline and sertindole. In a preferred embodiment the reference compound is astemizole. It is a further object of this invention to provide assays wherein the reference compound is labeled, preferably radiolabeled.

**[0045]** In a preferred embodiment, the assay for screening test compounds for their capability to induce cardiotoxicity in a subject consists of a) incubating membrane preparations of cells expressing on the surface thereof HERG polypeptide channels encoded by the amino acid sequence consisting of SEQ ID NO:2 with i) [<sup>3</sup>H]-astemizole, ii) the compound to be tested; and measuring the effect of the test compound on the amount of reference compound bound to HERG. The label of the reference compound is used to measure this effect wherein said label can be measured using amongst others scintillation counting.

**[0046]** A specific embodiment of the assays according to the invention, consists of an high-throughput assay for screening test compounds, the assay comprising: a) contacting membrane preparations of cells expressing on the surface thereof HERG polypeptide channels having an amino acid sequence that is at least 80% identical to that of SEQ ID NO:2 or fragments thereof, with a labeled reference compound for a time sufficient to allow binding of the reference compound with the HERG polypeptide channel; b) contacting membrane preparations of cells expressing on the surface thereof HERG polypeptide channels having an amino acid sequence that is at least 80% identical to that of SEQ ID NO:2 or fragments thereof, with the labeled reference compound of step a) together with the test compound for a time sufficient to allow binding of the reference compound and of the test compound with the HERG polypeptide channel; c) measuring the amount of labeled reference compound bound to the HERG channel in step a); d) measuring the amount of labeled reference compound bound to the HERG channel in step b); and e) compare the amount of labeled reference compound bound to the HERG channel measured in step a) with the amount of labeled reference compound bound to the HERG polypeptide channel measured in step b).

**[0047]** In a further embodiment the membrane preparations of the high-throughput screening assay consist of membrane preparations of cells expressing on the surface thereof the HERG polypeptide channel comprising the amino acid sequence of SEQ ID NO:2 or fragments thereof.

**[0048]** In a preferred embodiment of this invention the membrane preparations of the high-throughput screening assay consist of membrane preparations of cells, preferably HEK 293 cells, expressing on the surface thereof HERG polypeptide channels consisting of the amino acid sequence of SEQ ID NO:2.

**[0049]** In a further preferred embodiment, the labeled reference compound in the high-throughput screening assay consists of [<sup>3</sup>H]-labeled astemizole. Said label can be measured using amongst others scintillation counting.

**[0050]** In another specific embodiment the present invention provides a high-throughput proximity detection assay for screening test compounds the assay comprising:

**[0051]** i) HERG labeled with a first label capable of participating in a proximity detection assay;

**[0052]** ii) a reference compound labeled with a second label capable of participating in a proximity detection assay;

**[0053]** iii) contacting HERG of step i) and a reference compound of step ii) together with a test compound for a time sufficient to allow binding of the reference compound and of the test compound to HERG; and

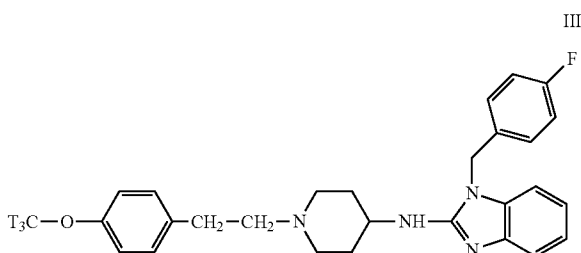
**[0054]** iv) detect an interaction between HERG of step i) and a reference compound of step ii) by means of proximity of the first label with the second label when HERG and the reference compound interact.

The proximity of the first label to the second label, brought about by the interaction of HERG and the reference compound results in the production of a detectable signal. This may be achieved by e.g. a scintillation proximity assay (SPA) system, in which one of the labels is a radiolabel suitable for use in SPA and the other label is a fluorophore comprised in a solid phase. The detectable signal is light energy emitted when the labeled HERG protein interacts with the labeled reference compound, bringing the radiolabel sufficiently close to the fluorophore. Scintillation proximity assay technology is described in U.S. Pat. No. 4,568,649.

**[0055]** Alternatively, the detectable signal may be a change in an existing signal output, eg. fluorescence. Fluorescence resonance energy transfer (FRET) is a method which works on this principle and is described by Tsien R. et al. (Tsien R. et al. (1993) Trends Cell Biol. 3: 242-245). It employs two different fluorescent molecules, a donor and an acceptor, such that when these are in sufficient proximity to one another the fluorescence of the donor molecule is absorbed by the acceptor molecule and light of another wavelength is emitted. Thus, when there is an interaction between two molecules such as HERG and a reference compound, each of which is labeled with one of these fluorescent molecules, a detectable signal is produced.

**[0056]** By such proximity assays as are described above, the screening assay according to the invention may be performed in a single step, i.e. without the need of a separation step to remove the excess of labeled reference compound from the incubation mixture using separation means such as filtration.

**[0057]** In a preferred embodiment of the high-throughput proximity detection assay, HERG is labeled with the fluorophore comprised in a solid phase, such as coated scintillation proximity assay beads and the reference compound is labeled with the radiolabel preferably the reference compound is radiolabeled astemizole of formula (III).



**[0058]** It will be readily appreciated by the skilled artisan that the binding of astemizole with HERG may also be used in a method for the structure-based or rational design of compound which affects the aforementioned binding, by:

**[0059]** a) probing the structure of the binding site of the HERG polypeptide channel with astemizole;

**[0060]** b) identifying contacting atoms in the binding site of the HERG polypeptide channel that interact with astemizole during binding;

**[0061]** c) design test compounds that interact with the atoms identified in (b) to affect the HERG-astemizole interaction; and

**[0062]** d) contact said designed test compound with a source containing HERG or a fragment thereof, to measure the capability of said compound to affect the amount of labeled astemizole bound to HERG.

It will be further appreciated that this will normally be an iterative process.

#### Kits

**[0063]** The present invention also provides kits that can be used in the above assays. In one embodiment the kit comprises a) a source containing HERG; b) a reference compound.

