JOR 2-35665652721-0134403.000

The Journal of Publishing and Pharmacological Characterization of Human

Cloning and Pharmacological Characterization of Human
Alpha-1 Adrenergic Receptors: Sequence Corrections and 0022-35650502721-0134403.000

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Direct Comparison with Other Species Homologues¹ **Direct Comparison with Other Species Homologues¹
Direct Class by The American Society for Pharmacology and Experimental Therapeutics

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DITECT COMPORTISOM WITH OTHET SPECIES HOMIOIOGUES
DEBRA A. SCHWINN, GEOFFREY I. JOHNSTON, STELLA O. PAGE, MICHAEL J. MOSLEY, KATRINA H. WILSON,
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Accepted for publication August 22, 1994

ABSTRACT

We have cloned cDNAs encoding three human *alpha*-1 adren-
ergic receptor (AR) subtypes and characterized pharmacolog-**ABSTRACT**
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significant sequence corrections We have cloned cDNAs encoding three human *alpha*-1 adren-
ergic receptor (AR) subtypes and characterized pharmacolog-
ical properties of the expressed receptor protein. A number of
previously published data, at both nucle **human** and **human** *alpha-1_{a/d}AR.* Pharmacological characterization was
performed simultaneously published data, at both nucleotide and parmino acid levels; the most major differences occur for the in
human *alpha-1_{a/d*} by particular and the provide of the most major differences occur for the human alpha-1_{a/d}AR. Pharmacological characterization was performed simultaneously using six cloned *alpha*-1AR subtypes (human and rat *alpha*-1_a blasts at approximately equal receptor concentration was
berformed simultaneously using six cloned *alpha*-1AR sub-
types (human and rat *alpha*-1_{a/d}, human and hamster *alpha*-1_b, cou
human and bovine *alpha*-1_a) st **performed simultaneously using six cloned alpha-1AR sub-
types (human and rat alpha-1_{a/d}, human and hamster alpha-1_b,
human and bovine alpha-1_a) stably expressed in rat-1 fibro-
blasts at approximately equal recepto** types (human and rat alpha-1_{a/d}, human and hamster alpha-1_t
human and bovine alpha-1_{a/d}, human and hamster alpha-1_t
human and bovine alpha-1_a) stably expressed in rat-1 fibro
blasts at approximately equal recept Furnan and bovine alpha-1.) stably expressed in rat-1 fibro-
blasts at approximately equal receptor concentrations (1–2
pmol/mg of total protein). In general, human alpha-1AR sub-
types have similar pharmacology compared t Ferences important for *alpha* 1.9 stating experiences in Tat 1 holds phases at approximately equal receptor concentrations (1–2 side pmol/mg of total protein). In general, human *alpha*-1AR sub-
types have similar pharmac

ergic receptor (AR) subtypes and characterized pharmacolog-
ical properties of the expressed receptor protein. A number of
ical properties of the expressed receptor protein. A number of
previous reports for both human and **addition, much lower inactivation (20%) by the alkylating addition, much lower inactivation (~20%) by the alkylating agent chloroethylclonidine is noted in this study compared to previous reports for both human and bovine alpha-1_cAR memprevious reports for both human and bovine alpha-1_cAR mem-
previous reports for both human and bovine** *alpha***-1_cAR mem-
brane preparations. All six** *alpha***-1AR subtypes couple to phos-
phoinositide hydrolysis in a per** addition, much lower inactivation (~20%) by the alkylating
agent chloroethylclonidine is noted in this study compared to
previous reports for both human and bovine *alpha*-1_cAR mem-
brane preparations. All six *alpha*-1A **including the cloned human** and bovine *alpha*-1_cAR membrane preparations. All six *alpha*-1AR subtypes couple to phosohologistic hydrolysis in a pertussis toxin-insensitive manner, including the cloned human *alpha*-1 gent onclocally. In spite of significant sequence to phos-
phoinositide hydrolysis in a pertussis toxin-insensitive manner,
including the cloned human *alpha*-1_{a/d}AR which had not been
expressed previously. In spite of s proparations. All six applies that subtypes couple to price
phoinositide hydrolysis in a pertussis toxin-insensitive manner,
including the cloned human alpha-1_{a/d}AR which had not been
expressed previously. In spite of si including the cloned human *alpha*-1_{a/d}AR which had not been expressed previously. In spite of significant sequence differences between human *alpha*-1ARs and their other species counterparts, previously established liga expressed previously. In spite of significant sequence differences between human *alpha*-1ARs and their other species counterparts, previously established ligand selectivity remains fairly comparable. In summary, these dat expressed preveasity. In spite of significant sequence differences between human *alpha*-1ARs and their other species counterparts, previously established ligand selectivity remains fairly comparable. In summary, these dat counterparts, previously established ligand selectivity remains
fairly comparable. In summary, these data represent the first
side-by-side comparison of pharmacological properties be-
tween species homologs of *alpha*-1AR fairly comparable. In subside-by-side comparas
side-by-side comparisc
tween species homolog
facilitate the developm
drugs for clinical use.

Alpha-1-ARs are members of the G-protein-coupled rece
 p family, coupling *via* Gq to the hydrolysis of membral Alpha-1-ARs are members of the G-protein-coupled receptor family, coupling *via* Gq to the hydrolysis of membrane
phospholipids and ultimately to smooth muscle contraction *Alpha*-1-ARs are members of the G-protein-coupled receptor family, coupling via Gq to the hydrolysis of membrane G
phospholipids and ultimately to smooth muscle contraction 1
(Minneman, 1988a; McGrath *et al.*, 1989; Ruff Alpha-1-ARs are members of the G-protein-coupled receptor family, coupling *via* Gq to the hydrolysis of membrane phospholipids and ultimately to smooth muscle contraction (Minneman, 1988a; McGrath *et al.*, 1989; Ruffolo *Alpha*-1-ARs are members of the G-protein-coupled receptor family, coupling via Gq to the hydrolysis of membrane Grophospholipids and ultimately to smooth muscle contraction 1Al (Minneman, 1988a; McGrath *et al.*, 1989; R tor family, coupling *via* Gq to the hydrolysis of membrane phospholipids and ultimately to smooth muscle contraction (Minneman, 1988a; McGrath *et al.*, 1989; Ruffolo *et al.*, 1991
Lomasney *et al.*, 1991a). *Alpha*-1ARs phospholipids and ultimately to smooth muscle contraction (Minneman, 1988a; McGrath *et al.*, 1989; Ruffolo *et al.*, 1991; Lomasney *et al.*, 1991a). *Alpha*-1ARs have been implicated in many human diseases such as benign (Minneman, 1988a; McGrath *et al.*, 1989; Ruffolo *et al.*, 1991;
Lomasney *et al.*, 1991a). *Alpha*-1ARs have been implicated in
many human diseases such as benign prostatic hypertrophy,
hypertension, myocardial hypertrop Lomasney *et al.*, 1991a). *Alpha*-1ARs have been implicated in id
many human diseases such as benign prostatic hypertrophy, 19
hypertension, myocardial hypertrophy and myocardial ar-
rhythmias (Caine *et al.*, 1975; Nicho many human diseases such as benign prostatic hypertrophy, 1988

hypertension, myocardial hypertrophy and myocardial ar-
 rhythmias (Caine *et al.*, 1975; Nichols and Ruffolo, 1991; we re

Terzic *et al.*, 1993). Two sub

and Creese, 1986; Han *et al.*, 1987; Minneman *et al.*, 1988b;
Gross *et al.*, 1988), whereas cDNAs encoding three *alpha*and Creese, 1986; Han *et al.*, 1987; Minneman *et al.*, 1988
Gross *et al.*, 1988), whereas cDNAs encoding three *alph*
1ARs [cloned rat *alpha*-1_{a/d} (also referred to as *alpha*-1_a and Creese, 1986; Han *et al.*, 1987; Minneman *et al.*, 1988b;
Gross *et al.*, 1988), whereas cDNAs encoding three *alpha-1*
1ARs [cloned rat *alpha-1*_{a/d} (also referred to as *alpha-1*_a or
*alpha-1*_a), hamster *alp* and Creese, 1986; Han *et al.*, 1987; Minneman *et al.*, 1988b;
Gross *et al.*, 1988), whereas cDNAs encoding three *alpha*-
1ARs [cloned rat *alpha*- 1_{ad} (also referred to as *alpha*- 1_{a} or
alpha- 1_{d}), Gross *et al.*, 1988), whereas cDNAs encoding three *alpha*-1ARs [cloned rat *alpha*-1_{a'} (also referred to as *alpha*-1_a or *alpha*-1_a), hamster *alpha*-1_b and bovine *alpha*-1_c] have been identified by using mo 1ARs [cloned rat *alpha*- $1_{a/d}$ (also referred to as *alpha*- 1_a or *alpha*- 1_d), hamster *alpha*- 1_b and bovine *alpha*- 1_c] have been identified by using molecular techniques (Cotecchia *et al.*, 1988; Schwinn *et* $alpha-1_d$), hamster $alpha-1_b$ and bovine $alpha-1_c$] have been
identified by using molecular techniques (Cotecchia *et al.*,
1988; Schwinn *et al.*, 1990; Lomasney *et al.*, 1991b, Perez *et*
 $al.$, 1991, Schwinn and Lomasney, 1992) identified by using indectual decliniques (codecting *et al.*, 1988; Schwinn *et al.*, 1990; Lomasney *et al.*, 1991b, Perez *et al.*, 1991, Schwinn and Lomasney, 1992). In this manuscript we refer to pharmacologically def 1988; Schwinn *et al.*, 1990; Lomasney *et al.*, 1991b, Perez *et al.*, 1991, Schwinn and Lomasney, 1992). In this manuscript we refer to pharmacologically defined *alpha*-1AR subtypes by upper case subscripts $(e.g. \ alpha-1_B)$ al., 1991, Schwinn and Lomasney, i
we refer to pharmacologically define
upper case subscripts (*e.g. alpha*-1_i
subtypes by lower case subscripts (*i*
to current muscarinic nomenclature
The role of *alpha*-1ARs in many l Frefer to pharmacologically defined *alpha*-1AR subtypes by
pper case subscripts $(e.g. alpha-1_B)$ and cloned *alpha*-1AR
btypes by lower case subscripts $(e.g. alpha-1_b)$, in analogy
current muscarinic nomenclature.
The role of *alpha* upper case subscripts (*e.g. alpha-*1_B) and cloned *alpha-*1AR subtypes by lower case subscripts (*e.g. alpha-*1_b), in analogy to current muscarinic nomenclature.
The role of *alpha-*1ARs in many human diseases, togeth

Terzic *et al.*, 1993). Two subtypes of *alpha*-1ARs (*alpha*-1_A upper case subscripts (*e.g. alpha*-1_B) and cloned *alpha*-1AR and *alpha*-1_B) have been defined pharmacologically (Morrow subtypes by lower case subs subtypes by lower case subscripts (*e.g. alpha*-1_b), in analogy
to current muscarinic nomenclature.
The role of *alpha*-1ARs in many human diseases, together
with the development of *alpha*-1AR subtype-selective ago-
nis to current muscarinic nomenclature.
The role of *alpha*-1ARs in many human diseases, togeth
with the development of *alpha*-1AR subtype-selective ag
nists and antagonists, make it important to define the exa
pharmacologica The role of $alpha$ -1ARs in many human diseases, toge with the development of $alpha$ -1AR subtype-selective inists and antagonists, make it important to define the epharmacological properties of cloned human $alpha$ -1AR, types. This

HL49103 from **the** National Institutes **of Health (D. A. S.). Corrected nudeouting secuel for publication May 19, 1994.**

¹ This project has been supported by Pfizer Central Research and Grant
 HL49103 from the National Institutes of Health (D. A. S.). Corrected nucle-

poide sequences have b ¹ This project has been supported by
HL49103 from the National Institutes cotide sequences have been entered into
follows: rat *alpha*-1_e (L31771), human
(L31773) and human *alpha*-1_c (L31774).

