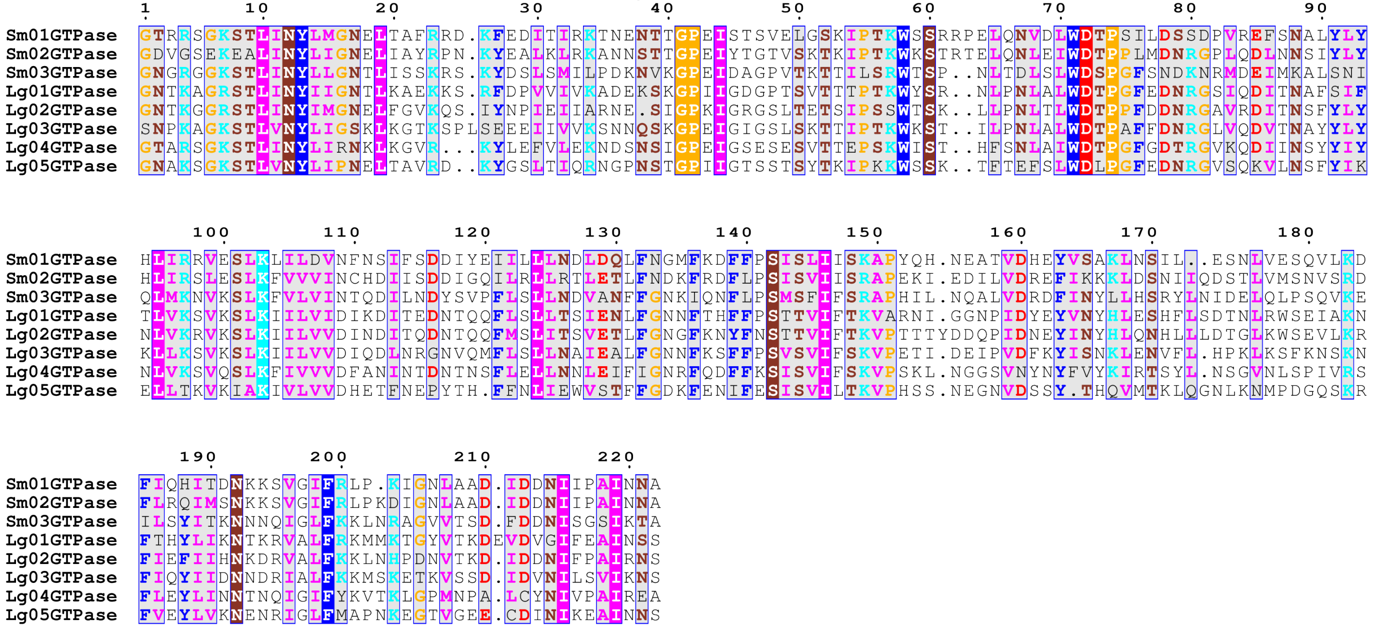
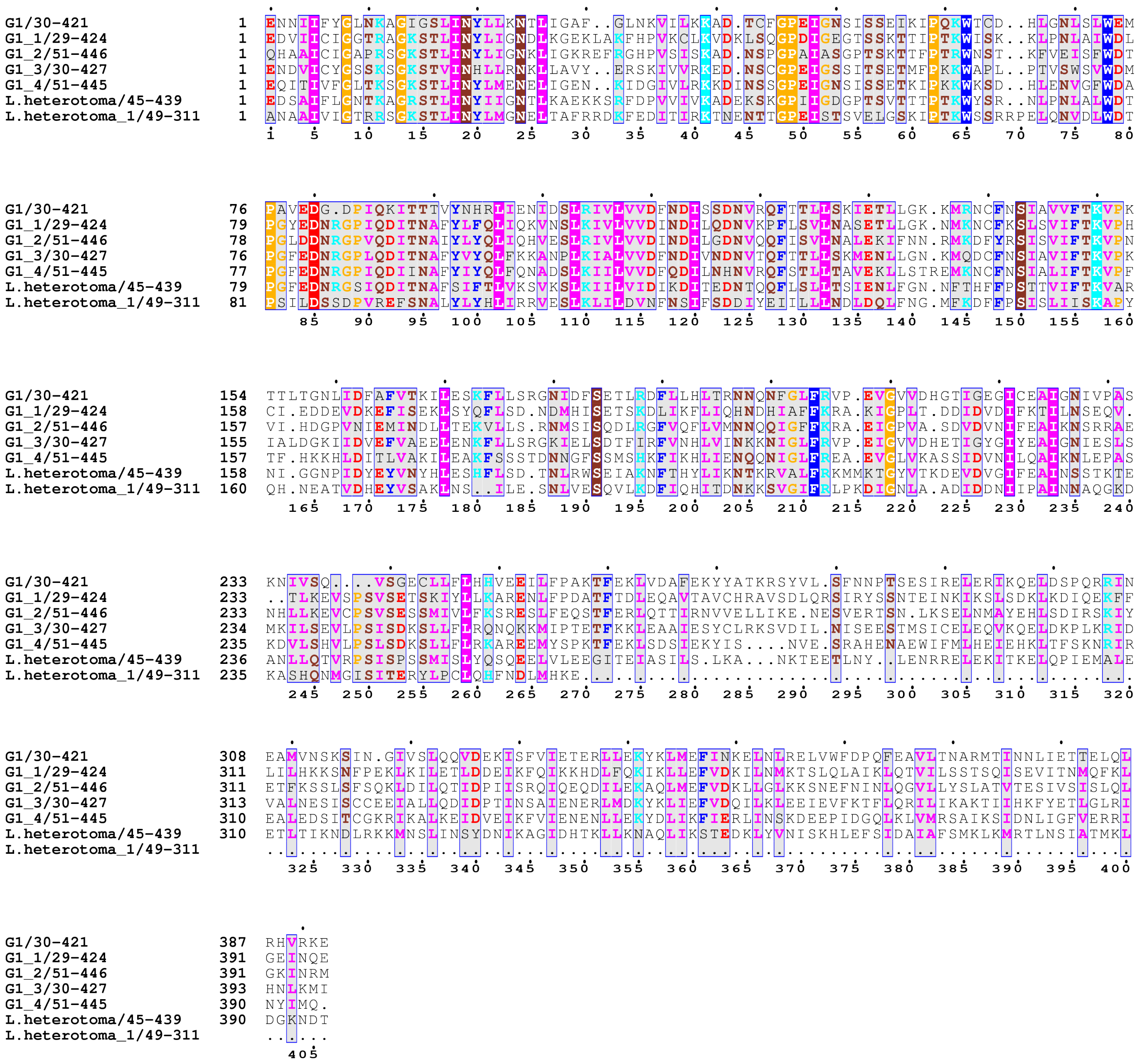
Data S2: *Lh* VLP GTPase alignments (Related to Main Figures 2, 3A, & 4A - C)

A Members of the novel *Lh* GTPase family



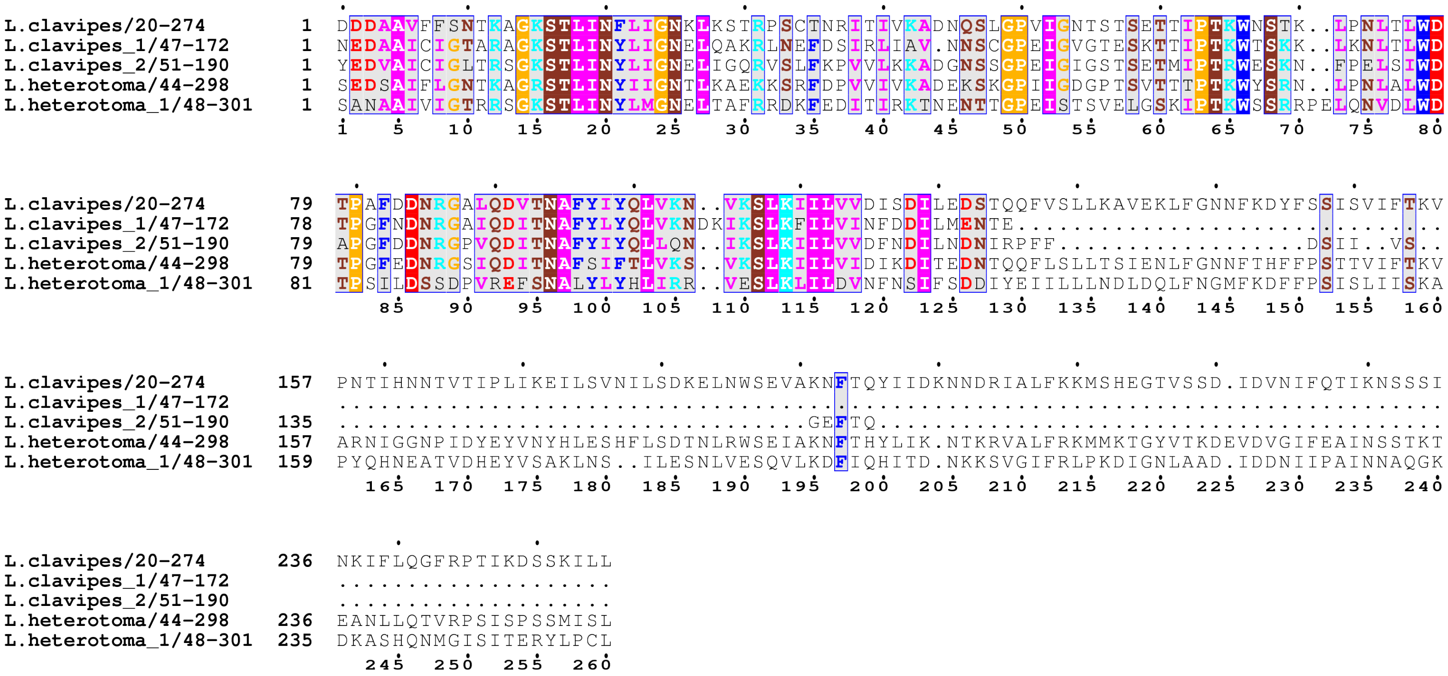
```
            1        10        20        30        40        50        60        70        80        90
Sm01GTPase  GTRRSGKSTLINYLMGNELTAFRRD.KFEDITIRKTNENTTGPEISTSVELGSKIPTKWSSRRPELQNVDLWDTPSILDSSDPVREFSNALYLY
Sm02GTPase  GDVGSEKEALINYLIGNELIAYRPN.KYEALKLRKANNSTTGPEIYTGTVSKTKIPTKWKSTRTELQNLEIWDTPPLMDNRGPLQDLNNSIYLY
Sm03GTPase  GNGRGGKSTLINYLLGNTLISSKRS.KYDSLSMILPDKNVKGPEIDAGPVTKTTILSRWTSP..NLTDLSLWDSPGFSNDKNRMDEIMKALSNI
Lg01GTPase  GNTKAGRSTLINYIIGNTLKAEKKS.RFDPVVIVKADEKSKGPIIGDGPTSVTTTPTKWYSR..NLPNLALWDTPGFEDNRGSIQDITNAFSIF
Lg02GTPase  GNTKGGRSTLINYIMGNELFGVKQS.IYNPIEIIARNE.SIGPKIGRGSLTETSIPSSWTSK..LLPNLTLWDTPPFDDNRGAVRDITNSFYLY
Lg03GTPase  SNPKAGKSTLVNYLIGSKLKGTKSPLSEEEIIVVKSNNQSKGPEIGIGSLSKTTIPTKWKST..ILPNLALWDTPAFFDNRGLVQDVTNAYYLY
