Supplementary Information

```
1       ACAAGACCGAAGCAACACACAGACCTCTCGACAGCATACGTATTGCAGAGATGGAGCTCA
1                                                         M  E  L

61      GACTCAGGCCATATCAGGAGGAGGTGGTCCAGGCGGCTTTAAGAGGAGAGAACAGCATCA
4       R  L  R  P  Y  Q  E  E  V  V  Q  A  A  L  R  G  E  N  S  I

121     TCTGGCTGCCCACTGGTGGAGGAAAAACTCGTGCTGCGGTTTACGTCGCTGAGAAACATC
24      I  W  L  P  T  G  G  G  K  T  R  A  A  V  Y  V  A  E  K  H

181     TAGAGACCAAGGCCAATGCCAAAGTGGCAGTGCTCGTCAATAAGGTGCACCTGGTAGACC
44      L  E  T  K  A  N  A  K  V  A  V  L  V  N  K  V  H  L  V  D

241     AGCACTATATGAAAGAATTTGGCCATTACCTAAGGCACAAATACAGGATAAAGGCCATCA
64      Q  H  Y  M  K  E  F  G  H  Y  L  R  H  K  Y  R  I  K  A  I

301     GTGGTGACAGCAGTGAGAAAGACTTTTTTGGGCGTCTTGTTAGAGTCTCAGACTTGGTCA
84      S  G  D  S  S  E  K  D  F  F  G  R  L  V  R  V  S  D  L  V

361     TCTGCACGGCTCAGATTCTGGAAAACGCCTTGAACAACATGGATGAGGACAAGCACGTGG
104     I  C  T  A  Q  I  L  E  N  A  L  N  N  M  D  E  D  K  H  V

421     AGATCACTGATTTTACCCTACTGATCATAGATGAATGTCATCACACAAATAAGGAGAGTG
124     E  I  T  D  F  T  L  L  I  I  D  E  C  H  H  T  N  K  E  S

481     TCTATAACAAGATTATGTGGCGTTACGTGGAGAAGAAAGTGAGAAAAGAAGGCAGACTGC
144     V  Y  N  K  I  M  W  R  Y  V  E  K  K  V  R  K  E  G  R  L

541     CTCAGATTTTGGGCCTCACAGCATCACCTGGTACAGGAGGAAACAAGTCATTGGATAAAG
164     P  Q  I  L  G  L  T  A  S  P  G  T  G  G  N  K  S  L  D  K

601     CTGTTGAACACGTCCTGCAGATCTGTGCCAATCTGGATTCAAAAATTGTGTCCACCAAGA
184     A  V  E  H  V  L  Q  I  C  A  N  L  D  S  K  I  V  S  T  K

661     ATTACACACCGATGCTGCAGAACTTTGTGCCAAAACCCAAAAAGGAATACGACATTGTCG
204     N  Y  T  P  M  L  Q  N  F  V  P  K  P  K  K  E  Y  D  I  V

721     AAAGAAGAGATAAAGATCCATTTGGTGACCACTTGAAGTCAATGATGTTAATGATTCATG
224     E  R  R  D  K  D  P  F  G  D  H  L  K  S  M  M  L  M  I  H

781     AGTTTATGCCAGCAACGGTGGGTAGCAGCCTGAGAGAACTAGGCACCCAGGAATATGAGG
244     E  F  M  P  A  T  V  G  S  S  L  R  E  L  G  T  Q  E  Y  E

841     CTGATGTGGTGGAACTGGAGAAAGCAGGTGTAAAAGTAAAGAACAGACTGATCGCTCAGT
264     A  D  V  V  E  L  E  K  A  G  V  K  V  K  N  R  L  I  A  Q

901     GCGCTTTGCATCTACGCAAATACAATGATGCCCTTCTCATTAATGACACCATTCGCATGG
```

Figure S1. *Cont.*

```
284     C  A  L  H  L  R  K  Y  N  D  A  L  L  I  N  D  T  I  R  M

961     TGGATGCGTTCAGAGTGCTGGAAGAGTTTTACAATACAAGAAGCAGCAAGTTGCTGGATG
304     V  D  A  F  R  V  L  E  E  F  Y  N  T  R  S  S  K  L  L  D

1021    GAACAGACATCTTTCTACAAGGACTTTTCGATGAGAACAGTCTGGAGTTAAAACATCTGG
324     G  T  D  I  F  L  Q  G  L  F  D  E  N  S  L  E  L  K  H  L

1081    CGTCGGACGCCCGATATGAAAACCCCAAACTAGCTCAACTGCAGAGCAGATTGCTGGAAG
344     A  S  D  A  R  Y  E  N  P  K  L  A  Q  L  Q  S  R  L  L  E

1141    AGTTCCAAGACACTAATTCTCGTGGAATCATCTTCTCAAAGACACGCAGAGGCACGCATT
364     E  F  Q  D  T  N  S  R  G  I  I  F  S  K  T  R  R  G  T  H

1201    GTCTGAATGACTGGGTGAAAACAAACCGTGAGCTGCAGAGGGTCAACATCACTGCTGGCA
