Table S1. Oligonucleotide primers used in this study

Oligonucleotide	**Sequence (5’-3’)**	**Relevant description**
BAP2569	CGGAATTCCATCATGCCTTGTTTGATCG	*PetL* internal forward primer with EcoRI site. For *petL* mutagenesis using pUA826.
BAP2570	CGGAATTCTTGAACAGCGATTGATTTGG	*PetL* internal reverse primer with EcoRI site. For *petL* mutagenesis using pUA826.
BAP3425	CCCAGTCGACAATTCCGTCCAGTTGTTGC	*petK* internal forward primer with SalI site. For *petK* mutagenesis using pUA826.
BAP3426	TACCGTCGACGAACTCAAACGGATCATGG	*petK* internal reverse primer with SalI site. For *petK* mutagenesis using pUA826.
BAP5870	AAAAAAGCTTATAATTATCCTTATGTGTCTACAGAGTGCGCCCAGATAGGGTG	TargeTron IBS primer for mutagenesis of *petL.*
BAP5871	CAGATTGTACAAATGTGGTGATAACAGATAAGTCTACAGACGTAACTTACCTTTCTTTGT	TargeTron EBS1d primer for mutagenesis of *petL.*
BAP5872	TGAACGCAAGTTTCTAATTTCGGTTACACATCGATAGAGGAAAGTGTCT	TargeTron EBS2 primer for mutagenesis of *petL.*
BAP6116	TCGCGGATCCTGTAATGATATACCACTC	Anneals upstream of *petG*, contains BamHI site. For *petG* expression plasmid.
BAP6117	TTATGTCGACCGGTTCATATTGTACCGC	Anneals downstream of *petG*, contains SalI site. For *petG* expression plasmid.
BAP6617	AAAAAAGCTTATAATTATCCTTAAAAAACAATTTAGTGCGCCCAGATAGGGTG	TargeTron IBS primer for mutagenesis of *petG.*
BAP6618	CAGATTGTACAAATGTGGTGATAACAGATAAGTCAATTTATTTAACTTACCTTTCTTTGT	TargeTron EBS1d primer for mutagenesis of *petG.*
BAP6619	TGAACGCAAGTTTCTAATTTCGGTTTTTTTCCGATAGAGGAAAGTGTCT	TargeTron EBS2 primer for mutagenesis of *petG.*
BAP6715	AAAAAAGCTTATAATTATCCTTAAATTGCCACACCGTGCGCCCAGATAGGGTG	TargeTron IBS primer specific for *petK.*
BAP6716	CAGATTGTACAAATGTGGTGATAACAGATAAGTCCACACCTGTAACTTACCTTTCTTTGT	TargeTron EBS1d primer specific for *petK.*
BAP6717	TGAACGCAAGTTTCTAATTTCGGTTCAATTCCGATAGAGGAAAGTGTCT	TargeTron EBS2 primer specific for *petK.*
BAP7478	CATTGGATCCGTTTCTAACAGAAGTCGA	Anneals upstream of *petL*, contains BamHI site. For *petL* expression plasmid.
BAP7479	AGCTGTCGACGGCTTTTATTCAATGTCC	Anneals downstream of *petL*, contains SalI site. For *petL* expression.
BAP7509	TCATGGATCCGGATGTCTATCCATTTTGC	Anneals upstream of *petK*, contains BamHI site. For *petK* expression plasmid.
BAP7510	AACGTCGACGGGTATTGGCTAAAATAATGG	Anneals downstream of *petK*, contains SalI site. For *petK* expression plasmid.
EBS Universal	CGAAATTAGAAACTTGCGTTCAGTAAAC	TargeTron Universal primer for retargeting intron.

Figure. S1

COBALT multiple sequence alignment

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Sf-plasmid-SFxv_5135/LptO      ---------------------------------------------------------------------------MFLIS  5
Pm-X73-A0R63_09570/PetK        --MYSNS-----EKNHRTL---------LFPIF--FFVFVNLIVFTLSRLGLSLWQAERVSAVNGWVELFVQGLRIDIVS  62
HI-KW20-HI_1246                -MLVVFT-----MKKAHSP---------LFPIF--TFVLINLIILSLSRLGLAVWQSERVSAVDGWLQLFLQGVRMDVVA  63
Mh-M42548-MHH_c23440           -MYQ--------RSQSRTV---------LFPIL--LFVGINLVILTLSRLVLGVWQSDRVSAVDGWIPLILQGIRIDISS  60
Acti.p-L20-APL_0804            -MRFILNLKGEIMEQRRSV---------LFPIL--FFVGINLLILSLSRLGLSLWQAERVSAVDGWLPLFLQGIRIDISA  68
Aggr.a-D11S1-D11S_0415         MSRQLFK-----TEKMHSL---------LYPIF--FFCLLNLIVFTLSRLGLSLWQIERVNAVHGWGELFLQGLRMDIVS  64
Aero.s-A449_ASA3698            MCPRTGANRL----VGTTMTTIKQWLGPFWPIA--VFSFIALVSLSASRVGLGVWQLERVDAVAGWPEMLLQGLRVDIAT  74
Shew.p-CN32-Sputcn32_3803      MLSVLSA-RG----RGHAY-------GPFHAIL--IFCLLVLFVTTVSRICLGLWQTERVVAVEGWSHLILQGLRVDIAT  66
Vh-1DA3-VME47170               --------------------MKKPAFGPLQPI--AVFALFSLAFLSVSRILLAIWLSDRIESFNDLIYILGQGLRVDFAT  58
Vp-UCMV493-VPUCM_1817          --------------------M----FGPLQPL--AVFSLFSLAFLSISRILLAFWQFDRIESFNDFLYILGQGVRVDIAT  54
Vc-M10-VchoM_02105             ------------------MNKLKLFFGPLYPIVCAVFAL--LVIFALSRLGLAMWHFDRVTNADGWIRIFTSGLRVDFAS  60
Vc-O1ElTorN16961-VCA802        ---------------VTTLNKLKLFFGPLYPIVCAVFAL--LVIFALSRLGLAMWHFDRVTNADGWIRIFTSGLRVDFAS  63
Bp-TahomaI-BP3136              -MRVFFCNEAD-----EALALPPPTRNPVRRLT-IRFAIAILVLLTLSRLGLSAWQWERVQAAGGLGPIMLGGLRMDLRL  73
Pm-X73-A0R63_06305/PetL        -------------MKKLR-F-RWS--------LSSSKLLALTAFYF--SVILNYPFYAKVLSIHPLTHTSADYF---IYT  52
Hd-3500P-Hd0852/EptA           -------------MKFKC-S-TWQ--------LSSTQLVAIVSFYF--TVVLNIPFFRESFKLYEFTQTSADYF---IYT  52
Nm-Mc58-NMB1638/EptA           -------------MIKPN-L-RPK--------LGSSALIAFLSLYS--SLVLNYAFFAKVVELHPFNGTGADIF---LYT  52
Ng-FA19-NGEG_02067/LptA        -------------MIKPN-L-RPK--------LGSSALIAFLSLYS--SLVLNYAFFAKVVELRPFNDTGADIF---LYT  52
Hp-6695-Hp0022/EptA            ------------MASLFHLRFLKP--------LSCLQAGLLYSLIF--GVLYHFPLF---VYVYKESNQVSFIA---MMV  52
Cj-NCTC11168-Cj0256/EptC       ------------MLRLTW---------------------FQFTFFN--SLMIVLLNFNLFYFVYEKNTQ-NWLI---TFV  41
Vp-UCMV493-VPUCM_20416         ------------MKTVDS-PK-KG--------IPYVAFTVLLALYF--ALVVNIPIYKELIGIFSKLDEVKIGF---IIT  53
Vc-M10-VchoM_02405             ------------MVIMPT-FNIKP--------FSYLQLVFLLAAYF--ALPLNLPVYAQLAHIFNQSTSLDWGF---ALS  54
Vc-O1ElTorN16961-VCA1102       ------------MVIMPT-FNIKP--------FSYLQLVFLLAAYF--ALPLNLPVYAQLAHIFNQSTSLDWGF---ALS  54
ST-L2-PmrC                     -------------MLKRF-LKRPV--------LGQIAWLLLFSFYI--AVCLNIAFYKQVLQDLPLNSLRNVLV---FIS  53
Ec-plasmid-mcr1                ------------MMQHTSVCYRRS--------VSPFVLVASVAVFL--TATANLTFFDKISQTYPIADNL--GF---VLT  53
Ec-plasmid-mcr2                ------------MTSHHS-WYRYS--------INPFVLMGLVALFL--AATANLTFFEKAMAVYPVSDNL--GF---IIS  52
Pm-X73-A0R63_02570/Lpt3        --------------------------------------------------------------------------------
Nm-MC58-Lpt3                   --------------------------------------------------------------------------------
Ng-FA19-Lpt_3                  --------------------------------------------------------------------------------
Hi-RdKW20-Lpt_6                --------------------------------------------------------------------------------
Nm-MC58-Lpt6                   --------------------------------------------------------------------------------
Ng-FA19-Lpt_6                  --------------------------------------------------------------------------------
Pm-X73-A0R63_03465/PetG        -----MKLD----FIFSR-I---S--------KEEYFLFCLLGVY---VFVSHFILCLSLT----FLSLLGSFI---FWI  49
Pm-P1059-PetG                  -----MKLD----FIFSR-I---S--------KEEYFLFCLLGVY---VFVSHFILCLSLT----FLSLLGSFI---FWI  49
Pm-P2100-A0R72_03015           ----MMKLD----FIFSR-I---K--------KEQYFLLFSLGLY---VVVSHFILCLSLT----FLSLLGSFI---FWI  50
Pm-HN06-PMCN06_0886            ----MMKLD----FIFSR-I---K--------KEQYFLLFSLGLY---VVVSHFILCLSLT----FLSLLGSFI---FWI  50
Hd-3500P-Hd0371/PdtA           ----MI--K----KLF---A---Y--------LHYRLFYIWLLLF---SFLSVMISPEKST----EYAVISVFI---LLY  46
Hd-3500P-Hd1598/PdtB           -----MKLK----LTPKQ-A------------------CFSLIAIFLTLFASYVMLKGSGFFPEPNLIQLLLTS---ILI  49
Acti.s-130Z-Asuc_1041          -------------MEQ---T---N--------KQTNIFCFLLILY---SLFSNYSLGYPPN----IYALAGNFL---LLF  43
Hh-CCUG3714-B0186_06625        ----MFSEK----KMKPN-F---L--------LQPI-FILVLSLY---SFTTTLALSPYYPNFLYQNWFETLLL---FAF  53
Aggr.a-RhAA1-RhAA1_04486       ----MFQSK----KF--H-F---L--------YNDISFFLLLLLF---AFLSHIALGIL---DHYANHILSIFA---LGV  49
Hf-CCUG31170-B0188_07100       ----MMFNK----IIT---S---S--------KKNYLFFILLFIY---AILSNYALGYPPN----LYAIIAIYL---SIY  48
Hh-11P18-AAX18_01700           ----MNKVS----IF----------------------FHLSLFIF---SFLTNIGLGKAHTGNIFSSSHITLYV---FLI  44
Ec-K12-OpgE                    ----MNLTL----KES---L---V--------TRSRVFSPWTAFYFLQSLLINLGLGYPFS----LLYTAAFTA---ILL  51
Ng-FA19-DcaA/PptA              -----MKQS----ARIKN-MDQTL--------KNTLGICALLAFCFGAAIASGYHLEYEYGYRYSAVGALASVV---FLL  59
Ec-W3110-EptB                  ----MLSPVCPGFVCMRY---IKS--------ITQQKLSFLLAIYI--GLFMNGAVFYRRFGSYAHDFTVWKGI---SAV  60
Ec-K12-EptC/CptA               ----MHSTE---VQAKPL----FS--------WKALGWALLYFWFF--STLLQAIIY---ISGYSGTNGIRDSL---LFS  53
ST-L2-EptC/CptA                ----MQSTL---LQTKPA----FS--------WKALGWALLYFWFF--STLLQAIIY---LTGYSGTNGLRDSL---LYS  53
Ec-plasmid-ECH74115_B0113      ----MHLNT---GQNRPT----FS--------WSALGWAIFYFGFF--STLLQVIIF---SSGYSGTNGIRDSL---LFS  53
