Supplemental Table S1. Comparison of the amino acid sequences of GPIHBP1, SLURP1, and four Ly6E-like chicken proteins.

Alignment between Ly6E-like proteins and GPIHBP1

```
45170      MKTTPVI--------LLVAVLCVEQ------------------------------------------ 17
39585      MKALLVA--------LLVAVLCAEQ------------------------------------------ 17
41621      MKAFLLA--------VLAAVLCVER------------------------------------------ 17
43582      MKASLLV--------VLVIALCTES------------------------------------------ 17
hu GPIHBP1 MKALGAV--------LLALLLFGRPGR-GQTQQ-EEEEEDEDHGPDDYDEEDEDEVEEEETNRLPGG 57
pl GPIHBP1 MKALMTALLTALLTALLTALFCAAQGVVGKEVGPDRPETEDGEEEEDYDDEDL------EYEAPTDG 61
           **:            :*.  :

45170      --VYPFMCYVCQQQESNKDCLTISMCAKEDKYCVTVRDNVGTNPDKPKYVISKMCSPTCNATSQQQN 82
39585      --ASSLFCYTCENEHSNWNCLKTYKCEDHEKYCTTTYSAAGFGKD-MGYRITKKCSADCPETNTDFG 81
41621      --AHTLICFSCSDASSNWACLTPVKCAENEEHCVTTYVGVGIGGK-SGQSISKGCSPVCPSAGINLG 81
43582      --AFSLRCFSCKDAPSNIHCFSTTTCADHEKYCLTTYSTKGLGDD-RQQSITKKCAAFCPSIDLNIG 81
hu GPIHBP1 RSRVLLRCYTCKSLPRDERCNLTQNCS-HGQTCTTLIAHGNT-ESGLLTTHSTWCTDSCQPITKTVE 122
pl GPIHBP1 KRGGELRCYTCESQFSKEFCLNDTPCPSSSNYCKTLISSGLT-DSGHLTTYSMWCADFCEPLTKTVH 164
                : *: *..   .  *     *    : * *         .      :  *:  *

45170      QAHRNVSCCEKPLCN 97
39585      VVAISTKCCKTSLCN 96
41621      IAAASVYCCDSFLCN 96
43582      IAGLATSCCQTSLCN 96
hu GPIHBP1 GTQVTMTCCQSSLCN 137
pl GPIHBP1 GTFFMVSCCSSSLCG 179
            .     **.. **.
```

Alignment between Ly6E-like proteins and SLURP1

```
hu SLURP1  MASRWAVQLLLVAAWSMGCGEALKCYTCKEPMTSASCRTITRCKPEDTACMTTLVTVEAEYPFNQSP 67
45170      --MKTTPVILLVAVLCVEQVYPFMCYVCQQQESNKDCLTISMCAKEDKYCVTVRDNVGTNPD-KPKY 64
39585      --MKALLVALLVAVLCAEQASSLFCYTCENEHSNWNCLKTYKCEDHEKYCTTTYSAAGFGKD--MGY 63
41621      --MKAFLLAVLAAVLCVERAHTLICFSCSDASSNWACLTPVKCAENEEHCVTTYVGVGIGGK--SGQ 63
43582      --MKASLLVVLVIALCTESAFSLRCFSCKDAPSNIHCFSTTTCADHEKYCLTTYSTKGLGDD--RQQ 63
              :     :*. . .      : *: *.:  :.  * .   *  .:  * *.

hu SLURP1  VVTRSCSSSCVATDPDSIGAAHLIFCCFRDLCN 100
45170      VISKMCSPTCNATSQQQNQAHRNVSCCEKPLCN 97
39585      RITKKCSADCPETNTDFGVVAISTKCCKTSLCN 96
41621      SISKGCSPVCPSAGINLGIAAASVYCCDSFLCN 96
43582      SITKKCAAFCPSIDLNIGIAGLATSCCQTSLCN 96
            ::: *:  *   . :   .     **   ***
```