Lg04GTPase  GTARSGKSTLINYLIRNKLKGVR...KYLEFVLEKNDSNSIGPEIGSESESVTTEPSKWIST..HFSNLAIWDTPGFGDTRGVKQDIINSYYIY
Lg05GTPase  GNAKSGKSTLVNYLIPNELTAVRD..KYGSLTIQRNGPNSTGPIIGTSSTSYTKIPKKWSSK..TFTEFSLWDLPGFEDNRGVSQKVLNSFYIK

                100       110       120       130       140       150       160       170       180
Sm01GTPase  HLIRRVESLKLILDVNFNSIFSDDIYEIILLLNDLDQLFNGMFKDFFPSISLIISKAPYQH.NEATVDHEYVSAKLNSIL..ESNLVESQVLKD
Sm02GTPase  HLIRSLESLKFVVVINCHDIISDDIGQILRLLRTLETLFNDKFRDFLPSISVIISRAPEKI.EDILVDREFIKKKLDSNIIQDSTLVMSNVSRD
Sm03GTPase  QLMKNVKSLKFVLVINTQDILNDYSVPFLSLLNDVANFFGNKIQNFLPSMSFIFSRAPHIL.NQALVDRDFINYLLHSRYLNIDELQLPSQVKE
Lg01GTPase  TLVKSVKSLKIILVIDIKDITEDNTQQFLSLLTSIENLFGNNFTHFFPSTTVIFTKVARNI.GGNPIDYEYVNYHLESHFLSDTNLRWSEIAKN
Lg02GTPase  NLVKRVKSLKIILVVDINDITQDNTQQFMSLITSVETLFGNGFKNYFNSTTVIFTKVPTTTYDDQPIDNEYINYHLQNHLLLDTGLKWSEVLKR
Lg03GTPase  KLLKSVKSLKIILVVDIQDLNRGNVQMFLSLLNAIEALFGNNFKSFFPSVSVIFSKVPETI.DEIPVDFKYISNKLENVFL.HPKLKSFKNSKN
Lg04GTPase  NLVKSVQSLKFIVVVDFANINTDNTNSFLELLNNLEIFIGNRFQDFFKSISVIFSKVPSKL.NGGSVNYNYFVYKIRTSYL.NSGVNLSPIVRS
