

Figure S1. Amino acid sequence of putative Mn oxidase enzymes in the multicopper oxidase (MCO) family

CotA [*Bacillus pumilus* WH4] Accession no. JQ797387

MNLEKFVDELPIPEVAEPVKKNPRQTYYEIAMEEVFLKVHRGLPPTKLWTYNGSLPGPTIKANR
NEKVKVKWMNKLPLKHFLPVDHTIHAGHHDEPEVKTVVHLHGGVTPASSDGYPEAWFSRDPEAT
GPFEREVEYEPNHQQACTLWYHDHAMALTRLNVYAGLAGFY LISDAFEKSLELPPKDEYDIPLM
IMDRTFQEDGALFYPSRPNNTPPEESDLPDPSIVPFFCGETILVNGKVWPYLEVEPRKYRFRILN
ASNTRTYELHLDNDATILQIGSDGGFLPRPVQHQSFSIAPAERFDV I IDFSAYENKTIVLKNTA
GCGQEVNPETDANIMQFKVTRPLKGRAAKTLRPIFKPLPLRPSRADNERTLTLTGTQDKYGRP
ILLLDNRFWNDPVTENPRLGSEVWNIVNPTRGTHPIHLHLVQFRVIDRPFDTDIYQSTGEIV
YTGPN EAPPLHEQGYKDTIQAHAGEVIRI IARFVPYSGRYVWHCHILEHEDYDMMRPMDI I

CopA [*Brevibacillus panacihumi*]NCBI Reference Sequence: WP_023554169.1

MKKWIPLPAILTATLVLAACSNQTKMPGHDM SKMDSASTAEHENLKQMSASLDPPFEVL TGN
TFTLTAKESMLMLDDNTMKTAWTYNGTVPGPQLRVKQGETIKVVLNNELPEPVTIHHWGLPVPN
NMDGIPGITQNAV KPKESFTYEFKVDVPGTYWYHSHQNGVNQVDKGLYGSIVVEPKDAEPVDKD
FTLVLD EWMEDDSMAEMHSAGSSSHSAHSQSKDSSEHANMDMSGMSDAEMMPLMYTIF SANGKTG
SAIQPLIVKKGEKVRIRLINAGYLSHKMHLPGHSFTIVSTDGQPIHNPPETQDQLLN IAPGERY
DVEFVANHPGKWL LDEHSTNPGAKSLAIP IVEYEGEEHASVKSESMDLPVVDITKYGEAAKGTFS
LDDQYDV TY SMDLNTDMSHGDMTFTINGKTYPDTPPLDVREGDLVKVKMVNRSPEDIHPMHLHG
HFFQVLSKDGQPISGSPLVKDTLNLIPGEEYVVA FKADNPGNWMFCHDLGHA AKGMMSEVKYD
GFKPDFTIDPTVNNMPE

MnxG [*Pseudomonas putida* GB-1] Accession number ABY98346.1

MTTPRKGPLLSSLV LALLGWESTSEAAVQCQRTL VANVVALDQPLMFNRLGAQNANGMLFALRE
DVVDDKQVPLSKGGA AVPGKVTLRPKRPRPIVLRVAAGDCLTVNL TNLLDYRANPNKHGIEAE
GPEGEEVENEADEGFVADEQVAERMVGFQVNGMQAVNSIADISAYTGRNGNFFVSPGSTRSYTL
YAEREGAF AATSKAATFGGEGTAGNVANGLFGQVVVVPKLGRTYRNTLTTEEMLRATTGRTATG
QPVIDYEARYPQVEPWIAEGKAGKPIIAMVNGNEIINSETDAIVMGPNPDGSFPKSTYPLESMG
KRN PALPNRLEAFRDFASQFADEVAGTQAFFPGYWADPVMGHVLEPTRDSFMINYGSGGMGA EVV
ANRLGVGPMHDC LSCAYEEFFLSAHTVGDIGTLVDVPANVGLEHIRPGEVPPASAVGVKASMAL
YPSEPANVHHSYIGDFTKFRNTHNGHEQHIFHLHG HQWLFNPNDNDSYIDAQGIGAGVGYTYE
IANGGSGNRNRVAGDAIYHCHFYPHFAQGMWAMWRVHDVFEEGTRLEVSGQGENG FHSTPFALR
SGKPAAGARALPDGEIVAGTPIPAIVPLPGKAMAPMPGKVVVVVPKLSETLVAANDDDDDDEEGD
DDHANQPPVRKAVGSLALVDRTEANRNADGTLKNPGYPFWIGGMESSVGNRPPTPPLDMLDPAL
ARQLKDSGKALWANLDANQVDGWDGGLGRHALDGVSAGGEAETTTTKLDFTKV VHKAKPIYLP E
EGTDVEQAAMQFHAMA EHPSYALIPGSQPVAKA FRTNGALPTAGAPYYEPCMDDRGKRLTQSSG
VGEFFSGESPTGLNFRGASAFTADR PRIYKGANIQF DAVYNKVG YHFPQARI IALWEDAWPVIT
KQRPPEPLVMRMNTFDCTMYQHTNLI PN IYEMDDYQVRTPTD VIGQHIHL PKWDLTAADGSANG
WNYEDGILSPG SVVERVHAIRAYNGCTEGDSRDGTAACPKAKQHPYFGRFGRADWL GARTAMQR
WFADPLVNVYNVDRGLGTIFTHDHLGPSTHQQLGLYATVLAEPAGSTWYHAETGEQLYNPATRQ

DGGPTSWQAVIQTDHGDGKND SYREFFLEYSDFQHAYEAGVYVGAGPDGIPNAQSY PATADS
FRYAINPPVRGKASNLLEAIVEERGGINPGCPSRPCQAI SVDDPGMFVVNYRNEPLALRVYDP
NKVGPDPGKRGMQADGLAGDLSYALQTRTDRAIPAMNLSPSAITS AVGPTGGTTLFP PHINKAGA
EPGDPFTPLLR TYSGDNVRLRMHAGGHEEEHNVTLHG VKWLQNGTGFGNSSNSGWKSSQMIGIS
EQLGFMAPVSMISSAATNGDYLSLDAALEGYWNGIWGIMRNYTVQRADLFALPNNPQPVAMR
NTVNFDGICPKTTANPNGIGTRTTVKRNYEIVAALANDILENRNGVSINDPAGIGQHVG GALK
NGGTLVFNSRRTAIPLVSGVDPEDGE PFTIGGHSAPLHDPTAILYVRKADLDASTGKLKAGVPV
EPLVLRANAGDCISITLENRLPLVMPDLPSTAVMHN VVKRDRFGSEGSTAFANNLMRPSSSHVGL
HAQLLAYDITKSDGANVGLNPVQTVPPRAGTSGAYPTKVYQYYAGHLEREGKPVSQLGR TVDNI
NTTAIEFGGLNLTPSDFIKQPQKGLVGAMSILPQTATWTEDTATRAQATVKVSGQPDYRDFVTV
WQRALNMRWADGRPVEGINTEGNGAAGDPQDNGNMAVNYKTEPLWLRFGMAPDSPFGRANGLGF
GDVPNAHMAYANALVGGDPQTPVLYAKPGQPVRNHIVMPSGGSRGMVYQLDGH IWLPHNYQAEK
SDVDGYPMSLPGIGSVRFGNNPMAMYIGA QESVLPAAHFSFMLPSAGGANAVAGDYLFRDYAAY
GNLSGLWGILRVTNEAPPATAPAQ

