>sp|P48734|CDK1\_BOVIN Cyclin-dependent kinase 1 OS=Bos taurus GN=CDK1 PE=2 SV=2

MEDYTKIEKIGEGTYGVVYKGRHKTTGQVVAMKKIRLESEEEGVPSTAIREISLLKELRH

PNIVSLQDVLMQDSRLYLIFEFLSMDLKKYLDSIPPGQFMDSSLVKSYLYQILQGIVFCH

SRRVLHRDLKPQNLLIDDKGTIKLADFGLARAFGIPIRVYTHEVVTLWYRSPEVLLGSAR

YSTPVDIWSIGTIFAELATKKPLFHGDSEIDQLFRIFRALGTPNNEVWPEVESLQDYKST

FPKWKPGSLASHVKNLENGLDLLSKMLIYDPAKRISGKMALNHPYFNDLDSQIKKM

>sp|P34556|CDK1\_CAEEL Cyclin-dependent kinase 1 OS=Caenorhabditis elegans GN=cdk-1 PE=1 SV=1

MDPIREGEVAHEGDSVYTLNDFTKLEKIGEGTYGVVYKGKNRRTNAMVAMKKIRLESEDE

GVPSTAVREISLLKELQHPNVVGLEAVIMQENRLFLIFEFLSFDLKRYMDQLGKDEYLPL

ETLKSYTFQILQAMCFCHQRRVIHRDLKPQNLLVDNNGAIKLADFGLARAIGIPIRVYTH

EVVTLWYRAPEILMGAQRYSMGVDMWSIGCIFAEMATKKPLFQGDSEIDELFRIFRVLGT

PTELEWNGVESLPDYKATFPKWRENFLRDKFYDKKTGKHLLDDTAFSLLEGLLIYDPSLR

LNAKKALVHPYFDNMDTSKLPAGNYRGELELF

>sp|P23572|CDK1\_DROME Cyclin-dependent kinase 1 OS=Drosophila melanogaster GN=Cdk1 PE=1 SV=1

MEDFEKIEKIGEGTYGVVYKGRNRLTGQIVAMKKIRLESDDEGVPSTAIREISLLKELKH

ENIVCLEDVLMEENRIYLIFEFLSMDLKKYMDSLPVDKHMESELVRSYLYQITSAILFCH

RRRVLHRDLKPQNLLIDKSGLIKVADFGLGRSFGIPVRIYTHEIVTLWYRAPEVLLGSPR

YSCPVDIWSIGCIFAEMATRKPLFQGDSEIDQLFRMFRILKTPTEDIWPGVTSLPDYKNT

FPCWSTNQLTNQLKNLDANGIDLIQKMLIYDPVHRISAKDILEHPYFNGFQSGLVRN

>sp|P79432|CDK4\_PIG Cyclin-dependent kinase 4 OS=Sus scrofa GN=CDK4 PE=3 SV=1

MATSRYEPVAEIGVGAYGTVYKARDPHSGHFVALKSVRVPNGGGAGGGLPISTVREVALL

RRLEAFEHPNVVRLMDVCATARTDRETKVTLVFEHVDQDLRTYLDKAPPPGLPVETIKDL

MRQFLRGLDFLHANCIVHRDLKPENILVTSGGTVKLADFGLARIYSYQMALTPVVVTLWY

RAPEVLLQSTYATPVDMWSVGCIFAEMFRRKPLFCGNSEADQLGKIFDLIGLPPEDDWPR

DVSLPRGAFSPRGPRPVQSVVPEMEESGAQLLLEMLTFNPHKRISAFRALQHSYLHKAEG

NPE

>XP\_008954060.1 PREDICTED: cyclin-dependent kinase 1 isoform X1 [Pan paniscus]