ABBREVIATIONS: AR, adrenergic receptor; CEC, chloroethylclonidine; bp, base pair; SSC(1X) (150 mM NaCl and 15 mM sodium citrate; pH 7);
ABBREVIATIONS: AR, adrenergic receptor; CEC, chloroethylclonidine; bp, base pair; SSC(otide sequences have been entered into GenBank. Accession numbers are as
follows: rat *alpha-1*_{a/d} (L31771), human *alpha-1*_{a/d} (L31772), human *alpha-1*_b
(L31773) and human *alpha-1*_{a/d} (L31774).
ABBREVIATIONS: (L31773) and human *alpha*-1_e (L31774).
 ABBREVIATIONS: AR, adrenergic receptor; CEC, chloroethylclonidine; bp, base pair; SSC(1X) (150 mM NaCl and 15 mM sodium citrate; pH 7);

SDS, sodium dodecyl sulfate; PCR, polyme

1995
because this cDNA has never been expressed and charac
ized pharmacologically (Bruno *et al.*, 1991). In addition, 1995
because this cDNA has never been expressed and character-
ized pharmacologically (Bruno *et al.*, 1991). In addition, it is
important to compare expressed human *alpha*-1ARs with 1995
because this cDNA has never been expressed and character-
ized pharmacologically (Bruno *et al.*, 1991). In addition, it is well
important to compare expressed human *alpha*-1ARs with know
those of other species to ev because this cDNA has never been expressed and characte ized pharmacologically (Bruno *et al.*, 1991). In addition, it important to compare expressed human *alpha*-1ARs with those of other species to evaluate species diffe because this cDNA has never been expressed and character-

ized pharmacologically (Bruno *et al.*, 1991). In addition, it is

important to compare expressed human *alpha*-1ARs with

those of other species to evaluate spec important to compare expressed human *alpha*-1ARs with
those of other species to evaluate species differences in phar-
macological properties of the receptor subtypes (as has been
macological properties of the receptor sub important to compare expressed human *alpha*-1ARs with

those of other species to evaluate species differences in phar-

macological properties of the receptor subtypes (as has been

reported for human and mouse *alpha*-2 those of other species to evaluate species differences in phar-
macological properties of the receptor subtypes (as has been
reported for human and mouse *alpha*-2AR homologs) (Link *et*
al., 1992). We have therefore clo reported for human and mouse alpha-2AR homologs) (Link et objection-
allows therefore cloned three human alpha-1AR
cDNAs, expressed them in rat-1 fibroblasts in approximately
equal concentrations (1-2 pmol/mg of total pro pared their pharmacological profile to their rat, hamster and
bovine counterparts. Significantly, our human *alpha*-1AR
cDNAs demonstrate substantial deviation in nucleotide se-
quence compared to recently published report cDNAs, expressed them in rat-1 fibroblasts in approximately
equal concentrations $(1-2 \text{ pmol/mg})$ of total protein) and com-
pared their pharmacological profile to their rat, hamster and
bovine counterparts. Significantly, pared their pharmacological profile to their rat, hamster and
bovine counterparts. Significantly, our human *alpha*-1AR
cDNAs demonstrate substantial deviation in nucleotide se-
quence compared to recently published report bovine counterparts. Significantly, our human *alpha*-1AR cDNAs demonstrate substantial deviation in nucleotide sequence compared to recently published reports, particularly to the human *alpha*-1_{a/d}. These sequence diff cDNAs demonstrate substantial deviation in nucleotide sequence compared to recently published reports, particularly for the human $alpha \cdot 1_{\alpha/d}$. These sequence differences result for significant changes at the nucleotide a quence compared to recently published reports, particularly teor the human $alpha_{\text{1}}$ λ_{dd} . These sequence differences result for significant changes at the nucleotide and amino acid levels from regions potentially i in significant changes at the nucleotide and amino acid levels
in regions potentially involved in receptor regulation (amino
terminus and carboxyl terminus) as well as isolated amino
acid changes which could impact ligand in significant changes at the nucleotide and amino acid leve
in regions potentially involved in receptor regulation (amin
terminus and carboxyl terminus) as well as isolated amin
acid changes which could impact ligand bind in regions potentially involved in receptor regulation (amino terminus and carboxyl terminus) as well as isolated amino acid changes which could impact ligand binding and interpretation of structure-function relationships terminus and carboxyl terminus) as well as isolated amino acid changes which could impact ligand binding and inter-
pretation of structure-function relationships in these recep-
tors. In addition to examining ligand bindin acid changes which could impact ligand binding and inter-
pretation of structure-function relationships in these recep-
tors. In addition to examining ligand binding characteristics
by competition experiments and saturatio tors. In addition to examining ligand binding characteristics
by competition experiments and saturation binding iso-
therms, we report CEC sensitivity and second messenger
coupling assays (phosphoinositide hydrolysis with tors. In addition to examining ligand binding characteristics
by competition experiments and saturation binding iso-
therms, we report CEC sensitivity and second messenger
coupling assays (phosphoinositide hydrolysis with by competition experiments and saturation binding isotherms, we report CEC sensitivity and second messenge coupling assays (phosphoinositide hydrolysis with and with out pertussis toxin) obtained simultaneously for all six therms, we report CEC sensitivity and second messenger
coupling assays (phosphoinositide hydrolysis with and with-
out pertussis toxin) obtained simultaneously for all six cloned
alpha-1AR receptors. These results repres coupling assays (phosphoinositide hydrolysis with and with-
out pertussis toxin) obtained simultaneously for all six cloned
alpha-1AR receptors. These results represent the first dem-
onstration of detailed pharmacology *alpha*-1AR receptors. These results represent the first demonstration of detailed pharmacology of human *alpha*-1AR subtypes as well as direct comparison with previously cloned *alpha*-1ARs from other species.

Methods

nda-1ARs from other species.
 Methods
 Isolation of alpha-1AR cDNA clones. General cloning methods the lized in isolating human alpha-1AR cDNA clones are listed first, **Methods**
 Usolation of *alpha***-1AR cDNA clones.** General cloning methods

utilized in isolating human *alpha*-1AR cDNA clones are listed first,

followed by the exact cloning strategy used for each individual *alpha***followed by heation** of *alpha-1AR* **cDNA clones.** General cloning methoutilized in isolating human *alpha-1AR* cDNA clones are listed fir followed by the exact cloning strategy used for each individual *alpha-1AR* subt 18 **Isolation of** *alpha***-1AR cDNA clones.** General cloning methods

utilized in isolating human *alpha*-1AR cDNA clones are listed first,

followed by the exact cloning strategy used for each individual *alpha*-

1AR subty utilized in isolating human *alpha*-1AR cDNA clones are listed first, P
followed by the exact cloning strategy used for each individual *alpha*-
1AR subtype. Human heart and prostate cDNA libraries (Stratagene
1
1
alpha-1A dillowed by the exact cloning strategy used for each individual *alpha*-
1AR subtype. Human heart and prostate cDNA libraries (Stratagene
1AR subtype. Human heart and prostate cDNA libraries (Stratagene
1La Jolla, CA] and conowed by the exact closing strategy these to call interviewed as intervalsed [La Jolla, CA] and Clontech [Palo Alto, CA], respectively) and a total human genomic library (Clontech) were used to clone three human stable First statistic conducts of the statistic conducts.

(La Jolla, CA] and Clontech [Palo Alto, CA], respectively) and a

human genomic library (Clontech) were used to clone three human
 $alpha$ -1AR cDNAs. Portions of previously probe (905 bp PvuII fragment, nucleotide no. 131-1036) and both the apples (905 bp PvuII fragment, nucleotide no. 433-1119), hamster alpha-1_cAR sprobe (905 bp PvuII fragment, nucleotide no. 433-1119), hamster alpha-1_c *alpha-1AR* cDNAs. Portions of previously published *alpha-1AR a*CDNAs were used as initial probes: rat *alpha-1*_{a/}*AR* probe (686 bp ^v PvuII fragment, nucleotide no. 433-1119), hamster *alpha-1*_a/*AR* sprobe (905 **1000).** DNAs were used as initial probes: rat $alpha_{1pha}$ AR probe (686 bp PvuII fragment, nucleotide no. 433-1119), hamster $alpha_{1pha}$ AR probe (905 bp PvuII fragment, nucleotide no. 131-1036) and bovine $alpha_{1pha}$ -1_cAR probe cDNAs were used as initial probes: rat $alpha_{rad}$ AR probe (686 bp were grown in monolayers in DMEM (Gibco, Grand Island, NY)
PvuII fragment, nucleotide no. 433-1119), hamster $alpha_{1}$ ₋₁_bAR supplemented with 10% fetal bovine From Tragment, indicedue no. 450-1115), indicate the temperature of the strep probe (905 bp PvuII fragment, nucleotide no. 131-1036) and bovine strep alpha-1. AR probe (694 bp BgIII/PvuII fragment, nucleotide no. 356-
105 species (300 specific activity fragment, nucleotide no. 356-
1050). DNA probes were labeled with ³²P by using random-priming
and were added to prehybridization solution (50% formamide, 5×
Denhardt's and 5× SSC, 0.1% SDS complished and were added to prehybridization solution (50% formamide, 5× **Rad** Denhardt's and 5× SSC, 0.1% SDS, 100 μ g/ml of denatured fish *alpha*-isperm DNA) to give a specific activity for each probe of 5×10^5 Denhardt's and $5 \times$ SSC, 0.1% SDS, 100 μ g/ml of denatured fish algebra DNA) to give a specific activity for each probe of 5×10^5 10 cpm/ml. After an overnight incubation at 42°C, the filters were PI washed to $55^$ rounds of plaque purification. DNA inserts were released from the phase DNA by EcoRI digestion. DNA inserts were released from the phase DNA by EcoRI digestion and ligated into pSP72 (Promega dilutional computer of the ph washed to 55°C in $0.2 \times$ SSPE $1(\times)$ (150 mM NaCl, 20 mM EDTA and 10 mM NaH₂PO₄), pH 7.4 and 0.1% SDS, and were subjected to 7 autoradiography. Positive clones were subjected to two further arounds of plaque purifica and 10 mM NaH₂PO₄), pH 7.4 and 0.1% SDS, and were subjected to 7.4, quickly frozen and stored at -70°C . Binding of the *alpha*-1-
autoradiography. Positive clones were subjected to two further adrenergic antag autoradiography. Positive clones were subjected to two further aduoratiography. Tositive clones were subjected to two further aduorations of plaque purification. DNA inserts were released from the Booghage DNA by EcoRI digestion and ligated into pSP72 (Promega dilustice, Madison, WI). rounds of plaque-purincation. Dividends were released from the hydrogen DNA by EcoRI digestion and ligated into pSP72 (Promega dBiotec, Madison, WI). Further cDNA library and genomic library necreasings to obtain missing p Biotec, Madison, WI). Further cDNA library and genomic library mM
Biotec, Madison, WI). Further cDNA library and genomic library mM
screenings to obtain missing portions of clones were performed by (5
initially screening a experimg to obtain missing portions of clones were performed by (5
initially screening amplified library subpools by polymerase chain treaction, then plating out positive pools at 10,000 plaque-forming ce
units per 230-mm by using standard musics of closes were performed by

initially screening amplified library subpools by polymerase chain

treaction, then plating out positive pools at 10,000 plaque-forming

eencoding each human *alpha*-1A reaction, then plating out positive pounits per 230-mm² plate. Sequencing encoding each human *alpha*-1AR subt by using standard ³⁵S-dideoxy sequencing automated fluorescent methods. Cloning of the human *alpha*-1_{a/d} units per 230-mm² plate. Sequencing of final full-length cDNAs per
encoding each human *alpha*-1AR subtype was performed manually 100
by using standard ³⁵S-dideoxy sequencing techniques as well as by
ascensing a human

encount each numan *atpha*-ARK subtype was performed manually
by using standard ³⁵S-dideoxy sequencing techniques as well as by
using automated fluorescent methods.
Cloning of the human *alpha*-1_{a/d} cDNA was accomplish by using standard 3-dideoxy sequencing techniques as wen as by ascorbing
using automated fluorescent methods. for 45
Cloning of the human *alpha*-1_{a/d} cDNA was accomplished first by HCl (p
screening a human prostate cDNA using automated intorescent methods.
Cloning of the human *alpha*-1_{a/d} cDNA was accomplished first by
screening a human prostate cDNA library (Clontech), from which a
portion of the coding region just before the NotI sit

