

Biochemical Characterization of a Novel Alkaline-Tolerant Xaa-Pro Dipeptidase from *Aspergillus phoenicis*

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Table S1. Xaa-Pro dipeptidases that were characterized by molecular and/or biochemical techniques.

Enzyme	Organism	GenBank accession No.	Optimum pH and temperature	pH stability and thermostability	Monomer/Multi mer (MW of subunits, or native enzymes) ^a	Inhibitor (cofactor) ^b	Substrate specificity ^c	Referen ce
Hyperthermophilic archaea								
PfPEPQ	<i>Pyrococcus furiosus</i> DSM 3638	P81535.1	pH 7.0, 100 °C	Half-life at 100 °C for native and recombinant enzymes is 4 h and 1 h, respectively	Homodimer (39.4 kDa, 100±10 kDa)	EDTA, Zn ²⁺ (Co ²⁺ , Mn ²⁺)	Xaa-Pro (Xaa=Met, Leu, Val, Phe or Ala)	[25,35,5 0]
PhPROL	<i>P. horikoshii</i> OT3	BAA30249.1	pH 7.0, 100 °C	Half-life at 90 °C is 21.5 h	39.27 kDa, NA	Zn ²⁺ (Co ²⁺)	Met-Pro, Leu-Pro, and organophosphorus nerve agents	[34,51]
Eubacteria								
AhOPA A	<i>Alteromonas</i> <i>haloplanktis</i> ATCC 23821	P77814.1	pH 7.5, 40 °C	ND ^a	Monomer (50 kDa, NA)	DFP analog Nipafox, pCMB, NEM (Mn ²⁺)	Xaa-Pro and OP compounds	[45]
AmOPA A	<i>A. macleodii</i> NCIMN1963	AEI26268.1			Dimer (50.6 kDa, 101.2 kDa)	cofactor: Mn ²⁺	Xaa-Pro and OP compounds	[9]
AsOPA A	<i>Alteromonas</i> sp. JD6.5	Q44238.3	pH 8.5, 50 °C		Monomer (60 kDa, 60 kDa)	pCMB, IAA, NEM, EGTA, Zn ²⁺ (Mn ²⁺)	DFP, NPMPP, NPEPP, paraaxon, and nerve agents such as sarin, soman, and O-cyclohexyl methylphosphonofluoridate; Xaa-Pro dipeptides such as Gly-Pro	[38,52,53]
AuOPA	<i>A. undina</i> ATCC		pH 8.0, 55 °C		Monomer (53	IAA, EGTA,	A wide range of nerve	[54]

