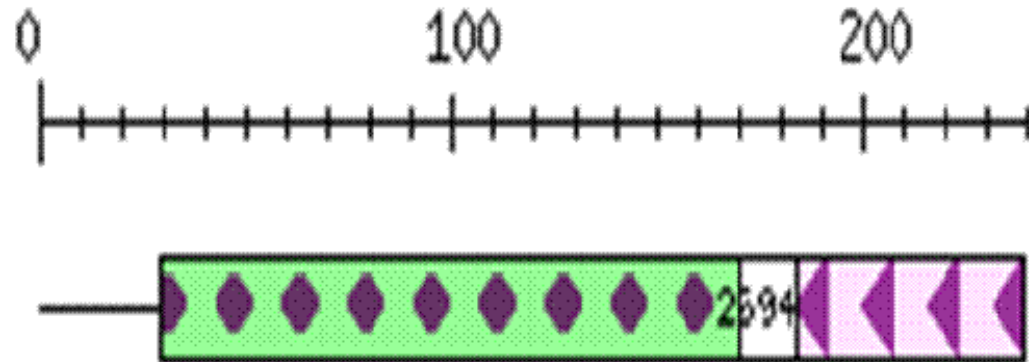


VirB1



	<u>Domain ID</u>	<u>BEGIN</u>	<u>END</u>	<u>Total ID</u>
1.	PD017223	29	169	28
2.	PD114911	184	238	4
3.	PD269425	170	234	2
4.	PD580287	91	125	275
5.	PD648112	169	237	1

1 10 20 30 40 50 60 70 80 90 100 110 120 130

066281_AGRTU(29-169) EFNNFARECAPSVSPSTLAAIAQVESRFDPFLVYHDM-----TTGETLHW-QNQQAQTQVYMDRLDARHSLDVGMLQINSRNF SVLGL-TPDEALQPCTLSAAANL LGSRYAGGDTA---DKKQLA
Q9R6C3_AGRTU(29-183) EFNNFARECAPSVAPSTLAAIAQVESRFDPFLVYHDM-----TTGETLHW-QNQQAQTQVYMDRLDARHSLDVGMLQINSRNF SVLGL-TPDEALQPCTLSVAANL LGSRYAGGNTR--DDEQLS
VIB1_AGRT5(29-183) EFNNFARECAPSVAPSTLAAIAQVESRFDPFLVYHDM-----TTGETLHW-QNQQAQTQVYMDRLDARHSLDVGMLQINSRNF SVLGL-TPDGALQPCTLSVAANL LGSRYAGGNTR--DDEQLS
VIB1_AGRTU(29-169) EFDHVARKCAPSVATSTLAAIAQVESRFDPFLVYHDM-----TTGETLHW-QDHTQATQVYRHRDLARHSLDVGMLQINSRNF SMLGL-TPDGALKACPSLSAAANML KSRYAGGETI--DEKQIA
VirB1(29-169) EFDHVARKCAPSVATSTLAAIAQVESRFDPFLVYHDM-----TTGETLHW-QDHTQATQVYRHRDLARHSLDVGMLQINSRNF SMLGL-TPDGALKACPSLSAAANML KSRYAGGETI--DEKQIA
Q8YTA2_AGRTU(27-167) EFSQLARECAPSVAPSTLAAIAQVESRFDPFLVYHDM-----TTGETLHW-KNPADATQSYNMRVYAGHSYDVGMLQVNSKNFANLGL-TAGNAINPCVLSAAADL LVRHYSGGDTV--ESEQLA
Q9F5A2_AGRRH(27-167) EFNQLARECAPSVAPSTLAAIAQVESRFDPFLVYHDM-----TTGETLHW-KNPADATQSYNMRVYAGHSYDVGMLQVNSKNFANLGL-TAGNAINPCVLSAAADL LVRHYSGGDTV--ESEQLA
Q8KJL3_RHILO(29-169) EFHRLSRKCAPVAPSTLAAIAQTESGFETLVAHDM-----TTGEQLRW-TDHLAETRGKLNLEAQHSYDVGMLQINSRNF SFLNL-TPEKAFEP CASLSAAAHLL ESRYAGGTTA--PAQLA
Q46694_ECOLI(33-175) LAQR CAPDVSP LTHAYIVGHESSENGPYRININ-----GSIQLKQPRTEREAVSVYAKVLLKDNKSFDMGLAQINSNMLVGLGL-SVDDIFKPCINLRASQTILKACYDSALKSY-PAGQVA
Q847E4_PSEPU(31-163) FSDLAARKCAPNVHASTLKALIGNESSFNPPYAIQVV-----GT-RLERQPKSLSEAIATAEKLERDGHRYAMGLGQLLMTNMRARGL-SYQDVFEPCRNLQAISKLFTEYYTQALKTS-ATEQEA
Q8VMF7_PSEPU(41-191) FSELAARKCAPVHPSTLKALIGNESTFNPPYAIQVV-----GT-HLQRQPSLSEAIATAEKLERDGHRYAMGLGQLLMTNMRARGL-SYEDVFEPCRNLQAISMLLVEYYKQALTT-SDKQEA
Q8KMV0_ECOLI(5-179) EFAVIAAMCAPAIHPTLSAVVYTESRGMIIYRIGIN-----GDHKLPRPQQTLEAIATAEKLERDGHRYAMGLGQLLMTNMRARGL-SYEDVFEPCRNLQAISKLFTEYYTQALKTS-ATEQEA
Q9PHK3_XYLFA(2-171) DFLALSQECAPVATQTHAAIVKTESGFNPLLSYV-----GGAKLVYRQPKENKAEVSTARMLTEKGYNIDLGLGQVNSNMLVYKVL-SVEDAFEPCKNLAAARITLQGNFQVAKGKY-HDDQAA
Q8PRJ6_XANAC(24-188) FEKLAARECAPDVHPTTLKGVVSTESSNMPYAIQVV-----GG-RLDRQPSLSEAVATARELERQGFNFMSHGLGQVNSRNLAKYGE-SYETVFEPCRNLKAGSVILKDFCQRAKAQH-GDDQAA
Q8YD25_BRUME(4-161) FLVLAQQCAPTVAPQTHAAIVQVESGFNPPYAIQVV-----GG-RLYRQPSLSEAITTAQSLERKGMNFSLGIQAVNRYNLPKYGS-TYQAFDPCKNLKMGSKILLEDYRRAIVKMPGQEQGA
Q9KIT0_BRUAB(4-161) FLVLAQQCAPTVAPQTHAAIVQVESGFNPPYAIQVV-----GG-RLYRQPSLSEAITTAQSLERKGMNFSLGIQAVNRYNLPKYGS-TYQAFDPCKNLKMGSKILLEDYRRAIVKMPGQEQGA
Q9RPY4_BRUSU(4-180) FLVLAQQCAPTVAPQTHAAIVQVESGFNPPYAIQVV-----GG-RLYRQPSLSEAITTAQSLERKGMNFSLGIQAVNRYNLPKYGS-TYQAFDPCKNLKMGSKILLEDYRRAIVKMPGQEQGA
Q91UQ4_RHIME(2-174) LEFLALAEQCAPTVAPQTHAAIVVYESSYFNPPYAIQVV-----GG-RLARQPSRDEAVATARELERQGFNFMSHGLGQVNSRNLAKYGE-SYETVFEPCRNLKAGSVILKDFCQRAKAQH-GDDQAA
Q91UX8_ECOLI(2-168) LEFLALAEQCAPTVAPQTHAAIVVYESSYFNPPYAIQVV-----GG-RLARQPSRDEAVATARELERQGFNFMSHGLGQVNSRNLAKYGE-SYETVFEPCRNLKAGSVILKDFCQRAKAQH-GDDQAA
Q93TD0_BBBB(7-165) FLALAMQCAPSIHPATLPIYKTESGFNPPYAIQVV-----GG-VLPRQPSLSEAITTAQSLERKGMNFSLGIQAVNRYNLPKYGLTSYEMAFKPCNLYAASKILAECHSRS-----GAN
Q8VP09_BBBB(37-181) FAQLARACAPNVDPATLALVRETESGFNPPYAIQVV-----GG-HLTRQPSLSEARATARELERQGFNFMSHGLGQVNSRNLAKYGE-SYETVFEPCRNLKAGSVILKDFCQRAKAQH-GDDQAA
Q9F522_ECOLI(10-157) ALSQCAPDVSPDTMNAIINTESGANNPYAIQVV-----SD-GTSKYFKDEKGAIEYAEKLTRENKRFSAQLTQYYSKFPSPNLN-TNKTVDFPCNLRKAGAVLTDNYLRQKE---GSSNQK
Q8P7X8_XANCP(15-138) VPEVVMQHVVRVYESSRNPYAIQVV-----GG-RLAREPRGLEAVATARELERQGFNFMSHGLGQVNSRNLAKYGE-SYETVFEPCRNLKAGSVILKDFCQRAKAQH-GDDQAA
Q8PJB8_XANAC(15-152) VPEVVMQHVVRVYESSRNPYAIQVV-----GG-RLAREPRGLEAVATARELERQGFNFMSHGLGQVNSRNLAKYGE-SYETVFEPCRNLKAGSVILKDFCQRAKAQH-GDDQAA
Q8KIM5_RHIET(5-150) FVEIAQTCAPMVQVQTLAGVVSLESFQFPFIRIN-----SGPPLAAQPPASKAEIEVATSLADRDQIQIGLGGIGMELRRLKL-SISDAFDPCLNLHATATL LDGYRRLAMKAGADPDHAE
Q92Y23_RHIME(5-147) FLDLAQTCAPIVARETLAGVVSLESFQFPFIRIN-----SGVPLSEQPAKTAEIAMATLSAERQDIQLGLGGIGMELRRLKL-SISDAFDPCLNLHATATL LDGYRRLAMKAGADPDHAE
Q8KI83_ACTAC(9-130) CSTIVHIETLHALIQTESYFNPPYAIQVV-----NDIPLAQPKTLQEAELVIDELEAKKINYSVGLGQVNSRNLAKYGE-SYETVFEPCRNLKAGSVILKDFCQRAKAQH-GDDQAA
Q9EUG1_ECOLI(7-140) FVALAMQCAASIHPTDAEQVARVYESSFNPPYAIQVV-----IPKNERKEGDSGVISHFQKTEALKTVQNIESRNRYSVGLMQLTSTNFSQYGV-NADKLFSPCTNLAVFEKVL LDGYRRLAMKAGADPDHAE
Q9F243_ACTAC(3-128) MTLALQAMCAPLVHPDTALSYMKESKLNQFATGIV-----DGMVYKQ-PTDFMSAVLTAQQLEAKKINYSVGLMQLTSTNFSQYGV-NADKLFSPCTNLAVFEKVL LDGYRRLAMKAGADPDHAE
Consensus .f..la..Cap.!..p.Tl.a....ES.f#pyai..vl..qp....eA...a..l...g.....Gl.Q.n.#f...glaf.pC.nl.a....L..c%.....q.a

