Figure S3. PLA2R CTLD domain alignment against CTLD1

CTLD1-CTLD1

Score	Expect	Method	Identities	Positives	Gaps
247 bits(630)	1e-91	Compositional matrix adjust.	118/118(100%)	118/118(100%)	0/118(0%)

```
CTLD1   1    NSHICYQFNLLSSLSWSEAHSSCQMQGGTLLSITDETEENFIREHMSSKTVEVWMGLNQL  60
             NSHICYQFNLLSSLSWSEAHSSCQMQGGTLLSITDETEENFIREHMSSKTVEVWMGLNQL
CTLD1   1    NSHICYQFNLLSSLSWSEAHSSCQMQGGTLLSITDETEENFIREHMSSKTVEVWMGLNQL  60

CTLD1   61   DEHAGWQWSDGTPLNYLNWSPEVNFEPFVEDHCGTFSSFMPSAWRSRDCESTLPYICK  118
             DEHAGWQWSDGTPLNYLNWSPEVNFEPFVEDHCGTFSSFMPSAWRSRDCESTLPYICK
CTLD1   61   DEHAGWQWSDGTPLNYLNWSPEVNFEPFVEDHCGTFSSFMPSAWRSRDCESTLPYICK  118
```

CTLD1-CTLD2

Score	Expect	Method	Identities	Positives	Gaps
45.8 bits(107)	2e-12	Compositional matrix adjust.	32/116(28%)	53/116(45%)	4/116(3%)

```
CTLD1   5    CYQFNLLSSLSWSEAHSSCQMQGGTLLSITDETEENFIREHMSSKTV-EVWMGLNQLDEH  63
             CY+       +W EA  SCQ     L+ IT   E  F+   +  +   E W+GL+
CTLD2   5    CYKLQK-EEKTWHEALRSCQADNSALIDITSLAEVEFLVTLLGDENASETWIGLSSNKIP  63

CTLD1   64   AGWQWSDGTPLNYLNW-SPEVNFEPFVEDHCGTFSSFMPSAWRSRDCESTLPYICK  118
               ++WS+ + + + NW + E +  P     C + +      W+ ++CE  L YICK
CTLD2   64   VSFEWSNDSSVIFTNWHTLEPHIFPNRSQLCVS-AEQSEGHWKVKNCEERLFYICK  118
```

CTLD1-CTLD3: No alignment

CTLD1-CTLD4

Score	Expect	Method	Identities	Positives	Gaps
43.1 bits(100)	2e-11	Compositional matrix adjust.	26/73(36%)	39/73(53%)	7/73(9%)

```
CTLD1   9    NLLSSLSWSEAHSSCQMQGGTLLSITDETEENFIREHMSSK-----TVEVWMGLNQLDE-  62
              +L   +W EA + C+  G  L S     EENF+ E + SK       + W+G N+ +
CTLD4   13   KVLMKRTWREAEAFCEEFGAHLASFAHIEEENFVNELLHSKFNWTEERQFWIGFNKRNPL  72

CTLD1   63   HAG-WQWSDGTPL  74
             +AG W+WSD TP+
CTLD4   73   NAGSWEWSDRTPV  85
```

CTLD1-CTLD5

Score	Expect	Method	Identities	Positives	Gaps
45.8 bits(107)	3e-12	Compositional matrix adjust.	36/119(30%)	54/119(45%)	10/119(8%)

```
CTLD1   6    YQFNLLSSLSWSEAHSSCQMQGGTLLSITDETEENFIR---EHMSSKTVEVWMGLNQLDE  62
             Y F+  +S  W      C      LL+I    E+ FI    + +S      W+GL +
CTLD5   6    YLFHTFAS-EWLNFEFVCSWLHSDLLTIHSAHEQEFIHSKIKALSKYGASWWIGLQEERA  64

CTLD1   63   HAGWQWSDGTPLNYLNWSPEVNFEPFVEDH---CGTFSSFMPSAWRSRDCESTLPYICK  118
             +  ++W DGTP+ Y NW  +   E  V +    CG  SS +   W S +C  ++P ICK
CTLD5   65   NDEFRWRDGTPVIYQNW--DTGRERTVNNQSQRCGFISS-ITGLWGSEECSVSMPSICK  120
```

CTLD1-CTLD6

Score	Expect	Method	Identities	Positives	Gaps
53.9 bits(128)	3e-15	Compositional matrix adjust.	26/67(39%)	38/67(56%)	3/67(4%)

```
CTLD1   15  SWSEAHSSCQMQGGTLLSITDETEENFIREHMSSKTVEVWMGLNQLDEHAGWQWSDGTPL  74
            +W+ A   C  +GGTL++I  E E+ FI  ++  +T  VW+GL   D      W +G P+
CTLD6   19  NWTHAQHFCAEEGGTLVAIESEVEQAFITMNLFGQTTSVWIGLQNDDYET---WLNGKPV  75

CTLD1   75  NYLNWSP  81
             Y NWSP
CTLD6   76  VYSNWSP  82
```

CTLD1-CTLD7

Score	Expect	Method	Identities	Positives	Gaps
45.4 bits(106)	3e-12	Compositional matrix adjust.	30/103(29%)	47/103(45%)	5/103(4%)

```
CTLD1   12  SSLSWSEAHSSCQMQGGTLLSITDETEENFIREHMSSKTVEVWMGLNQLDEHAGWQWSDG  71
            ++++W  A  +C M    L+SITD+  ++F+   ++      W+GL   D    + WSDG
CTLD7   11  ANMTWYAAIKTCLMHKAQLVSITDQYHQSFLTVVLNRLGYAHWIGLFTTDNGLNFDWSDG  70

CTLD1   72  TPLNYLNWSPEVNFEPFVEDHCGTFSSFMPSAWRSRDCESTLP  114
            T  ++  W  E   E  +   C    S     W S  CES L
CTLD7   71  TKSSFTFWKDE---ESSLLGDCVFADS--NGRWHSTACESFLQ  108
```

CTDL1-CTLD8

Score	Expect	Method	Identities	Positives	Gaps
56.6 bits(135)	2e-16	Compositional matrix adjust.	38/122(31%)	58/122(47%)	12/122(9%)

```
CTLD1   5   CYQFN-LLSSLSWSEAHSSCQMQGGTLLSITDETEENFIREHM---SSKTVEVWMGLNQL  60
            CY F+ +L S+S+  AH  C+ +G  LL+I DE E  F+ E +    S    VW+
CTLD8   5   CYSFSTVLDSMSFEAAHEFCKKEGSNLLTIKDEAENAFLLEELFAFGSSVQMVWLNAQFD  64

CTLD1   61  DEHAGWQWSDGTPLNYLNW---SPEVNFEPFVEDHCGTFSSFMPSA-WRSRDCESTLPYI  116
              +   +W DGTP +  NW    P+ ++  F   HC      +P   W+   C+    +I
CTLD1   65  GNNETIKWFDGTPTDQSNWGIRKPDTDY--FKPHHCVALR--IPEGLWQLSPCQEKKGFI  120

CTLD1   117 CK  118
            CK
CTLD1   121 CK  122
```

The PLA2R domains were aligned using the blast program.
https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome