

(12) PATENT
(19) AUSTRALIAN PATENT OFFICE

(11) Application No. AU 200010274 B2
(10) Patent No. 763515

(54) Title
**Isolated and purified human soluble guanylylcyclase alpha1/beta1
(hsGCalpha1/beta1)**

(51)⁷ International Patent Classification(s)
C12N 015/60 C12N 009/88
A61K 048/00 C12N 015/62
A61P 009/10 C12P 021/02
C07K 016/40

(21) Application No: **200010274**

(22) Application Date: **1999.08.16**

(87) WIPO No: **WO00/09711**

(30) Priority Data

(31) Number	(32) Date	(33) Country
19837015	1998.08.14	DE

(43) Publication Date : **2000.03.06**

(43) Publication Journal Date : **2000.05.04**

(44) Accepted Journal Date : **2003.07.24**

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PCT

WELTORGANISATION FÜR GEISTIGES EIGENTUM
Internationales Büro



INTERNATIONALE ANMELDUNG VERÖFFENTLICHT NACH DEM VERTRAG ÜBER DIE
INTERNATIONALE ZUSAMMENARBEIT AUF DEM GEBIET DES PATENTWESENS (PCT)

(51) Internationale Patentklassifikation ⁷ :
C12N 15/60, 15/62, 9/88, C12P 21/02,
C07K 16/40, A61K 48/00, A61P 9/10

A1

(11) Internationale Veröffentlichungsnummer: WO 00/09711

(43) Internationales
Veröffentlichungsdatum: 24. Februar 2000 (24.02.00)

(21) Internationales Aktenzeichen: PCT/DE99/02601

(22) Internationales Anmeldedatum: 16. August 1999 (16.08.99)

(30) Prioritätsdaten:
198 37 015.6 14. August 1998 (14.08.98) DE

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(81) Bestimmungsstaaten: AE, AL, AM, AT, AU, AZ, BA, BB,
BG, BR, BY, CA, CH, CN, CU, CZ, DK, EE, ES, FI, GB,
GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR,
KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN,
MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK,
SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW,
ARIPO Patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG,
ZW), eurasisches Patent (AM, AZ, BY, KG, KZ, MD, RU,
TJ, TM), europäisches Patent (AT, BE, CH, CY, DE, DK,
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI
Patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR,
NE, SN, TD, TG).

Veröffentlicht

Mit internationalem Recherchenbericht.

(54) Title: ISOLATED AND PURIFIED HUMAN SOLUBLE GUANYLYLCYCLASE $\alpha 1/\beta 1$ (hsGC $\alpha 1/\beta 1$)

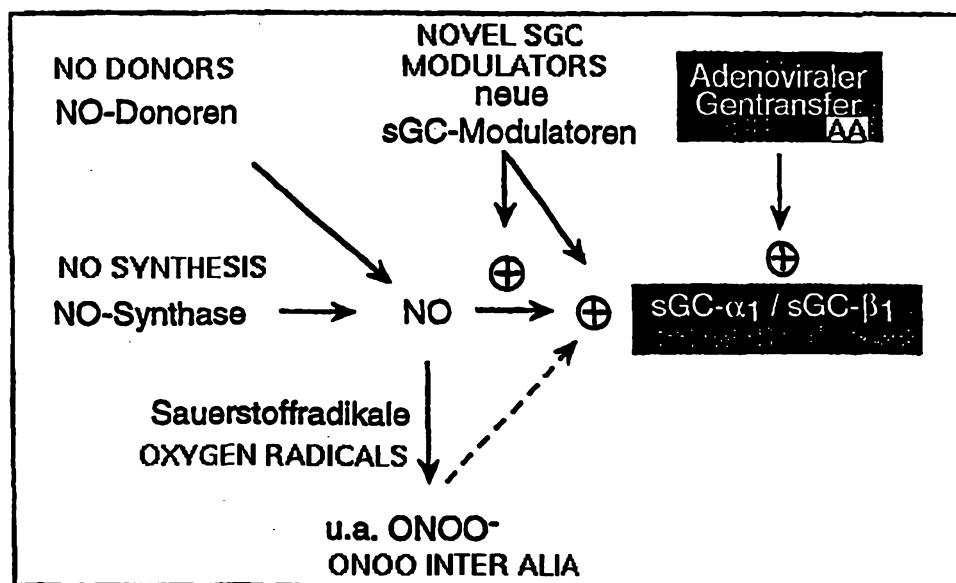
(54) Bezeichnung: ISOLIERTE UND GEREINIGTE HUMANE LÖSLICHE GUANYLYLCYCLASE $\alpha 1/\beta 1$ (hsGC $\alpha 1/\beta 1$)

(57) Abstract

The invention relates to the expression of the cDNA clone for sub-units a1 (hsGC $\alpha 1$) and b1 (hsGC $\beta 1$) of human soluble guanylylcyclase and the subsequent purification of the active enzyme and use thereof, the medical application of the expression of this clone by gene transfer, in addition to antibodies against peptides derived from said sequence and the use thereof.

(57) Zusammenfassung

Beschrieben ist die Expression der cDNA-Klone für die Untereinheiten a1 (hsGC $\alpha 1$) und b1 (hsGC $\beta 1$) der humanen



AA...ADENOVIRAL GENE TRANSFER

löslichen Guanylylcyclase und die nachfolgende Aufreinigung des aktiven Enzyms und dessen Anwendung, die medizinische Anwendung der Expression dieser Klone durch Gentransfer, sowie Antikörper gegen aus der Sequenz abgeleitete Peptide und deren Anwendung.

Abstract

5 The invention relates to the expression of the cDNA clone for sub-units a1 (hsGCa1) and b1 (hsGCb1) of human soluble guanylylcyclase and the subsequent purification of the active enzyme and use thereof, the medical application of the expression of this clone by gene transfer, in addition to antibodies against peptides derived from said sequence and the use thereof.

Isolated and purified human soluble guanylyl cyclase $\alpha 1/\beta 1$ (hsGC $\alpha 1/\beta 1$)

The technical field of the invention

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The present invention relates to the expression of the cDNA clones for the subunits $\alpha 1$ (hsGC $\alpha 1$) and $\beta 1$ (hsGC $\beta 1$) of human soluble guanylyl cyclase and the subsequent purification of the active enzyme and the use thereof, the medical application of the expression of these clones by gene transfer, as well as antibodies
10 to peptides derived from the sequence and the use thereof.

State of the art

15 The endogenous NO/cGMP signaling system mediates important functions such as vasodilation, inhibition of platelet aggregation, neurotransmission, and the immune response. In addition, it is involved in the development of various disease states such as ischemia-reperfusion and inflammatory injuries (Schmidt and Walter, 1994). Therefore, the NO/cGMP system has long been an important starting point for the
20 development of novel drugs for the therapy of coronary heart disease, susceptibility to thrombosis, cardiac insufficiency, angina pectoris, cardiac-dependent pulmonary oedema, hypertensive crises, inflammatory states and cardiac infarction. Until now, such therapies have employed various so-called NO donors, e.g. nitroglycerin, that release NO, thereby replacing endogenous NO and activating soluble guanylyl
25 cyclase (sGC) (Fig. 1). sGC forms cGMP, which mediates the effects of the NO/cGMP pathway via various intracellular receptor enzymes. The application of NO donors has two limitations: I) The repeated application of NO donors results in tolerance in the patient, i.e. loss of activity, when reapplied; II) NO reacts with O_2^- to form peroxynitrite, which is cytotoxic and less effective in activating sGC. Thus, direct
30 activation of sGC by novel, non-NO-containing pharmaceuticals for therapy or gene transfer of sGC would be desirable strategies. Non-NO-releasing activators of sGC are potentially lacking tolerance and NO toxication. Recently, "YC-1" (3-(5'-hydroxymethyl-2'-furyl)-1-benzylindazol) has been described as the first non-NO-releasing activator of sGC in platelets (Ko et al., 1994; Wu et al., 1995). YC-1 also

activates purified sGC from bovine lung and potentiates the activation of NO (Friebe et al., 1996). The effect on human sGC has not been investigated. The human isoform of sGC is not yet available for pharmacological screening.

5 The NO receptor sGC consists of two subunits, α and β , which together form an enzymatically active heterodimer. Three different isoforms of the α and three of the β subunits have been described in the literature, although from different species. The best investigated isoforms, the bovine α_1/β_1 and the rat α_1/β_1 isoforms, have particular significance for cardiovascular research. Until recently, a human
10 homologue of the bovine and rat sGC (e.g. sGC α_1 /sGC β_1 heterodimers) was unknown. cDNA sequences have been published that reportedly correspond to a human sGC α_3 and β_3 isoform (Giuli et al., 1992). While sGC β_3 showed a high homology to sGC β_1 (bovine/rat), the sGC α_3 sequence contained two restricted regions without homology to sGC α_1 (bovine/rat), here designated S1 and S2 (Fig. 2).
15 In addition, it was unknown whether sGC α_3 and sGC β_3 can form a functional sGC heterodimer and which role the S1 and S2 regions play. Furthermore, no other human sGC subunit has yet been expressed as a protein. Recently, a sequence designated hsGC α_1 was published in the GeneBank (Accession No. U58855) that lacks the sequence differences to sGC α_1 from bovine and rat tissues in the regions
20 S1 and S2. In addition, an alternatively spliced product of hsGC β_3 was recently published in the GeneBank (Accession No. AF020340) that was designated by the authors as an alternatively spliced form of hsGC β_1 . The physiological significance of this splice variant of hsGC $\beta_1/3$ is unclear. Thus, the question arises as to which of these isoforms is responsible for which physiological function in which cell types.

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Furthermore, no antibodies to the human sGC α_1/β_1 are currently available that are monospecific, directed against the human sequences, or that have been shown to be suitable for immunoblots with human tissues. Peptide antibodies reported thus far only partially show these features: Harteneck et al. and Guthmann et al. used a
30 peptide sequence (VYKVETVGDKYMTVSGLP) that is highly conserved in guanylyl cyclases. Therefore, cross-reaction with particulate guanylyl cyclases (e.g. GC-C) can be expected. Guthmann et al. used a peptide sequence (YGPEVWEDIKKEA) identical to hsGC β_1 and a peptide sequence (KKDVEEANANFLGKASGID) identical

to hsGC α 1 except for two amino acid exchanges. However, the function of these antibodies in immunoblots was only shown for *enriched* hsGC from human platelets. In addition, the antisera to hsGC α 1 detect a second, unspecific product. Humbert et al. and Koesling et al. used a peptide sequence (SRKNTGTEETE QDEN) of bovine sGC β 1 that partially (amino acids 1-10) overlaps with the peptide used here for the human sGC β 1 (amino acids 13-22) and is identical in this region. The C-terminus of this bovine peptide (amino acids 11-15), however, is clearly different from the human sequence. On the other hand, the antiserum to this peptide was not tested with a human protein but rather only used for immunoprecipitation of the bovine sGC.

Thus, for the human isoform α 1/ β 1 which is important for cardiovascular research, neither *native* protein nor *recombinant* protein, nor a one-step purification protocol, nor specific antibodies have been available. An approach for gene therapy (e.g. with adenoviruses or the like) has also not been described yet.

The NO-independent activation of the human sGC α 1/ β 1 is a promising approach to finding novel drugs or gene transfer techniques for cardiovascular therapy that neither result in tolerance in the patient nor form cytotoxic peroxynitrite. To find such pharmaceuticals, a mass screening for suitable active substances is necessary. Such a pharmacological screening for specific activators or inhibitors via animal testing is too expensive and is not reasonable due to species differences, possible side effects, and effects on other isoforms. Cell culture systems have the disadvantage that only with substantial additional effort can it be determined at which points of the signaling cascade substances are effective. In addition, cell culture is expensive and touchy. The purification of a protein from animal tissues is labor-intensive and results in a low yield. More importantly, because of species differences the results of such a screening are not generally transferable. Here, in particular, the question arises of the significance of the isoforms hsGC α 1 and hsGC α 3 and whether hsGC β 3 in fact corresponds to a human hsGC β 1. This is an important factor to consider in selecting the appropriate target protein for pharmacological screening or gene therapy. For optimal screening, the human homologue of the protein sGC α 1/ β 1 would have to be purified in large amounts and to be available at low cost. A purification of large amounts of human native sGC α 1/ β 1 protein from human tissues is not possible. Thus, other methods are needed for the drug screening protocol. In addition, no

purified antibodies are available for the detection of human sGC α 1/ β 1 that have been shown to be suitable for diagnostic uses, e.g. in normal immunoblotting, ELISA, RIA, or EIA, among other techniques. An approach for the artificial expression of hsGC by gene transfer in humans that could be used therapeutically is also not available.

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Therefore, the present invention is based on the technical problem of providing isolated and purified human sGC α 1/ β 1 as well as a process for its production and purification. In addition, a further technical problem of the present invention is to provide antibodies directed against human sGC α 1/ β 1. A further technical problem is the provision of expression vectors containing the cDNA of human sGC α 1/ β 1 based on adenoviruses. Finally, the technical problem of the present invention is the provision of human sGC α 1/ β 1 in purified form and in manageable amounts for drug screening assays aimed at detecting modulators, inhibitors, and activators of human sGC α 1/ β 1.

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The present invention relates to a human soluble guanylyl cyclase α 1/ β 1 (hsGC α 1/ β 1) in an isolated form purified to apparent homogeneity.

The present invention further relates to a process for the production of subunit α 1 and/or β 1 of human soluble guanylyl cyclase comprising the expression of expression vectors containing the DNA sequence for hsGC α 1 and/or hsGC β 1 in prokaryotic and eukaryotic host cells, and obtaining of the subunit or subunits.

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In a preferred embodiment of the process of the present invention for the production of subunit α 1 and/or β 1 of human soluble guanylyl cyclase, the step of obtaining the subunit or subunits comprises the lysis of cells, affinity chromatography of the cell lysate, and finally, the elution of the subunit or subunits.

In a further preferred embodiment of the process of the present invention for the production of subunit α 1 and/or β 1 of human soluble guanylyl cyclase, the expression vector contains additionally at least one DNA sequence of a domain for specific affinity chromatography (affinity tag) with attached protease cleavage site.

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The present invention also relates to a process for the production of human soluble guanylyl cyclase $\alpha 1/\beta 1$ (hsGC $\alpha 1/\beta 1$) comprising the separate expression of an expression vector containing the DNA sequence for hsGC $\alpha 1$ or hsGC $\beta 1$ in prokaryotic or eukaryotic host cells, obtaining the subunits, and combining the subunits hsGC $\alpha 1$ and hsGC $\beta 1$ into the dimeric guanylyl cyclase $\alpha 1/\beta 1$ (hsGC $\alpha 1/\beta 1$).

A further preferred embodiment of the process of the present invention for the production of human soluble guanylyl cyclase $\alpha 1/\beta 1$ (hsGC $\alpha 1/\beta 1$) also comprises the coexpression of the DNA sequences for hsGC $\alpha 1$ and hsGC $\beta 1$ in prokaryotic or eukaryotic host cells, the lysis of the cells containing hsGC $\alpha 1$ and hsGC $\beta 1$, affinity chromatography, and the subsequent elution of hsGC $\alpha 1/\beta 1$.

The present invention also relates to the use of a nucleic acid sequence that codes for subunits hsGC $\alpha 1$ and/or hsGC $\beta 1$ of human soluble guanylyl cyclase $\alpha 1/\beta 1$ for somatic gene therapy, particularly for the prevention and therapy of atherosclerosis and its complications, restenosis, ischemia (infarction), peripheral occlusive diseases, and arterial hypertension, as well as, in patients with risk factors, for the prevention of atherosclerosis, transient ischemic attacks, cerebral ischemia, stroke, coronary heart disease, status post coronary bypass grafting, carotid stenosis, heart insufficiency and liver dysfunction, and as a supplement to therapy with sGC activators, sGC-sensitizing substances, NO donors, or phosphodiesterase inhibitors.

In a particularly preferred embodiment, adenoviral vectors containing hsGC $\alpha 1$ or hsGC $\beta 1$ cDNA are used in somatic gene therapy. Other vector systems, however, can also be applied for gene therapeutic, medicinal use.

In a preferred embodiment, adenoviral Ad5 and other suitable vectors that contain the nucleic acid sequence of human soluble guanylyl cyclase $\alpha 1$ (hsGC $\alpha 1$) and/or human soluble guanylyl cyclase $\beta 1$ (hsGC $\beta 1$) are used for prevention and therapy of the diseases mentioned above. Likewise, a mixture of two vectors in which one vector contains the nucleic acid sequence of human soluble guanylyl cyclase $\alpha 1$ (hsGC $\alpha 1$) and the second that of human soluble guanylyl cyclase $\beta 1$ (hsGC $\beta 1$) can be used for somatic gene transfer. Especially preferred is somatic gene transfer into

endothelial cells, vascular smooth muscle cells, neointimal cells, fibroblasts, and other vascular cells as well as into blood particles (platelets, leukocytes, and others) and the liver.

- 5 The methods of gene transfer described in the present invention can also be used for gene transfer of human soluble guanylyl cyclase $\alpha 2$ (GeneBank: x63282) and of the human homologue of soluble guanylyl cyclase $\beta 2$ (from rat; GeneBank: m57507) as well as for other human soluble guanylyl cyclases.
- 10 The present invention further relates to antibodies to human soluble guanylyl cyclase $\alpha 1/\beta 1$ (hsGC $\alpha 1/\beta 1$), obtainable by immunization of a mammal with hsGC $\alpha 1/\beta 1$, either of subunits $\alpha 1$ or $\beta 1$, or immunogenic peptide fragments thereof, as well as isolation of the antibodies.
- 15 Reference to any prior art in the specification is not, and should not be taken as, an acknowledgment or any form of suggestion that this prior art forms part of the common general knowledge in Australia or any other country.

It will be understood that the term "comprises" or its grammatical variants as used in this specification and claims is equivalent to the term "includes" and is not to be taken as excluding the presence of other elements or features.

Figures:

Figure 1 shows various possibilities of modulation of soluble guanylyl cyclase (CsGC- $\alpha 1$ /sGC- $\beta 1$). Normal activation is mediated by NO synthase (NOS) and NO. NO, however, reacts with oxygen radicals to form peroxynitrite (ONOO⁻), which is cytotoxic and only poorly activates sGC. NO can also be released by NO donors such as nitroglycerin or sodium nitroprusside. sGC can be directly activated by modulators of sGC (e.g. YC-1); alternatively, the activation by NO of sGC is potentiated by these modulators. Additionally, sGC can be overexpressed by use of gene transfer (e.g. using adenoviral vectors) or a pathologically low expression level of sGC can be compensated. Adenoviral (or other) vectors with mutated sGC that

has a higher basal activity can also be used. Thus, an elevated cGMP level could be achieved permanently independent of NOS, NO, NO donors, or sGC modulators.

Figure 2 shows a schematic comparison of the bovine and rat sGC α 1 subunits together with the published sequence of the human cDNA clone termed 'sGC α 3' (Giuli et al., 1992). The bars represent the protein. 'N' represents the N-terminus and 'C' the C-terminus. The functional segments 'regulatory domain', 'sGC homology domain', and 'cyclase domain' of these proteins are marked with different patterns. The regions 'S1' and 'S2' for which no homologous regions are found in the bovine and rat sGC α 1 proteins are marked in black.

Figure 3 shows a schematic illustration of the human sGC α 3 clone with the sequence errors published (Giuli et al., 1992). The cDNA is shown above: the bar represents the coding region of the cDNA, the lines left and right of the bar represent the 5' and 3' untranslated regions, respectively. 'S1' and 'S2' represent the regions that have no homology to the bovine and rat isoforms of sGC α 1 (see Fig. 2). The positions of the sequence errors are marked below: line a shows the nucleotide insertions, line b the deletion, and line c the exchanges. A base-pair (bp) scale is shown below. The sequence errors for each of the 3 lines a, b, and c are listed at the bottom: the letter specifies the type of the base concerned, and the number its position in the cDNA.

Figure 4 shows the verification of the expression of human sGC α 1 (A) and sGC β 1 (B) in human tissues by means of PCR using cDNA libraries. Shown is a photo of an ethidium bromide-stained agarose gel under UV light with separated PCR products. The arrow on the left points to the specific product. The PCR primers are visible at the bottom of the photo. The tissues from which the cDNA libraries were produced are indicated at the top. No cDNA was added in the negative control, and in the positive control, plasmid containing the cDNA of hsGC α 1 was added.

