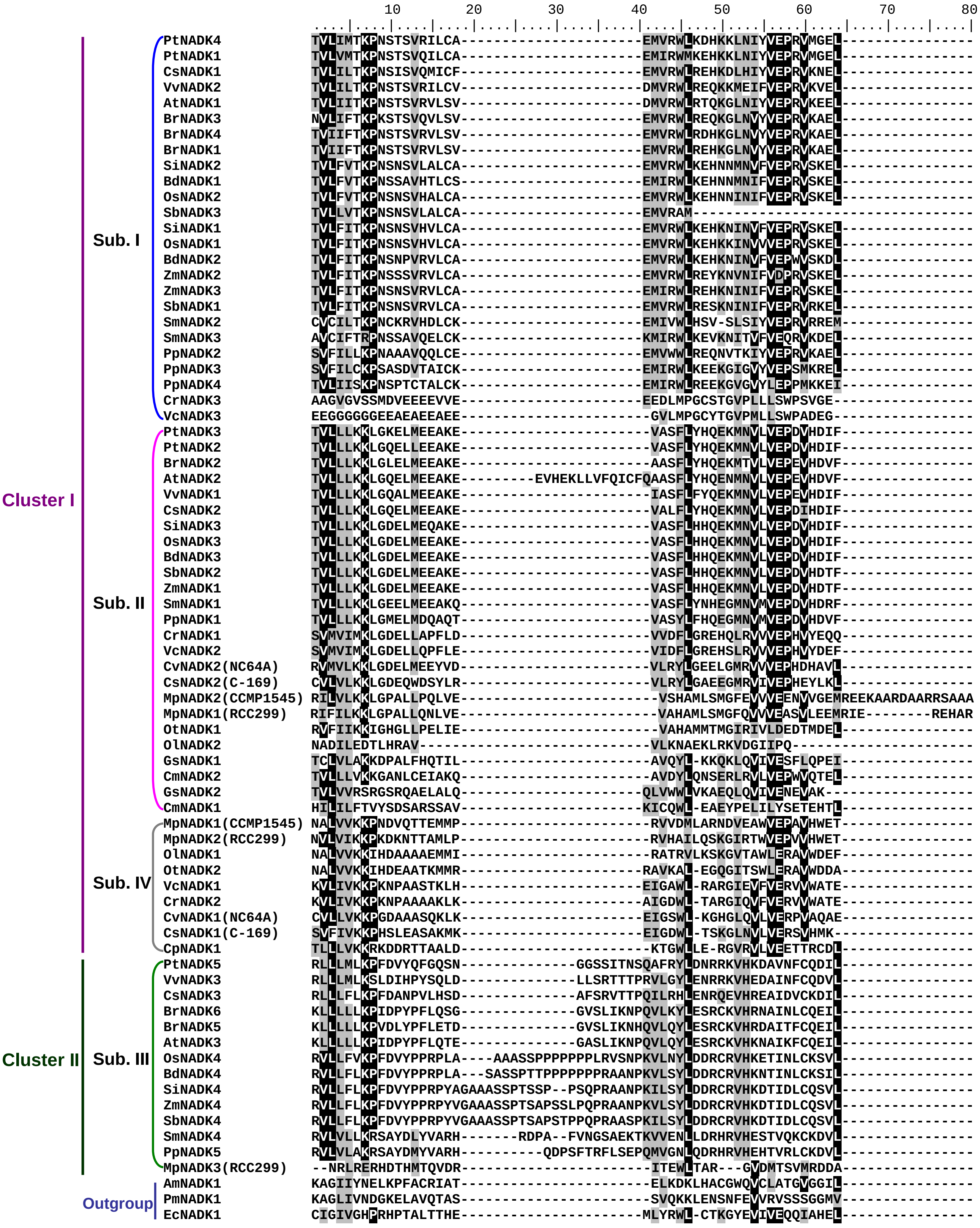
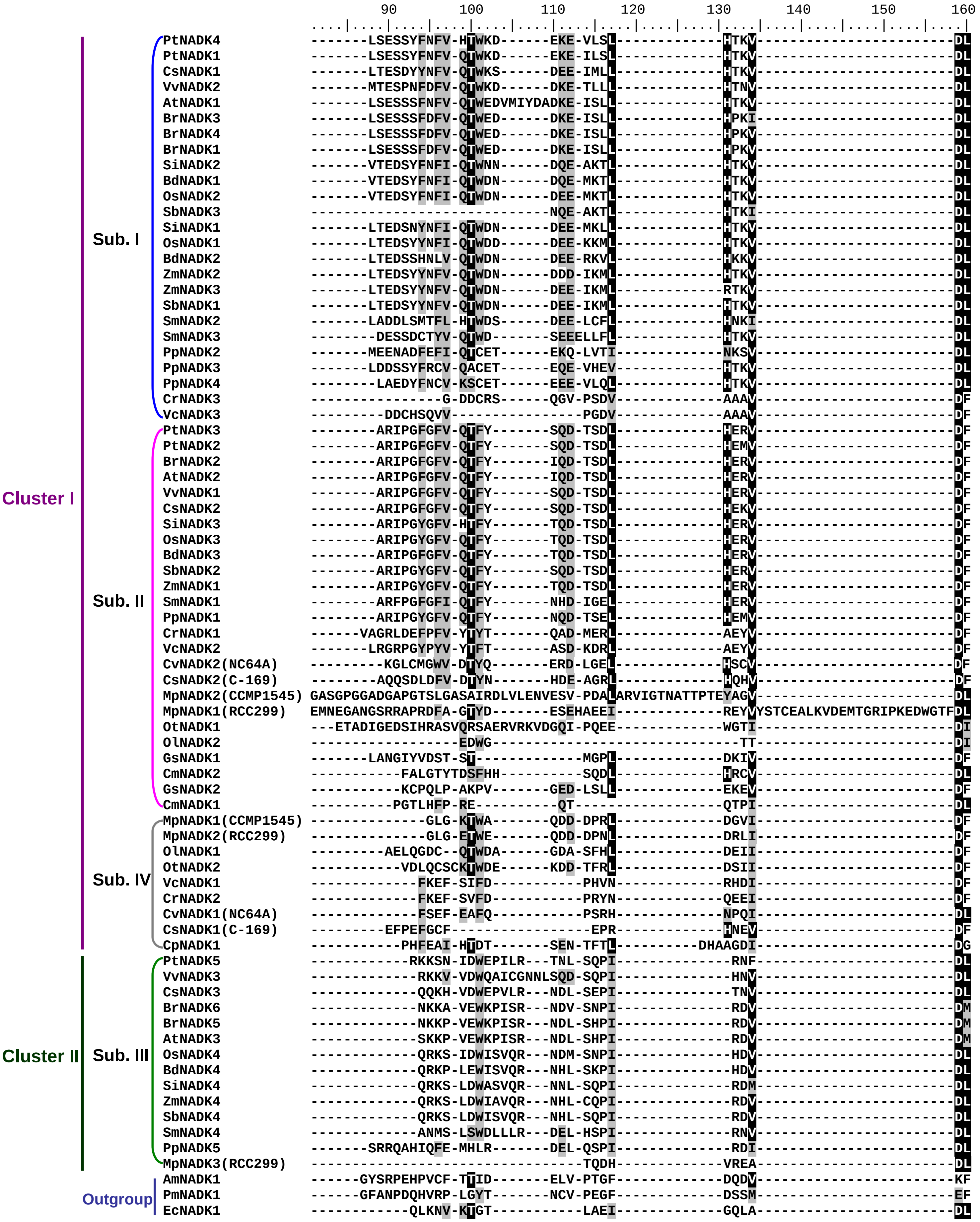
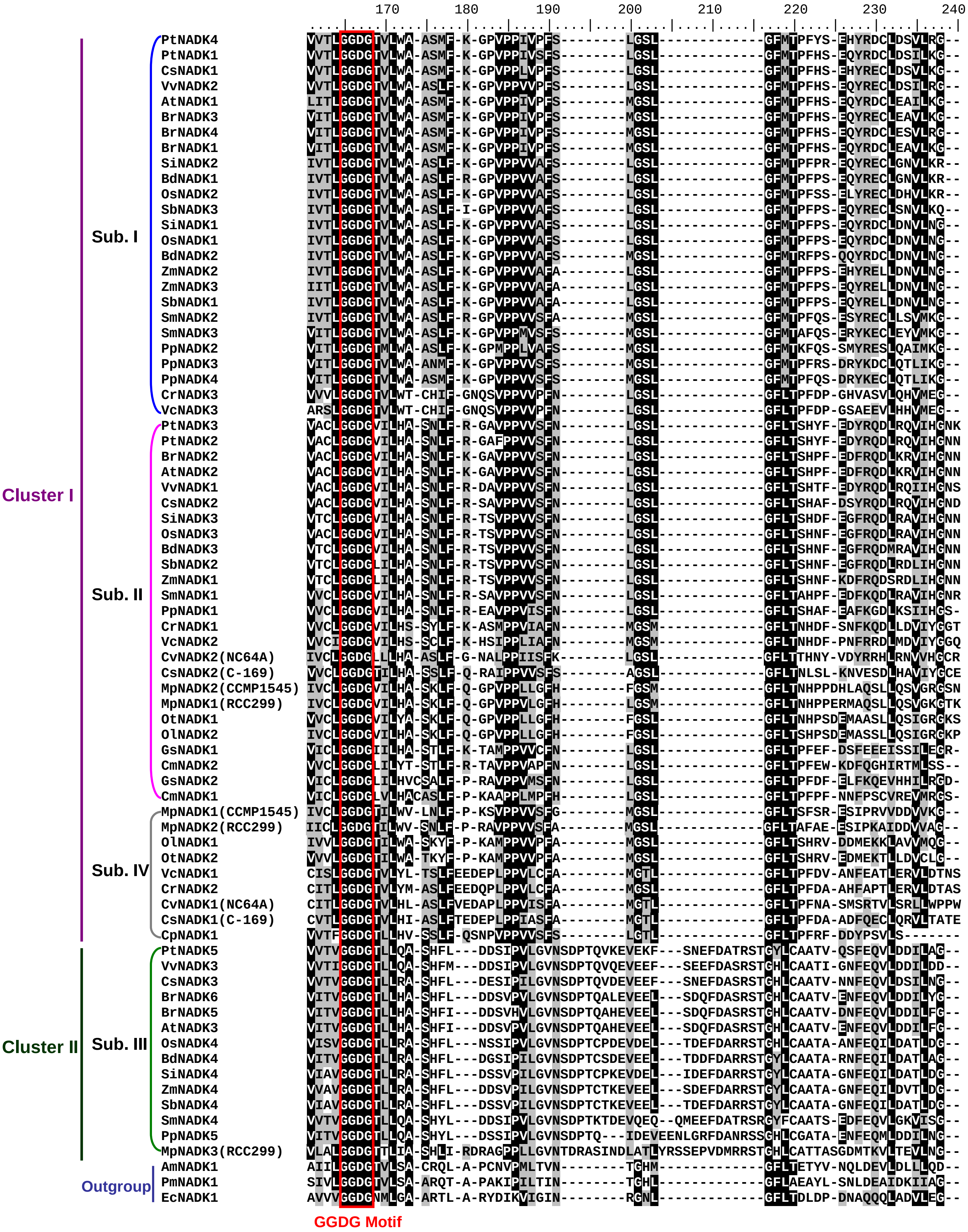
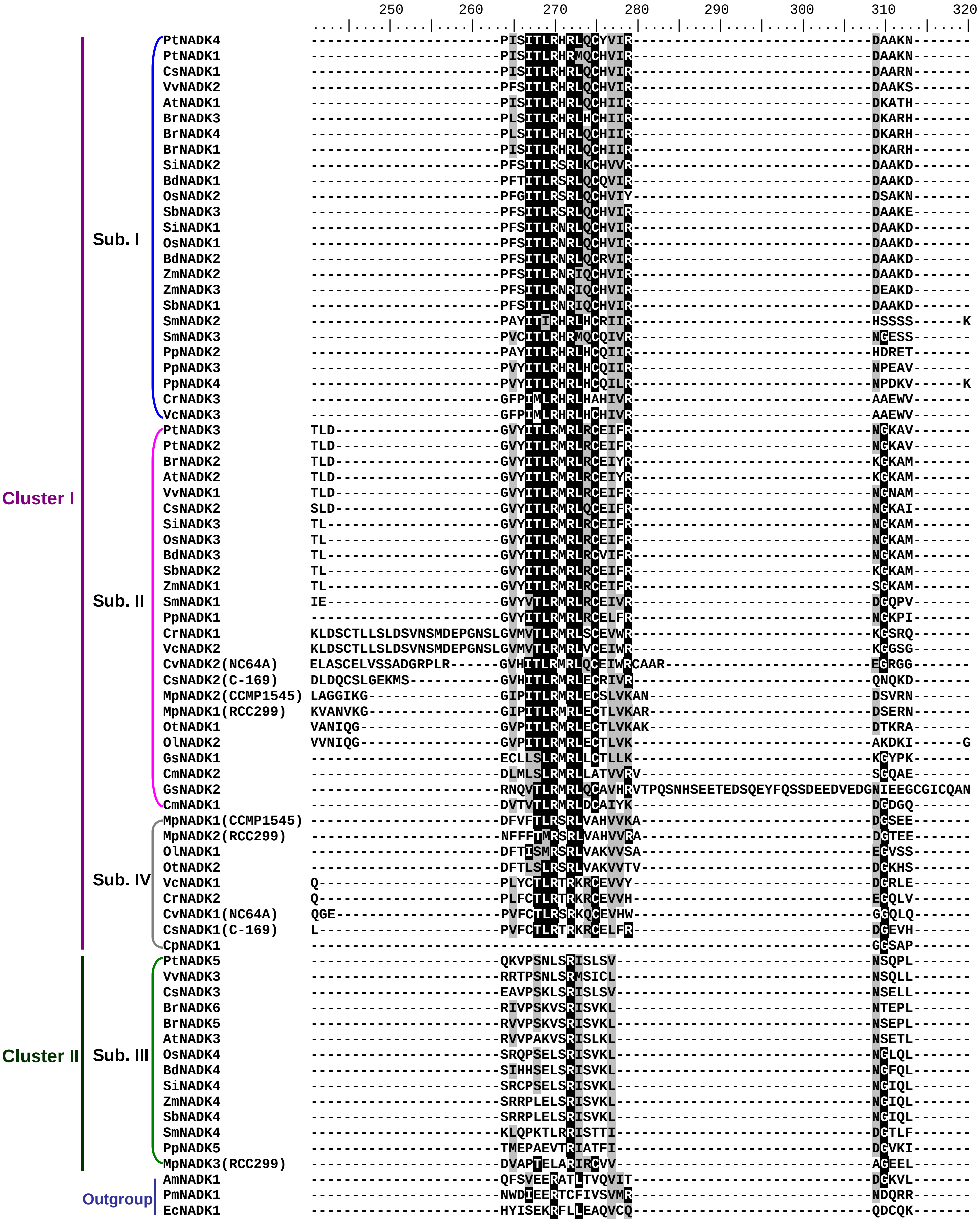


```
                             10        20        30        40        50        60        70        80
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
PtNADK4             TVLIMTKPNSTSVRILCA----------------------EMVRWLKDHKKLNIYVEPRVMGEL----------------
PtNADK1             TVLVMTKPNSTSVQILCA----------------------EMIRWMKEHKKLNIYVEPRVMGEL----------------
CsNADK1             TVLILTKPNSISVQMICF----------------------EMVRWLREHKDLHIYVEPRVKNEL----------------
VvNADK2             TVLILTKPNSTSVRILCV----------------------DMVRWLREQKKMEIFVEPRVKVEL----------------
AtNADK1             TVLIITKPNSTSVRVLSV----------------------DMVRWLRTQKGLNIYVEPRVKEEL----------------
BrNADK3             NVLIFTKPKSTSVQVLSV----------------------EMVRWLREQKGLNVYVEPRVKAEL----------------
BrNADK4             TVIIFTKPNSTSVRVLSV----------------------EMVRWLRDHKGLNVYVEPRVKAEL----------------
BrNADK1             TVIIFTKPNSTSVRVLSV----------------------EMVRWLREHKGLNVYVEPRVKAEL----------------
SiNADK2             TVLFVTKPNSNSVLALCA----------------------EMVRWLKEHNNMNVFVEPRVSKEL----------------
BdNADK1             TVLFVTKPNSSAVHTLCS----------------------EMIRWLKEHNNMNIFVEPRVSKEL----------------
OsNADK2             TVLFVTKPNSNSVHALCA----------------------EMVRWLKEHNNINIFVEPRVSKEL----------------
SbNADK3             TVLLVTKPNSNSVLALCA----------------------EMVRAM----------------------------------
SiNADK1             TVLFITKPNSNSVHVLCA----------------------EMVRWLKEHKNINVFVEPRVSKEL----------------
OsNADK1             TVLFITKPNSNSVHVLCA----------------------EMVRWLKEHKKINVVVEPRVSKEL----------------
BdNADK2             TVLFITKPNSNPVRVLCA----------------------EMVRWLKEHKNINVFVEPWVSKDL----------------
ZmNADK2             TVLFITKPNSSSVRVLCA----------------------EMVRWLREYKNVNIFVDPRVSKEL----------------
ZmNADK3             TVLFITKPNSNSVRVLCA----------------------EMIRWLREHKNINIFVEPRVSKEL----------------
SbNADK1             TVLFITKPNSNSVRVLCA----------------------EMVRWLRESKNINIFVEPRVRKEL----------------
SmNADK2             CVCILTKPNCKRVHDLCK----------------------EMIVWLHSV-SLSIYVEPRVRREM----------------
SmNADK3             AVCIFTRPNSSAVQELCK----------------------KMIRWLKEVKNITVFVEQRVKDEL----------------
PpNADK2             SVFILLKPNAAAVQQLCE----------------------EMVWWLREQNVTKIYVEPRVKAEL----------------
PpNADK3             SVFILCKPSASDVTAICK----------------------EMIRWLKEEKGIGVYVEPSMKREL----------------
PpNADK4             TVLIISKPNSPTCTALCK----------------------EMIRWLREEKGVGVYLEPPMKKEI----------------
CrNADK3             AAGVGVSSMDVEEEEVVE----------------------EEDLMPGCSTGVPLLLSWPSVGE-----------------
VcNADK3             EEGGGGGGEEAEAEEAEE-----------------------GVLMPGCYTGVPMLLSWPADEG-----------------
PtNADK3             TVLLLKKLGKELMEEAKE-----------------------VASFLYHQEKMNVLVEPDVHDIF----------------
PtNADK2             TVLLLKKLGQELLEEAKE-----------------------VASFLYHQEKMNVLVEPDVHDIF----------------
BrNADK2             TVLLLKKLGLELMEEAKE-----------------------AASFLYHQEKMTVLVEPEVHDVF----------------
AtNADK2             TVLLLKKLGQELMEEAKE---------EVHEKLLVFQICFQAASFLYHQENMNVLVEPEVHDVF----------------
VvNADK1             TVLLLKKLGQALMEEAKE-----------------------IASFLFYQEKMNVLVEPEVHDIF----------------
CsNADK2             TVLLLKKLGQELMEEAKE-----------------------VALFLYHQEKMNVLVEPDIHDIF----------------
SiNADK3             TVLLLKKLGDELMEQAKE-----------------------VASFLHHQEKMNVLVEPDVHDIF----------------
OsNADK3             TVLLLKKLGDELMEEAKE-----------------------VASFLHHQEKMNVLVEPDVHDIF----------------
BdNADK3             TVLLLKKLGDELMEEAKE-----------------------VASFLHHQEKMNVLVEPDVHDIF----------------
SbNADK2             TVLLLKKLGDELMEEAKE-----------------------VASFLHHQEKMNVLVEPDVHDTF----------------
ZmNADK1             TVLLLKKLGDELMEEAKE-----------------------VASFLHHQEKMNVLVEPDVHDTF----------------
SmNADK1             TVLLLKKLGEELMEEAKQ-----------------------VASFLYNHEGMNVMVEPDVHDRF----------------
PpNADK1             TVLLLKKLGMELMDQAQT-----------------------VASYLFHQEGMNVMVEPDVHDVF----------------
CrNADK1             SVMVIMKLGDELLAPFLD-----------------------VVDFLGREHQLRVVVEPHVYEQQ----------------
VcNADK2             SVMVIMKLGDELLQPFLE-----------------------VIDFLGREHSLRVVVEPHVYDEF----------------
CvNADK2(NC64A)      RVMVLKKLGDELMEEYVD-----------------------VLRYLGEELGMRVVVEPHDHAVL----------------
CsNADK2(C-169)      CVLVLKKLGDEQWDSYLR-----------------------VLRYLGAEEGMRVIVEPHEYLKL----------------
MpNADK2(CCMP1545)   RILVLKKLGPALLPQLVE------------------------VSHAMLSMGFEVVVEENVVGEMREEKAARDAARRSAAA
MpNADK1(RCC299)     RIFILKKLGPALLQNLVE------------------------VAHAMLSMGFQVVVEASVLEEMRIE--------REHAR
OtNADK1             RVFIIKKIGHGLLPELIE------------------------VAHAMMTMGIRIVLDEDTMDEL----------------
OlNADK2             NADILEDTLHRAV----------------------------VLKNAEKLRKVDGIIPQ----------------------
GsNADK1             TCLVLAKKDPALFHQTIL-----------------------AVQYL-KKQKLQVIVESFLQPEI----------------
CmNADK2             TVLLLVKKGANLCEIAKQ-----------------------AVDYLQNSERLRVLVEPWVQTEL----------------
GsNADK2             TVLVVRSRGSRQAELALQ----------------------QLVWWLVKAEQLQVIVENEVAK------------------
CmNADK1             HILILFTVYSDSARSSAV----------------------KICQWL-EAEYPELILYSETEHTL----------------
MpNADK1(CCMP1545)   NALVVKKPNDVQTTEMMP-----------------------RVVDMLARNDVEAWVEPAVHWET----------------
MpNADK2(RCC299)     NVLVIKKPKDKNTTAMLP-----------------------RVHAILQSKGIRTWVEPVVHWET----------------
OlNADK1             NALVVKKIHDAAAAEMMI-----------------------RATRVLKSKGVTAWLERAVWDEF----------------
