

Supplemental Figure 1. Alignment of amino acid sequence of ceramidases from different organisms using ClustalW: *Oryza sativa* cv. Nipponbare (OsCDase), *Arabidopsis thaliana* (NP_172218, NP_200706, NP_181337), *Dictyostelium discoideum* (XP_629027), *Homo sapiens* (NP_063946), *Canis familiaris* (XP_861054), *Mus musculus* (NP_061300), *Rattus norvegicus* (NP_446098), *Gallus gallus* (XP_421560), *Drosophila melanogaster* (NP_651797) and *Drosophila pseudoobscura* (XP_001357669). Dark and light grey shading indicate identical and similar residues, respectively.

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At-NP_172218      1  ----YISTVL---F-L-L--T-----GG--G---V---Y--SH-----
At-NP_200706     1  ----L---L---F-L-LRIT-----C---I---F---SD-----
At-NP_181337     1  ----I-L-FLL---L-L-L-LS-----RT---V---Y---A-----
OsCDase          1  GSSRVWL-WLI---LAL-VL-LN-----CS--L---V---L---SA-----
Dd-XP_629027    1  ----I-L--LLSVGF--IDAFKIS---I-----EN--H---I-K--L--SD---D-
Hs-NP_063946    1  ----T-V-ALLS--L-L-F-ITSCTIENHK-DLGG-HFFSTTQSPATQGSTAAQRSTA
Cf-XP_861054    1  ----T-V-ALLS--L-L-F-ITSCTIENHKGKFCRVHF--QTQGVPTTQSSITTLGSTA
Mm-NP_061300    1  ----T-V-ALLT--L-L-F-VTSCTIENHK-DSCN-HW---F-S--TTLGST---T-
Rn-NP_446098    1  ----T-V-ALLT--L-L-F-VTSCTIENHK-DSCN-HW---V-S--TTQGP-----T-
Gg-XP_421560    1  ----T-V-ALL--V-LH-F-VT-G--ESSS-SNGK-----L-S--SF-GSA--Q-EDY
Dm-NP_651797    1  ----L-AFL--A-V---S-F-I-----CG-----L---V---SA-----
Dp-XP_001357669 1  ----L-ALI--A-L---S-G-I-----CG-----L---A---SA-----

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At-NP_172218      18  -----SE-----YLLIGLSYDITGP-AADVNMGYA-NM
At-NP_200706     14  -----SD-----YLMGLGSYDITGP-AADVNMGYA-NM
At-NP_181337     16  -----YLLIGVGSYDITGP-AADVNMGYA-NS
OsCDase          25  -----SP-----YLVGMGSFDITGP-AADVNMGYA-NT
Dd-XP_629027    26  -----SS-----YQIGTGIYDITGP-GAETNMGYA--M
Hs-NP_063946    47  TQHSTATQSSSTATQTSPLVLTPE-SPLFQNFSGYHIGVGRADCTGQ-VADINLMGYGKS-
Cf-XP_861054    47  TQGSLTHGTTATPTPPVVTPE-PPLFQNFSGYHIGVGRADCTGQ-VADINLMGYSKT-
Mm-NP_061300    35  TQ-P-----P-----PITQTPNFP-SFRNFSGYHIGVGRADCTGQ-VSDINLMGYGKN-
Rn-NP_446098    35  TQ-S---SPT-TQT-PTTQTPDLPPS-QNFSGYHIGVGRADCTGQ-VSDINLMGYGKN-
Gg-XP_421560    32  GE-P---SP--TQK-PTT-TAG---S-EN---YLLIGVGRADCTGP-VAEIPLMGYA-NP
Dm-NP_651797    16  -----T-----YKVGVGRADITGPPV-EINFMGYA-NI
Dp-XP_001357669 16  -----T-----YKVGVGRADITGPPV-EINFMGYA-NI

