

Journal of Plant Pathology

Secondary Metabolite Gene Clusters from the phytopathogenic fungus
Gaeumannomyces tritici

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Predicted BGCs and backbone gene sequences. BGCs had the boundaries adjusted according to the cblaster and the expression profile results.

Backbone genes are indicated in bold.

Genes belonging to BGCs with adjusted boundaries are indicated in blue.

Predicted BGC and backbone gene sequences

>GtPKS1 backbone gene sequence (GGTG_13042)

MAGSRLPAEDDGGSNSSSSSSSAAVGLIVFSHELPGGDSVQDLLRRLHRHAKRPRHGLLAR
FLRECVAVLRHEAQALPRDERAPAPPFSDVAALGSCWEALRRGPVGGAWEGAMVCLYHLAVL
IGHHEATDQPYHSQDSAPPCLVGVSIGLFSAAVAVSPTLTDLVSCGAEAVRMAFVFCRHVG
RVSQLETTIPTTPGRSPSWASV IIGLPADVQAE LDLFNNGAEQQAGRQGDDGDDDDGGM
ATALTRVSISHVDHGSVGVGTGTPSRLAELFAKSKPLGASRHAALPISGGLCHVPHVYGDDDV
RAVLRAARVGERWGRGNRRRVVRPLLSPHTGSPFEAADAAGLIEEICA EALT KPLFFDKVAE
GAAQTLRSLDERELAAAGTQPSRLGVLHYRTSVVSDGIVA AVEGRLLSSRAVVVQRQDVVD
WVVQQERGGEVGMGRDHLVGNPGSPQDSKLAVVGMACRMPGDADTPDKFWELLVQGRDTLAE
VPPDRFDLDAHFD PAMKAENTVNTRFGNFVSGPGLFDAGFFNMSPREAQQTDPMQRLALVTA
YEAL EMAGFVPGRTASSHASRVGTYYGQASDDYREVNASQKIGTYGIPGTERAFGNRIN YF
FNFQGPSFNVD TACSSGLAAVYAACSALWAGEVD TVVAGGLNVITSPDIYCMLGKGHFLSPT
GQCKVWDAGADGYCRGDGVGSVVIK RLEDALADNDVVLATILAGATNHSSESVSITQPHAAI
QKNNYQ RVM DRAGVDPLDVS YVELHGTGTQVGDAVESESVLDFFAPDHSRQGQDQHLALGAL
KCNIGHGEAAAGIASLIKVLLMYRHGVIPRHIGIKTAVNPVVARHLAGRNAGVAFENKPWTA
PDGGDGK RYSIVNSFGAHGGNTTLLLEDGAPPAASLHHQGGDGGDDGRHEVVCISAKSKAS
LRGNVAALLGYLDANPDARLRDVAYTTSARRMH HIRVAEAVSSTARLG DVL RAMAADD AAL
DAHACHVARQGRKKVVF AFSGQGC FYRGAAAALCERSPDFARLVLELDRVVVQLGFPSVRAA
VVENKTDGSLVESDVGGSDLSPLVAQLALVVLQIALARYWALLGITPD AVVGHSLGEYAALC
AAGVLSAADALFLVGRRAQLTAARARGGAGSHAMLSVRGVSA AQLAEMYPPERFGYEVSCLN
GRADTVVSGPRDALVALRDATLLEEKKAATGLKCVLLDVPYAFHSAQMDPVLADFEAAARRR
VTFKRPQVPVISPLLGRCVLPSEAHVINETYLRRAARERVD FVS AVAAAAAAGLADDG SVWL
DIGPHPVCSTFVRNCRQE QKEEPAAVTALPSLRGDDSLA AWSSTLAALHRLGLPVAWDEYF
SRRGHGECSKAPQLLHLATYCWNNKNYWIPIYEGTWTLDKADPAAAAEMHRQRTSRRQPAGEV
PFLTSSVQRVAFEDVGEKTARLTAISDLRHPHLLGAATGHKIHGRSVLTASIWADICLTVGE
HAYKRLVPNATGVLMDVRDMRVVAAQLIAEEENDGDPAASPPAQQLIRIEAGLDLSLGRTNV
GLWTCRADGSRDPADRAFATAVVWYYPDDGTAAMARQDWAAEWRTAAHLVGSRIDALWDSTT
AAATGSGEAGGGASTSTSSALS NRATYELFANIVDYG PQYRAMRRVALDPDALEAAADVTL D
DDRHG DWRTPPHWIDGAFQLAGLVMNSFGDPAAGSPAR DFFFITPGWRRRLR LLEPLRGGVGA
GYRNYVRMAPEAGGASYVGDIYLLRGKT VVGLCEGIEFKRVPRALMAVMFPRRGGRGGGGA
KSSNGGGIRNHPLPTTINYGAGTAAAGGHAPSPKAAPPIEAATPTAAGTAETESIIVTPPSS
TASDGATGAGEKQH QH PHVAASMR LIARETGLDAEDMRPETAFADVGVDSLMSLT LADKLQA
ELGVPVKASLFLECATVADLERWLMKVGTHA

Predicted cluster (antiSMASH prediction)

GGTG_13028
GGTG_13029
GGTG_13030
GGTG_13031
GGTG_13032
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GGTG_13035
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GGTG_13045
GGTG_13046
GGTG_13047
GGTG_13048
GGTG_13049
GGTG_13050
GGTG_13051
GGTG_13052
GGTG_13053

>GtPKS2 backbone gene sequence (GGTG_11488)

MAAIAIVGIGCRFPGDASNVEELWGLMAEGRSAWSRIPSRMNAAGHYHPDPSRQGSFHIKG
GHFLKQNVAAFDPSFFAISPNEATAMDPQQRILLEVTYEAMESAGIPRESLDGSDTTVWIGS
FVKDYEQVCLRDQDDAPQYAATGNNGIAILANRISHSFNLTGTSQTVDTGCSASLVAIHQACQ
SLLSGECSTAIAGGVGLILTPNTIHPMTSLGFLSAEGKSFAFDSRADGYGRGEGAGIVILRR
LEDALASSDTIRGVIRSTVSNQDGRTPGITLPNMESQADNIIQAYDKAGLNPLRTGFVECHG
TGTKAGDVRELRAVHRSITSGRHIDDPVFGSIKTNIGHLEGAAGVAGLIKAALVVEKGIIP
KHLNFEKPNTEIDFSDLRVRVPMELTPWPEQGLRRASVNCFGFGGTNTHAIVEDAAHHLAEA

GLRGFHACHLFESSNTCPSTSQTSLNDEPRLFVYSAHEKNRVGVVARLHAS YFRKKLNQEDS
 SDLMDRYEHTLLNRRSRLEYRSYIIISRNHQDLVKKLSAGAVGAVIQCPRDTNTRLAFVFSGQ
 GAQWWAMGRELLDYPVFRDSIEAACRYMHKSLNGSPTLLHELEASTCEDDSIIDLPHLSQPL
 TTAIQVALVDLLQASNIMPAAVVGHSSGEIAAAYACGIIISRESAWKAAHFRGHCAEWQADK
 SQPTGKMLTVYLSEQEVQQYLDIVPPGSVGIACYNGPRFLTLSGDQEAILDIEKELKRKGLT
 SHLVNVQAAYHSHHMNAIAGSYRQAIGQIEMQMPPVDGAKMYSSLTGSEILPNDLHADYWVK
 NLVSPVLFDKAVTAMVQAIKPDVVVEVSPRVVWATTIGRILRAMGHPVSVPCLSVLHKGANA
 AESALNLLGDLWARGCDIETGWARGGGDGGRGDGGERSQAALPLQHLWDLPPYPWNHDKFW
 SESRISKGHRFRAHGREDLIGAPVNPMPPTDPAWRGFFRLGENPWIEDHQVQGAIIYPAAGL
 VAMAVQAAVQLAEGSGREVVGFEVSNFEILSPVIIIPRSADGIEHAILTRPAAVAAAEGGPVA
 RRAWAAHEFSIVTGTGGQAAHKHAQGLVTILYGGGGGGGSSQQGAEGALGFDPPQLREYEE
 ARFLCGDVVAPRHLYERLAGLGLNYGPMFRNMVAVARGQLGTHQCHSEIRVPDTRAGMPLAW
 EYPHVMHPATLDAMVQTVFALGEDEAMMPCSI RSVFISAKSPRAAGDRFVGYTKARGAGPRQ
 VSADVAMFDARAAAADPEMVVVKGLLLRSARPADGLGHLPNHRNLCAEVVWKEDLGGSAPES
 LETWDLRGHATPSLAVLQVGGGGGGGSAATTATTAAEFARVLAGGYETPRFASYTLCECPE
 AAMAELQAAGSLPSRVLERVAWDAPVEAVPEASHDLVVALVERS QLQDITAAGLN RVLVPG
 GHLVMAVEDGGAGCGGGEAGLEELRSVLVSAGFEEAGTLAGFGSLPEGQRYMLAKKPSAPAR
 LPPSAAGPAHEVVVLPQEPSARVVALGGLIESRIRGSSLAGGRCRFVRFSPELDALEGEAT
 HISLLEAEHPFIFGVDESQWPAVRRLLLLPSMIWVTGGGQMSVRDPRMAAAVGLTRTLRSED
 SQRRLVSVDDIDLQADHDDSTVRAIVAILQASMAEEGGGGGAAAQKEVEHVVRGGRRFIPRL
 MTLTALNSLIEKGDGRPEHVEDSALWQQEGGGAGRPRK LAPASVAGSDGLYFEDDAE AIRPL
 GKTEVRVKIETCQLLPDDMDAIANHS GG EVGSDAKGSVVEVGREVTSCRVGDAVVVFARGTI
 KTSVVVHEKFAWTL DGLAKSSSHLSPTAMLTATYGLV VYGRLEKGETVLVHAAASAYGQAAV
 HIARAKGAVVIAVVSSEEQRRVVREKLHMADNMILSEDRRLALSVQSLTGGNGADII FNPTP
 RHLAANFECCA EYGRVAQLAFKSLEAPDMRQAVVKQISFETFDIHNLA KR RPAMMDRTL LQL
 KELLPLKTLANMQAYPTREHGFDKLGA AFKAFTADTYLGSHTLV AHDTARIPIRIKLTRSAE
 LTAEGTYILVGGFGGIGRAIAQLLVKKGARHLVFLSRSGPKSEAAMGLLKMLKSLGVTTTRNV
 PVDVCDEDQLREAVATIQLDMPPIKGTIQCAAVLQDSAFVTMTFEKWQAAFRPKAMGSWNLH
 RCLPDDMDFFILLSSASGVLGNQGGQANYAAGNTFQDALAEHRQQQTS DGPDKSRTNLSLDLG
 LVLDAGMVAENERLLGAMLANGFFGVRLADVRYILERAMAQTAVVVKTPTEGILRLPAQVVT
 ALGTGGLTLQSGNEGGPRHWTSSGLFDYLN MVDVPADVAAAAASQPRTTAAAARRPGRKGAK
 ELAAEIRAAPSPDEAGNVAVAAVARQLGRLLDNNNNSSGGSSSESTTMDVTRSTRDYGVDSL V
 KLVNTRWIANQ TGVAVGDIDDFASIRDIGHHVSRRVLESGANDAE

Predicted cluster (antiSMASH prediction)

GGTG_11479
GGTG_11480
GGTG_11481
GGTG_11482
GGTG_11483
GGTG_11484
GGTG_11485

GGTG_11486
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GGTG_11490
GGTG_11491
GGTG_11492
GGTG_11493
GGTG_11494
GGTG_11495
GGTG_11496
GGTG_11497
GGTG_11498

>GtPKS3 backbone gene sequence (GGTG_10423)

MAPSIIHVNNDRFDEGLPASVDHSVLHGSKATRLNGSRQDATSNGHNGYLHSLNGHVNGNG
TGPPPLPAPTPDAPIAICGMACRLPGGLHTPQQLWEFLLAKGDAKSTVPESRYNVEAFYDPS
GRPGTVNTRHGYFLDVDLTKVDGAFSSFVRGSLERMDPHHIQMMEVARECLEDAGVTGWRGG
LIGCYVGSFGEDWVEMNAKENQPYSVYRTTGSDFMLSNHVSYELDLKGPSMTVRTACSAAM
VALHEACRAIQRGDCSSAIVGGANLILAPGMTQAMSEQGVLSPEGSCKTFSADADGYGRGEA
VSALYIKPLDAALRDGNPVRAI IKQTATNADGKTQGVSMPTESHEALIRKAYELAGIDDFS
KTTFVECHGTGTPTGDPDIETSAVARVFGSKERELYIGSVKPNLGHSEGASGLTSIIKVVMA
ENRVIPPNIKFSKPNPNIPFEESRLVVPVDPTWPAGRCERASINSFGIGGTNAHAILESAS
SYGVGAGALPLTPSSSSISSSSDEARVPAEEPQLLLYSANSSSSSLKNTVDNFQSFVESNPDK
LARLAYTLANGREHLAHRAFAVATRGGSSVVSFVRAPQQPPGVVMVFTGQGAQWPAMGAEL
LMQGSFVFRSTIRSLDAALAETLLVKPEWSLERELLKAGKQSRVDQAEVSQPLCTAVQVALV
DSFAAVGIRPAAVVGHSSEIAAAYAAGALTAREAIVVAWLRGVAAKMQQRKGSMAAVGLGW
DEVKPYLAGTTAAVACENSPHSVTISGDTPAVEAVLAKIKQSRPGGRDVLARLLKIDKAYHS
YHMAEVGGWYRNALEHHDVVAGGARSCLFYSSVTGKLLRPGDSLGPYWTSNLVSPVLFSTA
VSEMLRNPDVAGQPNRSVTLEVGPSAMAAPLRQIMADATPPATLPYVAAMIRSRNCVESYL
TAIGKLHQLNVAIDLRLSLPGGPGASPFLPDLPRYAWDHEETAWWESRTSKEWRLRKHPYHE
LLGIRTTESTDLEPTWRNVFHVHESPWVRDHHVIADNVVFPFAGYMAMAAEAARQVTGLEDDY
ALRHVIVSTALVVAEGKPLELLSTLRPVRLTDSLDSQWWEFSIASHNGVMWTKHCTGQVRSL
SRAADGAGILAAPGDDARHSMTRTLGSRKAYKIMQEVGLRYGPLFQPLRNIRTGTLDRSAAA
EVAAPRLEGSAALQPYHLHPIVLDACLQILSVAATKGYTQKLSMAIPTLVEELEVYRSESGV
EISSEAEISSLGAITGSCRCFAADGGGAVLSMSGARLAMPGGGPEGPVKGAHSTARYCWEP
HVDFLDERSLVDTPAAEDRSLYLPVLDEMTQLCLVYAQRRLASLRTELPMARYGAWISEQA
SRADAATVAMADWALFEAVESRLALRGTAAGTALAVFNVLSITGIFQGRIGASNVLLAD
DSLAKIKALRDAAFDTSRLLRQLARSRPDMRVLELEAGNGERTVEALRSLVHEQQPGGPVLY
STYTFTDPSSGVVTAAKERFRAAANMQYRALDISQPLEEQGFAGDSEEGYDVIIATNVIHAA

PRLSEGLTNLRRLLRPGGRVLLQEFSPGPSSRWLNFMGGMPRWWSGVADGRAEEPYIDLAA
 WGRALADAGLAVSASVPDSPREDLRQNNLMIVRHAGTVARSPSGREVTLPCRPGEDLPVLDE
 LKRELGVLG FVANQRGLGDEVPPGEDVIALLDHGPEAFFDGDIDEERYGAFRGLVGAAAAGGA
 AILWLTRLCQVAPVESPAHAQVIGVARALRSEVGAAALATCEVDDPRASAGSVAAVFHFAAA
 REEAAGSDGDPAALDPDYEYAVVGGVVHTGRFYPPFSLADELRCADAGDRVVLRTKPGLLAA
 LTWSRQAPTPLEGNLVDVKVSAAGLNFRDVL SANGIVDIPEEGFGLEASGVVSAVGPDVRHL
 RPDGRVFLNNGSFSTSTITIPEELCEKIPDGLSLEDAATMPCVYATAIYSLFNIGRLQRGQS
 VLIHSACGGVGIAAIQLARMAGAVIYTTVGSEEKVKYLMDTFDIPRHHIFNSRDTSFVEGIK
 SVTKGNGVDLALNSLSGELLHATWKCVAEFGIMVEIGKRDLLGSGRLEMDVFLANRSYCCVD
 LDQLCFKRRRAICKELLRRIVDCYNDGHIQPIRPVTVFSAGKVREAFRFMQQGLHMGKIVIKI
 LESPADADPEEELAAATRRELSLGGDGPDDASYLLVGGLGGLGQAVSRWLVGGRARHLVYLS
 RGAGSGAGDAAFIEELNSMGARATLVRGDVCECADVRRAVEAAGGPARLRGVMQMSMVLDR
 AWDSMTLDEWRGAVAPKVQGTWNHLHLATLG CARLDFVLFSSISGIVGQPGQANYAAANAF
 DSFARWRLSRGLPASSVDIGAIDDVGVVAENEAIRRAMKTTGAYMVSEAEELLEASMLLR
 EGGAATGANFVLGLASTTPLTSPNNRSLWRKDRMAAYRNMAAGEDGSGPGGSSSSSEALKT
 WLKAAQGGGDEGPLKEAGAVDFLAREIGKKLFTLVLRPEDEIQTSVALSDLGMDSLVAIEMR
 SWWRATFGFNISMLELLGMGNLEALGAFaingMLKAFEK

Predicted cluster (antiSMASH prediction)

GGTG_10413
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GGTG_10417
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GGTG_10420
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GGTG_10441
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GGTG_10443
GGTG_10444
GGTG_10445

>GtPKS4 backbone gene sequence (GGTG_11347)

MSPFLEADTAVQRSEDAIIIGLGCRFPGDATTPSRLWDLLEGRSAWSPVPASKWNAEAHYH
PSSDHGGSTWIKGGHFLQDGAQNGKEFDALFFNITRTEAMSMDLQQRIVMENVEALENAGL
RLEDVRGSRSTS FAGAF TDDSRVMNEDPDVVLKFKPTGTSNSII SNRVSYFYDLRGTS LTL
DTACSSSLVAFALACQDLRAGASAMSIVTGVNVIESPETMYRMSNLGFLSPDGRCFSFDARA
NGYSRGEVGT VILKPVA AALRDGDTIRAVVRGSGTNQDGQGTGGMTLPNKAAQEALIRDVY
ATYSLDLDTGTFVEAHATGTPAGDPLEAGAIAS TFKRVGPSAASKPPLWIGA AKTNHGHLEG
ASGVAAIIKTVLTLEKGIIPP NINF EKCNPRIPVDKWGIKLPLEPTPFLGADGLRRASINSF
GFGGTNAHAVLDDAASYFKQ RGLGGRHATEA ISETSAAAQSATPTSTFPSTHKVFLFSAHDE
AGIDRVLSTYAKHLEAEACPKDDAYLSSLAYTLSQRRSRLAWRVAVTADSHASLVVALKDSS
TKSRAVRTNAASKPALGFIFTGQGAQWFAMGRELLPYAVFRDSVAAADAYLRTVGCDFSILE
ELTQRDAETSRVDEPLLSQTLCTVLQVALVELLASWGAAPKR VVGHS SGEIAAAYAAGALDR
ESAWRVAYS RGVVSGRPSPSKGAMLA VGCSADSVAPLFKEVDGKLGTGGELVIACYN SPRSL
TISGNEAKIDELQAAAEKSKLFARKLRVSRAYHSSHMQPVADEYSKLMG LLTRPAEAPAGEK
VQVFSSVTGKAIDVLEMAQATYWTRNLVSPVR FQQAVHQLCTTNTAKRQLKVGGGAELPVTH
LVEVGPHGALQGAVRETLLSDPNLKALRYLSVLTRAKHAAVTALNAVSTLAAAGHPIELAAV
NREIRSSSAVLTDLPYPFHHGPAQEYWSESRRSKAWRFRKRARHDLLGATVPDWNPEEPRW
RNFLRVSELPWLKDHIVTGSIVVPGVSYLIMAIEGIRQLYEARGDGV LIGYNLRDIIISRAL
QVQEAEDTEVMLSMRRLAES AQADSAAWWEWKVTSFSPHDGSWLEHCRGQIAAELDSSAHIA
TGPIDSGREAAERTQLYRLLAESTALCNHKSANIARQYADLERVGLVFGPLFRNITAVQMA
DPSVTGRVQGALGTLVVPDIAAGMPARAIS SHVVCPPVFD SIIHLFLFAFQGSSTSDGRPLT
EPMVPVAIKSVWISADIEAEAGAQLLVHSA AQLASHKRFGADITVWSGEAVDRDIRLVLRGL
EAVPLQETQAGGGGEAREICFDLEWAADV D LLEETGATEAVLRSEVVSVEAPTARAANLERL
RNLQLAAAIYISEAVDDLERNPLTDEKGLPSHQQRYLAWLRHQAEFFHQGR LIHQDESWKTI
KGSPAERQRFLEDFEVNGGPEGRLTARMGRNIVPGLRGLEGADALHLMFGLDDLLEEYYRVI
LGTEQVHTQLGAYLRLLGHKRGADLRVLEIGAGTGGTSTAVLEALCPGGGRAHGDARLLRYT