384     C  L  N  D  W  V  K  T  N  R  E  L  Q  R  V  N  I  T  A  G

1261    TTCTGACCGGAGCCGGTAATGGCGCTAACAACATGACACAGACTGAACAGAAGAGCGTCA
404     I  L  T  G  A  G  N  G  A  N  N  M  T  Q  T  E  Q  K  S  V

1321    TCAGTCATTTTAGGCAAGGATACCTCAACCTCCTCATCTCCACCAGTGTAGCTGAGGAGG
424     I  S  H  F  R  Q  G  Y  L  N  L  L  I  S  T  S  V  A  E  E

1381    GACTGGATATTCCTGAATGCAACTTAGTTGTGCGTTACGGGCTGTTGACCAATGAAATCG
444     G  L  D  I  P  E  C  N  L  V  V  R  Y  G  L  L  T  N  E  I

1441    CTCAGCAGCAGGCCAGCGGACGAGCTCGAGCCTCCAACAGTGTCTACTCTGTGGTGGCTG
464     A  Q  Q  Q  A  S  G  R  A  R  A  S  N  S  V  Y  S  V  V  A

1501    ACGTAGGTGGACGGGAAGTGCGCAAAGAACTTGTCAATGAGTATCTAGAAGATCTCACCG
484     D  V  G  G  R  E  V  R  K  E  L  V  N  E  Y  L  E  D  L  T

1561    CAAGAGCTATTGATGAAGTACAGCGCATGAGTCCTGTGGACTTCAGACACAAGGTGTTTG
504     A  R  A  I  D  E  V  Q  R  M  S  P  V  D  F  R  H  K  V  F

1621    AGCTCCAGAAAACAGCTGTGGTGATTCGGATGGAGGCTGAACGGAAGAGGGATGCGAAAA
524     E  L  Q  K  T  A  V  V  I  R  M  E  A  E  R  K  R  D  A  K

1681    AGCAGCGCTATAGTCCAGGTCAGGTTCAGCTTCAGTGCAGAAGCTGCTTCGCTTCCGTCT
544     K  Q  R  Y  S  P  G  Q  V  Q  L  Q  C  R  S  C  F  A  S  V

1741    GCAGCGGAGGAGACATCAGGAAGATCGAGAACTCGCACCATGTCAACGTTAACACTGAGT
564     C  S  G  G  D  I  R  K  I  E  N  S  H  H  V  N  V  N  T  E

1801    TTAAAAATCACTATAAAGTTGGTGGCCAGGTGAATATGGAGAGGACCTTTGAAGACTGGG
584     F  K  N  H  Y  K  V  G  G  Q  V  N  M  E  R  T  F  E  D  W
```

Figure S1. *Cont.*

```
1861        AGCCTGGACGGATTATCAGCTGCAGACGTTGTGGAGAGGACTGGGGATTCGAGATTAAAT
604         E  P  G  R  I  I  S  C  R  R  C  G  E  D  W  G  F  E  I  K

1921        TCAAGAAAGTGGCAATTCTCCCCTGTCTGAACATAAAGAGCTTCTCCTTTAACACCCCTA
624         F  K  K  V  A  I  L  P  C  L  N  I  K  S  F  S  F  N  T  P

1981        AAGAAACAAAGCCTTACAAGAAGTGGAAGGATGTTGAGTTTCAGGTGACAGAGTTTGACT
644         K  E  T  K  P  Y  K  K  W  K  D  V  E  F  Q  V  T  E  F  D

2041        TTATTGAGTACATGAGCTGCCGTTTCCCTGACCTGGACTTGTCTGACTGATACAGCTCCA
664         F  I  E  Y  M  S  C  R  F  P  D  L  D  L  S  D  *

2101        TACCACTGATTTAATTGAAATATGAAATAATACATATTCTGATTATGTTAATGCTCCGTC
2161        TTGGGTCTTCATGCATGTTGGTGACAGTAGTAGAAGCAGATAGATGGTTTTATTCAAAAC
2221        TAGGGCTGTCAATTGATTTAAAAAATTAACTAAGTAATCACAGTTTTTTGTAATTAATCA
2281        TAATTAATCATGGAATGCCATGTTTATTACAGAAATAGAAACACAGGCATGTAAGTGCCA
2341        TTTGAATTTCAAAATAATCAATGCCAATAACAAACAAAAACATTTCCATGTTGGATTCTA
2401        ATTGGACTACAAAAAAATCCAAAATACAGGCATTGCAAATATAGAAAAAAAAAAAAAAAA
2461        AAAAAAAAAAAAA
```

Figure S1. Nucleotide and deduced amino acid sequences of DrLGP2a from *Danio rerio*. The start codon (ATG) was shown by underline. The termination code (TAG) was marked with an asterisk below. The motif associated with mRNA instability (ATTTA) was in bold underline. Shadow said DEXDc (DEAD/DEAH box helicase domain), double underline said HELICc, the box said RD (regulatory domin).

