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             429                                                                                                                  548
       1A-04 TSVDLMSTSEHQQLATFNDTAHPYPRDVLIHQLIEQQAAQRPDACAVRGDSGPLLTYAELNQQANQLAHRLIELDVEPDTRVAVSLRRGAEMVVALLGILKAGGAYVPIDPDLPSARQAY
       1B-06 TSVDLMSTSEHQQLATFNDTAHPYPRDVLIHQLIEQQAAQRPDACAVRGDSGPLLTYAELNQQANQLAHRLIELDVEPDTRVAVSLRRGAEMVVALLGILKAGGAYVPIDPDLPSARQAY
EntF-SyrE-A1 TSVDLMSTSEHQQLATFNDTAHPYPRDVLIHQLIEQQAAQRPDACAVRGDSGPLLTYAELNQQANQLAHRLIELGVEPDTRVAVSLRRGAEMVVALLGILKAGGAYVPIDPDLPSARQAY
             549                                                                                                                  668
       1A-04 MLEDSSPQAVLTTRDLSDNLPASDLPVLVLDGHDDRAQLARQQSVNPDAKALGLQPNHLAYVLYTSGSTGTPKGVMNEHLGVVNRLLWARDAYQVNSQDRVLQKTPFGFDVSVWEFFLPL
       1B-06 MLEDSSPQAVLTTRDLSDNLPASDLPVLVLDGHDDRAQLARQQSVNPDAKALGLQPNHLAYVLYTSGSTGTPKGVMNEHLGVVNRLLWARDAYQVNSQDRVLQKTPFGFDVSVWEFFLPL
EntF-SyrE-A1 MLEDSSPQAVLTTRDLSDNLPASDLPVLVLDGHDDRAQLARQQSVNPDAKALGLQPNHLAYVLYTSGSTGTPKGVMNEHLGVVNRLLWARDAYQVNSQDRVLQKTPFGFDVSVWEFFLPL
             669                                                                                                                  788
       1A-04 LAGAELVMAPPGGHQDPDYLAQVMSDAGITLLHFVPSMLDVFLEHRSTRDFPQLRRVLCSGEALPRALQRRFEQQLKGVELHNLYGPTEAAIDVTAWECRPTDPGDSVPIGRPIANIQIH
       1B-06 LAGAELVMALPGGHQDPDYLAQVMSDAGITLLHFVPSMLDVFLEHRSTRDFPQLRRVLCSGEALPRALQRRFEQQLKGVELHNLYGPTEAAIDVTAWECRPTDPGDSVPIGRPIANIQIH
EntF-SyrE-A1 LTGAELVMAPPGGHQDPDYLAQVMSDAGITLLHFVPSMLDVFLEHRSTRDFPQLRRVLCSGEALPRALQRRFEQQLKGVELHNLYGPTEAAIDVTAWECRPTDPGDSVPIGRPIANIQMH
             789                                                                                                                  908
       1A-04 VLDALGQLQPMGVAGELHIGGIGVARGYLNQPQLSAERFIADPFSNDPQARLYKTGDVGRWLANGALEYLGRNDFQVKIRGLRIEIGEIEAALAKHPAVHEAVVTAREDIPGDKRLVAYY
       1B-06 VLDALGQLQPMGVAGELHIGGIGVARGYLNQPQLSAERFIADPFSNDPQARLYKTGDVGRWLANGALEYLGRNDFQVKIRGLRIEIGEIEAALAKHPAVHEAVVTAREDIPGDKRLVAYY
EntF-SyrE-A1 VLDALGQLQPMGVAGELHIGGIGVARGYLNQPQLSAERFIADPFSNDPQARLYKTGDVGRWLANGALEYLGRNDFQVKIRGLRIEIGEIEAALAKHPAVHEAVVTAREDIPGDKRLVAYY
             909
       1A-04 TQSAEHTAVDLEALRSHLQQVLPEYMVPAIYVLLEAMPLTSNGKLDRKALPA
       1B-06 TQSAEHTAVDLEALRSHLQQVLPEYMVPAIYVLLEAMPLTSNGKLDRKALPA
EntF-SyrE-A1 TQSAEHTAVDLEALRSHLQQVLPEYMVPAIYVLLEAMPLTSNGKLDRKALPA
