A. FAD-binding oxidoreductases

```
R_eryth    1   --------------------------------------------MGFEQHREGVERLLASYRAIPADASVRLAKK
R_qingsh   1   --------------------------------------------MGFEQHREGVERLLASYRAIPADASVRLAKK
R_ruber    1   ---------------------------------MQKPKSVVVPSGESAHRAGVERLLRSYRAIPADAPVRLAKK
N_donost   1   ------------------------------MSLLGKAGHDPAAYESGFAAYRAGVSRLLESYRAIPAGADVLAKK
M_chloro   1   ------------------------------MSVPATDARAAHADGVERLLASYRAIPPGATVRLAKP
M_tuber    1   -----------------------MQGQLSRTRVYTVPVPGSAQSAYACGVERLLASYRSIPATASIRLAKP
C_urealy   1   MVGDMTVLGALKNIAVETVGKTTDALRIGNGLDARELQPVGWFAHGQAVEKLRASYEAIPPGENVRLAKK
A_orient   1   ------------------------MASGDGGPRATARLVRFAEHEARADALRAQLAGLHG--TIRLAKR

R_eryth    32  TSNLFRARAKTSAPGLDVSGLAGVIAVDAQAHTADVAGMCTYEDLVDATLPYGLAPLVVPQLKTITLGGA
R_qingsh   32  TSNLFRARAKTSAPGLDVSGLAGVIAVDAQARTADVAGMCTYEDLVDATLPYGLAPLVVPQLKTITLGGA
R_ruber    42  TSNLFRARARVNAPGLDVSGLGGVVAVDPVARTADVAGMCTYEDLVDATLPHGLAPLVVPQLKTITLGGA
N_donost   47  TSNLFRARARNTAPGLDVSGLTKVIAVDPDARTADVAGMTTYEDLVATTLPYGLAPLVVPQLKTITLGGA
M_chloro   38  TSNLFRARAKSTAPGLDVSGLTDVISVDPVARTADVAGMCTYEDLVAATLPHGLSPLVVPQLKTITLGGA
M_tuber    49  TSNLFRARVKHDARGLDASGLTGVIGIDPEARTADVAGMCTYEDLIAATLHYGLSPLVVPQLRTITLGGA
C_urealy   71  TSNLFRGRNQSTTPGLDVSGLGGVIAVDPVAGTADVQGMCTYEDLVDTVLPYGYSPTVVPQLKTITLGGA
A_orient   44  TSNLFRARAATSTPGLDVSGFTHVLDVDPLARTADVEGMVTYEQLVDATLPHGLMPLVVPQLKTITLGGA

R_eryth    102 VTGLGIESTSFRNGLPHESVLEIDVLTGSGEIITATPDGEHAELFFGFPNSYGTLGYSTRLKIALEPVKK
R_qingsh   102 VTGLGIESTSFRNGLPHESVLEIDVLTGSGEIITATPDGEHAELFFGFPNSYGTLGYSTRLKIALEPVKK
R_ruber    112 VTGLGIESTSFRNGLPHESVLEMDILTGAGEIVTATPDGEHADLFHGFPNSYGTLGYATRLKIELEAVKP
N_donost   117 VTGLGIESTSFRNGLPHESVLEIDVLTGAGEIVTATPDGEHADLFRGFPNSYGTLGYSTRLKIELEPVEP
M_chloro   108 VTGLGIESASFRNGLPHESVLEMDILTGCDVVRASP-TENPDLFHAFPNSYGTLGYSVRLKIELEPVKP
M_tuber    119 VTGLGIESASFRNGLPHESVLEMDILTGAGELLTVSP-GQLSDLYRAFPNSYGTLGYSTRLRIQLEPVRP
C_urealy   141 VTGLGVESACFRNGLPHEALIEMDVLTGEVVTCSP-TQNVDLFRGFPNTYGSLGYAVRLKIELEKVKD
A_orient   114 VTGLGIESSSFRNGLVHESVLEMELLTCDCRIVVARADNEHSDLFHGFPNSYGTLGYALRLKIELEPVKP

R_eryth    172 YVALRHVRFDSLKKLEETMDRIVTEREYDGIAVDYLDGVVFTDSESYLTLGVQTDEEGPVSDYTDQDIFY
R_qingsh   172 YVALRHVRFDSLKKLEETMDRIVTEREYDGIAVDYLDGVVFTDSESYLTLGVQTDEEGPVSDYTDQDIFY
