

Supplementary material

Short Linear Motifs Characterizing Snake Venom and Mammalian Phospholipases A2

Caterina Peggion and Fiorella Tonello

Clustal O sequence alignments

Group 1: 4 [myotoxins](#), 7 [neuro-myotoxins](#), 14 [neurotoxins](#), 10 [PLA2G1B](#) reviewed

Gruppo 2: 61 [myotoxins \(14 D49\)](#), (14) [neuromyotoxins \(9 D49\)](#), 12 [neurotoxins \(12 D49\)](#), 10 [PLA2G2A](#) (5 reviewed, 5 not reviewed)

Myotoxins Group 1 (all D49)

CLUSTAL O(1.2.4) multiple sequence alignment.

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SP|P80966|PA2A1_OPHHA  HLIQFGNMIQCTVPGFSLWIKYADYGCYCGAGSGTTPVDKLDRCQVHDNCYTQAQKLPA  60
SP|C0HLF0|PA2_POROP    NLFQFRKMIKKMTK--KEPVVYYAFYGCYCGKGGRGKPKDATDRCCFVHDCCYEKVTG---  56
SP|P81167|PA2BB_MICNI  NLIDFKNMIKCTNT--RHWVSFTNYGCYCGYGGSGTTPVDELDKCCQVHDKCYDTAKHVCK  58
SP|P81166|PA2BA_MICNI  NLYQLKNMIKCTNT--RHWVSFTNYGCYCGYGGSGTTPVDELDKCCQVHDKCYDTAKHVCK  58
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SP|P80966|PA2A1_OPHHA  CSSIMDSPYVKIYSYDCSERTVTCKADNDECAAFICNCDRVAAHCF AASPNN-----  113
SP|C0HLF0|PA2_POROP    CN-----PKWGYTTYSMNQ--IVCGGDDPCKKQVCECDKAAAICFRDNLKTYKKKYMSF  109
SP|P81167|PA2BB_MICNI  CS-----PSMTMYSYDCSEGKLTCKDNNTKCKDFVCNCDRTAALCF AKA PNN-----  106
SP|P81166|PA2BA_MICNI  CS-----PSMTMYSYDCSEGKLTCKDNNTKCKDFVCNCDRTAALCF AKA PNN-----  106
                        *.      *      *:  .  .  :          .:  *      *:  *:  .  **  **      .

SP|P80966|PA2A1_OPHHA  -NNYNIDTTTRC-  124
SP|C0HLF0|PA2_POROP    PNFFCTDPSEKC-  121
SP|P81167|PA2BB_MICNI  -KNFKIDPTKGCQ  118
SP|P81166|PA2BA_MICNI  -KNFKIDPTKGCQ  118
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Neuro-Myotoxins Group 1 (all D49)

CLUSTAL O(1.2.4) multiple sequence alignment

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SP|Q45Z47|PA22_OXYSC   NLAQFGFMIRCANGGSRSPLDYTDYGCYCGKGGRGTPVDDLDRCCQVHDECYGEAEKRLG  60
SP|P00608|PA2B_NOTSC   NLVQFSYLIQCANHGKRPTWHYMDYGCYCGAGSGTTPVDELDRCCKIHDDCYDEAGK-KG  59
SP|P00610|PA2B_HYDSC   NLVQFSYVITCANHNRRSSLDYADYGCYCGAGSGTTPVDELDRCCKIHDDCYGEAEK-QG  59
SP|P00604|PA2B3_NAJMO  NLYQFKNMIHCTVP-SRPWWHFADYGCYCGRGKGKTPVDDLDRCCQVHDNCYKAGK-MG  58
SP|Q9PSN5|PA2AE_NOTSC  NLYQFGNMIQCANHGRRPTRHYMDYGCYCGKGGSGTTPVDELDRCCKQTHDDCYGEAEK-LP  59
SP|P00602|PA2A1_NAJMO  NLYQFKNMIHCTVP-SRPWWHFADYGCYCGRGKGKTAVDLDRCCQVHDNCYGEAEK-LG  58
SP|P00603|PA2B2_NAJMO  NLYQFKNMIHCTVP-SRPWWHFADYGCYCGRGKGKTAVDLDRCCQVHDNCYGEAEK-LG  58
                        **  **  :  *  *  :          *  .:  *****  **  **  *:  *:  *:  :  **  **  :  *  *

SP|Q45Z47|PA22_OXYSC   CSP-----FVTLYSWKCYGKAPSCN-TKTDCQRFVCNCDAKAAECFARSPYQKKNWNIN  113
SP|P00608|PA2B_NOTSC   CFP-----KMSAYDYICGNGPYCRNIKKKCLRFVCDCEVA AFCFAKAPYNNANWNID  113
SP|P00610|PA2B_HYDSC   CYP-----KMLMYDYICGNSGPYCRNVKKCNKRVCDCEVA AECFARNAYNNANYNID  113
SP|P00604|PA2B3_NAJMO  CWP-----YFTLYKYKCSQGKLTCSGGNSKCGAAVCNCDLVAANCFAGARYIDANYNIN  112
SP|Q9PSN5|PA2AE_NOTSC  ACNYMMSGPPYYNTYSYECNEGELTCKDNND ECKAFICNCDRTAAICFARAPYNDANWNID  119
SP|P00602|PA2A1_NAJMO  CWP-----YLTLYKYEC SQGLTCSGGNNKCEAAVCNCDLVAANCFAGAPYIDANYNVN  112
SP|P00603|PA2B2_NAJMO  CWP-----YLTLYKYEC SQGLTCSGGNNKCAAAVCNCDLVAANCFAGARYIDANYNIN  112
                        .          *:  :  *          *  :  .  *  :  *:  **  **  ***  *  .  *:  *:  :

SP|Q45Z47|PA22_OXYSC   TKARCK  119
SP|P00608|PA2B_NOTSC   TKKRCK  119
SP|P00610|PA2B_HYDSC   TKKRCK  119
SP|P00604|PA2B3_NAJMO  FKKRCK  118
SP|Q9PSN5|PA2AE_NOTSC  TKTRCQ  125
SP|P00602|PA2A1_NAJMO  LKERCK  118
SP|P00603|PA2B2_NAJMO  LKERCK  118
                        *  **:  :
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Neurotoxins Group 1 (all D49)

