

KNC82246 hypothetical protein SARC 05472 [Sphaeroforma a  
CAMPEP 0196951544 /NCGR PEP ID=MMETSP1377-20130  
XP 001746195.1 cyclin B [Monosiga brevicollis MX1]  
XP 001746195 cyclin B [Monosiga brevicollis MX1]  
CAA62472.1 cyclin B, partial [Hydra vulgaris]  
CAA62471.1 cyclin B [Hydra viridissima]  
P20439.2  
XP 009019533.1 hypothetical protein HELRODRAFT 106476 [  
EAW51306.1 cyclin B1 [Homo sapiens]  
BAA92876.1 cyclin B1 [Danio rerio]  
Q95067.1  
AAH66507.1 Cyclin B2 [Danio rerio]  
XP 001439676.1 hypothetical protein (macronuclear) [Paramec  
AAD08957.1 mitotic cyclin-CYC1a [Paramecium tetraurelia]  
AAD01794.1 cyclin B2 [Paramecium tetraurelia]  
XP 001017313 amine-terminal domain cyclin [Tetrahymena th  
EAR96952 amine-terminal domain cyclin (macronuclear) [Tet  
EAS07022 amine-terminal domain cyclin (macronuclear) [Tet  
EAR83691 amine-terminal domain cyclin (macronuclear) [Tet  
XP 643591 hypothetical protein DDB G0275493 [Dictyosteliu  
XP 001013775.3 amine-terminal domain cyclin [Tetrahymena  
EAR93530 amine-terminal domain cyclin (macronuclear) [Tet  
CAA49202.1 CLB4 [Saccharomyces cerevisiae]  
CAA49201.1 CLB3 [Saccharomyces cerevisiae]  
AAT92875.1 YDL155W [Saccharomyces cerevisiae]  
PKK60365.1 A/B/D/E cyclin [Rhizophagus irregularis]  
EWH15581.1 Clb2p [Saccharomyces cerevisiae P283]  
CLB1 YGR108W SGDID:S000003340  
AAA34501.1 G2-specific B-type cyclin-like protein [Sacchar  
EWH15582.1 Clb5p [Saccharomyces cerevisiae P283]  
CAA49894.1 cyclin [Saccharomyces cerevisiae]  
AAT93114.1 YGR109C [Saccharomyces cerevisiae]  
XP 002111737 hypothetical protein TRIADDRAFT 56083 [Tric  
Q9I7I0.1  
CAC94915.1 cyclin B3 [Homo sapiens]  
Q5SCB7  
Q5SCB7 OSTTA Cyclin A  
XP 001745729 hypothetical protein [Monosiga brevicollis M  
XP 002109629 hypothetical protein TRIADDRAFT 53841 [  
AAH66425.1 Cyclin F [Danio rerio]  
AAB60342.1 cyclin F [Homo sapiens]  
CAMPEP 0199578094 /NCGR PEP ID=Symbiodinium-sp-C  
GAX81523.1 hypothetical protein CEUSTIGMA g8951.t1 [Chl  
XP 003589118.2 carboxy-terminal domain cyclin [Medicago ti  
XP 010494276.1 PREDICTED: putative cyclin-A3-1 isoform >  
Q9FMH5  
A0MEB5  
Q9C6A9  
Q3ECW2  
Q9FVX0  
Q9C6Y3  
Q38819  
Q9C968  
Q39071  
Q147G5  
P14785.3  
AAB49754.1 cyclin A1 [Homo sapiens]  
EAX05246.1 cyclin A2 [Homo sapiens]  
AAH45840.2 Cyclin A2 [Danio rerio]  
XP 002112749 hypothetical protein TRIADDRAFT 24944 [Tric  
CAA62470.1 cyclin A, partial [Hydra viridissima]  
KJE94017 cyclin A [Capsaspora owczarzaki ATCC 30864]  
CAMPEP 0196967952 /NCGR PEP ID=MMETSP1377-2013  
XP 004998950.1 cyclin A [Salpingoeca rosetta]  
XP 001743335 cyclin A [Monosiga brevicollis MX1]  
KJE97202 G2/mitotic-specific cyclin-B [Capsaspora owczarz  
EAS03328 amine-terminal domain cyclin (macronuclear) [Tr  
B7GES4  
KNC51496 hypothetical protein AMSP 07694 [Thecamonas  
XP 004365050.2 cyclin Dx [Capsaspora owczarzaki ATCC 50062  
KNC75563 hypothetical protein SARC 11916 [Sphaeroforma  
CAMPEP 0196951960 /NCGR PEP ID=MMETSP1377-20130  
NP066970.3 cyclin-O [Homo sapiens]  
KJE88973 hypothetical protein CAOG 000538 [Thecamonas  
