

# **Supplementary:**

## **Plastic-hydrolytic enzyme classification using explainable deep learning**

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## Supplementary Note 1. Transformer architecture.

We considered an encoder-only transformer for the benchmark. It is composed of an embedding module followed by four encoders. The embedding module relies on two layers: the amino acid matrix embedding and the positional encoding. The amino acid matrix embedding is a  $23 \times d_{model}$  ( $d_{model} = 256$ ) matrix learned during training such that the amino acid (assigned index  $a$ ) has its embedding in the  $a$ -th row of this matrix. Note that we need an embedding for the 20 different amino acids: the undetermined amino acid often referred to X, the classification token, as well as the padding token which account for the 23 rows of our matrix. The positional encoding module takes the position  $p$  of the amino acid as input and encodes it as:

$$PE(p, 2i) = \sin\left(\frac{p}{10000^{2i/d_{model}}}\right), \quad (1)$$

$$PE(p, 2i + 1) = \cos\left(\frac{p}{10000^{2i/d_{model}}}\right), \quad (2)$$

where  $2i$  and  $2i+1$  represent even and odd indices, respectively. The outputs of the two layers are then added to form the output of our embedding module, which is fed to the first encoder.

Each encoder comprises a multi-headed attention module followed by two fully connected layers activated by the ReLU function, a dropout layer, and a layer normalization. The multi-headed attention layer consists of projecting the input into 3 vectors  $Q$  (query),  $K$  (key), and  $V$  (value) of size  $d_k = 256$ . The output of the attention module is computed as:

$$\text{Attention Scores} = \text{Softmax}\left(\frac{Q \cdot K^T}{\sqrt{d_k}}\right), \quad (3)$$

$$\text{Attention output} = \text{Attention Scores} \cdot K. \quad (4)$$

Then, the output is fed to a dropout layer with a dropout rate of  $0.1$ . The multi-headed attention module incorporates a skip connection, which adds the input of this module to its output. The given result is normalized and fed to two successive position-wise feed-forward layers of size  $4 * d_k = 1024$  in which the first one uses ReLU as an activation function, and both layers apply a dropout of  $0.1$  to their output. These two layers are skipped through a skip connection that adds the module's input to its output.

The final output of the encoder is passed through a dropout layer with a dropout rate of 0.1. After going through the embedding module and the four encoders, the final prediction is made by a linear layer, which takes as input the representation of the classification token by the last encoder of the transformer and uses the sigmoid function as activation to produce a score between 0 and 1 for each of the 11 classes.

**Supplementary Note 2. Predictive performance comparison of CNNs across various encoders.**

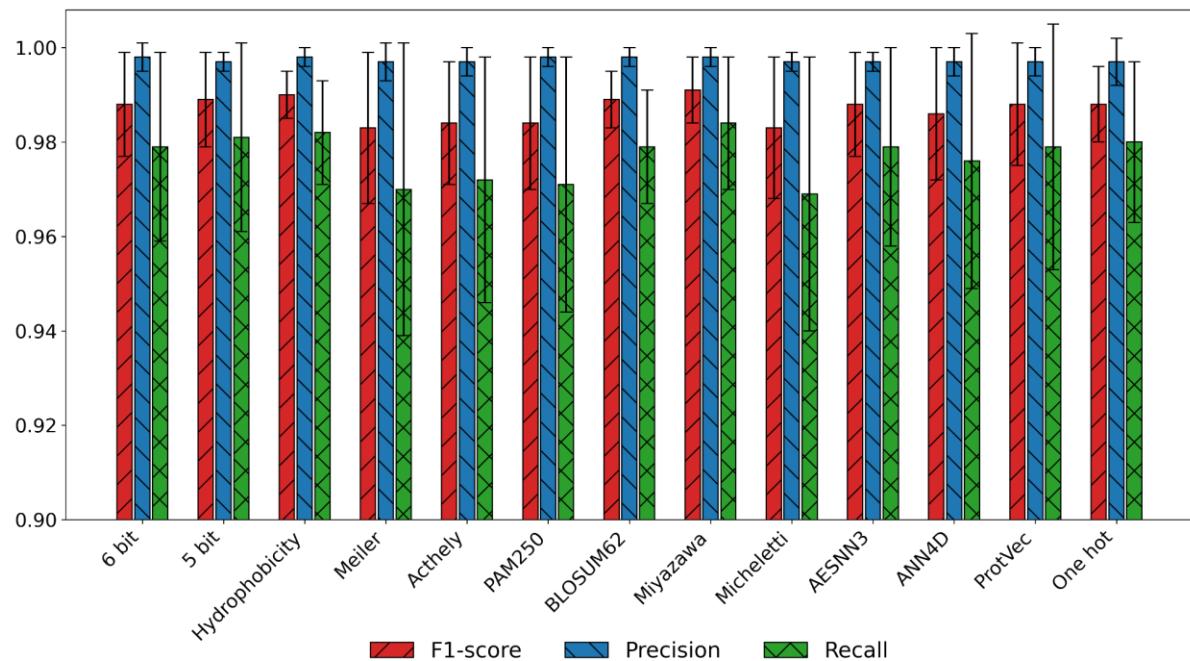


Fig. S1. Predictive performance of convolutional neural networks on the cross-validation dataset across multiple encoding methods

We evaluated the predictive performance of thirteen amino acid encoding methods using PEPIC on the cross-validation dataset (Fig. S1). Performance was assessed on the validation sets using micro-averaged F1-score across twenty repetitions to ensure statistical robustness. Among the tested encodings, Miyazawa energies achieved the highest micro-averaged F1-score ( $0.991 \pm 0.007$ ), followed closely by hydrophobicity matrix ( $0.990 \pm 0.005$ ), binary 5-bit encoding ( $0.989 \pm 0.010$ ), and BLOSUM62 ( $0.989 \pm 0.006$ ). Other encoding methods, such as one-hot ( $0.988 \pm 0.008$ ), AESNN3 ( $0.988 \pm 0.011$ ), and PAM250 ( $0.984 \pm 0.014$ ), also demonstrated competitive performance. Despite slight variations in the results, none of the differences were statistically significant. Given its strong performance, we adopted the Miyazawa energies encoding for the remainder of this study.

