

S.sche 1 :NNLLHEITSKPKKERIVHYHTALVQ--HESNLMRRLROLVGNHKLFAFNFOYADANLSVLGPWIIDRFWOIIPFRTEELAKQEAQAEIER-QPDDE-
P.anse 324 :-ITQHTISCPKBEIVLEYDRRPRQ--WTTPLHQSIKALVGNHDYETKAEVETSQATAELGPWCADRYWOLFFNQEDIAKLETQAEBSL-LRQGA-
N.cras 322 :-ALQHTICKPKTELVVVEYVRGRPD--SETVLNKQLRKLVGGQELFKPLNETTSAASKLGTWCADRYWOLFFKQEDIVKLESRTBRDL-MKVAA-
C.glob 297 :-ALHNSSTKLKREVTVEYGKCLPE--FETGLNRALKDLVGEHRLFOQPFATATAASELGPWCADRYWOLFFRGEVVKLEAKTEREI-LRKSA-
M.gris 313 :--LLKVTGSRPQEVKRSYARVLRO--EQTLCNQLRELVLGNHPLFKQTFDSAEFAVTELGAWCADKMLWELCFREEAVSTLDGRVEGSR-ARPD-
C.para 301 :-ALRRAVGRPKKEIYKYKNLVKP--IQTMLTFFKLRLPIANNKQFSKAEAFSEAAARELGTVWFVDRMWOLFLEDEELKLEAKTERSL-SKDMA-
S.scle 621 :-LMQYSIT-KGKPEITIAFYDCLGPR--FHTPLYLKMPLPLEENPIFOQPEIFEGKEASRTLGSWCADQIWTFTCLQEEESKKLOAKTEQAHHSKVPE
G.zeae 275 :-MRQATDFQVHVEETVKYNTLGLPDETKTQLWDSISKLVSRNKEFKASLDETKEASTILGPWCADRYWQVLIDDTETKRLADRTMAF-FGGGE-

S.sche 92 :GAGRNPLKLDGLGDEPVQYNSNVVAVRDASRFVELYRF-V-PP-----T-----MAQLSNKVQRLHDALFDVFTFRFS-GQKTRCIVFVEORY
P.anse 414 :FSQL-----M--GLDKNRVREAHVELVKNHEFEQPI-----D-----TRLFSSKVIELWKTLLHDQFSSQD--LVRRCIVFVKORN
N.cras 412 :LDEI-----T--EKHVQVREAHVELVNAHTFSPAAL-----D-----PTMLSSKVIMLVRLRDOFERGV--GAQRCIIFVRORN
C.glob 387 :YSQE-----T--AAQVNKVREAHRLVGOHEFASP-----S-----SDLSSSKVVILLRILRGEFRGVD--HKRRCIVFVRORN
M.gris 402 :EVGE-----S--SHEVSNAREALSLVQQWSE-S-PP-----E-----DGSISTKTHKLEILAEFCFSQASAGNAIQCIVFVKRRD
C.para 391 :APEV-----V--EKHRNAVRSARELIRSHEFPKPEPG--L-----LSSKLKTLTKLLEEYFT-DSS---IRCIVFVERRW
S.scle 712 :PLEV-----L--EERKEQLQEAKSIVKDHIFEPHPHFASKLSDDFATKVHYSTNLSTKVVALLSILKDRFORPTN---DKCIVFVRERY
G.zeae 367 :K-----LLARGDQA-EEAVREVQKVVAHEFRAISP-----Q-----SQELSAKVKCLHEILLVHAFTVDN---TKRCIVFVDQRH