YTDISAGFFEKAGNKFAKWKVGGVLEFRVLDVEKDIEAQGFDDGAYDIIVAANVLHATADLA
 KTLANVRRLLSPPGGKLLLQEITQPEFVAGPLCFGQLPGWWLSTENYRPWGPLLSNEGWVRAL
 RENGFSENVLALSDTPEANLHAQSLIIATVPTAALTQSPIDEKDKIVRVFVVAQTLEPAQLL
 FAEDLAQSLRGIGGAVPDVSVVAFADIAQQGTLKRTCIVIVALELFSPLLASAMTPDEFETLR
 QLITTAGGFLWLTGDPYESPDMALITGLVRTLRLWERDLDSADLVTGLRLTPSVEHVKTVYSH
 HFVGHCPPTDRHAEYLVSSGDVLQINRLVAAKPVNGFIAQRTTVLPPQPQALGADPTRSLML
 STSAPGRDLRLHFVDWPAYQEPLPAGQIEVEIKATGLNFRDVMVAMGEVAAATFGHEGAGVV
 TKVGAGVADVQIGDRMLVLSALHGTFTQTHTRIPRDIAAKIPDSMTFEDAAGIPVIFSTAYYC
 LCDVARLRKRETVLIHAAAGGVGQAAIQIAKNMGATVFATVSSAEKKQLLMQHYGIPETHIF
 SSRDLSFAAGVMRMTDGRGVDVILNSLAGEALRASFNCIATFGRFIEIGKRDI FANGKLD MF
 PFSRSVTFAACDLYTITKLDTATTARILVTVLDMFASGKVHAAMPQTTYSFAQIEEAFRLLO
 QGKHMKGKVVLTADAADVVKVVP RPPVPTRLRPDRTYLLPGGLGGLGRAIAKWMAQPQQGAKN
 ILFLSRSGGDGDVARELLGELEGMGVRARAACDVGDEAELTTTLNTASRDGFPRIGGVIQG
 AMQLVDSAFEFMQORSWEAALAPKVRGTWNLHRHTPPDVFDFVMLSSICGLVGNRGQANYAA
 GNTFQDALAAHRRARGLAAS TLDLGNILGVGYIAENAATLNANPLFFFAHDGVREDEF LSF I
 EFHLDAQRASRQPLGAQVAVGLATSADFRSRGLPEPTFMKTPLFTQLRSVGGTGGGGDDGGK
 DGGVSVAHALKFADGPEAAAALVQDALVGRLARTMTIPRDDIDAARPIHAYGVDSL VAMEFR
 NYIGSDCGYDIAVL DIMGNKSIAALSREIANGSRLCRFAKGNSEGLS

Predicted cluster (antiSMASH prediction)

GGTG_11330
GGTG_11331
GGTG_11332
GGTG_11333
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GGTG_11350
GGTG_11351
GGTG_11352
GGTG_11353
GGTG_11354
GGTG_11355

>GtPKS5 backbone gene sequence (GGTG_07526)

MDEPIAVIGLDARFPGDGDTAERFYEFLLAGRSARTEIPEDRYNADSFWHPSGDRSGNVRAK
AAHFLKGSISAFDAPFFSITPAEASAMDPQQRGMLEAVYKALENAGI PLEQVAGTQTGVVYG
CMYSDYDRMTLKDLDIPSKYSALGSVASMLSNRVSWCFNLRGPSMTIDTACSSSLVALHQAC
NSLKLREASMAVVGGCNLIISPEFSQLLDGAGVLGPDGVSYSFDSRNGYSRGEFGFVVILK
RVADAIRDGDVIRAVIRNTGSNQDGRSPIITAPSKAAQVDLIKRVYAGAGLDPSATRFFFEAH
GTGTAVGDPIEAGAIGQVFSSYRSPGAPLYVGALKSNVGHLEGAAGVAAVIKGVLTLERGVI
PANTWFEKRNPKILDEWNLEFPTAPMAWPQQRGLRRMSINSFGVGGNAHVVMDDALNFLAQH
YMSGCHRTIASPVAPAAAAAAVAPPVVVSRPPQRGLAALRGDEEDAGSATSAGSVSARSDSG
IDLTDNESSGSKSPAGSRSPLLAAVDAPVTATTTATATATAIATAHVTA AE PQDGSSQEPLL
FVFSAYDQEGVTRVQGGQIRDYIASAPKRSFRSPTARSSRSRTSSWSSTSSKSNRDELVADLS
YTLACRRTRHGWRACCTAKSRRELMTSLQAKPIVTRAATDPRLA FVFTGQGAQWPSMGRRLI
WAYPAFRESLYAADEYLNSLGCVWSLTYELCKNKESSRIDDAEFSQPICTAVQIALVDLLRT
WKVRPHAVVGHSSEIAAAYAAGQLSRKSAWRIAYYRGKLSKGLIRAETLASTGGS LDEQQS
KPKTGMAAVGLDKDKTMAAIKRV DAMMDHG TLEIACLNSQDSVTVSGDVGKLDALVEMLKND
KVFARRLNVEIAYHSRHMKPIVDDYRRYMGDISSDL PAPAQEGQTPVYFSSLEGGLIPT SRL
RSPDYWVDNLVSPVRFHEAVTQLLQSDLNTGSLGHGKEQITDLLEIGPHSALRGPLRSIIQQ
ARGAAASKVGYETILKRNESAVDTS LGAAGTLFCRGFPVDLA AVNRQRPAAAAAAGRLDGAD
GDPVKMLTDLPSYPFNHTKEYWLESRLSRNHRLRHAPRHELLGAPVPGWNRHGNAVWRNYIR
RSENTWVEDHRVGADVLYPAAGMLVMAIEASRQVAAL EAAENETRP AVSGFRFSQVSFHTAL
LVPDTELGVESHFFLRPSREAGRDGWSEFQLWTSEGD DWREHCRGFVRTEYSKDALT PADGQ
AVLEEAKRCTSKVKA AKLYRAFGDIGLGF GPTFQTLRDVKLSGNRVLAQADALVSKIRRAAP
LQYLQPHMVHPSTLDAVIQAGLVPLLDLGAASSGRGVKDS CVPIHASELWISA ADEHGGGV P
NLHDSSY MISALT KPGPGYRDARASIT ALHAETSLPVVTIKGLVFKALPGTGGQGRLEGVHR
PALALQWKPDPTLLNAAEAARVFGCP ESEKDKDVSLAIKSMADCEALAVLYMRQFLES LKES
EVDGMQWHHKHYVSWMRNVVATSAVQAAMGEMPELEARVAGTPEGKLVTVVGRNLSGMLLGA
TEPLDIIFGDRAAENVYRYSEGSRRC AAQLCSYLDALAHRNPKMKILEVGS GTGTTGHVLD
TLANVADGTRRFGHYDFTDISPSFFENAREAFKDHEENMSYRILNIDKDPAEQGF EAGSYDL
VLAANVLHATSDMTRTLGNVRRL LKPGGKLLVLELTNTDVAFS AF CFGALPGWWLSE DGREG
GPLMPVESWRSTLGKVGFSGLDAVFSDFPDSEYRTSSTLVSTALPPADATEGAAAAAAAVDG
FRKQQDSVFILVDVAPSALQVHVADALSAALSTQGAVVRTTTMTGT KGLPVEGATC IALTEL
DSPALCGMSEGFFTALRDLTSRCGTLVWLGRGGVGLVADPHHELV TGLARTVRGEGRAGGRG
ALQFVTVSFAESES GDTIAEKT LQILAQNKA AIAMDDAQPDNTFRVADGVVHVPRLVEATHL

VRHLQAASAPASAALAEEGEETPSSLTEAEATALGRLLAAWTALREMDAVREGDVVLIHAAPA
 SKSEASVTQAAVQLAHHHGAEVFVAVEAAGAAWGAQGAEAYGLAADHVLSGDDES LGPAIRD
 RTGGRGAKVVVEVSRSASEETRMLLD CVATFGRFVDMVPTGGDEGGSSSSSSSSSSSSSSSSSS
 SSSSRQQTAADVGRSNVRLDTVDVEALVSADAEGARAVLERAMAFFEGQPQQQRPASPTDGE
 AVPTTKSSARVSEALGRLLRDATMTVATPTSTAGHDDDDDDAAAADLKFKADASYVIAGGAGG
 VGRSVARWMVARGARHMILLSRGAASAEARELVAELLGEGGCEQAVAVACDVADAAAVRRA
 VDECRPAMPPIRGCVQGAMVLNDNKFAGMSLAEWDATVRPRVDGSLNLVECLGGQLDFFVML
 SSFAGLIGAPEQANYAAAATFQDALARSLSAAQSKTGGGCVFASLDLPVLQDVGFVAERPEL
 MEQLRAAGWSYLEEDELATLELYCLLQPQQQRFEDVVSRAQVAPRLWLATETMDEGLQAPS
 WVRDPLFSLRERSSSSSSSSPSSSGNKSSSSSSNNNNNNNSNNNNNNNTKKDKKEAAALLAATTSP
 AEAEAVVLEALLKLSRVLRLVELSNLDGARPLHAYGVDSLISVSLRAWLGRELGAELSVFEM
 SDRPSIDALAALVAERSRLVPKFA

Predicted cluster (antiSMASH prediction)

GGTG_07516
GGTG_07517
GGTG_07518
GGTG_07519
GGTG_07520
GGTG_07521
GGTG_07522
GGTG_07523
GGTG_07524
GGTG_07525
GGTG_07526
GGTG_07527
GGTG_07528
GGTG_07529
GGTG_07530
GGTG_07531
GGTG_07532
GGTG_07533
GGTG_07534

>GtPKS6 backbone gene sequence (GGTG_08683)

MERAMNGREERLPLVQGGGSVSSNKLCAHADGAFLRGQWYWDIRVQVCGRDAVEARLSN
 PAHPSVGPERSRRRQEMGREATEEEAGRPLQTATFQTEGDKAEVERTSLSLRIKAGEFPPEAR
 SSPLETPVDSPLQEDTPHIPLADSIALGMDDVPAAANEDDKIPIVSNNGSANGNDSTTPENAS
 NGNSNGNASGGVHPAAANGTNGTAAAKDTNGTATTSPADLPPTTELGPQDPPIAIIIGMSC

RLPGGASDPEAFYQLCCLGRSGWTPMPPDRFSKDGYYHHPDPDRLGCYNPAGGCFLAEDVALF
 DAPFFKITEREALAMDPQHRLILECAYEALENAGLPMASLAGKNVGVYAGGSFTDYELNNLR
 DLDTAPMHQSTGNAPSLLANRVSYFFDFRGPSYTVDTACSSSLTALHLAVQSLRSGDASVVV
 LASSHLNLLPDHFVSMSSQGLLSPDGRSYAFDSRANGFGRGEGAGVVILKPLSAAALRDNDPV
 RAVVVGTGLNQDGRITNGITMPNKEAQLDLMRKVYADNGLDPRETGYVEAHGTGTRVGDPLEM
 EALHRMFHDGRTSRRLWVGSVKTNVGHLEGASGIVSMIKSAMMLERGYLLPNHDFRDGNRE
 IPFDEWGVVRVPSRVMPWPRGMKYASINSFGFGGGNAHAVLAAPPRQAKPVAAAGGAAAAFTP
 GGYVEPKRVFVVSASKAALAEQMRSVTVYLERRPVAFQGSLLSDMAYTLGQRRSFLPYKFF
 AVGSEGNGLISTFVHDAPSSPVRSTRPRLGFVFTGQGAQWHAMGRELIAAYPVFKGSLERF
 DACLARLGARFSLLEELTDRDAKTSRISEAELSQPGCTAVQLALVDLLRAWGVRPDVAVGHS
 SGEIGAAYAAGALTHDECAAVAYLRGQSVLQLKAAYPDLRGMLAVGAGPDEVRRRIKTLKQ
 DDDEGHRRRVTVACVNSPGSVTASGDAAVEELQAKAEEAQLFNRRVRVETAYHSHHMELVA
 GWYGASVGELYPMAGNDNDDDGHEVEFYSSLRGDKLVSLAELDTSYVWQNLTPVLFSSQAVT
 RMCTPEPGRDKMDVLVEIGPHAALEGPVKQILKAVESLPKKPQYLASLVRNKDAVDTALNLA
 GSLFVHGAAVDFGAVNFPVPPPKAAKVLSDMPKYAWDHKTRYWWETRLSRAHLHRRFPRNDV
 LGSMADWSNDVEPTWRSILRADDVPWVRGHAMQGMTVFPMACYLSMAIEAAAQRAAAAAGLG
 AAQEAEEGGLVGKFIIFRDVTISRPLIVQEGVDSETNITLRPNPEGTRESSAVWDEFRIFSWN
 KEREWIEHCRGLIRVEHNKPGAVTTAAAASSQTNTVHDASADAAALLEARRRRVLDACEAV
 RADRLYGELEAVTARYGAQFRSMENCAGGDTACVADVVPDTAKVMPKGHEAPLHIHPALLD
 QFTHAAWVILGAGRGKLPALYMPRFFKGLTVSADVRRLAGRPGDRIRVYGEGNPNFANPGST
 KISMFATTMGQQELISMEGLVIDPIFDGDAVAEAVGARELCFKESWEPLYPEIAGSSPSS
 ELQVSNGVNGTNGTNGVHEEATDIATAPRPRATREITDSVVIVATQQQQDAEGLATALKNKL
 LASHTSDRAPPDVHLSSLEAAPADPTADSPYAAKVCVVLVELDGEPLLAGLDADAFARVQRL
 ILSAKGILWVVIRGAHSDATDPRLGMILGLARTVRSETGMKFATLDDLDEGAGAPSSSSSSSTV
 ARDAGLVAEVASHVFGKPTTPDSENDVASTGGDPDMEFQERRGLLSVCRVADDADLDAFV
 EQHTNPATPPFAQPFQPGRPLRLAVGTKGALDTLHFVDDDKACLPLGPDEIQIEIKVTSMN
 FKDIMVSMGEVPSPYLGVEACGLVSAVGSSVGDFKVGDRVCASSEGAYSTYTRSRSTSAARV
 PDDMTLEAAATVPVVFSTAYYGLFDVGRLLRGESVLIHAAAGGVGQAAVMLARMVGAEVYAT
 VGSAAKKDFLTSTYGVPEDHIFYSRDVSFAEAVRRATGGRGVDVVLNSLAGDALRETWECLA
 CFGRFVEIGKRSILANASLGMAVFDKNASFSSIDLTLVASEKPRTMRRLDDVFKLLSYGAV
 RPISPTTTFSSISEVEAAFRTLQAGKVHGKILVTAAPEDMVKATYSTKAFEKLLRPDATYIVV
 GGTGGIGRSIARWMTQKGARHITLVSRSAKVAPKVAQLIDEARSEHGARIVVSQCDVSLAAD
 VEKMIAELAAAQMPAVKGVVHSAMILDVSYIPEVVT

Predicted cluster (antiSMASH prediction)

GGTG_08672
GGTG_08673
GGTG_08674
GGTG_08675
GGTG_08676
GGTG_08677
GGTG_08678

GGTG_08679
GGTG_08680
GGTG_08681
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GGTG_08685
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GGTG_08687
GGTG_08688
GGTG_08689
GGTG_08690
GGTG_08691
GGTG_08692
GGTG_08693
GGTG_08694
GGTG_08695

>GtPKS7 backbone gene sequence (GGTG_07238)

MAPLMFNFSSSGTSPTTSTAFTMPSVANSETDSAADMANGHMSDHFGDMGTATRNQTPIAI
VGMACRMPGSVATPAEFWELCSRARSGFTKVPKERFNHDLFYHPNPGKTGAYHAEGGNFLDV
DLAAFDAPFFGLTEKEAISMDPQQRLLECTFEALENAGVPKHSIIGKDVGVFVGGSFAEYE
SHLFRDSDTI PMHQATGCAHAMQSNRLSHFFDLRGPSFTADTACSASLVALHLACQSLRTGE
SSQAIVG SCHLNMLPEFFVSFSTCRLLSDSGRSIAFDERGSGFGRGEGCGVILLKPLDQAIR
DNDSIRAVIMGSGINQDGKTPGITMPNGEAQEKLINQVYSNFGLDPLDCGYVEAHGTGTRVG
DPIEATALHNALGQGRSARDPLYIGSVKSNIGHLEAASGLAGVIKAAMMLERGFILPNHDFK
KPNSKI PWKEWMSVAKTQRPWPKGKKYISVNNFGFGGTNAHVVLAKAPYTPEPVTTTQPP
QAQQKPKSGGKKLVVLTANDKESLAGVMKKLVIYLEQRPEVFQADLMKNVAYTLGQRRSHLQ
WRLALPVATSFELVDTLNAGKVMPAKTQPEPLRLGFVYTGQGAQWYGMGRELYGQYPVYTAA
LDRADARLKDLGATWSLVEELNRDEKTSKVNEAHISQPACTAVQLAITDLLLSWGITPVAVA
GHSSGEICAAYAAGIITFDSAVAIAYHRGR LIPVLRKRHADLAGGMMAVGGSESNLQPMIDA
VKRKQQEVRIACYNSSSLTISGDAAVLGD LERVIEEEQPEMFRRRLQVDVAYHSHHMLVA
DEYRDSIDHLTKPRNTDVQFHSSLYGTRAEGYRCTSSYWVDNLTCPVRFSEALSGMLEQKAE
QGGINALVEIGPHSALQGPIKQILAAVGRPKTPYSAVLLRKKGAVDTALDLAGGLFMKGAF L
NMNAVNF PAGSLGAASQGSTRQPTLLTDLP RYVWNHSSKFWHESRMTQMHKHKRKFGRNDLIG
VEAIYSTDAEPVWRNIVHLDDLPWLRHHRVQSLTIFPFSGFVAMALEAAAQLAKGKDS PFDH
FELRDVAVSKPLALAE GDVEMTISMRSHDKQQGQIGWKTFRISSWTQGNWTDHCTGEIAT
LCDDNNEVDGERQKQAARAKVCAAI AALQSENVAEIPAAEMYQRLEELGVTFGPLFQGLKGC
TASSTHSSANVMTADIAQDMPNH YMTESVLHPSVLES LMQMYWPILGAGRAGSTAETVYLP S

SVGKITISREVTKHTKDTGSIIRAYGEARFPDSEHEPSPTNVSIMATAPESKDLLVQIQDLK
 VAPIMDGEAEVEANAPRELCYKLEWEQVLKPALVNGANATVGALPDADVIVHGDFAFQHTL
 ARCLADVIERATTLCPAMGTLGHMDTEGKLCIVLGEIDRPFADPTEQQFEAVRALAGSAQA
 LLWVVRGAYDSSTSPNSNICGLSRTVRSETLLPFATLDLDPATSKMSEDMARQKMAKSVFD
 VVKLAFSGGLSASKEMEFKERAGKLFTPRIVDDGDTNAYVHRQTNPNIIERQPFTQNGRPIK
 MVCGAKPYFVDDDSVQDAVGDEEIEFEVKAIGVNLSDAQRTAKLGSPAGLEASGVVTRVGQS
 VPSFKAGDRIAALTLEKGAYATLTRASAANTLPIPDMAFSEAAALPLAYSTAHHALVGQAR
 LEPGQTLLIHCASTPVGQAALCLATNIMRSVEGIYATVATAAEKTLLMECYGISESHIFHSR
 GVAFGPAIRAATGGRGVDVVLNQSTDGGAVRETWSCLDRFGCLVDTASASSRLDLGSDGRSS
 NASFASVDMLSLAAERPAMQRLIRDIARLLAEGKLRATIEAGAVFPPISEVQDAFKSVQSGKI
 AGKVVVAPKSQDMVMATPSKTTKNLLRSDGTYLLIGGTGGLGRSMKWMMAEKAGNVVLLSR
 SGSATGKVKELIDSASVNGANVVVRRCDVADKASVDELFATGLDGLPPVRGIVHGAMVLRDV
 LFEKMAYEDYTTVIESKVRGAWNFFHHALQASSSPLDFFIAISSAAGAVGNRGQAAYAAANTF
 LNALVQHRLSLGLPAASLDLTAVSDAGHLADGDPERAAEVAKNLGADSTISEAEVLALIGAC
 VDGRTTAACGGHVITGMRIPPAPGKPFWHSDAKFKTLLATAEEAEREAGGGGDASASAAALS
 PGAAVKAASTLAEAEADAVCRGLVDKISAVLMMEAEDIDVTRSLSHYPLDSLVAIEIRNFITR
 EFEEANMQVLELLSSGSVQTLTKAVCRKSKLCTGLS

Predicted cluster (antiSMASH prediction)

GGTG_07228
GGTG_07229
GGTG_07230
GGTG_07231
GGTG_07232
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GGTG_07235
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GGTG_07243
GGTG_07244
GGTG_07245
GGTG_07246
GGTG_07247

GGTG_07248
GGTG_07249
GGTG_07250
GGTG_07251

>GtPKS8 backbone gene sequence (GGTG_03165)