Figures 5 and 6 show the baculovirus transfer vectors pVL1393 and pAcG2T, respectively (both without the hsGC cDNA), which were used for the construction of recombinant baculoviruses for the expression of human sGC α 1/ β 1 in Sf9 cells. The circular plasmid with the restriction sites (short names and position in base pairs), the gene for ampicillin resistance (Amp^R), the 'origin of replication' (ColE ori), the

polyhedrin promotor, the glutathione-S-transfease sequence (only in Fig. 6), and the multiple cloning site (MCS) are shown at the top of the figures. Figure 5 shows the multiple cloning site with its unique restriction sites at the bottom. Figure 6 shows the multiple cloning site with the unique restriction sites as well as a thrombin cleavage site normal at the bottom.

Figure 7 shows the construction of the plasmids hsGC β 1-pVL1393 (without GST-tag) with the hsGC β 1 cDNA, which was used to obtain genetically modified, hsGC β 1-expressing baculovirus by homologous recombination. The procedure for the plasmid pAcG2T-hsGC β 1 (with GST-tag = glutathione-S-transferase cDNA from *Schistosoma japonicum*) is identical. A fragment was produced that carries an additional BamHI-site at its 5' end by means of PCR with the primers A (bases 89-116 of the hsGC β 1 cDNA + BamHI site at its 5' end) and B (bases 692-711 of the hsGC β 1 cDNA [noncoding strand] with natural KpnI site). Due to the additional restriction sites, fragment 1 (PCR fragment with new BamHI site) and fragment 2 (hsGC β 1 cDNA from KpnI site to EcoRI site) could be inserted together into the BamHI and EcoRI sites of the plasmid pVL1393. Thus, the complete hsGC β 1 cDNA is under the control of the polyhedrin promotor (PHP).

Figure 8 shows the construction of the plasmid hsGC α 1-pVL1393 (without GST-tag) with the hsGC α 1 cDNA which was used to obtain genetically modified, hsGC α 1-expressing baculovirus by homologous recombination. The procedure for the plasmid pAcG2T-hsGC α 1 (with GST-tag = glutathione-S-transferase cDNA from *Schistosoma japonicum*) is identical. A fragment was produced that carries an additional BamHI site at its 5' end and a natural BsaAI site within the sequence by means of PCR with the primers C (bases 524-541 of the hsGC α 1 cDNA + BamHI site at its 5' end) and D (bases 1232-1249 of the hsGC α 1 cDNA [noncoding strand]). Due to the added restriction site, fragment 3 cut with BsaAI (PCR fragment with new BamHI site to the BsaAI site) and fragment 4 (hsGC α 1 cDNA from BsaAI site to EcoRI site) could be inserted together into the BamHI and EcoRI sites of the plasmid pVL1393. Thus, the complete hsGC α 1 cDNA is under the control of the polyhedrin promotor (PHP).

Figure 9 shows the verification of the expression of hsGC α 1/ β 1 in Sf9 cells, which were infected with the genetically modified viruses described above (with hsGC α 1 or hsGC β 1 cDNA; both without GST-tag = glutathione-S-transferase cDNA from *Schistosoma japonicum*). On the left (A) a Coomassie-stained 10% SDS-polyacrylamide gel is shown on which were loaded the cell homogenates that had been separated into pellet (P) and supernatant (S) by centrifugation (20,000 x g). 'Co' designates the control with noninfected Sf9 cells. ' α 1' designates Sf9 cells that were infected with viruses containing the hsGC α 1 cDNA, and ' β 1' designates Sf9 cells that were infected with viruses containing the hsGC β 1 cDNA. The position of hsGC α 1 and hsGC β 1 in the gel are marked (α 1 or β 1). On the right an immunoblot is shown with supernatant (S) and pellet (P) of the cell homogenate from Sf9 cells that were either noninfected (Co) or coinfecting with hsGC α 1 and hsGC β 1 baculoviruses (α 1+ β 1). The peptide antibodies to hsGC β 1 described above (anti-hsGC β 1) were used in immunoblotting first (Fig. 9B. lines 1-4). Afterwards, the blot was redeveloped with the peptide antibodies to hsGC α 1 (anti-hsGC α 1; Fig. 9B, lanes 5-8), which additionally revealed the hsGC β 1 bands.

Figure 10 shows the activity of guanylyl cyclase (formation of cGMP from GTP) in intact Sf9 cells that were coinfecting with the genetically modified baculoviruses containing hsGC α 1 and hsGC β 1 cDNA described here (both without GST-tag). Shown is the content of cGMP in pmol per 10⁶ cells with different treatments, indicated at the bottom of the figure. Sample 1 is untreated in both panels A and B. 1 mM IBMX (3-isobutyl-1-methylxanthine) was added to each of the other samples (top line: black crossbar). In the middle line, the concentration of SNP added to the samples is indicated in μ M. The bottom line shows the concentration of added YC-1 (A, left) or ODQ (B, right) in μ M.

YC-1 = 3-(5'-hydroxymethyl-2'-furyl)-1-benzylindazol;

ODQ = 1H-[1,2,4]oxadiazolo[4,3,-a]chinoxalin-1-on;

SNP = sodium nitroprusside;

cGMP = cyclic 3', 5'-guanosine monophosphate

Figure 11 shows the activity of guanylyl cyclase (formation of cGMP from GTP) in homogenates of Sf9 cells that were coinfecting with the genetically modified baculoviruses containing hsGC α 1 and hsGC β 1 cDNA described here (both without

GST-tag). As shown at the top, (A), the soluble cell fraction (supernatant after centrifugation at 20,000 x g) was used, and at the bottom, (B), the respective pellet. In each case, the amount of cGMP formed in pmol per mg protein per minute is shown for homogenates of cells that were harvested at different time points (indicated in hours) after infection with the baculoviruses. cGMP formation was measured with (black boxes) and without (white boxes) the addition of 100 μ M SNP.

Figure 12 shows the activity of guanylyl cyclase (formation of cGMP from GTP) in Sf9 cells that were coinfectd with the genetically modified baculoviruses containing hsGC β 1 cDNA (without GST-tag) and hsGC α 1 cDNA (with GST-tag = glutathione-S-transferase cDNA from *Schistosoma japonicum*). The formation of cGMP in pmol per mg protein per minute during the purification procedure (affinity chromatography on glutathione sepharose 4B) is shown. In each case, activity was measured in the lysate (after removing the insoluble part by centrifugation at 20,000 x g), in the supernatant after binding of hsGC to glutathione sepharose 4B (flow-through), in both supernatants of the washes of hsGC bound to glutathione sepharose 4B (1. and 2. wash), as well as in the supernatant after elution of hsGC with reduced glutathione (1. and 2. elution). The formation of cGMP was determined without (black boxes, 'basal') and with (grey boxes, '+ 100 μ M SNP') addition of 100 μ M SNP.

Figure 13 shows the natural, endogenous expression of hsGC α 1 and hsGC β 1 in different human tissues in an immunoblot.

The peptide antibodies to hsGC α 1 described above (anti-hsGC α 1) were used on the left (A), and the peptide antibodies to hsGC β 1 (anti-hsGC β 1) were used on the right (B). On the right, the peptide to which the antibodies were raised was added as negative control (peptide: +), while no peptide was added on the left (peptide: -). The SDS extracts of rhsGC α 1- (in panel A of the figure) or rhsGC β 1-overexpressing Sf9 cells (in panel B of the figure) (Sf9), of human cerebral cortex (cortex), of human cerebellum (cerebellum), and of human lung (lung) were loaded on an 8% polyacrylamide gel. The specific bands of hsGC α 1 (α 1) and hsGc β 1 (β 1) are indicated by an arrow.

Figure 14 shows in immunoblots the purification of hsGC α 1 (as a hsGC α 1/hsGC β 1 dimer) from Sf9 cells that were coinfectd with the genetically modified baculoviruses

containing hsGC α 1 cDNA with GST-tag (= glutathione-S-transferase cDNA from *Schistosoma japonicum*) and hsGC β 1 cDNA (without GST-tag). Cell lysate was incubated with glutathione sepharose 4B, and after binding, the supernatant was loaded (supernatant after binding). The sepharose was washed twice and the
 5 respective supernatants of this wash were loaded (1. and 2. wash). Subsequently, elution was performed by cleavage of the hsGC α 1 protein from the GST-tag with thrombin and an aliquot was loaded ('elution with thrombin'). Then, SDS stop buffer was added to the glutathione sepharose 4B and an aliquot was loaded (GSH sepharose after elution). In addition, glutathione sepharose 4B with bound hsGC α 1
 10 without prior thrombin elution to which SDS buffer had been added was loaded (GSH sepharose before elution). The immunoblot was developed with the affinity-purified peptide antibodies to the C-terminus of hsGC α 1 described here. The arrows on the right point to the specific bands of hsGC α 1 with the GST-tag (GST-hsGC α 1) and hsGC α 1 without the GST-tag (hsGC α 1).

Figure 15 shows the purification of hsGC α 1/ β 1 from Sf9 cells that were coinfecting with the genetically modified baculoviruses containing hsGC α 1 cDNA with GST-tag (= glutathione-S-transferase cDNA from *Schistosoma japonicum*) and hsGC β 1 cDNA without GST-tag in a Coomassie Brilliant Blue R250-stained SDS-polyacrylamide gel.
 20 Cell lysate of these infected Sf9 cells (lysate) was incubated with glutathione sepharose 4B, and the supernatant loaded after the binding (supernatant after binding). The glutathione sepharose 4B was washed twice and the respective supernatants of this wash buffer were loaded (1. and 2. wash). In one sample, the bound GST-hsGC α 1/ β 1 was eluted by incubation with reduced glutathione and
 25 loaded (elution with glutathione). In the other samples, the glutathione sepharose was washed with the buffer for the thrombin cleavage—without thrombin—and the supernatant of this buffer was loaded (3. wash). Then, the hsGC α 1/ β 1 dimer was eluted by incubation with different amounts of thrombin and the eluates were loaded (elution with 0.25-1 U/ml thrombin) [U = unit]. The same relative amount of each of
 30 the samples was used. The bands visible with the different elution methods are indicated on the right: GST-hsGC α 1 = hsGC α 1 with GST-tag; hsGC α 1 = hsGC α 1 without GST-tag; hsGC β 1 = hsGC β 1 without GST-tag. On the left are the molecular

weight standards loaded on the gel, the size of which (in kDa) is indicated on the far left side.

Figure 16 shows the construction of the recombinant adenoviral hsGC vectors. The cDNAs of hsGC α 1 and hsGC β 1 (grey bars) were inserted in the adenoviral transfer plasmid pZS2, which has a deletion in the adenovirus E1 region (Δ E1) and a unique XbaI site in this plasmid. This resulted in the plasmids hsGC α 1-pZS2 and hsGC β 1-pZS2, respectively. hsGC α 1-pZS2 and hsGC β 1-pZS2 cut with the restriction enzyme XbaI (middle bar, indicated as 'sGCpZS2') were ligated into the XbaI site of the long arm (upper bar, 'RR5') of Ad5. This resulted in the adenovectors Ad5CMVhsGC α 1 and Ad5CMVhsGC β 1, respectively (lower bar, 'Ad 5 CMV sGC') in which the sGC cDNAs lie under the control of the CMV promotor and CMV enhancer (CMV = cytomegalovirus).

Figure 17 shows the stimulation of sGC activity by 100 μ M SNP (= sodium nitroprusside) in EA.hy926 cells that were coinfectd with both hsGC adenoviruses Ad5CMVhsGC α 1 and Ad5CMVhsGC β 1 (samples A-C) and in noninfected EA.hy926 cells (sample D). The amount of pmol cGMP formed per mg protein per minute is plotted on the Y axis. The dark bars represent basal cGMP formation without SNP stimulation, and the light bars represent cGMP formation with SNP stimulation.

Figure 18 shows the DNA sequence of human soluble guanylyl cyclase α 1 (hsGC α 1); SEQ ID NO: 1.

Figure 19 shows the amino acid sequence of human soluble guanylyl cyclase α 1 (hsGC α 1); SEQ ID NO: 2.

Figure 20 shows the DNA sequence of human soluble guanylyl cyclase β 1 (hsGC β 1); SEQ ID NO: 3.

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Figure 21 shows the amino acid sequence of human soluble guanylyl cyclase β 1 (hsGC β 1); SEQ ID NO: 4.

Figure 22 shows the amino acid sequence of the peptide that was used for the production of antibodies to human soluble guanylyl cyclase $\alpha 1$ (hsGC $\alpha 1$) (corresponds to amino acids 634-647 of hsGC $\alpha 1$); SEQ ID NO: 5.

- 5 Figure 23 shows the amino acid sequence of the peptide that was used for the production of antibodies to human soluble guanylyl cyclase $\beta 1$ (hsGC $\beta 1$) (corresponds to amino acids 593-614 of hsGC $\beta 1$); SEQ ID NO: 6.

- 10 Figure 24 shows the DNA sequence of the PCR primer pair for human soluble guanylyl cyclase $\alpha 1$ (hsGC $\alpha 1$). Upper primer (corresponds to nucleotides 524-541 of the hsGC $\alpha 1$ cDNA sequence with added BamHI restriction site); SEQ ID NO: 7. Lower primer (corresponds to nucleotides 1249-1232 of the hsGC $\alpha 1$ cDNA sequence [noncoding strand]); SEQ ID NO: 8.

- 15 Figure 25 shows the DNA sequence of the PCR primer pair for human soluble guanylyl cyclase $\beta 1$ (hsGC $\beta 1$). Upper primer (corresponds to nucleotides 89-106 of the hsGC $\beta 1$ cDNA sequence with added BamHI restriction site); SEQ ID NO: 9. Lower primer (corresponds to nucleotides 692-711 of the hsGC $\beta 1$ cDNA sequence [noncoding strand]); SEQ ID NO: 10.

- 20 Figure 26 shows the stimulation of sGC activity by 100 μ M SNP (sodium nitroprusside) in ECV 304 cells that had been coinfectd with different amounts of both hsGC adenoviurses Ad5CMVhsGC $\alpha 1$ and Ad5CMVhsGC $\beta 1$ (samples 1-6) and in noninfected ECV 304 cells (sample 7). The amount of pmol cGMP formed per mg protein per minute is plotted on the Y axis. The dark bars represent basal cGMP formation without SNP stimulation, and the light bars represent cGMP formation with SNP stimulation.
- 25

- 30 Figure 27 shows the stimulation of sGC activity by 100 μ M SNP (sodium nitroprusside) in A10 cells that had been coinfectd with different amounts of both hsGC adenoviurses Ad5CMVhsGC $\alpha 1$ and Ad5CMVhsGC $\beta 1$ (samples 1-6) and in noninfected A10 cells (sample 7). The amount of pmol cGMP formed per mg protein per minute is plotted on the Y axis. The dark bars represent basal cGMP formation

without SNP stimulation, and the light bars represent cGMP formation with SNP stimulation.

Figure 28 shows the stimulation of sGC activity by 100 μ M SNP (sodium nitroprusside) in ECV 304 cells that had been coinfectd with 5×10^{10} of each of the hsGC adenoviruses Ad5CMVhsGC α 1 and Ad5CMVhsGC β 1 and then have been harvested at different time points as well as the activity in noninfected ECV 304 cells. The time point of the harvest, in days after infection (0, no infection), is plotted on the X axis. The amount of pmol cGMP formed per mg protein per minute is plotted on the Y axis. The dark bars represent basal cGMP formation without SNP stimulation, and the light bars represent cGMP formation with SNP stimulation.

Figure 29 shows the stimulation of sGC activity by 100 μ M SNP (sodium nitroprusside) in A10 cells that had been coinfectd with 5×10^{10} of each of the hsGC adenoviruses Ad5CMVhsGC α 1 and Ad5CMVhsGC β 1 and then have been harvested at different time points as well as the activity in noninfected A10 cells. The time point of the harvest, in days after infection (0, no infection), is plotted on the X axis. The amount of pmol cGMP formed per mg protein per minute is plotted on the Y axis. The dark bars show basal cGMP formation without SNP stimulation, and the light bars represent cGMP formation with SNP stimulation.

Figure 30 shows the detection of sGC subunits in E304 cells and A10 cells, respectively, that had been coinfectd with 5×10^{10} of each of the hsGC adenoviruses Ad5CMVhsGC α 1 and Ad5CMVhsGC β 1 for two days in a protein immunoblot with the peptide antibodies to hsGC α 1 and hsGC β 1 described above. Lane 1, purified hsGC (according to Figure 12); lane 2, ECV 304 cells with hsGC gene transfer; lane 3, A10 cells with hsGC gene transfer; lane 4, purified hsGC (according to Figure 12).

Advantages of the present invention

1.) The cDNA clones described in the literature as sGC α 3 and sGC β 3 were identified as human homologues of bovine and rat sGC α 1 and sGC β 1, and in the following are termed human sGC α 1 (hsGC α 1) and human sGC β 1 (hsGC β 1). According to present knowledge, this sGC α 1/ β 1 isoform is pharmacologically more important due to its function in the cardiovascular system. Because the original clone of hsGC α 3 was examined, it could be shown that hsGC α 1 and hsGC α 3 do not exist in parallel but rather only the form hsGC α 1. Thus, an obvious target protein for pharmacological mass screening and gene therapy has been identified.

2.) With the methods described by the present invention, a functional, active expression of human sGC has been obtained for the first time. Thus, the respective protein can be produced by genetic methods for the first time.

3.) By use of the peptide antibodies to sGC of the present invention, it is possible to determine the expression of sGC in human tissues as well as diagnose dysfunctional conditions (if expression of sGC is too high, too low, or absent). In addition, the present invention provides the technical prerequisites needed to further elucidate the control of transcription and translation of hsGC. The peptide antibodies of the invention have the advantage that they are monospecific, directed at the human sequence, and that their suitability for immunoblots with human tissues has been demonstrated. Other peptide antibodies exhibit these features only partially: Harteneck et al. and Guthmann et al. used a peptide sequence (VYKVETVGDKYMTVSGLP) that is relatively highly conserved in guanylyl cyclases. Thus, cross-reaction with particulate guanylyl cyclases (e.g. GC-C) would be expected. Furthermore, Guthmann et al. used a peptide sequence (YGPEVWEDIKKEA) identical to hsGC β 1 and a peptide sequence identical to hsGC α 1 except for two amino acid exchanges (KKDVEEANANFLGKASGID), but the function of these antibodies in immunoblotting has only been shown for enriched hsGC from human platelets. In addition, these antibodies to hsGC α 1 recognized a second, unspecific product.

Humbert et al. and Koesling et al. used a peptide sequence (SRKNTGTEETE QDEN) from bovine sGC β 1 that is in part (amino acids 1-10) identical to the peptide used here (amino acids 13-22) for hsGC β 1, although the C-terminus (amino acids 11-15) differed markedly from that of the human sequence. The antiserum to this peptide, however, has not been tested on human protein and has only been used for immunoprecipitation of bovine sGC.

In addition to the peptides shown in Figures 22 and 23 and their immunogenic fragments for the production of the antibodies to hsGC α 1 or hsGC β 1 in rabbits of the present invention, the production of monoclonal or polyclonal antibodies to the whole hsGC α 1/ β 1 protein or its cleavage products is possible. Various animal species (preferably mouse, rat, or rabbit) can be used for the production of these antibodies.

4.) By use of the eukaryotic baculovirus/Sf9 expression system of the present invention, human soluble guanylyl cyclase α 1/ β 1 can be produced in high amounts. The attachment of a nucleotide sequence that codes for a polypeptide suitable for affinity chromatography (affinity tag, e.g. glutathione-S-transferase = GST-tag) with an attached protease cleavage site at the N-terminus of the cDNA of the α 1 subunit allows the rapid and simple purification of the coexpressed dimeric protein by means of a single affinity chromatographic step. The attached affinity tag is subsequently removed by digestion with a protease. Thus, a protein identical in primary structure to the native protein is obtained. This revolutionary, fast, and clean purification yielding high amounts of very pure, functional human sGC results in new possibilities for a mass screening for specific activators and inhibitors as well as for the pharmacological characterization of potential drugs.

Purification of hsGC α 1/ β 1 can also be accomplished by ion exchange chromatography, gel filtration, immunoaffinity chromatography, and other chromatographic procedures, e.g. on ATP-, GTP-, cGMP- or Blue-sepharose, and other similar chromatographic media.

5.) The process of the present invention can also be used for other isoforms of the human, rat, and bovine enzyme in an identical manner. In the process provided

in the present invention, various affinity tags (e.g. histidine oligomer) and different expression systems (e.g. *E. coli*) can be used. Other parts of the hsGC α 1 and hsGC β 1 sequences can also be used for the production of antibodies to peptides or the whole protein.