131 140 150 160 170 180 190 194

066281_AGRTU(29-169) LRRASAYNTGDFTHGF-----ANGYVRKV
Q9R6C3_AGRTU(29-183) LRRASAYNTGDFTHGF-----ANGYVRKVETAQQQLVPPLTAR
VIB1_AGRT5(29-183) LRRASAYNTGDFTHGF-----ANGYVRKVETAQQQLVPPLTAR
VIB1_AGRTU(29-169) LRRASAYNTGNFIRGF-----ANGYVRKV
VirB1(29-169) LRRASAYNTGNFIRGF-----ANGYVRKV
Q8YTA2_AGRTU(27-167) LQAASAYNTGNPARGF-----ANGYVRRV
Q9F5A2_AGRRH(27-167) IRRASAYNTGNPTRGF-----ANGYVRRV
Q8KJL3_RHILO(29-169) LRRASAYNTGDVTRGF-----TNGYVRKV
Q46694_ECOLI(33-175) LRHALSCYNTGSLTNGI-----SNGYVTKVINVA
Q847E4_PSEPU(31-163) LLKATSHYSGNERLGF
Q8VMF7_PSEPU(41-191) LLKAFSHYSGNELRGFRPDRP-GEHSYVEKVVHNA
Q8KMV0_ECOLI(5-179) LQAALSCYNTGNFQRF-----SNGYVQKVASHVGVYVPALEPVSGGTQEPAKLQAVPKGAA
Q9PHK3_XYLFA(2-171) LHAALSAyntGSFSGF-----LNGYVQKVLNNAAGVTVQGYV-----AQQAVKLRKAAEGKA
Q8PRJ6_XANAC(24-188) LRAAFSCYSGNFTRGFRPDKA-GQPSYVQKVYASADVTTKPI
Q8YD25_BRUME(4-161) LRAAFSCYAGNFTGGFKT-KP-GSPSYVQKVYASADVTTKPI
Q9KIT0_BRUAB(4-161) LRAAFSCYAGNFTGGFKT-KP-GSPSYVQKVYASADVTTKPI
Q9RPY4_BRUSU(4-180) LRAAFSCYAGNFTGGFKT-KP-GSPSYVQKVYASADVTTKPIAVVPMIRKTPDAAAVVAP
Q91UQ4_RHIME(2-174) LQAASCYSGNFTRGFRPDKA-GEPSYVQKVLQANVQPKAIPVYVPSIKPGEGBA
Q91UX8_ECOLI(2-168) LHAAFSCYSGNFTRGFKPDVA-GKPSYVQKVLASAGVQPKAIPVYVPSIQ
Q93TD0_BBBB(7-165) LKHAISCYSGNPRRGFKAEARAFGGSSHYQVRLANAGITTTVYVPA
Q8VP09_BBBB(37-181) LRAALSCYSGNFTTGF-----SSGYVSRVYVA
Q9F522_ECOLI(10-157) ILRALSLYSGNESTGFIKEKKFNNTSYLERVIRNA
Q8P7X8_XANCP(15-138) HGKSFSCYSGNFETGF-----KHGYVQKI
Q8PJB8_XANAC(15-152) HGKSFSCYSGNFETGF-----KHGYVQKIYASIRQSVASSGAE
Q8KIM5_RHIET(5-150) RVHLQSYGRDDPSLGA-----HYKYDEQVQLQEA
Q92Y23_RHIME(5-147) QVHLQSYGRDDPSVGA-----HYVYDQVV
Q8KI83_ACTAC(9-130) VAERALSCYAGNFSYGFV
Q9EUG1_ECOLI(7-140) LKNALSCYSGNFSTG
Q9F243_ACTAC(3-128) VNDALSCYSGNFLRGY
Consensus l..a.ScY.G#f..Gf.....yv.kv.....

1 10 20 30 40 50 60 68
 |-----+-----+-----+-----+-----+-----+-----+-----|
 Q8YTA2_AGRTU(168-235) EVAAQLVPPLTQSGKNQTHSEQSQDEPMDVYGAHDHSHSAGEADDSASPEARKPNKGESPEKDQVF
 Q9F5A2_AGRRH(168-232) EVAAQLLVPPLAQSGKKGDRDERSPEEPMDVYGSYDRSHSAV---GSSAPPEAQQPNERKSPEKDQVF
 VirB1(170-234) ETAAQSLVPALIEP-PQDDHKALKSEDTMDVYGSYQR-RSQEDGVGGSIAPQPPDQDNGKSADDNQV
 Consensus EvAAQ.LVPPl.#sgk..dh.e.s.##pH#VMGsy#rshSa.....gsSa.P#a..p#.gkSp#. #QVf

1 10 20 30 40 50 60 62
 |-----+-----+-----+-----+-----+-----+-----+-----|
 O66281_AGRTU(184-245) PKDDREKPRSEETMDVYGSYKRRSPEGGAGGSSGPPPPDQDNRKSEDDQQLLFDLNKGGQQ
 Q9R6C3_AGRTU(184-245) PKDDREKPGSEETMDVYGAAYKRRSPEGGAGGSSGPPPPDEDNRKSEDDQQLLFDLNQGGPQ
 YIB1_AGRT5(184-245) PKDDREKPGSEETMDVYGAAYKRRSPEGGAGGSSGPPPPDEDNRKSEDDQQLLFDLNQGGPQ
 YIB1_AGRTU(184-238) PQDDHKALKSEDTMDVYGSYQRRSQEDGVGGSIAPQPP-DQDNGKSADDNQVLFDL
 VirB1(184-238) PQDDHKALKSEDTMDVYGSYQRRSQEDGVGGSIAPQPP-DQDNGKSADDNQVLFDL
 Consensus PqDDhkaIkSE#TMDVYGSYqRRSqEdGvGGSiAPqPP.D#DNgKSaDD#QvLFDL.....