**[0064]** In a first embodiment the kit comprises a source containing HERG selected from: i) an isolated and purified protein which encodes HERG having an amino acid sequence that is at least 80% identical to that of SEQ ID NO:2 or a fragment thereof; ii) an isolated and purified protein which encodes HERG comprising the amino acid sequence of SEQ ID NO:2 or a fragment thereof; iii) cells expressing on the surface thereof the HERG polypeptide channel or a fragment thereof; or iv) membrane preparations of cells expressing on the surface thereof the HERG polypeptide channel or a fragment thereof.

**[0065]** In a further embodiment the kit comprises a reference compound is selected from the group consisting of astemizole, terfenadine, erythromycin, sparfloxacin, probucol, terodiline and sertindole. In a preferred embodiment the reference compound is astemizole. It is a further object of this invention to provide kits wherein the reference compound is labeled, preferably radiolabeled.

**[0066]** In a specific embodiment the isolated and purified HERG polypeptide channel is bound to a solid support, preferably to a fluorescer comprising solid support such as coated scintillation proximity beads.

**[0067]** Thus, in a specific embodiment the kit comprises a) an isolated and purified HERG polypeptide channel or a fragment thereof, bound to a solid support; and b) a labeled reference compound. Preferably this specific embodiment consists of a kit comprising a) an isolated and purified HERG polypeptide channel consisting of the amino acid sequence of

SEQ ID NO:2, bound to fluorescer comprising solid support; and b) a radiolabeled reference compound, preferably [<sup>3</sup>H]-labeled astemizole.

**[0068]** In another specific embodiment the kit comprises a) membrane preparations of cells, preferably HEK293 cells, expressing on the surface thereof the HERG polypeptide channel consisting of the amino acid sequence of SEQ ID NO:2; b) [<sup>3</sup>H]-labeled astemizole; and c) means for measurement of the amount of labeled reference compound bound to HERG.

**[0069]** The means of measurement consist of separating means to remove the excess of unbound labeled reference compound from the incubation mixture and of means for detection of the labeled reference compound. The person skilled in the art will know the separating means available for removing the excess of unbound labeled reference compound from the incubation mixture. Said separating means include, but are not limited to, magnetic beads, centrifugation techniques and filtration techniques. The means for detecting the labeled reference compound will be depended on the labeled used. Said labels may be fluorescent or radiolabels. The skilled man will know the detection means available depending on the label used.

**[0070]** In a specific embodiment the separating means consists of GF/B filtration (Whatman Inc, Clifton, N.J.). In another specific embodiment the detection means consists of scintillation counting in a TOPCOUNT™ (Packard, Meriden, Conn.).

**[0071]** In a further embodiment the kits of the invention further comprise instructions and/or multiple well plates for performing the assay.

**[0072]** This invention will be better understood by reference to the Experimental Details that follow, but those skilled in the art will readily appreciate that these are only illustrative of the invention as described more fully in the claims that follow thereafter. Additionally, throughout this application, various publications are cited. The disclosure of these publications is hereby incorporated by reference into this application to describe more fully the state of the art to which this invention pertains.

#### Example 1

##### DNA Constructs and Stable Transfection of HEK293 Cells

**[0073]** HERG cDNA (Genbank Accession number: U04270 (SEQ ID NO:1)) was subcloned into bamHI/EcoRI sites of the pcDNA3 vector (Invitrogen). This vector contains a CMV promoter and a SV40 promoter, which drive the expression of the inserted cDNA (HERG) and neomycin resistance gene, respectively. The HEK293 cells were transfected with this construct by a calcium phosphate precipitate method (Gibco) or a lipofectamine method (Gibco). After selection in 800 µg/ml geneticin (G418; Gibco) for 15-20 days, single colonies were picked with cloning cylinders and tested for HERG current. The stably transfected cells were cultured in minimum essential medium (MEM) supplemented with 10% fetal bovine serum and 400 µg/ml geneticin.

**[0074]** For electrophysiological study, the cells were harvested from the culture dish by trypsinization, washed twice with standard MEM medium and seeded on small petri-dishes coated with poly-L-lysine. Experiments were performed on the cells 1-2 days after plating.



## Example 2

## Membrane Preparations of HEK293 Cells Stably Transfected with the HERG Potassium Channel

[0075] HEK293 cells stably transfected with the HERG channel cDNA, were grown in DMEM culture medium enriched with 10% fetal calf serum and antibiotics. Collected cells were homogenized in Tris-HCl 50 mM pH 7.4 using an Ultraturrax homogenizer and the homogenate was centrifuged for 10 min at 23,500×g in a SORVALL™ centrifuge. The cell membranes were washed once by re-homogenization and re-centrifugation. The membranes were suspended in Tris-HCl 50 mM pH 7.4, aliquoted and stored at -80 C.