OtNADK2             NALVVKKIHDEAATKMMR----------------------RAVKAL-EGQGITSWLERAVWDDA----------------
VcNADK1             KVLIVKKPKNPAASTKLH----------------------EIGAWL-RARGIEVFVERVVWATE----------------
CrNADK2             KVLIVKKPKNPAAAAKLK----------------------AIGDWL-TARGIQVFVERVVWATE----------------
CvNADK1(NC64A)      CVLLVKKPGDAAASQKLK----------------------EIGSWL-KGHGLQVLVERPVAQAE----------------
CsNADK1(C-169)      SVFIVKKPHSLEASAKMK----------------------EIGDWL-TSKGLNVLVERSVHMK-----------------
CpNADK1             TLLLVKKRKDDRTTAALD-----------------------KTGWLLE-RGVRVLVEETTRCDL----------------
PtNADK5             RLLLMLKPFDVYQFGQSN--------------GGSSITNSQAFRYLDNRRKVHKDAVNFCQDIL----------------
VvNADK3             RLLLMLKSLDIHPYSQLD--------------LLSRTTTPRVLGYLENRRKVHEDAINFCQDVL----------------
CsNADK3             RLLLFLKPFDANPVLHSD--------------AFSRVTTPQILRHLENRQEVHREAIDVCKDIL----------------
BrNADK6             KLLLLLKPIDPYPFLQSG--------------GVSLIKNPQVLKYLESRCKVHRNAINLCQEIL----------------
BrNADK5             KLLLLLKPVDLYPFLETD--------------GVSLIKNHQVLQYLESRCKVHRDAITFCQEIL----------------
AtNADK3             KLLLLLKPIDPYPFLQTE--------------GASLIKNPQVLQYLESRCKVHKNAIKFCQEIL----------------
OsNADK4             RVLLFVKPFDVYPPRPLA----AAASSPPPPPPPLRVSNPKVLNYLDDRCRVHKETINLCKSVL----------------
BdNADK4             RVLLFLKPFDVYPPRPLA---SASSPTTPPPPPPPRAANPKVLSYLDDRCRVHKNTINLCKSIL----------------
SiNADK4             RVLLFLKPFDVYPPRPYAGAAASSPTSSP--PSQPRAANPKILSYLDDRCRVHKDTIDLCQSVL----------------
ZmNADK4             RVLLFLKPFDVYPPRPYVGAAASSPTSAPSSLPQPRAANPKVLSYLDDRCRVHKDTIDLCQSVL----------------
SbNADK4             RVLLFLKPFDVYPPRPYVGAAASSPTSAPSTPPQPRAASPKILSYLDDRCRVHKDTIDLCQSVL----------------
SmNADK4             RVLVLLKRSAYDLYVARH-------RDPA--FVNGSAEKTKVVENLLDRHRVHESTVQKCKDVL----------------
PpNADK5             RVLVLAKRSAYDMYVARH----------QDPSFTRFLSEPQMVGNLQDRHRVHEHTVRLCKDVL----------------
MpNADK3(RCC299)     --NRLRERHDTHMTQVDR-----------------------ITEWLTAR---GVDMTSVMRDDA----------------
AmNADK1             KAGIIYNELKPFACRIAT-----------------------ELKDKLHACGWQVCLATGVGGIL----------------
PmNADK1             KAGLIVNDGKELAVQTAS-----------------------SVQKKLENSNFEVVRVSSSGGMV----------------
EcNADK1             CIGIVGHPRHPTALTTHE----------------------MLYRWL-CTKGYEVIVEQQIAHEL----------------
```

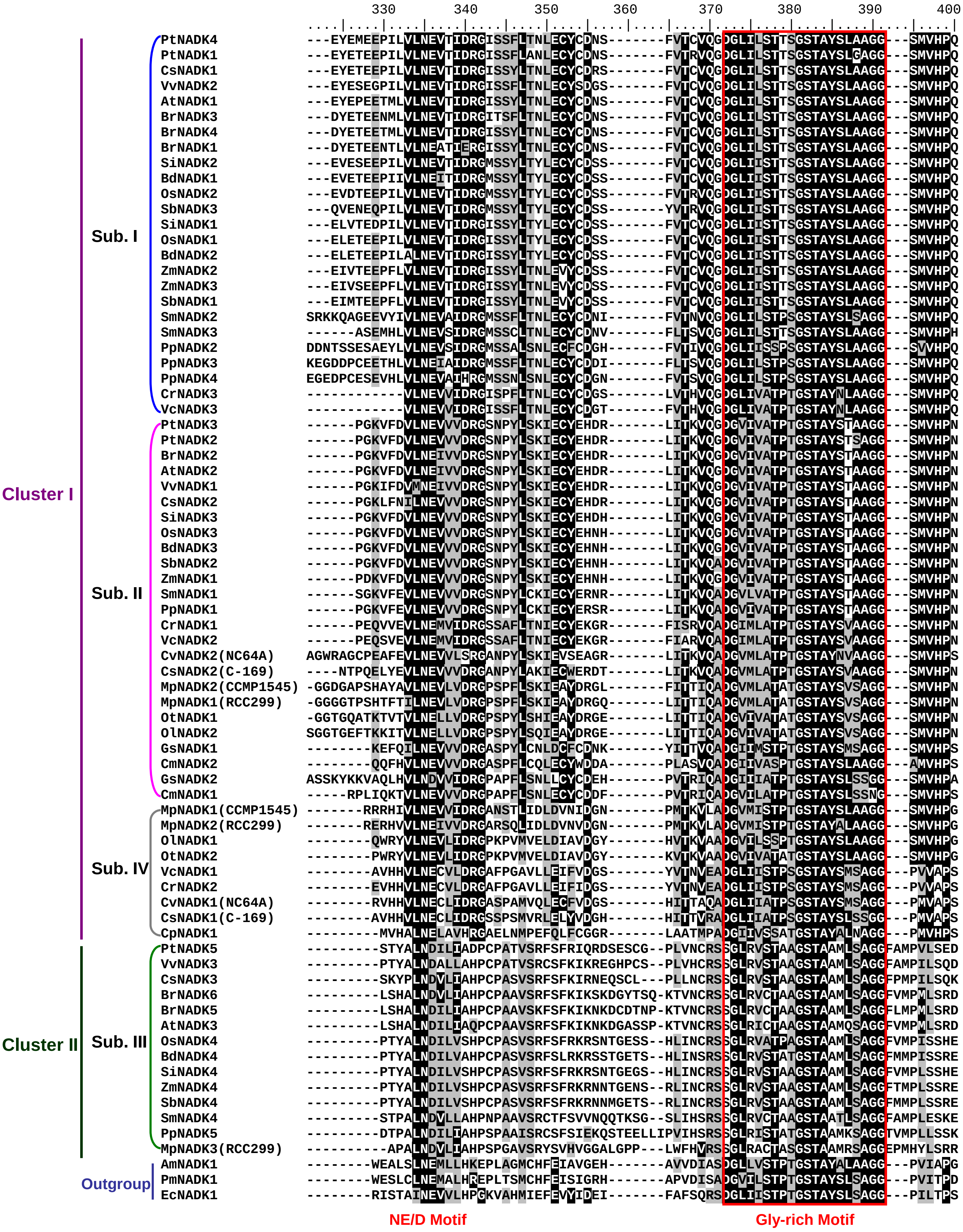


```
                             90       100       110       120       130       140       150       160
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
PtNADK4             -------LSESSYFNFV-HTWKD------EKE-VLSL-------------HTKV------------------------DL
PtNADK1             -------LSESSYFNFV-QTWKD------EKE-ILSL-------------HTKV------------------------DL
CsNADK1             -------LTESDYYNFV-QTWKS------DEE-IMLL-------------HTKV------------------------DL
VvNADK2             -------MTESPNFDFV-QTWKD------DKE-TLLL-------------HTNV------------------------DL
AtNADK1             -------LSESSSFNFV-QTWEDVMIYDADKE-ISLL-------------HTKV------------------------DL
BrNADK3             -------LSESSSFDFV-QTWED------DKE-ISLL-------------HPKI------------------------DL
BrNADK4             -------LSESSSFDFV-QTWED------DKE-ISLL-------------HPKV------------------------DL
BrNADK1             -------LSESSSFDFV-QTWED------DKE-ISLL-------------HPKV------------------------DL
SiNADK2             -------VTEDSYFNFI-QTWNN------DQE-AKTL-------------HTKV------------------------DL
BdNADK1             -------VTEDSYFNFI-QTWDN------DQE-MKTL-------------HTKV------------------------DL
OsNADK2             -------VTEDSYFNFI-QTWDN------DEE-MKTL-------------HTKV------------------------DL
SbNADK3             -----------------------------NQE-AKTL-------------HTKI------------------------DL
SiNADK1             -------LTEDSNYNFI-QTWDN------DEE-MKLL-------------HTKV------------------------DL
OsNADK1             -------LTEDSYYNFI-QTWDD------DEE-KKML-------------HTKV------------------------DL
BdNADK2             -------LTEDSSHNLV-QTWDN------DEE-RKVL-------------HKKV------------------------DL
ZmNADK2             -------LTEDSYYNFV-QTWDN------DDD-IKML-------------HTKV------------------------DL
ZmNADK3             -------LTEDSYYNFV-QTWDN------DEE-IKML-------------RTKV------------------------DL
SbNADK1             -------LTEDSYYNFV-QTWDN------DEE-IKML-------------HTKV------------------------DL
SmNADK2             -------LADDLSMTFL-HTWDS------DEE-LCFL-------------HNKI------------------------DL
SmNADK3             --------DESSDCTYV-QTWD-------SEEELLFL-------------HTKV------------------------DL
PpNADK2             -------MEENADFEFI-QTCET------EKQ-LVTI-------------NKSV------------------------DL
PpNADK3             -------LDDSSYFRCV-QACET------EQE-VHEV-------------HTKV------------------------DL
PpNADK4             --------LAEDYFNCV-KSCET------EEE-VLQL-------------HTKV------------------------DL
CrNADK3             ----------------G-DDCRS------QGV-PSDV-------------AAAV------------------------DF
VcNADK3             ---------DDCHSQVV----------------PGDV-------------AAAV------------------------DF
PtNADK3             --------ARIPGFGFV-QTFY-------SQD-TSDL-------------HERV------------------------DF
PtNADK2             --------ARIPGFGFV-QTFY-------SQD-TSDL-------------HEMV------------------------DF
BrNADK2             --------ARIPGFGFV-QTFY-------IQD-TSDL-------------HERV------------------------DF
AtNADK2             --------ARIPGFGFV-QTFY-------IQD-TSDL-------------HERV------------------------DF
VvNADK1             --------ARIPGFGFV-QTFY-------SQD-TSDL-------------HERV------------------------DF
CsNADK2             --------ARIPGFGFV-QTFY-------SQD-TSDL-------------HEKV------------------------DF
SiNADK3             --------ARIPGYGFV-HTFY-------TQD-TSDL-------------HERV------------------------DF