1 10 20 30 40 50 60 70 80 90 93
 |-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----|
 Q8KJL3_RHILO(170-260) ESAAKDITSHLERTLEPTAPDAPHLERASGRKAVPPLLQSQANGKQPNQNSMDIYGSYENRSGADPSGPTGSQAAEER--EPSNPNKLYFD
 VirB1(169-237) VETAAQSLVPALIEPPQDDHKALKSEDTMDVYGSYQRRSQEDGVGGSIAPQPPDQDNGKSADDNQVLFDL
 ConsensuslEaaarkaVPaLi#qpQ#angaqkn##sWD!WGSY#rrrqeadpgGpiapQaa##r..epa#dNqllFD

1 10 20 30 40 50 60 70 80 90 100 110 120 130

IAGB_SALTI(25-149) REKMFNIESELLYAIQAQESAMKPGAIGHNR--DG----STDLGLMQINSFHMKRLKKGMI--SEKQ--LLQDPCISVIVGASIL----SDMM-KIYGFSWEARVGVYAG--TSPKRSRDIR
IAGB_SALTY(25-149) REKMFNIESELLYAIQAQESAMKPGAIGHNR--DG----STDLGLMQINSFHMKRLKKGMI--SEKQ--LLQDPCISVIVGASIL----SDMM-KIYGFSWEARVGVYAG--TSPKRSRDIR
IPGF_SHIFL(24-141) AGERYNIPSSLLKAIAREKESGFNKFAVYVYNN--NG----SKDYGTIMQINDFHASKRLREMGY--SEEM--LISHPCLSVHYAAKLL----NEFM-HMYGRGWEAVGVYAG--TSPKPKKER
IPGF_SHISO(24-141) AGERYNIPSSLLKAIAREKESGFNKFAVYVYNN--NG----SKDYGTIMQINDFHASKRLREMGY--SEEM--LISHPCLSVHYAAKLL----NEFM-HMYGRGWEAVGVYAG--TSPKPKKER
052131_ECOLI(23-147) ITGKAYNDIPLILKAIAMNESKCKSGTISKXIN-KNG---TYDIGTGMQINSDDLKSKFNI--SEDD--LLNACINISVAGYIL----ASNI-KYRGNTWDAVGVYAGYFNTPNAYELR
095639_ECOLI(23-147) ITGKAYNDIPLILKAIAMNESKCKSGTISKXIN-KNG---TYDIGTGMQINSDDLKSKFNI--SEDD--LLNACINISVAGYIL----ASNI-KYRGNTWDAVGVYAGYFNTPNAYELR
08VL9_ECOLI(25-149) ITGKAYNDIPLILKAIAMNESKCKSGTISKXIN-KNG---TYDIGTGMQINSDDLKSKFNI--SEDD--LLNACINISVAGYIL----ASNI-KYRGNTWDAVGVYAGYFNTPNAYELR
09AJ25_ECOLI(23-147) ITGKAYNDIPLILKAIAMNESKCKSGTISKXIN-KNG---TYDIGTGMQINSDDLKSKFNI--SEDD--LLNACINISVAGYIL----ASNI-KYRGNTWDAVGVYAGYFNTPNAYELR
093FL8_BBBB(26-148) GKAYNDIPLILKAIAMNESKCKSGTISKXIN-KNG---TYDIGTGMQINSDDLKSKFNI--SEDD--LLNACINISVAGYIL----ASNI-KYRGNTWDAVGVYAGYFNTPNAYELR
08KQNI_SALTI(1-124) MAGROYRTEPDLRLAISFRSRRNANAVGINP-VTG---YAVGKMQIHSQNFHSLAQFGI--TPRQ--LYTDSCLNIYTGAYYL--AIAF-KKMGVSWRAVGVYAGFRETVEQEKRR
093GP2_SALTY(25-148) LAGROYKIDPDLRLAISMKESRRNANAVGINP-VTG---YVSGLMQVDSQHFNEFLARYGI--KPEQ--LYSDPCLNIYTGAYYL--AIAF-RKMGVSWRAVGVYAGFKKTPLDQARR
X191_ECOLI(25-148) LAGROYKIDPDLRLAISMKESRRNANAVGINP-VTG---YVSGLMQVDSQHFNEFLARYGI--KPEH--LTPDPCNIYTGAYYL--AIAF-KKMGVSWEARVGVYAGFRKTERQNR
X192_ECOLI(25-148) LAGROYKIDPDLRLAISMKESRRNANAVGINP-VTG---YVSGLMQVDSQHFNEFLARYGI--KPEH--LTPDPCNIYTGAYYL--AIAF-KKMGVSWEARVGVYAGFRKTERQNR
X193_ECOLI(25-148) LAGROYKIDPDLRLAISMKESRRNANAVGINP-VTG---YVSGLMQVDSQHFNEFLARYGI--KPEH--LTPDPCNIYTGAYYL--AIAF-KKMGVSWEARVGVYAGFRKTERQNR
X19F_ECOLI(25-148) LAGROYKIDPDLRLAISMKESRRNANAVGINP-VTG---YVSGLMQVDSQHFNEFLARYGI--KPEH--LTPDPCNIYTGAYYL--AIAF-KKMGVSWEARVGVYAGFRKTERQNR
093I74_ECOLI(26-146) AGYDSNDIPLILRAIAKVESNDNHLAIGKNP--VNG---FGVGLMQVDSQNFHELRQFDI--APEM--LL-DACINIVYAGAYFL--RLAV-NRMGNWDAVGVYAGFSKTPRQKRR
007378_ECOLI(45-171) AGARYQTEPILLKAIASAGESLSPGATINSL-DKKTGKASSTDYGLMQINSHTIPGLKRMGIIRSEME--LITKPCLNIIHIGSWIL--ARRH-QQCGVSNCLGSYNAGFRKDR--HETR
092I18_SALTI(29-151) ARAKYHYSPILLKSMATIGESNLDPHATINDNR--DKKTGKIKSTDYGLMNVNTHIPPLVSMGVIRKND--LLNKPCLNIIYGTWIL--AKHF-QVCGVSNCLGSYNAGFRPDR--HETR
093AE5_ECOLI(32-154) AGKRYSIDPGLLVYIARKESSLNPRAINHNR--NAS--GKIISTDYGLMQINSHTIPGLKRMGIIRSEME--LITKPCLNIIYGTWIL--AKHF-QQCGVSNCLGSYNAGFRKDR--HETR
093D61_ECOLI(50-172) AGKRYSIDPGLLVYIARKESSLNPRAINHNR--NAS--GKIISTDYGLMQINSHTIPGLKRMGIIRSEME--LITKPCLNIIYGTWIL--AKHF-QQCGVSNCLGSYNAGFRKDR--HETR
09F539_ECOLI(37-158) AGQRYLIDPILLKSIATVESLTPDRINHNK--E-K--GKILSTDYGLMQINSHTIPGLKRMGIIRSEME--LITKPCLNIIYGTWIL--AKHF-QQCGVSNCLGSYNAGFRKDR--HETR
088B7_PSESH(24-151) AGQRYGVDPVLLQAIGIQESKLPQGAVNLNR--DSS--GKVLSTDYGVYMQISTRNANRLVYRMLITRAED--LLTNACFNIVQAGAWVL--AQHL-RVCGNTWRCLGSYNAGFDPSPQRQERR
088B2_PSESH(11-138) AGQRYGVDPVLLQAIGIQESKLPQGAVNLNR--DSS--GKVLSTDYGVYMQISTRNANRLVYRMLITRAED--LLTNACFNIVQAGAWVL--AQHL-RVCGNTWRCLGSYNAGFDPSPQRQERR
046790_ECOLI(12-126) AGTHFRTEPMLIKAIALVESNLKKSISGKNR--DKN--NMIKSLDYGLMQINQHPMLKKGITKDER--LLDNPCLNIIKIGTEIL--YKHF-SRCGVTHQCLGTYNAGFAMD--QKRR
08X6H3_EC057(32-158) AGTHFRTEPMLIKAIALVESNLKKSISGKNR--DKN--NMIKSLDYGLMQINQHPMLKKGITKDER--LLDNPCLNIIKIGTEIL--YKHF-SRCGVTHQCLGTYNAGFAMD--QKRR
083X60_BBBB(76-178) VNPVYLRAIAQESRGRADATHRNN--NG----TYDYGKMQINSIHLRRLSSYGI--SRDA--LM-HPCISVYVAARWL--REMT-NKYGNTWAAVGVYAGS----ETPGER
08PQB1_XANAC(27-129) VNPVYLRAIAQESRGRADATHRNN--NG----TYDYGKMQINSIHLRRLSSYGI--SRDA--LM-HPCISVYVAARWL--REMT-NKYGNTWAAVGVYAGS----ETPGER
08RJP7_XANCV(46-148) VNPVYLRAIAQESRGRADATHRNN--NG----TYDYGKMQINSIHLRRLSSYGI--SKDA--LM-PCVSVYVAARWL--REMT-NKYGNTWAAVGVYAGS----ETPGER
09LB05_XANOR(28-134) VNPVYLRAIAQESRGRADATHRNN--NG----TYDYGKMQINSIHLRRLSSYGI--SKDA--LM-PCVSVYVAARWL--REMT-NKYGNTWAAVGVYAGS----ETPGER
08PB82_XANCP(27-131) VNPVYLRAIAQESRGRADATHRNN--NG----TYDYGKMQINSIHLRRLSSYGI--SRDA--LM-PCVSVYVAARWL--REMT-NKYGNTWAAVGVYAGS----ETPGER