Q9NG21  
Q9NG21 9TRYP Cyclin  
KZV13424 CLN3 [Saccharomyces cerevisiae]  
EAR87477 amine-terminal domain cyclin (macronuclear)  
KZV09052 CLN1 [Saccharomyces cerevisiae]  
CAA97982 CLN2 [Saccharomyces cerevisiae]  
CAA21630.1 G1/S-specific cyclin-D [Caenorhabditis elegans]  
Q24158  
AAM00355.1 cyclin D1 [Danio rerio]  
AAH23620.1 Cyclin D1 [Homo sapiens]  
XP 002110607 expressed hypothetical protein [Trichoplax  
AAA52137.1 cyclin D3 [Homo sapiens]  
CAA48493.1 cyclin D2 [Homo sapiens]  
XP 022808428.1 G1/S-specific cyclin-D2-like [Stylophora  
CAMPEP 0192418040 /NCGR PEP ID=Symbiodinium-sp-  
Q8IEW7 9TRYP Cyclin 8  
CAMPEP 0199594322 /NCGR PEP ID=Symbiodinium-sp-  
EEC50966 predicted protein [Phaeodactylum tricornutum  
EEC43733 predicted protein [Phaeodactylum tricornutum  
EEC44236 predicted protein [Phaeodactylum tricornutum  
EEC49106 predicted protein [Phaeodactylum tricornutum  
EEC43258 predicted protein [Phaeodactylum tricornutum  
EEC51801 predicted protein [Phaeodactylum tricornutum  
EEC51851 predicted protein [Phaeodactylum tricornutum  
EEC43747 predicted protein [Phaeodactylum tricornutum  
EEC51859 predicted protein [Phaeodactylum tricornutum  
EEC51223 predicted protein [Phaeodactylum tricornutum  
XP 009036810.1 hypothetical protein AURANDRAFT 715  
EEC43271 predicted protein [Phaeodactylum tricornutum  
AAH43175.1 Cyclin J [Homo sapiens]  
EEC45903 predicted protein [Phaeodactylum tricornutum  
CCND OSTTA RecName: Full=Cyclin-D  
XP 001747385 hypothetical protein [Monosiga brevicollis  
KNC56049 cyclin Dx [Thecamonas trahens ATCC 50062]  
KNC79761 hypothetical protein SARC 07852 [Sphaeroforma  
AAC41978.1 cyclin G2 [Homo sapiens]  
AAC41977.1 cyclin G1 [Homo sapiens]  
BAA08849.1 cyclin I [Homo sapiens]  
XP 020611600.1 cyclin-I-like [Orbicella faveolata]  
CAMPEP 0192409796 /NCGR PEP ID=Symbiodinium-sp-  
Q9LZM0  
Q2V3B2  
Q9ZR04  
P42751  
P42753  
Q9SN11  
AED98321.1 CYCLIN D3;2 [Arabidopsis thaliana]  
P42752  
Q8LGA1  
Q0WQ9N  
EAS06644 amine-terminal domain cyclin (macronuclear)  
EAR95548 amine-terminal domain cyclin (macronuclear)  
EAR88519 amine-terminal domain cyclin (macronuclear) [T  
EAR92814 amine-terminal domain cyclin (macronuclear) [T  
EAR82991 amine-terminal domain cyclin (macronuclear)  
EAS07794 amine-terminal domain cyclin (macronuclear) [T  
EAR94831 amine-terminal domain cyclin (macronuclear) [T  
EAS01638 amine-terminal domain cyclin (macronuclear) [T  
EAS00010 amine-terminal domain cyclin (macronuclear)  
XP 002116348 hypothetical protein TRIADDRAFT 5539, pa  
EAR96531 amine-terminal domain cyclin (macronuclear)  
XP 001747412 hypothetical protein [Monosiga brevicollis  
KJE91793 cyclin L beta [Capsaspora owczarzaki ATCC 50062  
KNC81896 hypothetical protein SARC 05809 [Sphaeroforma  
XP 002113496 hypothetical protein TRIADDRAFT 378  
AAH45378.1 Cyclin L1 [Danio rerio]  
Q96S94.1  
AAH67812.1 Cyclin L1 [Homo sapiens]  
XP 638121 hypothetical protein DDB G0285553 [Dictyostelium  
Smic33082 SmicGene33082 sp S micro  
CAMPEP 0192409358 /NCGR PEP ID=Symbiodinium-sp-C  