A conserved motif in GPIHBP1 and its absence in the Ly6E-like proteins

```
Opossum          YSAWCSDTCQ 131
Tasmanian devil  FSAWCSDTCK 114
Elephant         YTAWCADDCE 116
Hyrax            YTGWCTDECE 108
Platypus         YSMWCADFCE 120
Dolphin          YSGWCADTCQ 112
Sheep            YSGWCADTCQ 116
Kangaroo rat     YSMWCTDSCR 113
Shrew            YSAWCSDTCH 54
Guinea pig       YSMWCKDSCQ 114
Mouse            YSMWCTDTCQ 114
Rat              YSMWCTDTCQ 122
Hedgehog         YSAWCSDTCQ 109
Squirrel         YSMWCVDTCQ 123
Horse            YSAWCADMCQ 115
Dog              YSAWCADACK 114
Panda            YSAWCADACQ 115
Cat              YSTWCADTCQ 73
Ferret           YSVWCTDTCH 112
Lesser hdg tenrc FSTWCTDACE 55
Marmoset         HSTWCADSCQ 113
Macaque          HSAWCTDNCQ 115
Olive baboon     HSAWCTDNCQ 115
Vervet-AGM       HSAWCTDNCQ 117
Gibbon           HSTWCADSCQ 115
Chimpanzee       HSTWCTDSCQ 78
Orangutan        HSTWCADSCQ 115
Gorilla          HSTWCTDSCQ 115
Human            HSTWCTDSCQ 115
Bushbabby        YSMWCADSCK 119
Mouse-lemur      YSTWCADSCQ 110
                 .: ** * *.

45170            ISKMCSPTCN 76
39585            ITKKCSADCP 75
41621            ISKGCSPVCP 75
43582            ITKKCAAFCP 75
hu SLURP1        VTRSCSSSCV 78
```

Alignment between Ly6E-like proteins and GPIHBP1. CLUSTAL O (1.2.4) multiple amino acid sequence alignment showing little similarity (aside from the cysteine residues in the Ly6 structural motif) between ENSGALG00000041621, ENSGALG00000043582, ENSGALG00000039585, ENSGALG00000045170, human (hu) GPIHBP1, and platypus (pl) GPIHBP1. The residues comprising the acidic domain of GPIHBP1 are in *blue*; cysteine residues are in *green*.

Alignment between Ly6E-like proteins and SLURP1. CLUSTAL O (1.2.4) multiple amino acid sequence alignment showing little similarity (aside from the cysteine residues of the Ly6 structural motif) between ENSGALG00000041621, ENSGALG00000043582, ENSGALG00000039585, ENSGALG00000045170, and human SLURP1.

A conserved motif in GPIHBP1 and its absence in the Ly6E-like proteins. CLUSTAL O (1.2.4) multiple amino acid sequence alignment of GPIHBP1, revealing conservation of W109 (orange) and D112 (blue) in 31 mammalian species. These two residues are not found in the corresponding regions of ENSGALG00000041621, ENSGALG00000043582, ENSGALG00000039585, ENSGALG00000045170, and human SLURP1. * Conserved residue; : amino acids of similar properties; . amino acids with weakly similar properties. Lesser hdg tenrc, lesser hedgehog tenrec; vervet-AGM, African green monkey.

Supplemental Table S2. Amino acid sequence alignment of platypus GPIHBP1 against 14 chicken Ly6 proteins.

PSCA (ENSGALG00000045875); identity to GPIHBP1 = 27.0%

```
GPIHBP1  MKALMTALLTALLTALLTALFCAAQGVVGKEVGPDRPETEDGEEEEDYDDEDLEYEAPTDGKRGGELRCYTCESQFSKEFCLNDTPCPSSSNYCKTLISSGLTDSGHLTTYSMWCADFCE
120
PSCA     --------MKVFFILLLAAI--------------------------------------LCTDPGSSLQCYSCKTKLSNSNCQATMNCKENE-MCKTDVI---RVIGFFSIISKGCEASCQ
70
                 :..::  **:*:                                         . *..*:**:*::::*:. *     * ...  *** :       *.::  *  *   *:

GPIHBP1  PLTKTVHGTFFMVSCCSSSLCGADSLDRKEERDGAAAVAGGSLAALGASVLLGLLGAGL 179
PSCA     EDYQDFKVGNRNVSCCSTNLCNVNAAGSVRSSYGMA-------AGISASLLWTFLNNRL 122
            : .:     *****:.**..:: .  ..  * *       *.:.**:*  :*.  *
```

