CLONING AND EXPRESSION ANALYSIS OF *KFNCED*₁ FROM *KALIDIUM FOLIATUM* (CHENOPODIACEAE) IN RESPONSE TO NACL TREATMENT

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Abstract

Kalidium foliatum exhibits strong tolerance to salinity. $NCED_1$ from *K. foliatum* was cloned, and its expression level was analysed under salt treatment. Whole plants were subjected to 0, 150, 200, 250, 300, 350 and 400 mM NaCl for 72 h. Total RNA was extracted from the leaves of 4-month-old *K. foliatum* seedlings. The full-length *KfNCED*₁ cDNA was cloned with reverse transcription PCR, the *KfNCED*₁ expression levels were analysed with semiquantitative RT-PCR, and the ABA contents from *K. foliatum* were examined. The *KfNCED*₁ cDNA was 1500 bp long and included an open reading frame that encoded a polypeptide of 499 amino acids. The deduced amino acid sequence of *KfNCED*₁ had significant similarity with that of *AiNCED*₁. Semiquantitative RT-PCR showed that the expression of *KfNCED*₁ could be markedly induced by salt treatment.

Key words: Kalidium foliatum, Halophyte, ABA, Gene cloning, Salt treatment.

Introduction

Salinity is a severe environmental stressor that is responsible for agricultural production losses worldwide (Alzahrani et al., 2019; Ravindran et al., 2007). High NaCl induces ionic toxicity and osmotic stress (Hossain & Dietz, 2016). Correspondingly, plants have evolved physiological adaptations such as osmolysis synthesis and Na⁺ exclusion. ABA (abscisic acid) is a stress hormone that participates in plant tolerance to salinity (Sah et al., 2016), and it plays a critical role in stress tolerance during plant life cycles (Nambara & Marion-poll, 2005). Therefore, ABA is very important for the plant response to salt (Hou et al., 2013). The biosynthesis of ABA is regulated by environmental signals such as salt and drought (Seung et al., 2012), and ABA mediates stress signals to increase the expression of resistance genes. Although the importance of ABA in abiotic stress tolerance in plants has been well recognized, the molecular mechanisms of the ABA response to salt in K. foliatum remain poorly understood.

ABA in plants is regulated by ABA biosynthesis (Ng et al., 2014); ABA is synthesized in the cytoplasm through the ABA biosynthesis pathway that starts with the catalysis of several enzymes for carotenoid precursors found in plants (Xu et al., 2013). To date, ABA biosynthesis genes, such as NCED (9'-cisepoxycarotenoid dioxygenase) and ZEP (zeaxanthin epoxidase), have been cloned (Hauser et al., 2011). The first step in ABA biosynthesis is the cleavage of 9-cisneoxanthin or 9-cis-violaxanthin by the NCED enzyme to produce xanthoxin (Milborrow, 2011). ZEP catalyses the conversion of zeaxanthin into violaxanthin (Leng et al., 2014). NCEDs have been cloned from plant species such as maize (Schwartz et al., 1997), tomato (Burbidge et al., 1999), Arabidopsis (Tan et al., 2003), Brassica napus (Xu & Cai, 2017), avocado (Chernys & Zeevaart, 2000) and Malus (Xia et al., 2014).

NCED is a multigene family. There are five *NCED* members in *Arabidopsis*, each of which is located in different tissues and regulates the development and control ABA biosynthesis (Tan *et al.*, 2003). Studies have shown that increasing *NCED* transcripts could increase ABA accumulation in plants (Martínez-Andújar *et al.*, 2011). *AtNCED*₃ is induced by water stress and controls ABA contents under water stress (Hao *et al.*, 2009). *OsNCED*₁ is suppressed by water stress (Ye *et al.*, 2011). *OsNCED3*, *OsNCED4*, and *OsNCED*₅ are also induced by water stress (Teng *et al.*, 2014). Little is known about the function of *NCEDs* in plant tolerance to salt stress.