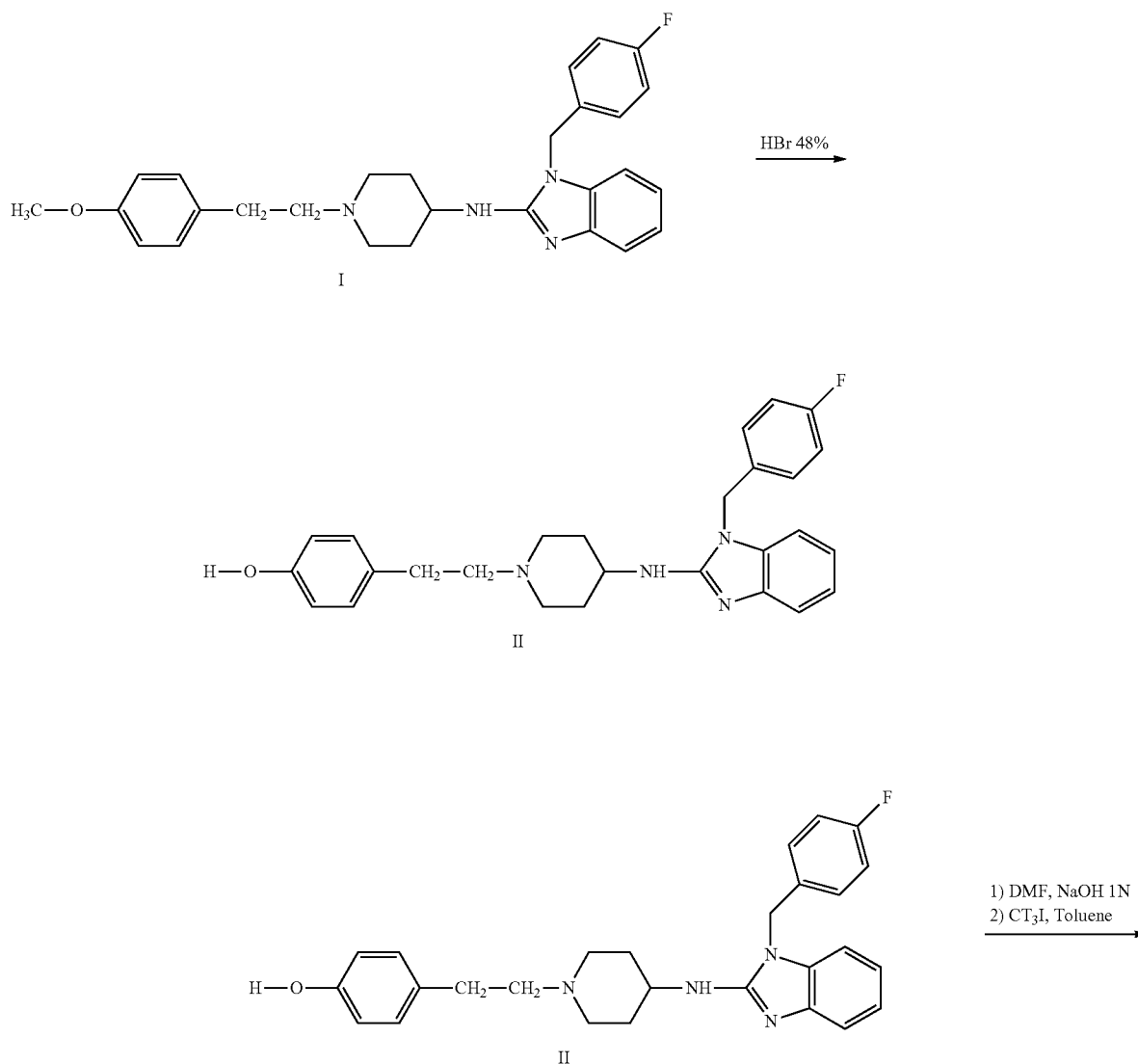
## Example 3

## Radiolabeling of Astemizole

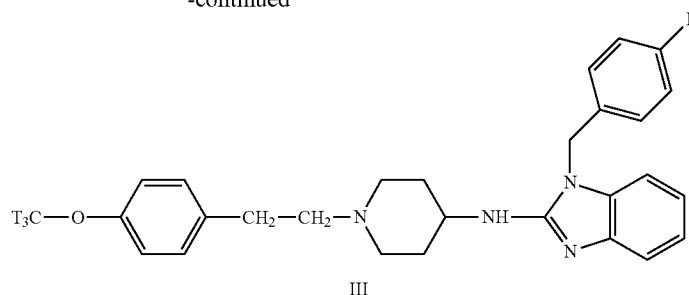
[0076]

[0077] A solution of 4.6 g of astemizole (I) (10 mmol) in a 48% aqueous hydrobromic acid solution (80 ml) was stirred and refluxed for 2 hours. The reaction mixture was allowed to cool to room temperature and the formed precipitate was filtered and washed with water. The solids were dissolved in a mixture of N,N-dimethylformamide (20 ml) and water (20 ml) and the mixture was made alkaline by introducing slowly and with stirring a concentrated aqueous ammoniumhydroxide solution. Then water (100 ml) was added and the mixture was stirred for 1 h. The precipitate was filtered off and dried to the air for 18 h to yield desmethylastemizole (II).

[0078] From this amount a fraction was taken and thoroughly purified in portions via preparative HPLC on a Hyper-syl ODS (5 μm) bonded phase stainless steel column (7.1 mm ID×300 mm) to yield astemizole free desmethylastemizole. Detection took place at 282 nm and elution was performed isocratically with acetonitrile-water-diisopropylamine (56:44:0.2, v/v) at a flow rate of 4.0 ml/min.



-continued



**[0079]** A fraction of the HPLC purified desmethylastemizole (II) (26.7 mg, 60  $\mu$ mol) was dissolved in N,N-dimethylformamide (1.0 ml). To this solution 1N aqueous sodium hydroxide solution (60  $\mu$ l, 60 mop was added. The mixture was stirred for 25 minutes at room temperature and added dropwise to a precooled solution ( $-78^{\circ}$  C.) of [ $^3$ H]-methyl iodide (370 MBq) in toluene. The reaction mixture was vortexed and then left without cooling for 3 hours. The toluene was evaporated from the reaction mixture on a waterbath of  $40^{\circ}$  C. at aspirator pressure and the residue was purified in portions via preparative HPLC as described above. The product containing fractions were combined and depleted to 70 ml with methanol to give [ $^3$ H]-astemizole (III) with a total radioactivity of 198 MBq and a specific activity of 3.14 TBq/mmol (85 Ci/mmol).

#### Example 4

##### Radioligand Binding Assay

**[0080]** Membranes were thawed and re-homogenized in incubation buffer (Hepes 10 mM pH 7.4, 40 mM KCl, 20 mM  $\text{KH}_2\text{PO}_4$ , 5 mM  $\text{MgCl}_2$ , 0.5 mM  $\text{KHCO}_3$ , 10 mM glucose, 50 mM glutamate, 20 mM aspartate, 14 mM heptanoic acid, 1 mM EGTA, 0.1% BSA) and 20-100  $\mu$ g protein was incubated with [ $^3$ H]-astemizole for 60 min at  $25^{\circ}$  C. with or without competitor followed by rapid filtration over GF/B filter using a Filtermate 196 harvester (Packard, Meriden, Conn.). Filters were rinsed extensively with ice-cold rinse-buffer (Tris-HCl 25 mM pH 7.4, 130 mM NaCl, 5.5 mM KCl, 5 mM glucose, 0.8 mM  $\text{MgCl}_2$ , 50  $\mu$ M  $\text{CaCl}_2$ , 0.1% BSA). Filter bound radioactivity was determined by scintillation counting in a TOPCOUNT<sup>TM</sup> (Packard, Meriden, Conn.) and results were expressed as counts per minute (cpm).

