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Supporting Information

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Supporting Information

for

Insights into Sequence–Activity Relationships amongst Baeyer–Villiger Monooxygenases as Revealed by the Intragenomic Complement of Enzymes from *Rhodococcus jostii* RHA1

Claudia Szolkowy, Lindsay D. Eltis, Neil C. Bruce, and Gideon Grogan*

S1. Amino acid sequences encoded by twenty-three open reading frames (MO1-MO23 as described in the manuscript) encoding putative Baeyer-Villiger mono-oxygenases in *R. jostii* RHA1.

>MO1

MSTAAPAVTEVLDVLVVGAGFAGLYQLENLRSRGYSVKVVEAGEGLGGIWHWNRYPGARVDSEGPI
YQFTRPDLWDEFAFSELYPGGDELRRYFKYVDAKLDLSKDIYYNTRIISAEFDDTANTWTVTAENGSS
FVCKYFVLCTGFAAKPIFPKLPGMDSFTGINHHTGLWPEGGIEFAGKRIAIIGTGASGVQVAQEASKKA
AQLTVFQRTPVQALPMRQRQLTDEDNAKIKFDLADRFSRRSASFSGFDFDFIPKSALGVSDEERITTY
ERLWECGFEFWLGTYQDVFVDDDANDTAYEFWRDRTRARIKDPVIAEKLAPTKKAYPFGVKRPSLEQ
TYYDIFNQDNVRVVDLHEDPIETITPTGLKTTSEQHEFDIIVYATGFDAVTGGLTAMDIRGTDGTLLRDK
WSNGVRANLGVATAGFPNLLFLYGPLSPSGFCNGPSCAEIQGDLIVNTIDYMRDNGLNRIESEADADA
AWSDHVAELTAEALYDKADSWYMGANVPGKPRQLLNYPGGLPLYLAKWDETVCAGYKGFTLS

>MO2

MNLPQHVHTLIVGAGFAGMGLAARILQTQPQADVLIIERGDDVGGTWRDNTYPGCACDVPTSLYSYS
FAPSADWSHTFARQPEIHRYLKKVAADTGVRSRVVTDCELQEAHWDADEAVWTVRTSRGTVTADVV
VAATGALSTPSVPDMPGLETFGGTTFHSATWNHDHDLTGERVAVIGTGASAVQFVPEIAPVAEHLTVF
QRTPAWVIPRLDRELSGSEKRLYRRLPLVQKAVRGTVYGFREALGGVLAHATGLLPVFEMVAKAHLR
RQVRDPELRRKLTPNFTIGCKRMLLSNDWLRTLDRPDVTLVDAGLAGVTPDGVVDALGNEHKVDTIIF
ATGFTPTEPPVAHALRGANGRTLAEHWDGSPSAYKGTTVAGFPNLFLMYGPNTNLGHSSIVYMLESQ
SAYIADALNVMHHSEITAFEVTEEAQRRYNTRIQSELQTTVWNKGGCSSWYYDSEGRNSVQWPTFT
WKFRSQLQRFDQENYVSRRRAAKETVA

>MO3

MNTTLLEELDVLVIGGGFSGVYQLDRLRTLGYNVKIYEAGTGLGGVWHWNSYPGARVDTWAPVYQF
SREELWRDWNWSEMYPGRDELVRYFEYVDEKLDLSKDVRYETRVLAGRFDEETHRWTLVSRNERT
GEEFTTQAQFVIMCLGAGSKPLFPNIPGLEKFGGDCFHTARWPLEGYDLAGKRVAVIGTGASGVQVIQ
EASKVADHLTVFQRTPNTALPMNQRALGEADNAEMKKTYPERFANRKNTWAGFDYDFLKENIQDLTE
ERRNEILEELWTNGGLQPWLGGFLNVLFDKDDNDILYAFWRDKTRQRITRPELVELLAPTEPIHPWGV
KRVSLEQNYFESLCRDNVELVDTSANPIREVASDAIITADGTRHEVDVIVLATGFDSVTGGLTAIDIRGT
GNETFEEVFRGGSRTALGKATVGFPNLLYVYGPQSPNAFCNGPTCAELEGEHLIQIVEHMRNNGYTRI

EAKPEAQQYWGAHIAELTSATLFPLAKSWYMGANVPGKTVEMLMYPGGLSVYLEILEKAAAGGYQEQ
FELV

>MO4

MTAIHAPKNDLAQSAETPTYDVIVVGGGFGGIYQLRHLRDRGFSVILLEASGGFGGAWSLNRYPGARV
DSHAPVYQFTDEYLWKDWDFSQMYPDHEEMRSYFNYVDSKLDLSKDSRFNTKVVGATFDEEQRMW
SLETQDGATFRARFVVFATGSTTEPYTPSIPDMDAYQGELVHTARWRSDLDMTGKRVAIIGTGASAV
QVVQEAGPVVENLTVFQRTPNISLPMQQKYLDDEEQAALKNKMPDVAAKCRETHAAIDYDFDPRSGF
ETPEDERNAVFERLWNQGGFAFWLGNFSDYLFNDKTNALTYEFWKNKIKPQIKDPVKAELLVPEIAPH
PFGAKRPALHQNYYEVMNQTNVSLVSTKETPIVGFTETGIRTADGVEHGEFDIIVLATGFNNNTGALTS
IDVQNANGVTLRDKWSQGVDAYLGAVTAGFPNAIFVYGPQSPAAFANGSTNAELQGEVMVDFFEFLR
SNGLTRFESTVEADKAWTAHINETDDTALFNRAKSWYNGGNIPGKKMQMLQYLNGVPTYLQFWQKE
KESGYTDGLTVS

>MO5

MGGEVHRCRVLVIGTGFSGLGTAIQLRRRGRDDFILLEKAREVGGTWRENTYPGCACDVPSHLYSFS
FEPNPDWTRMWSGQEEIFDYLRGLADKYDLRRNIHFGRTMTGGHWDAERRRWHVHTESGDEYVAQ
FVVSGIGALHIPNVPDLPGADTFDGTEFHSARWNHDYDLRGKKVAVIGTGASAVQFVPEIVGDVAELH
LYQRTPPWVIPGLNFGIPPEARRLFGRVPLARRMVRAAVYWTYESLALGFNGHSRLMRPIESMARKN
LNRTVADPELRRKLTPSYRIGCKRILGSDVYYPALISPKTVVITEGIAEVRPHSIVAGDGAERVVDAIIYA
TGFHVTDGFDNVELTGVGGRRLADEWEEHGIRTHLGITVAGYPNAFFLFGPNTGLGHNSVVFMIESQI
RYALELMDLVDRRGADSAAVRPAVQSGFNADIQRKLARGVWSTGGCVSWYLDSHGVNRTIWPGSTV
RYWQRTRSVEPADFEFTPG

>MO6

MTHYDILIVGAGISGIGAAIRLKQSGIDNFAILEKGDALGGTWRDNTYPGCACDVPSALYSYSFAPNRE
WSRLFAGQDEIRRYIERTAAEHGVPAHVKFGTEMQRAQWSEQSRRWTVDTSAGTFTANAVIAAAGP
WNEPLVPTVPGLDTFTGEVFHSSRWNHTYDLTGKRVAVVGTGASAVQFVPAIQPTVESLHLYQRTAQ
WVLPKPDHTLPGVERAILRRVPGAIRALRRVEYAIMESLGLGFRHPWILRVIQQVGKAQLRAQVRDPK
LRKALTPDYTLGCKRLLLSNTYYPALTRPNVEVHANAVESVRGNVVVGSDGAEREVDAIIFGTGFHILD
MPIGSKVFDGDGRSLDDHWKGSPQAYLGTTVAGFPNAFVLLGPALGTGHTSAFMILEAQLDYLIQAVT
AARSNGWTRMEPRREVQDAFNAQVQEALATTVYNAGGCQSYFLDVNGRNSFNWPWSTDRMRQRL
GRFDEAAYDVSREPASATATSR

>MO7

MVSYMSLPVTDTSAPPAGVRHIDTLIIGSGFAGLGAAIKLTQAGKTDFLVLERGSDVGGTWRDNTYPG
AACDVPSHLYSYSFALNPEWTRSFSTQPEIQKYIQSVADKYKVRNKHLFGCDVQSAHWNESTTRWEV
TTTKGNFVAKVLVSAVGALCEPSLPDIKGIEGFEGEIFHSARWNHDADLTGKRVAVIGTGASAIQIVPAI
GKKVSHLDVYQRTAPWILPRADREYTKLEHTAFKYLPGFQKLCRTGIYWMRESQVVGLAKAPVFMKP
LQFAAERHLRRQIKDKALRKKVTPNFQIGCKRMLISNNYYPTLAQDNVDLVTDGIAEVTADSVVSKDGT
VREVDAIVVATGFHVTDSPTFEGIFGKDGRSLADVFDEGGQQGYKGAAIANFPNMFFLVGPNTGLGH
TSMVFMIESQLNYLVDALQTLDKYDIGKIEVRQDAQDRYNAELQEKLSHSVWNNGGCASWYLDKHGN
NTTLWPGFTFQFRNETKRFDLTAYDSVATADLPAPVHVNGKTPGPAAIPAQIDLDDDKVTAQ

>MO8

MDRGDTPHRREYSTPQGFCGDHRFRVLNSPNKTDIPGLDTFEGTVVHTAEWDPSLDLTGKRVVVVG
TGCTAVQIVASIVDDVATVDAIVRSPHWIVPEKLWSTRYRPGRSGQCGTCRTSRIGSGSEPTGLPQNN
LYMMPRIDPEWAATHLSVSPVNDLVMQTSLQYLEQTLPDRPDLREKLTPSIRPYAKRIVKDPGFLEALE
RDHVSLHRASPKHVHPGGVSLSSGEFVEADVIVLATGFKVEYASFIDITGRNGKKLADKWDHGQDPR
AYLGIQVSGFPNLFVTAGPNAAPNHGAGHNITSEERVHYIVECLQYLVENDFSAMDVKPEALTVYNEK
VDEALDQTVWAHPGEGVTGYYRNQQG

>MO9

MTVQDNDFDAVVVGAGISGLYAVYKLRQRGMRVHGFESAEGVGGTWYHNRYPGARCDVESIDYSY
SFDEELQQEWTWTERFATQDEILRYLEHVADRHDLRSAYDFLTRVTSATYDEETTRWSITTDTGQNV

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TARFCVLATGVLSATNKPDIPGRDTFGGATYHTGEWPHEPVDFAGKRVGVIGTGSSGIQSIPVIAEEAA
EVFVFQRSPNYSIPAGNRPLTGEYIAEVKANYAERRRLSRMSGGGTPNSAYPKGALEVDAEERRRVY
DEWWQRGGYLFAKAFPDQTISQAANDTAREYVEAKIREMVTDPDIADQLVPTDHPIGTKRIVTDNGYF
KTFNRGNVTLVNLRRTPITEITEAGVLTTNSFYGLDMLVFATGFDAMTGSLSRIDIRGRAGRNLRDEWS
AGPRTYLGLSVAGFPNMFILAGAGSPSVLANMVLMAEQHVDWISNCLDYLDEHNIETIEATDESVDEW
VAECNEKAAGTLFPTADSWYMGANIPGKPRVFMPYIGGFGNYNTICAEVAAAGYKGFELGERRVDVD
Q

>MO10

MTETIAAGLAVPSDRDAQLYNAIAESDPAPLLMALVHATGDTGLLDEFGARLTIEEPGNHYRTGIRPTA
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VPVTVAPPADFDVIVIGAGIVGINAGIKLGEAGFRYTIIEEREDVGGTWYRNTYPGAAVDTPSHYYSYSF
ELNPNWSKYYPTGPEYQNYLLDVVEKYRLREHIRFRTRVLSARWLDDEHRWEVVTEDGEGSVVRHR
ARAVITAMGMLNAANIPEVDGLDSFAGRVVHTAEWDSDLDLSGKRVVVLGTGCTSVQVVANIVDQVE
ALDVVVRSPHWLVPEKAVSGDVTEGEKWALANLPFYDRWFRLRSYWFASDNLYPLPRIDKEWAATH
LSASPANDMVLRTAQEYLQTSFTDRPDLIAKLTPDFRPYAKRIVKDPGFFAALNREHVSLHRASFEKVT
PEGVYTTEGAFIPADVIILATGFKLQFTTSIEIEGRDGRTLSEVWNGGDDPRAYLGVQVAGFPNLFITAG
PNSAPNHGAGHNILSEEHVHYIVECLQYLLENGHDAMDVRQDVLDTYNRKVDAALDDTVWVHPGAE
VNGYYRNSSGRAIVPCPWRLVDYWTMLREPNPDDLTFIGRRAEGRREASAR

