```
Lmon; Listeria monocytogenes         1 --------------------------MAKGLGKGINALFN-----------NVDT-----------------------------------------------------------------  18
Bsub; Bacillus subtilis              1 --------------------------MAKGLGKGINALFN-----------QVDL-----------------------------------------------------------------  18
Bant; B. anthracis                   1 --------------------------VAKGLGRGINVFFP----------DLDVK-----------------------------------------------------------------  19
Bste; B. stearothermophilus          1 --------------------------VAKGLGKGISALFDNL------SLNELNG-----------------------------------------------------------------  23
Efae; Enterococcus faecalis          1 ------------------------------------------------------------------------------------------------------------------------   1
Mavi; Mycobacterium avium            1 --------------------MTQPLRKKGGLGRGLASLIPTG------PAEGD-----------AGPATLGPRMG----------------------DAAADVLIGGPAPQEAS------  55
Mbov; M. bovis                       1 --------------------MTQPSRRKGGLGRGLAALIPTG------PADGE-----------SGPPTLGPRMG----------------------SATADVVIGGPVPDTS-------  54
Mtub; M. tuberculosis                1 --------------------MTQPSRRKGGLGRGLAALIPTG------PADGE-----------SGPPTLGPRMG----------------------SATADVVIGGPVPDTS-------  54
Mlep; M. leprae                      1 --------------------MTQSLCKKGGLGRGLASLIPTG------PVDAD-----------SGPATYGPQMG----------------------NTAADVLIGGSAQKDN-------  54
Cdip; Corynebacterium diphtheriae    1 ---------------------MAQETRKGGLGRGLAALITSS------PSAGSRIGDTAADVVFGGPSTTPPKPGEKKKPEAPKPAAKRHRSGGNINPILADVVESHEREESAVRERRTQ  93
Scoe; Streptomyces coelicolor        1 ----------------------MPRRPWGARLSAAPGAMPLL------PNERG---------VAAAKVATLQHVS----------------------RETEELTAPQGVEGLRP------  55
Cdif; Clostridium difficile          1 --------------------MENKSKRSNRLGRGLSALIP--------EIKGETS-----------------------------------------------------------------  27
Cace; C. acetobutylicum              1 ------------------------MNKKGGLGRGLNALIV--------DTDVKEE-----------------------------------------------------------------  23
Rpro; Rickettsia prowazekii          1 ------------------------MVKNKGLGRGLSSLLG------------E-EVLP--------------------------------------------------------------  21
Hpyl; Helicobacter pylori            1 ------------------------MAKNKVLGRGLADIFPEIN-----EVYEQGLYER--------------------------------------------------------------  29
Cjej; Campylobacter jejuni           1 --------------------------MGLNKDRGLSSLIS--------DMDTVYSKELG-------------------------------------------------------------  25
Ctep; Chlorobium tepidum             1 -------------------------MSKKALGRGLKALISEE---GFAVAEKAEETEK--------------------------------------------------------------  30
Pgin; Porphyromonas gingivalis       1 -----------------------MKHTKKTLGRGLDSLLD------------A-EVIG--------------------------------------------------------------  22
Gsul; Geobacter sulfurreducens       1 ----------------------------------MAALLPVV------EEEGKRYFS---------------------------------------------------------------  17
Drad2.6; Deinococcus radiodurans     1 ------------------------MSKKSSLGRGLDALLTK--------K-GEPVAQA--------------------------------------------------------------  25