OsNADK3             --------ARIPGYGFV-QTFY-------TQD-TSDL-------------HERV------------------------DF
BdNADK3             --------ARIPGFGFV-QTFY-------TQD-TSDL-------------HERV------------------------DF
SbNADK2             --------ARIPGYGFV-QTFY-------SQD-TSDL-------------HERV------------------------DF
ZmNADK1             --------ARIPGYGFV-QTFY-------TQD-TSDL-------------HERV------------------------DF
SmNADK1             --------ARFPGFGFI-QTFY-------NHD-IGEL-------------HERV------------------------DF
PpNADK1             --------ARIPGYGFV-QTFY-------NQD-TSEL-------------HEMV------------------------DF
CrNADK1             ------VAGRLDEFPFV-YTYT-------QAD-MERL-------------AEYV------------------------DF
VcNADK2             -------LRGRPGYPYV-YTFT-------ASD-KDRL-------------AEYV------------------------DF
CvNADK2(NC64A)      ---------KGLCMGWV-DTYQ-------ERD-LGEL-------------HSCV------------------------DF
CsNADK2(C-169)      --------AQQSDLDFV-DTYN-------HDE-AGRL-------------HQHV------------------------DF
MpNADK2(CCMP1545)   GASGPGGADGAPGTSLGASAIRDLVLENVESV-PDALARVIGTNATTPTEYAGV------------------------DL
MpNADK1(RCC299)     EMNEGANGSRRAPRDFA-GTYD-------ESEHAEEI-------------REYVYSTCEALKVDEMTGRIPKEDWGTFDL
OtNADK1             ---ETADIGEDSIHRASVQRSAERVRKVDGQI-PQEE-------------WGTI------------------------DI
OlNADK2             ------------------EDWG------------------------------TT------------------------DI
GsNADK1             -------LANGIYVDST-ST-------------MGPL-------------DKIV------------------------DF
CmNADK2             -----------FALGTYTDSFHH----------SQDL-------------HRCV------------------------DL
GsNADK2             -----------KCPQLP-AKPV-------GED-LSLL-------------EKEV------------------------DF
CmNADK1             ----------PGTLHFP-RE----------QT------------------QTPI------------------------DL
MpNADK1(CCMP1545)   --------------GLG-KTWA-------QDD-DPRL-------------DGVI------------------------DF
MpNADK2(RCC299)     --------------GLG-ETWE-------QDD-DPNL-------------DRLI------------------------DF
OlNADK1             ---------AELQGDC--QTWDA------GDA-SFHL-------------DEII------------------------DF
OtNADK2             -----------VDLQCSCKTWDE------KDD-TFRL-------------DSII------------------------DF
VcNADK1             -------------FKEF-SIFD-----------PHVN-------------RHDI------------------------DF
CrNADK2             -------------FKEF-SVFD-----------PRYN-------------QEEI------------------------DF
CvNADK1(NC64A)      -------------FSEF-EAFQ-----------PSRH-------------NPQI------------------------DL
CsNADK1(C-169)      ---------EFPEFGCF----------------EPR--------------HNEV------------------------DF
CpNADK1             -----------PHFEAI-HTDT-------SEN-TFTL----------DHAAGDI------------------------DG
PtNADK5             ------------RKKSN-IDWEPILR---TNL-SQPI--------------RNF------------------------DL
VvNADK3             -------------RKKV-VDWQAICGNNLSQD-SQPI--------------HNV------------------------DL
CsNADK3             -------------QQKH-VDWEPVLR---NDL-SEPI--------------TNV------------------------DL
BrNADK6             -------------NKKA-VEWKPISR---NDV-SNPI--------------RDV------------------------DM
BrNADK5             -------------NKKP-VEWKPISR---NDL-SHPI--------------RDV------------------------DM
AtNADK3             -------------SKKP-VEWKPISR---NDL-SHPI--------------RDV------------------------DM
OsNADK4             -------------QRKS-IDWISVQR---NDM-SNPI--------------HDV------------------------DL
BdNADK4             -------------QRKP-LEWISVQR---NHL-SKPI--------------HDV------------------------DL
SiNADK4             -------------QRKS-LDWASVQR---NNL-SQPI--------------RDM------------------------DL
ZmNADK4             -------------QRKS-LDWIAVQR---NHL-CQPI--------------RDV------------------------DL
SbNADK4             -------------QRKS-LDWISVQR---NHL-SQPI--------------RDV------------------------DL
SmNADK4             -------------ANMS-LSWDLLLR---DEL-HSPI--------------RNV------------------------DL
PpNADK5             -------SRRQAHIQFE-MHLR-------DEL-QSPI--------------RDI------------------------DL
MpNADK3(RCC299)     ---------------------------------TQDH-------------VREA------------------------DL
AmNADK1             ------GYSRPEHPVCF-TTID-------ELV-PTGF-------------DQDV------------------------KF
PmNADK1             ------GFANPDQHVRP-LGYT-------NCV-PEGF-------------DSSM------------------------EF
EcNADK1             ------------QLKNV-KTGT-----------LAEI-------------GQLA------------------------DL
```


170
180
190
200
210
220
230
240
Cluster I
Sub. I
Sub. II
Sub. IV
Cluster II
Sub. III
Outgroup
PtNADK4 VVTLGGDGTVLWA-ASMF-K-GPVPPIVPFS-------LGSL-----------GFMTPFYS-EHYRDCLDSVLRG--
PtNADK1 VVTLGGDGTVLWA-ASMF-K-GPVPPIVSFS-------LGSL-----------GFMTPFHS-EQYRDCLDSILKG--
CsNADK1 VVTLGGDGTVLWA-ASMF-K-GPVPPLVPFS-------LGSL-----------GFMTPFHS-EQYRECLDSVLKG--
VvNADK2 VVTLGGDGTVLWA-ASLF-K-GPVPPVVPFS-------LGSL-----------GFMTPFHS-EQYRECLDSILRG--
AtNADK1 LITLGGDGTVLWA-ASMF-K-GPVPPIVPFS-------MGSL-----------GFMTPFHS-EQYRDCLEAILKG--
BrNADK3 VITLGGDGTVLWA-ASMF-K-GPVPPIVPFS-------MGSL-----------GFMTPFHS-EQYRECLEAVLKG--
BrNADK4 VITLGGDGTVLWA-ASMF-K-GPVPPIVPFS-------MGSL-----------GFMTPFHS-EQYRDCLESVLRG--
BrNADK1 VITLGGDGTVLWA-ASMF-K-GPVPPIVPFS-------MGSL-----------GFMTPFHS-EQYRDCLEAVLKG--
SiNADK2 IVTLGGDGTVLWA-ASLF-K-GPVPPVVAFS-------LGSL-----------GFMTPFPR-EQYRECLGNVLKR--
BdNADK1 IVTLGGDGTVLWA-ASLF-R-GPVPPVVAFS-------LGSL-----------GFMTPFPS-EQYRECLGNVLKR--
OsNADK2 IVTLGGDGTVLWA-ASLF-K-GPVPPVVAFS-------LGSL-----------GFMTPFSS-ELYRECLDHVLKR--
SbNADK3 IVTLGGDGTVLWA-ASLF-I-GPVPPVVAFS-------LGSL-----------GFMTPFPS-EQYRECLSNVLKQ--
SiNADK1 IVTLGGDGTVLWA-ASLF-K-GPVPPVVAFS-------LGSL-----------GFMTPFPS-EQYRDCLDNVLNG--
OsNADK1 IVTLGGDGTVLWA-ASLF-K-GPVPPVVAFS-------LGSL-----------GFMTPFPS-EQYRDCLDNVLNG--