>MO11

MTTASIDTRELDEANGVLDVLVVGGGFAGLYQLDQLRSRGFSVKVVEAGDSLGGIWYWNCYPGART
DSTGQIYQYSREDLWKDWSYDELYPSWSGVRDYFAYVDRKLDLSRDIIFSTRVTSADFDGERNQWT
VRTDTGRMLRARSVVICTGFGAKPHIPSINGLNSFAGESHHTALWPQEGLDMAGKRVGIIGTGSSGVQ
VTQEAAADAEQITIFQRTPNLALPMRQQQLTGQLKEKLKENLPERFAQRRRSFAGFDMDFIPKSVFEV
SDEERADTYERMWATGGFELWLANYQDILLDERANRIMYDFWRDKVRQRVTDPVKAEKLAPMDPPH
PFGTKRPSLEQNFYDVVNQENVDIVDVNEDPIERITPAGVQTKSGLHEFDILVFATGFDANRGGITSIDI
RGTNDQLLSHKWSERLDTFMGLTTAGFPNLMFVYGPQSPAGFCNGPTCAEVQGEIVVDFLTHVRDG
GYQRFETSEDAEQSWTAHVEEVFHMSLFPRAKSWYHGANIPGKPSQMLNYSGGLPSYFDHWEENV
AAGYKAFTLS

>MO12

MVRSAIPVELPVDSVDHPPEVVDVLVVGAGFGGLGTAIRLKQAGIDDFVVLDRAEDIGGTWRVNTYPG
AQCDIPSILYSFSFAPNPNWTRLYPLQQEIHDYLRSCAENFGIVPHLRMGHDVQDAAWDDDSQVWHV
TTSRGTWEARILVGAMGPFSEPAVPNLPALESFRGAVFHSAAWDHEHDLAGERVAVIGTGASAVQIIP
RIQPIVGSMTVFQRTPTWILPHPDQPMTGWPRKLFARVPVAQRLARSGLDLVQEAMVPGFVYKPALL
KGLAALGRAHLRRQVHDPELRTKLTPTYAFGCKRPTFSNSFYPALAQPNVDVITDGIREVRSNGIVTE
DGVLHEVDTIVMGTGFRLTDNPAFDVVRGRDGRTLAEAWNGNARAYLGTTISGFPNFFMLLGPNSVV
YTSQVVTIEAQIAYILSCLQEMNAQGAASIDVRPEIQQAFVDEVDERLQTSVWNTGGCNSYYLSGEGR
NFTFYPGFNRRFRARTRRVDLHHYIISGAGASAKSIVRTAG

>MO13

MKHITTSHDSDQETPVTITTIPEVETMDFDVLIIGAGISGIGAAYHLKTRRPDTTFAILEGKDAIGGTWTQ
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TVTAQRSGSDETVQITARFLFSGTGYYNHEAGFTPEFDGIEDFTGQVVHPQHWPEELDYSGKKVVVI
GSGATAATLIPAMAGTAAHITMLQRSPSYVLSLPAEDAIANTLNKLIGPKRAYPIIRRKNIMMHRGIFKAC
RRSPKLMRKLLIANARRQLPKNFDVDTHFTPRYNPWDQRLCMVPNGDLFKAISTGHASVVTDRIERFT
ATGIRLESGQELEADIVVTATGLNMLAFGAIQLSVDGEPVNPPDTTVYKSMMLSGLPNFVFALGYTNIS
WTLKVDLISEHFCRLLDHMDERGYTTVEPVLTDPGMERVPLLDLTSGYVQRAVAAFPRAGTSGPWTA
AMAYEKDVERLREGPIEDADLRFTANQPALLAS

>MO14

MSKTISADVDVVVVGAGFAGLYALRKLRDTMKLSTRVFEAGSEVGGTWFWNRYPGARCDIESVHYS
YSFDEDLQQEWQWSERFAGQPEILRYLEHVADRFDLRKDITFDTRVVGVHWDDENSVWTVRTDDGA
VVRSRYFISGAGNLSVPKTPEFGGIDNFRGEVLLTGNWPREGADFTGKRVAVIGTGASGIQAIPFIAED
AAELVVFQRTPNFATPLGNGPMDPNELADIKSNYADVRTAARNHFLGVPFNQVQPSALAVDAEERRR
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KWEHGPRTYLGIMVNEFPNLFLITGPQSPSVLYNMPLAIEDHVDFATDAIDYLDRRDLDVIEPTAQAES
DWGALTNEIADQTLLPETNSWYMGANIPGKPRACMVYLGGAPTYRATCDEVVAGGYSGFALTRAEA
RAASTVS

>MO15

MSARTEVDARANRIGDVDAVVVGAGFAGLYAVHKLRSLGLTVQGVEAAGGVGGTWFWNRYPGARC
DVESVDYSYSFSRELEQEWDWSEKYATQPEILAYINHVADRFDLRDRFLFGTRVTSAELDEESLRWE
VRTDRGDVLSARYCIFATGALSTANMPNIAGRESFTGDTHHTGQWPHEGVDFTGRRVGIIGTGSSGIQ
SIPLIAEQAEHLYVFQRSANYSVPAGNQAWDDEMRRAIKAGYEERRRLSRESGGGSPYNAHPKSALD
VSDEERREAYETRWKLGGVLFAKTFPDQTKTEAANATAREFAEEKIRLLVDDPAVADKLIPNDHPIGTK
RIVTDTHYFETYNRPNVTLVDLKAAPIESITPSGITTADADYALDTLVFATGFDAMTGALDRMRIVGRGG
VPLSEYWSEGPKTYLGLGVPGFPNLFVVTGPGSPSVLANMVLGAEQHVDWIADCIEHLWEKDYDAIE
ASVPATEQWVEHCRDLAAQTLFPLANSWYMGANIPGKPRVFMPYLGGFGAYGRICADVAEEGFRGF
EFSRSRTRLADPVG

>MO16

MSHTETAAETTGAKTPVEHVDVLIIGAGLSGIGAAYHLQDNFPRRTYAILESRESIGGTWDLFRYPGIR
SDSDMYTLGYRFKPWSGEKSIADGPSILEYVKDTAAEHGIDRNIRFRHKVVRAEWSTADSHWTVDAE
RTDTGETVRLTADFLMSCSGYYRYDEGYTPEFPGLDRFGGRVVHPQQWPEDLDYEGKRVVIIGSGA
TAVTLAPSMAADAAHVTMLQRSPTYIISMPAKDKLANKLRRHLPAKLAYGLTRLKNASVATAIYQLCQR
YPEFMKGRIRQLQEKWLPKGYDIDTHFTPRYNPWDQRLCLVPNGDLFRAIRNDEVSIVTDHIDTFTET
GITLKSGEELHADVVVTATGLNLLAFGGMTLAVDGHDIDLTETMAYKGMMLSGVPNFAFVIGYTNASW
TLKADLVCEYVCRLLAHMDANGFTQCAPERDSSVEEEPFLDFAAGYVLRSVESFPKQGSKAPWRLR
MNYFRDLVALRHGKILDDAMTFSRP

>MO17

MTTGTTEPDVLVVGTGFAGLCMAIKLKEAGEENVVVLEKADRVGGTWRENTYPGCGCDVMSLMYSF
SFAPNRKWTRMYARQPEILDYIERVVRDYDLAPHIRFGAEVISYEFDETTDRWRVETRSGSVYHPRIV
VAGPGPLHKPSVPDLPGRKSFSGVAFHSAEWDHSVDLTGKRVAVVGTGASAVQFVPEVAKTAAHVD
VFQRTPHWILPKLDRPITAGEKAVFKAVPGVQKAYRGAIYWSHESLIAGFLHPRLMTVLESAARGLLRR
QVRDPELRATLTPDYIIGCKRILVSSNFYPALQRGNVDLVTSGISEVTERGIRTDDGTMHEADVIVYGT
GFAAGDRFENEHIVGRRGLTIQRAWRDGMEAYLGVAVAGFPNFFLMMGPNSGGGNQSIVFVIEAQA
HYITRCLALMKKRDATRIEVRAGAQREFNRVVHRKLAGSVWNSGGCDSWYLDSTGHNRAAWPGSS
ASYWRRMRTPDDRHFELSSLAEREDDTEYRGPGVLTSGDLTVAVEVFLNGHIEPLDGLYHWYGRVV
GDGVDAAKGRNRTPLFLTIGDGPEVPAALAERDPWGHFRIAGVGTPPFPLAPVEVEVPISRAKLASAE

>MO18

MKAAQQVQEAGAATDDRINPDRLTESEIRTAVARANVPSLLMVVFQTTGDEKWLAAPYRPTRGKGLG
DHDSGGLEEPIQDEIREAAVKAILDLQNGALPAVETPSPELTVRMISVCTGEEVGEEYGPMLSLELARR
AAPDAPSLALEPVDAPEGYSVVVIGTGVAGIAAAQQLEDMGIDYVILEKQPEAGGNWWQNTYPGAGV
DTPSHLYSFSFAKNDWTTHFELRNELQAYFGAVLKDLGAGERVRYGTEVRSTRYDEAAAQWSVDMI
NPDGSSSTLRADVVISAVGVLNRPKTPNVPGMDSFTGTSFHSAAWPDDLDLDGKRVAIVGTGASSMQ
IAPAIADRVAHLSIYQRSPQWVAPFEKFRAPIPMELRRLMQTCPIYHSWYWIRLFWQFGDKVIESLRVD
PEWEHPERSVNARNDAHREYFTRYITSQVGDRTDLLDKVMPDYPPFGKRILLDNGWYSTLRKDNVDL
VDRSVTAVRPEGLVDDQGAENDVDVIVWATGFEAARFVSSMDVVGMDGRTLREVWNDDDPKAYLG
VSVPGFPNFFMLGGPNSFPGSGSFMFFMEVQMRYIRGLLTEMFKKGIKAIDARPEANEEYNELVDST
HARTVWTHRGMSTYYRNSHGRVVFVMPFLNVEYWQMTRRPDLENYTAR

>MO19

MTATTTQHAAAPDGGGDERHLRVVVVGAGLSGIAAAVKLERAGITDFVVLEKSDRVGGVWRENTYP
GCGVDIPAPVYSFSFHPNPRWRSNFALQPELLSYIEDTVDTFGLQSRISMQTDVREAAWSDERRRWI
LDTSRGTIVAQHVIFAAGPITEPSTPAVPGIDRFDGDVFHSARWNHDVDLTGKRVAVVGTGASAVQFIP
EIQPDVEELYVFQRTPAWVVPRLDFPFPRIAQWAFARVPAVQRALRRLLDVILRTLTWVMRCERTARL
LNPIGTRWLARQVPDPALRAALTPNFTLGCKRLLLSNTYLPALTKSNVELIPHALAEVDGRVVVGADGT
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RREVDVIIFGTGFDVSHPPIASRIRGRDGTLLSEKWSKSPEAYLATTTPGAPNAYIMLGPNILVYNSFLG
LAETQLDYVIDGLTTAERQGIEVLEVRDQPFRRFNDAVQKGLEPTVFNNGGCSSYYLDADGRNFAAW
PWSTGSLRRRLARFDLENYAIRPYRTEQSPALHPSGKSR

>MO20

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QWTARSADGKVQNARQVIVATGFGAKPLYPNLEGLDLFAGDCYHTARWPQEGVDMTGRKVVVMGT
GSSGVQVVQEAGHVAEHVTVFQRTPNLAIPMQQRALTHDDNEQFRKGLPERFEARYKAFAGFDFDF
LPQNAADLSMEERDAIYEKMWAEGGFEMWLGNFQDILVDEDANRTFYDFWRNKVLERVTDPKKAAIV
APETPPHPYGVKRPSLEQDYFDVINQSNVEVIDSNLTPIRRVLPHGIETDDGVIECDLLVLATGFDNNS
GGIMAIDITGVDGLSIQDKWKSGVDTCMGLSTRGFPNMMFLYGPQSPSGFCNGPTSAEYQGEIVVEF
LQHLRDNGITRFENTEESEKQWRAHVDELFVNSMFTKARSWYWGANVPGKPAQMLNYSGGVPQYF
ARWDKIKANGYAAFETN