Lg05GTPase  ELLTKVKIAKIVLVVDHETFNEPYTH.FFNLIEWVSTFFGDKFENIFESISVILTKVPHSS.NEGNVDSSY.THQVMTKLQGNLKNMPDGQSKR

             190       200       210       220
Sm01GTPase  FIQHITDNKKSVGIFRLP.KIGNLAAD.IDDNIIPAINNA
Sm02GTPase  FLRQIMSNKKSVGIFRLPKDIGNLAAD.IDDNIIPAINNA
Sm03GTPase  ILSYITKNNNQIGLFKKLNRAGVVTSD.FDDNISGSIKTA
Lg01GTPase  FTHYLIKNTKRVALFRKMMKTGYVTKDEVDVGIFEAINSS
Lg02GTPase  FIEFIIHNKDRVALFKKLNHPDNVTKD.IDDNIFPAIRNS
Lg03GTPase  FIQYIIDNNDRIALFKKMSKETKVSSD.IDVNILSVIKNS
Lg04GTPase  FLEYLINNTNQIGIFYKVTKLGPMNPA.LCYNIVPAIREA
Lg05GTPase  FVEYLVKNENRIGLFMAPNKEGTVGEE.CDINIKEAINNS
```

B *Lh* GTPases aligned with G1 GTPases



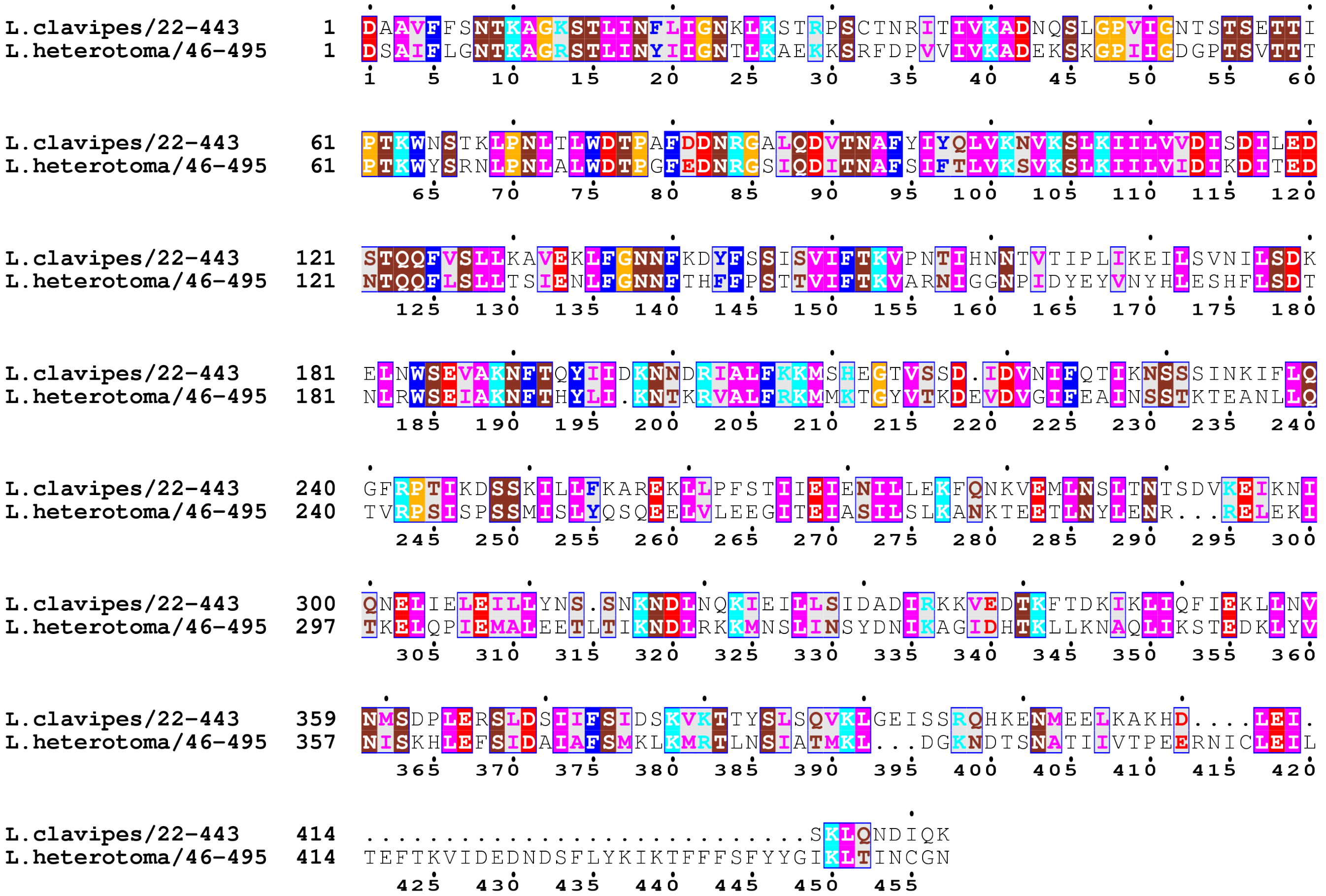
```
G1/30-421                 1  ENNIIFYGLNKAGIGSLINYLLKNTLIGAF..GLNKVILKKAD.TCFGPEIGNSISSEIKIPQKWTCD..HLGNLSLWEM
G1_1/29-424               1  EDVIICIGGTRAGKSTLINYLIGNDLKGEKLAKFHPVKCLKVDKLSQGPDIGEGTSSKTTIPTKWISK..KLPNLAIWDL
G1_2/51-446               1  QHAAICIGAPRSGKSTLINYLIGNKLIGKREFRGHPVSISKAD.NSPGPAIASGPTSKTTFPTRWNST..KFVEISFWDT