BdNADK2 IVTLGGDGTVLWA-ASLF-K-GPVPPVVAFS-------MGSL-----------GFMTRFPS-QQYRDCLDNVLNG--
ZmNADK2 IVTLGGDGTVLWA-ASLF-K-GPVPPVVAFA-------LGSL-----------GFMTPFPS-EHYRELLDNVLNG--
ZmNADK3 IITLGGDGTVLWA-ASLF-K-GPVPPVVAFA-------LGSL-----------GFMTPFPS-EQYRELLDNVLNG--
SbNADK1 IVTLGGDGTVLWA-ASLF-K-GPVPPVVAFA-------LGSL-----------GFMTPFPS-EQYRELLDNVLNG--
SmNADK2 IVTLGGDGTVLWA-ASLF-R-GPVPPVVSFA-------MGSL-----------GFMTPFQS-ESYRECLLSVMKG--
SmNADK3 VITLGGDGTVLWA-ASLF-K-GPVPPMVSFS-------MGSL-----------GFMTAFQS-ERYKECLEYVMKG--
PpNADK2 VITLGGDGTMLWA-ASLF-K-GPMPPLVAFS-------MGSL-----------GFMTKFQS-SMYRESLQAIMKG--
PpNADK3 VITLGGDGTVLWA-ANMF-K-GPVPPVVSFS-------MGSL-----------GFMTPFRS-DRYKDCLQTLIKG--
PpNADK4 VITLGGDGTVLWA-ASMF-K-GPVPPVVSFS-------MGSL-----------GFMTPFQS-DRYKECLQTLIKG--
CrNADK3 VVVLGGDGTVLWT-CHIF-GNQSVPPVVPFN-------LGSL-----------GFLTPFDP-GHVASVLQHVMEG--
VcNADK3 ARSLGGDGTVLWT-CHIF-GNQSVPPVVPFN-------LGSL-----------GFLTPFDP-GSAEEVLHHVMEG--
PtNADK3 VACLGGDGVILHA-SNLF-R-GAVPPVVSFN-------LGSL-----------GFLTSHYF-EDYRQDLRQVIHGNK
PtNADK2 VACLGGDGVILHA-SNLF-R-GAFPPVVSFN-------LGSL-----------GFLTSHYF-EDYRQDLRQVIHGNN
BrNADK2 VACLGGDGVILHA-SNLF-K-GAVPPVVSFN-------LGSL-----------GFLTSHPF-EDFRQDLKRVIHGNN
AtNADK2 VACLGGDGVILHA-SNLF-K-GAVPPVVSFN-------LGSL-----------GFLTSHPF-EDFRQDLKRVIHGNN
VvNADK1 VACLGGDGVILHA-SNLF-R-DAVPPVVSFN-------LGSL-----------GFLTSHTF-EDYRQDLRQIIHGNS
CsNADK2 VACLGGDGVILHA-SNLF-R-SAVPPVVSFN-------LGSL-----------GFLTSHAF-DSYRQDLRQVIHGND
SiNADK3 VTCLGGDGVILHA-SNLF-R-TSVPPVVSFN-------LGSL-----------GFLTSHDF-EGFRQDLRAVIHGNN
OsNADK3 VACLGGDGVILHA-SNLF-R-TSVPPVVSFN-------LGSL-----------GFLTSHNF-EGFRQDLRAVIHGNN
BdNADK3 VTCLGGDGVILHA-SNLF-R-TSVPPVVSFN-------LGSL-----------GFLTSHNF-EGFRQDMRAVIHGNN
SbNADK2 VTCLGGDGLILHA-SNLF-R-TSVPPVVSFN-------LGSL-----------GFLTSHNF-EGFRQDLRDLIHGNN
ZmNADK1 VTCLGGDGLILHA-SNLF-R-TSVPPVVSFN-------LGSL-----------GFLTSHNF-KDFRQDSRDLIHGNN
SmNADK1 VVCLGGDGVILHA-SNLF-R-SAVPPVVSFN-------LGSL-----------GFLTAHPF-EDFKQDLRAVIHGNR
PpNADK1 VVCLGGDGVILHA-SNLF-R-EAVPPVISFN-------LGSL-----------GFLTSHAF-EAFKGDLKSIIHGS-
CrNADK1 VVCLGGDGVILHS-SYLF-K-ASMPPVIAFN-------MGSM-----------GFLTNHDF-SNFKQDLLDVIYGGT
VcNADK2 VVCIGGDGVILHS-SCLF-K-HSIPPLIAFN-------MGSM-----------GFLTNHDF-PNFRRDLMDVIYGGQ
CvNADK2(NC64A) IVCLGGDGLLLHA-ASLF-G-NALPPIISFK-------LGSL-----------GFLTTHNY-VDYRRHLRNVVHGCR
CsNADK2(C-169) VVCLGGDGTILHA-SSLF-Q-RAIPPVVSFS-------AGSL-----------GFLTNLSL-KNVESDLHAVIYGCE
MpNADK2(CCMP1545) IVCLGGDGVILHA-SKLF-Q-GPVPPLLGFH-------FGSM-----------GFLTNHPPDHLAQSLLQSVGRGSN
MpNADK1(RCC299) IVCLGGDGVILHA-SKLF-Q-GPVPPVLGFH-------LGSM-----------GFLTNHPPERMAQSLLQSVGKGTK
OtNADK1 VVCLGGDGVILYA-SKLF-Q-GPVPPLLGFH-------FGSL-----------GFLTNHPSDEMAASLLQSIGRGKS
OlNADK2 IVCLGGDGVILHA-SKLF-Q-GPVPPLLGFH-------FGSL-----------GFLTSHPSDEMASSLLQSIGRGKP
GsNADK1 VICLGGDGIILHA-STLF-K-TAMPPVVCFN-------LGSL-----------GFLTPFEF-DSFEEEISSILEGR-
CmNADK2 VVCLGGDGLILYT-STLF-R-TAVPPVAPFN-------LGSL-----------GFLTPFEW-KDFQGHIRTMLSS--
GsNADK2 VICLGGDGLILHVCSALF-P-RAVPPVMSFN-------LGSL-----------GFLTPFDF-ELFKQEVHHILRGD-
CmNADK1 VICLGGDGLVLHACASLF-P-KAAPPLMPFH-------LGSL-----------GFLTPFPF-NNFPSCVREVMRGS-
MpNADK1(CCMP1545) IVCLGGDGTILWV-LNLF-P-KSVPPVVSFG-------MGSL-----------GFLTSFSR-ESIPRVVDDVVKG--
MpNADK2(RCC299) IICLGGDGTILWV-SNLF-P-RAVPPVVSFA-------MGSL-----------GFLTAFAE-ESIPKAIDDVVAG--
OlNADK1 IVVLGGDGTILWA-SKYF-P-KAMPPVVPFA-------MGSL-----------GFLTSHRV-DDMEKKLAVVMQG--
OtNADK2 VVVLGGDGTILWA-TKYF-P-KAMPPVVPFA-------MGSL-----------GFLTSHRV-EDMEKTLLDVCLG--
VcNADK1 CISLGGDGTVLYL-TSLFEEDEPLPPVLCFA-------MGTL-----------GFLTPFDV-ANFEATLERVLDTNS
CrNADK2 CITLGGDGTVLYM-ASLFEEDQPLPPVLCFA-------MGSL-----------GFLTPFDA-AHFAPTLERVLDTAS
CvNADK1(NC64A) CITLGGDGTVLHL-ASLFVEDAPLPPVISFA-------MGTL-----------GFLTPFNA-SMSRTVLSRLLWPPW
CsNADK1(C-169) CVTLGGDGTVLHI-ASLFTEDEPLPPIASFA-------MGTL-----------GFLTPFDA-ADFQECLQRVLTATE
CpNADK1 VVTFGGDGTLLHV-SSLF-QSNPVPPVVSFG-------LGTL-----------GFLTPFRF-DDYPSVLS------
PtNADK5 VVTVGGDGTLLQA-SHFL---DDSIPVLGVNSDPTQVKEVEKF---SNEFDATRSTGYLCAATV-QSFEQVLDDILAG--
VvNADK3 VVTIGGDGTLLQA-SHFM---DDSIPVLGVNSDPTQVQEVEEF---SEEFDASRSTGHLCAATI-GNFEQVLDDILDD--
CsNADK3 VVTVGGDGTLLRA-SHFL---DESIPILGVNSDPTQVDEVEEF---SNEFDASRSTGHLCAATV-NNFEQVLDSILNG--
BrNADK6 VITVGGDGTLLHA-SHFL---DDSVPVLGVNSDPTQALEVEEL---SDQFDASRSTGHLCAATV-ENFEQVLDDILYG--
BrNADK5 VITVGGDGTLLHA-SHFI---DDSVHVLGVNSDPTQAHEVEEL---SDQFDASRSTGHLCAATV-DNFEQVLDDILFG--
AtNADK3 VITVGGDGTLLHA-SHFI---DDSVPVLGVNSDPTQAHEVEEL---SDQFDASRSTGHLCAATV-ENFEQVLDDILFG--
OsNADK4 VISVGGDGTLLRA-SHFL---NSSIPVLGVNSDPTCPDEVDEL---TDEFDARRSTGHLCAATA-ANFEQILDATLDG--
BdNADK4 VITVGGDGTLLRA-SHFL---DGSIPILGVNSDPTCSDEVEEL---TDDFDARRSTGYLCAATA-RNFEQILDATLAG--
SiNADK4 VIAVGGDGTLLRA-SHFL---DSSVPILGVNSDPTCPKEVDEL---IDEFDARRSTGYLCAATA-GNFEQILDATLDG--
ZmNADK4 VVAVGGDGTLLRA-SHFL---DDSVPILGVNSDPTCTKEVEEL---SDEFDARRSTGYLCAATA-GNFEQILDVTLDG--
SbNADK4 VIAVGGDGTLLRA-SHFL---DSSVPILGVNSDPTCTKEVEEL---TDEFDARRSTGYLCAATA-GNFEQILDATLDG--
SmNADK4 VVTVGGDGTLLQA-SHYL---DDSIPVLGVNSDPTKTDEVQEQ--QMEEFDATRSRGYFCAATS-EDFEQVLGKVISG--
PpNADK5 VITVGGDGTLLQA-SHYL---DSSIPVLGVNSDPTQ---IDEVEENLGRFDANRSSGHLCGATA-ENFEQMLDDILNG--
MpNADK3(RCC299) VLALGGDGTTLIA-SHLI-RDRAGPPLLGVNTDRASINDLATLYRSSEPVDMRRSTGHLCATTASGDMTKVLTEVLNG--
AmNADK1 AIILGGDGTVLSA-CRQL-A-PCNVPMLTVN-------TGHM-----------GFLTETYV-NQLDEVLDLLLQD--
PmNADK1 SIVLGGDGTVLSA-ARQT-A-PAKIPILTIN-------TGHL-----------GFLAEAYL-SNLDEAIDKIIAG--
EcNADK1 AVVVGGDGNMLGA-ARTL-A-RYDIKVIGIN-------RGNL-----------GFLTDLDP-DNAQQQLADVLEG--
GGDG Motif



```
                          250       260       270       280       290       300       310       320
                   ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
PtNADK4            -----------------------PISITLRHRLQCYVIR-----------------------------DAAKN-------
