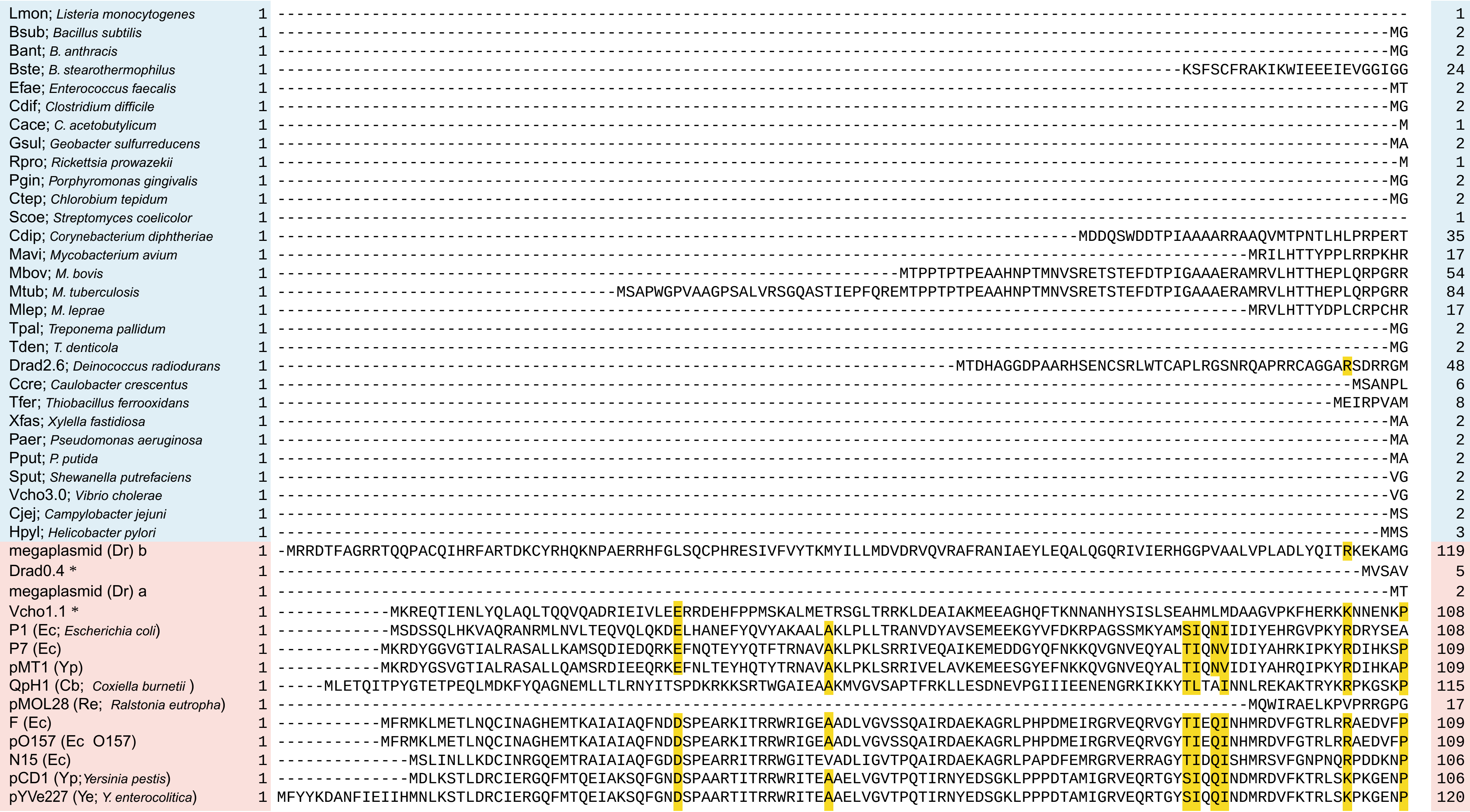

```
Lmon; Listeria monocytogenes          1 -----------------------------------------------------------------------------------------------------------------------    1
Bsub; Bacillus subtilis               1 ----------------------------------------------------------------------------------------------------------------------MG   2
Bant; B. anthracis                    1 ----------------------------------------------------------------------------------------------------------------------MG   2
Bste; B. stearothermophilus           1 ------------------------------------------------------------------------------------------------KSFSCFRAKIKWIEEEIEVGGIGG  24
Efae; Enterococcus faecalis           1 ----------------------------------------------------------------------------------------------------------------------MT   2
Cdif; Clostridium difficile           1 ----------------------------------------------------------------------------------------------------------------------MG   2
Cace; C. acetobutylicum               1 -----------------------------------------------------------------------------------------------------------------------M   1
Gsul; Geobacter sulfurreducens        1 ----------------------------------------------------------------------------------------------------------------------MA   2
Rpro; Rickettsia prowazekii           1 -----------------------------------------------------------------------------------------------------------------------M   1
Pgin; Porphyromonas gingivalis        1 ----------------------------------------------------------------------------------------------------------------------MG   2
Ctep; Chlorobium tepidum              1 ----------------------------------------------------------------------------------------------------------------------MG   2
Scoe; Streptomyces coelicolor         1 -----------------------------------------------------------------------------------------------------------------------    1
Cdip; Corynebacterium diphtheriae     1 -------------------------------------------------------------------------------------MDDQSWDDTPIAAAARRAAQVMTPNTLHLPRPERT  35
Mavi; Mycobacterium avium             1 -------------------------------------------------------------------------------------------------------MRILHTTYPPLRRPKHR  17
Mbov; M. bovis                        1 ------------------------------------------------------------------MTPPTPTPEAAHNPTMNVSRETSTEFDTPIGAAAERAMRVLHTTHEPLQRPGRR  54
Mtub; M. tuberculosis                 1 ------------------------------------MSAPWGPVAAGPSALVRSGQASTIEPFQREMTPPTPTPEAAHNPTMNVSRETSTEFDTPIGAAAERAMRVLHTTHEPLQRPGRR  84
Mlep; M. leprae                       1 -------------------------------------------------------------------------------------------------------MRVLHTTYDPLCRPCHR  17
Tpal; Treponema pallidum              1 ----------------------------------------------------------------------------------------------------------------------MG   2
Tden; T. denticola                    1 ----------------------------------------------------------------------------------------------------------------------MG   2
Drad2.6; Deinococcus radiodurans      1 ------------------------------------------------------------------------MTDHAGGDPAARHSENCSRLWTCAPLRGSNRQAPRRCAGGARSDRRGM  48