MAPGALLPDSPGGTPTSETTGGGFVGGYWARLRGAAVARLSTGFQNTNDHTSDGHQADEHS
 NGDTNGHANGHVNSDVNSRENSGSNEHVPHVSSAVPSTAASTAPISGLRDGAAANGHRPAIG
 PKASTGAIAIVGMSCRMPGNVSSPDEFWELLSRNRSGFSEIPEERFNSASFYHPNPKGKGCY
 NPVGGNFLQCDLRDLDAFFFGLTEKEAISMDPQQRLLECTFEALENAGIPKHHIAGGNVGV
 FIGGSFPEYESHLFRSDTIPMHQATGCAYAMQSNRISHFFDLRGPSFTSDTACSSSTVAVH
 LACQSLRAGESSLALVGGCHLNMLPEFWISFSTCRLLSDSGKSMAFDSRGTFGRGEGCAMI
 VLKPLEQALKDNDRAIRAVIAGSGINQDGKTPGITMPNGEAQESLMRQVYRDFNLNPWDCGFV
 EAHGTGTKVGDPTEATAIHNVLGKRRTAREPLIGSVKSNIGHLEGASGIAGILKGVMMLE
 SFVLPNHDFKSPNPKIPWKEWSLKVPMPQRPFPGRGKKYVSVNNFVGFGGTNGHVVLKTAPFRV
 KEELTENELDNQPKLIVFSANDKTSLQAILKDTVIYLERRPEAFEGALMRNIAYTLGQRRSL
 LPWRAAMQARKSLSLIEVLNGGRAVVNKEMESVRIGYIFTGQGAQWWAMGRELYNHYPVYTD
 SLDRADRCLASLGSGWSLVEELAKSELSTIVSEARISQPSCTAVQALALVDLLQNWGVRPTAV
 AGHSSGEIAAAYAAGVISFESAIAKIAYHRGRLIPVLRQRFPGQLQGRMAVGGSKDEVQELID
 GLDESQVRIACFNSSSLTISGDEVALAALERLVQQKQMFNRRLVVDVAYHSHHMNLVSKEY
 HAALADLPAPVPSDVKFHSSLAGGLVHGAE LRPSYWVNNLTCPVRFSEAVESMLQPADGSKA
 GVDMLVELGPHSALQGGPIKQILKAVGGSAAKTTYESALIRKRDAVETALDLAGSLFTKGVNL
 NLGAINFPKPGIPPIQLIDMPRYPWNQTKYWQESRMTAKHKQRSQPRSDILGVEAIYSNDL
 EPTWRNIIRLDDLPLWRQHKVQSLTMCMSVFIVMALEAASQRVVSSDRFRDRIEMRDVNIV
 KPLIIPDDDIEVTTTTLRPHQEGTLVSSDVWDEFRICSYSNKIGWTEHCVGLVTS LAHETNDV
 DGVRQRLDSEAMLHTAASAVQDSEPVVVRVEQMYGALAGVGVALGPAFQGLKDCEASSTHAT
 AKVHMDDLAKEMPSECLASPLMHPCVIESLIGMYWPVLLSGQSKIATVYLPSAVSRVSISTQ
 AMEISKAAGRSLRAHCSADFGQGASKPARVTTMAVDGDHGREPLIILEGLLIAPILDGETQM
 QADAPREL CYKLEWEPVLVPVHCSSEKSNGAPNGESGPGPLHPLSVVIVHDDSVLQRSVTQ
 KLATAMDKAVGRMPEIGQLSTIQPEGKILVFLSELDTLLSTISAAQFELLRGALAKADGCL
 WVVRGAYASSTNPEANMITGLSRSIRSETAMKFATLDLDGHEPLAEELVCGAVMRV FREVFG
 PSAANMRELEFMERGGGAFFTPRIVNDDLMAFVQEQINPAALSDSPFDSedrQLRLSISTPG
 ALETLHFVDDPMASQRLAGDQVEIDIRATGVSFRDVMAAKGQTAEDIGYEVS GVVSVVGPEA
 VGLAVGDRVAALVQGGYASKVRTPIRNAFKLPAMTFEAAATLPLAYCTAYYSLFEIGGLER
 GESVLIHSAAGPVGQAAIVLAQTAQAAIFVTVGTAEKKALIMEEYGIPDERILYSRRRTAFS
 NTLREATDGKGIDVVLNSATGDALRESWECLNEFGRFIDIGRRDGSVKTRLEVTRAGKNSAF
 ISLDFFAVVAERPRVIGRVVGEVSRLLD SGRI RPLTPITVFGISEVETALKKMQSARLAGKL
 VVVRPGEIVQATQSRPTNRLLRADATYVLIGGTGGLGRSMARWMVGNGAHHIALVSRSGSA
 EGKVRELIQELEELGAEVVRKCNVVS RDEVDLVTNGLRGMPAVRGVVHGT MVLHDVLF EK
 MTWDEYVKVTEGKVQGAWNLHHALAGKELDFVVAISSAAGAVGNRGQAAYAAANCFLNALVQ
 HRLSLGLPASSDLTMVSDAGYLAGNADKLAEVARNLGSDSICESEVLALLRAAIEGR LAAT
 CNNHAITGMRITPAMQPFWTSDAKFKHLRLAMEAQAAQGE GGGISTVSFGAAAKAAKSLEEA

ESAVCRGLVDKISTVLMLEPEEMDVTRSLSHYPLDSLVAIEIRNFIAREFEANMQVLELLSS
GSIQALARAVCVKSKLISFT

Predicted cluster (antiSMASH prediction)

GGTG_03156
GGTG_03157
GGTG_03158
GGTG_03159
GGTG_03160
GGTG_03161
GGTG_03162
GGTG_03163
GGTG_03164
GGTG_03165
GGTG_03166
GGTG_03167
GGTG_03168
GGTG_03169
GGTG_03170
GGTG_03171
GGTG_03172
GGTG_03173
GGTG_03174

>GtPKS9 backbone gene sequence (GGTG_00407)

MEKLLVFLFLFGDQSLDTHGFLADFYRREDQGILAKAFLDQAGEALRSEVDRLPRLERSKLPI
FRNLRQLNERYHSQVLKHSGIDSALLAISQLVDYIDHAEKHYEDVTQHENTHLVGLCSGLFA
ASAIASSTSVSSLVPLAVQTVLMAFRTGSQVAALAELEPSTDCSESWTCIVPGLTEEEAAQA
EISEFHSTQAISPASRAWVSATSTANCAISGPPSTLKAFRAASTYASKATSIPVYGPYHAAH
LHRPADVESILQLDSPAVVDAFVNTKPRSKVMSCESGTWLDVSSTKALFTSVVTEILTQPLR
FRKVLGDGCLQQARDFTGKASLIIPFGPTQHAATLANLLKENTELEVTLRQAAQISRESQTPI
GNHGSTGRCKLAIVGMSGVFPDAADHEKLWDLCKGLDVHREVPPERFPVATHVDPTGKAVN
TSHTPYGCWIENPGMFDPRFFNMSPREAFQTDPMQRMALTTAYKALEMSGYVNPRTSPSTRLD
RIGTFYGGTSDDWREINAAQTVDTYYITGGVRAFGPGRINYHFGFSGPSLNIDTACSSSAAA
MNVACSSLWARDCDTAIVGGLSCMTNSDIFAGLSRGQFLSKKGPCATFDNEADGYCRGDGCA
SVIVKRLEDAVADNDRVLAVILGTATNHSADAISITHPHGPTQSILSSAILDEAGVDPLDVD
YVEMHGTGTQAGDGTEMVSVTDVFAPASRKRPADRPLYLGAVKANLGHGEAASGITALCKVL
LMLQNNAIPPHVGIIKKGSVINKTFPKDLAERNVNIAFHMTPFKRRDGKLRVFINNFSAAGG
NTGLLLEDAPILSPATPDPRSVHVVTITGKSKTSMNLNNAERMVSWIDKHPDTPLSHLAYTTT

ARRQQHYWRMNVAASDLAEAQQLLRARLQENFVPVSSEQPKVAFLEFTGQGSHYAGLGKELYA
 NHSVFHQSI NEFDHIAQIHGFPSFMPLIDGSEPDVSKLSPVVVQLGLACFEMALARLWISWD
 VKPSAVLGHSLGEYAALNVAGVLSASDAIYLVGVRAQLLVEKCTAGTHAMLA VQGAVSVVQD
 ALGDKAATTNVACINGPRETVLSGEAGEMAEIAQQLTAAGFKCTQLKVPFAFHS AQVDTILD
 EFETLARSVRFS LPKVPIISPLL GKLVENEPINPKYLRDHAREAVN FLGGLVSAQQSGTIDE
 TTAWIEVGPHPVCSNMVKA AFGASTVAVPTLRNEPSLYKTL SASLCTLHTAGLKIDWNEFH
 NDFISSVRNLDTPAYAFDEKNYWIQYEGDWSLIKNRGFNKALPPATVVKPKLETTTVHKVLS
 EEVKGDVSIVEIETNLSREDIRGVVTGHLVNGAPLCPS SLYADMAITVCDYAYKLVKPDAKN
 LGVNVSHMEVPKTLIFDENLEAHVLRMTTTVNTATNSAEVVYHTGEGAKRIGHANCKVLFGN
 TEDWQGEFDRVSYLIKSRIDSLIAAEKEGKASKIGRGLAYKLFNALVDYNPRYRGMEEVTL D
 SDTCEATAKIKFQTSEQDGKFVFS PYWIDSLCHISGFIVNGTDAIDSRDQVFISHGWGAMKF
 TELPVATKEYRSYVRMQPVRGSKVYAGDVYVYDGDKIIGMCGELKFQCI PRKVLNMMMPPRG
 AA AVGAPAAPRIA AAARPATKAAPAKKSKGVTPKTI AKVNQKLATVVSQVLDILAQEVGVSH
 DELADNIAFTDLGVDSLMSLTVSGRIREDMDLNIDSHAFVDHPTIGAFKDFLAQFEGPPGPS
 EDSSSSASSDSGDLETDSDVTTPADESETGSLKGDKSAGAEVSNN DALREAVRNTIATEMGM
 EVDEIIAAPDLANLGMDSLMSLQILGTLRERTGMDISADLFVNNSSLK DVERALGISAVPKP
 VPQAAPAKAHKVKA EKVRPLPPTTAIPPSQVTASIVKPPPPKEIVDNYPHRKATS VLLQGSH
 RTATHNLFMPVDGSGCATSYTEISEIGQDWAVWGLFSPFMKTPDEYN CGVYGMAAKFIEEMR
 RRQPAGPYSLAGWSAGGVIAYEIVNQLTKVGESVSNLIIIDAPCPITIEPLPRSLHAWFAEI
 GLLGDGDETKIPDWLLPHFAASVTALSNYTAEPIPKDKCPKVM AIWCEDGVCHLPTDPRDP
 YPTGHALFLLDNRVDFGPNRWDEYLDVGKMTMRHMPGNHFSMMHG SFAKQLGSFMREALC

Predicted cluster (antiSMASH prediction)

GGTG_00395
GGTG_00396
GGTG_00397
GGTG_00398
GGTG_00399
GGTG_00400
GGTG_00401
GGTG_00402
GGTG_00403
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GGTG_00406
GGTG_00407
GGTG_00408
GGTG_00409
GGTG_00410
GGTG_00411

GGTG_00412
GGTG_00413
GGTG_00414
GGTG_00415

>GtPKS10 backbone gene sequence (GGTG_02434)

MPSDAPIAVVGMAYRAPGIGRKGIWDYLSEARSAWSEVPAGRFDQWAYRKPGADKSGVYHAE
 GAHFLPGDVYAFDAGFFNMRAEEARNSDPQHRLLECAFEAAEDAGYGLADLAGRRVGVFVG
 SGLHEYSERMGDDVFATKTFTATGLAPCMLANRISYFFDISGPSIVLDAACASSVYAAHQAC
 SAIRNGDCDAAFVGASALSLGPGTWLALEKTGALSTQGRSFSYDAKAAGFGRGEGGACLLIK
 RLDAALEAGDPIHAVIRSSACNHGGRSEGITMPNGVAHRKLLWETHQAAGLDPSDTPVVEGH
 GTGTAAGDPIEAGFTAVLARDRTAENPIYVGSVKSNGHLEGASGMLGMIKAILMVKHGVV
 LPTAGFESINPRIQDKEKIRVPDVPIWPENEPRIIVTNFGFGGSNSAIIFDQAPERPIAS
 HDGLNGVKEANGVNGTKNAANGHTNGHANGDTNGHTNGHTNGHTNDHGNGHTNGHSNGLTDG
 QTNGHANGHANGHGAVGKTSQPRLFVFSKSEASLTAYLPSFGEYLDEAEVPDDDDVFLRDLG
 YTLGQRRTOHAFRTFVAVADSVEGLQEKLSVKPARVRDRAIAFVFTGQGAQYEQMAAGLRRY
 KVFSAAALDRAESHLRTMGAPWSLGEELARAAGGGSRVHEAEISQPACTAVQLALVALLRSWG
 VEPAAAAGHSSGEIAAFAAGLVSFRTAVGVAYFRGLAAARLSRERGDRKGAMLALGVGPDE
 AAALLREHAAAAGYATVAAINSKSVTVSGDVPAIERLHEAADAAGIFARRLKIQMAYHSHK
 MEDVADYYLDAIKGYCDEAQEASATEEGDDRPLFVSSVTGKVEHAVGASYWVQNLVRPVMFA
 SAIQTLMTTPGRKTKTGQAAAPPVSLVEIGPHAALKSPIKQTVELLEQQRRRDGGAQAQPS
 APFTYLPVSLVRGTEAGLALMELAGNLFVLGTPLRIGDVNQTGPHNSNVVTGVPAYAWNKSAT
 YEMCPRATREKIFPGRPYNNLLGRILPSSGGRQQRQYRQVFTLDEFWVRDHAVAGIVVFPMT
 GYIACAIEAARGCLGPQPAAAFILRDVNVGARLEINEDETVDMTTSIWPSATGPGVASSSAW
 DFDVSTWSASGGWVVAHQGTIVPETTEMTADTPTFRASLPIVEAGASGLVEHDMQEAYEKSA
 ARATRFGPTRNTERFFEGRGYTLLHKLKRDVHADSWDGADPRGSPVTVDPPTLDGFLQGGG
 PLQVTADGRKPAQMPNYISRFISNNIPSTPGQRIDVVTRLLAYDVKGGRMSIGIAAFARGA
 DGSITPVAEWESIAFRSIGSAEEDLDPAAALPSSWAFELLPRPDCLSTGELTKRMMGVGELD
 GDAETAQWIKFEQIAWHYIHKGLDATMDQDPAEMPHHLAQLVKWGRRYRDSAPASHQAAALS
 SEDVAVLCGKAASADARGEMLVRVGENIVPILRGEIEPLELMLADGLLSRHYEADKINGHLS
 RVLGRVLASFSDIEPNMRILEIGAGTGGTTLPVLEALSPAVGEPGEPAFVSYTYTDISSGFF
 ENASAKLARWSQRITYKKLDVTQDPVAQGFELGEYDVVIAANVLHATEDMAVTMANVRKLLK
 PRGHVLLLEANRHAAAMLPPVMLPGWWYAKDAYRDRDEGPLMPLDVWDRLLRDSGFTGVDAH
 IGDGLTEAGEAPAMSIICSSRTGKWTDDRGVVVVGPFMDDEEVEFAQLVADAVVDRFGCPAE
 IRPFAELDPADEPCYIVIDSPRHSLMAGVDAERFEGQLQTVMLRNAGILWVVPEDGPVEASSA
 KGLMRTIRLENEPRNFLTLEVPITADQGLPAILRMTQTLRDPEATRLHDQDFTWHQGAIHV
 SRMLDRDASELLAVEQGASYRKEQRLWAGTETRALEMTMDAAGSPDSIYFRRTDVLQRPLG
 PEEVIVRVEAAGVSHRDLSLITGAIPWEAPGFDGAGVVERCGSDVASLQEGDRVMFLAADA
 GASAFATHRQVPAWLAARVPARVEPTDAASIPLAYSLAVLALFRTAHIRAGESVLIHSAAGA
 LGQACLALARHVGAEVFATAGTEAKRKFLHESCDLARNRIFSSRTAEFRDRVLAATGNRGVD
 VIVNSLGGELMAETWAVAAPLGRFVDVGKKDAFQNSYLPMPGFNNGVITYTAVDVRELGRHRP
 EEMKAVFAEVAALMRKRVALPIQPVTVLPISQLAAALRRIRSGEAQGKLVVTTLEADDRVVAE

SDLQASDAQLRADATYLVTTGGTRGIGLNLARWMLENGARNIVVLGRSGASGPEVQQLMKEYE
 ERPDVAIRAPPCDVGSRESLEGALESIKDLPAVRGVIHSALLLKDSLFFENATFENWQIVNNP
 RVDAAWYLDELLPKDMDFFIGLSSFLGDTGNAGQAIYAGTAVFYHEFAKYRSARGQHTVSIA
 LPVVLVDVGYVADNNLTDSLRLNTIGATLTIIQDIRALIKGAIAGPASRGMAFYPSHKAVAFSMY
 LDGARVRDGGPWKYFHPTLATEWLKDERRRRRAKGAAGAGGVGGGAEAYLSGSWATAEDPLT
 GLTEALVSKVSAMTMMDRSEVSPDTPLAAFSLSLVSVELRNWIRRETAVDLPLSGIMQAES
 LRAMATEILAQRAKGEGNKAT

Predicted cluster (antiSMASH prediction)

GGTG_02419
GGTG_02420
GGTG_02421
GGTG_02422
GGTG_02423
GGTG_02424
GGTG_02425
GGTG_02426
GGTG_02427
GGTG_02428
GGTG_02429
GGTG_02430
GGTG_02431
GGTG_02432
GGTG_02433
GGTG_02434
GGTG_02435
GGTG_02436
GGTG_02437
GGTG_02438
GGTG_02439
GGTG_02440
GGTG_02441
GGTG_02442

>GtPKS11 backbone gene sequence (GGTG_02129)
 MASAPRFYSPRRGELDGDAVEPVVAIVGFSLKFPQDATSPDAFWDMLAERRSAMTDVPADRWS
 AEGYYTADSGKPGMNNVEGAHFVKEDVSLFDAPFFSITPTEARSMDPQQRWLLECSYRAFEN

AGMSLEQVAGSDTTVHMGCSGFEFNSLSHHDHELHTPYFLTGTGNALIANRVSWFFDLRGSS
ATIDTGCSSSMVALHQACESLRSGHSSMGLVGGINLILTPHTFTHLTDLGMLNPAGKSYTFD
SRAHGYPAGEGIGVLVLKRLRDALRDGDCVRAVVRNTGSNQDGRTPGISQPSAAQEDLIRT
VYARAGLSLADTGYFEAHGTGTPLGDGIEARAIGAVFGPVREPGRPLYVGAVKTNLGHLEGA
SGVAGVIKTIILVLEKGIIPPNMWFEKPNPAIEDGWNLKFPTEPTPWQTRGLRRASINSFGYG
GTNVHAVLDDARSYLESRGLRGHNHTAGDPSLVTSEHVDVSGSGGGGCGQPVALLPVPRPL
LFVWSTHDEDGLRRVAEAYSGLLATTRAARGEHPGRCGGEAEFLCRLAHTLASRRTRLPWRS
FTVAASRSELLARLGDGKSAPSPPVRAASSPPLKVGFFVSGQGVQWHAMGRELLVYPVYRRA
LEEADALQTLGCWWSLIDELTKNADSSNVDNPAYSQPLCAAVQIALARLLASWGVRPASVA
GHSSGEIAAAYCAGALSRAAMKVAYFRGALSADLLVRQLTSGGGGSGRGMMAAALSEAAA
NSYLERGGLANVAVGCVNSPQNVTFGTDRGQLVRLEQTLKSEGVFCQLLNVGSAHYHXYMEV
VALRYQKCMGSLETNGDADPATSPVMFSSTTGRRATADEVSRAEYWVKNLVSPVLFSAALSE
MLREETVSTNGGEKTGVNYILEVGPHGALRRYVQEIRDALPQGLIGRSAMYDSALTRNVSAT
ETVLNAAAGRLFCAGLSSLDLGAVMASGADGGAYHGAAGREKMLVDLPEYFPNHSQGYWAESR
ISRNMLRRQPRSDFLGSQVADWNPADARWRMYLKLAEHGWVRDHEVTGQLIYPAAGMLVMA
IEAARQLADTGRAVAGYRLKEVVFDDKALTLPAAASEGVEVQLRVRTGRVSNFTGGASGWSDF
ELASHGDGGWTEHCRGSIRVEYGEATATAKSAASGSWGSASAAREKKAREERVLGEAAALDR
RCVPLDSGSLYGMIEGIVFGPSFRTMRDVRQSSRSSIKRSARDPASNTPSSDAVASIRV
MEQRPGARPNGHQVIHPATLDGILQTVFPSLAAGDKQTAMRTLVP SFLENMWIASDICQDDP
ASLKAHTTARKRGLREAECTVTVTTPGGDSLLAELSGFRLTALSNGAGGGATSAMKGRDGNW
RRLCYNLAWAPDVLDDLDKQAPDWFFFEPLATAEATARGESLGLLEEELEFLCFYYVTKALDYL
DQGGTGPPAGGHLEKYVDWMMHMRHVSLATGGSAPTGP HAINAKSAWLRQVRDEAYVDEM
MERVRETPEAPIILLRLGPPELPAIAGLVDPLELMFRDDVLQRLYRDGFGAKGTAAHERLID
ALAHKKPGMRILEIGAGTGGTTVPLIETLSRHGQGESESEDGTPRFEHYTFTDISPSFFEKAQ
EMFKDHSSRMSFKVLDIERDPIKQGFKAEGYDLIVAANVLHATKQMQVTLANTRLLKPGGK
LLLFELTNLNLMLGAGFAMGLLPGWVLGTEANRKGWPLMSRTDWDAAALRSSGFTGNELPTQWP
GSEKTQTSVMMSTATDHARAQKAPPASAPSNQIVIVVSERSNLQRAVAAELARYLEAGPGR
TRKSDPVRIYSIAEASRTPLRDAVCVFLPEFEHPFLETMDEARFACLKQLTGAKGLLWATRS
PVAGTWTPAFDLVHGFARTIREEKGEDFDFVTAALDTRVDPASVATKLGRIIRSTGLLTSG
RRGEERAEQEFVERDGVLCIGRVVEANYLNDEIATSLVPAAQRTPEMQPLQPNRPVKLTIGS
LGLLDTLRFVDADDGTSGEPSPLHIEDGYEVEIEVRACGLNFFDVMAAMGQIPEDLGIECS
GVVSRVGTRISRLKVGDRVLTAQMSSLRTMVRAPENLVYPIPEHMSFEEAATLP IVYWTAYY
SLFEVARLKEGETVLIHSASGGLGQAAINMARLRRARVLATVGTAEKAAFLVREFGLREEDI
FSSRDVDSFVLGVERATGGRGVDVALNSLSGEALRATWERCMAPLGRFVEVGKHDLATFASL
PMHPVARGVSFASGDGLYASRSNPALLSRILGEVAALAHAKAIEPPKPLHVYGFQVVEEAFR
LMQGGKHIGKIVLRPEPGQKIPIAPDTRPQYHLRADATYVVAGGLGGLGQSVARWMVRRGAK
HLLLSRSGADKDNTLVADLVSMGAAVVLTPRCDVSNKQELAATLDACKLMMPPPIAGCFNAQ
MVLKDDSFSTMSLDDFHAALAPKVKGSWNLHSLLPDGLDFFVMLSSMTGVMGSHGQSNYAAG
NSYQDALARYRLASGQRAVSLDLGMLLSVGFFVAQQGQDGNAALIHRLRDRGYMPIREAEFLS
LIEIYCDPTTALPPRRAAGPLDVLHAQVITGIETPASLRRRGVELPFASRTSALFDALHHMG
VGRYGDSESGDADAGSGSADGKGGLKARLAAAASVAEAGVVVAEALAAKLARMLSVPSADV
DMSRPLHVYGVDSLVAVELRNWLAREARADVAVLELMGGSNISRLGAAIAAKAQAVPGII

Predicted cluster (antiSMASH prediction)

