

### **S1:The Amino acid sequence of LsfLEA genes**

>LsfLEA1-5  
MHSAKEKLSDMASAACEHVDIYKAKAKEKIAHEGRKAKEAQAKMEMHEAKARHAEEK  
LNAKQSHLYGHQVHEPPLVAHIIGTMNQWWVSMDTMGRSLLELRPLYLYR  
>LsfLEA1-4  
MQAGKNAAASAKETAANAAASAKSGMDKTKATMQEKAERMTARDPMQKEMATEKKE  
TKKTEAELNKQEAEHNAARQMASTGGTAGTYTHSATGATGHPTGGHQMSAMPGHGT  
GQTTEGYVAEGAAGSKPTGINTGTGQTTAHNTRAGGGNTGGFGTGDTYT  
>LsfLEA1-1  
MQSAKEAVSNMTASAKAGMDKTKATVQQKVEKMTAHDPIEKDMATQRKEAKITEAELN  
KQETREHNAASKQAGKAGVAGGTTTHHSTTGLGGFSTGGHPPTHSTTGTGGYTTGGH  
PTTTHSTTEAAGGYPTGGHHMSAMPGEGTWQPTWQEAEEELLVPRGTGTGGTTGNTR  
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>LsfLEA1-3  
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>LsfLEA1-2  
MHSAKEKLSDMASAACEHVDIYKAKAKEKVEKAAARTEEEKKIAHEGRKAKEAQAKM  
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>LsfLEA2-42  
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TTTNWNVSFYIRNPNRMSFSYDMVQASFYKDAQFLSPGTIPPFSGTEDSTSVQAKL  
AASSVYVDDGLRKAILDCWSRRGAAVDLNVKVQALIRFDPGTNSESRGSVWVFCKDVKT  
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>LsfLEA2-33  
MAEEKPTQEEQIQQPQTNKMNP GCGCGGKTHPSHHLRRGICTCIAIFLLL AGVTALT VWL  
VYRPHKPKFAVVGAAIYDLNTTSPPLISTTMQFTIVTRNP NKRVSIYYDQLSAFMSYRNQAI  
TPQTMLPPLYHRKHSTVALSPMLGGGMVPVSVEVTNGLAMDEAYGVVALRLVLLGRLR  
WKAGAIRTGRYGVYVKCDMLVGVKKGVTGQVPLLGAPECKVDI  
>LsfLEA2-3  
MTKSDGQKRKCFAYVAAFVVFQTIIIVVFA LTVMRIKSPKLRFGAVEVENFSTANANSVSM  
RLNAQVTVKNTNFGHKYPNSTATILYGGVAVGEAFIPSRAKARQT KRFNITVDITSAQIS  
SNDVNSGVLT LTSEAKLNGKVHLMKVIKKKSAEMSCNMAVNLA TRAVQNL TCK  
>LsfLEA2-53

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FKLRKIKTGRFKPKIKCDLK  
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>LsfLEA2-23

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>LsfLEA2-20

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HIRDF  
SVP  
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QVNG  
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VTFN  
VTARN  
ANQN  
IGIY  
DSMV  
GSVY  
FEDQR  
IGST  
PLL  
FPY  
QEP  
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QRWT  
DFKN  
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PTYFT

>LsfLEA2-52

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KYIK  
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>LsfLEA2-49

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>LsfLEA2-37

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>LsfLEA2-11

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QVVIPKGKAGLRSTKKRDVVVELNSAALTSTSSLGSDINSRILTLSSQARLNGKVELMFVM  
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>LsfLEA2-36

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KLDHMDVSMVARLRVNLNITLNIDLSVKNPNKVGFKYTNSAHLNYRGQVGEVPIA  
GKISADSTMPMSVTLLADRFLSNSDIYSDVLSGTLPLSTYTKISGKVYILKVFKFHVTE  
STCDVVVNVLNRTTPCECKYKTKL

>LsfLEA2-30

MAEKNQQVYPLALSTGGQPRSADEESATLQSKEFRRKRQIKIAAYVAFFVQTIIIAIFAV  
TVMKYRTPKFRVGKVTVDLVSTAAPSPSFNTRFIAQFTVKNTNFGPYKFDNTTAVFTYGG  
GMTVGQVIPKGKAGLRSTKKMDVTVELNSDGLMGTALSALGSDISSGVLKLSSQAKLNGK  
VELMFVMKKKSAEMNCLTFDLSAKALQALECN

