Fig. S3

```
                    10        20        30        40        50        60
                     |         |         |         |         |         |
BtaurDIA1R   MEP-RLGPKAAALHLGWPF-LLLWVSGLSYSVSSPASPSPSP--VSRVRTSYNLGKTFLG
EcabaDIA1R   MEP-WLGPEAAALRPGWPA-LLLWVSALRCSVSSPASPSPSL--VPRVRTSYNFGRTFLG
DordiDIA1R   MDP-QLGPEAAALHPGWQV-LLLLVVSVLSCFSSPASPPPSL--VSRVRTSYNLGRTFLG
MmulaDIA1R   MEP-QLGPEAAALRPGWLA-LLLWVSALSCSFSLPASSPSSL--VSQVRTSYNFGRTFLG
HsapiDIA1R   MEP-QLGPEAAALRPGWLA-LLLWVSALSCSFSLPASSLSSL--VPQVRTSYNFGRTFLG
RnorvDIA1R   MELGRPGAAATAFRQRWPAWMLLWVSTLSCSFSLPASLPPSL--VPRVRSSYTLGKTFLG
MmuscDIA1R   MESQWRGAAATAFHQHWLARLLLWVSTLSCSFSLPASLPPSL--VPRVRSSYTMGKTFLG
MdomeDIA1R   MES-VIHGPLASPCLGWLT--LLQLVTLSCISSTESLTAPSS--VPRVKSSYNFGRTFLG
OanatDIA1R   MGL-RLGCRLFSAALSWMT--LLQFLTRGHGPVADASPAPSL--VPRVKPSYSFGRTFLG
GgallDIA1R   MGR--WICCLCSRVADWLM--LLLVLARSSNPSAAATASPS---APHVRPSYSFGRTFLG
SsalaDIA1R   MPL--KRCDQRAVGSVRLT--VCVLSWLLCVCWAPSVVEPAGTPPAPQQKALILQRAFLG
DreriDIA1R   ----------MAG--------IWSGVWILCFILVFGTADPS---PAPQDKSHDFRKIFLG
                        :         :              .   .:    .    :  : : ***
Consensus    MEP22LGPEAAALRPGWLA2LLLWVS2LSCSFSLPASPPPSLTPVPRVRTSYNFGRTFLG

                    70        80        90       100       110       120
                     |         |         |         |         |         |
BtaurDIA1R   LDKCNACIGTSICKKFFKEEIRFDNGLALHLGPPPDDLPSYSANYSDDFKTWRPVEISRL
EcabaDIA1R   LDKCNACIGTSICKKFFKEEIRFDNRLASHLGLPSGYLPSYSANYSDDSKTWRPVEVSRL
DordiDIA1R   LDKCNACIGTSICKKFFKEEIRFDNSLASDLELASDYLPSYSANYSDDSKTWRPVEIFRL
MmulaDIA1R   LDKCNACIGTSICKKFFKEEIRSDNWLASHLGLPPDFLLSYPANYSDDSKIWRPVEIFRL
HsapiDIA1R   LDKCNACIGTSICKKFFKEEIRSDNWLASHLGLPPDSLLSYPANYSDDSKIWRPVEIFRL
RnorvDIA1R   LDKCNACIGTSICKKFFKEEIRLDNSLVSHLGLPSQDLLSYAANYSDDSKTWRPVEISRL
MmuscDIA1R   LDKCNACIGTSICKKFFKEEIRFDNSLASHLGLPPQDLHSYAANYSDDSKTWRPVEISQL
MdomeDIA1R   LDKCNACIGTSICKKFFKEEIRFDNWLASHLKLPPDYFSTYPANYSDDTKSWRPVEISRL
OanatDIA1R   LDKCNACIGTSICKKFFKEEIRFDNWPASHLKPPPDHFPGYSANYTDDSKSWRLVEISRL