A	29660				kDa, 53 kDa)	NEM, Ni ²⁺ and Zn ²⁺ (Mn ²⁺)	agents and several chromogenic phosphinates	
DrXPD	<i>Deinococcus radiodurans</i> R1	WP_02747955 3.1			Dimer (45 kDa, NA)	cofactor: Mn ²⁺	Xaa-Pro	[43]
EcPEPQ	<i>Escherichia coli</i> BL21 (DE3)	P21165.2	pH 8.0, 60 °C	Incubation at 4-30 °C for 10 min (> 80%), incubation at pH 7.0-9.0 for 1 h (30 °C, > 60%)	Dimer	cofactor: Mn ²⁺	Xaa-Pro dipeptides, DFP, organophosphate diesters and triesters, and nerve agents GB (sarin), GD (soman), GF, and VX	[37,47,55]
LcXPD	<i>Lactobacillus casei</i> subsp. <i>casei</i> IFPL 731		pH 6.5-7.5, 55 °C	Retain 36% activity after incubation at 30°C for 30 min	Monomer (41 kDa, 41 kDa)	EDTA and 1,10-phenanthroline, DTT, ME, pHMB and IAA , Cu ²⁺ , Zn ²⁺ , Fe ³⁺ (Mn ²⁺ , Co ²⁺)	Hydrolyze Xaa-Pro, Ala-Ala, and Ala-Phe except for Pro-Pro and Gly-Pro	[40]
LdPEPQ	<i>L. delbrueckii</i> subsp. <i>bulgaricus</i> CNRZ 397	CAA73815.1	pH 6.0, 50 °C		Homodimer (45 kDa, 68-70 kDa)	Bestatin, DTT, EDTA (Zn ²⁺)	Hydrolyzes Xaa-Pro dipeptides except for Pro-Pro and Gly-Pro	[26]
LIXPDI	<i>Lactococcus lactis</i> subsp. <i>cremoris</i> AM2		8.3–9.0 (universal buffer)		NA, 42 kDa	NEM, benzamidine, bestatin, bacitracin, PMSF, pCMB, IAA, leupeptin	Xaa-Pro, Pro-Pro, Pro-Ala, Pro-Val, etc.	[56]
LIXPDII	<i>L. lactis</i> NRRL B-1821	ABW84230.1	pH 7.0, 40-50 °C	Incubation at 20-50 °C for 30 min (> 60%)	Dimer (40 kDa, 80 kDa)	cofactor: Zn ²⁺	Leu-Pro, Arg-Pro, Val-Pro, Phe-Pro, and Lys-Pro; does not hydrolyze Gly-Pro, Glu-Pro, Asp-Pro, Pro-Pro, Leu-Leu-Pro, and Leu-Val-Pro	[42]
MtXPD	<i>Mycobacterium</i>	P9WHS7.1	pH 7.5–8.0, 55	Completely lost its		Phosphate ion,	Hydrolyze only dipeptides,	[4]

	<i>tuberculosis</i> H37Rv		°C	activity at 50°C and 65°C in the absence and presence of 1 mM Mn ²⁺ , respectively Incubation at pH 5.0-8.0 for 2 h (> 60%); half-lives at 55, 60 and 65 °C are 88.87, 78.77 and 33.49 min, respectively		cacodylate	but failed to cleave tripeptides or long chain peptides like bradykinin	
PIOPAA	<i>Pseudoalteromonas lipolytica</i> SCSIO04301	WP_036973676	pH 8.5, 55 °C		Tetramer (53 kDa, 200 kDa)	EDTA, Ca ²⁺ , Mg ²⁺ , Co ²⁺ , Ni ²⁺ , Fe ³⁺ (Mn ²⁺)	Gly-Pro shows a preference for oxon-phosphoryl than thiono-phosphoryl, hydrolyzes dichlorvos, methyl-paraoxon, paraoxon, and profenofos	[13,39]
ScXPD	<i>Streptococcus cremoris</i> H61		pH 6.5-7.5, 40 °C	Quickly lose activity at temperatures above 40 °C	Monomer (NA, 43 kDa)	EDTA and 1,10-phenanthroline, pCMB, NEM, ME, Zn ²⁺ , Cu ²⁺ , Hg ²⁺ , Fe ²⁺ (Co ²⁺)	Xaa-Pro, e.g., Leu-Pro	[41]
TsPROL	<i>Thermococcus sibiricus</i> MM 739	ACS89882.1			Homodimer (39 kDa, 70-75 kDa)	cofactor: Zn ²⁺		[57,58]
XcXPD	<i>Xanthomonas campestris</i> pv. <i>campestris</i> ATCC 33913	Q8P839	pH 7.5–8.0, 55 °C	Completely lost its activity at 60 °C and 80 °C in the absence and presence of 1 mM Mn ²⁺ , respectively	Dimer	Phosphate ion, cacodylate (Mn ²⁺)	Hydrolyze only dipeptides, but failed to cleave tripeptides or long chain peptides like bradykinin	[4,33]
XmXPD	<i>X. maltophilia</i>		pH 7.5, 35 °C	pH 6.0-8.5; half-life at 37 °C is 60 min	Dimer (51 kDa, 100 kDa)	pCMB, o-phenanthroline, Z-L-proline, and phenylacetyl-thio proline, Cu ²⁺ , Zn ²⁺ , Hg ²⁺ (Mn ²⁺)	Xaa-Pro, e.g., Leu-Pro	[59]

