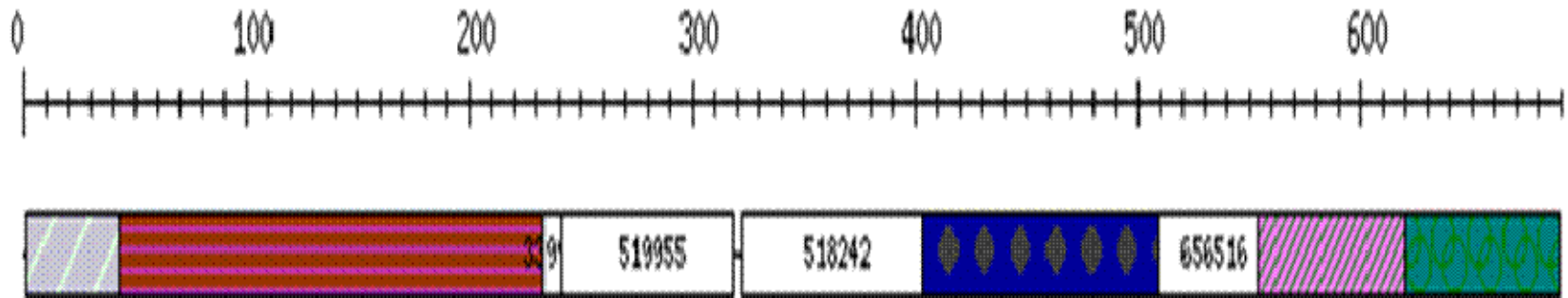


VirD4



	<u>Domain ID</u>	<u>BEGIN</u>	<u>END</u>	<u>Total ID</u>
1.	PD007793	43	232	76
2.	PD003889	403	508	111
3.	PD518242	322	402	53
4.	PD519955	241	307	9
5.	PD101064	620	688	1
6.	PD016707	554	619	5
7.	PD604423	93	138	2
8.	PD686139	43	92	4
9.	PD656516	509	553	8
10.	PD187518	1	42	9
11.	PD339970	143	256	9