MnxG [*Bacillus* sp. PL-12] Accession number ABP68890.1

MLRK FHVVGISTRIVVNTFGDHNPNGRIYVLKENESK LKDLVRKNPYKPIDLVQPLAIRANEGD
IVEILFENQLSFSAGMHFQEADYSVLSSDGADAGYNPDTTVEPGGEILYRLNVNQEGICFFTDL
GNVSSTEQGSSVQGLFGALLVQKRGSSWTD PVTGGPINSGVYADIHHPFLPSFREYAWFFNDEM
EIRDLTGERPLNPMTNQEAE SFHGVNLRYEPM TNRKRLMEAGVVCPCDSEEVH HDSWVFGDPA
TPILRGYVGDPVIRLIHG GVKETHVFHYHVHQLG DSSNINAEILDAQSISPQTHYSIQPLYG
LGSLHGAIGDSIIHCHLYPHFGIGMWGMNRVFD TQLQDGSQCYPNGVRIKALMPLPDRPEPPKPT
PEKPGFPNFI PGKVGYKAPRPPLGIVGGREMT ELERNAAIENPRPGAVFVDPCLDQDPVVVEFN
VSAIEMPVVYNKQGWHDPKARFYVMDEDLDD ILSGKKEPEPLVFHVPAGTCIRMNYTNRMPHIL
DGDAFQLVTRTYENG FHIHFVKFDVLACD GGNVGWNYDSAVLPGQTIRYEWYAETELKAFF FHD
HLFANSHQQHGVFGAGVIQPRFSKFLDSRTGDEVDHGTQISVEHPLIPDYRDQTLFVHDFALLF
DKNGRPIQPPEYPGSEDDPGVFGVNFKCEPLKFRLGEDCDPAYSFSSYVHGDPVTPI LRAYEGD
PIRIRLLQGAHEESH SFNIHGLRWKEERPD LGSSMKAQQHIGISESFTTFETEIPASGDYLWAFE
DEEDVWLGTWGLIRAYKGRMEDLIVLTDREALPEG SAETPKPTGKPPEKANPLASLPPGAYQGS
PVKKFEVVA FQTPIQYNSYGDHDPYGIIFALKEDVEDILT GKKNPVPLILRANVGDLVEVTLTS
ELKKELFPFQDGIHPYPPVKEQS FYPPSLRISLHTSLLNYDVKTSSGDTVGYNPDQTVGPGETI
TYRWFVDGQFGMCSMWMADLRNHR SFGTFGAFVAESRFTTYLDPYSLEKAITGENVILRHPLL
PATREFVLILHDGVRLEDKDGKVIIDPMDGVVPDTEELEEVDTYDYGSRGFNYR SERLINRYKE
HPVMHELFSSEVFGDPATPLFEAYPGEPVVMRITTPAERRRAHTFHLHG HYWKFD SKDLD SRIQ
SFLGHMVTGHTDDLRLIGGAGGVFNFP GDYLYRSGNIRWDIELGMWGI FRVHKDSKENLPRLEE
VEGGWDNEEKA

McoA [*Pseudomonas putida* GB-1] Accession number ABY98562.1

MKTPAVIHPNRYVFQLSSVTALMLSGLITAMASPLDDNSPPPTDPSAYTDQPD DPTPALLNL
STLPEANEGSLELTDGVYGNRDTVRTDNVLPALQTS DRYPTNGKPSPLFGAQPF TQQLLLFEE
FGPEKLDPTLPPDLTFPVPTLGAAPAQDPNVVARSGPSGTALEAFLKQPGLYPFPTQFSNVLD

RNPWKAQIEMFLNRHPVGS PAEGRPPGKGWSHQRWNEFYPPQAAFKTAQAGARINLGLRDRRQMH
NYTVGEFAPGGLYYQTS DIPTTLGTTKGIDTRFHPNFPLQNHKSLWTFDGTFFPKLLMVRYGQP
ILMRHYNALPIDPSANGGFLHTISTHEHNGHSPAESDGFANAYFFPGQYYDYRWVPVQLAGYDT
INTRAQDPRAAFPCSPGETLFVNDGTPGLKTCQNGSIKIRGDWRETMS THWFHDHMMDFTAQNV
YKGNVMMNYYSALDRGNEALQDGVNLRFPSSGSGMPWGNRDYDVNLVIADKAWDANGQLWFNPF
NTDGFLGDQILVNWQYQPKLKVRARSYRFRI LNGSVSRYFKFAVVREIAGTSGEFKGPSGSNVS
YARVPFHMIANDGNIMEHAVPFDGTLDLNGDGNLQDNNGILPLQGIAERYDIIINFAKNGIKAG
DKLYFVNLEEHR TGKGPEGTISLADVLSEKYKAVIKQTSKGPQWDKGDPAVGKFLQLLVQPYTG
QDLSMDPVAYEPAKPGKAAGLKMLPLPIDRNSATDLAKIKDARHREFIFGRSDGTDTPWTIKT
DGGFGYSMDPRRISAAPQLANQSTDGGFSGDGTLEVWKIKNGGNGWSHPVHVHFEEGVILSRDG
KAPPEWEKWARDVYRIGPDADSSEEVEMAIRFRE FAGTYMEHCHNTQHEDSSMLLRWDIEHPG
QFQVMPTPLPGWDGVQYMASVGLPTFR TKGHDDND DPANKPPVAANDSAATTAGKPITLNVLAN
DTPDGNVPLTVTGLSQPD SGQGT VSTDGTTVTYTPPATVETPFTASFNYTARDAKGAESVTPA
TVSIAVSPAAAVDQVQVTSATVQVRSGNRYTWDVAGTTSVATGNSISVTAASTSGPLNLGNATL
TVATSGARWKL SVTTTGTGPATPATVTVKSALGQSVTVPI SIK