human Alpha-1ARs 135
brary (Clontech, one donor) and the rest of the coding sequence (as
well as some 5' sequences) was obtained. Once the sequence was **well as some 5' sequences)** was obtained. Once the sequence (as well as some 5' sequences) was obtained. Once the sequence was known from these two cDNA libraries, the region between the initial ATG and the NotI site was brary (Clontech, one donor) and the rest of the coding sequence (as well as some 5' sequences) was obtained. Once the sequence was known from these two cDNA libraries, the region between the initial ATG and the NotI site w brary (Clontech, one donor) and the rest of the coding sequence (as
well as some 5' sequences) was obtained. Once the sequence was
known from these two cDNA libraries, the region between the initial
ATG and the NotI site w well as some 5' sequences) was obtained. Once the sequence was ATG and the NotI site was amplified by using PCR to optimize the ATG and the NotI site was amplified by using PCR to optimize the Kozak consensus sequence, and the two fragments were spliced together. The entire coding sequence was fully sequenced including matching PCR sequence with or together. The entire coding sequence was fully sequenced including
matching PCR sequence with original genomic coding sequence, and
ensuring splice sites were joined correctly. In the case of the *alpha*-
1_bAR, while stu maximity I out sequence what stighting problems counting sequence, the ensuring splice sites were joined correctly. In the case of the *alpha*-1_bAR, while studies were in progress to complete cloning of this cDNA from a $1_{\rm b}AR$, while studies were in progress to complete cloning of this cDNA from a human heart cDNA library (Stratagene), the sequence of the human $alpha_1$, gene was published (Ramarao *et al.*, 1992). Therefore, the missing of the human *alpha*-1_b gene was published (Ramarao *et al.*, 1992).
Therefore, the missing portion of this gene (the carboxyl terminal
third of the clone) was amplified from human heart mRNA (Clon-
tech) by using PCR (from **the published sequence.** PCR products **were subcloned into the** third of the clone) was amplified from human heart mRNA (Clontech) by using PCR (1 min at 94°C, 1 min at 55°C and 2.5 min at 72°C for 30 cycles in the presence of 10% formamide) with primers derived from the published seq pCRII vector (InVitrogen) and subjected to sequence analysis. Sequencing of several distinct PCR products $(n \geq 3)$ was performed to confirm the sequence in regions in which PCR had been used; differences with previously confirm the sequence in regions in which PCR had been used; differences with previously published sequences were noted only when at least three identical PCR products differed from published results. The human *alpha*-1_c between the vertical PCR products differed from published results.
The human *alpha*-1_cAR was cloned from a human prostate cDNA
library (Clontech, 65-year-old patient), and a large fragment encod-
ing the initial two-thi least three identical PCR products differed from published results.
The human *alpha*-1_cAR was cloned from a human prostate cDNA
library (Clontech, 65-year-old patient), and a large fragment encod-
ing the initial two-th Information the observation of the coding sequence was obtained. The carboxyl one-half of the coding sequence was obtained. The carboxyl one-half of the coding sequence was obtained from another human prostate cDNA library ing the initial two-thirds of the coding sequence was obtained. The carboxyl one-half of the coding sequence was obtained from another human prostate cDNA library (Clontech, 25-year-old patient) and the overlapping sequenc man prostate cDNA library (Clontech, 25-year-old patient) and
e overlapping sequence was validated. The entire coding block was
en amplified by using PCR and the sequence again was validated
ainst original cDNA sequences.

the overlapping sequence was validated. The entire coding block was
then amplified by using PCR and the sequence again was validated
against original cDNA sequences.
Stable expression of human *alpha***-1AR subtypes in ratinterpolarity in the either properties** against original CDNA sequences.
 Stable expression of human alpha-1AR subtypes in rat-
 fibroblasts. Transfection constructs consisted of the appropriat

human, rat, hamster or **Stable expression of human** *alpha***-1AR subtypes in rat-1**
fibroblasts. Transfection constructs consisted of the appropriate
human, rat, hamster or bovine *alpha*-1AR coding sequence inserted
in either pZipNeo (Cepko *et* human, rat, hamster or bovine *alpha*-1AR coding sequence inserted
in either pZipNeo (Cepko *et al.*, 1984) or pcDNA3 (InVitrogen) vec-
tors. Transfection of each cDNA into rat-1 fibroblasts was accom-
plished by using the in either pZipNeo (Cepko et al., 1984) or pcDNA3 (InVitrogen) vectors. Transfection of each cDNA into rat-1 fibroblasts was accom-
plished by using the calcium phosphate precipitation method as
described previously (Cullen, 1987). Individual colonies were iso-
lated, subcloned and scree plished by using the calcium phosphate precipitation method as
described previously (Cullen, 1987). Individual colonies were iso-
lated, subcloned and screened for high expression $(1-2 \text{ pmol/mg})$ of
total protein). Rat-1 fi absoluted, subcloned and screened for high expression $(1-2 \text{ pm}0/\text{mg} \text{ of }$
lated, subcloned and screened for high expression $(1-2 \text{ pm}0/\text{mg} \text{ of }$
stably expressing either rat $alpha_1L_{\text{wd}}$, human $alpha_1L_{\text{wd}}$, hamster
 total protein). Rat-1 fibroblasts and transfected rat-1 fibroblasts stably expressing either rat $alpha_{1-\omega,d}$, human $alpha_{1-\omega,d}$, hamster $alpha_{1-\omega,d}$, human $alpha_{1-\omega,d}$, human $alpha_{1-\omega,d}$, hamster $alpha_{1-\omega,d}$, human $alpha_{1-\omega,d}$, human stably expressing either rat $alpha_{1}$, human $alpha_{1}$, human $alpha_{1}$, hamst $alpha_{1}$, human $alpha_{1}$, human $alpha_{1}$, bovine $alpha_{1}$ _{-c} or human $alpha_{1}$. Alwere grown in monolayers in DMEM (Gibco, Grand Island, N'supplemented with 10 otic **0418 (0.8** mg/mi) **to the media.**

supplemented with 10% fetal bovine serum, penicillin (100 U/ml) and
streptomycin (100 μ g/ml) in 5% CO₂ at 37°C. Selection was main-
tained in cells expressing *alpha*-1AR subtypes by adding the antibi-
otic G418 (0.8 otic G418 (0.8 mg/ml) to the media.
Radioligand binding. Rat-1 cells stably expressing individual *alpha*-1AR subtypes from culture flasks (150 cm²) were scraped into 10 ml of TE. A lysate was prepared with a Brinkman **Radioligand binding.** Rat-1 cells stably expressing individual $\alpha lpha$ -1AR subtypes from culture flasks (150 cm²) were scraped into 10 ml of TE. A lysate was prepared with a Brinkman Polytron (model PT3000, setting 8 f *Alpha***-1AR subtypes from culture flasks (150 cm²) were scraped in 10 ml of TE. A lysate was prepared with a Brinkman Polytron (mc PT3000, setting 8 for 10 sec); after pelleting, membranes were suspended in 150 mM NaCl,** alpha-Trix subtypes it out calcule has as (100 cm) were straped into 10 ml of TE. A lysate was prepared with a Brinkman Polytron (model PT3000, setting 8 for 10 sec); after pelleting, membranes were resuspended in 150 mM Io in of 12. A iyaace was prepared with a Drinkman I ofyton (inoder
PT3000, setting 8 for 10 sec); after pelleting, membranes were re-
suspended in 150 mM NaCl, 50 mM Tris HCl and 5 mM EDTA, pH
7.4, quickly frozen and sto **F13000, setting 6 for 10 sec); after perieting, membranes were resuspended in 150 mM NaCl, 50 mM Tris HCl and 5 mM EDTA, pH 7.4, quickly frozen and stored at** -70° **C. Binding of the** *alpha***-1-adrenergic antagonist [^{** 7.4, quickly frozen and stored at -70° C. Binding of the *alpha*-1-
7.4, quickly frozen and stored at -70° C. Binding of the *alpha*-1-
adrenergic antagonist $[^{125}]$ HEAT (DuPont-New England Nuclear,
Boston, MA) w **(5)** the approximation of (125 H) in the approximate properties and solved at -10 C. Binding of the approximate process $[125]$ HEAT (DuPont-New England Nuclear, Boston, MA) was measured using a total volume of 0.2 Boston, MA) was measured using a total volume of 0.25 ml including
diluted membranes $(5-10 \mu g$ of total protein) in 150 mM NaCl, 50
mM Tris HCl and 5 mM EDTA, pH 7.4, with protease inhibitors
 $(5 \mu g/ml$ leupeptin, $10 \mu g/ml$ mM Tris HCl and 5 mM EDTA, pH 7.4, with protease inhibitors (5 μ g/ml leupeptin, 10 μ g/ml of benzamidine and 10 μ g/ml of soybean trypsin inhibitor). For saturation binding isotherms, [¹²⁵I]HEAT concentrations ra contrations ranged from 10 to 960 pM. Competition curves were performed in triplicate, with a final $[^{125}]$ HEAT concentration of 100 pM; agonist competition was performed in the presence of 1 μ M ascorbic acid to preve performed in triplicate, with a final $[^{125}]$ HEAT concentration of 100 pM; agonist competition was performed in the presence of 1 μ M ascorbic acid to prevent agonist oxidation. Incubations were at 25°C for 45 min; the 100 pM; agonist competition was performed in the presence of 1μ M ascorbic acid to prevent agonist oxidation. Incubations were at 25°C for 45 min; the reaction was terminated with ice-cold 50 mM Tris HCl (pH 7.4) and the entire reaction mixture was filtered rapidly over GF/C filters by u **HCl** (pH 7.4) and the entire reaction mixture was filtered rapidly over GF/C filters by using a Brandel harvester. Nonspecific binding was measured in the presence of $1 \mu M$ prazosin with nonspecific binding 5 to 10% of

CEC inactivation. For CEC experiments, 100 μ M CEC was (1)

cubated with transfected rat-1 fibroblast cell membrane lysates in **incubated with transfected rat-1 fibroblast cell membrane lysates** incubated with transfected rat-1 fibroblast cell membrane lysates in $(50-100 \mu g)$ of protein) in hypotonic TE at 37° C for 10 and 20 min. 136 Schwinn et al.

CEC inactivation. For CEC experiments, $100 \mu M$ CEC was

incubated with transfected rat-1 fibroblast cell membrane lysates
 $(50-100 \mu g$ of protein) in hypotonic TE at 37°C for 10 and 20 min.

The reac **CEC inactivation.** For CEC experiments, 100 μ M CEC was (1 incubated with transfected rat-1 fibroblast cell membrane lysates in (50–100 μ g of protein) in hypotonic TE at 37°C for 10 and 20 min. followed The reaction **but CEC inactivation.** For CEC experiments, 100 μ M CEC was (1) incubated with transfected rat-1 fibroblast cell membrane lysates ir (50–100 μ g of protein) in hypotonic TE at 37°C for 10 and 20 min. The reaction was incubated with transfected rat-1 fibroblast cell membrane lysates

(50-100 μg of protein) in hypotonic TE at 37°C for 10 and 20 min.