```
1           ACAAGACCGAAGCAACACACAGACCTCTCGACAGCATACGTATTGCAGAGATGGAGCTCA
1                                                            M  E  L

61          GACTCAGGCCATATCAGGAGGAGGTGGTCCAGGCGGCTTTAAGAGGAGAGAACAGCATCA
4           R  L  R  P  Y  Q  E  E  V  V  Q  A  A  L  R  G  E  N  S  I

121         TCTGGCTGCCCACTGGTGGAGGAAAAACTCGTGCTGCGGTTTACGTCGCTGAGAAACATC
24          I  W  L  P  T  G  G  G  K  T  R  A  A  V  Y  V  A  E  K  H

181         TAGAGACCAAGGCCAATGCCAAAGTGGCAGTGCTCGTCAATAAGGTGCACCTGGTAGACC
44          L  E  T  K  A  N  A  K  V  A  V  L  V  N  K  V  H  L  V  D

241         AGCACTATATGAAAGAATTTGGCCATTACCTAAGGCACAAATACAGGATAAAGGCCATCA
64          Q  H  Y  M  K  E  F  G  H  Y  L  R  H  K  Y  R  I  K  A  I

301         GTGGTGACAGCAGTGAGAAAGACTTTTTTGGGCGTCTTGTTAGAGTCTCAGACTTGGTCA
84          S  G  D  S  S  E  K  D  F  F  G  R  L  V  R  V  S  D  L  V

361         TCTGCACGGCTCAGATTCTGGAAAACGCCTTGAACAACATGGATGAGGACAAGCACGTGG
104         I  C  T  A  Q  I  L  E  N  A  L  N  N  M  D  E  D  K  H  V
```

Figure S2. *Cont.*

```
421     AGATCACTGATTTTACCCTACTGATCATAGATGAATGTCATCACACAAATAAGGAGAGTG
124     E  I  T  D  F  T  L  L  I  I  D  E  C  H  H  T  N  K  E  S

481     TCTATAACAAGATTATGTGGCGTTACGTGGAGAAGAAAGTGAGAAAAGAAGGCAGACTGC
144     V  Y  N  K  I  M  W  R  Y  V  E  K  K  V  R  K  E  G  R  L

541     CTCAGATTTTGGGCCTCACAGCATCACCTGGTACAGGAGGAAACAAGTCATTGGATAAAG
164     P  Q  I  L  G  L  T  A  S  P  G  T  G  G  N  K  S  L  D  K

601     CTGTTGAACACGTCCTGCAGATCTGTGCCAATCTGGATTCAAAAATTGTGTCCACCAAGA
184     A  V  E  H  V  L  Q  I  C  A  N  L  D  S  K  I  V  S  T  K

661     ATTACACACCGATGCTGCAGAACTTTGTGCCAAAACCCAAAAAGGAATACGACATTGTCG
204     N  Y  T  P  M  L  Q  N  F  V  P  K  P  K  K  E  Y  D  I  V

721     AAAGAAGAGATAAAGATCCATTTGGTGACCACTTGAAGTCAATGATGTTAATGATTCATG
224     E  R  R  D  K  D  P  F  G  D  H  L  K  S  M  M  L  M  I  H

781     AGTTTATGCCAGCAACGGTGGGTAGCAGCCTGAGAGAACTAGGCACCCAGGAATATGAGG
244     E  F  M  P  A  T  V  G  S  S  L  R  E  L  G  T  Q  E  Y  E

841     CTGATGTGGTGGAACTGGAGAAAGCAGGTGTAAAAGTAAAGAACAGACTGATCGCTCAGT
264     A  D  V  V  E  L  E  K  A  G  V  K  V  K  N  R  L  I  A  Q

901     GCGCTTTGCATCTACGCAAATACAATGATGCCCTTCTCATTAATGACACCATTCGCATGG
284     C  A  L  H  L  R  K  Y  N  D  A  L  L  I  N  D  T  I  R  M

961     TGGATGCGTTCAGAGTGCTGGAAGAGTTTTACAATACAAGAAGCAGCAAGTTGCTGGATG
304     V  D  A  F  R  V  L  E  E  F  Y  N  T  R  S  S  K  L  L  D

1021    GAACAGACATCTTTCTACAAGGACTTTTCGATGAGAACAGTCTGGAGTTAAAACATCTGG
