

C13F10.2

Fig.1

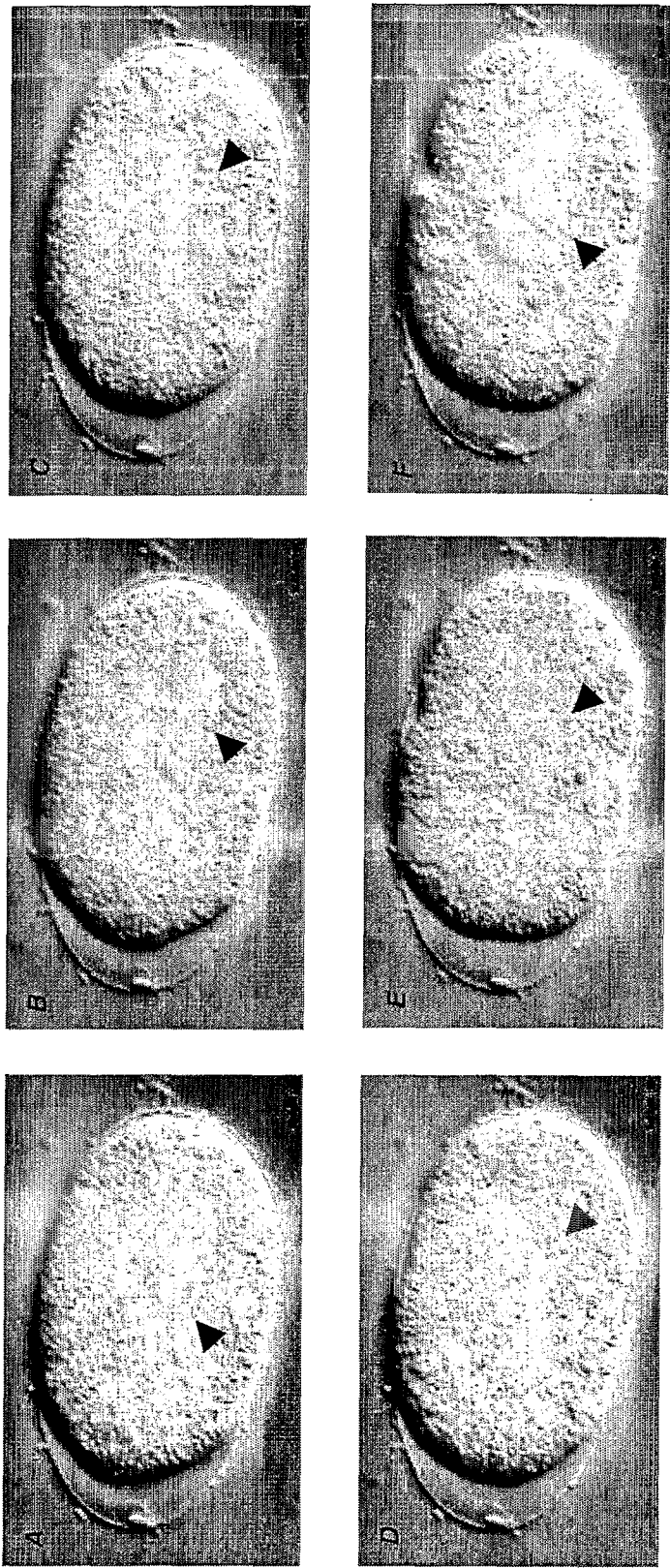


Fig. 2

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CLUSTAL W (1.8) multiple sequence alignment

NP_076974
AAF49911
C13F10.2
-----MDLPDSASRVFCGRILSMVNTDDVNAIILAQKNML
---MSHLGLADVHQSEDATEPDLESFTGFGNSAAEAFIQSLAGMVNQDVETMIRAQKQML
MAEKNHQQOERLPGNPFPPSRSNAGSSFDMPETPHLIDSLTSQIDEFTIQSLIDTQRQSL
      .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
      .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:

NP_076974
AAF49911
C13F10.2
DRFEKTNEMLLNFNNLSARLQOMSERFLHHTRTLVEMKRDLDSEFRIRITLKGKLARQH
ORFEKTNEMLLNCNALSQSLKASAEFKRHVKCLSEMKKDLDIYIFRKIRIICKQLSQSF
KRFEKTNEMLMNCAQLGDRRIEKAKRDSVGHKETILQMKTDLEFIFKKIRMFKTVLSSKY
*****:*      *..*:.:. . . * . : : ** ** : ** : ** : * * : * .
      .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:

NP_076974
AAF49911
C13F10.2
PEAFSHI-PEASFLEEDEDPIPPSTTTTATSEQSTG-----SCDTSPTDVSPSLSPGFE
PAIYAEVQPQRSSLAEEAEDDEAQAKKTAETPAPAAAKPVLSTKKSAATIEYVQMEEA
PEVYAEVSAELTPKRSEDE-----
      .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:

NP_076974
AAF49911
C13F10.2
DLSHVQAGSPAIN-----GRSQTDDEEMTGE---
DNGTVEIENELIKRVCVETANPNDS DCTSED TG
-----
*

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C25A1.9

Fig.3

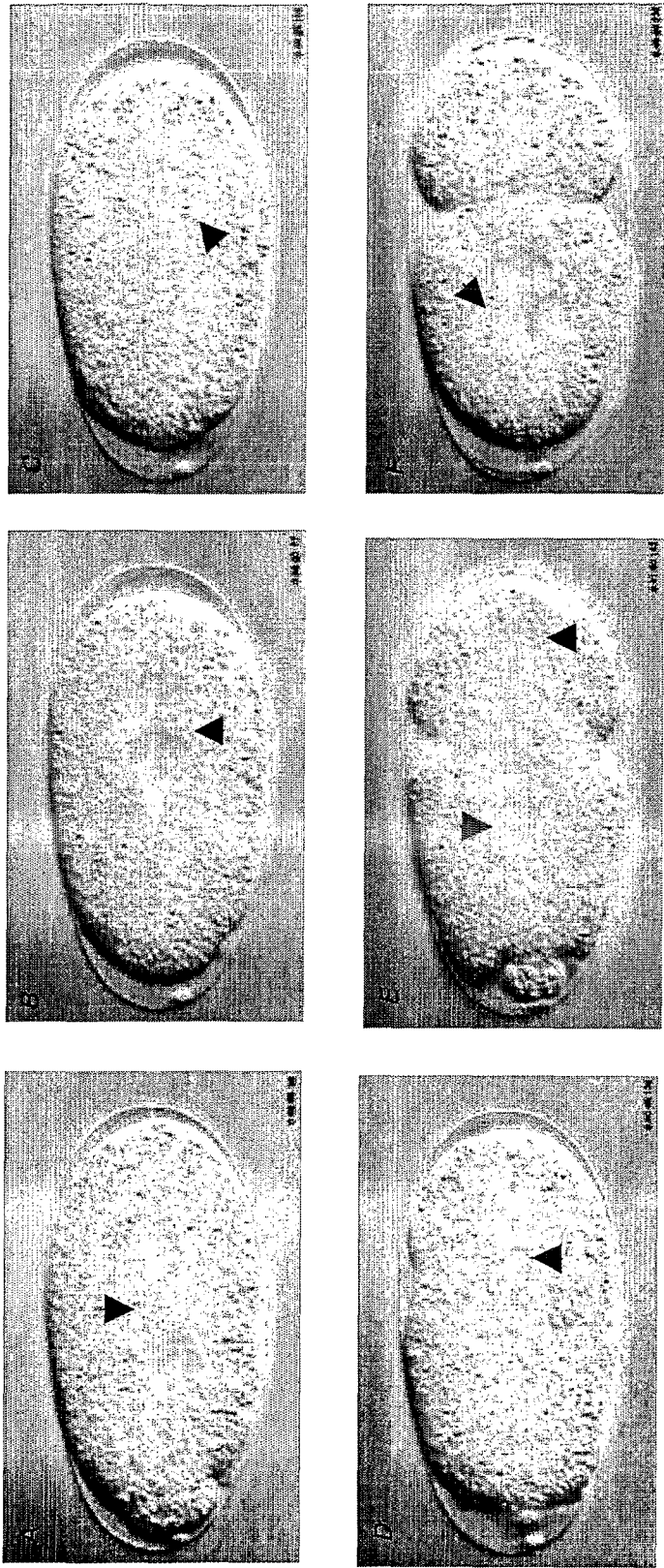


Fig. 4

CLUSTAL W (1.8) multiple sequence alignment

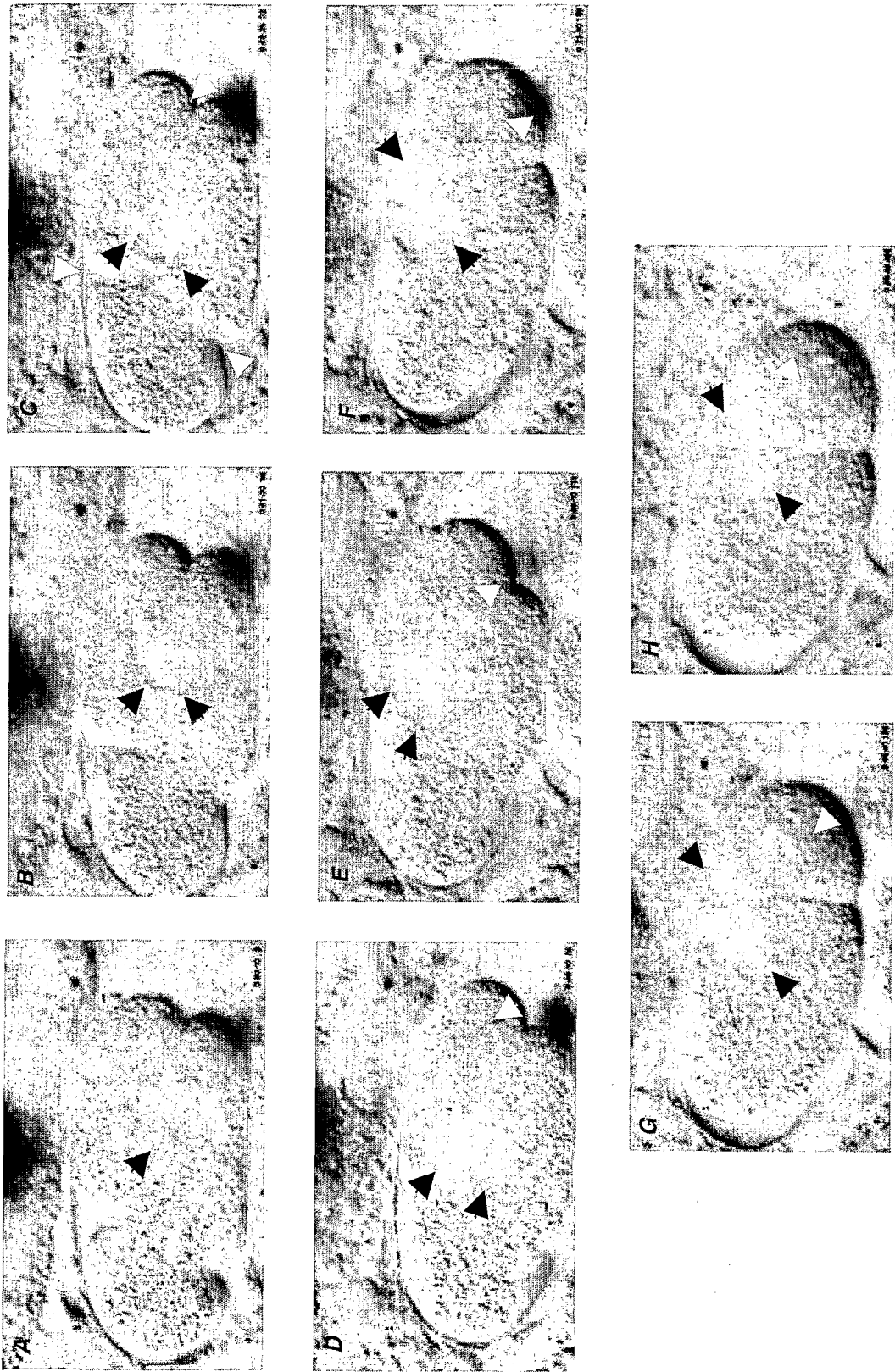
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C25A1.9      MPTDEPSKRKRSILPTIPTSLMLKKNEALSDFERTFNDRVMDIFAENRRRIDVEEFFKNAE
NP_060387    MDWKEVLRRR--LATPNTCPNKKKSEQELKDEEMDLFTKYSEWKGRKNTNEFFYKTIPR
               .* :.* :.* * .***:.* * : : : .*: * :.* . .
C25A1.9      CFLNIIRSNKIDLNWGEG-----GESRYV
NP_060387    FYYRLPAEDEVLQKLREESRAVFLQRKSRELLDNEELQNLWFLDKRQTPPMIGEEMI
               : . : .*** :* : .
C25A1.9      TITRLMKILKTSFQSIKDLLPHNTVSNFVKITNYNLTIDITLLEELVRTVTHAESYIKL
NP_060387    NYENFLKVGEKAGAKCKQFTAKVFAKLLHTDSYGRISIMQFFNYVMRKVWLHQTRIGLS
               .***: :. : * .***: :.***: : . : : : : .*: :
C25A1.9      LPFSENSTEISSYSLQDFVATHFIPIMIEEPENP---VYTYAVAGTIFFILGARRRDCV
NP_060387    LYDVAGQGYLRESDLNRYILELPTLPQLDGLEKSFYSFYVCTAVRKFFFLDPLRTCKI
               .. : .*.***: : : : : : : : : : : : : : : : : * . :
C25A1.9      YLKDLLASTLLQLLEECIHAENHCLSPPKIDVFTVAQFRTTLSEFRFLDSQRKGLLAPAD
NP_060387    KIQDILACSFLLDLELRDEE--LSKESQETNWFSAFSAALRVYGYQLNLDKDHNGMLSKEE
               :*:***:.* : * . * . . : : * : : : : : : : : : : : : :
C25A1.9      LKFFRDGIFNEVFTKRIFEISITYEDGRIDFKAFVDVFTALKFRHTTASAKYHFEILDIK
NP_060387    LSRHGTATMTNVFLDRVFQECITY-DGEMDYKTYLDFVLALLENRKEPAALQYIFKLLDIE
               . . . :*:*** .*: : : : : : : : : : : : : : : : : : : : : :
C25A1.9      DDGILLDEEEIRSISFQLQNLDPYVPEDNSVNPEVATAELRDMMR-LNQNGITLLEEFLLAN
NP_060387    NKGYNLVFSLN--YFFRAIQELMKIHGQDPVSFQDVVKDEIFDMVKPKDPLKISLQDLINS
               .* * : . : . * : : : : : : : : : : : : : : : : : : : : : :
C25A1.9      RMNSTFAGFLSNSDDYMKYERREQ-----
NP_060387    NQGDVTVTILIDINGFWYENREALVANDSENSADLDDT
               .*. : : : : : : : : : : : : : : : .

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Fig. 5

F54B3.3



CLUSTAL W (1.8) multiple sequence alignment

[illegible]