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AnPEPP	<i>Aspergillus nidulans</i> WG312	CAC39600.1	pH 7.0	Stable at 40°C for 60 min	Homodimer (58 kDa, 125 kDa)	cofactor: Mn ²⁺	Met-Pro, Ala-Pro, Phe-Pro, Leu-Pro, and Val-Pro; could not hydrolyze Pro-Ala, Ala-Ala, and Ala-Pro-Gly	[16]
HsPEPD I	<i>Homo sapiens</i>	AAA60064.1	pH 7.8, 50 °C	37 °C for at least 8 days	Dimer (54 kDa, NA) ^c	Cbz-Pro, guanidine hydrochloride (Mn ²⁺)	Gly-Pro>Ala-Pro>Phe-Pro>Leu-Pro, DFP, sarin, soman, tabun, and cyclosarin	[34,46,60]

ND, not determined; NA, not available.

^a Molecular weight of subunits and native enzymes were determined by SDS-PAGE and gel filtration, respectively;

^bpCMB, *p*-chloromercuribenzoic acid; IAA, iodoacetic acid; EDTA, ethylenediaminetetraacetic acid; EGTA, ethylene glycol-bis(β-aminoethyl ether)-N,N,N',N'-tetraacetic acid; pHMB, *p*-hydrocymercuribenzoic acid; NEM, *N*-ethylmaleimide; DTT, dithiothreitol; ME, β-mercaptoethanol

^c DFP, diisopropylfluorophosphate; NPMPP, *p*-nitrophenylmethyl(phenyl)phosphinate; NPEPP, *p*-nitrophenylethyl(phenyl)phosphinate; GF, *O*-cyclohexylmethylphosphonofluoridate; VX, *S*-2(diisopropylamino)ethyl *O*-ethyl methylphosphonothioate; OP compounds, organophosphate compounds.

PfPEPQ	- - - - -	1
PhPROL	- - - - -	1
TsPROL	- - - - -	1
LIXPDII	- - - - -	1
LdPEPQ	- - - - -	1
MtXPD	- - - - -	1
XcXPD	- - - - -	1
ApXPD	MLDKQTESLPLAEEIPLLRQPPHQHRKTVLRFITGAGLLLLTIYTLFPRLSPFTSIKQPL	60
DrXPP	- - - - -	1
AnPEPP	- - - - -MQAALHRTEIKAP	13
HsPEPDI	- - - - -	1
EcPEPQ	- - - - -	1
AnOPAA	- - - - -	1
AsOPAA	- - - - -	1
AhOPAA	- - - - -	1
PIOPAA	- - - - -	1
Consensus	- - - - -	1

PfPEPQ	- - - - -MKERLEKLVKFMDENSIDRVFIAKPV	26
PhPROL	- - - - -MDIMNEKVKKIIIEFMDKNSIDAVLIAKNP	29
TsPROL	- - - - -MDYKRRIHKKFQAHFGKKGFEGALVAPGS	28
LIXPDII	- - - - -MSKIERISAFLLNDKEVDMFTITNPT	25
LdPEPQ	- - - - -MNLDKLQNWQENGMDVAVVSSPT	24
MtXPD	- - - - -MGSRRFDAEVYARRLALAAAATADAGLAGLVITPGY	36
XcXPD	- - - - -MSTQIGGMSLDQARTQLAPWTQRAAPIGADEYQQRIERARVLMRAQGVDAALLIGAGT	57
ApXPD	SVSPYSEFERCSIENLRQTGYFFLDATPIAVEEFNERRNRLARALVADGADAFVVEPGY	120
DrXPP	- - - - -MSTPIPAMQAALAAATDLGWLVDYDFQ	26
AnPEPP	HRPTRLALSNLFTARNRIAMTSLDSILADKYPAKAHARRVAEGLKALGHSGGAIYLEAQKT	73
HsPEPDI	- - - - -MAAATGSPFWLGNETLKVPLALFALNRQRLCERLRKNPAVQAGSIVVLQGGEE	53
EcPEPQ	- - - - -MESLASLYKNHIATLQERTDALARFKLD	29
AnOPAA	- - - - -MSQHKATYQQHIEELQARTREALQREGLD	29
AsOPAA	- - - - -MNKLAVLYAEHIAITLQKRTREIERENLD	29
AhOPAA	- - - - -MEKLAVLYAEHIAITLQQRTRTICEQEGLE	29
PIOPAA	- - - - -MDKLAVLYAEHIAITLQQRTRTITEREGLE	29
Consensus	- - - - -	29