MEDYTKIEKIGEGMFRSIYGTNEGYIPSPVPRLQQNILDSPGTYGVVYKGRHKTTGQVVAMKKIRLESEE

EGVPSTAIREISLLKELRHPNIVSLQDVLMQDSRLYLIFEFLSMDLKKYLDSIPPGQYMDSSLVKSYLYQ

ILQGIVFCHSRRVLHRDLKPQNLLIDDKGTIKLADFGLARAFGIPIRVYTHEVVTLWYRSPEVLLGSARY

STPVDIWSIGTIFAELATKKPLFHGDSEIDQLFRIFRALGTPNNEVWPEVESLQDYKNTFPKWKPGSLAS

HVKNLDENGLDLLSKMLIYDPAKRISGKMALNHPYFNDLDNQIKKM

Bos, elegans, drosphila, sus, Pan:

1. sp|P48734|CDK1\_BOVIN Cyclin-dependent kinase 1 OS=Bos taurus GN=CDK1 PE=2 SV=2

2. XP\_008954060.1 PREDICTED: cyclin-dependent kinase 1 isoform X1 [Pan paniscus]

3. sp|P23572|CDK1\_DROME Cyclin-dependent kinase 1 OS=Drosophila melanogaster GN=Cdk1 PE=1 SV=1

4. sp|P34556|CDK1\_CAEEL Cyclin-dependent kinase 1 OS=Caenorhabditis elegans GN=cdk-1 PE=1 SV=1