Fig. 6 2/3

CLUSTAL W (1.8) multiple sequence alignment (Con't)

```

NP_060658      -----AMRRATVEREMELRHKNEMLRVEAEARAK-----AFRENADIIREQIRLK
AAF55289      -----AMRQTIIEHEIEMEKENRLKLEHELRAKAR-----VDRENRDINLEKIRLK
F54B3.3       -----QLRKQTIIEHELALKHKELEKIDAEARAK-----AARDNRDVNLEQMKLH
XP_109399     IFIDELDAIAPKREKTHGEVERIVSQLLTLMMDGLKQRAHVIVMAATNRPNPIDPALRRF
P46462        IFIDELDAIAPKREKTHGEVERIVSQLLTLMMDGLKQRAHVIVMAATNRPNPIDPALRRF
NP_015349     -----RHSEADAVRQNLITASSAGAVNPSSSS-----NQSGYHGNFPMSYSP
               :      .      .      :      :      .      .      :
NP_060658     AAHRQTIVLESIRTAG--TLFGEGFRAFVTDWDKVTATVAGLTLLAVGVYSAKNATLVAG
AAF55289     AQEHRTIVLEGIKTAG--TVIGAGAEAMLTWDKVLTAAGGLSLLALGVYTAAGATGVVS
F54B3.3     EENRKTIVIEKIKTSG--ELIGSGLNQFLNDKTKIAAAVGGLTALAVGWYTAARGTGVT
XP_109399     GRFDREVDIGIPDATGRLEILQIHTKNMKLADDDVDLEQVANETHGHVGADLAALCSEAL
P46462       GRFDREVDIGIPDATGRLEILQIHTKNMKLADDDVDLEQVANETHGHVGADLAALCSEAL
NP_015349     IYGSRKPELHVVSSESTFTVVSRRVWVWKLVLVFGILTYSFSEGFKYITENTTLK-SSEVAD
               *      :      :      :      :      :      :      :
               :      :      :      :      :      :      :
NP_060658     RFTIARLGKPSLVRETSTRITVLEALRHPIQVSRRLSRPQ-DALEGVVLSP-----
AAF55289     RYVEARIGKPTLVGETSRFAFDALKNPLHYLKRRLRAKPT-DALQGVVLNP-----
F54B3.3     RYIESRLGKPSLVRETSTRITPLEVLKHPKSVQMMTRQKK-DPLNGVVLPP-----
XP_109399     QAIRKKMDLIDLEDETIDAENVNSLAVTMDDFRVALSQSNPSALRETVEVPQVTWEDIG
P46462       QAIRKKMDLIDLEDETIDAENVNSLAVTMDDFRVALSQSNPSALRETVEVPQVTWEDIG
NP_015349     KSVDVAKTNVKFDDVCGCDEARAELFELVDFLKDPKYES-----
               :      :      *      :      :
               :      :      :      :      :
NP_060658     SLEARVRDIAIATRN-----TKKNRSLYRNILMYGPPGCTGKTLFAKKLALHSGMDYA
AAF55289     KLEERLRDIAIATKN-----TRINKGMYRNVLMHGPPGCTGKTMFAKKLAHSGMDFA
F54B3.3     ALERRLRDIAITTSN-----TKRNNGLFRNVMFYGPPTGKTLFAKSLAQHSGLDYA
XP_109399     GLEDVKRELQELVQYPVEHPDKFLKFGMTPSKGVLFYGPPTGKTLAKAIANECQANFI
P46462       GLEDVKRELQELVQYPVEHPDKFLKFGMTPSKGVLFYGPPTGKTLAKAIANECQANFI
NP_015349     -----LGGKLPKGVLLTGPPGTGKTLARATAGEAGVDF
               .      :      :      :      :      :      :      :
               :      :      :      :      :      :      :
NP_060658     IMTGGDVAPMGR-EGVTAMHKLFDWANTSRRLGLLFVDEADAFIRKRAT--EKISEDLR
AAF55289     IMTGGDVAPMGK-EGVTAHKVFDWSHTSRRLGLLFVDEADAFIRKRSS--EKISEDLR
F54B3.3     VLTGGDIAPLGR-DGVSAHKVFDWASKRGLVIFIDEADAFLOKRSK--NGMSEDTFA
XP_109399     SIKGPELLTMWFGESEANVREIFDKARQAP-CVLTFDELDSIAKARGNIGDGGGAADR
P46462       SIKGPELLTMWFGESEANVREIFDKARQAP-CVLTFDELDSIAKARGNIGDGGGAADR
NP_015349     FMSGSEFDEVYGVGAKRIRDLFAOARSRAP-AIIFIDELDAIGGKRN-----KDQAYAKQ
               :      :      :      :      :      :      :
               :      :      :      :      :      :      :

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Fig. 6 3/3

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CLUSTAL W (1.8) multiple sequence alignment (Con't)

NP_060658      TLNAFLYRTG--QHSNKFMLVLASNQPEQFDWAIN--DRINEMVHFDLPGQERERLVRM
AAF55289      ALNAFLYRTS--EQNPKFMLVLASNTPEQFDYAIN--DRIDEMVVEFTLPGLEERERILLRL
F54B3.3       ALNAFLFRTG--EQSRKFMLVLASNQPEQFDWAVN--DRFDQLVEFTLPGMEERERILLQ
XP_109399     VINQILTEMDCGMSTKKNVFIIGATNRPDIIDPAILRPGRLDQLIYIPLPDEKSRVAILKA
P46462        VINQILTEMDCGMSTKKNVFIIGATNRPDIIDPAILRPGRLDQLIYIPLPDEKSRVAILKA
NP_015349     TLNQLLVLDGFSQTSGLIIGATNPFPEALDKALTRPGRFDKVVNVNVDLPDVRGRADILKH
:* : * . . . . . : : : * : * : * : * : * : * : * : * : * : * : * :
NP_060658      YFDKYVLKPATEGK--QRLK--LAQFDYGRKCEVARLITEGMSGRELAQLAVSWQA--TA
AAF55289      YFDKYVLQPAAGA--KRFK--LDTFDYGKTCSKMAALCEGMSGREISKLGVSQA--AV
F54B3.3       YFNEHIVTPATSGRSRQLK--LDNFDWVAKNEVAKKTSGMSGRELSKLVIGWA--SA
XP_109399     NLRKSPVAKDVDFLEFLAKMTNGFSGADLTEICQACKLAIRSEIESEIRRERERTNPSA
P46462        NLRKSPVAKDVDFLEFLAKMTNGFSGADLTEICQACKLAIRSEIESEIRRERERTNPSA
NP_015349     HMKKITLADNVDPPTIARGTPEGLSGAELANLVNQAAYVACQKNAVSVDMSHFEWAKDKIL
: : : . . . . . : : : : . . . . .
NP_060658      YASEDG-----VLTEAMMDTRVQDAVQHQK-----
AAF55289      YASEDG-----LLTEKMVLDRCSAAQQHKQKRWPG-----FR
F54B3.3       YASETG-----VLTEAIVDRNTADAMVQHEHK-MEW-----LE
XP_109399     MEVEED-----DPVPEIRRDHFEEAMRFARRSVSDND-----IR
P46462        MEVEED-----DPVPEIRRDHFEEAMRFARRSVSDND-----IR
NP_015349     MGAERKTMVLTDAAARKATAFHEAGHAIMAKYTNGATPLYKATILPRGRAIGITFQLPEMD
*           :           *           .           .
MCWLKAEGP-----GRGDEPSPS-----
IRSVLITNP-----SQAQLPHSP-----
KEQLKARNQEV-----KFGTTLKRETAV-----
KYEMFAQTLQQ-----SRFGSFRFPSCNQGGAGPSQSGGGTG
KYEMFAQTLQQ-----SRFGSFRFPSCNQGGAGPSQSGGGTG
KVDITKRECQARLDVCMGGKIAEELIYGKDNNTISGCGSDIQAATGTARAMVTQYGMSSDV
:           .           .           :

