CLUSTAL 2.0.12 multiple sequence alignment (1/3)

```
ScNDE1          MIRQS-----LMKTVWANSSRFSLQSKSGLVKYAKNRSFHAARNLLEDKKVILQKVAPTT 55
ScNDE2          MLPRL-----GFARTARSIHRFKMTQIS--------KPFFHSTEVG--KPGPQQKLSKSY 45
ScNDI1          MLSKN-----LYS------NKRLLTSTN-----------------------TLVRFASTR 26
NcNDE2          MASTSRALGRLSAP-SMGVARLQTQAVSRLLSSAPRRALISESRQVAVTQQIRRAHTETT 59
YI              MLRLRPAVRAVSVARSVALTRSLHVSVAKFN-KIEGTAPAGLPKEVKQTAGHQGHHQEIP 59
StuNDA          ---------------------------------------------MPWFKNLIKISKTITN 16
AtNDA1          ---------------------------------------------MLWIKNLARISQTTSS 16
Tb              ------------------------------------------------------------
No              ------------------------------------------------------------
No2             ------------------------------------------------------------
Sy              ------------------------------------------------------------
Re              ------------------------------------------------------------
Sm              ------------------------------------------------------------
Av              ------------------------------------------------------------
Ec              ------------------------------------------------------------

ScNDE1          GVVAKQSFFKRTGKF--TLKALLYSALAGTAYVSYSLYREANPSTQVPQSDTFPNGSKRK 113
ScNDE2          TAVFKKWFVR-------GLKLTFYTTLAGTLYVSYELYKESNPPKQVPQSTAFANGLKKK 98
ScNDI1          STGVEN----------------------SGAGPTSFKTMKVIDP-----------QHSDKP 54
NcNDE2          PLPEPPKERRRFRKLRWLWRAPLFVSLAGIAYVGWGVYEERNPGPQVE------PDPSKK 113
YI              KPDENHPRRKKFHFWRSLWRLTYLSAIASLGYIGYRIYVIRNPSDQLP------ADPSKK 113
StuNDA          -------QSSSYKSITPLASPLLTQFLQFTKQYSTNDHVV---------GLEATKSDQKP 60
AtNDA1          SVGNVFRNPESYTLSSRFCTALQKQ--QVTDTVQAKEDVVNALEPQRYDGLAPTKEGEKP 74
Tb              ------------------------------------------------MICRTSFLRKP 11
No              ------------------------------------------------MVASLENHQPH 11
No2             ------------------------------------------------MVEALDNNPPH 11
Sy              ------------------------------------------------MNSPTSPRRPH 11
Re              ------------------------------------------------------MDTH 4
Sm              -------------------------------------------------------MQERH 5
Av              ------------------------------------------------------MT---H 3
Ec              ------------------------------------------------------MTTPLK 6

                                                P92-L93-L94
ScNDE1          TLVILGSGWGSVSLLKNLDTTL-----YNVVVVSPRNYFLFTPLLPSTPVGTIELKSIVE 168
ScNDE2          ELVILGTGWGAISLLKKLDTSL-----YNVTVVSPRSFFLFTPLLPSTPVGTIEMKSIVE 153
