



Figure 1

Nocardia 1 --AVDSPDERLQRRHAQLFAEEDCVKAAARPLEAVSAAMSAAPGMRLAQHAATVMAGYADRP  
MtfadD 1 ---MSINDQRLTRRVEDLMASDAQFAAASPNEALHQAHQDQPGVALPOLIRMVMEGYADRP  
MBCG 1 ---MSINDQRLTRRVEDLMASDAQFAAASPNEALHQAHQDQPGVALPOLIRMVMEGYADRP  
MlAcS 1 MSTTKQEKQLARRVDDLITANDPQFAAAKPDPAVAALAAQPGRLPOLITOTALDGYADRP  
Msmeg 1 -MTTETREDRFNRRLDHLFETDPQFAAARPDPAVAALAAQPGRLPOLITOTALDGYADRP  
consensus 1 v d rl RRie Lfa D QfaAA P eAvs Av Pgm Lpqii vm GYADRP

Nocardia 59 AAGORAFELNTHDADTGRTSRLLPRFETITYRELWQVCEVAAAWHHHPENPLRAGDFVA  
MtfadD 58 ALGORALRFVTDPSGRTMVELLPRFETITYRELWARACTLATALSAAP--AIRPGDRVC  
MBCG 58 ALGORALRFVTDPSGRTMVELLPRFETITYRELWARACTLATALSAAP--AIRPGDRVC  
MlAcS 61 ALGORVAEFTKDKPKGRTSMELELSEFETITYROLGDRVCAARAWRHE---LLHAGYRVC  
Msmeg 60 ALGKRAVEFVTD-EEGRITAKLLPRFETITYROLAGRIQAVTNAWHNH---PUNAGDRVA  
consensus 61 ALGqRa f tD tGRT l LLPrFeTITYR L R g va A d lr GdrV

Nocardia 119 ILGFTSVDYATIDIALHLCGAVTVPLQASAAVSOILIAITETSPREJASTPEHLDAVEFC  
MtfadD 116 VLGFNNSVDYTTIDIALHRLCGAVSVPLQTSAPVITGLRFIVTETEPTMIASSIDNLGDAVEV  
MBCG 116 VLGFNNSVDYTTIDIALHRLCGAVSVPLQTSAPVITGLRFIVTETEPTMIASSIDNLGDAVEV  
MlAcS 118 VLGFNNSVDYATIDIALGAVTVGAVVPLQTSAAITQLOQSTVTEPEPSMIASSVNLQDPITVEL  
Msmeg 116 ILGFTSVDYTTIDIALHLCGAVSVPLQTSAPVACLQPTVAETEPKVIASSVDFLADAVL  
consensus 121 ILGF SvDY tidlAli lGAVtVPLQtSA vs L IvtETeP liAssie L daVev

Nocardia 179 LLAGTTPERLVVFDYHPEDDDQRAAFESARRRLADAGSSVIVETLDANRARGRDLPAAPL  
MtfadD 176 LAG-HAPARLVVFDYHGKVDTHREAVEAARARLAG---SVTIDTLABELTERGRALPAT--  
MBCG 176 LAG-HAPARLVVFDYHGKVDTHREAVEAARARLAG---SVTIDTLABELTERGRALPAT--  
MlAcS 178 LSGCAPAKLVVFDYHPEVDEQHDVATARARLADS--SVVVESTVAVLGRCKTLPATPI  
Msmeg 176 VESGAPSRLLVVFDYSHEVDDQRAAFEAAGKRLAGT--GVVVEITTDALDRGRSLADAP-  
consensus 181 l aP rLVVFDYh vD reA e ArarLA sV vetl evi RGr Lpa

Nocardia 239 FVPTDDDPLALLIYTSGSTGTPKGAMYTNRLAAIMVQOQ---NSMLQNSQRVGINLNFMM  
MtfadD 230 PFIADSADDALALLIYTSGSTGAPKAGAMYRESQVMSFWRK---SSGWFEPSGYPSITLNFMM  
MBCG 230 PFIADSADDALALLIYTSGSTGAPKAGAMYRESQVMSFWRK---SSGWFEPSGYPSITLNFMM  
MlAcS 236 PFIADSADPLALLIYTSGSTGAPKAGAMYLSNVGKMWRR---SDGNWFGPTAASITLNFMM  
Msmeg 233 LYVPDEADPLTLLIYTSGSTGTPKGAMYPEKTAAMVQAGSKARWDETLGVMPISITLNFMM  
consensus 241 v d D LaLLIYTSGSTG PKGAMY s t W sitLNFMM

Nocardia 296 PMSHVAGRISLFCVILARGGTAYFAAKSDMSTLFEDLGLVRPTELFVPRICDMVFQRYQS  
MtfadD 287 PMSHVGGROVLYGTLNNGGTAYFAKSDLSTLFEDLALVRPTELCFVPRIDWMMVFAEYHS  
MBCG 287 PMSHVGGROVLYGTLNNGGTAYFAKSDLSTLFEDLALVRPTELCFVPRIDWMMVFAEYHS  
MlAcS 293 PMSHVMCRGILYGTLCNCGGTAYFAAKSDLSTLFEDLKLVRPTELNFVPRIEWETLYDESKR  
Msmeg 293 PMSHVMCRGILCSTLASCCTAYFAAKSDLSTLFEDLALVRPTQLNFVPRIDWMMVFCQYQS  
consensus 301 PMSHv GR vLfgtL GGTAYf AKSDlStl EDlgLVRPTel FVPRiwdmvf ey s

Nocardia 356 EIDRRSVAG--ADLDTEDREVKAIDIRONYLGGRFVAVVGSAPLAEMKTFMES-VLDLP  
MtfadD 347 EIDRRRLVDG--ADRAALEAQAQKAEIRENVLGGRFVMAHTGSAPLSAEMTAVVESLLADVH  
MBCG 347 EIDRRRLVDG--ADRAALEAQAQKAEIRENVLGGRFVMAHTGSAPLSAEMTAVVESLLADVH  
MlAcS 353 AVDRRLANSAGSADRAALEAQAQKAEVMDIQOSILGGRVLAAMTGSAPLSAEMKHGVES-LLDMH  
Msmeg 353 RIDNRRRAEG--S-EDRAALEAVLEVMTQILLGGRFVSAITGSAPLSAEMKSWVED-LLDMH  
consensus 361 lDrR g ad lda V eIR nvLGGRfI AvtGSAPlsaEm fvEs l dlh

Nocardia 413 LHEGYGSTEAGSVLLDNOIQRPVLDYKLVDPPELGYFRTRDRPHPRGELLKKAETTIPG  
MtfadD 405 LHEGYGSTEAG-MVLNDGMVRRPAVIDYKLVDPPELGYFGTDQPYPRGELLKKTQTMFPG  
MBCG 405 LHEGYGSTEAG-MVLNDGMVRRPAVIDYKLVDPPELGYFGTDQPYPRGELLKKTQTMFPG  
MlAcS 412 LHEGYGSTEAG-MVLFDCVQRPVLDYKLVDPPELGYFSTDPYPRGELLKKTQTMFPG  
Msmeg 409 LHEGYGSTEAG-AVFDGQIQRPVLDYKLVDPPELGYFATDRPYPRGELLKKSQMFPG  
consensus 421 LveGYGSTEAG V1 Dg i RP ViDYKLVDPPELGYF TD PyPRGELLlKt mfPG

Nocardia 473 YYKRPEVTAETFD DGFYK TGDIVAE LGEH DRLVYV DRRNNVLKLSQGEFVTVAKLEAVFA  
MtfadD 464 YYQRPDVTAEVFDE DGEYR TGDIMAKVGP DQFVYV DRRNNVLKLSQGEFVAVSKLEAVFG  
MBCG 464 YYQRPDVTAEVFDE DGEYR TGDIMAKVGP DQFVYV DRRNNVLKLSQGEFVAVSKLEAVFG  
MlAcS 471 YYKRPEVTAETVFDSDGMYQTGDI VAEVGP DRLVYV DRRNNVLKLSQGEFVTVAKLEA AFS  
Msmeg 468 YYKRPEVTAETFD DGFYR TGDIVAE LGGPDHLE YV DRRNNVLKLSQGEFVTVSKLEAVFG  
consensus 481 YY RPeVTAeiFD DGFyKtGDIvA lgpD vYvDRRNNVLKLSQGeFv V kLEAvFa

Nocardia 533 SSPLVRQIFIIYGNSSERSYLLAVVVPD DALRGRDTAT LKSA LAESHORTAKDANLQPYEI  
MtfadD 524 DSPLVRQIFIIYGN SARAYPLAVVVPSCDALSRHG IENLKPVI SESLQEVARAAGLQSYEI  
MBCG 524 DSPLVRQIFIIYGN SARAYPLAVVVPSCDALSRHG IENLKPVI SESLQEVARAAGLQSYEI  
MlAcS 531 NSPLVRQIMIYGN SAHPYLLAVVVPTE DALATNDIEVLKPLI IDSLQKVAKEADLQSYEV  
Msmeg 528 DSPLVRQIIVYGN SARSYLLAVVVPTEEALSRWDG EELKSRI SD SLQDAARAAGLQSYEI  
consensus 541 SPLvRQIfiYGnSar Y LAVvVPT dAL e LK i eSlQ iAk A LQsYei

Nocardia 593 PRDFLIETTPFTLENGLLSGIAK L LREN LKERYCAQLEQMYTDLATGCAD ELLALRRBAA  
MtfadD 584 PRDFLIETTPFTLENGLLTGIRKLAR PQLKKFYCERLERLYTELADSCSNELRELROSGP  
MBCG 584 PRDFLIETTPFTLENGLLTGIRKLAR PQLKKFYCERLERLYTELADSCSNELRELROSGP  
MlAcS 591 PRDLIVETTPFSL ENGLLTGIRKLAWPKL KQHVCARLEQLYADLVEGCANALIVLQOSVA  
Msmeg 588 PRDLIVETTPFTLENGLLTGIRKLAR PQLKAHYCERLEQLYTDLAFGCANELRELERNGA  
consensus 601 PRDfliETtPftleNGLLtGirKLarP LK YG rLE lytdLad Q neLr Lr a

Nocardia 653 DLPVLETIVSRAAKAM LGVASADMRP DAHFTDLGGDSL SALSFSNLLHEIFGVVDPVGVIV  
MtfadD 644 DAPVLP T LCRAAAAL LGSTAADVRP DAHFADLGGDSL SALS LANLLHEIFGVVDPVGVIV  
MBCG 644 DAPVLP T LCRAAAAL LGSTAADVRP DAHFADLGGDSL SALS LANLLHEIFGVVDPVGVIV  
MlAcS 651 NAPVLQTVSRAVGT LIGVATTD E PNAHFTDLGGDSL SALSIFGSLLELFDVDPVGVIV  
Msmeg 648 DRPVLETIVSRAAVALLGASVTD MRSDAHFTDLGGDSL SALSFSNLLHEIFD VDPVGVIV  
consensus 661 d Pvl Tv RAa amLG Dmr dAHF DLGGDSL SALS nLLheif vDPVGViv

