>CYP51B1 Mycobacterium tuberculosis (Actinobacteria) Rv0764c

MSAVALPRVSGGHDEHGHLEEFRTDPIGLMQRVRDECGDVGTFQ

LAGKQVVLLSGSHANEFFFRAGDDDLDQAKAYPFMTPIFGEGVVFDASPERRKEMLHN

AALRGEQMKGHAATIEDQVRRMIADWGEAGEIDLLDFFAELTIYTSSACLIGKKFRDQ

LDGRFAKLYHELERGTDPLAYVDPYLPIESFRRRDEARNGLVALVADIMNGRIANPPT

DKSDRDMLDVLIAVKAETGTPRFSADEITGMFISMMFAGHHTSSGTASWTLIELMRHR

DAYAAVIDELDELYGDGRSVSFHALRQIPQLENVLKETLRLHPPLIILMRVAKGEFEV

QGHRIHEGDLVAASPAISNRIPEDFPDPHDFVPARYEQPRQEDLLNRWTWIPFGAGRH

RCVGAAFAIMQIKAIFSVLLREYEFEMAQPPESYRNDHSKMVVQLAQPACVRYRRRTG

V

>CYP51B1 Mycobacterium marinum MM4932

MTTAIVPRVS GGEEEHGHLE EFRTDPIGLM QRVRDECGDV GWFQLANKHV VLLSGAKANE

FFFRSSDEEL DQAEAYPFMT PIFGKGVVFD ASPERRKEML HNSALRGEHM KGHATTIERE

VHRMIENWGQ EGEIDLLEFF AELTIYTSTS CLIGTKFRNQ LDSRFAHFYH ELERGTDPLC

YVDPYLPIES FRRRDEARKG LVALVQDIMH QRVANPPTDK RDRDMLDVLV SITDEQGNPR

FCADEVTGMF ISLMFAGHHT SSGTSAWTLI ELLRHPDAYA AVIDELDELY ADGQPVSFHA

LRQIPRLENV LKETLRLHPP LIILMRVAKG EFQVEGYPIH EGELVAASPA ISNRIAEDFP

DPDEFVPERY QEPRQEDLIN RWTWIPFGAG RHRCVGAAFA TMQIKAIFSV LLREYEFEMA

QPADSYRNDH SKMVVQLARP ARVRYRRRKM SDNRGH\*

>CYP51B1 Mycobacterium ulcerans

MTTAIVPRVSGGEEEHGHLEEFRTDPIGLMQRVRDECGDVGWFQLANKHVVLLSGAKANE

FFFRSSDEELDQAEAYPFMTPIFGKGVVFDASPERRKEMLHNSALRGEHMKGHATTIERE

VHRMIENWGQEGEIDLLEFFAELTSYTSTSCLIGTKFRNQLDSRFAHFCHELERGTDPLC

YVDPYLPIESFRRRDEARKGLVALVQDIMHQRVANPPTDKRDRDMLDVLVSITDEQGNPR

FCTDEVTGMFISLMFAGHHTSSGTSAWTLIELLRHPDAYAAVIDELDELYADGQLVSFHA

LRQIPRLENVLKETLRLHPPLIILMRVAKGEFQVEGYPIHEGELVAASPAISNRIAEDFP

DPDEFVPERYQEPRQEDLINRWTWIPFGAGRHRCVGAAFATMQIKAIFSVLLREYEFEMA

QPADSYRNDHSKMVVQLARPARVRYRRRKLSDNRGH

>CYP51B1 Mycobacterium bovis subsp. bovis AF2122/97 (Actinobacteria)

MSAVALPRVSGGHDEHGHLEEFRTDPIGLMQRVRDECGDVGTFQ

LAGKQVVLLSGSHANEFFFRAGDDDLDQAKAYPFMTPIFGEGVVFDASPERRKEMLHN

AALRGEQMKGHAATIEDQVRRMIADWGEAGEIDLLDFFAELTIYTSSACLIGKKFRDQ

LDGRFAKLYHELERGTDPLAYVDPYLPIESFRRRDEARNGLVALVADIMNGRIANPPT

DKSDRDMLDVLIAVKAETGTPRFSADEITGMFISMMFAGHHTSSGTASWTLIELMRHR

DAYAAVIDELDELYGDGRSVSFHALRQIPQLENVLKETLRLHPPLIILMRVAKGEFEV

QGHRIHEGDLVAASPAISNRIPEDFPDPHDFVPARYEQPRQEDLLNRWTWIPFGAGRH

RCVGAAFAIMQIKAIFSVLLREYEFEMAQPPESYRNDHSKMVVQLAQPACVRYRRRTG

V

>CYP51B1 Mycobacterium avium (Actinobacteria)

000 TSTVVPRVSGGEEEHGHLEEFRTDPIGLMQRVRDECGDVGWFQLVDKHVILLSGAQANEF 3021539

3021540 FFRSADEDLDQAEAYPFMTPIFGKGVVFDASPERRKEMLHNSALRGEQMKGHASTIEGEV 3021719

3021720 KKMIADWGDEGEIELLDFFAELTIYTSTACLIGLKFREQLDHRFAEYYHDLERGTDPLCY 3021899

3021900 VDPYLPIESFKRRDEARVKLVALVQEIMDQRLANPPKDKADRDMLDVLVSIKDEDGKPRF 3022079

3022080 SADEITGMFISLMFAGHHTSSGTSAWTLIELIRHPDVYAEVLAELEELYADGQEVSFHAL 3022259

3022260 RSIPKLDNVVKETLRLHPPLIILMRVAKGEFEVEGFPIHEGDYVAASPAISNRIPEDFPD 3022439

3022440 PDAFKPDRYNKPEQADIVNRWTWIPFGAGRHRCVGAAFAQMQIKAIFSVLLREYDFEMAQ 3022619

3022620 PADSYRNDHSKMVVQLARPAKVRYRKR 3022700

>CYP51B1 Mycobacterium smegmatis (Actinobacteria)

000 VPRVSGGEEEHGHLEEFRTDPIGLMKRVRSECGDVGWFQLADKQVVLLSGAEANEFFFRS 4858988

4858989 SDSELNQAEAYPFMTPIFGEGVVFDADPERRAEMLHNTALRGEQMKGHAATIENEVRRMV 4859168

4859169 ESWGDEGEIDLLEFFAELTIYTSTACLIGVKFRNQLDKRFADYYHLLERGTDPLCYVDPY 4859348

4859349 LPIESFRIRDEARANLVELVQEVMNGRIANPPKDKSDRDLLDVLVSIKDEDGTPRFSANE 4859528

4859529 VTGMFISLMFAGHHTSSGTASWTLIELLRHPEFYAKVQAELDDLYADGQEISFHALRQIP 4859708

4859709 NLDNALKETLRLHPPLIILMRVAQDEFEVAGRPIHKGQMVAASPAISNRIPEDFPDPDTF 4859888

4859889 DPDRYDKPRQEDLINRWTWIPFGAGKHRCVGAAFAQMQIKAIFSVLLRDFEFEMAQPSES 4860068

4860069 YRNDHSKMVVQLARPAKVRYRRR 4860137

>CYP51B1 Methylococcus capsulatus (Proteobacteria)

908332 MSHPPSNTP 000

908305 PVKPGGLPLLGHILEFGKNPHAFLMALRHEFGDVAEFRMFHQRMVLLTGSQASEAFYRAP 908126

908125 DEVLDQGPAYRIMTPIFGRGVVFDARIERKNQQLQMLMPALRDKPMRTYSEIIVAEVEAM 907946

907945 LRDWKDAGTIDLLELTKELTIYTSSHCLLGAEFRHELNTEFAGIYRDLEMGIQPIAYVFP 907766

907765 NLPLPVFKRRDQARVRLQELVTQIMERRARSQERSTNVFQMLIDASYDDGSKLTPH 907598

907597 EITGMLIATIFAGHHTSSGTTAWVLIELLRRPEYLRRVRAEIDALFETHGRVTFESLRQM 907418

907417 PQLENVIKEVLRLHPPLILLMRKVMKDFEVQGMRIEAGKFVCAAPSVTHRIPELFPNPEL 907238

907237 FDPDRYTPERAEDKDLYGWQAFGGGRHKCSGNAFAMFQIKAIVCVLLRNYEFELAAAPE 907061

907060 SYRDDYRKMVVEPASPCLIRYRRRDAP 906980

>CYP51B1 Rhodococcus sp. RHA1 (Actinobacteria) Rha05830

MNLATPQRVSGGEHEHGHLEELRTDPIALMRRVREECGNVGVFQLADKKVVLLSGAEANEFFFRSTDEDLDQQAAYPFMKPIFGEGVVFDASPERRKEMLHNQALRGEQMKGHAATIAHEVDRMVAQWGDEGEIDLLEFFAELTIYTSSACLIGKKFREQLDGRFAHLYHELEQGTDPIAYVDAYAPIESFRRRDEARVQLVALVQEIMNGRIENPPQGKEDRDMLDVLVSIKDEDGNERFTADEITGMFISMMFAGHHTTSGTAAWTLIELLRHPDYAKQVVAELDDLYSDGSDISFGALRQIPKLEAVLKETLRLHPPLIILLRVARGEFEVGGYRIAENDLVAATPAISNRIAEDFPNPDTFDPERYIDPNQEDIVNRWTWIPFGAGRHRCVGAAFALMQLKAIFSILLQDWEFEMAQPSETYRNDHSKMVVQLQQPCTVRYRKRST

>CYP51B1 Nocardia farcinica IFM 10152 (Actinobacteria)

MTLVKPRRVSGGEHEHGHLEEFRTDPIALMRRVRQECGDVGAFE

LAGKQVILLSGAEANEFFFRSGDEDLDQGAAYPFMKPIFGEGVVFDASPERRKEMLHN

SALRAEQMRGHATTIAAEVDRMIAGWDDEGEIDLLDFFAELTIYTSSACLIGVKFRNE

LDDRFARLYHELERGTDALAYVDPYAPIESFRRRDEARAALVALVQAIMDERAANPPA

DKSDRDLLDVLVSVPNEDGGPRFSASEITGIFISMMFAGHHTTSGTAAWTVIELLRHP

ELRDRVVAELDELFADGKDVSFHALRQIPLLEATLKETLRMHPPLIILMRVAQGDFEV

CGHHIAAGDHVAATPAISNRLPEDFPDPDTFDPGRYIDPNQEDLVNRWTWIPFGAGRH

RCVGAAFALMQLKAIFSILLRDWEFEMAQPSESYRNDHSKMVVQLQQPCRVRYRRRVR

TS

>CYP51B1 Mycobacterium vanbaalenii

MTAVKEVPRVSGGEEEHGHLEEFRTDPIGLMKRVREECGDVGWFQLADKQVILLSGAEANEFFFRSSDSE LNQAEAYPFMTPIFGEGVVFDADPERRAEMLHNTALRGEHMKGHATTIEAEVRKMIEGWGESGEIDLLEF FAELTIYTSTACLIGLKFRNQLDSRFANYYHLLERGTDPLCYVDPYLPIESFRIRDEARAGLVELVQDVM HGRIANPPKDKSDRDMLDVLVSIKDEDGNPRFTANEITGMFISLMFAGHHTSSGTSSWTLIELLRHPEFY AKVQQELDDLYADGQEVSFHALRQIPSLDNALKETLRLHPPLIILMRVAQDEFEVAGYPIHKGQMVAASP AISNRIPEDFPNPDDFDPDRYEKPRQEDLINRWTWIPFGAGKHRCVGAAFAQMQIKAIFSVLLREYEFEM AQPPESYQNDHSKMVVQLARPAKVRYRRRVRD

>CYP101A1 Pseudomonas putida

MTTETIQSNANLAPLPPHVPEHLVFDFDMYNPSNLSAGVQEAWA

VLQESNVPDLVWTRCNGGHWIATRGQLIREAYEDYRHFSSECPFIPREAGEAYDFIPT

SMDPPEQRQFRALANQVVGMPVVDKLENRIQELACSLIESLRPQGQCNFTEDYAEPFP

IRIFMLLAGLPEEDIPHLKYLTDQMTRPDGSMTFAEAKEALYDYLIPIIEQRRQKPGT

DAISIVANGQVNGRPITSDEAKRMCGLLLVGGLDTVVNFLSFSMEFLAKSPEHRQELI

ERPERIPAACEELLRRFSLVADGRILTSDYEFHGVQLKKGDQILLPQMLSGLDERENA

CPMHVDFSRQKVSHTTFGHGSHLCLGQHLARREIIVTLKEWLTRIPDFSIAPGAQIQH

KSGIVSGVQALPLVWDPATTKAV

>CYP101B1 Novosphingobium aromaticivorans

MLPHDRGQNSTRRITAMEAPAHVPADRVVDIDIYMPPGLAEHGF

HKAWSDLSAGNPAVVWTPRNEGHWIALGGEALQEVQSDPERFSSRIIVLPKSVGEMHG

LIPTTIDPPEHRPYRQLLNAHLNPGAIRGLSESIRQTAVDLIEGFAAQGHCNFTAQYA

EQFPIRVFMALVGIEASEAPRIRHWAECMTRPGMDMTFDEAKAVFFDYVGPLVDARRE

TPGEDMISAMINADLGDGRRLTRDEALSVVTQVLIAGLDTVVNVLGFIMRELAGNPAL

RADLRQRGADILPVVHELFRRFGLVSIAREVRRDIEFHGVHLKAGDMIAIPTQVHGLD

PRVNPDPLAIDPSRKRARHSTFGSGPHMCPGQELARKEVAITLEEWLRRIPDFALGPN

SDLSPVPGIVGALRRVELVWNT

>CYP101C1 Novosphingobium aromaticivorans

MIPAHVPADRVVDFDIFNPPGVEQDYFAAWKTLLDGPGLVWSTA

NGGHWIAARGDVVRELWGDAERLSSQCLAVTPGLGKVMQFIPLQQDGAEHKAFRTPVM

KGLASRFVVALEPKVQAVARKLMESLRPRGSCDFVSDFAEILPLNIFLTLIDVPLEDR

PRLRQLGVQLTRPDGSMTVEQLKQAADDYLWPFIEKRMAQPGDDLFSRILSEPVGGRP

WTVDEARRMCRNLLFGGLDTVAAMIGMVALHLARHPEDQRLLRERPDLIPAAADELMR

RYPTVAVSRNAVADVDADGVTIRKGDLVYLPSVLHNLDPASFEAPEEVRFDRGLAPIR

HTTMGVGAHRCVGAGLARMEVIVFLREWLGGMPEFALAPDKAVTMKGGNVGACTALPL

VWRA

>CYP101D1 Novosphingobium aromaticivorans

MNAQTSTATQKHRVAPPPHVPGHLIREIDAYDLDGLEQGFHEAW

KRVQQPDTPPLVWTPFTGGHWIATRGTLIDEIYRSPERFSSRVIWVPREAGEAYDMVP

TKLDPPEHTPYRKAIDKGLNLAEIRKLEDQIRTIAVEIIEGFADRGHCEFGSEFSTVF

PVRVFLALAGLPVEDATKLGLLANEMTRPSGNTPEEQGRSLEAANKGFFEYVAPIIAA

RRGGSGTDLITRILNVEIDGKPMPDDRALGLVSLLLLGGLDTVVNFLGFMMIYLSRHP

ETVAEMRREPLKLQRGVEELFRRFAVVSDARYVVSDMEFHGTMLKEGDLILLPTALHG

LDDRHHDDPMTVDLSRRDVTHSTFAQGPHRCAGMHLARLEVTVMLQEWLARIPEFRLK

DRAVPIYHSGIVAAVENIPLEWEPQRVSA

>CYP101D2 Novosphingobium aromaticivorans

MGTTRMDTFNPQESRLATNFDEAVRAKVERPANVPEDRVYEIDM

YALNGIEDGYHEAWKKVQHPGIPDLIWTPFTGGHWIATNGDTVKEVYSDPTRFSSEVI

FLPKEAGEKYQMVPTKMDPPEHTPYRKALDKGLNLAKIRKVEDKVREVASSLIDSFAA

RGECDFAAEYAELFPVHVFMALADLPLEDIPVLSEYARQMTRPEGNTPEEMATDLEAG

NNGFYAYVDPIIRARVGGDGDDLITLMVNSEINGERIAHDKAQGLISLLLLGGLDTVV

NFLSFFMIHLARHPELVAELRSDPLKLMRGAEEMFRRFPVVSEARMVAKDQEYKGVFL

KRGDMILLPTALHGLDDAANPEPWKLDFSRRSISHSTFGGGPHRCAGMHLARMEVIVT

LEEWLKRIPEFSFKEGETPIYHSGIVAAVENVPLVWPIAR

>CYP101D3 Sphingomonas sp. SKA58

1 MPEHVPETMS RARAPRPEHI PEQYVHEIDM YALEGIEQGY HEAWKNIPKP DMPDLIWTPF

61 TGGHWIATNG DTVREVYSDP TRFSSEVIFL PKEAGEKYEM VPTRMDPPEH TPYRKALDKG

121 LSLAQIRKVE SKVRKVAVDL IDSFVSRGEC DFSAEYANVF PVRVFMALAD LPESDVPTLS

181 RFAKMMTRPE GNTPEEMAKH LEEGNKGFFA YVEPIIQARR GKEGEDLITV MVNAEINGER

241 ITHDKALGLI SLLLLGGLDT VVNFLSFMMI HLAKNPQVVE ELRADPLKLM RSAEEMFRRF

301 PVVSEARMVA KDQDFRGIEL KRGDMILLPT ALHGLDDQLN DDPWRINLER RGISHSTFGG

361 GPHRCAGLHL ARMEVIVTIE EWLKRIPTFA MKPGAQPIYH SGIVAAVDNV PLIWSER

>CYP102A1 Bacillus megaterium

MTIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFE

APGRVTRYLSSQRLIKEACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHN

ILLPSFSQQAMKGYHAMMVDIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFN

YRFNSFYRDQPHPFITSMVRALDEAMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVD

KIIADRKASGEQSDDLLTHMLNGKDPETGEPLDDENIRYQIITFLIAGHETTSGLLSF

ALYFLVKNPHVLQKAAEEAARVLVDPVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSL

YAKEDTVLGGEYPLEKGDELMVLIPQLHRDKTIWGDDVEEFRPERFENPSAIPQHAFK

PFGNGQRACIGQQFALHEATLVLGMMLKHFDFEDHTNYELDIKETLTLKPEGFVVKAK

SKKIPLGGIP

>CYP102A2 Bacillus subtilis

MKETSPIPQPKTFGPLGNLPLIDKDKPTLSLIKLAEEQGPIFQI

HTPAGTTIVVSGHELVKEVCDEERFDKSIEGALEKVRAFSGDGLFTSWTHEPNWRKAH

NILMPTFSQRAMKDYHEKMVDIAVQLIQKWARLNPNEAVDVPGDMTRLTLDTIGLCGF

NYRFNSYYRETPHPFINSMVRALDEAMHQMQRLDVQDKLMVRTKRQFRYDIQTMFSLV

DSIIAERRANGDQDEKDLLARMLNVEDPETGEKLDDENIRFQIITFLIAGHETTSGLL

SFATYFLLKHPDKLKKAYEEVDRVLTDAAPTYKQVLELTYIRMILNESLRLWPTAPAF

SLYPKEDTVIGGKFPITTNDRISVLIPQLHRDRDAWGKDAEEFRPERFEHQDQVPHHA

YKPFGNGQRACIGMQFALHEATLVLGMILKYFTLIDHENYELDIKQTLTLKPGDFHIS

VQSRHQEAIHADVQAAEKAAPDEQKEKTE

>CYP102A3 Bacillus subtilis

MKQASAIPQPKTYGPLKNLPHLEKEQLSQSLWRIADELGPIFRF

DFPGVSSVFVSGHNLVAEVCDEKRFDKNLGKGLQKVREFGGDGLFTSWTHEPNWQKAH

RILLPSFSQKAMKGYHSMMLDIATQLIQKWSRLNPNEEIDVADDMTRLTLDTIGLCGF

NYRFNSFYRDSQHPFITSMLRALKEAMNQSKRLGLQDKMMVKTKLQFQKDIEVMNSLV

DRMIAERKANPDENIKDLLSLMLYAKDPVTGETLDDENIRYQIITFLIAGHETTSGLL

SFAIYCLLTHPEKLKKAQEEADRVLTDDTPEYKQIQQLKYIRMVLNETLRLYPTAPAF

SLYAKEDTVLGGEYPISKGQPVTVLIPKLHRDQNAWGPDAEDFRPERFEDPSSIPHHA

YKPFGNGQRACIGMQFALQEATMVLGLVLKHFELINHTGYELKIKEALTIKPDDFKIT

VKPRKTAAINV

>CYP102A4 Bacillus anthracis str. Ames

1 MDKKVSAIPQ PKTYGPLGNL PLIDKDKPTL SFIKLAEEYG PIFRMQTLSD TIIVVSGHEL

61 VAEVCDETRF DKSIEGALAK VRAFAGDGLF TSETQEPNWQ KAHNILMPTF SQRAMKDYHA

121 MMVDIAVQLV QKWARLNPNE NVDVPEDMTR LTLDTIGLCG FNYRFNSFYR ETPHPFITSM

181 TRALDEAMHQ LQRLDIEDKL MWRTKRQFQH DIQSMFSLVD NIIAERKSSE NQEENDLLSR

241 MLNVQDPETG EKLDDENIRF QIITFLIAGH ETTSGLLSFA IYFLLKNPDK LKKAYEEVDR

301 VLTDSTPTYQ QVMKLKYIRM ILNESLRLWP TAPAFSLYAK EDTVIGGKYP IKKGEDRISV

361 LIPQLHRDKD AWGDNVEEFQ PERFEELDKV PHHAYKPFGN GQRACIGMQF ALHEATLVMG

421 MLLQHFEFID YEEYQLDVKQ TLTLKPGDFK IRIVPRNQTI SHTTVLAPTE EKLKNHEIKQ

481 QVQKTPSIIG ADNLSLLVLY GSDTGVAEGI ARELADTASL EGVQTEVAAL NDRIGSLPKE

541 GAVLIVTSSY NGKPPSNAGQ FVQWLEELKG DELKGVQYAV FGCGDHNWAS TYQRIPRYID

601 EQMAQKGATR FSTRGEADAS GDFEEQLEQW KQRMWSDAMK VFGLELNKNM EKERSTLSLQ

661 FVSRLGGSPL ARTYEAVYAS ILENRELQSS SSERSTRHIE ISLPEGATYK EGDHLGVLPI

721 NSEKNVNRIL KRFGLNGKDQ VILSASGRSV NHIPLDSPVR LYDLLSYSVE VQEAATRAQI

781 REMVTFTACP PHKKELESLL EDGVYQEQIL KKRISMLDLL EKYEACEIRF EPFLELLPAL

841 KPRYYSISSS PLVAQDRLSI TVGVVNAPAW SGEGTYEGVA SNYLAQRHNK DEIICFIRTP

901 QSNFQLPENP ETPIIMVGPG TGIAPFRGFL QARRVQKQKG MNVGEAHLYF GCRHPEKDYL

961 YRTELENDER DGLISLHTAF SRLEGQAKTY VQHVIKEDRI HLISLLDNGA HLYICGDGSK

1021 MAPDVEDTLC QAYQEIHEVS EQEARNWLDR LQEEGRYGKD VWAGI

>CYP102A5 Bacillus cereus ATCC 14579

1 MEKKVSAIPQ PKTYGPLGNL PLIDKDKPTL SFIKIAEEYG PIFQIQTLSD TIIVVSGHEL

61 VAEVCDETRF DKSIEGALAK VRAFAGDGLF TSETHEPNWK KAHNILMPTF SQRAMKDYHA

121 MMVDIAVQLV QKWARLNPNE NVDVPEDMTR LTLDTIGLCG FNYRFNSFYR ETPHPFITSM

181 TRALDEAMHQ LQRLDIEDKL MWRTKRQFQH DIQSMFSLVD NIIAERKSSG DQEENDLLSR

241 MLNVPDPETG EKLDDENIRF QIITFLIAGH ETTSGLLSFA IYFLLKNPDK LKKAYEEVDR

301 VLTDPTPTYQ QVMKLKYMRM ILNESLRLWP TAPAFSLYAK EDTVIGGKYP IKKGEDRISV

361 LIPQLHRDKD AWGDNVEEFQ PERFEELDKV PHHAYKPFGN GQRACIGMQF ALHEATLVMG

421 MLLQHFELID YQNYQLDVKQ TLTLKPGDFK IRILPRKQTI SHPTVLAPTE DKLKNDEIKQ

481 HVQKTPSIIG ADNLSLLVLY GSDTGVAEGI ARELADTASL EGVQTEVVAL NDRIGSLPKE

541 GAVLIVTSSY NGKPPSNAGQ FVQWLEELKP DELKGVQYAV FGCGDHNWAS TYQRIPRYID

601 EQMAQKGATR FSKRGEADAS GDFEEQLEQW KQNMWSDAMK AFGLELNKNM EKERSTLSLQ

661 FVSRLGGSPL ARTYEAVYAS ILENRELQSS SSDRSTRHIE VSLPEGATYK EGDHLGVLPV

721 NSEKNINRIL KRFGLNGKDQ VILSASGRSI NHIPLDSPVS LLALLSYSVE VQEAATRAQI

781 REMVTFTACP PHKKELEALL EEGVYHEQIL KKRISMLDLL EKYEACEIRF ERFLELLPAL

841 KPRYYSISSS PLVAHNRLSI TVGVVNAPAW SGEGTYEGVA SNYLAQRHNK DEIICFIRTP

901 QSNFELPKDP ETPIIMVGPG TGIAPFRGFL QARRVQKQKG MNLGQAHLYF GCRHPEKDYL

961 YRTELENDER DGLISLHTAF SRLEGHPKTY VQHLIKQDRI NLISLLDNGA HLYICGDGSK

1021 MAPDVEDTLC QAYQEIHEVS EQEARNWLDR VQDEGRYGKD VWAGI

>CYP102A6 Bradyrhizobium japonicum USDA 110

1 MSSKNRLDPI PQPPTKPVVG NMLSLDSAAP VQHLTRLAKE LGPIFWLDMM GSPIVVVSGH

61 DLVDELSDEK RFDKTVRGAL RRVRAVGGDG LFTADTREPN WSKAHNILLQ PFGNRAMQSY

121 HPSMVDIAEQ LVQKWERLNA DDEIDVVHDM TALTLDTIGL CGFDYRFNSF YRRDYHPFVE

181 SLVRSLETIM MTRGLPFEQI WMQKRRKTLA EDVAFMNKMV DEIIAERRKS AEGIDDKKDM

241 LAAMMTGVDR STGEQLDDVN IRYQINTFLI AGHETTSGLL SYTLYALLKH PDILKKAYDE

301 VDRVFGPDVN AKPTYQQVTQ LTYITQILKE ALRLWPPAPA YGISPLADET IGGGKYKLRK

361 GTFITILVTA LHRDPSVWGP NPDAFDPENF SREAEAKRPI NAWKPFGNGQ RACIGRGFAM

421 HEAALALGMI LQRFKLIDHQ RYQMHLKETL TMKPEGFKIK VRPRADRERG AYGGPVAAVS

481 SAPRAPRQPT ARPGHNTPML VLYGSNLGTA EELATRMADL AEINGFAVHL GALDEYVGKL

541 PQEGGVLIIC ASYNGAPPDN ATQFVKWLGS DLPKDAFANV RYAVFGCGNS DWAATYQSVP

601 RFIDEQLSGH GARAVYPRGE GDARSDLDGQ FQKWFPAAAQ VATKEFGIDW NFTRTAEDDP

661 LYAIEPVAVT AVNTIVAQGG AVAMKVLVND ELQNKSGSNP SERSTRHIEV QLPSNITYRV

721 GDHLSVVPRN DPTLVDSVAR RFGFLPADQI RLQVAEGRRA QLPVGEAVSV GRLLSEFVEL

781 QQVATRKQIQ IMAEHTRCPV TKPKLLAFVG EEAEPAERYR TEILAMRKSV YDLLLEYPAC

841 ELPFHVYLEM LSLLAPRYYS ISSSPSVDPA RCSITVGVVE GPAASGRGVY KGICSNYLAN

901 RRASDAIYAT VRETKAGFRL PDDSSVPIIM IGPGTGLAPF RGFLQERAAR KAKGASLGPA

961 MLFFGCRHPD QDFLYADELK ALAASGVTEL FTAFSRADGP KTYVQHVLAA QKDKVWPLIE

1021 QGAIIYVCGD GGQMEPDVKA ALVAIRHEKS GSDTATAARW IEEMGATNRY VLDVWAGG

>CYP102A7 Bacillus licheniformis ATCC 14580

1 MNKLDGIPIP KTYGPLGNLP LLDKNRVSQS LWKIADEMGP IFQFKFADAI GVFVSSHELV

61 KEVSEESRFD KNMGKGLLKV REFSGDGLFT SWTEEPNWRK AHNILLPSFS QKAMKGYHPM

121 MQDIAVQLIQ KWSRLNQDES IDVPDDMTRL TLDTIGLCGF NYRFNSFYRE GQHPFIESMV

181 RGLSEAMRQT KRFPLQDKLM IQTKRRFNSD VESMFSLVDR IIADRKQAES ESGNDLLSLM

241 LHAKDPETGE KLDDENIRYQ IITFLIAGHE TTSGLLSFAI YLLLKHPDKL KKAYEEADRV

301 LTDPVPSYKQ VQQLKYIRMI LNESIRLWPT APAFSLYAKE ETVIGGKYLI PKGQSVTVLI

361 PKLHRDQSVW GEDAEAFRPE RFEQMDSIPA HAYKPFGNGQ RACIGMQFAL HEATLVLGMI

421 LQYFDLEDHA NYQLKIKESL TLKPDGFTIR VRPRKKEAMT AMPGAQPEEN GRQEERPSAP

481 AAENTHGTPL LVLYGSNLGT AEEIAKELAE EAREQGFHSR TAELDQYAGA IPAEGAVIIV

541 TASYNGNPPD CAKEFVNWLE HDQTDDLRGV KYAVFGCGNR SWASTYQRIP RLIDSVLEKK

601 GAQRLHKLGE GDAGDDFEGQ FESWKYDLWP LLRTEFSLAE PEPNQTETDR QALSVEFVNA

661 PAASPLAKAY QVFTAKISAN RELQCEKSGR STRHIEISLP EGAAYQEGDH LGVLPQNSEV

721 LIGRVFQRFG LNGNEQILIS GRNQASHLPL ERPVHVKDLF QHCVELQEPA TRAQIRELAA

781 HTVCPPHQRE LEDLLKDDVY KDQVLNKRLT MLDLLEQYPA CELPFARFLA LLPPLKPRYY

841 SISSSPQLNP RQTSITVSVV SGPALSGRGH YKGVASNYLA GLEPGDAISC FIREPQSGFR

901 LPEDPETPVI MVGPGTGIAP YRGFLQARRI QRDAGVKLGE AHLYFGCRRP NEDFLYRDEL

961 EQAEKDGIVH LHTAFSRLEG RPKTYVQDLL REDAALLIHL LNEGGRLYVC GDGSRMAPAV

1021 EQALCEAYRI VQGASREESQ SWLSALLEEG RYAKDVWDGG VSQHNVKADC IART

>CYP102A8 Bacillus thuringiensis serovar konkukian str. 97-27

1 MDKKVSAIPQ PKTYGPLGNL PLIDKDKPTL SFIKLAEEYG PIFQIQTLSD TIIVVSGHEL

61 VAEVCDETRF DKSIEGALAK VRAFAGDGLF TSETDEPNWK KAHNILMPTF SQRAMKDYHA

121 MMVDIAVQLV QKWARLNPNE NVDVPEDMTR LTLDTIGLCG FNYRFNSFYR ETPHPFITSM

181 TRALDEAMHQ LQRLDIEDKL MWRTKRQFQH DIQSMFSLVD NIIAERKSSE NQEENDLLSR

241 MLNVQDPETG EKLDDENIRF QIITFLIAGH ETTSGLLSFA IYFLLKNPDK LKKAYEEVDR

301 VLTDSTPTYQ QVMKLKYIRM ILNESLRLWP TAPAFSLYAK EDTVIGGKYP IKKGEDRISV

361 LIPQLHRDKD AWGDDVEEFQ PERFEELDKV PHHAYKPFGN GQRACIGMQF ALHEATLVMG

421 MLLQHFEFID YEDYQLDVKQ TLTLKPGDFK IRIVPRNQTI SHTTVLAPTE EKLKKHEIKK

481 QVQKTPSIIG ADNLSLLVLY GSDTGVAEGI ARELADTASL EGVQTEVVAL NDRIGSLPKE

541 GAVLIVTSSY NGKPPSNAGQ FVQWLEELKP DELKGVQYAV FGCGDHNWAS TYQRIPRYID

601 EQMAQKGATR FSTRGEADAS GDFEEQLEQW KQSMWSDAMK AFGLELNKNM EKERSTLSLQ

661 FVSRLGGSPL ARTYEAVYAS ILENRELQSS SSERSTRHIE ISLPEGATYK EGDHLGVLPI

721 NNEKNVNRIL KRFGLNGKDQ VILSASGRSV NHIPLDSPVR LYDLLSYSVE VQEAATRAQI

781 REMVTFTACP PHKKELESLL EDGVYQEQIL KKRISMLDLL EKYEACEIRF ERFLELLPAL

841 KPRYYSISSS PLVAQDRLSI TVGVVNAPAW SGEGTYEGVA SNYLAQRHNK DEIICFIRTP

901 QSNFQLPENP ETPIIMVGPG TGIAPFRGFL QARRVQKQKG MKVGEAHLYF GCRHPEKDYL

961 YRTELENDER DGLISLHTAF SRLEGHPKTY VQHVIKEDRI HLISLLDNGA HLYICGDGSK

1021 MAPDVEDTLC QAYQEIHEVS EQEARNWLDR LQEEGRYGKD VWAGI

>CYP102A9 Bacillus weihenstephanensis KBAB4

1 MDKKVSAIPQ PKTYGLLGNL PLIDKDKPTL SFIKIAEEYG PIFRIQTLSD TIIVVSGHEL

61 VAEVCDETRF DKSIEGALAK VRAFAGDGLF TSETHEPNWK KAHNILMPTF SQRAMKDYHA

121 MMVDIAVQLV QKWARLNPNE NVDVPEDMTR LTLDTIGLCG FNYRFNSYYR ETPHPFITSM

181 SRALDEAMHQ LQRLDIEDKL MWRTKRQFQH DIQSMFSLVD NIIAERKSSG NQEENDLLSR

241 MLNVQDPETG EKLDDENIRF QIITFLIAGH ETTSGLLSFA IYFLLKNPDK LKKAYEEVDR

301 VLTDPTPTYQ QVMKLKYIRM ILNESLRLWP TAPAFSLYAK EDTVIGGKYP IKKGEDRISV

361 LIPQLHRDKD AWGDNVEEFQ PERFEELDKI PHHAYKPFGN GQRACIGMQF ALHEATLVMG

421 MLLQHFEFID YQDYQLDVKQ TLTLKPGDFK IRILPRNQTI SHTTVLAPIE EKLKNDEIEQ

481 QVQKTPSIIG ADNLSLLVLY GSDTGVAEGI ARELADTASL EGVQTEVVAL NDRIGSLPKE

541 GAVLIVTSSY NGKPPSNAGQ FVQWLEELKS DELKGVQYAV FGCGDHNWAS TYQRIPRYID

601 EQMAQKGATR FSTRGEADAS GDFEEQLEQW KQSMWSDAMK AFGLELNKNI EKERSTLSLQ

661 FVSRLGGSPL ARTYEAVYAS ILENRELQSS SSERSTRHIE ISLPEGATYQ EGDHLGVLPI

721 NSEKNVNRIL KRFGLNGKDQ VILSASGRSV NHIPLDSPVS LFDLLSYSVE VQEAATRAQI

781 REMVTFTACP PHKKELELLL EEGVYHEQIL KKRMSMLDLL EKYEACEIRF ERFLELLPAL

841 KPRYYSISSS PLVAQDRLSI TVGVVNAPAW SGEGTYEGVA SNYLAQRHNK DEIICFIRTP

901 QSNFQLPENP ETPIIMVGPG TGVAPFRGFL QARRVQKQKG INLGQAHLYF GCRHPEKDYL

961 YRTELENDER DGLISLHIAF SRLEGYPKTY VQHLIKQDRI NLISLLDNGA HLYICGDGSK

1021 MAPDVEDTLC QAYQEIHEVS EQEARNWLDR VQEEGRYGKD VWAGI

>CYP102A10 Erythrobacter litoralis HTCC2594

1 MDAPTALAPI PQPPGKPIVG NAFTVDSSRL IQSLMELAEE YGPIFQLEVM GTPLVFVSGA

61 DMVAEICDES RFDKTVRGPL KRLRLIAGDG LFTGDTDDPN WAKAHHILLP SFSQKAMGSY

121 LPMMTDIASQ LMLKWERLNS DDVIDVPMDM VRLTLDTIGV CGFGYRFNSF YREDFHPFIE

181 ALNRTLDTTQ KMRGLPGEKL LKRQQIEQLN EDAAYMNNLV DEIIRERRQT GESGQGDLLD

241 FMLSGRDPVT GERLSDENIR YQINTFLIAG HETTSGLLSF TLYYLLKNRD VLQRAYAEVD

301 EVLGRNIDQT PTLSQIGRLP YIRAILSEAL RLWPTAPAMG LAPFEDEVLG GKYAIAKGTF

361 TTVLIPSLHR DKLVWGENPE AFNPDNFSPK AEAARPPHAY KPFGNGQRAC IGRQFAIQES

421 ILVLGMLLQR FELFDHADYQ LRIKETLSIK PDGFTIKARL RHDVERGGVA TVEPESKTPD

481 QAAAVPSHGT PLLVLYGSNL GSSEGFAREL AQRGEFSGFD VTMAPLDAHV AKLPTDGAVA

541 IACASYNGMP PDNAAKFVDW LEQADAADAP LSNVSYLVLG CGNSDWAATF QVVPRKIDAL

601 MEQHGAERLV PAEELDARGD LDTQFHDWLD GLIPQLGDAF DIDLESGFDA VFEPLYTVEI

661 TDSITGNTVA DRVGAREVEV VANRELKDTS KDEGRSTRHL EVRLPEGMEY EPGDHLCVVP

721 VNDPAVVDRL LKRFGLDRDT FVRIESRSDM RGPFPSGSTF SVLNLAETAG ELQAVATRKD

781 IATLARYSEC PNSRAALEAL AAPPSADGTD RYTSEVLEKR RSVLDMLEEF PACDVPLAVF

841 LELIPFLSPR YYSISSAPEA NQGLCSITVG VVKGPALAGT GEFKGTCSAY LADLPPGDRF

901 RAVVRKPTAQ FRLPDNPETP VIMIGPGTGV APFRAFLQRR DHLQEDGAVL GEAMLFFGCR

961 HPDIDYLYRE ELDDYDQRGV ATVHAAFSRH DGSRTYVQDL IAREADRVWE LIEQDARIYV

1021 CGDGARMEPD VRKALMAIYA EKKSSDEASA KAWIDDLVAQ DRYLLDVWVG

>CYP102A11 Erythrobacter sp. NAP1

1 MATNATLTPI PQPPGKPLIG NALTVDASQQ IQSLMELAEE YGPIFQLDMM GTPIVIISGA

61 DLVAEVCDEK RFDKSVRGPL KRLRLIGGDG LFTGDTDAPN WSKAHNILLP SFSQKAMGSY

121 LPMMTDIATQ LVMKWERMNS DDVIDVPKDM IRLTLDTIGV CGFGYRFNSF YREDFHPFIR

181 ALTRTLETTQ KIRGIPGEKL LKGDAVKQLH RDAKYMNNLV DEIIRERQRS GGDGPEDLLD

241 FMLSGRDPLT GERLSDENIR YQINTFLIAG HETTSGLLSF TLYYLLKNRD VLTRAYAEVD

301 TVLGRNIDQP PSLKQIGQLP YIRAILFEAL RLWPTAPAFG LAPFEDEVLG GKYLIPKGTF

361 TTVLIPSLHR DKSVWGENPE VFDPENFTAE AEAARPPHAY KPFGNGQRAC IGRQFAIQES

421 ILVLAMILQR FELFDHSDYK LDIKETLSIK PDEFTIKARM RKDVERGGKA TEDAEEASTE

481 PAEPKVPKHD TPLLVLYGSN LGSSESFARE VAQKGEFSGF EVEMAPLDDY VGKLPEDGAV

541 AIACASYNGM PPDNAAKFID WIEGKDGAAP DLSGVSYMML GCGNSDWAAT FQAVPRLIDA

601 RMEELGAKRI VPTTELDARS DVDTQFHTWL DALMPQLGEH FDLDLSGEAA GIAEPLYKVE

661 VTQSVTANTV ASRVGAHAVK MVANRELKNT DIGEGRSTRH IEVELAQGET YQPGDHLCVV

721 PENDDAVVER LLRRFNLDAD TYVRIESRSE MRGPFPSGST FSVYNLAKTA GELQAVATRK

781 DIATLALYTE CPNSKPALEK LAQPPQEDGT DQYATDVLAK RKSVLDLLED YPACDLPLAV

841 FLEMIPFLSP RYYSISSAPG DTPQTCSITV GVVKGPALSG KGTFKGTCSN YLAELEPGAS

901 FNAVVREPTA NFRLPDDPKV PLIMVGPGTG LAPFRGFLQE RDALASSGEE LGPARLYFGC

961 RTPDEDFLYR DELEDYDKRG IVTLRTAFSR VDEGKCYVQD HIADDADAIW EMLEAGGRIY

1021 VCGDGARMEP DVRAALAKIH SDKTGSTPAE AQSWVGDLIT NERYSLDVWV G

>CYP102A12 Rhodopseudomonas palustris HaA2

1 MSSSNKLAPI PHPPKQPVVG NMLSIDTKAP VQHLVRLAEE LGPIFWLDMM GAPIVIVSGY

61 DLVDEISDEK RFDKAVRGAL RRVRTVGGDG LFTADTSEPN WSKAHNILLT PFGGRAMQSY

121 HPSMVDIAEQ LVKKWERLNA DDEIDVVHDM TALTLDTIGL CGFDYRFNSF YRRDYHPFVE

181 SLVRSLETIM MTRGLPLENL WMKKRRDTLA EDVAFMNAMV DEIIAERRKA AAVADKMDML

241 GAMMTGVDKV TGEPLDDVNI RYQINTFLIA GHETTSGLLS CAIYALLKHP EVLQKAYDEV

301 DRVLGADTSV EPSYQQVNQL GYITQILKET LRLWPPAPAY GVAPIQDETI GGQYHLKRGT

361 FTTVLVLALH RDPSIWGPNP DAFDPENFSR EAESKRPANA WKPFGNGQRA CIGRGFAMHE

421 AALALGMILQ RFKLIDHTRY RMVLKETLTI KPEGFKIKVR PRSDKDRATR IASGVSHSVA

481 PAPAAPRARP GHNTPLLVLY GSNLGTAEEL AHRVADLADL NGFATRLGAL DQYVGQLPEE

541 GGVLIFAASY NGAPPDNATQ FVRWLSGDLP PDAFAKLRYA VFGCGNRDWT ATYQAIPRLI

601 DERLAAHGGR NIFVRGEGDA RDDLEGQFEA WFATLGPLAV KEFGIDAAFD RGADDTPLYG

661 IEPLAPAASQ PLAATGVAVA MRVLENRELQ DRAASGRSTR HIEIALPQGM SYRVGDHLSV

721 IPRNDPALVA AVAQRFGFAP DDQIRLSAAP GRRAQLPVGE AVSIGGLLGD HVELQQVATR

781 KQIVALAAHT RCPQTRPKLQ ALAGGDGAAD DAYRAEVLGK RRSVFDLLQE HPACELPFAA

841 YLEMLTPLQP RYYSISSSPA RDPARASVTV AVVEGPALSG RGIYRGACSS WLAGRGSGDT

901 VQATVRATKA CFRLPDDDRV PLIMIGPGTG VAPFRGFLQE RSARKVGGAT LGPALLFFGC

961 RHPAQDYLYA DELQGFAADG IVELHAAFSR GDGPKTYVQH LIAAQKDRVF ALIEQGAIVY

1021 VCGDGGRMEP DVKAALCAIH RERSGADATA AAAWIADLGA RDRYVLDVWA SV

>CYP102A12 Rhodopseudomonas palustris HaA2

1 MPSTNKLDPI PHPPKKPVVG NMLSLDTTAP VQHLVRLAKE LGPIFWLDMM GAPLVIVSGY

61 DLVDEISDEK RFDKAVRGAL RRARAVGGDG LFTADTKEPN WSKAHNILLT PFGGRAMQSY

121 HPSMVDIAEQ LVKKWERLNA DDEIDVVHDM TALTLDTIGL CGFDYRFNSF YRRDYHPFVE

181 SLVRSLETIM MTRGLPLENL WMKKRRETLA DDVVFMNAMV DEIIAERRKA SESAADKKDM

241 LGAMLAGVDR ATGEPLDDVN IRYQINTFLI AGHETTSGLL SCAIYALLKH PDVLQKAYDE

301 VDRVLGSDTA VRPSYQQVNQ LSYITQILKE TLRMWPPAPA YGVAPIKDEV IGGKYHLKRG

361 TFVTVLVLAL HRDPAIWGPN PDAFDPENFS REAESKRPAN AWKPFGNGQR ACIGRGFAMH

421 EAALALGMIL QRFQLIDHQR YRMVLKETLT IKPEGFKIKV RPRSDKDRGD FVAAGASQVS

481 TPALAQAAPR ARPDHNTPLL VLYGSNLGTA EELATRVADL AELNGFSTRL GALDQYVGHL

541 PEEGGVLIFT ASYNGAPPDN ATQFVQWLSG DLPKDAFAKL RYAVFGCGNR DWTATYQAIP

601 RLVDERLAAH GGRNIFLRGE GDARDDLEGQ FESWFAKLGP LAVKEFGIDA KFARAVDDAP

661 LYRIEPVAPA AGNAVAAAGG AVPMKVLANR ELQDCAASGR STRHIEIALP EGISYRVGDH

721 LSVMPRNDPA LVAAVAQRLG FAPDDQIKLQ VAPGRRAQLP IGEAISVGRL LGDFVELQQV

781 ATRKQIAVMA EHTRCPQTRP KLQALAGGDG AADEAYRAGV LAKRKSVYDL MQEHPACELP

841 LHAYLEMLSP LAPRYYSISS SPLRDPSRAA ITVAVVDGPA LSGRGHYRGV CSTWLAGRSV

901 GDTIHATVRA TKAGFRLPDD DRVPLIMIGP GTGLAPFRGF LQERAARQQN GATLGPALLF

961 FGCRHPAQDY LYADELQGFA AEGVVELHTA FSRGEGPKTY VQHLIAAQKD RVFTLIEQGA

1021 IIYVCGDGGK MEPDVRAALM AIHRERSGAD AAAASTWIDD LGACNRYVLD VWASA

>CYP102A13 uncultured soil bacterium

1 MASNNKMSPI PQPPTRPVVG NMLSLDSAAP VQDLTRLAKE LGPIFWLDMM GAPIVIVSGY

61 TLVDELSVET RLDKVVRGAL RRVRAIGGDG LFTADTAEPN WSKARNILLQ PFGNRAMQSY

121 HPSMVDIAEQ LVKKWERLNA DDEIDVVHDM TALTLDTIGL CGFDYRFNSF YRRDYHPFVE

181 SLVRSLETIM MIRGLPLENF WMRRRRSDLA TDVAFMNKMV DEIVAERRKS AEASDGKKDM

241 LNAMMSGVDR STGEQLDDVN IRYQINTFLI AGHETTSGLL SYAIYALLKH PDVLKKAYAE

301 VDRVLGADIE ARPSYQQVTQ LTYITQILKE ALRLWPPAPA YGIAPLKDET IAGGKYSLKK

361 NTFISILVTA LHHDPAVWGP NPDLFDPENF SPEAEAKRPV NAWRPFGNGQ RACIGRGFAM

421 HEAALALGMI LQRFKLIDHQ RYQIRLKETL TIKPDGFKIK VRPRSGHDRT VHAEAATAAV

481 ATGAALPRAR PRPGHNTPLL VLYGSNLGTA EDLATRVADL AEVNGFATRL APLDDCAGQL

541 PDSGGVLIFC ASYNGAPPDN ATKFVGWLRG ELPNDAFAKL RYAVFGCGNR DWAATYQSVP

601 RLIDETLSAH GGKRVFPRGE GDARSDLDGQ FESWFAALGA AAVKEFGLES RFSRSADDAP

661 LYSVEPVAPS AVNAVAALGG TVPMTILVSR ELQNKSGPDA SERSTRHIEV QLPGGMTYRV

721 GDHLSVVPCN APALVDRVAR RFGFLPADQI RLAVAEGRRA QLPVGEAVSI GQLLTDFVEL

781 QQVATRKQIQ IMSEHTRCPV TKPKLVAYVG DDADSSERYR ADILSRRKSV YDLLEEFPAI

841 ELPFPAYLEM LSLLAPRYYS ISSSPTGDAS RCSITVGVVS CPASSTGRGL YRGVCPYYLA

901 SRREGESVFA TVRETKAGFR LPDDPSVPII MIGPGTGLAP FRGFLQERAA RKAGGATLGP

961 AMLFFGCRHP EQDYLYADEL KAFADEGITE LFVAFSRSEG PKTYVQHLLA TQKARVWDLI

1021 EQGAVIFVCG DGSKMEPDVK ATLVQIYRDC TGADANGGAK WIADLGAQNR YVLDVWAGG

>CYP102A14 uncultured soil bacterium ABD83817

1 MASNNKMSPI PQPPTRPVVG NMLSLDSAAP VQDLTRLAKE LGPIFWLDMM GAPIVIVSGY 61 TLVDELSVET RLDKVVRGAL RRVRAIGGDG LFTADTAEPN WSKARNILLQ PFGNRAMQSY 121 HPSMVDIAEQ LVKKWERLNA DDEIDVVHDM TALTLDTIGL CGFDYRFNSF YRRDYHPFVE 181 SLVRSLETIM MIRGLPLENF WMRRRRSDLA TDVAFMNKMV DEIVAERRKS AEASDGKKDM 241 LNAMMSGVDR STGEQLDDVN IRYQINTFLI AGHETTSGLL SYAIYALLKH PDVLKKAYAE 301 VDRVLGADIE ARPSYQQVTQ LTYITQILKE ALRLWPPAPA YGIAPLKDET IAGGKYSLKK 361 NTFISILVTA LHHDPAVWGP NPDLFDPENF SPEAEAKRPV NAWRPFGNGQ RACIGRGFAM 421 HEAALALGMI LQRFKLIDHQ RYQIRLKETL TIKPDGFKIK VRPRSGHDRT VHAEAATAAV 481 ATGAALPRAR PRPGHNTPLL VLYGSNLGTA EDLATRVADL AEVNGFATRL APLDDCAGQL 541 PDSGGVLIFC ASYNGAPPDN ATKFVGWLRG ELPNDAFAKL RYAVFGCGNR DWAATYQSVP 601 RLIDETLSAH GGKRVFPRGE GDARSDLDGQ FESWFAALGA AAVKEFGLES RFSRSADDAP 661 LYSVEPVAPS AVNAVAALGG TVPMTILVSR ELQNKSGPDA SERSTRHIEV QLPGGMTYRV 721 GDHLSVVPCN APALVDRVAR RFGFLPADQI RLAVAEGRRA QLPVGEAVSI GQLLTDFVEL 781 QQVATRKQIQ IMSEHTRCPV TKPKLVAYVG DDADSSERYR ADILSRRKSV YDLLEEFPAI 841 ELPFPAYLEM LSLLAPRYYS ISSSPTGDAS RCSITVGVVS CPASSTGRGL YRGVCPYYLA 901 SRREGESVFA TVRETKAGFR LPDDPSVPII MIGPGTGLAP FRGFLQERAA RKAGGATLGP 961 AMLFFGCRHP EQDYLYADEL KAFADEGITE LFVAFSRSEG PKTYVQHLLA TQKARVWDLI 1021 EQGAVIFVCG DGSKMEPDVK ATLVQIYRDC TGADANGGAK WIADLGAQNR YVLDVWAGG

>CYP102A15 Bacillus pumilus ATCC 7061 ZP\_03053227

1 MQQTSIIPKP KTYGPFKNIP HIKKGELSQT FWRLADELGP IFQFEFSKAT SIFVSNHELF 61 QEICDESRFD KYIGTSLNKV RAFAGDGLFT SWTEEPNWRK AHHILMPAFS QQAMKGYHEM 121 MLDIATQLVQ KWQRTGRDEE IEVAEDMTKL TLDTIGLCGF DFRFNSFYKE NQHPFIESMV 181 NGLSEAMDQA SRLPVADKLM IKRRKKFEEN VDFMKQLVDD IIQERKKQDK TGDDLLSLML 241 HAKDPETGER LSDENIRYQI ITFLIAGHET TSGLLSFAIY FLLKNPEKLK KAVQEADDVL 301 QGGLPTFKQV QKLNYTRMVL NESLRLWPTA PTFSLYAKED TVIGGKYSIE KNQSVSVLLP 361 KLHRDQAVWG EDAEEFKPER FLHPEKIPQH AYKPFGNGQR ACIGMQFALH EATMVLAMVL 421 HNLELIDHTS YELDLKESLT IKPNDFKIKV RPRKQQLFMV PPKEETKKST TTDESKVKSH 481 GTPLLVLYGS NLGTAQQIAN ELAEEGKAKG FDVTTAPLDD YTRQLPDKGA VFIVTASYNG 541 HPPDHAKKFV DWVTQEKEQD LTNVTFAVFG CGDRNWASTY QRIPRLIDEA LERKGAKRAA 601 DLGEGDAGGD MDEDKEAFQK TVFKQLAKEF QLTFQEKGKE NPKLSVAYTN ELVERPVAKT 661 YGAFSAVVLK NEELQSEKSE RQTRHIELQL PEGKKYKEGD HIGIVPKNSD ALVQRVINRF 721 NLDPKQHIKL YSEKKANHLP LDQPIQMREL LASHVELQEP ATRTQLRELA AYTVCPPHRV 781 ELEQMAGEAY QEAILKKRVT MLDLLDQYEA CELSFVHFLA LLPGLKPRYY SISSSPKVDE 841 KRVSITVAVV KGKAWSGRGE YAGVASNYLC GLKEGEEVAC FLHEAQAGFQ LPPSSEVPMI 901 MIGPGTGIAP FRGFVQAREV WQKEGKPLGE AHLYFGCRHP HEDDLYFEEM QLAAQKGVVH 961 IHRAYSRHKE QKVYVQHLLK EDGGMLIKLL DQGAYLYVCG DGKVMAPDVE ATLIDLYQHE 1021 KQCSKEAAEN WLTTLANNNR YVKDVWS

>CYP102B1 Streptomyces coelicolor cosmid F43.

MAQTAREPARDGLPKGFRSAELGWPELHRIPHPPYRLPLLGDVV

GASRRTPMQDSLRYARRLGPIFRRRAFGKEFVFVWGAALAADLADEARFAKHVGLGVA

NLRPVAGDGLFTAYNHEPNWQLAHDVLAPGFSREAMAGYHVMMLDVAARLTGHWDLAE

ASGRAVDVPGDMTKLTLETIARTGFGHDFGSFERSRLHPFVTAMVGTLGYAQRLNTVP

APLAPWLLRDASRRNAADIAHLNRTVDDLVRERRANGGTGGGTGSGSGSGDLLDRMLE

TAHPRTGERLSPQNVRRQVITFLVAGHETTSGALSFALHYLAQHPDVAARARAEVDRV

WGDTEAPGYEQVAKLRYVRRVLDESLRLWPTAPGFAREAREDTVLGGTHPMRRGAWAL

VLTGMLHRDPEVWGADAERFDPDRFDAKAVRSRAPHTFKPFGTGARACIGRQFALHEA

TLVLGLLLRRYELRPEPGYRLRVTERLTLMPEGLRLHLVRRTAAAPAPGRRTAAPGAA

DDAGDTVSAPGCPVHRAGD

>CYP102B2 Streptomyces avermitilis

MAQSTRTVIPKGFRSAELGWPELHRIPHPPHRLPVVGDVLGVNV

RTPVQDSLRIGRRLGPVFRRKAFGKEIVFVGGADLAAELADESRFAKHVGLGVANLRP

VAGDGLFTAYNHEPNWQLGHDVLAPGFSREAMAGYHPMMLAVTERLIDHWDREQTAGR

AVDVPGDMTKLTLETIARTGFGHDFGSFERARPHPFVTAMVGTLTYAQRRNVVPEPLA

PLLLRTATRRNAADLAYLNRTVDALVRARRTTSGEGDLLDRMLDTARPGTGERLAPEN

IRRQVITFLVAGHETTSGALSFALHYLSRHPDVAARARAEVDRVWGGTARPGYDQVAK

LRYVRRVLDESLRLWPTAPAFAREARRDTVLGGVHPMREGAWALVLTAMLHRDPGVWG

ADAERFDPDRFDAQAVRSRAAHTFKPFGTGARACIGRQFALHEATLVLGLLLRRYELR

AEPGYRLRVAERLTLMPEGLRLRLDRRVPAVEDVPVANPEVSSGPRCPVTGAGE

>CYP102B3 Rhodococcus sp. RHA1 Rha05872

MPVTVLLDTGSVRGTLRTRHQFSNAGHIDTGVDMSVESLHTTADATIPHPRWRLPVVGDVFGISIRTPLQNSMEIGRKLGPIFERNVLGNRFVFASGADMVAELSDESRFAKHLAPGVASLREVGGDGLFTAYNHEPNWSKAHNLLAPAFTKSAMRSYHRTMLDVAGELTEHWDERVDGSPVDVSSDMTKLTLETIGRTGFSYSFDSFGRERPHPFVQAMVGALSHSQRTTFVKSSALGRLLMRRSDRRNIANLEHMAEVVDEVIRARRDSAEDGPEDLLELMLRAARENDPHRIDELNIRHQVVTFLVAGHETTSGALSFALYYLSRHPDVLAKAQAEVDAVWGDEEPAFEQIAKLRYVRRVLDESLRLWPTAPAYGREATVDTTLVGKYPMKVGDWVLVLIPALHRDPVWGDDPEAFDPDHFLPERIRSRPAHVYKPFGTGERACIGRQFALHESVLVLGTILRRYDIVGDPDYRLKVAERLTLMPEGFTLQLRRR

>CYP102B4 Streptomyces scabies SCAB9321

MTATTAATAI SGFRSAELGW PELHRIPHPP FRIPLLGDVL GTNVRTPVQE STRLGQRLGP

IFRRKAFGKE IVFVGGAELA AEMADEARFA KHVGVGVANL RPVAGDGLFT AYNHEPNWQL

AHDVLAPGFG REAMAGYHPM MLDVAERLIE HWDREETAGS AVDVPGDMTK LTLETIARTG

FGHDFGSFER TRPHPFVAAM VGTLTYAQQR NVVPDPLVPV LLRGAAQQNR ADMAFLVETV

DAVVRARRSP GGGRGAGDGD LLDRMLETAH PETGERLSAE NVRRQVITFL VAGHETTSGA

LSFALHYLAR YPDLAARARA EVDRVWGDAA RPGYEQVAKL RYVRRVLDEA LRLWPTAPAF

SREAREDTVL GGVHPMRRGA WALVLTSMLH RDPEVWGADA ERFDPDRFDA AAVRGRAPHT

FKPFGTGARA CIGRQFALHE ATLVLGLLLR RYELTPEPGY RLRVVERLTL MPDGLRLRVR

RRAGAGTDAP RTPSSPPTPS SAPSGRPVTG AGE

>CYP102C1 Rhodococcus sp. X309

AAAGGKIDATADANKLALDVIGLAGFGYDFASFDGDEHPFVGAM

SRVLEHVNRTSNDIPFLRKLRGNGADLQYEKDIAFVRTVVDDVITERQAKPGEHQDDL

LDLMLNNIDDETGEKLDPVNIRNQVLTFLVAGNETTAGAIAFALYFLSRHPEIADAAR

AEVADITGGETPAFEDVARMRYLRRVVDETLRLWPSAPGYFRKVRTDTTLGGRYAMPK

GSWVFVLLPQLHRDPVWGENPDSFDPDRFKPENVKKRPAHAYRPFGTGPRSCIGRQFA

LHEAVLSLATILQRYSFQSDPEYKLDVREALTLKPVGLELSLQRL

>CYP102C2 Rhodococcus erythropolis PR4

1 MNGPRGSRTR PRRASLVNLA VLGVVLVHTV LMSADKCPYP KSATRAGEIT AVQPQVFESI

61 PSPAWRLPLL GDLLTVDSEK PIQKEMALAS KLGPIFEWKI VNNRVTVVSG VDLVAEVNNE

121 ALWAKSVGLP ILKLRKVAED GLFTAFNSEP NWRKAHNILS EGFSRSALRN YHPSMLRALG

181 GLTDSWDRVA DAGETIDASS DANKLALDVI GLAGFGYDFA SFIGEEHPFV GAMSRVLAHV

241 NSTSNDIPFL RKLRGNGADL QNEKDIALLR TVVDNVIAER QSKPGEHQDD LLDLMLHSAD

301 AETGEKLDPV NIRNQVFTFL VAGNETTAGT LAFALYFLSR HPDVADTARA EVADVTAGET

361 PAFEDVARMR YLRRVVDETL RLWPSAPGYF RKVRTDTTLG GRYDMPKGSW VFVLLPQLHR

421 DPVWGEDPES FDPDRFKPEN VKKRPAHAYR PFGTGPRACI GRQFALHEAV LALAIILQRY

481 NFQSDPEYKL DIRETLSLKP VGFELSLQRR

>CYP102D1 Streptomyces avermitilis

MTTQPETDLRPIRSPRGVPLFGHTPQIPSTNPVEYFGKLSKQFP

EGLYGMEIAGIEQVFVWDPDLVAEVCDETRFFKQIDKTPLAHVRDYAGAGLFTAHQHE

EEWGMAHRVLLPVFSQRAMKGYFGQMLEIAQNLVGKWERKEGQPVNITDDYTRLTLDT

IALSGFGYRFDSFAKEDLHPFLNALLQALVESLRRSQELPVMTKMRKADDKKYRENIR

LMRDLVENVIKERREGKGTGEDDLLGLMLEATDPETGKGLDDDNVRDQVVTFLIAGHE

TTSGLLSFATYSLMRNPHILAQAYAEVDRLLPGDTVPDYDTIMQMDVIPRILEETLRL

WAPIPMIGKSPLEDTVIGGCYGLKKGARVNILEGPLHTHPKAWERPEEFDINRWLPEN

RVNHHPHAYKPFGNGVRACIGRQFALTEARLALALVLQKFKFADTDDYKMDVKEALTR

KPGGFELNVRARQEHERTVFGAAD

>CYP102E1 Ralstonia metallidurans

MSTATPAAALEPIPRDPGWPIFGNLFQITPGEVGQHLLARSRHHDGIFELDFAGKRVPFVS

SVALASELCDATRFRKIIGPPLSYLRDMAGDGLFTAHSDEPNWGCAHRILMPAFSQRAM

KAYFDVMLRVANRLVDKWDRQGPDADIAVADDMTRLTLDTIALAGFGYDFASFASDELDP

FVMAMVGALGEAMQKLTRLPIQDRFMGRAHRQAAEDIAYMRNLVDDVIRQRRVSPTSGMD

LLNLMLEARDPETDRRLDDANIRNQVITFLIAGHETTSGLLTFALYELLRNPGVLAQAY

AEVDTVLPGDALPVYADLARMPVLDRVLKETLRLWPTAPAFAVAPFDDVVLGGRYRLRKD

RRISVVLTALHRDPKVWANPERFDIDRFLPENEAKLPAHAYMPFGQGERACIGRQFALTE

AKLALALMLRNFAFQDPHDYQFRLKETLTIKPDQFVLRVRRRRPHERFV

TRQASQAVADAAQTDVRGHGQAMTVLCASSLGTARELAEQIHAGAIAAGFDAKLADLDDA

VGVLPTSGLVVVVAATYNGRAPDSARKFEAMLDADDASGYRANGMRLALLGCGNSQWATY

QAFPRRVFDFFITAGAVPLLPRGEADGNGDFDQAAERWLAQLWQALQADGAGTGGLGVDV

QVRSMAAIRAETLPAGTQAFTVLSNDELVGDPSGLWDFSIEAPRTSTRDIRLQLPPGITY

RTGDHIAVWPQNDAQLVSELCERLDLDPDAQATISAPHGMGRGLPIDQALPVRQLLTHFI

ELQDVVSRQTLRALAQATRCPFTKQSIEQLASDDAEHGYA

>CYP102F1 Actinosynnema pretiosum subsp. auranticum

MVATGTRIPGPKPLPLVGNLLDVLTSDLDTDVDFLDRCHREHGG

IVALTFAGQRQVFASSHELVARMCSDPSWGKAVHPALEQVRDFAGDGLFTARGDEPNW

GKAHRLLMPAFGPTAMRDHFPAMLDIAEQMLVRWRRFGPDHRIDVADDMTRLTLDTIA

LCAFGARFNSFYRDRAHPFVDAMVRSLVEAGERAERLPGVQPFLVGRNQRYRDDIATM

NRIADGIVAARAALPAGERPDDLLERMLTCADPVTGERLSARNVRYQLATFLIAGHET

TSGLLSFAVHRLLAHPEVLRKAKDAVDGVLGDRVPAFEDLARLDYLGQVLRETLRLHP

TAPAFALAPDEPAELGGHAIGAGEPVLVMLPTLHRDPAVWRDPDVFDPERFAPERMDE

IPACAWMPFGHGARACIGRPFALQEATLVLALVLQRFDLALADPDHRLTIKQTLTLKP

DSLVVRARPRADRPGATATVETVVPHQVPATHRHGTPLHVFYGSNGGSGEGLARTIAG

DGAARGWATSVAPLDDAVRALPASGPVVIVSSSYNGAPPDNAAHFVRWLTQDGPDLSG

VDYLVLGCGNLDWSATYQRVPTLIDEAMAAAGARRLRERGATDARADFFGDWERWYEP

LWPLLSAECGVEVGEIGPRFRVVESDAADGLGDLASAVVLENRELVRGPDAGSKRHLE

LRLPDGTSYRTGDYLSVLPQNHPDLVRRAVARLGTRAERVVTVESSAPTGLVPVGRAL

RVDELLTRCVDLSAPAGAGVVARLAERCPCPPERAELAATTGATLLELLERFPSCAVD

LALALELLPAPRTRLYSISSAAEEQRAEVALTVSVTGVTSGYLSRVRPGDRVAVGIAS

PPESFRPPADNTVPVVLIAAGTGIAPFRGFLRARAALGGEPGPALLLFGCRGPELDDL

YAEEFAALGDWLEVDRAYSRHPDGEVRHVQHRLWQRRDRVRELVDAGARVYLCGDATR

VGPAVEEVLGRIGPGAGWLDALRAGGRYATDVF

>CYP102G1 Streptomyces scabies SCAB5931

MTHATERGTE SIPERSALPL VGHAFDIPGG ADGLLHLMKE ARELGPLFKL RVFGNEINIA

SGLDLVTELS DESRFRKNVH ADLVLVREIT GDGLFTAFND EPNWRKAHDV LMPAFSLGAM

RGYHATMLKV ARELIGKWDG AAGTEPVDVA EDMTRLTFDT IGLCGFGHDF ESFGRPEPHP

FVTALSRALG FAQAKGESIP GLDLFKWKQA EQFRTDVAVM RDLVDDVIRE RRASGDTGTD

DLLGRMLHTR DQVTGEPLDD VNIRHQAITF LIAGHETTSG ALSFALYYLT KHPEVLARAQ

AEVDALWGDT DTPDPDYGDI GKLTYIRQVL NEGLRLWPTA PAYAVEPLED TVIGGRYAVR

EGETIQVLIP QLHRDPAWGE NVELFDPDRF LPEREQERPV HLFKPFGSGE RACIGRQFAL

HEATLVLALV IHRYRLIDHT DYQLKIKQSL TIKPDEFTLR LARRTAGERR LPLVASDRAP

AGEAPPAVRR AAGTTLTLLH GSNLGTCAGI ARELAEDGEQ HGFAPTVASL DSAAGTLSAV

DGPVVIVAAS YNGRPTDDAT RFMEWLDDLA PGSLDGLRYA VLGVGDRNWA ATYQRVPALI

DERLSAAGAT ALLERGAADA SGDFAGTVDR WTGELWTTLL DRHGTAQDGV AAQPDTDAEG

GLYVLEDTTD SVIGGLAARH GVQPMEVLDA RELVDMSHGL GRSKRFLRLR LPEGVTYRTG

DHLAVLPRNP DHLVRRVTDR FGLDPDRTVR LRARRRGRNT LPVDRPLTVR RLLTDFVELQ

DPATREQIAV LAEHTACPPE KRPLTELAAA DPETFREQVT AAGRSVLDLL ERHRACELPF

ERFLELLPVL RPRPYSISSS ALAAPGEVDL MVSLLAAPHR AGEGMFHGIG SHFLQTVRPG

DTLQARVLPC SEAFRLPDDT SASVILVSAG TGLAPFRGAV LDRRHAGSTG TLLCYFGCDH

PDVDYLHRAE FEAAEAAGAV SMRPAFSCAP EDGVRFVQDR IGKESDEVWA ALEAGARVHV

CGDGRRMAPA VREAFRALYR ENTGADDAEA TAWLDALTES GHYVEDVWAG

>CYP102G2 Saccharopolyspora erythraea NRRL23338

MTQTPLHHDDVPVADVSGTGLTATPTQQAMELARRHGPVFRRRTREFQSLLVSDVDLVAE

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RVARRLLDSWDRAAAASAPVDVPDDMTRMTLDTIGLAGFGFDFGSFGRAEPHPFVGAMVR

CLDWSMTRLSRVPGTDHSERDEAFRADARYLASVVDEVINTRAAEGDTSGEDLLGLMLGA

RHPADGTTLDAANIRNQIITFLIAGHETTSGTLSFALHYLAKNPTVLRLVQREADELWGD

SPDPEPSFEDIGRLTYTRQVLNETLRLWPSAPAFGRQARHDTVLGGRIPMRAGEAAAVLI

PMLHRSPVRGDNPELFDPARFAPEAEAARGPHAFKPFGTGERACIGRQFALDEATMVLAM

LAHRYRLVDHAGYRLKVKETLTLKPEGLTLAVRARTAADRVTNRLALPVGLPSAAPGEPA

DAARRPGRVLPGTGLLLLHGSNYGTCRDFAAQLALAAGELGCDTAVAPLDEYAGNLPSDR

PVIVVAASYNGRPTDDAVSFSRWLDEAEPGAADGVDFAVLGVGDRNWAATYQHVPTRIDA

RLAELGGTRILERGEADASGDLAGAVRRFSAALETALLERSGDPDAVAAAPEGDGPAYTV

SEVTGGALDSLAARHGMVEMTVTEVADLTAPDYPRTKRFVRLALPEGTAYRTADHLAVLP

VHDAALVERAAGVLGVDLDTVLDIRAKRPGRLTFDRSLTVRELLSHHVELQDPPTPDGLD

ALAALNPCPPERAALRGLAEEARSGTADHRTLWDLIEDHPALRDALSWSALLELLPATRP

RQYSVSSSPAVDPRHVDLMVSVLRAPARSGRGEFRGAGSRHLSEVRPGDTVLARVQPCRE

DFRVAPDEPLIMVAAGTGLAPFRGVIADRRERVANGARQAPALCYFGCDAPDADYLHSAE

LRAAESAGAVAMRPAFNEAPVGGQCFVQHRIAAEAGEVWALLESGARVLVCGDGRHMAPG

VREAFRGIYRERTPGADDASAHEWLQAMIAGGCYVEDVYAG

>CYP102H1 Nocardia farcinica IFM 10152 plasmid pNF1

MAVTTSTTSGGHSNPPLPHPKWRLPIINDLLTINPIKPTLTSLR

DAEQLGGIFERRLVDWPMIVVSDSELITEICDERNWAKHLGVPLRKMRHIARDGLFTA

RNDEPNWAKAHAVLAPAFTKEAMRSYHQTMLTTIGELLDYWAKRDGQWVDVGEDMNKL

TLEIIARTGFDYTFDSFTRSEVHPFVAAMLRGLTYISRNSNMPPFLQKTIGARAAARH

SRDITYVRTVVDDVIKARQASGTVGDHHDLLDRMLTVPDPASDELLDTTNVRSQILTM

LVAGHETSAGVLAFALYELSRRPELVAAARAEIETRFADGDLSTIAYDDVAKLRTLRR

IVDETLRLYPVAPGFFREARHETTIGGGRYRFGPGDWVLVLTLHAHRDPATWGPDAGE

FQPDRWLPERMRSLDGRQVFKPFGTGLRACIGRQFAYHEIVLALAHILHTFEFTPDPG

YELDIAEQITLKPHRFRLRLNHR

>CYP102J1 Burkholderia sp. 383 ABB05850 50% to CYP102A4

1 MKSSSLVPQP PLKPVIGHLM EVLGPSPLAK MMDLARTYGP VYWFEVFGQG YYVVSGQTLV 61 DEVCDETRFQ KCVHQSLLEL RPAIGDGLFT AFGDEPNWAK AHRVLMQAFG PLSIWSMFDK 121 MVDIADQMFL HWERFGPETP VDVSDHMTRL TLDTIALCAF DCRFNSFYRE DQHPFVDAMV 181 NTLSEAGKRE LRPKLVSKLM VKRSRQFDAD IEVMRSLATK MIEDRRKNPH VNEESMDLLD 241 RMLNGIDPVT GEKLDDENIV FQMITFLIAG HETTSGLLSF ATYFLLKNPD ILQKARDMVD 301 EVVGSETPRI EHLARLRYVE QILMETLRIW PTAPGFAVKP LADTTFGGKY AVSPDDIIMI 361 LTPMLHRDVS VWGEDVEAFR PERFAPENAE QLPPNSWKPF GNGARACIGR PFAMQEAHLV 421 LIMLLQRFDF SFADPDYELD VAETLTLKPA GFRVNVKPRA RGALKVPDTA LHARSNAQSP 481 SVAPVQSIAP GEDLSNLLVL FGGNTGSAES FARRIAGDAS RHGFHATCAP LDDFAGKLGG 541 YPAIVIVTAS YEGQPPDNAK SFVPYVEALD EGALDGVHFS VLGCGNKQWA RTYQAIPKRV 601 DEALEKAGAT RVHFRGELDS GGDFFGEFDR WYTEMWNRFA ISAGKEIPVI QHDDVALKVS 661 FAGSSREKVL NLGDMAHASI VDNRELVDIS VAGSRSKKHI ELKLPEAMTY RSGDYLAVLP 721 RNAKNNVDRV LRRFRVSWDT QVVIEGTSSN PRLPLGQAIG CGELFSSYVE LAVPATRSQV 781 SSLAAATRCP PEKVELERLS ADGFECEILG KRTTVMDLLE RFGSVDLSLE KFLDMLPALK 841 ARQYSISSSP LWKADHVTLT VAVVDAPALS GNGRHEGVAS SYLARLNTGD SLSVAVRPSN 901 ARFRPPAEPD LPMILICAGS GIAPFRGFLQ ERALQKQRGE NVGTSLLFFG IDDPDVDFLY 961 RDELDEWARC GVVEVMPAYS NRPEEGARFV QDKVWLERER ISALFSQGAT VFVCGDGKNM 1021 APAVRATLGR IYQETTGEND ESASAWIDTM EREHGRYVAD VFA

>CYP103A1 Agrobacterium tumefaciens

MIANSSTDVSVADQKFLNVAKSNQIDPDAVPISRLDSEGHSIFA

EWRPKRPFLRREDGIFLVLRADHIFLLGTDPRTRQIETELMLNRGVKAGAVFDFIDHS

MLFSNGETHGKRRSGLSKAFSFRMVEALRPEIAKITECLWDDLQKVDDFNFTEMYASQ

LPALTIASVLGLPSEDTPFFTRLVYKVSRCLSPSWRDEEFEEIEASAIELQDYVRSVI

ADSGRRMRDDFLSRYLKAVREAGTLSPIEEIMQLMLIILAGSDTTRTAMVMVTALALQ

NPALWSSLRGNQSYVAAAVEEGLRFEPPVGSFPRLALKDIDLDGYVLPKGSLLALSVM

SGLRDEKHYEHPQLFDVGRQQMRWHLGFGAGVHRCLGETLARIELQEGLRTLLRRAPN

LAVVGDWPRMMGHGGIRRATDMMVKLSFDL

>CYP103A2 Agrobacterium tumefaciens

MITSSISGTDQQFQNATQPKELDPDAVPVSRLDSEGHEIFAEWR

PKRPFLRREDGVFLVLRADDIFLLGTDPRTRQIETELMLNRGVTRGAVFDLIRYSMLF

SNGEVHVKRRSAFAKTFAFRMIDALRPEITKLTEHLWDDVPRVDDFDFAEMYASKLPA

LTIASVLGLPFGDAPFFTRLVYNVSRCLSPSWGEDDFPEIEASAVELQDYVRAVVADR

SRRISDDFLSCYLKAVREEGTLSPIEEIMQLVFLILAGSDATRNAMVMLPTLLLQNPV

VWSSLCHDQSGVAAAVEEGLRFEPSVGSFPRLALEDIDLDGYVLPKGSFLALSIMSGL

RDERHYEHPQLFDIKRKQMRRHLGFGAGVHRCLGEALARIELQEGLRTLLRRAPSLRV

TGDWPRMIGHGGARRATGMTVNLGVDR

>CYP103A3 Agrobacterium tumefaciens plasmid pTiAB2/73 vir

MNARGPEKVSQTSGPIISASLDPDNVSVSDLDRSGHAIFAEWRP

KRPFLRRQDGVYVLLRADDVLGLSSDPRTRQIETELMLNRGINEGAVFDFVRYSMLFS

NNEVHSRRRSPFTRTFAFRMIENLRPQVSQLTETLFQDLKELDSFNFVEEFASKLPAV

AIAGLLGLPPSDIPYFTQLVYRVARCLSPSWRDADLPDIEASAAEFKNYVQAVIDDRR

SNPRDDFLSSFIRATREAEDLSPDEGLAQLMLIVLAGTDTTKTGLTALTGQLLRHRHV

WEALLKDESLVPAAVEEGLRFEPPVGSYPRLALADIDLEGFILPKGSLLALCTMSALR

DEKHFAHPELFDIHRKQMHWHMVFGAGAHRCLGEALARLELQEGLATVLRYAPTLSIE

GEWPTVQGHGGVRRIAEMRVGFRRQI

>CYP104A1 Agrobacterium tumefaciens

MEERRVSISSITWRFPMLFAPVDDVTTIDDLTLDPYPIYRRMRV

QNPVVHVASVRRTFLTKAFDTKMVKDDPSRFSSDDPSTPMKPAFQAHTLMRKDGTEHA

RERMAMARAFAPKAIADHWAPIYRDIVNEYLDRLPRGDTVDLFAEICGPVAARILAHI

LGICEASDVEIIRWSQRLIDGAGNFGWRSELFERSDEANAEMNCLFNDLVKKHRSAPN

PSAFATMLNAPDPIPLSQIYANIKIAIGGGVNEPRDALGTILYGLLTNPEQLEEVKRQ

QCWGQAFEEGLRWVAPIQASSRLVREDTEIRGFIVPKGDIVMTIQASANRDEDVFEDG

ESFNVFRPKSAHQSFGSGPHHCPGAQISRQTVGAIMLPILFDRFPDMILPHPELVQWR

GFGFRGPINLPVTLR

>CYP104A2 Agrobacterium tumefaciens

MQLAPVDRVTTIDDLTLDPYPIYRRMRAQTPVVRVASVMRTFLT

KASDTKMVKDQPRRFSSDDPNTPMKPAFQAHTLMRKDGAEHARERMAMAKAFAPKTTA

EHWAAIYRDIVNEYLDRLSRGSTVDLFAEICGPVAARILAHVLGISEASDAEMIRWSQ

RLIEGAGNFGWRPEPFERANEANAEMNRLFDNLVEKHRAEPNPSAFAIMVTASDPIPM

SQIYANIKIAVGGGINEPRDALGTIIYGLLTNPEQFEEVKRQQCWGQVFEEGVRWVAP

IQASSRLVLEDTEIRGFLVPKGDTVMTIQASANRDEDVFDDGERFNVFRQNNAHQSFG

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>CYP105A1 Streptomyces griseolus

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LYDGRQAWVVTKHEAARKLLGDPRLSSNRTDDNFPATSPRFEAVRESPQAFIGLDPPE

HGTRRRMTISEFTVKRIKGMRPEVEEVVHGFLDEMLAAGPTADLVSQFALPVPSMVIC

RLLGVPYADHEFFQDASKRLVQSTDAQSALTARNDLAGYLDGLITQFQTEPGAGLVGA

LVADQLANGEIDREELISTAMLLLIAGHETTASMTSLSVITLLDHPEQYAALRADRSL

VPGAVEELLRYLAIADIAGGRVATADIEVEGHLIRAGEGVIVVNSIANRDGTVYEDPD

ALDIHRSARHHLAFGFGVHQCLGQNLARLELEVILNALMDRVPTLRLAVPVEQLVLRP

GTTIQGVNELPVTW

>CYP105A2 Amycolata autotrophica

MTTDATDPRTTDAAPFPSNRSAPYRFSDGYAQLRDPPGPLRLGT

RYDGRQAWVVVIHEAARKLLASRFESADAHRTGFPFLTAGGRDMIGTNPTLFRMDDPE

HARLRRMTISHYTVKRIKTISEFVEEVVLVFLRRMTISGPTADLVSQFLIGAGHMVIC

RLLGVPYEDHAFFQERSRVLLTLRSTPEEVRAAQDELLQYLARLARTKRERPDDAIIS

RLVARGEILREEDISDAMLLLIAGHATDANLTSMSLYALADRSEQYAALRADRSLVPG

AVEDPLRYVAIADIATEDVPIRGRTIAAGNTQIAMGSSANLDHEYYEDPDALTARVED

LVHLAFGFGRHQCLGQNLARADQLREDLMTARNDPTLRLAVPVQSSARLEGTTIQGVN

ELPVTW

>CYP105A3 Streptomyces carbophilus

MTEMTEKATTFLTSQEAPAFPADRTCPYQLPTAYSRLRDEPDAL

RPVTLYDGRRAWVVTKHEAARRLLADPRLSSDRLHADFPATSPRFKAFRQGSPAFIGM

DPPEHGTRRRMTISEFTVKRIKGMRPDVERIVHGFIDDMLAAGPTADLVSQFALPVPS

MVICHMLGVPYADHEFFQDASKRLVQAVDADSAVAARDDFERYLDGLITKLESEPGTG

LLGKLVTHQLADGEIDRAELISTALLLLVAGHETTASMTSLSVITLLEHPDQHAALRA

DPSLVPGAVEELLRVLAIADIAGGRIATADIEIDGQLIRAGEGVIVTNSIANRDSSVF

ENPDRLDVHRSARHHLSFGYGVHQCLGQNLARLELEVILTVLFDRIPTLRLAVPVEQL

TLRPGTTIQGVNELPVTW

>CYP105B1 Streptomyces griseolus

MTTAERTAPPDALTVPASRAPGCPFDPAPDVTEAARTEPVTRAT

LWDGSSCWLVTRHQDVRAVLGDPRFSADAHRTGFPFLTAGGREIIGTNPTFLRMDDPE

HARLRRMLTADFIVKKVEAMRPEVQRLADDLVDRMTTGRTSADLVTEFALPLPSLVIC

LLLGVPYEDHAFFQERSRVLLTLRSTPEEVRAAQDELLEYLARLARTKRERPDDAIIS

RLVARGELDDTQIATMGRLLLVAGHETTANMTALSTLVLLRNPDQLARLRAEPALVKG

AVEELLRYLTIVHNGVPRIATEDVLIGGRTIAAGEGVLCMISSANRDAEVFPGGDDLD

VARDARRHVAFGFGVHQCLGQPLARVELQIAIETLLRRLPDLRLAVPHEEIPFRGDMA

IYGVHSLPIAW

>CYP105B2 Streptomyces tubercidicus strain R-922

MTTAERTEAERNTGSTGPSEDLAPLSPLAVPAARADGCPFDPAPGVERARREEPVTRATLWDGSTCWLVTRHQDVR

EVLGDPRFSADAARPGFPFLTAGGRVLATSKPTFIRQDDPEHARLRRMLTADFMVKKMEAMRPEVQRLADDLLDRM

TAGRNAADLVAEFALPLPSLVICLLLGVPYDDHEFFQDRSRLLLSLRSTAEEVRTAQADLQRYLSRLAAAKQREPD

DGIVSRLVARGELDFEEIASMGRLLLIAGHETTANMTALSTLALLRNPGQLARLREDPSLIKGAVEELLRYLTIVH

NGLPRVATEDVTLGGRTIRAGEGVLCTLNSANRDEDVFPGGDALDVGRDARRHVAFGFGVHQCLGQPLARVELQIA

VETLLRRLPDLRLGIPFEDVPFRHDMGIYGVHALPVAW

>CYP105B3 Saccharopolyspora erythraea NRRL23338

MTSTLDESTPDYPMPRARGCPFDPPPALRDLQRETPMARVRLWDGSTPWLVTRYADQRAV

LRDSHVSADMNHPTYPRQAPGGGTLSFIGMDDPEHARLRRMVGSAFAVKNVERMRPWVQR

IVDEAVDELLAGPRPADLVEEFALPVPSLVICGLLDVPYADHAFFQSNSKTMINRDSTPE

QRSQASGRLAEYLSDLLSSKMDTRGDDLRSRLCGRIEAGDLTLRQATEMAVLLLIAGHET

TANMIALSTLLLLRHPDQLALLRESDDPDVARRAVEEMLRYLNITHGGRRRVALEDVEVA

GQRVRAGEGLVLPNEIANRDPDAFPDPDRLDITREARHHVAFGFGVHQCLGQPLARLELE

IVYRTLYRRAPRLALAAGIEDIPFKHDGFVYGVYELPVTW

>CYP105B4 SBI\_7395 Streptomyces bingchengensis

59% to CYP105B3 Saccharopolyspora erythraea NRRL23338

VTGAAANTTSGTPLDTPEYNIDRSARCPLDPAPAMRARQAEGPLVRVRLW

DGTLAWLVTGWEEHRALMSDQRVSVDPFRPGAPKLSPGEVTAIDVLKKEG

KRSTGTSFILMDDPEHARLRRMVTSAFTIKRVEALRPPTQRITDDLIDTM

LAGPKPVDLVEALALPVPSLVISNLLGVPYDDHEFFQANSRTIINRETTA

AERAAARGRLVDYLDGLLGEKLAQPREDLLSGLAERIKTGELAREDATEM

GVLMLFAGHETTANMITLGTLALLQHPDQLALLRDTEDPKLIASAVDELL

RYLTITHGGQRRVALADIEIAGQVIRAGEGVIPVNEIANRDPSVFPDPDR

LDLRRDARRHVAFGFGIHQCLGQPLARMELQVVYPTLLRRIPTLALAADL

AEIPFKHDGFVYGAYRLPVTW

>CYP105C1 Streptomyces sp.

MTQAAPVTFSTVRENYFGPPAEMQALRHKAPVTRTAFADGRPGW

LVTGYSAARAVLSDSRFTARGEREHPAVPRAATLEDERCRRLIAGQFTARRMRQLTGR

TERIVREHLDAMEHMGSPADLVEHFALPVPSLVIAELLGVPPPDREHFQHDTLRWGGF

GRSTEEVTEAFVSLGGQLQRLVRLKRTEPGDDLLSGLIAADPALTDEELASIAFLLLV

AGHGTTAHQIALGAFLLLEHPDQLAALRADPALTESAVEELLRHLSVVHHGPTRAALQ

DADIEGTPVKAGEVVVVSLGAANRDPARFERPDAVDVTREDTGHLAFGHGMHQCLGRQ

LARIELRVALTALLERFPHLRLACPAAEIPLRHDMQVYGADRLPVAW

>CYP105D1 Streptomyces griseus

MTESTTDPARQNLDPTSPAPATSFPQDRGCPYHPPAGYAPLREG

RPLSRVTLFDGRPVWAVTGHALARRLLADPRLSTDRSHPDFPVPAERFAGAQRRRVAL

LGVDDPEHNTQRRMLIPTFSVKRIGALRPRIQETVDRLLDAMERQGPPAELVSAFALP

VPSMVICALLGVPYADHAFFEERSQRLLRGPGADDVNRARDELEEYLGALIDRKRAEP

GDGLLDELIHRDHPDGPVDREQLVAFAVILLIAGHETTANMISLGTFTLLSHPEQLAA

LRAGGTSTAVVVEELLRFLSIAEGLQRLATEDMEVDGATIRKGEGVVFSTSLINRDAD

VFPRAETLDWDRPARHHLAFGFGVHQCLGQNLARAELDIAMRTLFERLPGLRLAVPAH

EIRHKPGDTIQGLLDLPVAW

>CYP105D2 Streptomyces griseus

LLIAGHETTANMISLGTFTLLNHPEQLEALRSGRTTTAAVVEEL

LRFLSIAEGLQRLATEDIEVAGTTIREGEGVFFSTSLINRDTEVYENPETLDWDRPSR

HHLAFGFGVHQCLGQNL

>CYP105D2 SGR264 Streptomyces griseus

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>CYP105D3 Streptomyces sclerotialus

LLIAGHETTANMISLGTYTLLRHPDRLAELRADPGLAPAAVEEL

LRMLSIADGMLRVATEDIEAGGTVIRAGDGVIFGTSVINRDETVYTDPDALDWHRPAR

HHVAFGFGIHQCLGQNL

>CYP105D4 Streptomyces lividans

MTDTDTTTNTHPAAPVAFPQDRTCPYHPPAAYDPLRTARPLARI

TLFDGRPAWLVTGHAAARRLLADQRLSTDRTRDGFPATSARLAAVRERRTALLGVDDP

EHRAQRRMVLPEFTLKRAGALRPSIRRIVGERLDAMIAQGPPADLVTAFALPVPSMVI

CALLGVPYADHEFFEEQSRRLLRGPLPADTRDARDRLEAYLGELIDRKRRAPGEGLLD

DLVRRQASEGATDREQLIAFAVILLVAGHETTANMISLGTYTLLTNPGRLAELRADPA

LLPGAVEELMRVLSIADGLLRMATEDIDVDGQTIRAGDGVVFSTSVINRDESVYPEPD

ALDWHRPARHHVAFGFGIHQCLGQNLARAELEIALESLFDRLPTLRLAAPADEIPFKP

GDTIQGMLELPVAW

>CYP105D5 Streptomyces coelicolor

3343 MTDTDTTTNTDTTTNT

3295 HPAAPVAFPQDRTCPYHPPAAYDPLRAARPLARITLFDGRPAWLVTGHAAARRLLADQRL 3116

3115 STDRTRDGFPATSARLAAVRERRTALLGVDDPEHRAQRRMVLPEFTLKRAGALRPSIRRI 2936

2935 VGERLDAMIAQGPPADLVTAFALPVPSMVICALLGVPYADHEFFEEQSRRLLRGPLPADT 2756

2755 RDARDRLEAYLGELIDRKRRAPGEGLLDDLVRRQASEGATDREQLIAFAVILLVAGHETT 2576

2575 ANMISLGTYTLLTNPGRLAELRADPALLPGAVEELMRVLSIADGLLRMATEDIDVDGQTI 2396

2395 RAGDGVVFSTSVINRDESVYPEPDALDWHRPARHHVAFGFGIHQCLGQNLARAELEIALE 2216

2215 SLFDRLPTLRLAAPADEIPFKPGDTIQGMLELPVAW\* 2105

>CYP105D6 Streptomyces avermitilis

MNAALPMFERHDMTETEIRLTGSPAPSFPQDRTCPYQPPKAYEE

RRGESPLTQVTLFDGRPAWLITGHAEGRALLVDPRLSSDWGHPDFPVVVRRTEDRGGL

AFPLIGVDDPVHARQRRMLIPSFGVKRMNAIRPRLQSLVDRLLDDMLAKGPGADLVSA

FALPVPSVAICELLGVPYGDHDFFEECSRNFVGAATSAEADAAFGELYTYLHGLVGRK

QAEPEDGLLDELIARQLEEGDLDHDEVVMIALVLLVAGHETTVNAIALGALTLIQHPE

QIDVLLRDPGAVSGVVEELLRFTSVSDHIVRMAKEDIEVGGATIKAGDAVLVSITLMN

RDAKAYENPDIFDARRNARHHVGFGHGIHQCLGQNLARAELEIALGGLFARIPGLRLA

VPLDEVPIKAGHDAQGPIELPVVW

>CYP105D7 Streptomyces avermitilis

MEIGKSKSSPARSFMTEPGTSVSAPVAFPQDRTCPYDPPTAYDP

LREGRPLSRVSLYDGRSVWVVTGHAAARALLSDQRLSSDRTLPRFPATTERFEAVRTR

RVALLGVDDPEHRTQRRMLVPSFTLKRAAALRPRIQETVDGLLDAMEAQGPPAELVSA

FALPLPSMVICALLGVPYADHDFFESQSRRLLRGPGIAEVQDARAQLDDYLYALIDRK

RKEPGDGLLDDLIQEQLNRGTVDRAELVSLATLLLIAGHETTANMISLGTFTLLRHPE

QLAELRAEPGLMPAAVEELLRFLSIADGLLRVATEDIEVAGTTIRADEGVVFATSVIN

RDAAGFAEPDALDWHRSARHHVAFGFGIHQCLGQNLARAEMEIALGTLFERLPGLRLA

APADEIPFKPGDTIQGMLELPVTW

>CYP105D8 Streptomyces tubercidicus strain I-1529

VTEAISYFQDRTCPYHPPAGYQPLRETGPLTHVALYDGRKVWAVTGHSEARALLSDQRLSSDRQNPAFPMPFERFA

SIAQVRTPLIGVDDPEHNTQRRMLIPSFSVKRVAALRPDIHRIVDELLDRMLAEGPPAELVSTFALPVPSMVICSL

LGVPYSDHEFFEGESRRLLRSRTAEEAKQARIKLEEYFTDLIAHKEKNPGDGLLDELIEERLRTGTLAHEDLVRLV

MILLVAGHETTANMISLGTFTLLEHPEQLAQLKAEESLMPTAVEELLRFLSIADGMLRVAKEDIEIGGQLIRADDG

VLFPTSLINRDEATYPSPDELDLDRSARHHIAFGFGIHQCLGQNLARAEMEIALRSLFTRIPGLRLAVPAAEIPFK

PGDTLQGMIELPLAW

>CYP105D9 Streptomyces sp. JP95

MTDTLDEPQTLADGAEDAPAYPVKRTCPYRMPPGYEELREKGPI

SRVTLWNGRTAWLVTGNDLGRRLFPDARLSSDVLDPRFPLLAPRIEAQRQQAAAPPLV

GVDDPVHARQRRMVLPSFGIRQINALRPEIQKYADDLLDTMLAKGPGVTVDLLTEYAL

PMPSAVICMLLGVPYEDHHYFDERSRHVLSSSGEEQAAQAQQAFTEILAYLDDLIVRK

QAEPGDTLLDELIARQLEEGKVDRQELAMIATVLLVSGHETTSNMIALSTMALLADPD

QLAALRADESLMPRAVDELMRFSSIGDMLMRVAKEDIEIEGHLIRAGDGVILSTMLMN

RDPGAFERPDELDIRRPAGRHVAFGYGIHQCIGQNLARAEMEIALATLFRRVPTLKLA

VPAEQVPVNAPFVLQGVSELPVTW

>CYP105E1 Rhodococcus fascians

MAGTADLPLEMRRNGLNPTEELAQVRDRDGVIPVGELYGAPAFL

VCRYEDVRRIFADSNRFSNAHTPMFAIPSGGDVIEDELAAMRAGNLIGLDPPDHTRLR

HILAAEFSVHRLSRLQPRIAEIVDSALDGLEQAGQPADLMDRYALPVSLLVLCELLGV

PYADRDELRDRTARLLDLSASAEQRAVAQREDRRYMATLVTRAQEQPGDDLLGILARK

IGDNLSTDELISIISLIMLGGHETTASMIGLSVLALLHHPEQAAMMIEDPNCVNSGIE

ELLRWLSVAHSQPPRMAVTEVQIAGVTIPAGSFVIPSLLAANRDSNLTDRPDDLDITR

GVAGHLAFGHGVHFCLGHSLARMTLRTAVPAVLRRFPDLALSPSHDVRLRSASIVLGL

EELQLTW

>CYP105F1 Streptomyces lavendulae

MSDTEQHAPTLPRQRTCPFSPPPELEELRRTDPISRMRFADDSP

GWLLTRHADVRAALADPGVSSHPGKAPQPWRNLAPEMRAEHYLPGFLIFMDPPDHTRY

RRLLTKWFTMRAIRKLEPRIEQIVTETLDAMEAQGGTVDLVQSFALPIPLLVICELMG

IRYEEREEFMDMVLRLQALDATPEELGALGARMNEFMMKLAAAKRANPGDDLLSHLAH

DPDADPALTDLEIAGIGVLMLIAGHETSANMLGVGTYTLLENADQWALLRDDISLIDR

AVEELLRHQTIVQQGLPRGVTRDMEIAGHQVKTGESLLASLPAANRDPAVFPDPDRLD

ITREHNPHLAFGHGIHLCLGMELARVEMRQAWRGLVTRFPGLRMAAAPEDIRWRDDQI

VYGVYNLPVTWDEAK

>CYP105F2 Streptomyces peucetius

VSETDQRPPTLPRQRTCPFSPPPELEELRGTDPISRMRFADDSEGWLLTRHADVRAALAS

RSVSSHPGRTPQPWRNLAPEMRAEEYLPGFLIFMDPPNHSRYRRLLTKWFTMRAIRKLEP

RIEQIVSDALDAMEAEGGPVDLVQSFALPIPLLVICELMGIRYDDRVEFMDMVLRLQDLE

ATPEELGALGAKMNQFMIDLCAAKRKNPGDDLLSHLIQDPDAEPALTDLEVAGIGVLMLI

AGHETSANMLGIGTYTLLQNPGQWDLLRNDIGLIDQAVEELLRHQTIVQQGLPRGVTEDM

EIAGHAIKPGETLLASLPAANRDPEVFPDPDRLDITREHNPHLAFGHGIHLCLGMELARV

EMRCAWRGLVKRFPDLRMAARIEDIPWRDDQIVYGVYKLPVTWGDAP

>CYP105G1 Amycolatopsis mediterranei

MTTKVTENAPSTESLRSPLPPEFVRREDPFHVPPALVAVSERGP

VARATLAAGDPFWLVSGYEEARAVLSDPRFSSDRFQYHPRFKELSPEFAFPAPSLMIC

ELLGVRYEDRAEFQQRASALLQMNAPVAEAVKNADALRAFMQALVTDKRANPAGDIIS

GLIHHAGADPALTDDELINIANLLLIAGYDTTASMLGLGIFVLLQRPAQLATLRDDPS

RIADAVEGLLRYLSVVNPGIFRFAKEDLEFAGEHIPAGSTVVVSVVATNRDARHWPDP

DLDLTRPRGPHLAFGHGVHQCLGQQLARMEMQAGYAELLRRLPNVRLAVPPEEVPLRN

DMLTYGVHSLPIAWDAP

>CYP105H1 Streptomyces noursei ATCC 11455 nyst

MSTEADARTAAPQCPVAFPLRRPGRPFPPPEYATYRGGAGLVRS

ELPSGPVWLVTRHEDVRAVLTDPRISADPSKPGFPKAGRTGGAPSQYEVPGWFVAMDP

PEHGRFRKTLIPEFTVRKVRELRPVIQQIVDERIDAMLAAGTSADLVESFALPVPSLV

ISSLLGVPKVDRDFFEDRTRVLVRLSSTDEERDKATQALLRYLGRLIQIKQRRPGDDL

ISRLIAAGTLSRQELSGVAMLLLIAGHETTANNIGLGVVQLLTNPRWIGDDRIVEELL

RYYSVADLVAFRVAVEDVEIGGQLIRAGEGIVPLIAAANHDATAFAAPSEFDPERSAR

SHVAFGYGVHQCLGQNLVREEMDIAYRTLFARIPSLTLAVPVEELPLKYDGVLFGLHE

LPVTWK

>CYP105H2 Streptomyces albus

LLIAGHETTANNIGLGVVTLLSHPQWAGDERAVEELLRLHSVAD

MVALRVAVDDVEIAGQVIRKGEGIVPLLAAANHDTEVFGCPHAFDPERSERRHVAFGY

GVHQCLGQNL

>CYP105H3 Streptomyces natalensis

MTYTDPAAPETDPPAVDFPQRKPGVPFPPPDYADYRDRKGLVLS

QLSDGKRVWLVTRHEDVRAVLTSPSISSNPEHKGFPNVGNLGVPKQDQIPGWFVGMDS

PEHDRFRKALIPEFTVRRVRAMKPAIERTVDAQLDAMLAAGNTADLVADFALPIPSLV

ISALLGVPPADREFFESRTRVLVSLRSSTDDDRMAAAKDLLRYINRLVEIKQKWGGDD

LITRLLATGAIAPHEMSGVLMLLLIAGHETTANNIALGVVTLLANPQWIGDDRAVEET

LRFHSVADLVSLRVAVQDVEIAGQLIKAGEGIVPLVAAANHDENAFECPHAFDPSRSA

RHHVAFGYGVHQCLGQNLVRIEMEVAYRKLFERIPNLELAVPTDGLDIKYDGVLYGLN

ELPVRW

>CYP105H4 Streptomyces nodosus

MTAETEMTTFAPGCPVAFPLRRPGRPFPPPEYADYRAGEGLVRS

ELPASGPVWLVTRHEDVRTVLTDPRISADPSRPGFPRARRTGGAPSQSEIPGWFVALD

PPEHDRFRKTLIPEFTVRKVRELRPAIQQIVDERIDALLAAGNSADLIADFALSVPSL

VISDLLGVPKADRDFFEAKTKVLVTLSSTDEQRDEASKALLRYLNRLIQIKGRRPGED

LISRLLQAGTMNRQELSGVSMLLLIAGHETTANNIGLGVVQLLTNPQWIGDDRIVEEM

LRYYSVADLVSFRVAVEDVEIGGQLIKAGEGIVPLIAAANHDGSVFDKPEEFNPERSA

RSHVAFGYGVHQCLGQNLVRVEMEIAYRTLFERIPTLELAVPVEELPLKYDGVLFGLH

ELPVTWS

>CYP105H5 Streptomyces griseus

MTTSPGPTVVDFPRRTPREPLPLSQYAEHRKQNGLVQTHLPNGR

PIWLVTRHEDVRAVLTHPRISANPDNEGFPNVGETMGVPKQEQIPGWFVGLDSPEHDR

FRKVLIPEFTVRRVRELRPAIERTVDERIDAMLAGGNTADLVNDFALPVPSLVISALL

GVPSADRDFFESRTRTLVAIRTSTDEERAEATRQLLRYINRLIVIKKKWRGEDLISRL

LSTGKLSDEELSGVLLLLLIAGHETTANNIGLGVVTLLSHREWIGDDRLVEELLRLHS

VADMVALRVAVDDVEIAGQTIRKGEGIVPLLASANHDTEAFGCPHAFNPERTERRHVA

FGYGVHQCLGQNLVRVEMEIAYRKLFERIPELRLAVPEDQLAYKYDGILFGLHELPVR

W

>CYP105H6 SBI\_4165 Streptomyces bingchengensis

67% to CYP105H4 Streptomyces nodosus

VGSVKMATADAIPIEFPRRQPGRLTPPAEYAGLRSQEGLVKSSLPGGSTV

WLVPRHEDVRSVLTDPRISSNPLHEGFPSMGKNGTVPPPDQVPGWFVAYD

PPEHGRFRKALIPEFTVRRIKEMQPAIQRIVDRLIDALLDGGNSADLVAQ

FALPVPSLVICELLGVPYSDHEYFESRTRVLVTFTSTDEQRESAAKELIT

YLTKLISIKHKFPGNDLISGLLKNETLTAQEVSGIALLLLIAGHETTANN

IALGVVMLLLNREWIGDPRAVEEALRYLSVADRVALRVAVEDVEIGGQLI

KAGEGIVPLGAAANHDENAFERADQFDPGRPARHHVAFGYGVHQCLGQHL

VRAEMGTAYRTLFERIPTLRLAVPPEELPFKDEGILFGLHELPVTW

>CYP105J1 Amycolatopsis mediterranei rifamycin

MTETVAFPQDRTCPYQPAPGYEPLADRRPIAEVTLYDGRKAWAV

TGHELARKLLCDPRISSDRTNPAWPMVSAAAAVEFTDVQQKVIKLLTALVGVDGPAHR

ARRKLVQAGFTVKRIDSLRPKIQALVDRQIDEMIAEGAPVDLLKKFASPVPLIALCDL

LGIPHEDQDYFEKKAHQILFGPDAGGAYDELMAYLTKLIDKAEQNPGEEGFLQALLAE

RDPSSDVDHEEILQMFLIVLVTGHDTTSSSIGLGAFTLLQHPERLAELRADPSLMPAA

VDELTRFVVVPDGLQRVAADDIEVDADTTIRKGDGVFFLFSLINRDEEAYEDGDRLDW

HRPTFRDHLTYGFGTHQCAGMNHARAIMEIAFRRLIDRLPGLRLAVPADEVRVKPGDA

FQGLAELPVTW

>CYP105K1 Streptomyces tendae strain Tue901

MTETFGHDIPSFPMARECPMHPPAEYRKLRVQEPVSRVRMPDGQ

VAWLVLKHDLARKLLADPRVSADRLHPAFPGRLTAEQRTATERVRRLSTRRSMIHLDG

DEHGAHRKILTGEFSLRRIAALRPRVQEIVDRSIDEMLAAPQPADLVEHVSQAVPSLV

ICELLGVPHEQRRDFHEWAGMLVSRSVSIRERAAASDALNDFLEDLVTEKERGEPTDD

LIGRLIARNRRTPVMTHDEIVGTAVMLLIAGHQTTANMISLGVVALLENPEHKARIAA

DPSLLPPAIEEMLRYFSVVENAPARVATEDIEIGGVTIRKDEGIVVSGLAADWDDEVF

EHPDRLDFERGARHHVAFGYGVHQCLGQNLARVELEIVFETLLRRVPGLSLAVPAEEL

PYKDDAGIYGIYRVPVNC

>CYP105K2 Streptomyces ansochromogenes

MTEAFDHDIPSFPMARECPMHPPAEYRELRGQEPVSRVRMPDGQ

VAWLVLKHALARKLLADPRVSADRLHPAFPGRLTAEQRAATERVRRLTTRRSMIHLDG

DEHGAHRRILTGEFSLRRIAAQRPRVQEIVDRSIDEMLAAPQPADLVEHVSQAVPSLV

ICELLGVPHEQRRDFHEWAGMLVSRSVSIQERAAASDALNDFLEALVTEKERGEPADD

LIGRLIARNRQTPVMTHDEIVGTAVMLLVAGHQTTANMISLGVVALLENPEHKARIAA

DSSLLPPAIEEMLRYFSVVENAPARVATEDIAIGGVTIRKNEGIVVSGLAADWDDEVF

GHPDRLDFERGARHHVAFGYGVHQCLGQNLARVELEIVFETLLRRVPGLSLAVPAEEL

PYKDDAGIYGIYRVPVNC

>CYP105L1 Streptomyces fradiae

MSSSGDARPSQKGILLPAARANDTDEAAGRRSIAWPVARTCPFS

PPEQYAALRAEEPIARAELWDGAPVWLISRQDHVRALLADPRVSIHPAKLPRLSPSDG

EAEASRSLLTLDPPDHGALRGHFIPEFGLRRVRDVRPSVEQIVTGLLDDLTARGDEAD

LLADFALPMATQVICRLLDIPYEDRDYFQERTEQATRPAAGEEALEALLELRDYLDRL

ISGKTGRESGDGMLGSMVAQARGGGLSHADVLDNAVLLLAAGHETTASMVTMSVLVLL

QHPTAWRELTVNPGLLPGAVDELLRYLSIADGLRRSATADIEIDGHTIRAGDGLVFLL

AAANRDEAVFSEPEAFDIHRSARRHVAFGYGPHQCLGQNLARMELEVALGAVLERLPA

LRPTTDVAGLRLKSDSAVFGVYELPVAW

>CYP105L2 Micromonospora griseorubida

MDRTCAWALPEQYAEFRQRATGWPAKVWDGSPTWLVSRYEHVRA

LLVDPRVTVDPTRQPRLSEADGDGDGFRSMLMLDPPEHTRLRRMFISAFSVRQVETMR

PEIEKIVDGILDRLLALEPPVDILTHLALPMSTQVICHLLGVPYEDREFFQERSELAS

RPNDDRSMPALIELVEYLDGLVRTKTAHPDTGLLGTAVTERLLKGEITHQELVNNAVL

LLAAGHETSANQVTLSVLTLLRHPETAAELREQPELMPNAVDELLRYHSIADGLRRAA

TADIVLGDHTIRAGDGLIILLSSANHDGNTFGAEATFDIHRPARHHVAFGYGPHQCLG

QNLARLEMEVTLGKLFRRVPALRLAQEPDALRVRQGSPIFGIDELLVEW

>CYP105M1 Streptomyces clavuligerus clavulanic

MNEAAPQSDQVAPAYPMHRVCPVDPPPQLAGLRSQKAASRVTLW

DGSQVWLVTSHAGARAVLGDRRFTAVTSAPGFPMLTRTSQLVRANPESASFIRMDDPQ

HSRLRSMLTRDFLARRAEALRPAVRELLDEILGGLVKGERPVDLVAGLTIPVPSRVIT

LLFGAGDDRREFIEDRSAVLIDRGYTPEQVAKARDELDGYLRELVEERIENPGTDLIS

RLVIDQVRPGHLRVEEMVPMCRLLLVAGHGTTTSQASLSLLSLLTDPELAGRLTEDPA

LLPKAVEELLRFHSIVQNGLARAAVEDVQLDDVLIRAGEGVVLSLSAGNRDETVFPDP

DRVDVDRDARRHLAFGHGMHQCLGQWLARVELEEILAAVLRWMPGARLAVPFEELDFR

HEVSSYGLGALPVTW

>CYP105N1 Streptomyces coelicolor

MTPPESPTASHTPGATPPRDFPIQRGCPFAAPAEYAALRTDDPV

ARVTLPTRREAWVVTRYDDVRELLSDPRVSADIRRPGFPALGEGEQEAGARFRPFIRT

DAPEHTRYRRMLLPAFTVRRVRAMRPAVQARVDEILDGMLAAGGPVDLVSAYANAVST

SVICELLGIPRHDLEFFRDVTRISGSRNSTAEQVSEALGGLFGLLGGLVAERREEPRD

DLISKLVTDHLVPGNVTTEQLLSTLGITINAGRETTTSMIALSTLLLLDRPELPAELR

KDPDLMPAAVDELLRVLSVADSIPLRVAAEDIELSGRTVPADDGVIALLAGANHDPEQ

FDDPERVDFHRTDNHHVAFGYGVHQCVGQHLARLELEVALETLLRRVPTLRLAGERDQ

VVVKHDSATFGLEELMVTW

>CYP105N2 Streptomyces glaucescens cytochrome P450

LLIAGHETTTSMIALSTLLLLDRPELPAELRNDPDLMPAAVDEL

LRVLSVADSIPLRVAAEDIELSGRTVPADDGVIALLAGANHDPEQFDDPERVDFHRTD

NHHVAFGYGMHQCLGQNL

>CYP107N3 SP0881 91% to 107N1 AJ605544.1

VTGRATDPATEGSRCPFAAGEAPAYPFGSPDRLEPDPYWEPLRREQPLQRVTLPYGGEAW

LATRYQDVRKVFADRRFSRALAVAPGAPRFLPHQPPADAVLSVEGPDHARLRRLVGKVFT

PRRVEAMRPLIQSTADRLLDAMEEIGPPADLVEDFSLPFAVSMICELLGVPPEDRKRFCT

WSDALLTTTAHTPAQVRDHMMQMHDYLGGLVAQRRTRPTEDLIGSLVTARDAEDKLTEGE

LVRLAEAILIAGYETSASQIPNFLYVLFRNPHLLERLRNDHDLIPDAVEELLRYVPIGTV

DGFPRTATEDVELGGVLIRAGETVVPSMGAANRDPELFADPEELDLTRSPNPHLGFGAGP

HHCLGAQLARVELQITLTTLFRRYPRLRLAVPEESLAWKAGLMVRGMHTMPITW

>CYP105P1 Streptomyces avermitilis

MPEPTADAPTVPKARSCPFLPPDGIADIRAAAPVTRATFTSGHE

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AKEFTVRRMQALRPNIQRIVDEHLDAIEARGGPVDLVKTFANAVPSMVISDLFGVPVE

RRAEFQDIAEAMMRVDQDAAATEAAGMRLGGLLYQLVQERRANPGDDLISALITTEDP

DGVVDDMFLMNAAGTLLIAAHDTTACMIGLGTALLLDSPDQLALLREDPSLVGNAVEE

LLRYLTIGQFGGERVATRDVELGGVRIAKGEQVVAHVLAADFDPAFVEEPERFDITRR

PAPHLAFGFGAHQCIGQQLARIELQIVFETLFRRLPGLRLAKPVEELRFRHDMVFYGV

HELPVTW

>CYP105P2 Streptomyces peucetius

MSQPTAGAPAAPKARSCPFLPPDGIADIRAAAPVTRATFTSGHEAWLVTGYEQVRAVLRD

PSFSVGVPHALHTQDGVVTQKPGRGSLLWQDAPEHTDDRKLLAKEFTVRRMQALRPNIQR

IVDEHLDAIEARGGPVDLVKTFANPVPSMVISDLFGVPAERRAEFQEIAEAMMRVDQDAA

ATEAAGMRLGGLLYQLVQERRANPGDDLISALITTEDPDGVIDDMFLMNAAGTLLIAAHD

TTACMIGLGTALLLDRPDQLALLQKDPSLIGNAVEELLRYLTIGQFGAERVATQDGEIGG

VRIAKGEQVVTHLLSADFDPAFVEDPERFDITRRPAPHLAFGFGAHQCIGQQLARIELQI

VFGTLFRRFPTLRLAKPVEELRFRNDMVFYGVHELPVTW

>CYP105Q1 Streptomyces avermitilis

MADALAGRAPDATPPVAAYPMPRAVSCPLAPPPALQPLRDEQPI

TKVRIWNGSTPWLITRHADQRALLTDPRVSNDDRDPGFPYVNAHRAEIAHATPRLITN

TDAPEHTRLRRTVNAPFLIKRIEAMRPAVQRIVDGLIDDMLDGPNPADLLTALALPVP

SLVIAQLLGVPYADHEFFQRNSNLVLDNSVPAEEARAASGALAAYLDTLLAEKTAAPD

ADVLSEMGGRIKAGEMTHREAVHMGVAMLIAGHETTATMISLGTLALLEHPEQLAVLR

DAEDPKVIAAAVEELLRYLTIVHSGIRRVAKEDIEIGDRVIGAGDGLLFDLHAANWDS

EAFPEADRLDLSRPARHHQAFGYGPHQCLGQSLARLELQVVYGTLYRRFPTLRLAAPI

DRLAFHHTGTTYGVRCLPVTW

>CYP105Q2 Streptomyces sp.

LIAGHETTATMISLGTLALFEHPDQLAVLRDTEDPKVVAGAVDELLRYLSIVHSGLRRVA 182

183 KGDIEIDGRLIRKGDGLLFDLQTANWDPNAFPGAERLDLARPARQHNAFGFGTHQC 350

>CYP105Q3 Streptomyces sp.

MADTLTDAAPDTDGRVPEYPMPRATGCPLAPSPAAAELRGDRPITRVRIWNGSTPWLITR 318

319 HADQRTLLTDPRVSNDDHEPDFPHVNAHRAAIAPHTPKLITNTDAPEHTRLRRSVNAPFL 498

499 VKRIEAMRPAVQKIVDDLIDDMLAGPSPADLLTALALPVPSLVIAELLGVPYEDHHFFQE 678

679 NSNRVLDNSLTAEEAQESSRALGGYLDTLFRTKLEQPGEDVLSEMGSKVKAGEMTHQEAV 858

859 SMGVAMLIAGHETTATMISLGTLALFEHPDQLAVLRDTEDPKVVAGAVDELLRYLSIVHS 1038

1039 GLRRVAKGDIEIDGRLIRKGDGLLFDLQTANWDPNAFPGAERLDLARPARQHNAFGYGPH 1218

1219 QCLGQNLARLELQVVYGTLYRRVLTLRPAVPVDQLAFNHTGTTYGVKCLPVTW 1377

>CYP105Q4 Mycobacterium marinum MM4762

MSDTLASPSP ETASGIPDYP MSRSAGCPFA PPPGVMALAA AKPLTRVRIW DGSTPWLITG

YEQVRELFSD SRVSVDDRLP GFPHWNAGML STVHKRPRSV FTADGEEHTR FRRMLSKPFT

FKRVEALRPT IQQITDEHID AMLAGPQPAD LVAKLALPVP SLVISQLLGV PYEDAEMFQH

HANVGLARYA TGADTVKGAM SLHKYLAELV EAKMANPAED AVSDLAERVK AGELSVKEAA

QLGTGLLIAG HETTANMIGL GVLALLVNPD QAGILRDAQD PKIVANAVEE LLRYLSIIQN

GQRRVAHEDI HIGGETIRAG EGIIIDLAPA NWDAHAFTEP DRLYLHRAGA ERNVAFGYGR

HQCVGQQLAR AELQIVYRTL LQRIPTLTLA TALEDVPFKD DRLAYGVYEL PVTW\*

>CYP105Q4 Mycobacterium ulcerans

VSDTLASPSPETAAGIPDYPMSRSAGCPFAPPPGVMSLAAAKPLTRVRIWDGSAPWLITG

YEQVRELFSGSRVSVDDRVPGFPHWNAGMLSTVHKRPRSVFTADGEEHTRFRRMLSKPFT

FKRVEALRPTIQQITDEHIDAMLAGPQPADLVAKLALPVPSLVISQLLGVPYEDAEMFQH

HANVGLARYATGADTVKGAMSLHKYLAELVEAKMANPAEDAVSDLAERVKAGELSVKEAA

QLGTGLLIAGHETTANMIGLGVLALLVNPDQAGILRDAHDPKIVANAVEELLRYLSIIQN

GQRRVAHEDIHIGGETIRAGEGIIIDLAPANWDAHAFTEPDRLYLHRAGAERNVAFGYGR

HQCVGQQLARTELQIVYRTLLQRIPTLTLATALEDVPFKDDRLAYGVYELPVTW

>CYP105Q5 Streptomyces scabies SCAB11341

MAGTPTDAAS GTDGQLPEYP MPRAAACPLA PPPAAAGLRG EHPISRVRIW NGSTPWLITR

HADQRTLLTD PRVSNDDHEP DFPHVNAHRA AIAPHTPKLI TNTDAPEHTR LRRSVNAPFL

VKRIEAMRPA AQKIVDDLID EMLAGPNPAD LLTALALPVP SLVIAELLGV PYEDHRFFQE

NSNRVLDNSL TAEEAQESSR ALGGYLDTLF RTKLEQPGDD VLSEMGAKVR AGEMTHQEAV

SMGVAMLIAG HETTATMISL GTLALFEHPD QLAVLRDTEE PRVVAGAVDE LLRYLSIVHS

GLRRVAKDDI EIDGRVIRKG DGLLFDLQTA NWDPNAFPEA ERLDLGRPAR QHNAFGHGPH

QCLGQNLARL ELQVVYGTLY RRVPTLRPAV PVDRLAFHHT GTTYGVTCLP VAW

>CYP105Q6 Mycobacterium vanbaalenii PYR-1

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>CYP105Q7 Mycobacterium smegmatis

MSETLTQPSATDIPGYPMERAAACPFAPPPQMLDMNKAKGLSRVRIWDGS

TPWLITGHEEARALFADSRVSVDDRRPGFPHWNEHMLATVHKRPRSVFTS

DAEEHTRFRRMLSKPFTFRRVEGLRPAIQKITDECIDAILAGPQPADIVD

KLALPVPTVVISEMLGVPYEDHEFFQEHANAGLARYAAADAMQKGAMSLH

QYLIDLIEKKQAEPAEDAVSDLAERVTAGELSVKEAAQLGTGLLIAGHET

TANMIGIGILALLENPEQADFLRNAEDPKVIANAVEELMRYLSIIQTGQR

RVAVEDIEIGGETIKAGEGIIIDLVPANWDAKAFPEPDKLDLTRDAGQQL

GFGYGRHQCVGQQLARAELQIVFHTLLRRIPTLRLAIPLEEVPFKHDRLA

YGVYELPVAW

>CYP105R1 Streptomyces avermitilis

MTQTAAVTTAWPLHRTCPMSQPPALAAFRDGPPRQVLLRGDQPA

WLITRYADVRQALADPRLSVNDQHPNWPNRLLFPVPPRAVSFWRMDPPEHGAYRKMVA

AEFIAHRTQALRPLLQSITDELLDEMAAMPKPVDFHSVFALPLPCIAIARIFGVPDED

MSEFKENTSALLNQKEPEKAVQAFLATTAYLDGLARAKEREPKDDLLSRLVVNFVRPG

QLSHDDLVAMVRLMLVAGHETTANQIALSIFTLLDRPGVLAELRADPRLLTPVVDELL

RYWSIAQDNVVRTATEDLSVGDARIAAGDAVVISVPGANHDEAVFPDAADFDIHRDNS

RHLAFGHGPHFCPGGPLARTELEIAITSVFRRFPDLRLAIGRDQVPVHTDTLVYGLEC

LPVTW

>CYP105S1 Mycobacterium smegmatis

MTQAQALPPLHIRRDAFDPTPELGEIRAGEGVHVTVNPFGMQVYLVTRHE

DVKTVLSDHERFSNSRPPGFVLPGAPQISAEEQASNRAGNLLGLDPPEHQ

RLRRMLTPEFTIRRIKRLEPRIVEIVDAHLDAMESAGPPADIVADFALPI

PSLVICELLGVPYEDRTDFQQRSARQLDLSAPMPERLELQRQGRAYMRGL

VERSRTRPGDDILGMLVREHGTELTDDELIGIAGLLLLAGHETTSNMLGL

GVLALLRHPDQLACVRDDPDAVGPAIEELLRWLSIVSTALPRITTTDVEL

AGVTIPAGHLVFASLPAGNRDPEFIDDPDTLDIRRGAPGHLAFGHGVHHC

LGAPLARMEMRIALPALLRRFPTLALAEPFEDVRWRPFHFIYGLQSLAVAW

>CYP105S2 Mycobacterium vanbaalenii PYR-1

MSQAVRPELPPVHMRRDGFDPTPQLREIRETEGVRVITSAFGMSAYLVTRHEDVKTVLSDHTRFSNTRPP GFVVPGAPPIDEDEQARSRAGNLLGLDPPEHQRLRRMLTPEFTLRRMRRLQPRIAEIVDAQLDALAAARD GEASADLVQHFALPIPSLVICELLGVPYADRDDFQRRSARQLDLSIPIPERIELAREGRAYMGSLVAGAR TNPGDDILGMLVREHGAELTDDELVGIAGLLLLAGHETTSNMLALGTLALLRHPEQLAAVREDPDAVAPA VEELLRWLSIVHTAIPRITTTDVEIAGVSIPAGQLVFASLPSGNRDDEFIERPEVFDITRGAMGHLAFGH GVHHCLGAPLARMEMQIAFPALLRRFPTLAPAGEFDDVPFRSFHFIYGLKSLEVTW

>CYP105S3 Frankia alni ACN14a

MRRAQFDPISELSTARDTVGVCPVVTPFGVPAHLVSRYDDVREVLSDSVRFSTADRHALMPPDAAGPTEQ

EYAQARVGNLLAYDPPEHTRLRRMLTPEFTMRRMRALEPRIVDIVSAALDDVERAGRPADLVSTFALPVP

SLVICELLGVPYADRAEFQRRTVDQLDASHPPEHRLALQQASRAYMATLVERARRDPGEDILGMLVREHG

DDISAEELVGIASLLLLAGHETTANMLGLGTLALLRHPDQLARVRDDPASVEPAVEELLRWLSIVHAGIP

RTATTEVTIAGSTIAAGEHVVLALPGANRDPALVDDPDRLDITREPAGHVAFGHGLHHCLGAPLARLELR

IAYPALLRRFPGLALAVPYEQIAFRPYSVIHGLQALPVTW

>CYP105S4 Frankia sp. CcI3

MAAAPIVPLHIRRAQFDPIEELVRIRDTDGVCRVVTVFGIPAYLVSRYEDVREILADPGRFSNVNQWVVG

PGGPVLSDEEIAELRAGQMLAFDPPDHTRLRRMLTPEFTVRRMRGLEPRIRDIVDAALDEVERAGRPADL

VATFALPVPSLVICELLGVPYSDRAEFQQRTRRQIDASLPIEQRLALQREARAYMAGLVTRAQAAPGEDL

LGMLVREHGDELSTAELVGIASLLLVAGHETTSNMLALGTLALLRHPDQLAMVRDDPAQVEPAVEELLRW

LSIVPSGVPRTTTTEVEIAGHRIPAGEQLLLALPAANRDPALVGDPDRLDITRGAPGHVAFGHGVHHCLG

APLARMEMRIAFPALLRRFPDLALAVPYEQVAFRAHHVVHGLHALPVTW

>CYP105T1 Burkholderia fungorum

MRKTMTSAINDVRPQTTSTFPFARTGSPLHPPAEYARYRDGQPV

TRVQMWDGRYAWIFTRMEDVKAVLSSPHFSVVPSKPGYPFLTPARAATVKSYQTFITM

DPPDHTRFRRMLTRDFTQKRMEELRPQIAAYVNRLIDEMLARGSPGDLVSALALKLPV

TVVSMLVGVPYEDHEDLVKWSGQRLDLEQNPTVSESAADNMLAYFDGLLQRKERDPGD

GADMLSRLVIEQIKPGHLSRLEAIHMVNLLYFAGHETTANQIALGTLSFLLDPRQRAL

LENNPGLLKNAIEEMLRFHTISHYNSCRVATADVEVGGTLIREGEGAYALIMAANRDP

AAFPAPDRFDIERPNSQEHVAFSYGLHMCLGQPLARLELQVCFEALFRRLPRLRLAVP

LEELPFKREMYVYGLHALPVTW

>CYP105U1 Streptomyces hygroscopicus strain NRRL 3602

MDEIRDYPESRAAACPFSPPLGYEELRERSAVTRVRMWDGSTPF

LVTGYHEARAALGDSRFSADGTHKAMPRFVKFEVPAEVFNLGRMDDPEHARIRRMLTA

NFTIRRTEAMRPMIQGIVDGLLDRLIAQGPPADLVADFAFPLPSQVIGVMLGVSDADF

AEFQQASQGVMDFTASAEEMGAALGVMVDYVARMCAAKRADPGDDLLSRLIVDQELTG

GLTQQQVVATALVLLLAGHETTANMIALSTVLLLSHPEQLARLRADAGLMGNAVDELL

RYITIVQEGTGRVATEDVEVGGVLIPGGEGVIINLPSANRDPHFADAHELDLSRPNAR

EHVAFGFGVHQCLGQTLARVELQIALETLLRRLPTLRLEVPFDDLAFLYESMNFGVAR

VPVAW

>CYP105V1 Streptomyces sp. HK803

MSQLSSELPAFPMSKAKGCPLDPPPEYAQLRSDRPVAKARLWDG

KEVWLITGYDEIRSIFTDPRISVDNTQPGYPWLSEQARTVVLTGGVKPVGRMDPPEHT

AMRRMLGQGFLVKKIQNMRGDVEALVNELIDDILAGPRPTDLVPSLAMPVPSTALGWV

LGVPPADKRLISLVPRLFDEDSGLEGAMEARAELFAYIDELITHRENQPGDDIISHLV

GYYQKGELSRVSVLTQSVTLIAAALDTTRSMITNGILALLQHPEQAAALIEDPDLVPA

AVEELLRYTVVTEFSSKRVAAADIEIAGETIKAGDGIICLISAGNRDEKVFTDPDTLD

VRRDAKQHLGFGAGIHTCIGKQLARMELEVVYGTLFRRIPELRLAVPFDQLVFRNTFD

VQGVRALPVTW

>CYP105W1 Micromonospora echinospora

MPRRCPFGPPAEYARLRTERPVARLPMLGGNTAWVVSRYADVKR

VLSDPRMSADRRRAGFPRFAPTTESQRQASFANFRPPLNWMDPPEHTAARRQIVDEFA

ARRVRQLRPLVERVVDEHLDAMTAGRSSADLVPSFSYPVPSRVICEMLGVPYGEHAFF

ERRSTRMLSRGVPADERARCAREIREFLDGVVTDKERHPGDDVLSRLLAAQRAAGEPD

HEAVVSMAFVLLVAGHVTTSNMISLSVLALLTHPERLARLRAEPDRFPAAVEELLRYF

TIVEAATARTATADVTVGGVTIRAGEGVVALGQAANRDPAAFDRPDEFDPDRDARHHL

AFGYGRHICPGQHLARLELDVALSRLVRRLPGLRLTVDVDDLPLKEDGNIFGLHALPVAW

>CYP105X1 Pseudonocardia autotrophica same as Amycolata

MAEDTLGQDFPMQRQCPFEPPKEYERLRAEQPISRVRMPDGTPA

WLVTLHEDVRTVLASPAFSSDLAHPGMPAVNPEIRTIARQQRPPFSRMDPPEHSFFRR

MLIPEFTVKRTKTLRAGIQSVVDGLIDDLLRKSPPVDLVDEFALPVPSLVICQLLGVP

YSRHEFFQQQARVILSRQSTREQVGAAFTALRAYLDTLVEEKLHTPGDDLTSRLATEH

LEPTGDVRRQDLVASCMLLLTAGHETTSHMISLGVTALLEHPDQLAALQNDLTLLPEA

VEELVRYLSIADYVPSRVALEDVVIGGTVIRAGEGVVPLLAAADWDPKVFDNPGTLDI

HRGNRRHACFGYGVHQCIGQHLARTELEVAFSTLFTRIPTLQIAAPSDELDYDHDGML

FGLHELPVTW

>CYP105X2 Amycolata autotrophica same as Pseudonocardia

LLIAGHETTSHMISLGVTALLERPDQLAALQNDLTLLPEAVEEL

LRYLSIADYVPSRVALEDVVIGGTVIRAGEGVVPLLAAADWDPKVFDNPGTLDIHRGN

RRHVAFGYGVHQCLGQNL

>CYP105X3 Micromonospora inyoensis

LLIAGHETTSHMISLGVTALLEHPDQLAALQNDLTLLPEAVEEL

LRYLSIADYVPSRVALEDVVIGGTVIRAGEGVVPLLAAADWDPKVFDNPGTLDIHRGN

RRHVAFGYGVHQCLGQNL

>CYP105Z1 Streptomyces scabies SCAB17851

MTTHPPHPPL PTLRPLLDPS PEYAKWRTEE PIRRVTIWGD NSPWLITRHE DARVVLADPR

FSADATRDGF PGFRPQSPPR GPGQFFMMDP PDHTRLRRVL IPDFTFRRIE QLRPAIARIC

GELLDAMTAD DATAADLVEA YALPLPSLAI CELLGVPYED HDFFQRQANA FSSFSSGPEE

MMAARTALHT YLGDLLARRG REPADDLLTR LARDRVATGE ISAPEAVGIA SLLLVAGHET

TANMFPLAVL DLLRHPAQLA ALRADPALWP GAVEELLRHL TVTHAGLRRI ATEDVVVSGV

RIRAGEGVIV ALQAANRDPS AFTAPDTLDV RRTTTGHLAF GHGLHQCIGQ SLARAELQVG

LPALFDRLPG LRTAGEPEDF TPAISAVHGV RSLPVSW

>CYP105AA1 Streptomyces tubercidicus strain R-922

MTGRSACGSGARSAPSVRTPASPPVGPSAAPVTPVTPSQPLTLL

EKDCPMTAMQPTARTQPMERTCPFSPPEGYRTLREEDPITQVTFPDGAKGWLVSRYSD

VRAVLADPRFGANGQQPPLPGMFLTMDPPEHTRFRRLLTGQFTVRRMRKLAPAVEQIV

AERLAEMAAAEGPVDLVQAFALPVPSLVICELLGVPYADREEFQENSSRMLRLDASQE

QFEQAQMAMYERIHQLVVAKRAHPTDDILSGLVQSGVLTDEEVTGVGVLLLIAGHETT

ANMIALGTMCLLGHPGQLASLRADPELMDDAVEELLRYLTIVQYGLRRMALEDVELGG

QRIKAGSVVVAALPSGNRDATHFSGDPETLDVRRPYSPHLAFGHGVHQCIGQQLARVE

MKAALSALIDRFPGLRLAVPAREVPMRDDMLIYGVHELPVTW

>CYP105AA2 Streptomyces tubercidicus strain I-1529

MTRTVPGPQALPTERDAGPFAPPRDISRMREARPVSPMVFPDGH

EGWIVTGYDAVRRLMADTRFSSRQDIGILHVPYETPGMPAPTEPSPQIPGLFIAMDPP

DHTRLRRKLTGAFTVKRMKQLEEHISDIVERQLDELTRLAPPVDLVKEFALPVPSLVI

CALLGVPYADRETFQVNSAKFLEKDVSLDEKMAAYTGLTTYLSELVTRKRAAPGEDIL

SDLARHDDLTIEELTGMAFLLLLAGHETTANMLALGTFALLEHPEQLAELRADPDLMP

GAVEELLRYLSIADIFYRYATEDIELGGETIGKGSTVVVSLLAANHDPQRFDNPDTLD

IHRTARGHLSFGHGIHQCLGQQLARIEMRAGFEGLLRRFPTLELAIPADEVKLKTDMN

IYGVHELPVTWTDTAR

>CYP105AA3 = old CYP105Y1 Rhodococcus sp. RHA1 Rha04313

MSKTVAVPYGLPMERDAGPFDPPRRITRLRETRPVSPMVFPDGHEGWLVTGYDAVRQLMADTRFSSRQDIGILHVPYETPGMPAATEPSPQMPGVFIAMDPPDHTRMRRKLAGAFTVKRMKQLEDHIIDVAERQLDAMARLTPPVDLVKEFALPVPSLVICELLGVPYADRDNFQVNSAKFLIKDQPLDDKMAAYGALSTYLADLVTRKRAAPGDDILSDLARDDDLTIEELTGAAFLLLLAGHETTANMLALGAFALLENPEQLTELRTDPDLLPDAVEELLRYLSVADIFYRYATEDIELGGETIRAGSTVVVSLLAANRDPQRFDNPDTLDIRRKARGHLSLGHGVHLCLGQQLARLEMRAGFEGLLRRFPTLGLAIPAGDVKLRTDMNIYGVHELPVTWTETSR

>CYP105AA4 Amycolatopsis azurea GenPept BAD91667 80% to CYP105AA2

1 MTETVPVPQG LPMQRDAGPF APPSEITRLR GARPVSPMVF PDGHEGWLVT GYDEVRQMMA 61 DTRFSSRQDL GILHLPYETP GMPAPTEPSP PMPGMFVAMV PPDHGRLRKR LTGAFTVKRM 121 KQLEEHIVEI TEQHLDAMTK LVPPVDLVKE FALPVPSLVI CELLGVPYED RENFQANSAQ 181 LMVRDQTLEE KMAAFIGMNT FLTELVTRKR ETPGDDILSD LGRYDDLTIE ELAGAAFLLL 241 LAGHETTANM LALGTFALLE HPEQLAELRA DAELLPAAVE ELLRYLSVAD IFFRYATEDL 301 ELGGETIRAG STVIVSLLAA NRDPRRFENP DTLDLHRNAR GLLSFGHGVH QCLGQQLSRI 361 EMRAGFEGLL RRFPTLSLAV PADEVKLKTD MNIYGVHELP VTW

>CYP105AA5 Streptomyces lydicus GenPept BAG50414.1 79% to CYP105AA4

1 MSRTVPVPQG LPMERDAGPF DPPRDLTRLR EARPVSPLLF PDGHEGWLVT GYEAVRRLMA 61 DTRFSSRQDI GVLHVPYETP GMPVATEPSP QVPGLFIAMD PPDHTRLRRR LTGAFTVKRM 121 KMLEEHIHDI VERQLDAMAR LAPPVDLVKE FALPVPSLVI CEMLGVPYED RETFQVNSAK 181 FLVKDQPLDE KMAAYGALTT YLAELVTRKR ATPGEDILSD LARQDDLTVE ELTGIAFLLL 241 LAGHETTANM LALGTFALLE HPGQLAELRA HPELLPGAVE ELMRYLSVAD IFYRYATEDI 301 ELGGETIGKG STVVVSLLAA NRDPLRFDNP DALDVRRAAR GHLSFGHGVH QCLGQQLARI 361 EMRAGFDGLL RRFPTLELAL PADEVRLRTD MNIYGVHELP VTW

>CYP105AA6 Rhodococcus opacus B4 GenPept BAH51173.1 78% to CYP105AA4

1 MTVKQTHTVS VPHGLPMERD AGPFDPPGDI TRLRDARPVS PLIFPDGHEG WLVTGYDAVR 61 QLLADTRFSS RSDLGIVHVP YETPGMPAAT EPSPQVPGLF IAMDPPDHTR LRRKLTGAFT 121 VRRMKQLEEH IADIVERQLD EMARLTPPVD LVQEFALPVP SLVICELLGV PYADRDTFQV 181 NTAKFLVKDQ ALDEKMAAYG ALTTYLAELV ALKRVTPGED ILSDLARDDD LTIEELIGIA 241 FLLLLAGHET TANMLALGAF ALLEHPEQLA ELRADPELMP NAVEELMRYL AVADIFYRYA 301 TEDIELGGET IGQGSTVVVS LLAANRDPRH FDNPDTLDLH RKARGHLSFG HGVHLCLGQQ 361 LARLEMRAGF AGLLRRFPAL ELAVPAGEVK LKTDMNIYGV HSLPVCLQPV STY

>CYP105AA7 Actinosynnema mirum DSM 43827 GenPept EEH76286.1 69% to CYP105AA4

1 MDLTSPIPIP DGLPQERDAG PFAPTTFVAD LRARRPVCPL VFPDGHVGWL VTGHAAVRQV 61 LADTRFSSRL DLGVLHVPHP TPGMPQATEP SPQVPGLFVA MDPPDHTRLR RKLTGAFTVK 121 RMRALEERVA QVVEERLTAM AALTPPVDLV REFALPVPSL VICELLGVPY ADREVFQANT 181 ARFLVKDVEL AEKAAAYGAL TGYLAGLVAS KRAEPGEDVL SDLARHEDLT VEELTGCAFL 241 LLLAGHETTA NMVALGTFAL LEHPDQLAAL RAEPGLLGGA VEELTRYLSV GDLFYRYATE 301 DLELHGELIP AGSTVVLSLL AANHDPEAFE DAGALDVRRD ARGLVAFGHG VHQCLGQQLA 361 RVEMRAGFAG LLRRFPDLAL AVPAGEVPLK TDMNVYGVHA LPVTWGTAAG

>CYP105AB1 Saccharopolyspora erythraea NRRL23338

LRSQEPVKRVRTIGGGTAWLVTRHEDVRRVLSDPRMSSDRTMPGFPSLVPGRRAIVAENK

QAMIGMDGQEHAEARRAVIGEFTVRRINRMRPRIQEIVDECVDRMLAAGGPVDLVRELSL

PVPSLVICELLGVPYSDHDFFQSRSALMISRSTPPERRRDVVLELRRYLDELVAEKVREP

ADDLLGRQVAQQSEKGEVDREGLVSLAFLLLIAGHETTANMISLGTLALLDNPDQLARIT

EDPARTPAAVEELLRYFSIVDGATSRTALADIEIGGVLIREGEGVVAVGLSANRDPEAFD

SPDELDLDRQARNHVAFGFGAHQCLGQNLARVELQIVFDTLFRRIPGLRLADGLDGIRFK

DDALVYGAHEMSVTW

>CYP105AB2 Salinispora tropica (marine actinomycete)

MTETASIATTRTASGQLTDAEFPVQRGCPFTTPTEYEQIREESSIAKVRLKNGGEAWWIA

GHELGRSVLADRRFSSDRRRDNFPFVSTDPETRAQLQSQPTSMLGMDGAEHAQTRRALMG

EFTVRRMAGLRPRIQQIVDQHIDEMLATPQRSVDLVEALSLPVPSLVICELLGVPYADHD

FFQGLTGPLLRHTTPPEVRLRIQEELNTYLGTLIDRKLTDPTDDLLSRQIAKHRDNGTFD

RASMVSLAFLLLVAGHETTANMISLGVVGLLQHPDQLVIIKDDPDKTPLAVEELLRYFTI

ADSVTARVATEDVQLGDTTINAGDGVVISGLAADRDPTVFAEPDRLDLERGARHHVAFGF

GPHQCIGQTLARMELRIVFDTLFHRIPTLRLAAPLDDIPFKSDAFVYGIEELPVAW

>CYP105AB3 Nonomuraea recticatena AB180844 Gene name moxA

64% to CYP105AB2 Salinispora tropica (marine actinomycete)

MTKNVADELAGLELPVERGCPFAPPAAYERLRERAPINKVRLTS GGQAWWVSGHEEARAVLADGRFSSDKRKDGFPLFTLDAATLQQLRSQPPLMLGMDGAE HSAARRPVIGEFTVKRLAALRPRIQDIVDHFIDDMLATDQRPVDLVQALSLPVPSLVI CELLGVPYTDHDFFQSRTTMMVSRTSMEDRRRAFAELRAYIDDLITRKESEPGDDLFS RQIARQRQEGTLDHAGLVSLAFLLLTAGHETTANMISLGVVGLLSHPEQLTVVKANPG RTPMAVEELLRYFTIADGVTSRLATEDVEIGGVSIKAGEGVIVSMLSANWDPAVFKDP AVLDVERGARHHLAFGFGPHQCLGQNLARMELQIVFDTLFRRIPSLRLAVPMEDVPFK GDSVIYGVHELPVTW

>CYP105AC1 Saccharopolyspora erythraea NRRL23338

MQKHAPHNADDVLESLPRDRPSGCPFDPPEGLAEIRGQRPLTRLVYGDGHVGWLATGHAV

VRAVLADRRFSSRYELMHFPVAMPGLPAQIPPAQVGDITGIDPPEHTRYRKLLTGKFTVR

RMRALTERVEQITAERLDAMQRLGPPVDLVEAYAQPIPALMICELLGVPYDRLEEFLGLV

AASGDRDLTPEEQFDAFAKIQEFVRELVPAKRAKPTDDLLSDLTTTELTDQELAGIGGLL

LAAGLDTTANILALGTFALLRNPEQIAALREGDADRAVEELLRYLSIAHTGMRSALEDVE

IDGTLIRAGETVTLSIQAANRDPRRFTDPDALDLRRHAAGHLSFGHGIHQCLGQQLARVE

MRVAFPALFNRFPGLRLAVAPEEVPLRGDMNIYGVHGLPVTWDGA

>CYP105AD1 Frankia alni ACN14a

MTQAPQYPQTRTCPYEPPPAYKEIGQEGPVVKVSLFDGRESWMVTGYRESREILTHPNLSSLRTHPNFPI

VAPRFRSPVARSLALLAMDPPIHDVYRRYLNPHFSLRSVRAMRPELERIIAGYVDRIIDHGPPADLIEML

AVPMPSLIICHHLGVPYADHDFFQDCSGKVMLAGEEEAGKAAQDLVEYLDNLVTEQQRNPTDGLIGQLVR

ERVSDGDIGHDELVSIALVLLIAAHETTASTLAIGIINLLGHPEELAKLRADISLLPGAIEELLRYVATT

DLVAVRIAKGDIEIAGHHIREGEPVLVSGTLANRDPQVHQRADEFDIQRDDTFHLTFGFGIHQCLGQNLA

RLEIELALRELITRLPGLRLAVPMEELPILSAGTVQRVLELPVEW

>CYP105AE1 Frankia alni ACN14a

MNRVTLFDGATAWLVTGHSHSRRLLADPRVSADRSRPDFPVVLPRFEADVFKPLAIIGFDPPQHGLQRGL

LTADFSMRSVRAKRESIERLVESLADRMLAAGPPADLVLDYSLPIPSMVVADLLGVPYADHQFFEDATVR

LLQATTPQGAEAAGEELLNYLDEQIRLRERDPDDTLLSRLGEHVHDEGLGRDIINKIALALLVGGHDTTS

QMIALGVVTLLDHPDQLAILRSDPSALPGVVEELLRMVSVTDLAGVRVATEDVEIDGQVIARGEGLIFCN

SMANRDPAVYDAPYEFDVRRSADDPPATRRHLTFGHGPHQCIGRNLARMELEIAYRVLFEKIPNLRLAVP

RDELPMRHGSTMQGVHRLPVTW

>CYP105AF1 Frankia sp. EAN1pec

MSSNQAVVATPPAFPMDRGCPYHPPAGYAQLQQDGPITRATLFDGREVWVVTGYEEARRLLVDPRLSSDR

SRPDFPVLVPRMAAAKLVALVGMDPPEHDIQRRMLIGSFTVRRANALRPDIERIVGGRVDALLAHEPGEV

VDLVPEFALPIPSTVICELLGVPYGDHEFFEEQTRRMVIATSTAAEAAAASRALVDYFDELIARKRERPG

EGLLDELIAERLVTGQIGQDDLASMAMFLLVAGHETTANMLGLSVLALLEHPDQRARLIEDPAGRAAGAT

EELLRFLSVADEIQRIAAADIEVAGVVIRAGDGVYLPTAAANRTAATFPDPDALDIGRVPRGHLAFGYGI

HQCIGQNLARVELEIGLRELFGRIPTLRLAEPVEALGAKPGGSVQGVYRLPVVW

>CYP105AF2 Frankia sp. EAN1pec

MTGTEIPEYPLARTCPFHPPAGYARYREHGPVNPVRLYDGRRVWAVTGHAEAREVLLNTRLFSSERADPR

YPATSPRFEAARKVRNFIGMDPPDHTAQRRMLQSSFTMRRINGLRPGIQRLVDELLDAIVAKGPVVDLVP

EFALPIPSIVISELLGVPYGDHAFFEQQSRRVASGTSTLEESADAFTQLLQYLDGLIQDKERSAGDGLLD

VLIAEQVRPGVLTRRELVDISLLLLVAGHETTASAIALGVVALLEHPDQLAALRADPALLPSAVEELLRF

TTIADSVARFATADTELAGQPVAAGDGVLVVLSAANRDGTVFPDPDLLDLARRARSHVAFGHGAHQCIGH

NIARAELEIAFSTLFARLPGLRLAVPLDRLPGKDAGGVQGVFELPVAW

>CYP105AG1 Frankia alni ACN14a

MTTRHLIDQPISRDLAHPLDPPAAYTELRENQPVVRARFPNGSTGWLVTRFEEGSQVFSDPRFSAKRRRH

DTPEGEQAEAGDDAPFDAGFVMMDEPDHGVYRRLLTARFTPKAVQTRLQPYLDRIVAEHLDAIAAGPETF

DFVQALSLPIPCLVICELLGVPYADRDGFHHATEVMMDTGVSRAERDRGAHWLVDYITALVADKRRTGDT

EGILAELIGKADDEGSILSERQLVGLGVLLLFAGHDTTAAMMGLSTLTLLTHPEQRRDLTEHPERIGTAV

EELMRYLTIVQFGLGRVAAQDVELGGAHIGRGELVVVAMNAANRDPRVFADPDALDLDRTMVRHLGFGYG

VHACLGQNVARAELRTVLPALFRRFPHLRLATPPNEVPMDFTGTNYGVRKLMVTR

>CYP105AH1 Frankia sp. EAN1pec

MRELPPCAVRIPAGAADSRLAWLVTRYPDARQALMDPRLSADETLPGAPVRIQVPPDQKPGSFLRMDDPE

HARLRGTITTEFTARRVRGLRPAVQRLIDELLDGLAAGPRPTDLQDAFSRTLPTLVIARVLGVPDADSPF

FVEKTRVTISQGDTARSYAAYQEMSEYLGVLATRKQKEPADDLMSRLAVNHLATGKITLDELVGIARLVL

VAGHETTTNQIALNILSMLLDDDLRRTVLADDGVRIPQFVEESMRYWSISQDAIVRLAVEDFELGGTTMH

KGDAVVISIPAGNHDESMFPDPDRIDLDRDSGDHLQWGVGPHYCQGAPLARLEMELALKTLFGRFPGLRL

ATDDPDSVFRTGTVFHGVRELPVTW

>CYP105AJ1 Frankia sp. CcI3

MQNAHSDLRMSSRGDLLRSPIPLPMAGERTEPAPGMFTAMDPPEHTRYRRHIVEWFSTRRTRSLEPRVIE

IVDQHLDAMIAGGGPADLVSAFAEPVSALVICELLGVPVEQREVFGAAIAALFTVHSSAEEAISGWQNIG

GLLMGLIQAKRVASADDLLGTLVARGELSDEELMTIGSVLLVAGHDTSTNMIAMGTFALLEHPEQYAALA

ADPGLAPGAVEELLRYLTIVHAGSIRAVSADLEFDGHQLTAGDAVSLSLAAANRDPALCDAPDRLDITRE

PVPHLAFGHGIHQCVGQQLSRLELRIAFESLARRLPNLHVAVPTSEIRTRSEMIIYGVRELPVTW

>CYP105AK1 SBI\_6930 Streptomyces bingchengensis

47% to CYP105S3

MSNLRSNIITWLGRKYFSRIQKNGFDLSKMSFLPSATLAPLRRNGLDPVD

ELSRTRAKEPISKLPLPFGMKGWLVTGYDETKAVLGRTNGFSSDFTNLAE

KNIGIAAQQNPGGLGFSDPPTHTRLRRLLTPEFTMRRLSRLTPRIHSIVE

ERLDEMAAMGAAGDPVDLVQSFALPIPSLVICELLGVPYEDRADFQQLSM

ARFDLFDGADASFGAISDSLSYLLDIVKKQRESPGDGLLGMLVKEHGDEI

DDQELAGLADGVLTGGFETTASMLALGTLVLLRNPEQFAEIRDNDDVVDR

YVEELLRYLTVVQVAFPRFAKEDMEIAGTKISSGDLVLCSLSGANREEKL

GPDMERFDPHRQTPSHLAFGHGIHRCIGAELAKMELRAAYPALVRRFPEM

RLAVPQEKLAFRKLSIVYGVEALPVTLK

>CYP105AL1P Frankia alni ACN14a YP\_710901.1 CAJ59294.1 42% to CYP105AB1 Saccharopolyspora erythraea

MEAPLMTLSVESHLPSCPMERSSPFEPPPGYARARSEAPITKVRLVDGSTGWFVTGHALVRRLLNDPKVS KNGLRPGYPPLVPDQEALVRGQKGFLVWMDPPDHTMYRRMLAGEFSVNTLERLRPHVEHIVNECIDQLLD AGPPADLVQVLSLPVPTMTICELLGVPYTDRQLFQESTAATVNLRTTQEERNRTVAELRQCATRAGDRLP HALPAAPGPARRAADALGADRLRAGRGRTGEDGLVVLLTEDPPEERRQEVIDAAGSCPAQAILVDGE

>CYP105 fragment Streptoalloteichus hindustanus

LLIAGHETTANMLALGAFALLEHPEQLAELRANPDLMPGAVEEL

MRYLSIVHIGPVRTAVADVEIEGQLIRAGESVTVSVPAANWDPAKFPEPERLDLTRRT

SGHLAFGHGVHQCLRQNL

>CYP106A1 Bacillus megaterium

MNKEVIPVTEIPKFQSRAEEFFPIQWYKEMLNNSPVYFHEETNT

WNVFQYEHVKQVLSNYDFFSSDGQRTTIFVGDNSKKKSTSPITNLTNLDPPDHRKARS

LLAAAFTPRSLKNWEPRIKQIAADLVEAIQKNSTINIVDDLSSPFPSLVIADLFGVPV

KDRYQFKKWVDILFQPYDQERLEEIEQEKQRAGAEYFQYLYPIVIEKRSNLSDDIISD

LIQAEVDGETFTDEEIVHATMLLLGAGVETTSHAIANMFYSFLYDDKSLYSELRNNRE

LAPKAVEEMLRYRFHISRRDRTVKQDNELLGVKLKKGDVVIAWMSACNMDETMFENPF

SVDIHRPTNKKHLTFGNGPHFCLGAPLARLEMKIILEAFLEAFSHIEPFEDFELEPHL

TASATGQSLTYLPMTVYR

>CYP106A2 Bacillus megaterium

MKEVIAVKEITRFKTRTEEFSPYAWCKRMLENDPVSYHEGTDTW

NVFKYEDVKRVLSDYKHFSSVRKRTTISVGTDSEEGSVPEKIQITESDPPDHRKRRSL

LAAAFTPRSLQNWEPRIQEIADELIGQMDGGTEIDIVASLASPLPIIVMADLMGVPSK

DRLLFKKWVDTLFLPFDREKQEEVDKLKQVAAKEYYQYLYPIVVQKRLNPADDIISDL

LKSEVDGEMFTDDEVVRTTMLILGAGVETTSHLLANSFYSLLYDDKEVYQELHENLDL

VPQAVEEMLRFRFNLIKLDRTVKEDNDLLGVELKEGDSVVVWMSAANMDEEMFEDPFT

LNIHRPNNKKHLTFGNGPHFCLGAPLARLEAKIALTAFLKKFKHIEAVPSFQLEENLT

DSATGQTLTSLPLKASRM

>CYP106B1 Bacillus anthracis str. Ames

1 MASPENVILV HEISKLKTKE ELWNPYEWYQ FMRDNHPVHY DDEQDVWNVF LYDDVNRVLS

61 DYSLFSSRRE RRQFAIPPLE TRININSTDP PEHRNVRSIV SKAFTPRSLE QWKPRIQSIA

121 NELVKDIENC SEVDIVEQFA APLPVTVISD LLGVPTTDRK KIKAWSDILF MPYSKEKFND

181 LDAEKGIALN EFKAYLLPIV QEKRYHLTDD IISDLIRAEY EGERLTDEEI VTFSLGLLAA

241 GNETTTNLII NSFYCFLVDS PATYKEVREK PKLISKAVEE VLRYRFPVTL ARRITEDTNI

301 FGPLMKKDQM VVAWVSAANL DEKKFSQASK FNIHRIGNEK HLTFGKGPHF CLGAPLARLE

361 AEIALTTFIN AFEKIALSPS FNIEQCILEN EQTLKFLPIR LKPQ

>CYP106B2P Bacillus cereus ATCC 14579

1 MTSVITDGEI VTFSLGLLAA GNETTTNLII NSFYCFLVDS PGIYEELRKE PNLILKAIEE

61 VLRYRFPVTL TRRITALSER ESPSPLGMG

>CYP106B3P Bacillus cereus ATCC 14579

LKEDTNIFGPF

1 MKKNQMIVAW VSAANLDEKK FSQASQFNVH RTGNEKHLTF GKGPHFCLGA PLARLEAEIA

61 LTTFINAFEK IELFPSFCLE KCILENEQTL KYLPIRLKAT

>CYP107A1 Saccharopolyspora erythraea

MTTVPDLESDSFHVDWYRTYAELRETAPVTPVRFLGQDAWLVTG

YDEAKAALSDLRLSSDPKKKYPGVEVEFPAYLGFPEDVRNYFATNMGTSDPPTHTRLR

KLVSQEFTVRRVEAMRPRVEQITAELLDEVGDSGVVDIVDRFAHPLPIKVICELLGVD

EKYRGEFGRWSSEILVMDPERAEQRGQAAREVVNFILDLVERRRTEPGDDLLSALIRV

QDDDDGRLSADELTSIALVLLLAGFEASVSLIGIGTYLLLTHPDQDQLALVRRDPSAL

PNAVEEILRYIAPPETTTRFAAEEVEIRGVAIPQYSTVLVANGAANRDPKQFPDPHRF

DVTRDTRGHLSFGQGIHFCMGRPLAKLEGEVALRALFGRFPALSLGIDADDVVWRRSL

LLRGIDHLPVRLDG

>CYP107A2 Streptomyces rochei plasmid pSLA2-L

MTTDAHTAVPSLDSDLFHIDQYEAYAALREREPVSKVSFIGREA

FLITRHAEAKAALGDLRLSNDFKKQPPGVELPTYHGIPEDVRPYFANNMGSNDPPAHT

RLRRLVSREFTARRVESMRTRVAQLAEHLLDGLAGERETDLVERFAYPLPITVISELL

GVEERYQGDFGRWSNEFLVIDADRVEQREHAARALVGFILELVDRRRADPGSDLLSAL

IHVHDEDEDRLSTDELASVVLILLIAGFETSVSLIAMATYLLLTHPGELAKVRADPSL

VPNAVDEVLRFLGPAEITTRGTLEPVEIGGVHIPAHSTVLIAGAAANRDPRRFPDPER

FDVTRDTGGHLSFGHGIHFCVGGPLARLEGEIALRALLNRFPGLDLAIPAEQVRWRRS

FLRGIESLPVRLGR

>CYP107B1 Saccharopolyspora erythraea NRRL23338

MTTGEVPDLLAFDDAFAQDRHNRYARMREEPVQRIRTVNGLDAWLITRYEDVKQALLDPR

IAKDFGRTQQIIEKRLADAERRPGFSPDLGPHMLNTDPPDHTRLRKLVVKAFTARRVEGL

RPRIEQITDDLLDRLAGRSEVDLIDEFAFPLPITVISELMGVEDSRRDDFRSWTNVLVDG

SQPEAQAQASVAMVEYLTELIAKKRTEPGDDLLTALLEAVEDGDRLSEGELIAMVFLLLV

AGHETTVNLIGNCVLSLLGNPDQLAALRNDPSLLPGAIEETLRYESPVANGTFRHTAEAV

RFGDVVIPEGELVWVALGAANRDGERFEDPDRFDITRETTGHVAFGHGIHFCVGAALARL

EAQIAVGRLLERFPDLRMAASPDDLRWRFSVLMRGLEKLPVRPGA

>CYP107B2 Streptomyces sp.