Tpal; Treponema pallidum             1 -------------------------MGKDKLGKGIDALLQES------SDRYDVRDS---------------------------------------------------------------  26
Tden; T. denticola                   1 ------------------------VAKKSALGRGLNALLEEQ------PANQIVESLN--------------------------------------------------------------  28
Ccre; Caulobacter crescentus         1 -----------------------MSEGRRGLGRGLSACWAS-------RR-RAGSGPG--------------------------------------------------------------  27
Paer; Pseudomonas aeruginosa         1 -----------------------MAAKKRGLGRGLDALLGG-----SSPAKLQEEAVQ--------------------------------------------------------------  30
Pput; P. putida                      1 -----------------------MAVKKRGLGRGLDALLSG-----PSVSALEEQAVK--------------------------------------------------------------  30
Sput; Shewanella putrefaciens        1 -----------------------MTLKKRGLGKGLDALLSHS--HAANKKQTEEVAVV--------------------------------------------------------------  33
Vcho3.0; Vibrio cholerae             1 -------------------------MTKRGLGKGLDALLATSSLAREKQQVASLSQSM--------------------------------------------------------------  33
Xfas; Xylella fastidiosa             1 ------------------MNKPSPPLKKRGLGRGLEALLGSK---GGSSVPPTVAEGQ--------------------------------------------------------------  37
Tfer; Thiobacillus ferrooxidans      1 -------------------------MKRVGLGRGLDALFAS-------EG-GAG------------------------------------------------------------------  21
megaplasmid (Dr) b †                 1 -----------------------MSRKLPPPKAAISPLSLR-------QLMDEHEGVS--------------------------------------------------------------  28
Drad0.4                              1 -----------------------MTRRRPERRRDLLGLLG--------ETPVDLS-----------------------------------------------------------------  24
megaplasmid (Dr) a †                 1 ----------------------------MTRREGLAALLG--------ESAKLAQG----------------------------------------------------------------  20
pMOL28 (Re; Ralstonia eutropha)      1 ------MSLREKLAAKAGNIKVTAEDLEKAAARGPQAPRTAPGQLMHMQGKVERQANEIAQLR---------------------------------------------------------  57
QpH1 (Cb; Coxiella burnetii )        1 ---------MDNSKRNIHNSGPLGMLMKNGQIKKIENSAESNEGTVVLNKAAPSYFKT--------------------------------------------------------------  49
F (Ec; Escherichia coli )            1 -MKRAPVIPKHTLNTQPVEDTSLSTPAAPMVDSLIARVG---VMARGNAITLPVCGRD------------------------------------------------------------VK  56
pO157 (Ec  O157)                     1 -MKRAPVIPKHTLNTQPVEDTSLSTPAAPMVDSLIARVG---VMARGNAITLPVCGRD------------------------------------------------------------VK  56
N15 (Ec)                             1 -MKNRSILKNAPNIETFMSNNHNAPQKAPSVSPMVGDLQSKLSSLSGNSITLPVCGRN------------------------------------------------------------VT  59
pCD1 (Yp; Yersinia pestis)           1 -MKRSPVLRNAPSINFDDAKPAISNAEPSVSAPAVSQLASRVSGMKGNTIVLPVCGRN------------------------------------------------------------VA  59
pYVe227 (Ye; Y. enterocolitica)      1 MMKRSPVLRNAPSINFDDAKPAISNAEPSVSAPAVSQLASRVSGMKGNTIVLPVCGRN------------------------------------------------------------VA  60
Vcho1.1 *                            1 ---------MAIKTSELNAKLFGKADKRRATTPAEAQSAVKAQAQMIELAVAGEEVVT--------------------------------------------------------------  49