```

Fig. 7

F08B6.2

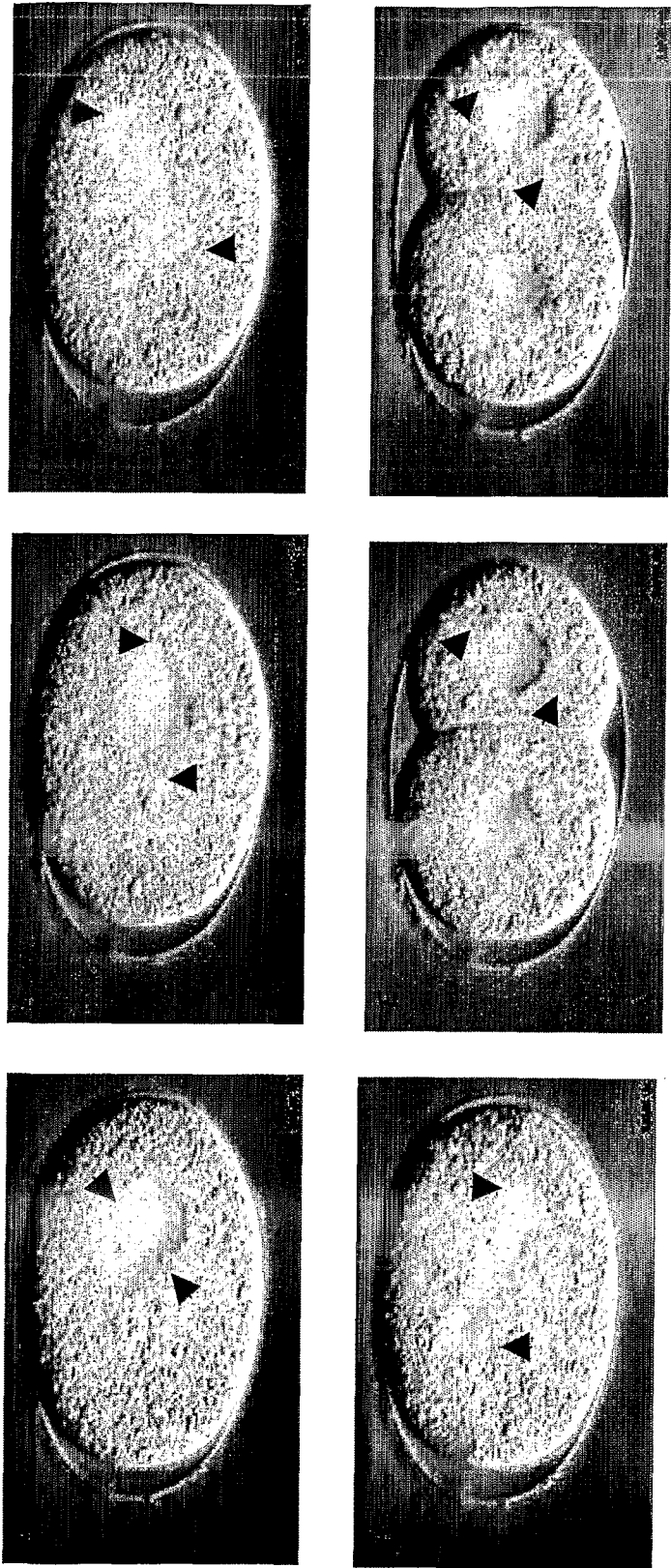


Fig. 8

CLUSTAL W (1.8) multiple sequence alignment

```

NP_057625      -----MEEWDVPQMKKEVESLKYQLAFQREMAKTIPELLKWIEDGIPKDPFLNPDLMKN
AAF52761      MDPSALQNMDRDALKKQIENMKYQASMERWPLSKSIAEMRSFIEENEKNDPLINAPDKKN
F08B6.2      -----MDKSDMQRTVDSLRSQNLIERTPITVSAAEELRRFTES--QEDPLVNPIDKKV
AAA73553      ----MSNNMAKIAEARKTVEQLKLEVNIDRMKVSQAAAELLAFCEETHAKDDPLVTPVPAAE
               .   :: ::::: :  ::*   :  : .*:   :  *   .**:::..  *

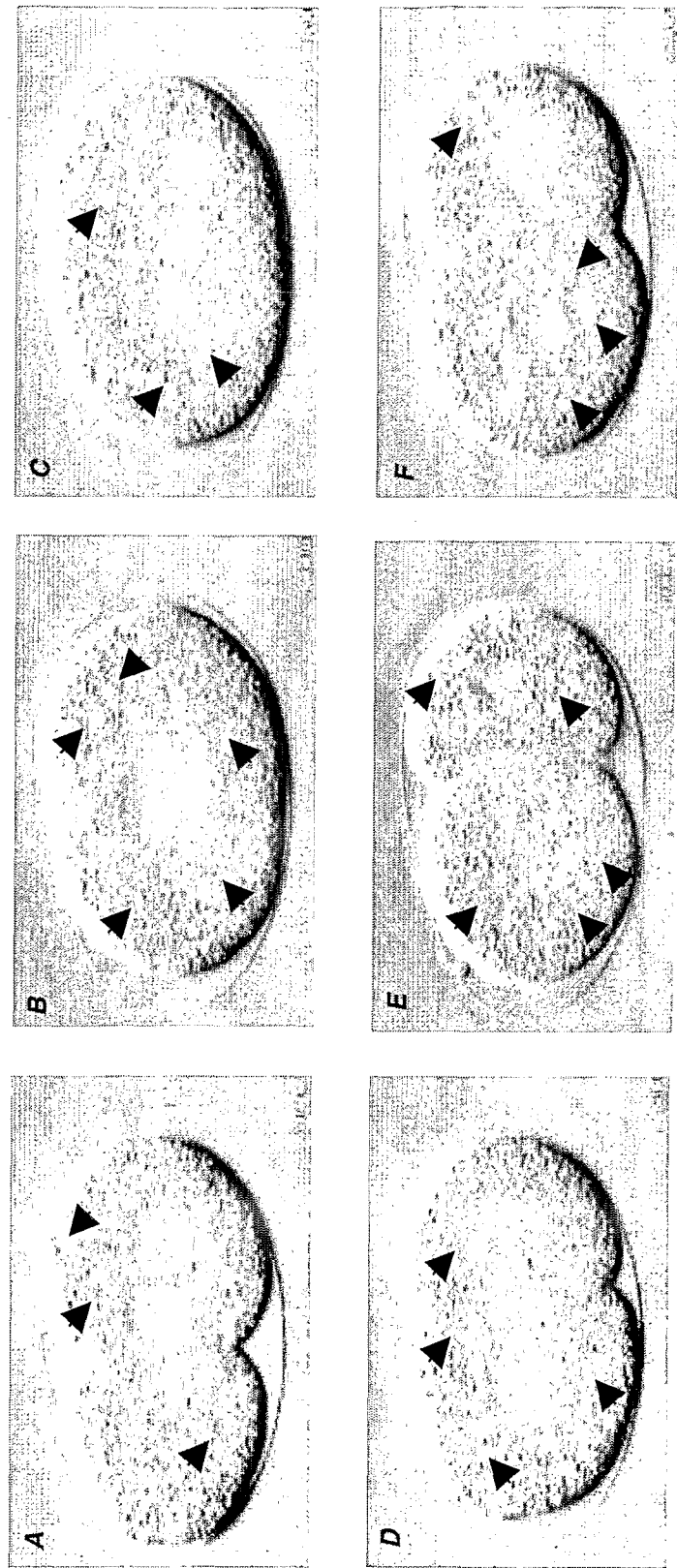
NP_057625      NPWVEKGK-C-----TIL-----
AAF52761      NPWAEKGK-CPQHHQQLDTPSQCSQVLGQDLGESPDLPVPEMQHYNNNNYYYYYNNLSY
F08B6.2      NPWAEKSK-C-----SML-----
AAA73553      NPFRDKRLFC-----TLL-----
               *:  :*   *           :*

NP_057625      -----
AAF52761      EPPVDRSLGGGKRSIQRLQQLVRRTRYELQQWPILLMQLLLFVILWLNKFWQLVNEQVTY
F08B6.2      -----
AAA73553      -----

NP_057625      -----
AAF52761      RRRRWH
F08B6.2      -----
AAA73553      -----
               *
```

Fig. 9

CD4.4



```
NP_078943      -----MAGASEARFAGLSLVQLNELLEDEGQLTENVQKMEETQNVLN  
CAD38936      DAWARLFNPRWRRRPPWQRMETLKDKTLOELEELQNDSEAIQLALESPEVQDLQLE  
AAF52060      -----MYQEYLYQLRATITPMCHHEIKELLNDDDKLDEKVD--EVLQVLRTO  
CD4.4         ---MFSONPYESHVDVAASAANLRNMTNEQLISLLDDALLESIIVNLQVRSMPD  
  
NP_078943      KEMTLASNRSLAEGNLLYQPQLDTLKARTOKYQELQVLFEAYQIKTKLDRQSSASLE  
CAD38936      REMALATNRSILAERNLEFGPLEISRNSLDRYQELRKIVERCQEQAQKLEKFSSALQPG  
AAF52060      KTSVFEDNRSRAERNIEREQJIELRGQLAELSEDGRTRCSSVQEKLSQIKEKSGGVGLE  
CD4.4         KESALAANKSLAEWNLAQKPRIIDAAKTQTVDLYDQVKKLQGEVAVLKSQSDSVSSSKSLD  
              .: *:* ** *: : : : : : : : : : : : : : : : : : :  
  
NP_078943      TLLALLQAEAKIEEDTENMAEFLDGELPLDSFDIVYQSKRKLAHMRVRKIEKLQEMVL  
CAD38936      TLDLLQVEGMKIEESEAMAEKFLEGEVLETLENFSMMRLSHLRVRVEKLVVVVR  
AAF52060      TALALLQTAASEEEQTEEMVKKENDS DIGVEDFLDAFLPIRRTMHRLRLKAEMOELMR  
CD4.4         TTSSLMQVAAQEAADDAEALFTQFENGELSVELFKQDKKTTIAHLRKIKSDRLAALLR  
              *:*. . . : : : : : : : : : : : : : : : : : : : : : :  
  
NP_078943      KGQRLPQALA-----PLPPR-----LP--ELAPTAPL--PYPAPEASGP---P-A  
CAD38936      K-PRASQELAGADAPPPRPVPDPQGTPPVVEEQPPPLAMPYPPLPSPSPSLFVGF  
AAF52060      K-----QRQG-----  
CD4.4         E-----Q-TYS-----  
              *  
NP_078943      VAPRRIPPPPPVP-----AGRLATPTTAA MSSGQ-AVPYPGLQCPLPVRVGLP-TQQ  
CAD38936      TAHGALPPAPFPVWSQPSFYSGPLGTYPAAQLGPRGAAGYSWSPQRSMPRPFGVPTFM  
AAF52060      -----AYGNVPSSGFFPASGCS-----  
CD4.4         -----MP-----HAQPGYPTGNHMPGIGNIQFG-  
              * *  
  
NP_078943      QFS-S-----QFVSYP-----PPLPQR---P-----P--PRILPHQPG  
CAD38936      GASGPGYPLRGGRAPSPGYQQSPYATGCKPPYIOPQLPSFGQPQPSVLPQPPYPGP  
AAF52060      -----APYIMG--PLMPMP-----  
CD4.4         -----SGYSG-----YPNISQP-----SAGRHPF  
              : *. * . * .  
  
NP_078943      -----FILQ-----  
CAD38936      PAPPYGFP PPPGPAWPGY  
AAF52060      -----  
CD4.4         F-----  
              :
```