R_ruber    182 YVALRHLRFDTLDEMQSALDRIATERVHAGVPVDYLDGVMFSATESYLTLGTQTDAPGPVSDYTGEHIYY
N_donost   187 YVALRHLRFHDLGELEAALTRIVTERDHDGERVDYLDGVVFSAGESYLTLGTQTDAPGPVSDYTGMDIYY
M_chloro   177 FVALRHVRFHAIDALIEAMDRIIETGGWNGERVDYLDGVVFSADESYLCLGVQSATPGPVSDYTGQQIYY
M_tuber    188 FVALRHIRFSSLTAMVAAMERIIDTGGLDGESVDYLDGVVFSADESYLCIGMQTSVPGPVSDYTGQDIYY
C_urealy   210 YVELRHVRFHDVHALTETMEQIIETGEYDGEAVDYLDGAVFSLEECYLMLCRQTDEPGPTSDYTRDRIYY
A_orient   184 YVRLDHVRYDDTEEYFAALGEACRTG-----AADFVDGTVFGPGEQYLTLGTFTTSAPATSDYTWLDIYY

R_eryth    242 RSIQHPSLTQPKTDRLTIRDYLWRWDTDWFWCSRAFGAQNPKIRRFWPKQYLRSSFYWKLIALDHKYDIG
R_qingsh   242 RSIQHSSLTQPKTDRLTIRDYLWRWDTDWFWCSRAFGAQNPKIRRFWPKQYLRSSFYWKLIALDHKYDIG
R_ruber    252 RSIQHASVNHPRTDRLTVRDYLWRWDTDWFWCSRAFGAQNPRIRRLWPKRLLRSSFYWKLIALDHRYGVA
N_donost   257 RSLQHEGG-TPKHDRLTIHDYLWRWDTDWFWCSRAFGTQNPKIRRFWPKRYRRSSFYWKLIALDHRYHIG
M_chloro   247 RSIQHPSG--EKHDRLTIHDYLWRWDTDWFWCSRAFGAQDPRIRRFWPRRLRRSSFYWKLIGYDQRFDIA
M_tuber    258 RSIQHEAG--IKEDRLTIHDYFWRWDTDWFWCSRSFGAQNPRLRRWWPRRYRRSSVYWRLMALDQRFGIA
C_urealy   280 RSIQHPEG--VLRDRLSIRDYLWRWDVDWFWASRAFGTQNPTIRRMWPRDLLRSSFYWKIIGWDRKYDLA
A_orient   249 KSIRERET-----DHLSVRDYLWRWDTDWFWCSRAFGVQHRLPRLLLGRRLLRSSVYWKAVALDRRFGIA

R_eryth    312 DRLEKRKGKPPRERVVQDVEVPIERTADFVSWFLEEIPIEPLWLCPLRLR------------EPSPAAASA
R_qingsh   312 DRLEKRKGKPPRERVVQDVEVPIERTADFVSWFLEEIPIEPLWLCPLRLR------------EPSPAAASA
R_ruber    322 DRIERRKGNLPRERVVQDIEVPIERTAEFLRWFLDEIPIEPVWLCPLRLR------------EGGPAARDA
N_donost   326 DKLEARKGNPPRERVVQDIEVPVERTADFMEWFLREIPIKPIWLCPLRLR------------RTG--SGGS
M_chloro   315 DRIEKRNGRPPRERVVQDVEVPIERTAEFVEWFLATVPIEPIWLCPLRLR----------------DAPNS
M_tuber    326 DRFENSRGRPARERVVQDIEVPIERTCEFLEWFGENVPISPIWLCPLRLR----------------DHAG-
C_urealy   348 DRIEAANNRPARERVVQDIEVTPLHLPEFLEWPFHSCEIEPVWLCPIRIRGTGADGNELVGEGETLGADK
A_orient   314 AKILKLRGLPPEETIVQDIEVPLSRAAEFLDFFRREIPISPVWICPLKQR-------------------PG

R_eryth    371 SRPWPLYPLEPKRTYVNIGFWSSVPIVPGER---EGAANRLIEEKVSDFDGHKSLYSDSYYSKEDFEELY
R_qingsh   371 SRPWPLYPLEPKRTYVNIGFWSSVPIVPGER--EGAANRLIEEKVSDFDGHKSLYSDSYYSKEDFEELY
R_ruber    381 QRPWPLYPLEPKRTYVNVGFWSSVPTVAGEI---EGAANRRIEHKVAELDGHKSLYSDSYYTRAEFEQLY
N_donost   383 ARPWPLYPLHPDRTYVNAGFWSSVPITSGEI---EGAANRAIEKAVTDFCGHKSLYSDSYYRQDEFADLY
M_chloro   370 TGGWPLYPIRPHHSYVNVGFWSSVPVGPE-----ECYTNRMIERKVSDLDGHKSLYSDAFYSPEEFDELY