>MO21

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RTDRGETITTRFLVTCSGMLSAPMSYVFEGQEEFSGPIFHTSRWPKEGADLDGKRVAVIGVGATGIQV
IQTVADKVEHLKVFIRTPQYALPMKNPTFDESDVAAYKSRFAELKETLPNTFSGFEYDFEHVWADLTP
EQRNDVLEEIYENGSLKLWLASFGEMFYDEEISEEISEFVRRKMRARLQDPHLCDLLIPTDYGFGTHR
VPLETNYLETYHRPNVEAIGVRDNPITRIVPQGLVLADGTLHEVDVIVMATGFDAGTGSLTRIDIRGRG
GRALKDDWNRDIRTTMGLMVHGYPNMLTTGAPLAPSAALCNMTTCLQQQTEWIAECIRYMRAHDHT
VIEPTLAGEDEWVAHHDETANATLVSKTDSWYNGANVPGKPRRVLSYIGGVGTYREKTLAAAAAGYK
GFQLS

>MO22

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TKATNIRIAEDRTPPRLVERAGIPCLEVIFEFDTLAGSAVGVARLVDVPERGLLVRSLFTTLDQLADHPE
RTGEHRPVGQADSSKFGGPNWLDRRIAAQAYENRDPDVLIVGGGQSGLTLAARLGQLDVDALVVDT
HARPGDNWRTRYHALTLHNAVWLNDLPYMPFPATWPQFVPKDKLAGWFEAYVEAMEINFWGTTAFI
GGDYDEQSQSWVARVRRGDGTVRTLRPKHVVIATGVSGIPYVPELPGLSQFAGRTLHSSEYDDAND
FAGQRVVIIGTGNSAHDVAQDLHAHGIDVTMVQRSSTTIVSVDPSAAAADASYLTAPTLEDCDLLSMAT
VYPDLYTGSQMITATMKELDKDLVAALNRIGFRTDYGEEDTGQQMKFMRRGGGYYLNVGCSDLLISG
QVGLVQYADTAGFVAEGLSLTNGDVVEADAVILATGYQTQQEGVRALLGDEIADAVGPIWGYDDEGE
VRNTWRRTAQPGLWFSSGNFQLCRIYSKVLAMQIRTELDNG

>MO23

MSTTASAPTETSATESLELDALIIGAGVAGLYQLHQLREQGLRVRAYDTAGDVGGTWYWNRYPGARF
DSEAYIYQYLFSEELYKNWSWSQRFPGQPEIERWMHYVADTLDLRRDIQLSTMITSAHYDERADKWIV
RTDRGETITTRFLVTCSGMLSAPMSYVFEGQEEFSGPIFHTSRWPKEGADLDGKRVAVIGVGATGIQV
IQTVADKVEHLKVFIRTPQYALPMKNPTFDESDVAAYKSRFAELKETLPNTFSGFEYDFEHVWADLTP
EQRNDVLEEIYENGSLKLWLASFGEMFYDEEISEEISEFVRRKMRARLQDPHLCDLLIPTDYGFGTHR
VPLETNYLETYHRPNVEAIGVRDNPITRIVPQGLVLADGTLHEVDVIVMATGFDAGTGSLTRIDIRGRG
GRALKDDWNRDIRTTMGLMVHGYPNMLTTGAPLAPSAALCNMTTCLQQQTEWIAECIRYMRAHDHT
VIEPTRAGEDEWVAHHDETANATLVSKTDSWYNGANVPGKPRRVLSYIGGVGTYREKTLAAAAAGYK
GFQLS

S2. Full amino acid sequence alignment of soluble BVMOs from *R. jostii* RHA1 and other sequences of enzymes used to create the phylogram in Figure 1, derived using default parameters in ClustalW.[22]

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BVMO_Pf           ------------------------------------------------------------
BVMO_Rv3049c      ------------------------------------------------------------
HAPMO             ----------MSAFNTTLPSLDYDDDTLREHLQGADIPTLLLTVAHLTGDLQILKPNWKP 50
MO10              --MTETIAAGLAVPSD-------RDAQLYNAIAESDPAPLLMALVHATGDTGLLDEFGAR 51
MO18              MKAAQQVQEAGAATDDRINPDRLTESEIRTAVARANVPSLLMVVFQTTGDEKWLAAPYRP 60
CHMO_arthro       ------------------------------------------------------------
CHMO_rhodo1       ------------------------------------------------------------
CHMO-brachy       ------------------------------------------------------------
CHMO_Xantho       ------------------------------------------------------------
CHMO_9871         ------------------------------------------------------------
MO9               ------------------------------------------------------------
MO15              ------------------------------------------------------------
MO14              ------------------------------------------------------------
PAMO              ------------------------------------------------------------
CHMO_Brevi1       ------------------------------------------------------------
BVMO_mekA         ------------------------------------------------------------
MO21              ------------------------------------------------------------
MO20              ------------------------------------------------------------
CHMO_Brevi2       ------------------------------------------------------------
MO11              ------------------------------------------------------------
CPMO              ------------------------------------------------------------
MO3               ------------------------------------------------------------
MO4               ------------------------------------------------------------
BVMO_EtaA         ------------------------------------------------------------
MO16              ------------------------------------------------------------
BVMO_KT2440       ------------------------------------------------------------
CPDMO             ------------------------------------------------------------


BVMO_Pf           ------------------------------------------------------------
BVMO_Rv3049c      ------------------------------------------------------------
HAPMO             SIAMGVARSG---------MDLETEAQVREFCLQRLIDFRDSGQPAPGRPTSDQLHILGT 101
MO10              LTIEEPGNHYRTGIRPTAPPGIYPEDVAEDIRIRAREILTPDVVAELGVPDDELFVRMAT 111
MO18              TRGKGLGDHDSGGLEEPIQDEIREAAVKAILDLQN------GALPAVETPSPELTVRMIS 114
CHMO_arthro       -----------------------------------------MSTRSWPGGPPSWHRSSTS 19
CHMO_rhodo1       ------------------------------------------------------------
CHMO-brachy       ------------------------------------------------------------
CHMO_Xantho       ------------------------------------------------------------
CHMO_9871         ------------------------------------------------------------
MO9               ------------------------------------------------------------
MO15              ------------------------------------------------------------
MO14              ------------------------------------------------------------
PAMO              ------------------------------------------------------------
CHMO_Brevi1       ------------------------------------------------------------
BVMO_mekA         ------------------------------------------------------------
MO21              ------------------------------------------------------------
MO20              ------------------------------------------------------------
CHMO_Brevi2       ------------------------------------------------------------
MO11              ------------------------------------------------------------
CPMO              ------------------------------------------------------------
MO3               ------------------------------------------------------------
MO4               ------------------------------------------------------------
BVMO_EtaA         ------------------------------------------------------------
MO16              ------------------------------------------------------------
BVMO_KT2440       ------------------------------------------------------------
CPDMO             ----------------------------MSQLIQEPAEAGVTSQKVSFDHVALREKYRQE 32


BVMO_Pf           ---------------------------------MNAHSDSIDIAIIGSGFAGLCMAIKLK 27
BVMO_Rv3049c      ------------------MSIADTAAKPSTPSPANQPPVRTRAVIIGTGFSGLGMAIALQ 42
HAPMO             WLMGPVIEPYLPLIAEEAVTAEEDLRAPRWHKDHVASGRDFKVVIIGAGESGMIAALRFK 161
MO10              VCTSQRVDAEFAPIL---LEQAGFTKNRRHVPVTVAPPADFDVIVIGAGIVGINAGIKLG 168
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MO18              VCTGEEVGEEYGPMLSLELARRAAPDAPSLALEPVDAPEGYSVVVIGTGVAGIAAAQQLE 174
CHMO_arthro       SRPGTGNNPATLRSHTIHYFVPCIRTTKEFAMTAQNTFQTVDAVVIGAGFGGIYAVHKLH 79
CHMO_rhodo1       -------------------------------MTAQISPTVVDAVVIGAGFGGIYAVHKLH 29
CHMO-brachy       ------------------------------MSSSPSSAIHFDAIVVGAGFGGMYMLHKLR 30
CHMO_Xantho       --------------------------MTMTVEKTRTGGADYDAVVVGAGFGGLYAVHKLR 34
CHMO_9871         ----------------------------------MSQKMDFDAIVIGGGFGGLYAVKKLR 26
MO9               ------------------------------MTVQDN---DFDAVVVGAGISGLYAVYKLR 27
MO15              ------------------------MSARTEVDARANRIGDVDAVVVGAGFAGLYAVHKLR 36
MO14              ------------------------MSKTISAD--------VDVVVVGAGFAGLYALRKLR 28
PAMO              ------------------------MAGQTTVDSRRQPPEEVDVLVVGAGFSGLYALYRLR 36
CHMO_Brevi1       --------------------------------MPITQQLDHDAIVIGAGFSGLAILHHLR 28
BVMO_mekA         ---------------------MSAQSKLAAGSCAYGNVTSLDAMVIGAGVAGLYQLYRLR 39
MO21              ---------------------MSTTASAPTETSAT-ESLELDALIIGAGVAGLYQLHQLR 38
MO20              --------------------MTASQADTATRTGKHSNNDVLDVLIIGGGFSGLYALDRIR 40
CHMO_Brevi2       --------------------MTSTMPAPTAAQANADETEVLDALIVGGGFSGPVSVDRLR 40
MO11              --------------------MTTASIDTRELDEANG---VLDVLVVGGGFAGLYQLDQLR 37
CPMO              --------------------TTMTTMTTEQLGMNNSVNDKLDVLLIGAGFTGLYQLYHLR 40
MO3               --------------------------------MNTTLLEELDVLVIGGGFSGVYQLDRLR 28
MO4               ---------------------MTAIHAPKNDLAQSAETPTYDVIVVGGGFGGIYQLRHLR 39
BVMO_EtaA         ------------------------------------MTEHLDVVIVGAGISGVSAAWHLQ 24
MO16              ---------------------MSHTETAAETTGAKTPVEHVDVLIIGAGLSGIGAAYHLQ 39
BVMO_KT2440       -----------------------------MSSHTALPVEPLDVLIMGAGVSGIGAAAYLR 31
CPDMO             RDKRLRQDGQEQYLEVAVTCDEYLKDPYADPIVRDPVVRETDVFIIGGGFGGLLAAVRLQ 92
                                                              ::* *  *      :