PfPEPQ	NVYYFSG - - - - TSPLGGGY - - - - IIVDGDEATLYVPELEY - - EMAKE - ESKLPVVKFKK	74
PhPROL	NVYYISG - - - - ASPLAGGY - - - - ILITGESATLYVPELEY - - EMAKE - ESNIPVEKFKK	77
TsPROL	NFYLTG - - - - FNPLGTLERLFVLILPSEGLLTAIAPRLY - - EKELE - EFNGEVVLWSD	80
LIXPDII	TLNYLTG - - - - LAIDPHERIAGLMIFRDS TPMLFTPALV - - EKAKEHTSGLDIFGYED	78
LdPEPQ	TINYFTG - - - - FITDPEERIFKLFAFKDAEPFLFCPALNY - - EEAKASAWDGDVVGGLD	77
MtXPD	DLCYLIGSR - - - - AETFERLTALVLAAGAPAVVLPRLAAL - KQSAAEGLGLRVDWVD	92
XcXPD	SLRYFSG - - - - VPWGASERLVALLLTTEGDPVLICPAFEEG - QSDAVLQLPVRKRLWEE	111
ApXPD	TFKYFANVSQPEWEVWEPEERPFPLMVVQPYRHSSGHVTAKTT - FLAPSFEAERARLLNMP	179
DrXPP	GLNPHARRVLGIGDDVFLTRFFVWVPRAGRAVVLHNNHIEGGNWNRIITQEWDAELRPFGS	86
AnPEPP	RLIEDNDP - - - - VFRQRRPFFYL SGCLLPDSSLVYNIDSD - QLTLFIPPINPDVIEWS	128
HsPEPDI	TQRYCTDTG - - - - VLFLQESFFHWAFGVTEPGCYGVIDVDTGKSTL FVPRLPASHATWMG	109
EcPEPQ	ALLIHSGL - - - - FNVFLDDHPPYFVKVNPQFKAWVPVTQVPN - - CWLLVDGYNKPKLWFYL	84
AnOPAA	GLVIHSGQG - - - - KRLFLDDNHYPFKVNPQFKAWVPVIDNPN - - CWLVVNGVDKPTLIFYR	84
AsOPAA	GVVFHSGQA - - - - KRQFLDDMYYPFKVNPQFKAWLPVIDNPN - - CWIVANGTDKPKLIFYR	84
AhOPAA	GLVIHSGQA - - - - KRQFLDDMYYPFKVNPQFKAWLPVIDNPN - - CWIVVNGSDKPKLIFYR	84
PIOPAA	GLVIHSGQA - - - - KRQFLDDMYYPFKVNPQFKAWLPVIDNPN - - CWIVVDGASKPKLIFYR	84
Consensus	- - - - -	84