M_tuber    380 ---WPLYPIRPDRSYVNIGFWSSVPVGAT-----EGATNRKIENKVSALDGHKSLYSDSFYTRKEFDELY
C_urealy   418 EHPWPLYPLTVGQTMVNVGFWSSVPVDLLGKDAPAGAFNKLVEEKVSALGCHKSLYSEAFYDRETFEQLY
A_orient   366 GVNSPLYELDPETLYVNPGFWSAVPLDPGEE---PDTHNRLIEAEVTRLGCRKSLYSDSFYTEDEFWRLY

R_eryth    438 YGGDRYIGLKERYDPKSRLLDLFSKAVQRK
R_qingsh   438 YGGDRYIGLKERYDPKSRLLDLFSKAVQRK
R_ruber    448 YGGGDYPTLKKRYDPESRLLDLFSKAVHNK
N_donost   450 GG-DDYIQLKKRYDPDQRLLDLYSKAVORK
M_chloro   435 GG-EVYTTVKKIYDPDSRFLDLYAKAVRRQ
M_tuber    442 GG-ETYNTVKKAYDPDSRLLDLYAKAVQRR
C_urealy   488 GG-SFPAQLKEVYDPQGRFPGLYEKTVDWA
A_orient   433 NC-DAYRKLKTAYDPDGRLLDLYAKCVRRR
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B. SAM-dependent methyltransferases

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M_chloro    1  MTTFRERPTDAANPADGRLTLAEILEIFASC-TRPLKFTAYDGSSAGPDDAALGLDLLTPRGTTYLATAP
M_tuber     1  --------------------MAEILEIFTATGQHPLKFTAYDGSTAGQDDATLGLDLRTPRGATYLATAP
R_eryth     1  -MTTFKDSK----SQD-KLSIAEILETLSDC-MLPLRFTAYDGSTAGPEDADYGLHLKSTRGTTYLATAP
R_qingsh    1  -MTTFKDSK----SQD-KLSIAEILETLSDC-MLPLRFTAYDGSTAGPEDADYGLHLKSTRGTTYLATAP
R_ruber     1  -MTTLREPR----TPDGRLTLAQILETVTGC-ELPVRFTAYDGSSAGPTDAPYGLRLTSTRGTTYLATAP
N_donost    1  -MTTFRERSDVFADLGTKLSIAEIFDLLVDC-EIPIRLTAYDGSATGPADSEFALDIRNARCINYLATAP
A_orient    1  ---------------MAETTTVGKIFERLLGP-STEVSITAYDGSTSGPADAPVSIQVRSPLALTYLMSSP
C_urealy    1  ------------------MTVAEIVEAITAP-PLPFHVLGFDGSETGPADARLRLDITSSDALAYIVTAP

M_chloro   70  GDLGLARAYISGNLEAHGVHPGDPYELLNALTE--KLDFKRPSARVLAQVIRSIG-IEHLKPISPPPQEA
M_tuber    51  GELGLARAYVSGDLQAHGVHPGDPYELLKTLTE--RVDFKRPSARVLANVVRSIG-VEHILPIAPPPQEA
R_eryth    64  GDLGMARAYVSGDLEAEGVHPGDPYEILRIMGD--ELHLKRPSALTLASITRSLG-WDLLRPIAPPPQEH
R_qingsh   64  GDLGMARAYVSGDLEAEGVHPGDPYEILRIMGD--ELHLKRPSALTLASITRSLG-WDLLRPIAPPPQEH
R_ruber    65  GDLGMARAYVSGDLEAEGVHPGNPYELLKALG---DLHFQRPPALTLAQIARSLG-LETLKPIAPPPQEH
N_donost   69  GDLGMARAYISGDMTATGVHPGDPYEILKAMQ---DLKFRRPSALALLTIARSLG-WERLRPVPPPPQET
A_orient   56  GDLGLARAYVACALDVDCDLYTALRALVAQVDQ--LSTADR------LWLLRELC-PRHLRRVAPPAEEL
C_urealy   52  GDLGLARAYITCALQVSCENPCHPYGMFDALQTFYYESFRKPSAATGARIARSLKHLDAIRPMPIPPQED

M_chloro  137  LPRWRRFAEG--LRHSKTRDAEAIHHHYDVSNTFYEWVLGPSMTYTCACYQHPE----------------
M_tuber   118  RPRWRRMANG--LLHSKTRDAEAIHHHYDVSNNFYEWVLGPSMTYTCAVFPNAE----------------
