

sp|Q16795|NDUA9_HUMAN MAAAQSRVVRVLSMSRSAITAIATSVCCHGPPCRQLHHALMPHGKGRSS 50
sp|Q5R5S0|NDUA9_PONPY MAAAQSRVVRVLSMSRSAITAIATSVCCHGPPRRQLHHALIPHGKGRSS 50
sp|P34943|NDUA9_BOVIN MAAAVHPRVVRVLPMSRSVVALAASVFHSPQRQLHHAVIPHGKGRSS 50
sp|Q9DC69|NDUA9_MOUSE MAAAVRFRVVRALPMSRPAITAAATSVCSSHRQLHHAVIPHGKGRSS 50
sp|P25284|NDUA9_NEUCR -MAPLTAAMRSTPRIIVSNAFGFQRRATSDVTITRTGKPIIRN-QGGRSS 48
sdrA1 -----MYAVYPEVLMNNYVPV-----DGL 19
sdrA2 -----VSAMTENDYTKAK-----GDGI 17

sp|Q16795|NDUA9_HUMAN VSGIVATVFGATGFLGRYVNVNHLGRMGSQVIIPYRCDKYDIMHLRPMGDL 100
sp|Q5R5S0|NDUA9_PONPY VSGIVATVFGATGFLGRYVNVNHLGRMGSQVIIPYRCDTYDIMHLRPMGDL 100
sp|P34943|NDUA9_BOVIN VSGIVATVFGATGFLGRYVNVNHLGRMGSQVIVPHRCEPYDTMHLRPMGDL 100
sp|Q9DC69|NDUA9_MOUSE VSGVATVFGATGFLGRYVNVNHLGRMGSQVIIPYRCDVYDIMHLRPMGDL 100
sp|P25284|NDUA9_NEUCR LGGHTATVFGATGQLGRYIVNRLARQGGCTVVIIPFR-DEYNKRHLKVTGDL 97
sdrA1 LNGRVIIIVTGAGEGIGRCAAVEFARLGAEVVLLGRTQRKLEGVYDEIVDS 69
sdrA2 LDGKTIIVTGAGDGI GRAVAIEYAHQGATVVLLGKTKRNLEGVYDEITDY 67
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sp|Q16795|NDUA9_HUMAN GQLLFLEWDARDKDSIRRVVQHSNVVINLIGRDWETKNDFDFEDVFKIPQ 150
sp|Q5R5S0|NDUA9_PONPY GQLLFLEWDARDKDSIRRVVQHSNVVINLIGRDWETRNDFDFEDVFKIPQ 150
sp|P34943|NDUA9_BOVIN GQIFMDWNGRDKDSIRRAVEHSSVIVNLVGREWETQNFDFEDVFKIPQ 150
sp|Q9DC69|NDUA9_MOUSE GQLTFLEWDARDKDSIRKAVQHSNVVINLIGREWETRNDFDFEDVFNIPR 150
sp|P25284|NDUA9_NEUCR GKVVMIIEFDLRNTQSIEESVRHSDVVYNLIGRDYPTKNFSFEDVHIEGAE 147
sdrA1 G-----YKEPVIHPMDLLTAKGRDYQDFAQRLKESLGRLDG 105
sdrA2 G-----YAEPAIVVLDLADPASDAFKTIGAAISSEFTQLNG 103
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sp|Q16795|NDUA9_HUMAN AIAQLSKEAGVEKFIHVSHLNANIKSSSRYLNRNKAVGEKVVVRDAFPEAII 200
sp|Q5R5S0|NDUA9_PONPY AIAQLSKEAGVEKFIHVSHLNANIKSSSRYLNRNKAVGEKVVVRDAFPEAII 200
sp|P34943|NDUA9_BOVIN AIAQVSKEAGVEKFIHISHLNADIKSSSKYLRSKAVGEKEVRETFPEAII 200
sp|Q9DC69|NDUA9_MOUSE AIAQASKEAGVERFIHVSHLNAMKSSSKLRSKAVGEKEVRSVFPPEAII 200
sp|P25284|NDUA9_NEUCR RIAEAVAKYDVDRFIHVSSYNADPNSECEFFATKARGEQVVRISFPETTI 197
sdrA1 ILHN---AAELDILTPIQYDEELWESAMKVVNTAP-YLLTQACLPLLLA 151