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

025260_HELPY(215-304 VIYGRRLGDFIAYAGQAFIG
09JHY0_HELPY(215-304 VIYGRRLGDFIAYAGQAFIG
092LV3_HELPJ(215-304 VIYGRRLGDFIAYAGQAFIG
032582_ECOLI(79-232) LAAPAFIHWLNQKDAPLFGDAKFASSDLSKSKLLKWEKE---ND---TDILVG---R---YKGYLYHTAPDFVS
086LV7_RICTY(115-248 VYGDASHANQSDIEAAGL---RSKK---GMLIG---V---DAGGYFVADGFQHAL
092DN4_RICPR(115-248 VYGDASHANQSDIEAAGL---RSKK---GMLIG---V---DAGGYFVADGFQHAL
092TH9_RICCN(115-248 VYGDASHANQSDIEAAGL---RSKK---GMLIG---V---DAGGYFVADGFQHAL
08RPL3_ANAHP(73-251) PKLFGIANSKLMGSSFFAPIGLVCLYAMNLRHVLIDMRPFKKESLHGDSRWASEKDIRKAGL---RSRR---GILLG---K---DQRGYLVDGFQHAL
09KH36_BBBB(76-251) YSLELKITLISSALPTIIVLHILWNLRERIEMRPFKKESLHGDSRWASEKDIRKAGL---RSKK---GMLIG---K---DKRGYFVADGFQHAL
09KH43_BBBB(114-251) KESLHGDSRWASEKDIRKAGL---RSKK---GMLIG---K---DKRGYFVADGFQHAL
08RPL9_EHRCH(116-253) KESLHGDSRWATEKDIRKIGL---RSRR---GILLG---K---DKRGYFVADGFQHAL
08RPD6_LEGPN(116-273) FLMLLALALYLFHMLRPNKALGNHAFSNGFETKAGFFERQEQ---SIIIG---K---KYAAPLYSNGFEHVL
09RLR2_LEGPN(195-351) ILTFLALALYLFHMLKPNKALGNHAFSNGFETKAGFFERQEQ---SIVIG---K---KYAAPLYSNGFEHVL
MLLKVAAPLSVDTYMSYVKALDLPQFAPYASKIKLAGAIGFVPLAWIALLIPLFK-PKAAALHGDAARFASGSDLAKKDMLKPSPT---GIVVG---K---HGKVVRLPGQQFVI
08P577_XANCP(31-230) MLLKVAAPLSVDTYMSYVKALDLPQFAPYASKIKLAGAIGFVPLAWIALLIPLFK-PKAAALHGDAARFASGSDLAKKDMLKPSPT---GIVVG---K---HGKVVRLPGQQFVI
093T4_XANCP(1-200) DTYRYYSAMGLPEVAPYVTKIKLAGAIGFVPLAWIALLIPLFK-PKAAALHGDAARFASGSDLAKKDMLKPSPT---GIVVG---K---HGKVVRLPGQQFVI
08P7X2_XANCP(40-228) DTYRYYSALGLPQVAPYATKIKLAGAIGFVPLAWIALLIPLFK-PKAAALHGDAARFASGSDLAKKDMLKPSPT---GIVVG---K---HGKVVRLPGQQFVI
08PJB2_XANCP(40-228) DTYRYYSALGLPQVAPYATKIKLAGAIGFVPLAWIALLIPLFK-PKAAALHGDAARFASGSDLAKKDMLKPSPT---GIVVG---K---HGKVVRLPGQQFVI
091UR9_RHIME(47-235) TWTYMQFYAADPVYAKRLKVALI-VAAVYVYGVPLVAIIRAM---REVRSLHGDAARFASGSDLAKKDMLKPSPT---GIVVG---K---HGKVVRLPGQQFVI
091UH5_ECOLI(50-228) TYMQFYAADPVYAKRLKVALI-VAAVYVYGVPLVAIIRAM---REVRSLHGDAARFASGSDLAKKDMLKPSPT---GIVVG---K---HGKVVRLPGQQFVI
09PH19_XYLF(57-214) ISSGISLAVLLAPLFFFS-HAEKSLGDAARFASGSDLAKKDMLKPSPT---GIVVG---K---HGKVVRLPGQQFVI
09F254_ACTAC(35-216) IEAFKRYPTLTDIAINGNPKIQSLLISFVSLVLLIMLKLFFY---QPKKSLYGNAEFATKSEVQKAGLLE-EKN---GIIIG---K---YMNLLRFGSQHVS
08VRC7_HREAE(49-253) ITTIFDLIKSINESTPKATKGYILGAGIGLYITLIPLLIYAVFFGLKQKEEYVGSASFADKDIRKAGLPTPKQRKGLKY---PSIIG---K---YKDFLHFAGQQFLI
09F531_ECOLI(59-251) PQYKLVFMAHFGVSPVIFFAIFHLIYVI-GIMPKKVYGDARLATDMDLSKSGFFPDKKSP---YKH---PPILIG---KHFKGRYKQQFYFAGQQFLI
0981R7_RHIL0(113-244) YGDARFATDKEIAALTSGSS---GMLIG---K---HGKVVRLPGQQFVI
08U6E9_AGR15(109-242) HGARFATDKEIAALTSGSS---GMLIG---K---HGKVVRLPGQQFVI
08KJL1_RHIL0(93-232) HGTARHARVDEMRRTGYLRRYRQ---V---TGPVFG---KTSGPFMPGYYLTNGEQPHSL
08V785_AGR15(43-232) TFSAFAYLYPEFYLYGYASPPFYRGLAIIMATATLVLLSLLLSM---RDRHHHGTAARHAGSGEMRHAGYLQRYRQ---V---TGPVFG---KTSGPFMPGYYLTNGEQPHSL
09F585_AGR15(52-232) ETPLPYGHATPYVYGLAIVVSTIYVLLSLLLSM---RERHHHGTAARHAGSGEMRHAGYLQRYRQ---V---TGPVFG---KTSGPFMPGYYLTNGEQPHSL
09R6B7_AGR15(52-220) ETPLPYGHATPYVYGLAIVVSTIYVLLSLLLSM---RNEHHHGTAARHAGSGEMRHAGYLQRYRQ---V---TGPVFG---KTSGPFMPGYYLTNGEQPHSL
VID4_AGR15(52-220) ETPLPYGHATPYVYGLAIVVSTIYVLLSLLLSM---RNEHHHGTAARHAGSGEMRHAGYLQRYRQ---V---TGPVFG---KTSGPFMPGYYLTNGEQPHSL
VID4_AGR15(52-220) ETPLPYGHATPYVYGLAIVVSTIYVLLSLLLSM---RNEHHHGTAARHAGSGEMRHAGYLQRYRQ---V---TGPVFG---KTSGPFMPGYYLTNGEQPHSL
08KH18_BBBB(90-227) HGTARHARVDEMRRTGYLRRYRQ---V---TGPVFG---KTSGPFMPGYYLTNGEQPHSL
08VLK3_AGR15(139-220) GQTHAQSAARENKANGFFGAPG---GMLIG---K---HGKVVRLPGQQFVI
VIR04(43-232) QPHSL
VID4_AGR15(139-220) TFDVFAHYETPLLYGYASTVFRHRLSVVIFTSLAVLSSQLIISL---RNQKHNGTARHAEIEMQHAGYLQRYRQ---V---TGPVFG---KTSGPFMPGYYLTNGEQPHSL