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Sf-plasmid-SFxv_5135/LptO       IIQMFSVMIIMLNI-----KI-KDAFRAIILLLLLL-LSMVISIEISSIISIGEY------IPTLALANISETNSVGWKI  72
Pm-X73-A0R63_09570/PetK         LCYLFGVPALFTVLLYHHNAL-GRVWQKILRVWLTFGSVFILFMEIATPAFIETYDFRPNRLFIEYLIYPKEVFTMLFEG  141
HI-KW20-HI_1246                 LCYLFGVPALLTTLFHS-----SKVWVKILRLWLTFGSVFIIFMEIATPAFIETYDYRPNRLFIEYLIYPKEVFSMLAEG  138
Mh-M42548-MHH_c23440            LCWLFGLPALFSVLCFHKNVL-GSIWQTVLRIWLTVGSVFILFMEVATPNFIETFDLRPNRLFIEYLVHPREVFTMLING  139
Acti.p-L20-APL_0804             LCWLFGVPALFTALFLNHNKL-GAIWRVILRIWLTAGSVFILFMEAATPNFIETFDLRPNRLFIEYLVHPKEVFSMLING  147
Aggr.a-D11S1-D11S_0415          LCYLFGVPALFSVLFYHDNTL-GRIWKGILRVWLTVGSVFILFMELSTPAFINTYDYRPNRLFIEYLIYPKEVFTMLMEG  143
Aero.s-A449_ASA3698             LCWIWGVPAMLTMLLAGPHAI-GRAWLQLIRVWLTLGLWLMLFLEISTPSFVTEYGVRPNRLYVEYLIYPKEVLSMLWAG  153
Shew.p-CN32-Sputcn32_3803       LCWLWGIAALGTALFSGDHFV-GRLWQPILRIWLTFGLWVIVFLEISTPTFIEEYGIRPNRLYVEYLIYPKEVLSMLWAG  145
Vh-1DA3-VME47170                ICWLFILPGLLSALLPVQGKV-GECWKWVLRCWMVAGLWILVYMELATAPFIQEYDLRPNRLFVEYLIYPKEVFSMLWTG  137
Vp-UCMV493-VPUCM_1817           LCWLFILPALLSSFMPLKGKV-GECWKWVLRLWMVAGLWILVYMELATAPFIQEYDLRPNRLFVEYLIYPKEVMSMLWTG  133
Vc-M10-VchoM_02105              ICYLFILPALLTSLISGEHWL-GRIWNWILRLWITAGLWIVVYMEVATPPFIIEYDLRPNRLFVEYLIYPKEVFGMLWSG  139
Vc-O1ElTorN16961-VCA802         ICYLFILPALLTSLISGEHWL-GRIWNWILRLWITAGLWIVVYMEVATPPFIIEYDLRPNRLFVEYLIYPKEVFGMLWSG  142
Bp-TahomaI-BP3136               LALVLALPAVLAPWFGHRAWA-ASATAWWYRVWW----MLFVLLEVSTPQFIAEYDTRPNRLYFEYLVHPREVASMLWEG  148
Pm-X73-A0R63_06305/PetL         MPLVIF-VILNAAFQII-AI--PVIHKIIMPCLIVISAAISYNTLFFDIY----FNR--EMLQNVVQSNLAEGSRLITWT  122
Hd-3500P-Hd0852/EptA            MPLVLF-VALNIVLNIL-AL--LIVHKIIIPLLLILGSAISYNSLFFNVY----FDR--NMLNNVLQTNVAESYRMLTPS  122
Nm-Mc58-NMB1638/EptA            MPVVLF-FLSNFVFHVI-AL--PFVHKVLIPLILVISAAVSYQEIFFNIY----FNK--SMLNNVLQTTAAESARLITPG  122
Ng-FA19-NGEG_02067/LptA         MPVVLF-FLSNFVFHVI-AL--PFVHKVLIPLILVISAAVSYQEIFFNIY----FNK--SMLNNVLQTTAAESARLITPG  122
Hp-6695-Hp0022/EptA             VVLFCVNGALFLALGLI--S--ASLMRWSAIVFSLLNSVAFYFISAYKVF----LNK--SMMGNVLNTNTHEVLGFLSVK  122
Cj-NCTC11168-Cj0256/EptC        FIVAYF-ALVHVICSLL-FI--KFFTKFFSILFIISSFLSVYFISFYGVL----IDS--DMMQNVVQTDIKEVKDLLNLK  111
Vp-UCMV493-VPUCM_20416          IPIFFF-AALNFLFNLF-SW--PWVGKPFFILLLVVSSLVSYAGYNYGTL----FDS--GMIANIVETDSSEASSYLSTY  123
Vc-M10-VchoM_02405              IPLFFL-FALNFIFQIF-SW--PYLFKPFFAVLLVLSALISFAGFQYGVI----VDQ--DMLVNVLETDRGEAGSYLTIY  124
Vc-O1ElTorN16961-VCA1102        IPLFFL-FALNFIFQIF-SW--PYLFKPFFAVLLVLSALISFAGFQYGVI----VDQ--DMLVNVLETDRGEAGSYLTIY  124
ST-L2-PmrC                      MPVVAF-SVVNSVLTLA-SF--IWLNRLLACVFILVGAAAQYFILTYGII----IDR--SMIANMMDTTPAETFALMTPQ  123
Ec-plasmid-mcr1                 IAVVLF-GAMLLITTLLSSY--RYVLKPVLILLLIMGAVTSYFTDTYGTV----YDT--TMLQNALQTDQAETKDLLNAA  124
Ec-plasmid-mcr2                 MAVAVM-GAMLLIVVLL-SY--RYVLKPVLILLLIMGAVTSYFTDTYGTV----YDT--TMLQNAMQTDQAESKDLMNLA  122
Pm-X73-A0R63_02570/Lpt3         -----------------------------------------------------------------------MKKSLFILL  9
Nm-MC58-Lpt3                    ----------------------------------------------------------------------MMKKSFLTLV  10
Ng-FA19-Lpt_3                   -----------------------------------------------------------------------MKKSLFVLF  9
Hi-RdKW20-Lpt_6                 ------------------------MIAYIFLALFTIAAVIFIVNSHYRWTYF---------FAITLFTFLFGGMLMVSSQ  47
Nm-MC58-Lpt6                    ------------------------MIAYVFLFLFVTAALVLIIRSHYRWTYF---------FASALFVFLAGGMLMLTAQ  47
Ng-FA19-Lpt_6                   ------------------------MVAYAFLFLFVTAVVLLIVRSHYRWTYF---------FASALFVFLAGGMLMLTAQ  47
Pm-X73-A0R63_03465/PetG         FIYHLSLR----------------LFILLFCFYTLLVGMMIPL-YLYKGI-----NL--SIIASIFESNLSESIEYISTL  105
Pm-P1059-PetG                   FIYHLSLR----------------LFILLFCFYTLLVGMMIPL-YLYKGI-----NL--SIIASIFESNLSESIEYISTL  105
Pm-P2100-A0R72_03015            FIYNLSLR----------------LFLFLFPCYTLLVALMLPL-YTYDGI-----NL--GIVASIFETNLSESVEYIATF  106
Pm-HN06-PMCN06_0886             FIYNLSLR----------------LF-FLFPCYTLLVALMLPL-YTYDGI-----NL--GIVASIFETNLSESVEYIATF  105
Hd-3500P-Hd0371/PdtA            LIYAFNKQL----------------FTWVIIFLSITLSLYYPIYLRYGSL-----NS--GIVAAFLETNISESLGFLERI  103
Hd-3500P-Hd1598/PdtB            IVLGSSRLS----------------FYLLLLPITFSYAIYTPIGLSFGPP-----SY--QYIASLFATDLLEAREFLSQL  106
Acti.s-130Z-Asuc_1041           LAFRLSKFL----------------FFTVLLFHSLICSVYIPEAIFYGSP-----SV--GIIASLFETNMQESWEYLQSL  100
Hh-CCUG3714-B0186_06625         LYASFLLS-NK-------------FFYLVTSVIFLPALLYLPQIILYGGL-----TI--GVVASLHETNSAESIEYLRSI  112
Aggr.a-RhAA1-RhAA1_04486        LLFTFKKHDNR-------------LFLVAFVFIFAISFGYVPSGILYGPV-----SI--GVIASVYETNFSETLGFFRAM  109
Hf-CCUG31170-B0188_07100        LSIYLSIYLSIYLSIYLSIYLSRIIFQLLFLIHSLVCTIYIPEAIFYGKP-----SI--GLISSLFETNRNEALEYLQSL  121
Hh-11P18-AAX18_01700            LIFSSSRI----------------IGLITSSILFITSMIYYPAGVSYGAP-----SF--GIIASIYETNINETLEYLSSI  101
Ec-K12-OpgE                     LLWRTLPRVQ----------------KVLVGVSSLVAACYFPFAQAYGAP-----NF--NTLLALHSTNMEESTEILTIF  108
Ng-FA19-DcaA/PptA               LARGFPRVS----------------SVVLLIYVGTT-ALYLPVGWLYGAP-----SY--QIVGSILESNPAEAREFVGNL  115
Ec-W3110-EptB                   VELAATVLVTFFLLRLL-SLFGRRSWRILASLVVLFSAGASYYMTFLNVV----IGY--GIIASVMTTDIDLSKEVVGLN  133
Ec-K12-EptC/CptA                SLWLIP---------VF-LF--PKRIKIIAAVIGVVLWAASLAALCYYVIYGQEFSQ--SVLFVMFETNTNEASEYLSQY  119
ST-L2-EptC/CptA                 SLWLIP---------VF-LF--PGRIRVIAAVIGVVLWAASLAALSYYVIYGQEFSQ--SVLFVMFETNANEASEYLSQY  119
Ec-plasmid-ECH74115_B0113       CLWLIP---------VF-LY--PDRIKIIAAVVGFILWGTSLAALCYYFLYGHEFSQ--SVLFVMFETNAREAGEYFSQY  119
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Sf-plasmid-SFxv_5135/LptO    K--LLPFLVFLSFMIASLILKR-LIKEKKIRNIMVVVF----LLSL--LI---------------PISPINAFFS-----  123
Pm-X73-A0R63_09570/PetK      H--LLSMVISLVVTATATLCYW-KLAGWAVKNLSSPSWKFRPVIAL--LVIAIAFIGARSTFAHRGINPAMVAFSSDGLV  216
HI-KW20-HI_1246              H--LSAVIFSLVFTILAAVIYW-KISGWAVKNLRSMSWKLRPVIAL--LVIVVSFLGARSSFQHRGINPAMVAFSSDALV  213
Mh-M42548-MHH_c23440         H--LWAVICGIGIAMISLIIYW-KLSGWATKNLHFPSWKMRPLLAL--LVAAIVFVGGRSSFAHRGINPAMVAFSSDPLV  214
Acti.p-L20-APL_0804          H--LSSVIISTLLAVVSLVVYW-KLSGWATNNLRFPNWKFRPLIGL--LVAALVFVGGRSSFAHRGINPAMVAFSSDPLV  222
Aggr.a-D11S1-D11S_0415       H--LSAVILSLVFTVIAAVVYW-KLAGRAVRDMQPMSWKWRPLVAL--LVIAVSFLGARSSLQHRGINPAMVAFSSDAMV  218
Aero.s-A449_ASA3698          R--KGELLIAVLFSLLTLGGGW-WLSGRLLRGLSFPRWYLRPAFAL--LILAIGFLGARSSLGHRPLNPAMVAFASDPLI  228
Shew.p-CN32-Sputcn32_3803    R--KVELIFSVIVSMATLWGGW-VLSGKLTSYLRFPRWYWRPVLAV--VVVVLVFLGARSTLGHRPLNPAMVAFADDPLV  220
Vh-1DA3-VME47170             Y--KLELFIGAVGTAITLFLGW-KWSKKLTDNAQQVNWKWRPVLAI--LVVLIGVAGARSSLGHRPLNPAMVAFSNDPLM  212
Vp-UCMV493-VPUCM_1817        Y--KLELFIGAIGTALTLVLGW-KWSKKLTDSAQQINWKWRPLLAI--FVVLLCVAGARSSLGHRPLNPAMVAFSNDPLL  208
Vc-M10-VchoM_02105           Y--KLELFIGLVVSVLTVVLGW-RWSKTLVSNLHYPKWYWRPVIAV--LVVTVGVLGARSSLGHRPMNPAMVSFSSDPLM  214
Vc-O1ElTorN16961-VCA802      Y--KLELFIGLVVSVLTVVLGW-RWSKTLVSNLHYPKWYWRPVIAV--LVVTVGVLGARSSLGHRPMNPAMVSFSSDPLM  217
Bp-TahomaI-BP3136            Y--KGVLLASFVVLVLAAWLAV-RLFPTGRQD-GFMKWWKRPFVTL--AVLAVVVLAARGTLQHRPINASMVAFSSDAMV  222
Pm-X73-A0R63_06305/PetL      Y---LEWLLAFGF--VPALLYC--LTRVN--YHHVVKEVLVRLSMI---LLSVLLFVGVAA-----------FFYQDYSA  179
Hd-3500P-Hd0852/EptA         Y---LAWLFCLGI--LPALVYL--NIKIK--YRKWYKEIAVRLATI---FAASLVIGLIAS-----------QYYQSYAS  179
Nm-Mc58-NMB1638/EptA         Y---VLWIVCLGV--LPALAYI--AVKVK--YRVWYKELLTRLVLA---AVSFLCALGIAM-----------LQYQDYAS  179
Ng-FA19-NGEG_02067/LptA      Y---VLWIVCLGV--LPALAYI--AVKVK--YRVWYKELLTRLVLA---AVSFLCALGIAM-----------LQYQDYAS  179
Hp-6695-Hp0022/EptA          L---FVFIVVFGV--LPGYVIY--KIPLKN---SSKKA---PFLAI---LALVFIFIASAL-----------ANTKNWLW  175
Cj-NCTC11168-Cj0256/EptC     L---ILFVV-LAL--LLVFYVV--KVKIDY-YGSFKSHIKIKIINI---ISGLIVVCAVLI-----------PLSKTFLP  168
Vp-UCMV493-VPUCM_20416       S---VVWTTLMGV--IPALIVF--KVKLQPQRGQWLRFVLTKLVAM---LASLAVIAVIAG-----------LYYQDYAS  182