P1 (Ec)                              1 ------------------MSKKNRPTIGRTLNPSILSGFDSSSASGDRVEQVFKLSTG----------------------------------------------------------RQAT  44
P7 (Ec)                              1 --------------------MKKIVSRGRVLGKNSSEFARMLEGSEGTKTFTLKSGRQ------------------------------------------------------------AK  40
pMT1 (Yp)                            1 --------------------MKQVIARGRVLGNSNSEFARMLEGDGDVKTFTLKSGVQ------------------------------------------------------------AR  40
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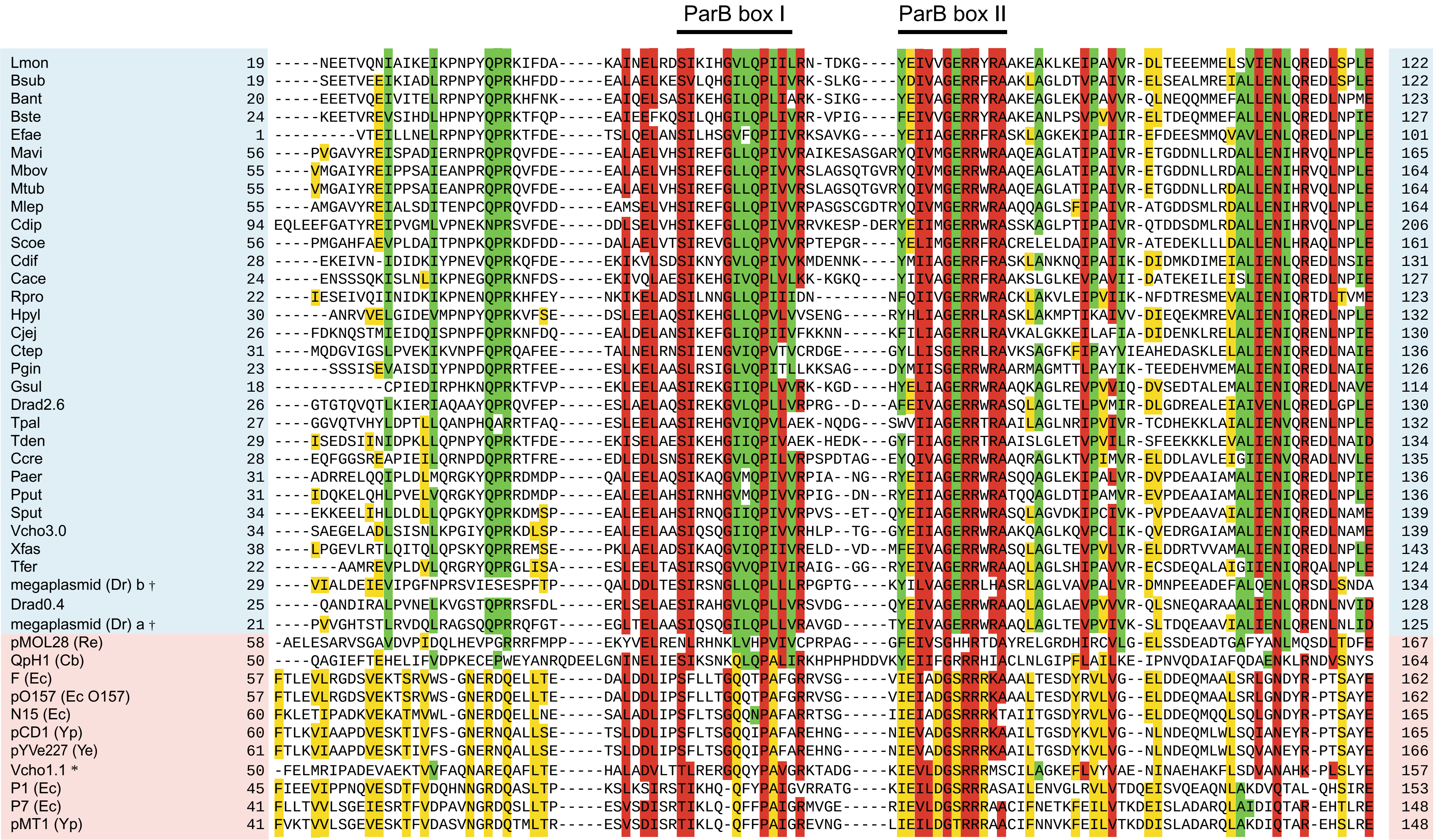
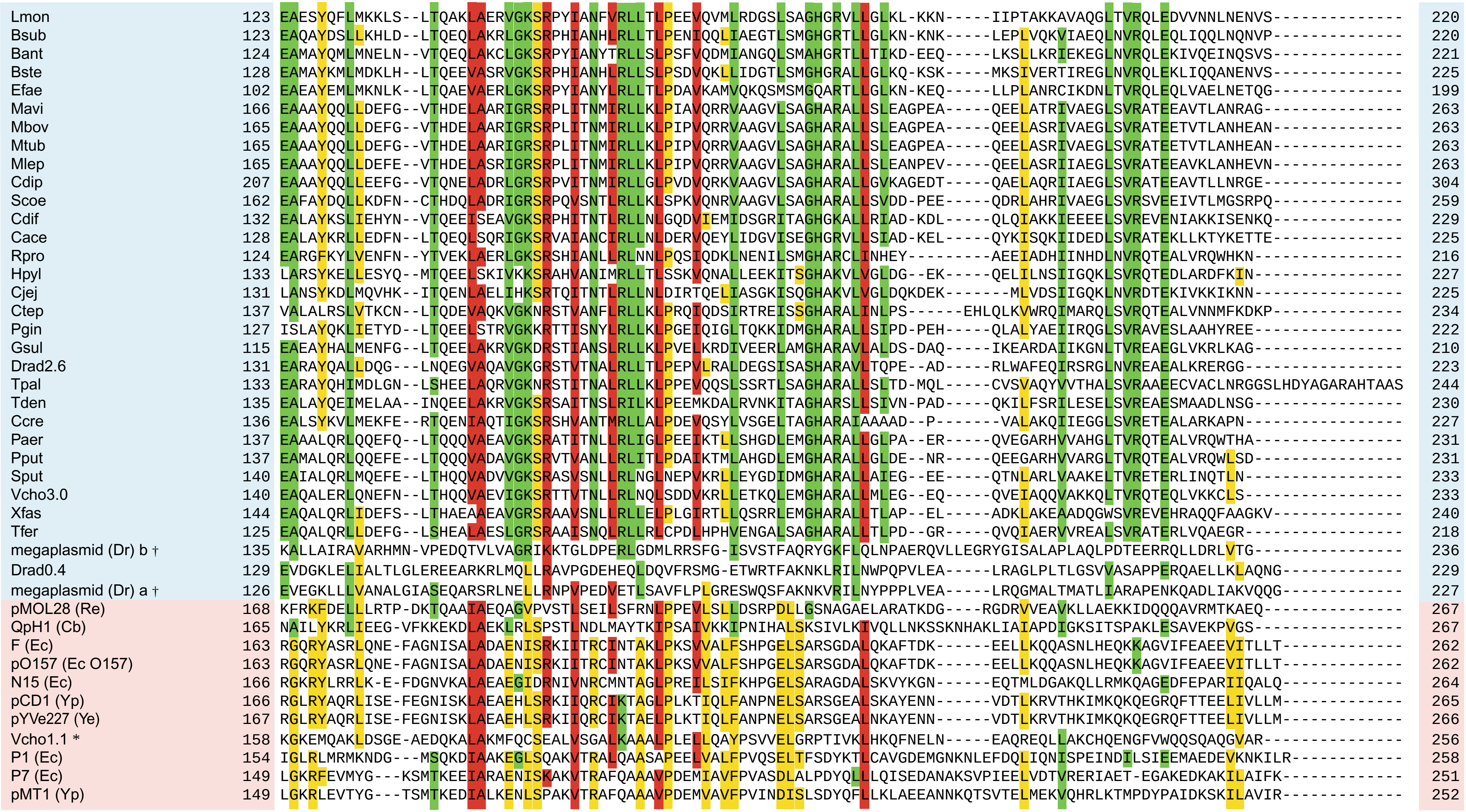


Lmon	19	-----NEETVQNIAIKEIKPNPYQPRKIFDA-----KAINELRDSIKIHGVLQPIILRN-TDKG----YEIVVGERRYRAAKEAKLKEIPAVVR-DLTEEEMMELSVIENLQREDLSPLE	122
Bsub	19	-----SEETVEEIKIADLRPNPYQPRKHFDD-----EALAELKESVLQHGILQPLIVRK-SLKG----YDIVAGERRFRAAKLAGLDTVPAIVR-ELSEALMREIALLENLQREDLSPLE	122
Bant	20	-----EEETVQEIVITELRPNPYQPRKHFNK-----EAIQELSASIKEHGILQPLIARK-SIKG----YEIVAGERRYRAAKEAGLEKVPAVVR-QLNEQQMMEFALLENLQREDLNPME	123
Bste	24	-----KEETVREVSIHDLHPNPYQPRKTFQP-----EAIEEFKQSILQHGILQPLIVRR-VPIG----FEIVVGERRYRAAKEANLPSVPVVVR-ELTDEQMMEFALLENLQREDLNPIE	127
Efae	1	---------VTEILLNELRPNPYQPRKTFDE-----TSLQELANSILHSGVFQPIIVRKSAVKG----YEIIAGERRFRASKLAGKEKIPAIIR-EFDEESMMQVAVLENLQREDLNPLE	101
Mavi	56	----PVGAVYREISPADIERNPRQPRQVFDE-----EALAELVHSIREFGLLQPIVVRAIKESASGARYQIVMGERRWRAAQEAGLATIPAIVR-ETGDDNLLRDALLENIHRVQLNPLE	165
Mbov	55	----VMGAIYREIPPSAIEANPRQPRQVFDE-----EALAELVHSIREFGLLQPIVVRSLAGSQTGVRYQIVMGERRWRAAQEAGLATIPAIVR-ETGDDNLLRDALLENIHRVQLNPLE	164
Mtub	55	----VMGAIYREIPPSAIEANPRQPRQVFDE-----EALAELVHSIREFGLLQPIVVRSLAGSQTGVRYQIVMGERRWRAAQEAGLATIPAIVR-ETGDDNLLRDALLENIHRVQLNPLE	164
Mlep	55	----AMGAVYREIALSDITENPCQPRQVFDD-----EAMSELVHSIREFGLLQPIVVRPASGSCGDTRYQIVMGERRWRAAQQAGLSFIPAIVR-ATGDDSMLRDALLENIHRVQLNPLE	164
Cdip	94	EQLEEFGATYREIPVGMLVPNEKNPRSVFDE-----DDLSELVHSIKEFGLLQPIVVRRVKESP-DERYEIIMGERRWRASSKAGLPTIPAIVR-QTDDSDMLRDALLENIHRVQLNPLE	206
Scoe	56	----PMGAHFAEVPLDAITPNPKQPRKDFDD-----DALAELVTSIREVGLLQPVVVRPTEPGR----YELIMGERRFRACRELELDAIPAIVR-ATEDEKLLLDALLENLHRAQLNPLE	161
Cdif	28	-----EKEIVN-IDIDKIYPNEVQPRKQFDE-----EKIKVLSDSIKNYGVLQPIVVKMDENNK----YMIIAGERRFRASKLANKNQIPAIIK-DIDMKDIMEIALIENLQREDLNSIE	131
Cace	24	-----ENSSSQKISLNLIKPNEGQPRKNFDS-----EKIVQLAESIKEHGIVQPLVLKK-KGKQ----YIIVAGERRFRAAKSLGLKEVPAVII-DATEKEILEISLIENIQREDLNPIE	127
Rpro	22	----IESEIVQIINIDKIKPNENQPRKHFEY-----NKIKELADSILNNGLLQPIIIDN--------NFQIIVGERRWRACKLAKVLEIPVIIK-NFDTRESMEVALIENIQRTDLTVME	123
Hpyl	30	------ANRVVELGIDEVMPNPYQPRKVFSE-----DSLEELAQSIKEHGLLQPVLVVSENG-----RYHLIAGERRLRASKLAKMPTIKAIVV-DIEQEKMREVALIENIQREDLNPLE	132
Cjej	26	----FDKNQSTMIEIDQISPNPFQPRKNFDQ-----EALDELANSIKEFGLIQPIIVFKKNN-----KFILIAGERRLRAVKALGKKEILAFIA-DIDENKLRELALIENIQRENLNPIE	130
Ctep	31	----MQDGVIGSLPVEKIKVNPFQPRQAFEE-----TALNELRNSIIENGVIQPVTVCRDGE-----GYLLISGERRLRAVKSAGFKFIPAYVIEAHEDASKLELALIENIQREDLNAIE	136
Pgin	23	------SSSISEVAISDIYPNPDQPRRTFEE-----ESLKELAASLRSIGLVQPITLLKKSAG----DYMIISGERRWRAARMAGMTTLPAYIK-TEEDEHVMEMALIENIQREDLNAIE	126
Gsul	18	------------CPIEDIRPHKNQPRKTFVP-----EKLEELAASIREKGIIQPLVVRK-KGD----HYELIAGERRWRAAQKAGLREVPVVIQ-DVSEDTALEMALIENIQREDLNAVE	114
Drad2.6	26	----GTGTQVQTLKIERIAQAAYQPRQVFEP-----ESLAELAQSIREKGVLQPLLVRPRG--D---AFEIVAGERRWRASQLAGLTELPVMIR-DLGDREALEIAIVENLQREDLGPLE	130