Nocardia 713 SPANHLRDLIANYI EAERN SCAKR PFTTSVHG-GGSETRAADL TLDKF IDARTLAAADSIIP  
MtfadD 704 SPASDLRALADHI EAAR-TGVR RPSFASIHGRS ATEVHASDL TLDKF IDAATLAAAPNL P  
MBCG 704 SPASDLRALADHI EAAR-TGVR RPSFASIHGRS ATEVHASDL TLDKF IDAATLAAAPNL P  
MlAcS 711 SPVNNLVATADYI ERER-QCTKR PTEIA THGRDAGKVFHASDL TLDKF IDVSTLTAAPVLA  
Msmeg 708 SPATDLACVAAYI ECEL-RCSKR PTVASMHGRD ATEVHARDL TLDCKF IDAKTL SAAAGLP  
consensus 721 SPa eL aLa IEa r G kRptf svHG r asevrA DLtLdKfIda TL Aap lp

Nocardia 772 HAPVPAQTVLLTGANGYLG RFLCLEWLERUDKTCG TLIICVVRGSDAAAARKRLDSAFDSG  
MtfadD 763 APSAQV R TVLLTGATGFLGRYLALEW LDRMDLVNCKIICLVRA RSDDEAARLDATFD SG  
MBCG 763 APSAQV R TVLLTGATGFLGRYLALEW LDRMDLVNCKIICLVRA RSDDEAARLDATFD SG  
MlAcS 770 QPGTEV R TVLLTGATGFLGRYLA LKWLERM DLVECKVIALVRAKSNEDARARLDKTFDSG  
Msmeg 767 RSCTEV R TVLLTGATGFLGRYLALEW LERM DLV DCKV ICLVRA RSDDEARARLDATFD TG  
consensus 781 vrTVLLTGatGfLGRyLaLeWLeRmDlv GkIiClvRars eeA aRLD tFDsG

Nocardia 832 DPGLEEHYQQLAART LEVLAGDKG EADLGLDRVTWQR LADTVDLIVDPAALVNHVLPYSQ  
MtfadD 823 DPYLMRHYREL GACRLEVL AGDKGEADLGLDRVTWQR LADTVDLIVDPAALVNHVLPYSQ  
MBCG 823 DPYLMRHYREL GACRLEVL AGDKGEADLGLDRVTWQR LADTVDLIVDPAALVNHVLPYSQ  
MlAcS 830 DPKLEAHYQELATD HLEVL AGDKGEVDLELDRQ TWRLADTVDLIVDPAALVNHVLPYS E  
Msmeg 827 DATLEEHYRALAAD HLEVL AGDKGEADLGLDRVTWQR LADTVDLIVDPAALVNHVLPYSQ  
consensus 841 Dp Ll HY Laa rLEVLAGDKGe dLgLDr TwqRLAdTVDLIVdPAALVNHVLPysq

Nocardia 892 LFGPNVVGTAELVRIALTARRK E VTYLSTVGVADQMDPAEYQ EESD YREMSAVR VVRESY  
MtfadD 883 LFGPNAAGTAE LRLALTGKRKPYIYVSTIANG EOIIPPEAFTEADIRAI SPTRRIDDSY  
MBCG 883 LFGPNAAGTAE LRLALTGKRKPYIYVSTIANG EOIIPPEAFTEADIRAI SPTRRIDDSY  
MlAcS 890 LFGPNTLGTAE LRLALTSKQKPYIYVSTIANG EOIIPPAKFTEDSDIRVI SPTRRINNNY  
Msmeg 887 MFGPNALGTAE LRLALT TTIKPYIYVSTIANG EOIIPPEAFVEDADIREI SATRRIDDSY  
consensus 901 lFGPN GTAElvRlALT r KPyiY STigVg qi P f ED DiR iS tR v esY

Nocardia 952 ANGYGNSKWAGEVLLREAHdLCGLPVAVFRSDMILAHsRYAGQLNVDVfTRlLlSLVAT  
MtfadD 943 ANGYGNSKWAGEVLLREAHdCGLPVtVFRCDMILADtSYTGQLNlPDMFTRlMLSLAAT  
MBCG 943 ANGYGNSKWAGEVLLREAHdCGLPVtVFRCDMILADtSYTGQLNlPDMFTRlMLSLAAT  
MlAcS 950 ANGYGNSKWAGEVLLREAHdLCGLPVtVFRCDMILADtSYAGQLNlPDMFTRlMLSLAAT  
Msmeg 947 ANGYGNSKWAGEVLLREAHdWCGLPVtVFRCDMILADtSYSGQLNlPDMFTRlMLSLVAT  
consensus 961 ANGYGNSKWAGEVLLREAHd CGLPVtVFRCDMILADtSY GQLNvpDmFTRlMLSL AT

Nocardia 1012 GIAPGSFYRTDADCNQRRAHYDGLPVEFVAEAItlG---IQATEGFRtYDvlnpYDDGI  
MtfadD 1003 GIAPGSFYELDAHCNRQRAHYDGLPVEFVAEAItlG---THSPDRFVtYHVMNpYDDGI  
MBCG 1003 GIAPGSFYELDAHCNRQRAHYDGLPVEFVAEAItlG---THSPDRFV-----  
MlAcS 1010 GIAPGSFYELDAESNRQRAHYDGLPVEFVAEAItlGdQSLHdRdGfTtYHVMNpHDDGI  
Msmeg 1007 GIAPGSFYELDADCNQRRAHYDGLPVEFVAEAItlG---SQVtDGFtYHVMNpYDDGI  
consensus 1021 GIAPGSFYelDA gNRQRAHYDGLPveFvAeAI tlG d F ty vlnp ddgi

Nocardia 1069 SdDEFVDWLVESG----HPIQRHtDYSDWfHRfETAIRALPEKQRQASMLPLLDAYRNPC  
MtfadD 1060 GdDEFVDWLVNSPTSGSGCTIQRHAdYGEWlQRfETSIRALPDRORHASLLPLLNpYREBA  
MBCG -----  
MlAcS 1070 GdDEFVDWLIID----ACCPfORHNDYDEWLRfEISIRALPEORHSSlLPLLNpYQKPE  
Msmeg 1064 GdDEFVDWLIIEAG----YPVHMDDYATWLSRFETAIRALPEKQRQASMLPLLNpYQCPs  
consensus 1081 ldefvdwl i ri dy w rfe iralpekqr svlpll y p

Nocardia 1125 PAVRCAHLPAKEfQAaVQTAkIGPEQDIpHfSAPtIDkYMSDLpHLQLL SEQ ID NO:2  
MtfadD 1120 KPfHCStAPtDQfRAaVQEAkIGPEKDIpHLtAAAtkYtSNLrLLGLL SEQ ID NO:32  
MBCG ----- SEQ ID NO:33  
MlAcS 1126 KPfHCStAPtIRfRTAVQNAntGQDKDIpHfSAPtIAkYMSDLpHLGLV SEQ ID NO:34  
Msmeg 1120 PpVCCAMApTDfRfRAaVQDAkIGPEKDIpHVAADkVtYSNLQMLGLL SEQ ID NO:35  
consensus 1141 v g i p f avq a ig e dipHs li kyvs l ll ll SEQ ID NO:36