084EN5_BBBB(64-212) FDAYAPRYVDIGGAIAGGSGLYVAVLVAIGMSINRS---RQSRLVTTYGSARMAAEADIRKAGL---QPHSL
08XN89_RALS0(67-212) YAPHVVDIGGAIAGGSGLYVAVLVAIGMSINRS---RQSRLVTTYGSARMAAEADIRKAGL---QPHSL
08KJN0_RHIL0(170-319) QFDAYAPEVFDKAGMLAGTSFGMCAARAIAGSLMRA---RQRGLVTTYGSARMAAEADIRKAGL---QPHSL
0989J7_RHIL0(122-271) QFDAYAPEVFDKAGMLAGTSFGMCAARAIAGSLMRA---RQRGLVTTYGSARMAAEADIRKAGL---QPHSL
089YB1_BRAJA(117-227) KNAETVYGSARMAAEADIRKAGL---QPHSL
098NT6_RHIL0(127-232) YGSARMAAEADIRKAGL---QPHSL
08RSH2_PBB02(74-249) YSQYDPEINRAGSIGMVTATVGLLGVAVYKVVTSN---SSKANEYLHGSAARHAEKKDIAQAGLLPRERNVLEIYTGKAPRTATGVYVY---GMDQKDNFFYLPHSGPEHVL
0937B8_PSED(60-249) VYAPWSI-LHMTYKMSYQYDPEINRAGSIGMVTATVGLLGVAVYKVVTSN---SSKANEYLHGSAARHAEKKDIAQAGLLPRERNVLEIYTGKAPRTATGVYVY---GMDQKDNFFYLPHSGPEHVL
TRG5_ECOLI(60-249) VYAPWSI-LHMTYKMSYQYDPEINRAGSIGMVTATVGLLGVAVYKVVTSN---SSKANEYLHGSAARHAEKKDIAQAGLLPRERNVLEIYTGKAPRTATGVYVY---GMDQKDNFFYLPHSGPEHVL
TRG4_ECOLI(115-248) LHGSAARHAEKKDIAQAGLLPRERNVLEIYTGKAPRTATGVYVY---GMDQKDNFFYLPHSGPEHVL
082XL2_NITEU(37-215) AVPYFLALGAVLLIKGVLVSLYLLIQLFRFRKRAMKPTDRSGSAAHNS-SRDIEKHGLYNR---RGGFLA---GVH---ENRPVYDIESSGL
086JE7_CAHJE(57-205) LKLKAYVAVFALILPFVICTLIFHFPQMLKENYGNARFAKE---KDFEHNICND---RGLILGCIKKGKIDIEIYIRAKNPLSAL
08RHY0_HELPY(67-217) MLISLMPFVATYINFPKTTIETSHGYARAWVKDIECFKIFSKGFCFKYVHRLGVQFD---NGFILG---KFGFP---KLRWICYDKPLGAM
082YL7_ENTFA(64-216) TPSLLGFSVGLLGLLGLLHYVNDNRGIRYHGGEEYGSARFATPAMKKYEDPIPEN---NIIYSKHYK---ISLFNKRLPIKLNKKNLRA
085A4_STR13(40-230) LFPAPYTYVFEKITEPPYFYANTSPILAILSALVGFVGLLFLYKIRLDGNYRHGEEYGSARFATPAMKKYEDPIPEN---NIIYSKHYK---ISLFNKRLPIKLNKKNLRA
0832B2_ENTFA(68-226) GAVVAVIIRAVYVYKAKNAKRYRHGVEYGSARHAGTAKDIAPYIDPKFEN---NILLTQTER---LTHGRPKDPTARNKNVL
09L900_ENTFA(94-232) YGSARHAGTAKDIAPYIDPKFEN---NILLTQTER---LTHGRPKDPTARNKNVL
08R8F9_THETN(59-229) LKAYLIFLLISIPAIIVLILARATDYRTQGVKYLRODGTHTANMNTYQEAKKILGIGTNG---GLILGRI---GSKVYVLPDPSFLNKNVA
097HP1_CLOAB(112-249) GTANMKNSEIKKYLITGGGE---GLVFGSIKEGFGNKMVILPKDTEFNKNVA
08CR29_STAEP(94-257) YFLIFHLKIICILPFVILYIYTIQILYRKNRNVDFGEEGDSRMTLKEIQEYKEIPDS---DKHYSIGRGGFISHYKDNVYIDTETHNTC
093M96_CLOPE(88-247) KYPLRF-LIYIVLCIPILKL---VFDLKSFSISLEDGQKTSRFTLLEIKAYKEVPEK---KEGFKGGGVPISRHKKIYIDTSPVNNL
09RN16_BACAN(101-254) FGL-LASTVHMGFLVYSK---VN---YRSDENVYAGQKGDSDRTTIEIQEYRIPEK---TDFEGYGGVPSHYKQSDYDTDYNTA
09M76_PEDPE(116-236) GKAHFVSETGLKGNLHMKD---VIVFG---KKGRLVAKPNLDGNYA
084HU0_RHIET(138-300) RGRKRALHGEAEAMKLEAATLFSDTGGIYIGERYVYDOKSTAAR---AFRADEPETHAGGKSPILLCFDGSFGSSHGI
TRAG_RHISN(153-315) RGRKRALHGEADMMHQAARLFSDBGVYIGERYVYDOKSTAAR---SFRADDPETHAGGKSPILLCFDGSFGSSHGI
09F5E3_AGR15(153-315) QGKRALHGEADMMKTEARLFSDBGVYIGERYVYDOKSTAAR---SFRADDPETHAGGKSPILLCFDGSFGSSHGI
TRAG_AGR15(111-315) VLAYADPVTMIGASIFISGMFALRVAIKGNARFATPAPKIGGKRAYVHGEADMMKLEAATLFSDBGVYIGERYVYDOKSTAAR---SFRADDPETHAGGKSPILLCFDGSFGSSHGI
TRAG_AGR15(155-315) KRAYVHGETDMKNGEAKLFPDGTGGIYIGERYVYDOKSTAAR---SFRADDPETHAGGKSPILLCFDGSFGSSHGI
09R6F3_AGR15(222-315) VLAYADPVTMIGASIFISGMFALRVAIKGNARFATPAPKIGGKRAYVHGEADMMKLEAATLFSDBGVYIGERYVYDOKSTAAR---SFRADDPETHAGGKSPILLCFDGSFGSSHGI
093UY7_AGR15(222-315) VLAYADPVTMIGASIFISGMFALRVAIKGNARFATPAPKIGGKRAYVHGEADMMKLEAATLFSDBGVYIGERYVYDOKSTAAR---SFRADDPETHAGGKSPILLCFDGSFGSSHGI
08KL68_RHIET(215-312) RQDFDSTHML
092Z13_RHIME(215-312) RQDFDSTHML
08UKJ4_AGR15(220-312) STHML
086J55_BBBB(216-294) GSTHMI
087219_BBBB(26-100) VN
07713_STAAR(36-119) LLAESDGLILGK---FPSGKYVIQPEDSKISNRNIF
08L1D0_ENTFA(4-120) LLAESDGLILGK---FPSGKYVIQPEDSKISNRNIF
09AL10_ENTFA(4-120) LLAESDGLILGK---FPSGKYVIQPEDSKISNRNIF
08E4N7_STR13(141-212) NLI
09E2G5_STRPN(1-71) HA
08CH35_STR13(329-411) YIDDSTNLI
08GCH5_MYCFE(154-229) NSV
Consensus