Fig. 11

ZK546.1

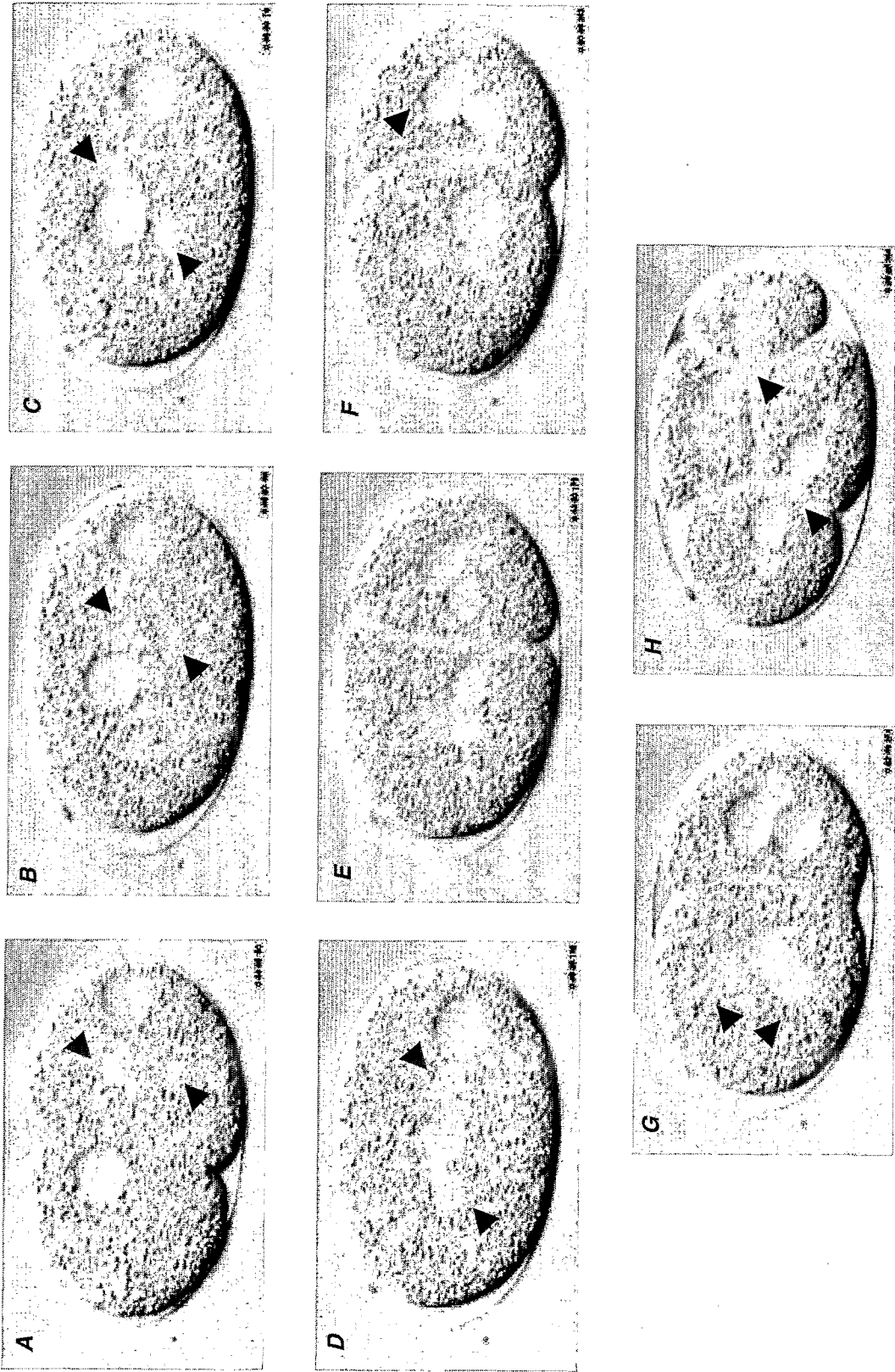


Fig. 12 1/7

CLUSTAL W (1.8) multiple sequence alignment

```
NP_056972      -----
AAA74950      ---MAQQAADKYL YVDKNF INNPLAQADCGAKK-LVWVPSTKNGFEPASLKEEVGEEAIV
ZK546.1        -----
NP_010225      -----MDIIQGLIQPKIQSVDETIP-TLCDRVENSTLISDRRS AVLGLKAFS
AAF53605      MSDDTSASGGTSAPFPSPVTADPEPGATASKLPGPIRSNIPTPATSGTGIPQPSKMKAPS
XP_109474      -----

NP_056972      -----
AAA74950      ELVENGKKVKVNKDDIQKMNP PKFSKVEDMAEL TCLNEASVLHNLKERYYSGLIYTSGL
ZK546.1        -----
NP_010225      RQYRESVIASGLKPLLNTLKR DYMDSDSVKAILETILILFIRGDGHDDL TRGWISQQS-R
AAF53605      SFGSTGSVSKIGRPCCNHTTPKSGPPPREATSMSRESDDLSSINSAYTDNSSAVLTANT
XP_109474      -----MAQSRRHMSSRTPSGSRMSTEASAR

NP_056972      -----
AAA74950      FCVVINPYKNLPIYSEEIVDMYKGKKRHEMPPHIYAITDTAYRSMMQDREDQSILCTGES
ZK546.1        -----
NP_010225      LQNGKYPSPLVMKQEKEQVDQFSLWIADALTQSEDLIHLLVEFW EIDNFHIRLYTIQLLE
AAF53605      EQFIIGQRVWLGGTRPGQIAFIGDTHFAAGEWAGVVLDEPNGKNDGCVSGKRYFQCEPKR
XP_109474      PLRVGSRVEVIGKGHRGT VAYVGATLFATGKWVG VILDEAKGKNDGTVQGRKYFTCDEGH

NP_056972      -----
AAA74950      GAGKTENTKKVIQYLAHVASSHKS KKDQGELERQLLQANPILEAFGNAKTVKNDNSSRFG
ZK546.1        -----
NP_010225      AVMATRPLKARSALISLPTSISTMVSLLDDMHEPIRDEAILLLMAVVNDSPHVQKLVAFE
AAF53605      GIFSRLTRLTTYPLAGAQTP TSPLAKSSPDRSRTVSPTASIRSSMLRSPGIGGKNGMAVG
XP_109474      GIFVRQSQIQVFEDGADTTSPETPDSSASKVLK-----

NP_056972      -----
AAA74950      KFIRINFVNGYIVGANIETYLLEKSRAIRQAKEERTFHIFYLLSGAGEHLKTDLLLEP
ZK546.1        -----
NP_010225      NIFERLFSIIIEEGGLRGLSVVNDCLSLINNILKYNTSNQTLFLETGNLPKLAHLLSEPI
AAF53605      ----DRVIVSSGFGSRPGILRYLGETQFAPGNWCGVELDEPSGKNDGTVD DIRYFECKPK
XP_109474      -----REGADAAAKTSKLRGL
```

Fig. 12 2/7

NP\_056972 -----  
AAA74950 YNKYRFLSNGHVTIPGQQDKDMFQETMEAMRIMGIPEDQMGLLRVISGVLQLGNIVFKK  
ZK546.1 -----  
NP\_010225 SQDEVFFWNDQRIVNINTALDIVSLTVEPGNTVTTKHQNALLDSSVLMVVLRLAFFHNIP  
AAF53605 YGVFVPIAKVSLSPSSKKTRL SRTGSRESLTSIGTMNSIATTATSRMRMNAQQRKSSTPV  
XP\_109474 KPKKAPTARKTTTRRPKPTRPASTGVAGPSSSLGPSGSASAGELSSSEPSTPAQTPLAAP

NP\_056972 -----  
AAA74950 ERNTDQASMPDN----TAAQKVSHLLGINVTDFTRGILTPRIKVGRDYVQKAQTKEQADF  
ZK546.1 -----  
NP\_010225 KKVRPVALLTAANMVRSNEHAQLEFSKIDVPYFDPSPVNSTANGGPIKLIPVVSILINW  
AAF53605 KPILATPKSQFS-MQDLLREKQQHVEKLMVERDL DREDAQNQALQLQKNINELKARIVEL  
XP\_109474 IIPAL TSPGAAPPLSPSPSKEEEGLRAQVRDLEEKLET LRLKRSEDK---AKLKELEKH

NP\_056972 -----  
AAA74950 AIEALAKATYERMFRWL VLRINKALDKTKRQGASFIGILDIAGFEIFDLNSFEQLCINYT  
ZK546.1 -----MLDLTNKESESSDNG  
NP\_010225 MLYANSVHTFDTRVACSRLLKAYFMDNFDLQRDFLLKQVQLCNNSTNNVGDNAKENGGSN  
AAF53605 ESALDNERKKTEELQCSIDEAQFCGDELNAQSQVYKEKIHDL ESKITKLVSATPSLQSIL  
XP\_109474 IQLEQVQEWKSKMQEQQADLQRRLKEARKEAKEALEAKERYMEEMADTADAIEMATL DK

NP\_056972 -----MEETQPPP-----  
AAA74950 NEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGLDLQPCIDLIEKPAGPPGILAL---LD  
ZK546.1 NSKYEDSID-----GREVGTSKPFKEERSLED-----  
NP\_010225 KSDKESDSD-----KDTDGKDGTEYEGSFKANLFEVLLNYDAELNLPFKLFFTTDIF  
AAF53605 PPDLP SDDG-----ALQEEIAKLQEKMTIQQKEVESRIAEQLEEEQRLREN-----  
XP\_109474 EMAEERAES-----LQQEVEALKERVDELTTDL-----

:

NP\_056972 -----QPKLPLCDSLMIWLQTFNTASPCQD-----VKQLTSGVAMAQVLHQIDA AW  
AAA74950 EECWF PKATDKSFVEKV VQE QGTHPKFQK-----PKQLKDKADFCIIHYAGKVDY  
ZK546.1 -----LQADLADMAVWMEGLDATKLPLND-----PQLLCNGRAFSEVLHNVDKNF  
NP\_010225 MFFFQ QD HKYSEELREITRNVT TGN DLEDEEPLKAIQTISELLTTS LTAADIRIPISYLT  
AAF53605 --VKYLNEQIATLQSELVSKDEALEKFSLSECG-----IENLRRELELLKEENEKQAQE  
XP\_109474 ---EILKAEIEEKGS DGAASSYQLKQLEE-----Q NARLKDALVRMRDLSSEK

Fig. 12 3/7

NP\_056972 FNESWLSRIKEDVGDNWR-----  
AAA74950 KADEWLMKNMDPLNDNIATLLHQSSDKFVSELWKDVDRIIGLDQVAGMSETALPGAFKTR  
ZK546.1 FTDGWLETMPENRTTNIMVFR-----  
NP\_010225 FLIYWLF GDFKATNDFLSDKS-----  
AAF53605 AQAEFTRKLAEKSVEVLRLLSS-----  
XP\_109474 QEHVKLQKLMEKKNQELEVVR-----

NP\_056972 -----IKASN-----VKKVLQ  
AAA74950 KGMFRTVGQLYKEQLAKLMATLRNTNPNFVCCIIPNHEKKAGKLDPHLVLDQLRCNGVLE  
ZK546.1 -----SCTRKLW  
NP\_010225 -----VIKSLLSFSYQIQDEDVTIKCLVTMLLG VAYEFSSKESPFPRKEYFEFIT  
AAF53605 -----ELQNLKATSDSLESERVN-----KTDECEILQT  
XP\_109474 -----QQRERLQE

NP\_056972 GIM--SYHFEFLGQQISEALIPDLNQITECSDPVELG-----  
AAA74950 GIR--ICRQGFNPRVVFQEFRQRYEILTPNSIPKGFMDGKQACVLMIKALELDSNLYRIG  
ZK546.1 RKM--FDYVNHINRTTVSSRWTDIHERIDGIYESDLP-----  
NP\_010225 KTLGKDNYASRIKQFKDSYFSKVD MNEDSILTPELDETG-----  
AAF53605 EVRMRDEQIRELNQQLDEVTTQLNVQKADSSALDDMLRLQ-----  
XP\_109474 ELSQAESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVR-----