The reaction was stopped by addition of 4 ml of ice-cold TE, followed

by immediate ce In tractation was suppled by a
by immediate centrifugation s
then washed 2 to 3 more times
binding. A saturating concense was used to determine *alpha*-
CEC treatment in triplicate.
IP determination in interen washed 2 to 3 more times with 5 ml of ice-cold PBS before ligand
nding. A saturating concentration of $[^{125}]$ HEAT (300 pM final)
as used to determine *alpha*-1AR receptor number before and after
EC treatment in triplic

binding. A saturating concentration of $[1^{28}]$ HEAT (300 pM final)
was used to determine *alpha*-1AR receptor number before and after
CEC treatment in triplicate.
(1 cells/dish), were labeled with $[{}^{8}H]$ inositol (DuP The Hall contribution of the Indian CEC treatment in triplicate.
 P determination in intact cells. Rat-1 fibroblasts stably expressing individual *alpha*-1AR subtypes, grown in 30-mm dishes $(1 \times 10^6 \text{ cells/dish})$, were labe **IP determination in intact cells.** Rat-1 fibroblasts stably expressing individual *alpha*-1AR subtypes, grown in 30-mm dishes $(1 \times 10^6 \text{ cells/dish})$, were labeled with $[^{8}H]$ inositol (DuPont-New openland Nuclear) for 18 hr $\frac{1 \times 10^6 \text{ cells/dish}}{1 \times 10^6 \text{ cells/dish}}$, were labeled with $\frac{19 \text{ H}}{1 \text{ in DMEM}}$ supplemented in Fig. 25 μ Ci/ml in DMEM supplemented in With 5% fetal bovine serum (GIBCO). After labeling, cells were washed and incubated i England Nuclear) for 18 hr at 2.5 μ Ci/ml in DMEM supplemented in which
with 5% fetal bovine serum (GIBCO). After labeling, cells were
washed and incubated in PBS (no added calcium) for 30 min, fol-
lowed by a 30-min inc **languary 10.8 ml and 10.6 ml packed calcium) for 30 min, followed by a 30-min incubation in PBS with 20 mM LiCl. IPs were extracted as de** washed and incubated in PBS (no added calcium) for 30 min, fol-
lowed by a 30-min incubation in PBS with 20 mM LiCl. IPs were
extracted as described by Martin (1983) and were separated on AG
1-X8 columns (0.8 ml packed, 1 **before** increase in the P1 experiments with a momentum of the Formate-0.1 M formic acid. For experiments with pertussis toxin, coincubation with 100 ng/ml of pertussis toxin was performed for 18 hr before initiation of th Sources: EDTA, epinephrine, methoxamine, NE, oxymetazoline, phenologymetric phenomenologymetric methoxamine, Materials. Drugs and reagents were obtained from the following sources: EDTA, epinephrine, methoxamine, NE, oxyme

incubation with 100 ng/ml of pertussis toxin was performed for 18 hr
before initiation of the PI experiment. (
Materials. Drugs and reagents were obtained from the following
sources: EDTA, epinephrine, methoxamine, NE, o measured what is to the PI experiment.
 Materials. Drugs and reagents were obtained from the followin,

sources: EDTA, epinephrine, methoxamine, NE, oxymetazoline

phentolamine, phenylephrine, prazosin and propranolol (S Seison minimum of the 11 caperiments.
 Materials. Drugs and reagents were obtained from the following

sources: EDTA, epinephrine, methoxamine, NE, oxymetazoline,

phentolamine, phenylephrine, prazosin and propranolol (S sources: EDTA, epinephrine, methoxamine, NE, oxymetazoline, phentolamine, phenylephrine, prazosin and propranolol (Sigma que Chemical Co., St. Louis, MO); 5-methylurapidil, (+)-niguldipine, (Capperone and WB4101 (Research Definition (Fig. 1912). The properties of the control of the spiperone and WB4101 (Research Biochemical Inc., Wayland, MA);
spiperone and WB4101 (Research Biochemical Inc., Wayland, MA);
and pertussis toxin (List Biologica Example 2013, 2014, 2015, 2016

Results

Mucleotide sequence differences with previously

oned human *alpha*-1AR cDNAs. Comparisons of the **cloned human** *alpha***-1AR cDNAs.** Comparisons of the *algence differences* with previously be
cloned human *alpha*-1AR cDNAs. Comparisons of the *algences* for all three cloned human $\frac{a l_i}{d}$ **Results**

Nucleotide sequence differences with previously

cloned human *alpha*-1AR cDNAs. Comparisons of the

translated amino acid sequences for all three cloned human
 alpha-1AR cDNAs and their mammalian counterparts **Alpha-1AR cDNAs.** Comparisons of the translated amino acid sequences for all three cloned human *alpha*-1AR cDNAs and their mammalian counterparts (rat, hamster and bovine) are shown in figure 1; differences be-Nucleotide sequence differences with previously
cloned human *alpha*-1AR cDNAs. Comparisons of the
translated amino acid sequences for all three cloned human
alpha-1AR cDNAs and their mammalian counterparts (rat,
hamster **cloned human** *alpha***-1AR cDNAs.** Comparisons of the $\frac{al}{alpha}$ -1AR cDNAs and their mammalian counterparts (rat, id hamster and bovine) are shown in figure 1; differences between our sequences and those published previou translated amino acid sequences for all three cloned human $a lpha$ -1AR cDNAs and their mammalian counterparts (rat, identify hamster and bovine) are shown in figure 1; differences bewitween our sequences and those publishe alpha-1AR cDNAs and their mammalian counterparts (rat,
hamster and bovine) are shown in figure 1; differences be-
tween our sequences and those published previously (Bruno
et al., 1991; Ramarao et al., 1992; Hirasawa et al hamster and bovine) are shown in figure 1; differences between our sequences and those published previously (Bruncet al., 1991; Ramarao et al., 1992; Hirasawa et al., 1993) are highlighted in boxes. The largest variation b tween our sequences and those published previously (Bruncet al., 1991; Ramarao et al., 1992; Hirasawa et al., 1993) are highlighted in boxes. The largest variation between our cloned human *alpha*-1AR cDNAs and other previ *Et al.*, 1991; Ramarao *et al.*, 1992; Hirasawa *et al.*, 1993) are highlighted in boxes. The largest variation between our the contained human *alpha*-lAR cDNAs and other previously pub-
lished sequences occurs for the cloned human *alpha*-1AR cDNAs and other previously pub-
lished sequences occurs for the human *alpha*-1_{a/d}AR subtype. the
The translated sequence of the human *alpha*-1_{a/d}AR contains *ph*
572 amino acids; comparison lished sequences occurs for the human $alpha_{1}$ _{a/d}AR subtype.
The translated sequence of the human $alpha_{1}$ _{a/d}AR contains *pi*
572 amino acids; comparison with the human $alpha_{1}$ _{a/d}
clone published by Bruno *et al.* (1991 The translated sequence of the human $alpha \cdot 1_{\alpha/d}$ AR contains ph
572 amino acids; comparison with the human $alpha \cdot 1_{\alpha/d}$ ho
clone published by Bruno *et al.* (1991) reveals that our clone se-
does not match bases 1 to 178 572 amino acids; comparison with the human $alpha_{1}$
clone published by Bruno *et al.* (1991) reveals that our clone
does not match bases 1 to 178 of this human sequence in spite
of the fact that this region of our clone is clone published by Bruno *et al.* (1991) reveals that our clone does not match bases 1 to 178 of this human sequence in spit of the fact that this region of our clone is homologous with the rat $alpha_{1}$ _{a/d}AR (Lomasney *et* does not match bases 1 to 178 of this human sequence in spite
of the fact that this region of our clone is homologous with the
rat $alpha\-l_{\alpha/d}AR$ (Lomasney *et al.*, 1991b; Perez *et al.*, 1991).
When bases 1 to 172 are rever of the fact that this region of our clone is homologous with th
rat *alpha*-1_{a/d}AR (Lomasney *et al.*, 1991b; Perez *et al.*, 1991
When bases 1 to 172 are reverse-complemented and com
pared to the entire human *alpha*-1 rat $alpha \cdot 1_{\alpha/d}AR$ (Lomasney *et al.*, 1991b; Perez *et al.*, 1991).
When bases 1 to 172 are reverse-complemented and compared to the entire human $alpha \cdot 1_{\alpha/d}AR$ coding sequence, 1
this fragment matches bases 454 to 626, su When bases 1 to 172 are reverse-complemented and compared to the entire human $alpha^{-1}$ _{a/d}AR coding sequence, this fragment matches bases 454 to 626, suggesting the presence of a cloning artifact at the 5' end of the previ pared to the entire numan $aipha-1_{a/d}AR$ coung sequence, here of a cloning artifact at the 5' end of the previously published human $alpha-1_{a/d}AR$ cDNA (Bruno *et al.*, 1991). ce Another discrepancy between our human $alpha-1_{$ ence of a cloning artifact at the 5' end of the previously publ
published human $alpha \cdot 1_{\alpha/d}AR$ cDNA (Bruno *et al.*, 1991). cept
Another discrepancy between our human $alpha \cdot 1_{\alpha/d}AR$ G. T
cDNA and that published by Bruno *et* published human $alpha_{1}$ _{1a/d}AR cDNA (Bruno *et al.*, 1991). cept
Another discrepancy between our human $alpha_{1}$ _{a/d}AR G. T
cDNA and that published by Bruno *et al.* (1991) occurs in the glut
carboxyl terminus where again s cDNA and that published by Bruno *et al.* (1991) occurs in the glutamine (CAG), which is the same residue that is found in carboxyl terminus where again significant deviations in the bovine *alpha*-1_cAR. It is important amino acid sequence are noted. Of note, the human *alpha*-
 $1_{\alpha/d}AR$ clone published by Bruno *et al.* (1991) also differs in ot
this region from previously reported rat *alpha*- $1_{\alpha/d}AR$ se-
quences (Lomasney *et al.*, 1 $1_{\alpha/4}$ AR clone published by Bruno *et al.* (1991) also differs in ot this region from previously reported rat *alpha*- $1_{\alpha/4}$ AR sequences (Lomasney *et al.*, 1991b; Perez *et al.*, 1991). In order be to clarify these this region from previously reported rat $alpha_{1\bullet}$ AR sequences (Lomasney *et al.*, 1991b; Perez *et al.*, 1991). In order to clarify these sequencing differences, in addition to cloning the human $alpha_{1\bullet}$ AR cDNA, we also r

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(1991b). Resequencing the rat $alpha\-l_{\alpha/d}$ cDNA in this region
indicates two errors, a two bp insertion (GC) at base 1749 *Vol. 272*
 indicates two errors, a two bp insertion (GC) at base 1749
 indicates two errors, a two bp insertion (GC) at base 1749
 followed 177 bp later by a single base insertion (C), leading to *Vol. 272*
(1991b). Resequencing the rat *alpha*-1_{a/d} cDNA in this region
indicates two errors, a two bp insertion (GC) at base 1749
followed 177 bp later by a single base insertion (C), leading to
a 59 amino acid frame (1991b). Resequencing the rat $alpha \cdot 1_{\alpha/d}$ cDNA in this region indicates two errors, a two bp insertion (GC) at base 1749 followed 177 bp later by a single base insertion (C), leading to a 59 amino acid frame shift in the indicates two errors, a two bp insertion (GC) at base 1749 followed 177 bp later by a single base insertion (C), leading to a 59 amino acid frame shift in the carboxyl terminus; this mistake is present in both published r followed 177 bp later by a single base insertion (C), leading to
a 59 amino acid frame shift in the carboxyl terminus; this
mistake is present in both published rat $alpha_{1}$ cDNAs
(Lomasney *et al.*, 1991b; Perez *et al.*, a 59 amino acid frame shift in the carboxyl terminus; this mistake is present in both published rat *alpha*- 1_{ad} cDNAs (Lomasney *et al.*, 1991b; Perez *et al.*, 1991) and may have resulted from the GC rich nature of (Lomasney *et al.*, 1991b; Perez *et al.*, 1991) and may have resulted from the GC rich nature of this region which makes sequencing more difficult. When these corrections are inserted into the rat $alpha1_{\mathbf{a}/\mathbf{a}}$ R sequ (Lomasney *et al.*, 1991b; Perez *et al.*, 1991) and may have resulted from the GC rich nature of this region which makes equencing more difficult. When these corrections are is serted into the rat $alpha_{1}$ _{a/d}AR sequence, resulted from the GC rich nature of this region which makes
sequencing more difficult. When these corrections are in-
serted into the rat $alpha_{1-\alpha}A$ R sequence, the reading frame
shows greater alignment to the human sequence sequencing more difficult. When these corrections are inserted into the rat $alpha_{1}l_{\text{ad}}AR$ sequence, the reading frame shows greater alignment to the human sequence and homology increases significantly from 83 to 87%. Clo serted into the rat $alpha\cdot1_{\alpha/d}$ as sequence, the reading frame shows greater alignment to the human sequence and homology increases significantly from 83 to 87%. Close to the area in which this marked divergence is noted shows greater alignment to the human sequence and homology increases significantly from 83 to 87%. Close to the area
in which this marked divergence is noted between our human
and rat $alpha_{1}$ _{a/d} cDNAs, we found a single ogy increases significantly from 83 to 87%. Close to the area
in which this marked divergence is noted between our human
and rat $alpha_{1}$ _{a/d} cDNAs, we found a single base missing in
the published human sequence (Bruno *et* in which this marked divergence is noted between our humand rat $alpha_{1}$ $_{\text{bd}}$ cDNAs, we found a single base missing the published human sequence (Bruno *et al.*, 1991) (at bas 1393–1394 there are two adenines in the pub the published human sequence (Bruno *et al.*, 1991) (at bases 1393–1394 there are two adenines in the published sequence instead of three in our sequence). This results in the translated sequence moving into another readin the published human sequence (Bruno *et al.*, 1991) (at base 1393–1394 there are two adenines in the published sequent instead of three in our sequence). This results in the tran lated sequence moving into another reading 1393–1394 there are two adennes in the published sequence
instead of three in our sequence). This results in the trans-
lated sequence moving into another reading frame, and ac-
counts for differences between the publishe instead of three in our sequence). This results in the trans-
lated sequence moving into another reading frame, and ac-
counts for differences between the published human *alpha*-
 $1_{\omega d}$ clone (Bruno *et al.*, 1991) and lated sequence moving into another reading frame, and accounts for differences between the published human *alpha*- $1_{a/d}$ clone (Bruno *et al.*, 1991) and rat *alpha*- $1_{a/d}$ AR cDNAs (Lomasney *et al.*, 1991b; Perez *et a* counts for differences between the published human *alpha*- $1_{\mathbf{a}/\mathbf{d}}$ clone (Bruno *et al.*, 1991) and rat *alpha*- $1_{\mathbf{a}/\mathbf{d}}$ CDNAs (Lomasney *et al.*, 1991b; Perez *et al.*, 1991). Other minor differences bet $1_{\mathbf{a}/\mathbf{d}}$ clone (Bruno *et al.*, 1991) and rat *alpha*- $1_{\mathbf{a}/\mathbf{d}}$ AR cDNAs (Lomasney *et al.*, 1991b; Perez *et al.*, 1991). Other minor differences between the published human *alpha*- $1_{\mathbf{a}/\mathbf{d}}$ AR seque (Lomasney *et al.*, 1991b; Perez *et al.*, 1991). Other minor differences between the published human $alpha$ -l_{a/d}AR sequence and our sequence include a silent base change at 1358 (C to A) and a GC inversion at base 1492 to differences between the published human *alpha*-1_{a/d}AR sequence and our sequence include a silent base change at 135 (C to A) and a GC inversion at base 1492 to 1493. Due to the complexity of these corrections in the hum quence and our sequence include a silent base change at 1358 (C to A) and a GC inversion at base 1492 to 1493. Due to the complexity of these corrections in the human $alpha_{1}$ A R nucleotide and translated amino acid sequen to A) and a GC inversion at base 1492 to 1493. Due to the mplexity of these corrections in the human $alpha_{1}$ -1_{a/d}AR is cleotide and translated amino acid sequences, the openading frame of the human $alpha_{1}$ -1_{a/d}AR is giv