Figure 2

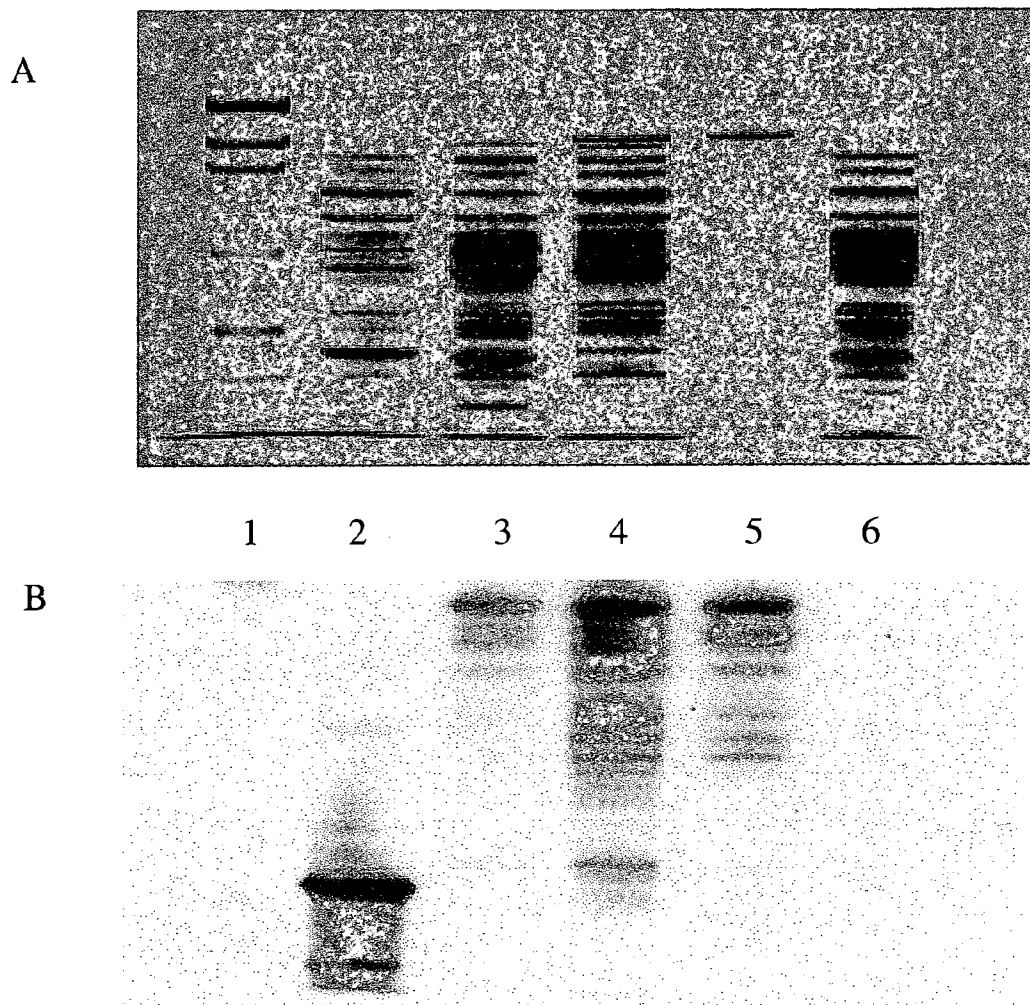


Figure 3

<b>Car-C</b>	LIYTSGSTGTPKGAMY	SEQ ID NO:40
FadD9	LIYTSGSTGAPKGAMY	SEQ ID NO:41
yeast AAR	LSFTSGSEGIPKGVLG	SEQ ID NO:42
motif-Pc	---TSGSEGRPKG---	SEQ ID NO:43
consensus	l yTSGS G PKG m	SEQ ID NO:44
<b>Car-D</b>	DLPLHDGYGSTEAG	SEQ ID NO:45
FadD9	DVHLVEGYGSTEAG	SEQ ID NO:46
yeast	NCRIVNMYGTTETQ	SEQ ID NO:47
motif-Pc	---IVNMYGTT---	SEQ ID NO:48
consensus	lv YGSte	SEQ ID NO:49
<b>Car-F</b>	DEDGFYKTGDIVAE	SEQ ID NO:50
FadD9	DPDGFYRTGDIMAK	SEQ ID NO:51
yeast	PRDRLYRTGDLGRY	SEQ ID NO:52
motif-Pc	---RLYRSGDL---	SEQ ID NO:53
consensus	d YrtGDI	SEQ ID NO:54
<b>Car-H</b>	DANLQPYEIPRDF-	SEQ ID NO:55
FadD9	AAGLQSYEIPRDF-	SEQ ID NO:56
yeast	EPTLITFMVPR-FD	SEQ ID NO:57
motif-Pc	---LVSYFVP----	SEQ ID NO:58
consensus	L sy iPr f	SEQ ID NO:59
<b>Car-I</b>	NGLLSGIAKLLRPNLKER	SEQ ID NO:60
FadD9	NGLLTGIRKLARPQLKKF	SEQ ID NO:61
yeast	KLPLNPNGKVDKPKLQFP	SEQ ID NO:62
motif-Pc	---LNPNGKIDKPAL---	SEQ ID NO:63
consensus	L gKv kP L	SEQ ID NO:64
<b>Car-J</b>	FTDLGGDSLSALSF	SEQ ID NO:65
FadD9	FADLGGDSLSALS	SEQ ID NO:66
yeast	FFDLGGHSILATKM	SEQ ID NO:67
motif-Pc	---LGGHSILAQ--	SEQ ID NO:68
consensus	f dLGG Si A	SEQ ID NO:69
<b>Car-NADP</b>	LLTGANGYLGRFL	SEQ ID NO:70
FadD9	LLTGATGFLGRYL	SEQ ID NO:71
yeast	FVTGVTGFLGSYI	SEQ ID NO:72
motif-Pc	---GATGFLGAHI	SEQ ID NO:73
consensus	vtGatGfLG yi	SEQ ID NO:74
<b>Car-Reduct</b>	YANGYGNSKWAGE	SEQ ID NO:75
FadD9	YANGYANSKWAGE	SEQ ID NO:76
yeast	LTGGYGQSKWAAE	SEQ ID NO:77
motif-Pc	---GYGQSKW---	SEQ ID NO:78
consensus	GYgqSKWaae	SEQ ID NO:79

Fig. 4

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	
LIY[ <u>TSGSTGT</u> ]	[ <u>PKG</u> AMYTNR	AATMWQGNM	LQGNSQRVGI	NLNYMPMSHI	<b>C</b> 300
AGRISLFGVL	ARGGTAYFAA	KSDMSTLFED	IGLVRPTEIF	FVPRVCDMVF	
QRYQSELD	RR SVAGADLDTL	DREVKADLRQ	NYLGGRFLVA	VVGSAPLAAE	400
MKTFMESVLD	LPL[ <u>HDGYGST</u> ]	EAGASVLLDN	QIQRPPVLDY	KLVDVPELGY	<b>D</b>
FRTDRPHPRG	ELLLKAETTI	PGYYKRPEVT	AEIFDE[ <u>DGFY</u> ]	[ <u>KTGDI</u> ]VAELE	<b>F</b> 500
HDRLVYVDRR	NNVLKLSQGE	FVTVAHLEAV	FASSPLIRQI	FIYGSSERSY	
LLAVIVPTDD	ALRGRDTATL	KSALAESIQR	IAKDAN[ <u>LQPY</u> ]	[ <u>EIPRDFLI</u> ]ET	<b>H</b> 600
EPFTIANGLL	[ <u>SGIAKLLRPN</u> ]	[ <u>L</u> KERYGAQLE	QMYTDLATGQ	ADELLALRRE	<b>I</b>
AADLPVLETV	SRAAKAMLG	V ASADMRPDAH	FTD[ <u>LGGDSLS</u> ]	[ <u>ALSFSNLL</u> ]HE	<b>J</b> 700
IFGVEVPVGV	VVSPANELRD	LANYIEAERN	SGAKRPTFTS	VHGGGSEIRA	
ADLTLDKFID	ARTLAAADSI	PHAPVPAQTV	LLT[ <u>GANGYLG</u> ]	RFLCLEWLER	<b>NADP bind.</b> 800
LDKTGGTLIC	VVRGSDAAAA	RKRLDSAFDS	GDPGLLEHYQ	QLAARTLEVL	
AGDIGDPNLG	LDDATWQRLA	ETVDLIVHPA	ALVNHVLPYT	QLFGPNVVG	900
AEIVRLAITA	RRKPVTYLST	VGVADQVDP	AEYQEDSDVRE	MSAVRVVRES	
YAN[ <u>GYGNSKW</u> ]	AGEVLLREAH	DLCGLPVAVF	RSDMILAHSR	YAGQLNVQDV	<b>Reduction</b> 1000
FTRLILSLVA	TGIAPYSFYR	TDADGNRQRA	HYDGLPADFT	AAAITALGIQ	
ATEGFRTYDV	LNPYDDGISL	DEFVDWLVES	GHPIQRITDY	SDWFHRFETA	1100
IRALPEKQRQ	ASVLPLLDAY	RNPPCAVRGA	ILPAKEFQAA	VQTAKIGPEQ	1150
DIPHLSAPLI	DKYVSDLELL	QLL (SEQ ID NO:2)			

Fig. 5

SINDQRLTRR	VEDLYASDAQ	FAAASPNEAI	TQAIDQPGVA	LPQLIRMVME	
GYADRPALGQ	RALRFVTPDP	SGRTMVLLP	RFETITYREL	WARAGTLATA	100
LSAEPAIRPG	DRVCVLGFNS	VDYTTIDIAL	IRLGAVSVPL	QTSAPVTGLR	
PIVTETEPTM	IATSIDNLGD	AVEVLGAGAP	ARLVVFDYHG	KVDTHREAVE	200
AARARLAGSV	TIDTLAELIE	RGRALPATPI	ADSADDALAL	LIY <u>TSGSTGA</u>	<b>C</b>
<u>PKG</u> AMYRESQ	VMSFWRKSSG	WFEPSPYPSI	TLNFMPMSHV	GGRQVLYGTL	300
SNGGTAYFVA	KSDLSTLFED	LALVRPTELC	FVPRIWDMVF	AEFHSEVDRR	
LVDGADRAAL	EAQVKAELRE	NVLGGRFVMA	LTGSAPISAE	MTAWVESLLA	400
DVHL <u>VEGYGS</u>	TEAGMVLNDG	MVRRPAVIDY	KLVDVPELGY	FGTDQPYPRG	<b>D</b>
ELLVKTQTMF	PGYYQRPDVT	AEVFDPD <u>GFY</u>	<u>RTGD</u> IMAKVG	PDQFVYLDRR	<b>F</b> 500
NNVLKLSQGE	FAVSKLEAV	FGDSPLVRQI	FIYGNSARAY	PLAVVVPSPG	
ALSRHGIENL	KPVISESLQE	VARAAG <u>LQSY</u>	<u>EIPRDFI</u> ET	TPFTLENGLL	<b>H</b> 600
<u>TGIRKLARPO</u>	<u>LKKFY</u> GERLE	RLYTELADSQ	SNELRELRQS	GPDAPVLPPL	<b>I</b>
CRAAAALLGS	TAADVRPDAA	FAD <u>LGGDSL</u> S	<u>ALSLANLL</u> HE	IFGVDVPVGV	<b>J</b> 700
IVSPASDLRA	LADHIEAART	GVRPSPFASI	HGRSATEVHA	SDLTLDKFID	
AATLAAAPNL	PAPSAQVRTV	LLT <u>GATGFLG</u>	RYLALEWLDR	MDLVNGKLIC	<b>NADP</b>
LVRARSDEEA	QARLDATFDS	GDPYLVRHYR	ELGAGRLEVL	AGDKGEADLG	
LDRVTWQRLA	DTVDLIVDPA	ALVNHVLPYS	QLFGPNAAGT	AELLRLALTG	900
KRKPYYTST	IAVGEQIPPE	AFTEDADIRA	ISPTRRIDDS	YANG <u>YANSKW</u>	<b>Reduction</b>
<u>AGEVLL</u> REAH	EQCGLPVTVF	RCDMILADTS	YTGQLNLPDM	FTRLMLSLAA	1000
TGIAPGSFYE	LDAHGNRQRA	HYDGLPVEFV	AEAICTLGTH	SPDRFVTYHV	
MNPYDDGIGL	DEFVDWLNSP	TSGSGCTIQR	IADYGEWLQR	FETSLRALPD	1100
RQRHASLLPL	LHNYREPAKP	ICGSIAPTDQ	FRAAVQEAKI	GPKKDIPHLT	1150
AAIIAKYISN LRLGLL (SEQ ID NO:32)					



Fig. 6.

TNEKVWIEKL	DNPTLSVLPH	DFLRPQQEY	TKQATYSLQL	PQLDVPHDSF	
SNKYAVALSV	WAALIYRVTG	DDDIVLYIAN	NKILRFNIQP	TWSFNELYST	100
INNELNKLNS	IEANFSFDEL	AEKIQSCQDL	ERTPQLFRLA	FLENQDFKLD	
EFKHHLVDFA	LNLDTSNNAH	VLNLIYNSLL	YSNERVTIVA	DQFTQYLTA	200
LSDPNCITK	ISLITASSKD	SLPDP'TKNLG	WCDVFGCIHD	IFQDNAEAFP	
ERTCVVETPT	LNSDKSRSFT	YRDINRTSNI	VAHYLIKTGI	KRGDVVMIYS	300
SRGVDMVCV	MGVLKAGATF	SVIDPAYPPA	RQTIYLGVAK	PRGLIVIRAA	
GQLDQLVEDY	INDELEIVSR	INSIAIQENG	TIEGGKLDNG	EDVLAPYDHY	400
KDTRTGVVVG	PDSNPTLSFT	<u>SGSEGI</u> PKGV	LGRHFSLAYY	FNWMSKRFNL	<b>C</b>
TENDKFTMLS	GIAHDPIQRD	MFTPLFLGAQ	LYVPTQDDIG	TPGRLAEWMS	500
KYGCTVTHLT	PAMQQLLTAQ	ATTPFKLHH	AFFVGDILTK	RDCLRLQTLA	
ENCRIVNMYG	<u>TTETQ</u> RAVSY	FEVKSKNDDP	NFLKCLKDVM	PAGKGMNLVQ	<b>D</b> 600
LLVVNRNDRT	QICGIGEIGE	IYVRAGGLAE	GYRGLPELNK	EKFVNNWFVE	
KDHWNYLDKD	NGEPWRQFWL	GPRDRLYRTG	<u>DLGRYL</u> PNGD	CECCGRADDQ	<b>F</b> 700
VKIRGFRIEL	GEIDTHISQH	PLVRENITLV	RKNADNEPTL	<u>ITFMV</u> PRFDK	<b>H</b>
PDDLKSFQSD	VPKEVETDPI	VKGLIGYHLL	SKDIRTFLKK	RLASYAMPSL	800
IVVMDKLP LN	<u>PNGKVDKPKL</u>	QFPTPKQLNL	VAENTVSETD	DSQFTNVERE	
VRDLWLSILP	TKPASVSPDD	SFFD <u>LGGHSI</u>	LATKMIFTLK	KKLQVDLPLG	<b>J</b> 900
TIFKYPTIKA	FAAEIDRIKS	SGGSSQGEVV	ENVTANYAED	AKKLVETLPS	
SYPSREYFVE	PNSAEGKTTI	NVFVT <u>GVTGF</u>	<u>LSYILADLL</u>	GRSPKNYSFK	<b>NADP bind.</b> 1000
VFAHVRAKDE	EAAFARLQKA	GITYGTWNEK	FASNIKVVLG	DLSKSQFGLS	
DEKWMDLANT	VDIIIHNGAL	VHWVYPYAKL	RDPNVIISTIN	VMSLAAVGKP	1100
KFFDFVSS'TS	TLDTEYYFNL	SDKLVSEGKP	GILESDDL MN	SASGLTG <u>GYG</u>	
<u>QSKWAAEYII</u>	RRAGERGLRG	CIVRPGYVTG	ASANGSSNTD	DFLLRFLKGS	<b>Reduction</b> 1200
VQLGKIPDIE	NSVNMVVDH	VARVVVATSL	NPPKENELAV	AQVTGHPRIL	
FKDYLYTLHD	YGYDVEIESY	SKWKSLEAS	VIDRNEENAL	YPLLHMVLDN	1300
LPSTKAPEL	DDRNAVASLK	KDTAWTGVDW	SNGIGVTPPEE	VGIYIAFLNK	1350
VGFLPPP'HTN	DKLPLPSIEL	TQAQISLVAS	GAGARGSSAA	A (SEQ ID NO:80)	