CLUSTAL O(1.2.4) multiple sequence alignment

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SP|P00598|PA2A1_NAJAT  NLYQFKNMIQCTV-PSRSWWDFADYGCYCGRGSGTTPVDDLDRCCQVHDNCYNEAEKISG  59
SP|Q9DF52|PA2B_BUNCE   NLIQFKNMIQCA--GTREWTA YVNYGCYCGKGGSGTTPVDELDRCCTHDCYNEAEKIPG  58
SP|Q90WA8|PA2B2_BUNFA  NLLQFKNMIECA--GTRTWMA YVKYGCYCGPGGTGTPLELDRCCKQTHDQCYDNAKKFGN  58
SP|P00609|PA2B5_NOTSC  NLVQFSYLIQCANHGRRPTRHYMDYGCYCGWGGSGTTPVDELDRCCKIHDDCYSDAEK-KG  59
SP|P10116|PA2B2_LATCO  NLIQFSELIQCANKGKRATYYMYDYGCYCGKGGSGTTPVDDLDRCKKTHDDCYGQAEK-KG  59
SP|A4FS04|PA2A_NAJAT   NLYQFKNMIQCTV-PSRSWWDFADYGCYCGKGGSGTTPVDDLDRCCQVHDNCYNEAEKISG  59
SP|P14556|PA2B_NAJPA   NLYQFKNMIHCTV-PSRPWWHFADYGCYCGRGKGKTPIDDLDRCCQVHDNCYKAGK-MG  58
SP|Q90WA7|PA2B1_BUNFA  NLLQFKNMIQCA--GSLRWVA YVKYGCYCGPGGTGTPLDQLDRCCQTHDHCYDNAKKFGN  58
SP|Q8UUH8|PA2BH_LATCO  NLVQFSELIQCVNKGKRATYHYMDYGCYCGKGGSGTTPVDALDRCKKTHDDCYGQAEK-KG  59
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SP|Q8UUH9|PA2B9_LATCO NLIQFSQLIQCANKGKRPTLHYMDYGCYCGKGGSGTPVDALDRCKKTHDDCYGQAGK-KG 59
SP|Q8UUH7|PA2BK_LATCO NLIQFSQLIQCANKGKRATYHYMDYGCYCSKGGSGTPVDALDRCKKTHDDCYGQAEK-KG 59
SP|Q8UW08|PA2B0_HYDHA NLVQFSYVITCANHGRRSSLDYADYGCYCGAGGSGTPVDELDRCCKIHDDCYGEAEK-QG 59
SP|Q8UW30|PA2B7_HYDHA NLVQFSYVITCANHNRRSSLDYADYGCYCGAGGSGTPVDELDRCCKIHDDCYGEAEK-QG 59
SP|Q8UU10|PA2B1_LATCO NLVQFSELIQCVNKGKRATYHYMDYGCYCGKGGSGTPVDALDRCKKTHDDCYGQAEK-KG 59
** *. : * . * : .*****. **.***.* ***** **.*** . * * .

SP|P00598|PA2A1_NAJAT CWPYFKTYSYECSQGTLTCTCKGGNNACAAAVCDCLRLAAICFAGAPYNNNNYNIDLKARCQ 119
SP|Q9DF52|PA2B_BUNCE CNPNIKTYSYTCTEPNLTCTDTADTCARFLCDCDRTAACIFASAPYNSNNVMISSTNCQ 118
SP|Q90WA8|PA2B2_BUNFA CIPYFKTYVYTCKNKPDLTCTDAKGSCGRTVCDCDRAAALCFAAAPYNLANFGINKETHCQ 118
SP|P00609|PA2B5_NOTSC CSPKMSAYDYCYGENGPYCRNIKKKCLRFVCDVDVEAAFCFAKAPYNNANWNIDTKKRCK 119
SP|P10116|PA2B2_LATCO CFPFLTLYNFICFPGGPTCDR-GTTCQRFVCDCDIQAACFCFARSPYNNKNYNINISKRCK 118
SP|A4FS04|PA2A_NAJAT CWPYFKTYSYECSQGTLTCTCKGGNNACAAAVCDCLRLAAICFAGAPYTDANYNIDLKARCQ 119
SP|P14556|PA2B_NAJPA CWPYFTLYKYKCSKGTLTCTNGRNGKCAAAVNCNLDVAANCFAGAPYINANYNIDFKKRCK 118
SP|Q90WA7|PA2B1_BUNFA CIPYFKTYEYTCNKPDLTCTDAKGSCARNVCDCDRAAALCFAAAPYNLANFGINKETHCQ 118
SP|Q8UUH8|PA2BH_LATCO CFPFLTLYNFGCFPGGPTCGK-GNTCQRFVCDLKAALCFAKSPYNNNNYNIDTKKRCK 118
SP|Q8UUH9|PA2B9_LATCO CIPFVTLYNFGCFPGAPQCGK-GNTCQRFVCADLKAALCFAKSPYNNNNYNIDTKKKCK 118
SP|Q8UUH7|PA2BK_LATCO CFPLLSLYNFACFPGAPQCGK-GNTCQRFVCADLKAALCFAKSPYNN-NYNIDIKKKCK 117
SP|Q8UW08|PA2B0_HYDHA CYPKMLIYDYCYGSDGPYCRNVKKKCNRMVCDVDVAAAKCFARNAYNNANYNIDTNKRCK 119
SP|Q8UW30|PA2B7_HYDHA CYPKMLIYDYDCGSNGPYCKNVTKKCNRKVCDCDVAAAKCFARNAYNNANYNIDTKKRCK 119
SP|Q8UU10|PA2B1_LATCO CFPLLSLYNFACFPGAPQCGK-GNTCQRFVCADLKAALCFAKSPYNNNNYNIDIKKKCK 118
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SP|P00598|PA2A1_NAJAT -----
SP|Q9DF52|PA2B_BUNCE -----
SP|Q90WA8|PA2B2_BUNFA -----
SP|P00609|PA2B5_NOTSC -----
SP|P10116|PA2B2_LATCO -----
SP|A4FS04|PA2A_NAJAT -----
SP|P14556|PA2B_NAJPA -----
SP|Q90WA7|PA2B1_BUNFA -----
SP|Q8UUH8|PA2BH_LATCO -----
SP|Q8UUH9|PA2B9_LATCO TLIYARLQTQ 128
SP|Q8UUH7|PA2BK_LATCO TLIYMRLQTQ 127
SP|Q8UW08|PA2B0_HYDHA -----
SP|Q8UW30|PA2B7_HYDHA -----
SP|Q8UU10|PA2B1_LATCO TLIYMRLQTQ 128

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PLA2G1B reviewed (PLA2G1B of camel has been removed because it is very different).