Vc-M10-VchoM_02405           S---VLWLLGFGL--VPALALL--FTPIRP-EKSALRFLMKKGLSM---LVSVVVIGVIAG-----------LYYQNYSS  182
Vc-O1ElTorN16961-VCA1102     S---VLWLLGFGL--VPALALL--FTPIRP-EKSALRFLMKKGLSM---LVSVVVIGVIAG-----------LYYQNYSS  182
ST-L2-PmrC                   M---VLTLGLSGV--LAAVIAF--WVKIRP-ATPRLRSGLYRLASV---LISILLVILVAA-----------FFYKDYAS  181
Ec-plasmid-mcr1              F---IMRIIGLGV--LPSLLVA--FVKVDY--PTWGKGLMRRLGLI---VASLALILLPVV-----------AFSSHYAS  181
Ec-plasmid-mcr2              F---FVRIIGLGV--LPSVLVA--VAKVNY--PTWGKGLIQRAMTW---GVSLVLLLVPIG-----------LFSSQYAS  179
Pm-X73-A0R63_02570/Lpt3      G---YSAVLLLSEILYRYFFKI--------NSL--YRISESFLIIF---VVLSLFYFSKYKVSRFF---IALFFSCSTLI  70
Nm-MC58-Lpt3                 L---YSSLLTASEIAYRFVFGI--------ETLPAAKIAETFALTF---VIAALYLFARYKVTRLL---IAVFFAFSIIA  73
Ng-FA19-Lpt_3                L---YSSLLTASEIAYRFVFGI--------ETLPAAKMAETFALTF---MIAALYLFARYKASRLL---IAVFFAFSMIA  72
Hi-RdKW20-Lpt_6              W----QRALNFSSVLFVVLMLF---------HRLKIHYYKQPLLIS--DFFLVVDWRNWETLIHYK------------GA  100
Nm-MC58-Lpt6                 W----QRALNFASVWFVVLILF---------HRLKIHYYKQPLLIS--DFLLIADWRNWETLFHYK------------EA  100
Ng-FA19-Lpt_6                W----QRALNFASVWFVVLILF---------HRLKIHYYKQPLLIS--DFLLIADWRNWETLFHYK------------EA  100
Pm-X73-A0R63_03465/PetG      --SYYQFISIFVYFYFGFFILY-RLV-LYSKLGNKNKEFKNILLLL-LFLLLVTFYKPVKEYIK----------------  164
Pm-P1059-PetG                --SYYQFISIFVYFYFGFFILY-RLV-LYSKLGNKNKEFKNILLLL-LFLLLVTFYKPVKEYIK----------------  164
Pm-P2100-A0R72_03015         --SYYQILAIFTYISFGFILLY-KLATLHNKYRSLN--IRKVLFLF-IFLLLIAFYKPVKEYMK----------------  164
Pm-HN06-PMCN06_0886          --SYYQILAIFTYISFGFILLY-KLATLHNKYRSLN--IRKVLFLF-IFLLLIAFYKPVKEYMK----------------  163
Hd-3500P-Hd0371/PdtA         R--LEHLLFPICYILFAVILIR-LKK--YNKPSPYDKRKRQLYIVLSATFIFTLLFEPTRFYLG-----------SYVAE  167
Hd-3500P-Hd1598/PdtB         S--LFNYLAGLSIILAVVFFR---KINQKYHINLLNNRTFVVIAFV---IS-----------------------------  149
Acti.s-130Z-Asuc_1041        P--LYSYVISLLFLLFSVGFAV-FAL--KVKFLPMKKTTVSTLIFL---IVIAVLYKPW----------------SNYHK  156
Hh-CCUG3714-B0186_06625      PYSIYIYCFLYIVLFLTLIILS-KKT---AKP---KVSLSIFILLW-GLILGSTFDAPIKKYNK----------------  168
Aggr.a-RhAA1-RhAA1_04486     PISIYFFTALYVVLFIALLVIN-RHI---H---SNKKYRPAYYSLY-FAALLLSLYTPVNKLINHT---------DKTQS  172
Hf-CCUG31170-B0188_07100     P--IYSYIIALLFFIFSLIIIF-LSN--QIQLKRIKKSTFFIYFTL---FITAVLYKPI----------------SNVYK  177
Hh-11P18-AAX18_01700         PNYIYTLMCIYFLVLISVIYSS-KQV---SKFITLRKKKKIFILIW-ITLLSYVLTKPINGIIK-----------SKSSD  165
Ec-K12-OpgE                  P--WYSYLVGLFIFALGVIAIR-RKK--ENEKARWNTFDSLCLVFS----VATFFVAPVQNLA-----------------  162
Ng-FA19-DcaA/PptA            P--GSLFVQALFFIFGLTVWKYCVSVGVFADVKNYKRRSKIWLTIL---LTLILSCAVMEKIAGD-------------KD  177
Ec-W3110-EptB                F---ILWLIAVSA--LPLILIW--NNRCRYTLLRQLRTPGQRIRSL---AVVVLAGIMVWAPIRLLDIQQKKVERATGVD  203
Ec-K12-EptC/CptA             F---SLKIVLIALAYTAVAVLL--WTRLRP----VYIPKPWRYVVS---FALLYGLILHPIAMNTF-IKNK--------P  178
ST-L2-EptC/CptA              F---SLKIVLVALAYTVAAILL--WTRLRP----VYIPSPWRYLVS---FALLYGLILHPIAMNTF-IKHK--------S  178
Ec-plasmid-ECH74115_B0113    F---SLKLLLISLVYTAVSVFL--WTRLRP----VYIPLPWRRIVS---FLLLYALLLHPVVLKSL-IRQE--------P  178
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Sf-plasmid-SFxv_5135/LptO    ------SSYEVYSEAKEYN-----------MSPHEIS-----------------------------DI------------  145
Pm-X73-A0R63_09570/PetK      NSLVLNSGYSVIYAAQQFKDEDNAASLYGKMADDEML-----------------------------RIV-----------  256
HI-KW20-HI_1246              NSLVLNSGYSVIYAAQQFKDEEKSSEMYGKMDADEMF-----------------------------RIV-----------  253
Mh-M42548-MHH_c23440         NSLVLNSGYSVLYAVQQLKDEDKSSEQYGKMSVEEMF-----------------------------NIV-----------  254
Acti.p-L20-APL_0804          NSLVLSSGYSVLYAVQQLKDEDKSSEQYGKMSAEEMF-----------------------------ALV-----------  262
Aggr.a-D11S1-D11S_0415       NSLVLNSGYSVIYAAQQFKDEGTSSESYGKMETAEML-----------------------------DII-----------  258
Aero.s-A449_ASA3698          NALTVNSAYSVFFAIKQMGGEEDASQFYGQLPRQQIL-----------------------------DLI-----------  268
Shew.p-CN32-Sputcn32_3803    NSLVTNSSYSLVFAIKQMGNEEDAAEVYGDLNDAEII-----------------------------ATI-----------  260
Vh-1DA3-VME47170             NDLALNSSYSLLFAVNNMKSEKSAEEFYGKMDNQKML-----------------------------DLV-----------  252
Vp-UCMV493-VPUCM_1817        NDLALNSSYSLLFAVNNMKSEKSAEQFYGKMDNQKML-----------------------------DLV-----------  248
Vc-M10-VchoM_02105           NDLALNSAYSVIFAAKQMGSEANAFEFYPKMDKQLVI-----------------------------DQV-----------  254
Vc-O1ElTorN16961-VCA802      NDLALNSAYSVIFAAKQMGSEANAFEFYPKMDKQLVI-----------------------------DQV-----------  257
Bp-TahomaI-BP3136            NTLPLNSLGNVLDAAYRMQDERSSAALYPPMKTEEMN-----------------------------RIV-----------  262
Pm-X73-A0R63_06305/PetL      FFRNNKSLTHLLVPSNFIGATINVIQDLRAAN-LPYV-------------------------------------------  215
Hd-3500P-Hd0852/EptA         FFRNHKYLTHLIVPSNFVGATIGKIKRDRLAN-QPFI-------------------------------------------  215
Nm-Mc58-NMB1638/EptA         FFRNNKSVTHLIVPSNFIGAGVSKYKDWKRSN-IPYT-------------------------------------------  215
Ng-FA19-NGEG_02067/LptA      FFRNNKSVTHLIVPSNFIGAGVSKYKDWKRSN-IPYT-------------------------------------------  215
Hp-6695-Hp0022/EptA          FDKHAKFIGGLILPFAYSVNAFRVSALKFFAP------------------------------------------------  207
Cj-NCTC11168-Cj0256/EptC     FFRNYNEIRMYNTPFYQIYAVYRYYVRFVKAKP-EFK-------------------------------------------  204
Vp-UCMV493-VPUCM_20416       VGRNNSYLKKMIIPTQYVYSATSYVKENYLTTPQPYR-------------------------------------------  219
Vc-M10-VchoM_02405           VGRNNSSLKKMIIPTHFLYSSFGLVKQRYFTEPMVYQ-------------------------------------------  219
Vc-O1ElTorN16961-VCA1102     VGRNNSSLKKMIIPTHFLYSSFGLVKQRYFTEPMVYQ-------------------------------------------  219
ST-L2-PmrC                   LFRNNKQLIKALSPSNSIVASWSWYSHQRLAN-LPLV-------------------------------------------  217
Ec-plasmid-mcr1              FFRVHKPLRSYVNPIMPIYSVGKLASIEYKKASAPKD-------------------------------------------  218
Ec-plasmid-mcr2              FFRVHKPVRFYINPITPIYSVGKLASIEYKKATAPTD-------------------------------------------  216
Pm-X73-A0R63_02570/Lpt3      NNVHYEVYQNWINGTNYLLMFKEYWEVTHAGLHMLDKLAGGIIWGALDILIFISISRFRQKTHWVADISFILVMGYIFVR  150
Nm-MC58-Lpt3                 NNVHYAVYQSWMTGINYWLMLKEVTEVGSAGASMLDKLWLPVLWGVLEVMLFCSLAKFRRKTHFSADILFAFLMLMIFVR  153
Ng-FA19-Lpt_3                NNVHYAVYQSWMTGINYWLMLKEVTEVGSAGASMLDKLWLPALWGVAEVVLFCSLAKFRRKTHFSADILFAFLMLMIFVR  152
Hi-RdKW20-Lpt_6              LFGVIGLLALLGYAIFGFNDVESLGVLGNSIGALLFIVSFSLMWHYSKNPSAVQ-VWLDSLPDDGRDVFL----------  169
Nm-MC58-Lpt6                 VIGMAGLLALAAYAVFGWSGADALGLPWRWAGTVLFAAAFVSMRHFSKHPGAVK-TWLDSLPDDGRDVFL----------  169
Ng-FA19-Lpt_6                VIGMAGLLALAAYAVFGWSGADSLGMPWRWAGAVLFAAAFVSVRHFSKHPGAVK-TWLDSLPDDGRDVFL----------  169
Pm-X73-A0R63_03465/PetG      -GSSFSVLNIRVYPIQLVSNIYYLTFSYFNQKEMLEY-------------------------------------------  200
Pm-P1059-PetG                -GSSFSVLNIRVYPIQLVSNIYYLTFSYFNQKEMLEY-------------------------------------------  200
Pm-P2100-A0R72_03015         -GGDFYFLNIRVYPIQIVGKIYHLTYSYLHQKALLEQ-------------------------------------------  200
Pm-HN06-PMCN06_0886          -GGDFYFLNIRVYPIQIVGKIYHLTYSYLHQKALLEQ-------------------------------------------  199
Hd-3500P-Hd0371/PdtA         EDRDWTLENSPVNIVSFYANIYDSITHYYQEKQELLV-------------------------------------------  204
Hd-3500P-Hd1598/PdtB         -----SFS---LAPFKLFHEFFNEGMKVKQELAILNS-------------------------------------------  178
Acti.s-130Z-Asuc_1041        GRD-FRLTDTRVSLIGFYWVNYHLIKDYLRQKSEMIA-------------------------------------------  192
Hh-CCUG3714-B0186_06625      VSFPVALESSPFYPIAFTTKAINLKNAYQKEKSEFDQ-------------------------------------------  205
Aggr.a-RhAA1-RhAA1_04486     FTAAEFFKASDFYPMSFISNAVKVNNTYLTQRALLND-------------------------------------------  209
Hf-CCUG31170-B0188_07100     YNEPFDLQNTRVSIVGFYVLNYQLIKNYHLEKEKLEQ-------------------------------------------  214