08XVD5_RALSO(51-161) AGAYQGVNPTVLRRAIAVESKGDPRAVHRNA--DG---SYDIGQAQINSIHFGTLARYGV--PQHA--LT-DACVNIYVAARWL--KQKH-VKHGNTWAAVGVYAGS----ETPAQR
092F7_BURPS(30-138) AAKYQVNPVLLRAIAQESGHNKPEALNKNA--NG---STDYGLMQINSIHLRRLSSYGI--TKDT--LM-EPKCVYVAARWL--RRKH-DKYGNTWAAVGVYAGS----ETPSLR
09KKJ1_YEREN(37-137) ILEAIIIESSGKPDARLNINK--NG---SHDYGLMQINTINDPLKSGQITKNAQA--LM-OPCTNIEAGAYL--SKKF-KKHGNTWAAVGVYAGS----ETPAER
08XRJ0_RALSO(43-129) VNPQYLRAIGYQESRLNPQARNLNR--NG---SEDLGHFQINSIHLPELRYGI--GRQH--LF-DPCVYVAARWL--SRKI-RQHGNTWAAVGVYAGS----ETPAQR
067519_AQUE(69-161) AAKYQVNPVLLRAIAQESGHNKPEALNKNA--NG---STDYGLMQINSIHLRRLSSYGI--TKDT--LM-EPKCVYVAARWL--RRKH-DKYGNTWAAVGVYAGS----ETPSLR
0882F0_PSESH(189-284) AAKATGVSPVIGIARQESRGLNARTTNY--NG---KDAAGLQVINDTFKSLQKQMPNLLGND--VN--DSHTNIMAGALYL--RDQN-KEFGSVMAGALRAYNSG
046781_ECOLI(22-134) NIEPALLSVMTVEG--GKPGSVSINK--NG---SHDLGIMQINTHAHLKLSKSFNGDERSAYAKLDDACFNISVGAAIL--RRSIFEGGNLWEGVGRYHS----ATPEYK
047073_ECOLI(22-134) NIEPALLSVMTVEG--GKPGSVSINK--NG---SHDLGIMQINTHAHLKLSKSFNGDERSAYAKLDDACFNISVGAAIL--RRSIFEGGNLWEGVGRYHS----ATPEYK
08QFN6_CITFR(36-117) G-GKPGMKNK--NG---TYDYGAFQINT--IANKLADDFVYRAEQ--LQDDFCASMASAYIL--KYNIIIEGGDFWQGVGRYHS----NTPARK
09L5L2_SALTI(45-125) G-GKYGVTFRNK--NG---TYDIGPQMINS--SNLPELRDHFVSVYTRV--LAYDACSASFVGTWIL--YRKIVDRKGMVFEIGADYNS----KTPK
P71189_ENTRE(21-99) AAVKYEYVPIVLAIAVEKEG--GKPGQVYRNS--NG---THDVGPQMFNTAYLVDLARYGITAND--VAARAGCSYFDLAARWL--RHHIR
09AHG6_COMTE(21-99) AAVKYEYVPIVLAIAVEKEG--GKPGQVYRNS--NG---THDVGPQMFNTAYLVDLARYGITAND--VAARAGCSYFDLAARWL--RHHIR
08RS14_PRBO2(21-99) AAVKYEYVPIVLAIAVEKEG--GKPGQVYRNS--NG---THDVGPQMFNTAYLVDLARYGITAND--VAARAGCSYFDLAARWL--RHHIR
087BU8_XYLFT(20-98) AAVKYEYVPIVLAIAVEKEG--GKPGQVYRNT--NG---THDVGPQMFNTAYLVELRQYGITPQD--VARGGCYSYDLAARWL--RGHLR
09PB00_XYLFA(20-98) AAVKYEYVPIVLAIAVEKEG--GKPGQVYRNT--NG---THDVGPQMFNTAYLVELRQYGITPQD--VARGGCYSYDLAARWL--RGHLR
09PH69_XYLFA(20-98) AAVKYEYVPIVLAIAVEKEG--GKPGQVYRNT--NG---THDVGPQMFNTAYLVELRQYGITPQD--VARGGCYSYDLAARWL--RGHLR
003538_ECOLI(51-144) AAVKYEYVPIVLAIAVEKEG--GKPGQVYRNT--NG---TYDVGELQFNTAYLVDLARYGITAND--VAARAGCSYFDLAARWL--RHHIR
048376_BPP1(755-850) KYGLPEGLTYAIARTESSGNPNKSTLT--RSPNG---KLSGGLGMFQTSVAREETGLSKREDS--FNPEKSAARALLN--SKYLKQANGDLNEAITRYNAGF
09K028_BACHD(93-194) LAGTSQQYGVDPILVYELLRTETGGFPNTVGP--ETQYG---RAYGMAQFMHTAPVIAREKAGLRYEDD--LLDFVYSIAQLAVVYI--D-FLYDKEYDDHALTAYHRG
08R8B6_THETN(442-526) AGEKYGTPTVLAIAVAYRES--SFTFNAYG--YLPDY--NTS--AVGMDLAPETFEYGVVDGND--GIISPFDPDSD--AVYTA--AHYLSANYNLY
08GHP9_PSERE(106-189) TDIGTGMQINRYRNGNRVSP--L--LDDPEVNIIRIGAQIL--CESTARQYVDMQLAIGGYHT---RNPKRLDRA
08KJ4_PROVU(103-185) TDIGTGMQINRYRNGNRVSP--L--LDDPEVNIIRIGAQIL--CESTARQYVDMQLAIGGYHT---RNPKRLDRA
081I40_BACCR(51-160) AKKYVNLPEMIPLAIAHEESRLNPR---SVGDNGTSFGLFQLHRGGGLAPDHLTDELDKPRTHAQIA--MPLMKGYKRGVQKGLTDF--ALLKYIANTSGPGLGPEMTDNMNY
081VH9_BACRA(51-160) AKKYVNLPEMIPLAIAHEESRLNPR---SVGDNGTSFGLFQLHRGGGLAPDHLTDELDKPRTHAQIA--MPLMKGYKRGVQKGLTDF--ALLKYIANTSGPGLGPEMTDNMNY
09SA28_ARSH(74-176) LDSEMICIAELSDRKLTHRYSKTKETGLGILQVFEKTAAMLAGGGQYAYVDDNPDLKHPFINVYFAGAYLKLTDY---QNNQRSEFVYRAYNGGTTK
085R5_VVVV(108-227) GYPPDLVVALARRESFNPHYDRV---AYALQISKNGATCASGSEIPLQVQPCAFRQVGMPTDILLNHSIPARVQYATAGIR---YLAKLKGQFTWCDVLAHNRGPTAYRRGERN
08KQ4_VIBCH(32-172) AAQSYGIDPVMLYAVALAESASHRGLNMTSPMYPAIRNGSNATYAKSKEAREQLLQALQESEYQLDILGLMQINLHMHGRVYSSAEL--LDPITNLTVGSSILAEIKSSPNDELIGIGRY
08KQ9_VPROE(32-172) AAQSYGIDPVMLYAVALAESASHRGLNMTSPMYPAIRNGSNATYAKSKEAREQLLQALQESEYQLDILGLMQINLHMHGRVYSSAEL--LDPITNLTVGSSILAEIKSSPNDELIGIGRY
08UHV7_AGR75(36-162) AARKYGVPEGLTVYVGLTETGRKGLRD---PNANIEGKPVFASTEEARVYFAAKRNGAKL--IDLGMQIMQINRYHFGENFSAEM--FDPRRNVEYAMFLRM--LHNRHETMTAVARY
08VPH3_BBBB(65-184) AQATNFPPGVIAAQLFESRFDPNAYQPSSGASGIAQFIRSTWETMGNAGDHF---DALKIDAQGRYHQAQYVTSRRIEL---ALAYNAGPAAVTRAGGIPAIPTQNYYSQIM
MLTC_ECOLI(199-281) ASRKYGVDESILAIHQTESFNPIYVRSDD--ALGLMQVYQHTAGKDVFRS--QKSGTSPS--RSFLDPASNIDTGTAYL--AMLNNVY
08XC56_EC057(200-282) ASRKYGVDESILAIHQTESFNPIYVRSDD--ALGLMQVYQHTAGKDVFRS--QKSGTSPS--RSFLDPASNIDTGTAYL--AMLNNVY
083Q83_SHIFL(200-282) ASRKYGVDESILAIHQTESFNPIYVRSDD--ALGLMQVYQHTAGKDVFRS--QKSGTSPS--RSFLDPASNIDTGTAYL--AMLNNVY
082319_SALTI(201-283) ASRKYGVDESILAIHQTESFNPIYVSHAD--ALGLMQVYQHTAGKDVFRS--QKSGTSPS--RNFLDPASNIDTGTAYL--AMLNNVY
082M39_SALTY(201-283) ASRKYGVDESILAIHQTESFNPIYVSHAD--ALGLMQVYQHTAGKDVFRS--QKSGTSPS--RNFLDPASNIDTGTAYL--AMLNNVY
082HE6_YERPE(203-279) AARYGVDESILAIHQTESFNPIYVRSDD--ALGLMQVYQHTAGKDVFKL--KGSQGPS--RSYLFDPENNIDAGTAYL--SI
MLTC_HREIN(196-299) AARYGVDESILAIHQTESFNPIYVRSDD--ALGLMQVYQHTAGKDVFKL--KGSQGPS--RSYLFDPENNIDAGTAYL--SI
09CLB8_PASHU(200-302) AARYNDESILAIHQTESFNPIYVRSDD--ALGLMQVYQHTAGKDVFKL--KGSQGPS--RSYLFDPENNIDAGTAYL--SI
VirB1(91-125) SLDVGLMQINSRNFSLGLTPDGLKRCPSLAA