**Supplementary Table 1. Sequences for interpretation of plastics-hydrolyzing enzymes.**

Class	Accession number (Nr)	Sequence
PET	MAA58622.1	MNTYLLRTLSICLFAGLFSMQVQAITPDPDPPSTCSNCYQRGPNP VSALeadSGPSVRTINVSSWVSGFGGGTIHYPVGTEGTMGAIAVIPGYVS YERSIKWWGPRLASWGFVVITTDNTIYDQPDSRADQLSAALDYVISQSNS SRSPiYGMVDANRLGAMGWSMGGGTLKLSTERELKAAIPQAPYYAGFNP FDEITTPTLIIACELDVAVPAQHASPFYREIPGSTAKAFLEINGGDHFACS GYPDDEDILGKYGIAMKRFIDEERRYDQFLCGPNHEADRSISEYRDTNCY
	RLP53020.1	MLEGRYMKTVRFNTAAA VFTSALLSSQVFAITDDPVDPVDPVDPSSGT GPDP TL SALES TRSGPSVR TENVS NLS ASGF GGGT IHYP TNA IPGYVSYESSIEWWGPRLASWGFVVITIDNTIYDQPDSRADQLSAALDH DEGS SSSPISGLVDA SRLGVIGWMSMGGGTLKLA TERNLKAIPQAPWYSG FNSFDRITTPTMIIAC ESDAIAPVGQHASPFYNDIPNSTAKAFLEINGGSHYC ANSGYSD E DILGKYGIWMKRFMDNDTRYSQFLCGPNHESDRSISEYRDT NY
	WP_0210188 94.1	MNVLTCKKLALGIIAIFSLPSFAVPCSDCSNGFERGQVPRVDQLESSRGPS VKTINVSR LARGFGGGTIHYSTESGGQQGIIAVPGYVSVLEGSIKWGPRL ASWGFTVITIDNTIYDQPDSRASQLSAIDYVIDKGNDRSSPIYGLVDPNR VG VIGWMSMGGGSLKLATDRKIDAVIPQAPWYLGLSRFSSITSPTMIIACQA DV VAPV SVHASRFYNQIPGTTPKAYFEIALGSHFCANTGYPSE DILGRNGVA WMKRFIDKDERYTQFLCGQNFDSSLRVSEYRDNCSYY
	WP_0773153 88.1	MKF LIKVNFILSIFA VFISP QI FAATVACSDCSNGFQRGTL PRV DQLESSRGP Y SVKTSN VS FVARGFGGGTIHYSTDSGGQQGIIAVPGYVSYESSIKWWGPRL LA SWGFTV ITINTNTIYDQPNSRANQLSAIDYVIDKGNDRSSPIYGLVDP VG VIGWMSMGGGTLKLATDRD IDAI IPQAPWY SGLNSFSRITTPTMVIACQA DAVAPVAL HASIF YNQIPR STPKAFFEIAAGSHFCGN SGYPNEDILGRNGVA WMKRFIDNDTRYNQFLCGQNFDSSLRVSDYKDT CNTY
	RMH89651.1	MKL KAYLARITSLV TSLLASSL AYAPGPSAPCADC SRGP NP TVASLQSR GPFTV STFSVSGYLRGFGNSTV HYP TNA TGM GAI AIPGYL SYED SIRWW GP RLASHGFV VITMNT NTIYDQPDSRATQLS RALD YVIEQSNSRSPISGKV DSTR LGAI GWMSMGGGSLKLSTERSLN AII P QAP YYA GLNRFNT INTPTMIL ACSADVVAPVGSHASP FYNRIPEATPKA FLEIYGGSHFCANGD N GYPNEDLLG MYGISWMKRFIDFDSRYSQFLCGPNHAADLRISEYRENCNY
	OUS39971.1	MPNPNPAPCQEDCDFTRGPDP TISSLEASAGPSVANQGVSRVDGFGGGT FYPMNTTGTMGAI AIPGFLAGESSIEWWGP RFASHGFVII TIA TNSV FDQ SRETQLSSALDYVISQNSNSGNSPISGMV DSTRVGAMGWMSMGGGALR LAS GDRLSAV IPLAPWHQGRNSFDQLETPTLIIACENDTVAPVNRHASSFYNSIPS STD KALLE ISNGAHS CANGGGANGLLKG YGV SWM KRFIDN DLRYDQFL GPN HAANS A VSEYRGTCNY
	WP_0859886 67.1	MPLSMNK LQKLPLTL T S A ALLCAGGLTVNTAVAETRGPDPT EAYVEAE GP Y NVDT INVSS L ALGFGGGTIHYPTNTTGQMGGIVIPGYL SYESSIEWWGER LASHGFV VMTIDNTIYDQPGSRRDQIDAALDYL VDRSDSSFS A ISGMV DG DRLGAVGWSMGGGTLQLASGDR LSA A I PLAPW NSFND FDDI ETPTL IFA CENDTVAPVGV HASP FYYDIPASTDKAFFEIN NGNHCANGDNANDA VLS KG YGV SWM K LHIDQDARYGQFLCGPNHESQYRISEYRGTC PY
	MBF78136.1	MPFNKKGILA CAGAGA GALLFSMSA LANNP PPTD PDPG DGGSSPYQRGP DPSV SF LEADRG NYSV STS RVSG LVSG FG GGTI HYP SGTT GT MAA IVV PGF VSAE SSIEWWGP KLAS YGFV VMTIDTNSGF DQPGS R ATQINN ALDYL VLS QNT SSS

		SPVRGMIDTSRLGVVGWSMGGGTLRVAREGRIKAAIPLAPWDTSTYYSSRSQAPTLIFACESDVIAPVYQHASPFYNALPSSIDKAFVEINNGSHYCGNGGSIYNDVLSRGVSMKLHLDDEDARYKQFLCGPNHTSDSQISDYRGNCPY
WP_1181318 88.1		MSALANNPPPTDPDPGNGGSSPYQRGPDPSSVNFEADRGQYNVDDERVSSFVSGGGGTIHYPHTGTTGMAAIIVIPGVSAESSIEWWGPKLASGYGVVMТИDTNSGFQPGSRATQINNALDYLVDQNTSVGPVRGMIDTDRLGVIGWSMGGGTLRVGREGRIKAAIPLAPWDTSSYYASRAQAPTLIFACESDVIAPVYQHASPFYNALPSNIDKAFVEINNGSHYCGNGGSIYNDVLSRGVSMKLHLD EDARYKQFLCGPNHTSDSQISDYRGNCPY
WP_0918498 96.1		MSDHYASNPLRSVVAASALLFSASVFAAGGGGSDGGDDGCTSNCGYERGPAPTESFLEASSGPYSVRTDRVSSLVGGFGGGTIHYPTGTSGMTGAVVVIPGVVSAESSIEWWGPKLASHGFGVVMТИDTNSGFQPGSRATQINNALDYLIEQN GSSSSPVSGMIDTNRLGVIGWSMGGGTLRVASEGRIQAAIPLAPWDTSSFRFRNIETPTLIIACESDIIAPVRSHADPFYEAPISTDKAFVELNNGSHYCGNGGNSYNDVLSRGVSMKLHLDNDQRYNQFLCGPDHERDWDISEYRGTCPY
CAH17554.1		MAVMTPRRERSSLLSRALRFTAAAATALVTAVSLAAPAHAANPYERGPNP TDALLEARSGPFSVSEERASRGFADGFGGGTIYYPRENNTYGAVAISPGYTGTQASVAWLKGRIASHGFVVITIDTNTLDQPDPSRARQLNAALDYMINDASS AVRSRIDSSRLAVMGHSMGGGSLRLASQRPDLKAAIPLTPWHLNKNWSS VRVPTLIIGADLDTIAPVLTHARPFYNSLPTSISKAYLELDGATHFAPNIPNKI IGKYSVAWLKRFVDNDTRYTQFLCPGPRDGLFGEVEEYRSTCPF
G8GER6.1		MPPHAARPGPAQNRRGRAMAVITPERRSSLLSRALRFTAAAATALVTAVSLAAPAHAANPYERGPNP TDALLEARSGPFSVSEERASRGFADGFGGGTIYYPRENNTYGAVAISPGYTGTQASVAWLKGRIASHGFVVITIDTNTLDQPDPSRARQLNAALDYMINDASS AVRSRIDSSRLAVMGHSMGGGSLRLASQRPDLKAAIPLTPWHLNKNWSS VRVPTLIIGADLDTIAPVLTHARPFYNSLPTSISKAYLELDGATHFAPNIPNKI IGKYSVAWLKRFVDNDTRYTQFLCPGPRDGLFGEVEEYRSTCPF
WP_1247733 20.1		MSSPTTRPRSVVARLALAALAVLAAGGVLAGPAGVAQAASPYERGPAPTTAILEASRGPFATASQSVSSLVSGFGGGVIYYPTSTSEGTFGAIAISPGFTASWS SISWLGPRIASHGFVVIGIETNTRLDQPDPSGRQLLAALDYLTERSSVRSRID SSRLAVAGHSMGGGSLEAASSRPSLQAAVPLAPWNTDKSWSELRVPTLII GGESDSVAPVATHSVFVNSIPASAECAYLELNGASHFFPQTNTPTARQM VAWLKRFVDDDTRYEQFLCPGPGSGSQIQEYRNTCPA
TKK88911.1		MSRIATAALAFLATGTAVTLAPSQAAGFERGPNPSTAILEASRGPFVAT TSVSSLVSGFGGGTIYYPTDTSQGTFGAIAISPGYTARWSSLELGPRIASHGFVVIGIETNTRLDQPDPSGRQLLAALDYLVNSSSTTVRSRIDRNRLAVAGHS MGGGGTLHAAEDRPSLKAAPVIAPIWPWNTDKTWGSVRVPTLIVAGESDSVAS PTTHASPFYNSITQTEKAYLELNSASHFFPQTNTPTFAKQFVAWLKRWVDE DTRYSQFICPGPSGLAIEEYRSTCPF
WP_1608756 56.1		MTTTTWRTRIASLALAAAAATGLTSGVGLGAPISAVAATANPYERGPAPTR ASIEATRGAYATAQTSVSSLVSGFGGGTIYYPTTADGTFGAVIAPGYTAT SSSLAWLGPRLASQGFVVFIDTDSRYDQPSARGDQLLEADYLRTSVA SRVDARRVALMGHSMGGGTLAEIKDRPSKAAIPLTPWNLDKTWPEVTT PTLIIGADNDSVAPVASHAEPFYGSLPSTLDKAYLELRNASHFAPNSANTTI ASYSIAWLKRFVDDDTRYSQFLCPPTPASSLAIAYEYRSTCPF
WP_1425690 56.1		MVTRLALVVLALAGGLTAPAAHAAVHGPDPDTDALLESSRGPYATAQTD VSSLVSGFGGGTIYYPTTSEGTFGGVIAIPGYTADKSSLAWLAARLASH GFVVFNIIDLTRLDQPDPSGRQLLAALDYLQRSSVRGRVDA TRGLVMGH SMGGGTLAEVDDRPSVRAAVPLTPWNLDKTWSGVRTPTLIIGAEADTVA PVASHAEPFYTSLSSSLDKAYLELNGATHFAPNTTNTTIGKYAVAWMKRF VDDDTTRYDQFLCPGPGRSLTVEEYRSTCPF

