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Rosazza et al.

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(54) **CARBOXYLIC ACID REDUCTASE
POLYPEPTIDE, NUCLEOTIDE SEQUENCE
ENCODING SAME AND METHODS OF USE**

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patent is extended or adjusted under 35
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Related U.S. Application Data

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Mar. 11, 2003, now Pat. No. 7,056,714.

(51) **Int. Cl.**

C12N 9/02 (2006.01)
C12N 15/00 (2006.01)
C12P 21/04 (2006.01)
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C12Q 1/26 (2006.01)
C07H 21/04 (2006.01)

(52) **U.S. Cl.** **435/189**; 435/440; 435/25;
435/69.1; 435/71.1; 435/132; 536/23.2

(58) **Field of Classification Search** None
See application file for complete search history.

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(57) **ABSTRACT**

The invention provides the nucleotide sequence and amino
acid sequence for the enzyme carboxylic acid reductase iso-
lated from bacteria. Expression cassettes, vectors, trans-
formed cells, and variants are also provided as methods for
use of recombinant biocatalytic reagents in production of
synthetic, aromatic, aliphatic and alicyclic aldehydes and
alcohols.

3 Claims, 8 Drawing Sheets

Nocardia	1	--AVDSPDERLQRPTAQLRAEAEQVKAARELEAVSAAVSAPGMRLAQLAATVMAGYADRP
MtfadD	1	---MSINDORLTRRVEDLYASDAQFAAAASENEAITQATDQPGVALPQLIRMMVEGYADRP
MBCG	1	---MSINDORLTRRVEDLYASDAQFAAAASENEAITQATDQPGVALPQLIRMMVEGYADRP
MIAcS	1	MSTITKQEKQLARRVDDLTANLPQFAAAKEDPAVAAALAQPGRLRPLQIQTALDGYAERE
Msmeg	1	-MTIETREDLFRNRI DHELETLPQFAAAAREDEATSAABADELRLPAAVKOLLAGYADRP
consensus	1	v d r l RRie Lfa D QfaAA P eAvs Av Pgm Lpqii vm GYADRP
Nocardia	59	AAGQRAFELNTLDATGRTSIRLLPRFETITYRELWQRVGEVAAAWHHDPENPLRAGLFVA
MtfadD	58	ALGQRALREVTDPDSGRIMVELLPRFETITYRELWARAGTLATALSAEP--AIRPGDRV
MBCG	58	ALGQRALREVTDPDSGRIMVELLPRFETITYRELWARAGTLATALSAEP--AIRPGDRV
MIAcS	61	ALGQVAVFTKLPKTKGRTSMELLPSEFETITYRQLGDRVGALARAWRH---LLHAGYRVC
Msmeg	60	ALGKRAVEVTD--EEGRITAKLLPRFDITITYRQLAGRIQAVTNAWHNH---PYNAGDRVA
consensus	61	AlGqRa f tD tGRT l LLPrFeTITYR L R g va A d lr GdrV
Nocardia	119	ILGFTSLDYATLIDLADHILGAVTVPLQASAAVSQLIALITETSPRLLIASTPEHIDAAVEC
MtfadD	116	VLGFNSVDYTTIDIALIRLGAHSVPLQTSAPVTGLRPIVTETEPTMIATSIDNLGDAVEV
MBCG	116	VLGFNSVDYTTIDIALIRLGAHSVPLQTSAPVTGLRPIVTETEPTMIATSIDNLGDAVEV
MIAcS	118	VLGFNSVDYTTIDMALGVIGAVAVPLQTSAAITQLQSVTETEPESMIATSNVQLPDTVEL
Msmeg	116	ILGFTSLDYATLIDLADHILGAVTVPLQTSAPVVAQLQPIVAETEPKVIASVDFLADAVL
consensus	121	ILGF SvDY tiDlAlI lGAVtVPLQtsA vs L IvtETeP liAssie L daVeV
Nocardia	179	ILAGTTPEIRLVVFDYHPEDLDQRAAFESARRLADAGSSVIVETLDAMRAEGDFEPAAPL
MtfadD	176	LAG-HAPARLVVFDYHGKVDTHREAVEAARARLAG---SVTIDTLAELIERGRALPAT--
MBCG	176	LAG-HAPARLVVFDYHGKVDTHREAVEAARARLAG---SVTIDTLAELIERGRALPAT--
MIAcS	178	ILSGQAPAKLVVFDYHPEDLDQRAAFESARRLADAGSSVIVETLDAMRAEGDFEPAAPL
Msmeg	176	VESGPAPSRLVVFDYHSHVDLDQRAAFESARRLADAGSSVIVETLDAMRAEGDFEPAAPL
consensus	181	l aP rLVVFDYh vD reA e ArarLA sV vetl evi RGr Lpa
Nocardia	239	FVPDITDDLP LALLIYTSGSTGTPKGAMYTNRLAATMWQG---NSMLQGNSQRVGINLHNYM
MtfadD	230	PIADSADL LALLIYTSGSTGAPKGMAYRESQVMSFWRK---SSGWFEPSGYPSITLNFEM
MBCG	230	PIADSADL LALLIYTSGSTGAPKGMAYRESQVMSFWRK---SSGWFEPSGYPSITLNFEM
MIAcS	236	PVADSADL LALLIYTSGSTGAPKGMAYRESQVMSFWRK---SDGNVFGPPTAASITLNFEM
Msmeg	233	LYVPDEADPL LLLIYTSGSTGTPKGAMYPEKKTATMWQAGSKARWDET LGVMSITLNFEM
consensus	241	v d D LaLLIYTSGSTG PKGAMY s t W sItLNFEM
Nocardia	296	PMSHLAGRISLEGVLRGGTAYFAAKSDMLSTLFEDI GLVRPTEL FVPRVCDMVFQRYQS
MtfadD	287	PMSHVGGQVLYGTLNSGGTAYFVAKSDMLSTLFEDLALVRPTELCEVPRIDMVFQRYQS
MBCG	287	PMSHVGGQVLYGTLNSGGTAYFVAKSDMLSTLFEDLALVRPTELCEVPRIDMVFQRYQS
MIAcS	293	PMSHVMGRGILYGTLSNGGTAYFAARS DLSTLFEDLALVRPTELNEVPRIVETLYDESKR
Msmeg	293	PMSHVMGRGILCSTLASGGTAYFAARS DLSTLFEDLALVRPTELNEVPRIVETLYDESKR
consensus	301	PMSHv GR vLfgtL GGTAYf AkSDlStl EDlgLVRPtel FVPRiwdmvf ey s
Nocardia	356	ELDRRSVAG--ADLDTLDREVKADLRONYLGGREFLVAVVGSAPLAAEMKTFMES-VLIDL
MtfadD	347	EVDRPLVDC--ADRAALEAQVKAELPENVLGGREFVMALTSAPISAEMTAWVESILLALVH
MBCG	347	EVDRPLVDC--ADRAALEAQVKAELPENVLGGREFVMALTSAPISAEMTAWVESILLALVH
MIAcS	353	AVDPPLANSGSADRAATKAEVMDEQRFQSLGGRYIAAMTGSAPTSPELKHGVE3-LLEMH
Msmeg	353	RLDNRRAEC--S-EDRAEAALVEEVRTQLLGGRFVMSALTSAPISAEMKSWED-LLDMH
consensus	361	lDrR g ad lda V elR nvLGRfl AvtGSAPlsaEm fvEs l dlh
Nocardia	413	LHDGYGSTEAGSVLLDNOIQREPVLDYKLVDPPELGYFRTDRPHPRGELLKTAETTIFG
MtfadD	405	LVEGYGSTEAG-MVLNDCMVRPAPAVIYKLVDPPELGYFRTDRPHPRGELLKTMFPG
MBCG	405	LVEGYGSTEAG-MVLNDCMVRPAPAVIYKLVDPPELGYFRTDRPHPRGELLKTMFPG
MIAcS	412	LLEGYCSTEAG-MVLFDCGEVORPPVLDYKLVDPPELGYESTDQYPRGELLKTMFPG
Msmeg	409	LLEGYGSTEAG-AVFIDGQIQREPVLDYKLVDPPELGYEATDRPHPRGELLKTMFPG
consensus	421	LveGYGSTEAG V l Dg i RP ViDYKLVDPPELGYF TD PyPRGELLKt mfPG

FIG. 1A

Nocardia 952 ANGYGNSKWAGEVLLREAHDCGLPVAVFRSDMILAHSRVAGQLVQVDFTRILMLSLVAT
MtfadD 943 ANGYANSKWAGEVLLREAHDCGLPVTVFRCDMILADTSYTGQLNLPDMFTRMLMLSLAAT
MBCG 943 ANGYANSKWAGEVLLREAHDCGLPVTVFRCDMILADTSYTGQLNLPDMFTRMLMLSLAAT
MlAcS 950 ANGYGNSKWAGEVLLREAHDCGLPVTVFRCDMILADTSYAGQLVMPDMFTPMMLSLAAT
Msmeg 947 ANGYGNSKWAGEVLLREAHDCGLPVSVFRCDMILADTSYTGQLNLPDMFTRMLMLSLVAT
consensus 961 ANGYgNSKWAGEVLLREAHd CGLPVtVFRcDMILAdtsY GQLNvpDmFTRlmLSL AT

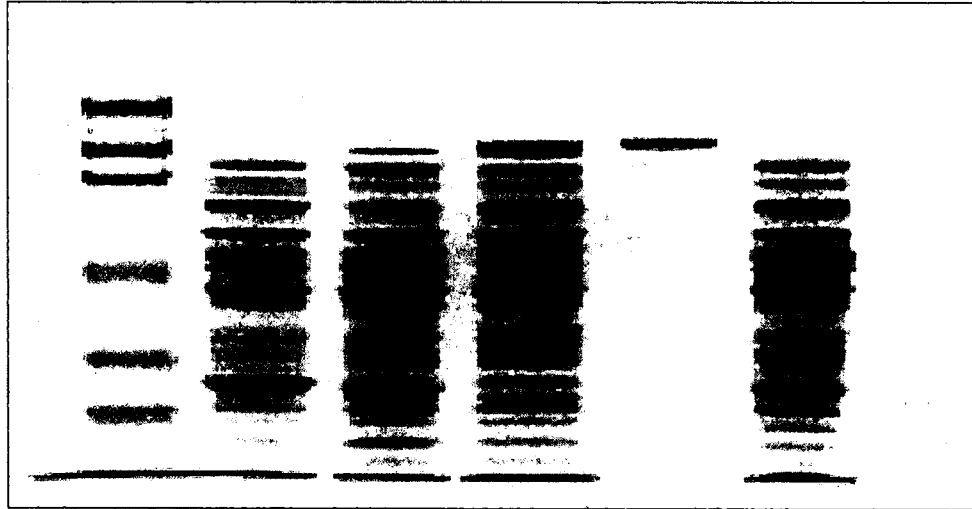
Nocardia 1012 GIAFYSFRTDADGNRQRAHYDGLPADFTAAAITALG---IQATEGRTYDVLNPNYDDGI
MtfadD 1003 GIAFGSFYELDAHGNRQRAHYDGLPVEFVAEAITCLG---THSPURFVTVYHVMNPNYDDGI
MBCG 1003 GIAFGSFYELDAHGNRQRAHYDGLPVEFVAEAITCLG---THSPURFV-----
MlAcS 1010 GIAFGSFYELDAESIRQRAHYDGLPVEFTAAEISTLGDQSLHDRUGFTTYHVMNPHDDGI
Msmeg 1007 GIAFGSFYELDADGNRQRAHYDGLPVEFTAAEISTIG---SQVTIGFETTHVMNPNYDDGI
consensus 1021 GIAPgSFYelDA gNRQRAHYDGLPveFvAeAI tIG d F ty vlnp ddgi

Nocardia 1069 SLDEFVDWLIVESG----HPTRITIDYSDWFHRFETALRALPEKQRQASVLPDLLDAYRNEC
MtfadD 1060 GLDEFVDWLNSTSGSGCTIORTIALYGEFLORFETSLRALPDRQPHASLPLLLHNYREBA
MBCG -----
MlAcS 1070 GMDEFVDWLID---AGCPTRINDYDEWLRFEISLRALPERQRHSSLLELLHNYQKPE
Msmeg 1064 GLDEFVDWLEIAG----YPVHFVDDYATWLSRFEETALRALPERQRQASLPLLLHNYQOQS
consensus 1081 ldefvdwl i ri dy w rfe iralpekqr svlpll y p

Nocardia 1125 PAVRGAILLAKEFQAAVQTEKIGPEQDIPHLSAPLIDKYVSDLETLQLL (SEQ ID NO:81)
MtfadD 1120 KPICGSLAETDQFRAAVQEAKEGPKDKDIPHLTAAALAKYISNLRLLGLL (SEQ ID NO:32)
MBCG ----- (SEQ ID NO:33)
MlAcS 1126 KPLHGSIAETIRFERTAVQNANIGQDKDIPHISPATIAKYVSDLQHLGLV (SEQ ID NO:34)
Msmeg 1120 PPVCGAMAETDRFRAAVQDAKIGPKDKDIPHVTADVIVKYISNLQMLGLL (SEQ ID NO:35)
consensus 1141 v g i p f avq a ig e diphls li kyvs l ll ll (SEQ ID NO:36)

FIG. 1C

A



B

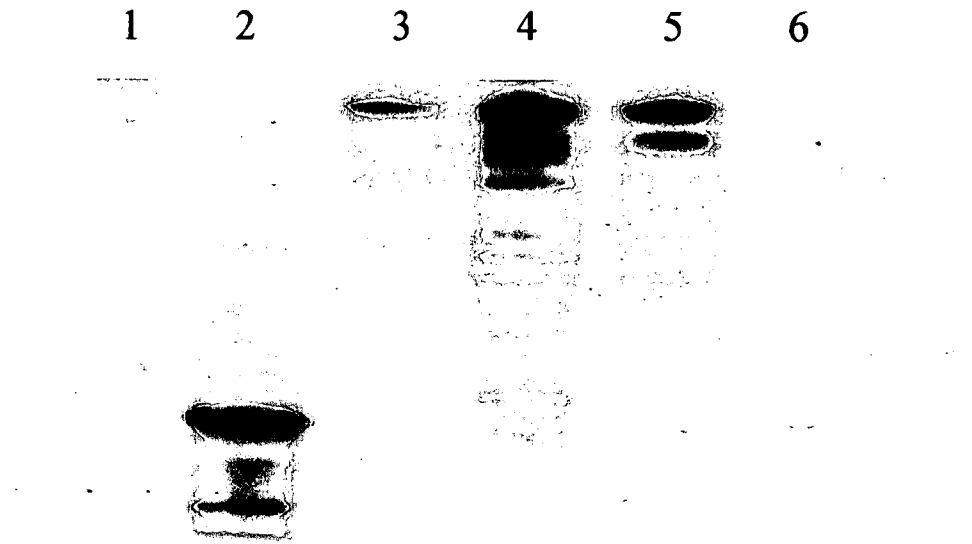


FIG.2

Car-C	LIY TSGSTG TPKGAMY (SEQ ID NO:40)
FadD9	LIY TSGSTG APKGAMY (SEQ ID NO:41)
yeast AAR	LS F TSGSEGI P KGVLG (SEQ ID NO:42)
motif-Pc	--- TSGSEGR PKG--- (SEQ ID NO:43)
consensus	l y TSGS G PKG m (SEQ ID NO:44)
Car-D	DLPLHDGY G STEAG (SEQ ID NO:45)
FadD9	DVHLVEGY G STEAG (SEQ ID NO:46)
yeast	NCRIVNMY G TTETQ (SEQ ID NO:47)
motif-Pc	--- IVNMYG TT--- (SEQ ID NO:48)
consensus	lv YG sTe (SEQ ID NO:49)
Car-F	DE D GFYKTGDIVAE (SEQ ID NO:50)
FadD9	DPDGFY R TGDIMAK (SEQ ID NO:51)
yeast	PRDRLY R TGDLGRY (SEQ ID NO:52)
motif-Pc	--- RLYR SGDL--- (SEQ ID NO:53)
consensus	d Yrt GDl (SEQ ID NO:54)
Car-H	DANLQ P YEIPRDF- (SEQ ID NO:55)
FadD9	AAGLQ S YEIPRDF- (SEQ ID NO:56)
yeast	EPTLIT E MVPR-FD (SEQ ID NO:57)
motif-Pc	--- LVS YFVP---- (SEQ ID NO:58)
consensus	L sy iPr f (SEQ ID NO:59)
Car-I	NGLLSGIA K LLRPNLKER (SEQ ID NO:60)
FadD9	NGLLTGIR K LARPQLKKF (SEQ ID NO:61)
yeast	KLPLNPNG K VDPKPLQFP (SEQ ID NO:62)
motif-Pc	--- LNPNG KIDKPAL--- (SEQ ID NO:63)
consensus	L gKv kP L (SEQ ID NO:64)
Car-J	FTDLGG D SLSALSF (SEQ ID NO:65)
FadD9	FADLGG D SLSALS (SEQ ID NO:66)
yeast	FFDLGG H SILATKM (SEQ ID NO:67)
motif-Pc	--- LGGH SILAQ-- (SEQ ID NO:68)
consensus	f d LGG Si A (SEQ ID NO:69)
Car-NADP	LLTG A NGYLGRFL (SEQ ID NO:70)
FadD9	LLTG A TGFLGRYL (SEQ ID NO:71)
yeast	FVTG V TGFLGSYI (SEQ ID NO:72)
motif-Pc	--- GATG FLGAHI (SEQ ID NO:73)
consensus	vt GatG FLG yi (SEQ ID NO:74)
Car-Reduct	YANGY G NSKWAGE (SEQ ID NO:75)
FadD9	YANGY A NSKWAGE (SEQ ID NO:76)
yeast	LTGGY Q SKWAAE (SEQ ID NO:77)
motif-Pc	--- GYG QSKW--- (SEQ ID NO:78)
consensus	GY qqSKWaae (SEQ ID NO:79)

FIG.3

AVDSPDERLQ	RRIAQLFAED	EQVKAARPLE	AVSAAVSAPG	MRLAQIAATV	
MAGYADRPAA	GQRAFELNTD	DATGRTSLRL	LPRFETITYR	ELWQRVGEVA	100
AAWHHPENP	LRAGDFVALL	GFTSIDYATL	DLADIHLGAV	TVPLQASAAV	
SQLIAILTET	SPRLLASTPE	HLDAAVECLL	AGTTPERLVV	FDYHPEDDDQ	200
RAAFESARRR	LADAGSLVIV	ETLDAVRARG	RDLPAAPLFV	PDTDDDPLAL	
LIYTSGSTGT	PKGAMYNRL	AATMWQGNM	LQGNSQRVGI	NLNYMPMSHI	C 300
AGRISLFGVL	ARGGTAYFAA	KSDMSTLFED	IGLVRPTEIF	FVPRVCDMVF	
QRYQSELDRR	SVAGADLDTL	DREVKADLRQ	NYLGGREFVA	VVGSAPLAAE	400
MKTFMESVLD	LPLHDGYGST	EAGASVLLDN	QIQRPPVLDY	KLVDVPELGY	D
FRTDRPHPRG	ELLLKAETTI	PGYYKRPEVT	AEIFDEEDGFY	KTGDIVAELE	F 500
HDRLVYVDRR	NNVLKLSQGE	FVTVAHLEAV	FASSPLIRQI	FIYGSSERSY	
LLAVIVPTDD	ALRGRDTATL	KSALAESIQR	IAKDANLOPY	EIPRDFLIET	H 600
EPFTIANGLL	SGIAKLLRPN	LKERYGAQLE	QMYTDLATGQ	ADELLALRRE	I
AADLPVLETV	SRAAKAMLV	ASADMRPDAH	FTDLGGDSLS	ALSFSNLLHE	J 700
IFGVEVPVGV	VVSPANELRD	LANYIEAERN	SGAKRPTFTS	VHGGGSEIRA	
ADLTLDKFID	ARTLAAADSI	PHAPVPAQTV	LLTGANGYLG	RFLCLEWLER	NADP bind. 800
LDKTGGTLIC	VVRGSDAAAA	RKRLDSAFDS	GDPGLLEHYQ	QLAARTLEVL	
AGDIGDPNLG	LDDATWQRLA	ETVDLIVHPA	ALVNHVLPYT	QLFGPNVVG	900
AEIVRLAITA	RRKPVTYLST	VGVADQVDP	EYQEDSDVRE	MSAVRVVRES	
YANGYGNSKW	AGEVLLREAH	DLCGLPVAVF	RSDMILHSR	YAGQLNVQDV	Reduction 1000
FTRLILSLVA	TGIAPYSFYR	TDADGNRQRA	HYDGLPADFT	AAAITALGIQ	
ATEGFRTYDV	LNPYDDGISL	DEFVDWLVES	GHPIQRITDY	SDWFHRFETA	1100
IRALPEKQRQ	ASVLPPLDAY	RNPCPAVRGA	ILPAKEFQAA	VQTAKIGPEQ	1150
DIPHLSAPLI	DKYVSDLELL	QLL (SEQ ID NO:81)			

FIG.4

SINDQRLTRR	VEDLYASDAQ	FAAASPNEAI	TQAIDQPGVA	LPQLIRMVME	
GYADRPALGQ	RALRFVTPDP	SGRTMVELLP	RFETITYREL	WARAGTLATA	100
LSAEPAIRPG	DRVCVLGFNS	VDYTTIDIAL	IRLGAVSVPL	QTSAPVTGLR	
PIVTETEPTM	IATSIDNLGD	AVEVLGHAP	ARLVVFDYHG	KVDTHREAVE	200
AARARLAGSV	TIDTLAELIE	RGRALPATPI	ADSADDALAL	LIYTSGSTGA	C
PKGAMYRESQ	VMSFWRKSSG	WFEPGYPYPSI	TLNFMPMSHV	GGRQVLYGTL	300
SNGGTAYFVA	KSDLSTLFED	LALVRPTELC	FVPRIWDMVF	AEFHSEVDRR	
LVDGADRAAL	EAQVKAELRE	NVLGGRFVMA	LTGSAPISAE	MTAWVESLLA	400
DVHLVEGYGS	TEAGMVLNDG	MVRRPAVIDY	KLVDVPELGY	FGTDQPYPRG	D
ELLVKTQTMF	PGYQRPDVT	AEVDFDPDGFY	RTGDIMAKVG	PDQFVYLDRR	F 500
NNVLKLSQGE	FIAVSKLEAV	FGDSPLVRQI	FIYGNSARAY	PLAVVVPSPD	
ALSRHGIENL	KPVISESLOE	VARAAGLOSY	EIPRDFIET	TPFTLENGLL	H 600
TGIRKLARPO	LKKFYGERLE	RLYTELADSQ	SNELRELRQS	GPDAPVLPT	I
CRAAAALLGS	TAADVPRDAH	FADLGGDSL	ALSLANLLHE	IFGVDVPVGV	J 700
IVSPASDLRA	LADHIEAART	GVRPSPFASI	HGRSATEVHA	SDLTLDKPID	
AATLAAAPNL	PAPSAQVRTV	LLTGATGFLG	RYLALEWLDR	MDLVNGKLIC	NADP
LVRARSDEEA	QARLDATFDS	GDPYLVRHYR	ELGAGRLEVL	AGDKGEADLG	
LDRVTWQRLA	DTVDLIVDPA	ALVNHVLPYS	QLFGPNAAGT	AELLRLALTG	900
KRKPYYTST	IAVGEQIPPE	AFTEDADIRA	ISPTRRIDDS	YANGYANSKW	Reduction
AGEVLLREAH	EQCGLPVTVF	RCDMILADTS	YTGQLNLPDM	FTRLMLSLAA	
TGIAPGSFYE	LDAHGNRQRA	HYDGLPVEFV	AEAICTLGTH	SPDRFVTYHV	
MNPYDDGIGL	DEFVDWLNSP	TSGSGCTIQR	IADYGEWLQR	FETSLRALPD	1100
RQRHASLLPL	LHNYREPAKP	ICGSIAPTQD	FRAAVQEAKI	GPKDIPHLT	1150
AAIIAKYISN LRLGLL (SEQ ID NO:82)					

FIG.5

TNEKVVIEKL	DNPTLSVLPH	DFLRPQQEY	TKQATYSLQL	PQLDVPHDSF	
SNKYAVALSV	WAALIYRVTG	DDDIVLYIAN	NKILRFNIQP	TWSFNELYST	100
INNELNKLNS	IEANFSFDEL	AEKIQSCQDL	ERTPQLFRLA	FLENQDFKLD	
EFKHHLVDF	LNLDTSNNAH	VLNLIYNLL	YSNERVTIVA	DQFTQYLTA	200
LSDPSNCITK	ISLITASSKD	SLPDPTKNLG	WCDFVGCIRD	IFQDNAEAFP	
ERTCVVETPT	LNSDKRSRFT	YRDINRTSNI	VAHYLIKGTI	KRGDVVMIYS	300
SRGVDLMVCV	MGVLKAGATF	SVIDPAYPPA	RQTIYLGVAK	PRGLIVIRAA	
GQLDQLVEDY	INDELEIVSR	INSIAIQENG	TIEGGKLDNG	EDVLAPYDHY	400
KDTRTGVVVG	PDSNPTLSFT	SGSEGIPKGV	LGRHFSLAYY	FNWMSKRFNL	C
TENDKFTMLS	GIAHDPIQRD	MFTPLFLGAQ	LYVPTQDDIG	TPGRLAEWMS	500
KYGCTVTHLT	PAMGQLLTAQ	ATTPFPKLHH	AFFVGDILTK	RDCLRLQTLA	
ENCRIVNMYG	TTETQRAVS	FEVKSKNDDP	NFLKCLKDVM	PAGKMLNVQ	D 600
LLVVRNRDRT	QICGIGEIGE	IYVRAGGLAE	GYRGLPELNK	EKFVNNWFVE	
KDHWNYLDKD	NGEPWRQFWL	GPRDRLYRTG	DLGRYLPNGD	CECCGRADDQ	F 700
VKIRGFRIEL	GEIDTHISQH	PLVRENITLV	RKNADNEPTL	ITFMVPRFDK	H
PDDLKSFQSD	VPKEVETDPI	VKGLIGYHLL	SKDIRTFLKK	RLASYAMPSL	800
IVVMDKLP LN	PNGKVDPKPL	QFPTPKQLNL	VAENTVSETD	DSQFTNVERE	
VRDLWLSILP	TKPASVSPDD	SFFDLGGHSI	LATKMIFTLK	KKLQVDLPLG	J 900
TIFKYPTIKA	FAAEIDRIKS	SGGSSQGEVV	ENVTANYAED	AKKLVETLPS	
SYPSREYFVE	PNSAEGKTTI	NVFVTGVTGF	LGSYILADLL	GRSPKNYSFK	NADP bind. 1000
VFAHVRAKDE	EAAFARLQKA	GITYGTWNEK	FASNIKVVLG	DLSKSQFGLS	
DEKWMDLANT	VDIIHNGAL	VHWVYPYAKL	RDPNVISTIN	VMSLAAVGKP	1100
KFFDFVSSTS	TLDTEYYFNL	SDKLVSEGKP	GILESDDL MN	SASGLTGGYG	
QSKWAAEYII	RRAGERGLRG	CIVRPGYVTG	ASANGSSNTD	DFLLRFLKGS	Reduction 1200
VQLGKIPDIE	NSVMMPVDH	VARVVVATSL	NPPKENELAV	AQVTGHPRIL	
FKDYLYTLHD	YGVDVEIESY	SKWKSLEAS	VIDRNEENAL	YPLLHMVL DN	1300
LPESTKAPEL	DDRNAVASLK	KDTAWTGVDW	SNGIGVTPEE	VGIYIAFLNK	1350
VGFLPPPTHN	DKLPLPSIEL	TQAQISLVAS	GAGARGSSAA	A (SEQ ID NO:80)	

FIG.6

1

**CARBOXYLIC ACID REDUCTASE
POLYPEPTIDE, NUCLEOTIDE SEQUENCE
ENCODING SAME AND METHODS OF USE**

CROSS-REFERENCE TO RELATED
APPLICATIONS

This is a Continuation Application of U.S. patent application Ser. No. 10/386,329 filed Mar. 11, 2003, now U.S. Pat. No. 7,056,714, which application is hereby incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

Microorganism-produced enzymes are widely used as a class of biocatalytic reagents in production of synthetic, aromatic, aliphatic and alicyclic aldehydes and alcohols are useful chemical intermediates in chemical, agrochemical, pharmaceutical and food industries. These enzymes are useful in a wide variety of reactions including, e.g., oxidations, reductions, hydrolyses, and carbon—carbon bond ligations.