**[0081]** Initially, various parameters including buffer, radioligand and compound to determined non-specific binding, were investigated in order to select the optimal conditions.

**[0082]** In a saturation binding experiment, increasing concentrations of [ $^3$ H]-astemizole were incubated with membranes, re-suspended in buffer. Non-specific binding was measured in the presence of 10  $\mu$ M R66204 (FIG. 1).

**[0083]** The effect of BSA and/or cyclodextrine present in the incubation buffer, and of various ways of compound addition prior to the experiment, was investigated by comparing the binding affinities of 22 reference compounds to the electrophysiology data. Compounds were dissolved in DMSO and further diluted in the same solvent using a MULTI-PROBEII<sup>TM</sup> pipetting station (Packard, Meriden, Conn.). The final DMSO concentration in all experiments was 1%. From this analysis it appears that compounds can be added directly from the DMSO stock solution. Attempts to increase the

solubility of the compounds by addition of BSA and/or cyclodextrin did not improve the correlation significantly.

#### Example 5

##### Whole-Cell Voltage Clamp Technique (Patch Clamp)

**[0084]** Solutions: The bath solution contained (in mM) 150 NaCl, 4 KCl, 5 glucose, 10 HEPES, 1.8  $\text{CaCl}_2$  and 1  $\text{MgCl}_2$  (pH 7.4 with NaOH). The pipette solution contained (in mM) 120 KCl, 5 EGTA, 10 HEPES, 4  $\text{MgATP}$ , 0.5  $\text{CaCl}_2$  and 2  $\text{MgCl}_2$  (pH 7.2 with KOH). Compounds were dissolved in DMSO to obtain a stock solution of  $10^{-2}$  M or  $10^{-1}$  M. Control (=bath solution+DMSO) and test solutions (=bath solution+DMSO+compound to be tested) contained 0.3%, 0.1% or 0.03% DMSO. Test and control solutions were applied to the cell under study using an Y-tube system, allowing to rapidly change solutions (less than 0.5 s) in the vicinity of the cell under study.

Electrophysiological measurements: A Petri dish containing attached HEK293 cells expressing HERG was fixed on the stage of a Patch Clamp Tower. An inverted microscope was used to observe the cells. The Petri dish was constantly perfused with the bath solution at room temperature.

**[0085]** Patch pipettes were pulled from borosilicate glass capillaries using a horizontal Flaming/Brown micropipette puller without further fire-polishing. The microelectrodes used had an input resistance between 1.5 and 3 M $\Omega$  when filled with the pipette solution.

**[0086]** The membrane current of the cells was measured at distinct membrane potentials with the patch clamp technique by means of an EPC-9 patch clamp amplifier. Data were acquired and analysed using the programs Pulse and Pulsefit (HEKA), DataAccess (Bruxton) and Igor (Wavemetrics). The current signals were low-pass filtered and subsequently digitised. The liquid junction potential was electronically corrected, before establishing the seal. After disruption of the membrane, the cell capacitance and the series resistance were compensated using the circuit of the EPC-9 patch clamp amplifier.

**[0087]** The holding potential was  $-80$  mV. The HERG current ( $\text{K}^+$ -selective outward current) was determined as the maximal tail current at  $-40$  mV after a 2 second depolarization to  $+60$  mV. Pulse cycling rate was 15 s. Before each test pulse a short pulse (0.5 s) from the holding potential to  $-60$  mV was given to determine leak current. After establishing whole-cell configuration a 5 minute equilibration period allowed for internal perfusion of the cell with the pipette solution. Thereafter test pulses were given for 5 minutes to quantify the HERG current under control conditions. While continuing the pulse protocol, perfusion was switched from control solution to drug-containing solution. The effect of the

drug was measured after 5 minutes of drug application. One to three concentrations of the drug were tested per cell (applied cumulatively).

Parameter analysis of the measurements: The HERG current was determined as the maximal tail current at  $-40$  mV after a 2 second depolarization to  $+60$  mV, starting from a holding potential of  $-80$  mV.

**[0088]** During the initial 5 minutes measured in the presence of the control solution, the amplitude of the HERG-mediated membrane  $K^+$  current gradually decreased with time (run-down). In order to quantify accurately the extent of block by the compounds, this continuous run-down of the  $K^+$  current has to be taken into account. Therefore the time course of the  $K^+$  current (measured at  $-40$  mV) was fitted exponentially to the initial period of 5 minutes in control solution and extrapolated for the remainder of the experiment. These extrapolations give the estimated amplitude of the current if no drug would have been given. To determine the extent of block by the compounds, the ratio of the measured current was calculated by dividing each measured current amplitude by the value of the fitted current at the same point in time.

#### Example 6

##### Pharmacological Evaluation of the Binding Assay

**[0089]** For the pharmacological evaluation of the binding assay, 322 compounds were tested at 8 concentrations, for their ability to inhibit  $[^3H]$ -astemizole binding to the HERG channel and  $pIC_{50}$ -values were calculated by non-linear

regression analysis. If  $pIC_{50}$  values were available, the rank order (Spearman) of the potencies for binding and patch clamp was compared.

**[0090]** If in the patch clamp assay, compounds only have been tested at  $<4$  concentrations, a score was assigned to both binding- and patch clamp data according to the following criteria:

**[0091]** score 1:  $pIC_{50} < 6$  or % blockade  $< 50\%$  at  $10^{-6}$  M or higher

**[0092]** score 2:  $pIC_{50}$  between 6-8 or % blockade  $< 50\%$  between  $10^{-6}$  and  $10^{-8}$  M

**[0093]** score 3:  $pIC_{50} > 8$  or % blockade  $> 50\%$  at  $10^{-8}$  M or lower

**[0094]** The rank order of potencies of 42 reference compounds to displace the  $[^3H]$ -astemizole binding from the HERG channel, correlates well with the electrophysiological data for the functional blockade of the rapid activating delayed rectifier  $K^+$  current ( $r_{SP} = 0.87$ ) (FIG. 2).

**[0095]** For 94% of the compounds tested, the binding data correlate with the patch clamp data. In 2% of the cases the binding assay scored higher than the patch clamp assay, for the remaining 4% it is the other way around, i.e. the patch clamp assay scores higher than the binding assay.