PtNADK1            -----------------------PISITLRHRMQCHVIR-----------------------------DAAKN-------
CsNADK1            -----------------------PISITLRHRLQCHVIR-----------------------------DAARN-------
VvNADK2            -----------------------PFSITLRHRLQCHVIR-----------------------------DAAKS-------
AtNADK1            -----------------------PISITLRHRLQCHIIR-----------------------------DKATH-------
BrNADK3            -----------------------PLSITLRHRLHCHIIR-----------------------------DKARH-------
BrNADK4            -----------------------PLSITLRHRLQCHIIR-----------------------------DKARH-------
BrNADK1            -----------------------PISITLRHRLQCHIIR-----------------------------DKARH-------
SiNADK2            -----------------------PFSITLRSRLKCHVVR-----------------------------DAAKD-------
BdNADK1            -----------------------PFTITLRSRLQCQVIR-----------------------------DAAKD-------
OsNADK2            -----------------------PFGITLRSRLQCHVIY-----------------------------DSAKN-------
SbNADK3            -----------------------PFSITLRSRLQCHVIR-----------------------------DAAKE-------
SiNADK1            -----------------------PFSITLRNRLQCHVIR-----------------------------DAAKD-------
OsNADK1            -----------------------PFSITLRNRLQCHVIR-----------------------------DAAKD-------
BdNADK2            -----------------------PFSITLRNRLQCRVIR-----------------------------DAAKD-------
ZmNADK2            -----------------------PFSITLRNRIQCHVIR-----------------------------DAAKD-------
ZmNADK3            -----------------------PFSITLRNRIQCHVIR-----------------------------DEAKD-------
SbNADK1            -----------------------PFSITLRNRIQCHVIR-----------------------------DAAKD-------
SmNADK2            -----------------------PAYITIRHRLHCRIIR-----------------------------HSSSS------K
SmNADK3            -----------------------PVCITLRHRMQCQIVR-----------------------------NGESS-------
PpNADK2            -----------------------PAYITLRHRLHCQIIR-----------------------------HDRET-------
PpNADK3            -----------------------PVYITLRHRLHCQIIR-----------------------------NPEAV-------
PpNADK4            -----------------------PVYITLRHRLHCQILR-----------------------------NPDKV------K
CrNADK3            -----------------------GFPIMLRHRLHAHIVR-----------------------------AAEWV-------
VcNADK3            -----------------------GFPIMLRHRLHCHIVR-----------------------------AAEWV-------
PtNADK3            TLD--------------------GVYITLRMRLRCEIFR-----------------------------NGKAV-------
PtNADK2            TLD--------------------GVYITLRMRLRCEIFR-----------------------------NGKAV-------
BrNADK2            TLD--------------------GVYITLRMRLRCEIYR-----------------------------KGKAM-------
AtNADK2            TLD--------------------GVYITLRMRLRCEIYR-----------------------------KGKAM-------
VvNADK1            TLD--------------------GVYITLRMRLRCEIFR-----------------------------NGNAM-------
CsNADK2            SLD--------------------GVYITLRMRLQCEIFR-----------------------------NGKAI-------
SiNADK3            TL---------------------GVYITLRMRLRCEIFR-----------------------------NGKAM-------
OsNADK3            TL---------------------GVYITLRMRLRCEIFR-----------------------------NGKAM-------
BdNADK3            TL---------------------GVYITLRMRLRCVIFR-----------------------------NGKAM-------
SbNADK2            TL---------------------GVYITLRMRLRCEIFR-----------------------------KGKAM-------
ZmNADK1            TL---------------------GVYITLRMRLRCEIFR-----------------------------SGKAM-------
SmNADK1            IE---------------------GVYVTLRMRLRCEIVR-----------------------------DGQPV-------
PpNADK1            -----------------------GVYITLRMRLRCELFR-----------------------------NGKPI-------
CrNADK1            KLDSCTLLSLDSVNSMDEPGNSLGVMVTLRMRLSCEVWR-----------------------------KGSRQ-------
VcNADK2            KLDSCTLLSLDSVNSMDEPGNSLGVMVTLRMRLVCEIWR-----------------------------KGGSG-------
CvNADK2(NC64A)     ELASCELVSSADGRPLR------GVHITLRMRLQCEIWRCAAR-------------------------EGRGG-------
CsNADK2(C-169)     DLDQCSLGEKMS-----------GVHITLRMRLECRIVR-----------------------------QNQKD-------
MpNADK2(CCMP1545)  LAGGIKG----------------GIPITLRMRLECSLVKAN---------------------------DSVRN-------
MpNADK1(RCC299)    KVANVKG----------------GIPITLRMRLECTLVKAR---------------------------DSERN-------
OtNADK1            VANIQG-----------------GVPITLRMRLECTLVKAK---------------------------DTKRA-------
OlNADK2            VVNIQG-----------------GVPITLRMRLECTLVK-----------------------------AKDKI------G
GsNADK1            -----------------------ECLLSLRMRLLCTLLK-----------------------------KGYPK-------
CmNADK2            -----------------------DLMLSLRMRLLATVVRV----------------------------SGQAE-------
GsNADK2            -----------------------RNQVTLRMRLQCAVHRVTPQSNHSEETEDSQEYFQSSDEEDVEDGNIEEGCGICQAN
CmNADK1            -----------------------DVTVTLRMRLDCAIYK-----------------------------DGDGQ-------
MpNADK1(CCMP1545)  -----------------------DFVFTLRSRLVAHVVKA----------------------------DGSEE-------
MpNADK2(RCC299)    -----------------------NFFFTMRSRLVAHVVRA----------------------------DGTEE-------
OlNADK1            -----------------------DFTISMRSRLVAKVVSA----------------------------EGVSS-------
OtNADK2            -----------------------DFTLSLRSRLVAKVVTV----------------------------DGKHS-------
VcNADK1            Q----------------------PLYCTLRTRKRCEVVY-----------------------------DGRLE-------
CrNADK2            Q----------------------PLFCTLRTRKRCEVVH-----------------------------EGQLV-------
CvNADK1(NC64A)     QGE--------------------PVFCTLRSRKQCEVHW-----------------------------GGQLQ-------
CsNADK1(C-169)     L----------------------PVFCTLRTRKRCELFR-----------------------------DGEVH-------
