



15220806.p -PPSKRPFKDIYVVFELMESDLHQVIKANDLTLREHQQFLYOMRLALKFMHTANVHRDLK
18406088.p -PPSRPFKDIYVVFELMESDLHQVIKANDLTLREHQQFLYQLLRKLYIHTANVHRDLK
30685711.p -PPSRPFKDIYVVFELMESDLHQVIKANDLTLREHQQFLYQLLRKLYVHAANVHRDLK
15220976.p -PPSRPFKDIYVVFELMESDLHQVIKANDLTLREHQQFLYQLLRKLYVHAANVHRDLK
18410420.p -PPSRPFKDIYVVFELMESDLHQVIKANDLTLREHQQFLYQLLRKLYFHTANVHRDLK
18401750.p -PPSRPFKDIYVVFELMESDLHQVIKANDLTLREHQQFLYQLLRKLYFHTANVHRDLK
30677926.p -PPCRKFQKDIYVVFELMESDLHQVIKANDLTLREHQQFLYQLLRKLYFHTANVHRDLK
15239634.p -PPSRPFKDIYVVFELMESDLHQVIKANDLTLREHQQFLYQLLRKLYFHTANVHRDLK
C04G6.1.AA -AEGAAKGDKIYLVWDLMTDLHQVIKANDLTLREHQQFLYQLLRKLYFHTANVHRDLK
F09C12.2.A -RESGGQDLYIVMMDLMETDLHQVIKANDLTLREHQQFLYQLLRKLYFHTANVHRDLK
27369906.p -DL-QGEFLFKFSVAVIVOBMETDLARLLEQ-GTMEHEHAFMFYQMLLRLGLKLYIHSANVLHRDLK
Erk4 -DL-QGEFLFKFSVAVIVOBMETDLARLLEQ-GTMEHEHAFMFYQMLLRLGLKLYIHSANVLHRDLK
27679318.r -DL-QGEFLFKFSVAVIVOBMETDLARLLEQ-GTMEHEHAFMFYQMLLRLGLKLYIHSANVLHRDLK
31560797.m -TDD-VGSLTELNSVYIVOBMETDLARLLEQ-GPGLIEEHHAFMFYQMLLRLGLKLYIHSANVLHRDLK
Erk3 -TDD-VGSLTELNSVYIVOBMETDLARLLEQ-GPGLIEEHHAFMFYQMLLRLGLKLYIHSANVLHRDLK
13928856.r -TDD-VGSLTELNSVYIVOBMETDLARLLEQ-GPGLIEEHHAFMFYQMLLRLGLKLYIHSANVLHRDLK