GgallDIA1R   LDKCNACIGTSICKKFFKEEIRFDTWLSSHLKLPPSYLLSYLGNYTDDAQSWRMVDITRL
SsalaDIA1R   LDKCNACVGTSICKKLLKDQIRFDWWMSPDTTLPLAEKQSFPGNLTDDSLSWRPVVLSFL
DreriDIA1R   LDKCNACIGTSICKKFFKDEIRFERRLTAQSNLSSADVRSYEGNYTDSTAGWRPVVVSRL
             *******:*******::*::** :     .   .      : .* :*.   ** * :  *
Consensus    LDKCNACIGTSICKKFFKEEIRFDNWLASHLGLPPD2L2SY2ANYSDDSKTWRPVEISRL

                   130       140       150       160       170       180
                     |         |         |         |         |         |
BtaurDIA1R   VSKQQNKISDGRICASAAAPKTCSIERVLRKTGRFQKWLQAKRLTPDLVRGLSSPLLRCP
EcabaDIA1R   VSKQQNEISDRRICAFAAAPKTCSIERVLRKTRRFQKWLQAKRLTPDLVRGLPSPLLRCP
DordiDIA1R   VSKEQNEISDRRICAFASAPKTCSIERILRKTGRFQKWLQAKRLTPDLVQGLPSPFLRCP
MmulaDIA1R   VSNYQNEISDRRICASASAPRTCSIERVLRKTERFQKWLQAKRLTPDLVQGLASPLLRCP
HsapiDIA1R   VSKYQNEISDRRICASASAPKTCSIERVLRKTERFQKWLQAKRLTPDLVQGLASPLLRCP
RnorvDIA1R   VSKYQSEISDKRICASASGPKTCSIERILRKTGRFQKWLQAKRLTPDLVQGLPSPFLHCP
MmuscDIA1R   VSRYQIEISDRRICASVSAPKTCSIERILQKTGRFQKWLQAKRLTPDLVQGLPSPFLRCP
MdomeDIA1R   ISKYQHELSDRRICASASGSKTCSIERVLRKTERVKKWLKAKRLTPDLVQGLPSPMLRCP
OanatDIA1R   IGKDQNELSDQKICTSVSLVKTCSIERVLRKTERFQKWLKARRLTPALVQGLPSLLLRCP
GgallDIA1R   TTKYQHDRADQHICTSLLKTKTCSLERALRRTHRFQKWLRAKRLTPDLVQGLSSPMLRCP
SsalaDIA1R   SSPCLHSSSDRSICRSVGRQGPCSIEAVLRVTPRFQSLNQSHLLLPHIVKGLAPPLLRCP
DreriDIA1R   MSPHLHQLSDNSICTSAGKGKSCSIEGVLRATSRFQTWVHSNLLLPSMVKGLVTPMLRCP
                   . :*  **       .**:*  *: * *.:.  ::. * * :*:** . :*:**
Consensus    VSKYQNEISDRRICASASAPKTCSIERVLRKT2RFQKWLQAKRLTPDLVQGLPSPLLRCP

                   190       200       210       220       230       240
                     |         |         |         |         |         |
BtaurDIA1R   SQRLLDRVVRRYAEVADAGSIFMDHFTDRDKLRLLYTLAVNTHPVLLQIFPGAEGWPLPQ
EcabaDIA1R   SQRLLDRVVRRYAEVPDAGSIFMDHFTDRDKLRLLYTLAVNAHPILLQIFPGAEGWPLPR
DordiDIA1R   SQRLLDRVVRRYAEVADAGSIFMDHFTDRDKLRLLYTLAVNAHPIFLQIFPGAEGWPLPK
