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                   10        20        30        40        50        60        70        80        90       100       110
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TgNTPDase2 LETRCHDSLQALVVIDAGSSSTRTNVFLAKTRSCPNKGIDPDIQLIREGKRFTGLRVVLEEWLDTRPVDARLLFQYVPQMQLLEEDTVAILDSQLNEEQKVQVKALG--I
TgNTPDase1 LETRCHDSLQALVVIDAGSSSTRTNVFLAKTRSCPNKGIDPDIQLIGAGKRFAGLRVVLEEWLDTRPVDARLLFQYVPQMQLLEEDTVAILDSQLNEKQKVQVKALG--I
NcNTPDase  AERRCHDAWQAIVVIDGGSSATRTDVFLAKTRSCPRGGIDPDIRLLGAGKRFAGLRGVLESWLDARSVDSKRLFQHVPEMQLLEDDAVRILDEKLTEEQKVQVQAMG--V
TcNTPDase  SDVGRRQ---TADVFAAIAKEFDEWEDAAQNKTELLTNNAMRRYSIVFDAGSTGSRVHVFRYNLTSLTSFLRLDDELFVEAN-PNDAVASLSPLIEAAKAYIPESLHACV
TbNTPDase  AAVSLQR---AANLIDSLTHQTESWLKKAADTTPSLAAKSPRRYSVVFDAGSTGSRVHVYRYNLTSLLPYLKLEDELFIESD-PRGAAASLVPLLDAAKARVPTDMHACV
LmNTPDase1 VRRMTQQSKRLRVASTLVLSALVIFGFLVYHQSPLFSPSAYAVYDVVIDAGSTGSRVHVFQYERG--RTGFVLLRERFKRATDLDGAKASLEGLLRFADTVVPQSYQKCT
LmNTPDase2 GAVQLRSSSEIRALQAALFHEMRASKKKAENGVASGAAKSSVKYSVVFDIGSTGNRVHVYKYRVASELSDIDLVEELFELENSVQDAPEALWELFVKAKDFVPAELHACT
PfNTPDase  IEGEKKEKKIKERLFLCLICLLVIIWLIYFCYKNHIFLLQNEEYGIIIDAGSNGTRIHLFEWKKRKEIFNAKVKKSISTIDILIYLINKVIDHLIEKKIYVYNKQKWKSY
hNTPDase1  KESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENKYGIVLDAGSSHTSLYIYKWPAEQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQET
hNTPDase2  -MAGKVRSLLPPLLLAAAG----LAGLLLLCVPTRDVREPPAKYGIVLDAGSSHTSMFIYKWPADQHSSCDVPGGGISSYADNPSGASQSLVGCLEQALQDVPKERHAGT
hNTPDase3  EQAGLKALYRTPTIIALVVLLVSIVVLVSITVIQIHKQLPPGKYGIVLDAGSSRTTVYVYQWPAEQTFKCSVKGSGISSYGNNPQDVPRAFEECMQKVKGQVPSHLHGST
hNTPDase4  AVSLLYFSVVIIRNKYGRLTRDKKFQRYLARVTDIEATNNPNNYGIVVDCGSSGSRVFVYCWPRHIRQMRDKNRKPVVMKATSPEKVSDYISPLLNFAAEHVPRAKHKET
hNTPDase5  CVCSAVSHRNQQT----WFEGIFLSSMCPINVSAST------LYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVDQPKQGAETVQGLLEVAKDSIPRSHWKKT
hNTPDase6  YVAYIKWHRATATQAFFSITRAAPGARWGQQAHSPLGTDGHEFYGIMFDAGSTGTRVHVFQFTR-PPRETPTLTHETFKAADDVEKSAQGIRELLDVAKQDIPFDFWKAT
hNTPDase7  SCLLLLMLIIDFRHWSASLPRDRQYERYLARVGELEATEDPNNYGLVVDCGSSGSRIFVYFWPRHIKQMRDRNSQPVVKKADTPEHASDYLRPLLSFAAAHVPVKKHKET