	EFL43114.1	MHRPAGGSQRQGPLVVQQHPTGRRTRFAALAAAVALVGLTLLGG PGAHADNPYERGPAPTESSIEALRGPYAVSETSVSSLVTGFGGGTIYYPT STADGTFGAIAVSPGFTAYQSSIAWLGPRLASQGFVVFTIDNTTLQDQASR GDQLLAALDYLTQRSAVRGRIDSSRLGVMGHSMGGGTLEAKDRPSLQ AAIPLTPWNLDKTWPEVRTPTLLFGADGDTVAPVGTHAEPLYTGLPSSLDR AYLELNGATHFTPNSNTTIAKYSISWLKRFIDNDTRYEQFLCPLPRPSLTIE ESRGNCPHTS
	WP_0855761 51.1	MQQHPHTSRRGTGRFAALTAAVAVALVGLTLLNGPGQAQAADNPYERGPAP TESSIEALRGPYAVSDVSVSSLVTGFGGGTIYYPTSTADGTFGAIASPGFT AYQSSIAWLGPRLASQGFVVFTIDNTTLQDQASRQGDQLLAALDYLTQRSA VRGRVDSSRLGVMGHSMGGGTLEAKDRPSLQAAIPLTPWNLDKTWPE VRTPTLLFGADGDTVAPVSSHAEPLYSGLPSSLDRAYIELNGATHFTPNSN TTIAKYSVSWLKRFIDNDTRYEQFLCPLPRPSLTVEESRGNCPHTS
	WP_1504740 04.1	MQQQARTGAHHRVPTGSPHRRSARFAGLATAIAAVGLTLLNGAGAQAA DNPYERGPAPTTSSIEAARGSYSVSQTSVSSLAVTGFGGGTIYYPTSTADGT FGAVAISPGYTGTQSTMALWLGPRLASQGFVVFTIDNTTLQDQPSRGRQOLL AALDYLTQRSSVRGRVDSTRLGVMGHSMGGGSLEAAKTRPSLQAAIPLT PWNTDKSWPEISTPTLIFGADGDTIAPVASHAEPFYSSLPSLDRAYLELNGT SHLTISSNTTIAKYSVSWLKRFIDNDTRYEQFLCPLPRPSLTIEEYRGNCPH S
	WP_0537570 25.1	MQQHPRSTTASAAPGPARGAGRRGTRRFAGAAAAIAAVALSTLTGPGAR AADNPYERGPAPTTASIEASRGPSVSETSVSSLAVSGFGGGTIYYPTSTAD GTGAVAVSPGYTGTQSSIAWLGPRLASQGFVVFTIDTLTLDQPSRGRQ LLAALDYLTTRSSVRGRVDSTRLGVMGHSMGGGSLEAAKSRSRPSLQAAIP LTPWNLDKSWPEVTPTLIVGADGDSIAPVSSHAEPFYGSLRSSLDRAYLEL NGASHFTPNSNTTIAKYSVSWLKRFIDNDTRYEQFLCPLPRPSLTIEEYRGN CPHTS
	BCL25765.1	MQQHSQNSSLTAGTVPPESAGRPRRDGRGGWAALKITGALAALTTVVG LSSLASPGAHADNPYERGPAPTTSSIEAARGSYVSQTTVSSLAVTGFGGG TVYYPTSTADGTFGAVVISPGYTGTQSSISWLGARLASQGFAVFTIDTLT DQPSRGRQLLAALDYLTTERSSVRTRVDGSRALVMGHSMGGGSLEAAK SRPSLQAAIPLTWNTDKSWPEVSTPTLIVGADGDTIAPVASHAEPFYGSLPS STDKAYLELNATHFTPNSDDTTIAKYSISWLKRFIDNDTRYEQFLCPLPRP SLTIEEYRGNCPHTS
	WP_0699337 76.1	MRNAPAHRRRGSGRLRSLVAGLAALLAVGLSSVATPAQAQAADNPYERG PAPTTASIEAPNGPYAVSQTSVSSLVTGFGGGTYYPTTGDGTGAVAIS PGFTAGESSIAWLGPRLASQGFVVFTIGLTRYDQPSRGSQLLAALDYLTQ RSTVRARIDSGRGLGVMGHSMGGGSLEAAKSRSRPSLQAAIPLTGWN PEIKPTLVVGADGDTVASVGHSEPFYESLPSLSDKAYLELNATHFTPNT SNTTIAKYSISWLKRFIDNDTRYEQFLCPLPRPSLTIEEYRGNCPHTS
	WP_2373253 67.1	MQQHLLARRQTPHPSRSRTLTGLTAAAATAGLLTALAPGAQAVAANPY ERGPAPTNASIEASRGSYATSQTSVSSLAVSGFGGGTIYYPTSTADGTFGAV VISPGFTAYQSSIAWLGPRLASQGFVVFTIDNTTLQDQPSRGRQLLSALDY LTQRSSVRTRVDASRLGVMGHSMGGGSLEAAKSRTSLKAAIPLTGWN KTWPELRTPTLVVGADGDTVAPVGTHSKPFYESLPGSLDKAYLELRGASHF TPNSSDTTIAKYSLSWLKRFIDNDTRYEQFLCPIPRPSLTIAEYRGTCPHTS
	WP_1612676 37.1	MQQHLLARRQAPRPSRSRTLTGLTAAAATAGLLTGLAPGAQAVAANPY ERGPAPTNASIEASRGSYATSQTSVSSLAVSGFGGGTIYYPTSTADGTFGAV VISPGFTAYQSSIAWLGPRLASQGFVVFTIDNTTLQDQPSRGRQLLSALDY LTQRSSVRTRVDASRLGVMGHSMGGGSLEAAKSRTSLKAAIPLTGWN KTWPELRTPTLVVGADGDTVAPVATHSKPFYESLPGSLDKAYLELRGASHF TPNSSDTTIAKYSLSWLKRFIDNDTRYEQFLCPIPRPSLTIAEYRGTCPHSS