Ccre; Caulobacter crescentus          1 ------------------------------------------------------------------------------------------------------------------MSANPL   6
Tfer; Thiobacillus ferrooxidans       1 ----------------------------------------------------------------------------------------------------------------MEIRPVAM   8
Xfas; Xylella fastidiosa              1 ----------------------------------------------------------------------------------------------------------------------MA   2
Paer; Pseudomonas aeruginosa          1 ----------------------------------------------------------------------------------------------------------------------MA   2
Pput; P. putida                       1 ----------------------------------------------------------------------------------------------------------------------MA   2
Sput; Shewanella putrefaciens         1 ----------------------------------------------------------------------------------------------------------------------VG   2
Vcho3.0; Vibrio cholerae              1 ----------------------------------------------------------------------------------------------------------------------VG   2
Cjej; Campylobacter jejuni            1 ----------------------------------------------------------------------------------------------------------------------MS   2
Hpyl; Helicobacter pylori             1 ---------------------------------------------------------------------------------------------------------------------MMS   3
megaplasmid (Dr) b                    1 -MRRDTFAGRRTQQPACQIHRFARTDKCYRHQKNPAERRHFGLSQCPHRESIVFVYTKMYILLMDVDRVQVRAFRANIAEYLEQALQGQRIVIERHGGPVAALVPLADLYQITRKEKAMG 119
Drad0.4 *                             1 -------------------------------------------------------------------------------------------------------------------MVSAV   5
megaplasmid (Dr) a                    1 ----------------------------------------------------------------------------------------------------------------------MT   2
Vcho1.1 *                             1 ------------MKREQTIENLYQLAQLTQQVQADRIEIVLEERRDEHFPPMSKALMETRSGLTRRKLDEAIAKMEEAGHQFTKNNANHYSISLSEAHMLMDAAGVPKFHERKKNNENKP 108
P1 (Ec; Escherichia coli)             1 ------------MSDSSQLHKVAQRANRMLNVLTEQVQLQKDELHANEFYQVYAKAALAKLPLLTRANVDYAVSEMEEKGYVFDKRPAGSSMKYAMSIQNIIDIYEHRGVPKYRDRYSEA 108
P7 (Ec)                               1 -----------MKRDYGGVGTIALRASALLKAMSQDIEDQRKEFNQTEYYQTFTRNAVAKLPKLSRRIVEQAIKEMEDDGYQFNKKQVGNVEQYALTIQNVIDIYAHRKIPKYRDIHKSP 109
pMT1 (Yp)                             1 -----------MKRDYGSVGTIALRASALLQAMSRDIEEQRKEFNLTEYHQTYTRNAVAKLPKLSRRIVELAVKEMEESGYEFNKKQVGNVEQYALTIQNVIDIYAHRQIPKYRDIHKAP 109
QpH1 (Cb; Coxiella burnetii )         1 -----MLETQITPYGTETPEQLMDKFYQAGNEMLLTLRNYITSPDKRKKSRTWGAIEAAKMVGVSAPTFRKLLESDNEVPGIIIEENENGRKIKKYTLTAINNLREKAKTRYKRPKGSKP 115
pMOL28 (Re; Ralstonia eutropha)       1 -------------------------------------------------------------------------------------------------------MQWIRAELKPVPRRGPG  17
F (Ec)                                1 -----------MFRMKLMETLNQCINAGHEMTKAIAIAQFNDDSPEARKITRRWRIGEAADLVGVSSQAIRDAEKAGRLPHPDMEIRGRVEQRVGYTIEQINHMRDVFGTRLRRAEDVFP 109
pO157 (Ec  O157)                      1 -----------MFRMKLMETLNQCINAGHEMTKAIAIAQFNDDSPEARKITRRWRIGEAADLVGVSSQAIRDAEKAGRLPHPDMEIRGRVEQRVGYTIEQINHMRDVFGTRLRRAEDVFP 109