5

6.) The availability of high amounts of an isolated human protein in high purity and in high quality is essential for modern pharmaceutical development. Until now, this requirement was not fulfilled in the search for alternatives to the classical NO donors. Mass screening for specific activators or inhibitors in animal testing is too
10 expensive and would not make sense due to species differences, possible side effects, and effects on other isoforms. Cell culture systems have the disadvantage of requiring substantial additional effort to determine precisely at which point within the signaling cascades substances act. In addition, cell culture is expensive and touchy. Compared with the expression of a protein using
15 recombinant DNA technology, the purification of a protein from animal tissues is more labor intensive and results in lower yields. In particular, the results of a pharmacological screening can only be generalized to a limited extent because of differences between species. In contrast, processes of the present invention provide for recombinant, inexpensive hsGC α 1/ β 1 in high amounts, and
20 unequivocal predictions concerning modulation, activation, or inhibition of this particular human enzyme can be made from a screening procedure. Species differences and lack of applicability to human are excluded a priori by the use of a human enzyme.

25

In addition, hsGC is available thereby in high amounts and adequate purity for crystallization and clarification of its structure. Thus, an important prerequisite for rational drug design by means of molecular modeling is fulfilled.

30

7.) In addition to the use of isolated hsGC α 1/ β 1, intact Sf9 cells that express hsGC α 1/ β 1 by being infected with the recombinant baculoviruses described here can be used in in vitro experiments.

8.) Transient (e.g. with adenoviral vectors) or stable overexpression can be achieved by means of gene transfer. Thus, the cGMP level can be elevated even at low

NO concentration or in the case of poor activation of sGC due to peroxynitrite formation. This approach also has conceptual advantages compared to the gene transfer of NOS (NO synthase) because the formation of cytotoxic peroxynitrite, which is less effective in activating sGC, is circumvented with the approach of the present invention. Furthermore, a permanent increase in the cGMP level could be achieved (e.g. for therapeutic purposes) independently of NOS, NO, NO donors, or sGC modulators by gene transfer of mutated sGC with elevated basal activity.

9.) In addition to the purification procedure for hsGC α 1/ β 1 described here, purification from Sf9 cells is also possible after infection with the described baculoviruses containing hsGC α 1 or hsGC β 1 cDNA if coinfection is performed with hsGC α 1 baculoviruses without a GST-tag (GST-tag = appended glutathione-S-transferase sequence from *Schistosoma japonicum*) and hsGC β 1 baculoviruses having a GST-tag as well as with hsGC α 1 baculoviruses having a GST-tag and hsGC β 1 baculoviruses having a GST-tag.

Furthermore, use of a column containing glutathione sepharose 4B is possible in addition to the use of glutathione sepharose 4B alone in a batch-wise step.

Purification can also be performed by digesting the dimeric fusion protein GST-hsGC α 1/ β 1 with thrombin after elution of the fusion protein from the glutathione sepharose 4B with reduced glutathione. After dialysis (to remove the reduced glutathione), the GST-tag which has been cleaved from the protein can be removed from the mixture by additional affinity chromatography on glutathione sepharose 4B.

10.) The process of the present invention can also be used for human soluble guanylyl cyclase α 2 (GeneBank: x63282) and any potentially existing human homologue of the soluble guanylyl cyclase β 2 (from rat; GeneBank: m57507) as well as for other human soluble guanylyl cyclases (in all technical variations described in the present invention).

11.) Using the adenoviral, somatic gene transfer of hsGC α 1 or hsGC β 1 by means of coinfection with Ad5CMVhsGC α 1 or Ad5CMVhsGC β 1, respectively, it was demonstrated in endothelial (ECV 304) and smooth muscle (A10) cells that the intracellular sGC activity measured as cGMP content after stimulation of sGC with SNP was increased from undetectable levels (≤ 100 pmol/mg/min) to 12-fold higher values. An optimal concentration, regarding the amount of adenovirus (pfu) as well as an equimolar ratio of both adenoviruses (based on pfu), corresponding to the homodimeric structure of the enzyme, was determined. This effect on intracellular sGC activity was still detectable 15 days after a single infection, a period sufficient for the intended applications.

The examples illustrate the present invention.

Example 1

The corrected sequence of hsGC α 1 and hsGC β 1

The original clone of the human isoform sGC α 3 and sGC β 3 (Giuli et al., 1992) was sequenced again. While the sequence of the sGC β 3 clone was confirmed (see SEQ ID NO: 3 and Figure 20), the sequencing of sGC α 3 showed that the original publication (Giuli et al., 1992) contained 19 sequencing errors, which are summarized in Figure 3. The corresponding corrected α 3-cDNA sequence is shown in SEQ ID NO: 1 and Figure 18. The deduced amino acid sequence is shown in SEQ ID NO: 2 and Figure 19. Furthermore, the corrected sequence (see SEQ ID NO: 1 and Figure 18) is identical with the human sGC α 1 sequence published in the GeneBank (accession No. U58855), whereby the 5' untranslated region of the sequence provided here is 506 base pairs longer. Therefore, 'sGC α 3' is now classified as human sGC α 1 (hsGC α 1). Thus, it was shown that two different hsGC α subunits α 1 and α 3 do not both exist in humans, which could be important for cardiovascular research but rather—in analogy to the situation in bovine and rat tissues—only hsGC α 1.

Table 1 Revised terminology of soluble guanylyl cyclase cDNAs and proteins and their detection in human tissue.

human sGC subunits		
	α	β
isoform 1	cDNA and protein detectable	cDNA and protein detectable
	active, when coexpressed	
isoform 2	cDNA detectable	
	active, when coexpressed with bovine $\beta 1$	

- 5 The expression of sGC $\alpha 1$ and sGC $\beta 1$ mRNA in human tissues was demonstrated by means of PCR (Figure 4). The amplification of a hsGC $\beta 1$ fragment with a PCR primer pair (5'-AAAAGGATCCATGTACGGATTTGTGAAT-3' = nucleotides 89-106 of the hsGC $\beta 1$ cDNA sequence with added restriction site; 5'-ATGCGTGATTCCTGGGTACC-3' = 692-711 of the hsGC $\beta 1$ cDNA sequence) with
- 10 an annealing temperature of 54°C resulted in one specific band each in cDNA libraries from brain, heart, kidney, lung, pancreas, and skeletal muscle. The identity of the amplified fragment was confirmed by sequencing. The amplification of a hsGC $\alpha 1$ fragment with a PCR primer pair (5'-AAAAGGATCCATGTTCTGCACGAAGCTC-3' = nucleotide 524-541 of the hsGC $\alpha 1$ cDNA sequence with added restriction site; 5'-ATTATGGAAGCAGGGAGG-3' =
- 15 1249-1232 of the hsGC $\alpha 1$ cDNA sequence) with an annealing temperature of 54°C resulted in one specific band each in cDNA libraries from heart (Figure 4A) and lung (not shown). In each case, the sequencing of the fragments resulted in the corrected hsGC $\alpha 1$ sequence; and the 'hsGC $\alpha 3$ ' sequence published by Giuli et al. was not
- 20 found. Thus, it was shown that in humans, only one hsGC $\alpha 1/\beta 1$ exists, and that the potential hsGC $\alpha 3/\beta 3$ is a result of sequencing errors. This results in a clear picture for cardiovascular research concerning which sGC isoform should be the target protein for pharmacological screening.

Example 2

Construction of recombinant baculoviruses for the expression of human sGC α and sGC β in insect cells

5 In order to verify that hsGC α 1 and hsGC β 1 can form a functional, heterodimeric sGC protein, both cDNAs were inserted into baculoviruses. Using these baculoviruses, the recombinant protein was expressed under the control of the strong polyhedrin promoter in insect cells (Sf9 cells). For the production of the recombinant baculoviruses, the baculovirus transfer vector pVL1393 (Pharmingen, San Diego,
10 California, USA; Figure 5) and the baculovirus transfer vector pAcG2T (with glutathione-S-transferase sequence from *Schistosoma japonicum* and thrombin cleavage site; Pharmingen; Figure 6) were used in which the foreign genes hsGC α 1 and hsGC β 1 were cloned, respectively. The cotransfection of such a recombinant pVL1393 or pAcG2T plasmid with BaculoGold baculovirus DNA (Pharmingen)
15 allowed the direct isolation of the genetically modified baculoviruses with hsGC α 1 or hsGC β 1 cDNA formed by homologous recombination from the cell culture media.

The construction of pVL1393-hsGC β 1 is schematically shown in Figure 7 (identical procedure for pAcG2T-hsGC β 1). The coding region of the hsGC β 1 cDNA with the 3' untranslated region but without the 5' untranslated region was cloned into pVL1393.
20 For this, a BamHI site was introduced by means of PCR with primers A and B immediately upstream of the codon coding for the start methionine. The thus amplified fragment 1 was digested with BamHI/KpnI; fragment 2 was isolated from the sGC β 1 cDNA clone with KpnI/EcoRI. Fragments 1 and 2 as well as the vector
25 opened with BamHI and EcoRI were ligated (see Figure 7).

The construction of pVL1393-hsGC α 1 is shown schematically in Figure 8 (identical procedure for pAcG2T-hsGC α 1). The coding region of the hsGC α 1 cDNA with the 3' untranslated region but without the 5' untranslated region was cloned into pVL1393.
30 For this, a BamHI site was introduced by means of PCR with primers C and D immediately upstream of the codon coding for the start methionine. The thus amplified fragment 3 was digested with BamHI/BsaAI; fragment 4 was isolated from

the sGC α 1 cDNA clone with BsaAI/EcoRI. Fragments 3 and 4 as well as the vector opened with BamHI and EcoRI were ligated (see Figure 8).

For the production of the recombinant hsGC α 1 and hsGC β 1 baculoviruses, the
 5 baculovirus transfer vectors (pVL1393-hsGC α 1, pAcG2T-hsGC α 1, pVL1393-hsGC β 1, pAcG2T-hsGC β 1) were each cotransfected with baculovirus DNA (Baculo-Gold; Pharmingen, San Diego, California, USA) in monolayers of Sf9 cell cultures. For this, the cells were cultivated at 27°C in IPL-41 media (Gibco) supplemented with 10% (vol/vol) fetal calf serum (Biochrom), 4% (vol/vol) tryptose-phosphate-broth
 10 (Gibco), 1% (vol/vol) Pluronic F68 (Gibco), 0,5% amphotericin B (Gibco), 80 µg/ml gentamycin sulfate (Gibco), and 0.5 mM δ -aminolevulinic acid (Merck). Recombinant hsGC α 1 and hsGC β 1 baculovirus clones were obtained from the culture media by means of plaque purification. For the production of virus stock solutions with high titer, Sf9 shaking cultures (0.5×10^6 cells/ml) were infected with a M.O.I. (multiplicity
 15 of infection) of 0.1 pfu/cell (pfu = plaque forming units) and harvested 6 days after infection.

Example 3

Production of recombinant hsGC α 1 and hsGC β 1 in Sf9 cells

20 Ten of each recombinant hsGC α 1 and hsGC β 1 baculovirus clones were tested for expression of recombinant protein in Sf9 cells. For this, Sf9 monolayer cell cultures were infected with plaque-purified, recombinant hsGC α 1 or hsGC β 1 baculoviruses, incubated at 27°C for 5 days, harvested with a cell scraper, resuspended in 0.5 ml
 25 lysis buffer (25 mM TEA, pH 7.8, 50 mM NaCl, 1 mM EDTA, 5 mM DTT, 1 µM leupeptin, 0.5 mg/l trypsin inhibitor), and homogenized by sonication ('Sonifier 250', 'standard'-tip, Branson; 15 times, 'duty cycle': 15%, intensity: 1). After centrifugation of the homogenates at 20,000 x g, the supernatant and pellet were analyzed by SDS-PAGE. Three of the hsGC β 1 baculovirus clones and two of the hsGC α 1 baculovirus
 30 clones yielded recombinant protein in amounts that were visible in the insoluble fraction by staining with Coomassie Brilliant Blue R250. Recombinant human sGC α and sGC β (rhsGC α and rhsGC β) migrated with an apparent molecular weight of 79.5 (hsGC α 1) and 68.5 kDa (hsGC β 1), which is very close to the predicted molecular

weights deduced from the amino acid sequence (77.5 and 70.5 kDa, respectively) (representative clones in Figure 9). The baculovirus clones that showed the highest expression of recombinant proteins in the immunoblot were used for the expression of functional heterodimeric hsGC [see examples 4-7].

5

Example 4

Recombinant human sGC in intact insect cells is active and stimulated by NO

10 For the production of functional heterodimeric human sGC, rhsGC α 1 and rhsGC β 1 were coexpressed in Sf9 cells with recombinant baculoviruses. For this, Sf9 monolayer cultures [2.5×10^6 cells/dish, Ø 90 mm; supplements see example 2] were coinfectd with a M.O.I. (multiplicity of infection) of 2 pfu/cell of each recombinant baculovirus (hsGC α 1 and hsGC β 1; both without GST-tag) and cultivated for 48 hours
15 at 27°C. The basal as well as the NO-stimulated activity of the sGC in the cells was determined by measurement of the cGMP content in the cells in the presence of the phosphodiesterase inhibitor IBMX (3-isobutyl-1-methylxanthine).

For the determination of the cGMP content, the culture media was replaced by
20 Krebs-Ringer-buffer (KRB; 119 mM NaCl; 4.74 mM KCl; 2.54 mM CaCl₂; 1.19 mM MgSO₄; 1.19 mM KH₂PO₄; 25 mM NaHCO₃; 10 mM HEPES; pH 7.4; 0.1% BSA) which, in addition, contained 1 mM IBMX. The cells were incubated for one hour at 27°C. Then the cells were washed with ice-cold KRP and harvested in 1 ml ice-cold ethanol (80 %) with a cell scraper. The cells were homogenized by sonication [see
25 Example 3] and centrifuged at 20,000 x g for 20 minutes. The supernatant was dried in a speed-vac and the residue resuspended in 25 mM TEA, pH 7.8. The cGMP content was determined by means of RIA (Biotrend).

The coexpression of rhsGC α 1 and rhsGC β 1 resulted in the formation of functional
30 sGC with basal activity in Sf9 cells (Figure 10): While noninfected Sf9 cells contained approximately 0.1 pmol cGMP/ 10^6 cells (not shown), approximately 20 pmol cGMP/ 10^6 cells was found in rhsGC-expressing cells (Figure 10). This basal activity of recombinant hsGC was increased by an NO donor, SNP (sodium nitroprusside). When the cells were incubated with 10, 100, or 1000 μ M SNP for 2 minutes prior to

the harvest, the cGMP content increased in a concentration-dependent manner by up to 50 fold (Figure 10).

5

Example 5

Recombinant human sGC in insect cell extracts is active and stimulated by NO

The activity of the recombinant hsGC (after expression with the recombinant baculoviruses described above) was not only determined in intact Sf9 cells but also
 10 in Sf9 cell extracts. For the production of such extracts, Sf9 shaking cultures [2×10^6 cells/ml; supplements see Example 2] were coinfectd with a M.O.I. (multiplicity of infection) of 1 pfu/cell of each virus (hsGC α 1 and hsGC β 1; both without GST-tag) and incubated at 27°C. Samples were taken (4 ml) at 0, 24, 48, 72, 96, and 118 hours after infection, the cells sedimented, resuspended in 1 ml lysis buffer and
 15 homogenized by sonication [see Example 3]. The homogenates were centrifuged at 20,000 x g for 15 minutes and the insoluble pellet was resuspended again in lysis buffer. The samples were adjusted to 50% glycerin (vol/vol) and stored at -20°C. The protein concentration was determined spectrophotometrically with the standard method of Bradford (Bradford, 1976). The sGC activity was determined by the
 20 formation of [32 P]cGMP from [α - 32 P]GTP (Schultz and Böhme, 1984). The reactions contained 50 mM TEA (pH 7.4), 3 mM MgCl₂, 3 mM DTT, 1 mM IBMX, 1 mM cGMP, 5 mM creatine phosphate, 0.25 mg/ml creatine kinase, and 500 μ M GTP in a total volume of 100 μ l. After incubation at 37°C for 10 minutes, the reaction was started by simultaneous addition of cell extract and the sGC activators SNP, CO, or YC-1. The
 25 [32 P]cGMP formed was measured as described (Schultz and Böhme, 1984). Basal rhsGC activity (i.e. cGMP formation by rhsGC *without* activation of the enzyme by addition of NO or other activators), mainly found in the soluble Sf9 cell fraction (Figure 11A), reached its maximum 72 hours after infection of the cells and was increased up to 5 fold with 100 μ M SNP (Figure 11A). The pellet fraction did not
 30 contain measurable basal sGC activity at any time point; although in the presence of SNP a low degree of sGC activity was found (Figure 11B).

Example 6

Influence of YC-1 and ODQ on recombinant human sGC

YC-1 (3-(5'-hydroxymethyl-2'-furyl)-1-benzylindazol) and ODQ (1H-[1,2,4]oxadiazol[4,3,-a]chinoxalin-1-on) are substances that were described to specifically influence the activity of sGC. Thus, it was investigated if this also holds true for rhsGC.

After expression with the recombinant baculoviruses (without GST-tag) described above, rhsGC was activated in intact Sf9 cells by YC-1. The NO-potentiating effect was also found: the cGMP content of cells expressing rhsGC was increased 3.4 fold by incubation with 10 μ M YC-1 for 2 minutes (Figure 10A). 100 μ M YC-1 had the same effect (Figure 10A). When the cells were simultaneously treated with YC-1 and 100 μ M SNP, the cGMP levels doubled compared to the cGMP levels after stimulation with SNP alone (Figure 10A). Similar results were obtained with rhsGC in cell extracts.

ODQ is described as a selective inhibitor of NO-stimulated sGC that, however, does not inhibit the basal activity (Garthwaite et al., 1995). In Sf9 cells expressing rhsGC (after expression with the recombinant baculoviruses described above, without GST-tag), ODQ did not have an influence on the basal cGMP levels; the stimulation of rhsGC in intact cells with SNP, however, was inhibited by simultaneous incubation with ODQ (Figure 10B).

Example 7

Extraction of the purified human soluble guanylyl cyclase $\alpha 1/\beta 1$ (hsGC $\alpha 1/\beta 1$)

For the purification of recombinant human hsGC $\alpha 1/\beta 1$ from Sf9 cells, a recombinant baculovirus [see Example 2] was used in which a fusion protein composed of hsGC $\alpha 1$ and attached GST [so-called GST-tag, GST = glutathione-S-transferase from *Schistosoma japonicum*; see Example 2] is formed. Using this GST-tag, which binds to glutathione with high affinity, specific affinity chromatography on glutathione sepharose 4B (Pharmacia, Freiburg, Germany) can be performed. The Sf9 cells coinfecting with hsGC $\alpha 1$ baculoviruses (with GST-tag) and hsGC $\beta 1$ baculoviruses (without GST-tag) were lysed in 25 mM triethanolamine pH 7.8 / 1 mM EDTA / 5 mM DTT / 1 μ M leupeptin / 0.5 μ g/ml trypsin inhibitor / 0.2 mM PMSF (30 min hypotonic

lysis at 4°C). After addition of NaCl (75 mM final concentration), the homogenate was centrifuged at 75,000 x g for 1 hour at 4°C. The supernatant was mixed with the GSH sepharose 4B for 1 hour at room temperature. The glutathione sepharose 4B was then pelleted by centrifugation at 500 x g for 5 minutes and the supernatant removed.

- 5 A 10-fold volume of 50 mM Tris-HCl (pH 8.0) / 150 mM NaCl / 2.5 mM CaCl₂ / 0.1% 2-mercaptoethanol was added to the glutathione sepharose 4B and mixed for 1 minute. The mixture was centrifuged again at 500 x g for 5 minutes. The supernatant was removed and the glutathione sepharose 4B was washed again in the same way. To elute from the sepharose, the hsGC α 1 protein (with the bound hsGC β 1) was
- 10 cleaved by thrombin from the GST-tag, which remained bound to the glutathione sepharose 4B at the specific cleavage site. Digestion with thrombin was performed in 50 mM Tris-HCl (pH 8.0) / 150 mM NaCl / 2.5 mM CaCl₂ / 0.1% 2-mercaptoethanol with 0.25 to 1 units thrombin/ml buffer for 1 or 3 hours at room temperature. The glutathione sepharose 4B (with the GST-tag) was pelleted again by centrifugation at
- 15 500 x g for 5 minutes and the supernatant containing the hsGC α 1/ β 1 was removed. Another elution method was performed by addition of 50 mM Tris-HCl (pH 8.0) / 5 mM reduced glutathione and mixing for 30 minutes at room temperature. In this manner, hsGC α 1/ β 1 with the GST-tag bound was removed from the glutathione sepharose 4B. After centrifugation at 500 x g for 5 minutes, the supernatant
- 20 containing dissolved GST-hsGC α 1/ β 1 was removed.