	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	60																							
CG2309.AA	NICGDRRYSLEDMKKNCDDGH-LVKAALVLMHNRLTAKEAIRPYPYRSRFA-SADLMDVPPRLRVH-RYDVDPYR C05D10.2.A	MPCPRPKRPLDNLITTSQTAIDMVRLRIFPAKQRKLTVQECLVPEPYVQPHN-SSEPBVNPYEVPELPDHI 28486935.m	LGSGPQQTLDPTPBPADDLKLRLAFA-PDKRLSAEQLCPYQRP-HCPDREWAR-SDVRVLPVHEGD 20903997.m	LGSGPQQTLDPTPBPADDLKLRLAFA-PDKRLSAEQLCPYQRP-HCPDREWAR-SDVRVLPVHEGD 29244575.m	LGSGPQQTLDPTPBPADDLKLRLAFA-PDKRLSAEQLCPYQRP-HCPDREWAR-SDVRVLPVHEGD 27662128.r	LGSGPQQTLDPTPBPADDLKLRLAFA-PDKRLSAEQLCPYQRP-HCPDREWAR-SDVRVLPVHEGD 27545428.r	LGSGPQQTLDALLPDPDPEPALDLKLRLAFA-PDKRLSAEQLCPYQRP-HCPDREWAR-TRGSDVRLPVHEGD Erk7	LGSGPQQTLDALLPDPDPEPALDLKLRLAFA-PDKRLSAEQLCPYQRP-HCPDREWAR-ADRV-RAHGV 2erk_	LGPHNKVPNRLP-NADSKADLLKLRLAFA-PDKRLSAEQLCPYQRP-HCPDREWAR-ADRV-RAHGV 16758698.r	LGPHNKVPNRLP-NADSKADLLKLRLAFA-PDKRLSAEQLCPYQRP-HCPDREWAR-ADRV-RAHGV 6754632.m	LGPHNKVPNRLP-NADSKADLLKLRLAFA-PDKRLSAEQLCPYQRP-HCPDREWAR-ADRV-RAHGV Erk2	LGPHNKVPNRLP-NADSKADLLKLRLAFA-PDKRLSAEQLCPYQRP-HCPDREWAR-ADRV-RAHGV 21489933.m	LGPSKTKVVAWAKLPP-KSDSKADLLRMLDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD 8393331.r	LGPSKTKVVAWAKLPP-KSDSKADLLRMLDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD Erk1	LGPSKTKVVAWAKLPP-KSDSKADLLRMLDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD mpk-1.AA	LGPHNKVPNRLP-GADPFALELLRMLDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD 6754634.m	LGPHNKVPNRLP-GADPFALELLRMLDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD Erk5	LGPHNKVPNRLP-GADPFALELLRMLDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD 15231196.p	LGPNPFRPLAKLPS-HVNPNAILDVLRFMDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD 15224359.p	LGPPYQPRQSINDKGP-TVHPDIAIDLIEKMLDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD 15231753.p	LPTLPRQSFTEKGP-NVPPAIDLVKMLDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD 18378855.p	LGQXPRQNFARGP-NMSVNADLQKMLDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD 15234152.p	LGQXPRQNFARGP-NMSACAVDLMLVDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD 30690210.p	LGPRYKPKQFARGP-KMPTTAIDLLRMLDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD 15223026.p	LPHVKQJSPRKGP-NISPAIDLLRMLDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD 18406388.p	LPPYSPGMSLSRLYMP-CANVIAIDLLQKMLVDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD 15218451.p	LPPYSPGMSLSRLYMP-CANVIAIDLLQKMLVDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD 15224120.p	LPSYRGTHLNSLGP-CANPAIDLLQKMLVDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD 15234397.p	LPSYRGTHLNSLGP-CANPAIDLLQKMLVDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD 15231915.p	MRKQNLVFSKGP-NADPAIATILLORLIAFPDKRPTAAEALADPYFKCLAKVVERBSCPIKSMFEER-RRKQKODIR 15220806.p	MRKQNLVFSKGP-NADPAIATILLORLIAFPDKRPTAAEALADPYFKCLAKVVERBSCPIKSMFEER-RRKQKODIR 30685711.p	MRKQNLVFSKGP-NADPAIATILLORLIAFPDKRPTAAEALADPYFKCLAKVVERBSCPIKSMFEER-RRKQKODIR 15220976.p	MRKQNLVFSKGP-NADPAIATILLORLIAFPDKRPTAAEALADPYFKCLAKVVERBSCPIKSMFEER-RRKQKODIR 18410420.p	MRKQNLVFSKGP-NADPAIATILLORLIAFPDKRPTAAEALADPYFKCLAKVVERBSCPIKSMFEER-RRKQKODIR 30677926.p	MRKQNLVFSKGP-NADPAIATILLORLIAFPDKRPTAAEALADPYFKCLAKVVERBSCPIKSMFEER-RRKQKODIR 15239634.p	MRKQNLVFSKGP-HDPHPLAIDLLRMLDFPENKRIT-EEAALAPYI-EQYYDPDDEPVAE-EPTEFDME-DD C04G6.1.AA	CGRCPPLPFCAIPE-XASPARNMVYQIOLCPKRYSAQDOLCPFMQAHQDOYDPLCP F09C12.2.A	FGRCPPLPFCAIPE-XASPARNMVYQIOLCPKRYSAQDOLCPFMQAHQDOYDPLCP 27369906.m	TWEVLRPLRKLPD-VNSEAIDFLKLIIDTFNEMDLDLAEMLCPYNSPSCPDEPTS-HPFPRIEDBDIDIVLMAASQDSLSNWD Erk4	TWEVLRPLRKLPD-VNSEAIDFLKLIIDTFNEMDLDLAEMLCPYNSPSCPDEPTS-HPFPRIEDBDIDIVLMAASQDSLSNWD 27679318.r	TWEVLRPLRKLPD-VNSEAIDFLKLIIDTFNEMDLDLAEMLCPYNSPSCPDEPTS-HPFPRIEDBDIDIVLMAASQDSLSNWD 31560797.m	TWEVLRPLQLPG-ISRAFALDEQIITFSPMDRMLTAAEALCPYNSPSCPDEPTS-HPFPRIEDBDIDIVLMAASQDSLSNWD Erk3	TWEVLRPLQLPG-ISRAFALDEQIITFSPMDRMLTAAEALCPYNSPSCPDEPTS-HPFPRIEDBDIDIVLMAASQDSLSNWD 13928856.r

