

Cd-hit clusters of the LEA transcripts:

>Cluster 0

0 502aa, >PdU002998_v1.1... at 100%
1 593aa, >PdU053999_v1.1... at 82%
2 1002aa, >PDT19L04... *

>Cluster 1

0 339aa, >PdU001599_v1.1... at 99%
1 594aa, >PDT20F06... *

>Cluster 2

0 272aa, >PdU010487_v1.1... at 100%
1 207aa, >PdU017016_v1.1... at 96%
2 593aa, >PDT30I10... *

>Cluster 3

0 320aa, >PDT06A14... *

>Cluster 4

0 307aa, >PdU055885_v1.1... at 89%
1 288aa, >PDF06F09... at 95%
2 317aa, >PDF40F19... *
3 306aa, >PDF16M17... at 99%
4 201aa, >PDF82L15... at 94%

>Cluster 5

0 240aa, >PdU015612_v1.1... at 91%
1 119aa, >PdU017506_v1.1... at 89%
2 282aa, >PDF80K07... *

>Cluster 6

0 235aa, >PdU055084_v1.1... *
1 235aa, >PDT10D20... at 99%

>Cluster 7

0 209aa, >PDF96E03... *

>Cluster 8

0 169aa, >PdU013001_v1.1... *

>Cluster 9

0 150aa, >PdU014555_v1.1... *

>Cluster 10

0 90aa, >PDF39E07... at 82%
1 98aa, >PDT45G14... *

>Cluster 11

0 78aa, >PDF77N04... *

>Cluster 12

0 54aa, >PDT56F11... *

Sequences:

>PdU013001_v1.1

MAGITENVKEMLNTVAEKSSEFKDYATGEELRNPSDTSMDISDAKDKASEIADAADKDKASD
LADAASNKASEVKDAASNKASEMKDAASSKASDLSDKASEMKDAAADKASEMYEGAKQ
KASDLGAAKVKADEMTSQETKDAARDMADKAGSKLEDAGHKIREQKDAI

>PdU055084_v1.1

MSTEKSYTETVQDAITAREKIIETAEAVKEKAAELATAAAGETLGLTSEEAKDKVDDVKDQ
AKEKASEVADAAGKKLDSAKEQVKDKVDETKQKASKAADAAGEKLESAKEHVKDKVGE
AEEKMDDGPELKGNHPPADKMSGGVRIARKKRPSESARHEHGNQEENAASGSADEDEEAP
STTEIAVQKQEKKLQQNFQEDAVKSYHEKPMPTHQPDHGYHSGRAHKDPAFQPKKQ

>PdU014555_v1.1

MPTLYKKVGPLSTTFDSLMSDNEDKTLGEKAKDAIANAAEAVKEAATDLKNKIVGEKSTE
EKAADKVKDAADAAADKIGDMKDSANNAGDKIKEAATDLKNKVVGKSTEDKVADKVK
DAADAAADKVGEMKESARDGAHKAGDKLKDA

>PDF40F19

MDSTNDSSPTLAEIAAEAAHNIAEKAQNVA AAAARDKLADAYEAVAEYAHDGKEKAEDLAE
AGKEKAEDLGASVKESAQNAAEKVKDLAHDGKEKVKDLAQAGKEKAEDLAEAGKEKVK
HASKAKDLAHDGKEKAEDLGERAKEKSHDLAEAGKEKAQRATEKAKDVAQSGKEKAH
DLAESGKQKANELGDRAKEKADHASDKAKDLAHAGKEKAHDLAQAGKEKAQHASKA
KDLAQDGKEKAQELGDRSKENAHASNKAKELANRGNKAQELGDHAKEKASHASKA
KELANRGNKAQELGDRAKEKAESNK

>PDF96E03

MLLKRLKILHMMVKKRLKILLKLEKKPKILLKLERKKPNMLLIKQKILHMMVKKRLKILE
NVQKSHDLAEAGKEKAQRASEKAKDVAQSGKEKAHDLAESGKQKANELGDRAKEKAD
HASKAKDLAQAGKEKAHDLAQAGKEKAQHASKAKDLAQDGKEKAQELGDRSKEKA
SHASKAKELANRGNKAQELGDRAKEKAESNK

>PDT06A14

MNRKIITLCFIGLFALSAFADETVGDKVDEGIN KASSGVQDAADSVKEKAEEAKQRFRRDT
VGDKLDQGLDSASQSVQNAADSVKDSAKDAKYKVG EALERKRRET VGDVDEKINDAS
DSVQNAADSVKDKAEDAKQRMKRET VGDVDEGIN KASSGVQDAADSVKEKAEEAKQK
RET VGDVDEKINDAKMTAEKAGESIKETGQELKQDRET V GAKINHGIDAASEKTQDAAE
SVKDTAKDAKYKAGEAIDDAKEGGKTF FENVGETISNAAESVKKAVVNAKDAVVGSSSS
ESHEEIATTMLIPRYRRHVAYSL

>PDF80K07

MNRKIITLCFIGLFALTAFADETVGDKVDEGIN KASSGVQDAADSVKEKAEEAKQRFRRDT
VGDKLDQGLDSASQSVQNAADSVKDSAKDAKYKAGEAL ERKRRET VGNKVDEKINDAS
DSVQNAADSVKEKAEEIKQKRET VGDVDEKINDAKMTAERAGESIKETGQELKQDRET V
GSKINHGMDAASEKTQDAAESVKDTAKDAKYKAGEAIDDAKEGGKTF FENVGETISNAAE
SVKKAVVNAKDAVVGSSSSSESHEEIATTMLIPRYRRHVAYSL