N15 (Ec)                              1 --------------MSLINLLKDCINRGQEMTRAIAIAQFGDDSPEARRITRRWGITEVADLIGVTPQAIRDAEKAGRLPAPDFEMRGRVERRAGYTIDQISHMRSVFGNPNQRPDDKNP 106
pCD1 (Yp;Yersinia pestis)             1 --------------MDLKSTLDRCIERGQFMTQEIAKSQFGNDSPAARTITRRWRITEAAELVGVTPQTIRNYEDSGKLPPPDTAMIGRVEQRTGYSIQQINDMRDVFKTRLSKPKGENP 106
pYVe227 (Ye; Y. enterocolitica)       1 MFYYKDANFIEIIHMNLKSTLDRCIERGQFMTQEIAKSQFGNDSPAARTITRRWRITEAAELVGVTPQTIRNYEDSGKLPPPDTAMIGRVEQRTGYSIQQINDMRDVFKTRLSKPKGENP 120
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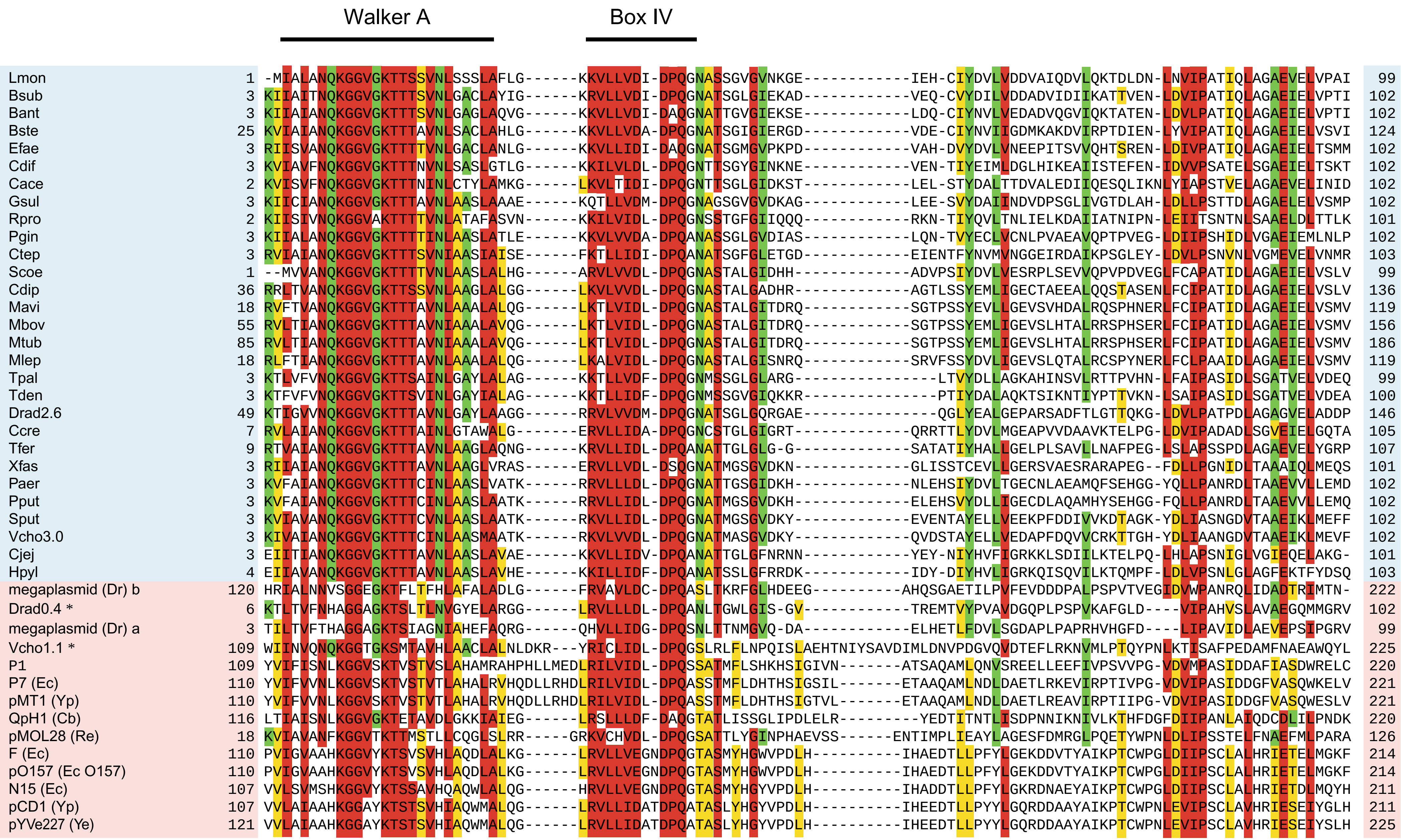

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Lmon                   1 -MIALANQKGGVGKTTSSVNLSSSLAFLG------KKVLLVDI-DPQGNASSGVGVNKGE------------IEH-CIYDVLVDDVAIQDVLQKTDLDN-LNVIPATIQLAGAEVELVPAI  99
Bsub                   3 KIIAITNQKGGVGKTTTSVNLGACLAYIG------KRVLLVDI-DPQGNATSGLGIEKAD------------VEQ-CVYDILVDDADVIDIIKATTVEN-LDVIPATIQLAGAEIELVPTI 102
Bant                   3 KIIAIANQKGGVGKTTTSVNLGAGLAQVG------KKVLLVDI-DAQGNATTGVGIEKSE------------LDQ-CIYNVLVEDADVQGVIQKTATEN-LDVLPATIQLAGAEIELVPTI 102
Bste                  25 KVIAIANQKGGVGKTTTAVNLSACLAHLG------KKVLLVDA-DPQGNATSGIGIERGD------------VDE-CIYNVIIGDMKAKDVIRPTDIEN-LYVIPATIQLAGAEIELVSVI 124
Efae                   3 RIISVANQKGGVGKTTTTVNLGACLANLG------KKVLLIDI-DAQGNATSGMGVPKPD------------VAH-DVYDVLVNEEPITSVVQHTSREN-LDIVPATIQLAGAEIELTSMM 102
Cdif                   3 KVIAVFNQKGGVGKTTTNVNLSASLGTLG------KKILVLDL-DPQGNTTSGYGINKNE------------VEN-TIYEIMLDGLHIKEAIISTEFEN-IDVVPSATELSGAEIELTSKT 102
Cace                   2 KVISVFNQKGGVGKTTTNINLCTYLAMKG------LKVLTIDI-DPQGNTTSGLGIDKST------------LEL-STYDALTTDVALEDIIQESQLIKNLYIAPSTVELAGAEVELINID 102
Gsul                   3 KIICIANQKGGVGKTTTAVNLAASLAAAE------KQTLLVDM-DPQGNAGSGVGVDKAG------------LEE-SVYDAIINDVDPSGLIVGTDLAH-LDLLPSTTDLAGAELELVSMP 102
Rpro                   2 KIISIVNQKGGVAKTTTTVNLATAFASVN------KKILVIDL-DPQGNSSTGFGIIQQQ------------RKN-TIYQVLTNLIELKDAIIATNIPN-LEIITSNTNLSAAELDLTTLK 101
Pgin                   3 KIIALANQKGGVGKTTTTINLAASLATLE------KKVLVVDA-DPQANASSGLGVDIAS------------LQN-TVYECLVCNLPVAEAVQPTPVEG-LDIIPSHIDLVGAEIEMLNLP 102
Ctep                   3 RVIAIANQKGGVGKTTTSVNIAASIAISE------FKTLLIDI-DPQANATSGFGLETGD------------EIENTFYNVMVNGGEIRDAIKPSGLEY-LDVLPSNVNLVGMEVELVNMR 103
Scoe                   1 --MVVANQKGGVGKTTTTVNLAASLALHG------ARVLVVDL-DPQGNASTALGIDHH-------------ADVPSIYDVLVESRPLSEVVQPVPDVEGLFCAPATIDLAGAEIELVSLV  99
Cdip                  36 RRLTVANQKGGVGKTTSSVNLAAGLALGG------LKVLVVDL-DPQGNASTALGADHR-------------AGTLSSYEMLIGECTAEEALQQSTASENLFCIPATIDLAGAEIELVSLV 136
Mavi                  18 RVFTVANQKGGVGKTTTAVNLAAALALQG------LKTLVIDL-DPQGNASTALGITDRQ------------SGTPSSYEVLLGEVSVHDALRQSPHNERLFCIPATIDLAGAEIELVSMV 119
Mbov                  55 RVLTIANQKGGVGKTTTAVNIAAALAVQG------LKTLVIDL-DPQGNASTALGITDRQ------------SGTPSSYEMLIGEVSLHTALRRSPHSERLFCIPATIDLAGAEIELVSMV 156
Mtub                  85 RVLTIANQKGGVGKTTTAVNIAAALAVQG------LKTLVIDL-DPQGNASTALGITDRQ------------SGTPSSYEMLIGEVSLHTALRRSPHSERLFCIPATIDLAGAEIELVSMV 186
Mlep                  18 RLFTIANQKGGVGKTTTAVNLAAALALQG------LKALVIDL-DPQGNASTALGISNRQ------------SRVFSSYDVLIGEVSLQTALRCSPYNERLFCLPAAIDLAGAEIELVSMV 119