K. foliatum belongs to the *Chenopodiaceae* family and is a halophyte with succulent leaves. This species is widely distributed in saline soil; however, little is known about the mechanisms responsible for its tolerance to salt stress. Thus, the objective of this study was to clone the ABA biosynthesis gene $NCED_1$ in *K. foliatum*, analyse the ABA content and evaluate the expression of *NCEDs* under different NaCl concentrations.

Materials and Methods

Plant materials and salt treatment: Seeds from K. foliatum were collected from an area in Bayannaoer City, Inner Mongolia, China. The soil in the area was strongly saline, the major cation in the soil was Na⁺, and the major anion was Cl⁻. K. foliatum seeds were treated with sublimate for 8 min and washed with sterilized dH₂O. The seeds were cultured in a growth chamber at 27°C until the beginning of germination. A mixture of composted sheep manure and soil at a ratio of 1:3 was mixed with vermiculite at a ratio of 5:1 to increase soil porosity. The soil mixtures were then transferred to nutritive pots. The germinating seeds were planted in the nutritive pots and allowed to grow for 4 months (25°C in daytime, 15°C at night, light cycle of 14 h/10 h, and 5000 lux light intensity). The seedlings were irrigated with 30 ml of tap water every 2 days during the growing period. All tests involved the use of 4-month-old seedlings that were treated with 0, 150, 200, 250, 300 and 400 mM NaCl.

Total RNA extraction and cDNA synthesis: Fourmonth-old seedlings were treated with NaCl for 72 h. After harvesting, freshly collected leaves were frozen in liquid nitrogen, and total RNA was extracted from the leaves with the SDS-LiCl method. mRNAs were reversetranscribed into cDNA with an M-MLV reverse transcriptase kit (Promega) for genetic identification and expression model analysis.

Identification of differentially expressed genes: Total RNA was extracted from *K. foliatum* leaves that were treated with 0 mM and 250 mM NaCl using TRIzol reagent (TransGen Biotech, China). The mRNAs were purified using magnetic oligo (dT) beads and fragmented into small strands. The fragments were used as templates to synthesize double-stranded cDNAs. The cDNAs were purified using AMPure XP beads, the purified cDNAs were ligated into sequencing adapters, and the ligated fragments were enriched by PCR for 18 cycles. Finally, the library was sequenced with an Illumina HiSeq 2500 platform.

To identify DEGs (differentially expressed genes), adapters, reads containing more than 10% unknown bases in raw reads and low-quality reads (more than half of the bases with a quality score of less than 5) were removed. Clean reads were assembled to obtain the unigene library, and the expression level of each gene was calculated by the RSEM tool (Leng *et al.*, 2014).

KfNCED1 gene cloning and bioinformatics analysis: According to the sequence of the $NCED_1$ gene from the transcriptome sequencing of *K. foliatum*, two primer pairs (*KfNCED*₁-F₁: 5'-TGACATGGTTGAGAAGGCTTTG-3', *KfNCED*₁-R₁: 5'-CACCTTATGCTTGCTTCAGTAA-3') were designed to amplify the full cDNA of *KfNCED*₁. The evolution of *KfNCED*₁ was analysed by MEGA5 software.

Semi-quantitative RT-PCR analysis: The primers *Kf28SrRNA*-F (5'-GCCGACCCTGATCTTCTGTGA-3') and *Kf28SrRNA*-R (5'-TACCCAAGTCAGA CGAA CGATT-3') were designed according to the conserved sequence of 28S rRNA for *K. foliatum* (Accession No. AY5566443.1) available in the NCBI database. The specific primers *KfNCED1*-F₂ (5'-ACCAGCGGGG AAGAGATT-3') and *KfNCED1*-R₂ (5'-TGTCGAGAC GCC AGTGAC-3') were designed based on the *KfNCED*₁ gene sequence.