CLUSTAL O(1.2.4) multiple sequence alignment

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SP|P04054|PA21B_HUMAN AVWQFRMKIKCVIPGSDPFLEYNNYGCYCGLGSGTPVDELDKCCQTHDNCYDQAKKLDS 60
SP|Q9Z0Y2|PA21B_MOUSE AVWQFRNMIKCTIPGSDPLKDYNNGYGCYCGLGWGTVPVDDLDRCCQTHDHCYSQAKKLES 60
SP|P06596|PA21B_CANLF AVWQFRNMIKCTIPESDPLKDYNNDYGCYCGLGSGTPVDELDKCCQTHDHCYSEAKKLDS 60
SP|P04055|PA21B_RAT AVWQFRNMIKCTIPGSDPLREYNNYGCYCGLGSGTPVDDLDRCCQTHDHCYNQAKKLES 60
SP|P00594|PA21B_HORSE AVWQFRSMIQCTIPNSKPYLEFNNDYGCYCGLGSGTPVDELDACCQVHDNCYTQAKELSS 60
SP|P00593|PA21B_BOVIN ALWQFNGMIKCKIPSSPEPLDFNNGYGCYCGLGSGTPVDDLDRCCQTHDNCYKQAKKLDS 60
SP|P43434|PA21B_CAVPO ALWQFRDMIKCAIPGSRPYSEYNNYGCFCGLGSGTPVDELDRCCEIHDACYTQAKHLES 60
SP|P00592|PA21B_PIG ALWQFRSMIKCAIPGSHPLMDFNNGYGCYCGLGSGTPVDELDRCCEIHDNCYRDAKNLDS 60
SP|Q7M334|PA21B_RABIT ALWQFRGMIQCTIPGSSPYLEFNNGYGCYCGLGSGTPVDELDRCQTHDQCYTQAKKLSS 60
SP|P14419|PA21B_SHEEP ALWQFNGMIKCKIPSSPEPLDFNNGYGCYCGLGSGTPVDDLDRCCQTHDNCYKQAKKLDS 60
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SP|P04054|PA21B_HUMAN CKFLLDNPNYTHYTSYSCSGSAITCSSKNKECEAFICNCDRNAAICFSKAPYNKAHKNLDT 120
SP|Q9Z0Y2|PA21B_MOUSE CKFLIDNPNYTNYSYSCSGSEITCSAKNNKCEDFICNCDREAAICFSKVPYNKEYKNLDT 120
SP|P06596|PA21B_CANLF CKFLLDNPNYTKIYSYSCSGSEITCSSKNKDCQAFICNCDRSAAICFSKAPYNKEHKNLDT 120
SP|P04055|PA21B_RAT CKFLIDNPNYTNYSYKCSGNVITCSDKNNDCEFSFICNCDRQAAICFSKVPYNKEYKDLD 120
SP|P00594|PA21B_HORSE CRFLVDNPNYTESYKFCSGTEVTCSDKNNACEAFICNCDRNAAICFSKAPYNPENKNLDS 120
SP|P00593|PA21B_BOVIN CKVLVDNPNYTNYSYSCSNNEITCSSENNACEAFICNCDRNAAICFSKVPYNKEHKNLDT 120
SP|P43434|PA21B_CAVPO CKSVIDNPNYTNYSYFSCSGTNIICSSKNKECEEFICNCDRAAICFSKAPYNNENKNINK 120
SP|P00592|PA21B_PIG CKFLVDNPNYTESYSCSNTEITCNSKNNACEAFICNCDRNAAICFSKAPYNKEHKNLDT 120
SP|Q7M334|PA21B_RABIT CSFLVDNPNYTNYSYSCSGTTVCSSKNKECEAFICDCDRKAAICFSKRPYNKEYKPIK 120
SP|P14419|PA21B_SHEEP CKVLVDNPNYTNYSYSCSNKQITCSSENNACEAFICNCDRNAAICFSEVPYNNEHKNLDT 120
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SP|P04054|PA21B_HUMAN KKYCQS 126
SP|Q9Z0Y2|PA21B_MOUSE GKFC-- 124
SP|P06596|PA21B_CANLF KKYC-- 124
SP|P04055|PA21B_RAT KKHC-- 124
SP|P00594|PA21B_HORSE KRKCA- 125
SP|P00593|PA21B_BOVIN KNC--- 123
SP|P43434|PA21B_CAVPO KERC-- 124
SP|P00592|PA21B_PIG KKYC-- 124
SP|Q7M334|PA21B_RABIT --YC-- 122
SP|P14419|PA21B_SHEEP KYC--- 123

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Myotoxins Group 2, NOT family:"D49 sub-subfamily"

NOT D49 CLUSTAL O(1.2.4) multiple sequence alignment

SP|P24605|PA2H2_BOTAS SLFELGKMILQETGKNPAKSYGAYGCNCGVLGRGKPKDATDRCCYVHKCCYKKLTGTCNPK 60
 SP|P0DJJ9|PA2B2_PROFL SLVQLWKMI FQETGKEAAKNYGLYGCNCGVGRGKPKDATDSCCYVHKCCYKKVTGTCNPK 60
 SP|Q90249|PA2B1_BOTJR SLFELGKMILQETGKNPAKSYGAYGCNCGVLGRGKPKDATDRCCYVHKCCYKKLTGCDPK 60
 SP|P82114|PA2H1_BOTMO SLVELGKMILQETGKNPAKSYGAYGCNCGVLGRGKPKDATDRCCYVHKCCYKKLTNCDPK 60
 SP|P80963|PA2H_BOTSC SMYELGKMILLETGKNAATSYIAYGCNCGVGRGQPLDATDRCCYVHKCCYKKLTGTCNPL 60
 SP|I6L8L6|MTX2_BOTBZ SLFQLGKMILQETGKNPAASYGAYGCNCGVLGRGKPKDATDRCCYVHKCCYKKLTGCDPK 60
 SP|O57385|PA2H_DEIAC SLFELGKMIWQETGKNPVKNYGLYGCNCGVGRGEPLDATDRCCFVHKCCYKKLTDCDSK 60
 SP|P49121|PA2H1_AGKCL SLEELGKMILQETGKNATSYSGSYGCNCGWGHRRGQPKDATDRCCFVHKCCYKKLTDCNPK 60
 SP|P04361|PA2HB_AGKPI SVLELGKMILQETGKNATSYSGSYGCNCGWGHRRGQPKDATDRCCFVHKCCYKKLTDCNPK 60
 SP|Q6JK69|PA2H1_BOTAT SLVELGKMILQETGKNPLTSYGAYGCNCGVGRGKPKDATDRCCYVHKCCYKKMTDCDPK 60
 SP|Q9I834|PA2H2_BOTMO SLFELGKMILQETGKNPAKSYGVYGCNCGVGRGKPKDATDRCCYVHKCCYKKLTGCDPK 60
 SP|P84776|PA2H_PROMB SLIELTKMVFQETGKNPVTTYTYLYGCNCGVGRGKPKDATDRCCFVHRCCYKKLTGCDPK 60
 SP|Q2PWA3|PA2HP_PROMU SVIELGKMVFQETGKNPVKNYGLYGCNCGVGRGKPKVDATDSCCFVHRCCYKKVTGCDPK 60
 SP|P0DJJ8|PA2B1_PROFL SLVQLWKMI FQETGKEAAKNYGLYGCNCGVGRGKPKDATDSCCYVHKCCYKKVTGCDPK 60
 SP|Q2YHJ9|PA2HA_TRIPE SVIQLGKMILQETGKNPVKYGYAYGCNCGPLGRRKPLDATDRCCYMHKCCYKKLTDSNPI 60
 SP|Q2YHJ8|PA2HB_TRIPE SVIQLGKMILQETGKNPVKYGYAYGCNCGPLGRRKPLDATDRCCYMHKCCYKKLTDSNPI 60
 SP|Q2YHJ4|PA2HB_TRIBO SVIELGKMILQETGKNPVTTYGYAYGCNCGPLGRRKPLDATDRCCFMHKCCYKKLTDSNPI 60
 SP|B5U6Y4|PA2HS_ECHOC SVVELGKMI IQETGKSPFSPSYTSYGCFCGGGEKGT PKDATDRCCFVHSCCYDKLPDCSPK 60
 SP|C0HKC1|PA2HB_AGKPC SVLELGKMILQETGKNATSYSGSYGCNCGWGHRRGQPKDATDRCCFVHKCCYKKLTDCNPK 60
 SP|Q6H3D4|PA2HE_TRIST SVIELGKMI FQETGKNPATSYGLYGCNCGPGGRRKPKDATDRCCYVHKCCYKKLTDCDPI 60
 SP|Q6H3D5|PA2HI_TRIST SLVQLGKMI FQETGKNPATSYGLYGCNCGPGGRRKPKDATDRCCFLHKCCYKKLTDCDPI 60
 SP|C0HKC2|PA2HB_AGKPL SVLELGKMILQETGKNATSYSGSYGCNCGWGHRRGQPKDATDRCCFVHKCCYKKLTDCNPK 60
 SP|Q6H3D6|PA2HD_TRIST HLLQLRKMIKKMTNKEPILSYGKYGCNCGMAGRGPVVDGTDRCCSIHNCCYGVKNGCSPK 60
 SP|P0DTS8|BBTX2_BOTBZ SLFELGKMILQETGKNPAKSYGAYGCYCGVLGRGKPKDATDRCCYVHKCCYKKLTGTCNPK 60