Biocatalysts are valued for their intrinsic abilities to bind organic substrates and to catalyze highly specific and selective reactions under the mildest of reaction conditions. These selectivities and specificities are realized because of highly rigid interactions occurring between the enzyme active site and the substrate molecule. Biocatalytic reactions are particularly useful when they may be used to overcome difficulties encountered in catalysis achieved by the use of traditional chemical approaches.

Carboxylic acid reductases are complex, multicomponent enzyme systems, requiring the initial activation of carboxylic acids via formation of AMP and often coenzyme A intermediates (see, e.g., Hempel et al., *Protein Sci.* 2:1890-1900 (1993). Chemical methods for carboxylic acid reductions are generally poor usually requiring prior derivatization and product deblocking with multifunctional reactants.

An enzymatic reaction offers significant advantages over existing methods used in chemical reductions of carboxylic acids, or their derivatives. Unlike many substrates subjected to biocatalytic reactions, carboxylic acids are generally water soluble, rendering them of potentially broad application to this class of enzyme. The carboxylic acid reduction reaction appears to bear the usual desirable features of functional group specificity. It also functions well under mild reaction conditions and produces a high yield of product. The reduction of the activated carboxylic acid intermediate occurs stepwise to give aldehyde products (Gross et al., *Eur. J. Biochem.* 8:413-419; 420-425 (1969); Gross, *Eur. J. Biochem.* 31:585-592 (1972)).

The reduction of carboxylic acids by microorganisms is a relatively new biocatalytic reaction that has not yet been widely examined or exploited. Jezo and Zemek reported the reduction of aromatic acids to their corresponding benzaldehyde derivatives by Actinomycetes in *Chem. Papers* 40(2): 279-281 (1986). Kato et al. reported the reduction of benzoate to benzyl alcohol by *Nocardia asteroides* JCM 3016 (*Agric. Biol. Chem.* 52(7):1885-1886 (1988)), and Tsuda et al. described the reduction of 2-aryloxyacetic acids (*Agric. Biol. Chem.* 48(5): 1373-1374 (1984)) and arylpropionates (*Chem. Pharm. Bull.* 33(11):4657-4661 (1985)) by species of *Glomeraella* and *Gloeosporium*. Microbial reductions of aromatic carboxylic acids, typically to their corresponding alcohols, have also been observed with whole cell biotransformations by *Clostridium thermoaceticum* (White et al., *Eur. J. Biochem.* 184:89-96 (1989)), and by *Neurospora* (Bachman et al., *Arch. Biochem. Biophys.* 91:326 (1960)). More recently,

2

carboxylic acid reduction reactions have reportedly been catalyzed by whole cell preparations of *Aspergillus niger*, *Corynespora melonis* and *Coriolus* (Arfmann et al., *Z. Naturforsch* 48c:52-57 (1993); cf., Raman et al., *J. Bacteriol* 84:1340-1341 (1962)), and by *Nocardia asteroides* (Chen and Rosazza, *Appl. Environ. Microbiol.* 60(4):1292-1296 (1994)).

Biocatalytic reductions of carboxylic acids are attractive to traditional chemical catalysis because the substrates are water soluble, blocking chemistry is not necessary, reductions are enantioselective (7), and the scope of the reaction is very broad (23, 32).

Aldehyde oxidoreductases are also known as carboxylic acid reductases (CAR), require ATP, Mg²⁺, and NADPH as cofactors during carboxylic acid reduction (15, 16, 20, 23). The reduction reaction is a stepwise process involving initial binding of both ATP and the carboxylic acid to the enzyme, to form mixed 5'-adenylic acid-carbonyl anhydride intermediates (8, 14, 24, 26, 40) that are subsequently reduced by hydride delivery from NADPH to form the aldehyde product (15, 24).

Aromatic carboxylic acid reductases have been purified to homogeneity only from *Neurospora* (16) and *Nocardia* (20, 23). Although details of N— and internal amino acid sequences have been reported for the *Nocardia asteroides* enzyme (23), complete gene sequences for these or any other carboxylic acid reductases are unknown.

It is an object of the present invention to provide a purified and isolated bacterial carboxylic acid reductase (CAR) gene and the protein encoded thereby.

It is yet another object of the invention to provide homologous nucleotide sequences and/or amino acid sequences which encode CAR.

It is yet another object of the invention to provide recombinant DNA using expression constructs, vectors, and recombinant cells using the sequences of the invention for production of recombinant CAR.

It is yet another object of the invention to provide for large scale production of and recovery of recombinant CAR, for use in production of synthetic, aromatic, aliphatic and alicyclic aldehydes and alcohols.

It is yet another embodiment of the invention to provide methods of synthesis of chemical compounds such as those for biocatalytically reducing a carboxylic acid, or a derivative thereof, to its corresponding aldehyde product(s), to provide a method of biocatalytically reducing a carboxylic acid, or a derivative thereof, to its corresponding intermediary by-product(s), as exemplified by acyl-AMP analogs, or to provide a method of biocatalytically reducing vanillic acid, or a precursor or derivative thereof, to vanillin, all using recombinant CAR as described in the invention disclosed herein.

Additional objects, advantages and novel features of the invention will be set forth in part in the description which follows, and in part will become apparent to those skilled in the art on examination of the following, or may be learned by practice of the invention.

BRIEF SUMMARY OF THE INVENTION

The present invention provides polynucleotides, related polypeptides and all conservatively modified variants of purified and isolated CAR. The nucleotide sequence of CAR comprises the sequence found in SEQ ID NO: 1, 3, and 5. Sequences 3 and 5 provide examples of conservatively modified polynucleotides of SEQ ID NO: 1 and sequences 7, and 9, 11, are examples of sequences with 80, 90, and 95% sequence identity to SEQ ID NO:1 as also described herein.

Therefore, in one aspect, the present invention relates to an isolated nucleic acid comprising an isolated polynucleotide sequence encoding a CAR enzyme. In a further aspect, the present invention includes a nucleic acid selected from: (a) an isolated polynucleotide encoding a polypeptide of the present invention; (b) a polynucleotide having at least 80%, 90% or 95% identity to a polynucleotide of the present invention; (c) a polynucleotide comprising at least 25 nucleotides in length which hybridizes under high stringency conditions to a polynucleotide of the present invention; (d) a polynucleotide comprising a polynucleotide of the present invention; and (e) a polynucleotide which is complementary to the polynucleotide of (a) to (d).

In another aspect, the present invention relates to a recombinant expression cassette comprising a nucleic acid as described, supra. Additionally, the present invention relates to a vector containing the recombinant expression cassette. Further, the vector containing the recombinant expression cassette can facilitate the transcription and translation of the nucleic acid in a host cell. The present invention also relates to host cells able to express the polynucleotide of the present invention. A number of host cells could be used, such as but not limited to, microbial, mammalian, plant, or insect. In a preferred embodiment the host cell is a bacterial cell. In a more preferred embodiment the bacterial host cell is *E. Coli*. Thus the invention is also directed to transgenic cells, containing the nucleic acids of the present invention as well as cells, strains and lines derived therefrom.

This invention also provides an isolated polypeptide comprising (a) a polypeptide comprising at least 80%, 90% or 95% sequence identity to a polypeptide of the present invention (SEQ ID NO:2); (b) a polypeptide encoded by a nucleic acid of the present invention; and (c) a polypeptide comprising CAR activity and modeled and designed after SEQ ID NO:1.

Another embodiment of the subject invention comprises a method for biocatalytically reducing a carboxylic acid, or a derivative thereof, to its corresponding aldehyde product(s), to provide a method of biocatalytically reducing a carboxylic acid, or a derivative thereof, to its corresponding intermediary by-product(s), as exemplified by acyl-AMP analogs, or to provide a method of biocatalytically reducing vanillic acid, or a precursor or derivative thereof, to vanillin, all using recombinant cells, extracts, CAR protein purified therefrom or derivatives and modifications of this CAR protein.

Yet another embodiment of the invention comprises a method of making a polypeptide of a recombinant gene comprising:

- a) providing a population of these host cells; and
- b) growing the population of cells under conditions whereby the polypeptide encoded by the coding sequence of the expression cassette is expressed;
- c) isolating the resulting polypeptide.

A number of expression systems using the said host cells could be used, such as but not limited to, microbial, mammalian, plant, or insect.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. 1A-1C are alignments of the deduced amino acid sequence of *Nocardia* CAR with a representative sample of putative homologous molecules from other organisms. Identical amino acids are highlighted in black, and similar amino acids are highlighted in gray. The Clustal W program was used to align the above sequences, and Boxshade (0.7 setting) was used to determine the degree of residue shading. The corresponding nucleotide sequence encoding *Nocardia* CAR

has been deposited in the GenBank/EMBL database. Accession numbers for the other protein sequences above are: MtfadD, *M. tuberculosis* (Z77724), Mlacl, *M. leprae* (NP_301424), Msmeg, *M. smegmatis* (Contig 3313), MBCG, *M. bovis* BCG (unnamed hypothetical protein at bases 2,885, 319-2,888,822).

FIGS. 2a and b are SDS-PAGE (a) and Western blot (b) analysis of *Nocardia* CAR expression in *E. coli* carrying pHAT10 based vectors. Samples taken from the lysates of *E. coli* cells carrying different vectors were separated in duplicate by 10% SDS-PAGE and either stained with 0.1% Coomassie blue R-250 (A) or subjected to Western blotting using a HAT-specific antibody (B). Lane assignments for panels A and B: 1, molecular weight markers: myosin (209 kDa), beta-galactosidase (124 kDa), BSA (80 kDa), ovalbumin (49.1 kDa), carbonic anhydrase (34.8 kDa), soybean trypsin inhibitor (21.5 kDa) and lysozyme (20.6 kDa), aprotinin (7.1 kDa); 2, *E. coli* cells BL21-CodonPlus®(DE3)-RP carrying PHAT-DHFR; 3, *E. coli* BL21(DE3) cells carrying pHAT-305; 4, *E. coli* BL21-CodonPlus®(DE3)-RP cells carrying pHAT-305 (uninduced); 5, purified HAT-CAR; 6, *E. coli* CodonPlus®(DE3)-RP cells carrying pHAT10.

FIG. 3 depicts the alpha-Aminoacidate reductase motifs that were described by Casqueiro et al. and Hijarrubia et al. that are present in Car. Red letters indicate identical amino acids and blue letters indicate similar amino acids. Bold letters are matches within the motif.

FIG. 4 depicts the location of motifs within Car.

FIG. 5 depicts the location of motifs within FadD9.

FIG. 6 depicts the location of motifs in Aar: yeast AAR.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Unless mentioned otherwise, the techniques employed or contemplated herein are standard methodologies well known to one of ordinary skill in the art. The materials, methods and examples are illustrative only and not limiting. The following is presented by way of illustration and is not intended to limit the scope of the invention.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of botany, microbiology, tissue culture, molecular biology, chemistry, biochemistry and recombinant DNA technology, which are within the skill of the art. Such techniques are explained fully in the literature. See, e.g., *The Microbial World*, (1986) 5th Ed., Prentice-Hall; O. D. Dhiringra and J. B. Sinclair, *Basic Plant Pathology Methods*, (1985) CRC Press; Maniatis, Fritsch & Sambrook, *Molecular Cloning: A Laboratory Manual* (1982); *DNA Cloning*, Vols. I and II (D. N. Glover ed. 1985); *Oligonucleotide Synthesis* (M. J. Gait ed. 1984); *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); and the series *Methods in Enzymology* (S. Colowick and N. Kaplan, eds., Academic Press, Inc.).

Units, prefixes, and symbols may be denoted in their SI accepted form. Unless otherwise indicated, nucleic acids are written left to right in 5' to 3' orientation; amino acid sequences are written left to right in amino to carboxy orientation, respectively. Numeric ranges are inclusive of the numbers defining the range. Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted

single-letter codes. The terms defined below are more fully defined by reference to the specification as a whole.

In describing the present invention, the following terms will be employed, and are intended to be defined as indicated below.

By "amplified" is meant the construction of multiple copies of a nucleic acid sequence or multiple copies complementary to the nucleic acid sequence using at least one of the nucleic acid sequences as a template. Amplification systems include the polymerase chain reaction (PCR) system, ligase chain reaction (LCR) system, nucleic acid sequence based amplification (NASBA, Cingene, Mississauga, Ontario), Q-Beta Replicase systems, transcription-based amplification system (TAS), and strand displacement amplification (SDA). See, e.g., *Diagnostic Molecular Microbiology: Principles and Applications*, D. H. Persing et al., Ed., American Society for Microbiology, Washington, D.C. (1993). The product of amplification is termed an amplicon.

The term "conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refer to those nucleic acids that encode identical or conservatively modified variants of the amino acid sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations" and represent one species of conservatively modified variation. Every nucleic acid sequence herein that encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of ordinary skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, one exception is *Micrococcus rubens*, for which GTG is the methionine codon (Ishizuka, et al., *J. Gen'l Microbiol.*, 139:425-432 (1993)) can be modified to yield a functionally identical molecule. Accordingly, each nucleic acid disclosed herein also includes each silent variation of the nucleic acid, which encodes a polypeptide of the present invention. It is implicit in each described polypeptide sequence and incorporated herein by reference. Examples of conservatively modified variants with silent mutations are SEQ ID NO:37 (where some gca codons have been replaced with gcg codons both of which code for Alanine) and 38 (where a tca codon has been replaced with an agt codon both of which code for serine).

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" when the alteration results in the substitution of an amino acid with a chemically similar amino acid. Thus, any number of amino acid residues selected from the group of integers consisting of from 1 to 15 can be so altered. Thus, for example, 1, 2, 3, 4, 5, 7, or 10 alterations can be made. Conservatively modified variants typically provide similar biological activity as the unmodified polypeptide sequence from which they are derived. For example, substrate specificity, enzyme activity, or ligand/receptor binding is generally at least 80%, or 95%, preferably 80-95% of the native protein for its native substrate. Conservative substitution tables providing functionally similar amino acids are well

known in the art. Sequence ID no 39 is a protein sequence with a conservative substitution of A for S.

The following six groups each contain amino acids that are conservative substitutions for one another:

- 1) Alanine (A), Serine (S), Threonine (T);
- 2) Aspartic acid (D), Glutamic acid (E);
- 3) Asparagine (N), Glutamine (Q);
- 4) Arginine (R), Lysine (K);
- 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V);
- and
- 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W).

See also, Creighton (1984) *Proteins* W.H. Freeman and Company.

By "encoding" or "encoded", with respect to a specified nucleic acid, is meant comprising the information for translation into the specified protein. A nucleic acid encoding a protein may comprise non-translated sequences (e.g., introns) within translated regions of the nucleic acid, or may lack such intervening non-translated sequences (e.g., as in cDNA). The information by which a protein is encoded is specified by the use of codons. Typically, the amino acid sequence is encoded by the nucleic acid using the "universal" genetic code. However, variants of the universal code, such as is present in some plant, animal, and fungal mitochondria, the bacterium *Mycoplasma capricolum* (*Proc. Natl. Acad. Sci. (USA)*, 82: 2306-2309 (1985)), or the ciliate Macronucleus, may be used when the nucleic acid is expressed using these organisms.

When the nucleic acid is prepared or altered synthetically, advantage can be taken of known codon preferences of the intended host where the nucleic acid is to be expressed. As used herein, "heterologous" in reference to a nucleic acid is a nucleic acid that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention. For example, a promoter operably linked to a heterologous structural gene is from a species different from that from which the structural gene was derived, or, if from the same species, one or both are substantially modified from their original form. A heterologous protein may originate from a foreign species or, if from the same species, is substantially modified from its original form by deliberate human intervention.

By "host cell" is meant a cell, which contains a vector and supports the replication and/or expression of the expression vector. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, plant, amphibian, or mammalian cells. Preferably, host cells are bacterial cells to provide for production of the enzyme in large quantities. A particularly preferred bacterial host cell is an *E. coli* host cell.

The term "hybridization complex" includes reference to a duplex nucleic acid structure formed by two single-stranded nucleic acid sequences selectively hybridized with each other.

The term "introduced" in the context of inserting a nucleic acid into a cell, means "transfection" or "transformation" or "transduction" and includes reference to the incorporation of a nucleic acid into a eukaryotic or prokaryotic cell where the nucleic acid may be incorporated into the genome of the cell (e.g., chromosome, plasmid, plastid or mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (e.g., transfected mRNA).

The terms "isolated" refers to material, such as a nucleic acid or a protein, which is substantially or essentially free from components which normally accompany or interact with it as found in its naturally occurring environment. The

isolated material optionally comprises material not found with the material in its natural environment. Nucleic acids, which are "isolated", as defined herein, are also referred to as "heterologous" nucleic acids.

Unless otherwise stated, the term "CAR nucleic acid" means a nucleic acid, including all conservatively modified variants, encoding an CAR polypeptide. The term CAR, unless otherwise stated encompasses CAR and its functional, conservatively modified variants.

As used herein, "nucleic acid" includes reference to a deoxyribonucleotide or ribonucleotide polymer in either single- or double-stranded form, and unless otherwise limited, encompasses known analogues having the essential nature of natural nucleotides in that they hybridize to single-stranded nucleic acids in a manner similar to naturally occurring nucleotides (e.g., peptide nucleic acids).

By "nucleic acid library" is meant a collection of isolated DNA or RNA molecules, which comprise and substantially represent the entire transcribed fraction of a genome of a specified organism. Construction of exemplary nucleic acid libraries, such as genomic and cDNA libraries, is taught in standard molecular biology references such as Berger and Kimmel, *Guide to Molecular Cloning Techniques, Methods in Enzymology*, Vol. 152, Academic Press, Inc., San Diego, Calif. (Berger); Sambrook et al., *Molecular Cloning—A Laboratory Manual*, 2nd ed., Vol. 1-3 (1989); and *Current Protocols in Molecular Biology*, F. M. Ausubel et al., Eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc. (1994 Supplement).

As used herein "operably linked" includes reference to a functional linkage between a first sequence, such as a promoter and a second sequence, wherein the promoter sequence initiates and mediates transcription of the DNA sequence corresponding to the second sequence. Generally, operably linked means that the nucleic acid sequences being linked are contiguous and, where necessary to join two protein coding regions, contiguous and in the same reading frame.

As used herein, "polynucleotide" includes reference to a deoxyribopolynucleotide, ribopolynucleotide, or analogs thereof that have the essential nature of a natural ribonucleotide in that they hybridize, under stringent hybridization conditions, to substantially the same nucleotide sequence as naturally occurring nucleotides and/or allow translation into the same amino acid(s) as the naturally occurring nucleotide(s). A polynucleotide can be full-length or a subsequence of a native or heterologous structural or regulatory gene. Unless otherwise indicated, the term includes reference to the specified sequence as well as the complementary sequence thereof. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "polynucleotides" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are polynucleotides as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art.

The term polynucleotide as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including inter alia, simple and complex cells. The terms "polypeptide", "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue

is an artificial chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers.

As used herein "promoter" includes reference to a region of DNA upstream from the start of transcription and involved in recognition and binding of RNA polymerase and other proteins to initiate transcription. An "inducible" or "regulatable" promoter is a promoter, which is under environmental control. Examples of environmental conditions that may effect transcription by inducible promoters include anaerobic conditions or the presence of light. Another type of promoter is a developmentally regulated or tissue specific promoter. Tissue preferred, cell type specific, developmentally regulated, and inducible promoters constitute the class of "non-constitutive" promoters. A "constitutive" promoter is a promoter, which is active under most environmental conditions.

The term "CAR polypeptide" refers to one or more amino acid sequences. The term is also inclusive of conservatively modified variants, fragments, homologs, alleles or precursors (e.g., preproteins or proproteins) thereof. A "CAR protein" comprises a CAR polypeptide.

As used herein "recombinant" includes reference to a cell or vector, that has been modified by the introduction of a heterologous nucleic acid or that the cell is derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found in identical form within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all as a result of deliberate human intervention. The term "recombinant" as used herein does not encompass the alteration of the cell or vector by naturally occurring events (e.g., spontaneous mutation, natural transformation/transduction/transposition) such as those occurring without deliberate human intervention.

As used herein, a "recombinant expression cassette" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements, which permit transcription of a particular nucleic acid in a target cell. The recombinant expression cassette can be incorporated into a plasmid, chromosome, mitochondrial DNA, plastid DNA, virus, or nucleic acid fragment. Typically, the recombinant expression cassette portion of an expression vector includes, among other sequences, a nucleic acid to be transcribed, and a promoter.

The term "residue" or "amino acid residue" or "amino acid" are used interchangeably herein to refer to an amino acid that is incorporated into a protein, polypeptide, or peptide (collectively "protein"). The amino acid may be a naturally occurring amino acid and, unless otherwise limited, may encompass known analogs of natural amino acids that can function in a similar manner as naturally occurring amino acids.

The term "selectively hybridizes" includes reference to hybridization, under stringent hybridization conditions, of a nucleic acid sequence to a specified nucleic acid target sequence to a detectably greater degree (e.g., at least 2-fold over background) than its hybridization to non-target nucleic acid sequences and to the substantial exclusion of non-target nucleic acids. Selectively hybridizing sequences typically have about at least 40% sequence identity, preferably 60-90% sequence identity, and most preferably 100% sequence identity (i.e., complementary) with each other.

The terms "stringent conditions" or "stringent hybridization conditions" include reference to conditions under which a probe will hybridize to its target sequence, to a detectably greater degree than other sequences (e.g., at least 2-fold over background). Stringent conditions are sequence-dependent

and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences can be identified which can be up to 100% complementary to the probe (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Optimally, the probe is approximately 500 nucleotides in length, but can vary greatly in length from less than 500 nucleotides to equal to the entire length of the target sequence.

Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C. for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C. for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide or Denhardt's. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37° C., and a wash in 1× to 2×SSC (20×SSC=3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55° C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1 M NaCl, 1% SDS at 37° C., and a wash in 0.5× to 1×SSC at 55 to 60° C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37° C., and a wash in 0.1×SSC at 60 to 65° C. Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl, *Anal. Biochem.*, 138:267-284 (1984): $T_m = 81.5^\circ \text{C.} + 16.6 (\log M) + 0.41 (\% \text{GC}) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. T_m is reduced by about 1° C. for each 1% of mismatching; thus, T_m , hybridization and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with $\geq 90\%$ identity are sought, the T_m can be decreased 10° C. Generally, stringent conditions are selected to be about 5° C. lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4° C. lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10° C. lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20° C. lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T_m , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T_m of less than 45° C. (aqueous solution) or 32° C. (formamide solution) it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes*, Part I, Chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays", Elsevier, N.Y. (1993); and *Current Protocols in*

Molecular Biology, Chapter 2, Ausubel, et al., Eds., Greene Publishing and Wiley-Interscience, N.Y. (1995). Unless otherwise stated, in the present application high stringency is defined as hybridization in 4×SSC, 5×Denhardt's (5 g Ficoll, 5 g polyvinylpyrrolidone, 5 g bovine serum albumin in 500 ml of water), 0.1 mg/ml boiled salmon sperm DNA, and 25 mM Na phosphate at 65° C., and a wash in 0.1×SSC, 0.1% SDS at 65° C.