LIAGHETTTNFIGNAALALLRHPESLAHLRAEPQLLGGALDELLRYDSPVGIATFRFSTE 182

183 ALTLGGTEIPEGVPVLIAPGAANRDPDRFPDPDRLDLTRGATGHLAFGFGMHHC 344

>CYP107C1 Streptomyces thermotolerans

MTALNLMDPEVLRDPFGAYAEIRAQAPLVRASYPWGAVQWLATR

YSDVKAVLTDPRLVNNPANVPEMHLPHPYEQALGDGGIPDEYVRYLAGSILSQDGPGH

LRLRRLSSRAFTVRRVNALRPRVTELAHRLLASLPDRAQDGVIDVLEDFSYPLSIDVI

CEIVGIPEEAREQWHTWGSAFYTMDPAVIGPAVRGMADHLHLLIEQRRATPTGDLLTG

LVQAEDEQGEPLTDEEIATLVLTFVTAGNETTAHLIGNGVAALLTHSDQLALLRSDRR

LLSQAVDELMRWCTPVQVTQPRYATEDLDVGGVTVRKGEQVVAVIGAAGHDPDRFPDP

ERFDITRNHRAPHEAHVGFGFGPHYCLGAALAHQETAIALDTLFDRFPSLALAVPPSA

LERQPFPGAWRLKSLPVRL

>CYP107D1 Streptomyces antibioticus

MTDTHTGPTPADAVPAYPFSLPHALDLDPHYAELRRDEPVSRVR

LPYGEGTAWLVTRMSDARIVLGDSRFSTAAATDPATPRMFPTPPEPDGVLAQDPPDHT

RLRRLVGKAFTARRVEEMRPRVRSLVDSLLDDMVAHGSPADLVEFLAVPFPVAVICEL

LGVPLEDRDLFRTFSDAMLSSTRLTAAEIQRVQQDFMVYMDGLVAQRRDAPTEDLLGA

LALATDNDDHLTKGEIVNMGVSLLIAGHETSVNQITNLVHLLLTERKRYESLVADPAL

VPAAVEEMLRYTPLVSAGSFVRVATEDVELSTVTVRAGEPCVVHFASANRDEEVFDHA

DELDFHRERNPHIAFGHGAHHCIGAQLGRLELQEALSALVRRFPTLDLAEPVAGLKWK

QGMLIRGLERQIVSW

>CYP107E1 Micromosospora griseorubida

MTSAEPRAYPFNDVHGLTLAGRYGELQETEPVSRVRPPYGEEAW

LVTRYEDVRAVLGDGRFVRGPSMTRDEPRTRPEMVKGGLLSMDPPEHSRLRRLVVKAF

TARRAESLRPRAREIAHELVDQMAATGQPADLVAMFARQLPVRVICELLGVPSADHDR

FTRWSGAFLSTAEVTAEEMQEAAEQAYAYMGDLIDRRRKEPTDDLVSALVQARDQQDS

LSEQELLDLAIGLLVAGYESTTTQIADFVYLLMTRPELRRQLLDRPELIPSAVEELTR

WVPLGVGTAFPRYAVEDVTLRGVTIRAGEPVLASTGAANRDQAQFPDADRIDVDRTPN

QHLGFGHGVHHCLGAPLARVELQVALEVLLQRLPGIRLGIPETQLRWSEGMLLRGPLE

LPVVW

>CYP107E2 Saccharopolyspora erythraea NRRL23338

MPEPRPYPFSAAERLNLDPFYARLRAQEPMSRVKLPYGEAAWLATRYEDAKVVLADPRFS

RAAVLEKDEPRMRPGITGGGILSMDPPDHTRLRRLVAKAFTQRRVERLRPRTQEIADGLV

DRMIEHGSPADLVEEFALPLPITVICELLGVPYEDRDDFREWSDAFLSTTKLTPEQVVDY

MDRMFGYMAGLIAKRRVDPQDDLMSALIEARDEHDKLTEQEMVQLAAGILVAGHETTATQ

IPNFVYVLLTHPDQLEGLLADLDGLPRAVEELTRYVPLGVAAVFARYAVEDVELGGVTVR

AGEPVLVSASSANRDEAVFDDPDRLDLTRENNAHIGFGHGPHHCLGAQLARLELQVGLRT

LLTRLPGLRFAGGEDDVVWKEGMLVRGPSKLEVAWQSE

>CYP107E3 Salinispora tropica (marine actinomycete)

MTIDQEIRKYPFCESPGIGIDPTYGLLRSTEPLARVQLPYGEVSWLATRYEDVKTVLTDP

RFSRAAAQGKDQPRTREEMTYEGIIGLDPPDHTRLRKLAGKALTARRVNAIRADAQRIAN

EYVDEMIAKGSPGDLVELFALPYPVTVICELLGVPFEDRAQFRIWTEGLTSTSEQLMVYA

EQLFGYMGKLVAQRREEPTDDLLGALVKARDEGDRLTEQELLSIAGVGLLLTGVETVSTH

IPNFVYALLTHPELMAQLRADRSLVPAAVEELLRMIPLNPAAMFPRYAVEDVTLSGITVR

AGEPVLVSLPGANRDPEVFENPETFDFTREQNPHVAFGHGPHHCLGAQLARMELQVALHT

VLDRFPDLSLADGDEGVSWKSGLLVRGPSRLLVAW

>CYP107E4 Actinoplanes sp. ATCC 53771

MTTTDTEFVAYPFNEDAGLELNEAYAAARATEGMLRVRLPHGEP AWLATRYADARFVLGDRRFSRAMAVERDEPRMAPGRRPGGILSMDPPDHTRLRTLVAK AFTMRRVELLRPRVAELASGLIQDMKAKGQPADLVEDYALPIPVAVICELLGVPVEDR PKFRVWSDAALSTSPLTTEEMMANQDELRAYMHVLVEQHRAEPQDDLMTALIEARDVR DRLSELELVDMCIGILIAGHETTASQIPNFVYALLEQPDQLARLRADLDLIPAAVEEL LRFIPLGAGAGFARYATEDIQVGDVLVKEGEPVMVAIGAANRDALQFTSADTLEFGRE SNPHLGFGHGVHHCLGAPLARLELQEALRALLRDLPGLHLDGDIVWKTQMLVRGPRSM PIGW

>CYP107E5 SBI\_8067 Streptomyces bingchengensis

57% to CYP107E2 Saccharopolyspora erythraea NRRL23338

VTTAETTVQSEAIAYPFNSSEGLGLSQAYQEARNRPGLVRVRMAYGEPAW

LVTRYAEARLVLGDRRFSRAAALHRDEPRQGEGRRNSGILTMDPPEHTRL

RTLVAKAFTVHQVEKLRPSVRQLTHELLDGLEAAGPPADLVDRYALPIPV

GVICRLLGVPEEDRPKFRAWSDAALSTSSLSAEEFDRNRDELRAYMAGLI

EIHRAAPQDDLMTSLIEARDAGDRLSELELVDLCVGILVAGHETTATQIP

NFVLTLLDHPGELRRLREEPALLNGAVEELLRFVPLGKGASQPRYATEDI

EVGGQLVRAGEPVLVAVGSANRDALRFDEPGKLNVARPATQHLGFGHGVH

HCLGAPLARLELQEALGALITRFPGLCLTGDVVWKDQMLVRGPRVMPVGW

>CYP107F1 Streptomyces griseus D45916

MENTSVQNKETVRNCPFDYAHELEFDPQLRQLLTEEPVSRIRMA

YGEGEAWLVTRYEDVRTVTTDRRFSRSAVLGRDFPRMTPEPIVQAESINLMDPPASSR

LRGLVAKSFTPRRVEQMRGGTQRVVDRLLDEMEEEGSPGDFVARVSAPLPLITICEAL

DIPEADRPWLRAHAMTMMNVGAAGKQDAVRAKAELRGYFQELTADRRRSPGEDLISTL

ATARDGDELLDDDELAVMAMVLLITGQDTTTYQLGNIAYTLLTRPDLLRSLRAEPQRL

PRTLEELLRHIPFRKGVGIPRIALEDVELSGVLIKAGDVVHVSYLTANRDSAKFDRPD

ELDPDRPTIPHMTFGWGAHHCLGAPLATMELEVAFSTLLTRFPALRLDVPPEDVSWNT

TSIWRYPLALPVTW

>CYP107F1 SGR6619 Streptomyces griseus 1 aa diff to D45916

MENTSVQNKETVRNCPFDYAHELEFDPQLRQLLTEEPVSRIRMAYGEGEAWLVTRYEDVRTVTTDRRFSRSAVLGRDFPRMTPEPIVQAESINLMDPPASSRLRGLVAKSFTPRRVEQMRGGTQRVVDRLLDEMEEEGSPADFVARVSAPLPLITICEALDIPEADRPWLRAHAMTMMNVGAAGKQDAVRAKAELRGYFQELTADRRRSPGEDLISTLATARDGDELLDDDELAVMAMVLLITGQDTTTYQLGNIAYTLLTRPDLLRSLRAEPQRLPRTLEELLRHIPFRKGVGIPRIALEDVELSGVLIKAGDVVHVSYLTANRDSAKFDRPDELDPDRPTIPHMTFGWGAHHCLGAPLATMELEVAFSTLLTRFPALRLDVPPEDVSWNTTSIWRYPLALPVTW

>CYP107F2 Streptomyces avermitilis

MTPSDEAIMCPFDFSKGLEFDPSLAELMARDSITRIRLPYGDAD

AWLVTGFDAVRQVTTDQRFSRAGIMGSDYPRLTPEPIVSPESINVVDPPHSSRLRRLV

SQAFTKGHVERMRRRIVRLADTLLDEMAAQGPPADLAHHLSNRLPQHTICDVLGIEQD

DWPRMEQYVHQLLSTGPDSRQSAATAKSELREYFGGLVEKRRSSPGNDLISALAAAKD

GEDVLDDQELAVMALTLMLSGHDTATCQISNICYLLLTRPELMKHLRSRPDTLTAVLN

EMLRFIPFRKGVGIPRVAVEDAEVDGVKIRAGDFVHVSYLTANRDPERYPDPDAIDPD

RPSLPHMTFGWGGHRCIAVPLAMAELEVAIGRLLERFPELRLAVPPEEVRWDTETIRR

FPIELPVAW

>CYP107G1 Streptomyces hygroscopicus

MSTTDQGETGKACPYPFAEMERLEIHPEYNRLRDAGELGRVLML

DGREAWLAASWEDVAKVFVDPRFSRSATLGKDVPRVLPAIQDQPVIMLMDPPEHTRLR

RVATKALTSRRMEALRPRTQEVADDLIDKMLAKGAPADLMEDFALPLPIIMICELLGV

PIEDQTKFRTWSDQMLSNGAYSQEVVMAAGQSLYLYLSELIAERRKQDTNDLLGSLVR

ARDKDDRLSETELVGFAVTLLIAGYETTANAIGNSVYTLLTHPEKLAELRKDLSLIPK

AVDELLRIIPIAKQASWVRMAVEDVELSGTIVKAGEAVAIQTHSANTDPKVYDHPEEI

DFHRTSNPHMSLGHGAHHCMGAQLVRVEMQTALGSLISRIPALRFAVPEPRIKFLRGR

LVPSLEALPLTW

>CYP107H1 Bacillus subtilis

MTIASSTASSEFLKNPYSFYDTLRAVHPIYKGSFLKYPGWYVTG

YEETAAILKDARFKVRTPLPESSTKYQDLSHVQNQMMLFQNQPDHRRLRTLASGAFTP

RTTESYQPYIIETVHHLLDQVQGKKKMEVISDFAFPLASFVIANIIGVPEEDREQLKE

WAASLIQTIDFTRSRKALTEGNIMAVQAMAYFKELIQKRKRHPQQDMISMLLKGREKD

KLTEEEAASTCILLAIAGHETTVNLISNSVLCLLQHPEQLLKLRENPDLIGTAVEECL

RYESPTQMTARVASEDIDICGVTIRQGEQVYLLLGAANRDPSIFTNPDVFDITRSPNP

HLSFGHGHHVCLGSSLARLEAQIAINTLLQRMPSLNLADFEWRYRPLFGFRALEELPV

TFE

>CYP107J1 Bacillus subtilis

MSSKEKKSVTILTESQLSSRAFKDEAYEFYKELRKSQALYPLSL

GALGKGWLISRYDDAIHLLKNEKLKKNYENVFTAKEKRPALLKNEETLTKHMLNSDPP

DHNRLRTLVQKAFTHRMILQLEDKIQHIADSLLDKVQPNKFMNLVDDYAFPLPIIVIS

EMLGIPLEDRQKFRVWSQAIIDFSDAPERLQENDHLLGEFVEYLESLVRKKRREPAGD

LISALIQAESEGTQLSTEELYSMIMLLIVAGHETTVNLITNMTYALMCHHDQLEKLRQ

QPDLMNSAIEEALRFHSPVELTTIRWTAEPFILHGQEIKRKDVIIISLASANRDEKIF

PNADIFDIERKNNRHIAFGHGNHFCLGAQLARLEAKIAISTLLRRCPNIQLKGEKKQM

KWKGNFLMRALEELPISF

>CYP107J2 Bacillus anthracis str. Ames

1 MAMKNKVGIR IEDGINLASA QFKEDAYEIY KESRKVQPVL FVNKTELGAE WLITRYEDAL

61 PLLKDNRLKK DPANVFSQDT LNVFLTVDNS DYLTTHMLNS DPPNHNRLRS LVQKVFTPKM

121 IAQLEGRIQD IADDLLNEVE RKGSLNLVDD YSFPLPIIVI SEMLGIPKED QAKFRIWSHA

181 VIAYPETPEE IKETEKQLSE FITYLQYLVD MKRKEPKEDL VSALILAESE GHKLSARELY

241 SMIMLLIVAG HETTVNLITN TVLALLENPN QLQLLKENPK LIDAAIEEGL RYYSPVEVTT

301 SRWADEPFQI HDQTIEKGDM VVIALAAANR DETVFENPEV FDITRENNRH IAFGHGSHFC

361 LGAPLARLEA KIAITTLFER MPELQIKGNR EDIKWQGNYL MRSLEELPLT F

>CYP107J3 Bacillus cereus ATCC 14579

1 MKNKVGLSIE DGINLASAQF KEDAYEIYKE SRKKQPILFV NQVEIGKEWL ITRYEDALPL

61 LKDNRLKKDW TNVFSQDIKN MYLSVDNSDH LTTHMLNSDP PNHSRLRSLV QKAFTPKMIA

121 QLDGRIQRIA DDLISDIERK GTLNLVDDYS FPLPIIVISE MLGIPKEDQA KFRIWSHAVI

181 ASPETPEEIK ETEKQLSEFI TYLQYLVDIK RKEPKEDLVS ALILAESEGH KLSARELYSM

241 IMLLIVAGHE TTVNLITNTV LALLENPNQL QLLKDNPKLI DSAIEEGLRY YSPVEVTTAR

301 WAAEPFQIHH QTIQKGDMVI IALASANRDE TVFENPEIFD ITRENNRHIA FGHGSHFCLG

361 APLARLEAKI AITTLFNRMP ELQIKGNREE IKWQGNYLMR SLEELPLTF

>CYP107J4P Bacillus cereus ATCC 14579

1 MKEPQLQQHL EKFIQYIEAL VNEKRLNPDA DLISELVQTK EQEDKLSNNE LLSTIWLLII

61 AGHETTVNLI SNGLLALLQH PEQMNLIREN PSLIPSAVDE LLRHSGPVMF ISRLASEDMT

121 IHGKRIPKGD LVLLSLTAAN IDPQKFTYPE TLNISREENN HLAFGAGIHH CLGAPLARLE

181 GQIALGTLLQ RLPNLRLAIK PDQLNYNHSK IRSLVNLPVV F

>CYP107K1 Bacillus subtilis

MQMEKLMFHPHGKEFHHNPFSVLGRFREEEPIHRFELKRFGATY

PAWLITRYDDCMAFLKDNRITRDVKNVMNQEQIKMLNVSEDIDFVSDHMLAKDTPDHT

RLRSLVHQAFTPRTIENLRGSIEQIAEQLLDEMEKENKADIMKSFASPLPFIVISELM

GIPKEDRSQFQIWTNAMVDTSEGNRELTNQALREFKDYIAKLIHDRRIKPKDDLISKL

VHAEENGSKLSEKELYSMLFLLVVAGLETTVNLLGSGTLALLQHKKECEKLKQQPEMI

ATAVEELLRYTSPVVMMANRWAIEDFTYKGHSIKRGDMIFIGIGSANRDPNFFENPEI

LNINRSPNRHISFGFGIHFCLGAPLARLEGHIAFKAAFEEIS

>CYP107L1 Streptomyces venezuelae

MRRTQQGTTASPPVLDLGALGQDFAADPYPTYARLRAEGPAHRV

RTPEGDEVWLVVGYDRARAVLADPRFSKDWRNSTTPLTEAEAALNHNMLESDPPRHTR

LRKLVAREFTMRRVELLRPRVQEIVDGLVDAMLAAPDGRADLMESLAWPLPITVISEL

LGVPEPDRAAFRVWTDAFVFPDDPAQAQTAMAEMSGYLSRLIDSKRGQDGEDLLSALV

RTSDEDGSRLTSEELLGMAHILLVAGHETTVNLIANGMYALLSHPDQLAALRADMTLL

DGAVEEMLRYEGPVESATYRFPVEPVDLDGTVIPAGDTVLVVLADAHRTPERFPDPHR

FDIRRDTAGHLAFGHGIHFCIGAPLARLEARIAVRALLERCPDLALDVSPGELVWYPN

PMIRGLKALPIRWRRGREAGRRTG

>CYP107L2 Streptomyces avermitilis

MGNVIDLGEYGARFTEDPYPVYAELRERGPVHWVRTPPPEAFEG

WLVVGHEEARAALADPRLSKDGTKKGLTSLDVELMGPYLLVVDPPEHTRLRSLVARAF

TMRRVEALRPRIQEITDGLLDEMLPRGRADLVDSFAYPLPITVICELLGVPDIDRVTF

RALSNEIVAPTGGDAELAAYERLAAYLDELIDDKRSTAPADDLLGDLIRTRAEDDDRL

SGEELRAMAFILLVAGHETTVNLITNGVHTLLTHPDQLAALRADMTLLDGAVEEVLRF

EGPVETATYRYAAESMEIGGTAIAEGDPVMIGLDAAGRDPARHPDPHVFDIHRAPQGH

LAFGHGIHYCLGAPLARLEARVALRSLLERCPDLALDGPPGARPPGMLIRGVRRLPVRW

>CYP107L3 Streptomyces tubercidicus strain I-1529

VSEDRIVDLAALGEEFTRDPHPVYAELRARGPVHRVRLPEGFEAWLVVGYEAARAALSDPRLSNDWRRAAGADEGD

PAAAPHMLISDPPRHTRLRRLVVKEFTPRRIEALGPRVREITDELIDAMLSRPGGRADLVEDFAFPLPAAVICELL

GVPYADRKTFHEWSTEVTKRSGGPRAEAAMGELAGYLMRLLEEKGRRPGDDLLSALIRTTGEDGDRLSSDELLGMA

VLLLIAGHETTAGLISNGMLALLRHPDQLAALQADFGLLDGAVEEMLRHSGPTGTSLHRFTTGPVDIAGTRIPGGG

ELVLIGNTPANHDPGRYPDPGRFDIRRDHRGHLAFGHGIHYCFGAPLARLEARTAIRTLLQRCPGLALDAAPDELV

WHHSAMMRGLPHVPVRTVPAPAAPAPQVHQVSSAH

>CYP107L4 Streptomyces tubercidicus strain R-922

VSEDRIVDLAALGEDFTRDPHPVYAELRDRGPVHRVRLPEGFEAWLVVGYEAARAALADPRLSNDWRHAAGAGAGD

PAAAPHMLISDPPRHTRLRRLVVKEFTPRRIEALGPRVREITDELIDAMLSRPDGRADLVEDFAFPLPAAVICELL

GVPYADRKAFHGWSTEVTKRSGGPQAEAAMGELAGYLVRLLEDKGRRPGDDLLSALLRTTGEDGDRLSSDELLGMA

VLLLIAGHETTAGLLSNGMLALLRHPDQLAALHADFDLLDGAVEEMLRHSGPTGTSLHRFTTAPVDLAGTLIPGGG

ELVLIGNTPANHDPGRFPDPGRFDIRRAPHGHLAFGHGIHYCFGAPLARLEARTAIRALLERCPGLALDADADRLV

WHHSAMMRGLPHVPVRVRPAPGTPAAQVHHASSAR

>CYP107L5 Streptomyces sp.

LIAGHETTVNLITGAVHALLTHPGQLAQVRGDMSLVDAVVEETLRHEGPVENATFRFAAE 182

183 PLEIGGTVIPAGDPVLIGLAAADRDGARYPGPDRFDIHRDTRGHLAFGFGTHRC 344

>CYP107L6 Streptomyces sp.

MGHEHVIDLGEYGPGFTENPHPVYAELRARGPVHRVRLPKHDAHHEAWLVVGYEEARAAL

ADPRLSKDGSTIGVTFLDEELIGKYLLIADPPQHTRLRGLIAREFTGRRVERLRPRVQEI

TDSLLDEMLPRGRADLVESFAYPLPLTVICELLGVPEIDRAAFRKLSTEAVAPTSGESEY

AAFVQLAAYLEELVEEKRCAPPADDLLSALIRTTDEDGDRLSPAELRGMAFILLIAGHET

TVNLITGAVHALLTHPGQLAQVRGDMSLVDAVVEETLRHEGPVENATFRFAAEPLEIGGT

VIPAGDPVLIGLAAADRDGARYPGPDRFDIHRDTRGHLAFGHGIHFCLGAPLARLEARVA

LRALLERCPGLTPDGAPGEWLPGMLIRGVRSLPVRW

>CYP107L7P Streptomyces narbonensis

MSRTHQGTTASRPVLDLAALGQDFAADPYPTYARLRAEGPAHRV

RTPEGDEVWLVVGYDTARAVLADPRFSKDWRNSATPPTEAEAALSHNMLESDPRCGPT

(deletion)

ALRADLTLLDGAVEEMLRYGGPVESATYRFPVEPVDLDGTVLPAGETVLVVLAD

AHRTPERFPDPHRFDIRRDTAGHLAFGHGIHFCTGAPLARMEARIAVRALLERCPDLALD

VSPGELFWYPNPMIRGLESLPIRWRSGREAGRRVPVEPACRP\*

>CYP107L8 Streptomyces sp. HK803

MVTVDLSAYGPGFFTDPYPYYARLREAGPVHEIVLADGDRFWLI

VGYDEARAALADPRLAKSLDPPSEDERHVLITDPPDHTRLRRLVSREFTARRVEAMRP

RVQEITDGLLDEMVAGRRRADLVPSLGSPLPITVLCELLGVPLADREDFRGWTERVLV

PAEPDTIAWWKSRGFAQAGMALTDYLKNMIEDKRRSTPTGDLISSLLRTTAEDNDRLS

AAELHSMVFILIVAGHETTANLITNGVRALLAHPEQLAALRTDPEGLIDQAVEEMLRY

DGPVETSTKRFTLEAVRYGATKIPPGETLLVSIAATGRDPAQFERPDTFDIHRGTTGT

RSGHVAFGHGIHFCLGAGLARMESRVAILTLLRRCPDLALDIDPAGLDWLPGIRVRGV

RSLPVRW

>CYP107L9 Streptomyces peucetius

MTIVDLADYGPDFTANPYPYYERLRASAPAHRVRGADGGEFWLIVGHEEARAALGDARLS

KSPATMGTTMLDEQVIGPNLLVVDPPDHTRLRKLVVREFTPRRAEALRPRVQRITDDLLD

AMVPAGRADLVDALAFPLPIVVICELLGIPAADRDAFRTWSNEVVAPTSPETGEDAVRQL

GAYLDGLIADKRCAGPTDDLLSALIRTKDEDGDRLSFTELRALAYLLLIAGHETTVNLIS

NGVRALLAHPDQLAALRADFSLLDGAVEEMLRYDGPVETATVRFSAAPVPVGDLVIPPGE

VVL SAWRPPTATPPATPDPTASTSAGTPAAISPSGTASTSASALRWPAWRPGSPSAPSWS

AAPPSPWTKRRTRTNGSRAS

>CYP107L10 SGR1278 Streptomyces griseus

MTTEPLVDLAALGEQFTRDPYPAYAALRAKGPVHRVRIPEGAEAWLVVGYEQGRALLADQRLSKHWSRASPSLGVSKVSAGSSMLGSDAPDHTRMRKLVAREFTPRRMEQLAPRVQEMTDGLLDAMLAAPDRTADLVEALSFPLPMAVICELLGVPSLDREAFRTWSGQAVSSVDPSLRASSTQAMTAYIAGLLADKRERPGEDLLSALIHTSDEDGDRLSGDELIGMAWLLLVAGHETTVNLITNGVHNLLAHPDQLAALRADFTLIDNAVEEILRFEGPVETPTYRFTTDPIEVGGTVIPGGGELVLVAMSDANRDPARYPDGSRFDITRDARGHIAFGHGIHYCLGAPLARIEARIAIRSLLERCPELRSAADPATLPWRTGILMRGPLSLPVGW

>CYP107L11 SGR1279 Streptomyces griseus

MAVLDLRDLPDFTTNPYPYYAKLRAEGPVHAVRTEEMEQRVWLVVGHAEARAALADQRLGKDWRHTGLWTESEAALSANMLELDAPHHTRLRRLVSREFTARRIEALRPRVTEITGELLDAMAPRGSADLVDALAFPLPMTVICELLGVPDIDRDAFRALSNGIVTPTPEQRGADPAGAMGAYLDGLIENKRRSPGDDLLSGLIRTGEADGEGLSSAELVGMAFLLLVAGHETTVNLIANGVRALLDHPDQLALLRADPGLLDNAVEEMLRYDGPVETATFRFARETLTIGDTEIHVDEPVLVALASADRDPLRFRDPDTFDIRREPQGHLGFGHGVHYCLGAPLARMEARIAIGALLERFPGLARDPSGGELDWLPGLLMRGARGLPVRW

>CYP107M1 Actinomadura hibisca

MPSSKDAPTVDPRPDVTPAFPFRPDDPFQPPCEHARLRASDPVA

KVVLPTGDHAWVVTRYADVRFVTSDRRFSKEAVTRPGAPRLIPMQRGSKSLVIMDPPE

HTRMRKIVSRAFTARRVEGMRAHVRDLTSGFVDEMVEHGPPADLIAHLALPLPVTVIC

EMLGVPPEDRPRFQDWTDRMLTIGAPALAQADEIKAAVGRLRGYLAELIDAKTAAPAD

DLLSLLSRAHADDGLSEEELLTFGMTLLAAGYHTTTAAITHSVYHLLREPSRYARLRE

DPSGIPAAVEELLRYGQIGGGAGAIRIAVEDVEVGGTLVRAGEAVIPLFNAANRDPEV

FADPEELDLGRTDNPHIALGHGIHYCLGAPLARLELQVVLETLVERTPALRLAIDDAD

ITWRPGLAFARPDALPIAW

>CYP107N1 Streptomyces lavendulae

MTGPEAAVRGCPFGAGEAPAYPFHAPDRLEPDPYWEPLRRERPL

QRVTLPYGGEAWLATRYQDVRAVFADRRFSRQLAVAPGAPRFLPHQPPPDAVLSVEGP

DHARLRRLVGKVFTPRRVEDMRPLIQRTADGLLDAMEEMGPPADLVEDFSLPFAVSMI

CELLGVPPEDRKRFCVWSDALLTTTAHTPAQVRDYMMQMHDYLGGLVAQRRVRPTADL

IGSLVTARDEEDKLTEGELVRLAEAILIAGYETSASQIPNFLYVLFRHPQLLERIRND

HDLIPDAVEELLRFVPIGTVDGFPRTATEDVELGGVLVRAGETVVPSMGAANRDPELF

TDPDELDLARRPNPHLGFGAGPHHCLGAQLARVELQITLTTLFRRYPRLRLAVPEESL

SWKEGLMVRGMHTMPVTW

>CYP107N3 Streptomyces peucetius

VTGRATDPATEGSRCPFAAGEAPAYPFGSPDRLEPDPYWEPLRREQPLQRVTLPYGGEAW

LATRYQDVRKVFADRRFSRALAVAPGAPRFLPHQPPADAVLSVEGPDHARLRRLVGKVFT

PRRVEAMRPLIQSTADRLLDAMEEIGPPADLVEDFSLPFAVSMICELLGVPPEDRKRFCT

WSDALLTTTAHTPAQVRDHMMQMHDYLGGLVAQRRTRPTEDLIGSLVTARDAEDKLTEGE

LVRLAEAILIAGYETSASQIPNFLYVLFRNPHLLERLRNDHDLIPDAVEELLRYVPIGTV

DGFPRTATEDVELGGVLIRAGETVVPSMGAANRDPELFADPEELDLTRSPNPHLGFGAGP

HHCLGAQLARVELQITLTTLFRRYPRLRLAVPEESLAWKAGLMVRGMHTMPITW\*

>CYP107P1 Streptomyces coelicolor cosmid H10

MTAATDGPHVSGPAFDPWDPAFVADPYPAFAELRARGRVLYYEP

SDQWLVPHHADVSALLRDRRLGRTYQHRFTHEDFGRTPPPPEQEPFHTLNDHGMLDLE

PPDHTRIRRLVSKAFTPRTVERLKPYVHGLADDLVARLVAAGGGDLLTDVAEPLPVAV

IAEMLGIPESDRAPLRPWSAEICGMYELNPSEETAAKAVRASLDFSDYLRALIAARRK

EPGDDLISGLIAAHDEDDRLTEQEMISTCVLLLNAGHEATVNATTNGWLALFRHPDQL

AALRADHSLVPSAVEELMRYDTPLQLFERWVLDEIEIDGTTLPRGAEVAMLFGSANHD

PAVFTDPERLDLTRRDNPHISFSAGIHYCIGAPLARIELAASMTSLLKRAPGLRLAAE

PERRPNFVMRGLTELRVEL

>CYP107P2 Streptomyces avermitilis

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IRRLVSKAFTPRTVEQLKPYVAKLAGELVDRLVAAGGGDLLADVAEPLPVAVIAEMLG

IPESDRAPLRPWSADICGMYELNPPKDVAAKAVRASVEFSDYLRELIAERRKEPGDDL

ISGLIAAHDEGDRLTEQEMISTCVLLLNAGHEATVNATVNGWYALFRNPDQLAALRAD

HSLVPAAVEELMRYDTPLQLFERWVLDEIEIDGTTVPRGAEIAMLFGSANHDPEVFRN

PEKLDLTREDNPHISFSAGIHYCIGAPLARIELAASMTALLEKAPTLGLVAEPKRKPN

FVIRGLEGLSVAV

>CYP107P3 Streptomyces peucetius

MLGIPVPDRPLLRPWSADICGMYELNPSQETAARAVQASVEFSAYLRELIAARRAEPGED

LVSALIAAYDEGDRLSEQEMISTCVLLLNAGHEATVNTTVNGWWTLFRYPEQLAALRADH

SLLSTAVEELMRYDTPLQLFERWVLDDIEIDGTLVPRGCELALLFGSANRDGARFDHPDE

LDLARQDNPHVSFGAGIHYCLGAPLARIELAAT

FGERCGSARRCGSRRSHGGRGAL\*

>CYP107P4 SBI\_9576 Streptomyces bingchengensis

75% to CYP107P1 Streptomyces coelicolor

MSSSAAPAPVFDPWQPSFVADPYPAYAALRERGRAHYFEASRQWLIPRHE

DVRVLLRDRRLGRTYLHRFSHEEFGRTAPPPEHEPFHTLNGHGMLDLEPP

DHTRLRRLVSKAFTPRTVERLAPVVERLADELVEAFVAEGGGDLVAAVAE

PLPVAVIAEMLGIPPADRAQLRPWSADICGMFELNPGDEAARRAVRASVE

FSEYLRELIAARRRNPGEDLISGLVAAYDEGDRLTEQEMISTCVLLLNAG

HEATVNSTGNGWLALFRHPDQLALLRSDPDALLPTAVDELLRYDTPLQLF

ERWVLDDIEVGGTVIPRGSEVALLFGSANRDPERFPDPDRLDLSRTDNAH

FSFGGGIHYCLGAPLARLELAASFGALLRRAPGLRPAAEPRWNPGFVIRG

LQELLVEV

>CYP107P7 SGR3408 Streptomyces griseus

MHVSFDPWSPAFVADPYPAYTALRAAGRAHWFEPTGQWLIPHHSDVSALLRDRRLGRTYLHRFSHEEFGRTPPPAAHEPFTTLNGQGILDLEAPDHPRIRRLISRAFTPRTVENLAPTVRRLAAELVDAFVAKGGGDLLAEVAEPLPVAVIAEMLGVPEADRGLLRPWSAAICGMFELNPSEETAEAAVRASVDFSAYLRGLIAERRADPGEDLVSALIAAHDEGERLTEQEMISTCVLLLNAGHEATVNTTVNGWRTLFHHPEQLAALRADPALLPSAVEELLRYDTPLQMFERWVLDDIELDGQVIERGAEVALLFGSANRDPERFARPDTLDLSRQDNPHLTFGAGIHFCLGAPLARLELAASFGELLRKAPALRMTAEPEWHPGYVIRGLKELRAEV

>CYP107Q1 Amycolatopsis mediterranei

PVPLSIVSRDRVSIQRLACKVFGETRSGPPGRASFVLIAPRRPQ

TVHKGHNSEHCQVGGCSTGRPLPTVRNRACRTRAGRPRRHQEGMAMTATAKPSAKPVD

LFSPEVVADPFGWYARLREEPLPHTGTLNLGTMMGGPDMWLATRYEDVLTVLTDPRFL

TNPPADSPLADIRDGVFKAMNFPEDLIPWMANKLNTADGEDHTRLRKLVSYALTARRV

NALRPRVEKITEDLFDRMAEQGKDGSPVDIVEEFCFPLPVTVICELVGIDEPDRAAWH

AWGNAMATMDGPKIPPALRECIALSRELMARRRVEPKDDLVTALVQAQADDPGRVSDD

EIVGILFSLVTAGHQTTTYLIGNSVLFLLEQPEQLARLKAEPALWAQAVRELQRLGPL

QFTQARFPSEDVELGGVTIPRGTPVAPLLLAANTDPRKFPEPDKLVVDRLSVANEMHL

SFGKGIHRCLGQHLAYQEAEVALHGLFTRFPDLALAVPRDEIPWILRPAFTRTKTLPL

KLA

>CYP107Q2 Amycolatopsis mediterranei

MTTTAETSAEPVDLFSPEVVADPWGAHAAVREAPTLQIGGFMGG

PPMYLAARYEDVRQVLMDQRFQCNPLADSPAEDIRNGVFRHLDMPEELIPWLKNLINA

SDGEEHARLRKLVSYALTAHRVGKFRPRVEELTAELLDKLEAAGGDGTPIDLVESFCY

PLPVTVICELVGVDHEDRPQWRAWSDAMATLDGKRLPEEVRKTLAAARGMIERRRAEP

KDDMVTALVEAQAKNPGIATDDELVGVLFSLVTAGHQTTTYLIGNSVLALHEHPDQLA

RLKADPSLWPQAVRELQRLGPIQFGQPRFATEDIEVGGTVIPRGMPVVPLIMAANSDP

RKFPEPEKLQIDRLAVGSESHLGFGKGIHRCLGQHVAYLEAEVALRGLYTRFPDMTLA

VPREEIPWILRPGFTRTKDLPVRLARPAS

>CYP107R1 Streptomyces maritimus

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REQLRGWSDALLSTTACTPAESAAAAQAMADHFAALVSQRRRQPTDDLLGALVQTWDR

EEGLLRDEELVLLTRDLLIAGHETTASQIANCTYLLLQRPHDMDRLRTDPSAMASAVE

ELLRFIPLGSGSFRARVATEPVELCGVRIQPGDTVFAPTVAANWDPDVFAEPGRLDID

RSPNPHVAFGHGVHHCLGAQLARLELQVALGVLLRRLPRLRLAVDEAEIVWKTGMQVR

GPKTLPVKW

>CYP107S1 Pseudomonas aeruginosa

VPDRKLRLGEELISPLHALYDGLQVDGAPRPAHRAAEHPVWVVTRYRDAR

KVLNHPGVRRDARQAAELYAKRTGSPRAGIGEGLSHHMLNLDPPDHTRL

RSLVGRAFTPRQVERLQPHIERITEALLDAMAGREQADLMADFAIPLTI

AVIFELLGIPEAEREHARQSWERQAELLSPEEAQALADAQVDYLRVLLE

AKRRQPADDVYSGLVQAADESGQLSEAELVSMAHLLMMSGFETTMNMIG

NALVTLLVNPEQLALLRAQPELLPNAMEELVRHDSPVRASMLRFTVEDV

ELDGVTIPAGEYILVSNLTANHDAERFDDPDRLDLTRNTDGHLGYGFGV

HYCVGASLARLEGRIAIQRLLARFPDLQLAVPHAELQWLPITFLRALIS

VPVRTGCSAPANTASHANPIERIAQ\*

>CYP107T1 Streptomyces coelicolor

MGSAPRLIVSLTGGPMTAPTYEELAALRAVGAVHRVFVPGSGESRLVVTRDAARAALTDPRL 16234

16235 RNDIRHSASWDSDGGHAIGHNMLQSDPPQHTRLRRLVAGHFTPGRTAALRPRVERIAHDL 16414

16415 LDALPPAGTADLVARYALPLPVTVICELLGVPESDRGTFHTWSNELVMPTSPEAAGSA 16588

16589 ATALTGYLTELTDAKRRTPDGTLLGDLVAAADSGELTPGELLGMAFLILVAGHETTVN 16762

16763 LISATVHGLLTHPGQLARLRAEPELTEAAVEESLRYHSPVHASAFRFAAEPLELAGTAIA 16942

16943 AGDPVLVSLAAASRDPAHFPDPDRFDIGRRPRGHLGFGHGPHHCLGAPLARVEAAVAVRL 17122

17123 LLDRHPALALAAGPATLTWRTSTLLRGLVELPVRLG\* 17233

>CYP107U1 Streptomyces coelicolor

MTGSSSAPVPELFSWEFASDPYPAYAWLREHAPVHRTRLPSGVEAWLVTRYADAKQALADP 8557

8556 RLSKNPAHHDEPAHAKGKTGIPGERKAELMTHLLNIDPPDHTRLRRLVSKAFTPRRVAEF 8377

8376 APRVQELADGLIDRFADTGSADLIHDFAFPLPIYAICDLLGVPREDQDDFRDWAGMMI 8203

8202 RHQGGPRGGVARSVKKMRGYLADLIHRKRAALPPEPAPGEDLISGLIRASDHGEHLTEN 8026

8025 EAAAMAFILLFAGFETTVNLVGNGTYALLTHPEQRERLQTSLAAGERGLLETGVEELLRY 7846

7845 DGPVELATWRFATRPLTIGGQDVAAGDPVLVVLAAADRDPERFTDPDTLDLARRDSQHLG 7666

7665 YGHGIHYCLGAPLARLEGQTALATLLTRLPDLRLAADPAELRWRGGLIMRGLRTLPV 7495

SFTPPASSAGNGPSPTQK\*

>CYP107U2 Streptomyces avermitilis

MAGSARRRGRHGGGVGTVAGSAAGTRRLQRERGSRYRHPVNAPH

SEPELFTWEFATDPYPAYAWLREHAPVHRTTLPSGVEAWLVTRYADAKQALADARLSK

NPVHHSEDAPGKSKTGIPGERSANLMTHLLNIDPPDHTRLRRLVSKAFTPRRVAEFAP

RVQELTDHLIDQFAQTGSADLIHEFAFPLPIYAICDLLGVPREDQDDFRDWAGMMIRH

GGGPRGGVARSVKKMRGYLAELIHRKREALPADPGPGEDLISGLIRASDHGEHLTENE

AAAMCFVLLFAGFETTINLIGNGTYALLRNPQQRARLQQSIERGEQDLLDTGIEELLR

YDGPVELATWRYATEPLDMGGQRIASGDPVLVVLAAADRDPARFDEPDTLDLSRSDNQ

HLGYGHGIHYCIGAPLARLEGRTALATLLRRLPDLRLAADPADLRWRGGLIMRGLRNL

PVEFTAT

>CYP107U3 Streptomyces peucetius

MTHLLNIDPPDHTRLRRLVSKAFTPRRVAEFAPRVQELTDRLIDAFIDKGEADLIHEFAF

PLPIYAICDMLGVPREDQDDFRDWAGMMIRHGGGPRGGVARSVKKMRGYLAELIHRKREQ

PGDDLISGLIKASDHGEHLTENEAAAMAFILLFAGFETTVNLIGNGVYALLCNPEQRERL

QASLAAGERGLLETGVEELLRYDGPVELATWRFATEPLTVGGQRIAAGDPVLVVLAAADR

DPERFADPDTLDLSRSDNQHLGYGHGIHYCLGAPLARLEGQTALATLLRRVPDLRLTGDP

ADLRWRGGLIMRGLRTLPVAWGAGGAPGGIKPGTAQTN\*

>CYP107U4 Streptomyces scabies SCAB54411

MTNQPAPSSA VPTGTGAPEL FTWEFATDPY PAYAWLREHA PVHRTRLPSG VEAWLVTRYG

DAKQALADGR LSKNPAHHAE PAHARGKTGI PGERKAELMT HLLNIDPPDH TRLRRLVSKA

FTPRRVAEFA PRVQELTDRL IDGFADRGEA DLIHEFAFPL PIYAICDLLG VPREDQDDFR

DWAGMMIRHG GGPRGGVARS VKKMRGYLAD LIHRKREGLT DHPAPGEDLI SALIRASDHG

EHLTENEAAA MAFILLFAGF ETTVNLIGNG TYALLTHPEQ RARLQTSLAA GETGLLETGV

EELLRYDGPV ELATWRFATE PLTLGGQDIA PGDPVLVVLA AADRDPARFD DPDTLDLSRR

DNQHLGYGHG IHYCLGAPLA RLEGQTALAT LLTRLPDLRL AVDSADLRWR GGLIMRGLRT

LPVEFTPRKR S

>CYP107U5 SBI\_8392 Streptomyces bingchengensis

80% to CYP107U2 Streptomyces avermitilis

MSDRHHPACSPALFSWEFAADPYPAYAWLREHAPVHRTTLPSGVEAWLVT

RYADARATLADPRLSKNPIHHSEAAHAKGKVGIPGERSADLMTHLLNIDP

PDHTRLRRLVSKAFTPRRVAAFAPRVQELTDGLIDGFQRRGEADLIHEFA

FPLPIYAICDLLGVPREDQDDFRDWAGMMIRHGGGPRGGVARAVKRIRAY

LADLIHRKRESLRENAEGKAGEKADDLISGLIRASDHGEQLTENEAAAMC

FVLLFAGFETTVNLIGNGTYALLRDPAQCDRLRRAAQEGDEGLLATGVEE

LLRYDGPVEISTWRFATEPVVIGGQRIAAGEPVLVVLAAADRDPERFDSP

DVLDLSRADNQHLGYGHGIHYCLGAPLARLEAQTAIGTLLRRLPDLRLAV

EPEEIRRRGGLIMRGLRELPVTWGPII

>CYP107U8 SGR4436 Streptomyces griseus

MNDSPAPRPSEPSACPHSPAGPHGAPELFTWEFATDPYPAYAWLREHRPVHRTALPSGVEAWLVTRYGDAREALADARLSKNPANHAESPHAKGKTGIPGERKAELMTHLLNIDPPDHTRLRRLVSKAFTPRRVAEFAPRVQELTDRLIDDFVEKGSADLIHDFAFPLPIYAICDLLGVPEEDQDDFRDWAGMMIRHGGGPRGGVARSVKKMRGYLAELIHRKRENPGDDLISGLIRASDHGEHLTENEAAAMAFILLFAGFETTVNLIGNGTYALLRHPGQRARLEASLAAGESALLATGLEELLRFDGPVEMATWRYATEALTLGGEEIAAGDPVLVVLAAADRDPARFTDPDTLDLARRDNQHLGYGHGIHYCLGAPLARLEGQTALTTLLRRLPDLRLAGEPGDLRWRGGLIMRGLRTLPVAFEPGSRTRKSDTASTL

>CYP107V1 Streptomyces avermitilis

MSGASARCPFSGAGGGTDVLPLPADPGTAAGAPAPGPPDAPAAP

APRTADRSAPHAADPHAPSTADLPRFPFPGLSGIPLDPVLLDRYRGEPLVPVGLANGR

EALLVTRYADVRTVLSDDRFSREAWANGTLFARRSGALALVTSDAPTHTRRRSRVQSR

FTHRRAEEDRPRIARIAAELLDSLQAADTGRPVDLIAEFTTPFPYRVICEMLGVPVAD

LDRLLPSVTVMMSAGRFSADEAARAHEVMYGYFFGQLAARREAIAAGCPGDDLLTSLL

SAPRETRLSDEEIVVFGFGLMMAGGETTASHLAMCVLQVLGTPGLADRLRRDASAVPA

VVEELLRWVWFAGTGGQPHVALEDVELAGRVLPAGQVVIPLTDAANRDPGVFPDADEF

RPDRAPNPHIGFGHGRHMCLGAAHARVELQEGLTAVLERLDHLELAVEPAELRWRDQM

FMRGVWELPVRWHTKEDGRC

>CYP107W1 Streptomyces avermitilis

MAEAPSEPIAFPFPDPPSVCELPPELAEIRDGQSVVEVKFPDGI

SGWMVTKHADVRKVLVDSRFSSKVMATAAAAMSETETGKLMNESLVGMDAPEHTRLRK

LVTKAFTARRVETLRPRITELVGQLLDELETLPRPVDLVKNFSVPLPVRVICELLGVP

AGDQDTFHAWSNALLGDWQQVVEKEAATVSLVNYFGELIAVKRENPADDLISELIAIS

DGDSTLTEREIIALSIGILSAGHETTANQISMFLVTLLHNPEELDKLRDNREAIPKAV

DELLRFVPLTTTGGIIPRLTTAEVELSGGQVLPAGAVVLPAVATANRDPEVFEDGERL

NVTRENNPHLAFGAGIHHCLGAQLARIELQEALGAILDRMPQVRLAVPESELRLKSAS

IIRGLESLPITW

>CYP107X1 Streptomyces avermitilis

MDPAEGLLADPYAVYDRLRDTAPVHRIAGTDGKPAWLVTRYDDV

REGLANPLLSLDKKHALPGNYRGLALPPALDANLLNMDAPDHTRIRRLVGRAFTLRRV

EQLREPVRETAHRLLDALGTHGSTDLIASYAAPLPITVICDLLGVPDEHRRDFRAWTD

PLVTPDPARPDVARESVVSLLGFFTGLLADKRKNPADDLLSDLIAVQEEGDRLTEDEL

MSLAFLILFAGYENTVHLIGNAVLALLRHPEQLAALREDPARLPDAVGEFARYEGPAL

LAIRRFPVRDVTIGGVTVPAGETVLLSLSAANRDPSRFPDPDRLDLGRDAAGHLALGH

GVHYCLGAPLARLETEVALAALLERFPDLALAETEPRRRPSLRARGLLALPVTY

>CYP107X2 Saccharopolyspora erythraea NRRL23338

MRPVEIDDEFVTCPHAAYARLREQGPVHRAVAPDGSRVWLVTRYDDVRAALADSRLSLDK

AHATDGYRGLSLPPALDANLLNMDAPEHTRLRRTVTRAFTAHRTELLRPRVQEIADELLA

AVAGQERAELMSAFAGPLPITVICELLGVDARDRPDFRAWTDEMLAPSTPDRARDSLRSL

YAFLVDLIARKRAEPGADMPSTLVGLRDEDGSLTEDELTSTAFLVLFAGYENTVNLIGNG

LAALLARPAQLAAVRSDRGLLPSTVEELLRFDPPPQLSIRRFPKEDLEIGGVRIPAGDTV

LLSLVSAHHDPARFTSPGELIPDRADNAHLAFGHGPHFCIGAPLARMEAEVAFSTVLTRF

PALSLAVDPAELRWRPSFRNRGLRELPVRLS

>CYP107X3 SBI\_2046 Streptomyces bingchengensis

67% to CYP107X1 Streptomyces avermitilis

MQNTANTAVPGPPEPFDTRVLLEDPHTAYAELREAGPVHRIPGPDGRPAW

LVTRYDDVRRALADPRLSLDKSNALPGNFRGFALPPALDANLLNMDPPDH

TRVRRLVTKAFTPGRVERMREPVRRAADELLDAVEPAGRADLIAAYAGPL

PITVICDLLGVPQRDRRDFRAWSDALIAPDPERPHVAKEAVGNMLRFYTG

LIASKREEPGDDLLSDLIAVRDDAVGGAGEGGDRLTEDELTSLAFLLLMA

GYENVTHLIGNAVLSLLDHPPLLRELRERPAGIAAAGGXAVEEFARHDGP

APLAIRRFPLEDVEIGGVTVPAGETVLLSLASANRDPGHFKEPDRLDPDF

GRLGHLAFGHGIHYCLGAPLARLEAETALAALLSRLPRLRLDISHTELRR

RPTIRARGLISLPVAW

>CYP107Y1 Streptomyces avermitilis

MDFGADPYPEYAWLRAEEPVRQVLEGRGLYGLLVTRYEDVRKLL

SDPRMSKDPRNAPLDWQEAGKGRPLEDRTGLGTHLLTTDAPEHTRLRRLVSTAFTARR

VEGLRAQVQHITDGLLDTIVPRGQAELIGDFAFPLAITVICELLGVPKADQDVFRQWT

KDFRRWTNTDSAQADRGDARPVGLRDLLEYLTRLVDKRRQDPADGLVDALIAARDDDD

RLNEAELLSMMSLLLVGGFETTVNLIGNGTLALLRHPDQLALLRERPELVDSALEEML

RYDGSFETATWRFPLEPIEVAGTRIEKGHPVLLSLASANRDGAKFPAPDDFDVTRADP

AHVAFGRGAHFCLGAPLARLEGRIAFHGLLRRLPGLALSVPPEQLRWQRSLTVRGLEA

LPVTFDA

>CYP107Z1 Streptomyces rimosus ssp. paromyceticus strain R-2374

MTTSPTESRAATPTGSTASPSTASAPATTPSAATSSDTTYPATTDRTTLPSYVGLHPGEPNLMEPELLDNPYTGYG

TLREQAPLVRARFIDDSPIWLVTRFDVVREVMRDQRFVNNPTLVPGIGADKDPRARLIELFGIPEDLTPYLADTIL

TSDPPDHTRLRRLVSRAFTARRIQDLRPRVEQITDALLERLPDHAEDGVVDLVEHFAYPLPITVICELVGIDEEDR

TLWRRFGADLASLNPKRIGATMPEMIAHIHEVIDERRAALRDDLLSGLIRAQDDDGGRLSDVEMVTLVLTLVLAGH

ETTAHLISNGTLALLTHPDQRRLIDEDPALLPRAVHELMRWCGPIQATQLRYAMEDTEVAGVQVRQGEALMFSLVA

ANHDPRHYTGPERLDLTRQPAGRAEDHVGFGHGMHYCLGASLARQEAEVAYGKLLTRYPDLELALTPEQLEDQERL

RQPGTWRLRRLPLKLHARS

>CYP107Z2v1 Streptomyces albofaciens strain C-0083

MTTSPTESRAATPPDSTASPSTAAAPATTPSAAASPDTTSPATTDRTTLPSYVGLHPGEPNLMEPELLDNPYTGYG

TLREQAPLVRARFIDDSPIWLVTRFDVVREVMRDQRFVNNPTLVPGIGADQDPRARLIELFGIPEDLAPYLTDTIL

TSDPPDHTRLRRLVSRAFTARRIQDLRPRVERITDELLARLPDHAEDGVVDLVEHFAYPLPITVICELVGIDEEDR

ALWRRFGADLASLNPKRIGATMPEMIAHIHEVIDERRADLRDDLLSGLIRAQDDDGGRLSDVEMVTLVLTLVLAGH

ETTAHLISNGTLALLTHPDQRRLIDEDPALLPRAVHELMRWCGPIQATQLRYAMEDTEVAGVQVRQGEALMFSLVA

ANHDPRHYTGPERLDLTRQPAGRAEDHVGFGHGMHYCLGASLARQEAEVAYGKLLTRYPDLALALTPEQLEDQERL

RQPGTWRLRRLPLRLHAES

>CYP107Z2v2 Streptomyces rimosus ssp. paromyceticus strain BOEH-4355

MTTSPTESRAATPPDSTASPSTASAPATTPSAAASPDTTDRTTLPSYVGLHPGEPNLMEPELLENPYTGYGTLREQ

APLVRARFIDDSPIWLVTRFDVVREVMRDQRFVNNPTLVPGIGADKDPRARLIELFGIPEDLAPYLTDNILTSDPP

DHTRLRRLVSRAFTARRIQDLRPRVERITDELLERLPDHAEDGVVDLVEHFAYPLPITVICELVGIDEEDRALWRR

FGADLASLNPKRIGATMPEMISHIHELIDERRAALRDDLLSGLIRAQDDDGGRLSDVEMVTLVLTLVLAGHETTAH

LISNGTLALLTHPDQRRLIDEDPALLPRAVHELMRWCGPIQATQLRYALEDTEVAGVQVRQGEALMFSLVAANHDP

RHYTGPERLDLTRQPAGRAEDHVGFGHGMHYCLGASLARQEAEVAYGKLLTRYPDLALALTPEQLEDQERLRQPGT

WRLRRLPLRLHAQS

>CYP107Z3 Streptomyces sp. strain IHS-0435

MTELADSPFSEHVGKHPGEPNVMEPALLTDPFTGYGELREQGPVVRGRFADDTPVWFITRFEEAREVLRDHRFANA

PAFAAGGGSGDTPSNRLMEIMGLPEHYRVYLANTILTMDAPDHTRIRRLVSRAFTARKITDLRPRVEDIADDLLRR

LPEHAEDGVVDLIKHYAYPLPITVICELVGIPEEDRLQWRDWGSAFVSLQPDRLSKAFPAMIEHIHALIRERRAAL

TDDLLSELIRVHDDDGGRLSDVEMVTMVLTLVLAGHETTAHLIGNGTAALLTHPDQLHLLKSDPELLPRAVHELMR

WCGPVQMTQLRYATEDVEVAGVQVKQGEAVLAMLVAANHDPRHFADPARLDLTRQPAGRAENHVGFGHGMHYCLGA

SLARQEGEVAFGNLLAHYPDVSLAVEPDALQRVPLPGNWRLAALPVRLR

>CYP107Z4 Streptomyces lydicus strain NRAB-0114

MSASTSSPLSAHVGKHPGEPHVMDPALISDPFGGYGALREQGPVVRGRFFDDSPLWLVTRFEEVRQVLRDQRFVNN

PADPALGVAPEDSPQLRALAMLGIPEHLHGYLLNSILNYDAPDHTRLRRLVSRAFTARKITDLRPRVAQITAELLD

RLPEHAEDGVVDLIEHFAYPLPITVICELVGIAAEDRPQWRSWGADLVSVDPDRLGRTFPAMIDHIHALIGQRRAA

LTDDLLSELIRTHDDDGSRLSDVEMVTLVLTLVLAGHETTAHLIGNGTAALLTHPDQLRLLKDDPALLPRAVHELM

RWCGPVHVTQLRYAAEDVDLAGTRIRRGDAVQAVLVSANHDPRHYTDPERLDLTRQPAGRAENHVGFGHGAHYCLG

ASLARQEGEVALGALFDRYPDLALAVAPEELERTPVPGTWRLTSLPVRLG

>CYP107Z5V1 Streptomyces lydicus strain NRRL-2433

MSALPSNTFTEHVGKHPGEPNVMDPALIGDPFAGYGALREQGPVVRGRFVDDSPVWFVTRFEEVREVLRDQRFRNN

PVSSAPDADPEDTPLSRLMDMMGFPEHLRVYLLGSILNNDAPDHTRLRRLVSRAFTARKITDLRPRVAQIADELLA

RLPEHAEDGVVDLIQHFAYPLPITVICELVGIPEEDRPQWRTWGADLVSLQPDRMSRSFPAMIDHIHELIAARRRA

LTDDLLSELIRTHDDDGSRLSDVEMVTMVLTVVLAGHETTAHLIGNGTAALLTHPDQLRLLKDDPALLPRAVHELM

RWCGPVHMTQLRYAAEDVELAGVRIRKGDAVQLILVSANRDPRHYTEPDRLDLTRHPAGHAENHVGFGHGAHYCLG

ATLAKQEGEVALGALLRHFPELSLAVAPDALERTPVPGSWRLNALPLRLR

>CYP107Z5v2 Streptomyces chattanoogensis DSM-40241

MSASPSNTFTEHVGKHPGEPNVMDPALIGDPFAGYGALREQGPVVRGRFMDDSPVWFVTRFEEVREVLRDPRFRNN

PVSAAPGAAPEDTPLSRLMDMMGFPEHLRVYLLGSILNNDAPDHTRLRRLVSRAFTARKITDLRPRVTQIADELLA

RLPEHAEDGVVDLIQHFAYPLPITVICELVGIPEEDRPQWRTWGADLVSLQPDRMSRSFPAMIDHIHELIAARRRA

LTDDLLSELIRTHDDDGSRLSDVEMVTMVLTVVLAGHETTAHLIGNGTAALLTHPDQLRLLKDDPALLPRAVHELM

RWCGPVHMTQLRYAAEDVELAGVRIRTGDAVQLILVSANRDPRHYTDPDRLDLTRHPAGHAENHVGFGHGAHYCLG

ATLAKQEGEVALGALLRHFPELSLAVAPDALERTPVPGSWRLNALPLRLG

>CYP107Z5v3 Streptomyces lydicus strain R-401

MSASPSNTFTEHVGKHPGEPNVMDPALIGDPFAGYGALREQGPVVRGRFMDDSPVWFVTRFEEVREVLRDPRFRNN

PVSAAPGAAPEDTPLSRLMDMMGFPEHLRVYLLGSILNNDAPDHTRLRRLVSRAFTARKITDLRPRVTQIADELLA

RLPEHAEDGVVDLIQHFAYPLPITVICELVGIPEEDRPQWRTWGADLVSLQPDRMSRSFPAMIDHIHELIAARRRA

LTDDLLSELIRTHDDDGSRLSDVEMVTMVLTVVLAGHETTAHLIGNGTAALLTHPDQLRLLKDDPALLPRAVHELM

RWCGPVHMTQLRYAAEDVELAGVRIRTGDAVQLILVSANRDPRHYTDPDRLDLTRHPAGHAENHVGFGHGAHYCLG

ATLAKQEGEVALGALLRHFPELSLAVAPEALERTPVPGSWRLNALPLRLR

>CYP107Z5v3 Streptomyces kasugaensis strain A/96

MSASPSNTFTEHVGKHPGEPNVMDPALIGDPFAGYGALREQGPVVRGRFMDDSPVWFVTRFEEVREVLRDPRFRNN

PVSAAPGAAPEDTPLSRLMDMMGFPEHLRVYLLGSILNNDAPDHTRLRRLVSRAFTARKITDLRPRVTQIADELLA

RLPEHAEDGVVDLIQHFAYPLPITVICELVGIPEEDRPQWRTWGADLVSLQPDRMSRSFPAMIDHIHELIAARRRA

LTDDLLSELIRTHDDDGSRLSDVEMVTMVLTVVLAGHETTAHLIGNGTAALLTHPDQLRLLKDDPALLPRAVHELM

RWCGPVHMTQLRYAAEDVELAGVRIRTGDAVQLILVSANRDPRHYTDPDRLDLTRHPAGHAENHVGFGHGAHYCLG

ATLAKQEGEVALGALLRHFPELSLAVAPEALERTPVPGSWRLNALPLRLR

>CYP107Z6 Streptomyces sp. strain I-1525

MSALSSSPFAEHIGKHPGEPNVMEPALINDPFGGYGALREQGPVVRGRFMDDSPVWFVTRFEEVRQVLRDQRFVNN

PASPLLGSQVEEMPMVKLLEQMGLPEHLRVYLLGSILNSDAPDHTRLRRLVSRAFTARKITGLRPRVEQIADELLA

RLPEHAEDGVVDLIQHFAYPLPITVICELVGIPEADRPQWRAWGADLVSLEPDKLSTSFPAMIDHTHELIRQRRGA

LTDDLLSELIRAHDDDGSRLSDVEMVTMVFALVFAGHETTAHLIGNGTAALLTHPDQLRLLKDDPALLPRAVHELM

RWCGPVHMTQLRYASEDIDLAGTPIRKGDAVQLILVSANFDPRHYSDPDRLDLTRHPAGHAENHVGFGHGMHYCLG

AALARQEGEVAFGKLLAHYPDVALGVEPEALERVPMPGSWRLNSLPLRLAKR

>CYP107Z7 Streptomyces tubercidicus strain DSM-40261

MSAISSSPFAAHVGKHPGEPNVMDPALITDPFGGYGALREQGPVLPGRFMDDSPVWLVTRFEEVRQVLRDQRFLNN

PAASSPGHSIDESPTARLLDMMGMPEHFRPYLMGSILNNDAPDHTRLRRLVSRAFTARKITDLRPRVEQLADELLA

RLPEHAEDGVVDLIKHFAYPLPITVICELVGIPEADRPQWRKWGADLVSLQPERLSTSFPAMIEHIHELIRERRGA

LTDDLLSELIRTHDDDGSRLSDVEMVTMVLTVVLAGHETTAHLIGNGTAALLTHPDQLRLVKDDPELLPRAVHELL

RWCGPVQMTQLRYASEDVEIAGTPIRKGDAVQLILVSANFDPRHYTAPERLDLTRHPAGHAENHVGFGHGMHYCLG

ATLAKQEGEVAFGKLFTHYPELSLAVAPDELERTPVPGSWRLDSLPVRLG

>CYP107Z8 Streptomyces platensis strain Tu-3077

MSALSSSPFAAHVGKHPGEPNVMDPALIADPFGGYGALREQGPVVRGRFMDDSPVWLVTRFEEVRQVLRDQRFLND

PTAPSLGRSFDDSPTARLLEMMGLPEHFRPYLLGSILNNDAPDHTRLRRLVSRAFTARKITDLRPRVEQIADELLT

RLPEYAEDGVVDLIKHFAYPLPIAVICELVGIAEADRPQWRKWGADLVSLQPDRLSTSFPAMIEHIHELIRERRGA

LTDDLLSELIRAHDDDGGRLSDVEMVTMILTVVLAGHETTAHLIGNGTAALLTHPDQLRLLRDDPALFPRAVHELL

RWCGPVHMTQMRFASEDVDIAGTKIRKGDAVQLILVSANFDPRHYTDPERLDLTRHPAGHAENHVGFGHGMHYCLG

ATLAKQEGEVAFEKLFAHYPEVSLGVAPEQLERTPLPGSWRLDSLPLRLR

>CYP107Z9 Streptomyces tubercidicus strain NRAA-7027

MSALSNSPLAAHVGKHPGEPNVMDPALITDPFGGYGALREQGPVVRGRFMDDSPVWLVTRFEEVRQVLRDQRFVNN

PAAPSLGRSIDESPAVRLLEMLGLPDHFRPYLLGSILNYDAPDHTRLRRLVSRAFTARKITDLRPRVEQITDDLLT

RLPEHAEDGVVDLIQHFAYPLPITVICELVGIAEADRPQWRKWGADLVSLEPGRLSTAFPAMVEHIHELIRERRGA

LTDDLLSELIRTHDDDGGRLSDIEMVTMILTIVLAGHETTAHLIGNGTAALLTHPDQLRLLKDDPALLPRAVHELM

RWCGPVHMTQLRFASEDVEVAGTPIHKGDAVQLILVSANFDPRHYTDPDRLDLTRHPAGHAENHVGFGHGMHYCLG

ATLAKQEGEVAFSRLFTHYPELSLGVAADQLARTQVPGSWRLDTLPLRLG

>CYP107Z10 Streptomyces tubercidicus strain I-1529

MSALSSSPFAAHVGKHPGEPNVMEPALLTDPFAGYGALREQAPVVRGRFVDDSPVWFVTRFEEVRQVLRDQRFVNN

PAAPPLAPSAEENPLTRLMDMLGLPEHLRVYMLGSILNYDAPDHTRLRRLVSRAFTARKITDLRPRVEQIADELLA

RLPEYAEDGVVDLIQHFAYPLPITVICELVGIPEADRPQWRKWGADLISMDPDRLGATFPAMIEHIHEMVRERRAA

LTDDLLSELIRTHDDDGGRLSDVEMVTMILTLVLAGHETTAHLISNGTAALLTHPDQLRLLKDDPALLPRAVHELM

RWCGPVQMTQLRYAAADVDLAGTRIHKGDAVQLLLVAANFDPRHYTDPDRLDLTRHPAGHAENHVGFGHGAHYCLG

ATLAKQEGEVAFGKLLAHYPEMSLGIEPERLERLPLPGNWRLNSLPLRLG

>CYP107Z10 Streptomyces platensis strain I-1548

MSALSSSPFAAHVGKHPGEPNVMEPALLTDPFAGYGALREQAPVVRGRFVDDSPVWFVTRFEEVRQVLRDQRFVNN

PAAPPLAPSAEENPLTRLMDMLGLPEHLRVYMLGSILNYDAPDHTRLRRLVSRAFTARKITDLRPRVEQIADELLA

RLPEYAEDGVVDLIQHFAYPLPITVICELVGIPEADRPQWRKWGADLISMDPDRLGATFPAMIEHIHEMVRERRAA

LTDDLLSELIRTHDDDGGRLSDVEMVTMILTLVLAGHETTAHLISNGTAALLTHPDQLRLLKDDPALLPRAVHELM

RWCGPVQMTQLRYAAADVDLAGTRIHKGDAVQLLLVAANFDPRHYTDPDRLDLTRHPAGHAENHVGFGHGAHYCLG

ATLAKQEGEVAFGKLLAHYPEMSLGIEPERLERLPLPGNWRLNSLPLRLG

>CYP107Z11 Streptomyces platensis strain NRAA-7479

MSALPTSPFAAHVGKHPGEPNVMDPALITDPFTGYGALREQGPVVRGRFVDDSPVWLVTRFEEVRQVLRDQRFVNN

PAAPSLGHAAEDNPLTRLMDMLGLPEHLRPYLLGSILNYDAPDHTRLRRLVSRAFTARKITDLRPRVEQIADALLA

RLPEHAEDGVVDLIRHFAYPLPITVICELVGIPEADRPQWRTWGADLVSMEPDRLTASFPPMIEHIHRMVRERRGA

LTGDLLSELIRAHDDDGGRLSDVEMVTLILTLVLAGHETTAHLISNGTAALLTHPDQLRLLQDDPALLPRAVHELM

RWCGPVQMTQLRYAAADVDLAGTTIHRGDAVQLILVSANFDPRHYTDPDRLDLTRHPAGHAENHVGFGHGAHYCLG

ATLAKQEGEVAFGKLLAHYPEMALGVAPERLERTPLPGNWRLNALPVRLG

>CYP107Z12 Streptomyces tubercidicus strain R-922

MSELMNSPFAAHVGKHPGEPNVMDPALITDPFTGYGALREQGPVVRGRFMDDSPVWLVTRFEEVRQVLRDQRFVNN

PASPSLNYAPEDNPLTRLMEMLGLPEHLRVYLLGSILNYDAPDHTRLRRLVSRAFTARKITDLRPRVEQIADALLA

RLPEHAEDGVVDLIQHFAYPLPITVICELVGIPEADRPQWRTWGADLISMDPDRLGASFPAMIEHIHQMVRERREA

LTDDLLSELIRTHDDDGGRLSDVEMVTMILTLVLAGHETTAHLISNGTAALLTHPDQLRLVKDDPALLPRAVHELM

RWCGPVHMTQLRYATADVDLAGTPIRQGDAVQLILVSANFDPRHYTDPDRLDLTRHPAGHAENHVGFGHGAHYCLG

ATLAKQEGEVAFGKLLTHYPDISLGIAPEHLERTPLPGNWRLNSLPVRLG

>CYP107AA1 Mycobacterium smegmatis

MTPYSRRDRNH

MLRLGNSFVQNPHEVYDRLRRSGPVQRVEMWGGVPVWLVTRYQEARNLLT

DPRIGKDGAAASALFPPGTDGSIGTVLGDNMLFRDPPDHTRLRRFVTSAF

TAHAVRRLRPTIAGFADALLDDIAASVPGQVDLLQAFAQPLPVQVIGELL

GVPERDRELFAALVVPIFTSTDTTVLRRAQKELTQLLTDMLAEKRQSPAD

DVLSSLVHRRDGTDQLSEAELLGTAFLLIVAGYETTVNLLANGILALLRN

PEQLRAVRADRSLLPRAVEEALRFESPLNTATVRYTSAPVTVGDVEIPSG

ELVVIGLLAANHDDEQFPDAHRFDVSRTHNRHLAFGYGVHHCVGAPLARM

EAEIGFDRLLSRFEVMELVDSGPPRYRPSTLMRGVERLPVILGYPHDIAS

TMREWSGSLPSSGEADSSFAH

>CYP107AB1P Mycobacterium smegmatis

MILDEQFAQDPEGLYRMLRSEAPVCEVELIGGVRGWLVTRYADVMALLKD

PRVSKDHTSALPRLAPDRVRPYISPQLHNHMLNLDPPEHTRLRRLVVQAF

TPKALARMQPVIDAIADELLDDIDLRSGDEPIDLMADYAEPLPIQVIAEL

LGVAVEYA\*PFRAAVTPLLMSVTVEEKAESGRATIEILNAVIDEKIREPG

EDLLSGMIGASVDGHGLTRDELMAMCFLLITAGYETTVNLIGNGTLALID

NPSQLEKVRENPDLTAGAVEEILRFDGPVNIATWRYATADIDVDGVVIPA

NEQIFLSLLSANRDTGRFENADRFDIERNTRGHIAFGHGIHYCLGAPLAR

MEGVTAIGRIVQRYDSITLDPTAELRYHNGTLMHGLKSLPVRLTRVPQPRP

>CYP107AC1 Streptomyces atroolivaceus

MSATRRVHIYPFEGEVDGLEIHPKFAELRETDPLARVRLPYGGE

GWMVTRYDDVRAANSDPRFSRAQIGEDTPRTTPLARRSDTILSLDPPEHTRLRRLLSK

AFTARRMGAMQSWLEELFAGLLDGVERTGHPADIVRDLAQPFTIAVICRLLGVPYEDR

GRFQHWSEVIMSTTAYSKEEAVSADASIRAYLADLVSARRAAPHDDLLGVLVSARDDD

DRLTEDELITFGVTLLVAGHETSAHQLGNMVYALLTHEDQLSLLREQPELLPRAVEEL

LRFVPLGNGVGNARIALEDVELSGGTVRAGEGVVAAAVNANRDPRAFDDPDRLDITRE

KNPHLAFGHGAHYCLGAQLARMELRVAIGGLLERFPGLRLAVPADQVEWKTGGLFRGP

QRLPIAW

>CYP107AD1 Streptomyces hygroscopicus

MSGRHFEQGERGTAMADTPEEELRILDPQSVAQELRKHGPPRQI

TMHGTTAWLVSRYEEVRDCLGHPGMSPAAAYAASQGQTNPVSGLFEDTVAGTNPPQHT

RLRRLLAKAFTVRRVESLRPRVQEITDTLLDRIAVDGRADLVSALAIPLPMQVICELL

GVPIADRTEFHQWADLMLTPPLDPDTAARSQDASAKLWTYMEDLAEARRKAPEDDLIS

DLMSAHEDDRLSHREVVATARMMLIAGYELTGSFISNAVFSLLSQPDQMELLRKDPEL

AGRGLEELLRHAGPGILIVRFANEDVEIGSVSIRAGDQVLLDMDAAHSDPAHFTDGER

LDLTRDSAVHLQFGHGIHYCIGAPLARVEGQIALESLVRRFPGLRLSVPAAEISHSKN

PFIRSLTALPVEFEAQQPVAG

>CYP107AE1 Streptomyces sp.

VILLKSLAANGLTASSCFTVSPLPIRSASPSIAFLTSSSERDSGVRNDRPSDAQPAIARF

RFPTPPHPRNPTQPHPTPPRPSPTDDPLQAPTFFADPYPTYARLRDTAPVLKVPTGSGGG

GRHSYVVTGYAEAREAFTDPRLSKDTASFFAGRPSQRDLHPAVSRNMLATDPPQHARLRA

LVTKAFTTGAVARLRPYISSLVDELLDTWPTHGTVDLIADLAVPLPVTVICELLGVPDSD

RASVRTWSSDLFAAGDPQRIDAASHAVGDYMTALVAAKRTAPGDSLLDDLIAVRDGQDHL

SEDELVSLAVLLLVAGHETTTNFIGNAALALLRHPESLAHLRAEPQLLGGALDELLRYDS

PVGIATFRFSTEALTLGGTEIPEGVPVLIAPGAANRDPDRFPDPDRLDLTRGATGHLAFG

HGIHRCLGAPLARAEAELALHAVITRYPQAALATPPETLPWRHTRLTRGLASLPITLRDH

PK\*

>CYP107AE3 SGR420 Streptomyces griseus

69% to CYP107AE2

MNDASEDSRSAPDLSSGCTAPRPRCPVRAVTSGSDGRESYLVTGYAEARDALSDVRLSKDTAAFFAGKGSRRRLHAAVAHTMLASDPPRHTRLRKLVTGAFTSGSIAALRPSIARLTDELLDRWPAGGAVDVVAALAVPLPVMVICELLGVPETDRPRVQRWSADLFAAGDPGRTDAASHAVAAYMTGLIVSKRLHPGDSLLDRLIAARERGDRLGEEELVSLAVLLLVAGHETTTNFLGNAVLALLRHPAELNRLRGDPGTIPRALDELLRFDPPVSTSTFRFATEAMSLGGTEIPAGVPVLVDINAANRDPERFTAPDRLDLDRDATGHLGFGHGIHRCLGAPLAKAEAHIALRAILTRFPDIRLAVAADRLDRRRTRLISGLDSLPVLL

>CYP107AF1 Streptomyces collinus DSM2012

MARTDAPQAAPPADLFTPAFHQNPHEALAGLRRTAPAVPVMTPN

GLRTWLVTGHEHARALLADPRLSKDMRVGRDLIPRNFVDPDKQREFLAESGERSQFPH

VLSVHMLDSDPPDHTRLRRLVGRAFTARRVESLRPRITELTDELLDAMARHERLDLME

ALAFPVPFTVICWLLGVPPDDRAAFRRWSNLLVSGAGTDEVREASASMITYLTELIEA

KRNEPADDMLTDLVHARDAGDQLSSDELISMAFLLLVAGHETTVNLIGNGALALLTHP

EVREQLAADESLWPGAVEEFLRYDGPVTNATWRFTTEPVEVGSVTIPEGEFVTISIGA

AGRDPDRYPDPDRLDITRAHSGSVAFGHGIHHCLGAPLARLEGRIVLSRLFARLPGLR

LAADPDELSWRSSLMMRGLEELPVFTA

>CYP107AG1 Streptomyces atroolivaceus

MSTEVETEKPAPVAYPFTGSEGLELSQSYAKLFEDGDPIRVQLP

FGEPAWLVTRYDDARFVLTDRRFSRHLATQRDEPRMTPRAVPESILTMDPPDHTRLRT

LVSKAFTPRRIESKRAWIGELAAGLVADMKAGGAPAELVGSYALAIPVTVICELLGVP

EDDRTRLRGWCDAALSTGELTDEECVQSFMDLQKYFEDLVKERRAEPRDDLTSALIEA

RDAHDRLAEPELIGLCISILIGGFETTASEISSFVHVLQQRRELWTRLCADPEAIPAA

VEELLRFVPFAANGISPRYALEDMTVGGVLVREGEPVIVDTSAVNRDGLVFDNADEVV

IDRADNRHMVFGHGAHHCLGAHLARVELQEALKALVEGMPGLRLSGDVEWKADMIIRA

PRVMHVEW

>CYP107AH1 Streptomyces peucetius

VTTTQDPVTAAERCTADFRRNPHPVYASLRDTAPVCPMKPPHGVETYLITRYEDARAALS

DPRLSKDMYGAMDAYRRIFGDSSVSLDDNMLNADAPKHTRLRRLVNSEFTPRRVEALRPK

IQDIVDQLLDACPTGEPVDLLPAFAFPLPITVICELLGVPAEERPHMQRLSTTVAQTGFS

KESKQAQQKAEEDLHSYFTQLIARKRERPGEDLLSALTEARDKDGGLSENELVSTAFLLM

FAGHKTTAYLIGNAVHHLMANPAQLRAVRENPELVGPAVEELVRYDGSVESATFRFATED

VEIGGTRIPKGALVQISLLSANRDPRKFESPDEFDVRRPGNAQSGHLGFGHGSHYCLGAP

LARLEMQLALTTLFGRFPAIAPADPSAEAKWMEVPFPAFRGLAELPVVLCPES\*

>CYP107AJ1 Streptomyces peucetius

MVNTGGEMPLATERLGDSFFQDPQGLFARLRSSAPVTPVITPEGTRVWLVTRYEDVRAAL

ADPRLAKDWVTHMTPDDFDINVDPVQAYLDQHMLNLDPPDHTRLRRLVVKAFTPRRVAAL

RPRISAVNGELLDAMADGPAETDLIEAFAFPLSVTVICELIGIPVGDRESFREWSGTLLS

SRGTREESRAAAVDMYEYFTRMVAERRRSPADDLLSALIAARDSGDSLSEHELLSMVFLL

LVAGHETMVNLIASGVLALLTHPAELGRLRDDPSLLPSAVEELLRYANPLNHATERFTLE

PVTIGDAIIPAKEWVMLATSSANRDASRFAD

ARPAGRGPGRVGPRRVRARDPLLSRRATG

AAGGRDRVRDAAVPVPGADAGGARVVAEVAALQPHPRAGGPPRPTALTRAGETCPARPDE

LGSTVDVADPKGRRPALPADG\*

>CYP107AK1 Streptomyces scabies SCAB79691

MVLGAEFVRN PHEVNARLRE QGAVHEVVMP TGLKVWWVTR WEEGRALLAD ARLSKNVADA

GKLFERHQSD MSRQRDYSHV INRSMVNMDP PDHTRLRGLV AKAFTMRQVT GLRPWIEKIA

DEVLGSLEGR VEFDVIADFA VPMVRTVISE FLGVPVADRA EFCAHAAVLT SDGDRESAAE

ASNALAELVS RIVTAKRADL GEDLLSSLIL AADGSDRLSD DEIISFTVLL FVGGFDTTVN

LLGNGMLALL RNPDQLAAVR DDPALLAGAV EEFLRYDGSA NISHWRRTVE PVTVGEVTIP

AGEFVFIALG SANRDPARFP EPDRLDVTRS AQGHLAFGHG IHHCIGAPLA RAEGEIAFRR

LLARFPSLEL TVDPEELEWR PSMLHHGLRS LPVRTAQR

>CYP107AL1 Streptomyces scabies SCAB63301

MDTASASPAG NGTDTETAYE YPFHRPSAVE VPPVYEELRA KCPVAKVRLP SGDEGYVVSR

YDDARVVLAD PRFSRAAMLD EGAPRLTAAP PMPGSLFTMD APEHTRVRRL VSREFTARRV

QNLRPRIQQM TDELLDDMEK LSPPVDLNPA FAFPLPVMVI CELLGVPFED RDRFRGWSDA

FVSLTAHTAE EVMEQRMSMV QYLAQLVQRK REEPADDLMS ALVAVHDEDG DRLSEHELIT

MGITLLVAGH ETTVSMIGKC VLTLLRHPEH LAALRERPET IDQVVEELLR INPIGDGGPF

RVTLEDVEIA GTTIPKGSGV IAAVASANQD PERFGADSGV FDPARSSAGA HLALGHGAHF

CLGAALARAE LQIAVSSLIR RFPRLALADE VGNLSLTSGM MVHALSRMPV TW

>CYP107AM1 Streptomyces scabies SCAB44031

MSQVETSGGT ASGSGTASGS GSGTSGGDRT RTGAPPDDEV IRLPMTGEGP LDPPAAWERL

RERCPVATVE LPSGDRAKFV SRYDDVRALL SDPRFARPRA GDDSARLSAD GSGGVATDAS

AAYPLAIPEA GEPHLRWRRQ VGRYFTAKRM AALRPGMTRI AGSLLDDMIE RGQPADLKAA

LGFPLPVYVI CELLGAPAED RDLFSHWSDA FLNVSRFSKE ETRTAFTEFT RYMADLVAAK

RSEPGEDLLS MLVVDSTALP EAERLTDAEL LATGMGLLVA GHETTANMIG KMAALLLADR

RRWEQLLADP SLVRTAVEEV LRFDANLSAF GMRRQLSEDV ALGREVLPGG TTVFCGMSSA

NRDDRVFSSP AEMDLTRSPN PHLTFGAGPH SCLGQALART ELQVALEVLL HRLPTLELAV

PPAELRRLEG LLVGGLREVP VRW

>CYP107AM2 SBI\_7397 Streptomyces bingchengensis

68% to CYP107AM1 Streptomyces scabies SCAB44031

MSQNDPTVRLPLPTDGPLDPPPEWELLRGRCPVATVELPSGDTGTLLTRY

DHIKALLSDPRFSRPAPEDDSARIAPEGAGGVSTNSGMSLSLQSNGEGHQ

RWRRHVGKYFTARRVTALRPGMEEMAETLIDAMVQSGSPADLKAALGFPL

PVYVICNLLGAPAEDRDRFSYWSDAFLNVSRYSVAETGAAHEDFVTYMSE

LIAAKRAEPSEDLISTLIEESRAEGEGLTDLELRDTGMALLVAGHETTAN

MIGKMVAMLLADRTRWDSLLADPSLIRTAVDEVLRSDANLGGYGVRRYLT

EDYEVDGAVLPGGTTVFCGLSAANRDERVFADPDEMDLTRSPNPHLTFGA

GAHSCLGQSLARTELQVVLEVLLHKLPSLDLAVPVARLRQIEGLTVGGLR

EVPVRW

>CYP107AN1 Bradyrhizobium japonicum USDA 110

1 MVTPGSGAAI GVFVSCGNRF EVTMNEQAQP AGGDPLFNPL SPDFIRNPYP HYDRLRAIDP

61 IHVTPFGQFV ASRHADVSLV MRDKRFGKDF VERSKRRYSE KIMDEPVFRS MSHWMLQADP

121 PDHTRLRGLV VKAFTARRVE DMRPRIQEIV DEAIDAVIDR GHMDLIEDFA FRLPVTIICD

181 MLGIPEDHRE VFYKSSRDGG RLLDPVPLTP EEIAKGNAGN MMAQMYFQQL FELRRRNPAD

241 DLTTQLVQAE EDGNKLTNEE LTANIILLFG AGHETTVNLI GNGLLALHRN PDQLALLKAR

301 PELMVNAIEE FLRYDSSVQM TGRVTLEDID DLGGRKIPKG ETVLCLLGSA NRDPAVYPDR

361 PDRLDVTRPN VKPLSFGGGI HFCLGAQLAR IEAEIAIATL LRRLPDLRID DVENPEWRPT

421 FVLRGLKSLP ASW

>CYP107AP1 Streptomyces rochei plasmid pSLA2-L

MNQPQLPEIPALNSELFHTDQYATYREILEQRPVTRVRFYDGSL

VWLVNRHEDVRAALTDPRLSNDPMKQSDIDLSAATGIPADLIEYFQRNMFRSDEPDHG

RLRKLVTREFTVRRINALRPRIRQIADDLLEKFAATGGGDLVEALARPLPLTVMCELL

GVPEEDRADFQTWSQHIVESSPEFAERNAVSYRSLFECVRSLIRRRRDEPGDDLLSAL

VDLRDVADRLSENELISTVFLLLVAGIETTVNVLGTGTFLLLTHPGELARLRADGALL

GPAVEEMLRYMAPIEITSRHTLEPVEIGGVSIDAQSTVLINLAAANRDPARFEDPQSF

RVDRNDGGHLTFGHGIHYCLGAALARAEAEVTFEALLERFPDLRLAASASDLTWRHAF

MRGPVELPVSWG

>CYP107AQ1 Saccharopolyspora erythraea NRRL23338

MFDTADPAFVADPYPCFAELRRRGEVHRHPGLGMAVAVSHAAASEVLRHRGLGRIWVDAQ

PAADFPAFNLLHRTSLLETEGAEHTRLRRSISAAFARGHVERVRPWVAGLADALVGGLVE

RGGGDVVEEVAAPLPVQVIAELLGVPESDRNLLRPWSNAIVKMYEPGLPERRRAAAESAA

AEFAEYMRALADRRRSAPADDMVSDLVAAEELSADEVVGTAVLLLMAGHEASVNLVANGV

LALLRHPGQWRRLVDDPGLVPTAVEELIRYDSPLQLFERTAVEDVVVAGHRVAAGSKIAA

LLGAAARDPEVFESPDVLDVGRQPNPHLGFGAGIHYCLGAPLARVEAAAALSALVRLAPR

LEQAGEPVRRPEFVIRGLRELPVSV

>CYP107AR1 Saccharopolyspora erythraea NRRL23338

VQPDQSPTPRPESRHSPAAACPHAAVHREERPGGLVTWQISAFSEARAALGDSRFSKDPR

RLGEALRAGGRSMFAEYGDNLLDNLLNSDPPDHTRLRRLVGKAFSPATIERLGPTTQRLA

DELVASMLPAGRADLLAQFAYPFAFGVIARVLGLPPDSYRIFQRWTESMTAPREQGTDRM

VAARHLCEHVTELVRRSREWLASAPAETLLDELVSARDDGDRLSENELVATVLLLIIAGH

ETTVNLIGNGVHALLQHPGQLALLRDHPDLIDGAVEELLRFQPPISKTTLRVTTTDVEVA

GTEIPAGSIVNVLVPAANRDQRQFPDADRLDITRPPSAHMSFGHGIHYCIGAPLARMEGR

IAIGALLRGLPGLRLAEPAAEIPWRASNILRGLQRLPVRFDSAGADDEVRDRRHAGAARV

HA

>CYP107AS1 Saccharopolyspora erythraea NRRL23338

MTESIQRDADSQEAACPHARAYPFGDPGALDLDPDYARVRDEEPLTRIRMPYGEQGWLVT

RYDDVRTVLADPRFSRSEVLKRDVPRPTPQQVERPGTLVTTDPPEHGRLRRLVAGAFTHR

RAESMRPRIRGVVDELVDEMLAGDKPADLVAAVSMPLPVNVICELLGVPREDRHVFHSGA

VLSDYTVPADEREATFKSLADYLAVLIAERRARPEGPGDDVLGALISARDTDGDRLSEDE

LIELWVDILVAGYASIMSVTPDMVVTLLTERDRWDGLVADPGGVPDAVEEMLRVMPTIIE

SGHSRVATEDVEIAGGTVRAGEAVLPCLPAANRDPAVFDAAEEMRLDRDAGKHIAFGFGP

HYCLGASLARVQLQSVLTALVRKVPTLDLVEAVREDSTRVAAAVQGQLLVTW

>CYP107AT1 Saccharopolyspora erythraea NRRL23338

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RLRPTAERLVGELLAAAMSGPADEPVDLMAELAFALPSNLISELLGMPPQDKPLFEQWSS

ALGRGLDPDFMLSPEEMQRRDQARTEFDGYFAELARRRRAEPADDLVSALVAVEEDGRNL

SMSELVSTCRLLLSAGYLSTAHLIGNGVNALLRHPEQFEWFRAHPDQVAGVVEELLRYDS

PVQTAGMRTALQDTEIGDQPVSAGEGAMLLVGAANRDPAAFPDPDRLDVSRKPERNLGFG

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>CYP107AT2 Saccharopolyspora erythraea NRRL23338

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VSAVLRDQAFGWGEAELAAGHFTTDDEGNTVRPLTFADPPEHTRIRSLVTSAFSARIVER

LRPRAQELARESLAAALAGGGSADVIQQVAYPLTGRLLCELLGVDPEYQERFRAWAEAMG

RGLDPDFMQSPDQLARREEARAHFHEYFAELAARRRAEPGDDLVSALVAVEQEGDRLTAT

ELVVTCTLLLSAGYATTVHLIGNGMLALLENPDQLAWLRANPGRVGDAVEEVLRFDGPIQ

LVSRVALRDTEVDGHAVAAGSPVLLLLAAANRDPAVFDDPDRLDVSRKPGRNLGFGVGIH

FCLGAPLARLTAQAALSLLVEHELVLDGPRPAPTGSLVLRGLAELPLRSA

>CYP107AU1 Saccharopolyspora erythraea NRRL23338

MTAGTNNAGRLGALAEAVLGYNPVDPEYHANAHEHHRRMAERGPIFRTPGGMWTAVSHAA

CSAVLRDDRFGHDPGSAAQNLFDSTQRPSVAQRSFEFMDGPDHSRLRRLVNRAFTARRVE

RLRPAVRTLADQLLTDVSGRIDVLADFILPLAMTTIVDMLGAPTEDNHLFRAWAEPIVRG

LDPDFLLSSSELAAREQANAEFAEYFDRLVALRRAEPKDDLISALIAVEDDGVVLSGNEL

ISMCLLLLAAGHESIMHLVGNGTVALLRDEDQLEHFRGHPGEVTNAVNELLRYDPPVVLL

VRTALADAEVLGNRVRRGEIVWLQIGAANRDPAVFPDPDRLDLTRDTGGSLAFGLGIHFC

IGASLARLEAAAALSALLHRDVALASEQLVHQKNVVIRGYEEVPVVLR

>CYP107AV1 Saccharopolyspora erythraea NRRL23338

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RLRKLAAPAFRPRKLENYRQRIEDTAHELLDRALAKGEFDLIRDFATPLPIRVICELLGL

PELGAERLAVHGAALSGALDGIRSIRHLRRMRASTLELNELFGDLIEQRRRQPGEDIVSD

LVTALDQDRLDSTELVQMCDLLLVAGFETTVNLIGNGVLALLERPDQWRLLCDDPDQAVG

VVEETLRWDPPVQTTMRVAHEPVEVAGRLLPRNSAVLPMLGAAGRDPAVHFAPDRFDITR

GTRGDHLAFSSGIHYCLGAPLARLESEIAFRCLATRVPELRRSGALVRRPTSVIHGLSAL

PVAASKATAGGRR

>CYP107AW1 Salinispora tropica (marine actinomycete)

MESVTSTSAPPPVPYIADPYPALARIRANGPVSILHSDEGIPMWVIARYRNVRAALADPR

FGQDARRAQTLADNRVAGVTLGGDVIHMLNSDPPDHTRLRHLVQGAFTARRVAAMRPLVE

RITTSLLDGVGGRQTVDLVQDFAFPLPMLVICELLGFPAEERDAYRSWSTAILTHNDDPA

AFATALRDMTDYIEVQLRHRRARPGEDLLTELLAARDAGQLTDDEIVGMVFLLLIGGHET

TVNLLGTATLALVRNPDQHRWLLANPHALSEAIDEFLRYESPVAMATLRFTTAPVTVDDV

VIPAGELVLVSLGGANRDPDRFPDADRLILDRRDTGHLAFGHGLHRCLGAFLGKLEGEVA

LGALLGRYPGLTLAAEVRQLRWRDTIMLRGLESLPVSLHG

>CYP107AX1 Salinispora tropica (marine actinomycete)

MTSRPTAVFDQCLLRDPHSRYNALRDQAPVHHVLTPDGAPAWLVTRYNDVRAAFTDPRLS

VDKRFSGTDGEHGSSLPPELDAHLLNRDPPDHTRLRRLAAAACTPRRVADLHPAVERIVS

TLLDGLAGHDRAELIGSLASPLPLQVMHELLGLPTQANIDFRTWTNTLLSADANQPAQSR

AAMANMRRFLIEQLAHKRAQPGDDLLTGLLAAREDDDRLTDDELVAMVFLLMFAGYDNTA

ALIGTVTHALLTNAELHEAVRGGSLALDELIDEVLRWNPAFPLAVRRFAREPITIAGQTI

PAGDRIWLCLASANRDPAQFTQPDELGIIGLRRSHLSFGHGIHYCLGAPLARLQTTIAVT

SLLNRFPEMRLAVPAHDIRWRESFRLRGLIALPVYL

>CYP107AY1 Salinispora tropica (marine actinomycete)

MSQDPTMRAELAPIPRSGARLGQEYDQLRNAGDVHQVLLPDSSLAWLVTNPKLVSRALTD

PRLALNRRHSRGSWSGFALPPALDANLLNLDAPDHTRLRRLVGPAFSPQRVSALRPRIRR

TAEHLLDTLVATSGPVDLVTGYCTPLSVQVIADLMGVPEAGRADLRTWTDTMLTSYPPDR

DAIRQAVVELHGYVVDLIDTKRQQPGDDLLSALVTIEQDGDRLTRDELTSLAFLILFAGY

ENTANLIASTVLRLLDHGGLRGVQLPEAIEETLRLEPPAPAAVRRFPTEEMTIGGATIPA

GDIVLLSIAAATRGTAGNAARLAFGNGPHFCLGAALARVEAEEALTVLARRLPDLALALP

VAQVRWRPTFRTHGPAELLVTW

>CYP107AZ1 Roseiflexus sp. RS-1, complete genome.

MHHPTEPPPELWSAAAISDPYPIYDRLRAEQPIRWTGGDWQIFR

YADAQALLRDPRLGADRLQVDPQWLIASGLEPLFKTRDSMMLFADPPDHTRLRTLVHR

AFTPRVVESYRPLVQRIVDQLLDAAAARGAIELIGEFAYPLPVTVIAHMLGVPVNMHD

QFRRWSDSLAAFIGGTTRPEADVLPAALKAVLEMTDFFLALVAERRRAPRDDLLSALA

QAEDGGDRLSEQELVANSILLLLAGHETTTNLIGNGMLALMRHPDQFALLRDHPELTP

SAIEELLRYDSPVQVTSRRALTDIEFQGHRIEEGQAVTVFIGAANRDPAQYQDPARLD

VTRGDVRHLSFGHGPHYCLGAPLARLEGQVAISALVRRFPHMRTLDEQVVWRDNFALR

GLQSLHIELE

>CYP107BA1 Roseiflexus sp. RS-1, complete genome.

4472327 MTPTIVARLASPEFLADPYPVYRQLIEQTPVFWLPHANAPGGMWCIARYDDIAFVLREAPIFKDT 4472133

4472132 SRIAPPDTLTPLDRAMLQRDPPDHTRLRRLASHAFTPRRVHDLMPRIEQI 4471983

4471982 SLDLIERIGARGEADFIADYA 4471920

4471920 PLPIIVIAELLGVPFEDHEQFSTWSDQIMAGSDSVLGGEEAARQSHQAMASLVDYFTTLI 4471741

4471740 RQRRHSPRDDLISALIAAHDAGDSLSEDELLGMCVLLLIAGHETTVNLIGNGLLTLLRH 4471564

4471563 PDQLNLLRRQSEYLTSAIEEMLRYESPVQRSTPRFAAEPFVIGGEQIEAGQQISLMFGAA 4471384

4471383 NRDPAHFSDPDRFDITRQPNPHLGFGMGIHYCLGAPLARIEARVAFTHILERLPAIRLAT 4471204

4471203 DTPAWKPVTWLRGLKSLPVLV\* 4471138

>CYP107BB1 PlaO2 [Streptomyces sp. Tu6071].

1 MDRVLDFLSS ADSAGELQPR LVELSRQETL PRVLLADGQE AWLVTRNEDV RTVLSDRSFT

61 RDVMGERARQ AGETPDGARS VNMDGRPHNE LRALVSKAFT VRRIEAMRPR IQAWTDELID

121 AMEETGPPAD LVAHLAVPLP ALAICELLGF PVEDRQVLSG WCERITRLGE GGPDQRAWQE

181 LSAYIARRVP VERAAARGGL APETSILTRL VHAHDSEDAL SMEELLSLTV VVLAGGLETT

241 QTAIGAGMVR LFRNPAQLDK VRADPDLVVP AVEEILRYQP VIDVNRVQVA TRTVRLGGQE

301 IRAGDLVQVS VNAANRDETV FPDSERCDVT RGPNPHLAFG YGAHHCLGAA LARLELKTAF

361 STLLRRLPDL RPAVPLESLG WRGGHVTLGL EELPVAW

>CYP107BC1 PlaO5 [Streptomyces sp. Tu6071].

1 MTESLETTSP DPTRSGNSDT GATPGYTVPK QVNDMWREKP VRRFSMRDGR EAWLVTGRAE

61 VRTVLADPRF SRVEARRLDA VMSPAVIFTR PGILDMDPPE HTRLRRLVAG EFSARRMRAL

121 RPRIQQIADE LIGTMKAAGP PADLAEGLSY PLPIAVICEI LGVPYADRER FRAWADRVSA

181 PGTQPQEAMA ALRSLFDYMG GLVDDKHAHP DGSLLHGLVT ARDEQGRLDN EELVTLGCGL

241 LLAGYETTAT MLGKGLLALL DNPDQLAVVR SDPRAVPAAV SEVLRHVTPG VDPHTGLIRA

301 TTADVELGGT VIPAHSVVVA CNTAANFDPA TFRDPDRFDV TRENAAAHLT FGHGMHRCVG

361 AQLAQIELEA AFAALFPAIP GLRLAVPADE ITYTQSTLIR GLRSLPVLW

>CYP107BD1 Frankia alni ACN14a

MAETGGFAEVGGVAQTGGAREIFDPRWRSDPYPLYRTLRESARCHWLSPARIGVLTRHADCVAVLQDSAW

GHVPMETSAFRPVTDQDEGLRSMLRANPPTHTRLRRLVSRAFTPARIARFRPMAEALAGELLAAAVDRGE

VDLVEAFTRPLPLRVICSLLGVPAHDEKVFSGWASALTRGLDPDQVLDPVERAQRTEATRAFADYFTALI

ARRRAEPADDLLSDLIAVQDQGDRLGADELLEICVLLLVAGYDTTVNLVANAVLALARDPGQYAALQANR

TLVPAAIEETLRHDPPVQWTGRTALTDTDLAGQAFRAGDGIILVAGAAHRDPAAFPDPDRFDLTRYASAS

APAARHLGFGHGLHYCLGAPLARLEAETMLTALLDRVARLEIVAEPTYRPHLAVRGVDALQIRLHPAG

>CYP107BD2 Frankia sp. CcI3

MDADSPSGAAAVGTPPAFGAFDPARRHDPYPSYHALREADPFYRLPLGAQQVTLLTRYQDCMHVLQDAAW

GRGEGGTNAWRSANSFDGGLRSLLGVNPPDHTRLRGLVSKAFTPRVISGLRPQITVLVESLLDAALAAGE

VDLIDAFARPLPLRIICDLLGVPVRDEETFRAWGTALTRGLDPDYLLTPDELALRGKATVEFDAYFTDLI

AARRARPTDDLLGLLVAVREQGDSLTEAELLELCALLLVAGYETTINLIGNAVLALLRDTDQLTALRADP

DLAPALVDETLRHDPPVQFVGRLALRGTEVAGHSFAAGEVGVIMLAAAGRDPRTFAEPDRFDIRRYAGPT

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>CYP107BE1 Frankia alni ACN14a

MATVPASRSASERRSPLLAAFDAARQVDPYSTYRAIREADPLAGHDLAGHRVTLVTRHGDTAAVLQDPAF

GHGYKENISPFRPDGDADDGLESLLRSDPPDHTRLRRLVSRTFTPGTLVELAPDITSFVAGLLDAALEAG

EIDAIRALARPVPTRMICRLLGVPAADEKIFGEWSETLIRGIDPDFLLTPDEITERRRAARELDAYFRDL

IARVRVRPGTDLVSQLVAIHLGEDALTESEVLALCAVLLVAGHETTVNLIGGGVLALVQHPDQLALLRAD

PGLIPAAVEEMLRHDSPVQFIPRTALRDTEVGGRQFRRGEGALLLVGSANRDPDAFDEPDRFLVARYAGS

TPAARHFAFGTGVHYCLGAPLARMEAEIIFRLLLERTSELALIGSTPTYRNQSIIRGLQTLPLRLAA

>CYP107BE2 Frankia sp. EAN1pec

MTTVGGMDTSEGGTSAIIAAVTATRLADPYPRYREIREVGAFIPGEIADRTVTLVTRLAEASAVLAHPAV

GHGYTDGINYRTGMDDGLGSLLRADPPDHTRLRRLVGRAFTPAVIEALAPEVTSLANVLLDEAIERGEID

AVAAFARPLPLRLISRLLGVPAADEEEFGGWADALTLGLDPHYLLTDEAKAACNRAAVEFDAYFLDLIAR

RRKEPRDDLLSRLVAIHDRGDMLAERELLELCTLLLVAGYETTANLISGGILALTRNPGQLAALRADPAL

VGPAVEEMLRFDPPVQFIARTVLADAEIGGRPFARGDGAIMMIGAANRDPEAFDEPDRFLVARHTRSDRT

RRHLGLGVGIHYCLGAPLARLEAEIAFRALFSRTSSFALAEDTVAYREQIVVRGLKRLPLHLSA

>CYP107BF1 Frankia sp. EAN1pec

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PGVDPDDVPGSMLRMDPPDHTRMRGLVKRAFVPRHTEGLRPRVEGLVNELIDTAIEAGEVDLMEALARPL

PLTVIGDMLGIPPEDYTAVKKWSLEIVRGTDPDILQSPESLARRPEAMREFEAYFAGLIAQRRKDPRDDL

LSDLCAAQERDSVLSDREMLGLSVGLLIGGYETVSDLIGKGLVALLRNPDQVALWRSNPELAPYAVDELL

RYEPPVQFTHRVALEERELAGRAFARGEGVVVLIAAANRDPAVYSDPERLDITRFAGRSPAPRHLSLSEG

IHYCLGAHLGRLQTQIAVDTLLLRAPGLSLTDDEPVWRDTVAIHGLDTLPIRLRD

>CYP107BG1 Frankia alni ACN14a

MFPVPQVRGTEGAYEGAGFMTTAEIDGDRVDAHRVVDAHDVFDTAHRIDPYPRYRRLRQAGSPTPVRLGD

AEVTLMSRFSDCAAVLQSQAWGHGNVDRLSPFWDQQASLPGSFIRMDPPDHRRLRTLVNKAFSARMVADL

TPMITSLVDTLVDRALAAGGLDVISGLSAPLAQAMVGQRLLGVPAADAEMLRSWELAIARGTDPDALLSA

EDAARRDSAGANVVAYLQDLVARRKAHPEDDLLSRLVAVEESGEVLTAAEVLGICVLLLVAGMETSINLV

GNGILALLAHPDQLALLRARPELAPSAVEEILRYDTPTQFTMRVALTDTTVGERRFRRGDGAIVLMGSAG

RDTDVFDGGERLDVTRYAEPGRSPRHLGFSLGLHYCLGAPLARLEATTAIRTLVERAPALSLATDELSYQ

PSLIHRGLSSLPVDLSPAAA

>CYP107BG2 Frankia sp. EAN1pec

MVAAEVTAGVAAESAPVEFTAFHPTHKADPYAVYQRVREARPLCPFMLGDIPVTVLTRYADCEAVLQSDD

WVHGYDAGISPFRDGAASAPRSFLRMDPPDHTRLRGLVNKAFTPRIVNQMAPGIQALADRLVDGALATGS

IDVIGEYAALIASATLGHLLGVPDDVGASLRGWALAIARGTDPDNLLTEAELVARRQATQDFQAYFEELI

AQRRANPTDDLISRMAAARDRDDALSELELLGVSSLLVVAGMETSINYVGSAVLSLLRHPDQLALLRARP

ELLPSAVEEVLRYDPPTQFTMRTACRRTELAGHTFARGDGVLLVSAAAGRDPAAFTDPDRFDITRYHGPR

PARRHLGFSVGIHFCLGAPLARIEAAAAIGALVRRTTTLELAVDEAELVYLPSLIHRALATLPVRVR

>CYP107BH1 Frankia alni ACN14a

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GPLGLRLVTRYREVEAILADSAWSHAEEGAIMHPDSDGSDLPTSFLWMEPPDHTRIRRLVGKAFSARRIE

ALRARVTEVAGGLVDAAIAAGEVDLVEAIAYPLPLTMIAELMGVPVADHAAVRSMSFGLARGLDPDVLLS

QAEIDLRRESAAAFREYFTDLVARRRADPADDLVSALALAEAEGDRLTADEMLSTLVVLLVAGHETTVSL

ISSTFLMLMRHPDQYAALRARPDLAAPAVDELMRYCTPSHLTTRVATRDVEVLGEQFAAGDGVIILLASA

NRDAGRYADPERLDLARYAGGAAVPRHLAFGRGHHYCIGAPMVRLEMELLLRTLARRAPRLTPLVDPPPY

RPNLVVRGIAELPVRIDG

>CYP107BH2 Frankia sp. EAN1pec

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CAAILADPVWSHAEESELLHPDSDVELPGSFLWMEPPDHTRLRGLVSRAFTPRTIEATRPLARRVVDGLI

DDALAAGELDLIEGLAYPLPLTMICELLGVPISEHPAVRRMSAGIARGLDPDVLLSPAELAARTAAVEEF

REFFGALVTARRADPRDDLISALAQVHAEGDRLTTTELLGTLLILVVAGHETTVNLIGNGVLALLRDPAQ

LDALRRDPGLALPAVEEILRFDAPAQVTTRTARAEVTVAGRTFTPGEAVICMLGSANRDPRAFDRPDEFL

VDRYAGGARVSRHLALGMGLHYCLGAPLVRLEVGEVLRGIATRLTGMTLLADPPPYRPNIVVRGMSSLPV

RVTGRPG

>CYP107BH3P Frankia sp. CcI3 YP\_481037.1 ABD11308.1

MDSAAPSLGAPDWPARSDPEMEPPGHTRLRGLVSKAFTPRTIEGMRPWAEQVVDDLLSRLIQR

GLTSLPLSLTPGGVA

>CYP107BJ1 Frankia alni ACN14a

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AVLGSQEWGHDREPHQLHPTIPAEAFPASFLWMEPPDHTRLRGLVTKAFTARTVAALRPRIAALVDELLD

NALRQGEFDLIATIAYPLPLTVVCEILGVPAEDHPLVQVWSQALARAFDPDVLMTPEALAERNRAIPEFL

SYFRALVSRRRREATGDDLITQLAAVEEQGDRLTEEELLGTCVTLLIAGHETTVNLVGNGMMALIRHPDQ

VALLRERPELIGPAVDELLRYDSPIHMNTRAAKRELVVGGEVFAPGEGIVALIACANRDPLVYDDPERLD

VTRFHTSKPIARHLSFSLGHHYCLGAPLALLEMELLLAGVLDRVADMELLTDTPPYKPNMLIRGLAELPT

RFHAA

>CYP107BJ2 Frankia sp. CcI3

MAVTTDSVFAGADAGTGVAADHGKPLPDQAPDLLAALFDPANRPNPYPLYARLRAAGRLHETPFGLRVAT

RHDDCVAVLSNQSWGHDQEAHQLHPTLPAEEFPATFLWMEPPDHTRLRGLVSKAFTPGRVADLRPRITAL

VDDLLDTALRAGEFDLIETIAYPLPLTIICEILGVPAADHGIIQIWSQALARAFDPDVLMSPEALAERND

AIPEFLAYFRALVARSRRSGGDDLLSALAAVEEQGDRLTEDELLGTCVTLLIAGHETTVNLVGNGALALL

RNPDQTALLRDEPDLIRPAVDELLRYDSPIHLNTRAATREMTVGGRTFSPGEGVVALIACANRDPEAFDD

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AELPVRFRG

>CYP107BJ3 Frankia sp. EAN1pec

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LANQDWGHDLEAHQMHPTLPAESFPTTFLWMEPPDHTRLRGLVSKGFTPRSVQLLRPRITALVDELLDNA

LAAGEFDLVETIAYPLPLTVICEILGVPAADHPAVQVWSQALARAFDPDALMSPEALAERNRAIPEFLEY

FGALVERHRREPGDNLISALAQVEEAGDRLTADELLGTCVTLIIAGHETTVNLVGNGMLALLRNPDQLAL

LRAEPELIPAAVEELLRYDSPIHLNTRAAKRELEVAGRVFAPGEGVVALIACANRDPRAYPDPDRLDVRR

FTSSAGGPPARHLSFSLGHHYCLGAPLALLEMELLLAAFVRRVSHAEITDNNPPYKPNLLIRGLAELPVR

FRG

>CYP107BK1 SBI\_9749 Streptomyces bingchengensis

42% to CYP107AN1 Bradyrhizobium japonicum USDA 110

MEMSIIFDPRDPSVRTDPYPIYRRLRETDPIHQSHFGYWILSRYADVDAV

LRAPGASSEFYRDRTWANRRGGPDSPLVQSVRKWMLMLDGPAHRRIRGAI

SKVFTRASVERLRPRIAAETARLLDAAGEGKTDLIHSLALPLPVTVTCEL

LGLPGSDRDQCRRWTEQISRVIDPSITAEDAVEMNAAEVEFREYVADHLK

ERRSAPRDDILSLLLHAEVDGGQLTEEEIIANVQFLFVAGHETTVNLIGN

GLLALLRHPDQLRMLRDNPEIITDSIDEITRYDPPVQIVSRLLTEDVPLT

DVTLPAGAKVMLLFGAAGRDPERYPDPDRLDLTRTGVKTLAFSGGPHYCI

GAALGKLETSMMLTELLRRYSTIELTGDDLVWRPNVSFRGLQELPLQLVR

>CYP107BM1 Streptomyces hygroscopicus ATCC 53653 ACEX01000414.1 3915-5168 (+) strand

MSENAMSENATHLTPEQVEDPVRGYADLRTRDELPH AVLPGLTTPVRLVTRYADVKAALTEPRLIRDRTRIPGDADEAQASDAQDELLEAASAGLP AEYVKYFAGHLALFDGEEHAHRRAPLTRAFTARRIAALRTFVERTADALVAEAEANGGTD LLGAFAYPLATQVICELIGVEERDRDQVCSWMRDFAFGDGSRAGEALVALVEYAKELIAR RRAEPTEDLISALLDGDQLTEDDLIGIVFLLINTGITPPALFLAHAALALLDHPEQAARL HAAPELLPRAVPELLRYVSIVRIGATLYATEDVDFAGTALRRGESVTVALLAADHDPEEF GDGAGQLDVGREFGRGDGHLAFGHGAHYCIGAALGRLVTSVVLDRLFVRHDGLRLAVPRA ELEFGHWPGDGFHLLRLPVRL\*

>CYP107BM2 Streptomyces sp. C strain C ACEW01000053.1 15059-16303 (+) strand

MNETVHHLSPDRLQDPATGYAGLGDGDGLPRVVLPGLRTPV RLVTRYADVKAALTEPRLIRDRTKVPGATDGPDAQDELLAPLGDLPPEYARYVSAHLAFL DGAEHARLRTPLTRAFTARRVASLRPFVEESAARLIGELAGRKEADLLNEFAYPLATSVI CELVGVDEADRARVCDWIRDFAYGDGSRMGDGLAGVVEYVKALIARRTAAPADDLISALL GGAREGGAGALDEEEITAMVFLLINTGITPPALFLAHAVLALLDHPGQLDRLRAEPELLG RAVPELLRHVTLLRIGATLYATEDFVFAGTGLRRGDSVTVALLAANHDPAVYGEASARLD VTREAARGRGHLAFGHGAHHCIGAALGSLVTGVVFERLLVRRPVPELAVARGELEFGHWP GDGFHLLRLPVRL\*

>CYP107BM3 = old CYP107BL1 SBI\_9870 Streptomyces bingchengensis

51% to CYP107L1 Streptomyces venezuelae

MTQQPIVLPYGDPAFVADPFPFYRMLCQGQPGEDGPVRRAVIAGGLEVWL

VTPFEECLAALSDPRLSSDVRLATDPRLMRQLPVAERESVLGNMLRADPP

DHTRLRRLVSRAFTARRVAELRPHVQEIADRLLDAVVPTGRADLIEDFAL

PLPVTVISELLGVPTDDRRAFQRWVDHLLPWGAEPQDPAVVERAWRQMRA

YLTGLLATKRVRPGEDLLSALIEARDEQRRLTEDELVSMAFLLLAAGYIT

TVNLIGGGIAALLAHPDQLRTLRDDPALLPDAIEELLRYDGPVNPGVARF

ASEDVSIAGVDIPRGATVLVGSALADRDPERFPDPDRLDISRGDSAHLAF

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ERLPVTFTPGASLAAVPS

>CYP107BN1P

MQQCLGEAMRSLHDCAVEMVLREREEPGNGALGALTVVRDEDGTGFSDEELVSTVLLTAIAGYESTVVQI GNGFLAMFRHPEQMEHLKRGRTDIAAAVEEILRYAQSSTGFAGMTYAMADVELGSVTVPAGATVFVSLDS AARDEAHVDSPQRFELSRGSARHHVTFGSGHHYRA

>CYP107BP1P

MPSRDIAAAGYMRSPRAKSTESREILMSVDETTEGCVTDANGNLIAYGATSCMVSQLEPSTDVNVSPPAA APHTTFDEFHA FDVFDPEHWPNPYPRYAMARKARPLIRTPLGVHLVTRYQDCATILQDNNWSHAHKAELF HPGVEHVDLPTSFLWMDPPDHTRLRALVSKAFTPRTVANLRPRIEQLVKDLFDAIIEAREVDVISALAYP LPLTIIAELLGAPAEDHPDLQRWSRALARGFDPEPLLSP GNVTHAPMPPVSSWPTSADWAPGNGVSGTRR AGKHALSVVNPVSTRRRLVTAGVEETDDWSGWLRERRHDDIPLSQRENPHERAVRSTTNTAGRTSGRKGG PRSRRTEPGCRYRSACSCSRCRSCCRRCRTTPTSRAEQQIGVGATRR

>CYP107BQ1P MTIRTASQEVPMSPTDPIPLYgpqykrdpyplyrrlratgpvhrvrfpsgvigwlvtgyraahealndhr lgknHALGTSDALSALIDEEGLRHLDLFSLRDILGDLPYDDKRSSVSRRYGPTSEQLRAEVRSDEDTRRL YQGITRFLVEDTAEFVGSRSALQRECRQRAYGVIGRSRAWGRLVAEHHPRAVRLSIHPQRRGTSKFGIRL LESSDAWMTPWHATVLRRADGASELMRRADAQRLGRLVTRDGRPSHFQAHAAV

>CYP107BR1

MALTTTGTEQHDLFSGTFWQNPHPAYAALRAEDPVRKLALPDGP VWLLTRYADVREAFVDPRLSKDWRHTLPEDQRADMPATPTPMMILMDPPDHTRLRKLV GRSFTVRRMNELEPRITEIADGLLAGLPTDGPVDLMREYAFQIPVQVICELLGVPAED RDDFSAWSSVLVDDSPADDKNAAMGKLHGYLSDLLERKRTEPDDALLSSLLAVSDEDG DRLSQEELVAMAMLLLIAGHETTVNLIGNGVLALLTHPDQRKLLAEDPSLISSAVEEF LRFDSPVSQAPIRFTAEDVTYSGVTIPAGEMVMLGLAAANRDADWMPEPDRLDITRDA SGGVFFGHGIHFCLGAQLARLEGRVAIGRLFADRPELALAVGLDELVYRESTLVRGLS

RMPVTMGPRSA

>CYP107BR2 MTAVDASVFEGSFWRDPYPAYERLRAQAPVREVALPRGGTTWLVTRYDDVRAAFTDPRLV KDHRATLPPEVRAQAPRLPGPFGSMMILLDPPDHTRLRRLVSRAFTARRTAELRPRIEAL AAALLDAVPETEPVDLLAGYAVPLPMAVICELLGVPDTDRDAFGTWSRALVDDQDDVDEQ QATAGLAQYLYALVETKRRAPDGALISALVEVSEAGDQLSTEEVVAMGVLLLIAGHETTA NLIGNAVLGVATDAALREHLLADPQRIPAAVEEFLRWDGPVHNAPLRFAAEDVEYSGTTI PAGSVVTLSVGAANRDPGRFDRPELLDPDRETGGHLAFGHGLHYCLGAPLARLEGEVALR SLLDRFPDLRLAVPPEELRHRRSVLVHALETLPVVLRPEAAGSASA

>CYP107BX1 SGR810 Streptomyces griseus

MHRLFFEEPGPPRPAELPGGDPAWLVSRYADVRQVLSDPRFGRARLYAPEAPALSGVPDLVNNPDLMFNQDGSDHLRLRRTLRRAFTPRAVARWRPWIAATVEGILDRLESRPQPADVVAEFALPLPVAVISRLMGLDESVWDRMRYWSEHAFSDGTHEREQVAAALKEFSAFGAHLLAERRSTPGEDLVSGLVTAADEEGGVPEAQLVSLVCGLVVGGHDSTMTMLGNALLYLLGERRETWPRLGADEEAAGLLVERLVHLVPLGDDRGSTRHAAEDVEVSGVRIPAGAIVIADCGMANRDPEVFPPATLYDLFAPLEAPTLSFGAGPHYCLGAWLARTELQLALHRLAARFPELRLADPVDAVVWRTGTTSRSPRRLGVRW

>CYP107BY1 SGR895 Streptomyces griseus

*SGR895* putative cytochrome P450 376-aa MW:41055.09

42% to CYP107L2 Streptomyces avermitilis

MTADPYPGYAWLREHDPVCPVGGPHVPGRMWLVTRYDDVRACLADRRLGSRAPVDPDPHPPGLSHLDGPGHARLRRLVAAAFTPAAVARLRDRTARTCAHAVESFAGRGHADLVAEYTREIPVAVMHDLLGVPETERAPAADVLDMWYRAKFRQPRDEASLAELLDYVGELVAYKRTHPGDDLTTRLIDSDALTGEELEVMVMTLIGAGHITTIQFLGTTVLHLLDHPGHRAALLRGDLDWPRAVNELLRLDSPSHVAEYRYAGEDMTLADARVGEGDVVLLSLAAANRDPDRFPDPGTLDLTRDARPHLAFGHGAHTCLGSHLVRLETEIAVTTLFGRLPDLALDIPGGEVAWGYAPTFRGPLALPVTFTPSTSR

>CYP107BZ1 SGR3274 Streptomyces griseus

MTGTQTLSKYWMLTNEFTQNPYPVLDHVRREGPVRELSFPDGGRAWVVTRYEEAKAALADPRLSRDIHVHYRLMSRRTGRALTPPPEEANHLANLEPPRHTPLRRAISFAFTPRRAEALRPKVERIADDLLDRLGEAPEAELIAGYADPLPVITIAELMGVPADAWPDFLRWSTALRTHSPTDGSGVLDRNVQELSAYMADLIARKEREPGEDLLSALIHAAPENRLTPTEILSTGFALMTGGNDTTASLVGGVIAALLTHPRERARLLADTGRWGKSMDELIRYVSPISNALQRVTTEPVDVGGVTIPAGEVVVVCVMSTNRDTGQFPGHPDRLDLDRVKPAHLSFGFGIHYCSGAHLAKVITEVSARRLFERFPAARLAVDPSRLRYQQNVVVRPLEALPVLLRP

>CYP107CA1 SGR6789 Streptomyces griseus

MTATGHEIRDYPFGPVDRLDLDPALVEICGEHPVLRVRLPFGGDGWLVTRYADVRAVLSDPRFSRSAAAGDHVPRTVAVAPPPTSIMGMDPPDHTRLRRRVMRAFTVRSIDALRPRIAEIVNDLVDTMTEGDGPADLAAVLTWPLPITVICEMLGVPRADQDRFTEWVDGLLILDDPERSADARRQLGDYLAVLIAQRRAEPTDDLLGELAADSGKDPLSEEELVGLGVSLLSAGQEATANQIGNFVYTLLTRPALWRELVADPSIVPRAVEELSRFIPISATAGFTRVATEDLELGGQLIRAGDAVVAELGMANRDSAVFDRPEEIDFHREQIPHVTFGYGIHHCLGAQLARVELRVVLETLVTRLPGLRLAVPADQLAWRTERLIRGVAALPVRW

>CYP107 fragment Streptomyces noursei

63% to CYP107A2 Streptomyces rochei

WTTPTRWSCSAPSLICLPRHGRNTAHRRTSRSHHPGRARRHPDR

DTLIPARSTVFIAGAAANRDPQKFPNPDTFDITRNTQGHLAFGYGVHHCIGRPLAQME

GEVAITALLRRFPHLHLTTPSQNLTWRRSFLRGLTALPVTLN

>CYP108A1 Pseudomonas spp.

MDARATIPEHIARTVILPQGYADDEVIYPAFKWLRDEQPLAMAH

IEGYDPMWIATKHADVMQIGKQPGLFSNAEGSEILYDQNNEAFMRSISGGCPHVIDSL

TSMDPPTHTAYRGLTLNWFQPASIRKLEENIRRIAQASVQRLLDFDGECDFMTDCALY

YPLHVVMTALGVPEDDEPLMLKLTQDFFGVHEPDEQAVAAPRQSADEAARRFHETIAT

FYDYFNGFTVDRRSCPKDDVMSLLANSKLDGNYIDDKYINAYYVAIATAGHDTTSSSS

GGAIIGLSRNPEQLALAKSDPALIPRLVDEAVRWTAPVKSFMRTALADTEVRGQNIKR

GDRIMLSYPSANRDEEVFSNPDEFDITRFPNRHLGFGWGAHMCLGQHLAKLEMKIFFE

ELLPKLKSVELSGPPRLVATNFVGGPKNVPIRFTKA

>CYP108B1 Mycobacterium smegmatis

MFLTPVKFSPSEVPD

MSTPVINDAARVLAEPRAYADEPRLHAALAELRSQTPVAYVDVPGYYPFW

AITKHADVMAIERDNELFINAPRPMLITKEKDDLAKANLAAGGGIRTLIH

MDDPLHRDIRKIGADWFRPKAMRALKERVDELAKIYVDKLVEKGPECDFV

QEVAVNYPLYVILSLLGLPESDFDRMLKLTQELFGNDDDEMGRGSSAEEL

NAVILDFFNYFTELTADRRANPTEDLASAIANAKLNGEYLNDVDCLSYYV

IVASAGHDTTSAAISGGLLALTENQDQLARLKADMSLMPLATEEIIRWSA

PVKEFMRTATRDTEVRGVPIKEGESVLLSYVSANRDEEIFENADKFDVGR

DPNKHLSFGYGVHFCLGAALARMEINSFFTELIPRLESIELAGDPEFMAT

TFVGGLKHLPIRYSVR

>CYP108B2 Mycobacterium smegmatis

MSTPTMDDAAKALADPTAYADDARLHEALARLRAENPVAWVDQAPYRPFW

AITKHADIMAIERANDLWLSAPRPLLATAEADDLGRSQQEMGIGLRTLIH

MDDPHHRKVRAIGADWFRPKAMRELKVRVDELARIYVDKMREIGPECDFV

TDIAVNFPLYVILSLLGLPEEDFGRMHMLTQEMFGGDDDEYKRGTTVEEQ

MAVLTDFFNYFSALTNSRRENPTDDLASAIANGRVDGELMSDMDTLSYYV

IVASAGHDTTKDAISGGLHALIENPGELARLKADPGLMGTAVEEMIRWST

PVKEFMRTAAEDTEVRGVPIAKGESVYLAYVSGNRDEEVFTDPFRFDVGR

DPNKHLAFGYGVHFCLGAALARMEMNSLFSELLPRLDSIELAGEPELSAT

TFVGGLKHLPIRYSIR

>CYP108B3 Mycobacterium smegmatis

MTARTIDDAAKVFAMPSAYTDEAKFHEALTHLRVNAPVSWVDVPPYRPFW

AITRYADIMAIERANDLFTNSPRPVLMTAEEDEQQAAVGISTLIHMDDPQ

HRVIRAIGADWFRPKAMRALKIRVDELAKIHVDKMVAAGGECDFVQEITV

NYPLYVIMSLLGIPEADFPLMLKLTQELFGNKDDEYQRSADEGDSMAALL

EMFQYFTELTASRRANPTDDLASAIANATVNGEPLNDIETVSYYAIVAAA

GHDTTSATISGGMLALLEHPDQLERLRNDPSLMGTATEEMIRWVTPVKAF

MRTAATDTVVRDVPIAAGESLLLAYPSGNRDEEVFTDPFRFDVGRDPNKH

VAFGYGVHFCLGAALARMEINSFFAELIPRLESIELTGSPRHTATTFVGG

LKHLPVRYALR

>CYP108B4 Mycobacterium marinum MM3999

MSAPTMDEAA LLADPLAYTD ETRLHAALTR LRAQAPVALV DVPNYRRFWA ITRHADVMDI

ERDNTLFTNW PRPVLATVAG DELQAAAGVR TLIHLDDPQH RVARAIGADW FRPKAMRALK

VRVDELAKNY VDAMMAAGPE CDFVQQIAVN YPLYVIMSLL GLPEADFPRM LKLTQELFGS

DDSEFKRGST SEDQLPALLD MFGYFNAVTT ARREHPTEDL ASAIANARID GEPLSDIDTV

SYYLIVATAG HDTTSATISG GLHALIEHPD QLARLQADPA LIPLATEEMI RWVTPVKQFM

RTASRDTVVR GIPIAAGESV LLSYVSANRD EEVFDQPFRF DIGREPNKHV AFGYGVHFCM

GAALARMEVG SFFTELLPRL KSIELSGDPQ FTATTFVGGL KHLPVSYSLV \*

>CYP108B4 Mycobacterium ulcerans

MSAPTMDEAALLADPLAYTDETRLHAALTRLRAQAPVALVDVPNYRRFWAITRHADVMDI

ERDNTLFTNWPRPVLATVAGDELQAAAGVRTLIHLDDPQHRVARAIGADWFRPKAMRALK

VRVDELAKNYVDAMMAAGPECDFVQQIAVNYPLYVIMSLLGLPEADFPRMLKLTQELFGS

DDSEFKRGSTSEDQLPALLDMFGYFNAVTTARRAHPTADLASAIANARIDGEPLSDIDTV

SYYLIVATAGHDTTSATISGGLHALIEHPDQLARLQADPALMSLATEEMIRWVTPVKQFM

RTASSDTVVRGIPIAAGESVLLSYVSANRDEEVFDQPFRFDIGREPNKHVAFGYGVHFCM

GAALARMEVASFFTELLPRLKSIELSGDPQFTATTFVGGLKRLPVSYSLM

>CYP108B5 Mycobacterium avium subsp. paratuberculosis K-10.