G1_3/30-427               1  ENDVICYGSSKSGKSTVINHLLRNKLLAVY..ERSKIVVRKED.NSCGPEIGSSITSETMFPKKWAPL..PTVSWSVWDM
G1_4/51-445               1  EQITIVFGLTKSGKSTLINYLMENELIGEN..KIDGIVLRKKDINSSGPEIGNSISSETKIPKKWKSD..HLENVGFWDA
L.heterotoma/45-439       1  EDSAIFLGNTKAGRSTLINYIIGNTLKAEKKSRFDPVVIVKADEKSKGPIIGDGPTSVTTTPTKWYSR..NLPNLALWDT
L.heterotoma_1/49-311     1  ANAAIVIGTRRSGKSTLINYLMGNELTAFRRDKFEDITIRKTNENTTGPEISTSVELGSKIPTKWSSRRPELQNVDLWDT
                             1   5    10   15   20   25   30   35   40   45   50   55   60   65   70   75   80

G1/30-421                76  PAVEDG.DPIQKITTTVYNHRLIENIDSLRIVLVVDFNDISSDNVRQFTTLLSKIETLLGK.KMRNCFNSIAVVFTKVPK
G1_1/29-424              79  PGYEDNRGPIQDITNAFYLFQLIQKVNSLKIVLVVDINDILQDNVKPFLSVLNASETLLGK.NMKNCFKSLSVIFTKVPH
G1_2/51-446              78  PGLDDNRGPVQDITNAIYLYQLIQHVESLRIVLVVDINDILGDNVQQFISVLNALEKIFNN.RMKDFYRSISVIFTKVPN
G1_3/30-427              76  PGFEDNRGPLQDITNAFYVYQLFKKANPLKIALVVDFNDIVNDNVTQFTTLLSKMENLLGN.KMQDCFNSIAVIFTKVPK
