

A

Glo_vio : -----MRWLTF-----MFWFVAGFAVLTVPVAALFVR---SAHTEAELHSEVRSVQFGRPFVADRLKMDPWHYVWLNPGSGSTATTQ-----WQQPAGIQAGPLRWFPQRTAAAPP---LASYGYEGLVYLLSEIQ : 119
Myx_xan : --MTHQSKRLGVVGGIGLLVAAVAVADLPASAVASSAPDEGDFRIEGADLVDATEVVKFGDTFRVGRFRDPPSWHYVYWRNPGSGLETEVA-----WDTFG-VTVGFLQWFPQTFRTPDGFIITHGYDGBAILIADAK : 133
Cau_cre : -----MFLKKAVLALQALVMGAMLLGGHALAGPVVN---SGHVESELDVAQEAGIAPGGTIYVAIRQKIDAPGSHVYWRNPGDAGEPTKIT-----WTLEEGWSAGDMVWFTF---VKTRLGLHLLDYAYKGEVLIIPVET : 121
Hyp_nep : -----MD---ERRAEALADRVSVAFGDTFYAAIKMTDESWHYVWQAGAGLPPRLILEEGTSLBED-AVGAFIWEHPLHLPVVEGIMDYGYDDEVIYFAFFVT : 98
Sac_deg : MFVPPCFKRFGLKATKAVRVLGVVVFVFAICLAAQAQAQSTAFGDHVKVWMLAPDS-LIAGQOEVIIGFYFVLDLSEHYVYWRNPGSGAAPRFD-----IQVQGATLGEVWVWF---TFLPIEHLNLYGESHAYLLLET : 132
Sal_typ : -----MMILFRRILFCLLMLLPLVSWAAES-GWLRSPDNHDHSTRIRADTSANG---ETRLLDVWLENKRTYWRPAGGGVAPSLA-----WKG-DMPEVSWWVWF---SRFVANIITQGYHDETFPMIVR : 118
Rho_rub : -----MSRFLALCLFLCLPQAQAGNDPGASAVWEKSHSRMRLSVAASAAGKAEIALQVQEVAPKHYWRSPGAGYPPSFD-----WTGSLNLGATPFRWVFP---TRFSVLGETYGYEHOVLIPLMAR : 123
Chl_tra : -----MIRQWYGFLLCLLFSYTSCEFVEENSGRATPTVELVSESEQAIECEVLRIGVLIAPBESEHYVWRNPGKLEMPLRIS-----WDLSEGCRLLEEHWFP---EIFEEDGWVYFYKSHTMVVALIR : 118
1 g 6 gwh YW npGd G w WP P 6 gY v

Glo_vio : APADLPKGAATRAKAEQTECKVCELGAGTVALELTVQA-EATAPSVHADAIAAARGHIVVTIA-DWKLRAAVQEGQLIIRA---TRPEWFAGEIGPVTFPEQDILLPEAAHVLLEV-----RFDGLFKLKRSAV : 248
Myx_xan : AVEGSPSTG-LIIVSAAEYHVEVHCIPAEMLMTRSLPHGP-QTVRDAETAAVVDTEKIKRPPAK-DSGPAATVALDAPQITAGQDFTGTLTAPGGAAPVAVGDFVADRIFGVVRVGLASDGGFRFKKGAKEPD : 270
Cau_cre : AANAQPGTTLSTLADWFLVCEQVCHIEQAQKLSLLELVVAGTPADPKPWGAVIGKVLADAPKPAKGLKAVFK---LEGQALKAV---TGGPLKGMAGAYFSPYSSKVEHAHAERAIER---GAEGLTLKPG-Y : 249
Hyp_nep : VEPDASG---EVRIKVAEADYHCESTICTHETADVSHLTPVGA---PIENAVAGAEIGKVARVDFVDFGEARIIDDAEPWTLISRQ-----PGGFPEGAQIR---FSPFK-HEHSHPAAPQKA-----GAEGASHLTPDRA : 221
Sac_deg : AD---LQTSEVIVNVSLEWLVKVDCTIEFGFMSRILPHTN-QSLWLADPLDALRDGYLALVQOQNTSPWQAVKAQVGTQQLTLANHSTRLAQGDFFNSVSVGPEVDEGLVATKPKIKSN-----AAGLELTFNRVPG : 262
Sal_typ : GT---LEPAT---LRGVTLSTGASNVCLLT---DYFYSVPTTV---QNAD-FAHDYARAWKILRIS---GLTDSLVDVYRPEGLV---VTATRAAGWSPPGLDLDVDDVDFAKPRIRVDEGDRLOQATVPTVDSWGEKAP : 238
Rho_rub : LE---RPGDPTIRLAWDYLCAEVCFVDRGDFLIVPEGPP---SGASPAQALARSIMQVGPSPSHGTYDEAVIETGGVVR---VAVRADPPLAAPDLVEAPAGAFARFQVTVVEGGRAVLRAGVGGD--- : 249
Chl_tra : VS-KEIETRPEIKAQEELISGASCLFGSSSRVIVIPDEGPLIPNSKETETTFSRALGCEVLRIGVLIAPBESEHYVWRNPGKLEMPLRIS---KADRATQAWFIAENTRDFAYAQEVPLELATTYIWKLKHPEGNMFKGILGSG : 253
6 1 C C6p 1 6p a P q