>LsfLEA2-48

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SAAVEGIAPRVSPLIIRIQLNITLDLKLLVENPNHASFKHGTGKSVLLYNGHQVGEADIFPG  
NIPARGSTTLACRLTLQVDELASDVTPLIRDVLAGELLMETHHTGIPGRVSFLGILRKHAVAI  
DCQIAIGIPDMKIRRQDCKQRAKL

>LsfLEA2-45

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>LsfLEA2-24

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LSATWDITFRVRNPNEKLSVYYHRIEAWVVYGEEDLLYGTDLPPFYQEKRNETTVEAQLA  
VVSDTADGYVLRAISEEKARGLVSFDVRVLALINFRKGWQTRRHLLRASCEGVIFGFSAP  
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>LsfLEA2-4

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LRSTILNATAELKVLTKIRYKMWGRKSKHHGMNLQGQIRIGSDGKISGKNKKIKLKHT  
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>LsfLEA2-50

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MTVGQVIPKGKAGLRSTKKMDVTVELNSDGLSSTSALGSDISSGVLKLSSQAKLNGKV  
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>LsfLEA2-9

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QISSNDINSGVLT廖SEAKLNGKVHLMKVIKKKSAAMSCTMAVNLATRAVQNLKCK

>LsfLEA2-54

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>LsfLEA2-16

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>LsfLEA2-1

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DSIVSSLFYEEAFLSRTTLPPFDQDTRNLTVRAEFAAGVYVDGRLVNEINSERARGAVG  
FDVTVQARVRFSAAGAWKARRRFLRVLCEDVAVGSSNGASGTLVGGPKECRVGL

>LsfLEA2-21

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>LsfLEA2-8

MASSPKTQPTLYYHPIPPPDDHHHPQNYVVLPLYYPAGHRRRLPCRLICTISFLLLALAVYV  
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LGHVRSSHGHVRARGSSDVDAELEFNGVEVLYDVVYLEDLAKGTVPDFVTKVRGQL  
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>LsfLEA2-13

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>LsfLEA2-28

MEDQKTLAIGYPLQFGYPTNTNSASTTTTVATNNNNNAVDAHVVQLPPVPYPEPPCR  
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WNISFYVRNPNRWTASIAYDVIWLFYQDQLLSDGTTSPFQQGRRGQTVVTASLAAKSVH  
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MVGGSRKCKTYLDDDERGG

>LsfLEA2-38

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>LsfLEA2-35

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>LsfLEA2-22

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KFTVMYRGIPGRASVPGFYQPAHSVRQVETTVAVDRVNLQADAADLIKDASLNDRVEL  
RVLGEVGAKIRVLDFTSPGVQSVDCAVVISPRKQSLSYKQCGFDGLSV

>LsfLEA2-34

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SPNFLTSNIQVTVLSRNPNNLIGVYYEKLDIYASYRNQQITLPTSLPTTYQGHKDIVVWSPF  
VYGNINIPVAPYLAVALSQDQMAGMVLVNIKINGRVWKVGTWISSRYHLYVNCPAYIAFG  
NRNTGIPVGPAMKFQLAQGCSVVGK

>LsfLEA2-10

MAEKNQKQSAAGHTRSDEESATLQSKEFRRKRRIRIAAYIVALGKITVETLVSTPAPLPSFN  
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ALASTSSLGSDISSGILKLSTHARLSGTVELMFVMKKKSAQMNCNTLFDLASKALQALD  
CN

>LsfLEA2-26

MAEKNERQGYPLAPAAGHLRSDQVSATLQSKEFRRKRRIRIAAYIVAFVVFQSIIIAIFAVTV  
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VGQVIPKGKAGLRSTKNIDVTVDLNSDALASTSSLGSDISSGILKLSTQAKLSGKVELMF  
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>LsfLEA2-43

MAKEDSKRNTKCLAYVAAFVVFTIIIVVFALTVMRIKSPKLRFGAVALVENFSTANTNSVS  
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>LsfLEA2-5

MVEKDQQAYPLSPVAAGHPRSDEESATFQSKELRRKKRIKIAAYVVAFAVFQSIIIAIFAVTV  
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GRVVIPKGKVGFRSTKKIDVTVDLNSGLSTDGLGSDISSGILKVNSQAKISGKVELMF  
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>LsfLEA2-56

MADNQRIHPVVHDPEAPHTPTAPLVPRGSSKSEKGAPADQYHQVPLRRTIPVMHSKPPKK  
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VAITARNPNKKIGIYYESGSQITVWYTGTQLCQGSLPKFYQGHRNTTILNVPLTGQTQNAT  
GLLSTLQAQQQTGSIPLNLRVNVPVRIKLGKLKLMVKFRVRCRLLVVDLSAADNAISIKSS  
SCKFRLRL