Tpal                   3 KTLVFVNQKGGVGKTTSAINLGAYLALAG------KKTLLVDF-DPQGNMSSGLGLARG----------------LTVYDLLAGKAHINSVLRTTPVHN-LFAIPASIDLSGATVELVDEQ  99
Tden                   3 KTFVFVNQKGGVGKTTSVINLGAYIALAG------KKTLLIDF-DPQGNMSSGVGIQKKR---------------PTIYDALAQKTSIKNTIYPTTVKN-LSAIPASIDLSGATVELVDEA 100
Drad2.6               49 KTIGVVNQKGGVGKTTTAVNLGAYLAAGG------RRVLVVDM-DPQGNATSGLGQRGAE---------------QGLYEALGEPARSADFTLGTTQKG-LDVLPATPDLAGAGVELADDP 146
Ccre                   7 RVLAIANQKGGVGKTTTAINLGTAWALG-------ERVLLIDA-DPQGNCSTGLGIGRT-------------QRRTTLYDVLMGEAPVVDAAVKTELPG-LDVIPADADLSGVEIELGQTA 105
Tfer                   9 RTVAIANQKGGVGKTTTAVNLAAGLAQNG------KRVLLIDL-DPQANATTGLGLG-G-------------SATATIYHALLGELPLSAVLLNAFPEG-LSLAPSSPDLAGAEVELYGRP 107
Xfas                   3 RIIAIANQKGGVGKTTTAVNLAAGLVRAS------ERVLLVDL-DSQGNATMGSGVDKN-------------GLISSTCEVLLGERSVAESRARAPEG--FDLLPGNIDLTAAAIQLMEQS 101
Paer                   3 KVFAIANQKGGVGKTTTCINLAASLVATK------RRVLLLDL-DPQGNATTGSGIDKH-------------NLEHSIYDVLTGECNLAEAMQFSEHGG-YQLLPANRDLTAAEVVLLEMD 102
Pput                   3 KVFAIANQKGGVGKTTTCINLAASLAATK------RRVLLIDL-DPQGNATMGSGVDKH-------------ELEHSVYDLLIGECDLAQAMHYSEHGG-FQLLPANRDLTAAEVVLLEMQ 102
Sput                   3 KVIAVANQKGGVGKTTTCVNLAASLAATK------RKVLLIDL-DPQGNATMGSGVDKY-------------EVENTAYELLVEEKPFDDIVVKDTAGK-YDLIASNGDVTAAEIKLMEFF 102
Vcho3.0                3 KIVAIANQKGGVGKTTTCINLAASMAATK------RKVLVVDL-DPQGNATMASGVDKY-------------QVDSTAYELLVEDAPFDQVVCRKTTGH-YDLIAANGDVTAAEIKLMEVF 102
Cjej                   3 EIITIANQKGGVGKTTTAVNLAASLAVAE------KKVLLIDV-DPQANATTGLGFNRNN------------YEY-NIYHVFIGRKKLSDIILKTELPQ-LHLAPSNIGLVGIEQELAKG- 101
Hpyl                   4 EIIAVANQKGGVGKTTTAVNLAASLAVHE------KKILLIDF-DPQANATSSLGFRRDK------------IDY-DIYHVLIGRKQISQVILKTQMPF-LDLVPSNLGLAGFEKTFYDSQ 103
megaplasmid (Dr) b   120 HRIALNNVSGGEGKTFLTFHLAFALADLG------FRVAVLDC-DPQASLTKRFGLHDEEG----------AHQSGAETILPVFEVDDDPALPSPVTVEGIDVWPANRQLIDADTRIMTN- 222
Drad0.4 *              6 KTLTVFNHAGGAGKTSLTLNVGYELARGG------LRVLLLDL-DPQANLTGWLGIS-GV------------TREMTVYPVAVDGQPLPSPVKAFGLD----VIPAHVSLAVAEGQMMGRV 102
megaplasmid (Dr) a     3 TILTVFTHAGGAGKTSIAGNIAHEFAQRG------QHVLLIDG-DPQSNLTTNMGVQ-DA------------ELHETLFDVLSGDAPLPAPRHVHGFD----LIPAVIDLAEVEPSIPGRV  99
Vcho1.1 *            109 WIINVQNQKGGTGKSMTAVHLAACLALNLDKR---YRICLIDL-DPQGSLRLFLNPQISLAEHTNIYSAVDIMLDNVPDGVQVDTEFLRKNVMLPTQYPNLKTISAFPEDAMFNAEAWQYL 225
P1                   109 YVIFISNLKGGVSKTVSTVSLAHAMRAHPHLLMEDLRILVIDL-DPQSSATMFLSHKHSIGIVN-------ATSAQAMLQNVSREELLEEFIVPSVVPG-VDVMPASIDDAFIASDWRELC 220
P7 (Ec)              110 YVIFVVNLKGGVSKTVSTVTLAHALRVHQDLLRHDLRILVIDL-DPQASSTMFLDHTHSIGSIL-------ETAAQAMLNDLDAETLRKEVIRPTIVPG-VDVIPASIDDGFVASQWKELV 221
pMT1 (Yp)            110 YVIFVVNLKGGVSKTVSTVTLAHALRVHQDLLRHDLRILVIDL-DPQASSTMFLDHTHSIGTVL-------ETAAQAMLNDLDAETLREAVIRPTIIPG-VDVIPASIDDGFVASQWESLV 221
QpH1 (Cb)            116 LTIAISNLKGGVGKTETAVDLGKKIAIEG------LRSLLLDF-DAQGTATLISSGLIPDLELR---------YEDTITNTLISDPNNIKNIVLKTHFDGFDIIPANLAIQDCDLILPNDK 220
pMOL28 (Re)           18 KVIAVANFKGGVTKTTMSTLLCQGLSLRR-----GRKVCHVDL-DPQGSATTLYGINPHAEVSS------ENTIMPLIEAYLAGESFDMRGLPQETYWPNLDLIPSSTELFNAEFMLPARA 126
F (Ec)               110 PVIGVAAHKGGVYKTSVSVHLAQDLALKG------LRVLLVEGNDPQGTASMYHGWVPDLH----------IHAEDTLLPFYLGEKDDVTYAIKPTCWPGLDIIPSCLALHRIETELMGKF 214