R_eryth   131  LPRWRRVAEG--LRHSKTRDAEVIHHHYDVSNTFYEYVLGPSMTYTCAAYDNAE----------------
R_qingsh  131  LPRWRRVAEG--LRHSKTRDAEVIHHHYDVSNTFYEYVLGPSMTYTCAAYDNAE----------------
R_ruber   131  LPRWRRFAEG--LRHSRSRDAEVIHHHYDVSNAFYEHVLGPSMTYTCALFDSEA----------------
N_donost  135  LPRWRRIAEG--LRHSKLRDAEAIHHHYDVSNAFYEMVLGPSMTYTCACYGDQD----------------
A_orient  117  PSRAKRVFDC--LRHSKARDSNALSNHYDVSNRFYELVLGPSMAYTCAAYPSAD----------------
C_urealy  122  QPGWKKALFEGLSRHSRERDKEVVQRHYDVGNDLYELFLCGDSMTYTCAYYPADESDTPEGWDKSQWAKGT

M_chloro  189  ---ATLEEAQDNKYRLVFEKLRLQPGDRLLDVGCGWGGMVRYAARHG-VTAIGVTLSKQQAEWAQKAIAE
M_tuber   170  ---ASLEQAQENKYRLIFEKLRLEPGDRLLDVGCGWGGMVRYAARRG-VRVIGATLSAEQAKWGQKAVED
R_eryth   183  ---QTLEEAQENKYRLVFEKLGLQKGDRLLDIGCGWGSMVRYAARRG-VKVIGVTLSREQADWAQKAIED
R_qingsh  183  ---QTLEEAQENKYRLVFEKLGLQKGDRLLDIGCGWGSMVRYAARRG-VKVIGVTLSREQADWAQKAIED
R_ruber   183  ---QSLEDAQENKYRLIFEKLRLQPGDRLLDVGCGWGGMVRYAARRG-VKALGVTLSREQAEWAQKTIAD
N_donost  187  ---WTLEQAQENKYRLIFEKLRLSPGDRLLDLGCGWGGMVRYAASRG-VQAIGATLSAEQAEWAQRKIAE
A_orient  169  ---ASLEEAQHRFDLVCRKLDLKPGMRLLDVGCGWGGMVEHAVEHYGVEALGVTLSREQAQWAQKDIVT
C_urealy  192  AVKEPLDRAQENKYRLVFDKLRLAEGDRLLDVGCGWGGMVRYAAARG-VKAIGVTLSEEQVAWGNEKIRE

M_chloro  255  EGLCDLAEVRHSDYRDVRESQFDAVSSIGLTEHIGVANYPAYFRFLKSKLRTGGLLLNHCITRHDNRHGA
M_tuber   236  EGLSDLAQVRHSDYRDVAETGFDAVSSIGLTEHIGVKNYPFYFGFLKSKLRTGGLLLNHCITRHDNRSTS
R_eryth   249  EGLADLAQVRFSDYRDVAETGFDAVSSIGLTEHIGVGNYPAYFEFLKGKLREGGRLLNHCITRPDNRSSA
R_qingsh  249  EGLADLAQVRFSDYRDVAETGFDAVSSIGLTEHIGVGNYPAYFEFLKGKLREGGRLLNHCITRPDNRSSA
R_ruber   249  EGLTDLAEVRFSDYRDVPETGFDAESSIGLTEHIGVQNYPAYFRRLHDKLREGGLLLNHCITRPVNRGPV
N_donost  253  EGLSDLAEVRHCDYRDVPESEFDAVSSIGLTEHIGVHNYPTYFEFIKGKLREGGLFLNHCITRPDNTRGT
A_orient  236  KGLADRAEVRHLDYRDVTETGFDAVSSIGLTEHICARNLPSYFRFLAGKLKPRGRLLNHCITNPDTTVPH
C_urealy  261  QGLEEFAEIRLMDYRDVPETGFDAISAIGVLEHVCRRQYEEFPQLMYCRLREGGRMLNHCITRPTNERIN

M_chloro  325  AAGGFIDRYVFPDGELTGSGRIITEVQDVGLEVVHEENLRNHYAMTLRDWNRNLVEHWDEAVAEVGLATA
M_tuber   306  FAGGFTDRYVFPDGELTGSGRITTEIQQVGLEVLHEENFRHHYAMTLRDWCGNLVEHWDDAVAEVGLPTA
R_eryth   319  KAGGFIDRYVFPDGELTGSGRIISEIQNVGLEVRHEENLREHYALTLAGWCQNLVDNWDACVAEVGEGTA
R_qingsh  319  KAGGFIDRYVFPDGELTGSGRIISEIQNVGLEVRHEENLREHYALTLAGWCQNLVDNWDACVAEVGEGTA