MSTTTMDEAA KLLADPMAYT DEQRLHAALT HLRANAPVSW VEVPNYKPFW AITKHADVMD

IERENMLFTN WPRPVLTTAE GDEMQAAAGV RTLIHMDDPQ HRVVRAIGSD WFRPKAMRAL

KVRVDELAKI YVDKMLAAGP ECDFVQEVAV NYPLYVIMSL LGLPEADFPR MLKLTQELFG

SDDSEFKRGS SNEDQLPALL DMFGYFNGVT AARREHPTED LASAIANARV DGEPLSDIDT

VSYYLIVATA GHDTTSATIS GGLQALIENP DQLQRLRDNL DLMPLATEEM IRWVTPVKEF

MRTAAKDTVV RGVPIAAGES VLLSYVSANR DEDVFDEPFR FDVGRDPNKH LAFGYGVHFC

MGAALARMEV NSFFTELLPR LKSIELTGDP ELVATTFVGG LKHLPVRYSL A

>CYP108B6 Mycobacterium flavescens PYR-GCK

MSVRVADEAG KVFADPTAYA DEQRLHAAMT HLRANAPVSW VDVEGYNPFW AITKHADIMA

IERDNTVFTN SPRPVLTTAE GDAQHASMGV STLIHMDDPQ HRKVRAIGAD WFRPKAMRAL

KVRVDELAKT FVDQMYDRGG ECDFVQEVAV NFPLYVIMSL LGIPESDFGR MLTYTQELFG

SDDAELQRGT TMEERGLALF DMFTYFNELT ASRRAQPTED LASAIANARI NGEPLSDIDT

VSYYLIVATA GHDTTSATIS GGLQALIENP DQLARLQQAP ELLPLAVEEM IRWVTPVKEF

MRTAQQDTEV RGVPIAAGES VLLSYPSGNR DEDVFTDPFR FDIGRDPNKH VAFGYGVHFC

LGAALARMEI NSFFSELLPR LTSVELAGRP EHIATIFVGG LKHLPIRYSL TR

>CYP108B7 Mycobacterium vanbaalenii PYR-1

MSVRIADEAARVFADPSAYADEARLHAAMTHLRANAPVSWVEVPGYNPFWAITKHADIMAVERDNLVFTN SPRPVLTTAEGDAQHEAMGISTLIHLDDPQHRKVRAIGADWFRPKAMRALKVRVDELAKTFVDQMYERGG ECDFVQEVAVNFPLYVIMSLLGIPESDFQRMLTYTQELFGNDDAELQRGESMEERGLALFDMFTYFNEIT AARRARPTEDLASAIANARIDGAPLSDIDTVSYYLIVATAGHDTTSATISGGLQALIENPDQLQRLQQNP GLMPLAVEEMIRWVTPVKEFMRTAQQDAEVRGVKIAAGESVLLSYPSGNRDEDVFTDPFRFDVGRDPNKH VAFGYGVHFCLGAALARMEINSFFTELLPRLKSVELAGRPEHIATIFVGGLKHLPIRYSLTR

>CYP108B8 Mycobacterium vanbaalenii PYR-1

MSTPTMNQESQEAAKVLADPTAYADDQRLHKALAHLRANDPVAWVDHPPYRPFWAITKHADIMAIERAND LFLSEPRPVLVTAEADDMARAQLEAGFGLRTLIHMDDPHHRKVRAIGADWFRPKAMRDLKIRVDELAKRY VDKMRDIGPECDFVTEIAVNFPLYVILSLLGLPEEDFGRMHMLTQEMFGGDDDEYKRGATVEEQMAVLTD FFNYFGALTASRRANPTDDLASAIANGLVDGELMSDVDTLSYYVIVASAGHDTTKDAISGGLHALVENPG ELARLQGDLDLMPTAVEEMIRWSTPVKEFMRTAAEDTTVRGVPIAKGESVYLAYVSANRDEDIFDDPFRF DVGRDPNKHLSFGYGVHFCLGAALARMEINSLFSELLPRLDSIELAGRPELSATTFVGGLKHLPVRYSLR

>CYP108B9 Mycobacterium vanbaalenii PYR-1

MSTPVIDEAASDAARVLADPKAYTDEARLHAALAHLRAHAPVSYVDVPDYRPFWAVTKHSDIMAIERDNE LWINEPRPLLTTAATDDLSQANLAAGGGIRTLIHMDDPLHRDIRKIGADWFRPKAMRDLKTRVDELAKIY VDKMVEKGPECDFVQEVAVNFPLYVILSLLGLPESDFGRMLKLTQEMFGGDDDELTRGKSPEELHEVITD FFRYFTALTAERRANPTEDLASAIANAKLDGEYLNDIDCLSYYVIVASAGHDTTSAAISGGMLALIENQD QLARLKAQPELMGTAVEEIIRWTTPVKEFMRTATADTEVRGVPIREGESVLLSYVSANRDEDIFDEPAKF DVGRDPNKHLSFGYGVHFCLGAALARMEINSFFTELIPRLESIELAGDPEYIATIFVGGLKHLPIRYSVR

>CYP108B10 Frankia sp. EAN1pec

MDIEAAATVFTDPRAYADNERFHTATALLRRESPIHRIEHPNFHPFWAVTKHEDVMAISRASDIWINEPR

PALGPKPKDAERENIPIRSLVQMDAPDHPVYRHVSADWFKPAGVRRLRDRIAELAKRFVDRMADQGGECD

FFTDIVSHYPLYVILSLLGLPEEDFPRMLRLTQELFGADDEDLARDQDKQAQRAPLVDFFNYFQALIQDR

RENPTDDLGSVIANATIQGEQIGKLEAAGYYTLIATAGHDTTSAALAGGLHALLESPGQWQRLVDDPRMV

ATGVDEMIRWVSPVKHFMRTAREDTVVRGVALAAGESVLLSYPSANRDEDVFENPDTFDVGRSPNRHVAF

GFGAHYCLGTHLARLEGQALYAELVPRVRSIELAGTPEYMEALFVGGPKRLPIRYTMA

>CYP108B11 Frankia sp. EAN1pec

MGFRSRALVIDNIPNRRASALGSLPLGSPWRGTHEGGPGMDIAEAATVFTDPTAYADNQRFHTATALLRR

AAPVQRVEHEDFESFYAITKHDDVMTISRGSDIWRNAPRPALGPKPKDGRAAEDAPVRTLIQMDAPDHPV

YRHISAEWFKPLGVRRLAGRIAELAKRYVDTMADFGGACDFFADVACHYPLYVILSLLGLPEDDFPRMLK

LTQELFGANDPDMARGSGDEQALMAALLDFFTYFQALTADRRANPTDDLASVIANATIDGEPIGELEAIG

YYVLIATAGHDTTSSALAGGMHALLQYPDQWRRLSENPGLVPTAFDEMIRWVTPVKQFMRTAARDTEIRG

VPIAAGESVLLSYPSANRDEDVFDNPDTFDVGRTPNRHVAFGFGAHYCLGTHLARLEGQALYAELVPRLR

SIDLAGTPEYMETLFVGGPKRLPIRYTMT

>CYP108B12P Frankia sp. EAN1pec YP\_001509055.1 ABW14149.1 67% to CYP108B7 Mycobacterium vanbaalenii PYR-1

MDLDEAGSVFTDPTAYADEKRWHTATALLRRHSPVHRVESAGFAPFWAVTRHEDVFTDPEAFDVGRTPNK HVGFGFGAHYCLGTHLARLEGRALYTELVPRLREVELAGTPEYMQTLFVGGPKHLPIRYTIT

>CYP108C1 Saccharopolyspora spinosa strain NRRL 18395

VNIKLMGAGRTLADPAAYANDDRIHKALALLRREAPVHWVEAPGYRPFWAITRHADVMEIERQPDLFRNAPRPILV

PDAMEKRTAAQGTNFRTLVSMDGAEHRQVRAIGTDWFGPGALRHLETRVTELARQYVDRMLEFDGECDFVTDIAVH

YPLDVILSLLGLPRSDFPRVLSLAKELLGNADQEINGGRGAEGFVAVQQELLTYFNELTAARRATPTTDLASAIAN

ARLDGALLSEFDAASYYILIATAGHDTTSASIAGGLQALIENPQQLRQLQDDLTLLPTAVDEMIRWVTPIKCFLRT

ATEDYVLRGTTIRKGDSVLLSYPSANRDEDLFEEPFRFDIRRTPNRHLAFGFGVHYCLGAALAKMEARAFFAELLP

RLDSVQLAGKAELFATNFIGGLKHLPIRYKLRPSV

>CYP108D1 Novosphingobium aromaticivorans

MTNTSRLTKRRRPRRSDGKREGFMDSIPMVPAEVGRAVIDPKSY

GTWEPLLDRFDALRAEAPVAKVVAPDDEHEPFWLVSSFDGVMKASKDNATFLNNPKST

VFTLRVGEMMAKAITGGSPHLVESLVQMDAPKHPKLRRLTQDWFMPKNLARLDGEIRK

IANEAIDRMLGAGEEGDFMALVAAPYPLHVVMQILGVPPEDEPKMLFLTQQMFGGQDE

DMNKSGLKDLPPEQISQIVAGAVAEFERYFAGLAAERRRNPTDDVATVIANAVVDGEP

MSDRDTAGYYIITASAGHDTTSASSAGAALALARDPDLFARVKADRNLLPGIVEEAIR

WTTPVQHFMRTAATDTELCGQKIAAGDWLMLNYVAANHDPAQFPEPRKFDPTRPANRH

LAFGAGSHQCLGLHLARLEMRVLLDVLLDRVDSLELAGEPKRVNSTFVGGFKSLPMRW

KAA

>CYP108E1 Ralstonia metallidurans

MTIASDFDTELASHEIYSDPERMHEMFETLRREDPVHWTTAPGH

PPFWAVTKQADVIEVGKHPDVFIASPKSFLMNDVEQRVRIEETAATGGKLVRTMIHMD

DPDHKKYRGLTQSYFMPANIKRLESVIQERARALVGRLIEKGTSEFCSEIAVWYPLQI

VMTLLDVPESEHPYLLKLTQQFLAPKDPTLRRDGPDERGKGAVAKEYFAYFGKMLAER

RAAPLKEDLGSLIAHATVDGEPLPLMEAVSYYVILATAGHDTTSSSMCSGLYYLLTQP

GELDRLRARPELMPSAIEEMFRHGSPVKHFVRTATRDFELRGKKIQAGDEVALMYHSA

SFDEEVFDEPRSFRIDRGPNKHVAFGFGIHACLGQNLARASMRTFFTELLARTESIEV

VGKAEFIASNQVGGMKTLNIRVTPSKQSTTDRIEVAA

>CYP108F1X = 108B4 Mycobacterium marinum MM3999

MSAPTMDEAA LLADPLAYTD ETRLHAALTR LRAQAPVALV DVPNYRRFWA ITRHADVMDI

ERDNTLFTNW PRPVLATVAG DELQAAAGVR TLIHLDDPQH RVARAIGADW FRPKAMRALK

VRVDELAKNY VDAMMAAGPE CDFVQQIAVN YPLYVIMSLL GLPEADFPRM LKLTQELFGS

DDSEFKRGST SEDQLPALLD MFGYFNAVTT ARREHPTEDL ASAIANARID GEPLSDIDTV

SYYLIVATAG HDTTSATISG GLHALIEHPD QLARLQADPA LIPLATEEMI RWVTPVKQFM

RTASRDTVVR GIPIAAGESV LLSYVSANRD EEVFDQPFRF DIGREPNKHV AFGYGVHFCM

GAALARMEVG SFFTELLPRL KSIELSGDPQ FTATTFVGGL KHLPVSYSLV \*

>CYP108F1X = 108B4 Mycobacterium ulcerans

MSAPTMDEAALLADPLAYTDETRLHAALTRLRAQAPVALVDVPNYRRFWAITRHADVMDI

ERDNTLFTNWPRPVLATVAGDELQAAAGVRTLIHLDDPQHRVARAIGADWFRPKAMRALK

VRVDELAKNYVDAMMAAGPECDFVQQIAVNYPLYVIMSLLGLPEADFPRMLKLTQELFGS

DDSEFKRGSTSEDQLPALLDMFGYFNAVTTARRAHPTADLASAIANARIDGEPLSDIDTV

SYYLIVATAGHDTTSATISGGLHALIEHPDQLARLQADPALMSLATEEMIRWVTPVKQFM

RTASSDTVVRGIPIAAGESVLLSYVSANRDEEVFDQPFRFDIGREPNKHVAFGYGVHFCM

GAALARMEVASFFTELLPRLKSIELSGDPQFTATTFVGGLKRLPVSYSLM

>CYP108G1 Caulobacter crescentus CB15

1 MTISTDIANT IIDPKAYADG DRIDQAFAHL RREAPLAVAQ PDGFDPFWVV TRHADILEVE

61 RQNELFHNGD RATVVTTIEP DKKVREMMGG SPHLVRSLVQ MDNPDHFAYR KITQGALLPQ

121 NLRALEARIR EIARGFVDRM AEHGDRCDFA RDVAFLYPLH VIMEVLGVPE SDEPRMLKLT

181 QELFGNADPD LNRTGKSVTD VGEGVDSIQS VVMDFMMYFN AITEDRRANP RDDLATLIAN

241 GKINGEPMGH LEAMSYYIIA ATAGHDTTSS TTAGALWALA ENPDQFAKVK ADPSLIPGLI

301 EESIRWVTPV KHFMRTATAD AELGGQKIAK GDWIMLSYPS GNRDEAVFED PFTFRVDRTP

361 NKHVAFGYGA HICLGQHLAR MEMRVLWEEL FARLDHVELD GAPTRMVANF VCGPKSVPIR

421 FKMH

>CYP108G2 Ectocarpus bacterium, 67% to CYP108G1 Caulobacter crescentus AE005918

159023 MIDPNIPDDIAITVVDPRSYADGNAIDEAFAKLRKDTPLGVAGPQGFEPFWVVTKHKD

IVEVERNNEVFHNGDKSTTLVDANTDTA 158766

158765 VREMMGGSPHLIRSLVQMDNPDHKNYRGITAANFMPQELKALEVQVRKIAKSFVDHMEEL 158586

158585 GRKNDGRCDFAKDVAFLYPLHVIMELLGVPQSDEPKMLKLTQELFGAADPELNRTGKE 158412

158411 RDDPKEALAALSGTVAEFVEYFTAVTEDRRKTPRADIASVIANGKVNGEAIGIFEAMGYY 158232

158231 IIVATAGHDTTSGTTAGTMWELAKDRQKFLQVKNDPKLIPLLVEESIRWVTPVKHFMRSA 158052

158051 TQDTVLGGQEIKKGDWMMLCYQSGNRDEDVFDDPFEFKVNRQPNRHIAFGHGAHVCLGQH 157872

157871 LARMEMRALWEELLPRLDSVELDGEPTRMLANFVCGPKSVPIKFKMS\* 157728

>CYP108G3 ABS63163.1 Parvibaculum lavamentivorans DS-1

CDS complement(1684831..1686087) locus\_tag="Plav\_1544"

56% to CYP108G1 Caulobacter crescentus

MTDKTIDNAIVNPKTYAHVDEFHRLFTQLRKEEPVRWTEPDGFRPFWTVSKHADIMEVERQNDKFLNDPR

LTLQTIEVEEEVKKFTGGNSKLIRSLVDMDNPDHRNYRGLTQAWFMPPNLKAISARVEALAEKYIDRLEA

KGGECDFVSDVAVWYPLRVIMTVLGVPAEDEPIMLKLTQELFGSTDPDMKRPDATETVNTVTEFFNYFTA

MTEDRRKNPKDDVASVIANATIDGEPIGHLEAISYYIIVATAGHDTTSSTAAGGLLALMQNPEEFAKLKA

NPEGLLGGAIDEMIRWTTPVKHFFRTAAVDYELRGQKIKAGDNLLMCYWSANRDEEAFDDPFSFKIERSP

NKHLAFGYGAHLCLGQHLAKMEIRALYKELLARLDHIELAGDPAWVEASFVSGLKRLPIRYSMKRKAA

>CYP108H1 Ectocarpus bacterium, 49% to CYP108G1 Caulobacter crescentus CB15 AE005918

1535540 MGAASHKAQTSLSELVAPIFNPASFSHRDKIDG

1535639 IFTTLRQDNPLACVEVPGYDPHWMVTKYSDVKEITRQDNLFHSGDRPKILHSQAGEA 1535809

1535810 LARSFTGGSPNLFQSLVQLDPPEHTAYRNVLQGEFMPGGIAKMKENVAKTAQEFVDQMAS 1535989

1535990 LAPTCDFADDVAMNYPLQVVLDIVGVPREHHPKMLQLTQWLFSYADPDLKRPGSDIT 1536160

1536161 DPEEIIKTWNVVFTQFHEFFMPLVEARRANPKEDIASLIANAKINGESMEERKMISYFG 1536337

1536338 ILATAGHDTTSATTALGMKMLAENPDMLARLKEKPDLIPSFVEECIRWGSPVQHFIRSAT 1536517

1536518 EDYVLRGQTIRKGDLLYISYLSANRDEEEFDDPFTFKMDRAPNRHVGFGFGGHVCLGQH 1536694

1536695 LARLEIRTIWQTLLPRLTEVELTGPVKFTESEFVCGPKSVPIRFKMDG\* 1536841

>CYP108H2 Marine metagenome 1093018949056, AACY022454370, 57% to CYP108H1

APPRRGPQQSAEHTETWNRVYKEFEEYYEPVIKDRQTCPREDLASLISNGKIDGCPMEHR

AQISYFIIASTAGHDTTSATLATAISVLAERPEVLEQLKANLELIPAFIEETIRWASPVK

HFLRHATQDYELRGQQIKKGDLMYLSYISGNRDEDLIEDPFEFRIDRKPNRHVAFAFGNH

ICLGQHLARLELKIMLEELLPRLESLQLTGKPKLAISDLVCGPKSVPIQYDFKRTA\*

>CYP108-un1 Mycobacterium smegmatis

LTDHYAMAHPKALNDTPDTAQPGQPQTRNPTTPGDLPPLQFFARTVHAET

SLGGVQFSENQRLVMNLAAANRDPRQFDDPESFDADRPRNPHVAFGGGLH

SCQGQHIARAEMRAVLRVLLTRLPDVHLTGEVGEAGVLAGLMAVISLPVA

FTPERSQT

>CYP109A1 Bacillus subtilis

MTNQTARSSKKERYANLIPMEELHSEKDRLFPFPIYDKLRRESP

VRYDPLRDCWDVFKYDDVQFVLKNPKLFSSKRGIQTESILTMDPPKHTKLRALVSRAF

TPKAVKQLETRIKDVTAFLLQEARQKSTIDIIEDFAGPLPVIIIAEMLGAPIEDRHLI

KTYSDVLVAGAKDSSDKAVADMVHNRRDGHAFLSDYFRDILSKRRAEPKEDLMTMLLQ

AEIDGEYLTEEQLIGFCILLLVAGNETTTNLIANAVRYLTEDSVVQQQVRQNTDNVAN

VIEETLRYYSPVQAIGRVATEDTELGGVFIKKGSSVISWIASANRDEDKFCKPDCFKI

DRPSYPHLSFGFGIHFCLGAPLARLEANIALSSLLSMSACIEKAAHDEKLEAIPSPFV

FGVKRLPVRITFK

>CYP109B1 Bacillus subtilis

MNVLNRRQALQRALLNGKNKQDAYHPFPWYESMRKDAPVSFDEE

NQVWSVFLYDDVKKVVGDKELFSSCMPQQTSSIGNSIINMDPPKHTKIRSVVNKAFTP

RVMKQWEPRIQEITDELIQKFQGRSEFDLVHDFSYPLPVIVISELLGVPSAHMEQFKA

WSDLLVSTPKDKSEEAEKAFLEERDKCEEELAAFFAGIIEEKRNKPEQDIISILVEAE

ETGEKLSGEELIPFCTLLLVAGNETTTNLISNAMYSILETPGVYEELRSHPELMPQAV

EEALRFRAPAPVLRRIAKRDTEIGGHLIKEGDMVLAFVASANRDEAKFDRPHMFDIRR

HPNPHIAFGHGIHFCLGAPLARLEANIALTSLISAFPHMECVSITPIENSVIYGLKSF

RVKM

>CYP109C1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_111

MNLFPDEMRR DPYPLYDQLR TGSPVFHVAP LDLWMVFDYD GVKRALTDHE AFSSAVAPPT

GKAPDWIVFS DPPRHTKLRS IVLRAFTPRS IAGLEPRIRE LSRDLLDPWI ERGEMDLAAD

YAGPLPTMVI AEMLGVPPED RARLLRFSEV IVNLSHAISG GEEAARAVSE HAVVKEEMKV

YLAGLIEARR RAPAEDLLTR LVEAEVDGER LTEGDILNFF QFLLAAGTET ATNLIDNAIL

CFLESPAELF RLRAAPELLP SAIEEVLRHR SPLQMVFRET RRAVEVHGQV IPAGKLVLPV

IGSANRDPHQ FHDPGRFDIG RDPNPHVAFG HGIHFCIGAA LARLEARIAL PDLLCRLKGL

RRASDEPWEP RKAIIVHGPA RLPIRFEPGR RAAVHAAGAH TPCPG

>CYP109C2 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_8140

MNLFSEEMRR NPYPAYDQLR SRTPVLHYPP SDSWLIFDHD GVKRALHDHD AFSSVVSPPG

TRTAEWLIFS DPPRHTKLRA LITRAFTPRA VAGLEPRIRR LSRELLDRTI ESGQMDVAED

YAVPLPLLVI AEMLGAPAAD QPHFKRWSDA ILDLSHTVSG SEEAARALDA FTAVTAEMQA

YLRGLVEQRR AAPEDDLLTR LVEAEVDGER LNEDEILGFF QLLLVAGHET TTNLIGNAML

CFLENPDELA RLRAAPELLP SAIEEVLRYR SPVQAMFRVT RRDVPMHGQV IPAGKAVLAM

IGSANRDSQQ FRDPDRFDIA RDPNPHIAFG HGIHFCIGAP LSRLEARVAL ADLVARLGGL

ERASDAPWEP RRAIHVHGPA RLPIRFAPGP RLGGAPG

>CYP109D1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_4257

METETAPSPS PEQIDLSAPS VIADPYPAYR ALRGRSPVLY ARVPAGGAAG LGEPIRAYAL

LRHAEVLAAL RDPQTFSSNV TDKIRVLPRI TLLHDDPPRH THLRRLVSRS FTPRRIAELE

PWIGRLAASL LEATGDGPSD LMGAYAMPLP MMVIATLLGI PAERYVQFRS WSESVMSYSG

IPAEERASRG KAMVDFFAAE LEARRRAPSG DLISALVEAE IDGARLDTPE AVGFCVGLLV

AGNDTTTNLI GNMAHLLSER PELYRRAQQD RSLVGPIIEE TLRHSSPVQR LLRVTTRPVD

VSGVMIPAGH LVDVVFGAAN RDPAVFEEPD AFRLDRPPAE HLAFGQGTHF CIGAALARME

ARIALNALLD CYESITPGEA PPLRQTRAIM PLGFESLPLV LRRSRATA

>CYP110A1 Nostoc sp. PCC 7120 same as Anabaena sp. PCC

1 MLTQLPNPIS VPSWWQLINW IADPIGFQKK YSKKYGNIFS MQLAGIGSFV ILGEPQALQE

61 IFTQDSRFDV GRGNTLAEPL IGRTSLMLMD GDRHRRERKL LMPPFHGERL QAYAQQICLI

121 TNQIASEWQI GQPFVARSAM QKLSLEVIIQ IVFGLADGER YQQIKPLFTD WLNMTDSPLR

181 SSMLFLKSLQ KDWGTWTPWG QMKHKQRSIY DLLQAEIEEK RTKENEQRGD VLSLMMAARD

241 ENGQAMTDEE LKDELLTILF AGHETTATTI AWAFYQILKN VNVQEKLQQE LDRLGANPNP

301 MEIAQLPYLT AVSQETLRMY PVLPTLFPRI TKSSINIAGY QLEPDTTLMA SIYLIHYRED

361 LYPNPQQFRP ERFIERQYSP SEYIPFGGGS RRCLGYALAL LEIKLVIATV LSNYQLALAE

421 DKPVNVQRRG FTLAPDGGVR VIMTGKKSLK FEQSSKIFN

>CYP110A2 Anabaena variabilis (a cyanobacterium)

MLTQLPNPISVPSWWQLINWIADPIGFQKKYSQKYGDIFSMQLA

GIGSFVILGEPQAIQEIFTQDSRFDIGRGNKLAEPLIGRTSLMLMDGDRHRRERKLLM

PPFHGEKLQAYAQQICLITHQIASQWQIGQPFVARSAMQKLSLEVIIQIVFGLANGER

YQQIKPLFTDWLNMTDSPLRSSMLFLKSLQQDWGNRSPWGQMKYQQRCIYDLLQAEIE

EKRTKENERRGDVLSLMMAARDENGQAMTDEELKDELLTILFAGHETTATTIAWAFYQ

IFRNVNVREKLQQELDSLGENPNPMEIAQLPYLTAVCQETLRMYPVLPTLFPRITKSS

INIAGYQLEPNTTLMASIYLIHYREDLYPHPQQFRPERFIERQYSPSEYIPFGGGSRR

CLGYALALLEIKLVIATVLSNYQLALAEDKPIKVQRRGFTLAPEGGVRMIMTGKKSLR

FEQSNKIFN

>CYP110B1 Nostoc sp. PCC 7120 Same as Anabaena

1 MHLPKGPQTP VFVQVLRWVF SPMSFLEDCA KRYGDIFSVK LAKDVPAIVF LSNPKDIQQI

61 LTNDNNQLDS PGDWNDLFEP LLGKRSVITL SGAEHQRQRQ LLMPPFHGER MRGYSQVITD

121 VTEKVISQHQ IGQPFQVRSV TQAITLRVIM QAVFGLYEGS RAEKLQHLLS DLLEKSSSPF

181 SVALLYFPSL RRDFGPIKFW GEQVQIQQQA DELIYQEIQE RRENPDPSRT DILSLLMDAR

241 DADGQPMTDV ELRDELMTLL VAGHETTATA LAWAMYWIHK LPPVKARLLE ELDSLGDNPD

301 STTIFKLPYL NAVYSETLRI YPVAMLTFAR RVIETMALGG YELPPGTPVL GSIYLTHHRE

361 DLYPEPKKFK PERFLERQFS PYEYLPFGGG TRRCLGLAFA QWEMKLALAK ILTSYELELV

421 NNSVEVRPKR RGLVTGPHRP IEMVIKSQRQ ITSRILETTT VS

>CYP110B2 Nostoc punctiforme

MKLPKGPQSPAVLQMLRWITSPMSFMETCAKRYGDMFTIRLDSK

SPPLIFVSKPEVLEQILTNDIKGLEAPGDTNLVFESLLGKHSVITISGAEHQRQRQLL

LPPFHGERMRSYSQIISDITEKVISQYQIGQPFNIRSVTQAITLRVIMQAVFGLDEGP

RAEKLQHCLAEMLEKGSSVLSAALLYFPALQRDFGPINFWGKQMRRQQAADKLIYEEI

RERQEQPDPSRTDILSLLMAARDEAGQPMTDEKLRDELMTLLVAGHETTATALAWAFY

WIQKIPTVRQKLLKELDSLGDNPDPSTIFKLPYLNAVCSETLRIYPVAMLTFARVVRT

PLSLGGYELEPGIGVIGSIYLTHHREDLYPEPKQFKPERFLERQFSPYEYLPFGGGAR

RCIGLAFAQLEMKLALAKILSTRELELVDNSEVRPKRRGLVTGQDRPIQMVVTSQRQV

KFPILQTATV

>CYP110C1 Nostoc sp. PCC 7120 Same as Anabaena

1 MKYQIQRPNP LKTHPFLQKL QWIADPVEYM KKASLQHPDM FTAEVIGFGD TVVFVSHPQG

61 IQTLFANDRK KLVAVGEANR ILYPLVGNNS MFLLEGVKHK QRRQLLMPSF HGERMREYGH

121 LIRNITENLF SQLQQDVTFS ALTAMREISM QVILQAVFGF YEGERCQQFK HLLPIFLSEL

181 FQSPLASSIL FFPSLQKDLG NLTPWGRFVR QREKIDKLLY AEIAERRQEI NSDRIDILSL

241 LISARDETGD SMSDKELRDE LITLMISGHE TTGTAMAWSL YWILQTPEVF QRLIQELDSL

301 GDSPDPMSIF RLPYLTAVCN ETLRINPVAM LTLPRVVKEP IELLGNRLET STTVVGCIYL

361 THHREDLYPE SKLFKPERFL KREFSQYEFM PFGGGVRGCI GQALAMFEMK IVLATVLSRY

421 QLALADRKPE RPQRQGFTLT PTNGVKMLIT GQHKRQNYSM AASTTFNA

>CYP110C2 Nostoc punctiforme

1 MQLPNILKSP SLLQKLHWVS DPIGYMENAA QEYPDIFTGK IVGFGDTVVF VNHPQAIQEI

61 LTNDRKKFTA VGELNGILKP LLGDNSVLML ESDRHKRQRQ LVTPSFHGER MQAYGQLICN

121 VSKKIFNQLP LNKPFVARNL TKEISLQVIL QSIFGFYEGE KIQKLRQLLP LLLELFESPL

181 SSSLFLFSFL QQDLGAWSPW GNFLRVREKI DQFLYTEIAE CQQQADPERI DILSLLISCR

241 DEAGQPMTDQ ELRDQLITLI LAGYDTTATA MAWGLYWIHK QPLVCEKLLQ ELDTLGDSPD

301 PMSISRLPYL TAVCNETLRI HPVTMFSFPR VVQEPLELLG HSLEPGTILL PSIYLTHHRE

361 NLYPQSKQFK PERFIERQFS PYEFLPFGGG VRRCMGEALA LFEIKLALAT IVSHYHLALV

421 DQRPEQPQRR GFNLAPGSGV KMVMTDQRAR KESLINMTTT PLS

>CYP110C3 gi|75908202| YP\_322498 Anabaena variabilis ATCC 29413

95% to 110C1

MKYQIKRPNPLKTHPFLQKLQWIADPVEYMEKASLQHRDMFTAEVIGFGDTVVFVSHPQGIQTIFANDRK

KLVAVGEANRILYPLVGNNSMFLLEGVKHKQRRQLLMPSFHGERMREYGHLIRNITETLFSQLQQNVTFS

ALTAMREISMQVILQAVFGFYEGERCQQFKHLLPVFLSELFQSPLASSILFFPFLQKDLGNLTPWGRFVR

QREKIDKLLYEEIAERRQEINSDRIDILSLLISSRDETGNSMSDQELRDELITLMISGHETTGTAMAWSL

YWILQTPEVFQRLIQELDSLGDSPDPMSIFRLPYLTAVCNETLRINPVAMLTLPRVVKEPVELLGNRLES

GTTVVGCIYLTHHREDLYPESKLFQPERFLKREFSQYEFMPFGGGVRGCIGQAIAMFEMKIVLATVLSRY

QFALADGKPERPQRQGFTLTPANGVKMLITGKHQRQNYSTAASTTFTT

>CYP110C4 gi|119510163| ZP\_01629302 Nodularia spumigena CCY9414

MSTPNRLKTPAFFQQLQWVADPVGYMEKAAQQYPDIFTAQVVGFGNNLVFVNHPQAMQEILTNDRKKLFA

GGKENKILQPLLGDYSMIMLDGDRHRKRRQLVMPSFHGDRMRSYGEIISNITEEVWSNLPTDKSFLARNV

TQDITLQVMIQAVFGVYQGERSQQLKKQLELMANIFRSPLSSSMLFFSSLQQDLGAWSPWGKFVRDRQEL

DNLIYTEIAERRQQNLENRIDILSLLMSAEDESGNPMTVQELRDELMTLLFAGYETTATALAWGLYFIQK

HPEVQEKLLQELDTLGDSPDPMSIFRLPYLTAVCNETLRIHPVAMLTFPRTVKEPVEISGYALDPGTILV

GSMYLTHQREDLYPEPKQFKPERFLERQFSPYEFIPFGGGVRRCVGEALAVFELKLVLATILSRYELALT

DDQPEVPRRRGVTLAPGRGVNMMITGQRLA

>CYP110C5 gi|67925622| ZP\_00518945 Crocosphaera watsonii WH 8501

MKTIPTPKTPTLVQQLQWVLNPTGYLQTNHHRYPDLFKAKIIGLGNDIILISNPEIMQYILTHDRQEFTA

PSSLNTLLKPLLGDYSVVMLDGDGHRQRRQLVMPSFHGERLKVYGDLTCRITREAMEKLPENQPFLAREV

MQDISLKVIMEAVFGVTEGERYEELQYRLKELLDLFDSPITSGFLFFPSLQKDLGNWSPWGYFLRQRQAL

DKLIYAEISDRRANPDPERTDILSLLMFAKDEQGESMKDQELRDELITLLMAGHETTASAMAWALYWLHH

IPEIKDKLIEELNTLSPDAEGMDIFRLPYLTAVCNETLRLSPSAMLTFTRLAQQTVEVGGYTFKPGDIVA

GCLYLTHLREDIYANPKQFNPQRFLDHKYSAYEFIPFGGGSRRCMGEALAKFEMKLVIAIIISEYCLKLA

DTQPEKQQRRGLTLSPKRGVKMILEGKRQPQKARELELSTR

>CYP110C6 gi|126660859| ZP\_01731952 Cyanothece sp. CCY0110

MKTIPGSKTPKLIQQLQWIFNPTKYLKTNHRRYPDIFKAKIIGFGDKMILTSRPEIMQYILTHDRKQFTS

PSGLNAILRPLLGDSSVLMLDGDRHRQRRQLVMPSFHGERLKVYGDLTCRITEEVMAKVPQNQPFLAREI

MQDISLKVIMEAVFGVTEGKRYEQLQDRLKKMLDLFNSPLTSAFLFFPFLQKDLGSWSPWGHFLRQRQAI

DELIYAEISDRKAHPDSDRTDILSLLMSAKDEQGQGMKDQELRDELMTLLTAGHETTASAMAWALYWIHH

TPEVKDKLIEELNTLSPDAEGMDIFRLPYLTAVCNETLRLSPSAMLTFTRVAQEKVEVAGYTFEPGDMIM

GCMYLTHLREDLYTNPEQFNPQRFVDRQYTPYEFIPFGGGSRRCVGEALAQFEIKLVIATIMSQYCLKLA

DTQPEKQQRRGVTLSPARGVKMILEGKRQPQPVRELELSRQ

>CYP110C7 gi|119486461| ZP\_01620519 Lyngbya sp. PCC 8106

MKTLNSPKTSPLIQRLQWVFNPLEYMETNVKINRDIFNTQVTGGVGLIFVNSPEGMQELLTRDTKEFYAP

GSINEILKPLLGEQSVMLLDGDRHKRQRKLLMPPFHGERMRTYGELILNITQQATAKLKPGQPFIARNAM

QEITLAVILQAVFGIYEGSRYDKLKQLITSLLAVTDSPVSSSLLFFTSLQKDWGAWSPWGRFLRMRQKVD

QLLFAEIEERRQNWDENRTDILNLMMAARDEDGQPMADEELRDELLTLLVAGHETTATAMAWALYWIHRQ

PEVYQKLIQELESLPENADPMTIFRLPYLTAVCNEALRIYPVAMLTFPRVTKEPTQLLGYELEANIGLAG

CIYLLHHREDLYPEPKQFKPERFLERKFSPYEFLPFGSGARQCIGMALAQFEMKLALAQILLDYDLTLLE

KRPVKAARRGVTLSPVGGIKMMMNGKRTPSKSVAIPATV

>CYP110D1 Nostoc sp. PCC 7120 Same as Anabaena

1 MTVTQNLPNG PRIPRLLRLF KFITQPIQYV EDFAKVYGDN FTIWGSGESY FVYFSHPQAL

61 EQIFTNVSCF ESSGGGSPLL ELLLGKNSLI LLEGDRHQRQ RQLLTPPFHG ERMRAYGQTI

121 REITQQVTQA WQMGKPFNIR ASMQEITMRV ILRVVFGVDE GELFQELRQL LTTLLDFMGS

181 PLMSSTFFFS FTQKDYGAWS PWGRMVRLIK KIDQLIYALI AQRRAEFGEN RQDILSLLIS

241 ARYDDGQPMS DVELRDELMT MLVAGHETTA SALTWAFYWI DSVPEVREKL FQELDTLNDD

301 SEPSIIAKLP YLTAVCQETL RFYPIVLNAF FRRTKNPMEI MGYKLPKATL VVPSIYLAHH

361 REEVYPQSKQ FRPERFLEKQ FSPYEYLPFG GGNRRCIGLA FAQYEMKIVL ATILSQFQVS

421 RLSKRPVQPV RRGLTLAAPG GMKMVANKRM RNS

>CYP110D2 Nostoc punctiforme

MNIPLSVTLSNMKSRNNKIQKPSNLQTPMTATYNLPDGPQMPRW

LRTIKFISQPVKYVDDFAKTYGDTFTIRSSRSDNHIVYFSQPQALEEIFTADSRHFEV

GRGNTGLRFLLGDRSFMLVDGDRHQRQRQLLAPPFHGERMRAYGEDIRKITQQVSHEW

KIGKPFNIRESMQEITLRVILRVVFGLNEGELFEELRRSLSDLLDFISSPIMSSAFFF

RFIQKDFGAWSPWGRILLQRQKVDLLIYTLLRERRAQTDQNRQDILSLMMAARYDDGQ

GMSDEELHDELMTLLVAGHETTASALTWAFYWIDHLPEVREKLLQELNTIGVNPDLSS

VAKLPYLTAVCQETLRIYPIAMTAFVRIVKTPITIMGYELREGTAIVPSIYLAHHREE

VYPQSKQFKPERFLERQYSPYEYLPFGGGNRRCIGMAFAQYEMKIVLATVLSEFQVSL

VNKRPVHPVRRGLTVATPAGMRMVATPQVKRANTPALV

>CYP110D3 Trichodesmium erythraeum

MTLPDGPSLSPLQRRLRTWKFIFSPLSAIEERYSEYGDIFRTNT

NSLYPFIYFCNPKAIQQIFTADPDTFTSGSINGILKYFVGLNSLLLQDGDRHKRQRKL

LMPPFHGDRMRKYGDLIYNITSNVISQWKIEQPFPIRKSTQEISLKVILAAVFGLDQE

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EIQTAKKEGNHRDDILSLLLEARDEAGNAMSDEEIKDELLTMLFAGHETTASALAWAL

YWIDMIPSVGEKLMAELATIPSNSDQVAITKLPYLSAICQETLRIYPIAMNAFPRVVQ

KPIEIMGYQLEPGMVAIVPIYLTHHREDIYPEPKKFKPERFLERQFSPYEYLPFGGGS

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WQKVSQPILTSG

>CYP110D4 gi|119486457| ZP\_01620515 Lyngbya sp. PCC 8106

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AGGVLLFLLGDNSVLMVDGERHERQRKLLMPPFHGERLKTYNQLICEITKEVMSQVKIGQPFRVRTLMQD

ITLRVILKAVFGLTEGERYEQLRHLLSAMMESIGSPLAASLMFFPSLRQDWGEWSPWGRFLRYKQQADEM

IYAEIRERKQQRDFDGDDILTLLMSARDETGKPMNETELRDELVTLLIAGHETTASSLTWALYWTHYLPE

VKDKLCFELANLGENPHLSEIARLPYLTAVCNETLRIYPVTLTSGVRVLKKPLELGGYSFEPGTVLFPCT

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>CYP110D5 gi|67920042| ZP\_00513562 Crocosphaera watsonii WH 8501

MNLPPTLSQPRLLRLFKLIFYPLDYLEDNYQRYGDIFVAGKSETPFVYISNPQGIQTILTRDKTDFKTGG

GSGFLSTLLGDNSLLFLQGERHRRERKLLMPPFHGERLKSYANLIYSISDKVTDKLQINRSFNVRDIMQE

ITLKVILKAVFGITEGERYQRLQELLKSWLSFFDSPANAILIFFPWLRKNWGNWTPWGRFLQIKAEIQEL

IYTEIRERREQKKYEGTDILTLLMLAKDEEGKPLSDQELHDELITLLIAGHETTASALTWALYWIHFCPD

VEDKLRFHFSNLNNNTDLLDIVKLPYLDAVCKETLRIYPVLLTTFIRVLQTPLELMGYQFKPGTVFAPAI

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PLKAVRRGLTVAPPSNFKMILSN

>CYP110D6 gi|126654866| ZP\_01726400 Cyanothece sp. CCY0110

MVLPPSISTPRLLRLFKLIFYPLDSLENYYERYGDIFIVGQSETPFVYISNPQGIQEILTKDKTHFRTGG

GSGFLTTFLGNNSLLSLKGEKHQRERKLLTPAFHGERLQSYATLIYSISDEVSEKLEINQSFNVREIMQE

ITLQVILKAVFGIAEGKRYQKLKNLLTSWLSFFDSPINATIIFFPFLQKDWGNWTTWGRFLRIKAQIDDL

IYTEINERRQQKNYQGKDILTLLILARDEDGNPMSDQELHDELITLLIAGHETTASSLTWALYWIHYCPE

VEEKLRSHFSILDKNIDLLNIIKLPYLDAVCSETLRIYPVVVNAFIRVLETPLELMGYQFKPGTVFAPAI

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PLKPVRRGLTIAPPNSFKMIITQKLAYT

>CYP110E1 Nostoc sp. PCC 7120 Same as Anabaena

1 MKLPDSPKIP KFMQLVQWIY QPLQLMEASA KAHGDSFTLW LTNKRPIVFL SNPQAIQELF

61 TTPLEQLDAR GTAQVLQPLL GENSLLLLSG ETHQRQRKLL TPPFHGDRMR AYGDIITNIT

121 KEVISNWQLG KPFSVRDSMQ EITLRVILQA VFGLREGERY TQLQKRLCDI LDLSGSALRS

181 TLSFLPALQI DLGRWSPWGH FLRQREAIDQ LLYAEIQDRR DHPDPSRTDI LSLMMAARDE

241 NGEAMTDVEL RDELMTLLVA GHETTASALT WALYWIHKLP QVREKLLAEL DNFGDNGDVN

301 EITRLPYLTA VCQETLRIYP IAMVTIPRIT KTNLEIGGHQ FAPGTMLVGC IYLMHRRPDL

361 YPQPQEFKPE RFLEKQYSLY EYLPFGGSNR RCVGMAFALY EMKLILATVL ANVDLALVDN

421 YPVKPTRRGV TLAPSGGKWL IATAQHQKIK NPVEV

>CYP110E2 Nostoc punctiforme

MSLLKLPNGPQTHPWIQMYQWLTNPLEYMEACTKRYGDIFTLKL

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KSPLQIGEYNFEPGTILIPSIYLTHHREDLYPESKQFKPERFLERQFSPYEYLPFGGG

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LQNQPILQTSSSSV

>CYP110E3 Trichodesmium erythraeum

1 MIKLPGPKSP ALTQILQWTA KPIKFMEKCA REYGDTFEVK LNYPIVFISH PKAIEEIFKA

61 NPKKFDCGSS NKLAQPLLGD YSLLLLDDIP HQRQRKLLMP PFHGKRMQAY GELICNVAQE

121 VASKWEIGQV FSMREFTAEI SLKVILQAVF GLYEGERYSK LEKLLGSLLE SLSSPLKTSM

181 LFFQFLQIDL GPWSPWGNFI KNREEIYELL CAEISERRQK LDPERSDILT MLLLARDEEG

241 EGMSDIELRD ELMTLLIAGH ETTATSLSWA FYWIHHQPEI YQKLSRELET FGDDLNPMTV

301 INLPYMNAVC SETLRIYPVV IIVSPRKTKL PITIMGQT

>CYP110E4 gi|37522632| NP\_926009 Gloeobacter violaceus PCC 7421

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ASNVALRPTLGANSLLLLDGERHQQQRRLLTPPFHGERMRAYGELIRQVTEEVIVRWQPGKPFLVRNAMQ

RISLAVILQAVFGLHDGTRLVRLRQALGSMLDAMSSPLSMAMLLMLPEDFGPWSPRARLQAHLGAIDELL

YAEIRERREHFDAGAGDILGLLLAARDEAGAAMGDAELRDELMTLLVAGHETTATAMAWALYWIHYLPQV

RERLLAELDSLGSDPDPEAIARLPYLGAVCSETLRIYPVALIASPRVARHTVRILERDYEAGTRLAAGIY

LAHHRPETYPEPERFRPERFLERTFSPYEFVPFGGGSRRCIGMAFALYEMKLVIATVLLERDLRLVQPRL

LRPVRRGVTLAPPEGLYLVPTGERSASRLLSRTSTAGQ

>CYP110E5 gi|37522633| NP\_926010 Gloeobacter violaceus PCC 7421

MSLPAGPASPPPLQLLQWIGRPTDYLERTARRYGDPFTMRLGLHSPVTGVFFSSPEAFQQLFNTEPGLFD

SGGANASSTFNLLFGTNSLILLDGERHQQQRRLLTPPFHGERMRSYGELIRTLAEQVTARWNLGTPFQAR

RSMQRISLGVILKAVFGLHDGTRYLRVCRLLGNLIDASASPLLFGLRLIFPQDAGPMSPMGQLKAQIDAI

DELLYAEIRERRERPDPRADDILSLLMAARDEAGQGMGDVELRDELMTLLVAGHETTATAMAWALYWIHR

LPQVRERLLAELDSLGSDPDPEAIARLPYLGAVCSETLRIYPVAMVAFARVPRRPVRILDREYPAGTFLI

PNIYLAHRRPEAYPDPERFRPERFLERTFSPYEFVPFGGGSRRCIGVAFALYEMKLVLATVLSRVELRLA

DPRPRLPVRRGLTLAPPEDLHLIPTALRSGHRDLLPAC

>CYP110E6 gi|75908324| YP\_322620 Anabaena variabilis ATCC 29413

MKLPDSPKIPRFMQLVQWIYQPLQLMEASAKAHGDCFTLWLTNKRPIVFLSNPQAIQELFTTPLEQLDAR

GTAQVLQPLLGENSLLLLSGETHQRQRKLLTPPFHGDRMRAYGDIITNITQEVISKWQLGEPFSVRDSMQ

EITLRVILQAVFGLREGERYTQLQKRLCDILDLSGSALRSTLSFLPALQIDLGSWSPWGHFLRQRAAIDQ

LLYAEIQDRRDHPDPSRTDILSLMMAARDENGEAMTDIELRDELMTLLVAGHETTASALTWALYWIHKLP

QVREKLLAELDNFGDNGDVNEITRLPYLTAVCQETLRIYPIAMVTIPRIVKTTLEIGGHQFAPGTMLVGC

IYLMHRRPDLYPQPQEFKPERFLEKQYSLYEYLPFGGSNRRCVGMAFALYEMKLVLATVLANMDLALVDN

YPVKPTRRGVTLAPSGGKWLIATGQHQKVKSPVEV

>CYP110E7 gi|119512554| ZP\_01631632 Nodularia spumigena CCY9414

MPALQLPDGPKNHPWLQTYRWLTSPLEYMEDCAKNYGDIFTIRVGPLSTPQVFVSNPQAIQQIFSTDPKY

LDSGAAAGFKSPLLGNQSLLSLDGKPHQRQRKLLTPPFHGERMLAYGELIRDISQQVTNKWQVGETVSVL

SSMQAISFQVILKAVFGLAEGPRYEKIKEALIAILNPKKPLLRSMLLMFPSLRRDLGAWSPWGEFLRLRQ

QIDELVYAEIQERKAQLDSSRTDILSLMMATRDEAGEPMTDLELRDELMTLLVAGHETTATALSWALYWI

HHQPQVREKLLQELDTLGEKPDPNAIFRLPYLNAVCSETLRLYPVAMLLLSRLVKSPLQIGEYQFEPGTL

LIPCVYLTHHREDLYPDSQTFKPERFLERQFSNSEFIPFGGGNRRCIGMAFALFEMKLVLATVLSNWQME

LANTQPVLPVRKGLLFGPKGGVQMVVKGRRELS

>CYP110F1 Nostoc punctiforme

MKILDSLTTPSLLQTLQLIAKPTKTLENYATKYGDIFTMRVMGL

KSPPIVFFSHPQAISDCFAVPAHKLDFKKATHVFKPLFGENSIVFKEARSHQQQRQLL

LPAFHGDNLKSYGQAICQIAEELTQSWTSGTNICIHKLMSKITLEIILQVVFGITHGV

RYQQLKEQLSALLEDVTKPWYSSLFFFPSLQKDLGAWSPWGIFLKRREQIDKLIYAEI

SERRWQNDAMRTDILSLLMSAHDVNGQQMTDEELRDQLVSLLLLGYETTSGVLAWIFY

LIHSHPEVKHRLMQELSTLDNLTNPEAITQLPYLTAVCQETLRIHPIALICTPRMLKE

PVEIMGHKFTSETVLVPCIHLAHRRTDTYPEPEQFRPERFLNQKFSPYEYLPFGGGYR

GCIGAAFSMYELKLVTAIILSRFELSLTDKRPAYPVRRGITIVPSGGVKMVVTKKAKF

KRQTILST

>CYP110G1 Trichodesmium erythraeum

1 MKQVCALKTP LWLQRFNYIT NPVSYWQKAY SSYKDAFYAQ GINFGKPLMV FYTPSAAKQI

61 IENCQGDLTT TSFDSELTAI FGDSSFFILE GTNHKKMRKL LIPALHGKHI KTYGELICNL

121 VNNLIENLPF NQSFSALEIA QEISMQVMIK LLFGNYQQER YQKIKQLMIN MVSLFAANVF

181 GFPLFFKFLQ QDLGLVSPWG NFLQQRRKIQ QLIYQEIAER RNHPNQERTD ILSLLMTAQD

241 EKGNFLNDEE LLGQLLSLLF TGNESTAASI AWSWYEVYRN SKIKEKLLEE INNLGDSPEP

301 LSLFNLPYLS AVCNETLRKY PVTMFMIPRI VKNTTEINGY QLDKGMLVTV GTYILHHRED

361 IYDQPEEFKP ERFIEHRFSS FEFLPFGRGM RGCIGADIAL YQMKLTLATI ISHHRLELTN

421 YGQIFPKRRN TILTPIKLRI IKAC

>CYP110H1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_2802

MSQLPRGPRS RLLTTYKFLT RPFEFLTHCA ATYGDVFNVP VVSGDVVIAG GPRTVQDVMT

APPETFLPFA TRAIAPLVGE HSLLMLSDER HRRERKLLTP PFHGDRMRAY AAAMADTAAR

RLTEAARAPR AVAQELTQAI SLDVIIRAVF GVEEPSRTSA FARAVVAMTD ALTPALTFLP

PLQRELGGLG PYARFRRRVG ELDALFRAQI ERARAAPGDD ILSLMVSARY DDGSRMSDQA

IFDELRTLLF AGHETTALAL AWALDHVHRH PGVLARLRDE IDALGPEPDP ERLAALPYLD

AVCKEALRVY PIVTESPRLL AQPFRLGEHE LLPGTGVAPC ILLVHHHPEL YPEPSRFRPE

RFLERKFSPF EYLPFGGGHR RCIGAAFAMF EMKIVLGVAL SAWEFRLLDE RPPRPVRRNL

TLSPSGGVPL VLRARGRSRL YAAA

>CYP110J1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_5885

MGNLPPGPKS LSLVDTIRAG FISSEPVFRR YAAEYGPTFR LRSPNGILTI TGDPEAIRAV

YTADPDEFDV WGVQLTEPVF GTSSVVVTAG ARHRRDRRLL APPFSAGAMR GYGDAIAEIS

LDVASRWRPG RSFSMLAATQ AIALDVIVRV VFGVRGEARV GRTREAVLGL IESLSPSFMI

IPALRRDFAG FGPYARHKRA ARALDALLFE EIRARRAEGD ASQDILGLMM SARHDDGAGM

SDVEIADQLR ALLFAGHETT AMSLGWAMYW LHREPAVLAR LLDELDTLGP APEADALASL

PYLEAVCLEA LRLHPPVVDV ARVVKRPFRL KGYTIPAGEA IAASPLLLHG REDLYPSPER

FRPSRFLDRK FTPFEFIAFG GGARRCLGAA FAMYEMKVAL GTILGRYRLR LESQAPIHHV

RRGLTMGPSG DVAMILEGER ERARAEGRPA AVQGSPAEPA LRPAAPQPAG RCPMGFS

>CYP110K1 gi|126660674| ZP\_01731775 Cyanothece sp. CCY0110

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ALFTADPDLFNSGTSNAAFQPLLGSQSILQLDGEPHKKRRKLLMPSFHGQRLQTYGEIITNITQSIISHW

QKEDIFSMREVTQEITLSVILQAVFGITQGNNYQSLRKQLGRYLDLFNSPLYTSTLFLPILQKNWGTWTP

WGNFIAQRDKVYELLSQEIDKRTTTKDGEDILTLLLSVIDEEGEHLTKSEVMSELMTLLFAGHETTASAL

AWAFYWIHFHPEIYHNLKDELDTIDLDTDPMEIAKLPYLSAVVSETLRIYPIALFAFSRTLTTSWEFMGY

SLDKGMSLAPCIYLVHHHPDIYPNSKQFKPERFLERQFSPYEFIPFGGSNRRCLGYALALYEMKLVLATV

LKQVNLKLVSSQPILPVRRGFTMSPQGGVKMQVI

>CYP110L1 gi|113954988| changed from 110H1 YP\_731620 Synechococcus sp. CC9311

MLEAILRPIAYYRRCFFRNSGVVRVRMSPTLPPQQVLISDPSVIKELINEDGGRHITAPGQLNGLLSQVL

GKHSIILLAPATHRQRRKLLTPPFHGERLKAYGQLISSLADQSLIDLNVGDVFDAREQMQGITMRVILTA

VFGLHEGDAFRQLERSLASSISIRSGPLGSLLLFFPFLRRDLGRWSPGGRIKAADAAIRRLLLEQIASRR

RAVERCGEENMSADILSLLLSCKDDEGQGLSDDELHDELLTLLFAGHETTATALTWAFYWIHRNPLVLER

LMNELNGLLDHSDPEAIARLPYLSAVVNEVLRIHPVAMLTFPRRIESAITLGGYAFRSGDVVMACIQAVH

ERPDLYPKPLQFNPERFMNQTYGLHEFLAFGGGSRRCIGAALALYEMKLILAKILLNNQFELTPKSNRWN

KPRRRGFTLGPSIPVKLKMVSLRP

>CYP110M1 gi|119485435| changed from 110J1 ZP\_01619763 Lyngbya sp. PCC 8106

MRLPDGPRLPALLQTLQIIAQPTQFLERCANQFGDCFTLRVLGFNSPPIVFFSNSEAIEAIFTTDTDKFE

LGKITHVFQPLTGSQSLIMQDGKRHQRLRQLLMPSLHSKQLPAYGQTICNLTLKATQNWSPGDFISIRDY

TSEIALEVILQVVLGLKENRRYFQLKHLIEPYLESVNKPLNSIQFFLPPLQQNLGQKSPWGKFLKQRKKI

DDLIYAEIAERRTKPLGEDVLSLLISAKDEAGQPLTDQELRDQLITLLLLGHDTTASALAWAFYWIHRYP

KIVNQLVEELNSLGENPDPMDIVQLPYLNAVCQETLRIHPIALISQPRVVKESIKIENYQFKPGTILVPC

IHLAHHREQIYPNSKQFNPNRFLEQKFSPYEYLPFGGGNRSCIGMALSLFEMKLILATILLNYQLAFNQS

HVVKPVRRGITIVPSINFRLTVLTRKQAGIASKSVNH

>CYP110M2 gi|56750197| changed from 110J2 YP\_170898 Synechococcus elongatus PCC 6301

MLPPGPSQLALLQTLRIITQPVSFLLSCADRYGDWFTLRVLGPQSPPVVFVSDPEAILAIFSSLADQLEL

GRIADVFRPLVGNESLIMQNGDRHRQQRQLLMPALQGERLFDYTPAMTAITQAAIAQWPLGQPLDLRRQM

SQISLAVILQVVFGLTPGPRYRDLYQRLDQLLEAITDPLYSLQFFWPALQQDWGNWSPWGRFCRQREAID

ALITAEIQEGRQSQQPRQDVLELLLAARDRDGNPLSDQELRDQLMTLLLLGHETTASALTWAVFWLLRHP

DCLNRLQSELVAIGDNDRAIAKAPYLDAVCREALRLQPIALIAQPRRVASPLSLGGYDFASGTILVPCVL

TAHRRAATYPNPDQFQPNRFLERRFSNGEFLPFGGGQRSCIGMALSLIEMKMVLATLLRQCQIAEVSQRP

VRPARRGITFVPSQDFRIQVQQWHNPSAQTAIASV

>CYP111A1 Pseudomonas incognita

MERPDLKNPDLYTQQVPHDIFARLRREEPVYWNPESDGSGFWAV

LRHKDIIEVSRQPLLFSSAYENGGHRIFNENEVGLTNAGEAAVGVPFISLDPPVHTQY

RKVIMPALSPARLGDIEQRIRVRAEALIERIPLGEEVDLVPLLSAPLPLLTLAELLGL

DPDCWYELYNWTNAFVGEDDPEFRKSPEDMAKVLGEFMGFCQELFESRRANPGPDIAT

LLANAEINGQPVALRDFIGNLTLTLVGGNETTRNSISHTIVTLSQQPDQWDILRQRPE

LLKTATAEMVRHASPVLHMRRTAMEDTEIGGQAIAKGDKVVLWYASGNRDESVFSDAD

RFDVTRTGVQHVGFGSGQHVCVGSRLAEMQLRVVFEILSTRVKRFELCSKSRRFRSNF

LNGLKNLNVVLVPK

>CYP111A2 Novosphingobium aromaticivorans

MLDLKNPDTYQGGVPYAALQDLRAEGPVHWNPESDGAGFWAVLG

HDEIVAVSRQPDLFSSAFENGGHRIFNENQVGLTGAGESAIGIPFISRDPPSHTQYRK

FVMPALSPARLQGIEERIAKRVERLFAQVPLGETVNILPLLTVPLPLLTLAELLGVPA

DLWPDLHRWTDAFVGEDDPDFRQSPEAMQAVLAEFMGFATALFEDRRANPGPDIASLL

ANTEIRGEPAPLRDFIANLILALVGGNETTRNSINHTMIALAENPGQWDILRADPSLM

TAAVKEMVRFASPVIHMRRTAMRDTQLGQQAICKGDKVVIFYPAGNRDPAVFENPDRF

EITRPVRQHLAFGSGAHVCVGSRLAEMQLRLAFAEMARHVRAFEVVGEPSRVRSNFIN

GFKRLEVRLLV

>CYP111B1 ABS61652.1 Parvibaculum lavamentivorans DS-1

CDS complement(33622..34875) locus\_tag="Plav\_0029"

49% to CYP111A1 P450 lin L23310 Pseudomonas incognita

MLRPQAKAIDLNGKPDLKDPDLYLHEQHHEAFRRLRAEEPVYWNPEADGPGFWAVTRYDDIEAVSKNPKL

FSSAKHNGGHRIFNENEIGGNDTDASMISMDPPAHAGYRRMVTPGFVPKRISNMEERIRARVTRLLDAMP

KTGEAEFISAVAAALPIEVLAELFGVPESDGPKLFEWSNATVGEDDPELRVSDEYMQKCIMEMAGYAAGL

WQQRLETPGDDLISMLAHSKIGGEAMNFPTYIGTFILLVVAGNETTRNSISGGLLALSENPGERQKLLDD

PSLIPSAVQEIVRWVSPVLHMRRTATEDTELRGQKIRKGDKVVMWYASGNRDEAQWADPYRFDVARYAAP

GVPAQIGFGVGQHFCLGSRLAELQLTILFEELLRRFPDINVSGPIRRLRSNFIYGIKEMPVSYTPEG

>CYP112A1 Bradyrhizobium japonicum

MSEQQPLPTLPMWRVDHIEPSPEMLALRANGPIHRVRFPSGHEG

WWVTGYDEAKAVLSDAAFRPAGMPPAAFTPDSVILGSPGWLVSHEGREHARLRAIVAP

AFSDRRVKLLVQQVEAIAAHLFETLAAQPQPADLRRHLSFPLPAMVISALMGVLYEDH

AFFAGLSDEVMTHQHESGPRSASRLAWEELRAYIRGKMRDKRQDPDDNLLTDLLAAVD

QGKASEEEAVGLAAGMLVAGHESTVAQIEFGLHAMFRHPQQRERLVGDPSLVDKAVQE

ILRMYPPGAGWDGIMRYPRTDVTIAGEHIPAESKVLVGLPATSFDPHHFDDPEIFDIE

RQEKPHLAFSYGPHACIGVALARLELKVVFGSIFQRLPALRLAVAPEQLKLRKEIITG

GFEQFPVLW

>CYP112A2 Rhizobium sp. NGR234 plasmid pNGR234a

MPEQPLPTLPMWRVDHIEPSPTMLALRANGPIHNVRFPRGHEGW

WVTGYDEAKAVLSDAAFRPAGMPPAAFTPDCVILGSPGWLVSHEGGEHARLRTIVAPA

FSDRRVKLLAQQVEAIAAQLFETLAAQPQPADLRRHLSFPLPAMVISALMGVLYEDHA

FFAGLSDEVMTHQHESGPRSASRLAWEELRAYIRGKMRDKRQDPGDNLLTDLLAAVDR

GEATEEEAIGLAAGMLVAGHESTVAQIEFGLLAMLRHPQQRERLVGNPSLVDKAVEEI

LRMYPPGAGWDGIMRYPRTDVTIAGVHIPAESKVLVGLPATSFDPRHFEDPEIFDIGR

DAKPHLAFSYGPHYCIGMALARLELKVVFGSIFQRFPALRLAVAPEELKLRKEIITGG

FEEFPVLW

>CYP112A3v1 Mesorhizobium loti

1 MSEQPLPTLP MWRVDHIEPS PEMLALRANG PIHHVRFPSG HEGWWVTGYD EAKAALSDAA

61 FRPAGMPPAA FTPDSVILGS PGWLVSHEGG EHARLRTIVA PAFSNRRVKV LAQQVEAIAA

121 QLFETLAAQP QPADLRRHLS FPLPAMVISA LMGVLYEDHA FFAGLSDEVM THQHESGPRS

181 ASRLAWEELR AYIRGKMWDK RQDPGDNLLT DLLAAVEQGN ATEEEAIGLA AGMLVAGHES

241 TVAQIEFGLL AMFRHPQQRE RLVGDPSLVD KAVEEILRMY PPGAGWDGIM RYPRTDVTIA

301 GVHIPAESKV LVGLPATSFD PRHFDDPEIF DIGRDENPHL TFSHGPHYCI GMALARLELK

361 VVVGSIFQRF PALRLAVAPE ELKLRKEIIT GGFEEFPVLW

>CYP112A3v2 Mesorhizobium loti

GenEMBL AL672112 complement(85404..86606)

Strain R7A symbiosis island

Gene = msi071

2 DIFFS with CYP112A3v1

>CYP112A4 Rhizobium etli symbiotic plasmid p42d

MSEQSLPTLPMWRVDHIEPSPEMLALRAKGPIHRVRLPSGHECW

WVTGYDEAKAVLSDAAFLPAGMPPADFTPDSVILGSPGWLVSHEGDEHARLRTIVAPA

FSNSRVKLLTQQVEAITVQLFDTLAVQPQPADLRRHLSFPLPAKVISALMGVPFEEHA

FFAGLSDEVMTHQHESGPRSASGLAWEELRAYIHGKIRGKRQDPGDNLLTDLLAAVDQ

GKATEEEAIGLAAGVLVAGHESTVAQIEFGLLAMFRHPQQRERLVRDPSLVDKAVEEI

LRMYSPGAGWDGIMRYPRTDVTIAGVHIPAESKVLVGLPATSFDPCHFKDPEVFDIGR

DANPHLAFSYGQHNCIGAALARLELKAIFGSIFQRFPALRLAVAPEELKLRKEIITGG

FEEMPVLWCGRPPASQSSHLAAPGAHRSDQPLDR

>CYP113A1 Saccharopolyspora erythraea NRRL23338

MTTIDEVPGMADETALLDWLGTMREKQPVWQDRYGVWHVFRHAD

VQTVLRDTATFSSDPTRVIEGASPTPGMIHEIDPPEHRALRKVVSSAFTPRTISDLEP

RIRDVTRSLLADAGESFDLVDVLAFPLPVTIVAELLGLPPMDHEQFGDWSGALVDIQM

DDPTDPALAERIADVLNPLTAYLKARCAERRADPGDDLISRLVLAEVDGRALDDEEAA

NFSTALLLAGHITTTVLLGNIVRTLDEHPAHWDAAAEDPGRIPAIVEEVLRYRPPFPQ

MQRTTTKATEVAGVPIPADVMVNTWVLSANRDSDAHDDPDRFDPSRKSGGAAQFSFGH

GVHFCLGAPLARLENRVALEEIIARFGRLTVDRDDERLRHFEQIVLGTRHLPVLAGSS

PRQSA

>CYP113B1 Streptomyces fradiae

MTTQTLEAEKPPEPERTANSVHPLAQPAGAGARGLLEWFARARA

EAPVFWDESRQAWQVFRYDDYLTVSTNPQLFSSDFSPVFPVPEELAILMGPGTFGGID

PPRHGPLRKLVSQAFTPRRIATLEPRIAEITRGLLDGLREKGQIDVVSDLAYPLPVIV

IAELLGIPAEDRDLFREWVDVILNNEGMEYPNLPDDFSETMGPAIKEWGDYLYRRIAL

KRETPTDDLMSGLIEAEVEGRRLTDEEIVNIVALLLTAGHISSATLLGNLFLVLDEHR

EAQAELRADRDLIPGAIEETLRYRSPFNNIFRLLKEDTDILGHPMKAGQMVVAWIASA

NRDSAHFSDPDTFDVRRQPNKHMSFGHGIHHCLGSFLARLEAKVFLELFFDEFSDYRV

EHDEVEFYEEDELTARRLPVTVTRH

>CYP113B2 Streptomyces caelestis

MVDSVTGPMELSKDANAKELLDWFSHNRTHHPVFWDEGRQAWQV

FRYDDYLTVSNHPEFFSSDFTEVAPTPPELEMILGPGTIGALDPPAHGPMRKLVSQAF

TPRRMAGQEQRIRVIAEELLDRVRGQKTIA

>CYP113B3 Streptomyces mycarofaciens

MSEAPTVPLELSKEANAQELLGLGSPSTGTHHPVFWDENWACLG

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ALTPRRMARLGPRIRAVTQGLLDAVRGQETIDVVGDLSYALPVIVIAELLGIPSGDRD

VFRGWVDTLLTNEGLGYPSLPDNFSETIAPALKEMTDYLLHQIHAKREAPVDDLICGL

VQAEQDGRKLTDVEIVNIVALLLTAGHVSSSTLLSNLSLVLEENPQALADLRADRELV

TGAVEETLRYRSPFNNIFRFLKEDTDILGPEMKKGQMVIAWSQSANRDPEHFPEPDTF

DIRRSSSSRHMAFGIGIHHCLGAFLARQEGKVVLELML

>CYP113C1 Streptomyces virginiae

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DLEPRVTELAGRLLEKVEGSEFDLVGDFAYPLPVIVIAELLGVPAEDRELFRGWSDRM

LSMQVDDPLEIQFGDEAGEDYERLVKEPLKEMHAYLQRHVDARRETPGDDLLSRLVTA

EIAGERLTDRQIVEFGALLLMAGHVSTSMLLGNTVLCLEENPETAAALRADRALISGV

IEEVLRMRPPITVAARVTTGEVVVGGVTIPKDRMVMASLLSANHDERHIQDPEVFDPR

RSPNPQLAFGHGIHYCLGGPLARLEGRVALEMLLDRFEDIRVTPGAPYDFHREGLFVP

ARSPLTVRRG

>CYP113D1 Saccharopolyspora erythraea NRRL23338

MSIPADTWGIPASQFWLRGRRPERTVDYDAATGMWNVYGYPEIQHVLSDPRTFSSDTTRL

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DRMEMVEDLAYPLPVIVIAELLGVPGSDRHLFKKWVDALLQRDQQFSLVDESDEQVQQVE

EAIAQVKHLTDYLGEHAAERRRAPREDLLTKLVQAEVDGHRLSDTEVVNFANILLLAGHI

TTTMLLGNTVLCLDTHPRQRDAVRADRSLVPSAIEESLRFFSPFAVLGRVTQREVEVGGQ

TIPQDQMLMLWIAAANRDPRQFADPDVFDVTRDPNPQIAFGRGIHFCVGAPLARLEGKVA

LNILLDRFPHLRTDPDEGPTFLPAPTTTGVRKLPLLLTPSA

>CYP113E1 Salinispora tropica (marine actinomycete)

MATVPRLTFADGGVSVLPWFRQMRDDQPVWYDQGTGSWNVFRYADIAQILTDPATFSSDP

GRTMPPELVEEAEGSLVAVDPPRHGRLRALISTAFTPRLVEQLAPRVRSIAERLLDRTFV

DRGPEGEFDAIGDVAYLLPVYVIGELLGLPETDREYLVRTADEFYAISADDPFDGTYMAS

MQSTLDGLGTYMLDQAERRRARPGDDLMSALAHAEIDGEQLNDREIRNFAVLLLTAGHIT

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VPGDQLLRLWIASGNRDERQFADPDTFVLGRDSRHLGFGLGIHYCLGASLARMESSVVLE

VLAERTTTLAPAVQGLSYYDAPGIFCLRSLPVSYRRS

>CYP113F1 Streptomyces sp. Tu6071

1 MTASEEGTRL ADQSADAATM LAWFRRMRES EPVSHDEEAG VWHVFRHADV ERVLADPGTF

61 SSDFSSFMPA QEDVDRFIKG NLLRKDPPQH RKLRTLVSKA FTPGVVARLA PRIEVIADEL

121 LDAKAGADQL ELVADLASPL PVTVIAELLG IPAEDRPMFG RWADSLVAPE SQTSFIPNED

181 RTKAMAVVMR EMNAYCLEHI RRRRAAPSQD LVSKLVAAEV DGQRLDDDEI IGFVGLLLLA

241 GHITTTALLT NVILCLDEFP DIAAALRADP SALPGAIEEV LRFRTPLAPS MRRTTREVRV

301 GEHTVPAGRI LLAWLASANR DERQFTAPDT FDIHRAPNPH LSLGHGIHFC LGAPLARLEV

361 RIAVEKMLGR WSGITVADGV ECHDARGIVG AKKLPLRLRW A

>CYP113F2 Frankia sp. EAN1pec

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RLELIDDLAYPLPVIVIAELLGLPAADRPMFRGWADALFDREVADPDQPLTELAAANTRAAVPVLREMNA

YLLDRIRACRAHPGDDLTGRLVQVEVDGQRLADEEIVGFVGLLLLAGHITTTATLGNAALALDEHPGAAA

ELRAEPELLPATIEEVLRLRTPFPRLVRRAVADTRVGDEVIPAGAVVTVWLTAANRDERVFAEPDRFDPR

RAPNPHIAFGQGIHFCLGAPLARLEARTALGILLDRYSDIAVAADVPVEHRDPWAMVSVNSLPLDVRPR

>CYP113G1 SBI\_3232 Streptomyces bingchengensis

47% to CYP113C1 Streptomyces virginiae

MSEQAISLTPPSAADGGATLFGWLRRMREESPVVQDNNGSWYVFRHADVQ

HVLTEYADFSSDPTPISPKAAEIAKGDLAQIDPPEHHGLRRQISRVFTPR

MVAELEPRIEEIGRLLLDEAGDAGELDLVRQLTHPLPVIVIAEMLGVPAE

DRPVFRHWADRIIAAKIAGIDDPETYERLRSAIEEMDFYLEGQLDERRSR

PGDDLLSKMVTAEVDGDPISGAEAVNFARLLLVAGHITTTMMLSSSILCF

DEYPEAAREVREDRSLLPAAIEEVMRYRPPFTITGRYTTRDVELSGVTIP

ERSVVIPWLASANRDERRFMDPDVFDIHRSPNPHVAFGKGIHFCIGAPLA

RLEGKVALNLLFDRYSDVRIDRDASLEFYEHNFFGVKSLPVSVKHA

>CYP114A1 Bradyrhizobium japonicum

MLSRHADIFWAFKATGDAFRGPAPGELARYFSRAATSPSLNLLA

STLAMKDPPTHTRLRRLISRDFTMGQIDNLRPSIARIVAARLDGITPALERGEAVDLH

REFALALPMLVFAELFGMPQDDMFELAAGIGTILEGLGPHASDPQLAAADAASARVQA

YFGDLIQRKRTDPRRDIVSMLVGAHDDDADTLSDAELISMLWGMLLGGFVTTAASIDH

AVLAMLAYPEQRHWLQADAARVRAFVEEVLRCDAPAMFSSIPRIAQRDIELGGVVIPK

NADVRVLIASGNRDPDAFADPDRFDPARFYGTSPGMSTDGKIMLSFGHGIHFCLGAQL

ARVQLAESLPRIQARFPTLAFAGQPTREPSAFLRTFRTLPVRLHAQGS

>CYP114A2 Rhizobium sp. NGR234 plasmid pNGR234.

MDMQETTTACADAFAELASPACIDDPYPFMRWLREHDPVHRAAS

GLFLLSRHADICWALKATGDAFRGPAPGELARYFPRAATSLSLNLLASTLAMKEPPTH

TRLRRLISRDFTMREIDNLRPSIARFVAARLDGMAPALERGEAVDLHRQFALALPMLV

FAELFGMPQDDMFGLAAGIGAILEGLSPHASDPQLAAADAASARMKAYFGDLIQRKCI

DPRHDIVATLVGAHDDDADTLSDAELISMLWGMLLGGFATTAATIDHAVLAMLAYPDQ

RHWLQGDAAGVEAFVEEVLRCDAPAMFSSIPRIAQSDIELSGVVIPKNADVRVLIAAG

NRDPDAFADPDRFDPARFYGTSPGMSTDGKIMLSFGHGIHFCLGAQLARVQLAESLPR

IQARFPTLTVAEQPTREPSAFLRTFRALPVRLHAQGDSPRLTSAFLNGQRGVEGGASF

EHGDGERRSATDRRAQP

>CYP114A3v1 Mesorhizobium loti

1 MDVQETTAAC RDAFAELASP ACIQDPYTFM RWLREHDPVH RAASGLFLLS RHADIYWALK

61 ATGDVFRGPA PGELARYFPR AETSLSLNLL ASTLAMKEPP THTRLRRLIS RDFTIRQIDN

121 LRPSIARIVA ARLDGMAPAL ERGEAVDLHW EFALAVPILV FAELFGMPQD DMFGLAAGIG

181 AILEGLSPHA SDPQLAEADA ASARVQAYFG DLIQRKRTDP RNDIVSMVVG AHDDDADTLS

241 DAELISMLWG MLLGGFATTA ATIDHAVLAM LAYPEQRHWL QGDAVGVKAF VEEVLRCDAP

301 AMFSSIPRIA QRDIELGGVV IPKNADVRVL IAAGNRDPDA FSDPDRFDPA RFYGTTPGMS

361 TDGKIMLSFG HGIHFCLGAQ LARVQLAESL PRIEARFPTL ALAEQPTREP SAFLRTFRAL

421 PVRLHAQGG

>CYP114A3v2 Mesorhizobium loti

GenEMBL AL672112 complement(84020..85309)

Strain R7A symbiosis island

Gene = msi070

10 DIFFS with CYP114A3v1

>CYP114A4 Rhizobium etli symbiotic plasmid p42d

MDVQDTTAACHDAFAELASPACIQDPYPFMRWLREHDPVHRAAS

GLFLLSRHADIYWAFKATGDAFRGPAPSELARYFPRAASSLSLNLLASTLAMKEPPTH

TRLRRLISRDFTVGQIDNLRPSIARIVAARLDGMAPALERGEAVDLHREFALALPMLV

FAELFGMPQDDVFELSAIVSAILEGLSPHASDPQLAAADVASARVKAYFGDLILRKRA

DPRRDIVSTLVGAHTDDADTLSDAELISMLWGMLLGGFATTAATIDHAVLAMLAYPEE

RHWLQGDAAGVEAFVEEVLRCEAPAMFSSIPRIAQRDIELHGVVIPKDADVRVLIAAG

NRDPDAFADPDRFDPVRFYGTRPGMSSDGKIMLSFGHGIHFCLGAQLARVQLAESLPQ

IQARFPTLALAEQPTREPSAFLRTFRALPVRLHAQAAAEVRVVVDQDLCGTTGQCVLT

LPGTFRQREPDGVAEVCMATVPQALHAAVRLAASQCPVAAIRVIESEAGDDHCTNPGP

TPSPADAERHAAKDLRNPGEHDGTI

>CYP115A1P Bradyrhizobium japonicum

1 MADTSGARSN LLHQSVRSIY

GDADRFDVTR RHNPHLSFGQ GPHFCLGAAL ARLELGCAFP

61 ALFVRLEHLA LTIAAEDVVY MPSYVIRCPQ RLPVTFRPSI A

>CYP115A2v1 Mesorhizobium loti

1 MPAAPTQLDR LSSAILRQGG MARVSLPGDV VTWAAARHQT LRQMLSDQRF NKDWRQWRAL

61 QDGEIPEDHP LIGICKVDNM TTAHGADHRR LRGLLSSSFA PSRIALLAPR VEQCVDRLLA

121 EMAQRGGSAD LMSEFAAPLP TNVIAELFGL PDEQREEIVA LTYSLASTSA TAEEVRQTRQ

181 RIPEFFRRLI ALKRGQLGDD LASALIVARD KGELVSDTEL IDMLFMVLSA GFVTTAGVIG

241 NGVLALLTHP QQLHLVRSGQ VPWSQAIEEI LRWGTSAANL PFRYATQDVE IDGCLVRRGD

301 AVLMAFHAAN RDEKAFGPGA NRFDVTRRHN PHLSFGEGPH SCLGAALARL ELRCAFPPLF

361 GRLEDLALTI AAEDVVYMPS YVIRCPQRLP VSFRPSVA

>CYP115A2v2 Mesorhizobium loti

GenEMBL AL672113 41375..42607

Strain R7A symbiosis island

Gene = msi159

10 DIFFS with CYP115A2v1

>CYP115A3P Rhizobium etli symbiotic plasmid p42d

ANSYGRPTYGDTDMFDFNRLQNPHLPLGQGPHLCLGAALARLELGSVFPPPFVRPEDLALAIAAE

>CYP116A1 Rhodococcus erythropolis

MTVDHAPEGVKSPTGCPVSGMAADFDPFRGAYQVDPSSSLRQAR

KDEPVFFSPLLDYWVVTRYEDIKQIFKTPSVFSPSITVDQITPISDEALQILGSYQFA

AGRMLVNEDEPIHTERRRLLMQPFEADNVATLEPKIREVVNTYLDRVIKDGRADLIGD

LLYEVPCIVALIFLGVPDEDIETCRQYGMQQTLFTWGHPTGDEQTRVATGMGKFWEFA

GGLVDKLKADPNAKGWIPHAIEMQRQHPDLFDDNYLQNIMFGGVFAAHETTTNATGNA

FRTLLENRSSWDEICADPTLIPKAIEECLRYSGSVVAWRRKAVVDTTVGEVDIPAGGR

LLIVMASANRDDSMFPEPDDFDIHRGNAQRHLTFGIGSHTCLGATLARLEMKVFLEEV

SRRLPHMSLVAGQEFSYLPNTSFRGPEHVLVEWDPQQNPVPADRP

>CYP116A2 Saccharopolyspora erythraea NRRL23338

VEELQVDATRVGAGCPISRIAEEFDPFGEAYQQDPAGVLKAAREREPVFYSPELDHWVVT

RYADIKEIFRDTRRFSASNALDPITPLGAKARERLAEYDFAPGPVLVNEDEPLHMRRRRA

LAGPLAADEVAKLEGRIRDLVTRYVDGFAGRGRADLVDDLLWEVPAIVGLLVCGVPDEDI

DRARHYTIKMGSFTWGRPTEEHQVEIADQVGQWWSLSGRLVERLKREGGEGWVPTAIEVH

REDPELVNDNHLQNMMMSGLVAAHETTTNATANALRHLLSNRSSWEALCADPSAIPNAVE

ECLRFSSSVLCWRRKALVDVPVGGVTIPAGARVLLVIGSGNHDDDVFGDPGELDIARSNA

KRHLTFGIGSHACIGAPLARLEMRIILEELTRRLPGMRLVEGQDFGYLRNASFHGPRHLL

VEWEPAGA

>CYP116B1 Ralstonia metallidurans

MPQTNAPASSGSCPIDHSALRAPNGCPISHQAAAFDPFEDGYQQ

DPPEYVRWSRAQEPVFYSPKLGYWVVTRYDDIKAIFRDNITFSPSIALEKITPTGEAA

NAVLASYGYAMNRTLVNEDEPAHMPRRRALMEPFTPAELAHHEPMVRKLTREYVDRFI

DTGRADLVDEMLWEVPLTVALHFLGVPEEDMDLLRQYSIAHTVNTWGRPKPEEQVAVA

HAVGNFWQLAGRILDKMREDPSGPGWMQYGLRKQRELPEVVTDSYLHSMMMAGIVAAH

ETTANASANAIKLLLQHPDVWREICEDPALIPNAVEECLRHNGSVAAWRRLVTRDTEV

GGMSLAAGSKLLIVTSSANHDEHHFADADLFDIHRDNASDQLTFGYGSHQCMGKNLAR

MEMQIFLEELTSRLPHMRLAGQRFTYVPNTSFRGPEHLWVEWDPARNPERTDPTVLAP

RDAVRIGEPTGGTTGRTLIVERVETAAQGVSRIRLVSPDGRALPRWSPGSHIDIECGH

TGISRQYSLCGDPADTSAFEIAVLREPESRGGSAWIHASLRAGDKLKVRGPRNHFRLD

ETCRRAIFIAGGIGVTPVSAMARRAKELGVDYTFHYCGRSRASMAMIDELRALHGDRV

RIHAADEGQRADLAQVLGAPDANTQIYACGPARMIEALEALCATWPEDSLRVEHFSSK

LGTLDPSREQPFAVELKDSGLTLEVPPDQTLLATLRAANIDVQSDCEEGLCGSCEVRV

LAGEIDHRDVVLTRGERDANNRMMACCSRAAKGGKIVLGL

>CYP116B2 Rhodococcus sp. NCIMB 9784

MSASVPASAPACPVDHAALAGGCPVSANAAAFDPFGSAYQTDPA

ESLRWSRDEEPVFYSPELGYWVVTRYEDVKAVFRDNILFSPAIALEKITPVSAEATAT

LARYDYAMARTLVNEDEPAHMPRRRALMDPFTPKELAHHEAMVRRLTREYVDRFVESG

KADLVDEMLWEVPLTVALHFLGVPEEDMATMRKYSIAHTVNTWGRPAPEEQVAVAEAV

GRFWQYAGTVLEKMRQDPSGHGWMPYGIRKQREMPDVVTDSYLHSMMMAGIVAAHETT

ANASANAFKLLLENRAVWEEICADPSLIPNAVEECLRHSGSVAAWRRVATADTRIGDV

DIPAGAKLLVVNASANHDERHFERPDEFDIRRPNSSDHLTFGYGSHQCMGKNLARMEM

QIFLEELTTRLPHMELVPDQEFTYLPNTSFRGPDHVWVQWDPQANPERTDPAVLHRHQ

PVTIGEPAARAVSRTVTVERLDRIADDVLRLVLRDAGGKTLPTWTPGAHIDLDLGALS

RQYSLCGAPDAPSYEIAVHLDPESRGGSRYIHEQLEVGSPLRMRGPRNHFALDPGAEH

YVFVAGGIGITPVLAMADHARARGWSYELHYCGRNRSGMAYLERVAGHGDRAALHVSE

EGTRIDLAALLAEPAPGVQIYACGPGRLLAGLEDASRNWPDGALHVEHFTSSLAALDP

DVEHAFDLELRDSGLTVRVEPTQTVLDALRANNIDVPSDCEEGLCGSCEVAVLDGEVD

HRDTVLTKAERAANRQMMTCCSRACGDRLALRL

>CYP116B3 Rhodococcus ruber

MSASVPASACPVDHAALAGGCPVSTNAAAFDPFGPAYQADPAES

LRWSRDEEPVFYSPELGYWVVTRYEDVKAVFRDNLVFSPAIALEKITPVSEEATATLA

RYDYAMARTLVNEDEPAHMPRRRALMDPFTPKELAHHEAMVRRLTREYVDRFVESGKA

DLVDEMLWEVPLTVALHFLGVPEEDMATMRKYSIAHTVNTWGRPAPEEQVAVAEAVGR

FWQYAGTVLEKMRQDPSGHGWMPYGIRMQQQMPDVVTDSYLHSMMMAGIVAAHETTAN

ASANAFKLLLENRPVWEEICADPSLIPNAVEECLRHSGSVAAWRRVATTDTRIGDVDI

PAGAKLLVVNASANHDERHFDRPDEFDIRRPNSSDHLTFGYGSHQCMGKNLARMEMQI

FLEELTTRLPHMELVPDQEFTYLPNTSFRGPDHVWVQWDPQANPERTDPAVLQRQHPV

TIGEPSTRSVSRTVTVERLDRIVDDVLRVVLRAPAGNALPAWTPGAHIDVDLGALSRQ

YSLCGAPDAPTYEIAVLLDPESRGGSRYVHEQLRVGGSLRIRGPRNHFALDPDAEHYV

FVAGGIGITPVLAMADHARARGWSYELHYCGRNRSGMAYLERVAGHGDRAALHVSAEG

TRVDLAALLATPVSGTQIYACGPGRLLAGLEDASRHWPDGALHVEHFTSSLTALDPDV

EHAFDLDLRDSGLTVRVEPTQTVLDALRANNIDVPSDCEEGLCGSCEVTVLEGEVDHR

DTVLTKAERAANRQMMTCCSRACGDRLTLRL

>CYP116C1 Rhodococcus sp. RHA1 Rha08932

MTETTPAPNAEDIVAGKCPVSHFAAEFNPFDEEYQQDPYPVFKSVREQEPVFYSPEIDYWIVSRYEDIIEIFKDTESYSASEAGVMITPPCPAAMDVLAEANFVPSTMLVDEDAPLHPKRRRVFRKGLNDNKVAELEPYTRRFVSECLDTIVKNGRADMVGDMTFSVPALTAFILMGVPEAEVERVRGYAARFALWLWGRPTDEQQVALAGDYAAYLQYAREHVDKLAENPGEDYMSNVIKAWQKDGNDEVWDKTYLASIMQSHLYASHETTTNAAASGIKSLLENRDQWDAICADPSLIPGAVHEILRYQSSVPTWRRITTRPVRLGGYDLPAGSRVMMLTGSANHDDAKFEDGESFDITRENADEHLAFGWGVHLCLGQGLARMEMRVMLEETTKRLPHLRLVEDQEWTYSPNTSFRGPDHVRVEWDASQNPLPEDRP

>CYP116C2 Rhodococcus sp. RHA1 Rha10704

MTETSAEPHRSQGAGKCPVSHIAAEFNPFADDYLQDPYAVFTRARAEEPVFFSPSLGYWVVSRHEDVRQVFQDPAFSASISITPLKELCPAAVDELVKAEMVMGPSLVNEDPPLHTKRRRLIQKAMISPARIEAVTPRIRALTTSYIDGFVRRGHADLVADFAWEIPALVAFALMGVPDEDVERAKEFAGRLALFTWGYPSEEEQRKLAAGMGQYWIYAKEHVKRRLEDPTDDYISNLIAAWRKPGNEDLFDENYLVTTMMNFLFAGHETTTNATANGLRALLEHRDQWAALCADPSLVPGAVEEILRFSSSVVAWRREATEDTHIGDVPIPAQAKVLVLTGSANHDEEVFPEPERFDITRTNADEHLAFGFGRHLCLGAPLARIEMGIFLEELTRRLPHMQLAEGQTFTYSPNTSFRGPDHLFVGWDPSQNPVPEDRP

>CYP116D1 Saccharopolyspora erythraea NRRL23338

MHERFDPLATDYLADPFPILAAIREETPVFYSSELDMWPVTRHEDIKRIFTDYETFSGAI

TQTPVYPLAEEAKDILAAGFHTTPTVSNCDPPKHTRVRAHNVKAFSARRIAVLEPTIRAY

VTEMIDRILHQDRFDIVQEVTFPLPATIVFNLIGFPESDMEMLKGLAINRMAFTWGRSTE

AEQVRIAKNQVDYWQYCTEFVASRLAEPKDDFTSDLIRTHLADPDELSVDEITNVVHALS

FAGHETTTNVSSSMIQRLLTHREQWEELCADPALIPKAIEEGLRFDPSLFTWRRITTKPV

SIGGVEVPAGAKLLLLVGSANHDPAKFPDPEAFNIHRSGAQAHLTFGRGIHSCFGAPLAR

LEMQIMLEELTARMPGLRLVEDQDVQYHVNACFRGPVELWLDNSAHR

>CYP117A1 Bradyrhizobium japonicum

MFGGTLVAQDGIAHRQARDAIQAALLPKGLTLAGIGELFAPVIR

ARVQRWRERGDVTILRETGDLMLKLIFSLMGIPAQDLPGWHRKYRQLLQLIVAPPVDL

PGLPLRRGRAARDWIDARLREFVRAAREHASRTGLINDMVSAFDRSDDALSDDVLVAN

IRLLLLGGHDTTASTMAWMVIELARQPGLWDALVEEAQRVGAVPTRHADLAQCPVAEA

LFRETLRVHPATPLLVRRALRELRIGQQRIPTGTDLCIPLLHFSTSALLHEAPDQFRL

ARWLQRTEPIRPVDMLQFGTGPHFCMGYHLVWLELVQFCIALALTMHEAGVRPRLLSG

VEKGRRYYPTAHPSMTIRIGFS

>CYP117A2 Rhizobium sp. NGR234 plasmid pNGR234a

MNVLLNPLNRRHRLRYDIPVMPGAFPLVGHLPAIVCDLPRLLRR

AERTLGSHFWLDFGPAGHLMTCVDPHAFALLRHKDVSSALIEEIAPELLGGTLVAQDG

GAHRQARDAIKAAFLPEGLTQAGIGDLFAPVIRARVQAWRDRGDVTILPETGDLMLKL

IFTLMGVPAQDLPGWHRKYRQLLQLIVAPSVDLPGLPLRRGRAARDWIDAQLRQFVRD

ARAHAARTGLINDMVSAFDRSDDALSDDLLVANIRLLLLAGHDTTASTMAWMVIELAR

QPMLWDALVEEAQRVGAVPTRHADLEQCPVAEALFRETLRVHPATTLLPRRALQELQL

GQRRIPAGTHLCIPLLHFSTSALLHEAPDQFRLARWLQRTEPIRPVDMLQFGTGPHVC

IGYHLVWLELVQFSIALALTMHKAGVRPLLLSGVEKGRRYYPTAHPSMTIRIGFS

>CYP117A3 Mesorhizobium loti

1 MDMLLNPLDR RHRLRDDIPV VPGAFPLVGH LPAIVCDLPR LLRRAERTLG SHFWLDFGPA

61 GHLMTCVDPD AFALLRHKDV SSALIEEIAP ELLGGTLVAQ DGGAHRQARD AIKAAFLPKG

121 LTQAGIGNLF APVIQARVQA WRDRGDVTIL RETGDLMLKL IFSLMGIPAQ DLPGWHRKYR

181 QLLQLIVAPP VDLPGLPLRR GRAARDWIDA QLRQFVRDAR AHAARTGLIN DMVSSFDRGD

241 DALSDDVLVA NIRLLLLAGH DTTASTMAWM VIELARQPGL WDALVEEAQR VGAVPTRHAD

301 LAQCPVAEAL FRETLRVHPA TTLLPRRALQ ELQLGQRRIP AGTPLCIPLL HFSTSALLHE

361 APDQFRLARW LQRTEPIRPV DMLQFGTGPH VCIGYHLVWL EMVQFCIALA LTMHKAGVRP

421 RLLSAVEKGR RYFPTAHPSM KIRIGFS

>CYP117A3v2 Mesorhizobium loti

GenEMBL AL672112 complement(81551..82888)

Strain R7A symbiosis island

Gene = msi068

2 DIFFS with CYP117A3v1

>CYP117A4 Rhizobium etli symbiotic plasmid p42d

MDMLLNPLNRWRRLRDDIPVMPGAFPLVGHLPAIVCDLPRLLRR

AERTLGSHFWLDFGPAGHLMTCLDPDALALLRHKEVSSALIEEMAPDILGGTLVTLDG

SAHRQARDGIKAAFLPRGLTEAGIGELFEPIIRAQVKAWRDRGEVAILPDTRNLMLKL

TFSLMGIPAQDLSEWHRKYRQLLQLMVAPPIDLPGMPLRRGRAARDWIDAQSRQFIRD

ARARAARTGLINDMVSAFDCSDGALSDDVLVANIRLLLLAGHETSASTIAWMVIELAQ

HPELWDALVEEAQRVGAVPTGHEDLAQCPVAEALFRETLRMHPASSLVPRRAMQELQL

GQRRIPSGTHLCIPLLHFSTSPLLHEAPDQFRLGRWLQRTEPIRPVDMLQFGAGPHVC

MGYHLVWLELVQFSIALALTMQEAGVRPRLMSGVEKGRRYYPTAHPSMTVRIGFS

>CYP117B1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_5081

MTTALPASFA DLPLLQGRNP LARRIETRHG FPILPGRFPV VGHMPAIAVD ELGLLREGQR

RFGSLFFWAP GVDAWQLIYA SNEAFSLFKS KAVDSSYLTE GGVGHLFGQT LMAHDGASHR

RLRTAMNGPF SPKGLDAAEV GAIVATSVER KVRSWLGRRD VQLLRETREL ALEVMFKITG

VEDDELPEWR HYYEDLMLVI LSLPFDVPGS PRRRGLRARA WLDERIGRIL AGVRARGDAK

GLLPALLTAR DEQGEPLSEQ DLVGNLRLLL LAGHETSASV MAWCVAHLAE SPAVWRALRE

EASSAPDLPR SPADLRRFPF AEAVFREALR LHPPVPHDAR RAVADFELDG RAVPAGTHVA

IPLVLLSRDP ELYPDPDSYR PERWLGRKEA LSPLEIAQFG GGAHFCLGYH LAWMEIVQFL

VALGRELPAS GPRLQGGFPA SRYLPVLRPS GGTRVRFDG

>CYP118P1/CYP102 PSEUDOGENE Mycobacterium leprae

RLGSGIVEQRISVLSIIALADPXXXXXXXDETVWENI

XXXXXXRLLMGDELFTXXXXESNWGKAHN

TASQHDDILDIMLYSADPSTGEQLDTDNVVNQILTLLVSGSQTLANAIAFALHYLLSIHH

DIAAQTRREIYQNRSDRGIANVSY

FGDVVKLRCLRRVVDATLRLWS

VPCYLRQARRD

TTLGNGTSLFHKGQWVIVLLTAPMPG

WGPDANEFNPDRVLPEICRKLPYTYIL

FGTGLRTCIGRRFALHEMALELTMIVHQYILSRADPG

YCLSISEAFTLKTVGL

>CYP119A1 Sulfolobus solfataricus (an archaebacterium)

MYDWFSEMRKKDPVYYDGNIWQVFSYRYTKEVLNNFSKFSSDLT

GYHERLEDLRNGKIRFDIPTRYTMLTSDPPLHDELRSMSADIFSPQKLQTLETFIRET

TRSLLDSIDPREDDIVKKLAVPLPIIVISKILGLPIEDKEKFKEWSDLVAFRLGKPGE

IFELGKKYLELIGYVKDHLNSGTEVVSRVVNSNLSDIEKLGYIILLLIAGNETTTNLI

SNSVIDFTRFNLWQRIREENLYLKAIEEALRYSPPVMRTVRKTKERVKLGDQTIEEGE

YVRVWIASANRDEEVFHDGEKFIPDRNPNPHLSFGSGIHLCLGAPLARLEARIAIEEF

SKRFRHIEILDTEKVPNEVLNGYKRLVVRLKSNE

>CYP119A2 Sulfolobus tokodaii

GenPept BAB66184

64% to CYP119A1 U51337 Sulfolobus solfataricus

1 MYDWFKQMRK ESPVYYDGKV WNLFKYEDCK MVLNDHKRFS SNLTGYNDKL EMLRSGKVFF

61 DIPTRYTMLT SDPPLHDELR NLTADAFNPS NLPVDFVREV TVKLLSELDE EFDVIESFAI

121 PLPILVISKM LGINPDVKKV KDWSDLVALR LGRADEIFSI GRKYLELISF SKKELDSRKG

181 KEIVDLTGKI ANSNLSELEK EGYFILLMIA GNETTTNLIG NAIEDFTLYN SWDYVREKGA

241 LKAVEEALRF SPPVMRTIRV TKEKVKIRDQ VIDEGELVRV WIASANRDEE VFKDPDSFIP

301 DRTPNPHLSF GSGIHLCLGA PLARLEARIA LEEFAKKFRV KEIVKKEKID NEVLNGYRKL

361 VVRVERA

>CYP120A1 Synechocystis sp. (strain PCC6803) Cyanobacterium

MITSPTNLNSLPIPPGDFGLPWLGETLNFLNDGDFGKKRQQQFG

PIFKTRLFGKNVIFISGALANRFLFTKEQETFQATWPLSTRILLGPNALATQMGEIHR

SRRKILYQAFLPRTLDSYLPKMDGIVQGYLEQWGKANEVIWYPQLRRMTFDVAATLFM

GEKVSQNPQLFPWFETYIQGLFSLPIPLPNTLFGKSQRARALLLAELEKIIKARQQQP

PSEEDALGILLAARDDNNQPLSLPELKDQILLLLFAGHETLTSALSSFCLLLGQHSDI

RERVRQEQNKLQLSQELTAETLKKMPYLDQVLQEVLRLIPPVGGGFRELIQDCQFQGF

HFPKGWLVSYQISQTHADPDLYPDPEKFDPERFTPDGSATHNPPFAHVPFGGGLRECL

GKEFARLEMKLFATRLIQQFDWTLLPGQNLELVVTPSPRPKDNLRVKLHSLM

>CYP120A2 Trichodesmium erythraeum

MTANYLEKWVEMGTLTWYPEIRNYTFDIASLLFMGSDESSQTKL

VSLFEEWVKGLFSIPLSLPWTRFGKSLRCRQKLLQHIEEIILQRQQQQNLGEDALGIL

LQAQDKEVNGLSLDELKDQILLLLFAGHETLTSAIASFCLLTSQHLDVLTRLRQEQKQ

FSAIEPLTLENLKRMTYLDMVLKEVLRLIPPVGGGFRQVTQDCEFCGYSIPKGWLVQY

QIAKTHQDETLYPDDKNFDPERFAPENAVDKQKVFGYVPFGGGMRECLGKEFARLEMK

IFAVMLLRGYEWELLPEQDLSVVAAPTPYPRDGLKVKFRKVE

>CYP120A3 gi|126659238|ref|ZP\_01730375.1| cytochrome P450 [Cyanothece sp. CCY0110]

54% to CYP120A1

MLIFFFYNKSKLIYNFDQKMTNIESQKSVSLPPGETGLPFIGETLSFLFDPDFAKKKKSKYGQIYKTNIF

GNDTVTMIGAEANQFLFRNENKYVVSTWPKSTRVLLGKLSLAVKDGNFHTSRRKLLAQAFQPRALNSYIP

KMTEITQQYVEKWLQTKELTWYPELRKYTFDVACSLLISIDNASQTKLASDFETWCQGLFTLPINLPWTN

FGKALKCRAKLLQEIETIIINRQQQPKHQNDALGILLEAKDEEGNSLTIEELKDQILLLLFAGHETLTSS

LSSFVLLMAQHPNILEKVRTEQENLNITEDITSEKLKEMTYLEEVLKEVLRFIPPVGGGFRKVIEEFEFQ

GYRIPKDWTVQYQIAQTHKESDIFPDYQTFDPERFSPENMADKQKNFGYIPFGGGLRECLGKEFARLEMK

IFASVLVHNCHWQLLPDQDLEMITIPSPRPRDGLKVKITEV

>CYP120A4 gi|119485417|ref|ZP\_01619745.1| cytochrome P450 [Lyngbya sp. PCC 8106]

53% to CYP120A1

MTTSEKKQSYPTPPGSLGLPLIGETLSFLRDRDFATKRHQKYGSVFKTNIFGNPTIMMIGTEANQFIFTN

EKKYFENSWPPSTTALLGPASLTIQTGDIHKSRRKLLAQAFQPRVLAGYVPTMEIMTRRYLQKWEQQKTF

AWYPELRKYTFDVACKLFVGDEKASETEMGEWFETWCQGLFTLPLRLPGTKFNKALNCRKKLLNQIETII

RQRQQQAEPGEDALGLLLQAKDEDGNSLSVEELKDQILTLLFAGHETLTSSVTAFCFLLAQHPDVLAKAR

LEQQQIQLTEPLSFEQLKLMSYLDQVLKEVLRFIPPVGGAFREVIETCEFNGYTFPKGWTVLYQIGKTHQ

DNSIYNQPEKFDPDRFSPERTEEKPYGYIPFGGGMRECLGKEFAKLEMKVLATMLLREYEWELLPNQNLE

MTVSPTPHPKDELLVNFKRLSEVH

>CYP120A5 gi|119509406|ref|ZP\_01628555.1| cytochrome P450 [Nodularia spumigena CCY9414]

53% to CYP120A1

METTNSQTQNKLPLPPGNLGLPLIGETISFLRDPEFAEQRYQQYGPIFKTHLFGQPTIMMIGAEANRFLF

SNENQNFTISWPDSTKTLLGPASLALQTGGTHQKRRKLLSQAFQPRALAGYTSKMEEITHNYLHKWQRMG

TFKWYPELRNYTFDVACKLLIGTDAASDSHFGELFEEWCAGLFTIPINLPWTKFGRALRCRQQLLVKIEE

IILQRQQQPHSDADALGLLLQAEDEDGNRLSLAELKDQVLLLLFAGHETLTSAIASFCLQLAQHPEVLAQ

ALAEQQQLAIEESLTLEHLKQMQYLDQVLKEVLRTIPPVGGGFRRVIQSSEFNGYQIPEGWSVLYQIGKT

HQDSSTYTEPESFDPQRFAPERVEDKQKPFGYVPFGGGVRECLGKEFAKLEMKLFAALLIREYHWELVPG

QNLDLIMVPTPHPRDDLQVNFSTQRGAEGSAKVRGVLDLGGEVAM

>CYP120A6 ORF00071 [Synechococcus sp.PCC7002]

53% to CYP120A1

MTSPSELPLPPGKFGLPVIGETIEFFTDRNFQKKRLEKYGDVFKTSIFTKPTVVMVGAEA

NEVLFRNENKYVKATWPKSTRILLGADSLATQEGGIHSSRRRIIFQAFQPRALESYIPTI

EKITQRYLTQWEQKQEFAWYDELRKYTFDVASTLFIGKDGGAETPLANLFEEWVKGLFSL

PINLPWTAFGKAMKCRRKLLRELEMIIGDRLKTYDANAEPTDALDLLIRAKDEDGNSLSI

DELKDQILLLLFAGHETLTSSLVSFGLLVGQHRDVFEKIRAEQDALDIGNGLDMAVLQQM

TYLDQVFKEVLRLVPPVGGGFREVINTFEYKNFQIPQGWAVQYQIAQTHKDEALYPDHEK

FDPERFSPERLADKQKKFGFIPFGGGMRECIGKEFARLEAKILASMLARDYDWELLPDQD

LSMQVIPTPLPKDGLQIRFYRRQESSSTTA

>CYP120B1 Nostoc punctiforme

MKTNQIPPGSFGLPVLGETLSFVFDRDFAKKRYHQYGPIFKTHL

LGRPTVVMAGPEALEFVLSSHIENFSWREGWPDNFKTLLGESLFLQDGEEHRRNRRLM

MPALHGPALASYFSTMEDITRSYLQKWEKKQEFTWFQEFKQLTFDIASQLFLGTRPGP

ECVRLSQLFTTLTNGLLAINPLPLPFTTFGKAIAARNEILEHLTQVVRERQQNPTQDT

ISLLIKAKDEDGNSLSEKEIIAQAVLLLFAGHETTTSMLTWLCTELACHPEVLEKARV

EQLQLASQGDLDLEQLGKMPYLEQVLWEVERLHQPVGGGFRGVIKDFELNGYHVPTGW

QLYYSIGVTHQIEEIYSEPELFDPDRFSPQRQEHKKYPFSLVGFGGGPRICIGIAFAK

MEMKIVAAHLLRSYHWEILPNQSLEVVAVPTNRPKDGLRVRFQPR

>CYP120C1 Nostoc punctiforme

MQQLKSAEEIPGSYGLPILGETLEIFRDSELYLWRRFQQYGSVF

KTSVLGRKRAYLIGPSANRLVLVEQAENMSSRIGWYFLESTFGNNILLQDGEEHRLTR

RLMYPAFHGKAIATYFDTIQNIVQDFLKDWGERGTISLNSSFRQLTLMIATRLFLGSQ

NKSEVEQTSQWFTQLLDSSMAIFKWNVPFTLYGRGQNARGKLVAFLREAIAQRIEQGN

LEESKDVLGLLLAAVDEDGNKLSETQVINEALLLLFAGHETTASLLTWVIFELGNHPE

WRERLRQEQLAVVGNNPLSLSHLKQFPQLTNVLKEAERLYPPVYAYNRGVLKDIEYGG

YRIPAGWFVTISPMLTHRLPELYTEPDRFDPDRFAPPREEDKKHPLALMGFGYGSHSC

LGMEFAQMEMKIVLSTLLRHYDWTVKPDYSAIAPVRQPSKVKDILQAYIEPLLIKHPL

DS

>CYP120D1 gi|126661226|ref|ZP\_01732300.1| cytochrome P450 [Cyanothece sp. CCY0110]

48% to CYP120A1

MLFGNSSISVQVGEIHKQRRQILYEVFKPRMLDSYFNTMVKITEKYLDYWMKQENIVWYPEIENYTFDLA

FKFLIGLDKASESSFKPLYEQWQKGIFSLNTIKLPWTKFGKAWKARNLLKKELKEIIIKRQKEQEANDSD

ALDILIKAKDEDGKQLLVDEISDHLLNILFAGYGTLTSTLASFCRLMAQEGEILGKIREEQQRFPKQLTI

MQLKEMPYLDLVLKELLRTNTPVGTGFRQTINNCEINGYHIPKNWFIFYQISNTHKDTDIYQDPDVFDPD

RFGLDRAEGEKPFSYLPFGGGIRECLGKDFARLEMKIFSSLLVRKCQWDLLPNQNLEIEFTPVAKPKDGL

KVKISSY

>CYP120E1 gi|113476367| YP\_722428 Trichodesmium erythraeum IMS101

MNMNFKSSNPASSLALPPGDLGLPFIGQNKKIFKNPQNFIEEVYQKYGPVYKTNFLGKNFIYFQGYEAIK

FILTNENKYFTYSQILRNYQRIFGENDITVLAGKEHRERQKILAKTIKSKNLNNYIDIIHDLSQSYFLKW

IKSDYVDLYSEINNYTLDMILKLLLGIDYASKSEISNYLKDMSSGLNTIPVVFPWTKFGSALESKNKLFN

QFEQIIVRRKKENNFGSDILGILLTVQEQMNYELTPREIVGQMVNLLSLGKKELSSALSSFFILTSEHLD

VLKLLQIEQEKMDVSEPLSLDKYKKMVYLEQVIKEVLRLVPPVSGGLRKIIEDCSFQGFRIPKGWHAYYY

ISSVLKDPEIYKQPEIFNPERFNPTNAEDKKKPLCYIPFGGGARECIGKEFAYLVIKIFISALLDNCSWK

FKENQDLTINTFPVARPAHKIEVCFTPK

>CYP121A1 Mycobacterium tuberculosis

MTATVLLEVPFSARGDRIPDAVAELRTREPIRKVRTITGAEAWL

VSSYALCTQVLEDRRFSMKETAAAGAPRLNALTVPPEVVNNMGNIADAGLRKAVMKAI

TPKAPGLEQFLRDTANSLLDNLITEGAPADLRNDFADPLATALHCKVLGIPQEDGPKL

FRSLSIAFMSSADPIPAAKINWDRDIEYMAGILENPNITTGLMGELSRLRKDPAYSHV

SDELFATIGVTFFGAGVISTGSFLTTALISLIQRPQLRNLLHEKPELIPAGVEELLRI

NLSFADGLPRLATADIQVGDVLVRKGELVLVLLEGANFDPEHFPNPGSIELDRPNPTS

HLAFGRGQHFCPGSALGRRHAQIGIEALLKKMPGVDLAVPIDQLVWRTRFQRRIPERL

PVLW

>CYP121A1 Mycobacterium bovis subsp. bovis AF2122/97,

MTATVLLEVPFSARGDRIPDAVAELRTREPIRKVRTITGAEAWL

VSSYALCTQVLEDRRFSMKETAAAGAPRLNALTVPPEVVNNMGNIADAGLRKAVMKAI

TPKAPGLEQFLRDTANSLLDNLITEGAPADLRNDFADPLATALHCKVLGIPQEDGPKL

FRSLSIAFMSSADPIPAAKINWDRDIEYMAGILENPNITTGLMGELSRLRKDPAYSHV

SDELFATIGVTFFGAGVISTGSFLTTALISLIQRPQLRNLLHEKPELIPAGVEELLRI

NLSFADGLPRLATADIQVGDVLVRKGELVLVLLEGANFDPEHFPNPGSIELDRPNPTS

HLAFGRGQHFCPGSALGRRHAQIGIEALLKKMPGVDLAVPIDQLVWRTRFQRRIPERL

PVLW

>CYP122A1 Streptomyces sp.

MSTDTPAGTPQAGRCPFAIQDAHRAILDSATVGSFDLFGIKHWL

VAAAEDVKLVTNDPRFSSAAPSEMLPDRRPGWFSGMDVPEHSRYRQKIAGDFTLRAAR

RQEEFVFEAADACLDEIEAAGPGADLVPGYAKRLPSLVINALYGLTPEEGAVLETRMR

GITGSTDLDSVKTLTDDFFAHALELVRAKRDERGDDLLHRLASAEDGEIPLSDDEATG

VFATLLFAGHDSVQQMVGYCLYALLSHPEQEGALRTRPELIDGAVEEMLRFLPVNQMG

VPRVCVADVDLRGVRISVGDNVIPLYSTANRDPEVFPDPDTFDVSRPTEGNFAFGHGV

HKCPGQHVARLLIKVACLRLLERFPDVRLVGDVPMNEGLGLFSPAELRITWGAA

>CYP122A2 Streptomyces hygroscopicus

MSTEAQQESTPTARCPFSIQDGHRTILETGTVGAHELFGVKQWL

VAAAEDVKLVTNDPRFSSAAPSGILGDRRPGWFSGMDSPEHNRYRQKIARDFTLRAAR

KQEEFIVRAADSCLDDIEASGPGTDLVPGYAKRLASLAIHDLYGLNEEGPVLEGQMRA

MEGGTDMESIKRLTDEFGHVLALVRAKRDEAGDRLLHRLAESGEDEILLSDEEATGVF

ATLLFAGHDSMQQMVGYSLYALLSHPEQRAALRENPDLIDGAVEELLRFLPLNQLGVP

RVCVEDVELHGQTISAGDNVIPLYSTANRDPGVFADPDTFDITRKPEHNFAFGYGIHG

CPGQHLARVLIKVATVRLFERFPDVRLAGDVPMNEGLGLFSPAELRVTWGAE

>CYP122A3 Streptomyces hygroscopicus var.

MSTDTHEGTPPAGRCPFAIQDGHRAILESGTVGSFDLFGVKHWL

VAAAEDVKLVTNDPRFSSAAPSEMLPDRRPGWFSGMDSPEHNRYRQKIAGDFTLRAAR

KREDFVAEAADACLDDIEAAGPGTDLIPGYAKRLPSLVINALYGLTPEEGAVLEARMR

DITGSADLDSVKTLTDDFFGHALRLVRAKRDERGEDLLHRLASADDGEISLSDDEATG

VFATLLFAGHDSVQQMVGYCLYALLSHPEQQAALRARPELVDNAVEEMLRFLPVNQMG

VPRVCVEDVDVRGVRIRAGDNVIPLYSTANRDPEVFPQPDTFDVTRPLEGNFAFGHGI

HKCPGQHIARVLIKVACLRLFERFPDVRLAGDVPMNEGLGLFSPAELRVTWGAA

>CYP123A1 Mycobacterium tuberculosis

MTVRVGDPELVLDPYDYDFHEDPYPYYRRLRDEAPLYRNEERNF

WAVSRHHDVLQGFRDSTALSNAYGVSLDPSSRTSEAYRVMSMLAMDDPAHLRMRTLVS

KGFTPRRIRELEPQVLELARIHLDSALQTESFDFVAEFAGKLPMDVISELIGVPDTDR

ARIRALADAVLHREDGVADVPPPAMAASIELMRYYADLIAEFRRRPANNLTSALLAAE

LDGDRLSDQEIMAFLFLMVIAGNETTTKLLANAVYWAAHHPGQLARVFADHSRIPMWV

EETLRYDTSSQILARTVAHDLTLYDTTIPEGEVLLLLPGSANRDDRVFDDPDDYRIGR

EIGCKLVSFGSGAHFCLGAHLARMEARVALGALLRRIRNYEVDDDNVVRVHSSNVRGF

AHLPISVQAR

>CYP123A1 Mycobacterium bovis subsp. bovis AF2122/97,

NC\_002945 complete genome complement(861053..862261)

Gene = CYP123 100% match

locus\_tag = Mb0789c

>CYP123A2 Mycobacterium smegmatis

MSLPTVEPVLDPYDYDFHEDPYPYYKRLRDEAPLYRNDERNFWALSRHED

VLKGFRNSTALSNKHGVSLDPVSRNDEAHRVMSFLALDDPAHLRLRTLVS

KGFTPRRIRELEARVTEIAVQHLEIALQSDSFDFVDDFAGKLPMDVISEL

MGVPEEDRVRIRALADGVMHREDGVADVPASAIAASGELLVYYADMVKRR

RRNVSDDLTSALVEAEIDGDKLTDDEIMAFLFLMVVAGNETTTKLLANAA

YWGFKNPDQLAPVFDDHSQIPLWVEETLRYDTSSQILARAVVEDLTFYGT

TVPAGDVLVLLAGSANRDERAFDDPDEYRIGRDIGSKLVSFGSGAHFCLG

AHLARMEARVALAELFKRIRGYDVDESASVRVHSSSVRGFAHLPITVEKR

>CYP123A3 Mycobacterium marinum MM4930

MSVHVGGPEL VLDPYDYDFH EDPYPYYRRL RDEAPLYHNQ ELGFWALSRH RDVHQGFRNS

TTLSNRDGVS LDPVSRGPHA TKTMSFLAMD DPAHLRLRTL VSKGFTPRRI RELEPRVTEL

AVAHLDTMLD MAGGSQTVDY VAEFAGKLPM DVISELMGVP VADRDQIRAM ADGVMHREDG

VTDVPASAIE ASINLIVYYQ QMIAERRKKP SDDLTSALLA ADVDGDRLTD EEVLGFMFLM

VIAGNETTTK LLANAAFWGH KNTDQLTPIY ADLSRVPLWV EETLRYDTSS QILARTVVGE

LTLYDTTIPE GDVVLLLPGS AHRDERAFRD PDEYLIGREI GSKLLSFGSG AHFCLGAHLA

RMEARVALTE LFKRIRGYQV DEGNAVRVHS SNVRGFAHLP ITVEVA\*

>CYP123A3 Mycobacterium ulcerans

MSVHVGGPELVLDPYDYDFHEDPYPYYRRLRNEAPLYHNQELGFWALSRRRDVHQGFRNS

TTLSNRDGVSLDPVSRGPHATKTMSFLAIDDPAHLRLRTLVSKGFTPRRIRELEPRVTEL

AVAHLDTMLDMAGGSQTVDYVAEFAGKLPMDVISELMGVPVADRDQIRAMADGVMHREDG

VTDVPASAIEASINLIVYYQQMIAERRKKPSDDLTSALLAADVDGDRLTDEEVLGFMFLM

VIAGNETTTKLLANAAFWGHKNTDQLTPIYADLSRVPLWVEETLRYDTSSQILARTVVGE

LTLYDTTIPEGDVVLLLPGSAHRDERAFRDPDEYLIGREIGSKLLSFGSGAHFCLGAHLA

RMEARVALTELFKRIRGYQVDEGNAVRVHSSNVRGFAHLPITVEVA

>CYP123A4 Mycobacterium vanbaalenii PYR-1

MTISEVRLDPYNYDFHEDPYPYYKRLRDEAPLYRNEELGFWALSRHADVLKGFRNSTTLSNKFGVSLDPA SRGPHASKTMSFLAMDDPAHLRLRTLVSKGFTPRRIRELEPRVTEIAVTHLDAMLEQATTGDAVDYVDEF AGKLPMDVISELMGVPDADRVQVRAWADAVMHRDDGVTDVPDSAIEASLNLIVYYQEMVAERRKKLTDDL TSALLEAEIDGDRLTDDEIIGFMFLMVIAGNETTTKLLANAAFWGHRNPDQLTSVYQDLARVPLWVEETL RFDTSSQILARTVSGELTLYDTTIPDGDVVLLLPGSAHRDERVFENPDDYVIGREIGSKLMSFGSGAHFC LGAHLARMEARVALAELFKRIRGYEVDEANAVRVHSSNVRGFAHLPIRVEIR

>CYP123A5 Rhodococcus sp. RHA1 Rha05833 and Rha05832

MTAASMPGVSHNPVTFNPYDYGFHEDPYVTYRRLREEAPLYYNEELDFWALSRHEDVVAAFRDNQRLSSANGVSLDPAAYGPHAHKTMSFLALDDPRHMRMRQLVSRGFTPRRVNELEGRILDLTRQYLDPALAAGEFDWIGEFAGKLPMDVISELMGVPEADRVELRRLADLVVHREEGVLDVPHAAMEASLYLVGYYADMLAERRRKPTEDLTSALLEAEIDGDRLTDDEIIAFMS

MRCTGVSAIRARLGNVFEDASRVPEWVEXTLRFDTSSQMVARTASVDLDFHDRTIPAGDKVLILIGSANRDSAVFEDADEYRIGRDTSNKLASFGGGTHFCLGAHMARLEARIALTELVSRIDDYDIDEANSVRVHSTNVRGFATLPMKVQVRDA

>CYP123B1 Mycobacterium marinum MM4833

MWQETLMSTV QLRYDPFDPE IQDDPYPVYR QLRDDAPVYH ATDTNTWVLS RHADVISALL

DHHSYSSVDG VFPTPPGSTF RESLLPMMIL MDPPRHDQLR ALVSKAFTPR RIAALTSAIE

DLADHLTGGL IQEAGSADFV ADFAAVLPAM VIADLLGVPR EDRTQFRQWS NALVQSNPTH

GETGEALAAA AAIYGYFTDF LADRRRQPRD DLMSALVCAE IDGKHLSDDE LLGFCLLLLI

AGHETTSNLL ANAAVVLADY RDTRRQLAGD ESLLGAAVEE LLRYDSPAQG LSRTLTRDVT

VHGVRMSAGE SVLLLFGSAN RDERVFADPD VFDIGRKPEH QVAFGRGIHF CLGASLARME

ARIALRALLA RVPNWEVDLE RAQRLRSGPI RGYLSLPISW SAN\*

>CYP123B2 Mycobacterium vanbaalenii PYR-1

MVSVQIRYDPFDASILNDPYPTYRLLRDVAPVYRAEESHTWVLSRHADVQAAALDHSTYSSVDGIFPTPP GSDFIGSFLPMMIVMDPPRHDQLRALVSRAFTPRRVAGLQGTITQMAAELFERLDEGSGSADFVTDFAAI LPAAVIADLLGVPATDRDQFRLWSSQLVQVDVNHGQTTDALAAAAAIYAYFTDFLADRRKNPREDLMSAL ANATVDGIGLTDEEVLGFCALLLVAGYETTTNLLGNSAVVLAQHRQTRRRLAADRTLLGPAVEELLRYDS PAQGLSRTLTRDVTLHDTTMRQGEKVLLLFGSANRDERAFPDPDVFDIERTSEHQVAFGRGIHFCLGAAL ARMEARIALNALLDKVPDWEVDLESARRLRSGPIRGYTSLPITWTTPV

>CYP124A1 Mycobacterium tuberculosis

MGLNTAIATRVNGTPPPEVPIADIELGSLDFWALDDDVRDGAFA

TLRREAPISFWPTIELPGFVAGNGHWALTKYDDVFYASRHPDIFSSYPNITINDQTPE

LAEYFGSMIVLDDPRHQRLRSIVSRAFTPKVVARIEAAVRDRAHRLVSSMIANNPDRQ

ADLVSELAGPLPLQIICDMMGIPKADHQRIFHWTNVILGFGDPDLATDFDEFMQVSAD

IGAYATALAEDRRVNHHDDLTSSLVEAEVDGERLSSREIASFFILLVVAGNETTRNAI

THGVLALSRYPEQRDRWWSDFDGLAPTAVEEIVRWASPVVYMRRTLTQDIELRGTKMA

AGDKVSLWYCSANRDESKFADPWTFDLARNPNPHLGFGGGGAHFCLGANLARREIRVA

FDELRRQMPDVVATEEPARLLSQFIHGIKTLPVTWS

>CYP124A1 Mycobacterium bovis subsp. bovis AF2122/97,

NC\_002945 complete genome 2519058..2520344

Gene = CYP124 100% match

locus\_tag = Mb2289

>CYP124A1 Mycobacterium avium subsp. paratuberculosis str k10

MSLKTRPKKGLATRINGAPPPRVPLADIHLESLDFWGYDDDFRD

GAFATLRREAPISFWPAIEMDGFVAGNGYWALTKHEDVHFASRHPEIFSSVPNITIND

QTPELAEYFGSMIVLDDPRHQRLRSIVSRAFTPKVVARIEASVRERARRLVSSLVANH

PNGEAELVSELAGPLPLQVICDMMGIPEEDHQRVFHWTNVILGFGDPDLATDFEEFLQ

VSMDIGAYATALAEDRRVNHHDDLTTSLVEAEVDGERLTSSEIASFFILLVVAGNETT

RNAISHGVLALSRYPDERDKWFSDFDRLTPTAVEEVVRWASPVVYMRRTLTRDVKLRG

TKMKAGDKVALWYNSANRDESTFGNPWLFDVARTPNPHLGFGGGGAHFCLGANLARRE

IRVVFDELRHEIPDIVATEEPARLLSQFIHGIKRLPVAWTPPR

>CYP124A1 Mycobacterium marinum MM3361

MDLSTNLNTG LLPRVNGTPP PEVPLADIEL GSLEFWGRDD DFRDGAFATL RREAPISFWP

PIELAGLTAG KGHWALTKHD DIHFASRHPE IFHSSPNIVI HDQTPELAEY FGSMIVLDDP

RHQRLRSIVS RAFTPKVVAR IEASVRERAH RLVAAMIENH PDGQADLVSE LAGPLPLQII

CDMMGIPEED HEQIFHWTNV ILGFGDPDLT TDFDEFLQVS MAIGGYATAL ADDRRVNHHG

DLTTSLVEAE VDGERLSSSE IAMFFILLVV AGNETTRNAI SHGMLALSRY PDERAKWWSD

FDGLAATAVE EIVRWASPVV YMRRTLSQDV DLRGTKMAAG DKVTLWYCSA NRDEEKFADP

WTFDVTRNPN PQVGFGGGGA HFCLGANLAR REIRVVFDEL RRQMPDVVAT EEPARLLSQF

IHGIKRLPVA WSR\*

>CYP124A1 Mycobacterium ulcerans

MDLSTNLNTGLLPRVNGTPPPEVPLADIELGSLEFWGRDDDFRDGAFATLRREAPISFWP

PIELAGLTAGKGHWALTKHDDIHFASRHPEIFHSSPNIVIHDQTPELAEYFGSMIVLDDP

RHQRLRSIVSRAFTPKVVARIEASVRERAHRLVAAMIENHPDGQADLVSELAGPLPLQII

CDMMGIPEEDHEQIFHWTNVILGFGDPDLTTDFDDFLQVSMAIGGYATALADDRRVNHHG

DLTTSLVEAEVDGERLSSSEIAMFFILLVVAGNETTRNTISHGMLALSRYPDERAKWWSD

FDGLAATAVEEIVRWASPVVYMRRTLNQDVDLRGTKMAAGDKVTLWYCSANRDEEKFADP

WTFDVTRNPNPQVGFGGGGAHFCLGANLARREIRVVFDELRRQMPDVVATEEPARLLSQF

IHGIKRLPVAWSR

>CYP124A1 Mycobacterium smegmatis

MGIAPRVNGAAPPDVPLSEINLGSWDFWALDDDIRDGAFATLRREAPISF

HPAFDTEEGFPQGAGHWALTRHDDVFYASRHPELFSSASGIVIGDQTPEL

AEYFGSMIAMDDPRHTRLRNIVRSAFTPRVLAVIEDSVRDRARRLVAGMV

DRNPDGHAELVTELAGPLPLQIICDMMGIPESDHQQIFHWTNVILGFGDP

DLTTDFDEFVTVAMDIGAYATALADQRRSAPADDLTTSLVQAEVDGERLT

SAEVASFFILLVVAGNETTRNAISHGVLALTRYPEQRRLWWSRFDELAPT

AVEEIVRWASPVSYMRRTVTRDTELAGTALPAGSKVTLWYGSANRDETKF

DNPWMFDVQRHPNPHVGFGGGGAHFCLGANLARREITVLFSELHRHLPDI

VATEEPDRLQSAFIHGIKRLPVAWR

>CYP124A1 Mycobacterium vanbaalenii PYR-1

MSLGMGIEKSAVTRTNGVAPPEVPLADIDLGSWDFWGLDDDYRDGAFATLRREAPISFHEAYVIDPDNEV AGHWALTRHDDVFYASRHPEIFSSALGITVGDQTPELAEYFGSMIAMDDPRHTRLRNIVRSAFTPRVLAL IEDSVRQRARSLVQQMVAAHPDGNGELVAELAGPLPLQIICDMMGIPEEDHQKIFHWTNVILGFGDPDIA TDFDEFVSVAMGIGAYATQLADDRRDHPGDDLTTSLVAAELDGERLTSAEVASFFILLVVAGNETTRNAI SHGVLALSRYPEQRQRWWSDYQGMAPTAVEEIVRWASPVAYMRRTATRDVEMSGVRIAAGDKVSLWYGSA NRDESKFENPWLFDVGRHPNPHVGFGGGGAHFCLGANLARREITVAFEELHRLVPGIRAVEEPDRLHSAF

IHGIKRLPVSWSA

>CYP124B1 Streptomyces cinnamonensis

MGLTVGPDNAKRGIVPITDSKPAATFPDLVDPSFWARPHAERVA

LFEEMRGLPRPAFIRQNMPGVPWTFGYHALVKYADIVEVSRRPQDFSSNGATTIIGLP

PELDEYYGSMINMDNPEHSRLRRIVSRSFGRNMIPEFEAVATRTARRIIDELIARGPG

DFIRPVAAEMPIAVLSDMMGIPAEDHDFLFDRSNTIVGPLDPDYVPDRADSERAVIEA

SRELGDYIAGLRAERLAAPGNDLITKLVQVQADGEQLTRQELVSFFILLVIAGMETTR

NAISHALVLLTEHPEQKQLLLSDFDTHAPNAVEEILRVSTPINWMRRVATRDCDMNGH

RFRRGDRIFLFYWSGNRDESVFPDPYRFDITRGTNAHVTFGAVGPHVCLGAHLARMEI

TVLYRELLAALPQIHAVGQPRRLDSSFIEGIKHLHCAF

>CYP124B2 Streptomyces nanchangensis NS3226

MNRGVVSPTEATPASSAKATRPPDFMDPSFWLRPRDERAEVFEK

LRALPGPEFVPPRLPWGPLASGYYALSKHADICEVSRRPQDFSSEGATAILPPEMDEF

YGSMINMDNPEHSRLRRIVARSFGRGMAPKFDAMSRRVARRIVDELIERGPGDFIRPA

AEMPIAVLSTMMGIPGEDYEFLFERTNTIMGGADPELAADPEKMAAAVLGALRDLGDY

IGRLREDRLARPGPDVITKLVQVQEDGEQLTNQELVSFFILLINAGMETTRNVIAQAL

VLLTEHPDQRQLLLSDFELHAKGAVEEILRVGTPINWMRRTATGDCEMNGHRFRKGDE

IFLFYWSANHDEKVFEDAYRFDITRDPNPHLSFGAVGPHFCLGAHLARIEIIAMLREL

LASLPDIRVEGEPVRLASSFIEGFKELSCTF

>CYP124B2 ortholog SBI\_3705 Streptomyces bingchengensis

99% to CYP124B2 Streptomyces nanchangensis NS3226

only 3 aa diffs

MDPSFWLRPRDERAEVFEKLRALPGPEFVPPRLPWGPLASGYYALSKHAD

ICEVSRRPQDFSSEGATAILPPEMDEFYGSMINMDNPEHSRLRRIVARSF

GRGMVPKFDAMSRRVARRIVDELIERGPGDFIRPAAEMPIAVLSTMMGIS

GEDYEFLFERTNTIMGGADPELAADPEKMAAAVLGALRDLGDYIGRLRED

RLARPGPDVITKLVQVQEDGEQLTNQELVSFFILLINAGMETTRNVIAQA

LVLLTEHPDQRQLLLSDFELHARGAVEEILRVGTPINWMRRTATGDCEMN

GHRFRKGDEIFLFYWSANHDEKVFEDAYRFDITRDPNPHLSFGAVGPHFC

LGAHLARIEIIAMLRELLASLPDIRVEGEPVRLASSFIEGFKELSCTF

>CYP124C1 Rhodococcus sp. RHA1 Rha04649

VTGSASEKIISPASRAFWDRSFAGRRAMFEELRQRSPIEFHAETAGPGFWSVVGYDDVVAVSRNPEVFSSAKGFTIDDVPAEILEFAMSMIAMDDPRHRRLRGIVQSAFTAASVRGIAERVRGTAAQIAADLPRDAEFDFVPDVATRLPVQVICELIGIPENDRPMILAAAADVVAGGGDQEFVTAPGGAAGLGQIYGYALELGERRKADPGEDLTSRLVSTMVDGEALAPTEFGSFVILLITAGFETTRQALAWALLLLSEHPDQKELLLADFAGHIDNTIDEVIRFASPVPYMRRTATVDTELGGAHIAAGDKVVMWYLSANHDERVFDGPGRFDITRANAGKHLGFGAKDIHHCLGVNLARLELRVMLEELFTAHPTLHAVGEPELLLSAFISGVAALPARTRDGR

>CYP124F1 Frankia alni ACN14a

MSLIADVDLDDLDWWTRPAAERDAYFASVRASGERPYFPELDLAGNTRGRGFYAVTRYADVMEVSRRPED

FCSGEGTNIFDQPLDLREFFGSIIAMDNPQHARQRRIISRGFTAKNLEALRANVGEVTREVLATVAEKGE

CDFVTEVAALIPLRIVNDMMGIPRSQEQFIFESTNKLLGASDPEYVPDQSPRGVAKNLSRVGDDFAELLR

ELAADRQRNPGDDLISLLVAAEGENLTAQELASFFILLVGAGNETTRNAIAHGLLALTQNPDQRALWASD

VDGLTPTAVDEVVRWASPVLHMRRTVTADGVRLGDQEFREGDKLVLWYRSANQDESVFPDGTRFDVRRDL

TPPHLGFGAPGPHFCLGAHLARLELSVVFKALFEYLPDIHAVEEPQFLRTNFLHGIKHLKAAYTPTTVRA

>CYP124F2 Frankia alni ACN14a

MPGTRGLPGDVLDDLSWWTRPAAERDATFAWLRAHDPRPYVPELDLTGAPRGGGFWALTRLDDVREVSRR

PADFCSGQGSLIFDQPPRLREFRGSIIDMDNPEHARQRRIVARGFTPKAVAALVEDIARTSREVISAVAR

RGECDFVTEVAALLPLRIVNNLLGIPRSEERFLFEQTNILMGASDPEYVPDQTPRSVARAVHGAGQAMSG

LLEELARDRIRNPQDDLVSSLVAAQEEENLTPTELATFFNLLVGAGNETTRNALAHGLSALTRFPDQREL

WRSDLDRYTPGAVEELLRWASPVLYMRRTVARDGVTLGEQRFDAGDKVVLWYRSANQDEAYFDDATAFRV

TRDPNPHVTFGAPGPHHCLGANLARVELAIAFRTLFELLPDIEATAEPDLLRSNFLHGVKHLPARFTPTA

PRP

>CYP124G1 SGR529 Streptomyces griseus

42% to CYP124B1 Streptomyces cinnamonensis

42% to CYP268A2 Mycobacterium marinum MM3761

top 19 hits are CYP124 or CYP268. These families overlap

MLLAAGGRTMAWRTVEVMDMTVPYQLSEGRVLRAADVDLADPAFWRLPRPVRLRAFALLRELEEPVLFTPRAGTARTAGKPFRALVRHADVRTASRTPQVFASAPGVTTPEPAGWAKALFGNSMVNMDGPEHAALRRIISRRFTPRLLAEAEENVGRLAGRLVDELIAERPRDFMPSAASRLPLEVICDLMGVPAAYRARIAEQIDHASEHVGVERRGRARLRIPGRGLASLARMQFVMGRLARERRQRPEDDLVSALVNADIDGEALSGRQLGAFFSLLLVAGVETTRNAIAHGLFLLDRHPEQRELLRSDFDRYIDGAVDEIVRHSTPIIQFRRTVAEECALGGRTFLPGEKVALIYASANRDETVFTHPDRFDITRSPNPHLGYGGGGPHHCLGAHLARLEMTALFRELIARRPVMRDLGDPDLVDSNFDNRVGSLPFTFGPTFT

>CYP125A1 Mycobacterium tuberculosis

MSWNHQSVEIAVRRTTVPSPNLPPGFDFTDPAIYAERLPVAEFA

ELRSAAPIWWNGQDPGKGGGFHDGGFWAITKLNDVKEISRHSDVFSSYENGVIPRFKN

DIAREDIEVQRFVMLNMDAPHHTRLRKIISRGFTPRAVGRLHDELQERAQKIAAEAAA

AGSGDFVEQVSCELPLQAIAGLLGVPQEDRGKLFHWSNEMTGNEDPEYAHIDPKASSA

ELIGYAMKMAEEKAKNPADDIVTQLIQADIDGEKLSDDEFGFFVVMLAVAGNETTRNS

ITQGMMAFAEHPDQWELYKKVRPETAADEIVRWATPVTAFQRTALRDYELSGVQIKKG

QRVVMFYRSANFDEEVFQDPFTFNILRNPNPHVGFGGTGAHYCIGANLARMTINLIFN

AVADHMPDLKPISAPERLRSGWLNGIKHWQVDYTGRCPVAH

>CYP125A1 Mycobacterium bovis subsp. bovis AF2122/97,

NC\_002945 complete genome complement(3927359..3928660)

Gene = CYP125A1 100% match

locus\_tag =Mb3575c

>CYP125A2 Streptomyces avermitilis

MPCPALPDGFDLTDPDLLHQRVPLPEFAELRRTAPVHWVPQQHG

LAGFQDDGYWAVTRHADVKYVSTHPELFSSYLNTAIIRFHETMQREQIDAQRLFMLNM

DPPEHTRVRQIVQRGFTPRAIRALEDTLRRRARSIVETALADAGPDGSFDFVTQVACE

LPLQAIAELIGIPQDDRAKIFDWSNKMIAYDDPEYAITEEVGAESATELIAYAMNMAA

DRKQCPAKDIVSTLVAAEDVGNLASDEFGFFVLMLAVAGNETTRNAITHGMHAFLTHP

DQWDLYKRERPATAAEEIVRWATPVVSFQRTATQDTELGGKQIRKGDRVGIFYSSANH

DPEVFEHPDVFDITRDPNPHLGFGGGGPHFCLGKSLAVVEIDLIFGAIADVMPGLRLT

GDPRRLRSAWLNGVKGLQVSAG

>CYP125A3 Mycobacterium smegmatis

MPTPNIPSDFDFLDATLNLERLPVEELAELRKSEPIHWVDVPGGTGGFGD

KGYWLVTKHADVKEVSRRSDVFGSSPDGAIPVWPQDMTREAVDLQRAVLL

NMDAPQHTRLRKIISRGFTPRAIGRLEDELRSRAQKIAQTAAAQGAGDFV

EQVSCELPLQAIAELLGVPQDDRDKLFRWSNEMTAGEDPEYADVDPAMSS

FELISYAMKMAEERAVNPTEDIVTKLIEADIDGEKLSDDEFGFFVVMLAV

AGNETTRNSITHGMIAFAQNPDQWELYKKERPETAADEIVRWATPVSAFQ

RTALEDVELGGVQIKKGQRVVMSYRSANFDEEVFEDPHTFNILRSPNPHV

GFGGTGAHYCIGANLARMTINLIFNAIADNMPDLKPIGAPERLKSGWLNG

IKHWQVDYTGAGKASVSGAPGTCPVAH

>CYP125A4 Mycobacterium smegmatis

MSDSALHLPAGFDFTDPDIYAERLPVDELAELRRVAPIWWNAQPIGAGGF

DDGGFWVVTKHKDVKEISLRSDVFSSLEKTALPRYPEGTVQDQIEQGRFV

LLNMDAPHHTHLRKIISRAFTPRAVERLRDDLAERARAIVRAAAEEGSGD

FVEQVACELPLQAIAGLMGVPQEDRRKLFDWSNQMVGNQDPEFVANDGAS

AAVELITYGMQLAAQRAAAPGDDLVTKLVQADVEGHKLSDDEFGFFVVLL

AVAGNETTRNSITQGMMAFTDHRDQWELFKRERPVTTADEIVRWATPVTS

FQRTALADTEVSGVRIKKGQRVVMFYRSANFDEDVFTDPYRFDILRDPNP

HVGFGGTGAHYCIGANLARMTIDLIFNAIADEMPDLTPISEPVRLRSGWL

NGIKHWQVDYRGDAAKHRAAQASSQADR

>CYP125A5P Mycobacterium smegmatis

MATMNTCPFGNGYDFTDPDVLFRGIPVEEFAVLRKTAPVWWNQQGESIFDDGG

YWVISRHEDIKTISRDGGEVWSTNAKGAVMRLPDGVTAEQLDLTKALLIN

HDAPEHTRLRKLVSRLFTPRSVAALEEKLAVAAHDIVAEAKAEGSGNFVE

DIAMKLPLLAIADLIGVPEADREKIFAWSNAIINTDDPDFDSDPTVANAE

LMGYAYTMAEERRRCPADDIVTRLVQADVSGESLGEVEFAFFVILLAVAG

NETTRNAITHGMNAFFENPDQWELFKRERPITAVDEIVRWATPVHCFQRT

AVVDTEIGGVPIKAGQRAGLFYSSANYDEDVFDDPFRFDILRDPNPHLGF

GGNGAHYCIGANLARMEIRLMFDEIADQIPDITKVGEPQRLRSGWINGVK

DLQVSYRG\*PARLIYYSRMRTHGWSGSAPATD

>CYP125A6 Mycobacterium marinum MM2783

MPAAEPTATS VPNLPPGFDF TDPDIYAERL PVAELAEMRR SAPIWWNEQP TGCGGFDDGG

FWVVTKHKDV KEISLRSDVF SSLQKTALPR YKDGTVDEQI ERGKFVLLNM DAPQHTRLRK

IVSRAFTPRA VERLRDDLRE RARRIVEAAA AEGRGDFVEQ VSCELPLQAI AGLMGVPQED

RKKLFHWSNE MVGDQDPEFA TNDALTASVE LIMYGMQMAA DRAKNPGQDL VTKLVEADID

GHKLSDDEFG FFVILLAVAG NETTRNSITQ GMMAFTDFPD QWELYKRERP VTTADEIVRW

ATPVTSFQRT ALQDYELSGV RIKKGQRVVM FYRSANFDED VFDDPYTFNI LRDPNPHVGF

GGTGAHYCIG ANLARMTIDL MFNAIADVMP DLESISQPER LRSGWLNGIK HWQVDYHSDS

SGKCPVAH\*

>CYP125A6P Mycobacterium ulcerans

MPAAEPTATSVPNLPPGFDFTDPDIYAERLPVAELAEMRRSAPIWWNEQPTGCGGFDDGG

FWVVTKHKDVKEISLRSDVFSSLQKTALPRYKDGTVDEQIERGKFVLLNMDAPQHTRLRK

IVSRAFTPRAVERLRDDLRQRARRIVEAAAAEGRGDFVEQVSCELPLQAIAGLMGVPQED

RKKLFHWSNEMVGDPGLRRC LLEANSGQDPRFAAADHDDRELRRALRRQGVGDQDPEFATNDALTASAELIMYGMQMAAD

RAKNPGQDLVTKLVEADIDGHKLSDDEFGFFVILLAVAGNETTRNSITQGMMAFIDFPDQ

WELYKRERPVTTADEIVRWATPMTSFQRTALEDYELSGVRIKKGQRVVMFYRSANFDEDV

FDDPYTFNILRDPNPHVGFGGTGAHYCIGANLARMTIDLMFHAIADVMPDLESISRPERL

RSGWLNGIKHWQVDYHSDSSGKCPVAH

>CYP125A7 Mycobacterium marinum MM5032

MPCPNLPPGF DFTDPDIYAE RLPVEEFAEL RSSEPIWWDE QLPGQGGGFH DGGFWAITKL

KDVKEVSRRS DVFSSYENGV IPRFKNDIAR EDIDVQRFVM LNMDAPHHTR LRKIISRGFT

PRAIGRLHDE LNDRAQNIAK AAAAAGSGDF VEQVSCELPL QAIAGLLGIP QEDRGKLFDW

SNEMTGTEDP EFAHIDAKAS SVELIGYAMK MAEEKAKNPG DDIVTQLIQA DIDGEKLSDD

EFGFFVVMLA VAGNETTRNS ITQGMMAFAD NPEQWELYKR ERPETAADEI VRWATPVTSF

QRTALEDYEL SGVQIKKGQR VLMFYRSANF DEEVFEDPFS FNILRNPNPH VGFGGTGAHY

CIGANLARMT INLIFNAVAD HMPDLTPIAA PERLRSGWLN GIKHWQVDYT GKCPVSH\*

>CYP125A7 Mycobacterium ulcerans

VPCPNLPPGFDFTDPDIYAERLPVEEFAELRSSEPIWWDEQFPGQGGGFHDGGFWAITKL

KDVKEVSRRSDVFSSYENGVIPRFKNDIAREDIDVQRFVMLNMDAPHHTRLRKIISRGFT

PRAIGRLHDELNDRAQNIAKAAAAAGSGDFVEQVSCELPLQAIAGLLGIPQEDRGKLFDW

SNEMTGTEDPEFAHIDAKASSVELIGYAMKMAEEKAKNPGDDIVTQLIQADIDGEKLSDD

EFGFFVVMLAVAGNETTRNSITQGMMAFADNPEQWELYKRERPGTAADEIVRWATPVTSF

QRTALEDYELSGVQIKKGQRVLMFYRSANFDEEVFEDPFSFNILRNPNPHVGFGGTGAHY

CIGANLARMTINLIFNAVADHMPDLKPIAAPERLRSGWLNGIKHWQVDYTGKCPVSH

>CYP125A8 Streptomyces scabies SCAB65311

MLRQESPMPC PALPDGFDLT DPDLLHHRVP LPEFAELRRA EPVHWIPQAP GIAGFADEGY

WAVTRHADVK YVSTHPELFS STVNTAIIRF NEHIERDAID AQRLILLNMD PPEHTRVRQI

VQRVFTPRAI RALEDNLRHR ALNIAREAGA HAGPFDFVTE VACELPLQAI AELIGIPQED

RIRIFEWSNR MISYDDPEYA ITEEVGQQSA MELIAYAMNM AADRKQCPAK DIVTTLVAAE

DEGNLTSDEF GFFVLMLAVA GNETTRNAIT HGMHAFLTHP DQWDLYKRER PATAAEEIVR

WAAPVNAFQR TATQDLELGG KRISKGDRVG IFYASANHDP DVFTDPDTFD ITRDPNPHLG

FGGGGPHFCL GKSLAVLEID LIFNAIADAM PGLRLAGEPS RLRSAWINGV KHLQVTTA

>CYP125A9 Mycobacterium vanbaalenii PYR-1

MPGPNSCPISPEFDFLDASLNLERLPVEELAELRKSEPVHWVDVPGGTGGFGDRGYWLVTKHADVKEVSK HNEIFGSSPDGAIPVWPQEMTREAIDLQKAVLLNMDAPQHTRLRKIISRGFTPRAVGRLEDELRARAQRI AATAATEGSGDFVEQVSCELPLQAIAELLGVPQEDRDKLFRWSNEMTAGEDPEYADVDPAMSSFELITYA MKMAEERAKNPTEDIVTKLIEADIEGEKLSDDEFGFFVVMLAVAGNETTRNSITHGMIAFSRNPDQWELY KKERPETAADEIVRWATPVSAFQRTALEDTELGGVQIKKGQRVVMSYRSANFDEEVFENPHSFDIMRNPN PHVGFGGTGAHYCIGANLAKMTINLMFNAIADAMPDLKPIGDPERLKSGWLNGIKHWQVDYTGQCPVQH

>CYP125A10 Mycobacterium vanbaalenii PYR-1

MATPTLPPGFDFTDPDLNLERLPVEELAELRRCAPIWWNEQTSGGAGPFGDGGYWVVTKHRDVKEISKHS EVFSSQQKTALPRYPEGSTTEQVETGSLVLLNMDAPRHTHLRKIISRGFTPRAVERLREDLAQRAHNIAK SAAAAGAGDFVEQVSCELPLQAIAGLLGVPLEDRKKLFDWSNQMVSDDDPEFAHYDNRNAATELIMYAMQ LAALRAEQPGEDIVTKLIEADVDGHKLTDDEFGFFMVLLAVAGNETTRNSITHGMIAFTEHPDQWELFKR ERPATAVDEIVRWATPVTSFQRTALRDYELSGVQIKKGQRVVMSYRSANFDEEVFDDPFTFDIMRDPNPH VGFGGTGAHYCIGANLARMTIDLMFNAIADHLPDLSSAGTPDRLRSGWLNGIKHWQVDYTGPSGCPVAH

>CYP125A11 Mycobacterium vanbaalenii PYR-1

MTATQSCPFLPHGYDFTDPDVLLKGIPVTEFAELRRTAPVWWNEQADSIFDDGGYWVISRHEDVKAISRN STQWSTNTKGAVMRLPDGVTAEQLDLTKALLINHDAPEHTRLRKIVSRLFTPRAIAGMEDRLADAAREIV RSAAEKDSGDFVDDVAMMLPLQAIADLIGVPEEDREKLFHWTNAIMNTDDPEFDADPTMANAELMGYAYS MAEERRRCPADDIVTRLVQADIDGESLGEVEFAFFVILLAVAGNETTRNAMTHGMNAFFDNPAQWELFKR ERPETAIDEIIRWATPVHCFQRTALEDVEVGGVTIAEGQRVGLFYSSANFDEDVFDRPFDFDILRDPNPH LAFGGNGAHFCIGANLARMEIKLMFNEIADQIPDISKLAEPQRLRSGWINGVKNLQVAYR

>CYP125A12P Mycobacterium leprae

1 PGFDFPDPEIYTEQLSV\*EPAEMCQAETI\*\*NEQPIGRSGFYDDDY 138

XXXXXXXXXXXXXX

174 HSGTFSNLEKTALACYQEGMNDEQISRGKLVLLNIDASQYTRLHKIISPGFIP\*AAEQLR 353

354 DDLXXXXXXXXXXXXXXX 362

410 SGDFVEHVSCELSRQAAIAGLPSG 481

480 VPQEDCKKLFHWSN 521

522 QTVGAQDPKFATNDPMVTSVKLIM\*AMQIAADRAKPLGQVIVTNLVEADIEGHKLSKDEFGSF 710

713 VIMLTAAGKENTRNCIMQSMMQFTNFPD\*WELYK 814

816 KKAPGTTADKIIRQATLVMS 875

876 FQRTVLK\*YELSSVSIKKGQRVVVIYRSANFDEKVLTIRLPCSIMRNPT 1022

1022 PHAGFNDTNVHYCIGIN 1072

1073 LARMTIDRMFHAIAESMPNL\*STGKPK\*LRSGWLNGVKHWQVD 1201

>CYP125A13 Streptomyces peucetius

MSCPHLPQGFDFTDPDLLQARVPHPEFAEMRRTAPVWWCEQPAGISGFDDEGYWAVTRHA

DVRHVSTHPELFSSNTNTAVIRFNESISRDQIEVQKLIMLNMDPPEHTRVRQIVQRGFTP

RAVRSLEAALRRRARSIVETAAAGAKPDGSFDFVTNIAVELPLQAIAELVGVPQEDRSKI

FDWSNKMAAYDDPEYAITEEVGTEAAMEIVSYAMNLAAARKECPAQDIVSRLVAAEGERQ

PVLRRIRLLRHPAGGGRGTRPPR

NAISHGMH

GVPHPPRAVGELYSGCAPTRRPRENLRLGGTPGGFLSNGPGTQERGSLGGAAYX

>CYP125A14P Rhodococcus sp. RHA1 Rha05823

VGSFPCPQKIEQVLLSGQGLNELSFASRPACASMLVERVPHHGVVYGLGQETAVAQPNLPEGFDFTDPDVYAERIPYQEFAELRKTAPIWWNPQPPEIGGFHDDGYWVVSKLEDVKEVSRRSDVFSTHENTAIVRFADDIPRENIEMQRFILINKDAPEHTKLRKLVSRGFTPRAINSLREELTERAEKIVKEAAESGAGDFVTQVACELPLQAIAELLGVPQEDRLKVFDWSNQMTGYDDPELDIDPQAASMEILGYAYQMADERKKCPADDIVTTLIEADIDGNELSPEEFGFFVILLAVAGNETTRNAITHGMMAFLDHPDQWELYKKERPKTTADEIVRWATPVNSFQRTALEDTELGGVQIKKGQRVVMLYGSANFDEDAFENPEKFDIMRENNPHVGFGGTGAHFCLGANLARLEIDLIFNAIADHLPDISKLGDPRRLRSGWLNGIKEFQVDYKTASGGCPVRH

>CYP125A15 Salinispora tropica (marine actinomycete)

MTEPRIPVGFDFTDPAVLERRVPREEFAELRRTAPVWWNVQPRGSAGFDDDGYWVVTRYA

DVMAVSRDSDTYSTRENTAIARFQPGTTRADLEMQRVIMLNVDPPEHTKLRAIVSRGFTP

RAINALRGSLAERAERIVRDAAVRGTGDFVADVACELPLQAIAELIGVPQHHRRKVFDWS

NQLIGYDDPAYGVDPLTAAAELLAYAMEMANERQLNPSDDLVTKLVNAQIDGEHLTTDEF

GFFVMLLAVAGNETTRNAITHGMLAFLEHPEQWELFKAERPRSAVEEIIRWATPVNVFQR

TALVDTTLGGQAISAGQRVALFYGSANFDESVFEEPERFDITRSPNPHLGFGGSGAHFCL

GANLARLEIELIFHSIADHMPDIRKVAEPRRLRSGWINGIREMPVRYR

>CYP125A16 SBI\_1118 Streptomyces bingchengensis

79% to CYP125A2 Streptomyces avermitilis

MSCPALPEGFDFTDPDIYQQRLPFPEFAQLRQTDRVWWIPQPHGVAGFDD

DGYWAVTRHADVKEVSTKPEIFSSHLNTAIIRFNEHIHRDQIDVQKLIML

NMDPPEHTRVRQIVQRGFTPRAIRALEDALRERATRIVAGAKEDGSGDFV

TDVAFGMPLQAIAELIGVPQQDRSKIFDWSNKMVAYDDPELAITEEIGAE

SAMELISYAMNLAADRKACPAKDIVSQLVAAEDQGNLASDEFGFFVLLLA

VAGNETTRNAISHGMHAFLTHPDQWELFKRERPASAADEIVRWATPVMSF

QRTATQDTELGGQRIAAGQRVGIFYSSANHDPEVFDRPEDFDITRDPNPH

LGFGGGGPHFCLGKSLAELEIRLIFNAIADAMPDVRLAGDPRRLRSPWLN

GIKELQVNYG

>CYP125A19 SGR5169 Streptomyces griseus

MRCPHLPDGFDFTDPDLLQSRVPHPEFALMRETAPVWWCTQPRNISGFGDEGYWAVTRHADVKYVSTHPELFSSNTNTAVIRFNETISRDQIDVQKLIMLNMDPPEHTRVRQIVQRGFTPRAVRSLEAALRSRARSIVGTAQASADAHGSFDFVTDIAVELPLQAIAELIGVPQEDRSKIFDWSNKMAAYDDPEYAITEEVGAEAAMEIVAYSMNLAAARKECPAQDIVSQLVAAEGEGNLSSDEFGFFVILLAVAGNETTRNAISHGMHAFLTHPEQWELYKRERPKTTAEEIVRWATPVVSFQRTATQDVELGGQRIRKGERVGLFYSSANNDPEVFDAPEAFDITRDPNPHLGFGGGGPHFCLGKSLAVMEIDLIFNAIADVLPDLRLLEDPRRLRSAWLNGIKELRVTTAAA

>CYP125B1 Rhodococcus sp. RHA1 Rha05835

MTASRIDLKCPDVYTEGVPYAFFDHLRSSEPVYWQPEENGTGFWAVTRHADVVAVSRDSVTFSSAVGTTQIDDFDEQTRAKQAAMLVNLDPPDHTRLRQLVSRGFTPRTVKVLEGHIRDICTRIVDRLLEARDVDFVPEAAAPLPLEVIAALLGAPPGDVDRLYDWSNRMIGFDDPEYGTTQADGELAAAEIFLYANELAAQRRIEPRDDIVTKLVQPDENGDTLTEMEFNMFFVLLVVAGNETTRNATAGGMQAFIDHPDQWRRLQSEPDLASSAVEEILRWVTPVMDFRRTATRDAYIGDQLVRAGDKVVIYYPSANRDEAVFDEPYRFDIGRSPNPQIAFGGSGVHFCLGAHLARLELRILFETLAARIDRVESTGPVARLRSNFISGIKTMPVRIHPRSPV

>CYP125C1 Rhodococcus sp. RHA1 Rha04272

MTLSALHTDLGSPDAYIHGVPHQVFAELRRHEPVAWIEEPAGEGFAGGPGFWAVTRYDDVMTVSKKPDVFSSHKGASFLRDQSPQDLAALQQMMLNLDPPDHSQMRSIVSKVFTPKMVRGMFDSIADHARAIVDALPDDGEIDLVEHVSAEMPLRVLADVLGVPSEDRHLLYDWTNRMVGLDDPSYGGREAFLSAFIEMFEYSAAQTRAKRTEPGSDVWSLIVNAEVDGTQLSPEELNRFFQLLVIAGNETTRNLLTGAILTLGEHPGEREKLADDPALLPNAIEEVLRFHSPVIQFRRTVTRSTELGGKQMHEGQKVVIFYVSANRDEAQFDDPDTFRIDRGAANHLAFGAGTHFCLGNSLARLEAKVLLEALFTRFPHWQVTGPPDRFRSNFIHGIKKLPVHLGKATS

>CYP125D1 Rhodococcus sp. RHA1 Rha05286

VQLADVDLYNPDTFAKGVPHEMFAVLRREAPVYRHLDERGDPFWCVTRHADIVTVNRDAETYSSWRGATYIDDLSPDDLAGQQLMMLNMDPPDHTALRKIVSKGFTPRRIGQLHEILARRATTIVDAVIERGECDFVVDVASELPLQAIADFLGVPQEDRKLIFDLTNQMIGSSDPEFHLEDGQERAAAAQMFAYSLEMFEDRKKHPRDDIATALIQADVHGEKLGELDFNMFFMLLAVAGNETTRNAISHTQLALMEHPEERRKVLEDPSKLDALIEEGLRWATPVMQFRRTATTDTVLHDVEISEGDRVVIWHMSGNRDEAVFDDPYTFDIDRPTGHYSQHIAFGGGGHHFCLGANLARAEMKVMLSEILRRMPDMEQTAPAQRLRSNFINGLKHMPVTFTPSSL

>CYP125E1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_7184

MTPQTVDILD PDLYLAGAPH DRFELLRREA PVHWHPEPAG RGFWAITRHA DVARISRDPA

AFCSGRGLFI EDLPPGDMRD NPDVMIMMDP PRHARFRALV SKGFTPRVIQ RLESHVRELV

TRLIDDACER GGCDFASDIA GKLPLSVILE VIGVPREDQE QMLDWTTRFF GASDPAYGVT

PEELNAVLHN MNAYAHQLAE QRRKEPKDDM LSLLMAAEVD GEKLSYTEFG GFFNLLLTAG

HDTTKNLISN GMLALLEHPD QRRRLLDDPS LLPTAIEEML RFTPPVYYFR RSAVRDIELH

GQRIAAGDKV VLWYVSANRD ETVFSDPHRF DVGRTPNEHL SFGIGPHVCL GLVLARLEAR

VAFEELLRRL PDLELAGPAV RLRSNWVSGV KSMPVRCARP AR

>CYP125F1 Mycobacterium avium subsp. paratuberculosis str.