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

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 step-wise 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 *Glomerella* 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, 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. Bacterial 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, Mg<sup>2+</sup>, 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 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 methods 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

FIG. 1 is an alignment 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 nos. 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-Aminoacidopate 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. Dhingra 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 condons 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 func-

tionally 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. Examples of proteins with conservatively modified variants are SEQ ID NO:\_\_\_\_\_.

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, New York (1993); and *Current Protocols in Molecular Biology*, Chapter 2, Ausubel, et al., Eds., Greene Publishing and Wiley-Interscience, New York (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, New York (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 (GG-GAGG) (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 attach-

ment 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 catalytic 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 prokaryotic or eukaryotic 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 prokaryotic or eukaryotic 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<sup>+</sup> 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) radioimmuno 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 comprises 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<sub>L</sub> 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 (Hitzeman, 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 rbC12 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 MgCl<sub>2</sub>, 5 mM dithiothreitol, 1-2 mM ATP, 1.75y pmoles γ<sup>32</sup>P-ATP (2.9 mCi/mmole), 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 μg of plasmid or DNA sequence is cleaved by one unit of enzyme in about 20 μl 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 pre-

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, 6 mM MgCl<sub>2</sub>, 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 µl volumes under the following standard conditions and temperatures: for example, 20 mM Tris-Cl pH 7.5, 10 mM MgCl<sub>2</sub>, 10 mM DTT, 33 µg/ml BSA, 10 mM–50 mM NaCl, and either 40 µM 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 µg/ml total DNA concentrations (5–100 nM total end concentration). Intermolecular blunt end ligations are performed at 1 µM 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 µg 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, o4 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 µg/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 µg/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×g for 15 min and 4° C. Cells (1.5 g, wet weight) were resuspended in 5 ml of lysis solution I (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  $\mu$ g/ml proteinase K) was then added, and the sample was incubated at 55° C. for 4 hrs. Then 45  $\mu$ l Rnase (500  $\mu$ 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  $\mu$ 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 CARBOXYLIC ACID REDUCTASE (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  $\mu$ l reaction in 1×PCR buffer contained 500 ng *Nocardia* DNA, 5 mM<sup>++</sup>, 500  $\mu$ M of each dNTP, 0.5  $\mu$ M of each primer, 1% DM50 (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° for 45 s, 56° 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  $\mu$ 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  $\mu$ g/ml ampicillin. Ampicillin resistant colonies were picked and used to inoculate 5 ml LB broth supplemented with 100  $\mu$ 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 asteriodes car* gene sequence. To prepare the template for Inverse PCR analysis, 1  $\mu$ g of *Nocardia asteriodes* 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 asteriodes 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 asteriodes car* gave a 4.6 Kb sequence which contained the entire *Nocardia asteriodes 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 asteriodes car* in *E. coli*, a DNA fragment containing *Nocardia asteriodes car* was generated by PCR using the primers *car*-F and *car*-R with *Nocardia asteriodes* gDNA as the template. For cloning purposes, those two primers incorporated a BamHI site at the 5' end and a 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  $\mu$ g/ml ampicillin at 37° C. Overnight broth cultures were diluted 20 fold in fresh LB medium containing 100  $\mu$ 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×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 MgCl<sub>2</sub> 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  $\mu$ mol of benzoate to benzaldehyde.min<sup>-1</sup> 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  $K_2HPO_4$  (pH 7.5) buffer containing 0.3 M NaCl, 10% (vol/vol) glycerol, 0.2 mM PMSF and 3 mM  $\beta$ -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  $K_2HPO_4$  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  $K_2HPO_4$  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  $K_2HPO_4$  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 Western 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-Codon-Plus® (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  $MgCl_2$ , 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 1,000 $\times$ g. Organic phases were removed and used to spot silica gel GF<sub>254</sub> 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 posttranslational 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* Codon-Plus® (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  $852\pm 82$  mM,  $69\pm 6.6$   $\mu\text{M}$ , and  $57\pm 3.6$   $\mu\text{M}$ , respectively. These are similar to the Km values of the natural protein. Vmax was determined to be  $0.135\pm 0.004$   $\mu\text{mol}\cdot\text{min}^{-1}\cdot\text{mg}^{-1}$  protein, which is lower than that of the natural protein at  $0.902\pm 0.04$   $\mu\text{mol}\cdot\text{min}^{-1}\cdot\text{mg}^{-1}$  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 CARBOXYLIC ACID REDUCTASE 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-CARBOXYLIC ACID REDUCTASE) to the catalytically active form of the enzyme (CARBOXYLIC ACID REDUCTASE) may occur

by posttranslational modification. One such modification that has precedence in the type of reaction catalyzed by carboxylic acid reductase would be phosphopantetheinylation (12). In this type of model, inactive pre-carboxylic acid reductase would be converted to active carboxylic acid reductase by attachment of phosphopantetheine prosthetic group possibly attached to Ser688 to function as a Swinging arm. In the active enzyme, carboxylic acid reductase, the SH of the phosphopantetheine prosthetic group would react with acyl-AMP to form an acyl-S-pantotheine-carboxylic acid reductase intermediate. The C-terminal reductase domain finishes the catalytic cycle by delivering hydride from NADPH to the acyl-S-pantotheine carboxylic acid reductase intermediate freeing an aldehyde product.  $\alpha$ -Aminoacidate reductase is well studied, and motifs responsible for adenylation of  $\alpha$ -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 carboxylic acid reductase (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* carboxylic acid reductase homologs (FIG. 1). Whether benzoate induction (23) increases the expression of carboxylic acid reductase, 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 <sup>r</sup>	Stratagene
<i>E. coli</i> BL21-CodonPlus® (DE3)-RP	having argU and proL tRNA genes	Stratagene

TABLE 1-continued

Strains and plasmids used in this study		
Strains or plasmids	Relevant properties	Reference or source
pGEM-T easy	T/A PCR cloning vector, Amp <sup>r</sup>	Promega
pHAT10	Cloning vector for addition of HAT-tag to the N-terminus, Amp <sup>r</sup>	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	
GTSGATTCACCSGATGAG	This study 11
CCSGATGARGCSCTACAG	This Study 12
TSGGCSACSGTSACGAAC	This Study 13
SACGAAYTCSCCCTGSGAC	This Study 14
GGTCGGGATCAATCTCAACTACATG	This Study 15
CTTCAGCTGCTCTGACGGATATCAG	This Study 16
CCTGCTCATCTTCTGCAAACAACTG	This Study 17
<u>CGCGGATCCG</u> CAGTGGATTACCCGG	This Study 18
ATGAGC	
CGGGGT <u>ACCC</u> CTGATATCCGTCAGA	This Study 19
GCAGCTG	
<u>Sequencing primers</u>	
TAATACGACTCACTATAGGG	Sigma-Genosys 20
CATACGATTTAGGTGACACTATAG	Sigma-Genosys 21
CAGGAAACAGCTATGACC	Sigma-Genosys 22
CTCGACTGGCCGATATCCAC	This Study 23
GAGGACGGCTTCTACAAGAC	This Study 24
GACGCGCACTTACCACCTG	This Study 25
GTCGACTGATCGTCCATCC	This Study 26
ACCTACGACGTGCTCAATC	This Study 27
CGTACGACGATGGCATCTC	This Study 28
GTGGATATCGCCAGGTGCGAG	This Study 29
GGTGGCAGGATGGAATCGG	This Study 30
CGTCGATTCGCGATTCCCTG	This Study 31

<sup>a</sup>Restriction cleavage sites are underlined; R = A or G, Y = C or T, S = G or C.

TABLE 3

Purification of recombinant HAT-CAR from <i>Nocardia</i> .					
Step Purification	Total protein (mg)	Total activity (U) <sup>1</sup>	Specific activity (U/mg)	Yield (%)	
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

<sup>1</sup>One 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.

### 15 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 amino acid 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-amino acid reductase. 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 acid 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-amino acid 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-Amino acid semialdehyde is in chemical equilibrium with 1-piperidine-6-carboxylate. It is of interest that



there is some similarity in structure between the 1-piperideine-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 piperideine-6-carboxylate (a-aminoadipate semialdehyde) into a-aminoadipate exists in *Nocardia*, *Streptomyces*, *Flavobacterium* and *Pseudomonas*, by use of 1-piperideine-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 piperideine-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-Aminoacidate 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"	$2.4 \times 10^{-213}$	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>	SCO2561	Putative fatty acid-CoA ligase	251	$3.5 \times 10^{-29}$	29	50
<i>S. coelicolor</i>	SCO4383	Putative 4-coumarate: CoA ligase	221	$6.8 \times 10^{-18}$	28	42
<i>Drosophila</i>	CG3961-PA	Hypothetical protein	211	$4 \times 10^{-53}$	31	49
<i>Mus</i>	AAH31544	Similar to fatty acid Co-A ligase	202	$2 \times 10^{-50}$	27	46
<i>T. fusca</i>	Scaf 1	Not annotated	121	$3 \times 10^{-28}$	25	41
<i>Stigmatella aurantica</i>	MxaA	<b>Non-ribosomal peptide synthetase</b> (in myxalamid biosynthesis)	39	$7 \times 10^{-5}$	26	41
<i>Schizosaccharomyces pombe</i>	P40976	□-Aminoadipate reductase	25	0.14	23	43
<i>Candida albicans</i>	AAC02241	□-Aminoadipate 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 score	% 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"	$3 \times 10^{-155}$	60	74
<i>M. leprae</i>	ML0484	Putative acyl-CoA ligase	555	$1 \times 10^{-157}$	58	74
<i>M. smegmatis</i>	3.11301	Not annotated	"1597"	$4.8 \times 10^{-164}$	62	77
<i>S. coelicolor</i>	SCO6273	Putative polyketide synthase	323	$1.6 \times 10^{-27}$	35	51
<i>S. coelicolor</i>	SCO1273	Putative reductase	248	$4.7 \times 10^{-28}$	39	52
<i>Stigmatella aurantica</i>	MxaA	<b>Non-ribosomal peptide synthetase</b> (in myxalamid biosynthesis)	148	$2 \times 10^{-34}$	33	46
<i>Schizosaccharomyces pombe</i>	P40976	□-Aminoadipate reductase	116	$9 \times 10^{-25}$	27	46
<i>Pichia farinosa</i>	CAB97252	□-Aminoadipate reductase	108	$2 \times 10^{-22}$	25	42
<i>T. fusca</i>		No Hits				