	AOS64284.1	MQSSSIASRRARVRSAGRPRTRLAGLVLALTMVATGLAAAPAATAQENPY ERGPAPTERSIEALRGPFAVAEDRVSSLVIGFGGGTIYYPTDTSEGTGFAVA VSPGYTGTQSSMAWLGPRLASQGFVVFTIDNTTVDQPDSRGRQLLAALD YLVEDSDVRNRIDPNRLGVMGHSMGGGSLSAAESRPALQAAIPLTGWHL SKNWSRVTVP TLVVGAEIDLIA PVRSHSIPFYESLSSLDKAYLELDGASHF APNISNTTIAKYSISWLKFIDDDLRYEQFLCPPDDREISEYRNTCPHS
	KOV83888.1	MPNEVYSAVQLRTLIPALTLVLTGTAAQAAADNPYERGPAPTVSSIEALR GPFAVSETSVSSLVGGFGGGTIYYPTSTSGTGFAVA VSPGYTGTQSSISWL GPRLASQGFVVFTIDNTIYDQPDSRASQLAALDYL TQQSSVRSRIDATRL GVMGHSMGGGTLRAASQRPTLQAAIPLTAWHTKNWSSVRVPTLVGA EDDSIAPVATHSEPFYTTLPSTLDKAYLELNNA THFAPNSNNTTIAKYSISW LKRFIDNDTRYEQFLCPAPGRSTLIEYRDTCPHS
	WP_3738731 95.1	MDKVIPKLFGIAAAVALGGAGITLIPDADAATASFAKG PAPSNASIEAVRGP FAVAQSNVSRSASVSGFGGGDIYAPTD TGAGTFGAVVIAPGFTARKSSMAW LAPRLASQGFVVFNIDT LSTSDQPASRGRQLAAADFLTQRSTVRARIDAGR VAVIGHSMGGGALLEAAGSRPALAAAIPLTPWNLTKSFSRNAVPTLVIGAE ADSIAPVRSQAQPFFQSLPAVPGKAFLNLNGASHFAPNTPNTTIAKFSISWL KLFVDDDTRYQQFVCPGPAGAAVQEYRSTCDQFTP
	WP_3285947 53.1	MPRTTLRTLAAVLAAGAVGVLP TAPAHAAAGFERGPAPTEASVTAAGP AIDRIEV PAGSGTGFNSGTIYYPTSTAEGTGFAVAISPGFVSPKSWIDWYGR LASQGFVVMTLETFSYFDAPDGRADQLAALDYLTA KSKVKDRIDPNRLA AMGHSMGGGALSAAVKRPSLKA VVPLAPWYVGGGLEQSTVPTMIFGAD NDFIAPVASNARPYQSLTKVPEKAYLELENAGHVGFSNPNNTTIAKYAISW LKRFVDDDTRYSQFLCPAPKFPSSTIQEYRDTCPHS
	G9BY57.1	MDGVLWRVRTAALMAALLALA AWALVWASPSVEAQSNPYQRGPNPTRS ALTADGPFSVATYTVSRLSVSGFGGGVIYYPTGTSLTFGGIAMSPGYTADAS SLAWLGRRFLASHG FVVLVINTNSRFDYPD SRSASQLSAALNYLRTSSPSAVR ARLDANRLAVAGHSMGGGTLRIA EQNPSLKA A VPLTPWHTDKTFNTSVP VLIVGAEADTVAPVSQHAI PFYQNL PSTTPKVYV ELDNASHFAPNSNNAIS VYTISWMKLWVDNDTRYRQFLCNVNDPALSDFRTNNRH CQ
	P19833.1	MFIMIKKSELAKAIIVTGALVFSIPTLA EVTLSETTVSSIKSEATVSSKKALP ATPSDCIADSKITAVALSDTRDNGPFSIRTKRISRQS A KGFGGGTIHYPTNAS GCGLLGAIAVPGYVSYENS IKWWGPRLASWG FV VITINTNSIYDDPDSRA AQLNAALDNMIADD TVGSMIDPKRLGAI GWSMGGGALKATERSTVRAI MPLAPYHD KSYGEVKTPTLVIACEDDRIAETKKYANAFYKNAIGPKMKVE VNNGSHFCPSYRFNEILLSKPGIAWMQRYINNDTRFDKFLCANENYSKSPRI SAYDYKDCP
PCL	WP_0258041 84.1	MSTLSWVRGVNGTLGWVAPKLVASKMRLAFMTPREHLP RDWELPLLARS ERITLRFGLSALRWGQGP AVLLMHGWEGRPTQFASLIDALVGAGYSVVAL DGP AHGRSPGHEANVLFARAMLEAAAELPPLRAVIGHSMGGASAMLAV QLGLRTETLV SIAAPARILGVLRGFARYVRLPPKARSAFIRQVEKDVG MRAA AAMDVAHYQLDMPGLIVHAEDDNFV PVKESELIHD AWFDSRLLRK EGG HQ RVLADPRVIEGVLTLLAGRS LQARQSA
	WP_0591812 12.1	MSTLK WVRGVNGTLGWFAPQLVASRMRLAFMS PRALPPRDWELPLLAKS ERITLRFGLSALRWGQGP AVLLMHGWEGRPTQFASIITALVDAGYSVVALD GPAHGRSPGEEANVLFARAMLEAAAELPPLQAVIGHSMGGASAMLAVQ LGLRTETLV SIAAPARILGVLRGFARYVRLPPKARSAFIRQVEKDVG MRAA ALDVAHYQLDMPGLIVHAEDDRFVSAKESQLIHEAWFDSRLLRLEEGGHQ RVLADPRVIDGVL SLLAGRS LHSRQSA
	WP_0521451 36.1	MERYRGMGRAALDRAYNNTRAIANFP AVLADFRTRSAAL YER VRG RRD LRYGDRPRERFDWLPGGRANAPTFVFIHGGYWQNCAKEDFAFVAHGPLAR

		GFNVLVLAEYTLAPDASMTQIVDEIGRLIDHLRADRDGLGTAGRPLCLSGHS AGGHLSALHRGHAFVTSALAIISPVLDEPISLWLNEKLQLSERIAAYSPL WHVGKGAPTVVAVGADELPELVRQADDYTAACAAAGEPVWGAHVPGCT HFSVLDLAAQPNGLMRLDAAIAGSGHGGDERADEERR
WP_1243200 71.1	MSTLSWVRGVNGTLGWVAPKLVASKMRLAFMTPRERLPRDWELPLLARS ERITLRFGSALRWGQGPVLLMHGWEGRPTQFASLIDALVGAGYSVVAL DGPAHGRSPGQEANVMLFARAMLEAAAELPPLRAVIGHSMGGASAMLAV QLGLRTETLVRIAAPARILGVLRGFARYVRLPPKARSAFIRQVEQDVGMRA AAMDVAHYQLDMPGLIVHAEDDNFVPVKESDLIHEAWFDSRLLRLKEGG HQRLADPRVIEGVLTLLAGRSLQARQSA	
WP_1341743 23.1	MNTLKWRGVNGTLGWIAPIKRVASKMRLAFMTPRSPLRDWELPLASSE RITLRFGSALRWGQGPVLLMHGWEGRPTQFAALITALVDAGYTVALD GPAHGRSPGREANVVLFARAMLEAAAELPPLQAVIGHSMGGASAMLAVQ LGLRTETLVRIAAPARILGVLRGFARYVGMPPRARSAFIRQVEQDVGMRA TLDVAHYQLDMPGLIVHAEDDNFVSVKESQLIHESWFDSRLLREGGHQ RVLADPRVIDGVLSLLAGRSLQARQSA	
WP_0967961 49.1	MNTLKWRGVNGTLGWIAPIKRVASKMRLAFMTPRSPLRDWELPLASA ERITLRFGSALRWGQGPVLLMHGWEGRPTQFAALITALVEAGYTVALD DGPAHGRSPGREANVVLFARAMLEAAAELPPLQAVIGHSMGGASAMLAV QLGLRTETLVRIAAPARILGVLRGFARYVGMPPRARSAFIRQVEQDVGMRA ATLDVAHYQLDMPGLIVHAEDDTFVSVKESQLIHESWFDSRLLREGGHQ RVLADPRVVDGVLSLLAGRSLQARQSA	
WP_0545966 12.1	MSTLSWVRGVNGTLGWVAPQWVASKMRSVFMTPRELPPRDWEMPLLA SERITLRFGSALRWGQGPVLLMHGWEGRPTQFASLITALVDAGYTVALD DGPAHGRSPGREANVVLFARAMLEAAAELPPLQAVIGHSMGGASAMLAV QLGLRTETLVRIAAPARILGVLRGFARYVGMPPRARSAFIRKVERDVGQAS RLDVAHYQLDMPGLIVHAEDDNFVSVKESQLIHESWFDSRLLREGGHQ RVLADPRVIEGVLSLLSGRSLQARQSA	
WP_1235928 31.1	MNTLKWRGVNGTLGWIAPIKRVASKMRLAFMTPRSPLRDWELPLASS RITLRFGSALRWGQGPVLLMHGWEGRPTQFAALITALVDAGYTVALD GPAHGRSLGREANVVLFARAMLEAAAELPPLQAVIGHSMGGASAMLAV QLGLRTETLVRIAAPARILGVLRGFARYVGMPPRARSAFIRQVEQDVGMRA ATLDVAHYQLDMPGLIVHAEDDNFVSVKESQLIHESWFDSRLLREGGHQ QRVLADPRVVDGVLSLLAGRSLQARQSA	
WP_0597283 96.1	MTILYRGMDRAALDAAYLNTKVPDFPALLASMQARSAALYDTAHRRD LRYGAQPAQRFDWLSCGRPDAPLFVFIHGGYWQHCAKEDFAYAASGPLAR GFDVILAETLAPVATMTGIVGEIGALDYLANDPDAIGTAGRPPIHLSGHSA GGHLTAVYRAHPAVVSALAISPLVDLEPISLCVNDKLQLGAREVDAYSP RHVGPGAPTVAVGDAELPELVRQARDYATACEAAGERVVHVGGLPMRH FDVLDLAKPDGAMLAALQSIAPR	
WP_0386312 69.1	MSTLSWVRGVNGTLGWVAPTLVASKMRLAFMTPRERLPRDWELPLLARS ERITLRFGSALRWGQGPVLLMHGWEGRPTQFASLIDALVGAGYSVVAL DGPAHGRSPGHEANVMLFARAMLEAAAELPPLRAVIGHSMGGASAMLAV QLGLRTETLVRIAAPARILGVLRGFARYVRLPPKARSAFIRQVEQDVGMRA AAMDVAHYQLDMPGLIVHAEDDNFVPVKESDLIHEAWFDSRLLRLKEGG HQRLADPRVIEGVLTLLAGRSLQARQSA	
AIC18917.1	MTMTLLYRDMNQAQLDAAYNNTQAVPDFPGYAALQARSASFYASAAGR LNLPYGTAPRQRYDWLPCGKADAPTLIFIHGGYWQNCSKEDFAFIAAGPLA AGFNIVLAETLAPQASMTQIVSEIGSLLEHLQADADQLGIAGHKVVLSGH SAGGHLALQFRSHPWVTDLAISALVDLEPISLWLNEKLSLSEAEIDAYSP LYHIDKGANTWWAVGADELSELVRQSDEYAKQALARGESVQLIHPGCTH FSVLDDEMAKPQGALLQALSSIR	