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SP|P24605|PA2H2_BOTAS KDRYSYSWKDKTIVCGENN-SCLKELCECDKAVAICLRENLTYNKKYRY-YLPLCKKA 118
 SP|P0DJJ9|PA2B2_PROFL MDSYSYSWKNAIVCGEKNPPCLKQVCECDKAVAICLRENLTYNKKYT-IYKPFCKKA 119
 SP|Q90249|PA2B1_BOTJR KDRYSYSWKDKTIVCGENN-PCLKELCECDKAVAICLRENLTYNKKYRYH-LKPFCKKA 118
 SP|P82114|PA2H1_BOTMO KDRYSYSWKNAIVCGEEN-PCLKQLCECDKAVAICLRENKGTYNKK-RDVYLPFCNPK 118
 SP|P80963|PA2H_BOTSC TDRYSHSLKNKTIVCGENK-PCLKEMCECDKALAICLGKNVNTYNKNYKI-TMKMFCKKP 118
 SP|I6L8L6|MTX2_BOTBZ KDRYSYSWKDKTIVCGENN-PCLKELCECDKAVAICLRENLTYNKKYRYH-LKPFCKKA 118
 SP|O57385|PA2H_DEIAC KDRYSYSWKNAIVCGKNQ-PCMQUEMCECDKAFIACLRENLDTYNKSFRYH-LKPSCKKT 118
 SP|P49121|PA2H1_AGKCL TDRYSYSWKNAIICEEKN-PCLKEMCECDKAVAICLRENLDTYNKKYKA-YFKFKCKKP 118
 SP|P04361|PA2HB_AGKPI TDRYSYSWKNAIICEEKN-PCLKEMCECDKAVAICLRENLDTYNKKYKA-YFKLKCKKP 118
 SP|Q6JK69|PA2H1_BOTAT KDRYSYSWKDKTIVCGEKN-SCLKELCECDKAVAICLRENLDTYNKKYKNYLYKPFCKKA 119
 SP|Q9I834|PA2H2_BOTMO KDRYSYSWKDKTIVCGENN-SCLKELCECDKAVAICLRENLDTYNKKYRYNYLYKPFCKKA 119
 SP|P84776|PA2H_PROMB KDRYSYSWENKAIVCGEKN-PCLKELCECDKAVAICLRKNLGTIDKNYRF-TMKFLCDKP 118
 SP|Q2PWA3|PA2HP_PROMU KDRYSYSWENKAIVCGEKNPPCLKQVCECDKAVAICLRENLTIDYDKKHRV-TMKFLCKAP 119
 SP|P0DJJ8|PA2B1_PROFL MDSYSYSWKNAIVCGEKNPPCLKQVCECDKAVAICLRENLTYNKKYT-IYKPFCKKA 119
 SP|Q2YHJ9|PA2HA_TRIPE KDRYSYSWENKAIVCKEKN-PRLKEMCECDKAVAICFRENMRITYNKKERI-NTKIFCKKT 118
 SP|Q2YHJ8|PA2HB_TRIPE KDSYSYSWENKAIVCKEKN-PRLKEMCECDKAVAICFRENMDITYNKKERI-NTKIFCKKT 118
 SP|Q2YHJ4|PA2HB_TRIBO KDSYSYSWENKAIVCKEKN-PRLKEMCECDKAVAICFRENMGITYNKKERI-NTKIFCKKT 118
 SP|B5U6Y4|PA2HS_ECHOC TDRYKYQRENGEIIICENST-SCKKRICECDKAVAVCLRENLTQTYNKKYTY-YPNFLCKGE 118
 SP|C0HKC1|PA2HB_AGKPC TDRYSYSWKNAIICEEKN-PCLKEMCECDKAVAICLRENLDTYNKKYKA-YFKLKCKKP 118
 SP|Q6H3D4|PA2HE_TRIST KDRYSYSWVNAIVCGEDN-PCLKEMCECDKAVAICFRENLDTYDKKKKI-NLKLFCCKT 118
 SP|Q6H3D5|PA2HI_TRIST KDSYSYSWVNAIVCGGDD-PHLKEMCECDKAMAICFRENLDTYDKKKKI-NLKLFCCKT 118
 SP|C0HKC2|PA2HB_AGKPL TDRYSYSWKNAIICEEKN-PCLKEMCECDKAVAICLRENLDTYNKKYKA-YFKLKCKKP 118
 SP|C7G1G6|PA2B3_PROFL MDSYSYSWKNAIVCGENNPPCLKQVCECDKAVAICLRENLTYNKKYT-IYKPFCKKA 119
 SP|Q6H3D6|PA2HD_TRIST WDYYTYSSENGDIVCEEKH-PC-KDVCECDKAVATCFRDNLDITYKKRNIF-HPKSSSCVKV 117
 SP|P0DTS8|BBTX2_BOTBZ KDRYSYSWKDKTIVCGENN-PCLKELCECDKAVAICLRENLTYNKKYRYH-LKPLCKKA 118