MofA [*Leptothrix discophora* SS-1] Accession number CAA81037.2

MRKSTGFHRTPVAAATGLLALLLGAAMPAQAGVGFGAAIDRS GADMNKTNGNAVRSYFAHSPRG
ERETLNPDSISEADALFGAGKFTGRSATDTGKALRK FIDPLPLPGKLSTLADGVTQRTIPVAVP
AKWINPQTGAATSDDYFEIALVEYKQKLHSDLKNPTTLRGYVQLSV DGTGLYLYYPNSSGKVAF
ANAADAPADAKPVMINA VDAKGFM TGAKVQARVVM EPHMYGPLIQARKGTPTRLKFVNLLPGGR
AETTVGADGKVQVTARN GDI FLPLDKSIAHAGLGP DGFTEFTQNR SNIIHLHG GDT PWISDGTPH
QWITPIEEANAANPKALVNQGIDPEFLPSFLRGASAQNV PDM PDGAGASTYYFPNGQSARMLW
YHDHTIGVTRLNVYAGMAAVYTLGDEVDDQLTGKTTGGALNKVLPPAEDTIPLVLTDRTFVPAD
VALQDARWNTSAWGGESDSWFP HVYETVQDPNQMN GFNSVGRWHWGPWFVPVFPAMYDLPSGEY
GDVTVTPEAWMDT PLVNGVAYPTIELDPKVYRMKVLNASNDRFFNISLFVADEAQRLNDPLLGG
ATEVKMVDA AVSATPCAAGVTRAVVATDGSYCTPETWPTDNRPGGVPS PAAQGPSFFQIANEGG
LLPKVAEIAPTPVGYQLDKGRITVLNVLTTGLYLGNAERADVLVDLSAYAGKTLIVYND SGAPV
PAGDPRNDYFTAVGDQSDAGGAEDTKPGYGPNTRTMMQIKVRAAITTPSFDGQIRDARQRGDST
ALKA EIPKAYAIAQEKPVVGQDVYNQALGTTWGATPSLNGNPGNFADIFTGSLKQPVFNYPGE
PHAGFNSVKVTSIGAGYTSAPT VSFADPSVTTESGAKAQATLKIGKVNLTDPGSGYTIAPQVTI
TAVAGGGSGAMGEHLAVDNV IITNGGAGYTSAPT VKFSSSPKATAGNATATAEGVAVISGGKVI
GVTVTNPGFGYAARRTVSFQGG LCHQHRASATTTGYVADVSLIAPDPLQPIVIDPATGIRHQPG
QRGGGGYTDLNQVTVA FNNGGVAPAGGHGGH RHTVGSVFDITMLNNGSGYTNATTVTTLTGGGAPN
GSVAKAEVDTKNGVATGSHLVKTKAIHELFE PVFGRMNAILAVEIPFTSALTQTTIPLAMIDAP
TERFADGETQIWKITHNGVDTHPVHFHLLNVQLINRVGWDGWIEPPAANEIGWKETIRMNPLED
VIVAVRAKR PPLPGFGVPNSIRPMDPSQPLGSSFGFTQIDPLTGNPQSVVNAVMMNYQWEYVWHC
HILGHEENDFMRPIVFEANEAVPLAPTTLALKN GASTLGATSTAATTVTEITWVDQSQTEYQYL
VERSLNGGAWQSVGTSLANATSHTLATPVAIDSGSKVD FRVTAVGANGTASASASVSVPPANVI
ETPTGLVSMGVTSVNNNLRPSVTLNWIDASRTETEFQVWRKVTGSTAPAVLVGTVTRNAAATAA
LGGVVSFVDGSQPNGQALLRPAFGTSYDYTIVARKTTNPTSKSVDSAALTVKIGTRSPVNAFGA
DAPVLT SVGAVRAATTGTAANTDTVVLGWTEEATNSNSSYAVQYRSCATQTSTSTTCRYPVTD S

RYWGAWTAGALVPAAGGAANSTGGSFSITNQVRNKPQVQVQARNSIGSSAWSAALDVTLP

MoxA [*Pedomicrobium* sp. ACM 3067] Accession number CAJ19378.1

MSINRRSFMAASGLALAGVSQVSGRAAFANVPEAPTQKSPLMQPPLKPTSGVDYNPVVTNLNGWT
LPWRMKDGWKEFHLVAEPVIREIAPGMKAHLWGYNQSPGPTIEAVEGDKVRI FVSNRLPEHTT
IHWHGQILPCGMDGVGGLTQPQIKPGKTMVYEFVLQKSGTFMYHPHADEMVMAMGMMGFFVVH
PKDPAFMRVDRDFVFLNNAFDIDAGSYVPKVNTMLEFNLWTWNSRAFPIDHLVVAKDDRVRIR
FGNLTMTNHP IHMHGYDFEV SCTDGGWTRPESRWPEVTVDCAVGQMRAFD FKATNPGDWAIHCH
KSHHTMNAMGHDVKTYIGVDKTEVKQKIRKV VQGYMPMGSTGMAEMGEMEMPLPENTLPMMTGF
GQFGPIEMGGMFSVVKVREGLARDDYKDPGWYTFPQGTVAFEYDGDKPAAPQPPAPAAPMHGGH
KKS DVVPNPAVKPVTLRAVKPRGGHGH

CueO [*Escherichia coli*] Accession number OAEC32945.1

MQRRDFLKYSVALGVSALPLWSRAVFAAERPTLPIDLLTTDARNRIQLTIGAGQSTFGGKTA
TTWGYNGNLLGPAVKLQRGKAVTVDIYNQLTEETTLHWHGLEVPGEVDGGPQGIIPPGGKRSVT
LNVDQPAATCWFHPHQHGKTGRQVAMGLAGLVVIEDDEILKLMLPKQWGI DDVPVIVQDKKFSA
DGQIDYQLDVM TAAVGWFGDTLLTNGAIYPQHAAPRGWLRLRL LNCNARSLNFATSDNRPLYV
IASDGGLLXEPVKVSELPVLMGERFEVLVEVNDNKPFDLVTLPVSQMGMAIAPFDKPHPVMRIQ
PIAISASGALPDTLSSLPALPSLEGLTVRKQLSMDPMLDMMGMQMLMEKYGDQAMAGMDHSQM
MGHMGHGNMNMHNHGGKDFDFHHANKINGQAFDMNKPMFAAAKRQYERWVISGVGDMMLHPFHIH
GTQFRILSENGKPPAAHRAGWKDTAKVEGNVSEVLVKFNHDAPKEHAYMAHCHLLEHEDTGMM L
GFTV

MokA [*Lysinibacillus* sp. MK_1] Accession number AANQ47161.1

MQINPSVPATIPKFVDELPKPMIAKPKYSRGQQKNDYYELVMMEGQHRFHKHFPNTLIWGYNGL
YPGPTIEASKDKTIYVKYKNQLPLQHFLPVDFTLHAANDSQEVRTVTHLHGANVDWQSDGHPEA
WYTRDYRHTGPKFNKEIHEYTNHQPGTTMWYHDHAMALTRLNVYAGLAGFYLLRDALEERSNLP
CGDYEYPILIQDKSFNEDGSLFYPDEPPFPVPVHPSITPGFVGNTIVVNGKLWPYLDVEPRKYR
FRFLNGSNRRGYVISLSNDQPMFQIGTDGGFLPAPQLIQSVELLPAERTDVIIDFSSCAGQEIT
LLNTD TDFSDEHTNVIMQFRVTVPLKCEDTSEI PERLAVSMDLHPHHAHIERQLPLTAT TDEFG
RPMLLLNDRMYHDPATEKPSLDSVEVWNFINATPFIHPIHLHLIQFKILERRPFDLEIYQNEGI
VQFTGPPEEPRDYERGWKDTV KADAGKVTKIIMHWKDHIGNYMWHCHFLEHEDHDMMRPILVMK
DVHAVQQPHVAVEHPATHQEATAPTNPTSTSTTHHSESSAPLLNAVEHSSHEEERVDSPTTEE
SITFHIGDNTQHMP TLLFPALPSNTNTSRNRPQRRTRF