G1_4/51-445              77  PGFEDNRGPIQDIINAFYIYQLFQNADSLKIILVVDFQDILNHNVRQFSTLLTAVEKLLSTREMKNCFNSIALIFTKVPF
L.heterotoma/45-439      79  PGFEDNRGSIQDITNAFSIFTLVKSVKSLKIILVIDIKDITEDNTQQFLSLLTSIENLFGN.NFTHFFPSTTVIFTKVAR
L.heterotoma_1/49-311    81  PSILDSSDPVREFSNALYLYHLIRRVESLKLILDVNFNSIFSDDIYEIILLLNDLDQLFNG.MFKDFFPSISLIISKAPY
                                 85   90   95   100  105  110  115  120  125  130  135  140  145  150  155  160

G1/30-421               154  TTLTGNLIDFAFVTKILESKFLLSRGNIDFSETLRDFLLHLTRNNQNFGLFRVP.EVGVVDHGTIGEGICEAIGNIVPAS
G1_1/29-424             158  CI.EDDEVDKEFISEKLSYQFLSD.NDMHISETSKDLIKFLIQHNDHIAFFKRA.KIGPLT.DDIDVDIFKTILNSEQV.
G1_2/51-446             157  VI.HDGPVNIEMINDLLTEKVLLS.RNMSISQDLRGFVQFLVMNNQQIGFFKRA.EIGPVA.SDVDVNIFEAIKNSRRAE
G1_3/30-427             155  IALDGKIIDVEFVAEELENKFLLSRGKIELSDTFIRFVNHLVINKKNIGLFRVP.EIGVVDHETIGYGIYEAIGNIESLS
G1_4/51-445             157  TF.HKKHLDITLVAKILEAKFSSSTDNNGFSSMSHKFIKHLIENQQNIGLFREA.EVGLVKASSIDVNILQAIKNLEPAS
L.heterotoma/45-439     158  NI.GGNPIDYEYVNYHLESHFLSD.TNLRWSEIAKNFTHYLIKNTKRVALFRKMMKTGYVTKDEVDVGIFEAINSSTKTE