Hh-11P18-AAX18_01700         ISYSYYFSQSKLYPLSFYSETVRVVSEYFKQKHFLDR-------------------------------------------  202
Ec-K12-OpgE                  WGGVFKLKDTGYPVFRFAKDVIVNNNEVIEEQERMAK-------------------------------------------  199
Ng-FA19-DcaA/PptA            WEPDAGLL---LNIFDLYYDLASAPAQYAAKRAHILE-------------------------------------------  211
Ec-W3110-EptB                LPSYGGVVANSYLPSNWL-SALGLYAWARVDESSDNN-------------------------------------------  239
Ec-K12-EptC/CptA             FEKTLDNLASRMEPAAPWQFLTGYYQYRQQLNSLTKL-------------------------------------------  215
ST-L2-EptC/CptA              MEKTLDSLASRMEPAAPWQFITGYYQYRLQLASLNKL-------------------------------------------  215
Ec-plasmid-ECH74115_B0113    LNDTLGKLASRMEPAAPWQFVSSYYQYHQQLNALTTF-------------------------------------------  215
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Zinc co-ordination site 240/227/246 in EptA$_{Nm}$/EptC/Mcr-1 ↓

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Sf-plasmid-SFxv_5135/LptO   -----------KSK------------------------YTKEIVTNDSYSHEI-IN-GNGKNILVIFIEGMSSLVIS---  185
Pm-X73-A0R63_09570/PetK     ----KQTRGRPESD------------------------YISSQYPTLTRNQAT-YQ-GKPKNIVIILEESLGAQFIGSLG  306
HI-KW20-HI_1246             ----KASRGRPESD------------------------YISDKYPTLTKNVAT-YQ-GKPKNIVILLQESLGAQFIGTLG  303
Mh-M42548-MHH_c23440        ----KQVRNRPASD------------------------YISDEIPTLTQNKAT-YQ-GKPKNIVIILEESLGAQFVGSLG  304
Acti.p-L20-APL_0804         ----KQARGRADSD------------------------YISTEIPTLTYNQAT-YQ-GKPKNIVIVLEESLGAQFVGTLG  312
Aggr.a-D11S1-D11S_0415      ----KKSGSRPVEA------------------------YISDEFPTLTRNQAT-YQ-GKPKNIVIILEESFGAQFIGTLG  308
Aero.s-A449_ASA3698         ----RQESGRELHD------------------------FSSTALPSQTFNEAS-YS-GKPKNLVILLQESLGAQFVGSLG  318
Shew.p-CN32-Sputcn32_3803   ----RQESGRPASA------------------------FTSTDVPSLSFNQAS-YT-GKPKNLVILLQESLGARFVGSLG  310
Vh-1DA3-VME47170            ----RASSAKS--N------------------------FDPSVLPTMNSNVAS-YQ-GKPKNLVILLQESLGAQFVGSLG  300
Vp-UCMV493-VPUCM_1817       ----RASSTKV--D------------------------FDPTLLPTMNSNPAT-YQ-GKRKNLVILLQESLGAQFVGSLG  296
Vc-M10-VchoM_02105          ----RASMTVAPED------------------------FISDDKPSLANHVAT-YQ-GAPKNIVILLMESHGARYVKSLG  304
Vc-O1ElTorN16961-VCA802     ----RASMTVAPED------------------------FISDDKPSLANHVAT-YQ-GAPKNIVILLMESHGARYVKSLG  307
Bp-TahomaI-BP3136           ----RAAAGLE-DP------------------------PLDARYPSLHKQTAT-VRRDKPLNLVIILQESLGAQYVGSLG  312
Pm-X73-A0R63_06305/PetL     ---------------------------------------QLDLKASQA----K-TDQD-RHVTVLIIGETTRAKNWGLNH  250
Hd-3500P-Hd0852/EptA        ---------------------------------------KQAEQVKML----K-KDNY-RTVSVIVVGETTRAANWGLSG  250
Nm-Mc58-NMB1638/EptA        ---------------------------------------QLDMAVVQN----R-PAGSLRRFVVLVVGETTRAANWGLNG  251
Ng-FA19-NGEG_02067/LptA     ---------------------------------------QLDMAVVQN----R-PAGSLRRFVVLVVGETTRAANWGLNG  251
Hp-6695-Hp0022/EptA         ---------------------------------------------TIKPLPLF-SPNHSHSFVVLVIGESARKHNYALYG  241
Cj-NCTC11168-Cj0256/EptC    ---------------------------------------TIANDAY------R-ENNHTKKLLVLVVGETARAANYSLGG  238
Vp-UCMV493-VPUCM_20416      ---------------------------------------EIGTDAQQSPTALQ-QAQDKPTLLVFVVGETARTQNYQLNG  259
Vc-M10-VchoM_02405          ---------------------------------------EIGQDAQQKPSAVR-QATQKPTLVFFVLGETARVQNYQYLG  259
Vc-O1ElTorN16961-VCA1102    ---------------------------------------EIGQDAQQKPSAVR-QATQKPTLVFFVLGETARVQNYQYLG  259
ST-L2-PmrC                  ---------------------------------------RIGEDAHRNP--LM-LKGDRKNLTILIVGETSRGDDFSLGG  255
Ec-plasmid-mcr1             ---------------------------------------TI-YHAKDAVQATK-PDMRKPRLVVFVVGETARADHVSFNG  257
Ec-plasmid-mcr2             ---------------------------------------TI-YHAKDAVQTTK-PSERKPRLVVFVVGETARADHVQFNG  255
Pm-X73-A0R63_02570/Lpt3     SFYTNQELGITSNPGYSRIKANFFAFGYFIGKTLPYDLFNLSNVSVYYRDKPNMIQPPMAKNIILIMGESLSASNVGTFG  230
Nm-MC58-Lpt3                SFDTKQEHGISPKPTYSRIKANYFSFGYFVGRVLPYQLFDLSRIPAFKQPAPSKIGQGSVQNIVLIMGESESAAHLKLFG  233
Ng-FA19-Lpt_3               SFDTKQEHGISPKPTYSRIKANYFSFGYFVGRVLPYQLFDLSKIPVFKQPAPSKIGQGSIQNIVLIMGESESAAHLKLFG  232
Hi-RdKW20-Lpt_6             --------NLPMSC-----RGIFFKVPNFDGNSQNF----IEKMTALSSDANN--LSETKPDIVVTLMESTLNPH--QFA  228
Nm-MC58-Lpt6                --------NLPMSC-----RAVFFQVPVFEGDGEAF----AKQMPS-ETQPYG--MSDEKPDIVVTLMESTLDPH--CFD  227
Ng-FA19-Lpt_6               --------NLPMSC-----RAVFFQVPVFEGDGEAF----ARQMPS-ETQPYG--MSDEKPDIVVTLMESTLDPH--CFD  227
Pm-X73-A0R63_03465/PetG     ---------------------------------------GINIEPDWKIQSVN--S--KYDNYVLVIGESMRADYMSLYG  237
Pm-P1059-PetG               ---------------------------------------GINIEPDWKIQSVN--S--KYDNYVLVIGESMRADYMSLYG  237
Pm-P2100-A0R72_03015        ---------------------------------------GLNVKPDWKIQSVN--P--KYGNYVLVIGESMRANYMSLYG  237
Pm-HN06-PMCN06_0886         ---------------------------------------GLNVKPDWKIQSVN--P--KYGNYVLVIGESMRADYMSLYI  236
Hd-3500P-Hd0371/PdtA        ---------------------------------------VSTKPSLWQITQVE--P--RYDNYVLIIGESARRDYLATYG  241
Hd-3500P-Hd1598/PdtB        ---------------------------------------SSVIPSEWGESTLS--SDAKYDDYVLIIGESARKDYHHAYG  217
Acti.s-130Z-Asuc_1041       ---------------------------------------VKNQQSTWEISSVS--P--KYRNYVVIIGESMRADYLSMYG  229
Hh-CCUG3714-B0186_06625     ---------------------------------------ALKQPNSWEIISTN--A--KYKNYILIIGESMRKDYMSAYG  242
Aggr.a-RhAA1-RhAA1_04486    ---------------------------------------ALTKTPEWDIVSVE--P--KYQNYVLIIGESMRRDYTSLYG  246
Hf-CCUG31170-B0188_07100    ---------------------------------------AKQIPSTWKIKHSL--P--KYKNYVLIIGESMRADYLSLYG  251
Hh-11P18-AAX18_01700        ---------------------------------------AFDEDSKWEIVSVS--P--KYKNYILIIGESMRKDYMSLYG  239
Ec-K12-OpgE                 ---------------------------------------LSGMKDTWTVTAVK--P--KYQTYVVVIGESARRDALGAFG  236
Ng-FA19-DcaA/PptA           ---------------------------------------AAKKASTWHIRHVA--P--EYKNYVVVIGE-ARSDYMNVYG  247
Ec-W3110-EptB               ---------------------------------------SLLNPAKKF-TYQA-PQNVDDTYVVFIIGETTRWDHMGIFG  278
Ec-K12-EptC/CptA            ---------------------------------------LNENNALPPLANFKDESGNEPRTLVLVIGESTQRGRMSLYG  256
ST-L2-EptC/CptA             ---------------------------------------LNENDALPPLANFQDHSGDAPRTLVLVIGESTQRGRMSLYG  256
Ec-plasmid-ECH74115_B0113   ---------------------------------------LNENSALPPLGNLRDESGERPRTLVLVIGESTQRERMSLYG  256
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Catalytic nucleophile 280/266/285 in EptA$_{Nm}$/EptC/Mcr-1

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Sf-plasmid-SFxv_5135/LptO     -KE--LTPNLYEF---RKKSISFN---NYYNHTAATFRGLRGQLTSSYQMTGGYYKDNSGLGQASKAEIEHKLNTYNYIT  256
Pm-X73-A0R63_09570/PetK       GLP--LSPEFDKL---AQEGWLFE---NLYATGTRSVRGIEAVTAGFTPTPAR--------------AVVKLSNSQHGFF  364
HI-KW20-HI_1246               GKP--LSPNVDQL---AKEGWLFE---NLYATGTRSVRGIEATTAGFTPTPAR--------------AVVKLNNAQSGFF  361
Mh-M42548-MHH_c23440          GKN--LTPNLDKL---SEQGWYFT---NLYATGTRSVRGIEAVTAGFTPTPAR--------------SVVKLTKSQTNFF  362
Acti.p-L20-APL_0804           GKP--LTPNFDRL---AQEGWLFE---NLYATGTRSVRGIEAVTTGFTPTPAR--------------AVVKLTKSQHNFF  370
Aggr.a-D11S1-D11S_0415        GLP--LSPAFDKL---AQQGWLFD---NLYATGTRSVRGIEAVTAGFTPTPAR--------------AVVKLNNSQNGFF  366
Aero.s-A449_ASA3698           GLP--LTPNLDAL---SQQGWAFE---QLYATGTRSVRGIEAVLTGFTPTPAQ--------------AVVKLGKSQTNFF  376
Shew.p-CN32-Sputcn32_3803     GLP--LTPNIDAL---SQEGWYFD---HLYATGTRSVRGIEAVTTGFTPTPAR--------------AVVKLGKSQTGFF  368
Vh-1DA3-VME47170              GLP--LTPNVDKL---MAEGWSFT---QLYATGTRSVRGIEAVTTGFPPSPSR--------------AVVKLSKSQTNFF  358
Vp-UCMV493-VPUCM_1817         GLP--LTPNLDEL---MQEGWQFT---QMYATGTRSVRGIEAVTTGFPPSPSR--------------AVVKLSKSQTGFF  354
Vc-M10-VchoM_02105            GID--VSPNMDKL---INEGWAFT---RMYATGTRSVRGIEAVTTGFSPTPAR--------------SVVKLGKSQNNFF  362
Vc-O1ElTorN16961-VCA802       GID--VSPNMDKL---INEGWAFT---RMYATGTRSVRGIEAVTTGFSPTPAR--------------SVVKLGKSQNNFF  365