hNTPDase8  MGLSRKEQVFLALLGASGVS--GLTALILLLVEATSVLLPTDKFGIVFDAGSSHTSLFLYQWLANQALACQVEGPGISSYTSNAAQAGESLQGCLEEALVLIPEAQHRKT
DrNTPDase1 MEVKVKNPWHRPVVIFLMAVVAVGIVIMVSISVVQHKPLPQKKYGIVLDAGSSHTSVFIYKWPAEQHHTCNVKGKGISSYFDKPHGAGASLEECMKEAKEKIPAHRHSET
DrNTPDase2 -MVSTGNRQQCQIITATGALFLAVGGILLLVLPSEDIKGSPGMYGIVLDAGSSHTSMFIYKWPADQHSECHAKGGGISSYAGVKGGAARSLKECMDKAMREIPTVRYKHT
DrNTPDase3 SRRGVR-MAKVAVVLAAAFMLASIAVIISIAVVQTNKKVSRGKYGIVLDAGSSRTTVYLYEWPAEQTTKCLVKGPGISDLGDQDQNTWYSLKECMKKMTEAIPSHQHNST
DrNTPDase4 VMGLLYLLLVTGKGQYSWLREDRHIHTRLGRVPDMEATNNPNNYGLVVDCGSSGSRVFVYTWPRHIKQMRDKHRKPVVMKASTPDKASDYISPLLSFAAQHIPKNKHQET
DrNTPDase6 YLTYVKRHYDDSK---LSVPEQLPQYRTDTRKHPTSGQS-ENQYGIMIDAGSTGTRIHIFKFQM-EPNEAPKLAHETFRAADEPEKSKEGILELLNVAKDTVPEVLWSST
DrNTPDase8 -MVHMKAILLGAAMAAVAVT--TIIALILALANRQTLDQPYSQFGIVFDAGSSHTALFLYQWQGNQKQSCDVDGDGISSYVQNPAGAGESLKKCLDIAKAAIPTEQQKST
XtNTPDase5 MIDFSLCHMEPTN----TLKSVLPLATSGQTSHSDT------IYGIMFDAGSTGTRIHIYRFKQRARGSHLELEGEVFESADQPKKGAATVRLLLDLAQKEVPSTQWSHT
XtNTPDase7 VFILVFAAVADLQLWSSRAFRDRQFRRYLDQIEDLEATKDTKNYGVVVDCGSSGSRVFVYFWPPHIKQMRDRGSKPVVKKALTPEKSSDYINPLLSFAASYIPKHKHKET
LpNTPDase  ---MYHSKTSILALYQLMFRVLIFLSCLVILTPNTIADPCEKSCIAVIDAGSTGSRLHIYSYDTDPIHIEEIWNKKIKPGFASIQPNSVTIDAYLTMLLADAP---IHNI
LiNTPDase1 VRRMTQQSKRLRIAGTLVLSALVIFGFLVYYQSPLLSPSAYAVYDVVIDAGSTGSRVHVFQYERG--RTGLVLLRERFKRATDPDGAKESLAGLLRFADKVVPQSYQKCT
LiNTPDase2 GAVELRRSSEIRALQAALFHEMRASKKKAENGVANGEAKTSDKYSVVFDIGSTGNRVHVYKYRVASELSDIDLVEELFELDNPVQDAPEALWELFMKAKYFVPAELHACT
LdNTPDase1 VRRMTQQSKRLRIAGTLVLSALVIFGFLVYYQSPLLSPSAYAVYDVVIDAGSTGSRVHVFQYERG--RTGLVLLRERFKRATDPDGAKESLAGLLRFADKVVPQSYQKCT
LdNTPDase2 GAVELRRSSEIRALQAALLHEMRASKKKAENGVANGEAKTSDKYSVVFDIGSTGNRVHVYKYRVASELSDIDLVEELFELDNPVQDAPEALWELFMKAKYFVPAELHACT

                  120       130       140       150       160       170       180       190       200       210       220
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TgNTPDase2 PVMLCSTAGVRDFHEWYRDALFVLLRHLINNPSYKFFTNWTRPITGAEEGLFAFITLNHLSRRLGCRNDLAGVVEVGGASAQIVFPLQVRAVLQRERLLPERYPSADVVS