Q92I73_RICCN(492-580) IPPHLYGIIRQESVFDHKAVSYAN-----AMGLMQLIKGTACDTR-RSINVK-CNV--ADLTRNPVYNIKLGAAHF---KLLLDNH--KGSYLSIASYNAG
Q92DD1_RICPR(490-581) ISSSLTYGIIRQESVFDHKATCSN-----AMGLMQLIKGTACDIA-KSINMK-CDV--GQLIKNPSYNIKLGSHHF---KLLLDH--KGSYLSIASYNAGSNW
Q9AZF1_THEMEA(72-180) AKETNFDPLIISVIOVESDF-RNVVGLYG-----ELGMMQIKKETAEMVA-NL YGLEIPEESGATEL VMYRNLNIKYGAYL---KYLDFDKF---NNLRALALEYNGG-----N
Q9X023_THEMEA(38-145) DPILLIQSIIMVESDFORNAVSSLG-----AFGLMQLIMPSTAVMLK-KKFSLE-----EDFNKPEGNIITVYLV---KFLKDLV---GDLDKAIIMAYNVPALSEGRLD
Q9X3X0_ZYMMO(164-267) MHYDPLYLYAHALQESQFRSRVSNKGG-----ARGVMQITPATRALVA-KQATNID----IEDLDKPTISFEYGGQAYI---EMLRDLTSYTGZLLPKVIARAYNAGPALPRAKRD
Q82U27_NITEU(86-178) ATRAGLDPELVLSIIQVESNFRKYAVSSAG-----ARGYMQVMPFVYDTIGNPE-----HNLFHLRYMLRYGCTIL---RHYLDLE---QGDYFRALGRYNGSLGKAGY
Q8XVL5_RALSO(98-202) AKRAGLDPELVLSIIQVESNFRKYAVSSAG-----AMGLMQLMVPFATRSIGDKDV-----RKL FHLQSNLRYGCTIL---RHYLDME---GGNLYLALGRYNGSRGQYPPNAV
Q9JT07_NEIMA(104-196) GLDTQIVLGLIEVESAFRQYRISGVG-----ARGLMQVMPFKNYIGKPPA-----HNLFDIRTNLRYGCTIL---RHYRNL---KGIIVRALARFNGSLGSKNYPNAV
Q9JYR6_NEIMB(104-196) GLDTQIVLGLIEVESAFRQYRISGVG-----ARGLMQVMPFKNYIGKPPA-----HNLFDIRTNLRYGCTIL---RHYRNL---KGIIVRALARFNGSLGSKNYPNAV
Q31608_BACSU(67-152) AADKYGVDEKLIRAVIKQESGFNAKAVSSAG-----AMGLMQLMPTASSLG---VSN-----PLDPQQNVEGGTKYL---KQMLDKY-DGNVSH-ALAYNAG
Q9K900_BACHD(117-202) AAKKYGVDPNLIYAVIKHESNFMNPLAKSRAG-----ASGLMQLMPTARQLN---VNN-----MFDQQNIDGGTRYL---KQMLDRY-DGNIQL-ALAYNAG
Q8EP68_OCEIH(111-196) ASQKYGVDESINAVIKHESNFMNPLAKSRAG-----AQGLMQLMPTARAGL---VTN-----AYDPVQNIAGTKYL---SQMLQRY-NGDNQL-ALAYNAG
Q8RBD9_THETN(72-156) ASQKYGVDMNLIIRSVIKAESNFMNPLAKSRAG-----AMGLMQLMPTARELN---VKN-----PFDPSONIDGGVRYL---KNLLDLY-K-DVRL-ALAYNAG
Q97FQ1_CLOAB(122-206) ASKKYGVDKKLIISVIOQESGFDPNATSGVG-----AEGLMQLMPTARELG---VTN-----PYDVQNIIDGGTKYL---KQLLNF-S-DMKL-AVAYNAG
Q891H5_CLOTE(87-172) AARRFNDKDLILLVSIKQESGFQDCVSSAG-----AMGLMQLMPTARAGL---VSN-----PYDIEQNIIDGGTKYL---KEHLNHY-GNSKEL-ALAYNSG
Q88HD8_PTEP(73-158) AARLHNLPPALLHAVIKAESGYNPKARSRAG-----AVGLMQLMPTAREHG---VDQ-----RLDPEDNVQGGARYL---KMLDIT-DMDITL-AVAYNAG
Q9X2M1_PSEPG(14-99) AARTHNYPALLHALIKAESGYNPKARSRAG-----AVGLMQLMPTAREHG---VED-----RLDPEDNVQGGARYI---KMLTLF-DMDITL-AVAYNAG
Q8E8K4_SHEON(119-204) AADKHQDLPALIRAVIAHESAFNARAVSRAG-----AMGLMQLMPTAKDMG---VTN-----AFLPEENILGGSKYL---AQMLKQF-NGDIAL-ACAYNAG
Q87AP5_XYLFT(174-258) AGEFGVEEALVRAIIHAESESNPLSLSSAG-----AQGLMQLMPTARRFG---VTD-----SYDPLQNIIRGGVQYL---AWLLKRF-NGNLT-ALAYNAG
Q9PEX1_XYLF(174-258) AGEFGVEEALVRAIIHAESESNPLSLSSAG-----AQGLMQLMPTARRFG---VTD-----SYDPLQNIIRGGVQYL---AWLLKRF-NGNLT-ALAYNAG
Q8P888_XANCP(199-284) AAREFGVEESIVRAIIHAESESNPLSLSSAG-----AQGLMQLMPTARRFG---VSD-----AYDAQNIIRGGVQYL---SMLLKRK-NGDITL-AAAYNAG
Q8PJS2_XANAC(204-289) AAREFGVEESIVRAIIHAESESNPLSLSSAG-----AQGLMQLMPTARRFG---VSD-----AYDAQNIIRGGVQYL---SMLLKRK-NGDITL-AAAYNAG
Q8X27_RALSO(77-162) AGRKHWYPELLRAIIVAESKFNPRAVSKRG-----ARGLMQLMPTARRFG---AGD-----LFDPRANVLAGAQLY---RFLDLDF-GMDVEL-AVAYNAG
Q8Y0R6_RALSO(113-207) AARKKHGVDPALYKAVIAEESGFNPQAVSPKG-----ATGLMQLMPTARRFG---VTD-----MQLRMF-SGDLE-ALAYNAG
Q9A5N1_CAUCR(97-181) AAQRSQISPDLLTAVARRESGLNPQARSAGK-----ALGYMQLMPTAKDLA---VD-----PLDPAANVDDGGTRYL---KTLARY-DGVIK-ALAYNAG
Q81FD2_BACCR(141-222) YGIPKTLIQKHEVESDFNPKTVSHAG-----AMGLMQLMPTARRFG---VKN-----PFSPAESIEGGVKEL---SGYLKKK-NGDYL-ALAYNAG
Q81SF1_BACRA(150-231) YGIPKTLIQKHEVESDFNPKTVSHAG-----AKGLMQLMPTARRFG---VKN-----PFSPAESIEGGVKEL---SGYLKKK-NGDYL-ALAYNAG
Q8EX91_LEPIN(94-173) NLDPLRLVQSVIKAESDFKTDVAVSPKG-----ATGLMQLMPTARRFG---VED-----PFDPANVAGGTKFL---SMLLNKY-K-NLDH-ALAYNAG
Q31976_BACSU(1429-15) AASKYNDPDLIRAVIQQESGFNAKARSVG-----AMGLMQLMPTAKSLG---VNN-----AYDPQNVHGGTKYL---AQLEKF-GGVEK-ALAYNAGPGNVIKY-GGI
Q64046_BPSPC(1429-15) AASKYNDPDLIRAVIQQESGFNAKARSVG-----AMGLMQLMPTAKSLG---VNN-----AYDPQNVHGGTKYL---AQLEKF-GGVEK-ALAYNAGPGNVIKY-GGI
Q825S9_NITEU(167-277) YEIDPLVLLAVIIVAESGFNTQAVSPKG-----AQGLMQLMPTARRFG---VTD-----YDPEENIRGGMAYL---RMLLAFK-KGDVAL-VARAYNAGGAVEKY-RGI
P07_BPPRD(13-127) ASAQYNLDPRLVAGVQTESGPNRTTSGVG-----AMGLMQLMPTAKSLG---VTN-----AYDPQNIYGGAAAL---RENLDY--GQVNT-ALLAYHGGTQANAMK-AKI
Q8K30_BBBB(227-335) LYRANIEVESAYRQDAISSAG-----ATGLMQLMPTARRFG---V-D-----PRDPLQNLGDSARYL---AMLETF--GPHL-ALAYNAGPDALRQH-GGI
Q8K76_BBBB(170-273) DMQVLFHALVEAESNYPTAISPKG-----AYGLMQLMPTARRFG---V-D-----PRDPSQNLGDSARYL---LAQLATF--KIDOL-ALAYNAGPHRYVEY-SGI
Q85953_SPHAR(112-213) GLPASLLDVAVVAQESGFNAKARSRAG-----AMGMQVMPPTARRHLE---LNN-----PHDALANMRAGARYL---RQLDRF--ERVDL-ALAYNAGPERRSL-LGY
Q83YQ0_BBBB(2-105) ESGYRQDAISSAG-----ATGLMQLMPTARRFG---V-TNS-----ASSVSANLKAGTRYF---SLLQKYY-PGRDL-ATAAYNAGGAVEKY-GNE
Q8GY2_LISMO(119-198) AATKYGVPEALIKRVIQVESNFMNPNVSSAG-----ATGLMQLMPTARRFG---V-TNS-----DPATNIDAGTKQL---ASYIKKY-DGDLKL-ALAYNAGP
Q8Y925_LISMO(119-198) AATKYGVPEALIKRVIQVESNFMNPNVSSAG-----ATGLMQLMPTARRFG---V-TNS-----DPATNIDAGTKQL---ASYIKKY-DGDLKL-ALAYNAGP
Q92D7_LISIN(120-199) AATKYGVPEALIKRVIQVESNFMNPNVSSAG-----ATGLMQLMPTARRFG---V-TNS-----DPATNIDAGTKQL---ASYIKKY-DGDLKL-ALAYNAGP
Q88K3_PSEPK(18-103) QYGLPQGTFLKHSGEESFNLDAESGK-----AEGPQLMPTARRFG---VTD-----PHDYTQAADAAGRYM---RDSLAKY-NGMMDH-ALADYNGGPR
Q98158_SHELO(105-187) ARQYGFAPPLVLAVARAESRFSNGALSPKG-----AYGLMQLMPTARRFG---VD-----ICDPADNVKGGIGFL---RDLRRF-PNPIYH-LAYNAG
Q89JY0_BRAJA(105-186) VIMQESRFQADAVGPMTR-----SGEHAQGIQAFMPTARRFG---LLD-----PFNPQALPKSAREFL---NLRNQF--GNLGL-AAAYNAGPRRVQE
Q89R06_BRAJA(96-204) AAREASGIPVFFARLLMQRFSRFSNEVSPAG-----AQGVAQFMPTARRFG---LDD-----PFDPQKALPASAKFL---RKLROF--GNLGL-AAAYNAGPGRIQKALARE
Q8YIE4_BRUME(39-122) AEAHGIPKDFARLLMQRFSRFSNEVSPAG-----AQGVAQFMPTARRFG---LDD-----PFDPQKALPASAKFL---RKLROF--GNLGL-AAAYNAGPGRIQKALARE
Q8UBC3_AGR15(80-163) AARHAYPPDYFARLLMQRFSRFSNEVSPAG-----AQGVAQFMPTARRFG---LDD-----PFDPQKALPASAKFL---RKLROF--GNLGL-AAAYNAGPGRIQKALARE
Q92K01_RHIME(88-171) AKANDLPAARFARLLMQRFSRFSNEVSPAG-----AQGVAQFMPTARRFG---LDD-----PFDPQKALPASAKFL---RKLROF--GNLGL-AAAYNAGPGRIQKALARE
Q98F61_RHILO(148-217) LLQALIMQESRFTIGARSPVG-----AFGLTQIMPSTASDLG---INPEY-----YDPSYLVQVHGGARYL---AAQLNLF-DGNIIN-ALAYNAG
Q8K428_BBBB(164-241) PNLLAALLTQESGFNPKARSVPKG-----AQGVAQFMPTARRFG---LDD-----PFDPQKALPASAKFL---RKLROF--GNLGL-AAAYNAGPGRIQKALARE
Q848E2_STRLI(23-111) AADANGVSYDILLRKYAHTESRFVPTAKSKTG-----PLGIMQFTKATANALG---LRYTDGPD---DDRLNPELAINAARAKHL---AGLVGKF-DGDELK-AALAYNAG
Q858J9_VVVVV(19-111) ADANGVSYDILLRKYAHTESRFVPTAKSKTG-----PLGIMQFTKATANALG---LRYTDGPD---DDRLNPELAINAARAKHL---AGLVGKF-DGDELK-AALAYNAG
Q8M5T9_BPT3(20-111) ADANGVSYDILLRKYAHTESRFVPTAKSKTG-----PLGIMQFTKATANALG---LRYTDGPD---DDRLNPELAINAARAKHL---AGLVGKF-DGDELK-AALAYNAG
VIVD_BPT7(19-111) ADANGVSYDILLRKYAHTESRFVPTAKSKTG-----PLGIMQFTKATANALG---LRYTDGPD---DDRLNPELAINAARAKHL---AGLVGKF-DGDELK-AALAYNAG
Q9T100_VVVVV(18-110) AADKHGVSYDILLRKLAFNESNFMNPKARSPTG-----PKGLMQLMPTARRFG---LRYTDGPD---DDRLNPELAINAARAKHL---AGLVGKF-DGDELK-AALAYNAG
Q859E2_VVVVV(24-112) AADANGVSYDILLRKYAHTESRFVPTAKSKTG-----PLGIMQFTKATANALG---LRYTDGPD---DDRLNPELAINAARAKHL---AGLVGKF-DGDELK-AALAYNAG
Q8P704_XANCP(147-233) LPEALLFGIMAKESNGKYHASSRAG-----ARGLMQVMPATARRFG---LGPDTGF---DTRFDARSAREASARYL---NERHAGL-NRSIEL-ALAYNAG
Q8PJI6_XANAC(141-231) QKRGLPEALLFGIMAKESNGKYHASSRAG-----ARGLMQVMPATARRFG---LGPDTGF---DTRFDARSAREASARYL---NERHAGL-NRSIEL-ALAYNAG
Q89Y99_BRAJA(108-196) AAQRFGIPAAHIRAVMRVESNG-----DRRAY-----SPKGLMQLMPTARRFG---LRYTDGPD---DDRLNPELAINAARAKHL---AGLVGKF-DGDELK-AALAYNAG
Q98NT8_RHILO(68-153) RFRYPERKIRAIMHLESAR-----DPRAY-----SRKAVGLMQLMPTARRFG---LRYTDGPD---DDRLNPELAINAARAKHL---AGLVGKF-DGDELK-AALAYNAG
Q8K6V7_RHILO(46-140) ASARFHIPQAWICAVIDAESRGKTVLDGRPIT-----SRAGMQLMQLMPTARRFG---LRYTDGPD---DDRLNPELAINAARAKHL---AGLVGKF-DGDELK-AALAYNAG
Q88A23_RHILO(46-140) ASARFHIPQAWICAVIDAESRGKTVLDGRPIT-----SRAGMQLMQLMPTARRFG---LRYTDGPD---DDRLNPELAINAARAKHL---AGLVGKF-DGDELK-AALAYNAG
Q8X253_RALSO(19-105) KFGLPRTGTTARQITQESGM-----NPNAY-----SPKGLMQLMPTARRFG---LRYTDGPD---DDRLNPELAINAARAKHL---AGLVGKF-DGDELK-AALAYNAG
MLTD_ECOLI(105-201) IAGQVKKRNMPELVLLPIVESAFDPHATSSAN-----AAGIMQIPSTGRNYGLKQTRNYDAR---RDVYASTTAALNMHQL---NKMFI---DGMALLTVARYNSGEGR
Q8X722_EC057(105-201) IAGQVKKRNMPELVLLPIVESAFDPHATSSAN-----AAGIMQIPSTGRNYGLKQTRNYDAR---RDVYASTTAALNMHQL---NKMFI---DGMALLTVARYNSGEGR
Q8XFH2_SALTI(108-204) IAGQVKKRNMPELVLLPIVESAFDPHATSSAN-----AAGIMQIPSTGRNYGLKQTRNYDAR---RDVYASTTAALNMHQL---NKMFI---DGMALLTVARYNSGEGR
Q83MM0_SHIFL(59-155) IAGQVKKRNMPELVLLPIVESAFDPHATSSAN-----AAGIMQIPSTGRNYGLKQTRNYDAR---RDVYASTTAALNMHQL---NKMFI---DGMALLTVARYNSGEGR
Q8C4H0_YERPE(140-231) KKRKMPMELVLLPIVESAFDPHATSSAN-----AAGIMQIPSTGRNYGLKQTRNYDAR---RDVYASTTAALNMHQL---NKMFI---DGMALLTVARYNSGEGR
Q8ZH33_YERPE(132-223) KKRKMPMELVLLPIVESAFDPHATSSAN-----AAGIMQIPSTGRNYGLKQTRNYDAR---RDVYASTTAALNMHQL---NKMFI---DGMALLTVARYNSGEGR
Q9KX5_VIBCH(128-231) QRGLPELVLLPIVESAFDPHATSSAN-----AAGIMQIPSTGRNYGLKQTRNYDAR---RDVYASTTAALNMHQL---NKMFI---DGMALLTVARYNSGEGR
Q8GF74_PHOLA(132-209) VESAFNPHATSSAN-----AAGIMQIPSTGRNYGLKQTRNYDAR---RDVYASTTAALNMHQL---NKMFI---DGMALLTVARYNSGEGR
Q9JU39_NEIMA(108-198) KKRKMPREALLPFIEVSFVTKAKSHYV-----ASGLMQLMPTARRFG---LRYTDGPD---DDRLNPELAINAARAKHL---AGLVGKF-DGDELK-AALAYNAG
Q9JZ45_NEIMB(108-198) KKRKMPREALLPFIEVSFVTKAKSHYV-----ASGLMQLMPTARRFG---LRYTDGPD---DDRLNPELAINAARAKHL---AGLVGKF-DGDELK-AALAYNAG