pO157 (Ec O157)      110 PVIGVAAHKGGVYKTSVSVHLAQDLALKG------LRVLLVEGNDPQGTASMYHGWVPDLH----------IHAEDTLLPFYLGEKDDVTYAIKPTCWPGLDIIPSCLALHRIETELMGKF 214
N15 (Ec)             107 VVLSVMSHKGGVYKTSSAVHQAQWLALQG------HRVLLVEGNDPQGTASMYHGYVPDLH----------IHADDTLLPFYLGKRDNAEYAIKPTCWPGLDIIPSCLALHRIETDLMQYH 211
pCD1 (Yp)            107 VVLAIAAHKGGAYKTSTSVHIAQWMALQG------LRVLLIDATDPQATASLYHGYVPDLH----------IHEEDTLLPYYLGQRDDAAYAIKPTCWPNLEVIPSCLAVHRIESEIYGLH 211
pYVe227 (Ye)         121 VVLAIAAHKGGAYKTSTSVHIAQWMALQG------LRVLLIDATDPQATASLYHGYVPDLH----------IHEEDTLLPYYLGQRDDAAYAIKPTCWPNLEVIPSCLAVHRIESEIYSLH 225
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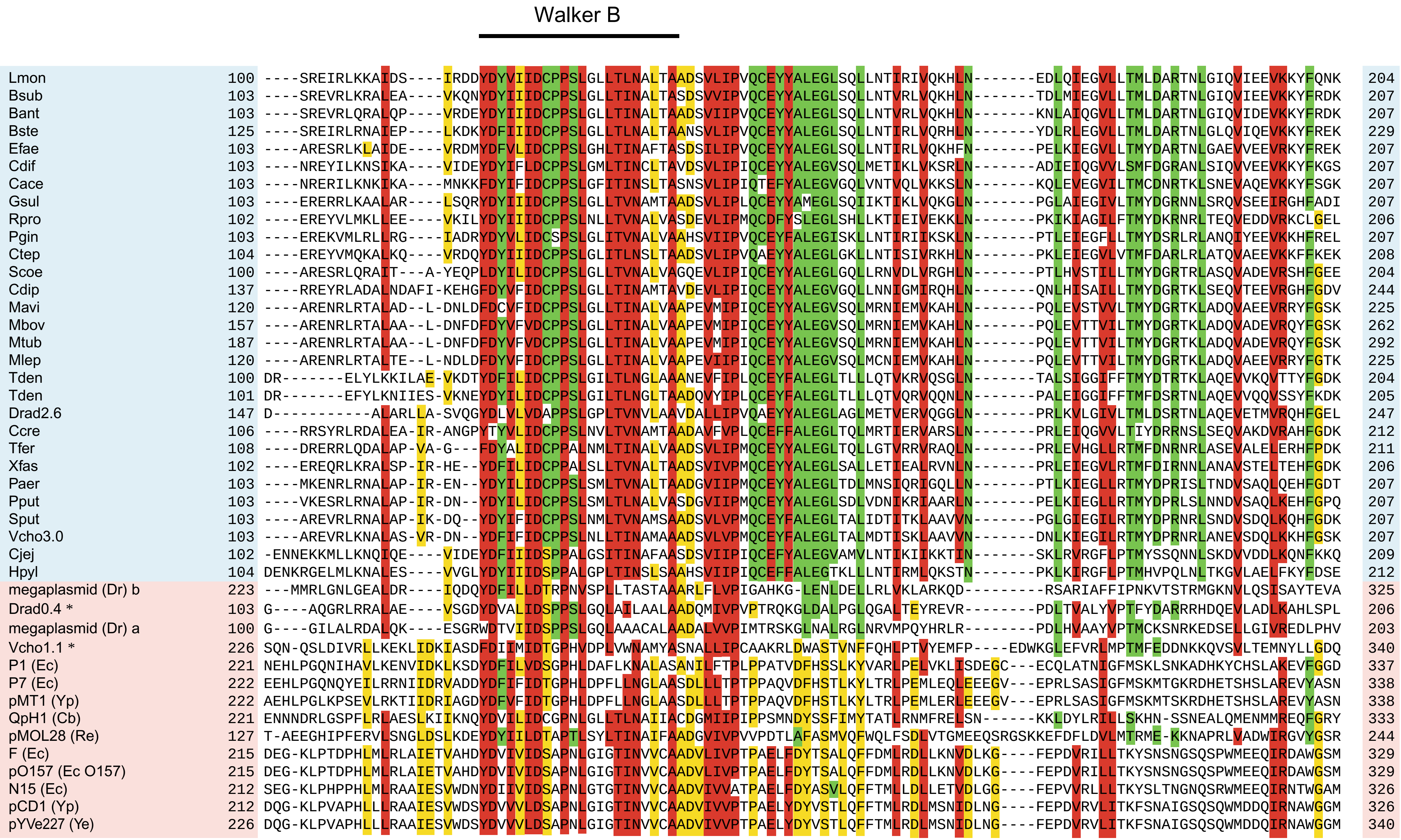

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Lmon                 100 ----SREIRLKKAIDS----IRDDYDYVIIDCPPSLGLLTLNALTAADSVLIPVQCEYYALEGLSQLLNTIRIVQKHLN-------EDLQIEGVLLTMLDARTNLGIQVIEEVKKYFQNK  204
Bsub                 103 ----SREVRLKRALEA----VKQNYDYIIIDCPPSLGLLTINALTASDSVVIPVQCEYYALEGLSQLLNTVRLVQKHLN-------TDLMIEGVLLTMLDARTNLGIQVIEEVKKYFRDK  207
Bant                 103 ----SREVRLQRALQP----VRDEYDYIIIDCPPSLGLLTINALTAADSVIIPVQCEYYALEGLSQLLNTVRLVQKHLN-------KNLAIQGVLLTMLDARTNLGIQVIDEVKKYFRDK  207
Bste                 125 ----SREIRLRNAIEP----LKDKYDFIIIDCPPSLGLLTLNALTAANSVLIPVQCEYYALEGLSQLLNTIRLVQRHLN-------YDLRLEGVLLTMLDARTNLGLQVIQEVKKYFREK  229
Efae                 103 ----ARESRLKLAIDE----VRDMYDFVLIDCPPSLGHLTINAFTASDSILIPVQCEYYALEGLSQLLNTIRLVQKHFN-------PELKIEGVLLTMYDARTNLGAEVVEEVRKYFREK  207
Cdif                 103 ----NREYILKNSIKA----VIDEYDYIFLDCPPSLGMLTINCLTAVDSVLIPIQCEYYALEGVSQLMETIKLVKSRLN-------ADIEIQGVVLSMFDGRANLSIQVVEEVKKYFKGS  207
Cace                 103 ----NRERILKNKIKA----MNKKFDYIFIDCPPSLGFITINSLTASNSVLIPIQTEFYALEGVGQLVNTVQLVKKSLN-------KQLEVEGVILTMCDNRTKLSNEVAQEVKKYFSGK  207
Gsul                 103 ----ERERRLKAALAR----LSQRYDYIIIDCPPSLGLLTVNAMTAADSVLIPLQCEYYAMEGLSQIIKTIKLVQKGLN-------PGLAIEGIVLTMYDGRNNLSRQVSEEIRGHFADI  207
Rpro                 102 ----EREYVLMKLLEE----VKILYDYIIIDCPPSLNLLTVNALVASDEVLIPMQCDFYSLEGLSHLLKTIEIVEKKLN-------PKIKIAGILFTMYDKRNRLTEQVEDDVRKCLGEL  206
Pgin                 103 ----EREKVMLRLLRG----IADRYDYVLIDCSPSLGLITVNALVAAHSVIIPVQCEYFALEGISKLLNTIRIIKSKLN-------PTLEIEGFLLTMYDSRLRLANQIYEEVKKHFREL  207
Ctep                 104 ----EREYVMQKALKQ----VRDQYDYIIIDCPPSLGLITLNSLTAADSVLIPVQAEYYALEGLGKLLNTISIVRKHLN-------PKLEIEGVLVTMFDARLRLATQVAEEVKKFFKEK  208
Scoe                 100 ----ARESRLQRAIT---A-YEQPLDYILIDCPPSLGLLTVNALVAGQEVLIPIQCEYYALEGLGQLLRNVDLVRGHLN-------PTLHVSTILLTMYDGRTRLASQVADEVRSHFGEE  204
Cdip                 137 ----RREYRLADALNDAFI-KEHGFDYVFIDCPPSLGLLTINAMTAVDEVLIPIQCEYYALEGVGQLLNNIGMIRQHLN-------QNLHISAILLTMYDGRTKLSEQVTEEVRGHFGDV  244
Mavi                 120 ----ARENRLRTALAD--L-DNLDFDCVFIDCPPSLGLLTINALVAAPEVMIPIQCEYYALEGVSQLMRNIEMVKAHLN-------PQLEVSTVVLTMYDGRTKLADQVAEEVRRYFGSK  225
Mbov                 157 ----ARENRLRTALAA--L-DNFDFDYVFVDCPPSLGLLTINALVAAPEVMIPIQCEYYALEGVSQLMRNIEMVKAHLN-------PQLEVTTVILTMYDGRTKLADQVADEVRQYFGSK  262
Mtub                 187 ----ARENRLRTALAA--L-DNFDFDYVFVDCPPSLGLLTINALVAAPEVMIPIQCEYYALEGVSQLMRNIEMVKAHLN-------PQLEVTTVILTMYDGRTKLADQVADEVRQYFGSK  292
Mlep                 120 ----ARENRLRTALTE--L-NDLDFDYVFIDCPPSLGLLTINALVAAPEVIIPIQCEYYALEGVSQLMCNIEMVKAHLN-------PQLEVTTVILTMYDGRTKLADQVAEEVRRYFGTK  225
