**S2 Table:** Protein sequences of selected terpene synthases

>AHY47823.1*\_Rubrobacter\_radiotolerans* MRGTAWPGLSYPFPPLINEHSDAVHAETVEWARSFGLMEEAGMREKVLATNIGRLAGRFHPSAPRERLRL

VSDWYAWMFFRDDLCDEAELGRRPDLLAAADLRYLGVLRGEEPGEEDGPLARAMRDLRERLLPVVPAALW

MRRFVRSVKEHFDSTLWEASNRVRREVPDLQTYTRMRPITGGMYVDADFIEITTGLYLPTEVRTDPTVSD

LTRMSNNAVCWANDIISLTKELASGDVHNIVLVLMAERDLSLEEAGRTAVGMHDREVTRFLALERELPSF

GRTIDENLARYVSVLRYRMRGNLDWSLESLRYRTV

>KYF56472.1*\_Sorangium\_cellulosum*

MPSERHSVVVSKGEVETFDYPFPASRNANVDIAERRTLQWIRRLQLAPEGRALSRLKATGFAQLAAWLLP

WANMRTLELASDFTAALFLLDDAYDEGDLSMDPEAVERLNEKYLGELFGYVEPDMSDPLTRGLLDVRDRI

KSSHPHFFLNRWLAHFQFYYEANLWEANNRRRARTPCVDEYLLMRRYSGAVYTYCDLLELLLERPLPLEV

VQHPTIQCVRDICNDILCWTNDYFSLGKELRSGDVHNLILVLRDNHAITLEEAIARLKQMHDERIAEYQD

VKEKVLALWDDEATRLYIGAADAMIAGNQRWALEARRYSGLESLIARAG

>KFG92939.1\_*Burkholderia\_paludis*

MKTDALKIELAALRIPVFDVPWAGACSPHAQRIETRMLEWADDHGLLVNDMYRKRVMRTRYGWLAARCYP

NADPALLQVIADYFVWYFLTDDLFIDRVETLGPGTLTHLVAIVDVLDYDQTARQPVYGERAWLDVCRRLR

ARLSAEHFARFAQGMRLWATTAGLQILNHIHAESVGIPQYETIRRHTSGMNPCLALADTANCGAVPPDTF

HRPDVQELCRHANHIVCWSNDIQSLGIEARQPGQFRNMVLIRRLEGHTLQEGVDYTAARVRDEIGEFVRC

ADALSQHADTRVRGLVDGCRYWIRGYLDWVARDTQRYAAAYADDADDRGLIAPSGSVARD

>AHY45426.1*\_Rubrobacter\_radiotolerans* MDPVRGGAGGVAVPPVVCRFDEGLSPHVGEVRKLHARWCERHGIYPSAAVGELFTAMDIGDLACRMHPGG