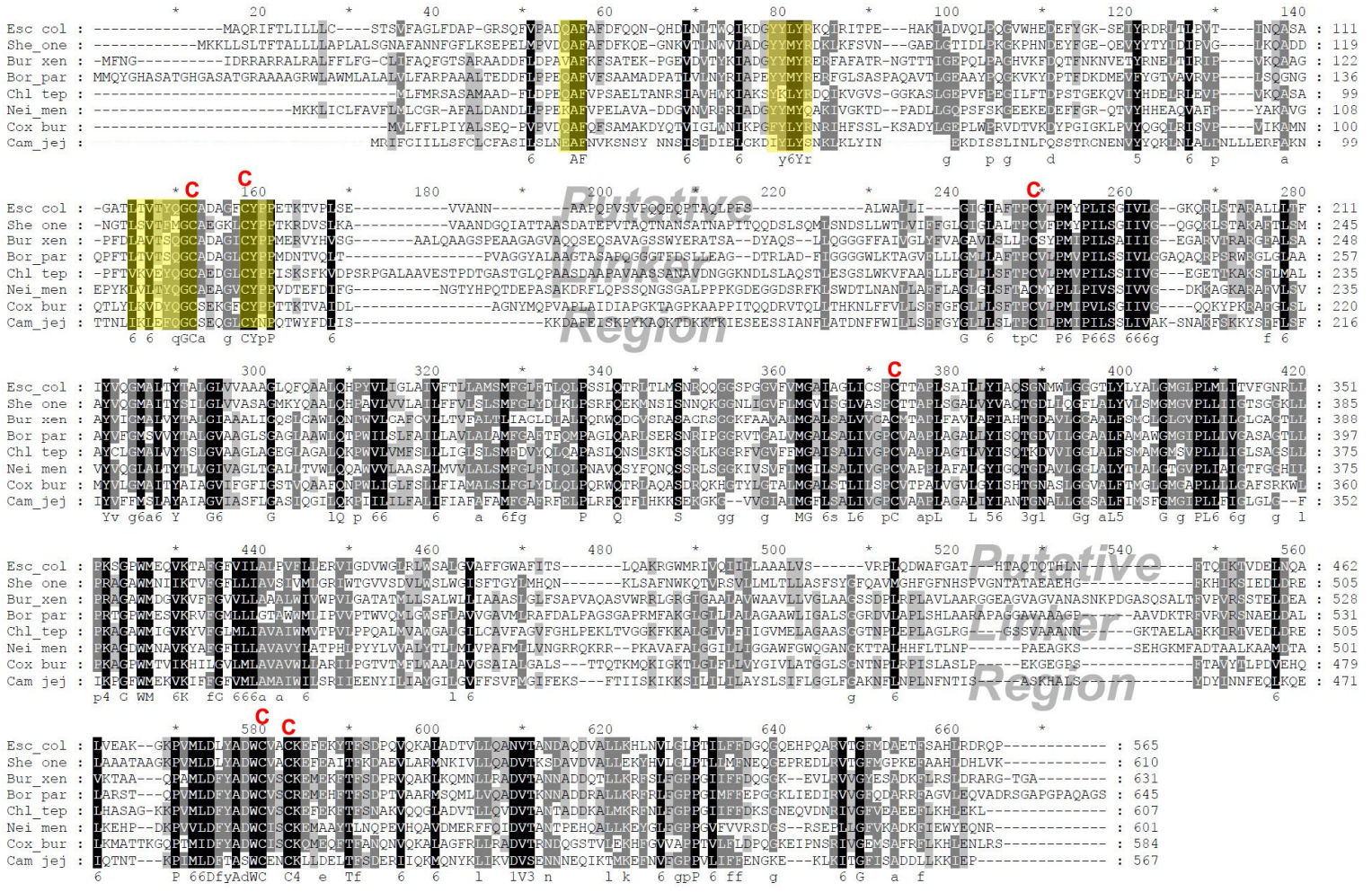
Glo_vio : STATPERIAGV-----VAPAGWRGAGSEQALSVR-----VALEFVAALISAG--APDLAG---LLVAVGFAHGGMILNLMPCVPLVLSIKVLEGFQEAR---TGHAWRYGATATAGVITASVWL : 355
Myx_xan : AQASAPDLTGVLRLGTAATGYQYLEVTAPLAPLVAAGGAAGTFAVVKPPSVKDSIAAVKFEVGAATTPPAEASSMG---LGLAVFAHGGMILNLMPCVPLVLSIKVLEGFQEAR---TGHAWRYGATATAGVITASVWL : 406
Cau_cre : DFVGGSTPPAEI-----VGLVATKAGAWVETATAGEAAGASG---LGPPEAAAPGGALAGG---LAGALFAHGGMILNLMPCVPLVLSIKVLEGFQEAR---TGHAWRYGATATAGVITASVWL : 363
Hyp_nep : GSTAETLDGVTR-----IDVPGAEPVGYEIASASRGEAFAGTADBNVQSALPGTSGAGAPDAGDGAALGWORIATLAFFAHGGMILNLMPCVPLVLSIKVLEGFQEAR---TGHAWRYGATATAGVITASVWL : 348
Sac_deg : AALPTATDEVVVD-----GNRAFWLN-----DIALVNQAVLLPANSQSQTQPSWTLIIGAFHGGMILNLMPCVPLVLSIKVLEGFQEAR---TGHAWRYGATATAGVITASVWL : 363
Sal_typ : DLRNKSITLIVADR-----ATAQFS---TQTGTAPAQTFDN-----AALPFOQVVMMAHGGMILNLMPCVPLVLSIKVLEGFQEAR---TGHAWRYGATATAGVITASVWL : 336
Rho_rub : ALIGQSLPVLVADG-----VRGVEAGVDTRRALAPPACAGDRPTALGEGSGGETGAPGAPTGLPLAFAMVSVALLGGMILNLMPCVPLVLSIKVLEGFQEAR---TGHAWRYGATATAGVITASVWL : 370
Chl_tra : ILIFKDDAGKVVAS-----YQVEENQVEQLSALSWR-----FLSILMFAHGGMILNLMPCVPLVLSIKVLEGFQEAR---TGHAWRYGATATAGVITASVWL : 344
A GG 6LN6MFCV P66 6K G 6 3F