Tpal	27	----GGVQTVHYLDPTLLQANPHQARRTFAQ-----ESLEELAASIREHGVIQPVLAEK-NQDG---SWVIIAGERRTRAAILAGLNRIPVIVR-TCDHEKKLAIALIENVQRENLNPLE	132
Tden	29	----ISEDSIINIDPKLLQPNPYQPRKTFDE-----EKISELAESIKEHGIIQPIVAEK-HEDK---GYFIIAGERRTRAAISLGLETVPVILR-SFEEKKKLEVALIENIQREDLNAID	134
Ccre	28	----EQFGGSREAPIEILQRNPDQPRRTFRE-----EDLEDLSNSIREKGVLQPILVRPSPDTAG--EYQIVAGERRWRAAQRAGLKTVPIMVR-ELDDLAVLEIGIIENVQRADLNVLE	135
Paer	31	----ADRRELQQIPLDLMQRGKYQPRRDMDP-----QALEELAQSIKAQGVMQPIVVRPIA--NG--RYEIIAGERRWRASQQAGLEKIPALVR-DVPDEAAIAMALIENIQREDLNPIE	136
Pput	31	----IDQKELQHLPVELVQRGKYQPRRDMDP-----EALEELAHSIRNHGVMQPIVVRPIG--DN--RYEIIAGERRWRATQQAGLDTIPAMVR-EVPDEAAIAMALIENIQREDLNPLE	136
Sput	34	----EKKEELIHLDLDLLQPGKYQPRKDMSP-----EALEELAHSIRNQGIIQPIVVRPVS--ET--QYEIIAGERRWRASQLAGVDKIPCIVK-PVPDEAAVAIALIENIQREDLNAME	139
Vcho3.0	34	----SAEGELADLSISNLKPGIYQPRKDLSP-----EALEELAASIQSQGIIQPIVVRHLP--TG--GYEIIAGERRWRAAKQAGLKQVPCLIK-QVEDRGAIAMALIENIQREDLNAME	139
Xfas	38	----LPGEVLRTLQITQLQPSKYQPRREMSE-----PKLAELADSIKAQGVIQPIIVRELD--VD--MFEIVAGERRWRASQLAGLTEVPVLVR-ELDDRTVVAMALIENIQREDLNPLE	143
Tfer	22	-------AAMREVPLDVLQRGRYQPRGLISA-----ESLEELTASIRSQGVVQPIVIRAIG--GG--RYEIVAGERRWRAAQLAGLSHIPAVVR-ECSDEQALAIGIIENIQRQALNPLE	124
megaplasmid (Dr) b †	29	----VIALDEIEVIPGFNPRSVIESESPFTP-----QALDDLTESIRSNGLLQPLLLRPGPTG----KYILVAGERRLHASRLAGLVAVPALVR-DMNPEEADEFALQENLQRSDLSNDA	134
Drad0.4	25	-----QANDIRALPVNELKVGSTQPRRSFDL-----ERLSELAESIRAHGVLQPLLVRSVDG-----QYEIVAGERRWRAAQLAGLAEVPVVVR-QLSNEQARAAALIENLQRDNLNVID	128
megaplasmid (Dr) a †	21	----PVVGHTSTLRVDQLRAGSQQPRRQFGT-----EGLTELAASIQSQGILQPLLVRAVGD-----TYEIVAGERRWRAAQLAGLTEVPVIVK-SLTDQEAAVIALIENLQRENLNLID	125
pMOL28 (Re)	58	-AELESARVSGAVDVPIDQLHEVPGRRRFMPP----EKYVELRENLRHNKLVHPVIVCPRPAG----GFEIVSGHHRTDAYRELGRDHIRCVLG-ELSSDEADTGAFYANLMQSDLTDFE	167
QpH1 (Cb)	50	----QAGIEFTEHELIFVDPKECEPWEYANRQDEELGNINELIESIKSNKQLQPALIRKHPHPHDDVKYEIIFGRRRHIACLNLGIPFLAILKE-IPNVQDAIAFQDAENKLRNDVSNYS	164
F (Ec)	57	FTLEVLRGDSVEKTSRVWS-GNERDQELLTE-----DALDDLIPSFLLTGQQTPAFGRRVSG-----VIEIADGSRRRKAAALTESDYRVLVG--ELDDEQMAALSRLGNDYR-PTSAYE	162
pO157 (Ec O157)	57	FTLEVLRGDSVEKTSRVWS-GNERDQELLTE-----DALDDLIPSFLLTGQQTPAFGRRVSG-----VIEIADGSRRRKAAALTESDYRVLVG--ELDDEQMAALSRLGNDYR-PTSAYE	162
N15 (Ec)	60	FKLETIPADKVEKATMVWL-GNERDQELLNE-----SALADLIPSFLTSGQQNPAFARRTSG-----IIEIADGSRRRKTAIITGSDYRVLVG--ELDDEQMQQLSQLGNDYR-PTSAYE	165
pCD1 (Yp)	60	FTLKVIAAPDVESKTIVFS-GNERNQALLSE-----TSLDDLIPSFLTSGQQIPAFAREHNG-----NIEVADGSRRRKAAILTGSDYKVLVG--NLNDEQMLWLSQIANEYR-PTSAYE	165
pYVe227 (Ye)	61	FTLKVIAAPDVESKTIVFS-GNERNQALLSE-----TSLDDLIPSFLTSGQQIPAFAREHNG-----NIEVADGSRRRKAAILTGSDYKVLVG--NLNDEQMLWLSQVANEYR-PTSAYE	166
Vcho1.1 *	50	-FELMRIPADEVAEKTVVFAQNAREQAFLTE-----HALADVLTTLRERGQQYPAVGRKTADG----KIEVLDGSRRRMSCILAGKEFLVYVAE-NINAEHAKFLSDVANAHK-PLSLYE	157
P1 (Ec)	45	FIEEVIPPNQVESDTFVDQHNNGRDQASLTP-----KSLKSIRSTIKHQ-QFYPAIGVRRATG----KIEILDGSRRRASAILENVGLRVLVTDQEISVQEAQNLAKDVQTAL-QHSIRE	153
P7 (Ec)	41	FLLTVVLSGEIESRTFVDPAVNGRDQSLLTP-----ESVSDISRTIKLQ-QFFPAIGRMVGE-----RIEVLDGSRRRAACIFNETKFEILVTKDEISLADARQLAIDIQTAR-EHTLRE	148
pMT1 (Yp)	41	FVKTVVLSGEVESKTFVDASVNGRDQTMLTR-----ESVSDISRTIKLQ-QFFPAIGREVNG-----LIEILDGTRRRAACIFNNVKFEILVTKDDISLADARQLAKDIQTAR-EHSLRE	148



