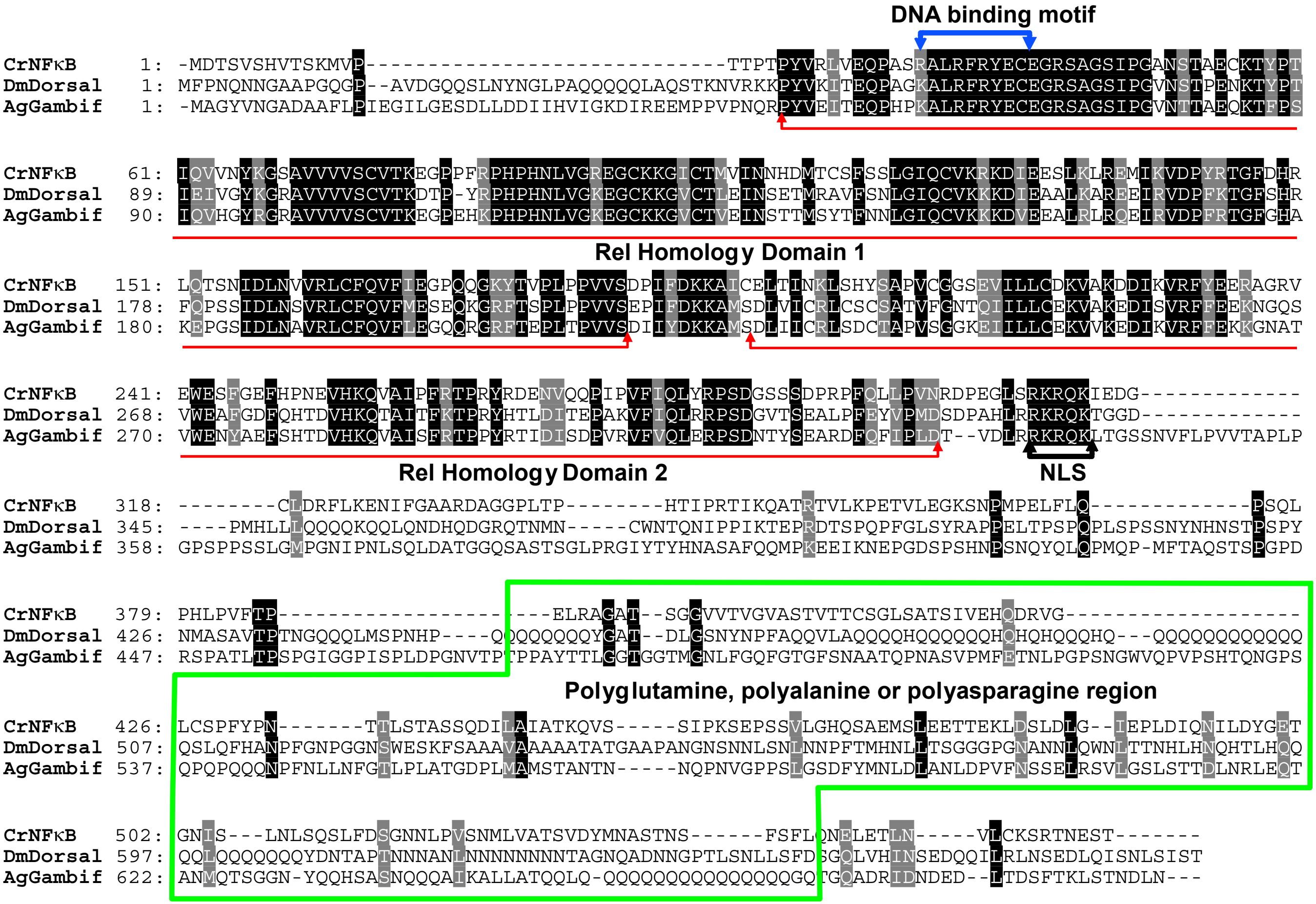

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CrNFκB      1: -MDTSVSHVTSKMVP-----------------------------TTPTPYVRLVEQPASRALRFRYECEGRSAGSIPGANSTAECKTYPT
DmDorsal    1: MFPNQNNGAAPGQGP--AVDGQQSLNYNGLPAQQQQQLAQSTKNVRKKPYVKITEQPAGKALRFRYECEGRSAGSIPGVNSTPENKTYPT
AgGambif    1: -MAGYVNGADAAFLPIEGILGESDLLDDIIHVIGKDIREEMPPVPNQRPYVEITEQPHPKALRFRYECEGRSAGSIPGVNTTAEQKTFPS