PfPEPQ	FDEIYEILKN - - - - TETLGIEGT - - - - LSYSMVENFKEKSNVKEFKK -	113
PhPROL	MDEFYKALEG - - - - IKSLGIESS - - - - LPYGFIEELKKKANIKEFKK -	116
TsPROL	SENPYKIFATKIKETFKEGEKLLIDDT - - - - MPVGVFLKAKDIFDKYSLHP -	127
LIXPDII	SQNPWEVVKNHVKS - - - - DVKSIAVEFSID - - - - IPLAKTEGLKAQFGDINFTN -	123
LdPEPQ	SEDPWKGIAEEIKQRTKDYQNWAVEKNG - - - - LTVAHYQALHAQFPDSDFSKD	126
MtXPD	GDDPYGLVSAVLGG - - - - APVATAVTD - - - - MPALHMLPLADALGVLPLVAT	137
XcXPD	HEDPYALVVQAMDEQHAAHALALDPG - - - - IAFAVHTGLRAHLGTAIRDAG	157
ApXPD	FLEPIEIPWEEHWNPDYTLKNSVIFSALDR - - - - LAPRLMVDEEMRDFIQRGLGHS	231
DrXPP	HAELDAALRGVVSQQLAMEYSPNGAVP - - - - YVSRVDAGTLERVRGAGAAEVA	136
AnPEPP	GLPLSAAEALERYDNDVLETTENVNATLANIAASHANNSTAFATAIEQVSEGTFEGFSET	188
HsPEPDI	KIHSKEHFKEKYAVDDVQYVDEIASVLT SQKPSVLLTLRGVNTDSGVSVCREASFDGISKF	169
EcPEPQ	PVDYWHNVEPLPTSFWTEDVEVIALPKADGIGSLLPAARGNIGYIGPVPERALQLGIEAS	144
AnOPAA	PEDFWHKVPPPEPNDFTDSFDIKLLQADAVEKFLPYDKSRFAYVGEYIEVAKALGFDN -	143
AsOPAA	PVDFWHKVPDEPNFYWADYFDIELLVKPDQVEKLLPYDKARFAYIGEYLEVAQALGFEL -	143
AhOPAA	PIDFWHKVPDEPRDFWAEYFDIELLLQPDQVEKLLPYDKAKFAYIGEYLEVAQALGFSI -	143
PIOPAA	PVDFWHKVPDEPRDFWAEYFDIELLVQPDQVEKLLPYDKANYAYIGEYLEVAQALGFSI -	143
Consensus	- - - - -	143