**[0096]** In view of this good correlation between binding data and electrophysiological data it may be concluded that the radioligand binding assay can be used as a primary screening tool for the prediction of potential cardiovascular side-effects.

---

#### SEQUENCE LISTING

```
<160> NUMBER OF SEQ ID NOS: 2

<210> SEQ ID NO 1
<211> LENGTH: 4070
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (184)..(3663)
<300> PUBLICATION INFORMATION:
<301> AUTHORS: Warmke, J. W.
<302> TITLE: Human putative potassium channel subunit (h-erg) mRNA,
        complete cds.
<308> DATABASE ACCESSION NUMBER: GenBank / U04270
<309> DATABASE ENTRY DATE: 1993-12-09
<313> RELEVANT RESIDUES IN SEQ ID NO: 1 TO 4070

<400> SEQUENCE: 1

acgcggcctg ctcaggctc cagcggcggg tcggagggga ggcgggaggc gagcaggac      60
ccgcgccgcg agtccagtct gtgcgcgccg gtgctcgctt ggcgcggtgc gggaccagcg      120
ccggccaccc gaagcctagt ggcgcgcggg gtgggtgggc ccgcccgcg ccatgggctc      180

agg atg ccg gtg cgg agg ggc cac gtc gcg ccg cag aac acc ttc ctg      228
Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Phe Leu
1          5          10          15

gac acc atc atc cgc aag ttt gag ggc cag agc cgt aag ttc atc atc      276
Asp Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Ile Ile
20         25         30

gcc aac gct cgg gtg gag aac tgc gcc gtc atc tac tgc aac gac ggc      324
Ala Asn Ala Arg Val Glu Asn Cys Ala Val Ile Tyr Cys Asn Asp Gly
35         40         45
```

-continued

ttc tgc gag ctg tgc ggc tac tcg cgg gcc gag gtg atg cag cga ccc	372
Phe Cys Glu Leu Cys Gly Tyr Ser Arg Ala Glu Val Met Gln Arg Pro	
50 55 60	
tgc acc tgc gac ttc ctg cac ggg cgg cgc acg cag cgc cgc gct gcc	420
Cys Thr Cys Asp Phe Leu His Gly Pro Arg Thr Gln Arg Arg Ala Ala	
65 70 75	
gcg cag atc gcg cag gca ctg ctg ggc gcc gag gag cgc aaa gtg gaa	468
Ala Gln Ile Ala Gln Ala Leu Leu Gly Ala Glu Glu Arg Lys Val Glu	
80 85 90 95	
atc gcc ttc tac cgg aaa gat ggg agc tgc ttc cta tgt ctg gtg gat	516
Ile Ala Phe Tyr Arg Lys Asp Gly Ser Cys Phe Leu Cys Leu Val Asp	
100 105 110	
gtg gtg ccc gtg aag aac gag gat ggg gct gtc atc atg ttc atc ctc	564
Val Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu	
115 120 125	
aat ttc gag gtg gtg atg gag aag gac atg gtg ggg tcc ccg gct cat	612
Asn Phe Glu Val Val Met Glu Lys Asp Met Val Gly Ser Pro Ala His	
130 135 140	
gac acc aac cac cgg ggc ccc ccc acc agc tgg ctg gcc cca ggc cgc	660
Asp Thr Asn His Arg Gly Pro Pro Thr Ser Trp Leu Ala Pro Gly Arg	
145 150 155	
gcc aag acc ttc cgc ctg aag ctg ccc gcg ctg ctg gcg ctg acg gcc	708
Ala Lys Thr Phe Arg Leu Lys Leu Pro Ala Leu Leu Ala Leu Thr Ala	
160 165 170 175	
cgg gag tcg tcg gtg cgg tcg ggc ggc gcg ggc ggc ggc gcc ccg	756
Arg Glu Ser Ser Val Arg Ser Gly Gly Ala Gly Gly Ala Gly Ala Pro	
180 185 190	
ggg gcc gtg gtg gtg gac gtg gac ctg acg ccc gcg gca ccc agc agc	804
Gly Ala Val Val Val Asp Val Asp Leu Thr Pro Ala Ala Pro Ser Ser	
195 200 205	
gag tcg ctg gcc ctg gac gaa gtg aca gcc atg gac aac cac gtg gca	852
Glu Ser Leu Ala Leu Asp Glu Val Thr Ala Met Asp Asn His Val Ala	
210 215 220	
ggg ctc ggg ccc gcg gag gag cgg cgt gcg ctg gtg ggt ccc ggc tct	900
Gly Leu Gly Pro Ala Glu Glu Arg Arg Ala Leu Val Gly Pro Gly Ser	
225 230 235	
ccg ccc cgc agc gcg ccc ggc cag ctc cca tcg ccc cgg gcg cac agc	948
Pro Pro Arg Ser Ala Pro Gly Gln Leu Pro Ser Pro Arg Ala His Ser	
240 245 250 255	
ctc aac ccc gac gcc tcg ggc tcc agc tgc agc ctg gcc cgg acg cgc	996
Leu Asn Pro Asp Ala Ser Gly Ser Ser Cys Ser Leu Ala Arg Thr Arg	
260 265 270	
tcc cga gaa agc tgc gcc agc gtg cgc cgc gcc tcg tcg gcc gac gac	1044
Ser Arg Glu Ser Cys Ala Ser Val Arg Arg Ala Ser Ser Ala Asp Asp	
275 280 285	
atc gag gcc atg cgc gcc ggg gtg ctg ccc ccg cca ccg cgc cac gcc	1092
Ile Glu Ala Met Arg Ala Gly Val Leu Pro Pro Pro Pro Arg His Ala	
290 295 300	
agc acc ggg gcc atg cac cca ctg cgc agc ggc ttg ctc aac tcc acc	1140
Ser Thr Gly Ala Met His Pro Leu Arg Ser Gly Leu Leu Asn Ser Thr	
305 310 315	
tcg gac tcc gac ctc gtg cgc tac cgc acc att agc aag att ccc caa	1188
Ser Asp Ser Asp Leu Val Arg Tyr Arg Thr Ile Ser Lys Ile Pro Gln	
320 325 330 335	
atc acc ctc aac ttt gtg gac ctc aag ggc gac ccc ttc ttg gct tcg	1236
Ile Thr Leu Asn Phe Val Asp Leu Lys Gly Asp Pro Phe Leu Ala Ser	
340 345 350	