**Bold** letters indicate genes known to make a particular enzyme.

## SEQUENCE LISTING

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tatttactta ggctaacgtg ttttaacgggt tgcagggctt ttcctactta 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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gca cag ttg ttt gca gaa gat gag cag gtc aag gcc gca cgt ccg ctc      278
Ala Gln Leu Phe Ala Glu Asp Glu Gln Val Lys Ala Ala Arg Pro Leu
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gaa cgc gtg agc gcg cgc gtg agc gcg ccc ggt atg cgg ctg gcg cag      326
Glu Ala Val Ser Ala Ala Val Ser Ala Pro Gly Met Arg Leu Ala Gln
35             40             45

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

cag cgt gcg ttc gaa ctg aac acc gac gac gcg acg ggc cgc acc tcg      422
Gln Arg Ala Phe Glu Leu Asn Thr Asp Asp Ala Thr Gly Arg Thr Ser
65             70             75

ctg cgg tta ctt ccc cga ttc gag acc atc acc tat cgc gaa ctg tgg      470
Leu Arg Leu Leu Pro Arg Phe Glu Thr Ile Thr Tyr Arg Glu Leu Trp
80             85             90

cag cga gtc ggc gag gtt gcc gcg gcc tgg cat cat gat ccc gag aac      518
Gln Arg Val Gly Glu Val Ala Ala Trp His His Asp Pro Glu Asn
95             100            105            110

ccc ttg cgc gca ggt gat ttc gtc gcc ctg ctc ggc ttc acc agc atc      566
Pro Leu Arg Ala Gly Asp Phe Val Ala Leu Leu Gly Phe Thr Ser Ile
115            120            125

gac tac gcc acc ctc gac ctg gcc gat atc cac ctc ggc gcg gtt acc      614
Asp Tyr Ala Thr Leu Asp Leu Ala Asp Ile His Leu Gly Ala Val Thr
130            135            140

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Val Pro Leu Gln Ala Ser Ala Ala Val Ser Gln Leu Ile Ala Ile Leu
145            150            155

acc gag act tcg ccg cgg ctg ctc gcc tcg acc ccg gag cac ctc gat      710
Thr Glu Thr Ser Pro Arg Leu Leu Ala Ser Thr Pro Glu His Leu Asp
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gcg gcg gtc gag tgc cta ctc gcg gcc acc aca ccg gaa cga ctg gtg      758
Ala Ala Val Glu Cys Leu Leu Ala Gly Thr Thr Pro Glu Arg Leu Val
175            180            185            190

gtc ttc gac tac cac ccc gag gac gac gac cag cgt gcg gcc ttc gaa      806
Val Phe Asp Tyr His Pro Glu Asp Asp Gln Arg Ala Ala Phe Glu
195            200            205

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acc	tcc	ggc	agc	acc	gga	acg	ccg	aag	ggc	gcg	atg	tac	acc	aat	cgg	998	
Thr	Ser	Gly	Ser	Thr	Gly	Thr	Pro	Lys	Gly	Ala	Met	Tyr	Thr	Asn	Arg		
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Leu	Ala	Ala	Thr	Met	Trp	Gln	Gly	Asn	Ser	Met	Leu	Gln	Gly	Asn	Ser		
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caa	cgg	gtc	ggg	atc	aat	ctc	aac	tac	atg	ccg	atg	agc	cac	atc	gcc	1094	
Gln	Arg	Val	Gly	Ile	Asn	Leu	Asn	Tyr	Met	Pro	Met	Ser	His	Ile	Ala		
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Gly	Arg	Ile	Ser	Leu	Phe	Gly	Val	Leu	Ala	Arg	Gly	Gly	Thr	Ala	Tyr		
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gta	cgt	ccc	acc	gag	atc	ttc	ttc	gtc	ccg	cgc	gtg	tgc	gac	atg	gtc	1238	
Val	Arg	Pro	Thr	Glu	Ile	Phe	Phe	Val	Pro	Arg	Val	Cys	Asp	Met	Val		
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ttc ggg gtc gag gtg ccg gtg ggt gtc gtc gtc agc ccg gcg aac gag Phe Gly Val Glu Val Pro Val Gly Val Val Val Ser Pro Ala Asn Glu 705 710 715	2342
ctg cgc gat ctg gcg aat tac att gag gcg gaa cgc aac tcg ggc gcg Leu Arg Asp Leu Ala Asn Tyr Ile Glu Ala Glu Arg Asn Ser Gly Ala 720 725 730	2390
aag cgt ccc acc ttc acc tcg gtg cac ggc ggc ggt tcc gag atc cgc Lys Arg Pro Thr Phe Thr Ser Val His Gly Gly Gly Ser Glu Ile Arg 735 740 745 750	2438
gcc gcc gat ctg acc ctc gac aag ttc atc gat gcc cgc acc ctg gcc Ala Ala Asp Leu Thr Leu Asp Lys Phe Ile Asp Ala Arg Thr Leu Ala 755 760 765	2486
gcc gcc gac agc att ccg cac gcg ccg gtg cca gcg cag acg gtg ctg Ala Ala Asp Ser Ile Pro His Ala Pro Val Pro Ala Gln Thr Val Leu 770 775 780	2534
ctg acc ggc gcg aac ggc tac ctc gcc cgg ttc ctg tgc ctg gaa tgg Leu Thr Gly Ala Asn Gly Tyr Leu Gly Arg Phe Leu Cys Leu Glu Trp 785 790 795	2582
ctg gag cgg ctg gac aag acg ggt gcc acg ctg atc tgc gtc gtg cgc Leu Glu Arg Leu Asp Lys Thr Gly Gly Thr Leu Ile Cys Val Val Arg 800 805 810	2630
ggt agt gac gcg gcc gcg gcc cgt aaa cgg ctg gac tcg gcg ttc gac Gly Ser Asp Ala Ala Ala Ala Arg Lys Arg Leu Asp Ser Ala Phe Asp 815 820 825 830	2678
agc ggc gat ccc ggc ctg ctc gag cac tac cag caa ctg gcc gca cgg Ser Gly Asp Pro Gly Leu Leu Glu His Tyr Gln Gln Leu Ala Ala Arg 835 840 845	2726
acc ctg gaa gtc ctc gcc ggt gat atc gcc gac ccg aat ctc ggt ctg Thr Leu Glu Val Leu Ala Gly Asp Ile Gly Asp Pro Asn Leu Gly Leu 850 855 860	2774

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gac gac gcg act tgg cag cgg ttg gcc gaa acc gtc gac ctg atc gtc Asp Asp Ala Thr Trp Gln Arg Leu Ala Glu Thr Val Asp Leu Ile Val 865 870 875	2822
cat ccc gcc gcg ttg gtc aac cac gtc ctt ccc tac acc cag ctg ttc His Pro Ala Ala Leu Val Asn His Val Leu Pro Tyr Thr Gln Leu Phe 880 885 890	2870
ggc ccc aat gtc gtc ggc acc gcc gaa atc gtc cgg ttg gcg atc acg Gly Pro Asn Val Val Gly Thr Ala Glu Ile Val Arg Leu Ala Ile Thr 895 900 905 910	2918
gcg cgg cgc aag cgg gtc acc tac ctg tcg acc gtc gga gtg gcc gac Ala Arg Arg Lys Pro Val Thr Tyr Leu Ser Thr Val Gly Val Ala Asp 915 920 925	2966
cag gtc gac ccg gcg gag tat cag gag gac agc gac gtc cgc gag atg Gln Val Asp Pro Ala Glu Tyr Gln Glu Asp Ser Asp Val Arg Glu Met 930 935 940	3014
agc gcg gtg cgc gtc gtg cgc gag agt tac gcc aac ggc tac ggc aac Ser Ala Val Arg Val Val Arg Glu Ser Tyr Ala Asn Gly Tyr Gly Asn 945 950 955	3062
agc aag tgg gcg ggg gag gtc ctg ctg cgc gaa gca cac gat ctg tgt Ser Lys Trp Ala Gly Glu Val Leu Leu Arg Glu Ala His Asp Leu Cys 960 965 970	3110
ggc ttg ccg gtc gcg gtg ttc cgt tcg gac atg atc ctg gcg cac agc Gly Leu Pro Val Ala Val Phe Arg Ser Asp Met Ile Leu Ala His Ser 975 980 985 990	3158
cgg tac gcg ggt cag ctc aac gtc cag gac gtg ttc acc cgg ctg atc Arg Tyr Ala Gly Gln Leu Asn Val Gln Asp Val Phe Thr Arg Leu Ile 995 1000 1005	3206
ctc agc ctg gtc gcc acc ggc atc gcg ccg tac tcg ttc tac cga Leu Ser Leu Val Ala Thr Gly Ile Ala Pro Tyr Ser Phe Tyr Arg 1010 1015 1020	3251
acc gac gcg gac ggc aac cgg cag cgg gcc cac tac gac ggt ctg Thr Asp Ala Asp Gly Asn Arg Gln Arg Ala His Tyr Asp Gly Leu 1025 1030 1035	3296
ccc gcc gat ttc acg gcg gcg gcg atc acc gcg ctc ggc atc caa Pro Ala Asp Phe Thr Ala Ala Ala Ile Thr Ala Leu Gly Ile Gln 1040 1045 1050	3341
gcc acc gaa ggc ttc cgg acc tac gac gtg ctc aat ccg tac gac Ala Thr Glu Gly Phe Arg Thr Tyr Asp Val Leu Asn Pro Tyr Asp 1055 1060 1065	3386
gat ggc atc tcc ctc gat gaa ttc gtc gac tgg ctc gtc gaa tcc Asp Gly Ile Ser Leu Asp Glu Phe Val Asp Trp Leu Val Glu Ser 1070 1075 1080	3431
ggc cac ccg atc cag cgc atc acc gac tac agc gac tgg ttc cac Gly His Pro Ile Gln Arg Ile Thr Asp Tyr Ser Asp Trp Phe His 1085 1090 1095	3476
cgt ttc gag acg gcg atc cgc gcg ctg ccg gaa aag caa cgc cag Arg Phe Glu Thr Ala Ile Arg Ala Leu Pro Glu Lys Gln Arg Gln 1100 1105 1110	3521
gcc tcg gtg ctg ccg ttg ctg gac gcc tac cgc aac ccc tgc ccg Ala Ser Val Leu Pro Leu Leu Asp Ala Tyr Arg Asn Pro Cys Pro 1115 1120 1125	3566
gcg gtc cgc ggc gcg ata ctc ccg gcc aag gag ttc caa gcg gcg Ala Val Arg Gly Ala Ile Leu Pro Ala Lys Glu Phe Gln Ala Ala 1130 1135 1140	3611
gtg caa aca gcc aaa atc ggt ccg gaa cag gac atc ccg cat ttg Val Gln Thr Ala Lys Ile Gly Pro Glu Gln Asp Ile Pro His Leu 1145 1150 1155	3656
tcc gcg cca ctg atc gat aag tac gtc agc gat ctg gaa ctg ctt Ser Ala Pro Leu Ile Asp Lys Tyr Val Ser Asp Leu Glu Leu Leu	3701