By the elution with thrombin, a two-fold selectivity is achieved in a single affinity chromatographic step:

- 1.) Only proteins that have an affinity to reduced glutathione are able to bind.
- 25 2.) Of these proteins, only the proteins that are cleaved by thrombin will elute (as cleavage products).

The thrombin can be separated from the sample with a p-aminobenzamidine column to which thrombin binds specifically.

30

Figure 12 shows the specific enrichment of sGC activity after elution from the GSH sepharose 4B with glutathione compared with the activity in the lysate of infected Sf9 cells.

Figure 14 shows the binding of GST-hsGC α 1 to glutathione sepharose 4B and the cleavage of hsGC α 1 from the GST-tag by thrombin in an immunoblot.

Figure 15 shows the purification of coexpressed hsGC α 1 with GST-tag and hsGC β 1 without GST-tag by affinity chromatography on glutathione sepharose 4B in a Coomassie Brilliant Blue R250-stained SDS-polyacrylamide gel. Upon elution with reduced glutathione, only two bands were visible, which correspond to GST-hsGC α 1 (larger product) and hsGC β 1 (smaller product) (detected in an immunoblot). After elution with thrombin (0.25, 0.5, or 1 unit/ml for three hours at room temperature), however, the lower band was identical (hsGC β 1; estimated molecular weight according to the migration in the gel of approximately 70 kDa), whereas the upper band was significantly smaller compared to elution with glutathione (hsGC α 1; estimated molecular weight of approximately 80 kDa) because the GST-tag was cleaved off by use of the thrombin elution. This approximately corresponds to the molecular weights of 77.5 kDa for hsGC α 1 and 70.5 kDa for hsGC β 1 deduced from the amino acid sequences. In contrast to the elution with reduced glutathione, an additional very small band of approximately 25 kDa was visible after the thrombin elution, which is likely thrombin itself. Thrombin can be removed from the eluate by means of an aminobenzamidine sepharose column to which thrombin binds specifically. Additional bands were not detectable in this experiment.

Example 8

Production of polyclonal rabbit antisera to hsGC α 1 and hsGC β 1

Antisera were obtained by immunization of rabbits with synthetic peptides corresponding to sequences from hsGC α 1 (Phe-Thr-Pro-Arg-Ser-Arg-Glu-Glu-Leu-Pro-Pro-Asn-Phe-Pro [Figure 22/SEQ ID NO: 5]; amino acids 634-647) and from hsGC β 1 (Lys-Gly-Lys-Lys-Glu-Pro-Met-Gln-Val-Trp-Phe-Leu-Ser-Arg-Lys-Asn-Thr-Gly-Thr-Glu-Glu-Thr [Figure 23/SEQ ID NO: 6] amino acids 593-614) that were coupled to KLH (keyhole limpet hemocyanin) via an additional C-terminal (α 1) or N-terminal (β 1) cysteine residue. The antisera were affinity-purified with the corresponding peptides coupled to epoxy-activated sepharose (Pharmacia, Freiburg, Germany) according to the manufacturer's instructions.

Example 9

Detection of hsGC α 1 and hsGC β 1 in different human tissues by immunoblotting

5 Human lung tissue was obtained from a tumor-free area of a lung resection, and human cortex and cerebellum were from a normal autopsy. All tissues were immediately frozen in liquid nitrogen and stored at -70°C . The frozen tissues were homogenized in a mortar and double-concentrated, hot SDS stop buffer (130 mM Tris-HCl, pH 6.8 / 16% [v/v] glycerol / 4% [w/v] SDS / 0.025% [w/v] bromphenol blue /
10 6.5% [v/v] 2-mercaptoethanol) was added to the powder. This was incubated at 95°C for 10 minutes and then centrifuged at $20,000 \times g$ for 20 minutes. The supernatant was used for immunoblotting (for antibodies used, see above).

Expression of both subunits (α 1 and β 1) was detected in all three tissues (Figure 13).
15 In contrast, expression could not be detected in kidney, liver, and pancreas (data not shown).

Example 10

Construction of recombinant adenoviral hsGC vectors

20 The cDNAs for hsGC α 1 and hsGC β 1 were isolated from the original plasmid with the restriction enzyme EcoRI as 3.0 kb (hsGC α 1) and 2.4 kb (hsGC β 1) fragments. The fragments were each inserted into the EcoRI restriction sites of the adenoviral transfer plasmid pZS2 (Figure 16), which contains an adenovirus type 5 sequence
25 (Ad5) with a deletion in the E1 region (ΔE1), followed by an expression cassette with a CMV (cytomegalovirus) promoter/enhancer and a unique XbaI restriction site. hsGC α 1-pZS2 and hsGC β 1-pZS2 digested with XbaI were inserted into the XbaI site of the long arm (RR5) of Ad5 (Figure 16). The resulting recombinant adenoviral vectors Ad5CMVhsGC α 1 and Ad5CMVhsGC β 1 are replication deficient because
30 they lack the E1 region. To propagate the viruses, 293 cells that express E1 were infected with these viruses. Viral plaques appeared 12-24 hours after the transfection. Viruses from single plaques were purified according to a standard procedure. Plaques containing recombinant viruses (Ad5CMVhsGC α 1 or Ad5CMVhsGC β 1) were identified by means of PCR analysis. The plaque material

was freeze-thawed three times, incubated at 37°C for 30 minutes in lysis buffer (16.6 mM ammonium sulfate / 67 mM Tris-HCl pH 6.8 / 6.7 mM MgCl₂ / 5 mM 2-mercaptoethanol / 6.7 mM EDTA / 1.7 mM SDS / 50 µg/ml proteinase K), and thereafter heat inactivated for 10 minutes at 85°C. Finally, the DNA was isolated from the lysate with a standard phenol/chloroform extraction and used for PCR analysis.

Example 11

Detection of cGMP formation in EA.hy926 cells after coinfection with the hsGC adenovectors Ad5CMVhsGCα1 and Ad5CMVhsGCβ1

10

Ten 10-cm cell culture dishes with 'EA.hy926' cells were coinfectd with each of the adenovectors Ad5CMVhsGCα1 and Ad5CMVhsGCβ1 at 2×10^{10} pfu (plaque forming units) per dish. After 72 hours, the cells were harvested by adding hypotonic lysis buffer (25 mM triethanolamine pH 7.8 / 1 mM EDTA / 5 mM DTT / 1 µM leupeptin / 0.5 mg/l trypsin inhibitor / 0.2 mM PMSF) and detaching with a cell scraper. The homogenate was centrifuged at 500 x g for 15 minutes and the supernatant was mixed with an equal volume of glycerol and stored at -20°C. The stimulation of hsGC by 100 µM SNP (sodium nitroprusside) was determined by measurement of the basal cGMP level and the cGMP level after treatment with SNP according to the procedure described above (see Example 5). In three samples (A, B, C), a 7-fold to 10.75-fold elevation in the cGMP concentration compared to the basal activity was detectable after SNP stimulation, while no significant elevation was measurable in the control without adenovirus infection (Figure 17).

25

Example 12

Detection of the cGMP formation in ECV 304 and A10 cells after coinfection with the hsGC adenoviruses Ad5CMVhsGCα1 and Ad5CMVhsGCβ1

30

Three 10-cm cell culture dishes with 'ECV 304' cells were coinfectd with 10^9 - 5×10^{10} pfu (plaque forming units) of each of Ad5CMVhsGCα1 and Ad5CMVhsGCβ1. After 72 hours, the cells were harvested by two washes with PBS buffer (phosphate-buffered saline), addition of hypotonic lysis buffer, and then further treated according to the procedure described in Example 11. The samples were stored and the activity was determined (cGMP content in pmol/mg/min) as described in Example 5. A

significant basal activity (without SNP) and a significant maximal activity (with addition of 100 μ M SNP to the assay) was only detectable after the gene transfer of Ad5CMVhsGC α 1 and Ad5CMVhsGC β 1 (5×10^{10} pfu each) (Figure 26). In control experiments without Ad5CMVhsGC α 1 or Ad5CMVhsGC β 1, no significant increase in cGMP formation by SNP was detectable. Qualitatively similar results were obtained in 'A10' vascular smooth muscle cells if these cells were also coinfecting with $10^9 - 5 \times 10^{10}$ pfu Ad5CMVhsGC α 1 and Ad5CMVhsGC β 1. Here, too, a significant basal activity (without SNP) and a significant maximal activity (with addition of 100 μ M SNP to the assay) was only detectable after the gene transfer of Ad5CMVhsGC α 1 and Ad5CMVhsGC β 1 (5×10^{10} pfu of each) (Figure 26). In control experiments without Ad5CMVhsGC α 1 or Ad5CMVhsGC β 1, again no significant increase in cGMP formation by SNP was detectable (Figure 28).

Example 13

15 *Kinetics of cGMP formation in ECV 304 and A10 cells after coinfection with the hsGC adenovectors Ad5CMVhsGC α 1 and Ad5CMVhsGC β 1*

Three 10-cm cell culture dishes containing either 'ECV 304' or 'A10' cells were coinfecting with 5×10^{10} pfu (plaque forming units) Ad5CMVhsGC α 1 and Ad5CMVhsGC β 1. The cells were harvested, and further treatment, storage, and determination of activity was performed as described in Examples 12, 11, and 5. Whereas at day 0 (before the coinfection), no significant increase in cGMP formation by SNP was detectable, 15 days after the gene transfer of Ad5CMVhsGC α 1 and Ad5CMVhsGC β 1, a significant increase in cGMP formation after SNP addition was detectable (Figure 28). Qualitatively similar results were obtained in 'A10' vascular smooth muscle cells if these cells were also coinfecting with 5×10^{10} pfu Ad5CMVhsGC α 1 and Ad5CMVhsGC β 1. Here, 15 days after coinfection, an increase in cGMP formation by SNP was also still detectable (Figure 29). Again, at day 0 (before the coinfection), there was still no significant increase in cGMP formation by SNP. In the same experiments, sGC subunits were detectable after adenoviral gene transfer, but not in noninfected control cells (Figure 30).

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EDITORIAL NOTE

APPLICATION NUMBER - 10274/00

The following Sequence Listing pages 1 to 8 are part of the description. The claims pages follow on pages "32" to "34".

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Vasopharm Biotech GmbH
 (B) STREET: Sedanstrasse 27
 (C) CITY: Würzburg
 (D) STATE: Bayern
 (E) COUNTRY: Deutschland
 (F) POSTAL CODE: 97082

(ii) TITLE OF THE INVENTION: Isolated and purified human soluble
 guanylyl cyclase $\alpha 1/\beta 1$ (hsGC $\alpha 1/\beta 1$)

(iii) NUMBER OF SEQUENCES: 10

(iv) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) DATA TO SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3015 basepairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: doublestrand
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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	CCTAGTGGGT	GGGACTCAGC	TCAGAGTCAG	TTTTCCAGAA	GCAGGTTTCA	GTGCAGAGTT	120
	TTCCTACACT	TTTCCTGCGC	TAGAGCAGCG	AGCAGCCTGG	AACAGACCCA	GGCGGAGGAC	180
	ACCTGTGGGG	GAGGGAGCGC	CTGGAGGAGC	TTAGAGACCC	CAGCCGGGCG	TGATCTCACC	240
	ATGTGCGGAT	TTGCGAGGCG	CGCCCTGGAG	CTGCTAGAGA	TCCGGAAGCA	CAGCCCCGAG	300
45	GTGTGCGAAG	CCACCAAGAC	TGCGGCTCTT	GGAGAAAGCG	TGAGCAGGGG	GCCACCGCGG	360
	TCTCCGCGCC	TGTCTGCACC	CTGTGCGCTG	AGCTGCCTGA	CAGTGACAAT	GACATCCCAG	420
	TTACCAGTGT	CCTTGAATTG	ATAGTGGCTT	CTGTTTGTCA	GTCTCATATA	AGAACTACAG	480
	CTCATCAGGA	GGAGATCGCA	GCAGGGTAAG	AGACACCAAC	ACCATGTTCT	GCACGAAGCT	540
	CAAGGATCTC	AAGATCACAG	GAGAGTGTCC	TTTCTCCTTA	CTGGCACCAG	GTCAAGTTCC	600
50	TAACGAGTCT	TCAGAGGAGG	CAGCAGGAAG	CTCAGAGAGC	TGCAAAGCAA	CCGTGCCCCAT	660
	CTGTCAAGAC	ATTCCTGAGA	AGAACATACA	AGAAAGTCTT	CCTCAAAGAA	AAACCAGTCG	720
	GAGCCGAGTC	TATCTTCACA	CTTTGGCAGA	GAGTATTTGC	AAACTGATTT	TCCCAGAGTT	780
	TGAACGGCTG	AATGTTGCAC	TTCAGAGAAC	ATTGGCAAAG	CACAAAATAA	AAGAAAGCAG	840
	GAAATCTTTG	GAAAGAGAAG	ACTTTGAAAA	AACAATTGCA	GAGCAAGCAG	TTGCAGCAGG	900
55	AGTTCCAGTG	GAGGTTATCA	AAGAATCTCT	TGGTGAAGAG	GTTTTTAAAA	TATGTTACGA	960
	GGAAGATGAA	AACATCCTTG	GGGTGGTTGG	AGGCACCCTT	AAAGATTTTT	TAAACAGCTT	1020
	CAGTACCCTT	CTGAAACAGA	GCAGCCATTG	CCAAGAAGCA	GGAAAAAGGG	GCAGGCTTGA	1080
	GGACGCCTCC	ATTCTATGCC	TGGATAAGGA	GGATGATTTT	CTACATGTTT	ACTACTTCTT	1140
	CCCTAAGAGA	ACCACCTCCC	TGATTCTTCC	CGGCATCATA	AAGGCAGCTG	CTCACGTATT	1200
60	ATATGAAACG	GAAGTGAAG	TGTCGTTAAT	GCCTCCCTGC	TTCCATAATG	ATTGCAGCGA	1260
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	GTCCCCCAGC	AAACCCAGT	CCTCGCTGGT	GATTCCCACA	TCGCTATTCT	GCAAGACATT	1380

	TCCATTCCAT	TTCATGTTTG	ACAAAGATAT	GACAATTCTG	CAATTTGGCA	ATGGCATCAG	1440
	AAGGCTGATG	AACAGGAGAG	ACTTTCAGG	AAAGCCTAAT	TTTGAAGAAT	ACTTTGAAAT	1500
	TCTGACTCCA	AAAATCAACC	AGACGTTTAG	CGGGATCATG	ACTATGTTGA	ATATGCAGTT	1560
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5	CAAAGGCCAA	ATGATCTACA	TTGTTGAATC	CAGTGCAATC	TTGTTTTTGG	GGTCACCCTG	1680
	TGTGGACAGA	TTAGAAGATT	TTACAGGACG	AGGGCTCTAC	CTCTCAGACA	TCCCAATTCA	1740
	CAATGCACTG	AGGGATGTGG	TCTTAATAGG	GGAACAAGCC	CGAGCTCAAG	ATGGCCTGAA	1800
	GAAGAGGCTG	GGGAAGCTGA	AGGCTACCCT	TGAGCAAGCC	CACCAAGCCC	TGGAGGAGGA	1860
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	TGTTTCAGATA	GCGCTGATGG	CCCTGAAGAT	GATGGAGCTC	TCTGATGAAG	TTATGTCTCC	2220
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	CGTTGGAGTT	AAAATGCCCC	GTTACTGTCT	TTTTGGAAAC	AATGTCACTC	TGGCTAACAA	2340
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	CAAAGACTGT	CCTGGTTTCG	TGTTTACCCC	TCGATCAAGG	GAGGAACTTC	CACCAAACCT	2460
	CCCTAGTGAA	ATCCCCGGAA	TCTGCCATTT	TCTGGATGCT	TACCAACAAG	GAACAAACTC	2520
20	AAAACCATGC	TTCCAAAAGA	AAGATGTGGA	AGATGGCAAT	GCCAATTTTT	TAGGCAAAGC	2580
	ATCAGGAATA	GATTAGCAAC	CTATATACCT	ATTTATAAGT	CTTTGGGGTT	TGACTCATTG	2640
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(2) DATA TO SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 695 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase a1 (hsGCa1))

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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	Glu	Glu	Tyr	Phe	Glu	Ile	Leu	Thr	Pro	Lys	Ile	Asn	Gln	Thr	Phe	Ser
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	Ser	Asp	Ile	Pro	Ile	His	Asn	Ala	Leu	Arg	Asp	Val	Val	Leu	Ile	Gly
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	Asp	Glu	Val	Met	Ser	Pro	His	Gly	Glu	Pro	Ile	Lys	Met	Arg	Ile	Gly
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			600					605					610			
60	Ser	Cys	Ser	Val	Pro	Arg	Lys	Ile	Asn	Val	Ser	Pro	Thr	Thr	Tyr	Arg
	615						620					625				
	Leu	Leu	Lys	Asp	Cys	Pro	Gly	Phe	Val	Phe	Thr	Pro	Arg	Ser	Arg	Glu