SLURP1 (ENSGALG00000046632); identity to GPIHBP1 = 26.8%

```
GPIHBP1  MKALMTALLTALLTALLTALFCAAQGVVGKEVGPDRPETEDGEEEEDYDDEDLEYEAPTD--------GKRGGELRCYTCESQFSKEFCLNDTPCPSSSNYCKTLISSGLTD---SGHLT
109
SLURP1   ------------------------------------------------------MKMPLVGLLLGLACIELAQSLQCYTCKEPTDISKCRTPTECPPKAKVCTTTLHSVDLGYPFFGNVT
66
                                                                : *           : . .*:****:.  . . * . * ** .:: *.* : *   .    *::*

GPIHBP1  TYSMWCADFCEPLTKTVHGTFFMVSCCSSSLCGADSLDRKEERDGAAAVAGGSLAALGASVLLGLLGAGL 179
SLURP1   -VTRSCEEECI--TYDGIGSNRPTSCCYTDLCSDDTKSSKGERSSSAALG--VMAMVFGTLLQGVL---- 127
           :  * : *   *    *:   .*** :.**. *: . * **..:**:.   :* : .::* *:*
```

LYPD2 (ENSGALG00000035166); identity to GPIHBP1 = 22.7%

```
GPIHBP1  MKALMTALLTALLTALLTALFCAAQGVVGKEVGPDRPETEDGEEEEDYDDEDLEYEAPTDGKRGGELRCYTCESQFSKEFCLNDTPCPSSSNYCKTLISSGL--TDSGHLTTYSMWCADF
118
LYPD2    ---------------------------------------MKTTWGSGWLATQIPIVIGNKGEVAQSLKCYTCHEPTASEKCMKIQKCAKNETMCKTTMYSLEEVYPFVGLSTVTKMCSSV
81
                                                 .    ..:   ::     ..*: . .*:****..  :.* *::   * .... *** : *         *:* :  *:..

GPIHBP1      CEPLTKTVHGTFFMVSCCSSSLCGADSLDRKEERDGAAAVAGGSLAALGASVLLGLLGAGL 179
LYPD2        CSPSDVDGIGMTRPVSCCYSNLCNIDGAASLRIKITFF--------PLLVWLILN------ 128
             *.*      *    **** *.**. *.    . :             * . ::*.
```

ENSGALG00000041621; identity to GPIHBP1 = 25.4%

```
GPIHBP1  MKALMTALLTALLTALLTALFCAAQGVVGKEVGPDRPETEDGEEEEDYDDEDLEYEAPTDGKRGGELRCYTCESQFSKEFCLNDTPCPSSSNYCKTLIS-SGLTDSGHLTTYSMWCADFC
119
41621    MK--------AFLLAVLAAVLC--------------------------------------VERAHTLICFSCSDASSNWACLTPVKCAENEEHCVTTYVGVGIGG-KSGQSISKGCSPVC
73
         **        *:* *:*:*::*                                       :*.  * *::*..  *:  **. . * ...::* *     *: .     : *  *: .*

GPIHBP1  EPLTKTVHGTFFMVSCCSSSLCGADSLDRKEERDGAAAVAGGSLAALGASVLLGLLGAGL------- 179
41621    PSAGINLGIAAASVYCCDSFLCNISGSSSVKAS----------YAV----LALGILVSFVYVLRARE 126
              .:  :   * **.* **. .. .  :             *.    : **:* : :
```