ScNDI1          NVLILGSGWGAISFLKHIDTKK-----YNVSIISPRSYFLFTPLLPSAPVGTVDEKSIIE 109
NcNDE2          TLVVLGTGWGSVSLLKKLDTEH-----YNVIVISPRNYFLFTPLLPSCTTGLIEHRSIME 168
YI              TLVVLGSGWGSVSFLKKLDTSN-----YNVIVVSPRNYFLFTPLLPSCPTGTIEHRSIME 168
StuNDA          RIVVLGSGWAGCRLMKDIDTNI-----YDVVCVSPRNHMVFTPLLASTCVGTLEFRSVAE 115
AtNDA1          RVLVLGSGWAGCRVLKGIDTSI-----YDVVCVSPRNHMVFTPLLASTCVGTLEFRSVAE 129
Tb              KVVVVGTGWAGCYFVRDTKPQL-----AELHVLSTRNHHVLTPLLPQTTTGTLEFRSICE 66
No              EVVIVGGGFGGLYAAKALAKTN-----VNVTLIDKRNFHLFQPLLYQVATGTLSPADISA 66
No2             KVVIVGGGFGGLYAAKALAKAK-----VDVTLIDKRNFHLFQPLLYQVATGTLSPADISS 66
Sy              -VVIVGGGFAGLYTAKNLRRSP-----VDITLIDKRNFHLFQPLLYQVATGSLSPADIAS 65
Re              RVVVVGGGFAGLQLAKDLKCPD-----TSITIVDRRNHHLFQPLLYQVATTVLATSEIAW 59
Sm              HVVVVGGGFGGLQLVNDLKGAP-----VKVTLIDRRNHHLFQPLLYQVATTVLATSEIAW 60
Av              RIVIVGGGAGGVELATRLGKTMGRNFQAKITLVDANMTHLWKPLLHEVAAGSLNST--GD 61
Ec              KIVIVGGGAGGLEMATQLGHKLGRKKKAKITLVDRNHSHLWKPLLHEVATGSLDEG--VD 64
                 ::::* * ..                 .:  :. .   :  *** .  .  :

ScNDE1          PVRTIARRS--HGEVHYYEAEAYDVDPENKTIKVKSSAKNNDYDL-------------DL 213
ScNDE2          PVRSIARRT--PGEVHYIEAEALDVDPKAKKVMVQSVSEDEYFVS-------------SL 198
ScNDI1          PIVNFALKK--KGNVTYYEAEATSINPDRNTVTIKSLSAVSQLYQPENHLGLHQAEPAEI 167
NcNDE2          PIRTILRHK--KANVKFYEAEASSVDPERKVVRVL-DTSEIRGDV----------VETEI 215
YI              PIRGIIRHK--QAECQYLEADATKIDHEKRIVTIRSAVSENSKEE----------VIKEI 216
StuNDA          PIGRIQPAVSTQPASYFFLANCNAIDFDNHMIECETVTEGVETLEAWK---------FNV 166
AtNDA1          PISRIQPAISREPGSYYFLANCSKLDADNHEVHCETVTEGSSTLKPWK---------FKI 180
Tb              PITRIQPALAHLP-NRFSRCFVYDINFEQKRVDCISVDNTSVGPHALVN-------TFDV 118
No              PLRSVLSKS---KNTKVLLGEVNDIDPNLQQIIVGDKV----------------------V 102
No2             PLRAVLSKS---KNTQVLLGEVNDIDPEAQELVMGDEK----------------------I 102
Sy              PLRGVLKGQ---KNIRVLMDKVIDIDPDKQKVVLEDHAP---------------------I 102
Re              PIRALFRGR---KDVSTLLGEVVGVDTEARVVSLKDGNA---------------------I 96
Sm              PIRRLYRDR---QEVTTLLGEVAGVDMIAKEVTLAHGQS---------------------I 97
Av              ELNYVAQAK--WNNFEFQYGRMCGLDRANKRIRLAAQPAQEDRAPLPER---------EL 110
Ec              ALSYLAHAR--NHGFQFQLGSVIDIDREAKTITIAELRDEKGELLVPER---------KI 113
                 :  .                    ::   . :                           :
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CLUSTAL 2.0.12 multiple sequence alignment (2/3)

```
                                          L195
ScNDE1          KYDYLVVGVGAQPNTFGTPGVYEYSSFLKEISDAQEIRLKIMSSIEKAASLSPKDPERAR 273