	α7	α8	
PfPEPQ	-----IDDDVIKDLRIIKTKEEIEIEEKACEIADKAVMAAIE-----EITEGKREREVAAK		163
PhPROL	-----VDDVIRDMRIIKSEKEIKIEEKACEIADKAVMAAIE-----EITEGKKEREVAAK		166
TsPROL	-----ISPVISELREIKDKDEIKAHKKAAEIVDKVFYRFIE-----GKLEGKSERELANR		177
LIXPDII	-----LTPLIERMRLIKSADEIEKMKVAGDFADKCFEIGFATA--AERNGVTESDIVAK		175
LdPEPQ	-----LSDFIAHIRLFKTESELVKLRKAGEEADFAFQIGFE-----ALRNGVTERAVVSQ		176
MtXPD	-----DVLRLRLRMVKEETEIDALRKAGAAIDRVHARVPE-----FLVPGRTEADVAAD		185
XcXPD	-----AIIIDGCRMCKSPAELALMQQACDMTLLVQRLAAG-----IAHEGIGTDQLVRF		205
ApXPD	GFEIVGLMGEVERVRQIKSDTEVGILRAVNTGTVEAVRQMRK-----CLYPGLTESEIASA		287
DrXPP	-----SSADLLQAFLVWTPDDLAHRRRAAALLMRAKDDAFRLIHDRLRAGQSVTEWEVQ		190
AnPEPP	-NFNVLKGVIERTRVVKDSYIEALLRKANDISAKGHIAAIK-----ASKSATNEREIEAA		242
HsPEPDI	EVNNTILHPEIVESRVFKTDMELVLRVYTNKISSEAHREVMK-----AVKVGMEYGLESL		225
EcPEPQ	NINPKGVIDYLHYYSFKTEYELACMREAQKMAVNGHRAAEE-----AFRSGMSE--FDIN		198
AnOPAA	-VNPDRVLHYLHYQRAYKTDYELDCMREANKLAVAGHKAAEQ-----AFREGKSE--FDIN		196
AsOPAA	-MNPPEVMNFYHYHRAYKTQYELACMREANKIAVQGHKAARD-----AFFQGGKSE--FEIQ		196
AhOPAA	-MNPPEVLNYIHYHRAYKTQYELECLRNANRIAVDGHKAARD-----AFFNGGSE--FDIQ		196
PIOPAA	-MNPPEVMNYLHFHRAYKTQYELECLRQANRIAVEGHKAARD-----TFFNGGSE--FDIQ		196
Consensus			
	α9	β7	η2
PfPEPQ	VEYLMKMN-GAEKPAFDTIIASGHRSAHPHGVASDK-----RIERG-DLVVIDLGALYN-		215
PhPROL	VEYLMKMN-GAEKPAFDTIIASGYRSALPHGVASDK-----RIERG-DLVVIDLGALYQ-		218
TsPROL	IEYMIKNEFGADDVSFEPIVASGPNGANPHHRP SHR-----KIRKG-DVVIDYGAAYL-		230
LIXPDII	IEYEMK-RMGVPQMSFDTLVLSGAANAAPHGAPENV-----EIQEN-KLLLFDLGVMMSG-		227
LdPEPQ	IEYQLKLQKGVMTSFDTIIVQAGKNAANPHQGP SMN-----TVQPN-ELVLFDLGTMHE-		229
MtXPD	IAEAIVAEGHSEV--AFVIVGSGPHGADPHHGYSDR-----ELREG-DIVVVDIGGTYGP		237
XcXPD	IDEAHRALGADNGSTFC-IVQFGHATAFPHGIPGVQ-----HLRAG-ELVLIDTGCITVQ-		257
ApXPD	LDNTLR--SAGLEPFFDIVLFDENAAANPHGGTNGS-----KVLEPETFVLIDVGAHL-		338
DrXPP	QLIMDQIRAAGMQAGHDVNVSVFGVNAADSHYEPSEQR-----SATLHPGECVLIDLWAQEPG		247
AnPEPP	FIACTIAN-GAREQSYHPIVACGNGATLHYGKNDIDLDPVTNRRKDNVLIDAGAEYR-		300
HsPEPDI	FEHYCYSRGGMRHSSTYTCICGSGENSAVLHYGHAGAP--NDRTIQNGDMCLFDMGGEYY-		282
EcPEPQ	IAYLTATGHRDITDVPYSNIVALNEHAAPVHYTKLDH-----QAPPEMRSFLLIDAGAEYN-		252
AnOPAA	LAYAAASRQGDNDVPYTSIVALNEHASILHYMQCDT-----VAPKESRSFLIDAGANYH-		250
AsOPAA	QAYLLATQHSENDNAYGNIVALNENCAILHYTHFDR-----VAPATHRSFLIDAGANFN-		250
AhOPAA	QAYLMATRQSENEMPYGNIVALNENCAILHYTHFEP-----KAPQTHNSFLIDAGANFN-		250