L.heterotoma_1/49-311   160  QH.NEATVDHEYVSAKLNS..ILE.SNLVESQVLKDFIQHITDNKKSVGIFRLPKDIGNLA.ADIDDNIIPAINNAQGKD
                                 165  170  175  180  185  190  195  200  205  210  215  220  225  230  235  240

G1/30-421               233  KNIVSQ....VSGECLLFLHHVEEILFPAKTFEKLVDAFEKYYATKRSYVL.SFNNPTSESIRELERIKQELDSPQRRIN
G1_1/29-424             233  ..TLKEVSPSVSETSKIYLLKARENLFPDATFTDLEQAVTAVCHRAVSDLQRSIRYSSNTEINKIKSLSDKLKDIQEKFF
G1_2/51-446             233  NHLLKEVCPSVSESSMIVLFKSRESLFEQSTFERLQTTIRNVVELLIKE.NESVERTSN.LKSELNMAYEHLSDIRSKIY
G1_3/30-427             234  MKILSEVLPSISDKSLLFLRQNQKKMIPTETFKKLEAAIESYCLRKSVDIL.NISEESTMSICELEQVKQELDKPLKRID
G1_4/51-445             235  KDVLSHVLPSLSDKSLLFLRKAREEMYSPKTFEKLSDSIEKYIS....NVE.SRAHENAEWIFMLHEIEHKLTFSKNRIR
L.heterotoma/45-439     236  ANLLQTVRPSISPSSMISLYQSQEELVLEEGITEIASILS.LKA...NKTEETLNY..LENRRELEKITKELQPIEMALE
L.heterotoma_1/49-311   235  KASHQNMGISITERYLPCLQHFNDLMHKE...................................................