BVMO_Pf           E-AGFTDLFVAEQADTLGGTWRDNHYPGCACDVQSHVYSFSF----APNPDWTRQFAPQA 82
BVMO_Rv3049c      K-QG-VDFVILEKADDVGGTWRDNTYPGCACDIPSHLYSFSF----EPKADWKHLFSYWD 96
HAPMO             Q-AG-VPFVIYEKGNDVGGTWRENTYPGCRVDINSFWYSFSF----ARG-IWDDCFAPAP 214
MO10              E-AG-FRYTIIEEREDVGGTWYRNTYPGAAVDTPSHYYSYSF----ELNPNWSKYYPTGP 222
MO18              D-MG-IDYVILEKQPEAGGNWWQNTYPGAGVDTPSHLYSFSF----AKN-DWTTHFELRN 227
CHMO_arthro       N-EQGLTVVGFDKADGPGGTWYWNRYPGALSDTESHVYRFSFDKGLLQDGTWKHTYITQP 138
CHMO_rhodo1       N-EQGLTVVGFDKADGPGGTWYWNRYPGALSDTESHLYRFSFDRDLLQDGTWKTTYITQP 88
CHMO-brachy       D-QLGLKVKVFDTAGGIGGTWYWNRYPGALSDTHSHVYQYSFDEAMLQEWTWKNKYLTQP 89
CHMO_Xantho       N-EQGMNVKAYDNAADIGGTWFWNRYPGAVSDTESFVYRFSFDRELLQRGRWKNRYVTQP 93
CHMO_9871         D-ELELKVQAFDKATDVAGTWYWNRYPGALSDTETHLYCYSWDKELLQSLEIKKKYVQGP 85
MO9               --QRGMRVHGFESAEGVGGTWYHNRYPGARCDVESIDYSYSFDEELQQEWTWTERFATQD 85
MO15              --SLGLTVQGVEAAGGVGGTWFWNRYPGARCDVESVDYSYSFSRELEQEWDWSEKYATQP 94
MO14              D-TMKLSTRVFEAGSEVGGTWFWNRYPGARCDIESVHYSYSFDEDLQQEWQWSERFAGQP 87
PAMO              --ELGRSVHVIETAGDVGGVWYWNRYPGARCDIESIEYCYSFSEEVLQEWNWTERYASQP 94
CHMO_Brevi1       --EIGLDTQIVEATDGIGGTWWINRYPGVRTDSEFHYYSFSFSKEVRDEWTWTQRYPDGE 86
BVMO_mekA         --EMGLTVRAYDTASGVGGTWYWNRYPGARFDSQAEIYQYWFSEELYKSWQPTERFPAQP 97
MO21              --EQGLRVRAYDTAGDVGGTWYWNRYPGARFDSEAYIYQYLFSEELYKNWSWSQRFPGQP 96
MO20              --DLGFTAKVWDAAGGLGGIWWWNCYPGARTDSTGQIYQFSH-KDLWKKYDFAELYPGHD 97
CHMO_Brevi2       --EDGFKVKVWDAAGGFGGIWWWNCYPGARTDSTGQIYQFQY-KDLWKDFDFKELYPDFN 97
MO11              --SRGFSVKVVEAGDSLGGIWYWNCYPGARTDSTGQIYQYSR-EDLWKDWSYDELYPSWS 94
CPMO              --KLGYKVHLVDAGADIGGIWHWNCYPGARVDTHCQIYQYSI-PELWQEFNWKELFPNWA 97
MO3               --TLGYNVKIYEAGTGLGGVWHWNSYPGARVDTWAPVYQFSR-EELWRDWNWSEMYPGRD 85
MO4               --DRGFSVILLEASGGFGGAWSLNRYPGARVDSHAPVYQFTD-EYLWKDWDFSQMYPDHE 96
BVMO_EtaA         DRCPTKSYAILEKRESMGGTWDLFRYPGIRSDSDMYTLGFRF-----RPWTGRQAIADGK 79
MO16              DNFPRRTYAILESRESIGGTWDLFRYPGIRSDSDMYTLGYRF-----KPWSGEKSIADGP 94
BVMO_KT2440       RNQPNKTFAILESRERMGGTWDLFRYPGIRSDSDLYTFGFDF-----KPWTKAKSLADAA 86
CPDMO             Q-AGVSDYVMVERAGDYGGTWYWNRYPGAQCDIESYVYMPLL---EEMGYIPTEKYAFGT 148
                             :     .* *    ***   *

BVMO_Pf           EIRAYLEDCAVRFGLAPYLRFGMGLKRAVFDEQLQRWQLSFSDGR-----HVSARVLVSG 137
BVMO_Rv3049c      EILGYLKGVTDKYGLRRYIEFNSLVDRGYWDDDECRWHVFTADGR-----EYVAQFLISG 151
HAPMO             QVFAYMQAVAREHGLYEHIRFNTEVSDAHWDESTQRWQLLYRDSEGQT--QVDSNVVVFA 272
MO10              EYQNYLLDVVEKYRLREHIRFRTRVLSARWLDDEHRWEVVTEDGEGSVV-RHRARAVITA 281
MO18              ELQAYFGAVLKDLGAGERVRYGTEVRSTRYDEAAAQWSVDMINPDGSSS-TLRADVVISA 286
CHMO_arthro       EILEYLEDVVDRFDLRRHFRFGTEVKSATYLEDEGLWEVTTGGGAV-----YRAKYVINA 193
CHMO_rhodo1       EILEYLESVVDRFDLRRHFRFGTEVTSAIYLEDENLWEVSTDKGEV-----YRAKYVVNA 143
CHMO-brachy       EILAYLEYVADRLDLRPDIQLNTTVTSMHFNEVHNIWEVRTDRGGY-----YTARFIVTA 144
CHMO_Xantho       EILAYLNEVADHLDLRRSYEFNTKVSAAQFDDATGLWKVTTDKGQA-----VTAKYLITG 148
CHMO_9871         DVRKYLQQVAEKHDLKKSYQFNTAVQSAHYNEADALWEVTTEYGDK-----YTARFLITA 140
MO9               EILRYLEHVADRHDLRSAYDFLTRVTSATYDEETTRWSITTDTGQN-----VTARFCVLA 140
MO15              EILAYINHVADRFDLRDRFLFGTRVTSAELDEESLRWEVRTDRGDV-----LSARYCIFA 149
MO14              EILRYLEHVADRFDLRKDITFDTRVVGVHWDDENSVWTVRTDDGAV-----VRSRYFISG 142
PAMO              EILRYINFVADKFDLRSGITFHTTVTAAAFDEATNTWTVDTNHGDR-----IRARYLIMA 149
CHMO_Brevi1       EVCAYLNFIADRLDLRKDIQLNSRVNTARWNETEKYWDVIFEDGSS-----KRARFLISA 141
BVMO_mekA         ETEEWLNFVANRLNLKKDIQFNTRIASAHFCEDSGRWVVTTAAGET-----INTQYLISC 152
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MO21              EIERWMHYVADTLDLRRDIQLSTMITSAHYDERADKWIVRTDRGET-----ITTRFLVTC 151
MO20              GVRNYFEYVDSQLDLTRDVVFDTFAESCTWDEETRQWTARSADGKV-----QNARQVIVA 152
CHMO_Brevi2       GVREYFEYVDSQLDLSRDVTFNTFAESCTWDDAAKEWTVRSSEGRE-----QRARAVIVA 152
MO11              GVRDYFAYVDRKLDLSRDIIFSTRVTSADFDGERNQWTVRTDTGRM-----LRARSVVIC 149
CPMO              QMREYFHFADKKLDLSKDISFNTRVQSAVFDEGTREWTVRSIGHQP-----IQARFVIAN 152
MO3               ELVRYFEYVDEKLDLSKDVRYETRVLAGRFDEETHRWTLVSRNERTGEEFTTQAQFVIMC 145
MO4               EMRSYFNYVDSKLDLSKDSRFNTKVVGATFDEEQRMWSLETQDGAT-----FRARFVVFA 151
BVMO_EtaA         PILEYVKSTAAMYGIDRHIRFHHKVISADWSTAENRWTVHIQSHGT--LSALTCEFLFLC 137
MO16              SILEYVKDTAAEHGIDRNIRFRHKVVRAEWSTADSHWTVDAERTDTGETVRLTADFLMSC 154
BVMO_KT2440       DILEYLSEAIDEHQLAPFIQYQQKVISANWQSDKGLWSVRVEDGRTAQIRTVECRWLFSA 146
CPDMO             EILEYSRSIGRKFGLYERTYFQTEVKDLSWDDEAARWRITTDRGDK-----FSARFVCMS 203
                      :                               *

BVMO_Pf           MGAL--ARPALPEIPGLETFKGKRFHSQQWD---HAYALKG-------KRVAVIGTGASA 185
BVMO_Rv3049c      AGAL--HIPSFPEIAGRDEFAGPAFHSAQWD---HSIDLTG-------KRVAIVGTGASA 199
HAPMO             VGQL--NRPMIPAIPGIETFKGPMFHSAQWD---HDVDWSG-------KRVGVIGTGASA 320
MO10              MGML--NAANIPEVDGLDSFAGRVVHTAEWD---SDLDLSG-------KRVVVLGTGCTS 329
MO18              VGVL--NRPKTPNVPGMDSFTGTSFHSAAWP---DDLDLDG-------KRVAIVGTGASS 334
CHMO_arthro       VGLL--SAINFPNLPGIDTFEGETIHTAAWP---QGKSLAG-------RRVGVIGTGSTG 241
CHMO_rhodo1       VGLL--SAINFPDLPGLDTFEGETIHTAAWP---EGKNLAG-------KRVGVIGTGSTG 191
CHMO-brachy       LGLL--SAINWPNIPGRESFQGEMYHTAAWP---KDVELRG-------KRVGVIGTGSTG 192
CHMO_Xantho       LGLL--SATNLPKFKGMDTFKGRILHTGAWP---EGVELAG-------KRVGIIGTGSTG 196
CHMO_9871         LGLL--SAPNLPNIKGINQFKGELHHTSRWP---DDVSFEG-------KRVGVIGTGSTG 188
MO9               TGVL--SATNKPDIPGRDTFGGATYHTGEWPH--EPVDFAG-------KRVGVIGTGSSG 189
MO15              TGAL--STANMPNIAGRESFTGDTHHTGQWPH--EGVDFTG-------RRVGIIGTGSSG 198
MO14              AGNL--SVPKTPEFGGIDNFRGEVLLTGNWPR--EGADFTG-------KRVAVIGTGASG 191
PAMO              SGQL--SVPQLPNFPGLKDFAGNLYHTGNWPH--EPVDFSG-------QRVGVIGTGSSG 198
CHMO_Brevi1       MGAL--SQAIFPAIDGIDEFNGAKYHTAAWPA--DGVDFTG-------KKVGVIGVGASG 190
BVMO_mekA         CGML--SAPLSDRFPGQADFQGQIYHTGLWPK--DPVDFNG-------KRVAVVGTGATG 201
MO21              SGML--SAPMSYVFEGQEEFSGPIFHTSRWPK--EGADLDG-------KRVAVIGVGATG 200
MO20              TGFG--AKPLYPNLEGLDLFAGDCYHTARWPQ--EGVDMTG-------RKVVVMGTGSSG 201
CHMO_Brevi2       TGFG--AKPLYPNIEGLDSFEGECHHTARWPQ--GGLDMTG-------KRVVVMGTGASG 201
MO11              TGFG--AKPHIPSINGLNSFAGESHHTALWPQ--EGLDMAG-------KRVGIIGTGSSG 198
CPMO              LGFG--ASPSTPNVDGIETFKGQWYHTALWPQ--EGVNMAG-------KRVAIIGTGSSG 201
MO3               LGAG--SKPLFPNIPGLEKFGGDCFHTARWPL--EGYDLAG-------KRVAVIGTGASG 194
MO4               TGST--TEPYTPSIPDMDAYQGELVHTARWR---SDLDMTG-------KRVAIIGTGASA 199
BVMO_EtaA         SGYYNYDEGYSPRFAGSEDFVGPIIHPQHWP---EDLDYDA-------KNIVVIGSGATA 187
MO16              SGYYRYDEGYTPEFPGLDRFGGRVVHPQQWP---EDLDYEG-------KRVVIIGSGATA 204
BVMO_KT2440       GGYYRYDQGFSPRFEGSEQFKGQIIHPQHWP---EDLDYTG-------KRVVVIGSGATA 196
CPDMO             TGPLQ--RPKLPGIPGITSFKGHSFHTSRWDYSYTGGDQTGNLEGLKDKRVAIIGTGATS 261
                   *           . .   : *    .  *          .       :.: ::* *.:.