ENSGALG00000043582; identity to GPIHBP1 = 27.8%

```
GPIHBP1  MKALMTALLTALLTALLTALFCAAQGVVGKEVGPDRPETEDGEEEEDYDDEDLEYEAPTDGKRGGELRCYTCESQFSKEFCLNDTPCPSSSNYCKTLISSGLTDSGHLTTYSMWCADFCE
120
43582    MKA-------SLL---------------------------------------VVLVIALCTESAFSLRCFSCKDAPSNIHCFSTTTCADHEKYCLTTYSTKGLGDDRQQSITKKCAAFCP
74
         ***       :**                                       :        : . .***::*:.  *: .*:. * * . .:** *  *:   ...:  : :  ** **

GPIHBP1  PLTKTVHGTFFMVSCCSSSLCGADSLDRKEERDGAAAVAGGSLAALGASVLLGLLGAGL 179
43582    SIDLNIGIAGLATSCCQTSLCNISGASSVKT--SYTVIAVGVLASLACILRLGL----- 126
          :  .:  : : .***.:***. .. .  :   . :.:* * **:*.. : ***
```

ENSGALG00000039585; identity to GPIHBP1 = 23.4%

```
GPIHBP1  MKALMTALLTALLTALLTALFCAAQGVVGKEVGPDRPETEDGEEEEDYDDEDLEYEAPTDGKRGGELRCYTCESQFSKEFCLNDTPCPSSSNYCKTLISSGLTDSGHLTTYSMWCADFCE
120
39585    --------MKALLVALLVAVLCA--------------------------------------EQASSLFCYTCENEHSNWNCLKTYKCEDHEKYCTTTYSAAGFGKDMGYRITKKCSADCP
74
                 :.***.***.*::**                                      ::...* *****.:.*:  **:   * . .:**.*  *:.  ...     :  *:  *

GPIHBP1  PLTKTVHGTFFMVSCCSSSLCGADSLDRKEERDGAAAVAGGSLAALGASVLLGLLG---AGL------------------- 179
39585    ETNTDFGVVAISTKCCKTSLCNFSGANSVKLSYA-VMFLGT---------CLGVLSWLPFSIDSIASSSSRKTLHKDTCSD 145
           .. .  . : ..**.:***. .. :  :   . . . *           **:*.    .:
```

ENSGALG00000045170; identity to GPIHBP1 = 26.0%

```
GPIHBP1  MKALMTALLTALLTALLTALFCAAQGVVGKEVGPDRPETEDGEEEEDYDDEDLEYEAPTDGKRGGELRCYTCESQFSKEFCLNDTPCPSSSNYCKTLISSGLTDS-GHLTTYSMWCADFC
119
45170    MK--------TTPVILLVAVL--------------------------------------CVEQVYPFMCYVCQQQESNKDCLTISMCAKEDKYCVTVRDNVGTNPDKPKYVISKMCSPTC
74
         **        :  . **.*::                                        ::   : **.*:.* *:: **. : * ...:** *: ..  *:      . *  *:  *

GPIHBP1  EPLTKTVHGTFFMVSCCSSSLCGADSLDRKEERDGAAAVAGGSLAALGASVLLGLLGAGL 179
45170    NATSQQQNQAHRNVSCCEKPLCNVNGGSSKQGSYGAMFL--GVLASITYIF-----ACGR 127
         :  ::  : :.  ****.. **..:. . *:   **  :  * **::   .     ..*
```