324     G  T  D  I  F  L  Q  G  L  F  D  E  N  S  L  E  L  K  H  L

1081    CGTCGGACGCCCGATATGAAAACCCCAAACTAGCTCAACTGCAGAGCAGATTGCTGGAAG
344     A  S  D  A  R  Y  E  N  P  K  L  A  Q  L  Q  S  R  L  L  E

1141    AGTTCCAAGACACTAATTCTCGTGGAATCATCTTCTCAAAGACACGCAGAGGCACGCATT
364     E  F  Q  D  T  N  S  R  G  I  I  F  S  K  T  R  R  G  T  H

1201    GTCTGAATGACTGGGTGAAAACAAACCGTGAGCTGCAGAGGGTCAACATCACTGCTGGCA
384     C  L  N  D  W  V  K  T  N  R  E  L  Q  R  V  N  I  T  A  G

1261    TTCTGACCGGAGCCGGTAATGGCGCTAACAACATGACACAGACTGAACAGAAGAGCGTCA
404     I  L  T  G  A  G  N  G  A  N  N  M  T  Q  T  E  Q  K  S  V

1321    TCAGTCATTTTAGGCAAGGATACCTCAACCTCCTCATCTCCACCAGTGTAGCTGAGGAGG
```

Figure S2. *Cont.*

```
424     I S H F R Q G Y L N L L I S T S V A E E

1381    GACTGGATATTCCTGAATGCAACTTAGTTGTGCGTTACGGGCTGTTGACCAATGAAATCG
444     G L D I P E C N L V V R Y G L L T N E I

1441    CTCAGCAGCAGGCCAGCGGACGAGCTCGAGCCTCCAACAGTGTCTACTCTGTGGTGGCTG
464     A Q Q Q A S G R A R A S N S V Y S V V A

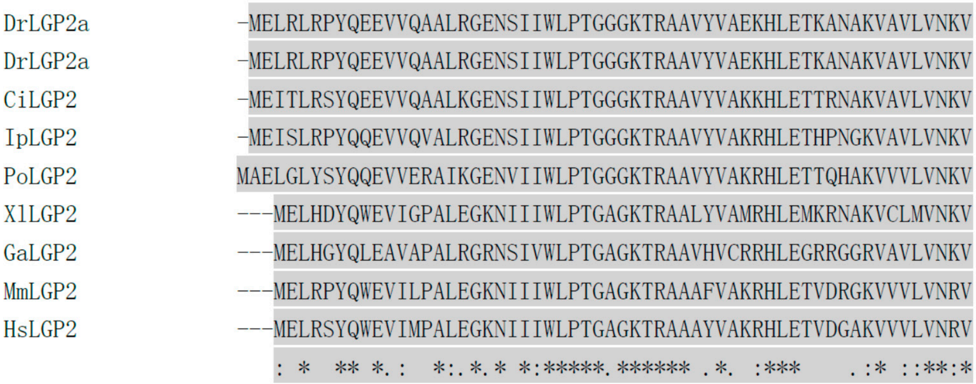
1501    ACGTAGGTGGACGGGAAGTGCGCAAAGAACTTGTCAATGAGTATCTAGAAGATCTCACCG
484     D V G G R E V R K E L V N E Y L E D L T

1561    CAAGAGCTATTGATGAAGTACAGCGCATGAGTCCTGTGGACTTCAGACACGAGGTTTGTG
504     A R A I D E V Q R M S P V D F R H E V C

1621    TTTGACTTTTTACTATTAAATCTGACTGTGTTTGTAATAGAATAGAAAAACTTAAAAGGA
524     V *

1681    CAATTCACCTAGACTTCACAATTCTGTCATCATTTACCCAAACATGAGTTTCTTTCTTCT
1741    GTTGAACACAAAAAGAAGTTACTTTTGAATAGTGTTGGAAGCCTGTAACCATTGACTTCC
1801    ATAGTATTTGTTTTTTCTACCATTTAAGTCGGTGGTTACCGGTTTCTAACATACTTCAGA
1861    ATATCCATTTTGTGTTTAACAGAAAAGAGAAACTTCTTAAGGTTTGGAATCACGTGAGTA
1921    AACAGTGAGTACATTTTCATTTTTGAGTAAACTATATTTTTAAAGGTGTTTCACATACGA
1981    AATCTACTGTAAGTCTGTTGACAGATTAGAGTTCTTTGTTAGTATTGCTCCCCAAGTCTA
2041    GGCGAAAACAACATGGGCATAATAAACAAAGAAAACAAATGTGTTAGGGTGGTGGATTTC
2101    CCAAACAAAACAAAAACTTAATGCAAAAGATCCCTTTCGGTCGACAACCAAACTCGGACA
2161    CTCAGTTGAGAGTATTTAAATAGATTTATTATAGGAAAAAGTAGTAAATATAAATGAGCA
2221    TCCCTTCAGGATCTCCACAGGCCAAAAAAAAAAAAAAAAAAAAAA
```

Figure S2. Nucleotide and deduced amino acid sequences of DrLGP2b from *Danio rerio*. The start codon (ATG) was shown by underline. The termination code (TAG) was marked with an asterisk. The typical polyadenylation signal AATAAA was bolded. The motif associated with mRNA instability (ATTTA) was in bold underline. Shadow said DEXDc (DEAD/DEAH box helicase domain), double underline said HELICc domain structure.