>LsfLEA2-12

MADSAIRKTEDSPPSSKPPSNPTSKPVRHVFSEIPRRPHKPDKERRGRCCSGCFVVCCA  
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EVSNKNDRAKLSYGTMTVDVSSEKISLGQTKVVAFSQPKPNSTELKIHTKVTRLAVDKED

GAFLKSNVKDGEMVFDVVLSGTIGVGVRFTINGLPVTMACHGIQQSQVDIGQEPKCSV  
KMFSFRLYTFLFILIIHYL

>LsfLEA2-19

MEGQKPPVIGYPLQFSHGQSPNPLSDNPTAQPPHSTTTTAAAHVVQLPIVGHQDQPRP  
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NWNVTFYVRNPNRWASIAYDVTQASVFYEDQLLSAGTISPQQGRREQTLVTASLDAKS  
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>LsfLEA2-57

MGRIKFSRRGLKICCGVTAILFIIILVVVIVSLTIFKPQPKITTQSVTLEHAKLVIFPVFKLN  
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VKF

>LsfLEA2-55

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LTVIYDDIKSTYDDIKPGSIIPYKIKVELIVDPVFGRLTLPLEKTGEIIPYKPDIDIEKIQFKR  
FSFEETVAVLHLKLENKNDFDLGINPAELSESTKLDKNGIGHINIPITFKPKDFGSALWDMIR  
GKGTGYTMKGNI DVTDPFGAMKLPISEGTT RLKKNKGE GEGDDDDNVDDHALGA  
VE

>LsfLEA2-51

MAEKKNQKQSAAGHTRSDEESATLQSKEFRRKRRIRIAAYIVAFAVFQSIIIAIFAVTVMKYRT  
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DLSARALQALECN

>LsfLEA2-27

MAEKNNQQVYPLALSTGGQPRSADEESATLHSKEFRRKRQIKIAAYVA AFVVFQTIIIAIFAL  
TVMKYRTPKFRVGKVTVDLSTA PPSFNTRFVAQVTVKNTNFGPYRFDNTTAVFTY  
GMTVGQVIPKGKAGLRSTKKMDVTVELNSDSLTSMSLGNIDISSGVLKLSSQAKLNGK  
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>LsfLEA2-39

MADHQKIHPVV DVEAPPTTPLVPHGSFRSENGDPVQQNPPKHATVIPVIHSIPPTERSRC  
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NPNKKIGIYYEKGGRLSVWYTGTRLCEGSLPKFYQGHNTVLDVSLTGQTQYGSTLMT  
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RLKL

>LsfLEA2-2

MADQTRHNKIIKCSIIVATIVVLI AYVLITVKTIQPRPPRFRVTSVLVSPNQLNVTLNNNST  
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ASSLEVNNNGVMN AIAADMSHGAVGFNMVVARVRVDRRTWIQKMRGM RVT CEDVKV  
GLWSHTTAGTMLGGSTPCNVHL

>LsfLEA2-40

MTDRVYPQT KPTTTTNPPQTVNGGATTNPTFSTTKPQLYNPT RHPYRPQPRNNRRSRR  
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TTFNITLSAQNPNKLTFFYDPFTISVLSNDVLLANGSFPLFTSYAKNTTILRTTLSASRDLD  
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VASTSESQCKVDLRIKIWKWTF

>LsfLEA2-14

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>LsfLEA2-6

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PKSKAGFRSTKKIDVTVDLNSSGLTSTEGLASDINNGILKVNSHAKISGKVELMFVMKCR  
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>LsfLEA2-7

MAEKNQQVYPLAPAVANPRSDEESDLQSKEFRRKRRIKIAGYIVAFVFQCIVIAVFATVM  
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VGEVVIPKGKAGFRSTKKINVVVNLDSALASTSSLGTDINSVNLSTDALKSGKVELM  
FVMKKKSAKMNCMTMTNLPTKAFVLECNQKHEAV

>LsfLEA2-32

MADSAIRKTEDSPPSSKPSPNPTSKPVRHVVFSEIPCRPHKPDKERRGRCCSGCFVVCCA  
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VSNKNDRAKLSYGTMTVDVSSEKIRLGQTKVVAFSQKPKNTELKIHTKVTRSAVDKEDG  
AFLKSNVKNGEMVFDVVLSGTIGVGVRFTINGLPVTMACHGIQQSQVDIGQEPKCSVK  
MFSFRLHTFLFILINY