	131	140	150	160	165
	-----+	-----+	-----+	-----+	-----
IAGB_SALTI(25-149)	KR-----	YAKKIMENYRKLKEMSAEE			
IAGB_SALTY(25-149)	KR-----	YAKKIMENYRKLKGMSAEE			
IPGF_SHIFL(24-141)	LK-----	YAEDIYRRYLRI			
IPGF_SHISO(24-141)	LK-----	YAEDIYRRYLRI			
O52131_ECOLI(23-147)	RQ-----	YAMKIYKTYNKLKNN			
O85639_ECOLI(23-147)	RQ-----	YAMKIYKTYNKLKNN			
Q8VLC9_ECOLI(25-149)	RQ-----	YAMKIYKTYTKLKNN			
Q9AJ25_ECOLI(23-147)	RQ-----	YAMKIYKTYTKLKNN			
Q93FL8_BBBBB(26-148)	RQ-----	YAMKIYNTYTKLKNN			
Q8KQNI_SALTI(1-124)	QQ-----	YAKEIQAIYVAIKKN			
Q93GP2_SALTY(25-148)	LD-----	YATDVHRIWIAIKQS			
X191_ECOLI(25-148)	LA-----	YASEVYRIYTHIKSS			
X192_ECOLI(25-148)	LA-----	YASEVYRIYTGIKSS			
X193_ECOLI(25-148)	LA-----	YASDVYRIYTGIKSS			
X19F_ECOLI(25-148)	LA-----	YASDVYRIYTGIKSS			
Q93I74_ECOLI(26-146)	YQ-----	YASKVRQYQSIKK			
O07378_ECOLI(45-171)	EQ-----	YANKIMRIYRDHK			
Q92IU8_SALTI(29-151)	ER-----	YANRIWKIY			
Q93AE5_ECOLI(32-154)	MK-----	YARLIYAAYM			
Q93D61_ECOLI(50-172)	MK-----	YARLIYAAYM			
Q9F539_ECOLI(37-158)	IK-----	YARYVYNKYM			
Q88BM7_PSESM(24-151)	LH-----	YAQQVRNVYDRLK			
Q88BT2_PSESM(11-138)	LH-----	YAQQVRNVYDRLK			
Q46790_ECOLI(12-126)	QQ-----	YA			
Q8XGH3_EC057(32-158)	LQ-----	YAKKIYIYVYTRLNE			
Q83XG0_BBBBB(76-178)	DK-----	YAHAIHSI			
Q8PQB1_XANAC(27-129)	DK-----	YAHAIHSI			
Q8RJP7_XANCV(46-148)	DK-----	YAHAIHSI			
Q9LBD5_XANOR(28-134)	DK-----	YAHAIHSLRL			
Q8PB82_XANCP(27-131)	DK-----	YAHAIHALI			
Q8XVD5_RALSO(51-161)	DA-----	YARSIQRVLV			
Q92F87_BURPS(30-138)	DK-----	YARQIADI			
Q9KKJ1_YEREN(37-137)	DK-----	YASKIMKI			
Q8XRJ0_RALSO(43-129)					
O67519_AQUAE(69-161)					
Q882F0_PSESM(189-284)					
Q46781_ECOLI(22-134)	YR-----	YIDKYKNVY			
Q47073_ECOLI(22-134)	YR-----	YIDKYKNVY			
Q8GFN6_CITFR(36-117)					
Q9L5L2_SALTI(45-125)					
P71189_ENTAE(21-99)					
Q9AHG6_COMTE(21-99)					
Q8RSI4_PRB02(21-99)					
Q87BU8_XYLFT(20-98)					
Q9PBU0_XYLFA(20-98)					
Q9PHG9_XYLFA(20-98)					
Q03538_ECOLI(51-144)					
O48376_BPP1(755-850)					
Q9KD28_BACHD(93-194)					
Q8R8B6_THETN(442-526)					
Q8GHP9_PSERE(106-189)	RE-----	YASNVLRIWRLQLK			
Q8KJX4_PROYU(103-185)	LN-----	YARNVLRIWKRLIEN			
Q81IM0_BACCR(51-160)					
Q81VH9_BACAA(51-160)					
Q9SA28_ARATH(74-176)					
Q859R5_VVVVV(108-227)	DA-----	YVGQI			
Q8KQU4_VIBCH(32-172)	HS-----	MNEERARHYGQRVLSIYR			
Q8RKV9_PRORE(32-172)	HS-----	MNEERARHYGQRVLSIYR			
Q8UHV7_AGR5(36-162)	HA-----	GPNNDPQKKY			
Q8VPM3_BBBBB(65-184)	Q				
MLTC_ECOLI(199-281)					
Q8XCS6_EC057(200-282)					
Q83Q83_SHIFL(200-282)					