Tden                 100 DR-------ELYLKKILAE-VKDTYDFILIDCPPSLGILTLNGLAAANEVFIPLQCEYFALEGLTLLLQTVKRVQSGLN-------TALSIGGIFFTMYDTRTKLAQEVVKQVTTYFGDK  204
Tden                 101 DR-------EFYLKNIIES-VKNEYDYILIDCPPSLGILTLNGLTAADQVYIPLQCEYFALEGLTLLLQTVQRVQQNLN-------PALEIGGIFFTMFDSRTNLAQEVVQQVSSYFKDK  205
Drad2.6              147 D-----------ALARLLA-SVQGYDLVLVDAPPSLGPLTVNVLAAVDALLIPVQAEYYALEGLAGLMETVERVQGGLN-------PRLKVLGIVLTMLDSRTNLAQEVETMVRQHFGEL  247
Ccre                 106 ----RRSYRLRDALEA-IR-ANGPYTYVLIDCPPSLNVLTVNAMTAADAVFVPLQCEFFALEGLTQLMRTIERVARSLN-------PRLEIQGVVLTIYDRRNSLSEQVAKDVRAHFGDK  212
Tfer                 108 ----DRERRLQDALAP-VA-G---FDYALIDCPPALNMLTINALVAADSVLIPMQCEYYALEGLTQLLGTVRRVRAQLN-------PRLEVHGLLRTMFDNRNRLASEVALELERHFPDK  211
Xfas                 102 ----EREQRLKRALSP-IR-HE--YDFILIDCPPALSLLTVNALTAADSVIVPMQCEYYALEGLSALLETIEALRVNLN-------PRLEIEGVLRTMFDIRNNLANAVSTELTEHFGDK  206
Paer                 103 ----MKENRLRNALAP-IR-EN--YDYILIDCPPSLSMLTVNALTAADGVIIPMQCEYYALEGLTDLMNSIQRIGQLLN-------PTLKIEGLLRTMYDPRISLTNDVSAQLQEHFGDT  207
Pput                 103 ----VKESRLRNALAP-IR-DN--YDYILIDCPPSLSMLTLNALVASDGVIIPMQCEYYALEGLSDLVDNIKRIAARLN-------PELKIEGLLRTMYDPRLSLNNDVSAQLKEHFGPQ  207
Sput                 103 ----AREVRLRNALAP-IK-DQ--YDYIFIDCPPSLNMLTVNAMSAADSVLVPMQCEYFALEGLTALIDTITKLAAVVN-------PGLGIEGILRTMYDPRNRLSNDVSDQLKQHFGDK  207
Vcho3.0              103 ----AREVRLKNALAS-VR-DN--YDFIFIDCPPSLNLLTINAMAAADSVLVPMQCEYFALEGLTALMDTISKLAAVVN-------DNLKIEGILRTMYDPRNRLANEVSDQLKKHFGSK  207
Cjej                 102 -ENNEKKMLLKNQIQE----VIDEYDFIIIDSPPALGSITINAFAASDSVIIPIQCEFYALEGVAMVLNTIKIIKKTIN-------SKLRVRGFLPTMYSSQNNLSKDVVDDLKQNFKKQ  209
Hpyl                 104 DENKRGELMLKNALES----VVGLYDYIIIDSPPALGPLTINSLSAAHSVIIPIQCEFFALEGTKLLLNTIRMLQKSTN-------PKLKIRGFLPTMHVPQLNLTKGVLAELFKYFDSE  212
megaplasmid (Dr) b   223 ---MMRLGNLGEALDR----IQDQYDFILLDTRPNVSPLLTASTAAARLFLVPIGAHKG-LENLDELLRLVKLARKQD---------RSARIAFFIPNKVTSTRMGKNVLQSISAYTEVA  325
Drad0.4 *            103 G----AQGRLRRALAE----VSGDYDVALIDSPPSLGQLAILAALAADQMIVPVPTRQKGLDALPGLQGALTEYREVR--------PDLTVALYVPTFYDARRRHDQEVLADLKAHLSPL  206
megaplasmid (Dr) a   100 G----GILALRDALQK----ESGRWDTVIIDSPPSLGQLAAACALAADALVVPIMTRSKGLNALRGLNRVMPQYHRLR--------PDLHVAAYVPTMCKSNRKEDSELLGIVREDLPHV  203
Vcho1.1 *            226 SQN-QSLDIVRLLKEKLIDKIASDFDIIMIDTGPHVDPLVWNAMYASNALLIPCAAKRLDWASTVNFFQHLPTVYEMFP----EDWKGLEFVRLMPTMFEDDNKKQVSVLTEMNYLLGDQ  340
P1 (Ec)              221 NEHLPGQNIHAVLKENVIDKLKSDYDFILVDSGPHLDAFLKNALASANILFTPLPPATVDFHSSLKYVARLPELVKLISDEGC---ECQLATNIGFMSKLSNKADHKYCHSLAKEVFGGD  337
P7 (Ec)              222 EEHLPGQNQYEILRRNIIDRVADDYDFIFIDTGPHLDPFLLNGLAASDLLLTPTPPAQVDFHSTLKYLTRLPEMLEQLEEEGV---EPRLSASIGFMSKMTGKRDHETSHSLAREVYASN  338
pMT1 (Yp)            222 AEHLPGLKPSEVLRKTIIDRIAGDYDFVFIDTGPHLDPFLLNGLAASDLLLTPTPPAQVDFHSTLKYLTRLPEMLERLEEEGV---EPRLSASIGFMSKMTSKRDHETSHSLAREVYASN  338
QpH1 (Cb)            221 ENNNDRLGSPFLRLAESLKIIKNQYDVILIDCGPNLGLLTLNAIIACDGMIIPIPPSMNDYSSFIMYTATLRNMFRELSN------KKLDYLRILLSKHN-SSNEALQMENMMREQFGRY  333
pMOL28 (Re)          127 T-AEEGHIPFERVLSNGLDSLKDEYDYIILDTAPTLSYLTINAIFAADGVIVPVVPDTLAFASMVQFWQLFSDLVTGMEEQSRGSKKEFDFLDVLMTRME-KKNAPRLVADWIRGVYGSR  244
F (Ec)               215 DEG-KLPTDPHLMLRLAIETVAHDYDVIVIDSAPNLGIGTINVVCAADVLIVPTPAELFDYTSALQFFDMLRDLLKNVDLKG----FEPDVRILLTKYSNSNGSQSPWMEEQIRDAWGSM  329