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At-NP_172218      45  E-Q-VASGIHFRLRARAFIVASEP-QG-KRVVFNLDACMASQIV-KLKVIERLKARYGD-
At-NP_200706     41  E-Q-VASGVHFRRLARAFIVAEP-YK-KRIAFVNLDAGMASQLV-TIKVIERLKORYGE-
At-NP_181337     41  D-Q-IASGIHFRLRARAFIVAEP-QG-NRVVFNLDACMASQIV-TIKVLERLKARYGE-
OsCDase          52  E-Q-IASGIHFRLKSRAFIVAEP-NG-KRVVFNLDACMASQIV-TIKVLERLKARYGD-
Dd-XP_629027    52  PGC-ITGGIHFRRARAFVVIDS-EG-NRAVVSTDSCMIFQEV-KIQVIQDLOEIFGPT
Hs-NP_063946    104 G-Q-NAQGILTRLYSRAFVMAEP-DGSNRTVFSIDIGMVSQRL-RLEVLNRLQSKYGS-
Cf-XP_861054    104 G-Q-NARGILTRLYSRAFVMAEP-DGSNRVVFVSDIGMVSQRL-RLEVLNRLQTKYGS-
Mm-NP_061300    80  G-Q-NARGLLTRLYSRAFILADP-DGSNRMAFVSVELCMISQRL-RLEVLKRLQSKYGS-
Rn-NP_446098    85  G-Q-NAQCLLTRLYSRAFILADP-DGSNRMAFVSVELCMISQRL-RLEVLKRLQSKYGS-
Gg-XP_421560    74  D-QVGG-GLLTRLYSRAFIVAEPND-SRRVVFVSDIGMVSQRL-RLEVLKELKNKYGE-
Dm-NP_651797    42  K-Q-VGRGIHTRVFARAFVVEDE-KG-NRVAFVSADAGMMGYGLKR-EVIKRLQARYGN-
Dp-XP_001357669 42  K-Q-VGRGIHTRVFARAFVVEDE-KG-NRVAFVSADAGMMGYGLKR-EVIKRLQARYGN-

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At-NP_172218      99  LYTEQNVGTSGIHTHAG-PGGYLOQVYIVTSLGF-V-RQSFDAIVDGI-ENSI-IQAHE
At-NP_200706     95  LYTEENVVAISGTHTHAG-PGGYLOQVILYLVTSLSGF-V-HQSFNAIVDGI-EQSI-IQAHE
At-NP_181337     95  LYTEKNVAISGIHTHAG-PGGYLOQVYIVTSLGF-V-RQSFVIVVNGI-EQSI-VQAHE
OsCDase          106 LYNENNVVAISGIHTHAG-PGGYLOQVYIVTSLGF-V-RQSFVIVDGI-EQSI-VEAHN
Dd-XP_629027    108 LYTHDNVLLSGTHTHSG-PAGFSEYALYGITALGF-Y-KKNFDITCDGI-VQAI-VKAHK
Hs-NP_063946    159 LYRRDNVILSGTHTHSG-PAGFYQYTVFVIASEGF-S-NQTFQHMVTGI-LKSIDI-AHT
Cf-XP_861054    159 LYGRDNVILSGTHTHSG-PAGFYQYTVFVIASEGF-S-NRTFQYVMTGI-VKSIDI-AHR
Mm-NP_061300    135 LYRRDNVILSATHTHSG-PAGFYQYTYLILASEGF-S-NRTFQYIVSGI-MKSIDI-AHT
Rn-NP_446098    140 LYRRDNVILSATHTHSG-PAGFYQYTYLILASEGF-S-NRTFQYIVSGI-VKSIDI-AHT
Gg-XP_421560    129 LYRRDNVILSGTHTHSG-PGGFYQYTLFWITSKGLIKPN--LNALVNGI-VKSIDI-AHQ
Dm-NP_651797    96  LYHNDNVVAISGTHTH-GAPGGFLMHLLYDISILGF-V-PQTFEVMAQGLYL-CIKR-ATD
Dp-XP_001357669 96  LYHTDNVAISGTHTH-GAPGGFLMHLLYDISILGF-V-PQTFEVMAQGLYL-CIKR-ATD