MRTPVTVGQHRHPFGRDIYVGRSGYVTEDAISIGGVNLADPDTY

RAGMPYGAFRKLRERAPVAWHPQKDGSGFWALTGYEEIHAVSRDSATWSSQINGAMFD

APPPGEVPPVMIFMDPPQHTALRKLINKGFTPRQVTRLNEHIVEMAKQIVDDVIERGE

CEFADDVAGALPSYVIAEMLGIPLEDGRRLYQITEILHTGSVGDSDDERQQAMVEMFQ

YGVELAVRKRAEPGDDIATSLLHAEVDGQSLSDLEFNLFFMLLIDAGGDTTRNLVAAG

ILALLEHPQELQRLKADPSLMPTAIEEMLRYTSPVTAFLRTATKDTELRGVPVKAGER

VAMFYPSGNRDDSHFADPDRLDVGRAPNPHLAFGGGGTHFCLGANLARVEASAMVPEV

LSRMNDLELAGPVERLRSDLINGIRSMPVRFTPGKRLGTA

>CYP125F2 Mycobacterium vanbaalenii PYR-1

MATDAISIGGVDLADPDTYVGGMPHGAFRELRRHAPVAWHPYGDNPGFWALTGYDEVLAVSRDSRTWSSQ TTGVFLDVPAPEDSYQLSLMMLTMDPPRHTALRALVSRGFTPRHLARLNARTADMARDILDAALQRGECE FVDDVAGALPSYVIAELLGIPLDDGRRLYALTEIMNTRPLHDPELMQTQVELFGYAGDLAASKRAAPGDD IATALLHAEVDGQRLTDLEFNLFFMLLLNAGGDTTRNLVAAGTLALIEHPEQWARLAADPSLMPTAIEEM LRWTSPVNVFTRTATRDTEVGGVPLRAGERVAMFYPSANRDEKHFADPDRFDIGRAPNHHLAFGGGGTHF CLGASLARVEATAIFGEILTRTAHIELAGPVERVRSVLMNGIRSMPVRLTPASVPA

>CYP125F3 Mycobacterium flavescens PYR-GCK

MQDRVDHPEY EVRRHEQNCG AQPLGEGHLV AQESAQVAEH AHYVNDYSRL CLQYRGANQT

GRSTVRPMPA DAITLGGADL ADPDTYLAGM PYDAFRTLRR EAPVAWHPQV DKPGFWALTG

YDEIYAVSRD SETWSSQATG VFLDVPAPED SYQLALMMLT MDPPRHTALR ALVSRGFTPR

HVARLGARTA DMARAIVDDA LAHGQCEFVD EVAGALPSYV IAELLGIPLE DGRRLYTLTD

IMNTRPLHDP ELVAAQMQMF EYAAELAARK RSEPGDDIAT ALLHAEVDGR RLTDLEFNLF

FLLLINAGGD TTRNLVAAGT LALIEHPDQW RRLAADPSLM PTAVEEMLRW TSPVTVFSRT

ATRDTDVGGI RLREGERVAM FYPSANRDEK HFADPDRFDI GRMPNPHLAF GGGGTHFCLG

ASLARVEAAA IFRELITRTR EIGLVGPVER VRSVLMNGIR SMPAQFTPAV VPA

>CYP125G1 Salinispora tropica (marine actinomycete)

MSTEVVSTGNRADIAHPATYAAGVPYAEFARLRRDKPVSWVPEAALWRRSGEGRILSQGP

GFWAVTTHEGVVAASRQPEVFSSGRQGAFLADPRTTADLEQARQLLVNMDAPQHARVRKL

VTAVFTPRAIRALGDSVTAHARNLVERAVRQEECDVVADLAAELPLLVLADLLGLPREDR

HLLYQWSNNLVGFDDPEYGGGDVEAYRKTFFEAFQYALSVAGERRRAPREDLMTLLATSE

VDGRRLTDREFCNFWLLLVVAGNETTRHLITGSVLALVDNPMQRERLVADDTLLPSAVDE

LLRWVSPIMQFRRTAIVDTELCGTPIAAGDKVVLWYTSANRDAAVFEAPDELRLHRNPNP

HLSFGMGPHFCLGAHLARLEARTMLRELAPHLSRFRLTGPVVRLESNFVNGVKSLPGSFT

GQ

>CYP126A1 Mycobacterium tuberculosis

MTTAAGLSGIDLTDLDNFADGFPHHLFAIHRREAPVYWHRPTEH

TPDGEGFWSVATYAETLEVLRDPVTYSSVTGGQRRFGGTVLQDLPVAGQVLNMMDDPR

HTRIRRLVSSGLTPRMIRRVEDDLRRRARGLLDGVEPGAPFDFVVEIAAELPMQMICI

LLGVPETDRHWLFEAVEPGFDFRGSRRATMPRLNVEDAGSRLYTYALELIAGKRAEPA

DDMLSVVANATIDDPDAPALSDAELYLFFHLLFSAGAETTRNSIAGGLLALAENPDQL

QTLRSDFELLPTAIEEIVRWTSPSPSKRRTASRAVSLGGQPIEAGQKVVVWEGSANRD

PSVFDRADEFDITRKPNPHLGFGQGVHYCLGANLARLELRVLFEELLSRFGSVRVVEP

AEWTRSNRHTGIRHLVVELRGG

>CYP126A1 Mycobacterium bovis subsp. bovis AF2122/97,

MTTAAGLSGIDLTDLDNFADGFPHHLFAIHRREAPVYWHRPTEH

TPDGEGFWSVATYAETLEVLRDPVTYSSVTGGQRRFGGTVLQDLPVAGQVLNMMDDPR

HTRIRRLVSSGLTPRMIRRVEDDLRRRARGLLDGVEPGAPFDFVVEIAAELPMQMICI

LLGVPETDRHWLFEAVEPGFDFRGSRRATMPRLNVEDAGSRLYTYALELIAGKRAEPA

DDMLSVVANATIDDPDAPALSDAELYLFFHLLFSAGAETTRNSIAGGLLALAENPDQL

QTLRSDFELLPTAIEEIVRWTSPSPSKRRTASRAVSLGGQPIEAGQKVVVWEGSANRD

PSVFDRADEFDITRKPNPHLGFGQGVHYCLGANLARLELRVLFEELLSRFGSVRVVEP

AEWTRSNRHTGIRHLVVELRGG

>CYP126A2 Mycobacterium smegmatis

MRADLTDLDNFADGFPHALFEAHRREAPVYWHEPTEHTPDGEGFWSVATY

AETLAVLRDPVTFSSVTGGSRPYGGTLLQDLAIAGQVLNMMDDPRHAQIR

RLVSSGLTPRMIARVEEDLRVRARRLLDAVEPGVPLDFLVEVAAELPMQM

ICILLGVPESERHWLFHAIEPQFDFSGSRTASVGQLTPEEAGNRMYRYGM

ELIAAKRAAPTDDMLSVVANAHDAELSDLELYLFFSLLFSAGAETTRNAV

AGGLLALIEHPSQMALLRADLALLPTAVEEMVRWTSPSPSKRRTATRDVE

LGGCRIAAGDKVQIWEGSANRDPLVFTDPDVFDITRKPNPHLGFGQGVHY

CLGANLARLELRVLFEELLSRFSAARLVKPVEWTRSNRHTGIRHLVVEFDA

>CYP126A3 Mycobacterium marinum MM4915

MTSAGVLSKI DFTDLDNFAD GFPHALFAIH RREAPVYWHE PTDNTPDGEG FWSVATYPET

LEVLRDPVTY SSVTGGQRPF GGTLLQDLAI AGQVLNMMDD PRHAQIRRLV SSGLTPRMIR

RVEDDLRART RRLLDAVVPG EPFDFLVDVA AELPMQMICI LLGVPESERH WLFEAIEPQF

DFGGSRKAAV SQLSVAQTAE EAASRMYSYG QELIASKRAA PTDDMLSVVA NAMVDGGDEP

ALSDLELYLF FSLLFSAGAE TTRNAVAGGL LALAEHPEQL RALRGDLDLL PTAVEEMVRW

TSPSPSKRRT ATRDVTLAGC SIEAGQKVQI WEGSANRDAR IFDHADEFDI TRKPNPHLGF

GQGVHYCLGA NLARLELRVL FEELLGRFGA VLVGQPVEWT RSNRHTGIRH LVVELFGG\*

>CYP126A3 Mycobacterium ulcerans

VTSAGVLSKIDFTDLDNFADGFPHALFAIHRREAPVYWHEPTDNTPDGEGFWSVATYPET

LEVLRDPVTYSSVTGGQRPFGGTLLQDLAIAGQVLNMMDDPRHAQIRRLVSSGLTPRMIR

RVEDDLRARTRRLLDAVVPGEPFDFLVDVAAELPMQMICILLGVPESERHWLFEAIEPQF

DFGGSRKAAVSQLSVAQTAEEAASRMYSYGQDLIASKRAAPTDDMLSVVANAMVDGGDEP

ALSDLELYLFFSLLFSAGAETTRNAVAGGLLALAEHPEQLRALRGDLDLLPTAVEEMVRW

TSPSPSKRRTATRDVTLAGCSIEAGQKVQIWEGSANRDARIFDHADEFDITRKPNPHLGF

GQGVHYCLGANLARLELRVLFEELLGRFGVVLVGQPVEWTRSNRHTGIRHLVVELFGG

>CYP126A4 Mycobacterium vanbaalenii PYR-1

MRVAGALAAVDFTDLDNFAAGFPHGLFALHREQAPVYWHEPTENTPDGEGFWSVATHAETLAVFRDPETY SSVTGGERAFGGTLLQDLPIAGQLLNMMDDPRHSAVRRLVSSGLTPRMIRRVEDDLRERARRLLDEVEPG TPVDFLTDIAAEVPMQMICILLGVPESERHWLFEAIEPSFDFGGARKASITRLSVEEAGSRMFEYGQELI AAKRAQPGDDMLSVVVNSGDPQLSDLESYLFFNLLFSAGAETTRNAIAGGLLALIENPDAYRALRADPGL LPTAIEEMIRWTSPSPSKRRTATRRATLGGHTIEAGQKVLVWEGSANRDAAVFASPDHFDITRKPNPHLG FGQGVHYCLGANLARLELRVIFEEILRRHPAAHLARPVEWTRSNRHTGIRHLVVEFASR

>CYP126A5P Mycobacterium leprae

DRSLIPSAIEEGSRSETPNWASVTRITIA\*LAIGGKTILPNAGVDILMGSANRDGSRWTE 363

364 PNTFDIHWPRQAHTTLAGSHMCLGIGLAQLDTRVMLNNLFD 486

>CYP126B1 Saccharopolyspora erythraea NRRL23338

VTVDQPELPTSRNASESVSDQLPAVLGGFDLTDQVRFSGGFPHEVFNRLRADEPILLHPP

GRTRDGESFWVLSRYEDVVEAAANPVFSSQGGGSREGGGTHLDDLPAGTYAGGMLNMMDD

PRHQLIKDIVSPAVCPSAVAALEPVVRERASALVSTVLERGTCDLQAEVAGRYSVEVVAA

LLGVPRQDWSRLVDWAEIAMGYEDRDEGEATGRSQAALLDMYKYGCELVRAKRAEPAGDF

MSLIATGEIPEGHGQAPLVDYEREVFFNLISLAGTEPTRNAIAIGLLALVEHPEQWQALR

ADRSLLDGAVEEALRWSSPTPYNRRTATEDIRFRDVLIREGDKVTLWWASANRDERVFAD

PFRFDVRRSPNPHLAFGHGAHTCLGPALARMELRVLLEELLDRVERIELTGPVPWARNSK

HTVALRVPVALTASS

>CYP127A1 Rhizobium sp.

MSDLRRKRVKTNPIPDHVPPALVRHFSLFTSPGMAPTPNGDPHA

AVACVHDDGPPIFYSPSNTRDGRGTWVITRARDQRRVLEDTETFSSHRSIFASALGEH

WPVIPLELDPPAHGVFRALLNPLFSSRRVLALEPTIHARAGALIDCIAKEKTSCDVMK

DFALPFTFSVFLSFLGLSQRRSEVLVGWVSDLLHGNAEKRRAAARSVVAFIDEMAAMR

RKSPAVDFMTFVVQAKIEGRSLTEEEVRGIGVLFLVAGLDTVAAAIGFDMAYLARNPK

HQELLRNEPARLGLAAEELLRAYSTVQIIRVATKDIEFEGVPIREGDYVSCPAMIANR

DPSEFKCPNTIDLARQDNQHTAFGYGPHLCHGAHLARREIVIGLREWLARIPAFRIKE

GTAPITHGGHVFGISNIILTWA

>CYP127A2 Rhizobium sp. BR816

MILRRNHVALKPVPDHVPPEMVRDFSLFTSPGMQRMPNGDPHAA

VARVHGGPPIFYSPDNTRDSRGTWVITRAKDQRRVLQDSESFSSHRSIFASALGENWP

MIPLELDPPAHGVFRSLLNPLFSPKRVMALEPAIRQRAMALIDRICASRTSCDVMSDF

AFPFAVNIFLRFLGLSDERLDTYVGWGKDLLHGDSVKRTAAALAIVAFIDELAAMRRK

EPTDDVMTFVVETEVDGRRLTDEEVRGIGVLVFVAGLDTVATAIGFDLAHLARNPNDQ

ALLRGEPDRIVPAVEELLRAYSTVQIIRVARKNIDFEGAPIRKGDYISCATMIANRDP

AEFECPNTIDLAREDNRHTAFAYGPHRCLGSHLARREIVIGLEEWLSRIPDFRIKEGT

APITFGGHVFGIENLILDWS

>CYP127A3v1 Mesorhizobium loti

1 MAINPVPDHV PPEMVRDFSL FTSPGMPPTP NGDPHAAVAC AHDGPPIFYS PYNTQDGRGT

61 WVITRAADQR KVLQDTETFS SHRSIFSSIL GETWPTIPLE LDPPAHGAFR SLLSPLLSPK

121 RVTALEPAVR ERAIALIDRI TASATSCDVM KDFAFPFTVS IFLRFLGLPD QGLDTFVGWA

181 KDLLHGDDVE RPVAARKIVA FIDELATNRR KDPVDDLMTF IVQAQIEGRR LTDGEIRGIG

241 VLVFVAGLDT VAAAIGFDLA YLARNLKDQE LLRSEPARIL LATEELLRAY PPIQLIRVAT

301 KDIDFEGAPI RKGDYVSCAT MIANRDPEEF ESPNTVDLAR DHNRHAAFGY GPHRCLGSHL

361 ARREIVIGLE EWLARIPTFR IKEGTAPITC GGHVFGIENL ILDWS

>CYP127A3v2 Mesorhizobium loti

GenEMBL AL672114 complement(100678..101895)

Strain R7A symbiosis island

Gene = msi332

2 DIFFS with CYP127A3v1

>CYP127A4 Rhizobium etli symbiotic plasmid p42d

MHLCSERIYRKRGTRENPMSTGRAGEASKKFRLRPTKQRGFRAA

RRSDRCIACHWRLALLRLEIWRSTILLAPSPRRIRSRRRGFDDRRKAVATIRVPEHVP

PEMVKDFSLFTSPGMERMPNGDPHAAVACLHNGPRIFYSPCNTRDGRGTWVIVRAQDQ

RKLLQDTGTFSSHRSLFASALGENWPLIPLELDPPAHSVFRSLLNPLLSPRRIMELEP

AVRDRAIALISKISASSTSCDILTDFAFPFAVSIFLRLLGLSDERLNTFVGWGKDLLH

GDGIRRTAAARTILAFIDELAAMRRKEPADDFMTFVVQAKVDGRLLRDQEIHGIGVLL

FVAGLDTVATAIGFDLAYLARNPTEQELLRSKPDRIVLAAEELLRAYSTVQMIRVATK

DINFEGAPIRKGDYISCATMIANRDPVEFENPNTIDLAREDNRHTAFAYGPHRCLGSH

LARREIIIGLEEWLSRIPDFRIKDGTAPITYGGHVFGMENLILDWS

>CYP128A1 Mycobacterium tuberculosis

MTATQSPPEPAPDRVRLAGCPLAGTPDVGLTAQDATTALGVPTR

RRASSGGIPVATSMWRDAQTVRTYGPAVAKALALRVAGKARSRLTGRHCRKFMQLTDF

DPFDPAIAADPYPHYRELLAGERVQYNPKRDVYILSRYADVREAARNHDTLSSARGVT

FSRGWLPFLPTSDPPAHTRMRKQLAPGMARGALETWRPMVDQLARELVGGLLTQTPAD

VVSTVAAPMPMRAITSVLGVDGPDEAAFCRLSNQAVRITDVALSASGLISLVQGFAGF

RRLRALFTHRRDNGLLRECTVLGKLATHAEQGRLSDDELFFFAVLLLVAGYESTAHMI

STLFLTLADYPDQLTLLAQQPDLIPSAIEEHLRFISPIQNICRTTRVDYSVGQAVIPA

GSLVLLAWGAANRDPRQYEDPDVFRADRNPVGHLAFGSGIHLCPGTQLARMEGQAILR

EIVANIDRIEVVEPPTWTTNANLRGLTRLRVAVTPRVAP

>CYP128A1 Mycobacterium bovis subsp. bovis AF2122/97,

MTATQSPPEPAPDRVRLAGCPLAGTPDVGLTAQDATTALGVPTR

RRASSGGIPVATSMWRDAQTVRTYGPAVAKALALRVAGKARSRLTGRHCRKFMQLTDF

DPFDPAIAADPYPHYRELLAGERVQYNPKRDVYILSRYADVREAARNHDTLSSARGVT

FSRGWLPFLPTSDPPAHTRMRKQLAPGMARGALETWRPMVDQLARELVGGLLTQTPAD

VVSTVAAPMPMRAITSVLGVDGPDEAAFCRLSNQAVRITDVALSASGLISLVQGFAGF

RRLRALFTHRRDNGLLRECTVLGKLATHAEQGRLSDDELFFFAVLLLVAGYESTAHMI

STLFLTLADYPDQLTLLAQQPDLIPSAIEEHLRFISPIQNICRTTRVDYSVGQAVIPA

GSLVLLAWGAANRDPRQYEDPDVFRADRNPVGHLAFGSGIHLCPGTQLARMEGQAILR

EIVANIDRIEVVEPPTWTTNANLRGLTRLRVAVTPRVAP

>CYP129A1 Steptomyces sp.

MSGEAPRVAVDPFSCPMMTMQRKPEVHDAFREAGPVVEVNAPAG

GPAWVITDDALAREVLADPRFVKDPDLAPTAWRGVDDGLDIPVPELRPFTLIAVDGED

HRRLRRIHAPAFNPRRLAERTDRIAAIADRLLTELADSSDRSGEPAELIGGFAYHFPL

LVICELLGVPVTDPAMAREAVGVLKALGLGGPQSAGGDGTDPAGDVPDTSALESLLLE

AVHAARRKDTRTMTRVLYERAQAEFGSVSDDQLVYMITGLIFAGHDTTGSFLGFLLAE

VLAGRLAADADGDAISRFVEEALRHHPPVPYTLWRFAATEVVIRGVRLPRGAPVLVDI

EGTNTDGRHHDAPHAFHPDRPSRRRLTFGDGPHYCIGEQLAQLESRTMIGVLRSRFPQ

ARLAVPYEELRWCRKGAQTARLTDLPVWLR

>CYP129A2 Streptomyces peucetius

MAVDPFACPMMTMQRKPEVHDAFREAGPVVEVNAPAGGPAWVIT

DDALAREVLADPRFVKDPDLAPAAWRGVDDGLDIPVPELRPFTLIAVDGEAHRRLRRI

HAPAFNPRRLAERTDRIAAIAGRLLTELADASGRSGKPAELIGGFAYHFPLLVICELL

GVPVTDPAMAREAVSVLKALGLGGPQSGGGDGTDPAGGVPDTSALESLLLEAVHSARR

NDTPTMTRVLYERAQAEFGSVSDDQLVYMITGLIFAGHDTTGSFLGFLLAEVLAGRLA

ADADEDAVSRFVEEALRYHPPVPYTLWRFAATEVTIGGVRLPRGAPVLVDIEGTNTDG

RHHDAPHAFHPDRPSWRRLTFGDGPHYCIGEQLAQLESRTMIGVLRSRFPEARLAVPY

DELRWCRKGAQTARLTELPVWLR

>CYP130A1 Mycobacterium tuberculosis

MTSVMSHEFQLATAETWPNPWPMYRALRDHDPVHHVVPPQRPEY

DYYVLSRHADVWSAARDHQTFSSAQGLTVNYGELEMIGLHDTPPMVMQDPPVHTEFRK

LVSRGFTPRQVETVEPTVRKFVVERLEKLRANGGGDIVTELFKPLPSMVVAHYLGVPE

EDWTQFDGWTQAIVAANAVDGATTGALDAVGSMMAYFTGLIERRRTEPADDAISHLVA

AGVGADGDTAGTLSILAFTFTMVTGGNDTVTGMLGGSMPLLHRRPDQRRLLLDDPEGI

PDAVEELLRLTSPVQGLARTTTRDVTIGDTTIPAGRRVLLLYGSANRDERQYGPDAAE

LDVTRCPRNILTFSHGAHHCLGAAAARMQCRVALTELLARCPDFEVAESRIVWSGGSY

VRRPLSVPFRVTS

>CYP130A1X Mycobacterium bovis subsp. bovis AF2122/97,

NC\_002945 complete genome

CYP130 lies in a deletion in M. bovis

>CYP130A2 Mycobacterium smegmatis

MSHPAVAFELANADTWADPWDMYTALRDHDPVHHVVPPERPHHDYF

VLSRHADIWAAARDHETYSSAQGLTVNYGELELIGLADNPPFVMQDPPTH

TEFRKLVSRGFTPRQVEAVEPQVREFVVERLERLRAEGGGDIVAELFKPL

PSMVVAHYLGVPEADRAQFDGWTEAIVAANSEAGSALGAGDAVMSMTGYF

AELIERRRREPGDDTISHLVAAGADDEAVDVLSILAFTFTMVTGGNDTTT

GMLGGAVQLLQQHPDQRRVLTDDPDLIPDAVDEFLRLTSPVQGLARTATR

DVTIGDTTIPAGRKVLLLYGSGNRDEREFGPDAAQLDVRRRPRNILTFSH

GAHFCLGAAAARMQSRVALTELLTRCPDFTVDLDAVVWAGGSYVRRPLSV

PFRAGA

>CYP130A3 Rhodococcus sp. RHA1 Rha08652

MGNVSHYRYMTAHVSSVSFVPRSGQSWRAPWQMYAGLRDHDPVHHVVPEDAPGNDYWVLSRHADVYAAARDPETFSSAAGLTTTYGELEKIGLQDNPPLVMLDPPDHTAFRRLVSKGFTPRQVTAVEPNVRAFVVERIERLREAGAGDVVKELFKPLPSMVVAHYLGVPDEDRAQFDGWTEAIVAANAQGDTLQATGAVTELMGYFTGLIERRRTDPGDDTISHLVAGGMGADGDITGLLSILGFAFTMVTGGNDTTTGMLGGAVQLLTEHRDQRRDLIEHPELVRDAVEELLRLTAPVQGLARTVTRDVEIEGTVVPEGRKVLLLYGSANRDPRRFGPDAEVLDVRRSPKQILTFSHGAHHCLGAAAARMQARIALEELLARCPDFTVDIDAVVYADGNYVRRPTSVPFRVREA

>CYP130A4 Mycobacterium marinum MM4184

MSVDVSHRAP VAFQLATAAT WPDPWPMYRA LRDQDPVHHV IPAHQPDQDY YVLSRHADVW

AAARDHQTFS SAQGLTVNYG DLEMIGLQDN PPMVMQDPPA HTEFRKLVSR GFTPRQVEAV

EPKVRDFVVE RIERLRAQGG GDIVTELFKP LPSMVVAHYL GVPEQDRTQF DGWTQAIVAA

NTAEGGIAGA LATVGDAVGS MMAYFTSLIE RRRAKPEDDT ISHLVAAGVG ADGDIAGTLS

ILAFTFTMVT GGNDTVTGML GGSMPLLHRR PDQRRLLTDN PELITDAVEE LLRLTSPVQG

LARTVTHDVT IGNVTIPAGR RALLLYGSAN RDERQYGPDA GELDVRRCPR NILTFSHGAH

HCLGAAAARM QSRVALTELL ARCPDFEVDE SRIVWSGGSY VRRPLSLPFE VRS\*

>CYP130A4P Mycobacterium ulcerans

MSHRAPVAFQLATAATWPDPWPMYRALRDQDPVHHVIPTHQPDQDYYVLSRHADVWAAAR

DHQTFSSAQGLTVNYGDLEMIGLQDNPPMVMQDPPAHTEFRKLVSRGFTPRQVEAVEPKV

RDFVVERIERLRAQGAATSSPTCSSPCRRWWSHTISGYPNRTGHSSMGGPRPSSRPTPPR

AASRARWPRSAMWSGR\*LSSMVVAHYLGVPEQDRAQFDGWTQAIVAANTAEGGIAGALAT

VGDVVGSMMAYFTSLIERRRAKPEDDTISHLVAAGVGADGDIAGTLSILAFTFTMITGGN

DTVTGMFGGSMPLLHRRPDQRRLLTDNPELITDAVEELLRLTSPVRGLARTVTHDVTIGN

VTIPAGRRALLLYGSANRDERQYGPDAGELDVRRCPRNILTFSHGAHHCLGAAAARMQSR

VALTELLARCPDFEVDESRIVWSGGSYVRRPLSLPFEVRS

>CYP130A5 Mycobacterium vanbaalenii PYR-1

MTAVLSHGSPVHFALADASTWADPWPMYRALRDHDPVHHVVPEDRPNHDYYVLSRHADIWAAARDHQTFS SALGLTVNYGELDLIGLADNPPMVMQDPPVHTEFRKLVARGFTPRQVEAVEPKVHDFVVDRIEHLRANGG GDIVAELFKPLPSMVVAHYLGVPDEDRGKFDGWTDAIVAANTSAGGLGGALDTLGDALGEMMSYFTALIE RRRTEPEDDTISHLVAAGVGADGDISGVLSILAFTFTMVTGGNDTTTGMLGGSVQLLHRRPDQRTMLAEN PDLIPDAVDEFLRLTSPVQMLGRTVTHDVTIGDVTIPEGRRVMFLYGSGNRDERQYGDDAGELDVTRKPR NILTFSHGAHHCLGAAAARMQSRVALTELLTRIPDFEVDESGIAWAGGSYVRRPVSVPFTVTH

>CYP130A6P Mycobacterium leprae strain TN

VMSHRFRFTTADIWPNPWSMYRTLRDHEAVHHVVPANQPEDDYYVLPRHADVWSMAMRS

HAKLSSAQRLTVNYSDMELIGLQDNPPMVMQDQPV\*TKCRKLVSRRFTPRQTNVVEPKVR

HFVVEHIEQLRAKGSVDIVTELFKPLPPMVVAHYFGFPEKVRSQFDGW

TTAADGGGALFRFPRKSPITIRRLAPAIVAANTADAGGITNELDVAGYAVESMLAYFTR

IATGGNNTVTGMLGG\*MPL

SHRRKQHRHWHARRLDAVKDTAEAD

LLRLTSSVRGLMRTTTRDVAIGHTTVSPGRRVLMRYGQAKRDER\*YSAAAS\*LDVTW\*

PPNILIFSHGAH

YLGAKVTRMQRR

VRLTELLARYPDFEVDESSIAWAGGKLHTTP

>CYP131A1 Streptomyces peucetius

MPTPTSAPPAAPTDSELGRHLLTVRGFHFVFGALGDPYARRLRG

EADHLSLGELVRDRGPLHGSALGTWVTADGGISARLLDDPLLGPRHPASEGPQEHVLE

NVWETWRTCHVTPLGEDLLTPAAADSDRLAALLGPVLGPRTCTAWQVDAGRAVHRVLD

GLPPHFDVVSDLARPAIAGSLAAVLGLPDEARAELPDLLAACGPVLDSALCPPRLPVA

RAMTQALRRVRELMAAAVANHLTAPADGAVSALLAVDPGGGRDPGDTVTAAVLSTVVG

AETAITTVANAVMALLKHDEQWSLLRADPGRAADAVEETLRWAPPVTLRSLITQGEVQ

IGGETLEADQHVVVLVDAAQRDPALYEDPDRFRLDRPRSPGFTHMALAGRDHLGLVAP

LVRVQCTAVLRALAERLPGLRAEGEPLRRGRSPVVRAPLSLRLAQK

>CYP131A2 Streptomyces sp.

MTMPTPTSAPPAAPTNSELGRHLLTVRGFHFVFGALGDPYARRL

RGEADHLSLGELVRDRGPLHRSALGTWVTADGETSAGLLDDPLLGPRHPASEGLQ

>CYP132A1 Mycobacterium tuberculosis

MATATTQRPLKGPAKRMSTWTMTREAITIGFDAGDGFLGRLRGS

DITRFRCAGRRFVSISHPDYVDHVLHEARLKYVKSDEYGPIRATAGLNLLTDEGDSWA

RHRGALNSTFARRHLRGLVGLMIDPIADVTAARVPGAQFDMHQSMVETTLRVVANALF

SQDFGPLVQSMHDLATRGLRRAEKLERLGLWGLMPRTVYDTLIWCIYSGVHLPPPLRE

MQEITLTLDRAINSVIDRRLAEPTNSADLLNVLLSADGGIWPRQRVRDEALTFMLAGH

ETTANAMSWFWYLMALNPQARDHMLTELDDVLGMRRPTADDLGKLAWTTACLQESQRY

FSSVWIIAREAVDDDIIDGHRIRRGTTVVIPIHHIHHDPRWWPDPDRFDPGRFLRCPT

DRPRCAYLPFGGGRRICIGQSFALMEMVLMAAIMSQHFTFDLAPGYHVELEATLTLRP

KHGVHVIGRRR

>CYP132A1 Mycobacterium bovis subsp. bovis AF2122/97,

NC\_002945 complete genome complement(1566263..1567648)

Gene = CYP132 1 aa diff

locus\_tag = Mb1429c

>CYP133A1 Erwinia herbicola

MQLHELMDPDYSDNPFPLYRKLHQQGPLIPAGDKIIISGSHAVVDALLNDRRVGKNYMESVRVRFGDDAAGLPLFQGISRMFLVLNPPDHNRL

>CYP133B1v1 Xylella fastidiosa 9a5c

1 MKLTDLSNPA FLENPYPLYE TLRAQAPFVS IGPNALMTGR YSLVDSLLHN RNMGKKYMES

61 MRVRYGDSAA DMPLFQAFSR MFITINPPAH THLRGLVMQA FTGRESESMR PLAIDTAHQL

121 IDNFEQKPSV DLVAEFAFPF PMQIICKMMD VDIGDAVTLG IAVSKIAKVF DPSPMSADEL

181 VHASTAYEEL AQYFTKLIEL RRTHPGTDLI SMFLRAEEDG EKLTHDEIVS NVIMLLIAGY

241 ETTSNMIGNA LIALHRHPEQ LALLKSDLSL MPQAVSECLR YDGSVQFTMR AAMDDIEVEG

301 ELVPRGTVVF LMLGAANRDP AQFTHPDQLD ITRKQGRLQS FGAGIHHCLG YRLALIELEC

361 ALTTLFERLP HLRLAHLDAL NWNQRSNLRG VNTLIVDLHA KN

>CYP133B1v2 Xylella fastidiosa Temecula1

1 MKLTDLSNPA FLENPYPLYE TLRAQAPFVS IGPNALMTGR YSLVDSLLHN RNMGKKYIES

61 IRLRYGDTAA DMPLFQAFSR MFITINPPAH THLRGLVMQA FTGRESESMR PLAIDTAHQL

121 IDNFEQKPSV DLVAEFAFPF PMQIICKMMD VDIGDAVTLG MAVSKIAKVL DPSPMSADEL

181 VHASTAYEEL AQYFTKLIEL RRTHPGTDLI SMFLRAEEDG EKLTHDEIVS NVIMLLIAGY

241 ETTSNMIGNA LIALHRHPEQ LALLKSDLSL MPQAVSECLR YDGSVQFTMR AAMDDIEVEG

301 ELVPRGTVVF LMLGAANRDP AQFTHPDQLD ITRKQGRLQS FGAGIHHCLG YRLALIELEC

361 ALTTLFERLP HLRLAHLDAL NWNQRSNLRG VNTLIVDLHA KN

>CYP133B1v3 Xylella fastidiosa Dixon

MKLTDLSNPAILENPYPLYETLRAQAPFVSIGPNALMTGRYSLV

DSLLHNRNMGKNYMESMRVRYGDSAADMPLFQAFNRMFITINPPAHTHLRGLVMQAFT

GRESESMRPLVIDTAHQLIDNFEQKPSVDLVAEFAFPFPMQIICKMMDVDIGDAVTLG

MAVSKIAKVFDPSPMSADELVHASTAYEELAQYFTKLIELRRTHPGTDLISMFLRAEE

DGEKLTHDEIVSNVIMLLIAGYETTSNMIGNALIALHRHPEQLTLLKSDLSLMPQAVS

ECLRYDGSVQFTMRAAMDDIEVEGELVPRGTVVFLMLGAANRDPAQFTHPDQLDITRK

QGRLQSFGAGIHHCLGYRLALIELECALTALFERLPHLRLAHLDALNWNQRSNLRGVN

TLIVDLHAKN

>CYP133B2v1 Xylella fastidiosa, section 33 of 22

AE003887 CDS 6723..7925

82% to AE003889 48% to CYP133A1

>CYP133B2v2 Xylella fastidiosa Ann-1

MKLADLSSPAFLENPYPLYETLRRQGPFVSIGPNALMTGRYSIV

DGLLHNRNMGKSYMESIRVRYGDDALDMPLFQGFNRMFLMLNPPVHTHLRGLVMQAFT

GRESESMRPLATDTAHRLIDDFEQKSSVDLVTEFSFPLPMRIICRMMDVDISDAISLS

VAVSNIAKVFDPAPMSPDELVHASAAYEELAHYFTRLIELRRAQPGTDLISMLLRAEE

EGQKLTHDEIVSNVILLLLSGYETASNMIGNALIALHRHPKQLARLKSDLSLMPQTVL

ECLRYDGSVQFTVRAAMDDVSIEGDVVPRGTIVFLMLGAANRDPAQFTDPDHLEITRK

QGRLQSFGAGVHHCLGYRLALVELECALTVLLERLPHLRLANLDTLSWNQRGNLRGVN

ALIADLHP

>CYP133B2v3 Xylella fastidiosa Dixon

MKLADLSSPAFLENPYPLYETLRRQGPFVSIGPNALMTGRYSIV

DGLLHNRNMGKSYMESIRVRYGDDALDMPLFQGFNRMFLMLNPPVHTHLRGLVMQAFT

GRESESMRPLAIDTAHRLIDDFEQKSSVDLVTEFSFPLPMRIICRMMHVDISDAISLS

VAVSNLAKVLDPAPMSPDELVHASAAYEELAHYFTRLIELRRAQPGTDLISMLLRAEE

EGQKLTHDEIVSNVILLLLGGYETTSNMIGNALIALHRHPKQLARLKSDLSLMPQAVL

ECLRYDGSVQFTIRAAIDDVSIEGDVVPRGTIVFLMLGAANRDPVQFTDPDHLEITRK

QGRLQSFGAGVHHCLGYRLALVELECALTVLLERLPHLRLANLDTLSWNQRGNLRGVN

ALIADLHP

>CYP133B3 Xanthomonas axonopodis pv. citri str. 306

1 MLLSDLATPQ FRHDPYPTYA RLREEGPLVQ VADGRLMSGR YAVVDRLLSD RRVGRDYLQS

61 VRLRYGEAAV HLPLFQGMSR MFLLLNPPLH TQLRGLMTQA FGARQMESMR EVASDIAAGL

121 IDAFQANGHC DLLTEFAFPL PIAIICRMLD IAAADVTALS HATSALAKVF DPMMTAEELQ

181 ATSVAYDQLA TYFHGVIAQR RSAGGDDLIA RFIQAEDNGR RLSEEEIVSN VILLFFAGHE

241 TTSNMICNAL VALHRHPQQL RLLQETPGLL PNAVLECMRY DSSVQMATRT ALQDFEIEGV

301 AVPRGTMLYL MLGAANHDTL QFTDPQVLDI RRQQGRALSL GGGIHHCLGN RLALIEVEAA

361 LACLLARLPA LRLEQLDTLS WNDRANLRGV DALLASW

>CYP133B4 Xanthomonas campestris pv. Campestris str. ATCC 33913

1 MQLSDFATPA FRQDPYPMYA RLRAAGPLVQ ISDNGWVSGH YTVVDALLSD RRVGRNYLDS

61 IRVRYGANAA EMPLFQGMSR MFLLLNPPVH TQQRALMTKA FGARQLEALR EVAVDTADAL

121 LDQHEDRRSC DLLNDFAMPM TISLICRMLG LAVTDVAALG QASSALAKVF DPLMRPEDMA

181 QATAAYTTLE QYFRAIVLQR RDTQEDDLIA RLIAAEDHGQ RMPVDDIVSN VIMLFTAGHE

241 TTANMICNAL IALHRHPEQL QLLRDTPTLM PNAVLECMRY DSSVQVAMRS VLQPLQVEGT

301 TLPVGAILYL MLGSANHDAE QFTAPQQLDL RRQQGRALSF GGGVHHCLGN RLALIELETA

361 LERLLQRAPA LRLPELDNLS WNERANLRGI QALHATW

>CYP133B5 Ralstonia solanacearum GMI1000 megaplasmid

MKLADLSTPSFLENPYPLYETLRSQGPFVRIGPNALMTGHYSIV

DALLHNRQMGKSYMESIRLRYGDEGPNMPLFQGFSRMFLMLNPPMHTRLRGLMMQVFN

ARQIESMREVATATAHQLIDDFEQKPSADLVAEFAFPLPVRIICQMMDLDIDDAMALG

VGVSKLAKVFDPAPMSADALVETSAAYEELAQYFTKVIEARRAQPGTDLISMLMRAEE

NGETLTHDEIVSNVILLFIAGHETTSNMIGNALIALHRNPQQLDLLKREPSRMPNAVL

ECLRYDGSVQVTIRAALEDVEVEGEVLPRGTTVFLMLGAANRDPAQFTDPDQLDIGRQ

QGRLQTFGAGIHHCLGYRLALIELESALGALFERLPNLRLTNLDQLSWNQRGNLRGVN

ALMAAW

>CYP134A1 Bacillus subtilis

MSQSIKLFSVLSDQFQNNPYAYFSQLREEDPVHYEESIDSYFIS

RYHDVRYILQHPDIFTTKSLVERAEPVMRGPVLAQMHGKEHSAKRRIVVRSFIGDALD

HLSPLIKQNAENLLAPYLERGKSDLVNDFGKTFAVCVTMDMLGLDKRDHEKISEWHSG

VADFITSISQSPEARAHSLWCSEQLSQYLMPVIKERRVNPGSDLISILCTSEYEGMAL

SDKDILALILNVLLAATEPADKTLALMIYHLLNNPEQMNDVLADRSLVPRAIAETLRY

KPPVQLIPRQLSQDTVVGGMEIKKDTIVFCMIGAANRDPEAFEQPDVFNIHREDLGIK

SAFSGAARHLAFGSGIHNCVGAAFAKNEIEIVANIVLDKMRNIRLEEDFCYAESGLYT

RGPVSLLVAFDGA

>CYP134A2P Bacillus cereus ATCC 14579

1 MIGATNCDSN VFERPDKFNV YRPDIDIKKA FSGTARHLAF GLSIYNCVGV AFAKLKIEID

61 STIKDNISRK KLRDIKDFVK KTSKMN

>CYP134B1 Photorhabdus luminescens subsp. laumondii TTO1

MAKLSSFNIHDPKFIKNPYDFYDILHKQDLVYFEQSQNSYFIGK

YEDVDAILKSSIFNTKPLTALAEPVMGDRVLAQMEGEEHACKRKFIMQGLSRDYFNRY

YEPMIRKITEDLLQPYMEKGNIDIVNDFGRDYAVLVTLSILGLPSDNYRDIAEWHKGI

ASFITQFDQTELEKMHSLECSQKLIRLLKPIIDQRRRNPSKDIISIFCQDTAMSMSEI

TALCLNILLAATEPADKILAMMLNHLISNPSMLDVVLKDRSLVRDAFEETLRLTSPVQ

LIPREASEDVTISGIDIPKGAVVFCMIGAANRDPSVFHKPNEFDLYRRKNTTSPQKAN

RKRHLAFGAGTHACAAAAFSLSQLEVSSNIILDLLHNLRFADHYHYQETGVYTRGPSK

LLLSFDPIASSAIKE

>CYP135A1 Mycobacterium tuberculosis

MASTLTTGLPPGPRLPRYLQSVLYLRFREWFLPAMHRKYGDVFS

LRVPPYADNLVVYTRPEHIKEIFAADPRSLHAGEGNHILGFVMGEHSVLMTDEAEHAR

MRSLLMPAFTRAALRGYRDMIASVAREHITRWRPHATINSLDHMNALTLDIILRVVFG

VTDPKVKAELTSRLQQIINIHPAILAGVPYPSLKRMNPWKRFFHNQTKIDEILYREIA

SRRIDSDLTARTDVLSRLLQTKDTPTKPLTDAELRDQLITLLLAGHETTAAALSWTLW

ELAHAPEIQSQVVWAAVGGDDGFLEAVLKEGMRRHTVIASTARKVTAPAEIGGWRLPA

GTVVNTSILLAHASEVSHPKPTEFRPSRFLDGSVAPNTWLPFGGGVRRCLGFGFALTE

GAVILQEIFRRFTITAAGPSKGETPLVRNITTVPKHGAHLRLIPQRRLGGLGDSDPP

>CYP135A1 Mycobacterium bovis subsp. bovis AF2122/97,

NC\_002945 complete genome complement(393726..395075)

Gene = CYP135A1 1 aa diff

locus\_tag = Mb0334c

>CYP135B1 Mycobacterium tuberculosis

MSGTSSMGLPPGPRLSGSVQAVLMLRHGLRFLTACQRRYGSVFT

LHVAGFGHMVYLSDPAAIKTVFAGNPSVFHAGEANSMLAGLLGDSSLLLIDDDVHRDR

RRLMSPPFHRDAVARQAGPIAEIAAANIAGWPMAKAFAVAPKMSEITLEVILRTVIGA

SDPVRLAALRKVMPRLLNVGPWATLALANPSLLNNRLWSRLRRRIEEADALLYAEIAD

RRADPDLAARTDTLAMLVRAADEDGRTMTERELRDQLITLLVAGHDTTATGLSWALER

LTRHPVTLAKAVQAADASAAGDPAGDEYLDAVAKETLRIRPVVYDVGRVLTEAVEVAG

YRLPAGVMVVPAIGLVHASAQLYPDPERFDPDRMVGATLSPTTWLPFGGGNRRCLGAT

FAMVEMRVVLREILRRVELSTTTTSGERPKLKHVIMVPHRGARIRVRATRDVSATSQA

TAQGAGCPAARGGGPSRAVGSQ

>CYP135B1 Mycobacterium bovis subsp. bovis AF2122/97,

NC\_002945 complete genome 660693..662111

Gene = CYP135B1 100% match

locus\_tag = Mb0583

>CYP135B2 Mycobacterium smegmatis

MSTPGTLPPGPPLPAFVQTAMMLRHWSRFVSACRRRYGDVFTLRIASMGT

WVYLADPADIKTVFAGDPTVFHAGEANSMLSGLLGETSVLVIDEDVHRDR

RRLMLAPFARDAVARQTGVMAEVAATNIASWPVGTPFPVAPKMAEIALEV

ILRTVIGATEPARLAALRHVMPQLLGIGPWQSLAIASPGLQRRRPWRTLQ

RNLAEADRLLYAEIAACRAGPDLASRPDALAMLVRAANDEGRTMTDRELR

DQLMTLLVAGHETTATGLSWTLERLIRHPAVLDKAVAAARTTDGSGEAYL

DAVVRESLRIRPVVFEAGRVLTEPVELGGYLLPAGTLVAPSIGLVHASAD

VYPDPDRFEPDRMLASTQAPSTWLPFGGGNRRCLGATFALVEMRVVLREI

LHRVDLFATTARGEKQRLKHVTMIPHRGGRICVRALRDVAPAPMTCPAEA

RRA

>CYP135B3 Mycobacterium marinum MM4483

MKGNAYDVTT MIARTRTALP PGPRLPRSVQ DALLIRHGPR FLAACRRRYG DVFTLRVASI

GTMVYVADPA VIKSVFAGDP NTLHGGAASM LRGLLGDSSL LVVDDRAHRD RRRLMLAPFH

RDVIERQAGL IAEIAAENVT GWPVGTPFAA ATKMSEITLE VILRTVIGTS DAARLAALRA

VMPRLLDLRP WETLALAKPN LLQRGPWRSL HRRIAEADEL LYAEIAEHRT DPGLSGRADT

LAMLIQAAYD DGRTMADGEL RDQLMTLLVA GHDNTAAGLC WALERLTRHP AVLAKAVQAA

DASAAGDPAG NEYLDAVVKE TLRARPVVFD LGRVLRKPIE LAGYLLPEGV MVVPSIGLVH

GSAALYPGPE RFDPDRMLGV ILGPTGWLPF GGGSRRCLGA AFAMAEMRVV LREILRRVEL

CPTTAVDERQ KLKNVILVPH RGGRILVRAM RGVPAPD\*

>CYP135B4 Mycobacterium marinum MM0938

MTKTATLPPG PRLPRAVQAA LMLRHAPRFL TACKRRYGSV FTLRVAGLGT MVNVTDPVVI

KKVFAGDPRV FHAGEANTML AGLLGESSLL VVDDDVHRDR RRMMLPPFQR EAVAHQAQLM

SEIAAENIAG WPVGRTFAVA PKMAEITLEV ILRTVIGATD PDRLAALRKV MPRLLNVGPW

ETLALAKPDL LSRRAWRRLR RAIDEANELL YAEIAERRAD PNLAERTDVL ATLVRAVDGD

TAKPSGRMTD EELRDQLMTL LVAGHDTTAT GLAWALERLT RHPAILAKAV RAAEASAAGD

PSGDEYLDAL AKETLRIRPV VFDVGRILTE PTELAGYQLP AGTMVVASIG LVHANAEVYP

DPDRFDPDRM IDATLTPTTW LPFGGGNRRC LGATFAMVEM RVVLREILRR VDLATTTAPD

ERYKLKHVIL VPHRDARIRV RAITAVSPAV PEAPGCPVAH AKS\*

>CYP135B5 Mycobacterium vanbaalenii PYR-1

MRDPRYGRGRAFYAGVMTPTSLPPGPRLPRSVQAALMLRCGPRFVAACRRRYGSAFTLRVASMGTLVYLT DPADIKTVFAGDPDIYHAGEANSMLKGLLGDTSVLVIDGDLHRDRRRLMLAPFARDAVAAQAGVIAEIAA DNIAGWPVGETFPVAPKMSEITLEVILRTVIGASDQARLAALRTVMPRVLSVGPWETLAIANQDLLRRRP WRAVRDAIAEADRLLYAEIADRRADPDLDTRTDALAMLVRAGDMSDKELRDQLITLLVAGHDTTATALSW ALERLTRHPAVLAKAVRAARDGDDDYLDAVAKETLRDRPVVFDVGRVLKAPVELAGYRLPAGVMVIPGLV AVHADSQIYPHADRFDPDRMLGATLSPSSYLPFGGGNRRCLGATFAMVEFKVVLREILRRVELETTTARG

EHRRLKHVIFVPHRGARIRVRAKRVVAAEAPKCPMSGPA

>CYP135B6 Mycobacterium marinum MM2978

MPHSNSGVLP PGPPLSRSLQ AALMLLRGPQ FLAACRRRYG DVFTLRIARM GTQVYLADPR

DIKTVFTGDT HIFHAGDANA LLSGLIGDSS LMVLDEEAHR CRRRTMLAPF HRDAVARQAG

LMAEIAADNV AGWPAGRTFP VTVRMSEITL EVILRTVIGA TDPARLAALR TAVPRLLSMG

PWGTLALANP KLLSRRPWRG LRKRIADVDN LLYAEITDRR NDAELGKRAD VLAMLIRTEG

NDNAMTDREL RDQLVTLLVA GYDTSATGLA WALERLTRHP TILTRAVAAA HASAAGDAAG

DEYLDAVVKE TLRIRPLAFA VGRVLAAPVE VAGYQLPAGA WALPGIGLVH ASAALYPDPD

RFDPDRMIGV SPGPTTWLPF GGGARRCLGA TFALVEMRVV LREVLRRAEL ITTTAADETP

KLKYVTLIPS RGARISVRTI KNIPPASPVG AEKPATTPGC PATENVGATR PAF\*

>CYP136A1 Mycobacterium tuberculosis

MATIHPPAYLLDQAKRRFTPSFNNFPGMSLVEHMLLNTKFPEKK

LAEPPPGSGLKPVVGDAGLPILGHMIEMLRGGPDYLMFLYKTKGPVVFGDSAVLPGVA

ALGPDAAQVIYSNRNKDYSQQGWVPVIGPFFHRGLMLLDFEEHMFHRRIMQEAFVRSR

LAGYLEQMDRVVSRVVADDWVVNDARFLVYPAMKALTLDIASMVFMGHEPGTDHELVT

KVNKAFTITTRAGNAVIRTSVPPFTWWRGLRARELLENYFTARVKERREASGNDLLTV

LCQTEDDDGNRFSDADIVNHMIFLMMAAHDTSTSTATTMAYQLAAHPEWQQRCRDESD

RHGDGPLDIESLEQLESLDLVMNESIRLVTPVQWAMRQTVRDTELLGYYLPKGTNVIA

YPGMNHRLPEIWTDPLTFDPERFTEPRNEHKRHRYAFTPFGGGVHKCIGMVFDQLEIK

TILHRLLRRYRLELSRPDYQPRWDYSAMPIPMDGMPIVLRPR

>CYP136A1 Mycobacterium bovis subsp. bovis AF2122/97,

NC\_002945 complete genome 3376038..3377516

Gene = CYP136 1 aa diff

locus\_tag = Mb3085

>CYP136A1 Mycobacterium marinum MM1634

MATISTPAYL LDQAQRRLTP SFNNFPGMGM VERWLLKTQF PETTLADPPP GSDLKPVVGD

AGLPILGHLI EMLRGGPDYL MFLYRTKGPV VFGDSPVLPA VVALGPDAAQ VIYSNRNKDY

SQQGWVPVIG PFFRRGLMLL DFEEHMFHRR IMQEAFVRSR LVGYVEHMDE VASRAIAGEW

ATNDARFLLY PAMKKLTLDI ASMVFMGHEP GTDHELVTKV NRAFTTTTRA GNAVIRTSVP

PFTWWRGIRA RQLLENYFAA RVTERRGQEG NDLLTVLCHT ADEDGNRFSD QDIVNHMIFL

MMAAHDTSTS TATTMAYHLA AHPEWQQRCR DESDRLGDGP LDIEALEKLE SLDLVMNESI

RLVTPVQWAM RQTVRDTELL GYYLPKGTNV IAYPGMNHRL PEFWTDPMTF DPDRFAEPRN

EHKRHRYAFT PFGGGAHKCL GMVFGQLEIK TILHRLLRRY RLELARPDYR ACWDYGGMPV

PKDGMPIVLR PL\*

>CYP136A1 Mycobacterium ulcerans

VATISTPAYLLDQAQRRLTPSFNNFPGMGMVERWLLKTQFPETTLADPPPGSDLKPVVGD

AGLPILGHLIEMLRGGPDYLMFLYRTKGPVVFGDSPVLSAVVALGPDAAQVIYSNRNKDY

SQQGWVPVIGPFFRRGLMLLDFEEHMFHRRIMQQAFVRPRLVGYVEHMDEVASRAIAGEW

ATNDARFLLYPAMKKLTLDIASMVFMGHEPGTDHELVTKVNRAFTTTTRAGNAVIRTSVP

PFTWWRGIRARQLLENYFAARVTERRGQEGNDLLTVLCHTADEDGNRFSDQDIVNHMIFL

MMAAHDTSTSTATTMAYHLAAHPEWQQRCRDESDRLGDGPLDIEALEKLESLDLVMNESI

RLVTPVQWAMRQTVRDTELLGYYLPKGTNVIAYPGMNHRLPEFWTDPMTFDPDRFAEPRN

EHKRHRYAFTPFGGGAHKCLGMVFGQLEIKTILHRLLRRYRLELARPDYRACWDYGGMPV

PKDGMPIVLRPL

>CYP136A1 Mycobacterium smegmatis

MPTTISTPRYLLDQARRRFTPTPNTIPGMGAIEKRLKRKQWDQFVFSTPP

AGSGLKPIMGDSGLPVLGHMIEIFRGGPDFILEQYRRNGPIHYAYSPALS

SVMALGPDATQTVFSNRNKDYSQRAWDPVIGPFFEGGLMLLDFDEHMYHR

RIMQDAFTRSRLTGYIPHIDSVASQVLANDWVSDDPRFLFYPAIKELTLD

IASEVFMGVPAGTDKKLVTTVNHAFTTTTRAGNAIVRTPVPPLKWWRGIQ

ARKTLEDYFLSRIDEKRRAESTDMFSVLCHSADEDGQTFTDDQIVSHMIF

LMMAAHDTSTSTMTTMAYHLAANPEWQDRLRDESERIGDGPLDIEALEKL

ETYDLVINEALRMMTPLPFNFRQAVRDTELLGYFIPAGTNVVTWPSINHR

LPELWTDPEKFDPERFAEPRSEHKKHRYAFAPFGGGAHKCIGMVFGQLEI

KTVMHRLLRQYRLELPRPGYTPRYDYGGMPVPIDGMPIVLRPLR

>CYP136A1 Mycobacterium vanbaalenii PYR-1

MPSISTTDYVLDQAKRRLKPTPVTIPGMGAVEKRLKDKHWDQFVLAEPPAGSDLKPILGDAGLPIIGHMI EIFRGGPDFILEIYRKHGPVYFAESPALSSVMALGPDATQAVFSNRNKDFSQRAWDPVIGPFFEGGLMLL DFDEHMFHRRIMQEAFTRSRLTGYVSHIDSVASAVLANDWVANDPRFLFHPAIKELTLDIASEVFMGVPA GTDRALVTTVNQAFTTTTRAGNAIVRKPVPPLTWWRGIKARKTLEDYFSSRIGEKRRSESTDMFSVLCHS ADEDGQSFTDDQIVSHMIFLMMAAHDTSTSTMTTMAYHLAANPEWQDRLREESARIGDGPLDIEALEKLE TYDLVINEALRMMTPLPFNFRQAIRDTDLLGYYIPAGTNVVTWPSINHRLPELWTDPEKFDPERFAEPRS EHKKHRYAFAPFGGGAHKCIGMVFGQLEIKTVVHRLLQNYRLELPRPDYQPRYDYGGMPVPLDGMPIVLR PLH

>CYP136B1 Mycobacterium smegmatis

MTIPAAEAAADAKVRLQTAVAGITARYPSREHALAAPPPGSGLKPV

MGNYGFPILGHVMSTLVEPLAFARERYERYGPVSWAGGVGFRVALLMGPE

ALETVWINKDKAFSSTLGWAPVIGPFFHRGIMLLDFEEHRDHRRIMQQAF

TRSALNGYLDLMRPGIDRTVRSWPAAQRFPFYTSVKHLLLDQAAEVFIGA

ELGPEADQLSRDFHDTVCGGQAVIRADVPGGVWSRGLRARRRLERYFAGQ

LPARRSGEGTDLFSMLCRSRSDEGERFSDTDIVNHMIFLLMAAHDTSAIA

ISMLVYELGRNLRWQNTLRDEALSGPQGEITMEDLDSAYPLLDAAFKESL

RMYAPAGTLFRQTLTATAVAGHFIPRKTQVAIGVYASMRLADWWPEPDEF

DPARFLTGSDATAVQRYAFAPFGGGAHKCIGQQFANMNVKAIMLHLLRHF

RWHVPAGYQPRMTWGTGPTPADGLPITLERLSA

>CYP136B2 Mycobacterium flavescens PYR-GCK

MSALPQSLPG LPAASAKLRF QSAAASVTSR YPSRVRPLSR PPAGSGLKPV LGNYGFPVLG

HHLSTFVEPL EFARERYERF GPVSWAGGIG FRVVQLMGPE ALETAWINRD KAFSSTRGWA

PVIGPFFHRG IMLLDFEEHR DHRRIMQQAF TRSALDGYLT LMRPGISRTV TSWPTAAGFP

FYTAIKKLLL DQAAEVFVGA VLGAEADRLS SDFHDTVCGG QAMIRADVPG GTWARGLRAR

ERLERYFAAQ IPDRRAGTGA DLFSMMCRSR SEDGDSFSDA DIVNHMIFLL MAAHDTSAIA

ISMLVYELGR NLRWQDALRD EADAGDGLGL ADLDGAYPLL DAAFKEILRM YAPAGTLFRQ

TVTDTEVCGH YIPRRTQVAI NVYASLRLAD WWPDPDRFDP GRFLGGGDAA AVHRYAFAPF

GGGVHKCIGQ QFADMNVKLV MHQLLRQFRW RVAPGYRPLM TWGTGPTPAD GLPISLQRLSGG

>CYP136B3 Mycobacterium sp. KMS

MTALTAQLTS PANTHRLQVA GAALTSRFPS REEPLATPPP GSNLKPVMGN YGFPFLGHTL

SALAEPLDFA RRRYDMYGPV SWAGGVGFRV VALMGPDALE TAWINRDKVF SSTRGWAPVI

GPFFHRGIML LDFEEHRDHR RIMQQAFART ALDGYLELMR PGIDRTLGGW PASDAFPFYP

SIKHLLLEQA AEVFVGTHLG PESDQLSADF HDTVRGGQAL LRADVPGGVW ARGLRARKRL

ERYFGDQIAD RQRGDGADLF SMLCRSEDDD GARFTPADIV NHMIFLLMAA HDTTAIALSM

LVYELGRNQK WQKTLRDEAV GRPNDAPAVG DLDAYPLLDA AFKEILRMYA PAGTLFRQTT

RDTDILGHFV PAKTQVAINV HASMRLADWW PDPDTFDPAR FIDQPGARAA VSRYAFAPFG

GGAHKCIGQQ FADMTVKTTM HQMLRRFEWS VADGYRIPLT WGTGPTPADD LPITLRTLTT

>CYP136B4 Nocardia farcinica IFM 10152

MVEITRSVAK GFGMSLQLPT TVSAVSDNAR HLRTRLSWQA QRAGLQVVKR YPTRIRPLAE

PPPGSGLKPV LGDFGPPGIG YTLHTLADPM GFSRERFERL GPVSWLGVLG RPVVSVAGPE

AFEEVLLDRD KVYSAQRGWE WLIGPFFHGG VMLRDFDDHM FHRRILQQAF TRPRLHGYQD

LTSPLLRRGI ESWRPAAEFH IHTAIKQLLL QQATEVFAGA ELGRESVALA HAFEDAVHGG

TAMVRANVPG GVWARGLRGR RRLEDYFRRE LPAKRAGEGN DLFSVLSRAT TEEGHTFTDE

EVVQHMIFVM LAAHDTSTIA SSMLVYELGR HPEWQDKLRA EAIGLGKESV GYDDLDELPL

LDMAFKEALR MYAPVAQQAR ETIADTALCG HYLPRGTLVM CGPYMMMRTA RYWRDPDEFD

PERFAPERRE DKSHRFAWAP FGGGAHKCIG LYFGGMTVKA VLYQMLTRFR WSVRPGYEPL

LVAGTGPTPA DGLPIRLERL AR

>CYP136C1 Rhodococcus sp. RHA1 Rha02367

MPKVLAAPPPQSTLQPISGNAGFPVIGHSLDYFRDPMGLLQSRWDRYGPVSWLSMAGKRWVTVLGPDGCQTVLQNKDRAFVNSDGWSVLIGPFFHRGLMLLDGDEHLAHRRIMQQAFTRDRLSRYTEALHPAVEKGLDGWQPTAGFAAYPALKELTLDLATSIFMGGAEGSTPREMAEINRAFIDCVQAATSVIRYPLLGTRWKRGIDGRARLEEFFRRYLPARRAGAGEDLFSALCHIESEEGQRFSDDDVVNHMIFLLMAAHDTSTITLSTMMQYLGQHPDWQERCRRQSAALGTSTPTYDQLDELTDLDLVMKECLRLVPPVPVVARRAVEDTEVLGHYIPRGTYMSVVVHFTHHMPEYWPDPERFDPERFAPERREDKVHRFAWEPFGGGVHKCLGMHFAGAEIKTVMHHLLRRFHWHVSPGYVAPLNYTSLPFPSDGQPVDLYHRVGGADTP

>CYP136C2 Rhodococcus sp. RHA1 Rha06567

MRRELRFVMSKILAVPPAQSQLQPVSGRSGLPGVGHVLEYIRDPLALMQKHWDRYGEVSWFSMVGRRWVAVLGPDACQEVLQNKDRAFVNGDGWSVLIGPFFHGGLMLLDSEEHLRHRRIMQQAFTRSRLENTVDVLNPAIDSALDAWTPTNGFRAYTALKALTLDLATDIFMGGAEGSTESEISSVKKAFVDCVQAATSVVRYPVPGTRWKRGLDGRRVLEDFFRQYLPARRSHETDDLFSVLCHIESEAGQRFSDDEVVDHMIFLLMAAHDTSTITISTMMQYLGQHPQWQDRCRAESLALGTPAPSYADLDGLDSLDLVMKECLRIVSPVPVMARRAVRDTQVQGHFVPAGTYAAVVPHFTHHMPQYWPEPERFDPERFAEHRREDKVHRYAWEPFGGGVHKCLGMHFAGAEIKAIMHHLLLRFDWHVDADYVAPLNFTSLPFPSDGQPVDLRLLATS

>CYP136C3 Frankia sp. CcI3

MAVRGSRGPVPGDGGPPLVGYTLRYLHDPAQHWRQRYDRYGPVSWERTFGLRVVSLLGPDATGLALRNHE

QAFANGPGQQRIAGPFFRRGLSMLDFDEHRHHRRILAGAFAPDRLRGYLAGMNPSIERGVAGWRPGARFQ

VYPAVKQLTLELATRIFMGERLGPEADRFNAALFACIRAPGAVVRVPAPGLRWSRGLAGRRYLEEFLRLR

VPAKRAGSGTDMFSRLCHAEAEDGSRLSDDDVVNHMILMMVAAHDTSTITMTSMSYYLARHPEWQQRCRE

ESLALGTPAVDHADLDRLPSLALVMKEALRLVTPVPILLRATVKDIDVLGVTVPAGTVAALALAFTHQMP

EYWPSPERFDPERFADHRREDKVHPYAWQPFGGGPHTCIGLHFAGQQVKAILHQMLLRYRWSLAPGYRIS

LDRFPLPVPRDGLPVQLEKIT

>CYP136D1 Mycobacterium abscessus

1 MDAVEAAQRP GGTMTNHLLA PAHHVKERLS SVIMVPAPHA VDDRWRRWSR DWPVRELAPA

61 PAGSGLKAVR GDAGLPFVGH TLDYIRFGSD FSRERYDRLG SVSWMGAFGT KMVVIAGPDA

121 TREAFTSEAK AFSQDGWSFL IDAFFHRGLM LMSFDEHLMH RRIMQEAFTR PRLTGYVEQV

181 TPCVRSAVPA WPVGPSVRIY PLLKELTLDI ATDVFMGGRG KDESDAVNKA FVATVRAASS

241 LVRAPLPGTR FRAGVQGRRV LEDYFFRHLP AARAGETEDL FAALCQATTE DGERFSDEDV

301 VNHMIFLMMA AHDTSTITTT AVTYFLAKYP QWQEAAAAEA AAIGDGLPDI EALEKMTVID

361 RVIKEALRLL APVPLVMRKT VRDVAIDGYH IPSNTLCAIT PAVNHFDRTI WNDPERFDPS

421 RFDEPRREDQ HHRFAWVPFG GGAHKCIGMQ FGTLEVKAIL HRMLRSFTWK VPENYHVRWD

481 NTSLPIPVDG LPLEMKRR

>CYP136D2 Mycobacterium marinum MM3135 OR 3315 (TYPO)

MANQLLAITR HPKERLTSVL LAPAPRVVDD KWRQWSRDWR VRELAPAPAG SGLRAVLGDA

GLPLLGHTVD YIRFGSEFSR ERYERLGSVS WMGAFGTKMV VIAGPDATRE AFTSEAKAFS

QDGWSFLIDA FFHRGLMLMS FDEHLMHRRI MQEAFTRPRL TGYVGQVAPC VRAAVPAWPT

GPSVRIYPLL KNLTLDIATD VFMGGRGKDE SAAVNEAFVS TVRAASSFVR VPLPGTRFRA

GVHGRRVLED YFSRHLPAAR AGETDDLFAA LCQATTEDGE RFSDEDVINH MIFLMMAAHD

TSTITTTAVT YFLAKHPEWQ EKAAAEARSF GHDSPDIDEL ERMTVLDLIL KEALRLLAPV

PLVMRKTVRD VAIDGYHIPR ETLCAITPAV NHFDRRIWSD PDRFDPSRFD EPRREDQQHR

FAWVPFGGGA HKCIGMQFGT LEVKAILHQM LRTYTWTVPN DYHVRWDNTS LPIPVDGLPV

TLRHR\*

>CYP137A1 Mycobacterium tuberculosis

MVLRSLASPAALTDPKRCASVVGVAAFAVRREHAPDALGGPPGL

PAPRGFRAAFAAAYAVAYLAGGERRMLRLIRRYGPIMTMPILSLGDVAIVSDSALAKE

VFTAPTDVLLGGEGVGPAAAIYGSGSMFVQEEPEHLRRRKLLTPPLHGAALDRYVPII

ENSTRAAMHTWPVDRPFAMLTVARSLMLDVIVKVIFGVDDPEEVRRLGRPFERLLNLG

VSEQLTVRYALRRLGALRVWPARARANTEIDDVVMALIAQRRADPRLGERHDVLSLLV

SARGESGEQLSDSEIRDDLITLVLAGHETTATTLAWAFDLLLHHPDALRRVRAEAVGG

GEAFTTAVINETLRVRPPAPLTARVAAQPLTIGGYRVEAGTRIVVHIIAINRSAEVYE

HPHEFRPERFLGTRPQTYAWVPFGGGVKRCLGANFSMRELITVLHVLLREGEFTAVDD

EPERIVRRSIMLVPRRGTRVRFRPAR

>CYP137A1 Mycobacterium bovis subsp. bovis AF2122/97,

NC\_002945 complete genome complement(4064642..4066072)

Gene = CYP137 1 aa diff

locus\_tag = Mb3710c

>CYP137A2 Mycobacterium marinum MM5175

MPASAPSART PPALRRPPGL PAPRRLRTVF AAAYAVAYLV GGERRMLRLI RRYGPIMTMP

ILSLGDVAIV SDPALVKEVF TAPPDVLLGG EGVGPAAAIY GAGSMFVQEE PEHLRRRKLL

TPPLHGTALG RYVPIIEEST RAAMRDWPVD RPFELLGAAR ALMLDVIVKV IFGVDDPDEV

RRLGRPFERL LDLGVSEQLT VRYALRRAGA LRVWPQRARA YREIEDVVMP LIAQRRSDLG

RTEQRDILGL LISARGDDGE QLSDQEIRDD LITLMLAGHE TTATTLAWVF DLLLHHPDAL

RRVQEEAEGG TETFTTAVIN ETLRVRPPAP FTARVAARPF RLGGYLIDPG TRIVVHMIAI

NRNPDVYEQP NRFRPERFLG TRPQTYAWVP FGGGAKRCLG AAFSMRELVT VLHVLLREGQ

FTAVDEAPER IVRRSIMLAP RHGTRVRFRP RLQESV\*

>CYP137A2P Mycobacterium ulcerans

VPASAPSARTPPALRRPPGLPAPRRLRTVFAAAYAVAYGWWRAANAAIDPALRADHDDAH

PEPGRRGDRLGPGTGQRSLHRAARRAPGW\*MLRLIRRYGPIMTMPILSLGDVAIVSDPAL

VKEVFTAPPDVLLGGEGVGPAAAIYGAGSMFVQEEPEHLRRRKLLTPPLHGTALGRYVPI

IEESTRAAMRDWPVDRPFELLGAARALMLDVIVKVIFGVDDPDEVRRLGRPFERLLDLGV

SEQLTVRYALRRAGALRVWPQRARAYREIEDVVMPLIAQRRSDLGRTEQRDILGLLISAR

GDDGEQLSDQEIRDDLITLMLAGHETTATTLAWVFDLLLHHPDALRRVQEEAEGGTETFT

TAVINETLRVRPPAPFTARVAARPFRLGGYLIDPGTRIVVHMIAINRNPDVYEQPNRFRP

ERFLGTRPQTYAWVPFGGGAKRCLGAAFSMRELVTVLHVLLREGQFTAVDEAPERIVRRS

IMLAPRHGTRVRFRPRLQESF

>CYP137A3 Mycobacterium vanbaalenii PYR-1

MAEHSPHESYRCEMVHIVRPPSLPAPPPLAPVFGGLYAAAFGMGGQAIVAQMVRRYGPVVALPVLGFGKV VAVADAALAKQVFTENPDVLLGGEGVGPAAAIYGPRSMFVLEEPGHLRRRRLLTPPLHGELLGSYVPIIE SSTRSAMATWPVGRPMRMLDAARELTLDVIVQVVFGVHDPESVARFGKPFHELLDLALSEETPVRYALRR FGALRRWGRLSDANRRIDELVLPLIAERRSDPLSAERADILSMLANSHTDDGETLSDNEIRDDLITLVLA GHETTATTLSWLIDLLLHHPRALARVRAEAVSGDTGYTEAVIAETLRLRPAAPITGRMTTGPYRLGDYTL EPDTRIVLLLDVINRNPDTYPQPDEFRPERFLGSRPHPYAWIPFGGGVKRCIGAAFAMRELTTTLHTVLR EGELEPVSARPETPPLRAAPVLVPRDGTRVRFTPARPAASPRCADRTSTV

>CYP138A1 Mycobacterium tuberculosis

MSEVVTAAPAPPVVRLPPAVRGPKLFQGLAFVVSRRRLLGRFVR

RYGKAFTANILMYGRVVVVADPQLARQVFTSSPEELGNIQPNLSRMFGSGSVFALDGD

DHRRRRRLLAPPFHGKSMKNYETIIEEETLRETANWPQGQAFATLPSMMHITLNAILR

AIFGAGGSELDELRRLIPPWVTLGSRLAALPKPKRDYGRLSPWGRLAEWRRQYDTVID

KLIEAERADPNFADRTDVLALMLRSTYDDGSIMSRKDIGDELLTLLAAGHETTAATLG

WAFERLSRHPDVLAALVEEVDNGGHELRQAAILEVQRARTVIDFAARRVNPPVYQLGE

WVIPRGYSIIINIAQIHGDPDVFPQPDRFDPQRYIGSKPSPFAWIPFGGGTRRCVGAA

FANMEMDVVLRTVLRHFTLETTTAAGERSHGRGVAFTPKDGGRVVMRRR

>CYP138A1 Mycobacterium bovis subsp. bovis AF2122/97,

NC\_002945 complete genome 163556..164881

Gene = CYP138 100% match

locus\_tag = Mb0141

>CYP138A2 Mycobacterium smegmatis

66% to CYP138A1

MTATVERPESAIRAAQLPPVLPLPKTVQGLAFSVARRWVVKQAARRYGDV

VTLDIPVFGRTVLVTEPQLAKQVYAAHPDDVGNVQPNLSRMLGPGSVFAL

DGTDHRRRRKLLTPPFHGRSIKNYERIFEEETLREAASWPDGQEFRTLEP

MMRITLNVILRAVFGADGEQLDELRRIIPPWVTLGSRLAVLPTPKRNYGR

LTPWGRLAAYRAEYDDVVDRLIDRVEADPDFDQRDDILALLLRSAYEDGS

SMSRKDIGDELLTLLAAGHETTASTLGWAFERISRHPGVLEKLVAEAATD

DNEYRQAAIAEVQRVRTVIDFSGRHVYAPSFQLGQWTIPRGYSIMVAIAH

IQEREEEFSDPHRFDPQRFVGNRPGLGWLPYGGGTRRCVGAVFANIEMDV

VLRTILRHFVIETTTAPDEKVHPRGVAYTPASGGRVVMRRRREPLGA

>CYP138A3 Mycobacterium marinum MM0346

MNQAISDAPA VPAVKMAQAT RIPKLLQGLA FATSRRRMMD WLSRRNGDVF ALNVPIYGHM

VVVNDPQLAK QVFTASPEDL GNIQPNLSRM FGSGSVFGLD GDDHRRRRRL LAPPFHGKSM

KNYEIIIEQE TLRETANWPE GQLFPTLPSM MRITLNAILR AVFGADGAEL DELRRIIPPW

TTLGSRLASM PKPKRRYGRF SPWGRLAEYR RQYDVIIDRL IDQERSDPNF SDRTDVLALM

LRSTYDDGSR MSRKDIGDEL LALLAAGHET TASTLSWAFE RVTRHPELLA ALVAEAEDAG

GELRQATILE VQRARTVIDF AARHVYAPQY QLGQWMIPRG QSILVNIAQM HANPDIFPDP

QRFDPQRFIG GRPSTFGWIP FGGGTRRCVG AAFANMEMDV VLRTVLRNFT IEPTTAAGER

LFCRGVAYTP KNGGRIVVHR R\*

>CYP138A3P Mycobacterium ulcerans

MNQAISDAPAVPAVKMAQATRIPKLLQGLAFATSRRRMMDWLSRRNGDVFALNVPIYGYM

VVVNDPQLAKQVFTASPEDLGNIQPNLSRMFGSGSVFGLDGDDHRRRRGLLVPPFHGKSM

KNYEIIIEQETLRETANWPEGQLFPTLPSMMRTTLNAILRAVFGADGAELDELRRIIPPW

TTLGSRLASMPKPKRRYGRFSPWGRLAEYRRQYDVIIDRLIDQERSDPNFSIGPTCWP\*V

LALMLRSTYDDGSRMSRKDIGDELLALLAAGHETTASTLSWAFERVTRHPDLLAALVAEA

EDAGGELRQATILEVQRARTVIDFAARHVYAPQYQLGQWMIPRGQSILVNIAQMHANPDI

FPDPQRFDPQRFIGGRPSTFGWIPFGGGTRRCVGAAFANMEMDVVLRTVLRNFTIEPTTA

AGERLFCRGVAYTPKNGGRIVVHRR

>CYP138A4 Mycobacterium marinum MM3976

MTELVAAAAV PPAVRLPPEF RMPKALQAIT YVALRRWLLL RLARRYGKVF SVNLPLYGHI

VVVGDCLLAK QVLATSPEEL GNIEPNLGRL FGPGSIFSLD GEEHRQRRRL LMPLFHGNLM

KSYESIIEDE TLREVANWPE GQSFPAMPAM AQITLGGILR ALFGPECAEL DELRRLVPPW

VTLGLRIALL PRPRRDYGRY SPWARLAEMR HQCEIVIEKL IEAARTGPNL AERTDVLALM

LRSCYDDGSA MSHNDIVDEL LTMMAAGHET TAATLTWAFE RLGRHPDVLA ALVEEADRGG

RALRQATILE VQRTRPAIDR VVRRVCSPYY RLGQWVLPQG YSVHLHIEQV QSDPEIFPDP

ERFDPHRHMG GKPSSLGWIP FGGGTRRCIG AALANLEIDV VLRTVLRNFT IEPNAAPDER

WHNRGIAFTP KDGGQIVVHR RH\*

>CYP138A4P Mycobacterium ulcerans

MTELVAAAAVPPAVRLPPEFRMPKALQAITYVALRRWLLLRLARRYGKVFSVNLPLYGHI

VVVGDSLLAKQVLATSPEELGNMEPNLGRLFGPGSIFSLDGEEHRQRRRLLMPLFHGNLM

KSYESIIEDETLREVANWPEGQSFPAMPAMAQITLGGILRALFGPECAELDELRRLVPPW

VTLGLRIALLPRPRRDYGRYSPWAGLAEMRHQCEIVIKKLIEAARTGPNLAERTDVLALM

LRSCYDDGSAMSHNDIVDEPLTMMAAGHETTAATLTWAFERLGRHPDVLAALVEGGRPGR

SRPPAGDDPGSPADQAGDRSSSSTRLLALLPARSMSSAPRVFGPPSYRTSSIRSRGLSRP

GALRSASPHGGASHRRSDGSHSVAGLAAASGLPVVLRTVLQHFTIQPNAAPDERWHNRG

IAFTPKDGGQIVVHRRH

>CYP138A5 Mycobacterium vanbaalenii PYR-1

MSEATIAAHRSTADAESAPPRPVRLPPTPRIPKLLQGLGFSFSRQWTVAQIVRRYGDVFSMTLPVFGPTV MVADPALAKQLFMANTDDVGNIQPNLSRVLGSGSVFALDGGDHRKRRKLLTPPFHGKSIKNYETIFEEET LREAANWPEGQPFETLEPMMRITLNAILRAVFGADGAHLDELRRIIPPWVTLGSRLAVLPTPHRTYGRFS PWGRLAAYRRQYDDVIGRLIDAVQADPDFDTRDDILALLLRSTYEDGSTMSRQDIGDELLTLLAAGHETT AATLGWAFERISRHPEVLAKLVAEAETDGNEYRQATILEIQRSRTVIDFAGRHVYAPTFELGEWVIPQGY SIVVAIGQVHKRAQDFDDPDRFDPQRYIGQRPPTFAHIPFGGGTRRCVGAAFANVEMDIVLRTVLRHFVI

ETTAAPGEKMHSRGVAYTPKDGGRVVMRRR

>CYP138A6P Mycobacterium leprae

1 NRVAREIVVEVIYGALFGAFEALSGLVPQDTVLGPMGRYSMAPSLIR

439 ITINVIMRAGFGSELDELRRLHPTAATL 522

RWTVERQARCNHDIFMLDSRSTAERLRRRLHGTCMKNH 351

352 VRIFEAEPLWGLRTGLKASLLPHCRLINRITINVIMRAGFGSELDELRRLHPTAA 516

517 TLVGLF\*LLSQHLGVLADPSSMGATMPGDDPAPALRQATIPG

638 LGVQWTRTVIDFAARRVYSSVYHLSEWAIPREDSILISIAQIYXXXXXXXXXXXX 766

795 DPRRYVEHKPSSFAWI 842

PFSGGT 861

862 SRCVSICQDGDGMNVVLKMVLRYWIIDTTTAPGER\*HLRGVVYTPRNGGR 1011

>CYP138B1 Mycobacterium marinum MM4430

MAEATTDPIQ LPPGPNASKL TQTLVYVFAK ARARTRLTNR YGSGYSLNLP KYGPTLVISD

PAMLKELFTS GNDLVTRPTT LGKLLGPGSI LSMIGVEHRQ RRKLMVPPFS GRRIDAYVKI

VEEEFLREAQ TWPEETEFES LQALVNITGS IVLRTILGAH GAIFEELQYL GPRTIVLAAR

MIALPEWLRR DLGPWSPWGK IQAARSRFDE LIAQLIAEAR ADPNFETRTD MLAMMLQARY

DDGSPITDAH ISDEMLTMIV AGHETTATTL AWAVERLRRS PSFVAQLVDE IDNGGTALMQ

ATVWEVQRTR PVLDFIARRV ETQLRLGPWV LPKGHMIVGD VWAAQHASSS FKDPERFDPT

RFADGPPESY AWIPFGGGIH RCIGAAFANM EMTTVLRTLL RKFELVPTDA PAEPIRSRGI

TNAPGHGGRI VVRSRPAGAR AAYASEDGHS AVAQSV\*

>CYP138C1 Mycobacterium vanbaalenii PYR-1

MATATTDPVRLPPGPRIPKLIQGAAVLTQRYGAIAALGRRYGPTFTLNIPVFGETVVISDPVLVKDLFST HRDLVGRPQNNLGGDVLGPGSIFNLEGDALQARRKLLLPPFNGKSMRGYASITEEEAIREIRTWPEGVEF ETLEPMMRITLNTILRAVFGAEGEQLDELRELMPKAVEFGSKIALMPSIVRKDFGPWSPGGKFARYRKRM DELLNGLLNDARSDPNFTERNDVLSLLLQARYDDGSPMPDSFILDELLTMLVAGHETTSTQLAWTIERIR RHPQLLVRLTEEVDAGGNELLLATIAESQRTRPVLTAALRRARTRIRLGEWVIPEGDTILASTQLAMAAE SSFPDADKFNPDRFVGNPPNPFAWIPFGGGMMRCIGASFATMEMEVTLRALLREFTIEPTTEPDEKPHSR

GVTVTPGRNGRLVVHRREHKAARATDSVSVAESS

>CYP138C2 Mycobacterium flavescens PYR-GCK

MATATTDPVR LPPGPRFPKL IQGGAVLAFR YGSVAALGRR YGSTFTLQLP VFGETVVISD

PVLVKDLFST SRELVGRPQN NLGGDVLGPG SIFNLEGDEL LARRKLLLPP FNGKNMRAYE

DITEQEVIRE MQSWPEGVEF ETLEPMMRIT LNTILRAVFG AKGDELDELR VVIPAAVEFG

SKIALLPSVV RKDLGAWSPG GKFARYRRRM DEICTQLIAD ARSDPDFTDR GDVLSLLLQA

RYDNGDPIPD AFVVDELLTM LVAGHETTST QLAWTIERIR RHPDLLARLS DEVDAGGNEL

MAATIAESQR TRPVLTAALR RARTRIRLGE WVIPEGDTIM ASTQLAMAAE QSFPDAEKFN

PDRFVGNPPN PFAWIPFGGG MMRCIGASFA TMEMDVTLRT MLREFRLEPT DEPDEKPHSR

GVTVTPGRGG RAVVRRRRTP ASGDANSVSV AETSR

>CYP139A1 Mycobacterium tuberculosis

mrtyrtvRYPLGEALLALYRWRGPLINAGVGGHGYTYLLGAEANRFVFAN

ADAFSWSQTFESLVPVDGPTALIVSDGADHRRRRSVVAPGLRHHHVQRYVATMVSNID

TVIDGWQPGQRLDIYQELRSAVRRSTAESLFGQRLAVHSDFLGEQLQPLLDLTRRPPQ

VMRLQQRVNSPGWRRAMAARKRIDDLIDAQIADARTAPRPDDHMLTTLISGCSEEGTT

LSDNEIRDSIVSLITAGYETTSGALAWAIYALLTVPGTWESAASEVARVLGGRVPAAD

DLSALTYLNGVVHETLRLYSPGVISARRVLRDLWFDGHRIRAGRLLIFSAYVTHRLPE

IWPEPTEFRPLRWDPNAADYRKPAPHEFIPFSGGLHRCIGAVMATTEMTVILARLVAR

AMLQLPAQRTHRIRAANFAALRPWPGLTVEIRKSAPAQ

>CYP139A1 Mycobacterium bovis subsp. bovis AF2122/97,

NC\_002945 complete genome complement(1877656..1878948)

Gene = CYP139 start codon differs by 6 aa

locus\_tag = Mb1694c

>CYP139A2P Mycobacterium leprae

GAAVATTSMTVILARLASRTRLHLLAHYTHRVRARNFAALIP\*LSLTVEVINSMPTQ

>CYP139A3 Mycobacterium marinum MM2475

MSTYRTVPYR PGEALLALYR RRGAFIDAGV GRHGFVYLLG PEANRFVFAN ADAFSWRETF

ESLVPVDGPT ALIVSDGEDH RRRRSIVAPG LRHRSVQDYV ATMVSTIDNV IDSWRPGQPL

DIYQEFRCAV RRSTTESLFG PRLASHSDYL GRQLQPLIDL THRLPQVMQL QQRLNSPGWR

RAMAARTRID ELIDAEIANA RAEPSPDDRM LTALINGRSE EGCALSDNEI RDSIVSLIAA

GYETTSGALA WATYSLLTLP GAWETAAREV ARVLGGTAPS AETLGALTYL NGVVHETLRL

YSPGVVSARR LIRDLWFDGH RINSGRLLIF SAYVTHRIPE VWPNPTQFLP QRWDPAAPDY

RKPAPHEFIP FSGGLHRCIG AVMATTELVV LLARLVARTR LRLPAQRIRA ANFAALAPKP

GLRVEFVDSV PAQ\*

>CYP139A3P Mycobacterium ulcerans

VPYRPGEALLALYRRRGAFIDAGVGRHGFVYLLGPEANRFVFANADAFSWRETFESLVPV

DGPTALIVSDGEDHRRLCSTVAPGLRHRSVQDYVATMVSTIDNVIDSWRPGQPLDIYQEF

RCAVRRSTTESLFGPRLASHLDYLGRQLQPLIDLTHRLPQVMQLQQRLNSPGWRRAMAAR

TRIDELIDAEIANARAEPSPDDRMLTALINGRSEEGCALSDTRFATPSFRSSRPATRPPA

QRWRGPPTPCSRCPAPGRRRPARLPGCSAAPRPAPRPSALSPTSMALCTKRFGSTHREWS

RRAG\*LRGAPQHDREPVRPTAGLPFGLSGPTTAASDRPDPPVAPGDATTAAAQLTGLAAG

DGRAHPHRRTDRCRNRQRSRGAQPRRPHADRTDQRPFRRRLRVERHEIRDSIVSLIAAGY

ETTSAALAWATYTLLTLPGAWETAAREVARVLGGTAPSAETLGALTYLNGVVHETLRLYS

PGVVSARRLIRDLWFDGHRINSGRLLIFSAYVTHRIPEVWPNPTQFLPQRWDPAAPDYRK

PAPHEFIPFSGGLHRCIGAVMATTELVLLARLVARTRLRLPAQRIRAANFAALAPKPGLR

VEFVDSVPAQ

>CYP140A1 Mycobacterium tuberculosis

MKDKLHWLAMHGVIRGIAAIGIRRGDLQARLIADPAVATDPVPF

YDEVRSHGALVRNRANYLTVDHRLAHDLLRSDDFRVVSFGENLPPPLRWLERRTRGDQ

LHPLREPSLLAVEPPDHTRYRKTVSAVFTSRAVSALRDLVEQTAINLLDRFAEQPGIV

DVVGRYCSQLPIVVISEILGVPEHDRPRVLEFGELAAPSLDIGIPWRQYLRVQQGIRG

FDCWLEGHLQQLRHAPGDDLMSQLIQIAESGDNETQLDETELRAIAGLVLVAGFETTV

NLLGNGIRMLLDTPEHLATLRQHPELWPNTVEEILRLDSPVQLTARVACRDVEVAGVR

IKRGEVVVIYLAAANRDPAVFPDPHRFDIERPNAGRHLAFSTGRHFCLGAALARAEGE

VGLRTFFDRFPDVRAAGAGSRRDTRVLRGWSTLPVTLGPARSMVSP

>CYP140A1 Mycobacterium bovis subsp. bovis AF2122/97,

MKDKLHWLAMHGVIRGIAAIGIRRGDLQARLIADPAVATDPVPF

YDEVRSHGALVRNRANYLTVDHRLAHDLLRSDDFRVVSFGENLPPPLRWLERRTRGDQ

LHPLREPSLLAVEPPDHTRYRKTVSAVFTSRAVSALRDLVEQTAINLLDRFAEQPGIV

DVVGRYCSQLPIVVISEILGVPEHDRPRVLEFGELAAPSLDIGIPWRQYLRVQQGIRG

FDCWLEGHLQQLRHAPGDDLMSQLIQIAESGDNETQLDETELRAIAGLVLVAGFETTV

NLLGNGIRMLLDTPEHLATLRQHPELWPNTVEEILRLDSPVQLTARVACRDVEVAGVR

IKRGEVVVIYLAAANRDPAVFPDPHRFDIERPNAGRHLAFSTGRHFCLGAALARAEGE

VGLRTFFDRFPDVRAAGAGSRRDTRVLRGWSTLPVTLGPARSMVSP

>CYP140A2 Mycobacterium smegmatis

MRERLRWMALHGFVRSMATLGLRRGDPQARLIADPVVRADPTTFADQMRKQGPVIRG

RVVLLTFDHAVAFDLLRSDDFQVSQLGANLPKPLRWIADKTNPGLLHPIE

PPSLLSIEPPDHTRMRKLVSSVFTTRAVATLRERVEQTAHELLDGLEAES

GVVDIVERYCAQLPVAVIGDILGVPEPDRPNILRYGELGAPSLDIGLSWS

QYQQVNEGIIGFETWLNRHLRTLRRDPGDDLLSQIITASESGATGEPLTD

RELKALAGLVLAAGFETTVNLLGNGIRMLLDHREHLETLAARPDVWPNAV

EEILRLDSPVQMTARAAVRDVDVAGTAVGRGELVVLHIAGANRDPKVFDD

PHRFDIERDNAGRHLSFSGGRHFCLGAALARAEGEVGLRAFFDRFPDARL

AGDPVRRDTRVLRGWSTLPIALGKARAAVGS

>CYP140A3P Mycobacterium leprae TN

VRQRLHWFAQYGFIRGIAATHH

RRSDPLARLDIALAIKANPVP

YCHKPRPRRPLVQSRISYLTANRAITHELLQSEDFHVFWLNVTLPAPSHWL

RRRTGYRTSSQYNL

LHPLLAIQ\*AYHIHYRKTVSPLFAPKAVATLRDRIEQTTLALLDQLAHQHDVVDVVNRY

CSQLPVAVISDILGYP

VPDRDRSHILKFGELVAPSLDVELT\*Q\*YQQA\*REVAGFNFWL

LKHLPQLQRTPGDNLVRHLSH\*EDNKPTEISLSKSKLQAISG

GLVLATGGETTVNLLGRGI

LLLDTPEHMVMLQACPEPGHKRG\*EILRLDSPIQMAARVARKDVDLAGSTIKRSQVVVLY

FGRSQPGPVRLCRSR\*VQHRTPQCGKESRIFR\*QEFCLENALTRAYNAVGLRAFFDHLP\*

TRAAGTRSRLDTRVLRGWSTLPIALGPTRSMVS

>CYP140A4 Mycobacterium avium subsp. paratuberculosis

GAAARQSRPVGPRRSRRSCDRQPGPDDRAHAPPATSTSAPAMVG

LVPRRARNRDPKVFSDPTTFDVTRPNAREHLAFASGIHACLGAALARIEGATCARSFE

NFPDRSSRARNGGR

>CYP140A5 Mycobacterium marinum MM2768

MKDKLHWFAM HGVIRGMANI GLRRGELEAR LIADPAVAAN PGPFHDELRR HGRMVRTRVN

YLTVDYQLAH DVLRSDDFHT ISFGENLPGP LRWLERRTRD EQLHPLRPPS LLAVEPPDHT

RYRKTVSAVF TSRAVAALRD RVEQTANSLL DQLAQRPGVV DVVGQYCSQL PIMVISEILG

VPEQDRGRVL EYGELAAPSL DIGVPYRQYR RIQQGITGFN SWLTAHLEQL RRNPGDDLMS

QLIRVAESGD AGTYLDESEL RAVAGLVLVA GFETTVNLLG NGIRMLLDAP EQLETLRQRP

ELWPNAVEEI LRLDSPVQLT ARVARTDVEI ASWPINRGEM VVAYLAGANR DPAVFPNPHR

FDVERANAGR HLAFSTGRHF CLGAALARAE GEVGLRTFFE RFPDVRAAGA GSRRDTRVLR

GWSTLPVTLG PARALAAS\*

>CYP140A5 Mycobacterium ulcerans

VKDKLHWFAMHGVIRGMANIGLRRGELEARLIADPAVAANPGPFHDELRRHGRMVRTRVN

YLTVDYQLAHDVLRSDDFHTISFGENLPGPLRWLERRTRDEQLHPLRPPSLLAVEPPDHT

RYRKTVSAVFTSRAVAALRDRVEQTANSLLDQLAQRPGVVDVVGQYCSQLPIMVISEILG

VPEQDRGRVLEYGELAAPSLDIGVTYRQYRRIQQGITGFNSWLTAHLEQLRRNPGDDLMS

QLIRVAESGDAGTYLDKSELRAIAGLVLVAGFETTVNLLGNGIRMLLDAPEQLETLRQRP

ELWPNAVEEILRLDSPVQLTARVARTDVEIASWPINRGEMVVAYLAGANRDPAVFPNPHR

FDVERANAGRHLAFSTGRHFCLGAALARAEGEVGLRTFFERFPDVRAAGAGSRRDTRVLR

GWSTLPVTLGPARALAAS

>CYP140A6 Mycobacterium vanbaalenii PYR-1

MAADLQQRIRWLALHGVIRGLSKVAVRRGQDPQARLIADPAVRADPAAFADELRGRGPVIRCRAVLMTVD HQVVNEILRSDDFRVSSLGAGLPKPLQWINRKTHPGLLHPIEPPSLLSIEPPDHTRCRKLVSSVFTTRAV AALRERVQQTANDLLDDLERESGVVDIVERYCSQLPVAVISDILGVPERDRRHILHFGELGAPSLDIGLS WRQYTQVHEGLVGFNEWLGGHMDELRRNPGDDLMSQLIQASQAADEGSRLTDRELQATAGLVLAAGFETT VNLLGNGIRMLLETPGHLETLAARPELWPNAVEEILRLDSPVQMSARFARRDVTVGGTEIKRGELVILHL AGANRDPEVFTDPHRFDIERDNAGRHLSFSGGRHFCLGAALARAEGEVGLRTFFERYPDARLAGQGSRRD TRVLRGWSTLPITLGTARAALGS

>CYP140A7 Mycobacterium ulcerans

MVMANPAPFCDELRAIGPVVSSYGTHLV

VSHAIAHELLRSEDFEVVSLGSNLPAPMRWLERRTRDDTPHLLLPPSLLAVEPPNHTRYR

KAVSSVFTPKAVAGLRDHVEETASALLDQLTDQASAVDIIARYCSQLPVAVICDILGVPS

RDRNRVLKFGQLAGPCLDFGLTWRQHQQVRQGLQGLHFWITEHLEELRSNPGDDLMSQMI

HASENGSSETHLHATEVRMIGLVLGASFATTMDLLGNGIQVLLDAPELRDALSQRPQLWP

NAVEEILRLEPPVQLAGRMARKDTEVAGTAIKRGQLVAIYLGAVNRDPSVFADPHRFDIT

RANANRHLAFSGGRHFCLGAALARVEGEVGLRMLFERFPDVRAAGPGNRRDTRTLRGWSQ

LPVQLGAARSMAIR\*

>CYP140B1 Mycobacterium vanbaalenii PYR-1

MGQHAGRQAGPGGAGRPVGRSGARRSGGGQPWAARAAGRRRAQVGAGAGPGSGRAAHGRHLRRPSPRQPD RRMRSRPAVWLRWATVHGVPRAFLTVRARRGEPLARLILGRGDRLALIEEIRAAGPLMRTPVVWATADYD VCRTVLRDNDFGVADPSETGLPDALLGLIRRVDPGLPNPVEPPAMLMTDPPQHTEYRKLVSRSFTPRSIA ALDTRIGELTAELLDDLGRRREVDLIADYAAQLPAAVISRMLGVPDEDRARILGWGETGAALLDIGIGWR PFRAAIDGLVDVDTHLGAHFRRLHQNGADGTPFSSLALDGSLSGRELISNAALLVGAGVETTVNLIGNGI AALLDHPDQLALLRDDPGLWPSAVEEILRYDSPVQMTARTAHRDTEIAGVGIRKGAVIVMLLGGANRDPK VFDRPQTFDITRANARDHLAFASGIHVCLGAALARIEGATALRELFTRYPDLHLTAPAEPRDLVTLHGYR HLPVRLGRAATATRRAS

>CYP141A1 Mycobacterium tuberculosis

MTSTSIPTFPFDRPVPTEPSPMLSELRNSCPVAPIELPSGHTAW

LVTRFDDVKGVLSDKRFSCRAAAHPSSPPFVPFVQLCPSLLSIDGPQHTAARRLLAQG

LNPGFIARMRPVVQQIVDNALDDLAAAEPPVDFQEIVSVPIGEQLMAKLLGVEPKTVH

ELAAHVDAAMSVCEIGDEEVSRRWSALCTMVIDILHRKLAEPGDDLLSTIAQANRQQS

TMTDEQVVGMLLTVVIGGVDTPIAVITNGLASLLHHRDQYERLVEDPGRVARAVEEIV

RFNPATEIEHLRVVTEDVVIAGTALSAGSPAFTSITSANRDSDQFLDPDEFDVERNPN

EHIAFGYGPHACPASAYSRMCLTTFFTSLTQRFPQLQLARPFEDLERRGKGLHSVGIK

ELLVTWPT

>CYP141A1P Mycobacterium bovis subsp. bovis AF2122/97,

IAFGYGPHACPASAYSRMCLTTFFTSLTQRFPQLQLARPFEDLERRGKGLHSVGIKELLVTWPT\*

>CYP142A1 Mycobacterium tuberculosis

MTEAPDVDLADGNFYASREARAAYRWMRANQPVFRDRNGLAAAS

TYQAVIDAERQPELFSNAGGIRPDQPALPMMIDMDDPAHLLRRKLVNAGFTRKRVKDK

EASIAALCDTLIDAVCERGECDFVRDLAAPLPMAVIGDMLGVRPEQRDMFLRWSDDLV

TFLSSHVSQEDFQITMDAFAAYNDFTRATIAARRADPTDDLVSVLVSSEVDGERLSDD

ELVMETLLILIGGDETTRHTLSGGTEQLLRNRDQWDLLQRDPSLLPGAIEEMLRWTAP

VKNMCRVLTADTEFHGTALCAGEKMMLLFESANFDEAVFCEPEKFDVQRNPNSHLAFG

FGTHFCLGNQLARLELSLMTERVLRRLPDLRLVADDSVLPLRPANFVSGLESMPVVFT

PSPPLG

>CYP142A1aP Mycobacterium bovis subsp. bovis AF2122/97,

NC\_002945 complete genome complement(3898119..3898736)

gene = CYP142A1a aa 1-197 100%

locus\_tag = Mb3548c

In Mycobacterium bovis, a frameshift due to a single base

deletion (c-\*) splits CYP142 into 2 parts (pseudogene)

>CYP142A1bP Mycobacterium bovis subsp. bovis AF2122/97,

NC\_002945 complete genome complement(3897541..3898122)

gene = CYP142A1b aa 207-end 100%

locus\_tag = Mb3547c

In Mycobacterium bovis, a frameshift due to a single base

deletion (c-\*) splits CYP142 into 2 parts (pseudogene)

>CYP142A2 Mycobacterium smegmatis

MTQMLTRPDVDLVNGMFYADGGAREAYRWMRANEPVFRDRNGLAAATTYQ

AVLDAERNPELFSSTGGIRPDQPGMPYMIDMDDPQHLLRRKLVNAGFTRK

RVMDKVDSIGRLCDTLIDAVCERGECDFVRDIAAPLPMAVIGDMLGVLPT

ERDMLLKWSDDLVCGLSSHVDEAAIQKLMDTFAAYTEFTKDVITKRRAEP

TDDLFSVLVNSEVEGQRMSDDEIVFETLLILIGGDETTRHTLSGGTEQLL

RHRDQWDALVADVDLLPGAIEEMLRWTSPVKNMCRTLTADTVFHGTELRA

GEKIMLMFESANFDESVFGDPDNFRIDRNPNSHVAFGFGTHFCLGNQLAR

LELRLMTERVLRRLPDLRLADDAPVPLRPANFVSGPESMPVVFTPSAPVLA

>CYP142A3 Mycobacterium marinum MM5003

MTKPLIKPDV DLTDGNFYAS RQAREAYRWM RANQPVFRDR NGLAAASTYQ AVIDAERQPE

LFSNAGGIRP DQDALPMMID MDDPAHLLRR KLVNAGFTRK RVKDKERSIA QLCDTLIDAV

CERGECDFVR DLAAPLPMAV IGDMLGVLPE QREMFLRWSD DLVTFLSSHV SQEDFQVTID

AFAAYNDFTR ATIAARRAEP TDDLVSVLVS SEVDGERLSD DELVMETLLI LIGGDETTRH

TLSGGSEQLL RNRDQWDLLQ SDRELLPGAI EEMLRWTAPV KNMCRMLTAD TEFHGTALSE

GEKIMLLFES ANFDEAVFTD PEKFDIQRNP NSHLAFGFGT HFCMGNQLAR LELSLMTARV

VQRLPDLRLA DQDSRLPLRP ANFVSGLESM PVVFTPSRPL S\*

>CYP142A3 Mycobacterium ulcerans

MAMTKPLIKPDVDLTDGNFYASRQAREAYRWMRANQPVFRDRNGLAAASTYQAVIDAERQ

PELFSNAGGIRPDQDALPMMIDMDDPAHLWRRKLVNAGFTRKRVKDKEHSIAQLCDTLID

AVCERGECDFVRDLAAPLPMAVIGDMLGVLPEQREMFLRWSDDLVTFLSSQVSQEDFQVT

IDAFAAYNDFTRATIAARRAEPTDDLVSVLVSSEVDGERLSDDELVMETLLILIGGDETT

RHTLSGGSEQLLRNRVQWDLLQSDRELLPGAIEEMLRWTAPVKNMCRMLTADTEFHGTAL

SKGEKIMLLFESANFDEAVFTDPEKFDIQRNPNSHLAFGFGTHFCMGNQLARLELSLMTA

RVVQRLPDLRLADQDSRLPLRPANFVSGLESMPVVFTPSRPLR

>CYP142A4 Mycobacterium vanbaalenii PYR-1

MTSTLPALDVDLADGNFYADGRAAREAYKWMRANQPVFRDRNGLAAATTYQAVLDAERNPELFSSTGGIR PDQPGMPYMIDMDDPAHLLRRKLVNSGFTRKRVMDKVPSIENLCDTLIDAVCERGECDFVRDIAAPLPMA VIGDMLGVLPDERDMLLKWSDDLVCGLSSTVDEQTIQKLMDTFAAYTAFTTEVIADRRANPRDDLFSVLV NAEVEGQRMSDDEIVFETLLILIGGDETTRHTLSGGTEQLLRHQDQWRQAVADPELLPGAIEEMLRWTSP VKNMCRTLTADTEFHGTSLKAGEKIMLMFESANFDEAVFENPDEFDIHRNPNSHMAFGFGTHFCLGNQLA RLELRLMLTKILQRLPDLRLADESMLPLRPANFVSGLESMPVVFTPTAPVGA

>CYP142A5 Rhodococcus sp. RHA1 Rha05910

MRRSASMTNRPDFDLIDGRFYSGELGDPRQAYAWMRAHEPVYRADGILGAASYEAVLAAERDPELFSNAGGIRPGLGPLPQMIDMDDPQHLQHRRLVNAGFTRKQVEAKIGRIREICDHLIDAACDKDEVDFVRDLAAPLPMAVVGDMLGMRPEERDTFLQWSDDLMNALGSNATPEELQAQANAYLAFNEFTLRTIEERRQNPTDDLTSILVHSEIDGHRLSDPDIVGETLLILIGGDETTRHVLSGGMEQLMRHPDQHQRLVNDPDGIPAAVEEMLRWSSPIKNMCRTVTRDVEFFGTDLRQGEKMMLLFESANFDDAVFDSPEVFDIERSPNPHVAFGFGTHFCLGNQFARLEAKIMFEQLLSRLPDMVLVDDGPLRRRPANFVSGLEEMPVKL

>CYP142B1 Mycobacterium vanbaalenii PYR-1

MTTAVPTHRDIDLSDRNFWARPHEERDAAFAVLRRENPVPWSRPADSDLLPPEQNLKGFWSLTKHEDIRY ASRHPEIFSSAEGITVEDFPVEIRMMSQSFIAMDAPRHTQLRGITLDAFKPRNMLRLQDWIQGHARDLIS EISHLGEGDFVDLVSVKLPGRIFGSFFGLPPGELHEKTINAAQRTLGWTDPEVRGDLTAVELFVGAVMDL HETVTTLLPERRANPGDDLLSWMVQAEFDGEKMTDDELKAFFTLLAVAANDTTRHASAHAILAFSQFPDQ RDLLVADVEGRVDTAVEEVLRWASPLVHMRRTAVQDVTLRGSEIKAGDKVVLWYSSANRDEDIFEDPFKF DIARNPNPHIAFGGGGPHFCLGAALARTMLRSLLTEVYTRIPDISAPEPRYQVANFINGINSLPATWTPERR

>CYP142B2 Mycobacterium sp. JLS

MTTVFPETTH GDIDLSAREF WAKPPVERDA AFAVLRRENP VAWSRPADSD LLPPEQNLKG

FWSLTKHEDI RYASRHPEIF SSAQGITMED FPHEILMMSQ SFIAMDAPRH TQLRGITLDA

FKPRNMRRLQ GWVQEHARDL ISEMSHLGEG DFVELVSVKL PGRIFGSFFG LPPGEIHEKT

IDAAQRTLGW TDPDVRGDRT ALELFAGAVM DLHETVTTLL PERRANPGDD LLSWMVQAEF

DGVKMTDDEL KAFFTLLAVA ANDTTRHASA QAIYAFSQFP DQRDLLVADV EGRVDSAVEE

ALRWASPLIH MRRTATQDVT VRGAEIKAGD KVVLWYSSAN RDEDVFDDPF TFDIERNPNP

HLAFGGGGPH FCLGAALART MLRSLLTEVY TRIPDIHAPE PKFQVANFIN GINSLPATWT

PERR

>CYP143A1 Mycobacterium tuberculosis

MTTPGEDHAGSFYLPRLEYSTLPMAVDRGVGWKTLRDAGPVVFM

NGWYYLTRREDVLAALRNPKVFSSRKALQPPGNPLPVVPLAFDPPEHTRYRRILQPYF

SPAALSKALPSLRRHTVAMIDAIAGRGECEAMADLANLFPFQLFLVLYGLPLEDRDRL

IGWKDAVIAMSDRPHPTEADVAAARELLEYLTAMVAERRRNPGPDVLSQVQIGEDPLS

EIEVLGLSHLLILAGLDTVTAAVGFSLLELARRPQLRAMLRDNPKQIRVFIEEIVRLE

PSAPVAPRVTTEPVTVGGMTLPAGSPVRLCMAAVNRDGSDAMSTDELVMDGKVHRHWG

FGGGPHRCLGSHLARLELTLLVGEWLNQIPDFELAPDYAPEIRFPSKSFALKNLPLRWS

>CYP143A1 Mycobacterium bovis subsp. bovis AF2122/97,

MTTPGEDHAGSFYLPRLEYSTLPMAVDRGVGWKTLRDAGPVVFM

NGWYYLTRREDVLAALRNPKVFSSRKALQPPGNPLPVVPLAFDPPEHTRYRRILQPYF

SPAALSKALPSLRRHTVAMIDAIAGRGECEAMADLANLFPFQLFLVLYGLPLEDRDRL

IGWKDAVIAMSDRPHPTEADVAAARELLEYLTAMVAERRRNPGPDVLSQVQIGEDPLS

EIEVLGLSHLLILAGLDTVTAAVGFSLLELARRPQLRAMLRDNPKQIRVFIEEIVRLE

PSAPVAPRVTTEPVTVGGMTLPAGSPVRLCMAAVNRDGSDAMSTDELVMDGKVHRHWG

FGGGPHRCLGSHLARLELTLLVGEWLNQIPDFELAPDYAPEIRFPSKSFALKNLPLRWS

>CYP143A2P Mycobacterium leprae

1 MSTSAKANPTHFTYCSLNYSALSMITDRGVIWKTLXX 105

113 AKPVVFMNG\*YYLNVSRKCILHTTSITKGFSSREAXXX 217

225 PGNALPVLPXXXXXXXXXXXXXXXXXXX 251

278 SLNNLNKALPALRTYTVTMANAITSRGEW 364

366 EAMTDFANX 389

391 LFPLQLFLVL\*GLXX 429

434 AQDRDHLIALLKDVVIGMSDKPFLSQADIADQGELCEYLVDTIAERKQNPA 586

585 PDVLSQVLIGEDPLSEIKVLDLESL 659

659 MLILAELDTVTATVGFSLLQPACRQQLRTMLRDKPKQIRILIED 790

792 ILQLEPPAQITPYITTEFVNVDGMTLSPGSRVRLC 896

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

993 GSHLARLKLTLAVDEWLINI 1052

XXXXXXXXXXXXXXXXXX

1116 LFALKALALHW 1148

>CYP143A3 Mycobacterium marinum MM2631

MSAPRDERDI PHFVYAELPM ATDRGRGWAT LRDAGPVVIG DGFYYLTRRD DVLDALRHPE

VFSSKRAFDI LGSPLPLVPL AFDPPEHTRF RKVLQPFFSP HALAAMLPSL QAQAIEIIDA

IAAGSQCEVI TELAIPYPSQ VFLTLFGLSL ADRDRLIRWK DAIIALGLLA SLDDADLTPA

LELTSYLVDA IAAHRRHPGT DILSQVLLGD DPLDDSEALG LSYVFVLAGL DTVTSAIGAA

LLELARRPQL RQLLRENHGQ IAVFVDEIVR LEPPAPVVPR VTTREVNIAG AKIPAGSRVW

LCLGAINRDG SDATSVNDVV MDGKVHKHWG FGGGTHRCLG SHLARMELSL VISEWLRRIP

QFELACGYTP EIDWPSATLG LSTLTLQFTS \*

>CYP143A3 Mycobacterium ulcerans

MSAPRDERDIPHFVYAELPMATDRGRGWATLRDAGPVVIGDGFYYLTRRDDVLDALRHPE

VFSSKRAFDILGSPLPLVPLAFDPPEHTRFRKVLQPFFSPHALAAMLPSLQAQAIEIIDA

IAAGSQCEVITKLAIPYPSQVFLTLFGLSLADRDRLIRWKDAIIALGLLASLDDADLTPA

LELTSYLVDAIAAHRRHPGTDILSQVLLGDDPLDDSEALGLSYVFVLAGLDTVTSAIGAA

LLELARRPQLRQLLRENHGQIAVFVDEIVRLEPPAPVVPRVTTREVNIAGAKIPAGSRVW

LCLGAINRDGSDATSVNDVVMDGKVHKHWDFGGGTHRCLGSHLARMELSLVISEWLCRIP

QFELACGYTPEIDWPSATLGLSTLPLQFTS

>CYP143A4 Mycobacterium marinum MM2666

MSTPGEGSAS SFYLPRLEYS TLPLAADRAV GWNTLRDAGP VVFMNGHYYL TRREDVLAAL

RNPKIFSSRI LQPPGNPLPV VPLAFDPPEH TRYRKALQPY FSPHALGKSR PVLERHAAEM

IAGFAGRGEC DAMAEFARLY PFQVFLDLYG LPLQDRDRVI AWKDAIIGDK LYLTREELEV

GQLELLEYLN NAIQQRRQNP GSDMLSQVMT GPGEFTDLEL LGMSHLLILA GLDTVTAAIG

FSLLELARRP QLRTQLRDNP KEIRVFIEEI VRLEPSAPVA PRITTDFVNV GGMTLPPGSQ

VRLCMAAVNR DGSDAMSTNE LVMDGKVHRH WGFGGGPHRC LGSHLARIEL TVIVAEWLKQ

LPDFELAPDY SPEIAFPSKT FALKSLPLRW A\*

>CYP143A4 Mycobacterium ulcerans

MSTPGEGSASSFYLPRLEYSTLPLSADRAVGWNTLRDAGPVVFMNGHYYLTRREDVLAAL

RNPKIFSSRILQPPGNPLPVVPLAFDPPEHTRYRKALQPYFSPHALGKSRPVLERHAAEM

IAGFAGRGECDAMAEFARLYPFQVFLDLYGLPLQDRDRVIAWKDAIIGDKLYLTREELEV

GQLELLEYLNNAIQQRRQNPGSDMLSQVMTGPGEFTDLELLGMSHLLILAGLDTVTAAIG

FSLLELARRPQLRTQLRDNPKEIRVFIEEIVRLEPSAPVAPRITTDFVNVGGMTLPPGSQ

VRLCMAAVNRDGSDAMSTNELVMDGKVHRHWGFGGGPHRCLGSHLARIELTVIVAEWLKQ

LPDFELAPDYSPEIAFPSKTFALKSLPLRWA

>CYP143A5 Mycobacterium vanbaalenii PYR-1

MSALPHVLYGDLPMAADRGAGWATLREFGPVAYGDGWYYLTRRDDVLAALRNPEVFSSRIAYDDMISPVP LVPLGFDPPEHTRYRRILHPFFSPQALGVLLPSLQAQAADIVETIAQRDACEVMAELATPYPSQVFLTLF GLPLQDRERLIAWKDAIIAFSLTNDPTSVDLTPAVELYGYLTEAVARQREKPREGILSHLLHGDEQLTDN EAVGLSLVFVLAGLDTVTSTIGATMLELARRPELRAALLGDPDGIAGFVEEMIRLEPAAPVVGRVTTREV TVAGVTLPKGAEVRLCLGAINRDGADEHSGDDFVLDGKLHKHWGFGGGPHRCLGSHLARMELRLVVTEWL SRIPDFELAPGYVPEITWPSATCTLPTLPLILTRKTP

>CYP143B1 Frankia alni ACN14a

MSAGEAQPLTFEDLPVRDDRDAAWRLIRERGGIVQLEPDVALTDHTLVEAAFRNPAVFSSRQAFDSLGSP

LPLVPIAFDPPEHARYRHILQPFFSPRSIRPLEPELRRQLAELIAPLPARGACDFVADVASVFPVQAFLT

FFGLPLDMRDQFVAWKDAILALSDPSGAISTDEADLRHAGELFTYLSELVAARRGVPGPDVLSELLCLDG

DDALTDAEVIGLCFLFVLAGLDTVTDALGFGMERLARNPDRRQEIVDDPGLVPAAVEELLRLDPPAPFVP

RITTAQTELGGRTLPAGTRVTAYIAACNRDEARYPDPYGVDFHRGDNPHASFGVGVHRCLGSHLARLEMR

LVYEEWHRLIPHYDIAPGFAPTVKFPRGTVGLEALPLVLTPGASR

>CYP143B2 Frankia alni ACN14a

MTHKRDMRHSASHAWNESWVTRRAGERVEGTAMTDDRNNEKVTLSNLPIARDRDAAWRQLREHGRTVLLD

GGLAATDVETVETVLRQPAIFSSKKAFDVLGSPLPLVPIAFDPPDQTRYRRILQPFFSPRAIRPLEDELR

RQIVEIVEPLVRRGSCEYVSEVAGIFPVQVFLTLFGLPLEMRDQFIEWKDAILGLSDPSGNTALDEAATE

AAMATALGLFSYLADLVPARRGVAGDDVLSQLLCLEGDEALTDEEAVGLCFLFVLAGLDTVVDALSFGTD

RLIRNPDRRREIVDDPALIPAAIEELLRLDPPAPFVPRVTTEQTVLDGRTLPAGTRVTTNLAAANRDPAR

HPDPYTVNFHRGESPHLSFGAGVHRCLGSHLARLEMRLVFEEWHRLIPDYDLAPGASPQVKWPRGTLGLD

ALPLVFPASAPAAGAGGQAS

>CYP143C1 SBI\_7215 Streptomyces bingchengensis

51% to CYP143B2 Frankia alni ACN14a

MTSVDSDTVHVVRDLPVAERRDDAWRMLMARPEPAPMDNGLAVTSLAAVK

AVLKEPNRFSAKKAFDAVETGYPLIPLAFDPPEQTHYRRILQPFFGPRRI

RALEESLRAQAIDLVEAVKARGGCDFVADIAVPFPAQALLTLLGLPLADR

DRFIESKNAALELTADAAGELTLTDEERAARVEQTMALGNYLGELIQTRR

AQPGDDILSEILAIDGDDHLSDTEAMGVCLMLVLAGLETVTDALSLAMER

LATHPGRRRELVEDPSLVPAAVEELLRLDPPAPFLPRVTTEDVEIAGCPV

PAGTLVNTHLTTANRDETCWPRPHDIDFHRPDNPHTSFGVGVHRCLGTHL

ARLEMQLLFEEWHRRIPEYAIAEGTSPRARLVRANIGMESLRLTIPTA

>CYP144A1 Mycobacterium tuberculosis

MRRSPKGSPGAVLDLQRRVDQAVSADHAELMTIAKDANTFFGAE

SVQDPYPLYERMRAAGSVHRIANSDFYAVCGWDAVNEAIGRPEDFSSNLTATMTYTAE

GTAKPFEMDPLGGPTHVLATADDPAHAVHRKLVLRHLAAKRIRVMEQFTVQAADRLWV

DGMQDGCIEWMGAMANRLPMMVVAELIGLPDPDIAQLVKWGYAATQLLEGLVENDQLV

AAGVALMELSGYIFEQFDRAAADPRDNLLGELATACASGELDTLTAQVMMVTLFAAGG

ESTAALLGSAVWILATRPDIQQQVRANPELLGAFIEETLRYEPPFRGHYRHVRNATTL

DGTELPADSHLLLLWGAANRDPAQFEAPGEFRLDRAGGKGHISFGKGAHFCVGAALAR

LEARIVLRLLLDRTSVIEAADVGGWLPSILVRRIERLELAVQ

>CYP144A1 Mycobacterium bovis subsp. bovis AF2122/97,

NC\_002945 complete genome 2001114..2002418

Gene = CYP144 1 aa diff

locus\_tag = Mb1806

>CYP144A1P Rhodococcus sp. RHA1 Rha02971

VLADTTLGGAELPAGSHLLLLWGAANRDPAVFERPDEIVLDRPHIRSHLAFGKGVHFCVASALARMEALAATTALLARTGRFALAADSEPRWVPSLSVRRHSALPLRLEQVTPED

>CYP144A2 Mycobacterium smegmatis MC2

MTFGCMTPPEGLGLALFRPECIQDPYPLYRRMLDTAPVHPIADSGFYAVC

GWDAVNDAIARPENFSSNLTATMTYQADGTVGAFEMESLGGKSHVLATAD

EPAHTAHRKALLPQLAARRIRAFEPFILETANSLWHSHLHDGHIEWMSAV

ANRLPMMIVGRLIGVPDADVDKLVRWGYSATQVVEGLVGQDQLTQATVAV

MELAGYITDQFRHAAQDPQDNLLGDLATACATGEMDELTAQSMMIILFSA

GGESTASLIGSAAWILASRPDIQEHLRAKPELLGAFVEEVLRYEPPFRGH

YRHVVHDTTLGGVDLPAGSRLLLLWGAANRDPSHFDAPDEFRLDRSSAKS

HLSFGKGTHFCVGAALARLEALVVLRHLLHNTANITAGDTGPWLPSLLVR

RLAHLELVTT

>CYP144A3 Mycobacterium vanbaalenii PYR-1

MTVGHTDLGLALFHDEFLQDPHPLYARMHAEAPVHRVGDSDFYAVCGWDAITEAVARPGDFSSNLTGAMR YQADGTVSLLPLDTLGSPTQALATADDPAHAAHRKLLVPYLAAKRVRALETFAENTMHALWQQMPAGAPV EWMAVVADRLPMTVVCKLIGVPAEDVDRIAAWAYASTQILEGRVDEHTLTAAGTAALELAGYISDKLGRA SLDPGDNLLGCIATACAAGELNNLTAQVMLVTLFSAGGESTAALIGSATQIIATRPDVQRRLRADPGLIP AFLEEVLRFEPPFRGHYRHVVRDCALAGKELTAGSRLLLLWGAANRDPARFDAPNEFQIERPNSKAHIAF GKGAHFCIGAALARFEARIVIDLLLRHTSWVDAAGPGWWLPSLLVRRLDELPLTMT

>CYP144A4 Mycobacterium ulcerans

MKVASDAMTFFGTESLQNPYPLYERMRAEGPVHRIADSEFYAVCGWDAVNDAISRPGDFS

SNLTATMTYSPDGKVAAFEMDQLGGPTHVLATADDPAHAVHRKLLVRHLAARRIRSLERF

VSETAERLWFDGLQGGRIEWMDAIANRLPMMVVAELIGLPDADIAQLVQWGYGATQLLEG

LVDQDQLADAGIAVMQLSGCITEQFARAAADPQENLLGELATACAAGELDSLTANLMMVM

LFAAGGESTASLLGSAVWILATRPDIQQQVRDNPQLLGAFVEETLRYEAPFRAHYRHVRN

DTTLGGLTLPADSHLLLMWGAANRDPVQFDAPEEFRLDRPGGKGHISFGKGAHFCVGAAL

ARLEAQIVLRLLLERTTVIEAADVGRWLPSMLVRRLENLELAVR

>CYP144A4 Mycobacterium marinum MM2654

MKVASDAMTF FGPETLQNPY PLYERMRAEG PVHRIADSDF YAVCGWDAVN DAISRPEDFS

SNLTATMTYS PAGKIAAFEM DQLGGPTHVL ATADDPAHAV HRKLLVRHLA ARRIRSLERF

VSETAERLWF DGLQGGRIEW MDAIANRLPM MVVAELIGLP DADIAQLVQW GYGATQLLEG

LVDQDQLADA GIAVMQLSGY ITEQFARAAA DPQENLLGEL ATACATGELD SLTANLMMVM

LFAAGGESTA SLLGSAVWIL ATRPDIQQQV RDNPQLLGAF VEETLRYEAP FRGHYRHVRN

DTTLGGLTLP ADSHLLLMWG AANRDPVQFD APEEFRLDRP GGKGHISFGK GAHFCVGAAL

ARLEAQIVLR LLLERTTVIE AADVGRWLPS MLVRRLENLE LAVR\*

>CYP145A1 Nocardioides sp.