pO157 (Ec O157)      215 DEG-KLPTDPHLMLRLAIETVAHDYDVIVIDSAPNLGIGTINVVCAADVLIVPTPAELFDYTSALQFFDMLRDLLKNVDLKG----FEPDVRILLTKYSNSNGSQSPWMEEQIRDAWGSM  329
N15 (Ec)             212 SEG-KLPHPPHLMLRAAIESVWDNYDIIVIDSAPNLGTGTINVVCAADVIVVATPAELFDYASVLQFFTMLLDLLETVDLGG----FEPVVRLLLTKYSLTNGNQSRWMEEQIRNTWGAM  326
pCD1 (Yp)            212 DQG-KLPVAPHLLLRAAIESVWDSYDVVVLDSAPNLGIGTINVVCAADVIVVPTPAELYDYVSTLQFFTMLRDLMSNIDLNG----FEPDVRVLITKFSNAIGSQSQWMDDQIRNAWGGM  326
pYVe227 (Ye)         226 DQG-KLPVAPHLLLRAAIESVWDSYDVVVLDSAPNLGIGTINVVCAADVIVVPTPAELYDYVSTLQFFTMLRDLMSNIDLNG----FEPDVRVLITKFSNAIGSQSQWMDDQIRNAWGGM  340
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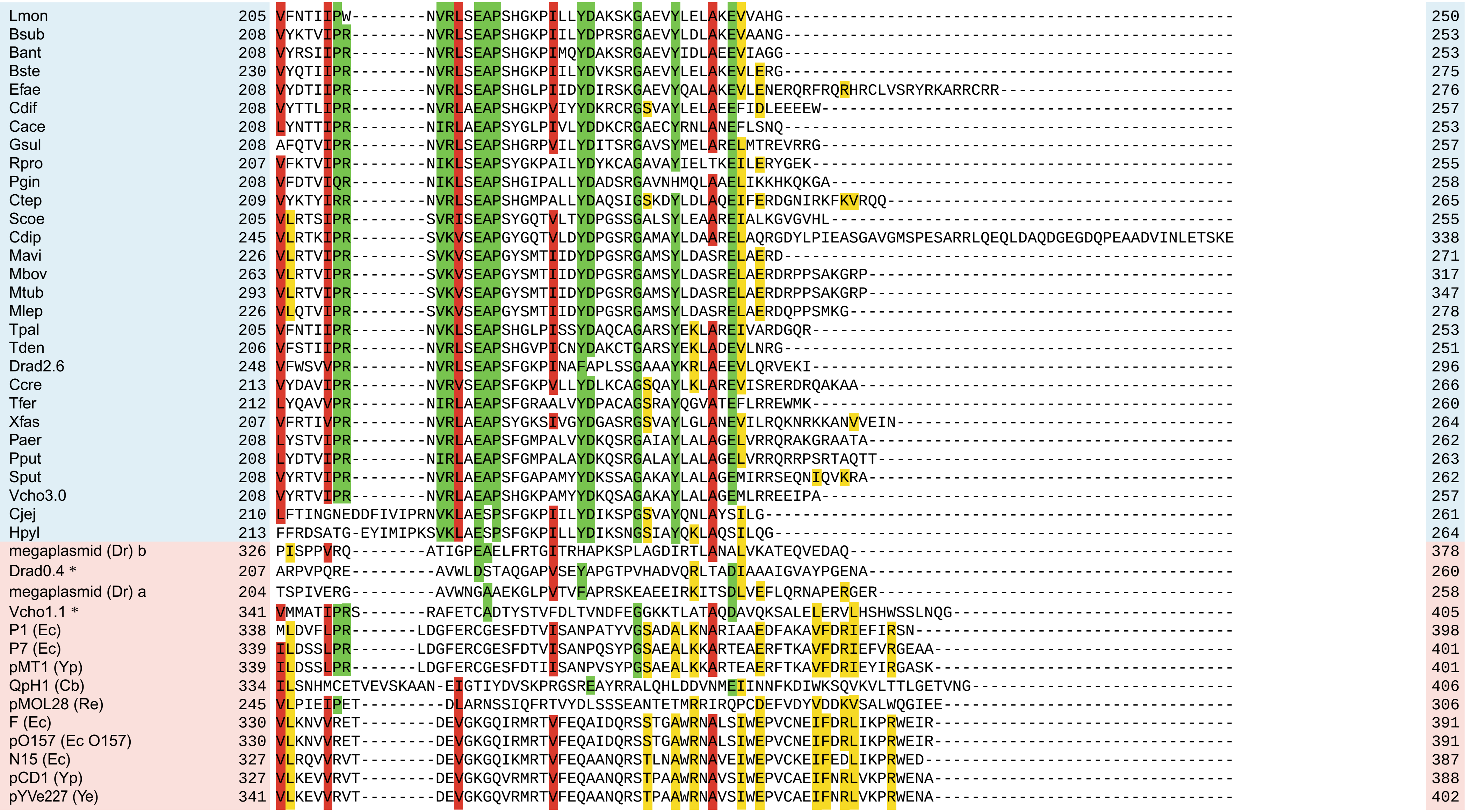

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Lmon                  205 VFNTIIPW--------NVRLSEAPSHGKPILLYDAKSKGAEVYLELAKEVVAHG------------------------------------------------ 250
Bsub                  208 VYKTVIPR--------NVRLSEAPSHGKPIILYDPRSRGAEVYLDLAKEVAANG------------------------------------------------ 253
Bant                  208 VYRSIIPR--------NVRLSEAPSHGKPIMQYDAKSRGAEVYIDLAEEVIAGG------------------------------------------------ 253
Bste                  230 VYQTIIPR--------NVRLSEAPSHGKPIILYDVKSRGAEVYLELAKEVLERG------------------------------------------------ 275
Efae                  208 VYDTIIPR--------NVRLSEAPSHGLPIIDYDIRSKGAEVYQALAKEVLENERQRFRQRHRCLVSRYRKARRCRR------------------------- 276
Cdif                  208 VYTTLIPR--------NVRLAEAPSHGKPVIYYDKRCRGSVAYLELAEEFIDLEEEEW-------------------------------------------- 257
Cace                  208 LYNTTIPR--------NIRLAEAPSYGLPIVLYDDKCRGAECYRNLANEFLSNQ------------------------------------------------ 253
Gsul                  208 AFQTVIPR--------NVRLSEAPSHGRPVILYDITSRGAVSYMELARELMTREVRRG-------------------------------------------- 257
Rpro                  207 VFKTVIPR--------NIKLSEAPSYGKPAILYDYKCAGAVAYIELTKEILERYGEK--------------------------------------------- 255
Pgin                  208 VFDTVIQR--------NIKLSEAPSHGIPALLYDADSRGAVNHMQLAAELIKKHKQKGA------------------------------------------- 258
Ctep                  209 VYKTYIRR--------NVRLSEAPSHGMPALLYDAQSIGSKDYLDLAQEIFERDGNIRKFKVRQQ------------------------------------- 265
Scoe                  205 VLRTSIPR--------SVRISEAPSYGQTVLTYDPGSSGALSYLEAAREIALKGVGVHL------------------------------------------- 255
Cdip                  245 VLRTKIPR--------SVKVSEAPGYGQTVLDYDPGSRGAMAYLDAARELAQRGDYLPIEASGAVGMSPESARRLQEQLDAQDGEGDQPEAADVINLETSKE 338
Mavi                  226 VLRTVIPR--------SVKVSEAPGYSMTIIDYDPGSRGAMSYLDASRELAERD------------------------------------------------ 271
Mbov                  263 VLRTVIPR--------SVKVSEAPGYSMTIIDYDPGSRGAMSYLDASRELAERDRPPSAKGRP--------------------------------------- 317
Mtub                  293 VLRTVIPR--------SVKVSEAPGYSMTIIDYDPGSRGAMSYLDASRELAERDRPPSAKGRP--------------------------------------- 347
Mlep                  226 VLQTVIPR--------SVKVSEAPGYSMTIIDYDPGSRGAMSYLDASRELAERDQPPSMKG----------------------------------------- 278
Tpal                  205 VFNTIIPR--------NVKLSEAPSHGLPISSYDAQCAGARSYEKLAREIVARDGQR--------------------------------------------- 253
Tden                  206 VFSTIIPR--------NVRLSEAPSHGVPICNYDAKCTGARSYEKLADEVLNRG------------------------------------------------ 251