CpNADK1            --------------------------------------------------------------------GGSAP-------
PtNADK5            -----------------------QKVPSNLSRISLSV-------------------------------NSQPL-------
VvNADK3            -----------------------RRTPSNLSRMSICL-------------------------------NSQLL-------
CsNADK3            -----------------------EAVPSKLSRISLSV-------------------------------NSELL-------
BrNADK6            -----------------------RIVPSKVSRISVKL-------------------------------NTEPL-------
BrNADK5            -----------------------RVVPSKVSRISVKL-------------------------------NSEPL-------
AtNADK3            -----------------------RVVPAKVSRISLKL-------------------------------NSETL-------
OsNADK4            -----------------------SRQPSELSRISVKL-------------------------------NGLQL-------
BdNADK4            -----------------------SIHHSELSRISVKL-------------------------------NGFQL-------
SiNADK4            -----------------------SRCPSELSRISVKL-------------------------------NGIQL-------
ZmNADK4            -----------------------SRRPLELSRISVKL-------------------------------NGIQL-------
SbNADK4            -----------------------SRRPLELSRISVKL-------------------------------NGIQL-------
SmNADK4            -----------------------KLQPKTLRRISTTI-------------------------------DGTLF-------
PpNADK5            -----------------------TMEPAEVTRIATFI-------------------------------DGVKI-------
MpNADK3(RCC299)    -----------------------DVAPTELARIRCVV-------------------------------AGEEL-------
AmNADK1            -----------------------QFSVEERATLTVQVIT-----------------------------DGKVL-------
PmNADK1            -----------------------NWDIEERTCFIVSVMR-----------------------------NDQRR-------
EcNADK1            -----------------------HYISEKRFLLEAQVCQ-----------------------------QDCQK-------
```


330
340
350
360
370
380
390
400
Cluster I
Cluster II
Sub. I
Sub. II
Sub. IV
Sub. III
Outgroup
PtNADK4 ---EYEMEEPILVLNEVTIDRGISSFLTNLECYCDNS-------FVTCVQGDGLILSTTSGSTAYSLAAGG---SMVHPQ
PtNADK1 ---EYETEEPILVLNEVTIDRGISSFLANLECYCDNS-------FVTRVQGDGLILSTTSGSTAYSLGAGG---SMVHPQ
CsNADK1 ---EYETEEPILVLNEVTIDRGISSYLTNLECYCDRS-------FVTCVQGDGLILSTTSGSTAYSLAAGG---SMVHPQ
VvNADK2 ---EYESEGPILVLNEVTIDRGISSFLTNLECYSDGS-------FVTCVQGDGLILSTTSGSTAYSLAAGG---SMVHPQ
AtNADK1 ---EYEPEETMLVLNEVTIDRGISSYLTNLECYCDNS-------FVTCVQGDGLILSTTSGSTAYSLAAGG---SMVHPQ
BrNADK3 ---DYETEENMLVLNEVTIDRGITSFLTNLECYCDNS-------FVTCVQGDGLILSTTSGSTAYSLAAGG---SMVHPQ
BrNADK4 ---DYETEETMLVLNEVTIDRGISSYLTNLECYCDNS-------FVTCVQGDGLILSTTSGSTAYSLAAGG---SMVHPQ
BrNADK1 ---DYETEENTLVLNEATIERGISSYLTNLECYCDNS-------FVTCVQGDGLILSTTSGSTAYSLAAGG---SMVHPQ
SiNADK2 ---EVESEEPILVLNEVTIDRGMSSYLTYLECYCDSS-------FVTCVQGDGLIISTTSGSTAYSLAAGG---SMVHPQ
BdNADK1 ---EVETEEPIIVLNEITIDRGMSSYLTYLECYCDSS-------FVTCVQGDGLIISTTSGSTAYSLAAGG---SMVHPQ
OsNADK2 ---EVDTEEPILVLNEVTIDRGMSSYLTYLECYCDSS-------FVTRVQGDGLIISTTSGSTAYSLAAGG---SMVHPQ
SbNADK3 ---QVENEQPILVLNEVTIDRGMSSYLTYLECYCDSS-------YVTRVQGDGLIISTTSGSTAYSLAAGG---SMVHPQ
SiNADK1 ---ELVTEDPILVLNEVTIDRGISSYLTYLECYCDSS-------FVTCVQGDGLIISTTSGSTAYSLAAGG---SMVHPQ
OsNADK1 ---ELETEEPILVLNEVTIDRGISSYLTYLECYCDSS-------FVTCVQGDGLIISTTSGSTAYSLAAGG---SMVHPQ
BdNADK2 ---ELETEEPILALNEVTIDRGISSYLTYLECYCDSS-------FVTCVQGDGLIISTTSGSTAYSLAAGG---SMVHPQ
ZmNADK2 ---EIVTEEPFLVLNEVTIDRGISSYLTNLEVYCDSS-------FVTCVQGDGLIISTTSGSTAYSLAAGG---SMVHPQ
ZmNADK3 ---EIVSEEPFLVLNEVTIDRGISSYLTNLEVYCDSS-------FVTCVQGDGLIISTTSGSTAYSLAAGG---SMVHPQ
SbNADK1 ---EIMTEEPFLVLNEVTIDRGISSYLTNLEVYCDSS-------FVTCVQGDGLIISTTSGSTAYSLAAGG---SMVHPQ
SmNADK2 SRKKQAGEEVYIVLNEVAIDRGMSSFLTNLECYCDNI-------FVTNVQGDGLILSTPSGSTAYSLSAGG---SMVHPQ
SmNADK3 ------ASEMHLVLNEVSIDRGMSSCLTNLECYCDNV-------FLTSVQGDGLILSTTSGSTAYSLAAGG---SMVHPH
PpNADK2 DDNTSSESAEYLVLNEVSIDRGMSSALSNLECFCDGH-------FVTIVQGDGLIISSPSGSTAYSLAAGG---SVVHPQ
PpNADK3 KEGDDPCEETHLVLNEIAIDRGMSSFLTNLECYCDDI-------FLTSVQGDGLILSTPSGSTAYSLAAGG---SMVHPQ
PpNADK4 EGEDPCESEVHLVLNEVAIHRGMSSNLSNLECYCDGN-------FVTSVQGDGLILSTPSGSTAYSLAAGG---SMVHPQ
CrNADK3 ------------VLNEVVIDRGISPFLTNLECYCDGS-------LVTHVQGDGLIVATPTGSTAYNLAAGG---SMVHPQ
VcNADK3 ------------VLNEVVIDRGISSFLTNLECYCDGT-------FVTHVQGDGLIVATPTGSTAYNLAAGG---SMVHPQ
PtNADK3 ------PGKVFDVLNEVVVDRGSNPYLSKIECYEHDR-------LITKVQGDGVIVATPTGSTAYSTAAGG---SMVHPN
PtNADK2 ------PGKVFDVLNEVVVDRGSNPYLSKIECYEHDR-------LITKVQGDGVIVATPTGSTAYSTSAGG---SMVHPN
BrNADK2 ------PGKVFDVLNEIVVDRGSNPYLSKIECYEHDR-------LITKVQGDGVIVATPTGSTAYSTAAGG---SMVHPN
AtNADK2 ------PGKVFDVLNEIVVDRGSNPYLSKIECYEHDR-------LITKVQGDGVIVATPTGSTAYSTAAGG---SMVHPN
VvNADK1 ------PGKIFDVMNEIVVDRGSNPYLSKIECYEHDR-------LITKVQGDGVIVATPTGSTAYSTAAGG---SMVHPN
CsNADK2 ------PGKLFNILNEVVVDRGSNPYLSKIECYEHDR-------LITKVQGDGVIVATPTGSTAYSTAAGG---SMVHPN
SiNADK3 ------PGKVFDVLNEVVVDRGSNPYLSKIECYEHDH-------LITKVQGDGVIVATPTGSTAYSTAAGG---SMVHPN
OsNADK3 ------PGKVFDVLNEVVVDRGSNPYLSKIECYEHNH-------LITKVQGDGVIVATPTGSTAYSTAAGG---SMVHPN
BdNADK3 ------PGKVFDVLNEVVVDRGSNPYLSKIECYEHNH-------LITKVQGDGVIVATPTGSTAYSTAAGG---SMVHPN
SbNADK2 ------PGKVFDVLNEVVVDRGSNPYLSKIECYEHNH-------LITKVQADGVIVATPTGSTAYSTAAGG---SMVHPN
ZmNADK1 ------PDKVFDVLNEVVVDRGSNPYLSKIECYEHNH-------LITKVQGDGVIVATPTGSTAYSTAAGG---SMVHPN
SmNADK1 ------SGKVFEVLNEVVVDRGSNPYLCKIECYERNR-------LITKVQADGVLVATPTGSTAYSTAAGG---SMVHPN
PpNADK1 ------PGKVFEVLNEVVVDRGSNPYLCKIECYERSR-------LITKVQADGVIVATPTGSTAYSTAAGG---SMVHPN
CrNADK1 ------PEQVVEVLNEMVIDRGSSAFLTNIECYEKGR-------FISRVQADGIMLATPTGSTAYSVAAGG---SMVHPN
VcNADK2 ------PEQSVEVLNEMVIDRGSSAFLTNIECYEKGR-------FIARVQADGIMLATPTGSTAYSVAAGG---SMVHPN
CvNADK2(NC64A) AGWRAGCPEAFEVLNEVVLSRGANPYLSKIEVSEAGR-------LITKVQADGVMLATPTGSTAYNVAAGG---SMVHPS
CsNADK2(C-169) ----NTPQELYEVLNEVVVDRGANPYLAKIECWERDT-------LITKVQADGVMLATPTGSTAYSVAAGG---SMVHPN
MpNADK2(CCMP1545) -GGDGAPSHAYAVLNEVLVDRGPSPFLSKIEAYDRGL-------FITTIQADGVMLATATGSTAYSVSAGG---SMVHPN