GGTG_02119
GGTG_02120
GGTG_02121
GGTG_02122
GGTG_02123
GGTG_02124
GGTG_02125
GGTG_02126
GGTG_02127
GGTG_02128
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GGTG_02131
GGTG_02132
GGTG_02133
GGTG_02134
GGTG_02135
GGTG_02136
GGTG_02137
GGTG_02138
GGTG_02139
GGTG_02140

>GtPKS12 backbone gene sequence (GGTG_02166)

MAQDIPSNEPLAVVGSSCRFAGGVDSPSKLWDLLEKPRDLSKRVPADRFNVEGFYHPNGEYH
GTTDATKGYWLEGNHRVFDTSFFSITPKEAETIDPQQRLLEVVYESLESAGYDLKQYAGKK
VAVFAGIMTADFDTLCQRDDLLGSQYLATGNARSIISNRISYFYDFHGPSMTIDTACSASLV
ALHQAVLSLRSGESTMACVAGANMMLAPEQFITESSLHMLSPSGRCRMWDAGADGYARGE
ACLLKPLSRALADGDIAIQAIVRETGVNSDGRITKGITMPNPVAQSAIIRDTYSRAGLDPRRE
ADRCQYFEAHGTGTHAGDPREAAAIADAFFGDGDTYAEGVPPNQEAQRKLLVGSVKTVIGH
TEGAAGLAGVLKVIQAMKHKTVPNNLHLETNPSVEPFYTNLEIPVSATPWPAVENNQPLRA
SVNSFGFGGTNSHAILERYTPDIHCPIGISFGQTGRNSIPPTIAQELQQSEVPLPLVLSANS
QHSLYLMVEKYRDFLVGKADVFA SPKPFSQLLYHLYAKQNPFPFRLAVTARTATETIEKLNQ
LLLGAPASKHPQLGSRTATQQLEPNKLRILGVFTGQGAQWATMSRD LFNCEGYRRSISELD
AVLRSCPDRPNWTLQEILADPSVSRIGAA AISQPLCTALQVAMVDLLTTLGVTFHSHVVGHS
SGEIGAAYAAGYVTAKQAILIAYYRGKFASLARPKVAVSVRDETAPKQAGGMI AVGLSRVE
AEELCSQQKYVGRVLAASNSPTSATLSGDFDGVIEIQKELEAQGKFARIL AIDTAYHSQHM
QLPAARYGPALEACGVAHMPKITDSKTRWFSSVHGGSEAFSAAQIEPTYWVENMTAPVLFRE

ALEKAVDEAASFDLAIEVGPHQPLKGPATQITIEALGGTKLPFTYLGVLDRKKGDLAAFSDFL
 GSLWTNFGPSATAVGAAITSSSESGGVEPDELPTYPWDHSQVHYRESRISHQYSNRTHAPHEL
 LGVTRRDDSELEMRWRNLIKLETIPWIEHHKFQGGQALLPASAYCVMALDAARVFLNGKSATV
 IELQDVEFVNGITIEPGTYGVEVLFTLSVSPPPKDSRSRSPQEIHATFTVSSAYADGTTMPR
 PNFSGHMRIELGTPSADVLPPRPSLHPETMAVSTDGFYKMMEGLDLGYTGPFGRGIETIQRRF
 NFASTTLPKTHPEDTTTLKVSPAMLDTCFQACFSAFSSPGDRALWTPFLPRSISKVRFNMAV
 CDRNDDEPDQKTTVDALLTDFRPISKQGAATITGMSIYNSRGQMEVQIESMVVASFAATKP
 EDDYELYLHTVMQADPEDEIAGLMAFDNDRAEEEQRVLEECFERVKSFYKTNRAPHPMRDS
 VFSNRSNASTIASFEPPPFVVEGRATSAWPHETHQSLRQFIESSRYPAALELLSSLAANLSS
 SILDVMVPNVTMEALTLLRFQKHLETVTCQIAHRYPRMNILGVTDPLFLVEHVLAGLGSSF
 LSFTTVGADERFDRRVLDRLPQNVRDKVVTDNHLLSDKAKSDDNGTAYDMVVLPTSVMEPGQ
 AAVLKVIRHLMKPGGFLVLIHASTNPLKDNIRRCAGSLAGSPSVSNGALTPPDWPDALEDC
 GFVRGPANADQHFPFGYTILVRQAESAEEKMLRPFPGPAGPGPAGTMEGDAPSRAKAVFGTLT
 SQLLIVGGGSRQTSDDLTEEIVDMIEASCSNDVCVARAFEDIDPADISSCTAAIVLADLDSPV
 LSRMTEERLETLKALMRPDMRILWVTNIDGETGTEQSASFARTLIAEMPSLALQMLDLDT
 LGGAAKTIVESFARLCQQASVSSNSSSPDSRDPDSILYSYEHEIHIKKGRRIVPRVLPYQPA
 IDRVNSARRIITTPVNTTAKSVEIVPVQFSDGAMHYEARHVNFSISDVPPGETPVQVLYSAL
 NPISGSEHFQYLCVGKMLDPQEEGRSVVMFSKMNASLIHVKRESIYDAPHVEGVLNSSLFAT
 CLLQALRAQILCHAARLPMVLVNAESALLESMKATLSTLWPQMVIAVTSNKEVADANSDYIY
 IHRSSPQAIKSALPTSRAYIVDYSADNDGYAQLICDCLPNGSQYIRFGDNCFSKPDILPGE
 AAELTNAIDVAAELMFTVGARDTNLPTVSVPHLLQRSSLAPFSPDIVDWRAERTVAVSPT
 DQRQPQSLARSASYAEKPTLLRHDRTYVLIGITRDLGQSLCQLFVNNGARHIVLASRSPPPA
 SLSWVSALAGRGVTQVETLDVTDLDSVRRFARRLPAPLCLPPVAGVVNGAMVLEDRVFA
 QMTLETNLNRVMRPKTIGSQNLDAVFGPSADLDFIMTSSFAAVGGHAGQANYAAANMFMNGL
 AADRRRRGLAASVLNIGVIYGLGFLHREREGLYAGLEREGYPPISERDLHMHFVEAVVAGRP
 GADGPEALTGTLSRYRVGDPNQLHWHRDPRFCHFTTTAGGEEAAAGPGQSAGDGSPRQRVEQA
 RGADEVRAVVLAELVARLEAVLRLPAGSVAAQDDSVSGLGIDSLMAVELRAWLHRATGRDVP
 VMKILSAPSIARLADDIAGLVLADREV

Predicted cluster (antiSMASH prediction)

GGTG_02156
GGTG_02157
GGTG_02158
GGTG_02159
GGTG_02160
GGTG_02161
GGTG_02162
GGTG_02163
GGTG_02164
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GGTG_02167
GGTG_02168
GGTG_02169
GGTG_02170
GGTG_02171
GGTG_02172
GGTG_02173
GGTG_02174
GGTG_02175
GGTG_02176

>GtPKS13 backbone gene sequence (GGTG_02313)

MVPDALTPGMGATGLLTPAMPATAAMTSGTGPTGLLTPATTTLSQTTTPSTINNGLDGHRTM
GTSIVESEKNSSTGTHPAHDESSAKPSHGVKKNPYPPYEPIAIIGMGMRLPGGVHDDVSYWD
LLVNGKDGRRCRVPESTRYHAEAWVQPPGSNKPPSAGLAVPSTHGYFLATDADGSDPLQRLDGS
FWTLGRHEAEALDPQQRLFLEVVEAELETAGLTPSSYRGADVGMVVGQMCDDWAGMQRMDRL
DHGAARAEVVGDIIVANRASYEFDLRGPSVVVRTACSSSLVALHMACRDLQARTCGAAIVGG
VNIMVTPLDVTGMNVQGVLSPSGRCMAFDADADGYARGEVSAICVKRLDDALRDGDPIRAV
IRASCVSNDGQGGGRGITS PDGGAHERIMRRAYDIAEIGDLGRTAMVECHGTGTAVGDPIEA
GAVAKLWGKDGIYIGSVKGNIGHGGGASGLSSLMKMLALEHSTIPPNIHFNTPNPRI PWQD
AKLTVPTKASPWPADRLERSVNSFGIGGTNAHASIRSNPFCIGVETSENRDDDVSSQRLLV
FSAKHPKALERSAEAVRNYLADRPVKLSDMAYSLATHRAAYSQRAFAVVGSDASSFRVEAG
GTALETQPSVAWVFTGQGAQWPQMGKELLEKEPLVRQRVEHFDRLLASLSKPPPTIKDEIM
KPPAHSRLYEAQYSQPCMVALLQSLIVDLLKSWGKPAAVVGHSSGETAAAYAAGAVTADDAF
LLAYHRGQITPTLAKAHDGSMAGLGRDAVTPFLQPGVIIGCENSPESTVLSGEKDVLTSTV
MAAISAARPEVLCRKLKVECGYHSQHMAVVADEYWSRVTPGDGVRGQAVEPAITFYSSVNAG
LTKDLSPKHFLDNLLSPVLFDGAVRALLRDLTPPPVFVEIGPHAALAGPIRQIVHSEAAAHT
YIPTLVRSRDGMVCLLETAGKLWLAGAAIQPRAVNPPGGSFLRDMPTYQWHYEDGSHPWRET
RISREWRLRRFPHELLGSRVETGDACPAWRCRLSPADEAPWLREHVVRGTPVLPAAAFVV
MVGEALRQLGAGRDGFSLKS VVFSAPLALDRDETVELITALMPIPDGEHAGWYHFSISSIAD
IKSGGACTQHATGSCAAGAKFQLPAPNMAASTASLVRQVNHGGFYDTWRRFGLDYGPPQFRRI
RDARSHVSERRAAATIDTSCAPEDEDAYCQAAMHPTSLDAAFHACMVAGCVGLERNFERLAV
PQHIEEVYVKPQTGAATAAEMTVVTEAFENVNGVSCSNVFGTSKTSGEILLHVRGLKATPLP
EEISPEGPADRHAAVLQWKPDVDFGSWSYWIRPNKRQYKAQVASLMGLLGHKTPAMRILEV
ETQHGTNMTDAALQALKSGQGTPLYSEYALVSGSDASSKLAREHFGQTARMRFKANLGP
FDLAQALKTPAPFDLVILNSDDSDSLKDLLQATRPLLSARGRLIISDTIATAGNDDTVVDKY
KHYMGRMDSLRRTLSTAGFLTQREVVYSYGASTIMATPTPPDDPQPATPPSRPNKTINVLR
STRSPRVSAASQLRARGYRIQWFLPGQLLPTRKATVSLDLDEERGPFLLHGMGPDDLAAALK
ASVLSLQGTAAATAPQMLWVTGAAQVRCVDPRWALVLGFARSVRRETGVDLVLTLELESFDADG
WGAVVRVLDGFDTRWRGGDEEDGVDPESYVFSGGEIQIGRFDSDVLPKLLERAPDGEDED
KSRKVLTM SKHGDHTSLEWKQEA VTTGGKVNGNTVQVQVQAFSIPHGGLQTTSEPSLTSTEL

TFLTSGVISAIGPQVDKLGVGDRVVMLASGSIATSVQISED MCFRIRDDMKFEEAVKLPLLE
YCSAFQSLDTLAGLEKGQSILIHRAETPIGRAALEIALERHGDKSDDIFATVTNAAEAEVVM
TKFHLASDHVFISGSTTSFLHSVTEATAVKGVNIVLSTFADPRLVEASWKCLTPYGHLIQLA
GWDASPRTRDSGEQLRGIDILRDSKTF SRVDLAQVLNRRPHSLHSHLRKAMAYCRTGNISAI
NRHIKVLEGDSIKNGIKVPRSPGDGTSLLVAKLPEDAGALRVAPARRKLALREDRTYIVVGG
VGGLGIPCARFLAERGARRMLFSRSAERFATDNPLLCDEFKAMGCSVKFVSGSITQAADVE
RLVAAAEIPVGGIIHSAMVLQDSHLANMTHRQWRDVIDAKVQGTWNLHSATTESSSQPLDFF
VLFSSLAGLGQVGQANYAAANAFQDAFVQHRRARGLPCAALDIGIMEGVGILARETARLEA
LRSVEHHILHERELLDALAILDDGAGGGGGGGGDNINNSVAPKSSSAVPAAAGYVSAGQ
MAIGLGFTAAGQGLTRQSAWRRDPRMQMGRSSAGHDNYDDETTSSKEQQQKSNSGAQQQLADA
LAHDAHEQTAASREALTRTLARELAATVRQLTMRDADDGNLDQDAGAPMRS LGVDSLVSVEL
RGWLRRRAKVALSVQDVRGAETLADLARLVTQKTADARGAADRHS DSRVPIGVPG

Predicted cluster (antiSMASH prediction)

GGTG_02299
GGTG_02300
GGTG_02301
GGTG_02302
GGTG_02303
GGTG_02304
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GGTG_02319
GGTG_02320
GGTG_02321
GGTG_02322

GGTG_02323
GGTG_02324
GGTG_02325
GGTG_02326
GGTG_02327

>GtPKS14 backbone gene sequence (GGTG_01184)

MAAPQSSFRELGLSILGVGSQYPPYSLKPDVETLGKRFYPDSPAMKKVLDINRYTGIEGRS
SIGNPDHPLVNGPTAPSIAELHSTFMSDGVPLAISAARRALEDAGLGGDDAAAQITHVVSTT
CTDSANPGYDHFVARALGLSPSVEKVLLHGVGCSGGLAALRTAANLALGHAMRGLPARILVL
ALEVSTTFVRSELD SINSEQTTRIGVCLFSDCASAVVLSNGVGQAPTTEPAFDLLGWQNRTI
PDSEVDLGFVDVPAGWKVILTQRVPKLTAEVL RPTFDSLMSLPPLPKTYGAAADF DWAMHP
GGATILMGAEKAMGMAPEHMRASYDTYMNHGNSSSATIFSVLDRLRQKMDAHTPGGRPPAD
YVVGCAFGPGITVEMCMLRRRRQGAAAVTGLQTPPETESEASRSDDEDDVQSKRAAPQSSSR
NGNKSSGVAGSSNGFVESAGSDAFISEALAGVELD

Predicted cluster (antiSMASH prediction)

GGTG_01171
GGTG_01172
GGTG_01173
GGTG_01174
GGTG_01175
GGTG_01176
GGTG_01177
GGTG_01178
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GGTG_01187
GGTG_01188
GGTG_01189
GGTG_01190

GGTG_01191
GGTG_01192
GGTG_01193
GGTG_01194
GGTG_01195

>GtNRPS1 backbone gene sequence (GGTG_13228)

MAGGGTNEVRGTRHTPSQAMKAHTESSAVRRQEASHERKLDYWRTQLADGVSAEFLTDQPRP
AGALSGKTAVAAFTIEDSLHEAVQGFSRAREATTFAVLLAAFRAAHYRFTGAEDAIVGTSKA
GPVGAVRLLPADTLCLRIAVGGSDTLAELTARAEAAAAAALAHGDVPLGRIASALQKAGQKE
KSRAHLVRILFGLHSQGEGLPVEPSVAAAAEVALDLELHLAETTHGGLDGKITYSTDLFQTR
SIDGIIAAFREILRGGIEQPAEPVSALPLGGLDELATMGLLGVKRTGYARDSSVVDLFRSHV
AATPHALAVVDAAERLTYAQLDARS DVTAAWLRRRAMSAEALVAVLAPRSCEAVA AFLAVLK
ANLAYVPLDPAVPAARVAEILSAMPGGGRRLLVLVGRGVCgaeIPGVDVELVRLDEAVDTAGA
ASAAASTVMPLATSLAYVMFTSGSTGRPKGVMIEHRGIVRLVTD RSVLPVDKAAVPVAHIAN
PAFDMATWEIYTALLNGGTVVCVDHMTVLDPKALAAVFEREKVRAAVFTPAFLKQYLYESPS
TFSQLDMLLSGGDAIRPQDALRAAQLVRHAFcNAYGPTENTGISTMYRMGANEQCANGVPIG
RAYSNSGAYVMDPLMRPVPLGVLGELVVTGDGLARGYTDAALDRDRFVTIQVGE GEPVRAYR
TGDRVRWRPTDGQIEFFGRIDQQVKIRGHRIELAEVEKALLGHGGLRDAAVVVHKDDSGEPE
MIGFVEPRAGDTAGDEEDGQVEIWVNHYEQQNYATLGGVDGSAVGND FVGWTSMYDGSAIDR
TEMQEWLDDTIRTVLNGRPPGRVLEIGTGSGMILFNLA KAGGLENYVGIEPSKSAASFVTQR
VASIPELAGRVQMNVGTAEDLGSIDAQQPELVVNSVAQLFPSPEYLLDLVRTIAAMPTVRR
VYFGDMRSHAIDRQFLAGRALHSLGENPRIAKAEFRARIEEMEDREEELLVGPAFFTGLTAL
LPNRVRHVEVIPKRMVATNELSCYRYAAVIHLNCPHGIEEPRIVDTS AWVDFRESAMDRDS
LAELLKGAAGEPATVAVANIPYSKTIVERQILASLEDEANDEDDEAWVVAARLAAQRCP SLS
ALDLARMAEEAGFRVEISWARQLSRRAALDAVFHRFPAAAEGARVLF EFPTDDAGAPPATFA
NRPMQKLQSRRIEAEVRDRVQALLPSYMVPDRIVVLDRMPV NANGKVDRKELARMAKTTAKK
TKVASSPTRVAPRDEVEAAVCDEFLAVLGIEVGIEDNFFDQGGHSLMATRLASRLSRRLDAD
VSVKDIFDQPV LKDLAASIRRSSSAYS PITGAPYSGPVEQSFAQGRLWFLGQLNISTAYVVP
LATRLRGQLQVDALEAALHTLEQRHETLRTTFQNGDDGVGIQVVRSAGARKKL RVIDASGDF
AQILREEQAVSFDLGSEPGWKVSLRLRIAPDDYILSIVMHHI IADGWSFGVV RKDL SRLYSAA
ANGRDPLAALEPLPIQYRDFSLWQKLPEQAAEHQRQLEYWKTQLADSSPAELLCDRKRPAFL
SGEAGIVQFTIEGAAYERLQAFcRAHQTTAFVLLAAFRAAHYRLTGADDATVGTPIANRNR
PELENLIGFFVNTQCMRITVEEEDTTFDTLVKQVRATATAAFANQDV PFERIVSALLRGSQD
ASRNPLVQLLFALHSQTNLDRVELEGMSAEPAPGPMATRLDMEFHLFQAEHSLSGKVLYSVD
LFERKTIEGVVAVFQEVLRRLDRPQTPI SALPLTDGLDGLDAMGLMHIERTAYPRDSSVVD
IFRQQAALPNATAVTDSSGRRLTYAQLDAESDQAAAWLRRRGIPAE TLIGVLAPRSCEAVV
AFMGILKAKLAYIPLDVNVPGARIGAILEAAECRLLLLGRGVPPPDTDLTGVDVIRINSTLD
HSSAGGLSSPLGAEVADGPLATNLAYVMFTSGSTGKPKGVMIEHRGIVRLVKDTNVV TSAAS
AVPVAHVTTLSFDLSTWELYAPLLNGGSVVCIDYMTLLDPAALAKVFEREQVRAALLTPAFL
KQCLASPESAAA IARLDALLACGERLDVQDAIAACKVATKCGIVNAYGPTENTVFSTIFKMT
LQEGCPNGVPIGRSLTNSGSYIMDGRQRLVPIGVVGELVLTGDGLARGYTDSALDRDRFTEV