NAGDLALLADWSAWLLLRDDRWDAGEYLVEWERLAERDRVYLRLMRSGRTGEEPGSRRDGTRQDGLYTGL

EDLCARLRRRAADNGLPDPVSAGFLTTMGTFFRGSVRQAFLQRRREVPDLKEYLELRRVTGGLDILTHVR

AATDGFSLAGDALSGADARRLTLAADNICCWHNDLVSLNKELAGGEVNNLALVLVGDPASPCQTVEEGVE

AVVGMIYSEQDEFARLGELLRRRGGPHARTTAWYVKMLEERISGIISWQDRCSRYQVERLQGERYGSP

>KPH97530.1*\_Actinobacteria\_bacterium OV450*

MDTALSGEYVINGCSPADFAQAVGDIAPWMRQRLAEIYRPMASALADELNLWPIPGGIPGEYTFPPLPEH

IAKIDAEVQSWIDHHGLNPPGRTYPHPRLAHHVYAILHDAPVEVLRVQILWWERIIRHDDSTVEPGLLTA

SFPSEVDQILRNRVLPGEPDRHHLAFLDLRDAIADIDGGPTLLPTMADEAVALLQGSLTEQHYRTTGTVP

TLRQYLHYAADLIGIKDTIALGRLAPGGLLPGEIPPAFLPPLWRLATDIIRLTNDVIGAHRESVEGSPTV

FAAMAAQYDLAPADAARAVLALIDVLMRDFQHTIDEILPECPPKIHRELVLLQRRVCAAYAWDLTVISTR

YDPATRRREAR

>ADU09376.1\_*Micromonospora sp. L5*

MRDFALSALHEPPFPSRRHPAVDQTAAESAAWVRDFGLVEDQAGRRRLAGAHAAELAARACPEASPSGLR

LLTDLVNWLFVVDDACDDDGLGATPTLLAPTLAALLAVLDRHGDPEAPAPADGGPIALALHDLCRRARDR

GRPAHLLRLVSQLREYLLALLWEAANRERRRVPGVAEYTQMRRHTGGVRPSFTVTDLARPSAPRADQRVA

PALTVLDALATDLICWCNDLFSYGKERGATPEAHNLVTTIAGETGQDESAALYAAADRFNKTLATYAERD

AALSAVADKGMRAFLDTRRDWIRATYDWSRAASRYA

>CAN96536.1*\_Sorangium\_cellulosum*

MHRALLCPFPATTPHPQAAQLANDCLEWTRKCGLLPDESPRTLDKVRSYSALAAHCYPDAHFERLRAICD

YYSWLFFFDDVCENTSLNGAEPKVVSSLLFDVYGVLRGPTAAVGHAPFAQALADIWRRIGDGCPGFWRRR

LIRHVENYIDGCVWEAQNRQLDRVPSRAVFEGMRMHTSTMYEFWDFIEYAGDLFLPDEVVEHPLVAEVRR

AGNAIASFANDIYSLRKETSNRDVHNLVVVLMHEERIELEAAYARAAGIHDAQVEHFLDLVKHLPTFSAT

IDRNLARYVEGIRIWIRANHDWSIVTPRYNEPDAR

>ABU58787.1\_*Roseiflexus\_castenholzii DSM 13941*

MMTIEPWYWQAVESINYPFPQRMHQAVSWLEDEIVTWCYVHKLIRDHAQEQHLRSALLAEFIARANAEIP

PSMLRLIGLWTVWFFLLDDLTDTLPSVEELADLQMRILTVVSEGRAYDYDHPLILAAADLSDLLKQCAGS

VTLVRFLRALAQTLEAHLWEVSTRLADIQPDSQTYTNMRLWSGAFFPMIALADMAQGSVLPSHIFEHAIV

QELIRAATQAVLWYNDLWSYPKEIQKHKMPHNIVHILAHENRIPLSEALSLTIAQHDRAIQQFLRLKKQI

HTLNGAEDVVLRFVESIEAWLRATQDWSHRTDRYRQQMVRAIHP

>KFF23441.1\_*Chryseobacterium\_vrystaatense*

MNTLELLNKQFNYPFPTLKNPNADQLQEITENQWIDGEYLWLYEQNPDLRKKYKKTKTAHIAAQWFPTAS

PERFKPICRLMLWTLYNDDLYEESVSGDIKNIHAQSIAVLNGEISAAESTIPLASMLASLRQELLEFIPQ

ESIARFTKMISRYFTGLETELIYKEKKMFPTIAECIALRENSICLYPFLQLTEVETGIVLPPEIHEHPVI

CRLQTLACHLVTYFNEVQSVVKDEATDSVYYNIVKVIQHERQISLEDACLKDLRLHNEDLKEFVALQASL