LYPD6B (ENSGALG00000028759); identity to GPIHBP1 = 23.1%

```
GPIHBP1  MKALMTALLTALLTALLTALFCAAQGVVGKEVGPDRPETEDGEEEEDYDDEDLEYEAPT-DGKRGGELRCYTCESQFSKEFC---LNDTPCPSSSNYCKTLISSGLTDSGHLTTYSMWCA
116
LYPD6B   ----MLLFCHTLVGAFLPLFLLSGNWVSAKNIN-------------FYN-----VRPPLDPTPFPNSFKCFTCDNAVDNYNCNRWAEDRWCPESTQYCLTVHL--FTDHGKSTSVTKKCA
96
             *  :  :*: *:*  :: :.: * .*::.              *:      . *       ..::*:**:. ..:  *    :*  **.*::** *:    :** *: *: :  **

GPIHBP1  D--FCE---PLTKTVHGTFFMVSCCSSSLCGADSLDRKEERD----GAAAVAGGSLAALGASVLLGLLGAGL- 179
LYPD6B   TGDECHFVGCHHHRESGHTECVSCCEGMICNVEIPTNHTNAVFAVLHARRTSGGSRRTVSIAVLVSVMAIALS 169
             *.      :   *    ****.. :*..:   .: :       *  .:***  ::. :**:.::. .*
```

```
LYPD1 (ENSGALG00000012176); identity to GPIHBP1 = 18.3%

GPIHBP1  MKALMTALLTALLTALLTALFCAAQGVVGKEVGPDRPETEDGEEEEDYDDEDLEYEAPTDGKRGGELRCYTCESQFSKEFCLNDTP---CP-SSSNYCKTLISSGLTDSGHLTTYS----
112
LYPD1    ----------RMRLFLLAATFCGLCL---------------------------------APGFGLQIQCYQCEEFQLNNDCSSPEFIVNCTVNVQDMCQKE----VMEKSFGIMYRKSCA
73
                    :   **:* **.                                        * :::** **.   :: * .      *  . .: *:.     : :...   *

GPIHBP1  ---------MWCADFCEPLTKTVHGTFFMVSCCSSSLCGADSLDRKEERDGAAAVAGGSLAALGASVLLGLLGAGL----- 179
LYPD1    SSAACLIASAGYQSFCSPGK----VNSVCISCCNTPLCNGPRPKKRGNS-GV--MLRAHM--ITTALL---LEFSLLFLYC 142
                      .**.* .     . . :***.: **..   .:: :  *.  :  . :  : :::*   *  .*
```

```
ENSGALG00000033369; identity to GPIHBP1 = 19.4%

GPIHBP1  MKALMTALLTALLTALLTALFCAAQGVVGKEVGPDRPETEDGEEEEDYDDEDLEYEAPTDGKRGGELRCYTCESQFSKEFCLNDTPCPSSSNYCKTLISSGLTDSGHLTTYSMWCADFCE
120
33369    -------MLS------------------G-----HMPGGAHG----ILSLMTVVFVL----PEVSGLQCYGCNIIVGTKYVDTGCSNPEV-------ITCSHS-------HQGFKHRFCI
68
                :*:                  *     . *   .*      .   : :       . . *:** *:  ...::  ..   *.        *:.. :       :. :   **

GPIHBP1  PLTKTVHGTFF------------------MVSCCSSSLCGADSLDRKEERDGAAAVAGGSLAA--LGASVLLGLLGAGL 179
33369    KTESVVLGILLTSGCATSRHCQQQELPGVRIHCCDTDLCNGSPQPPP-------SLAGGCLLLPSLLAALLLS------ 134
            ..* * ::                   : **.:.**...            ::***.*    * *::**.
```

```
LYPD6 (ENSGALG00000012470); identity to GPIHBP1 = 20.1%

GPIHBP1  MKALMTALLTALLTALLTALFCAAQGVVGKEVGPDRPETEDGEEEEDYDDEDLEYEAPTDGKRGGELRCYTCESQFSKEFC---LNDTPCPSSSNYCKTLISSGLTDSGHLTTYSMWCAD
117
LYPD6    MA-SQPRLAHVLLL-----------GLVAG--------WLRAAQPRDFTVKDIVYLHPSTTPFPHGFKCFTCERAADNYECNRWAPDVYCPRGTRYCFSQHMMRVTGES------VSVTK
94
         *      *  .**            *:*.            . : .*:  :*: *  *:       ::*:***   .:  *     *. ** .:.** :     :*...      :  :.