EIAGEIVKAYRTGDKARYRPTDGEMEFFGRMDQQVKIRGHRIELAEVEAGLLRHEAVTDAAV
VVRNTQEGQEPEMIAFVRAPRLVEQQSQAAAEAEILSRLRVFLPKYMVPEGVVLMQDMPNA
NGKVDRKELGRLAQTAARSEVQVAVAVAAARDEVELAVCDECAGVLGAAEVGVNDDFFALGGH
SLMATKLAARLSRRLGTAVSVKDVFDPRVLAADLAAKIRRSASHSPIKRVGGYSGPVQQSF
AQGRVWFMEQLAGGTASYLSMATRLRGALNIHALEAALGALEQRHETLRTVFDEVGVGVQ
KVLDSGRVKKLVMSLSPEDDDFSGLLLKQQTTPFDLKSEPAWRVSLIQLPGVDDNLSIVMH
HIIADGWSIDVLRQELGAYYAAALRGGHVPLLEQIAPLPIQYRDFSVMQREPAQAEDHGRQL
EYWKTQLADSTPAEFLPDRPRPSVLSSGAGVDFDAIDGALYERLQAFCRAGRSTTSFIALLA
FRAAHYRLTGVEDATIGSLIANRNHPEIENLIGFFVNTQCMRMAVGDDGSFQGLVEQTRTTA
AAAFANQDVPFERIVSSRLGTNDMSRNPLVQTMLVLHSQEDLDRIQLEGLIADPVPGTATT
RLDVEFHMLQRAGSLSGRALYSTDLFEPKTIRCLVFVFLTVLRQGLEQPQEPISTLPLIKDG
LDEICGNSGTFVMDRRQQLVPPGVMGELVVTGYGLARRYAGSDSDRNRVVEIEMVVGNTPIK
AYRTGDRARYRPTDGQLEFFGRMDQQIKVGGHHIEVAEVEAAILKQDAVADAADVQAGKII
AFMTTKATKNTPPDHDDASGQVDGWVTHFDKATYTDIDKIEDTTLGNDFMGWTSMYDGLI
DRAEMQEWLDETMQAMLEGAAPGRVLEIGTGSGMILFNLARAAAGGLERYWGLEPSPAATRF
VNDRVKADAMLAGRVHMHVGTAAADVGHLELRPELVVINSVIQYFPTCEYLAEIIDQLVTRPG
VQRIFFGDVRSYAINKQFLASRALRSLGASATKAGVRQIIAELTESEEEELLVDPAFFTSLKK
RLPDLVHHVEILPKRMTASNELSSYRYAAVVHVSQENARPVHTIDQAAWVDFEASGMSREGL
ASLLRSAPADATIAIENIPWRKTMLERLVVESLDTEGDAQNNTVDGAAWISTARSAAERRES
LSAADLARLAGEAGFRAEVSWARQRSRAGALDAVFHRIAAEGGARVLYRFPTDDEPEGSPAA
PLTSQPLERLHRRRVEAQIREGLQKMLPAHMVPQKIVVLGCQLPVGANGKVDREELGRMAQA
IQKPSAVASVHASPKDDTEAVVCEEFGSVLGVGVGINDNFFDQGGHSLMATKLAARLSRRLN
TDISVKNIFDQPVLSDLADTIRRISASHKPIAKTTHDGPVKLSFAQGRLWFLDQIDLGKTAY
IIPLATRLRGPLNTEALEAAIRALETREHETLRRTTFHETDGVGMQAVGPVSTIKINMVDMSAK
THQEYQAQLLWKEQTTAFDLAAQPGWRVALIKLGQNDHILSVVMHHIISDGWSIDVMRRELQ
FYAAAVRGRDPLSAVPALPIQYRDFAAWQAQQSAEHGRQLQYWKMLADSSPAELLTDKPRP
ATLSGDAGVVPLAIDGPMYEDLQAFCRYHQTTSTFTVLLAAFRAAHYRLTTGAEIATIGTPIA
NRNRPELENMIGFFVNTQCMKIAVGKDDTFEGLVRQVRSTTTAAAFANQDVPFERVSELLPG
LRDSSTSRNPLVQLMFALHSQQDLERIPLEGLAAEAVPGNPTTRMDLEFHLLQGRKGLDGRV
LYSKDLFEEKTADGIVAVFLEILRRGLDRPRTPLSTLPLTDGLGEVRSMGLLDIRQTDYPKG
SVVDAFRKQAAAHPDATAVIDSSARMYRELDEKSSRLETWLRRRKGTSPESLVGLAPRSC
EAIVAFLGVLKANLAYIPLDTNAPAARIATILSTVAGKTLVLLGRDTPPPDCSTTAGVELIR
IADALRSAGPAEAAALAYQQQPSASSLAYVMFTSGSTGRPKGVMVEHRGVVRLASEPDVALRG
APIAHMANTAFAATWEIYTAILSGGTLVCIGHTTVLDPVELGGVFADKGIRGALFTPALLK
QCMTSAPAALAGLDLLVVGADRFPQSAIEAARLVRGAVFNAYGPTENSCISTKYRVPVGEE
NYVNGVPIGRAIANSCTFVMDGQQKVVPVIGVMGELVVTGDGLARGYTDPALNDGRFVSVTIN
GRTRAYRTGDRVRYRADGQIEFFGRMDQQIKIRGHRIELAEVEHAIIGHDAVQDAAVIVRV
QKGQVPEMVGFVAARPDGAAKQPRNREEQFAAQVEEEICRRLQALLPSYMPERIVVLDQMP
LNANGKVDRKTLARMAQTVPKRVDSTTDEVFVPTGEVDKIMHAVIAEVVNLPNRPANRSF
IGLGGDSITAMQVMALCRQGGVSLGVQDILKSATIADMAARANRLSLAGAPAQDGSTETLGE
EDEFAPFPLSPIQKLYFAQFPDGENHYNQSMMLKLQRPTPESVVREALSELVRHHSMLRARF
QRDPAKGQWMQRVSPNADEAFSFARSNVPTWEEAQGAMLEAERCLDITSGPMLAARSLHIGE
STSFLFLVAHHLVVDLVSWRVLLRDLEQLIGGISLPKTQESWSYQRWVRSLQSYAETEASAAA
LTLPFAVPEPNIEFWGIDESSPNNDSTNLAQGEFTLGPFLTDILLRAAEKTLRAEVPDVL

MAAHTFAVIFPERAAPSFHTETHGRDHPRGGTAIPVHETVGWFTAIVPLVITAAGGSDYVDS
 VIQAKDIRRTVPGLGVPYFTSKMLRGPPQKPTMEIMFNYLGRFQQLERPDGLFELLPGSTHP
 VDVGLSVARLSVIDVSAVVERGALTVSWNNAKIIHHQDKLARWFSLYEQALTEVTSALQKAL
 PRLTSSDVPLLCLPHARLGALNEALAAVVSRRGGVEAVQDVYPTSPMQRGILLRSRKDASQYD
 VHAVWEISPCEGRGAAKVDTSRLRRARHVRHVRHMLRTVFI DAGLRDDSPFDQVVLRELDP
 SITFFTCDGDDKAAAMEKLWDSCRGDGDPDASAHRLAICACPGGKAYAHLQVSHALVDATSL
 QILLRDWARAYADDLPAGPGLSYSSYIAHIQNTSPESSLRFWTARLEGATVCRLPRLTDGIV
 RTGHGGMRLRHVDVPFGHRLDALARRLRVSVANIFQLAWALVLRSYTNAQDVCFGYIASGRD
 VELDGISDAVGPFINILVSRLVFDQHSTAATMLRRFFAAYVDGLPHQHAPLADILHALQVPG
 GQLFNTALS FQKLPTGQPQDLELSFRFIRGDDPTEFDVMLNVLSGDSINFSIDYRDNFLTQA
 QAINIGQSLVQALSAIEATPDAGVDSLELLPPKHLSQLKRWGEAIPPLVDRTVHCLFGDACR
 ARPDASAIHAWDAHFSYAELDDASSRLAGLLVERGIEPGSFVAMCFEKSAAWVAVAF LAIHKV
 GAAFLLELPDAPRERTQYMLEKTEISMVLCSAACSASVEGWGMASMVVDKDAIATPASHACQ
 LPDVPSSSAAYVVF TSGTTGQPKGAVVEHGAFCTAAVAQAQNMSIGPESRCLQFASF AFDIA
 MLEMVTPLL VGVCVCMPPQKQDMVADLPGVVRNMKV TWAF LTPSFARTLSPEAGLAPLETFL
 GGEPLSQRDIDAWADKVRLGNGYGPAECAVISSAMPRATRSTEASNIGHPSGCARWVTELGN
 RQRLVPIGAVGELLLEGAPLSRGYVNDPARTAEVFFVGLAWAPHVGRTPETRFYATGDLVRL
 NSDGS LTFVGRRDGQVKIHGQRIELGEIHHHLATMHEIRHSVVLSPSEGPLRGRLVAVLELK
 DFCSTADAADAAATHEPMRLVAPSMRPRAAECVGRIRNALARRLPAYMVPTTWIAVHQIPMM
 VSRKLHLPTVQAWIEGIDEDTYRNILAVADATAELDPSEKVARQISRRLGDLLGGAGNVLQD
 VVGKDIVPMQFGLDSIAAITLSSWIRKTFTATVPMATLLSPQASVRTLAALVQEEKTG PSTA
 RRATAAAIVNLRAELQRLDQRLARLLAVPKKVTPKRLRRNHQTPSTFLVTGSTGFLGSQIV
 RQLLLRAAVKRVFCLVRADNDDQAWERMMDAARKGEWWRPD LAERLTTWSGDLARPHLGLDA
 ARWARVAGGDVD AIIHNGAVVHWHLGYHDIRAANVGSTFDLLSALSTATSPPRLAYVSGGYF
 GTADETDNQVADLLSDSGGYAQTKFISEVLVGRHGERLAAASPDFPMPVVLKPGFIIGDGDL
 GVSNLDDFLWRVVGSAVRVGGYNADDPDAWLLAAGSDQIASAAVDACMLPPSAASKRAV
 RFVDGVPVKELWRVLAEDPELGFELKPMSCRDWLATLERDMNARGPAHPIFPVFDFLRSRRG
 TVGVRIRDEEAVFPETELRERVRRSLIYLKTIGFFSANGAASQPKVGVFNRSGWSLRLVD

Predicted cluster (antiSMASH prediction)

GGTG_13215
GGTG_13216
GGTG_13217
GGTG_13218
GGTG_13219
GGTG_13220
GGTG_13221
GGTG_13222
GGTG_13223
GGTG_13224
GGTG_13225

GGTG_13226
GGTG_13227
GGTG_13228
GGTG_13229

>GtNRPS2 backbone gene sequence (GGTG_08621)

MASEITAGLREETALSILNPTPTRLPGPALLHHLLKLELRQQDTAIHYLSSSSWDKTSLTIGE
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LDAPPDRVQFILGDISARLVLTTELSQKVPSEESNVIVIAVDAPEEAGPGDEACPTPTPRR
DARASDLAYVMYTSGSTGTPKGVGISHDAVTQSLLAHDQHIPSFSRFLQFAAPTFDVSVFEI
FFPLFRGATLVCADRRLMLDDLPAVLRVMDVDGCELTPTVAGSLLRKRDSSASSLKLTLTIGE
MLTGPVVEEFGGVEHGAESMLWAMYGPTEAAIHCTLQPAFDANSTINNIGVPLATVSTYVLS
IPDESPQVDTSPQAMPHPVILPVGEMGELAVGGFQLAEGYINRPEQTAAAFIETISYGRLY
RTGDKARLRPDGILECFGRISEGQVKLRGQRIELGEIEAVVLRVDGCHGAVAGVVEGRVLV
FCEMDSPDTRHWAEDKVMEACSCWLPRFMHPNDVVVFGNLPRLASGKVDKRLISEYQSSR
DSAKTMLPPGPTCTDPLEADLCNTAEKVLGKAISPLDNLASLGLDSLLSIQLASLLRQSGLA
ISTIDVLESRTISHLCSRIRARKDQESSSEVLLHEHINVELELEYVLEQAPSLLPDQEQIEV
VLPCTPLQVSMLAETARNPEAYCNWIELEFPTDCHENQILAAFEHLSQRNEILRAGFVHLLN
GRFVQVWRNLPLPQQAEDDASVPHRNPQDNMPLDGHDIHRPLKLRLVRRDGLRMLIAIHH
ALYDGWSMDMMLLDLEVLLRGQEPAPRPQFRAVSQFYASDAYAHASDEARAFWAQQLLGFQP
SPFLLVSATSEGSSTTLSQTYTIDIEPGYLEGMARHIECSPQAVFQASLVWLWGAILGADD
IVIGTVTSGRTIPIMGVEDIVGPCLASVPLRAKLGEVRTLKGLVGYLQASARALIPHICILPL
SEVKKSADIPLTQSLYDVLFFVYQESLASRRQGERSLVREVAHQDYLESKLLVEIEPSVHQFS
CRITYHTGFVPSDYVSGFAEQFCFILNHLIHNI DAQVTSLRDAFPD TLLSQHNTPPRALEGN
ADLASLVEGTAARFPEKPAVCFADA IPTDGEAQTRTLSYSDLNMTANTIGRLIQSFGVEVGA
PVAIVMEKSVDLYAGILGILKAGCAYLPLLPSTPPQRIDTILRQAGVQICLTDTATSQSLQS
LGNNLHVINIMKSNLEALSSENLGVAPDSTRVANI IYTSGSTGTPKGVCVTQLNIASNLDVL
SRIYPLSSRGASRMLQSCSQAFDVSVEI IFFAWKTGMCLCSATNDMLFVDLEHAIRALQITH
LSMTPTVASLVDPQNVPTVEFLVTSGEPMTEQVAEKWTGLLYQGYGPSETTNICTVKKMSPG
DPIRHLGHGFENTSSFVLYKDGTSELVPHGCMGELCFGGDQVVKGYLGMPELTSQKFIEHPS
HGRLYRTGDLGRMLPDGSLVTIGRMDDQIKLRGQRIETKEVDSVVRESGKVTSVLTMIVARS
DSEVDQLATFYVPAASCSDVSATQHRKSRI FINAASPLLAVNETIFRLLASSLAAYMVPSY
LIPVSSIPTTPSGKVDKGLLRQLFENLSQPTLELASAGAGDSHDDGESWSELETTAKTIAD
ALGVDAHHVRKWSPLSSIGLDSISAITVARRLR TSMGLKLSISQVLQSACVARLAHLAHEAV
SPTDESASSHHADITFFTDSFVAEIQGRLGDRRVEAILPCTPLQAGMLAMSSGSSNSSYLNQ
MVFKLSVPGKGMQKCWEALVSRHAILRTCFLATE MATHPIIQVALKDWAPKWQVFDLSADQA
ALDECLRACELTLAPAIDSMEPPVSFALARSHDAEYFI FTCHHALYDGVAVGRLLQEAEWLL
ELGDQKPLPPPPRYEHFLREMLALPEDSDAFWKDQLD GFLPRSLPSPGAHVHRDQSLPENLD
LGVPLDEINGRLKDMGVSLLAMCQSSWAVCLSILLGQADVCFGNVVSGRSVAIDGIENLVAP
CFNTIPVRADVSNARHHVDLARSLOKSGIEALRYQFTPLRQLQSMHAGAGSSTRLFD TMLLL
QRPPRPLDNNIWVLNRDDGTMDVPLVCELIPDPQSNLLQVKLHHDSSQISASLVFFVFGLFS
HAFRTALAYPSSPILARASLPNELSRMMHSLELRQDTSAAASVSPVYQTPQSEEWSTESVV

RGVLSTISSTAEAVIGKHTTIYQLGLDSISAVQIAAALRKRQFQVSATDVM EHPTCHRLAVF
VDSATSND AAGLPVYDLHAFQAECHGQLARDPAYRHASAAIFPCTPLQHGM LTEFINSNGHN
YFNFLRLDISNSGATPGSILESWKRVVSSHEILRVGFFAVDHK DASFAMVGRSDVDAILVAQ
IDVVADGDTGAFDMERWRS DARGVRDELGRPPWRLALVEDDQGI IQIHLAIHHVLYDAHSL
NAILEDFAAASGGTDVHPSRNSRIAATISDIMAQSMNNKSEAQDFWKSLS SRRAVVNRFPVMT
PLRVEQRAICVEKTVGSFPFSGIEGA AKLSGVSVQALIQAAWSRILCSYLG EPSVVFVGVLS
GRNTDATQSAAFPCITTL PVIENRASNRELLQQMAYNTRLHRHQQVPLAQIQGWLGLPDT
RLFD TLLVYQKFEDRATPSGEQSWRIVDDTA AVDYPISLEIEPCG DLLHHQLAFYNDVIPRD
QATLL LKQFDSALAH LAFHPDAQEDDLWPSAPSLFSTTPASNPELPSEIVFLHQFVERMA LS
SPERAAL E FVSSF KPDGEP MRRTWSYEELEANGNR IANLLEPHTQTGGIVAVCFDKCPEAYF
SILGILKAGCA FVALDPGAPPARRQFILEDSGATALLTD TDRSAALDFVASVPVITVDEQVL
DALSPDPLHERQIQ LSPNDR CYCLYTS GTTGT PKGCEI THENAVQAM LAFQELFSGHWD EDS
KWLQFASFHF DVSVLEQYWSWGVGITLVAAPRDLILEDLVAMISRLEITHIDLTPSLARLVH
PDEVPSLCRGVFITGGEQLKQEILDVWGDAGVIYNAYGPTEATIGVTTYQRVPRTGRSTNIG
RQFSNVGSYIFKPGTEIPVLRGAVGELCVSGKLVGKG YLNRDDLTRERFP SLAGFGEERVYR
TGDLVRILHDGCFDFLGRADDQVKLRGQRLEIGEINH SIRAGVPQLEDVATLVIRDEKKYKD
LLVTFVVSKNLATAGSGRGETLRPVTTADDGIGGSTLARDVQAACRTRLPGYMP TYIVQLP
FIPLSSNNKAEVKQLREL FNSLTPEDLMAASAAGPRASSALDGGVAQKVVAALRAMHLLDGS
QSPSAETSIFELGIDSISVLRFSRALKRGGLDQATPALILKHPVIGDLVHALQTDSVSRDAG
AALEARQLVEACQHRNRAQACRALGVASDQIEYIAPCSALQHGMISISKNEESTGAYFNVFT
FELHETVDVFRLKDSWQTIVDSFSILRTRFLASTEGFIQVALKEVALPWAEIDVEEVQQNET
GQGV LQSLQNRWIQLNSKDVIVPMELHLVKLPAQQRVLLKLHIFHGLYDANSLGMI IAKVAA
LYLGTEPIESRTTFIDALIHGPLRNF SYTKSFWESHLLGAELVPLPQLCPTPATSVTSASLS
LDFHVLEPARQQNLNVTHSAVVQALWLSVLCARIQSSMTIGVVLFGR AIDVENAEHVVGPLFN
TLPFHLPDAA NCQTWADLVEYCHNFNTSTLPFQH TPLRDIQKWCSSGRPLFDTL FSCQRESL
PSAAITGGLWTEVPPEDLTPDYPLAFEATLTRGNRLELL LVAQAGVADNGTLASMLDDFHQA
MLQMEQSVEGQWSARPRPGVVGTGLRPSNAPPKQSTD SHTAHAVPFIWTD AALILRSEMASL
AGVAPGDISDTTRLLELGLDSIDI I KLSARLKKQGLVLTNSQLVKGQTIKAFVDILGQPAGG
DGRNPTS NSTEQSHPSRTAALRSRIQDIPGALDADMVEAVLPPTPLQDAMVADTLD SGFRRY
YNHDVLEIPPGVELSRLHEAWQTVMDGSPVLR TVFVQVDDTDLDFAFCQVVLREMKLHWEVR
ELHTTAEIQGEIEQLRQRAESSAGMANLLQLTPIQVGKQNF LILSIAHALYDGWSLDDLHRD
VRDAYAGRFKPRPPYVDYLDHMLLSATAEANDFWVDSL TGATPTS IQPQKLQVGSVKQRDQL
QSSPILVHRLERESTVAAADLLSFCRRQAAS PQVAGQVCWAAVLSRRTQSLDVTFGSVLSGR
ETEA AEALLFPTMNTVAVRTVLHGT VGTLLRYVQENMAGINQFQH FPLRKAQRLGGAGGTGE
ALFNTL FIMQKRRVDEADDNEDMIMRSVDGSSSV EYPVCVEMEIVGSQKVVRTACDDYFLS
RRETAELLGELDSVLRFLLRSSHDT SIFTSTVASAAGGASASSEVSVCGLP PFHLRTRNSSS
SATEFSAQTDTSTLVEDQHWTPLEETIRDVLARVSGATDPSSVKKTYNVYHLGLDSISAIKV
ASLLHKRGVELRVPELLGAESLEEMATIASGRAASQSSYSQISTHPEPVAA APEGAKVYEEA
ASQAMLDRI SHLDLVQNAGLRLEDIQNVLPASAMQVHMISAWQKSGGEVFFPEFRYQLSGVA
DDFSADELA AAWRSLVHQTPMLRTVFLPTGVPDAPFIQVVLDPAAPYCLRTYGDVSAPDGGS
RGETSPDYPIQPLVHLAANKDSVGTGRNWTLSL KILHALYDGFSLP AIMTRFEELLARSNEG
KLLLLQHVPKSDVAGEWASRLAQQVSRPTMDARRAFWTDY LREAASTPFAAPSPTLTSGPDI
DRTRVSKFTPQAIGDASLLREACASKGVSIQSAFLAAVWRMLQ RDERTDVVFGVYLANRQWH
DQDGRDEGEQDPLASYPTLALLPLRVRCGAGADLITAARAIQQDLG SIMSDPANTS VGLWEI

EEWAGIRVDCFVNFLGRPFAERAGATEGVRLGQLHFSDETQPPLPASAPFGTKPCGQLILEN
NVVREAF PDTIDIEAALGHEGGLDIGVFGPSSMLGGDRGAEDLISMLTEYLALEA

Predicted cluster (antiSMASH prediction)

GGTG_08614
GGTG_08615
GGTG_08616
GGTG_08617
GGTG_08618
GGTG_08619
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GGTG_08621
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GGTG_08632
GGTG_08633
GGTG_08634
GGTG_08635
GGTG_08636
GGTG_08637
GGTG_08638
GGTG_08639
GGTG_08640

>GtNRPS3 backbone gene sequence (GGTG_06444)

MDYSMQPLASPKHQLPHIDTTTNSWDASDIIREEPLGSKLMWAIAHVQLDAGSIQAMDSFQ
DLGGDQRTATLLRRKCRSLGLDVRTKDILSCVTIAELETICKPCRRDDTITPADASDSHNPL
QLRPRKPSRFSYASDASTLHSRNSSTLSAVLSPPAVEVDVDKLIDDNAAVERSVVIKPRAGP
FDGKGVAFLELHGIEISGSPTS DVEVIPQSHMFLAGTKVAAIRRS LQETARGCEIPEVWIVL