006958_SALTY(364-440)
09K461_ECOLI(364-440)
004230_ECOLI(363-471)
0847F1_PSEPH(376-480)
08VHG2_PSEPH(376-448)
08PRK2_XANAC(381-472)
085919_SPHAR(482-531)
080619_VIEPH(449-558)
08KKN0_SALTY(433-539)
087742_ECOLI(432-510)
TR01_ECOLI(432-510)
TR02_ECOLI(432-510)
093GL8_SALTY(432-510)
09EUJ3_BBBB(432-510)
025260_HELPY(558-668)
09JHY0_HELPY(558-668)
052LY3_HELPY(558-668)
032582_ECOLI(428-529)
08P579_XANCP(250-352)
0931C4_XANCP(383-485)
08P742_XANCP(410-508)
08PJB2_XANAC(410-508)
091UR9_RHIME(495-606)
091UW5_ECOLI(429-540)
09PH19_XYLFAC(392-498)
09F254_ACTAC(409-509)
08VRC7_HAREE(450-549)
087219_BBBB(299-404)
08L1D0_ENTFR(307-415)
08RL10_ENTFR(307-415)
09M476_PEDPE(400-508)
08K418_BBBB(399-507)
0981R7_RHIL0(416-524)
08R8F9_THEW(412-516)
097HP1_CLORR(427-532)
084EN5_BBBB(416-524)
09X489_RAL50(416-524)
09Y811_BRAJA(429-537)
098NT6_RHIL0(434-542)
08V438_KLEPN(125-233)
08KJN0_RHIL0(527-635)
088917_RHIL0(479-587)
08RSH2_PRR02(457-583)
093788_PSES0(457-583)
TR65_ECOLI(457-583)
TR64_ECOLI(456-582)
08R6E9_AGR75(418-520)
08RPD6_LEGPN(444-550)
08RLR2_LEGPN(522-628)
08BLV7_RICTY(416-525)
092DM4_RICPR(416-525)
092TH9_RICCN(416-525)
08RPL3_AWAPH(418-527)
08RPL9_EHRCH(420-529)
09K436_BBBB(418-527)
09K443_BBBB(418-527)
08KJL1_RHIL0(403-508)
08VLK3_AGR70(403-508)
V1rD4(403-508)
VID4_AGR7U(403-508)
09R687_AGR7U(403-508)
VID4_AGR75(403-508)
VID4_AGRRH(403-508)
08V185_AGR7U(403-508)
09F585_AGRRH(403-508)
084HU0_RHIET(476-582)
TRAG_RHISN(491-597)
093UY7_AGR7U(491-597)
09F5E3_AGRRH(491-597)
089T11_BRAJA(291-386)
09R6F3_AGR7U(502-597)
TRAG_AGR75(502-597)
TRAG_AGR7U(502-593)
08GJ55_BBBB(489-593)
08KL68_RHIET(487-593)
08UKJ4_AGR75(487-593)
092Z13_RHIME(487-593)
082YL7_ENTFR(428-524)
083282_ENTFR(413-521)
09L900_ENTFR(425-528)
08E4N7_STRR3(446-534)
09E265_STRPW(327-415)
08E584_STRR3(444-527)
08CR29_STRAP(587-686)
08KYG5_BACRN(1-87)
Y015_BACRN(1-87)
093H96_CLDPE(618-708)
025652_HELPY(38-131)
08RMV0_HELPY(480-576)
086JE7_CRRJE(432-536)
089X12_HITED(404-496)
09X9L9_STRTR(307-403)
089YH4_BACTN(310-407)
08H415_BACTN(474-571)
08R8K0_BACTN(474-571)
08R5D3_BACTN(474-569)
08R8Z0_BACTN(320-412)
092F54_BACFR(371-461)
007713_STRR3(307-379)
08CK35_STRR3(804-877)
082EY4_STRRH(437-518)
08G6E9_ARTNI(440-516)
08KJL7_STRCO(424-517)
093882_STRCO(277-371)
08G480_BIFLO(453-561)
08VPM3_BBBB(426-532)
09EU11_CUREU(456-573)
08YK90_AWRSP(406-489)
08YK58_AWRSP(397-472)
082SH1_AWRSP(427-497)
09F531_ECOLI(441-508)
097852_THEV0(298-363)