TgNTPDase1 PVMLCSTAGVRDFHEWYRDALFVLLRHLINNPSYKFFTNWTRPITGAEEGLFAFITLNHLSRRLGCRNDLAGVVEVGGASAQIVFPLQVRAVLQRERLLPERYPSADVVS
NcNTPDase  PVLLCSTAGVRDFHDWYREALFVILRFLINHPKYKFFTNWTRPITGAEEGLYAFLALNHLSGRLGCRNDLVGVVEVGGASTQIVFPLQIRAVLQHERFLPSRFPCADVIS
TcNTPDase  PIEMKATAGLRRIGREHAEAVLDVVRRLFARGPFWMQSESVRILEGWEEGPLAWLTVNYLLGALNGDKNTATILDLGGGSTQIVMHPSIEAYAEFSYALKVNGRSFVVYQ
TbNTPDase  GIELKATAGLRRIGAEQAGRVLDAVRREFQKGPFWVHSESVRILEGREEGPLAWLTVNFLIGSLSGTKETATILDLGGGSTQVVMRPNLEGHEEFTDTFAINGKSIKLYQ
LmNTPDase1 SVTLKATAGLRLLPESAQQALLDVAQHTLNASPFQSR--GASIISGAQEGVYGWLTVNYLLDRLDTDVATVATIDMGGASTQVVFETTEWLPFNYAYQLRTPKRTIAMYQ
LmNTPDase2 AAEFKATAGLRMLGMEKANEILAGIRARYRNETFWLRGN-VRILDACEEGPMAWLTVNYLLGAFSATDSTVAVIDLGGGSTQIVFEPGHGMRTDFRYAATLGSRSVRAYQ
PfNTPDase  PFYFQATGGMRNLKQEDRNLRMKYIKNILSNDNNPFYFLYARILSGEEEGIYGWLAVNNLLNSIF--NNTYGAIDLGGSSTQITFYPM--HNLENYNSILLNNILIRLYS
hNTPDase1  PVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFGARIITGQEEGAYGWITINYLLGKFSNNQETFGALDLGGASTQVTFVPQQTIEPDNALQFRLYGKDYNVYT
hNTPDase2  PLYLGATAGMRLLNLTNPEASTSVLMAVTHTLTQYPFDFGARILSGQEEGVFGWVTANYLLENFIRK-GTLGAMDLGGASTQITFETTSPAERASEVQLHLYGQHYRVYT
hNTPDase3  PIHLGATAGMRLLRLQNETAANEVLESIQSYFKSQPFDFGAQIISGQEEGVYGWITANYLMGNFLHGVETTGALDLGGASTQISFVAGKMDLTSDIMQVSLYGYVYTLYT
hNTPDase4  PLYILCTAGMRILPESQQKAILEDLLTDIPVHFDFLFSDHAEVISGKQEGVYAWIGINFVLGRFEVRKRTAGILDMGGVSTQIAYEVPNLLAFNLGCDVHQTEHVYRVYV
hNTPDase5  PVVLKATAGLRLLPEHKAKALLFEVKEIFRKSPFLVPKGSVSIMDGSDEGILAWVTVNFLTGQLHHRQETVGTLDLGGASTQITFLPQLEQTRGYLTSFEMFNSTYKLYT
hNTPDase6  PLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWITINFLTGSLKPGGSSVGMLDLGGGSTQIAFLPRLQASPGYLTALRMFNRTYKLYS
hNTPDase7  PLYILCTAGMRLLPERKQLAILADLVKDLPLEFDFLFSQQAEVISGKQEGVYAWIGINFVLGRFDGRRRTVGILDMGGASLQIAYEVPILLAFNLGCDVQHTEHVYRVYV
hNTPDase8  PTFLGATAGMRLLSRKNSSQARDIFAAVTQVLGRSPVDFGAELLAGQAEGAFGWITVNYGLGTLVPEEMLVGALDMGGASTQITFVPGGPILKSTQADFRLYGSDYSVYT
DrNTPDase1 PVYLGATAGMRLLKMEDEMASEKVLTSVAHSLKTYPFSYGARILSGQEEGAFGWITVNYLSENLR--AGTLGALDLGGASTQITFVPQQIIESDNSIDFRLYGNDYHLYT
DrNTPDase2 PVYLGATAGMRLLNISKPKESAEVLKEVEEKLKSYPFSFGASILTGQEEGAYGWITVNYLLENYIGR-DTVGALDFGGASTQITFVTKQTVEKDDLMKLRLYGRDYQIYT