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1160	1165	1170	
cag ctg ctc tga cgg Gln Leu Leu Arg 1175	ata tca gcc cgc cgc Ile Ser Gly Arg Arg 1180	gcg cac ctc gtc ggt Ala His Leu Val Gly 1185	3746
gcg ttc gcc gcc ttc Ala Phe Gly Ala Phe 1190	gcg ccg gag gcg aaa Ala Pro Glu Ala Lys 1195	cag gaa tac cgc cga Gln Glu Tyr Arg Arg 1200	3791
gcc acc cag gac agc Ala Thr Gln Asp Ser 1205	ggc gta gac gat gac Gly Val Asp Asp 1210	gaa gct gtt gat cag Glu Ala Val Asp Gln 1215	3836
gac ctg gcc gac cgg Asp Leu Gly Asp Arg 1220	cca cca cgg cgg gaa Pro Pro Arg Arg Glu 1225	cag gaa cag ccc gac Gln Glu Gln Pro Asp 1230	3881
gac aac gta gtc cgg Asp Asn Val Val Arg 1235	gct gta ttc cca cgt Ala Val Phe Pro Arg 1240	cca cgc gcc gat cga Pro Arg Ala Asp Arg 1245	3926
gac gaa gag cgc ggc Asp Glu Glu Arg Gly 1250	cga ggc aag cca cca Arg Gly Lys Pro Pro 1255	cca cgg ctg cga ctg Pro Arg Leu Arg Leu 1260	3971
cgc cct gtg cag tag Arg Pro Val Gln 1265	ata gac gaa cag ggg Ile Asp Glu Gln Gly 1270	aac gaa cca cac cca Asn Glu Pro His Pro 1275	4016
gtg gtg gtc cca gga Val Val Val Pro Gly 1275	gaa cgg cga gac cgc Glu Arg Arg Asp Arg 1280	gca ggc ggt gag gcc Ala Gly Gly Glu Ala 1285	4061
ggc gag ggt gac cgc Gly Glu Gly Asp Arg 1290	gag ctg ttc gcc acg Glu Leu Phe Ala Thr 1295	ccg ata cag gcc Pro Ile Gln Ala 1300	4106
gat ggt gac gcc cag Asp Gly Asp Gly Gln 1305	act cgc cag cgc gac Thr Arg Gln Arg Asp 1310	gga gcc cgc gat gag Gly Ala Arg Asp Glu 1315	4151
cag cca cag cca cac Gln Pro Gln Pro His 1320	cgg cgc cgg gtg atg Arg Arg Val Met 1325	ggt cag gtg cgc gat Gly Gln Val Arg Asp 1330	4196
ggc gcc cgc gat gga Gly Ala Ala Asp Gly 1335	ttg att gga cgg gtg Leu Ile Gly Arg Val 1340	cat atc gtc cgc gat His Ile Val Arg Asp 1345	4241
ccg att gga ctg gaa Pro Ile Gly Leu Glu 1350	gaa cgt cga ggt cca Glu Arg Arg Gly Pro 1355	gta ctg ccg gga atc Val Leu Pro Gly Ile 1360	4286
ggc ggg cag cac gat Gly Gly Gln His Asp 1365	cca ggc gag gac gat Pro Gly Glu Asp Asp 1370	gga cgc gat gaa cac Gly Arg Asp Glu His 1375	4331
cgc cac gcc ggt gca Arg His Gly Gly Ala 1380	cgc gga ccg cca ctg Arg Gly Pro Pro Leu 1385	ccg caa cgc gag gaa Pro Gln Arg Glu Glu 1390	4376
ttg cac gac gaa gta Leu His Asp Glu Val 1395	gcc agg gac gag ctt Ala Arg Asp Glu Leu 1400	gat gcc cgc cgc cac Asp Ala Arg Arg His 1405	4421
ccc gac gcc gag gcc Pro Asp Ala Glu Ala 1410	gcg cag ctt gct gcg Ala Gln Leu Ala Ala 1415	gtc ggg ccg gga gaa Val Gly Pro Gly Glu 1420	4466
gtc cca cag cac cag Val Pro Gln His Gln 1425	cag cat cag cat cag His Gln His Gln Val 1430	ggt gat ctg gcc gta Val Asp Leu Ala Val 1435	4511
gaa cag cgt tgt ccg Glu Gln Arg Cys Pro 1440	gac ggc ctc gat gaa Asp Gly Leu Asp Glu 1445	cgc gca ggt gag cgc Arg Ala Gly Glu Arg 1450	4556
cag tag gcc gct gac 1455	gac ggc cag tct gcc 1460	ggt gat ccg gta cc 1465	4600

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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: PRT  
 <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  
 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

Ala Thr Leu Asp Leu Ala Asp Ile His Leu Gly Ala Val Thr Val Pro  
 130 135 140

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

Thr Ser Pro Arg Leu Leu Ala Ser Thr Pro Glu His Leu Asp Ala Ala  
 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

Gly Ser Thr Gly Thr Pro Lys Gly Ala Met Tyr Thr Asn Arg Leu Ala  
 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  
 305 310 315 320

Ala Lys Ser Asp Met Ser Thr Leu Phe Glu Asp Ile Gly Leu Val Arg  
 325 330 335

Pro Thr Glu Ile Phe Phe Val Pro Arg Val Cys Asp Met Val Phe Gln  
 340 345 350

Arg Tyr Gln Ser Glu Leu Asp Arg Arg Ser Val Ala Gly Ala Asp Leu  
 355 360 365

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Asp Thr Leu Asp Arg Glu Val Lys Ala Asp Leu Arg Gln Asn Tyr Leu  
 370 375 380

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

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



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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 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  
 1160 1165 1170  
 Leu

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<211> LENGTH: 90  
 <212> TYPE: PRT  
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 3

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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

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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

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

<400> SEQUENCE: 5

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

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

<400> SEQUENCE: 8

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

<400> SEQUENCE: 9

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

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<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: X can be any amino acid

<400> SEQUENCE: 10

Gly Xaa Xaa Gly Xaa Leu Gly
1           5

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

<400> SEQUENCE: 11

gtsgattcac csgatgag 18

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

<400> SEQUENCE: 12

ccsgatgarc gsctacag 18

<210> SEQ ID NO 13
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Nocardia

<400> SEQUENCE: 13

tgsqcsacsg tsacgaac 18

<210> SEQ ID NO 14
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Nocardia

<400> SEQUENCE: 14

sacgaaytcs cctgsgac 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 tctgaaaca actg 24

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<210> SEQ ID NO 18  
 <211> LENGTH: 31  
 <212> TYPE: DNA  
 <213> ORGANISM: Nocardia  
 <400> SEQUENCE: 18  
 cgcggatccg cagtggattc 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  
 <400> SEQUENCE: 20  
 taatacgact 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  
 gaggacggct tetacaagac 20

<210> SEQ ID NO 25  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Nocardia  
 <400> SEQUENCE: 25  
 gacgcgact tcaccgacct g 21

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<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  
 <213> ORGANISM: Nocardia  
 <400> SEQUENCE: 28  
 cgtacgacga 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  
 cgtcgattcg 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

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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 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  
 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

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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  
                   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





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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  
 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

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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
				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				

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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

<210> SEQ ID NO 34  
 <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

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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
	385					390					395				400
Lys	His	Gly	Val	Glu	Ser	Leu	Leu	Glu	Met	His	Leu	Leu	Glu	Gly	Tyr
				405					410					415	
Gly	Ser	Thr	Glu	Ala	Gly	Met	Val	Leu	Phe	Asp	Gly	Glu	Val	Gln	Arg
			420					425					430		
Pro	Pro	Val	Ile	Asp	Tyr	Lys	Leu	Val	Asp	Val	Pro	Asp	Leu	Gly	Tyr
		435					440					445			
Phe	Ser	Thr	Asp	Gln	Pro	Tyr	Pro	Arg	Gly	Glu	Leu	Leu	Leu	Lys	Thr
	450					455					460				
Gln	Asn	Met	Phe	Pro	Gly	Tyr	Tyr	Lys	Arg	Pro	Glu	Val	Thr	Ala	Thr
	465					470					475				480
Val	Phe	Asp	Ser	Asp	Gly	Tyr	Tyr	Gln	Thr	Gly	Asp	Ile	Val	Ala	Glu
				485					490					495	
Val	Gly	Pro	Asp	Arg	Leu	Val	Tyr	Val	Asp	Arg	Arg	Asn	Asn	Val	Leu
			500					505					510		
Lys	Leu	Ala	Gln	Gly	Gln	Phe	Val	Thr	Val	Ala	Lys	Leu	Glu	Ala	Ala
		515					520						525		
Phe	Ser	Asn	Ser	Pro	Leu	Val	Arg	Gln	Ile	Tyr	Ile	Tyr	Gly	Asn	Ser
	530					535					540				
Ala	His	Pro	Tyr	Leu	Leu	Ala	Val	Val	Val	Pro	Thr	Glu	Asp	Ala	Leu
	545					550					555				560
Ala	Thr	Asn	Asp	Ile	Glu	Val	Leu	Lys	Pro	Leu	Ile	Ile	Asp	Ser	Leu
				565					570					575	
Gln	Lys	Val	Ala	Lys	Glu	Ala	Asp	Leu	Gln	Ser	Tyr	Glu	Val	Pro	Arg
			580					585					590		
Asp	Leu	Ile	Val	Glu	Thr	Thr	Pro	Phe	Ser	Leu	Glu	Asn	Gly	Leu	Leu
		595					600					605			
Thr	Gly	Ile	Arg	Lys	Leu	Ala	Trp	Pro	Lys	Leu	Lys	Gln	His	Tyr	Gly
	610					615					620				
Ala	Arg	Leu	Glu	Gln	Leu	Tyr	Ala	Asp	Leu	Val	Glu	Gly	Gln	Ala	Asn
	625					630					635				640
Ala	Leu	His	Val	Leu	Lys	Gln	Ser	Val	Ala	Asn	Ala	Pro	Val	Leu	Gln
				645					650					655	
Thr	Val	Ser	Arg	Ala	Val	Gly	Thr	Ile	Leu	Gly	Val	Ala	Thr	Thr	Asp
			660					665					670		
Leu	Pro	Ser	Asn	Ala	His	Phe	Thr	Asp	Leu	Gly	Gly	Asp	Ser	Leu	Ser
		675					680					685			

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Ala Leu Thr Phe Gly Ser Leu Leu Arg Glu Leu Phe Asp Ile Asp Val  
690 695 700

Pro Val Gly Val Ile Val Ser Pro Val Asn Asn Leu Val Ala Ile Ala  
705 710 715 720