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Lmon                  123 EAESYQFLMKKLS--LTQAKLAERVGKSRPYIANFVRLLTLPEEVQVMLRDGSLSAGHGRVLLGLKL-KKN-----IIPTAKKAVAQGLTVRQLEDVVNNLNENVS--------------  220
Bsub                  123 EAQAYDSLLKHLD--LTQEQLAKRLGKSRPHIANHLRLLTLPENIQQLIAEGTLSMGHGRTLLGLKN-KNK-----LEPLVQKVIAEQLNVRQLEQLIQQLNQNVP--------------  220
Bant                  124 EAMAYQMLMNELN--VTQEQLAKCLGKSRPYIANYTRLLSLPSFVQDMIANGQLSMAHGRTLLTIKD-EEQ-----LKSLLKRIEKEGLNVRQLEKIVQEINQSVS--------------  221
Bste                  128 EAMAYKMLMDKLH--LTQEEVASRVGKSRPHIANHLRLLSLPSDVQKLLIDGTLSMGHGRALLGLKQ-KSK-----MKSIVERTIREGLNVRQLEKLIQQANENVS--------------  225
Efae                  102 EAEAYEMLMKNLK--LTQAEVAERLGKSRPYIANYLRLLTLPDAVKAMVQKQSMSMGQARTLLGLKN-KEQ-----LLPLANRCIKDNLTVRQLEQLVAELNETQG--------------  199
Mavi                  166 EAAAYQQLLDEFG--VTHDELAARIGRSRPLITNMIRLLKLPIAVQRRVAAGVLSAGHARALLSLEAGPEA-----QEELATRIVAEGLSVRATEEAVTLANRAG---------------  263
Mbov                  165 EAAAYQQLLDEFG--VTHDELAARIGRSRPLITNMIRLLKLPIPVQRRVAAGVLSAGHARALLSLEAGPEA-----QEELASRIVAEGLSVRATEETVTLANHEAN--------------  263
Mtub                  165 EAAAYQQLLDEFG--VTHDELAARIGRSRPLITNMIRLLKLPIPVQRRVAAGVLSAGHARALLSLEAGPEA-----QEELASRIVAEGLSVRATEETVTLANHEAN--------------  263
Mlep                  165 EAAAYQQLLDEFE--VTHDELASRIGRSRPLITNMIRLLKLPIPVQRRVAAGVLSAGHARALLSLEANPEV-----QEELASRIIAEGLSVRATEEAVKLANHEVN--------------  263
Cdip                  207 EAAAYQQLLEEFG--VTQNELADRLGRSRPVITNMIRLLGLPVDVQRKVAAGVLSAGHARALLGVKAGEDT-----QAELAQRIIAEGLSVRATEEAVTLLNRGE---------------  304
Scoe                  162 EAFAYDQLLKDFN--CTHDQLADRIGRSRPQVSNTLRLLKLSPKVQNRVAAGVLSAGHARALLSVDD-PEE-----QDRLAHRIVAEGLSVRSVEEIVTLMGSRPQ--------------  259
Cdif                  132 EALAYKSLIEHYN--VTQEEISEAVGKSRPHITNTLRLLNLGQDVIEMIDSGRITAGHGKALLRIAD-KDL-----QLQIAKKIEEEELSVREVENIAKKISENKQ--------------  229
Cace                  128 EALAYKRLLEDFN--LTQEQLSQRIGKSRVAIANCIRLLNLDERVQEYLIDGVISEGHGRVLLSIAD-KEL-----QYKISQKIIDEDLSVRATEKLLKTYKETTE--------------  225
Rpro                  124 EARGFKYLVENFN--YTVEKLAERLGKSRSHIANLLRLNNLPQSIQDKLNENILSMGHARCLINHEY---------AEEIADHIINHDLNVRQTEALVRQWHKN----------------  216
Hpyl                  133 LARSYKELLESYQ--MTQEELSKIVKKSRAHVANIMRLLTLSSKVQNALLEEKITSGHAKVLVGLDG--EK-----QELILNSIIGQKLSVRQTEDLARDFKIN----------------  227
Cjej                  131 LANSYKDLMQVHK--ITQENLAELIHKSRTQITNTLRLLNLDIRTQELIASGKISQGHAKVLVGLDQKDEK-------MLVDSIIGQKLNVRDTEKIVKKIKNN----------------  225
Ctep                  137 VALALRSLVTKCN--LTQDEVAQKVGKNRSTVANFLRLLKLPRQIQDSIRTREISSGHARALINLPS------EHLQLKVWRQIMARQLSVRQTEALVNNMFKDKP--------------  234
Pgin                  127 ISLAYQKLIETYD--LTQEELSTRVGKKRTTISNYLRLLKLPGEIQIGLTQKKIDMGHARALLSIPD-PEH-----QLALYAEIIRQGLSVRAVESLAAHYREE----------------  222
Gsul                  115 EAEAYHALMENFG--LTQEELAKRVGKDRSTIANSLRLLKLPVELKRDIVEERLAMGHARAVLALDS-DAQ-----IKEARDAIIKGNLTVREAEGLVKRLKAG----------------  210
Drad2.6               131 EARAYQALLDQG---LNQEGVAQAVGKGRSTVTNALRLLTLPEPVLRALDEGSISASHARAVLTQPE--AD-----RLWAFEQIRSRGLNVREAEALKRERGG-----------------  223
Tpal                  133 EARAYQHIMDLGN--LSHEELAQRVGKNRSTITNALRLLKLPPEVQQSLSSRTLSAGHARALLSLTD-MQL-----CVSVAQYVVTHALSVRAAEECVACLNRGGSLHDYAGARAHTAAS  244
Tden                  135 EALAYQEIMELAA--INQEELAKRVGKSRSAITNSLRILKLPEEMKDALRVNKITAGHARSLLSIVN-PAD-----QKILFSRILESELSVREAESMAADLNSG----------------  230