"Transgenic" is used herein to include any cell, cell line, or tissue, the genotype of which has been altered by the presence of heterologous nucleic acid including those transgenics initially so altered as well as those created by sexual crosses or asexual propagation from the initial transgenic. The term "transgenic" as used herein does not encompass the alteration of the genome (chromosomal or extra-chromosomal) by conventional breeding methods or by naturally occurring events such as random cross-fertilization, non-recombinant viral infection, non-recombinant bacterial transformation, non-recombinant transposition, or spontaneous mutation.

As used herein, "vector" includes reference to a nucleic acid used in transfection of a host cell and into which can be inserted a polynucleotide. Vectors are often replicons. Expression vectors permit transcription of a nucleic acid inserted therein.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides or polypeptides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence identity", and (e) "substantial identity".

(a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence.

(b) As used herein, "comparison window" means includes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence may be compared to a reference sequence and wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of nucleotide and amino acid sequences for comparison are well known in the art. The local homology algorithm (Best Fit) of Smith and Waterman, *Adv. Appl. Math* may conduct optimal alignment of sequences for comparison. 2: 482 (1981); by the homology alignment algorithm (GAP) of Needleman and Wunsch, *J. Mol. Biol.* 48: 443 (1970); by the search for similarity method (Tfasta and Fasta) of Pearson and Lipman, *Proc. Natl. Acad. Sci.* 85: 2444 (1988); by computerized implementations of these algorithms, including, but not limited to: CLUSTAL in the PC/Gene program by Intelligenetics, Mountain View, Calif., GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, Wis., USA; the CLUSTAL program is well described by Higgins and Sharp, *Gene* 73: 237-244 (1988); Higgins and Sharp, *CABIOS* 5: 151-153 (1989); Corpet, et al., *Nucleic Acids Research* 16: 10881-90 (1988); Huang, et al., *Computer Applications in the*

Biosciences 8: 155-65 (1992), and Pearson, et al., *Methods in Molecular Biology* 24: 307-331 (1994). The preferred program to use for optimal global alignment of multiple sequences is PileUp (Feng and Doolittle, *Journal of Molecular Evolution*, 25:351-360 (1987) which is similar to the method described by Higgins and Sharp, *CABIOS*, 5:151-153 (1989) and hereby incorporated by reference). The BLAST family of programs which can be used for database similarity searches includes: BLASTN for nucleotide query sequences against nucleotide database sequences; BLASTX for nucleotide query sequences against protein database sequences; BLASTP for protein query sequences against protein database sequences; TBLASTN for protein query sequences against nucleotide database sequences; and TBLASTX for nucleotide query sequences against nucleotide database sequences. See, *Current Protocols in Molecular Biology*, Chapter 19, Ausubel, et al., Eds., Greene Publishing and Wiley-Interscience, N.Y. (1995).

GAP uses the algorithm of Needleman and Wunsch (J. Mol. Biol. 48: 443-453, 1970) to find the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps. GAP considers all possible alignments and gap positions and creates the alignment with the largest number of matched bases and the fewest gaps. It allows for the provision of a gap creation penalty and a gap extension penalty in units of matched bases. GAP must make a profit of gap creation penalty number of matches for each gap it inserts. If a gap extension penalty greater than zero is chosen, GAP must, in addition, make a profit for each gap inserted of the length of the gap times the gap extension penalty. Default gap creation penalty values and gap extension penalty values in Version 10 of the Wisconsin Genetics Software Package are 8 and 2, respectively. The gap creation and gap extension penalties can be expressed as an integer selected from the group of integers consisting of from 0 to 100. Thus, for example, the gap creation and gap extension penalties can be 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, 50, or greater.

GAP presents one member of the family of best alignments. There may be many members of this family, but no other member has a better quality. GAP displays four figures of merit for alignments: Quality, Ratio, Identity, and Similarity. The Quality is the metric maximized in order to align the sequences. Ratio is the quality divided by the number of bases in the shorter segment. Percent Identity is the percent of the symbols that actually match. Percent Similarity is the percent of the symbols that are similar. Symbols that are across from gaps are ignored. A similarity is scored when the scoring matrix value for a pair of symbols is greater than or equal to 0.50, the similarity threshold. The scoring matrix used in Version 10 of the Wisconsin Genetics Software Package is BLOSUM62 (see Henikoff & Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915).

Unless otherwise stated, sequence identity/similarity values provided herein refer to the value obtained using the BLAST 2.0 suite of programs using default parameters. Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997).

As those of ordinary skill in the art will understand, BLAST searches assume that proteins can be modeled as random sequences. However, many real proteins comprise regions of nonrandom sequences, which may be homopolymeric tracts, short-period repeats, or regions enriched in one or more amino acids. Such low-complexity regions may be aligned between unrelated proteins even though other regions of the protein are entirely dissimilar. A number of low-complexity filter programs can be employed to reduce such low-complexity alignments. For example, the SEG (Wooten and

Federhen, *Comput. Chem.*, 17:149-163 (1993)) and XNU (Claverie and States, *Comput. Chem.*, 17:191-201 (1993)) low-complexity filters can be employed alone or in combination.

(c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences includes reference to the residues in the two sequences, which are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g. charge or hydrophobicity) and therefore do not change the functional properties of the molecule. Where sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences, which differ by such conservative substitutions, are said to have "sequence similarity" or "similarity". Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., according to the algorithm of Meyers and Miller, *Computer Applic. Biol. Sci.*, 4: 11-17 (1988) e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, Calif., USA).

(d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

(e) (i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has between 50-100% sequence identity, preferably at least 50% sequence identity, preferably at least 60% sequence identity, preferably at least 87%, more preferably at least 90%, more preferably at least 95%, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of between 55-100%, preferably at least 75%, preferably at least 80%, more preferably at least 90%, and most preferably at least 95%.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions. The degeneracy of the genetic code allows for many amino acids substitutions that lead to variety in the nucleotide sequence that code for the same

amino acid, hence it is possible that the DNA sequence could code for the same polypeptide but not hybridize to each other under stringent conditions. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is that the polypeptide, which the first nucleic acid encodes, is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

(e) (ii) The terms "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with between 55-100% sequence identity to a reference sequence preferably at least 55% sequence identity, preferably 60% preferably 70%, more preferably 80%, most preferably at least 90% or 95% sequence identity to the reference sequence over a specified comparison window. Preferably, optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch, *J. Mol. Biol.* 48: 443 (1970). An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution. In addition, a peptide can be substantially identical to a second peptide when they differ by a non-conservative change if the epitope that the antibody recognizes is substantially identical. Peptides, which are "substantially similar" share sequences as, noted above except that residue positions, which are not identical, may differ by conservative amino acid changes.

Carboxylic acid reductase (CAR) catalyzes the first and rate limiting step in the reduction of carboxylic acids to aldehydes, and later alcohols. According to the invention, analysis of a cloned 6.9 Kb sequence revealed that the entire open reading frame of *Nocardia* CAR and its 5' and 3' flanking regions had been cloned. ATG was identified as the translation start codon by matching the N-terminal amino acid sequence from purified *Nocardia* CAR (23) with an amino acid sequence deduced from the DNA sequence. The assignment of ATG as the start codon is supported by 5' flank region analysis: 6 bp upstream from the start codon ATG lies a conserved *Streptomyces* ribosomal binding site (GGGAGG) (27, 35). The 2.5 Kb sequence upstream of CAR showed fair homology to a putative transmembrane efflux protein (33% identity) in *S. avermitilis*, and a putative efflux protein (32% identity) in *M. tuberculosis*. The sequence downstream of *Nocardia car* showed 40%, 35%, 34% and 28% identities to putative membrane proteins in *Corynebacterium efficiens*, *M. tuberculosis*, *M. leprae*, and *S. coelicolor*, respectively. Although the CAR gene was flanked by genes encoding membrane proteins, the actual function of CAR in *Nocardia* remains unknown at this time.

BLAST analysis also showed that CAR contained two major domains and a possible phosphopantetheine attachment site. The N-terminal domain (aa 90-544) showed high homology to AMP-binding proteins. The C-terminal showed high homology to NADPH binding proteins. If a 4'-phosphopantetheine prosthetic group exists in active CAR, it likely acts as a "swinging arm" for transferring acyl-AMP intermediates to the C-terminal reductase domain. This arrangement of the CAR protein would reflect its sequential catalytic mechanism wherein the N-terminal domain catalyzes substrate activation by formation of an initial acyl-AMP intermediate, while the C-terminal portion then catalyzes the reduction of acyl-AMP by cofactor NADPH to finish a cata-

lytic cycle. The existence of a possible 4'-phosphopantetheine prosthetic group for the catalytic process remains to be shown.

By BLAST analysis, the deduced amino acid sequence of *Nocardia* CAR showed high similarity to those of the putative enzymes in *M. tuberculosis* (fadD9, 61% identity), *M. leprae* (acyl-CoA synthetase, 57% identity), *M. smegmatis* (unnamed hypothetical protein on contig:3313, 61.8% identity), *M. bovis* strain BCG (unnamed hypothetical protein at bases 2,885,319-2,888,822, 60.3% identity), suggesting that possible functions of these proteins may relate to carboxylic acid reduction.

The present invention provides, inter alia, isolated nucleic acids of RNA, DNA, and analogs and/or chimeras thereof, comprising a CAR nucleic acid.

The present invention also includes polynucleotides optimized for expression in different organisms. For example, for expression of the polynucleotide in a maize plant, the sequence can be altered to account for specific codon preferences and to alter GC content as according to Murray et al, supra. Maize codon usage for 28 genes from maize plants is listed in Table 4 of Murray, et al., supra.

The CAR nucleic acids of the present invention comprise isolated CAR nucleic acid sequences which, are inclusive of:

(a) an isolated polynucleotide encoding a polypeptide of the present invention; (b) a polynucleotide having at least 80%, 90% or 95% identity to a polynucleotide of the present invention; (c) a polynucleotide comprising at least 25 nucleotides in length which hybridizes under high stringency conditions to a polynucleotide of the present invention; (d) a polynucleotide comprising a polynucleotide of the present invention; and (e) a polynucleotide which is complementary to the polynucleotide of (a) to (d).

The following description sets forth the general procedures involved in practicing the present invention. To the extent that specific materials are mentioned, it is merely for purposes of illustration and is not intended to limit the invention. Unless otherwise specified, general cloning procedures, such as those set forth in Sambrook et al., *Molecular Cloning*, Cold Spring Harbor Laboratory (1989) (hereinafter "Sambrook et al.") or Ausubel et al. (eds) *Current Protocols in Molecular Biology*, John Wiley & Sons (1999) (hereinafter "Ausubel et al.") are used.

A. Preparation of CAR, Antibodies Specific for CAR and Nucleic Acid Molecules Encoding CAR

1. Proteins and Antibodies

CAR may be prepared in a variety of ways, according to a variety of methods that have been developed for purifying CAR from bacteria which are detailed in the materials incorporated herein by reference. Alternatively, the availability of amino acid sequence information, such as (SEQ ID NO: 2), enables the isolation of nucleic acid molecules encoding CAR. This may be accomplished using anti-CAR antibodies to screen a cDNA expression library from a selected species, according to methods well known in the art. Alternatively, a series of degenerate oligonucleotide probes encoding parts or all of (SEQ ID NO: 1) FIG. 2 may be used to screen cDNA or genomic libraries, as described in greater detail below.

Once obtained, a cDNA or gene may be cloned into an appropriate in vitro transcription vector, such as pSP64 or pSP65 for in vitro transcription, followed by cell-free translation in a suitable cell-free translation system, such as wheat germ or rabbit reticulocytes. In vitro transcription and translation systems are commercially available, e.g., from

Promega Biotech, Madison, Wis. or BRL, Rockville, Md. The pCITE in vitro translation system (Novagen) also may be utilized.

According to a preferred embodiment, larger quantities of the proteins may be produced by expression in a suitable procaryotic or eucaryotic system. This is particularly beneficial for CAR as *Nocardia* sp. are difficult to propagate and maintain in culture. For example, part or all of a CAR-encoding DNA molecule may be inserted into a vector adapted for expression in a bacterial cell (such as *E. coli*) or a yeast cell (such as *Saccharomyces cerevisiae*), or a mammalian cell. Such vectors comprise the regulatory elements necessary for expression of the DNA in the host cell, positioned in such a manner as to permit expression of the DNA in the host cell. Such regulatory elements required for expression include operably linked promoter sequences, transcription initiation sequences and, optionally, enhancer sequences.

CAR produced by gene expression in a recombinant procaryotic or eucaryotic system may be purified according to methods known in the art and incorporated herein. In a preferred embodiment, a commercially available expression/secretion system can be used, whereby the recombinant protein is expressed and thereafter secreted from the host cell, to be easily purified from the surrounding medium. If expression/secretion vectors are not used, an alternative approach involves purifying the recombinant protein by affinity separation, such as by immunological interaction with antibodies that bind specifically to the recombinant protein or with expression/secretion systems (e.g. a C-terminal tag on a secreted protein). Such methods are commonly used by skilled practitioners.

The present invention also provides antibodies capable of binding to CAR from one or more selected species. Polyclonal or monoclonal antibodies directed toward part or all of a selected CAR may be prepared according to standard methods. Monoclonal antibodies may be prepared according to general methods of Kohler and Milstein, following standard protocols. In a preferred embodiment, antibodies are prepared, which react immunospecifically with selected epitopes of CAR distinguishing it from other enzymes.

2. Nucleic Acid Molecules

Once sequence information is obtained, nucleic acid molecules encoding CAR may be prepared by two general methods: (1) they may be synthesized from appropriate nucleotide triphosphates, or (2) they may be isolated from biological sources. Both methods utilize protocols well known in the art.

The availability of nucleotide sequence information enables preparation of an isolated nucleic acid molecule of the invention by oligonucleotide synthesis. Synthetic oligonucleotides may be prepared by the phosphoramidite method employed in the Applied Biosystems 38A DNA Synthesizer or similar devices. The resultant construct may be purified according to methods known in the art, such as high performance liquid chromatography (HPLC). Long, double-stranded polynucleotides, such as a DNA molecule of the present invention, must be synthesized in stages, due to the size limitations inherent in current oligonucleotide synthetic methods. Thus, for example, a long double-stranded molecule may be synthesized as several smaller segments of appropriate complementarity. Complementary segments thus produced may be annealed such that each segment possesses appropriate cohesive termini for attachment of an adjacent segment. Adjacent segments may be ligated by annealing cohesive termini in the presence of DNA ligase to construct an entire long double-stranded molecule. A synthetic DNA molecule so constructed may then be cloned and amplified in an appropriate vector.

Nucleic acid molecules encoding CAR also may be isolated from microorganisms of interest using methods well known in the art. Nucleic acid molecules from a selected species may be isolated by screening cDNA or genomic libraries with oligonucleotides designed to match a nucleic acid sequence specific to a CAR-encoding gene. If the gene from a species is desired, the genomic library is screened. Alternatively, if the protein coding sequence is of particular interest, the cDNA library is screened. In positions of degeneracy, where more than one nucleic acid residue could be used to encode the appropriate amino acid residue, all the appropriate nucleic acids residues may be incorporated to create a mixed oligonucleotide population, or a neutral base such as inosine may be used. The strategy of oligonucleotide design is well known in the art (see also Sambrook et al., *Molecular Cloning*, 1989, Cold Spring Harbor Press, Cold Spring Harbor N.Y.).

Alternatively, PCR (polymerase chain reaction) primers may be designed by the above method to encode a portion of CAR protein, and these primers used to amplify nucleic acids from isolated cDNA or genomic DNA. In a preferred embodiment, the oligonucleotides used to isolate CAR-encoding nucleic acids are designed to encode sequences unique to CAR, as opposed to other homologous proteins.

In accordance with the present invention, nucleic acids having the appropriate sequence homology with a CAR-encoding nucleic acid molecule may be identified by using hybridization and washing conditions of appropriate stringency. For example, hybridizations may be performed, according to the method of Sambrook et al. (1989, supra), using a hybridization solution comprising: 5×SSC, 5× Denhardt's reagent, 1.0% SDS, 100 µg/ml denatured, fragmented salmon sperm DNA, 0.05% sodium pyrophosphate and up to 50% formamide. Hybridization is carried out at 37-42° C. for at least six hours. Following hybridization, filters are washed as follows: (1) 5 minutes at room temperature in 2×SSC and 1% SDS; (2) 15 minutes at room temperature in 2×SSC and 0.1% SDS; (3) 30 minutes-1 hour at 37° C. in 1×SSC and 1% SDS; (4) 2 hours at 42-65° in 1×SSC and 1% SDS, changing the solution every 30 minutes.

Nucleic acids of the present invention may be maintained as DNA in any convenient cloning vector. In a preferred embodiment, clones are maintained in plasmid cloning/expression vector, such as pGEM-T (Promega Biotech, Madison, Wis.) or pBluescript (Stratagene, La Jolla, Calif.), either of which is propagated in a suitable *E. coli* host cell.

CAR-encoding nucleic acid molecules of the invention include cDNA, genomic DNA, RNA, and fragments thereof which may be single- or double-stranded. Thus, this invention provides oligonucleotides (sense or antisense strands of DNA or RNA) having sequences capable of hybridizing with at least one sequence of a nucleic acid molecule of the present invention. Such oligonucleotides are useful as probes for detecting CAR-encoding genes or mRNA in test samples, e.g. by PCR amplification.

B. Uses of CAR Protein

CAR can reduce many types of carboxylic acids. Previous work by the inventors(23, 32) showed that CAR from *Nocardia* has wide ranging substrate capabilities and that the enzyme is enantioselective versus racemic carboxylic acid substrates such as ibuprofen (7). Recombinant CAR shown in the examples herein indicate that CAR effectively reduced benzoic acid, vanillic acid and ferulic acid in preparative scale reactions. However, CAR is different than coniferyl aldehyde dehydrogenase, which uses NAD⁺ as the cofactor to catalyze the oxidation of aldehydes to acids, which does not use ATP, and which has no homology with CAR (1). ATP-dependent

CAR catalyzes the energetically unfavorable reduction of acids to aldehydes by using ATP as an energy source to drive the reaction forward. It can also catalyze the oxidation of aldehyde to acid without ATP, but the cofactor for CAR is NADP(H) instead of NAD(H). From the gene sequence, we know that CAR (3.5 kb) is much larger than aldehyde dehydrogenases (1.5 kb) (1). The enzyme also differs from fatty acid reductases in luminescent bacteria which contains three polypeptide components (31).

1. Proteins and Antibodies

Purified CAR, or fragments thereof, may be used to produce polyclonal or monoclonal antibodies which may serve as sensitive detection reagents for the presence and accumulation of the proteins in cultured cells or tissues and in intact organisms. Recombinant techniques enable expression of fusion proteins containing part or all of a selected CAR. The full length protein or fragments of the protein may be used to advantage to generate an array of monoclonal or polyclonal antibodies specific for various epitopes of the protein, thereby providing even greater sensitivity for detection of the protein. In a preferred embodiment, fragments of CAR that distinguish CAR from serum SAAs are utilized for generating epitope-specific antibodies.

Polyclonal or monoclonal antibodies immunologically specific for CAR may be used in a variety of assays designed to detect and quantitative the proteins. Such assays include, but are not limited to, (1) immunoprecipitation followed by protein quantification; (2) immunoblot analysis (e.g., dot blot, Western blot) (3) radioimmune assays, (4) nephelometry, turbidometric or immunochromatographic (lateral flow) assays, and (5) enzyme-coupled assays, including ELISA and a variety of qualitative rapid tests (e.g., dip-stick and similar tests).

Polyclonal or monoclonal antibodies that immunospecifically interact with CAR can be utilized for identifying and purifying such proteins. For example, antibodies may be utilized for affinity separation of proteins with which they immunospecifically interact. Antibodies may also be used to immunoprecipitate proteins from a sample containing a mixture of proteins and other biological molecules.

2. Nucleic Acids

CAR-encoding nucleic acids may be used for a variety of purposes in accordance with the present invention. The DNA, RNA, or fragments thereof may be used as probes to detect the presence of and/or expression of the genes. Methods in which CAR-encoding nucleic acids may be utilized as probes for such assays include, but are not limited to: (1) in situ hybridization; (2) Southern hybridization (3) northern hybridization; and (4) assorted amplification reactions such as polymerase chain reactions (PCR) and reverse transcriptase-PCR (RT-PCR).

The exemplified CAR-encoding nucleic acids of the invention (e.g., cow, sheep, horse) may also be utilized as probes to identify related genes from other species, including s. As is well known in the art and described above, hybridization stringencies may be adjusted to allow hybridization of nucleic acid probes with complementary sequences of varying degrees of homology.

In addition to the aforementioned uses of CAR-encoding nucleic acids, they are expected to be of utility in the creation of transgenic cells, tissues and organisms.

The present invention provides novel purified and isolated nucleic acid sequences encoding CAR protein. In presently preferred forms, the DNA sequences comprise cDNA sequences encoding the novel CAR, or its conservatively modified variants, which are expressed in *Nocardia* cells. In a more preferred embodiment the nucleic acid sequence com-

prises at least about 80% identity to (SEQ ID NO:1) or 80% identity of the encoded amino acid sequence. Specifically, the sequence isolated is depicted in (SEQ ID NO:1). Alternate DNA forms such as genomic DNA, and DNA prepared by partial or total chemical synthesis from nucleotides as well as DNA with deletions or mutations, is also within the contemplated scope of the invention.

Association of DNA sequences provided by the invention with homologous or heterologous species expression control DNA sequences such as promoters, operators, regulators, and the like, allows in vivo and in vitro transcription to make mRNA which, in turn, is susceptible to translation to provide the proteins of the invention, and related poly- and oligopeptides in large quantities. In a presently preferred DNA expression system of the invention CAR encoding DNA is operatively linked to a regulatory promoter DNA sequence allowing for in vitro transcription and translation of the protein.

Incorporation of DNA sequences into prokaryotic and eucaryotic host cells by standard transformation and transfection processes, potentially involving suitable viral and circular DNA plasmid vectors, is also within the contemplation of the invention and is expected to provide useful proteins in quantities heretofore unavailable from natural sources.

Most of the techniques which are used to transform cells, construct vectors, extract messenger RNA, prepare cDNA libraries, and the like are widely practiced in the art, and most practitioners are familiar with the standard resource materials which describe specific conditions and procedures. However, for convenience, the following paragraphs may serve as a guideline.

Hosts and Control Sequences

Both prokaryotic and eucaryotic systems may be used to express CAR encoding sequences; prokaryotic hosts are, of course, the most convenient for cloning procedures. Prokaryotes most frequently are represented by various strains of *E. coli*; however, other microbial strains may also be used. Plasmid vectors which contain replication sites, selectable markers and control sequences derived from a species compatible with the host are used; for example, *E. coli* is typically transformed using derivatives of pBR322, a plasmid derived from an *E. coli* species by Bolivar, et al, *Gene* (1977) 2:95. pBR322 contains genes for ampicillin and tetracycline resistance, and thus provides multiple selectable markers which can be either retained or destroyed in constructing the desired vector. Commonly used prokaryotic control sequences which are defined herein to include promoters for transcription initiation, optionally with an operator, along with ribosome binding site sequences, include such commonly used promoters as the beta-lactamase (penicillinase) and lactose (lac) promoter systems (Chang, et al, *Nature* (1977) 198:1056) and the tryptophan (trp) promoter system (Goeddel, et al, *Nucleic Acids Res* (1980) 8:4057) and the lambda derived P_L promoter and N-gene ribosome binding site (Shimatake, et al, *Nature* (1981) 292:128).

In addition to bacteria, eucaryotic microbes, such as yeast, may also be used as hosts. Laboratory strains of *Saccharomyces cerevisiae*, Baker's yeast, are most used although a number of other strains or species are commonly available. Vectors employing, for example, the 2μ origin of replication of Broach, J. R., *Meth Enz* (1983) 101:307, or other yeast compatible origins of replication (see, for example, Stinchcomb, et al, *Nature* (1979) 282:39, Tschumper, G., et al, *Gene* (1980) 10:157 and Clarke, L., et al, *Meth Enz* (1983) 101:300) may be used. Control sequences for yeast vectors include promoters for the synthesis of glycolytic enzymes (Hess, et

al, *J Adv Enzyme Reg* (1968) 7:149; Holland, et al, *Biochemistry* (1978) 17:4900). Additional promoters known in the art include the promoter for 3-phosphoglycerate kinase (Hitzman, et al *J Biol Chem* (1980) 255:2073). Other promoters, which have the additional advantage of transcription controlled by growth conditions and/or genetic background are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, the alpha factor system and enzymes responsible for maltose and galactose utilization. It is also believed terminator sequences are desirable at the 3' end of the coding sequences. Such terminators are found in the 3' untranslated region following the coding sequences in yeast-derived genes.

It is also, of course, possible to express genes encoding polypeptides in eucaryotic host cell cultures derived from multicellular organisms. See, for example, Axel, et al, U.S. Pat. No. 4,399,216. These systems have the additional advantage of the ability to splice out introns and thus can be used directly to express genomic fragments. Useful host cell lines include VERO and HeLa cells, and Chinese hamster ovary (CHO) cells. Expression vectors for such cells ordinarily include promoters and control sequences compatible with mammalian cells such as, for example, the commonly used early and late promoters from Simian Virus 40 (SV 40) (Fiers, et al, *Nature* (1978) 273:113), or other viral promoters such as those derived from polyoma, Adenovirus 2, bovine papilloma virus, or avian sarcoma viruses. The controllable promoter, hMT11 (Karin, M., et al, *Nature* (1982) 299:797-802) may also be used. General aspects of mammalian cell host system transformations have been described by Axel (supra). It now appears, also that "enhancer" regions are important in optimizing expression; these are, generally, sequences found upstream or downstream of the promoter region in non-coding DNA regions. Origins of replication may be obtained, if needed, from viral sources. However, integration into the chromosome is a common mechanism for DNA replication in eucaryotes.