Asp Tyr Ile Glu Arg Glu Arg Gln Gly Thr Lys Arg Pro Thr Phe Ile  
725 730 735

Ala Ile His Gly Arg Asp Ala Gly Lys Val His Ala Ser Asp Leu Thr  
740 745 750

Leu Asp Lys Phe Ile Asp Val Ser Thr Leu Thr Ala Ala Pro Val Leu  
755 760 765

Ala Gln Pro Gly Thr Glu Val Arg Thr Val Leu Leu Thr Gly Ala Thr  
770 775 780

Gly Phe Leu Gly Arg Tyr Leu Ala Leu Lys Trp Leu Glu Arg Met Asp  
785 790 795 800

Leu Val Glu Gly Lys Val Ile Ala Leu Val Arg Ala Lys Ser Asn Glu  
805 810 815

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

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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

&lt;400&gt; SEQUENCE: 35

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

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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	
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



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705	710	715	720
Glu Gly Glu Leu Arg 725	Gly Ser Lys Arg 730	Pro Thr Tyr Ala Ser Val His 735	
Gly Arg Asp Ala Thr 740	Glu Val Arg Ala Arg 745	Asp Leu Ala Leu Gly Lys 750	
Phe Ile Asp Ala Lys Thr 755	Leu Ser Ala Ala Pro 760	Gly Leu Pro Arg Ser 765	
Gly Thr Glu Ile Arg Thr 770	Val Leu Leu Thr Gly 775	Ala Thr Gly Phe Leu 780	
Gly Arg Tyr Leu Ala Leu 785	Glu Trp Leu Glu Arg 790	Met Asp Leu Val Asp 795	800
Gly Lys Val Ile Cys 805	Leu Val Arg Ala Arg 810	Ser Asp Asp Glu Ala Arg 815	
Ala Arg Leu Asp Ala Thr 820	Phe Asp Thr Gly Asp 825	Ala Thr Leu Leu Glu 830	
His Tyr Arg Ala Leu Ala 835	Ala Asp His Leu Glu Val 840	Ile Ala Gly Asp 845	
Lys Gly Glu Ala Asp Leu 850	Gly Leu Asp His Asp 855	Thr Trp Gln Arg Leu 860	
Ala Asp Thr Val Asp Leu 865	Ile Val Asp Pro Ala 870	Ala Leu Val Asn His 875	880
Val Leu Pro Tyr Ser Gln 885	Met Phe Gly Pro Asn 890	Ala Leu Gly Thr Ala 895	
Glu Leu Ile Arg Ile Ala 900	Leu Thr Thr Thr Ile 905	Lys Pro Tyr Val Tyr 910	
Val Ser Thr Ile Gly Val 915	Gly Gln Gly Ile Ser 920	Pro Glu Ala Phe Val 925	
Glu Asp Ala Asp Ile Arg 930	Glu Ile Ser Ala Thr 935	Arg Arg Val Asp Asp 940	
Ser Tyr Ala Asn Gly Tyr 945	Gly Asn Ser Lys Trp 950	Ala Gly Glu Val Leu 955	960
Leu Arg Glu Ala His Asp 965	Trp Cys Gly Leu Pro 970	Val Ser Val Phe Arg 975	
Cys Asp Met Ile Leu Ala 980	Asp Thr Thr Tyr Ser 985	Gly Gln Leu Asn Leu 990	
Pro Asp Met Phe Thr Arg 995	Leu Met Leu Ser Leu 1000	Val Ala Thr Gly Ile 1005	
Ala Pro Gly Ser Phe Tyr 1010	Glu Leu Asp Ala Asp 1015	Gly Asn Arg Gln 1020	
Arg Ala His Tyr Asp Gly 1025	Leu Pro Val Glu Phe 1030	Ile Ala Glu Ala 1035	
Ile Ser Thr Ile Gly Ser 1040	Gln Val Thr Asp Gly 1045	Phe Glu Thr Phe 1050	
His Val Met Asn Pro Tyr 1055	Asp Asp Gly Ile Gly 1060	Leu Asp Glu Tyr 1065	
Val Asp Trp Leu Ile Glu 1070	Ala Gly Tyr Pro Val 1075	His Arg Val Asp 1080	
Asp Tyr Ala Thr Trp Leu 1085	Ser Arg Phe Glu Thr 1090	Ala Leu Arg Ala 1095	
Leu Pro Glu Arg Gln Arg 1100	Gln Ala Ser Leu Leu 1105	Pro Leu Leu His 1110	
Asn Tyr Gln Gln Pro Ser 1115	Pro Pro Val Cys Gly 1120	Ala Met Ala Pro 1125	

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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

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Ala Pro Glu Ala Val Ser Ala Val Pro Gly Met Leu Pro Gln Ile Ile  
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Val Met Gly Tyr Ala Asp Arg Pro Ala Leu Gly Gln Arg Ala Phe Thr  
 35 40 45

Asp Thr Gly Arg Leu Leu Gly Phe Ser Val Asp Tyr Thr Ile Asp Leu  
 50 55 60

Ala Leu Ile Leu Gly Ala Val Thr Val Pro Leu Gln Thr Ser Ala Val  
 65 70 75 80

Ser Leu Ile Val Thr Glu Thr Glu Pro Leu Ile Ala Ser Ser Ile Glu  
 85 90 95

Leu Asp Ala Val Glu Val Leu Ala Pro Arg Leu Val Val Phe Asp Tyr  
 100 105 110

His Val Asp Arg Glu Ala Glu Ala Arg Ala Arg Leu Ala Ser Val Val  
 115 120 125

Glu Thr Leu Glu Val Ile Arg Gly Arg Leu Pro Ala Val Asp Asp Leu  
 130 135 140

Ala Leu Leu Ile Tyr Thr Ser Gly Ser Thr Gly Pro Lys Gly Ala Met  
 145 150 155 160

Tyr Ser Thr Trp Ser Ile Thr Leu Asn Phe Met Pro Met Ser His Val  
 165 170 175

Gly Arg Val Leu Phe Gly Thr Leu Gly Gly Thr Ala Tyr Phe Ala Lys  
 180 185 190

Ser Asp Leu Ser Thr Leu Glu Asp Leu Gly Leu Val Arg Pro Thr Glu  
 195 200 205

Leu Phe Val Pro Arg Ile Trp Asp Met Val Phe Glu Tyr Ser Leu Asp  
 210 215 220

Arg Arg Gly Ala Asp Leu Asp Ala Val Glu Leu Arg Asn Val Leu Gly  
 225 230 235 240

Gly Arg Phe Leu Ala Val Thr Gly Ser Ala Pro Leu Ser Ala Glu Met  
 245 250 255

Phe Val Glu Ser Leu Asp Leu His Leu Val Glu Gly Tyr Gly Ser Thr  
 260 265 270

Glu Ala Gly Val Leu Asp Gly Ile Arg Pro Val Ile Asp Tyr Lys Leu  
 275 280 285

Val Asp Val Pro Glu Leu Gly Tyr Phe Thr Asp Pro Tyr Pro Arg Gly  
 290 295 300

Glu Leu Leu Leu Lys Thr Met Phe Pro Gly Tyr Tyr Arg Pro Glu Val  
 305 310 315 320

Thr Ala Glu Ile Phe Asp Asp Gly Phe Tyr Lys Thr Gly Asp Ile Val

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325					330					335					
Ala	Leu	Gly	Pro	Asp	Val	Tyr	Val	Asp	Arg	Arg	Asn	Asn	Val	Leu	Lys
			340					345					350		
Leu	Ser	Gln	Gly	Glu	Phe	Val	Val	Lys	Leu	Glu	Ala	Val	Phe	Ala	Ser
		355					360					365			
Pro	Leu	Val	Arg	Gln	Ile	Phe	Ile	Tyr	Gly	Asn	Ser	Ala	Arg	Tyr	Leu
	370					375					380				
Ala	Val	Val	Val	Pro	Thr	Asp	Ala	Leu	Glu	Leu	Lys	Ile	Glu	Ser	Leu
	385					390					395				400
Gln	Ile	Ala	Lys	Ala	Leu	Gln	Ser	Tyr	Glu	Ile	Pro	Arg	Asp	Phe	Leu
				405					410					415	
Ile	Glu	Thr	Thr	Pro	Phe	Thr	Leu	Glu	Asn	Gly	Leu	Leu	Thr	Gly	Ile
			420					425					430		
Arg	Lys	Leu	Ala	Arg	Pro	Leu	Lys	Tyr	Gly	Arg	Leu	Glu	Leu	Tyr	Thr
		435					440					445			
Asp	Leu	Ala	Asp	Gln	Asn	Glu	Leu	Arg	Leu	Arg	Ala	Asp	Pro	Val	Leu
	450					455					460				
Thr	Val	Arg	Ala	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	Glu
				485					490					495	
Ile	Phe	Val	Asp	Val	Pro	Val	Gly	Val	Ile	Val	Ser	Pro	Ala	Glu	Leu
			500					505					510		
Ala	Leu	Ala	Ile	Glu	Ala	Arg	Gly	Lys	Arg	Pro	Thr	Phe	Ser	Val	His
		515					520					525			
Gly	Arg	Ala	Ser	Glu	Val	Arg	Ala	Asp	Leu	Thr	Leu	Asp	Lys	Phe	Ile
	530					535					540				
Asp	Ala	Thr	Leu	Ala	Ala	Pro	Leu	Pro	Val	Arg	Thr	Val	Leu	Leu	Thr
	545					550					555				560
Gly	Ala	Thr	Gly	Phe	Leu	Gly	Arg	Tyr	Leu	Ala	Leu	Glu	Trp	Leu	Glu
				565					570					575	
Arg	Met	Asp	Leu	Val	Gly	Lys	Leu	Ile	Cys	Leu	Val	Arg	Ala	Arg	Ser
			580				585						590		
Glu	Glu	Ala	Ala	Arg	Leu	Asp	Thr	Phe	Asp	Ser	Gly	Asp	Pro	Leu	Leu
		595					600					605			
His	Tyr	Leu	Ala	Ala	Arg	Leu	Glu	Val	Leu	Ala	Gly	Asp	Lys	Gly	Glu
	610					615					620				
Asp	Leu	Gly	Leu	Asp	Arg	Thr	Trp	Gln	Arg	Leu	Ala	Asp	Thr	Val	Asp
	625					630					635				640
Leu	Ile	Val	Asp	Pro	Ala	Ala	Leu	Val	Asn	His	Val	Leu	Pro	Tyr	Ser
				645					650					655	
Gln	Leu	Phe	Gly	Pro	Asn	Gly	Thr	Ala	Glu	Leu	Val	Arg	Leu	Ala	Leu
			660					665					670		
Thr	Arg	Lys	Pro	Tyr	Ile	Tyr	Ser	Thr	Ile	Gly	Val	Gly	Gln	Ile	Pro
		675					680					685			
Phe	Glu	Asp	Asp	Ile	Arg	Ile	Ser	Thr	Arg	Val	Glu	Ser	Tyr	Ala	Asn
	690					695					700				
Gly	Tyr	Gly	Asn	Ser	Lys	Trp	Ala	Gly	Glu	Val	Leu	Leu	Arg	Glu	Ala
	705					710					715				720
His	Asp	Cys	Gly	Leu	Pro	Val	Thr	Val	Phe	Arg	Cys	Asp	Met	Ile	Leu
				725					730					735	
Ala	Asp	Thr	Ser	Tyr	Gly	Gln	Leu	Asn	Val	Pro	Asp	Met	Phe	Thr	Arg
			740				745						750		