-continued

ccc acc agt gac cgt gag atc ata gca cct aag ata aag gag cga acc	1284
Pro Thr Ser Asp Arg Glu Ile Ile Ala Pro Lys Ile Lys Glu Arg Thr	
355 360 365	
cac aat gtc act gag aag gtc acc cag gtc ctg tcc ctg ggc gcc gac	1332
His Asn Val Thr Glu Lys Val Thr Gln Val Leu Ser Leu Gly Ala Asp	
370 375 380	
gtg ctg cct gag tac aag ctg cag gca ccg cgc atc cac cgc tgg acc	1380
Val Leu Pro Glu Tyr Lys Leu Gln Ala Pro Arg Ile His Arg Trp Thr	
385 390 395	
atc ctg cat tac agc ccc ttc aag gcc gtg tgg gac tgg ctc atc ctg	1428
Ile Leu His Tyr Ser Pro Phe Lys Ala Val Trp Asp Trp Leu Ile Leu	
400 405 410 415	
ctg ctg gtc atc tac acg gct gtc ttc aca ccc tac tcg gct gcc ttc	1476
Leu Leu Val Ile Thr Ala Val Phe Thr Pro Tyr Ser Ala Ala Phe	
420 425 430	
ctg ctg aag gag acg gaa gaa ggc ccg cct gct acc gag tgt ggc tac	1524
Leu Leu Lys Glu Thr Glu Glu Gly Pro Pro Ala Thr Glu Cys Gly Tyr	
435 440 445	
gcc tgc cag ccg ctg gct gtg gtg gac ctc atc gtg gac atc atg ttc	1572
Ala Cys Gln Pro Leu Ala Val Val Asp Leu Ile Val Asp Ile Met Phe	
450 455 460	
att gtg gac atc ctc atc aac ttc cgc acc acc tac gtc aat gcc aac	1620
Ile Val Asp Ile Leu Ile Asn Phe Arg Thr Thr Tyr Val Asn Ala Asn	
465 470 475	
gag gag gtg gtc agc cac ccc ggc cgc atc gcc gtc cac tac ttc aag	1668
Glu Glu Val Val Ser His Pro Gly Arg Ile Ala Val His Tyr Phe Lys	
480 485 490 495	
ggc tgg ttc ctc atc gac atg gtg gcc gcc atc ccc ttc gac ctg ctc	1716
Gly Trp Phe Leu Ile Asp Met Val Ala Ala Ile Pro Phe Asp Leu Leu	
500 505 510	
atc ttc ggc tct ggc tct gag gag ctg atc ggg ctg ctg aag act gcg	1764
Ile Phe Gly Ser Gly Ser Glu Glu Leu Ile Gly Leu Leu Lys Thr Ala	
515 520 525	
cgg ctg ctg cgg ctg gtg cgc gtg gcg cgg aag ctg gat cgc tac tca	1812
Arg Leu Leu Arg Leu Val Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser	
530 535 540	
gag tac ggc gcg gcc gtg ctg ttc ttg ctc atg tgc acc ttt gcg ctc	1860
Glu Tyr Gly Ala Ala Val Leu Phe Leu Leu Met Cys Thr Phe Ala Leu	
545 550 555	
atc gcg cac tgg cta gcc tgc atc tgg tac gcc atc ggc aac atg gag	1908
Ile Ala His Trp Leu Ala Cys Ile Trp Tyr Ala Ile Gly Asn Met Glu	
560 565 570 575	
cag cca cac atg gac tca cgc atc ggc tgg ctg cac aac ctg ggc gac	1956
Gln Pro His Met Asp Ser Arg Ile Gly Trp Leu His Asn Leu Gly Asp	
580 585 590	
cag ata ggc aaa ccc tac aac agc agc ggc ctg ggc ggc ccc tcc atc	2004
Gln Ile Gly Lys Pro Tyr Asn Ser Ser Gly Leu Gly Gly Pro Ser Ile	
595 600 605	
aag gac aag tat gtg acg gcg ctc tac ttc acc ttc agc agc ctc acc	2052
Lys Asp Lys Tyr Val Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr	
610 615 620	
agt gtg ggc ttc ggc aac gtc tct ccc aac acc aac tca gag aag atc	2100
Ser Val Gly Phe Gly Asn Val Ser Pro Asn Thr Asn Ser Glu Lys Ile	
625 630 635	
ttc tcc atc tgc gtc atg ctc att ggc tcc ctc atg tat gct agc atc	2148
Phe Ser Ile Cys Val Met Leu Ile Gly Ser Leu Met Tyr Ala Ser Ile	
640 645 650 655	