CumA [*Pseudomonas putida* GB-1] AAD24211.1

MSFTRRQMLKGLTGLVVVGLGAGGAARYWL GKVEDDNAGHDYELIAAPLDVELVPGFKTEAWAF
GPSAPGTELVRV RQGTWLRVRFINHLPVETTIHWHGIRLPLEMDGV PYVSQLPVKPGEYFDYKFR
VPDAGSYWYHPHVSSSEELGRGLVGPLIVEEREPTGFLHER TLSLKNWHVDEQGAWLPFSIPRE
AARNGTAGRLITINGQADSVTELPAGQVVRVRLNLNDNTW TYRLNLKGNCEAKIYALDGNPVTP
RPLEDDYWLGP GMRICLAIRIPQAGEEISLRDGFVRLGTLRSVASNDAPSDWPPALPPNP IAE
PLENAEKLNFNF EWAASVTVPDPDKPSSMWQINGQAWDITDKTCADRPIATLQKGKSYIFELK
NMTQYQHPIHLHGMSFKVIGSNRHDIKEPWF TDTYLLGKNERAQVALVADNP GTWWMFCHVIDH
METGLMAAIAVV

Figure S2. Amino acid sequence of putative Mn oxidase enzymes in the animal heme peroxidase (AHP) family

Pseudomonas putida GB-1 MopA ABY99243.1

MANFSKSDLEFILKQIFIAEAHADGASLIDLLPNSQVPFGLRTVDGSYNNLVAGQSEFGAADNS
FLRLLDASYRANYVGTGNVVDSPRTISNLIVDQTANNPAAVEANGGAAPVMSPGIDGVFGTAD
DKPVFFIPNVSPDVGLTAGFNAWMTFFGQFFDHGLDLVTKSSTDIVFIPLRPDDPLYNASSPTN
FMVLSRAVRTAGADGVVGTADDGQPNNTTSPFVDQSQTYSSHPSHQVFLREYMLDAAGDPVATGR
LITNRDLGADGKFGTADDGNSSENGGMATWAVVKAQARDLLGINLTDADVHSVPLLATDAYGNFL
RGPNGMPQVVMRVNNGADGIAGTADDVTTLVEGNRAAPISLANAVSTGHGFLDDIAHNAEPVKV
GGVLQADADSAVGNVQPVGPGGNNLTYNELLDHYIAGDGRVNENIGLTAVHHVFHSEHNRLV
QQTKDTLLAAGDLAFLNEWLIDDVIAIPTTPAGIAALVWDGERLFQAAKFGTEMQYQHLVFEEF
ARTIQPQIDEFLAPNGYDTSINPAILAEFAHVYRFGHSMLTETVDRFDPSFNPVSGDPANPDQ
QLGLIAAFLNPLAFAGSGATADEAAGAIIRGVTRQLGNEIDEFVTEALRNLLGLPLDLPALNI
ARGRDTGIPSLNEARREFYGATGDSQLKAYISWADFADHLKHPASLINFIAAYGTHSSITGATT
EAAKRAAAVALVLGGAGAPADRLDFLNSTGAWANVTLAGKDGIAGTADDIAGVTVSGVDAIDFW
VGGLAEKKMPFGGMLGSSFNFFVETQLEALQNGDRFYLSRTAGMNFGTELENNSFAKLIMLNS
DVTHLSNTVFLTPFTTLEVNQANQFTGLGADGKADPTGGIEINGVEIVPLVIRDNPDTVGPDSN
YLHYTGEDHVVLGGTSGNDIIISGDGDDTVYGDAGDDVLEGGAGNDAVLGGAGDDIITDSFGDN
RLEGNAAGNDVIVAGSMLAAGNLILGGDGQDFIITTEDISTTFFGGQGDDFILGAKTNLPPTGNEG
DDWIEKGTQDGAPGDNFAPLLGDEVVGNDFVGGGGFDEMIGEGGDDIFVGSDAQDKMDGMSGF
DWITKNKNDKVGVTVDLSLAALAQPHGNAPNQAGVFNPVGASPASILDRFAEVEGVSGSNYADV
LKGDDVDAVTILNHGGATGSALTNVALIRGLQQFLADAGLPTTGATGNIMLGNGSDLIEGRG
GDDLIDGDKWLNVRIVAPGDVNHTGPEIASFDSMVDMIPFMLDRTYNPGQLKAVREILPGTS
TGGAADFDTAIFSGVQSEYVVSQNTKGTADVADDVWTVTDTVAGRDGVDTLHIERLQFADSQRV
LVTGVNAQPTGSPTITDGNAAITVGDLLTVSVAGVRDADNISAGNPLGTLADRSVSYYWQFEA
DPGSGVFQDIILLPAGDLAFQSADGTSFKVSPDLAGLSLRVKAIYQDAHGTTEVLFSAPTAVVQ
PGAPVVPTPATPVVDATAGGEGHLMVRSDLNFI LAQIKIAEADAAGQDILSLIPNIRAPLGLRA
VDGSNNLMNLNGHNNTQFGAADNVFRLTDPVFNPVPAEGAPAGFFGPGSPAIPGSSYQQTSGPV
FDSQPRTISNLIVDQTSNNPAAAYATAYDPGADGVLNFGAPGNDDVLKDGVRIVASPGMDGQFGT
TDDHDVYLFENTAADAGLSAPFNAWMTFFGQFFDHGLDLVTKGSGTIYIPLQPDDPLYVEGGF
TNFMVVTRATNLPDPDGILGNADDIHEHTNTTTPFVDQNQTYSSHPSHQVFLRAYVMTDDGPVA
TGRITNRDLGADGKFGTADDTEIGGMATWKVVKAQARDLLGINLTDADVDNVPLLATDAYGNF
IKGPNGYPMVVMKGVVDGIAGTADDQQVEGNPLAPISLTNAVTRTGHQFLADIAHNAVVPVSGGVL
APDADNAVGNAPVNPQTGANLAYDNELLDHYIAGDGRVNENIGLTAVHAI FFAEHNRLVAQT
MDTVLDSHDLAFLNEWLLNPVTALPVTAEIDALVWNGERLFQAAKFGTEMQYQHLVFEEFART
VQPRVDLFFAPTQVYDVLDLASIVAEFAHTVYRFGHSMLTETVDRFDIDFNVIKDPASANPDQQ
LGLIAAFLNPLAYAASGVTPEDATSAIVRGVTRQGGNEIDEFVTEALRNLLGLPLDLPAINIA
RGRDVGIPSLNAVRRDVYGTGDTQLKPYTSWVDLVQHLKHPESLINFIAAYGTHSSITGATTL
LEKRAAAMALVFGGEGAPADRLDFLNSSGAWANVTLPKDGVLGTADDLKAVTITGVDAIDLWI
GGLAEKTPFGGMLGSTFNFFVFENQMEKLQDGDRFYLYLERTSGLSMNAELESNSFAKLIMANTS
AAHLPLGLVFSDPGLYLELDQSKQYNDGLGHADPLGENGEQVVFRRDSPLTAGPDSNYIRYAGAEH