DrNTPDase3 PVFLGATAGMRLLHMTNEGRSNDVLTQMKNYLSSLPFKFNASIISGQEEGLYGWITVNYLKGNFLHGAKTVGSLDLGGASTQIAFATS--DAGEDIIKVSLYGYEYNIYT
DrNTPDase4 PLYILCTAGMRVLPESQQEALLEDLRTDIPVNFNFLFSDHVEVISGKQEGVYAWIGINFVLGRFNLRKRTAGVLDMGGVSTQIAYEVPNLLAFNLGCDAHRTEHVYRVYV
DrNTPDase6 PLMLRATAGLRLLPGEKATILLDKVREVFSESLFLYKPDSVSIMDGTDEGMSAWITINFLIGALHTETPTVGMLDLGGGSTQITFALQIQTSIDYVTSFQMFNISHALYS
DrNTPDase8 PVYLGATAGMRLLNLQNQTQSDSILAEVAKTIQTYPFDFGARILTGMEEGAYGWITTNYLLESFIKAGKIIGALDLGGASTQISFTPKDPVRPNSAFNLQLYGYKYELYT
XtNTPDase5 PVVLKATAGLRLLSETQSDALLSEVREVFHESPFLVPENSVSIINGADEGIFAWITVNFLTGRLHHR--TVGILDLGGGSTQITFLPLLDQTHDFLASVELFNSTYRLYT
XtNTPDase7 PLYILCTAGMRILPESQQIAILQDLVKDVPQEFDFLFSEHAEVISGKQEGVYAWISINFVLGRFDIRKRTVGVIDMGGGSLQIAYEVPSMLAFNLGCDLQHTEHVYRVYV
LpNTPDase  PVYFYATAGMRLLPQSQQKKYYDELEYWFRQQS---QWQEAKTITGNDEALFDWLAVNYKLDTLK--NKSVGVMDMGGASVQIVFPMP-AEIKHNQVELNIYGQNINLYV
LiNTPDase1 FVTLKATAGLRLLPESVQQVLLDAAQHTLNASPFQSR--GASIISGAQEGVYGWLTVNYLLNRLDTDVATVATIDMGGASTQVVFETTEWLPFNYAHQLRTPKRTITMYQ
LiNTPDase2 AVEFKATAGLRMLGMEKATEILDGIRARYRNETFWLRGN-VRILDACEEGPMAWLTVNYLLGVFSATASTVAVIDLGGGSTQIVFEPGHGMRTDLRYSATLGSRSVSAYQ
LdNTPDase1 FVTLKATAGLRLLPESVQQVLLDAAQHTLNASPFQSR--GASIISGAQEGVYGWLTVNYLLNRLDTDVATVATIDMGGASTQVVFETTEWLPFNYAHQLRTPKRTITMYQ
LdNTPDase2 AVEFKATAGLRMLGMEKATEILDGIRARYRNETFWLRGN-VRILDACEEGPMAWLTVNYLLGVFSATASTVAVIDLGGGSTQIVFEPGHGMRTDLRYSATLGSRSVSAYQ

                  230       240       250       260       270       280       290       300       310       320       330
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TgNTPDase2 VSFMQLGMASSAGLFLKELCSNDEVRPDGSASVNEDVRKNPLATYCSVHNFKVTNEMQCRENSITKPLAMKIENCSIIEGTGNVSQVESILVAPKLPLPFESVFRFASST
TgNTPDase1 VSFMQLGMASSAGLFLKELCSNDEVRPDGSASVNEDVRKNPLATYCSVNNFKVTNEMQCRENSITKPLAMKIENCSIIKGTGNVSQVESILVAPKLPLPFESVFRFASST
NcNTPDase  VSFMQLGVASSSGLFFKELCSNAEILPDGTIVVDEDVRKNPVATSCSANNFKAMNEMQCRENKITKSLALRIDDCFQIVGTGDQAQVEELLVSPRFPLPFESVFKFASTA
TcNTPDase  HSYEGNGLHAAKEQLLQAVAANNAVDAFPCFPKGYVHTE-GISN-TRDGGMEECSALFRRHVVRHQPCGSCGFNGVFQPDISAPVYAFSFYYDRLKPY-IKD-IRVQDVL