MSSVLAPESDVDLFAGEVLADPYPIYAALRSLGPVVWLPRHGFY

VVVRYAEAREVLNDHERFVSGRGVGFNQQFNDVRSGSIIASDPPRHDILRSVLNERLG

PRALKDTEVMIRSRASDLVAEMAQRRSFDAVKDFAEVFPVQVVGELIGLPEGSRGRLL

QWANGAFNAFGPSGERTAAGLEAIAEQFDYIRTVANREQLMPDSMGAAVYQAADEGII

SEDDCLPLLSAYLTAGMDTTVNALSAMLLLLSTDPDQWQELRSSPSLAPSVVNEVLRI

EAPAQLFSRVTATRVDLAGTRIEAGERVAVIYASANRDEKKYPDPDRFDIRRNPAGHL

AFGSGLHVCAGQFLAKTELRAVLDALIEQIETMTVGEPVRKINNVLRGLSSLPATFVP

VQTSR

>CYP145B1 Streptomyces scabies SCAB90301

MISTTTPVSD VDLFADEVLD DPYPVYEELR DLGAAVHLSR HGCWVLPRYA QVRAALGDHG

RFSSVDSVGL DPALNERRRG GVLASDPPEH DVLRGVLSES LAPRALATLR TDIGRRAEEL

VAPLVERRTF DVVRDLARVF PVSVVADLIG MPLAAREEVL RFADAFFNTF GPLNDRTRQS

LPVAETLFDE LTAMMSRDNL EPGGWGQAVH RAADRGVIGE HQVVPLLRAY LVASMDTTIN

AIGSGLWLLA QRPGAWRSLR EDRSLVPSVF EEILRYESPV QMFFRRTTCP VRYGDVVIPE

QAQVSLLFGS ANRDPREWTD PDRFRVDRAP TGHVGFGYGV HGCAGQGLAR MEAQAVFSAL

LDRVDSIELA GPPRRHLNNV IRGLDSLPVT VTTRKV

>CYP145C1 Streptomyces scabies SCAB90701

MPMRTEIPVY HPDLYAASAI RDTYPHYAAL RALGPVVHLS KHNVHALPRY AECKQVLLDD

DTFISSHGVA LNPVANRVGQ GTTLFSDGED HARRRSLLGH RLTPRALRTM KDTVDQQAAA

VVEDAVARRT VDAVEIATAL PMSVVPDLVG WPRQGREHLL RWAGATFDAL GPLNCQAART

LPASLGMLRY ARAVVRDRSV LDGSMGHDLL LAADEGRIMP AECATMMIDY LAPSLDTTIS

AISSALYLFA VHPEQWRLLK ADPDLAPKAV NEVVRYESPI RAFSRTAARD TEVAGIPLRK

GSRVLVLYGS ANRDPLEWDD PDTFDIRRDA ARQLGFGQGT HGCAGQGLAR METSAILRAL

IERVDRIEVT GPPEWALNNV IHRLGRLPLE LIPA

>CYP146A1 Amycolatopsis orientalis

MQTTTAVGDLGNPDLYTTLDRHARWRELAARDAMVWSEPGSSPT

GFWSVFSHRACAAVLAPSAPFTSEYGMMIGFDRDHPDKSGGQMMVVSEQEQHRKLRRL

VGPLLSRAAARKLSERVRTEVSGVLDQVLDGGVCDVATAIGPRIPAAVVCEILGVPAE

DEDMLIELTNHAFGGEDELFDGMTPRQAHTEILVYFDELITARRERPADDLVSTLVTD

DELTIDDVLLNCDNVLIGGNETTRHAITGAVHALATVPGLLTGLQDGSADVDTVVEEV

LRWTSPAMHVLRVSTDDVTINGQDLPAGTPVVAWLPAANRDPAEFDDPDTFLPGRKPN

RHITFGHGMHHCLGSALARIELSVVLRVLAERVSRVELVKEPAWLRAIVVQGYAELSA

RFTGR

>CYP146A2 Amycolatopsis balhimycina biosynthetic gene cluster for balhimycin, strain DSM 5908. Y16952.3 90% to CYP146A1

MFEESNALRGTEIHRRDRFAPGPELRSLMGEGTMSILQPPDSPG GRTGWLATGHDEVRQVLGSDKFSAKLLYGGTVAGRIWPGFLNQYDPPEHTRLRRMVTS AFTVRRMQDFRPRIEQIVQASLDAIEAAGGPVDFVPRFAWSVATTVTCDFLGIPRDDQ ADLSRALHASRSERSGKRRVAAGNKYWTYMTEIAARARRDPGDDMFGAVVRDHGDAIT DAELLGVAAFVMGAGGDQVARFLAAGAWLMVEHPDQFALLREKPDTVPDWLNEVERYL TSDEKTTPRIAQEDVRIGDQLVKAGDAVTCSLLAANRRKFPAPEDEFDITRERPVHVT FGHGIHHCLGRPLAEMVFRAAIPALAQRFPKLRLAEPDREIKLGPPPFDVEALLLEW

>CYP147A1 Myxococcus xanthus Partial missing C-term

MAQASIFEQILDPANRANPYPLYAELRKTPVAREADGTYIVSTY

DEIVALLHDPRVSSDIRNLVRQAGATPSPQEGPPGLPEPFIRRDPPDHDRLRKLAMRP

FGRTPPDALMPFVPGWSRPRRACLTRSRARTKSTSSDDVAYPFPVTVICKLLGVPRED

EARFHELADAGVETLDPTTGTIEQRKAKRDRTKAELGQYLAALADAHLRQPGGDLLSG

FLTDNGPDGRMSREEVLSTAALLLVAGHETTVNLIANGMLTLLRHPGVFERLRREPEL

SIPLVEELLRYEPPVQFLPDRVTLADIDIAGTTIPQG

>CYP147B1 Streptomyces avermitilis

MASDTLLARITDYANRPDPYPLYAELREAGPVVRQADGSYLIGT

YHEIVALLHDPRMSADPRSRTAPAPYEVTRKPSFLRLDDPEHHRLRNSAMRPFGPPHS

PGRVDSMRGEIVQLTKELAEVFQEGRQIDVVDDFAYPLPVTVICRLLGIPDKDEQLFQ

DWTDTLVASADIGPEGDTAERDQAADQAQQEMGQYLVQLAEQRRGRPTGDMLSDLVNE

PDPAARLSEEDLAANTILLFIAGHETTVNLIANGVLTLLRRPDQLDRLREDPSLLPRA

VEELLRYEPPVHMRERVPLVDIDVAGTTIPGGTSVILALASGSRDPMRFSEPDRFDPT

RPDNQHVGFGSGIHLCFGAPLARIEAEAALGALLPHLGTARLVQDPPPYRQNAMLRGP

RHLPIQL

>CYP147B2 Rhodococcus sp. RHA1 Rha05428

MSRAQLFQRITDQASRPNPYPLYEELRETRVAPQDNGSFLVGRYYDVKALLHDPRISSDLHNRGPGLPGADRAGDGPESFLKLDPPEHDRLRRLTTRQFGPPHSPDRIDSMRGELAALVTKLVDGLDGKERIDIVDDFAYPFPVTVICRLLGVPHEEEPRFHAWADALVAAIDPRRAGADNEQVKVAQKAQMEMAMFMAGLIEDRRRDPGDDMLSGLANDSGPDGQLNTVELVTNSILLFIAGHETTVNLITNGMLTLLRNPDVLERLRAEPELMPQAVEELLRFEPPVHLLGQRTPIVDIEIGGVTVPKGSPLVLALASANRDPERFVDADKFVPDRADNQHVGLGSGIHSCFGAPLARLEGQMALAELIRRLPNPRLVEDPPPYRPNPVLRGPRHLLVDCG

>CYP147C1 Streptomyces tubercidicus strain I-1529

VVEETPWQQALRYANRANPYPFYEELRKTPVARQPDGTYVVSTYQEIVALLHDPRVSSDVRKLPDPATAPAEGSAE

AEPITEAVILEPNIITQDPPEHDRDRRMMMPHFAGPPHSPHLISDLEPEIRRIVDGLLDTMQGKTRIDAVDEFAYP

LPVTVICKVLGVPLEDEPRFHSWIETALDALDFGPEAASEEIQSRRAGGRQAVEEFGQFAAELLDRYAQQPGPGML

SAMVNEDGPEGRMSKGVLVSNALLLIFAGHETTVNLIAHSVLTLLRHPDALEKLRRRPELIVPGVEELLRFESSVQ

FWHTRSAVEDIDIAGTTIPKGAPIFLAYGSANRDPKRFAHPDELDLERRDNQHLGFSQGIHFCFGAPLARLEVQAA

VGEFIRRVENPRLVEDPPPYRHNQIFRGPRHVLVDIDGIRD

>CYP147D1 Magnetospirillum magnetotacticum

MCAPGPGRDPQCGTGRSSSGDPPDHDRLRGQVMRCFTPQRVRGM

REKTRRITDDLIAKMAGKTRIDLVDDFSYPLPVTVICELLGVPPEDEAQFHGWATQLA

TALEPNQRGDEETQAKNEVCFNEIADYIQGLIKEKRKNPQEDILSDLATDTDGMNDFD

LIATAVLLLVAGHETTVNLITNGMLTLLRFPEHLERLRAEPETAPRLIEELLRYEPPV

HYRTRLALADIPVAGITIPKDAPVILLLAAANRDPLRFSDPDRFDPDRPDNRHLGFGG

GLHYCVGAPLARIEAEVALVSLVRRLKGLSLTENPPPYRPGASLRGPCHLRLALEEVA

EG

>CYP147E1 Methanosarcina barkeri Archaea; Euryarchaeota

MYRQGSGPNDRRQTMTQQSLYEQVLDYANRANPYPLYAKLRQTP

ITRQIDGSYVVSTYREIVSLLHDPRIGSDFRMRSA

HDRPSAGLSANQELASKNQAQDEGAETSSSNQGSETEVV

PSFIGLDPPEHDRLRRQATWPFGPPHTPGRVADMEPELILLA

NRQIDTIKGRTSIDIVEDFAYPIPVTMISELLGVPPEDQPRLHALSEAIIEDIDLDPR

QSPEEQKRRQEQSSQTFKELEQYMEVLIEHHRKQPGSDLLSGLITDHGSDGPMAQADL

VSTASLLLIAGHETTVNLITNGMLTLLRHPDVLERLRREPDLVIRLVEEFLRYEPPVQ

ILPNRVALSDITIAGTTIQKGSPVILLLASGSRDPARFHDPEKFDPDRRDNMHLGFGS

GIHYCYGAPLARLETQIALTELVQRLENPRLAHDPPPYRQSATLRGPRHLIVEIDGVK

DWEFHL

>CYP147F1 Streptomyces peucetius

PSFLR

MTQSLLHQILDYANRADPYPIYEELRKTPVHHEEDGPYVVGTYYEIRSLLHDPRISSDAR

NLASTAGDPLAESAQEEDSALPPSFLRLDPPEHDRLRRMTNRSFGPPHSPHRVDGMRGEL

HGIVSGLIDGIGDTGRIDLVEQFSYPFPVTVICRLLGVPREDEARFHTWADTIAASLDPN

PDADPAERGKASHDARTQLGMYLAGLIEERRKNPGDDILSELATAKGRDGTMTTMELLST

AALLLIAGHETTVNLVTNGMLTLLRNPDVLQRLRADPRLAVPIVEELLRFEPPVQLVPQR

TTLTDIEVRGVTIPKGASLWLVLASGNRDPQRFEDPDRFDPDRRDIQHLGLGSGIHSCFG

APLARLEAHIALSELARRLENPRLLEDPPPYRQNAVLRGPRHLPIACDGIRP\*

>CYP147F2 SBI\_7351 Streptomyces bingchengensis

57% to CYP147F1 Streptomyces peucetius

60% to CYP147F3 Streptomyces bingchengensis

MTLGSMSARINDYANRADPYPLFAELRKQPVIREDDGTYLVSTYYEVKSL

ANDPRLSNDTRNRAPGCARTGGSEENTGLPPSFIFTDPPEHDRLRGTANR

PFGPPHSPRFLHDLQADLAKVVTELLDAFEGKDQVDIVEDFSYPLPVTAI

CKVLGVPREDEPRFHGWADALAAGVDPHPGENGQERADTARQEMGSYLAD

LIDASRRHPRPGILSALAPHTGPGGRMTPKDLVATAVLLLVAGHETTVNL

ITNTTLTLLRHPDVLRRFQHDQDLATPLIEEVLRYEPPVQFVPWTTALAD

IDIADTTIPKGSPVWLMLAAANRDPRRFEDPDRFMPERKDNEHLGFYTGI

HYCFGAPLARIEAHLALPELFRRVKDFRLLEDPPPYRANAVLRGPRHLPV

AIEGVTA

>CYP147F3 SBI\_9076 Streptomyces bingchengensis

68% to CYP147F1 Streptomyces peucetius

60% to CYP147F2 Streptomyces bingchengensis

MTYGTYLRKITDPANRADPYPLYAELRKTPVLRDEGGPYLVSTYWEIHGL

LHDPRLSSDPRNLDPDAAAALAVTEEADDPTLPPSFLRLDPPEHDRLRRI

ATYPFGPPHTPRRIHDMRGELARIVTDLIDDFEGRDRVDLVDDFAYPFPV

TVICRLLGVPRADEPLFHAWADTMLTSLDPAAAEADVAQRRRAVRQARVE

LGMYLSELIEDRRRAPAEDMLSSLIHGDGPDGRMSHAELVSTAVLLLIAG

HETTVNLIANGMLTLLRHQDVLKRLHDDSRLAVPLVEEVLRYEPPVQLLP

HRTPLTDIDIAGVTIPKGAAIWLVLASGNRDPKRFPDPDRFDPDRKDNQH

LGFGSGIHICYGAPLARLEGQIALAELARRLENPRLLEDPPPYRHNAVLR

GPRHLPVGFDGVRPAREP

>CYP147G1 Mycobacterium marinum MM2930

MNAETAWAEA MKFENRPNPY PYFDELRKTP VAKVAEKTYV VTGYRELLAL AHDPRISSDI

TRSPSGFGGE APQPEPGSEH VQAYGQDASI IVSDPPDHDR ARRQVMRHFA PPHSPDLIPS

MEPFVVRLAN DLLNQASARG STRLDVVEDF AYPIPVAVIC KILGVPIEDE PKFHAWIFDF

MAGTDLGPEG DTEEGQVLAE KGRVSTAALT DYLGDLVRSY AKTPGEGLLS KLLHDDGPDG

PMSVPETTAN ALLLLVAGHD STVNTITNCV MTLLRNPGSW DLVRQRPELI PRTIEEVQRL

QSAVQFFPSR SATDEIEIGG TVIPAGSAVH LIYAAANRDP RRFDNPNRFD PLREDNEHFG

WGSGIHTCMG GPLARLEVNL AVEIFLRRVQ SPKLVVDPPP YRHNQIFRGP RHLWVDFAAI TE\*

>CYP147G2 Mycobacterium vanbaalenii PYR-1

MTTASQAWAQAMAFAHRADPYPFFAELRKTPVARVADDLYVVTGYYELLALAHDPRVSSDFRRSPLSSDR APAEPADDVGAYGSEPSLIVTDPPSHDRARRQVSRHFAPPHSPDLIPSMEPAVVALCNDLLDTAKANGRT RIDVVDDYAYPVPVMVICKILGVPLEDEPRFHAWIFDMLAGVDLGPDATTDEGQGRAARARDAQAALRDY LAGLIEGYRGAGGDGLLSALVNDASGPDGAMPPGQALANAVLLLIAGHDSTVNTISNCVLTFLRNPGTVE LLRDRPELIPRAIEEVQRLQSAVQFFPSRSATADIEVGGTVIPEGAAVHLMYGAANRDPRRFADPDTFDI FRPDNEHFGWGSGIHTCVGGPLARLEVNLALEIFLRRVHRPRLVSDPPPYRQSQIFRGPRHVLVDVEAIG D

>CYP147H1P Frankia sp. EAN1pec YP\_001510211.1 ABW15305.1 58% to CYP147B2 Rhodococcus sp. RHA1 I-helix

MAELAAKRHDAPRDHMLSGLVSDDGPQGRMSQAEPITTAILLFVAGHETTVDLITDGMLIFLRHPELLEW MRREPDLMAGAVEELLRYEPPVHMLPQRTTLTDVEIAGTTIPRALRSP

>CYP148A1 Deinococcus radiodurans R1

MTASSGSSAPSSGPLLAAVQGLWSGAALADPHPIYEQIRGFANA

DGLVRLPEWNTAFAVGHAATSAVLRSPAARSGEWDHGPSDGGKLLQHMMLFRNGIPHA

RLRGLVQKAFTPRVVEEQRDLVRSLLDELLSDMARAGGPVDLVAGLSGPLPGRVIMRM

LGLRGADEERFLGWSASVAELLGGADRSPALLARIEADAREMRGYFRDLADELRVSPQ

PGLLSALAAVEDGGERLSGDELLSNAVLLLAAGHETTSNLIPGGVLALSQQPGAWAAL

LNHPRHPGVADELLRHVSPVQLDGRMLTEAQTVGETPLPAGTPVQLLLAAANRDPQVF

PDPERLDWDRPNASRHLAFAAGPHYCLGASLARLEIAETFAALAERFPDLRVSAAPHY

KANFVLRGPQELWVTLG

>CYP149A1 Microcystis aeruginosa

MIKQPIAIVGMGCRFPGANNPSEFWEILQNGVHKITKDPIDRPT

QMTGWAGFLDGIDKFDAAFFGIYSEEAIKMDPQHRLLLETSWEALEDAKLVPANLAGT

DTGVFIGLSGSEYPNLLIEDSTFNTTIGTLDCMLANRISSYFDFQGLSITINTACSSV

LVAIDSACQSLWNEDICLALVGGTHLTFSPVIASRASLNAMRPKIQAIVDDLLDRFAP

RGEMEIIADFATPLPAFAITKILGLPIEDYQQLIRWSAKTVFIFDQPVSLEEYKEQNQ

ILIEHRAYFAQKVAEYKRQPNDGLISQLANYNDNINALTEDEIISTSILLIATSQESM

KGLLSNGLLALLKHPQSLEYVRQNPGNIENIVEELLRYDSPIQYVSRRAIEDVEVSGK

IIHRGEYVVIYLGAVNHDPEYFSNPQQLDFSRRKPNLGFGGGLHYCVGMFLARLQVQI

ALNAMVQRFPDICLNTDKLDWCDSKISRRLKTLPVKFTPVA

>CYP150A1 Mycobacterium species

MSDFDTIDYFTDPALVPDPHPYFDHLRAQCPVVKEPHYGVLAVT

GYDEAATVLKDNETFSSCIAVAGPFPPLPFTPEGDDITDQITAHRPQMPMFEHMVTMD

PPDHTNARSLLNRLLTPSRLKENEDFMWRLADEVLDDFVTDGRCEFLTAFAKPFSLLV

IADMLGVPEEDHDEFRAVLGAPRPGANVGSLDHSDLVGTNPLEWLDEKFIGYLEDRRR

EPRNDVLTALATAKYPDGSTPPVIEVVRSATFLFAAGQETTTKLLSASMRVLGDHPDV

QERLRRDRSRIPVFVEEALRMDAPVKSQFRLAKKNTKVGDMNVPAGTTMMVCPGAVNR

DPNRFEHPHEFDLDRKNVREHIAFGRGVHSCPGGPLARVEGRVSIERILDRMADIQID

EELHGPPGARRYTYEPTFILRGLTDINITFSPVG

>CYP150A2 Mycobacterium smegmatis mc2155

MTDSTATDPAATTPDFDTVDYFTDQSLVPDPHPYFDHLRSKCPV

VREPHYGVLAITSFEEATTVLKDTETFSSCIAVGGPFPPLPFTPEGDDITGQIEQHRT

QLPMFEHMVTMDPPEHTNARSLLNRLLTPKRLKENEDFMWRLADECLDDFIDDGSCEF

LKQYAKPFSLLVIADLLGVPEEDHDEFRHVLGAPRPGAIVGSLDGDQLAMNPLAWLDD

KFVRYLEDRRKEPRDDVLTALATAKYPDGSTPEVIDVVRSATFLFAAGQETTTKLLSA

SLRVLGDRPDIQQALREDRSRIPTFVEEALRMDAPVKSQFRLAKKTTQLGGVDVPAGT

TLMVCPGAVNRDPVRFEDPHTFSLDRKNVREHIAFGRGVHSCPGGPLARVEGRVSLER

ILDRMADIRIDEEHHGPADNRRYTYEPTYILRGLTDLHIKFEPVR

>CYP150A3 Mycobacterium smegmatis

mtakrrcgnvilnnerhvlirlspsgngvth

MAIDPAGIDWFKDPRLVDDPYPYFNALRDKCPVQSEDHYGVTMVTGWEEA

VSVYNDEKSFSSCTSVTGPFPGFPVPLEGRDDVAELIEKHRDELPFSDQL

PTLDPPVHTNHRSLMMRLITPKRLKENEDAMWQLADEVLDDFLAPGKGEF

IKGFASPFTLLVIADLLGIPAEDRNAFVDGISQNSGGGVGSTGDESLSHS

PLEFLYGQFEAYIEDRRSNPREDILTGMATALFPDGTTPSPGDVARVATN

VFSAGQETTVRLLGTALKVLGDRPDVQKMVREDRSLLPNFIEEALRHESP

VKGDFRLSRCPVTVGDKDLPSGRTVMVVNGAANRDPRRFENPDDFDPARK

NARQHLAFGRGIHSCPGAPLARAETRVGLERLLDRTTDIRISEEHHGPAA

NRDYKYIPTFILRGLTHLHLEFDVK

>CYP150A4 Mycobacterium smegmatis

MTDLASVDYFSDPAVAQDPYEYYDFLRSRGPVTTEPHYGVVAVTGYQEVM

AAFKDHDSFSAVNAIGGPFPPLPFTPEGDDITEQIEAHRHLFPIHEHMVV

MDPPAHERARSLLSKLLTPRRLKENEDFMWQLVDRQLDAIIGNQADEGRC

EFLSEYAKPFATSAIIDLLGVPEEDRAEFLEALGAAPREGARVGALDGEP

VGLDPLQYLDCKFAGYLAERRREPRGDVLSGMATATYPDGSTPDLMEVVK

PATFLFAAGQETVTKLLSSAVQTLAERPEFQERLRKEPDLIPVFIEEALR

TQSPTKVDFRLARKTTTLGGVEIKAGTVLMLCLGAANRDPRKFEDPHEFR

IDRPNVREHIAFGRGIHTCAGAPLARVEGQITVRRMLDRLRDIRIDATRH

GPADSRTYAYEPTFLLRGLTKLHIEYTPA

>CYP150A5 Mycobacterium marinum MM4737

MNDCAEPDFF RDSGLVENPY PYYETLRQRC PVTGEGHHGV TMVTGWDEAV SVLNDAETFS

SCISVTGPFP GFPVPLEGDD VTELIERHRS ELPFSDQLPT LDPPTHTNHR ALLMRLITPK

RLKENEDAMW VLADRVLDDY LAAGEGEFIK GFASPFTLLV IADLLGVPPE DRQTFVNNIH

HHAGGGVGGT GKEALAHNPL EFLYGAFADY VRDRRREPRE DVLTGLATAT FPDGTVPDVE

DVARVACNVF SAGQETTVRL LGAALQIIGE RADIQQQLRR DRSLIPNFIE EALRIESPVK

GDFRLSRVPT TVGEVDLPAG TTVMVLQAAA NRDPRRFVEP ATFDPARKNA RQHLSFGRGI

HSCPGAPLAR AETRVAIERL LDRTADITIS ERVHGPANDR RYQYVPTYIL RGLTELHLDF TPA\*

>CYP150A6 Mycobacterium marinum MM4694

MSSYESIDFF TDPSLIPDPH PYFDYLRSQS PVLRLPQYGV VAVTGYEEAT AVYKDTDSFS NCVALGGPFP PLPFAPNGDD VNAQIDAHRE QFPMYEHMVT MDPPEHSRAR SILSRLLTPS RLKQNEEFMW RLADRQLDEF LGAGECEFIS EYAKPFATLV IADLLGVPED DRKDFRVVLG ADRMGRVGAL DHESVGVNPL QWLDDKFSAY IEDRRRQPRN DVLTALATAT YPDGSTPEVI DVVRSATFLF AAGQETTAKL LTAAMRVLGD RPDIQRRLRE NRSLIPNFIE ESLRMDSPVK SDSRLARKRT TVGGLDIAAG TVVMVLPGAA NRDPRRFEDP HEFRLDRPNV REHMAFARGV HSCPGGPLAR VEGRVSLERI LDRMLDIAIN EDRHGPADDR RYTYEPTYIL RGLTELHITF TPAG\*

>CYP150A6 Mycobacterium ulcerans

MSSYESIDFFTDPSLIPDPHPYFDYLRRQSPVLRLPQYGVVAVTGYEEATAVYKDTDSFS

NCVALGGPFPPLPFTPNGDDVNAQIDAHREQFPMYEHMVTMDPPEHSRARSILSRLLTPS

RLKQNEEFMWRLADRQLDEFLGAAECEFISEYAKPFATLVIADLLGVPEDDRKDFRVVLG

ADRMGRVGALDHESVGVNPLQWLDDKFSAYIEDRRRRPRNDVLTALATATYPDGSTPEII

DVVRWATFLFAAGQETTAKQLTAAMRVLGDRPDIQRQLRENRSLIPNFIEESLRMDSPVK

SDSRLARKRTTVGGLDIAAGTVVMVLSGAANRDPRRFEDPHEFRLDRPNVREHMAFARGV

HSCPGGPLARVEGRVSLERILDRMLDIAINEDRHGPADDRRYTYEPTYILRGLTELHITF

TPAG

>CYP150A7 Mycobacterium vanbaalenii PYR-1

MSDFDTIDYFTDPSLVPDPHPYFDHLRSKCPVVREPHYGVLAVTGYEEAATVLKDSDTFSSCIAVAGPFP PLPFTPEGDDITGQIAAHRSQMPMFEHMVTMDPPDHTNARSLLNRLLTPSRLKENEDFMWRLADEVLDDI ISRDPVGRCEFLSAYAKPFSLLVIADMLGVPEADHEEFRTVLGAPRPGANVGSLDHSDLVGANPLEWLDE KFIGYLEDRRKEPRDDVLTALATAKYPDGSTPPVIEVVRSATFLFAAGQETTTKLLSASLRVLGDHPDIQ ERLRRDRSRIPIFVEEALRMDAPVKSQFRLAKKNTRVGDMDVPAGTTMMVCPGAVNRDPSRFEHPHEFDL DRKNVREHIAFGRGVHSCPGGPLARVEGRVSIERILDRMGDIAIDEELHGPPGARRYNYEPTFILRGLTD LNITFTPVR

>CYP150A8 Mycobacterium vanbaalenii PYR-1

MTDLASADFFSDYALSQDPHPYWDHLREQNPVYREPHYGVVAVTGYQEVLAAFKDHDSFSAVNAIGGPFP PLPFTPEGDDITEQIEAHRHLFPIHEHLVVMDPPAHERARSLLNKLLTPRRLKENEDYMWQLVDSQIDQV IGKGRCEFLSEYAKPFATSAIIDLLGVPEEDRPEFLAALGAEQPDGARVGALDGEPVGLDPLQYLDDKFA GYLAERRREPRGDVLSGMATAVYPDGSTPELIEVVKPATFLFAAGQETVTKLLSAAVKTLAEQPEYQRIL RAHPDRIPTFIEESLRMNAPTKVDFRLVRKTTTLGGVHLKAGTIVMLCLGAANRDPRKFEDPHEFRPERK NVREHIAFGRGIHTCAGAPLARVEGQITVRRWLDRTDEIHLDESVHGPAGQHHFAYDPTFLLRGLSQLNI EFTAAT

>CYP150A9 Mycobacterium vanbaalenii PYR-1

MAEDLTTVDFFRDSRLTDDPYTFYEALRNKCPVSREEHYGVTMVTGWQEAVDVYNDAESFSSCVSVTGPF PGFPVSLEGRQDDDITALIEQHRDEIPFSDQLPTLDPPTHTNHRALLMRLITPKRLKENEDAMWQLADDI LDDYLAQGEGEFIKGFAGPFTLRVIADLLGVPEEDRPELLERLAKGTHGGGLGNADKTLTKTPLEYLYDV FATYVEERRAEPRDDVLTGLATANFPDGTVPEVGDVVRVATNVFSAGQETTVRLLSTALKVIGDRPDIQE RLRADRSLLPNFIEECLRIESPVKGDFRLSRVPTTIGDQALGAGCTVMVINGAANRDPRRFEDPDAFDPE RKNARQHLAFGRGIHSCPGAPLARAETRVGLERLLDRTSDIRISESKHGPAGNRRYDYIPTYILRGLTEL HLEYDVR

>CYP150A10 Mycobacterium vanbaalenii PYR-1

MTEQLTPTDIDEVDFFTDNTVLHDPYGYLAAMRNECPVRRERHHDVVMITGYEEAVAVYNDNARFSSCTA VTGPFPGFPVPLVGDDVSGLIAEHRDKLPFNDQLPTLDPPLHTDHRALLSRMITPKRLKENEEFMWRLAD RQYDEALAGGRCEFVGEFGNPFAMLVIADLLGVPESDHNDFKDQLLTSTGTIGSSGGDAMHHSPLEYLYG KFTDYITDRRENPRDDVLTGLASALFPDGRTPPVIDVVCVAANLFAAGQETTVRLLSTAVMMIAEDPALQ AKLRADRSLIPGFVEEALRFESPIRGDFRLSKVPVSVGGVELPAGTTVMLNNAAANRDPRRFTDPDTFDL QRPNARQHIAFGRGAHSCPGAPLARAEAKVSINRLLDRTSDIWIDEDKHGPVDARRYKYLPTFILRGLTR LHIEFS

>CYP150A11 Frankia sp. EAN1pec

MREFEAMDFFRDETLVADPYPYLDALRRKCPVQRERHHDVVMVTGYEEAVEVFHDSEAFSSCVSVTGPFP

GFPVPLDGDDVSALIERHRHELPMNDQLPTMDPPTHTDHRALLMRLITPKRLKENEALMWDLADRMLDPF

LTPGEGEFISGFAGPFTLLVIADLLGVPEEDQDEFLDKLQRQPAQTGGVGGTGAETLAHSPLEFLYGKFT

GYIEDRRRNPRADVLTGLAGATFPDGSTPEVIDVVRVAANLFSAGQETTVRLLSSALKILAERPDLQRQL

RVERERIPAFIEETLRWESPVKGDFRLSRVPVTVGGVQLPAGTTVMVVNGAANRDPRRFENPETFDVARS

NARQHLAFGRGIHSCPGAPLARAEARASLERLLDRTTDIRVNERVHGPAGNRRYEYMPTFILRGLTALHL

EFDLAPAPPRDFPPAGSPVGWIKG

>CYP150A12 Frankia sp. EAN1pec

MSELETKDFFRDEELVADPYPFLEAMRGKCPVQRENHHDVVMVTGYDEAVQVFHDSATFSSCVSVTGPFP

GFPVPLEGDDVTELIERHRGELPMNDQLPTLDPPTHTAHRALLMRLITPKRLKENEAQMWRLVDQMVEPY

LAGGEGEFITGFAGPFTLLVIADLLGVPEEDQEEFLDRLQRQPQESGGIGSTGDDHMAHNPLEFLYNKFT

AYIEDRRREPREDVLTGLALATFPDGSTPEVIDAVRVAANLFSAGQETTVRLLSSALKILAEDRELQQLL

RAEPDRVGNFIEETLRLESPVKGDFRLSRVPTTVGGVDLPAGTTVMVVNGAANRDPRRFENPSVFDVARP

NARHHVAFGRGIHTCPGAPLARAEARASIERLLERTTDIRISESVHGPADDRRYSYLPTFILRGLTHLNL

EFTLAESKTP

>CYP150A13 Frankia sp. EAN1pec

MKDIEAIDFFRGDELVADPYPYFHALREQCPVRREPHHGVVMVTGYEEAVSVFHDSDRFSSCTSVTGPFP

GFPVPLEGLEGDDISELIERHRAELPMSDQLPTFDPPMHTDHRALLMRLITPKRLKENEEFIWRLADRLL

DEYLASGEGEFIRGFAGPFALLVIADLLGVPEEDHEEFTDRLQHRPAEGGGVGSTGDHSMEHSPLQFLYD

RFTTYIEDRRREPRDDVLTGLATATFPDGSTPEVIDVVRVAANLFSAGQETTVRLVSTAAKLIADNPGLQ

RLLRAERDRIPNFIEETLRLESPVKGDFRLARVPTTVGGVDIPAGSTVMVVNGAANRDPRRFADPDTLDV

ARPNARQHIAFGRGIHSCPGAPLARAEARAGLERLLDRTADIRISERVHGPAGARNYQYLPTFILRGLTH

LQLEFTPAASDSR

>CYP150A14 Frankia sp. EAN1pec

MTDWTTTDFFNDESLAEDPYPYFDELRSVCPVLPLPHLGVVAVTGYDEAHEVYRDVDTFSSCNSVVGPFA

TFPVPLEGDEVGAIIDRHRDQLPMNEHMVTMDPPMHTRERALVMRMLTPKRLQENEAFIWRLADQQLDEF

IADGRCEFIRAYAQPFSMLAVADVLGVLESDHQRFREGFGLTVSPGQIGAGEQTDGELNALGWLDAWFAR

YIESRRHEPRNDVLTQMAAATYPDGTTPEVTSVVRAATFLFAAGQETTARLLGAALKFIAENPGLQEEIR

EHRERIPDLIEETLRVESPVKADFRLARRTTTIGDVEVPAGTPVMLLNGAANRDPRQFECPAEFRISRRN

VRQHIAFGRGIHSCPGGPLARVEGRISLERILDRTRDIRISEEHHGPPDARRFDYEPTWILRGLTNLHLE

FTPVESAR

>CYP150A15P Frankia sp. EAN1pec YP\_001505067.1 ABW10161.1 59% to CYP150A2 Mycobacterium smegmatis

MSDWKTIDYFTDESLVADPYPYFDELREAGPVLPLPHLGMVAVTGYEEASQVYREAETFSSCSSVVGPFA TFPVPLEGDDVSEIIDRYRTRLPMFEHMVTMDPPDHTRERALLMRLLTPRRLKENERFISRQADRQLDEF IDRGTCEFVREYAQPFTMTGPLTSGCPKSTTGRRVPGVSPTTPPGSCAA

>CYP151A1 Mycobacterium smegmatis

MSSTTLDSVPSFDVTDPAFSITSDEVHEAREKSWYATTPYGLAV

LRYEQVNRLIKHPKLRQGSAAWPAHNGVTEGPFAEWFASWILNKEGEEHHRLRRLMNP

AFSPKLIGSLVPRFQALANELIDNFAEPDRCEFVSEFAEPYAARVIAIMLGLPEEEWK

VISTESATIGLALGVTLREDLPKIEAAVQRLYEYSDELIADRRANPRDDFMTTLVNAS

RPDDGRLSDKELRDAILLLIFGGFDTTRNQLGLAMQTFMKHPDQWRLLGERPDLGGKA

VEEVMRVNPTVRWVTREVVEDFEYEGVTLKAGTTVHLYSESAGTDPRVFEPGFDITAE

RKPHFGFGGGVHHCLGHFVARSDMSEALPLLARRLRDPHELPGATWLPDSGNTGPNTL

PIGFTPAP

>CYP151A2 Mycobacterium sp. strain RP1

MSSLALGPVAAFDVADPSFSITSNEVHAARERSWYATTPYGIAV

LRYEQFSRLLKHPKLRQGSVAWPAHNGVTEGPFAEWFASWILNKEGEEHHRLRRLMNP

AFSPKLIGSLVPRFQALANELVDNFAEPYRCEFMSEFAEPYAARVIAIMLGIPEDEWK

VISTEAATMGLCLGVTLGKDLPKIEAALQRLYEYCDALITDRRANPREDFVTALVEAS

REEDGRLSDTELRDAMVLLIFGGFDTTRNQLGLAMQTFMAHPDQWRLLAERPELGGKA

VEEVMRVNPTVRWVTREVLEDFEYEGVLLKAGTTVHLYSESAGTDPRVFDGSFDITAE

RKPHFGFGGGAHHCLGHFVARSDMSEALPLLARRMRDPQALPGATWLPDSGNTGPIQL

PIGFTPAR

>CYP151A3 Mycobacterium vanbaalenii PYR-1

MSSATVGSVPAFAVTDPGFSITSAEVHAARERSWYATTEYGLAVLRYEQVNRLLKHPKLRQGSAAWPAHN GVTEGPFADWFAGWILNKEGEEHHRLRRLMNPAFSNKLIGGLVPRFQALAAELIDGFAEPGRCEFVGEFA EPYAARVIAIMLGLPESEWKVIATESATIGLALGVTILDDLPRIEAALAHLYEYCDELIADRRASPRDDF VTTLVNASRPEDGRLSDNELRDAMVLLIFGGFDTTRNQLGLAMQTFMAHPDQWRLLAERPELGGNAVEEV MRVNPTVRWVTREVLEDFEYEGVELAAGTTVHLYSESAGTDPRVFEPGFDITAERKPHFGFGGGVHHCLG HFVARSDMSEALPLLARRMLDPHELPGATWLPDSGNTGPITLPIGFTPAS

>CYP152A1 Bacillus subtilis

MNEQIPHDKSLDNSLTLLKEGYLFIKNRTERYNSDLFQARLLGK

NFICMTGAEAAKVFYDTDRFQRQNALPKRVQKSLFGVNAIQGMDGSAHIHRKMLFLSL

MTPPHQKRLAELMTEEWKAAVTRWEKADEVVLFEEAKEILCRVACYWAGVPLKETEVK

ERADDFIDMVDAFGAVGPRHWKGRRARPRAEEWIEVMIEDARAGLLKTTSGTALHEMA

FHTQEDGSQLDSRMAAIELINVLRPIVAISYFLVFSALALHEHPKYKEWLRSGNSRER

EMFVQEVRRYYPFGPFLGALVKKDFVWNNCEFKKGTSVLLDLYGTNHDPRLWDHPDEF

RPERFAEREENLFDMIPQGGGHAEKGHRCPGEGITIEVMKASLDFLVHQIEYDVPEQS

LHYSLARMPSLPESGFVMSGIRRKS

>CYP152A2 Clostridium acetobutylicum

1 MLLKENTAKD KGIDSTLDLL KEGYLFIKNR ADHYQSDLFE TRLMGQRIIC MTGEEAARIF

61 YDSDKFKRQG AAPKRVQETL LGENAIQTLD GESHLHRKKL FMLLTNQVQQ KRLAELTTEK

121 WEASASKWHT KSIVLFNEAN EILCQVACHW AGVPLMESDI KNRAEDFSSM IDSFGAVGPR

181 HWKGKKARNT IEAWIKEIIE NVRSGRIRAE EGSPLHEIAF YIDVNGQQMP AEMAAIELIN

241 ILRPIVAIST FITFSALALY EHSEYREKLQ SKDIRYLEMF TQEVRRYYPF APFVGARVRK

301 DFLWNNCEFK KEMLVLLDIY GTNHDSRIWQ KPYEFIPDRF RSYKGNLFDF IPQGGGDPSS

361 THRCPGEGIT LEIMKTSLDF LSTKIDFTVP DQDLSYSLSK IPTLPKSGFI IDNINLKL

>CYP152B1 Sphingomonas paucimobilis

MPKTPHTKGPDETLSLLADPYRFISRQCQRLGANAFESRFLLKK

TNCLKGAKAAEIFYDTTRFEREGAMPVAIQKTLLGQGGVQGLDGETHRHRKQMFMGLM

TPERVRALAQLFEAEWRRAVPGWTRKGEIVFYDELHEPLTRAVCAWAGVPLPDDEAGN

RAGELRALFDAAGSASPRHLWSRLARRRVDAWAKRIIEGIRAGSIGSGSGTAAYAIAW

HRDRHDDLLSPHVAAVELVNVLRPTVAIAVYITFVAHALQTCSGIRAALVQQPDYAEL

FVQEVRRFYPFFPAVVARASQDFEWEGMAFPEGRQVVLDLYGSNHDAATWADPQEFRP

ERFRAWDEDSFNFIPQGGGDHYLGHRCPGEWIVLAIMKVAAHLLVNAMRYDVPDQDLS

IDFARLPALPKSGFVMRNVHIGG

>CYP152B2 Azotobacter vinelandii

MHRIPRDKGLDSTLALLHDPYRFIARRCRLHGSNLFETRLLLRKTLCMSGAEAARLFYDP

ERFVRHGAMPPRLQKTLFGVGGVQGLDGEAHRHRKHMFVALLMDAERVAQLVEAVRGEWR

TCARRWERMEKVVLYD

CAWAGIPLAEEEAGPRAREIALLFDYAGSVGPKHWRSRLARRRSEAWMGALVESIRASRR

QPPAETAAQVISWHRGLDGNLLEAR

VAAVELLNVIRPVVAIAVYLTFVAHALHRYPHCRHGLRSGDAEYREWFVQEVRRFYPFFPA

VVARVRQDFEWRGYAFPAGRRVMLDLYGTDHDVRLWQAPETFRPERFGSREYGPCDFIPQ

GGGEHESGHRCPGERIVMKLGADVLARELSYAVPMQNLEIDFSRLPALPRSRFVMSDIHGAP\*

>CYP152C1 Rhodobacter sphaeroides

MTTDEGRRPEEPGTPASLREMPRDPRIDASMALMSEGYRFVSNL

CDRMDSDAVATRLRLREVVCLRGSAAARLLYGAEGLTRVGAMPSTVLHLLQDKGSVQQ

LEGPAHRHRKALFLSICMDPARVEALVSEMRLAWRERLPAWEAEGRIVLQQEAARLLT

RAGCRWAGVAHQPEAQLADEIFDMIDKAGSVGPRNWLAQMRRAGTEKRLRTLVEEVRA

GEVVPEAATALHAIAFHREEDGTLLDPSVAAVELLNLLRPIVAVGRYITFAALALHRE

TTWRELFRSGNLELAGDFAEEVRRASPFFPFTAAVTTRPITWEGYDFPEGQWLLLDLY

GTTHDPRHFPEPTRFRAERMLSWTGQDEAFIPQGAGDVARTHRCPGEMITVELMKEAI

RLLCCEMDYEVPAQDLGVRLNRMPAQPRSGMILSAISRRAGTEASRNG

>CYP152C2 Rhodobacter sphaeroides

MSNSDARHEA GPSDTTCGRE IPRDPRLDAS MGLLSEGYRF VSNLCDQLDS DIVSTRIRLR

EVICLRGGTA ARLLYGAEGL TRVGAMPSSV LHLLQDKGSV QQLEGPAHRH RKALFLGICM

DPARVEALVA EFRAAWRAAL DEWEEADSIV LQQEAARVLT RAACRWAGVE NQPEARLAEE

IFDMIDKAGS IGPRNWLAQM RRSGTERRLR KLIEQVRAGE VVPGSATALH AIAFHREADG

ALLDDTVAAV ELLNVLRPIV AVGRYITFTA LALHRETNWR DLFRSGTLEL AADFAEEVRR

ISPFFPFTAA VTTRPLQWEG YDLPADQWLL LDLYGTLHDA RNFPDPARFR AERMLSWSGQ

DDCFVPQGGG EVAVTHRCPG EMITVELLKE AIRLLCLEMD YEIPPQDLGV RLNRLPAQPR

TGMVLASIRR RPGTEPCVAG

>CYP152D1 Streptomyces scabies fSCAB80661

MGMMHSRRTP LVDSSLSLLV RGYTWLPDRR RRTTGPLVRA RLTGRPAVAL RGPEAVRFFY

DERHVERASA LPGPVLGTLF GHGAVHTLDG PPHRVRKDLF LSLLTGPKAV AGLVDHVTRA

WDAAEASWPH RPSVVLFDEA SRVLTLGVCR WAGIPLHDRD ADGAAPAADL VAMVDGFATP

GPRHWRARRA RGRREAWLAR LVSDVREGAA TAPAGSALDV VARHEDADGL PLDPHTAAVE

LLNVIRPTVA VCWFVAYAGH ALHLRPDVRE RLAEADPEYA VAFAHELRRF YPFAPFVGGR

AVTDLEWRGE PIPAGALVLL DLYGQNHDPG QWDLPYTFEP QRFLERPPGR DDLVPQGGGD

RATGHRCPGE DVTVALLRTL GPRLARLEYA VPPQDLRIPL TRMPARVRSG FVMESVRVPE

RVRVAGRAAG

>CYP152E1 gi|126657198| ZP\_01728364 Cyanothece sp. CCY0110

MIKKIPQDKWIDSSLALIFDGYDFISKRCKRYQSNIFQTRLMLEKTICFKGEEAAKIFYDKTKFTRKNAA

PDRVKKTLFGEKGIQGMDGDAHLHRKQMFMSLMSKERIQEVGTLTQKQWHNYAKKWERMDTIVLFEEARE

VLCRVACTWAGVPLEESEVKLRSQQFEAMIAGSGVVGPKHWQGRKARKENEQWIETIIEKVRNHQLEVPE

ISATYIFANHRDLSGELLDKRVAAVELINVLRPIVAIDRYITFGALALHEHPECRPKLLESEDYLRAFVE

EIRRFYPFFPFASARVRQDFDWQGYHFPEGTRVLLDLYGTNRDPQSWDKHDVFYPERFLNFSELDSFKFI

PQGGGDYHTNHRCPGEWITIELLKVTMTFLIQSINYNVPKQDLRINHLKMPTVPASGFVIKNVNLC

>CYP153A1 Acinetobacter calcoaceticus

MNSVAEIFEKITQTVTSTAADVATTVTDKVKSNEQFQTGKQFLHGQVTRFVPLHTQVRGIQWMQKAKFRVFNVQEFPAFIEQPIPEVATLALAEIDVSNPFLYKQKKWQSYFKRLRDEAPVHYQANSPFGAFWSVTRYDDIVYVDKNHEIFSAEPVIAIGNTPPGLDAEMFIAMDPPKHDVQRQAVQDVVAPKNLKELEGLIRLRVQGVLDQLPTDQPFDWVQNVSIELTARMLATLFDFPYEKRHKLVEWSDLMAGTAEATGGTVTNLDEIFDAAVDAAKHFAELWHRKAAQKSAGAEMGYDLISLMQSNEATKDLIYRPMEFMGNLVLLIVGGNDTTRNSMTGGVYALNLFPNEFVKLKNNPSLIPNMVSEIIRWQTPLAYMRRIAKQDVELNGQTIKKGDKVVMWYVSGNRDERVIERPDELIIDRKGARNHLSFGFGVHRCMGNRLAEMQLRILWEELLQRFENIEVLGEPEIVQSNFVRGYAKMMVKLTAKA

>CYP153A2 Caulobacter crescentus CB15

1 MMSQNTDPRE DLMSDGSIDL KADARARAYS IPLEDYHVAD PALFQADAMW PYFERLRKEA

61 PVHYSKGDEE VGPYWSVTRY NDIMTVDTTH QVFSSDAHLG GITIRNFDED FVLPMFIAMD

121 QPKHDIQRKT VSPIVSPANL GRLEGIIRER VCGILDALPI NEPFDWVDKV SIELTTQMLA

181 TLFDFPWEER RKLTRWSDIA TASPESGLIE SEEARRAELL ECLAYFTNLW NERVNLTEPG

241 NDLISMLAHG EATRDMPPME YLGNVILLIV GGNDTTRNSL TGGLYALSKN PQEEAKLRAD

301 PGLIPNMVSE IIRWQTPLAH MRRTALEDYE LAGQTIKKGD KVVMWYVSGN RDDTVIENAD

361 QFIVDRPNAR RHLSFGFGIH RCVGNRLAEM QLKIVWEEIL KRFPKIEVLE EPKRVYSTFV

421 KGYERMMVRI PERI

>CYP153A3 Bradyrhizobium japonicum USDA 110

1 MHYCKDSMFG PYWSVTRYND IMEIETNHSV FSSASALGGI TIRDIDPDLR RESFISMDPP

61 RHAAQRKTVA PMFTPTHLDN LALNIRARSA ECLDNLPRGE VFDWVDRVSI ELTTQMLAVL

121 FDFPWEDRRK LTRWSDIATT IPGPDGLVAT EDERQAELTE CAGYFARLWK ERIEQPPKSD

181 LLSMMAHGAA TRDMDAKNFL GNLVLLIVGG NDTTRNTMSG SIYALSQHPE QYRKLRENPA

241 LLDSFVPEVI RWQTPLAHMR RTALSDFEFR GKQIKKGDKV VMWYVSGNRD EEAIEKPYDF

301 IIDRARPRTH LSFGFGIHRC VGLRLAELQL KIIWEEILKR FDHIDVVGEP KRVYSSFVKG

361 LETLPVKIAA

>CYP153A4 Bradyrhizobium japonicum USDA 110

1 MDGRRRRPMP LPQAGEVRKT TGATTMNIQT PVKVDKAERM RRARGEAYAT PLAQFHPGAP

61 RLFQDDTLWP WFERLRKEEP VHYCTNAPIE PYWSVVKYND IMHVDTNHGI FSSDSTLGGI

121 SIRDVPEGYD YPSFIAMDQP RHSAQRKTVS PMFTPTHLDE LAKLIRQRSQ TVLDNLPRNE

181 TFNFVERVSI ELTTQMLATL FDFPWEERRK LTRWSDVSTA LPKSGIVASA EERRREMDEC

241 YAYMSKLWNE RVNSAPRNDL LSLMAHNDAT RFMDPDNLMG NIILLIVGGN DTTRNTMTGS

301 VLALNENPEQ YDKLRANPAL IDSMVPEVIR WQTPLAHMRR TALQDTEIGG KQIKKGDRVV

361 MWYVSGNRDE EAIDRPNEFI IDRPRPRTHL SFGFGIHRCV GMRLAELQLK IVWEEMLKRF

421 DRIEVVGEPK RIYSSFIKGY ESLPVRIPG

>CYP153A5 Rhodopseudomonas palustris

MTWPGRTTMHGTIETGKAARLRAAREEAYATPLKDFHPGAPRHF

RDDTLWPWFERLRAEEPVHYCTNAPIEPYWSVTKYNDIMHVDTNHQIFSSDSTLGGIS

IRDAPVGYDWPSFIAMDEPRHSAQRKTVSPMFTPQHLDELAVLIRGRTQKVLDGLPRG

ETFNFVDRVSIELTTQMLATLFDFPFDERRKLTRWSDVATALPKSGVVDSEQQRRDEL

NECAAYFARMWNDRVNSEPRNDLLSMMAHHDATRTMDRDNLIGNILLLIVGGNDTTRN

TMSGSVLALNENPHEFEKLRANPKLIDTLVPEVIRWQTPLAHMRRTALQDAELGGKTI

RKGDRVVMWYVSGNRDDEVIERPEEFIIDRARARIHLSFGFGIHRCVGMRLAELQLRI

VWEEMLKRFERIEVVGEPKRVYSSFVKGYESLPVRVS

>CYP153A6 Mycobacterium sp. HXN1500

MTEMTVAASDATNAAYGMALEDIDVSNPVLFRDNTWHPYFKRLREEDPVHYCKSSMFGPYWSVTKYRDIMAVETNPKVFS

SEAKSGGITIMDDNAAASLPMFIAMDPPKHDVQRKTVSPIVAPENLATMESVIRQRTADLLDGLPINEEFDWVHRVSIEL

TTKMLATLFDFPWDDRAKLTRWSDVTTALPGGGIIDSEEQRMAELMECATYFTELWNQRVNAEPKNDLISMMAHSESTRH

MAPEEYLGNIVLLIVGGNDTTRNSMTGGVLALNEFPDEYRKLSANPALISSMVSEIIRWQTPLSHMRRTALEDIEFGGKH

IRQGDKVVMWYVSGNRDPEAIDNPDTFIIDRAKPRQHLSFGFGIHRCVGNRLAELQLNILWEEILKRWPDPLQIQVLQEP

TRVLSPFVKGYESLPVRINA

>CYP153A7 Sphingomonas sp. HXN200

MEHTGQSAAATMPLDSIDVSIPELFYNDSVGEYFKRLRKDDPVHYCADSAFGPYWSITKYNDIMHVDTNHDIFSSDAGYG

GIIIDDGIQKGGDGGLDLPNFIAMDRPRHDEQRKAVSPIVAPANLAALEGTIRERVSKTLDGLPVGEEFDWVDRVSIEIT

TQMLATLFDFPFEERRKLTRWSDVTTAAPGGGVVESWDQRKTELLECAAYFQVLWNERVNKDPGNDLISMLAHSPATRNM

TPEEYLGNVLLLIVGGNDTTRNSMTGGVLALHKNPDQFAKLKANPALVETMVPEIIRWQTPLAHMRRTAIADSELGGKTI

RKGDKVVMWYYSGNRDDEVIDRPEEFIIDRPRPRQHLSFGFGIHRCVGNRLAEMQLRILWEEILTRFSRIEVMAEPERVR

SNFVRGYAKMMVRVHA

>CYP153A8 Sphingomonas sp. HXN200

MDTDMVEPNIREKVAFIPIDEIDVARPSLFQKDTVGLFFERLRREEPVHYCRESYVGPYWSITKFDDIMAVDTNHKVFSS

EAKLGGIAIEDMHSAKSALELEMFIAMDPPKHNQQRKAVTGAVAPSNLLLLEPTIRERACQILDDLPVGEDIDWVDKVAV

ELTTMTLATLFDFPWEERRKLTRWSDVTTAAPETGIVASYEARRAELIECAMYFKGLWEQRINAEPKNDLISMMAHSPAT

RDMPFLEFLGNLLLLIVGGNDTTRNSISGGVLALNQNPDAYLKLNNDPGLITSMVPEIIRWQTPLTHMRRTALQDWEIGG

KKIRKGDKVVMWYLSGNRDETVIDRADEFIIDRKNPRHHLSFGYGIHRCMGNRLAELQLRIIWEEIHKRFAKIEVTGEPE

RLFSNLVRGITKLPVRLHAR

>CYP153A9 Bradyrhizobium japonicum USDA 110

1 MNRRLEIHRA DDGYIIPLSE LDVSEGKRFQ DDSIWGCFER LRREDPVHYC QNSAHGPYWS

61 ITKYRDIVAV DTNHHAFSSQ QGVTIVEVPD KHWTPSFIKM GPPQHAEQRN TVSPIVGPES

121 LTRLETLIRS RVRMILDGLP RNEVFNWVTK VSIELTTQTL ATLFDFPFED RRLLTYWSDA

181 AVTTPKAGYA IDSWDKRSTI LSECLDYFTR LWNERINAEP RLDLISLMAH SPVTRHMEPT

241 EFLGNLILLI VGGNDTTRNS ITGGLLFMSQ YPSELRKLTD NPKLISSAVS EIIRYQTPIA

301 HMRRTAAIDS IVGGKPIRTG DKVVMWYISG NRDEEVIENA NSFVIDRKNV RQHLSFGFGI

361 HRCLGRHLAE LQLRVLWEEI LDGGLKIKVV GEPERIASNF VHGYSALPVR IEA

>CYP153A10 Burkholderia fungorum

MRHVSCLRRSRLERSRGRARRPGGFHADLFTDPQGQLAALLPDR

GARGTRRTGPAPSRRPALTTLARHSNPVPDKALAPLTRNCHSAKVNCMNTLVVDSSHV

RLAPDALSQPVEDIDPSLPYRFQQQTHFAMFDRLRRESPVHYVKDSEYGPFWSVHRYN

DIIDVEIDHATFSSDVKYGGMLIKDLPENMRRTSFINADPPLHDHQRRVVSPIVAPGN

LNRLEHTIRREAADILDGLPRGETFDWVDNVSIELTGRVLCELMDFPRADRRLLTYWS

DIVNVDLEVGGEINTEEKRYVKLKECASYFGVLFKERMNSEPKDDLISMLAHSEYTKN

MPEQEFLGMIVLLMVGGNDTTRNSISGGLVALNQFPEQYAKLHNDPGLIPKLVPEILR

WVTPVTHMRRTATRDIEFRGKQIRQGDKVVVWYASGNRDSDVIKDPYQFIIDRANPRL

HLSFGFGIHRCLGNRLAELQLRVLWEEILKRQMLIEMMGEPVRKYANNITGVMALPVRIAA

>CYP153A11 Sphingomonas sp. HXN200

MQSGPDREEPDRPIAEIPLAEIDVSRPSLFQSDKVGAFFERLRREDPVHYCSESAFGPYWSITRYNDIMAVDTNHKLFSS

EAKLGGIAIQDMHNDATNLELEMFIAMDQPKHDAQRKAVTPAVAPSNLLLLEPVIRERAGAILDSLPVGEEIDWVKSVSV

ELTTMTLATLFDFPWDERAKLTRWSDVTTAIPGSGIVESNEQRRQELIECAMYFKGLWDQRIDRSEGSDLITMMANSPAT

REMPFLEFLGNLLLLIVGGNDTTRNSISGGVIALNQNPDQYEKLRQHPSLIGSMVPEIIRWQTPLTHMRRTALADSEIGG

KRIRKGDKVVMWYLSGNRDETVIERPEEFIIDRKNPRQHLSFGYGIHRCMGNRLAELQ

>CYP153A12 Alcanivorax borkumensis

MSTSSSTSNDIQAKVINATSKVVPMHLQIKALKNLMKVKRKTIGTSRPQVHFVETDLPDVNDVAIEDIDTSNPFLYRQSK

SNSYFKRLRDEAPVHYQKDSAFGPFWSITRYEDIVFVDKNHELFSSEPQITLGEFPEGLSVEMFIAMDPPKHDVQRRAVQ

GVVAPKNLKEMEGLIRKRTGDVLDSLPLDTPFNWVPVVSKELTGRMLASLLDFPYDEREKLVGWSDRLSGASSATGGEFT

NEDVFFDDAADMAWSFSKLWRDKEARQKAGEEPGFDLISMLQSNDDTKDLINRPLEFIGNLALLIVGGNDTTRNSMSGGV

LAFNQFPEQFEKLKANPKLIPNMVSEIIRWQTPLPHMRRVATQDVELNGQTIKKGDRVLMWYASGNQDERKFENPEQFII

DRKEARNHVAFGYGVHRCMGNRLAELQLRILWEEILPRFEKLEVIGEPERVQSNFVRGYSKMVVKLTAKK

>CYP153A13 Alcanivorax borkumensis Strain AP1

MSTSSSTSNDIQAKVINATSKVVPMHLQIKALKNLMKVKRKTIGTSRPQVHFVETDLPDVNDLAIEDIDTSNPFLYRQGK

ANAYFKRLRDEAPVHYQKNSAFGPFWSVTRYEDIVFVDKSHDLFSAEPQIILGDPPEGLSVEMFIAMDPPKHDVQRRAVQ

GVVAPKNLKEMEGLIRKRTGDVLDSLPLDTPFNWVPVVSKELTGRMLASLLDFPYDEREKLVGWSDRLSGASSATGGEFT

NEDVFFDDAADMAWAFSKLWRDKEARQKAGEEPGFDLISMLQSNEDTKDLINRPLEFIGNLALLIVGGNDTTRNSMSGGV

LALNQFPEQFEKLKANPKLIPNMVSEIIRWQTPLAYMRRVAKQDVELNGETIKKGDRVLMWYASGNQDERKFENPEQFII

DRKDTRNHVSFGYGVHRCMGNRLAELQLRILWEELLPRFENIEVIGEPERVQSNFVRGYSKMMVKLTAKK

>CYP153A13a Alcanivorax borkumensis Strain SK2

MSTSSSTSNDIQAKIINATSKVVPMHLQIKALKNLMKVKRKTIGTSRPQVHFVETDLPDVNDLAIEDIDTSNPFLYRQGK

ANAYFKRLRDEAPVHYQKNSAFGPFWSVTRYEDIVFVDKSHDLFSAEPQIILGDPPEGLSVEMFIAMDPPKHDVQRRAVQ

GVVAPKNLKEMEGLIRKRTGDVLDSLPLDTPFNWVPVVSKELTGRMLASLLDFPYDEREKLVGWSDRLSGASSATGGEFT

NEDVFFDDAADMAWAFSKLWRDKEARQKAGEEPGFDLISMLQSNEDTKDLINRPLEFIGNLALLIVGGNDTTRNSMSGGV

LALNQFPEQFEKLKANPKLIPNMVSEIIRWQTPLAYMRRVAKQDVELNGQTIKKGDRVLMWYASGNQDERKFENPEQFII

DRKDTRNHVSFGYGVHRCMGNRLAELQLRILWEELLPRFENIEVIGEPERVQSNFVRGYSKMMVKLTAKK

>CYP153A13b Alcanivorax borkumensis Strain SK2

No accession number

Jan van Beilen

Submitted to nomenclature committee 7/21/2004

Nearly identical to CYP153A13 from strain AP1

Two genes in this strain code for identical proteins

>CYP153A14 Mycobacterium marinum

MDRIIQGAHLYDRTRRWVTGTNGEKIFIERPIPPADEVELTDIDLSNPFLYRQGRWKSYYERLRNEAPVHYQAHSAFGPF

WSVTRHADIVAVDKNHEVFSSEPFIVIGSPPRFLDIAMFIAMDPPKHDRQRQAVQGVVAPKNLREMEGLIRERVVDVLDA

LPLGEPFNWVQHVSIELTARMLATLLDFPFEQRRKLVQWSDLATSMEQANGGPSDNDEIFRGMVDMARGLSAHWRDKAAR

TAAGELPGFDLITMLQSDESTKDLIDRPMEFLGNLVLLIVGGNDTTRNSMSGGVLALNEFPDQFEKLKANPELIPNMVSE

IIRWQTPLAHMRRIAKADTVLNGQFIRKGDKVLMWYASGNRDERVFDRPDDLIIDRANARNHISFGFGVHRCMGNRLAEM

QLRILWEELLPRFENIEVVGEPEYVQSNFVRGISKLMVRLTPKGGA

>CYP153A15 Hyphomonas neptunium

859136 MAADTVSFVNHPALERPKVTEREPLHPHNLRFGANIPPAADIDLSTLDLIDGELWRQGKY 858957

858956 WDRFERLRNEDPLHYCPDSFPGPFWSVTRYEDVMAIDTDHKRFSSSWEYGGITLGEPISD 858777

858776 FEMPMFIAMDEPRHSEQRKTVQPAVAPDMLKVYEPLIRSRTQGLLDSLPVNEPFDWVDKV 858597

858596 SVELTTMMLATLFDYPFENRRDLTHWSDVATGMHNPDICPGGEEEWKATMMKCLMTFMGI 858417

858416 YQERQQQPQKPDLMSLLAHGEKTKNMTPMELLGNVILLIVGGNDTTRNSMTASVFALNKF 858237

858236 PKEYEKLKADPSIIPNMVSETIRWQTPLAYMRRTALEDVEMHGKTIKKGDQVAMWYVSAN 858057

858056 RDERFWDKPNDFIADRPEARRHISFGFGIHRCVGNRLAELQLRILWEEIMERFEHIEVLA 857877

857876 EPSLNQNAFVKGYNWMPVVLHPK 857808

>CYP153A16 Mycobacterium marinum MM3154

MSNIREAVTA KAQATIPMDR IIQGAHLYDR TRRWVTGTNG EKIFIERPIP PADEVELTDI

DLSNPFLYRQ GRWKSYYERL RNEAPVHYQA HSAFGPFWSV TRHADIVAVD KNHEVFSSEP

FIVIGSPPRF LDIAMFIAMD PPKHDRQRQA VQGVVAPKNL REMEGLIRER VVDVLDALPL

GEPFNWVQHV SIELTARMLA TLLDFPFEQR RKLVQWSDLA TSMEQANGGP SDNDEIFRGM

VDMARGLSAH WRDKAARTAA GELPGFDLIT MLQSDESTKD LIDRPMEFLG NLVLLIVGGN

DTTRNSMSGG VLALNEFPDQ FEKLKANPEL IPNMVSEIIR WQTPLAHMRR IAKADTVLNG

QFIRKGDKVL MWYASGNRDE RVFDRPDDLI IDRANARNHI SFGFGVHRCM GNRLAEMQLR

ILWEELLPRF ENIEVVGEPE YVQSNFVRGI SKLMVRLTPK GGA\*

>CYP153A17 Ectocarpus bacterium, 59% to CYP153A2 Caulobacter crescentus CB15 GenPept AAK22050

1458016 MTQATAATPLTDEFNPAEVALRDIDLSDANHFFNQHHWK

1458133 LFERLRNEDPVHFFEHEEFGRFWSVTRHADIMSIDTNHQQFSSEPSIFLGNTNSDEDENF 1458312

1458313 NPATFIAMDPPKHDAQRNAVNPAVAPPALRDLEPLIRQRVSAVLDSLPIGETFNWVDLVS 1458492

1458493 IEITTQMLATLFDFPFEDRYMLTRWSDMTTANPETLAAMGLTIEDRRNAMYECLEIFG 1458666

1458667 GLYAERAQLPPANDFISLMAHNEDMKNLDPMNLLGNLVLLIVGGNDTTRNSMSGGVLAL 1458843

1458844 HENPAEFAKLKADPSIIPNMVSEIIRWQTPLAYMRRTANEDLEFRGKQIKQGDRIMMWYV 1459023

1459024 SGNRDERAIERPNEFLIDRENARRHLSFGFGIHRCMGNRVGEMQVRILWEEILKRFDRVE 1459203

1459204 VVGKPARTLSNFVMGFTELPVRLHPKK\* 1459287

>CYP153A18 Ectocarpus bacterium, 70% to seawater bacterial sequence CYP153A25 JCVI\_PEP\_1096681995831

2416172 MTTANQTSPNGAIDVNDIPLAELDVSQPHLFKNDTWRPWFARLRAEAPVHYLADSENG 2416345

2416346 PFWSVTSHDMTKAVDANHKVFSSEEGGIAIVDPQPLDGEQLMRDPSFISMDEPKHATQRK 2416525

2416526 AVSPAVAPKNLAELEPLIRERAADILDNLPVGETFNWVDRVSVELTARMLATLFDFPYER 2416705

2416706 RRDLIRWSDVATAVPKVTGEANDMGARRDALIECATTFYQLWQERAAQPPKFDFVSM 2416876

2416877 LAHGEATKHLSEDPLLMLGNIILLIVGGNDTTRNSISGGVVALNQYPEEYQKLRDTPAL 2417053

2417054 IPNMVAETVRWQTPVIHMRRTALEDVELGGKTIRKGDKVVMWYLSGNRDEAVFPDADRLI 2417233

2417234 IDRPNARQHVSFGFGVHRCMGNRLAEMQLRVLWEEIMKRFHTVEVVGEVERLSNNFI 2417404

2417405 RGIASVPVRLHPL\* 2417446

>CYP153A19 Ectocarpus bacterium, 59% to CYP153A8 Sphingomonas sp. HXN200

2455477 MSQAFTHTPTSDVELSSTTNIADPDIWSNYEY

2455381 FPIFEKMRAEEPVHYCAESTYGPYWSVTRYEDIMAVDTNHQVYSSEADFGGIVID 2455217

2455216 DRIAIDPETNYKSASFISMDQPKHDDQRKSVNGITNPNNLQYFGDIIRTRTVNMLDSLPV 2455037

2455036 GEEFDWVPTVSIELTTQMLATLFDFPFEDRHKLTRWSDVITAEPESDIVENQE 2454878

2454877 ARVAELNEMAEYFVELQKGRINKPDSIDLLTMMTHSPAMAKMPPEEFMGNLALLIVGGN 2454701

2454700 DTTRNSMSGSIFGMHLFPDEFKKMVDDPSLTDNAVAEIIRWQTPLSHMRRTALQDAVL 2454527

2454526 GGKQIRKGDKVVMWYASGNRDTSIFDDPDKIIIDRKNARRHLSFGFGIHRCMGNRIGELQ 2454347

2454346 LRILWEEILKRFSRVEVTGEPVLTHSNFVKGYASLPVKLHAL\* 2454218

>CYP153A20 Ectocarpus bacterium, 58% to CYP153A2 Caulobacter crescentus CB15 GenPept AAK22050

2456749 MSQAFKHTPPATQPLTSKTNVADPALWESYSY

2456653 FPIFEQMRQEDPVHYCAESTYGPYWSVTRYEDIMAVDTNHHVYSSDAHLGGIIID 2456489

2456488 DGIQNDPENDFKAVNFIAMDKPKHDEQRKSVNGITNPNNLQHFGEIIRKRTSNLLDSLPV 2456309

2456308 GEEFDWVSTVSIELTTQMLATMFDFPFEDRHKLTRWSDVSTAEPGSGIVETQQQRI 2456141

2456140 DELMEMAAYFSDLQQSRKDKPDNIDLLTMMTHSPAMANMPPEEFLGNLSLLIVGGNDTT 2455964

2455963 RNSMTGGVFGFSLFPEQWDKMVADPTLIDNAVAEIIRWQTPLAHMRRTALEDAILGG 2455793

2455792 KQIRKGDKVVMWYASGNRDTSIFDDPDKIIIDRKNARRHLSFGFGIHRCMGNRIGELQLR 2455613

2455612 ILWEEVLKRFSRIEVTGEPELTNSNFVKGYTSLPVKLHAL\* 2455490

>CYP153A21 Ectocarpus bacterium, 68% to CYP153A2 Caulobacter crescentus CB15 GenPept AAK22050

2728336 MSQAAVQPEGEIDHTERAWSMPLKDINIADPDIFQADAIW

2728456 PYFERLRKEAPVHKAYSPDFGEYWSVTRYEDIMAVDTNHHVFSSSWEHGGITLFDQISDF 2728635

2728636 QLPMFIAMDPPKHDQQRITVQPIVAPNNLKNWEGLIRERTGQILDSLPRGEVFDWVDNVS 2728815

2728816 VELTTMMLATLFDFPFEQRRKLTRWSDVATGRNNPEIVADDDQWRAELLECLEAFT 2728983

2728984 DIWNERINSDTPGNDLITMLTRGESTKNMDPMEYLGNIILLIVGGNDTTRNSMTASVYA 2729160

2729161 LNKFAGEYDKLLAKPDLIPNLSSEIIRWQTPLAHMRRTALEDIVLNGAHIKKGDKVAMWY 2729340

2729341 VSGNRDESVFEDADKVIIDRPNARRQMSFGYGIHRCVGNRLGELQIKILWEEILKRFPKI 2729520

2729521 EVMEEPTRTKSVFVKGYTYMPVRIPA\* 2729601

>CYP153A22 Ectocarpus bacterium, 71% to CYP153A2 Caulobacter crescentus CB15 GenPept AAK22050

2729680 MSQAAAETPSTVDHQERAWS

2729740 MPLEDINVADGALFQDDAIWPYFERLRKEAPVHKGHSDEFGDYWSVTRYEDIMAVDTNHH 2729919

2729920 VFSSEGAITLADPLEDFRAPMFIAMDPPKHDKQRITVQPIVAPKNLQNWEGLIRERTGLI 2730099

2730100 LDQLPRNETFDWVDKVSIELTTMMLATLFDFPFEERRRLTRWSDVATGRDNPEIYK 2730267

2730268 SEEQWRGELMECLEAFTGLWNDRVNSDTPGNDLISMLASGESTKNMDPMEYLGNIILLI 2730444

2730445 VGGNDTTRNSMTGSVYALNKFAGEYDKLIADPSLIPNLSSEIIRWQTPLAHMRRTALEDI 2730624

2730625 ELNGQMIKKGDKVAMWYVSGNRDTAVFENADDVIIDRPNARRQMSFGYGIHRCVGNRLGE 2730804

2730805 LQIKILWEELLKRFPKIEVMEEPTRTRSPFVKGYTYMPVRIPA\* 2730936

>CYP153A23 Ectocarpus bacterium, 68% to CYP153A2 Caulobacter crescentus CB15 GenPept AAK22050

2731016 MSQAVAEPQTDVDHAERAWS

2731076 MPLNEINPARRDLFQNDVIWPYFERLRKEAPVHKAYDEDFGEYWSVTRYEDIMAVDTNHH 2731255

2731256 VFSSDWTNGGITLFDAAEDFRLPMFIAMDPPKHDQQRITVQPIVAPNNLKNWEGLIRERT 2731435

2731436 AYVLDSLPRGETFDWVDNVSIELTTMMLATLFDFPFEERRKLTFWSDMVTTDPKT 2731600

2731601 LEGGVEEKRGHLLACLEYFTGLWNERINSDTPGNDLITMLTRGESTKNMDPMEYLGNI 2731774

2731775 ILLIVGGNDTTRNSMTASVYGLNKFPGEYDKLIADPSLIPNLSSEIIRWQTPLAHMRRTA 2731954

2731955 LEDIELNGTMIKKGDKVAMWYVSGNRDADVFENADDIIIDRPNARRQMSFGYGIHRCVGN 2732134

2732135 RLGELQIKILWEEILKRFPKIELMEEPTRTPGCFVKGYTYMPVRIPA\* 2732278

>CYP153A24 Ectocarpus bacterium, 68% to CYP153A2 Caulobacter crescentus CB15 GenPept AAK22050

2732360 MSQAVAEPHTEIDHTERAWS

2732420 MPLNEFNPAQRDLFQNDVIWPYFERLREEAPVHKCFDEEFGEYWSVSSYEHIMAVDTNHQ 2732599

2732600 VFSSSWEHGGITLFDGPEDFQLPMFIAMDQPKHDEQRKTVQPIVAPNNLKSWEPLIRERT 2732779

2732780 GMVLDSLPRGETFDWVDNVSIELTTMMLATLFDFPFEDRRKLTFWSDMVTTDAN 2732941

2732942 TLEGGEEEWKGHLLECLAYFTELWNQRINSDKPGNDLITMLTRGEATKNMDPMEYLGN 2733115

2733116 IILLIVGGNDTTRNSMTGSVYALNKFPTEYDKLIADPGLIPNLSSEIIRWQTPLAHMRRT 2733295

2733296 ALEDFELGGKMIKKGDKVAMWYVSGNRDKTVFENADDVIIDRANARRQMSFGYGIHRCVG 2733475

2733476 NRLGELQIMILWEEILKRFPKIELMAEPTRSPGCFVKGYTYMPVRIPE\* 2733622

>CYP153A25 JCVI\_PEP\_1096681995831 seawater sequencing, 70% to CYP153A18

MSIHPEIDNSSGPLRELDVSLPEHYENDTWRPMFARLRKEAPVHYLSDSVNGPFWSVTSHALIKEVDANNSIFSSEKGGI

SIVDLKPVEGQVQGKNFIAMDEPEHSIQRSAVAPSVAPKNLVELEPLIRERAVDILENLPVGETFNWVQEVSIELTARML

TTILDFPYDQRHKLVQWSDLATDVPQVTGKEGTDMQARYDELMNCAAAFYQLWVSKSGQPPSFDLISMLQNNPDTARMNE

DMELFLGNMLLLIVGGNDTTRNSISGGVMALNQYPDEYQKLRDNPALIPNMVSEIIRWQTPVIHMRRTALEDYELGGQHI

KKGEKVIMWYLSGNRDESVFEDPDRLIIDRPNARSHVAFGFGVHRCMGNRMAELQLRVLWEEIMERFHTIEVVGDITRLP

NNFIRGIKEVPVRVHAH\*

>CYP153A26 ABS61648.1 Parvibaculum lavamentivorans DS-1

CDS 27133..28401 locus\_tag="Plav\_0025"

73% to CYP153A2 Caulobacter crescentus

MSDAAVKYEADEARDEAYSIPLAEINVADPSLFRDYKMWPYFERLRAEAPVHYSQGNEDTGPYWSVTRYN

DIMSVDTNHQVFSSEGGITLRDQDEDFKLPMFIAMDPPKHDDQRKVVSPIVAPGNLAKLEGTIRERAGKI

LDELPTGEPVDWVDRVSIELTTQMLATLFDFPFEERRKLTRWSDVATATEESGIIESEEQRRAELLECAE

YFMGLWNERVNAREPGNDLISMLAHGESTRNMDKMEYLGNLILLIVGGNDTTRNSISGGLYALNKFPDQY

KKLLANPGIIPNMVPEIIRWQTPLAYMRRTALQDAEVGGQTIRKGEKVAMWYVSGNRDESVIQNPNELVI

DRERPRQHLSFGFGIHRCVGNRLAEMQLRIIWEEILKRWDQPIRVLSEPQRVHSSFVKGYEKMMVELPKR

KH

>CYP153A27 ABS63384.1 Parvibaculum lavamentivorans DS-1

CDS complement(1917064..1918329) locus\_tag="Plav\_1765"

68% to CYP153A2 Caulobacter crescentus

MSETLVAARDKSIADAYAIPLEKIDVSNPELFRANAIWPYFERLRREDPVHYCKESEYGSFWSVTKYKDI

MHVDTNHGIYSSEATLGGVALRNQEEGFFLPMFIMMDPPKHDAQRKVVSPIVAPGNLAKLEGTIRERAGN

ILDSLPVNETFDWVDRVSIELTTQMLATLFDFPWEERRKLTRWSDVAAAGTAFGDEETEKARRNELRDCA

AYFTELWNQRVNATEPGNDLITMLAQGEATKNMGPMEYLGNVLLLIVGGNDTTRNSITGGLLALNENPVQ

YKKLRDNPSLVESMVPEIIRWQTPLSHMRRTALQDTELGGKQIKKGDKVVMWYVSGNRDEEAIENANSFI

IDRKHPRQHLSFGFGIHRCVGNRLAEMQLRVVWEEILKRWPDKPIEVVGEPTRVFSNLIKGYSSMPVRIP

G

>CYP153A28P Pseudogene (their call) Parvibaculum lavamentivorans DS-1

CDS 1927820..1929084 locus\_tag="Plav\_1775"

67% to CYP153A2 Caulobacter crescentus

1927820 MSSMNVAERVQSLDDPYAIPLDKLNVSDPELFRSNRMWPYFERLRREDPVHYCAESAYGPFWSVTK 1928017

1928018 YKDIMHVETNHGVYSSDVEQ 1928077 (frameshift)

1928077 GGITIRDNNAGLKLP

1928122 MFIAMDPPKHDAQRKVVSPIVAPANLAKLEGTIRERAGKILDSLPVNETFNWVDRVSIEL 1928301

1928302 TTQMLATLFDFPWEERRKLTRWSDVATSEEAFKTPEGEAAREAELLECAAYFTELWNQRV 1928481

1928482 NATEPGGDLITMLAQGESTKNMSPAEYLGNVILLIVGGNDTTRNSLTGGLLALHE 1928646

1928647 NPDQYRKLRENPALVETMIPEIIRWQTPLTHMRRTALQDTELAGKRIKKGDRVVMWYVSG 1928826

1928827 NRDEEAIDEPNRFIIDRARPRQHLSFGFGIHRCVGNRLAEMQLRIVWEEILKRWPDKPIE 1929006

1929007 VVDEPKRVFSNFIKGYEALPVRIPG\* 1929084

>CYP153A29 Parvibaculum lavamentivorans DS-1 ABS63400, 73% to 153A8

CDS 1935500..1936753 locus\_tag="Plav\_1782"

temporarily named CYP153A26 but revised to match genome order of P450 genes

1 MTTDTLVGDT ASTVPLSQMD VSDPKLFQSD MIGSYFARLR REDPVHYCPE SAYGPYWSVT

61 KFNDIMQVEV NHQTFSSEAK LGGIALQDMQ SGEAALELEM FIAMDPPKHD AQRKAVSPAV

121 APSNLVLLEP IIRERAGIIL DSLPIGEEID WVDRVSIELT TMTLATLFDF PWEERRKLTR

181 WSDVATSTPE TGVVSSFEQR REELLECAHY FKGLWDQRVN EPPKPDLISM MVHSPATRDM

241 PYLEFLGNLI LLIVGGNDTT RNSISGGVLA LNQNPAEYRK LMADPDLIPK MIPEIIRWQT

301 PLTHMRRTAL MDAEIGGKKI RKGDKVVMWY LSGNRDDEVI DRPNEFIINR PNSRHHLSFG

361 FGVHRCMGNR VAELQLRIIW EEILKRFSKV EVVGAPERTL SNFIRGFTHL PVKLYVH

>CYP153A30 ABS63566.1 Parvibaculum lavamentivorans DS-1

CDS 2129237..2130550 locus\_tag="Plav\_1951"

58% to CYP153A26 Parvibaculum lavamentivorans DS-1

54% to CYP153A2 Caulobacter crescentus

MSEQVSVGRDYTRSNADLAAKWKIDVNRDPWSIPLEELDPAHDELFAANTVLPYFERLRKEDPVHLNETG

PYGRYWSVTKYEDIMHVDTNHKIFSSDIRNGGIRLGGQRIEGEPDPLTYLPMFIMEDPPKHDEQRKAVQP

MFTPQNLADLEPLIRERAGLILDALPRGETFNWVRQVSVELTGRTLATLFNVPQEDRHKLIHWSDTVERL

GDPEYFETPEEGFKELWNCWEYFDGVWKDRLANPGSDLISLLAHSPSTKNMPPNEYLGNMLLLIVGGNDT

TRNSITGGVLALNQYPDEYAKLIANPDIIPNMVSEIIRWQSPVAHMCRTATEDTELGGKKIRKWDKVAMW

YVSGNRDDSKIDRANEFLIDREGARHHLSFGFGIHRCIGNRVGEMQLRILWEEIMKRFKKVEVVGDPKYL

RSNFIRGITELPVIVRE

>CYP153A31 ABS63742.1 [Parvibaculum lavamentivorans DS-1]

CDS complement(2309535..2310806) locus\_tag="Plav\_2128"

64% to CYP153A2 Caulobacter crescentus

77% to CYP153A7 Sphingomonas sp. HXN200

MTATASAAAPAGIDDPYALSLDQIDVSKPELFERNAEGAYFARLRREDPVHFCADSAYGPYWSITKYKDI

MAVDTNHQVFSSEAGLGGIIIEDGIQKSSGEGSIDLPNFIAMDPPKHDGQRKAVSPIVAPANLANLEGTI

RERVGRVLDGLPVGEEFDWVPAVSIELTTQMLATLFDFPFEERSKLTRWSDVATAEPGSGIVDSWEQRTS

EIMECAECFQGLWNERMEKPGMDLVSMMAHSPATHDMTPQNYLGNVLLLIVGGNDTTRNSMTGGVLALHQ

NPAEFAKLKANHGLIDSMVSETIRWQTPLAHMRRTALADAEVGGKTIRKGDKVVMWYVSGNRDKDVIIQP

DDFIIDRERPRQHLSFGFGVHRCVGNRLAEMQLKILWEEILKRFSRIEVTSEPVRTRSNFVRGYASMPVR

LHA

>CYP153C1 Novosphingobium aromaticivorans

MAATLAPDRAINPHDVSLNALYTEDRWREPFRWLRENMPVSYRA

ESPFGAYWSVVTHDLIQQVELDPGTYSSSWQRGNITIADSVNETEFPNFIAQDPPIHT

AQRKVIAPAFGPSQMVKLERLVRERTTQLLDGLPMGEEFDWVERVSIPLTLGMLLILF

DMPFDEWRDIKRWSDWASGVSEDSLNDAYRAEFVQQMGQMLMRFDRELEARRALPPSD

DLLSRMVHSDAMGHLTPPERIANIALLIVGGNDTTRNSMSGLIEALHRYPAELDKLRA

DPALSANAAQEIIRWQSPVTHMRRTLTRDAELGGQRLAEGDKIVMWYISGNRDENVFP

DAERFDVTRENARRHIGFGHGIHRCVGARLAEVQIAAVIEEIATRRLRITPQGAPTRL

ASPFLHGFTAMPVVMSRD

>CYP153D1 Novosphingobium aromaticivorans

MATQLAPEVPQFTYHSSPTATEAFAAWLKDNPQAIPAHSHPWDV

SRSDIYVEDRWQPIFAEMRAKAPVNRVPDSPYGAYWNVASHKAIMHVESLPELFSSSW

QYGGITIGDPPEDVDPQKLAERQLPMFIAMDRPDHTGQRRTVAPAFTPAKMVEMEAEI

RRRTASVLDSLPWGERFDWVDKVSIELTTGMLAILFGFPWADRRLLTFWSDWAGDVEL

TLARELADTRFGFLGEMAHYFQRLWGARMQAPPSGDLISMMIHSEAMNHMSPQEFMGN

LVLLIVGGNDTTRNTMSGIVHALDKFPDQRELLERDASLIPNAVQECIRYVTPLAHMR

RTATADTELFGNQIKAGEKVILWYISANRDETVFENPDKLMVDRPNARRHLSFGHGIH

RCVGARLAELQLRILLEEMHERRMRVRVAGEVERVRANFVHGFRKLEVELEKR

>CYP153D2 Sphingomonas sp. HXN200

MATVIRETPADLHPLDLSRADLWREDQWQEPMRQLRAESPIYYCEDSKFGPYWSVTTYKPIQHIEALPKIFSSSWEYGGI

TVAGDGIEHLKEGEIPMPMFIAMDPPQHTAQRRTVAPAFGPSEIERMRADTQARTAALIDTLPVGEAFDWVERLSIELTT

DMLAILFDFPWENRHNLTRWSDALGDIESFNTLEERQQRLATAFEMGAAFKELWDHKAKNPGKHDLISIMLQSDAMNHMS

HEEFMGNLILLIVGGNDTTRNSMSAYAYGLHCFPEERAKLEANHDPDLAVNAMHEIIRWQTPLAHMRRTALEDTELFGHQ

IRARDKIALWYASANRDESIFPDGDRIIVDRENARRHLAFGYGIHRCVGARVAELQLTTLISEMQKRRLRVNVLAEPERV

NASFVHVSPHAGRTRALLTAVTAGPISAR

>CYP153D3 Sphingomonas sp. HXN200

MASTATLVRTASPIAPIDVSLPELYAEDRWQEPFRTLRAQAPIQYVPDSKFGPYWSVTTYKPIVYIEALPKLFSSSWQYG

GISIAFDSDKLLEHEVRQPMFIAMDPPQHTAQRRTVAPSFGPSEVAAMKAEVQLRTGALLDSLPVGDPFDWVQKVSIELT

TGMLARLFDFPWEERHNLTHWSDIGGDVELIRSPEGLVERNTKLLQMGMAFAALWQEKAQNPGKDLISVMLKSDAMNHMS

NEEFIGNLVLLIVGGNDTTRNSMSSYAYGLAQFPEERAKLEANPALIPNAVQELIRWQTPLAHMRRTVEEDTEIDGQLMK

KGDKVVLWYLSANRDETVFKDADRIIVGRENARRHLSFGYGIHRCVGARVAELQLVTLLEEMAKRRLRANVLAEPVRVPA

CFVHGYKSLQVELSHY

>CYP153E1 Erwinia chrysanthemi strain 3937

MKMTKQLQDVFEDIDAVPLEKINPASRDRFINAAELPMFERLRREDPVHFTPESEFGPYW 4874499

4874498 SLTLWEDIRAVGNNYRDFTSTQNIDLKSIEEKIKLEAALQALGHERRKNVGFITMDPPEH 4874319

4874318 TKHRKAVTPAVGPSSLAQMEPIMRERAGIILDSLPIGEPFDWVDLVSKELTATVLATLLD 4874139

4874138 FPFEERRKLTFWSDLLMFEPGHGLVKSWEQKAEETVKCYQVFEALWEKRRNGPPSYDLIS 4873959

4873958 MLAHHPDTRDMTLEQFRGTIVLLIIGGNDTTRNTISSSLYLLDKYPEEFAKLKANPKLVM 4873779

4873778 PMISETLRFHPPVNFMSRVATRDVEIRGKNIKEGDRVVMWYTSGNRDASAIEDPDTFSID 4873599

4873598 RERARRHLSFGVGVHACIGSRVAEMQLTVIWEEILKRFSRIEVLEEPERSYSNFLHGFEN 4873419

4873418 LKVII 4873404

>CYP154A1 Streptomyces coelicolor cosmid E6

MATQQPALVLDPTGADHHTEHRTLREGGPATWVDVLGVQAWSVS

DPVLLKQLLTSSDVSKDARAHWPAFGEVVGTWPLALWVAVENMFTAYGPNHRKLRRLV

APAFSARRVDAMRPAVEAMVTGLVDRLAELPAGEPVDLRQELAYPLPIAVIGHLMGVP

QDRRDGFRALVDGVFDTTLDQAEAQANTARLYEVLDQLIAAKRATPGDDMTSLLIAAR

DDEGDGDRLSPEELRDTLLLMISAGYETTVNVIDQAVHTLLTRPDQLALVRKGEVTWA

DVVEETLRHEPAVKHLPLRYAVTDIALPDGRTIARGEPILASYAAANRHPDWHEDADT

FDATRTVKEHLAFGHGVHFCLGAPLARMEVTLALESLFGRFPDLRLADPAEELPPVPS

LISNGHQRLPVLLHAG

>CYP154A2 Streptomyces avermitilis

MSEQQIIVLDPTGSDPDAEHQALRERGSAALVDILGVRAWSVSD

PALLKQLLTSKDVSKDGRAHWPAFAETVPTWPLALWVAVENMFTAYGDNHSRLRRMVA

PALSARRTAALQADIEALVNSMLDGLDAFPAGEVADLRKHLAYPLPIAVIGKLMGVPA

DRRTEFRTVVDNVFATHLSAEEQAANTAALYALLDALIEIRRAEPGQDMTSLLIAARD

EEDGSAFSDAELRDTLLLMISAGYETTVNVIDQAITTLLTDPCQLAHVREGRCTWQDV

VEETLRHQPAVKHLPLRYARIDIPLPDGQTIKTGEAILASYAAANRHPTWHEDADRFD

ATRPSKEHLAFGHGVHFCLGAPLARLEVATALRLLFERFPDARLATERTALEALPSLI

SNGHTSVPVHLRPTSSASS

>CYP154A3 Streptomyces peucetius

MFTAYGGDHRRLRRMVAPAFSARRIQAMRSAVEKVVTALLDDLDSKPAGEAVDLRKHLAY

PLPIEVIGQLMGVPHEQRDGFRAEVDGVFDTTLTTEQASANTAALYEALNQLIVAKRAEP

GDDMTSLLIASRDDEGDGSALTDDELRDTLLLMISAGYETTVNVIDQAVTALLTDPEQLA

HLQSGRADWSSVVEETLRHEPAVKHLPLRYALTDIPLPDGQTIAQGEAILASYAAANRHR

DWHGESADRFDLTRPTKEHLAFGHGVHFCLGAPLARLEVATALQQLFERFPEIELAVPAE

ELKPLPSLISNGHQALPVRLRPAAR\*

>CYP154A4 Streptomyces scabies SCAB20211

MIDPTGRDIH GEAARIRERG PATRVLLPGP HDVEAWAVSS PDLLKRLLTD PRVSKDARQH

WPRLAAGEIT PEWPLFTWVA VQNMFTAYGG DHRRLRILVS KALTARRTAA LRPRIEEITE

ELLDRVEEGL GHGGTVDLRK EFCYPLPIQV ISELFGLPEE KGLVLKDLVD KLFDTSAEPG

EMTAAYERMY GVLGELVADK RESPGDDLTS GLIAARDEDD TRLSEQELLD TLVLVVSAGH

ETTVNLLDRA VHSLLTHPGQ LAHVREGRAT WDDVIEETLR VEAPVANLPL RYAVEDLDLG

EFGGPAGVVI AKGDPILAAY AAAGRDPGRH GKDADVFDVT RADKEHLAFG HGVHHCLGAP

LGRMEARIAL PALFARFPDL ELAAPEAELG HVESFISNGH RRLPVRRS

>CYP154A5 SBI\_1147 Streptomyces bingchengensis

58% to CYP154A4 Streptomyces scabies SCAB20211

missing about 34 aa at N-term

VAWAITDPTLLKQLVTDARVSKDPRQHWPKFINGEIPATWPLIAWVAVEN

MFTAYGADHTRLRRLVAKAFTGRRTTALRPRIEHLVSRFLDGLAAGGPDT

AVDLKAAYCHPIPMEVICELLGVPEGEMRERELEFVSTMFRTNAPPEEAI

AAYQGHEALLRELVTLKRHSPGDDITSDLIAVRDEDGSHLNEQELADTVG

VLIAGGFETTVQLLDNAVHAMLTHPDQLALVRSGQASWDDVIEETLRAQP

PVVNVPLRYAVEDIELEGVTIKQGDAIILSLTAVNRHPEVHGEDSDHFDI

TRAVKEHLAFGHGVHYCLGAPLARLEARIALPALFDRFPELQLAVPAQDL

LPLPTLISNGHQTLPVRTGR

>CYP154B1 Streptomyces fradiae tylosin-biosynt.

MAPDPVLVPRVGTYSMRPTERSARMETTSCPYALDPLGRDLAGE

AAMLRSQGPATWVELPGGVGAWAVTGHRYVKQVVADPRVSREARHWPAFTEGRITEEW

PLYYWVAAQNMMFSYGERHARLRRMVAGAFTVRRTEALRPRIEGLVGELLDGLAASPA

GEPVDLRASFAKLLPMRVICALFGVPEADRDTLCAEVDTTFNTAATPEETTASQIKVF

RMLAELIALKRAEPEDDLTSALIAIRDSGDRLTEDELIGTLNLMIAAGAESTVHLIGN

AVAALLTRNDQRDLVRSGRAGWEDVIAETMRTKNPAAYLPLRYAVEDIDLDGVPIRKG

DPILVSFAAPGLDPERHGDDAAEFDLLRAGRDNLGFGHGVHYCLGAPLARLEAGIALE

KLFERFPAMSLARPVESLEPLSSLIVNGYAALPVLLGPAAS

>CYP154B2 Streptomyces avermitilis

MAETAEAPGTAEAPGTAEAPGTAEAPETAEVSGTAEAPRTAETA

EAPETNGTNRVAEGVGAAGVTGMNQCPYALDVTGRDLAGETAQLRTRGPAVEVELPGG

VAAWAVVRQKYVKQLLMDARVSKDARQHWPAFVSGQIDEAWPLYPWVANENMLFAHGD

RHARLRRLNAAAFTARRTEALRPRVEEITAALLDGLADRPAGEQVDLRAEFAKLLPMR

VICELFGIAEANREPLCTALELVFGTAVPADEMAAAQVKVFGMLAELVAEKRERPGGD

LTSALIEARDGDDSRLTEQELLGTLYLMIAAGQETTCTLITNAVAALCAHPDQLSHVR

EGRADWADVVGETLRTHGPAAYSPMRFAIDDIELDGVHIKKGDPILVSFAAAAADPEP

YGADAAVFDVLRPGRRDDLAFGYGVHRCLGAPLARLEATTALSALFTRFPDLTSVQPT

EELEPVRSFIVNGYGSLPVVLRPH

>CYP154C1 Streptomyces coelicolor cosmid 6D11

MTTGTEEARIPLDPFVTDLDGESARLRAAGPLAAVELPGGVPVW

AVTHHAEAKALLTDPRLVKDINVWGAWRRGEIPADWPLIGLANPGRSMLTVDGAEHRR

LRTLVAQALTVRRVEHMRGRITELTDRLLDELPADGGVVDLKAAFAYPLPMYVVADLM

GIEEARLPRLKVLFEKFFSTQTPPEEVVATLTELASIMTDTVAAKRAAPGDDLTSALI

QASENGDHLTDAEIVSTLQLMVAAGHETTISLIVNAVVNLSTHPEQRALVLSGEAEWS

AVVEETLRFSTPTSHVLIRFAAEDVPVGDRVIPAGDALIVSYGALGRDERAHGPTADR

FDLTRTSGNRHISFGHGPHVCPGAALSRMEAGVALPALYARFPHLDLAVPAAELRNKP

VVTQNDLFELPVRLA

>CYP154C2 Streptomyces avermitilis

MTTRIALDPFVSDLEAESAALRAAGPLAAVELPGGVPVWAVTHH

AEAKKLLTDPRLVKDINVWGAWQRGEIAPDWPLIGLANPGRSMLTVDGADHRRMRTLV

AQALTPRRVEQMRERITKLTEELLDRLTGEVVDLKADFAYPLPMYVVADLMGIDEARL

PRLGELFEKFFSTQTPPAEVIATLTELAGIMAETVAAKRAAPGDDLTSALILASEDGD

HLTDAEIVSTLQLMVAAGHETTISLIVNAVVNLSTHPEQRALVLSGEADWSSVVEETL

RYSTPTSHVLIRFATEDVPVGDKVLPAGDALIVSYGALGRDEAAHGPTAGEFDITRST

ENRHISFGHGPHVCPGAALSRLEAGVALPALYARFPKLDLAVPAAELRNKPVVTQNDL

FELPVRLG

>CYP154C3 SGR1085 Streptomyces griseus

MNCPHTAAAQTDPGAGTVVIDPMVQDLDGETARLRDAGVLARIDLLGVPAWTVTRHAEARQLLLDQRLVKDIDAWGLWQSGVVTRAWPLIGMIDAGRSMFTVDGAEHRRLRTKTSQALTPRRLEAIRPEIEKFTDELLDALDAARGEDGVVDLKSVFAQPLPMKVVGMLMGVDESQHAMLTRQYKAFFSMLTPQEERLALLAELDVFYTDLVREKTARPTDDLTSALILAEEGGEPLTEEEVVGNLKAMVAAGHETTIGLVLNAVRALLSHPDQLRMVLAGEAGWDAVIEETLRWDTPTTHLLMRFATEDITVGDDVIRKGEGVVVSYRAIGRDVGHHGPDADAFDITRPTRNRHMTFGHGPHICPGAALSRVEAGIALPALFTRFPGLRLAVPDEEITKLPVMTQNDMTAFPVLLG

>CYP154C4 SGR3108 Streptomyces griseus

MTRIALDPFVRDLDGESAALRAAGPLAEVELPGGVHVYAVTRHAEARALLTDSRVVKDINVWNAWQRGEIPMDWPLIGLANPGRSMLTVDGADHRRLRTLVAQALTVKRVERLRAGIEALTNASLDRLAAHPAGAPVDLKAEFAYPLPMNVISELMGVDAADHPRLKELFEKFFSTQTPPEEVPQMMADLGTLFTKIVDSKRANPGDDLTSALIAASEDGDHLTDEEIVNTLQLIIAAGHETTISLIVNVVEALATHPEQREKVLNGEIGWDGVIEETLRWNTPTSHVLIRFATEDIKVGDRVLPKGEGLIVSFGALGRDEEQYGPTAGDFDAGRTPNRHIAFGHGPHVCPGAALSRLEAGIALPALYERFPELDLAVPAAELRNKPIVTQNDLHELPVKLGCPFGHDA

>CYP154D1 Streptomyces avermitilis

MRGVPRAGRLVRRTAPTRRRSQETSLDTSSGTQPHRMDPAGGCP

HADNARLLARGAVAPVLLPGDIEGMAVLGHDALKEFLAHPEVAKNARHFTALQEGRTA

PGWPLLTFATVQGMTTADGEDHRRLRSLVSKAFTARRVERLRPWIEELTSALLDGLGR

AAEEGGQVADLRAHFALPLPMGVIGELLGVDAEHRDRLHHLSNQVVATDIGPEQAIAA

NRELVAVLSTVAAARAERPGDDLTSALIAARDEGGDRLSQQELIGTLVLMIIAGHETT

LNLITNAVRALCGNRDQLELVRKGDAGWPDVVEETLRWDAPVSYFPFRYPVRDLTVDG

TVIPAGTPVLAGYSAAGRDPAAHGPDADRFDVTRPARSETTRHLSLGHGAHYCLGAPL

ARMEATIALERLFTRFPDLELAVPEAELARHSSFVGNSVRALPVRPGVPRS

>CYP154D2 SBI\_870 Streptomyces bingchengensis

70% to CYP154D1 Streptomyces avermitilis

MTDATDETDATDATDATDGQCPVPHAAAPHAAQDPHRLDPTGAGQHAVNA

RLRERGAAVPVLLPGDVTAYAITRHEELKDFTTHPQVAKDACHFAALRDG

EIPPGWPLATFATVRGMTTADGADHKRLRSLVTRAFTPRRVETLRPAVEE

LTAALLDRLAEAAAEAPDGVVDLRRHFALPLPMGVICRLLGVGPEHQDRL

HALSNDIVGTRTAPERALAANREMIAILGQVAAARLRSPGDDLTSALIAA

HEEDGDRLSEEELIGTLVLMIIAGHETTLNLITNAVRALCAHRDQLELVR

SGVGEASWGDVVEETLRYDSPVSLFPFRYPTRDLTVGDTVIPQGAPVLVS

YTSAGRDPRAHGADADRFDITRHTRPDAARHLSFGHGAHYCLGAPLARME

ATIALDALFTRFPGLDLAVPDDALVPHPSFVGNSPQELPVRLRPAGPAAH

SG

>CYP154E1 Thermobifida fusca

MGQSRRPHTVYLDPAKGVDIPAQRRELLDKGPVVRVAFPGNLEV

WALTHDAPLRNALADESVFVRGWRNWRALMAGEVDPTHPVANMLRVESMLARSGADHK

RMRGLVQAAFTRRRVEALRPRIEEITNELLDRMAESDGVVDLKAAYSFPLPIRVISEL

LGLNEEDHLTLQTLVTRTLSGTDPEANADAFTFVASLIEAKRKNLDDGLISAMIEARA

EDGDRLSETELIHNTLLLIIGGFETTMGMISNSVQLLLTHPDQLHLLRTGQASWENAI

EECLRFESAVVMLPFLYTTRDVEIDGITIPAGDAVLIGFGPANRDPQAYDDPDRFDIT

RPRPRHLAFGHGAHLCLGAALARLELLIALPALFERFPDITLVGEAPPTPTVFMNHPL

SRPVLLRPKP

>CYP154F1 Thermobifida fusca

MAVSADHAAAGALPGARHPAGRRVRAGRRLLDHRLRSGTRRPGG

CPVHRPAQPVRDPRPPGVGDRAPRVPGAADLPADRGRRGECAAGPVAGRASRGSPRVA

GAAPFPVRPRTQGASCHLHPRRHHPTNGGT

MAAVPEPIVLVPGKSREQALQLREAGPL

ARVVVEGLEVWALTHDRELREALIDPRFRRNWRTWRALNEGEVATDHPVAAMVYLDNM

LTVDGEAHRRMRSPVAQAFTPRRVELLRPRVTEIVNALLDQLAERDGTVDFKTEFAYP

LSMRVFSALFGIPERDHGRMQQMVNTAFSPSSPEEVRAMREELDAFLDELIEDKRRSP

GEDLTSALVTATDEEHKLSDAELRDTLWLLVTAGFETTSSALANAVQTLLTHPDQLAH

LRSGSIAWEDAIEEVLRQSSSVATLPFLFAAEDVQIGDRTIRAGEPVLLAYLAANLDV

ERYGEDAAEFDATQSRPRHLAFGHGPHTCLGAALARLEMEVALTTLFTEFPEVSLAEG

EAPRLESVFIHAPAALPIRLGPRRTAA

>CYP154G1 Thermobifida fusca

MLDTERGLTEADIHALAEHGPVVRLSVMGLDVWAVTGYEELRTL

MADPEVKRGVEHWTAVAQGKVPAEHPLVKLVSMGSMLSKNPPEHTRLRRLVQHAFTTR

RVEGLRPVVQELTRACLDRIDASQPFDINAALSHPVPVGVIGRLLGIPETDQPALDSL

VTRLLSGTDATVHEELYAYVAAMVAARREQPDDGLISALLHVHDDDGSTLSEEDLMWT

VVLLVDAGFETTVGQISNSVRLLLEHPDQLALVTSGEVPWERAVEECLRHTASVVMLP

FCFPTREKELGGYTIGAGEPVMMVYGAANRDSRVHAAPKVFDVTRSDSRHITFGHGPH

HCLGAPLARLELNVVLPELFARFPKLALAERDIPRVKSLFVNRPSELWVTAGMG

>CYP154H1 Thermobifida fusca

MMASPTDNPIVLDPYVSDLEGERERLYEAGPIAWVELPGGVRTW

SVTHHQAARELLTDSRLSKNMAHWGAYNRGEISPTWPLLSVIPPTPTNLLGTDGAEHK

RLRTLTAQAFTPRRVEKLRPRIREITEELLDALEERANEPQDLKSEFSFKLPMRVIGE

LYGVEEAAHGQLRSLYDKFFSSVTPPEEFLATREALVQFYTELMERKKANPSDDLTTA

LLQANENGDRMTDEEVLGTLQIVVAAGHETTVNLLTNTVRALLRFPDQLELLRTGKAT

WEAAIEESLRWDPPTTNFIFRFATEDIEYGGVTIAKGDSVMISYGAIGRDRGQHGDNP

EVFDVTRKTSSRHISFGYGPHVCPGAPLARLEAQVALPMLFERYPDMKLAVDDSELVP

NPSVIVNSLKEFPVILRP

>CYP154J1 Streptomyces carzinostaticus subsp. neocarzinostaticus

MCPYRLDPEGADTHGETARLREQGPIARVELQDGVLAWSVHDYA

VAKQIMADERFSKNPRKNWPAYINGEISNGWPLITWVAMDTMATQDGADHARLRKLLL

KAFTERRVESMRPHIEKTVKELLDNMAAKADDEIVDIKEMFHAELPTRLMCDLFGVPE

ERRAEVLAGGHKNIDTRISSEAAEANLGQWQEAISDLVEYKRHHPGDDLTSALIEARD

EGSRLSDSELIGTLHLLLGAGSETLVNALAHSSLALLVDADLRKKVTSGEIPWVNVWE

ETLRVESPVAHLPFRYATEDFEIGGVKISKGDPLLVDFAGIGRDPAVHSDAPDEFDAL

RPDKTHLSFGHGVHYCLGARLAKHAWMIGIPALFERFPDMELAVRRDELKGQGSFVVN

GHASLPVHLKGRAAALAR

>CYP154K1 Streptomyces rochei plasmid pSLA2-L

MLRQEAPYVIDSAGRDLPGEAARLRERGPVVRVVLPGGVSAWAV

TDLDLIKQLLTDSRASKDAYRHWPAWAGGEVDESWQMSMWVSVRNMLTAYGEEHARLR

RLVAGAFTARRTADLRPRVERITARLLDGLAAVPPGAAVDVRNEFARPLSVLVMGETL

GLPEDLHADLQRMVDVLFKTTAEPEEARANQYELYALLTELVAARRSAPGTDLTSELI

AARDEDGGEGLSEKELVDTLLLLIGAGTETTVNLIDQAVHGLITHPAQLALVLGGEAT

WDSVIDETLRHQPVVANVPFRFAVEDIEVGGVTIPKGDPILLSLAAAARCPHRHGADA

DQFDVARPSRRDHVPFGYGVHHCVGRPLARLEVSIALESLFARYPRMAAAVPEAELAV

RESFISSGHVALPVVLVPGAAA

>CYP154L1 Streptomyces scabies SCAB32131

MRVELPGGIP AWAITRHTVL RDLLLDDRVS KDPRHWELWT SGWVEANPEA HWIYNWTGVT

NMFTAYGPDH RRLRNLVAPA FTGRRTLDLL PRIEEITTSL LDSLSTRAAS LPGRPADLRI

LFAYPLPLLV ISELFGLTEQ ERGDAAHFVD MIMDTTTPPE IAGQILTHTR SVMARLLARK

REQPGNDLTS ALITARDQGD RLSEQELVDT LILTLGAGFE TTVNLIGNAI AALLDHPDQL

DLLLNGAVPW KQAIEEVLRW APPITSLPLR FATTTIDLGE ETIIQGEAIL TTFGAVGWDP

DTHGPRAHEF DITREPGKHL AFGHGVHHCL GAPLARAEAT IALPALFTRF PDLRLTMPAP

ELTPFPSFVS HGHTTLPAHL TPSPATSTAT

>CYP154M1 Salinispora tropica (marine actinomycete)

MRRRCPVVIDPAGTDIHAEGARIRANGSVSQVELPGGVLAWSVTGQQVARKVLSDQRFSK

DPRKHWTDYLEGRIGQDFPLIGWVLMDNLTTAYGSDHSRLRKPCANAFTPRRVEALRPAV

ERAAVELLGELATVSPTESVDLKARYAHPLPSRVICDLFGVPEEDREEMLRGGEVNVDTR

VSAEEAAANVERWHQQMLDFIEEKRRNPGPDLTSDLIAAQQAEGSRLTDSEMVGTLHIML

ATGTEPVKNLIGNAVFALLTHPEQLDLVRSGRAGWDDVIQETLRMQAPVAHLPFRFAVED

VDIDGVTIRRGDPLLVNFAAIGRDPDVHGDTAAEFDITRADKEHLSFGHGVYRCIGQPLA

LREAEIALRMLFQRFPNLVLAVPPEEVTPQPTFIMNGLDTLPVLLKGRA

>CYP154M2 SGR622 Streptomyces griseus

MVVESRCPVVIDRTGQNIHAEADRLREQGPVARVELPGGVRAWSVTGYDVALSVLGDQRFSKDPRKHWTAYANGEIGDDFPLIGWVLMDNLTTAHGSDHSRLRRLTAKAFTPRRVSAMRSAIEQACTELLDELAESGPGDKVDLKARFAHPLPARVICDLVGVAPQDRAAMLRGGEVNVDTTTSPEDAAANVERWHQEMHEFVESKRRTPGDDLTSDLIAAQEEDGSRLSPSELVGTLHLMLGTGTEPVMNLIANAVHLLLTHPEQRAELRAGRISWDDVIEETLRAEAPVAHLPFRFPTEDVEIGGVTIPRGDPVLIAFAAAGRDPAVHGPSAGRFDPSRADKAHLAFGHGIYRCIGMPLAREEARIVLPALFTRFPDLDLAVAPEDIEPQGSFIMNGLRTLPVRLRSEGAGR

>CYP154N1 Frankia alni ACN14a

MVHVQPLSVAAAGPSLVAEAAALRARGPVAEVTLPGGIPAYAVNEHALLRALLLDPRVSKDPRRHWAQWD

EACRRPEWGWVLQWVGVVNMLSTYGVDHARLRRLVAPSFSARRTELLRPAVVAVTERLLDDLAAGSARAA

GSAGSVGSVGSVGSAGSVGSAGSVGSARSVGSAGSAGSVVDLVGTFAQPLPLAVISGLFGIPDRMRPDFA

HVVEQIMNTTVSSEQAAANLGRTRSVLATLVERKVREPGDDLTSELIGVRDAVTGDRLAHRELLDTLLLL

ISAGHETTRHLLGNAVHALLTHDRQLRRLRAGEITWDQVVEETLRWAPSIANIPLRFAVTDIDTGAVTIP

AGAAIVAGILAAGHDPGHHGPGASRFEPGRDAADHLAFGVGVHRCLGAPLARLEAGYALPALFARFPGLA

LATPADDLPQAPSFIVHGWQALPVRLAPPAPLVTASAR

>CYP154P1 SBI\_1935 Streptomyces bingchengensis

43% to CYP154D1 Streptomyces avermitilis

41% to CYP154H1 Thermobifida fusca

MDAISPVHLAPEPTDLHSVEGAALRAAGPVATVALPGGVVVKAVTTREAG

AQVLNDPRFSKSLRHWGAHQRGEIPAEWPLLFILEGEGLLNSDGDLHRRL

RQPVQRAFSPRRVRELRPRIEAVTDRLLAALDDVAPGQETDLQSRFALPL

PLDVICYLLGVPEEGGLREELHVLSAAALSNDAGAEELQRTMAERFPATL

MSIIERKRASGDHDDLTMDLVEAMDQGELTVPEVIGNLVVTVIGGHETTV

TLICHAVRGLLTHPETLAAARARQEAGEDPWPDVVEEALRWESPVRALLF

RYATEDVPVVGGGVVREGEAVLLPLATINRCPHAFSEPDRFDPDRPDASR

HLSFGYGAHRCPGASLAKVEAEIALRRLFETFPDIALAQRPAPRAASLGM

NSYRELPVVLRPATV

>CYP155A1 Streptomyces coelicolor cosmid 6D11

DPGDHVVEPGGRRGRTAGVGGGHVVQDGRVSARKADRGRAGPAC

PVDRAADGTWRVHDFAVARALLRGPGTVQAGLGIETVEKLPPRVRRPVLYRDGPEHRE

HRRQTARYFTPRRVDEHYREPMVRIAEEQLAVLRSAGEAPLSDLAFGLAVGVVSEVVG

LRYSRPGIRRRLERFFPEEFGEPGLTSVRGLYWLVRQNTNWLRIHLADVRPAVRAHRR

REHDDLISHLIAEGCSDVEILGECLTFAAAGMVTTREFVCLAAWHLFSDAELLGHYRS

ADETGRLAVLQELLRLEPVIGSLRRRATGPVELSCRDGPVTVRPGEYVEVHLDDANAD

PKAVGEEPLLVRPERAGAVGAGLSFGDGPHRCPGAHIALLETDVFLSRLFALDGVRMS

GGPRVAFQEAIDGYEIRDLTVALPRAGRG

>CYP155A2 Saccharopolyspora erythraea NRRL23338

MPTDSTDARKIDRGETEGGCPVHRRPDGVWEVRGYASARAVLRSTDTVQAGLGVETVEKM

PSRIRRPVLYRDGTEHREHRRQTARYFTPRRVDEHYRDIMERVTDEQLAKLRADGRAQLS

ELSFHLAIDVASSVIGLTESKPGIQARLERFFPEEFGEPGFTSINGIYWIFRQLRNWLGI

YLGDVRPAVRARKRRRQDDLISHLLDEGCSSAEILGECITFAAAGMVTTREFVNLAAWHL

FTDEALRERYRSAEEAERLEVLHELLRLEPVVGHLRRRTNAELRVPDGDSEVTVPAGEVV

DIVVSATNLDERVMGEQPASLCPGRELSDGAYAHGMSFGDGAHKCPGAHIAILETDTFLR

KLFALPGVTMETPPRVTFNDAIGGYELRDLVVSVSAN

>CYP155A3 Frankia sp. CcI3

MADPVVTDVGTSARKIDREDPNGGCPVVQGADGVWRISGYAAGQAVLRSLETKQAGLGIDASKAIPKRIR

RPVLHSDGPEHRERRRLTARFFTLRRVDEHYRELMHRVADEQIDRLRRERSVDLSELSFALAVEVAAAVI

GLTNSRPGMAARLERFAQGDLGPPNVTSIRGIRQFIRQNRHALAFYLADVRPAVRARRRRRTDDLISHMI

DQGCTNAEIFAECVTFAPAGMITTREFINVAAWHLFTDDTLRARYHDADQTERIAILHEFLRLEPVISTL

KRRTTADIQLPGPHGPLTIPAGAQIDIAVSSTNIDTQAIGADPYTVRPARPIGDGVSPAGLSFGDGPHKC

PGAHVAIHETDIFLHKLFMLDGLHMASPPQVTLRDEIAAYELRGLVVTLD

>CYP155A4 SBI\_1967 Streptomyces bingchengensis

68% to CYP155A2 Saccharopolyspora erythraea NRRL23338

MGYGARKIERAADSDGRSGCPVRRGPDGVWQVCGYAEARAVLRSTDTVQA

GLGIETVEKLPSGLRRPVLYRDGPEHREHRRQTARFFTPRRVDERYREVM

VRVAEAQLGKVRAAGRAHLADLSFHLAIEVAASVIGLTESRPGIRRRLER

FFPEKFGTPGLTSLHGIHWLLRQNVNWLRVYLADVRPAVRARRGQRRDDL

ISHLLDEGCSAGEILGECLTFAAAGMVTTREFINVAAWHLFTDDALLGRY

RAADEPGRIAVLHEILRLEPVIGRLRRRTTAALELPGDDGVVTVPTGALV

DVDLESANVDARTVGERPELIRPGRPLAEGAGAVGLAFGAGPHKCPGAHI

AILETDIFLSRLFALPGIRMATPPGVGFKDEIGGYELRGCTVECRA

>CYP155B1 Deinococcus radiodurans

MPSFLSFRSSAMTAHDAQPEPARCPFTGQAAPTETITRRHVPPQ

GDLAQPVETYARARDLLKSEQAQQAGFLADMVSRVPGSQHPPVLYLEGEEHTEMRRAT

AKYFTPTQVNTYQPDIARLADELIGKLARRGEAKLDDLSLELAVRVAAGVVGLTNSRL

PGMDRRIERFIPSGVDAEPGVKLEGASPLENARQAANMALFYALDVKPAIEARRKAPQ

DDLISYLLSRGYNDQDILTECVTYGTAGMITTREFISVAAWHLLKNPELRAAYVHGTE

KERHAVLHEILRLEPVVGTLYRRA

GTGDDCGRRSHPAGSVFALDIGQANLDPAVMGEGAEQLCPMRELPRGVQAQGLSFG

DGHHRCPGAFLAIKETDVFLRRLLIWNDLHVVSEPRVTYNEVIKGYELRGFRVRLGGARA\*

>CYP155B2P Deinococcus radiodurans

SGSTDAEILPYVVEAEPSSPVVHLDISQ

ANRDESVFTQAQQFCPHRKNVRQHLSFGKGEHACLGQSLVYTICRVMAHALELLSAPAGQ

RTDQVSQ\*

>CYP155C1 Brevibacterium linens strain ATCC 9175

MNSVSMRKAVGTHDETEPRVGHDGTMWRIRSYEAATTVLRARHQ

TTQAGFTAEKIPRGYFRQHPILISDGDDHDVQRREVARYFAPAVVSAKYGDFINKRAQ

ALVDSALANGRLRLDEAALNYSVEVTAEIVGLTDSPIDAMAKRLVGFFRQPPVDLAAP

AMGRTRRQWIQAAVNGLVPIGRFYISDVRPAIRARRDRRRDDVLSHLLSAGYSTADIL

VECVTYGTAGMVTTREFITMACWHLLTNDELGRRYTEASQPTRLEILEEIIRLDPVVG

HLYRRAQADIEVSDNGCPYTIPEGDLIDVCVRQTNTDPQAMGAAPETVIPGRDLRRGS

AATGLSFSDGAHTCPGQPLALYETDALLHKVLATRPRILREPTISWDNVIEGYRLRGL

DLSLMTRSRPVTTRMTT

>CYP155C2 Brevibacterium linens strain ATCC 9174 (JGI genome

MNSAGMRKAVGAHDETEPRVEHDGAMWRIRSYEAATTVLRARHRTTQAGFTAEKIPRGYFRKHPILISDGDEHDSQRKEV

ARYFAPAVVSAKYGEFINERAQALVDRAVANGGLRLDEAALNYSVEVTAEIVGLTESSTDAMAKRLVGFFRQPPVDLAAP

AMGRTRRQWAQAAVNGLLPIGRFYVHDVQPAIRSRRSRRRDDVLSHLLSAGYSTADILVECMTYGTAGMVTTREFITMAC

WHLLTDEELGRRYTESSQPTRLKILEEIIRLDPVVGHLYRRAQADIEVSDNGCPHTISAGDLIDVCVRQTNTDPHAMGTA

PETIIPGRDLGRGTAATGLSFSDGAHACPGQPLALYETDALVHKLLTIGPRILRKPEISWDNLIEGYRLRGMDLSLMERS

RPAATREPI

>CYP155D1 Frankia sp. EAN1pec

MTTTELPKCPMDPTRDDRKSAALAAQRVRADAGARVVGSFDFGRAILRSATMLQAGAGSEQVKVGGDEHG

PVFFLDGEEHRRRRTAIARFFTPKAISTRHRLVMERTSDELLARLRAKGGGQLDELSYQLAVAVAAEIVG

LTDSNQVAMARRIQATLLGTRLRGMHPVIRVGAQALTAVHAMRFFLRDVRPAIRSRRRERRDDVISHLID

EGYPDKAILIECMTYAVAGMVTTREFIVMVAWHLFDNDELRARFTAGGEADQTAIIEEILRLEPVAAMLH

RRATQDSDLGVGSVKEGELLAVSIRAANVDPETVGECPHALDPDRARRLKAVGSYMSFGDGSHRCPGAQV

AINETRVFLDRLMRLPDLRLARTPDMTWCDGLMSYELRGATVTCSRDLTPAAHEVGQDAGPDGEQT

>CYP156A1 Streptomyces coelicolor cosmid E6 gene

MTLPSTETAPTGEPGRIALYAPEFAADPHAAYRSMRRTHGPLVP

VDLAPGVPATLVIGYYQARRILNDPLRFPADPRAWEKLIPATCPVRPMMEWRPNALRS

GGAEHTRYRSANTHAIDQVDQHGLRALVEQVASDAIEGFRTAGSADLLTQYSFPIAFR

VLSALLGCPDEIGQRIADGMAKIFDTTNADQGNLILAQAVSDLVTLRRTHPGDDITSR

LALHPVRLTDEEMSHQLVTLYGAGIEPMTNLISNTILKILTDEEFSADLHAGLSTVRD

ALDAVLYTDPPMANYCISYPPYPVDVEGVLLPADQPVVISMAAANNDPALTEGVPAGQ

HGGNRAHLAWSTGPHTCPARSHAYLIAETAVTHLLDALPETDLARPAAELVWRPGPFH

RALESLPVTFPAAQSAAH

>CYP156B1 Streptomyces coelicolor cosmid IF3 gene

MDATTPAVPPPGCPAHADARIPLYGPDFAADPHAYYDYARSYGP

SAPVELAPGVDASLVTDYATALRLLQDNGTFRKDARRWKAFNEGLIPADSPVVPLLAY

RPNAMFSDGAEHLRLRQAITDAMARIDTARLARSTEQISDYLISQFGSRGSADLMADY

AKQLPLFVFNELFGCPADIGDRILFGISGMFDGVNAERAAEVLFGAVGELVALKRSRP

GEDVTSWLMQHETRMTDEEMVYQLSLILGAGADPLRNLIGNTLHRILIHDEYARQGGL

IDEAMEDTLWENPPVPNLAPHYPAADVEFAGQKFEAGELIMVSFAAANNSPSLAAARQ

SGSNRSHLAWSAGPHACPSKDPARQITMAAVENLLNRIPDIAAAVPEDSLTWRPGPFT

RGLTALPARFTPLPAPDRTPAPAQAPAGERAEQSGTARKAAGTGRWSQFLNWLTR

>CYP156B2 Streptomyces scabies SCAB79211

MTPDSSFPAP PPGCPAHDSG MRVPLYGPEY AADPQAYYAY MRHYGQTAPV EIAPGVDATL

VTDHATALRL LQDSGNFRKD ARRWRDVAEG KIGPESPVVP MLGYRPNAMF TDGAEHARLR

QAITDSLAKV DSRRISDMTK RASDYLLAQV SARGSIDLMN DYVKQLPLLV FNELFGCPAD

IGDRVVFGIS GVFEGVNAEK ANAVLGQAVF ELVALKRARP ADDVTSYLMR HEARLTDEEL

VHQLILLLGA GAEPLRNLIG NTLHRLLLHD RYADGGLIEE AIDDTLWENP PMANFAPHYP

ALDLEFGGTK MRAGDLVLIS MTAANTDPAL ATARQTGGRR AHLSWSAGPH ACPSKELARL

VTMVSIENLL NRLHDIELAV PADSLTWRPG PFHRALAALP CRFTPQVLQR PTPPRAETAA

RGESAPAGRK QERGVWGSFL SWLKG

>CYP156B5 SGR3494 Streptomyces griseus

59% to CYP156B4

MDPQPGATPYTAPAGCPMHQQRTALYGPEFAADPHRFYDAARTHGPAAPIELSPGVEATLIVQHEAALRVLQNPALFARDSRRWAALREGAVPMDSPVLPMMVYRPNCLFTDGAEHLRLRKAVTESLSRLNSSRLSRDVERIADYLIDQFIERGTADLLNEYAKLLPLLLFNQLFGCPGDIGDRLTRSMSAIFDGEDVLRANAELTECLMELVALKRRQPGEDITSWLIQHPAGLRDEELKDQLVVLMGAGVEPERNLIANALLLMLAGEAPGAPERRGSGMLVEDALDDVLWNNPPIANYATHFPVQDIELDGVVLKAETPVLISFAAANSDPGLTDARQTLSKGAHLAWGAGPHVCPAKSPATLIALTAIEKILNTVPDLALAVPASGVAWRPGPFHRALVALPVRFTPTAARRAATGAQPAAPVSAQLPDPFRNTPSAPSAAPRHAQEPAKKQKGWWSSFLDVFRV

>CYP156C1 Streptomyces scabies SCAB20221

MTAPPPAGPP PGCPAHQPMY GPEFAADPAA FYRRARAHGP TAPVELAPGV RATLVTSYDA

ALYVLRGTET FAKDARRWRD LGDGTVPPDS PVVPMMMYRP NALFSDGEEH RRLRGAITDS

LARVEPHTLR GYVERSADTL IDRLAPTGGA DLLGEYAQVL PLLVFNHLFG CPAELGVKLV

EGMSAIFDGV DAERADALLT ATLVELVTLK RERPGPDVTS WLTLHPAKLT DEEMIHTLVV

LMGAGTEPQQ NLIANALRLL LSDDRFAGDL SGGSLPVEDA LDEVLWTDPP MANYAVHYPK

RDVLHEGALL RAGDPVVVSL AAANTDPALG TDQRTGNRAH LAWSAGPHNC PARSEARLIA

SVAVEKLLDR LPDIELAVPV EALEWRPGPF HRALAALPVT FPPAPALAAS APVAPEPPAA

SARPAPEPPV TPGPRPPEPA RPTSGRGRLL SWWRGERPGR A

>CYP156C2P Saccharopolyspora erythraea NRRL23338

LINEFGSAGEADLLTQYAGPLTLRVLTWLFGCPTDLGQRLLADMAHIADAADAGAAGEAG

ADLDECLRRLVHLKRGHPGRGVTSRLMAHSAQLSDDEVVHQLVILMGVSGEAQQNLISNA

LRLLLSDERFAGDLSGGSLPVEDALDEVLWADPPIANHSTAYPTREVHLDGVHLPRVNRW

>CYP156C3 SBI\_1148 Streptomyces bingchengensis

57% to CYP156C1 Streptomyces scabies SCAB20221

VPTSTPDSGPTPPPGCPAHTGPGQAPGLPESLYGAEFAENPSAVYARLRA

YGPVAPVEISPGVHASLVTSYSTALEIMRNTETFPRDPRRWEALNNGTVP

MDSPVVPMMMYRPNPMYTDGEEHDRYRGAVSDTLNRLNPHALRTYVEESA

DLLIDLFGPEGEAELLSEYCARLPLLVFNQLFGCPPELSETMVKGMAALL

DASEDAVEANAVLIETLLALIALKRLEPGADITSWLLAHPARLNDEELVS

QLILLLGAGVEPVQNLICNALRLLLSDERFAGDLSGGTMPVDEALDEALW

TDPPIANYATHFPVRDVTIAGHRVGKGTPLLISMGAANNDPQLVSDRRGN

RAHLAFGAGPHACPAKDPARIIASTAVEKLLDRVPDIELAVDPAQLHWRP

GPFHRALAALPVHFPPVAAKYDQAGATATDQTTGGNAWTPSPAPSSSTPK

GATSTGREPGSGNGAQRPWWNSLITWWRGR

>CYP156C4 SBI\_1149 Streptomyces bingchengensis

59% to CYP156C1 Streptomyces scabies SCAB20221

80% to CYP156C3, 58% to CYP156C5

VPTSAPDSDPPPPPGCPAHSGQASEPGRPEPLYGPEFAADPAAVYARLRA

YGPVAPVELAPGVHASLATGYATALEILRSPDTFARDPRRWEALADGTVP

MDSPIVPLMMYRPTPMYTDGEDHERYRGAVSDTLNRLNPHTLRTYVEESA

DLLIDLFGPEGEAELLSEYCARLPLLVFNQLFGCPPELSETLVKGMAALF

DIDEDAMKADAVLREALSALITTKRAEPAADITSWLIAHPARLNDEEMTH

QLILLLGAGVEPVKNLIGNALRLLLSDDRFAGDLSGGTMPVDDALDEVLW

TDPPVANFCTHYPVHDVTVAGHRLAKGAPVLISMAAANNDPQLISDRRGN

RAHLSFGAGPHACPAKDPARIITSIAIEKLLDRLPDIELAVHPDQLRWRP

GPIHRALAALPVSFPPIAAKYDAVSAAATDQNPGGNAWNPSPAPSTSTRS

PSTPKDATSTERGRDSGNAAQRPWWNSLITWWRGR

>CYP156C5 SBI\_5524 Streptomyces bingchengensis

58% to CYP156C1 Streptomyces scabies SCAB20221

60% without insertion

VTYHPDATAAVGHSPDAEAGVGVAPPPGCPAHAGHAGFGGPARPAAQGLP

LYGPEFAADPHLFYERLRQYGPIAPVELSPGVEAYLITSYSLALEVLRDT

ERFAKDPRGWRALNEGRIPPDCPVGPMMMYRPNALFNDGEAHARLRGAIT

DSLTRLDPYALSEYVERSADTLINAFADRGEADLLADYAAAIPLLVFNEL

FGYPAEHGLRLVGTMARLFDSGEDAAEANQELLEYMAGLIAAKRERPAAD

ITSWMLAHPSRLADDELLQQLMLILAAGTEPQLNLIANALRLLLSDDRFA

GELSGGSLPVQDAIDEVLWTDPPLANFGTRFARHDLDLAGLRIRQGEPIL

TSYAAANTDPELISDGRFGNRAHLAWSIGAHRCPAESPARVIASVAIEKL

LDRLPDMELAVPVDQLAWRTGPFHRALTALPVRFPVTARPTAAAAPAAVS

AAVSPPAPAAAPAKPHGSPQTAPDASDTPSQSPRAAQRRRWGSLAAWWRGQ

>CYP156D1 Streptomyces scabies SCAB32121

MTTTAPLYLP HAYRLYEPGF AQDPHAYYTH MRAHFGDVAP IEISPGVFGH LVIGYRLALQ

LLRDTQTWSK DPTVWVSHLP KDSPVLGMLG PRPNPLFADG ERHARYRRVI TDSFGRIQPH

HLRDLVREIA ALLIGRFAGA GIADLIAQYA RPIPSYVMNR LFGQPDHAAP RLVTALAGLI

EGGENAAAAN AEFEAYMRRL LALKTGERGH DLTSWIMDHS AGLSPEEVLH HVVLTVGAGQ

EPTTNLIANA LAIMLSDDRY YAGVTNGALA PIHAVHRVLR DEPPMANYAA HYPRHNVRIN

NLSIPAHSLV MVSFAAANAD PQGPGAPLSG EGSHLAWSAG PHACPVKDPA ILIAVTAIEE

ITSRLPDLEL DGRREDLQRR IGPFHTAYRH IPATFTPLTA LPTTGDRAWP GNPFRTSSTP

PDAISPQKPP ACAPSAPPCA

>CYP156E1 SBI\_8426 Streptomyces bingchengensis

52% to CYP156C1 Streptomyces scabies SCAB20221

VSQPYESVAQPTAVPPPGCPAHAGGTGTGTGTGAEPLYTPEFFQDPYAVY

KRLRETHGPLAPVEIEPGVTAVLCVGYETALEIMRRPETFSKDARNWRAM

TEGRVPEATHAAQLIKPRAQAGWVDGEAHRRLRSAIDDSMSRIDLGALRG

YVERIADSLIDQFAAAGEADLIPEYCQLVSMLAVGELFGCPKDIADRLFA

AMAGLLDGRDPMAAAQEIDATMRALIELKRREPGPDVTSWLIAHPARLND

EEMVEQLLLMMGMGSEPVPSLISNALRVLLTDERFAGDLAGGGMLVEDAL

DEVLWTDPPLSNLAVHFPLRDVTVSGTRLRAGEPVIISFAGGNQDALDSS

QHKQGNRAHLAFSAGPHTCSGRNQGRLIATAAIEKLLDRIPDIELAVDAE

KLEWRPGMYQRGLTALPVRFAPVGELSKSEPAAPAAPAPQVPAAPEVPPA

PTGLPAVPDAEGAAGEPGGAPGDADAAKPKPTGLLGFLARWRRSRK

>CYP156F1 SBI\_8398 Streptomyces bingchengensis

56% to CYP156B2 Streptomyces scabies SCAB79211

missing N-term 165 amino acids

MLPLLVFNELFGCSPSIGDRLVIGTSGIFDASMDAEKANEELTQALIELI

ALKRRQPGDDVTSRLMAHPAKLTDEEMIHQLVMLISAGTEPQRNLIANGL

YLLLCDEKHAGGSQAGGLLVEDVIDDVLWNSPPMANYAPHYPVCDVELGG

NLLRAGDLVLISFAGANTDPALSSSRQILSKRAHLAWSAGPHACPAKDSG

QLIAVGAIENLLNQLPDVELAVPMESLQWRPGPFHRALTSLPARFAPVRA

QQTAMMSPAAQTGPVVTPAAIPQTRPQGKVQKSSAWSSFLAWWKS

>CYP157A1 Streptomyces coelicolor cosmid 6D11

MSTDAHDVPGAVPLGGPRFQTDPALLYRQMRREHGAVTPVVLDG

DVPAWLVLGYRELHQVTGDPVLFSRDSDLWNQWENIPDDWPLLPMIGRRQPSILYTVG

ERHRERAAMISDALEAVDPHLLRGHAERFADELVDRLCAKGEADLVGDYAMLLPVRVL

ARLYGFPDEQGPALVTALNDMIDGRERALAGQTHLGTSMARLLADRKAAPADDVASRM

LADESGFTEEEVAQDLMVMMAAGHQPTADWIGNSLRLMLTDDRFAASLFGGRNSVAEA

MNEVLWEDTPTQNVAGRWAARDTQLGGRRIRAGDLVLLGLQGANSDPQVRTDGSALTG

GNNAHFSFGHGEHRCPFPAQEVAEVIARTGIEVVLDRLPDIDLAVPAGSLTRRPSPWL

RGLTELPVRFTPTTALGGTSA

>CYP157A2 Streptomyces avermitilis

MTPAPAPAPVPLSGPRFQTDPAALYREMRREHGSVAPVLLDGDI

PAWLVLGYRELHQVTGDPVLFSRDSELWNQWPNIPADWPLLPMIGHKQPSILYTVGER

HRERAAMISDALEAVDPFELRSLTEKFADELIDAVCAKGETDLVADYAALLPVRVLAL

LYGFAEEQGPGLVTALNDMIDGRDRAIAGQTHLATSMAQLLADRKAEPANDVVSRMLA

DSGGFTDEEIAQDLMVMMAAGHQPTADWIGNSLRLMLTDERFAASLFGGRNSVAEAMN

EVLWEDTPTQNVAGRWASRDTQLGGRRVRAGDLLLLGLQGANNDPQVRIDGAALTGGN

NAHFSFGHGEHRCPFPAQEIAEVIARTGIEVVLDRLPDIDLALPAGSLARRPSPWLRG

LTELPVKFTPIPALGGSPA

>CYP157A3 Thermobifida fusca

MGPAVHRGARRSRPRRRPPTRRLLVLHRPAGGARHSLRRRPQQL

RVLLHPGPDPRGTRPGPLSPPPGMRRPGTRVRQTGAGHPGPTCDDDHRGGGRPMNAQR

GIPSSHQNAFRLYGPQFQNKPAELYRQMRTDYGPVAPVLLDGDIPAWLVIGYREVTHV

LNHPETFARSSRRWNAWDLVPENWPLYPMVTRTPNILYSEGEEHRRRATAISDALSGA

DQHEVRQYAVQAADRLIDGFCAASRADLRADYASRLPAIVLGRLYGLDQKHAEVLAEA

MTTMIDSGPDAVKAQQFLLQTMGTLVAERRKQPGPDVVSRLVHHPAKLRDEELIPDLV

VILGGGHQPTTEWLGNTLRLMLTDDRFAASLTGARSSVREALNEVLWEDTPTQIYLGR

YAAHDVELGGQLIRRGDLVLLGLAGANSDPQINPGPECRMSQGNQAYLSFSHGEHRCP

YPAPELAEIIVTAGIEVLLDRLPDVELAVPVDELRWRPSPWMRGLVALPVVFTPVPPI

GGQ

>CYP157A4 Streptomyces scabies SCAB51111

MDFATSDADG DQPFPTSALP PSASAPVPLL GARFRGAPAP LYRDLRREHG EVAPVLLDGG

VPAWLVLGYS ELHQVTSDPE LFSRDSGLWN QWRNIPADWP LLPVISPRQP SVLGTTGERH

RQRAALIEEA LEAVEPLELR GQVERFADEL IDEVCGVGAA DLVGQFAALL PVRVLACLFG

FREDHGPGLV AALNDILDGQ DRAMAAEGFL RTAMDRLVSE RLAQPGDDVV SRLLARARAY

EVTVEEVTHD VMVMLAVGHQ PTADWIGNSL HLMLTDERFA ASLFGGRSSV AEAMNEVLWE

DAPIQNAAGR WTTRDTRLGG RVLRAGDLVL LGLQGANSDP RVRTRGDALT GGNNAHFSFG

HGEHRCPFPA QETAEVIART GIEVVLDRLP DMDLTVPPTS LPRRASPWLR GLVELPVRFS

PGPVRGA

>CYP157A6 Streptomyces cyaneofuscatus IT17-157 AB426723.1

80% to CYP157A1 Streptomyces coelicolor

MTTTSGTPGTASGCPVTHGSVPLSGPRFQSDPVQLYRDMRRDHG AVAPVVLDGDVPAWLVLGYRELHQVTGDPALFSRDSDLWNQWDRIPDDWPLLPMIGRK QPSILYTVGERHSVRAMMISNALEGVDPFSLKRYAEEFADELIDRFCTKGAVDIIAEY AKLLPALVLARIYGFSDEEAYPLVGAINDMIDGRERALAGQQHLATSMFQLLADKHAE PGDDVASRMIADVGGFTDEEVAQDLMVMMAAGHQPTADWMGNSLRLMLTDDRFAASLS GGRHSVAEAMNEVLWEDTPTQNVAGRWAARDTHLGGRHIRAGDLLLLGIAAANGDPQV RTHASALTGGNNAFLSFGHGEHRCPFPAQETAEVIARTGIEVLLDRLPDVDLAVPAEQ LTRRPSPWLRGLTDLPVLFTPTPALGRPGSLGGPA

>CYP157A7 SGR1086 Streptomyces griseus

MTNPSSATPASTAGTGGGCPVGAGTGAVPLGGPGFLAEPREFYRSLRRDHGPVVPVELPGGLPAWLVIGYRELHQVTSDGEMFPRDVSLWNQWENVPADWPLLPMVGTPMPSIYFTAGAEHRRHVDMVVPALEEADPFEIRRHCEQLADRLIDAVCTRGTADLVAEYAEPLPVLVLARLVGFPDDEGADIARVLKDLADGGPGAQKAHLSFGEHMQRLVAAKRARPGDDVTSRMLAHPEPFTDQEYALDLMAITAAGHLTTADWISNSTRLMLTEDQFADALSGGRHSVAEAMNEVLWEDGPTQILAGRWAARDARLGGRDIARGDMLLLGLGAANADPHIRQQVTASAVRSGQGGNSAHLAFSHGEYRCPFPAQEIAEIIARTGIEVLLDRLPDLELAVPATELVRRPSAFLRGTTALPVRFTPVRTTGDAL

>CYP157A8 SGR3107 Streptomyces griseus

MTTVSGCPVTHTSVPLSGPRFQSDPVQLYREMRRDHGAIAPVVLDGDVPAWLVLGYRELHQVTGDPVLFSRDSDLWNQWDRIPDDWPLLPMIGRKQNSILYTVGERHSVRAMMISNALEGVDPFSLKRYAEEFADELIDRFCTKGSVDIIAEYAKLLPALVLARIYGFSDEEAHPLVGAINDMIDGRERALAGQQHLATSMFRLLADKHAEPGDDVASRMIADTGGFTDEEVAQDLMVMMAAGHQPTADWMGNSLRLMLTDDRFAASLSGGRHSVAEAMNEVLWEDTPTQNVAGRWAARDTHLGGRHIRAGDLLLLGLAAANGDPQVRTDGSALTGGNNAFLSFGHGEHRCPFPAQETAEVIARTGIEVLLDRLPDVDLAVAADQLTRRPSPWLRGLTDLPVLFTPTPAIGRPGSFGGPA