IVLGGTNGDDILVSSEGGDDTVWGDAGNDRIEGGDGNDQLRGGAGDDIIISDMGGDDNIQGGDGND
VLHGGNGVNLIIGGFGNDFIVTGEDASEAIGGQGNDFILGSKANEQDMGNEGDDWIEKGTSDGA
PGDNFDP LGNDPIIGNDVFIGGNENDKFNGEGGDDIMVGS LGFGDRYIGGSGYDWATFKGLAQG
VTIDYSDRFFDVPVPVPGSGASALVRFDIMEGLSGSAHGDFLRGDNEDAASLPTNGATGSVLTNI
SLINGLSSLLAAGATFYDGGNIILGGSGSDLIEGRGGDDILDGDKWLNVRISVRANHDGTGPEI
ASFDSMEPMVPFMLNGTYNPGQLVIVREILNGTDNYDTAVFSGVATDYSVVVDGNAVIVTDLVA
GRDGVDHLTGIERLQFSQRSQASGVGTAVNAGPTGHLVILDDATGVRDDTPVTGQLLRVTPLAV
HDADNVSAANLTGAVNGPVAYYWQVENLPGSGVYEDITFVAAGEVSRAIGTTYRVTDDVAGLSI
RVRAVYQDAKGTLEIVDSSPNSAPSAGPAVTGLLVQNQTLTANPATIVDADGLSNPQFTFQWQS
NRGVGVWNIAGAISSFTVLTQAQVGQNM RVVS YVDDFGVHESVASDILDPVANVNDAPTGA VL
ISDTTPDQGGQTLTALTGGIADLDGLGAFS FQWQQGTGGTFANIAGATAATFTP GFAQGNQQLRV
IVRYTDGFGTLESLSAATAAVTVPPGVVLTGTNAANTLTGGAGNDVISGLGGNDILNGLAGAD
QLFGGVGNDTLNGGDDADLLNGEDGNDILNGGLGADVMMGGAGNDTFVVDNVGDTVTEALNGGT
DLVQTSLASYT LGANVENLTYTGSSAFTGTGNALANTITGGAGNDLLNGGAGADRLVGGVGNDT
YVVDNAGDVVVEATGAGTDLVRTTLASYTMAANVENLTYTG VGNFSGTG NGLANI INGAAGNDT
LAGDGGNDILNGNAGNDTLNGDAGNDQLFGGLGADRLNGGGGDDSLDGGDGNDTLLGDAGNDTL
LGGAGDDSLDGGNGNDSLQGGDGNDTLFGDVGTDTLIGGAGNDFLNGAGGNDTVVGGAGNDTMM
ATDGNDVFQFAAGFGNDLIINFDAIAAGGQDRLDITALNITAAATFAASVTIADV GADTLVSIGA
ADSIRLVGVADATTVTAA DFILAG

***Aurantimonas manganoxydans* SI85-9A1 MopA Accession number EAS51309.1**

MAVKLNENDLRFILDQIKIAEAAHAGADLNDLVDPHPVWGLR TVDGTNNLV DGREQWGAADT
VMPRYLDGSFVTD TNSGAFFGVTNNNYAAPGSVVDTPRIISNLIVDMSVDNPAAVLAFLNNEL
AVETFKE LHGGLEPVAPGTVVNSATQLAVTDADLALIPNIAPDEGISAPFNGWTTFFGQFFDHG
LDLITKGTNGTVYIPLQPDPLYVPGGFTNFMVLTRAAKAEHLPGEDGVLGTADDIVSHTNTTT
PFVDQNQTYTSHASHQVFLREYKF NADGEPVSTGRLLDGLEGG LATWGQIKAEAAAKLGIALDD
QDALNIPLLRDTPYGEFIRGDNGLPMIVTGLGPDGIPNTADDIVVQGNLTTPVNTMAIGAIRIG
HAFLDDIAHNAAPVINGGVLPDADVL TGNTVASQQGQNT EYDNELLDRHYITGDGRGNENIAL
TAVHHVFHSEHNRLVDATRMEVLKSGDLAFINEWLATDIATLEGI PADGLPLLNFANTLDWDGE
RVFQAARFGTEMQYQHLVFEEFARKIQPAIDPFVFNSSTDIDPSIFSEFANVVYRFGHSMLTET
VARTNIHDGSADNIGLIQAFLNPVEFTKNSTVSAD EATASIVLGMTSEHGNAIDEFITSALRNN
LLGLPLDLAAINIARGRDTGMPTLNETREQLYQATGSSFLKPYDSWVDFAANLKNPMSVVFIA
AYGTHETIVAAGNNLQERRNAAMALVFNTEGAPADRLAFLNSTGGETAESVGLNDIDLWVGGLA
EQILLFGGMLGSTFAAIFEAQLEALQDGDRFYLYLSRTQGLNLLNELENNAFSKLI IANTDLSDP
GPDGIRGTGDDVIARHIGVDAFGQYDYVLEV NKS NQLIEDPTGVDPVLEALGLGKVIRDDP RTP
QDES AVSGYVASINALVKQYDASGTPTGILIDGSENVIPGITVGD LRENAEHLGIILTDEDLAN
APVLKLNPDGT LR FNTPGATTTASVLNNDFEATSLADGAPGVTTDANGNYTVGAPVGWEINGG
SGGLFDPAAIITDQAGPSGNNVWLRQGATLARNTGESAVAGAVYTLSFDIGDRTDHPWPGGQV
RISATDGANTTLLAFQLLPEPSNGMWSNVSISTSAIPTNLAGQELRIEIQQDGNGGANQILVDT
ISFSSTTEVFYSSDLTPAQMGVAYDPAADPFARDADGNVLR TGQAIVDGPATNETVIDPVGLAQ
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DDGDSGNFIKGEDGDDVIANSAGPFDILMGRGKDVIFVGPDDTEVFGGEGDDFIAGGEGVD FL

