

```

1      10      20      30      40      50      60
O17145_LUCCU MSDSMLYRKFDTFMPRSRIITLWLAFNLAMFLQEPKKQITVNAATAGGSM LGD VNI SA I
lcGABBATM2 .....
4COF .....ETGQSVNDP GNM SF... VKET
consensus>50 .....t.n.....g.m.....!sai

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70      80      90      100     110     120
O17145_LUCCU IDSFSVSYDKRVRPNYGGPPVEVGVMTMYVLSISSEV KMDFTLDFYFRQFRTPRLAYR
lcGABBATM2 IDSFSVSYDKRVRPNYGGPPVEVGVMTMYVLSISSEV KMDFTLDFYFRQFRTPRLAYR
4COF VDKLLKGYD IRLRPD FGPPVCVGMNIDIASIDMVSEVNDYTLTMYFQQYWRDKRLAYS
consensus>50 lDsfsvsYDkRvRP#%GGPPVeVGvtmy!lSisslSEV kMD%TLdfYFrQ%rtDpRLAYr

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130     140     150     160     170     180
O17145_LUCCU KRPGVETLSVGSEFIKNIWVPDTEFVNEKQSYFHIATTSNEFIRVHHS GSITRSIRITIT
lcGABBATM2 KRPGVETLSVGSEFIKNIWVPDTEFVNEKQSYFHIATTSNEFIRVHHS GSITRSIRITIT
4COF GIP...LNTLDNRVADQLWVPDTEFVNEKQSYFHIATTSNEFIRVHHS GSITRSIRITIT
consensus>50 krPgvetLsvgsefik#iWVPDTEFvN#KqS%fHiaTtsNefIRvHhsGs!trsIRITiT

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190     200     210     220     230     240
O17145_LUCCU ASCPMNLQYFPMDROLCHEIESFGYTMRDIRYKWNCGPNSVGVSNEVSLPQFKVLGHRQ
lcGABBATM2 ASCPMNLQYFPMDROLCHEIESFGYTMRDIRYKWNCGPNSVGVSNEVSLPQFKVLGHRQ
4COF AACMMDLRRYPLDEONCTLEIESYGYTTDDIEFYWRGGDKAVTGVERIE LPQFSIVEHRL
consensus>50 AsCpM#Lqy%P$DrQlChiEIES%GYTmRDir%kWneGpnsVgvs#e!sLPQFk!lgHRRq

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250     260     270     280     290     300
O17145_LUCCU RAMEISLTGTGNYSRLACEIQFVRSMGYLYIQIYIPSGLIVVISWVSFWLN RNATPARVAL
lcGABBATM2 RAMEISLTGTGNYSRLACEIQFVRSMGYLYIQIYIPSGLIVVISWVSFWLN RNATPARVAL
4COF VSRNVVFATGAYPRLSLSFRLKRNIGYFILOIYIMPSILITILSWVSFWLN YDASARVAL
consensus>50 ram#!sltGTGnYsRLaceiqfvRsmGY%liQiYiPSgLiv!iSWVSFWLNr#AtpARVAL

```

```

310     320     330     340     350     360
O17145_LUCCU GVTTLVLTMTTLMSSSTNAALPKISYVKSIDVYLGACFVMVFASLLEYATVGYMAKRIQM R K
lcGABBATM2 GVTTLVLTMTTLMSSSTNAALPKISYVKSIDVYLGACFVMVFASLLEYATVGYMAKLLGITP
4COF GITTLVLTMTTINTHLRETLPKIPYVKAIDMYLMGCFVFVFLALLEYAVVNIFFSQPARA
consensus>50 G!TTLVLTMTTlmsstnaaLPKISYVKSIDvYLGaCFVmVFasLLEYAtVgYmak....r.

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```

370     380     390     400     410     420
O17145_LUCCU QRFMTIQKMAEQKKQQQLDGVQQPPNPNNPTGVDHGGHGHGHGHSHSPHPVKQTVRFK
lcGABBATM2 SDIDKYSRIVFPVCFVCFNLMYWIIYLL...TETSQVAPA.....
4COF AAIDRWSRIVFPFTFSLFNLVYWLIVYVNGATETSQVAPA.....
consensus>50 ..id..srivfp..f..f#lvyw..y.n..t.....

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430     440     450     460     470     480
O17145_LUCCU VHDPKAHSKGGTLENTVNGGRGGPPVGP HGPQG GGGGGGGGGPPGGGGGGGGGAPPEGGD
lcGABBATM2 .....
4COF .....
consensus>50 .....

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490     500     510     520     530     540
O17145_LUCCU AEA AVPAHLLHPGKVKKDINKLLGITPSDIDKYSRIVFPVCFVCFNLMYWIIYLVHSDVV
lcGABBATM2 .....
4COF .....
consensus>50 .....

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550
O17145_LUCCU ADDLVLLGEE
lcGABBATM2 .....
4COF .....
consensus>50 .....

```