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           1                                                                                                                  120
       6A-16 MAHHHHHHVGTMLLQSMTSDPIARNSDLVSLFREVAATAPERTALSAEDDRISYGRLDAWSDAVARTLLAEGVRPGDRVALRMSPGAEAIVAILAILKCGAAYVPVDLRNPVSRSDFILA
       6B-19 MAHHHHHHVGTMLLQSMTSDPVARNSDLVSLFREVAATAPERTALSVEDDRISYGRLDAWSDAVARTLLAEGVRPGDRVALRMSPGAEAIVAILAILKCGAAYVPVDLRNPVSRSDFILA
       6C-06 MAHHHHHHVGTMLLQSMTSDPVARNSDLVSLFREVAATAPERTALSVEDDRISYERLDAWSDAVARTLLAEGVRPGDRVALRMSPGAEAIVAILAILKCGAAYVPVDLRNPVSRSDFILA
AdmK-CytC1-A MAHHHHHHVGTMLLQSMTSDPIARNSDLVSLFREVAATAPERTALSAEDDRISYGRLDAWSDAVARTLLAEGVRPGDRVALRMSPGAEAIVAILAILKCGAAYVPVDLRNPVSRSDFILA
             121                                                                                                                  240
       6A-16 DSGASALIGEPHEGCAVTRVVRTAAVAECKDAEPGPVTGAPGPGAEDMAYVIYTSGTTGNPKGVPVRHANVLALLAGAPSVFDFSGDDRWLLFHSLSFDFSVWEVWGAFSTGAELVVLPH
       6B-19 DSGASALIGEPHEGCAVTRVVRTAAVAECKDAEPGPVTGAPGPGAEDMAYVIYTSGTTGNPKGVPVRHANVLALLAGAPSVFDFSGDDRWLLFHSLSFDFSVWEVWGAFSTGAELVVLPH
       6C-06 DSGASALIGEPHEGCAVTRVVRTAAVAECKDAEPGPVTGAPGPGAEDMAYVIYTSGTTGNPKGVPVRHANVLALLAGAPSVFDFSGDDRWLLFHSLSFDFSVWEVWGAFSTGAELVVLPH
AdmK-CytC1-A DSGASALIGEPHEGCAVTRVVRTAAVAECKDAEPGPVTGAPGPGAEDMAYVIYTSGTTGNPKGVPVRHANVLALLAGAPSVFDFSGDDRWLLFHSLSFDFSVWEIWGAFSTGAELVVLPH
             241                                                                                                                  360
       6A-16 WAARTPEQYLAVIIDRGVTVINQTPTAFLVLTEAAVRGGRDVSGLRYVIFGGEKLTVPMLRPWAKAFGLDRPRLVNGYGITETTVFTTFEEITEAYLAQDASIIGRALPSFGTRVVGDDG
       6B-19 WAARTPEQYLAVIIDRGVTVINQTPTAFLVLTEAAVRGGRDVSGLRYVIFGGEKLTVPMLRPWAKAFGLDRPRLVNGYGITETTVFTTFEEITEAYLAQDASIIGRALPSFGTRVVGDDG
       6C-06 WAARTPEQYLAVIIDRGVTVINQTPTAFLVLIEAAVRGGRDVSGLRYVIFGGEKLTVPMLRSWAKAFGLDRPRLVNGYGITETTVFTTFEEITEAYLAQDASIIGRALPSFGTRVVGDDG
AdmK-CytC1-A WAARTPEQYLAVIIDRGVTVINQTPTAFLALTEAAVRGGRDVSGLRYVIFGGEKLTAPMLRPWAKAFGLDRPRLVNGYGITETTVFTTFEEITEAYLAQDASIIGRALPSFGTRVVGDDG
             361                                                                                                                  480
       6A-16 RDVAPGETGELWLSGAQLAEGYLRRPELTAEKFPEVTDEKTGESVRYYRTGDLVSELPDGRFAYEGRADLQIKLRGYRIELSDIETAVRRHDDVVDAVVTVREFKPGDLRLVCAYVAREG
       6B-19 RDVAPGETGELWLSGAQLAEGYLRRPELTAEKFPEVTDEKTGESVRYYRTGDLVSELPDGRFAYEGRADLQIKLRGYRIELSDIETAVRRHDDVVDAVVTVREFKPGDLRLVCAYVAREG