PIOPAA	HAYLMATRQSENEMPYGNIVALNENCAILHYTHFEP-----TAPHTHHSFLIDAGANFN-		250
Consensus			
	β10	β11	α10
PfPEPQ	HYNSDITRTIVVG--SPNEKQR-----EIIYEVLEAQKRAVEAAKPGMTAK----		259
PhPROL	HYNSDITRTIVVG--SPNEKQK-----EIIYEVLEAQKKAVEAAKPGITAK----		262
TsPROL	GYCSDVTRTVVG--PPSEEVK-----KVYEVKEAQETAVQKVAEGIPAE----		274
LIXPDII	GYASDATRTIAIG--QPNDFDA-----EIHKIVKEAQQAAMDFIKPGVTAH----		271
LdPEPQ	GYASDSSRTVAYG--EPTDKMR-----EIIYEVNRTAQQAIDAAPKGMTAS----		273
MtXPD	GYHSDSTRITYSIG--EPDSDAV-----QSYSMQLQRAQRAAFEAIRPGVTAE----		281
XcXPD	GYHSDITRTWIYG--TPSDAQV-----RIWELELAQAQAFAAARPGVACE----		301
ApXPD	GYSSDICRTFFPPFLEPPTPDMTPANRLREKLEVWDIVFEAQTRSIGQFQVNASAA----		394
DrXPP	RPFADVTVWVGFAG--EPGTEYL-----DAWQAVRAAREAALELLRSRFVAEGYGR		295
AnPEPP	TYCADITRAFPLNGKFLPETR-----QIIYEVLRMQLECIDMLKEGVQWE----		345
HsPEPDI	SVASDITCSFPFRNGKFTADQKA-----VYEAVALLSRAVMGAMKPGDWWP----		327
EcPEPQ	GYAADLTRTWSAK--SDNDYA-----QLVKDVNDEQLALIAMTKAGVSYY----		295
AnOPAA	GYAADITRTYAQEGVHNSAMFR-----DLIQAVDKVTLTLVDSLKPGLVAYT----		296
AsOPAA	GYAADITRTYDFT--GEGEFA-----ELVATMKQHQIALCNQLAPGKLYG----		293
AhOPAA	GYAADITRTYDFK--KQGEFA-----DLVNAMTAHQIELGKSLKPGLLYG----		293
PIOPAA	GYAADITRTYDFK--KSGEFS-----DLIQVMTEHQIALGKALKPGLLYG----		293
Consensus			
	α11	β12	β13
PfPEPQ	---ELDSIAREI---IKEYGYGDYFIHSLGHGVGLEIHEWPIRI		296
PhPROL	---ELDSIARNI---IIAEYGYGEYFNIHSLGHGVGLEIHEWPIRV		299
TsPROL	---VVDATARGI---IISKYGYGEYFIHRTGHGLGIDVHEEPIYI		311
LIXPDII	---EVDVAARDI---LITKAGYGEYFNIHRLGHGIGMDVHEEPIYI		308
LdPEPQ	---ELDGVARKI---IITDAGYGEYFIHRLGHGIGMEVHEEPIYI		310
MtXPD	---QVDAARDI---VLAEAGLAIFYFIHRTGHGIGLCVHEEPIYI		318
XcXPD	---AVDQAARAIVLQAAG---LGPDYRLPGLPIHRTGHGICGLAIHEAPYL		343
ApXPD	---SVDIAARKI---VITDGGYGEAFTHRVGHGIGIKAEHSPYL		431
DrXPP	LQGWELDRAARDI---AMGERWAPHFLHRTGHGIDLVQVIGHGAGAN		335
AnPEPP	---DVHAHAHRVAIRGLLELGILR-GSEDELFDKRI SVAFFPHGLGHYLGMDTHDTGGN		400
HsPEPDI	---DIDRLADRIHLEELAHMGILS-GSVDAMVQAHLGAVFMPHGLGHFLGIDVHDVGGY		382
EcPEPQ	---DYHIQFHQRIAKLLRKHQIITDMSEEAMVENDLTGPFMPHGHGIFLGLQVHDVAGF		351
AnOPAA	---DIHLLAHDGIAQILHDTGMVN-LTPPEIVEMGITRTFFPHGHGIFLGLQVHDVGGF		351
AsOPAA	---ELHLDCHQIRVAQTLSDFNIVD-LSADEIVAKGITSTFFPHGLGHGHLGLQVHDVGGF		348
AhOPAA	---DLHIDCHNRIAQLLSDFDIVK-LPAAEIVERQITSTFFPHGLGHGHLGLQVHDVGGF		348
PIOPAA	---ELHLECHQIRVAQVLSDFNIVK-LPAAEIVERGITSTFFPHGLGHGHLGLQVHDMGGF		348
Consensus			

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