Ccre                  136 EALSYKVLMEKFE--RTQENIAQTIGKSRSHVANTMRLLALPDEVQSYLVSGELTAGHARAIAAAAD--P-------VALAKQIIEGGLSVRETEALARKAPN-----------------  227
Paer                  137 EAAALQRLQQEFQ--LTQQQVAEAVGKSRATITNLLRLIGLPEEIKTLLSHGDLEMGHARALLGLPA--ER-----QVEGARHVVAHGLTVRQTEALVRQWTHA----------------  231
Pput                  137 EAMALQRLQQEFE--LTQQQVADAVGKSRVTVANLLRLITLPDAIKTMLAHGDLEMGHARALLGLDE--NR-----QEEGARHVVARGLTVRQTEALVRQWLSD----------------  231
Sput                  140 EAIALQRLMQEFE--LTHQQVADVVGKSRASVSNLLRLNGLNEPVKRLLEYGDIDMGHARALLAIEG--EE-----QTNLARLVAAKELTVRETERLINQTLN-----------------  233
Vcho3.0               140 EAQALERLQNEFN--LTHQQVAEVIGKSRTTVTNLLRLNQLSDDVKRLLETKQLEMGHARALLMLEG--EQ-----QVEIAQQVAKKQLTVRQTEQLVKKCLS-----------------  233
Xfas                  144 EAQALQRLIDEFS--LTHAEAAEAVGRSRAAVSNLLRLLELPLGIRTLLQSRRLEMGHARALLTLAP--EL-----ADKLAKEAADQGWSVREVEHRAQQFAAGKV--------------  240
Tfer                  125 EAQALQRLLDEFG--LSHEALAESLGRSRAAISNQLRLLRLCPDLHPHVENGALSAGHARALLTLPD--GR-----QVQIAERVVREALSVRATERLVQAEGR-----------------  218
megaplasmid (Dr) b †  135 KALLAIRAVARHMN-VPEDQTVLVAGRIKKTGLDPERLGDMLRRSFG-ISVSTFAQRYGKFLQLNPAERQVLLEGRYGISALAPLAQLPDTEERRQLLDRLVTG----------------  236
Drad0.4               129 EVDGKLELIALTLGLEREEARKRLMQLLRAVPGDEHEQLDQVFRSMG-ETWRTFAKNKLRILNWPQPVLEA-----LRAGLPLTLGSVVASAPPERQAELLKLAQNG-------------  229
megaplasmid (Dr) a †  126 EVEGKLLLVANALGIASEQARSRLNELLRNPVPEDVETLSAVFLPLGRESWQSFAKNKVRILNYPPPLVEA-----LRQGMALTMATLIARAPENKQADLIAKVQQG-------------  227
pMOL28 (Re)           168 KFRKFDELLLRTP-DKTQAAIAEQAGVPVSTLSEILSFRNLPPEVLSLLDSRPDLLGSNAGAELARATKDG----RGDRVVEAVKLLAEKKIDQQQAVRMTKAEQ---------------  267
QpH1 (Cb)             165 NAILYKRLIEEG-VFKKEKDLAEKLRLSPSTLNDLMAYTKIPSAIVKKIPNIHALSKSIVLKIVQLLNKSSKNHAKLIAIAPDIGKSITSPAKLESAVEKPVGS----------------  267
F (Ec)                163 RGQRYASRLQNE-FAGNISALADAENISRKIITRCINTAKLPKSVVALFSHPGELSARSGDALQKAFTDK------EELLKQQASNLHEQKKAGVIFEAEEVITLLT-------------  262
pO157 (Ec O157)       163 RGQRYASRLQNE-FAGNISALADAENISRKIITRCINTAKLPKSVVALFSHPGELSARSGDALQKAFTDK------EELLKQQASNLHEQKKAGVIFEAEEVITLLT-------------  262
N15 (Ec)              166 RGKRYLRRLK-E-FDGNVKALAEAEGIDRNIVNRCMNTAGLPREILSIFKHPGELSARAGDALSKVYKGN------EQTMLDGAKQLLRMKQAGEDFEPARIIQALQ-------------  264
pCD1 (Yp)             166 RGLRYAQRLISE-FEGNISKLAEAEHLSRKIIQRCIKTAGLPLKTIQLFANPNELSARSGEALSKAYENN------VDTLKRVTHKIMKQKQEGRQFTTEELIVLLM-------------  265
pYVe227 (Ye)          167 RGLRYAQRLISE-FEGNISKLAEAEHLSRKIIQRCIKTAELPLKTIQLFANPNELSARSGEALNKAYENN------VDTLKRVTHKIMKQKQEGRQFTTEELIVLLM-------------  266
Vcho1.1 *             158 KGKEMQAKLDSGE-AEDQKALAKMFQCSEALVSGALKAAALPLELLQAYPSVVELGRPTIVKLHKQFNELN-----EAQREQLLAKCHQENGFVWQQSQAQGVAR---------------  256
P1 (Ec)               154 IGLRLMRMKNDG---MSQKDIAAKEGLSQAKVTRALQAASAPEELVALFPVQSELTFSDYKTLCAVGDEMGNKNLEFDQLIQNISPEINDILSIEEMAEDEVKNKILR------------  258
P7 (Ec)               149 LGKRFEVMYG---KSMTKEEIARAENISKAKVTRAFQAAAVPDEMIAVFPVASDLALPDYQLLLQISEDANAKSVPIEELVDTVRERIAET-EGAKEDKAKILAIFK-------------  251
pMT1 (Yp)             149 LGKRLEVTYG---TSMTKEDIALKENLSPAKVTRAFQAAAVPDEMVAVFPVINDISLSDYQFLLKLAEEANNKQTSVTELMEKVQHRLKTMPDYPAIDKSKILAVIR-------------  252