Total RNA from *K. foliatum* subjected to NaCl for 72 h was used to synthesize first-strand cDNA with M-MLV reverse transcriptase (Promega). *KfNCED*₁ and the control (28S *rRNA*) were used to detect the expression levels via semi-quantitative RT-PCR. The amplification conditions were as follows: 94°C for 3 min; 94°C for 30 s, 63°C for 1 min, and 72°C for 1 min (26 cycles for 28S *rRNA*, 35 cycles for *KfNCED*₁); and 72°C for 10 min. PCRs were carried out with three biological repeats.

ABA content: Three hundred milligram samples of leaves were ground in liquid nitrogen. The powders were treated with 1.5 ml of extraction buffer (methanol: H₂O: methanoic acid=7.9:2:0.1) and kept at 4°C overnight. The extraction mixture was centrifuged at 4°C and 12 000 g for 15 min. The supernatants were collected, dried in nitrogen gas, and then dissolved in 2 ml of 0.1 M ammonia solution. Crude extracts were purified with a MAX column that was pretreated with 2 ml of methanol. After the supernatants were loaded onto the MAX column, the column was washed with 2 ml of 0.1 M ammonia solution and then 2 ml of methanol. ABA was eluted with 4 ml of methanol containing 1% formic acid. The eluent was dried in nitrogen gas, dissolved in 0.2 ml of methanol, and then filtered with a 0.2 µm nylon membrane. ABA was quantified by liquid chromatography-tandem mass spectrometry with three biological replicates.

Statistical analysis

The data determined in triplicate were visualized with Origin 8.6. Individual differences among means were determined by Duncan's test. Before ANOVA was performed, the data were checked for both homogeneity and normality of variance and were log-transformed to correct deviations from the assumptions when needed. Statistical analysis was conducted with SPSS 19.0 software.

Results

Bioinformatics analysis of $KfNCED_1$ **.** A cDNA fragment approximately 1500 bp in length was amplified by RT–PCR (Fig. 1) and found to encode 499 amino acid residues (Fig. 2). A comparison of the deduced amino acid sequences was performed with BLAST P amino acid sequence was mostly similar to 9'-cis-epoxycarotenoid dioxygenase $NCED_1$ from *Phaseolus vulgaris*, with a similarity of 72.9% (Fig. 3). The amino acid sequence clustered with $KfNCED_1$ by phylogenetic tree analysis (Fig. 4) indicating that $KfNCED_1$ had significant homology with $AiNCED_1$ (Fig. 4).

Expression of *KfNCED*₁**.** To test the expression level of *KfNCED*₁, semiquantitative RT–PCR was performed with *K. foliatum* leaves grown with different NaCl concentrations. After treatment with 200, 250 and 300 mM NaCl, the expression level of *KfNCED*₁ increased markedly; the highest expression was found in the leaves under 250 mM NaCl treatment (Fig. 5). The results suggested that NaCl treatment could induce an ABA content increase by increasing the expression of *KfNCED*₁ and indicated that *KfNCED*₁ may play an important role in salt resistance.