BVMO_Pf           IQFVPQIAPQ-VAHLDLFQRTPPWIMPKP--DRGISAFERWLFRHLPV-TQRLVRGAFYW 241
BVMO_Rv3049c      IQIVPEIVGQ-VAELQLYQRTPPWVVPRT--NEELPVSLRRALRTVPG-LRALLRLGIYW 255
HAPMO             TQFIPQLAQT-AAELKVFARTTNWLLPTPDLHEKISDSCKWLLAHVPH-YSLWYRVAMAM 378
MO10              VQVVANIVDQ-VEALDVVVRSPHWLVPEKAVSGDVTEGEKWALANLPF-YDRWFRLRSYW 387
MO18              MQIAPAIADR-VAHLSIYQRSPQWVAPFEKFRAPIPMELRRLMQTCPI-YHSWYWIRLFW 392
CHMO_arthro       QQVITALAPE-VEHLTVFVRTPQYSVPVGKRPVTTQQIDEIKADYDNI-WAQVKRSGVAF 299
CHMO_rhodo1       QQVITALAPE-VEHLTVFVRTPQYSVPVGNRPVTKEQIDAIKADYDGI-WDSVKKSAVAF 249
CHMO-brachy       VQLITAIAPE-VKHLTVFQRTPQYSVPTGNRPVSAQEIAEVKRNFSKV-WQQVRESAVAF 250
CHMO_Xantho       VQVITATAPI-AKHLTVFQRSAQFVVPIGNTPQDAETIARQKATYDDI-WKQVKSSAVAF 254
CHMO_9871         VQVITAVAPL-AKHLTVFQRSAQYSVPIGNDPLSEEDVKKIKDNYDKI-WDGVWNSALAF 246
MO9               IQSIPVIAEE-AAEVFVFQRSPNYSIPAGNRPLTGEYIAEVKANYAER-RRLSRMSGGGT 247
MO15              IQSIPLIAEQ-AEHLYVFQRSANYSVPAGNQAWDDEMRRAIKAGYEER-RRLSRESGGGS 256
MO14              IQAIPFIAED-AAELVVFQRTPNFATPLGNGPMDPNELADIKSNYADV-RTAARNHFLGV 249
PAMO              IQVSPQIAKQ-AAELFVFQRTPHFAVPARNAPLDPEFLADLKKRYAEF-REESRNTPGGT 256
CHMO_Brevi1       IQIIPELAKL-AGELFVFQRTPNYVVESNNDKVDAEWMQYVRDNYDEI-FERASKHPFGV 248
BVMO_mekA         IQVIQTIAPT-VGSMTVFVRTPQYVIPMRNPKYSKADWEKWGTQFHQL-KKRVRETFAGF 259
MO21              IQVIQTVADK-VEHLKVFIRTPQYALPMKNPTFDESDVAAYKSRFAEL-KETLPNTFSGF 258
MO20              VQVVQEAGHV-AEHVTVFQRTPNLAIPMQQRALTHDDNEQFRKGLPER-FEARYKAFAGF 259
CHMO_Brevi2       IQVIQEAAAV-AEHLTVFQRTPNLALPMRQQRLSADDNDRYRENIEDR-FQIRDNSFAGF 259
MO11              VQVTQEAAAD-AEQITIFQRTPNLALPMRQQQLTGQLKEKLKENLPER-FAQRRRSFAGF 256
CPMO              VQVAQEAALD-AKQVTVYQRTPNLALPMHQKQLSAEDNLRMKPELPAA-FERRGKCFAGF 259
MO3               VQVIQEASKV-ADHLTVFQRTPNTALPMNQRALGEADNAEMKKTYPER-FANRKNTWAGF 252
MO4               VQVVQEAGPV-VENLTVFQRTPNISLPMQQKYLDDEEQAALKNKMPDV-AAKCRETHAAI 257
BVMO_EtaA         VTLVPALADSGAKHVTMLQRSPTYIVSQPDRDGIAEKLNRWLPETMAY-TAVRWKNVLRQ 246
MO16              VTLAPSMAAD-AAHVTMLQRSPTYIISMPAKDKLANKLRRHLPAKLAY-GLTRLKNASVA 262
BVMO_KT2440       VTLIPAMADK-VASITMLQRTPSYIINQPANDGVAAFLRKVLPAQTAY-SLTRYKNAKIT 254
CPDMO             IQAVPHLAAY-AQELYVIQRTPISVGFRGNKPTDPEWAKSLQPGWQQARMDNFNAITHGM 320
                             .  : :  *:.
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BVMO_Pf           ALEGRVLG---------------------------------FALHPQLMKMVQKVALRHL 268
BVMO_Rv3049c      AQEALAYG---------------------------------MTKRPNTLKIIEAYAKYNI 282
HAPMO             PQSVGFLEDVMVDVGYP---------------------PTELAVSARNDRLRQDISAWME 417
MO10              FASDNLYPLPRIDKEWA---------------------ATHLSASPANDMVLRTAQEYLQ 426
MO18              QFGDKVIESLRVDPEWE---------------------HPERSVNARNDAHREYFTRYIT 431
CHMO_arthro       GFEESTVPAMSVTEEERRQVYEKAWEYGGGFRFMFETFSDIATDEEANETAASFIRNKIV 359
CHMO_rhodo1       GFEESTLPAMSVSEEERNRIFQEAWDHGGGFRFMFGTFGDIATDEAANEAAASFIRSKIA 309
CHMO-brachy       GFEESTVPAMSVSEAERQRVFQEAWNQGNGFYYMFGTFCDIATDPQANEAAATFIRNKIA 310
CHMO_Xantho       GFEESTIPAETASPEERDRVFEAAWQRGGGFYFMFGTFSDIATSQVANDAAADFIKRKLK 314
CHMO_9871         GLNESTVPAMSVSAEERKAVFEKAWQTGGGFRFMFETFGDIATNMEANIEAQNFIKGKIA 306
MO9               PNSAYPKGALEVDAEERRRVYDEWWQR-GGY-LFAKAFPDQTISQAANDTAREYVEAKIR 305
MO15              PYNAHPKSALDVSDEERREAYETRWKL-GGV-LFAKTFPDQTKTEAANATAREFAEEKIR 314
MO14              PFNQVQPSALAVDAEERRRTFDERWNA-GGFRLFIDSYQDILFDKKANDTIADYIRDRIH 308
PAMO              HRYQGPKSALEVSDEELVETLERYWQE-GGP-DILAAYRDILRDRDANERVAEFIRNKIR 314
CHMO_Brevi1       DMEYPTDSAVEVSEEERKRVFESKWEE-GGFHFANECFTDLGTSPEASELASEFIRSKIR 307
BVMO_mekA         DYDFDAGPWAEKTPDERQAVLEQLWKD-GSLAMWLASFPEMFFDEQVNEVVSQFVRIKMR 318
MO21              EYDFEH-VWADLTPEQRNDVLEEIYEN-GSLKLWLASFGEMFYDEEISEEISEFVRRKMR 316
MO20              DFDFLPQNAADLSMEERDAIYEKMWAE-GGFEMWLGNFQDILVDEDANRTFYDFWRNKVL 318
CHMO_Brevi2       DFYFIPQNAADTPEDERTAIYEKMWDE-GGFPLWLGNFQGLLTDEAANHTFYNFWRSKVH 318
MO11              DMDFIPKSVFEVSDEERADTYERMWAT-GGFELWLANYQDILLDERANRIMYDFWRDKVR 315
CPMO              DFDFIAKNATELSAAERTEILEELWNA-GGFRYWLANFQDYLFDDKANDYVYEFWRDKVR 318
MO3               DYDFLKENIQDLTEERRNEILEELWTN-GGLQPWLGGFLNVLFDKDDNDILYAFWRDKTR 311
MO4               DYDFDPRSGFETPEDERNAVFERLWNQ-GGFAFWLGNFSDYLFNDKTNALTYEFWKNKIK 316
BVMO_EtaA         -------------------------------------AAVYSACQKWPRRMRKMFLSLIQ 269
MO16              -------------------------------------TAIYQLCQRYPEFMKGRIRQLQE 285
BVMO_KT2440       -------------------------------------LAFWGFCQRFPKLSKKLLLWLTR 277
CPDMO             PVDVDLVQDSWTKIFGEIGVFLG---------------SDGSRAQMVDFQLMEQIRARVD 365


BVMO_Pf           RKQVPRPSLRKALTPDYT---IGCKRVLISN-DYYPALSRSNVEVVTDK---ILRIEADG 321
BVMO_Rv3049c      RRSVKDRELRRKLTPRYR---IGCKRILNSS-TYYPAVADPKTELITDR---IDRITHDG 335
HAPMO             PQFADRPDLREVLIPDSP---VGGKRIVRDNGTWISTLKRDNVSMIRQP---IEVITPKG 471
MO10              TSFTDRPDLIAKLTPDFR---PYAKRIVKDP-GFFAALNREHVSLHRAS---FEKVTPEG 479
MO18              SQVGDRTDLLDKVMPDYP---PFGKRILLDN-GWYSTLRKDNVDLVDRS---VTAVRPEG 484
CHMO_arthro       ETIKD-PETARKLTPTG----LFARRPLCDD-GYFQVFNRPNVEAVAIKENPIREVTAKG 413
CHMO_rhodo1       EIIED-PETARKLMPTG----LYAKRPLCDN-GYYEVYNRPNVEAVAIKENPIREVTAKG 363
CHMO-brachy       EIVKD-PETARKLTPTD----VYARRPLCDS-GYYRTYNRSNVSLVDVKATPISAMTPRG 364
CHMO_Xantho       QIVKD-PETARKLTPSD----LYAKRPLCGD-DYYGVYNRDNVTLADVKADPIAEFTLTG 368
CHMO_9871         EIVKD-PAIAQKLMPQD----LYAKRPLCDS-GYYNTFNRDNVRLEDVKANPIVEITENG 360
MO9               EMVTD-PDIADQLVPTDH--PIGTKRIVTDN-GYFKTFNRGNVTLVNLRRTPITEITEAG 361
MO15              LLVDD-PAVADKLIPNDH--PIGTKRIVTDT-HYFETYNRPNVTLVDLKAAPIESITPSG 370
MO14              ERVQD-PAKAATLAPTGY--AYGTKRPPLET-NYYEAFNRDSVSVVDVKSTPIDEITPTG 364
PAMO              NTVRD-PEVAERLVPKGY--PFGTKRLILEI-DYYEMFNRDNVHLVDTLSAPIETITPRG 370
CHMO_Brevi1       EVVKD-PATADLLCPKSY--SFNGKRVPTGH-GYYETFNRTNVHLLDARGTPITRISSKG 363
BVMO_mekA         ERLRSRPDLCDLLIPTD--YGFGTHRVPLEN-NYLEVYLQSNVKAVDCKQSPIERIVPQG 375
MO21              ARLQD-PHLCDLLIPTD--YGFGTHRVPLET-NYLETYHRPNVEAIGVRDNPITRIVPQG 372
MO20              ERVTD-PKKAAIVAPETPPHPYGVKRPSLEQ-DYFDVINQSNVEVIDSNLTPIRRVLPHG 376
CHMO_Brevi2       DRVKD-PKTAEMLAPATPPHPFGVKRPSLEQ-NYFDVYNQDNVDLIDSNATPITRVLPNG 376
MO11              QRVTD-PVKAEKLAPMDPPHPFGTKRPSLEQ-NFYDVVNQENVDIVDVNEDPIERITPAG 373
CPMO              ARIKD-PKVAEKLAPMKKPHPYGAKRPSLEQ-WYYEIFNQNNVTLVDVNETPVLRITEKG 376
MO3               QRITR-PELVELLAPTEPIHPWGVKRVSLEQ-NYFESLCRDNVELVDTSANPIREVASDA 369
MO4               PQIKD-PVKAELLVPEIAPHPFGAKRPALHQ-NYYEVMNQTNVSLVSTKETPIVGFTETG 374
BVMO_EtaA         RQLPEGYDVRKHFGPHYN--PWDQRLCLVPNGDLFRAIRHGKVEVVTDT---IERFTATG 324
MO16              KWLPKGYDIDTHFTPRYN--PWDQRLCLVPNGDLFRAIRNDEVSIVTDH---IDTFTETG 340
BVMO_KT2440       KELPKDYPVDVHFNPPYN--PWDQRLCSVPEGDLFKAISAGNADIVTDH---IERFTEHG 332
CPDMO             QEVKD-PATAESLKPYYN---IMCKRPGFHD-SYLPSFNKPNVTLVDTQGAGVERITEKG 420
                              . *         :                 .         .  .   .