-continued

ttc ggc aac gtg tgc gcc atc atc cag cgg ctg tac tgc ggc aca gcc	2196
Phe Gly Asn Val Ser Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr Ala	
660 665 670	
cgc tac cac aca cag atg ctg cgg gtg cgg gag ttc atc cgc ttc cac	2244
Arg Tyr His Thr Gln Met Leu Arg Val Arg Glu Phe Ile Arg Phe His	
675 680 685	
cag atc ccc aat ccc ctg cgc cag cgc ctc gag gag tac ttc cag cac	2292
Gln Ile Pro Asn Pro Leu Arg Gln Arg Leu Glu Glu Tyr Phe Gln His	
690 695 700	
gcc tgg tcc tac acc aac ggc atc gac atg aac ggc gtg ctg aag ggc	2340
Ala Trp Ser Tyr Thr Asn Gly Ile Asp Met Asn Ala Val Leu Lys Gly	
705 710 715	
ttc cct gag tgc ctg cag gct gac atc tgc ctg cac ctg aac cgc tca	2388
Phe Pro Glu Cys Leu Gln Ala Asp Ile Cys Leu His Leu Asn Arg Ser	
720 725 730 735	
ctg ctg cag cac tgc aaa ccc ttc cga ggg gcc acc aag ggc tgc ctt	2436
Leu Leu Gln His Cys Lys Pro Phe Arg Gly Ala Thr Lys Gly Cys Leu	
740 745 750	
cgg gcc ctg gcc atg aag ttc aag acc aca cat gca ccg cca ggg gac	2484
Arg Ala Leu Ala Met Lys Phe Lys Thr Thr His Ala Pro Pro Gly Asp	
755 760 765	
aca ctg gtg cat gct ggg gac ctg ctc acc gcc ctg tac ttc atc tcc	2532
Thr Leu Val His Ala Gly Asp Leu Leu Thr Ala Leu Tyr Phe Ile Ser	
770 775 780	
cgg ggc tcc atc gag atc ctg cgg ggc gac gtc gtc gtg gcc atc ctg	2580
Arg Gly Ser Ile Glu Ile Leu Arg Gly Asp Val Val Val Ala Ile Leu	
785 790 795	
ggg aag aat gac atc ttt ggg gag cct ctg aac ctg tat gca agg cct	2628
Gly Lys Asn Asp Ile Phe Gly Glu Pro Leu Asn Leu Tyr Ala Arg Pro	
800 805 810 815	
ggc aag tgc aac ggg gat gtg cgg gcc ctc acc tac tgt gac cta cac	2676
Gly Lys Ser Asn Gly Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu His	
820 825 830	
aag atc cat cgg gac gac ctg ctg gag gtg ctg gac atg tac cct gag	2724
Lys Ile His Arg Asp Asp Leu Leu Glu Val Leu Asp Met Tyr Pro Glu	
835 840 845	
ttc tcc gac cac ttc tgg tcc agc ctg gag atc acc ttc aac ctg cga	2772
Phe Ser Asp His Phe Trp Ser Ser Leu Glu Ile Thr Phe Asn Leu Arg	
850 855 860	
gat acc aac atg atc ccg ggc tcc ccc ggc agt acg gag tta gag ggt	2820
Asp Thr Asn Met Ile Pro Gly Ser Pro Gly Ser Thr Glu Leu Glu Gly	
865 870 875	
ggc ttc agt cgg caa cgc aag cgc aag ttg tcc ttc cgc agg cgc acg	2868
Gly Phe Ser Arg Gln Arg Lys Arg Lys Leu Ser Phe Arg Arg Arg Thr	
880 885 890 895	
gac aag gac acg gag cag cca ggg gag gtg tgc gcc ttg ggg ccg ggc	2916
Asp Lys Asp Thr Glu Gln Pro Gly Glu Val Ser Ala Leu Gly Pro Gly	
900 905 910	
cgg gcg ggg gca ggg ccg agt agc cgg ggc cgg ccg ggg ggg ccg tgg	2964
Arg Ala Gly Ala Gly Pro Ser Ser Arg Gly Arg Pro Gly Gly Pro Trp	
915 920 925	
ggg gag agc ccg tcc agt ggc ccc tcc agc cct gag agc agt gag gat	3012
Gly Glu Ser Pro Ser Ser Gly Pro Ser Ser Pro Glu Ser Ser Glu Asp	
930 935 940	
gag ggc cca ggc cgc agc tcc agc ccc ctc cgc ctg gtg ccc ttc tcc	3060
Glu Gly Pro Gly Arg Ser Ser Ser Pro Leu Arg Leu Val Pro Phe Ser	
945 950 955	

-continued

agc ccc agg ccc ccc gga gag ccg ccg ggt ggg gag ccc ctg atg gag Ser Pro Arg Pro Pro Gly Glu Pro Pro Gly Gly Glu Pro Leu Met Glu 960 965 970 975	3108
gac tgc gag aag agc agc gag act tgc aac ccc ctg tca ggc gcc ttc Asp Cys Glu Lys Ser Ser Asp Thr Cys Asn Pro Leu Ser Gly Ala Phe 980 985 990	3156
tca gga gtg tcc aac att ttc agc ttc tgg ggg gag agt ccg ggc cgc Ser Gly Val Ser Asn Ile Phe Ser Phe Trp Gly Asp Ser Arg Gly Arg 995 1000 1005	3204
cag tac cag gag ctc cct cga tgc ccc gcc ccc acc ccc agc ctc ctc Gln Tyr Gln Glu Leu Pro Arg Cys Pro Ala Pro Thr Pro Ser Leu Leu 1010 1015 1020	3252
aac atc ccc ctc tcc agc ccg ggt cgg cgg ccc cgg ggc gag gtg gag Asn Ile Pro Leu Ser Ser Pro Gly Arg Arg Pro Arg Gly Asp Val Glu 1025 1030 1035	3300
agc agg ctg gat gcc ctc cag cgc cag ctc aac agg ctg gag acc cgg Ser Arg Leu Asp Ala Leu Gln Arg Gln Leu Asn Arg Leu Glu Thr Arg 1040 1045 1050 1055	3348
ctg agt gca gag atg gcc act gtc ctg cag ctg cta cag agg cag atg Leu Ser Ala Asp Met Ala Thr Val Leu Gln Leu Leu Gln Arg Gln Met 1060 1065 1070	3396
acg ctg gtc ccg ccc gcc tac agt gct gtg acc acc ccg ggg cct ggc Thr Leu Val Pro Pro Ala Tyr Ser Ala Val Thr Thr Pro Gly Pro Gly 1075 1080 1085	3444
ccc act tcc aca tcc ccg ctg ttg ccc gtc agc ccc ctc ccc acc ctc Pro Thr Ser Thr Ser Pro Leu Leu Pro Val Ser Pro Leu Pro Thr Leu 1090 1095 1100	3492
acc ttg gac tcg ctt tct cag gtt tcc cag ttc atg gcg tgt gag gag Thr Leu Asp Ser Leu Ser Gln Val Ser Gln Phe Met Ala Cys Glu Glu 1105 1110 1115	3540
ctg ccc ccg ggg gcc cca gag ctt ccc caa gaa ggc ccc aca cga cgc Leu Pro Pro Gly Ala Pro Glu Leu Pro Gln Glu Gly Pro Thr Arg Arg 1120 1125 1130 1135	3588
ctc tcc cta ccg ggc cag ctg ggg gcc ctc acc tcc cag ccc ctg cac Leu Ser Leu Pro Gly Gln Leu Gly Ala Leu Thr Ser Gln Pro Leu His 1140 1145 1150	3636
aga cac ggc tcg gag ccg ggc agt tag tggggctgcc cagtgtggac Arg His Gly Ser Asp Pro Gly Ser 1155 1160	3683
acgtggctca cccagggatc aaggcgtgc tgggcccgtc cccttgagg cctgtctcag	3743
gaggccctga ccgtggaagg ggagaggaac tcgaaagcac agctcctccc ccagcccttg	3803
ggaccatctt ctctgcagt cccctgggcc ccagtgcagag gggcaggggc agggccggca	3863
gtaggtgggg cctgtgtgcc cccactgcc ctgagggcat tagctgttct aactgcccg	3923
aggcaccceg cccctgggct taggcacctc aaggactttt ctgctattta ctgctttat	3983
tgtaaggat aataattaag gatcatatga ataattaatg aagatgctga tgactatgaa	4043
taataaataa ttatcctgag gagaaaa	4070