                                 245  250  255  260  265  270  275  280  285  290  295  300  305  310  315  320

G1/30-421               308  EAMVNSKSIN.GIVSLQQVDEKISFVIETERLLEKYKLMEFINKELNLRELVWFDPQFEAVLTNARMTINNLIETTELQL
G1_1/29-424             311  LILHKKSNFPEKLKILETLDDEIKFQIKKHDLFQKIKLLEFVDKILNMKTSLQLAIKLQTVILSSTSQISEVITNMQFKL
G1_2/51-446             311  ETFKSSLSFSQKLDILQTIDPIISRQIQEQDILEKAQLMEFVDKLLGLKKSNEFNINLQGVLLYSLATVTESIVSISLQL
G1_3/30-427             313  VALNESISCCEEIALLQDIDPTINSAIENERLMDKYKLIEFVDQILKLKEEIEVFKTFLQRILIKAKTIIHKFYETLGLRI
G1_4/51-445             310  EALEDSITCGKRIKALKEIDVEIKFVIENENLLEKYDLIKFIERLINSKDEEPIDGQLKLVMRSAIKSIDNLIGFVERRI
L.heterotoma/45-439     310  ETLTIKNDLRKKMNSLINSYDNIKAGIDHTKLLKNAQLIKSTEDKLYVNISKHLEFSIDAIAFSMKLKMRTLNSIATMKL
L.heterotoma_1/49-311        ................................................................................
                                 325  330  335  340  345  350  355  360  365  370  375  380  385  390  395  400

G1/30-421               387  RHVRKE
G1_1/29-424             391  GEINQE
G1_2/51-446             391  GKINRM
G1_3/30-427             393  HNLKMI
G1_4/51-445             390  NYIMQ.
L.heterotoma/45-439     390  DGKNDT
L.heterotoma_1/49-311        ......
                               405
```

C *Lh* GTPases aligned with sequences from *L. clavipes*



```
L.clavipes/20-274        1  DDDAAVFFSNTKAGKSTLINFLIGNKLKSTRPSCTNRITIVKADNQSLGPVIGNTSTSETTIPTKWNSTK..LPNLTLWD
L.clavipes_1/47-172      1  NEDAAICIGTARAGKSTLINYLIGNELQAKRLNEFDSIRLIAV.NNSCGPEIGVGTESKTTIPTKWTSKK..LKNLTLWD
L.clavipes_2/51-190      1  YEDVAICIGLTRSGKSTLINYLIGNELIGQRVSLFKPVVLKKADGNSSGPEIGIGSTSETMIPTRWESKN..FPELSIWD
L.heterotoma/44-298      1  SEDSAIFLGNTKAGRSTLINYIIGNTLKAEKKSRFDPVVIVKADEKSKGPIIGDGPTSVTTTPTKWYSRN..LPNLALWD
L.heterotoma_1/48-301    1  SANAAIVIGTRRSGKSTLINYLMGNELTAFRRDKFEDITIRKTNENTTGPEISTSVELGSKIPTKWSSRRPELQNVDLWD
                            1   5    10   15   20   25   30   35   40   45   50   55   60   65   70   75   80

L.clavipes/20-274       79  TPAFDDNRGALQDVTNAFYIYQLVKN..VKSLKIILVVDISDILEDSTQQFVSLLKAVEKLFGNNFKDYFSSISVIFTKV
L.clavipes_1/47-172     78  TPGFNDNRGAIQDITNAFYLYQLVKNDKIKSLKFILVINFDDILMENTE...............................
L.clavipes_2/51-190     79  APGFDDNRGPVQDITNAFYIYQLLQN..IKSLKIILVVDFNDILNDNIRPFF..................DSII..VS..
L.heterotoma/44-298     79  TPGFEDNRGSIQDITNAFSIFTLVKS..VKSLKIILVIDIKDITEDNTQQFLSLLTSIENLFGNNFTHFFPSTTVIFTKV
L.heterotoma_1/48-301   81  TPSILDSSDPVREFSNALYLYHLIRR..VESLKLILDVNFNSIFSDDIYEIILLLNDLDQLFNGMFKDFFPSISLIISKA
                                 85   90   95  100  105  110  115  120  125  130  135  140  145  150  155  160

L.clavipes/20-274      157  PNTIHNNTVTIPLIKEILSVNILSDKELNWSEVAKNFTQYIIDKNNDRIALFKKMSHEGTVSSD.IDVNIFQTIKNSSSI
L.clavipes_1/47-172         ................................................................................