TbNTPDase  HSYEGNGLNAAREQLLASVATS-PLRAFPCFPQGYAHEK-GVSNGVGGGGMEECVALFRKHVVRGGECSSCGFNGVFQPDVRTPVYAFSFYHDLLRPH-MTAGIRLQDII
LmNTPDase1 HSYLGLGMNEAKKRLMTLFAEANGTLSFPCFPRGYTKRVN---GVELRNSFNACAGLFREHVITTSTCKACGARGVPQPLFPSPIYAFSYFYNRLYDFL--KEVYVSSYK
LmNTPDase2 HSYEGYGLHAATKKLLYHIQGKSAMEAFPCFAVGYEDPLGVKRNNAEEPVFQACANLFRDRLLKGLTCENCGIAGVMQPPLTNEIYAFSFIFDLLVLANVSKEVKLPDLA
PfNTPDase  HSFIGYGWIDSLFRVNIYLCLEIRNYPYNNFQQKYIHTNPNYTKGNINNSKNLSNILLQEIVKYHSQNDYSSLTDIYDYTYNIKPYDIENFIKTIKNFNLVQNPYPYEMK
hNTPDase1  HSFLCYGKDQALWQKLAKDIQVADLYKTPCTK--RFEMTLQQFEIQGIGNYQQCHQSILELFNTCPYS-QCAFNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEVSQEKVT
hNTPDase2  HSFLCYGRDQVLQRLLASALQTHDVYQSPCTMAQRPQNFNARVSLSGSSDPHLCRDLVSGLFSFCPFS-RCSFNGVFQPPVAGNFVAFSAFFYTVDFLRTSMGATLQQLE
hNTPDase3  HSFQCYGRNEAEKKFLAMLLQNSHVFDSLCTVDQRPESYNDVITFEGTGDPSLCKEKVASIFDFCHDQETCSFDGVYQPKIKGPFVAFAGFYYTASALNLSGSFSLDTFN
hNTPDase4  ATFLGFGGNAARQRYEDRIFANTMPYLDPCLPLDIKDEIQQTIYLRGTGDFDLCRETIQPFMNK--NETQTSLNGVYQPPIHFEFYGFSEFYYCTEDVLRMGGYNAAKFT
hNTPDase5  HSYLGFGLKAARLATLGALETE-HTFRSACLPRWLEAEWIVKYQYGGNQEFEPCYAEVLRVVRGHQPEERG------------SFYAFSYYYDRAVDTDDYEKLKVEDFE
hNTPDase6  YSYLGLGLMSARLAILGGVEGQPKELVSPCLSPSFKGEWEVTYRVSGQKAHELCAARVSEVLQNHRTEEHV------------DFYAFSYYYDLAAGVGDAEKLVVGDFE
hNTPDase7  TTFLGFGGNFARQRYEDLVLNETNPFLDPCLPVGLTDVVEQVLHVRGRGDWVSCGAMLSPLLAR--NTSQASLNGIYQSPIDFEFYGFSEFFYCTEDVLRIGGYHGPTFA
hNTPDase8  HSYLCFGRDQMLSRLLVGLVQ-SPLYESPCVHATPP--LSQNLTVEGTGNPGACVSAIRELFNFCQGQEDCAFDGVYQPPLRGQFYAFSNFYYTFHFLNLTS-QPLSTVN
DrNTPDase1 HSFLCYGKDQALKLAMAEKLRSTSVN-TPCMK--PLKMPKEQFSHVGLGNWSQCQESIRKVFNTCPYS-GCSFNGVFQPTVEGKFGAFSAFFFVMDFLNLKND-SLDKTK
DrNTPDase2 HSFLCYGRDQVLLRLLAHLITIQSVFGTPCVEKQTS--YNGELQIKGTGNYNQCLGNVSQLFSFCSYS-KCSFDGVFQPNITGNFMAFSAFFYTHSFLQEATGWTPAHLE
DrNTPDase3 HSFLCYGKNEAEKRVLAKLAKEPEIFGSECTKNNVPSRYNRLITFFGQSNPEQCKALVRSIFDLCQGTENCSFDGVYQPPLNGDFTAYAGFYWTALALKVNGSNSMEKFN
DrNTPDase4 STFLGFGGNAARQRYEENLISSTSPILDPCLPVDLQDELGQRLHLRGSGDFERCRLLLQPFLNR--NDTNTSLNGVYQPPIDFQFYGFSEFYYCTEDVLRMGGYNSTKYT
DrNTPDase6 HSYLGLGLMSARLAVLGGIEGQPQELVSPCLAPDYSGQWEVLYTVKGQKPYESCLRKVEKMIYKRKAEENM------------DFYAFSYYYDRAVDLGDERTVRVSDYI