GPIHBP1  FCEPLTKTV--------HG-TFFMVSCCSSSLCGADSLDRKEERD--------GAAAVAGGSLAALGASVLLGLLGAGL 179
LYPD6    RCVPLEDCLSTGCTYVKHEEYKICTSCCEGTICNLPLPRNASDAVFTTLSPLSSTPGL-SGRAVLTAVCLLLGLMA--- 169
          * ** . :        *    : .***..::*.     . .:          .: .: .*  .  ...:****:.
```

```
ENSGALG00000026884; identity to GPIHBP1 = 12.0%

GPIHBP1  ---------------------------------------------------------MKALMTALLTALLTALLTALFCAAQGVVGKEVGPDRPETEDGE--------------------
43
26884    MCSVLPVLIGALPNLRLPQLPLPQVADTSRSILLKPLWYIELCLARFGSSLYLQSISMKLFLGFSFLLTFLDSATMLQCEVCHSIGRSCSGHL-ETCSGNADTCGIILHEVTIGGMAIPS
119
                                                                  ** ::   :   :    * * * .   :*:. . .  ** .*:

GPIHBP1  ---------------EEEDYDDE---------------DLEYEAPTDGKRGGELRCYTCESQFSKEFCLNDTPCPSSSNYCKTLISSGLTDSGHLTTYSMWCADFCEPLTKTVHGTFFMV
133
26884    SIKTCVPSTVCQMGPVTMNYGKVKARSHLACCVGDACRTASVSLPPENNVPNGFQCPACYSVDSFQCHNETVNCTGSENQCVDLA--GLMNTGGLTVKA------------------AMK
219
                           :*..                  . . * :.:  . ::* :* *  * :   : . * .*.* *  *   ** ::* **. :                   *

GPIHBP1  SCCSSSLCGADSLDRKEERDGAAAVAGGSLAALGASVLLGLLGAGL--------------------- 179
26884    GCTTISECSVAGDGKN--NLGVMDIKIKRY-QCHPPTTLEMLSSGLVSPQSLFFPALSGFILEKLLF 283
         .* : * *.. . .::  . *.  :           . * :*.:**
```

```
HEP21 (ENSGALG00000000115); identity to GPIHBP1 = 23.4%

GPIHBP1  MKALMTALLTALLTALLTALFCAAQGV----VGKEVGPDRPETEDGEEEEDYDDEDLEYEAPTDGKRGGELRCYTCESQFSKEFCLNDTPCPSSSNYCKTLISSGLTDSGHLTTYSMWCA
116
HEP21    MKLLFVGLALVLCVGVVEALQCKVCKYKIPYVGCFHGANETTCER------------------------RERCAIIKTSLGKVTLYYQQGCTSALN-------CGRE-------------
76
         ** *:..*  .* ..:: ** * .       **   * :.   *                         . **   ::.:.*     :  * *: *       .*

GPIHBP1  DFCEPLTKTVHGTFFMVSCCSSSLCGADSLDRKEERDGAAAVAGGSLAALGASVLLGLLGAGL 179
HEP21    ----RASDAESRLTSRYSCCETDLCNEKWDDDPTD---------------------------- 107
               :.:        ***.:.**. .  *   :

CD59 (ENSGALG00000040371); identity to GPIHBP1 = 27.7%

GPIHBP1  MKALMTALLTALLTALLTALFCAAQGVVGKEVGPDRPETEDGEEEEDYDDEDLEYEAPTDGKRGGELRCYTCESQFSKEFCLNDTPCPSSSNYCKTLISSGLTDSGHLTTYSMWCADFCE
120
CD59     ----MIKMNCVLLTACI--------------------------------------VLLAFSSSGYALKCYHCENS--PSLCKTNSTCLSNEDTCLQMR------FGKLRTSSCWKLSQCN
70
             *  :  .**** :                                         : .. *  *:** **..   .:* .:: * *..: *  :        *:* * * *  . *:

GPIHBP1  PLTKTV--HGTFFMVSCCSSSLCGADSLDRKEERDGAAAVAGGSLAALGASVLLGLLGAGL 179
CD59     VNDIAVFYQLDNFDYFCCQQDLCNEGAVTGVNKAAF-------SIAPVMAM-LWMLL---- 119
             :*  :   *   **...**. .::   ::          *:* : *  *  **
```