	WP_1390555 57.1	MNTLKWRGVNGTLGWIAPQRVASKMRQAFMTPRTLPLRDWELP LASS ERITLRFGSALRWGQGPVLLMHGWEGRPTQFAALITALVEAGYTV VAL DGPAHGRSPGREANVVLFARAMLEAAEELPPLQAVIGHSMGGAS AMLA V QLGLRTETLV SIAAPARILGVLRGFARYVGMP RARS AFIRQVEQDVG MRA ATLDVAHYQLDMPGLIVHAEDDTFVS VKESQLIHE SWFDSRLLRLES GGHQ RVLADPRVVDGVLSLLAGRSLQARQSA
	WP_1033048 52.1	MNTLKWRGVNGTLGWIAPKQVASKMR LA FMTPR ALPLRDWELP LASS ERITLRFGSALRWGQGP T VLLMHGWEGRPTQFAALITALVEAGYTV VAL DGPAHGRSPGREANVVLFARAMLEAAEELPPLQAVIGHSMGGAS AMLA V QLGLRTETLV SIAAPARILGVLRGFARYVGMP RARS AFIRQVEQDVG MRA ATLDVAHYQLDMPGLIVHAEDDNFVS VKESQLIHE SWFDSRLLRLES GGHQ QRVLADPRVVDGVLSLLAGRSLQARQSA
	WP_0079692 26.1	MNTLKWRGVNGTLGWIAPKQVASKMR TA FMTPR ALPLRDWELP LASS ERITLRFGSALRWGQGP A VLLMHGWEGRPTQFAALITALVEAGYTV VAL DGPAHGRSPGREANVVLFARAMLEAAEELPPLQAVIGHSMGGAS AMLA V QLGLRTETLV SIAAPARILGVLRGFARYVGMP RARS AFIRQVEQDVG MRA ATLDVAHYQLDMPGLIVHAEDDNFVS VKESQLIHE SWFDSRLLRLES GGHQ QRVLADPRVVDGVLSLLAGRSLQARQSA
	WP_0476001 95.1	MNTLKWRGVNGTLGWIAPQRVANKMRQAFMTPR TLPLRDWELP LASS ERITLRFGSALRWGQGP A VLLMHGWEGRPTQFAALITALVEAGYTV VAL DGPAHGRSPGREANVVLFARAMLEAAEELPPLQAVIGHSMGGAS AMLA V QLGLRTETLV SIAAPARILGVLRGFARYVGMP RARS AFIRQVEQDVG MRA ATLDVAHYQLDMPGLIVHAEDDNFVS VKESQLIHE AWFDSRLLRLES GGHQ QRVLADPRVVDGVLSLLAGRSLQARQSA
	WP_1309278 96.1	MNALKWRGVNGTLGWFAPKL VASKMR LA FMTPR ALPLRDWELP LASS ERITLRFGSALRWGQGP T VLLMHGWEGRPTQFAS LINALVDAGYTV VAL DGPAHGRSPGREANVVLFARAMLE ASAEELPPLQAVIGHSMGGAS AMLA V QLGLRTETLV SIAAPS RILGVLRGFARMVGMP RARS AFIRQVEQDVG MRA ATLDVAHYQLDMPGLIVHAEDDNFVS VKESQLIHEAWFDSRLLRLES GGHQ QRVLADPRVVDGVLSLLAGRSLQARQSA
	WP_1234634 37.1	MNTLKWRGVNGTLGWIAPKR VASKMR LA FMTPR TLPLRDWELP LASS ERITLRFGSALRWGQGP T VLLMHGWEGRPTQFA ALITALVEAGYTV VAL DGPAHGRSPGREANVVLFARAMLE AAAELPPLQAVIGHSMGGAS AMLA V QLGLRTETLV SIAAPARILGVLRGFARYVGLPP RARS AFIRQVEQDVG MRA ATLDVAHYQLDMPGLIVHAEDDTFVS VKESQLIHE SWFDSRLLRLES GGHQ VLADPRVVDGVLSLLAGRSLQARQSA
	WP_1515516 51.1	MNALKWRGVNGTLGWFAPKL VASKMR LA FMTPR ALPLRDWELP LASS ERITLRFGSALRWGQGP T VLLMHGWEGRPTQFAS LINALVDAGYTV VAL DGPAHGRSPGREANVVLFARAMLE AAAELPPLQAVIGHSMGGAS AMLA V QLGLRTETLV SIAAPARILGVLRGFARMVGMP RARS AFIRQVEQDVG MRA ATLDVAHYQLDMPGLIVHAEDDNFVS VKESQLIHEAWFDSRLLRLES GGHQ QRVLADPRVVDGVLSLLAGRSLQARKSA
	WP_1234486 44.1	MNTLKWRGVNGTLGWIAPKR VASKMR LA FMTPR SLPLRDWELP LASS ERITLRFGSALRWGQGP T VLLMHGWEGRPTQFA ALITALVEAGYTV VAL DGPAHGRSPGREANVVLFARAMLE AAAELPPLQAVIGHSMGGAS AMLA V QLGLRTETLV SIAAPARILGVLRGFARYVGMP RARS AFIRQVEQDVG MRA ATLDVAHYQLDMPGLIVHAEDDSFVS VKESQLIHEAWFDSRLLRLEG GH QRVLADPRVVDGVLSLLAGRSLQARQSA
	WP_1276503 88.1	MNTLKWRGVNGTLGWIAPKR VASKMR LA FMTPR ALPLRDWELP LASS ERITLRFGSALRWGQGP A VLLMHGWEGRPTQFAALITALVEAGYTV VAL DGPAHGRSPGREANVVLFARAMLEAAEELPPLQAVIGHSMGGAS AMLA V QLGLRTETLV SIAAPARILGVLRGFARYVGMP RARS AFIRQVEQDVG MRA

		ATLDVAHYQLDMPGLIVHAEDDTFVSVKESQLIHESWFDSRLLLESGGHQ RVLADPRVVDGVLSLLAGRSLQARQSA
WP_1600571 37.1		MNTLKWRGVNGTLGWIAPQRVASKMRLAFMTPRALPLRDWELPLASS ERITLRFGLSALRWGQGPAVLLMHGWEGRPTQFAALITALVDAGYTVVAL DGPAHGRSPGREANVVLFARAMLEAAEELPPLQAVIGHSMGGASAMLAV QLGLRTETLVRIAAPARILGVLRGFARYVGMPRARSAFIRQVEQDVGMRA ATLDVAHYQLDMPGLIVHAEDDNFVSVKESQLIHESWFDSRLLLEGGGH RVLADPRVVDGVLSLLAGRSLQARQSA
WP_1085916 90.1		MNTLKWRGVNGTLGWIAPKQVASKMRTAFMTPRSPLLRDWELPLASS ERITLRFGLSALRWGQGPAVLLMHGWEGRPTQFAALITALVEAGYTVVAL DGPAHGRSPGREANVVLFARAMLEAAEELPPLQAVIGHSMGGASAMLAV QLGLRTETLVRIAAPARILGVLRGFARYVGMPRARSAFIRQVEQDVGMRA ATLDVAHYQLDMPGLIVHAEDDNFVSVKESQLIHESWFDSRLLLESGGH RVLADPRVVDGVLSLLAGRSLQARQSA
WP_3323732 21.1		MTIYRGMDRTALDAAYLNTKAVPDFPALLASCQTRSAALEYAATPGRRDL RYGAQPAQRFDWLPCGQPDAPLFVFIHGGYWQHCTKEDFAYAASGPLAR GYDVVLAEYTLAPVATMTDIVGEIGALLDHLAADRDGLGTAGRPIHLSGHS AGGHTAMRAHPAVVSALAISPLVDLEPIALCCLNDKLQLTAHEVDAYSP LHHIGPGAPT VIAVGDAELPELIRQADEVYATACEAAGERIARTWLRGMQHF AVLDDLATPDGAMLDALHAIAPR
WP_0341868 71.1		MTIYRGMDRAALDAAYLNTKAVPDFPALLASCQARSAALEYDETPGRRDL RYGAQPAQRFDWLSCGQAGAPLFVFIHGGYWQHCTKADFAYAASGPLAC GFDVILAETYLAPVATMTGIVAEIGMLLDHLAADPDRLGTARRPIHLSGHS AGGHTAMRAHPAVVSALAISPLVDLEPISLCCLNDKLQLTAHEVDAYSP LRHVGPGAPT VVAVGDAELPELIRQADEVYATACEAAGERIARVWLPGMQH FAVLDLAPDGAMLAALRSITPR
WP_1302070 01.1		MSALKWRGVNGTLGFAPKLVARKMRLAFMTPRDLPPRDWELPLAKS ERITLRFGLSALRWGQGPAVLLMHGWEGRPTQFASLITALVDAGYTVVAL DGPAHGRSPGREANVVLFARAMLEAAEELPPLQAVIGHSMGGASAMLAV QLGLRTETLVRIAAPARILGVLRGFARYVGMPKARSAFIRQVEQDVGMRA ATLDVAHYQLDMPGLIVHAEDDKLVSVKESQAIHEAWFDSRLLRLQEGGH RVLADPQVIDGVLSLLAGRSLQSRQSA
WP_1507739 89.1		MNTKWRGVNGTLGWIAPKRVASKMRLAFMTPRALPLRDWELPLASSE RITLRFGLSALRWGQGPAVLLMHGWEGRPTQFAALITALVDAGYTVVALD GPAHGRSPGREANVVLFARAMLEAAEELPPLQAVIGHSMGGASAMLAVQ LGLRTETLVRIAAPARILGVLRGFARYVGMPRARSAFIRQVEQDVGMRAA TLDVAHYQLDMPGLIVHAEDDNFVSVKESQLIHESWFDSRLLLEGGHQ RVLADPRVVDGVLSLLAGRSLQARQSA
WP_0697453 39.1		MTIYRGMDRAALDAAYLNTKAVPDFPALLASCQSRSAALYDAIAGRREL RYGALPAQRDYWLPCGQPGAPLFVFIHGGYWQHCAKEDFAYAASGPLAR GYDVVLAEYTLAPTASMTDIVAEIGALLDHLAADRDGLGIAGRPIHLSGHS AGGHTAMYRAHPAVAAALSISPLVDLEPISLCCLNDKLQLTAQEIEACSP RHIGPGAPT VVAVGDAELPELIRQAHDYAAACDAAGERIAHVQLPGMKHF AVLDDLANPDGKMLAALRAIAPR
WP_0032264 46.1		MNTLKWRGVNGTLGWIAPQRVASKMRLAFMTPRSPLLRDWELPLASA ERITLRFGLSALRWGQGPAVLLMHGWEGRPTQFAALITALVEAGYTVVAL DGPAHGRSPGREANVVLFARAMLEAAEELPPLQAVIGHSMGGASAMLAV QLGLRTETLVRIAAPARILGVLRGFARYVGMPRARSAFIRQVEQDVGMRA ATLDVAHYQLDMPGLIVHAEDDTFVSVKESQLIHESWFDSRLLLESGGHQ RVLADPRVVDGVLSLLAGRSLQARQSA
WP_1235329		MNTLKWRGVNGTLGWIAPQRVASKMRLAFMTPRVLPLRDWELPLANS