complexity of these corrections in the human $alpha-1_{\alpha/4}AR$
nucleotide and translated amino acid sequences, the open-
reading frame of the human $alpha-1_{\alpha/4}AR$ is given in figure 2.
Fewer differences between our cloned sequen nucleotide and translated amino acid sequences, the open-
reading frame of the human $alpha_{pha-1_{a/a}}AR$ is given in figure 2.
Fewer differences between our cloned sequences and pre-
viously published sequences were found for h reading frame of the human $alpha$ $1_{a/d}$ AR is given in figure 2.
 Fewer differences between our cloned sequences and previously published sequences were found for human $alpha$ 1_{b} A R and
 $alpha$ 1_{c} AR are 95 and 92% iden Fewer differences between our cloned sequences and pre-
viously published sequences were found for human $alpha_{1}$ _b and
and $alpha_{1}$ _c subtype cDNAs. The human $alpha_{1}$ _bAR and
 $alpha_{1}$ _cAR are 95 and 92% identical to the rat and *alpha*-1_c subtype cDNAs. The human *alpha*-1_cAR and *alpha*-1_cAR are 95 and 92% identical to the rat *alpha*-1_b and bovine *alpha*-1_c, respectively. Comparison of our human *alpha*-1_bAR sequence to the pr alpha-1_cAR are 95 and 92% identical to the rat alpha-1_c and bovine alpha-1_c, respectively. Comparison of our human alpha-1_cAR sequence to the previously isolated human alpha-1_cAR gene sequence (Ramarao *et al.*, bovine alpha-1_c, respectively. Comparison of our human bovine *alpha*-1_c, respectively. Comparison of our human *alpha*-1_bAR sequence to the previously isolated human *alpha*-1_bAR gene sequence (Ramarao *et al.*, 1992) showed identity, except for a three bp insertion (CG alpha-1_bAR sequence to the previously isolated human *alpha*-1_bAR gene sequence (Ramarao *et al.*, 1992) showed identity, except for a three bp insertion (CGC) at base 1114 which adds another arginine residue, three s alpha-1_bAR gene sequence (Ramarao *et al.*, 1992) showed identity, except for a three bp insertion (CGC) at base 1114 which adds another arginine residue, three single guanine insertions after bases 1486, 1490 and 1492 a identity, except for a three bp insertion (CGC) at base 111
which adds another arginine residue, three single guanir
insertions after bases 1486, 1490 and 1492 and a base sul
stitution at base 1489 (A to G). These latter c which adds another arginine residue, three single guanine
insertions after bases 1486, 1490 and 1492 and a base sub-
stitution at base 1489 (A to G). These latter changes alter
three amino acids (P-R-H) to encode four ami insertions after bases 1486, 1490 and 1492 and a base substitution at base 1489 (A to G). These latter changes alter three amino acids (P-R-H) to encode four amino acids (A-A-A-D) in the human $\alpha lpha$ -1_bAR. These change stitution at base 1489 (A to G). These latter changes alter
three amino acids (P-R-H) to encode four amino acids (A-A-
A-D) in the human $alpha^{-1}$ _bAR. These changes close a gap in
the published comparison between hamster a three amino acids (P-R-H) to encode four amino acids (A-A-
A-D) in the human $alpha^{-1}$ _bAR. These changes close a gap in
the published comparison between hamster and human al -
 pha^{-1} _BAR with the new human sequence being the published comparison between hamster and human *al-*
pha-1_BAR with the new human sequence being now more
homologous to the hamster (A-T-T-D). In addition, there is a
sequence difference between the publication and th the published comparison between hamster and human $a l$ -
pha-1_BAR with the new human sequence being now more
homologous to the hamster (A-T-T-D). In addition, there is a
sequence difference between the publication and homologous to the hamster $(A-T-T-D)$. In addition, there is a sequence difference between the publication and the Genbank entry for the human $alpha_1$ _b (Ramarao *et al.*, 1992); our sequence at amino acid 33 to 35 (S-N-S) and sequence difference between the publication and the Gen-
bank entry for the human $alpha$ -1_b (Ramarao *et al.*, 1992);
our sequence at amino acid 33 to 35 (S-N-S) and at amino
acid 486 (D) is identical to the sequence descr bank entry for the human $alpha_{1b}$ (Ramarao *et al.*, 1992);
our sequence at amino acid 33 to 35 (S-N-S) and at amino
acid 486 (D) is identical to the sequence described in
the manuscript (Ramarao *et al.*, 1992), but diffe our sequence at amino acid 33 to 35 (S-N-S) and at amino acid 486 (D) is identical to the sequence described in the manuscript (Ramarao *et al.*, 1992), but differs from the R-G-G and E present in Genbank, respectively. C acid 486 (D) is identical to the sequence described in the manuscript (Ramarao *et al.*, 1992), but differs from the R-G-G and E present in Genbank, respectively. Comparison of our human $alpha-l_cAR$ nucleotide sequence to the r the manuscript (Ramarao *et al.*, 1992), but differs from the R-G-G and E present in Genbank, respectively. Comparison of our human $alpha_{1}$ -1_cAR nucleotide sequence to the recently published human $alpha_{1}$ -1_cAR sequence s R-G-G and E present in Genbank, respectively. Comparison
of our human $alpha \cdot 1_c AR$ nucleotide sequence to the recently
published human $alpha \cdot 1_c AR$ sequence shows identity ex-
cept for base 1727, which is a C in our sequence ins of our human $alpha_{1}$ -1_cAR nucleotide sequence to the recently
published human $alpha_{1}$ -1_cAR sequence shows identity ex-
cept for base 1727, which is a C in our sequence instead of a
G. This changes the glutamic acid at p published human *alpha*-1_cAR sequence shows identity except for base 1727, which is a C in our sequence instead of a G. This changes the glutamic acid at position 431 (GAG) to a glutamine (CAG), which is the same residue cept for base 1727, which is a C in our sequence instead of a G. This changes the glutamic acid at position 431 (GAG) to a glutamine (CAG), which is the same residue that is found in the bovine *alpha*-1₄AR. It is import G. This changes the glutamic acid at position 431 (GAG) to glutamine (CAG), which is the same residue that is found it the bovine *alpha*-1_cAR. It is important to note at this poin that single bp differences could be the glutamine (CAG), which is the same residue that is found in the bovine *alpha*-1_cAR. It is important to note at this point that single bp differences could be the result of ethnic or other naturally occurring polymorphis the bovine *alpha*-1_cAR. It is important to note at this point that single bp differences could be the result of ethnic or other naturally occurring polymorphisms. However, inasmuch as changes noted above result in close that single bp differences could be the result of ethnic or other naturally occurring polymorphisms. However, inasmuch as changes noted above result in closer alignment between human and nonhuman homologs, the possibility other naturally occurring polymorphisms. However, inas-
much as changes noted above result in closer alignment
between human and nonhuman homologs, the possibility of
polymorphisms becomes less likely. Corrected nucleotide much as changes noted above result in closer alibetween human and nonhuman homologs, the possipolymorphisms becomes less likely. Corrected nucleo quences for all three human $alpha$ -1AR cDNAs, as we the rat $alpha$ -1_{a/d}, have be

Fig. 1. Translated amino acid sequences for cDNAs encoding human and rat alpha-1 (α_1) $_{\alpha/d}$ ARs, human and hamster α_{1b} ARs, human and bovine α_{1c} ARs. Differences with previously published sequences are highlighted in boxes.

Pharmacological characterization of alpha-1AR subtypes. In order to assess the pharmacological characteristics of human alpha-1ARs, each cDNA was stably transfected into rat-1 fibroblasts, and the resulting receptors were compared to other expressed alpha-1AR subtypes (rat alpha- $1_{a/d}$, hamster alpha- 1_b and bovine alpha- 1_c) in rat-1 fibroblasts. Expression levels were roughly equivalent between all six clonal lines tested (1-2 pmol/mg of total protein). Membranes prepared from these stable cell lines expressing alpha-1AR subtypes were both used in saturation binding isotherms to determine K_d for $[$ ¹²⁵I]HEAT and, in competition analysis with various alpha-1-subtype selective drugs, both agonists and antagonists (table 1). Of note, all alpha-1AR subtypes demonstrate high and approximately equal affinity for [¹²⁵I]HEAT. Although it is evident that human alpha-1ARs have approximately the same affinities for various agonists and antagonists compared to their rat $alpha$ -l_{a/d}, hamster alpha-1_b and bovine alpha-1_c homologs, some minor

These include slightly higher affinity for spiperone by the differences occur which impact on *alpha*-1AR classification.
These include slightly higher affinity for spiperone by the 1₄
bovine *alpha*-1_c compared to the human *alpha*-1_c, as well as ef
larger differences in aff differences occur which impact on *alpha*-1AR classification. af
These include slightly higher affinity for spiperone by the 1,
bovine $alpha$ -1_c compared to the human $alpha$ -1_c, as well as ef
larger differences in affinity bovine **homologs.** bovine $alpha\text{-}1_c$ compared to the human $alpha\text{-}1_c$, as well as larger differences in affinity for methoxamine between human $alpha\text{-}1_b$ and $alpha\text{-}1_c$ than seen between hamster and bovine homologs.
Further pharmacological char

larger differences in affinity for methoxamine between human $alpha_{1b}$ and $alpha_{1c}$ than seen between hamster and bovine homologs.
Further pharmacological characterization included inactivation of $alpha_{1c}$ -1AR subtypes by the man *alpha*-1_b and *alpha*-1_c than seen between hamster and
bovine homologs.
Further pharmacological characterization included inacti-
vation of *alpha*-1AR subtypes by the alkylating agent CEC.
Conditions were chosen bovine homologs.