RRVPTAETGEVNRRLRTWIQNVNAGTEQLIMSMDVEEAVKEPLTDIEKALRGAVGRALQMP
VENIGMNFSAQLGGNDISATQVVAIAKADSIFLNSSEVMQNHTLAQLARIASTRAEPSRW
DGSPLNSGVELSPMONLYFLTAMGGDSTNRSVRDGSYRFNQSVLLRTSRNFALDDVSAAVDA
VVGHHAMLRSRFSKASTGAWTQRVVPTGAGSYSLRFHTVSTDKELQAIIEESQTLVDIEQGP
VFAVDHVQTNDGHQMIYMAHHLVVDLLSWRVIIQDLDELLVNGSLLSQRSLPFQQWNQLQK
REIEQADISSPIPTGTPAGNYTYWGLQDAPNTYADSREVSFCLSPELTTILQTTCNKVFRD
SVDIYLAALLLSFSQTFHDRPVPVIWNQEHGRDVADPTVDITDTVGWFTSLSPIGSLVLEPGR
NDFLDVVRRLKDLRRAMPRRGAQYFASKFLNRSGPDLFTEDWPIELIFSHAGSMQQLERENG
VLEQLKIPGRTLASKTSDIGPRVGRIALFEVNTVISRGS AKVKLLYNRRSQHQELISQWVEN
FEHLLLEAIGRLRYHAPELTLADVPQLDVTYAGLEKLNKDRLATLGLSSVRDIEAVYPVTAV
QQAILIRQESVPESQLHGIYELTS AVGESVDISRLCAAWQNVTMKHAALRTVFIESVSETG
VYDQVVLQRCSPHMLFIDVHAGEDPIEALNNLPMVPAGTSR PQHRAVCKAPT KTLVKLDIN
GALCDAQSMNTIFVDVRRAYALNTPLQDATSLTYPEYLKFLETARTSQSLDFWMQRLKDVEP
CTFPRLLVITNEQRFYENSHFDLEIDAKTFMDFSRANQVTGDAVLRLAWGLVLRAVFGNDKV
CFGYRATGREAVSGGSSMRNVVGCFGNTIVCNLTLSPFKSLSSMLKTVESEYVASLRHQYVS
IPELHHILGVRGPERFFNSCVSLTYEPAGLDSRAATQTNFGLHGVSHRETSSFDLAVNARFM
NGSLVVDIASNSLLSEREARNVSNTLKKALNSILEMPSGSIEGVDLFTDHDYAQVVAWANER
DTPQPRSAVVHELVERNARESPQAIAIRAWDGELTYHQLDL LASRLAQRLMDAGVGHRTVP
LVLEKSFWSPVAMLA VLRTGA AFVPI DASDMGFIQPIFEQLNSSHVAIQCQNASAVLGNLFE
KVIVLNPPELLRELQLQPMRSTVTHTSEEDIACVFFVPASSRQVKGIAFSHASMSMALLTQGP
SAMISASSRVMQLSSYNVDIALSEIFATLIHGGCVCIPTDSERVL DFTGAVQRM EVNWSYMT
PLLSRKLNVDILPTLKTICFRTRSLDEDSYAPWVGKKKVL FAYGAPDICPLGISFLEVFGPH
QLNRIGGPLVGNFWIVNPDHRLMPIGAVGELVIEGPTLGYDFRNGQVDQAHWNSADFTG
GSNKKTRYFKTGHRVRYTEGGFIQIISSKKEDLEIGGHTIIISELEQHIRRSLDLGVDVITE
AIAFKGVQVEPVLTA FIELGEMFDGPEDLRQLSRTTRERLFAARRLVEIGLRNAVPSYMPVQ
IYIPVKHLPVTASLKVNRRLKQKIIYGLSRDQLVALSTVPNPGEVQRYCMQPAPLGQMEERM
RQIWAHVLNIEDETVISGADGFIKAGGDDILATKLLVCCRQEGIIISIADVLRNITLSELCK
TVKFADDTQQAHAQAHAPSHTPPQASVSSVASAPASEAAYPHVVLVQQQQQQQMLQRRRSRN
SIAAVPAAVDTSQQPRRGSNGDDLESVLATKIGVERATVREVAEASSMQSRFIESGMLRGRA
NINYFVFSFSGTIDCKKLEDACQTLVTIHPVLRTAFVPHKRRMYQIVFKSSAGADFKRYLCP
SWRLAAFAEKVIKKDQAAPLAFASPMTKFILLDGGKQSTLLLRLSRAQYDDL SVALLVKDLK
KLYDGAQNPPRRPSYVEFVRS AQVANSKGAHDYWRSLLEGASMTKV VQHARPYQLTNHSKI
KQRVAVGSLAHLDISFETVVKSAWAMTLAALSGSGDVVFGEVVDGRQVRLSGGQSVAGVLGP
TANAI PVRVKFPDQQVAPLDLLKAVQAQRVAGIQFENYGF LDLVQSC TTWPYWTRFSTVVHH
RYEETTVVPSEAKIFNLGKGGAGPS CRTIIIESRAQDV PDMYVHSLARGGGGPGSGSQTNNV
EMCITFCESRIPVSFAEETLRMLVDNVATFTSASITAPVVPSSSAFQRLQAHIPLPQAPSTP
SMIASELHPTPNNDVAPNHAAAIRKTIEKAWTLSSLN PATLNVPEEHRDHAAFYDLWGS LIP
ASQLASALTREVPKLGLPGIGGPGEFSLSMDEILDNPTMAKQFNLIARRMAGHGGGSSPGHR
RNV PSSSSLVSKIASKIKGHDQHAPVPQTTYLVVDSRTAADNARTPPPRSAGLPTPQAVHVS
SMLTPGLPATTPGAPTPLGASFTGP IRDDDELERQLERALHEISGEAQVRPQVPRKGS AEMR
RGGSSGGSSGDSSGGSGMESLTDGSSAVSSSVHEDLEQHTVFP GMAPVNYGGSPYRGGLRK
DSAVSAVSALAPVSPPTPGSKLVASAMTPAPISPPTPAMKQNAYHSHTQRHQRYRQNRPADL
NISLVRPPLPPIPADEAPDDVVS PVT PPTH SARYFDRAHRRADSSIVTPPAARAPRHFRSFS
RS

Predicted cluster (antiSMASH prediction)

GGTG_06438
GGTG_06439
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GGTG_06441
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GGTG_06443
GGTG_06444
GGTG_06445
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GGTG_06449
GGTG_06450
GGTG_06451
GGTG_06452
GGTG_06453

>GtNRPS4 backbone gene sequence (GGTG_03812)

MQLLHQVHNEGEFFSPISSLPGPKESVHSSIRPKFSQVERVFPATQIQRAIAAEGIQWAKAE
LSLWKKNPADFLAVFNAWTALASHHAALRSHLSTDPQTGELQVTILRRIGGITLQGMKDEQ
DASFDRLAHMALEATEHADSI RMVLHFHRA LLDAASISMIKLDFALLLHGIPCAEHTGFYLY
TRYLEQWRKSDEGSKSFWSNVLSGAVPRLALQAAPKHAHGAGSLAAGGGGARRSISVINGP
NLADLGGSHLAESQGQPLSSQTVLELLWGLVLGAHTGSDEVVYGTVRRDSTFVGADSCVGCL
DQTYLVRLPIPSRDRRLTVRDAVVGLERYHEQASHHAFVGLDEISRHL PANTS VETALTYTR
LGNPPCLAPGMSRFPVVLAI SGESSAALQVT LRYRDSY IASADA EVVLQHFVA AVRSAAAKV
ELANCLCSAVDLVSEDERDLLLAQSRSPRTAQPTTIPSLFEKAVKLHPQRTALEFEESVSLT
YAE LDGRANALARALKLQRG AIVPVLAERSPELIVALLAVLKSGAAYTVLDPDAPVQRNAQV
VAECDPPFVLATRRHSRVFPNTTAIEDALASCADRSPLDGVSIGPQDRCYIIYTSGSTGKPK
GAVLTHGAATSGMAHHS LGGLQRWLLFYNPIFSAAQRTMLATLVHGGTLVLASKERLTGDVA
GTINSLRADVVGITPSALSLLRPADV PGLKQVTLVGESVPQHLVDVWAGVEGLTLRNTYGLS
ECTQLNFRALLRSADDDDAVINPRVGVPGDTSDAFVLLPGTTELAPRLVAGELCLAGPQL
AEGYLN EPALTARAFVDNAFGPGRLYRTGDLARRLADGSVEILGRADLQVKINGQKVEPAEV
DGLLLGCGAVDASVTLPVEVEEGRGPSLVAFVVLAGGRTL RQAVVAGREYLRERLPGYMIPT
MWVPVEAIPKTASGKINLQQLRELARDMGAVGFAKAMFEGEAGSDTALEGLELEISKAWAAV
LDMDPSVIRKHHSLLDLGGTSIQAIKIISELRLSGLALDFSELLAGATLESIASAAQVIDKG
QDEIPQPFSLVQDNPRLLSKLEKDVGISDAYPATPFQAAMLTSLNTPSDPYTYSRTWDVSGL
DTDKLRESFEQVFRARAILRTGTFVPHKRSFVQVVRDDVPLPWHESQETLDSFVADKSHAKWD

MSEPLFRVTLTGGAQASKVLVVTMHHSFLDFWSHRFLYRDVAAAYQGKAMPVRTPFSAFVRH
VVLGQQPDAAAASRDFWAGYLAGAPTTTLNYAPVNSVDQAVKLKATLDFSLSQRARECGVTL
GGVYGAWAVLLSHHAAASDVYATTVSGREAPVLGIRDMDGPTMTSVPQVRVLQADATLGE
LVRRIMGEFVGKVKHSQVGMQEALRSGGASAGVLDTLVNVVLVGNEESDDDDTRSVFKQYAGR
PAWGSEYTVLEVEEASAANTTEVRLSSTMEARRLEYIRESFVKIVHLILEQPDTPLSQVTVL
GDAHSFLYSALSHRETQVPEPEFLHAAFERYARDTPDAVAIDFNGERQISYAELNTLANR
FAHELGRGRHGVRTGDLIPLMLDRSVDMMVVILGVMKAGAAVPLSPDNPAERNAFVVS DAGA
RLVVVHAEHEEFGRHLGAGVETLVVAPGMPDLLDDAENKQRP AIDDASPDNLAYVIYTS GST
GQPKG VKVPHRSAAA AVQSMAVEGRYEGAPWRTLQFANYVFDASVQDFFNTLSTGGALCMA
PTDVLLSDIAGCINRMDARQSIITPTVAKLFRPDDVPRFERLIVGGEPLTPDVVETWGRRCR
ILNVYGP TETSMVTTMKDVRQGGRIGNIGAPFPTVMAFIVDPEAGRDSLRLPYGAVGELCI
AGPQVTAGYVNRPDLTAAAYVDSEALGGVRVYRTGDLARWLPGGEIECLGRKDNQVKIHGHR
IELGEVENAIRRTGLVQDVVALATSIRDKLHLVAFCVFRNSAGGDDGSDDASGPDEVEALDP
TLFAGRMAELRENLGSLAAYMVPKFVVPMPGVFPKLP SRKVDRKALRKVADELDPVFLTGCAL
DRSGGGGEGGHVVPTETPAERALEAMWADIFSLPAEQIGREANFLALGGDSISAITLASFA
REAGYSLSPVNILKTPKLKDLATAMKEIRKDAAKARVVFKMPDSVKVTAEAVGLRWEEDVEY
AYPSPPGQAEFLQQGSRDEQMWVLQTVRHMPAELGQDAWVQATTALSQVNDILRTTWIQAGD
ALDDWVGVLRSRPDVARAACETDEDVTRFTEEFWESRFTFGKPFIKYAQLARPDGSWVLV
IKMDHAVYDGTLLRVFDDHFAAIVNGEPVPRHGEFRTFAEHMLQADKKGDLAYWARSMAGKP
AAIKAADSGDSAPIITAALRHEVATPNLERAARQLGVTPSIVFQAAFSLWLGGSAHGADVNF
DYLLSGRNLALPDPQSINGTLAQFLPVRTAVDPAEPLPGFLGRVQDDFWAMTEHASVGMDAI
YGAAGLARETHGNKVLFLFQPFEPAAPSEQERPRWLVMASKVRMFQPYELVVEVSKALGDR
HALKIMYDETCYAQGDAEKIAQDIAAIVDVMAEEEESEKLFVGAF

Predicted cluster (antiSMASH prediction)

GGTG_03802
GGTG_03803
GGTG_03804
GGTG_03805
GGTG_03806
GGTG_03807
GGTG_03808
GGTG_03809
GGTG_03810
GGTG_03811
GGTG_03812
GGTG_03813
GGTG_03814
GGTG_03815
GGTG_03816

GGTG_03817
GGTG_03818
GGTG_03819
GGTG_03820
GGTG_03821
GGTG_03822
GGTG_03823
GGTG_03824
GGTG_03825

>GtNRPS5 backbone gene sequence (GGTG_02228)

MQLSSARLGTPSNGLQTPEGRDRTSYATDRPDIPTPISFKSVSFDMREGDSLPLDSGP SHIP
 LSAALLAWRLLIARS GEEDAVDAIAIGRWPTQPADFPSPAPSTATFQVTIPKPPLAVDRRVT
 ETCDEIRRGLEQSLQQSHGQLGTQVGIDTTLCFSDAPAAENVEQHCSGNGTKVQSIWRVCLQ
 LAAVGDELRIVMQWQSSYMTETRAENGLHLFRTYLAAILAQTRVSAACSKAQQSSPKTVWDL
 IGPSTEDLSQIWNWNAAVPPTINRCIHDLVSDQCVVAPDKVAVEAWDGTFTTYREVDALSTIL
 ARQLRSSAGVHVGDIVVLVFEKSRWTTPALLGVLKAGAAFALTDPSQPEARLRSIVAQTRAR
 AVVSSELQVGLATRISHDANKDNGGKPAKVLVASDATLLEHAGWGFGASAMFLPVVPPSSPM
 YVIFTSGSTGIPKGVVCSHANFVSGAFPRAKAVGYRSSSRVFEFASYAFDVSIDCMLCTLMV
 GGTVCVPSEAGRVDLGAAILASGANMAHMTPSVARVLSDSERVMRALDVLGLGGEAVSAGD
 AAWSRLTKVIIAYGPSECTVGCTINDEVCAANTTIGKGKGAATWIVDPEDHDLMPVGSVG
 ELLVEGPVVGGLGYLGQPDKTAEVFISDPTWLVEGYAGKAPGRKGLLYKTGDLVKYDPNGFIV
 FVGRKDQQVKLRGQRVELSEIEHHLRGKLPBGVKIAAEVIKPGGADPTLVAFVSEPLAASPK
 LEGISKRPQDARFSSDLAAILADMDNLLGEELPRYMVPTAYIPLKEMPALPSAKTDRKK
 LRALGNAMSREDIAKLRLVNAVSTKPTTMEKALQGLWRKTLNTDLEIGLEDSEFFGVGGDSL
 RAMKLVSAAARAEIVLTVAEVFIHHTLKAMAAVAVADKDCAMSRAVEVAPFSILPSDWDLES
 ARKDAALCEDVDSEMIEDMYPCTPLQEGLMALS AKFQDSYVAQRVLQLADAAEAKRLADAF
 EWACRDCAIMRTRIVQLPGRGLLQVVIRESSIRWRS GKTVEEYLES DHGEHMDLGKPLVRYG
 LVHHDDSTVAFILTIHHALYDGWSMPLVVDRVNRSWDGLQTERPAEFKHFIFKLETVDKEAC
 EAYWRRRLDGATGLQFPPLPYEGYTTQADSLIERHIPVAARDNSHSSTSSPTAAITMATIFR
 GAWALVASQYIGGADDVVFGETLTGRNAPVAGADLIEGPMITTVPVRVRVDRHATAAEYLAA
 IQDEGVRQMEHEHTGLQHIRRVS PDAL EACELRTGLVLHPPTGEAGSPSLCPAEGLMPPADDA
 GAAREALTFTNTFALMLVCSIAADGFLVMAS FDSRTVDSGTMERVLQRMDRCIAELYRGLENG
 TKIAGILTSVGFDDVNDEFDELASLSKNGADGLGFDKPEHIWLVD PQDSQRLVPRGAVGEIL
 VDSTTQLNLPSVEIPAWYTKITSEQPERAVYLHVTGQLARYDGEGKLVVLARKEDRASSSKG
 KPDSNETKEEQSSSITSATLSSKESNVRELWADILHIDAASIDREDNFFRLGGDSIAAMKLV
 SEARPAGLKLTVAQIFKTKTLAAMAEMA EELPTCITS DQGPTKDA AAAAANTAPIPFSLLDVT
 SVSEFLEQQIQPRLANKHWKIDDVLPTRPLQAI AVKGSTDNPRFSIRYEALYFDDNTGLDKA
 RLVQSCQELVSRNEILRTVFVDDEKGV CYGVVLENLVADVEEYVLPQGGSDMQAFVHQLFNN
 DIGGSIPEGSAFVKFFLVEAGSEAGSRGALVMRISHAQYDEICLP LLLRQLATLYKGGGSDA
 AADQLVPFVSFVHHTLRVANPASAGYWADLLAGSP PPTVLRPGRADV PAGERAHFAVQRTAD

FSTAASPGVTAATFPTAAWALCLARRTGRRDVLFGFVSVSGRGGGLEGAGRVAGPCWQYVPFR
 VRLSPDDTPTGAALLELVQAQHAAGSAHEGMALPEMVAAVVAGLGWEADWFDTVVHQDVEHV
 EDLGFGAAAGLEAQGGGLGARTETIYPHQEPLREWKVQALVAEGGTRLTMEIVTFEAWRDEA
 VELLDELMGCVEELVYRPGDALVFP

Predicted cluster (antiSMASH prediction)

GGTG_02218
GGTG_02219
GGTG_02220
GGTG_02221
GGTG_02222
GGTG_02223
GGTG_02224
GGTG_02225
GGTG_02226
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GGTG_02228
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GGTG_02231
GGTG_02232
GGTG_02233
GGTG_02234
GGTG_02235
GGTG_02236
GGTG_02237
GGTG_02238
GGTG_02239
GGTG_02240

>GtNRPS-likel backbone gene sequence (GGTG_05648)
 MAHTSTTHLSCVDDLIRERASTISDAPLITYPNSAVRCAEWVEYTARDLDTFADEAAKELTR
 QGLVPKERKSAKSEVVALLGHSDLDYAITILALTRMGFAVLFLSTRLHTEAYVSLLDKCECF
 RIVTTSKYADTVRSVRGTGRELETFDVVPKAIYGLPSTTPRFKQTEFEDQSGVCAFIHSS
 GSTGLPKPIFQTHRACLSNYQIGSGMRAFVTLPLFHNGLSTTFRGIVAGRRTALYNAAIPI
 TNANMLEAMRAIDPQSFNCVPYVLKILAETEEGIRALARCKVVVFAGSGCPDDLGDLLVDNG
 VPLIAHYGQTEMGQLMMSSRDLDKTNWNLRLPTAKPYLVMEAIGEGMYELVVLDGLPSK
 VMSNCDTPAPNSYRTRDTFEKHPTMEDVWKHVGRLDDRLLTVNGEKVLPVPMENRIRLDERV

QDCVVFAGRAFPGLIVVRSENVPREWTDEQYLDAIWPTIQSANEGA EKFSQIDRDMVQVLG
VDTEYPRTDKGTIIRAASYKR FASLIDALYVRFEGGPSVAQIAVSGKRRMGADDWEPYLLNL
IHERLGLKDIGPDTDFFNAGMDSLQAIMARGHMMRQLDLGGAVLGQNAMFEHPSVRQLTKHL
TSLVRPESSSPAATSPLTPEEEAAVMREL VHEYGQFEPFVPGDQTPDGDVLLTGATGSLG
AHMLSQLLAMPVGHVYCLVRAPDPAAAASRVFGSLSDRGLGGALTPAQAAKVVALPADLSR
EADLGLGADVYARLRASVTSILHVAWAVNFNLGVRSFAPVHIAGVRNLLRLALSVPFPQPAR
FSFVSSVSAAAGTPLPARVAESFVADPRHAQGMGYARSKWVAEHVVRRAEEAWPPAAAAAT
VPPRVLRTGQVVGDSREGRWNATEA IPLMIQAAETMGCLPRLDERPSWIPVDVCARAVAE LS
GVVAAADEAEVVEDPGHVYHVLNPRTFDWTAEPLPALRAAGLAFEEVGQREWVARLRAAAE
RGEDPARNP TLKLLDFFADKYDNDRPGRRLAFETEK TERRSAAVAGRFDVIGAGLMRK CVE
SWRAREWAAVKKLE

Predicted cluster (antiSMASH prediction)

GGTG_05635
GGTG_05636
GGTG_05637
GGTG_05638
GGTG_05639
GGTG_05640
GGTG_05641
GGTG_05642
GGTG_05643
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GGTG_05654
GGTG_05655
GGTG_05656
GGTG_05657
GGTG_05658
GGTG_05659

GGTG_05660
GGTG_05661

>GtNRPS-like2 backbone gene sequence (GGTG_04908)

MAQLPDPTIDLDWSGHIGAIHEIFAANTHKHPDRVCVVETKSSEGPERSYTYRQIFEASNVL
 AHYLDAGVTNGDVVMIWAHRSVDLVVSIMGVLASGATFSVLDPLYPPARQQIYLEVSGPTA
 LVNIARATDEAGPLAPLVRKYIDEELKLKAEVPSLRIGDNGFLSGGEMDGRDVFASVRGKAA
 APPADVLVGPDSNPTLSFTSGSEGRPKGVLGRHYSKAKYFSWMAETFGLSGESRFTLLSGIA
 HDPVQORDIFTPLFLGAQLLVPSKEHIAHERLAEWFRFEPTVTHLTPAMGQILVGGASAEFP
 ALKTAFFVGDVLTSRDCRTLRLKLAANVDIVNMYGTTETSRVSYLVNPNRATDPDFLDRLDK
 DTIPAGRGMQNVQLLVNREDKTKLCGVGEVGEIYVRAAGLGEGYKGDVPMNEQKFLDNWVF
 DNNKWVEADKQHPSQGPWRKYKGPDRRLYRTGDLGKYLESGDVECTGRADDQVKIRGFRI
 ELNDIDSNLSQSSLIRDCKTLVRRDRNEEPSLVSYVPELKEWPLWLKAQGHEDAEDDAGVK
 LGPTRVFFKFRFRLQTELRDHLKGRLPAYAVPTLFIVLERLPLNPNGKVDKPNLPFPDIAEQ
 TTEASGEELKRWDLLSETEKRVATKASLIRGLNVKTIAPEDHFFDLGGHSILAQQMLLDVR
 KDTGASVSINTLYANPTLAAFSAQIDKHLGSAGADGADGTAPESSEADSYSRARDLVLKQLPA
 RYQSADPATIRASSRPTVFLTGATGFLGAFLIRDILQRTSRQVRLVAHVRAKDEKAATERLR
 RSLQGYGLWRDEWASRLSVAVGDLKQPLGMEQTVWDRLAGVDVVIHNGATVHVRRWQDM
 LAANVTSTVDAMRLCNEGRPKLFTYVSSTSVLDNEHYVSLSERQLSTGQGAVPESDDLEGSA
 AGLSTGYGQTKWMSEQLAREAGRRGLRGSVVRPGYILGDSESGCCNTDDFLIRFLKGCQILG
 SRPRIVNTVNSVPVNHVARVVAAAALNPLPGGGGVGVVHVTGHPRLRMSEYLSLLEYGYRV
 PEVGYGSWKGELERYVSAGGGVERDQEQHALLPLFHLCSIDLPAKPELDDENAVAVLKA
 DAENWTGVDESAGYGIGREDVGRYLRYLATVKFLPWPSGKGRPLPEISFDAGDALASGAADV
 GGRGGVSQSVPA

Predicted cluster (antiSMASH prediction)

GGTG_04896
GGTG_04897
GGTG_04898
GGTG_04899
GGTG_04900
GGTG_04901
GGTG_04902
GGTG_04903
GGTG_04904
GGTG_04905
GGTG_04906
GGTG_04907
GGTG_04908