BVMO_Pf           VITADG----IKHPADCLIFGTGFQATD-PLPRD--CIIGRDGVDLMDTW-R-DGAHAYK 372
BVMO_Rv3049c      IVTADGTGREVFREADVIVYATGFHVTD-SYTYV--QIKGRHGEDLVDRWNR-EGIGAHR 391
HAPMO             ICCVDG----TEHEFDLIVYGTGFHASK-FLMPI--NVTGRDGVALHDVWKG-DDARAYL 523
MO10              VYTTEG----AFIPADVIILATGFKLQ--FTTSI--EIEGRDGRTLSEVWNGGDDPRAYL 531
MO18              LVDDQG----AENDVDVIVWATGFEAAR-FVSSM--DVVGMDGRTLREVWND-DDPKAYL 536
CHMO_arthro       VVTEDGV----LHELDVIVFATGFDAVDGNYRRM--EISGRDGVNINDHWDG--QPTSYL 465
CHMO_rhodo1       VVTEDGV----LHELDVLVFATGFDAVDGNYRRI--EIRGRNGLHINDHWDG--QPTSYL 415
CHMO-brachy       IRTADGV----EHELDMLILATGYDAVDGNYRRI--DLRGRGGQTINEHWND--TPTSYV 416
CHMO_Xantho       IRLASGA----EHELDVVIFATGFDAVDGNYTRM--DMRGRNGVSLRDMWKE--GPLGYL 420
CHMO_9871         VKLENGD----FVELDMLICATGFDAVDGNYVRM--DIQGKNGLAMKDYWKE--GPSSYM 412
MO9               VLTTNS-----FYGLDMLVFATGFDAMTGSLSRI--DIRGRAGRNLRDEWSA--GPRTYL 412
MO15              ITTADA-----DYALDTLVFATGFDAMTGALDRM--RIVGRGGVPLSEYWSE--GPKTYL 421
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MO14              VRVGDR-----VYEVDTIVLATGFDAMTGPLMAM--DIRGRGGLPLAEKWEH--GPRTYL 415
PAMO              VRTSER-----EYELDSLVLATGFDALTGALFKI--DIRGVGNVALKEKWAA--GPRTYL 421
CHMO_Brevi1       IVHGDT-----EYELDAIVFATGFDAMTGTLTNI--DIVGRDGVILRDKWAQD-GLRTNI 415
BVMO_mekA         IQTADG-K---IHEVDIIVLAVGFDAGSGALSRI--DIRGRDSRSLKEQWQQ--EIRTAM 427
MO21              LVLADG-T---LHEVDVIVMATGFDAGTGSLTRI--DIRGRGGRALKDDWNR--DIRTTM 424
MO20              IETDDG-----VIECDLLVLATGFDNNSGGIMAI--DITGVDGLSIQDKWKS--GVDTCM 427
CHMO_Brevi2       VETPDG-----VVECDVLVLATGFDNNSGGINAI--DIK-AGGQLLRDKWAT--GVDTYM 426
MO11              VQTKSG-----LHEFDILVFATGFDANRGGITSI--DIRGTNDQLLSHKWSE--RLDTFM 424
CPMO              IVTAEG-----EAEFDLIVFATGFDAVTGGLTSI--DFRNNQGQSFKDVWSD--GIRTQL 427
MO3               IITADGT----RHEVDVIVLATGFDSVTGGLTAI--DIRGTGNETFEEVFRG--GSRTAL 421
MO4               IRTADGVE---HGEFDIIVLATGFNNNTGALTSI--DVQNANGVTLRDKWSQ--GVDAYL 427
BVMO_EtaA         IRLNSGR----ELPADIIITATGLNLQLFGGATA--TIDGQQVDIT--------TTMAYK 370
MO16              ITLKSGE----ELHADVVVTATGLNLLAFGGMTL--AVDGHDIDLT--------ETMAYK 386
BVMO_KT2440       VLLKSGK----MLKADIIVTATGLNVQLFGGITL--HKDGKPVVLS--------ETLAYK 378
CPDMO             LVVNGR-----EYEVDCLIYATGFEYQTKLSRRNGYEIHGRNGQPLSDKWKD--GLSTLW 473
                  :              * :: ..* .

BVMO_Pf           GTTVPGYPNLFLIIGPNTGLGHN-SMILMIEAQVTYILDALRQMQRHRIATVDVKPMVEQ 431
BVMO_Rv3049c      GITVANMPNLFFLLGPNTGLGHN-SVVFMIESQIHYVADAIAKCDRMGVQALAPTREAQD 450
HAPMO             GMTVPQFPNMFCMYGPNTGLVVYSTVIQFSEMTASYIVDAVRLLLEGGHQSMEVKTPVFE 583
MO10              GVQVAGFPNLFITAGPNSAPNHGAGHNILSEEHVHYIVECLQYLLENGHDAMDVRQDVLD 591
MO18              GVSVPGFPNFFMLGGPNSFPGSGS-FMFFMEVQMRYIRGLLTEMFKKGIKAIDARPEANE 595
CHMO_arthro       GVSTAKFPNWFMVLGPNGP---FTNLPPSIETQVEWISDTVAYAEENGIRAIEPTPEAEA 522
CHMO_rhodo1       GVTTANFPNWFMVLGPNGP---FTNLPPSIETQVEWISDTVAYAERNEIRAIEPTPEAEE 472
CHMO-brachy       GVSTANFPNMFMILGPNGP---FTNLPPSIEAQVEWITDLVAHMRQHGLATAEPTRDAED 473
CHMO_Xantho       GIMEAEFPNLFMILGPNGP---FTNLPPSIETQVEWIADMVKTMEAKGLKTSEPTAQARD 477
CHMO_9871         GVTVNNYPNMFMVLGPNGP---FTNLPPSIESQVEWISDTIQYTVENNVESIEATKEAEE 469
MO9               GLSVAGFPNMFILAGAGSP-SVLANMVLMAEQHVDWISNCLDYLDEHNIETIEATDESVD 471
MO15              GLGVPGFPNLFVVTGPGSP-SVLANMVLGAEQHVDWIADCIEHLWEKDYDAIEASVPATE 480
MO14              GIMVNEFPNLFLITGPQSP-SVLYNMPLAIEDHVDFATDAIDYLDRRDLDVIEPTAQAES 474
PAMO              GLSTAGFPNLFFIAGPGSP-SALSNMLVSIEQHVEWVTDHIAYMFKNGLTRSEAVLEKED 480
CHMO_Brevi1       GLTVNGFPNFLMSLGPQTP---YSNLVVPIQLGAQWMQRFLKFIQERGIEVFESSREAEE 472
BVMO_mekA         GLQIHGYPNLFTTGAPLAPSAALCNMTTCLQQQVDWITGCIEFAAEHGKHVVEASKALED 487
MO21              GLMVHGYPNMLTTGAPLAPSAALCNMTTCLQQQTEWIAECIRYMRAHDHTVIEPTLAGED 484
MO20              GLSTRGFPNMMFLYGPQSP-SGFCNGPTSAEYQGEIVVEFLQHLRDNGITRFENTEESEK 486
CHMO_Brevi2       GLSTHGFPNLMFLYGPQSP-SGFCNGTDFGGAPGDMVADFLIWLKDNGISRFESTEEVER 485
MO11              GLTTAGFPNLMFVYGPQSP-AGFCNGPTCAEVQGEIVVDFLTHVRDGGYQRFETSEDAEQ 483
CPMO              GVATAGFPNLLFGYGPQSP-AGFCNGPSSAEYQGDLLIQLMNYLRDNNISRIEAQSEAQE 486
MO3               GKATVGFPNLLYVYGPQSP-NAFCNGPTCAELEGEHLIQIVEHMRNNGYTRIEAKPEAQQ 480
MO4               GAVTAGFPNAIFVYGPQSP-AAFANGSTNAELQGEVMVDFFEFLRSNGLTRFESTVEADK 486
BVMO_EtaA         GMMLSGIPNMAYTVGYTNA-----SWTLKADLVSEFVCRLLNYMDDNGFDTVVVERPGSD 425
MO16              GMMLSGVPNFAFVIGYTNA-----SWTLKADLVCEYVCRLLAHMDANGFTQCAPER-DSS 440
BVMO_KT2440       GMMLSGVPNFAFAVGYTNS-----SWTLKVCLLCDHFCRLLGLMEREGYNVCEPKA-PEG 432
CPDMO             GYHIRDFPNCFILGNGQSA--VTPNFTHMLNEAGKHVAYVVKHCLDERVDVFEPTAEAEQ 531
                  *      **                               .

BVMO_Pf           AYNRQLQDQLKRTIWN--TGGCQS-WYLDPRTGKNTT-LWPAS--TWRFKRVTRQFALKD 485
BVMO_Rv3049c      RFNQELQRRLAGSVWN--SGGCRS-WYLD-EHGKNTV-LWCGY--TWQYWLTTRSVNPAE 503
HAPMO             SYNQRVDEGNALRAWG--FSKVNS-WYKN-SKGRVTQ-NFPFT--AVEFWQRTHSVEPTD 636
MO10              TYNRKVDAALDDTVWV--HPGAEVNGYYRNSSGRAIV-PCPWR--LVDYWTMLREPNPDD 646
MO18              EYNELVDSTHARTVWT--HRGMST--YYRNSHGRVVF-VMPFL--NVEYWQMTRRPDLEN 648
CHMO_arthro       EWTETCTQIANMTVF----TKVDSWIFGANVPGKKPS-VLFYLGGLGNYRGVLDDVTANG 577
CHMO_rhodo1       EWTQTCTDIANATLF----TRGDSWIFGANVPGKKPS-VLFYLGGLGNYRNVLAGVVADS 527
CHMO-brachy       AWGRTCAEIAEQTLF----GQVESWIFGANSPGKKHT-LMFYLAGLGNYRKQLADVANAQ 528
CHMO_Xantho       QWVELCRTIANMTLF----PKAESWIFGANIPGKKNT-VMFYLAGLGNYRKVLSGLSESG 532
CHMO_9871         QWTQTCANIAEMTLF----PKAQSWIFGANIPGKKNT-VYFYLGGLKEYRSALANCKNHA 524
MO9               EWVAECNEKAAGTLF----PTADSWYMGANIPGKPRV-FMPYIGGFGNYNTICAEVAAAG 526
MO15              QWVEHCRDLAAQTLF----PLANSWYMGANIPGKPRV-FMPYLGGFGAYGRICADVAEEG 535
MO14              DWGALTNEIADQTLL----PETNSWYMGANIPGKPRA-CMVYLGGAPTYRATCDEVVAGG 529
PAMO              EWVEHVNEIADETLY----PMTASWYTGANVPGKPRV-FMLYVGGFHRYRQICDEVAAKG 535
CHMO_Brevi1       IWNAETIRGAESTVMSIEGPKAGAWFIGGNIPGKSRE-YQVYMGGGQVYQDWCREAEESD 531
BVMO_mekA         NWVQHHDETAAKTLV----VKTDSWYMGSNVDGKPRR-LLSYIGGAGDYHRRCAEIAAQG 542
MO21              EWVAHHDETANATLV----SKTDSWYNGANVPGKPRR-VLSYIGGVGTYREKTLAAAAAG 539
MO20              QWRAHVDELFVNSMF----TKARSWYWGANVPGKPAQ-MLNYSGGVPQYFARWDKIKANG 541
CHMO_Brevi2       EWRAHVDDIFVNSLF----PKAKSWYWGANVPGKPAQ-MLNYSEASPHI----------- 529
MO11              SWTAHVEEVFHMSLF----PRAKSWYHGANIPGKPSQ-MLNYSGGLPSYFDHWEENVAAG 538
CPMO              EWSKLIADFWDSSLF----PRAKSWYQGSNIPGKKVE-SLNFPLGLPTYISKFNESAEKG 541
MO3               YWGAHIAELTSATLF----PLAKSWYMGANVPGKTVE-MLMYPGGLSVYLEILEKAAAGG 535
MO4               AWTAHINETDDTALF----NRAKSWYNGGNIPGKKMQ-MLQYLNGVPTYLQFWQKEKESG 541
BVMO_EtaA         VEERPFMEFTPGYVLR---SLDELPKQGSRTPWRLNQ-NYLRDIRLIRRGKIDDEGLRFA 481
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MO16              VEEEPFLDFAAGYVLR---SVESFPKQGSKAPWRLRM-NYFRDLVALRHGKILDDAMTFS 496
BVMO_KT2440       VETRPLLDFGAGYVQR---ALDSMPRQGPREPWVMSM-DYFRDVKLLRRGAVTDKCLKFT 488
CPDMO             AWVDHVMSFAGIKQQYDRECTPSYYNNEGQVNDVALTRNNFYPGGAVAFINILREWREKG 591


BVMO_Pf           YAVDLLPLTAPPRPATAPHSTAEGSLS 512
BVMO_Rv3049c      YRFFGIGNGLSSDRATVAAAN------ 524
HAPMO             YQLG----------------------- 640
MO10              LTFIGRRAEGRREASAR---------- 663
MO18              YTAR----------------------- 652
CHMO_arthro       YRG-FELKSEAAVAA------------ 591
CHMO_rhodo1       YRG-FELKSAVPVTA------------ 541
CHMO-brachy       YQG-FAFQPL----------------- 537
CHMO_Xantho       YPT-IIFDRAVECVA------------ 546
CHMO_9871         YEG-FDIQLQRSDIKQPANA------- 543
MO9               YKG-FELGERRVDVDQ----------- 541
MO15              FRG-FEFSRSRTRLADPVG-------- 553
MO14              YSG-FALTRAEARAASTVS-------- 547
PAMO              YEG-FVLT------------------- 542
CHMO_Brevi1       YAT-FLNADSIDGEKVRESAGMK---- 553
BVMO_mekA         YPG-FEMA------------------- 549
MO21              YKG-FQLS------------------- 546
MO20              YAA-FETN------------------- 548
CHMO_Brevi2       ---------------------------
MO11              YKA-FTLS------------------- 545
CPMO              YAG-FSLAS------------------ 549
MO3               YQEQFELV------------------- 543
MO4               YTDGLTVS------------------- 549
BVMO_EtaA         KRP-APVGV------------------ 489
MO16              RP------------------------- 498
BVMO_KT2440       AVPNAPLHADVQLQQQGSRR------- 508
CPDMO             DFAQFQQRKR----------------- 601
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S3. Gene Cloning