Transformations

Depending on the host cell used, transformation is done using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described by Cohen, S. N., *Proc Natl Acad Sci (USA)* 1972) 69:2110, or the rbCl2 method described in Maniatis, et al, *Molecular Cloning: A Laboratory Manual* (1982) Cold Spring Harbor Press, p. 254 and Hanahan, D., *J Mol Biol* (1983) 166:557-580 may be used for prokaryotes or other cells which contain substantial cell wall barriers. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, *Virology* (1978) 52:546, optionally as modified by Wigler, M., et al, *Cell* (1979) 16:777-785 may be used. Transformations into yeast may be carried out according to the method of Beggs, J. D. *Nature* (1978) 275:104-109 or of Hinnen, A., et al, *Proc Natl Acad Sci (USA)* (1978) 75:1929.

Vector Construction

Construction of suitable vectors containing the desired coding and control sequences employs standard ligation and restriction techniques which are well understood in the art. Isolated plasmids, DNA sequences, or synthesized oligonucleotides are cleaved, tailored, and relegated in the form desired.

The DNA sequences which form the vectors are available from a number of sources. Backbone vectors and control systems are generally found on available "host" vectors which are used for the bulk of the sequences in construction. Typical sequences have been set forth above. For the pertinent

coding sequence, initial construction may be, and usually is, a matter of retrieving the appropriate sequences from cDNA or genomic DNA libraries. However, once the sequence is disclosed it is possible to synthesize the entire gene sequence in vitro starting from the individual nucleoside derivatives. The entire sequence for genes or cDNA's of sizable length, e.g., 500-1000 bp may be prepared by synthesizing individual overlapping complementary oligonucleotides and filling in single stranded nonoverlapping portions using DNA polymerase in the presence of the deoxyribonucleotide triphosphates. This approach has been used successfully in the construction of several genes of known sequence. See, for example, Edge, M. D., *Nature* (1981) 292:756; Nambair, K. P., et al, *Science* (1984) 223:1299; Jay, Ernest, *J Biol Chem* (1984) 259:6311.

Synthetic oligonucleotides are prepared by either the phosphotriester method as described by Edge, et al, *Nature* (supra) and Duckworth, et al, *Nucleic Acids Res* (1981) 9:1691 or the phosphoramidite method as described by Beaucage, S. L., and Caruthers, M. H., *Tet Letts* (1981) 22:1859 and Matteucci, M. D., and Caruthers, M. H., *J Am Chem Soc* (1981) 103:3185 and can be prepared using commercially available automated oligonucleotide synthesizers. Kinasing of single strands prior to annealing or for labeling is achieved using an excess, e.g., approximately 10 units of polynucleotide kinase to 1 nmole substrate in the presence of 50 mM Tris, pH 7.6, 10 mM MgCl₂, 5 mM dithiothreitol, 1-2 mM ATP, 1.75y pmoles γ 32P-ATP (2.9 mCi/mmmole), 0.1 mM spermidine, 0.1 mM EDTA.

Once the components of the desired vectors are thus available, they can be excised and ligated using standard restriction and ligation procedures.

Site specific DNA cleavage is performed by treating with the suitable restriction enzyme (or enzymes) under conditions which are generally understood in the art, and the particulars of which are specified by the manufacturer of these commercially available restriction enzymes. See, e.g., New England Biolabs, Product Catalog. In general, about 1 μ g of plasmid or DNA sequence is cleaved by one unit of enzyme in about 20 μ l of buffer solution; in the examples herein, typically, an excess of restriction enzyme is used to insure complete digestion of the DNA substrate. Incubation times of about one hour to two hours at about 37° C. are workable, although variations can be tolerated. After each incubation, protein is removed by extraction with phenol/chloroform, and may be followed by ether extraction, and the nucleic acid recovered from aqueous fractions by precipitation with ethanol. If desired, size separation of the cleaved fragments may be performed by polyacrylamide gel or agarose gel electrophoresis using standard techniques. A general description of size separations is found in *Methods in Enzymology* (1980) 65:499-560.

Restriction cleaved fragments may be blunt ended by treating with the large fragment of *E. coli* DNA polymerase I (Klenow) in the presence of the four deoxynucleotide triphosphates (dNTPs) using incubation times of about 15 to 25 min at 20° to 25° C. in 50 mM Tris pH 7.6, 50 mM NaCl, 6mM MgCl₂, 6 mM DTT and 0.1-1.0 mM dNTPs. The Klenow fragment fills in at 5' single-stranded overhangs but chews back protruding 3' single strands, even though the four dNTPs are present. If desired, selective repair can be performed by supplying only one of the, or selected, dNTPs within the limitations dictated by the nature of the overhang. After treatment with Klenow, the mixture is extracted with phenol/chloroform and ethanol precipitated. Treatment under appropriate conditions with S1 nuclease or BAL-31 results in hydrolysis of any single-stranded portion.

Ligations are performed in 15-50 μ l volumes under the following standard conditions and temperatures: for example, 20 mM Tris-HCl pH 7.5, 10 mM MgCl₂, 10 mM DTT, 33 μ g/ml BSA, 10 mM-50 mM NaCl, and either 40 μ M ATP, 0.01-0.02 (Weiss) units T4 DNA ligase at 0 C (for "sticky end" ligation) or 1 mM ATP, 0.3-0.6 (Weiss) units T4 DNA ligase at 14° C. (for "blunt end" ligation). Intermolecular "sticky end" ligations are usually performed at 33-100 μ g/ml total DNA concentrations (5-100 nM total end concentration). Intermolecular blunt end ligations are performed at 1 μ M total ends concentration.

In vector construction employing "vector fragments", the vector fragment is commonly treated with bacterial alkaline phosphatase (BAP) or calf intestinal alkaline phosphatase (CIP) in order to remove the 5' phosphate and prevent self-ligation of the vector. Digestions are conducted at pH 8 in approximately 10 mM Tris-HCl, 1 mM EDTA using about 1 unit of BAP or CIP per μ g of vector at 60° for about one hour. In order to recover the nucleic acid fragments, the preparation is extracted with phenol/chloroform and ethanol precipitated. Alternatively, re-ligation can be prevented in vectors which have been double digested by additional restriction enzyme digestion and/or separation of the unwanted fragments.

For portions of vectors derived from cDNA or genomic DNA which require sequence modifications, site specific primer directed mutagenesis may be used (Zoller, M. J., and Smith, M. *Nucleic Acids Res* (1982) 10:6487-6500 and Adelman, J. P., et al, *DNA* (1983) 2:183-193). This is conducted using a primer synthetic oligonucleotide complementary to a single stranded phage DNA to be mutagenized except for limited mismatching, representing the desired mutation. Briefly, the synthetic oligonucleotide is used as a primer to direct synthesis of a strand complementary to the phage, and the resulting partially or fully double-stranded DNA is transformed into a phage-supporting host bacterium. Cultures of the transformed bacteria are plated in top agar, permitting plaque formation from single cells which harbor the phage.

Theoretically, 50% of the new plaques will contain the phage having, as a single strand, the mutated form; 50% will have the original sequence. The resulting plaques are washed after hybridization with kinased synthetic primer at a wash temperature which permits binding of an exact match, but at which the mismatches with the original strand are sufficient to prevent binding. Plaques which hybridize with the probe are then picked, cultured, and the DNA recovered.

Verification of Construction

Correct ligations for plasmid construction can be confirmed by first transforming *E. coli* strain MC1061 obtained from Dr. M. Casadaban (Casadaban, M., et al, *J Mol Biol* (1980) 138:179-207) or other suitable host with the ligation mixture. Successful transformants are selected by ampicillin, tetracycline or other antibiotic resistance by using other markers depending on the mode of plasmid construction, as is understood in the art. Plasmids from the transformants are then prepared according to the method of Clewell, D. B., et al, *Proc Natl Acad Sci (USA)* (1969) 62:1159, optionally following chloramphenicol amplification (Clewell, D. B., *J Bacteriol* (1972) 110:667). Several mini DNA preps are commonly used, e.g., Holmes, D. S., et al, *Anal Biochem Acids Res* (1979) 7:1513-1523. The isolated DNA is analyzed by restriction and/or sequenced by the dideoxy nucleotide method of Sanger, F., et al, *Proc Natl Acad Sci (USA)* (1977) 74:5463 as further described by Messing, et al, *Nucleic Acids Res* (1981) 9:309, or by the method of Maxam, et al, *Methods in Enzymology* (1980) 65:499.

Hosts Exemplified

Host strains used in cloning and prokaryotic expression herein are as follows:

For cloning and sequencing, and for expression of construction under control of most bacterial promoters, *E. coli* strains such as MC1061, DH1, RR1, C600hfl, K803, HB101, JA221, and JM101 can be used.

It can therefore be seen that the above invention accomplishes at least all of its stated objectives. All references cited herein are hereby expressly incorporated herein in their entirety by reference.

EXAMPLES

Materials and enzymes. Restriction enzymes, T4 DNA ligase and shrimp alkaline phosphatase were purchased from New England Biolabs (Beverly, Mass.); pGEM-T easy vector kit from Promega (Madison, Wis.); *Escherichia coli* BL21 (DE3) and BL21-CodonPlus®(DE3)-RP competent cells from Stratagene (La Jolla, Calif.); Polyclonal rabbit anti-HAT antibody, pHAT10 vector and Talon® resin from Clontech (Palo Alto, Calif.); goat anti-rabbit IgG-conjugated alkaline phosphatase and Immun-Star Chemiluminescent Substrate Kit from Bio-Rad (Hercules, Calif.); Qiaprep Spin Miniprep kit and Qiaquick kit from Qiagen Inc. (Chatsworth, Calif.). All other chemicals were from Sigma (St Louis, Mo.) unless specified.

Bacterial strains, plasmids, media and growth conditions. The bacteria and plasmids used in this study are given in Table 1. *Nocardia* sp. NRRL 5646 (9), maintained in the University of Iowa College of Pharmacy culture collection on slants of Sabouraud-Dextrose agar or sporulation agar (ATCC no. 5 medium), was grown in Luria-Bertani (LB) medium containing 0.05% Tween 80 (vol/vol, liquid medium only). With *E. coli* (JM109, BL21 (DE3), or BL21-CodonPlus®(DE3)-RP) as the recombinant host for pHAT based vectors, cells were grown at 37° C. on solid or in liquid LB medium. Ampicillin (100 μ g/ml) was incorporated into LB medium to select for recombinants. In addition, isopropyl- β -D-thiogalactopyranoside (IPTG, 1 mM) and/or 5-bromo-4-chloro-3-indolyl- β -D-galactopyranoside (X-Gal, 80 μ g/ml) were included for recombinant selection and identification.

Molecular biology techniques. All DNA manipulations used for this study were performed by standard protocols (33). *Nocardia* sp. NRRL 5646 chromosomal DNA (gDNA) was purified as described by Pelicic et al. (29) with modifications. Briefly, ampicillin (0.2 mg/ml) and glycine (1.5%, vol/vol) were added into 100 ml stationary phase cultures, two hrs before harvest by centrifugation at 4,000 \times g for 15 min and 4° C. Cells (1.5 g, wet weight) were resuspended in 5 ml of lysis solution 1 (25% sucrose in 50 mM Tris-HCl, pH 8.0 containing 50 mM EDTA and 12 mg/ml lysozyme), and incubated at 37° C. with shaking at 50 rpm for 1.5 hrs. Lysis solution II (3 ml of 100 mM Tris-HCl, pH 8.0 containing 1% SDS and 700 μ g/ml proteinase K) was then added, and the sample was incubated at 55° C. for 4 hrs. Then 45 μ l Rnase (500 μ g/ml) was added into the lysate, and incubated with shaking at 50 rpm and 37° C. for 1 h. The lysate was then extracted with phenol-chloroform-isoamyl alcohol (25:24:1, vol/vol/vol, Invitrogen Life Technologies), and gDNA was concentrated by ethanol precipitation, yielding a total of 90 μ g gDNA. Recombinant plasmids from *E. coli* were purified by using a Qiaprep spin miniprep kit, and Qiaquick kits were used for PCR cleanup and gel extractions with vector constructs as instructed by the manufacturer. All PCR cloning amplification was done with either Platinum Taq DNA polymerase or Platinum Pfx DNA polymerase (Invitrogen).

Restriction enzymes and DNA-modification enzymes were used according to the manufacturer's protocols. Sequencing was conducted using an Applied Biosystem 373A DNA sequencer.

PCR and cloning of PCR product. In order to obtain a portion of *Nocardia car*, oligonucleotides were constructed corresponding to N-terminal and internal amino acid sequences, which were determined with purified CAR (23). Forward primers (Noc-1 and Noc-2) were based on the N-terminal amino acid sequence AVDSPDERLQRRIAQL (SEQ ID NO:6), and reverse primers (Noc-3 and Noc-4) were based on the complementary strand sequence encoding the internal amino acid sequence KLSQGEFVTVAHLEAV (SEQ ID NO:7) (Table 2). Degeneracy of all four primers was minimized by taking advantage of the reported *Nocardia* codon preferences (10). A typical 50 μ l reaction in 1 \times PCR buffer contained 500 ng *Nocardia* DNA, 5 mM Mg⁺⁺, 500 μ M of each dNTP, 0.5 μ M of each primer, 1% DMSO (vol/vol) and 3.5 units of Taq DNA polymerase. The reaction mixtures were subjected to the following cycles: one cycle at 94° C. for 4 min, thirty cycles at 94° C. for 45 s, 56° C. for 45 s, and 72° C. for 2 min, and finally one cycle at 72° C. for 10 min. PCR products were separated on 1% agarose gel. The desired band was excised and extracted with a Qiagen gel extraction kit. The resulting PCR product was ligated into pGEM-T by T4 ligase. The ligation mixture was mixed with *E. coli* JM109 cells and chilled on ice for 30 min. Cells were transformed by heat shock, then placed immediately on ice. Transformed *E. coli* JM 109 cells were mixed with 800 μ l SOC medium and incubated at 37° C. for 1.5 hrs on a rotary shaker at 170 rpm. Plasmid transformants were spreadplated onto LB/X-Gal agar supplemented with 100 μ g/ml ampicillin. Ampicillin resistant colonies were picked and used to inoculate 5 ml LB broth supplemented with 100 μ g/ml ampicillin and incubated overnight at 37° C. on a rotary shaker operating at 170 rpm. Cultures were harvested by centrifugation and subjected to a plasmid miniprep procedure (Qiagen). The resulting recombinant plasmid was sequenced in both directions with sequencing primers (Table 2).

Inverse PCR. Inverse PCR was used to obtain the entire *Nocardia asteroides car* gene sequence. To prepare the template for Inverse PCR analysis, 1 μ g of *Nocardia asteroides* gDNA was completely digested with 20 U Sall or Acc65I at 37° C. Digested gDNA was diluted five fold and then circularized with T4 DNA ligase. PCR primers CA-5 (Forward) and CA-7 (Reverse) were designed based on part of the *Nocardia asteroides car* sequence obtained above. Inverse PCR was performed using Taq DNA polymerase for a total of 30 cycles with the following cycling pattern: melting at 94° C. for 45 s, annealing at 57° C. for 45 s, and polymerization at 72° C. for 2 min. The amplified PCR product was cloned in pGEM-T, and transformed into *E. coli* JM109 cells by heat shock treatment as described above. Plasmid preparations from independent clones were sequenced in both directions. The resulting sequence combined with the above part of *Nocardia asteroides car* gave a 4.6 Kb sequence which contained the entire *Nocardia asteroides car* gene (with Acc65I digested and then religated gDNA as the template). A sequence of 2.5 Kb upstream *car* was obtained with Sall digested and religated gDNA as the template for PCR.

Construction of expression vectors. To express recombinant *Nocardia asteroides car* in *E. coli*, a DNA fragment containing *Nocardia asteroides car* was generated by PCR using the primers *car*-F and *car*-R with *Nocardia asteroides* gDNA as the template. For cloning purposes, those two primers incorporated a BamHI site at the 5' end and an KpnI site at the 3' end of the *Nocardia* gene insert. PCR was performed

using Platinum Pfx DNA polymerase for a total of 30 cycles with the following cycling pattern: melting at 94° C. for 18 s, annealing at 59° C. for 30 s, and polymerization at 72° C. for 4 min. PCR products were sequentially digested with BamHI and KpnI was separated on a 1% agarose gel and purified using a Qiagen gel extraction kit, and then subcloned into the corresponding sites of pHAT10 to result in pHAT-305. One round of sequencing confirmed that *Nocardia car* had been correctly cloned into the pHAT vector by using sequence primers.

Expression of *Nocardia car* in *E. coli*. A 100 ml culture of *E. coli* cells (BL21(DE3) or BL21-CodonPlus®(DE3)-RP) harboring pHAT-305 were grown overnight in LB medium containing 100 μ g/ml ampicillin at 37° C. Overnight broth cultures were diluted 20 fold in fresh LB medium containing 100 μ g/ml ampicillin, and then incubated at 170 rpm in a rotary shaker at 37° C. to an optical density at 600 nm of 0.6, followed by addition of 1 mM IPTG and further incubation for 4.5 h. The cells were harvested by centrifugation (10 min, 5,000 \times g), and then stored at -65° C. before use.

Enzyme assay. The standard reaction mixture contained 1 mM ATP, 0.15 mM NADPH, 5 mM sodium benzoate, 10 mM MgCl₂ and enzyme in 0.05 M Tris buffer (pH 7.5) containing 1 mM EDTA, 1 mM DTT and 10% glycerol (vol/vol), in a final volume of 1.4 ml. The reference cuvette contained all components except benzoate. Reactions were initiated by adding enzyme, and were monitored by recording the absorption decrease at 340 nm at 25° C. with a Shimadzu UV-2010PC scanning spectrophotometer. One unit of the enzyme was defined as the amount of enzyme that catalyzed the reduction of 1 μ mol of benzoate to benzaldehyde.min⁻¹ under standard assay condition. Protein concentrations were measured by the Bradford protein microassay (4) with bovine serum albumin as the standard.

Purification of overexpressed HAT-CAR fusion protein. *E. coli* BL21-CodonPlus®(DE3)-RP cells (4.3 g wet weight) transformed with pHAT-305 were suspended in 26 ml of 0.05 M K₂HPO₄ (pH 7.5) buffer containing 0.3 M NaCl, 10% (vol/vol) glycerol, 0.2 mM PMSF and 3 mM P-mercaptoethanol. The cells were disrupted by passing through a French Press cell at 12,000 psi twice. The cell debris was removed by centrifugation for 60 min at 25,000 \times g and 4° C. The resulting supernatant (27 ml) was referred to as cell-free extract (CFE) and used for HAT-CAR purification. 24 ml of CFE was loaded on a 6 ml bed volume column of Talon resin (A cobalt complexed resin made by Clontech that specifically binds the HAT tag.) equilibrated with 0.05 M K₂HPO₄ buffer pH 7.5 containing 0.3 M NaCl, 10% (vol/vol) glycerol, at a flow rate of 0.4 ml/min. After the column was washed with 35 ml 0.05 M K₂HPO₄ buffer pH 7.5 containing 0.3 M NaCl, 10% (vol/vol) glycerol, the HAT-CAR was eluted sequentially by 16 ml of 5 mM, 7.5 mM, 10 mM, and 20 mM of Imidazole in 0.05 M K₂HPO₄ buffer pH 7.5 containing 0.3 M NaCl, 10% (vol/vol) glycerol. Active fractions were pooled and then concentrated by ultrafiltration in an Amicon concentrator (PM-10 membrane) and then diluted with 100 ml of 50 mM Tris buffer (pH 7.5) containing 1 mM EDTA, 1 mM DTT, and 10% glycerol. The resulting enzyme preparation was loaded on a DEAE Sepharose column (1.5 by 20 cm with a bed volume of 24 ml) equilibrated with 50 mM Tris buffer (pH 7.5) containing 1 mM EDTA, 1 mM DTT, and 10% glycerol. The column was washed with 30 ml of starting buffer and eluted with a 0 to 0.5 M NaCl linear gradient (total 100 ml). The active fractions (29 to 34) were combined for subsequent analysis (Table 3).

SDS-PAGE and Western blot analysis. Proteins were separated by SDS-PAGE as described by Laemmli (22). For West-

ern blot analysis, protein samples were subjected to SDS-PAGE and then transferred to a polyvinylidene difluoride (PVDF) membrane. To identify proteins containing the HAT tag, the PVDF membrane was first incubated with 2% fat-free milk in TBS, then with a polyclonal anti-HAT antibody (diluted 1:20,000) that recognizes epitopes throughout the HAT tag, and finally with a polyclonal goat anti-rabbit IgG conjugated to alkaline phosphatase (diluted 1:20,000), which was used with the Bio-Rad Immuno-Star Chemoluminescent Substrate. Proteins containing the HAT tag were identified with Kodak BioMax MR photographic film after 2 min exposures. *E. coli* JM 109 carrying an expression vector coding for HAT-tagged dihydrofolate reductase (DHFR, Clontech) was used as a positive control for each Western blot analysis, and *E. coli* BL21-CodonPlus® (DE3)-RP carrying the pHAT10 vector was used as a negative control.

In vitro and in vivo transformations of benzoate, vanillic acid, and ferulic acid. In vitro enzyme reactions were carried out in a reaction mixture of 50 ml of 50 mM Tris-HCl buffer (pH 7.5) containing 0.1 mmol of substrate, 12.5 mg of NADPH, 55 mg ATP, 101 mg MgCl₂, 33.6 mg glucose-6-phosphate, and 3 U of glucose-6-phosphate dehydrogenase, and 1 mg purified HAT-CAR (0.1 U). Reaction mixtures were incubated at 30° C. with gentle shaking at 50 rpm for 24 h.

In vivo whole cell reactions were typically conducted with 100 ml cultures of *E. coli* BL21-CodonPlus®(DE3)-RP carrying pHAT-305. Cultures were induced by 1 mM IPTG for 4 hrs before receiving 1 mg/ml of benzoic acid, vanillic acid, or ferulic acid.

Samples of approximately 2 mL were removed at various time intervals, sample pH was adjusted to pH 2.0 with 6N HCl, and samples were extracted with 1 ml ethyl acetate, and centrifuged for 2 min at 1,000xg. Organic phases were removed and used to spot silica gel GF₂₅₄ TLC plates for analysis, and comparison with authentic standards of benzaldehyde, vanillin and coniferaldehyde. For metabolite isolation, reactions were stopped by adjustment of mixtures to pH 2.0 with 6N HCl, and extracted three times with half-volumes of ethyl acetate. After removal of solvent by rotary evaporation, reduction products were purified by preparative TLC for analysis and comparison with authentic standards.

Four degenerate primers (two forward, CA-1 and CA-2; and two reverse, CA-3 and CA-4) incorporating *Nocardia* codon preferences (10) were initially designed to identify part of *Nocardia car*, based on the known N-terminal amino acid sequence and internal amino acid sequences (Li and Rosazza, 1997). PCR products were cloned into a pGEM-T vector and sequenced to give a 1.6 Kb sequence.

Gene sequence specific primers (CA-5 and CA-6) based on this identified fragment were synthesized for inverse PCR to clone the entire *Nocardia car* gene. The sequence derived from two inverse PCR experiments and the above-obtained sequence gave a total of 6.9 Kb of data, which included the entire *Nocardia car* gene and its flanking regions. The DNA sequence and the deduced amino acid sequence of *Nocardia car* will be deposited in the GenBank upon filing of a patent. *Nocardia car* consisted of 3525 bp, corresponding to 1174 amino acid residues with a calculated molecular mass of 128.3 kDa and an isoelectric point (pI) of 4.74. The N-terminal amino acid sequence of purified *Nocardia* CAR exactly matched the deduced amino acid sequence of the N-terminus, with Ala as the first amino acid. Met, encoded by the start codon ATG in *Nocardia car*, is apparently removed by post-translational modification in the mature form of the protein produced in wild type *Nocardia* cells.

Comparative sequence analysis. When the *Nocardia car* sequence was compared by BLAST analysis with DNA

sequences in the NCBI database, the BestFit analysis of two nucleotide sequences showed that the *Nocardia* CAR was 60% and 57% identical to the putative polyketide synthetase fadD9 of *M. tuberculosis* and putative acyl-CoA synthetase of *M. leprae* respectively. Putative proteins in *M. smegmatis* and *M. bovis* strain BCG were 61.8% and 60.3% identical to *Nocardia* CAR. The Clustal W program (35) was used to align CAR with these closely-related putative proteins from different species (FIG. 1).

Heterologous expression of *Nocardia car*. For expression of *Nocardia* CAR, the *Nocardia car* gene was successfully cloned in frame into pHAT10 to form the expression vector pHAT-305. Constructed vectors were found by complete sequencing to have a *car* that was 100% identical to the original *Nocardia car* sequence, proving that no errors were introduced by Pfx DNA polymerase cloning. Lysate from *E. coli* BL21(DE3) cells carrying pHAT-305 had moderate carboxylic acid reductase activity (0.003 U/mg of protein) versus that of *Nocardia* wild type cells (0.03 U/mg of protein) (23). However, the expression of pHAT-305 was much improved when it was transformed into *E. coli* CodonPlus® (DE3)-RP cells, where a crude extract specific activity of 0.009 U/mg of protein was observed. When these cultures were examined by SDS-PAGE, the Coomassie blue-stained band with an apparent molecular size of 132.4 kDa were confirmed to be the HAT-CAR by activity assay and Western blot analysis (FIG. 2). Also, the DHFR-positive control (lysate of *E. coli* carrying the DHFR gene cloned into the same pHAT 10 vector) and negative control (lysate of *E. coli* BL21-CodonPlus®(DE3)-RP cells carrying the pHAT10 vector) showed the absence of a 132.4 kDa band by SDS-PAGE and Western blot analyses.