5. sp|P79432|CDK4\_PIG Cyclin-dependent kinase 4 OS=Sus scrofa GN=CDK4 PE=3 SV=1

1. sp|P48734|CD ------------------MEDYTKIEKIGE-----------------------------G

2. XP\_008954060 ------------------MEDYTKIEKIGEGMFRSIYGTNEGYIPSPVPRLQQNILDSPG

3. sp|P23572|CD ------------------MEDFEKIEKIGE-----------------------------G

4. sp|P34556|CD MDPIREGEVAHEGDSVYTLNDFTKLEKIGE-----------------------------G

5. sp|P79432|CD MA----------------TSRYEPVAEIGV-----------------------------G

1. sp|P48734|CD TYGVVYKGRHKTTGQVVAMKKIRLES---EEEGVPSTAIREISLLKEL---RHPNIVSLQ

2. XP\_008954060 TYGVVYKGRHKTTGQVVAMKKIRLES---EEEGVPSTAIREISLLKEL---RHPNIVSLQ

3. sp|P23572|CD TYGVVYKGRNRLTGQIVAMKKIRLES---DDEGVPSTAIREISLLKEL---KHENIVCLE

4. sp|P34556|CD TYGVVYKGKNRRTNAMVAMKKIRLES---EDEGVPSTAVREISLLKEL---QHPNVVGLE

5. sp|P79432|CD AYGTVYKARDPHSGHFVALKSVRVPNGGGAGGGLPISTVREVALLRRLEAFEHPNVVRLM

1. sp|P48734|CD DVLM-----QDSRLYLIFEFLSMDLKKYLDSIPPGQFMDSSLVKSYLYQILQGIVFCHSR

2. XP\_008954060 DVLM-----QDSRLYLIFEFLSMDLKKYLDSIPPGQYMDSSLVKSYLYQILQGIVFCHSR

3. sp|P23572|CD DVLM-----EENRIYLIFEFLSMDLKKYMDSLPVDKHMESELVRSYLYQITSAILFCHRR

4. sp|P34556|CD AVIM-----QENRLFLIFEFLSFDLKRYMDQLGKDEYLPLETLKSYTFQILQAMCFCHQR

5. sp|P79432|CD DVCATARTDRETKVTLVFEHVDQDLRTYLDKAPP-PGLPVETIKDLMRQFLRGLDFLHAN

1. sp|P48734|CD RVLHRDLKPQNLLIDDKGTIKLADFGLARAFGIPIRVYTHEVVTLWYRSPEVLLGSARYS

2. XP\_008954060 RVLHRDLKPQNLLIDDKGTIKLADFGLARAFGIPIRVYTHEVVTLWYRSPEVLLGSARYS

3. sp|P23572|CD RVLHRDLKPQNLLIDKSGLIKVADFGLGRSFGIPVRIYTHEIVTLWYRAPEVLLGSPRYS

4. sp|P34556|CD RVIHRDLKPQNLLVDNNGAIKLADFGLARAIGIPIRVYTHEVVTLWYRAPEILMGAQRYS

5. sp|P79432|CD CIVHRDLKPENILVTSGGTVKLADFGLARIYSYQMAL-TPVVVTLWYRAPEVLLQST-YA

1. sp|P48734|CD TPVDIWSIGTIFAELATKKPLFHGDSEIDQLFRIFRALGTPNNEVWPEVESLQDYKSTFP

2. XP\_008954060 TPVDIWSIGTIFAELATKKPLFHGDSEIDQLFRIFRALGTPNNEVWPEVESLQDYKNTFP

3. sp|P23572|CD CPVDIWSIGCIFAEMATRKPLFQGDSEIDQLFRMFRILKTPTEDIWPGVTSLPDYKNTFP

4. sp|P34556|CD MGVDMWSIGCIFAEMATKKPLFQGDSEIDELFRIFRVLGTPTELEWNGVESLPDYKATFP

5. sp|P79432|CD TPVDMWSVGCIFAEMFRRKPLFCGNSEADQLGKIFDLIGLPPEDDWPRDVSLP--RGAFS

1. sp|P48734|CD KWKPGSLASHVKN-------L-ENGLDLLSKMLIYDPAKRISGKMALNHPYFNDLDSQ--

2. XP\_008954060 KWKPGSLASHVKN-------LDENGLDLLSKMLIYDPAKRISGKMALNHPYFNDLDNQ--

3. sp|P23572|CD CWSTNQLTNQLKN-------LDANGIDLIQKMLIYDPVHRISAKDILEHPYFNGFQSG--

4. sp|P34556|CD KWRENFLRDKFYDKKTGKHLLDDTAFSLLEGLLIYDPSLRLNAKKALVHPYFDNMDTSKL

5. sp|P79432|CD PRGPRPVQSVVPE-------MEESGAQLLLEMLTFNPHKRISAFRALQHSYLHKAEGN--

1. sp|P48734|CD --------IKKM

2. XP\_008954060 --------IKKM

3. sp|P23572|CD --------LVRN

4. sp|P34556|CD PAGNYRGELELF

5. sp|P79432|CD ----------PE

CLUSTAL O(1.2.4) multiple sequence alignment

sp|P79432|CDK4\_PIG ----------------MATSRYEPVAEI-----------------------------GVG

sp|P34556|CDK1\_CAEEL MDPIREGEVAHEGDSVYTLNDFTKLEKIGE-----------------------------G

sp|P23572|CDK1\_DROME ------------------MEDFEKIEKIGE-----------------------------G

sp|P48734|CDK1\_BOVIN ------------------MEDYTKIEKIGE-----------------------------G

XP\_008954060.1 ------------------MEDYTKIEKIGEGMFRSIYGTNEGYIPSPVPRLQQNILDSPG

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sp|P79432|CDK4\_PIG AYGTVYKARDPHSGHFVALKSVRVPNGGGAGGGLPISTVREVALLRRLEAFEHPNVVRLM

sp|P34556|CDK1\_CAEEL TYGVVYKGKNRRTNAMVAMKKIRLESE---DEGVPSTAVREISLLKE---LQHPNVVGLE

sp|P23572|CDK1\_DROME TYGVVYKGRNRLTGQIVAMKKIRLESD---DEGVPSTAIREISLLKE---LKHENIVCLE

sp|P48734|CDK1\_BOVIN TYGVVYKGRHKTTGQVVAMKKIRLESE---EEGVPSTAIREISLLKE---LRHPNIVSLQ

XP\_008954060.1 TYGVVYKGRHKTTGQVVAMKKIRLESE---EEGVPSTAIREISLLKE---LRHPNIVSLQ

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sp|P79432|CDK4\_PIG DVCATARTDRETKVTLVFEHVDQDLRTYLDKAPPP-GLPVETIKDLMRQFLRGLDFLHAN