ScNDE2          SYDYLVVSVGAKTTTFNIPGVYGNANFLKEIEDAQNIRMKLMKTIEQASSFPVNDPERKR 258
ScNDI1          KYDYLISAVGAEPNTFGIPGVTDYGHFLKEIPNSLEIRRTFAANLEKANLLPKGDPERRR 227
NcNDE2          PYDMLVVGVGAENATFGIPGVREHTCFLKEIGDAQRIRKKIMDCVETAAFKGQSQEEIDR 275
Yl              PFDYLVVGVGAMSSTFGIPGVQENACFLKEIPDAQQIRRTLMDCIEKAQFE-KDPEVRKR 275
StuNDA          SYDKLVIASGAHALTFGIKGVNEHATFLREVHHAQEIRRKLLLNLMLSDVPGVSEEEKRR 226
AtNDA1          AYDKLVLACGAEASTFGINGVLENAIFLREVHHAQEIRRKLLLNLMLSEVPGIGEDEKKR 240
Tb              QYDKLVLAHGAQPNTFNVPGAVERACFLREVNEARTIRKRLVQNIMTANLPVTSVEEKKR 178
No              PYDTLIVATGAKHSYFGKDNWQELAPGLKTVEDAIEMRRRIFGAFEAAEKETDLEK-RKA 161
No2             PYDTLIVATGAKHSYFGKDNWEEFAPGLKTVEDAIEMRRRIFTAFEAAEKEKDPAK-RRA 161
Sy              AYDWLVVATGVSHHYFGNDHWAALAPGLKTIEDALTIRQRIFAAFEAAEKESNPER-QQA 161
Re              PYDTLVLATGARHAYFGRDEWEPFAPGLKALEDATTIRRRLLLAFEKAELEADPER-RKA 155
Sm              PYDTLVLATGATHAYFGHDEWAAVAPGLKTLEDATTIRRRVLIAFEQAEVEEDTAR-RDA 156
Av              EYDTLVLSVGSTTNDFGTPGAAENCIFLEGRDQAERFRRPLLSHYLRAHASNDDGH---- 166
Ec              AYDTLVMALGSTSNDFNTPGVKENCIFLDNPHQARRFHQEMLNLFLKYSANLGANG---- 169
                 :* *: . *    *.          *   .:  ::  .
                         T239E242 E246
ScNDE1          LLSFVVVGGGPTGVEFAAELRDYVDQDLRKWMPELSK-EIKVTLVEALPNILNMFDKYLV 332
ScNDE2          LLTFVVVGGGPTGVEFAAELQDYINQDLRKWMPDLSK-EMKVILIEALPNILNMFDKTLI 317
ScNDI1          LLSIVVVGGGPTGVEAAGELQDYVHQDLRKFLPALAE-EVQIHLVEALPIVLNMFEKKLS 286
NcNDE2          LLHMVVVGGGPTGVEFAGELQDFFEEDIKKLIPDIAD-RFRVTLIEALPNVLPSFSKQLI 334
Yl              LLHTVVVGGGPTGVEFAAELQDFFEDDLRKWIPDIRD-DFKVTLVEALPNVLPSFSKKLI 334
StuNDA          LLHCVVVGGGPTGVEFSGELSDFILKDVHQRYAHVKD-YIHVTLIEAN-EILSSFDDRLR 284
AtNDA1          LLHCVVVGGGPTGVEFSGELSDFIMKDVRQRYSHVKD-DIRVTLIEAR-DILSSFDDRLR 298
Tb              LLHTVVVGGGPTGVEFSADLAEFLRDDVKNINPELVQ-FCKVTVLEAG-EVFSTFDLRVR 236
No              LLTFVIVGGGPTGVELAGAIAELAYKTLQEDFRNINTSETRILLLQGGDRILPHIAPELS 221
No2             WLTFVVVGGGPTGVELAGAIAELAYKTLKEDFRNIDTTETQVILLEGLDRILPPFAPELS 221
Sy              WLTFVIVGAGPTGVELAGAIAEIAHSSLKDNFHRIDTRQAKILLIEGVDRVLPPYKPQLS 221
Re              MLTFSIIGAGPTGVEMAGIIAQLAQRTLVEEFRSIDTRSARILLIEAGPRVLPVFPEALS 215
Sm              LLTFTIIGAGPTGVELAGIIAEMAHRTLPGEFRRIDTRLARVVLVEAGPRILPAFSEELS 216
Av              QVKVAIVGAGATGVELAAELRHASKELVAYGLERIPPENLSITLIESSPRVLAALPERIS 226
Ec              KVNIAIVGGGATGVELSAELHNAVKQLHSYGYKGLTNEALNVTLVEAGERILPALPPRIS 229
                 :   ::*.*.**** :. : .            :      : :::.   ::      :
                                                                     N341