	98.1	ERITLRFGLSALRWGQGPTVLLMHGWEGRPTQFAALITALVDAGYTVVAL DGAHGRSPGREANVLFARAMLEAAELPPLQAVIGHSMGGASAMLA QLGLRTETLVSIAAPARILGVLRGFARYVGMPRRARSEFIRQVEQDVGMRA ATLDVAHYQLDMPGLIVHAEDDNFVSVKESQLIHESWFDSRLLRLEAGGH QRVLADPRVIDGVLSLLAGRSLQARQSA
	WP_1023589 40.1	MSTLKWVRGVNGTLGWFAPKLVASKMRLAFMTPRSPLRDWELPLASS ERITLRFGLSALRWGQGPAVLLMHGWEGRPTQFAALITALVEAGYTVVAL DGAHGRSPGREANVLFARAMLEAAELPPLQAVIGHSMGGASAMLA QLGLRTETLVSIAAPARILGVLRGFARYVGMPRRARSAFIRQVERDVGMR ATLDVAHYQLDMPGLIVHAEDDSFVSVKESQLIHESWFDSRLLRLESGGH RVLADPRVVDGVLSLLAGRSLQARQSA
	WP_0079134 23.1	MNTLKWVRGVNGTLGWIAPQRVASKMRLAFMTPRSPLRDWELPLASS ERITLRFGLSALRWGQGPTVLLMHGWEGRPTQFAALITALVDAGYTVVAL DGAHGRSPGREANVLFARAMLEAAELPPLQAVIGHSMGGASAMLA QLGLRTETLVSIAAPARILGVLRGFARYVGMPPRARSAFIRQVEQDVGMRA ATLDVAHYQLDMPGLIVHAEDDNFVSVKESQLIHESWFDSRLLRLEGGGH QRVLADPRVVDGVLSLLAGRSLQARQSA
	WP_1507943 02.1	MNTLKWVRGVNGTLGWIAPQRVASKMRLAFMTPRSPLRDWELPLASS ERITLRFGLSALRWGQGPTVLLMHGWEGRPTQFAALITALVEAGYTVVAL DGAHGRSPGREANVLFARAMLEAAELPPLQAVIGHSMGGASAMLA QLGLRTETLVSIAAPARILGVLRGFARYVGMPPRARSAFIRQVEQDVGMRA ATLDVAHYQLDMPGLIVHAEDDNFVSVKESQLIHESWFDSRLLRLEGGGH QRVLADPRVVDGVLSLLAGRSLQARQSA
	WP_1332109 51.1	MNTLWIRSVNGTGLRAPEHIAGKMRHAFMTPRNLPPLRDWELPLASGE RITLRFGLSALRWGQGPTVLLMHGWEGRPTQFAHLITLVQAGYTA GPAHGHSPGNQAHVALFARSLEAAELPPLRAVIGHSMGGASVMLALQ WGLRAEMAVSVAAPAQLLGVLNRFAHRLGMPRSRARA AFVRQVERDVGIPISRLDVSRYQLEIPALIAHAEDDRIVP ASEALTIHQSWFDSRLLLPEGGHQRVLADPQLIEGV MALLLRRHSTARQSA
	WP_0389941 75.1	MNTLWIRSVNGTGLHIAPEHVARKMRRAFMTPRNPPRDWELPLA RITLRFGLSALRWGQGPTVLLMHGWEGRPTQFAHLIDSLVDAGYTA GPAHGHSPGNQAHVALFARSLEAAELPPLKAVVGHSMGGASML WGLRAEVAVSIAAPAQLLGVLNRFAHRLGMPRSRARA AFIRQIERDVGQISRLDVSRYQLELPGLIVHAEDDQL VPVDESDAIHRAWFDSRLLL PDGGHLRVLADPQLREGVLALLQRSSSPARQSA
	WP_1600878 82.1	MNSMSWVRGFNASIGLLAPHALASKLREFMTPHTLPPRDWELPLA QAE RITLRFGLSALRWGSGPAVLLMHGWEGRPTQFAELIKLVNAGYGV VALD APAHGRSPGREANVLFARALLEAAE LPLKAVVGHSMGGASALLATQLG LRT EALVSIAAPS RILTMLRRFSHYMGLP RQARAHFVRQL VEEQAGIPAGQL DSA HYQLDFP GLVVHA VDDPMV PFSE AEAIHQ RFDSR LLR L ERGGH QRV LADP QV V Q AV L T L L AS LN NQ AP SN ALAS
	NMY13981.1	MNQMAWVRGVNATLGRVAPQLIASRLRERFMTPT RFTSPRDWELPLASSE RITLRFGLSALRWGSGPTVLLMHGWEGRPTQFALL IRGLVDAGYGV VALD APA HGRSP GREAN VLFAR ALLEAA E LPLK AVV GHSM GGAS ALLAT QM GLR SET LT V IA APS RIL L RGF AR FM GL PA EAR AHF VRQ VE KT AGI PA AHL DV Q YR R LE L P GL IV HA ADD Q V V P V SE AD LI HK AW F DS SQL L R L S AG GH QRL LSD P L L Q AV L L LE EQ V P Q A S L K A L A S
PLA	WP_0341262 30.1	MGALTWVRGFNGTVGRLAPHAVASKMRRTFMT PRDLPPRDWELPLAQS ERITLRFGLSALRWG HGPAVLLMHGWEGRPTQFAS LITALVDNGY S VIALD GPAHGRSP GREAH VLLFAR AMLEAA E LPL YAVV GHSM GGAS AMLA VQ LGL RTQ ALV SIA APS RFL DVL RGF TRMV GLP PRAR SAF I QE VEL SMG PLK