	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	80
CG2309.AA	VAAAAAVARRKKSSWQSQQSCKGKHTEAHKAVQTAIQTQDKNICKDPPRMQESQSLTEAKAPIKNYSNKMCEKKYKKHHSMSCITRDTPSETBRQQRERRAYQRMKRELOLKESYRRTEAESEPILKETTEQESKTIKVIEKVCEHTEKADESLKDQQKDSITPFGTCVRERIHHLDEMEKCTEELV	C05D10.2.A	-NPSSIKQRKSVERAR-LEPANIKPSKILHPLKILSNTY-	28486935.m	ATGQPPSAPSGVKTQVRAMAPSLTSQAEQAANQALRSDPA-	20903997.m	ATGQPPSAPSGVKTQVRAMAPSLTSQAEQAANQALRSDPA-	29244575.m	ATGQPPSAPSGVKTQVRAMAPSLTSQAEQAANQALRSDPA-	27662128.r	ATGQPPSAPSGVKTQVRAMAPSLTSQAEQAANQALRSDPA-	27545428.r	ATGQPPSAPSGVKTQVRAMAPSLTSQAEQAANQALRSDPA-	Erk7	AKEAPPTLSLVPKSGRAAAPSLSQAAQANQPLRSDPA-	2erk_	16758698.r	6754632.m	Erk2	21489933.m

8393331.r
Erk1
mpk-1.AA
6754634.m
KAALLKSILSRRLRDGPSAPELEAPERPRKPVTAQEREREREEKRERRRQEAKEREKREKERGACTLGGPSTDPLAGLVLSDNDRSLLERWTRMARPPAP-----APAPAPAPAPAPSSAQPTSTPTGFVQSSTGP-LQPAGSIPGFASQFVCPPPGVPOPAG-----PIAPPLQTAPSTSLLASQSLVPPSGLPGSS
KAALLKSILSRRLRDGPSAPELEAPERPRKPVTAQEREREREEKRERRRQEAKEREKREKERGAGASGGPSTDPLAGLVLSDNDRSLLERWTRMARFAAFTSVPAPAPPTPTPVQPTSPPPGLAQPPTGPPQPSAGSTSGPVPQFACPPPFPAPHTGPPGPIFPVAPPQIATSTSLLAAQSLVPPPGLPGS
15231196.p
15224359.p
15231753.p
18378855.p
15234152.p
30690210.p
15223026.p
18406388.p
15218451.p
15224120.p
15234397.p
15231915.p
SKNGASSAAGHPSTSAYPELEAPERPRKPVTAQEREREREEKRERRRQEAKEREKREKERGAGASGGPSTDPLAGLVLSDNDRSLLERWTRMARFAAFTSVPAPAPPTPTPVQPTSPPPGLAQPPTGPPQPSAGSTSGPVPQFACPPPFPAPHTGPPGPIFPVAPPQIATSTSLLAAQSLVPPPGLPGS
15220806.p
18406088.p
ET-----TQNIPFNHATIQAQQRNLNAAKPSTFMQFVAFFDNGRISRDAYD-----PRSFIR-----STNLPSQOSAATVAMCKQQERRRTTMEPEKARQISQYN-----RYAPDVAINIIDNNPFIMARTGMNAEENISDRIIITDNLQATAGIVAAAAAAAFCGSAHRKVGAIVRYGMKMY
30685711.p
DVERRAAAAVASTLES-----EEADNGGGYSARNLMK-----ASISGSKCIGVQSCKIDKEDTTAEE-----EDNNEVATELDKVASLNS-----EDNNEVATELDKVASLNS
15220976.p
DVERRAAAAVASTLES-----EEADNGGGYSARNLMK-----ASISGSKCIGVQSCKIDKEDTTAEE-----EDNNEVATELDKVASLNS-----EDNNEVATELDKVASLNS
18410420.p
18401750.p
DIENRSIASLVTTESSPPTSQHEGSDYRNQTSQTYGYSARSLLKS-----ASISASCKCIGMKPRNKSE-----YGE-----SNNDTVDALSQKVALHT
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15239634.p
LSKCGSIRDERRGADRNAQPMMSRIPINVQTIQAAVARPKCKVVGSLVLRYNMC-----GAATGVEALEQOORRMRVNRPAAASQYKRTOPCKSNRGDEDCAAA-----EGPSRLKPNTQYYLPQKVSAADTAMSWY
C04G6.1.AA
F09C12.1.AA
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27369906.m
HHYSEPKLILDLSHWKQOAASAPP-----QCSSS-----RPCVT
Erk4
HHYSEPKLILDLSHWKQOAAGAPPATGLDTGAREDEPAFLIEIAQWVKSTQGAQSTPARPPPTPSAACLPRFPPPGPGGRRQPPVRFGRVHLPRPEALHQARGPAGQ
27679318.r
31560797.m
NHYKEPKLIIIDLGNWKEQSKKEKDKKKGKCKERNGLVKQAQIALEEASQQLA-----ERERGQGFDFFDSFTAIGTQQLSAQHQADVVDKLNDLNSSVSQLELKSLISKSVEKREQEKCRANIAQQLGALYQSWWDSQFVSGGECFLISQFCCERKDEIAEKENTYTSYLDKFFSRKEDSEMLETEFVEEGKREGERGREAGLHS
Erk3
NHYKEPKLIIIDLGNWKEQSKKEKDKKKGKCKERNGLVKQAQIALEEASQQLACKERKEKNQGFDFFDSFTAIGTQQLSSCHEPTDVVDKLNDLNSSVSQLELKSLISKSVEKGMANLAQLEALYQSWWDSQFVSGGEDCCFFINQFC-EVRKDEQVEKENITYTSYLDKFFSRKEDTEMLETEFVEGKLGGERGHEEGFLN
13928856.r
NHYKEPKLIIIDLGNWKEQSKKDSDKRGKSKCKERNGLVKRRLRKPSSWL-----RGRG-----AKALTIMPSSQAP-----FSSVPSVSLLT