>CYP157B1 Streptomyces coelicolor cosmid F55

MTDIDPSPHPVAAPGCPVHPDAVPLAGLEYQQTPSELYRGLRAE

HGAVAPVLLDGGIPAWLVLGYPEVSYVTSHDELFARDSRRWNQWGSIPPDWPLLPYVG

HQPSVLFTEGEEHRRRAGVITQALAGIDQFELARDCRHLADRLIAAFAGSGRAELMSG

YAHPLPMRAAVRMCGMPHTGVETRQLVEDLRISLDAAEGDDPVAAYTRVGERIHQLVR

HKRERPGPDVTSRMLTHPAGLTDEEIVQDLISVIAAAQQPTANWIGNTLRLLLTDERF

ALNVSGGRLSVGEALNEVLWLDTPTQNFIGRWAVNDTQLGGRHIRAGDCLVLGFAAAN

TDPQLWPEAHVGAENSAHLSFSNGEHRCPYPAPLLADVVARTAVETLLERLPDLVLAL

EPGELTWRPSIWMRGLTALPALFTPVVA

>CYP157B2 Streptomyces hygroscopicus subsp. yingchengensis

MGSATSELPSQRTPLTAAAETGLKIVVVGGFGVGKTTLVRSVSE

IRPLNTEELMTQAGQGIDETAGVERKTTTTVAFDFGRISLNDRMVLYLFGAPGQERFW

FLWDRLFAGTLGAVVLVDTRRMEDCWYAIDRLEHHGTPFVVAVNRFDGDEKRFSLDEV

RQALALGEHVPMIECDARVRASGKEVLIALVDHLYTRALAKESTACSDTTGFPSTDAP

PPGCPAHGSAVPLAGLEYQQTPSQLYRTLRREHGAVAPVLLDGGIPAWLVLGYPEVCY

VTAHDELFARDSRRWNQWEHIPPDWPLLPYVGYQPSVLFTEGAEHQRRAGVITQALEG

VDQFELARECQLIAARLISSFSGSGRAELMSMYAHALPARGVLWMCGMPAEDADTERL

VDDLRISLDAGEGDDPVAAYTRVGERIMRLVKEKRERPGPDVTSRMILHPAGLGDEEI

VQDLISVIAAAQQPTANWICNTLRLLLTDERFAVNVAGGRVSVGEALNEVLWLDTPTQ

NFIGRWAVRDTQLGGRHIREGDCLVLGLAAANTDPQIWPEPHAGSGNSAHLSFSNGEH

RCPYPAPLLADVMARTAVETLLEHLPDLVLAVEPEELTWRPSIWMRGLTSLPVEFTPA

MN

>CYP157B3 Saccharopolyspora erythraea NRRL23338

MTGASEVEWPAADAPSDCPVQEVPAAPQEHAVRMYGPILQRDPKELYREMRREHGPVAPI

LLEGDLPAWLVLGYREVHQVTTDSELFARNSRRWNHWDDVPEGHPLWPWLGIDHSVLVSE

GEEHRRRAGAISDALAAVDQFELWDHCARIADRLIDSFAGSGRADLIAEYTDRIPLLVVT

TMFGMTEEQTRNLIGDLSTTIDAAEGAGAAHNRVVDRMRALLAVKRERPGNDLPTRLLGH

PSTADDDECAIDLVILLTAAHQPTASWIGNTLRLLLTDERFALTLSGGRRSVGDALNEVL

WEDSPVSNLLGRWAARDTQLGGRAIRKGDLLLLGYNAANSDPQVWPDGTNAHMAGNHAHM

AFGHGEHGCPFPAPELAEVIAKSTIEVLLDRLPDLRLAVEPEALRWRQSTTIRGLVDLPV

EFSPTYAKRP

>CYP157B4 SBI\_9885 Streptomyces bingchengensis

56% to CYP157B2 Streptomyces hygroscopicus subsp. yingchengensis

VTNVHHPSPVDGPSPLTGCPAHPGAVRMHTEELQADPAELYRRLRRDHGA

VAPILLDGDIPAWLVLGYRELHRVTSDPTLFARDSRRWHAWEYIPADWPL

MPFVGYRPTMLFAEGAEHERRAEAMFDALASVDQFELRAESERVADELID

VFAGSGRAELVADYASQVPIRVVTRLFGLAPDTAVAIQRDTVEMVTANDG

SXLPPANDGSVAAYQRVHNRMVTLMAEVRRNPGMPGIPAQMAAHRAALTD

EEIVNDLIGTVYASHQSTTDWIGNALGLMLTDERFAVTMAGGRRSIGQAL

NEVLWENTPVPAFIGRWAAEDTILGGQRIKKGDCLVLGLAAANADPSVRP

DFRADASGNQAHMSFSHGEHSCPVPARELAEVISMTAIEVLLDRLPDVVL

AVSPEELVWRSSIWLRGIAALPVEFTPALG

>CYP157B5 SBI\_9382 Streptomyces bingchengensis

62% to CYP157B4

53% to CYP157D1 Frankia alni ACN14a

VTTPDPTLPPEDPDTSAAPLPGWPEQPDAVLLHAEDFSRSQEDLYRRLRR

DHGPVVPVLLDGQIPVWMVLGYRELVRVTTDPNVFARDSRRWHSWHLVPP

DWELMTFVGYRPTMLFTEGAEHERRAEAIIDSMEIVDAFELRALCERVAD

GLIDTFAGRGHADLIADYACQIPLRVLNRMYGMNEAESAELQQVTVDLVS

GKGGPEAHQNMVDRMVALMEHARATPDRKNISTVLVNHPAGLTDEEIIND

LLGNVYAAHQPTTDLIGNALRLMLTDERFAVTMSGGRRSVGQAINEVLWE

ATPVPNWVGRWAAEDTMLAGRHIRKGDCLMLGLAAANADPDVRPDFRSGA

AGNQAHMAFSHGTHGCPPVARELAEAIAMAAIEVLIDRLPDVSLTAAPED

LEWRSKLMMRGVSAIPVQFTPTSR

>CYP157B9 SGR4392 Streptomyces griseus

MSTSSPSFGPQAPASCPVGAGAGAVRLSGASYQQTPTQLYRSLRRDHGAVAPVLLDGDVPAWLVLGYAELSYVLTHDELFARDSRRWNQWETIPPDWPLMPFVGYQPSVLFTEGDEHRRRAGVITEALEGIDQFELARDCRRIADRLIADFAGSGRTELMSSYVHALPMRAVVEMCGMPVSGSDTQQLVDDLRISLDAGEGDDPVAAYGRVGDRLRQLVEDKRAAPGADITSRMVTHGAGLTDEEIVQDLISVIAAAQQPTANWICNTLRLLLTDERFALNVSGGRLSVGEALNEVLWLDTPTQNFIGRWAVRDTQLGGRHIRAGDCLVLGLAAANTDPEIWPESYVGAENSAHLSFSGGEHRCPYPAPLLADVMARTAVETLLEQLPDLMLAVDPTELSWRPSIWMRGLSTLPVQFSPMAQ

>CYP157C1 Streptomyces coelicolor cosmid I41

MTPESHSPTGTGEPLLEPPPGCPAHGLGPGGLHRLHEAEDLEEL

YEKLREQHGPVAPALLHDDVPMWVVLGHAENLHMVSTPSQFCRDSRIWTPLNEGMVKP

DHPLMPHIAWQPICSHAEGDEHKRLRGAVTSAMSDLDYRELRRHIKRYTQRVVNRFCE

EGRADLVSQFAEHLPMGVMCHLLGMPEEYNDRLVEAARDTLKGTETAIASHAYVMEAL

GRLTATRRADPADDIAGRLVTHPAGLTDDEVREHLRVVLLAAYEATVNLIGNVMRVVL

TDPGFRAQLSGGQMTVPQAVEQSLWDEPPFSTVFAYFAKQETELGGQRIRAGDGLLLG

IAPGNVDPRIRPDLDASMMGNRAHLAFGGGPHECPGQDIGRAIADAGIDALLMRLPDL

QLDCDEDDLRWRSSIASRHLVELPVRFEPRAQQDIMQQPSHAPTPERHAPWHVGLPKP

ERRAQPPLPAQPPQPVSVTAAEPQQAPGAGQPRPRGAWQRFLLWWRGY

>CYP157C2 Streptomyces avermitilis

MTPEPHPSTGTDDPTFGPPPGCPAHDPGLGGVRRLYGPEAEDLG

DLYEKLRAEHGAVAPVLLHNDVPMWVVLGHTENLHMVRSPSQYTRDSRVWTPVLDGTA

GPDHPLMPHIAWQPICSHAEGDEHLRLRGAVSGAISTIDHRGIRRYINRSSQALVNRF

CEEGRADLVGQFAEHLPMAVMCEILGMPDEYNDRMVQAARDMLKGTETAIASNAYVMD

ALMRLTARRRAHPEGDFTSHLINHPAQLSDDEVGQHLRLVLIAAYEATTNLLANVLRM

VLTDPRFRAQLNGGQMTVPEAVEQSLWDEPPFSTVLGYFAKQETELGGQLIRKGDGLL

LGIAPGNVDPHVRPDLSANMQGNRSHLAFGGGPHECPGQDVGRAIADVGVDALLMRLP

DVQLDCAEDELRWTASISSRHLVELPVRFAPKEPQDVSQRPSLRPLPQPVPSRPVRTQ

QPQATTPPPAPPAPPAAAPERGPGAWQRFLRWWRGY

>CYP157C3 Streptomyces griseus

MTTPFHHEPGTVPPPQCPAHNLDIGPGGLRRLHGPEAENNPAGL

YDKLRAEHGTVAPILLHGDVPAWLVLGHSENLHVTRTPSQFSRDSRRWRALQDGSVAP

DHPLAPIFTWQPICVFADGPKHERQRGAVTDSMERIDTRGVRRHINRFSNRLVNDFCE

KGTADLVGQFAEHLPMMVVCAIFGMPEEYDERLVQAARDMTRGTETAVASNAHIVSVL

TRLVERRRAEPSPDLASWLVEHPATMTDTEVIEHLRLIMIAAYESTANLIANVLRMVL

IDPRFRARLSGGHMTVPEAVEQTLWDEPPFTAVFGRWAVGDTELGGQQIKAGDALLVG

IAPANTDPTVRPDLGADMGGNRAHLAFSGGPHECPGQDIGRAIADVGVDALLMRLPDL

ELGVGESELHWVGNIMSRHLVELPVKFAPGPQQKLDADPLTVMARLLAPPTPGRSPPR

PGRSPSPATRGPWRRAHAPGAAPTAEPDPAPAAPPAPEPAAAPEPAPVATIPQQRRPA

APARFWQAVTRWWSGY

>CYP157C4 Streptomyces peucetius

MTTPEPSVPPGPVPPPGCPAHGMSPDALRRLYGAEAEADPQALYEVLRKEHGQVAPVLLH

GDLPAWLVLGHRENLEVMRSPSRFSNNSRLWSMFQQGRVGQDSPLLPIVGWQPICVFADG

ADHERLRSAVRDGLEQFDRRGIRRYVIRYTNQLVDSFAATGQADLIGDFAEKLPMLVMTQ

LFGMPEEYGPRLVDAALDLMKGSETALASNELVVDTLRTLAERKKAKPGHDFTTWLIGHE

ADLTDDEVMEHLRLVLVAANETTVNLIANTLRMVLTDRRFRANLAGGHMTLPDALEQVLW

DEPPLSVITGRWATGDTVLGGKQISKGDMLLLGLAAGNVDPEIRPDLQKPLMGNRAHLAF

SSGPHECPGQDIGRAIADTGIDTLLARLPDLQLGVSEGELRSSATWLSQRLESLPVRFTP

PGSTGGGGKESVNFASTMPGPLPATVPAPVPDASPAGQPKKRPVAKSWRSLFHRGG\*

>CYP157C5 Streptomyces scabies SCAB73721

MTPESHSLTG TDDPTLGPPP GCPAHGTGPG GIRRLYGPEA EDLGAVYEKL RAEHGPVAPA

LLHDDVPIWV VLGHGENMHM VSTPSQYSRD TRLWNKLQDG TFKPDNPLMP HIAWQPICCH

AEGDEHLRLR GAVTGAMSTI NFRGIRRSIN RYTQQLVNEF CEEGEADLVG QFAEHLPMAV

MCEILGMAEE YNDQIVHAAR DMLKGTETAI ASNAYIMEAL MRLTVRRRAE PQEDFTSHLI

NHPARLTDEE VGQHLRVVLI AAYEATTNLL ANVLRVVLTN PGFRAQLKGG QMTVPEAVEQ

SLWDEPPFST QLAYFAKQDT ELGGQRVRKG DGLLFGIAPG NVDPRVRPDL TANMQGNRSH

LAFGGGPHEC PGQDTGRAIA DVGVDALLAR LPDIRLNCEE SELRWRASIS TRHLVRLPVR

FEPKEREALE LRPVGRPVPA QREGRQTVTP DTPLQAASPE PRPATPAPDA EPKGRPGLLR

RALRWLSGR

>CYP157C6 Frankia sp. CcI3 old ver = 157C1 but name conflict

MSTPIPEAGAESGAAIPPPGCPAHAAFAQDAVRTALYGPEAQHDPGAVYEKLRAEHGGIAPVELEGGVPA

WLVLGYRENMEVARTPSRFTRDARLWRDWNEGRIAADDPLLPLIGWRPDVVSYDGEEHARLRAAVNECLT

RFDRHGTRRHVQRYANQLIDGFVEDGRADLVTQFAVYLPMLVLSRLVGLSEGYGRKLVEAIVGMVSGGED

AYAHNQYIIGTLRSLTEERRRAPAHDLASWFVQHPSGLNDEEVLNHLRLVIVLGYEATANLVSNTLRMVL

TDPRFRASLAGGLMTLPDAVEQMLWDDPPLLVCPARFATHDMHFADKEIREGDMLLLGIAAGNADPEIRP

DLGAPMHGNRSHLAFSRGPHECSGQEIARAITDTGVDVLLNRLPDLHLTVPEEQLTWTASTWSRHLDALP

VKFAPQCRPVPQSAPAAPAFSAPVVEPSAAKDALAAVAEADAQARADTRRGFWASLGGMFRGRR

>CYP157C7 SBI\_7811 Streptomyces bingchengensis

60% to CYP157C4 Streptomyces peucetius

VTPPPDHPGTDHLGTAPPPGCPAHAAIRSGTAGDLFGPEHEADPKGFYEW

LRAEHGAVAPVRLAGDLPAWLLLGYRENLEVARTPSRFSRDSRHWGDWRE

GRVASDSPLLPVVGWQPMCTFADGAEHERLRAALTESMNRFDRRGMRRQV

TRFTHQLVDEFAADGHAELVSGIAEQLPMLVLTHLLGMPDEYGPRLVEAT

RDLMKGTETALSSNAYVTETLENLVARKRAEPGSDLASWLLEHPSGLTEE

EVVQHLRLVLLTGNETTTNLMANTLRTVLTDPRFRASLAGGHMTLPDAIE

HVLWNEPPLAVIPGRWATGDTELGGRQIRAGDMLLLGLAAGNVDPAVRPD

IAAPMYGNRSHLSFSGGPHECPGQDIGRAIADTGIDTLLLRLPDLRLAVP

ETELSWTASWISRHLVSLPAEFTPRGGDSDTLETETGLLAPDFLARSAPQ

PDPPDQSKALDRPNTPDRPDVRRSSRRRSWWRSLWRRLRPGPRPPRR

>CYP157C10 SGR1059 Streptomyces griseus

MTTPFHHEPGTVPPPQCPAHNLDIGPGGLRRLHGPEAENNPAGLYDKLRAEHGTVAPILLHGDVPAWLVLGHSENLHVTRTPSQFSRDSRRWRALQDGSVAPDHPLAPIFTWQPICVFADGAKHERQRGAVTDSMERIDTRGVRRHINRFSNRLVNDFCEKGTADLVGQFAEHLPMMVVCAIFGMPEEYDERLVQAARDMTRGTETAVASNAHIVSVLTRLVERRRAEPSPDLASWLVEHPATMTDTEVIEHLRLIMIAAYESTANLIANVLRMVLIDPRFRARLSGGHMTVPEAVEQTLWDEPPFTAVFGRWAVGDTELGGQQIKAGDALLVGIAPANTDPTVRPDLGADMGGNRAHLAFSGGPHECPGQDIGRAIADVGVDALLMRLPDLELGVGESELHWVGNIMSRHLVELPVKFAPGPQQKLDADPLTVMARAPRPADAWEISSPARQVPEPRHEAVVAQPAHAPGAAPTAEPDPAPAAPPAPEPAAAPEPAPVATIPQQRRPAAPARFWQAVTRWWSGY

>CYP157D1 Frankia alni ACN14a

MTPPSHDRVDTWAPAPAAPELAAPAPGFPDHPGAVRLYGPRFQHNPAQMYREMRRVHGPVAPILLDGDIP

AWLVLGYRELHYVTSNPELYGRDPRRWNAWDRVPPDWPLLPVVGYQPYTMHLEGAEFERRSAIMNDVLGD

VDLFELRALCERTCDELIDGFAGRGEADLITEYAQSMPMLLIGRMIGIPEAGLPELLASMNAATDGSGPE

AVAGHSRFVAIINALLADRRARPRPDLPSAMLGHPGKLTDEEASWDLLLIVGIGQQPITDWIGNTLRLML

TDSRFAVTLSGGRRSVGQALNEVLWEDTPLQNMSGRWAVRSTQLAGQHIQAGDMLVLSCAAANGDPQVRP

DSFEGPGGNHAHMSFGHGEHRCPYPAQEIAETIVRGAVEVLLDRLPDAVLAVSPDALVWRPSPWMRGLSA

LPVHFSPS

>CYP157D2 Frankia sp. EAN1pec YP\_001509751.1

MTTAREPARESLRGPAREPAREPARAARERPPGGRTPPCHLGEAQFQGGPARAYRDLRRKHGAVAPVLLD

GGLPAWLVLGYRELHYVLSHPEIFAHDPRHWAGWDDVPPDWAALPGVGHRPSVLRAEGAEHRRRYTAIQD

VLGAVDLFELRARAEEITDDVIDAFAGRGETDLIDSFAHRVPALVLASLCGPPEVDTAGLVHDLIVLIDD

GPDAAESHQRVLDRLRWLLADRREHPDDDIVSRLIAHPAGLADEEVVEDLAVVFGFGARAVAGWIGNSLR

LLLTDGSFALDLSGGRRSVMQALNQVLWEDTPMQVVAGRWATRNTQLGGQRIEAGDMIALGLGAGNADPQ

VRRGHAPDTQTGAGTSANSAHLSFGHGEHRCPYPAQEIAEVVTRTAVEALLDRLPNMWIAVPADALGWRR

TAWNRALTALPVRFSPV

>CYP157E1 Frankia sp. EAN1pec YP\_001509752.1

MTHPNPRQLGTCASGMPRAFGAVRQLGALRQYGASCPAPTTRRGGPEDTPSGEPVPGPSSGPPSGPRGGP

VRGTAGAHPPARPDLDARWPAHATAVRLPADGPGDDRAAFYRRIRDEHGPVAPVLLEGDVPAWLVLGYRE

VVYVAGTPALFGRDCRIWNAWDLVPPAWPLQSMVGQRPSLRALDGPAHARRLGAIGDVLGMFEPHGLRAR

AASGADALIDAMASDGRAELMTQYASPLPAMVAAGMWGLPDTDLTALARDLTLLVSGGTGARDARRRAHA

MLTRVVRRRRAQPGDDAVSALLTHPAGLRDDEVVEDVMATLIAGQAPTADWIGNTLRLMLTDPRFATDLA

GGRLSAGDAMAEVLWADPPIQNLVARWARRDVRLGGRWIRAGDLLIFGLSAANSDPWARPQPSGRPSGNH

AHLAFGHGEHRCPFPAQMTAETIATTAIEVLLDRLPDLELAVEPRDLRWRPSVWARGVAALPVRFTPP

>CYP157F1 SBI\_871 Streptomyces bingchengensis

47% to CYP157C6 Frankia sp. CcI3

missing about 33 aa at N-term

VPLYGAAPAGDMPALYERMRRDHGPVVPVAIAPGIEAWLVLGHRELLHLT

RDEQHFSHDPRRWTPLRDGRVPPDSPLIPLVGWRPALLFADGQQHRRMRS

AVAEALGRLDGHELIRMVRSAAERLIAGFADRRKADLVPQYARLLPLQVV

TQILGLDEERGPRLVEAIAAIVNPTAAATGANRRMGGILLELIEQKKRQP

GADLTSWLLEHPVGLSDQEVLHNLVVIIVAGNQTTVNWIADTVRILLTDP

GFRSSLARGHLTVDDALDLVLWRHPPTANFPGRYATRDLRFGGQHIRAGD

MLILGLAGANADPEVLPEDGRPVIGNRSHLAFGAGPHTCPARDPARLITR

TAVDTLRHRLPDLELAVPEDQLAWITSPWSKNLAGLPVRFTAPQLAADAA

DSADAAAAGHPADSGDLR

>CYP157G1 SBI\_4984 Streptomyces bingchengensis

50% to CYP157B3 Saccharopolyspora erythraea NRRL23338

VTNPQDPQDLQDPQPPRSAPDTPPPGCPAHAARLYGPDFRREPAETYRRI

RREGQVTRVLLEGDVPVWFVVGYRETRQVLSDVETYGRDPRRWNGWDSVP

PDWSLMPWVQYSPMMPFTEGEEHLQRAAAVSEVLATLDPFVLRGHCERFA

DQLIDKFAVTGRADLVYDYIYSVPTLVMGEVFGLAEDEAGLAALAEGLTT

SFVSREDAMAGQQRAAAYVAGLVKAKREAPGPDLTSRFIQSTPNLTEEQH

IADVMMLMAAALPLTSYWIGNTLRLLLTDERFATTLTGNRRSIGQAMNEV

LWVDTPLQNLIGRYATRDTVLGGQRIRTGDLVVLGLAAANADPLLWPDGH

VGHAGNHSHVAFSGGEYGCPVGGPETARIIAETTIEVLLDRVPDLALAVA

PEELRWMDSVWYRCLESLPVAFTPTGVMGG

>CYP158A1 Streptomyces coelicolor cosmid 8F11

MTQETTTLTGQSPPPVRDWPALDLDGPEFDPVLAELMREGPLTR

VRLPHGEGWAWLATRYDDVKAITNDPRFGRAEVTQRQITRLAPHFKPRPGSLAFADQP

DHNRLRRAVAGAFTVGATKRLRPRAQEILDGLVDGILAEGPPADLVERVLEPFPIAVV

SEVMGVPAADRERVHSWTRQIISTSGGAEAAERAKRGLYGWITETVRARAGSEGGDVY

SMLGAAVGRGEVGETEAVGLAGPLQIGGEAVTHNVGQMLYLLLTRRELMARMRERPGA

RGTALDELLRWISHRTSVGLARIALEDVEVHGTRIAAGEPVYVSYLAANRDPDVFPDP

DRIDLDRDPNPHLAYGNGHHFCTGAVLARMQTELLVDTLLERLPGLRLAVPAEQVAWR

RKTMIRGPRTLPCTW

>CYP158A2 Streptomyces coelicolor 2StG58 [Full Sequence] MTEETISQAVPPVRDWPAVDLPGSDFDPVLTELMREGPVTRISL

PNGEGWAWLVTRHDDVRLVTNDPRFGREAVMDRQVTRLAPHFIPARGAVGFLDPPDHT

RLRRSVAAAFTARGVERVRERSRGMLDELVDAMLRAGPPADLTEAVLSPFPIAVICEL

MGVPATDRHSMHTWTQLILSSSHGAEVSERAKNEMNAYFSDLIGLRSDSAGEDVTSLL

GAAVGRDEITLSEAVGLAVLLQIGGEAVTNNSGQMFHLLLSRPELAERLRSEPEIRPR

AIDELLRWIPHRNAVGLSRIALEDVEIKGVRIRAGDAVYVSYLAANRDPEVFPDPDRI

DFERSPNPHVSFGFGPHYCPGGMLARLESELLVDAVLDRVPGLKLAVAPEDVPFKKGA

LIRGPEALPVTW

>CYP158A3 Streptomyces avermitilis

MTEKTITEALPPVRHWPALNLTGVEFDPVLSQLMSEGPVSRIQLPNGEGW

AWLVTRYDDVRMVANDPRFSRAAVMGRQVTRLAPHFIPTAGAVGFLDPPD

HTRLRRSVAAAFTARGVERVREKSRRMLDELIDELLRGGPPADLVETVLS

PFPIAVVCELMGVPAADRHSMHTWTQLILSSAHGAEVSEKARNDMGAHFE

RLIGERRGSTGEDVTSLLGAAVGSGEITLDEAVGLAVLIQIGGEAVTNNS

GQLFYILLTRPDLAERLRAEPKIRPQGIDELLRYIPHRNAVGLSRIATED

IEIRGVRIREGDTVYVSYLAANRDPDVFPDPERIDLTRSPNPHVSFGFGP

HYCVGGMLARLESELLVEALLDRVPGLRLAVPPGLVPFKKGALIRGPEAL

PVTW

>CYP158B1 Saccharopolyspora erythraea NRRL23338

MTDRCPARMYDPADLPGMTFDPVFLELLRDEPVARIRMRYGEGE

AWLLTRYEDVKFVTSDPRFSRKIMGRPFPKMTKHHIPMDRAISFSDPPEHARVRRVVA

RDFSPGSIERLRPTGREIMHRYLDELVASGPPADLVRHVTSPFPMAVLGELMGIPESD

RQWLIDCSSQVLSMAPDQAAVDRINGIKAEVAEYFLALVESRRADPRDDVVSTVAAAR

ERGDLDDEEVGAMTVLLALNGWHAVRNNSTNMVYVLLTDPELRSRLKADLALVPTAVE

ELLRYIPHKRGIGQPRIATEDVDIRGVRISKGDVVYVSYIAANWDEEVYPEPDRVDLD

RPEVPHLAFGHGPHYCMGPMLARMESQVLLSSLLTRLPDLALAVPPEQVAWQPNALIR

GPVELPVTW

>CYP159A1 Streptomyces coelicolor cosmid F55

MSTAQQVPDILSPEFAANPYPAYRTMRDSAPLIRHEATQSWIVS

RYEDVERVFKDRAGQFTTENYDWQIEPVHGRTILQLSGREHAVRRALVAPAFRGADLQ

ERFLPVIERNSRELIDAFRHTGRADLVADYATRFPVNVIADMLGLDKADHDRFHGWYT

SVIAFLGNLSGDQEVAAAGARTRTEFAEYMIPVIRERRENPGDDLLSTLCAAEVDGVR

MSDEDIKAFCSLLLAAGGETTDKAIAGIFANLLAHPEQLAAVREDRSLIPRAFAETLR

YTPPVHMIMRQTATDVTLSGGTIPAGATVTCLIGAANRDETRYRDPDRFDIMRDDLTT

TTAFSAAADHLAFALGRHFCVGALLAKAEVEIGVGQLLDALPGLRTEDGFEVVERGVF

TRGPQSLPVRFTPAA

>CYP159A2 Streptomyces hygroscopicus subsp. yingchengensis

MSAAHHLPDILSPEFAANPYPAYAVMREKEPLIWHEATQSYIIS

RYEDVERVFKDKKAEFTTDNYNWQLEPVHGKTILQLSGREHAVRRALVAPAFRGSDLE

QKFLPVIERNSRELIDAFRHTGSADIVNDYATRFPVNVIADMLGLDKADHARFHGWYT

AVIAFLGNLSGDPEVAAAGERTRVEFAEYMLPVIRERRANPGDDLLSTLCAAEVDGVR

MSDEDIKAFCSLLLAAGGETTDKAIAGILANLLSHPDQLAAVRADRSLIPAAFAETLR

YTPPVQMIMRQSATDVEVTGGTIPAGATVTCLIGAANRDERRYRDPDRFDIFRDDLAT

TSAFSAAAGHLAFALGRHFCVGALLAKAEVEVGLNQLLDAMPDLRLADGHDLVEQGVF

TRGPKTLPVRFTPVTA

>CYP159A3 Frankia alni ACN14a

MTTTPTTVPEKPDVLSAEFARDPHTYYKIMRDFYPVLHHEVSGYYFVSRY

EDVARIYKDSVGFSNENYAFQMEPVIGKTVIQMGGREHAINRQLITPALR

GNYLEELLPQVDELATEMIDKFRTAGRVDLAEDFTKWFPINVIVKMLDLP

REDLPKFHEWYSSLMAFLANLTNDPEIHAWGMRTQQEYPAYILPIIAERR

RNPGTDLISRLTQAEINDEQFSDEQIKALIGLLLIAGGETTDKSIASTLK

YLIMHPEQLEAVRQDPSLATRALVETLRYHPPVQIILRTTTDDVEVAGTV

IPVGSVVGCVNGAANRDERRFDDPDTYNIFRTDINIRQAFAGSADHIAFA

LGRHFCVGSLLAKREAETAINQILAAMPDIRFADGIEPTDAGLFTRGPES

LIVEFTPAS\*

>CYP159A5 SGR4391 Streptomyces griseus

MFMSVPAPDILSPEFERDPYRAYRLMRQDTPLMWHEATGSYIVSRYEDVERVFKDKEGEFTTENYDWQIEPVHGRTILQLSGREHAVRRALVAPAFRGSDLREKFLPVIERNSRELIDGFRDAGSADLVADYATRFPVNVIADMLGLDKSDYERFHGWYTAVIAFLGNLSGDAEVARAGERTRVEFAEYMLPIIRKRREAPGDDLLSTLCTAEVDGVRMGDEDIKAFCSLLLAAGGETTDKAIAGIFTNLLRHPEQLEAVRADRGLIPRAFAETLRYTPPVHMIMRKSATEVELSGGTVPAGVTVTCLIGAANRDEDRYRNPDSFDIFREDLTATNAFSAAADHLAFALGRHFCVGALLAKAEVEIGVGQLLDAMPDLRLADGFDPVERGVFTRGPQSLPVRFTPVSG

>CYP160A1 Streptomyces lavendulae LinA homolog.

MTSAAPPAFPFPPGPGGTVPPEYARLLTDDPVAEVRLADGSRIW

LVTRHEDVRTVLTDGRFSRHRAAMLPGSGFGRSQGSGIVDLDPPEHGRLRGPVVAAFG

ASRTARFAPRIEAAAEAALDRLPAGSGTVDLVAAYTAPFAGRVTAEFLGLPGDRWQDV

TSDVELLLLPRGATEQALKEARGRLGQVLDELLAARRAEPGDSVTDTLLDAEELTDDD

RRLLLHGLIISGFITIRDLLARHLFGVLSSPGLAARLREDPSVLPSAVQELLRYYPSS

NDGLLRVATEDVVLSGRRVAAGDAVLPLVSAASRDPEVFADPHVLDIERVADRGIAFG

AGQHACPATGLAVTELTVGIGRLLAAFPRIALAVPPEEVEHSSELLPLGVRSLPVVPG

PRN

>CYP161A1 Streptomyces noursei ATCC 11455 nyst.

MSTPTAPPSLKAEVPPVLRLSPLLRELQSRAPVCKVRTPAGDEG

WLVTRHTELKQLLHDDRLARAHADPANAPRYVHNPFLDLLVVDDFDLARTLHAEMRSL

FTPQFSARRVMDLTPRVEALAEGVLAHFVAQGPPADLHNDFSLPFSLSVLCALIGVPA

EEQGKLIAALTKLGELDDPARVQEGQDELFGLLSGLARRKRITPEDDVISRLCLKVPS

DERIGPIASGLLFAGLDSVASHIDLGTVLFIQHPDQLAAALADEKLMRGAVEEILRSA

KAGGSVLPRYATADVPIGDVTIRAGDLVLLDFTLVNFDRTVFDEPELFDIRRAPNPHL

TFGHGMWHCIGAPLARVNLRTAYTLLFTRLPGLRLVRPVEELRVLSGQLSAGLTELPV

TW

>CYP161A2 Streptomyces natalensis

MTAASHDLPCLNLEPPKMLKLSPLLRALQDRGPIHRVRTPAGDE

AWLVTRHAELKQLLHDERIGRTHPDPPSAAQYVRSPFLDLLISDADAESGRRQHAETR

RLLTPLFSARRVLEMQPKVEEAADTLLDAFIAQGPPGDLHGELTVPFALTVLCEVIGV

PPQRRAELTTLLAGIAKLDDREGAVRAQDDLFGYVAGLVEHKRAEPGPDIISRLNDGE

LTEDRVAHLAMGLLFAGLDSVASIMDNGVVLLAAHPDQRAAALADPDVMARAVEEVLR

TARAGGSVLPPRYASEDMEFGGVTIRAGDLVLFDLGLPNFDERAFTGPEEFDAARTPN

PHLTFGHGIWHCIGAPLARLELRTMFTKLFTRLPELRPELPVEQLRLKEGQLSGGFAELRVVW

>CYP161A3 Streptomyces nodosus

MVNPTPPPSLEDAAPSVLRLSPLLRELQMRAPVTKIRTPAGDEG

WLVTRHAELKQLLHDERLARAHADPANAPRYVKSPLMDLLIMDDVEAARAAHAELRTL

LTPQFSARRVLNMMPMVEGIAEQILNGFAAQEQPADLRGNFSLPYSLTVLCALIGIPL

QEQGQLLAVLGEMATLNDAESVARSQAKLFGLLTDLAGRKRAEPGDDVISRLCETVPE

DERIGPIAASLLFAGLDSVATHVDLGVVLFTQYPDQLKEALADEKLMRSGVEEILRAA

KAGGSGAALPRYATDDIEIADVTIRTGDLVLLDFTLVNFDEAVFDDADLFDIRRSPNE

HLTFGHGMWHCIGAPLARMMLKTAYTQLFTRLPGLKLASSVEELQVTSGQLNGGLTEL

PVTW

>CYP161B1 Streptomyces sp. Tu6071

1 MAAQIQLPLD PPHPARPQHN LRALQKRAPV HRVSTAVGDP AWLVTGYQEI KQLLADPRLG

61 RSHHDPENAA RSGASELLDG PRGDYDTEQK WIATMRSRLQ PFFSAGHVKA MRPRVEALVG

121 ELLDRLEKQG PPADLAEALA LLLPREVIGE LLGVPVEERE LLDEWTTAVS DARDRERSAA

181 GLAALHRYGH ELAARKRAHP TQDVVSWLCE DGTLSDDQVA QLAMGVLFAG YETTATALCV

241 GTALLLDSPE QWRALRENPG LAPTAAEESV RVVSRLLPPV IRYTREDLEI AGAEVRRGEL

301 VMLDIYAATH DESIFPDPDR FDITREDNPH LCFGFGLRYC IGAPLARLEL QAALTQLTTR

361 FPRMRLTVPV EDLTVRPGSF AAIPTSLPVI W

>CYP161C1 SBI\_10607 Streptomyces bingchengensis

42% to CYP161B1 Streptomyces sp. Tu6071 ABB69759

40% to CYP161A2 Streptomyces natalensis

MKELPRLPFDNPAMLGIAPQMRALQQEEPITRVRTAGEDAWLVTRYDEVR

ALLADRRLGLSNPNPEQSAKSAARRFMVALMAGDDYDTEATRHAQMRALL

VPRFSTRRMRLMKTRIEHHVDDLLDQLAAGTPPVDLHRALSFPLPTMVIC

DLLGVPLADRERFGQWARGTFDQSDNQHSANTFQQVVDYITELVARKRTE

PGDDLLSELIAHKDSALSDADIAHLGNAVLLFGYETTIVRIDLGTLLLLR

NPAQRALLAENPELAPAAVEEILRLGVGGKGSNAIIPRYAHSDITVGETV

IRTGDAVMLAIGAANYDGRAFPDGDLFDLARNKPKSHLAFGHGARHCIGR

TLARIELTAVFERLFRRLPNLRLAVPEESLRWQEHRITGGFDELPVTF

>CYP161C2 pntM Streptomyces arenae TU469 HQ292065

89% TO CYP161C1 SBI\_10607 Streptomyces bingchenggensis

MTDLPRLPFDNPDIMGIAPQMLALQKEGPIARVGTAGEDAWLVT RYDEVRTLLADRRLRLSNPNPQPSAKSAARAFMVALMAGDDHETEPARHAQMRSLLIP RFSTRRLRLMKTRIEHHVDELLDQLAASAPPVDLHRVLSFRLPTMVVCDLLGVPLADR ERFGQWARGTFDQSDNEHSANTFQQVVDYMLELVARKRVEPGDDILSELIAEKDGALS DADIAHLGNAVLLFGYETTIVRIDLGTLLLLRNPVQRAQLAEDPGLAPAAVEEILRLG VGGKGSNALIPRYAHGDITVGETVIRTGDAVMLAIGAANYDDRAFPDGGLFDLTRVRP RSHLAFGHGARHCIGRTLARIELTAVFERLFRRLPDLRLAVPEESLRWQEHRITGGFD EIPVTF

>CYP161C3 PenM Streptomyces exfoliatus strain UC5319

HQ292066 84% TO CYP161C1, 81% TO CYP161C2

MNELPRLPFDNPAILGIAPQMRALQKEGPIVRVRTAGEDAWLIT RYDEVKALLSDRRLGLSDPKPERAAKSTARITMMALMAGDDYDREATEHPQMRELLVP RFSTRRMRVMKARIEQHVDELLDQLAASVAPVDLHRALSFPLPTMVVCDLLGVPLADR ERIGQWARGTFDQSDSLHSVNTFQQVVDYMMELVQRKRTEPGDDILSELIAEKDGTLS DEYIAHLGCAVLLFGYETTIVRIDMGVLLMLRNPAQRALLAENPALAPAAVEEILRLA VGGKGSNALIPRYAHSDITVGETVIRTGDAVMLAIGAANIDGHAFPHADLFDLSREKP KAHMAFGHGTRHCIGRVLARIELTAVFERLFRRLPNLQLAVPEESLRWQEHRITGGFD EIPVTF

>CYP162A1 Streptomyces tendae nikkomycin

MRVDLSDPLLYRDSDPEPVWSRLRAEHPVYRNERANGEHFWAVM

THGLCTDMLTDPRVFSSQNGMRLDSDPQVLAAAAGKMLNITDPPRHDKIRKVVSSAFT

PRMVSRLEATMRETAAKAIDEALAAGECEFTRVAQKLPVSVICDMLGVAPADWDFMVE

RTRFAWSSTALDEAEEARKVRAHTEILLHFQDLAAERRREPKDDLMSALVCGEIDGAP

LTDQEILYNCDALVSGGNETTRHATVGGLLALIDNPDQWHRLRDEPALMPSAIQEIVR

YTSPVMHALRTATEDVEFGGERISAGDHVVAWLPSANRDEKVFDDPDRFDIEREPNRH

LGFIQGNHYCIGSSLAKLELTVMFEELLARVEVAELAGQVRRLRSNLLWGFDSLPVKF

VPRA

>CYP162A2 Streptomyces ansochromogenes

MRVDLSDPLLYRDSDPAPVWSRLRAEHPVHRNERANGEHFWAVM

THGLCTDMLTDPRVFSSRNGMRLDSDPKVLAAAAGKMLNITDPPRHDKIRKVVSSAFT

PRMVSRLEATMRKTAAEAIDEALAAGECEFTRVAQKLPVSVICDMLGVAPADWDFMVE

RTRFAWSSTALDEAEEARKIRAHTEILLHFQDLAAQRRREPQDDLMSALVCGEIDGAP

LTDQEILYNCDALVSGGNETTRHATVGGLLALIDNPDQWHRLRDEPALMPSAIQEIVR

YTSPVMHALRTATEDVEFGGELISAGDHVVAWLPSANRDEKVFDDPDRFDIGREPNRH

LGFIQGNHYCIGSSLAKLELTVMFEELLARVEIAELAGQVRRLRSNLLWGFDSLPVTF

VPRA

>CYP162B1 Saccharopolyspora erythraea NRRL23338

VIQAPTVDLTDPELFSSNRFWEVLAWLRANDPVHWHPDAEGSGFWVVTRYDDVTAVYADA

ETFSSRFGMRLGSNDDAVSAVSQRMLIVSDPPDHTHLKRVLSKTFGGSEMSRLEGLVRDV

VREVVADAVEAGETDFLDVAKLIPNYVVCAVMDLPREDWAWVGRTTTDAFEGEDEETRSG

AHGEIFLYFDDLLRQRRGGSGEDFISRVARDRRATDVPDQDRLLTDEEIVFNCNGVLAGA

NETTRYSTAGGVLALAENPDQWRKLREGGAAAIPAAVEEILRWTVPGVHALRTATRPATI

RGQSIGVGDRVTIWNVSANRDEAVFADADSFVVDRSPNRHITFGAGRHLCLGARLARLEL

SAFLSELLDRVEEIELCGEPQYNASNFTWGLRELPVRLVRKQKVP

>CYP162C1 SGR582 Streptomyces griseus

42% to CYP162A1 Streptomyces tendae nikkomycin

43% to CYP162A2 Streptomyces ansochromogenes

MSGEAGGCPAGTARGPDLTDPATYRDADYFAQWQRARRDHPVVRLESPRFGAFWSVTAHAAARQVLERPESFTSTRGMRLGGEPAAVSAASGRMLVVSDGPAHTRLRSAHAPWFAGQAVSRLKDALRSRLDALLADLADGSPVDVPARLARPLPTWLVCGMLGVPEEDWEELALLAAAAFDETETSTASARRAASAGVFAYFAELLEKRRADPGDDLVSALVHQPGGDRLTDEEILLTCDGLVNGGLGTTRHAVSGAVLAFAAHPRQWERLRADRGLVPTAVEEILRWVSPPLHIMRTATEDVLLGGARIRAGERVVLWIPSCNRDESVFAEPDAFRVDRRPNPHLGLGGGPHYCIGASLARLELRTLLRALLDHVARFESDPVLTRTPSTFLHGLDRLEVTLIPAADAAACSPAESEDP

>CYP163A1 Streptomyces spheroides novobiocin

MSTRPTVSPSELEQIDLASPVLHAEYELDEIFRHLRADEPVYWQ

QPRNEQPGFWVISRHADVNEVYKDKEHFTTEHGNALATLLTGGDSASGAMLAVTDGVR

HHQVRNVLSRGFSARMLDLIAHTLQETVDGLLLAALERGECDAAQDIAADVPLGAICD

LLEIPHADRKYLLGLTSHAWSTDYADEPPEESWVAKNEILLYFSKLLKERRGGVREDM

VSLLANCRIDGDPLKAAEQMANCYGLMIGGDETGRHAITGTILALIQNPDQWRALKNG

DVDLNTATEEALRWTVPSLHGGRKATGDVVINGRRINAGDVVSVWISSANRDETVFDA

PDEFNLARTPNKHFTFAYGSHYCLGHYLGRMEVYAVLDGLRRLVGDLEQIGEERWIYS

SILHGMSSLPIRITG

>CYP163A2 Streptomyces roseochromogenes subsp. oscitans

MSTRPTVSPDELEQIDLASPILHAEYELGEVFRYLRANRPMYWQ

QPRGEQPGFWVISRYADVNEVYKDKAHFTTEHGNALATLLTGGDSASGAMLAVTDGVR

HHQVRNLLSKGFSPQMLDLIANSLRETVDGLLLAALDRGECDAAQDIAANVPLGAICD

LLEIPQTDRKYLLGLTAHAWSTDYADETPEEGWVAKNEILLYFSKLLKERRGGDRDDM

VSLLANCRIDGHPLNAAEQVANCYGLMIGGDETGRHAITGTILALIENPDQWRALKNG

DVDLKTATEEALRWTVPSLHGGRKATGDVVINGQQIKAGDVVSVWISSANRDEAIFDA

ADEFKLARTPNKHFTFAYGSHYCLGHYLGRMEVYAVLDGLRRLVGDLEQIGEERWIYS

SILHGMSSLPIRITV

>CYP163A3 Streptomyces antibioticus

MNPRPMLSPDVLEDIDLNDRQLHADYDLSEVWRYLRAERPFYYQ

TARGSQPGFWVVTRHADCTAVYKDKTNFTAERGNVLPTLLAGGDSASRTMLALTDGDR

HTQVRNLLMKAFSPKMLSNIGQSLRTTVDGLLRDAIEKGECDFARDVSGKVPLVAICD

LLAVPQEDREYLLSLTAHALSADEADATAEDNWTAKNEILLYFADLAESRRSSGHNDV

VSLLATSSIEGEPLSDGELMANCYGLMIGGDETGRHAITGGLRALIHHPDQWRMLRNG

EADLQTATEEVLRWTVPSLHGARTATADVVVNGKQQIRAGEIVSVWFASANRDEEVFR

DADRFDLNRTPNKHLTFAFGPHFCLGHYLARMEVEAILDGLRRMVDDIQQTGPEKLIY

SSILQGISSFPALLKPDRRVPPQT

>CYP163B1 Salinispora tropica (marine actinomycete)

MTAADTGRVGSGESQTPAHTVDLADPATFANHDLTGFWQQLRDEEPIHWNPPTAGRRGFW

VVSRYADILDVYRDDVTFTSERGNVLVTLLAGGDAGAGRMLAVTDGPRHAELRKLLLRAL

GPRVLAPVCAAVRTNTRQMIREAVTKGECDFASDIASRIPMMTISNLLGVPDADRAFLLS

LTKTALSADDESISETESAMARNEILLYFQDLMEFRRDHPGEDVVSMLVNSSIDGAPLSD

DDIVLNCYSLIIGGDETSRLTMIDSVNTLAAHPQQWRRLKDGQCEIDKAVDEVLRWASPS

MHFGRVAARDTILHGVRIRADDIVTLWHASGNRDERVFHRPEVFDLGRTPNRHLSFGHGP

HYCIGSYLAKVEISELLIALRDLTSGFETTGEPQRIRSNLLTGFATMPVRFVPDRAGLAR

DALDG

>CYP163B2 SGR3267 Streptomyces griseus

MTTATSTLHGVDLTDPQTFLDRKDDLVGLWQEFRSHSPVHWHPVEGRQVPGFWVLSRYRDVMEVYRDNKRFTSERGNVLATLLEGGDSAAGQMLAVTDGRRHRELRNLLLKAFSPRLLASVVEGVRRRADRLVREAVGRGSCDFAQDVAEHIPMATIADLLGAPAADRDYLLSLTKQALSAEEAGQSAEEAVVARNELLYYFSELAEIRREDPRDDVVSVLATATVDGKPLTEQEIVFNCYSVIIGGDETSRLSMICAVHELMEHPDQWRRLVSGEVSVDSAVEEVLRWVTPAMHFGRRALTDVEIGGRTIRAGDVVTLWNSSANYDETVFDRPEEFDLARTPNKHVSFGYGPHFCLGAYLGRGEIHALLTALRTHVAAMEPTAPARPIHSNFLHGYSSLPVSLRPVTGDRT

>CYP163C1 SBI\_8210 Streptomyces bingchengensis

49% to CYP163A3 Streptomyces antibioticus

MDTRRALPPQPLDQLDLADPLLHAHHDLGPLWRRLRAEAPVHWQPETARG

PGFWAVSGYADVVSVLGDSETFTSERGNVLDTLLAGGDSAAGQMLAVTDG

RPHQALRSALLKPFSPRSLDVVVDSVRRGTRALVEEAVERGEVDFAADVA

AHIPLAAICDLLGVPAAERQHIIDLTSGALSSADGAPTEEATWASRNGLL

LYFSELAAERRAKPYDDVVSLLVTKEIDGRPLTHEEIVFNCYSIIMGGHE

TTRFAMVGGLRALMEHEDQWQALKSGRVATASAVEEVLRWTTPALHSGRT

ATRDVLLDDRFVEAGDIVVTWLASANRDERVFDRPDEFDLSRTPNKHLSF

AHGSHFCLGAFLARAELTALLESARDLVDKAEPAGPPRYVYSNFLSGMSA

LPVSLTPSCRVLAGPVAWEGPTAGLTVGNMTHTPAAVGAEAVSAVVCGMV

RLVAPRKLDQVELDHRLVGDLGFHSLVLAELGYNLEDLYGLRALTPEETM

KLERVKDVIEFVSTEVASGRAQLPDEEELSDLFARYGADAPTA

>CYP164A1 Mycobacterium leprae cosmid B1788

1 MRTCVPTRTC VYAFIEYLSH NRPMGTNPPS LVEAQMLLLR LIDPGTRADP FPVYRALIDY

61 GPMQLPGMPL TVFSSFSDCD EALRHPLSAS DRLKATLAQQ AIAAGAEPRP FYASSFMFLD

121 PPDHTRLRKL VSKAFAPKVV QALEGDIAAL VDSLLDKGAA AGQFDVIADL AFPLAVAVIC

181 RLLGVPYEDA PEFGRVSALL VQSVDPFITI TGEPPEATEE RLRAGVWLRD YLEQLVKCRR

241 GTPGEDLISR LIELDESGDQ LTEEEIIATC GLLLVAGHET TVNLIANAVL AMLRNPSQWK

301 ALSSNPQRAP LVVEETLRYD PAIHLIGRVA AKDMTIGQTT LTEGDTMVLL LAAANRDPAV

361 YSRPDEFDPD RPSSRHLAFA VGSHFCLGAA LARLEATVTL SAISARFPQV QLAGELVYKP

421 NVAMRGMSAL PVQV

>CYP164A2 Mycobacterium smegmatis

MHNGWMSTAATAQEAQGLLLQLLDPATRADPYPIYDRIRRGGPLALPEAN

LAVFSSFSDCDDVLRHPSSCSDRTKSTIFQRQLAAETQPRPQGPASFLFL

DPPDHTRLRGLVSKAFAPRVIKRLEPEITALVDQLLDAVDGPEFNLIDNL

AYPLPVAVICRLLGVPIEDEPKFSRASALLAAALDPFLALTGETSDLFDE

QMKAGMWLRDYLRALIDERRRTPGEDLMSGLVAVEESGDQLTEDEIIATC

NLLLIAGHETTVNLIANAALAMLRTPGQWAALAADGSRASAVIEETMRYD

PPVQLVSRYAGDDLTIGTHTVPKGDTMLLLLAAAHRDPTIVGAPDRFDPD

RAQIRHLGFGKGAHFCLGAPLARLEATVALPALAARFPEARLSGEPEYKR

NLTLRGMSTLSIAV

>CYP164A3 Mycobacterium marinum MM5268

MLRGPVTAAT HFDHTFFMRR HNVSMTTRPI EPIEFTEQVE PQAFLFQLLD PAIRADPYPL

CARLRDHGPL HLPEANFVLF SSFGDCDEVL RHPSSCSDQT KSTVAQRRVE EEPALGRDFP

PGFLFLDPPD HTRLRKLVSK AFAPKVVNAL RPEISSLVDG LLDRIAEQGR FDVVSDFAYP

LPVAVICRLL GVPLEDEPQF SQASALLAQA LDPFFAFTGQ NAENLNDSLE AGQWLRGYLR

DLIALRRSQP GEDLMSGLVA VEESGDQLTE DEIVSTCVLL LVAGHETTVN LIGNAILAML

RDRRQWAQLG ADPDRAAAVV EETMRYDPPV QLIGRIAGAD MVIGDVEVAK GDVMMMLVAA

AHRDPAEYDR PEEFDPDRGA LRHLGFGRGA HYCLGAPLAR LEASVALSAI AARFPQARLD

GEPQYKTNVT LRGLESMTVA LS\*

>CYP164A3P Mycobacterium ulcerans

MLRGPVTAATHFDHTFFMRRHNVSMTTRPIEPIEFTEQVEPQAFLFQLLDPAIRADPYPL

CARLREHGRLHLPEANFVLFSSFGDCDEVLRHPSSCSDQTKSTVAQRRVEEEPALGRDFP

PGFLFLDPPDHTRLRKLVSKAFAPKVVNALRPEISSLVDGLLDRIAEQGRFDVVSDFAYP

LPVAVICRLLGVPLEDEPQFSQASALLAQALDPFFAFTGQNAENLNDSLEAGAVAARIPA

\*MTRWKRGQWLHGYLRDLIALRRSQPGEDLMSGLVAVEESGDQLTEDEIVSTCVLLLVAG

HETTVNLIGNAILAMLRDRRQWARLGADPDLAAAVVEETMRYDPPVQLIGRIAGADMVIG

DVEVTKGDVMMMLVAAAHRDPAEYDRPEEFDPDRGPLRHLGFGRGAHYCLGVPLARLEAA

VALSAIAARFPQARLDGEPQYKTNVTLRGLESMTVALS

>CYP164A4 Mycobacterium vanbaalenii PYR-1

MRLLHLHALHPRVSAPLVQGQGDAVRDAVHDPQRAVRHPPRRRHPRRHPRGPVRRAARARPRPVLRQGVA SAGVFDLHPFRLVHNKSMTTAAEPQSLLLQMLAPEVRADPYPVYAQILAHGPMQLPGNNLTVFSSYADCD EVLRHPDASSDRLKSTAAQRAIADGAEARPFGPPGFLFLDPPDHTRLRWLVSKAFVPKVVKALEPDIVTM VDGLLREAEAGATFEAIGGLAYPLPVAVICRLLGVPLEDEPQFSAASALLAQSLDPFISVTGSAGSGFEE RMQAARWLRGYLRELIARRRRDPGEDLMSGLIHVEESGDQLTEDEIVATCNLLLVAGHETTVNLIANAIL ALLRNDGQWAALAADPGRAAAVIEETLRHDPPVQLVGRIAGQDMTIGGERSDGGNVAGGVTVPKGDNILL LTAAAHRDPDHVDRPDEFDPDRPVIRHLGFGKGAHFCLGAPLARLEATLALTALTSRFPDAKLAAEPVYK PNVTLRGMSELSITLA

>CYP164A5P Mycobacterium leprae cosmid B1450

AVDALLCFLSPPGLAGPRFAVTDVEIGQHTVVAGQTVRLYLASANHDPQRFNCTDELEPTRPAPHTA

>CYP164B1 Streptomyces peucetius

MPNLMNLDAPDHTRLRRLAGKAFKPRLVQQWRPRIEEIVRELLTDIAAGENTADLVSAFA

YPLPVRVICDMLGVPREDHPVFEKWARSIAYTVDPQLVPGRLSTEVVQEVEEARAGFVGY

FGRLIAERRHTPRADVLSELISAEEQGDQLTESELIITCILLLVAGHETTANLILNGILG

LLRHPGQLRLLRERPELAEAAVEEVLRYDAPAQMITRIAREPFTIGDTPVTPGTPLLVLL

AAANRDPDVHRDPDTFDISRGDPGHLGFAAGPHFCLGSVLARLEGSIALNAFAQAFVEPR

LDAESLRYRPHVAVRGPDRMRVSFKEIRVDAVRVTGTSERSVASRG\*

>CYP165A1 Amycolatopsis mediterranei

MFEESNALRGTEIHRRDRFAPGPELRSLMGEGTMSILQPPDSPG

GRTGWLATGHDEVRQVLGSDKFSAKLLYGGTVAGRIWPGFLNQYDPPEHTRLRRMVTS

AFTVRRMQDFRPRIEQIVQASLDAIEAAGGPVDFVPRFAWSVATTVTCDFLGIPRDDQ

ADLSRALHASRSERSGKRRVAAGNKYWTYMTEIAARARRDPGDDMFGAVVRDHGDAIT

DAELLGVAAFVMGAGGDQVARFLAAGAWLMVEHPDQFALLREKPDTVPDWLNEVERYL

TSDEKTTPRIAQEDVRIGDQLVKAGDAVTCSLLAANRRKFPAPEDEFDITRERPVHVT

FGHGIHHCLGRPLAEMVFRAAIPALAQRFPKLRLAEPDREIKLGPPPFDVEALLLEW

>CYP165A2 Amycolatopsis orientalis cosmid PCZA363.

MFAENNAVRGTEIHRREQFDPGPELRSLMAEGPMSILEADDPAE

GRTGWLATGYDEIRQVLGSDKFSAKLLYGGTVAGRIWPGFLNQYDPPEHTRLRRMLTS

AFTVRRMQGFRPRIELIVEATLDDIEATGGPVDFVPRFAWPIATTVTCDFIGIPRDDQ

ADLSRALLASRSERTGKRRVAAGNKFWTYMSQVAAQARRDPGDNMFGAVVREHGDAIT

DAELLGVAAFIIGAAGDQVARFLAAGAWLIAEHPEQFAVLRDKPDTIPDWLNEVARYL

TSDEKTTPRIALEDVYIGDQLVKAGDAVTCSLLAANRRNFPAPEDQFDITRERPAHVT

FGHGIHHCLGRPLAEMVFRTAITALTRRFPTLRLAEPGREIKLGPPPFDVEVLLLDW

>CYP165A3 Amycolatopsis orientalis

MFEEKNALRGTEIHRRERFDPGPELRALMAEGRMSVMESEESPG

GRTGWLATGYEETRQVLGSDKFSAKLLFGGTAAGRIWPGFLNQYDPPEHTRLRRMVAS

AFTVRRMRDFRPRIEAVVKATLDDIEATGGPVDFVPRFAWPIATTVICDFLGIPRDDQ

AELSRVLHASRSERSGKRRVAAGNKYWTYMGQVAAKTRRDPGDDMFGAVVREHGDDIT

DAELLGVAAFVMGASGDQVARFLSAGAWLMVEHPEQFAVLRDDPDSVPDWLNEVARYL

TSDEKTTPRIALEDVRIGDQLVKKGDAVTCSLLASNRHRFPDPEDRFDITREKPSHVT

FGHGIHHCLGRPLAEMVFRTAIPALAHRFPTLRLAEPDREIKLGPPPFDVEALLLDW

>CYP165A4 Streptomcyes toyocaensis strain NRRL 15009

MFEEINVVRASQLHRRDRFDPVPELHSLMKEGGLTVLGTEDSTE

GRTAWLATGIDEVRQVLGSDKFSARLLYGGTAAGITWPGFLTQYDPPEHTRLRRMVVP

AFSHRRMQKFRPRVEQIVQDSLDTIESLGGPVDFVPHFGWAIATPATCDFLGIPRDDQ

ADLARILLASRTDRSDKRRTAAGNKFMTYMKQHVAQSRRGSGDDLFGIVGRENGDAIT

DAELTGVAAFVMGAAADQVARLLAAGAWLMVEQPAQFALLREKPETVPEWLDETMRYL

TTDEKTHPRVATQDVRIGNQLVKAGDTVTCSLLAANRPNYPSAEDEFDITREKAEHLA

FGHGIHHCLGRAMAELMFKVSIPALAHRFPTLRLADPQREITLGPPPFDVEALLLDW

>CYP165A5 Actinomadura sp. ATCC 39727

MEVFEELNVVLPGELHWRDRFDPVPQLRSFMAEGPMTELGAEEG

PGGRTAWLATGFDEVRQVLGSDKFSSRLLYGGTAAGIVFPGFITQYDPPEHTRLRRVV

SPAFTVRRMERFRPQVDQVVEDCLDAIESIGGPLDFVPHFGWSIATTATCDFLGIPRD

DQAELSRSLHASRSQRAASRRGAAGNKFMTYMGQVVARTRRDPGDDMLSVVVREHGDE

ITDAELTGLAAFVMGAGGDQVARFLAAGAWLMAEVPEQFALLRDKPDVVPDWLEEMVR

YLTIDEKLTPRIALEDVRIGDRIVKAGDTVTCSLLGANRRHFPGPDDQFDLTRDRAPN

VAFGHGIHHCLGRPLAELIFRSAIPALARRFPALRLAEPEQEIRLGPPPFDVKALLLDW

>CYP165A6 Actinoplanes teichomyceticus Genpept CAG105017

GenEMBL AJ632270 CDS 47098..48273 teicoplanin gene cluster

80% to CYP165A4 Streptomcyes toyocaensis strain NRRL 15009

MFEEINVVRAAELHRRDRFDPVPQLRSLMAEGPLTTLGTEESPG GRTAWLATGYDEIRQVLSSDDFSARLLYGGTAAGITWPGFLTQYDPPEHTRLRRMVAP AFAVRRMQKFQPQVERVVQDSLDAIEALGGPVDFVPRFGWSVATTATCDFLGIPRDDQ ADLARSLHASRTERSGKRRTAAGNKFMTYMNKMTARTRRDPGDDMFGVVVREYGDEIT DAELTGVAAFVMGAGADQVARFLAAGAWLMADDPEQFALLREKPDTVPDWLDEVIRYL TTDEKTHPRVATDDVRIGDHLIKAGDTVTCSLLAANRRNFPRPEDRFDITRVRPEHLA FGHGIHHCLGRSLAELVFRTAIPALAHRFPTLRLAEPHREIRLGPPPFDVEALLLDW

>CYP165B1 Amycolatopsis mediterranei 9.9kB DNA

MNDDDPRPLHIRRQGLDPADELLAAGSLTRVTIGSGADAETHWM

ATAHALVRQVMGDHQRFSTRRRWDPRDEIGGTGTFRPRELVGNLMDYDPPEHTRLRQK

LTPGFTLRKMQRLQPYIEQIVNERLDEMARAGSPADLVAFVADKVPGAVLCELIGVPR

DDRATFMQLCHAHLDASRSQKRRAAAGEAFSRYLLAMIARERKDPGEGLIGAVVAEYG

DEATDEELRGFCVQVMLAGDDNISGMIGLGVLALLRHPEQIDALRGGEQPAQRAVDEL

IRYLTVPYGPTPRIAKQDVTVGDQVIKAGESVICSLPAANRDPALVPDADRLDVTRDP

VPHVAFGHGIHHCLGAALARLELRTVFTALWRRFPDLRLADPAQETKFRLTTPAYGLT

ELMVAW

>CYP165B2 Amycolatopsis orientalis cosmid PCZA363.

MVAQELSQSGDDDPRPLHIRRQDLDPADELLAAGALTRVTVGSG

ADAETSWMATTHGAVRQVMGDHKSFSTRRRWHQRDEIGGTGIFRPRELVGNLMDYDPP

EHTRLRQKLTPGFTLRKMQRMQPYIEQIVADRLDAMEQAGSPADLIEFVADEVPGAVL

CELIGVPRDDRAMFMQLCHGHLDASRSQKRRAAAGEAFSRYLLAMIARERKDPGEGLI

GAVIAEYGDEATDEELRGFCVQVMLAGDDNISGMIGLGVLALLRHPEQIAAFQGDEQS

AQRAVDELIRYLTVPYAPTPRIAMQDVIVASQMIKKGESVICSLPAANRDPALVPDPN

RLDVTREPVPHVAFGHGVHHCLGAALSRLELRTVYTALWQRFPTLRLADPAKETNFRL

TTPAYGVTSLLVAW

>CYP165B3 Amycolatopsis orientalis

MSEDDPRPLHIRRQGLDPADELLAAGALTRVTIGSGADAETHWM

ATAHAVVRQVMGDHQQFSTRRRWDPRDEIGGKGIFRPRELVGNLMDYDPPEHTRLRRK

LTPGFTLRKMQRMAPYIEQIVNDRLDEMERAGSPADLIAFVADKVPGAVLCELVGVPR

DDRDMFMKLCHGHLDASLSQKRRAALGDKFSRYLLAMIARERKEPGEGMIGAVVAEYG

DDATDEELRGFCVQVMLAGDDNISGMIGLGVLAMLRHPEQIDAFRGDEQSAQRAVDEL

IRYLTVPYSPTPRIAREDLTLAGQEIKKGDSVICSLPAANRDPALAPDVDRLDVTREP

IPHVAFGHGVHHCLGAALARLELRTVFTELWRRFPALRLADPAQDTEFRLTTPAYGLT

ELMVAW

>CYP165B4 Streptomcyes toyocaensis strain NRRL 15009

MSGDDRPPIHTLRQGFDPADELRAAGELTRVRLGSGADAEHTWL

ATGHDVVRQVLGDHTRFSTRRRFDRNDEIGGKGVFRPRELVGNLMDYDPPEHTRLRRL

LAPGFTHRKIRRMAPYIEQIVTERLDEMEREGSPADLIELFADEVPGPVLCELLGVPR

DDRAMFLQLCHRHLDASLSGRRRAAAGEAFSRYLVTMVARERKDPGDGLIGMVVAEHG

DTVTDEELRGVCVQMMLAGDDNISGMIGLGVLALLRNPEQIAALRGDVPAAERAVDEL

IRYLTVPYAPTPRTAIEDSTVGDQVIKAGETVLCSLPTANRDPALLPDADRLDVTREA

VPHVAFGHGVHHCLGAALARLELRIAYTALWRRFPDLRLADPDGATEFRLSTPAYGIS

RLMVTW

>CYP165B5 Streptomyces lavendulae

MPQQAQRQAPQQQPRAQQAYPELLYTRRTRFDPADDLRAAPPLS

RYVIGPNESDEWVWLATGYTEVRRILGDHTNFSTRRRWGAEGPNWRPPELVGHLMDYD

PPEHTRLRQMLTPEFTVRRLRRLEPDITAIIEEHLDTVEATGPGADLMPLFAQPVPGE

VLCELIGVPRDDRPEFLRHCHRHLDFSRSRKVRAADGAAFSRYLVSMVARQRKDPDDG

FIGALVREHGDDFTDEEMRGVCVLLILAGIDNIEGMIGLGVLAMLENPDQLPLLLGER

DSTGGPGAGKGDGGRLASDRALDELIRYMSVANAPTPRTAVNDVRIGDQLIKAGETVI

CSLTMANRDPALTDGPDRLDLAREPVAHVAFGHGVHHCLGAALARTELRIAYKALWRR

FPELRLAVPVEEVRFYNRALAHGVHRLPVAW

>CYP165B6 Actinomadura sp. ATCC 39727

MSGDGARPLHTRRQDLDPADELRAAGTLTRITIGSGADAETTWL

ATGYTVVRQVLGDHRRFSTRRRWNERDEIGGRGNFRPRELVGNLMDYDPPEHTRLRQK

LTPGFTLRRIRRLKPYIEQIVTERLDALERAGPPADLVELVADEVPGAVLCELIGVPR

DDRAMFMQLCHGHLDASRSQKRRAAAGAAFSRYLLAMIARERKDPGEGLLGAVLAEYG

DTATDEELRGFCVQVMLAGDDNISGMIGLGVLALLRHPEQIAALQGDDQSADRAVDEL

IRYLTVPYAPTPRVAMEDVTIGGQVIKEGETVSCSLPMANRDPALLPDAGRLDVRREP

VPHVAFGHGVHHCLGAALARLELRTVYTALWRRFPTLRLADPDREPSFRLTTPAYGLT

SLMVAW

>CYP165B7 Actinoplanes teichomyceticus Genpept CAG105019

GenEMBL AJ632270 CDS 49590..50636 teicoplanin gene cluster 82% to CYP165B4 Streptomcyes toyocaensis strain NRRL 15009

MRQVLGDHKRFSTRRRFDRRDEIGGTGVFRPRELVGNLMDYDPP EHTRLRHLLTPGFTQRRMRRLAPRIEEIVTDRLDAMEQAGPPADLIELFADEVPGAVL CELIGVPRDDQAMFLQLCHRHLDASLSARKRAAAGEAFARYLVAMMARERKDPGDGFI GSIVAEHGDTITDEELRGVCVQLMLAGDDNVSGMIGLGVLALLRHPEQIAALRGDDQS ADRAVDELIRYLTVPYAPTPRTAVEDVMVADQVIKEGETVLCSLPMANRDRALLPDAD RLDVTRTPVPHVAFGHGIHHCLGAALTRLQLRIAYTALWRRFPALQLADPAQEIMFRT

STPAYGLTSLLVAW

>CYP165C1 Amycolatopsis mediterranei 9.9kB DNA

MGHDIGQLAPLLPEPANFQLRTNCDPHADNFDLRAHGPLVRIAG

DSSAQLGREYVWQAHGYDVVRRILGDHENFTTRPQFTQAKSGAHVEAQFVGQISTYDP

PEHTRLRKMLTPEFTVRRIRRMEPAIQALVDDRLDRVAAEGPPADLQALFADPVGALA

LCELLGIPRDDQREFVRRIRRNTDLSRGLKARAADSAAFNRYLDNLIARQRRDADDGF

LGMIVREHGDTVTDEELKGLCTALILGGVETVAGMIGFGVLALLENPGQVPLLFAGPE

QADRVVNELLRYLSPVQAPNPSLAVKDVIIDGQLIKAGDYVLCSVLMANRDEALTPNP

NVFDANRAAVSDVGFGHGIHYCVGAALARSMLRMAYQALWQRFPGLRLAVPIAEVKYR

SAFVDCPDRVPVTW

>CYP165C2 Amycolatopsis orientalis hypothetical

ISTYDPPEHTRLRKMLTPEFTVRRIRRMEPAIQSLVDDRLDMLE

AEGSPADLQGLFADPVGAHALCELLGIPRDDQREFVRRIRRNADLSRGLKARAADSAA

FNRYLDNLIARQRADPDDGLLGTIVREHGGNVTDEELRGLCTALILGGVETVAGMIGF

GVLALLQHPGQIPLLFEGPEKADRVVNELVRYLSPVQAPNPRLAIKDVVVDGQLIKAG

DYVLCSVLMANRDEALTPDPNVFDANRTAVSDVGFGHGIHYCVGAALARSMLRTAYQT

LWRRFPGLRLAVPVEEVKYRSAFVDCPDQVPVTW

>CYP165C3 Amycolatopsis orientalis cosmid PCZA363.

MAHGIDQHGIDQHGIDQHGIDQHGIDQHGIDQHGIDQHSIDQHG

IDQHGMEQVAPLLQEPANFQMRTGCDPHEENFDLRAHGPLVRLVGDSSTQLGRDYVWQ

AHGYDVVRKILGDHENFTTRPQFTHAKSDAHVEAQFVGQISTYDPPEHTRLRKMLT

PEFTVRRIRRMEPAIQGLIDDRLDMVEAEGPPADLQGLFADPVGALALCELLGIPRDD

QREFVRRIRRNTDLSRGLKARAADSAAFNRYLDNLISRQRKDPDEGFLGMIVREHGDN

VTDEELKGLCTALILGGVETVAGMIGFGVLALLENPDQIQLLFAGPEKADRVVNELVR

YLSPVQAPNPRLAIKDVVIDGQLIKAGDYVLCSVLMANRDEALTPNPNVLDANRAAVS

DVGFGHGIHYCVGAALARSMLRMAYQTLWQRFPGLRLAVPIAEVKYRSAFVDCPDQVP

VTW

>CYP165C4 Amycolatopsis orientalis

MGHDIDQVAPLLREPANFQLRTNCDPHEDNFGLRAHGPLVRIVG

ESSTQLGRDFVWQAHGYEVVRRILGDHEHFTTRPQFTQSKSGAHVEAQFVGQISTYDP

PEHTRLRKMLTPEFTVRRIRRMEPAIQSLIDDRLDLLEAEGPSADLQGLFADPVGAHA

LCELLGIPRDDQREFVRRIRRNADLSRGLKARAADSAAFNRYLDNLLARQRADPDDGL

LGMIVRDHGDNVTDEELKGLCTALILGGVETVAGMIGFGVLALLDNPGQIELLFESPE

KAERVVNELVRYLSPVQAPNPRLAIKDVVIDGQLIKAGDYVLCSILMANRDEALTPDP

DVLDANRAAVSDVGFGHGIHYCVGAALARSMLRMAYQTLWRRFPGLRLAVPIEEVKYR

SAFVDCPDQVPVTW

>CYP165C5 Streptomcyes toyocaensis strain NRRL 15009

MRRTLCDPHEDMFALRAHGPLIRIEGNASDQMSTDYVWQAMGYD

VVRKILGDHENFTTRLRLTDAQPLSGEGVSVPPELAGQISIYDPPEHTRLRRMLTPEF

TVRRIRRLEPAIEGIIEEHLDALEGAGPPADLQVLFADPVGGETLCELLGVPRDDRNE

FIRRVRQNVDLSRGYKARAADSAAFNRYLMTLITRQRKDPDEGFLGMLVREHGDRITD

EELKGVCTALILGGVESVAGMIGFGVLALLEHPDQRRLLFGSREEADRLVNELLRFLS

AVQQPTPRMAVRDVVVEGQLIKAGEYVLCSILMANRDEGLTSDSHLLDANREPLPHVA

FGHGIHHCIGAAVARAVLRITYQSLWRRFPRLSLAVPAGEVKFRNAFIDSPDRLPVTW

>CYP165C6 Actinomadura sp. ATCC 39727

MRIDSEWSFDPGMDDDIDAGAPVLQPTANYMMRTHCDPHEDMFA

LRAHGPLVRIGGDAATQLRVDYVWQALGYDVVRRILGDHENFTTRPRWSSAPSIAGEP

IPPNLVGQLSVYDPPEHTRLRGMLTPEFTARRIRRLEPAMQDLIDDRIDELEAAGPPA

DVQALFADPVGGGVLCELLGIPRDDRIEFIRRVRQNVDLSRGFKARAADSAAFNRYLN

GLIIRQRKDPDEGFIGMLVREHGDDVTDEELKGVLTALILGGVETVAGSIGFGVLALL

DHPDQRQSLFAGREEADRVVGELLRFLSPVQQPNPRLAVRDVVVDGQLIKAGDYVLCS

ILMANRDEALTPNANVLDVRRDCGSHVGFGHGIHYCIGAAIARTLLRMAYQSLWRRFP

GLRLAVSAEEVKFRNAFIDCPDELPVTW

>CYP165C7 Actinoplanes teichomyceticus Genpept CAG105021

GenEMBL AJ632270 CDS 52502..53746 teicoplanin gene cluster

78% to CYP165C6 Actinomadura sp. ATCC 39727

MFTGMDHDIDEVAPVVEPTANYMRRTVCDPHEDMFALRAHGPLI RIGGDAAVQMGADYLWQAMGYDVVRQILGDHENFTTRLRLTASEPISGEGATKPQELV GQISTYDPPEHTRLRRMLTPEFTVRRVRRLEPAIQELIDDRIDAMEAAGPPVDVQTVF ADPVGGGALCELLGIPRDDRNQFMRRVRQNVDLSRGYKARAADSAAFNRYLQSLITRQ RKDPDEGFLGMLVRDHGDDITDEELKGVCTALLLGGVETVAGMLGFGVLALLDHPDQR RLLFAGREEADRLVNELLRYLSAVQQPTPRMAVKDVVVDGQQIRAGEYVLCSILMANR DEALTPHPNVLDAEREPAPHIGFGHGIHHCIGAAVARTVLRMAYQTLWRRLPGLRLAI PAGQVKLRNAFIDSPDQLPVTW

>CYP165D1 Streptomcyes toyocaensis strain NRRL 15009

MALPLPHRRHRLDPVPEFHDLQNEGPLHEYDTEPGMDGRKQWLV

TGYHEVRDILADPERFSSMRPVDDEADRALLPGILQAYDPPDHTRLRRTVAPAYSARR

MERLRPRIEEIVEECLDDLEDVGSPVDFVRYAAWPIPALIACEFLDVPRDDRAELSRM

IRESRESRLPRQRTSSGMGVVNYTQKLAARKRLDPGEGMIGVIVREHGAEVSDEELAG

LAEGNLIMAAEQMAAQLAVAVLLLVTHPDQMALLREHPELVDGATEELLRHASIVEAP

APRVALEDVSVAGRDIRAGDVLTCSMMAVNRPQGEHFDITRENPKHMAFGYGIHHCLG

APLARLQLRVALPAVLRRFPSLRLAVPEEDLRFKPGRPAPFAVEELPVEW

>CYP165D2 Actinomadura sp. ATCC 39727

MVVPLPHQRLRLDPVPALFDLQEDGPLHEYDTEPGLDGHKQWLV

TGYGEIREILADANRFSSMRPVEDEAERAWLPGILQSYDAPDHTRLRRTVTRANTARR

IESLRPVVEETVEDCLADLESMGSPVDFVRNAAWPIPALIACDFLGVPRDDQAELSRM

FRDSRESRVPRQRNVSGLGIVDYARKLAARERLDPGTGMIGGIVREHGGEVTDEELAG

LVEGIMIGAVEQMASQLAIAVLLLVTHPDQMALLRERPELADSAAEEVFRYASIVETP

SPRTALVDTRLAGRDIHAGDVLTCSILAGNRAREDRFDLTRGNPEHLAFGHGVHFCLG

APLARLQAQVALPALVRRFPSLRLAVPAEDLRFKPGKPAPFAVEELPVEW

>CYP165D3 Actinoplanes teichomyceticus Genpept CAG105018

GenEMBL AJ632270 CDS 48296..49450 teicoplanin gene cluster

86% to CYP165D1, 75% to CYP165D2

MALPLPHQRLRLDPVPEFEELQKAGPLHEYDTEPGMDGRKQWLV TGHDEVRAILADHERFSSMRPVDDEADRALLPGILQAYDPPDHTRLRRTVAPAYSARR MERLRPRIEEIVEECLDDFESVGAPVDFVRHAAWPIPAYIACEFLGVPRDDQAELSRM IRESRESRLPRQRTLSGLGIVNYTKRLTSGKRRDPGDGMIGVIVREHGAEISDEELAG LAEGNLIMAAEQMAAQLAVAVLLLVTHPDQMALLREKPELIDSATEEVLRHASIVEAP APRVALADVRMAGRDIHAGDVLTCSMLATNRAPGDRFDITREKATHMAFGHGIHHCIG APLARLQLRVALPAVVGRFPSLRLAVPEEDLRFKPGRPAPFAVEELPLEW

>CYP165E1 Streptomyces lavendulae

MASRDVPVYNRRDRLDPVPELVELRNRCPVLRTELHGGPSSQVV

GWLVTGIDESREVLSDQHRFTMLPPADTEAQSRRLQNIGNPLHYDPPEHTRLRKMLNP

EFTMRRLRRLQPRIDAVVEECLDAMEQAGAPADLMQHFAWQIPGHTACELLGVPRDDR

AELSRHLDITRDDGRGRARQMAAGRAYRAYFHQLTARQRRDPGDDLLGMLVREYGDEI

TDEELEGLAASLTSAGIENVASMLGLGTLVLLEHPDQLAELREKPELIDRAVEELLRH

VSVIPTLSPRTALEDVPLGGHVVPKGERVICSAFAANRIATPGDDLEDGFDITREPAP

HMAFGHGVHHCLGAPLARMQLRTAYQALWRRFPELRLAVPHEEIRFRMPSSRVYSVDA

LPVAW

>CYP166A1 Amycolatopsis mediterranei rifamycin.

MTDAISFEVPWDRTDKFDPPAVFDSLREERPLAKMVYPDGHVGW

IVSSYELVREVLSDLRFSHSCEVGHFPVTHQGQVIPTHPLIPGMFIHMDPPEHTRYRK

LLTGEFTVRRASRLIPRAEAVAAEQIEVMRAKGAPADVVMDFAKPLVLRMLGELVGLP

YEERDRYVPAVTLLHDAEADPAEAAAAYEVAGKFFDEVIERRRQRPQDDLISSLVTED

LTQEELRNIVTLLLFAGYETTEGALATGVFALLHHTDQLAALRAEPEKLDAAIEELLR

YLTVNQYHTYRTALEDVKLEGELIKKGDTVTVSLPAANRDPAKFGCPAELDIERDTSG

HVAFGFGIHQCLGQNLARIELRAGFTALLRAFPELRLAVPADEVPLRLKGSVFSVKKL

PVSW

>CYP166B1 Streptomyces peucetius

MTQSRESENRLARPFPTARPSGCPFDPPAPFAEAREECPVTPLRYPDGHLGRLVTGLQSA

RAVLGDVRFSSLPAGKRSPVKVPGSELSTDALPAGMFVNMDPPEHTRYRRLLSKHFTLRR

VRELRPRIQEMTDRLLDDTESSGGPVDLVAAFAKPLPMLVTSELLGLPEEDRAPFGHHVD

VLFSLSSSGEEMQQSMVLLAGMLHALINAARKDPGPDILGRLTVETELTDEELLGITTVL

LIAGLETTTHMLALGTYALLRHPEQLAALRADWSLMDDAVEELLRYLSVVQIGPIRVAAE

DFEFEGQSIRKGEVVTVSLPAANRDPQGFEDPDTFDIRRGAARHVAFGSGPHQCMGHHLA

RLELSIGYESLLRRFPRLELAVPAQEIGTREMMVTYGVPELPVRW\*

>CYP167A1 Sorangium cellulosum = Polyangium cellulosum

MTQEQANQSETKPAFDFKPFAPGYAEDPFPAIERLREATPIFYW

DEGRSWVLTRYHDVSAVFRDERFAVSREEWESSAEYSSAIPELSDMKKYGLFGLPPED

HARVRKLVNPSFTSRAIDLLRAEIQRTVDQLLDARSGQEEFDVVRDYAEGIPMRAISA

LLKVPAECDEKFRRFGSATARALGVGLVPQVDEETKTLVASVTEGLALLHDVLDERRR

NPLENDVLTMLLQAEADGSRLSTKELVALVGAIIAAGTDTTIYLIAFAVLNLLRSPEA

LELVKAEPGLMRNALDEVLRFDNILRIGTVRFARQDLEYCGASIKKGEMVFLLIPSAL

RDGTVFSRPDVFDVRRDTGASLAYGRGPHVCPGVSLARLEAEIAVGTIFRRFPEMKLK

ETPVFGYHPAFRNIESLNVILKPSKAG

>CYP168A1 Pseudomonas aeruginosa

MDDAFSEEGSAQPRHDAQRPALAPRSDGFDIHTYHPDFVADPYP

LLRLIRSRAPVCRDQASIWWISRYADVSACLRDRRFSADPARLGAAGVRQGGASWFGH

QQLQPLARFYDNFMLFNDAPRHTRLRRLFAPAFGPDAVRRWEARIEVLVEELLDSLLE

RREPDLLRDFAEPLTIRVAAELFGFPREDTGQLLPWGRDLAAGLDLAASHGDAGQINR

SAVAFSDYLQRQARGWSDGSSRPPSGAAPSILDGAAMLEAGLGLEDLVAAYAMVFMAA

FETTISMVGNATLALLTHPDQLDLLRRCPELAANAVEELLRFDGAVRGGVRCTLEEVE

IGGQRIPPGEKVWLSFLAANRDPEMFAAPDRLQLQRANAKQHVAFAHGPHYCLGAYLA

RLELQCALRGLVRRRFALASEPTDLRWRRSSVFRTLERLPIVPEGDAQKTCE

>CYP169A1 Pseudomonas aeruginosa

MQQTIDCPIRRRLAHLPWANDGRAGVRHWLEMQRDPLAWLQKMH

VAQPDLAVARMGPQRLWCLFHPQAVQELMVDRRDDLQRWQPALCMLKQWNGRSFMMRE

GAPAQARRKEVRPHLAPPPASEVRRLAAEWGERVEEGREYDLDLEMAAFSVTLSGHAL

FDVDLQPSAYRIAKAVRLLSRVALLEMSTGLPLGHWFPSKLCPRKRWALGQLREAVGE

VAERSPRPLADLRDELCTLLMASHQSTGVTLTWSLLLLAQRPELLARLRAELAGVNWT

AIRSVADLRDCALLRAVLQECLRLYPPAYGLAPRQVTADIEVFGQRLKRGDVTMVSSW

ITQRDPRWFEAPLEFRPERFLEPARWPRGAYFPFGLGDRACPGTAMAMIDLAAALAYW

VEHWDIMHDGDLAPRGWFSLRPQRARVRFRRRA

>CYP170A1 Streptomyces coelicolor cosmid 7E4 gene="SC7E4.20

MTVESVNPETRAPAAPGAPELREPPVAGGGVPLLGHGWRLARDP

LAFMSQLRDHGDVVRIKLGPKTVYAVTNPELTGALALNPDYHIAGPLWESLEGLLGKE

GVATANGPLHRRQRRTIQPAFRLDAIPAYGPIMEEEAHALTERWQPGKTVDATSESFR

VAVRVAARCLLRGQYMDERAERLCVALATVFRGMYRRMVVPLGPLYRLPLPANRRFND

ALADLHLLVDEIIAERRASGQKPDDLLTALLEAKDDNGDPIGEQEIHDQVVAILTPGS

ETIASTIMWLLQALADHPEHADRIRDEVEAVTGGRPVAFEDVRKLRHTGNVIVEAMRL

RPAVWVLTRRAVAESELGGYRIPAGADIIYSPYAIQRDPKSYDDNLEFDPDRWLPERA

ANVPKYAMKPFSAGKRKCPSDHFSMAQLTLITAALATKYRFEQVAGSNDAVRVGITLR

PHDLLVRPVAR

>CYP170A2 Streptomyces avermitilis

MTLESVKPEAPEAPQLRNPPLAGGGIPGLGHGWKLARDPLGFLAQLRDHG

DIVRLKLGPKTMYAVTTPALTGELALSPDYEIGGPLWESLEGLLGKHGVA

TANGPTHRRQRRTIQPAFRLDIIPEYGPIMEEEARAFAARWQPGEIIDCT

SESFRVAVRIAARCLLRGHYMDERAERLSIALTTVFRGMYRRMVIPAGPL

YRLPLPANRKFDRALADLHLLVDEIVAERRASGQKPDDLLTALLEAKDDN

GDPITEQEIHDQVVAILTPGSETIASTIMWLLQVLTEHPEHAAKVCAEVE

SVTGDRTVAFDDVRKLSHTNNVVVEAMRLRPAVWILTRRAVTETELGGYR

IPAGADIVYSPYAIQRDPRSYAEHLEFDPDRWLPERSKDLPKYAMRPFSL

GNRKCPSDHFSMAQLTLITATVAAKWRFEQVSESSDATRVGITLRPHRLL

LKAIPR

>CYP171A1 Streptomyces avermitilis polyketide synthase gene MMSQSTSSIPEAPGAWPVVGHVPPLMRQPLEFLRSAADHGDLLKLRLGPK

TAYLATHPDLVRTMLVSSGSGDFTRSKGAQGASRFIGPILVAVSGETHRR

QRRRMQPGFHRQRLESYVATMAAAAQETADSWSAGQVVDVEQAACDLSLA

MITKTLFFSDLGAKAEAALRKTGHDILKVARLSALAPTLYEVLPTAGKRS

VGRTSATIREAITAYRADGRDHGDLLSTMLRATDAEGASMTDQEVHDEVM

GIAVAGIGGPAAITAWIFHELGQNAEIESRLHAELDTVLGGRLPTHEDLP

RLPYTQNLVKEALRKYPGWVGSRRTVRPVRLGGHDLPADVEVMYSAYAIQ

RDPRWYPEPERLDPGRWETKGSSRGVPKGAWVPFALGTYKCIGDNFALLE

TAVTVAVVASHWRLHALPGDEVRPKTKATHVFPNRLRMIAEPRSVVRLEE

PAAMGA

>CYP171A2 Streptomyces nanchangensis

MPAPLQVPDVPGSWPVVGHLPQLARRPLDFLSSLADHGDLVRIR

LGRKPVYVATHPDLVRSLLVTDAHAYTRGAGHAKALAFIGPILVATTGEPHRRQRRMM

QPCFHRQRLGSYVSAMCSAATETADSWSAQDVVDVVPVMTELATAMIAKSLFVSERAA

HAEAELRKTGNAILTVARMSAILPGIYRRLPTPGNRQLPPARTVIEETIAAYRAEGQD

HGDMLSTLLRTTDATGTGLTDEEIRDEVMGLAITGIGGPAAIASWIFYELGQNPDLER

RLHEELDTVLDGRPPSSQDLTRLVFTQRLVKEALRKYPGWVGARRTRESVRLGGHEIP

ADAEVMYSAYALQNDPRWYPDPERFDPDRWDPQQNATRVKKGAWVPFSGGVYKCIGDA

FTETETAVAVAVIASRWRLRPADGRSVRASHLATHVVPRPLRMVVEPRSRNKDEAERS

PHEAPQVSR

>CYP171A2 ortholog SBI\_9777 Streptomyces bingchengensis

99% to CYP171A2 Streptomyces nanchangensis

only 2 aa diffs, missing 15 aa at N-term

VVGHLPQLARRPLDFLSSLADHGDLVRIRLGRKPVYVATHPDLVRSLLVT

DAHAYTRGAGHAKALAFIGPILVATTGEPHRRQRRMMQPCFHRQRLGSYV

SAMCSAATETADSWSAQDVVDVVPVMTELATAMIAKSLFVSERAAHAEAE

LRKTGNAILTVARMSAILPGIYRRLPTPGNRQLPPARTVIEETIAAYRAE

GQDHGDMLSTLLRTTDATGTGLTDEEIRDEVMGLAITGIGGPAAIASWIF

YELGQNPDLERRLHEELDTVLDGRPPSSQDLTRLVFTQRLVKEALRKYPG

WVGARRTRESVRLGGHEIPVDAEVMYSAYALQNDPRWYPDPERFDPDRWD

PQQNATRVKKGAWVPFSGGVYKCIGDAFTETEPAVAVAVIASRWRLRPAD

GRSVRASHLATHVVPRPLRMVVEPRSRNKDEAERSPHEAPQVSR

>CYP172A1 Campylobacter jejuni subsp. jejuni NCTC 11168

GenPept CAB73835

100% match

1 MSECPFFPKP YKNKASTLLT FLLKRRSWLD GLYERSYKMQ TGYVKMPNFD LYVINDTKEV

61 KRMMVDEVRE FPKSAFLHEL LSPLLGESIF TTNGEVWKKQ RELLRPSFEM TRINKVFNLM

121 SEAVADMMDR FSKYPNHAVI EVDEAMTFIT ADVIFRTIMS SKLDEEKGKK ILNAFVTFQE

181 QSVHTAMRRM FRFPKWLSYV LGDCKRAKAG DVIRQVLSDI IKPRYDMADN AEFEDILGSL

241 LLVVDADTNK RFSFEEILDQ VAMLFLAGHE TTASSLTWTL YLLSLYPKEQ EKAYEEITQV

301 LQGGVIEISH LRQFKYLTNI FKESLRLYPP VGFFAREAKK DTQVRDKLIK KGSGVVIAPW

361 LIHRHEEFWT NPHGFNPSRF EGEYKKDAYL PFGVGERICI GQGFAMQEAI LILANILKTY

421 KLELEEGFVP DVVGRLTVRS ANGMRIKFSK RKL

>CYP173A1 Mesorhizobium loti

1 MDTQPAPFVP PAPKPRTSPP STLEMIRIVY RNPLELWGEP TYNEPWISAN GVGGHLIVAN

61 DPGLIRHVLV DNAKNYKMAT VRQKILRPIL RDGLLTAEGE VWKRSRKAMA PVFTPRHIFG

121 FAQPMLKRTK EFVTRYEEGG ASDIAHDMTL LTYDILAETL FSGEIAGEPG SFANEIDRLF

181 ETMGRVDPLD LLRAPDWLPR LTRIRGRKTM AYFRKIVTDT VKMREEKFRR DPDAVPQDFL

241 TLLLKAEGPD GLTRSEVEDN IITFIGAGHE TTARALGWTL YCLAESPWER NRVEQEIDEV

301 LAREPDPTKW LDAMPLTRAA FDEALRLYPP APSINREPIE PEMWKDLYIP RHAAVLVMPW

361 VVHRHRKLWD RPDAFLPERF HPGNREKIDR FQYLPFGAGP RVCIGASFAM QEAIIALAIL

421 LSRFRFDTTA ETKPWPVQKL TTQPQGGLPM QVTPR

>CYP173A2 Sinorhizobium meliloti 1021

MDTRPEPFEPPAPVPRTGIPSRLEIIRTVLRNPLELWGEPSYTL

PWIETKFINQRTLIVNDPGLIRYILVENAANYEMSNVRRLILRPILRDGLLTAEGEVW

KRSRKAMAPVFTPRHAQGFAGQMLRVCEAFVDRYAGASSEPFVTNVAVDMTELTFEIL

AETLFSGEIAVEKQGFAANVEELLHRMGRVDPMDLLVAPSWVPRLTRIGGRKVLDRFR

GVVSETMSLRRRRTTEAPGDVPNDFLTLLLQLEGPDGLSTSEIEDNILTFIGAGHETT

ARALAWCFYCVANTPAYRETMEQEIDSVLASGADPVDWLGRMPHVLAAFEEALRLYPP

APSINRAAIEEDAWTSPEGERVPIRKGISVLVMPWTLHRHALYWQKPRAFMPERFLPE

NRDKINRFQYLPFGAGPRVCIGATFALQEAVIALAVLMHRFRFDLTDETHPWPVQRLT

TQPRGGLPMKVSARVK

>CYP173B1 Magnetospirillum magnetotacticum

NGLLTAEGDEWRLQRRTLAPIFSARHVAGFVAQMDAAGARLGRRLARRDGATVDIALEMT 1287

1286 RATLDVLERTIVHAKGLPGPIPDALGRAITRLLESVGPIDP 1164

1185 SDVFGFPAFVPRLGRLRAGRHCVSSRRW\*HLLDGRKQALARGEAPHDLM 1015

1014 TLLLAAQDPETGRGLSDIEVKANIVTFIAAGHETTANALTWALYCLSQDGAARARVEAEA 835

834 DAAAGPEGNLRLDRLPFTKAVMEETMRLFPPVPFLSRQALRDDRIGRVKIPRNSTVIV 661

660 APWVMQRHRKLWDEPDAFIPDRFFGSRRESIERYAYLPFGAGPRVCIGQSFSVQEATLVL 481

480 AHVARAVRFTLPDEHPPVTPLHRVTLRPKDGLRMVARRRM\* 358

>CYP174A1 Halobacterium sp. NRC-1

MGPMETYVVTEPALVERLLVSDAAEFRKPEFQADAIDDLLGDGL

LLSEGESWREQRGRANPAFSMARVAGFDADIAAHAADRVDDWPVGDTVDVEAAMTHIT

LDVILDVMLGVSLPEARVDAIGDALEPVGARFEPDPVRFAVPEWLPMPDDREYAAAVA

TLDDLVDDIVAAREGTASGGDGDDPMDLLSVLLRARDRGEQSLDRLRDEVMTTLLAGH

DTTALTLTYTWFLLSEHPDVEARLHAELDGALDDGAQPTVAQLQDLDYLEWVLQESMR

LYPPVYNVFRTPIEPVELAGSEVPAGAPIMLPQWAIHRSPDHWDDPEAFDPERWRPER

RADRPRFAYFPFGGGPRHCIGKQLALLEAKLIVATVASDYRLRYEGDTPLSFVPSLTI

HPEQEMRMRVEPR

>CYP174A2 Haloarcula marismortui ATCC 43049 (Euryarchaeota; Halobacteria)

YP\_134859, AAV45153 GenPept, NC\_006396.1:56503..57840 genomic

62% to 174A1

1 MSKTPPGPKG EPLFGSSRTY ARDPFRFISA LERAYGDVAR FDMGPMDTVM LCDPTAIERV

61 LVSEADRFRK PDFQGDALGD LLGDGLLLSE GETWEQQRKL ANPAFSMARL SGMADRITGH

121 AEDRIADWSH GDVIDAEQSM TRVTLDVILD LMMGVELSEQ RVQTIEEQLL PLGQRFEPDP

181 IRFAMPQWMP MPDDAEFNRA VRTLDEVLDD IIEVREDSLG TDEDGPMDFL SVLLRARDDG

241 NQSPEQLRDE MMTMLLAGHD TTALTLTYTW FLLSEHPEVE QRVHEELDDV IGDDRPGMEH

301 VRELDYLEWV IQEAMRLYPP VYTIFREPTE DVTLSGYEVE AGTTLMVPQW GVHRSERFYD

361 DPETFDPERW KPERASERPR FAYFPFGGGP RHCIGKHLAM LEAQLITATT ASQYRLEFQG

421 ETPLELLPSL TAHPRQKMSM RVQER

>CYP174A3

1 MAETPPGPKG EPLFGSSRTY AQDPFRFVEA LEDAYGGVAR FDMGPMDTLL IAEPELVQQI

61 LVDDDAKYRK PDFQDDALGD LLGDGLLLSE GDTWQEQRKL ANPAFSMARL ADMDDRIVDH

121 AESLVADWQD GSVVDAERGM THVTLDVILD LMMGVELPDE RVTTVQDQLV PLGARFEPDP

181 IRFAMPDWVP MPDDAEFDAA METLDGVLDD IFERRRGTTG DEDDGPMDFL SILMRARDRG

241 EQSDEQLRDE MMTMLLAGHD TTALTLTYTW FLLSEHPEVE QRLHEEIDAV VGDERPTIDH

301 VQELEFLDWV IDESMRMYPP VYTIFRTPTD PVELGGYDVA PSTNLMLPQW AVHHSERHWE

361 NPEEFDPERW SPERSEDRHR FAFFPFGGGP RHCIGKHLAL LEAKLIVATV AKDYRLRFEG

421 ETPLELVPSL TVHPRQEMSM RVEER

>CYP174B1 Halorubrum lacusprofundi ATCC 49239 (Euryarchaeota; Halobacteria)

ZP\_02017101.1, EDN48184.1 GenPept, NZ\_ABEB01000009.1

complement(36125..37534) genomic

63% to YP\_659381 Haloquadratum walsbyi, 53% to 174A1 with an insertion

1 MSATPPGPIG DPVFGNGRQY ADDPFSFMRA CADSYGDVVR FDLGPRETYM LTNPADVERV

61 LVADAERYRK PDFGDDAIDT LLGNGLLMSE GETWERQRRL ASPSFHSRRI GALAGTMVEH

121 TESQLADWAD GEVVDVQLEV ARLTVKIIVS AMFGADITDE EVKTVQEKLE PLGARFEPDP

181 RRFLIPNWMP TRENREFDAA IGTLESVIDG IVDRRRGTEY DPSVDPAGPG GVAVRGPVGD

241 GPDGDGAGDL PMDLLSVLLR ARDRGEQTDE NLRDELVTML LAGHDTTALA LTYTFYLLSN

301 HPEARERVAR EAAAATADGP PTAADAREMK FTERVLNESL RLYPPVYTLF REPKLDVKLG

361 GYRIPEGSAL MLSQWAIHRS PRWYDDPETF DPSRWEPERQ SKRPRFAFFP FGGGPRHCIG

421 KAFSLLEAKL ILAEVCSRYD LDYEGPDLSL RGSLTMHPDH PVPMRIRER

>CYP174B2 Haloquadratum walsbyi DSM 16790 (Euryarchaeota; Halobacteria)

YP\_659381 GenPept, NC\_008212.1:3112950..3114311 genomic

CAJ53807 GenPept, AM180088.1:3112950..3114311

1 MSTQPPGPNG VPVFGNSRQY ASDPFTFLRS VADAYGDVVR FSLGPLDTYM LTNPVDIERV

61 LVTDDQKYQK PDFQDDAIGT LLGDGLLLSE GETWQKQRQL AQPAFGPKRI TSLAGTMTDH

121 TRGMLDGWEP GDIKDVHLEM ARVTVRIIVE AMFGTSLTDT QTTAVQENLE PLGKRFEPDP

181 LRFIIPDWVP TQENQEYHKS VSVLEDIIDE IVSERRGTET NSDIDPGAGS DDDPMDLLSI

241 LLRAKQRGEQ TDKQLRDEMM TILLAGHDTT ALTLTYTWYL LSEHPKVRDQ VHEELASVCG

301 GETPTMADTR SLDYTERVLQ ESMRMYPPVY VIFREPQVDV RLGGYRIPAG SAIMLPQWVV

361 HRSPRWYDNP TTFDPDRWRP ERRADRPRFS YFPFGGGPRH CIGKHLSMLE AKLILGTVAQ

421 SYELDYVRDR PFDLRGSLTM HPDEPMGMRV TER

>CYP174B3 Halobaculum gomorrense Euryarchaeota; Halobacteria

BZ894476.1, BZ894445.1

54% TO 174A1, 60% TO 174B2, 66% TO 174B1

GRAGDLGRRRPHRRATGARAAHRPDHRHRDVGTDIDEETVRAVQENLEPLGQRFEPNPMR

AVIPNWAPTRENRRFDDAVATLEGVIDDLVARRRGTEETAPDPAGDAVDSPMPMDLLSIL

LRAHDRGDQTEGDLRDELMTMLLAGHDTTALALTYTFYLLSKHPEAKARFQREVDALDGT

PTAADLRDLSFTDRVLSEAXXXXXX

VYTLFRESKVDARVAGYRIPEGSLIMLPQWVVHRSDRWYDDPLAFDPDRWAPGRRADRPR

FAYFPFGAGPRHCIGKQFSLLEAKLILATVGRAFDLEYEGPELDLRGSLTMHPDHPMPLR

LSSR\*

>CYP174B4 Halogeometricum borinquense DSM 11551 (Archaea; Euryarchaeota)

ZP\_03998664, EEJ57769, ABTX01000001.1 1368411-1369736

76% to CYP174B2 Haloquadratum walsbyi DSM 16790 (Euryarchaeota; Halobacteria)

1 MPLFGNSREY AKDPFTFLRQ VSEAYGDVVY FGLGPLDTYM LTNPADIERV LVSEDAKFHK

61 PDFQDDAIGT LLGDGLLLSE GETWRKQREL AQPSFDPRRI AALGETMTDH ATAMVEGWND

121 GEVRDVQLEM ARVTVKIIVD AMFGSSLADE RVRTVQENLE PLGKRFEPDP LRFLIPDWAP

181 TRENREYKQS ISILEGIIDD VVAERLGTEN DPSAAVAGED GAPMDLLSVL LRAKQRGEQT

241 DQQIRDEMMT MLLAGHDTTA LTLTYAFYLL SQHPESEAKV QAEVDKVCGG ETPTVADVRQ

301 FDYLERVLQE AMRLYPPVYV IFREPQVDVR LGGYRIPSGS AIMLPQWVVH RSPRWYDAPT

361 EFDPDRWRPE RRASRPRFSY FPFGGGPRHC IGKQFSMMEA KLILATVAQA YELDYVRDRP

421 FSLRGSLTMH PEEPMGMRLR AR

>CYP174C1

1 MTTTDAPGPR GLPVIGNSHQ WARDPCAFRE RCAAEYGPVV NYEMLGWDTY MLTDPADVKR

61 VLEDPDTFPK HEPSNAQLEA FVGNGLLTSG GDLWERQREA IQPAFYMDHI RNYAERMVAQ

121 AAATADRWTA GESVDVRRAM TRCTLDILVD CLFGQEIDPA ERGLYEAVEA FQAPLEPSKQ

181 PITFFAPDWA PVPFLRRADR ALSHIDDQIY DIVETRRADE ADRDDLVAML IAADTAMDDE

241 QIRDELVTFL FAGHETTALS MTYVWDLLSR NPTAQRRLHE ELDALLDGRP TIEDVFDFEY

301 TGAVIEEAMR LYPPAHDIRR SPATTVEIGG YTIPEGSLVT LPTWVLHRDE RFWDDPEQFR

361 PGRFLDGGRS DRPEYAYFPF GGGPRRCIGQ QFAMTEAQLI LATIASEWTL EREYGDLELS

421 AAVTLQPSHD VAMTPHRRD

>CYP175A1 Thermus thermophilus

MKRLSLREAWPYLKDLQQDPLAVLLAWGRAHPRLFLPLPRFPLA

LIFDPEGVEGALLAEGTTKATFQYRALSRLTGRGLLTDWGESWKEARKALKDPFLPKN

VRGYREAMEEEARAFFGEWRGEERDLDHEMLALSLRLLGRALFGKPLSPSLAEHALKA

LDRIMAQTRSPLALLDLAAEARFRKDRGALYREAEALIVHPPLSHLPRERALSEAVTL

LVAGHETVASALTWSFLLLSHRPDWQKRVAESEEAALAAFQEALRLYPPAWILTRRLE

RPLLLGEDRLPPGTTLVLSPYVTQRLHFPDGEAFRPERFLEERGTPSGRYFPFGLGQR

LCLGRDFALLEGPIVLRAFFRRFRLDPLPFPRVLAQVTLRPEGGLPARPREEVRA

>CYP175A1 Thermus sp. NMX2.A1

MKRLSLREAWPYLKDLQQDPLAVLLEWGRAHPRLFLPLPRFPLA LIFDPEGVEGALLAEGTTKATFQYRALSRLTGRGLLTDWGKSWKEARKALKDPFLPKS VRGYREAMEEEARAFFGEWRGEERDLDHEMLALSLRLLGRALFGEPLSPSLAEHALKA LDRIMAQTRSPLALLDLAAEARFRKDRGALYREAEALIVHPPLSHLPRERALSEAVTL LVAGHETVASALTWSFLLLSHRPDWQKRVAESEEAALAAFQEALRLYPPAWILTRRLG RPLLLGEDRLPPGTTLVLSPYVTQRLHFPDGEAFRPERFLEERGTPSGRYFPFGLGQR LCLGRDFALLEGPIVLRAFFRRFRLDPLPFPRVLAQVTLRPEGGLPARPREGVRA

>CYP176A1 Citrabacter braakii

MTATVASTSLFTTADHYHTPLGPDGTPHAFFEALRDEAETTPIG

WSEAYGGHWVVAGYKEIQAVIQNTKAFSNKGVTFPRYETGEFELMMAGQDDPVHKKYR

QLVAKPFSPEATDLFTEQLRQSTNDLIDARIELGEGDAATWLANEIPARLTAILLGLP

PEDGDTYRRWVWAITHVENPEEGAEIFAELVAHARTLIAERRTNPGNDIMSRVIMSKI

DGESLSEDDLIGFFTILLLGGIDNTARFLSSVFWRLAWDIELRRRLIAHPELIPNAVD

ELLRFYGPAMVGRLVTQEVTVGDITMKPGQTAMLWFPIASRDRSAFDSPDNIVIERTP

NRHLSLGHGIHRCLGAHLIRVEARVAITEFLKRIPEFSLDPNKECEWLMGQVAGMLHV

PIIFPKGKRLSE

>CYP177A1 Rhodococcus rhodochrous strain 11Y

MTDVTVLFGTETGNAEMVADDIASALGEFDIEATVVGMEDFDVADLAASGTVVLVTSTYGEGELPATTQPFFDAMKAAEPDLTGLRFGAFGLGDSTYDTYNNAIDILVGAVTDAGATQVGATGRHDAASFQPADGPVAEWAKQFAEALSDRTRRGGHEMTAASIDRELVPWSDPEFRNNPYPWYRRLQQDHPVHKLEDGTYLVSRYADVSHFAKLPIMSVEPGWADAGPWAVASDTALGSDPPHHTVLRRQTNKWFTPKLVDGWVRTTRELVGDLLDGVEAGQVIEARRDLAVVPTHVTMARVLQLPEDDADAVMEAMFEAMLMQSAEPADGDVDRAAVAFGYLSARVAEMLEDKRVNPGDGLADSLLDAARAGEITESEAIATILVFYAVGHMAIGYLIASGIELFARRPEVFTAFRNDESARAAIINEMVRMDPPQLSFLRFPTEDVEIGGVLIEAGSPIRFMIGAANRDPEVFDDPDVFDHTRPPAASRNLSFGLGPHSCAGQIISRAEATTVFAVLAERYERIELAEEPTVAHNDFARRYRKLPIVLS

>CYP178A1 Streptomyces avermitilis

MIDLADLDLFTDGDPHEAWRVLRRDRPVHWNATGGDTASGVGPSGFWALT

RYQDVHDAYVDAGLFSSRWGTVMGGSHRRDADSASGRMLIASDDPQHRLM

RQQVHRAFLPALMDRARRVVRDYVNAALDRVLKDGGGDFATDVAPELPAG

LLAAMFGLERRDALHLLALTRSMIGFQDPRYHSDSTPPAVLVSSQVEIFD

VMMDLMETRRRAPSDDLVSILLGASINGRRFTEDEVLYNCLNVAVGGNET

TPFTASAAVQAFMDFPDQAQRLLDDGGLLPTAVEEIFRWTSTNAYVQRVA

TRDVELHGQLIRAGDPVTLWNASANRDEEKFPNPDRFDVRRTPNRHIAFG

VGVHRCIGMGAAQMEIALLLKEIVRRGITFEPAGPPARLRSNFMLGLTCL

PVHATVAQDAS

>CYP179A1 Streptomyces avermitilis

MDLELHGRLDELQRDPYPHYARARRFTALEHVPELDAWLVARDADVREVL

RRPDDFSSANALRPDVMPAPAALAVLGGGFGGRPVVVTADGARHQELRAP

IVRGLSPARVAAVLPYAAERATALVDRFLSGAESGRVELMAAYARRLPGD

VIGRIVGLDPADVPAVVYGGHRAEELLFRPLTEDEQVVAAQDVVAMQHLL

DAFVRDRRADPREDLASEIIASVAPGDGELTLDQRHDIVAHLQNLLLAGH

LTTTALIGTTVLNLLRHPRQWELLCAEPERIPAAIEEAARYDSALQGFRR

VTTRPVTLAGTELPAGASVFVAFGGANRDGGRHPRPDEFDITRTPRRHLA

FGFGVHGCPGAQLAREQLRLTLEQLTRRLPGLRPADDRPVTMRPTLIHRS

PRSLHLVW

>CYP179A2 Streptomyces scabies SCAB19191

MDAELHGRLD ELQRDPYPHY ARARAAEGLT YVPELDSWLV ARDADVREVL RRPEDFSSAN

ALRPDVMPAP AALAVLGGGF GGRPVVVTAD GTLHQELRAP LVRGLSPARV AAVLPYAEER

AAALIDGFVE GGRVELMSAY AGRLPGEVVG RLVGFEPEDV PALVRAGHRA ERLLFRPMTE

AEQIAAAEDV VAAAHRLDAF VRARHADPRE DLGTELIRSV VGHGTDAANA TATSSATDAS

ELTLDHRHQV VSHPQNLLIA GHLTTTALIG TTLLHLLRDR RQWELLCAEP ERIPAAVEEA

ARHDTALQGF RRVTTRPVTL SGTELPAGTP VFLAFGSANR DGSRHPRPDD FDITRPAAGR

HLSFGLGAHA CPGSQLAREQ LRITLRLLTS RLPGLRLAED QRITMRTTLI HRAPERLDLVW

>CYP180A1 Streptomyces avermitilis

MSVREQAPPVPDVFDPRRYAAGVPHAAYRTLRDHHPVARQAEPEVLGWPA

GPGFWAVTRHADVVRVLKDSTTYSSRFGATQIRDPDPDDLPFIRDMMLNQ

DPPDHGRLRRLVSRAFTPRRVDRFESLARDRARTLLAAALAGARAGDGSC

DLVATVTDDYALLNLADLLGVPESDRGLLLHWTRRVIGYQDPDEAGEPLL

DAAGKPVDPRSPGALRDMFEYARQLASYKREHPADDIMTTLATDPELTGP

ELAMFFFLLTVAGNDTVRGAAPGGLLALAEHPEAYARLRARPQQLPSAVE

ELLRWHPPVLTFRRTAVRDTDLAGQRIRAGDKVVVFHASANRDGRVFTAP

DRLDLSRSPNPHVSFGDGPHVCLGAHFARLQLRVLYAQTLRALPAPRVAG

PPGRLVSNFINGIKSLPLQVA

>CYP180A2 Saccharopolyspora erythraea NRRL23338

VTATGVPDVFDPRRYSSGIPHADFAWLRANAPVSWQPEHAVGDWPAGPGFWAVTGYDDVV

RVLRSPGEFSSWLGATQIRDPAPADLPFIRRMMLNLDPPEHGKLRRIVSRAFTPRRVERF

RAEVAARARRLVDAVAERGGCDVPPDLTDDFPLLNLADLMGVPEADRRMLLEWTNRIIGY

QDPEHSEVVRDADGRPLNPRSPAMLADMFGYAQELAAHKRRHPADDLMTALATAEVDGGR

LSGAELEMFFFLLSVAGNDTVRSALPGGLRAFAEHPGQHRLLLESPELLDRAIEETLRYH

PPVLSFRRTATTDVELAGQAIPVGAKVVVFHCSANFDPARFDDPLRFDIRRDPNEQLSFG

TGPHVCLGAHFARLQLRAFYSEALWRLRDLHVTGPVRHLVSNFINGIKHLPVAFTAVRPR

>CYP180A3 SBI\_2082 Streptomyces bingchengensis

51% to CYP180A2 Saccharopolyspora erythraea NRRL23338

54% without insertion

missing about 5 amino acids at N-term

VNPDVVFLPETYAAGVPYALFAEARATRPVCWIEESAVGAWPAGPGFWAV

FRHADVKHVLRTPEVFSSHLGATQIRDPDTPGDLEFVRAMMLNQDPPDHS

RTRRVVAAAFTPRAVRELQAVIEARARTLVEGVAPRGEADFVELAADLPV

WTLAHVMGVPESDRGLLFDWASRVIGYQDAEYAASSTADAAGLSPMGRAA

LAHRPRSLTRPDGRPMNPRSREALADMFAYAHALAERPRPGTVMAHLREG

GLSREEFENMFFLFAVAGNETLRNGIPGGLLTLLDHPESHELLLARPELT

DSAVEEMLRFWPPVIDFRRTATREVELGGQRIRRGDKVVVYHASANRDEA

VFNDPDRFDITRSLGDHVSFGHGPHFCLGAHLARLQMRAMLRGALTRLPG

LRRAGEPVRLMSNFQNGLKHLPVSWETDR

>CYP180B1 Streptomyces scabies SCAB9651

MKPRRTTDMT TSAHLPPALV REAVQEPLPL DDVNLADLDN FTDGVTPWRM FHTLRHEDPV

HWQPEEAPNS GFWAVTRHAD IARVDRDAET FTSTRFVNLE EVDENQIAIR ASILELDGVR

HRALRSVIQR QFGANVINSY TDFLRGLTAR TLDAALAKGT FDFVADVSAD FPINVLARLL

DVPPEDNQRL IDWGNRIIGN TDPDYADVLL HSAESERYRD LPFRSPASLE VFEYGRELAR

QRRGGEGTDL VSKLVNTTPR DGIPLSAQDF DNYFLLLVVA GNETTRHTIT HSMLALLQHP

EQLARLQEDP SLIPAATEEF LRWASPVYHF RRTATRDVEL GGKQVKEGDK VVMWYASGNR

DEAVFGNPYD FDVARADNDH VTFGKGSPHL CLGNLLARTE IRIMFEELIP RLADIRLVGD

VPRVRSNFVN GIKKLPVEVT LA

>CYP181A1 Streptomyces avermitilis

MLPAEYETLRERGIGQVELPTGKLVWMVVRPEYARIVLSDPRFSSDKTDD

RFPKLTPNSLMKLRYCAPFMINLDGPEHLKKKKSIMDEFSPEGLARLLPR

LRVAVEEKIDDMLRQPTKPVDLVKELAFPIAWQLQEMFLGIPAAELETMR

DNVWKLLLGTTTEAEEREAADRLNGHAEEVLKEKAKHLGDDMMSRLIVQE

REKHGEVNWYELAPLMLSNAQGIHNSVSTMISLGVLTLLNHPEQRPTLLA

HPDRMTTAVDEMLRYFSVNDGTPMRLATEDMLIGDTLVKAGDGVAVPTLP

VNRDPSVCPYPHQLDIMREEPARHLAFGHGPHKCPADRLVPSLLEIVYTT

LFERVPTLALAVPEAELTYKYHSIQAFGPAEMPVTW

>CYP182A1 Streptomyces avermitilis

MHGRCGMRSGMEAQPYATAPAGSPRLESLRVEPLLTSEFDADPAGVYERL

RRTYGPVAPVGLMGVPVWLVLDYHEVLEVLRDDSQWRRDIRYWRARAQGQ

LPRDWPLLAGYEVRQTMFLDGDEHHAARLTHHSALRPFQDGHSPQGWELR

AAVARYADELIALLAAESGSAGYADLGAQYTRPLLLMVTGKLFGCPVGLG

DELVMDLWRMLDGGPDAGPATDRAAAVMTRLAAHRRQRPGDDLTSYLLLA

DPGMTDEQLGRELLMNAVYLNDITGNMVMNTLLEVLRGNATVRRSVSDGH

LGETFHRVALVNPPVANMCFRFAAGDVRLGAFWIRAGDVVSPSAAAAHQD

LLTIGTSPLGDATASTRAHLGWGAGQHQCPGAARELAGMIVTTAVGRIFD

HFTKAELTLPADQLPWRSGPVVRGLRLLPVRYELRGTPSESHPVPPPRHD

GEAPDTAPTADHRSRGLLSALRRLMTGTGRAG

>CYP182B1 Streptomyces scabies SCAB81761

MVREIRSDEG VSVDLDGARL EELSPQPLLT RDYETRPSLV YERLRQRHGA VAPVDLLGVP

AWLVLGYRES LQVLQDDAGW PKGLENWRAR TEGRVPADWP LAPSLEVNHV LIQGGPGYKS

LRTAWDQALK PFQDPRNPQT KRLKAAVTAY ADELITLMGE AGGTGLADLS AQFSRPLPLM

VASHLLGFPG SQGDDALMDM WRVLDAGPDA GPALDRLLGA LAELAELKLK TPGEDFPSYL

LAAHPDLSLD QLARELFMLL GMTSDHVGIL ISNTVVEVLS GEDSVRASLS AGMVREAMNR

VVMRKPPLVN FVPRFAAADS RLGEYTIRAG DPVWVSSAAA HADPLFADHV APTTTVSTRA

HLSWGAGPRQ CPARELASTV AAVGVGRLFE RFAHLDLALP VDQLPWRSSP FMRGLRSLPV

RYELAPTDQQ PPALDPAESG AGAGAGAGTP ARDVSARQRS SLWRYLTGLI RSGR

>CYP183A1 Streptomyces avermitilis

MSQHTFVAGTAPGAVPVVGHAWQMMRRPLHFMSSLSAHGDLVKIRIGPTS

AYVPCHPELLRQVLTNDRVFDKGGVFYDRARDIAGNGLVTCPYRDHRRQR

RLMQSAFQRTQLERYSTAMRAEIDATAARWHDGTVIDAFPELYGMALRTV

ARTLYSTPVTEELAQRVEQAFDTVLNGLFRQMFLPHSLRRLPTPANLRYR

NNLRFLHDTVQDLITEYRRDDTQRDDLLSALLASRDEDGGRLGDTEIHDQ

VITVMAAGTETVAGTLTWIFHLLSRHPEIEARLYEEIDTVLDGKPPHWDD

LPSLSLTDRIITEALRMYPPAWIFTRLTASDVDLAGVRLPEGTTIVFSPS

SVQRHSEAYDDASRFDPDRWLPDRTSAVARQAFTAFGTGARKCIGDLFAR

TEATLALATMLSQWRVTVEPDADVRPVALATVYHPRRLRLRLTARTPGQ

>CYP183A2 SBI\_10598 Streptomyces bingchengensis

72% to CYP183A1 Streptomyces avermitilis

VNFMASLSAHGDLVEIKIGPTTAYVPTHPELLRHVLTNDRIFDKGGIFYD

RARDIAGNGLVTCPFADHRRQRRLMQSAFTRGQLKRYAEAMHAEIEDTAS

RWQDGMVVDAFQEMYGLALRTVGRTLYSTPVSPELAAKVERSFDVVLNGL

FRQMFLPASIRRLPLPSQRRYKSNLDFLHETTQQLIDDYRSSDTERDDLL

AALIASRDDDGGKLGDKEIHDQVITVMAAGTETVAATLTWVFYLLSQHPE

IEAALYDEIDTVLDSRAPQWDDLPNLSLADRIISETLRLHPPAWLFTRLT

ASPTELAGRQLPTGSTVVFSPAAVAQYEDAFDNPKKFDPDRWLPDRIAPA

SRHAYVPFGTGARKCIGDLYARTEATLGLATILGRWRVTCEPGMDIRPVP

LATVYHPRRLRLRLDARTPRRKTSAVPVPAGGDVT

>CYP183B1 Mycobacterium marinum MM0281

MPTSIPIAPA ALPLLGHTLP LLRNPLSFLL SLPARGDLVR IRIGPATAVV ACTAELTHEI

LCDDRIFDKG GIFFDRFREM LGDGLGTCPR SQHRRQRRLL QPAFHTQRLP GYAQTMTTEV

AATVGRWQNG QIIDVPAEMM AITGRTLLAT MFSNSLPNPA LRQALDDLTA IFAVLYWRML

TPPPLDRLPT VGNRRYHRAS ARLRHTIGSA VAGRRAAGVD RGDLLSAILA SHEVDSSTVA

FTDTEVIDQI VSFFIAGTET TALTVAWALY LLAEHPAIEQ RVHAEIDPVL AGRAATHADL

PRLGLVNRIV TETLRLYPPG WIISRVATAD VYLGGHRIPA GATVIFSPYL IHHRPDLYAE

PERFDPDRWL PERARAIGRN TYIPFGGGAR KCIGDNFGTT EAALALATIA ANWRMQRLPG

LPVRPAVAAS LRPRNLALRV TARTADRVPG EPGRRLTSRE IG\*

>CYP183C1 SBI\_7103 Streptomyces bingchengensis

43% to CYP183B1 Mycobacterium marinum MM0281

MGPWPVHVVCHPELVHRLLASDRCFDKGGPLYDRLRGLIGDGLASCPHAV

HRRRRRLVQPAFHHTRLPLYAKVMTQQIDETTRSWADGQILDLREELTGL

ATRVLSRTIFTADFSGPAIAALIPYAELITAKLSWRLLWDAALKGVPTPG

KRHFARRTEELRSAVYTMARRYRASDTDHGDLMSMLLSARDDDGSGLTDA

EIFAEVVTMVLAGTGTVPNTLSWAFHTLAQHPDIAKRLHSEVDKVLGGRS

ATWDDLPALPLTAAIFTEAMRHFPSDWLVTRVTTEDTELAGRRLAAGSVV

AYSGQVIHRRPDLYPQPDLFLPDRWLDTDRKPPRGAFLSFGGGARKCIGD

KFGTIEGVLALSTIAARWRLEPAHPGRARSTSSSRRSTRPPAMRLVARG

>CYP183D1 SBI\_7104 Streptomyces bingchengensis

44% to CYP183A1 Streptomyces avermitilis

MTMPNTFTTGLAPGALPLLGHARQLRRQPLPFLESLPGVGDLAEIRLGRE

RVYVPCHPELVRQVLTDDHTFDRGGALQDHFVELFGECVATATYRGHRRQ

RRLIQPAFCHDRLEGYAPVVEAEVAALPDSWREGQTFDLFPVLYTLTLRS

VIRMLFSDRVDEATMDEVRRLFLAMTGGAAPRQGVARLIRGTGPTEGRRR

RAAHQLRGVVDRIVADYRRAGETGKDMLSALLTAREENGGRLDDTEVRNQ

AIIMLAAGSHSPATVLTSVFYLLAEHGGAEHRLHREVDAVLGGRPARWTD

LPDLAFTGRVITETLRLYAPAWTIFRKTTKEVRLAGRDLPAGTTVLVVPL

IPHRRGDLFDCPREFTPDRWRPECDTVTQRGAFKAFGGGARKCVGDVLGM

AELKLVVATIASRWRLECLPDARVRPHAGAVAPPPRYLPVRLVERRP

>CYP183E1 SBI\_7185 Streptomyces bingchengensis

43% to CYP183B1 Mycobacterium marinum MM0281

MDSGSAVVQAPGAIPVVGHLTAFLRAPLPFLRGLPAHGPLVTIRLGRQRV

IVVCDPELTRTVLVQDRVFDKGGPLYERLREAGGQGLASCPSGEHRRQRR

LIQPAFHHSRFPGYAHVMAERMDTLLGGWHDGQTLDLTTETRRIAADVVI

SAIFGTGLDAAVHTRLATDFHTLLAGFTRHTLTPKPLRKVPTPGNLRYER

ATRRVRRTMADLTTTYRAHGDTGETNLLSLLISARDPESDSPALTDDELV

DQAVTMYSAGTETTASAVCWALFLAALHPEVHDRLITEIDTVLDGRTADW

SDLPRLIYTRQVFTEAIRMYPPGWFLTRRTESDTRLGSYDLPKGTTIAYS

PYLISHLPGLYPDPETFDPDRWKPAERGPEVPVTVFGGGARKCIGDQFAL

VEGVLLLASLVSHWHIDFHPDSLSLPRLPQLTLNPGKMKATVTARRGGED

RQRHTSQSRVP

>CYP184A1 Streptomyces avermitilis

MAAVTAAGAAQAPIVAGHPLLGSMNDLLNDPLATYLRARRDHGDVVRFRA

GPPGLRADIYAVFSAEGAQQVLATESGNFRKDNVFYGELRDSVGNGLLTS

QDATYLRQRRLVQPLFTRRRVDGYAGQVADEAAGLAEAWRGIPGGGVELV

GEMHRFALRVVGRILFGTDMETTFEVIERTLPLLQEYALKRGLAPVRTPR

TWPTPANRRAARTQAELFALCDGIIDSRRNRKNEGDGGEESGEDLVTLLV

RAGNAEDGSLDAAELREQVLIFLLAGHETTATALAFALHLLARHPEQQRR

VRDEADRVLGGPGGRAPTAADMEALPYLTMVLKEAMRLYPSAPVIGRRAV

ADAEVDGVRIPAGADLFVSPWVTHRHPDYWPDPERFDPERFTPEAEAGRP

RYAWFPFGGGPRACIGQHLSMLESVLGLAVLIREFEFEAVGEEEVPLGAG

ITLLAKGPARCRVIPRSSGPRSS

>CYP184A2 SBI\_734 Streptomyces bingchengensis

65% to CYP184A1 Streptomyces avermitilis

MATKASTTTAVDVSDVSDVTEVTEVTXXXXXKXXXXXPYAAGTPLLGSMS

DLLGDPLAAYLRARRDHGDVVRFRAGPPGLRREIYGVFSAEGIQQVLATE

AANFRKDNAIYEELRQALGNGLLTSQDEDYRRQRRLIQPLFTRRRVESYA

TAVTSEAAALAARWRETPGGADGALELVEEMRGYALRVVGRVLFGSDVEQ

TIEVVRDSLPMLNERARARALSPVKLPRDWPTPANRRAARAQAGLYALCD

AIISKRMDGREREEREEREQAPGPGHAPGPVPEDGAGPEDGAAEDLLTLL

IRAHNAEDGSLTRAELREQVLVFFLAGHDTTATALTFALHLLARHPAEQR

RVHEELDRALPDGRTPTAADLEALPRLTMVLKEAMRLFPPSPAVSRLAVA

ETVIGGRRIPAGAAVLVSQWVAHRHPAYWEDPERFDPERFTPQAEAGRPR

YAYFPFGGGPRACIGQHFSTLHSVLSLATLLRAYEVEDATDGGDIPLGAG

ITLLAKGPVRVRVRSRT

>CYP185A1 Mycobacterium smegmatis

MRADTRFMVETASPPLTELPLAPRNTLPCREQIRCLRSFIDGMQRLRDVGGPVTRIV

LGPRWLVPPALLVTSPQGAHDVLSLPDAVADRGGSRNMRQLQRLMGGNLL

DLPHDRWLPRRRTLQPLFTKKHVPRFAGHMAAAAQSVAVSWADGATVDLD

RACRALTLRALGRSVFGVDLDQRAEDVGPALRTSLSWVADRASRPVNLPQ

WVPTRGQRKARAGNATLHRLAAEILADVRADPDRDAPLVRALLEARDPET

GRGLTDDQICDELVLFMLAGHDTTSTTLCYSLWALGHHPDIQERVYAEVA

ALGDRELTTDDVPQLTYTMRVLHEALRLCPPGSGTMRMLNEEMTVDGYRV

EAGTVAIVNFYAMHRSPTLWDAPERFDPDRFSPERSAGRNRWQYLPFGGG

PRSCIGDHFAMLEATLALATVIRAVSVESQNTDLPVETPFTVIAAAPVPA

RVTRR

>CYP185A2 Mycobacterium smegmatis

MVSDVPAVTAPPGRSADASGANAKPDTGALPLAPRNPLSLRQMARAVRAL

DMGQQVIRAAGGAVTRVQFGPRWLVPPLVAVFSPEGIRDVLGRNDAFAER

CIVHDEVRHAAGDSLFVLPNEQWRPRKRALQPVFTKHSVRAFGGHMSRAA

QTLVDEWADQWAQADSLEVDLDAVCRRVTMQSLGRSVLGIDLNERADVIV

EHMHVASSYATDRALRPLRAPRWLPTPARRRARAAVAAMRAVTAEILQAC

RDDADRDAPLVRALMAAEDPETGERLSDEDICNDLLIFMLAGHDTTATAL

TYALWALGHHPEIQDRVAAEARALGDRELTPADVPQLGYTVQVLHESLRM

CPPAAGVGRLALRDIAVAGHRVEAGSLVALGIYAVHHDPQLWPDPEVFDP

DRFSPENSRERDRWHFIPFAGGARACIGEHFARLETTLALATIIRSVVVG

SVDAEFPVDVPFTTVAKGPIRANVAPRGPDHYTL

>CYP185A3 Mycobacterium avium subsp. Paratuberculosis old CYP277A1X

MSVAEPKRDIAGLPLAPKNPLSYRERLRAIKEFHTGTNKLRDAG

GPVTRVTLGPRWLISPIVLATSPQGIRDIVSVRDGSIDKTSTVATELRRLLGPNLFVL

PHTEWLPRRRTLQPVFTRQRVREFGGHMAEAAESVCAGWPEDTEIDLDAQCRTLTLRA

LGRSVLGLDLDERSDAIAEPLRVATSYAVRRALRPLRAPEWLPTPSRRRARAAAGAIR

ALADEILQACRADPGREAPLVHALIAATDPETGQALSDKEIRDEMIIFLFAGHDTTAT

TLTYALWALGRHPEYQARVAAEVAELPDRHLTPDDVARLGFTVRVLQEALRLCPPGPT

GTRMATRDVEVAGYRVEAGTMLAFGRMAVQTDPSLWDAPLRFDPDRFDPRRAGDRDRW

QYLPFGGGPRSCIGDHFAMLEATLALATIVRRVEIESLSDDFPLAVPFTMVAAAPIRA

MVRRRR

>CYP185A4 Mycobacterium marinum MM0852 old CYP277A2X

MVDSPDVRSL PLAPRNPLPY WQQLKALKTL HVGSEALRDA GGSVTRIWLG PKRLVPPMVM

VTSPQGARDV LGRSGALSDR GTLPLLKDLR RAIGESVLNL PHDTWLPRRR TLQPIFTKQR

VAGFAGHMSE AANHILLGWP DGAEVDLNAA SHALVLRVVG HSVFGLDLQD KADVITTGVT

LAAKWAADRS ARPVRAPHWL PTPARRRARG AYDAMYKIAA DMLAACRADP NREAPLIRAL

IDATDPNTGE SLSDQQICDE MVYFMILGED TTSTVLTYAL WALGRHSQLQ DRVAAEAAEL

GDRPLTPADV PRLGYTIQVL QEAMRLCPPG PTVARRAMQD IEVDGYRVQA GTYCLVGVYA

MHRDPALWDD PLAFDPDRFA PKKSKGRDRW QYLPFGGGGR SCLGDHFAML EASLALATII

REAEIHSLDG DFPVAIPLPI VPAGPIRARV NQRRPSQEVC TTTLSDSSAS SSAS\*

>CYP185A4 Mycobacterium ulcerans old CYP277A2X

VVDPPDIRSLPLAPRNPLPYWQQLKALKTLHVGSEALRDAGGSVTRIWLGPKRLVPPMVM

VTSPQGARDVLGRSGALSDRGTLPLLKDLRRAIGESVLNLPHDTWLPRRRTLQPIFTKQR

VAGFAGHMSEAANHILLGWPDGAEVDLNAASHALVLRVVGHSVFGLDLQDKADVITTGVT

LAAKWAADRSARPVRAPHWLPTPARPRARGAYDAMYKIAADMLAACRADPSREAPLITAL

IDATGPNTGESLSDQQICDEMVYFMILGEDTTSTVLTYALWALGQHCQLQDRLAAEAAEL

GDRPLTPADVPRLGYTIQVLQEAMRLRPPGPTVARRAMQDIEVDGYRVQAGTYCLVGVYA

MHRDPALWDDPLAFDPDRFAPKKSKGRDRWQYLPFGGGGRSCLGDHFAMLEASLALATII

REAEIHSLDGDFPVAIPLPIVPAGPIRARVNQRRPSQEVCTTTLSDSSASS

>CYP185A5 Mycobacterium vanbaalenii PYR-1

MVGTVEREDLGALPLAPRNPLPYRQQVRAIRTFHTGLETLRDAGGPVTRLKLAPKWLMPPMVVATSPQGA RDILARGGGHIDKTRVHHEMRRLLGANLFDLTHEPWLPRRRALQPIFTKQHVREFAGHMATAAQTVADSW ADGTELDLDTECRKLTLRALGRSVLGLDLDEHSDAIAEPLRTALEYIADRALQPISAPRWLPTPARRRAR AASSTLHKLADKILQACRTDPTRDAPLVQALIAASDPATGRPLSDDEIRDELIVFMLAGHDTTATTLTYA MWALGHHHDVQDRVRAEVVGIGDRELTPEDVPALGYTIQVLHEALRLCPPAAATARMAMRDVEVDGYRIE AGSMMAVGIYALHRDPALWERPLVFDPDRFSAQNSGGRDRWQYLPFGAGPRSCIGDHFAMLEATLALATI IRSAEIRSSDPHFPMIVPFTTVAAEPIRARVKSVNRIPAADSGGR

>CYP185A6 Mycobacterium vanbaalenii PYR-1

MTARDTAAAPEVGSLPLVPRNPLPLWKLVQLVRRLDTGQEVIRDAGGPITRIQLGPKKLMPPIVAVMSPA GMRDVLGRNDASSDRCIIHEQVQEMAGDSLWVLPNEQWRPRKRALAPVFTKTSVRAFGGHMSKAAQAFVD RWPSGGEVDLDAECRRVAMQSLGRSVLGVDLNERGETIARCMHVASSYTADRALRPVRAPRWLLTPARQR ARSAVNAMRAITDEMVKACRDDPTRDAPLVQALIAATDPETGRPLTDEEISNDLLIFMLAGHDTTATALT HALWVLGHHPDIQDRVAAEAAAIGDRELTPDDVPALGYTVQVLHESVRLCPPAAGVARLVTRDFAVDGYR VEAGSLVALGLYALHHDPALWPDPMAFDPDRFSPENVKARDRWQFLPFLGGGRPCIGEHFARLETTLALA

TVVRACRIESLDDLFECEVPLTTVAKGPIRARVTPRR

>CYP186A1 Mycobacterium smegmatis

MSDGGHQLRGAQALATLVDLGFPAIASGVIARRPPVLGLLERMQADERAGRR

MHRLRSEFGRGPVELVIPGRRIVVVTDPEDVAAVLVQAPEPFHPANRE

KRKALQWFQPHGVLISQGPIREQRRTVNEAALDSGAAMHRLAESFAAKVA

AEADTLVARTLPGQRLDADEFMTAWWRLVRRLTLGERARDDHAITDQLAR

LRRAGNWSFLSLPHYRARSRFLSHLYRYAEDPEPGTLVGALADVPAGGAV

DPVGQIPQWLFAFDAAGMALLRALAVLATHPLQRDRALEDAGEPNRPLLR

PYLRGCLLESVRLWPTTPAILRDTTEDTHWREGAERFTVAKGAGLLIVAP

AFHRDDQVLPFAHDFVPEIWIDGRAQLYPQLVPFSAGPAECPGRNLVLFT

TSTLAANLLNRLHFDVRSEPRPVPGEPLPMTFNHAGIEFSLRPARRAVTA

ATVDPAT

>CYP186A2 Mycobacterium sp. JLS

MGASGRRLTG ARAAATLADL GPASTAARAV RRMQQLREQF GAGPVELVLP GRRMVVVLDP

DDVRRVLAGA PEPFHPANRE ERKSLEWSQR RDLDDAALDS GAEMHRLAGA FGDVIAAEAR

ELTDEVTARG TMDANQFMAA WWRIVRRIAL GDRARDDDEI TDALLRLRRA RNWSFLSMPH

YRTRARFLER LYDYVEDPQI GTLAAAVPAS GAVDPVGPLP QWLFAFDAAG IAQLRALAVL

ATHPAAMARA IEDAAEPDRL RLRPFLRACV LESVRLWPTT PTILRETTEK GAGLMIVTPA

FHRDPKLLPF ANDFVPDIWL DGRARSYPQL VPFSAGPAEC PGRNLALFTT STLLANLLSA

LDFRISSMPH LSPDEPLPVT LNQHGLEFAV VTAPRWRHHR AGSAVRS

>CYP186A3 Nocardia farcinica

4523238 MSGRHPETVARDQDERSPAPVPTS

4523166 AEHGRRLDGTRAVAALTDLGFAAIAAGVIARRRPVMGLLEKAQADSRALQRMRQLRREFG 4522987

4522986 AGPVELVVPGRRIVVLLDPGDVGRVLAEAPTPFHPANREKRAALRQFQPHGVLLSKGVVR 4522807

4522806 EQRRAVNEAVLDTDAPLHRLAEPFAAIIADEAAQLMASALQRGHLDAEHFTIQWWRMVRR 4522627

4522626 LVLGERGRDDSAITDELWRLRSAANWSFLAPPHRRRREVFTEQLYRYVERPDPNSLAGAV 4522447

4522446 AAVQTGGAVDPVGQIPHWLFAFDAAGMAAQRALAVLATHPDQQAAATADAADPHQVHLRP 4522267

4522266 YLRACVLESVRLWPTTSTILRDITEPTQWRAGADAFTIAPGAALLILVPAFHRDADLLPF 4522087

4522086 ADRFAPEIWLDGQAAQYPQLVPFSAGPAECPGRNLVLFTTSTLLAHLLAAAEFRLRSGHR 4521907

4521906 MSPQTPLPLTLNNFGLDFDVTRLPNVAS\* 4521820

>CYP186B1 Saccharopolyspora erythraea NRRL23338

MTPKVSAALTTGVRTASPTDTARVAAQVVLPALATGVISRRPRVMALAERLRADRRAVGL

LRELRSRYGAGPLRLRVPGRDVVLVLSPEHVRRVLVSDAESFTPANREKQAALGHFQPHG

VLLSRGLDRARRRQFHEHVLETREHAHHLAPRFIQVVREEARVLLDEAERTGSLDWQTFG

AGWWRVVRRIVLGDQARDDRELTGELDALRSDANWAFLSPKRLSLRRDLRARLREHLRRA

EPGSLAETVARAETPVQAPEEQVPHWLFAFDAAGMAAFRALALLAAQPEQAARARSEIAE

SDLATPQPLHHLRACVLDALRLWPTTPMLLRDSVEETAWDGRQLPAGTAFLVFAPLFHRD

ETAADFAHAFTPEAWLDGRAEHHSALVPFSAGPGRCPGENLVLLVTSTLLAVLMRDAEFE

PGEGPALGPQGPLPATFDNFHTTVRLAR

>CYP187A1 Mycobacterium smegmatis

MDSRIRDDPAVDTAALLRDPYPIFARYRAQAGVFRGSVMDWSKTPKELMP

EHQYAAMSFDAVNTVFRDGKTFNSKIYDSTIGLFIGPSILAMEGKTHRDH

RNLVSAAFKSKSLARWEPEIARPICEALVDEFVDTGSADLVRDYTFEFPT

RVISKLLGLPEEDLPWFRRRAVELISYSVKYKRAFEASAALKDYFLDQIE

RRRSRPTEDIIGDLVTAEIDGEKLTDEAIYSFLRLLLPAGLETTYRSSGN

LLYLLLTHPDQFAAVQNDHDLIGAAIEEGLRYETPLTTVQRSATKDTELE

GVQIPAGAVIDVCIGSANRDENRWERPEEFDIFRKRIPHITFAAGEHTCM

GLHLARMETRVAMETLLNRVTDLRLIADDDPHIFGQPFRSPTAIPVTFRPAG

>CYP187A2 Mycobacterium avium subsp. Paratuberculosis old 273A1X

MMTNVPTAAGDETVSLRDPYPFFARKRREAGVFAGTVMDYSKTP

ESLMPKQEYSAVSFDAVNTVFRDGRVFSSKPYDKTIGLFMGPTILAMEGKKHRDHRNL

VSAAFKSKALARWEPTIVRPICNALIDDFIDAGTADLVRQFTFEFPTRVIARLLGLPD

EDLPMFHTRAVQLISYHVDYERAFEASAALKDYFLEQIEQRKSKPTEDIIGDLVTAEI

DGEKLSDEAIYSFLRLLLPAGLETTYRSSGNLLYLLLTHPDQFAALQADRELLAPAIE

EGLRFETPLTTVQRFTTEDTELQGVRIPARSVIGVCIGSANRDERRWERSEEFDIFRK

HVPHISFAAGEHTCLGLHLARLETRVAMECLLNRLTNVTLLSDGDPHIHGQPFRSPTA

LPVTFDAK

>CYP187A3 Mycobacterium avium subsp. Paratuberculosis old 273A2X

MPLSTGPTGQPVVPTLDFTGETSPYPFFEHMRRTDPVWHGSLAD

ASQLPEELRPEDEWVLFDYESVSQAFRDDRIFSSHKYDETIGLVMGHTILAMGGREHH

DHRNLVAKAFRATALERWEPSVIGPVCEQLVDEIKNDGHADLVKAVTFEFPTRIISTL

LGLPAEDLDLFRRLSLDLISIPTDIEAGLNAATELYDYFLKQVEQRRRKPTDDIIGDL

VAAEIDGEKLTDEAIIAFLRLLLPGGLETTYRSSGNLLYLLLTHPEQLAMVYRDRSLI

PMAIEEGLRFETPLTMVTRTTTEEVEIGGKTIPANAQIDMCMGSANRDETRWTDPNAF

DIRRPRQAHIAFAGGIHMCLGMHLARLETRVMLNSLFDRVRDLAFVPDDGTGEESKIV

GLTFRSPNKLPVTFAPAA

>CYP187A4 Mycobacterium marinum MM3996 old CYP273A3X

MTLRTDADGQ PVTLDLTGET SPYPFFEYMR RTDPVWHGAL MDHGQMPEEL RPNDEWVLFG

YDGVFQAFRD DRIFTSAGYD KTIGLVMGHT ILAMGGREHH DHRSLVAKAF RATALERWEP

SVIGPVCDQL IDEIRADGHA DLVKALTFEF PTRIISTLLG LPREDLDLFR RLSFDLISIP

TDIVAGFNAA TELHGYFLDQ VEQRRRKLTD DIIGDLVAAE IDGEKLDDEA IIAFLRLLLP

AGLETTYRSS GNLLYLLLTH PEQLAMVQRD RSLIPIAIEE GLRFETPLTM VMRTTTEEVD

IGGKTIPPDA QIDLCMGSAN RDESRWPDPN RFDIRRTRHA HIAFAGGIHM CLGMHLARLE

TRVMLNSLFD RVTNLAFTPD DGTGVQSRII GLTFRSPNKL PVTFTPAA\*

>CYP187A4 Mycobacterium ulcerans old CYP273A3X

MTLRTDADGQPVTLDLTGETSPYPFFEYMRRTDPVWHGALMDHGQMPEELRPNDEWVLFG

YDGVFQAFRDGRIFTSAGYDKTIGLVMGHTILAMGGREHHDHRSLVAKAFRATALERWEP

SVIGPVCDQLIDEIRADGHADLVKALTFEFPTRIISTLLGLPREDLDLFRRLSFDLISIP

TDIVAGFNAATELHGYFLDQVEQRRRKLTDDIIGDLVAAEIDGEKLDDEAIIAFLRLLLP

AGLETTYRSSGNLLYLLLTHPEQLTMVQRDRSLIPIAIEEGLRFETPLTMVMRTTTEEVD

IGGKTIPPDAQIDLCMGSANRDESRWPDPNRFDIRRTRHAHIAFAGGIHMCLGMHLARLE

TRVMLNSLFDRVTNLAFTPDDGTGVQSRIIGLTFRSPNKLPVTFTPAA

>CYP187A5 Mycobacterium marinum MM4008 old CYP273A4X

MTSPVHSVAG TGDQAVNPRN PYPFFAQQRR RGGVFPGTVM DYSKTPASLR PRREFSAMSF

AAVNTVFRDS RAFTSKTYDK TIGLFMGPTI LAMEGKQHRD HRNLVSAAFK SKALARWEPA

VIRPICNALI DDFIDAGRAE LVGDFTFEFP TRVIARLLGL PDEDLAMFHQ RAVQLISYTV

NYQLAFEASA ALKEYFLEQI DRRRSKPSED IIGDLVTAEI DGEKLSEEAI YSFLRLLLPA

GLETTYRSSG NLLYLLLAHP DQFMAVRAHR ELIPQAIEEG LRFETPLTTV QRFTTKDTEV

QGVPIPARSV IGVCMGSANR DEHRWQRPEV FDIFRERIPH ISFAAGEHTC LGLHLARLET

RVALECLLDR LTNIDLATAD DPHIHGQPFR SPTALPVTFE AVPT\*

>CYP187A5 Mycobacterium ulcerans old CYP273A4X

VTSPVHSVAGTGDQAVNPRNPYPFFAQQRRRGGVFPGTVMDYSKTPESLRPRREFSAMSF

AAVNTVFRDSRAFTSKTYDKMIGLFMGPTILAMEGKQHRDHRNLVSAAFKSKALARWEPA

VIRPICNALIDDFIDAGRAELVGDFTFEFPTRVIARLLGLPDEDLAMFHQRAVQLISYTV

NYQLAFEASAALKEYFLEQIDRRRSKPSEDIIGDLVTAEIDGEKLSEEAIYSFLRLLLPA

GLETTYRSSGNLLYLLLAHPDQFMAVRAHRELIPQAIEEGLRFETPLTTVQRFTTKDTEV

QGVPIPARSVIGVCMGSANRDEHRWQRPEVFDIFRERIPHISFAAGEHTCLGLHLARLET

RVALECLLDRLTNIDLATADDPHIHGQPFRSPKALPVTFEAVPT

>CYP187A6 Mycobacterium vanbaalenii PYR-1

MDQRPGRARRFGVRHVDDGGHSDRAVARRCTGKYCKRYSNEMETPVQDLAKDEPIDLRDPYPMFARRRAE GGVFRGSVMDWSRTPDSLRPENLYAAVSFDAVNRVFRDGKVFNSHIYDSTIGLFIGPTILAMEGKTHWEH RNLVSAAFKTRSLARWEPEIVRPVVNELIDEFIDDGRADLVRDFTFEFPTRVISRLLGLPEEDLPWFRKR AVELISYAVNYKKAFEASAALKDYFLGQIDKRRSAPTEDIIGDLVSAEIDGERLTDEAIFSFLRLLLPAG LETTFRSSGNLLYLLLTHRDQFEAVNADHALIGAAIEEGLRYETPLTTVQRFANEDTEIDGVEIPAGSVI DVCIGSANRDESRWERAEQFDIFRTRTPHISFAAGEHTCMGLHLARMETRVAAETLLSRLSAIELLTDGD PHIHGQPFRSPTALPVTFTPSRARP