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2443 basepairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: doublestrand
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCCCCCCCCG	CCGCTGCCGC	CTCTGCCTGG	GTCCCTTCGG	CCGTACCTCT	CGCTGGGGGC	60
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GAAGATGTTT	TTCGTCTTTT	GCCAAGAATC	TGGTTATGAT	ACAATCTTGC	GTGTCCTGGG	360
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CTACCCAGGA	ATGCGTGCAC	CTTCCTTTAG	GTGCACTGAT	GCAGAAAAGG	GCAAAGGACT	480
CATTTTGCAC	TACTACTCAG	AGAGAGAAGG	ACTTCAGGAT	ATTGTCAATT	GAATCATCAA	540
AACAGTGGCA	CAACAAATCC	ATGGCACTGA	AATAGACATG	AAGGTTATTC	AGCAAAGAAA	600
TGAAGAATGT	GATCATACTC	AATTTTTAAT	TGAAGAAAAA	GAGTCAAAAG	AAGAGGATTT	660
TTATGAAGAT	CTTGACAGAT	TTGAAGAAAA	TGGTACCCAG	GAATCACGCA	TCAGCCCATA	720
TACATTCTGC	AAAGCTTTTC	CTTTTCATAT	AATATTTGAC	CGGGACCTAG	TGGTCACTCA	780
GTGTGGCAAT	GCTATATACA	GAGTTCCTCC	CCAGCTCCAG	CCTGGGAATT	GCAGCCTTCT	840
GTCTGTCTTC	TCGCTGGTTC	GTCTCATAT	TGATATTAGT	TTCCATGGGA	TCCTTTCTCA	900
CATCAATACT	GTTTTTGTAT	TGAGAAGCAA	GGAAGGATTG	TTGGATGTGG	AGAAATTAGA	960
ATGTGAGGAT	GAAGTACTG	GGACTGAGAT	CAGCTGCTTA	CGTCTCAAGG	GTCAAATGAT	1020
CTACTTACCT	GAAGCAGATA	GCATACTTTT	TCTATGTTCA	CCAAGTGTC	TGAACCTGGA	1080
CGATTTGACA	AGGAGAGGGC	TGTATCTAAG	TGACATCCCT	CTGCATGATG	CCACGCGCGA	1140
TCTTGTTCTT	TTGGGAGAAC	AATTTAGAGA	GGAATACAAA	CTCACCCAAG	AACTGGAAT	1200
CCTCACTGAC	AGGCTACAGC	TCACGTTAAG	AGCCCTGGAA	GATGAAAAGA	AAAAGACAGA	1260
CACATTGCTG	TATTCTGTCC	TTCTCCGTC	TGTTGCCAAT	GAGCTGCGGC	ACAAGCGTCC	1320
AGTGCCTGCC	AAAAGATATG	ACAATGTGAC	CATCCTCTTT	AGTGGCATTG	TGGGCTTCAA	1380
TGCTTTCTGT	AGCAAGCATG	CATCTGGAGA	AGGAGCCATG	AAGATCGTCA	ACCTCCTCAA	1440
CGACCTCTAC	ACCAGATTTG	ACACACTGAC	TGATTCCCGG	AAAAACCCAT	TTGTTTATAA	1500
GGTGGAGACT	GTTGGTGACA	AGTATATGAC	AGTGAGTGGT	TTACCAGAGC	CATGCATTCA	1560
CCATGCACGA	TCCATCTGCC	ACCTGGCCTT	GGACATGATG	GAAATTGCTG	GCCAGGTTCA	1620
AGTAGATGGT	GAATCTGTTT	AGATAACAAT	AGGGATACAC	ACTGGAGAGG	TAGTTACAGG	1680
TGTCATAGGA	CAGCGGATGC	CTCGATACTG	TCTTTTTGGG	AATACTGTCA	ACCTCACAAG	1740
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TCTTATGTCT	CCAGAAAAAT	CAGATCCACA	ATTCCACTTG	GAGCACAGAG	GCCCAGTGTC	1860
CTGAAGGGC	AAAAAAGAAC	CAATGCAAGT	TTGGTTTCTA	TCCAGAAAAA	ATACAGGAAC	1920
AGAGGAAACA	AAGCAGGATG	ATGACTGAAT	CTTGATTAT	GGGGTGAAGA	GGAGTAGAGA	1980
CTAGGTTCCA	GTTTTCTCCT	AACACGTGCC	AAGCCCAGGA	GCAGTTCTTC	CCTATGGATA	2040
CAGATTTTCT	TTTGTCTCTG	TCCATTACCC	CAAGACTTTC	TTCTAGATAT	ATCTCTCACT	2100
ATCCGTTATT	CAACCTTAGC	TCTGCTTTCT	ATTACTTTTT	AGGCTTTAGT	ATATTATCTA	2160
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TTACCTAACA TGGTGATCTG CAAGTAGTAG GCACCCAATA AATATTTGTT GAATTTAGTT      2280
AAATGAAACT GAACAGTGTT TGGCCATGTG TATATTTATA TCATGTTTAC CAAATCTGTT      2340
TAGTGTTCCA CATATATGTA TATGTATATT TTAATGACTA TAATGTAATA AAGTTTATAT      2400
CATGTTGGTG TATATCATTa TAGAAATCAT TTTCTAAAGG AGT                        2443

```

5

(2) DATA TO SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 619 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase b1 (hsGCB1))

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

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

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Gly Leu Tyr Leu Ser Asp Ile Pro Leu His Asp Ala Thr Arg Asp Leu
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 Val Leu Leu Gly Glu Gln Phe Arg Glu Glu Tyr Lys Leu Thr Gln Glu
 355 360 365
 5 Leu Glu Ile Leu Thr Asp Arg Leu Gln Leu Thr Leu Arg Ala Leu Glu
 370 375 380
 Asp Glu Lys Lys Lys Thr Asp Thr Leu Leu Tyr Ser Val Leu Pro Pro
 385 390 395 400
 10 Ser Val Ala Asn Glu Leu Arg His Lys Arg Pro Val Pro Ala Lys Arg
 405 410 415
 Tyr Asp Asn Val Thr Ile Leu Phe Ser Gly Ile Val Gly Phe Asn Ala
 420 425 430
 Phe Cys Ser Lys His Ala Ser Gly Glu Gly Ala Met Lys Ile Val Asn
 435 440 445
 15 Leu Leu Asn Asp Leu Tyr Thr Arg Phe Asp Thr Leu Thr Asp Ser Arg
 450 455 460
 Lys Asn Pro Phe Val Tyr Lys Val Glu Thr Val Gly Asp Lys Tyr Met
 465 470 475 480
 20 Thr Val Ser Gly Leu Pro Glu Pro Cys Ile His His Ala Arg Ser Ile
 485 490 495
 Cys His Leu Ala Leu Asp Met Met Glu Ile Ala Gly Gln Val Gln Val
 500 505 510
 Asp Gly Glu Ser Val Gln Ile Thr Ile Gly Ile His Thr Gly Glu Val
 515 520 525
 25 Val Thr Gly Val Ile Gly Gln Arg Met Pro Arg Tyr Cys Leu Phe Gly
 530 535 540
 Asn Thr Val Asn Leu Thr Ser Arg Thr Glu Thr Thr Gly Glu Lys Gly
 545 550 555 560
 Lys Ile Asn Val Ser Glu Tyr Thr Tyr Arg Cys Leu Met Ser Pro Glu
 565 570 575
 30 Asn Ser Asp Pro Gln Phe His Leu Glu His Arg Gly Pro Val Ser Met
 580 585 590
 Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn
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 610 615

(2) DATA TO SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (amino acids 634-647 of hsGCa1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Phe Thr Pro Arg Ser Arg Glu Glu Leu Pro Pro Asn Phe Pro
 5 10

(2) DATA TO SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (amino acids 593-614 of hsGCb1)

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 6:

5 Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn
 5 10 15
 Thr Gly Thr Glu Glu Thr
 20

10 (2) DATA TO SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 basepairs

(B) TYPE: nucleotide

15 (C) STRANDEDNESS: single strans

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

20 (iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

25 (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 7:

AAAAGGATCC ATGTTCTGCA CGAAGCTC

28

30

2) DATA TO SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 basepairs

35 (B) TYPE: nucleotide

(C) STRANDEDNESS: single strans

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

40

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

45

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 8:

ATTATGGAAG CAGGGAGG

18

50

2) DATA TO SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 basepairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single strans

(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: genomic DNA

60