NP\_056972 -----RLLQLILGCAINCE-----KKQEHIQNIMTLEES--  
AAA74950 QSKVFFRSGVLAHLEERDLKITDVIIGFQACCRGYLARKAFARQQQLTAMKVLQRNCA  
ZK546.1 -----AMVNLGMAVVTLAHIG-----KNAKRFDYSKALTS--  
NP\_010225 ----LPKVYFSTYFIQLFNENIYRIRTALSHDPDEEPINKISFEEVEKLQRQCTKLKG--  
AAF53605 ----KEGTEEKSTLLEKTEKELVQSKEQAAKTLNDKEQLEKQISDLKQLAEQEKLVRMT  
XP\_109474 -----ELRETVGDLEAMNEMN-----DELQENARETELELR--

NP\_056972 -----VQHVVMTAIQELMSKEILSSP  
AAA74950 AYLRRLRNWQWWRLFTKVKPLLNSIRHEDELLAKEAELTKVREKHLAAENRLTEMETMQSQ  
ZK546.1 -----THKSMMSNVAKMVTTVIDEMP  
NP\_010225 -----EITSLQTETESTHENLTEKLIALTNEHKELDEKYQILNSSHSS  
AAF53605 EN-----AINQIQLEKESIEQQLALKQNELED FQKKQSESEVHLQEIKAQ  
XP\_109474 -----EQLDMAGARVREAQKRVEAAQETVAD

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NP\_056972 PNDVGELEQQLKR-----ALEELQEALAEK-EELRQRCEELDMQVTTLQDEKNSLVSE  
AAA74950 LMAEKLQLEQLQAKTELCAEAEELRARLTAKKQEELEEICHDLARVEEEEEERCQYLQAE  
ZK546.1 ENPCFHEISELHGSQSELN-SLSESSGKLNGN--GSSERRSNADQILVDAELEIERLRTE  
NP\_010225 LKENFSILETELKNVRDSLDEMTQLRDVLETKDKENQTALLEYKSTIHKQEDSIKTLEKG  
AAF53605 NTQKDFELVESGESLKKLQQQLEQKTLGHEKLQAALEELKKEKETIIEKEQELQQLQSK  
XP\_109474 YQQTICKYRQLTAHLQDVNRELTNQOEASVERQQQPPPETFDKIKFAETKAHAKAIEME  
: . . : :

NP\_056972 NEMMNEKLDQLDGSFDD---PNTVVAKKYFHAQLQLEQLQEE-----NFRLEAAKDD  
AAA74950 KKKMQQNIQELEEQLEEEEESARQKLQLEKVTTEAKLKKLEEDQI-IMEDQNCKLAKEKKL  
ZK546.1 TENQRKEIERLTKSFET---AQHDMSSNSESGDISILEKQNEE---LRQKRRELEEKNLE  
NP\_010225 LETILSQKKAEDGINKMGKDLFALSREMQAVEENCKNLQKEKDKSNVNHQKETKSLKED  
AAF53605 SAESESALKVVQVQLEQLQQQAAASGEEGSKTVAKLHDEISQLKSQAEETQSELKSTQSN  
XP\_109474 LRQMEVAQANRHMSLLTAFMPDSFLRPGGDHDCVLVLLLMPR-LICKAELIRKQAQEKFD  
: . :

NP\_056972 YRVHCEELEKQLIEFQHRNDELTSLAETRALKDEIDV----LRATS----DKANKLEST  
AAA74950 LEDRVAEFTTDLMEEEESKSLAKLKNKHEAMITDLEER---LRREE----KQRQELEKT  
ZK546.1 LDAAVDQFKGIVFELTNENDVLRSDKERQRLQTVLDAAQSDLDEWK----TVANQYQKE  
NP\_010225 IAAKITEIKAINENLEEMKIQCNNLSKEKEHISKELVEYKSRFQSHDNLVAKLTEKLKSL  
AAF53605 LEAKSKQLEAANGSLEEEAKKSGHLLQITKLKSEVGETQAALSSCHTDVESKTKQLEAA  
XP\_109474 LSENCSERPGLRGAAGEQLSFAAGLVYSLSLQATLHRYEHALSQCSVDVYKKVGSLYPE  
: . . : : :

NP\_056972 VEIYRQKLQDLNDLRKQVKTLQETNMMYMHN-----TVSLEEELKKANAARTQLETY  
AAA74950 RRKLEGDSTDLSQIAELQAQIAELKMQLAKKEEELQAALARVEEEAAQKNMALKKIREL  
ZK546.1 AELSKQQDKEIKELLSQNKALKSRLDHHVKS-----ATLEDANKNGIAQLRTQVGGL  
NP\_010225 ANNYKDMQAENESLIKAVEESKNESSIQLSNLQNKIDSMSQEKENFQIERGSIKNIQEL  
AAF53605 NAALEKVNKEYAESRAEASDLQDKVKEITDT-----LHAELQAERSSSSALHTKLSKF  
XP\_109474 MSAHERSLDFLIELLHKDQLDETVNVEPLTK-----AIKYYQHLYSIHLAEQPEDS  
: . . . :

NP\_056972 KRQVQDLHVKLSSSE-----SKR-----  
AAA74950 ETQISELQEDLESERACRNKAQKQKRDLGEELEALKTELEDTLSTAAQQELRSKREQEV  
ZK546.1 TALNTELKASLDSK-----KR-----  
NP\_010225 KKTISDLEQTKEEIISKSDSSKDEYESQISLLKEKLETATTANDENVNKISELTKTREEL  
AAF53605 SDEIATGHKELTSKADAWS-----QEMLQKEKEL  
XP\_109474 TMQLADHIKFTQSALD-----CM

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NP\_056972 -----ADTLAFEMKRLEEKHEALLKEKERLIEQRDTLKETNEELRCSQVQQD---  
AAA74950 SILKKTLEDEAKTHEAQIQEMRQKHSQAVEELAEQLEQTKRVKATLEKAKQTLENERGEL  
ZK546.1 -----CVEQLEIQLIQHKEKVKELEDKDELIEERNRLENQLIFKEAVTPRS----  
NP\_010225 EAELAAYKNLKNELETKLETSEKALKEVKENEHLKEEKIQLEKEATETKQQLNSLRAN-  
AAF53605 QELRQQLQDSQDSQTKLKAAGERKEKSFEESIKNLQEEVTKAKTENLELSTGTQTTIKD-  
XP\_109474 G-----VEVGRLRAFLQGGQEATDIALLLRDLETSCSDTRQFCKKIRRRMPGTDAPG

NP\_056972 -----HL  
AAA74950 ANEVKALLQKGKGDSEHKRKKVEAQLQELQVKFSEGERVTELADKVSKLQVELDSVTGLL  
ZK546.1 -----LH  
NP\_010225 -----LESLEKEHEDLAAQLKKYEEQIANKERQYNEEISQLNDEITST  
AAF53605 -----LQERLEITNAELQHKEKMASEDAQKIADLKTLEAI  
XP\_109474 -----IPAALAFG

NP\_056972 NQTDASATKSYENLAAEIMPVEYREVFIR-----LQHENKM-----LR  
AAA74950 NQSDSKSSKLTKDFSALESQLDQTQELLQEENRQKLSLS-TKLKQMEDEKNS-----FR  
ZK546.1 ESMFEAGNLSFEPFS-----EKNTLP-----LEIENK-----R  
NP\_010225 QQENESIKKKNDELEGEVKAMKSTSEEQSNLKKSEIDALNLQIKELKKKNETNEASLLES  
AAF53605 QVANANISATNAELSTVLEVLQAEKSETNHIFELFEMEADMNSERLIEKVTGIKEELKET  
XP\_109474 SQVSDTLLDCRKHLTWVAVLQEVAAAAAQLIAPLAENGLPVAALEELAFKAS-----E

NP\_056972 LQQEGSENERIEELQEQLQKHKRMNELETEQR-----LSKERIRELQQQIEDLQKSL  
AAA74950 EQLEEEEEAAKRNLEKQIATLHAQVTDMMKKMEDGVGCLETAEEAKRRLQKDLEGLSQRL  
ZK546.1 LTERIQELESLEPLKGELITLKSNGVLEEEKL-----FATKQIEELQQQIEDLQENL  
NP\_010225 IKSVESETVKIKELQDECNFKEKEVSELEDKLKAS-----EDKNSKYLELQKESEKIKEEL  
AAF53605 HLQLDERQKKFEELEELKQQAQQSEQKLQQESQ-----TSKEKLTEIQQSLQELQDSV  
XP\_109474 QIYGSPSSSPYECLRQSCITLSTMNKLATAMQEGEYDAERPSPKPPPVELRAAALRAEI

NP\_056972 QE-----  
AAA74950 EEKVAAYDKLEKTKTRLQQELDDLVDLDHQRQSVSNLEKKQKKFDQLLAEKTIKAKYA  
ZK546.1 LK-----  
NP\_010225 DAKTTELKIQLEKITN-----LS  
AAF53605 KQKEELVQNLEEKVRE-----S---SSIIE  
XP\_109474 TDAEG-----

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NP\_056972 -QGSKSEGESSSK-----  
 AAA74950 EERDRAEAEAREKETKALSLARALEEAMEQKA-----ELERLNKQFRTEMEDLMSSKDDV  
 ZK546.1 -NQEHASGDVVG-----  
 NP\_010225 KAKEKSESELSRLKKTSSSEERKNAEEQLEKLKNEIQIKNQAFEKERKLLNEGSSTITQEY  
 AAF53605 AQNTKLNESNVQLENKTSCLKETQDQLLES-----QKK--EKQLQEEAAKLSGELQQV  
 XP\_109474 -LGLKLEDRETVIK-----  
 : .