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SP|P24605|PA2H2_BOTAS D-AC 121
 SP|P0DJJ9|PA2B2_PROFL DTC- 122
 SP|Q90249|PA2B1_BOTJR D-PC 121
 SP|P82114|PA2H1_BOTMO R-DC 121
 SP|P80963|PA2H_BOTSC DAC- 121
 SP|I6L8L6|MTX2_BOTBZ D-PC 121
 SP|O57385|PA2H_DEIAC SEQC 122
 SP|P49121|PA2H1_AGKCL ETC- 121
 SP|P04361|PA2HB_AGKPI DTC- 121
 SP|Q6JK69|PA2H1_BOTAT D-AC 122
 SP|Q9I834|PA2H2_BOTMO D-PC 122
 SP|P84776|PA2H_PROMB EKC- 121
 SP|Q2PWA3|PA2HP_PROMU ESC- 122
 SP|P0DJJ8|PA2B1_PROFL DTC- 122
 SP|Q2YHJ9|PA2HA_TRIPE PEPC 122
 SP|Q2YHJ8|PA2HB_TRIPE PEPC 122
 SP|Q2YHJ4|PA2HB_TRIBO SEPC 122
 SP|B5U6Y4|PA2HS_ECHOC PEKC 122
 SP|C0HKC1|PA2HB_AGKPC DTC- 121
 SP|Q6H3D4|PA2HE_TRIST SEQC 122
 SP|Q6H3D5|PA2HI_TRIST SEQC 122
 SP|C0HKC2|PA2HB_AGKPL DTC- 121
 SP|C7G1G6|PA2B3_PROFL DTC- 122
 SP|Q6H3D6|PA2HD_TRIST STPC 121
 SP|P0DTS8|BBTX2_BOTBZ D-AC 121

Myotoxins Group 2, family:"D49 sub-subfamily"

D49 CLUSTAL O(1.2.4) multiple sequence alignment

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SP|P0DTS7|PA23_BOTBZ   SLWEWGMILKETGKNPFPPYGYGAYGCGWGGRRKPKDATDRCCFVHDCCRYKKLTGCPK 60
SP|P20474|PA2B3_BOTAS  SLIEFAKMILEETKRLFPFPYYTTYGCGYCGWGGGQPKDATDRCCFVHDCC-YGKLSNCKP 59
SP|Q71QE8|PA2BN_CROVV  NLLQFNKMIKMMTKKNAPFPYTSYGCGYCGWGGRRPKDATDRCCFVHDCC-YEKLTNCS 59
SP|Q7ZTA7|PA2AD_CROOA  SLVQFEMLIMKVAKRSGLFSYSAYGCGYCGWGGHGRPDATDHCCFVHDCC-YGKVTDCNP 59
SP|P86806|PA2BA_CRODM  SLLQFNKMIKFETRKSVPFPYAAAYGCGYCGWGGRR-RPKDPTDRCCFVHDCC-YGKLTCKNT 58
SP|P06859|PA2A1_PROFL  GLWQFENMI IKVVKKSGLISYSAYGCGYCGWGGRGKPKDATDRCCFVHDCC-YGKVTGCNP 59
SP|P45881|PA2B2_BOTJR  DLWQFGQMILKETGKLPFPYYTTYGCGYCGWGGGQPKDATDRCCFVHDCC-YGKLTNCKP 59
SP|P86805|PA2B9_CRODM  SLVQFNKMIKFETRKSGLPFPYAAAYGCGYCGWGGQ-RPKDATDRCCFVHDCC-YGKVAKCNT 58
SP|Q6EER4|PA2B_BOTSC  NLLQFNKMIKIMTRKNGIPYSSYGCGYCGWGGGQPLDATDRCCFVHDCC-YEKLTDCCSP 59
SP|Q9PVF4|PA2BD_CALRH  SMFNLWKIMIMVTGKEATKNYMGYGCNCGPMKRGKPKDATDQCCADHDCC-YKKLTDCDP 59
SP|Q8QG87|PA2A_BOTIN  NLWQFGKMMNVVMQSVVYKYFYFGYCGYCGWGGIGQPRDATDRCCFVHDCC-YGKVTGCDP 59
SP|Q6EER5|PA2B_CERGO  NLLQFNKMIKIMTKKNAPFPYTSYGCGYCGWGGRGKPKDATDRCCFEHDCC-YEKLTDCCSP 59
SP|P58464|PA2B3_BOTPI  DLWQFGQMILKETGKLPFPYYTYGGCYCGVGGRRGLGTKDDRCCYVHDCC-YKKLTGCPK 59
SP|Q6EER6|PA2B_SISMS  NLLQFNKMIKIMTKKNAPSYTSYGCGYCGWGGRRPKDATDRCCFVHDCC-YEKLTDCCSP 59
      .: :   : :   :   *   **   **
SP|P0DTS7|PA23_BOTBZ   TNDRYSYSRLDYTIVCGEDDPCK-EICECDKAAAVCFRENLRITYN-KKYMAHLRVLCKKD 118
SP|P20474|PA2B3_BOTAS  KTD RYSYSRKS GVIICGEGTPCEKQICECDKAAAVCFRENLRITYK-KRYMAYPDL LCKKP 118
SP|Q71QE8|PA2BN_CROVV  KTDIYSYSWKRGVIIICGKGTPECKQICECDRAAAVCFRENLRITYK-KRYMFYDLFLCTDP 118
SP|Q7ZTA7|PA2AD_CROOA  KTASYTYSEENGEIVCGGDDPCKQVCECDRAAICFRDNIPTYD-NKYWRFPPENCQEE 118
SP|P86806|PA2BA_CRODM  KWDIYSYSLKSGYITCGKGTWCKEQICECDRAAAECLRRSLNTYK-NEYMFYPDSRCRGP 117
SP|P06859|PA2A1_PROFL  KLGKITYSWNNGDIVCEGDGPCK-EVCECDRAAICFRDNLDTYDRNKYWRYPASNCQED 118
SP|P45881|PA2B2_BOTJR  KTD RYSYSRENGV IICGEGTPCEKQICECDKAAAVCFRENLRITYK-KRYMAYPDV LCKKP 118
SP|P86805|PA2B9_CRODM  KWDIYSYSLKSGYITCGKGTWCKEQICECDRAAAECLRRSLSTYK-NEYMFYPDSRCREP 117
SP|Q6EER4|PA2B_BOTSC  KTDIYSYSWKS GVIICGEGTPCEKQICECDRAAVCFGANLGYK-KSYMFPYDFLCTEP 118
SP|Q9PVF4|PA2BD_CALRH  KKESYSYKFEKEILCGETNPCLNQACECDKAVATCFRDNLDITYN-KKQQFNTGIFCSKA 118
SP|Q8QG87|PA2A_BOTIN  KTD SYTYSKENG DVVCGGDDPCKQICECDRAATCFRDNKDTYD-MKYWLYGAKNCQEE 118
SP|Q6EER5|PA2B_CERGO  KTDIYSYSWKS GVIICGEGTPCEKQICECDRAAVCFGTNLRTYK-KRYMFYPDFLCTDP 118
SP|P58464|PA2B3_BOTPI  TDDRYSYSWLDL TIVCGEDDPCK-ELCECDKAI AVCFRENLTGYN-KKYRYHLKPKCKAD 117
SP|Q6EER6|PA2B_SISMS  KTDIYSYSWKS GVIITCGEGTPCEKQICECDRAAVCFGENLPTYK-KRYMFYPDFLCTDP 118
      .   *: .   : *   *   : *****: * *:   .   **.
SP|P0DTS7|PA23_BOTBZ   KPC-- 121
SP|P20474|PA2B3_BOTAS  AEKC- 122
SP|Q71QE8|PA2BN_CROVV  SEKC- 122
SP|Q7ZTA7|PA2AD_CROOA  PEPC- 122
SP|P86806|PA2BA_CRODM  PEYTC 122
SP|P06859|PA2A1_PROFL  SEPC- 122
SP|P45881|PA2B2_BOTJR  AEKC- 122
SP|P86805|PA2B9_CRODM  PEYTC 122
SP|Q6EER4|PA2B_BOTSC  SEKC- 122
SP|Q9PVF4|PA2BD_CALRH  KAC-- 121
SP|Q8QG87|PA2A_BOTIN  SEPC- 122
SP|Q6EER5|PA2B_CERGO  SEKC- 122
SP|P58464|PA2B3_BOTPI  KPC-- 120
SP|Q6EER6|PA2B_SISMS  SEKC- 122