Further pharmacological characterization included inactivation of $alpha$ -1AR subtypes by the alkylating agent CEC.

Conditions were chosen such that the $alpha$ -1_bAR subtype Is

would be completely inactivate Further pharmacological characterization included inactivation of *alpha*-1AR subtypes by the alkylating agent CEC.
Conditions were chosen such that the *alpha*-1_bAR subtype I would be completely inactivated (100 μ M vation of *alpha*-1AR subtypes by the alkylating agent CEC.
Conditions were chosen such that the *alpha*-1_bAR subtype
would be completely inactivated (100 μ M CEC, 37°C, 20 th
min); for comparison, a slightly shorter Conditions were chosen such that the *alpha*-1_bAR subtype In this study we report the cloning and characterization of would be completely inactivated (100 μ M CEC, 37°C, 20 three human *alpha*-1AR cDNAs. *Alpha*-1ARs would be completely inactivated $(100 \mu M$ CEC, 37°C,
min); for comparison, a slightly shorter incubation time (
min) also was performed. Human *alpha*-1AR subtypes we
inactivated by CEC to the same extent as their rat, ha min); for comparison, a slightly shorter incubation time (10 bot

min) also was performed. Human *alpha*-1AR subtypes were ula

inactivated by CEC to the same extent as their rat, hamster *alp*

and bovine counterparts. F min) also was performed. Human *alpha*-1AR subtypes were ular (constituted by CEC to the same extent as their rat, hamster *alpha*-
and bovine counterparts. For 20-min incubations, *alpha*- has pr
 1_bARs were inactiv inactivated by CEC to the same extent as their rat, hamster and bovine counterparts. For 20-min incubations, *alpha* $1_{b}ARs$ were inactivated by CEC, 89 to 98%, followed b $alpha^{-1}$ _{a/d}ARs at 75 to 86% and $alpha^{-1}$ _cARs at 1 and bovine counterparts. For 20-min incubations, *alpha*-
 1_{b} ARs were inactivated by CEC, 89 to 98%, followed by c
alpha- $1_{\text{a}/4}$ ARs at 75 to 86% and *alpha*- 1_{c} ARs at 11 to 18% is
(table 1). Of note, CEC 1_{b} ARs were inactivated by CEC, 89 to 98%, followed by colo
 alpha- $1_{\text{a}/\text{d}}$ ARs at 75 to 86% and *alpha*- 1_{c} ARs at 11 to 18% sub

(table 1). Of note, CEC inactivation for the *alpha*- 1_{c} AR sub-

c alpha-1_{a/d}ARs at 75 to 86% and alpha-1_cARs at 11 to 18% (table 1). Of note, CEC inactivation for the alpha-1_cAR subtype is significantly less than that reported previously for membrane assays (Schwinn *et al.*, 1990 (table 1). Of note, CEC inactivation for the *alpha*-1_cAR subconed $(alpha-1_b)$ and pharmacological $(alpha-1_B)$ subtypes type is significantly less than that reported previously for have low affinity for several *alpha*-1AR test coupling to phospholipase C, PI hydrolysis experiments
were performed. All six cloned *alpha*-1AR subtypes stably
expressed in rat-1 fibroblasts produced IP with agonist stim-
ulation with the following NE efficacy: membrane assays (Schwinn *et al.*, 1990, 1991). In order to
test coupling to phospholipase C, PI hydrolysis experiments
were performed. All six cloned *alpha*-1AR subtypes stably
sxpressed in rat-1 fibroblasts produced IP test coupling to phospholipase C, PI hydrolysis experiments
were performed. All six cloned *alpha*-1AR subtypes stably
expressed in rat-1 fibroblasts produced IP with agonist stim-
ulation with the following NE efficacy:

dar (human and rat) (table 1). Of note, the human *alph*
 1_cAR couples to PI hydrolysis with almost twice the N **limes.**
 AR (human and rat) (table 1). Of note, the human *alpha*-

1_cAR couples to PI hydrolysis with almost twice the NE

efficacy as the bovine *alpha*-1_cAR. Activation of PI hydrolysis $A R$ (human and rat) (table 1). Of note, the human $alpha_{L}$
 $L_{c}AR$ couples to PI hydrolysis with almost twice the NE
efficacy as the bovine $alpha_{L}$ $A R$. Activation of PI hydrolysis
by the six cloned $alpha_{L}$ $A R$ subtypes is p **aAR** (human and rat) (table 1). Of note, the human *alph* 1_cAR couples to PI hydrolysis with almost twice the Γ efficacy as the bovine *alpha*-1_cAR. Activation of PI hydroly by the six cloned *alpha*-1AR subtypes aAR (human and rat) (table 1).
1_cAR couples to PI hydrolysis
efficacy as the bovine *alpha*-1_cAR
by the six cloned *alpha*-1AR s
insensitive (100 and 500 ng/ml).

Discussion

**IN 1989 Sensitive (100 and 500 ng/ml).

Discussion**

In this study we report the cloning and characterization of

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In this study we report the cloning and characterization
three human $alpha$ -1AR cDNAs. $Alpha$ -1ARs are defined
both a pharmacological $(alpha_{-1_A}$ and $alpha_{-1_B})$ and mole
ular (cloned rat $alpha_{-1_{\text{ad}}}$, hamster $alpha_{-1_b}$ In this study we report the cloning and characterization of
three human $alpha$ -lAR cDNAs. $Alpha$ -lARs are defined at
both a pharmacological $(alpha$ -l_A and $alpha$ -l_B) and molec-
ular (cloned rat $alpha$ -l_{a/d}, hamster $alpha$ -l_b and bo In this study we report the cloning and characterization of three human *alpha*-1AR cDNAs. *Alpha*-1ARs are defined at both a pharmacological $(alpha^{-1}A$ and $alpha^{-1}B)$ and molecular (cloned rat *alpha*-1_{a'd}, hamster *alpha* three human *alpha*-1AR cDNAs. *Alpha*-1ARs are defined both a pharmacological $\left(alpha_{1}h$ _A, and *alpha*-1_B) and moular (cloned rat *alpha*-1_{a/d}, hamster *alpha*-1_b and bov *alpha*-1_c) level, and merging of the t both a pharmacological $(alpha_1 - 1_A)$ and $alpha_1 - 1_B)$ and molecular $(closed \text{ rat } alpha-1_{\alpha/d})$, hamster $alpha_1 - 1_B$ and bovine $alpha_1 - 1_C)$ level, and merging of the two classification schemes has proven difficult. The best correlation be ular (cloned rat *alpha*-1_{a/d}, hamster *alpha*-1_b and bovine *alpha*-1_c) level, and merging of the two classification schemes has proven difficult. The best correlation between pharmacological and molecular classifi cloned *(alpha-1_b)* and pharmacological *(alpha-1_B)* subtypes have low affinity for several *alpha-1AR* subtype-selective compounds $[(+)$ -niguldipine, WB4101 and 5-methylurapidil], are sensitive to inactivation by CEC has proven difficult. The best correlation between pharma-
cological and molecular classification schemes for *alpha*-1AR
subtypes occurs for the *alpha*-1_BAR subtype, in which both
cloned (*alpha*-1_b) and pharmacologi cological and molecular classification schemes for *alpha*-1AR
subtypes occurs for the *alpha*-1_BAR subtype, in which both
cloned $(alpha-1_b)$ and pharmacological $(alpha-1_B)$ subtypes
have low affinity for several $alpha-1AR$ subt same rat tissues (Morrow and Creese, 1986; Han *et al.*, 1987; Minneman *et al.*, 1988; Gross *et al.*, 1988; Cotecchia *et al.*, 1988; Schwinn *et al.*, 1991). In contrast, alignment of the compounds $[(+)-$ niguldipine, WB4101 and 5-methylurapidil],
are sensitive to inactivation by CEC and are present in the
same rat tissues (Morrow and Creese, 1986; Han *et al.*, 1987;
Minneman *et al.*, 1988b; Gross *et al.*, are sensitive to inactivation by CEC and are present in the same rat tissues (Morrow and Creese, 1986; Han *et al.*, 1987; Minneman *et al.*, 1988); Gross *et al.*, 1988; Cotecchia *et al.*, 1988; Schwinn *et al.*, 1991).

A T G A D G A H G

S L S V R L L K F

I V V G V F V L C

S L P P O L K P S GCTACTTCAACAGCTGCGTGAACCCGCTC Y F N S C V N P L GCGCCTTCCTCCGTCTCCTGCGCTGCCAG A F L R L L R C Q GGCGTGTCTACGGCCACCACTGGCGGGCC R V Y G H H W R A CGAGTTCGGGCGACGCGCCCCCCCGGAGCG S S G D A P P G A ACCCCGAACCCCCAGGAACGCCCGAGATG **EPPGTPEM** CCAGCGCCTTCCGCGAGTGGAGGCTGCTG SAFREWRLL GCGCCAAAGTCTCCAGCCTGTCGCACAAG A K V S S L S H K CAGCGTGCGCCCAGCGCTCAGAGGTGGAG C A Q R S E V E CCGAGGGCGCCACCTGCCAGGCCTACGAA GATCQAY **ATATTTAAGGACCCCAGAGCTAGGCCGCG** AGAGAGGCGGGCTGGTGTTCTAAGAGCCC Fig. 2. The nucleotide sequence and translated amino acid sequence of the human alpha-1_{a/n}AR open-reading frame.

pha-1AR subtypes has been more difficult. The alpha-1, is defined as having high affinity for alpha-1AR subtype-selective drugs, resistance to inactivation by CEC and is the predominant alpha-1AR subtype present in the rat vas deferens and submaxillary gland (Morrow and Creese, 1986; Minneman et al., 1988b; Michel et al., 1989). Although the cloned bovine alpha-1_c, as described originally, has high affinity for all $alpha-1_AAR$ selective drugs, the encoded receptor protein deviates in its partial sensitivity to CEC, absence from pharmacologically predicted rat tissues as determined by Northern analysis (Schwinn et al., 1990, 1991) and lower than expected $(+)$ -niguldipine affinity (Schwinn and Lomasney, 1992). However, recent studies from our laboratory (Price et al., 1994a) and by others have suggested that the cloned alpha-1.AR might encode the pharmacological alpha-1AR after all. First, although CEC sensitivity is known in general to be lower in whole cells than in membrane preparations (Schwinn et al., 1991), a recent study suggests even less CEC sensitivity than described originally for human alpha-1.ARs in whole cells (Forray et al., 1994a); our current study suggests for the first time that lower CEC sensitivity exists $(\sim 20\%$ inactivation) for human and bovine alpha-1.ARs in membrane assays. Second, by using more sensitive techniques, the tissue distribution of the alpha-1-AR has now been shown to be more extensive than originally thought. RNase protection assays and in situ hybridization studies of alpha-1AR mRNAs have demonstrated recently the presence of cloned alpha-1.ARs in many human (Price et al., 1994b) and rat (Price et al., 1994a) tissues, particularly in the stroma of the human prostate (Price et al., 1993) where the

alpha-1 AR appears to be involved in smooth muscle contraction (Smith et al., 1993; Forray et al., 1994b). Finally, recent studies have demonstrated higher affinity for $(+)$ -niguldipine in the rat alpha-1.AR compared with the bovine homolog (Forray et al., 1994a). With the cloned alpha-1_c now thought to encode the pharmacological $alpha-1_A$ subtype, the only remaining cloned alpha-1AR not encoding a pharmacologically defined alpha-1AR subtype is the alpha- $1_{a/d}$. Historically, the cloned rat $alpha-1_{a/d}$ was first called the alpha-1.AR due to high affinity for phentolamine and WB4101, initial studies demonstrating resistance to inactivation by CEC and appropriate tissue distribution in the rat (Lomasney et al., 1991b). However, more extensive evaluation of this receptor (Perez et al., 1991) resulted in the name $alpha$ -1_dAR due to lower affinity for oxymetazoline and $(+)$ -niguldipine and some inactivation by CEC (Perez et al., 1991); until this controversy is resolved completely, this receptor has been called the $alpha$ -1_{a/d} (Schwinn and Lomasney, 1992).