810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 10

CG2309.AA
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C05D10.2.A
28486935.m
20903997.m
29244575.m
27662128.r
27545428.r
Erk7
2erk_
16758698.r
6754632.m
Erk2
21489933.m
8393331.r
Erk1
mpk-1.AA
6754634.m
APEVLPYFPPSGPPPPDPGLTPQPSSESVDVLNLTQQLSKSQVEDPLPPVFSGTPKGSGAGGYGVGFDEEFLNQSPDMGVADGPQDGQADASLASLADLWLEGHGMNPADIESLQREIQMDSPMLLSDLPLDQLP
Erk5
TPGVLPYFPPGLPPPDAGGAQSSMSESPDVNLTVTQQLSKSQVEDPLPPVFSGTPKGSGAGGYGVGFDEEFLNQSPDMGVADGPQDGQADASLASLADLWLEGHGMNPADIESLQREIQMDSPMLLADLPLDQLP
15231196.p
15224359.p
15231753.p
18378855.p
15234152.p
30690210.p
15223026.p
18406388.p
15218451.p
15224120.p
15234397.p
15231915.p
15220806.p
18406088.p
30685711.p
15220976.p
18410420.p
18401750.p
30677926.p
15239634.p
C04G6.1.AA
F09C12.2.A
27369906.m
Erk4
27679318.r
31560797.m
GGGEFLSKQLESIGTPQFISPVGSPLKS1QATLTPSAMKSSPQIPHHTYSSILKHLEN
Erk3
NSGEFLFKNQLESIGTPQFISPVGSPLKS1QATLTPSAMKSSPQIPHHTYSSILKHLEN

13928856.r

1010 1020

....|.....|....|....|

CG2309.AA HHAPYDHMRPTEDDIQEADSLPESN

C05D10.2.A

28486935.m

20903997.m

29244575.m

27662128.r

27545428.r

Erk7

2erk_

16758698.r

6754632.m

Erk2

21489933.m

8393331.r

Erk1

mpk-1.AA

6754634.m

Erk5

15231196.p

15224359.p

15231753.p

18378855.p

15234152.p

30690210.p

15223026.p

18406388.p

15218451.p

15224120.p

15234397.p

15231915.p

15220806.p

18406088.p

30685711.p

15220976.p

18410420.p

18401750.p

30677926.p

15239634.p

C04G6.1.AA

F09C12.2.A

27369906.m

Erk4

27679318.r

31560797.m

Erk3

13928856.r