       6C-06 RDVAPGETGELWLSGAQLAEGYLRRPELTAEKFPEVTDEKTGESVRYYRTGDLVSELPDGRFAYEGRADLQIKLRGYRIELSDIETAVRRHDDVVDAVVTVREFKPGDLRLVCAYVAREG
AdmK-CytC1-A RDVAPGETGELWLSGAQLAEGYLRRPELTAEKFPEVTDEKTGESVRYYRTGDLVSELPDGRFAYEGRADLQIKLRGYRIELSDIETAVRRHDDVVDAVVTVREFKPGDLRLVCAYVAREG
             481
       6A-16 SATTARELRNHIKTLLPAYMHPARYLPLPRLPRTVNGKVDRAAVARSAS
       6B-19 SATTARELRNHIKTLLPAYMHPARYLPLPRLPRTVNGKVDRAAVARSAS
       6C-06 SATTARELRNHIKTLLPAYMHPARYLPLPRLPRTVNGKVDRAAVARSAS
AdmK-CytC1-A SATTARELRNHIKTLLPAYMHPARYLPLPGLPRTVNGKVDRAAVARSAS
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             1                                                                                                                    120
       5A-06 MAHHHHHHVGTMHKMTENEKELILHFNNTKTDYPKNKTLHELFEEQAMKTPDHTALVFGAQRMTYRELNEKANQTARLLREKGIGRGSIAAIIADRSFEMIIGIIGILKAGGAYLPIDPE
AdmK-BacA-A1 MAHHHHHHVGTMHKMTENEKELILHFNNTKTDYPKNKTLHELFEEQAMKTPDHTALVFGAQRMTYRELNEKANQTARLLREKGIGRGSIAAIIADRSFEMIIGIIGILKAGGAYLPIDPE
             121                                                                                                                  240
       5A-06 TPKDRIAFMLSDTKAAVLLTQGKAADGIDCEADIVQLDREASDGFSKEPLSSVNDSGDTAYIIYTSGSTGTPKGVITPHYSVIRVVQNTNYIDITEDDVILQLSNYSFDGSVFDIFGALL
AdmK-BacA-A1 TPKDRIAFMLSDTKAAVLLTQGKAADGIDCEADIVQLDREASDGFSKEPLSSVNDSGDTAYIIYTSGSTGTPKGVITPHYSVIRVVQNTNYIDITEDDVILQLSNYSFDGSVFDIFGALL
             241                                                                                                                  360
       5A-06 NGASLVMIEKEALLNINRLGSAINEEKVSVMFITTALFNMIADIHVDCLSNLRKILFGGERASIPHVRKVLNHVGRDKLIHVYGPTESTVYATYYFINEIDDEAETIPIGSPLANTSVLI
AdmK-BacA-A1 NGASLVMIEKEALLNINRLGSAINEEKVSVMFITTALFNMIADIHVDCLSNLRKILFGGERASIPHVRKVLNHVGRDKLIHVYGPTESTVYATYYFINEIDDEAETIPIGSPLANTSVLI
             361                                                                                                                  480
       5A-06 MDEAGKLVPIGVPGELCIAGDGLSKGYLNREELTAEKFIPHPFIPGERLYKTGDLAKWLPDGNIEFIGRIDHQVKIRGFRIELGEIESRLEMHEDINETVVTVREDEESRPYICAYITAN
AdmK-BacA-A1 MDEAGKLVPIGVPGELCIAGDGLSKGYLNREELTAEKFIPHPFIPGERLYKTGDLAKWLPDGNIEFIGRIDHQVKIRGFRIELGEIESRLEMHEDINETIVTVREDEESRPYICAYITAN
             481
       5A-06 REISLDELKGFLGEKLPKYMIPAYFVKLDKLPLTKNGKVDRKALPEPAS
AdmK-BacA-A1 REISLDELKGFLGEKLPEYMIPAYFVKLDKLPLTKNGKVDRKALPEPAS
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