Because of the role of *alpha*-1ARs in many human diseases, and the possibility that species homologs with different pharmacologies may shed further light on alpha-1AR classification, it is important to define the exact pharmacologic properties of cloned human alpha-1AR subtypes. Therefore, we have cloned cDNAs encoding three human alpha-1AR subtypes and compared their pharmacological properties to the previously cloned rat, hamster and bovine alpha-1ARs. In addition to demonstrating sequence inaccuracies in human alpha-1ARs and the rat alpha- $1_{a/d}$ subtype, this study represents the first expression of human $alpha$ -1_n dAR protein and subsequent pharmacological characteriza-

Pharmacological characteristics of Alpha-1 AR subtypes
Mean ± S.E.M. Al results are rounded to two significant digits. TABLE₁

° Competition assays were performed in triplicate, with all six subtypes tested simultaneously, n = 3–5 separate experiments.
⁹ Ligand binding for CEC inactivation experiments was performed in triplicate, n = 3–5 separa

tion. Of importance, characterization of *alpha***-1AR** subtypes **gives** was performed simultaneously for all six subtypes, by using superceptors expressed in the same cell line (rat-1 fibroblasts) at receptors expressed in the same cell line $(rat - 1AR \text{ subtypes})$ and $rat - 1AR \text{ subtypes}}$ are vas performed simultaneously for all six subtypes, by using spectrors expressed in the same cell line $(rat-1 \text{ fibroblasts})$ at approximately equal e tion. Of importance, characterization of *alpha*-1AR subtypes give
was performed simultaneously for all six subtypes, by using sub
receptors expressed in the same cell line (rat-1 fibroblasts) at
approximately equal expres was performed simultaneously for all six subtypes, by usin
receptors expressed in the same cell line (rat-1 fibroblasts)
approximately equal expression level $(1-2 \text{ pmol/mg}$ of tot
protein). Although human and rat $alpha^{-1}$ _a hamster *alpha*-1_b and human and bovine *alpha*-1_cAR subtypes have similar pharmacological properties, some differences do exist.
In general, affinities for agonists and antagonists are similar between human, rat, hams types have similar pharmacological properties, some differ-

types have similar pharmacological properties, some differences do exist.

In general, affinities for agonists and antagonists are similar between human, rat, hamster and bovine *alpha*-1ARs.

However, subtle differences i ences do exist.
In general, affinities for agonists and antagonists are similar between human, rat, hamster and bovine *alpha*-1ARs.
However, subtle differences in ligand affinities noted in this
study do impact *alpha*-1A In general, affinities for agonists and antagonists are similar between human, rat, hamster and bovine *alpha*-1ARs.
However, subtle differences in ligand affinities noted in this effectively do impact *alpha*-1AR classif ilar between human, rat, hamster and bovine *alpha*-1ARs.

However, subtle differences in ligand affinities noted in this

study do impact *alpha*-1AR classification. One of these dif-

ferences is spiperone affinity, wher However, subtle differences in ligand affinities noted in t
study do impact *alpha*-1AR classification. One of these
ferences is spiperone affinity, where the pK_i value is 6.8
the human *alpha*-1_c and 7.5 for the bovin study do impact *alpha*-1AR classification. One of these of ferences is spiperone affinity, where the pK_i value is 6.8 the human *alpha*-1_c and 7.5 for the bovine *alpha*-1_c. though not a large difference, spiperone the human $alpha_{1c}$ and 7.5 for the bovine $alpha_{1c}$. Although not a large difference, spiperone is the only $alpha_{1c}$. Although not a large difference, spiperone is the only $alpha_{1b}$ -1_B-
selective compound available to date, the human *alpha*-1_c and 7.5 for the bovine *alpha*-1_c. Although not a large difference, spiperone is the only *alpha*-1_B-selective compound available to date, and original descriptions of spiperone in rat tissues d mougn not a large difference, spiperone is the only *alpha*-1_B-selective compound available to date, and original descriptions of spiperone in rat tissues demonstrated higher affinity for the pharmacological *alpha*-1_B selective compound available to date, and original descriptions of spiperone in rat tissues demonstrated higher affinity
for the pharmacological $alpha$ -1_BAR compared to the *alpha*-1_AAR (Michel *et al.*, 1989). Studies t for the pharmacological *alpha*-1_BAR compared to the *alpha*-1_AAR (Michel *et al.*, 1989). Studies to date with cloned (rat, hamster and bovine) *alpha*-1AR subtypes demonstrate spiperone affinities of *alpha*-1_c $\$ 1_A AR (Michel *et al.*, 1989). Studies to date with cloned (rat, hamster and bovine) *alpha*-1AR subtypes demonstrate spiperone affinities of *alpha*-1_c \geq *alpha*-1_b \geq *alpha*-1_e/d (Schwinn and Lomasney, 19 hamster and bovine) $alpha$ -1AR subtypes demonstrate
erone affinities of $alpha$ -1_c \geq $alpha$ -1_b \geq $alpha$ -1_{b/d} (Sch
and Lomasney, 1992). In this study, the human $alpha$ -1_p
higher affinity for spiperone compared with the huma and Lomasney, 1992). In this study, the human $alpha$ -1_b has higher affinity for spiperone compared with the human $alpha$ - pha -1_cAR, matching the previously described pharmacologiand Lomasney, 1992). In this study, the human $alpha_{1b}$ higher affinity for spiperone compared with the human $pha-1_cAR$, matching the previously described pharmacological $alpha^{-1}_{1B} > alpha-1_A$ (Michel *et al.*, 1989) and is content higher affinity for spiperone compared with the human al-
pha-1_cAR, matching the previously described pharmacologi-
cal alpha-1_B > alpha-1_c (Michel *et al.*, 1989) and is consis-
tent with the cloned alpha-1_c enco pha-1_cAR, matching the previously described pharmacological $alpha \cdot 1_B > alpha \cdot 1_A$ (Michel *et al.*, 1989) and is consistent with the cloned $alpha \cdot 1_c$ encoding the pharmacological $alpha \cdot 1_A$ subtype. Another subtle difference bet tent with the cloned $alpha$ -1_c encoding the pharmacological $alpha$ -1_A subtype. Another subtle difference between human and nonhuman homolog affinities occurs with the agonist methoxamine. Original descriptions of pharmacolo alpha-l_A subtype. Another subtle difference between human
and nonhuman homolog affinities occurs with the agonist
methoxamine. Original descriptions of pharmacological al-
pha-1AR subtypes demonstrated higher methoxamin alpha-1_A subtype. Another subtle difference between huma
and nonhuman homolog affinities occurs with the agonis
methoxamine. Original descriptions of pharmacological a
pha-1AR subtypes demonstrated higher methoxamine and nonhuman homolog affinities occurs with the agonist
methoxamine. Original descriptions of pharmacological *al-*
pha-1AR subtypes demonstrated higher methoxamine affin-
ity for the *alpha*-1_A compared with the *alpha pha-lAR* subtypes demonstrated higher methoxamine affinity for the $alpha_{1}$ compared with the $alpha_{1}$ _B (Minneman, 1988a). We demonstrate that whereas the cloned bovine $alpha_{1}$ pha_{1} , has approximately similar affinity fo pha-1AR subtypes demonstrated higher methoxamine affinity for the *alpha*-1_A compared with the *alpha*-1_B (Minneman, com
1988a). We demonstrate that whereas the cloned bovine *al-*
 pha -1_c has approximately similar **3.3**, respectively), the human *alpha-l_a* compared with the *alpha-l_B* (Minneman, compared with the hamster *alpha-l_b* (pK_i, 3.6 compared with assembly 3.3, respectively), the human *alpha-l_c* has higher affini 1988a). We demonstrate that whereas the cloned bovine *al-*

pha-1_c has approximately similar affinity for methoxamine

compared with the hamster *alpha*-1_c (pK_i, 3.6 compared with

3.3, respectively), the human *al* pha-1_c has approximately similar affinity for methoxamine
compared with the hamster $alpha_{1}$ (pK_i, 3.6 compared with
3.3, respectively), the human $alpha_{1}$ -1_c has higher affinity for
methoxamine (pK_i, 4.1) compared wi compared with the hamster $alpha_{1b}$ (pK_i, 3.6 compared wit
3.3, respectively), the human $alpha_{1c}$ has higher affinity fo
methoxamine (pK_i, 4.1) compared with the human $alpha_{1c}$
(pK_i, 2.7); this again is consistent with 3.3, respectively), the human $alpha\-l_c$ has higher affinity for potated methoxamine $(pK_i, 4.1)$ compared with the human $alpha\-l_b$ abil $(pK_i, 2.7)$; this again is consistent with the cloned $alpha\-l_c$ speed encoding the pharmacologi methoxamine (pK_i, 4.1) compared with the human $alpha_{1b}$ (pK_i, 2.7); this again is consistent with the cloned $alpha_{1c}$ encoding the pharmacological $alpha_{1c}$ subtype. Another difference between cloned bovine $alpha_{1c}$ -1AR p (pK_i, 2.7); this again is consistent with the cloned $alpha_{1c}$
encoding the pharmacological $alpha_{1c}$ subtype. Another dif-
ference between cloned bovine $alpha_{1c}$ and $alpha_{1c}$ and $alpha_{1c}$ and $alpha_{1c}$ and $alpha_{1c}$ and $alpha_{1c}$ a encoding the pharmacological $alpha \cdot 1_A$ subtype. Another difference between cloned bovine $alpha \cdot 1AR$ pharmacology and the classically described $alpha \cdot 1_AAR$ subtype is absolute $(+)$ -
niguldipine affinity, with the bovine $alpha \cdot 1_A$ ference between cloned bovine *alpha*-1AR pharmacology and
the classically described *alpha*-1_AAR subtype is absolute (+)-
niguldipine affinity, with the bovine *alpha*-1_cAR 10- to 100-
fold lower compared to experimen miguldipine affinity, with the bovine *alpha*-1_cAR 10- to 100-
fold lower compared to experiments performed in rat tissues
(Boer *et al.*, 1989; Han and Minneman, 1991). Of note,
whereas absolute (+)-niguldipine affinity niguldipine affinity, with the bovine *alpha*-1_cAR 10- to 10
fold lower compared to experiments performed in rat tissu
(Boer *et al.*, 1989; Han and Minneman, 1991). Of no
whereas absolute (+)-niguldipine affinity for th fold lower compared to experiments performed in rat tissues c

(Boer *et al.*, 1989; Han and Minneman, 1991). Of note,

whereas absolute $(+)$ -niguldipine affinity for the rat *alpha*-

1. AR has been reported to be higher (Boer *et al.*, 1989; Han and Minneman, 1991). Of note, whereas absolute $(+)$ -niguldipine affinity for the rat *alpha*-1_cAR has been reported to be higher than the bovine *alpha*-1_cAR (Forray *et al.*, 1994a), we find