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

5 (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 9:

AAAAGGATCC ATGTACGGAT TTGTGAAT

28

10 2) DATA TO SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 basepairs

(B) TYPE: nucleotide

15 (C) STRANDEDNESS: single strans

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

20 (iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

25 (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 10:

ATGCGTGATT CCTGGGTACC

20

THE INVENTION IS DEFINED BY THE FOLLOWING CLAIMS:

1. Isolated human soluble guanylyl cyclase $\alpha 1$ (hsGC $\alpha 1$; SEQ ID NO: 2)/ $\beta 1$ (hsGC $\beta 1$; SEQ ID NO: 4) purified to apparent homogeneity.
2. A method for the production of $\alpha 1$ (hsGC $\alpha 1$; SEQ ID NO:2) and $\beta 1$ (hsGC $\beta 1$; SEQ ID NO:4) subunits of human soluble guanylyl cyclase comprising the expression in prokaryotic or eukaryotic host cells of expression vectors containing the DNA sequence of hsGC $\alpha 1$ and hsGC $\beta 1$ and obtaining the subunits.
3. A method according to claim 2, wherein the step of obtaining the subunits comprises a lysis of the cells, the affinity chromatography of the cell lysate, and the subsequent elution of the subunits.
4. A method according to claim 2 or 3, wherein the expression vector contains at least one additional DNA sequence coding for a domain for the specific affinity chromatography (affinity tag) with appended protease cleavage site.
5. A method according to claim 4, wherein the expression vector contains the DNA sequence for hsGC $\alpha 1$ with affinity tag, the DNA sequence for hsGC $\beta 1$ with affinity tag, the DNA sequence for hsGC $\alpha 1$ with affinity tag, and the DNA sequence for hsGC $\beta 1$ the DNA sequence for hsGC $\beta 1$ with affinity tag and the DNA sequence for hsGC $\alpha 1$ or the DNA sequence hsGC $\alpha 1$ with affinity tag and the DNA sequence for hsGC $\beta 1$ with affinity tag.
6. A method for producing human soluble guanylyl cyclase $\alpha 1$ (hsGC $\alpha 1$; SEQ ID NO: 2)/ $\beta 1$ (hsGC $\beta 1$; SEQ ID NO: 4) comprising the separate expression in prokaryotic or eukaryotic host cells of an expression vector containing the DNA sequence for hsGC $\alpha 1$ or hsGC $\beta 1$, extraction of the subunits, and reconstitution of subunits hsGC $\alpha 1$ and hsGC $\beta 1$ to form the dimeric guanylyl cyclase $\alpha 1/\beta 1$ (hsGC $\alpha 1/\beta 1$).

7. A method according to claim 6, wherein the step for the purification of the subunits consists of a separate lysis of cells containing hsGC α 1 or hsGC β 1, the separate affinity chromatography of the cell lysates, and the subsequent elution of the subunits.
8. A method for producing human soluble guanylyl cyclase α 1 (hsGC α 1; SEQ ID NO: 2)/ β 1 (hsGC β 1; SEQ ID NO: 4) consisting of the coexpression of the DNA sequences of hsGC α 1 and hsGC β 1 in prokaryotic or eukaryotic host cells, a lysis of the cells containing hsGC α 1 and hsGC β 1, and affinity chromatography and subsequent elution of hsGC α 1/ β 1.
9. Use of a nucleotide sequence encoding the hsGC α 1(SEQ ID NO: 2) and/or hsGC β 1 (SEQ ID NO:4) subunits of human soluble guanylyl cyclase α 1/ β 1 for somatic gene therapy.
10. Use according to claim 9, wherein vectors or a mixture of vectors contain the nucleotide sequence of human soluble guanylyl cyclase α 1 (hsGC α 1) and/or human soluble guanylyl cyclase β 1 (hsGC β 1).
11. Use according to claim 9 or 10 for the prevention and therapy of atherosclerosis and its complications, of restenosis, ischemia (infarction), peripheral arterial occlusive diseases, and arterial hypertension as well as for the prevention of atherosclerosis in patients with risk factors, transient ischemic attacks, cerebral ischemia, stroke (Apoplex), coronary heart disease, status post coronary bypass grafting, carotid stenosis, heart insufficiency and liver dysfunction, and as a supplement to therapy with sGC activators, sGC-sensitizing substances, NO donors, or phosphodiesterase inhibitors.
12. Use according to any one of claims 9 to 11, wherein the somatic gene transfer is carried out with endothelial cells, vascular smooth muscle cells, neointimal cells, fibroblasts, or other vascular cells or blood particles (platelets, leukocytes, and others), or liver.

13. Antibodies against human soluble guanylyl cyclase $\alpha 1$ (hsGC $\alpha 1$; SEQ ID NO: 2)/ $\beta 1$ (hsGC $\beta 1$; SEQ ID NO: 4) obtained by immunization of a mammal with the peptide fragment Phe-Thr-Pro-Arg-Ser-Arg-Glu-Glu-Leu-Pro-Pro-Asn-Phe-Pro, or parts thereof, or immunogenic peptide fragments that overlap with this fragment, or obtained by immunization of a mammal with the peptide fragment Lys-Gly-Lys-Lys-Glu-Pro-Met-Gln-Val-Trp-Phe-Leu-Ser-Arg-Lys-Asn-Thr-Gly-Thr-Glu-Glu-Thr or immunogenic fragment or immunogenic peptide fragments that overlap with this fragment and isolation of the antibodies.
14. Isolated human soluble guanylyl cyclase $\alpha 1/\beta 1$ according to claim 1, substantially as hereinbefore described with reference to the examples.
15. A method according to claim 2, substantially as hereinbefore described with reference to examples 1 to 7.
16. A method of somatic gene therapy comprising introducing the nucleotide sequence encoding the hsGC $\alpha 1$ (SEQ ID NO: 2) and/or hsGC $\beta 1$ (SEQ ID NO: 4) subunits of human soluble guanylyl cyclase $\alpha 1/\beta 1$ into cells requiring treatment.

Vasopharm Biotech GmbH
By its Registered Patent Attorneys
Freehills Carter Smith Beadle

16 May 2003

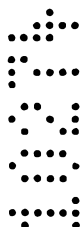


Fig. 1

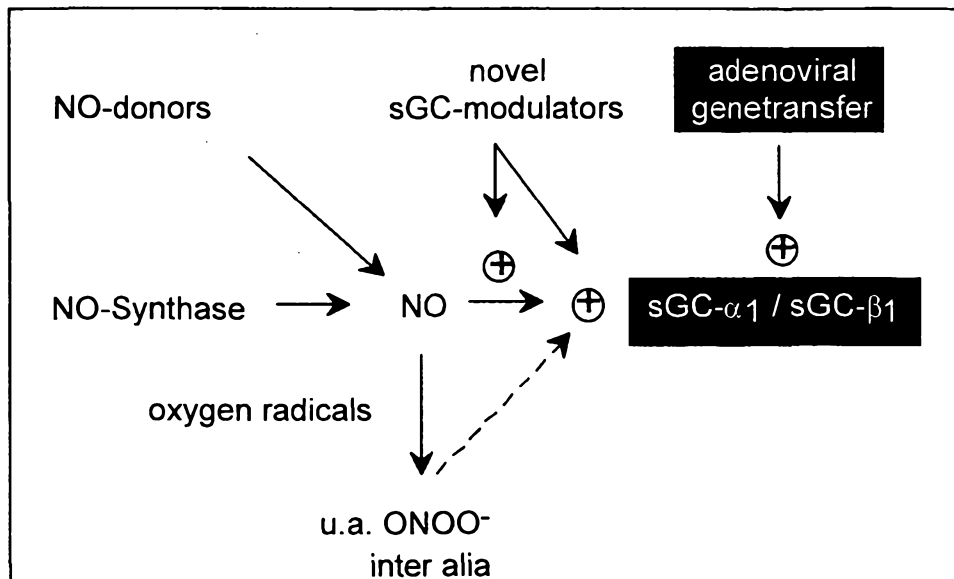
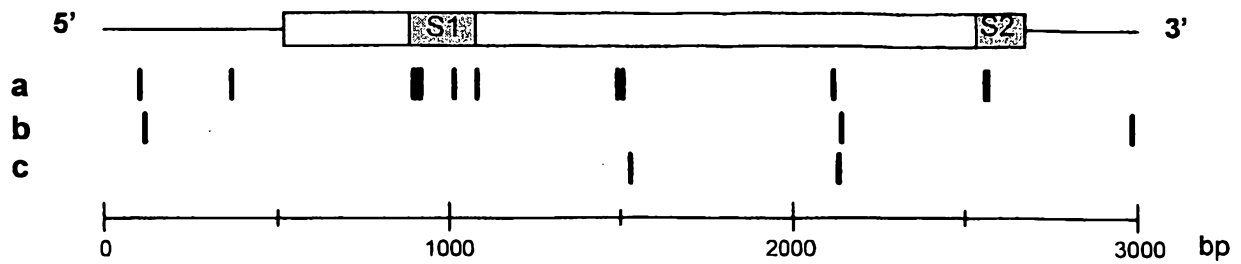


Figure 3

**a: nucleotide insertions**

C95, C367, T891, G900, T903, G913, T1006, G1074, G1487, A1488, A1489, G2108, G2555, T2560

b: nucleotide deletions

T between G111 and T112, T between T2128 and G2129, T between G2975 and T2976