MmulaDIA1R   SQRLLDRVVRRYAEVADAGSIFMDHFTDRDKLRLLYTLAVNSHPILLQIFPGAEGWPLPQ
HsapiDIA1R   SQRLLDRVVRRYAEVADAGSIFMDHFTDRDKLRLLYTLAVNSHPILLQIFPGAEGWPLPK
RnorvDIA1R   SQRLLDRVVRRYAEVVDAGSIFMDHFTDRDKLRLLYTLAVNAHPIILQIFPGAEGWPMPK
MmuscDIA1R   SQRLLDRVVRRYAEVVDAGSIFMDHFTAGDKLRLLYTLAVNAHPIILQIFPGAEGWPMPR
MdomeDIA1R   SQRLLDRIVRRYAEVADAGSVFMDHFTDRDKLRLLYTLSINAHPIMLQIFPGAEGWPLPR
OanatDIA1R   TQRLLDRIVRRYAEVPDAGSVYMDHFTDRDKLRLLYTLSVNAHPVLLQVFPGAEGWPFPK
GgallDIA1R   SQRLLDRIVRRYAEVPDAGSIYMDHLTDQDKLRLLYTLSVNSHPILLQIFPDVEGWPFPR
SsalaDIA1R   SQRLLDRIVRRYAEVVDVGSVQMKHFSERDKLRLLYTLAVNQQPLILQMFPGTEGWPFPR
DreriDIA1R   SQRLLDRIVRRYFEVTDVGSVQMKHFNEKDKLRLLYTLAVNQQPLILQMFPGTEGWPFLR
             :******:**** ** *.**: *.*:.  *********::* :*::**:**..****: :
Consensus    SQRLLDRVVRRYAEVADAGSIFMDHFTDRDKLRLLYTLAVNAHPILLQIFPGAEGWPLPR
```

```
                    250       260       270       280       290       300
                      |         |         |         |         |         |
BtaurDIA1R   YLGSCGRFLVSTSTSPLQEFYGAP--PDQAADLAYQLLGVLESLRSNDLNYFFYFTHVDA
EcabaDIA1R   YLGSCGRFLISTSTSPLQEFYSAP--PDQAADLAYQLLGVLESLRSNDLNYFFYFTHVDA
DordiDIA1R   YLGSCGRFFVSTSTRPLQEFYGAP--PDEAADLAYQLLGVLESLRSNDLNYFFYFTHVDA
MmulaDIA1R   YLGSCGRFLVSTSTRPLQEFYGAP--PDQAADLAYQLLGVLESLRSNDLNYFFYFTHIDA
HsapiDIA1R   YLGSCGRFLVSTSTRPLQEFYDAP--PDQAADLAYQLLGVLESLRSNDLNYFFYFTHIDA
RnorvDIA1R   YLGSCGRFLVSTSTRPLQEFYDAP--PEQAADIAYQLLGVLESLRSNDLNYFFYFTHVDA
MmuscDIA1R   YLGSCGRFLVSTSTRPLQEFYDAS--PEQAADLAYQLLRVLESLRSNDLNYFFYFTHVDA
MdomeDIA1R   YLGSCGRFLVSTSTQPLEEFYSSP--ADQAADLAYQLLGILDSLRNNDLNYFFYFTRIDA
OanatDIA1R   YLGSCGRLLVSTSTTPLLELSSGP--PDRAADLGHQLLGVIEFLRHNDWNYFFYFTRIHA
GgallDIA1R   YLGSCGRLVVSASTRPLRDFFRAA--PEVAADLALQLLAVLHSMGTNDLNYFFYFTRVDV
SsalaDIA1R   YQGSCGRLMVWASSRPLWGLYGSSREFVQRVDVAYQLLHITQGLGHNSLGFLLYYTRLGE
DreriDIA1R   YHGSCGRLMVWAASRALRTLFSSP--LERRADLAYQLLHITQSLSANSLRFRLFYTRIPE
             * *****:.: ::: .*  :  ..      .*:. *** : . :  *.  : ::*::
Consensus    YLGSCGRFLVSTSTRPLQEFY2APREPDQAADLAYQLLGVLESLRSNDLNYFFYFTHVDA