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Leu Met Leu Ser Leu Ala Thr Gly Ile Ala Pro Gly Ser Phe Tyr Glu  
 755 760 765

Leu Asp Ala Gly Asn Arg Gln Arg Ala His Tyr Asp Gly Leu Pro Val  
 770 775 780

Glu Phe Val Ala Glu Ala Ile Thr Leu Gly Asp Phe Thr Tyr Val Leu  
 785 790 795 800

Asn Pro Asp Asp Gly Ile Leu Asp Glu Phe Val Asp Trp Leu Ile Arg  
 805 810 815

Ile Asp Tyr Trp Arg Phe Glu Ile Arg Ala Leu Pro Glu Lys Gln Arg  
 820 825 830

Ser Val Leu Pro Leu Leu Tyr Pro Val Gly Ile Pro Phe Ala Val Gln  
 835 840 845

Ala Ile Gly Glu Asp Ile Pro His Leu Ser Leu Ile Lys Tyr Val Ser  
 850 855 860

Leu Leu Leu Leu Leu  
 865

<210> SEQ ID NO 37  
 <211> LENGTH: 4600  
 <212> TYPE: DNA  
 <213> ORGANISM: Nocardia

<400> SEQUENCE: 37

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tatttactta ggctaacgtg ttttacgggt tgcagggctt ttctactta tgacaaggga 180

ggcttgccat ggcgggtgat tcaccggatg agcggctaca gcgccgatt gcgcagtgt 240

ttgcagaaga tgagcaggtc aaggccgcac gtccgctcga agcggtgagc gcggcgggtga 300

gcgcgcccg tatgcccgtg gcgcagatcg ccgccactgt tatggcgggt tacgccgacc 360

gcccggccc cgggcagcgt gcgttcgaac tgaacaccga cgacgcgacg ggcgcacct 420

cgctgcgggt acttccccga ttcgagacca tcacctatcg cgaactgtgg cagcagatcg 480

gcgaggttg cgcggcctgg catcatgatc ccgagaacct cttgcgcgca ggtgatttcg 540

tcgccctgct cggttcacc agcatogact aogccaccct cgacctggcc gatatccacc 600

tcggcgcgggt taccgtgccg ttgcaggcca gcgcggcgggt gtcccagctg atcgctatcc 660

tcaccgagac ttgcgccgcg ctgctgcgct cgaccccgga gcacctgat gcggcggctg 720

agtgcctact cgcgggcacc acaccggaac gactggtggt cttcgactac caccgccagg 780

acgacgacca gcgtgcggcc ttcgaatccg cccgcgcgg ccttgccgac gcgggcagct 840

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cactgttcgt tcccgaacac gacgaogacc cgctggccct gctgatctac acctccggca 960

gcaccggaac gccgaagggc gcgatgtaca ccaatcgggt gcccgccacg atgtggcagg 1020

ggaactcgat gctgcagggg aactcgaac gggtcgggat caatctcaac tacatgccga 1080

tgagccacat cgcggctcgc atatcgtgt toggcgtgct cgctcgcgggt ggcaccgat 1140

acttcgcggc caagagcgac atgtcgacac tgttcgaaga catcggcttg gtacgtccca 1200

ccgagatctt cttcgtcccc gcgctgtgcg acatggcttt ccagcgtat cagagcgagc 1260

tggaccggcg ctccggtggcg ggcgcgacc tggacacgct cgatcgggaa gtgaaagccg 1320

acctccggca gaactaccte ggtgggcgct tcctggtggc ggtcgtcggc agcgcgccgc 1380

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tgctcgatta caagctcgtc gacgtgcccg aactgggtta cttccgcacc gaccggccgc	1560
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ccgaggtcac cgcggagatc ttcgacgagg acggcttcta caagaccggc gatatcgttg	1680
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cgagggcga gttcgtgacc gtcgcccacg tcgagccctg gttcggcagg agcccgtga	1800
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cgacaggcca gccgatgag ctgctcggcc tgcgcccga agccggcagg ctgcccgtgc	2160
tcgaaaccgt cagccgggca gcgaaagcga tgctcggcgt cgcctccgcc gatatcgtc	2220
ccgacgcga ctccaccgac ctggcgggcg attcccttcc cgcgctgtcg ttctcgaacc	2280
tgctgcacga gatcttcggg gtcgaggtgc cggtggtgtg cgtcgtcagg ccggcgaacg	2340
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ccttcacctc ggtgcacggc gccggttccg agatccgcgc cgcgatctg acctcgaca	2460
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ccgatttcac gccggcggcg atcacccgcg tcggcatcca agccaccgaa ggettcggga	3360
cctacgacgt gctcaatccg tacgaogatg goatctccct cgatgaattc gtcgactggc	3420
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tattcccacg tccacgcgcc gatcgagacg aagagcgcg cagaggcaag ccaccaccac 3960
ggctgcgact gcgccctgtg cagtagatag acgaacaggg gaacgaacca caccagtggt 4020
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acgacgaagt agccaggac gagcttgatg cccgccgcca ccccgacgc gaggccgcgc 4440
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<210> SEQ ID NO 38
<211> LENGTH: 4600
<212> TYPE: DNA
<213> ORGANISM: Nocardia

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<400> SEQUENCE: 38

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tatttactta ggtaacgtg ttttacgggt tgcaggcctt ttcctactta tgacaaggga 180
ggcttgccat ggcatggat agtccggatg agcggctaca gcgccgatt gcacagttgt 240
ttgcagaaga tgagcaggtc aagggccgac gtccgctcga agcggtgagc gcggcgggtg 300
gcgcgcccgg tatgcggctg gcgcagatcg ccgccactgt tatggcgggt tacgccgacc 360
gcccggcccg cgggcagcgt gcgttcgaac tgaacaccga cgacgcgacg ggcgcacact 420
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gcgaggttgc cgcggcctgg catcatgatc ccgagaaccc cttgcgcgca ggtgatttcg 540
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tcaccgagac ttccgcgcgg ctgctgcctc cgaccccgga gcacctcgat gcggcggctg 720
agtgcctact cgcgggcacc acaccggaac gactgggtgg cttcgactac caccocgagg 780
acgacgacca gcgtgcggcc ttcgaatccg cccgccgccc ccttgccgac gcgggcagct 840
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cactgttcgt tcccgcaccc gacgacgacc cgctggccct gctgatctac acctccggca 960
gcaccggaac gccgaagggc gcgatgtaca ccaatcggtt gcccgccacg atgtggcagg 1020
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tgagccacat cgcggctcgc atatcgctgt tcggcgtgct cgctcgcggg ggcaccgcat 1140
acttcggcgc caagagcgac atgtcgacac tgttcgaaga catcggttg gtaogtcca 1200
ccgagatcct cttcgtcccg cgcgtgtgct acatggtcct ccagcgctat cagagcgagc 1260

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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
Ala Thr Leu Asp Leu Ala Asp Ile His Leu Gly Ala Val Thr Val Pro
130         135        140
Leu Gln Ala Ser Ala Ala Val Ser Gln Leu Ile Ala Ile Leu Thr Glu
145         150        155        160
Thr Ser Pro Arg Leu Leu Ala Ser Thr Pro Glu His Leu Asp Ala Ala
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

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

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 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  
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 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  
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 740 745 750  
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 Asp Ser Ile Pro His Ala Pro Val Pro Ala Gln Thr Val Leu Leu Thr  
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 Gly Ala Asn Gly Tyr Leu Gly Arg Phe Leu Cys Leu Glu Trp Leu Glu  
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 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  
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 Asp Pro Ala Glu Tyr Gln Glu Asp Ser Asp Val Arg Glu Met Ser Ala  
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 Val Arg Val Val Arg Glu Ser Tyr Ala Asn Gly Tyr Gly Asn Ser Lys  
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 Trp Ala Gly Glu Val Leu Leu Arg Glu Ala His Asp Leu Cys Gly Leu  
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 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

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Asp	Phe	Thr	Ala	Ala	Ala	Ile	Thr	Ala	Leu	Gly	Ile	Gln	Ala	Thr
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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			

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Leu

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What is claimed is:

1. An isolated polynucleotide encoding a carboxylic acid reductase, said polynucleotide selected from the group consisting of:

- (a) a polynucleotide having at least 95% nucleotide sequence identity to SEQ ID NO:1 encoding a polypeptide having carboxylic acid reductase activity;
- (b) a polynucleotide comprising SEQ ID NO:1 encoding a polypeptide having carboxylic acid reductase activity; and
- (c) a polynucleotide which is complementary to the full length of the polynucleotide of (a) or (b).

2. A recombinant expression cassette comprising a polynucleotide selected from the group consisting of:

- (a) a polynucleotide having at least 95% nucleotide sequence identity to SEQ ID NO:1 encoding a polypeptide having carboxylic acid reductase activity;
- (b) a polynucleotide comprising SEQ ID NO:1 encoding a polypeptide having carboxylic acid reductase activity; and
- (c) a polynucleotide which is complementary to the full length of the polynucleotide of (a) or (b).

3. A vector comprising a recombinant expression cassette comprising a polynucleotide selected from the group consisting of:

- (a) a polynucleotide having at least 95% nucleotide sequence identity to SEQ ID NO:1 encoding a polypeptide having carboxylic acid reductase activity;
- (b) a polynucleotide comprising SEQ ID NO:1 encoding a polypeptide having carboxylic acid reductase activity; and
- (c) a polynucleotide which is complementary to the full length of the polynucleotide of (a) or (b).

4. An isolated host cell transformed with a recombinant expression cassette which comprises a polynucleotide selected from the group consisting of:

- (a) a polynucleotide having at least 95% nucleotide sequence identity to SEQ ID NO:1 encoding a polypeptide having carboxylic acid reductase activity;

(b) a polynucleotide comprising SEQ ID NO:1 encoding a polypeptide having carboxylic acid reductase activity; and

(c) a polynucleotide which is complementary to the full length of the polynucleotide of (a) or (b).

5. The host cell of claim 4 wherein the cell is a bacterial cell.

6. The host cell of claim 5 wherein the cell is an *E. Coli* cell.

7. An isolated bacterial cell transformed with a polynucleotide selected from the group consisting of:

- (a) a polynucleotide having at least 95% nucleotide sequence identity to SEQ ID NO:1 encoding a polypeptide having carboxylic acid reductase activity;
- (b) a polynucleotide comprising SEQ ID NO:1 encoding a polypeptide having carboxylic acid reductase activity; and
- (c) a polynucleotide which is complementary to the full length of the polynucleotide of (a) or (b).

8. A method of making a carboxylic acid reductase enzyme comprising the steps of:

- a) expressing a polynucleotide in a bacterial host cell transformed with said polynucleotide, wherein the polynucleotide is selected from the group consisting of:
  - i) a polynucleotide having at least 95% nucleotide sequence identity to SEQ ID NO:1 encoding a polypeptide having carboxylic acid reductase activity; and
  - ii) a polynucleotide comprising SEQ ID NO:1 encoding a polypeptide having carboxylic acid reductase activity;
- b) culturing said bacterial cell under cell growth conditions; so that carboxylic acid reductase is produced and
- c) harvesting said carboxylic acid reductase.

\* \* \* \* \*