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At-NP_172218 154 NLRPGSIFLNNGEILLDAGVNRSPSAYLNNPSKERSKHKYNVDKEMTLVKFVDDWG-PVG
 At-NP_200706 150 NLRPGSILINKGELLDAGVNRSPSAYLNNPAHERSKYEYDVKEMTLVKFVDDWG-PV-
 At-NP_181337 150 SLRPGSAFVNKGDILLDAGVNRSPSSYLNNPAAERSKYKYDVKEMTLVKFVDSQLG-PTG
 OsCDase 161 NLRPGKIFVNKGDILLDAGVNRSPSAYLNNPAAERSKYEYNVDKEMTLVKFVDELG-PVG
 Dd-XP_629027 163 SVQPARMLTQQGELWNSNINRSPYAYDNNPEEEKAMYDANVDKNTVIR-IEDMSGNPFA
 Hs-NP_063946 214 NMKPGKIFINKGNVDGVOINRSPYSYLQNPQSERARYPSNTDKEMTVLKMVDLN-GDDLG
 Cf-XP_861054 214 NMKPGKIFIKKGTVEGAQINRSPYSYLQNPESERARYSSNTDKEMVVLKMEDLD-GAELG
 Mm-NP_061300 190 NLKPGKIFINKGNVANVOINRSPSSYLLNPQSERARYSSNTDKEMVLKLVLDLN-GEDLG
 Rn-NP_446098 195 NLKPGKVLINKGNVANVOINRSPSSYLQNPQSERARYSSNTDKEMVVLKLVLDLN-GEDLG
 Gg-XP_421560 184 NMKRGRLFLNRGTVENSOINRSPYSYLQNPASERSRYSTNTDKEMVMLKMVDEN-GHDLG
 Dm-NP_651797 151 NLVDGRILLSKTTVLNVNINRSPSSYLQNPAAERAOYEHDTDKTLTQLRFVDLE-NNLLG
 Dp-XP_001357669 151 NLVDGRIFLSKTTVLNVNINRSPSSYLQNPAAERAOYEHDTDKTLTQLRFVDLE-NNLLG

At-NP_172218 213 SFNWFATHGTSMSRTNSLISGDNKGAASRFMEDWYE-----Q---NT--AESYSEEF
 At-NP_200706 208 -----A-----R---I-----MEDWFER---E---NG--C-RS-----
 At-NP_181337 209 SFNWFATHGTSMSRTNSLISGDNKGAARFMEDWFEN-G---QK--NS--V-SS-----
 OsCDase 220 SFNWFATHGTSMSRTNSLISGDNKGAARFMEDWAEQMGLPKQSAHANSDDL-RS-----
 Dd-XP_629027 222 AISEFCVHCTSMNNTNHLISGDNKGYAS-YL--W-EK-----HA---NG---QS-----
 Hs-NP_063946 273 LISWFATHPVSMNNSNHLVNSDNVGYAS-YL--L-EQ-----EK---N---KG-----
 Cf-XP_861054 273 LISWFAVHPVSMNNSNHLVNSDNMGYAA-YL--F-EQ-----EK---N---KG-----
 Mm-NP_061300 249 LISWFATHPVSMNNSNHLVNSDNMGYAA-YL--F-EQ-----EK---N---KG-----
 Rn-NP_446098 254 LISWFAVHPVSMNNSNHLVNSDNMGYAA-YL--F-EQ-----EK---N---RG-----
 Gg-XP_421560 243 LISWFAVHPVSMNNTNHL-----G--S-----
 Dm-NP_651797 210 AFNWMVAVHATSMNNTNRLVTSDNVGYAA-LL--L-EK-----EY---N---PN-----
 Dp-XP_001357669 210 AFNWMVAVHATSMNNTNRLVTSDNVGYAA-LL--L-EK-----EY---N---PN-----