		HLDVAHYHLNIPGLIVHAEDDTFV р VRAAQAIHEAWFDSRLLRLEQGGHQ KVLADPQVIDAVLALLAGCRLQERQSA
WP_0328961 34.1		MGALTWVRGNGTVGRLAPHAVASKMRRTFMTPRDLPPRDWELPLLAQS ERITLRFGSALRWGQGPAVLLMHGWEGRPTQFASLITALVDNGYSVIALD GPAHGRSPGREAHVLLFARAMLEAAAELPPLYAVVGHSMGGASAMLAVQ LGLRTQALVSIAAPSRLDVLRGFTRMVGLPPRARSAFIQEVELSGMPLK HLDVAHYQMNI PGLIVHAEDDTFV р VRAAQAIHEAWFDSRLLRLEQGGHQ KVLADPQVIDAVLALLAGCRLQERQSA
WP_0442747 07.1		MGALTWVRGNGTVGRLAPHAVASKMRRTFMTPRDLPPRDWELPLLAQS ERITLRFGSALRWGQGPAVLLMHGWEGRPTQFASLITALVDNGYSVIALD GPAHGRSPGREAHVLLFARAMLEAAAELPPLYAVVGHSMGGASAMLAVQ LGLRTQALVSIAAPSRLDVLRGFTRMVGLPPRARSAFIQEVELSGMPLK HLDVAHYQMNI PGLIVHAEDDTFV р VRAAQAIHEAWFDSRLLRLEQGGHQ KVLADPQVIDAVLALLAGCRLQERQSA
ABY53108.1		MGLAIAAAA VFSLPGVATATEPTGGVQPNIVGGGNATQVYSFMVSQQSSS GGHQCGGSLISSTVVVTAKHCGTPYQVRVGTTNRSGGTVARVAQRIAH SADLALLRLSTA VPQAPVTIADASGA VGTATRIIGWGQTCAPQGGCCAPITL QE LNTSIVSDSRCLGISGASEICTNNPNGNSGACYGDGGPQIKQVNGVWQ LIGATS RAGNNSTCATGPSIYDV PYFRSWIR TNTGV
WP_0570056 88.1		MGALT WIRGVNGTLGRLAPHTVANSMRRVFMTPRDLPPRDWELPLLAHA ERVTLRFGLSALRWGQGPAVLLMHGWEGRPTQFASLITALVQNGYSVFA DGPAHGRSPGREA HVLLFARAMLEAAAELPPLH A VVGHSMGGASAMLAV QLGLRTEALVSIAAPSRLDVLGGFAGMVGLPSRARSAFIQEVELTGMPL KHLDVAHYQM DLPGLIVHAEDDTFV р VSASQVIHD AWFDSRLLRLEQGGH QRVLADPRVVEAVLALLAGSCLQARQTA
WP_0432063 04.1		MGT LT WIRRFNGTLGRLAPQT VANMRRAFMTPRDLPPRDWELPLLAQSE RITLRFGSALRWGQGPAVLLMHGWEGRPTQFASLITALVDNGYSVIALDG PAHGRSPGREA HVLLFARAMLEAAAELPPLH A VIGHSMGGASAMLAVQL LRTEALVSIAAPSRLDVLRGFTQMVG LPARARSAFIQEVELTFGMLK HLD VAHYQMNI PGLIVHAEDDTFV р VKASQAIHEAWFDSRLLRLEQGGHQ KVL ADPRVIDAVLALLAGRRLQALQSA
WP_1166665 39.1		MGALTWVRGNGTVGRLAPHAVASKMRRTFMTPRDLPPRDWELPLLAQS ERITLRFGSALRWGQGPAVLLMHGWEGRPTQFASLITALVGDGYSVIALD GPAHGRSPGREA HVLLFARAMLGAAAELPPLYAVVGHSMGGASAMLAVQ LGLRTQALVSIAAPSRLDVLRGFTRMVGLPPRARSAFIQEVELSGMPLK HLDVAHYQLNIPGLIVHAEDDTFV р VRAAQAIHEAWFDSRLLRLEQGGHQ KVLADPQVIDAVLALLAGCRLQERQSA
WP_0640551 61.1		MMGTLTWIRRFNGTLGRLAPQT VANMRRAFMTPRDLPPRDWELPLLAQSE ERITLRFGSALRWGQGPAVLLMHGWEGRPTQFASLITALVDNGYSVIALD GPAHGRSPGREA HVLLFARAMLEAAAELPPLH A VIGHSMGGASAMLAVQL GLRTEALVSIAAPSRLDVLRGFTQMVG LPARARSAFIQEVELTFGMLK HLD DVAHYQMNI PGLIVHAEDDTFV р VKASQAIHEAWFDSRLLRLEQGGHQ KVL LADPRLIDAVLALLAGRRLQALQSA
WP_0769535 14.1		MGT LT WIRRFNGTLGHLAPQT VANKMRRVFMTPRTLPPRDWELPLLAQSE RITLRFGSALRWGQGPVLLMHGWEGRPTQFASLITALVDKGYSVIALDG PAHGRSPGREA HVVL FARAMLEAAAELPPLRA VIGHSMGGASAMLAVQL GLRTEALVSIAAPSRLCDALRGFTTMVGLPSRARSAFIREVEMTFAMPLK LDVAHYQMNI PGLIVHAEDDTFV р VKASQAIHEAWFDSRLLRLEQGGHQ KVL VLADPRVIDATSLLAGCGLQALQTA
WP_0198208 55.1		MGALTWVRGNGTVGRLAPHAVASKMRRTFMTPRDLPPRDWELPLLAQS ERITLRFGSALRWGQGPAVLLMHGWEGRPTQFASLITALVDNGYSVIALD

		GPAHGRSPGREAHVLLFARAMLEAAAELPPLYAVVGHSMGGASAMILAVQ LGLRTQALVSIAAPSRLDVLRGFTRMVLGPPRARSIFIQEVELSMGMALK HLDVAHYQLNIPGLIVHAEDDTFVVPVRAAQAIHEAWFDSRLLRLEQGGHQ KVLADPQVIDAVLALLAGCRLQERQIA
WP_0429370 80.1		MSTLSWIRGINGTLGRVAPRVVASRMRQMFTPRARLPRDWELPLLATAE RITLRFGSALRWGKGPTVLLMHGWEGRPTQFANLINALVAAGYTAVALD GPAHGRSPGREANVVVFARALLEAAAELPPLKAVVGHSMGGASAMILATQ LGLRTEALVSIAAPARVLGVLRGFARYVGLPPRARSAFIREVERDVGMRRAA HLDIEHYQMDMPGLIVHAEDDRMVRVDESRIHEAWFDSRLLRLESGGHL QVLADQRLLIDGVALLAGRSLAQRQSA
WP_0995840 16.1		MGALTWIRRFNGTGHVAPHTVANKMRRAFMTPRKLPPRDWELPLLAQS ERITLRFGSALRWGQGPVLLMHGWEGRPTQFASLIKALVDNGYCVIAL DGAHGRSPGREAHVLLFARAMLEAAAELPPLHAVVGHSMGGASAMILAV QLGLRTQALVSIAAPSRLDALRGFTRMVGLPARARSIFIQEVEMTFGMPL KYLDVAHYQMNIPGLIVHAEDDTFVVKASQAIHDIAWFDSRLLRLEQGGHQ QKVLAQRLIDGVALLAGRSLAQRQSA
WP_0567858 24.1		MGALTWVRGFNGTVGRLAPHAVASKMRRTFMTPRDLPPRDWELPLLAQS ERITLRFGSALRWGQGPVLLMHGWEGRPTQFASLITALVDNGYSVIALD GPAHGRSPGREAHVLLFARAMLEAAAELPPLYAVVGHSMGGASAMILAVQ LGLRTQALVSIAAPSRLDVLRGFTRMVGLPPRARSIFIQEVELSMGMPLK HLDVAHYQLNIPGLIVHAEDDTFVVPVRAAQAIHQAWFDSRLLRLEQGGHQ KVLADPQVIDAVLALLAGCRLQERQSA
WP_1976274 15.1		MGALTWIRGFNGTVGRLAPHMVASKLRRTFMTPRNLAQSE RITLRFGSALRWGQGPVLLMHGWEGRPTQFASLITALVADGYSVIALDG PAHGRSPGREAHVLLFARAMLEAAAELPPLHAVVGHSMGGASAMILAVQL GLRTEALVSIAAPSRLDALRGFAGMVGLPPRARSIFIHEVELTFGMLPKHL DVAHYQMNIPGLIVHAEDDTFVVKASQAIHDIAWFDSRLLRLEQGGHQKV LADPRVIDAVLSLLAGRRLQERQTA
WP_1106820 84.1		MSSMSWIRGFNATVGR LAPDLVASKMHR AFLTPRDLPPRDWELPLLAES RITLRFGSALRWGQGPVLLMHGWEGRPTQFAELIRALVRAGYGVVALD APTHGRSPGHEANVVLFARALLEAAGELPPLKAVIGHSLGGASALLATQLG LRTEALVTIAAPARILGALRRFAHFVGLPKQARARFVRMVEQSAGMPAAQ LDVARYQLDFPGLVVHAEDDPMPVYGEAQSIHAAWPGSRLPLERGGHSK PLGDP RV VEA VLELLGSADLHS AVS RRV LAATV LAS
XOQ14903.1		AQSVPWGISRVQAPAAHNRLGTSGVKVA VLDTGISTHPDLNIRGGASFVP GEPSTQDGNGHGTHVAGTIAALNNSIGVLGVAPS AELYAVKVLGASGS VSSIAQGLEWAGNNGMHVANLSLGSPSPSATLEQAVNSATSRGVLVVAAS GNSGAGSISYPARYANAMAVGATDQNNNRASFSQYGAGLDIVAPGVNVQ STY PG STY ASLNGTSMATPHVAGAA ALVKQKNPSWSNVQIRNLKNTATS LGSTNL YGS GLV NAE AATR
SPU21234.1		AQSVPWGISRVQAPAAHNRLGTSGVKVA VLDTGISTHPDLNIRGGASFVP GEPSTQDGNGHGTHVAGTIAALNNSIGVLGVAPS AELYAVKVLGADGRGA ISSIAQGLEWAGNNGMHVANLSLGSPSPSATLEQAVNSATSRGVLVVAAS NSGASSISYPARYANAMAVGATDQNNNRASFSQYGAGLDIVAPGVNVQST YPG STY ASLNGTSMATPHVAGAA ALVKQKNPSWSNVQIRNLKNTATS STNL YGS GLV NAE AATR
WP_0532580 10.1		MGALTWIRGFNGTVGRLAPRTVASKLRRTFMTPRNLP PRDWELPLLAQSE RITLRFGSALRWGQGPVLLMHGWEGRPTQFASLITALVDNGYSVIALD PAHGRSPGREAHVLLFARAMLEAAAELPPLQAVVGHSMGGASALLAVQL GLRTEALVSIAAPSRLDALRGFAGMVGLPARARAFAIREVELTFGMLKH LDVAHYQMNLPGLIVHAEDDTFVVKASQAIHDIAWFDSRLLRLEQGGHQK VLADPRVIDGVLTLLAGCRLQARQTA