The HAT-CAR protein from *E. coli* was purified to homogeneity on SDS-PAGE by Talon® resin affinity chromatography and DEAE sepharose column with an overall recovery of 85%. Western blot analysis showed that there were some HAT-tag positive smear bands with lower molecular weight than that of HAT-CAR. The purified HAT-CAR showed a specific CAR activity of 0.11 $\mu\text{mol}\cdot\text{min}^{-1}\cdot\text{mg}^{-1}$ protein, which was less than that of CAR purified from *Nocardia* cells (5.89 U/mg of protein) (23). Kinetic constants were determined by fitting experimental data with Cleland's kinetics program (9). Km values for benzoate, ATP and NADPH were determined to be 852±82 mM, 69±6.6 μM , and 57±3.6 μM , respectively. These are similar to the Km values of the natural protein. Vmax was determined to be 0.135±0.004 $\mu\text{mol}\cdot\text{min}^{-1}\cdot\text{mg}^{-1}$ protein, which is lower than that of the natural protein at 0.902±0.04 $\mu\text{mol}\cdot\text{min}^{-1}\cdot\text{mg}^{-1}$ protein (23).

In vitro transformations showed that pure HAT-CAR could reduce various carboxylic acids to their corresponding aldehydes in reactions that were not optimized. Benzoic acid was converted to benzaldehyde (96% yield), vanillic acid to vanillin (49% yield), and ferulic acid to coniferyl aldehyde (22% yield). In vivo studies on the transformation of the same substrates showed that benzoate was quickly converted to benzyl alcohol, while vanillin and coniferyl aldehyde converted to their corresponding alcohols.

Recombinant CAR bound weakly to Talon® affinity matrix, being eluted from columns by 10 mM imidazole, rather than the 100 mM imidazole usually required for HAT-tagged proteins elution. HAT-CAR can be easily purified to near homogeneity (SDS-PAGE) with Talon® matrix chromatography. Minor impurities in enzyme preparations after the affinity step were not completely removed by DEAE sepharose column chromatography. Although trace impurities were not detected by SDS-PAGE, they were detected by Western blot analysis (FIG. 2). These trace impurities were

HAT-tag containing proteins that are likely hydrolyzed fragments of HAT-CAR cleaved by metal proteases. Metal protease inhibitors were not used to prevent protease cleavage during cell disruption because they would be incompatible with Talon® matrix chromatography.

CAR was only moderately expressed in *E. coli* BL21 (DE3) cells carrying pHAT-305. It was thought that low expression was mainly due to the codon bias that can cause early termination and misincorporation of amino acids since the G+C content of the sequence is 66%. In searching for new hosts to overcome the codon bias, the expression of pHAT-305 was much improved when it was carried out in *E. coli* CodonPlus®(DE3)-RP cells. The protein bands were clearly seen on the SDS-PAGE (FIG. 2) with the CFE enzyme preparation. Although CAR of the correct molecular mass accumulates in cells, the specific activity of the crude extract was only improved about 3 fold. The specific activity of CAR in *E. coli* BL21 (DE3) may be higher than in *E. coli* CodonPlus®(DE3)-RP cells. We have shown that approximately 50 mg pure HAT-CAR can be obtained from a 1 liter culture of *E. coli* CodonPlus®(DE3)-RP cells.

Comparing relative protein expression and differing specific activities of CAR in these two different hosts, we speculate that two forms of the enzyme may exist in *E. coli* cells: one active, while the other is an inactive variant. It is possible that the conversion of an inactive form of the enzyme (pre-CAR) to the catalytically active form of the enzyme (CAR) may occur by posttranslational modification. One such modification that has precedence in the type of reaction catalyzed by CAR would be phosphopantetheinylation (12). In this type of model, inactive pre-CAR would be converted to active CAR by attachment of phosphopantetheine prosthetic group possibly attached to Ser688 to function as a Swinging arm. In the active enzyme, CAR, the SH of the phosphopantetheine prosthetic group would react with acyl-AMP to form an acyl-S-pantotheine-CAR intermediate. The C-terminal reductase domain finishes the catalytic cycle by delivering hydride from NADPH to the acyl-S-pantotheine-CAR intermediate freeing an aldehyde product. α -Aminoacidate reductase is well studied, and motifs responsible for adenylation of α -aminoacidate, reduction, NADPH binding and attachment of a phosphopantetheinyl group used in the reaction have been identified (5, 18). While traditional blast analysis does not reveal the expected common motifs in the N-terminal portion of car, they do appear in the C-terminal portion. A P-pantotheine attachment site, domain J, is clearly present in CAR (LGGxSxxA) (SEQ ID NO:8), as are the reduction domain (GYxxSKW) (SEQ ID NO:9) and the NADP binding domain

(GxxGxLG) (SEQ ID NO:10). These motifs are fully conserved in the *Mycobacterium* CAR homologs (FIG. 1). Whether benzoate induction (23) increases the expression of CAR, or catalyzes the conversion of inactive form enzyme to active form by a posttranslational modification remains to be established.

Biotransformation reactions using IPTG-induced whole growing cells of *E. coli* CodonPlus®(DE3)-RP cells carrying pHAT-305 were simple to conduct, and they smoothly converted carboxylic acids to aldehydes—and subsequently to alcohols. With whole cells, expensive cofactors are not needed (25), and the relatively slow reduction of aldehyde products formed by CAR to alcohols by an endogenous *E. coli* alcohol dehydrogenase similar to that in *Nocardia* (25) may be obviated by judicious biochemical engineering approaches with the recombinant organism.

The unique car sequence car for the carboxylic acid reductase enzyme, CAR, may be used to produce recombinant cultures such as *E. coli* for direct use in whole cell biocatalytic conversions of an enormous number of synthetic or natural carboxylic acids (23, 32) including aromatic, aliphatic, alicyclic and others. Alternatively, this gene sequence, or homologs of this gene sequence may be incorporated into the genomes of multiply recombinant strains through pathway engineering to be used as a part of a biosynthetic or biodegradative pathway leading to useful compounds.

TABLE 1

Strains and plasmids used in this study		
Strains or plasmids	Relevant properties	Reference or source
<i>Nocardia</i> sp. NRRL 5646	Wild type	8
<i>E. coli</i> JM 109	RecA ⁻ , recombinant vector host strain	Promega
<i>E. coli</i> BL21 (DE3)	Inducible T7 RNA polymerase, Amp ^r	Stratagene
<i>E. coli</i> BL21-CodonPlus® (DE3)-RP	having argU and proL tRNA genes	Stratagene
pGEM-T easy	T/A PCR cloning vector, Amp ^r	Promega
pHAT10	Cloning vector for addition of HAT-tag to the N-terminus, Amp ^r	Clontech
pHAT-305	pHAT-10 with car insert	This study
pHAT-DHFR	Positive control expression vector with dihydrofolate reductase gene tagged with HAT at the N-terminus	Clontech

TABLE 2

Oligonucleotides used in this study		
Oligonucleotides	Sequence (from 5' to 3') ^a	Source
<u>Cloning primers</u>		
CA-1	GTSGATTCACCSGATGAG	herein (SEQ ID NO:11)
CA-2	CCSGATGARGCSCTACAG	herein (SEQ ID NO:12)
CA-3	TGSGCSACSGTSACGAAC	herein (SEQ ID NO:13)
CA-4	SACGAAATCSCCCTGSGAC	herein (SEQ ID NO:14)
CA-5	GGTCGGGATCAATCTCAACTACATG	herein (SEQ ID NO:15)
CA-6	CTTCAGCTGCTCTGACGGATATCAG	herein (SEQ ID NO:16)
CA-7	CCTGCTCATCTTCTGCAAACTG	herein (SEQ ID NO:17)
carF	CGGGATCCGAGTGGATTCCCGGATGAGC	herein (SEQ ID NO:18)
carR	CGGGGTACCCCTGATATCCGTGAGCAGCTG	herein (SEQ ID NO:19)

TABLE 2-continued

<u>Oligonucleotides used in this study</u>		
Oligonucleotides Sequence (from 5' to 3') ^a		Source
Sequencing primers		
T7	TAATACGACTCACTATAGGG	Sigma-Genosys (SEQ ID NO:20)
SP6	CATACGATTAGGTGACACTATAG	Sigma-Genosys (SEQ ID NO:21)
M13 reverse	CAGGAACAGCTATGACC	Sigma-Genosys (SEQ ID NO:22)
Scar-1	CTCGACCTGGCCGATATCCAC	herein (SEQ ID NO:23)
Scar-2	GAGGACGGCTTCTACAAGAC	herein (SEQ ID NO:24)
Scar-3	GACGCGCACTTCACCGACCTG	herein (SEQ ID NO:25)
Scar-4	GTCGACCTGATCGTCCATCC	herein (SEQ ID NO:26)
Sacr-5	ACCTACGACGTGCTCAATC	herein (SEQ ID NO:27)
Scar-6	CGTACGACGATGGCATCTC	herein (SEQ ID NO:28)
Scar-7	GTGGATATCGGCCAGGTCGAG	herein (SEQ ID NO:29)
He-32	GGTGGCAGGATGGAATCGG	herein (SEQ ID NO:30)
He-33	CGTCGATTCGCGATTCCCTG	herein (SEQ ID NO:31)

^aRestriction cleavage sites are underlined; R=A or G, Y=C or T, S=G or C.

TABLE 3

<u>Purification of recombinant HAI-CAR from <i>Nocardia</i>.</u>					
Step	Total protein (mg)	Total activity (U) ¹	Specific activity (U/mg)	Yield (%)	Purification
Crude extract	600	5.21	0.009	100	1
Talon Matrix	69.1	4.57	0.066	87.7	7.62
DEAE Sepharose	49	4.43	0.09	85	10

¹One unit of the enzyme is defined as the amount of the enzyme that catalyzed the reduction of 1 μmol of benzoate to benzaldehyde per min at 25° C.

Homology

In conducting BLAST analysis the database proteins most similar to CAR are proteins of unknown function in mycobacteria. The most similar known enzymes are Alpha aminoadipate reductase and peptide synthetases, but it is unlikely that Car is either of these. Nonetheless, it is likely that the mechanism of benzoate reduction is similar to alpha-aminoadipate reduction. Piperidine-6-carboxylate dehydrogenase has no sequence similarity to CAR, and its mechanism is unlikely to be related to that of Car.

CAR shows very unique catalytic properties. It is very tolerant, taking carboxylic acids with different structures, as long as they are hydrophobic. In addition, when CAR was tested with alpha amino acids, none of them were reduced. If the alpha amino group is protected with a hydrophobic group, such as Boc, all were reduced with good efficiencies. Therefore, CAR is most likely different from alpha-amino adipate reductase despite the similar motifs.

CAR is most homologous to a set of proteins of similar large size, thus far found only among the mycobacteria. The best hit is with the *Mycobacterium tuberculosis* protein identified as a 'putative substrate-CoA ligase' (in Mtb CDC1551) or 'putative acyl CoA ligase' (FadD9; Rv2590, in Mtb H37Rv). These proteins give a score of 1336, E value of 0, and are 60% identical and 75% positive. The next best hit is with a 'putative acyl-CoA synthetase' from *Mycobacterium leprae*. Another strong hit is also obtained with the *Mycobacterium smegmatis* database.

A conserved domain search shows that the protein consists of two main domains, plus a small third domain. The N-terminal portion has homology with a variety of acyl-CoA synthetases and AMP-binding proteins, polyketide synthase, and

peptide synthetase modules. Between the N-terminal and C-terminal regions is a short section similar to phosphopantetheine attachment sites (aa 650-725). The C-terminal portion has homology with a variety of dehydrogenases and NAD(P)-dependent enzymes. The 740 N-terminal amino acids and the 482 C-terminal amino acids were blasted giving a bit of overlap. Tables 1 and 2 describe most of the best blast hits. Most protein homologues listed do not have known functions. It appears that the N-terminal and C-terminal Blast hits of CAR with *Streptomyces* are not with the same proteins, but this is not yet clear, since the *S. coelicolor* database is not yet fully annotated. The closest hits to known proteins are with alpha-aminoadipate reductase and a non-ribosomal peptide synthetase (for both N-terminal and C-terminal portions). These hits with known proteins are not very strong. alpha-Aminoadipate semialdehyde is in chemical equilibrium with 1-piperidine-6-carboxylate. It is of interest that there is some similarity in structure between the 1-piperidine-6-carboxylate and benzoic acid. This might suggest some evolutionary relationship between the benzoate reductase and the aminoadipate enzyme. However, given the low level of identity, it is unlikely that the benzoate reductase is actually an alpha-aminoadipate semialdehyde dehydrogenase. Furthermore, the *Mycobacterium* homologues would not be Aar because these organisms make lysine via the diaminopimelic acid path rather than the aminoadipate path.

Bacterial means for converting piperidine-6-carboxylate (α-aminoadipate semialdehyde) into α-aminoadipate exists in *Nocardia*, *Streptomyces*, *Flavobacterium* and *Pseudomonas*, by use of 1-piperidine-6-carboxylate dehydrogenase.

The gene for this enzyme has been identified in *Flavobacterium* and *Streptomyces clavuligerus*, and it has good homology with AldB (Rv3293 in *M. tuberculosis*). However, it has no homology with Car, despite the similarity of the piperidine-6-carboxylate dehydrogenase with the Car reaction. This makes sense, since this reaction does not involve ATP and NAD is used instead of NADP. Alpha-Aminoadipate reductase has been well studied. Motifs responsible for adenylation of alpha-aminoadipate, reduction, NADP(H) binding, and attachment of the P-pantetheinyl group used in the reaction have been identified. Given the similar overall sizes of Aar proteins and Car, and at least weak blast hits with both the N-terminal and C-terminal portions of the Car sequence, it might be reasonable to postulate a great similarity in mechanism between the two enzymes. However, traditional blast

analysis does not reveal the expected common motifs in the N-terminal portion of car, although they appear in the C-terminal portion. Nonetheless, when the motifs are searched for “visually”, many of them are found, as shown in FIG. 3. FIG. 4, FIG. 5, and FIG. 6 show the locations of these motifs within

Car, the *M. tuberculosis* homologue FadD9, and a yeast Aar. “Adenylation domain” motifs C, D, F, H and I are found in Car, although A, B, E, and G are not. The P-pantetheine attachment site, domain J, is clearly present, as are the reduction (R) domain and the NADP-binding domain.

TABLE 1

Comparison of amino acid sequence of N-terminal 740 aa of Car to database sequences using Blast analysis						
Organism	Sequence ID	Sequence function	Blast score	E value	% ID	% Positive
<i>M. tuberculosis</i>	FadD9	Putative acyl-CoA synthetase	764	0	57	72
<i>M. bovis</i> BCG	2.885331	Not annotated	“2074”	2.4×10^{-213}	57	72
<i>M. leprae</i>	ML0484	Putative acyl-CoA ligase	769	0	54	70
<i>M. smegmatis</i>	3.09264	Not annotated	“3528”	0	61	75
<i>S. coelicolor</i>	SC02561	Putative fatty acid-CoA ligase	251	3.5×10^{-29}	29	50
<i>S. coelicolor</i>	SC04383	Putative 4-coumarate:CoA ligase	221	6.8×10^{-18}	28	42
<i>Drosophila</i>	CG3961-PA	Hypothetical protein	211	4×10^{-53}	31	49
<i>Mus</i>	AAH31544	Similar to fatty acid Co-A ligase	202	2×10^{-50}	27	46
<i>T. fusca</i>	Scaf 1	Not annotated	121	3×10^{-28}	25	41
<i>Stigmatella aurantica</i>	MxaA	Non-ribosomal peptide synthetase (in myxalamid biosynthesis)	39	7×10^{-5}	26	41
<i>Schizosaccharomyces pombe</i>	P40976	<input type="checkbox"/> -Amino adipate reductase	25	0.14	23	43
<i>Candida albicans</i>	AAC02241	<input type="checkbox"/> -Amino adipate reductase	25	0.18	22	40

Bold letters indicate genes known to make a particular enzyme.

TABLE 2

Comparison of amino acid sequence of C-terminal 482 aa of Car to database sequences using Blast analysis						
Organism	Sequence ID	Sequence function	Blast score	E value	% ID	% Positive
<i>M. tuberculosis</i>	FadD9	Putative acyl-CoA synthetase	583	10^{-165}	61	74
<i>M. bovis</i> BCG	2.887365	Not annotated	“1531”	3×10^{-155}	60	74
<i>M. leprae</i>	ML0484	Putative acyl-CoA ligase	555	1×10^{-157}	58	74
<i>M. smegmatis</i>	3.11301	Not annotated	“1597”	4.8×10^{-164}	62	77
<i>S. coelicolor</i>	SCO6273	Putative polyketide synthase	323	1.6×10^{-27}	35	51
<i>S. coelicolor</i>	SCO1273	Putative reductase	248	4.7×10^{-28}	39	52
<i>Stigmatella aurantica</i>	MxaA	Non-ribosomal peptide synthetase (in myxalamid biosynthesis)	148	2×10^{-34}	33	46
<i>Schizosaccharomyces pombe</i>	P40976	<input type="checkbox"/> -Amino adipate reductase	116	9×10^{-25}	27	46
<i>Pichia farinosa</i>	CAB97252	<input type="checkbox"/> -Amino adipate reductase	108	2×10^{-22}	25	42
<i>T. fusca</i>		No Hits				

Bold letters indicate genes known to make a particular enzyme.

SEQUENCE LISTING

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<210> SEQ ID NO 1

<211> LENGTH: 4600

<212> TYPE: DNA

<213> ORGANISM: Nocardia

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (189)..(4598)

<400> SEQUENCE: 1

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tatttactta ggctaactgt ttttacgggt tgcagggtt ttctactta tgacaaggga 180

ggcttgcc atg gca gtg gat tca ccg gat gag cgg cta cag cgc cgc att 230
Met Ala Val Asp Ser Pro Asp Glu Arg Leu Gln Arg Arg Ile

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gac ctg ggc gac cgg cca cca cgg cgg gaa cag gaa cag ccc gac	3881
Asp Leu Gly Asp Arg Pro Pro Arg Arg Glu Gln Glu Gln Pro Asp	
1220 1225 1230	
gac aac gta gtc cgg gct gta ttc cca cgt cca cgc gcc gat cga	3926
Asp Asn Val Val Arg Ala Val Phe Pro Arg Pro Arg Ala Asp Arg	
1235 1240 1245	
gac gaa gag cgc ggc cga ggc aag cca cca cca cgg ctg cga ctg	3971
Asp Glu Glu Arg Gly Arg Gly Lys Pro Pro Pro Arg Leu Arg Leu	

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1250	1255	1260	
cgc cct gtg cag tag ata gac gaa cag ggg aac gaa cca cac cca			4016
Arg Pro Val Gln Ile Asp Glu Gln Gly Asn Glu Pro His Pro			
1265	1270		
gtg gtg gtc cca gga gaa cgg cga gac cgc gca ggc ggt gag gcc			4061
Val Val Val Pro Gly Glu Arg Arg Asp Arg Ala Gly Gly Glu Ala			
1275	1280	1285	
ggc gag ggt gac cgc gag gag ctg ttc gcc acg cgc ata cag gcc			4106
Gly Glu Gly Asp Arg Glu Glu Leu Phe Ala Thr Pro Ile Gln Ala			
1290	1295	1300	
gat ggt gac ggc cag act cgc cag cgc gac gga gcc cgc gat gag			4151
Asp Gly Asp Gly Gln Thr Arg Gln Arg Asp Gly Ala Arg Asp Glu			
1305	1310	1315	
cag cca cag cca cac cgc cgc cgg gtg atg ggt cag gtg cgc gat			4196
Gln Pro Gln Pro His Arg Arg Arg Val Met Gly Gln Val Arg Asp			
1320	1325	1330	
ggc gcc cgc gat gga ttg att gga cgg gtg cat atc gtc cgc gat			4241
Gly Ala Ala Asp Gly Leu Ile Gly Arg Val His Ile Val Arg Asp			
1335	1340	1345	
ccg att gga ctg gaa gaa cgt cga ggt cca gta ctg ccg gga atc			4286
Pro Ile Gly Leu Glu Glu Arg Arg Gly Pro Val Leu Pro Gly Ile			
1350	1355	1360	
ggc ggg cag cac gat cca ggc gag gac gat gga cgc gat gaa cac			4331
Gly Gly Gln His Asp Pro Gly Glu Asp Asp Gly Arg Asp Glu His			
1365	1370	1375	
cgc cac gcc ggt gca cgc gga ccg cca ctg ccg caa cgc gag gaa			4376
Arg His Gly Gly Ala Arg Gly Pro Pro Leu Pro Gln Arg Glu Glu			
1380	1385	1390	
ttg cac gac gaa gta gcc agg gac gag ctt gat gcc cgc cgc cac			4421
Leu His Asp Glu Val Ala Arg Asp Glu Leu Asp Ala Arg Arg His			
1395	1400	1405	
ccc gac gcc gag gcc cgc cag ctt gct cgc gtc ggg ccg gga gaa			4466
Pro Asp Ala Glu Ala Ala Gln Leu Ala Ala Val Gly Pro Gly Glu			
1410	1415	1420	
gtc cca cag cac cag cag cat cag cat cag gtt gat ctg gcc gta			4511
Val Pro Gln His Gln Gln His Gln His Gln Val Asp Leu Ala Val			
1425	1430	1435	
gaa cag cgt tgt ccg gac ggg ctc gat gaa cgc gca ggt gag cgc			4556
Glu Gln Arg Cys Pro Asp Gly Leu Asp Glu Arg Ala Gly Glu Arg			
1440	1445	1450	
cag tag gcc gct gac gac ggc cag tct gcc gtt gat ccg gta cc			4600
Gln Gly Ala Asp Asp Gly Gln Ser Gly Val Asp Pro Val			
1455	1460	1465	

<210> SEQ ID NO 2
 <211> LENGTH: 1174
 <212> TYPE: PRP
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 2

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

Leu Phe Ala Glu Asp Glu Gln Val Lys Ala Ala Arg Pro Leu Glu Ala
 20 25 30

Val Ser Ala Ala Val Ser Ala Pro Gly Met Arg Leu Ala Gln Ile Ala
 35 40 45

Ala Thr Val Met Ala Gly Tyr Ala Asp Arg Pro Ala Ala Gly Gln Arg
 50 55 60

Ala Phe Glu Leu Asn Thr Asp Asp Ala Thr Gly Arg Thr Ser Leu Arg

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65	70	75	80
Leu Leu Pro Arg	Phe 85	Glu Thr Ile Thr Tyr Arg	Glu Leu Trp Gln Arg 95
Val Gly Glu	Val Ala Ala	Ala Trp His His Asp	Pro Glu Asn Pro Leu 110
Arg Ala Gly Asp	Phe Val Ala	Leu Leu Gly Phe Thr	Ser Ile Asp Tyr 125
Ala Thr Leu Asp	Leu Ala Asp	Ile His Leu Gly	Ala Val Thr Val Pro 140
Leu Gln Ala Ser	Ala Ala Val	Ser Gln Leu Ile	Ala Ile Leu Thr Glu 160
Thr Ser Pro Arg	Leu Leu Ala	Ser Thr Pro Glu	His Leu Asp Ala Ala 175
Val Glu Cys	Leu Leu Ala	Gly Thr Thr Pro	Glu Arg Leu Val Val Phe 190
Asp Tyr His Pro	Glu Asp Asp	Asp Gln Arg Ala	Ala Phe Glu Ser Ala 205
Arg Arg Arg	Leu Ala Asp	Ala Gly Ser Ser	Val Ile Val Glu Thr Leu 220
Asp Ala Val Arg	Ala Arg Gly	Arg Asp Leu Pro	Ala Ala Pro Leu Phe 240
Val Pro Asp Thr	Asp Asp Asp	Pro Leu Ala Leu	Leu Ile Tyr Thr Ser 255
Gly Ser Thr Gly	Thr Pro Lys	Gly Ala Met Tyr	Thr Asn Arg Leu Ala 270
Ala Thr Met Trp	Gln Gly Asn Ser	Met Leu Gln Gly	Asn Ser Gln Arg 285
Val Gly Ile Asn	Leu Asn Tyr Met	Pro Met Ser His	Ile Ala Gly Arg 300
Ile Ser Leu Phe	Gly Val Leu Ala	Arg Gly Gly Thr	Ala Tyr Phe Ala 320
Ala Lys Ser Asp	Met Ser Thr	Leu Phe Glu Asp	Ile Gly Leu Val Arg 335
Pro Thr Glu Ile	Phe Phe Val	Pro Arg Val Cys	Asp Met Val Phe Gln 350
Arg Tyr Gln Ser	Glu Leu Asp	Arg Arg Ser Val	Ala Gly Ala Asp Leu 365
Asp Thr Leu Asp	Arg Glu Val	Lys Ala Asp Leu	Arg Gln Asn Tyr Leu 380
Gly Gly Arg Phe	Leu Val Ala Val	Val Gly Ser Ala	Pro Leu Ala Ala 400
Glu Met Lys Thr	Phe Met Glu Ser	Val Leu Asp Leu	Pro Leu His Asp 415
Gly Tyr Gly Ser	Thr Glu Ala Gly	Ala Ser Val Leu	Leu Asp Asn Gln 430
Ile Gln Arg Pro	Pro Val Leu Asp	Tyr Lys Leu Val	Asp Val Pro Glu 445
Leu Gly Tyr Phe	Arg Thr Asp	Arg Pro His Pro	Arg Gly Glu Leu Leu 460
Leu Lys Ala Glu	Thr Thr Ile	Pro Gly Tyr Tyr	Lys Arg Pro Glu Val 480
Thr Ala Glu Ile	Phe Asp Glu Asp	Gly Phe Tyr Lys	Thr Gly Asp Ile 495

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Val Ala Glu Leu Glu His Asp Arg Leu Val Tyr Val Asp Arg Arg Asn
 500 505 510