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Neuro-Myotoxins Group II, NOT family:"D49 sub-subfamily" (5)

NOT D49 CLUSTAL O(1.2.4) multiple sequence alignment

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SP|Q9IAT9|PA2H_BOTPA   SLFELGKMILQETGKNPAKSYGAYGCNCGVLGRGQPKDATDRCCYVHKCCYKKLTGCDPK 60
SP|P58399|PA2H1_BOTPI  SLFELGKMILQETGKNPAKSYGAYGCNCGVLGRGKPKDATDRCCYVHKCCYKKLTGCPNK 60
SP|P17935|PA2HL_VIPAA  SVIEFGKMIQEETDKNPLTYSYFYGCHGGLGNKGKPKDATDRCCFVHSCCYAKLPDCSPK 60
SP|P86453|PA2HB_BOTAL  SLFELGKMILQETGKNPAKSYGAYCYCGWGGGQPKDATDRCCYVHKCCYKKLTGCPNK 60
SP|P0DKU1|PA2H_GLOUS   SLLQFRKMIKMTGKEPVVSYAFYGYGCGSGGRGKPKDATDRCCFVHQCCYEKVTGCDPK 60
      *::: : *** : *.:* ** . * * * .:.*:*****:*.*** *: .*.**
SP|Q9IAT9|PA2H_BOTPA   KDRYSYSWKDKTIVCGENNPCLKELCECDKAVAICLRENLTYNKKYRYHLKPFCKKADP 120
SP|P58399|PA2H1_BOTPI  KDRYSYSWKDKTIVCGENNPCLKELCECDKAVAICLRENLTYNKLYRYHLKPFCKKADD 120
SP|P17935|PA2HL_VIPAA  TNRYEYHRENGAIVCGSSTPCKKQICECDRAAICFRENLTYNKKYKVYLRFKCKGVSE 120
SP|P86453|PA2HB_BOTAL  KDRYSYSWKDKTIVCGENNSCLKELCECDKAVAICLRENLTYNKKYRYLPLCKKADA 120
SP|P0DKU1|PA2H_GLOUS   WDDYTSYWKDGDIVCGGDDPCKKEVCECDRAAICFRDNLKTYKKIYMAPDIFCSSKASE 120
      : * * * : : ***** . * * :.:*****:*.***:*.*** *: * * :   * . .
SP|Q9IAT9|PA2H_BOTPA   C- 121
SP|P58399|PA2H1_BOTPI  C- 121
SP|P17935|PA2HL_VIPAA  KC 122
SP|P86453|PA2HB_BOTAL  C- 121
SP|P0DKU1|PA2H_GLOUS   KC 122

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Neuro-Myotoxins Group II, family:"D49 sub-subfamily" (11, two discarded as incomplete)

D49 CLUSTAL O(1.2.4) multiple sequence alignment

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SP|Q90W39|PA2BT_PROMU  NLLQFNKMIKIMTKKNAPFPYSSYGCGYCGWGGGQ-KPKDATDRCCFVHDCCYGKLTDCSP 59
SP|P59071|PA2B8_DABRR  SLLFEGKMILEETGKLAI PSYSSYGCGYCGWGGKG-TPKDATDRCCFVHDCCYGNLPDCNP 59
SP|P86804|PA2B2_BOTMA  DLWQWGMILKETGKIPFSYGYGAYGCGYCGWGGRGKPKAGTDRCCYVHDCCYGKLTSCPK 60
SP|P86803|PA2B1_BOTMA  DLWQFGQMILKETGKIPFPYGYGAYGCGYCGWGGRGKPKAGTDRCCYVHDCCYGKLTSCPK 60

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SP|Q805A2|PA2BN_PROFL NLLQFNKMIKIMTKKNGFPFYTSYGCYCGWGGRG-KPKDATDRCCFVHDCCYEKLTDCSP 59
SP|P0C8M1|PA2B1_BOTMO DLWQFNKMIKKEVGKLPFFFYGAYGCYCGWGGRGEKPKDGTDRCCFVHDCCYKLTGCPK 60
SP|P0CAS4|PA2BD_CRODR SLVQFEKMIKEETGKNAVPFYAFYGCYCGWGGRG-RPKDATDRCCIVHDCCYEKLVKCN 59
SP|P0CAS3|PA2BC_CRODR SLLQFNKMIKFETRKNNAIPFYAFYGCYCGWGGQG-RPKDATDRCCIVHDCCYKGLAKCN 59
SP|Q6EER3|PA2B2_SISTE NLLQFNKMIKIMTKKNAIPSYSSYGCYCGWGGRG-RPKDATDRCCFVHDCCYEKLTDCSP 59
.* :: :** . * . * *****:* ** .***** ***** :* *

SP|Q90W39|PA2BT_PROMU KSDIYSYSWKTGIIICGEGTECEKKICECDRAAAVCLGHNLRITYKKRYMFYPDFLCTDPS 119
SP|P59071|PA2B8_DABRR KSDRYKYKRVNGAIVCEKGTSCENRICECDKAAAIQFRQNLNTYSKKYMLYPDFLCKGEL 119
SP|P86804|PA2B2_BOTMA TDDRYSYSRLDLTIVCGEDDPCK-ELCECDKKIIVCFRENLTYNKKYRYHLKS-CKKAD 118
SP|P86803|PA2B1_BOTMA TDDRYSYSWLDGTIVCGEDDPCK-ELCECDKKIIVCFRENLTYNKKYRYHLKS-CKKAD 118
SP|Q805A2|PA2BN_PROFL KSDIYSYSWKTGVIICGEGTECEKQICECDRAAAVCFGQNLRTYKKKYMFYPDFLCTDPT 119
SP|P0C8M1|PA2B1_BOTMO WDDRYSYSWKDITIVCGEDLPCE-EICECDRAAAVCFYENLTYNKKYMKHLKP-CKKAD 118
SP|P0CAS4|PA2BD_CRODR KWDFYRYSLSRGYFQCGKGTWCEQQICECDRVAAECLRRSLSTYRYGKMIYPDSRCREPS 119
SP|P0CAS3|PA2BC_CRODR KWDFYRYSLSRGYFQCGKGTWCEQQICECDRVAAECLRRSLSTYRYGYMIYPDSRCREPS 119
SP|Q6EER3|PA2B2_SISTE KTDITYSYSLKSGVVICGNDPCKKQICECDKAAAVCFGENLSTYKKRYMFYPDFLCTDPS 119
* * *. : * . *: .:****: * *: ..* ** : . *