Q8ZHEG_YERPE(203-279)
MLTC_HAEIN(196-299)
Q9CLB8_PASMU(200-302)
VirB1(91-125)
Q87LI4_VIBPA(214-297)
Q8DCC6_VIBVU(214-297)
Q9KUR5_VIBCH(235-318)
Q8D3C6_WIGBR(198-272)
MLTE_BUCAI(79-158)
Q89AM2_BUCBP(57-137)
MLTE_ECOL6(84-161)
MLTE_ECOLI(84-161)
Q83RP9_SHIFL(14-91)
Q83RQ0_SHIFL(62-139)
Q8XDJ7_EC057(84-161)
Q8XGT6_SALTI(46-123)
Q8ZDM0_YERPE(61-138)
Q89FP5_BRAJA(63-150)
Q8G383_BRUSU(142-227)
Q8YEK0_BRUME(28-113)
Q8FZM5_BRUSU(102-190)
Q8YI79_BRUME(25-113)
Q98KA3_RHILO(172-260)
Q8UDL3_AGR5(84-185)
Q92NL1_RHIME(67-137)
Q8UDK8_AGR5(255-324)
Q98I80_RHILO(265-334)
Q92K36_RHIME(233-298)
Q8Y1I1_RALSO(190-262)
Q25362_HELPY(407-489)
Q9ZLI9_HELPJ(407-489)
Q9PP80_CAMJE(382-466)
Q51274_BORBU(583-672)
Q67665_AQUAE(221-312)
Q83083_TREPA(554-646)
Q8CVF3_LEPIN(610-698)
Q9A8M1_CAUCR(366-456)
Q55476_SYNY3(702-787)
Q8DKC6_SYNEL(568-655)
Q8YXU7_ANASP(578-664)
Q82U81_NITEU(479-572)
Q8Y392_RALSO(489-586)
Q9JW81_NEIMA(468-600)
Q9JXP1_NEIMB(468-600)
Q892J6_CLOTE(69-157)
Q8XIX1_CLOPE(45-134)
Q8RBE4_THETN(46-136)
Q97K21_CLOAB(46-134)
Q83N28_SHIFL(510-592)
Q8CVF5_ECOL6(500-582)
SLT_ECOLI(500-582)
Q83SR8_SALTI(482-564)
SLT_SALTY(500-582)
Q8Z0T5_SALTI(482-564)
Q8CZP1_YERPE(504-586)
Q8ZIP2_YERPE(494-576)
Q87ZA7_PSESM(498-579)
Q88L07_PSEPK(513-594)
Q9HZI6_PSEAE(498-579)
Q87S72_VIBPA(492-591)
Q8DEU4_VIBVU(477-570)
Q9KU29_VIBCH(492-585)
Q8EFE1_SHEON(484-578)
Q9CNU8_PASMU(535-617)
SLT_HAEIN(440-529)