1_cAR (Forray *et al.*, 1994a), we find no difference between human and bovine in (+)-niguldipine affinitiy in this study.
Compared with fairly subtle differences in ligand affinities, more striking differences from previ 1_cAR (Forray *et al.*, 1994a), we find no difference between
human and bovine in (+)-niguldipine affinity in this study.
Compared with fairly subtle differences in ligand affinities,
more striking differences from previo human and bovine in (+)-niguldipine affinity in this study.
 Compared with fairly subtle differences in ligand affinities,

more striking differences from previously reported pharma-

cological characterization of cloned Compared with fairly subtle differences in ligand affinities,
more striking differences from previously reported pharma-
cological characterization of cloned $alpha$ -1ARs are apparent
in CEC inactivation studies. In this stud more striking differences from previously reported pharm-
cological characterization of cloned *alpha*-1ARs are appare
in CEC inactivation studies. In this study, we find that bot
human and bovine *alpha*-1_cARs are inact cological characterization of cloned *alpha*-1ARs are apparent
in CEC inactivation studies. In this study, we find that both
human and bovine *alpha*-1_cARs are inactivated less by CEC
compared with that reported previous in CEC inactivation studies. In this study, we find that both
human and bovine $alpha-1_cARs$ are inactivated less by CEC cont
compared with that reported previously in hypotonic mem-
brane preparations (Schwinn *et al.*, 1990, human and bovine *alpha*-1_cARs are inactivated less by CEC contrompared with that reported previously in hypotonic mem-
brane preparations (Schwinn *et al.*, 1990, 1991; Perez *et al.*, 1991). CEC conditions in this stu compared with that reported previously in hypotonic mem-
brane preparations (Schwinn *et al.*, 1990, 1991; Perez *et al.*,
1991). CEC conditions in this study were chosen carefully to
mativate completely the $alpha_{1}$ -AR $(10$ brane preparations (Schwinn *et al.*, 1990, 1991; Perez *et al.*, 1991). CEC conditions in this study were chosen carefully to Refinactivate completely the *alpha*-1_bAR (100 μ M CEC, 37°C, 20 BER min). Under these con 1991). CEC conditions in this study were chosen carefully to
inactivate completely the *alpha*-1_bAR (100 μ M CEC, 37°C, 20
min). Under these conditions, *alpha*-1_bARs are 89 to 98%
inactivated, *alpha*-1_{g/A}ARs 75 inactivate completely the *alpha*-1_bAR (100 μ M CEC, 37°C, 20

min). Under these conditions, *alpha*-1_bARs are 89 to 98%

inactivated, *alpha*-1_{a/d}ARs 75 to 86% and *alpha*-1_cARs 11 to

18%. Hence although *alph* min). Under these conditions, *alpha*-1_bARs are 89 to 98% inactivated, *alpha*-1_{g/d}ARs 75 to 86% and *alpha*-1_cARs 11 to 18%. Hence although *alpha*-1_cARs are inactivated in part by CEC, they are clearly the most r

Human Alpha-1ARs 141
gives further support to the idea that the cloned *alpha-*1_c
subtype encodes the pharmacological *alpha-*1_aAR. Human *Alpha*-1A
gives further support to the idea that the clon
subtype encodes the pharmacological $alpha^{-1}A^AA$
All six $alpha^{-1}AR$ subtypes couple to the h

approximately equal expression level $(1-2 \text{ pmol/mg})$ of total membrane phospholipids *via* phospholipase *C*, as demon-
protein). Although human and rat $alpha_{1}$ _{a/d}, human and strated by production of IP isomers upon stimu Human *Alpha*-1ARs 141

ves further support to the idea that the cloned $alpha_{-1_c}$

btype encodes the pharmacological $alpha_{-1_A}$ AR.

All six $alpha_{-1}$ AR subtypes couple to the hydrolysis of

embrane phospholipids *via* phospholi gives further support to the idea that the cloned *alpha* subtype encodes the pharmacological *alpha*-1_AAR. All six *alpha*-1AR subtypes couple to the hydrolysis membrane phospholipids *via* phospholipase *C*, as demost gives further support to the idea that the cloned $alpha-1_c$
subtype encodes the pharmacological $alpha-1_AAR$.
All six $alpha-1AR$ subtypes couple to the hydrolysis of
membrane phospholipids *via* phospholipase C, as demon-
strated by subtype encodes the pharmacological $alpha-1_AAR$.
All six $alpha-1AR$ subtypes couple to the hydrolysis of
membrane phospholipids *via* phospholipase C , as demon-
strated by production of IP isomers upon stimulation with
NE. As r All six *alpha*-1AR subtypes couple to the hydrolysis of membrane phospholipids *via* phospholipase *C*, as demonstrated by production of IP isomers upon stimulation with NE. As reported previously, the bovine *alpha*-1_c membrane phospholipids *via* phospholipase *C*, as demonstrated by production of IP isomers upon stimulation with NE. As reported previously, the bovine $alpha-1_cAR$ couples with greater NE efficacy to PI hydrolysis compared t strated by production of IP isomers upon stimulation with NE. As reported previously, the bovine *alpha*-1_cAR couples with greater NE efficacy to PI hydrolysis compared to either the hamster *alpha*-1_b or the rat *alph* NE. As reported previously, the bovine *alpha*-1_cAR couples
with greater NE efficacy to PI hydrolysis compared to either
the hamster $alpha_1$ _b or the rat $alpha_1$ _{a/d} (Schwinn *et al.*,
1991). We now report similar results with greater NE efficacy to PI hydrolysis compared to either
the hamster $alpha_{1}$ _b or the rat $alpha_{1}$ _{d'd} (Schwinn *et al.*,
1991). We now report similar results with human $alpha_{1}$ ha-1AR
subtypes; in fact, the human $alpha_{1}$ the hamster $alpha_1$, or the rat $alpha_1$, $alpha_2$ (Schwinn *et al* 1991). We now report similar results with human $alpha_1$ $lambda_2$ -1A
subtypes; in fact, the human $alpha_1$, $lambda_1$, $lambda_2$ has the highest Nl
efficacy of coupling to PI hy 1991). We now report similar results with human *alpha*-1AR subtypes; in fact, the human *alpha*-1_cAR has the highest NE efficacy of coupling to PI hydrolysis of any of the *alpha*-1AR subtypes studied. Coupling of rat subtypes; in fact, the human *alpha*-1_cAR has the highest lefficacy of coupling to PI hydrolysis of any of the *alpha*-1
subtypes studied. Coupling of rat *alpha*-1_{a/d}, hamster
pha-1_b and bovine *alpha*-1_cARs to efficacy of coupling to PI hydrolysis of any of the *alpha*-1AR subtypes studied. Coupling of rat $alpha\text{-}1_{\alpha/d}$, hamster *al-*
pha-1_b and bovine *alpha*-1_cARs to PI hydrolysis has been reported to occur *via* Gq (Wu subtypes studied. Coupling of rat $alpha-1_{\bullet/4}$, hamster c *pha*-1_b and bovine *alpha*-1_cARs to PI hydrolysis has be reported to occur *via* Gq (Wu *et al.*, 1992) and to be insentive to pertussis toxin (Schwinn *et a* pha-1_b and bovine alpha-1_cARs to PI hydrolysis has been reported to occur *via* Gq (Wu *et al.*, 1992) and to be insensitive to pertussis toxin (Schwinn *et al.*, 1991; Perez *et al.*, 1993). Similar results are prese tive to pertussis toxin (Schwinn *et al.*, 1991; Perez *et al.*, 1993). Similar results are presented here for human *alpha*-
1AR subtypes. Typically, pertussis toxin ADP-ribosylates G_i (Simon *et al.*, 1991). However, G 1993). Similar results are presented here for human alpha-1993). Similar results are presented here for human *alpha*-
1AR subtypes. Typically, pertussis toxin ADP-ribosylates G_i
(Simon *et al.*, 1991). However, Gq associated with *alpha*-
1ARs has been classically described 1AR subtypes. Typically, pertussis toxin ADP-ribosylates G_i
(Simon *et al.*, 1991). However, Gq associated with *alpha*-
1ARs has been classically described as pertussis toxin-insen-
sitive (Blank *et al.*, 1991; Simon sitive (Blank *et al.*, 1991; Simon *et al.*, 1991). Isolated reports of *alpha*-1AR-mediated inhibition of PI hydrolysis in the rat heart have occurred (Han *et al.*, 1989), but not confirmed, with cloned *alpha*-1AR subt 1ARs has been classically described as pertussis toxin-insensitive (Blank *et al.*, 1991; Simon *et al.*, 1991). Isolated reports of *alpha*-1AR-mediated inhibition of PI hydrolysis in the rat heart have occurred (Han *et* sitive (Blank *et al.*, 1991; Simon *et al.*, 1991). Isolated reports of *alpha*-1AR-mediated inhibition of PI hydrolysis in the rat heart have occurred (Han *et al.*, 1989), but not confirmed, with cloned *alpha*-1AR subt pertussis **toxin-sensitive in rat-i fibroblasts.** with cloned *alpha*-1AR subtypes. These results demonstrate
that cloned *alpha*-1AR subtype-mediated PI hydrolysis is not
pertussis toxin-sensitive in rat-1 fibroblasts.
In summary, we have cloned three human *alpha*-1AR s

 I ype cDNAs, expressed them stably in rat-1 fibroblasts and that cloned *alpha*-1AR subtype-mediated PI hydrolysis is
pertussis toxin-sensitive in rat-1 fibroblasts.
In summary, we have cloned three human *alpha*-1AR s
type cDNAs, expressed them stably in rat-1 fibroblasts a
chara pertussis toxin-sensitive in rat-1 fibroblasts.
In summary, we have cloned three human *alpha*-1AR sub-
type cDNAs, expressed them stably in rat-1 fibroblasts and
characterized the expressed receptors pharmacologically;
th In summary, we have cloned three human $alpha$ -1AH
type cDNAs, expressed them stably in rat-1 fibroblast
characterized the expressed receptors pharmacologi
this is particularly important for the $alpha$ -1_{a/d} su
which has not pr type cDNAs, expressed them stably in rat-1 fibroblasts and characterized the expressed receptors pharmacologically; this is particularly important for the *alpha*-1_{a/d} subtype which has not previously been characterized this is particularly important for the $alpha_1_{\bullet/d}$ subtype
which has not previously been characterized pharmacologi-
cally. In addition, these data represent the first side-by-side
comparison of pharmacological properties ahomologically. In addition, these data represent the first side-by-side comparison of pharmacological properties between species homologs of *alpha*-1AR subtypes. Although pharmacological characterization of *alpha*-1AR s cally. In addition, these data represent the first side-by-side comparison of pharmacological properties between species homologs of *alpha*-1AR subtypes. Although pharmacological characterization of *alpha*-1AR subtypes i characterization of *alpha*-1AR subtypes is similar in many aspects between human and other species homologs, a few potentially important differences are apparent. The availability of clones for distinct *alpha*-1AR subtyp homologs of *alpha*-1AR subtypes. Although pharmacological characterization of *alpha*-1AR subtypes is similar in many aspects between human and other species homologs, a few potentially important differences are apparent. characterization of *alpha*-1AR subtypes is similar in man aspects between human and other species homologs, a fe potentially important differences are apparent. The ava ability of clones for distinct *alpha*-1AR subtypes aspects between human and other species homologs, a few potentially important differences are apparent. The availability of clones for distinct *alpha*-1AR subtypes in the same species should now facilitate refinement not potentially important differences are apparent. The availability of clones for distinct *alpha*-1AR subtypes in the same species should now facilitate refinement not only of the structural basis of receptor ligand interact ability of clones for distinct *alpha*-1AR subtypes in the same species should now facilitate refinement not only of the structural basis of receptor ligand interactions, but also of signal transduction mechanisms ultimate species should now facilitate refinement not only of the structural basis of receptor ligand interactions, but also of signal transduction mechanisms ultimately utilized by different *al-*
pha-1AR subtypes. In addition, tural basis of receptor ligand interactions, but also of signal
transduction mechanisms ultimately utilized by different *al-*
pha-1AR subtypes. In addition, these data may help in the
development of *alpha*-1AR subtype-se pha-1AR subtypes. In addition, these data may help in the pha-1AR subtypes. In addition, these data may help in the development of *alpha*-1AR subtype-selective drugs for use in clinical medicine.
 Note in proof. While this manuscipt was in review, a paper describing the sequen

development of *alpha*-1AR subtype-selective drugs for use in clinical medicine.
Note in proof. While this manuscipt was in review, a paper describing the sequences of all three human *alpha*-1ARs was published (Forray *et* clinical medicine.
Note in proof. While this manuscipt was in review, a paper
describing the sequences of all three human $alpha$ -1ARs was pub-
lished (Forray *et al.*, 1994b). Comparison of our human $alpha_{pha-1_{a/d}}$
sequence wi **Note in proof.** While this manuscipt was in review, a paper describing the sequences of all three human *alpha*-1ARs was published (Forray *et al.*, 1994b). Comparison of our human *alpha*-1_{a/d} sequence with results re describing the sequences of all the lished (Forray *et al.*, 1994b). Corrections sequence with results reported by reveals 100% sequence identity sour human *alpha*-1_{a/d} corrections

Acknowledgments

The authors are allows because the authors wish to acknowledge helpful discussions with, and
The authors wish to acknowledge helpful discussions with, and
thinued support by, both Drs. Robert J. Lefkowitz and Marc G. our human α *lpha*-1_{a/d} corrections.
 Acknowledgments

The authors wish to acknowledge helpful discussions with, and

continued support by, both Drs. Robert J. Lefkowitz and Marc G.

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