Glo_vio : LAGGHLRAGGECGHWGRCQCEHFLVLCVAVLEFGNIRGIEFVGTG-----LTRIGG-AGPAGTGCCEGEGVLTATVATPCTAFPMGSAIYALTPQVWAAIIVETALGIGMSPYLLGLSIALLRVVPKPG : 407
Myx_xan : LASVWVAVRAGSASVGGRCQCEHFLVLCVAVLEFGNIRGIEFVGTG-----LTRIGG-AGPAGTGCCEGEGVLTATVATPCTAFPMGSAIYALTPQVWAAIIVETALGIGMSPYLLGLSIALLRVVPKPG : 539
Cau_cre : LAGALAVRAGSAAVGGRCQCEHFLVLCVAVLEFGNIRGIEFVGTG-----LTRIGG-AGPAGTGCCEGEGVLTATVATPCTAFPMGSAIYALTPQVWAAIIVETALGIGMSPYLLGLSIALLRVVPKPG : 496
Hyp_nep : LAGAMAVRQATGSAIYGGRCQCEHFLVLCVAVLEFGNIRGIEFVGTG-----LTRIGG-AGPAGTGCCEGEGVLTATVATPCTAFPMGSAIYALTPQVWAAIIVETALGIGMSPYLLGLSIALLRVVPKPG : 481
Sac_deg : LEAVMLGLRAGCAALGGRCQCEHFLVLCVAVLEFGNIRGIEFVGTG-----LTRIGG-AGPAGTGCCEGEGVLTATVATPCTAFPMGSAIYALTPQVWAAIIVETALGIGMSPYLLGLSIALLRVVPKPG : 491
Sal_typ : LEAFMLLRLSNHAIYGGRCQCEHFLVLCVAVLEFGNIRGIEFVGTG-----LTRIGG-AGPAGTGCCEGEGVLTATVATPCTAFPMGSAIYALTPQVWAAIIVETALGIGMSPYLLGLSIALLRVVPKPG : 470
Rho_rub : LALAAALGKTAGMAGVGGRCQCEHFLVLCVAVLEFGNIRGIEFVGTG-----LTRIGG-AGPAGTGCCEGEGVLTATVATPCTAFPMGSAIYALTPQVWAAIIVETALGIGMSPYLLGLSIALLRVVPKPG : 505
Chl_tra : LAFCALILKVLQNLGGRCQCEHFLVLCVAVLEFGNIRGIEFVGTG-----LTRIGG-AGPAGTGCCEGEGVLTATVATPCTAFPMGSAIYALTPQVWAAIIVETALGIGMSPYLLGLSIALLRVVPKPG : 484
La 64 g gwGf Q p 6 6 6 1 l G Fe g g g f G la 6atPC P6f g a g a 6F aglG a P5 p 6P4PG