EIEERGD
EIEERGD
EIEERGD
SIEERGD

1 10 20 30 40 50 60 70 80 90 95

025260_HELPY(487-553 TSANDFDFRRL--RIDEVSIGVIANPKESTIVGPILELFFNVMIYSNLIIL-P----IHDPQCKRSCMLMDEF
Q9JHY0_HELPY(487-553 TSANDFDFRRL--RIDEVSIGVIANPKESTIVGPILELFFNVMIYSNLIIL-P----IHDPQCKRSCMLMDEF
Q9ZLV3_HELPJ(487-553 TSANDFDFRRL--RIDAVSIGVIANPKESTIVGPILELFFNVMIYSNLIIL-P----IHDPQCKRSCMLMDEF
O32582_ECOLI(360-426 DFDLRQM--RREDITYYGVNAEDHILAYDFLNLFFNLVVEYTLRENP----DFDPTLKHDCFLFLDEFPSIG
O87219_BBBB(215-294 FTDEEVSNFTSISDFHQLDI--GRKKIVLYVIIPVMD--NTYESFINLFFSQMFDELKYLAS----SNGAKLPQEVDFILDEFVNLGK
Q8L1D0_ENTFA(223-301 FVDKEYSEFTSTNDFFEEL--GTSKICLYLISPLD--RTWDGLVNLFFQQMFTELYFLGD----KHNAKLPVPLVMLDEFVNLG
Q9AL10_ENTFA(223-301 FVDKEYSEFTSTNDFFEEL--GTSKICLYLISPLD--RTWDGLVNLFFQQMFTELYFLGD----KHNAKLPVPLVMLDEFVNLG
Q07713_STAAR(232-301 TSDSDFDLRDV--GLRKTIIYVMLPVLG--NTVQSSLFFSQMFQQLYRLGD----ENGARLPVYPVDFLLDEWPNIG
Q82XL2_NITEU(314-391 PLEIFSPSGKLAECTSTCDFRFADL--KKKKMTYLLADPTRMAYAPMLGLLSMCALTELR-----FQNGKSVCFLCDIEITNI
Q8UG69_AGR5(341-413 PRHTAVLSRSDFRFADL--KRSNVTYFLVLPDRSLSTYSRMLRLVLSQSLLEHARD-----PTKATPVLYLDEFASLG
Q84EN5_BBBB(327-415 MSFLGLYR-DPTVAEYTSRCDWRIADLISAEHPVSLYLVYPPSDISRTKPLIRLILNQIGRRLTESLD---GSDGIARRHKLMLDEFPALG
Q8XW89_RALSO(327-415 MSFLGLYR-DPTVAEYTSRCDWRIADLISAEHPVSLYLVYPPSDISRTKPLIRLILNQIGRRLTESLD---GSDGIARRHKLMLDEFPALG
Q8KJN0_RHILO(438-526 MSFLGLYR-DPTVAAYTSDCDWRIADLMDAEPMSLYLVYPPSDISRTKPLVRLILNQIGRRLTERLE---GDPKSRKHQLMLDEFPALG
Q989J7_RHILO(390-478 MSFLGLYR-DPTVAAYTSDCDWRIADLMDAEPMSLYLVYPPSDISRTKPLVRLILNQIGRRLTERLE---GDPKSRKHQLMLDEFPALG
Q89TA9_BRAJA(1-86) MSFLGLHR-DPVVTEYTRRRDWRIIDIVGGDRPTTLYLVYPPSDINRTKPLIRLILNQLGRRLTEDLQ---AK---AGRRRFLMLDEFPALG
Q89YB1_BRAJA(343-428 MSFLGLYR-DPVVAEYTRCCDWRIIDIVGGERRATLLYLVYPPSDINRTKPLIRLILNQIGRRLTEDLQ---AK---AGRRRFLMLDEFPALG
Q98NT6_RHILO(348-433 MSFLGLYR-DPVVAQVTRACDWRIIDIVGGDRPTTLYLVYPPSDISRTKPLIRLILNQIGRRLTEDLQ---AR---ADRHRLLMLDEFPALG
Q8VM38_KLEPN(39-124) MSFLGLYR-DPVVARYTARCDWRIADLVGSRPVTLYLVYPPSDINRTKPLIRLILNQIGRRLTEELT---TS---GKRHRLLMLDEFPALG
Q8RS52_PRBO2(366-456 SYLALYR-DPVVARNVSRSDFRIKQLMHSDDPVSLYIVTQPNOKARLRPLVRYVMNMIVRLLADKMDFENGRPVYAHYKRLMLDEFPSLG
Q937B8_PSED(366-456 SYLALYR-DPVVARNVSRSDFRIKQLMHEDDPVSLYIVTQPNOKARLRPLVRYVMNMIVRLLADKMDFENGRPVYAHYKRLMLDEFPSLG
TRG5_ECOLI(366-456 SYLALYR-DPVVARNVSRSDFRIKQLMHEDDPVSLYIVTQPNOKARLRPLVRYVMNMIVRLLADKMDFENGRPVYAHYKRLMLDEFPSLG
TRG4_ECOLI(365-455 SYLALYR-DPVVARNVSRSDFRIKQLMHEDDPVSLYIVTQPNOKARLRPLVRYVMNMIVRLLADKMDFENGRPVYAHYKRLMLDEFPSLG
Q8GLV7_RICTY(332-415 SSELWA-NPLIDSATASSDFNIQEF--KKYKTTYVGLTPDNIQRLQKLMQVYFQQATEFLSRKMP----DLKEE--PYGVMFLDEFPTLG
Q92IM9_RICCN(332-415 SSELWA-NPLIDSATASSDFNIQEF--KKYKTTYVGLTPDNIQRLQKLMQVYFQQATEFLSRKMP----DLKEE--PYGVMFLDEFPTLG
Q9ZDN4_RICPR(332-415 SSELWA-NPLIDSATASSDFNIQEF--KKYKTTYVGLTPDNIQRLQKLMQVYFQQATEFLSRKMP----DLKEE--PYGVMFLDEFPTLG
Q8RPL3_ANAPH(335-417 SSELWA-NPLIDTATASSDFNIQDF--KRKRVSYYVGVTPDMLTRLRPLMQVYFQQATEFLCRTLP---S-DDE--PYGVLFLMDEFPTLG
Q8RPL9_EHRCH(337-419 SSELWA-NPLIDTATASSDFNIQEF--KRKKVTVYVGLTPDMLTRLRPLMQVYFQQATEFLCRTLP---S-DDE--PYGVLFLMDEFPTLG
Q9KW36_BBBB(335-417 SSELWA-NPLIDTATASSDFNILD--KKKKTTYVGLTPDMLTRLRPLMQVYFQQATEFLCRKLP---S-DDE--PYGVLFLMDEFPTLG
Q9KW43_BBBB(335-417 SSELWA-NPLIDTATASSDFNILD--KKKKTTYVGLTPDMLTRLRPLMQVYFQQATEFLCRKLP---S-DDE--PYGVLFLMDEFPTLG
Q8RPD6_LEGPN(361-443 YFELFD-DPTIDAATARSDFDLRQL--RREKITYIGFTDDMERLSPLLLFVQQLISVMIKNIP----DPVDE--PYPLLCIDEFSSLG
Q9RLR2_LEGPN(439-521 YFELFD-DPTIDAATARSDFDLRQL--RREKITYIGFTDDMERLSPLLLFVQQLISVMIKNIP----DPVDE--PYPLLCIDEFSSLG
Q8KJL1_RHILO(322-402 LNLWA-DPVKAATSRSDFSVYDL--RRRRTCIYLCVSPNDLEVIAPLIRLFFQQIVSILQRSPL---R-QDE--KHEVFLDEFKHLG
Q8VLK3_AGRU(322-402 LNLWA-DPLIKAATSRSDFSVYDL--RRRRTCIYLCVSPNDLEVIAPLIRLFFQQIVSILQRSPL---G-KDE--CHEVFLDEFKHLG
VirD4(322-402) LNLWA-DPLIKAATSRSDFSVYDL--RRRRTCIYLCVSPNDLEVIAPLIRLFFQQIVSILQRSPL---G-KDE--CHEVFLDEFKHLG
VID4_AGRU(322-402) LNLWA-DPLVKAATSRSDFSVYDL--RRRRTCIYLCVSPNDLEVIAPLIRLFFQQIVSILQRSPL---G-KDE--RHEVFLDEFKHLG
Q9R6B7_AGRU(322-402) LNLWA-DPLVKAATSRSDFSVYDL--RRRRTCIYLCVSPNDLEVIAPLIRLFFQQIVSILQRSPL---G-KDE--RHEVFLDEFKHLG
VID4_AGR5(322-402) LNLWA-DPLVKAATSRSDFSVYDL--RRRRTCIYLCVSPNDLEVIAPLIRLFFQQIVSILQRSPL---G-KDE--RHEVFLDEFKHLG
VID4_AGRRH(322-402) LNLWA-DPLVKAATSRSDFSVYDL--RRRRTCIYLCVSPNDLEVIAPLIRLFFQQIVSILQRSPL---G-KDE--RHEVFLDEFKHLG
Q8VT85_AGRU(322-402) LNLWA-DPLVKAATSRSDFSVYDL--RRRRTCIYLCVSPNDLEVIAPLIRLFFQQIVSILQRSPL---T-TDE--RHEVFLDEFKHLG
Q9F585_AGRRH(322-402) LNLWA-DPLVKAATSRSDFSVYDL--RRRRTCIYLCVSPNDLEVIAPLIRLFFQQIVSILQRSPL---L-GDE--RHEVFLDEFKHLG
Q8KW18_BBBB(316-398 SGLDQMQ-NPAIDEATAVSDFDFRTI--RKKPFSVYLVYQPLMYKPLAPLIRLFFSDLLSAMQEKDP---G-PDE--PWPVIMLDEFNRLG
Q98LR7_RHILO(335-415 LNPHT-NDLVRAATASTDFDISKL--RKDPTALFVIGCSVAQLDVFRIIILVQIHDVLMASLP---G-PDE--PYQVLMDEFRQLG
Q8P579_XANCP(167-249 LNQFI-NPILDASTSDNDFLLTDV--RKKKMSIYIGIQPNKLAESRLINLLFSQILNLTNREL---QNNPVEHQCLLLMDEFSTIG
Q93TC4_XANCP(300-382 LNQFI-NPILDASTSDNDFLLTDV--RKKKMSIYIGIQPNKLAESRLINLLFSQILNLTNREL---QNNPVEHQCLLLMDEFSTIG
Q8P7X2_XANCP(327-409 LNAMI-NPVLDAATSADDFLLTDL--RKKKMTIYIGIQPNKLAESRLINLLFSQILNLTNREL---KANPELKYQCLLLMDEFSTIG
Q8PJB2_XANAC(327-409 LNAMI-NPVLDAATSADDFLLTDL--RKKKMTIYIGIQPNKLAESRLINLLFSQILNLTNREL---KSNPELKYQCLLLMDEFSTIG
Q9PHI9_XYLFA(307-391 SKLELWM-NPIDAATSGNDFDLRDL--RKKRMSVYVGVTPDNLKRLAPLILNLLFYQQLIDLNTREL---EHNPAKYQCLLLMDEFSTALG
Q91UR9_RHIME(415-494 WA-SPIVDAATSANDFDLRDV--RKKRMSIYLGIPANKLSEAKLLNMFYTLVNLNTNQLL---HSTPELKFCTMLMDEFSTAPG
Q91UW5_ECOLI(349-428 NY-SPLVDAATAANDFYRDV--RKKRMTIYIGIQPNKLAESRLINLLFSQILNLTNREL---HSPPELKYQCLLLMDEFSTAPG
Q9F254_ACTAC(323-407 SPLTIFQ-NEIVEHATSASDFDLRAL--RREKITYYFHISANDLILAPQVANLFSMVIANNIDELP---ETNPALKYQLLLMDEFSTAVG
Q9F531_ECOLI(354-440 SPLSIFS-NPITAEATNFSDFDIRDI--RKKPMSIYLGITPDALITHEKIVNLLFFSLLVNECRELP---EHNPAKYQCLLLMDEFSTMSGKS
Q8VRC7_HAFAE(363-442 YT-NPTCAARLSDNDFDFENL--RRRMSIYVGLSPDGLVYSRLINLLFSQILNLTNREL---EYDSSLKYQVLLVDEFPALG
Q8GJE7_CAMJE(354-427 FT-NPQVANATSKMNFREFDL--REKRITHYVVIQTEDMDLAPLVRIFIESLFFKMLMSGQE-----NSNPDKFIYCLLDEF
Q8RMY0_HELPY(394-471 YK-DPKVREATSKMSDFYEEL--RTGNISYIVIAQIDIGTSSLVRAFLIESIAKMLMV-KE-----SSKPEERIFITAEDEFVRFK