Asn Val Leu Lys Leu Ser Gln Gly Glu Phe Val Thr Val Ala His Leu
 515 520 525

Glu Ala Val Phe Ala Ser Ser Pro Leu Ile Arg Gln Ile Phe Ile Tyr
 530 535 540

Gly Ser Ser Glu Arg Ser Tyr Leu Leu Ala Val Ile Val Pro Thr Asp
 545 550 555 560

Asp Ala Leu Arg Gly Arg Asp Thr Ala Thr Leu Lys Ser Ala Leu Ala
 565 570 575

Glu Ser Ile Gln Arg Ile Ala Lys Asp Ala Asn Leu Gln Pro Tyr Glu
 580 585 590

Ile Pro Arg Asp Phe Leu Ile Glu Thr Glu Pro Phe Thr Ile Ala Asn
 595 600 605

Gly Leu Leu Ser Gly Ile Ala Lys Leu Leu Arg Pro Asn Leu Lys Glu
 610 615 620

Arg Tyr Gly Ala Gln Leu Glu Gln Met Tyr Thr Asp Leu Ala Thr Gly
 625 630 635 640

Gln Ala Asp Glu Leu Leu Ala Leu Arg Arg Glu Ala Ala Asp Leu Pro
 645 650 655

Val Leu Glu Thr Val Ser Arg Ala Ala Lys Ala Met Leu Gly Val Ala
 660 665 670

Ser Ala Asp Met Arg Pro Asp Ala His Phe Thr Asp Leu Gly Gly Asp
 675 680 685

Ser Leu Ser Ala Leu Ser Phe Ser Asn Leu Leu His Glu Ile Phe Gly
 690 695 700

Val Glu Val Pro Val Gly Val Val Val Ser Pro Ala Asn Glu Leu Arg
 705 710 715 720

Asp Leu Ala Asn Tyr Ile Glu Ala Glu Arg Asn Ser Gly Ala Lys Arg
 725 730 735

Pro Thr Phe Thr Ser Val His Gly Gly Ser Glu Ile Arg Ala Ala
 740 745 750

Asp Leu Thr Leu Asp Lys Phe Ile Asp Ala Arg Thr Leu Ala Ala Ala
 755 760 765

Asp Ser Ile Pro His Ala Pro Val Pro Ala Gln Thr Val Leu Leu Thr
 770 775 780

Gly Ala Asn Gly Tyr Leu Gly Arg Phe Leu Cys Leu Glu Trp Leu Glu
 785 790 795 800

Arg Leu Asp Lys Thr Gly Gly Thr Leu Ile Cys Val Val Arg Gly Ser
 805 810 815

Asp Ala Ala Ala Ala Arg Lys Arg Leu Asp Ser Ala Phe Asp Ser Gly
 820 825 830

Asp Pro Gly Leu Leu Glu His Tyr Gln Gln Leu Ala Ala Arg Thr Leu
 835 840 845

Glu Val Leu Ala Gly Asp Ile Gly Asp Pro Asn Leu Gly Leu Asp Asp
 850 855 860

Ala Thr Trp Gln Arg Leu Ala Glu Thr Val Asp Leu Ile Val His Pro
 865 870 875 880

Ala Ala Leu Val Asn His Val Leu Pro Tyr Thr Gln Leu Phe Gly Pro
 885 890 895

Asn Val Val Gly Thr Ala Glu Ile Val Arg Leu Ala Ile Thr Ala Arg
 900 905 910

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Arg Lys Pro Val Thr Tyr Leu Ser Thr Val Gly Val Ala Asp Gln Val
 915 920 925

Asp Pro Ala Glu Tyr Gln Glu Asp Ser Asp Val Arg Glu Met Ser Ala
 930 935 940

Val Arg Val Val Arg Glu Ser Tyr Ala Asn Gly Tyr Gly Asn Ser Lys
 945 950 955 960

Trp Ala Gly Glu Val Leu Leu Arg Glu Ala His Asp Leu Cys Gly Leu
 965 970 975

Pro Val Ala Val Phe Arg Ser Asp Met Ile Leu Ala His Ser Arg Tyr
 980 985 990

Ala Gly Gln Leu Asn Val Gln Asp Val Phe Thr Arg Leu Ile Leu Ser
 995 1000 1005

Leu Val Ala Thr Gly Ile Ala Pro Tyr Ser Phe Tyr Arg Thr Asp
 1010 1015 1020

Ala Asp Gly Asn Arg Gln Arg Ala His Tyr Asp Gly Leu Pro Ala
 1025 1030 1035

Asp Phe Thr Ala Ala Ala Ile Thr Ala Leu Gly Ile Gln Ala Thr
 1040 1045 1050

Glu Gly Phe Arg Thr Tyr Asp Val Leu Asn Pro Tyr Asp Asp Gly
 1055 1060 1065

Ile Ser Leu Asp Glu Phe Val Asp Trp Leu Val Glu Ser Gly His
 1070 1075 1080

Pro Ile Gln Arg Ile Thr Asp Tyr Ser Asp Trp Phe His Arg Phe
 1085 1090 1095

Glu Thr Ala Ile Arg Ala Leu Pro Glu Lys Gln Arg Gln Ala Ser
 1100 1105 1110

Val Leu Pro Leu Leu Asp Ala Tyr Arg Asn Pro Cys Pro Ala Val
 1115 1120 1125

Arg Gly Ala Ile Leu Pro Ala Lys Glu Phe Gln Ala Ala Val Gln
 1130 1135 1140

Thr Ala Lys Ile Gly Pro Glu Gln Asp Ile Pro His Leu Ser Ala
 1145 1150 1155

Pro Leu Ile Asp Lys Tyr Val Ser Asp Leu Glu Leu Leu Gln Leu
 1160 1165 1170

Leu

<210> SEQ ID NO 3
 <211> LENGTH: 90
 <212> TYPE: PRT
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 3

Arg Ile Ser Gly Arg Arg Ala His Leu Val Gly Ala Phe Gly Ala Phe
 1 5 10 15

Ala Pro Glu Ala Lys Gln Glu Tyr Arg Arg Ala Thr Gln Asp Ser Gly
 20 25 30

Val Asp Asp Asp Glu Ala Val Asp Gln Asp Leu Gly Asp Arg Pro Pro
 35 40 45

Arg Arg Glu Gln Glu Gln Pro Asp Asp Asn Val Val Arg Ala Val Phe
 50 55 60

Pro Arg Pro Arg Ala Asp Arg Asp Glu Glu Arg Gly Arg Gly Lys Pro
 65 70 75 80

Pro Pro Arg Leu Arg Leu Arg Pro Val Gln
 85 90

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<210> SEQ ID NO 4
 <211> LENGTH: 191
 <212> TYPE: PRT
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 4

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

<210> SEQ ID NO 5
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 5

Gly Ala Asp Asp Gly Gln Ser Gly Val Asp Pro Val
 1 5 10

<210> SEQ ID NO 6
 <211> LENGTH: 16
 <212> TYPE: PRT
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 6

Ala Val Asp Ser Pro Asp Glu Arg Leu Gln Arg Arg Ile Ala Gln Leu
 1 5 10 15

<210> SEQ ID NO 7
 <211> LENGTH: 16
 <212> TYPE: PRT
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 7

Lys Leu Ser Gln Gly Glu Phe Val Thr Val Ala His Leu Glu Ala Val
 1 5 10 15

<210> SEQ ID NO 8

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<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: hypothetical
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: "X" can be any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: "X" can be any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: "X" can be any amino acid

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```

<400> SEQUENCE: 8

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Leu Gly Gly Xaa Ser Xaa Xaa Ala
1             5

```

```

<210> SEQ ID NO 9
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: hypothetical
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: X can be any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: X can be any amino acid

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```

<400> SEQUENCE: 9

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```

Gly Tyr Xaa Xaa Ser Lys Trp
1             5

```

```

<210> SEQ ID NO 10
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: hypothetical
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: X can be any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: X can be any amino acid
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: X can be any amino acid

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```

<400> SEQUENCE: 10

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Gly Xaa Xaa Gly Xaa Leu Gly
1             5

```

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<210> SEQ ID NO 11
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Nocardia

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<400> SEQUENCE: 11

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gtsgattcac csgatgag

```

18

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<210> SEQ ID NO 12
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Nocardia

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<400> SEQUENCE: 12	
ccsgatgarc gsctacag	18
<210> SEQ ID NO 13	
<211> LENGTH: 18	
<212> TYPE: DNA	
<213> ORGANISM: Nocardia	
<400> SEQUENCE: 13	
tgsgcsacsq tsacgaac	18
<210> SEQ ID NO 14	
<211> LENGTH: 19	
<212> TYPE: DNA	
<213> ORGANISM: Nocardia	
<400> SEQUENCE: 14	
sacgaaytcs ccttgsgac	19
<210> SEQ ID NO 15	
<211> LENGTH: 25	
<212> TYPE: DNA	
<213> ORGANISM: Nocardia	
<400> SEQUENCE: 15	
ggtcgggatc aatctcaact acatg	25
<210> SEQ ID NO 16	
<211> LENGTH: 26	
<212> TYPE: DNA	
<213> ORGANISM: Nocardia	
<400> SEQUENCE: 16	
cttcagctgc tctgacggat atcagc	26
<210> SEQ ID NO 17	
<211> LENGTH: 24	
<212> TYPE: DNA	
<213> ORGANISM: Nocardia	
<400> SEQUENCE: 17	
ctgctcatct tctgcaaaca actg	24
<210> SEQ ID NO 18	
<211> LENGTH: 31	
<212> TYPE: DNA	
<213> ORGANISM: Nocardia	
<400> SEQUENCE: 18	
cgcggatccg cagtggatc accggatgag c	31
<210> SEQ ID NO 19	
<211> LENGTH: 32	
<212> TYPE: DNA	
<213> ORGANISM: Nocardia	
<400> SEQUENCE: 19	
cggggtaccc ctgatatccg tcagagcagc tg	32
<210> SEQ ID NO 20	
<211> LENGTH: 20	
<212> TYPE: DNA	
<213> ORGANISM: Nocardia	

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<400> SEQUENCE: 20
 taatacgaact cactataggg 20

<210> SEQ ID NO 21
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 21
 catacgattt aggtgacact atag 24

<210> SEQ ID NO 22
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 22
 caggaaacag ctatgacc 18

<210> SEQ ID NO 23
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 23
 ctcgacctgg ccgatatcca c 21

<210> SEQ ID NO 24
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 24
 gaggaeggct tctacaagac 20

<210> SEQ ID NO 25
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 25
 gacgcgaact tcaccgacct g 21

<210> SEQ ID NO 26
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 26
 gtcgacctga tcgtccatcc 20

<210> SEQ ID NO 27
 <211> LENGTH: 19
 <212> TYPE: DNA
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 27
 acctacgacg tgctcaatc 19

<210> SEQ ID NO 28
 <211> LENGTH: 19
 <212> TYPE: DNA

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<213> ORGANISM: Nocardia

<400> SEQUENCE: 28

cgtagcagca tggcatctc 19

<210> SEQ ID NO 29

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Nocardia

<400> SEQUENCE: 29

gtggatatcg gccaggtcga g 21

<210> SEQ ID NO 30

<211> LENGTH: 19

<212> TYPE: DNA

<213> ORGANISM: Nocardia

<400> SEQUENCE: 30

ggtggcagga tggaatcgg 19

<210> SEQ ID NO 31

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Nocardia

<400> SEQUENCE: 31

cgtagattcg cgattccctg 20

<210> SEQ ID NO 32

<211> LENGTH: 1168

<212> TYPE: PRT

<213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 32

Met Ser Ile Asn Asp Gln Arg Leu Thr Arg Arg Val Glu Asp Leu Tyr
 1 5 10 15

Ala Ser Asp Ala Gln Phe Ala Ala Ala Ser Pro Asn Glu Ala Ile Thr
 20 25 30

Gln Ala Ile Asp Gln Pro Gly Val Ala Leu Pro Gln Leu Ile Arg Met
 35 40 45

Val Met Glu Gly Tyr Ala Asp Arg Pro Ala Leu Gly Gln Arg Ala Leu
 50 55 60

Arg Phe Val Thr Asp Pro Asp Ser Gly Arg Thr Met Val Glu Leu Leu
 65 70 75 80

Pro Arg Phe Glu Thr Ile Thr Tyr Arg Glu Leu Trp Ala Arg Ala Gly
 85 90 95

Thr Leu Ala Thr Ala Leu Ser Ala Glu Pro Ala Ile Arg Pro Gly Asp
 100 105 110

Arg Val Cys Val Leu Gly Phe Asn Ser Val Asp Tyr Thr Thr Ile Asp
 115 120 125

Ile Ala Leu Ile Arg Leu Gly Ala Val Ser Val Pro Leu Gln Thr Ser
 130 135 140

Ala Pro Val Thr Gly Leu Arg Pro Ile Val Thr Glu Thr Glu Pro Thr
 145 150 155 160

Met Ile Ala Thr Ser Ile Asp Asn Leu Gly Asp Ala Val Glu Val Leu
 165 170 175

Ala Gly His Ala Pro Ala Arg Leu Val Val Phe Asp Tyr His Gly Lys
 180 185 190

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

Gly Ser Val Thr Ile Asp Thr Leu Ala Glu Leu Ile Glu Arg Gly Arg
 210 215 220

Ala Leu Pro Ala Thr Pro Ile Ala Asp Ser Ala Asp Asp Ala Leu Ala
 225 230 235 240

Leu Leu Ile Tyr Thr Ser Gly Ser Thr Gly Ala Pro Lys Gly Ala Met
 245 250 255

Tyr Arg Glu Ser Gln Val Met Ser Phe Trp Arg Lys Ser Ser Gly Trp
 260 265 270

Phe Glu Pro Ser Gly Tyr Pro Ser Ile Thr Leu Asn Phe Met Pro Met
 275 280 285

Ser His Val Gly Gly Arg Gln Val Leu Tyr Gly Thr Leu Ser Asn Gly
 290 295 300

Gly Thr Ala Tyr Phe Val Ala Lys Ser Asp Leu Ser Thr Leu Phe Glu
 305 310 315 320

Asp Leu Ala Leu Val Arg Pro Thr Glu Leu Cys Phe Val Pro Arg Ile
 325 330 335

Trp Asp Met Val Phe Ala Glu Phe His Ser Glu Val Asp Arg Arg Leu
 340 345 350

Val Asp Gly Ala Asp Arg Ala Ala Leu Glu Ala Gln Val Lys Ala Glu
 355 360 365

Leu Arg Glu Asn Val Leu Gly Gly Arg Phe Val Met Ala Leu Thr Gly
 370 375 380

Ser Ala Pro Ile Ser Ala Glu Met Thr Ala Trp Val Glu Ser Leu Leu
 385 390 395 400

Ala Asp Val His Leu Val Glu Gly Tyr Gly Ser Thr Glu Ala Gly Met
 405 410 415

Val Leu Asn Asp Gly Met Val Arg Arg Pro Ala Val Ile Asp Tyr Lys
 420 425 430

Leu Val Asp Val Pro Glu Leu Gly Tyr Phe Gly Thr Asp Gln Pro Tyr
 435 440 445

Pro Arg Gly Glu Leu Leu Val Lys Thr Gln Thr Met Phe Pro Gly Tyr
 450 455 460

Tyr Gln Arg Pro Asp Val Thr Ala Glu Val Phe Asp Pro Asp Gly Phe
 465 470 475 480

Tyr Arg Thr Gly Asp Ile Met Ala Lys Val Gly Pro Asp Gln Phe Val
 485 490 495

Tyr Leu Asp Arg Arg Asn Asn Val Leu Lys Leu Ser Gln Gly Glu Phe
 500 505 510

Ile Ala Val Ser Lys Leu Glu Ala Val Phe Gly Asp Ser Pro Leu Val
 515 520 525

Arg Gln Ile Phe Ile Tyr Gly Asn Ser Ala Arg Ala Tyr Pro Leu Ala
 530 535 540

Val Val Val Pro Ser Gly Asp Ala Leu Ser Arg His Gly Ile Glu Asn
 545 550 555 560

Leu Lys Pro Val Ile Ser Glu Ser Leu Gln Glu Val Ala Arg Ala Ala
 565 570 575

Gly Leu Gln Ser Tyr Glu Ile Pro Arg Asp Phe Ile Ile Glu Thr Thr
 580 585 590

Pro Phe Thr Leu Glu Asn Gly Leu Leu Thr Gly Ile Arg Lys Leu Ala
 595 600 605

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Arg Pro Gln Leu Lys Lys Phe Tyr Gly Glu Arg Leu Glu Arg Leu Tyr
 610 615 620
 Thr Glu Leu Ala Asp Ser Gln Ser Asn Glu Leu Arg Glu Leu Arg Gln
 625 630 635 640
 Ser Gly Pro Asp Ala Pro Val Leu Pro Thr Leu Cys Arg Ala Ala Ala
 645 650 655
 Ala Leu Leu Gly Ser Thr Ala Ala Asp Val Arg Pro Asp Ala His Phe
 660 665 670
 Ala Asp Leu Gly Gly Asp Ser Leu Ser Ala Leu Ser Leu Ala Asn Leu
 675 680 685
 Leu His Glu Ile Phe Gly Val Asp Val Pro Val Gly Val Ile Val Ser
 690 695 700
 Pro Ala Ser Asp Leu Arg Ala Leu Ala Asp His Ile Glu Ala Ala Arg
 705 710 715 720
 Thr Gly Val Arg Arg Pro Ser Phe Ala Ser Ile His Gly Arg Ser Ala
 725 730 735
 Thr Glu Val His Ala Ser Asp Leu Thr Leu Asp Lys Phe Ile Asp Ala
 740 745 750
 Ala Thr Leu Ala Ala Ala Pro Asn Leu Pro Ala Pro Ser Ala Gln Val
 755 760 765
 Arg Thr Val Leu Leu Thr Gly Ala Thr Gly Phe Leu Gly Arg Tyr Leu
 770 775 780
 Ala Leu Glu Trp Leu Asp Arg Met Asp Leu Val Asn Gly Lys Leu Ile
 785 790 795 800
 Cys Leu Val Arg Ala Arg Ser Asp Glu Glu Ala Gln Ala Arg Leu Asp
 805 810 815
 Ala Thr Phe Asp Ser Gly Asp Pro Tyr Leu Val Arg His Tyr Arg Glu
 820 825 830
 Leu Gly Ala Gly Arg Leu Glu Val Leu Ala Gly Asp Lys Gly Glu Ala
 835 840 845
 Asp Leu Gly Leu Asp Arg Val Thr Trp Gln Arg Leu Ala Asp Thr Val
 850 855 860
 Asp Leu Ile Val Asp Pro Ala Ala Leu Val Asn His Val Leu Pro Tyr
 865 870 875 880
 Ser Gln Leu Phe Gly Pro Asn Ala Ala Gly Thr Ala Glu Leu Leu Arg
 885 890 895
 Leu Ala Leu Thr Gly Lys Arg Lys Pro Tyr Ile Tyr Thr Ser Thr Ile
 900 905 910
 Ala Val Gly Glu Gln Ile Pro Pro Glu Ala Phe Thr Glu Asp Ala Asp
 915 920 925
 Ile Arg Ala Ile Ser Pro Thr Arg Arg Ile Asp Asp Ser Tyr Ala Asn
 930 935 940
 Gly Tyr Ala Asn Ser Lys Trp Ala Gly Glu Val Leu Leu Arg Glu Ala
 945 950 955 960
 His Glu Gln Cys Gly Leu Pro Val Thr Val Phe Arg Cys Asp Met Ile
 965 970 975
 Leu Ala Asp Thr Ser Tyr Thr Gly Gln Leu Asn Leu Pro Asp Met Phe
 980 985 990
 Thr Arg Leu Met Leu Ser Leu Ala Ala Thr Gly Ile Ala Pro Gly Ser
 995 1000 1005
 Phe Tyr Glu Leu Asp Ala His Gly Asn Arg Gln Arg Ala His Tyr
 1010 1015 1020
 Asp Gly Leu Pro Val Glu Phe Val Ala Glu Ala Ile Cys Thr Leu

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1025	1030	1035
Gly Thr His Ser Pro Asp Arg Phe Val Thr Tyr His Val Met Asn 1040 1045 1050		
Pro Tyr Asp Asp Gly Ile Gly Leu Asp Glu Phe Val Asp Trp Leu 1055 1060 1065		
Asn Ser Pro Thr Ser Gly Ser Gly Cys Thr Ile Gln Arg Ile Ala 1070 1075 1080		
Asp Tyr Gly Glu Trp Leu Gln Arg Phe Glu Thr Ser Leu Arg Ala 1085 1090 1095		
Leu Pro Asp Arg Gln Arg His Ala Ser Leu Leu Pro Leu Leu His 1100 1105 1110		
Asn Tyr Arg Glu Pro Ala Lys Pro Ile Cys Gly Ser Ile Ala Pro 1115 1120 1125		
Thr Asp Gln Phe Arg Ala Ala Val Gln Glu Ala Lys Ile Gly Pro 1130 1135 1140		
Asp Lys Asp Ile Pro His Leu Thr Ala Ala Ile Ile Ala Lys Tyr 1145 1150 1155		
Ile Ser Asn Leu Arg Leu Leu Gly Leu Leu 1160 1165		

<210> SEQ ID NO 33

<211> LENGTH: 1047

<212> TYPE: PRT

<213> ORGANISM: M. bovis BCG

<400> SEQUENCE: 33

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

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Ala	Leu	Pro	Ala	Thr	Pro	Ile	Ala	Asp	Ser	Ala	Asp	Asp	Ala	Leu	Ala
225					230					235					240
Leu	Leu	Ile	Tyr	Thr	Ser	Gly	Ser	Thr	Gly	Ala	Pro	Lys	Gly	Ala	Met
				245					250					255	
Tyr	Arg	Glu	Ser	Gln	Val	Met	Ser	Phe	Trp	Arg	Lys	Ser	Ser	Gly	Trp
			260					265						270	
Phe	Glu	Pro	Ser	Gly	Tyr	Pro	Ser	Ile	Thr	Leu	Asn	Phe	Met	Pro	Met
		275					280					285			
Ser	His	Val	Gly	Gly	Arg	Gln	Val	Leu	Tyr	Gly	Thr	Leu	Ser	Asn	Gly
	290					295					300				
Gly	Thr	Ala	Tyr	Tyr	Val	Ala	Lys	Ser	Asp	Leu	Ser	Thr	Leu	Phe	Glu
305					310					315					320
Asp	Leu	Ala	Leu	Val	Arg	Pro	Thr	Glu	Leu	Cys	Phe	Val	Pro	Arg	Ile
				325					330					335	
Trp	Asp	Met	Val	Phe	Ala	Glu	Phe	His	Ser	Glu	Val	Asp	Arg	Arg	Leu
			340					345					350		
Val	Asp	Gly	Ala	Asp	Arg	Ala	Ala	Leu	Glu	Ala	Gln	Val	Lys	Ala	Glu
		355					360					365			
Leu	Arg	Glu	Asn	Val	Leu	Gly	Gly	Arg	Phe	Val	Met	Ala	Leu	Thr	Gly
	370					375					380				
Ser	Ala	Pro	Ile	Ser	Ala	Glu	Met	Thr	Ala	Trp	Val	Glu	Ser	Leu	Leu
385					390					395					400
Ala	Asp	Val	His	Leu	Val	Glu	Gly	Tyr	Gly	Ser	Thr	Glu	Ala	Gly	Met
			405						410					415	
Val	Leu	Asn	Asp	Gly	Met	Val	Arg	Arg	Pro	Ala	Val	Ile	Asp	Tyr	Lys
			420					425					430		
Leu	Val	Asp	Val	Pro	Glu	Leu	Gly	Tyr	Phe	Gly	Thr	Asp	Gln	Pro	Tyr
		435					440					445			
Pro	Arg	Gly	Glu	Leu	Leu	Val	Lys	Thr	Gln	Thr	Met	Phe	Pro	Gly	Tyr
	450					455					460				
Tyr	Gln	Arg	Pro	Asp	Val	Thr	Ala	Glu	Val	Phe	Asp	Pro	Asp	Gly	Phe
465					470					475					480
Tyr	Arg	Thr	Gly	Asp	Ile	Met	Ala	Lys	Val	Gly	Pro	Asp	Gln	Phe	Val
				485					490					495	
Tyr	Leu	Asp	Arg	Arg	Asn	Asn	Val	Leu	Lys	Leu	Ser	Gln	Gly	Glu	Phe
			500				505						510		
Ile	Ala	Val	Ser	Lys	Leu	Glu	Ala	Val	Phe	Gly	Asp	Ser	Pro	Leu	Val
		515					520					525			
Arg	Gln	Ile	Phe	Ile	Tyr	Gly	Asn	Ser	Ala	Arg	Ala	Tyr	Pro	Leu	Ala
	530					535					540				
Val	Val	Val	Pro	Ser	Gly	Asp	Ala	Leu	Ser	Arg	His	Gly	Ile	Glu	Asn
545					550					555					560
Leu	Lys	Pro	Val	Ile	Ser	Glu	Ser	Leu	Gln	Glu	Val	Ala	Arg	Ala	Ala
				565					570					575	
Gly	Leu	Gln	Ser	Tyr	Glu	Ile	Pro	Arg	Asp	Phe	Ile	Ile	Glu	Thr	Thr
			580					585					590		
Pro	Phe	Thr	Leu	Glu	Asn	Gly	Leu	Leu	Thr	Gly	Ile	Arg	Lys	Leu	Ala
		595					600					605			
Arg	Pro	Gln	Leu	Lys	Lys	Phe	Tyr	Gly	Glu	Arg	Leu	Glu	Arg	Leu	Tyr
	610					615					620				
Thr	Glu	Leu	Ala	Asp	Ser	Gln	Ser	Asn	Glu	Leu	Arg	Glu	Leu	Arg	Gln
625					630					635					640
Ser	Gly	Pro	Asp	Ala	Pro	Val	Leu	Pro	Thr	Leu	Cys	Arg	Ala	Ala	Ala