RY

PLEGAVYRETIPFSETRDYVKKVMANARYASLFG
PLEGAVYRETIPFSETRDYVKKVMANARYAALFG

Q87D58_XYLFT(546-639)
Q9PDL6_XYLFA(546-640)
Q8P5D5_XANCP(503-600)
Q8PGQ5_XANAC(526-623)
Q89K45_BRAJA(662-750)
Q89KX8_BRAJA(594-682)
Q8G1R3_BRUSU(501-596)
Q8YG59_BRUME(534-629)
Q985C0_RHIL0(525-611)
Q8UGL5_AGR5(542-631)
Q92R56_RHIME(528-612)
Q9A901_CAUCR(528-618)
Q92I73_RICCN(492-580)
Q92DD1_RICPR(490-581)
Q9WZF1_THEMA(72-180)
Q9X023_THEMA(38-145)
Q9X3X0_ZYMM0(164-267)
Q82UZ7_NITEU(86-178)
Q8XVL5_RALSO(98-202)
Q9JTQ7_NEIMA(104-196)
Q9JYR6_NEIMB(104-196)
Q31608_BACSU(67-152)
Q9K900_BACHD(117-202)
Q8EP68_OCEIH(111-196)
Q8RBD9_THETN(72-156)
Q97FQ1_CLOAB(122-206)
Q891H5_CLOTE(87-172)
Q88HD8_PSEPK(73-158)
Q9X2W1_PSEPG(14-99)
Q8E8K4_SHEON(119-204)
Q87AP5_XYLFT(174-258)
Q9PEX1_XYLFA(174-258)
Q8P8BB_XANCP(199-284)
Q8PJS2_XANAC(204-289)
Q8XX27_RALSO(77-162)
Q8Y0R6_RALSO(113-207)
Q9A5N1_CAUCR(97-181)
Q81FD2_BACCR(141-222)
Q81SF1_BACAA(150-231)
Q8EX91_LEPIN(94-173)
Q31976_BACSU(1429-15)
Q64046_BPSPC(1429-15)
Q82SS9_NITEU(167-277)
VP07_BPPRD(13-127)
Q8KM30_BBBBB(227-335)
Q8KM76_BBBBB(170-273)
Q85953_SPHAR(112-213)
Q83VQ0_BBBBB(2-105)
Q8GMY2_LISM0(119-198)
Q8Y925_LISM0(119-198)
Q92DT7_LISIN(120-199)
Q88KK3_PSEPK(18-103)
Q981S8_RHIL0(105-187)
Q89JY0_BRAJA(105-186)
Q89RQ6_BRAJA(96-204)
Q8YIE4_BRUME(39-122)
Q8UBC3_AGR5(80-163)
Q92KD1_RHIME(88-171)
Q98FG1_RHIL0(148-217)
Q8KM28_BBBBB(164-241)
Q848E2_STRLI(23-111)
Q858J9_VVVVV(19-111)
Q8M5T9_BPT3(20-111)
VIVD_BPT7(19-111)
Q9T100_VVVVV(18-110)

SRKS--YAQKILETY
SAKR--YLKKVKRTYL
H

AANKRM

PP-----FK-ETQNYVKKIMANY
PP-----FK-ETQNYVKKIMANY
PP-----YP-ETVKYVDKIMSRYNK
KS-----YPGKVMKNINLLFGNSGP
PP-----YR-ETQNHVARVMAYVARLEGSNS
PP-----FA-ESRDYIARIRGI
IP-----AIPETRNYVR
IP-----PYAETQAYVPKYMAQYEKLSGKS

SE-----LPRETRDYVRI

Q8M5T9_BPT3(20-111)
 YIVD_BPT7(19-111)
 Q9T100_VVVV(18-110)
 Q859E2_VVVV(24-112)
 Q8P7Q4_XANCP(147-233)
 Q8PJ16_XANAC(141-231)
 Q89YA9_BRAJA(108-196)
 Q98NT8_RHIL0(68-153)
 Q8KGV7_RHIL0(46-140)
 Q98A23_RHIL0(46-140)
 Q8X253_RALSO(19-105)
 MLTD_ECOLI(105-201)
 Q8X722_EC057(105-201)
 Q8XFM2_SALTI(108-204)
 Q83MN0_SHIFL(59-155)
 Q8CHH0_YERPE(140-231)
 Q8ZH33_YERPE(132-223)
 Q9KPY5_VIBCH(128-231) KKAG----K
 Q8GF74_PHOLU(132-209)
 Q9JU39_NEIMA(108-198)
 Q9JZ45_NEIMB(108-198)
 TBTA_ALTSM(35-125)
 Q83EK6_COXBU(99-185)
 Q8EE26_SHEON(109-196)
 Q840G8_PSESY(148-221)
 Q9JP38_PSESN(148-221)
 Q87YS7_PSESN(142-215)
 Q88FF2_PSEPK(131-213)
 Q9I2T2_PSEAE(132-217)
 Q82SC3_NITEU(116-191)
 Q87MF3_VIBPA(138-212)
 Q8DBD9_VIBVU(157-231)
 Q8X288_RALSO(125-196)
 026092_HELPHY(92-211) GTSD----IKILLDECKYLPKETREYIR
 Q9ZJ37_HELPIJ(94-213) GTSD----IKVLLDECKYLPKETREYIR
 Q9PHM2_CANJE(81-171)
 Q8AOM2_BACTN(139-248) GGET----DYAKIYNLL
 Q8KDR6_CHLTE(187-274) -----YNFVKERRKLPKETQNYVPLF
 067414_AQUAE(108-211)
 Q83CL1_COXBU(135-207)
 Q8EA91_SHEON(134-207)
 Q8PBV1_XANCP(104-184)
 Q8PNI1_XANAC(114-191)
 Q87JI9_VIBPA(97-170)
 Q89290_BACTN(128-200)
 Q83631_TREPA(400-473)
 Q51916_PROMI(220-302)
 Q8D0Z9_YERPE(332-418)
 Q82CQ1_YERPE(301-387)
 Q8FF25_EC0L6(297-388)
 Q8XRA45_EC057(251-342)
 YFHD_ECOLI(251-342)
 Q8Z4L5_SALTI(296-388)
 Q8ZM28_SALTY(296-388)
 Q9CPJ2_PASHU(276-366)
 YFHD_HAEIN(275-365)
 Q87RW1_VIBPA(322-407)
 Q8DF80_VIBVU(321-406)
 Q9KTN5_VIBCH(316-398)
 Q8EC56_SHEON(269-365)
 Q886H7_PSESN(256-346)
 Q88P17_PSEPK(266-351)
 Q9X3V4_PSEPG(302-388)
 Q9HXN1_PSEAE(267-351)
 Q87S67_VIBPA(308-403)
 Q88KH8_PSEPK(312-418) RRR
 Q9HZY1_PSEAE(313-415)
 Q8ABC7_BACTN(304-390)
 Q883U3_PSESN(312-382)
 Q82G15_STRAM(69-104)
 Q9KYD8_STRCO(74-109)
 Q83T33_SALTI(85-152)
 Q8ZKI8_SALTY(46-113)
 Q8Z6V7_SALTI(85-138)
 Q83MA9_SHIFL(1-52)
 Q89F42_BRAJA(99-164)
 Q8FUS7_BRUSU(94-159)
 Q8YDL8_BRUME(94-159)
 Q92KNO_RHIME(98-163)
 Q98HC3_RHIL0(56-119)
 Q92HT5_RICCN(152-205)
 Q9ZD86_RICPR(163-216)
 Q9RH77_BRAJA(447-524)
 Q8VRD8_HAEAE(80-115)
 Consensus