Consensus ..l.....p.....ats..DF....dl...r.....%.....p.....pl...lff.q....l....pe.....f.l.lDEF..lg

1 10 20 30 40 50 60 70 80 85
 |-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----|
 Q8KJL1_RHILO(233-317) ITAKGEGAE~~EGFVAGARDIFVAGILACIERGPTIGAYYDLFAQPGEKFKLFAQLAMETRNKEAQRIFDDMAGNDTKILTSYTSVL~~
 Q8VLK3_AGRTU(241-317) ~~EGFIDGARDLFVAGILTCIERGPTIGAYYDLFAQPGEKYKLFADLAEESLNKEAQRIFDNMAGNDTKILTSYTSVL~~
 VirD4(241-317) ~~EGFIDGARDLFVAGILTCIERGPTIGAYYDLFAQPGEKYKLFADLAEESLNKEAQRIFDNMAGNDTKILTSYTSVL~~
 VID4_AGRTU(241-317) ~~EGFIDGARDLFVAGILTCIERGPTIGAYYDLFAQPGEKYKLFADLAEESLNKEAQRIFDNMAGNDTKILTSYTSVL~~
 Q9R6B7_AGRTU(241-317) ~~EGFIDGARDLFVAGILTCIERGPTIGAYYDLFAQPGEKYKLFADLAEESRNKEAQRIFDNMAGNDTKILTSYTSVL~~
 VID4_AGRRH(241-317) ~~EGFIDGARDLFVAGILTCIERGPTIGAYYDLFAQPGEKYKLFADLAEESRNKEAQRIFDNMAGNDTKILTSYTSVL~~
 VID4_AGRT5(241-317) ~~EGFIDGARDLFVAGILTCIERGPTIGAYYDLFAQPGEKYKLFADLAEESRNKEAQRIFDNMAGNDTKILTSYTSVL~~
 Q8VT85_AGRTU(241-317) ~~EGFIDGARDLFVAGILTCIERGPTIGAYYDLFAQPGEKYKLFADLAEESRNKEAQRIFDNMAGNDTKILTSYTSVL~~
 Q9F585_AGRRH(241-317) ~~EGFIDGARDLFVAGILTCIERGPTIGAYYDLFAQPGEKYKLFADLAEESRNKEAQRIFDNMAGNDTKILTSYTSVL~~
 Q8KW18_BBBBB(237-313) ~~QGLLKGIDLVFVAGLLAFQKRPTLGEIYRIASGGNKQKEYFARGHEVDNRRAKLIFTRLASTNNDTLTSYVSL~~
 Consensus#GfidGarDIFVAGIL.ci#RgtPTiGa!YdlfaqpG#KyKl%aqlaeE..NkeAqrIFdn\$Agn#tkiLTSYtSvL

1 10 20 30 40 50 60 69
 |-----+-----+-----+-----+-----+-----+-----+-----+-----|
 VID4_AGRTU(620-688) LGCASRIDAGSGRSTAIIVGPDYCTSAKIEVRTGTACENKLNWVQFVSGGMLRFDKYARSQLSLYEYSV
 VirD4(620-688) LGCASRIDAGSGRSTAIIVGPDYCTSAKIEVRTGTACENKLNWVQFVSGGMLRFDKYARSQLSLYEYSV
 Consensus LGCASRIDAGSGRSTAIIVGPDYCTSAKIEVRTGTACENKLNWVQFVSGGMLRFDKYARSQLSLYEYSV