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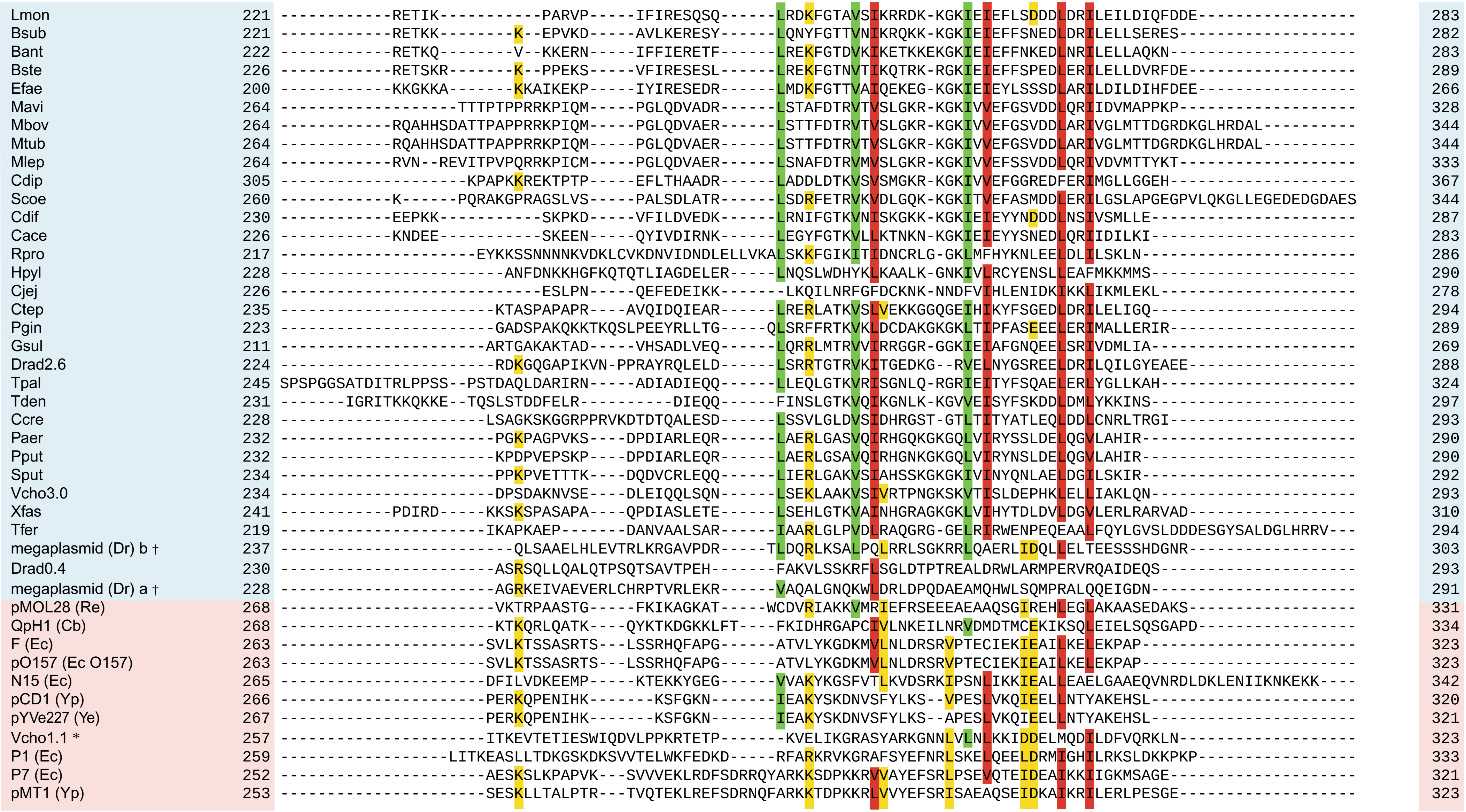

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Lmon                    221 ------------RETIK-----------PARVP-----IFIRESQSQ------LRDKFGTAVSIKRRDK-KGKIEIEFLSDDDLDRILEILDIQFDDE----------------- 283
Bsub                    221 ------------RETKK--------K--EPVKD-----AVLKERESY------LQNYFGTTVNIKRQKK-KGKIEIEFFSNEDLDRILELLSERES------------------- 282
Bant                    222 ------------RETKQ--------V--KKERN-----IFFIERETF------LREKFGTDVKIKETKKEKGKIEIEFFNKEDLNRILELLAQKN-------------------- 283
Bste                    226 ------------RETSKR-------K--PPEKS-----VFIRESESL------LREKFGTNVTIKQTRK-RGKIEIEFFSPEDLERILELLDVRFDE------------------ 289
Efae                    200 ------------KKGKKA-------KKAIKEKP-----IYIRESEDR------LMDKFGTTVAIQEKEG-KGKIEIEYLSSSDLARILDILDIHFDEE----------------- 266
Mavi                    264 -------------------TTTPTPPRRKPIQM-----PGLQDVADR------LSTAFDTRVTVSLGKR-KGKIVVEFGSVDDLQRIIDVMAPPKP------------------- 328
Mbov                    264 ------------RQAHHSDATTPAPPRRKPIQM-----PGLQDVAER------LSTTFDTRVTVSLGKR-KGKIVVEFGSVDDLARIVGLMTTDGRDKGLHRDAL---------- 344
Mtub                    264 ------------RQAHHSDATTPAPPRRKPIQM-----PGLQDVAER------LSTTFDTRVTVSLGKR-KGKIVVEFGSVDDLARIVGLMTTDGRDKGLHRDAL---------- 344
Mlep                    264 ------------RVN--REVITPVPQRRKPICM-----PGLQDVAER------LSNAFDTRVMVSLGKR-KGKIVVEFSSVDDLQRIVDVMTTYKT------------------- 333
Cdip                    305 --------------------KPAPKKREKTPTP-----EFLTHAADR------LADDLDTKVSVSMGKR-KGKIVVEFGGREDFERIMGLLGGEH-------------------- 367
Scoe                    260 ------------K------PQRAKGPRAGSLVS-----PALSDLATR------LSDRFETRVKVDLGQK-KGKITVEFASMDDLERILGSLAPGEGPVLQKGLLEGEDEDGDAES 344
Cdif                    230 ------------EEPKK-----------SKPKD-----VFILDVEDK------LRNIFGTKVNISKGKK-KGKIEIEYYNDDDLNSIVSMLLE---------------------- 287
Cace                    226 ------------KNDEE-----------SKEEN-----QYIVDIRNK------LEGYFGTKVLLKTNKN-KGKIEIEYYSNEDLQRIIDILKI---------------------- 283
Rpro                    217 ---------------------EYKKSSNNNNKVDKLCVKDNVIDNDLELLVKALSKKFGIKITIDNCRLG-GKLMFHYKNLEELDLILSKLN----------------------- 286
Hpyl                    228 ------------------------ANFDNKKHGFKQTQTLIAGDELER-----LNQSLWDHYKLKAALK-GNKIVLRCYENSLLEAFMKKMMS---------------------- 290
Cjej                    226 ----------------------------ESLPN-----QEFEDEIKK-------LKQILNRFGFDCKNK-NNDFVIHLENIDKIKKLIKMLEKL--------------------- 278
Ctep                    235 -----------------------KTASPAPAPR----AVQIDQIEAR------LRERLATKVSLVEKKGGQGEIHIKYFSGEDLDRILELIGQ---------------------- 294
Pgin                    223 -----------------------GADSPAKQKKTKQSLPEEYRLLTG-----QLSRFFRTKVKLDCDAKGKGKLTIPFASEEELERIMALLERIR-------------------- 289
Gsul                    211 ----------------------ARTGAKAKTAD-----VHSADLVEQ------LQRRLMTRVVIRRGGR-GGKIEIAFGNQEELSRIVDMLIA---------------------- 269
Drad2.6                 224 -----------------------RDKGQGAPIKVN-PPRAYRQLELD------LSRRTGTRVKITGEDKG--RVELNYGSREELDRILQILGYEAEE------------------ 288
Tpal                    245 SPSPGGSATDITRLPPSS--PSTDAQLDARIRN-----ADIADIEQQ------LLEQLGTKVRISGNLQ-RGRIEITYFSQAELERLYGLLKAH--------------------- 324