```
DrLGP2a     -MELRLRPYQEEVVQAALRGENSIIWLPTGGGKTRAAVYVAEKHLETKANAKVAVLVNKV
DrLGP2a     -MELRLRPYQEEVVQAALRGENSIIWLPTGGGKTRAAVYVAEKHLETKANAKVAVLVNKV
CiLGP2      -MEITLRSYQEEVVQAALKGENSIIWLPTGGGKTRAAVYVAKKHLETTRNAKVAVLVNKV
IpLGP2      -MEISLRPYQQEVVQVALRGENSIIWLPTGGGKTRAAVYVAKRHLETHPNGKVAVLVNKV
PoLGP2      MAELGLYSYQQEVVERAIKGENVIIWLPTGGGKTRAAVYVAKRHLETTQHAKVVVLVNKV
XlLGP2      ---MELHDYQWEVIGPALEGKNIIIWLPTGAGKTRAALYVAMRHLEMKRNAKVCLMVNKV
GaLGP2      ---MELHGYQLEAVAPALRGRNSIVWLPTGAGKTRAAVHVCRRHLEGRRGGRVAVLVNKV
MmLGP2      ---MELRPYQWEVILPALEGKNIIIWLPTGAGKTRAAAFVAKRHLETVDRGKVVVLVNRV
HsLGP2      ---MELRSYQWEVIMPALEGKNIIIWLPTGAGKTRAAAYVAKRHLETVDGAKVVVLVNRV
               : *  ** *.:  *:.*.* *:*****.****** .*. :***    .:* ::**:*
```

Figure S3. *Cont.*

```
DrLGP2a         HLVDQHYMKEFGHYLRHKYRIKAISGDSSEKDFFGRLVRVSDLVICTAQILENALNNMDE
DrLGP2b         HLVDQHYMKEFGHYLRHKYRIKAISGDSSEKDFFGRLVRVSDLVICTAQILENALNNMDE
CiLGP2          HLVDQHFNNEFNPYLGKAYRVKAISGDSSDKDLFGRLVKDSDLIICTAQILENALNSSEE
IpLGP2          HLVDQHFQKEFRPHLGSSVKMVPISGDSNEKDFFGCVVRDSSLVICTAQILENALINTEE
PoLGP2          HLVDQHYTKEFKPHLGSNYTLVPVSGESELKDLFGKVVQDSDVVICTAQILYNALTNSEE
XlLGP2          HLVDQHFSNEFHPHLKDKYKVVAISGDTEHKCFFAELVQNNDVIICTAQILQNALSSSSE
GaLGP2          HLVQQHLEKEFH-VLRDAFKVTAVSGDSSHKCFFGQLAKGSDVVICTAQILQNALLSGEE
MmLGP2          HLVSQHAE-EFRRMLDKHWTVTTLSGDMGSRAGFGLMARSHDLLICTAELLQLALNSSEE
HsLGP2          HLVTQHGE-EFRRMLDGRWTVTTLSGDMGPRAGFGHLARCHDLLICTAELLQMALTSPEE
                *** **   **   *     : .:**:   :  *. :.:  .::****::*  ** . .*

DrLGP2a         DKHVEITDFTLLIIDECHHTNKESVYNKIMWRYVEKKVRKEGRLPQILGLTASPGTGGNK
DrLGP2b         DKHVEITDFTLLIIDECHHTNKESVYNKIMWRYVEKKVRKEGRLPQILGLTASPGTGGNK
CiLGP2          EKHVELTDFSLLIIDECHHTQKESVYNKIMGRYVEKKVRKERKLPQVLGLTASPGTGGNK
IpLGP2          SKHVELTDFTLLIIDECHHTHKEGVYNKIMARYVRKKIERVKGLPQILGLTASPGTGGAK
PoLGP2          TKHVELSDITLLIFDECHHTHKGGVYNQIMKCYVEKKLKGERRLPQILGLTASPGTGGAR
XlLGP2          EIHVELTDFTLLIIDECHHTHKDGVYNKLMEGYLERKITQKGKLPQILGLTASPGTGRAT
GaLGP2          EARVELTDFSLLVIDECHHTQKEAVYNKIMLSYLQKKLSGQRDLPQILGLTASPGTGGET
MmLGP2          DEHVELREFSLIVVDECHHTHKDTVYNTILSRYLEQKLKKAEPLPQVLGLTASPGTGGAT
HsLGP2          EEHVELTVFSLIVVDECHHTHKDTVYNVIMSQYLELKLQRAQPLPQVLGLTASPGTGGAS
                  :**:  ::*::.******:*  *** ::  *:. *:     ***:**********

DrLGP2a         SLDKAVEHVLQICANLDS-KIVSTKNYTPMLQNFVPKPKKEYDIVERRDKDPFGDHLKSM