NP\_056972 -----LKQKLEAHMEKLTEVHEELQK-----KQELIEDLQPD  
 AAA74950 GKSVHELEKSNRALEQQVEEMKTQLEEEDELQATEDAKLRLEVNLQAMKAQFERDLQGR  
 ZK546.1 -----LKIQLEKAEVEAQQMREAKMRAETN-----QAQVDEILKKR  
 NP\_010225 SEKINTLEDELIRLQNENELKAKEIDNTRSELEKVSLSNDELLEEKQNTIKSLQDEILSY  
 AAF53605 QEANGDIKDSLKVVEELVKVLEEKLAATSQLDAAQATN--KELQELLVKSQENEGNLQGE  
 XP\_109474 -----ELKKSLKIKGEELSEANVRLSLLEKKLDS-----AAKDADERIEKV  
 : : : . :

NP\_056972 INQN-----VQKINELEAALQ-----KKDEDMKAMEERYKMYLEKARNV  
 AAA74950 DEQSEKKKKQLVRQVREMAELEDERKQRSIAMAARKKLEMDLKDLEAHIDTANKNREEA  
 ZK546.1 TAELEVN---ATALQKAKAVID-----ELEYNSRPVSEDSMTSVQAFKEM  
 NP\_010225 KDKITRNDEKLLSIERNKRDLESKEQLRAAQESKAKVEEGLKKLEEESSEKAELEKS  
 AAF53605 SLAVTEKLQQLEQANGELKEALCQKENGKELQG---KLDESNTVLESQKKSHNEIQDKL  
 XP\_109474 QTRLDETQTLLRKKEKDFEETMD-----ALQADIDQLEAEKAEKQRLNSQ  
 . : : : . . . .

NP\_056972 IKTL-----DPKLNPAEIMLLRKQLAEKE---  
 AAA74950 IKQLRKLQAQMKDCMRDVEDDTRASREEILAQAKENEKKLKSMEAMIQLQEELAAAERAK  
 ZK546.1 KEENEK-----LRQKVEKLEIELNTVTQGFEQEN---  
 NP\_010225 KEMMKK-----LESTIESNETELKSSMETIRKSD---  
 AAF53605 EQAQKK-----ERTLQEETSKLAEQLSQLKQAN---  
 XP\_109474 SKRT-----IEGLRGPPPSGIATLVSGIAGEE---  
 : : . : :

NP\_056972 -----RRIEILESECKVAKFRDYEEKLIVSAWYNKS--  
 AAA74950 RQAQQRDELADEIANSSGKGALALEEKRRLEALIALLEEELEEEQGNTELINDRLKKAN  
 ZK546.1 -----RLLTSASHQQVLNRSIDEVMSMRAHAGSEEPQ  
 NP\_010225 -----EKLEQSKKSAEEDIKNLQHEKSDLISRINESE  
 AAF53605 -----EELQKSLQQKQLLLEKGNFDTQLAEYQKVID  
 XP\_109474 -----PQRGGAPGQAPGALPGPGLVKDSPLLLQQISAMR

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|           |                                                               |
|-----------|---------------------------------------------------------------|
| NP_056972 | LAFQKLGME SRLVSGGGACSDTGACTPA-----RSFLAQQRHITNTRRNL SVKVP     |
| AAA74950  | LQIDQINTDLN LERSHAQKNENARQLE-----RQNKELKAKLQEMESAVKSKYK       |
| ZK546.1   | TLLDTQKMSGALPWRSLASETRRELPTA-----MASILVLGFLVFIWMFININS        |
| NP_010225 | KDIEELKSKLR IEAKSGSELETVKQELNNAQEKIRINAEENTVLKSKLEDIERELKDKQA |
| AAF53605  | EMDDAASVKSALLEQLQNRVAELETALRQANDAQKTAYLETKE LRRQLESLELEKSREVL |
| XP_109474 | LHISQLQHENSILRGAQMKASLAALPPLH-----VAKLSLPPHEGPGGNLVAGALY      |

. . . :

|           |                                                              |
|-----------|--------------------------------------------------------------|
| NP_056972 | ATTSD-----                                                   |
| AAA74950  | ASIAALEAK-----IAQLEEQLDNETKERQAASKQVRRAEKKLKDVL LQVED        |
| ZK546.1   | ALNAPPNA-----                                                |
| NP_010225 | EIKSNQEEKELLTSRLKELEQELDSTQQAQKSEEERRAEVRKFQVEKSQLDEKAM LLET |
| AAF53605  | SLKAQMNGAS-----SRSGKGDEVESLDIETSLAKINFLNSIIADMQQ             |
| XP_109474 | RKTSQLLEKLN-----QLSTHTHVVDITRSSPAAKSPSAQLME                  |

:

|           |                                                                 |
|-----------|-----------------------------------------------------------------|
| NP_056972 | -----                                                           |
| AAA74950  | ERRNAEQFKDQADKASTRLKQLKRQLEEAEEEEAQRANASRRKLQRELE DATETADAMNRE  |
| ZK546.1   | -----                                                           |
| NP_010225 | KYNDLVNKEQAWKRDEDTVKKTTDSQRQEIEKLAKELDNLKAENSKLKEANEDRSEIDDL    |
| AAF53605  | KNDALKAKVQTLETLPMDFTKPHAFDALTKRKPA PRL FCDICDEFDQHDTEDCPIQGS ED |
| XP_109474 | QVAQLKSLSDTIEKLKDEV LKETVTQRP GATVPTDFATFPSSAFLRAKEEQDDTVYMGK   |

|           |                                                  |
|-----------|--------------------------------------------------|
| NP_056972 | -----                                            |
| AAA74950  | VSSLKNKLRRGDMPFVVTRRIVRKGTGDCSDEEVDGKADGADAKATE  |
| ZK546.1   | -----                                            |
| NP_010225 | MLLVTDLDEKNAKYRSK LKDLGVEISSDEEDDEEDDEEDEEEGQVA- |
| AAF53605  | QDYSTPSSESNNNEKERKLPAPRKYCDSC EVFGHDTSECADDETY-- |
| XP_109474 | VTFSCAAGLGQRHRLVLTQEQLHQLHSRLIS-----             |