At-NP_172218 261 ISD-EI-PRRVSSLIEN---HQD-SHHELLELASYFESQPGKPVTRIS-SS-ARRVRSAL
 At-NP_200706 224 V-DVES-PRRVSSII SD-P-Y-D---QDLMEMASSLLSTGGKTVTRMS-SV-ARRVRSRF
 At-NP_181337 254 --R-NI-PRRVSTIVSDFSRN-Q-S-R-LLDIAATYKSSRGHSVDK-SLDVKTR-VRNG-
 OsCDase 274 LHKTSVLPRRVSTIPE-P-N-EIT-DDLIQLASSYEASGRRRLAG-S-SI-TRRIRST-
 Dd-XP_629027 261 ----SI-P---GT-----G-----
 Hs-NP_063946 311 ----YL-P---GQ-----G-----
 Cf-XP_861054 311 ----YL-P---GE-----G-----
 Mm-NP_061300 287 ----YL-P---GQ-----G-----
 Rn-NP_446098 292 ----YL-P---GQ-----G-----
 Gg-XP_421560 263 -----
 Dm-NP_651797 248 ----KM-P---GK-----G-----
 Dp-XP_001357669 248 ----KM-P---GK-----G-----

At-NP_172218 313 RKADKPGFVSAFCQINCGDVSPNVLGAFCLDTG-LPCDFNHSTC--G-GKNEMCYGRGP
 At-NP_200706 274 RHADKPRFVSAFCQINCGDVSPNVLGAFCLDTG-LPCDFNHSTC--G-GKNEQCYGRGP
 At-NP_181337 303 ---SKRK FVSAFCQSNCGDVSPNLTGTFCLDTG-LPCDFNHSTC--N-GQNEICYGRGP
 OsCDase 326 QQ-NKPK FVSAFCQSNCGDVSPNLTGTFCLDTN-LPCDFNHSTC--N-GKNEICYGRGP
 Dd-XP_629027 267 -----P-FIAAFGQSNCGDVSPNTRGPTCRD-G-KPCDYKTSTC--N-GKVEECWALGP
 Hs-NP_063946 317 -----P-FVAAFASSNLGDVSPNLTGPHCVNTG-ESCDNANSTCPIG-GP-SMCIKAGP
 Cf-XP_861054 317 -----P-YVAAFASSNLGDVSPNLTGPHCVNTG-ESCDNANSTCPIG-GS-SMCMATGP
 Mm-NP_061300 293 -----P-FVAGFASSNLGDVSPNLTGPHCVNTG-ESCDNDKSTCPNG-GP-SMCMASGP
 Rn-NP_446098 298 -----P-FVAGFASSNLGDVSPNLTGPHCVNTG-ESCDNDKSTCPNG-GP-SMCMASGP
 Gg-XP_421560 263 -----P-FVAAFASSNLGDVSPNLTGTFCLDTN-LPCDFNHSTC--N-GKNEICYGRGP
 Dm-NP_651797 254 -----K-FVGAFCSSNLGDVSPNLTGPHCVNTG-ESCDNPOSTCPVG-GA-SMCMAMGP
 Dp-XP_001357669 254 -----K-FVGAFCSSNLGDVSPNLTGPHCVNTG-ESCDNPOSTCPVG-GA-SMCMAMGP