Helicase C

S.sche 171 :TATLLADIFQCEOMK--IPNLRTGVLVGGG--SKD--MGKNTFFTOLLTISKFKRGQVNCLFATSIAEEGLDIPGLQPCHPRLRYGTMIOYIQSR
P.anse 480 :TANILVDILKOPELK--IPGLEPGILIGGGRNDSSWESSKTSYRDOVLTIIKFKKGELNCIFATSVAEEGLDIPDCNIIIRFDLYDTLTIQYIQSR
N.cras 478 :TAMLLADIFQCEIKSHIPSTIAAEVLVGGGTGSSSYNAKINFOQONRIIRKFKLGEINCLFATSVAEEGLDIPDCNIVIRFDLYDTLTIQCIQSR
C.glob 451 :VASLLTDILQCEPMR--IPGLEGILVGGGRPEASYNDAKVITYRDOVLTIIKFKKGELNCIFATSVAEEGLDIPDCNVIIRYDNLNTLTIQYIQSR
M.gris 468 :TAVLLNALCEQAEIRTKIPDLKGAFLIGAGR-GGN--AAFTTTRQOEQTVSRFRDGEINCLFATSIAEEGLDIPGCNVIRFDLHGHTTIQYIQSR
C.para 453 :TAKLLTDFFESHAAE--IPGLKVGSLMGANAEGGS---SQTSTFREQIRLILSFKKCNTNCIFATSVAEEGLDIPDCNLIIRFDICKTMIQYIQSR
S.scle 790 :TARLLASLLSTPEAG--TPFLKVAPLVGTTSTTSAG--EMHITFRSOTLTMHDFRNGKINCLIATSVAEEGLDIPDCNLVVRFDLYSTVIOYIQSR
G.zeae 433 :TACLLSDIYDQVSM--IPGMNASYMIGQQSSST--LGNMSTLRKQCSILKNFRDGVINCLFATSVAEEGIDIPSCDLVIRFDLYTSVIOYVQSK

Helicase C

dsRNA binding domain

S.sche 26 :GRARHQESTYIHMALGNVDHRRLLAENKASENKM RDFCNALPENRKLEGNDNDMDYFLR-DETDQOVYVVPSTQAKLTYRSSLVILAQYVSTLP
P.anse 573 :GRARQEKSTYIHMIERGNSEQLQKMKQLKQSEDGLRKFCAMPDTRKLTGNNFKMDYFLR-KEKGROYTVPETGAKLNYKOSLICLANFVSSLP
N.cras 573 :GRARPDSTRYIQMIEKQNYEHSRILRAKGAEDVLRKFCALPEDRKLTGNHMLDYLLR-KEKGROYTVPDTGAKLSYMQSLVCLANFTATLP
C.glob 544 :GRARQEGSTYIHMVSESENEEHVKKVCONQESDALRKFCALPADRKLTGNNFDMYFLR-KEKDQROYTVPETGARLNYKOSLICLAAFVASLP
M.gris 560 :GRARMNSWFIHMTTEFCNPEHNRRWFQDRVNEQKM RDFCLSIPKORIMEKAEVD-DV-LR-GDQSQKIFVVPGSKASLTFKQSLVVLAEFVATLP
C.para 543 :GRARQADSTYIHLIEGNGDHRRIMHONAENEKLLRRFCNTQPEDRLLKCSDYDMDFFLR-QERNROYTIKSTGARLTYKNSLPILQAFINTLR
S.scle 881 :GRARHVNSRYHYHMEESHNEEQRTIKEVLKHEKLLKHFFASALPEDRKLTGNNFNMDYFLR-KERTHRVYTVPGSNAKLTYSMLTIVLSAFVDSL
G.zeae 524 :GRARHESRYITMLEDGNMRQIRSLKQAARDATALREFCLRIPADRKLODDVDFDEETESQIKQIRFNVYKTIESTGAQLTFPSSLEILAREVASLG

dsRNA binding domain

S.sche 354 :EP---SE-GVPKPEYSVFCTADGFVCEVVLPSSSPIRQATGRPHSRKQVAKCAAAAFAMCLKLYEKKYIDKHLHPIFASRLPAMRNARLAVSSKKQ
P.anse 667 :HP---PE-TNLTPEYTVNTTEGGFQCEVILPAISPIRSAIGKVHGSKAVAKCSAAFEMCLQLVRGNYLDTHLRPTLTQOLPAMRNARLAISSKKK
N.cras 667 :HP---PE-TSLSP EYIITTVPGGFQCEVVM PDASPIKSAVGKVHLSKGVAKCAAAFELCIAALLKAGHLDNHLQSVFTQOLPEMRNARLAVSSKKK
C.glob 638 :HP---PE-VNLTAGYLVLSVPGGYQCEVTLPESSPIRSATGKVYASKAVAKCSAAAYEMCLMLIKGKYLDQHLRPTFTQOLPAMRNARLAVSSKKK
M.gris 652 :AR---PD-EILSVDYTVVPVFGGFQGEVYLPASSPLRSAMGGVYRSKOLAKCAAAAYAMCIQLYNSNYLDDHLKSTLAKVLPAMRNARLAVSSKKR
C.para 637 :NQDDYAE GMDIVADYSILSVQGGFICEVMPPLSPVTSAGKVYSTKQVAKCSAAFELCFOLIQKKFLDDHLRSKFVEKRVHMANARLAVSSKNK
S.scle 975 :QA---QD-SALRVDYVVTTVNKQFICEVILPEEAPIRGAIGRPATIKQVAKCSAAFE TCVILHQKGYIDQFLLSTFKKSAHMMRNALLAVDGKKR
G.zeae 619 :TA---ES-SHSKAEYHYVKVGTGYFTAAVNLPSSSPIVSOQTGYPQRSKLLAKCSAAFEVCKKLLINGKHIDDHLQPTFKKHPHKMRNARVGISPNKK