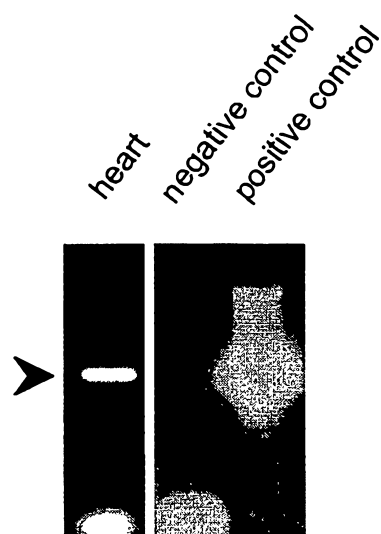
c: nucleotide exchanges

C1525>G, G2125>A

Figure 4

A

PCR
determination
of hsGC α 1



B

PCR
determination
of hsGC β 1

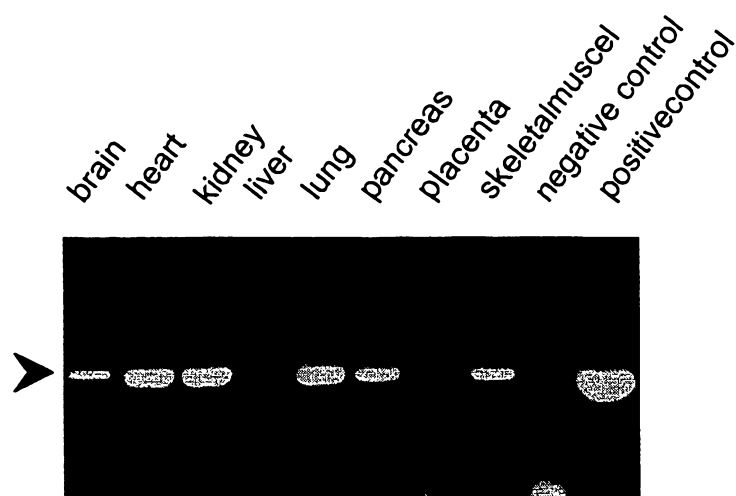
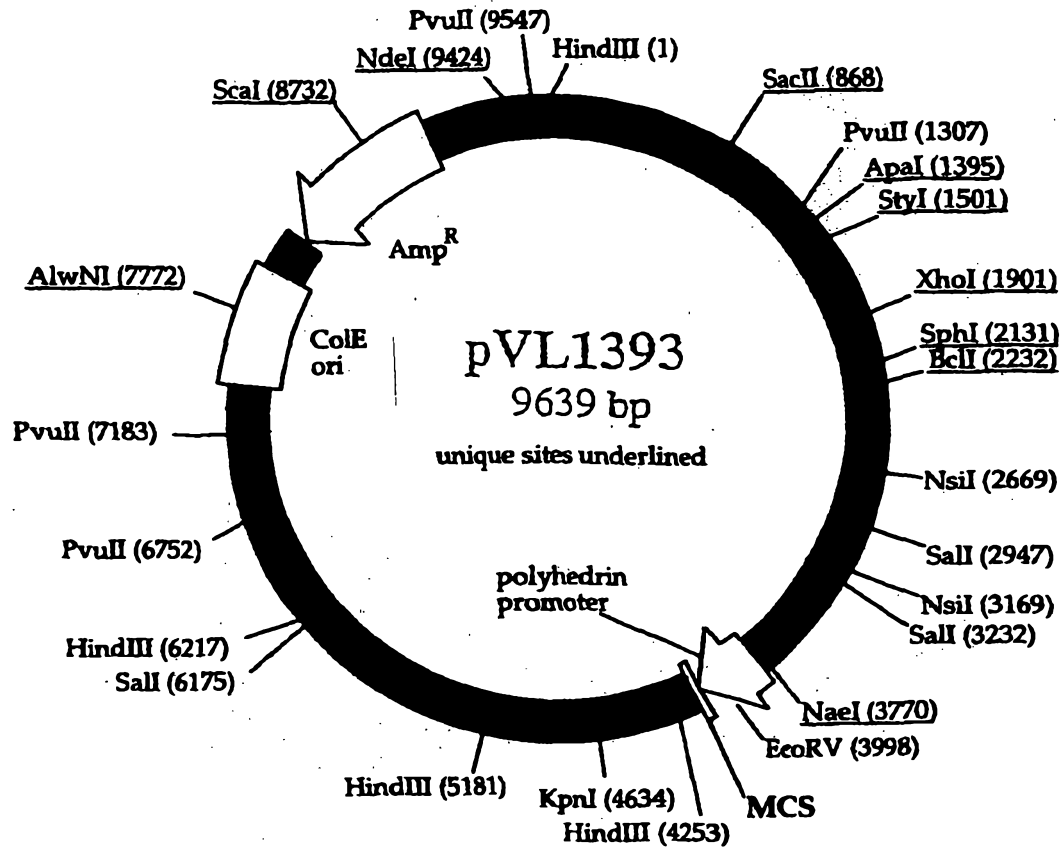


Figure 5

pVL1393 Baculovirus Transfer Vector



multiple cloning site (MCS) of pVL1393 with the unique restriction sites

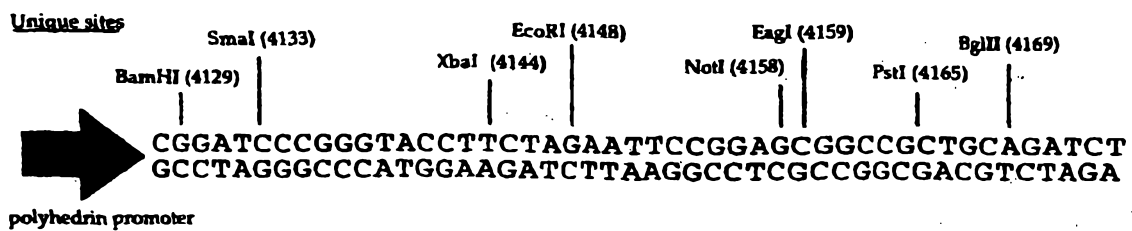
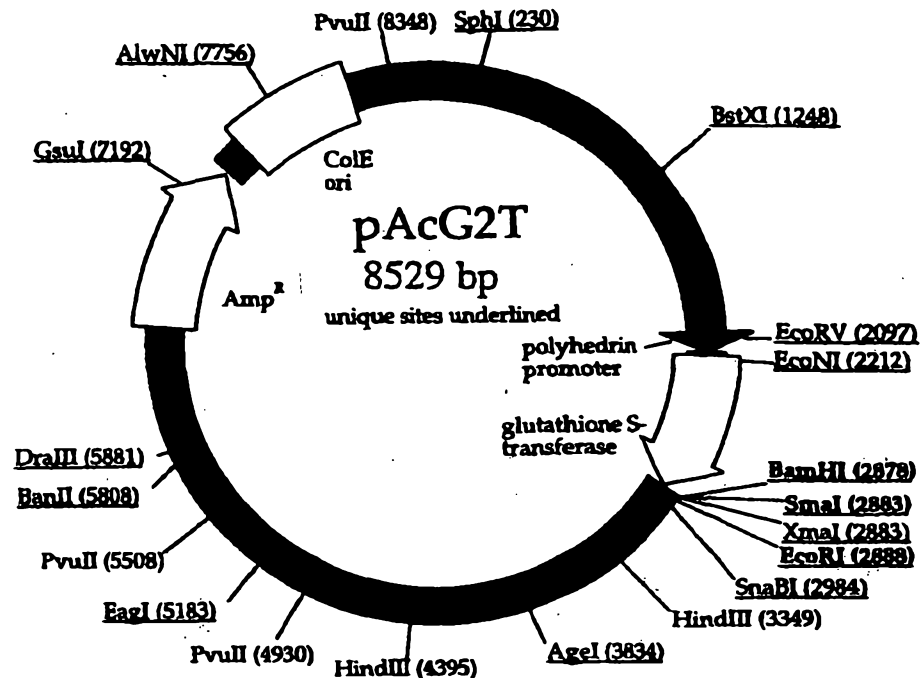


Figure 6

pAcG2T Baculovirus Transfer Vector



multiple cloning site (MCS) of pAcG2T downstream of glutathione-S-transferase sequence (GST) with the thrombin cleavage site and the unique restriction sites

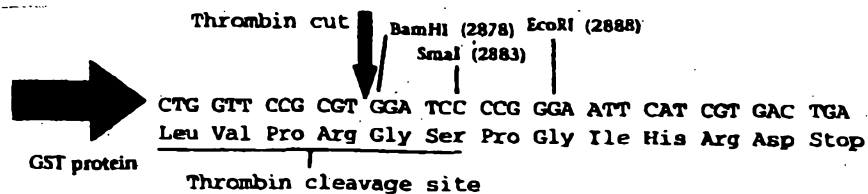
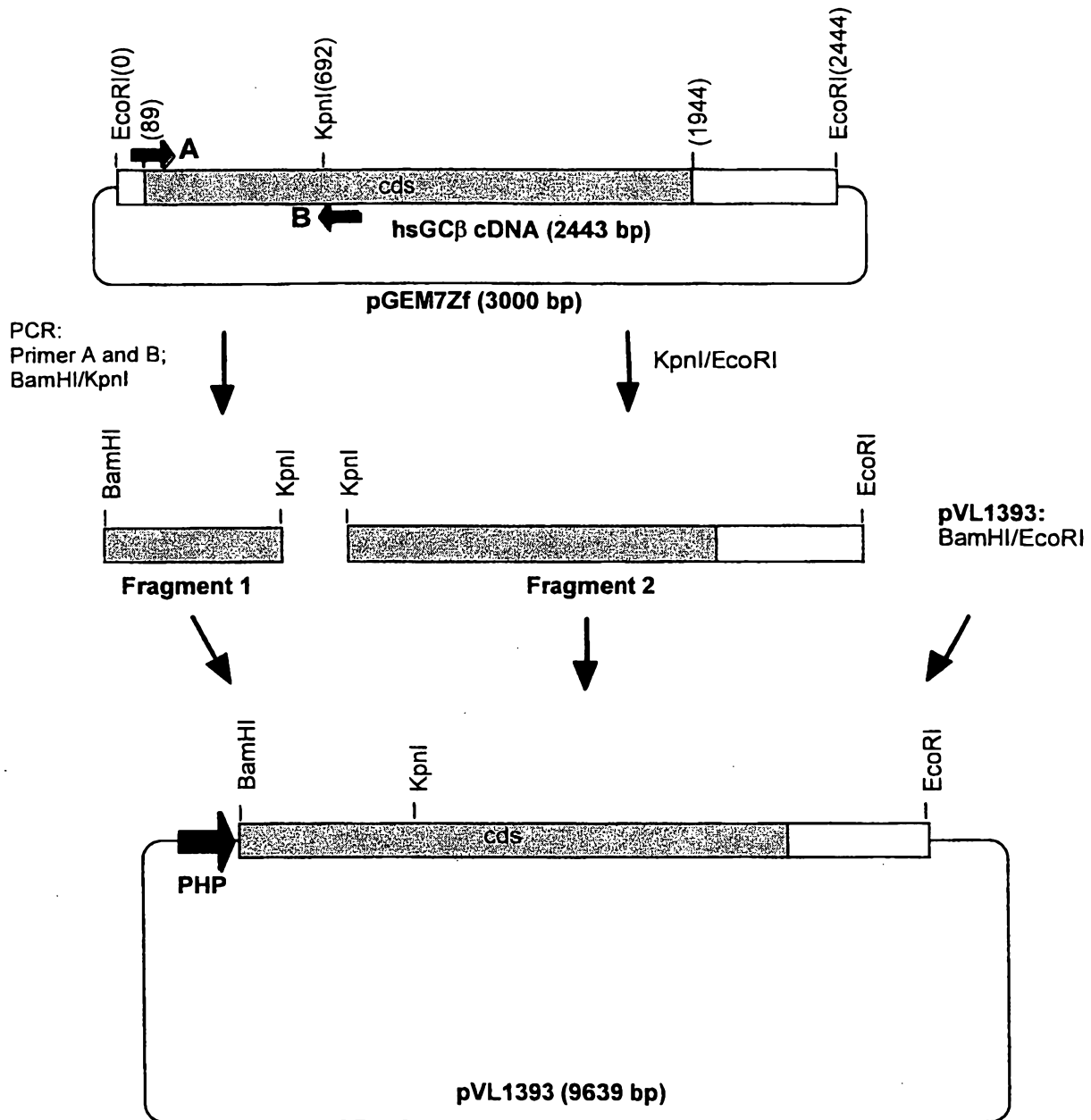
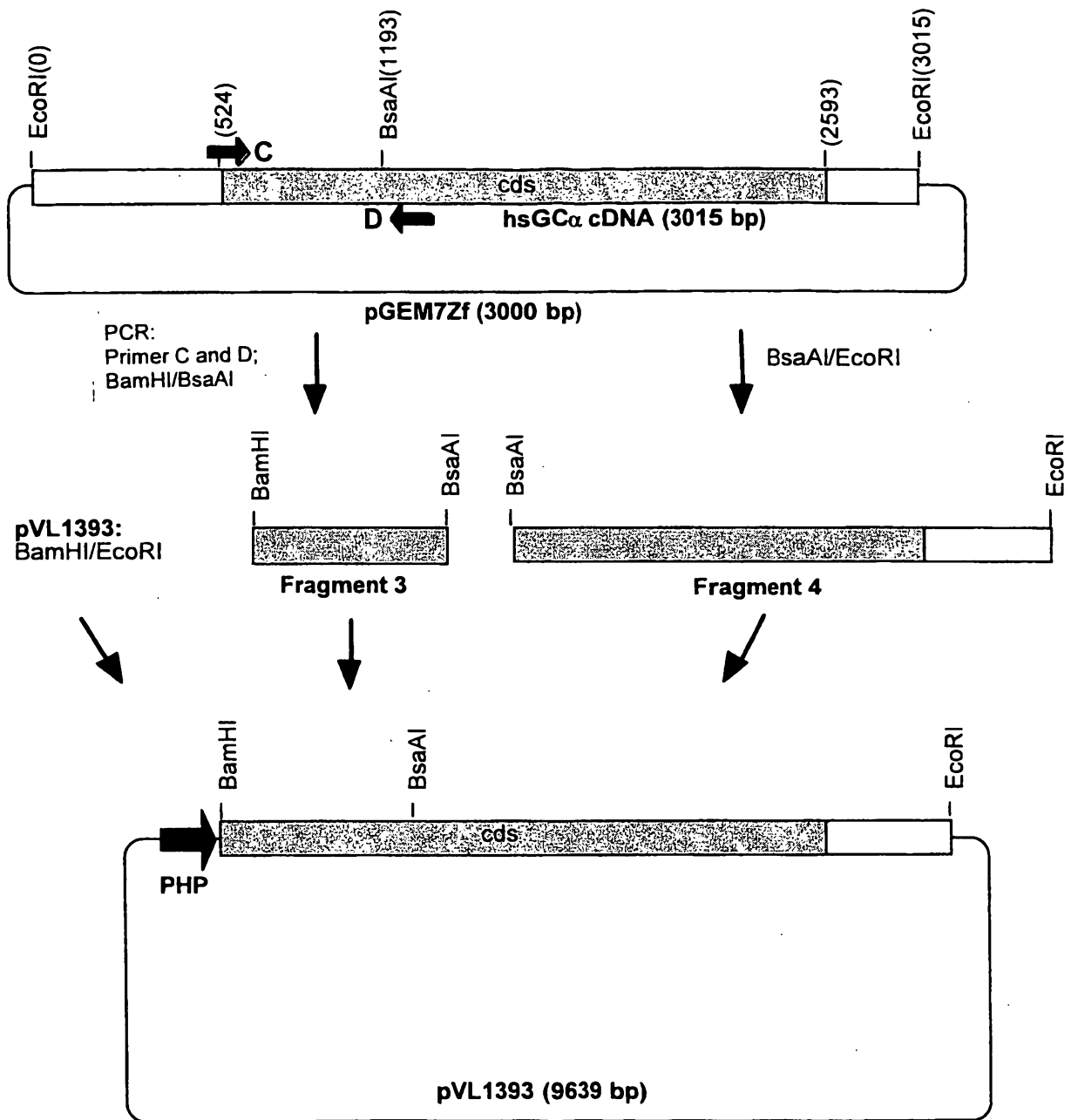


Figure 7: Cloning of hsGC β in pVL1393

Primer: A 5' AAAA **GGATCC** ATGTACGGATTTGTGAAT 3'
BamHI (89) (116)

B 3' **CCATGG** GTCCTTAGTGCGTA 5'
(692) KpnI (711)

Figure 8: Cloning of hsGC α in pVL1393

Primer: C 5' AAAA GGATCC ATGTTCTGCACGAAGCTC 3'
 BamHI (524) (541)

D 3' GGAGGGACGAAGGTATTA 5'
 (1232) (1249)

Figure 9

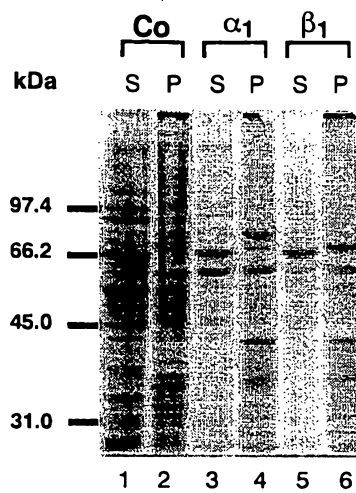
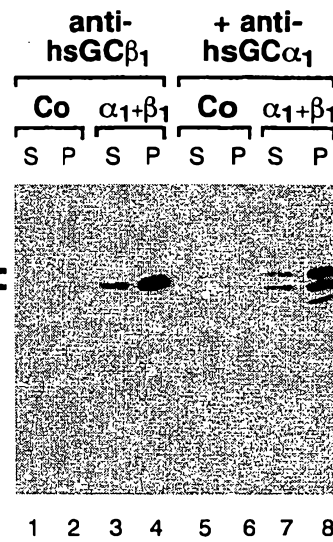
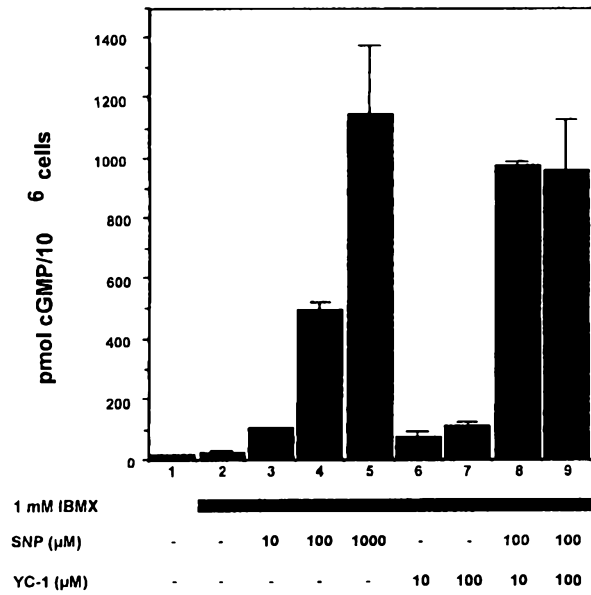
A SDS-PAGE**B Immunoblot**

Fig. 10

A



B

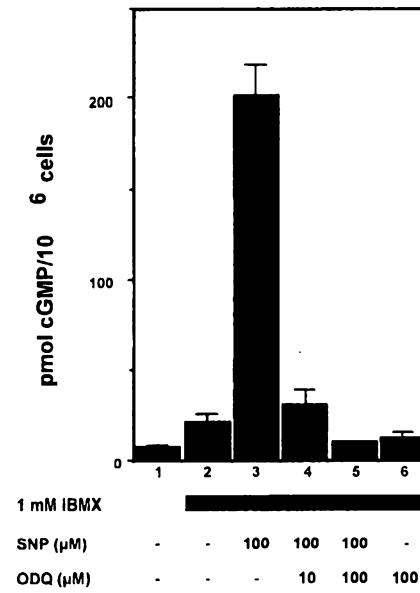


Fig. 11

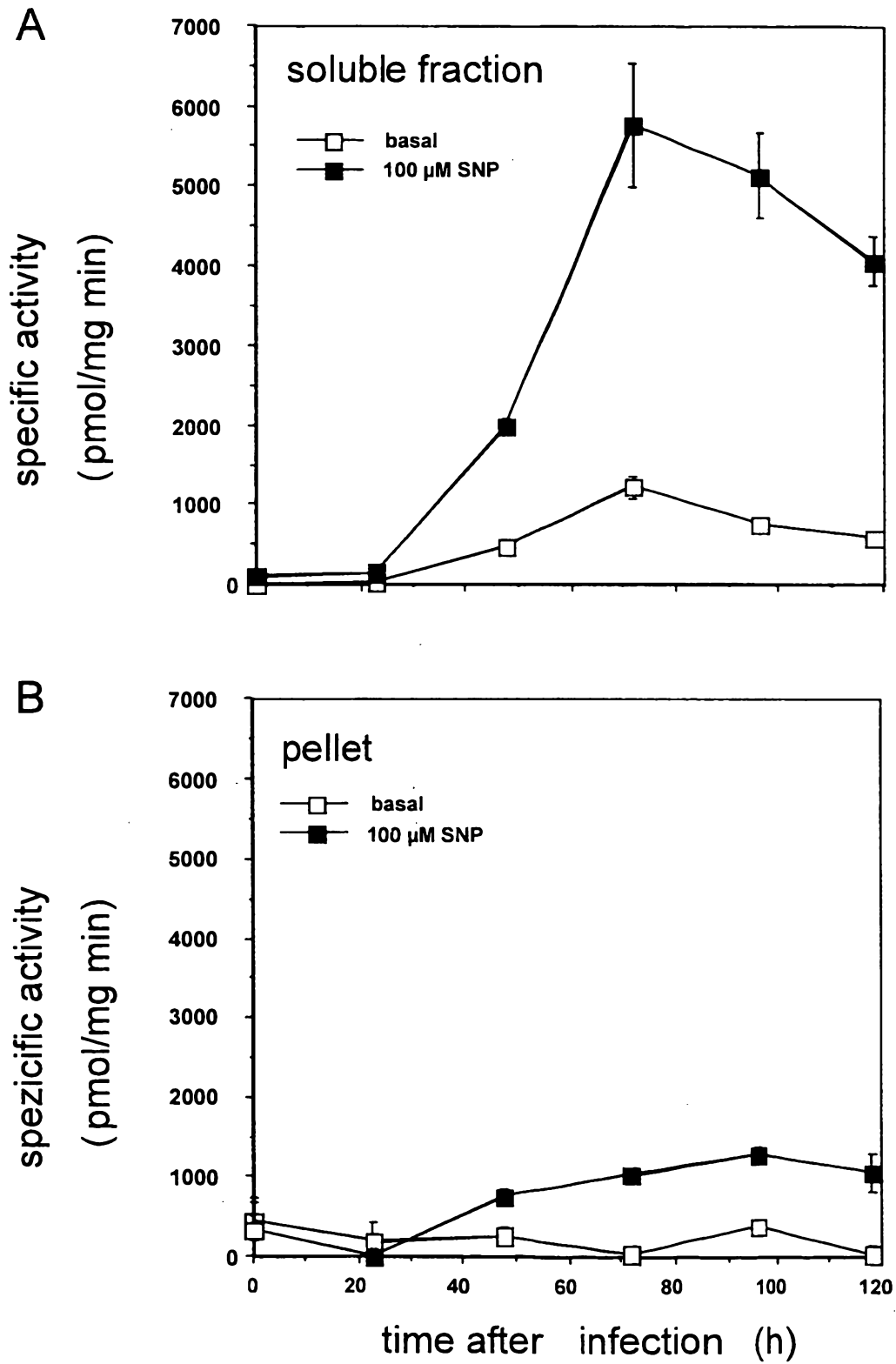


Figure 12: Purification of GST-hsGCalpha1/beta1 on GSH-Sepharose 4B

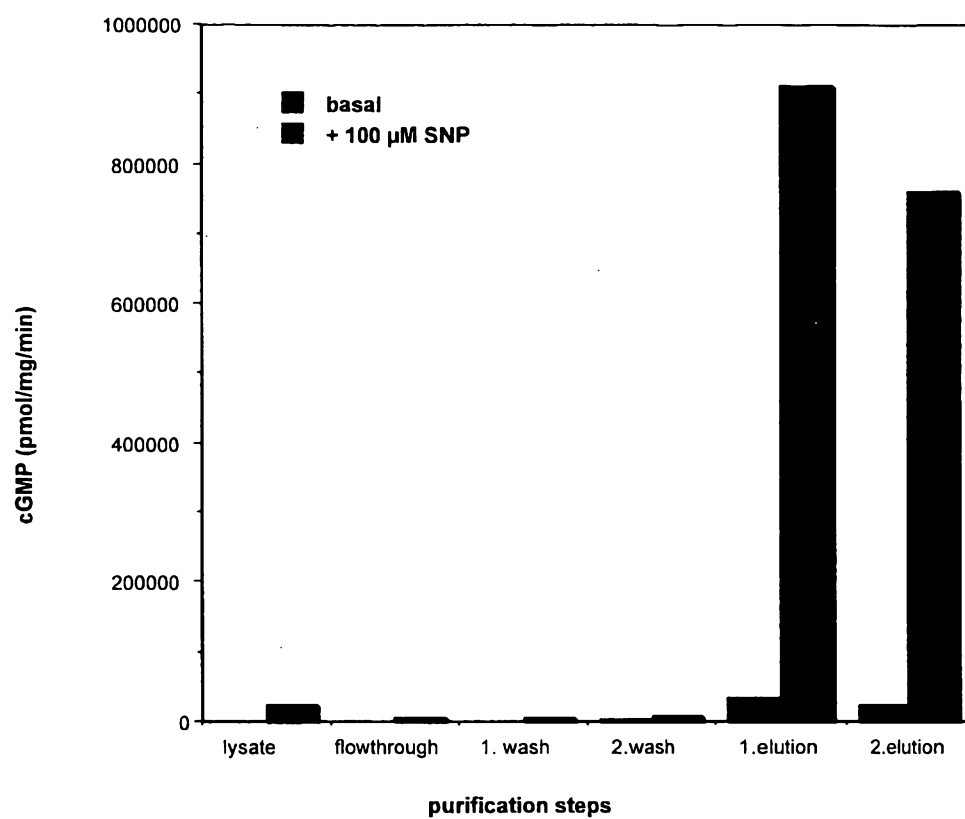


Figure 13

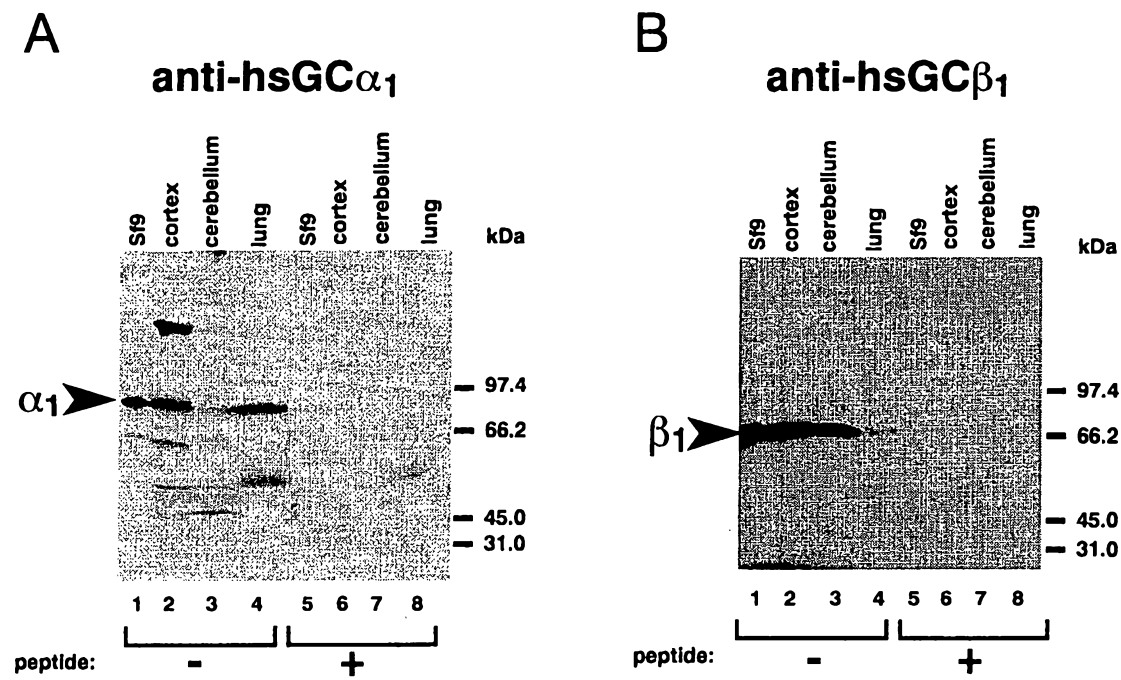


Figure 14

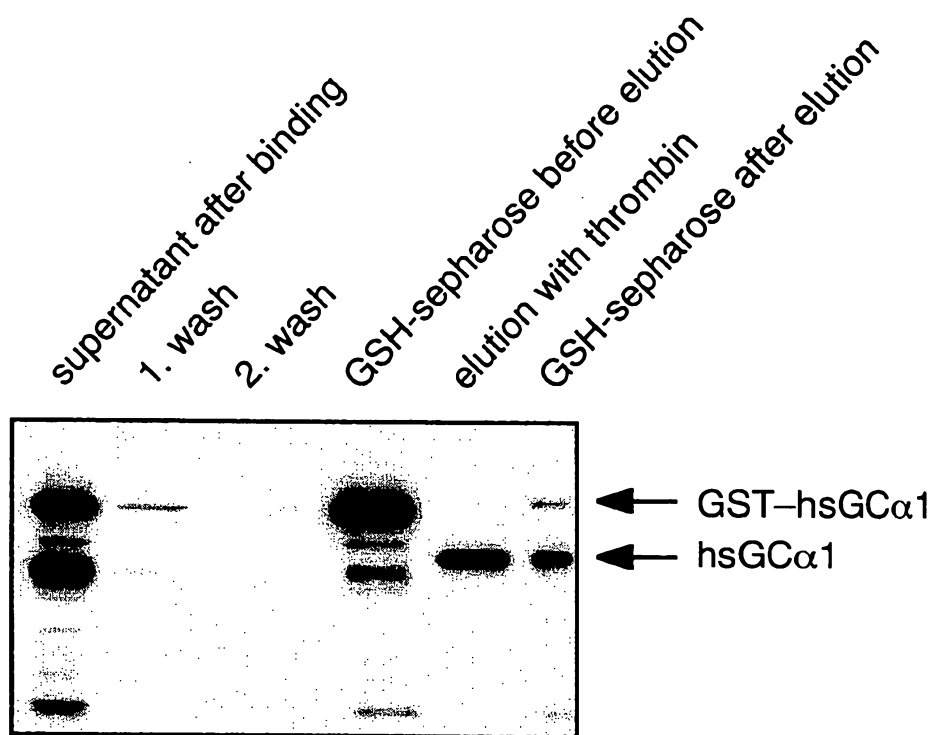


Figure 15: Purification of hsGC $\alpha 1/\beta 1$ in a Coomassie stained SDS polyacrylamide gel

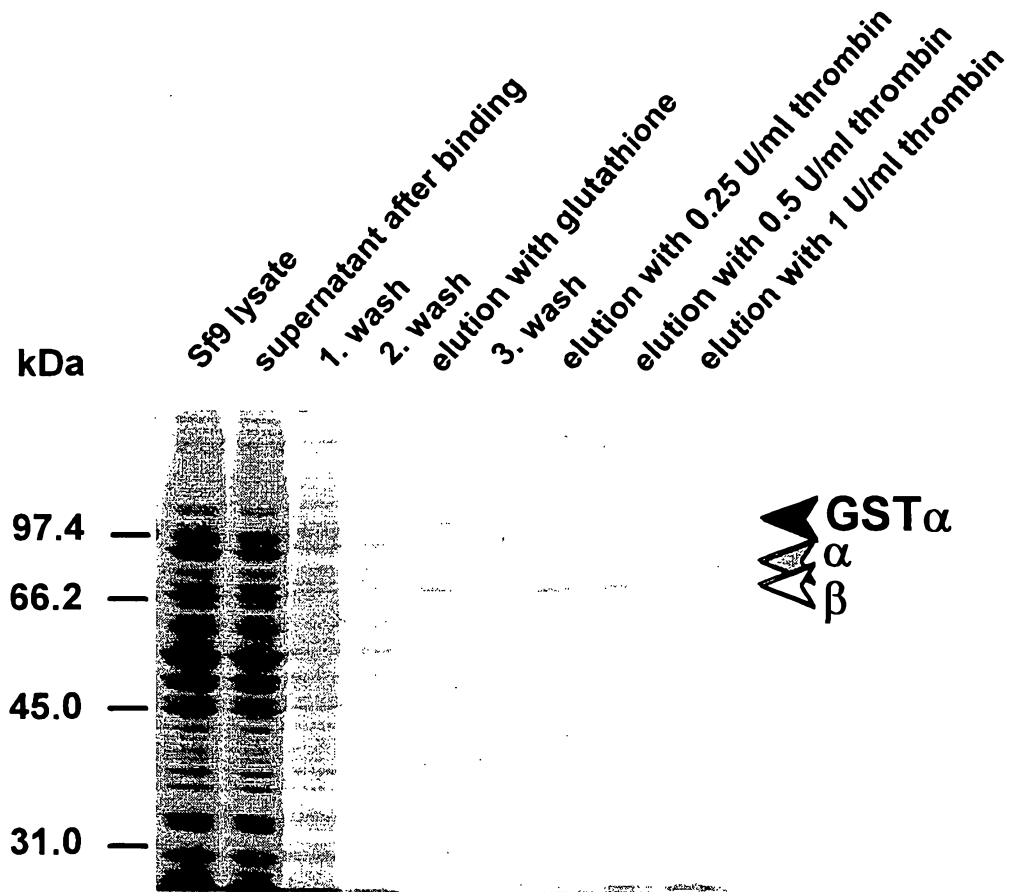


Figure 16: Construction of the hsGC-adenovectors

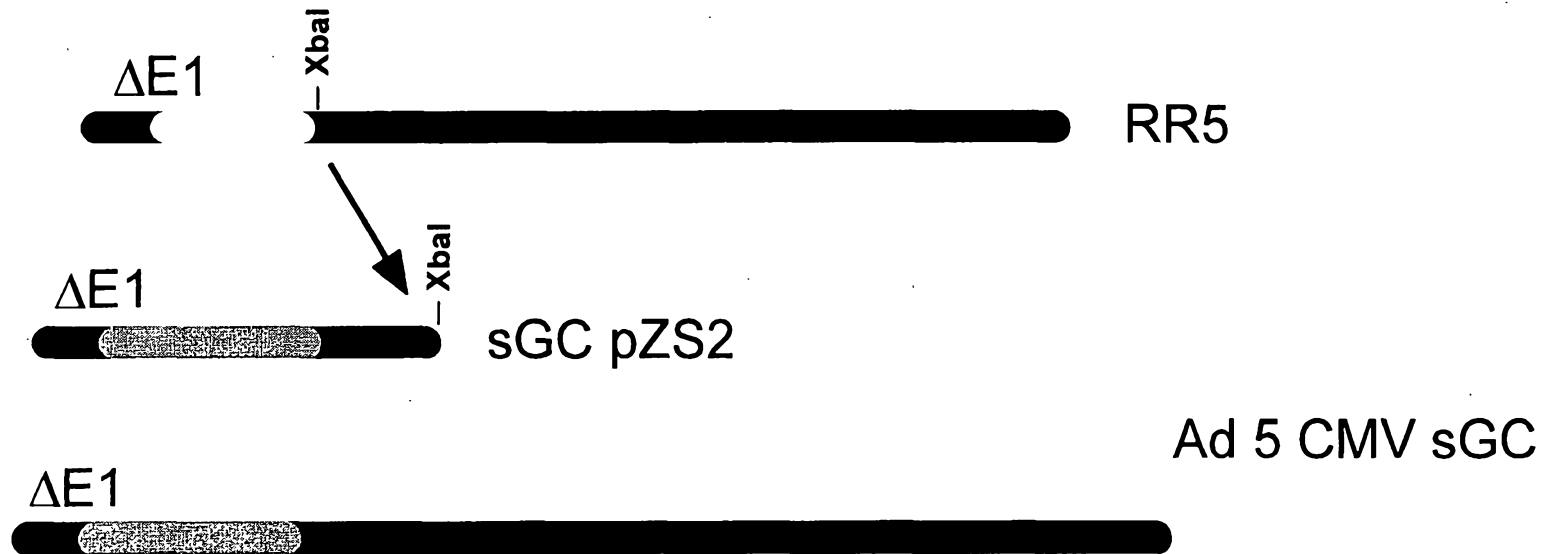


Figure 17:
Expression of human sGC in
adenovirus-infected EA.hy926
cells

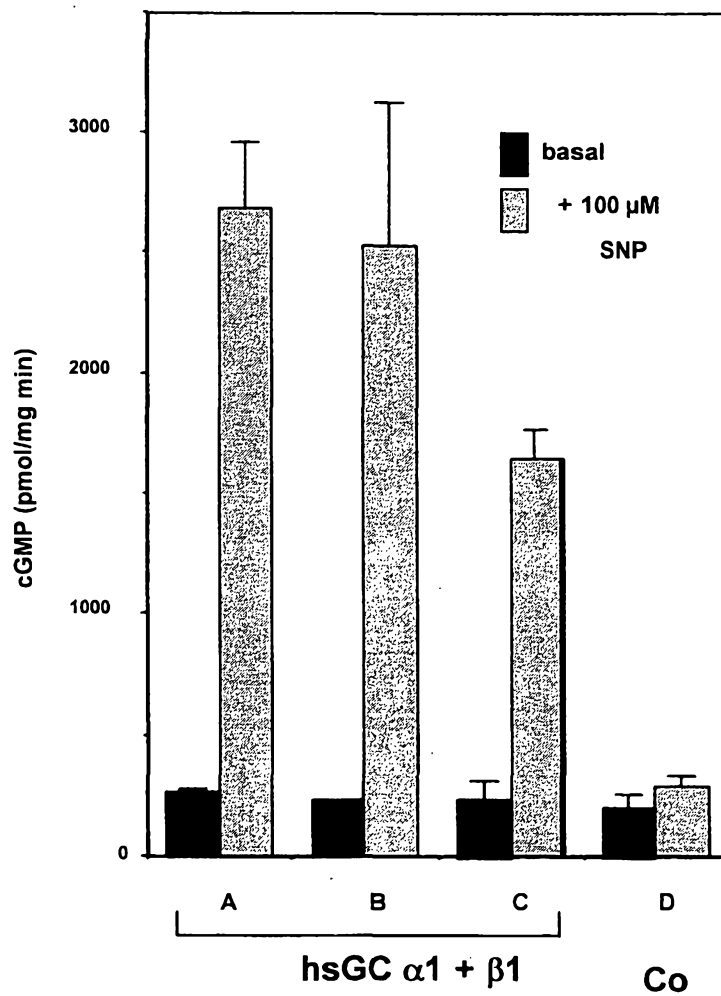


Figure 18

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GACCATTGGC GATGCCTATT GTGTAGCTGG GGGATTACAC AAAGAGAGTG ATACTCATGC
TGTTTCAGATA GCGCTGATGG CCCTGAAGAT GATGGAGCTC TCTGATGAAG TTATGTCTCC
CCATGGAGAA CCTATCAAGA TGCGAATTGG ACTGCACTCT GGATCAGTTT TTGCTGGCGT
CGTTGGAGTT AAAATGCCCC GTTACTGTCT TTTTGGAAAC AATGTCACTC TGGCTAACAA
ATTTGAGTCC TGCAGTGTAC CACGAAAAAT CAATGTCAGC CCAACAACCT ACAGATTACT
CAAAGACTGT CTGGTTTCG TGTTTACCCC TCGATCAAGG GAGGAACTTC CACCAAACTT
CCCTAGTGAA ATCCCCGGAA TCTGCCATTT TCTGGATGCT TACCAACAAG GAACAAACTC
AAAACCATGC TTCCAAAAGA AAGATGTGGA AGATGGCAAT GCCAATTTTT TAGGCAAAAGC
ATCAGGAATA GATTAGCAAC CTATATACCT ATTTATAAGT CTTTGGGGTT TGACTCATTG
AAGATGTGTA GAGCCTCTGA AAGCACTTTA GGGATTGTAG ATGGCTAACA AGCAGTATTA
AAATTTCAAG AGCCAAGTCA CAATCTTTCT CCTGTTTAA ACAGCAAAAT GTACTCACTT
CAGTACTTCA GCTCTTCAAG AAAAAAAAAA AAACCTTAAA AAGCTACTTT TGTGGGAGTA
TTTCTATTAT ATAACCAGCA CTTACTACCT GTACTCAAAA TTCAGCACCT TGTACATATA
TCAGATAATT GTAGTCAATT GTACAAACTG ATGGAGTCAC CTGCAATCTC ATATCCTGGT
GGAATGCCAT GGTATTATAA GTGTGTTTGT GATAGTGTCTG TCAAAAAAAAAA AAAAAAAAAA
AAAAAAAAAA AAAAA

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Figure 19

Met Phe Cys Thr Lys Leu Lys Asp Leu Lys Ile Thr Gly Glu Cys Pro
 Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu
 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln
 Asp Ile Pro Glu Lys Asn Ile Gln Glu Ser Leu Pro Gln Arg Lys Thr
 Ser Arg Ser Arg Val Tyr Leu His Thr Leu Ala Glu Ser Ile Cys Lys
 Leu Ile Phe Pro Glu Phe Glu Arg Leu Asn Val Ala Leu Gln Arg Thr
 Leu Ala Lys His Lys Ile Lys Glu Ser Arg Lys Ser Leu Glu Arg Glu
 Asp Phe Glu Lys Thr Ile Ala Glu Gln Ala Val Ala Ala Gly Val Pro
 Val Glu Val Ile Lys Glu Ser Leu Gly Glu Glu Val Phe Lys Ile Cys
 Tyr Glu Glu Asp Glu Asn Ile Leu Gly Val Val Gly Gly Thr Leu Lys
 Asp Phe Leu Asn Ser Phe Ser Thr Leu Leu Lys Gln Ser Ser His Cys
 Gln Glu Ala Gly Lys Arg Gly Arg Leu Glu Asp Ala Ser Ile Leu Cys
 Leu Asp Lys Glu Asp Asp Phe Leu His Val Tyr Tyr Phe Phe Pro Lys
 Arg Thr Thr Ser Leu Ile Leu Pro Gly Ile Ile Lys Ala Ala Ala His
 Val Leu Tyr Glu Thr Glu Val Glu Val Ser Leu Met Pro Pro Cys Phe
 His Asn Asp Cys Ser Glu Phe Val Asn Gln Pro Tyr Leu Leu Tyr Ser
 Val His Met Lys Ser Thr Lys Pro Ser Leu Ser Pro Ser Lys Pro Gln
 Ser Ser Leu Val Ile Pro Thr Ser Leu Phe Cys Lys Thr Phe Pro Phe
 His Phe Met Phe Asp Lys Asp Met Thr Ile Leu Gln Phe Gly Asn Gly
 Ile Arg Arg Leu Met Asn Arg Arg Asp Phe Gln Gly Lys Pro Asn Phe
 Glu Glu Tyr Phe Glu Ile Leu Thr Pro Lys Ile Asn Gln Thr Phe Ser
 Gly Ile Met Thr Met Leu Asn Met Gln Phe Val Val Arg Val Arg Arg
 Trp Asp Asn Ser Val Lys Lys Ser Ser Arg Val Met Asp Leu Lys Gly
 Gln Met Ile Tyr Ile Val Glu Ser Ser Ala Ile Leu Phe Leu Gly Ser
 Pro Cys Val Asp Arg Leu Glu Asp Phe Thr Gly Arg Gly Leu Tyr Leu
 Ser Asp Ile Pro Ile His Asn Ala Leu Arg Asp Val Val Leu Ile Gly
 Glu Gln Ala Arg Ala Gln Asp Gly Leu Lys Lys Arg Leu Gly Lys Leu
 Lys Ala Thr Leu Glu Gln Ala His Gln Ala Leu Glu Glu Glu Lys Lys
 Lys Thr Val Asp Leu Leu Cys Ser Ile Phe Pro Cys Glu Val Ala Gln
 Gln Leu Trp Gln Gly Gln Val Val Gln Ala Lys Lys Phe Ser Asn Val
 Thr Met Leu Phe Ser Asp Ile Val Gly Phe Thr Ala Ile Cys Ser Gln
 Cys Ser Pro Leu Gln Val Ile Thr Met Leu Asn Ala Leu Tyr Thr Arg
 Phe Asp Gln Gln Cys Gly Glu Leu Asp Val Tyr Lys Val Glu Thr Ile
 Gly Asp Ala Tyr Cys Val Ala Gly Gly Leu His Lys Glu Ser Asp Thr
 His Ala Val Gln Ile Ala Leu Met Ala Leu Lys Met Met Glu Leu Ser
 Asp Glu Val Met Ser Pro His Gly Glu Pro Ile Lys Met Arg Ile Gly
 Leu His Ser Gly Ser Val Phe Ala Gly Val Val Gly Val Lys Met Pro
 Arg Tyr Cys Leu Phe Gly Asn Asn Val Thr Leu Ala Asn Lys Phe Glu
 Ser Cys Ser Val Pro Arg Lys Ile Asn Val Ser Pro Thr Thr Tyr Arg
 Leu Leu Lys Asp Cys Pro Gly Phe Val Phe Thr Pro Arg Ser Arg Glu
 Glu Leu Pro Pro Asn Phe Pro Ser Glu Ile Pro Gly Ile Cys His Phe
 Leu Asp Ala Tyr Gln Gln Gly Thr Asn Ser Lys Pro Cys Phe Gln Lys
 Lys Asp Val Glu Asp Gly Asn Ala Asn Phe Leu Gly Lys Ala Ser Gly
 Ile Asp End

Figure 20