>LsfLEA2-15

MANPAAPPSQTPLPPRRSKLVRCIALILLALIVLGLVVLIIWLVVKPKRIVYTVEAASLSGF  
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>LsfLEA2-46

MGRGKCLAYVAAFFVVFQTIIILVFALTVMRIKNPKVRLGVVAVEDFSTTNSTSINMRLVAQV  
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ANDINSGVLAMSGEAKLSGVHLMKVIKKKSGEMNCTMAVNLATRAVQDLKCD

>LsfLEA2-29

MAEKNQQVYSLAPVAAHPRSDEESATLQSQEPRRKQRIKIAAYIVAFVFQSIIIAIFAITVM  
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>LsfLEA2-17

MAALLDKAKNFMVEKVAHVKKPEASVEDVDLKDVRECIDYNNAKVAKNPYGHTLAIC  
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EVGLTIDLPIIGNFTIPISKKGQMKLPTLTDIF

>LsfLEA2-25

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ISYRNPATFFGVHSSTPLEYYYQLKVASGHMREFYQSRKSNQNVMTVLGYQVPLYGG  
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TDSCIYQ

>LsfLEA2-31

MAEPVKPVLQKPPGYRDPNVPVQAPRPPVRKPALPPSFQPKKKRRSCCRIFCCSLCILTFIL  
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YYGGTRVKVTVGEDDTTELGTASLKQFTQGKKNNTSLKFTTRVKESEWVDDSVGKKLAR  
YRSRALVVFAEVTRVGLGVGRWRMGTVGVNLCGDMTLKKLAAGAMPKCTINLLKWI  
NIH

>LsfLEA2-41

MTDRVYPSSKPQAANGTTTANPAFPATKAQLYGATRPVYRPQPHPRQRSSCCSLCLW  
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LVFYYDAMSVSVSSNGVDVSDGTVPAFVHGKTNTALRVLTTSAAAQLDTSASTLKSD  
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RIKIWKWT

>LsfLEA3-3

MARSLSAKLLSAFVVDEISVAINRRGYSAAASQGVASNVARGGARMVKQGEEIAGKTE  
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>LsfLEA3-2

MAKVPINSFVILGRRSYAVVAENVRVQYSATNSVMRKAASEGCSTVTTEGAPEKQKEIFW  
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>LsfLEA3-1

MARSLSNALKFLAASVVDSLALICRGYAAASQGMVSASVSKGSRTGIVGRVEERAVIK  
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>LsfLEA4-1

MAELSDIKREDEEAIKWSLAKNNKQEREDVDVASDKAREAKEGAERSQEEKGVGEY  
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ALEKAREYKDSAAEKARETKDSTMKGKVGEYKDSAAEKARETKDSTMKGKVGEYKDSAAE  
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>LsfLEA4-2

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YKDSAAKAERRRTQRLGRQESTRIVPQRKRGKDSIMRRRWESIRIIVRESERGKEATLGKF  
SELKEICGDVARAMEFLSRKKEEQRERRDRGGDQGEAERDGRGSQTEDGRDEEMKLE  
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>LsfLEA5-3

MASNQKQREELDARARQGETVVPGGTGGKSLEAQEH LAEGRSRGGQTRREQLGTGGYQ  
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>LsfLEA5-1

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>LsfLEA5-2

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>LsfLEA6-2

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>LsfLEA6-1

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>LsfSMP-1

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>LsfDHN-1

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EFLSGEKEEEKHEDTTVPVEKCEEPVYVAPPPLYSEEKVEAVYAKPPPPLYTEEKVDYAKP  
PPPLYSD EKVGA VKA EPPPPPYSEEKVEAVYAEPPPPEEKKGILEKIKDKLPGQHKKTEE  
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>LsfDHN-4

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HPEGKKGILEKIKEKLPGQHKKGE EGATTIPP KCAPDGHSTE GEAKEKKGILEKIKEKLPG  
YHKNAEEEEKEEEN

>LsfDHN-2

MADLRDEYGSPIQLTDERGNPVQLTDEYGNPMHLSGVATTHGTTATTGMHGAPEIPIGLE  
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>LsfDHN-6

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>LsfDHN-5

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EEKKGILEKIKEKLPGQHKKGE EGATTIPPECAPVGPSEAEKKGILEKIKEKLPGYHKNA  
EEEKEEN

>LsfDHN-3

MANLRDEYGNPIQLTDERGNPVQLTDEYGNPMHLSGVATTHGTTATTGMHGGARETRTG  
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LSGGKSKDEREQTTGVTASTTTTSTTPGLHHQEHEKKSIVEKTKEKLPGRH NH