S.sche 445 :AQYTMVRVKPETWSVLGMPTQIYASII SLTQPESLDRPSRPLVFLSRHKMPLLPEFFPLFFSK---GRASKVRCVPVDIPMQPTPNELALAAAYTLR
P.anse 758 :EEYGMRMKPEVWSTLCEPTELFATALTLESPESLGRPSLPLLLLTRRRIPOVASFPIYFGK---SRSSIVNFVLADEPIEVDEAELTSLTAFTLS
N.cras 758 :TEYAMRLKPELWSVRGVVTQLFATAFVLENPDTLGRSSRPLLLLSRSALPEVASFPLFFGT---KRFSKVRCPVPIPGSVQADDTLVEQLTRFTLK
C.glob 729 :EQYKMRKPELWSVLGEPTTELFAMALTLADPTALARHSSPLLLLTROPIPOIASFPLYFGK---NRSSAVHCVPVPGRVELDDNQIQLVAVTLA
M.gris 743 :KSYNMRKPKVLWSEVGPLTELYAMVLSLAQPGAAYYHSRPIILLTRKPLPEIAQFPLFFGKGS-SRRSNVRCIPLAHPWSPTTTOVEGICAF TLC
C.para 732 :AKYDMRLKPOIWAELGVPEKLYATVLIILSKPSALERP SRPLFILTTRTPLPOLKPELLELGPVEQEMTSDLVCQVLNCPITPTEEDLQLLTKEFTLK
S.scle 1066 :EAYEMSTKPTLWLSKCEQGIFYMTILSLISPESLDRASQPLGLTRSPLEVLPOELLHFG---GGRNSPVSCVPLTSSVKLEGTTLDQVNMETLC
G.zeae 710 :GEHDMRLRENVWSIRGEWTHFFPTRITL-DRDCGEKN-RSLIILSRSPLEGLPSIPLFFGN---GRSAIVEVTCSQEPLPITTEEAGGLTAF TLK

S.sche 537 :AFYDVFSKEYEYEGTSKDMPYFIIAPYSEPTHDVVLDPKSTCPDARSILLDWTSTIHHVAAQIERITC----Q---G-DEPDSTFFENKFVSDPEDGSRKF
P.anse 850 :IFKDVFSKEYEATFYDLIPYFLAP-TCKDHSS---DFSAPA-SDEILDWDTVKYVQEN-NIVTY----N---F-DEPDSTFFEHKVVDVPWDGARKF
N.cras 850 :AFMDVFSKEYEATAVNLPYFLSP-MDGGHGF---DFRLAKSPAHLIDRKALAYVSEN-EKVPY----T---F-LEPDSTFFODKFVVDVPYDGARKF
C.glob 821 :IFKDIFSKEYEATAAQLPYFLAP-TLMQHGS---DFTSVTDLSRIVDWGAVTFVRDN-ERVAY----A---LDDEADEFFKNKVADVPYDGSRK F
M.gris 837 :IFRDIFS KDFQASGTDMPYFLAPSTGIEHGT---DLSSLVNPERIIDWATVHRTTTT-DRV PY----N---F-NEPDEFFODKYVSDPEDGSRKF
C.para 827 :IFVDIFNKKYAAANAQALPYFFAPT NK-DHVF---LFSNLQDP RNAVDWPLLRHVADR-DAEAY-----TGDEPEEFFODKYIVDPHDGARRE
S.scle 1158 :LFQDVFSKAYKSNPDSMPYFLVPINCPNHTG---DWKDY-EPMSIIDWETVQYVQDF-ENKQAGKPWEHKPWLGPDEYEFKNKFITDPEDGSRKL
G.zeae 800 :IFADVFSKEFEATCDQFPYLLAP-LAKD-----TNLN-EISRIDWDTVNLVRDH-DSLEW-----E-----NAPDSTFFDKLVVDVPYDGGRKL