LGNEGDDWIEGGGFDTTAGDNSDLFFDSKILGHDVMFAGNDEHDFDAESGDDIMVQGESVMRN
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TAFVSQNGQDTITGGAGDDTIQGLSGNDTLNGGAGDDDLLGHGGDDILVGGAGSDIINGGAGND
TAVLDFTVADATFFLTTPSGSLEIAAGADEDELIDIEQVEFS DGQILTTRQAENRIANFQ RGNQ
DNIINGDL DG VVADDTIRGLNGNDTISGGDGRDLLLG DGGSDTLNGDEDDDI LAGGRGNDTVNG
GAGDDTVFWFTGDGRDSVNGGGGTD TLSINGDEGVAETFRIYTRAAAI AANINPGGP NNEIVIT
RTVDGAPDSNADRIALVRNIEELEINTRPIGGATVARGDTVQIFGDFTTTSLALNTITIDGASG
DDTVDITALQSAHRIVFKSNGGNDTIIGTLRPQDVIELAPGATLADYQTTSMNGMTKMTFGGHS
IAFPSTSHPTFADNSSSQGGSGGGGESAPGGSFALTARDLAGLKNLVNGHQAFEDDDDDTAGAGG
VRELLGRNNNESHPEYGAADDEVFIRL TEARYGEYDGTNNRAINPIFAGLDARTISNVLGHQEA
DLSPAASGANTFFMAFGQYFDHGLDFLPKNSANGVLAIGGP GTSRAPGV DNPADLTRGEVYTID
ENGVPQH LNKASPFVDQ NQAYGSNALVGQFLRES DG DQGVGMRLLSGATDPSTPDFNLLPTLRE
LIAHHWENDTIFVDPSLP GGSVSFRDYFTDYPISDNATGSIFDEATGAYDPDVVASMVS NFMGG
GYPLLLDTNPYINLLDHYVAGDGRANENFALTS MHTIWARNHNFHVEMLLEAGFEGTEEEVFQA
AKMINEAEYQ RVVFTEFADMLIGGIRGE GDHGFNDYNPNADARISHEFASAVYRVGHS LVGQTM
TVIGPDGQPRQVELF DAF LNPTSELGAFKPGLPDGYVPQPGYAQLGAGAILAGVATQSAEEVDF
NIVDAIRNDLVRINADLFAFNVAR GWDVGLGT LNQVRADLKASGDPYIQEAVGFAGNLD PYASW
ADFQARNGLSDTIMDQMKVAYPDLILSTPEEIAAFI AVNPDIELTDGANGTKIVKGIDRVDLWV
GG LAEKHVLGGMVGQTFWVVLHEQFDRLQEGDRFY YLERFDNFDFYDNFIDGQEFSDIIARNTG
LTGLPEEIFRANDE NDDTADNDDGVGDDTSDE DGDSDTVGEDNDDTVVDDDDALAPVPPVVS G
LAVTGTAADVMMGGAEADVLSGGDGDDIILGGFGDDTLMGGSGSDLIKGDAGRDMIFGGAGDD
VVLGGADNDMIFGDAGDDRMFGDDGDDMLEGGGGFDTVYGGAGNDRFIARQGDGDDIYWG DAGN
DTLDYAAITANLTIDLNGMTMQHGSVHSSQSGHDAIFGFENVIGGAGNDEITASSVVNVMDGGG
GNDTFVFRTAADADGDRINGFASGDKIDLSGMNGSEGFTLETTVLTGAGQVLVTHLTGDDGEAL
TRIQGTVSDGA EADFTLEVAGRHLTQSDFIGVA

***Erythrobacter* sp. SD-21 Accession number WP_006834642.1**

MAVKLNKHDLEFILQQIKIAERHAAGENLV DILGNFHLPHYGLRTVDGSYNNLVEGRERWGASDE
IMPRMFTPNYRDDQDGDMMSF GPGMTITNTDYGAAGDVADVDPRIISNLIVDQTAGNPAAISAA
LTQTGYEGDATAAIQALHSAWADHENG LMTYEEFATLALD TYGLEMQGD TLVIPNTAPDEGLSS
PFNAWMTYFGQFFDHGLDLIPKADNGTVYVPLQ PDDPLFDAGPDGIPFTADDGR TNFMVMTRAQ
IDENGETMNTTTPFVDQNTY GSHASKQVFMREYELVNGRPEATGHLLLEGVNGGLATWADVKAQ
ALDVLGIVLSADADV LALPLIRSDPYGNFIPDENGYPQVVVGIGADGIPNTADDVVVSGSPTNPV
HLLTGMA GEIPPEGVPEGMAVIPVRTAHAF LDDIAHNAVVPVFDEGNLAADADTD TGNVATGTR
GENLEYDNELLDRHFITGDGRGNENIALTAVHHVFHSEHNRQIDSNKIEILKSGDLAFINEWLD
VDITAPEVAGLAALTDAQLAAYGESLDWDGERL FQMAKFSTEMQYQHLVFEEFGRRIQPNIDPF

VFNTTTDINPAIFAEFAHVYRFGHSMLTEDVNRMFNDAGEPVFYDELGNETPVTDLLEGWGN
TGLIEAFLNPVDYDLDDGNISAEQAAGAI FRGLNREQGNHIDEFVTDALRNLLGLPLDLAAINI
ARGRDTGMPTLNEARAELYDATGSTFLTPYGSWAEFAEGLKNPLSVINFIAAYGTHQTIIDAGD
NVDARRAAATDLVLGGGAVSEADRLAFLNGPAAETGVNDIDMWIGGLAEAPMAFGGFLGSTFNA
VFEAQMEALQDNDRFYYSRTQGLNFLNELENNAFSKMVMANTDMTDPGPDGIRGTEDDILNYH
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INGTAGDDTI IAGGGDDGIWGGAGNDRIEGGHGVDLIIAGAGNDIVTDSGDSDDFIKGEDEDDV
IANSNGLDVL MGGDGKDAFIVGVDTEVFEGGEDDFILGGEDADFLLGNEGDDWIEGGGGFDTT
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GANEIATVTSKNNVTIDGVTQSLVSHLLEGNVSPGQMHI VREL VNDGQEGDLDTAVYYDNAN
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AILSDNTPTEGQVISADVSGITDANGIVSSSIQWQVSSNGVDWVDVAGATGPDPFTPEDLAGTAF
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MEGSDNLSGGAGNDLLNGGVGADTTSGGLGNDDHHVDNAGDVVLEAVGEGTNDRVLSSATYVLN
AGAEIEVLVAKGSADIDLTGNEFDNVVWGNAGANSVDGADGNDRVFGLAGDDTVEGGDGDDEL F
GGAGVDVSDGGLGNDTHHIQ NAGDTVIEGVGQGLDIVRSSVSWALTAGAEVEVMFAKSGSNID
LAGNEFNNTIWGNAGMNVLSGLEGDDVLFGAGAADMLFGGEGNDQLFGGVAADTMDGGLGDDII
HVN NAGDVVEEAVGEGFDQVGTTVNYVLTAGAEVEVFFAKSGDINLTGNSLANSIWGNNGANT
LQGGAGDDVIGGGAGDDTIRGGLGNDTLYGVDGNDLFEQRGALDGRDFVNGGAGIDTWQLVAGA
GEDYTIYTRAEALAAGITGLNIATEIVVTLN GSDNASVIAELDNIEEIVVDSL DVASGGAANGG
TTASGASVTVVGDFTP TSLDLNTITVNGGNNDVVDITQLTSPHRIKFDASLGSDQVIGDLRPQ
DVVTFGDDFGVQMRPERIGEFDLFSHEDGRSDLSSLVSSFVAEARSSNLNASTAAQGSPPFGQP
AEFLKDDFGSVKFAPFEDGLFETFL