PDFGIWQDAVVNWVHYMSMVLSGWKNISTKLGRYNAMDFPEAKELKEKLNQM

>EJL71407.1\_*Chryseobacterium sp. CF314*

MNVPLLESQLPIMIHPQMNAIVDDIKEYYKTDIFNISSENARLYGDHMSTGALYSSYIHPLGNIDKVKAV

SRYYCYWALMDDQFFDNSVDLDSIIQTFDGFQSALNEAPDIEKIFLPISEFCSRTDWTMETKEMFKSEMN

RYLESVLKLRTIEVQMKVVSLEEYLSYRAFDVAMNVIYSLAWYIQHDMPSSLYYSAEFEKIFEYSGISIG

LLLDLYTLKAKKKEIRNYAHAIRIIQRAENCDEEEAINKGVRLFYEYDSKLEEEFNRLEAKYPDAIRYFR

YIQSGSVKYCNESRKIRYKQVDDIDENLVKGRTVI

>ACY98649.1\_*Thermomonospora\_curvata* DSM 43183

MDAALVLSLADRVASLADRSGMHPAAQLIGAQAEGWARSRGLLLGDPDATPLGRARFERLACRIFPHAQP

DRVVLFARWLMWLFALDDHFDDTPLGASATSVDGLYADLLGALRRGHTKPEAGALELALEELWRDTVPGT

SPQWRHHFLRLMEEHRAACAEEAVNRRTGRIAPLADYPVLRRRSAGPFLYELAEPVLQVALDPRLKRSPA

WKALVDGTADMITWANDVVSYPKESRQGTVPVTGNLVAVACRELGMAPAQAASWVVDRIARRAPQVREAA

RAVGAELDRLEIGPQGRKDTAAVVRVLLQAPRAHMDWLAETGRYTPPVRSPVVLLHRTAAGVARTIG

>KJK55818.1\_ *Saccharothrix sp. ST-888*

MNLPAPGPVLAPANRPRTGQTPRTPEEFAAAVVRHTGWVVARGLLPAQDVPRYQVFALHELIGHSYPRAR

GAELDLLLDILGWFTLLDDRFDGPTGYRPAEAHALIDPLLAVLRSPRPDVPAPDFPTSGLPAAAPDAAPD

AALIAAWQDLWHRQAGPMTDTWRRRAAADWRACLTTFVTETLHRARGTLPGLSETALLRRHASCLYPFMN

MLERVHGTGAAAQLHAEPSLHRLRAQTADAATLINDLFSLEREERQSAAQFNMVMTLQRTCGYRRDEAIT

AVRTKVRRIQDDSDALRRQLVRRHPAGHWYLHGTRELVDGVYTWTSTSHRYHGH

>KYF75876.1\_*Sorangium\_cellulosum* MGSELAAQRYLSNDIAGLMARWIPGAVGPDLDVTIDGVIVATLLDDQIDSGLADQPEEVARICQAMLSVI

RPDAAAPRSPSKPLINAFADVWGRLTQGRTATFCARTARHWQWYLDAYVDEAKNRNRAIMPTRAEHFELR

RRSGFVYAMMDMTERAYQFEAPELAWHTPQIQSMLTITADVVDTLNDLHSLEKEEGRGDLHNFVLVVQHE

RRCSRAEAIAETRDSVHEWIASFIKLTEEIPELCASLGLTEPERDNVRQLVTGMKTAMRGYFDWSCKTDR

YATTNLVRAGQAAYPHDLL

>KYF59190.1*\_Sorangium\_cellulosum*

MNPRSGFGASQGSGGAEGFGERLKGMELNFSGFEPVRTPALLVPVEHRVSEHLEQIRSPYVDWVVDAKLV

EPGTRGYDVLMRTKLDDCAALIFPDHPRELVLYGAISLALFFALDDVVDDVNADRSRKLAYIRRVEQIAS

GDAPAARDDHIVRAWHRWFEEIEALASPRAFEGFAGALRFHLRALRAQALNQQSAAPCPTTHLMRRRDNV

GSSYFMPLAAIFLEREHGLSMQEVLEDQHVKGITDLAAFVIVLHNELLGLYKDMRSGEANFVELLRREHG

IELQSACDLAGKLADDMVKAMVQMATDLSALVDGYEEKAEAIARCVRTAYSLIRGTFDWYMITRRYYDEE

CFSM

>EXG82599.1*\_Cryptosporangium\_arvum\_DSM\_44712* MTATTSPNPAATTGSARTAVRVVRLLRALRRWAAEVGPSFADAVEIDEVSAMVLVDAGPHAPTGELLAPA