S.sche 624 :YLRQVRRDM SALDPVPEGAP-APKHRAWNRPD TVRNILNYSVSLWSKSR-VNT-PIRQDQVVVEADIVYQRRNLLDERVFLDDFGPSRCFIVLDT
P.anse 931 :YLRGRRHDMKPTDPVPEGIV-APGHRAWRTTCAHDILNYSNLSWSKSR-AKF-KSRGDQAVVEAELLSTQRNLLDSDLEGENLEPKQCFVLLEP
N.cras 932 :FTHHRRHDMKPTDPVPDGIV-APNHRAWRGLGTHDILNYSNLSWSKSR-GFM-IFQADQPVVEAALISTRRDFLDDTLRDEDVEPQQCF LILEP
C.glob 904 :FLRGRRHDMKPTDMVPEGIV-TPGHRAWRVSKTHDILNYSLSAWSKSR-AFL-TPREDQPVVE-----
M.gris 920 :FMRKVRDLKEQDKVPEGVP-APSK--WRA-VE-HTILNYSVSLWKKSR-AGH-NSRQDQPVVEAE LAPLRRNLLDET DGENSTGPOTCYLVLET
C.para 909 :WLOGIRKDLTCTSPVPADVEHQPTHROWKRRREVPHDILHWSLTAWKATREAHENKWKENQPVVVGKYATLRRNFLAD--INETSKNPFCYFVLEP
S.scle 1248 :WSVGITKDYKLPDPVPNT--APRKGA-R-KN-NSNIMEYSCSLWAKAR-TRR-TFDEEQPVVEATYISLRRNLLDEFDTGEVETPKKCFVILEP
G.zeae 875 :ILKGIDKSKKPSDPTPEGVP-ESRSRAYRS-AE-QNIKOYSNLSFSKSR-LTA-QWRDDQPVVKAELLSLRRNLLDEFQVNEEINK-DCFVILEP

RNase3 domain

S.sche 716 :LRISPIPVDSIAMIFNLPPIIHRIESTLIALEAAAVIGLPSTIYGLALEACTKD CDVSDD---AG---ATETAINFOAGMGRNYERLEELLGDSF
P.anse 1023 :LKISPLPVQVAMAYNFPVIIHRVDSNLVALDACNMLGL-NIRPDLALEAFTKDSNTDE---QD---V-E-QVNFORGMGNNYERLEFLGD AF
N.cras 1024 :MRISPIPADVVAMLLCFPSIIHRVESNLVALDACKLIGL-DLRPDLALEAFTKDSDNSDE---HD---A-E-KENFOTGMGDN YERLEFLGDSE
C.glob 965 :---AELPVDIVAMAYNEPAIMHRIDSNLVALEACKMLNL-NVRPDLALEAFTKDSDNSGE---HD---A-E-QTSFQSGMGNNYERLEFLGD CF
M.gris 1008 :LLISOIPVDTVVMAYTFPAIIYRLNSLISLEACQNLGL-DIPIDIALIAMTKDSDNSDD---HD---E-A-PINFQSGMGONYERLEFLGD CF
C.para 1002 :MRISPLPVDVAMAYLLPSIIHRIEQNLIALDACRLLOL-DIHPDLALEALT KDSDNQGEDERMDSIQAF-E-PVNFOPGMGANYERLEEL LGDSF
S.scle 1336 :LKVSPLSTTVAMAYLLPAIIHRVESYLIALEATDLLHL-DIRPDLAEAVTKDSDNSEE---HG---E-E-QTNFORGMGNNYERLEFLGD CF
G.zeae 964 :LNVSPLPIDVVSMALKEPATIHRIDSALIALDACELFDL-STPDLALEAMTKDSNTED---HG---K-Q-QINFOAGMGSNYERLEFLGDSE