DrLGP2b         SLDKAVEHVLQICANLDS-KIVSTKNYTPMLQNFVPKPKKEYDIVERRDKDPFGDHLKSM
CiLGP2          TLAKAVEHVLQICANLDS-VIVSTKNYASKLKEVVPRPRKQYDIVEKRALDPFGDHLKLM
IpLGP2          SLDGAITHVLEICANLDS-VIVSTKNYEAELKEAVPRPMKNYDIVDERYWDPFGDHLKMM
PoLGP2          ILEKAVEHVLQICANLDS-SIVSTRLYAPELKKKVPRPIKTFDIVENRPEDPFGNHLKRM
XlLGP2          SFEKAEEHILQICANLDTWRIMSAEVHREDLEAKAKQPNKQYDLVTERPRDPFGDKLKEL
GaLGP2          SFEGAVEHILQICANLDTEVIASAQEHAQHLQSHVPQPTKQYDLCQEREQDPFGQRLKKI
MmLGP2          KLQGAIDHILQLCANLDTCHIMSPKNCYSQLLMHNPKPCKQYDLCQRRAQDPFGDLIKKL
HsLGP2          KLDGAINHVLQLCANLDTWCIMSPQNCCPQLQEHSQQPCKQYNLCHRRSQDPFGDLLKKL
                 :  *  *:*::*****:  * *..     *     :* * :::  .*  ****: :* :

DrLGP2a         MLMIHEFMPATVG-SSLRELGTQEYEADVVELEKAGVKVKNRLIAQCALHLRKYNDALLI
DrLGP2b         MLMIHEFMPATVG-SSLRELGTQEYEADVVELEKAGVKVKNRLIAQCALHLRKYNDALLI
CiLGP2          MSLIHEFMPSTVS-RSLREVGTQDYEADVVELEKTGVKEENRLITQCALHLRQYNDALLI
IpLGP2          MKLIHEFMMLDRK-FTLREMGTQEYEADVVELEKKGVQEQNRLLARCALHLRKFNDALLI
PoLGP2          MQMIQDYMNLPTSDFRLRECGTQEYEADVVILEQRGIREDNRRLAQCALHLRQYNDALLI
XlLGP2          MKTIHEYLRTTDF--CESDFGTQLYEQKVVELEKEGAVEANRMKRTCALHLRKYNDSLLV
GaLGP2          MAQIQEHMEMPEL--PQN-FGTQVYEQRIVELENRAAERFCRKTRVCALHLRRYNDALLI
MmLGP2          MNQIHQQLEMPDL--KQQ-FGTQMYEQQVVQLCKDAAEAGLQEQRVYALHLRRYNDALFI
HsLGP2          MDQIHDHLEMPEL--SRK-FGTQMYEQQVVKLSEAAALAGLQEQRVYALHLRRYNDALLI
                *  *:: :            *** **  :* * : .     :     *****::**:*::

DrLGP2a         NDTIRMVDAFRVLEEFYNTR--SSKLLDGTDIFLQGLFDENSLELKHLASDARYENPKLA
DrLGP2b         NDTIRMVDAFRVLEEFYNTR--SSKLLDGTDIFLQGLFDENSLELKHLASDARYENPKLA
```

Figure S3. *Cont.*

```
CiLGP2          HDTVRMVDAFNVLDEFYNSR--SNKLLDGTDFFLQGLFDENRVELKQLALDARYENPKLA
IpLGP2          NDTVRMVDALRLLEEFYTTE--TRNVLDITDEFLTGLFNENKVELLQLASEASNENPKLE
PoLGP2          NDTLLMMDAYRNLEEFYISK--STRAIDKTDFFLVGIFQDNQADLMKVARDSRYENPKMA
XlLGP2          HDTVRMMDAYELLDDYYQQEKVIRKQNDPTDAFLIQLFDGNRARLLELAQDVRFENPKLR
Gallus          NDTVRMMDAFQCLQQFYADK---RDTKDPTERFLATTFEENRATLQALAGDQRYENPRLS
MmLGP2          HDTVRARDALDMLQDFYDRERTTKTQMVRAESWLLKLFDDHKNVLGQLAAR-GPENPKLE
HsLGP2          HDTVRAVDALAALQDFYHREHVTKTQILCAERRLLALFDDRKNELAHLATH-GPENPKLE
                :**:   **   *:::*  .         ::  *   *: .   *  :*     ***::

DrLGP2a         QLQSRLLEEFQDT-NSRGIIFSKTRRGTHCLNDWVKTNRELQRVNITAGILTGAG--NGA
DrLGP2b         QLQSRLLEEFQDT-NSRGIIFSKTRRGTHCLNDWVKTNRELQRVNITAGILTGAG--NGA