AAAACTGCAG	CTGCTGCTCT	TGAC <mark>ATG</mark> GTT	GAGAAGGCTT	TGAATTCGTT	TGAAAGTGAA
CAACAACTAC	CCAAAACCGC	TGACCCACGG	GTCCAAATTA	AGGGCAATTT	TGCCCCGGTA
TCCGAACAAC	CTGTAAAGAG	TAATCTCCCG	GTAACCGGGT	CAGTCCCGGA	TTGTATTCGG
GGCGTGTACG	TACGAAACGG	GGCGAACCCG	CTTTATGAGC	CGGTTGCCGG	TCACCATTTC
TTCGACGGAG	ACGGCATGAT	CCACGCCGTA	CAATTCGACT	CAGACGGGTC	AGTGAGCTAC
TCTTGCAGGT	TCACCCAAAC	GAACCGTTTT	GTTCAAGAGC	GGGCTTTGGG	TCGACCCATT
TTTCCTAAGG	CAATTGGGGA	GCTGCACGGC	CACTCCGGTA	TTGCACGGCT	CATGTTGTTC
TACTCCCGTG	CATTGTGCGG	TCTGCTTGAC	CAGACGCACG	GCATCGGGGT	TGCCAACGCC
GGCGTGGTCT	ACTTCAATGA	CCGACTCCTC	GCGATGTCGG	AAGATGACCT	GCCATACCAG
GTAAAGGTAA	CGCCGTCGGG	TGACTTAACC	ACCGTTGGCC	GGTACGACTT	TAACGGACAG
CTGTCATCCA	CCATGATCGC	CCACCCGAAA	GTCGACCCTG	TTTCGGGTGA	GATGTTCGGG
TTAAGCTACG	ACGTCGTAAA	AAAGCCGTAC	TTGAAGTACT	TCTGGTTTAA	ACCCGACGGC
ACCAAGTCAG	CCGACGTGGA	CATCCACCTC	GACGCCCCAA	CAATGGTCCA	TGACTTCGCA
ATGTCGGAAA	ACAACATCAT	CATCCCGGAC	TCTCAGGTGG	TGTTCAAGTT	GCAGGAGATG
ATCAGGGGTG	GGTCCCCCGT	GGTTTTCGAC	AAGTCGAAAA	CCTCGAGGTT	CGGGATTCTC
CCCAAGTACG	CGACCAGCGG	GGAAGAGATT	CAGTGGGTTG	ACGTGCCCGA	CTGTTTCTGC
TTCCACCTCT	GGAACGCGTG	GGAAGAAGCT	GAAACTGATG	AGATAGTTGT	AATTGGTTCC
TGCATGACTC	CTGCAGACTC	CATCTTTAAC	GAGAGTGACG	AGAATTTGTC	GAGCGTGCTG
TCCGAAATTC	GGCTCAACAC	CGTCACTGGC	GTCTCGACAC	GACGAGAAAT	CGTGTCGGAA
ACCAACCTAG	AGGCCGGTAT	GGTCAACAGG	AATAAACTCG	GCCGGAAAAC	GCAATACGCC
TACTTGGCCA	TTGCGGAGCC	GTGGCCTAAG	GTGTCGGGTT	TTGCAAAAGT	TGATCTCTTC
AGCGGTGAAG	TAAAAAGTT	CATGTACGGT	GAAAATAAAT	ATGGGGGTGA	GCCCTTGTTT
GTTCCCAACC	ATGTCAATTC	TGCACAAGAA	GATGATGGTT	ACATTCTCAC	TTTTGTCCAC
GACGAAATGA	ATTGGGAATC	GAAGCTTCAG	ATCGTCAATG	CCGTCAATTT	AGAACTCGTC
GCCACCGTCG	ACCTTCCGTC	TAGGGTGCCT	TACGGTTTCC	ATGGGACCTT	CATCAGTGCT
AATGACTTAC T	'GAAGCAAGC A <mark>T</mark> A	AA			

Fig. 1. The nucleotide acid sequence of $K_f NCED_1$ gene.

Analysis of the ABA content in *K. foliatum* leaves. ABA has been described as a stress hormone (Mehrotra *et al.*, 2014). NCED and ZEP catalyse a key step in ABA biosynthesis (Ng *et al.*, 2014). Therefore, the ABA contents of the leaves of *K. foliatum* were measured, and the results showed that ABA levels increased markedly after treatment with 150, 200 and 250 mM NaCl. Additionally, ABA levels decreased markedly after treatment with 300 mM NaCl, and the ABA content increased again under 400 mM NaCl (Fig. 6). After moderate NaCl treatment, the ABA content in leaves of *K. foliatum* significantly increased, and the ABA content was higher than that at other NaCl concentrations. Therefore, increased NaCl stress could reduce endogenous ABA biosynthesis.