MpNADK1(RCC299) -GGGGTPSHTFTILNEVLVDRGPSPFLSKIEAYDRGQ-------LITTIQADGVMLATATGSTAYSVSAGG---SMVHPN
OtNADK1 -GGTGQATKTVTVLNELLVDRGPSPYLSHIEAYDRGE-------LITTIQADGVIVATATGSTAYSVSAGG---SMVHPN
OlNADK2 SGGTGEFTKKITVLNELLVDRGPSPYLSQIEAYDRGE-------LITTIQADGVIVATATGSTAYSVSAGG---SMVHPN
GsNADK1 --------KEFQILNEVVVDRGASPYLCNLDCFCDNK-------YITTVQADGIIMSTPTGSTAYSMSAGG---SMVHPS
CmNADK2 --------QQFHVLNEVVVDRGASPFLCQLECYWDDA-------PLASVQADGIIVASPTGSTAYSLAAGG---AMVHPS
GsNADK2 ASSKYKKVAQLHVLNDVVIDRGPAPFLSNLLCYCDEH-------PVTRIQADGIIIATPTGSTAYSLSSGG---SMVHPA
CmNADK1 -----RPLIQKTVLNEVVVDRGPAPFLSNLECYCDDF-------PVTRIQADGVILATPTGSTAYSLSSNG---SMVHPS
MpNADK1(CCMP1545) -------RRRHIVLNEVVIDRGANSTLIDLDVNIDGN-------PMTKVLADGVMISTPTGSTAYSLAAGG---SMVHPG
MpNADK2(RCC299) -------RERHVVLNEIVVDRGARSQLIDLDVNVDGN-------PMTKVLADGVMISTPTGSTAYALAAGG---SMVHPG
OlNADK1 --------QWRYVLNEVLIDRGPKPVMVELDIAVDGY-------HVTKVAADGVILSSPTGSTAYSLAAGG---SMVHPG
OtNADK2 --------PWRYVLNEVLIDRGPKPVMVELDIAVDGY-------KVTKVAADGVIVATATGSTAYSLAAGG---SMVHPG
VcNADK1 --------AVHHVLNECVLDRGAFPGAVLLEIFVDGS-------YVTNVEADGLIISTPSGSTAYSMSAGG---PVVAPS
CrNADK2 --------EVHHVLNECVLDRGAFPGAVLLEIFIDGS-------YVTNVEADGLIISTPSGSTAYSMSAGG---PVVAPS
CvNADK1(NC64A) --------RVHHVLNECLIDRGASPAMVQLECFVDGS-------HITTAQADGLIIATPSGSTAYSMSAGG---PMVAPS
CsNADK1(C-169) --------AVHHVLNECLIDRGSSPSMVRLELYVDGH-------HITTVRADGLIIATPSGSTAYSLSSGG---PMVAPS
CpNADK1 ---------MVHALNELAVHRGAELNMPEFQLFCGGR-------LAATMPADGIIVSSATGSTAYALNAGG---PMVHPS
PtNADK5 ---------STYALNDILIADPCPATVSRFSFRIQRDSESCG--PLVNCRSSGLRVSTAAGSTAAMLSAGGFAMPVLSED
VvNADK3 ---------PTYALNDALLAHPCPATVSRCSFKIKREGHPCS--PLVHCRSSGLRVSTAAGSTAAMLSAGGFAMPILSQD
CsNADK3 ---------SKYPLNDVLIAHPCPASVSRFSFKIRNEQSCL---PLLNCRSSGLRVSTAAGSTAAMLSAGGFPMPILSQK
BrNADK6 ---------LSHALNDVLIAHPCPAAVSRFSFKIKSKDGYTSQ-KTVNCRSSGLRVCTAAGSTAAMLSAGGFVMPMLSRD
BrNADK5 ---------LSHALNDILIAHPCPAAVSKFSFKIKNKDCDTNP-KTVNCRSSGLRVCTAAGSTAAMLSAGGFLMPMLSRD
AtNADK3 ---------LSHALNDILIAQPCPAAVSRFSFKIKNKDGASSP-KTVNCRSSGLRICTAAGSTAAMQSAGGFVMPMLSRD
OsNADK4 ---------PTYALNDILVSHPCPASVSRFSFRKRSNTGESS--HLINCRSSGLRVATPAGSTAAMLSAGGFVMPISSHE
BdNADK4 ---------PTYALNDILVAHPCPASVSRFSLRKRSSTGETS--HLINSRSSGLRVSTATGSTAAMLSAGGFMMPISSRE
SiNADK4 ---------PTYALNDILVSHPCPASVSRFSFRKRSNTGEGS--HLINCRSSGLRVSTAAGSTAAMLSAGGFVMPLSSHE
ZmNADK4 ---------PTYALNDILVSHPCPASVSRFSFRKRNNTGENS--RLINCRSSGLRVSTAAGSTAAMLSAGGFTMPLSSRE
SbNADK4 ---------PTYALNDILVSHPCPASVSRFSFRKRNNMGETS--RLINCRSSGLRVSTAAGSTAAMLSAGGFMMPLSSRE
SmNADK4 ---------STPALNDVLLAHPNPAAVSRCTFSVVNQQTKSG--SLIHSRSSGLRVCTAAGSTAATLSAGGFAMPLESKE
PpNADK5 ---------DTPALNDILIAHPSPAAISRCSFSIEKQSTEELLIPVIHSRSSGLRISTATGSTAAMKSAGGTVMPLLSSK
MpNADK3(RCC299) ----------APALNDVLIAHPSPGAVSRYSVHVGGALGPP---LWFHVRSSGLRACTASGSTAAMRSAGGEPMHYLSRR
AmNADK1 --------WEALSLNEMLLHKEPLAGMCHFEIAVGEH-------AVVDIASDGLLVSTPTGSTAYALAAGG---PVIAPG
PmNADK1 --------WESLCLNEMALHREPLTSMCHFEISIGRH-------APVDISADGVILSTPTGSTAYSLSAGG---PVITPD
EcNADK1 --------RISTAINEVVLHPGKVAHMIEFEVYIDEI-------FAFSQRSDGLIISTPTGSTAYSLSAGG---PILTPS
NE/D Motif
Gly-rich Motif

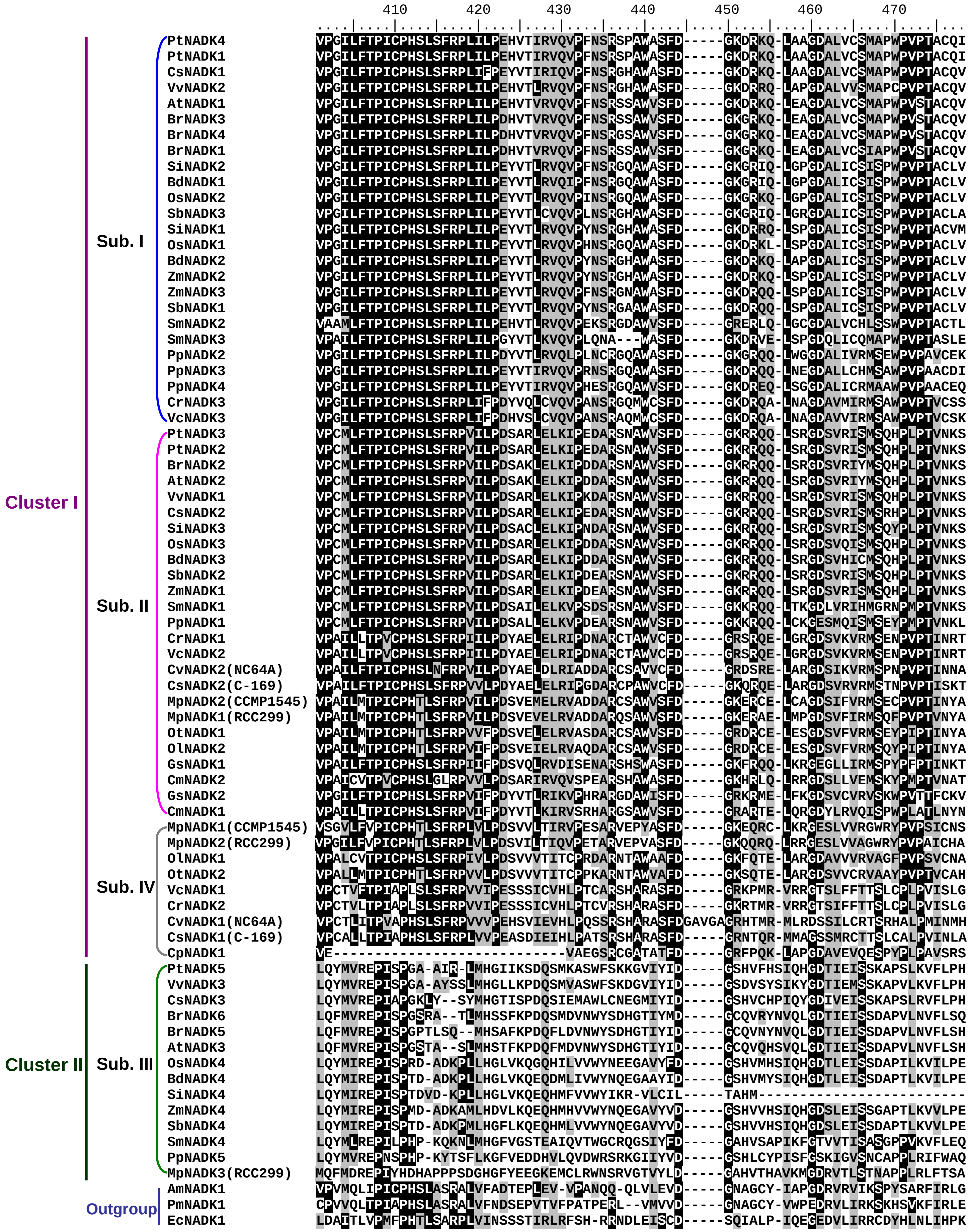

410
420
430
440
450
460
470
Cluster I
Sub. I
Sub. II
Sub. IV
Cluster II
Sub. III
Outgroup
PtNADK4 VPGILFTPICPHSLSFRPLILPEHVTIRVQVPFNSRSPAWASFD-----GKDRKQ-LAAGDALVCSMAPWPVPTACQI
PtNADK1 VPGILFTPICPHSLSFRPLILPEHVTIRVQVPFNSRSPAWASFD-----GKDRKQ-LAAGDALVCSMAPWPVPTACQI
CsNADK1 VPGILFTPICPHSLSFRPLIFPEYVTIRIQVPFNSRGHAWASFD-----GKDRKQ-LAAGDALVCSMAPWPVPTACQV
VvNADK2 VPGILFTPICPHSLSFRPLILPEHVTLRVQVPFNSRGHAWASFD-----GKDRRQ-LAPGDALVVSMAPCPVPTACQV
AtNADK1 VPGILFTPICPHSLSFRPLILPEHVTVRVQVPFNSRSSAWVSFD-----GKDRKQ-LEAGDALVCSMAPWPVSTACQV
BrNADK3 VPGILFTPICPHSLSFRPLILPDHVTVRVQVPFNSRSSAWVSFD-----GKGRKQ-LEAGDALVCSMAPWPVSTACQV
BrNADK4 VPGILFTPICPHSLSFRPLILPDHVTVRVQVPFNSRGSAWVSFD-----GKGRKQ-LEAGDALVCSMAPWPVSTACQV
BrNADK1 VPGILFTPICPHSLSFRPLILPDHVTVRVQVPFNSRSSAWVSFD-----GKGRKQ-LEAGDALVCSIAPWPVSTACQV
SiNADK2 VPGILFTPICPHSLSFRPLILPEYVTLRVQVPFNSRGQAWASFD-----GKGRIQ-LGPGDALICSISPWPVPTACLV
BdNADK1 VPGILFTPICPHSLSFRPLILPEYVTLRVQIPFNSRGQAWASFD-----GKGRIQ-LGPGDALICSISPWPVPTACLV
OsNADK2 VPGILFTPICPHSLSFRPLILPEYVTLRVQVPINSRGQAWASFD-----GKGRKQ-LGPGDALICSISPWPVPTACLV
SbNADK3 VPGILFTPICPHSLSFRPLILPEYVTLCVQVPLNSRGHAWASFD-----GKGRIQ-LGRGDALICSISPWPVPTACLA
SiNADK1 VPGILFTPICPHSLSFRPLILPEYVTLRVQVPYNSRGHAWASFD-----GKDRRQ-LSPGDALICSISPWPVPTACVM
OsNADK1 VPGILFTPICPHSLSFRPLILPEYVTLRVQVPHNSRGQAWASFD-----GKDRKL-LSPGDALICSISPWPVPTACLV
BdNADK2 VPGILFTPICPHSLSFRPLILPEYVTLRVQVPYNSRGHAWASFD-----GKDRKQ-LAPGDALICSISPWPVPTACLV
ZmNADK2 VPGILFTPICPHSLSFRPLILPEYVTLRVQVPYNSRGHAWASFD-----GKDRKQ-LSPGDALICSISPWPVPTACLV
ZmNADK3 VPGILFTPICPHSLSFRPLILPEYVTLRVQVPFNSRGNAWASFD-----GKDRQQ-LSPGDALICSISPWPVPTACLV
SbNADK1 VPGILFTPICPHSLSFRPLILPEYVTLRVQVPYNSRGAAWASFD-----GKDRQQ-LSPGDALICSISPWPVPTACLV
SmNADK2 VAAMLFTPICPHSLSFRPLILPEHVTLRVQVPEKSRGDAWVSFD-----GRERLQ-LGCGDALVCHLSSWPVPTACTL
SmNADK3 VPAILFTPICPHSLSFRPLILPGYVTLKVQVPLQNA---WASFD-----GKDRVE-LSPGDQLICQMAPWPVPTASLE
PpNADK2 VPGILFTPICPHSLSFRPLILPDYVTLRVQLPLNCRGQAWASFD-----GKGRQQ-LWGGDALIVRMSEWPVPAVCEK
PpNADK3 VPGILFTPICPHSLSFRPLILPEYVTIRVQVPRNSRGQAWASFD-----GKDRQQ-LNEGDALLCHMSAWPVPAACDI
PpNADK4 VPGILFTPICPHSLSFRPLILPEYVTIRVQVPHESRGQAWVSFD-----GKDREQ-LSGGDALICRMAAWPVPAACEQ
CrNADK3 VPGILFTPICPHSLSFRPLIFPDYVQLCVQVPANSRGQMWCSFD-----GKDRQA-LNAGDAVMIRMSAWPVPTVCSS
VcNADK3 VPGILFTPICPHSLSFRPLIFPDHVSLCVQVPANSRAQMWCSFD-----GKDRQA-LNAGDAVVIRMSAWPVPTVCSK
PtNADK3 VPCMLFTPICPHSLSFRPVILPDSARLELKIPEDARSNAWVSFD-----GKRRQQ-LSRGDSVRISMSQHPLPTVNKS
PtNADK2 VPCMLFTPICPHSLSFRPVILPDSARLELKIPEDARSNAWVSFD-----GKRRQQ-LSRGDSVRISMSQHPLPTVNKS
BrNADK2 VPCMLFTPICPHSLSFRPVILPDSAKLELKIPDDARSNAWVSFD-----GKRRQQ-LSRGDSVRIYMSQHPLPTVNKS
AtNADK2 VPCMLFTPICPHSLSFRPVILPDSAKLELKIPDDARSNAWVSFD-----GKRRQQ-LSRGDSVRIYMSQHPLPTVNKS