R_ruber   319  KAGGFIDRYVFPDGELTGSGRIITEVQDVGLEVLHEENLRQHYALTLKGWCENLVANWDACVAEVGEGTA
N_donost  323  KAGDFIDRYVFPDGELIGSGRIISDIQNVGLEVRHEENLRVHYAMTLRDWCGNLVDNWDACVAEAGEGTA
A_orient  306  RSRGFIDRYVFPDGELESVGEIATAMHDSGLEVRHSENLREHYATTLGAWCANLDENWDAAVAEAGAGRS
C_urealy  331  -AGKFIGRYIFPDGELTGSGTIVTRMQDVGFDVHHEENLRFHYQRTLHDWCELLAENWEEAVRIVGEGTA

M_chloro  395  KVWGLYMAGSRVGFEQNAIQLHQVLAVKLDERGRDGGLPLRPWWTA
M_tuber   376  KVWGLYMAASRVAFERNNLQLHHVLATKVDFRC-DDSLPLRPWWQP
R_eryth   389  RVWGLYMAGSRLGFERNVVQLHQVLAVKLGPKC-EAHVPLRPWWKA
R_qingsh  389  RVWGLYMAGSRLGFERNVVQLHQVLAVKLGPKG-EAHVPLRPWWKA
R_ruber   389  RVWGLYMAGSRLGFERNVVQLHHVLAVKLGPDQ-EPNVPLRPWWIA
N_donost  393  KVWGLYMAGSRLGFQRNVVQLHQVLCVKLGVNC-LPSVPLRPWWQP
A_orient  376  RVWALYMAACRLAFERREIELHQVLCVKVGPDC-DSGMPLRPDWGV
C_urealy  400  RLFGLYMAGSEWGFEFNIVQLHQVLAVKSYADC-STGLPVRQWWES
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Supplementary Figure 3. Alignments of amino acid sequences of homologous proteins of FAD-binding oxidoreductase WP_048472120 and SAM-dependent methyltransferase WP_048472121

A. Amino acid sequences of homologous proteins of FAD-binding oxidoreductase WP_048472120. R_eryth, WP_019746543 of *Rhodococcus erythropolis* R138; R_qingsh, WP_007731548 of *Rhodococcus qingshengii* BKS 20-40; R_ruber, WP_003935378 of *Rhodococcus ruber* BKS 20-38; N_donost, WP_077118793 of *Nocardia donostiensis* X 1654; M_chloro, WP_048472120 of *Mycobacterium chlorophenolicum* JCM 7439; M_tuber, WP_003917236 of *Mycobacterium tuberculosis* H37Rv; C_urealy, WP_012359407 of *Corynebacterium urealyticum* ATCC 43042; A_orient, WP_037303122 of *Amycolatopsis orientalis* DSM 40040. **B.** Amino acid sequences of homologous proteins of SAM-dependent methyltransferase WP_048472121. M_chloro, WP_048472121 of *Mycobacterium chlorophenolicum* JCM 7439; M_tuber, WP_003420415 of *Mycobacterium tuberculosis* H37Rv; R_eryth, WP_019746542 of *Rhodococcus erythropolis* R138; R_qingsh, WP_003943932 of *Rhodococcus qingshengii* BKS 20-40; R_ruber, WP_003935379 of *Rhodococcus ruber* BKS 20-38; N_donost, WP_077118797 of *Nocardia donostiensis* X 1654; A_orient, WP_037303124 of *Amycolatopsis orientalis* DSM 40040; C_urealy, WP_012359408 of *Corynebacterium urealyticum* ATCC 43042. Inserted sequences in *C. urealyticum* ATCC 43042 were indicated by red underlines.