Bp-TahomaI-BP3136             GRD--LTPQLDRL---AKDGWMFN---RAYATGTRSVRGLEAVTAGFLPTVAE--------------AVLKLPRSQTGFF  370
Pm-X73-A0R63_06305/PetL       YER-QTTPLLAKR---GEDVINFQ---HMTSCGTSTAVSVPCMFSSLDRKHFS-------------------NVQADHQD  304
Hd-3500P-Hd0852/EptA          YAR-QTTPKMAARIAQGDNLFNFS---EVTSCGTATAVSVPCLFSSQTRKQYD-------------------EVIAKNQD  307
Nm-Mc58-NMB1638/EptA          YSR-QTTPLLAAR---GDEIVNFP---QVRSCGTSTAHSLPCMFSTFDRTDYD-------------------EIKAEHQD  305
Ng-FA19-NGEG_02067/LptA       YSR-QTTPLLAAR---GDEIVNFP---QVRSCGTSTAHSLPCMFSTFDRTDYD-------------------EIKAEHQD  305
Hp-6695-Hp0022/EptA           YQK-PTTPRLSKRLA--DNELTLF---NATSCATYTTASLECILDSSFKNNA--------------------------YE  289
Cj-NCTC11168-Cj0256/EptC      YTKNDTNFYTKKD-----NVVFFD---NFSSCGTATAVSLPCMFSISKRENY---------------------SSSEFQE  289
Vp-UCMV493-VPUCM_20416        YER-ETNPYTSQL-----DVISFK---DVASCGTATAVSVPCMFSQLTRNQFD-------------------RKQADNQD  311
Vc-M10-VchoM_02405            YPR-DTNAYTAPF-----QPIFFK---DVASCGTATAVSVPCMFSNMNRQNFD-------------------RSRADNQD  311
Vc-O1ElTorN16961-VCA1102      YPR-DTNAYTAPF-----QPIFFK---DVASCGTATAVSVPCMFSNMNRQNFD-------------------RSRADNQD  311
ST-L2-PmrC                    YPR-DTNPRLAKD-----DVIYFP---HTTSCGTATAISVPCMFSDMPRKHYD-------------------EELAHHQE  307
Ec-plasmid-mcr1               YER-DTFPQLAKI----DGVTNFS---NVTSCGTSTAYSVPCMFSYLGADEYD-------------------VDTAKYQE  310
Ec-plasmid-mcr2               YGR-ETFPQLAKV----DGLANFS---QVTSCGTSTAYSVPCMFSYLGQDDYD-------------------VDTAKYQE  308
Pm-X73-A0R63_02570/Lpt3       YER-QTMPFLDQLVKNAPAETLLK---PAYSAGLGTAISLPAFFNAIPRPNGL-------------------EQIVSGRT  287
Nm-MC58-Lpt3                  YGR-ETSPFLTRL-SQADFKPIVK---QSYSAGFMTAVSLPSFFNAIPHANGL-------------------EQISGGDT  289
Ng-FA19-Lpt_3                 YGR-ETSPFLTRL-SQADFKPIVK---QSYSAGFMTAVSLPSFFNVIPHANGL-------------------EQISGGDT  288
Hi-RdKW20-Lpt_6               FSQ-QSIPPLSMF--EPQNDTVFASPLRVHTFAGATWKSEFAFLAGVPSTDFG-----------ALASGVFYSVVPHLQS  294
Nm-MC58-Lpt6                  FAA-AKIPDLKMF--GRQEDTVFSSPLRVHTFGGATWKSEFAFLAGVPSTDFG-----------ALASGVFYSVVPHLQT  293
Ng-FA19-Lpt_6                 FAA-AKIPDLKMF--GRQEDTVFSSPLRVHTFGGATWKSEFAFLAGVPSTDFG-----------ALASGVFYSVVPHLQT  293
Pm-X73-A0R63_03465/PetG       YPI-ETTPFLKRT-----RGIVFT---NYISSAPNTQPSLLHSF---YDKNN--------------------YE-IKPNN  284
Pm-P1059-PetG                 YPI-ETTPFLKRT-----RGIVFT---NYISSAPNTQPSLLHSF---YDKNN--------------------YE-IKPNN  284
Pm-P2100-A0R72_03015          YPI-DTTPFLKKT-----NAIVLD---NFISASSGTQVSLLRSF---YIKDK--------------------DDNFQTNN  285
Pm-HN06-PMCN06_0886           YPI-DTTPFLKKT-----NAIVLD---NFISASSGTQVSLLRSF---YIKDK--------------------DDNFQTNN  284
Hd-3500P-Hd0371/PdtA          FTL-PTTPFLDRT-----NGYINA---GYIASAPATYHSLLKSL---YLKQT---------------------GKRDYAY  288
Hd-3500P-Hd1598/PdtB          YPV-DNTPFMSNA-----KGTLID---GFTSGGTNTIASLKLLL---TKPDTQ-------------------NWEGNYRM  266
Acti.s-130Z-Asuc_1041         YPI-ETTPFLAKT-----KGLIID---GYISAAPNTQSSLARTL---YLYKE---------------------NDTQFQN  276
Hh-CCUG3714-B0186_06625       YPI-KTTPFLDKV-----NGIVFN---DYVAASGNTQLSLKNTL---YRKQD--------------------RETFIYTD  290
Aggr.a-RhAA1-RhAA1_04486      YPQ-KTTPFLEQV-----NGLIFN---LYVAAGPNTQPSLQRTL---YRSTNN-------------------NQETVYTD  295
Hf-CCUG31170-B0188_07100      YPL-ETTPFLNTT-----NGIIID---GYISAAPNTQTSLLRTL---YQFQG---------------------DKTQYEN  298
Hh-11P18-AAX18_01700          YPI-KTTPFLDSI-----NGTIFN---NYYSAAPNTQPSLQRTL---YRQE---------------------NYKTVYTD  286
Ec-K12-OpgE                   GHW-DNTPFASSV-----NGLIFA---DYIAASGSTQKSLGLTL---NRVVD---------------------GKPQFQD  283
Ng-FA19-DcaA/PptA             FPL-PDTPFLSRT-----KGLLIN---GYQSTAHATNLSLPQTL---GLP-------------------------GEPNN  290
Ec-W3110-EptB                 YER-NTTPKLAQE----KNLAAF----RGYSCDTATKLSLRCMFVRQGGAEDN-------------------PQRTLKEQ  330
Ec-K12-EptC/CptA              YPR-ETTPELDALHKTDPNLTVFN---NVVTSRPYTIEILQQALTFANEKNPD-------------------LYLT--QP  311
ST-L2-EptC/CptA               YPR-ETTPELDALHKTDPGLTVFN---NVVTSRPYTIEILQQALTFADEKNPD-------------------WYLT--KP  311
Ec-plasmid-ECH74115_B0113     YLR-ETTPELDALRKTDPGLTVFN---NVVASRPYTIEALQQALTFANEKNPD-------------------LYLT--QP  311
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Sf-plasmid-SFxv_5135/LptO    KLPIILEENGYHTYF-------------QASNSIDAPLSLMLSTLKFNHIYGREDYNKK----SGELTDKESFDLLFKK-  318
Pm-X73-A0R63_09570/PetK      TIAELLAKQGYHTSF------IY-----GGEKHFDNMASFFYGN-GFQYIIDELDYVNPKFKATWGVSDEDLFDKAHETF  432
HI-KW20-HI_1246              TIADLLHKQGYNTSF------IY-----GGEKHFDNMASFFYGN-GFKDIWDQQDYQNPKFTGTWGVSDEDLFDKANETF  429
Mh-M42548-MHH_c23440         SIAELLKRQGYHTSF------IY-----GGEKHFDNMASFFYGN-GFQQIIDEKDYKNPKFTATWGVSDEDLFDKANETF  430
Acti.p-L20-APL_0804          SIAELLRRQGYDTSF------IY-----GGEKHFDNMASFFYGN-GFTRIIDEKDYKNPKFKATWGMSDEDLFDKANETF  438
Aggr.a-D11S1-D11S_0415       TLAQLLSQRGYDTSF------IY-----GGEKHFDNMAGFFYGN-GFKRIIDQMDYQNPTFTGTWSVSDEDLFTKANETF  434
Aero.s-A449_ASA3698          TIADLLKQRGYNTSF------IY-----GGESHFDNMRSFFLGN-GFTTIVEQKDFKNPVFEGSWGASDEDLMTKADETF  444
Shew.p-CN32-Sputcn32_3803    SIAELLKNHGYTTQF------IY-----GGESHFDNMRSFFLGN-GFSDIIEQKDYKSPAFVGSWGVSDEDLMRKANSEF  436
Vh-1DA3-VME47170             TIADLLKANGYHTEF------IY-----GGEANFDNMKTFFFGN-GFDQIIEEKDYENPSFVGSWGVSDEDLYTKADQEF  426
Vp-UCMV493-VPUCM_1817        TIADLLKEQGYHTQF------IY-----GGEANFDNMKTFFFGN-GFDQIVEEKNYTNPGFVGSWGVSDEDLYNKADEEF  422
Vc-M10-VchoM_02105           SIAGLLKTQQYHTQF------IY-----GGESHFDNMKSFFLGN-GFVDMQDLPTFSNPKFVGSWGASDEDLFNKADEQF  430
Vc-O1ElTorN16961-VCA802      SIAGLLKTQQYHTQF------IY-----GGESHFDNMKSFFLGN-GFVDMQDLPTFSNPKFVGSWGASDEDLFNKADEQF  433
Bp-TahomaI-BP3136            TLADLLGRHGFHSRF------IY-----GGEAHFDNMRGFFLGN-GFNEVIDRQSFVDPVFVGSWGASDEDMFNQLDRLL  438
Pm-X73-A0R63_06305/PetL      NLLDILQRAGIAI--------KW-LNNNSDCKGVCKHIP----------YQNVTTLNLAEYCRNGECLDNILLTQVDQIL  365
Hd-3500P-Hd0852/EptA         NLIDILNRAGVKI--------VW-IQNNSDSKNVADRIG----------EINVFKGVESPLCVDGECQDNIMLPELDKAL  368
Nm-Mc58-NMB1638/EptA         NLLDIVQRAGVEV--------TW-LENDSGCKGVCGKVP----------NTDVTSLNLPEYCRNGECLDNILLTKFDEVL  366
Ng-FA19-NGEG_02067/LptA      NLLDIVQRAGVEV--------TW-LENDSGCKGVCGKVP----------NTDVTSLNLPEYCRNGECLDNILLTKFDEAL  366
Hp-6695-Hp0022/EptA          NLPTYLTKAGIKV--------FW-YSANDGEKNVKVTSY----------LKNYELIQKCPNCEAIAPYDESLLYNLPDLL  350
Cj-NCTC11168-Cj0256/EptC     NAMDVLYKTGVDA--------VWFDNNSGGCKGVCDRLAYKQKL--------------------SSDLDENLLAPFKEKL  341
Vp-UCMV493-VPUCM_20416       NALDIMQRAGIDL--------LW-KENDGGDKEVAHKIK----------KIEVDRKQQNALCNGQTCYDMALLSDFDQEV  372
Vc-M10-VchoM_02405           NVLDILQRAGISL--------LW-KENDGGDKNVAKNIP----------LKELARDNREGICDGDTCYDIAMLENLDQEI  372
Vc-O1ElTorN16961-VCA1102     NVLDILQRAGISL--------LW-KENDGGDKNVAKNIP----------LKELARDNREGICDGDTCYDIAMLENLDQEI  372
ST-L2-PmrC                   GLLDIIQRAGINV--------LW-NDNDGGCKGACDRVP----------HQNVTELNLPGQCIDGECYDEVLFHGLEDYI  368
Ec-plasmid-mcr1              NVLDTLDRLGVSI--------LW-RDNNSDSKGVMDKLPKAQFA----DYKSATNNAICNTNPYNECRDVGMLVGLDDFV  377
Ec-plasmid-mcr2              NVLDTLDRLGVGI--------LW-RDNNSDSKGVMDKLPATQYF----DYKSATNNTICNTNPYNECRDVGMLVGLDDYV  375
Pm-X73-A0R63_02570/Lpt3      NLFRLAKERGYQTYFYSAQP-----ENQMMIMSIMGKTWVDHLL----------FPSDIGYKRSEGMHDHALLPLFEQID  352
Nm-MC58-Lpt3                 NMFRLAKEQGYETYFYSAQA-----ENEMAILNLIGKKWIDHLI----------QPTQLGYGNGDNMPDEKLLPLFDKIN  354
Ng-FA19-Lpt_3                NMFRLAKEQGYETYFYSAQA-----ENQMAILNLIGKKWIDHLI----------QPTQLGYGNGDNMPDEKLLPLFDKIN  353
Hi-RdKW20-Lpt_6              GLVKNLKAQGYFCVALSPFTKGN-YNAKSAYDHFGFDLMLQPQDLG---------YPAPISKNLWDISSEEMMKYTRMIL  364
Nm-MC58-Lpt6                 GFVRNLREHGYFCVALSPFTKGN-YNAKAAYDHFGFNLMFQPQDLG---------YPAPMGKNLWHISSEEMMQYARMIL  363
Ng-FA19-Lpt_6                GFVRNLREHGYFCVALSPFTKGN-YNAKAAYDHFGFNLMFQPQDLG---------YPAPMGKNLWHISSEEMMQYARMIL  363
Pm-X73-A0R63_03465/PetG      NIINLANSAGFDT--------YW-ISNQGVLGNHDTVASRIGFL-----AKHHIFTKKGGYDDSET-RDLKLLEYFDEYL  349
Pm-P1059-PetG                NIINLANSAGFDT--------YW-ISNQGVLGNHDTVASRIGFL-----AKHHIFTKKGGYDDSET-RDLKLLEYFDEYL  349