1 10 20 30 40 50 60 70 80 90 100 103
 |-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----|
 Q8VLK3_AGRTU(554-619) ~~MLSDYSNDQVQSHLAEIANFNEDAAPRNRTVAEDHGSVKYGADIPERYMGINGDEQDADAREIPPE~~
 VirD4(554-619) ~~MLSDYSNDQVQSHLAEIANFNEDAAPRNRTVAEDHGSVKYGADIPERYMGINGDEQDADAREIPPE~~
 VID4_AGRTU(554-619) ~~MLSDYSNDQVQSHLAEIANFNEDAAPRNRTVAEDHGSVKYGADIPERYMGINGDEQDADAREIPPE~~
 Q9R6B7_AGRTU(584-668) ~~IPNNMEARTPQNSEMDDEQDSLPTGIDVPQGLIESDEVKEDAG--GVYPDFGVSAEMAPAMIAQQQLLEQIALQQRYPASSHSVK~~
 VID4_AGRT5(584-668) ~~IPNNMEARTPQNSEMDDEQDSLPTGIDVPQGLIESDEVKEDAG--GVYPDFGVSAEMAPAMIAQQQLLEQIALQQRYPASSHSVK~~
 VID4_AGRRH(585-669) ~~LVNNGETPTQQNSDMNDEQDNLAIIGIYAPQVSYEIDVVEDANARGVAPVSSVPAEMAPALSAQQQLLGQIALQQRYPVSSNP~~
 Consensus nlsdysndqvqshlaeiaNfnEdaaprNrtva##hgsvkvGadiP#rvngi#gde##Adare!pPe.....

1 10 20 30 40 46
 |-----+-----+-----+-----+-----+-----+-----|
 Q8VLK3_AGRTU(93-138) ~~HGTARWAEIGEMQHAGYLQRYSRKGPIFGKTCGPLWFGSYLTNGE~~
 VirD4(93-138) ~~HGTARWAEIGEMQHAGYLQRYSRKGPIFGKTCGPLWFGSYLTNGE~~
 VID4_AGRTU(93-138) ~~HGTARWAEIGEMQHAGYLQRYSRKGPIFGKTCGPLWFGSYLTNGE~~
 Consensus HGTARWAEIGEMQHAGYLQRYSRKGPIFGKTCGPLWFGSYLTNGE

1 10 20 30 40 50
 |-----+-----+-----+-----+-----+-----+-----|
 Q8KJL1_RHILO(44-92) ~~FDVFAFWYETPLYLGFATPVFYQGAARIYVLSAVVLLIQVVLRRKLEH~~
 Q8VLK3_AGRTU(43-92) ~~TFDVFADFWEYETPLYLGYASTVFWRGLSVYIFTSLAVLSSQLIISLRNQKH~~
 VirD4(43-92) ~~TFDVFADFWEYETPLYLGYASTVFWRGLSVYIFTSLAVLSSQLIISLRNQKH~~
 VID4_AGRTU(43-92) ~~TFDVFADFWEYETPLYLGYASTVFWRGLSVYIFTSLAVLSSQLIISLRNQKH~~
 VID4_AGRRH(43-92) ~~TFDVFADFWEYETPLYLGHATPVFFCGLSIIATSVVLLSLLIISLRNREH~~
 Consensus tFdVfAFW%ETPLYLGYAstVFWrGls!!ifTSLaVLssQl!!slRnqkH

1 10 20 30 40 50 60
 |-----+-----+-----+-----+-----+-----+-----|
 Q8KJL1_RHILO(509-568) NDEYEIVLIKGLPPLQLRKVRYFSORILKRIFESQTGALPEPAPLTEREEGFSAESRLDE
 Q9F585_AGRRH(509-568) DDDYEIVLIKGGPPLKLRKVRYYSDLILKRIFESQHGSLPEPASLMLPGDTNLVEGKLDQ
 Q8VT85_AGRU(509-558) DDNYQIVLIKGGPPLKLRKIRYYSDLILKRIFESQSGSLPEPASLTLPED
 Q9R6B7_AGRU(509-557) DDNMEIVLIKGHPPPLKLRKVRYYSDRMLRRLFECQIGALPEPASLMLSE
 VID4_AGRU(509-557) DDNMEIVLIKGHPPPLKLRKVRYYSDRMLRRLFECQIGALPEPASLMLSE
 VID4_AGRRH(509-558) DDKSEIVLIKGGPPLKLRKVRYYSDRMLRRLFECQIGALPEPASLMLAQD
 Q8YVK3_AGRU(509-553) DDQSEIVLIKGRPPLKLRKVQYYSDRTLKRLFERQMGSLPEPAPL
 VirD4(509-553) DDQSEIVLIKGRPPLKLRKVQYYSDRTLKRLFERQMGSLPEPAPL
 VID4_AGRU(509-553) DDQSEIVLIKGRPPLKLRKVQYYSDRTLKRLFERQMGSLPEPAPL
 Consensus DD.#IYLIK.G.PPLKLRK!r.YYSDr.LkRlFE.Q.GsLPEPAPL.....

1 10 20 30 40 42
 |-----+-----+-----+-----+-----+-----+-----|
 Q8KJL1_RHILO(1-42) MSSTKTTSPNIAISIA CSLALGFCAASLYATFRHGGSGEALM
 Q8YVK3_AGRU(1-42) MNSSKTSPPQRM TL SIYCSLAGFCAASCYVTFRRGFNGEAIM
 VirD4(1-42) MNSSKTSPPQRM TL SIYCSLAGFCAASCYVTFRRGFNGEAIM
 VID4_AGRU(1-42) MNSSKTSPPQRM TL SIYCSLAGFCAASCYVTFRRGFNGEAIM
 Q9R6B7_AGRU(1-42) MNSSKTPQRLAYSIYCSLAGFCAASLYVTFRRGFNGEAMM
 VID4_AGRU(1-42) MNSSKTPQRLAYSIYCSLAGFCAASLYVTFRRGFNGEAMM
 VID4_AGRRH(1-42) MNSSKTPQRLALSIYCSLAGFCAASLYATFRHGFNGEAMM
 Q8VT85_AGRU(1-42) MNSRYTPLRLAYSVACSLAYGFCAASLYATFRHGFASETLM
 Q9F585_AGRRH(1-42) MNSGKYTPIGLAASIA CSLAYGFCAASLYVTFRRHGFGETMM
 Consensus MnSsktTp.r.la.S!aCSLA.GFCAASLYvTFRhGf.gEa.M