RNase3 domain

S.sche 804 :LKMASTIALYTLAPDKNEFEYHVERMCMICNKNLFNNAL--EIGLEEYIRSKEFDRAWYPPVVDETVKLAEEAAAKTGTPDEN GKTP TALHGLIL
P.anse 1108 :LKMATTIAIYTLIPDKDEF EYHVERMVLICNRNLFNNAL--EVKLEEYIRSMAFNRRTWYPE--GLITL-----K-----RGK-----
N.cras 1109 :LKMATTIAIYTLIPDKGEFEYHVERMLLICNKNLFNNAL--EIGLEEYIRSMSEFNRRQWYPE--GLIIL-----K-----KGK-----
C.glob 1047 :LKMATTISIFTLIPDKAEFEYHVERMLLICNKNLFNNAL--EVKLEEHIRSMAFDRRSWYPE--GLITL-----K-----KGK-----
M.gris 1093 :LKMATSIALYTLV-EGDEF EYHVERMLDICNKNLLNWAL--ESNLOPHIRSKSFNRRTWYPP--GLKL-----L-----KGK-----
C.para 1094 :LKMATTIAVETLIPNKDEFDYHCDERMVMICNQNLFGVAKSDDLKHEYIRSKSFERGTWYPV--LKL-----E-----FGK-----T
S.scle 1421 :LKMGTISILYGLNPDSDEERYHVDRCMLICNKNLFNTAL--KLELYRIRSAAFNRRAWYPE--GP EL-----L-----RGK-----T
G.zeae 1049 :LKMATTISIEVLKEKSNECLYHVERMLLICNNNLFNTAV--DCKLPEYIRSLAFDRRTWYPD--LITL-----R-----KGK-----

RNase3 domain

S.sche 897 :KKGRKQQEGS--YHATSDKSIADVCEAMIGAAYLTITYEER--DFDLAVQAVSVVAKSKFHMPRTYKEYFAAYVLP EWQIAPATAAQVHMAKAVAR
P.anse 1176 :----RKDIRK--KHVLADKSIADVCEAIIIGAAYLT AQEAG--NFDMAIQAVTRMVNDKNHTMQTWSDY YAVYKKPAWQTMPTNSVQEDMAEKFHK
N.cras 1177 :----SKDARQ--RHVLADKSIADVCEALIGAAYLTGOEKG--SFDMAIKAVTAMVKDKKHRMISYGDYYAVYQKPTWQTESANSAQRDMAKKFSE
C.glob 1115 :----RKDLTR--QHVLADKTIADVCEALIGAAYLT AQEQTPPNFDLAIRAVTVMVKDKNHTMTSYSDYYAAYSPPAWQTAPCNSTOLDMAARFEA
M.gris 1160 :----KTEVDD--EHALGDKSIADVCEALIGAAYLT AQAQSSPNFDLAVKAVTVMTSKTHTMQAWSDY YASYQCP EWLSTPPSQTOLELCSQIKN
C.para 1164 :H---LKTLMQMD EHLADKSIADVCEALIGAAYMTTRKHD--DYDLAVRAVTRLVNHKQHPMTKWDDYHAAYVMPGWQTMPANAELDMAQK IHE
S.scle 1490 :----ATAPN--TEKLGDKSIADVCEAMIGALLSHHESK--SMDNAVRAVTEVVNSDNHKAIVWSDY YKLYQKPKGYQTAVATAAQIDLARQVET
G.zeae 1116 :----AFKATA--RQRLADKSIADVCEALIGAAYLSS--KDD--NLNMAVKAVSQMCKAKYHTMMAYDEYYASFV KVPDWOKASPNANQRRLVQKVAD

S.sche 988 :DVGYTFTYPRLLRCAVMHPSYPRVYEQLP SYQRL
P.anse 1263 :RMGYRFQYPRLLRSAFQHP TYPTSWEKLP SYQRL
N.cras 1264 :RMGYKFKHPRLLRAAFQHP TYPSLYERLP SYQRL
C.glob 1204 :RMGYATTHPRLLRSAFQHP TYPSVYEKLP SYQRL
M.gris 1249 :KMGYRFKNPRLLRCAFMHPSYPRQYENYQRL
C.para 1254 :ATGYQFKHPRVLRSAERHPSR PYVFDKVPHYQRL
S.scle 1576 :KHPYHFKYPRLLRSASTHPAYPFSYEQIP SYQRL
G.zeae 1202 :ATGYHFKSAPILLQSAFTHPSYAYS-GNVPNYQRL