CrNFκB     61: IQVVNYKGSAVVVVSCVTKEGPPFRPHPHNLVGREGCKKGICTMVINNHDMTCSFSSLGIQCVKRKDIEESLKLREMIKVDPYRTGFDHR
DmDorsal   89: IEIVGYKGRAVVVVSCVTKDTP-YRPHPHNLVGKEGCKKGVCTLEINSETMRAVFSNLGIQCVKKKDIEAALKAREEIRVDPFKTGFSHR
AgGambif   90: IQVHGYRGRAVVVVSCVTKEGPEHKPHPHNLVGKEGCKKGVCTVEINSTTMSYTFNNLGIQCVKKKDVEEALRLRQEIRVDPFRTGFGHA

CrNFκB    151: LQTSNIDLNVVRLCFQVFIEGPQQGKYTVPLPPVVSDPIFDKKAICELTINKLSHYSAPVCGGSEVILLCDKVAKDDIKVRFYEERAGRV
DmDorsal  178: FQPSSIDLNSVRLCFQVFMESEQKGRFTSPLPPVVSEPIFDKKAMSDLVICRLCSCSATVFGNTQIILLCEKVAKEDISVRFFEEKNGQS
AgGambif  180: KEPGSIDLNAVRLCFQVFLEGQQRGRFTEPLTPVVSDIIYDKKAMSDLIICRLSDCTAPVSGGKEIILLCEKVVKEDIKVRFFEKKGNAT

CrNFκB    241: EWESFGEFHPNEVHKQVAIPFRTPRYRDENVQQPIPVFIQLYRPSDGSSSDPRPFQLLPVNRDPEGLSRKRQKIEDG-------------
DmDorsal  268: VWEAFGDFQHTDVHKQTAITFKTPRYHTLDITEPAKVFIQLRRPSDGVTSEALPFEYVPMDSDPAHLRRKRQKTGGD-------------
AgGambif  270: VWENYAEFSHTDVHKQVAISFRTPPYRTIDISDPVRVFVQLERPSDNTYSEARDFQFIPLDT--VDLRRKRQKLTGSSNVFLPVVTAPLP

CrNFκB    318: --------CLDRFLKENIFGAARDAGGPLTP--------HTIPRTIKQATRTVLKPETVLEGKSNPMPELFLQ-------------PSQL
DmDorsal  345: ----PMHLLLQQQQKQQLQNDHQDGRQTNMN-----CWNTQNIPPIKTEPRDTSPQPFGLSYRAPPELTPSPQPLSPSSNYNHNSTPSPY
AgGambif  358: GPSPPSSLGMPGNIPNLSQLDATGGQSASTSGLPRGIYTYHNASAFQQMPKEEIKNEPGDSPSHNPSNQYQLQPMQP-MFTAQSTSPGPD

CrNFκB    379: PHLPVFTP----------------------ELRAGAT--SGGVVTVGVASTVTTCSGLSATSIVEHQDRVG-------------------
DmDorsal  426: NMASAVTPTNGQQQLMSPNHP----QQQQQQQQYGAT--DLGSNYNPFAQQVLAQQQQHQQQQQQHQHQHQQQHQ---QQQQQQQQQQQQ
AgGambif  447: RSPATLTPSPGIGGPISPLDPGNVTPTPPAYTTLGGTGGTMGNLFGQFGTGFSNAATQPNASVPMFETNLPGPSNGWVQPVPSHTQNGPS

CrNFκB    426: LCSPFYPN-------TTLSTASSQDILAIATKQVS-----SIPKSEPSSVLGHQSAEMSLEETTEKLDSLDLG--IEPLDIQNILDYGET
DmDorsal  507: QSLQFHANPFGNPGGNSWESKFSAAAVAAAAATATGAAPANGNSNNLSNLNNPFTMHNLLTSGGGPGNANNLQWNLTTNHLHNQHTLHQQ
AgGambif  537: QPQPQQQNPFNLLNFGTLPLATGDPLMAMSTANTN-----NQPNVGPPSLGSDFYMNLDLANLDPVFNSSELRSVLGSLSTTDLNRLEQT

CrNFκB    502: GNIS---LNLSQSLFDSGNNLPVSNMLVATSVDYMNASTNS------FSFLQNELETLN-----VLCKSRTNEST-------
DmDorsal  597: QQLQQQQQQQYDNTAPTNNNANLNNNNNNNNTAGNQADNNGPTLSNLLSFDSGQLVHINSEDQQILRLNSEDLQISNLSIST
AgGambif  622: ANMQTSGGN-YQQHSASNQQQAIKALLATQQLQ-QQQQQQQQQQQQQQQGQTGQADRIDNDED--LTDSFTKLSTNDLN---
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