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SP|Q90W39|PA2BT_PROMU EKC 122
SP|P59071|PA2B8_DABRR KC- 121
SP|P86804|PA2B2_BOTMA KPC 121
SP|P86803|PA2B1_BOTMA KPC 121
SP|Q805A2|PA2BN_PROFL EKC 122
SP|P0C8M1|PA2B1_BOTMO YPC 121
SP|P0CAS4|PA2BD_CRODR ETC 122
SP|P0CAS3|PA2BC_CRODR ETC 122
SP|Q6EER3|PA2B2_SISTE ETC 122

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Neurotoxins Group II (all D49)

CLUSTAL O(1.2.4) multiple sequence alignment

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SP|P00626|PA2BA_VIPAA SLLEFGMMILGETGKNPLTSYSFYGCYCGVGGKGTTPKDATDRCCFVHDCCYGNLPDCSPK 60
SP|P86169|PA2BA_CRODR HLLQFNKMIKFETRKNNAIPFYAFYGCYCGWGGRGRPKDATDRCCFVHDCCYKGLAKCN 60
SP|P11407|PA2BC_VIPAA SLLEFGMMILGETGKNPLTSYSFYGCYCGVGGKGTTPKDATDRCCFVHDCCYGNLPDCSPK 60
SP|P14424|PA2BB_VIPAA SLLEFGMMILGETGKNPLTSYSFYGCYCGVGGKGTTPKDATDRCCFVHDCCYGNLPDCSPK 60
SP|P0CAS5|PA2BE_CRODU HLLQFNKMIKFETRKNNAIPFYAFYGCYCGWGGQRRPKDATDRCCFVHDCCYKGLTKCN 60
SP|P14421|PA2N_GLOHA NLLQFNKMIKEETGKNAIPFYAFYGCYCGGGGQKPKDGTDRCCFVHDCCYGRVLVNCN 60
SP|P00622|PA2B_BITCA NLIQFGNMISAMTGKSSL-AYASYGCYCGWGGKGQPKDDTDRCCFVHDCCYGKADKCS 59
SP|P0CAS6|PA2BF_CRODU SLLQFNKMIKFETRKNNAIPFYAFYGCYCGWGGRRRPKDATDRCCFVHDCCYEKVT 60
SP|Q1ZY03|PA2B_DEIAC HLLQFNKMIKIMTRKNNAIPFYTSYGCYCGWGGRWPKDATDSCCFVHDCCYQKLTGC 60
SP|P04417|PA2B_GLOBL HLLQFRKMIKKMTGKEPVISYAFYGCYCGSGGRGKPKDATDRCCFVHDCCYEKVTG 60
SP|A8CG84|PA2BS_DABSI SLLEFGKMILEETGKLAIPSYSSYGCYCGWGGKGTTPKDATDRCCFVHDCCYGNLP 60
SP|A8CG87|PA2A2_DABRR NLYQFGEMINQKTGNFGLLSYVYGYCYCGWGGKGKPKQDATDRCCFVHDCCYGRV 60
* :* ** * : . * ***** **: *: * ** ***** . * . *

SP|P00626|PA2BA_VIPAA TDRYKYHRENGAIVCGKGTSCENRICECDRAAAICFRKNLKTNYIYRNPDLCKKESE 120
SP|P86169|PA2BA_CRODR WDIYPYSLKSGYITCGKGTWCEEQICECDRVAAECLRRSLSTYKYGYMFYPDSRCR 120
SP|P11407|PA2BC_VIPAA TDRYKYHRENGAIVCGKGTSCENRICECDRAAAICFRKNLKTNYIYRNPDLCKKESE 120
SP|P14424|PA2BB_VIPAA TDRYKYHRENGAIVCGKGTSCENRICECDRAAAICFRKNLKTNYIYRNPDLCKKESE 120
SP|P0CAS5|PA2BE_CRODU WDIYRYSLSKSGYITCGKGTWCKEQICECDRVAAECLRRSLSTYKNEYMFYPKSR 120
SP|P14421|PA2N_GLOHA SDIYSYSLKEGYITCGKGTNCEEQICECDRVAAECFRNLDTYNNGYMFYRDSK 120
SP|P00622|PA2B_BITCA MLYSYKFHNGNIVCGDKNACKKKVCECDRVAAICFAASKHSYNKNLWRYPSSKT 119
SP|P0CAS6|PA2BF_CRODU WDIYRYSLSKSGYITCGKGTWCKEQICECDRVAAECLRRSLSTYKNGYMFYP 120
SP|Q1ZY03|PA2B_DEIAC WDIYPYSWKTGVIICGEGTPEKEICECDRAAAVCLGENLRITYKTKYMFYPDL 120
SP|P04417|PA2B_GLOBL WDDYTYSWKNGDIVCGGDDPCKKEICECDRAAAICFRDNLKTYKKRYMAYPD 120
SP|A8CG84|PA2BS_DABSI SDRYKYKRVNGAIVCEKGTSCENRICECDKAAAIQFRQNLNTYSKKYMLYPDF 120
SP|A8CG87|PA2A2_DABRR TATYSYSFENGDIVCGGDDPCLRAVCECDRVAAICFRENMTYDKKYMYSIFDCK 120
* * * * * * . :****:..* *: . :*. * *

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SP|P00626|PA2BA_VIPAA KC 122
SP|P86169|PA2BA_CRODR TC 122
SP|P11407|PA2BC_VIPAA KC 122
SP|P14424|PA2BB_VIPAA KC 122
SP|P0CAS5|PA2BE_CRODU TC 122
SP|P14421|PA2N_GLOHA EC 122
SP|P00622|PA2B_BITCA KC 121
SP|P0CAS6|PA2BF_CRODU TC 122
SP|Q1ZY03|PA2B_DEIAC QC 122
SP|P04417|PA2B_GLOBL KC 122
SP|A8CG84|PA2BS_DABSI C- 121
SP|A8CG87|PA2A2_DABRR QC 122

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PLA2G2A, 5 reviewed sequences (the sequence of rabbit PLA2G2A has been discarded because incomplete)