MTAVWMQVADDHVDRFTHDQAEFDGLIQRWRSVSAGARPTPGDPLERGLADLVRRLRTAPRYPSLFPVWR

RSFGRMLDAWVFEQTTATRLARGEPAPSIESYLAHHHSFGLRPIVLAWWVTAGGDDLPDALEALLAALDE

IETAVRLANDLVMADRARTEPGSVDALLLGADATWVSDRATEHLRRGHDLLAPLIETGSPTGEALGRIGE

WLVTFYLLTDARLQGGGPGRRAAPAPIAT

>EST32145.1\_*Streptomyces\_niveus NCIMB 11891*

MTCVEEEVLARQLPAVPFYCPVEPAMHPGVDVLNDLTVDWMLRQNLDTDEHQRKRLAVCDFGGLTASTMP

YGRLEPLTLMAKIHAVLFSLDDGVCDETDATADLLAQETSRILRAVEAPAANSRSDSPHTAALRALRTEL

EQYASPQQVRRWTDAMRVYTSGLVWEASWRRSAELPSLNDYITLWMRAIGMAPTTAMIEVVGGFSVTDEE

LADPRVQALTEITWTLVSWDNDLYSRNKELLRAGDDLNLIDVLCHELGCEPREALNHAVAMRDRVMVLHG

RLSEQVLADASPELRSYLVGLGQFVRGHLDWASVCPRYSVPSGPAAQPGGWWKRHPSDAGREPLPIPTIS

WWWEQLAAPA

>KFE96946.1\_*Chryseobacterium\_luteum*

MNTPELLNEQSTYTDFATEQEPLQFYLRKFKDKQEYKCYPLYNEQVSKELIEWATKKSGIKKGTKAYQHT

ISSDISYWLALSFPLTKDLNKFKKTFYFFQMFSTMDDHADEDWGDGKADTEKIVKLWKKAIKLVDTIRDG

APWHIKALRTILMRMPNIPIYMRRNYSTMRKIMNDLSPVQRERYINSFKSYMENAMLQAQMSGKEKSTTL

QQYKEYRVKSIASIPCTLMVEYLYDIVLTNEEYFHPKLQELEKLGTLHVAFINDLFSLFKEYKGTFKNLH

HAVSIFILNEGLTFQQAIDKLCDEIEQLQKDYIDLKDEWFASGEYISDNVRRFIEGQQYYMAGNEKWHRL

SKRYHGENFNTTITSGTLKWSPEGTIYTPDDV

>KIZ18902.1\_*Streptomyces\_natalensis*

MPPVYAADSAPSRIGWELPPFYCPFNASLIHPKAEELEARAVEWIDRFGLYPDPTERAWGLATRGADFTS

RIIPYGDVEPMVLFAEWNYWAFALDDWQDAQDAGPARASAAAVADEGIRLFRSLEAPGSALLPPGPFTDA

LADLVQRTRALLTPYQLRRFGEGVRDWVLGATWQTANTERDVMPSLNDFCAMRMSVNGTRFTLTWCETAN

GAELPPDVLYAEPVQALTDAAGFVVSCDNDLFSYNKEDHQEPWEQNLVNVLVRERGCTPREAVRHAVALR

DQVLALVVRLGDKLARGANAPLRRYVEMLGEWIAGDVAYHALAPRYASPRNRNPLPVADASYDLVWADAP

SSARTAPPPVPSIAWWWAAERA

>ELQ82238.1\_*Streptomyces\_rimosus*

MAVRATVVIPQLYCPIPAAPHHETAGIERRVVEWMARFGFCDNDFHHAQVLANRTAEWACRIAPDGSSRL

LQIGADWSCLGLLLDDVYLDGGLFSRHPERFLPMAVQVIHGADHPETTDGGKADPYTVAFGEVSYRYRRH