CAMPEP 0199553876 /NCGR PEP ID=Symbiodinium-sp-C  
XP 022972922.1 cyclin-L1-1-like isoform X4 [Cucurbitur  
CEL98528.1 unnamed protein product [Vitrella brassicacae  
KNC49456 cyclin [Thecamonas trahens ATCC 50062]  
XP 002116531 hypothetical protein TRIADDRAFT 31C  
Q96433.2  
AAW56073.1 cyclin T2 [Homo sapiens]  
AAC39664.1 cyclin T1 [Homo sapiens]  
XP 637571 hypothetical protein DDB G0286617 [Dictyostelium  
KNC82244 hypothetical protein SARC 05471 [Sphaeroforma  
XP 002113606 hypothetical protein TRIADDRAFT 2730  
AAH15935.1 Cyclin K [Homo sapiens]  
XP 644320 hypothetical protein DDB G0274139 [Dictyostelium  
KNC51963 cyclin-C [Thecamonas trahens ATCC 50062]  
PKK73243.1 C/H/G cyclin [Rhizophagus irregularis]  
XP 004363813 cyclin C [Capsaspora owczarzaki ATCC 50062]  
XP 002115547 hypothetical protein TRIADDRAFT 296C  
CAA44720.1 Cyclin C [Drosophila melanogaster]  
AAR20478.1 cyclin C [Danio rerio]  
AAC50825.1 cyclin C [Homo sapiens]  
XP 002109341 hypothetical protein TRIADDRAFT 53C  
AAA57006.1 cyclin H [Homo sapiens]  
AAA57006 cyclin H [Homo sapiens]  
Q8W5S1  
Q5SCB4  
AAV68602 cyclin H [Ostreococcus tauri]  
XP 646851 hypothetical protein DDB G0268668 [Dictyostelium  
KNC56158 cyclin mcs2 [Thecamonas trahens ATCC 50062]  
EAR91248 amine-terminal domain cyclin (macronuclear)  
XP 642568 cyclin domain-containing protein [Dictyostelium  
EAW85912.1 chromosome 10 open reading frame 9, is  
XP 002116466 hypothetical protein TRIADDRAFT 30C  
KNC78856 hypothetical protein SARC 08730 [Sphaeroforma  
CAD43092 cyclin 5 [Trypanosoma  
KNC77900 hypothetical protein SARC 09649 [Sphaeroforma  
EAS05969 amine-terminal domain cyclin (macronuclear)  
CAD43049 cyclin 7 [Trypanosoma brucei]  
Q8IEW3  
Q382C9  
EAS03399 amine-terminal domain cyclin (macronuclear)  
CAMPEP 0196930664 /NCGR PEP ID=MMETSP1377-20130  
m.6019 g.6019 ORF g.6019 m.6019 type:5prime part  
m.7872 g.7872 ORF g.7872 m.7872 type:5prime part  
m.24931 g.24931 ORF g.24931 m.24931 type:5prime part  
CEM14973.1 unnamed protein product [Vitrella brassicacae  
PIM02140.1 cyclin2 related protein, partial [Toxoplasma gondii  
KFH13723.1 cyclin2 related protein [Toxoplasma gondii  
KYK64877.1 cyclin2 related protein [Toxoplasma gondii  
KFG29715.1 cyclin2 related protein [Toxoplasma gondii  
EWH15856 Pho80p [Saccharomyces cerevisiae P283]  
DAA08497 TPA: Pcl7p [Saccharomyces cerevisiae S288c]  
DAA07717 TPA: Pcl6p [Saccharomyces cerevisiae S288c]  
DAA11217 TPA: Pcl8p [Saccharomyces cerevisiae S288c]  
DAA07976 TPA: Pcl10p [Saccharomyces cerevisiae S288c]  
Q57YN6 9TRYP Hypothetical protein  
Q57YN5 9TRYP Hypothetical protein  
XP 001746391 hypothetical protein [Monosiga brevicollis MX1]  
Q8IEW6  
EAR96354 amine-terminal domain cyclin (macronuclear) [Tetrahymena  
EAS06402 amine-terminal domain cyclin (macronuclear)  
EAR86180 amine-terminal domain cyclin (macronuclear)  
EAS02326 amine-terminal domain cyclin (macronuclear) [Tetrahymena  
EAS06339 amine-terminal domain cyclin (macronuclear) [Tetrahymena  
KJE90681 cyclin E2 [Capsaspora owczarzaki ATCC 30864]  