Pm-P2100-A0R72_03015         NIATLANLAGFNT--------YW-ISNQGILGEFDTAASRLAYL-----FKHHKFTKKGDFDDVNI-HDIKLLEHFKDYL  350
Pm-HN06-PMCN06_0886          NIATLANLAGFNT--------YW-ISNQGILGEFDTAASRLAYL-----FKHHKFTKKGDFDDVNI-HDIKLLEHFKDYL  349
Hd-3500P-Hd0371/PdtA         NIITLAKGANFET--------NW-FSNQGSIGKYDTIASRMGQA-----SDFSYFTKVGGFNTTNNEDDFKLVEQLKQRL  354
Hd-3500P-Hd1598/PdtB         NVIELVNSAGINT--------FW-LSNQGYLGQFDTPISSLANK-----SNKKIFLKSGD-SFSQNISDFELLPKFIQII  331
Acti.s-130Z-Asuc_1041        NIITLAKQAGFKT--------YW-LSNQGFSGEFDSVAARVGVG-----SDKSHFTQLSSDSININ--DKTLLQIFRTEL  340
Hh-CCUG3714-B0186_06625      NIISLANKANFKT--------YW-LSNQGMLGQYDTIASRIGQQ-----ASYFFFSKKGSYDDKNY-FDTVLLEPFKKAL  355
Aggr.a-RhAA1-RhAA1_04486     NIISLAKLAHYKT--------YW-LSNQGKVGEWDTMASRIGIQ-----ADKSFFTKKGGYDSGNT-PDTALLEPLKQLL  360
Hf-CCUG31170-B0188_07100     NIITLAKQAGFAT--------FW-ISNQGQTSKFDTAASRVGYN-----ANEYYFTQEADSNLTIN--DTKLLPIFQEKI  362
Hh-11P18-AAX18_01700         NIISLLKLANIKT--------YW-LSNQGKMGEYDTMASRLGVN-----ADYNFFTKDLWYETEKK-FDTELLPKFKEIL  351
Ec-K12-OpgE                  NFVTLANRAGFQT--------WW-FSNQGQIGEYDTAIASIAKR-----ADEVYFLKEGNFEADKNTKDEALLDMTAQVL  349
Ng-FA19-DcaA/PptA            NIVSLAQ-AGFRT--------AW-LSNQGMLGHFANEISTYALR-----SDYPWFTQRGDYGKSAGLSDRLLLPAFKRVL  355
Ec-W3110-EptB                NIFAVLKQLGFSSDLYAMQSEMWFYSNTMAD-NIAYREQI----------------GAEPRNRGKPVDDMLLVDEMQQSL  393
Ec-K12-EptC/CptA             SLMNMMKQAGYKT--------FW---ITNQQTMTARNTMLTVFS----RQTDKQYYMNQQRTQSAREYDTNVLKPFQEVL  376
ST-L2-EptC/CptA              SLMNMMKQAGYKT--------FW---ITNQQTMTARNTMLTVFS----KQTDKQFYMNQQRTQSAREYDSNVLAPFKAVL  376
Ec-plasmid-ECH74115_B0113    SLMNMMKQAGYKT--------FW---ITNQQTITARNTMLTVFS----RQTDRQYYMNQQRTQSAREYDTNVLKPFREVL  376
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Sf-plasmid-SFxv_5135/LptO   ---LNEA------KQPFFYGVYTVGTHL------------GLDSPDVK---F-----YDGRNEYLNHFHQLDHWFGDFIS  369
Pm-X73-A0R63_09570/PetK     -TALHKE------GKPFFSLVFSSSNHD------------PFEFPDGKIELY-----EQPKQTRNNAAKYADYAIGHFFK  488
HI-KW20-HI_1246             -TKLQNE------GKPFFSLVFSSSNHD------------PFEYPDGKIELY-----EQPKATRNNAAKYADYALGHFFK  485
Mh-M42548-MHH_c23440        -NQLHKS------GKPFFSLVFSSSNHD------------PFEFPDGKIELY-----EQPKQTRHNAAKYADYAIGHFFE  486
Acti.p-L20-APL_0804         -TQLHKE------GKPFFSLVFSSSNHD------------PFEFPDDKIELY-----EQPKQTRNNAAKYADFAIGHFFE  494
Aggr.a-D11S1-D11S_0415      -TQLQKE------GKPFFSLVFSSSNHD------------PFEFLDGKIELY-----EQPKATRNNAAKYADYAIGHFFK  490
Aero.s-A449_ASA3698         -KALHKE------GKPFFSLVFSSSNHD------------PFEFPDDRIDLY-----EQPKQTRNNAAKYADYAIGEFFK  500
Shew.p-CN32-Sputcn32_3803   -ERLHNE------GKPFFSLVFSSTNHD------------PFEFPDDRIELY-----EQPKQTRNNAAKYADYAIGEFFK  492
Vh-1DA3-VME47170            -ERLSKN------GKPFFSLVFSSSNHS------------PYEYPQGKIEPY-----DSEYMTRNNAVKYSDYAIGTFFD  482
Vp-UCMV493-VPUCM_1817       -ERLSKG------DKPFFSLVFTSSNHS------------PYEYPEGKIEQY-----DSEHMTRNNAVKYSDYALGTFFD  478
Vc-M10-VchoM_02105          -TQMAKE------GKPFFSLVFTSSNHS------------PFEYPDGVITQY-----NEPKQTVENAVKYADYALGQFVE  486
Vc-O1ElTorN16961-VCA802     -TQMAKE------GKPFFSLVFTSSNHS------------PFEYPDGVITQY-----NEPKQTVENAVKYADYALGQFVE  489
Bp-TahomaI-BP3136           -R--ADD------GKSTFTLAFSVSNHS------------PWEYPAGRIEPV-----GDP-ASVDNTVRYADWAMGQFFD  491
Pm-X73-A0R63_06305/PetL     ---DST-------DKDTVLVLHTIGNHGPTYYERYTPEYRQFVPTCDTNQIN-RCSKQQLVNTYDNGILYVDQFIDQVIS  434
Hd-3500P-Hd0852/EptA        ---AENP------TQDLVVVLHTIGSHGPTYYERYTEAERLFTPTCDTNNIN-KCSREELVNTYDNSVVYLDQFLDKVIE  438
Nm-Mc58-NMB1638/EptA        ---NKN-------DKDAVLILHTIGSHGPTYYERYTEAERKFTPTCDTNEIN-KCTRATLVNTYDNTVLYVDQFIDKVIR  435
Ng-FA19-NGEG_02067/LptA     ---NKN-------DKDAVLILHTIGSHGPTYYERYTEAERKFTPTCDTNEID-KCARATLVNTYDNTVLYVDQFIDKVIR  435
Hp-6695-Hp0022/EptA         ---KEHS------NENVLLILHLAGSHGPNYDNKVPLNFRVFKPYCSSADLS-SCSKESLINAYDNTIFYNDYLLDKIIS  420
Cj-NCTC11168-Cj0256/EptC    ---NHL-------SDQNIIVLHLQGSHGPTYYKRYPSEFKKFTPTCDTNELS-KCDSEALINTYDNTLLYTDYLLSEIIK  410
Vp-UCMV493-VPUCM_20416      ---SNM-------NGNRVVAMHLIGSHGPTYFQRYPKEKAFFQPDCPRADIE-NCSVEEIVNTYDNTIRYTDFVLEQTIN  441
Vc-M10-VchoM_02405          ---ATQ-------QGNRMIFMHFIGSHGPTYFKRYPKEMAVYQPDCPRADIE-NCSVEQIVNTYDNTIRYSDYVMSQLLA  441
Vc-O1ElTorN16961-VCA1102    ---ATQ-------QGNRMIFMHFIGSHGPTYFKRYPKEMAVYQPDCPRADIE-NCSVEQIVNTYDNTIRYSDYVMSQLLA  441
ST-L2-PmrC                  ---DHL-------KGDGVIVLHTIGSHGPTYYNRYPPQFKKFTPTCDTNEIQ-NCSQEQLINTYDNTVLYVDYIVDKAIN  437
Ec-plasmid-mcr1             ---AANN------GKDMLIMLHQMGNHGPAYFKRYDEKFAKFTPVCEGNELA-KCEHQSLINAYDNALLATDDFIAQSIQ  447
Ec-plasmid-mcr2             ---SANN------GKDMLIMLHQMGNHGPAYFKRYDEQFAKFTPVCEGNELA-KCEHQSLINAYDNALLATDDFIAKSID  445
Pm-X73-A0R63_02570/Lpt3     -----LS------EGNHFIVLHQRGSHA-PYAYYLSEEEKAFK------ENT-------PLDNYDSTLYNTDQFIEKVFK  407
Nm-MC58-Lpt3                -----LQ------QGKHFIVLHQRGSHA-PYGALLQPQDKVFG------EAD-------IVDKYDNTIHKTDQMIQTVFE  409
Ng-FA19-Lpt_3               -----LQ------QGRHFIVLHQRGSHA-PYGALLQPQDKVFG------EAD-------IADKYDNTIHKTDQMIQTVFE  408
Hi-RdKW20-Lpt_6             ---EKQHPALENVDQPMFVYVLTMREHG----PYELGMENTFNLQMPNLGAK----SISALNDYTQRIVALNDAIEGINN  433
Nm-MC58-Lpt6                ---EKRHPDLENVRQPMFVYVLTMKEHG----PYRTDTDNVFDLDVPDLNAK----TVSALNDYIGRIADLDKAVESFDR  432
Ng-FA19-Lpt_6               ---EKRHPDLENVRQPMFVYVLTMKEHG----PYRTDTDNVFDLDAPDLNAK----TVSALNDYIGRIADLDKAVESFDR  432
Pm-X73-A0R63_03465/PetG     -LE-IDN------SKKNLFVFHLMGSHP-SFCMRLDSLPEI-----Y-FINQ-------DMTCYLETFKQTDLFLERLIA  407
Pm-P1059-PetG               -LE-IDN------SKKNLFVFHLMGSHP-SFCMRLDSLPEI-----Y-FINQ-------DMTCYLETFKQTDLFLERLIA  407
Pm-P2100-A0R72_03015        -VSSVNN------PSPNLFVLHLMGSHP-DFCNRLENSPKI-----N-LINK-------DISCYLETYKQTDFFISKIVD  409
Pm-HN06-PMCN06_0886         -VSSVNN------PSPNLFVLHLMGSHP-DFCNRLENSPKI-----N-LINK-------DISCYLETYKQTDFFISKIVD  408
Hd-3500P-Hd0371/PdtA        ALNKLVE------KRGRLFVLHLMGSHA-PFCDRITAKEKQ-----LTFVNE-------YMSCYVNSILKTDKLIENVVD  415
Hd-3500P-Hd1598/PdtB        ---EQKS------TAKRFIVLHLYGSHP-ITCDRLTDYPKIYDDTKIPAKYH-------DINCYLSSIKKTDQLIEKVYK  394
Acti.s-130Z-Asuc_1041       ---QKSD------EMPRLFVLHLMGSHP-VFCRRIDMSPF------IWFKNN-------EMSCYLETLRQTDALIKNVVD  397
Hh-CCUG3714-B0186_06625     -TE--QT------EQGKLIVLHLIGSHP-LFCERLEKQPSE-----KRF-SK-------EVDCYIETIKQTDHFIATINE  412
Aggr.a-RhAA1-RhAA1_04486    -NK--DK------DQTKLIVLHLIGSHP-TFCAHLNGEEPK-----FHLVSR-------EMSCYLDTLKQTDTLLSEINQ  418
Hf-CCUG31170-B0188_07100    ---NKLS------DKPRLFVLHLMGSHP-RFCKRILNKPI------FELKNK-------EMSCYLQSILETDKLIKEVND  419
Hh-11P18-AAX18_01700        -EK--EK------NTNKLIVLHLMGSHP-IFCERLPYKVEN-----Y-FINQ-------QMSCYLESIKYTDKFIEDINK  408
Ec-K12-OpgE                 ---AQEH------SQPQLIVLHLMGSHP-QACDRTQGKYE------TFVQSK-------ETSCYLYTMTQTDDLLRKLYD  406
Ng-FA19-DcaA/PptA           ---GNAG------TKPRLIVMHLMGSHS-DFCTRLDK-----DARRFQYQTE-------KISCYVSTIAQTDKFLEDTVK  413
Ec-W3110-EptB               ---GRNP------DGKHLIILHTKGSHF-NYTQRYPRSFAQWKPECIGVD-S-GCTKAQMINSYDNSVTYVDHFISSVID  461
Ec-K12-EptC/CptA            ---NDP-------APKKLIIVHLLGTHI-KYKYRYPENQGKFDGNTDHVPPGLNAEELESYNDYDNANLYNDHVVASLIK  445
ST-L2-EptC/CptA             ---ADP-------APKKFIIVHLLGTHI-KYKFRYPENQGKFDGKTDHVPPGLSSDELESYNDYDNANLYNDYVVASLIK  445
Ec-plasmid-ECH74115_B0113   ---NDP-------APKKLIIVHLLGTHI-KYKYRYPEGQGRFDGITGHIPTGLNAKELEVYNDYDNANLFNDHVVASLIK  445
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Zinc co-ordination sites Asp452/427/465 and His 453/428/466 in EptA$_{Nm}$/EptC/Mcr-1

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Sf-plasmid-SFxv_5135/LptO   HFN--KTSLSKDTIVIITSDHASYPSEDYKK-----TFKTDNTFFVDQIPLIIWSNGVEF------------KDINAHGL  430
Pm-X73-A0R63_09570/PetK     LAK--QADYWKDTLFLVIADHDSRVGGAALV-----PIKHF------HIPALLLGDHVEV------------K-RDARLV  542
HI-KW20-HI_1246             MAK--QSNYWKDTIFLIIADHDSRVGGASLV-----PIKHF------HIPALILGDGITP------------R-RDSRLV  539
Mh-M42548-MHH_c23440        LAK--KSEYWQDTVFLVIADHDSRAVGEHLV-----PIQHF------HIPALLLGEHIQP------------R-TDNRLV  540
Acti.p-L20-APL_0804         LAK--KSEYWQDTIFLVIADHDSRAVGEHLV-----PIQHF------HIPALFIGEGIEA------------K-RDSRLV  548