Glo_vio : AMMETRQAMGLLMDGIVWVWVGLQAVSALAAALLAVLVG-----AAAWLKGWGHMAAPATRLRVARVLAALGIVGLVALVGVQQAASGGPTQATATPSEGRWEAASFCRVAALRAAEETVEVIDETAA : 621
Myx_xan : AMMERKROVGGALLAMTIVWVWVGGGLAVDGMARLLAFIVAVG-----LVTALYQQG---QAQDGVKRLATVAVAAVGLVAGSLLTLRFDDQ---DPVEAPRVGTVQAQCPNSADRNAAALAGQVVIDETAD : 665
Cau_cre : DWMEVIRKGLIABEMYGAAILWLVVFAQQAPIALGOLLVAVGLAA-----FGAWLYGLAQRRAVGVKGSASVMIIGLLAVVGLALAAASALSAPVVAASSTPSPG-GLTAEANSERVQALQAEGRITVIDETAA : 629
Hyp_nep : KMMDTIKQAFABEFLLAAWLVSVVAGLAGAGAVGWTLAGATTLV-----FAIILG-----RQGGAVRKQVAALVAAAFIYPAVQANVPTSVAGSSEAPFTG---AYGEAANSVEVEAMLADCRVVIDETAS : 604
Sac_deg : FMMETRQFIAEFVAVVWLVVGLVGRVLEDIGLVGASLMLSFV-----VAIILAS-----TLQWGKIGRSVYICLGAVVAEVFSLSLAIP-----SGNKSQSETSQNNKEDSQTAQAPQCRVVIDETAA : 611
Sal_typ : FMMNIVRRIILGMLGSAIWAATLILPHFG-----AVVAARVCGGLLAVALGVRLRPIIS-----PLSGVAAALLGIAALALPALPEALSLPMAAFPSQALEETAWGRSPEVAVRIVDEKTVVIDETAD : 538
Rho_rub : FMMTRRRAVIGAVGLDPAWLVSVAVQICAVVAARVCGGLLAVALGVRLRPIIS-----PLSGVAAALLGIAALALPALPEALSLPMAAFPSQALEETAWGRSPEVAVRIVDEKTVVIDETAD : 625
Chl_tra : FMMSTRRQLTGMILANATWLVWVGVETSATAVITLVLVGLLAA-----VGAAILG-----RWGTLVSPNQRLLASVVFICILSSLVITSIGVRFIDENFPAHSSDWCSEPEHLDLREKIEFVWVNTAK : 610
WM 4 f 6 WL 6 w s 6 a g 6f61 TA