                    310       320       330       340       350       360
                      |         |         |         |         |         |
BtaurDIA1R   DMFGIFNNGHLFIRDASALGVIDRQEGSQAAS--GAGDNKDIFSCL-VSGCQTK-LPSCD
EcabaDIA1R   GMFGIFNNGHLFIRDASTLGVIDRQEGSQAAA--RAGENKDIFSCL-LSDCQAE-LPSCD
DordiDIA1R   AMFGIFSNGHLFIRDASALGVIDKQEGSQAAP--KAGENQDIFSCL-VSGCQAQLLPSCD
MmulaDIA1R   GMFGVFNNGHLFIRDASAVGVIDKQEGSQEAT--RAGENKDIFSCL-VSGCQAQ-LPSCE
HsapiDIA1R   GMFGVFNNGHLFIRDASAVGVIDKQEGSQEAN--RAGENKDIFSCL-VSGCQAQ-LPSCE
RnorvDIA1R   GMFGIFDNGHLFIRDASALGIIDKQEASQAAD--RTGENEDIFSCL-VSGCQVQ-MSSCD
MmuscDIA1R   GMFGIFDNGHLFIRDASALGIIDKQEGSQAAA--RTGENEDIFSCL-VSDCQIQ-LSSCD
MdomeDIA1R   GTFGIFDNGHLFIRDASTVGVIDKQRGSLTLD--RQEESKDIFSCL-VLDCQSP-FPSCS
OanatDIA1R   GTFGVFDNGHLFIRDASSLGVIDRQEGKRPAR--SSPEPRDIFSCL-AADCQSD-LPSCN
GgallDIA1R   GTFGVFSNGHLFIRDASTLGIIDKEEGSQPID--GQQEYKDIFSCL-TVDCQSA-FVSCN
SsalaDIA1R   DMFGLLDDQRVFITDASSIGVIDLEQGFPPDPPSQTGSDGDIFSCLGQGTSPCHRSPPCS
DreriDIA1R   DMFGILEDNKVFIVDTSTIGIIDLQEGHPPDK-DLLPEELDVFSCL-SG--SCVRPPPCE
               **::.: ::** *:*::*:** :..           .  *:****           .*.
Consensus    GMFGIFDNGHLFIRDASALGVIDKQEGSQAADP2RAGENKDIFSCLGVS2CQAQRLPSCD

                    370       380       390       400       410       420
                      |         |         |         |         |         |
BtaurDIA1R   TIPEKQNLVLVCSQVLP-LLLQAK-------------FPSPVQEEIDAELTRCADGTRPD
EcabaDIA1R   TVPEKQSLVLVCRQVLP-RLLQGK-------------FPSPVQEEIDATLTWCGEDTRPD
DordiDIA1R   NIPDKQSVVLVCQQLLP-QLLQGK-------------FPSPVQVEIDSALAQCGQGIRPD
MmulaDIA1R   SVSEKQSLVLVCQKLLP-RLLQGR-------------FPSPVQDDIDSALAQCGDSTRPD
HsapiDIA1R   SISEKQSLVLVCQKLLP-RLLQGR-------------FPSPVQDDIDSILVQCGDSIRPD
RnorvDIA1R   TVPEKQNLVLVCQQLLP-QLLRGK-------------FPSPVQQEIDSALSLCSKDASTN
MmuscDIA1R   TVPEKQSLVLVCQQLLP-QLLQGK-------------FPSPVQKEIDSALSLCSKDNSTD
MdomeDIA1R   SVKEKQSWVMACQQLLP-QLLKEK-------------FPQPIQEQIDSALVLCGNSSLSD
OanatDIA1R   TVQEHQSLVLVCRELLP-KLLEGK-------------FPKPVQEEIDALLDRCGDSSLDG
GgallDIA1R   SIREKQSLVMVCQELLP-KLLRGK-------------FLPPVQEKIDSFLQHCAEGLADD
SsalaDIA1R   SVRPTQSLTLLCTALLPRLLLTERGAQTTRLPMEGEAEAGRLARDVPLLLGVCADPSQPD
DreriDIA1R   TVREAQSFILLCKYILN-NLLTSN-----------DKQSG-LPRAAVDELLVCADPSQLD
             .:   *.  : *  :*   **  .                 :        *  *..    .
Consensus    TVPEKQSLVLVCQQLLPRQLLQGKGAQTTRLPMEG22FPSPVQEEIDSAL42CGDSSRPD

                    430       440       450
                      |         |         |
BtaurDIA1R   PEVLGAASRLKDILRPLRTCDPRFAYRYPDCKYDDKF
EcabaDIA1R   AEVLGAASRLKDILRPLRTCDPRFAYRYPDCKYNDKF
DordiDIA1R   SEVFGAASRLKDILRPLRTCDPRFAYRYPDCKYNDRF
MmulaDIA1R   PEVLGAASWLKHILRPLRTCDSRFAYRYPDCKYNDKF
HsapiDIA1R   PEVLGAASQLKDILRPLRTCDSRFAYRYPDCKYNDKF
RnorvDIA1R   LEVFGATSLLKNILRSLRTCDPRFAYRYPDCKYNDRF
MmuscDIA1R   LEVLGATSWLKDILRSLRTCDPRFAYRYPDCKYNDRF
MdomeDIA1R   QEVIEAASRLKAILKPLRTCDPRYAYRYPDCKYSDRY
OanatDIA1R   QTVIGGARRLMDILKSLRTCDARFAYRYPDCKYSEKY
GgallDIA1R   QDVNEAMAKLAQLLKPLRSCDSRFAYRYPDCKYSDKY
SsalaDIA1R   WRIMAAVGSLMDLLKPMRPCNPHYTYRYPECRYNQDY
DreriDIA1R   QTIIKSVQSLKNILKTLRPCSPQYAYRYPECLYSDKF
               :  .   *  :*:.:*.*..:::****:* *.: :
Consensus    QEVLGAASRLKDILRPLRTCDPRFAYRYPDCKYNDKF
```