GGTG_04909
GGTG_04910
GGTG_04911
GGTG_04912
GGTG_04913
GGTG_04914
GGTG_04915
GGTG_04916
GGTG_04917

>GtNRPS-like3 backbone gene sequence (GGTG_00281)

MATATETATARPQFGRLLPTILDEMARTQPGREMLSMPRSDKASDGWRPITFGQFADAVNR
VAALLIKRHPRPQTDDTAAIGSMLRASDEYTTFRPTLSYVGPSDVRYHIFLLACVKAGCKAL
LISPRNSLQAQLNLFDKTSCGALYYDVSEFKDRAAVWIKGRVGMQAFEAAASVAEWLGEGSTRP
APVVPYERTFEEARWDPLFVLHTSGSTGLPKPVVARAGSFATIDLSRAVPDFRGCRSIFWDT
FGAGRVFSPMPLFHAAGLYVSLTSSLFFDQPFALGFDPKPLTPQTVMDAVKHANVDVVVLP
AILEEMSHMPEAVAALAKLERVTFGGGPLSQEAGNTLVGRGVRLTNIIAATEMAPLYYYRQT
DPKLWNWFLINTEATCIDWRKFGESDGTLYEQVILRKAKDPGDQAPFYVFPEATEYSTKDL
YFKHPTVPNLWGYHGRSDDIIVFSNGEKLNPVSIIEAAVSRLPEVKSALVVGQGYFQPALFVE
PADDAATPEEQEALIARVWPAVERANRETVAHGRIVRELAVTRPDKPFPRAAKGTIQRFA
AVKLYAEAAAALYENFGGQDGFDRDGEDPLNGGSFVPDLSSDQALAQSLAELFRRLAGLKE
RGATLDVDTDFYTAGVDSLTIQAARILRKALGTATSKKLPVDAVAPRLIYANPTPNLLSSY
LMREVVSGHSHKQNGHTSGIDGVDPSIKIMQAQLDKYTQCLPDPAQKQKPPARTQGQTVIVT
GTTGGLGSYLLEQLQASPAVAKVICLNRTEDARERQVRGNTERGLDTALAKAEFLRADLSEP
RLGLASEVYERLLAETDRIVHNAWSVNFNMSIATFEPWVRGVRYLIDLSAACARRVPIAFVS
SIAAVEGWLGPPEPVPERQLPDLGLPGMGYGQSKLVASLVLDEARARGGVPSAIVRVGQIAGP
RSRRGEWTRREWLP TLVRSSLHLGLLPSDLGGGMAADVDPVEDVATLVLEVAGVLP
RREGWAAGEDDKVEGYHGINPTAAKWALLAQGIRGFYGPGRIRGLVPLSEWVAALERSAAETGA
VEDQVERNPAVKLLDFYQALVEGGTEARTYELARTVGMSPTEFAKLEAVTPELMNVNWC
RQWGFCA

Predicted cluster (antiSMASH prediction)

GGTG_00273
GGTG_00274
GGTG_00275
GGTG_00276
GGTG_00277
GGTG_00278
GGTG_00279

GGTG_00280
GGTG_00281
GGTG_00282
GGTG_00283
GGTG_00284
GGTG_00285
GGTG_00286
GGTG_00287
GGTG_00288
GGTG_00289
GGTG_00290
GGTG_00291

>GtTERP1 backbone gene sequence (GGTG_10466)

MGGLKDVAYLAFHPVQLRNIVQWKLWHEPVHHRDPAKDTPTQKKCFEYLDLTSRSFAAVIKE
LNPELLMPICLFYLVLRGLDTIEDDMTIDLKKEPLLRGFADNMEKDGWVFTENGPNKEDRE
LLVNFTVVEDELKLIDKKYYDVIRDITVKMGNMGADYAIKTQDTANCINTIEEYELYCHYVA
GIVGEGLTRLFLEGNLCNPKLGERMELTESMGQFLQKTNIIRDVREDYDDKRSWWPREIWSK
YFENYDDIFKPENRQQAVYLCSDMVNLALKHVEDCIYMGMRDQSCFNFVAIPQGMATL
ELVFQNPVAFDRNIKITKGDACSIMLSSTQNLRLVLCDVYRTYARRIHKKNDPRDPNYAKISM
QCAKIEQFIESIFPSQDPKAIALEKKTGKSMDKQPSMDATEAFWLLAAVVGTFLFLIGGSMVL
LAYFFGAKFDNYFREIDARARGAAPTITGHDEL

Predicted cluster (antiSMASH prediction)

GGTG_10461
GGTG_10462
GGTG_10463
GGTG_10464
GGTG_10465
GGTG_10466
GGTG_10467
GGTG_10468

>GtTERP2 backbone gene sequence (GGTG_10763)

MEAPETLVPIHAHDASTNRHEVSSTSQAKNHSANDAATTIILPDLFVSIMSPSPRLNPLYEV
VRPASEAFTKELLGLDAASFKKHRRVNFSLASMWMPEADAEGLRVMVDWLTWVFFFDDLFD
DGELRDDPVGAQAEAEATLALMSDHEQEVSRELHPLRYLFYTTWVRFRNVLLALQTRYRKCI

EEYITGVVRQTGASLVGADISVEQYLHWRRKSVGLRPCHALMEYACGIQLPDYVLAHPAVQE
 CVMVSIDLVS LQNDILSYRKELASCGTQNI IHILRRQGM TTQQA FDRAGGLTVTAIRRWHLA
 QLDMPIWGEEVDRQLQRYLQGCLDSCIGSLNWRLVSAV

Predicted cluster (antiSMASH prediction)

GGTG_10758
GGTG_10759
GGTG_10760
GGTG_10761
GGTG_10762
GGTG_10763
GGTG_10764
GGTG_10765
GGTG_10766
GGTG_10767
GGTG_10768
GGTG_10769

>GtTERP3 backbone gene sequence (GGTG_06480)

MGSSETAGAPADIHARLAEELRGRTIAVPNMLGDILQGWPSGRVNP HYVRLKHVVEGMLDSS
 VPEAWYRKKLSDSDFALFASIWHPDAAWEDLHTMGLLTVWAFVWDDTFDTGEQDLAGDYERG
 CAFRAQTLAYCRYWLGLELAACSPSEFPTWPSYPSP PQSSSFVPLFAGRRALHRALSWIGAR
 PPPPPPPNVGCALFKPLGEALCARFDERQQRKRVYSQIKFWIDSTAE EQQLRIRGSIPTSENY
 LRFRQGT TA FRMFALVGEISTVTNIPSAIMDTPEMGVIMTEANLGIII INDVLSLKKEMATL
 AMINLVPV MYHHENKSLEAIIESLCSELMASRQRFEAAASALARMAAREEAGGSDKSGKHGL
 QDELQRYMDTIKTSVTGTWEYT

Predicted cluster (antiSMASH prediction)

GGTG_06476
GGTG_06477
GGTG_06478
GGTG_06479
GGTG_06480
GGTG_06481
GGTG_06482
GGTG_06483
GGTG_06484
GGTG_06485

>GtTERP4 backbone gene sequence (GGTG_04211)

MTSNWIYSVPVDEDDVAHSTGCFTSLPIRIHSRNDIADATARSADWGSVHVGDGWEQKSGSC
WSPVGNWGAFIFPETVPERLGVLTLYLANMGNIHDDLCELDYDEAVTEHATLSHAMNVEPPE
RHHSEKSSDRKDKLQLSLAKCMLEALDLDRARALRMLDSYREKWLDVMESRDPQKIQTLDY
LVFRNLNGGMRPFWHMVQYGMADVSDAEEELIRPVFRAAEALVLTNDYWSWEREWAAAQQ
SKCGRIVNAVELFMRTGLAMADARATVREHIIAFEREYAAARREAFYATNRTVPDHLRAYVD
VCGLIIAGNHYWCANCPRHHGWRRSVRDQHQQVDGERYGERLVAFKQCEALALPGSPQKHEN
ELDSWTSATSSCLPSAGSGDPTSKTRSASQTSSTATSDLQDSTAASESAETGRDMALAADTC
ATSDRAAVDADGFKKPDSTRALMDPCNYICSMPSKGVRSLLIQSLRVWFPTSEESVAHIQRIV
DLLHNSSLILDDIEDGSGLRRSFPATHVVYGEAQAINSATYMFVQAVQLVRRLRNDSSLDLL
LEELECLFLGQSWDLYWRHNLQMPTEAQYMEMVDNKTGAMFRLRLARLLMSERSQSGWTSKA
VDASSLGRLCQLFGRFFQVRDDFMNLSADYSNQGFCEDLDEGKVSFLIVELCSKHQGTLR
DQAMGILRRQQAAMSHGPSGSAPPALSREAKKHVVKCLKEAGVMEATLARLRELEAAIILDCI
GSIEHERETENPMLRVLMLHKLSSVRDVTVV

Predicted cluster (antiSMASH prediction)

GGTG_04207
GGTG_04208
GGTG_04209
GGTG_04210
GGTG_04211
GGTG_04212
GGTG_04213
GGTG_04214
GGTG_04215

>GtTERP5 backbone gene sequence (GGTG_00032)

MTTMLASNILQSPNAIPPRTSSTGVYPITHAPSKPVLRLPEADWIAKSPPPSPHAAHAP
AANTNGMAGSAAPAPAAATTNGHHPRVNPRKASAGRSSQAPAASMQPPAPSSFDAGRYAHEDF
NFTTTKRTWSDHKEKIIISGPFDYLYGHPGKDFRTQVITAFNAWLEVPPESLEVITKVVGMLH
TASLLIDDVEDYSSLRRGLPVAHSIFGVPQTINSANYIYFCALQELQKLHNPNTLTIFADEL
LNLHRGQGMDLFWRDTLTCPTEDDYLEMVGNTGGFLRLGIKLMQAESRSQIECVPLVNI
LIFQIRDDYLNLFSSKEYSENKGMCEDLTEGKFSFPVIHSIRTPADLQLLNILKQKTTNEDL
KRYAVSYMEKTGSFDYTRRVLAVLIERARKMTDEIDGGRGKSEGIHKLLDKMIVAS

Predicted cluster (antiSMASH prediction)

GGTG_00031
GGTG_00032
GGTG_00033
GGTG_00034
GGTG_00035
GGTG_00036

>GtPKSNRPS1 backbone gene sequence (GGTG_11773)
MMEPIAVIGLAYRFPGGADSPARLWDVLTSGQNLSREPDSPRLNLRRFHSPGDPDRHGSTD
VTSSYFLDEDPSRFDAGFFGVSPLEAEAMDPQQRLLETVYEASESAGLSLASLKGSRCVSF
VGVMTS DYPEIQLKDTEDLSMYTASGASRAILANRISYFFDLRGSSVCLDTACSSSLVALHL
AVQDLRGGGGKGGGGGGMSDIAVVAGSNLIFGPDVYITESKLHMLSPTGT SKMWDEGADGY
ARGEGVAALFLKPLSKALRDGDPVVG LIRGTGVNSDGRTPGITMPSATAQARLIQET YRAAG
LDPDKVEDRCQYFEAHGTGTKAGDPVEARGIFQGFEEADPRRKRGRRQARRRQGDNNESP
LLVGSIKTVIGHLEGCAGLAGVVKVLLAMKKGVVPPNQHLEKLNPEIEPLRDFLRVPTEPVP
WPQPAPGQRKRASVNSFGFGGTNAHVIVESYEDDKPTQGS DGLVAEESPQERGEERLTAPIV
LSASSRTSLLRRVEQIAGYIRENPQTS LRDLAWTLQTRRSELGLRVAIPAATRDGLLEELD H
LVEEAKGSKQPAIGTPARQLVSPAEGVGILGIFTGQGAQWPGMGRELL LHNGVFRRAVRLCQ
EALAGLPDAPQWSLEEELLKDGR TT KSRVAEAEIAQPATTAVEIGLVDVLQSHGVRFTAVVG
HSSGEIAALYAAGILTMGDAIRIAYYRGKYAHLAGKGSMLAAGLSWDAALELCRSDRRFKGR
VWPAAKNSPSSVTLSGDVEAIQEMNQELQRLKVFSRPLHTDKAYHSPHMQSCADAYLEAMKR
CRVRPKLPSRSCVWVSSVGGTAESYWD AAPEDLQAALAGQYWVDNMVKPVL FADAVTAALTN
GGPFDA AEIVGPHAALKGPVSQT VQPLL NKELPYRGAMSRGEDC VEA VSQAVGFLW TNFGSA
AVPRFPGADKESSVGGFSDKTD RDRQSPPQVLTDLPSYPWDHRSFWRESRISRNNRLRGPS
KPD TAPSLLGRRCTDDTDQEPRWRNFLSLKEVPWLRGHSFQGGQALFPAAGYIVMVLEAAQAL
AQSGSRLGSAATSASLVEIENMIFERTLSIGESRPVELITSMTLNNSSGDTNGPIAGTVCFH
ICSDASTGVTERTCSGSVKILLSHADSGIDQEVPLPPRVVPKAAKTPVDVEKLYSTIRAGGL
QYDGRFMRMDSMHRAAGISTATASFDAD EARWTKLPPPFIDTGFQALFGALAAPTTDRLW
TPYLDHGFVKLTIDLRQKIAARSSSPGEKSQVKMVTDAHITLATATRVEGDLSIYLPASTGR
GAPLYTLCQIEGMALQALLKPDPSNDRHVFSETIWEPEIIIGGDLMTADYSPPQEDLVLLAE
RVAFYMLRVIIEQGEAVGPESLKRHERLFVEHARRQLRQARDGELYPYDAAWAEDDCDIIE
ILDRFAPQQVDFRLLRAVGEEVGAVFRGERQMLKVL FADDMLGEFYRVGLGLRNTQRQVARY
MRSITHRFPGADVLELGAGTGATTAAISEAVGNDFG SYTFTDVSAGFFPDARERFSGPRFQ
HHLDRMDFRRLDITLPLEEQGFDGTRLYDVIVAANVLHIAPNVD TALRRVRQLLRPGGYLVA
VEATSKLARIQVILGGLEGWWPPEDTKDVT PRDGCVLLSSEDWDARLVD TGFSGLDVFHGDQ
PDVRLHTCTSFVSQALGGSDDGRMSCLREPLRHVPLLSTTGSLLVIVGGATIATSRLVRNLD
SHLSSLGPCHLVHIRDLKSLSGASSASPVHFPDGASVLC LAHLDLAVSHKTGSGGVNATYLG
GMQTLLARAGRVLFVTQGAYSTDPMGAMLVGLLRCARSEQPSLAVQLLDIESDARPLSQDTG
VLLEHFLRFVFAGQQQQPDSAGGDILWSTETELL LRGGKLF LPRIRHDVELNERANAQRRPI
SKLVSKDTQIVEVRAASSGDVGAPASIELTAAPRLARDVREGEAEVEVSLSTLRPVVGLGSG
QQPRYLCAGTVSGYGDGGAHQSVLALAKTNASRLRLSNQALVDAGTGDTTPEALALVAVTLV

AQAWVASVAPGQTVVWHGDCEFGVEPDVLIDLLQREASKRSVQIVWTAPLGSGSNPKSSNIN
 SPSSPIRLHTQAPVRVIRDALPKKVAALIVTQSEHGSDFAKRMQAALGLRDEL CGGLWAPPG
 SWCDDKEAALRLTNSLHASRAAVEQGAVHFTTITSTLEELASTSGGNVESACKAQILDWTSS
 APITANIQPIDATELFRPDRTYLMIGLTGDLGLSICAWMIRQGVRRHLLSSRTPNIDEDWLA
 GMTRLGAKVVVKPMDVGSWESVRHTLDDALACMPVAGVCNGAMVLSDDLFSRMNVATAVAA
 MQPKVDGSLNLDYFSTPAMQQLDFFMLFSSVSGSIIGLPGQSNYHMANLFMATLAADRQRRG
 LVGSVIDVGVMLDIGYITRQSKFVQRNMQSMNVLTWEEEVHQLFAEGVFAGIPGNTRSSPE
 IIMGLKVSDNPADRPFWAADPRLAYFVKDRTKTFGETASVDGPSSSPSALEDLRTTLASEAP
 LDETRLSSLVRAALCAKLEKLLQSSAGSLDMGNALVGMGVDSLLAMEVRSWILKTIGAEVPV
 LQILGGITGDEICQNVVDSVLSKRPGSSSTVASEHTRHPTPTPPTRAATDTPSLASEDHTPSS
 QDSRSLMSSPGGNLPVVGQSADLTPLTLESSPLGDDSDVADTVHKRLDSLTPVELQRRCPMS
 LAQERIWFLHEYLEDPTSFNETAWYDVEGPLDIDRLKSAFNQLTARHEILRTRLSNDPITGL
 PVQTVWSSSACKFHHVDARQGRPGSDHEEQVVVEFEALKSHTWNLEAGECFGLTVVRRSSRK
 HTIIAAAHHIAVDGLTWVLLLRDLTHAYNQPGSLARMPPPRPYTDFAMRQRLVPSGALAPE
 LQFWKLELKGLPEDPLPLFPGLARVPRREATNVLRSLPVQRRDRDAVLTIKRASSALAVTP
 FHFHLAALRVLVGHLSGASDLICIGTCESGTLGDDAFAETVGFFLNMVPIRLASGADDQGETF
 GSLCKRASARAIAAMTHSRAPLDALLEELRVARSSACCSPLFQVIINYRLGALAYPPLGSSQL
 DYVKSHHSANPYDLALTVMMPNGACQVELAAQEALYSSDAASRIIDMYCRLVDDASRRPDI
 STLELAMDFCGVPRAKSGAVGAVKNDFSKRPRTPAKPAGNEWAESISGQVQAIARLYPNDVA
 VKDGTMTYSDLIRKSSTIASTLEELGRNDTGVRHCCLLFQPSADYITSLLGVLDCAVAV
 PLDTRLPKERLLAMVKDCRAATIIHHRDTADVASWLSSSFDNVPRIDVSRRLRSESTSTTSL
 RQPEMTAPMIMVYTS GTTGT PKGAVLTQANYWSII EAIARRMKMYGTDAGNTDSGGYRHTIL
 QQTSTFGFDLAMIPIVVGLCTGARLVVATAEQRRDPAALTSALQERVMTLAATPTEFEMWFR
 HGWEDLVRCNTLRTACVAGEAFPRRLAAEFHRLEEARGGKRLALFNVYGPTETTIIASNIGLV
 DYWNVPEVGQKDKAPSVGADHISVGPPLQGVYIILDEDDGHQLPPGSVGEVFIGGAGVGLGY
 LGRPDLTKAAVSDMFISGEGKKT PMMYRTGDSGVVRPDGSLVVLGRIDGGSQVKIRGIRIE
 LEDISSTILRAARGRISHAVATVRGEEKAI VAFVPSGSANHGGEVDGAYLES LAGSLPLPE
 YMRPAAILQIDKLPTNQNGKLDREALARMPLPTHKNQAIHKPPVTNSMVHVDPRKQPQAASS
 LSSLELEILDWQQVLPDAFRSSSGEAGPESDFFRMGGNSMSLVSLRNTIRQRWRAEVPLVR
 LYEGSTLRDMATILHDVKESDGDGVDWESETRFDPTAHQEVLT RTAAMNGPTTGLINERSR
 CSNGKTILITGATMQLGAELLKTLLARDDVATVHCVAVPPEEALQLTKVDDTRRTIQAAMKS
 RRLFIHEGYLDSAHLGLSDEEIQVLLRDVDAIVHAGA QGSCLNNYNSIRDQNVGSTKFLAAL
 GLACQKAPSFHLLSSARVILFSGKDEYPEESVSQFYPPRGASICGGGGGGGGGSKSREGFTA
 TKWASERFLENCAAATTHREGRRCMAAVTIHR TGYLMSDAASEMDAVNMIHRFADRVGAVPA
 MDRFSGFLDMCEVEWAAARMADSIVSPTAALSSGAVAVRYTHHTKGDAPFVGGFHAHLERKL
 GRSLDLSMEEWAERAERAGMSPFLASFLRAVCESRDEARYPKLLLGSGEGKAAGR

Predicted cluster (antiSMASH prediction)

GGTG_11764
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GGTG_11767

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>GtPKSNRPS2 backbone gene sequence (GGTG_10437)

MTVPQEPIAIIIGAGCRFPGASDRPSRLWDLLEPRELAVKIPHDRFNVESFYHPIGARGGST
NVKEAYIINDRNIRHFDAQFFSSPPAEADAIDPQHRHLLLEVVEALEDAGLGMEALQGSNTA
LFVGQMCTDYSALSSRDLDHVPKYSAPGIAPSNASSRVSYFFDWHGPTITIDTACSSSLVAL
AQAVQTLRAGTSDVAVAAGTNLILDPMFVSESNLGMLSPTGRSRMWDAADGYARGDGVAA
VILKTLAAVRDGDVIDCVVREVGCNHDGRTQGITMPSGAAQASLIRDYARAGLDPTKPDE
RCQYFEAHGTGTPAGDPQEASALDDAFFGTGGQRLPSDILYVGSIKTVIGHTEGTAGLAGVL
KASLALKHGLIPPNLLLKELSPGVRPYCKHLRIPQELMPWPDLP PGVPRRASVNSFGFGGSN
AHAILEAYEPPLSAATSPRGGELPVAGPRQAQRPATSLVPFVWSANSEASLEAALSSHARYI
RDHPSLDLEALRFTLATKRSALPHKIVFPALDAGELLSRMEDCLEARRSGDADAPLGMRSTP
RSPGGKGKHSILGVFTGQGAQWATMGARLVESAPARELMGRLDESLQTL PAPS DRPSWTLL
GELRKDEEGGSRVGEAALSQPLCTAVQLVLVDLLRAAGVRFAAVVGHSSGEIAAAYAAGFIS
ARDAIRIAYYRGFHAKLAAGAERP DGSR AKGAMMAVGTTLEDARELC ELDDLEGRLSVAACN
SPSSVTLSGDLDALELAREALEDEKKFTRVLRVD TAYHSHHMKDPVVAFRKSLANCDIEVLQ
PLGEEAQPAWFSSVKEGVVMEASPD LKANYWAENMAQT VLF SQALQH AVHIVTSKTEQSPFS
LAEVGPHPALKGPAIDTLEAAGVASIMYTGT LER GKDDVKALSGCLGAVWACLGSAAVDWA
GFICGYCGLEDGRALTALRGLPLY PWDH RREFWAEPRIGRLFRTQQDRVHELLGKKLPDGP
EDIRWKNVLPRIYPWLAGHSLQGQTVYPAAGYIALAMEAAMQIASSRLVQGQHVL CIELVD
LSIHRAIAFDENSGTELMVSLGDISVAGSDHDDAMIISANFVCRSPLDKESGRLGTNASGAL
TITIGNEADDDEASLLTLRECERSAGRLADVDIDAYYSGLAELGYGYSGPFGRGLASLQRRLG
FATGTISRELENQEDLEHHPLLFHPAMLDTSIHALFSSFGVPGDGTWSLMVPSKVRRVTLP
SLCGAALASTVEFDCSMSAMDRGCIDIVAADGVRKAIEVDGLEFVPFSPFTEKDDRLLFFSN