Glo_vio : WCISQVNERVAESSPQVREAGRGVVMKADWTRRDAATQAALQAFGRSGVFLVYLSTAGAPAFRILEPEVLPDITKAKIQELS----- : 708
Myx_xan : WCLTCKENERTVLSSTDVDRDAKKHQAFFIADWTRRDAITTRLAEGHGRAGVFLVLSLSTAGAPDPKPEVLPPELLTGGVWTDATRAAACAPSKLNGANVLAAGFPSSH : 774
Cau_cre : WCVTQVMEKVALSGPRVABAKQAQAVLIRADWTRRDPVIAKALADFGFRVGVPLVLY---PKNGGSEVILPQLLQEGMVLEAHERAGS----- : 716
Hyp_nep : WCASQVNMKLTLDKTRKVDANKSANVAFIVADFQKDPMAEBIKLRAAGVPMYLYW---PAGASEPQILPELLQELVIGLVEG----- : 688
Sac_deg : WCLTQVNMKLVLDQTPQDSKKNVYLVLRADWTRRDAITQSLAQQLGNSVPMYAWY---GKGADEVVILSOLLRAGSIDALFEQK----- : 696
Sal_typ : WCLTCKVKNYVILQKELVQALQDPVAVRBDWTRRDAITDFDKTRQVAVFVQVYGGGLP-EGEALFLLLRADVAIQTLKKAKGITQ----- : 628
Rho_rub : WCLTCKVKNYVILDAAPTRALLDSGRSGRADWTRRDPVIAKALADFGFRVGVPLVLY---PKNGGSEVILPQLLQEGMVLEAHERAGS----- : 715
Chl_tra : WCCTQVNMKLVLDQTPQDSKKNVYLVLRADWTRRDAITQSLAQQLGNSVPMYAWY---GKGADEVVILSOLLRAGSIDALFEQK----- : 692
WC 3C N 1 af ad5T d I La gr 6P y p Ip L3 6

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NP_697507Brucella      : -----MKICTSIIAPFIIAVIIAIP--AQASTSAWTETPGGRVRIIVIEGGDFAITGKQEVIRGALQIETLRFGWKTYWRNF : 71
NP_353804Agrobacteri  : MSVRIFFFFSHLRLAVVFAALIGGGCAAQAEITDWARSEGGCMRVAS----LAMDADGVVRGVLOIEPKIGWITTYWRFP : 75
YP_354084Rhodobacter : -----MLRRLFLASCIATAFAAATPPDQILKAELLEPC-----WREGGRHIAALRIKIAEGWKTYWRSP : 60
YP_180121Ehrlichia   : -----MLRISFIFIVLITLLTYQNGYSAKSPDPVNIKLIVG-----SMLMKNRITINIGVDFRIQEGWHIYYKSE : 64
                        :                               la l a gg                               6 GW tY54 P

NP_697507Brucella      : GLAGVPPQIS---IEGLAKAQTAFVAFVRFAGDEEGGIG---YKQVSIKIVTFHIEP---GGKR--LKGHAFIAGMCPN : 138
NP_353804Agrobacteri  : GEAGIPPCITPDFASGVSLTMMAYVVPKLIENGDIITDIG---YDHAVSIKPFQLKATD---FAASGTIDITAFIGVCCN : 147
YP_354084Rhodobacter : GEAGIPPEFDWSGSRNVSGVRMHWVPHVFSLNGMOTIG---YRDEVVLKPEEVETRD---AREPVRIRARVLDLGVCRD : 132
YP_180121Ehrlichia   : GDLGLETFVQWQ-ENIFKDVCIHWQPIQHTDTSNNIFHSNVYKDIIVMFIISFALKHDNLNLTKELSLSLRIKYAVCKD : 142
                        : G aG6Pp                               6 5P P Ig Y V 1P                               6 g6C 1

NP_697507Brucella      : TCVFVLAEEFDFFLLADRQKSSSENLAARTVVEVTAFAQLHAFASPD-FGVSAVKHDKDEAIFDVALPDPN---AFAELEFV : 213
NP_353804Agrobacteri  : ICIPFPAKFSISRGNAAADDSEE---RRLEEARETLPEASDD-FKVDFHTPDKTMLGVLQLEPENAPKETEIEFI : 221
YP_354084Rhodobacter : TCVHADFFELDGELGFPVG-----APDPIISAALRSREETGREAGVCRVACRVDPIDDGLRIETAELDFATGGAEVVV : 203
YP_180121Ehrlichia   : VCIEPQKVIILN-----RFIQDYVNOENLGLINFWKKK----- : 175
                        : 6C6P e                               a lp g                               e

NP_697507Brucella      : ASDT-VNLSAPVSVVE-DGKASQRFIAKMQCKTKLAVIDYT---IVQNG-KAVSGRLELD-- : 266
NP_353804Agrobacteri  : AGPSGFAYYEPQNTIV-RDKRRLSIFYMNIKGLPKTYQVPGNSWPIIVKSCDRAMETVLNFPKP : 282
YP_354084Rhodobacter : MEPGTFAIWTSEAVTSRQCARLVAVSDLVGPDGVFFALDRSAVTITVLEDRRAVEIRGCEAP : 265
YP_180121Ehrlichia   : ----- : -
                        :                               g g
    
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