ScNDE1          DYAQDLFKEEKIDLRLKTMVKKVDATTITAKTGDGD----IENIPYGVLVWATGNAPREV 388
ScNDE2          KYAEDLFARDEIDLQVNTAVKVVEPTYIRTLQNGQT----NTDIEYGMLVWATGNEPIDF 373
ScNDI1          SYAQSHLENTSIKVHLRTAVAKVEEKQLLAKTKHEDGKITEETIPYGTLIWATGNKARPV 346
NcNDE2          EYTESTFKEEKIDIMTKTMVKRVTEKTVEAEISKPDGTREKITLPYGLLVWATGNAVRPV 394
Yl              DYTEKTFSDEKISILTKTMVKSVDENVIRAEQTKGDGTKETLEMPYGTLVWATGNTVRPV 394
StuNDA          VYATNQLTKSGVRLVRGLVQHVQPDNIILSD---------GTNVPYGLLVWSTGVGPSPF 335
AtNDA1          HYAIKQLNKSGVKLVRGIVKEVKPQKLILDD---------GTEVPYGPLVWSTGVGPSSF 349
Tb              EWGKRRLDALGVRIVKGNVVAVQEKEVITKS---------GEVFSTGLVVWSTGVGPSPL 287
No              QAATTSLREFGVVVQTKTRVTSIENDIVTFKQGDE-----LQTITSKTILWAAGVKASPM 276
No2             QEAEISLKQLGVLVQTKTLVTNIENDIVTLKQGEE-----VKEIASKTVLWAAGVKASAM 276
Sy              ARAQRDLEDLGVTVLTERMVTDINPEQVTVHNNGQ-----TETIVTKTVLWGAGVRASSL 276
Re              RYAEQSLIKMGVEVRTGIPVTACNENGIAIG---------DEFVSSRTVIWAAGVQASNA 266
Sm              AYASRELEKLGVEVLTGTPVTDCTDEGVTIG---------ESFVPSRTLVWAAGVQASPA 267
Av              RSAHATLESLGVRVLVSTAVSEVTAEGVKTKD--------DQFIPADLMVWAAGVRAPAF 278
Ec              AAAHNELTKLGVRVLTQTMVTSADEGGLHTKD--------GEYIEADLMVWAAGIKAPDF 281
                      :    : :             :                    ::*.:*
                                                        D383          T392
ScNDE1          SKNLMTKLEEQDS-RRGLLIDNKLQLLGAK---GSIFAIGDCT------FHPGLFPTAQV 438
ScNDE2          SKTLMSRIPEQTN-RRGLLINDKLELLGSE---NSIYAIGDCT------AHTGFFPTAQV 423
ScNDI1          ITDLFKKIPEQNSSKRGLAVNDFLQVKGS----NNIFAIGDN-------AFAGLPPTAQV 395
NcNDE2          VKDLMERIPAQKDSRRGLAVNEYLVVQGT----RDIWAVGDC-------AVAGYAPTAQV 443
Yl              VRELMSKIPAQKGSRRGLLVNEYLVVEGT----EGIWALGDC-------SATKYAPTAQV 443
StuNDA          VNSLDIPK----AKG-RIGIDEWLRVP----SVQDVYSIGDCSGFLESTGRQVLPALAQV 386
AtNDA1          VRSLDFPK----DPGGRIGIDEWMRVP----SVQDVFAIGDCSGYLESTGKSTLPALAQV 401
Tb              TKELKVDR----TRQGRISVDEHLQVLRDGVPIPDVYAIGDCA----TNESNPLPTLAAV 339
No              GKVLAERTGVECDRAGRAIVEPDLSIKGH----QNIFVVGDLAN-FSHQNGQPLPSVAPV 331
No2             GKVLAEKTGVECDRAGRVIVESDLSIKGH----SNIFVVGDLAN-FSHQNGKPLPGVAPV 331
Sy              GKIIGDRTGAELDRAGRVVVNPDLSVASF----DNIFVLGDLAN-YSHQGDQPLPGVAPV 331
Re              ----AAWVGAEKDRAGRAVVQPDLTVGGK----PEIFIIGDTAS-VKAADGTPVPGVAPA 317
Sm              ----ARWVGADADRAGRVKVGPDLTAPHH----PDIFVIGDTAS-VIQEDGKPVPGIAPA 318
Av              LKELDGLET---NRINQLQVRQTLQTTLD----DDIFAFGDCASCPQPGTDRPVPPRAQA 331
Ec              LKDIGGLET---NRINQLVVEPTLQTTRD----PDIYAIGDCASCPRP-EGGFVPPRAQA 333
                                     :   :           :: .**               * .