CiLGP2          QLQRTLLKEFKENKMSRGIIFSKTRRGTHCLYDWVNANHELQKVKISAGILTGTG--TGV
IpLGP2          RLQRTLVDQFKDE-NSRGIIFAKTREITRCLYDWVRTNPELRRANIRAANLVGAG--TGA
PoLGP2          KLESVLLKQFSSGLQSKGILFSKTRKSIHCLNEWVLNNRALQEAGVKSAILTGAG--NGI
XlLGP2          KLEEILRDQFQFSSGSRGIIFTRTRQSTHSLHNWISSKHSFQIMGVKTAPLTGAGYSNQS
GaLGP2          KLEEILQEHFQPPGSSRGIVFTKTRQSAHSLLSWLQDTAGLCGQHIRAAVLTGSGHSNQA
MmLGP2          MLERILLKQFGSPGHTRGIIFTRTRQTASSLLLWLRQQPCLQTVGIKPQMLIGAGNTSQS
HsLGP2          MLEKILQRQFSSSNSPRGIIFTRTRQSAHSLLLWLQQQQGLQTVDIRAQLLIGAGNSSQS
                 *:  *  .*     .:**:*::**.   .*  *:     :    : .  * *:*  .

DrLGP2a         NNMTQTEQKSVISHFRQGYLNLLISTSVAEEGLDIPECNLVVRYGLLTNEIAQQQASGRA
DrLGP2b         NNMTQTEQKSVISHFRQGYLNLLISTSVAEEGLDIPECNLVVRYGLLTNEIAQQQASGRA
CiLGP2          NHMNQNKQKNTIKDFRLGHLNLLISTSVAEEGLDIAECNLVVRYGLLTNEIAQQQASGRA
IpLGP2          THMTQREQRDTIKTFREGELNLLISTSVAEEGLDIPECNVVIRYGLLTNEIAQQQASGRA
PoLGP2          TYMTQHEQADTICRFRQGTLNLLISTSVAEEGLDIPECNLVVRYGLLTNEIAQQQASGRA
XlLGP2          KHMTQNEQRETIEMFRKGQLNLLISTSVAEEGLDIPQCNIVVRYGLMTNEISMVQARGRA
GaLGP2          KGMTQNEQQDVITLFRYGELNLLFSTSVAEEGLDIPECNIVVRYGLMTNEIAMVQAQGRA
MmLGP2          THMTQKDQQEVIQEFRDGILSLLVATSVAEEGLDIAQCNVVVRYGLLTNEISMVQARGRA
HsLGP2          THMTQRDQQEVIQKFQDGTLNLLVATSVAEEGLDIPHCNVVVRYGLLTNEISMVQARGRA
                . *.* .* ..*  *: * *.**.:**********..**:*:****:****:  ** ***

DrLGP2a         RASNSVYSVVADVGGREVRKELVNEYLEDLTARAIDEVQRMSPVDFRHKVFELQKTAVVI
DrLGP2b         RASNSVYSVVADVGGREVRKELVNEYLEDLTARAIDEVQRMSPVDFRHEVCV--------
CiLGP2          RALNSVYSVVAEKGGRELRREFTNEYLESLTSNAIDQVQSMSPREFRIKITELQQMAVLI
IpLGP2          RAKNSVYSVVAKAGGREMRKEKTNEYLEELTSKAIAHVQSMEPGRFRQKIFELQHEAVTA
PoLGP2          RAQDSQYSVVALKGGREERREITNEYLEELTAKAIAQVQDMSIREFQRKITELQTQAVIK
XlLGP2          RHEDSCYSFLAKIGGKEIRREETNETLEGLMKRAIEAVQRMPEQEYQKKIKELQEESVIA
GaLGP2          RAQNSMYSVLAKANSREVYREQLNESLVGLMERAIRAVQAMPERKYRLKIVELQRNAVLS
MmLGP2          RAGQSVYSFLATEGSREMKRELTNEALEVLMEKAVAAVQKMDPDEFKAKIRDLQQASLVK
HsLGP2          RADQSVYAFVATEGSRELKRELINEALETLMEQAVAAVQKMDQAEYQAKIRDLQQAALTK
                *  :* *:.:*  ..:*  :*  ** *  *  .*:  ** *    :: ::

DrLGP2a         RMEAERKRDAKKQRYSPGQVQLQCRSCFASVCSGGDIRKIENSHHVNVNTEFKNHYKVG-
DrLGP2b         ------------------------------------------------------------
CiLGP2          RIEAERKKDARKQRYSPDQVHLQCRGCFVFVGLGEDIRKIENSHHVNINPEFQRHYRTG-