sp|P34556|CDK1\_CAEEL AVI-----MQENRLFLIFEFLSFDLKRYMDQLGKDEYLPLETLKSYTFQILQAMCFCHQR

sp|P23572|CDK1\_DROME DVL-----MEENRIYLIFEFLSMDLKKYMDSLPVDKHMESELVRSYLYQITSAILFCHRR

sp|P48734|CDK1\_BOVIN DVL-----MQDSRLYLIFEFLSMDLKKYLDSIPPGQFMDSSLVKSYLYQILQGIVFCHSR

XP\_008954060.1 DVL-----MQDSRLYLIFEFLSMDLKKYLDSIPPGQYMDSSLVKSYLYQILQGIVFCHSR

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sp|P79432|CDK4\_PIG CIVHRDLKPENILVTSGGTVKLADFGLARIYSYQMA-LTPVVVTLWYRAPEVLLQS-TYA

sp|P34556|CDK1\_CAEEL RVIHRDLKPQNLLVDNNGAIKLADFGLARAIGIPIRVYTHEVVTLWYRAPEILMGAQRYS

sp|P23572|CDK1\_DROME RVLHRDLKPQNLLIDKSGLIKVADFGLGRSFGIPVRIYTHEIVTLWYRAPEVLLGSPRYS

sp|P48734|CDK1\_BOVIN RVLHRDLKPQNLLIDDKGTIKLADFGLARAFGIPIRVYTHEVVTLWYRSPEVLLGSARYS

XP\_008954060.1 RVLHRDLKPQNLLIDDKGTIKLADFGLARAFGIPIRVYTHEVVTLWYRSPEVLLGSARYS

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sp|P79432|CDK4\_PIG TPVDMWSVGCIFAEMFRRKPLFCGNSEADQLGKIFDLIGLPPEDDWPRDVSLPRGA--FS

sp|P34556|CDK1\_CAEEL MGVDMWSIGCIFAEMATKKPLFQGDSEIDELFRIFRVLGTPTELEWNGVESLPDYKATFP

sp|P23572|CDK1\_DROME CPVDIWSIGCIFAEMATRKPLFQGDSEIDQLFRMFRILKTPTEDIWPGVTSLPDYKNTFP

sp|P48734|CDK1\_BOVIN TPVDIWSIGTIFAELATKKPLFHGDSEIDQLFRIFRALGTPNNEVWPEVESLQDYKSTFP

XP\_008954060.1 TPVDIWSIGTIFAELATKKPLFHGDSEIDQLFRIFRALGTPNNEVWPEVESLQDYKNTFP

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sp|P79432|CDK4\_PIG PRGPRPVQSVV-------PEMEESGAQLLLEMLTFNPHKRISAFRALQHSYLHKAEGNPE

sp|P34556|CDK1\_CAEEL KWRENFLRDKFYDKKTGKHLLDDTAFSLLEGLLIYDPSLRLNAKKALVHPYFDNMDTSKL

sp|P23572|CDK1\_DROME CWSTNQLTNQL-------KNLDANGIDLIQKMLIYDPVHRISAKDILEHPYFNGFQSGLV

sp|P48734|CDK1\_BOVIN KWKPGSLASHV-------KNL-ENGLDLLSKMLIYDPAKRISGKMALNHPYFNDLDSQIK

XP\_008954060.1 KWKPGSLASHV-------KNLDENGLDLLSKMLIYDPAKRISGKMALNHPYFNDLDNQIK

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sp|P79432|CDK4\_PIG ------------

sp|P34556|CDK1\_CAEEL PAGNYRGELELF

sp|P23572|CDK1\_DROME RN----------

sp|P48734|CDK1\_BOVIN KM----------

XP\_008954060.1 KM----------