Aggr.a-D11S1-D11S_0415      LAK--ESNYWKDTIFLVIADHDSRVAGASLM-----PIKHF------HIPALILGDGIAP------------H-RDDRLV  544
Aero.s-A449_ASA3698         KAK--QSDYWKDTLFLVIADHDSRVGGDSLV-----PIPRF------HIPGVIVGDGIAP------------K-QDPRIV  554
Shew.p-CN32-Sputcn32_3803   LAK--NAAYWKDTIFIVVADHDSRVVGADLV-----PVSRF------RIPGLIIGDGVTP------------K-RDHRIV  546
Vh-1DA3-VME47170            KAK--KSSYWDDTVFIIIADHDARVSGANLV-----PVKHF------HIPALILGKDIKP------------R-KDDRIA  536
Vp-UCMV493-VPUCM_1817       KAK--KSSYWDDTIFIVIADHDARVFGANLV-----PVKHF------HIPALIIGKDIQP------------R-KDDRIA  532
Vc-M10-VchoM_02105          KAK--KSPYWDNTVFVVVADHDARTQGTNPI-----PVEYF------HIPAVIFGGGIEA------------R-KDDRLL  540
Vc-O1ElTorN16961-VCA802     KAK--KSPYWDNTVFVVVADHDARTQGTNPI-----PVEYF------HIPAVIFGGGIEA------------R-KDDRLL  543
Bp-TahomaI-BP3136           KAR--KAPYWDNTVFLVIADHDSRVYGANLV-----PVRHF------QIPALILGGTVPP------------R-SDDRIV  545
Pm-X73-A0R63_06305/PetL     KLE--QRQH-LQSAVIYVSDHGESLGEKGVY-LHAAPYVIAPT-EQTHIPMIMWFSPRWKASQQVDLTCL-RQKAKEEAY  508
Hd-3500P-Hd0852/EptA        RLE--AHNE-WKSSLYYFSDHGESLGEKGIY-LHGTPYAFAPE-EQTHIPMLLWFSPTWIKHKPFDLACV-R-KNAAKAY  511
Nm-Mc58-NMB1638/EptA        KLE--NRDD-LESVVHYVSDHGESLGENGMY-LHAAPYAIAPS-GQTHIPMVMWFSKAFRQHGGIDFQCL-KQKAAENEY  509
Ng-FA19-NGEG_02067/LptA     KLE--NRDD-LESAVYYVSDHGESLGENGMY-LHAAPYAIAPS-GQTHIPMVMWFSKAFRQHGGIDFQCL-KQKAAENEY  509
Hp-6695-Hp0022/EptA         MLE--NAKQ--PALMIYLSDHGESLGEEAFY-LHGIPKSIAPK-EQYEIPFIVYANEPFKEKHSI----I----QTQTPI  486
Cj-NCTC11168-Cj0256/EptC    LLK--EQKS-YESSLFYLSDHGESLGENGIY-LHGMPYAIAPS-YQTHIPAIFWSNDKNLMNLAKEYKGL--------KL  477
Vp-UCMV493-VPUCM_20416      KLK--TLEDKYNTALIYVSDHGESLGESGMF-LHGMPYGLAPD-FQKRVPLIMWMSPSFKQAKHINTDCLSKEAQNAGKY  517
Vc-M10-VchoM_02405          KLD--SLQDRYNTALIYISDHGESLGENGLF-LHGMPYSLAPE-YQTRVPLLIWMSSGFSQSKGIDVECL--RSNSELPY  515
Vc-O1ElTorN16961-VCA1102    KLD--SLQDRYNTALIYISDHGESLGENGLF-LHGMPYSLAPE-YQTRVPLLIWMSSGFSQSKGIDVECL--RSNSELPY  515
ST-L2-PmrC                  LLK--SHQDKFTTSLVYLSDHGESLGENGVY-LHGLPYSIAPD-TQKHVPMLIWLSKDYQQRYQVDQACL-QKRASTLDY  512
Ec-plasmid-mcr1             WLQ--THSNAYDVSMLYVSDHGESLGENGVY-LHGMPNAFAPK-EQRSVPAFFWTDKQTG---------I-TPMATDTVL  513
Ec-plasmid-mcr2             WLK--THEANYDVAMLYVSDHGESLGENGVY-LHGMPNAFAPK-EQRAVPAFFWSNNTT----------F-KPTASDTVL  510
Pm-X73-A0R63_02570/Lpt3     QLK---QHHD-DWVLIYTSDHGQFVSNQVYN------QGTAKE-ANYLVPIMTYTENTVLQ-----------Q-LQRPFL  464
Nm-MC58-Lpt3                QLQ---KQPDGNWLFAYTSDHGQYVRQDIYN------QGTVQP-DSYLVPLVLYSPDKAVQ-----------QAANQAFA  468
Ng-FA19-Lpt_3               QLQ---KQPDGNWLFAYTSDHGQYVRQDIYN------QGTVQP-DSYIVPLVLYSPDKAVQ-----------QAANQAFA  467
Hi-RdKW20-Lpt_6             YLH----ERKKPFVLGYFGDHQVAFDNAIPPKKGDYAQPDYVT---QFVVRSNCASQFKQEQKFLDLAFAGGVLMNVAGL  506
Nm-MC58-Lpt6                YLH----ERGKPFVFGYFGDHQVPFEGVSVRKKWDYAQPDYVT---QFAVRSNIAGGFVQRQDFLDLAFAGGVLMEAAGL  505
Ng-FA19-Lpt_6               YLH----ERGKPFVFGYFGDHQVPFEGVSVRKKWDYAQPDYVT---QFAVRSNIAGGFVQRQDFLDLAFAGGVLMEAAGL  505
Pm-X73-A0R63_03465/PetG     RL-----EKLGSYSVIYFSDHGLQHYNT-RKDKLSLHVGNEYQ-ESFSVPLVKISSDDLK------------QIKIDARR  468
Pm-P1059-PetG               RL-----EKLGSYSVIYFSDHGLQHYNT-RKDKLSLHVGNEYQ-ESFSVPLVKISSDDLK------------QIKIDARR  468
Pm-P2100-A0R72_03015        EL-----KQYGSYSVIYFSDHGLSHYGK-DDKSLTLKHNNKFK-ENYHVPFIQISSDDIA------------QKRIHAYR  470
Pm-HN06-PMCN06_0886         EL-----KQYGSYSVIYFSDHGLSHYGK-DDKSLTLKHNNKFK-ENYHVPFIQISSDDIA------------QKRIHAYR  469
Hd-3500P-Hd0371/PdtA        ALK----STGQSYSLIYFSDHGLHHIDKTDKQKLTLDYGGEFK-SNYAVPFVKISSDDTE------------RLMVNTKR  478
Hd-3500P-Hd1598/PdtB        QLKQNETKTGRSFSMIYFSDHGLIHSEN-KNGIHILNT-AQSK-FHFDVPLFKISSDDQE------------RHVYKVFK  459
Acti.s-130Z-Asuc_1041       LVQ----AEGNDYSLIYFSDHGLSHRDK-ESKKMTLQVGNEHK-ENYQVPFIRISGDDSE------------RRIIKTQR  459
Hh-CCUG3714-B0186_06625     ILK----QNNQSYSVLYFSDHGLSHFK--DKSTLTLTVGNKYK-QNYEVPLIRFSSDDVK------------REYIQAPK  473
Aggr.a-RhAA1-RhAA1_04486    ILK----AQNQSYSVIYFSDHGLAHLG--EGKNLSMLNNKEYK-QSYAVPFIRFSSDDTK------------RTLIKNPQ  479
Hf-CCUG31170-B0188_07100    ILS----SKGN-YSLIYFSDHGLSHQGK-DSS-LTLLVGNKYK-QNYQIPFIKISSDDET------------REVIKTQR  479
Hh-11P18-AAX18_01700        LLI----KNNESFSVIYFSDHGLAH------KNDSLHVSNLYK-QDYEVPFIMFSSDSIK------------RIEINEKQ  465
Ec-K12-OpgE                 QLR----NSGSSFSLVYFSDHGLAFKER-GKDVQYLAHDDKYQ-QNFQVPFMVISSDDKA------------HRVIKARR  468
Ng-FA19-DcaA/PptA           I-----NENKESWSLVYFSDHGLMHV-G-KGGERTLTHGEWKR-QSYGVPLVKISSDDTR------------REMIKVRR  473
Ec-W3110-EptB               QVR--DKKA----IVFYAADHGESINER-EH-LHGTPRELAPP-EQFRVPMMVWMSDKYLENPANAQAFA--QLKKEADM  530
Ec-K12-EptC/CptA            DFK--AANP--NGFLVYFSDHGEEVYDTPPHKTQGRNEDNPTR-HMYTIPFLLWTSEKWQATHPRDFSQD-----VDRKY  515
ST-L2-EptC/CptA             DYK--ATDP--NGFLLYFSDHGEEVYDTPPHKTQGRNEDSPTR-HMYTVPFLLWTSEKWQAAHPRDFSQD-----VDRKY  515
Ec-plasmid-ECH74115_B0113   DFR--ATAP--DGFLLYFSDHGEEVYDTPPYKTQGRNEDNPTR-PMYTVPFLLWTSEKWHAAHPRDFSQY-----VDRKY  515
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Sf-plasmid-SFxv_5135/LptO   N----SLSLTPTILDIL-GIKESHNMFIGESLFE-------KEKNKNELNCTSAIGD---------------LYVKTC--  481
Pm-X73-A0R63_09570/PetK     S----QIDMPTTLLSLA-GISGDYPM-IGYDLTK--EDNPNRAFMQYDQTLAMMKGN-EVVILAPKVEAKGYLYDKQ---  610
HI-KW20-HI_1246             S----QIDMPTTLLSLA-GVSGNYPM-IGFDLTQ--DVNPDRAFMQYDQTQAMMKGNNDVVIQMPNKAAQGYHYDKS---  608
Mh-M42548-MHH_c23440        S----QLDMPTTLLSVA-GISGQYPM-IGYDLTQ--DIDPNRAFMQYDATQAMMRGN-DVVVMRPNLPIEGFSYDKA---  608
Acti.p-L20-APL_0804         S----QIDMPATLLSLA-GVSGEYPM-LGYDLTK--DVNPNRAFMQYDATQAMMKGDGSVVVMRPNTPIQGFIYNKA---  617
Aggr.a-D11S1-D11S_0415      S----QFDMPTTLLSLA-GISGDYPM-IGYDLTK--PNDPNRAIMQYDQVQALMRGN-DVVLQFPKVGAKTYRYDKT---  612
Aero.s-A449_ASA3698         S----QIDMAPTLLSLM-GISADYPM-LGKDLTRMPADWPGRAIMQYDKNFALMRGK-DVVILQPERPAQGFIYEDA---  624
Shew.p-CN32-Sputcn32_3803   S----QIDLPPTLLSLM-GISDSYPM-LGRDLTKVSDDWAGRALMQYDKNFALMEGK-DVVILQPEKAAQGFQYNQK---  616
Vh-1DA3-VME47170            N----NLDMPPTLLSLI-GVDAKTPM-IGRDLTKPLARKDERAMMQYDKNFGYLTRDN-LVVFSPGEKVSTMQYNFD---  606
Vp-UCMV493-VPUCM_1817       N----NIDMPPTLLSLI-GVDAKTPM-IGRDLTKPLAREDERAMMQYDKNFGYLTRDN-LVVLSPGEKVSTMEYDFE---  602
Vc-M10-VchoM_02105          S----QLDLAPTLLSLA-GISSQNPM-IGFDLTQDVPVEKQRAMMQRDKNFGWLTPDNQVVVLQPGQDITTYQYDSV---  611
Vc-O1ElTorN16961-VCA802     S----QLDLAPTLLSLA-GISSQNPM-IGFDLTQDVPVEKQRAMMQRDKNFGWLTPDNQVVVLQPGQDITTYQYDSV---  614
Bp-TahomaI-BP3136           S----QIDMGPTLLSLI-GLDNVNPM-LGSDLTQ---RDPNRAIMQYGDNFGYLKGD-SLLVIEPGKDPREYRYTAAASM  615
Pm-X73-A0R63_06305/PetL     S----HDHFFSTVFGLM-QMSEESET--------------------YQQDMDILRRC----------RI-R---------  543
Hd-3500P-Hd0852/EptA        S----HDNVFHTVFSLM-DIDMSKAS-----------------LPMYDEKLDMLAEC----------AHKVE--------  551
Nm-Mc58-NMB1638/EptA        S----HDHYFSTVLGLM-DISN-SQT--------------------YRKEMDILAAC----------RRPR---------  544
Ng-FA19-NGEG_02067/LptA     S----HDHYFSTVLGLM-DISN-SQT--------------------YRKEMDILAAC----------RRPR---------  544
Hp-6695-Hp0022/EptA         N----QNVIFHSVLGVFLDFKNPSVV--------------------YRPSLDLLKHK----------KE-----------  521
Cj-NCTC11168-Cj0256/EptC    S----QDNLFSTLLGYF-DVKT----------------------SVYEPEYDLLNPK----------LKANP--------  512
Vp-UCMV493-VPUCM_20416      S----HDNVFHSLLGIM-DVKT----------------------QAYDGQLDIFKTC----------RTVS---------  551
Vc-M10-VchoM_02405          A----HQNLFHSLLGVM-DVST----------------------KAYQANLDLFAKC----------RTSQS--------  550
Vc-O1ElTorN16961-VCA1102    A----HQNLFHSLLGVM-DVST----------------------KAYQANLDLFAKC----------RTSQS--------  550
ST-L2-PmrC                  S----QDNLFSTMLGLT-GVQT---T-----------------Y--YQAADDILQPC----------RRLSE--------  547
Ec-plasmid-mcr1             T----HDAITPTLLKLF-DVTADKVK-------------------------DRTAFI----------R------------  541
Ec-plasmid-mcr2             T----HDAITPTLLKLF-DVTAGKVK-------------------------DRAAFI----------Q------------  538
Pm-X73-A0R63_02570/Lpt3     AC----DRLFHQQLSTF------IIK-----------------MLGYDMPISDCQHG----------VINSLILTGDSGY  507
Nm-MC58-Lpt3                PC----EIAFHQQLSTF------LIH-----------------TLGYDMPVSGCREG----------SVTGNLITGDAGS  511