>CYP188A1 Mycobacterium smegmatis

MSIQDVTTDDDREKITYHFDRHTPEYRLQFEKITEEMHSRCPVAWTETYD

GHWVAAGSNEVFELARCPVVSNHHDISGETPFQGITIPKASRATVVRGGI

LEMDEPEHSAYRGALNPYLSPAAIKRWEPFVDEITRAAIDEHISSGRIDF

VEHLANVVPAVFTLAMMGIELKKWNVYSEPTHASVYTPEHAPEREKINEQ

HREMGIDLINNMMEIRQNPRPGLVNALLQL

RIDGEPAPDMEILGNLGLII

GGGFDTTTALTAHALEWLGEHPDERERLSRERDTLLNPATEEFLRFFTPA

PGDGRTFAEDAEVAGYKFKQYERLWLSWAMANRDPSVFDKPNEVILDRKG

NRHFSFGIGVHRCVGSNVARTVFKSMLTAVLDRMPDYVCDPEGTVHYDTI

GVIQGMRNLPATFTPSRPLGPGLDETLEKLQRICNEEELARPITERKERA

VID

>CYP188A2 Mycobacterium avium subsp. Paratuberculosis old CYP281A1X

MPDAWTDTYGGHRVAAGSHEVFELARCPAVSNDHDINGERRGYK

GISIPTASRVSAVRGGILEMDDPEHRIYRTVLNPYLSPAAVKRWEPFIDEVTRAALDE

KIEEGSIDFVDDLANIVPAVLTLAMLGIPLKKWKMYSEPVHAAVYTPEHSPDIERVTA

MHREMGLDMVNNMLEIRENPRPGIVNALLQMRIDGEPAPDLEILGNLGLVIGGGFDTT

TALTAHSLEWLSEHPEQRQLLSDERKTLLDPATEEFLRYFTPAPGDGRTFSEDFELDG

TVFKEGERLWISWAMANRDPAVFHDPDEVILDRKGNRHFSFGLGIHRCIGSNVARTVF

KSMLIAVLDRMPDYRCDPEGTVHYETIGVIQGMRKLPATFTPGRRIGAGLDETLEKLQ

RICDEQELARPITERKEAAVID

>CYP188A3 Mycobacterium marinum MM4717 old CYP281A2X

MSVDDVVSDS DHQKNRYQFD RHSPEYRSQF KAITEEMHTT CPMAWSDTYG GHWVAAGSHE VFELARCPAV SNDHDVNNQR RGYKGISIPT ASRINGVRGG ILEMDDPEHR IYRTVLNPYL SPAAVKRWEP FIDEVTRACL DERIEQGSID FVDDLANIVP AVLTLAILGI PLEKWNLYSE PVHAAVYTPE HSPDIQRVTE MHRQMGLDMV TNMIEIRDNP RPGLVNALVQ MRIDGQPAPD LEILGNLGLV IGGGFDTTTA LTAHALEWLS EHPDERERLW RNRDTLIDSA TEEFLRYFTP APGDGRTFSD DVEFDGIHFK EGERLWISWA MANRDPQVFP DPDELVLDRR GNRHFSFGIG VHRCIGSNVA RTVFKSMLSA VADRMPDYRC DPDGAVHYET IGVIQGMRKL PATFTPGRKA GAGLDETLAK LQRICDEQEL ARPVTERKQA AVID\*

>CYP188A3 Mycobacterium ulcerans old CYP281A2X

LSVDDVVSDSDHHQNRYQFDRHSPEYRSQFKAITEEMHTTCPMAWSDTYGGHWVAAGSHE

VFELARCPAVSNDHDVNNQRRGYKGISIPTASRINGVRGGILEMDDPEHRIYRTVLNPYL

SPAAVKRWEPFIDEVTRACLDERIEQGSIDFVDDLANIVPAVLTLAILGIPLEKWNLYSE

PVHAAVYTPEHSPDIQRVTEMHRQMGLDMVTNMIEIRDNPRPGLVNALVQMRIDGQPAPD

LEILGNLGLVIGGGFDTTTALTAHALEWLSEHHDERERLWRNRDTLIDSATEEFLRYFTP

APGDGRTFSDDLEFFGIHFKEGERLWISWAMANREPQVFPDPDELVLDRRGNRHFSFGIG

VHRCVGSNVARTVFKSMLSAVADRMPDYRCDPDGRSTTRPSASSRACASCPQRSPRAARS

ARAWTRLSRSCNASATNRNSRGPSPSANKPRSSTDAPPASRHKIASGSGR

>CYP188A4 Mycobacterium vanbaalenii PYR-1

MSVDDVVSGTADDSRKQNRYYFDRHTPEYRLQFEKITEEMQTKCPMAWSDTYGGHWVAADSKHVFELARC PVVSNHHDISGETPFQGITIPKASRATVVRGGILEMDEPEHSAYRGALNPYLSPAAIKRWEPFIHEITRA ALDEHIESGRIDFVDHLANVVPAVFTLAMMGIKLDKWNVYSEPTHASVYTPEHAPEREKINEQHRAMGLD LITNMMEIRENPRPGLVNALLQLRIDGEPAPDIEILGNLGLIIGGGFDTTTALTAHALEWLGEHPDQRQR LSSERATLLDPATEEFLRFFTPAPGDGRTFADDVEVEGQRFKKFERLWLSWAMANRDASVFDRPNEVVLD RKGNRHFSFGIGVHRCVGSNVARTLFKSMVTAVLDRMPDYVCDPEGTVHYDTIGVIQGMRNLPATFTPGK

RLGPGLDETLEKLQRICDEQELARPITERKEAAVID

>CYP188A5 Mycobacterium vanbaalenii PYR-1

MADQLDRRREARSFHFDRHTPQYRDRFQEITAQMQARCPLAWTDTYGGHWVAAGNREVFELARCPHVSND NDIDGTRRGYTGINIPRGDYSVAFRGGMLEMDDPEHREYRSPLNGYLSPAAVRRWVPVVDELVKACLDEK IEDGRIDFVDDLANIVPAVLTLGLLGVPLKDWEIYCEPAHASVYTPADSPDFPRVADLAIASAMGMMHHV AEIRQTPRPGLIDALVRTRIDGQPAPDTEIMGMLMLLIGGGFDTTTALTAHALEWLSQHPDERERLSRDR DTLLDPATEEFLRYFTPAPGDGRTVAEDIEVDGVVLKEGERLWLSWAMANRDPALFQNPDEVVLDRKGNR HFSFGLGVHRCIGSNVARTVFKSMLTAVLDRMPDFQCDAAGAVHYETIGVIQGMQHLPAAFTPGPRLGPG

LEATLEKLQRVCDEQQLAAPITVHKAAAVI

>CYP189A1 Mycobacterium smegmatis

MPPFDDGVPMAQPSTSATPDLYYDPYSVQLNMEPHEVFARIREEAPLYYN

EQHDFYALSRYHDVNKAVIDHETFISGRGALLELIKSGMEIPPGTLIFED

PPIHNIHRNLLSRMFTPRKVLALEPQIREFTTRCLDAVAGSDTFDFVNDL

GEQMPMRVIGMLLGIPEDRQRAITDHGEETLQGTTVDSLATGEVFAEFID

WRADNPSDDIMTDLLNAEFEDETGTVRKLRRDELLLYLTVIATAGSETTT

RALGWAGKTLADHPDQRRDLVENPALIPQAIEELLRWEPPALQIARYVTR

DVEYYGKTVPAGSAMLMLVGAANRDHRRFPPNGDVFDIHREQFSHMTFGA

GTHFCMGNALARLELRVALEEILKRFPEWEVDWDNARPSETAAVRGWAAM

PTFVR

>CYP189A2 Mycobacterium smegmatis

MTASATQNVYFDPYDVAINADPYPTFARLREEAPLYYNEQFDFYALSRFS

DVNKALIDHETFSSARGAIVELIKADIEIPSGALIFEDPPIHTAHRKLLS

RMFTPRKINALEPEIRRFCAQSLDAVAGVERFDIIKDFGAIMPMRVISAL

LGIPEEDQEKIRDHGNAQMRTEAGKPMKAAEEGLVDGSIFEAYIDWRKDN

PSDDIMTELLNVEFTDEHGVTRNLTREELLIYINVVAGAGNETTTRLIGW

AAKTLAEHPDQRRQLVENPALIPQAIEEILRFEPPAPHVARYVTRDVEYH

GRTVPEGSVMMLLIGAAVRDSRQFPPDGEVFDINRAPRQHLAFSVGTHFC

LGSALARLEGRVALEEILKRFPEWDVDLASAELSPTSTVRGWDSLPVIVR

>CYP189A3 Mycobacterium smegmatis

MTVDDSGVVVTGVAGPYYDPYDVGIVADPYPVYARLRDEAPLYHNERYGF

WALSRHADVESALANWETFSNSRSDILELVKSDFDMPPGVMMFTDPPMHT

MLRGLMSRVFTPRRMAEIEDQIRRYCVRCLDPLVGSDRFDIIAELASTMP

MRVIGMLLGIPESEQIGVRDANDANLRTKPGAPMKVAQADKIADGRIYAD

YVEWRSKNPSDDLMTALLGVEFTDEHGVTRKLTRKEVLHYTQVVAGAGNE

TTGRLIGWLAKVLAEHPDQRRQIEQDRSLLTRAVDETLRFEPTGPHVARW

VARDFEAYGQTVPAGSAMLLLFGAANRDPRRYTDPDVFDIHRDNISHLTF

GKGLHYCLGANLARLEGRVALDELLNRFPEWDIDYSTARLAPTSTVRGWE

RLDVLVG

>CYP189A4 Mycobacterium smegmatis

MRVLDELSYDPYDVEIDVDPYPTYRRLRDEAPVYFNGRFGFWALSRFADV

EAALRDVDNLSNAKGDILEVVKAEPKMPLGVFINEDPPLHTVHRLLVSRA

FTPRKMRAIEDQIRTFCAACLDPLTSGDRFDFTLDLGAEMPMRVIGMLIG

IPEELQRSVRKVAGQRLRNKPGEPLPVNKDNYFNGNMFRDYVEWRAQNPS

DDLVTELLNVEFEDVTGTTRKLSSEELLVFLGVIANAGTETVGRLFGWLG

KLLGEHPDQRRALVADPSLIPGAVEEVLRYEPPVHNIARYVSADVDYHGQ

TIPAGSALLLMTGAANRDERRFDDPDRFDIRRSPNHLSFGRGAHFCLGAS

LARVEGRVALEEILKRWPDWTVDMGNAVRAPTATVRGWDSMPAIVG

>CYP189A5 Mycobacterium avium subsp. Paratuberculosis old CYP275A1X

MVMTGTSAIELYYDPFDSGIDDNPYPVWQRMREEAPLYYNEKYN

FYALSRYEDVARELPNWQTYRSGRGTTADILFSNVEVPPGILLFEDPPLHDLHRRLLS

RVFTPRRMLAVEDLVRGFCVRELDPLVGAGGFDFIRDLGAMMPMRTIGYLLGIPEEDQ

EKIRDRSVANIELSRDSDPAAVDANVFANSIALFADYIEWRADHPSDDLMTELLRAEI

DEPDGTRRPLSRTEVLAYTAMIAGAGNETTARLIGFMGQLLSDHPDQRRELAADPSLI

PGAVEETLRFEPPSPVQARYVARDAEHYGRVVPEGSFMLLLNGSANRDPRRFTDPDRY

DIHRQGGGHLSFGQGLHFCLGSALARMEARVAFEEVLKRWPDWEVDYANAERARTASV

RGWARLPVVTGG

>CYP189A6 Mycobacterium marinum MM0928 old CYP275B1X

MATHIEAAQA HDTDVYYDPY DVNITANPYP TYARLREQAP LYYNQRYDFW AISRHADVEK

ALADWQTFSN SRSDILELIK SKYDMPPGVM MFEDPPVHTM LRGVMSRVFT PRRMAQLEDQ

IRRFCVRCLD PLVGRDSFDI IAELASMMPM RVIGMLLGIP ESDQIGVRDA NDANLRTQPG

TPMKVARPDK IADGSIYADY IDWRAKNPSD DLMTALLNVE FDDEHAVRRK LTRTEVLHYT

QVVAGAGNET TGRLIGWLAK VLAEHPDQRR QVHQDRSLLT RTVDETLRFE PTGPHVARFT

LRDYHCYDTT VPAGSAILML FGAANRDPRR YHDPDTFDIR RDNISHLTFG KGVHYCLGAN

LARLEGRVAL DELLNRWPQW DIDYDSLQLA PTSTVRGWER LRVLVS\*

>CYP189A6P Mycobacterium ulcerans old CYP275B1PX

MATHIEGAQAHDTDVYYDPYDVNITANPYPTYARLREQAPLYYNQRYDFWAISRHADVEK

ALADWQTFSNSRSDILELIKSKYDMPPGVMMFEDPPVHTMLRGVMSRVFTPRRMAQLEDQ

IRRFCVRCLDPLVGRDSFDIIAELASMMPMRVIGMLLGIPESDQIGVRDANDANLRTRPG

TPMKVARPDKIADGSIYADYIDWRAKNPSDDLMTALLNVEFDDEHAVRRKLTRTEVLHYT

QVVAGPETRPPAGSSAGWQKCSPSTPTSAGKSTRTGHCSPAPSTRRCASNRRDPMSRASR

CATTTVTTPRSPPAAPS\*VLAEHPDQRRQVHQDRSLLTRTVDETLRFEPTGPHVARFTLR

DYHCYDTTVPAGSAILMLFGAANRDPRRYHDPDTSDIRRDNISHLTFGKGVHYCLGANLA

RLEGRVALDELLNRWPQWDIGYDSLQLAPTSTVRGWERLRVLVS

>CYP189A7 Mycobacterium marinum MM4753 old CYP275B2X

MTVTAASDVY FDPYDVELNA DPYPMFRRLR EEAPLYYNAQ HGFYALSRFA DVDRAIVDYQ

TFSSARGAIL EIIKANIDIP AGVLVFEDPP VHDVHRKLLS RMFTPRKIND LEPKIREFCA

RSLDPLIGSG RFDFVADLGA QMPMRVIGML LGVPEEDQEA ARDFATAQLR TEAGKPMKAS

ADGMVSGDFF AHYIDWRAEH PSSDIMTELL NAEFEDETGT VRRLRRDELL TYVSVVSGAG

NETTTRLIGW AGKVLAEHPD QRRALVEDPS LIPQAVEELL RYEAPAPHVA RYVTRDLRYY

GESVPEGSIM MMLIGAANRD HRQFPPDGDV FDIRREPHQH LTFSVGTHYC LGSALARLEG

RIALEEILKR FPEWDVDLGN AKLSPTSTVR GWESMPAVFD \*

>CYP189A7 Mycobacterium ulcerans old CYP275B2X

VTVTAASDVYFDPYDVELNADPYPMFRRLREEAPLYYNAQHGFYALSRFADVDRAIVDYQ

TFSSARGAILEFIKANIDIPAGVLVFEDPPVHDVHRKLLSRMFTPRKINDLEPKIREFCA

RSLDPLIGSGRFDFVADLGAQMPMRVIGMLLGVPEEDQEAARDFATAQLRTEAGKPMKAS

ADGMVSGDFFAHYIDWRAEHPSSDIMTELLNAEFEDETGTVRRLRRDELLTYVSVVSGAG

NETTTRLIGWAGKVLAEHPDQRRALVEDPSLIPQAVEELLRYEAPAPHVARYVTRDLRYY

GQSVPEGSIMMMLIGAANRDHRQFRPDGDVFNIRREPHQHLTFSVGTHYCLGSALARLEG

RIALEDILKRFPEWDVDLGNAKLSPTSTVRGWESMPAVFD

>CYP189A8 Mycobacterium vanbaalenii PYR-1

MADDLYYDPYDQGIVADPYPTYARLRDEAPLYYNGRYDFWALSRHADVEKALQDWSTFSNSRSDILELIK SDFDMPKGVMMFEDPPEHTMLRGLMSRVFTPRRMAEIEDQIRRYCVNCLDPLVGSDGFDVIAELAAMMPM RVIGMLLGIPESEQVSVRDANDANLRTRPGAPMKVADPDRIADGRIYSDYVEWRAANPSDDLMTALLNVE FTDEAGVHRKLTRKEVLHYTQVVAGAGNETTGRLIGWLAKVLAEHPQQRREIVEDRSLLGRAVDETLRFE PTGPHVARYLARDFEYDGTTVPAGSAILLLFGAANRDERRYRNPDTFDIHRDNISHLTFGKGLHYCLGAN LARLEGRVALDELLNRWPEWNIDYDTARLAPTSTVRGWEHLRMLVG

>CYP189A9 Mycobacterium vanbaalenii PYR-1

MTISADDSDVQNADTAAELYYDPYNVDLNMDPHGVFARLREEAPLYYNDKHDFYALSRYEDVNKGVIDHQ TFISGRGALLEIIKSGMEIPPGTLIFEDPPIHNIHRNLLSRVFTPRKVQALEPQIREFTARCLDPLTGTN RFDFVRDLGAQMPMRVIGMLLGIPEEDQRRVTDHGEATLQSDSVDLMATGEVFAEFIDHRTEHPSDDIMT DLLNAEFEDETGTRRRLRRDELLMYLTVIATAGSETTTRLIGWAGKTLADYPEQRAQLVADPALIPQAIE EILRWEPPALQIARYVTRDVEYYGQVVPEGSAMLMLVGSANRDHRRFPPNGDVFDIHRELRSHMTFGAGT HFCMGNALARLEGKIALEEILKRFPTWEVDWPNAVPSQTTAVRGWESMPTIVS

>CYP189A10 Frankia sp. EAN1pec

MSLLRSKDIYYDPYDAQIDSDPYPVWRSMRNEEPLYYNEKYDFYALSRYGDVDACLSDRATYRSGRGSIL

EIIKANIEFPPGMILFEDPPIHDVHRGILARIFTPKKMNALESKVREFCVRSLDPLVGSGRFDFVEDLGA

QMPMRTIGFLLGIPEKDQEAIRDHSNAGQRLDEGQEPTVREPNGEHFEAYIDWRAEHPSDDLMTELLHAE

FDDETGTRRRLSRSEVLLYIQMLAGAGNETTTRLIGWTGKVLGEHPDQRREIAADRSLIPQAIEELLRYE

APSPVQARYVARDVEHYGRTIPENSAILLLNGSANRDERQFPDGDRFDIHRRRSRHLSFGYGIHFCLGAA

LARLEGRVALDEVLKRFPDWEIDRDSAIQARTSTVRGWQSLPVFVP

>CYP189A11 Frankia sp. EAN1pec

MTTVTTETSDAAGDVYYDPYDFEIDADPYPVWRRMRDSVPLYYNAKYDFFAISRFDDVEKVMGDFETYRS

GRGSVLEIIRSNIDFPPGNILFEDPPVHDIHRSILARVFTPRKMLAIEPKVREFCARSLDSLVAEGNFDF

IADLGAQMPMRTIGMLLGIPEQDQEAIRDAVDEGLTLTEGAPKPLNEDPLARSEGMFADYLDWRARNPSD

DLMTELITAEFEDETGTTRRLTRAEVLTYVNMLSSAGNETTTRLIGWTGKVLSDHPDQLRQVARDRSMVN

QVIEEVLRFEAPSPVQARYVARDVEVHGQTVPEGSVMVLLNGSANRDERQFVNGDSFDIHRSISRHVSFG

RGLHFCLGAALARLEGRVALDEVLKRWDRWEVDYDRAVQARTSTVRGWAKLPVTATPR

>CYP189A12 Frankia sp. EAN1pec

MPLTSPSDVYYDPYDAQIDADPYPVWRRMRDEASLYYNEKYDFYALSRFEDVEPCLSDWNTYRSGRGSIL

ELIKANIELPSGIILFEDPPIHDIHRSLLARVFTPRKMNALEPKIREFCARSLDPLVGTERFDFIRDLGA

QMPMRTIGFLLGIPESDQEAIRDRLDEGLQLREGEELSVSAEDFNADEFGAYIDWRAEHPSDDLMTELLN

AEFEDETGTVRKLHREEVLTYVTMLAGAGNETTTRLIGWTGKILAENPDQRRELVADRSLIPNAIEELLR

FEAPSPVQARYVARDVEHHGHTVPEGSIMVLLNGSANRDERRFADPDRFDVHRDVGRHLSFGYGIHHCLG

AALARLEGRVALDEVLSRFPTWEIDWDNAVQARTSTVRGWETMPAFVR

>CYP189A13 Frankia sp. EAN1pec

MSLASHLGDVYYDPYDFRIDADPYPVWRRMRDEAPIYYNEKYEFYALSRFEDVERALSEWGTFLSGRGTL

LEIIKANVPIPSGNILFEDPPVHHAHRGVMARVFTPKKMNAVESKVREFCGRALDPFIGTDGFDFIGDLG

THMAMRTIGYLLGIPEEDQEAIRSLFDDNLRIEDPDNPRPPDIGIDGAFVDYIEWRAEHPSDDLMTELMN

AEFEDETGTVRTLTRDEVIAYINLLAGAGNETTARLVGWVGKLLGEHADQRRELAADRSLIPNAVEEVLR

YEAPSPVQARYIEREVELHGRTIPAGSVVLLLNGSANRDERRFPDPDRFDIHRSVGRHLGFGYGIHHCLG

AALARLEGRVALDEVLQRFPDWEVDWDNAVQARTSTVRGWEKMPVRIG

>CYP189A14 Frankia sp. EAN1pec

MSRSGPVYWDPFDRDIAGDPYPVYQRLRAEAPLYYNDRQDFYALSRHEDIDRCLTDWKTFSSARGPILEI

IKANVEIPPGTLLMEDPPAHDIHRALLARVFTPRRVTSLEPQVRDFCRRCLDRLVDVDSFDLMAEFANEV

PMRVIGMLLGIPESDQPAIRERADAKLRTEPGQQMKVSQQALMDSDLFAEYIDWRAEHPSDDLMTELLRA

EFEETLRFEPTGHAIARYVTTGVELHGRTVPAGSAMMLLIASANRDENSWSDPDRFDVHRGTGHLRTFGL

GTHYCLGAALARLEARVALEEILKRFPRWNVDWENSALSSTSTMRGWETLPITVG

>CYP189A15 Frankia sp. EAN1pec

MQDESVYYDPYDFEIDANPYPVWRRLRDSAPLYYNEKYDFYALSRFEDVEKALTDFGTYTSGKGFILEVI

KAGIRLPPGNLLAEDPPLHDIHRGLLSRVFTPRKMAALEPQVRELCARILDELVGTDGFDFVADLGAIVP

MRVIGMMLGIPESDQVAIRDAGTRRHQLTEGEAPAPTDARSTAQPFADYIDWRATHPSDDLMTELLRAEF

EDETGTTRRLTRDEVLTYTSVLAGAGNETTRRLIGWTGQLLGEHPDQCRELAADHSNVPQAIEEILRFES

PSPVQGRVVSRDVEHHGGTIPGTIPEGSAVILLNASANRDERHFADPDTFDIHRRIDRHLAFGHGLHFCL

GASLARMEGRVVLDEVLKRWSSWEVDRDNSVLDHTSTTRGWMNLPVVTS

>CYP189A16 Frankia sp. EAN1pec

MTQDDLYYDPYDVEIDVDPYPTYRRLRDEEPLYYNERLDFWGLSRFADVGAALKDQKRLSSAKGDILEVI

KADPVMPPGVFINEDPPLHTVHRVLVSRAFTPKKMKALEDKIRAFCIACLEPLEGADRFDFVADLGDELP

MRAIGMLVGIPDAEQPTVRDHAQRGLRNERGKPLTVTKDKYFDGDFYADYVAWREKNPSDDLITELLNVE

FEDVSGTTRRLTKEEILIFLAVIAGAGVETTGNLFGWLGKVLAEHPDQRQQIVSDRSLIPNAIEELLRYE

PPGPHVARYVTEDVEYHGQTVPAGSALLLMLSSANRDERQFTDPGRFDIHRSISQHVTFGIGAHFCLGAA

LARMEGRIALDEVLNRFPEWDLDMANARRKPTTTVRGWDSMPAIVG

>CYP189B1 Frankia sp. EAN1pec

MTEDLYWDPFDREFHVDPHPVWHRMRDEAPVYRNEKMDFYALSRFADVDAAHLDTATYSSAYGTVLELMS

PEPLKTGQIIFMDPPIHTTLRVLVSRAFTPRRVGGLEGHIRQICAELLDRQVGGGGFDYIQDFAALLPSM

VISQLIGVDPADREEIRHTIDQTFHLDPEKGMVNDISMAASAKFHAYLSEQLEARRAAPRDDMMTALVQA

EIATDGGTRQLTTSEAADFTALLVAAGTETVARLLGWACDALEAHPDQRAELAVDPSLLGNAVEETLRYE

SPSPVQGRVTTRDVELHGTTIPARSKIILLTASAGRDGRRYDDPDRFDIRRRVDSHVAFGRGAHFCLGAA

LARMEGRIALEETLRRFPTWEVDRDNAARLHTSTVRGYEKLPIVV

>CYP189B2 Frankia sp. EAN1pec

MAELYWDPFDEVIDVNPYPLWKRMRDEEPVYRNDKFDFYALSRHADIDAAHVNADTYSSAHGTILEIMKP

EPMPPGFMIFTDAPAHHLLRSLVSRAFTPRRIAALEEHIRVLCAEMLDPQIGAGGFDYISDFAAQLPSKV

ISQLIGVDPADREEVRRTIDLTFHIEEGVGMVNETSHAATIKLRTYFAGLIEDRRRSPRDDMITGLAEAE

VTDGNGERRRLTTPEAASVTNEIVSAGTETVARLLGWACVLLEAHPDQRAELAADPSLLSNAVEETLRYE

APSPVQGRMLKNDVELHGTTIPTGAKVLLLTGSAGRDGRRYTDPDRYDIHRKFDGHVAFGRGAHFCLGAA

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>CYP189B3 Frankia sp. EAN1pec

MTELSWDPFDKVIHLAPYDVWRRMRDEAPVYRNDRLDFFALSRHADVEAAHRDPATYSSAHGTVLEIMSP

EPMQTGLIIFIDPPTHTELRTLVSRAFTPRRISALEDSIRALCAEMLDPQVGGSGFDYVQDFAAQLPSKV

ISELIGVDPADREDVRQLIDQTFHLEEGAGMINDISFGAQIKLHTYWSEQIELRRRQPRDDMMTALVEAE

VKSETGSRRLTTQEAADFTNLLVSAGTETVARLLGWAGFVLAAHPDQRAEITADPSLIGNTIEELLRYEA

PSPVQGRVLTREVELHGTVLPAKSKVLLLTGSAGRDERKYPDADRFDIHRRFDSHVSFGHGVHFCLGASL

ARLEGRVALQETLHRFPEWDVDHDRAVRLHTSTVRGYEKLPITLG

>CYP189B4 Frankia sp. EAN1pec

MTDDLYWDPFDKEIDVNPHPLWKRMRDEAPVYHNEKFDFYALSRFTDVDTAHLDPATYSSKYGTVLELMK

SEPWDTGQIIFMDPPTHTTLRVLVSRAFTPRRVGGLEGVIRDLCAELLDPQVGGGGFDFVQDFAAQLPSL

VISQLIGVDPADREDVRKMIDGTFYLDPEKGMFNETAMAATAKFHGYLNGQIQERVKNPRDDMMTALTQA

EITTDDGTRRLSLSEATDFTALLVSAGTETVARLLGWACVLLAAHPDQRADLAADPSLLGGAVEETLRYE

APSPVQGRVTTRDVELHGTEIPAKSKVLLLTGSAGRDDRKYDDPDRYDIRRRFDSHVSFGHGVHFCLGAA

LARMEGRIALEETLRRFPTWDVDHGNTVRLHTSTVRGYEELPIIV

>CYP189B5 Frankia sp. EAN1pec

MPPVTGRARAWRRELAVLGGSQRGPGTEKGSTVTEDLYWDPFDKIIDVNPHPLWRRLRDEAPVYRNEKHD

FYALSRHADVDAAHVEPETYSSAHGTVLELMGPEPFNTGQIIFMDPPTHTLLRVLVSRAFTPRRVGGLEG

SIREICAELLDPQIGGGGFDYVQDFAAQLPSLVISKLIGVDEADREEIRQTIDQTFHIEEGKGMINDVSF

AAQIKLHTYFSEQIDARRTAPRDDMMTGLAEAEITTDEGARRLTTSEAADFTNLLVAAGTETVARLLGWA

GDLLEAHPDQRAELAADPSLLGNAVEETLRYESPSPVQGRVNTREVELHGTTIPAKSRILLLTSSANRDE

RKYPDADRYDIRRNFDSHLAFGRGPHFCLGAALARMEGRIALEETLRRFPNYEVDRDNAVRLHTSTVRGY

EKLPIKV

>CYP190A1 Mycobacterium smegmatis

MTTPQMIFDPFSEQYFENPFDIYRQMRDDAPLYYDSEQDFYALSRHEDVA

AALKDHEAFSSSRGCDLAMVKGDEPPQKSIIFMDPPEHRHMRSLLNKAFT

PRAVQAQRDTVVEQVEHYLGQIDSDEFDVVQDFSGPFPVEVITRMAGVEP

EYRQQVRHWIDTSLSREPGQVAYSEAGMKANIDTAMYYYSLVQKRRENPQ

DDMISRLIAAEIPGENGEMRRLDDVEITGFATLLGGAGAETVTKLIGTAM

VTFAKFPDQWQKLLDDRSKVPAAVEELLRYEGPVQYNVRYTLKEARVPSG

TIPAGKPVFLLKASANRDERAWTDPDVFDIDRDRTEAQNLGLGYGIHSCL

GAALARLESTIALERLLDFMPRYEVKWDGLQRVHMQNVAGYSHVPVKVLR

>CYP190A2 Mycobacterium avium subsp. Paratuberculosis old 270A1X

MTKPKLVFDPYSEDYFNNPYEIYRRMREEAPLYYDEKEDFYALT

RHVDVAAAFKDYETYSSARGCDLAMVRRGISPEQKSIIFMDPPEHRHMRSLLNKAFTP

RAIQSQRETIIEVVDKYLSAADPDNFDVVQDFSGPFPVEVITRMAGVPEEYRQQVRHW

IDTSLHHEPGQIEVSEAGMQANIDTAMYYFGLVQERRQDPQDDMISRLIAAEIPGENG

QMRKLDDIEITGFATLLGGAGAETVTKLLGNAAVIFARHPDQWQKLQEDRDKIPGAVE

ELLRYEGPVQYNVRYTLKEAHVSGGVIPAGKPVFLCGAAANRDPEAFTDADTFDIERD

QTEAQHLGLGYGIHSCLGAALARLESRIALERLLDFMPRYDVDWAGCRRVTMQNVAGW

KNVPVKVLR

>CYP190A3 Mycobacterium marinum MM4733 old CYP270A2X

MTTSKVVFDP FSEEFFNGPW ETYRRMQAEA PVYYSEQYDF YALTRHADVA AGLKNFERYS

SAYGIDLSMV RSGQKPPQSI IFMDPPDHRH MRSLLNKVFT PRAIQAQRQT VIDKIDKYLG

ALDPEGFDAV QEFSGPFPVE VITTMLGVPE RHAQQVRHWI DESLTREPGQ VEVGEQGMQA

NINTAMLYYD LVKQRRDDPR DDLFTKLINA EIEREDGQVT NLDDLEIAGF ATLLGGAGAE

TVTKLVGNAA VVFARNPEQW QKLLDDRSKV PAAVEELLRY EAPSQYQVRR AMEDVELHGV

TIPAGKPVFL INGAANRDPH AWTDPDKFDI DRDPHEATNL GFGYGIHSCL GAALARMESA

IALEKLLDFM PAFEVDWAGC KRVHMQNVAG WQSVPVRVLR \*

>CYP190A4 Mycobacterium vanbaalenii PYR-1

MTAPELRFDPVSQDYFDNPYEIYRRMRDEAPIYYDAEEDFYALTRHEDVAAALKDHEAFSSARGCDLGMV RSEDGPVKSIIFMDPPEHRHMRSLLNKAFTPRAIQSQRETVIELVEHYLSKVDPDNFDVVQDFSGPFPVE VITRMAGVPEEFRQQVRHWIDKGLERKPGQIEWSDENMQANIDSGVYYYGLVQERRRNPQDDMISRLIAA EIPGENGEMRKLDDIEITGFTSLLGGAGAETVTKLLGSAVVEFARHPEQWQMLLDDRNLIPDAVEELLRY VGPVQYNVRYTVKEAHVPSGTIPAHKPVFLMKAAANRDPRAFDNAETFDITRDRTQAQNLGLGYGIHSCL GAALARTETAIALEHLLDFMPRFEVDFSGLQRVNMQNVAGYHHVPVKVLR

>CYP190A5 Mycobacterium vanbaalenii PYR-1

MAVVDVGRDPVVFDPFSEEFYRDPQG>CYPRLRAEAPVYYNATYDFYALSRHADVAAGLKDFATYSSAYGV DLGMVRRGEKVPAKMIISIDPPEHRAMRSLVNKVFTPRAIEALRTMVTDTVTRFLSAVRGDSFDVVQDFS VYFPVDVITQMLGVPEKYRQQVRLWIDESLHREPGQIDMSEAGMQAMAETWLMYYDLIKQRRADPRDDMI SALIAAEVEREDGTVDRLKDSEIAGFATLLGGAGAETVTKLVGSAVVTFARHPEQWQQLLDDRGKIGVAI EELLRYDAPVQYNVRRSNHPVTLHGVTIPAGAPVFLLGASANRDPDAWTAPDVFDINRDRTEAQNLGFGY GIHSCLGAALARLESSIALDMLLDFMPRYGVEWDGCRRVSMQNVSGWANVPVRIL

>CYP191A1 Mycobacterium smegmatis

MTTTVKPPVTEAVTGEFSYDPFDPAVMADPTPYYRVLREKYPLYHIEKWD

TWALSRFSDIWEVLEVNDGTFVASEGTLPAATVLAEHNDGAVPDPPWHPM

PFHANFDTPIYDSVRRCTSPQFRPRSVTKLADRIRTLANERLDELLPRGQ

FDLTQDYGGIVAASVVCELVGLPVDLAADVLATVNAGSLAEPGSGVEVAN

ARPGYLEYLTPVVQRRRAGEGRELPIVDNLLQYRLPDGSAFSDLEAAVQM

LGVFIGGTETVPKIVAHGLWELTRHPEQLAAVRTDLDANVPIAREEMIRF

CAPAQWFARTVRKPFTLHGTTLQPGQRVITLLASAGRDEREYPDPDSFIW

DRRIERLLAFGRGQHFCLGVHLARLEITIMVTEWLKRVGEFRVDERAARR

PPSSFQWGWNNVPVEV

>CYP191A2 Mycobacterium avium subsp. Paratuberculosis old CYP280A1X

MDFAYDPFDAEVMANPLPYYRILRDHHPVYYMPQWDTFALSRFD

DIWRVLEVNNGTFVASEGTLPPASVLAQHNDGPVDDPPLHPLPFHAMFDADLYGEIRR

THSRPFRPRAVTDLEGRIRTLANERLDELLARGSFDLTQEYGGVVVATIVCELLGIPT

DLAPQVLAAVNAGSLAEPGVGVDTGQARPNYFEFLLPAVQRRRADPSGPPLEVVDGLL

GYQLPDGSALDDLEVATQMLCIFIGGTETVPKIVAHGLWELSRHPDQLAAVRADPQHN

IPVAREEMIRYCAPAQWFARTVRKPFDIHGQTPNPGQRVITLLASANRDEREYPDPDD

FVWDRPIRRSLAFGRGQHFCIGYHLARLEVAVLLQEWLRRVPDYAIRADAATRLPSSF

QWGWNKIPVEV

>CYP191A3 Mycobacterium marinum MM0399 old CYP280A2X

MNFSYDPFGA RVMADPLPYY RVLRDQHPVY YLPQWDTFAI SRFDDIWRVL EVNDGTFVAS

EGTLPAASVL ARHNSGPVDD PPWHPLPFHA VFDAPLYGEI RRAHSPPLRP KSVAGLEARI

RELANERLDR LLPQGSFDLT QDYGGVVVAS IVCELLGMPA SLAPEVLAAV NAGSLTEPGV

GVDTAETRPN YLEFLVPVVR QRRADPTGEL PVVDGLLRYR LPDGSALDDT EVATQMLCIF

IGGTETVPKI VAHGLWELSR RPDQLAAVRT DPQSNVNVAR EEMIRYCAPA QWFARTARKP

FTIGDQTIEP GQRVITLLAS ANRDEREYPD PDEFIWDRPI RRSLAFGRGQ HFCIGYHLAR

LEISVLLQEW FRRVPEFQIC AAQATRLPSS FQWGWNKIPV EV\*

>CYP191A3 Mycobacterium ulcerans old CYP280A2X

VNFSYDPFGARVMADPLPYYRVLRDQHPVYYLPQWDTFAISRFDDIWRVLEVNDGTFVAS

EGTLPAALVLARHNSGPVDDPPWHPLPFRAVFDAPLCGEIRRAHSPPLRPKSVAGLEARI

RELANERLNRLLPQGSFDLTQDYGGVVVASIVCELLGMPASLAPEVLAAVNAGSLTEPGV

GVDTAETRPNYLEFLVPVVRQRRADPTGELPVVDGLLRYRLPDGSALDDTEVATQMLCIF

IGGTETVPKIVARGLWELSRRPDQLAAVRTDPQSNVNVAREEMIRYCASAQWFARTARKP

FTIGDQTIEPGQRVITLLASANRDEREYPDPDEFIWDRPIRRSLAFGRGQHFCIGYHLAR

LEIAVLLQEWFRRVPEFQICAAQATRLPSSFQWGWNKIPVEV

>CYP191A4 Mycobacterium vanbaalenii PYR-1

MVDIPARHRRQRRGPDHVRRAQQQDAGAVAGIGFPGRPGDSGSHADQAGPAGRLHQGTGTPLRAVVGVDG QALARLLHHHLQVQRGDPLLGARRRLGLLRESLPVVEGQPAGRDRHLDERRPRTARRLGGLHPGRPAPVP AAVSAKMSAAQQPDCRPGRRPFTYDPFDPDVMADPLPYYRVLRDEHPVYYLQKWDTYALSRFDDIWNVLE INDGTFVASEGTLPSAAVLAGHNDGPVADPPLHPMPFHANFDAPIYDEVRRCTAAPFRPRNVAKLADRIR VLANERLDELLPRGRFDLTQEYGGIVAASVVCELVGLPADLAPDVLATVNAGSLAQPGSGVEVANARPGY LEYLTPVVARRRAGQGSELPIVDNLLNYRLPDGSALSDTEAAVQMLGVFIGGTETVPKIVAHGLWELSSR PDQLAEVRSDMDANVPVAREEMIRYCAPAQWFARTLRRPFTLHDTTMRPGQRIISLLASANRDEREFPDA DRFVWNRPMPRLLAFGRGQHFCLGAHLARLEIAIMVTEWLKRVPEFRVDTAAAFRPPSSFQWGWSELPVE V

>CYP192A1 Caulobacter crescentus CB15

1 MDADVRSAPL IPPAPKVHPR QLGGSFVGEL RIALEMSRNL MGAWCEEDFD NLFTPYVFMG

61 QPGMVVSDPA AARRILSSPN YVRPVKAARS VRPIAGDGLL LSEGETWRRQ RKSLAPVFTP

121 MAVEGLLPHF VAAGASLAEA LSGHARADLS EAFHHATLDA VLSALFSRRA DAQGDQLAYM

181 VRRYMEGPAH FNLMDFVSRG ADDLTFLDVE RRRQGAAWFQ AVEHLIAQRQ AHPHAEARDL

241 LDRLLAARDE DGAPLSNQEI RDQCGTMLVA GFETTSRLLF WATYLLALDP ATQDRLRAEV

301 LAAPAAAVRT LDDLQAWPLM RSVLFETLRL YPTAPLLARE AIGPDTVMGH AVVPGQIITI

361 SPWLIHRHRK LWDAPTAFVP DRFIDQPHPW GIEAFLPFGA GPRVCIGASF ALAEAQIVLA

421 SLLERFEIGL VSDRPVIPIA SITLGPDHAP AFTLTPVS

>CYP193A1 Bradyrhizobium japonicum USDA 110

1 MARGCASRCS RPVSDASPAP RAGTLSGARL ECRLCRFMAL DERCLCVCRC PLLWVMRTRY

61 RARTPCPNRW GQTAAPERAS LAGHSRETAL STAPRIDIDP AAFWADPYPM LANMRKEAPI

121 AFVPQLGSTL LTSRDDISIS EKQIDVFSSH QPAGLMNRLM GHNMMRKDGE AHQVERRAMF

181 PTVSPKTVKG YWTALFQAHA DRIIDAIEPG RIDFMRDFAL PFSGECLKSI TGLTNIGFAE

241 MDAWSQGMIE GIANYVGDPA VEARCHAATS GIDAAIDDML PVMRKNPDQS ILGVLLASGM

301 PMESVRANVK LAISGGQNEP RKAIAGTVWA LMTHPEQLDL VRRGEVTWLQ AFEEYARWIS

361 PIGMSPRRIA KPWSIRDVAF ELDERVFLMF GSANRDEKHF ERADQFDVRR DTSKSVAFGA

421 GPHFCAGAWA SRAMIADVAL PTLFARAGRI EIADDEPVRI GGWAFRGLQN LPARWLH

>CYP194A1 Bradyrhizobium japonicum USDA 110

1 MSDVSEPVAH PPVTDWVNDF DHTDPQWTDD PFPIWDELRA ASPVVHTERF LGCYMPTTYE

61 AVREIANDTE HFSSRRIIVR DVRPEIARNA APPITSDPPV HKPAKQLLLP PFTPDAMKKL

121 EPRVRTICNE LIDGFISDGK VDAAARYSKY IPVRAIAHML GIPESDSDLF VNWIHMILEL

181 GIKDETMLLQ AVQEMSAYFR THIEERRSRP TDDLISYLMN AKDKEGQPLE ESHVLGSLRL

241 LLIAGIDTTW SAIGSSLWHL ARTPADRERL IAEPGLIPIA VEELLRAYSP VTMAREVVKE

301 TTISGCPVKA GNMVLLSFPA ANRDPKMFPD ADKVVIDRRE NRHAAFGLGI HRCVGSNLAR

361 MEMQVALEEW LKRIPDFRLD PAGTVTWSQG TVRGPRQLPF LLGKAM

>CYP194A2 Rhodopseudomonas palustris

MSERAPVTDWVNDFDHTDPRWTENPYPIWDELRSAGPLVHTDRF

LGCYMPTTFAAVKEISYDTDHFSSRRVIVRNVRSESPPPAPPITSDPPEHKPAKRLLL

PPFTPDAVAKLEPRVRAICNELIDAFIEDEGCDAATAYTKHIPVKTICHMLGIPEDDS

DIFIRWIHEILELGINDDAILMKAVFEMSTYFQGHIAHRKQKPTDDLISTLMNARDDK

GQPLSDAHVLGSLRLLLIAGIDTTWSAIGAALWHLATHPADRERLLAEPELMPTAIEE

FLRAYSPVTMAREVMKETSIAGCPVKPGNMVLLSFPAANRDPSVFPEADRVMIDRKEN

PHVAFGLGIHRCVGSNLARMEMTVAIEEWLKRIASFRLDPSQKVRWSEGTVRGPRSLP

LLFGKPS

>CYP194B1 SRE12854399 Streptomyces SN-593

51% to CYP194A1 Bradyrhizobium japonicum USDA 110

78% to CYP194 SRE12855425

MAADDRFNKDFRDPNRDQYHSVRSETISGPVTDWATDFSHLDPRWTADPFPIMDDLRQRCPIAHTERFGGAWVPTRYEDIAAVAYDTENFSSRSVNVGNFRPPRDLAPIGEAPPITSDPPFHHGARKLLLPAFTKTAVARLEPTTRAYCHSLIDGFEGRDVVDAAEAYAQKVPEQVIGDLLGIPQGDRKLFRDLIANINREDALDSRDEHVEQLSKMFVFLLAEIKEHVRNPREDLISYLLEVELRGRKLDPNHIISMMLLLFAAGIGTTTKAIGSSLWHLAGNPRDRERLVAEPELLPTALEEFLRAFTPVTMARLVKDDMHWRGVDMKADDWILLSFPAANRDPAQFERADEVVIDREANRHAAFGLGIHRCLGSHLARMELRVALEVWLERIPEFDLQDPSTVVWGGRLARGPVCLPLSVGRRTPLTPDGPR

>CYP194B2 SRE12855425 Streptomyces SN-593

52% to CYP194A1 Bradyrhizobium japonicum USDA 110

MAADDRFNKDFRHTDRDRFHVSRGEIVTGPVTDWATDFSHLDPRWTADPFPIMDDLRQRCPIAHTERFGGAWVPTRYEDVAAIAYDTDRFSSLGTNLSEFRPPRDLAPIGEAPPITSDPPFHHGARKLLLPAFTKTAVAKLEPGTRAYCHSLIDRFAGRAVVDAAEEYAQQIPSRVIGDMLGLPPEDRQRFHELATKLEGEGKQSRDERVKHMGRVFIYLLAEVDKHVEQPRDDLISYLLEAELHGRKLEPNHVIGTVMLLLIAGISTTYSAIGTSLWHLAGNPRDRERLVAEPELLPTALEEFLRAYAPVTMARLVKDDMHWRGVDMKADDWILLSFPAANRDPAQFERADEVVIDREANRHAAFGLGIHRCLGSHLARMELRVALEVWLERVPEFSLRDPSTVAWGGTQARGPKALPLRIR

>CYP195A1 Bradyrhizobium japonicum USDA 110

1 MNADAKELAA SFDLEKLTPE FYDNPYPTYR ALRENEPVKR LPNGTVFLTR YDDLVTTYKN

61 TKSFSSDKKR EFAPKYGNTP LYEHHTTSLV FNDPPAHTRV RRLIMGALSP RAIAGMEADL

121 IKLVDGLLDA IAAKGSCELI EDFAASIPIE VIGNLLDVPH DERTPLRDWS LAILGALEPV

181 VSPEAAARGN KAVKDFLSYL ETLVARRRGK PGNPERDVLT RLIQGEGNGE ENGERLTEKE

241 LLHNCIFLLN AGHETTTNLI GNGLVALDRH PDQKQRLIDH PDMIKTAVEE MLRYESSNQL

301 GNRMTTERVE LGGVMLDAGT SVTLCIGAAN RDPAQFPDPE SFDIARTPNR HLAFATGAHQ

361 CAGMALARLE VAIAISRFLA RFPNYAVNGR PVRGGRVRFR GFLSVPCAIG

>CYP195A2 Rhodopseudomonas palustris

MSVEEAALAAGPGPPTGRMTCVAPVPAARPDPQISRPFRQRRKS

PIDVKNGNDMETAPAELAEAFDLARLTPDFYDNPYPTYHALRAHQPVKRLASGGYFLT

RYDDLVAVYKNTTLFSSDKKREFTPKYGDSLLFEHHTTSLVFNDPPSHTRVRRLIMGA

LTPRAIAGMEPDLIALVDRLLDAMAAKGRVDLIEDFASAIPIEVIGNLLGVPHDERGP

LRGWSLAILGALEPVIGPEAFALGNAAVAEFLGYLDTLIARRTAEPGDPERDVLTRLI

RGEAGGEKLTAKELLHNCIFLLNAGHETTTNLIGNGLVTLAANPDQKRRLIAEPALIK

TAVEEILRYESSNQLGNRITTAEVEIGGVSMPANTSLTLCIGAANRDPAQFADPDRFD

VSRSPNRHLAFASGPHQCAGMALARLEGAIALSRFLAHFPDYVLDGPPQRGGRVRFRG

YLGVPCRLG

>CYP195A3 Burkholderia fungorum

MGAAIDVEVGALGDACIGNPDRVGVDDAGVRTARQRNERFVMVG

GKGRGALNDEVHGRRRSDTVEGGRAARAANPAIVTVRRFASPRAIRAKRCCARHPAWR

RAILRRAVHTDESNDASQPPRTPTVACTPSRRAKSGTRTQRHPRRGAPLRRHRMTPAT

ASDASTLARDFDLRHLNPAFHADPYPVYHALRAHEPVKRMPDGSLFLTRFRDVQAVYR

DPKTFSSDKTVEFKPKYGDSPLYAHHTTSLVFNDPPRHTRVRKLIAGALTARAIAAME

PGLVRLVDGLLDAAAARGRIDLIDEFASAIPVEVIGNLLDVPHTERAPLRDWSLAILG

ALEPSLSEAQLERGNRAVSEFIDYLRDLVARRRREPGDPQHDVLTRLIQGEAGGEQLS

EAELLQNCIFILNAGHETTTNLIGNGLVTLTQWPEQRAALLHEPSLIESAVEECLRFE

SSNQLGNRMATVDTEIGGVAVARGTPVTLCIGAANRDPEQFADPDRFDIRRDPNRHLA

FGFGIHQCAGLSLARLEARIAIGRFVQRFPAYRVNGEPTRGGRVRFRGFAAVPVELEP

AGRRTA

>CYP195A4 Stigmatella aurantiaca

MLRSVSASRPPSPANPVAAFDLARLDDAFYADPFPLYRAMRERD

PVHRMPDGSLFLTRWADLDCIYRDTRTFSSDKRAEFGAKYGDAPLFEHHTTSLVFNDP

PLHTRVRRLIVGALTPRALSTMEPGLRTLVDRLLDGLAVKGAADLIEDFAAAIPIEVI

GNLLDIPTEERGPLRGWSLAILGALEPRLTAEQEACGNEAVTEFLDYLRILVAQRRAR

PGDPATDVLTRLIQGESDGERLTETELLHQCVFLLNAGHETTTNLIGNALELLARFPD

ERARLLRAPALIPTAVEEVLRYESSNQLGNRRVAEDTEIGGVAVPTGTFLTLCIGAAN

RDPARFEDPEHFDVGRQPNRHLAFAGGAHTCAGMNLARIEARIALAAFLARFPDYALT

APPVRARRARFRGFTAMPTRLGSLR

>CYP196A1 Bradyrhizobium japonicum USDA 110

1 MLPRSAGAGR NKVAVARCPF GQPTGALVMS MQNVAAPALQ FTAPRRNELT HIPGDEGWPV

61 IGKTFQVLAD PKGHIEANGA KYGPVYRTHV FGETNVVLLG PEANELVMFD QQKLFSSTHG

121 WNKVLGLLFP RGLMLLDFDE HRLHRKALSV AFKSGPMKSY LSDLDRGISA RVAQWKAKPG

181 EMQLYPAMKQ LTLDLAAASF LGADIGPEVD EINRAFVDMV AAAVAPIRRP LPGTQMARGV

241 AGRKRIVAYF RQQIPLRRGN HGGDDLFSQL CRATHEDGAL LSEQDIIDHM SFLMMAAHDT

301 LTSSLTSFIG ELAANPDWQD RLRAEVLALG LAPGAPSSFD DLEKMPLSEM AFKEALRIKP

361 PVPSMPRRAM RDFTFKGFRI PAGTAVGVNP LYTHHMKDIW PEPDRFDPLR FTEEAQRNRH

421 RFAWVPFGGG AHMCLGLHFA YMQAKCFARH FLQNIEVSLA PGYKPDWQMW PIPKPRDGLK

481 VRVKAV

>CYP196A2 Rhodopseudomonas palustris

MSIQVADSSLVARLSPPKPSALAHVPGDEGWPIIGRTLAVLADP

KGEVEKMARTYGPVYRSRVLGETSITLLGPEANELVLFDNTKLFSSTHGWGPILGRLF

PRGLMMLDFDEHRLHRRTLSVAFKAGPMQSYLAELNAGIAHRVAEWRARPGEMLCYPA

MKQLTLDLAATSFLGTAIGAETEEVNRAFIDMVAASVAPIRKPWPGTAMARGVKGRQR

IVAYFAEQIPIRRAKGGDDLFSQLCRATHDDGALLSNQAIIDHMSFLMMAAHDTLTSS

LTSFVAALAAHPEWQQKLREEIAGLGLKPGEPISFEQLDALPLTEMAFKEAMRLRPPV

PSLPRRATRAFSFKGYTIPAGTMVAVNPLFTHHMPEIWPNPDQFDPLRFTDEASRGRH

RFAWIPYGGGAHMCLGLNFAYMQAKCFAVHLLQHLDLSLPPNYQASWQMWPIPKPKDG

LRVNVAPLN

>CYP196A3 Novosphingobium aromaticivorans

MASIAPDSRTDLHTERANPHWVRLGGDHKLDHVPGEDGWPVLGT

TLMQLADPLGFQRRMVETHGPVFRTRSFGRRGVNLIGADANELVLFDRDRLFSNEQGW

GPVLNLLFPRGLMLMDFEAHRVDRRALSIAFKPEPMRAYCSVLNTGIAQAVQGWGGQM

RFYDAIKALTLDTAASSFLGLPLGPEADRLNKAFVDMVQASGGVVRRPLPFTRMGKGV

AGRRLMVEYFGRLVRERRADPGQDMFSQFALATREDGSLLPEDVVVDHMIFLMMAAHD

TITSSATVLFWQLARNPDWQDRLRAEARAVTGGDGLPLAYEDLGRMELTEMAFKEALR

FMPPVPNMPRRALRDFEFGGYRIPAGTPVGISPAAVHADPAHWPEPDRFDPLRFTPEN

VSGRHKYAWVPFGGGAHMCLGLHFAYMQVKLLVSHILTRYEVAMQPGPAPSWQAWPIP

KPRDGLRVEMRRIC

>CYP197A1 Bacillus halodurans

1 MPTNTMPTGP KGNPVLGNTI EFGKDPLQFI TRCSQEYGEI VRLRFERERD TFLLNDPKHI

61 QYVFMNKGGE FSKGYQQDPI MGLVFGNGLL TSEGSFWLRQ RRLSQPAFHP KRIADYADTM

121 VGYCERMLNT WMDNDTRDIN DEMMQLTMAI ATKTLFDLDL HKGDTQEASR SLDTVMTAFN

181 EQMTNVFRHV LHLIGLGKLV PPVSRELREA VESLDKMIYS IIEERRKHPG DRGDLLSMLI

241 STYDEDDGSY MTDRQLRDEI ITLFLAGHET TANTLSWAFY LLSQHPHVEE KLYQEVSQVL

301 GNRPATLEDM PKLSYAEHVI KETLRVQPTV WLISRRAEKD VTLGDYHISA GSEIMISQWG

361 MHRNPRYFND PLTFLPERWD NNDNKPSKYV YFPFGGGPRV CIGERFALME ATLIMATIVR

421 EFRMELVDEL PIKMEPSITL RPKHGVTMKL RKR

>CYP197B1 Nostoc punctiforme

MVADVFELPAPSVNSIVGHLFELGQDPLGFLTRCRDYGDIVPLQ

LGLTPSCLIINPEYIEEVLKNRNDFIKSRGLRALKSLLGEGLLSAEGESWFWQRRLAQ

PVFHQKRINGYSQTMVEYTNRMVQTWHDGETHDIHEDMMRLTLQIVMKCIFSDDIDAG

EAKVVADALDVAMQWFESKRRQNFLVWEWFPRPENIRYRDAIAQMDEAIYKLIQERRN

GGEKTNDLLTMLMEAKDEQTLQQMDDKLLRDEVATLMLAGHETTANTLSWTWMLLAQN

PGVREKLESELNQVLQGKLPTLEDLGQLVYTQQIIKESMRLYPPVPLMGREAAVDTQI

GDYEIPQGMAIMISQWVMHRHPKYFENPEAFQPERWTQEFEKQLPKGVYIPFGDGPRI

CIGKGFAQMEAALLLATIAQRFQIDLVPGYPIVPQPSITLRPENGLKVQLKQIALDTS

K

>CYP197C1 Halogeometricum borinquense DSM 11551 (Archaea; Euryarchaeota)

ZP\_04000803, ABTX01000013.1 3913-2567

41% to CYP197A1 Bacillus halodurans (Firmicutes),

41% to CYP197B1 Nostoc punctiforme (Cyanobacteria)

1 MMSSDTPPVT DEMPPGPDGL PVVGNYPSYI REPFEFMTRN AREYGDIVGW EERNGPVYQL

61 NHPDHIEQVL VQNNQNYVKG DAFQSTLGPI TGSGILNSEG AIWRRNRHLI QPAFHPNRIE

121 EYSEMMTGYT EEMLETWSDG ETREIHEDMM TVTLKIVSRA LFGVDIDDHV EDIGEALESF

181 MEASESLSHY VLPEEIPTPS RKQIQGAREQ LDDVVYELIE DRRANPGEQD VISMLLDVTD

241 DDGNTLSTEQ IRDEVVTLLL AGHETTALSL SFTAYALARH PEAEAKLVEE LDEVLDGRTP

301 TMSDLSELTY TEQVVKESMR LYPPVPGIVR EPVKPDIIGG YEIPAGATVR MHQWVVHRDE

361 RWYDDPLAFE PERWTDDLEQ SIPKLAYFPF AAGPRRCIGD RFAMLEARLL LATIYQKYHL

421 ELTPGTELDL MATVTARPKS EIEMTVERR

>CYP198A1 Xanthomonas campestris pv. Campestris str. ATCC

1 MRRPAFPASV MNSSGAVWQH KRRTLMPAFR AALVRESAMQ ASAATRSLLH ELGDSCATQD

61 MRTLMTGLCA QLGAGFLLGD SANAADLLRM LPMVDAISKQ TRRQSLAPTW WPSSGRRRLR

121 RLRADIDMAL DRILMQSTQR PPRAASVLAL LLAETARDDG DWCRDEAAAI LMSALEPMSA

181 ALTWTLLLLA QHPHIAQEVA QEASALDGAD VASGTSLLDR LPQSRACVKE SMRLYPPAWI

241 TARIAQRDAT LNGFHVPRGT QLLVSAWVVH RDGRHFPDPE IFLPARWLDD SATHSLTRYS

301 YFPFGGGPRS CIGCMLALTQ MTIVIATVLH ACSLHLAPDA RPSPFPALVL RPMDVRIALR

361 PRVIRSVVPS RAHASPVRLA SVTPND

>CYP199A1 Bradyrhizobium japonicum USDA 110

1 MSAPGSAASG VPHLDVDPFD MNFFADPYAA HELLREAGPV VYLDKWNVYG VARYAEVHAV

61 LNDPATFCSS RGVGLSDFKK ETPWRPPSLI LEADPPAHTR TRAVLSKVLS PTVMKQVRDR

121 FAAAAEERVD ALIEKRSFDA IADLAEAYPL SIFPDALGLK SEGREHLIPY ASVVFNAFGP

181 PNQLRQEAIA RSTPHQAYVA EQCQRENLAP GGFGACIHAQ VDEGAITASE APLLVRSLLS

241 AGLDTTVNGI GAAVYCLARF PEQWQRLRGD LSLARSAFEE AVRFESPVQT FFRTTTREVE

301 LSGATIGEGE KVLMFLAAAN RDPRRWDKPD SYDVTRRSSG HVGFGSGIHM CVGQLVARLE

361 GEVMLTALAR RIAKIEITGE PKRRFNNTLR GLDGLPVTIT PA

>CYP199A2 Rhodopseudomonas palustris

MRPSGLGAAAADRRDFGGRDAPVMGMSAANACADIRTCHGISQV

AIEEDNMTTAPSLVPVTTPSQHGAGVPHLGIDPFALDYFADPYPEQETLREAGPVVYL

DKWNVYGVARYAEVYAVLNDPLTFCSSRGVGLSDFKKEKPWRPPSLILEADPPAHTRT

RAVLSKVLSPATMKRLRDGFAAAADAKIDELLARGGNIDAIADLAEAYPLSVFPDAMG

LKQEGRENLLPYAGLVFNAFGPPNELRQSAIERSAPHQAYVAEQCQRPNLAPGGFGAC

IHAFSDTGEITPEEAPLLVRSLLSAGLDTTVNGIAAAVYCLARFPDEFARLRADPSLA

RNAFEEAVRFESPVQTFFRTTTRDVELAGATIGEGEKVLMFLGSANRDPRRWDDPDRY

DITRKTSGHVGFGSGVHMCVGQLVARLEGEVVLAALARKVAAIEIAGPLKRRFNNTLR

GLESLPIQLTPA

>CYP199A3 Rhodococcus sp. RHA1 Rha06678

MFAPAPALPVSDADPFALDVLQDPLPFQANLRDAGPVVYLRRYDVFALGRYEQVHAALTDWQSFQSAAGVGLSNFRYETPWRPPSILLEADPPHHDAPRAVLSKILGPRALQKLRAAWIQDAEALVDQLLANTTEFDAVTDLAAAFPLRVFPDAVGIPDAGRENLLPYGDHAFNAFGPANGLVEKGAPRVAELSGWVNAQCARDALTGDGFGAQIWAAADRGDITYEQAPLVVRSLLTAGVDTTVNGLAAVLYAFATHPDQWARLRENRTLARTAFDEAVRWESPVQTFFRTATRDTEIGGATIPDGKKILMFLGAANRDPRRWENPEVFDLGRNPSGHVGYGMGIHQCVGQHVARLESEALLTALASRVHSLEIAGPVHRHLNNTLRSWESVPVKVRLP

>CYP200A1 Bradyrhizobium japonicum USDA 110

1 MAPRLDFTSE AFFRDPPAAI AALRASGPVV ATRFPLVGDV WITTTHDATA EVLKDGTTFT

61 LRKEDGKVAG LRWWMPKLVT TIANNMLTMD EPDHTRLRSI VDEAFRRRAI VAMEPRIRAI

121 ADGLANDLFA DGSPADLVQC YARILPVSVI CELLGLPAAD RPRFIAWANK MSSLTNVVSF

181 FRLLFAFRKM RAYLERQLQI ARVRGGEGLI AELVQVELEG GQITPDEMVS MVFLLLAAGS

241 ETTTHLISGS VYELLRNPAL RDWLEEDWSR ISLAVEEFLR FVSPVQFSKP RYLRRDVELA

301 GVRLKKGDRV MVMLAAANMD PAVHDRPERL DLTRKPNRHM SFGTGIHFCL GHQLARIEAT

361 CALQALLARW PKLELAVDPA QIHWRKRPGM RAIARLPVVA GGNRRPSRGA AAEPLLAD

>CYP201A1 Bradyrhizobium japonicum USDA 110

1 MNIASVRRPI VPPTPPRAPD DMSFLGRVAV IRQNMIATWG QRAYEEDVLE GRFFLHKSFI

61 LNRPDAIRHV LLSNYENYTR TPAGIRMLRP VLGEGLLIAE GHAWTFQRRT LAPAFTPRAT

121 ANLVPHMTAV LDETIAKLDA RSGETVDLRE TMQRMTLEIA GRTMFSFGMD RHGPTLRNFV

181 VEYGERLGRP YFLDMLLPVS WPSPMDFARA RFRKRWTEFV AMLIAERRAA GKKDGAPPRD

241 LFDLMDEARD PETGKGFSDE QLIDEVATMI LAGHETTATA LFWALYLLAL DPDTQEEVAS

301 ETRGEHLDSM ADIDRQKFTR AVIEETMRLY PPAFLIARAA RAKDNAAGIE IGRGDIIMIA

361 PWLLHRHEKL WDQPNAFVPK RFMSTEAPDR FAYLPFGAGP RVCVGAPFAQ AESVLALARL

421 IGAFRVELVD TVPVIPHGVV TTQPDRSPMF RITRR

>CYP201A2 Rhodopseudomonas palustris

MGSAGAFSLPVSHTTFVEQQRGSGFEVSIAAIDDRPASRAPLIP

PTPPRAPENLSALGRLAAIRHNAIASWGDRAYQDDVVRGRFFAHSSYILNTPDAIRHV

LVDNTDNYRRTATGIRVLRPMLGEGLLLAEGRAWKHQRRTLAPAFTPRAVATLVPHMA

SATDEVVEGLRRKTGVPLDLRETMQHLALEIAGRTMFSFEMGTHGQALRGFVIDYGTR

LASPRFLDLLLPLGWPTPQDVSRALFRRRWTRFIGELIAARRAAGKAEGAPPRDLFEL

MLAARDPETGEAFSDAQLGDQVATMILAGHETTATALFWALYLLALDPDAQERLANEV

RRVGFGGTEIERLPFTRAVLDETLRLYPPAFLIVREAAGPDRVAGFAVRKHDVMLIAP

WLLHRHDKLWSDPNAFVPERFLPGVPSPDRFAYLPFGVGPRVCIGAHFALVEATLALA

KIVGTFRIELIDTEPVIPIGVVTTQPDRSPLFRLTPR

>CYP201A3 Magnetospirillum magnetotacticum

675 LILAGHETTAV 643

640 PLLWACTLLALSPETQERVAAESGQADKPFTRAVIDETVRLYPPAFVLARR 488

487 AAGVDTLGGETVQPGDSVTISPWLLHRHRRLWRDPDAFDPGRFLPGASPVPRFAYLPF 314

313 GAGPRVCIGAAFALTEATLALSRIVGRFRLARADARPVLP 194

AAVVTTQPDHAPAFRLTLRT\* 131

>CYP202A1 Sinorhizobium meliloti

1 MSIAPGITID GPARRVSLDV RNPRFFRNPL PAYAALHAQC PAFFWEEPQQ WFFAGYEQVN

61 SLLRDRRFGR QILHVATREE LGMPEPKPHL KDFDALEAHS LLELEPPAHT RLRTLVNRAF

121 VSRQIEELRP EIEALSHAVI DGFEKDGETE LLKTYAETIP VTIIARMLGI PVEAAPRLLD

181 WSHRMVKMYV FNPSLETEFD ANNASAEFAD YLKGIIAEKR TNPADDLLTH MITSEKDGER

241 LSDAELISTT VLLLNAGHEA TVHQIGNAVR TILQSGLSPA ELFSDEKATE RTVEECLRFA

301 APLHIFQRYA LMDIELENGI ALRKGDKIGL MLGAANVDPR KFSSPDTFRP DRNEGANVSF

361 GAGLHFCIGA PLARLELQIS LPILFRRLPG MRLKNEPPVK DAFHFHGLER LDLVW

>CYP202A2 Mesorhizobium loti

1 MTNSTLPYLA FDPATRRLRL DPHEPAFFLN PYEAYGFLHD VSNAFFWEEF GFWCFGGFDD

61 VNRLLRDRRF GRQNPAGIPD SRGVGQDRSH LRAFDGIEAN SMLELEPPVH TRLRTLVNRA

121 FVSRQVERLR PRVEALANEL IDRFDPTGPV DLLPAFASPL PITIIAEMLG VPVEMGPQLL

181 DWSHQMVAMY IHGRTRETEE TANRAASEFA DFLRGYVAER RRNPGDDLLS LLISAQEDGE

241 RLSEDEMVSS AILLLNAGHE ATVHQTGNAV RSILAQGGDP SRFFTSAEAT AATVEECLRF

301 DAPLHMFMRY AYQEIEIAPG IVVRPGQTIG LLLGMANHDP RAFAEPQAFR PDRADQKNVS

361 FGAGIHFCIG APLARLELQV SLKTLFERHP RLHLAEQSRF RDTYHFHGLE TLAVGF

>CYP202A3 Agrobacterium tumefaciens strain C58

MTATFPFLKIDPATRRVSLNARDPAFYNDPNPVYAALHAQCPTF

YWEEQRQWFFTCYDHVSTLLRDRRFGRQILHVASREEIGLPEPLEHVKHFDLAEQHSL

LELEPPEHTRLRTLINRAFVSRHVDKMKPEIEELANRLIEAFEANGETELLSSYADII

PVTMIARMIGIPEEMGPQLLKWSHAYVGMYMFKRTPEDELLADKAAQEFSDYVRRVIA

ERRAEPKDDLLSHMIHTEHKGQYLTDDELVSTTIVLLNAGHEATVHQIGNSVRIILES

GLDPKTLFHDETATERTVEETLRICAPVHIFQRWVLEPVEIDGVQFKRGDKVSLILAA

ANLDPAKFSDPLAFQPDRNEGANVSFGAGIHFCIGAPLARLELNLALPLLFKRLPGLK

IAEPPKVKDVYHFHGLERLDLAW

>CYP202B1 Rhodobacter sphaeroides

MQTLSQSPHDRRFLRNPYRFYREARAAGPFFHWEELGLVCTTSY

AAANAILRDRRFGREVPPGRASAVPDHLAPFAAVEAHSMLELEPPRHTRLRNLVLRAF

TSRRIGTMQPEVAALSESLVAAVPEGPFDLLPAFSQRLPITLIARLIGIPESLAPELL

RWSSAMVAMYQAGRTRKTEERAALAAADFSDFLRLHIEARRHAPADDLLTHLIAAEAD

GQQLSTDEIVSTCILILNAGHEAAVHAIGNAAAVLLRHRTPPEALAPPHLLGTVEELL

RFDPPLHLFRRMAYERVEIMGRTIEEGCEVALLLGAANRDPGPWERPDRFLWNRPEKT

HLAFGAGLHFCLGAPLARLELATALPILFGRLPNLQLVKPPSYGDSWHFRGLERLIVSA

>CYP203A1 Rhodopseudomonas palustris

MFSFDPYSPIVDADPFPLYKTLRDEYPVFWSEPAQMWILSRYLD

VAGAGSNWQVFSSAKGNLMTELPNRAGATLGTTDPPRHDRLRGLVQHAFMKRNLEALA

EPMREIARDAAEALRGRDQFDFISDFSSKFTVRVLFAALGLPMGDEQTVRDKAVLMVQ

SDPVTRAKGPEHLAAYAWMQDYASSVIAQRRAEPKNDLISHFSMAEIDGDRLDEREVL

LTTTTLIMAGIESLGGFMSMLALNLADFADARRAVVADPALLPDAVEESLRYNTSAQR

FKRCLQSDLTLHGVTMKAGDFVCLAYGSANRDERQFPNPDVYDVKRKPKGHLGFGGGV

HACLGSAIARMAIRIAFDEFHKVVPDYTRTEQQLNWMPSSTFRSPLRLDFAVEQAASR

SAA

>CYP203A2 Novosphingobium aromaticivorans

MATVIERPQFRFDPYSPAIDADPFPAYKVLRDEYPCFWSEEAGK

WVLSRYDDVLAALQDWRTYSSAKGNLVDEFPGRAGSTLGSSDPPRHDRLRALIQSAVT

KRALEHIIAPARASAQAHLAALADKPVFDLVGDYTSKLTVDLLFYLFALPDEGAQQVR

ENAVLMVQTDPVTRQKSPEHLAAFHWMADYAEKLVASRKANPGDDLLSSFITAEIDGE

KLLDKEVQLTVTTLIMAGIESLSGFMAMFGLNLADYPEARSALVADPSLIPDAIEESL

RFNTSAQRFKRTLTRDVELHGQVMKAGDAVILAYGSANRDERMFENPDVYDITRKPRR

HLGFGGGVHACLGSMIGRLATQIAYEELLKAVPDFRRADAPLDWVPSSNFRSPKSLML

EKKA

>CYP204A1 Novosphingobium aromaticivorans

MARAATAAGNGLPLLDGGVPLLGHLAQFFRDPVSVLKRGYRSKG

RLFAMNFMGQRMNVMLGPEHNRFFFEETDKLLSIRESMPFFLKMFSPEFYSFAEMDEY

LRQRSIIMPRFKAASMKQYVPVMVEESLNLVERLGEEGEFDLIPTLGPVVMDIAAHSF

MGREFHEKLGHEFFELFRDFSGGMEFVLPLWLPTPKMVKSQRAKRKLHAILQSWIDKR

RAAPLDPPDFFQTMIETKYPDGRPVPDEIIRHLILLLVWAGHETTAGQVSWALADLLQ

NPDYQKVLRGEISSLLGGSDGRDLGWEQAVAMEKMDLALRETERLHPVAYMLSRKARA

DIERDGYVIRKGEFVLLAPSVSHRMEETFRNPDAYDPERFNPANPDAQIESNSLIGFG

GGVHRCAGVNFARMEMKVLVAILLQNFDMELMDEVRPIAGASTYWPAQPCRVRYRRRK

LDGSEAGADMAALARAAGCPAHT

>CYP204B1 Saccharopolyspora erythraea NRRL23338

MLSGARPLVGHAGEFIRNPVAMAERGYAECGEAFSVRIPGWTAHMFIGPEHNRFFFSETD

RRLSIRTAYPFFVRMFDPAFYFFAGDDEYRRQRALVLPRFQGRQLENYVATMVDEVCELD

RALGNSGEFDLVRTMGPLVMRIAARAFLGREFSARLENGFFEKFRRFSAGMDPVMAGWLP

LPHLVRSRFAKRELHRLMGELIRQRRRSPVEPGDFLQTLIEARYDDGEVVPDRVLINLIL

LFSWAGHETTTGHISWAVIDLLRNPEALRKVLEETHGVLGSRSFGELTLSDVGKLKYLGH

ALHETERLHPVAFTMARTAAEAFEYAGYRIPEGAMLMISPAVTHRLPGLYPEPDRFRPER

FQDNPKDTRYLVGFGGGVHRCLGVHFAYLEMTIALAHLFREFEFELLDTNPRPVPGAHTK

WPRSPCRVRYVRRAGTGRAA

>CYP205A1 Chloroflexus aurantiacus

MIPAIPVLIGDTAMIRFPSPVAIRNLQQLRREPLTLLEELAARG

DVVPFRVGPQMMVLVNHPDLIREVLVTQHRSFVKGRVLERAKRLLGEGLLTSEGELHL

RQRRLMQPAFHRQRIAAYGDAMVAVAEARSARWQDGLVLDVSREFMAITLQIVGITLF

SADTEADADEVFAAMHDLVAMFDLAVLPFADWLFALPLPPVRRFQAVKARLDAIIYRL

IAQRRANPVDRGDLLSMLLTAVDHEGDGYRMTDTQLRDELLTIFLAGHETTANALTWA

LYLLAQYPSLAAHLAAELDTVLGGRKPTVADLPKLTYTSWFFAEALRLYPPAWLIGRR

AIAPVTLGDVRIAPDTIVLLSPWLMHHDPRFFHEPYHCDPLRHTPEAQAQRPKFAFFP

FGGGPRTCIGEPFAWMEGILVLATLAQRWQFLPVADHPVVLQTGITLRPRYGMQLQLR

ERRTVLGAA

>CYP205B1 Frankia sp. CcI3

MSRAPHVRSVAAPPSTAKTSDIKTSDRVPGSGEGPVEAIRRLRADPLTRLNELARAHGPVVRLASWPVSA

FLVTDPDAIADALVSGHRAYAKGAVRRGAGSRRTVVQPLALLLGQGLLTSAGDTHRQQRRLLQPLFHKQR

IAGYADAFAAIADKTADGWRDGQRLDVHTEMTEMTLAIVARTLFDVDLDSHVVDVIRAALDQNMPAARRA

QLPGFTTLERLPLPAPRRRRDARNALDRVVHDLIADRRATGATGNDLLSLLLTARDADTGASMDDSQVRD

EALTLLLAGHETTANALTWTFHLLGRDPEVLATLQAELDRVLGERRPTIDDLPQLPYTNAVISEAMRLYP

PVWAMGRHLVEDRDVAGYRLPAGSTLVFSQWVVHRDERWWPRPELFDPIRWTGPDTADEPADAGPKMRPR

FAYFPFGAGPRQCIGNTFAITEGVLALAAIARRWSFTPVPGLPVTPQPLVTLRPKDGLPMIAHGRYPNR

>CYP205B2 Frankia sp. EAN1pec

MSIDRLPTAGHTGAQAPGPGRATPAFLRELLADPLRLFTRLRTSYGPIVRVPVGRGGFHLVCGPEAVEQV

LVGEQRAYAKGLRRRTMPPGEGIQPLSLLLGSGLLTSGGDLHRTRRRLIQPMFHRERIAGYGAAISELSR

ATALGWADGSRREVHTDMSELTLAIVARTVFGVDVDSEVVRRVRRAVAANMRLSQLAVLPGAIRLQQHLP

IGPLRAARDARDDLTAVVMEMIEQRRSLDAAGSDLLSTLLATRDADTGAPLDDTSIRDEALTILLAGHET

TANAMAWAYHLLATNPQARDRMHTELDDVLNGRKPTTADLAELPYTRAVFSETLRLYPPAWILLRRTTRD

VTLTGYHLPADTNVLLSQWVIHRDPTWWPAPEEFRPQRWLTPDPTRPKYAYFPFGGGTRQCIGNTFAEME

GALALAAISSIRTLTPTPGRPVTPIPRVTLRPQPLQMTAHPRTPHPTPATHQPH

>CYP206A1 Agrobacterium tumefaciens (strain C58, Cereon)

1 MTEIGFRTPS TDTTGAQPVS KLATARLALS LIRNPLKALP PEIFSEPAVF TRLGGVMRVH

61 LADPVLIHEA LVKNAALLGK GEDVRRALGP ALGQGLLTAD GDHWKWQRQS VAAAFRHEKL

121 LELLPVMIET ARRTQKRWRS SSTADIDIGH EMMRTTFDII VETMMSGGYG IDIARVEQSI

181 TDYLKPTGWT FALAMLGAPE WLPHPGRRKS RAAVDYLRAS LATVITGRRK NPTDRPDLVS

241 MLLEAKDPET GRMMSDEEII DNLLTFITAG HETTALGLAW TFHLLSQNPE TERKAVEEIE

301 AVTGGEPVAA EHIANLAYVR QVFSEAMRLY PPAPVITRTA LQDFRLGEHD IPAGTVLYVP

361 IYAVHRHTAL WDEPERFDPS RFEPEKVKAR HRYAYMPFGA GPRVCIGNAF AMMEAVAILA

421 VILQKNHLEN RTMASAEPLM RVTLRPQERL MMKITQRQNK SPAV

>CYP207A1 Kitasatospora griseola

1 MKGNLPAMST ATSSSVTGSV TTPRTATTPG RRPGLAPGGV PVLGHLPMIL RSRFEFIETV

61 RNAGPVTRVK LGPKTAYFVN DYELLAQILV SDADKFVRGI HFKKMRNMVG NGVVTTSGDL

121 HRRQRRIMLP SFSQRRLAMH LPVMRKIMSE FVASVPERRP YDLMGPVMGV GCDIVTSTML

181 GEKTPPEVLR LVREAVPVFV ENAAIQAVDV TGIYKHLPTK SNRDFERLLN AFNEYMYSVI

241 DDKFRNGAGE EAGLLDMLIN ATDPETGEKF DRTEVRDQAA TILLASTETT ANTISWACYE

301 LARHPRIFAE CRAEIDALVK DRDWLDIEIG RHDLPALKRV LFEALRMYPS SYLLSRQASV

361 DTTLGGYAIP KDAAILYSHY GQQRDERNFP HGDEFDPDRW LDKDGAEVTA SAFMPFGFGA

421 YRCLGESVAV LEATYCLAMM VHQWDFALSD YSEPKMNATI TLSPKDLEFL FTKRTESGAH

481 DE

>CYP208A1 Streptomyces globisporus

1 MRIDPPGPPL RALPGLLRKL AVDRLGMMRD AAGLGDAVRV SMGPKKLYIF NRPDYAKHVL

61 ADNSDNYHKG IGLVQSRRVL GDGLLTSDGE TWREQRRIVQ PAFKPGRINQ QAAAVAEEAA

121 KLVALLRGHE GGGPVDVLQE VTGLTLGVLG RTLLDSNLTA HESLAHSFEE VQDQAMLEMV

181 SQGTVPAWLP LPPQARFRRA RRELYRVADL LVADRRSRMA DGGPGDDALS RIIVAADRRR

241 DDPARARNRL REELVTLLLA GHETTASTLG WTLHLLERHP EVRDRVRAEA RAALGDGVPG

301 PEDLHRLTYT TMVVQEAMRL FPPVWILPRV AQQRDVVGGY TVSAGSDVLV CPYIMHRHPG

361 LWEDPERFDP ERFEPRQTAD RPRYAYIPFG AGPRFCVGSN LGMMEAVFVT ALVTRDLDLR

421 TVAGHRAVAE PMLSLRMRGG LPMTVSTAR

>CYP208A2 Streptomyces carzinostaticus subsp. neocarzinostaticus

MNGRRPVSPPLRALPGLLRKLAVDRLGMMRDAAALDDAVLVSMG

PKKLFVFNRPDYAKHVLADNAANYRKGIGLIESRKMLGDGLLTSEGELWREQRRTVQP

AFRPARVAAQADAVAEETMNLRDLLMRRGADGPVDVLQEVTGFTLGVLGRTVLNTDLG

GYGGIAHAFEAVQDQAMFDMVTQNMVPTWAPLATQRRFRRARRELIRTVDELVADRSA

RMTDGEEADDAFSLMIAAARRQTDPRTGQGRLRDELVTLLLAGHETTASTLAWTLLLL

ARHPHMRDLVREEARGVLADGRAPDAGDLRKLTYTTQVVQEAMRLYPPVWILPRVARQ

SDEVGPYSVSAGADVLICPYTLHRHPDLWERPEQFDPGRFDPARVADRPRYAYIPFGA

GPRFCVGSNLGMMEAVFVTALLTRDLVLEVVPGDERTPEPMMSLRMRGGLPMTVRPVR

>CYP208A3 Actinomadura madurae

MSIDELDARGGTPRAAGRVPPGPPRRATPNLLRMLATDRLGMMQ

AALRHGDAVRVGLGPKALYLFNRPEHAKHVLADNSGNYHKGIGLVQARRALGDGLLTS

EGDLWREQRRVVQPAFQHKRIAGLADAVVEEAGALVARLRARAGGPPVDVVGEMTALT

LGVLGRTLLDADLTAHTSLGRAFETVQDQAMFEMVSQGMVPMWLPLPGQLRFRRARRE

LDRIVRALVAERLREGGGAEDALSRLIESARREPDGRVGRRRLRDELVTLLLAGHETT

ASTLGWTFHLLDRHPLVRARVRAEARAVFGDGTPTLDDLSALSYTTMVVQEVMRMYPPVWI

>CYP208A4 Salinispora tropica (marine actinomycete)

MTVAAAGRTFSGPTGAALLRSLWQLGQDRLGLMTSAARYGDAVRLGVGSRSLYFFNHPDH

AKHVLADNSGNYTKGLGLVHARRALGDGLLTSEGELWREQRRVIQPVFQAKRVAGQAHAV

AEEADRLIARLRARRGRGPVNLTDEFTALTLGVLGRTLLDANLDAFTTVGAAFEEMQNQA

MFEMASMSMVPMWVPLPQQLRFRRARRELERIVGRLVADRTARGEGTGADDALSRLIAST

RDEPDPGVARRRMRDELVTLLLAGHETTASTLGWTFHLINQDPRVRVRLREEAIDVLGGR

LPEYADLARLTYTKMVVSEAMRLYPPVWMLSRLARDADVVDGYPVPARADVLICPYTLHR

HPAFWPEPERFDPERFDPEVTTDRPRYAYVPFGAGPRFCVGNHLGLMEAVFVVAMVSREF

DLVAPVGQPVVAEPMLSLRVRGGLSMTVEPVS

>CYP208A5 SGR611 Streptomyces griseus

MRTDPPGPPVSALPGLLRKLAVDRLEMMKDAAALGDAVRVSMGPKKLYIFNRPDYAKHVLADNSDNYHKGIGLVQSRRVLGDGLLTSDGEVWRAQRQTVQPAFKPGRINRQANAVAEEGAKLVALLRAHEGGGPVDVLHEVTGLTLGVLGRTLLDSDLSSQDTLAPSFEEVQDQAMLEMVSQGMVPGWLPLPPQARFRRARRELYRVADLLVADRSARMADGEPGDDALARIIEAAGRGNGPPRRVRGKLREELVTLLLAGHETTASTLGWTLHLLERHPEVRAAVREEARSVLGERLPDLDDLHRLTWTTKVVQEAMRLYPPVWVLPRVAQREDEVGGYTVSARADVLICPYIMHRNPRLWEDPERFDPERFDPQAVASRPRYAYIPFGAGPRFCVGSNLGMMEAVFVTALITRDLDLRTVPGHRAVAEPMLSLRMRGGLPMTVSVAG

>CYP209A1 Myxococcus xanthus

1 MGTSEPVEPD HALSKPPPVA PVGAQALPRG PAMPGIAQLM MLFLRPTEFL DRCAARYGDT

61 FTLKIPGTPP FIQTSDPALI EVIFKGDPDL FLGGKANNGL KPVVGENSLL VLDGKRHRRD

121 RKLIMPTFLG ERMHAYGSVI RDIVNAALDR WPVGKPFAVH EETQQIMLEV ILRVIFGLED

181 ARTIAQFRHH VHQVLKLALF LFPNGEGKPA AEGFARAVGK AFPSLDVFAS LKAIDDIIYQ

241 EIQDRRSQDI SGRQDVLSLM MQSHYDDGSV MTPQELRDEL MTLLMAGHET SATIAAWCVY

301 HLCRHPDAMG KLREEIAAHT VDGVLPLAKI NELKFLDAVV KETMRITPVF SLVARVLKEP

361 QTIGGTTYPA NVVLSPNIYG THHRADLWGD PKVFRPERFL EERVNPFHYF PFGGGIRKCI

421 GTSFAYYEMK IFVSETVRRM RFDTRPGYHA KVVRRSNTLA PSQGVPIIVE SRLPS

>CYP210A1 Polyangium cellulosum = Sorangium cellulosum

1 MISISKSKQK LLPPGPRSPM ALQTLQWLKN PVPFLEACGA RYGEMFTLKL PTQWPVVVVQ

61 HPEAVKEVFA LDSNAGHAGE ANNILKPFLG KYSLLVLDGE EHMRQRKMMM PAFHGERMEA

121 YGHAMIDAAH ASIDAWPVGS PFGVHAPMQA ITLQVILRTV VGMTDGPLLA ELEALYPQVI

181 DAASAPAMHF ELFRKDLGPW SPWGKFKRRS ARGKEIMIHE IRRAREKGTA GRTDVLAMII

241 DAKDENGELL TEDEIHGELM TLLVAGHETT ATALCWALRW LLRDAALTRR VAEEAAEVAD

301 DPVKIAKSEL LDRVVKEALR LQPIGPVVAR VLKQPLTIQG RELPADVMVA PCVQLLHHRP

361 SLYPEPTRFD PDRYATFTPK PWEFIPFGGG LRKCIGAAFS MYEMKMVLAT AFSRLSMELA

421 TDDIKIIRRG VTLAPSGGLP LVIRKKSPRA TKPIAA

>CYP211A1 Streptomyces globisporus

MAGLVMSPVEALDALGTVQGRQDPYPFYEAIRAHGQAVPTKPGR

FVVVGHDACDRALREPALRVQDARSYDVVFPSWRSHSSVRGFTSSMLYSNPPDHGRLR

QVVSFAFTPPKVRRMHGVIEDMTDRLLDRMARLGSGGSPVDLIAEFAARLPVAVISEM

IGFPAKDQVWFRDMASRVAVATDGFTDPGALTGADAAMDEMSAYFDDLLDRRRRTPAD

DLVTLLAEAHDGSPGRLDHDELMGTMMVLLTAGFETTSFLIGHGAMIALEQRAHAARL

RAEPDFADGYVEEILRFEPPVHVTSRWAAEDLDLLGLSVPAGSKLVLILAAANRDPGR

YPEPGRFDPDRYAPRPGGPEATRPLSFGAGGHFCLGAPLARLEARIALPRLLRRFPDL

AVSEPPVYRDRWVVRGLETFPVTLGS

>CYP211B1 Salinispora tropica (marine actinomycete)

MDASEAVALLMSPLGRIDPYPTYERLRAHGPVVQTAAGFFVVTGYTEADTVLRNARLAFE

VMDDELRDDVFPHWQDSPAMKSIARSMIRANPPNHGRMRRLAAGAFTPRRIAALREVVTA

QADELADEMIRAGRDGAPVDFMGSFAYPLPVAVICALLGVPAADWARFRGWASDLTAVLE

PEITPQELTVADAGASELRDYFTELIAQRRRAPADDLTTALVQTHDADGDRLSGEELLAN

LVLLLVAGFETTTNLLGNGLVVLLAHPDSATALRDQPELAPGHVDELLRYDSPVQLTTRT

VRESVLLAGVELPAGSWVLVLLGAANRDPERFTDPTRFDPGRAQSPPLSFGAGAHYCLGA

GLARLEAQVAFPLLLRRLPELALAGEPTRRNRLTLRGYETLPVTVSAIAADHGTPAGVAR

GTP

>CYP211C1 Salinispora tropica (marine actinomycete)

MLDVEGLLTRLYSEQGRQDPYPVYAGLHAQGAIAALAPRPEGQRVAAVAVGYDLVGAVLR

DPEWSKQPPPGWMEQEILRTLQSSMMFINPPDHGRMRKVFAGTFTPRRLGTLEPVINRVA

DELLDRMADAGPGEVDFVAEFAYPLPARVMAEFIGIPATELAWYRDRVDRIDAFLDVAGK

TPERLAAANAAAAELRVFYADLLARRRRTPGEDLISGLVEAVDAGGVQLTEDELINNLIV

LFNASFVTTVYMLSNGLPVLLEHPEVAAALADDPELTAGAIDEILRLQTPVHLLARAAPR

DTVLGGVPIPQGQNVLLLIAAANRDPAHFPDPDRFDPRRPGPPSLAFGLGLHYCLGAAVS

RLEGRLALPRLLSRFPRLRIMEQPVYSGSLFLRGIDKLSVSPGGRMHP

>CYP212A1 Chromobacterium violaceum ATCC 12472

MKTPPQSSCPFHAVGRPPTPPRSSAGRWPPGPESGLTGWGLLKL

MSRDLMGTLAGWQREFGDLVHVRTWPEHQVIVSDPQLARELLVNQADALQRWERALTV

YRRVHGHSVLIAEGQVWREKRQALQPDFTRKSVQAFSPSIVEAARRAFEQWPARHAAW

PIESELTSVTMEVILRMMFSSGVGSEAQQAEEAVHTLMVASTEELWRPASLPDWVPWQ

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>CYP212A2 Ralstonia metallidurans

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>CYP213A1 Synechococcus sp. WH 8102

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>CYP213A2 Prochlorococcus marinus str. MIT 9313

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1661946 DLADELQAAKTALPLAERMRRFAFSVIATTVLGLEGTDRDELFVDFEIWT 1662095

1662096 RALFSIPIALPGSSFAKALKARERLLRRLQKVLLKASNGNGGLDLLAGGLDE 1662251

1662252 AGIPLTDEDMVEQLLLLLFAGYETTASSLSCLMRELLLNPQVETWLREEINGVDWPPAPE 1662431

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1662603 ASNRHGAGDLEAFRPQRHLEDGCSATLLPFGGGERVCLGKPLAELEIRLMVVGLFHQLR 1662779

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>CYP213A3 gi|124022066| YP\_001016373 Prochlorococcus marinus str. MIT 9303

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>CYP213A4 gi|78213054| YP\_381833 Synechococcus sp. CC9605

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>CYP213A5 gi|148242205| YP\_001227362 Synechococcus sp. RCC307

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>CYP213A6 gi|148239342| YP\_001224729 Synechococcus sp. WH 7803

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>CYP213A7 gi|88808336| ZP\_01123846 Synechococcus sp. WH 7805

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DTSR

>CYP213A8 gi|113953002| YP\_730662 Synechococcus sp. CC9311

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>CYP213A9 gi|78184536| YP\_376971 Synechococcus sp. CC9902

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>CYP213A10 gi|116070800| ZP\_01468069 Synechococcus sp. BL107

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>CYP213A12 gi|87303613| ZP\_01086392 Synechococcus sp. WH 5701

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>CYP214A1 Trichodesmium erythraeum IMS101

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>CYP215A1 Thermobifida fusca

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>CYP216A1 Thermobifida fusca

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>CYP218A1 Thermobifida fusca

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>CYP220A1 Burkholderia fungorum

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40% to CYP222A1 Thermobifida fusca over 340 aa

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>CYP226A1 Burkholderia fungorum

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>CYP226A2 Burkholderia fungorum

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KGDFVATHLGIPTNAGASAAKCEVTLFRYQDVLAVMRDATTFTNGFIAEGLGGFFDGL

IILAMDGDAHRRARGLLQPVFMPETVNRWRPELDRVIREDFLAPLVPNRHADLMDFGL

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AVMEVVLQRRAAGADGNDLISRLMRAEYEGHKLDDHEVTTFVRSLLPAAGETTTRTFS

SVITLLLERPALVERVRNDRSLIPRLIDEAVRYEPVATFKVRQAARDIEIGGVKVRSG

GLVQCMVMSANRDEDVFENADTFDIDRKPKPSFGFGFGAHMCIGQFVAKIELQCAVNA

ILDLFPNVRLDPARPAPKIAGAQLRGAKSVPVIWD

>CYP226A3 Pseudomonas diterpeniphila

MSGPAHSNLEQVFANVASNYRGADVDLHAVYREMREKSPVLPEN

FMARLGVPSIAGLDPNRPTFTLFKYDDVMAVMRDATNFTSGFIAEGLGSFFDGLILTA

MDGEAHKNIRSLLQPVFMPETVNRWKETKIDRVIREEYLRPMVASKRADIMEFALYFP

IRVIYSLIGFPEDRPEEIEQYAAWALAILAGPQVDPEKAAAARGAAMEAAQALYDVVK

VVVAQRRAEGATGDDLICRLIRAEYEGRSLDDHEITTFVRSLLPAASETTTRTFGTLM

TLLLERPELLARIREDRSLVGKAIDEAVRYEPVATFKVRQAAKDVEIRGVAIPKGAMV

SCIVTSANRDEDAFENADTFDIDRRAKPSFGFGFGPHMCIGQFVAKTEINCALNAILD

LMPNIRLDPDKPAPEIIGAQLRGPHHVHVIWD

>CYP226B1 Mycobacterium marinum MM0272

MSPSVAELSQ ELGEAFRLSS MDDPYPMLAE RRRETPVMKG DIMVALGAPS YMGQHAGETH

TVFRHDDVMA ILRNHETFSS SIWEISQGPL IGRSILAMDG AEHRQWRGYL QSVFGGKLLS

SWDESIFRPL AAKYVADLAS KRGADLIAMA LEYPLRAIYE ILGLEDFKDN YEEFHADVLT

ILLALWSTPD PAQADQFLLR FQKATEASAR SWDRLLPIVQ RKRAAGASRN DLISSLIRAE

YEGGVLDDEQ ITSFLRSLLL AATDTTTRQF LNTLTLLLQR PDELDRIRRD RSRLRLALAE

GERLEPPALF IPRMITRDVV IRGTELTAGT PLLLAIGSAN RDPEAYPPDP DEFRIDRTGP

HHATFGFGTH ICSGMNTTRR EIAALIDAML DGLPGLRVDP DAPAPLISGI HFRGPSALPV VWD\*

>CYP226B1P Mycobacterium ulcerans

LALAEGERLEPPALFIPRMITRDVVIRGTELTAGTPLLLAIGSANRDPEAYPPDPDEFRI

DRTGPHHATFGFGTHICSGMNTTRREIAALIDAMLDGLPGLRVDPDAPAPLISGIHFRGP

SALPVVWD

>CYP227A1 Nostoc punctiforme

MTVNIMTLKDKVLKGQDRQLWLAPILAKVGYDTAIGKFLRLIFY

YTDASIILKAWRDFLYIRKDNIGDKYFAVDQAIMHSSHSQVRELMQTQPQLRGNDLGI

IRILAPSYLLDNPLSLGTNGNEHTGLRTVILQALPEPSQKIDFLGNLVEQSLLEAAKQ

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AQRL

>CYP228A1 Magnetospirillum magnetotacticum

MGPRPHARLVRRPPLPARARGHPVTGTALAPAPAGLAAAMRWEE

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ERVDLVAETATMAGTVVCAMTGLPPTDSAVREAMTAAQSVVGLVRLHRRSLTPSQVRH

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RLVALTADTGWLDRLLAADPGAGPEAAALRGRVVEEALRVTAPTPAMLRSVRAATTVG

DVRVRAGDRVVIATISCCKDAGPFDPDAPVDPAVRHLWFGAGPHFCLGMPLATAQVDA

VLDALRPVAAAGRSLQVTDRAVARGVLIPAYRSLV

>CYP229A1 Pseudomonas fluorescens PfO-1

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EVGALVSARLITNDSDGLYKAMFRGPVCVVASLLGFTPAQARVISELTADFAACLSPL

SNDLQLAAAHRAAEQLRGYFIEMLADPNPFLADIRQRFVGNEEVLLANLIGLCSQTFE

ATAGLIGNALVALHRQPELRNASVDSLLAEVQRFDPSVQNTRRFMANSCEIDGVRLEA

GDVILVLLASANRDPALNENPDRFRVDRPNRRSFTFGSGRHQCPGQTLAMTIASATLT

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>CYP230A1 Pseudomonas fluorescens NCIMB

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DGDAHRFQRNLMKPLFSKSAFNERIPMLAQIFTDTLQARYGVDQKVSALFRHVLSQQI

GGSLQGYQPTPDEVEALMRYQNTAMNVCALKKWPRLALRLPGYRAAKKQVQALADRII

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LFKQPHLHQALRDEVDACFSQGLPDADGLENMETLKNFIREVMRLYPTAYAVRRTRRK

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GPHTCIGAGLANILLSLNLALFLYHTDLRPACKLSDIKMDFSNPAAGLSERFAISFTPRNRP

>CYP231A1 Ferroplasma acidarmanus Archaea; Euryarchaeota

MEHDVFQYYRKMRKESPVHFNNDTGSWDVFDYKSVYFVLMNPDI

YSSDPSYAGNIPENRQGPGASFITMDNPDHKELRNVTTPYFLTSKITGYRDMIESTSK

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NDILNKFKHVKINAEKTSMLKNPMVYGFSTMQLDD

>CYP231A2 Picrophilus torridus, Archaea; Euryarchaeota

MRLNDPVHYDGAWHVYKYSDVKHVLMNDKIFSSNPGNRYSNAGG

ISFITMDNPEHKEFRDISAPYFLPSKINDYKDFIEETSNDLIKNIDNKDIISEYAVRL

PVNIISKILGIPDSDMPLFKLWSDYIIGNKRDENFNYVNNRMVSRLLEIFKSDSHGII

NVLAGSSLKNRKLTMDEKIKYIMLLIIGGNETTTNLIGNMIRVIDENPDIIDDALKNR

SGFVEETLRYYSPIQFLPHRFAAEDSYINNKKIKKGDQVIVYLGSANRDETFFDEPDL

FKIGRREMHLAFGIGIHMCLGAPLARLEASIALNDILNHFKRIKIDYKKSRLLDNKMV

LGYDKLFLS

>CYP232A1 Ferroplasma acidarmanus Archaea; Euryarchaeota

MEIPTYKEEPFEWYREMRKNSPVYREGNMIHIFKYNTISKILSD

HQNFSSQFRDLLGEEMAAMLNEKTTPSILLLDPPLHTTLRGLVGSAFTPRSIELFEPR

IREIARMLAHAIVEKENSDIVSDLSYQLPIRVISEMLGVPESDSEIFRDWSDKLATSL

GRGPDIETQYDMADYFYKKIDRNSKGNNLISRLSTVEMDGRKLSDKEIAGFAILLLVA

GNETTTNLITNAILSLYDHPEIYNEMRKTPSLIPGVVEETLRYRSPVQSTRRYSKIDT

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RLEARIALEEFSKAVPGFEIEKPSPDDRIDSDIMYGFRKLNLKVNRS

>CYP232A2 Picrophilus torridus, Archaea; Euryarchaeota

MYIPSYKEEPFEWYKSMRTQRIVREGNSVHVFKYNDVVTVLSNH

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RELAAKMIENIIEKRRCDLVSEISYPLPIMVISNMLGVPEKDLKKFKEWSDALATSLG

RGPDLRTQREMSEYFLNMIDRDSNDDNLISRLSNVSIDDKKLTDQEITGFSILLLVAG

NETTTNLITNALIELSNHPDIYKELVDNNKIAGDIVEETLRFRSPVQSTRRYAKYDYQ

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LESRIVLEEFAKRIESFSIERLNPDDRIDSDIMYGYKRAIINVKKINQ

>CYP233A1 Gloeobacter violaceus

MSALPPPRFNPFDSEFRQDPYRVYAHLRVAAPIHRSLGMWVLTR

YADVLAVLKDPHFSSSQIPLAVRQRSERPDQAQSHPLARLAAKSIVFTDEPDHTRLRH

LVVRAIKRRTPEQEQAHLTRIASALLERVGPKGRMDAVADYAERLPLQFMAESMALPP

DSWQTVRDWTHQLRYLLEPGLMGRGDFERVQAVLDEVIAFFEDMLAVRRQQPGDDLIS

ALDAAHREAQADRLSDEEIVYCCIMMFVAGHETTRSLIASGLLALLQHPEQLAYLRMH

PERMGAAVTEMLRYESPLQQTKRRATAAVAVGGRTIQPQEQVLLCLGAANRDPARFEQ

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SFILRGLKTLPVQWDR

>CYP233A2 Frankia sp. CcI3

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EDFTRVSDVVETFAQALDDVVTERRSRPGDDLISRLLAARTAGGDRLSDEEVVFVCIMCFVAGNETTKSL

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IVRGLKQLPVSVRGVG

>CYP233A3 Frankia alni ACN14a

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>CYP233A4 Frankia sp. EAN1pec

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GLMRAGDFEHVCDVVETFARALDGVVAERRQRPGGDLISRLLAARTAGGDALTPEELIFVCIMCFVAGNE

TTKSLLGNGLLALLRHPDQAARLHRAPELAGDAVTEALRYDSPLQMTKRVATRDVDVDGRRIRAGDQVLL

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QDHSSIVRGLRHLPVTLHPAAPR

>CYP234A1 Photorhabdus luminescens subsp. laumondii TTO1

MMNVLINEYKKKMDSVRLGDPERKGFFYDAKQAIWHCYSYDICS

YFLNSDYVTKKKLSIPLEIFSASDQSRVARFILYLNNSLIFNDDKYNTDAVSFIRGKF

NEMNFEVIANDLLSPLKQCDLLTAKHLRGVNNLLAASLVGLKASAFFSAHALNVGMFF

DGSMSGRAHFVSIAESFIAIYQQVLRQITINGGAEDVIHIEKFVADLSVTFIAAHETT

MQLIIATFLYIKSHVITVTENNIKSIVTETYRLSSPVLAVNRVFKERLIYKNSCFNKG

DRVLFYTGLANFDATVFDHPYQFQLDREGCPLSFGVGVKKCIGMNIAIHFTCQLITKI

LSCYQLDDVEIHEVTVGSLAIGCSKFTLKISKK

>CYP235A1 Streptomyces antibioticus

MEDSELGRRLQMLRGMQWVFGANGDPYARLLCGMEDDPSPFYDA

IRTLGELHRSRTGAWVTADPGLGGRILADRKARCPEGSWPVRAKTDGLEQYVLPGHQA

FLRLEREEAERLREVAAPVLGAAAVDAWRPLIDEVCAGLAKGLPDTFDLVEEYAGLVP

VEVLARIWGVPEEDRARFGRDCRALAPALDSLLCPQQLALSKDMASALEDLRLLFDGL

DATPRLAGPADGDGTAVAMLTVLLCTEPVTTAIGNTVLGLLPGQWPVPCTGRVAAGQV

AGQALHRAVSYRIATRFAREDLELAGCEVKSGDEVVVLAGAIGRNGPSAAAPPAPPGP

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LHRAPVAAA

>CYP236A1 Microscilla sp. PRE1 plasmid pSD15

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DSPVDGDKAKILYDYIDQQIDRALEKPGEDLYTVLLNSEINGKKLSREEVKGVMILTF

AGGRDTVINAVTNSVAYFAVHPESLELLRKEPEITGRAVEELIRYFAPLTHMGRVVTE

DTQVCEYAVKADSRISLVWASANRDSSVFEKPNEVVLDRKINPHVSFGFSHHNCLGAT

HARQIMHILLKTLAEKVGSIEIQEHEDNIETWGEFERKVGYDRLKVQFNPLQ

>CYP237A1 Pirellula sp.

MRNGTSYLQNFFPGYRRLSRLPKQCLAINPFAGDCMPSRVRLLA

PRSDRPTQPFPHRWNYEDPVRILETYFWKADEEQGPGRHNRYLDVPGFAPVLVTRDPG

MIRAIATATGDREGQFDRDTLPSVGIARATGTDTLLYANGAEWKKQRKIAACPFGKTT

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GADISYEELREKYVPALERVIDHIVKDTVKNRLGIPWRKFPSVSDRIVRAKADDATFE

ELTQRILVPRGEKKALWKQFKSDAPDAKLISNLKVFLAGALEATTSYATWAISHLARH

PDAQEKVFEEVKDIDVYTPEILAGAKYLRAVLDETLRLTPSLYFLPRRATADTWVTSA

DGRKMFIPWGTHLLLDVWHANRHEDHWGVQVSGYPANEFEPDRWRILAEWGRATKDTL

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MSLRLS

>CYP238A1 Pseudomonas putida KT2440

MEILDRPQAPSDFNPMSEQSFRDPASICQRAREETPVFFYAPLG

VWMVTRREDAERVLSEWETFSSLANSPNVPEEFRSRFAPSVMADSIVAIDPPRHTQAR

NVIQRGFMKPKIDPLEPIIEQRAHEIIDRFAGESGTEIMNNYCLELTTRTLMALYDLP

LEDRPMFERIRDVSIKVLASVYEPMQEPEKSRVWNEYVSGYEYFYQLVEQRRNSDARD

IISTMASQKDNQGNPALSTERIALHLVEIAFAGTDTTAQMMANAILFLDSHPEALAAA

KADKTLWSRVFEETVRRRPSAPFAGRITTTEVEIQGVKIPAGSPVWVSLAAANTDPRH

VGCPMNFDINREAPQDHLAFTKGRHTCPGAPLARLQGATGLRVLFERLPELKVVPDQP

LNFAPMALLPVRLSLQVIW

>CYP239A1 Pseudomonas aeruginosa strain SG17M

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QELKKLEQPIRDTARKLAEEFAKEGSGADASYHYSRPLPTIIFSRLAGYPEQDWPKFD

KWVDDIIYERVEKPEVANQASKDVFSYFENLLDNWKDDSESANLIDYLCRAKINGRPL

TRDELLRYCYLLFLAGLDTTAWSIRAGLWYLANNPADQQKLRDNPDLIPLACEEFLRT

LSPVQVMARTCLKDTVIRDQEIKAGERVMLVFGAGNRDEEVFPNPDKIDIERQENRHL

AFGGGIHRCLGSNLGRRELVVGIEEFLRAVPQFKPADPSEKWHGVGPLKLAF

>CYP239A2 Pseudomonas sp. KIE171

MKDVNEVARNFDFHGEALDEIFDTYSTLRNGCPVGRSENYGGFW

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QELKKLEQPIRDTARKLAEDFAKEGTGADASYHYSRPLPTIIFSRLAGYPEKDWPKFD

KWVDDIIYERVEKPEVANQASKDVFSYFENLLDNWKDNGESANLMDYLCRAKIDGRPL

TRDELLRYCYLLFLAGLDTTAWSIRAGLWYLANNPEDQQKLRDNPELIPLACEEFLRT

LSPVQVMARTCLKDTVIRGQDIKAGERVMLVFGAGNRDEEIFPNPDKIDIERQENRHL

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>CYP240A1v1 Bordetella bronchiseptica

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GRTPALLHAAQALAHALRHGVDAPALARRVRYRPLPNARVPRFHFPPGDTP

>CYP240A1v1 Bordetella parapertussis

NC\_002928 3527249..3528406

locus\_tag = BPP3270

100% to B. bronchiseptica

>CYP240A1v2 Bordetella pertussis

MIADTARQHRGDSMQPADPLEAVAHPDPYPYYAALARERPFYHD

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>CYP241A1 Enterococcus faecium

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>CYP242A1 Kitasatospora griseola

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RLDATRRPNDHLAFATGMFYCLGAALARMEADEFFRILLDRFPDVNPGYETPDWQPVL

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>CYP243A1 Mycobacterium avium

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TFAPGKSRKTLRPW

>CYP244A1 Streptomyces sp. TP-A0274

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EAERRLRSITDVMLYSSDYPARQEAVGALFGAVESWVQNPAPLRDGVITGFLAAADGP

DKVTEGEVIVWTVGMIITGYETTGSLISASLYEALRRPPEERPGTDEEIKSWIEEALR

VHPPFPHPTWRFPTEDIELGGYLIPKGAPVQVSIAAANRQPGEGADSFEAARGGHGHL

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>CYP245A1 Streptomyces sp. TP-A0274

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>CYP245A2 Lechevalieria aerocolonigenes

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PMLTR

>CYP246A1 Streptomyces acidiscabies

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TFHETIGVILMLIVGGYDTTASTISLSLVSYALQPEKFSVVHEHPERIPLLVEELLRY

HTVSQLGLGRIATEDVEVGGVTVRAGQMVVAALPLANRDESVFPNPDELDFDRPSVPH

VGFGYGPHQCVGQALARVELQEAIPAVIRRLPGMRLACALEDLPFRHDMATYGIHELPMTW

>CYP246A1 Streptomyces scabies SCAB31761

MESPATQVDP ANSPLEPYHI YPEAKSCPVA KVGLWNGTPA HVFSGYEDVR TVLQDRRFSS

DSRRPNFTEL TPTLQSQAAA PPFVRTDNPD HRRLRGTIAR EFLPKHIELL RPAIREIVQG

VLDGLAETAP PQDMLEAFAV PVASATVFRL LGIPAEDRAL LTRCVKGVVS AVGSEDEGAE

VFRTLGEYIG GLVQDPSELP EDSLIRRLVT GPYQEKQLTF HETIGVILML IVGGYDTTAS

TISLSLVSYA LQPEKFSVVH EHPERIPLLV EELLRYHTVS QLGLGRIATE DVEVGGVTVR

AGQMVVAALP LANRDESVFP NPDELDFDRP SVPHVGFGYG PHQCVGQALA RVELQEAIPA

VIRRLPGMRL ACALEDLPFR HDMATYGIHE LPMTW

>CYP247A1 Actinomadura verrucosospora

MRARAPLHHQVLPDGREFWSVTRYDDVCRVLGEHQRFTSERGTV

VTHLGVDDVAAGTLLTSTDPPRHTLVRRAIGARLTARAVAPWRERIPERDWDELVQLT

AMVTAPSDPHFRHGSEAATLAIAHHELVTYVKEWAARRRSAGGDDGSLLDHLMTVRVA

GAPLTDEEIALDGYSILLGANVTTPHTVSGTVLALIERPEQFGKVQADPSLVPNLVEE

GLRWTSAACNFMRYAVDDVRIAGGTIPARGAVVAWIGSANRDESQFADPHTFDVTRNA

SRQVAFGYGPHYCVGAPLARLTLRVFFKELLRRFGSLSSGGS

>CYP247A2 Frankia alni ACN14a

MRLSPGAASDVDLDRLDLFDLDLYSSGDPHAIWEVMRAQAPLHHQVLADGRAFWSVTRYDDVRAVLGDHR

RFTSERGTVVTHLGEDDLTAGKLMTSTDPPRHTQVRRAIGTRLTARAVASRQNQIRQAIVRFLEPLLDGG

TDDLAERALRLPMVVAGPLLGIPERDWDELVQLTAMVTAPSDPHFQCGGRAATLAIAHHEIVTYVTDWVR

RRRSSGERDGSLLDHLMSVRAGDAPLTDEEIAYDGYSLLLGANVTTPHTISGTVLALVELPEQFDKAQAD

PTLVPSLVEEGLRWTSAACNFMRYAACDTEIGGGTVRRGDAVVAWIASANRDESRFADPHEFDLTRDANR

HVAFGVGPHYCIGAPLARLTAQIFFDELLDRCASIELGGAPEHLRSYFIAGMTHLPVVARKRRSS

>CYP248A1 Micromonospora echinospora

MTAFDPTDADVRRDPYPSYHWLLRHDPVHRGAHRVWYVSRFADV

RAVLGDERFARTGIRRFWTDLVGPGLLAEIVGDIILFQDEPDHGRLRGVVGPAFSPSA

LRRLEPVIAGTVDDLLRPALARGAMDVVDELAYPLALRAVLGLLGLPAADWGAVGRWS

RDVGRTLDRGASAEDMRRGHAAIAEFADYVERALARRRREGGEDLLALMLDAHDRGLM

SRNEIVSTVVTFIFTGHETVASQVGNAVLSLLAHPDQLDLLRRRPDLLAQAVEECLRY

DPSVQSNTRQLDVDVELRGRRLRRDDVVVVLAGAANRDPRRYDRPDDFDIERDPVPSM

SFGAGMRYCLGSYLARTQLRAAVAALARLPGLRLGCASDALAYQPRTMFRGLASLPIA

FTPGG

>CYP249A1 Rhodococcus ruber

MTLSLATAQERYATDADVFAHDTLVDPYDTYRSLRDIGRVSYMT

RYDTWALTRYDEVRHALGDWQTFSSAQGIGMSTALNEAWKDFAPCKDGADHLPMRKLM

MQDLGPKAAAAYKEKIQQAAVTLVEELLDRREFDAVLDFAQMMPMRVFMEVLGVEPDI

EQRRTMLHWGTDTYNCAAPDGLYDDTLPSMDKLYSWALENITPETAREGSVAASTWES

VERGDITDVQAVATLAAYVTAGLDTTAGTLGNTIAQFAANPDQWAIVRDDPKTIPGAI

LEGIRFDSVAQWFTRVTTRDVEYDDIVIPAGSRTYHSYAAANRDERHYRDPDSFDVLR

NPTDHVGFGYGPHMCVGKSVSNTEMIALWTELGRRVDRIEQIGPKKQHINNLIRSLDS

LPVRIYPK

>CYP250A1 Arthrobacter aurescens

MKEPLDFADPTLYQNPVPAFNKMREEHPVFWSDSAGSWVVSRHA

DVVRVLNNLEDAQASLFKINDYAEQCPFGKGTAISRGIENALVTTDLPDHPRLRRHTA

PLLTRRSVERDYAETVEQTVIALLEGIEEDTRFDVLDSISVPLPLAVVTKLIGFDAED

>CYP251A1 Streptomyces peucetius

MQPAASRSVPVAPGAVPLLGHALKLWRDPLGFLKSLRENGDLVRVNLGTMPMYVATSAEL

IHEVTVRQARSFEKGRFFDRLRPLAGDGLATANGEVHRKHRRLIQPMFHPGRITMYAETM

SSNALALADSWTAGQEVEMEQAMAQFAIETLATTLFSTDIGQPAVVAIRENLPVVLQNLL

IRAASPKFLDRFPIRPNRDFDAAAAKLRSVIDEVVATTRRAGTSEHNDLLSVLLGARDSE

TGEYLSDTEVRDELSTILFAGAETTASTLSWTFYQLAEHPEVEAELVAEIKDVVGDRPVS

IEDVPKLEAVRRVLDEVIRLHGVTMLMRRTTAPVELGGHLLPVGTEVGFSLYAMHRDPTL

YDDPDRFDPDRWLPERRGDITRQAYIPFGAGNRKCIGDAFVWTEATIALATVLARWQLRP

LPGHTPKEVASAVAHPDRMPMTVLPRDA\*

>CYP251C1 Amycolatopsis mediterranei U32 ADJ49978.1

44% to CYP251A1 Streptomyces peucetius

MPAHGEIVKLYLGPAPVYFVASPRLVHEVLVNEGPKFRKGAMFD KFRPFVGNGLVLSNGEFHLRQRRLMQPAFHRDRLTAYAEIMRRAAAEMSGSWRAGEVR QIDDDLQSLAVTIVGEALFSTELGKAAIAEARRSIYVIIQQGMIRALSPKFVEKLPVP GNRRFDEAIARMQAIVIEVIHDWRRDGTDRGDLLSTLLLAGMTDEQARDEVLTLLTAG IETTALALAWTFHELGRHPDIEARVHTELDEVLDGRPVTIDDLPRLTYVRQVVDEVLR QYPLWMLMRRTLTEVDLGGTRLPEGAEVIVSPHALHHDPTSFADPDRFDPDRWAPDRV EAIPKGAFVPFGAGNRQCIGNRFAQNEIVITVATVAACWRLVPVAGKPVRVKFTSAAY PDSLPMTAVPR

>CYP252A1 Streptomyces peucetius

MSPSTRSETADPQPPGERGTMSPTLSGHLRRPPGPAGYPVVGCGPDLVRDLVGTFTRAWR

EYGDIVSFRLPGKRNLFLIVHPDHIKHVLDDRQPNYPKDPLSVGKFEPWVGQGLFTSNGD

FHFRQRRLAQPAFKGSRISGFGPAMVEATSDLVRDWHGRATREETFDITPEMFRLALTIV

MQTLFSTDVSNRAGELARAVRICNAYTNVRLQRFVELPQALPSKARSRFLRARATLDSFV

YGLIAERRRDPAPPDDLLTRFLNAQDEQTGERMSDKQLRDEVVTMFLGGYETTALSLVWA

FSLLSRHPEAERKVRSEVAEVCGDREPAASDLPRLRYLRAFYQEVLRLYPSVWTLSRSPL

EDDEIGGYHIPAGSQVFISPYLMHRHPGFWENPEGFRPERFEKSATGGAPLYAYIPFSRG

PRLCPGSSVAVLEAPLVIARMLQDYRLTLAGGHVCEPTSNVFLYPRAGMPMRLQHFKSTG

EGAA\*

>CYP253A1 Streptomyces peucetius

MCPPSSPTTYPSSPCDPPPLRKGLVRMTTTLVPPGPRGHPVLGSIREIQRDNVSAFMEAF

RHHGDIVNFRGPLRINLLAHPDYVQHVLRDQHKRYPRPRKVQGCLSTIVGDGLVAAEGTS

WLRSRRLTQPAFHRDILRRFGDSFTASTAELLDGWERRARDGEPLDIKSEMMHLSLANLA

RALFRTEWTDEVSRIEPAVQEALGFTHRRMTSPVDPLKFPSAARTRFRGALETINSLLYP

MVAERRRDGGGDDLVSLLIDAVDPESGGMFTDEQIRDEVSGFFVAGHETVSTALSWTWYL

LSLNPESRRRLQAEVDEVLAGRVPTVDDLPKLTYTTMVLQESMRLYPPIFVYMRCAAEDD

VIGGYHIPEGRWVVVCPYVTHRHPEFWDNPEGFEPERFTPENSANRHRMAYLPFGAGPRK

CIGDSFAMLQMPLVVAMIAQRFRLDLVEGQQVFPEPAISLRPRDPLMMWLRPNEETP\*

>CYP253A2 SBI\_4844 Streptomyces bingchengensis

85% to CYP253A1 Streptomyces peucetius

VLGSIREIQRDNVSAFMHAFRHHGDIVNFRGPLRINLLAHPDHVQHVLRD

QHKHYPRPRKVQGCLSTIVGDGLVAAEGGSWLRSRRLTQPAFHRDILRRF

GETFTRTTSGMLDDWERRRGQGRPLDIKSEMMHLSLANLARALFKSDLTD

AIARIEPAVQGALSFTHRRMTSPVDPLRIPSKARGRFRDALGTINSVLYP

MIVARRREGGEDDLVSMLIDAKDPGSGEAFTDEQIRDEVSGFFVAGHETV

STALTWTWYLLSLNPESRRRVQDEVDRTLSGRVPTVDDLPKLAYTTMVLQ

EAMRLYPPIFVYMRCAARDDEIGGYRVPAGRWVVVCPYVTHRHPEFWDNP

EGFEPERFTTENSEGRHRMAYLPFGAGPRKCIGDSFAMLQMPLVVAMVAQ

RFRLDLVEGQRVFPEPAISLRPRDPMWMWLRPVEEGSR

>CYP253B1 Streptomyces peucetius SP\_4173 44% to CYP253A1 EU725716.1

MATPTVLTARQAPGPKGEPVLGNARSFQADILGALQQGRRGYGDVVRFDGIGPLFPVFFVAHPEGIKEILQDKHRNFPKTPFVSDRWRALVGDGLICSEGDFWKRQRRLCQPAFHRRLVNSFGENMTEVTGELLDRWEAASRSNQEVDVTLDMTRLALGVLGGALFGANWRQDSEVMAHAVEVAIGEAYKKFGKFVSLPESVPTPANLRFAKARRSLDDVIYRVINARRTDRGEHPDDLLEALMTATEDDGSGMTVEQVRNEVMTFMFGGHETVASGLTWALYLLSRHPEVYGRMEQEVDEVLGSRVPTVDDLPQLPYIDRVVRESLRLYPPVSLISRTPQEDDTVMGYDIPKGSMVLLSAFVTHRHPEFWPNPEGFDPDRWIELGEQGPHRFAWWPFSGGPRKCIGDVFGLQEMKLVLAMMAQRVRVRLVPGHAVVPKPGITLGQQNGVIATVGMRERSRTTVSTAPRTAVAAAQGCPVTGAQAAPPAAASGCPVAHD

>CYP253B2 SBI\_4843 Streptomyces bingchengensis

83% to CYP253B1 Streptomyces peucetius SP\_4173

MTRQAPGPKGEPVLGNARAFQADILQALQRGRREYGDVVRFEGIGPLFPV

FFVGHPDGIKEILQDKHRNFPKTPFVSDRWRALVGDGLICSEGELWKRQR

RLCQPAFHRRLITSFATGMTEVTAELLDRWEAAARAHREVDVTLDMTRLA

LSVLGGALFGANWRQDSEVMAHAVEVAIGEAYKKFGKFVSLPEGVPTPAN

LRFARARKQLDRIIYRVIEDRRADRGPHPDDLLEALMTATEDDGSGMTVE

QVRNEVMTFMFGGHETVASGLTWALYLLSRHPEVAARLEAEVDEVLGGRL

PGVEDLPRLPYVDRVVRESLRLYPPVSLISRTPLEDDTVQGYDIPKGSMV

LLSSFVTHRHPDFWPNPEGFDPDRWIPLGEQGPHRYAWWPFSGGPRKCIG

DVFGLQEMKLVLAMMAQRVRVRLAPGHPVIPRPGITLGQEHGVIATVALR

EKAPPAAPRALAGADSEAIAAAAAAAGCPVHGGGAR

>CYP253C1 Streptomyces peucetius SP\_9081 EU725718

45% to CYP253A1 42% to CYP253B1

MGVSVGQGLVTTEGEVWRAQRRTVAPTFRREPLERFAGVMVDSTQRMLGRWDRIARYGQTLDARTEMQSLTLEILARCLFRADWSRDALALGSAVATQLEHINSKLIAVADIPEKVPTPRNRRFRAARKLLDDTVYRLIAERRAEPADGDAQDLLSMLMHTPDPETGRLMTDEQLRDQVMTLFIAGHETVAATLSWICHLLSTRPAETDRARAEVQKVLGGRTPTMEDLPQLKYLKLFIQEALRLYPPLWQVARMPLKDDVLSGYHIPAGSFLLLSTYITHRNPEFWDNPEGFDPERFTRERAAARSRYAYVPYAGGPRNCVGMAFANMELTIVVACLLQRFHLDMVPGHPIVMQPDISLRAKHGILMTLRPVTDAGARAVAAPEVTMPEAAPAPAGCPVERDAPDAADPVASSASEPEADVPRCPHRPAETAGSE

>CYP254A1 Rhodococcus sp. RHA1 Rha02824

VTTTQLPDRLIVDFDVYDQTLAMPEDVFQERAAALRAIGPVVYSKAHGGHWIVTRYEEIHQVLRDPETFSSYPNNLVNAGQGKFIPIELDPPEHTYYRQALQPLFSPKRMKELEPRIRDVINELIDDFAARGEAEFISEFAHELPTRVFLALMGWPLEDAEMFTTTTDVALQGVPGGTEEESATAREAAANQIFGYFGAIVAGVRSGEITSDTLTAQIINAPIEMGDGVRLLTDEELYRMFFLLLIAGLHTVQGSLAWAIIHLANNPGQRQEIVDDPDTVSAAVEEILRIEAAVIAGRRATRDVEIGGVTIREGDQLIVLLCSANRDGAEFEDPDELRVDRSPNRHLSFGAGPHRCIGSHLARIELKLAMEEIHKRLPDYRLVPEDPPILHATQVRGCIRLPITFTPAS

>CYP254A2 Rhodococcus sp. RHA1 Rha02853

MTSTQLDLPEHLITDFDVYDPSLAVPADVFQERVAALRKQGPVLYSPHHGGHWVVTRYKEALQVLQDPETFSSFPNNLLNAAQGKFLPLELDPPEHSYYRQALQPLFSPKQMKALEPEIRKIITELIDQFADRGECEFISEFAHELPTRIFLALMGWPLSDAPQFTEWTDITLQGIPGASEAESAEARAKAAGEIYEYFGKVVARVRSGEDSSESLTAQIINTPLDIDGTPRSLTDEELSRMFFLLLVAGLHTVQGALAWGLIHLSHNLEQREAIIDDPTLIPSAVEEILRIETATSSGRRATRDAEIGGVSIKAGDQLLVVMTSANRDNDEFDSPEELQIERHPNRHIGFGAGPHRCLGSHLARLELRLAMEEIHRRIPDYALVPDNPAVFHSSQVRGCEKLPITFTPPTH

>CYP254A3 Rhodococcus sp. RHA1 Rha02973

VFCLKTHDIATDLMVDFDVYDPALAAPVDVFQAKAAGLRARGPILYSPHYGGHWIVTRYDDIFRILRDAETFSSYPNNLVDAGQGKFIPVEIDPPEHTQYRQALQPLFGPARMKELEPKIREIINELIDGFASSGRCEFVAEFAHALPTRVFLTLMGWPLDDAERFTEWTDIALQGIPGAGEEESARARAEAATNVFEYFGAFVDRVRSGQEDGESVTAQIINTPILMDGVERYLTDEELRRMFFLLLIAGLHTVQGSLGWAMVHLANNPAQRNALIEDTSLVPDAVEEILRIEAAVSMGRRATRDVEIAGVKVEAGDQLLLLLCSANRDDTEFDDPDAFVIDRGSNRHLSFGAGPHRCLGSHLARLELTLAMEEIHRRIPDYALVESDPPLMHGTSVRGCVRLPLTFTPEL

>CYP255A1 Rhodococcus sp. RHA1 Rha04605

MTTSTTWIESITMEELDRDPNPIYDRLRREAPVAFVPAVGMHVVASRDLCLQIAQDSETWSTVIAPSGGRTFGKGTVLAANGEQHEKIREWIDPQLRPSAVDSYVEALVRPQARSLLEGIEDLGAADIQEAYFAPISVRSVGDLMGLTEIPSETLVRWFETLAQSYGNAEVDENGNFANPGPFEAGDRVKAEIVAAVGPMLDHWTEHPDHTLISHWLHDGMPDGQVRDRSEIYPNIYVFLLGALQEPGHVMTTTLAGLFQHPDQLERVIDDPTLIPRAVNEGARWVAPIWSAAVKVAGRDVTIGGIDLPTGTPVMLAYGSANRDESVWENAEAYEIDRPIMPHLAFGAGNHACAGTYLGTAIVRIALEALFETIPNIEPDPDRAPQFWGWTFRGPQGLHVTWEV

>CYP255A2 Rhodococcus sp. RHA1 Rha05312

NGEIHRDLRSMVDPALQPSEVDRWVDGLVRPIARRYVEQFENDGKADLVSQYCEPVSVRALGDLLGLNEVSSDTLRDWFHRLSNSFTNAGVDADGEFTNPEGFVQGDEAKAEIRAVVDPLIDKWTVHPDDSAISHWLHDGMPEGQVRDREYIYPTLFVYLLGAMQEPGHGMASTLVGLFTRPEQLEAVIDEPALIPRAISEGMRWTSPIWSATARISTKDVTLGDVFLPEGSVVLLSYGSANHDTAVYDAPSDYDMTRPPLPHLAFGSGNHACAGIYFANHVCRIGLEELFEAIPNLERDSGADVEFWGWGFRGPTALRATWEV

>CYP255A frag Rhodococcus rhodochrous

TSTLSWLDEITMEELERNPY

>CYP256A1 Rhodococcus sp. RHA1 Rha09714

MTTVDEPVLDTTYPFGPVEPTEAAARYAAIAAERPMTKMTMPIGGDVWVIHRESTARAMLADNRFVREPFRTGERPVPYFVEFPDFLKSTIQFEDPPHHTKLRKLVQRSISPKRVRSMRDSAVEFANSLLDAMIEKGAPSNLVEDYAVALPIQMISNLLGVPPEDRPKFQKWSSATLSVADMPQDEVMANMGELVQYMMELIDARRREPREDLLSDLANARDRDESLTDEEILPIALILIVAGFDNTANFICAGVLSLLHNPDQLEILLEDVDGVAPTAVEEVLRHGRFELGRPVAGGGGLVPFVATEDIELDGQMVAKNEAILVDPGSTGHDGAAVEHGEKFDVRRANNPHLTLSYGLHHCLGAPLARMEMQVAISELFKRLPGLALAGDVQIDDTNLTQPITMLPVTW

>CYP257A1 Rhodococcus sp. RHA1 Rha10525

MTVRTELQGIPDLSDPETFKEGIPYEAYDQLRSLPGLPWHPAESGTLNGGFWVVTRYDEVVEILQDPARFSSVQGSIYPLPNPTGDGPMTKHILLMDPPEHSRVRRAAAKSFGPRIVANFESWIRDVVVETLDDALPLERFDWVYEVSRLVPSRVIAQILGIPLEHRGYIVEATNALFESQTVNDGGASLTREFMKIGEFMTRLGEEKLRNPADDMTTVLAQSLESGEIDLVEYQLYTASLFAAGFETTHTTISHIGHLLATEPAIRAATTRALDEGKSAALVDEFLRYITPAMRFARTATQDTEFRDQAIKKGDTLLVVFSAANRDPAAFPNPNEFNPFREDPKPLAGTGGAGLTFGAGAHRCIGHMLAKLELRILLEELHVRNIAIEMDGDAQRGASGLVNQLLALPVTVAVG

>CYP258A1 Rhodococcus sp. RHA1 Rha10666

VLDPFAPGLSVAEADRLHERLRAAGPVVEATDADGLRVWIITRYDDVSRLLADPGIVNVRPGGPSGSPGLPLPPALARNLLNMVPDDHRRVRALAAPAFSRRRIGAVRQMVTARVDGLLDELDPNETGVVDLFPAYASPLPADIIAEILGVTDTDADEFRTAAATVMAMNPGEPTADDPRIPAMTTIVLVLMRVIAAKRKSPGDDVITDWITARDAEDRLTEEELISLAFLTFLAGFENSVYQIANAIGILAGLDRDQLLVEIADDQLWRARVKQLVLDAAPGSYAIRRFPIDDITVGGTRIPAGSPLYLSLRAATNDPARGERPDLAFGRGPHYCLGADLAVMQLDIATRHLFQRHPGLSLVKPWETLDRRHTWRTHGPTEMPVNLI

>CYP259A1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_4259

MLSLGRTDHD SFPTAAGELP VLGHLPVLYR DAIGLLRRSR SALGPLFWVN LGFAQRRLFY

VGADALDLLR APEVVMDHPE HIKGIVGRSM AAQDGPLHRH MRSAINPSFS PQGFAKEAAA

AIASAIAAKI DAWLQQESFA VHPAMRDLTL DIILRICGVP TGDIRAWSRA YRELFLGVYP

IPGRLPGMPA YRSDRARAWI DDRLRKLLAL ARGGGAAGSL VEMLSNARDD EGEPLSDQGI

VDNLRAIVLA GHETSASILA WIVIVLSRRS EVWSALCDEH AAAPDAPVPM SAREADRLPV

ANAIFREVLR MYTPVWFIFR TVTETITLSG RRIPRNTPLA LSPAQFGYDP SLFPDPDRFD

LSRWRDRSIP PGPLELAAFG GGPHFCLGYN VACVEALQLQ FILVRALRRA GLVPHLEGAS

PKHVYFPTGH PTAATRVAFR RC

>CYP260A1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_1461

MADEKAPERE HNQGARADGE RSSGAARRVA AFAAALPRLT LHDDLHSVSS MDFPLANLFF

VPSEDATAFG RRLRAAAQQA PIVFDTAFGM PILLRKSHIT TAYRDTATFS TRMFQAGILN

GGLAAMQGDE HARMRRVYNM FFLPRAVSQY EERFVRPISE QVVDRLAGKP RVDLLEDFAM

ELPRRVIGEL FGFPAEKLHE TDERVRAMLR GLVRMHDPAA VAESQRAYGE TLGLITEVVE

RESRDTSDTL LGEILRTLKA EHMDTIEASR QIVLSLILGG YETTSWLVAN TIHALLAHPD

TLARVRQDPS LLPAAIEEGM RWCPSSFGVL RMVERDVRLD DQALSAGTVV CLAGIAGNYD

ETAYPSPEVY DIDRKPLPAA NVFGGGAHFC VGAPLARMEA RVGLQALLAR FPGLRAVPEE

RPSFMYGAKD SVAHGPDKLP VLLH

>CYP260B1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_4416

MLPRKNLFSF TSKDPSAFGI HLAAAAREHS VYFDEGLGVP VVLRGADVVA VLRDSETFST

RTYDTGIMKG ALVTLGGEAH TRMRRLFNAV LSPRVISRYE EATVTPVARR VVERLVRKER

AELFDDFAIS MPMGVTSALF GLPEERIAEN DALIRKMIRS VVMPQDPVVV AEGRSAHAAM

EAQLREIAER EVAHPSDTLL GEIARAIVAE GLGGVEACEG VVLTLILGSY ETTSWMLANL

LVALLAHPDA MNQLRQQPSL LPQAIEESTR WCSSAAGIVR FVEREATIGG ETLAAGTILY

LSLIARHYDE EIYPRPETFD IHRRPVGMLN FGGGLHYCVG APLARMEARV GVSLLLERFP

ALRADPTVQP TFSTAPRGAA AFGPDQIPAL LV

>CYP261A1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_182

METARAEVAP SAGMRDLSTL PGPRRLPLLG NLLEIRPSQF HLTLEGWNRK YGDLYTFWLG

RTPVVVVGSA ELVQRILRER PKEFRRWSPL QELIDEMGFG GVFSAEGDQW TRQRRLVMSA

FTAGQLRESH GTLSTITRRL RERWRASAAR GAPVDARRDL ARYTVDVTTA VAFGLDMNLI

ERGTDPLSDQ LETVFASLNR RVFAPFPYWR HVKLPADRAL DQALSEVRTR MLDILRTTRA

ELDRDPARAA APRSLLEALL VARDADDPKA RLSEQEVLGN VLTLLLAGED TTADTMAWML

HFMALRPDVQ ARMRAEVDAE LGDADLPESP EHAQRLRYLG AVAQETLRLK SAAPILFMEA

CADTVVGSLR LAAGTRMILL TRQIALKEEH FHDAASFMPE RWLTPRPAGA GKHDPRAALA

FGSGPRVCPG RALSMVESAM VGAMVARDFD VSLVDPARPV KELLGFTMKP EGLFVRFPPR

HR

>CYP261B1 sce5725 49% to CYP261A1

MKGGMNATPP AMEDAIGRGE AAARPRRTLA DLPGPPGLPV LGNLLALHPD RWHLEFERWW

RAHGDLFVVR MGRQPVLVVV DGELVRDVLQ RRPAVFRRVR AIEAVSREAD MVGLFSADGD

AWRKQRQLIH PTFHPRHVEG FFPSIRDITG RLRELWARAA DERAARDVLG DLMRYSVDVT

SSVAFGRDLN TLERGADALQ EHLQRVFLGL NRRMLAPLPY WRYLGLPADR AYDRALVAVK

RLILDLVTAA RREIEGGADR PARPRTLLEL MIAARDGEDP RARLSDAEVY ANVLTMLLAG

EDTTANTLAW ILYYLGSRPD VQARAREEVD RVLGGGLIPT LEQCKRLEYT AAVTQETLRL

RSAAPLLFLE ANHDTAVGDV AVPAGAGVVA LTRATGRKPE YFGDPESFRP ERWLGGAPST

LPHEPRMALA FGGGPRVCPG RAMALLECAV TVGMVLRSFT VHLADHTAPV QERMAFAMQP

EGLRIRFTKR ASA

>CYP261C1 Photobacterium profundum SS9

YP\_133374 46% to CYP261D1, 97% to CYP261C2, 39% to CYP261B1,

42% to CYP261A1

1 mtesvvrenq likrtlddlp qpkgwpllgn flqlqsknlh qvleqwcley gdtykvdiag 61 llfvviadpv vvkdilrrrp ksfnrtasle rvfkelgihg vlsangeswk rqrrlimpaf 121 skkslasffp lleqtterlr lrlvkkrgqd tlaihddlrr ftvdittslv fghdtrlleh 181 dgdglqkhle vifpqlnsrt rmpfpywqyi kfkkdrkldq alievekyal kiveqtrdel 241 qfnpqladap etilqamvaa sdddnrltne elfaniltll lagedttsnl iawmlyfisq 301 rpdiqckine eaeqirlkhk gqinvqglde ltyleavare tlrlkstapm isaetadqvt 361 lldgtelpag tglflmtrlg glnkehfkda eqfrperwqe eavaaeacph katshfpfgg 421 garhcpgetl afmetkmvia mlcqqfdisq pesppvveey aitmrpknlq iclrlkpvgr