VvNADK1 VPCMLFTPICPHSLSFRPVILPDSARLELKIPKDARSNAWVSFD-----GKRRQQ-LSRGDSVRISMSQHPLPTVNKS
CsNADK2 VPCMLFTPICPHSLSFRPVILPDSARLELKIPEDARSNAWVSFD-----GKRRQQ-LSRGDSVRISMSRHPLPTVNKS
SiNADK3 VPCMLFTPICPHSLSFRPVILPDSACLELKIPNDARSNAWVSFD-----GKRRQQ-LSRGDSVRISMSQYPLPTVNKS
OsNADK3 VPCMLFTPICPHSLSFRPVILPDSARLELKIPDDARSNAWVSFD-----GKRRQQ-LSRGDSVQISMSQHPLPTVNKS
BdNADK3 VPCMLFTPICPHSLSFRPVILPDSARLELKIPDDARSNAWVSFD-----GKRRQQ-LSRGDSVHICMSQHPLPTVNKS
SbNADK2 VPCMLFTPICPHSLSFRPVILPDSARLELKIPDEARSNAWVSFD-----GKRRQQ-LSRGDSVRISMSQHPLPTVNKS
ZmNADK1 VPCMLFTPICPHSLSFRPVILPDSARLELKIPDEARSNAWVSFD-----GKRRQQ-LSRGDSVRISMSQHPLPTVNKS
SmNADK1 VPCMLFTPICPHSLSFRPVILPDSAILELKVPSDSRSNAWVSFD-----GKKRQQ-LTKGDLVRIHMGRNPMPTVNKS
PpNADK1 VPCMLFTPICPHSLSFRPVILPDSALLELKVPDEARSNAWVSFD-----GKKRQQ-LCKGESMQISMSEYPMPTVNKL
CrNADK1 VPAILLTPVCPHSLSFRPIILPDYAELELRIPDNARCTAWVCFD-----GRSRQE-LGRGDSVKVRMSENPVPTINRT
VcNADK2 VPAILLTPVCPHSLSFRPIILPDYAELELRIPDNARCTAWVCFD-----GRSRQE-LGRGDSVKVRMSENPVPTINRT
CvNADK2(NC64A) VPAILFTPICPHSLNFRPVILPDYAELDLRIADDARCSAVVCFD-----GRDSRE-LARGDSIKVRMSPNPVPTINNA
CsNADK2(C-169) VPAILFTPICPHSLSFRPVVLPDYAELELRIPGDARCPAWVCFD-----GKQRQE-LARGDSVRVRMSTNPVPTISKT
MpNADK2(CCMP1545) VPAILMTPICPHTLSFRPVILPDSVEMELRVADDARCSAWVSFD-----GKERCE-LCAGDSIFVRMSECPVPTINYA
MpNADK1(RCC299) VPAILMTPICPHTLSFRPVILPDSVEVELRVADDARQSAWVSFD-----GKERAE-LMPGDSVFIRMSQFPVPTVNYA
OtNADK1 VPAILMTPICPHTLSFRPVVFPDSVELELRVASDARCSAWVSFD-----GRDRCE-LESGDSVFVRMSEYPIPTINYA
OlNADK2 VPAILMTPICPHTLSFRPVIFPDSVEIELRVAQDARCSAWVSFD-----GRDRCE-LESGDSVFVRMSQYPIPTINYA
GsNADK1 VPAILFTPICPHSLSFRPIIFPDSVQLRVDISENARSHSWASFD-----GKFRQQ-LKRGEGLLIRMSPYPFPTINKT
CmNADK2 VPAICVTPVCPHSLGLRPVVLPDSARIRVQVSPEARSHAWASFD-----GKHRLQ-LRRGDSLLVEMSKYPMPTVNAT
GsNADK2 VPGILFTPICPHSLSFRPVIFPDYVTLRIKVPHRARGDAWISFD-----GRKRME-LFKGDSVCVRVSKWPVTTFCKV
CmNADK1 VPAILLTPICPHSLSFRPVIFPDYVTLKIRVSRHARGSAWVSFD-----GRARTE-LQRGDYLRVQISPWPLATLNYN
MpNADK1(CCMP1545) VSGVLFVPICPHTLSFRPLVLPDSVVLTIRVPESARVEPYASFD-----GKEQRC-LKRGESLVVRGWRYPVPSICNS
MpNADK2(RCC299) VPGILFVPICPHTLSFRPLVLPDSVILTIQVPETARVEPVASFD-----GKQQRQ-LRRGESLVVAGWRYPVPAICHA
OlNADK1 VPALCVTPICPHSLSFRPIVLPDSVVVTITCPRDARNTAWAAFD-----GKFQTE-LARGDAVVVRVAGFPVPSVCNA
OtNADK2 VPALLMTPICPHTLSFRPVVLPDSVVVTITCPPKARNTAWVAFD-----GKSQTE-LARGDSVVCRVAAYPVPTVCAH
VcNADK1 VPCTVFTPIAPLSLSFRPVVIPESSSICVHLPTCARSHARASFD-----GRKPMR-VRRGTSLFFTTSLCPLPVISLG
CrNADK2 VPCTVLTPIAPLSLSFRPVVIPESSSICVHLPTCVRSHARASFD-----GKRTMR-VRRGTSIFFTTSLCPLPVISLG
CvNADK1(NC64A) VPCTLITPVAPHSLSFRPVVVPEHSVIEVHLPQSSRSHARASFDGAVGAGRHTMR-MLRDSSILCRTSRHALPMINMH
CsNADK1(C-169) VPCALLTPIAPHSLSFRPLVVPEASDIEIHLPATSRSHARASFD-----GRNTQR-MMAGSSMRCTTSLCALPVINLA
CpNADK1 VE----------------------------VAEGSRCGATATFD-----GRFPQK-LAPGDAVEVQESPYPLPAVSRS
PtNADK5 LQYMVREPISPGA-AIR-LMHGIIKSDQSMKASWFSKKGVIYID-----GSHVFHSIQHGDTIEISSKAPSLKVFLPH
VvNADK3 LQYMVREPISPGA-AYSSLMHGLLKPDQSMVASWFSKDGVIYID-----GSDVSYSIKYGDTIEMSSKAPVLKVFLPH
CsNADK3 LQYMVREPIAPGKLY--SYMHGTISPDQSIEMAWLCNEGMIYID-----GSHVCHPIQYGDIVEISSKAPSLRVFLPH
BrNADK6 LQFMVREPISPGSRA--TLMHSSFKPDQSMDVNWYSDHGTIYMD-----GCQVRYNVQLGDTIEISSDAPVLNVFLSQ
BrNADK5 LQFMVREPISPGPTLSQ--MHSAFKPDQFLDVNWYSDHGTIYID-----GCQVNYNVQLGDTIEISSDAPVLNVFLSH
AtNADK3 LQFMVREPISPGSTA--SLMHSTFKPDQFMDVNWYSDHGTIYID-----GCQVQHSVQLGDTIEISSDAPVLNVFLSH
OsNADK4 LQYMIREPISPRD-ADKPLLHGLVKQGQHILVVWYNEEGAVYFD-----GSHVMHSIQHGDTLEISSDAPILKVILPE
BdNADK4 LQYMIREPISPTD-ADKPLLHGLVKQEQDMLIVWYNQEGAAYID-----GSHVMYSIQHGDTLEISSDAPTLKVILPE
SiNADK4 LQYMIREPISPTDVD-KPLLHGLVKQEQHMFVVWYIKR-VLCIL-----TAHM-------------------------
ZmNADK4 LQYMIREPISPMD-ADKAMLHDVLKQEQHMHVVWYNQEGAVYVD-----GSHVVHSIQHGDSLEISSGAPTLKVVLPE
SbNADK4 LQYMIREPISPTD-ADKPMLHGFLKQEQHMLVVWYNQEGAVYVD-----GSHVVHSIQHGDSLEISSDAPTLKVVLPE
SmNADK4 LQYMLREPILPHP-KQKNLMHGFVGSTEAIQVTWGCRQGSIYFD-----GAHVSAPIKFGTVVTISASGPPVKVFLEQ
PpNADK5 LQYMVREPNSPHP-KYTSFLKGFVEDDHVLQVDWRSRKGIIYVD-----GSHLCYPISFGSKIGVSNCAPPLRIFWAQ
MpNADK3(RCC299) MQFMDREPIYHDHAPPPSDGHGFYEEGKEMCLRWNSRVGTVYLD-----GAHVTHAVKMGDRVTLSTNAPPLRLFTSA
AmNADK1 VPVMQLIPICPHSLASRALVFADTEPLEV-VPANQQ-QLVLEVD-----GNAGCY-IAPGDRVRVIKSPYSARFIRLG
PmNADK1 CPVVQLTPIAPHSLASRALVFNDSEPVTVFPATPERL--VMVVD-----GNAGCY-VWPEDRVLIRKSKHSVKFIRLE
EcNADK1 LDAITLVPMFPHTLSARPLVINSSSTIRLRFSH-RRNDLEISCD-----SQIALP-IQEGEDVLIRRCDYHLNLIHPK

Figure S1. Amino acid sequences alignment analysis of NAD_Kinase domain of NADK proteins.

Amino acid sequences alignment and WebLogo analysis of NAD_Kinase domain in NADK genes from 24 species representing eight major lineages of the plantae: the glaucophytes (*Cyanophora paradoxa*), the rhodophytes (*Cyanidioschyzon merolae* and *Galdieria sulphuraria*), the chlorophytes (*Ostreococcus tauri*, *Ostreococcus lucimarinus*, *Micromonas pusilla* RCC299, *Micromonas pusilla* CCMP1545, *Chlorella variabilis* NC64A, *Coccomyxa subellipsoidea* C-169, *Chlamydomonas reinhardtii* and *Volvox carteri*), the bryophytes (*Physcomitrella patens*), the lycophytes (*Selaginella moellendorffii*), the gymnosperms (*Picea sitchensis*), the eudicots (*Arabidopsis thaliana, Populus trichocarpa*, *Cucumis sativus*, *Brassica rapa* and *Vitis vinifera*) and the monocots (*Brachypodium distachyon*, *Oryza sativa*, *Setaria italica*, *Sorghum bicolor* and *Zea mays*). Only CpNADK2 (ID, Contig53995) protein in *Cyanophora paradoxa* without complete NADK_Kinase domain is excluded, while the three outgroups of EcNADK1 (ID, EBESCP00000000630 or A7ZQ55) from *Escherichia coli* K-12, AmNADK1 (ID, AM1_1113 or B0C2T6) from *Acaryochloris marina* MBIC11017 and PmNADK1 (ID, P9301_14541 or A3PEA2) from *Prochlorococcus marinus* MIT 9301 are included in the alignment. Positions of the alignments where more than 50% of the sequences are identical are shown with black boxes. The four conserved NADK subfamilies are represented as sub. I, sub. II, sub, III and sub. IV at the left side of the alignment.