This table shows CLUSTAL O (1.2.4) amino acid sequence alignment of platypus GPIHBP1 (ENSOANG0000009983) against 14 chicken Ly6 proteins in the Ensembl and Uniprot databases. * Conserved residue; : amino acids of similar properties; . amino acids with weakly similar properties.

Supplemental Table S3. CLUSTAL O (1.2.4) multiple amino-acid sequence alignment covering the carboxyl-terminal end of the LPL in a variety of avian species, platypus, mouse, and human.

```
                    435          448                      Gene ID
Kea                 FVKCLEQPVKRKRGGTKQASKENSAHESA 462     Nno_R011707
Zebra finch         FVKCSEQPANRKRGGTKKASKENSAHESA 462     ENSTGUG00000000287
African ostrich     FVKCLEQPVNRKRGGAKKASKENSAHESA 462     Sca_R002339
Chicken             FVKCLEQPVSRKRGGAKKASKENSAHESA 490     ENSGALG00000015425
Brown roatelo       FVKCLEQPVNKKRGGAKKASNENSAHESA 462     Mun_R009276
Annas hummingbird   FVKCLDQPVNTKKGGAKKASRENSAHESA 460     Aan_R005563
American crow       FVKCSEQPVNRKRAGTKKASKENSAHESA 462     Cbr_R012597
Rifleman            FVKCLEQPVNKKREGAKKASKENSAHESA 462     Ach_R005439
Barn owl            FVKCLEQPVNRKRGGAKKASKENSAHESA 459     Tal_R012814
White-tailed eagle  FVKCADEPVNRKRGGAKKASKENSADESA 462     Hal_R007162
Royal crane         FVKCLEQPIHRKRGGAKKASKENSALESA 462     Bre_R010180
Houbara bustard     FVKCLEQPVNRKRGGAKKASKENSAHESA 462     Cun_R002946
Great cormorant     FVKCLEQPVNRKRGGAKKASKENSAYESA 462     Pca_R011895
Red-legged seriema  FVKCLEQPVNRKRGGAKKASKENSAHESA 462     Ccr_R011587
Adelie penguin      FVKCLEQPVNRKRGGAKKASKENSAHESA 462     Pad_R007755
Cuckoo roller       FVKCLEQPVNRKRGGAKKASKENSAHESA 462     Cdi_R000849
Red-throated loon   FVKCLEQPVNRKRGGAKKASKENSAHESA 462     Gst_R001718
American flamingo   FVKCLEQPVNRKRGGAKKASKENSAHESA 462     Pru_R009349
Crested ibis        FVKCLEQPVNRKRGGAKKASKENSAHESA 462     Nni_R004651

Platypus            FVKCHDKSLKSPKFLKKKTV--------- 454     ENSOANG00000005949
Human               FVKCHDKSLNKKSG--------------- 448     ENSG00000175445
Mouse               FVKCHDKSLKKSG---------------- 447     ENSMUSG00000015568
```

Avian lipoprotein lipase (LPL) sequences were retrieved by “blasting” the amino acid sequences of chicken LPL (Uniprot P11602), duck LPL (Uniprot U316M2), and flycatcher LPL (U3JR79) against the national avian research facility database (avianbase.narf.ac.uk). In birds, LPL has a 15–amino acid extension when compared to the human LPL sequence. This extension is rich in lysine residues and is highly conserved among birds. Numbers on the top refer to the residue’s position in the human sequence. *Black* residues are perfectly conserved; *orange* residue indicates conservation between amino acids of strongly similar properties; *green* residue indicates conservation between amino acids of weakly similar properties; *blue* residue indicate a non-conservative change.