At-NP_172218 368 GYP-DEFESTRIIGERQF-KMA----LEL-FNKASEQLQGGK-V-DYRHHVYVDFSOLE-VT
 At-NP_200706 329 GYP-DEFESTRIIGERQF-KKA----ADL-FTKASEEIQGGK-V-DYRHAYVDFSOLE-VT
 At-NP_181337 355 GYP-DEFESTRIIGERQF-KMA----VEL-FNKATEKLQGGK-I-GYQHAYLDFSNLD-VT
 OsCDase 380 GYP-DEFESTRVIIGNRQFLK-A----RDL-FDSASEEIQGGK-I-DYRHTYLDFSKLE-VK
 Dd-XP_629027 315 GTDGMFESTQIIGNQFNK-A----LEL-FNNAIQVSGK-I-QYRHTWKPFITNVS-VE
 Hs-NP_063946 367 GQ--DMFDSTQIIGRAMYQR-A----KEL-YASASQEVGTGP-L-ASAHQWVDMTDVTV-VW
 Cf-XP_861054 367 GL--DMFNSTQIIGRIIYER-A----KEL-YASASQELTGP-L-AAAHQWVNMDDVTV-IW
 Mm-NP_061300 343 GQ--DMFESTHIIGRIIYQK-A----KEL-YASASQEVGTGPVL-A-AHQWVNMDDVTV-VQ
 Rn-NP_446098 348 GQ--DMFESTHIIGRVIYQK-A----KEL-HASASQEVGTGPVL-T-AHQWVNMDDVTV-VQ
 Gg-XP_421560 312 GT--DMFDSTRIIAQNIYLK-A----KEL-YANAAQELTGP-LRS-AHQWVNMDSNVQ-VQ
 Dm-NP_651797 303 GK--DMFESTQIIGORLADA-ALGLLNEQSQESTAREVTGD-V-REIHQFVDMPNYNGST
 Dp-XP_001357669 303 GR--DMVESTQIIGORLADA-ALGLLNEQSQESTAREVTGD-V-REIHQFVDMPNYNGSA

At-NP_172218 418 LPKKDGKSEVV-KT--C-PAAMGEFAAGTTDGPADFDFIQGDDKG-NPFWRILVRN-VL-
 At-NP_200706 379 INGQNGGSEVV-KT--C-PAAMGEFAAGTTDGPADFDFKQGGDDQG-NPFWRILVRN-LL-
 At-NP_181337 405 VPKAGGGSETV-KT--C-PAAMGEFAAGTTDGPADFDFKQGGDDQG-NVFWRLVRN-VL-
 OsCDase 430 VSTSAGGQIV-KT--C-PAAMGEFAAGTTDGPADFDFRQGDVKG-NPFWKLVRN-LL-
 Dd-XP_629027 366 APYNSG-VEGA-TT--C-RGAMGYSFAGTTDGPADFNFIIQGDNSTINPFWNFTGG-IIA
 Hs-NP_063946 416 L--N-S-THAS-KT--CKP-ALGYSFAAGTIDGVGCLNFTQGTTEG-DPFWDTLRDQILG
 Cf-XP_861054 416 L--N-S-THSV-KT--CKP-ALGYSFAAGTIDGFGSENFQTGTTEG-DPFWDTLRDQLLG
 Mm-NP_061300 392 L--N-A-THTV-KT--CKP-ALGYSFAAGTIDGVSCLNITQGTTEG-DPFWDTLRDQLLG
 Rn-NP_446098 397 L--N-A-THTV-KT--CKA-ALGYSFAAGTIDGVSCLNITQGTTEG-NLFWDTLRDQLLG
 Gg-XP_421560 361 L--N-A-THTV-KT--CKP-ALGHSFAAGTIDGVGAFNFTQGAVER-DPFWDNTRDQLLG
 Dm-NP_651797 358 Y--N-PLSRKVDKIRGCQP-AMGYSFAAGTTDGPADFDFEQGTTD-NPMWNFVRD-FIA
 Dp-XP_001357669 358 Y--N-PLSRKIDKIRGCQP-AMGYSFAAGTTDGPADFDFEQGTTD-NPMWNFVRD-FIA