IpLGP2          RILMANQRERRRLRYDAAEVEFDCRGCFTAVARGDDMRLVNDTQHININPDFERFYKVG-
PoLGP2          SRIEESCKMQKRSRYTASSIQLLCRNCFKSVASGSDIKLIDNVHHVNVNPAFEKHYKVG-
```

Figure S3. *Cont.*

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XlLGP2          RKVKQAKRDQKRNTFYPEQVRFYCRCCSQAVAHGDDFRTIEGTHYVNINSDFRIYYEVCS
GaLGP2          WQVKEARSSERRQLHDPDDVYFHCVNCNVAVCRGSDIRTVEAMHHVNINPNFRFYYTVSS
MmLGP2          RAARAAHREIQQGQFLPEHVQLLCINCMVAVGYGSDLRKVEGTHHVNVNPNFSVYYTTSQ
HsLGP2          RAAQAAQRENQRQQFPVEHVQLLCINCMVAVGHGSDLRKVEGTHHVNVNPNFSNYYNVSR

DrLGP2a         GQVNMERTFEDWEPGRIISCR--RCGEDWGFEIKFKKVAILPCLNIKSFSFNTPKETKPY
DrLGP2b         ------------------------------------------------------------
CiLGP2          KQVFLEKTFEDWEPGQVINCR--KCGKDWGMEIKFKKVAILPCLNIKSFSLDTPGGKFTH
IpLGP2          GQVYLERTFEDWEPGRTISCV--ACGQNWGMEVKLKN-LVLPCLNIKGFSMKTRQSSRTA
PoLGP2          GQVILPKMFDDWEPGRIISCNNGNCNKEWGFEMKYKEIALLPNLAIKHLFLQTPDGRMTV
XlLGP2          PPLDFGKKMVDWTPGGKIRC---LCGQDWGFEMIYKH-VNFPAISVKNFVVETPEIKRPY
GaLGP2          GKIHFERTFRDWEPGCRIVCS--ECRQEWGMEMIYRN-VTLPILSIKNFVVVTPDEKKKY
MmLGP2          NPVVINKVFKDWRPGGTIRCS--NCGEVWGFQMIYKS-VTLPVLKIGSMLLETPRGKIQA
HsLGP2          DPVVINKVFKDWKPGGVISCR--NCGEVWGLQMIYKS-VKLPVLKVRSMLLETPQGRIQA

DrLGP2a         KKWKDVEFQVTEFDFIEYMSCRFPDLDLSD-
DrLGP2b         -------------------------------
CiLGP2          KQWKDVEFQVTEFDFIDYMSSRFPDLDLDD-
IpLGP2          KQWKDIEFLVEEFDFVQYVKNRYPDLEQD--
PoLGP2          KKWKDVPFTVDNFSFEEYCQDNFPDLLD---
XlLGP2          ARWKDVPFPVDELNYVQHVRIHPELLVHFED
GaLGP2          KKWSTVTFPIEEFSYLEYCSSTQDESL----
MmLGP2          KKWSRVPFSIPVFDILQDCTQSLSELSLD--
HsLGP2          KKWSRVPFSVPDFDFLQHCAENLSDLSLD—
```

Figure S3. Multiple alignment of LGP2 using the Clustal X2 program. LGP2 are conserved in vertebrates. Identical amino acids among all sequences are indicated by asterisks whereas those with high or low similarity are indicated by “:” and “.” respectively. Marked conserved domains include the DEXDc (DEAD/DEAH box helicase domain) (Shadowed), the HELICc (bold underlined) and the RD (regulatory domin) (double underlined). CiLGP2 (*Ctenopharyngodon idella*, AFQ93565.1), Gg (*Gallus gallus*, AEK21509.1), HsLGP2 (*Homo sapiens*, NM_024119.2), IpLGP2 (*Ictaluruspunctatus*, AFS34610.1), MmLGP2 (*Mus musculus*, NM_030150.2), PoLGP2 (*Paralichthys olivaceus*, ADM18136.1), XlLGP2 (*Xenopus laevis*, NP_001085915.1).