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CCCCCCCCCG CCGCTGCCGC CTCTGCCTGG GTCCCTTCGG CCGTACCTCT GCGTGGGGGC
TGCTCCCCCG GCTCCCGGTG CAGACACCAT GTACGGATT TGTGAATCACG CCCTGGAGTT
GCTGGTGATC CGCAATTACG GCCCCGAGGT GTGGGAAGAC ATCAAAAAAG AGGCACAGTT
AGATGAAGAA GGACAGTTTC TTGTCAGAAT AATATATGAT GACTCCAAAA CTTATGATTT
GGTTGCTGCT GCAAGCAAAG TCCTCAATCT CAATGCTGGA GAAATCCTCC AAATGTTTGG
GAAGATGTTT TTCGTCTTTT GCCAAGAATC TGGTTATGAT ACAATCTTGC GTGTCCTGGG
CTCTAATGTC AGAGAATTTT TACAGAACCT TGATGCTCTG CACGACCACC TTGCTACCAT
CTACCCAGGA ATGCGTGCAC CTTCTTTAG GTGCACTGAT GCAGAAAAGG GCAAAGGACT
CATTTTGCAC TACTACTCAG AGAGAGAAGG ACTTCAGGAT ATTGTCATTG GAATCATCAA
AACAGTGGCA CAACAAATCC ATGGCACTGA AATAGACATG AAGGTTATTC AGCAAAGAAA
TGAAGAATGT GATCATACTC AATTTTAAAT TGAAGAAAAA GAGTCAAAAG AAGAGGATTT
TTATGAAGAT CTTGACAGAT TTGAAGAAAA TGGTACCCAG GAATCACGCA TCAGCCCATA
TACATTCTGC AAAGCTTTTC CTTTTCATAT AATATTTGAC CGGGACCTAG TGGTCACTCA
GTGTGGCAAT GCTATATACA GAGTCTCCC CCAGCTCCAG CCTGGGAATT GCAGCCTTCT
GTCTGTCTTC TCGCTGGTTC GTCCTCATAT TGATATTAGT TTCCATGGGA TCCTTTCTCA
CATCAATACT GTTTTGTAT TGAGAAGCAA GGAAGGATTG TTGGATGTGG AGAAATTAGA
ATGTGAGGAT GAACTGACTG GGACTGAGAT CAGCTGCTTA CGTCTCAAGG GTCAAATGAT
CTACTTACCT GAAGCAGATA GCATACTTTT TCTATGTTCA CCAAGTGTCA TGAACCTGGA
CGATTTGACA AGGAGAGGGC TGTATCTAAG TGACATCCCT CTGCATGATG CCACGCGCGA
TCTTGTCTT TTGGGAGAAC AATTTAGAGA GGAATACAAA CTCACCCAAG AACTGGAAAT
CCTCACTGAC AGGCTACAGC TCACGTAAAG AGCCCTGGAA GATGAAAAGA AAAAGACAGA
CACATTGCTG TATTCTGTCC TTCTCCGTC GTTGCCAAT GAGCTGCGGC ACAAGCGTCC
AGTGCCTGCC AAAAGATATG ACAATGTGAC CATCCTCTTT AGTGGCATTG TGGGCTTCAA
TGCTTTCTGT AGCAAGCATG CATCTGGAGA AGGAGCCATG AAGATCGTCA ACCTCCTCAA
CGACCTCTAC ACCAGATTTG ACACACTGAC TGATTCCCGG AAAAACCCAT TTGTTTATAA
GGTGGAGACT GTTGGTGACA AGTATATGAC AGTGAGTGGT TTACCAGAGC CATGCATTCA
CCATGCACGA TCCATCTGCC ACCTGGCCTT GGACATGATG GAAATTGCTG GCCAGGTTCA
AGTAGATGGT GAATCTGTTC AGATAACAAT AGGGATACAC ACTGGAGAGG TAGTTACAGG
TGTCATAGGA CAGCGGATGC CTCGATACTG TCTTTTGGG AATACTGTCA ACCTCACAAG
CCGAACAGAA ACCACAGGAG AAAAGGGAAA AATAAATGTG TCTGAATATA CATACAGATG
TCTTATGTCT CCAGAAAATT CAGATCCACA ATTCCACTTG GAGCACAGAG GCCCAGTGTC
CATGAAGGGC AAAAAAGAAC CAATGCAAGT TTGGTTTCTA TCCAGAAAAA ATACAGGAAC
AGAGGAAACA AAGCAGGATG ATGACTGAAT CTTGGATTAT GGGGTGAAGA GGAGTACAGA
CTAGGTTCCA GTTTCTCCT AACACGTGCC AAGCCCAGGA GCAGTTCTTC CCTATGGATA
CAGATTTTCT TTTGTCCTTG TCCATTACCC CAAGACTTTC TTCTAGATAT ATCTCTCACT
ATCCGTTATT CAACCTTAGC TCTGCTTTCT ATTACTTTTT AGGCTTTAGT ATATTATCTA
AAGTTTGGCT TTTGATGTGG ATGATGTGAG CTTCATGTGT CTTAAAATCT ACTACAAGCA
TTACCTAACA TGGTGATCTG CAAGTAGTAG GCACCCAATA AATATTTGTT GAATTTAGTT
AAATGAAACT GAACAGTGTT TGGCCATGTG TATATTTATA TCATGTTTAC CAAATCTGTT
TAGTGTTCCT CATATATGTA TATGTATATT TTAATGACTA TAATGTAATA AGTTTATAT
CATGTTGGTG TATATCATTA TAGAAATCAT TTTCTAAAGG AGT

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Figure 21

Met Tyr Gly Phe Val Asn His Ala Leu Glu Leu Leu Val Ile Arg Asn
 Tyr Gly Pro Glu Val Trp Glu Asp Ile Lys Lys Glu Ala Gln Leu Asp
 Glu Glu Gly Gln Phe Leu Val Arg Ile Ile Tyr Asp Asp Ser Lys Thr
 Tyr Asp Leu Val Ala Ala Ala Ser Lys Val Leu Asn Leu Asn Ala Gly
 Glu Ile Leu Gln Met Phe Gly Lys Met Phe Phe Val Phe Cys Gln Glu
 Ser Gly Tyr Asp Thr Ile Leu Arg Val Leu Gly Ser Asn Val Arg Glu
 Phe Leu Gln Asn Leu Asp Ala Leu His Asp His Leu Ala Thr Ile Tyr
 Pro Gly Met Arg Ala Pro Ser Phe Arg Cys Thr Asp Ala Glu Lys Gly
 Lys Gly Leu Ile Leu His Tyr Tyr Ser Glu Arg Glu Gly Leu Gln Asp
 Ile Val Ile Gly Ile Ile Lys Thr Val Ala Gln Gln Ile His Gly Thr
 Glu Ile Asp Met Lys Val Ile Gln Gln Arg Asn Glu Glu Cys Asp His
 Thr Gln Phe Leu Ile Glu Glu Lys Glu Ser Lys Glu Glu Asp Phe Tyr
 Glu Asp Leu Asp Arg Phe Glu Glu Asn Gly Thr Gln Glu Ser Arg Ile
 Ser Pro Tyr Thr Phe Cys Lys Ala Phe Pro Phe His Ile Ile Phe Asp
 Arg Asp Leu Val Val Thr Gln Cys Gly Asn Ala Ile Tyr Arg Val Leu
 Pro Gln Leu Gln Pro Gly Asn Cys Ser Leu Leu Ser Val Phe Ser Leu
 Val Arg Pro His Ile Asp Ile Ser Phe His Gly Ile Leu Ser His Ile
 Asn Thr Val Phe Val Leu Arg Ser Lys Glu Gly Leu Leu Asp Val Glu
 Lys Leu Glu Cys Glu Asp Glu Leu Thr Gly Thr Glu Ile Ser Cys Leu
 Arg Leu Lys Gly Gln Met Ile Tyr Leu Pro Glu Ala Asp Ser Ile Leu
 Phe Leu Cys Ser Pro Ser Val Met Asn Leu Asp Asp Leu Thr Arg Arg
 Gly Leu Tyr Leu Ser Asp Ile Pro Leu His Asp Ala Thr Arg Asp Leu
 Val Leu Leu Gly Glu Gln Phe Arg Glu Glu Tyr Lys Leu Thr Gln Glu
 Leu Glu Ile Leu Thr Asp Arg Leu Gln Leu Thr Leu Arg Ala Leu Glu
 Asp Glu Lys Lys Lys Thr Asp Thr Leu Leu Tyr Ser Val Leu Pro Pro
 Ser Val Ala Asn Glu Leu Arg His Lys Arg Pro Val Pro Ala Lys Arg
 Tyr Asp Asn Val Thr Ile Leu Phe Ser Gly Ile Val Gly Phe Asn Ala
 Phe Cys Ser Lys His Ala Ser Gly Glu Gly Ala Met Lys Ile Val Asn
 Leu Leu Asn Asp Leu Tyr Thr Arg Phe Asp Thr Leu Thr Asp Ser Arg
 Lys Asn Pro Phe Val Tyr Lys Val Glu Thr Val Gly Asp Lys Tyr Met
 Thr Val Ser Gly Leu Pro Glu Pro Cys Ile His His Ala Arg Ser Ile
 Cys His Leu Ala Leu Asp Met Met Glu Ile Ala Gly Gln Val Gln Val
 Asp Gly Glu Ser Val Gln Ile Thr Ile Gly Ile His Thr Gly Glu Val
 Val Thr Gly Val Ile Gly Gln Arg Met Pro Arg Tyr Cys Leu Phe Gly
 Asn Thr Val Asn Leu Thr Ser Arg Thr Glu Thr Thr Gly Glu Lys Gly
 Lys Ile Asn Val Ser Glu Tyr Thr Tyr Arg Cys Leu Met Ser Pro Glu
 Asn Ser Asp Pro Gln Phe His Leu Glu His Arg Gly Pro Val Ser Met
 Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn
 Thr Gly Thr Glu Glu Thr Lys Gln Asp Asp Asp end

Figure 22

Phe Thr Pro Arg Ser Arg Glu Glu Leu Pro Pro Asn Phe Pro

Figure 23

Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn
Thr Gly Thr Glu Glu Thr

Figure 24

upper primer

AAAAGGATCC ATGTTCTGCA CGAAGCTC

lower primer

ATTATGGAAG CAGGGAGG

Figure 25

upper primer

AAAAGGATCC ATGTACGGAT TTGTGAAT

lower primer

ATGCGTGATT CCTGGGTACC

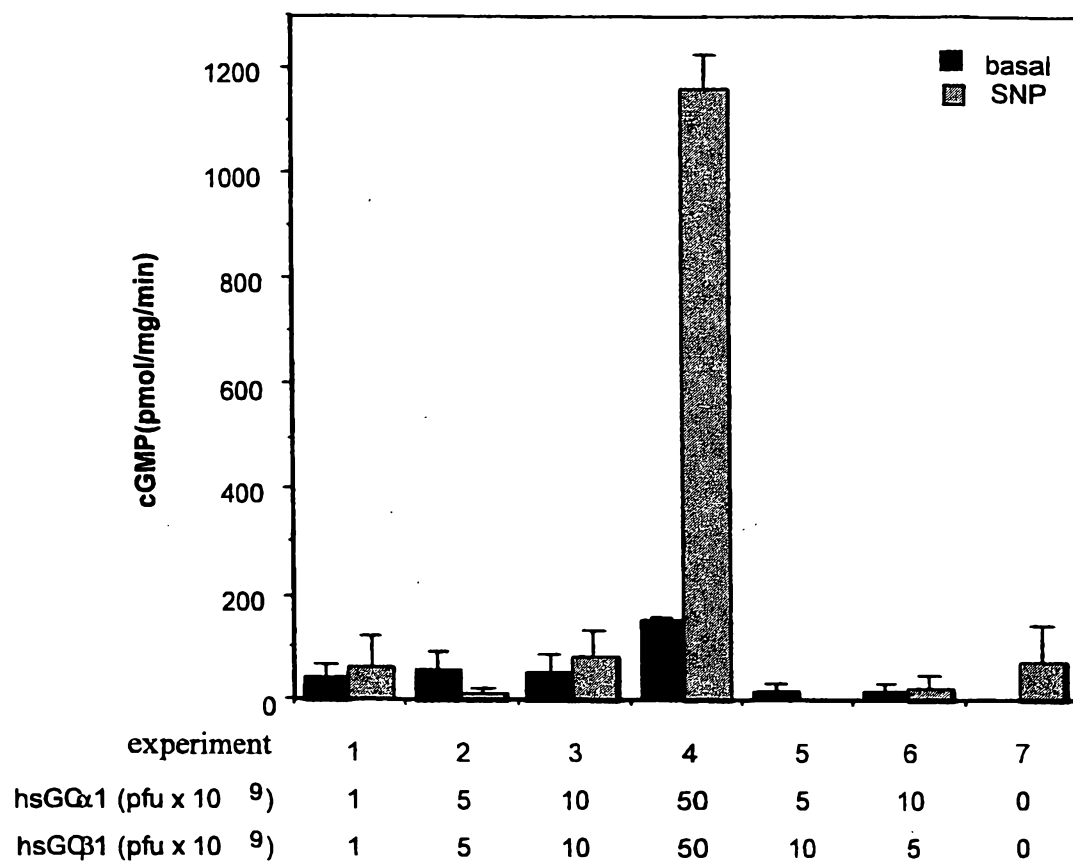
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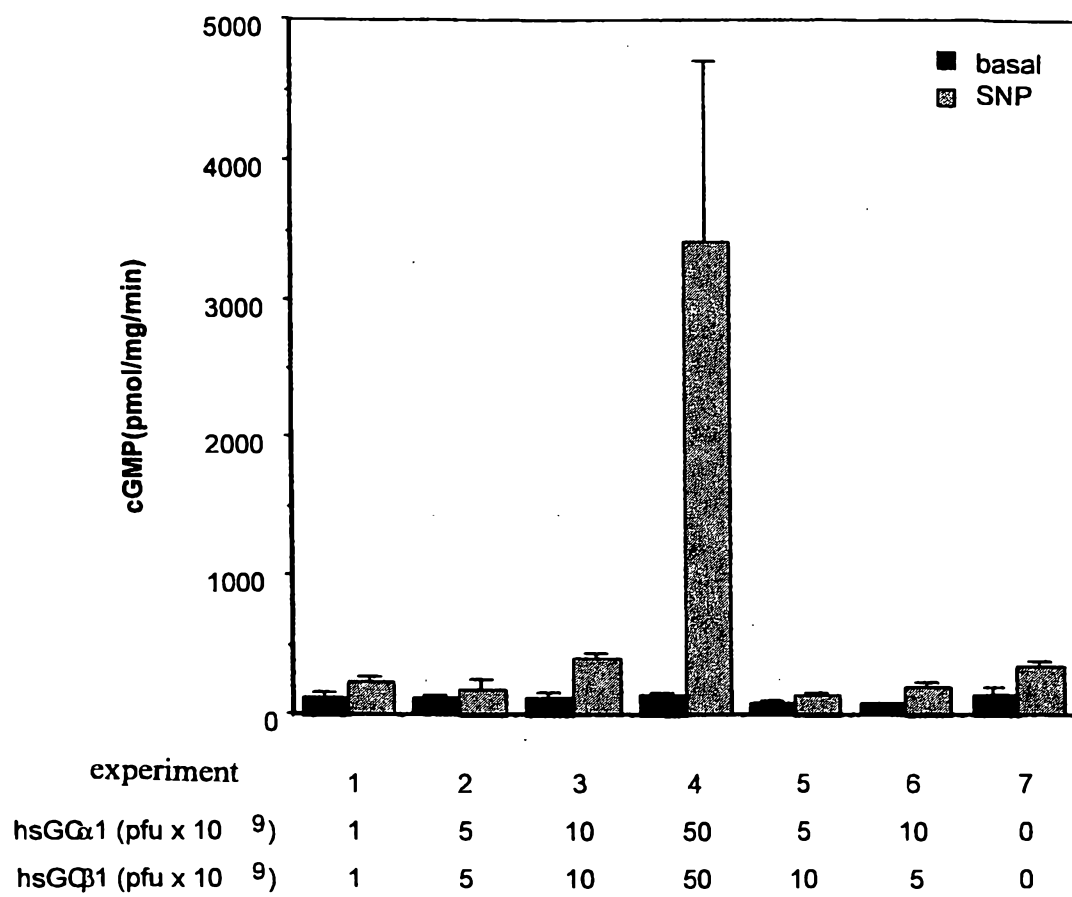
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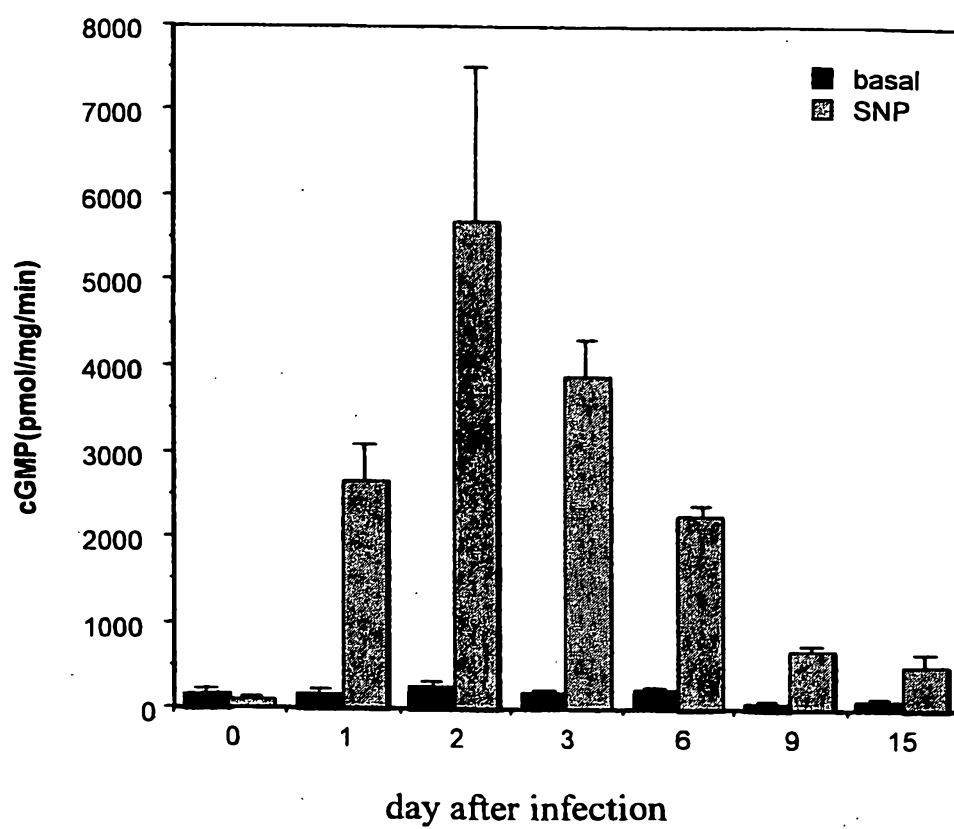
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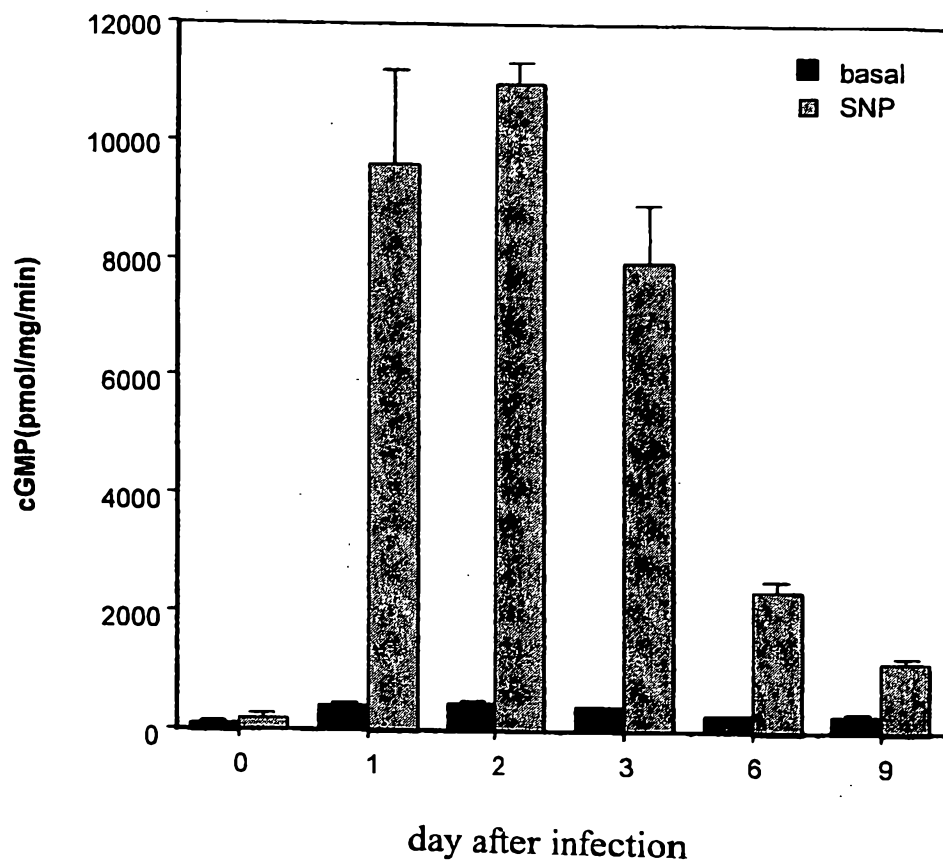
Figure 29

Figure 30