Discussion

The world population is projected to increase by more than 2.4 billion by 2050; to feed this growing population, crop production must be increased by 70% by 2050 (Wani & Sah, 2014). Abiotic stresses affect plant growth and limit plant productivity (Bailey-Serres *et al.*, 2012). Salt is a major factor limiting plant production and quality worldwide. Halophytes are plant species that are tolerant to high salt and have developed strategies to survive and complete their life cycles in such a harsh environment. *K. foliatum*, a halophyte from the family Amaranthaceae, is resistant to salt. At present, there are few reports concerning the effects of salt stress on *K. foliatum*.

Phytohormone engineering can improve productivity and combat salt stress. Phytohormones are key regulators of stress responses. ABA is a central regulator of abiotic stress resistance in plants and enables plants to cope with different stresses. When environmental conditions are harsh, ABA in plants increases through biosynthesis. Then, ABA binds to its receptor to initiate signal transduction, which leads to a cellular response to stress (Ng *et al.*, 2014); therefore, ABA is also considered a stress hormone (Mehrotra *et al.*, 2014).

ABA biosynthesis occurs in two places: it starts in plastids and ends in the cytosol. The first step of ABA biosynthesis is the conversion of antheraxanthin and zeaxanthin to all-trans-violaxanthin, which is catalysed by zeaxanthin epoxidase. After that, all-trans-violaxanthin is converted to 9'-cis-neoxanthin or 9'-cis-violaxanthin. The enzymes involved in this reaction are still unknown (Seiler *et al.*, 2011). Then, the oxidative cleavage of 9'-cis-neoxanthin and 9'-cis-violaxanthin is catalysed by the enzyme NCED (9'-cis-epoxy carotenoid dioxygenase), which yields a C15 intermediate product called the C25 metabolite and xanthoxin (Tan *et al.*, 2003). Therefore, NCEDs are the key enzymes in ABA biosynthesis.

NCED is supposed to increase ABA content and improve stress tolerance in plants (Bang *et al.*, 2013). Transgenic crops that overexpressed *NCED*₁, a key ABA synthesis gene, exhibited improved tolerance to drought, as seen in tomato (Thompson *et al.*, 2000), tobacco (Qin & Zeevaart, 2002), bent grass (Aswath *et al.*, 2005) and petunia (Estrada-Melo *et al.*, 2015). In the present study, RT–PCR analysis revealed that *KfNCED*₁ was significantly induced by NaCl (Fig. 5).

In conclusion, we cloned the *NCED*1 gene from the halophyte *K. foliatum*, and the RT–PCR results revealed that $NCED_1$ expression in *K. foliatum* was NaCl dependent, which was similar to $NCED_1$ found in most plants. Furthermore, the results of ABA level analysis demonstrated that these levels were markedly affected by NaCl concentration. This finding concerning *KfNCED*₁ is highly advantageous for exploring the synthesis mechanisms of ABA and salt tolerance in the halophyte *K. foliatum*.