Fig. 13

C56C10.3

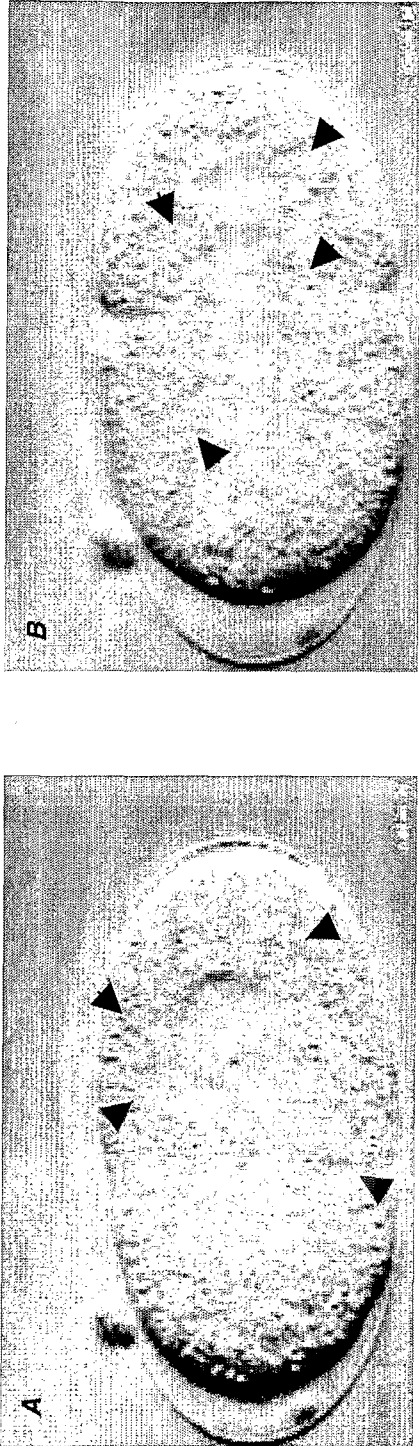


Fig. 14

```

CLUSTAL W (1.8) multiple sequence alignment for C56C10.3

XP_059282      MSVFGKLFAGAGGKAGKGGPTPQEAIQRLRDTEEMLSKKQEFLEKKIEQELTAAKKGHTK
NP_083638      MSVFGKLFAGAGGKAGKGGPTPQEAIQRLRDTEEMLSKKQEFLEKKIEQELTAAKKGHTK
C56C10.3      MSLFGKIF---GGRKQEAAPSTPQESIQKLRETEEMLEKKQEFLEKKVIDEQNAVYGYTK
AAAF58977      MSFFGKMF---GGKK-EVAPTTGEAIQKLRETEENMLIKKQEFLEAKIEDELNIARKNASK
               *.***:*      **:      :      *.***:***:*** ***** *: : * * .:***
               NKRAALQALKRKKRYEKQLAQIDGTLSTIEFQREALENANTNTVLKMGYAAKAMKAAH
               NKRAALQALKRKKRYEKQLAQIDGTLSTIEFQREALENANTNTVLKMGYAAKAMKAAH
               NKRMALQCLNRKRNFEKQLAHIDGVLSTIGYQREALENASTNAEVLNVMTASKALKAAH
               NKRVALQALKKKRLEKQLQIDGTLSTIEMQREALE SANTNTAVLTTMKNAADALKRAH
               ** ***.*:*. ***:****:**** *****.*.***:*** * *.:* *:*
               DNMDIDKVDELMQDIADQQELAEFISTAIKSPVGFGEFFDEDELMAELEEELEQEELDKNL
               DNMDIDKVDELMQDIADQQELAEFISTAIKSPVGFGEFFDEDELMAELEEELEQEELDKNL
               NNMDIDQVHLMEDIAEQQEVANEIAEAISNPVGFSTAVDDDDLMRELEALEQEELDDEL
               QNMDVDKVHDMDDIAEQQDVAREISDAISNPVAFGADLDDDELRELEDELEQENFDKEI
               ***:*:*:***:***:***:***:***:***:***:***:***:***:***:***:***:***:
               LEISGPETVPLPNVPSIALPSKPAKK-----KEEEDDDMKELENWAGSM
               LEISGPETVPLPNVPSVALPSKPAKK-----KEEEDDDMKELENWAGSM
               LDARAP-PVTLPDTPNIALPAVPASRP-----RAKEADKDLLEDLESWANA-
               IGIPEP-TPTLPEAPTEDLPEKAKEKKKATTTTAVEDDDDDPDMKQLLSWSN--
               * . ***:*. * . * . * . * . * . * . * . * . * . * . * . * . * .

```

Fig. 15 Wild type

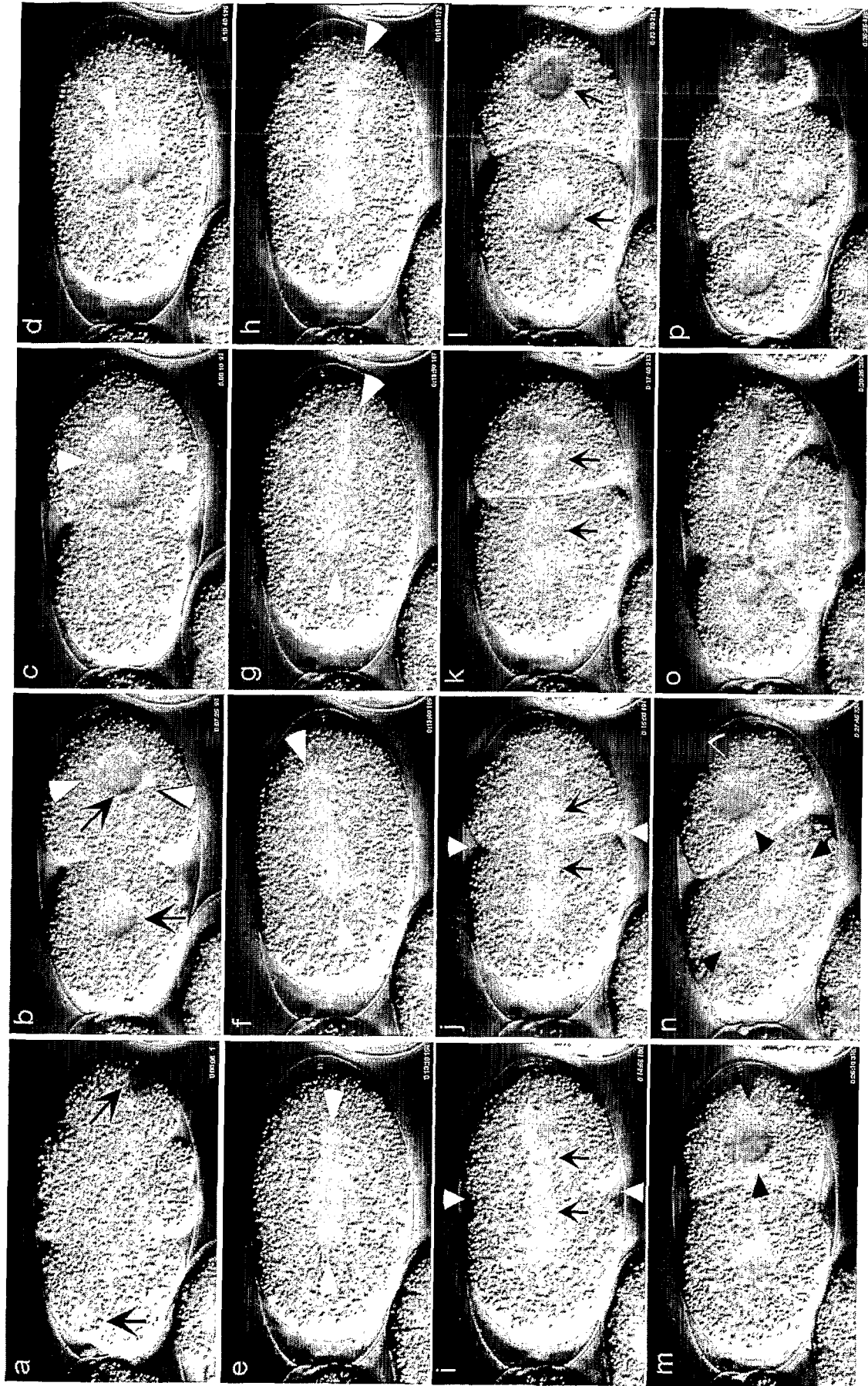


Fig.16

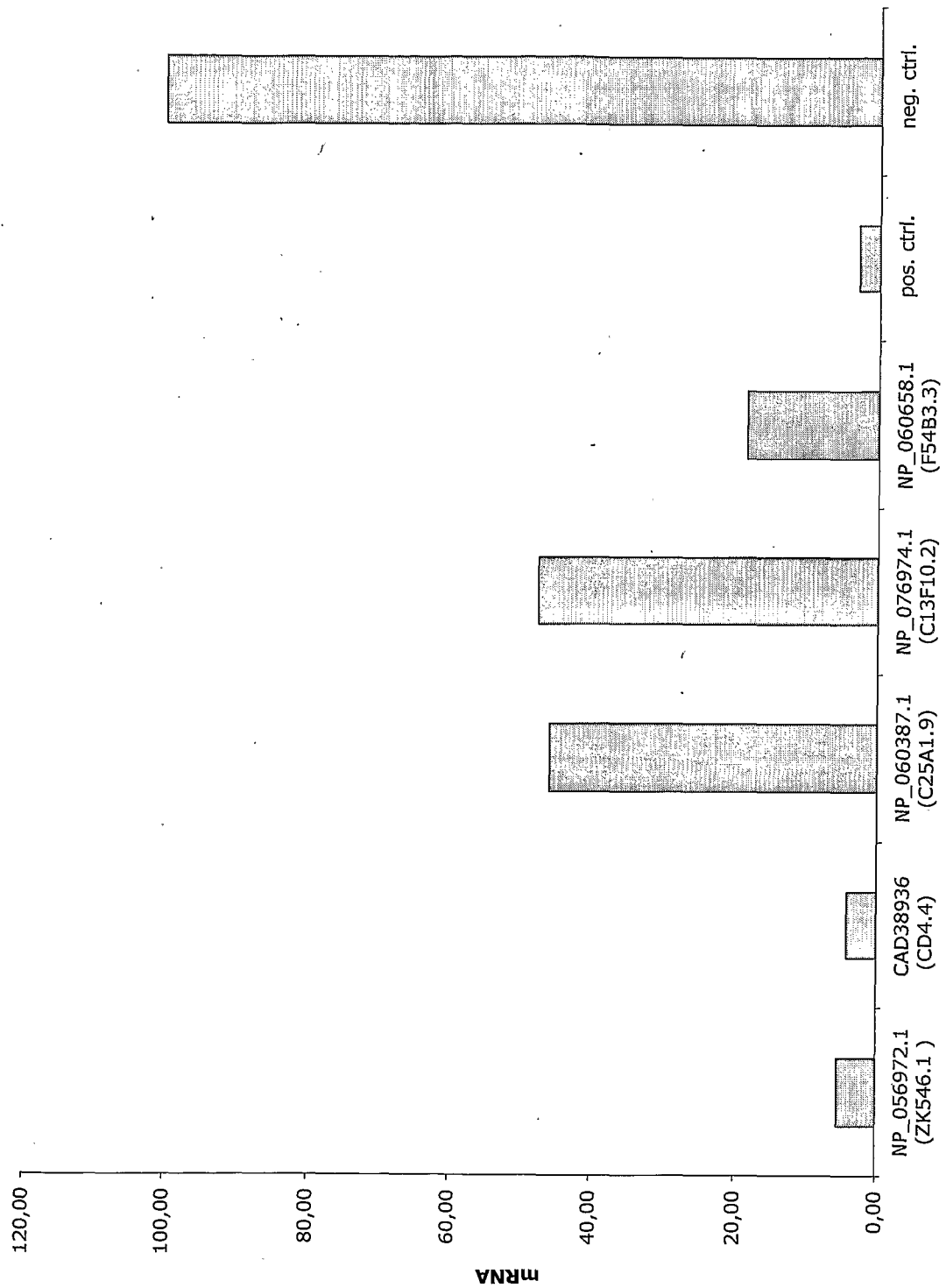


Fig. 17