Tden                    231 -------IGRITKKQKKE--TQSLSTDDFELR----------DIEQQ------FINSLGTKVQIKGNLK-KGVVEISYFSKDDLDMLYKKINS---------------------- 297
Ccre                    228 ----------------------LSAGKSKGGRPPRVKDTDTQALESD------LSSVLGLDVSIDHRGST-GTLTITYATLEQLDDLCNRLTRGI-------------------- 293
Paer                    232 -----------------------PGKPAGPVKS----DPDIARLEQR------LAERLGASVQIRHGQKGKGQLVIRYSSLDELQGVLAHIR----------------------- 290
Pput                    232 -----------------------KPDPVEPSKP----DPDIARLEQR------LAERLGSAVQIRHGNKGKGQLVIRYNSLDELQGVLAHIR----------------------- 290
Sput                    234 -----------------------PPKPVETTTK----DQDVCRLEQQ------LIERLGAKVSIAHSSKGKGKIVINYQNLAELDGILSKIR----------------------- 292
Vcho3.0                 234 -----------------------DPSDAKNVSE----DLEIQQLSQN------LSEKLAAKVSIVRTPNGKSKVTISLDEPHKLELLIAKLQN---------------------- 293
Xfas                    241 ------------PDIRD-----KKSKSPASAPA----QPDIASLETE------LSEHLGTKVAINHGRAGKGKLVIHYTDLDVLDGVLERLRARVAD------------------ 310
Tfer                    219 ----------------------IKAPKAEP-------DANVAALSAR------IAARLGLPVDLRAQGRG-GELRIRWENPEQEAALFQYLGVSLDDDESGYSALDGLHRRV--- 294
megaplasmid (Dr) b †    237 -------------------------QLSAAELHLEVTRLKRGAVPDR-----TLDQRLKSALPQLRRLSGKRRLQAERLIDQLLELTEESSSHDGNR------------------ 303
Drad0.4                 230 -----------------------ASRSQLLQALQTPSQTSAVTPEH-------FAKVLSSKRFLSGLDTPTREALDRWLARMPERVRQAIDEQS--------------------- 293
megaplasmid (Dr) a †    228 -----------------------AGRKEIVAEVERLCHRPTVRLEKR------VAQALGNQKWLDRLDPQDAEAMQHWLSQMPRALQQEIGDN---------------------- 291
pMOL28 (Re)             268 -----------------------VKTRPAASTG-----FKIKAGKAT-----WCDVRIAKKVMRIEFRSEEEAEAAQSGIREHLEGLAKAASEDAKS------------------ 331
QpH1 (Cb)               268 -----------------------KTKQRLQATK----QYKTKDGKKLFT----FKIDHRGAPCIVLNKEILNRVDMDTMCEKIKSQLEIELSQSGAPD----------------- 334
F (Ec)                  263 ----------------------SVLKTSSASRTS---LSSRHQFAPG------ATVLYKGDKMVLNLDRSRVPTECIEKIEAILKELEKPAP----------------------- 323
pO157 (Ec O157)         263 ----------------------SVLKTSSASRTS---LSSRHQFAPG------ATVLYKGDKMVLNLDRSRVPTECIEKIEAILKELEKPAP----------------------- 323
N15 (Ec)                265 ----------------------DFILVDKEEMP-----KTEKKYGEG------VVAKYKGSFVTLKVDSRKIPSNLIKKIEALLEAELGAAEQVNRDLDKLENIIKNKEKK---- 342
pCD1 (Yp)               266 ----------------------PERKQPENIHK-------KSFGKN-------IEAKYSKDNVSFYLKS--VPESLVKQIEELLNTYAKEHSL---------------------- 320
pYVe227 (Ye)            267 ----------------------PERKQPENIHK-------KSFGKN-------IEAKYSKDNVSFYLKS--APESLVKQIEELLNTYAKEHSL---------------------- 321
Vcho1.1 *               257 ----------------------ITKEVTETIESWIQDVLPPKRTETP-------KVELIKGRASYARKGNNLVLNLKKIDDELMQDILDFVQRKLN------------------- 323
P1 (Ec)                 259 ------------------LITKEASLLTDKGSKDKSVVTELWKFEDKD-----RFARKRVKGRAFSYEFNRLSKELQEELDRMIGHILRKSLDKKPKP----------------- 333
P7 (Ec)                 252 ----------------------AESKSLKPAPVK---SVVVEKLRDFSDRRQYARKKSDPKKRVVAYEFSRLPSEVQTEIDEAIKKIIGKMSAGE-------------------- 321
pMT1 (Yp)               253 ----------------------SESKLLTALPTR---TVQTEKLREFSDRNQFARKKTDPKKRLVVYEFSRISAEAQSEIDKAIKRILERLPESGE------------------- 323
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