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645					650					655					
Ala	Leu	Leu	Gly	Ser	Thr	Ala	Ala	Asp	Val	Arg	Pro	Asp	Ala	His	Phe
			660					665					670		
Ala	Asp	Leu	Gly	Gly	Asp	Ser	Leu	Ser	Ala	Leu	Ser	Leu	Ala	Asn	Leu
		675					680					685			
Leu	His	Glu	Ile	Phe	Gly	Val	Asp	Val	Pro	Val	Gly	Val	Ile	Val	Ser
	690					695					700				
Pro	Ala	Ser	Asp	Leu	Arg	Ala	Leu	Ala	Asp	His	Ile	Glu	Ala	Ala	Arg
705					710					715					720
Thr	Gly	Val	Arg	Arg	Pro	Ser	Phe	Ala	Ser	Ile	His	Gly	Arg	Ser	Ala
				725					730						735
Thr	Glu	Val	His	Ala	Ser	Asp	Leu	Thr	Leu	Asp	Lys	Phe	Ile	Asp	Ala
			740					745					750		
Ala	Thr	Leu	Ala	Ala	Ala	Pro	Asn	Leu	Pro	Ala	Pro	Ser	Ala	Gln	Val
		755					760					765			
Arg	Thr	Val	Leu	Leu	Thr	Gly	Ala	Thr	Gly	Phe	Leu	Gly	Arg	Tyr	Leu
		770				775					780				
Ala	Leu	Glu	Trp	Leu	Asp	Arg	Met	Asp	Leu	Val	Asn	Gly	Lys	Leu	Ile
785						790					795				800
Cys	Leu	Val	Arg	Ala	Arg	Ser	Asp	Glu	Glu	Ala	Gln	Ala	Arg	Leu	Asp
				805					810						815
Ala	Thr	Phe	Asp	Ser	Gly	Asp	Pro	Tyr	Leu	Val	Arg	His	Tyr	Arg	Glu
			820					825					830		
Leu	Gly	Ala	Gly	Arg	Leu	Glu	Val	Leu	Ala	Gly	Asp	Lys	Gly	Glu	Ala
		835					840					845			
Asp	Leu	Gly	Leu	Asp	Arg	Val	Thr	Trp	Gln	Arg	Leu	Ala	Asp	Thr	Val
		850				855					860				
Asp	Leu	Ile	Val	Asp	Pro	Ala	Ala	Leu	Val	Asn	His	Val	Leu	Pro	Tyr
865					870						875				880
Ser	Gln	Leu	Phe	Gly	Pro	Asn	Ala	Ala	Gly	Thr	Ala	Glu	Leu	Leu	Arg
				885					890						895
Leu	Ala	Leu	Thr	Gly	Lys	Arg	Lys	Pro	Tyr	Ile	Tyr	Thr	Ser	Thr	Ile
			900					905						910	
Ala	Val	Gly	Glu	Gln	Ile	Pro	Pro	Glu	Ala	Phe	Thr	Glu	Asp	Ala	Asp
			915				920						925		
Ile	Arg	Ala	Ile	Ser	Pro	Thr	Arg	Arg	Ile	Asp	Asp	Ser	Tyr	Ala	Asn
	930						935				940				
Gly	Tyr	Ala	Asn	Ser	Lys	Trp	Ala	Gly	Glu	Val	Leu	Leu	Arg	Glu	Ala
945					950					955					960
His	Glu	Gln	Cys	Gly	Leu	Pro	Val	Thr	Val	Phe	Arg	Cys	Asp	Met	Ile
				965					970					975	
Leu	Ala	Asp	Thr	Ser	Tyr	Thr	Gly	Gln	Leu	Asn	Leu	Pro	Asp	Met	Phe
			980					985					990		
Thr	Arg	Leu	Met	Leu	Ser	Leu	Ala	Ala	Thr	Gly	Ile	Ala	Pro	Gly	Ser
			995				1000						1005		
Phe	Tyr	Glu	Leu	Asp	Ala	His	Gly	Asn	Arg	Gln	Arg	Ala	His	Tyr	
	1010						1015					1020			
Asp	Gly	Leu	Pro	Val	Glu	Phe	Val	Ala	Glu	Ala	Ile	Cys	Thr	Leu	
	1025					1030					1035				
Gly	Thr	His	Ser	Pro	Asp	Arg	Phe	Val							
	1040					1045									

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<211> LENGTH: 1174
<212> TYPE: PRT
<213> ORGANISM: M. leprae

<400> SEQUENCE: 34

Met Ser Thr Ile Thr Lys Gln Glu Lys Gln Leu Ala Arg Arg Val Asp
 1           5           10          15

Asp Leu Thr Ala Asn Asp Pro Gln Phe Ala Ala Ala Lys Pro Asp Pro
 20          25          30

Ala Val Ala Ala Ala Leu Ala Gln Pro Gly Leu Arg Leu Pro Gln Ile
 35          40          45

Ile Gln Thr Ala Leu Asp Gly Tyr Ala Glu Arg Pro Ala Leu Gly Gln
 50          55          60

Arg Val Ala Glu Phe Thr Lys Asp Pro Lys Thr Gly Arg Thr Ser Met
 65          70          75          80

Glu Leu Leu Pro Ser Phe Glu Thr Ile Thr Tyr Arg Gln Leu Gly Asp
 85          90          95

Arg Val Gly Ala Leu Ala Arg Ala Trp Arg His Asp Leu Leu His Ala
 100         105         110

Gly Tyr Arg Val Cys Val Leu Gly Phe Asn Ser Val Asp Tyr Ala Ile
 115         120         125

Ile Asp Met Ala Leu Gly Val Ile Gly Ala Val Ala Val Pro Leu Gln
 130         135         140

Thr Ser Ala Ala Ile Thr Gln Leu Gln Ser Ile Val Thr Glu Thr Glu
 145         150         155         160

Pro Ser Met Ile Ala Thr Ser Val Asn Gln Leu Pro Asp Thr Val Glu
 165         170         175

Leu Ile Leu Ser Gly Gln Ala Pro Ala Lys Leu Val Val Phe Asp Tyr
 180         185         190

His Pro Glu Val Asp Glu Gln His Asp Ala Val Ala Thr Ala Arg Ala
 195         200         205

Arg Leu Ala Asp Ser Ser Val Val Val Glu Ser Leu Thr Glu Val Leu
 210         215         220

Gly Arg Gly Lys Thr Leu Pro Ala Thr Pro Ile Pro Val Ala Asp Asp
 225         230         235         240

Ser Ala Asp Pro Leu Ala Leu Leu Ile Tyr Thr Ser Gly Ser Thr Gly
 245         250         255

Ala Pro Lys Gly Ala Met Tyr Leu Gln Ser Asn Val Gly Lys Met Trp
 260         265         270

Arg Arg Ser Asp Gly Asn Trp Phe Gly Pro Thr Ala Ala Ser Ile Thr
 275         280         285

Leu Asn Phe Met Pro Met Ser His Val Met Gly Arg Gly Ile Leu Tyr
 290         295         300

Gly Thr Leu Gly Asn Gly Gly Thr Ala Tyr Phe Ala Ala Arg Ser Asp
 305         310         315         320

Leu Ser Thr Leu Leu Glu Asp Leu Lys Leu Val Arg Pro Thr Glu Leu
 325         330         335

Asn Phe Val Pro Arg Ile Trp Glu Thr Leu Tyr Asp Glu Ser Lys Arg
 340         345         350

Ala Val Asp Arg Arg Leu Ala Asn Ser Gly Ser Ala Asp Arg Ala Ala
 355         360         365

Ile Lys Ala Glu Val Met Asp Glu Gln Arg Gln Ser Leu Leu Gly Gly
 370         375         380

Arg Tyr Ile Ala Ala Met Thr Gly Ser Ala Pro Thr Ser Pro Glu Leu

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Asp Ala Arg Ala Arg Leu Asp Lys Thr Phe Asp Ser Gly Asp Pro Lys
 820 825 830

Leu Leu Ala His Tyr Gln Glu Leu Ala Thr Asp His Leu Glu Val Ile
 835 840 845

Ala Gly Asp Lys Gly Glu Val Asp Leu Glu Leu Asp Arg Gln Thr Trp
 850 855 860

Arg Arg Leu Ala Asp Thr Val Asp Leu Ile Val Asp Pro Ala Ala Leu
 865 870 875 880

Val Asn His Val Leu Pro Tyr Ser Glu Leu Phe Gly Pro Asn Thr Leu
 885 890 895

Gly Thr Ala Glu Leu Ile Arg Ile Ala Leu Thr Ser Lys Gln Lys Pro
 900 905 910

Tyr Ile Tyr Val Ser Thr Ile Gly Val Gly Asn Gln Ile Glu Pro Ala
 915 920 925

Lys Phe Thr Glu Asp Ser Asp Ile Arg Val Ile Ser Pro Thr Arg Asn
 930 935 940

Ile Asn Asn Asn Tyr Ala Asn Gly Tyr Gly Asn Ser Lys Trp Ala Gly
 945 950 955 960

Glu Val Leu Leu Arg Glu Ala His Asp Leu Cys Gly Leu Pro Val Thr
 965 970 975

Val Phe Arg Cys Asp Met Ile Leu Ala Asp Thr Ser Tyr Ala Gly Gln
 980 985 990

Leu Asn Val Pro Asp Met Phe Thr Arg Met Met Leu Ser Leu Ala Ala
 995 1000 1005

Thr Gly Ile Ala Pro Gly Ser Phe Tyr Glu Leu Asp Ala Glu Ser
 1010 1015 1020

Asn Arg Gln Arg Ala His Tyr Asp Gly Leu Pro Val Glu Phe Ile
 1025 1030 1035

Ala Glu Ala Ile Ser Thr Leu Gly Asp Gln Ser Leu His Asp Arg
 1040 1045 1050

Asp Gly Phe Thr Thr Tyr His Val Met Asn Pro His Asp Asp Gly
 1055 1060 1065

Ile Gly Met Asp Glu Phe Val Asp Trp Leu Ile Asp Ala Gly Cys
 1070 1075 1080

Pro Ile Gln Arg Ile Asn Asp Tyr Asp Glu Trp Leu Arg Arg Phe
 1085 1090 1095

Glu Ile Ser Leu Arg Ala Leu Pro Glu Arg Gln Arg His Ser Ser
 1100 1105 1110

Leu Leu Pro Leu Leu His Asn Tyr Gln Lys Pro Glu Lys Pro Leu
 1115 1120 1125

His Gly Ser Leu Ala Pro Thr Ile Arg Phe Arg Thr Ala Val Gln
 1130 1135 1140

Asn Ala Asn Ile Gly Gln Asp Lys Asp Ile Pro His Ile Ser Pro
 1145 1150 1155

Ala Ile Ile Ala Lys Tyr Val Ser Asp Leu Gln Leu Leu Gly Leu
 1160 1165 1170

Val

<210> SEQ ID NO 35

<211> LENGTH: 1168

<212> TYPE: PRT

<213> ORGANISM: M. smegmatis MBCG

<400> SEQUENCE: 35

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Met Thr Ile Glu Thr Arg Glu Asp Arg Phe Asn Arg Arg Ile Asp His
 1 5 10 15
 Leu Phe Glu Thr Asp Pro Gln Phe Ala Ala Ala Arg Pro Asp Glu Ala
 20 25 30
 Ile Ser Ala Ala Ala Ala Asp Pro Glu Leu Arg Leu Pro Ala Ala Val
 35 40 45
 Lys Gln Ile Leu Ala Gly Tyr Ala Asp Arg Pro Ala Leu Gly Lys Arg
 50 55 60
 Ala Val Glu Phe Val Thr Asp Glu Glu Gly Arg Thr Thr Ala Lys Leu
 65 70 75 80
 Leu Pro Arg Phe Asp Thr Ile Thr Tyr Arg Gln Leu Ala Gly Arg Ile
 85 90 95
 Gln Ala Val Thr Asn Ala Trp His Asn His Pro Val Asn Ala Gly Asp
 100 105 110
 Arg Val Ala Ile Leu Gly Phe Thr Ser Val Asp Tyr Thr Thr Ile Asp
 115 120 125
 Ile Ala Leu Leu Glu Leu Gly Ala Val Ser Val Pro Leu Gln Thr Ser
 130 135 140
 Ala Pro Val Ala Gln Leu Gln Pro Ile Val Ala Glu Thr Glu Pro Lys
 145 150 155 160
 Val Ile Ala Ser Ser Val Asp Phe Leu Ala Asp Ala Val Ala Leu Val
 165 170 175
 Glu Ser Gly Pro Ala Pro Ser Arg Leu Val Val Phe Asp Tyr Ser His
 180 185 190
 Glu Val Asp Asp Gln Arg Glu Ala Phe Glu Ala Ala Lys Gly Lys Leu
 195 200 205
 Ala Gly Thr Gly Val Val Val Glu Thr Ile Thr Asp Ala Leu Asp Arg
 210 215 220
 Gly Arg Ser Leu Ala Asp Ala Pro Leu Tyr Val Pro Asp Glu Ala Asp
 225 230 235 240
 Pro Leu Thr Leu Leu Ile Tyr Thr Ser Gly Ser Thr Gly Thr Pro Lys
 245 250 255
 Gly Ala Met Tyr Pro Glu Ser Lys Thr Ala Thr Met Trp Gln Ala Gly
 260 265 270
 Ser Lys Ala Arg Trp Asp Glu Thr Leu Gly Val Met Pro Ser Ile Thr
 275 280 285
 Leu Asn Phe Met Pro Met Ser His Val Met Gly Arg Gly Ile Leu Cys
 290 295 300
 Ser Thr Leu Ala Ser Gly Gly Thr Ala Tyr Phe Ala Ala Arg Ser Asp
 305 310 315 320
 Leu Ser Thr Phe Leu Glu Asp Leu Ala Leu Val Arg Pro Thr Gln Leu
 325 330 335
 Asn Phe Val Pro Arg Ile Trp Asp Met Leu Phe Gln Glu Tyr Gln Ser
 340 345 350
 Arg Leu Asp Asn Arg Arg Ala Glu Gly Ser Glu Asp Arg Ala Glu Ala
 355 360 365
 Ala Val Leu Glu Glu Val Arg Thr Gln Leu Leu Gly Gly Arg Phe Val
 370 375 380
 Ser Ala Leu Thr Gly Ser Ala Pro Ile Ser Ala Glu Met Lys Ser Trp
 385 390 395 400
 Val Glu Asp Leu Leu Asp Met His Leu Leu Glu Gly Tyr Gly Ser Thr
 405 410 415

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

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835					840					845					
Lys	Gly	Glu	Ala	Asp	Leu	Gly	Leu	Asp	His	Asp	Thr	Trp	Gln	Arg	Leu
	850					855					860				
Ala	Asp	Thr	Val	Asp	Leu	Ile	Val	Asp	Pro	Ala	Ala	Leu	Val	Asn	His
865					870					875					880
Val	Leu	Pro	Tyr	Ser	Gln	Met	Phe	Gly	Pro	Asn	Ala	Leu	Gly	Thr	Ala
				885					890					895	
Glu	Leu	Ile	Arg	Ile	Ala	Leu	Thr	Thr	Thr	Ile	Lys	Pro	Tyr	Val	Tyr
			900						905					910	
Val	Ser	Thr	Ile	Gly	Val	Gly	Gln	Gly	Ile	Ser	Pro	Glu	Ala	Phe	Val
		915					920					925			
Glu	Asp	Ala	Asp	Ile	Arg	Glu	Ile	Ser	Ala	Thr	Arg	Arg	Val	Asp	Asp
	930					935					940				
Ser	Tyr	Ala	Asn	Gly	Tyr	Gly	Asn	Ser	Lys	Trp	Ala	Gly	Glu	Val	Leu
945				950						955					960
Leu	Arg	Glu	Ala	His	Asp	Trp	Cys	Gly	Leu	Pro	Val	Ser	Val	Phe	Arg
				965					970					975	
Cys	Asp	Met	Ile	Leu	Ala	Asp	Thr	Thr	Tyr	Ser	Gly	Gln	Leu	Asn	Leu
			980						985					990	
Pro	Asp	Met	Phe	Thr	Arg	Leu	Met	Leu	Ser	Leu	Val	Ala	Thr	Gly	Ile
		995					1000					1005			
Ala	Pro	Gly	Ser	Phe	Tyr	Glu	Leu	Asp	Ala	Asp	Gly	Asn	Arg	Gln	
	1010					1015					1020				
Arg	Ala	His	Tyr	Asp	Gly	Leu	Pro	Val	Glu	Phe	Ile	Ala	Glu	Ala	
	1025					1030					1035				
Ile	Ser	Thr	Ile	Gly	Ser	Gln	Val	Thr	Asp	Gly	Phe	Glu	Thr	Phe	
	1040					1045					1050				
His	Val	Met	Asn	Pro	Tyr	Asp	Asp	Gly	Ile	Gly	Leu	Asp	Glu	Tyr	
	1055					1060					1065				
Val	Asp	Trp	Leu	Ile	Glu	Ala	Gly	Tyr	Pro	Val	His	Arg	Val	Asp	
	1070					1075					1080				
Asp	Tyr	Ala	Thr	Trp	Leu	Ser	Arg	Phe	Glu	Thr	Ala	Leu	Arg	Ala	
	1085					1090					1095				
Leu	Pro	Glu	Arg	Gln	Arg	Gln	Ala	Ser	Leu	Leu	Pro	Leu	Leu	His	
	1100					1105					1110				
Asn	Tyr	Gln	Gln	Pro	Ser	Pro	Pro	Val	Cys	Gly	Ala	Met	Ala	Pro	
	1115					1120					1125				
Thr	Asp	Arg	Phe	Arg	Ala	Ala	Val	Gln	Asp	Ala	Lys	Ile	Gly	Pro	
	1130					1135					1140				
Asp	Lys	Asp	Ile	Pro	His	Val	Thr	Ala	Asp	Val	Ile	Val	Lys	Tyr	
	1145					1150					1155				
Ile	Ser	Asn	Leu	Gln	Met	Leu	Gly	Leu	Leu						
	1160					1165									

<210> SEQ ID NO 36

<211> LENGTH: 869

<212> TYPE: PRT

<213> ORGANISM: hypothetical

<400> SEQUENCE: 36

Val Asp Arg Leu Arg Arg Ile Glu Leu Phe Ala Asp Gln Phe Ala Ala
 1 5 10 15

Ala Pro Glu Ala Val Ser Ala Val Pro Gly Met Leu Pro Gln Ile Ile
 20 25 30

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450				455				460						
Thr	Val	Arg	Ala	Ala	Met	Leu	Gly	Asp	Met	Arg	Asp	Ala	His	Phe
465				470				475						480
Asp	Leu	Gly	Gly	Asp	Ser	Leu	Ser	Ala	Leu	Ser	Asn	Leu	Leu	His
				485				490						495
Ile	Phe	Val	Asp	Val	Pro	Val	Gly	Val	Ile	Val	Ser	Pro	Ala	Glu
			500					505					510	Leu
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		515					520					525		His
Gly	Arg	Ala	Ser	Glu	Val	Arg	Ala	Asp	Leu	Thr	Leu	Asp	Lys	Phe
	530					535					540			Ile
Asp	Ala	Thr	Leu	Ala	Pro	Leu	Pro	Val	Arg	Thr	Val	Leu	Leu	Thr
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Gly	Ala	Thr	Gly	Phe	Leu	Gly	Arg	Tyr	Leu	Ala	Leu	Glu	Trp	Leu
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Arg	Met	Asp	Leu	Val	Gly	Lys	Leu	Ile	Cys	Leu	Val	Arg	Ala	Arg
			580					585					590	Ser
Glu	Glu	Ala	Ala	Arg	Leu	Asp	Thr	Phe	Asp	Ser	Gly	Asp	Pro	Leu
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His	Tyr	Leu	Ala	Ala	Arg	Leu	Glu	Val	Leu	Ala	Gly	Asp	Lys	Gly
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625				630						635				640
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Gln	Leu	Phe	Gly	Pro	Asn	Gly	Thr	Ala	Glu	Leu	Val	Arg	Leu	Ala
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Thr	Arg	Lys	Pro	Tyr	Ile	Tyr	Ser	Thr	Ile	Gly	Val	Gly	Gln	Ile
		675					680					685		Pro
Phe	Glu	Asp	Asp	Ile	Arg	Ile	Ser	Thr	Arg	Val	Glu	Ser	Tyr	Ala
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His	Asp	Cys	Gly	Leu	Pro	Val	Thr	Val	Phe	Arg	Cys	Asp	Met	Ile
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Ala	Asp	Thr	Ser	Tyr	Gly	Gln	Leu	Asn	Val	Pro	Asp	Met	Phe	Thr
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	755						760					765		Glu
Leu	Asp	Ala	Gly	Asn	Arg	Gln	Arg	Ala	His	Tyr	Asp	Gly	Leu	Pro
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Glu	Phe	Val	Ala	Glu	Ala	Ile	Thr	Leu	Gly	Asp	Phe	Thr	Tyr	Val
785				790						795				800
Asn	Pro	Asp	Asp	Gly	Ile	Leu	Asp	Glu	Phe	Val	Asp	Trp	Leu	Ile
				805					810					815
Ile	Asp	Tyr	Trp	Arg	Phe	Glu	Ile	Arg	Ala	Leu	Pro	Glu	Lys	Gln
			820				825						830	Arg
Ser	Val	Leu	Pro	Leu	Leu	Tyr	Pro	Val	Gly	Ile	Pro	Phe	Ala	Val
		835					840					845		Gln
Ala	Ile	Gly	Glu	Asp	Ile	Pro	His	Leu	Ser	Leu	Ile	Lys	Tyr	Val
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<210> SEQ ID NO 37
 <211> LENGTH: 4600
 <212> TYPE: DNA
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 37

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<210> SEQ ID NO 38
<211> LENGTH: 4600
<212> TYPE: DNA
<213> ORGANISM: Nocardia

<400> SEQUENCE: 38

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<210> SEQ ID NO 39
<211> LENGTH: 1174
<212> TYPE: PRT
<213> ORGANISM: Nocardia

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<400> SEQUENCE: 39

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20          25          30
Val Ser Ala Ala Val Ser Ala Pro Gly Met Arg Leu Ala Gln Ile Ala
35          40          45
Ala Thr Val Met Ala Gly Tyr Ala Asp Arg Pro Ala Ala Gly Gln Arg
50          55          60
Ala Phe Glu Leu Asn Thr Asp Asp Ala Thr Gly Arg Thr Ser Leu Arg
65          70          75          80
Leu Leu Pro Arg Phe Glu Thr Ile Thr Tyr Arg Glu Leu Trp Gln Arg
85          90          95
Val Gly Glu Val Ala Ala Ala Trp His His Asp Pro Glu Asn Pro Leu
100         105        110
Arg Ala Gly Asp Phe Val Ala Leu Leu Gly Phe Thr Ser Ile Asp Tyr
115         120        125
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130         135        140
Leu Gln Ala Ser Ala Ala Val Ser Gln Leu Ile Ala Ile Leu Thr Glu
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165         170        175
Val Glu Cys Leu Leu Ala Gly Thr Thr Pro Glu Arg Leu Val Val Phe
180         185        190
Asp Tyr His Pro Glu Asp Asp Asp Gln Arg Ala Ala Phe Glu Ser Ala
195         200        205
Arg Arg Arg Leu Ala Asp Ala Gly Ser Ser Val Ile Val Glu Thr Leu
210         215        220
Asp Ala Val Arg Ala Arg Gly Arg Asp Leu Pro Ala Ala Pro Leu Phe
225         230        235        240
Val Pro Asp Thr Asp Asp Asp Pro Leu Ala Leu Leu Ile Tyr Thr Ser
245         250        255
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260         265        270
Ala Thr Met Trp Gln Gly Asn Ser Met Leu Gln Gly Asn Ser Gln Arg
275         280        285
Val Gly Ile Asn Leu Asn Tyr Met Pro Met Ser His Ile Ala Gly Arg
290         295        300
Ile Ser Leu Phe Gly Val Leu Ala Arg Gly Gly Thr Ala Tyr Phe Ala
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Ala Lys Ser Asp Met Ser Thr Leu Phe Glu Asp Ile Gly Leu Val Arg
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Gly Gly Arg Phe Leu Val Ala Val Val Gly Ser Ala Pro Leu Ala Ala
 385 390 395 400