	WP_0995254 09.1	MNQMTWVRGVNATLGRVAPQLIASRLRERFMPRTQPPRDWELPLLASAE RITLRFGSALRWGSGPTVLLMHGWEGRPTQFALLIRGLVDAGYVIALDA PAHGRSPGREANVVLFARALLEAASELPLLRAVIGHSMGGASALLATQMG LCETLTVAAAPSRLGLRGFARFMGLPAEARAHFVRAVETTAGIPA AHL DVQRYQLDLPGLIVHAEDDQVVPVGEADLIHKAWFDSQLLRLPAGGHQRL LSDPLLLQAVLELLEQVPQASLKALAS
	WP_0540638 32.1	MNTLRWIRGINGTLGRVAPRVAASMRMRFQVMPTRERSPRDWEPLLATAE RITLRFGSALRWGQGPVLLMHGWEGRPTQFASLIALVAAGYTAVALD GPAHGQSPGHEANVVAFARALLEAAAELPLLRAVIGHSMGGASAMLAQQL GLRTEALVSIAAPARVLGVLRGFAQHVGLPPRARSAFIREVERDVGMR AEH LDIGHYQMDMPGLIVHAEDDQLVAVDESRRIHEAWFDSRLLRLES GHQ RL VLADPRLIDGVLALLAGRSMAQRQSA
	WP_0714881 09.1	MGTLTWVRRFNSTLGHLPQTVANRMRAFMPTRPLPPRDWELPLLAQSE RITLRFGSALRWGQGPVLLMHGWEGRPTQFASLITALVDNGYSVIALDG PAHGRSPGREAHVLLFARAMLEAAAELPLLRAVIGHSMGGASAMLAQVL LRTEALVSIAAPSRFLDVLRGFTRMVGLPARARSAFIQEVELTFGMPLKH VAHYQMNIPGLIVHAEDDTFVPKASQAIHEAWFDSRLLRLEQGGHQKV L ADPRVIDAVLALLAGCRLQERQSA
	WP_0714863 26.1	MGALTWIRGFNGTVGRLAPHTVASKMRRTFMPTRDLPPRDWELPLLAQSE RITLRFGSALRWGQGPVLLMHGWEGRPTQFASLITALVDNGYSVIALDG PAHGRSPGREAHVLLFARAMLEAAAELPLLRAVIGHSMGGASAMLAQVL GLRTQALVSIAAPSRFLDVLRGFAGMVGLPPRARSAFIQEVELTFGMPLKH LDVAHYQMNIPGLIVHAEDDTFVPKASQAIHEAWFDSRLLRLEQGGHQ KV VLADPRVIDAVLALLAGRRLQERQTA
	WP_1258815 20.1	MNQMTWVRGVNATLGRVAPQLIASRLRERFMPRTQPPRDWELPLLASAE RITLRFGSALRWGSGPTVLLMHGWEGRPTQFALLIRGLVDAGYVIALDA PAHGRSPGREANVVLFARALLEAASELPLLRAVIGHSMGGASALLATQMG LCETLTVAAAPSRLGLRGFARFMGLPAEARAHFVRAVETTAGIPA AHL DVQRYQLDLPGLIVHAEDDQVVPVGEADLIHKAWFDSQLLRLPAGGHQRL LSDPLLLQAVLELLEQVPQASLKAMAS
	WP_0549216 54.1	MGALTWVRGFNGTVGRLAPHAVASKMRRTFMPTRDLPPRDWELPLLAQS ERITLRFGSALRWGQGPVLLMHGWEGRPTQFASLITALVDNGYSVIALD GPAHGRSPGREAHVLLFARAMLEAAAELPLLYAVVGHSMGGASAMLAQ V LGLRTQALVSIAAPSRFLDVLRGFTRMVGLPPRARSAFIQEVELSMGMLK HLDVAHYQMNIPGLIVHAEDDTFVPKASQAIHEAWFDSRLLRLEQGGHQ K KVLADPQVIDAVLALLAGCRLQERQSA
	WP_1698517 37.1	MSTLSWIRRNVNGTVGRLAPQTIANQMRRAFMPTRDLPPRDWELPLLAQAE RVTLRFGLSALRWGQGPVLLMHGWEGRPTQFASLITALVGAGYSVIALD GPAHGRSPGREAHVVLFARAMLEAAAELPLLA VVGHSMGGASAMLA IQ LGLRTNALVSIAAPSRLLDVLRGFAGVVGMPARARAFAFIQEVESLGIP LK HLDVAHYQMNIPGLIVHAEDDTFVPKASQMIHEAWFDSRLLRLEQGGHQ K KVLADPRVVEGVLALLAGCREPTRQTA
	WP_0584268 95.1	MGTLTWIRRFNGTLGLAPQTVANRMRAFMPTRDLPLRDWELPLLAQSE RITLRFGSALRWGQGPVLLMHGWEGRPTQFASLITALVDNGYSVIALDG PAHGRSPGREAHVLLFARAMLEAAAELPLLRAVIGHSMGGASAMLAQVL LRTEALVSIAAPSRFLDVLRGFTKMVGLPARARSAFIQEVELTFGMPLKH D VAHYQMNIPGLIVHAEDDTFVPKASQAIHEAWFDSRLLRLEQGGHQKV L ADPRVIDGVLALLAGARLQERQTA
	WP_0031925 69.1	MGALTWVRGFNGTVGRLAPHAVASKMRRTFMPTRDLPPRDWELPLLAQS ERITLRFGSALRWGQGPVLLMHGWEGRPTQFASLITALVDNGYSVIALD GPAHGRSPGREAHVLLFARAMLEAAAELPLLYAVVGHSMGGASAMLAQ V LGLRTQALVSIAAPSRFLDVLRGFTRMVGLPPRARSAFIQEVELSMGMLK

		HLDVAHYQMNPGLIVHAEDDTFVPVRAAQAIHEAWFDSRLLRLEQGGHQ KVLADPQVIDAVLALLAGCRLQERQSA
WP_0607651 21.1		MGALTWVRGFNGTVGRLAPHAVASKMRRTFMTPRDLPPRDWELPLLAQS ERITLRFGSALRWGKGPTVLLMHGWEGRPTQFASLIAALVDNGYSVIALD GPAHGRSPGREAHVLLFARAMLEAAAELPPLYAVVGHSMGGASAMLAQV LGLRTQALVSIAAPSRLFVLRGFTRMVGLPPRARSASIQEVELSGMPLK HLDVAHYQLNIPGLIVHAEDDTFVPVRAAQAIHEAWFDSRLLRLEQGGHQ KVLADPQVIDAVLALLAGCRLQERQSA
WP_1547432 90.1		MSTFKWTRGVNGALGRLAPQIASKMRRVFMTPRNFPPRDWELPLLAQSE RITLRFGSALRWGKGPTVLLMHGWEGRPTQFASLISALVGAGYSVIALEG PAHGRSPGREAHVLLFARAMLEAAAELPPLHAVIGHSMGGASAMLAQLG LRTEALVSIAAPSRLFVLRGFAGMVGLPARARSASIQEVEHAFGMLKYL DVAHYQMNPGLIVHAEDDTFVSVRASQVIHEAWFDSRLMRLKQGGHQK VLADPHVIKGVLALLAGCRPAQRQTA