```

CLUSTAL 2.0.12 multiple sequence alignment (3/3)

```
ScNDE1      AHQEGEYLAQYFKKAYKIDQLNWKM-------------THAKDDSEVARLKNQIVKTQSQ 485
ScNDE2      AHQEGEYLAKILDKKLQIEQLEWDM-------------LNSTDETEVSRLQKEVNLRKSK 470
ScNDI1      AHQEAEYLAKNFDKMAQIPNFQKNL-------------SSRKD-------KIDLLFEENN 435
NcNDE2      ASQEGNFLAGLFNNMARTEVLEQRVRELS--GSLNLAPGNAAEISKEIEEHERQLRRIKD 501
Yl          ASQEGSYLANLLNGIAKTEDLNNEITNLEKQSEHTFDEQERKNIFAQLESKSRKLRRSRA 503
StuNDA      AERQGKYLASLLNKVGKQGGGHANC-----------------------------AQNINL 417
AtNDA1      AEREGKYLANLFNVMGKAGGGRANS-----------------------------AKEMEL 432
Tb          ASRQGVYLAKKIN--AELAG-----------------------------------KPF 360
No          AIQEGEYVAKLIKKRLQG-------------------------------------KT 351
No2         AKQEGEYVAALVQKRLQG-------------------------------------QT 351
Sy          AMQEAAYLSKLIPARLAEKE-----------------------------------QI 353
Re          AKQQGKYVASVIEARRLG-T-----------------------------------PT 338
Sm          AKQQGAYVAQVIRGRLTG-S-----------------------------------PA 339
Av          AHQQASLLAKSLHRKLQEDS-----------------------------------L 352
Ec          AHQMATCAMNNILAQMNGKP-----------------------------------L 354
            *:.     .

ScNDE1      IEDFKYNHKGALAYIGSDKAIADLAVGEA--KYRLAG-SFTFLFWKSAYLAMCLSFRNRV 542
ScNDE2      LDKFNYKHMGALAYIGSETAIADLHMGDS--SYQLKG-MFAFLFWKSAYLAMCLSIRNRI 527
ScNDI1      FKPFKYNDLGALAYLGSERAIATIRSGKR--TFYTGGGLMTFYLWRILYLSMILSARSRL 493
NcNDE2      IKPFHYSHQGSLAYIGSEKAVADVSWFNG---NLASGGSLTFLFWRSAYLSMCFSTRNRL 558
Yl          MLPFEYSHQGSLAYIGSDRAVADLSFNFWGIMNWSSGGTMTYYFWRSAYVSMCFSMRNKI 563
StuNDA      GDPFVYKHLGSMATIGRYKALVDLRESKEAKGVSLAG-FTSFFVWRSAYLTRVVSWRNKI 476
AtNDA1      GEPFVYKHLGSMATIGRYKALVDLRESKEGKGISMAG-FLSWFIWRSAYLTRVVSWRNRF 491
Tb          AAPFKYESLGSMVSLGTSSAVVELNGPRK---LDFVG-LKALFFWRSAYLSIVGSWRNRL 416
No          LPAFKYNDHGSLAMIGQNAAVVDLG------LLKLKG-FSAWAFWLLIHIYFLIEFDSKL 404
No2         LPAFNYTDKGSLAMIGQNAAVVDLG------FIKLKG-FFAWLFWLVIHIYFLIEFDNKL 404
Sy          MVPFRYIDYGSLAVIGQNKAVVDLG------FAQFTG-LVAWMIWVWAHVYYLIEFDNKL 406
Re          PSAFRYRHLGNLATIGPNSAVIDFG------KIRLKG-GIAWWIWGLAHIYFLIGTRSRL 391
Sm          PGPFRYRHQGSLATIGKRAAIIDFG------RIKLRG-SLAWWIWGIAHIYFLIGTRSRF 392
Av          CWSIATANHGSLISLSSFSAIGNLMGNLT-GNVTLEG-WLARKFYISLYRMHQMALYGTF 410
Ec          KN-YQYKDHGSLVSLSNFSTVGSLMGNLTRGSMMIEG-RIARFVYISLYRMHQIALHGYF 412
                     *:  :.   ::  .          *  :  .:  :       . .