sdrA2 IVHN---AAELGLMTPLENYEGALWDHVFQVNVKSP-LLVTQQCLPLLKE 149
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sp|Q16795|NDUA9_HUMAN VKPSDIFGREDRFLNSFASMHFRGPIPLGSLGWKTVKQPVYVVDVSKGIV 250
sp|Q5R5S0|NDUA9_PONPY IKPSDIFGREDRFLNSFASMHFRGPTPLGSLGWKTVKQPVYVVDVSKGIV 250
sp|P34943|NDUA9_BOVIN IKPAEIFGREDRFLNYFANIRWFGGVPPLISLGGKTVKQPVYIVDVTKGII 250
sp|Q9DC69|NDUA9_MOUSE IRPSDIFGREDRFLNHFANYRWFVAVPLVSLGFKTVKQPVYVADVSKGIV 250
sp|P25284|NDUA9_NEUCR VRPAPMFGFEDRLLHLKASVKN---ILTSNGMQEKYNPVHVIDVQALE 243
sdrA1 SEDASIVFITDDCAREAKYWGAVAVSRAAVQHLGLTLAIELQNTNVRVN 201
sdrA2 APYASIIIFTTDESQVKKPKYWGAVGVSRAAILHMARMWAIEYANTPIRVN 199
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sp|Q16795|NDUA9_HUMAN NAVKDPDANGKSFVFGPSRYLLFHLVKYIFAVAHRLFLPFPPLPFAYRW 300
sp|Q5R5S0|NDUA9_PONPY NAVKDPDANGKSFVFGPNRYLLFHLVKYIFAVAHRLFLPFPPLPFAYRW 300
sp|P34943|NDUA9_BOVIN NAIKDPDARGKTFVFGPSRYLLFDLVQYVFAVAHRPFLPYPLPHFAYRW 300
sp|Q9DC69|NDUA9_MOUSE NATKDPDAVGKTFVFGPNRYLLFHLVKYIFGMTHRTFIPYPLPFVYSW 300
sp|P25284|NDUA9_NEUCR QMLWDDNTASETFELYGPKTYTTAEISEMVDREIYKRRRHVNVPKKILKP 293
sdrA1 VINPGPCRTG----MRVTRHPGASIMSVPPP IAIMPLYEYLLGPD SKNT 246
sdrA2 IVDPGPCRTG----LRLLTHPGMPMKRYTPPEAITSIYTQLMDCDVLGH 244
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sp|Q16795|NDUA9_HUMAN VARVFEISPFEPWITRDKVERMHITDMKLPPLGLEDLGIQATPLELKAI 350
sp|Q5R5S0|NDUA9_PONPY VARVFEISPFEPWITRDKVERMHITDMKLPPLGLEDLGIQATPLELKAI 350
sp|P34943|NDUA9_BOVIN IGRLEISPFEPWITRDKVERIHITDKILPHLPGLLEDLGVQATPLELKAI 350
sp|Q9DC69|NDUA9_MOUSE IGKLFGLSPFEPWITRDKVERIHISDVMPDLPGLLEDLGVQATPLELKI 350
sp|P25284|NDUA9_NEUCR IAGVLNKAALWPPIMSADEIEREFHDQVIDPEAKTFKDLGIEPDIANFTY 343
sdrA1 RGQIMNARDWLD AEHDDRQIVAVLEQ----- 272
sdrA2 NGELFYAQNFINPDLDDRTEKDLATSTV----- 272
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sp|Q16795|NDUA9_HUMAN EVLRRHRT--YRWLSAEIEDVKPAKTVNI--- 377
sp|Q5R5S0|NDUA9_PONPY EVLRRHRT--YRWLSAEIEDVKPAKTVNI--- 377
sp|P34943|NDUA9_BOVIN EVLRRHRT--YRWLSSEIEDVQPAKTIPTSGP 380
sp|Q9DC69|NDUA9_MOUSE EVLRRHRT--YRWLSSEIEETKPAKTVNY--- 377
sp|P25284|NDUA9_NEUCR HYLQSYRSNAYYDLPPEATEKERREDREYIHML 375