DrNTPDase8 YSYLCYGKDQALKKLQAYLHKNAELYNSPCVVPPSS--FNDTILFKGTGNSSLCLSLIENIVNLCALSPDCGFNGIYQPPVNGEFFAFSAYFYTFDFLGLTP-APLTKVL
XtNTPDase5 HSYLGLGLKLARLAVLGVSEDN-QFFHSNCFLHGVKGEWSVTLKYEKKSDFDACYSEILPIIQDHQVPEHS------------PFYAFSYYYDRAADANDHMHLQVYDFA
XtNTPDase7 TTFMGFGGNFARQRYEDMVFNDTSPLQDPCLPVGLIDQVRHDLHVLGKGNWDSCRQQLEPLLLK--NDTQAYLNSVYQPSIDFEFYGFSEFFYCTEDVLRMGGYNSQKFA
LpNTPDase  HSFLGLGQTEMSHQFLN---------SPSCFANDYPLPDG------GQGNAPSCKEEVTSLMNSKVNQQPLLALNPVNEWYSINLASSQLFHFENSELT-----NQSLLQ
LiNTPDase1 HSYLGLGMNEAKKKLMMSFAEANGTSSFPCFPRGYAKRLN---DVELRNSFDACAGLFREHVITKTTCKACGARGVPQPLFPSLIYAFSYFYDRLYHFS--KEVYVSSYK
LiNTPDase2 HSYEGYGLHAATKELLFHIQGKSAVEAFPCFAVGYEDPLGIKKNNTGEPAFQACANLFRDRLLKGLTCENCGIAGVMQPPLTNEIYVFSFIFDLLALANVSREVKLPDLA
LdNTPDase1 HSYLGLGMNEAKKKLMMSFAEANGTSSFPCFPRGYAKRLN---DVELRNSFDACAGLFHEHVITKTTCKACGARGVPQPLFPSLIYAFSYFYDRLYHFS--KEVYVSSYK
LdNTPDase2 HSYEGYGLHAATKELLFHIQGKSAVEAFPCFAVGYEDPLGIKKNNAGEPAFQACANLFRDRLLKGLTCENCGIAGVMQPPLTNEIYVFSFIFDLLALANVSREVKLPDLA

                  340       350       360       370       380       390       400
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TgNTPDase2 APMFITGREMLASIDTLKDEELAEAAREFCSSEVIIRTDGPVLPNARGEQKLNSLDLCKTMALTVSLLRHMA
TgNTPDase1 APMIVTGGGMLAAINTLKDEELAEAAREFCSSEVIIRTDGPVLPNARGEQKLNSLDLCKTMALTVSLLRHMA
NcNTPDase  SPMVITGGAMYASISTMQGEQLIAASRTYCSSPVVNSGDGLVLPNA--EQKLTSMDLCKTIALTVSLIQHME
TcNTPDase  DIASQVCRSMKSVRELLEQPEMECFELSYLFTLLRYGFGFPPEQKLHIAKKINGFETAWALGASLVSLEGQS
TbNTPDase  GIASQVCKSMKSVEQLRREPELECLHLSYVVALLRDGFHYPLDQELHIAKKIDGYETAWTLGASLVSLEEHC
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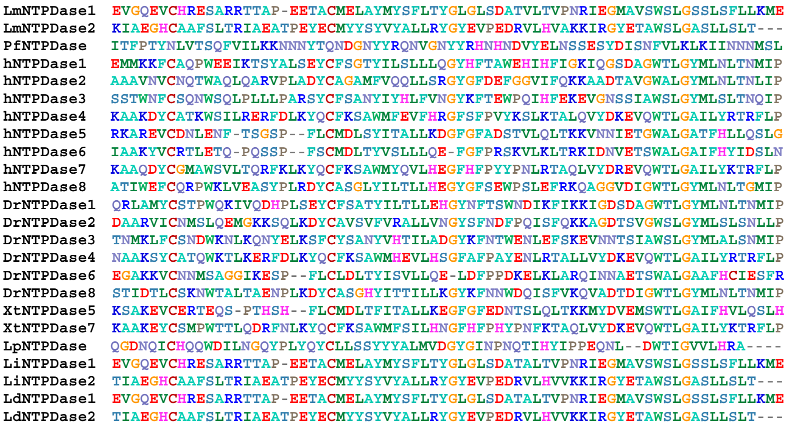

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LmNTPDase1  EVGQEVCHRESARRTTAP-EETACMELAYMYSFLTYGLGLSDATVLTVPNRIEGMAVSWSLGSSLSFLLKME
LmNTPDase2  KIAEGHCAAFSLTRIAEATPEYECMYYSYVYALLRYGYEVPEDRVLHVAKKIRGYETAWSLGASLLSLT---
PfNTPDase   ITFPTYNLVTSQFVILKKNNNYTQNDGNYYRQNVGNYYRHNHNDVYELNSSESYDISNFVLKLKIINNNMSL
hNTPDase1   EMMKKFCAQPWEEIKTSYALSEYCFSGTYILSLLLQGYHFTAWEHIHFIGKIQGSDAGWTLGYMLNLTNMIP