>CYP261C2 Photobacterium profundum-3TCK

ZP\_01217946 46% to CYP261D1, 97% to CYP261C2, 38% to CYP261B1,

41% to CYP261A1

mtesvvrenq likrtlddlp qpkgwpllgn flqlqskklh qvleqwcley gntykidiag 61 llfvviadpv vvkdilrrrp ksfnrtasle rvfkelgihg vlsangeswk rqrrlimpaf 121 skkslasffp lleqtterlr lrlvkkkgqd tlaihddlrr ftvdittslv fghdtrlleh 181 dgdglqkhle vifpqlnsrt rmpfpywkyi kfkkdrkldq alievekyal kiveqtrdel 241 qfnpqladap etilqamvaa sddnnrltne elfaniltll lagedttsnl iawmlyfisq 301 rpdiqckine eaeqirlkhk gqinvqglde ltyleavare tlrlkstapm isaetvdqvt 361 lldgtelpag tglflmtrlg glnpehfkda eqfrperwqe eavaaeacph katshfpfgg 421 garhcpgetl afmetkmvia mlcqqfdisq pesppvveey aitmrpknlq iclqlktvgk

>CYP261D1 Moritella sp. PE36

ZP\_01899073 46% to CYP261C1, 34% to CYP261A1 Sorangium cellulosum

32% to CYP261B1

1 mnakmvkgvn spvlptisfd elpgpkqqai lgnftqisae sfhthleqwa keygsayqmr 61 llnkpylvis dpkigleiik qrpklfnrte rlewlfedlg ihgvfssngd kwkrqrrlim 121 pafsyntlan fvpqlkslsi nlqvaidkki atgeafnvhk llqhftidit tslvfgyqtn 181 mlsgssdthl rdnidrlfra lnkrskypfp wwryirtpet rridkareev yqlavsmitk 241 akvvlaensa laeepetilq amivasdsee nkltddelva niltlllage dttsnmlawt 301 lfylaqnpsl qqqvidevsr vcdgdienvd ltaleqfefi dailreglrl kgtaplisae 361 ptedtvlsng iklpkgtaif iltrpgglde kvvacpekfn perwlstpek pvcphlqssh 421 ipfgagarhc pgerlammeg kaviarlcwy yvisqpeqap evgeefaftm rptnlaltlt 481 prk

>CYP262A1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_2000

VVGLLPALAR DAPSLLRQLA RQYPGELIEL DLGLTRAYLA THPEQVQYVL HDNWRNFGKE

GGMWKPIGRL LGNGLVTAGG DEWLRNRRRM QPLFSSRQLA GLVDRMFDVV EGDLPRLEER

ARAGAVVDMD KEMMQLTQRV ILATMFGVSI TPREADSLGE VLLVAIQALN ARMFLYFMPD

RLLPGERALR DAIARIDEAI LRLVRERRRS KEERDDLLSL LLRARDESGS GMDDRQLRDE

LVTMFIAGNE TTAITMTWLF YLLDRNPGIE RKLRAEIEEV VGDRRPTAAD LSRMEYTKMV

IQEAMRMYPP SWLVPRTVKE DDQICGYPVP AGATVILSQY VMHHDPAFWE APAEFDPERF

TPERSASRPR YSYMPFGGGP RQCIGNLFSI MEAQIVIAVL LRRLRMRLVP GHPVSPQAVA

TLRPRHGLKM TLHAV

>CYP262B1 sce1860 41% to CYP262A1

MQPDLLSGTP ARAAAGAAAR GSTPPSTRGF PLVGVLPHLL KDRLDYLLSA REQLGDLYTI

DLGVARLVAL NHPRHAQHVL RDNARNYRKG GAIWESVRSL IGNGLPTSEG DLWLRQRRMI

QPEFHRDRLA AMCDLMVQAI DDGMAGFGAA AAAGRPVNAE RELPHITMKV ILNTMFGSGI

TKEEADAVGG SLRYALDYML LGAALRALPS WIPAPGRRRF ERSAKAIDEH VFRFIAQRRA

QPGRGGDLLS ILLATVDAET GEQMTNQQLR DEAVSMFLAG YETTSVALAW ALHLLVEHPD

LLRALATEVD EALGDRRPGF ADVPRLPLAL AVVQEALRLY PPAYWIPRTA IEDDEIDGFH

IPAGTMVGVM TYVLHRHPDH WEAPARFDPG RFTPEHARAR HPLAFIPFGI GQRQCVGKEF

ALMEGQLILA RLLQRYRISA VPGRTTRLHF ATTLRTSGGV WLRLEPRPGR

>CYP263A1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_4484

MSATLERQPP GPGPLASLRY LANFRTGDMR HYEDLFARHG DVVRLRAPGA EDFVMAFHPN

DIAHVLRTNA RNYPKGKRYH ELAPVLGWGL VNSEGELWRR QRRHVQPQFN HANTLKFVPI

IVEHMEAVLR RWDAQPGEFE RDINDDMMDV TFGIAGEAFF GAALHAHTDT VREAFKYALS

IALKRMYSLV NPPLSWPLPS HLRFRRAMDR VHAVIDGIID GYQRGAGGED NVLVRLMNSV

DPETGAKMDR AQLRDEIKTI LMVGHETSSV TASWALYQLA RHPEVCARLT DEIDRVLGGR

SPTARDIESM PYLTMVFNEC LRLLPSVPFI LRSPLEDDVI GGYKVAAGST VAIVPWVTHR

HPEFWSDPLE FKPERFANHR RSADDKLAFI PFGAGQRICL GEFMGQLEGK IMVAMALQRY

RLRLVPGFDP RCRGFISLQP VNGMRMILKR REPSSAVRAA PAGREEPAGA EPVVTEPVAA

AMSAHGCPYS ARA

>CYP264A1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_5791

MSERVDIMTP AFRADPYTPY AAMRREAPVC QVDPGGMWAV SRYADVATVL RSPERFSSQG

FRAAWQPAWV GHNPLASSIL AMDGPDHARL RGLVSRAFGA PAIARIEQRA RDLCERLAGR

LDGEVDFIAA AAAPLPAFVI SELLGLDHAL EPHFKRWMDD LLSVTPEPAS AEHAARVRAT

IAELDRYMAD VIAARRRSPS DDLVSELARA GELLGDREII DLLVSILGGG LETTTHFLGS

SMLLLAERPA ELERLRASPQ LIPRFIEEMM RYDGPTQSVP RLTTSDVALA GVTIPAGSLV

LALVGSANRD EVRFTDPDRF DLHRGQPSLT FGHGAHFCLG AALARMEAKV ALEVLVPRIG

EVTRAPGEIP YNRTLTVRGP VSLPLRFRPA

>CYP264B1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_7808

MTRLNLFAPE VRENPYPFYA ALRRESPVCQ VDPNGMWVVT RYDDIVAAFK NTQVFSSAGL

RMATEPPYLR RQNPLSGSMI LADPPRHGQL RSISSRAFTA NMVSTLEHHM RSMAVRLTDD

LVHRRVVEFI SEFASRAQVS VLAKLIGFDP GLEGHFKRWA TDLVIVGVIP PEDHARIAEV

RRTIDEMEQY MLGLLASRRR HLENDLVSEL LRSRRDDDGI TDQDLVSLLS LLLVAGLETS

TSLMTHMVLI LAQRPMWMDR LRAEPALIPH FIEEVMRFEA PVHATMRLTV TETELGGTRL

PAHAVVALLI SSGLRDEARF QEPDRFNPER GDQANLAFGH GAHFCLGVFL ARVQARIVLE

ELLRRCHRIV LRTDRLEWQA ALNTRSPVAL PIEVIPVSTT AARESPVVQG IW

>CYP265A1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_7503

MSTPHTLQPD DLMEEGGDVV RRAQEACWYA ETSMGKAVLR YREVHDLLRD ARFRNMGTDV

LTRQGVTEGL VRRMYEGFLL STEGAAHARL RGLLKKGFTP DAVDALRPRM RERMHALLDE

IGDRTEFDFV TAVAERFPGQ VIIELLGLPV SFEDPDFRRW CSDLGYIVGL EVKKHLPRLE

AAFEGLRGYI EPTIAARRAE PRGDLISTLA AAEQNGDRFS EEELVCQIVA LLFGGLDTTR

RTIGKAFLVM LEHPDQRRLL QERPDLAEPA AEEILRYAPG TRVAVRVATC DLELHGVPIR

AGEMVIAATG AANRDPRVFE APETFDITRR GAAPLSLGAG PHHCLGAYLA RAELQEAVPI

LTRRLTEAAL ASPVVVRTAR EGSPGPRVIP LRCRVRPR

>CYP266A1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_5168

VETQVAATQP EINIIAPENL RWPYPMFRRL LLEEPVFYDK NTGSWVVSRY EDVNALLRDA

RMSADRYVAL ADTVPPEQKE MNSYIVKSLS MFMLNVENPT HFRLRNLTNR SFTPKSIAAM

RPSAHAVVNE LLDAVQPRGH MDVVADLAYP MPIKFICGIL GMPVEDMGLI KQLSDDVSVY

IGSAGKAAGC IPPAYHAIVE FSKLFRPLVE ARRKEPKDDL ISSMVTTRVD GDSLSDDEVI

ANCILFLVAG FETVTNLIAC GTLALLEHPD QLELLKRDSR LMEGAIDEML RYYPPVNRTA

RLCVEDIPLR GKVIKKGQIV VLMLGAGNRD PSEYPDPDRF DIARENRSRP LSFGGGHHFC

IGSHLARMEG EVALGALLQR MPNLRLATQE VEWRGNSRFR GLRALPVSF

>CYP266B1P sce6630 only the C-terminal, probable pseudogene

MGQAPATCTA ASPVAAPSSR GVAGRARSTG AYRSCPSPAA TDWTGHGHDR RRGGSGVRRN

CHLEPDRFDI TRQQSRHLTF GSGAHYCPGA SLIRMEVEES VRALLSLPRW ELAEETLSYA

GSNLQDRGPS SLRV RFPAAC SGRARPIGRR AAGR

>CYP267A1 Sorangium cellulosum So Ce56 (myxobacterium) sce\_040811\_619

MNSPDAPKPD APPAANPAAD ADLDPFRLQS PETLANPYPV YARLRQEAPV YFSAAYNGWL

ITRYDQVAAG FRDPRLSAKR SSAFVTKLPD EVRQRLEPLR RNLASWALLL DPPEHTRIRS

LINKAFVPRL VEGLRSRVET LVNELLDAVA PAGRMDVLRD LGDLLPLLVI GEVLGVPAED

RHRLKGWSNA LSGFLGAGRP TLEIAGGALS AVAELEDYFR GVIAARRQSP GNDLLSQLIL

AEEQGMILGE QELLSTCCML LFGGHETTKN LIGNGLLALL LHRSEREALR ATPSLIGPAV

EELLRYDSPV QWMSRVALDD IELDGVRIPK GDRAFLVLGA ANRDPAQFPD PDKLDFRRTD

IRHISLGLGV HYCAGSALAR VEAQAAISTF LRRFPDAELS PGPLTWRMNP GMRGVTALPI

ELGPQSSAS

>CYP267B1 sce7167 (CYP107 related) 43% to CYP267A1

MVDQDAFPEL FHPSSRAEPH AIYARMRAAG RLHRLVHPRL DVPIWVAVRY DDCVELLKDP

RLIRDFRKLP DEVRRRYFPL SDRTTFMDQH MLDADPPDHT RLRAIVQRAF SPRMMEGLRP

RIQEIADGLI DAVIDRRRME LIADFAFPLP TAVIAELLGL PVEDRGRFRR WTKILLAPAK

DREFVERAQP VVEEFAAYFR ALADARRKAP RDDLISGLLL AEEQEHKLSP AELSSMVFLL

LVAGHETTVH LIASGMLLLL SHPAERRRLD EDPGLVGSAV EEALRCEGPA ELSTIRWSLE

DIELFGARVP AGEGVAAGLL AANRDPQHFP DPDRFDIGRS PNRHIGFGGG IHFCLGAMLA

RIEAAIAFST LLRRLPRIEL ATSTRDIVWS EWPTIRGPAA VPVVF

>CYP268A1 Mycobacterium avium subsp. Paratuberculosis

MTGVIAERIGIMAVLTGESGTDRSGRPYDEIDLSSRAFWSGTAA

ERERSFAVLRAERPVSWHPPVEDSLLPDPTDPGFWAVTRRADIVTVSRNNDVFLSGHG

VMFESIPAELLEASQSFLAMDPPRHTKLRKLAHAALSPRQVRRIEDSIKANAKAIVEE

LRSAGSGCDFVDHCAKELPIRTLSDMMGIPESERERMAHATDALVSWADPEFLNGRPA

LEVLLENQMYLHQVVGDLATQRRERPGDDLISSLVTAEVDGDRLEDAEVAAFFVLLSV

AGNDTTRQTISHTLRALTVFPDEKFWLLEDFGHRIGTAVEEFIRWASPVMTFRRTAAA

DVELGGQTILAGEKVVMFYPSGNWDTEAFDHPERLNLGRDPNPHVGFGGGGLHFCLGA

HVARAQLRAIFSELFRQLPGIQAGEPTYLAGNFVHAIRAMPCTF

>CYP268A2 Mycobacterium marinum MM3761

MTAISASVRP YDTIDLSSRA FWASSASQRE SSFSELRAER PVSWHPPVED ALIQDPNDPG

FWAVTRRADI VAVSRTNEVF LSGNGVLFEN VPAELLEASQ SFLAMDPPRH TKLRKLVSAA

FTPRQVRRIE DSIKINAKGI VDELRMAGGG VDFVEHCAKE LPIRTLSDMV GIPEADRERV

AHAADALVSW ADPRYLNGRE PLAVLFENQM YLHQVAASLA AERRDRPGDD LFSALVNAEV

DGDRLADADV AAFFVLLAVA GNDTTRQTIS HGLKALTDFP SQKAWLLADF DTRIGTAVEE

LVRWATPVMT FRRTAAADFE LGGQLIRAGE KVVMFYASGN WDEDAFCHPE RLDLSRSPNP

HVGFGGGGVH FCLGAHLARA QLRAIFGELL VQLPDIQAGD PVYVPGNFVH AIRSMPCTF\*

>CYP268A2P Mycobacterium ulcerans

MTAISASVRPYDTIDLSSRAFWASSAAQRESSFSVLRAERPVSWHPPVEDALIQDPSDPG

FWAVTRRADIVAVSRTNEVFLSGNGVLFENVPAELLEASQSFLAMDPPRHTKLRKLVSAA

FTPRQVRRIEDSIKINAKGIVEELRMAGGGVDFVEHCAKELPIRTLSDMVGIPEADRERV

AHAADTLVSWRTPAT\*VLFENQMYLHQVAASLAAERRDRPGDDLFSALVNAEVDGDRLAD

ADVAAFFVLLAVAGNDTTRQTISHGLKALTDFPGEKAWLLADFDTRIGTAVEELVRWATP

VMTFRRIAAADFELGGQLIRAGEKVVMFYASGNWDEDAFCHPERLDLSRSPNPHVGFGGG

GVHFCLGAHLARAQLRAIFGELLVQLPDIQAGDPVYVPGNFVHAIRSMPCTF

>CYP268A3 Mycobacterium smegmatis

MTVLPITRPYDAVDLSSRAFWATTAADREVAFAQLRAERPVSWHPPVEDA

LMHDPDDKGFWAVTRHADIVAISRDSETFLSGQGVLFENVPQELLEASQS

FLAMDAPRHTLIRKLVHSAFTPRQVARIEDSIKANAAAIVAELKAAGSGV

DFVDHCAKELPIRTLSDMVGIPEGEREKVAHAADALVSWADPIYLAGRHP

LEVLLENQMYLHQVANTLAAERRENPGNDLISALVHAEVDGDRLTDAEVA

AFFVLLAVAGNDTTRQTTSHALKALTDFEDQRAWLMEDFDDRIGVAVEEM

VRWASPVMTFRRTAAVDVELGGRQIAAGEKVVMFYASGNWDTTVFDRPDV

LDLGRKPNPHLGFGGGGRHFCLGAHVARTQLRAIFGELLHQLPDIRAGEP

EYLQGNFVHAIRAMPCTFS

>CYP268A4 SBI\_1278 Streptomyces bingchengensis

53% to CYP268A2 Mycobacterium marinum MM3761

55% without the small insertion

MDAPRAVHAGEKRYDSVDLSSLAFWSQTAEERERSFALLRAERPVSWHRP

VEGRLLPDPDDTGFWAVVRHEDIMTVSRRTDLFASSAGVLLENIPEGLLE

GSQSLLAMDPPRHTKIRRLVSGAFTPRHILGMRKRIEAHARRIVGELARR

PDGRADFMRDCASLLPMRVISDVMGIPREWQDTVAATVSQSISGSGTDGE

DGEGGERGERGEGGDEQSPLELLIEGNRRLRAMALNLAGLRRGRPAQDLM

TVLVQAEVDGDRLTDDDIADFFLLLCLAGNDSTTQTIGHGLRLLTDLPEQ

RAWLLAGLDGRIGPAVEEILRYATPVLTFRRTAVAPTRLGGRHISAGDKV

VMFYASGNRDAAVFREPGRFDLARDPNPQLSFGGGGAHYCLAAQLARAQL

RILFRELLRMLPDIEAGEPEFVTGTSIHGMTRLPCRFTPHA

>CYP268B1 Mycobacterium vanbaalenii PYR-1

MSGSPDRRRSADHDHPAAVAACRQLYKLTVKCHANSVTAPSLHEREHSAIDITSHDFWSRPFAQRDESFA RLRAGDGLSWHAPFPSLFPMEEPGYWAVTRRADIAYVSQHPELFTSERGVALDPMPAEVQRFASFFLTMD PPQHTTYRRLISSAFTPRNVRQIEEQIQRNAVAIVDDLVGAGDIDFVADCSARLPMLTIMEMLGVPGADQ PAVALAAEKLFSMSDDEYSSLEERAANTLNEIMLLSSTGAELAKFRRAHPGDDLMTGIVNAEVDGQRLTD EEIGAFLILLASAGNDTTKQTTTHAMMALVENPQQRAWLMADFDGRIGAAVEEFVRWSSPVLQFARFATR DTEINGQPVAEGDKVGLFYCSANRDEAVFDNPAGFDLSRSPNPHLGFGGGGPHFCLGNQLAKAELRNLFR

ELLTRLKTVEFGEPDLLHSSFVHGVKRLPAHVR

>CYP268B2 Mycobacterium smegmatis

MTVASSAQAREYSPFDITSHEFWSRPFAVRDETFAQLRAAEGLSWHQPLS

TLFDVEEPGFWALTRRADIQFVSQHPELFTSAQGVALDPMPADVQKFATF

FLMMDPPEHTVYRRLISSAFTPRNVRRIEEQIHANAVDVVDQLIGVGNVD

FVEACSAQLPMRTISDMLGVPKADQPALAKAAEKLFSMSDDEYSSLEERA

VATINEIMLISNTGVELAKFRRANPGDDLMTSIVNAEVDGHRLTDEEIGA

FLILLASAGNDTTKQTTTHAMMALAAHPDQRDWLMADFDGRIGPAVEEFV

RWATPVIQFARFATEDVEVAGQTIRAGEKVGLFYCSANRDEAVFTDPQRF

DLSRSPNPHLGFGGGGPHFCLGNQLAKTELRNLFRELLTRLKTIEFGEPE

LLHSSFVHGIKRVPAYIR

>CYP268C1 Mycobacterium vanbaalenii PYR-1

MQIDEYLAATSDNKPDHCDIDISRKAFWARPADEKMEIFAALRAEHPVSWQRPIEGAVVPDPDDPGFWAV VRHADIRQVSHDNRTFISGQGVMFDRLPPLFLEMALSFLAMDPPRHDKLRRLVNKAFTPRQITRIEDKID LVAKEVVDGFIADPTGEIEFMDRCASRLPLRMFCEMFGVPDHLEERTVEHVIGSVSWSDEEILAGRSAAD MQLESIGGLHQVAQEIIEMRRQQPGDDIISSLVHAEIDGQMLTDFEISSFFCLLSGAATDTTKTTLGHAV RALSLFPEQHAWLLEDFDNRIGTAVEEFIRWATPLLTFTRTAAVETELGGRRIMPGDRVVMIYQAGNFDE DVFDRPRELDLARSPNPHVSFGGGGVHYCLGANLARSMLRAELRELLLRITEFETDAPDMLATNFIHGLK RLPFRFTPQ

>CYP269A1 Mycobacterium marinum MM3969

MAYPETNTAT DYPFTQPDAL SAPRDLGKLR QRCPVADVRF PSGDPAVVVT RYDDAKRVLD

DPRVSRNMYR ADAARLSTTQ LNMLELEFVS TLVDPPNHTR IRRLFAKALR RGRIEELRPR

IVTIVDELLD AMLAGPMPAD AVDALARPLP RQIIGEMFGF PPGEGDRAQY WAERLFSLSL

HTAEEMAAGQ QEFAAFICEL AEKRRAEPTG DFFSDLVAVS DVDDGQLSHL ELVYLAQALF

AAGIDSTWVM ISRMIGLLLH KGCYGRLVAD PKLIEPTVEE VLRYLPPSNL GALRYAVEDI

ELDDAVIPKG TTIAVSTTAA NRDPRFFDDP DEFLVDRSEN RHVSFGHGRF LCPGAWLARC

EMQSLLRGLV TRVPTLELAA DVNDLKVRTG MMNEGMLSLP VRW\*

>CYP269A1P Mycobacterium ulcerans

LAYPETNTATDYPFTQPDALSAPRDLGKLRQRCPVADVRFPSGDPAVVVTRYDDAKRVLD

DPRVSRNMYRADAARLSTTQLNILELEFVSTLVDPPNHTRIRRLFAKALRRGRIEELRPR

IVTIVDELLDAMLAGPMPADAVDALARPLPRQIIGEMFGFPPGEGDRAPILGGAAVQPLA

PHGRGNGRRPAGVRGVHLRAGRETAGRADGRLLQRSSRGVRRRRRAAQSPRTGLPRTGPL

RRRHRLHLGDDLPDDRSTAAQGLLWPGGC\*LSSPATTMPSECWTTLESAGTCTARTPPGC

RPPSSTSSSWSSSRRWLTRPITPGSAGCSPRHCAGGESKSCGRGSSRSSMSCWTQCWPGR

CPPTPSMPSPAHCRGRSSARCSAFHRARATAPQYWAERLFSLSLHTAEEMAAGQQEFAAF

IYELAEKRRAEPTGDFFSDLVAVSDVDDGQLSHLELVYLAQALFAAGIDSTWVMISRMIG

LLLHKGCYGRVVADPKLIEPTVEEVLRYLPPSNLGALRYAVEDIELDDAVIPKGTTIAVS

TTAANRDPRFFDDPDEFLVDRSENRHVSFGHGRFLCPGAWLARCEMQSLLRGLVTRVPTL

ELAADVNDLKVRTGMMNEGMLSLPVRW

>CYP271A1 Mycobacterium marinum MM0274

MEGNERFVPR LAPLTLAVKS LANPQFIYNA KAQGVRAERT EAGVVTLYRR DDLMRISRHP

AVLGPGGRGG NFGNDNPLIP LEIDGEEHKK WRRLLDPLFA PKQMARLEAA VRNRAAQLVD

GFASQTSAEL YQAYCAPLPC FTFLELLGAP LEDIEFFTAF KNGVLHPQGE TREEIQANQA

AAGAMLLEYF TRLVARQRAE GAQGEEVLAV LLRSRIDGQP LTDAELFNII HLLIFAGLDT

VTASMSCILA WLGQHPHERR RLVEDTARIP AAIEELMRYE SPAPSGIRYA TADIDLGDGL

TIRAGEAIHV SWAAANVDPT AHPDPLHVDF DRARFHHLAF GSGIHRCLGS HLARLELRVA

LEEFLARIPD YAVDTAGLVY DNVSVRTVQQ LRITFNANTP SPVDPSQRHA FMAPLTGQRD

SVLERNGHEH R\*

>CYP272A1 Mycobacterium avium subsp. paratuberculosis

MTEAGGFVDQTVTGVAEPQPMYKALRESNPVFRSTQAVVLSRLA

DIEMALKHTELFSSNMDAVDLGNVRPLIPLQIDPPDHAKYRRILDPLFTPREMARREP

LVTELVNEMIDRFAPRGECDFHAEFAVPLPCTVFLQLLGLPLEDLDRFLLWKDGVIRP

AGDSGFDRRHESSAGVAQQIYEYFDKAIDEHIAVPRDDVLSAMIAADVGGQPLSREEL

LDICFLFLIAGLDTVTDSLDCFFVYLARHPQHRRQLVERPDVLPGAVEELLRWETPVP

GVARVATQDVEVGGCPISKGERVSPLLGAANTDPAEFPDPEIVDFTRSPNRHRAFGGG

PHRCLGSHLARMELRVALREFHRRIPDYEIRPGTQLTYTAALRSVESLPLVFPVR

>CYP272B1 Frankia alni ACN14a

MPDDTAGAAAPADGGHGLRAATLDWLEFERQRAEDPRAYFSRLRAKCPVDYDEGHEGWIQILRRAEIDEV

LRNPEVFSNLIPELMSSPLPAIPMGVDPPDHAKYRRILDPLFSPRRMAALEAEVVANTVATIESFLDRGS

CDFATDLAVPLPCSVFLTLFGLPQSELPGLLHMKDALIRPESLTDDPDEKLRIQTEAGTQVFTLFGTVLA

QRRAEPRDDLITELLKAEIEGRPLTEPELLGICFMLMMAGLDTVTISLTCILAYLLEHPEARQRIVADPE

TIPAIVEELLRWETPVMAVPRIVTRDTEVAGCPVRKGEMVHVMLASGNLDPDADPRAGVVDLDRADKRHL

AFGGGPHRCLGSHLARMELRTVLREWHRLIPEYSLAPGASITWNGSTLRGLDSLALTWPTDAGQA

>CYP274A1 Mycobacterium marinum MM0283

MTVAGSPTLR TPPVAPGRLP GLGHLSALAR DPLGYLARLR SVADVVTIYL GPRPSYLVTS

HDLVRDMLVS QSECFTRGAV FERAGKALGQ GLLVSDGEFH RCQRRLLQPA FHHRQTPRYA

EVMADAAQTL SRAWRPGVPI EVTHEIHTMA LAVVCRGLFH TDLGGSAVSR VERALTGINQ

GVIWQTLYPF DWLARLPIPV NRRFRSAITD VRDLVTQLIS ACRTTGEGRE GVLAMLLQAR

DEETGRPMSD DQVRDEVLTL LLAATETSST TLSWLFYELD RHPEIERGVA RELDDKLANQ

SITHDNLRDL DLMKRVVDET LRLHTPNSIL TRRAVREVQL GQFRIPAGAE VAFSPTAIHR

DPTVYDDPLS FKPDRWLSEN SAHVPRHMFI PFGMGKHKCI GDSFAITEMH VTAATVLRDW

RLSLAPNAHV RERPWAIVQP HGLRMIPFPR R\*

>CYP274A1 Mycobacterium ulcerans

VYDDPLSFKPDRWLSENSAHVPRHMFILFGMGKHKCIGDSFAITEMHVTAATVLRDWRLS

LAPNAHVRERPWAIVQPHGLRMIPFPRR

>CYP276A1 Mycobacterium marinum MM1564

MTDTMLARFD PHDQQLRDDP YAVYATYRQA DPVHWGQPFK PGDNGCWYLF RHDHVVAMLR

DPRFRRKLVP ADPLASGRVF GAPRGFAELS GRLLLSLDPP HHGRLRSIVA PTFTPSAIES

YRMIAAKAAD RLIDGLDEAT AFDVIDNYAV PLSMTLIAAM LGLTADELHP DLPVWVSRFG

DGFDLRKEPA AIARADDAAA NMLWFFETAA ASHDRLRPGL ISALIAAREA GQLTHEELLA

LCVQLMFAAH GTTVAQIGNM IADLWTRPDQ LALLRAHPEL MAAAVNESLR FNGSVQSTAA

RKPIEDVTLG GAHIRAGQPV IAFVGAANRD PKVFEEPDRF DITRARGAAV MFGAGIHYCL

GARLARLECQ IAVGTLMRRL PRLKLTERTQ LHRHTNIVLP ALLHLKAVTA A\*

>CYP278A1 Mycobacterium marinum MM2877

MSTETVSGTV PAVELLTTPQ GIANPYPLYD ELRGLSPVAG YRDWPPGTVP GADEPVTAWA

LFRYDQVFAA ARDAATFSSR DPLQEASSAP SLMLVNTDPP KHEVERKLVS QAFSPRRVKR

LEGWLDDLIP QLLNDLEKDS RDGAEDGSPD GVVEVMGFAA EIPTRAMVRL LGLPDGDHVR

FRRWANAFML SSSLTPEERM ASNQEMVGTF ATRLAEHTAR LAEREASDDV EDAEDLISAL

LRAEVDGQRL TPEEIVRFCV TLVVAGSETT TFLIGNLLHA LAREPEVQAR VRADRTLLNI

FVEETLRLDG PPQRLFRIAT RDVEVGDKLI RKGEWVALFF GSANRDPAVF PDPGRLDIDR

PNIRQHLSLG HGLHFCLGAS LARLEVLAVL NAVLDRYQKI ALTDDPGTKQ TASLLTHAFV

RLPLHLS\*

>CYP278A1P Mycobacterium ulcerans

MSTETVSGTVPAVELLTTPQGIANPYPLYDELRGLSPVAGYRDWPLEPSRAPTNRLPPGR

CSATTRSLPRRATRQPSRPAIPCRRRRRRRA\*LQEASSAPSLMLVNTDPPKHEVERKLVS

QAFSPRRVKRLEGWLNDLIPQLLNDLEKDSRDGAEDGSPDGVVEVMGFAAEIPTRAMVRL

LGLPDGDHVRFRRWANAFMLSSSLTPEERMASNQEMVGTFATRLAEHTARLAEREASDDV

EDAEDLISALLRAEVDGQRLTPEEIVRFCVTLVVAGSETTTFLIGNLLHALAREPEVQAR

VRADRTLLNIFVEETLRLDGPPQRLFRIATRDVEVGDKLIRKGEWVALFFGSANRDPAVF

PDPGRLDIDRPNIRQQLSLGHGLHFCLGASLARLEVLAVLNAVLDRYQKIALTDDPGTKQ

TASLLTHAFVRLPLHLS

>CYP278A2 Mycobacterium vanbaalenii PYR-1

MTMSSTTASALELLTTASGIADPYPLYNQLRRLSPVAGYRDWPPGTIPGADEPVTAWALFRYDQVFEAAR DSATFSSRDPLQEASSAPSLMLVNTDPPKHEIERKLVSQAFSPRRVKRLEGWLGELVPRLLEDLGSGEVD VMEFAAEVPTRAMVRLLGLPDGDHVRFKRWANAFMLSSSLTPDERIASNDEMVAAFAGRLTEHTARLAEQ APTDDVEDAEDLISALLRAEVGGQRLTPEEIVRFCVTLVVAGSETTTFLIGNLLHAMARDPETTARMRAD RALLNVFVEETMRLDGPPQRLFRIATRDVEVGGKLIRKGEWVALFFGSANRDPDVFADPNVLDLDRPNIR QQLSMGHGLHFCLGASLARLEVMAVLNAVLDRYRTIALTDDPGTKQTASLLTHAYVRLPLHLS

>CYP278A3 Ectocarpus bacterium 54% to CYP278A1 Mycobacterium marinum MM2877

302460 MADDIAALVADLPSGDTIAN

302400 PYPLYTRLRPHAPVQGYRDYPPGTVPGEDEPVNAWVLLDYDQVSKAARDHRTFSSRDPLQ 302221

302220 EGSSAPTLMLVNHDNPEHDRLRNIVNLAFSRKRIEELSPYVSKMVHTLLDEVESASGGKV 302041

302040 EAMSDICAALPARVMVHLLGLPNEIAAKFRHWGTAFMLSADLTPEERQTSNV 301885

301884 ELYTYFVEQVTAMDEALAAGKDVPDSLMRALLTAEADGEKLTRDEVIRFCLTLVVAGAE 301708

301707 TTTFLLGNLLHHLATMPEMTERLRANRDDIEGFMNESLRHSGPPQRLFRIAEADVEVGGQ 301528

301527 QIRKGDWVALFFAAANHDPAMFPDPEKFDIDRTNLNKQLTFGVGVHHCLGSALAKAEARE 301348

301347 LMNALLDRYGAITETGSGSEPQRASLLNHGLATLNLHLTPKIKDAAQ\* 301204

>CYP278A4 Parvibaculum lavamentivorans DS-1 CP000774.1

CDS complement(3745637..3746905) locus\_tag="Plav\_3499"

35% to CYP107L1 AF087022 Streptomyces venezuelae

MQEIRKSDRADDLAALVAALPAGDTIASPYALYDRLRPYGPVYG

YRDYPPGTVPDADEAVTAWVLLNYDHVSAAARDHRIFSSRDPLQEQSSAPTLMLVNHD

NPEHDRLRSIVNLAFSRPRIEALDPWVREIVGGMVAGLGDGDTEVMEALAARIPARIM

VGLLGLPEEVVDRFRHWATAFMLSADLDPAEREASNAELVRYFTETVDSLYGALEAGD

PVPDGLIAALLKAEVDGEQLTLDEVIRFCITLVVAGSETTTFLLGNLLHNLAVMPDIR

AQLAANRALIGPFIDESLRHSGPPQRLFRIATQDVEVGGARISKGDWVALFFAAANHD

PAMFPDPEKFDISRPNLNKQLTFGVGIHHCLGSALARMEGRALIEAILDRMDDVSLGA

LPPVPQRASLLNHGFDSLTLRFTAREDETQ

>CYP278B1 JCVI\_PEP\_1096680833653 seawater sequencing

VAVAEMAIQAARLNSPEVIANPYPYYDQLRAASPVHGYVDLPPGTVPGQDEPKISWAVLRHADVVEA

ARDAQTFSSADPLQAESTAPTLMLVNDDPPRHSKLRAIAHKAFTPRRILEKGPWVAQVAAEILAPCG

GRCFDFMTDVAPVLPTRVMAKVIGVDDAQAPRFRNWATAFMLSADLTPAAREASNREVAAFFVDHVN

RRYALIERGGDPPDDLVTALILEDSDGQRLTRDEVTRFCITLLVAGAET

>CYP279A1 Mycobacterium avium subsp. paratuberculosis

MTVGAAPPSVFDSDLPTLHYHSDETPAQVYPRLREAQRRAAVAI

GPHGPEVLSYHLVRSVLRDPRFQIPPGINLLAQGIDSGPLWDKVANSLLCLEGDAHHR

LRSLCSKAFTPRTVARLHDTMAAVMNELVDRVAAAGRCDVVTDIARPYPVPIICALLG

APREDWRRFSSWADDVFKAFSFTVDLREVEPVVMRAWRELDDYVDEMVARRRHNLTDD

LLSDLIRVGDEGDRLDAAELRMLAGGLLLAGTDTTRNQVAASVQVLCEHPDQWELLRQ

RPELAMRAVEETMRHSPIACGTLRLVVEDAELDGHLFPAGTAVLVNTFAANRDPVVYN

DPDRVDITREAAPPILTFGGGVHYCLGANLARREIAEALNVLANRLRNPRLAGPAPWK

PMVSLSGPTSLPIEFDR

>CYP279A2 Mycobacterium marinum MM0122

MTSTVDRQVA PNVFAAGLPN IDYQNAQSPD EAHQILAEAR CRSPIALGPH GPELLTYDLV

HTVLRDPRFR MPPGMFLAAQ GITSGPLWDR LAANLISLDG PAHHRLRRLV SQAFTPRATG

RLNTTITEVI TDLVDRCADR GRCDVVADIA RRYPIPIICA LLGAPAGDWK LFSGWTDDIL

KAFSWDAAAQ QPAILAAWDE LDAYIDDMVA ARRGSLTEDL ISALIRAEDD GDCLSSDELR

MLVAGLLIGG TDTTRNQLAA SAQALCDHPD QWVLLAQHPD LAANAAEETM RHSPITFSTL

RIALDDVELA GVMIPTGTLV IANTGAANRD PALYRDPDRL DISRPIAGPI QTFGAGMHYC

LGANLARREL TEALRIITQR MPGARRTGAA PWKSLTGLSG PTTLPIEFDA GH\*

>CYP279A3 Mycobacterium vanbaalenii PYR-1

MSGDYVRDSARDHAFPCPYPPHGHTLFSIRKSNRPGSEATMVVSPTVANVFDAGLPTLTYDVFSTPAQVW PDLHDAQRTAPIAIGPMGPEVLSYEMARAVLRDTRFTIPPGINLAAQGITSGPLFDKVMSTLLCLEGSEH QRLRKLVSKAFTPRATERLHDTIVAVVDELVDNIAGARRCDVVADIARPYPIPIICALLGAPREDWRLFS DWTEDVFRAFSFSTDVATVQDDVMRAWNELDDYVDRMVAHRRRHLTDDLLSDLIRAEDDGDRLSTSELQM LAASLLMAGTDTTRNQLAASVQALSERPDQWALLADRPELAMRAVEETMRHSPVVCGAPRIVLDDVEFDG YLFPAGTFVFVNTFAANRDPAVYADADRLDLTREQAPAILTFGGGVHYCLGANLARRELAEALRILAGRL

SNPRRSGSAPWKPMLGMTGPTVLELEFDA

>CYP279A4 Mycobacterium vanbaalenii PYR-1

MALPHSRLRTRTRLRPRDHLAVGDVHAAHAAADPDEEDAVTAAATKPSVFDAGLPTLSYDVTDTPQQIYP QFRAAQRIAPIALGPIGPEVLSYEMARTVLRDPRFVIPPGIHLSAHGITSGPLWDRVTRSILNMEGDEHR RLRSLVSRAFTPRATARMHDAIHLVVNELLDAIQDTGRCEFVAEVARPYPIPIICALLGAPREDWQLFSR WAEDIFKIVSFDCDLAEEEPVVLKAWAEFDDYIDGMIADRRRHLSDDLLSDLIRIEDGGDRLDAAELRML AFSVLVAGTDTTRSQLAASVQVLCEHPDQWALLRADSDLAMRTVEETMRHSPSMCSTVRSVTADVEVGEY TFPAGTFILVNTYAANRDHTVYDDPTRFDITREDPPPILTFGGGVHHCLGANLARLELAEALKILSHRFR

YARRTGPVPWKPLLGLSGPTSLPLEFGP

>CYP279A5 Mycobacterium smegmatis

MTRMTVAELTPISYHHATMPAEVHDIIRQARANGPLALGPYGPEILGYEL

VRAVLRDERFEVPRGMFLAAQGITSGPLWERANNTLVGLGGPAHLRLRRL

VARAFIPKAAERLRATCVDIVTELVARCVPAGRCDVVADLAVPYAVPVIC

ALLGAPARDWARFSAWADEIFKMFSWDLGEHAEAVETAWKELDAYVDDMV

VRRRHTLTDDLLSDLIRAEDDGDRLTHHELLMLAGGVLLAGTDTTRNQLA

AAVETLCDHPREWDLLAEHPELAPTFVEELMRFSPATLGTVRIAKEEVEI

AGVTIPAGTLVTVNTAAANRDPQVFADPDRFDVHRRASPPMLGFGGGLHY

CLGVHLARVELAEALCVITAAMRHPHRDGPPPGNR

>CYP282A1 Streptomyces scabies SCAB14541

MDVTKSIDEH VKHFDIRDTA FDDPELVYKV YEAMRTIGAI VPTDQLDFSG RFKETLQVIG

YAECHQLLKD WRRVSNDPRK AFDNLSEIER RSDLPVDDSA TPISTDPPVQ KELRKVLSPS

FTPERMVALE PKVRAVANRL IDEFIEEGKG DLADFSWKLP SEILFAEFLG FPAELLGEAL

AAQGASLLAS DAAERDQSAA RVFELIADVL KERVGQPPRD DIIDGLLNSE IGGRPLTVGE

RMANATLLVA ASLETTSNAL SAAYYWLAHH PAERSRLVAD PSLLPAAVEE FVRYSGSVHG

LPRYITADVE ICGYGFKRGD AVIVNYAAAN RDENEFADAG KCIIDREPNR HLGFGFGTHR

CLGAPLARLE LRVGFSEVLR RLPDYRIANE DTCEFSGSSF TRGYQALPVA FTPGRREHS

>CYP282B1 Mycobacterium vanbaalenii PYR-1

VTRTPERHAENWDLRHPDFNDNDFLYDVYAVMRAKSPFARTDNPFLSATPAGAWVAVRYA 261343

261344 ECVQILQDWEHFSSNPTPEGAEQLAGDLVITLDPPRQQKFRKVLNPYFS 261490

261491 PARMKALRPEIGVETDRLIDDFIETGSGDLAAVAWRQPGIVFFKYLLGMPVDDVPLCV 261664

261665 ELTDTALNGATEQDRMAAWGGLYQHLHDAVTARRGQPPRDDMIDVLLSAEIDGEKLAFAD 261844

261845 VVSNAMLLVQAGLETTASAMSFAYHYLATNPAERDRLIDDPDLLTRAVEEFIRFAGSIHG 262024

262025 IPRTVAREVELSGCTFSPGESVIVNYAAANRDEQEFPDAHRCILDRRDNRHLGFGAGVHR 262204

262205 CLGSNLARLEFQVGLERVLTRMPDFALSPTSKAEFHGNSVTRGFRSVPVVFTPGKR 262372

>CYP283A1 Streptomyces scabies SCAB56621

MDFDFFAAPQ QYRDAAAAHA GEHGAFYSDR GFWVLTTYDG IVDAFKDEGT FTVGRVSAAE

GAEEERWIPL TVEGREHTAW RQRLGAWFTP QRVRELTPSV RAGARRRIEE FLDKGEVSFN

EDFARPYVLD NLMTAVGWPP DAFDLLLAID RAMIDSRSAP DPRVAAYGEL GLPALERFAR

EHVARRRAEP ADDLTTASFG WEIDGTPVSD DDRASLLCTL FLAGVDSTVN HLANAVQHLA

HHEEDRRRFL AAPEARPPAV EEFLRVNSCM YPGRQAATGG AGGVADRGDT VLLPLALANH

DPEVFPEPGR IDFGRPRNPH IAFGTGPHQC LGAAFARAQI LVALEEWHAL VPDYAPHPGQ

RATEPRFLRN SYDLRLVW

>CYP284A1 Nostoc sp. PCC 7120 (cyanobacteria same as Anabaena)

1 MLQYITAQID NSSSFPYLVT VLSVTTIAGT FAWRWWKQKK KYKSLQSLPS PPKHWLLGNL

61 PQVLAAVKQK KLFQLFFDWS QQLGPMYVVW NGSSPVVILS KPKVIEDTIV NGMRDGSLIR

121 SARLRQAWND ISGPILIGET GNEWQWRRKV WNPEFSSSSL AKYLKIINQA CVQVIDTLKE

181 TALPKEVEVD PLFVELTMRV ISSLVLGIPV DRKITTNEGP PLEVLKVYEA MCVVGYRFLR

241 QATGEKIWMK YLPTKNSQDY WASRRYLEEF LTPRVDLALQ MREQSTDFPQ VSPLFRESML

301 VRIAAKEPKY NRQTLIAESV EFLIAGTDTT AHTLSFAVGE LSLNPRVFQK AREIVDQAWQ

361 GQDNINTESF KELAYISAIL KETLRLYSIA SGSTSLEAQR DTVIEGKVIP SGTRISWSML

421 AAGRDPEVYA NPEEFLPERW LDKSKETSSL PMIDFGSGPH RCLGEHLSML EGTMMLALLL

481 RHFDWELVNG RSSLEQLQQN LLIYPSDKMP VRFRLRN

>CYP284A2 Nostoc punctiforme

MFQQIAAQITFSDSFPYLVTALGITSTAGIFGWRWWKQKNTYKS

LQSFPSPKRHWLLGNIPQVLAAVKEKKFFQLLFDWSQQLGPMYVYWTGFP

18635 VLVLSKPKVIEDTIVNGMRDGSLIRSQRASKAWNDIGGPILLGQNGSEWQYRRKAWNPEF 18456

18455 SSSGLSKYVEIINQACEQIIEKIQSVASPEVQVDPLFVELTMRVISCLVLGIPVDKN 18285

18284 IATNEGQPLDVLKVYEAMSIVGYRFLRVATGEKIWMKYLPTKNSRDYWAARRYLEEFIT 18108

18107 PRVDLALQMREQNQTDLTQVSPLFQESMLVKIAAKEPKYNRETLVAEVIELLIA 17946

17945 GTDTTAHTLSFAIGELALNPRVFHQAQAVVDQVWESQGTINGESLKELNYIRAILKETLR 17766

17765 LYSDDS 17748

XXXSLXAQR

DTVIEGTVIPRGTKIYWSMLAAGRDPEVYSHPDEFLPERWLEKGKEN 17579

17578 SQLPMIDFGSGSHRCLGEHLSMLEGTMMLALLVYYFDWELVNGRSSLEQLQQNLLIYPPD 17399

RMPVRFRLRK\* 17366

>CYP284A3 gi|75910266| YP\_324562 Anabaena variabilis ATCC 29413

MLQYVTAQMNNSSSFPYLVTIFSFTTIAGTFAWRWWKQKKKYKSLQSLPSPPQHWLLGNLPQVLAAVKQK

KLFQLFFDWSQQLGPMYVVWNGSSPVVILSKPKVIEDTIVNGMRDGSLIRSARLRQAWNDISGPILIGET

GNEWQWRRKVWNPEFSSSSLAKYLKIIHQACEQVIDTLKETAPPKEVEVDPLFVELTMRVISSLVLGIPV

DRTITTNEGPPLEVLKVYEAMCVVGYRFLRQATGEKIWMKYLPTKNSQDYWASRRYLEEFLTPRVDLALQ

MREQKTDFPQVSPLFRESMLVRIAAKEPKYNRQTLIAESVEFLIAGTDTTAHTLSFAVGELSLNPRVFQK

ARDIVDQAWQSQDNINTESFKELAYISAILKETLRLYSVASGSTSLEAQRDTVIEGKVIPSGTRISWSML

AAGRDPEVYAHPEEFLPERWLDKSKETSSLPMIDFGSGPHRCLGEHLSMLEGTMMLALLLRHFDWELVNG

RSSLEQLQQNLLIYPSDKMPVRFRLRN

>CYP285A1 Streptomyces tubercidicus strain I-1529

MKLSQSVPPEQIDLDSVDLTDSVLYGEGDPHSIWNAMRQRDPVR

WQQVDDTLGFWSVTKFEDADLVLRDHTLFTSQRGTMLFLLGKDDPARGRQMAATDPPR

HTRMRAPMQRALTNKQVEKYREAVTGEVRRLLEPALSEEPFDFAESMMTLPMTAAGTM

MGLPREDWTRLTQLTTMSIAPDDPEFAGPGSAEETLKAAHRELFAYFHDILRDRRNNL

GDDLISLLLGMEIDGRSLETGAILSNCYSLILGANVTTPFVPTGAMAEIVGTPLLHEW

RTDPKLMNTGVDEALRWSSPTNHFMRYALQDIELRGKKIRAGDAVVVWLGSANRDEEV

FANPFTFDIRRKPNRHMAFGSGPHYCVGHTVARMSMKILFTELFESFEDFELVGEVEH

LHSNFVAGIKHMPMVAKVRAGAARSHTGLVK

>CYP286A1 Deinococcus radiodurans

1 MVPAPPFLGH AAEMGTIKLR PFLTRCYQAY GPVFQLTVPG QKITVLAGPE ANLFAMKEGH

61 RVLRSLEAWR DNDHEMGSDR SMISLDGAEH RAYRRVEGRA FARSFFAAGL RPALAVLAED

121 LAPFQPGDVL PVATWCKKTI TEQLARMAVG GTVRPYLPDL LHFIQTALQV TVNRQLPPAV

181 LRLPKYRRAK ARIFQMVDDL IEDHRQNPPE KSGRAPDLID DVLADQQVNP ERWEHPDVRL

241 AALGAFIAGM DTAANSLAFV LYRMHLHSEF LPALRAEADA LFRDGPPTAE ALGRSPLLHR

301 FVMETLRVHP IAPALSRTLT EDVEFAGHRI PAGTPVIIGT TVPHGLPELF PDPEHFDPGR

361 FAPGRAEHRQ PGAYAPFGVG SHTCAGSGMA EGLIMLGAAA ALRTLDLSLE PDYVLRQTAK

421 PTPSLDNKLQ LRVNAVRHNP VFLVH

>CYP287A1 Deinococcus radiodurans

1 MLSSLHDLPE PASRPGSGHL QDWAARPLAL IEEGATQALA AGQDLFRLRL GLPAVVGLSP

61 AWNRRVLTDL NTFVSAGSFS AVVPYLAGGV ILTDAPGHGA RRRALNPGFG KGSVQQLRER

121 MRQASSPVPT GRFNALAWAD ETVRRQLNAA YFASEFDDRL LAAFLAPLRR PFPVPALPRP

181 LLFRRVEQEI RRLAERRLRE GGDDLLSTLA PLPGGLLETR ISLAAAHDTT THALAYAVWE

241 LAKAPQDQTP HTHSAVLKEV LRLYPPGWMG SRRLSRAAEW QGTEIPRGTL ALYSPYLTGR

301 DPTLWERPLD FRPERWEKSP PAWAYLPFGG GERTCLGVHL AQTLILDVLA ELPPLQAHWG

361 NDEPHPGITL GPRGPLVVER R

>CYP288A1 Corynebacterium efficiens YS-314

1 MIHNMETRCG SYHRATGILT GDDMTSDSTT ALSTAPETTS GGCPYGHGNP DATGTPGTSH

61 HGYEPFNMTN PFPAYEELRR EEPVMFDERI GYWVVTRYDD IKATFDDWET FSSENAQAPV

121 RKRGPQATKI MEEGGFTAYS GLSARIPPEH TRIRAIAQKA FTPRRYKALE PDIRANVVAR

181 LETMLKQGAP ADIVPALAYD IPTITILTLI GADVSMVDTY KRWSDSRAAM TWGDLSDEEQ

241 IPHAHNLVEY WQECQRMVAD AHANGGDNLT ADLVRAQESG QEITDHEIAS LLYSLLFAGH

301 ETTTTLISNC FRVLLAHRDQ WEALIEDPKK IPAAIDEVLR YSGSIVGWRR KALRDTEIGG

361 QPIKKGDGVL LLMGSANRDE ARFDDGETFD ITRPNAREHL SFGFGIHYCL GNMLAKLQAK

421 ICLEEATRLV PSLELADDQS VEFRENLSFR VPVSVPVTWS N

>CYP288A2 Corynebacterium glutamicum ATCC 13032

1 MTSQTSQQST STGGCPFGHT SESTSHHGYQ PFDMHNPFPA YKELRQEEPV MFDERIGYWV

61 VTKYDDIKTT FDDWETFSSE NAQAPVRKRG PQATQIMTDG GFTAYSGLSA RIPPEHTRIR

121 AIAQKAFTPR RYKALEPDIR AMVIDRVEKM LANDQHVGDM VSDLAYDIPT ITILTLIGAD

181 ISMVDTYKRW SDSRAAMTWG DLSDEEQIPH AHNLVEYWQE CQRMVADAHA HGGDNLTADL

241 VRAQQEGQEI TDHEIASLLY SLLFAGHETT TTLISNCFRV LLDHPEQWQA ILENPKLIPA

301 AVDEVLRYSG SIVGWRRKAL KDTEIGGVAI KEGDGVLLLM GSANRDEARF ENGEEFDISR

361 ANAREHLSFG FGIHYCLGNM LAKLQAKICL EEVTRLVPSL HLVADKAIGF RENLSFRVPT

421 SVPVTWNA

>CYP289A1 Brucella melitensis 16M

1 MRAGGIMTSP TERPKQDWDP RSEAVLSDQI GAYDAMRHQC PVAHSDYLGW SLFSYDDVVR

61 VLDDHETFSS VVSAHLSVPS GMDPPQHTAF RQLVERYFEP ERIKAFEPIC REISKKLVCE

121 LPRDAEIDLV TQFAQLYAVR IQCAFLGWPD SLQGPLLDWV HKNHAATLAR DTKAMAAIAL

181 EFDEYIRDLL DERRKLGADA PDDVTTRLLR DRIDRRNLTH EEIVSILRNW TVGELGTITA

241 CVGILCHYLA KSQQTQALMR GGPDLLPAAI DEILRLHAPL ISNRRVTTRA VVVGGREIPA

301 GEKITLMWAS ANRDEAVFDK PDELRLNRDP ALNLLYGRGI HVCPGAELAR AGLRILMEEL

361 LGQTRKLDLV PGSVPALAVY PASGFSRLPA RIS

>CYP290A1 Caulobacter crescentus CB15

1 MDLISQTVVD GKAGPGAPPT YPTLKDVDLA DIFRFTKGQP WADFARMRQE APVMWHPEPM

61 GGPGFWALTR YEDVHRVNGD PETFSSQRGG ILMSMGAPEK RHALLFRASM DTMINMDAPH

121 HLQLRREHMP YFTPSYLRGL TERVKGEVTR LLDEMEPLLA NGAEIDMVEH FSSVLPLFTL

181 CEILGVPPED RPKFLTWMHY LERAQDLAVK QANAPMQPTL ELMQFVMDFN NNVEEMFEYG

241 RTMLHKRRED PKEDLMTAIA RAQLDGAVLP DEYLDGSWLL IVFAGNDTTR NTLSGAMRLL

301 TEFPDQKQKL IADPSLLGGA VDEFIRMVSP VVYMRRTATR DVEVNGQLIR EGEKAIMYYG

361 AANRDPAMFE NPDQLDVTRA NAGKHIAFGY GPHTCIGKRV AQIQLEEAYR QILARFPDLN

421 WTGNIEIAPN NFVHAISKLG VKRG

>CYP290B1 Ectocarpus bacterium, 46% to CYP290A1 Caulobacter crescentus CB15 GenPept AAK22930

75% to seawater bacterial sequence CYP290B3 JCVI\_PEP\_1096682145269

3343594 MPLRKLSPHLIRWHRHTPRPIFLVSSLSKKPGRTRHIMRLVSDD 3343463

3343462 ILTDSNRQRPTFDAVYPELKEFELWNPASWTQGH

3343360 PHEFYKTMRESAPVMWSDIRKGGDGFWSVSRYDDLKAVELAPTVFSSERGSINLGVAPKD 3343181

3343180 KWKPEKLVSAALNALINLDAPRHMEMRIQQMDFFAPAYVATLRDKVSAKIDSLLDDMESK 3343001

3343000 GPVVDMVPVFSEQLPLFTLCEMLGVDEEDRPKIAHWMHYLELASQYLTNPWQVIIKEPLF 3342821

3342820 PFRFFKAVKDMFAYGEAIMADRRANPREDLLTAIAKTKLSDEELPQEFL 3342674

3342673 DGSWLLIIFAGNDTSRNSLSGTIRLMTEFPDQRQMVLDDPSLIPRMSQEALRMISPVRHM 3342494

3342493 RRTAVEDTEINGQRIAKDEKVVLWYGAANRDPSMFPDPDRFDMMRDSVDKHLAFGHGVHK 3342314

3342313 CLGSRIAQMQLRLSYERIFDRYPNITWTGHQKVAPNALVHAISSLKVNLYGTDGTRPTQVQVKAA\* 3342116

>CYP290B2 Maricaulis maris MCS10 CP000449.1, synonymous with Caulobacter halobacteroides, 67% to CYP290B1

MQLVSDVILEDRPQTEPGFGATYPGFDDFKLWDPAAWTSGHPHD

FFRKMREQAPVMWQSADKSKAGYWSVTRYDDIKTVELAPEIYSSERGSINMFVMPRKE

WKPKKLIPAAFNSIINLDQPHHMQMRIQQKDFFIPRFVSELQERVDAKIDDLLDEMER

RGPVVDFVKLFSQELPLFTLCEMLGVDEADRPKIIEWMHYLELANQYFVNPWSLLSRR

PWFPIKFYHHVNAMFAYGERVMAERRANPRRDLMTAIANTEMAGKPLPQEYLDGSWLL

IIFAGNDTSRNSLSGTIRLMTQFEDQREAILSDPSLIPAMTNEALRMISPVQHMRRTA

MEDTELNGQRIARDEKVVLWYPAANRDPSVFPDPDRFDMTRENGDKHLAFGHGAHKCL

GSRIAQMQLQSAFRKIFERFPKIAWTGRQTIAPNTLVHAISSLEVNLYGRDGERPRPV

QERWP

>CYP290B3 JCVI\_PEP\_1096682145269 seawater sequencing, 70% to CYP290B1

QRGSINMMVGDRKLWKPEKLAPAAFNSLINLDAPAHMEMRMQQSEFFFPAYIETLRDKVEAKIDAMLDELERQGPVVDFA

KLFSEELPLFTLCEMLGIDEEDRPRIKLWMHHLELAGQFLANPWQTFLSEPMFPFRFNKVVQEMFAFGERIMKDRRANPR

DDLLTVIAQSKLEGELLPQEYLDGSWLLIIFAGNDTSRNSLSGTIRLMTEFPTQRTLVLDDPSLIPQMSEEALRMVSPVI

HMRRTAVEDTEINGQPIAKDEKVVLWYGAANRDPDIFPDPDTFNLHRDNVEKHLAFGHGVHKCLGSRIAKMQLRLAFEQI

FKRFPNIYWTGKQKIAPNSLVHAISSLKVNLYGPDARRPTRIAANK\*

>CYP291A1 Mycobacterium vanbaalenii PYR-1

MSRLSNPLHSPAFYAGDPFPVYRELRATDPVCWNDEHEFWALLKYEDIRYVSTNPALFSSARGVTVPDPA LENPVMEGSLIFTDPPRHRQLRKLINSGFTRRQVAILEPKLRAFARAALDAIDPSATEFAEQVAAPLPTR MIAELLGAPDEDWEQFRTWSDATVGMDDPDVELDTFAAMGELYQYFEAQIARRRDGTLRDSDDLLSVLVA AEVDGVRLTDQDLLQFCLLLLVAGNETTRNLVALGTLALIENPDQFRLLRQRRDLVPTAVEEMLRYASPV ANMTRCATRDVDIRGRSIRAGQYVTMLYGSANRDKDVFGPTSEQFDITRNPNPHLAFGCGEHSCLGAQLA RLEARVLFEELLNRFDHIELDGDVLRMQATMVPGVRQMPVRLSATAAEPRETGTAAVSV

>CYP291A2 Mycobacterium flavescens PYR-GCK

MGRRTDLESP CGALHPSARI HPARTSPARQ RHRRRLGRRR ALGVPARPAR HPDRPAAHVT

PAVISAIPPV ASLAQKEIAL PPPLHSPAFY AGDPFPAYRE LRATDPVTWN EEHGFWALLK

YEDIRYVSTN PALFSSARGI TVPDPAIENP VMEGSLIFTD PPRHRRLRKL INSGFTRRQV

AILEPKLRAF ARTALDAIDP AGGTEFAERI AAPLPTRMIA ELLGAPDEDW EQFRRWSDAA

VGMDDPDVEL DTFTAMGELY QYFEKLIALR RNGALRDSDD LLSVLVAAEV DGVRLSDQDL

LQFCLLLLVA GNETTRNLIA LGTLALIEHP QQFRLLREHP ELIPTAVEEF LRYTSPVANM

TRCATRDVEM RGRLIREGQY VTMLYGSANR DEDIFGPTSE QLDVTRNPNP HLAFGCGEHS

CLGAQLARLE ARVLFEELLA RFEHIEPAGE VLRMQATMVP GVRAMPVRLR AATDPRRAKARAG

>CYP291A3 Mycobacterium avium subsp. Paratuberculosis

MQTHPPLRSP SFPLHSPDFY AGNPYPAYRE LRATAPVCWN DVTNFWALLK YEDIRFVSSN

PALFTSTRGI TIPDPQLPNP VQQGSLIFTD PPRHRQLRKL INSGFTRRRV SVLEPKIRKI

VRGILDGIER GAVHEFAEQI AAPLPTRMIA ELIGAPPDDW EQFRAWSDAA TGTADPEIEL

DPAVAAGQLY EYFQRLIAAR RARPRADLLS VLAEAEIDEH RLTDEDLLNF AFLLLVAGNE

TTRNLIALGT LALIAHPDQY RLLVEEPARI PLAVEEMLRW NSPVVHMART ATADVEIRGQ

RIRAGEVVVM LYGSANRDED VFGPDSEEFD VTRHPNPHIA FGCGEHSCVG AQLARLEATV

FFEELLRRYP RIELVGEVDR MRATMVPGVK RMPVRMGA

>CYP292A1 Mycobacterium vanbaalenii PYR-1

MTRTPERHAENWDLRHPDFNDNDFLYDVYAVMRAKSPFARTDNPFLSATPAGAWVAVRYAECVQILQDWE HFSSNPTPEGAEQLAGDLVITLDPPRQQKFRKVLNPYFSPARMKALRPEIGVETDRLIDDFIETGSGDLA AVAWRQPGIVFFKYLLGMPVDDVPLCVELTDTALNGATEQDRMAAWGGLYQHLHDAVTARRGQPPRDDMI DVLLSAEIDGEKLAFADVVSNAMLLVQAGLETTASAMSFAYHYLATNPAERDRLIDDPDLLTRAVEEFIR FAGSIHGIPRTVAREVELSGCTFSPGESVIVNYAAANRDEQEFPDAHRCILDRRDNRHLGFGAGVHRCLG SNLARLEFQVGLERVLTRMPDFALSPTSKAEFHGNSVTRGFRSVPVVFTPGKRVTA

>CYP292A2 Mycobacterium flavescens PYR-GCK

MSPTVEQHAE NWDLRHADFN DPDFLYDVYT VMRGNSPFAR TDNPFLSATP SGAWVAVRYA

ECVQILQDWE HFSSSPTPEG AEQLAGDLVI TLDPPRQQKF RKVLNPYFSP ARMKALRHEI

AAETDDLIDV FIESGSGDLA EVAWRQPGIV FFKYLLGMPV DDVPLCVELT DTALNGATEE

ARMGAWGGLY QHLHDAVTAR TAEPPRDDMI DVLLSAEIDG EKLAFGDVVS NAMLLVQAGL

ETTASAMSFA YHYLATHPAE RDRLIAEPDL LARAVEEFIR FAGSIHGIPR TVAKEVELSG

CTFSPGESVI VNYASANRDE EQFPEADRCI LDRRENRHLG FGAGVHRCLG SNLARLEFQV

GLERVLTRMP DFTLTAGAEA KFHGNSVTRG FRSVPVTFTP AARTR

>CYP293A1 Saccharopolyspora erythraea NRRL23338

VDVFDRNFGYDSDTLAAARERHWYARIPNGLMVLGHEEVNDLLRDHRLVSDGKRYLEMHG

VTSGPLYDWFVPMILHREGQDHARLRSVVRRTFTPRVIEGLRPYMRETVGRIADGIAETG

ECEFVETLANPFPVMVMGRLLGVPPQDHELFHGWSTDVGLVFSLAYGGDVRERVERAVSE

LGDYFDGLIERRRAEPADDLISSMIAAQTEEEVISGEELRNLLVALVSAGHDTTRHQFGS

AMLTLCRNPEQWTAFRDDPDRAVEEILRWCPAAPVLFRFAQEDIAYRDTTIPAGTFVMLC

VHTANRDPKRFDRAEVFDTTASRQTPHLTLSAGPHFCLGAAAARAELSEAFTVLSTRFGA

PRIAGEVTWRNPVGIYGPETLPVRFV

>CYP293A2 Saccharopolyspora erythraea NRRL23338

MPTSIESASQAPFLDVTDPGFTFEAPEVARARERHWYARTPVGPIVLRHAEVQELIRDPR

LAQDGARYLAMHGITSGPVHDWFVPLILHRNGVDHLRLRRVVQKSFTPRVVNNLRPFMRA

TAERLAERIAAEGACDFVEMFADPYPVAVMCELLGVPPQDYELFHRCSTDIGLVFSLSQG

DGVRERVERGVVELYAYVDSLIARRRAAPTGDLVSRMISAHEDDARLSSEELRNLVVALV

FAGHDTTRHQLGRAMVALCAHSEQWTALREEPQRAGAIVEELLRLFPTAPVIFRFATEDL

EYQDTAIPAGTFVMLCVQSAHRDVRAFGPDVESLDPAAERGAAQMVFGGGPHFCLGAATA

RAELAEALPVLARRLGAPAPAGPVAWRHPIGIYGPESLPLRFG

>CYP294A1 Saccharopolyspora erythraea NRRL23338

MEQASTGQLGPLPEFLRQATDEVERIVAPSGDKVLLVRGYALGRQVLTDKRFSRAAAVQP

DAPRFNDAQPVPDSMMSMDGAKHARLRRVVAGTFTTGRVSAMAPAVERLVDEHLNRVADI

GPGADLVEELAAPLSLSVLCSLLGIPLDDSARFREWVEVLFDITASTPREKARHRLELIG

YMTDTIEQKLQRQDDDLLTTLIRAHTQGKMSRPELLTLGLTLLMAGYETTAGQIGLSVLS

LLSDRETHDELRAHPELLPDAVEEFLRLTPATPLSFPRVAVEPVELNGVTIQAGEAVVVS

LLHGNRDTEVFAEPGQLMLRSRDAVHLTFGHGVHRCLGAPLAKLQVQLVLGRLLERFPAL

RLTPGPDSVVWKDGLATRGLSRLRVEW

>CYP295A1 Saccharopolyspora erythraea NRRL23338

MLGTRTVRPPGPKGRWLVGNTLDYDRDRMAFLVRCRQEYGDVFSFDERTIVVLDPGLVHD

LLTRTNDDFHSESVPLATRIDPERAAADAQAWMTARRKGWHGLNRAVAQAHAGRLRLLFE

QTLAETRGETVDVLPVMERFAGLATADFCLGADADGMAEILTENVRAIEPLGGSSQLFPA

WWPSRHIRRFLRAREGTLNAVTERIHRRRDKPPADHPQDLLDVLLAAGEPELTEQQVQLL

LRGIMLAAFGVPATALTWLVWTLASRPDLHRRVAEEAAAWPGEEAPPLSALPQTEAVVKE

VLRLWPPTWLIGRTARRGTTLGEWQLRPDDHVMFSPYLMHRDPRWWTDPDELTPDRWLDP

ARTPKRHTYIPFGAGPRVCVGTQLGMIQLCLAAHWLTRNHEIRPTTETCAPKFHDLLLPQ

GFRARFTPRTP

>CYP296A1 Saccharopolyspora erythraea NRRL23338

MLEQDVLDEVTNPFPGLAALQEQTPAVRVRTPDGPPAWLVTRYADVRDLLRDDTRLSVDP

DHGAGEDYAGFELPPQLRPHLLAVDAAQHDRLRELISSPFTGTGLHRTVEVVEAEAHRLV

AALAPDQPVDLVAELAFPLALTAVRAVLPLPDPAHQAFAEWAHDALLAPRRQEDGAEVRA

RDTLGRMAEIIQTATTVPGDGLLGELQAAYHHGRLSAHELAAQVFYLLFVPTEPLVDAFG

VVLLRLLAGTRHRAVLRDSPAARHVAVAEALRFDTPQGLAAPRFALVDLDIDGVRVRAGQ

TLLLSLAAANRDPRQFDDPDELVLTRSPNPHLALGRGDHACPATALSYQLLSSSVAALLS

RYPSTTVVPEKTQWRGNFRHRGPASVWADLKP

>CYP297A1 Saccharopolyspora erythraea NRRL23338

MAGPVLSSSDIPGPPPSAGGHNLRDIAEAGGLPGFQVRLHRTYGEIAHFAMPNAQVVSVA

SPEVLESTLDLPECPMELAPFLTPLADAANVLLSGEQDRARWRRTVIPALSCPHRAESDH

PRFIDIIEESAQRWSSTGEPVALERELDTLALRLMCTSVLGSTPGQAAIVERVTDAFERL

PEFFLGQVYGVRTTSQEPAVDSALTTLRDVVTFLVDEVAPSDLISAARRAGQSSKDLVNT

LLAILIGAHRTTGTVVSHALRQLMRHRDVAKRLRAELKTVLGGKAAPAFHELPCLRYLRR

TLNESVRLASPVPGIARRAPDGIALGAYRIPAGTVVHYAIRAVHMNPRVWPRPDEFDPDR

FDTAPQNSRPAMAFVPFGIGRNDCPGALVAMEHALLMLAVLAHRFRFESRTAGKQGSRFS

LGGPCADPVRVRPRRSR

>CYP298A1 Saccharopolyspora erythraea NRRL23338

MSVPTAVGAACPGEVFDPLSPSMLADPYLVYERLRTEAPVHWHEHLRAWVLTRHEDCVGV

LRRPEVFGSDPRKLAKPIPESVISLQTMDPPEHSAVRHHFLAKLRRQDLDAWSARVRRIA

VELLSNAGPDPFDFVAEVAEPLALHSMCSLCGVPYPEDDERFRTASRTMVLGMDAGLEPA

RREPALAARGVLNEIIEDWIARAPRESLISGLDEVSGIERGYLVNSARAVFDAGYSTTGN

MLGNIVKWLLGPGGVRETAPLGGLDSRAVEELGRIEGVVQAVSRHCLAAVEIGGRTLRRG

DVVIVMLAAANHDPKVFPDPRRADFSRESGPHLVFGRGVHSCLGGHVAGRVALALLHALA

DGFERIEPAGPHRQRPTATQRGLDHLPIRLS

>CYP299A1 Natronomonas pharaonis DSM 2160 (Euryarchaeota; Halobacteria)

1 MSTRLPEPPE AGLLNALRFG TDTFRFLEGI QARFDDGTSV SIPGRPPLVV LTGPDLVGEA

61 LDRPEDFPRV PAQDAVTMIA ENGLVQSEGA LWSQQRSVMA PSFSGEQVTA YANTTGRRIE

121 ARADQWAAAG ARTTDLHREM TSLTVRVASE ILLGEDIGTE RADQFHEWMQ VAGEEFEFGI

181 ETVLPDWVPT PTSGEFEQAA AGIRELSEQL IERRRESLAA GERPDASDML TMLIRAEDNP

241 DIDYPENQIR DEVATFLIAG HETTALSLTY TLCLLSWHPE ARRRVRQEAD EALGDGPPTH

301 DDLAELTYTR RVYDEALRLY PPAWGVFRQA NGDVTLGQYT IPDGSAVIMP LWSIHRDGSY

361 FEQPDTFDPD RWERRTPRAV DAYRPFSSGP HACIGRGFAL AGSTLVLARL VRDFDIDVPE

421 SALDDLRLTP TLRPADGVEA TIQPVGGR

>CYP1001A1 uncultured haloarchaeon FLAS10H9 (Euryarchaeota; Halobacteria)

1 MTRAPHTPPG PPVVGNVPRF ADDPLRFLVG VQEAYGGQYP VVRLEPAGGQ RIVVILDAAL

61 VHEILADRER FVRPRAGPEA SRREGLLSSR GPLWERQRSV IQPELVGGQL AAYADIAARS

121 VEEMLDRWPE NGEIDLVAEL SMLTMQVIAR SLLGRDATRE QARTVYEALD TFAEEFEFGA

181 DALLLPDALQ SGPSAAFERA DADLEAVARD FVDWQREHED PPDSMLTALI EAERDGVELS

241 EDELIDQTVL FLTAGQETTA LTIAYAFHHL SRSPDVRAGV TEEATGVLDG AAPSWEHLSG

301 FDLTERVVRE TLRLTPAAWN VTREVRGPTT LGGTRFETDD LVLLPTYAHQ REDRVWGDGD

361 AFRPARWTDE VSRSHDSYFP FGSGPRVCIG RQVALTEAQF TLAHTLQQYE VDVHGDELAF

421 EPAITLRPAD GLRATVTERE

>CYP1001A2 Haloarcula marismortui ATCC 43049 (Euryarchaeota; Halobacteria)

1 MERTAHTPPG LPVVGNLPRL ARDPLRFLTG MQDAYANQYP LVRVDPQVGQ SVTVVLDPDI

61 AHEVLADRDR FRRPNVGAQE QRRQGLVSSD GALWEQQRSV LDPEFVGGRL ADYAEIAGDT

121 LEETLTAWPE SGRVDLFEEL SILTMRVITR SLFSQDTDRE RGETVHEALA ALNDEFDASV

181 FDLVLPEQLQ SGVSAEFEEA DAVLDSVATE FVDWHLNHED PPRDVITALI DAKADPDIEL

241 SENELIDQTV LFMTGGQETT ALTIAYAFYW LSQNPAAKER VRAEAQDVLD GGQPGWADLS

301 DLTYTERVVR ETLRLTPAVW SVSREAREPV TLAGTDLDAG EFVMLPIYAH HRDSRVWSDP

361 LTFDPDRWAG SASRGDSAYY PFGSGPRVCI GRQVALTEAQ FALAHVLQHY DVQVTADELD

421 LQPSVTLRPS GPMEAEISAL E

>CYP1002A1 Halorubrum lacusprofundi ATCC 49239 (Euryarchaeota; Halobacteria)

1 MCNPITRSDD DRARQSGGSE RTDTADADVD VADAPPPPDP GGLPVLGNVH ELASDALGFY

61 ERRSAEYGGI VRYDVFGTES YLVTDPGAIG RILVEDHDRF VKGEMPREQL GGLLGDGLFL

121 AEGEAWREQR TAIRSAFFRE RVAAYGDSMV EHAREAVDSW GDGAVVDVHA ASTEYAFAVL

181 AESLLGSDIE GERETVRAAA EAITDRFDMS RPTSFLPEWL PTPANRRYRR RLGALRATIR

241 DLVTERRAAG PPADPSAADD LLGTLVAAAK LGALDDEELV DNAVTFLFAG HETSALGLTY

301 ALYCLARRPA FQDRIRSEIA PLHGDPTPAD LRECPALTAA VDEALRLYPP VHSFFREPTE

361 PIALGEYRIP SGVVLTLAPW SVHRDGRWWN APETYRPERW LRETEDGGVV HGDDRSGPAV

421 GEHPEHAFFP FGGGPRHCIG MRFARQELRL AVATILRRVR LEPVTEELSL QASANTRPDG

481 PVHVRILTRD EPSDPESLDQ DEPSKTSW

>CYP1002B1 Halogeometricum borinquense DSM 11551 (Archaea; Euryarchaeota)

ZP\_04000149, ABTX01000002.1 262288-260948

49% to CYP1002A1 Halorubrum lacusprofundi (Euryarchaeota; Halobacteria)

1 MSTEGGYPPG DGGLPVVGNT VELSRDILEF YEGLRNEYGR IASYRVFGTD ACMVADPEAI

61 RQILLEDHDA YEKGDVLTRS LGDAMGDGLF LSAGEQWHRQ RTRMQPAFYR ERLDTYVPAM

121 RDTASQSLDD WHDEAVIEVN DAMTAMTIDV LGRTLFGVDV ADEPVVTDAS DAILARFDTN

181 RFWSFLPDSV PTPTNRRYRR EIERLREFVD GLADQRRRRP REERGDDLLS ILVGFVESGD

241 LTMSEFRDNL ITFLFAGHET TALGLTYTVL CLARNPDEQE RIRAEVDSVC DGSVTAADLP

301 ELEQTGRAID EALRLYPPVY LFFRETARDV KLAGYRIPNG TTLVLSPWVV HRDSAWWDDP

361 QTYRPDRFAG ESDRPEYAYF PFGGGPRHCI GMRFARMEMK TVIASILRRY EFELVSDPDP

421 ELIASSNLKP AEDIEIRVSE RASTTSN

>CYP1002C1 Halorhabdus utahensis DSM 12940

1 maetqgsste rgeqpsetpp gpgglpllgn tldlyrdpwa lyeelesygd vvhytaggnd

61 fnvvldptlv eqvlltdhda ygkwalgdvg ggigseglvl tegeqwqrqr rviqdaftmd

121 riraygdamg qyaaeaveaw ddgeeialne afsrltlril ahslfdldid aeagtvaeft

181 rtvndrmdvd nltafvplwv plprnrrfkr rvaafesfve elieqrrada terddllsll

241 lahegdglte teirdqmttf lfaghettsl altyacmala thpgprerln rehervldgg

301 ipslaqlpql eateraikea lrlyppvyvl freanrdvel ggyrvpsgqk vtvpqfwihr

361 keafyddpde fdpsrwtdgf edelhdyayf pfgggprhci gmrfamqelk tvlptvlqrv

421 dfellsdpdp dfsmgatlrp aedvrvrvrk rd

>CYP1003A1 Haloarcula marismortui ATCC 43049 (Euryarchaeota; Halobacteria)

1 MDTQQAIRET PEPVTPGDRP PRLGRVPFVD NTAAMLRDPL GFYDRAGAHE ADMVGYSVAG

61 TTGCFVCHPD LVEQVLVTDA DVYEKGQLLQ DTLGQFIGEG LFLLEGEEWQ QQRTALQPAF

121 YRERIAAYGD TMTEFADRAA AGWSDGQRID VLPHMQSLTL NILGKTLLDV DIETTADALE

181 PLLDALRTRL DPRSLSAYLP LWVPTATNRA VTNSLAEFQS TLDDVIAARQ REDEHAREAR

241 DDVLSLLLSL DDETMDRERL GHQLLTFLVA GHDTTALTLT YAWFLLANNP KRQQRLHDEL

301 DATLGERQPT PEDLFELPYL DAVLNEVLRL YPPAFTVFRQ PTEPVTLGGY ELSTDAQLTL

361 PQWLVHRDDR WYDAPDAFRP ERWDDDLEAS LPDYAYYPFG GGPRHCIGMR FARMEAKLAL

421 ATIAQQYAVE AVTEPPLSLA MQITLSPTAP VEVRLRER

>CYP1004A1 Salinispora tropica (marine actinomycete)

MSTFSLERVACDRMLGLAVRGRLADSLLMRANTARPHLSAAFLATKDDPYPAYAELRARG

PLTRAELGQWLVTGHGAVSALLRDGRLESRMPAEYTRLTLGDSPGVDFLHRIVLTRTPPE

HTRLRRFIGRALGTPVVRRLHDRIAAATDALLEPALDRGRLDVVTELAVPLPVGVVCDLI

GIPTGDRPAVLTRVTALAKVFDAANLSPADLADINTALPWLHDYFGDLLAVRRAGSGGPT

LTEMYWEESASDRLAVADFVDNMLFLFHAGFETTMGLVSNGVAALLNNPEQLGRLRADPA

LVPSAVEEFLRYDAPIQNVIRVARKPVEVAGQKIRAGRTVLLLLGAANRDEEVFADAERL

DVGRDPNPHLGFGGGLHHCVGTALARLMAVVVFERLVDRVTVLGPAAPAVRRRHASLRSY

DHLPLAVAAR

>CYP1004B1 Salinispora tropica (marine actinomycete)

MTTSALAPRFDALDPNVVEDPYPEYARLRAAGPLCRLGPGSWGVTRFADVTNLQHDPRLG

SEFPAGYHEISVGDGPASAFFQRVMLYRDPPDHIRLRRLMSGAFTPAVVRRLRSHIEDLV

DELLAPALAAGRMDLVPELAYPLPVRVVCRLMGIPPESTEDVRHHATNIGRAFTAVVPEQ

ARTEADEAVSWLREHLGALLEQRRSHRGDDLLSRLLDAEESGDNLSADEIVDNTVFSFFA

GFETTVHMITTGTAALLAHPDQLARLRADPSLVTTAVDEFLRWDAPIQGTARYVREPIEI

GGRTIRRGRVLVLMIGSANHDERRFAQPDRLDVGRQDNPHVAFGGGAHLCLGAFLARMEG

AVVFDRLARLAVLEPDGPTVREPNTPFRAYASVPVRIGDR

>CYP1005A1 Salinispora tropica (marine actinomycete)

MSAVLFRSWTKTAGTHWPAITRVADQQGTEHLVVTQHALVRQVLTDQLTYRPDNALDAVT

PIPVAALRVLAGHRFRLPPTLANNGGVSHPAIRALVADALHPAKVAAQRPWLTGLVAERV

AAIRRTLDSGGSTDLHAELNADLPLLVLARLVELPDAPVSAVKQFARAALELFWAPLDAD

RQLALADEVGRFHQVLREFADTGGGLAAALRATGHPPDVLVGALFFLLVAGQETTSQFLT

LLLHRLADEPTVRAALRADSVSVADVVEEGLRLEPPIVTWRRVAAVDSTLGGSTVAAGTS

VLLWLARAGRDPAVVPAPDEFRPGQRGSRRHLAFGAGAHRCLGDQLARMEAAVVVEQVTP

LLDGVTVVRPPWYPDNLTFRMPDAFVVRR

>CYP1005A2 Acidothermus cellulolyticus 11B (Actinobacteria)

MSGATDAAERETEILYRDWYATDPRRPVIRVGRHWLVSSRALVK

AVLLDQETFAADNTLDAETPMSVAALRILAGHRFRLPHTLANNSGPSHAGWRRLLAPY

FSPSAIERHRAYVDRVAEQLVAEAAAVLARDGVVDLHAAVSQPLPLVVLDRIIGLPPD

DIATVKRFAAAALELFWAPLTPERQRVLADQVGAYHARLRRFAQTAGGLGAELRDHAQ

RTGLSDDDVVGVLFFLVVAGQETTSQFLTALFARLLAEPAVLAGLRRGRIAVADVVAE

GLRLLTPVVTWRRVATRDVVLGGTTIPRGGSIVLRLAAAGRDPDEVAEPEHFLPGQRG

SRRHLAFGAGAHRCLGAQLATMEAEIVVTRIADLLAEAEVVRAPRHPLNLSFRMPDAL

VVRSAAVSAGVAPAGGSCRGRSRSM

>CYP1006A1

WRYAEDVARALFGVDIDDDVETVGSALDEFMLATESLSHMMLPPRVPTPSRRRIQRARES

LDAVVYRMIEERRANPTDRDVISKLLEVTDEDGTKLSDEQIRDEVVTLLLAGHETTALSL

TFTAYLLATNPAAEERLVDELDDVLGGETPTMADLDDLTYTEQVVEESMRLYPPVPGIVR

EPAKPDIIGGYEIEPGATVRMHQWGGPPRP

>CYP1007A1 gi|119491070| ZP\_01623228 Lyngbya sp. PCC 8106

MLASAADQAEFIDLGVKKMTTIANQKAWTIPGPSPLPLVGRIVNTINFAKDSIGYSSELFKTYGKVASIV

AGGGTNLYSAASDCPGTVIAYGPEIVRQVATQSHIYHKAPLSGILYRYKDVSERTKPLKNYGVGLFGVND

ETHLKQRKLMMPAFHHQQLRSYRDDMVAITQSELEQIKVNEPCEINQLMKRLTLRIATQSLFGEDVIEKD

HSAGNLLQEIISIQISPFTRLLPLDLPGFSFHRYLDLLSLFETQMKGIIAEKKAKTTPDSDVLSMLVKAR

YEDTGHLLTEDELIAHTGVLFLAGHETTANALTWILLLLSQHPQVCSDLFDELDSTLHGNSPSVEQLQKL

PLLERVIKESLRVITSVPWNGRVTSQTTELGGYVLPKGTEVFVSIYHTHHLPDIYPDPEAFNPQRWESIN

PSVYEYNPFSAGPRLCLGAAFAMMEIKIVLAMLLQRFRWEYLPVQKIDRNGFISIKPKFGMQMKVCSQDR

EFMHGVGSVEGNVREMVKLPS

>CYP1008A1 Ectocarpus bacterium 56% to seawater bacterial sequence CYP1008A2

2052003 MTGAPTPEVEDDGWAGANPFAPSFRDDPYPAMNQLREKDPVNETPVG 2052143

2052144 PWRISRHADVVDVFRNAPTSQTLADGSSPNMDDQDRRGS 2052260

2052261 FRDFMLNMDGPEHARLRRLVLGAFTPKALKHIEGEIDRVVDEAMHTALKQGGMEVVEDFA 2052440

2052441 LRIPSRMICRIMGLPEEDIDQFTVWTAARTNAFFARFLPEDVVEHTRQAGEQMAD 2052605

2052606 YFEAQIKLRRANPREDLLTNLIQSEEKGDRLGDVELAIQAIGLLIAGFETTIGLIGNGTK 2052785

2052786 ALIENPDQAELLKQNPDLAKNTVEECLRYDTPVLFNWRVLTEPYEVGGKTLPENAVLWMM 2052965

2052966 LGAANHDPRVHDDPDTMDITRQGISHASFGGGAHTCLGNQLARMEASRAFHAFVSRL 2053136

2053137 PKAEIQYDDCAWSESFFRVLGKMPIEFH\* 2053223

>CYP1008A2 JCVI\_PEP\_1096696260773 seawater sequencing 56% to CYP1008A1

MMSETNQAAIGDWVGADFFDPSFRDDPYPKLAHLRENDPVNLTPVGTWRISRYEDVKAVFNDAPTSMTDKLGDSPNFDP

LDTKGSFLEFVLNKDGDAHRRLRMLVQKSFGQKTVRLMEEEVAKTVAAAFDKAQADGGMDVVPALAHEVPSRMICQIMGV

PMQDRQIFNEWTAARTNAFFAKFLPPDVQERTRNAGAAMEDYFRALIAERKRDLGDDLLSSMIMASEGGDKFTDDELIIQ

AIGVIVAGYETTIGLLGNGTRAFVEHPDQLAKLRNNPELVSNATDECLRYDTPILFNWRVLEEPYELSGVTLPAEAVIWQ

LLGAANRDPARFADPDQFDIEREDVAHQSFGGG

>CYP1009A1 58% to CYP1009A2 partial Metagenome sequence AAFZ01017524.1

2103615 MSSAQIDPSNPDLHSYAFESNPEPTLAWLREHDPVHWSQHGYWFVTRYEDVRAVLGDPARFSSQKAGFGA 2103406

2103405 NNPIGKDAKGPEGKSGKKASDAEKTMSKGLALSFNQQDPPDHSRVRKLVNQAFSRREISE 2103226

2103225 RADKIQAVVDALMADVKAKGEFDLITDFAFHLPIIVASDIIGIPAEDRDLFRRNFELAA 2103049

2103048 RLMAPKRSDEEWAEALTGAKWQSTYMGELIASRAREPRADLISALIQTSEDDQKLT 2102881

2102880 GGEVASAIMTIFTAAGTTTERMISSGAFLLLTHPEQLAALRADHSLMDNVLEEILRFHHP 2102701

2102700 NQSTSTNRRATQDVELGGKTIRAGDTVRVSLGSANRDAAQFDEPDAFNIQRTGTKHMSFG 2102521

2102520 FGIHFCLGSALARYETKAALEALLLGPKSIELITQNPVKDPDRPDRYKEIRVRMS\* 2102353

>CYP1009A2 AAFZ01017524.1 Metagenome sequence, microbial mat from gray whale carcass in the Pacific Ocean

34 NQMDALDNTYRALVHRAFSRRTVEERRPRIVEVVNGLLDAASAKG

170 LFDLVHDFAFHVPIIVASEIIGIPTDARELFRAAFEKSAGLMQPKRDEESWAESLDAA 343

344 RWIGRYIKGLIAERRASPQDDLITGLIRAEEEGDRLSEAEMSSAISTIYTAAGTTTERFI 523

524 SSGIFILLSHPEQWRALVADPKLLDGAIEEILRFHHPMQSTSNNRRCTVDTPLG 685

682 GRQLIRAGDTIRVGLGAANRDPAV\*SDPDTFNI 780

>CYP1010A1 ABS61705.1 Parvibaculum lavamentivorans DS-1

CDS complement(82741..84153) locus\_tag="Plav\_0082"

37% to CYP205A1 Chloroflexus aurantiacus (eukaryote-like P450)

MAMRAERFDEEAPEIFIPARPVPPKEAPGIGAAVFRPQLLANLIASYPEFWYSARSCPFRVGIARGGRGM

LVNDPDAIRRILVSDAEHFPKDDNQLAILKPLLGNGLLTAEGATWRRNRKLAAPIFQHSSVRDFAPLFVR

AAERSARRALEQQGFFPLDREMTKLTLEIIGETVLSANLEDDIDGISHTVTSVLDKFPAMFLASAFLPGQ

LRNRVIDTVVRPGRRALDVFARRIIDEARKSGEETTLLQRLMVSQSKAGHEMTLDQVRDEVATFLLAGHE

TTATTMSWVWYLLTVHPEWQERLYEEVWAVTEGRRLTIDDVPALVETRAVIEEALRLYPPVANLMRRAIK

TTELTPDITIERGQTVLISPWLLHRHRFFWREPDRFDPTRFLGEEAATRPRHLYIPFGGGPRICIGASFA

LLEAVLILATFMQRARVKVINADQVMPQARIVLRPNVALQAVVTPRRPGG

>CYP1011A1

gi|67924282| similar to CYP107 family ZP\_00517718 Crocosphaera watsonii WH 8501

MTKTKKNKTQNKLVFNPFYRAFHNNPYPIYERLRNEDPIHWSFLKAWIITRYQDVDTILKDNLFQVDDLP

LRLEEKSAYLKQGNFLPLAKTIDKWLFFQQPPNHTRLRSLVNKSFSPASVGNMKEEIEAKVNHLLDKVIP

TGKMDLIDDLASPLPAMTVTNILGLPPEDYYKLIHWSYELFFVFDQPMSLEGYEKQNKMAMEAREYLLRF

IANIDENSQGLIADLVKAKDEENKLDEDEILGFCIMLLIVGQETTKSFISNSILALLQHPEKLQELKDNP

EIIKEASEELLRYDTPVQVIARLAREDVEIGGKTILKGDKVILCLGGANRDENKFPNPEKIEFQRSNRNL

PFGGGIHFCLGAFLARLQGQISINRIVQRLPNLQLVNQTPDWRESITLRGLKSLPLTFDKNDIKTD

>CYP1011B1 gi|37521511| similar to CYP107 family NP\_924888 Gloeobacter violaceus PCC 7421

MDSVANLNQDAFGNTLPQTEAPFKFNVFDPAFHEDPYPFYDRLRRESPIYRNFMGAWVFTRYSDIKSILR

DRRFRVLDKPGWIKNKNRYLTPDQGNFDALVRSSSKFFFFLEPPDHGRLRGLITKAFSASFVDRLRPHVE

ATLADLLGKVREQGAMDIMADLACPLPAIVIARLIGVPAADYARLGHLSDELARIFDPVISLEGYLHLNA

VVEEFGSYFLDLVAEHKRQPGTDLIDSLIAAQEEGNRLSEEEVVAVCMQLFAGGEETTVNLIGNGMLALL

THPEQLELLRSKPEIIAGAVEELLRYDSSIQLVARAAIEDIEIEGCTIGAGEHVHLYLGAANRDPAQFFD

PHSLDLTRVDNRHLAFGDGIHHCFGGPLARVEGQVVFQTLVQQFPKLRLAESRRPERREGTLLRGLKTLP

VTF

>CYP1012A1 Streptomyces peucetius SP\_7691 new P450 family EU725717.1

MGRLRQVLSIWARPDTFLKSCRAKYGSRFRVTIIPGIRIHVISAPEDVKQMFLAPRDVLHTGSSNGPIEKWIGQNGLAWQDEDVHTERRRRVMPSFRGDAVKRVEQAVGQLAKETVASLPRDKVVSVHPYAHRYTTKVILEVLFGEHRPSCENEMFEEVMKMLDFNSRPASMTMFHRMPSWRVKLLRLLRPNGVNEFLTRRERVYRMLDAAIEERGRSGKSGDDLLGLMLGTTNADGSTPSRIEMRDEIMTQFLAGTETTAAAICWALEFLTRSPHVVERVRAEIEEGTGDEYLTAVVHEVLRLGPPTQQIVPREVVKPIEIGGVRYESGDRLWASAYLLHRDEHNYPQPDEFRPERFLGVKPASHTWIPFGGGHTRCLGDRIAFVELKATLTEILTTCDVERADPEPELAHSRTVVNIPKKGARMVFRPRKVKAELGS

>CYP1013A1 Streptomyces peucetius SP1171 EU770695.1

MTTTAPTTVTTARGKTATGPRGVPVLGNLPQWKGDTAEFLLRVQRDHGEVARLRLGPYTVHLVTEPDAVSRVLKENSANYVRGTLYEQFRTVMGNGLLTTDGDDWKAHRRAVQPVFLRKAVAAIEPNVVRATNEMLDEWEVKACRGEPVDLVTETLRLTLVTLSRSLFGYDIRPATPVLKDVVNNVIEVMFKHGSVAEMLPSWLPTRRNRLISRDRRIFTRLVTEIRDNHAATGEGPLMELIEAATDPVTGARWSDEEIRDEMLTIYLAGHETTAVALLWTLVSIANHPGVADEMDEELARELGRATPTAQDVERLSYTNQVVDESLRMYPPIWIYPRDAVADDELAGFHIPAKSSVLLSPLASHRNPRYWKNPQAFDPHRFDPDRVKERPRMAYFPFGAGARMCIGNFMALLELRMIVAMIHQRFRLSLVPGDSLRYGDTAISLRPLSKVLVVPESRDRGVRA

>CYP1014A1 Halogeometricum borinquense DSM 11551 (Archaea; Euryarchaeota)

ZP\_04000645, ABTX01000007.1 36825-35530

38% to CYP174A2, 37% to CYP1003A1

1 MGDNGPPTPG GLPVLGNTVA FARDPFSFID SAVTTHGDVI RLSMLGRDRY IVAHPDLFER

61 ALVTDRDAFV KTEDFRLAFG DSVLAVDGDE WREQRDLLDP FFFFRQITDY IPKMRKQADR

121 RAESWTPGQT YSAVEEMKGL TFDILGSTLL GQDPGKRSGD DSLRRAADDL NAYFAPTSWA

181 LPGSLPTPSR RRFNRAVTTL REEVDRLLAA DHSGDDLLSV LAEARGEEGY PRSETAVSDQ

241 LVGIIFAGHE TTALALTYTW YLLSEHPSVR ERVEHEIDEV VGDDPVGAEH LSDLTVLERV

301 IKESLRVYPP IHTLPRTTTR EIELGGYSIP EGSEVLLSVR NVHRDERFFE HPDQFDPDRW

361 ERNDAPEYAY VPFGAGPRRC IGQSFAMIEA KTALTELMKR YRLEWAGNGE LDLSPQMTTQ

421 PRGDVPMIVR ER

>CYP1015A1 Natrialba magadii ATCC 43099 EEG13968

MTDPQSTADD RSPRTDAEAG TEPARNDGET GSMRATARTP PPGPRGLPLI DSTLTFVREP

LEFLSDLSTY GDVAGYEAFG REFVAVSDPG LVEEVLVSRD DEFWRGEFEN EFSDAVAIEG

VFFAEGDRWR RQRVLLQNAF TPARIQSYAD DMVDETTRLV ERWSDGDVVD LREASSTLTL

RALTRSLFDL EFGDDRAERV RRWVHAMGVY NDTEFFGVRA VLPTWLPSGA EREYRRATAD

VEALVEGLVA DRRQSGTDGD DLLSLLATGA YPDGSRPSAE EITDQLLLFL LAGHETTATA

LTYACWLLAG DDADVDVDAD IDADADAGAD FDVDVDGGAD ADADFDTASV RSQLEREVDA

VCGDRNPTFT DLPELSVTEA VSREALRLYP PLPFLQREPH ESTAVGGYRI DPGTTVQLNM

YGIHRDDRWW SEPDAFRPAR WLSADEDGRP VLDARTDTNR PEYAYFPFGG GPRHCIGMRF

AMTELQLSLA TLVQHADFDR ITESIDPSFK VSLDPGPVEM RVRKR

>CYP1016A1 Mycobacterium parascrofulaceum ATCC BAA-614

NZ\_ADNV01000115.1 3646-4842 (-) strand, EFG78513.1

4 aa diffs to CYP1016A1 Mycobacterium indicus pranii

MSASHEDLIEKLRNFSSDETTPELAYELFAEAREACPVGRSDKQGGFRLLLNYDDVKAAQ  
GDWKTYASSPSVTRPFAERPAFPPLEQDPPEHTSWRELFSRILNNETAAQIEPLVRADVI  
TLIDRLRESGSFDLVADFAEELPLLALCHFLGFDAEKRDAVRAKALEMVGSLGDQELAGA  
TFMALAQLGVEEVLARRDQPRDDFLTELSTAEIDGELLSVEQIAMTMSSFLVAGHGTTVA  
ALSSLLCDVLSAPEVKARLCADHDLIPVAIEETLRLHPPFFGLFRRAVKPATIGDADIAE  
NESVLLCWAAANRDPKVYDDPDAFSLERKQSRRNRHLTFGFGIHACPGAPIARMQMKVAL  
EELLTRAPDIALVDPAAAVYEFRGTETAAIPSLPAVFKS

>CYP1017A1 Sphingomonas wittichii RW1

GenPept ABQ67388

MSGSRDIDHH AVAFARDHLA IYRDARAHCP VLRSDAHGGF AILTRYADNR AALRNHDTFA

SGRIRAGDRL GGGVAIPPNG LRIGMIEMDG AEARALRALL QPWFTIAAVE AAAPRMAQLS

AWLVDRIIAR GACDVVEDLA KPMPSLLILD ILGLPLDRWR DYGRVLHEAV AKSSGSIDGL

RWLASDLRAS VERREVHPEG LIAAMIAAEV DGRPLGDALV CELAMMLLFG GTDTTIAAIG

HALRHLTEHP ADRAALVARP ALIPAAVEEI LRLYSPSTGV ARTVTAPVEI GGERFEPGQR

VLCAINSANR DEEMFADAER FDLDRPKRPH LAFGWGVHAC LGQNLARADL RILLGELLAR

MPDFAVDVAA SERYASIPLV NGHARMPMRF TPGTPAGTGG GELPILTAPR LRPLP

>CYP1017B1 Mycobacterium parascrofulaceum ATCC BAA-614

NZ\_ADNV01000115.1 4886-5812 (-) strand,

95% to CYP1017B1 Mycobacterium indicus pranii, probable ortholog

MTVTHTSRTPTGAAAPPGGEAVTELTVESVEHAAADVIKLTLRA EDSGPLPMWTPGSHVDVIIDEATVRQYSLCGDPDDVRRWQIAVRRVPDGRGGSIRLHD QVTEGSVLTVRGPRNGFPLVSEAPRYVFLAGGIGITPLLPMMAELARRGAHWQLHYGG RTRSAMPFLAELSTYGNRVVSRPEDEEGLLDLQAICADLEPGTAVYCCGPEPMIEATE QICETRDDVTLHVERFAPKQNAILEPESAFEVYCSTSDLTFTVPPGRSILEVAQEAGL ELLSSCMEGTCGTCEVDVLEGLPDHRDSFLSPQERASNESMMICVSRCLGTKLTIDI

>CYP1017c1 Mycobacterium parascrofulaceum ATCC BAA-614

NZ\_ADNV01000109.1 13577-14839 (+) strand

46% to CYP1017A1

MTQFDHHSEDFAQNWREIYASMRNECPVAHSDEHGGFYVLTRYD DAKRVLRDSDTFVCGRDLTFGDTVVKGGVTVPTNPVRMGMMEMDPPQSQAYRQVLAPW LSRKAVEKYRPRMQEIVTWIVDRVIEAGEIDFVDDIANPLPAMVSLDYFGLSLEKWSD YATILHKAVYREPGSARDLAGLLDDLRATVKARRATAHTPATNLTEALLNAEVEGVPI DDETVTEMVFMLLNGGVDTSTALIASMFLYLDEHPDERARLQADPGLIPAAIDEMLRY FTPGPGVARTVARPVDINGQHLEPGDRVWLALGSANADPDTFTDPERINFDRDRGGTH LAFGFGMHRCLGAFLAPVEIAILLEEVLRRLPDYRIDRERVRHYPTIPLVNGYLAMPA TFTPGPRVLSGYAEALPIRLEPEVVGRG

>CYP1018A1 Mycobacterium indicus pranii

synonym Mycobacterium parascrofulaceum ATCC BAA-614

NZ\_ADNV01000109.1 29026-30219 (-) strand

100% the same except the last 17 aa of the pranii seq

these were probably frameshifted. These are

replaced here by the last 37 aa of parascrofulaceum

Submitted by Vikram Saini Oct. 7, 2009

Clone name MIP0241

52% to CYP1018A2, 40% to CYP1018B1

32% to CYP239A2 Pseudomonas sp. KIE171 GenEMBL AJ311159 4194..5354

MTSARTDRDLAALLESYDPFDRDHVEWKYDAFAYARQHCPVVRTETELTGPMWMITRYED  
VRRVLEDPETFSSVGGSPAPAPVRLGPLDSDPPEHTGFRALLSPYLTRKFALTYADEMRK  
TANELIDGFIENGKVELLSEFASPFVSRILARMVFNENDMSKMERAKEIVYRVTEDGTEE  
SFMNLGMLSAEYLFAAIENPPEEDGILRALATGTINGERLTNEQALGAISVLFLGGLDTT  
RSAIGAIAMYMALNPELEQRVRDPRWVRNDMDEFIRLTSPVGTFGRTVMKDTEIAGCPVK  
KGERLLIRFDSANRDDAKFPNADQLQFDPPRGGNAGFGLGIHRCIGMHLARVEIAIAFEE

LLARVTNFRLDADPADLKWVPGIANYPDRVPLIFDKV

>CYP1018A2 Mycobacterium parascrofulaceum ATCC BAA-614

NZ\_ADNV01000108.1 3707-4894 (-) strand

98% to CYP1018A2 Mycobacterium indicus pranii probable ortholog

MSNPAIDYEELLPHFDMWDPAHEKIKWDVLAYAREKCPVAHTDA DGGQYIVFRYEDVRRILEDPYTFSSKGVAPRPSPVGLNPLDADPPYQPDLRKILNPLF TRTFLTKFEPEMRKNAAELIDGFIGNGRFDFVREFAGPFVGNALSRAVFNEDDPVRMA HAQDVVVRVAVEGTDEAYGELVALSVQYLAEQTENPNPANEVMNAISTGTVEGGRHLT EMERLGVVAVLFLGGLDTTRGALGGIAHQLAIHPELETRLRDPAWIRQDMDELIRLTS PVGCLGRTATKDVEVGGLPIKAGEQILVRFDSANRDETHFEDASHLRFDLRRGGHVGF GLGLHRCLGAHFARIQIAIAFDELFKRITNLRLADPEAEVHWAAGIANGPESLPLVFD VVH

>CYP1018B1 Mycobacterium parascrofulaceum ATCC BAA-614

NZ\_ADNV01000108.1 6175-7389 (-) strand

97% to CYP1018B1 Mycobacterium indicus pranii probable ortholog

MTDTANSDAELASVLTETEIAALLPDFDFFDKEHADRSVQILGY ARRHCPVPPTSANGGYHIVTRYDDVRRVLTDSETFSSTEYTNIAGNGGVPLPPLDTDP PLQHGFRQLLNPFFHPKRLAASDERVREIARCTMDTWVASGRCDAMQDFAGPFVTNVL ASVIFEDDDGELFRNAAECNERFITGDTQGVLDFYQLMVQFVEKRAASSQPGAIVDAV TTGTVLGRPLTGAERIGVVQVLFVGGLDTTKVAIGDMVLQLATEPSFEELVREPGWER TILDEFLRYTSPVNAMGRIVTRDVELNGTQLHAGDRVLVHFGSANRDADVFDHADELD YTRERNPHVGFGMGVHRCIGMHLARQQIRIAIDTLLERITNLRLAPGAEIARRPGMSR VLYALPIEFDIR

>CYP1019A1 Mycobacterium parascrofulaceum ATCC BAA-614

NZ\_ADNV01000109.1 3763-4911 (-) strand

97% to CYP1019A1 Mycobacterium indicus pranii probable ortholog

MHQTLADLRSRCPVGWSDNYGGFWTLTRYDDVVDAARDHSVFTT TQGIMIPPTGASMRLVPAEFDPPEHSAYRKMVMPFFTNKVVALNHDAIRELVRECFDK FVADGHADLVSAVSDPVPPAVLAHYLGLDRNRADEMRQLMMEYLSSAKVSLDEKIASA KRFEAFVQREIDERIDEPGDDTLSKIIGVALSDENGAPLEPAAILGMVRLIISAGHET TVHGISSLCYRILAEPGLRDRLLADPSLRHVAIAEALRLDAPVMHMARTVVTGHEKRG QHLHSGDKVMLCFGAANRDDEVFPEPDTFSLDRPRSPSDVTFGTGRHRCLGEHLAVAE LSAVVDELLSRLPDARIAPEAEIRWTGGGNTRGVESLPIVFTPEKTGP

>CYP1019A2 Mycobacterium parascrofulaceum ATCC BAA-614

NZ\_ADNV01000107.1 7908-9125 (-) strand

98% to CYP1019A2 Mycobacterium indicus pranii probable ortholog

MTTDAPGSVRCPAIDYDFADPTVQSHLHETLAAIRQTCPVGWSD QYGGFWLLATYDDVLEVARDHERYTTTAGIMIPPTGASMPVVPAELDPPGHTPYRKLV MPFFTAPAVAAMEPQLREIVRDCIATFSADGHTDLVHSVAEIVPSLAIGLALGLPRED WSVARRLTGNFLSTAKVGIEAKRAAATELEDWLEELIRIRRANPTDDTLSKLVNARID GAEIPPQIALGMVQLTVLAGHETTVHGIGSMLFRVAAEPGLKDRLLSDADLMKATVHE SLRVDPPIIHMARTVVDDHDRAGARLHRGDKVMLNFGAANRDPAKFSEPFSFNIDRTP NPHLTFGSGRHRCLGEHLAVTEMLIVLEEILATIPDYRLSGEGGPADIEWRGGGNTRG PAKLEVVFTPVPR

>CYP1020A1 Frankia sp. CcI3

MRNTAPRASKGPNQLLTTLLATLPRPDPFPLYAELHQQGESFRSPLGTVYLVSHARCSESLRDPRLAVED

AALRARHRPGWADEAWSPFFDSLLFLNGADHRAVKTVAQSLLVPRALRLLEEGLETATDEVLGALAGAAK

AGEAIDVCHDVAWPLQLYTLSTFLGVGPGELDFLPGLMPRLVVLGSPLMWHSADDAKHAAEASRTLVAFF

KRIIEQRSELAARLGARWEHGLVHRLLASADAGGLDTSDVLATLVAVVVAGVETTIGLIANAVVEILRDP

RGTDFGDLRGPDSTPFVEEVIRLAAPIHIVGRRALESGTVVAGHEVPAGAHVVLLLGAALRDPAMFPEPN

QIDPTRAAGSSLAFGSGPHYCLGAALARIQLRAVVGGLFTRYPQLRLSGEPQLGRHLNPHSYSSVPVLLA

>CYP1021A1 Frankia sp. EAN1pec

MSVTETVPQDQDQDLPSFPFPDTFSPLPSGTLAEIARRAPAIRVRFGPGQIPIWLIVRHSPARAMLSDPR

FSRTKTLEFRPPLTGAQIPDPNSLLWLDPPDHTRIRRLVSTGFAHRRIEQLRPWVAETARRHVTAMTAKD

APADLRAALAAALPVDVICQILGVPEIDRENVRTWSETLFRFATNREAAAAGQKALYGYMDSLVRERQAQ

LAAGEPVTKLFDVLITTQDTDDGRLNEVELRSLALTLLIGGFETTAGVITNAVTTLLTDRSQWESLVGNP

ALLPNAVEELLRYHPLSMTFPRVATEDVDLGEFTVRAGEVAIAPFAATNRDPDLYDDPDRLDLTREPVAN

LAFGHGAHHCIGAHLARVELTEVLSALIDIVPTLRLAVPVSELRYELAAPIGRPEKLPVAW

>CYP1021A2 Frankia alni ACN14a

MSITEAVQNDQEIPSFPFDDTFSPHSSERLAEYAREAPAIRVRFGPGQLPIWLIVRYAPARAMLADSRFS

RTRTLDFSPPLTAGQMPDPNSMLWLDPPEHTRIRRMVNAGFAHRRIERMRPWIAATARARIDAMTAQGAP

GDIRTLAFHLPIEVICQLLGVPDLDREKVRTWSESLFRFHLDPKGAAEGLFALYGYMGELVRARKAAAGD

THSPEGLLDVLIAAADDDGTLTEPELHSLAMTLLIGGFETTGGVISNVITTLLTQRSHWESLVADPSGMP

NAIEELLRYHPLSMTFPRVATEDVDLGGFVVRAGEVVVVPLAAMSRDPAVFTDPDRLDLTREPVPNLTFG

AGVHHCIGAHLARVELTEVLTALIETVPGLRLAVAPAELRYELKAPIGRPETLPVVW

>CYP1022A1 Frankia sp. EAN1pec

MSTQAFEDFDPFDLAQAERHHAVMADMRERCPVARLSSGMIAVTRFADVRATLHEPALRNSHAARAPGVT

VPPEDRFFFFEYDPPEHHELRRLLLDLLSRRQSEQLAPSIRALVTELLTPLVGRGGAELVNEFSIPLASR

LMMRVAGFPEDDAPQWRQWIRDMVRSGFSFTNRNERGAGFEQCYPDVLAYLDGRLASAPATDSAQHGVLA

RVRDAQIDGEPLTRTQQRMILFSVVSAGTNTLANFMSNTLASLTREPGLFESLRDDRSLVPVVVEESLRR

DSPSMHLTRLCAEATTIADVPVAPGEKVLLSLASANRDATVFPDPDEFRTDRRDQPSHVAFGWGAHLCLG

APVARQAGVTMVDTFLGLVGAITLEPGTSPVPYLSPQGNGLDELRVCLAPTRAPARAET

>CYP1023A1 Frankia sp. CcI3

MATLPDLGDADALRDWHTSFRAIREHQRMYWDDAVGAWLVTRHADVEMGLYDHRLSSQGPTSFMAQLSAE

DLAKFADLQRFYESWMVFSNEPYHTVVRGSVQRVLTPRAVQKRQEAVRAAARSLLDRARAEVVDVNSDFA

RPLATAVISEVLGVPEQEWDNCSRWSHHIIDFISAPQPDASRAMAAAESYDQMCDYVYHLVEEHRRTGRD

DSPMLAVADVGAHAVVGTFAQFMTGGCDPISAAIANAVATLLAHPDQMQRLERDRSLIPTAIEEFIRYES

PFTLVPRVVTEPMTVAGQHLHEGSRVLFMLLAANRDPGVFERPDEVDVGRSPNPHLGFGKGSHYCIGAGL

ARLEMTESIEAIIDMAPNLELAGQVEWSSSLGLRSAVKLPVSVSR

>CYP1024A1 Frankia alni ACN14a

MTIVETESIDLYSLASFEHGHPHALYARLREHDPVHWNDEPNGPGFWAVTRWEDIRAVNRDDENFSHWPV

SMIEDFMETEDKSMVNLDPPLHTVIRRAVVPGFMPSAVRRRMTRFVDAAEAIVDEIRPAGGCDLAVDVAG

KIAAYVTADVLRIPREDAVRLYEYIEIGLGGGAYTEQERQGATEALIRYSIQVWEDRRAHPGDDVCSMLA

ACEVDGAPMSLENFSANMTLLIVGAGDTTRHLIGGGLHALFTHPDQRELLQADLDGRMPAAVEEMLRWVT

PVVYNRRTALRDVEIGGRSISAGDKVCVYYGAGNRDPREFADPERFDITRSPNRHLAFSGLGQHFCLGAH

VARAEAIAMITTLLRAFPGIHPAGEMEWTRSNFVMGPAHLPVTW

>CYP1025A1 Frankia sp. EAN1pec

MNQMPTPAAAAAPMPDEWCLKDFDHLSTDLAAVFPETMDRMRTLCPVTHTGQHGGFWVVTKYGDVLDVAQ

DWESFSSAYGLAIPPSTTHVRNIPVEVDPPEQRVYKKLVNSHFTPKAIAGWEAPARALVTDLIDEFIERG

ECEFMDDFARPFPSLSFFKFALDAPTEDLDKVSFLASKASIPNDPIGKECWAGLSEWINGFVEQRRQRPP

RGDVVDALLKAEFEGRPLTQKEIVGIVQLLILGGLETTAGALGLMLLRFSRQPEIPAYLRAHPERIPAGV

EELLRLDGPFIAIARTATRDIELDGKQISKGDRVLIYWASANHDDAEFTNPKTFDIDRSPNRHLAFGAGP

HRCLGSNVARLNMRIALEELLRRMDDIRLREDADIHFHSTLTRAPLHVPITFTPGPRSAPVG

>CYP1025A2 Frankia sp. EAN1pec

MSYDSTAASGERAGPAGESIDDDWCRNQFDHLSQELVDNLYPALTRMRSLCPVTHSNQYGGYWVVTKYDD

VLRVAQEWETFSSAFGLTVPPSPIATRNLPVEIDPPLQREFKRLINAYFTPKAVRPWEPRTRALVNRLID

GFVERGECDFMAEFARPYPALSFFDVAIGAPADQIERVAYLASKSGAPKDPDAAACWRGLSEWINGFLEQ

RRCEPPRGDVVDAILSAEIQGRPITHEEIIGTVQLLILGGLETTAGALGQIMLRFCRQPEIPAALRENPD

LLPQAVEELLRLDGPFVQITRTAMHDTEIDGHQIKQGEKVIIYWASANRDEGEFPASDEFDLDRKINRHV

AFGVGPHRCVGSNLARMNLRIALDELLRRLHDLRLRDGAEIHFHPTVNRAPVAVPVTFTPGPRVGADG

>CYP1025A3 Frankia sp. EAN1pec

MTDAATGQLDAEWVEHHFDHLSPELARDLHPTLALARSRCPVAHSDQYDGFWVVTGYEDVLRVAQDWETF

SSELGITVPHTPTPMKILPVTIDPPLQRTFKRLINTHFRPVVVVEWEQQTRALVNRLIDGFIEAGECDFM

TEFARPLPGLAFFDMALHAPAEDLEMVNHWATLASLSHLEESRESHGKLAAWIGALMAKRREEGPRGDVV

DAVMNADIEGRPITPAEAVGTVQLLVLGGLETTAGALGMSMIRFCRHPEILARLRENPELIPDAVEELLR

LDGSFICIARTARHDTELGGRQIKAGERVLIYWASANRDESEFDNADTFDLDRGRNRHIAFGAGPHRCAG

SNLARMNLRIALEEIVTRLVDVRLQPGADIDYHSTFNRAPQSVPITFTPGPRLTPAG

>CYP1025B1P Frankia alni ACN14a CAJ58987 CT573213.2, no YP#

42% to CYP188A5 Mycobacterium vanbaalenii

VLSDLTEAEIDGERLSDEELSGIVMPLLLGGMDTTAGRTGNAFLRIDADP ALRRRLLEDPAVLEIATEEFLRRDTPVQGLTRVVTRDAQFHGRQLKKGDR VMLMFAAANRDPSTFACPHDIDLDCGTNRHLAFAPVVHRCLGSNFARAMF RVMITALLRRLPDGHVAPPVERLADAGDVYTVKHLPVRLTPGPREGVGPP

ACASRTA\*

>CYP1026A1 Frankia sp. EAN1pec

MSVDDTEASAPTTQRGYATAPTLAGFSHAANERLNADPWGELDRLRDESPTFRSDMPNPLVPGASLWYLL

DYESVYTALRDWETFSNVGSAHPFSDSDPYSMIPGELDPPDHTKFRRPLNAHFSPGAIRALEPDIRRTAV

ELIESFKDSGQCDFVTDFALHFPTRVFERMFGVPLEDHDQLTAWVHTFGQQMATQTAIDKAVAAEQEVLA

YLGKKLDEREQSPREDLLGAIAFMEVDGARISRKEQVAVAYLMFQAGMDTVASQLGWSFRHLAENEVDRQ

AILADPKLIPSTVEELLRSYDILSHTMIVAKDVEFNGCPMKKGDRVVTMISAANRDPNEFPDPDTFDVSR

KPNRHMAFGVGPHRCIGAHLARIELNIALEEWHQRIPNYKVAEGAEFGQSMKWAVTSMESLPLEWDVEAV

N

>CYP1027A1 Frankia alni ACN14a

MTTPTTEITDHRIVGVGTVGDAGDRFDALRSLHRIVRVTEPDRSYWMVLDHDLARECLQNPAVFSSEVIT

PLSPDPPLSMIPIQLDPPEHTQWRRLLAQYFSPRTMGLLRPRLEERTTELVAAIRARGECDYVEDFALEL

PTVVFLELMGLPIDELPTFLEWEKQALAPTDSGDFDKDRQIGGIFSVVGYFQAEIARRRDSGERGDGLLG

AMLDWELDGAPAPDDALVNCSLLLFLAGLDTVAMSLSFAMHHLATHDADRRHVAGLAAAGEPLDGVVEEL

LRFYAVPEVGRKVKQDIEIGGQQLRAGDLVLFPLVAANRDEALVAGAGTVDLVSRPPAPHLAFGAGPHRC

LGSHLARIEMNVALAGWHRVIPAYALGEGTAPQAYWGNVHGIFSLPLAEFGS

>CYP1027B1 Frankia alni ACN14a

MDYVTGPPPAPALSLFQRMDDHQAAGRPAVRTGEAGGYWIFTDHDVILEGLQQPDLWSSSVIVPTESDPP

YRWIPIMLDPPEHTKWRHLLGSYFSPGRTKAMKAGQHRLAVELIEGLRDQGECDFVRDFAQVFPSTIFLE

IMGMPREQLGEFLRWEHMILHQNNDSDPDGSVRLAGMQAVQTYFAGLVAQRRANPDPHAQDVVSAAISWE

IDGEPVSDADVLNCLLLLFMAGLDTVAGQSSYALLHLATHPADRARIVAEPALIPHAVEELLRAYPIVQT

ARKATRDAQFHGCPIRKGDMAAFPLSAAGRDEQAYPDARRVDLDRPTTRHLSFGGGPHRCLGSHLARQEL

AVLLQEWHRLIPDYELAELPLEHGGGVWGLESLPLRWAV

>CYP1027C1 Frankia sp. EAN1pec

MSVTEPVPSRCPAVTYSPHEQRPVGEWTAFFDQLRDEAPVVRNTFANGYYVLTRYEDILSAYQDTDTFST

QAVTVLEPDPSYRWIPHMLGGNEHRQWRRQLGPYFSPRAIEGLDDRIRARAVGLIESFADRGSCDVITDF

SFHFPTTIFLELMGLPVGDLDRFMAWEANILHSNGSTPEEIAHNRTTAMAAVYEYFGSVIADRRRRPGDD

LVSHAIAFKVDGRPVTDDEVLSYCFFMFMAGLDTVAAALGYSLYHLATHPEDRARIVADPALIPSAIEEI

LRAYAFTIPARKVTRDIEVAGCPIAAGSMVQLPIKAAMRDGAAFASASEVLIDRKPNNHIAFGAGPHRCL

GSHLARHELAIALEEWHKRIPDYRLADDAVITELGRSSGPDTVPVVWAR

>CYP1028A1 Frankia sp. EAN1pec

MSTVGDRELNGAVGIVHTSIEAVNDGANPYQTLAPLHDYGEAVIMPEGYLAVWGHQACMDIMRSSAWGRH

LPDSSIRAAWQHDLTAEQAELLRQEEPPHIAPWLQTFDGPEHARQRSLVSKPFTPRRLQVMRQRTTEVVG

RLAAAAPRGVPFDFMSTIAFPIPNQVVGELVGLPLQDRDWFAERAVLLLAERDPRSSFDQLRRSTRAIRE

LGDYIRGLLRGETCPTEGLASDLLEAEETGARLTEPELLSLMLLMYVAGHGTTAHSMGNGLYVLLQHPDQ

LAALRADRGLTRSAVEEILRWDSGVTSVDYSAVEDTDIDGIRVPAGTPAHLFLSAANRDPRVYTDPGSFD

IRRTEGPTVVFGAGPHFCLGAALARLELEIALDVLLAGFASIELATSTPPRGDSFNYRYFTQLPIVVSDN

>CYP1029A1 Frankia sp. CcI3

MDGQGSVRRYINVYRNDNDIRGLENLETRVEESDVVWIIPAVAGGSIRPAVQEPKVPEVLPSEFFLNPGP

SPHATNAELRSKCPVHQINYPPGSEAYAVLGHRAVAEAFTDSRLSKEAENLPPRFRDRALSSSLLMVRNL

GFADPPDHARLRRPISRAFLPNAIADLRPRIQDVVDDLIDTFPAPGEIDLLGAFALPLPLTVICEYLGIP

VQDRPLFLEWGYILSQDPFQHAESELKAATEEFTDYFTRLVARRRTDLRKDLLSELVRAADSDALSEREL

LSTILLLLIAGHKTVANLIGNGTALLLGHPGQLDLLRTTPELIPAAVEEMLRFEGSAAWASMRVAVEDMR

LAGTEIPRGSFVHLLLSSAGHDPEAYDEPERFDVTRSPNHHLAFGHGAHFCVGAPLGRLQGDIAFTTLLR

RLPGFELAVRQDEVEWLADSSLSRGLRALPIRVRERLPR

>CYP1030A1 Frankia sp. EAN1pec

MPVQTMDFAAPSFRTDPFPAWSDLRRAGPLHRDVSGAWIVVSHREVGRLLADPRVGKDLRRLSTYGAQRP

YGPDGLAEYYIEQWMECRLPTMHRRWRQLVLPGFTHRAVHGLRAELCRTADDLLTHALTHAPSDGQVDLL

RDFARPFPVAVIVRVLGLTDLDTDRLAQLSRTIAAVLEPNAAVSAREAGDAALAELAGLLWDAVRADRGP

HPDGFLRRLVDANKGLLSPEQLIATVLLLFLSGNDTITGLIANGVLALASVPDQADRLRAHPELLPMAVE

EVLRFDAPACVAVRTTYEPMTIDGVTVERGAALLLAISSANRDPAAFAEPDVFRVDRRPIRHFAFGSGDH

TCVGIGLARMEATIALEALLHRFPRLTHDPSTLRWSDALYLRSPENLVLLCTVPPAPERACGVPEVGLGR

DLG

>CYP1031A1 Frankia sp. EAN1pec

MTDTRTPRAASGPYVFNPFADGFAEDPYPHYAQLRENAPAHRHPLGFWLVSRYEDVARIQRSGHSVDERH

ITELPEWKSESRTLGKQNRLMHGLSMLDQDPPNHTRLRRLVTKAFTRRAVDALEGRIERIVDDALDRMAE

AGRVDLVAELAFPLPFTVISELLGIPVLEHGRLRELTGTMVRALEPLPDPGLQAEIRAANDEVAAIMRAV

TDWKRDNPGDDLLTALIGAEHDGDVLSAEELVAQVMLLYVAGHETTVNLVAGGILTLLRHPDQMRRLRDE

PELAGNAVEELLRYDSPVHLMRRITLEPLSVRGTEIPPGVFVTVCLAAANRDPDFWGPDADEVRLDRTDA

HRHVSFGAGIHHCVGAALARLEARVAISRFVGRFPAPALEDVRWNGRINVRGPASLTVAVR

>CYP1031A2 SBI\_7216 Streptomyces bingchengensis

57% to CYP1031A1 Frankia sp. EAN1pec

VSTPPQSEPVIFNPFTPEFMEDPYPHYAELRRHVPVHEHPGGFWMLSRYE

DVDALMRSGLSVEQRHVAPGPFRDAYTNAGVTDEPRLKGLALLDRDPSDH

TRLRKLVSKAFTPRAINAMEPRIRSLVDDALDAIAEAGTVDLVEALAFPL

PFTVISQMLGMPPTDNDRLRLLSHTLMRSVEPTTDIEVMRAVEAADAELF

ALVGEAVSWKRDHPADDLLTALIAAEDNGDALTHDELVAQVAMLYVAGHE

TTVNLLSGGTLALLRNPDQLKLLRDTPDLIENAVEELLRYDAPVHNSRRV

TLETYHVDGFEIPPGSFILANLAGANRDETFWGPDAEELRLERENARRHL

AFGGGIHHCLGAALARIEGRVAIGELVRRFPALSLDGDVEWNGLLSLRGA

ARLPVRV

>CYP1032A1 Frankia sp. EAN1pec

MRFDPTAAAIKADPYPAYARLRAEAPVEWNDLGFWTVARHQDCLFALRDKRLGKEHPFAWAIENPDLPLI

QIHDAMMIFHDGQAHRRVRRLFTSAFTTRAADRLRPDIAAIVDELLAELVERDEFDLVSQFCYPVTLRTI

CYMLGVPRSDIDWCHSLTKNVQRLLEQDLSRAELVQISDSTVTLSEYFAEHVRDRRRNPKDDLISLLVQA

EIDGERLTEEEIIANSILLYLGGEDTNANLMANSTLALLAAPDQAELLRHDAGVVHATAFDELLRYDSSF

QMLTRYANEPVEIGGQRIEEGQTVMCLLGSANRDEREYERPDELDLRRVVKRGVSFGGGPHLCVGAPLAR

AQLQEALPRLFRAFPWMQNLTEELEYPLLVVRGPKELTLATGKQRVMA

>CYP1033A1 Frankia sp. EAN1pec

MLKPVQPADRIVGDVDDDVDYVDGQITDFHARLAALRAEKGVARLRFGPDTGLMLLRHADVVVALRDETR

FSKSGAFRPITFPFLGPNITGYDGHEHNVKRALVSPTFRRTMIPRYIQPVIRPIAEELVADLATLGEADL

MATFAKKYPMRITSRLLGIPSDEEDKLASWAFSMLHIAGDPDGAMKANAEFTEYVGPLIDTRRAHPRDDL

LSALLTEEVEGQHLDHDEVLGFLRLLFPAGVDTTWQALGSLVHAVLEHPEVHQRLRRDEEERAWAVEETL

RWESPVAADSRLTLQDVVVSGVEIAAGELVRLGLSVANRDPDVFPDPDRWNLDRRPTNHITFGLGRHFCL

GAHLARVELQVALDVLLQRLPNLRLLEQPQITGIGIRGPKTLRVAWDAPSTPGAP

>CYP1034A1 Frankia sp. EAN1pec

MSTTATLDRERVRQLFDLRSSYNVHMGGGYRQDPYPVWHRLREQAPVHPGIVHELTGFDGPAMFSGLPYP

DRPHFSAFSYAACDAAYRDPEVFASAAGPVDPNNGPYGATNSMLSMGGRQHRRYRGLVQPSFVPGKAKWW

ISNWIEETVDLLIDGFVDAGRAELNVDFCAAIPVLTITSSFGVPVDRALDIRAALTRPDEIVRMLEPIVA

ARRADPQDDLISILVQAEMTDENGVTHRLTDAEIYSFSVLLLTAGSGTTWKQMGITLTALLQHPEALAAV

RADRSLLRLAIEESLRWSPTDPMFSRWVTEDVDFFGVHMPAGSVLHLCIGAANRDPARWDRPDEYDITRA

LRPSFAFGGGAHVCLGMHVARAEMRVGIGALLDRLPDLRLDPDREAPRFIGMYERGATEIPVVFG

>CYP1034A2 Frankia sp. EAN1pec

MTRPDSIVLLDRARLREVFDLRNEANLGTVAGYEEDPYPRWHELRELAAVHPGTLHELTGFSGPVLFQGL

PFEDRPHFTAFTFAACDEALKNQEVFASSPVAVDLEGGRLAPLNSIFSMAGAQHRRYRRLVQSSFVPPRM

AWWTEKWIETTVHALIDWFAGDGSADLNVDFSAAVPVLTITGSFGVAVEQAIAIREALSSPERLVPLLAP

IIAARRETREDDLISVLVDAEVQDDDGNPHRLSDAEIYSFAVLLLMAGSGTTWRQMGIVLTALLQRPEIL

DAVRRDRQLLRNAIDESLRWMPTNPMFSRFLTKDVEFHGAHLPKGAVLHLALGAGSRDPRRWERPDEFDV

TRPPKPSLGFGGGPHVCLGMHVARAEMYTGIGALLDRLPNLRLDPDANPPRIIGMYHRGPTAIPVLFG

>CYP1035A1 SBI\_8399 Streptomyces bingchengensis

34% to CYP107BH1 Frankia alni ACN14a

MGDVVPAPWGGHLLLSHELCDQVLRSKAWATFDAEWRARQGDGNRWSAPA

SQQLSKTLQGLNPPVHTQQRRSLGNVFDRSTLAGLQPFVRQTVEELLDRL

SDRLRATGEADFATLVGEELPVATISHWLKLPQADHALLRELTHGQAYAQ

ELLPSASQLVQANAAAEGLREYFTAVVAERRRSLGDDALSRWIRTWDELE

PDREVADETLYHLVMFVVIASLETTSTLLSNMVWLLDQNPRQRSWLLTHP

EATPNAVEEVLRYDPPIHLTTRVATEDTELAGTRIERDEVVHVMIAAANH

DPSQFDDPDTFDIGRTAAHLGFGGGIHFCIGAMLARLEATELLQSLNRRF

PTLRVTTPPEWEPRMAFRRLLALHVAEH

>CYP1036A1 SBI\_10544 Streptomyces bingchengensis

43% to CYP145C1 Streptomyces scabies SCAB90701

42% to CYP217A1 Thermobifida fusca

LSQIPASDVDLYTESARTDPYEIYAELRALGPVVHLSRYDLYALPRYDEV

RAALMDWQTFSSARGVFVDPDVNAQLEGITLCSDPPEHTAMRSVLGRPLR

PDRMREVTPRIEAEADQVVERVVGRGRFEVVTELAEYLPMTVVSDLVGLP

DHGREKMLEWAAAIWNTQGPADDRAAAAGPAVEEFMAFAMNDAVPGKIDP

DGWAAQLYEAADRGEIPHDKCPVMMLDYVTPSLDTTILAIANAVALFAQN

PDQWDLLREDRSLIPHAINESLRLESPVPQFSRVLTEDHEIGGVPLAAGS

RVALLYASANRDERHYPNPTRFDITRRPSDHLAFGRGEHVCVGMHLARLE

MSALLERLADRVARFEILERRPMINNGLRGLDYLDVAVTPAP

>CYP1037A1 SBI\_3522 Streptomyces bingchengensis

38% to CYP163B1 Salinispora tropica (marine actinomycete)

MTDITFTPADVVDPELHASGEVHRLWRWMRQHAPVHWHEPGDLPGFWSLT

RYDDIRQVYQNPAVFSSAQGVLLRPTDLGEDPGSGLTMALTDPPRHRALR

GQVADRFSERCARSLAGEMRAEIRSVVTRAVESGTCDVVHDIGARLSSHN

IGRLLGVAPEDRERLLTWTTEAFESGKPLTSHLELMRYFIDMMYARMEEP

ADDAMGMFVNNEVQGGLLTETEILLSCENLVGAAENAGLSMASGILALAA

YPQAWQRLVRERDGELVRTAAEEVLRWTSSATHSMRTATADTAVQGRRIA

AGDRVVLWIPSANRDESVFPEPERFDLGRQPNRHLALGTGEHVCIGSTMA

RHQMRMLLETLAELVAVIEPAGDVEPLRSIAVNGPAHAPVRLVPR

>CYP1038A1 SBI\_7163 Streptomyces bingchengensis

33% to CYP208A1 Streptomyces globisporus

VVDLLAQARELGGVSAVRLGPRPTVLVTDPQAVQHVLALHPDRYVKRSHR

ARVLVGDGVLSAVGEPWKRQRRLLQAQFTGAGIRRYEQRIVGAARRAADH

WAECARTGTPTDVGDDMRFFALDTIWRSLTGHPLDETTNRELAAVEAVGA

ALPATPSASADVAELRAAVAADLARIDAVAEHAIAAARRGEAGPEGPGLL

RVLVEAGQTHAEYTDQLIRDELVTLLAAGHETTATTLSWLYLLLDRHPEA

RRWALNAGPAGSPEREKAFRALASETLRLYPPAWLIPRHATEDDALAGYH

IAASTDIYVCPYLTHRDPALWPEPERFDPERFTTADEGRPSSRHGAYSPF

GLGARACLGAQFAMREMTMLLEHLLPAFTPSFHTTPPSAVFGLTVRPDGP

TPATITPTPNGS

>CYP1039A1 SBI\_7500 Streptomyces bingchengensis

42% to CYP107AV1 Saccharopolyspora erythraea NRRL23338

MMGMGIRGARTAIKLATFRTMMAGAALTGDPAAKLLGRRQPANPFPLYEQ

IREHGDVYRSRLGIFCTVSHAQCRAVLKDPRFGMPVPPSPPAWEMYQGDA

DTLIHPIERSLLAVNPPEHTRLRRLVAPWFTASALRTRAARVEKIVHSHL

DRISDGQDFDLVRDFTAQVPTAVIGDMLGIEIENYEQFGRWGMALATTID

GVRTMGERRMVRAVLAEMTSFFTQLIEENRRAPRDNAISGLVGAEVDGRP

VTDEELIGLIGLLLAAGLETTVNLISNSVRFLLEHPDQKRLFLDNPDTAP

DVVEEALRYDPPAMFTVRMALEDVELDGRLIPRGGWXGGWLVQLLGGANR

DPKVFTDPHRFDVTRGNIREHIAFSAGAHHCVGSGLARLEAEIALRELFA

RFPDMRIAGDVTMRTARSARGPQSIPISVAQAVGPDPSRRA

>CYP1045A2 Streptomyces sp. MP39-85

ML-449 biosynthetic gene cluster [ACO94495.1](http://www.ncbi.nlm.nih.gov/protein/226973362)

MTTEATPTFQQADDALIKLLSPPFPDDPFPIYETLQSVNRVHKS ALGIYALSGYEEVTALLKMPDVHSGARAAAQMREDWADHISLRMYLNSMVTLNAPDHG RVRGLASRVFTPNKIKKMQPAVERRTDELINDIIEKSAGGEPVDLVEMLAMPFPVAVI SDMLGLPYEDGKRTWELADDWSRVFSGIYTEEDLVVADSAAEELTGYFRDVIKAVRAE PKDDLMSSLVQEATNGKLDEEELLALILFLFTAGFAATTNLIATGVLALMEHPDELKR WRADKSITPTAVEELLRHTAHTTASSRLTTRPITIGGTEIPEGVLVLALLSAANRDPA KFPDPHRLDLTRDNGTHLSFSAGGHFCFGGSLARMEAADLFPKLIDTFATMELAGTPG RRAIMGLTGYTSLPVRLGR

>CYP1045A3 Streptomyces sp. DSM 21069 FJ872523.1 gene = BecO

BE-14106 biosynthetic gene cluster

MTTEATPTTQQADEALMKLLSPPFPDDPFPIYETLQSVNRVHKS ALGIYALSGYEEVTELLKMPDVHSGARAAAQMREDWAEHISLRMYLNSMVTLNAPDHG RVRGLAARVFTPSKIKKMQPAVEKRTDELINELVERSAGGEPVDIVELLAMPFPVAVI SDMLGLPYEDGKRTWELADDWSRVFSGVYTDEDLAAADAAAEELTGYFNDVIKAVRAE PKDDLMSALVQEAANGKLDEEELMALILFLFTAGFAATTNLIATGVLALIEHPDELKR WRADKSITPTAVEELLRHTAHTTASSRLTTRPITIGGTDIPEGVLVLALLSAANRDPA RFPDPHRLDLSRDNGAHLSFSAGGHFCFGGSLARMEAADLFPKLIDTFTNIELAGTPG RRAIMGLTGYTSLPVTLGR

>CYP1046A1

MSVDRTACPGQPSVPPGEGMLTHSRALRFWLDPANLAARREQAGPVVPTRTGPATAFQVNDPALLRKIGTDEDTFRFWGPDPSLRDFTEDGVVGLEGAAHRKRRAVMRPAFSASRLTTLGPAAQARTRRLLAGLPADRPLDMRMEMSRLACGLLVSCVLNSELAPDTLSRIASARSTLSSGMFWRYALAPWPWVPVPRRRACRRALAELDEAVRQLLARHQPHPDGRDLVSVLEAATPENPRVVQRDVRALLIAGMETSASTLAWACYELGRHPHYQQALRDEADAAPDPSRLHADQLPLATAFVQEVTRLHGIPFLVRRTRHQTVQGGVRIPAGAVVTLPLGALRRDRDRYRDPDAFDPKRWLPHAEPPPAPTALLAYGLGPRYCPGAAAADAMLPVALATLAGSRTLRPARPNRKIGMSLELTPTPKGLTMYATPR\*

>CYP1046A2

HM038106.1 Streptomyces anulatus actinomycin biosynthetic gene cluster

89% to CYP1046A1

63362 MSVDRTTCPGQPFAQPGAGVLAHSRALRFWLDPANLAARLEQAGPVVPTRTGPATAFQVN 63541

63542 DPALLRKVGSDEDTFRFWGPDPSLRDFNENGVVGLEGTAHRERRAVMRPAFTASRLTALG 63721

63722 PSVQARTRQLLADLPADRPLDMRVEMSRLACGLLVSCVLNSELAPDTLSKIAAARSTLSG 63901

63902 GMFWRYALAPWPWVPVPRRRACRRALAELDEAVRQVRARHRPDPDGGDLVSLLEAAAPGN 64081

64082 SHVVQRDIRALLIAGMETSASTLAWTCYELGRNPHYQQALQEEADATPDPSRLQAHQLPL 64261

64262 ATAFVQEVTRLHGIPFLVRRTRHQTNQGGVQIPAGAVVTLPLGALRRDRNRYRDPDVFDP 64441

64442 QRWLPHAEPSPAPTALLAYGLGPRYCPGAAAADAMLPVALATLAGSRTLRPARPGRKIGV 64621

64622 SLELTPTPKGLTMYATP 64672

>CYP1046A3

CP002475.1 Streptomyces flavogriseus ATCC 33331

84% CYP1046A1

51195 MNVDRSACHGQPPVPPGPGTLAHSRALRFWLDPANLDQAGPVVRTRTGPATAYQVN 51028

51027 DPALLRKVGSDENTFRFWGPDPSLRDFTENGVVGIEGAAHRERRTVMRPAFTASRLTALG 50848

50847 PEVQARTLSLLADLPADRPLDMRVEMSRLACGLLVSCILNSELAPGTLSKIAAARSTLSG 50668

50667 GIFWRYALAPWPWVPVPRRRASSRALTELDEAVHEVRDRHRPDPDGQDLVSLLEAAAPGN 50488

50487 PHVVLRDIRALLIAGMETSASTLSWACYELGRYPHYQQALQDEADAAPDTSRLQADQLPL 50308

50307 ATAFVQEVTRLHGIPFLVRRTRHETCQGGVRIPAGAVVTLPLGALRRDRNRYPDPDVFDP 50128

50127 QRWLPNAEPPSAPAALLAYGLGPRYCPGAAAADAMLPVALATLASSRTLRPARPGRRIGV 49948

49947 SLELTPTPKGLTMYATPR 49894

>CYP1047A1 SGR1079 Streptomyces griseus

MSTQTGPALGTPPRGHAFVPGPRGLPLVGNLPQFGKNPLAFFELLRGHGDMVRWRFGRKRCVFLADPDLVGELLTETERTFDQPRLGIAFRTVLGNGMLVARGRDWRRKRSLVQPSVRPKQVTSYATTMAGCAVELADRLADGQRIDVKREMSALTQKIAVRTIFGVDTPADSEAMGRAMDVAQMEIGKEFAGLGALLPDWVPTPGRTRIRKAAGVIDAEVRRVVARHRDGDEERPDLLSRLLTAVDESGTRLSDEEIRDEAVTLYIGGHETTSTTLVWAWYLLARNPRVREALAEELDRVLGDRDPGFGDYAQLTYAQAVVKETLRLFPAVWLITGIAKEGATIGGLPVAEGTRVWSSQWATHRDARWFPEPEEFRPERWDAESGDAIPEYAWFPFGGGPRVCIGTRFAMVESVLLLAVLARRFTLDVDPGEITPLTGLTLQPDRDVLATVRAR