Ng-FA19-Lpt_3               PC----EIAFHQQLSTF------LIH-----------------TLGYDMPVSGCREG----------SVTGNLITGDAGS  510
Hi-RdKW20-Lpt_6             SA---EDEFMKANMAMC-KLSDGKLE----DSSD-IQLLNNYRHYLYQTLAIAR--------------------------  551
Nm-MC58-Lpt6                EA---KDGFMRANMAMR-GLCGGGLE----DCPN-RKLVGDYRNYLYDVLKIAR--------------------------  550
Ng-FA19-Lpt_6               EA---KDGFMRANMAMR-GLCGGGLE----DCPN-RELVGNYRNYLYDVLKIAR--------------------------  550
Pm-X73-A0R63_03465/PetG     S----GMFFLNAFSEWL-GIDEESL------------------KLPYLFFSNDVDKK----------PTIVFDWE-NYII  514
Pm-P1059-PetG               S----GMFFLNAFSEWL-GIDEESL------------------KLPYLFFSNDVDKK----------PTIVFDWE-NYII  514
Pm-P2100-A0R72_03015        S----GMDFLNGFAEWL-GIEESSL------------------KRPYSFFSEDNMNL----------PLKVFDWE-KYID  516
Pm-HN06-PMCN06_0886         S----GMDFLNGFAEWL-GIEESSL------------------KRPYSFFSEDNMNL----------PLKVFDWE-KYID  515
Hd-3500P-Hd0371/PdtA        S----AFNFMYGFSQWL-GIRSAEL------------------DQNYDFFSNK-DDE----------HIKVFNFK-ENVE  523
Hd-3500P-Hd1598/PdtB        S----GLNFTDGIGKWI-GIINKKL------------------NPTVDLFSNQ-ADD----------NDYGLK-Q--IIE  502
Acti.s-130Z-Asuc_1041       S----AFNFIYGFAHWL-GIQEKTL------------------SNGYQFFSEI-PDD-----------VKVFNWY-QDVN  503
Hh-CCUG3714-B0186_06625     S----AFHFMGGFAQWL-GIQEKHL------------------QQEQNFFSEE-TTL----------PIKIFNWQ-KFVN  518
Aggr.a-RhAA1-RhAA1_04486    S----AFNFINGFAQWL-GIKETHL------------------SQEDFFNPKP-Q------------PIKVFNWR-ALVD  522
Hf-CCUG31170-B0188_07100    S----AFNFIYGFAEWL-GISEENL------------------DTGYRFFSHS-PDK-----------VKVFDWE-NIVD  523
Hh-11P18-AAX18_01700        S----AFNFMYGFTQWL-GIKEKHL------------------SGVDFFNPKE-Q------------KIKVFDWE-NIID  508
Ec-K12-OpgE                 S----ANDFLGFFSQWT-GIKAKEI------------------NIKYPFISEK-KAG----------PIYITNFQLQKVD  514
Ng-FA19-DcaA/PptA           -----AFNFLRGFGSWT-GIETDELP-----------------DDGYDFWGNV-PDV----------PGEGNNLA--FID  517
Ec-W3110-EptB               KVPRRHVELYDTIMGCL-GYTSPDGG-----------------INENNNWCHIPQAK----------EAAAN--------  574
Ec-K12-EptC/CptA            S----LAELIHTWSDLA-GLSY----------------------DGYDPTRSVVNPQ----------FKETTRWI-----  553
ST-L2-EptC/CptA             S----SSELIHTWSDLA-GLTY----------------------DGYDPTRSITNPQ----------FKETTRWI-----  553
Ec-plasmid-ECH74115_B0113   S----LAELIHTWSDLA-GLTY----------------------DGYDPTRSLVNPQ----------FRETTRWI-----  553
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Sf-plasmid-SFxv_5135/LptO    -NGKMEI--EKRKEKIELIKQLQLFGDR-------------------  506
Pm-X73-A0R63_09570/PetK      -TNRFTE-ANLSEALKKEALAHSLLGSYLYKNRLYKSEDKK------  649
HI-KW20-HI_1246              -TETLTP-KDVPDAMKKEALAHALLGSYLYKNRLYSSGENK------  647
Mh-M42548-MHH_c23440         -NYKLTP-KEQPESFKKEALAHALLGSYLYKNQLYKLPEETKQ----  649
Acti.p-L20-APL_0804          -DHSLKA-QEQPEAMKKEALAHALLGSYLYKNQLYKLPKPEKE----  658
Aggr.a-D11S1-D11S_0415       -TETLTE-EEVPPAMVKEALAHALLGSYLYKHRLYTTPEIKQTEGKR  657
Aero.s-A449_ASA3698          -SETLTP-APQPDAMKDAALGLALWGSLAYQKGLYQTAPDTRTVLN-  668
Shew.p-CN32-Sputcn32_3803    -TEQLTPHIPAAKILEKKALSWALWGSLAYQQELYRLPK--------  654
Vh-1DA3-VME47170             -SQTMKP-IEVDPTIVERAKANALFASKAYQNDWYNSKAIQ------  645
Vp-UCMV493-VPUCM_1817        -SQTMKP-LEVDESVIDRAKANALFASKAYQNNWYSSKRTN------  641
Vc-M10-VchoM_02105           -THKMTP-LQLDESIVTRAHANAMWGSLAFKENFYTAQKSYELEK--  654
Vc-O1ElTorN16961-VCA802      -THKMTP-LQLDESIVTRAHANAMWGSLAFKENFYTAQKSYELEK--  657
Bp-TahomaI-BP3136            RDEKYVP-IDLDPALRDEALAFALWPSWAYREERYKLPK--------  653
Pm-X73-A0R63_06305/PetL      -----------------------------------------------
Hd-3500P-Hd0852/EptA         -----------------------------------------------
Nm-Mc58-NMB1638/EptA         -----------------------------------------------
Ng-FA19-NGEG_02067/LptA      -----------------------------------------------
Hp-6695-Hp0022/EptA          -----------------------------------------------
Cj-NCTC11168-Cj0256/EptC     -----------------------------------------------
Vp-UCMV493-VPUCM_20416       -----------------------------------------------
Vc-M10-VchoM_02405           -----------------------------------------------
Vc-O1ElTorN16961-VCA1102     -----------------------------------------------
ST-L2-PmrC                   -----------------------------------------------
Ec-plasmid-mcr1              -----------------------------------------------
Ec-plasmid-mcr2              -----------------------------------------------
Pm-X73-A0R63_02570/Lpt3      ----LEV-----------------QANQPPAFFI---PKNRFKKE--  528
Nm-MC58-Lpt3                 ----LNI-----------------R-DGKAEYVY---PQ--------  525
Ng-FA19-Lpt_3                ----LNI-----------------R-NGKAEYVY---PQ--------  524
Hi-RdKW20-Lpt_6              -----------------------------------------------
Nm-MC58-Lpt6                 -----------------------------------------------
Ng-FA19-Lpt_6                -----------------------------------------------
Pm-X73-A0R63_03465/PetG      ----FDS-----------------LPKDSAKK---------------  525
Pm-P1059-PetG                ----FDS-----------------LPKDSAKK---------------  525
Pm-P2100-A0R72_03015         ----FNL-----------------LPSDPVLL-----PENI------  531
Pm-HN06-PMCN06_0886          ----FNL-----------------LPSDPVLL-----PENI------  530
Hd-3500P-Hd0371/PdtA         ----FEQ-----------------LKED--VI-----PEFNTTISN-  541
Hd-3500P-Hd1598/PdtB         ----KIP-----------------AKPDPAVIIPIHQHKLNGHVQE-  527
Acti.s-130Z-Asuc_1041        ----FEQ-----------------LLSDPAVV-----ESR-------  517
Hh-CCUG3714-B0186_06625      ----FED-----------------LDSDPAII-----NIKKEINYE-  538
Aggr.a-RhAA1-RhAA1_04486     ----YNS-----------------LKEDPAKK---------------  533
Hf-CCUG31170-B0188_07100     ----FEQ-----------------LTEDPAVR-----P---------  535
Hh-11P18-AAX18_01700         ----VNL-----------------LKDDPAKL-----H---------  520
Ec-K12-OpgE                  ----YNH-----------------LGTD--IF-----DPKP------  527
Ng-FA19-DcaA/PptA            ----RQS-----------------DDPAPWYA---GKGKAKNTSKK-  539
Ec-W3110-EptB                -----------------------------------------------
Ec-K12-EptC/CptA             ----GNP-----------------YKKNALIDYD-TLPYGDQVGNQ-  577
ST-L2-EptC/CptA              ----GNP-----------------YKKNALIDYD-TLPYGDQVGNQ-  577
Ec-plasmid-ECH74115_B0113    ----GNP-----------------YKKNGLTDFD-TLPYGEP-----  573
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Supplementary Figure 1. Multiple alignment of a representative number of known and predicted phosphoethanolamine (PEtn) transferases. Bacterial species are as follows; Acti. p, *Actinobacillus pleuropneumoniae*; Aero.s, *Aeromonas salmonicida*, Aggr.a, *Aggregatibacter actinomycetemcomitans*; Bp, *Bordetella pertussis*; Cj, *Campylobacter jejuni*, Ec, *Escherichia coli*; Hd, *Haemophilus ducreyi*, Hf, *Haemophilus felis*; Hh, *Haemophilus haemolyticus*; Hi, *Haemophilus influenzae*; Hp, *Helicobacter pylori*; Mh, *Mannhaeimia haemolytica*; Ng, *Neisseria gonorrhoeae*; Nm, *Neisseria meningitidis*; Pm, *Pasteurella multocida*; Sf, *Shigella flexneri*; Shew.p, *Shewanella* *putrefaciens*; ST, *Salmonella enterica* subsp. *enterica* serovar Typhimurium; Vc, *Vibrio cholerae*; Vh, *Vibrio harveyi*; Vp, *Vibrio parahaemolyticus*. *, amino acids common to all proteins. Labels indicate species, strain and gene/locus tag, separated by hyphens. The presumed catalytic nucleophile is Thr280 in EptA_{Nm} (Nm-Mc58-NMB1638/EptA), Thr266 in EptC (Cj-NCTC11168-Cj0256/EptC), Thr285 in Mcr-1 (Ec-plasmid-mcr1) (1-3). Nucleophile Thr280 or the equivalent was present at the equivalent position in all other putative PEtn transferases with the exception of all proteins that align/clustered with *P. multocida* Kdo-specific PEtn transferase PetK/A0R63_09570 where serine is in the equivalent position. The metal binding sites that help co-ordinate a Zn molecule in the nucleophile site in EptA homologues are residues Glu240/227/246, Asp452/427/465 and His 453/428/466 in EptA_{Nm}/EptC/Mcr-1 (1-3) and are completely conserved across all PEtn proteins.

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