Glu Met Lys Thr Phe Met Glu Ser Val Leu Asp Leu Pro Leu His Asp
 405 410 415

Gly Tyr Gly Ser Thr Glu Ala Gly Ala Ser Val Leu Leu Asp Asn Gln
 420 425 430

Ile Gln Arg Pro Pro Val Leu Asp Tyr Lys Leu Val Asp Val Pro Glu
 435 440 445

Leu Gly Tyr Phe Arg Thr Asp Arg Pro His Pro Arg Gly Glu Leu Leu
 450 455 460

Leu Lys Ala Glu Thr Thr Ile Pro Gly Tyr Tyr Lys Arg Pro Glu Val
 465 470 475 480

Thr Ala Glu Ile Phe Asp Glu Asp Gly Phe Tyr Lys Thr Gly Asp Ile
 485 490 495

Val Ala Glu Leu Glu His Asp Arg Leu Val Tyr Val Asp Arg Arg Asn
 500 505 510

Asn Val Leu Lys Leu Ser Gln Gly Glu Phe Val Thr Val Ala His Leu
 515 520 525

Glu Ala Val Phe Ala Ser Ser Pro Leu Ile Arg Gln Ile Phe Ile Tyr
 530 535 540

Gly Ser Ser Glu Arg Ser Tyr Leu Leu Ala Val Ile Val Pro Thr Asp
 545 550 555 560

Asp Ala Leu Arg Gly Arg Asp Thr Ala Thr Leu Lys Ser Ala Leu Ala
 565 570 575

Glu Ser Ile Gln Arg Ile Ala Lys Asp Ala Asn Leu Gln Pro Tyr Glu
 580 585 590

Ile Pro Arg Asp Phe Leu Ile Glu Thr Glu Pro Phe Thr Ile Ala Asn
 595 600 605

Gly Leu Leu Ser Gly Ile Ala Lys Leu Leu Arg Pro Asn Leu Lys Glu
 610 615 620

Arg Tyr Gly Ala Gln Leu Glu Gln Met Tyr Thr Asp Leu Ala Thr Gly
 625 630 635 640

Gln Ala Asp Glu Leu Leu Ala Leu Arg Arg Glu Ala Ala Asp Leu Pro
 645 650 655

Val Leu Glu Thr Val Ser Arg Ala Ala Lys Ala Met Leu Gly Val Ala
 660 665 670

Ser Ala Asp Met Arg Pro Asp Ala His Phe Thr Asp Leu Gly Gly Asp
 675 680 685

Ser Leu Ser Ala Leu Ser Phe Ser Asn Leu Leu His Glu Ile Phe Gly
 690 695 700

Val Glu Val Pro Val Gly Val Val Val Ser Pro Ala Asn Glu Leu Arg
 705 710 715 720

Asp Leu Ala Asn Tyr Ile Glu Ala Glu Arg Asn Ser Gly Ala Lys Arg
 725 730 735

Pro Thr Phe Thr Ser Val His Gly Gly Gly Ser Glu Ile Arg Ala Ala
 740 745 750

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Asp Leu Thr Leu Asp Lys Phe Ile Asp Ala Arg Thr Leu Ala Ala Ala
 755 760 765
 Asp Ser Ile Pro His Ala Pro Val Pro Ala Gln Thr Val Leu Leu Thr
 770 775 780
 Gly Ala Asn Gly Tyr Leu Gly Arg Phe Leu Cys Leu Glu Trp Leu Glu
 785 790 795 800
 Arg Leu Asp Lys Thr Gly Gly Thr Leu Ile Cys Val Val Arg Gly Ser
 805 810 815
 Asp Ala Ala Ala Ala Arg Lys Arg Leu Asp Ser Ala Phe Asp Ser Gly
 820 825 830
 Asp Pro Gly Leu Leu Glu His Tyr Gln Gln Leu Ala Ala Arg Thr Leu
 835 840 845
 Glu Val Leu Ala Gly Asp Ile Gly Asp Pro Asn Leu Gly Leu Asp Asp
 850 855 860
 Ala Thr Trp Gln Arg Leu Ala Glu Thr Val Asp Leu Ile Val His Pro
 865 870 875 880
 Ala Ala Leu Val Asn His Val Leu Pro Tyr Thr Gln Leu Phe Gly Pro
 885 890 895
 Asn Val Val Gly Thr Ala Glu Ile Val Arg Leu Ala Ile Thr Ala Arg
 900 905 910
 Arg Lys Pro Val Thr Tyr Leu Ser Thr Val Gly Val Ala Asp Gln Val
 915 920 925
 Asp Pro Ala Glu Tyr Gln Glu Asp Ser Asp Val Arg Glu Met Ser Ala
 930 935 940
 Val Arg Val Val Arg Glu Ser Tyr Ala Asn Gly Tyr Gly Asn Ser Lys
 945 950 955 960
 Trp Ala Gly Glu Val Leu Leu Arg Glu Ala His Asp Leu Cys Gly Leu
 965 970 975
 Pro Val Ala Val Phe Arg Ser Asp Met Ile Leu Ala His Ser Arg Tyr
 980 985 990
 Ala Gly Gln Leu Asn Val Gln Asp Val Phe Thr Arg Leu Ile Leu Ser
 995 1000 1005
 Leu Val Ala Thr Gly Ile Ala Pro Tyr Ser Phe Tyr Arg Thr Asp
 1010 1015 1020
 Ala Asp Gly Asn Arg Gln Arg Ala His Tyr Asp Gly Leu Pro Ala
 1025 1030 1035
 Asp Phe Thr Ala Ala Ala Ile Thr Ala Leu Gly Ile Gln Ala Thr
 1040 1045 1050
 Glu Gly Phe Arg Thr Tyr Asp Val Leu Asn Pro Tyr Asp Asp Gly
 1055 1060 1065
 Ile Ser Leu Asp Glu Phe Val Asp Trp Leu Val Glu Ser Gly His
 1070 1075 1080
 Pro Ile Gln Arg Ile Thr Asp Tyr Ser Asp Trp Phe His Arg Phe
 1085 1090 1095
 Glu Thr Ala Ile Arg Ala Leu Pro Glu Lys Gln Arg Gln Ala Ser
 1100 1105 1110
 Val Leu Pro Leu Leu Asp Ala Tyr Arg Asn Pro Cys Pro Ala Val
 1115 1120 1125
 Arg Gly Ala Ile Leu Pro Ala Lys Glu Phe Gln Ala Ala Val Gln
 1130 1135 1140
 Thr Ala Lys Ile Gly Pro Glu Gln Asp Ile Pro His Leu Ser Ala
 1145 1150 1155
 Pro Leu Ile Asp Lys Tyr Val Ser Asp Leu Glu Leu Leu Gln Leu

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1160	1165	1170
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Leu

<210> SEQ ID NO 40
 <211> LENGTH: 16
 <212> TYPE: PRT
 <213> ORGANISM: Nicordia

<400> SEQUENCE: 40

Leu Ile Tyr Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Met Tyr
 1 5 10 15

<210> SEQ ID NO 41
 <211> LENGTH: 16
 <212> TYPE: PRT
 <213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 41

Leu Ile Tyr Thr Ser Gly Ser Thr Gly Ala Pro Lys Gly Ala Met Tyr
 1 5 10 15

<210> SEQ ID NO 42
 <211> LENGTH: 16
 <212> TYPE: PRT
 <213> ORGANISM: Saccharomyces

<400> SEQUENCE: 42

Leu Ser Phe Thr Ser Gly Ser Glu Gly Ile Pro Lys Gly Val Leu Gly
 1 5 10 15

<210> SEQ ID NO 43
 <211> LENGTH: 10
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 43

Thr Ser Gly Ser Glu Gly Arg Pro Lys Gly
 1 5 10

<210> SEQ ID NO 44
 <211> LENGTH: 11
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 44

Leu Tyr Thr Ser Gly Ser Gly Pro Lys Gly Met
 1 5 10

<210> SEQ ID NO 45
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: Nicordia

<400> SEQUENCE: 45

Asp Leu Pro Leu His Asp Gly Tyr Gly Ser Thr Glu Ala Gly
 1 5 10

<210> SEQ ID NO 46
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 46

Asp Val His Leu Val Glu Gly Tyr Gly Ser Thr Glu Ala Gly

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1 5 10

<210> SEQ ID NO 47
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: *Saccharomyces*

<400> SEQUENCE: 47

Asn Cys Arg Ile Val Asn Met Tyr Gly Thr Thr Glu Thr Gln
 1 5 10

<210> SEQ ID NO 48
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 48

Ile Val Asn Met Tyr Gly Thr Thr
 1 5

<210> SEQ ID NO 49
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 49

Leu Val Tyr Gly Ser Thr Glu
 1 5

<210> SEQ ID NO 50
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: *Nicordia*

<400> SEQUENCE: 50

Asp Glu Asp Gly Phe Tyr Lys Thr Gly Asp Ile Val Ala Glu
 1 5 10

<210> SEQ ID NO 51
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: *M. tuberculosis*

<400> SEQUENCE: 51

Asp Pro Asp Gly Phe Tyr Arg Thr Gly Asp Ile Met Ala Lys
 1 5 10

<210> SEQ ID NO 52
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: *Saccharomyces*

<400> SEQUENCE: 52

Pro Arg Asp Arg Leu Tyr Arg Thr Gly Asp Leu Gly Arg Tyr
 1 5 10

<210> SEQ ID NO 53
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 53

Arg Leu Tyr Arg Ser Gly Asp Leu
 1 5

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<210> SEQ ID NO 54
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 54

Asp Tyr Arg Thr Gly Asp Leu
 1 5

<210> SEQ ID NO 55
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Nicordia

<400> SEQUENCE: 55

Asp Ala Asn Leu Gln Pro Tyr Glu Ile Pro Arg Asp Phe
 1 5 10

<210> SEQ ID NO 56
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 56

Ala Ala Gly Leu Gln Ser Tyr Glu Ile Pro Arg Asp Phe
 1 5 10

<210> SEQ ID NO 57
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Saccharomyces

<400> SEQUENCE: 57

Glu Pro Thr Leu Ile Thr Phe Met Val Pro Arg Phe Asp
 1 5 10

<210> SEQ ID NO 58
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 58

Leu Val Ser Tyr Phe Val Pro
 1 5

<210> SEQ ID NO 59
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 59

Leu Ser Tyr Ile Pro Arg Phe
 1 5

<210> SEQ ID NO 60
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Nicordia

<400> SEQUENCE: 60

Asn Gly Leu Leu Ser Gly Ile Ala Lys Leu Leu Arg Pro Asn Leu Lys
 1 5 10 15

Glu Arg

-continued

<210> SEQ ID NO 61
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 61

Asn Gly Leu Leu Thr Gly Ile Arg Lys Leu Ala Arg Pro Gln Leu Lys
 1 5 10 15

Lys Phe

<210> SEQ ID NO 62
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Saccharomyces

<400> SEQUENCE: 62

Lys Leu Pro Leu Asn Pro Asn Gly Lys Val Asp Lys Pro Lys Leu Gln
 1 5 10 15

Phe Pro

<210> SEQ ID NO 63
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 63

Leu Asn Pro Asn Gly Lys Ile Asp Lys Pro Ala Leu
 1 5 10

<210> SEQ ID NO 64
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 64

Leu Gly Lys Val Lys Pro Leu
 1 5

<210> SEQ ID NO 65
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: Nicordia

<400> SEQUENCE: 65

Phe Thr Asp Leu Gly Gly Asp Ser Leu Ser Ala Leu Ser Phe
 1 5 10

<210> SEQ ID NO 66
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 66

Phe Ala Asp Leu Gly Gly Asp Ser Leu Ser Ala Leu Ser Leu
 1 5 10

<210> SEQ ID NO 67
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: Saccharomyces

<400> SEQUENCE: 67

Phe Phe Asp Leu Gly Gly His Ser Ile Leu Ala Thr Lys Met

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 1 5 10

<210> SEQ ID NO 68
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 68

Leu Gly Gly His Ser Ile Leu Ala Gln
 1 5

<210> SEQ ID NO 69
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 69

Phe Asp Leu Gly Gly Ser Ile Ala
 1 5

<210> SEQ ID NO 70
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Nicordia

<400> SEQUENCE: 70

Leu Leu Thr Gly Ala Asn Gly Tyr Leu Gly Arg Phe Leu
 1 5 10

<210> SEQ ID NO 71
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 71

Leu Leu Thr Gly Ala Thr Gly Phe Leu Gly Arg Tyr Leu
 1 5 10

<210> SEQ ID NO 72
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Saccharomyces

<400> SEQUENCE: 72

Phe Val Thr Gly Val Thr Gly Phe Leu Gly Ser Tyr Ile
 1 5 10

<210> SEQ ID NO 73
 <211> LENGTH: 10
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 73

Gly Ala Thr Gly Phe Leu Gly Ala His Ile
 1 5 10

<210> SEQ ID NO 74
 <211> LENGTH: 11
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 74

Val Thr Gly Ala Thr Gly Phe Leu Gly Tyr Ile
 1 5 10

-continued

<210> SEQ ID NO 75
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Nicordia

<400> SEQUENCE: 75

Tyr Ala Asn Gly Tyr Gly Asn Ser Lys Trp Ala Gly Glu
 1 5 10

<210> SEQ ID NO 76
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: M. tuberculosis

<400> SEQUENCE: 76

Tyr Ala Asn Gly Tyr Ala Asn Ser Lys Trp Ala Gly Glu
 1 5 10

<210> SEQ ID NO 77
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Saccharomyces

<400> SEQUENCE: 77

Leu Thr Gly Gly Tyr Gly Gln Ser Lys Trp Ala Ala Glu
 1 5 10

<210> SEQ ID NO 78
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 78

Gly Tyr Gly Gln Ser Lys Trp
 1 5

<210> SEQ ID NO 79
 <211> LENGTH: 10
 <212> TYPE: PRT
 <213> ORGANISM: hypothetical

<400> SEQUENCE: 79

Gly Tyr Gly Gln Ser Lys Trp Ala Ala Glu
 1 5 10

<210> SEQ ID NO 80
 <211> LENGTH: 1391
 <212> TYPE: PRT
 <213> ORGANISM: Saccharomyces

<400> SEQUENCE: 80

Thr Asn Glu Lys Val Trp Ile Glu Lys Leu Asp Asn Pro Thr Leu Ser
 1 5 10 15

Val Leu Pro His Asp Phe Leu Arg Pro Gln Gln Glu Pro Tyr Thr Lys
 20 25 30

Gln Ala Thr Tyr Ser Leu Gln Leu Pro Gln Leu Asp Val Pro His Asp
 35 40 45

Ser Phe Ser Asn Lys Tyr Ala Val Ala Leu Ser Val Trp Ala Ala Leu
 50 55 60

Ile Tyr Arg Val Thr Gly Asp Asp Asp Ile Val Leu Tyr Ile Ala Asn
 65 70 75 80

Asn Lys Ile Leu Arg Phe Asn Ile Gln Pro Thr Trp Ser Phe Asn Glu

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85					90					95					
Leu	Tyr	Ser	Thr	Ile	Asn	Asn	Glu	Leu	Asn	Lys	Leu	Asn	Ser	Ile	Glu
			100					105					110		
Ala	Asn	Phe	Ser	Phe	Asp	Glu	Leu	Ala	Glu	Lys	Ile	Gln	Ser	Cys	Gln
		115					120					125			
Asp	Leu	Glu	Arg	Thr	Pro	Gln	Leu	Phe	Arg	Leu	Ala	Phe	Leu	Glu	Asn
	130					135					140				
Gln	Asp	Phe	Lys	Leu	Asp	Glu	Phe	Lys	His	His	Leu	Val	Asp	Phe	Ala
145					150					155					160
Leu	Asn	Leu	Asp	Thr	Ser	Asn	Asn	Ala	His	Val	Leu	Asn	Leu	Ile	Tyr
			165						170					175	
Asn	Ser	Leu	Leu	Tyr	Ser	Asn	Glu	Arg	Val	Thr	Ile	Val	Ala	Asp	Gln
		180						185					190		
Phe	Thr	Gln	Tyr	Leu	Thr	Ala	Ala	Leu	Ser	Asp	Pro	Ser	Asn	Cys	Ile
		195					200					205			
Thr	Lys	Ile	Ser	Leu	Ile	Thr	Ala	Ser	Ser	Lys	Asp	Ser	Leu	Pro	Asp
	210					215					220				
Pro	Thr	Lys	Asn	Leu	Gly	Trp	Cys	Asp	Phe	Val	Gly	Cys	Ile	His	Asp
225					230					235					240
Ile	Phe	Gln	Asp	Asn	Ala	Glu	Ala	Phe	Pro	Glu	Arg	Thr	Cys	Val	Val
				245					250					255	
Glu	Thr	Pro	Thr	Leu	Asn	Ser	Asp	Lys	Ser	Arg	Ser	Phe	Thr	Tyr	Arg
			260					265					270		
Asp	Ile	Asn	Arg	Thr	Ser	Asn	Ile	Val	Ala	His	Tyr	Leu	Ile	Lys	Thr
	275						280					285			
Gly	Ile	Lys	Arg	Gly	Asp	Val	Val	Met	Ile	Tyr	Ser	Ser	Arg	Gly	Val
	290					295					300				
Asp	Leu	Met	Val	Cys	Val	Met	Gly	Val	Leu	Lys	Ala	Gly	Ala	Thr	Phe
305					310					315					320
Ser	Val	Ile	Asp	Pro	Ala	Tyr	Pro	Pro	Ala	Arg	Gln	Thr	Ile	Tyr	Leu
				325					330					335	
Gly	Val	Ala	Lys	Pro	Arg	Gly	Leu	Ile	Val	Ile	Arg	Ala	Ala	Gly	Gln
			340					345					350		
Leu	Asp	Gln	Leu	Val	Glu	Asp	Tyr	Ile	Asn	Asp	Glu	Leu	Glu	Ile	Val
		355					360					365			
Ser	Arg	Ile	Asn	Ser	Ile	Ala	Ile	Gln	Glu	Asn	Gly	Thr	Ile	Glu	Gly
	370					375					380				
Gly	Lys	Leu	Asp	Asn	Gly	Glu	Asp	Val	Leu	Ala	Pro	Tyr	Asp	His	Tyr
385					390					395					400
Lys	Asp	Thr	Arg	Thr	Gly	Val	Val	Val	Gly	Pro	Asp	Ser	Asn	Pro	Thr
				405					410					415	
Leu	Ser	Phe	Thr	Ser	Gly	Ser	Glu	Gly	Ile	Pro	Lys	Gly	Val	Leu	Gly
			420					425					430		
Arg	His	Phe	Ser	Leu	Ala	Tyr	Tyr	Phe	Asn	Trp	Met	Ser	Lys	Arg	Phe
		435					440					445			
Asn	Leu	Thr	Glu	Asn	Asp	Lys	Phe	Thr	Met	Leu	Ser	Gly	Ile	Ala	His
	450					455					460				
Asp	Pro	Ile	Gln	Arg	Asp	Met	Phe	Thr	Pro	Leu	Phe	Leu	Gly	Ala	Gln
465					470					475					480
Leu	Tyr	Val	Pro	Thr	Gln	Asp	Asp	Ile	Gly	Thr	Pro	Gly	Arg	Leu	Ala
				485					490					495	
Glu	Trp	Met	Ser	Lys	Tyr	Gly	Cys	Thr	Val	Thr	His	Leu	Thr	Pro	Ala
			500					505					510		

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Met Gly Gln Leu Leu Thr Ala Gln Ala Thr Thr Pro Phe Pro Lys Leu
515 520 525

His His Ala Phe Phe Val Gly Asp Ile Leu Thr Lys Arg Asp Cys Leu
530 535 540

Arg Leu Gln Thr Leu Ala Glu Asn Cys Arg Ile Val Asn Met Tyr Gly
545 550 555 560

Thr Thr Glu Thr Gln Arg Ala Val Ser Tyr Phe Glu Val Lys Ser Lys
565 570 575

Asn Asp Asp Pro Asn Phe Leu Lys Lys Leu Lys Asp Val Met Pro Ala
580 585 590

Gly Lys Gly Met Leu Asn Val Gln Leu Leu Val Val Asn Arg Asn Asp
595 600 605

Arg Thr Gln Ile Cys Gly Ile Gly Glu Ile Gly Glu Ile Tyr Val Arg
610 615 620

Ala Gly Gly Leu Ala Glu Gly Tyr Arg Gly Leu Pro Glu Leu Asn Lys
625 630 635 640

Glu Lys Phe Val Asn Asn Trp Phe Val Glu Lys Asp His Trp Asn Tyr
645 650 655

Leu Asp Lys Asp Asn Gly Glu Pro Trp Arg Gln Phe Trp Leu Gly Pro
660 665 670

Arg Asp Arg Leu Tyr Arg Thr Gly Asp Leu Gly Arg Tyr Leu Pro Asn
675 680 685

Gly Asp Cys Glu Cys Cys Gly Arg Ala Asp Asp Gln Val Lys Ile Arg
690 695 700

Gly Phe Arg Ile Glu Leu Gly Glu Ile Asp Thr His Ile Ser Gln His
705 710 715 720

Pro Leu Val Arg Glu Asn Ile Thr Leu Val Arg Lys Asn Ala Asp Asn
725 730 735

Glu Pro Thr Leu Ile Thr Phe Met Val Pro Arg Phe Asp Lys Pro Asp
740 745 750

Asp Leu Ser Lys Phe Gln Ser Asp Val Pro Lys Glu Val Glu Thr Asp
755 760 765

Pro Ile Val Lys Gly Leu Ile Gly Tyr His Leu Leu Ser Lys Asp Ile
770 775 780

Arg Thr Phe Leu Lys Lys Arg Leu Ala Ser Tyr Ala Met Pro Ser Leu
785 790 795 800

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

Lys Pro Lys Leu Gln Phe Pro Thr Pro Lys Gln Leu Asn Leu Val Ala
820 825 830

Glu Asn Thr Val Ser Glu Thr Asp Asp Ser Gln Phe Thr Asn Val Glu
835 840 845

Arg Glu Val Arg Asp Leu Trp Leu Ser Ile Leu Pro Thr Lys Pro Ala
850 855 860

Ser Val Ser Pro Asp Asp Ser Phe Phe Asp Leu Gly Gly His Ser Ile
865 870 875 880

Leu Ala Thr Lys Met Ile Phe Thr Leu Lys Lys Lys Leu Gln Val Asp
885 890 895

Leu Pro Leu Gly Thr Ile Phe Lys Tyr Pro Thr Ile Lys Ala Phe Ala
900 905 910

Ala Glu Ile Asp Arg Ile Lys Ser Ser Gly Gly Ser Ser Gln Gly Glu
915 920 925

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Val Val Glu Asn Val Thr Ala Asn Tyr Ala Glu Asp Ala Lys Lys Leu
 930 935 940

Val Glu Thr Leu Pro Ser Ser Tyr Pro Ser Arg Glu Tyr Phe Val Glu
 945 950 955 960

Pro Asn Ser Ala Glu Gly Lys Thr Thr Ile Asn Val Phe Val Thr Gly
 965 970 975

Val Thr Gly Phe Leu Gly Ser Tyr Ile Leu Ala Asp Leu Leu Gly Arg
 980 985 990

Ser Pro Lys Asn Tyr Ser Phe Lys Val Phe Ala His Val Arg Ala Lys
 995 1000 1005

Asp Glu Glu Ala Ala Phe Ala Arg Leu Gln Lys Ala Gly Ile Thr
 1010 1015 1020

Tyr Gly Thr Trp Asn Glu Lys Phe Ala Ser Asn Ile Lys Val Val
 1025 1030 1035

Leu Gly Asp Leu Ser Lys Ser Gln Phe Gly Leu Ser Asp Glu Lys
 1040 1045 1050

Trp Met Asp Leu Ala Asn Thr Val Asp Ile Ile Ile His Asn Gly
 1055 1060 1065

Ala Leu Val His Trp Val Tyr Pro Tyr Ala Lys Leu Arg Asp Pro
 1070 1075 1080

Asn Val Ile Ser Thr Ile Asn Val Met Ser Leu Ala Ala Val Gly
 1085 1090 1095

Lys Pro Lys Phe Phe Asp Phe Val Ser Ser Thr Ser Thr Leu Asp
 1100 1105 1110

Thr Glu Tyr Tyr Phe Asn Leu Ser Asp Lys Leu Val Ser Glu Gly
 1115 1120 1125

Lys Pro Gly Ile Leu Glu Ser Asp Asp Leu Met Asn Ser Ala Ser
 1130 1135 1140

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

Ile Ile Arg Arg Ala Gly Glu Arg Gly Leu Arg Gly Cys Ile Val
 1160 1165 1170

Arg Pro Gly Tyr Val Thr Gly Ala Ser Ala Asn Gly Ser Ser Asn
 1175 1180 1185

Thr Asp Asp Phe Leu Leu Arg Phe Leu Lys Gly Ser Val Gln Leu
 1190 1195 1200

Gly Lys Ile Pro Asp Ile Glu Asn Ser Val Asn Met Val Pro Val
 1205 1210 1215

Asp His Val Ala Arg Val Val Val Ala Thr Ser Leu Asn Pro Pro
 1220 1225 1230

Lys Glu Asn Glu Leu Ala Val Ala Gln Val Thr Gly His Pro Arg
 1235 1240 1245

Ile Leu Phe Lys Asp Tyr Leu Tyr Thr Leu His Asp Tyr Gly Tyr
 1250 1255 1260

Asp Val Glu Ile Glu Ser Tyr Ser Lys Trp Lys Lys Ser Leu Glu
 1265 1270 1275

Ala Ser Val Ile Asp Arg Asn Glu Glu Asn Ala Leu Tyr Pro Leu
 1280 1285 1290

Leu His Met Val Leu Asp Asn Leu Pro Glu Ser Thr Lys Ala Pro
 1295 1300 1305

Glu Leu Asp Asp Arg Asn Ala Val Ala Ser Leu Lys Lys Asp Thr
 1310 1315 1320

Ala Trp Thr Gly Val Asp Trp Ser Asn Gly Ile Gly Val Thr Pro

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1325						1330									1335
Glu	Glu	Val	Gly	Ile	Tyr	Ile	Ala	Phe	Leu	Asn	Lys	Val	Gly	Phe	
1340						1345					1350				
Leu	Pro	Pro	Pro	Thr	His	Asn	Asp	Lys	Leu	Pro	Leu	Pro	Ser	Ile	
1355						1360					1365				
Glu	Leu	Thr	Gln	Ala	Gln	Ile	Ser	Leu	Val	Ala	Ser	Gly	Ala	Gly	
1370						1375					1380				
Ala	Arg	Gly	Ser	Ser	Ala	Ala	Ala								
1385						1390									

15

What is claimed is:

1. An isolated carboxylic acid reductase polypeptide having carboxylic acid reductase activity, said polypeptide selected from the group consisting of:

(a) an isolated polypeptide having at least 95% sequence identity to SEQ ID NO:2; and

(b) an isolated polypeptide encoded by the nucleic acid of SEQ ID NO:1.

2. The isolated carboxylic acid reductase polypeptide of claim 1 wherein said polypeptide comprises the amino acid sequence of SEQ ID NO: 2.

3. A method of reducing a carboxylic acid substrate to an aldehyde product comprising:

- a) obtaining the carboxylic acid reductase of claim 1; and
- b) exposing said carboxylic acid substrate to said recombinant carboxylic reductase, thereby reducing said acid substrate to an aldehyde product, wherein said substrate is a vanillic acid, benzoic acid or ferulic acid.

* * * * *