hNTPDase2   AAAVNVCNQTWAQLQARVPLADYCAGAMFVQQLLSRGYGFDEFGGVIFQKKAADTAVGWALGYMLNLTNLIP
hNTPDase3   SSTWNFCSQNWSQLPLLLPARSYCFSANYIYHLFVNGYKFTEWPQIHFEKEVGNSSIAWSLGYMLSLTNQIP
hNTPDase4   KAAKDYCATKWSILRERFDLKYQCFKSAWMFEVFHRGFSFPVYKSLKTALQVYDKEVQWTLGAILYRTRFLP
hNTPDase5   RKAREVCDNLENF-TSGSP--FLCMDLSYITALLKDGFGFADSTVLQLTKKVNNIETGWALGATFHLLQSLG
hNTPDase6   IAAKYVCRTLETQ-PQSSP--FSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVETSWALGAIFHYIDSLN
hNTPDase7   KAAQDYCGMAWSVLTQRFKLKYQCFKSAWMYQVLHEGFHFPYYPNLRTAQLVYDREVQWTLGAILYKTRFLP
hNTPDase8   ATIWEFCQRPWKLVEASYPLRDYCASGLYILTLLHEGYGFSEWPSLEFRKQAGGVDIGWTLGYMLNLTGMIP
DrNTPDase1  QRLAMYCSTPWQKIVQDHPLSEYCFSATYILTLLEHGYNFTSWNDIKFIKKIGDSDAGWTLGYMLNLTNMIP
DrNTPDase2  DAARVICNMSLQEMGKKSQLKDYCAVSVFVRALLVNGYSFNDFPQISFQKKAGDTSVGWSLGYMLSLSNLLP
DrNTPDase3  TNMKLFCSNDWKNLKQNYELKSFCYSANYVHTILADGYKFNTWENLEFSKEVNNTSIAWSLGYMLALSNMIP
DrNTPDase4  NAAKSYCATQWKTLKERFDLKYQCFKSAWMHEVLHSGFAFPAYENLRTALLVYDKEVQWTLGAILYRTRFLP
DrNTPDase6  EGAKKVCNNMSAGGIKESP--FLCLDLTYISVLLQE-LDFPPDKELKLARQINNAETSWALGAAFHCIESFR
DrNTPDase8  STIDTLCSKNWTALTAENPLKDYCASGHYITTILLKGYKFNNWDQISFVKQVADTDIGWTLGYMLNLTNMIP
XtNTPDase5  KSAKEVCERTEQS-PTHSH--FLCMDLTFITALLKEGFGFEDNTSLQLTKKMYDVEMSWTLGAIFHVLQSLH
XtNTPDase7  KAAKEYCSMPWTTLQDRFNLKYQCFKSAWMFSILHNGFHFPHYPNFKTAQLVYDKEVQWTLGAILYKTRFLP
LpNTPDase   QGDNQICHQQWDILNGQYPLYQYCLLSSYYYALMVDGYGINPNQTIHYIPPEQNL--DWTIGVVLHRA----
LiNTPDase1  EVGQEVCHRESARRTTAP-EETACMELAYMYSFLTYGLGLSDATALTVPNRIEGMAVSWSLGSSLSFLLKME
LiNTPDase2  TIAEGHCAAFSLTRIAEATPEYECMYYSYVYALLRYGYEVPEDRVLHVVKKIRGYETAWSLGASLLSLT---
LdNTPDase1  EVGQEVCHRESARRTTAP-EETACMELAYMYSFLTYGLGLSDATALTVPNRIEGMAVSWSLGSSLSFLLKME
LdNTPDase2  TIAEGHCAAFSLTRIAEATPEYECMYYSYVYALLRYGYEVPEDRVLHVVKKIRGYETAWSLGASLLSLT---
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Figure S1. Sequence alignment of NTPDases used to build the evolutionary tree of Figure 2. TrimAl software was used to delete sites exhibiting a high proportion of gaps(GAPPYOUT function). NTPDases and their accession numbers are listed in Figure 2.