CLUSTAL O(1.2.4) multiple sequence alignment

```

SP|P14555|PA2GA_HUMAN  NLVNFHRMIKLTGKEAALSYGFGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGCG  60
SP|P14423|PA2GA_RAT    SLLEFGQMILFKTGKRADVSYGFGCHCGVGGRGSPKDATDWCCVTHDCCYNRLEKRGCG  60
SP|P31482|PA2GA_MOUSE  NIAQFGEMIRLKTGKRAELSYAFYGCHCGLGGKGS PKDATDRCCVTHDCCYKSLEKSGCG  60
SP|Q56JZ2|PA2GA_BOVIN  DLLNFRKMIKLTGKEPATRYSFYGCYCGMSGRGTPKDATDWCCRAHDCCYKNLESRGCR  60
SP|P47711|PA2GA_CAVPO  HLKQFTEMIKLTGKNGLTSYGAYGCHCGVGGKGT PKDATDRCCVRHDCCYDRLMKRGCG  60
      :  :*  .*  :  ***.      *  .***:*:*:*:*:*  *  *  *  *  *  *  *  *
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

SP|P14555|PA2GA_HUMAN  TKFLSYKFSNSGSRITCA-KQDSCRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRG  119
SP|P14423|PA2GA_RAT    TKFLTYKFSYRGGQISCSSTNQDSCRKQLCQCDKAAAE CFARNKKSYS LKYQFY PNKFCKG  120
SP|P31482|PA2GA_MOUSE  TKLLKYKYSHQGGQITCSANQNSCQKRLCQCDKAAAE CFARNKKTYS LKYQFY PNMFCKG  120
SP|Q56JZ2|PA2GA_BOVIN  TKFLKYNVTYQEDQIVCE-DADDCKSQVCQCDKIAANCF AANLKTYNKKLRFY NKFRCRG  119
SP|P47711|PA2GA_CAVPO  TKFLNRYRFT HKGSSITCSVKQNSCQKQLCECDKAAAYCFAANLKSYSRRYQFY YNGLCRG  120
      **:*.*. :      . * * . :.*:.*:*:*:* *  *  *  *  *  *  *  *  *  *  *  *
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

SP|P14555|PA2GA_HUMAN  STPRC  124
SP|P14423|PA2GA_RAT    KTPSC  125
SP|P31482|PA2GA_MOUSE  KKP KC  125
SP|Q56JZ2|PA2GA_BOVIN  AAPAC  124
SP|P47711|PA2GA_CAVPO  KTPSC  125
      *  *

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PLA2G2A 5 reviewed sequences and 5 unreviewed sequences

CLUSTAL O(1.2.4) multiple sequence alignment

```

SP|P14555|PA2GA_HUMAN      NLVNFHRMIKLTGKEAALSYGFGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGCG  60
SP|P14423|PA2GA_RAT        SLLEFGQMILFKTGKRADVSYGFGCHCGVGGRGSPKDATDWCCVTHDCCYNRLEKRGCG  60
SP|P31482|PA2GA_MOUSE      NIAQFGEMIRLKTGKRAELSYAFYGCHCGLGGKGS PKDATDRCCVTHDCCYKSLEKSGCG  60
SP|Q56JZ2|PA2GA_BOVIN      DLLNFRKMIKLTGKEPATRYSFYGCYCGMSGRGTPKDATDWCCRAHDCCYKNLESRGCR  60
SP|P47711|PA2GA_CAVPO      HLKQFTEMIKLTGKNGLTSYGAYGCHCGVGGKGT PKDATDRCCVRHDCCYDRLMKRGCG  60
TR|A0A5K1UTF7|A0A5K1UTF7_HORSE  HLLDFRKMIRLMTGKEATSSYGFYGCHCGVGGKGS PKDATDWCCVAHDCCY YRLQKRGCG  60
TR|H2PY77|H2PY77_PANTR      DLVNFHRMIKLTGKEAALSYGFGCHCGVGGKGS PKDATDRCCVTHDCCYKRLEKRGCG  60
TR|G3QZ00|G3QZ00_GORGO      DLVNFRMIKLTGKEAALSYGFGCHCGVGGKGS PKDATDRCCVTHDCCYKRLEKRGCG  60
TR|A0A452FN06|A0A452FN06_CAPHI  SLLDFRKMIFATGKEPATNYSFYGCYCGMRGRGTPKDATDRCCRAHECCYRSLESRGCR  60
TR|A0A2R8ZCM9|A0A2R8ZCM9_PANPA  DLVNFHRMIKLTGKEAALSYGFGCHCGVGGKGS PKDATDRCCVTHDCCYKRLEKRGCG  60
      :  :*  .*  :  ***.      *  .***:*:*:*:*  *  *  *  *  *  *  *  *
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

SP|P14555|PA2GA_HUMAN      TKFLSYKFSNSGSRITCA-KQDSCRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRG  119
SP|P14423|PA2GA_RAT        TKFLTYKFSYRGGQISCSSTNQDSCRKQLCQCDKAAAE CFARNKKSYS LKYQFY PNKFCKG  120
SP|P31482|PA2GA_MOUSE      TKLLKYKYSHQGGQITCSANQNSCQKRLCQCDKAAAE CFARNKKTYS LKYQFY PNMFCKG  120
SP|Q56JZ2|PA2GA_BOVIN      TKFLKYNVTYQEDQIVCE-DADDCKSQVCQCDKIAANCF AANLKTYNKKLRFY NKFRCRG  119
SP|P47711|PA2GA_CAVPO      TKFLNRYRFT HKGSSITCSVKQNSCQKQLCECDKAAAYCFAANLKSYSRRYQFY YNGLCRG  120
TR|A0A5K1UTF7|A0A5K1UTF7_HORSE  TKLLNFKFSYRGGKIICA-KQDSCRSEL CQCDKTAASC FARNRKTY SKKYQYYNNKSCRG  119
TR|H2PY77|H2PY77_PANTR      TKFLSYKFSNAGSRITCA-KQDSCRSQLCECDKAAANCFARNKTTYNKKYQYYSNKHCRG  119
TR|G3QZ00|G3QZ00_GORGO      TKFLSYKFSNVGSRITCA-KQDSCRSQLCECDKAAANCFARNKTTYNKKYQYYSNKHCRG  119
TR|A0A452FN06|A0A452FN06_CAPHI  TKFLKYNATYEEDQIIICE-DTDDCKSQVCQCDKIAASC FATNLKTYNKKLRFY NKLR CRG  119
TR|A0A2R8ZCM9|A0A2R8ZCM9_PANPA  TKFLSYKFSNAGSRITCA-KQDSCRSQLCECDKAAANCFARNKTTYNKKYQYYSNKHCRG  119
      **:*.*. :      . * * . :.*:.*:*:*:* *  *  *  *  *  *  *  *  *  *  *  *
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

SP|P14555|PA2GA_HUMAN      STPRC  124
SP|P14423|PA2GA_RAT        KTPSC  125
SP|P31482|PA2GA_MOUSE      KKP KC  125
SP|Q56JZ2|PA2GA_BOVIN      AAPAC  124
SP|P47711|PA2GA_CAVPO      KTPSC  125
TR|A0A5K1UTF7|A0A5K1UTF7_HORSE  KTPRC  124
TR|H2PY77|H2PY77_PANTR      STPRC  124
TR|G3QZ00|G3QZ00_GORGO      STPRC  124
TR|A0A452FN06|A0A452FN06_CAPHI  PAPQC  124
TR|A0A2R8ZCM9|A0A2R8ZCM9_PANPA  STPRC  124
      *  *

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