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MVFVNTNDLKHILDQIRIAEQHAAGTPLTDLVANPLL PYGLRLVDGTLNNLT PGREEWGSADQV
MPRLLESTFLTQPDA AHLADPSPRGAPGA EPTSYLQTS GSVYDAEPRVISNLIADQTL SNPAVI
AAALSHAGMTGQAMLTTANEIVQAYQRVIDAQAAAGNV DQALELQRQELQTALDTATAELTAAQ
GDVAAKTTAKNEADQAVTQAQDTLDNAAATMVTLQGGQQAEMQVALNAAVA AHTQAEADLKAA
QDELLQAESAAASMLTMHNAKQTTVTNLQGGQKATADQELATAEGLLSDARAALALETDAAGAVT
EAQTAVENATTAVSNAQTRVNELDAQLTQAEADLADLNTQLQAAEQTRDAAQTRVTAAQEAAAA
TQADREDAQALFDTEVSELATAQAEMLSALTNYITGGSLADFSVASAAYSAA REEKLAETALN
DAIDADDEADQAVIDETAALTTAQSRVSTLT TQRDNDMTTRDGLSTQLDEANGLL TSAQNTLTA
AEQTLQTAQDDNQAMSMRRTPLIWPRPMSMRLKGSSMASWHSWGLLKANLQR

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MGVAEGELATLNTNLGNADA EVTRLEGVVQTETTDLETAAGGVTTAQQN LAAAQMADAAILAQL
DVIADATVTLTEATATAAQAALDLTAAEGVEATKQVAVD TATSDLNALTAPGAAEALAAAQAT
AAEAQTTLDTLLTTHNITMDGNNVLLPDVTPDEGLSAPYNSWMTLFGQFFDHGLDLVGKGGSGT
VYIPLQPDDPLYDANSPTNFMVLTRATNQPGPDGILGTADDIREHFNKTPWVDQNQTYTSHPS
HQVFLREYDIDANGNPVSNGYLLHGQTGGMATWGDVKAQAATKLGIQLNDSVDLDGP LLATDPY

GNFIPGANGLPQLVVPNPAYVEGGTEPLNILIEGDLANPVDASQALRNGHAFLEDISHTAFPKG
MIDHDRNPMTPEIEVLPDADTDGTGNAIMPNI FGMNETYDNELLDRHFIAGDGRGNENFGLTAVH
HVFHTEHNRQAAEMKQTILDSGELAFINEWLATPITEADLATATVDTVEWDGGRLFQAAKFTTE
MQYQHIAFEFEGRTVQPQIAAFGVNGSAEIDCAVMADSPMWCTASPLDADRVDHTMDPNGVNTS
NGLIEAFLNPVAFDLDQTLTSDQAAGAVARGMSRETGANIDEFITSALRDNLVGLPLDLAALNI
ARGRETGVPSLNAAREQFY SATGSEFLKPYEGWSEFAANLKNPASI INFIASYGTHETIVNATT
VVEKRAAATDLVLGGDNAPADRLDFVNGTGAWADAETGINDVEFWIGGLAEDIMPFGGMLGSSF
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PQDPTVELRSINSLFEISNELLDGSI SPGQLQIVREILDAGQEGDVTAVYFDVRANYNIRTNA
DGSVTVDHIAPPIEGAFIDPINGQPNVEGGDGTDRLTNVEILRFADMEIDLRTDPASNGLIQGT
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TDMLVINGDGTEDGFTMYTVAAWTGQAPVDPSS EIIITRTVAGVETAIMEVRGIEEVAINGVQG
IETINAVGDFAGTSLAPNTIYVNGTAGREVIDFSGFTSTQRLVVDAGDGRDVI TGGAGNDILNA
GAGDDEITWSVGGGSDVDGGAGEDTYTINGDASDETFRVYAADSWTGAPLATGTDIVITRDAG
AGEQVIGQLQNI EIIQINTAGGVDNVEVIGDFNPTALNFNTIAVTGDDVSVDVTQRLSTHRVVF
DVGGNTQDVPKSLNVAGVVTEGDVFLIPVDPTTLTRTVDSR

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MATVNEQTGLPEEGFGFVLTGATLVTADDIAALKYMGASNVAPILPPEAGEPADNEPADLL
QEVRLGLEGLTNNLQNAEISGGATLPFMRVTEARYAGIGEDGAGI INPVFDRLDTRDISNTLGAQ
DLDAKAASANMFMMSFQGYFDHGLTFIPKSGSGPMQOTLGQIEIGGPSMDRGPMADNPADLTRG
SVIGYDEDGTPLQENITSPVVDQNQVYGSSSLIGQLLRES DGEMGVGARI LMGGDDPSAAPGFK
ILSTLRETLDHHIDAGTVFKGAGLGENGMTLLDYYPGLRDADRNYDAALVKELSGDFMDEGWPL
LIDTNPFMNLLDHFVGGDGRANENVGLTSMHTVWARNHNYHVDQINKQAGPDFTPEQLFQAARI
LNIGEYQQVVFND FADALIGGLQSGRHHGNEYNPNADARISHEFAAAAYRFGHSQIGETMLVE
KDGQMVELPLIDLFLNPTSDPNAFQYVDRETGELVTGEAALAALAQMDYVPQDGYAQYGVNSIL
GGLVAQPSEEVLDLQVVDVAVRDNLVRVSADLFAFNAAGRD LGLGLTNQVKADLAASDPYIVEA
IEQSNMNMDPYASWDDFQWRNNLSETEITKFKTAYPDLVLEGDAIAAFQQVNPDITLIPGENGA
MIVQGIDRVDMWVGGLAEPHIEGGVVGHTFWVLIHEQLDRLQEGDRFYIIDRIGDLPVYNNFIS
NLTFGDIVTRNTGMTDLPLDVFSYVPEVPEGAAADAGNQIQITDQANANRTDDPAIDTADTEGGG
TTTDTDVTGGADDETEAAATEGNAEPDPLETEANALSEGAVEGGVDETEQPDADVTGSTLEQSA
EEEEETEEDDATQ NATGAASGGEDLEATSSETNEEMPEDNTSMSPPDAGGADTGGADDETEAAAT
EGDNEPDPLETEVNALSEGAGEGEGGAEQPDADVTGSTLEQSAEEEEETEEDDATQ NATGAASG
GAALAE EEEEEETEEDDATQ NAMGAASGGADLEAE EEEEEETEEMPEDNTSMSPD TDTS AEGIVESDT
DMGAPLVGAAGDDILSGMAGDDMLVGNAGDDMLFGGEGRDDMLGGDGADMLSGGAGSDHILGGD
GDDMIIGGTGSDILMGNAGDDTFLGTNGDCNDLIYGGEGTDTIDMASVTSDLTVRLGNTGTDRG

SVTTEEGGRDTIWSIENFVGGAGDDTIFASDAANVLDGGDGNDTFVFETAASAQGDHINGLNAG
DVLQFGTGADMFELTWGDTDMQDGLSFSGGEEAGTTKISGTIEDDQFELTVSGRFDYDQIT