Table S1. Primers used for cloning the Baeyer-Villiger monooxygenase genes from *Rhodococcus* sp. RHA1 and the cyclohexanone monooxygenase gene *chnb* from *Acinetobacter* NCIMB 9871 in the pETYSBLIC-3C vector via ligation independent cloning

ORF	Forward Primers (F) and Reverse Primers (R)
RHA1_ro06679	F: CCAGGGACCAGCAATGAGCACTGCCGCACCAGCAG R:GAGGAGAAGGCGCGTTATCAGGAAAGCGTGAAGCCCTTGTATCC
RHA1_ro04304	F: CCAGGGACCAGCAATGAATCTTCCGCAGCACGTACACACC R: GAGGAGAAGGCGCGTTATCACGCGACGGTCTCCTTCG
RHA1_ro03247	F: CCAGGGACCAGCAATGAACACCACACTCCTCGAGGAGC R: GAGGAGAAGGCGCGTTATCAGACGAGTTCGAACTGCTCCTGATATC
RHA1_ro03063	F: CCAGGGACCAGCAATGACCGCAATCCACGCTCCAAAGAAC R: GAGGAGAAGGCGCGTTATCATGACACGGTCAGCCCATCG
RHA1_ro02109	F: CCAGGGACCAGCAATGGGCGGCGAGGTGCACCGGTG R: GAGGAGAAGGCGCGTTATCAGCCGGGTGTGAACTCGAAG

RHA1_ro01874	F: CCAGGGACCAGCAATGACGCATTACGACATTCTGATCGTCG R: GAGGAGAAGGCGCGTTATCATCGCGAAGTCGCTGTAGCCGAC
RHA1_ro06008	F: CCAGGGACCAGCAATGGTTTCTTACATGAGTCTCCCCGTCAC R: GAGGAGAAGGCGCGTTATCACTGTGCTGTCACCTTGTCGTCG
RHA1_ro08998 + 83 additional N-terminal amino acids in protein	F: CCAGGGACCAGCAATGGACCGTGGTGACACG R: GAGGAGAAGGCGCGTTACTACCCCTGCTGATTGCGGTAGTAC
RHA1_ro09035	F: CCAGGGACCAGCAATGACAGTCCAGGACAACGATTTCGATGC R: GAGGAGAAGGCGCGTTATCATTGGTCCACGTCCACG
RHA1_ro09039	F: CCAGGGACCAGCAATGACCGAGACCATCGCTGCAGG R: GAGGAGAAGGCGCGTTATCATCGCGCGCTCGCTTCC
RHA1_ro06698	F: CCAGGGACCAGCAATGACCACGGCATCGATCGATACGAGG R: GAGGAGAAGGCGCGTTATCAGGACAGTGTGAAGGCCTTGTAC
RHA1_ro07112	F: CCAGGGACCAGCAATGGTCAGGTCTGCAATACCG R: GAGGAGAAGGCGCGTTATCATCCTGCTGTCCTCACTATC
RHA1_ro03773	F: CCAGGGACCAGCAATGAAACACATCACAACCTC R: GAGGAGAAGGCGCGTTATCACGAGGCCAGCAGAG
RHA1_ro03437	F: CCAGGGACCAGCAATGTCAAAGACCATTTCTGCCGAC R: GAGGAGAAGGCGCGTTATCAGGACACGGTGGAGGCCGCG
RHA1_ro02492	F: CCAGGGACCAGCAATGAGTGCACGCACCGAAGTTG R: GAGGAGAAGGCGCGTTACTACCCCACCGGGTCGGCCAG
RHA1_ro02919	F: CCAGGGACCAGCAATGTCACACACCGAGACC R: GAGGAGAAGGCGCGTTATCACGGGCGGCTGAAGGTC
RHA1_ro05228	F: CCAGGGACCAGCAATGACAACCGGGACCACCGAAC R: GAGGAGAAGGCGCGTTATTATTCCGCCGAGGCGAGTTTG
RHA1_ro05396	F: CCAGGGACCAGCAATGAAGGCAGCGCAGCAGGTCCAGGAG R: GAGGAGAAGGCGCGTTACTATCGCGCGGTGTAGTTCTCCAG
RHA1_ro05522	F: CCAGGGACCAGCAATGACAGCGACAACCACTCAG R: GAGGAGAAGGCGCGTTATCATCGTGACTTTCCTGAC
RHA1_ro08137	F: CCAGGGACCAGCAATGACGGCATCCCAGG R: GAGGAGAAGGCGCGTTATCAGTTCGTCTCGAAGG
RHA1_ro10187	F: CCAGGGACCAGCAATGTCGACTACGGCTTCTGCG R: GAGGAGAAGGCGCGTTATCAGCTCAGTTGAAAACCCTTG
RHA1_ro00824	F: CCAGGGACCAGCAATGACCACCACTTTCAGTGACAC R: GAGGAGAAGGCGCGTTATCAGCCGTTGTCGAGTTCGGTG
RHA1_ro08185	F: CCAGGGACCAGCAATGTCGACTACGGCTTCTGCG R: GAGGAGAAGGCGCGTTATCAGCTCAGTTGAAAACCCTTG
chnb	F: CCAGGGACCAGCAATGTCACAAAAAATGGATTTTGATGC R: GAGGAGAAGGCGCGTTATTAGGCATTGGCAGGTTGCTTG

Table S2. DNA fragments obtained by treating the recombinant pET-YSBLIC-3C plasmids with the restriction endonucleases NcoI and NdeI

pET-YSBLIC-3C	Size (bp)	Fragment 1	Fragment 2	Fragment 3	Fragment 4
MO1	7013	5311	1248	454	
MO2	6887	5311	1576		
MO3	7028	5311	1717		
MO4	7046	5311	1735		
MO5	6872	5311	1561		
MO6	6878	5311	1567		
MO7	7010	5311	1699		
MO8	6557	5311	1246		
MO9	7022	5311	1711		
MO10	7388	5311	1723	354	
MO11	7034	5311	1546	177	
MO12	6941	5311	1630		
MO13	6944	5311	1489	144	
MO14	7040	5311	1242	487	
MO15	7058	5311	1747		
MO16	6893	5311	696	516	370
MO17	7208	5311	1897		
MO18	7355	5311	1173	442	429
MO19	6944	5311	1633		
MO20	7043	5311	1732		
MO21	7037	5311	1335	391	
MO22	7139	5311	988	840	
MO23	7037	5311	1335	391	
chnb	7028	5311	1717		

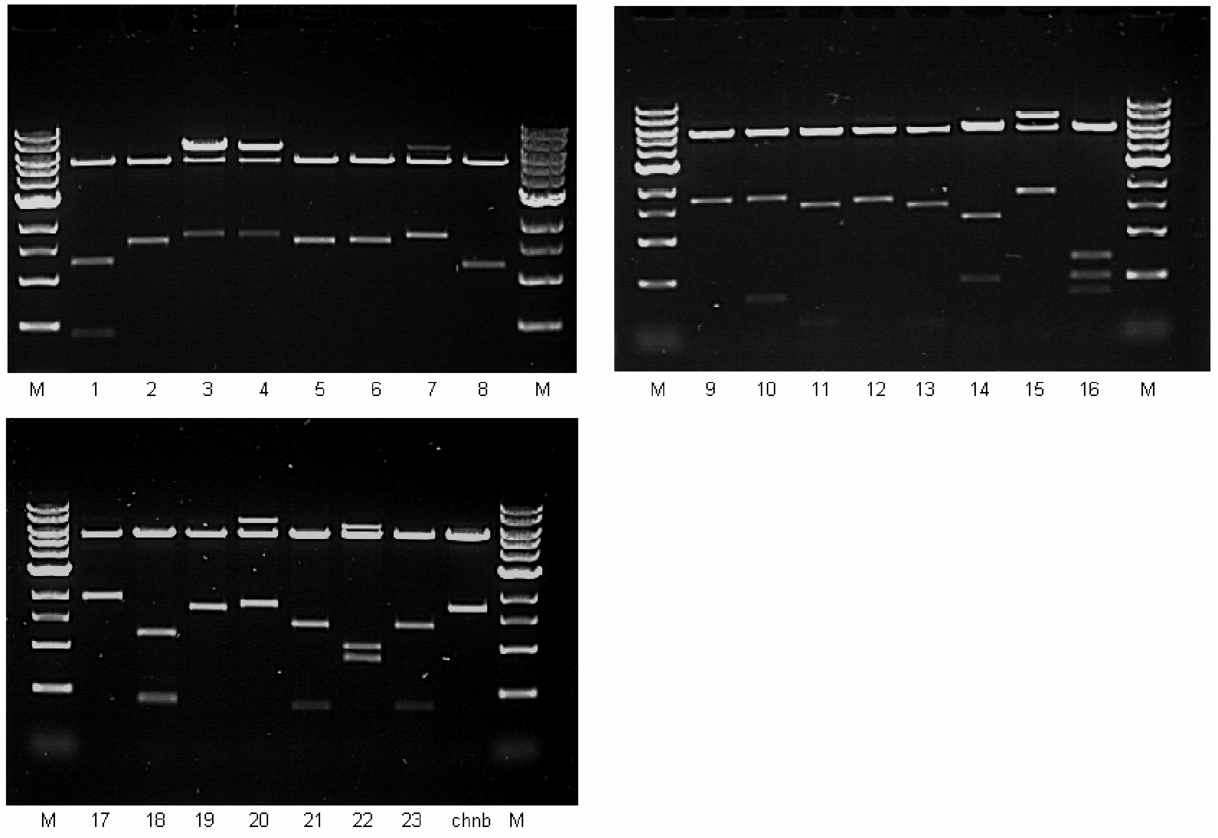

Figure S1. 0.8% (w/v) agarose gel electrophorsis of the restriction analysis of the recombinant pETYSBLIC-3C plasmids treated with the restriction endonucleases NdeI and NcoI (M = 1 kb DNA ladder from New England Biolabs (0.5, 1, 1.5, 2, 3, 4, 5, 6, 8, 10 kb), the number of each lane corresponds to the plasmid encoding MO1 to MO23 and cyclohexanone monooxygenase (*chnb* gene))

Table S3. DNA fragments obtained by treating the recombinant pET-YSBLIC-3C plasmids with the restriction endonucleases PvuI or XmaI

pET-YSBLIC-3C	Full length (bp)	Fragment 1	Fragment 2	Fragment 3	Fragment 4
MO1 (XmaI)	7013	4234	1435	1044	300
MO2 (PvuI)	6887	5048	1839		
MO3 (XmaI)	7028	7028			
MO4 (PvuI)	7046	5087	1486	293	174
MO5 (XmaI)	6872	4225	2647		
MO6 (PvuI)	6878	5216	1662		
MO7 (XmaI)	7010	4267	2270	473	
MO8 (PvuI)	6557	4520	2037		
MO9 (PvuI)	7022	4479	1443	1100	
MO10 (XmaI)	7388	4326	3062		
MO11 (XmaI)	7034	4252	2782		
MO12 (XmaI)	6941	4267	1438	653	583
MO13 (XmaI)	6944	4291	2653		
MO14 (XmaI)	7040	5676	1364		
MO15 (XmaI)	7058	4419	1468	1171	
MO16 (PvuI)	6893	4358	1719	816	
MO17 (XmaI)	7208	4857	1355	608	388
MO18 (XmaI)	7355	5734	1621		
MO19 (PvuI)	6944	4353	1677	654	260
MO20 (PvuI)	7043	5177	1866		
MO21 (XmaI)	7037	7037			
MO22 (PvuI)	7139	7139			
MO23 (XmaI)	7037	5602	1435		
chnb (XmaI)	7028	5557	1471		