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1 1	AAAAC K T	TGCA A	AGCT	GCT(A	A	L	D D	ATG(M	V	GAG. E	AAG K	GCT A	TTG. L	AAT N	TCG S	TTT F	GAA. E	AGT S	GAA E	Q Q	Q	L	P P	AAA/ K	ACC(T	GCT A
82 28	GACCC D P	ACGO R	GTC V	CAA Q	ATT) I	AAG(K	GGC. G	AAT: N	FTT F	GCC A	CCG P	GTA V	TCC S	GAA E	CAA Q	CCT P	GTA V	AAG K	AGT. S	AAT N	CTC(L	CCG P	GTA. V	ACC(T	GGG G	TCA S
163 55	GTCCC V P	GGA1 D	TGT. C	ATT(I	CGG R	GGC(G	STG V	TAC(Y	GTA V	CGA R	AAC) N	GGG G	GCG. A	AAC N	CCG P	CTT L	TAT Y	GAG E	CCG P	GTT V	GCC(A	GGT G	CAC H	CATI H	FTC F	TTC F
244 82	GACGG D G	AGAC D	GGC. G	ATG M	ATC I	CACO H	SCC A	GTA(V	CAA Q	TTC F	GAC D	TCA S	GAC D	GGG G	TCA S	GTG. V	AGC S	TAC Y	тст S	TGC. C	AGG R	FTC.	ACC T	CAA Q	ACG: T	AAC N
325 109	CGTTT R F	TGTI V	CAA Q	GAG E	CGG R	GCT1 A	rTG L	GGT(G	CGA R	CCC. P	ATT I	TTT F	CCT. P	AAG K	GCA A	ATT I	GGG G	GAG E	CTG L	CAC H	GGC(CAC H	TCC S	GGT2 G	ATT I	GCA A
406 136	CGGCT R L	CATO M	TTG L	TTC: F	FAC Y	rcco	CGT R	GCA' A	TTG L	TGC	GGT G	CTG L	CTT L	GAC D	CAG. Q	ACG T	CAC H	GGC G	ATC I	GGG G	GTT(V	GCC. A	AAC N	GCC(A	GCC G	GTG V
487 163	GTCTA V Y	CTTC F	CAAT N	GAC	CGA R	CTCC L	CTC L	GCG2 A	ATG M	TCG S	GAA(E	GAT D	GAC D	CTG L	CCA P	TAC Y	CAG Q	GTA V	AAG K	GTA V	ACG(T	CCG P	TCG S	GGT(G	GAC' D	TTA L
568 190	ACCAC T T	CGTI V	GGC G	CGG R	FAC Y	GAC1 D	FTT.	AAC(N	GGA G	CAG Q	CTG L	TCA S	TCC. S	ACC T	ATG. M	ATC I	GCC A	CAC H	CCG P	AAA K	GTC	GAC D	CCT P	GTT: V	rcg s	GGT G
649 217	GAGAT E M	GTTC F	cece G	TTA L	AGC' S	TACO Y	GAC D	GTC	GTA V	AAA K	AAG K	CCG P	TAC Y	TTG L	AAG K	TAC Y	TTC F	TGG W	TTT. F	AAA K	CCC	GAC D	GGC. G	ACC/ T	AAG' K	TCA S
730 244	GCCGA A D	CGTO V	GAC. D	ATC I	CAC H	CTCC L	GAC D	GCC(A	CCA P	ACA. T	ATG M	GTC V	CAT H	GAC D	TTC F	GCA. A	ATG M	TCG S	GAA E	AAC. N	AACI N	ATC. I	ATC. I	ATC	CCG P	GAC D
811 271	TCTCA S Q	GGTO V	GTG V	TTCI F	AAG K	TTGC L	CAG Q	GAG	ATG M	ATC. I	AGG R	GGT G	GGG G	TCC S	CCC P	GTG V	GTT V	TTC F	GAC. D	AAG K	TCG2 S	AAA K	ACC T	TCG/ S	AGG R	TTC F
892 298	GGGAT G I	тсто	CCCC.	AAG K	FAC	GCG2 A	ACC.	AGC	GGG	GAA	GAG	ATT I	CAG	TGG W	GTT	GAC	GTG V	CCC P	GAC	TGT C	TTC	rgc C	TTC F	CAC	CTC	TGG W
973 325	AACGO N A	GTGG	GAA	GAA	GCT	GAAJ E	ACT T	GAT	GAG	ATA	GTT	GTA V	ATT I	GGI	TCC	TGC.	ATG. M	ACT T	CCT	GCA	GAC:	rcc.	ATC	TTT	AAC	GAG
1054	AGTGA	CGAG	- SAAT	TTG	rcg	AGCO	- STG V	CTG	rcc s	GAA	ATT	CGG	CTC.	AAC N	ACC	GTC.	ACT	GGC	GTC	TCG.	ACA	CGA	CGA	GAA	ATC	GTG
1135 379	TCGGA	AACO	CAAC	CTA	GAG	GCCC	GT.	ATG	GTC	AAC.	AGG	AAT.	- AAA K	CTC	GGC	CGG. R	AAA	ACG	CAA	TAC	GCC:	FAC V	TTG	GCCI	- ATT(GCG
1216 406	GAGCO	GTGG	SCCT.	AAG	GTG	TCGO	GT	TTT(GCA	AAA	GTT(GAT	CTC	TTC	AGC	GGT	GAA	GTA	AAA K	AAG K	TTC	- ATG	TAC	GGT	GAAJ	AAT
1297	AAATA K Y	TGGG	GGT	GAG	CCC	TTG1	TTT F	GTT	CCC	AAC	CAT(GTC	- AAT N	TCT	GCA	CAA	GAA	GAT	GAT	GGT	TAC	ATT	- CTC.	ACT:	- TTT(GTC
1378	CACGA	CGAA	ATG.	AAT	rGG	GAAT	rCG.	AAG	CTT	CAG	ATC	GTC	AAT	GCC	GTC.	× AAT N	TTA	GAA	сто	GTC	GCC	ACC	GTC	GAC	CTT	CCG
1459 487	TCTAG S R	GGTO V	CCT P	TAC	G	TTC(F	CAT	GGG2 G	ACC T	TTC. F	ATC.	AGT S	GCT. A	AAT N	GAC	TTA	CTG. L	AAG K	CAA Q	GCA A	TAA *	•	•	2	-	-