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VFVNTNDLKHILDQIRIAEQHAAGTPLTDLVANPLLPYGLRLVDGTLNNLTPGREEWGSADQVM
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AALSHAGMTGQAMLTANEIVQAYQRVIDAQAAAGNVDQALELQRQELQ TALDTATAELTAAQG
DVAAKTTAKNEADQAVTQAQDTLDNAAATMVTLQGGQVAEMQVALNAAVAHAHTQAEADLKAAQ
DELLQAESAAAASMLTMHNAKQTTVTNLQGGQKATADQELATAEGLLSDARAALALETDAAGAVTE
AQTAVERNATTAVSNAQTRVNELDAQLTQAEADLADLNTQLQAAEQTRDAAQTRVTAAQEAATA
QADREDAQALFDTEVSELATAQAEMLSALTNYITGGSLADFSVASAAYSAREEKLAAETALND
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LTAAEGVEATKQVAVDTATSDLNALTAPGAEEAALAAQAATAEAQTTLDTLLTTHNITMDGNN
VLLPDVTPDEGLSAPYNSWMTLFGQFFDHGLDLVGKGGSGTVYIPLQPDPLYDANSPTNFMVL
TRATNQPGPDGILGTADDIREHFNKTPWVDQNQTYTSHPSHQVFLREYDIDANGNPVSNGYLL
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LAFINEWLATPITEADLATATVDTVWDDGGRLFQAAKFTTEMQYQHLAFEEFGRTVQPQIAAFG
VNGSAEIDGAVMAEFAHVYRFRGHSMILTENVHTMDPNGVNTSNGLIEAFINPVAFDLDQTLTSD
QAAGAVARGMSRETGANIDEFITSALRDNLVGLPLDLAALNIARGRETGVPSLNAAAREQFYSAT
GSEFLKPYEGWSEFAANLKNPASIIINFIASYGTHETIVNATTVEKRAAATDLVLGGDNAPADR
LDFVNGTGAWADAETGINDVEFWIGGLAEDIMPFGGMLGSSFGFVQQQMEALQNGDRFYLLAR
TAGNMIAELENNSFASMIVRNTDIKDGGAHIPANIFSSMDVILEVDQAVQSMPPDPVSTDVDPF
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DDLIGDAGVNTLRGGAGNDILKDGDVVSFLHGEGDDVISAAGGIGELMFGGKGNDAIILMGSD
DAATAFGMDGNDFIYGGAGGEFMMFGGEGDDWIEGGDGFDMVMDNGDPFGGSRVVGHVDVLDGGA
NDNDLLGEGGDDILIQREGVHVNEGDLGFDWVAHKDAMTGADIDLSSRLETNETQAALRDYDL
VEAASGTQFDDFLYGDDREGAALPDGIDLLANDATL FANELTQAGVDRIAGLRELLADMMGVDP
ADTFTGGNILLGGGSDVIQGRGGDDVIDGDKALNVRISVRDPQDPTVELRSINSLFEISNELL
DGSISPGQLQIVREILDAGQEGDVDVAVYFDVRANYNIRTNADGSVTVDHIAPPIEGAFIDPIN
GQPNVEGGDGTDRLTNVEILRFADMEIDLRTDPASNGLIQGTGDDVLNGSNSGRDAIFAGAGND
VINGLAGNDVIFGEGGSDTITWNAPNGGYDVVVGHGIVNDGGTDMLVINGDGTEDGFTMYTVAA
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VDNVEVIGDFNPTALNFNTIAVTGDDVSVDVTQRLSTHRVFDVVGNTQDVPKSLNVAGVVTEG
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AAKAASANMFMSFGQYFDHGLTFIPKSGSGPMGQTLGQIEIGGPSMDRGPMADNPADLTRGSVI
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TNPFFMNLDDHFDVGGDGRANENVGLTSMHTVWARNHNYHVDQINKQAGPDFTPEQLFQAARILNI
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QMVELPLIDLFLNPTSDPNAFQYVDRETGELVTGEAALAALAQM DYVPQDGYAQYGVNSILGGL
VAQPSEEVDLQVVD AVRDNLV RVVSADLFAFNAARGRDLGLGTLNQVKADLAASTDPYIVEAIEQ
SNMNMDPYASWDDFQWRNNLSETEITKFKTAYPDLVLEGDAIAAFQQVNPDITLIPGENGAMIV
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ETEEDDATQ NATGAASGGEDLEATSSETNEEMPEDNTSMSPDDAGGADTGGADDETEAAATEGD
NEPDPLETEVNALSEGAGEGEGGEAEQPDADVTGSTLEQSAEEEEETEEDDATQ NATGAASGGAA
LEAEEEEETEEDDATQ NAMGAASGGADLEAEEEEETEEMPEDNTSMSPD TDTSAEGIVESDTDMG
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QFGTGADM FELTWGDTDMQDGLSFSGGEEAGTTKISGTIEDDQFELTVSGRFDYDQIT

Figure S3. Amino acid sequence of the first heme-binding domain of *P. putida* GB-1 MopA.

LPNSQVPFGLRTVDGSYNNLVAGQSEFGAADNSFLRLLDASYRANYVGTGNVVDSQPRTISNLI
VDQTANNPAAVEANGGAAPVMSPGIDGVFGTADDKPVFFIPNVSPDVGLTAGFNAWMTFFGQFF
DHGLDLVTKSSTDIVFIPLRPDDPLYNASSPTNFMVLSRAVRTAGADGVVGTADDGQPNTTSPF
VDQSQTYSSHPHQVFLREYMLDAAGDPVATGRLITNRDLGADGKFGTADDGNSENGGMATWAV
VKAQARDLLGINLTDADVHSVPLLATDAYGNFLRGPNMPQVVMRVNNGADGIAGTADDVTTLV
EGNRAAPISLANAVSTGHGFLDDIAHNAEPVKVGGVLQADADSAVGNVQPVGPGGNNLTVDNEL
LDAHYYIAGDGRVNENIGLTAVHHVFHSEHNRLVQQTKDTLLAAGDLAFLNEWLIDDVIAIPTTP
AGIAALVWDGERLFQAAKFGTEMQYQHLVFEEFARTIQPQIDFLAPNGYDTSINPAILAEFAH
VVYRFGHSMLTETVDRFDPSFNPVSGDPANPDQQGLGLIAAFLNPLAFAGSGATADEAAGAIIRG
VTRQLGNEIDFVTEALRNLLGLPLDLPALNIARGRDTGIPSLNEARREFYGATGDSQLKAYI
SWADFADHLKHPASLINFIAAYGTHSSITGATTEAAKRAAAVALVLGGAGAPADRLDFLNSTGA
WANVTLAGKDGIAGTADDIAGVTVSGVDAIDFWVGGLAEKKMPFGGMLGSSFNVFETQLEALQ
NGDRFYLYLSRTAGMNFGTELENNNSFAKLIMLNSDVTHLSNTVFLTPFTTLEVNQANQFTGLGAD
GKADPT