At-NP_172218 471 KTPDKKQ-ID-CHYPKPILLDTGEMTK-PYDWAAPSIL-SLQVLRIGQLFILSVPGFFTMM
 At-NP_200706 432 KNPTEEQ-VR-CORPKPILLDTGEM-KOPYDWAAPSIL-PVQILRIGQLVILCVPGFFTMM
 At-NP_181337 458 RTPGPEQ-VQ-COKPKPILLDTGEM-KEPYDWAAPSIL-PIQILRIGQLVILSVPGFFTMM
 OsCDase 483 KTPGKQ-VE-CHSPKPILLDTGEM-KEPYDWAAPAIL-PVQMLRIGQLVILCVPGFFTMM
 Dd-XP_629027 420 K-PTPQQ-TA-CQAPKPILIDVGM-VEPIPWVDPVM-PLQIITLQIVLVAVPGEFTMM
 Hs-NP_063946 467 K-PS-EE-IKECHKPKPILLHTGEL-SKPHPWHPDIV-DVQIITLGLSLAITAIPGEFTMM
 Cf-XP_861054 467 K-PS-EE-IKCCOKPKPILLHTGEL-TKPHPWHPDIV-DVQMITLGLSLAITAIPGEFTMM
 Mm-NP_061300 443 K-PS-EE-IVECOKPKPILLHSGEL-TIPHPWQPDIV-DVQIVTVGLSLAIAAIPGELTTM
 Rn-NP_446098 448 K-PS-EE-IIECOKPKPILLHTGEL-TKPHPWQPDIV-DIQIVTLGLSLAIAAIPGEFTMM
 Gg-XP_421560 412 E-PS-NE-TKACHQPKPVLSTGEM-TWPHPWHPDIV-DVQIATLGLSLAIAVAVPGEFTMM
 Dm-NP_651797 412 A-PT-QEDIK-CHPKPILLATGRA-TFPYEWQPKIVSD-QLLKIIGDVIIAAVPCEFTMM
 Dp-XP_001357669 412 T-PT-QEDIK-CHPKPILLATGRA-TFPYEWQPKIVSD-QLLKIIGDVIIAAVPCEFTMM

At-NP_172218 527 AGRRLRYAVKTQL-KNSGNKDLGSG-EI----HVV-IAGLANGYSQYVT-TFEEYQVQRYE
 At-NP_200706 488 AGRRLRDAVKTVL-KE-GS---NGREF----SVV-IAGLINSYSQYIA-TFEEYQVQRYE
 At-NP_181337 514 AGRRLRDAIKSFL-IS-SDP--K--EFSNNMHVV-IAGLINTYSQYIA-TFEEYQVQRYE
 OsCDase 539 AGRRLRDAVKTVL-TS-GN---S--EFDKNIHVV-IAGLINSYSQYIT-TFEEYQVQRYE
 Dd-XP_629027 474 SGRRLRNTVREII---GQ---SI-EN---PIVLIAGLANTYSQYIA-TFEEYQVQRYE
 Hs-NP_063946 522 SGRRLREAVQAEF-ASHGM---Q--NM---TVV-ISGLCNVYTHYIT-TYEEYQAQRYE
 Cf-XP_861054 522 SGRRLREAVQAEF-ATYGM---K--NM---TVV-ISGLCNVYTHYIT-TFEEYQVQRYE
 Mm-NP_061300 498 SGRRLREAVKKEF-ALYGM---K--DM---TVV-IAGLSNVYTHYIT-TYEEYQAQRYE
 Rn-NP_446098 503 SGRRLREAVKKEF-ALYGM---K--DM---TVV-IAGLSNVYTHYIT-TYEEYQAQRYE
 Gg-XP_421560 467 SGRRLREAVKSEF-GSHGT---E--GM---DVV-IAGLCNVYTHYIT-TYEEYQVQRYE
 Dm-NP_651797 467 AGRRLRNQIRAAASAVGGI-----DT----EVI-IAGLNIYTSY-TVTPPEEYQAQRYE
 Dp-XP_001357669 467 AGRRLRNQIRAAASAAGGL-----DT----EVI-IAGLNIYTSY-TVTPPEEYQAQRYE