>PDT19L04

MLFYANANFVQKSWIHEQRTTKMFSKNLIFIAIAIFAITALADETVGDKVDQGINKAAGGVQ
DAAQSVKDTAKDAQRMKRET VGDVDEKINAASESVQNAAGQAVKDKAEEMKQERKRR
ETVGEKVDKINAASDAVQNAGEAVKEKGQEMKQERIKRET VGDVDEKINEASDSVQN
AGQAVKDKAEEMKQERMRRRETETIGEKLDSTLNSAGDSIKSAGQSVKEKGQDIKDRKRRE
TVGDVDEKINAASESVQNAAGQAVKDKAEEMKQERKRRET VGEKVDKINAASDAVQNA
GEAVKEKGQEMKQERMRRRET VGDVDEGIN KAADGVQDAAQSVKDTAKDAQRMKRE
TVGDVDEKINEASDSVQNAAGQAVKDKAEEMKQERLRRET VGDVDEKINQASDSVQAA
GEKTKEMAKEAKQHKRETETIGEKLDSTLNSAGDSIKSAGQSVKEKGQDIKDRKRRET
VGEKVDKINAASDAVQNAGEAVKEKGQEMKQERIKRET VGDVDEKINEASDSVQNA
GAVKDKAEEMKQERMRRRETETIGEKLDSTLNSAGDSIKSAGQSVKEKGQDIKDRKRRET V
GDVDEKINAASESVQNAAGQAVKDKAEEMKQERKRRET VGEKVDKINAASDAVQNAGE

AVKEKGQEMKQERMRRRETVGDKVDEGINKAADGVQDAAQSVKDTAKDAQQRMKRETV
GDKVDEKINEASDSVQNAGQAVKDKAEEMKQERLRRETVGDKVDEKINQASDSVQAAGE
KTKEMAKEAKQHKRETETIGEKL DSTLNSAGDSIKSAGQSVKEKGQDIKDRKRRETVGEK
VDEKINAASDAVQNAGEAVKEKGQEMKQERKRRETVGEKVDEKINEASDSVQNAGQAVK
DKAEEMKQERLRRETVGEKVDEKINAASDAVQEAGEAVKDKGEEMKQDRKRRETVGEK
VDSGVSSARDTMTETGESIKQTGKNMQQDRKRRTILGSDIEQVNDIPVTQITPRHRRYVL
>PDT30I10

MFSKNLIFIAIAIFTITACADETVGDKVDQGINKAAGGVQDAAQSVKDTAKDAQQRMKRET
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EAVKEKGQEMKQERIKRETVGDKVDEKINEASDSVQNAGQAVKDKAEEMKQERMRRRETE
TIGEKL DSTLNSAGDSIKSAGQSVKEKGQDIKDRKRRETVGDKVDAKINAASDAVQNAGQ
AVKDKAEEMKQERMRRRETVGDKVDEKINAASDAVQNAGEAVKEKGQEMKQERKRRETV
GDKVDEKINQASDSVQAAGEKTKEMAKEAKQHKRETETIGEKL DSTLNSAGDSIKSAGQS
VKEKGQDIKDRKRRETVGDKVDAKINAASESVQNAGQAVKDKAEEMKQERLRRETVGEK
VDEKINAASDAVQNAGEAVKEKGQEMKQERKRRETVGDKVDEKINAASDAVQNAGEAVK
EKGQEMKQERKRRETVGDKVDEKINAASDAVQEAGEAVKDKGEEMKQDRKRRETVGEK
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>PDT20F06

MKTIFTFVLLCIGLTLAETIGQKLDATLDAVSESIGNAADVVEKTRGSKYTAADAVDKTK
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DAAGNLRDHGGEIAYNAGKYVYDKTGNLLIDASEYVKDNGGNLLDKSGKIAYKAGEYVI
NQANRVVSNAKDRAQEMASDASDYVKDNAGNLRKTSGEIAYKAGEYVIDKANKVVQNA
KDSVSGTAEDAKNRAQEAL EDASQYVKDSMGNLKNKAGEIVYKAGEY AIDQKNKIVRQA
SNAKDDAINRAQEAL EDASQYVKDSMGNLRNKKDEIVYKAGEYVVDQKNKIVRQASNAK
DDAKNKAGKYAEDA KYRAQQA AEDASQYVKDKMGNLRDKSNNIVYKVNEYVIDSQNM
VSRKADDAKSRAQELGEDLSQYVKDKKNNYLNKAGEIVYHAGQYVIDEKKNLIRKVS DQ
ADDLGDYVRDAQGNLRDQAGNLIYKAGEQVKKR KASQMADQAGDYAEAARDAAGNLME
DAGDKLHSAGKKLKSTDKDDVKDA AHRAGEK LKETGEEVQSGGIYDSIREKVSNAAKTV
REKLDL

>PDF77N04

MSKDNNNPPEKEKYRGFASWPKEKIQEAGKKGGEARKEQLGLKGYIDMGRKGGMARSN
AAAKGDPSTSDKSDKKDGKK

>PDT45G14

MSTEDKSYVEQAKDAAASAAETAKEYAQSA AETATQLATDLKNKVVG EKSTEDKAADKV
KDAADATADKVSDMKDSAKDA A HKAGDKVKEAGNKIQNA

>PDT56F11

MSLKRVLIAEQRFLSTKSTKDSMKDSAASVAENAKEAAKNVAEKLQHAAAAARE