1 10 20 30 40 50 60 70 80 90 100 110 120 130
 |-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----|
 Q82EV4_STRAW(159-376) MHVDIMGPRGTGKTRRAIPAILDGP GAVL VTSNKR---DIVDATRGPR TAR G-PVMVFDPPQVA---QET-PSHWNPLSYVTDYAKARKMA DHFASGSRDANASTDAFFDPAGQDLLANLLLAAATAKA
 Q8GAE9_ARTNI(160-378) IMGPRGTGKSTSRVMPAILDAPGAVVSTSNKR---DYYDGTGRVRETVA-PVMVFDPPQIA---QEE-PGWNWNPLSYVTDDEEKAYKLTQHFAVGSRVPGSKPDAYFDPKAEIDLSSYFLAALGGL
 Q8VFN3_BBBBB(161-374) IMGPRAGKTTTCVCPQIVETGGPVLATSNKR---DIVDLTRGPRSEK G-VVMVHDVQGI---GEP-ASWNNPLSFVTSMMRAEALTDVYVSSATQVGAQADAYFESDGKRLLSHLFFAAAVADR
 Q8CJL7_STRCO(150-364) VAIMAPRSGKTTSLAIPSNLGA PGVLLTSNKA-AGDAFTTAYEARARAG-TVWMDPQQA---HAD-REMANPLAGATTLDGANRLAGHFLASVDSQQGD-FMSKAGSNLSQLLLAALDER
 Q9X8A2_STRCO(3-217) VAIMAPRSGKTSGLAIPAILSAPGPVLLTSNKA-ANDAFTTVDARAEV G-TIINTLDPQQA---HHP-REMANDILADARDLAGAKRLAGHFVTASVDESSGSD-FMSTASNTL GALFLAASHRR
 VirD4(143-256) LVVAPTRAGKGVGIYIP TLLTFKGSVIALDVKG---ELFELTSRARKASGDVYFKFSPLDSEKTHCYNPVLDIATLPPERQFTETRRLANLITAK---GKGAEFGIDGARDL FVAGIL
 Q8G4B0_BIFLO(171-399) MAIYLAGPRSGKSLCYAIPAVLSAPGPCLATSNGDILDYVAPIRRLDHPNG-EINTFDPERIADPNRKS-APVMVDLIASVQSIADAKRIADCHRYASGQPQTGGDDFFPGTAAQQLADYLF A AHLGGR
 Q9EU11_COREQ(170-408) LAYAGARMGKSAGLAIPAI CHAPGATIYASNRG---DYYSHYVGLRRKSG-RVWFLDLQGYTTGDRRQRATFHFNPLRNVTDLPSAARVCGYFISAATDANAKVDAYFDGNARDL FASYMLAASLAGG
 Q82FZ8_STRAW(248-445) TAAATQAIHDAAGPVL VLTSNP---ALWSETKDARAKL G-PVLLYDPTHRG---DTPARLHMSPSAGCEDKPTAVARAALL-APVPRTAKIDQALAE TAETLLRSYLHAAIEGR
 Q9KYE4_STRCO(210-398) DAEGAALVITSNP---ALWSETKDARAKL G-PTHLYDPNHLC---DTPARVHMSPTGGCEDRQATARAALL-TPVPRTARLDQAIGDTAELLRSYLHAAIDGR
 Consensusgpr.gk....aipail.apG.vl.tsnk....d....t....r...G.vu.fDpq.....a.uw.pl.v.d...A...a.f..a.....a.D.f...a..ll..yl.AAa..gr

131 140 150 160 170 180 190 200 210 220 230 240 247
 |-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----|
 Q82EV4_STRAW(159-376) PVTQIYTHLSNPKDDTPERILRGAG-H-TMSADGLSGVISAPDKRSGTYGVVAQQMASCLVNPEVNRHVTPP-----ADPS-----APEFDPHFVVRTGGTL YSLSRE
 Q8GAE9_ARTNI(160-378) PITKYVLYVTEQVSEPIEILREHD-Y-ELQYKGLESTLKLADKQRDGFGTAEKMIQCLKSRNTLRVAP TGGATV-ASDA-----RQQFNPHAFASQETIYILSKE
 Q8VFN3_BBBBB(161-374) PITDVARAVQDPEDET PVREL RQAG-H-SQLAESLSRIQELTPKQRDGFVGTARPHWVNLTYDTYIPHIRDTG-----QVG-----RAEFDHRRFASTDTLFLISKE
 Q8CJL7_STRCO(150-364) PITDIMQWLAFPADRTPLDILRDHD-F-TAVAAQLKGTVEGPPETRDGIYETARQYARALLNSEIARAVTP-----QKD-----VAEFRPEQFVSTDTLFLLSKD
 Q9X8A2_STRCO(3-217) PITDVLALAMPADRT PVDLLTDAG-H-HAVAAQLQGTYSGATETRDGIYETARQYARALLNDPDVAARVTP-----NDD-----LPEFPFAFATSRDTLYLLSKD
 VirD4(143-256) SVSDVFRWCSNERDTSPADILSEYPRY-AGIASRVSSVIALTPETRSGVFGSLQTMVAFLLADPEIIDWIDPHRDTNGNIDER-----RGLFDPYEFATSEDTLYLLS
 Q8G4B0_BIFLO(171-399) DIRHVVEHLTNTQSQIPAILKQYG-Y-PDLAKTMRGKQSVNAKQRDGFYDMARRFLAPLDEPRYAEAVLPNQRTIIGTDPDGNITFAPGDVYVHDLPEFIAEEFVARTDTMYMSKD
 Q9EU11_COREQ(170-408) TVRHVHRVAQGTQVQEA VRALRANPKAAPGAGGELLESALTSHPERRDMAQELTARALSSLFTVNI REACTPNR-----NDSLALDSFVDEGGTLY
 Q82FZ8_STRAW(248-445) TIRHVHRASQGLQVQAVRILRTHPKAAPGSAGLEGLTAPERRDMAQQLTARALALSTVNI REACTPNR-----TDALALDSFVHEQGTLY
 Q9KYE4_STRCO(210-398) TIRHVHRASQGLQVQAVRILRTHPKAAPGSAGLEGLTAPERRDMAQQLTARALALSTVNI REACTPNR-----TDALALDSFVHEQGTLY
 Consensus .!.!.!.u.....p..ilr.....a..l.....p..Rdg...a.....L.....u..p.....f.....Fv...dtl%..s..