L.clavipes_2/51-190    135  ..................................GEFTQ.........................................
L.heterotoma/44-298    157  ARNIGGNPIDYEYVNYHLESHFLSDTNLRWSEIAKNFTHYLIK.NTKRVALFRKMMKTGYVTKDEVDVGIFEAINSSTKT
L.heterotoma_1/48-301  159  PYQHNEATVDHEYVSAKLNS..ILESNLVESQVLKDFIQHITD.NKKSVGIFRLPKDIGNLAAD.IDDNIIPAINNAQGK
                                165  170  175  180  185  190  195  200  205  210  215  220  225  230  235  240

L.clavipes/20-274      236  NKIFLQGFRPTIKDSSKILL
L.clavipes_1/47-172         ....................
L.clavipes_2/51-190         ....................
L.heterotoma/44-298    236  EANLLQTVRPSISPSSMISL
L.heterotoma_1/48-301  235  DKASHQNMGISITERYLPCL
                                245  250  255  260
```

D The most similar *Lh* GTPase and *Lc* sequences



```
L.clavipes/22-443      1  DAAVFFSNTKAGKSTLINFLIGNKLKSTRPSCTNRITIVKADNQSLGPVIGNTSTSETTI
L.heterotoma/46-495    1  DSAIFLGNTKAGRSTLINYIIGNTLKAEKKSRFDPVVIVKADEKSKGPIIGDGPTSVTTT
                          1   5    10   15   20   25   30   35   40   45   50   55   60

L.clavipes/22-443     61  PTKWNSTKLPNLTLWDTPAFDDNRGALQDVTNAFYIYQLVKNVKSLKIILVVDISDILED
L.heterotoma/46-495   61  PTKWYSRNLPNLALWDTPGFEDNRGSIQDITNAFSIFTLVKSVKSLKIILVIDIKDITED
                              65   70   75   80   85   90   95  100  105  110  115  120

L.clavipes/22-443    121  STQQFVSLLKAVEKLFGNNFKDYFSSISVIFTKVPNTIHNNTVTIPLIKEILSVNILSDK
L.heterotoma/46-495  121  NTQQFLSLLTSIENLFGNNFTHFFPSTTVIFTKVARNIGGNPIDYEYVNYHLESHFLSDT
                              125  130  135  140  145  150  155  160  165  170  175  180

L.clavipes/22-443    181  ELNWSEVAKNFTQYIIDKNNDRIALFKKMSHEGTVSSD.IDVNIFQTIKNSSSINKIFLQ
L.heterotoma/46-495  181  NLRWSEIAKNFTHYLI.KNTKRVALFRKMMKTGYVTKDEVDVGIFEAINSSTKTEANLLQ
                              185  190  195  200  205  210  215  220  225  230  235  240

L.clavipes/22-443    240  GFRPTIKDSSKILLFKAREKLLPFSTIIEIENILLEKFQNKVEMLNSLTNTSDVKEIKNI
L.heterotoma/46-495  240  TVRPSISPSSMISLYQSQEELVLEEGITEIASILSLKANKTEETLNYLENR...RELEKI
                              245  250  255  260  265  270  275  280  285  290  295  300

L.clavipes/22-443    300  QNELIELEILLYNS.SNKNDLNQKIEILLSIDADIRKKVEDTKFTDKIKLIQFIEKLLNV
L.heterotoma/46-495  297  TKELQPIEMALEETLTIKNDLRKKMNSLINSYDNIKAGIDHTKLLKNAQLIKSTEDKLYV
                              305  310  315  320  325  330  335  340  345  350  355  360

L.clavipes/22-443    359  NMSDPLERSLDSIIFSIDSKVKTTYSLSQVKLGEISSRQHKENMEELKAKHD....LEI.
L.heterotoma/46-495  357  NISKHLEFSIDAIAFSMKLKMRTLNSIATMKL...DGKNDTSNATIIVTPEERNICLEIL
                              365  370  375  380  385  390  395  400  405  410  415  420

L.clavipes/22-443    414  ............................SKLQNDIQK
L.heterotoma/46-495  414  TEFTKVIDEDNDSFLYKIKTFFFSFYYGIKLTINCGN
                              425  430  435  440  445  450  455
```