At-NP_172218 579 GASTLYGPHTLSYIQEF-KKLSKSI-VL-D-M-P-V-Q-P-GPQPPDLL-DKQISL--LT
At-NP_200706 537 GASTLYGPHTLSYIQEF-KKLANDI-L-SAQ-T-T-D-P-GPQPPDLL-HKQISL--LT
At-NP_181337 566 GASTLYGRHTL IAYIQEF-KKLATAL-V-N-GLT-I---PRGPQPPDLL-DKQISL--LS
OsCDase 590 GASTLYGPHTLSAYIQEF-QKLAMAM-IAN-K-E-V---PTNFQPPDML-DKQIGL--L-
Dd-XP_629027 521 GASTVFGPHTLGAYIQEF-ANLAQSI-V-D-G-SQA-D-P-GTFERNMSGHTPE-F--LP
Hs-NP_063946 570 AASTIYGPHTLSAYIQLF-RNLAKAI-ATD---T-VANLSRGPPEPP-FFKQLIVPL--I-
Cf-XP_861054 570 AASTIYGPHTLSAYIQLF-RALAKAI-ATD---T-VANLSRGPPEPP-FFKQLIASL--I-
Mm-NP_061300 546 AASTIYGPHTLSAYIQLF-RDLAKAI-ATD---T-VANMSSGPPEPP-FFKNLIASL--I-
Rn-NP_446098 551 AASTIYGPHTLSAYIQLF-RALAKAI-ATD---T-VANMSSGPPEPP-FFKNLIQSL--I-
Gg-XP_421560 515 AASTIYGPHTLSAYIQLY-RGLARAI-AMN---T-VQDLPSGPPEPP-LF-N-VTSLTLV-
Dm-NP_651797 515 AASTIFGPHTHSIYMDVFER-LTKAM-MRN-E-T-V-D-A-GPSPP-YMNDVMLSL--N-
Dp-XP_001357669 515 AASTIFGPHTHSIYMDVFER-LTKAM-MRN-E-T-V-E-P-GPSPP-YMNDVMLSL--N-

At-NP_172218 628 P-V-MMDTTP-SGDSFGDVISDVP-KNLSLK--RNG-QVTV-V-FR-SACPRNDLLTE-
At-NP_200706 586 P-V-VADMTP-IGTAFGDVTSVDP-R-LS-K-ER-KGADI-VRVQFR-SANPRNDLMTE-
At-NP_181337 615 P-V-VVDSTP-LGVKFGDVKADVPPK--S-T-ER-RGQOVNA-T-FW-SGCPRNDLMTE-
OsCDase 638 PGV-VFDSTP-LGVKFGDVNSDVPGN--S-T-EN-KGSTVNA-T-FY-SACPRNDLLTD-
Dd-XP_629027 570 P-V-IVDVAPKF-DDFGDIYIDVS-T--T-TPYS-INQTVTV-I-FY-GANLRNFMTE-
Hs-NP_063946 620 PSH-V-DRAP-KGRTFGDV-LQ-PAK--P-E-YR-VGEVAEV-I-FV-GANPKNS--VQN
Cf-XP_861054 620 PNI-V-DRAP-IGKTFGDV-LQ-PAK--P-T-YR-VGEVAEV-T-FV-GANPKNS--AES
Mm-NP_061300 596 PNI-A-DRAP-IGKHFGDV-LQ-PAK--P-E-YR-VGEVVEV-I-FV-GANPKNS--AEN
Rn-NP_446098 601 PNI-A-DRAP-IGKQFGDV-LQ-PAK--P-E-YR-VGEVVEV-V-FV-GANPKNS--AEN
Gg-XP_421560 565 PAVTA-DRAP-VNKTFGDV-LQ-GVN--V-Q-YR-AGEVAEV-T-FV-GANPKNS--AEN
Dm-NP_651797 563 TGV-LFDGHP-INTDFGYVKSQ-PNK----E-YG-INETVKV-T-YISG-NPRNMLFTE-
Dp-XP_001357669 563 TGV-LFDGHP-INTDFGYVKIQ-PEK----E-YG-INDTVKV-T-YISG-NPRNMLFTE-