AAM78547.1 cyclin E [Caenorhabditis elegans]  
XP 002111485 hypothetical protein TRIADDRAFT 15757, partial  
P54733.2  
AAD08816.1 cyclin E2 [Homo sapiens]  
AAH75747.1 Cyclin E [Danio rerio]  
AAH35498.1 Cyclin E1 [Homo sapiens]  
CAMPEP 0196853782 /NCGR PEP ID=MMETSP1374-20130  
CAMPEP 0196858170 /NCGR PEP ID=MMETSP1374-20130  
AAU93350.1 mitotic cyclin 1, partial [Lingulodinium polyedrum  
CAMPEP 0192466248 /NCGR PEP ID=Symbiodinium-sp-C  
CAMPEP 0199563964 /NCGR PEP ID=Symbiodinium-sp-C  
symbB.v1.2.020228.t2 S B1  
symbB.v1.2.020228.t1 S B1  
m.35670 g.35670 ORF g.35670 m.35670 type:5prime part  
m.28300 g.28300 ORF g.28300 m.28300 type:complete len  
m.36255 g.36255 ORF g.36255 m.36255 type:5prime part  
CAMPEP 0192615964 /NCGR PEP ID=Symbiodinium-sp-M  
CAMPEP 0192526882 /NCGR PEP ID=Symbiodinium-sp-C  
CAMPEP 0192594040 /NCGR PEP ID=Symbiodinium-sp-M  
CAMPEP 0192534670 /NCGR PEP ID=Symbiodinium-sp-CC  
CAMPEP 0192534476 /NCGR PEP ID=Symbiodinium-sp-CC  
CAMPEP 0192513094 /NCGR PEP ID=Symbiodinium-sp-CC  
CAMPEP 0192512154 /NCGR PEP ID=Symbiodinium-sp-CC  
Smic39017 SmicGene39017 sp S micro  
CAMPEP 0196987114 /NCGR PEP ID=MMETSP1377-20130  
CAMPEP 0192465250 /NCGR PEP ID=Symbiodinium-sp-C1  
CAMPEP 0199568816 /NCGR PEP ID=Symbiodinium-sp-C1  
m.34531 g.34531 ORF g.34531 m.34531 type:complete len:3  
symbB.v1.2.002641.t1 S B1  
m.6207 g.6207 ORF g.6207 m.6207 type:5prime part len:4  
m.13663 g.13663 ORF g.13663 m.13663 type:5prime part len:1  
SymbF.scaffold2170.1 SymbF.scaffold2170:3083-6120(-) S F  
CAMPEP 0192419630 /NCGR PEP ID=Symbiodinium-sp-C1  
CAMPEP 0199635470 /NCGR PEP ID=Symbiodinium-sp-C1  
m.14528 g.14528 ORF g.14528 m.14528 type:complete len:3  
m.26466 g.26466 ORF g.26466 m.26466 type:complete len:3  
symbB.v1.2.033807.t1 S B1  
CAMPEP 0192602738 /NCGR PEP ID=Symbiodinium-sp-Mp  
Smic26768 SmicGene26768 sp S micro  
CAMPEP 0192534772 /NCGR PEP ID=Symbiodinium-sp-CC  
CAMPEP 0196927910 /NCGR PEP ID=MMETSP1377-20130  
OMJ78392.1 hypothetical protein SteCoe 21825 [Stentor coeruleus]  
XP 002111135 hypothetical protein TRIADDRAFT 22525, partial  
EAR91121 cyclin-dependent kinase-like protein (macronuclear)  
XP 005835589.1 hypothetical protein GUITHDRAFT 157506 [C  
EEC47805 predicted protein [Phaeodactylum tricornutum CCA  
KNC46921 G2/mitotic-specific cyclin-B [Thecamonas trahens  
EEC47909 predicted protein, partial [Phaeodactylum tricornutum  
Q8IEW9 9TRYP Cyclin 6  
CAMPEP 0196944882 /NCGR PEP ID=MMETSP1377-20130  
Q48790  
P30183  
P39069  
Q39067  
Q9SA32  
Q9SFW6  
Q9LDM4  
Q39070  
Q39068  
CDW78836.1 n-terminal domain containing protein [Stylonychia  
OMJ68918.1 hypothetical protein SteCoe 33501 [Stentor coeruleus]  
CAMPEP 0196876038 /NCGR PEP ID=MMETSP1374-20130  
CDW74673.1 UNKNOWN [Stylonychia lemnae]  
XP 005706828.1 G2/mitotic-specific cyclin 1/2 [Galdieria sulphuraria]  
OMJ84746.1 hypothetical protein SteCoe 14065 [Stentor coeruleus]  
Q5SCB6  
XP 005850047.1 hypothetical protein CHLNCDRAFT 10568, partial  
XP 001701288.1 B-type cyclin [Chlamydomonas reinhardtii]