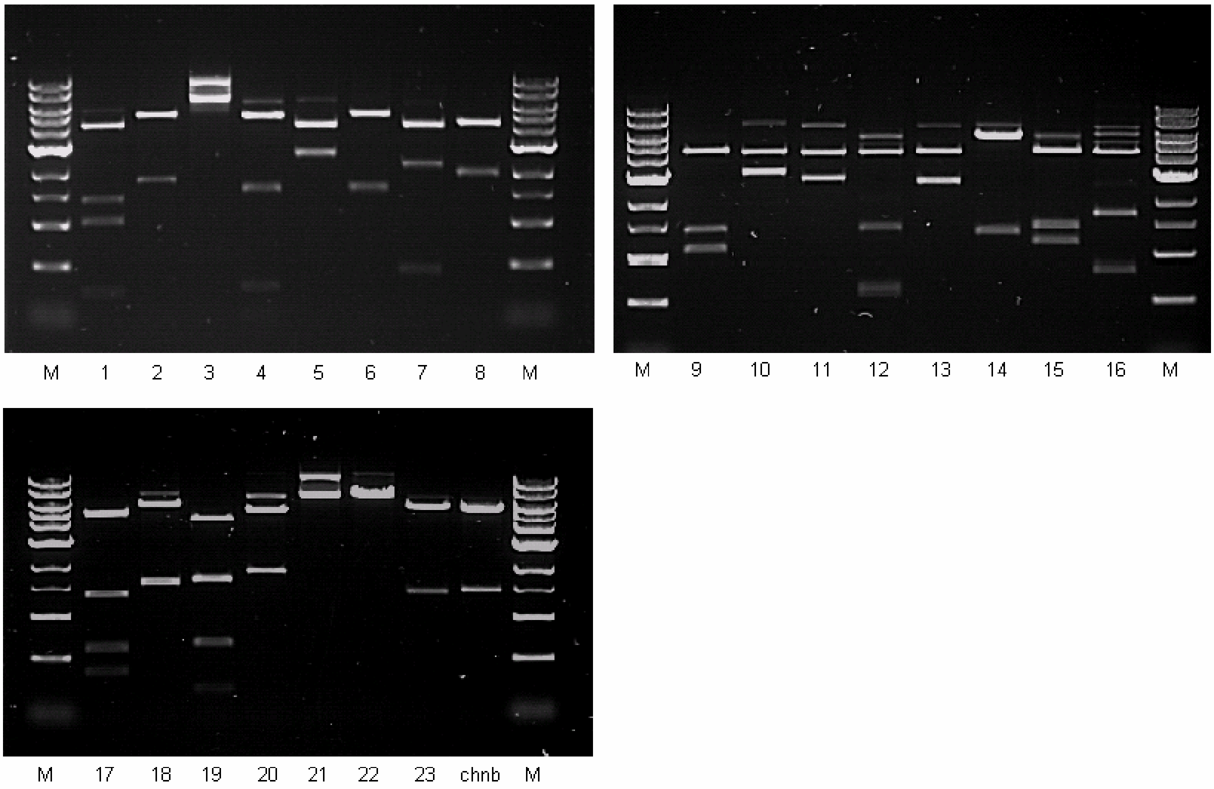

Figure S2: 0.8% (*w*/*v*) agarose gel electrophorsis of the restriction analysis of the recombinant pETYSBLIC-3C plasmids treated with the restriction endonucleases XmaI or PvuI (M = 1 kb DNA ladder from New England Biolabs (0.5, 1, 1.5, 2, 3, 4, 5, 6, 8, 10 kb), the number of each lane corresponds to the plasmid encoding MO1 to MO23 and cyclohexanone monooxygenase (*chnb* gene))

S4. Analysis of soluble overexpression by SDS-PAGE

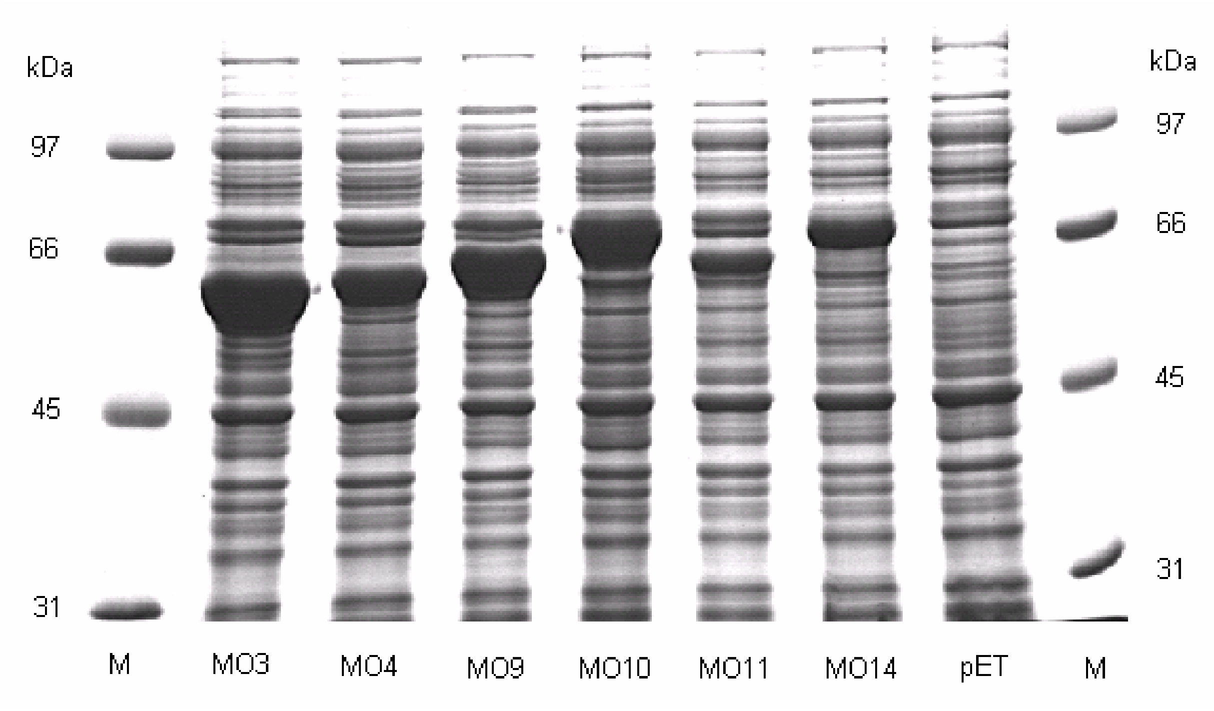

Figure S3.

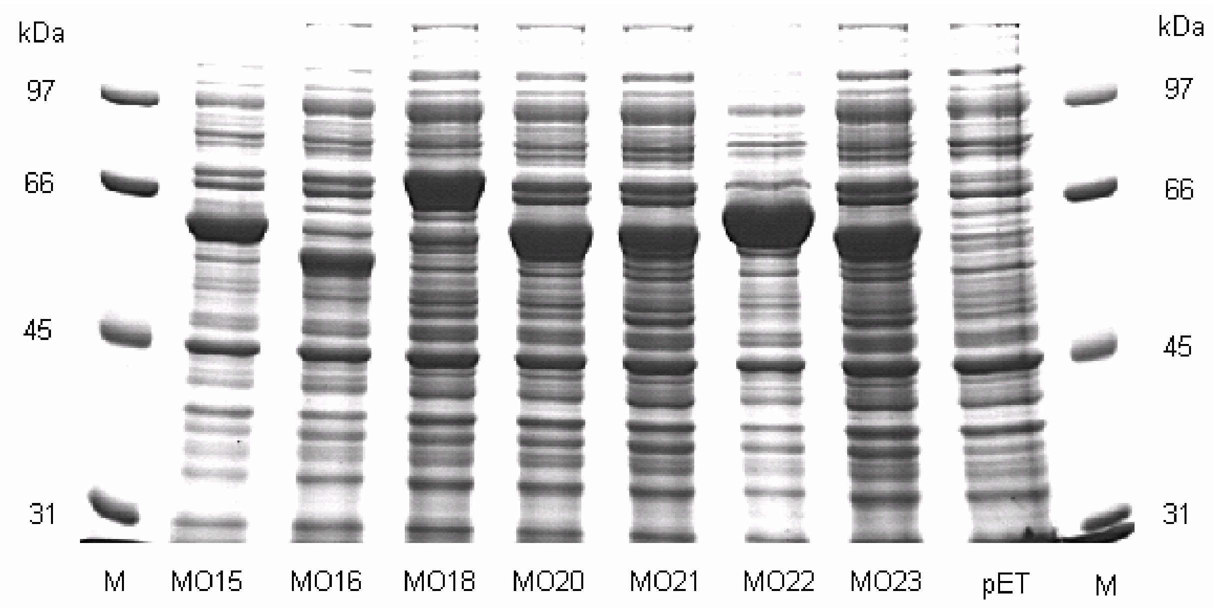

Figure S4.

S5. The fingerprint motif FXGXXXHXXXW(P/D)

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BVMO_Pf           GLETFKGKRFHSQQWD---HAYALKG-------KRVAVIGTGASA 185
BVMO_Rv3049c      GRDEFAGPAFHSAQWD---HSIDLTG-------KRVAIVGTGASA 199
HAPMO             GIETFKGPMFHSAQWD---HDVDWSG-------KRVGVIGTGASA 320
MO10              GLDSFAGRVVHTAEWD---SDLDLSG-------KRVVVLGTGCTS 329
MO18              GMDSFTGTSFHSAAWP---DDLDLDG-------KRVAIVGTGASS 334
CHMO_arthro       GIDTFEGETIHTAAWP---QGKSLAG-------RRVGVIGTGSTG 241
CHMO_rhodo1       GLDTFEGETIHTAAWP---EGKNLAG-------KRVGVIGTGSTG 191
CHMO-brachy       GRESFQGEMYHTAAWP---KDVELRG-------KRVGVIGTGSTG 192
CHMO_Xantho       GMDTFKGRILHTGAWP---EGVELAG-------KRVGIIGTGSTG 196
CHMO_9871         GINQFKGELHHTSRWP---DDVSFEG-------KRVGVIGTGSTG 188
MO9               GRDTFGGATYHTGEWPH--EPVDFAG-------KRVGVIGTGSSG 189
MO15              GRESFTGDTHHTGQWPH--EGVDFTG-------RRVGIIGTGSSG 198
MO14              GIDNFRGEVLLTGNWPR--EGADFTG-------KRVAVIGTGASG 191
PAMO              GLKDFAGNLYHTGNWPH--EPVDFSG-------QRVGVIGTGSSG 198
CHMO_Brevi1       GIDEFNGAKYHTAAWPA--DGVDFTG-------KKVGVIGVGASG 190
BVMO_mekA         GQADFQGQIYHTGLWPK--DPVDFNG-------KRVAVVGTGATG 201
MO21              GQEEFSGPIFHTSRWPK--EGADLDG-------KRVAVIGVGATG 200
MO20              GLDLFAGDCYHTARWPQ--EGVDMTG-------RKVVVMGTGSSG 201
CHMO_Brevi2       GLDSFEGECHHTARWPQ--GGLDMTG-------KRVVVMGTGASG 201
MO11              GLNSFAGESHHTALWPQ--EGLDMAG-------KRVGIIGTGSSG 198
CPMO              GIETFKGQWYHTALWPQ--EGVNMAG-------KRVAIIGTGSSG 201
MO3               GLEKFGGDCFHTARWPL--EGYDLAG-------KRVAVIGTGASG 194
MO4               DMDAYQGELVHTARWR---SDLDMTG-------KRVAIIGTGASA 199
BVMO_EtaA         GSEDFVGPIIHPQHWP---EDLDYDA-------KNIVVIGSGATA 187
MO16              GLDRFGGRVVHPQQWP---EDLDYEG-------KRVVIIGSGATA 204
BVMO_KT2440       GSEQFKGQIIHPQHWP---EDLDYTG-------KRVVVIGSGATA 196
CPDMO             GITSFKGHSFHTSRWDYSYTGGDQTGNLEGLKDKRVAIIGTGATS 261
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Figure S5. Partial sequence alignment illustrating the nature of the Baeyer-Villiger mono-oxygenase motif[7] in the soluble targets from *R. jostii* RHA1 and other selected BVMOs from the literature.