VTWQLARPDGNKIGTHNPTEWDLKKVADRERVAFWYLRTLQERTSALLQAALPDGHARYQET
PAEGCAQDETATPKNKPEVAWHHQAMFDFAAMCVEQVKRGSDPVAKPEWCSDTHDQVLGLMA
PYGDDADFNIMRAVGEQMPAVVRGDKTILEVMMKDDMLPRFYSHGIGGEAANSVALMLQQI
TNRFPHINMLEVGAGTGGATWEVMSRGTFFATYTYTDVSAGFFEKARDKFAAYADKMI FKFV
DMEREPPGQGFKENSYDVVVASHCLHATASLERTMGNLRRLKPGGFIVVLEVVQINTMPLG
LIMGGLPGWWIGRDDGRVHGPNITLPQWNRLLRRTGFGGVDFTFTPMTAPRLHTATIFAAQAV
DEKISLMRRPFAARTEDIRFPHLVVLGGESMATAALVDELEEVLRPRCQTLVVASTLEELEA
MPLPPLTAVLSVADLDS PVLGHGLGEARWQALQRLLG SASAMLWVTHGSRCEEPDSGTMLGL
LQSIWYELEHLRSQ LLEVVDLGD LTAGLLAQ LMLQMQLDQQWKGGVDGDSVLDPESTLYSI
EPELLLD RGGVLRILRQKQDDEANARYNSHRRLITKPVHLGKGAKVEARIGQSAAVAGGLEL
ELTELQTPPALGANLHVASHCSSAPMVHVHMSTAWAVQSPAGLHFVALGREQSSTGNSRAVV
ALSHTNASAI AADPDASVPVDAPGALHHA AFLALVTARVLARHILASTAPCAVLLVHEPGPV
LAAALEASCEPLGTRLLFSSTVGRHAKNRQGWIAVHPRMPHAALKRALPGRVDSFLDLSKSR
AAKDAGARLSSVLPQACRRQHVADLV SHEATVAHTLQAGSSTRVGVLQDAVDFAQSQMALLP
ELGDATTSRLRFRDDGDSSPTLNLPRQLSAEPLALLDWSSRPGVPVAVKTEPIDVRTDIFQD
GKTYWLLGLAGDLGQSLVDWMASHGARNIVISSRSVKSQVLPGWIAAHAARGVTVLLVEADV
TNTCSLKCARDVIEASLPPIRGVANGALVLRDRLFINTDFDTFQAVLRPKALGTANLDAMFS
APGSLDWFIGFSSIVAVVGNYGQSAYSAGNNFVKALVNKR RRVGLPGATIDISTVRGVGYVE
REQKAGVMTAKMVERIENSAMPMSERDLHQLFAEAVKAAPPDSGRHANITSGIQLVRS DRIN
KTFWANNLKFSHFVVEIGLGNQDALGSGSKVLVRSLLLEAGSVAEAVKIVRDAFTAKLNATI
QNPATEKIPDSQPLIDLGIDSLVAVEVRTWFRQELGLDMPMLKILGGATMAELVEDAVARLP
QELLPRVKKTGTNDPATLSPPPDEAEQT TALAKEKEHDAEDDKDKTGSSSDGNQTS EDTGDT
SITSRSGTPVSEPAARPSAPALNPFQPEIIRTEPMNFGQARFWFLRKYLDDPTTANVAFYFR
ITSNFSPSGLSQALYWACERHEALRTCFFSNPVDATTCQGIMRKS AIRMEHRLVSNHTEARY
TFETVKKHVYDLERGETLRLVLCEESPTSYYFILGYHHILMDGFSWEVLFSELQNYRRASTR
QDYIPPPVTRQYADWSRKQLSDVLGGLELATDRKFWRETLSPLPPVLPLLPLSRAAGRKPLG
TYELNRAETRIEQGLAQLV RNVA AAHKASPFHVHLTVFHALLFRLTGEPDVCIGMADAGRTE
EEDVGIVGLLLNLLPLRFGVAYGIDGRVDEAKSKVGECSFADALRQTRAKVYAGMARARVPF
NVILDDLAVPRSTSHHPLIQAFIEYRPARKIQFAGITGEIPNNTSHARTPYDIELNVNENH
AGDVTVSIGLQSSLYSASAAELVLG SYTTLLECFARSPESAIRD PDVYPRGDIELALRLGRG
PSAAVQHSTVSQFVDAVA SENPKTALRHTDDSGKTRSLSYGEMLARVMDIHSS LADAGAKA
GSRVAVAVQPSTDWVCCMLAVMRAGAVYIPLDCSLGTARLTQMGALVKADFALVDSVDVGAQ
VEGWLASAKGKVAAILDVHGISAAPAETGKVQLANLSAPDEAAA ILFTSGTTGTPKGILLRH
SSLANVVETTMAPRFYGPGLGRQTVLQHSAPSFDM SFEQVFLALCGGGTLIIADRSLRGDS
RALTRLIADEGVTF TKATPPEYSSWFRNGEALGPDTSLKHI FAGGDRMTQGMVDELKRRLPT
AVSKGAVRLFNSYGAEGTVIVTKTEIPLDSL PDIGGPEAANQQAMIPIGFPLQNCAYYVVD
DSLRLLPPGVSGEILIGGAGVAMGYLGSDDTPAGGNGGDKFLTNPWADEDFVQRGWTKLYRT
GDKGKLTREGTLLFEGRIEGDTQIKLRGVRIELEDIEHNIVQASRGAI AEAVCSLRGSAAVP
ETQFLVAHVVLSAPEPSPLEKAAREQTEGQEDEPQPADLLVHV LASLEFPNHMKPARLIPLP
RFPRTRHGKLDRAAIAALPLDSALDSASEASDNRALTETEEKVASI WVQMLSPEAAPALGMR
PSTDDFFALGGSSMLLEVQA HIRASLGGVDVSLRDLYRAHTLSALASRIDELAHASSLDWEE
ECAPPRADELVLLPESSVVPGGPRTTVDSGGAEVILT GATGHLGPYLLERLVSDPKVSKIHV
VAVRSEDRLRSVISAMAPAATAAADKVL SYPGDLTAPLLGLSTEAA SQLAGRATAVLHAGA
ARLSWETFETLRVNTLSTRELLRLAAPRRLPFHF ISSGGVFPAEEAPAEVSSAPFAPAQLG

ADGYVASKWASERMLERAARDLGVDVRIYRTVRCDGADDPASPLDESLPEDIAAGMARATIE
 SGTMLDHGGWAWSGWFDLVSVHQVVEAIVGRLLGAADAGAIQQAEDDGEDGGMVEFTHIKGT
 YRVWKVEQLHQVLRLRPEIQANMGRLKLVPPQLWLGLKRSGLFPWMMGANQATYKDWVSNRR

Predicted cluster (antiSMASH prediction)

GGTG_10413
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GGTG_10441
GGTG_10442
GGTG_10443

GGTG_10444

GGTG_10445

>GtPKSNRPS3 backbone gene sequence (GGTG_07560)

MSAPEPIAVIGSACRFPGDSDTPSKLWELLRAPRDLLRQVPPERDADAWHHTNGKHHGATN
VRHAYYLNESPAHFDNGFFSIQAGEAEAIDPQQRMLMETVYDSLCAAGQTIEGLRGSQTSVF
VGLMCDDWAGLMARDTETFPQYGATGTARSIMSNRISYFFDWHGSPMTIDTACSSSLVAVHQ
AIQTLHSGESEVAVATGANLLLSPPAMFMAESNLSMLSPHGRSRMWDKDVNGYARGEGLASVV
LKTLSSAAIRDGDHIECVIRATGVNQDGRGTGGITMPSAKAQATLVRSTYARAGLDINKPEDRP
QFFHAHGTGTPAGDPQEAESAISKAFYSQQQHDDKLYVGSIKTIVGHTEGTAGLASLIGTSLA
LQHGIIPPNMHFKTLNPKLKPFYTHLQVPTKCIWPPEPRPGQPRRASINSFGFGGTNAHAIL
EAYQPPPKARAKAAPMGALFTPLVFSAASESSLRAMLSLYVDLSTCQQKELHDLAYTLQHR
RSALSRYVAISAPTPAEARHQLEAILGGEKMSITIGTRQLAKGSSSKILGVFTGQGAQWARMG
ARLLETSPFVFQRLAQLDQALAESPAGDAPDWRLRDMILADPKTSRIGEAAISQPLCTALQI
VLVDMLGFAVRLHSAVGHSSGEIGAAYAAGLLSAADAIRVAYYRGLYAKLAESPNGGAKGA
MMAVGTTFEDATEFCELEWFKGRIQVAALNSSSSITLSGDEDAIDEAVIIFQDEGKFARKLK
VDTAYHSSHVMPCAAPYLAAMEKCGIEGGVATGVKWHSSVHAKTVMSQDKMSPQYWVDNMVN
PVLFSAPAAGDAWTESGPFDLAIEVGPAVLKTPALDSIESVSGGQRPPTYGVLARGKDDVQE
FSNALGYVWTQLGAGSVAFASLQRAVSGSEAVGRFLPNLPKYPFDSREFMALSRVSGLHKT
AQDPIHPLLGRRCHDRETSQSMQWRNILSPKEVPWLAGHQIQGQMVFAPATGYISMTVEAISL
LAGASDVGLFELRDLQIVRALTFNDEDDKVETLFDLKDIRRSSGEITADFALYSGSPYDIKS
TLALNTAGTVRMMLAAPQADQLPRVELDEVSLSSVDTDRFYAFLSKLGYNIAWPFHGTTSIR
RKADYSLGTIEDQSASAWEDQLIVHPGMLDTALQTAFAAFSCPGDERMWDLHLPKSFERSILI
NPYFTPLGVGKQANFGYVSAARVGSKLVRAAADITLFSSEGGHTFLQVDEMEIVPFSAAVQA
NDAVVFSRFQYKVAEPDAALVDDGCEGKTAAGEEIAAAAERLAFYYLGRLLEKVTAEERAG
ALPHFKSLLDYADECVPRVARGENGLVPAAAQDTASDIDALVARHGQDASIRLLQSVGENL
AQVILENGDMLQHASMDAMLQSSGLAKGDEWIASLAEQMSHRFPKMNLLEIGAGSGSSAREI
VTRLGDAFLTYTYADVSGSVVPAQQLFKGFENRMVFKPYDLDESPAGQGLTGAYDVVCS
SVLRAARDVEATLKHVRSVLKPGGYVVFVQEVVATDDSLRACLAMGSLPGWWPVSGVADDAGR
NKPMTLDRWGALLQKTGFRGVESATPEMPWVGPRVFVAQAVDERTEMLRDPVAHLAVLPAA
RAPQLYLVGKGKTAEVKQMCDAALYATLSPRFPKTVRHEVSAFNQDAPLEGSTVLCLTELEQ
PLMEVITPEKLDALRLVYKRARDVMFVTRGARRETPHSYMMLGMGRCMRFEYPGLNLLAFDL
DRVGDDAAATVARQLLRLELAGRWALELQPGELLSVEPEVYIEDGRMVIPIRYKDDERNRR
YNTTRRVKEDVDPATSRVLFESREGPWAEQVPSPLDMPAPLPFDVPATRTLRTLVTHFVPATI
TVGQGARMPLVGRAEPGGELYLAAAHLTESPATVPVDWTFALQDGTDPVAALASFAAALAA
RRIASLAGSGDTIVVHEPPAVIADALQACARDLGISVRLTTSDRHSSSDRQQQYLDKELSE
HALKALLPRAATKFLDLSQARSSAAQKMAKCLPRGCDVIIIPGSVFHQNTLRSSASPADIA
AVKAAWSASQKQLGGSSSREVQAIMLQDLAAGQADNNNSGRLAVVDCTSPVPAAVRAIDDG
TLFRGDRTYWLVLGLANEMGLSICRWMVERGARHVALTSRSPKVHFAFIDRMARLGAHVKTFA
MDVTDRAHLAAAYASLTEAMPPVAGVANGAMLMRDSLFEENMSYENFTACTNPKVIGSLLLDE
LFGDAPLDFVFVAFSSIAAVTGNNGQCNVSSNLFMNGLAEKRRARGVVGSAADISPVIGLGF
VERTDSLTEDTFTMGYRPVSEQDVQVIFAESILAGRVDGPGGESEVISGVQPLFDDFVGRDQ
YMKDVKFNHFWMERTDARDLAGGRPLAVSVRAQLALALAASKAEVLDIVREEFLVRLRKILSLG

ADEAVNERVT FVEQGLDSLMAVEVRAWLVKELDVDVPVLKILGGSSIADLLDHAIKSLPESI
 VDVSKLGDGTPGQAKKKAPAPVPAAPPVSASLPASPPRDVSPQKTSSNSGTGTGTGSGTPV
 DDKSVSGSATPLSTPDESLTASAFFGGSVENKKLAEVPDDSTDMLTSPMSFGQTGFWFLNEY
 LAGKAVFNIAMMYKFTGPIRMSALEDAVRLVGGRHETFRTRFFWAGEGDARVPMQGIGATSP
 VELRSRRISSEAEAVEEMNRVRAQPWDLESNLIITLTVLSLSNKVHYMVAGMHHLFDGYSF
 TVLFKELELAYNTKNLSPLPAESQYRAFASRQREDYEAGKMAHSVEYYRSVLPAAEDLQPIA
 LLPFAKTTTTRQALTRYGQYEATFQIEAELA AKVRQLARRSRSTSFHVYLVALEVLLFRLLPD
 ADDVFIGIADANRSDKTFMDSMGFFLNLPLRFCRPQADAKLGSVIEQGRDAAYA ALEHSRL
 PFDALLRELVNPRSSSEHTPLFQVFLDYKQIYQERSTWCGCKVENERWELASTGYDVSLEVSE
 DTSGGVMLRLDLQDTLYTEESTRLMLRSYGVGVIEYMTSAADGGILGDV PKWSPQDVQATLVT
 GKGTPLDAQWQPTIIHRIEELAQTQPDKTALKDDNGRILTYQQMTARIDAIQHALETAGLQK
 GG VGVVFQEPSADWTC SMLAVLRAGGVYVPLDLRNSIPRLASIVKASKPAFLLLTDRTTESQV
 SLIGADAAAQVSVSNLKADDA AAAAAAAAAAAAAA PPTTNRAERGAPAVVLTSGSTGEPKGIV
 MTHANLVANAEANSHVYAATAQDGADLVVLQQSAYSFDFSIDQTLAALTNGGRLHVVAARHR
 GDPAAISKIMLDEGVTYTSSSTPSEFEMWLRYGRET LRRCASWRWAFSGGEP MHPGLPREFSK
 LKLGGSLRLFTGYGPAETT CFSTKIELPYTSPDAIPDPLPAGRMLRGYTV CVVDEALRPVPH
 GVPGEIVIGGACVVS GYLDNAAFTSAKFLADEFFGSETKVYRS GDRGRLLGDGTLFC DGRLE
 GDLQVKIRGFRVELVEVEEAILRCSAGTLSQAVVSVRGGE GEDRYLAAHV VFRPGITSDEQA
 MTLRALRHSLPLPPYMRPSAIATLDEIPRTAHLKVDRKAIAALPVVVTGNEDDESAGEDSLT
 DTERRLAALWREVM PVGPGALGSHSDFFLVGGNSILLVKLQSRIRASFGAAPKLVALMGAHT
 LAAMAAVESSSGSAKALIDWQAETE VPEVLLATKPRPRAPKTDNIRV LMTGSQGYLGRHIL
 AALVKDPKVSSVQCLVRKENTTAPLDAKVTEIEADV SQPSLSLSPSTFSALSSSIDVVVHCA
 ANRSFWDRIYETLRADNLSSVKELARLAAPRSVPLHILSSGAVATYDGPAGVTTPTDGS DGY
 VATKWAAETFLRRLAAATNLPVHSHRPTGDGAPVADEAGAAAPLLEELMGLVAKVGARPDFS
 GVRGHVGLVPVERTVEDITKAVLASSA AVASVGGGVQVQSHKAAVRVAVDVFEKRVA ADEEG
 AMKLLPAVGVLDFWFGMAKRAGWGQLMTSWELVMGSSSTDGTGELELR

Predicted cluster (antiSMASH prediction)

GGTG_07548
GGTG_07549
GGTG_07550
GGTG_07551
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GGTG_07570
GGTG_07571
GGTG_07572

>GtIND1 backbone gene sequence (GGTG_03398)

MSSMPHKPDVPPALVSSTEHSVKQFRDRVVSQRQTTLRELTRFLHTIWLFTESDVKTVLVP
SALFGLANAVALWLLLPEAGVPHPRVVLGRAPQILLYVWVNLVVIDIQNRDPDAIEEDRI
NKPGRPLPSGKVSPNEAGSLLVASVIIAVLASCYCLGAPGASVLVILLGYAYSIDLGGSEHPLL
RNLLNALGMPCFAVGALQVALNPTYPNPYPTPSSPSGGNGPWVPLLAGRWWLVLAAAIYST
ISIQDIKDQEGDAARGRRTLPLVVGDAARWLVALPVLAWSALLPWLWGCATAAAYAPVLGL
GLVVAARTVAVRGDVPADKRTFKIWCLWLVAIYCLPLTRALLGGEGMLMLVTA

Predicted backbone (SMIPS prediction)

GGTG_03398

>GtIND2 backbone gene sequence (GGTG_04287)

MIASPILRRLRLVSCSLTGANMAAKGASRPSLMHSGTFGLRNHSPRPVGLSCYHASKTALAP
PLPVLNQESPLKSQGPEPTALSTGAPVLAPAPPKSWILSRLPAAWVPYGELIRIDKPAGTYY
LFFPTLFSTLMAAPMTTPMTDPGAVVGTSLLFFTALVMRGAGCTINDLWDRNLDPHVARTR
LRPIARGAVTPLQGLVFTGAQLLTGLAVLLQFPASCFFYAVPSLVLVAGYPLAKRVITYYPQF
VLGLTFSWGAIMGFPALGVDVLSNGSALAAMGLLYSSNVAVTVLYDMIYAHMDIKDDAKAGI
KSIALKHDAQTKQVLTGLAAVQIALLAGAGAAAGAGPAFFIGSCGGAAVTLGLMIKRVNLKS
VKDCWWWVFNCGWITGGAIAGLAIDYGVRYTKDDEAENKVSS

Predicted backbone (SMIPS prediction)

GGTG_04287

>GtIND3 backbone gene sequence (GGTG_04539)

MSDHLRVFRNLVEPLWDGAGTDENPFTGAQMPAFLPLL RQAAGPDADTRWFEQAWDAWHVPG
AKARTARRALPPHLARMPQVYLAFDLHGGRALKSYHFPTTKHLATGRPTEDLAYDL SGTSS
PAARLWPGRRMPVEMLAIDNVDPADGSVRVKIYARTPSNCKDALRDGLTLGGAQTDAATLAA
VEHAERFWHLVLDDRGRKVASVAEGLRRLMPALVVPEVLLLSGQQSSYAFRRRRRTAEAEAG

Predicted backbone (SMIPS prediction)

GGTG_04539

>GtIND4 backbone gene sequence (GGTG_07454)

MAATETQHAVAPLQPKDAVLRDTATTPWELVNNAIALGSPDAQFWWQGAGRIFARLLEAAHY
APDKQIAELTFFALFVAPELGPAPDPPTGESARGTVRYAFEP IGP HAGTSADPLNRHATDLW
IKKLQTHGLVPGLDTSWYDHSARQVLPQEDVVRTKTADGFIEETTPLAGCFVARDLEPTGPV
VKVYVYPGLKAAEPGLTNLETGIAGIDCKAPDEGARIKIYRGRRVRDLLAFWDAFPGEAPDV
LPADLPGRASPGFYITVGCGRPVPAPKLYPAVILWAPVSRGDDVIGPL

Predicted backbone (SMIPS prediction)

GGTG_07454

>GtIND5 backbone gene sequence (GGTG_09818)

MPGPRPLLPGVGALDNVCWRCCRRRLPARQRFLAPLSTTARPRSAAGGGAPSAPAQSPRVKG
AYFLSNTLLDRFGGIQFRPRARNMGAAAVTSRPPAKPASNTFSSSPYPRGADEPPPSAASTT
THDVLPHRRRQAAKRAADPSTSATSGPDKPSSSSSPADAPLPPDASSILAEAAAKQPADSLR
RKLSALLSLSKPRLTFLVLSAMAPYALYPVPAFLSPGAAEATLPSLSPLTLLFLTGTGTTLC
SAAANALNMLYEPRTDALMSRTRARPLVRGLVSTRAAVLFAVGCAVAGVAALHLGVNPTVAF
LGAANIALYAGVYTPMKRLSAANTWVGAVVGGIPPLMGWAAAAGESAVGDG SWRELL LAPDG
SSAGGWLFAALLFAWQFPHFMALSWGVRDEYRTAGLRMLAWTNPARNARVALRYGLLGFLPI
CVGLCAVGVTDW SFAVTS LPVNVWLARES VRFWRLRGAGGSARGLFWASVWHLPVVMVLALL
QKKGMWGRVWRS LTGEGELVGDDDDDEGWEYVEDDDGGGAK

Predicted backbone (SMIPS prediction)

GGTG_09818