ScNDE1      LVAMDWAKVYFLGRDSSI------------------------------------------ 560
ScNDE2      LIAMDWTKVYFLGRDSSV------------------------------------------ 545
ScNDI1      KVFFDWIKLAFFKRDFFKGL---------------------------------------- 513
NcNDE2      LVINDWVKSKLFGRDVSRE----------------------------------------- 577
Yl          LVCIDWMKVRVFGRDISRE----------------------------------------- 582
StuNDA      YVLINWLTTLVFGRDISRI----------------------------------------- 495
AtNDA1      YVAINWLTTFVFGRDISRI----------------------------------------- 510
Tb          YVIVNWLGSAIFGRDLTLINDYNDERTWLSLASEGAAREKVSRMNKVKTDGDGSNGNETT 476
No          LVMIQWAWNYITRKRGSRLITGKESLAFANNFDDSNDTNNYSAANNRQPLNV-------- 456
No2         VVMIQWVWNYITRNRGARLITGQEIHLAVN---TVNNSGHYQPLEKRLPVNV-------- 453
Sy          IVMLQWGWNYFTRGRGARLIT-------------DTPNPQSTSTVQKELVRP--------- 445
Re          AVGLSWLWIFVSGHHSARLIT-------------------QKETLKDEV------------ 421
Sm          AVAWSWLWTYLSGQHSARLIT-------------------QKDTLREER------------ 422
Av          RTLMMMLGDRFRSSTEPRLKLH-------------------------------------- 432
Ec          KTGLMMLVGSINRVIRPRLKLH-------------------------------------- 434
                      .

ScNDE1      ---------------
ScNDE2      ---------------
ScNDI1      ---------------
NcNDE2      ---------------
Yl          ---------------
StuNDA      ---------------
AtNDA1      ---------------
Tb          ARSKVDLPATKKQNE 491
No          ---------------
No2         ---------------
Sy          ---------------
Re          ---------------
Sm          ---------------
Av          ---------------
Ec          ---------------
```

Supplemental Fig. 4. Alignment of the amino acid sequences from selected Group A enzymes. The conserved amino acid in Ndi1 (Pro92, Leu93, Leu94, Leu195, Thr239, Glu242, Glu 246, Asn341, Asp383, and Thr392), are shown with a glay background. AtNDA1, *Arabidopsis thaliana* (NP_563783.1); Av, *Azotobacter vinelandii* (AAK19737.1); Ec, *Escherichia coli* (CAA23586.1); NcNDE2, *Neurospora crassa* (XP_331372.1); No, *Nostoc* sp. (BAB73083.1); No2, *Nostoc* sp. (BAB73084.1); Re, *Rhizobium etli* (AAM54916.2); ScNDE1, *S. cerevisiae* (CAA87359.1); ScNDE2, *S. cerevisiae* (CAA98651.1); ScNDI1, *S. cerevisiae* (CAA89160.1); Sm, *Sinorhizobium meliloti* (CAC46658.1); StuNDA, *Solanum tuberosum* (CAB52796.1); Sy, *Synechocystis* sp. (BAA17787.1); Tb, *Trypanosoma brucei* (AAM95239.1); Yl, *Yarrowia lipolytica* (CAA07265.1).