Drad2.6               248 VFWSVVPR--------NVRLSEAPSFGKPINAFAPLSSGAAAYKRLAEEVLQRVEKI--------------------------------------------- 296
Ccre                  213 VYDAVIPR--------NVRVSEAPSFGKPVLLYDLKCAGSQAYLKLAREVISRERDRQAKAA---------------------------------------- 266
Tfer                  212 LYQAVVPR--------NIRLAEAPSFGRAALVYDPACAGSRAYQGVATEFLRREWMK--------------------------------------------- 260
Xfas                  207 VFRTIVPR--------NVRLAEAPSYGKSIVGYDGASRGSVAYLGLANEVILRQKNRKKANVVEIN------------------------------------ 264
Paer                  208 LYSTVIPR--------NVRLAEAPSFGMPALVYDKQSRGAIAYLALAGELVRRQRAKGRAATA--------------------------------------- 262
Pput                  208 LYDTVIPR--------NIRLAEAPSFGMPALAYDKQSRGALAYLALAGELVRRQRRPSRTAQTT-------------------------------------- 263
Sput                  208 VYRTVIPR--------NVRLAEAPSFGAPAMYYDKSSAGAKAYLALAGEMIRRSEQNIQVKRA--------------------------------------- 262
Vcho3.0               208 VYRTVIPR--------NVRLAEAPSHGKPAMYYDKQSAGAKAYLALAGEMLRREEIPA-------------------------------------------- 257
Cjej                  210 LFTINGNEDDFIVIPRNVKLAESPSFGKPIILYDIKSPGSVAYQNLAYSILG-------------------------------------------------- 261
Hpyl                  213 FFRDSATG-EYIMIPKSVKLAESPSFGKPILLYDIKSNGSIAYQKLAQSILQG------------------------------------------------- 264
megaplasmid (Dr) b    326 PISPPVRQ--------ATIGPEAELFRTGITRHAPKSPLAGDIRTLANALVKATEQVEDAQ----------------------------------------- 378
Drad0.4 *             207 ARPVPQRE---------AVWLDSTAQGAPVSEYAPGTPVHADVQRLTADIAAAIGVAYPGENA--------------------------------------- 260
megaplasmid (Dr) a    204 TSPIVERG---------AVWNGAAEKGLPVTVFAPRSKEAEEIRKITSDLVEFLQRNAPERGER-------------------------------------- 258
Vcho1.1 *             341 VMMATIPRS-------RAFETCADTYSTVFDLTVNDFEGGKKTLATAQDAVQKSALELERVLHSHWSSLNQG------------------------------ 405
P1 (Ec)               338 MLDVFLPR-------LDGFERCGESFDTVISANPATYVGSADALKNARIAAEDFAKAVFDRIEFIRSN---------------------------------- 398
P7 (Ec)               339 ILDSSLPR-------LDGFERCGESFDTVISANPQSYPGSAEALKKARTEAERFTKAVFDRIEFVRGEAA-------------------------------- 401
pMT1 (Yp)             339 ILDSSLPR-------LDGFERCGESFDTIISANPVSYPGSAEALKKARTEAERFTKAVFDRIEYIRGASK-------------------------------- 401
QpH1 (Cb)             334 ILSNHMCETVEVSKAAN-EIGTIYDVSKPRGSREAYRRALQHLDDVNMEIINNFKDIWKSQVKVLTTLGETVNG---------------------------- 406
pMOL28 (Re)           245 VLPIEIPET---------DLARNSSIQFRTVYDLSSSEANTETMRRIRQPCDEFVDYVDDKVSALWQGIEE------------------------------- 306
F (Ec)                330 VLKNVVRET--------DEVGKGQIRMRTVFEQAIDQRSSTGAWRNALSIWEPVCNEIFDRLIKPRWEIR-------------------------------- 391
pO157 (Ec O157)       330 VLKNVVRET--------DEVGKGQIRMRTVFEQAIDQRSSTGAWRNALSIWEPVCNEIFDRLIKPRWEIR-------------------------------- 391
N15 (Ec)              327 VLRQVVRVT--------DEVGKGQIKMRTVFEQAANQRSTLNAWRNAVEIWEPVCKEIFEDLIKPRWED--------------------------------- 387
pCD1 (Yp)             327 VLKEVVRVT--------DEVGKGQVRMRTVFEQAANQRSTPAAWRNAVSIWEPVCAEIFNRLVKPRWENA-------------------------------- 388
pYVe227 (Ye)          341 VLKEVVRVT--------DEVGKGQVRMRTVFEQAANQRSTPAAWRNAVSIWEPVCAEIFNRLVKPRWENA-------------------------------- 402
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