&lt;210&gt; SEQ ID NO 2

&lt;211&gt; LENGTH: 1159

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 2

Met	Pro	Val	Arg	Arg	Gly	His	Val	Ala	Pro	Gln	Asn	Thr	Phe	Leu	Asp
1				5					10					15	

-continued

---

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



-continued

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

-continued

---

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

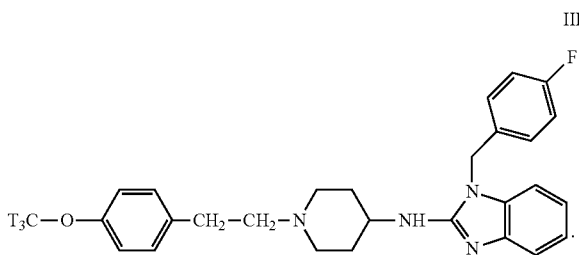
---

What is claimed is:

**1-36.** (canceled)

**37.** A kit comprising:

- a) a source containing a HERG polypeptide or functional fragment thereof;
- b) radiolabeled astemizole of formula III:



**38.** A kit according to claim **37** wherein the source containing said HERG polypeptide or functional equivalent thereof is selected from:

- i) an isolated and purified nucleic acid which encodes a HERG polypeptide having an amino acid sequence that is at least 80% identical to that of SEQ ID NO: 2 or a functional fragment thereof;
- ii) an isolated and purified nucleic acid which encodes a HERG polypeptide comprising the amino acid sequence of SEQ ID NO: 2 or a functional fragment thereof;
- iii) cells expressing on the surface thereof a HERG polypeptide having an amino acid sequence that is at least 80% identical to that of SEQ ID NO: 2 or a functional fragment thereof;

or

- iv) membrane preparations of cells expressing on the surface thereof a HERG polypeptide having an amino acid sequence that is at least 80% identical to that of SEQ ID NO: 2 or a functional fragment thereof.

**39.** A kit according to claim **37** wherein the source containing HERG is an isolated and purified HERG polypeptide having an amino acid sequence that is at least 80% identical to that of SEQ ID NO: 2 or a functional fragment thereof, bound to a solid support.

**40.** A kit according to claim **39** wherein the solid support is a fluorescer comprising solid support.

**41.** A kit according to claim **39** wherein the source containing HERG consists of membrane preparations of cells expressing on the surface thereof HERG polypeptide channels encoded by the nucleic acid sequence consisting of SEQ ID NO: 2.

**42.** A kit according to claim **41** wherein the cells are HEK293 cells.

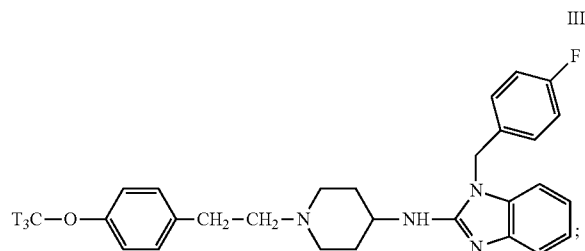
**43.** A kit according to claim **42** optionally comprising means to remove the excess of unbound labeled reference compound from the incubation mixture.

**44.** A kit according to claim **42** wherein the separating means consist of GF/B filtration.

**45.** An assay for screening test compounds, comprising:

- a) incubating an isolated and purified polynucleotide which encodes HERG comprising the nucleic acid sequence of SEQ ID NO: 2 or a functional fragment thereof with:

- i) radiolabeled astemizole of formula III

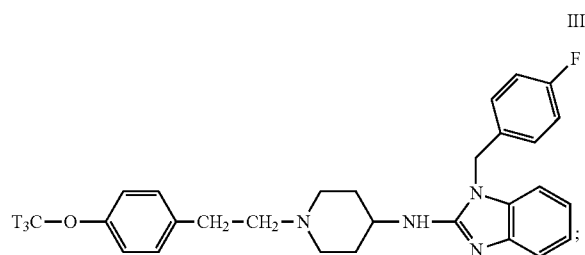


- ii) the test compound; and
- b) measuring the effect.

**46.** An assay for screening test compounds, comprising:

- a) incubating an isolated and purified polynucleotide which encodes a HERG polypeptide having an amino sequence that is at least 80% identical to that of SEQ ID NO: 2; said nucleic acid sequence comprising the nucleic acid sequence of SEQ ID NO: 1 or a functional fragment thereof with:

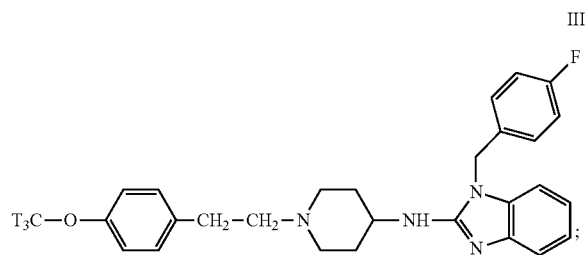
- i) radiolabeled astemizole of formula III



- ii) the test compound; and
- b) measuring the effect.

**47.** An assay for screening test compounds, comprising:

- a) incubating membrane preparations of cells expressing on the surface thereof a HERG polypeptide encoded by nucleic acid sequence consisting of SEQ ID NO: 1 with:
- i) radiolabeled astemizole of formula III



- ii) the test compound; and
- b) measuring the effect.

\* \* \* \* \*