ATGTVVRRWVDGVAEWFLAACVGMGQRASGTVPSLEEYFVIGPRDRGTKASIAVIEMAEGTSLPSEESET

PRIRALTQVASALVTFANDVYSYHREVKEQSLESNLVGILEHELRVPPQEAMTRAAALHDRLMCLYLALR

ERIARRATPEVRCYLGQLDHFIRGNLDYSAVSPRYRDDPGAAPDPAPAFGVWADSPSDGSLEPLPLRTVA

WWWDQLSPAA

>CFM47198.1\_*Burkholderia\_pseudomallei*

MPATPAPAPMPPARRLVGEACRIASIERSFERRFDPHRRALHAHCVRWIDEQSLAPAGSPPADLRALRYP

DLVAGYYVGAPPAVLEAIAGLSVWFFVWDDRHDEDARRLRRAAWARLRDALCAVLASPRARVADAEPIVG

ALSDCIVLRIRAWLGDAWNRRFTGHLRQMIDAYDDEFRARLAARIPTRDAYMRLRERTFGCEVWLDCLEL

AAGRALPDAVRAAPPYRLAGPARRSNSPRFTTISVRCARSAKPKKSTISAFR

>Q9X839.3\_*Streptomyces\_coelicolor* A3 (2)

MTQQPFQLPHFYLPHPARLNPHLDEARAHSTTWAREMGMLEGSGVWEQSDLEAHDYGLLCAYTHPDCDGP

ALSLITDWYVWVFFFDDHFLEKYKRSQDRLAGKAHLDRLPLFMPLDDAAGMPEPRNPVEAGLADLWTRTV

PAMSADWRRRFAVATEHLLNESMWELSNINEGRVANPVEYIEMRRKVGGAPWSAGLVEYATAEVPAAVAG

TRPLRVLMETFSDAVHLRNDLFSYQREVEDEGELSNGVLVLETFFGCTTQEAADLVNDVLTSRLHQFEHT

AFTEVPAVALEKGLTPLEVAAVGAYTKGLQDWQSGGHEWHMRSSRYMNKGERPLAGWQALTGPGTSAADV

GALLADAVAQRARSYTYVPFQKVGPSVIPDIRMPYPLELSPALDGARRHLSEWCREMGILSEGVWDEDKL

ESCDLPLCAAGLDPDATQDQLDLASGWLAFGTYGDDYYPLVYGHRRDLAAARLTTTRLSDCMPLDGEPVP

PPGNAMERSLIDLWVRTTAGMTPEERRPLKKAVDDMTEAWLWELSNQIQNRVPDPVDYLEMRRATFGSDL

TLGLCRAGHGPAVPPEVYRSGPVRSLENAAIDYACLLNDVFSYQKEIEYEGEIHNAVLVVQNFFGVDYPA

ALGVVQDLMNQRMRQFEHVVAHELPVVYDDFQLSEEARTVMRGYVTDLQNWMAGILNWHRNVPRYKAEYL

AGRTHGFLPDRIPAPPVPRSSPALTH

>AHH94051.1

MAMQPFELPTFYMPHPARLNPHLEGARVHTKAWAREFGMIEGSNVWDERQFDGMDYALLCAYTHPECDQEMLDLI

TDWYVWVFFFDDHFLEVFKRTKDQPGAKAYLDRLSLFMPHSGPITEKPTNQVEAGLEDLWNRTIPRMSDAWRQRF

IVSTENLLKDCVWELANIVEGRVANPIEYIEMRRKVGGAPWSADLVEVATEAEVPASVAHSRPLRVLKETFSDGV

HLRNDLFSYQREVEDEGENANAVLVLKEFLGYDTQRAADAVNDMITSRLHQFENTFFTELPLLCEENGLDPAERM

RVLVYARGLQDWQSGGHEWHMRSNRYMNEGGTAATASPSLGSFLGGPRGLGTATASIGSLVGLGG