At-NP_172218 677 GT----FTL-VER-L-E-QK-DKTWTPVYDDDDCLRFKWSRHK-KLSSRSQATVEWRI-
At-NP_200706 635 GT----FAL-VERWL-E-GR-E-TWVPVYDDDDCLRFKWSRPF-KLSTQSTATIEWRI-
At-NP_181337 663 GS----FAV-VET-LRE-GG-K--WAPVYDDDDSLKFKWSRPA-KLSSRSQATIEWRV-
OsCDase 687 GT----FAL-VEK-L-D-GN-N-NWVPVYDDDDSLRFKWSRPA-RLSSRSFATIEWTV-
Dd-XP_629027 618 SS----F-LTVDQ-L-Q-SN-G-QWTTILNDGDWDTKLYW-KMH-DLGF-SLITVDWTTIS
Hs-NP_063946 665 QT-HQTF-LTVEK-Y-EATS-T-SWQIVCNDASWETRFYWHK-G-LLGL-SNATIEWHI-
Cf-XP_861054 665 QT-HRTF-LTVEK-Y-EATS-A-TWQIVHNDASWETRFYWK-G-LLGH-SNATIQWHI-
Mm-NP_061300 641 QT-HQTF-LTVEK-Y-E-DSVA-DWQIMYNDASWETRFYWHK-G-ILGL-SNATIYWHI-
Rn-NP_446098 646 QT-HQTF-LTVEK-Y-E-DSVA-NWQIMHNDASWETRFYWHK-G-VLGL-SNATIHWHI-
Gg-XP_421560 611 MTEHN-F-LTVER-Y---TSVSGSWQVQNDASWTRFYWTK-G-SSGQ-SNVTIEWHI-
Dm-NP_651797 610 KT-Y--F--TIER-K-I-NE-D-RWKVAYTDASWETKMWHRNTNILGF-SEMDIYWDIS
Dp-XP_001357669 610 KT-Y--F--TVER-K-I-NE-D-RWKVAYTDASWETKMIWHRNTNILGF-SDLEIYWNIS

At-NP_172218 726 PE-SASPGVYRITHFG-AAKK--LF--G-S-VHHE-TGSSSA-FVV-T--
At-NP_200706 684 PE-TASPGVYRITHFG-SAKT-PI---S-S-IHHE-SGSSSA-FVV-Y--
At-NP_181337 711 PE-SAVAGVYRIRHFG-ASKS--LF--G-S-SSSE-SGSSSA-FVV-V--
OsCDase 735 PE-DAAAGVYRLRHFG-ASKP--MF--G-S-VRHE-TGTSRA-FAV-R--
Dd-XP_629027 665 PI-T-QPGTYRITHSGYAKKN--PF--SDN-LT-FYQGISSN-FNV-Q--
Hs-NP_063946 715 PD-TAQPGIYRIRYFG-HNRKQDEL--KPAVILSF-EG-TSPAFAVVT-I
Cf-XP_861054 715 PD-TAQPGIYRIRYFG-HNRKQDEL--KPAVILSF-ES-TSPAFAVVT-T
Mm-NP_061300 691 PD-TAYPGIYRIRYFG-HNRKQELL--KPAVILAF-EGISSP-FAVVT-T
Rn-NP_446098 696 PD-TALPGVYRIRYFG-HNRKQELL--KPAVILAF-EGISSP-FAVVT-T
Gg-XP_421560 661 PSGT-EPGTYRIQYFG-HYRR--LF--KQ--FYPE-EG-TSAAFET-TNL
Dm-NP_651797 659 PQ-T-LPGEYRIRHSG-EYKY--ILGGK----YPY-EGLTHS-FTVKE-D
Dp-XP_001357669 659 PQ-T-LPGVYRIRHSG-EYKY--ILGGK----YPY-EGLSHS-FTVKE-D