Fig. 2. The deduced amino acid sequence of $KfNCED_1$ gene.

А	:	MPSSA <mark>S</mark>	NTWFNAT	' <mark>lps</mark> pp	FKDI	P <mark>S</mark> TS <mark>S</mark>	-P <mark>T</mark> NL	LPI	I <mark>rk</mark> tss	S <mark>N</mark> T <mark>I</mark> I	C <mark>SLQ</mark>	:	48
В	:	MPLPAS	NTCF <mark>NT</mark> T	' <mark>lps</mark> p-	FKDI	P <mark>S</mark> TS <mark>S</mark>	-P <mark>T</mark> TL	LLPRN	I <mark>KK</mark> T <mark>S</mark> SS	S <mark>N</mark> I <mark>I</mark> I	S <mark>SLQ</mark>	:	49
С	:	MPSTA <mark>S</mark>	NTF FNT T	LPSP-	FKDI	P <mark>S</mark> TS <mark>S</mark>	-PITL	LPI	KKR <mark>S</mark> SS	S <mark>n</mark> tit	'S <mark>SLQ</mark>	:	47
D	:	MAAT <mark>S</mark>	NTWINTK	LPS <mark>SC</mark>	SSLKG-AS	C <mark>S</mark> PQ <mark>T</mark>	PS <mark>S</mark> FT	MRSSN	I <mark>kr</mark> r <mark>t</mark> no	C <mark>n</mark> tik	(C <mark>SLQ</mark>	:	53
Е	:	MATAS <mark>S</mark>	SN <mark>W</mark> GVVT	SNKPK	FS	- <mark>s</mark> skk	SQ	FHF	'VNS <mark>S</mark> LÇ	2LP <mark>L</mark> I	JD <mark>S</mark> PK	:	43
F	:							N	IGSEKKE	E <mark>n</mark> g <mark>v</mark> i	LE <mark>VE</mark>	:	15
G	:	MPSPA <mark>S</mark>	NTWINT	' <mark>lps</mark> sc	SS-PFKDI	A <mark>S</mark> TS <mark>S</mark>	SP <mark>T</mark> TL	LPFKK	(<mark>r</mark> ss <mark>s</mark> ni	r <mark>n</mark> tit	C <mark>SLQ</mark>	:	54
Η	:	MASQAPI <mark>S</mark>	NTWINTK	LS <mark>S</mark> SS	SFSKELGS	lnst <mark>t</mark>	TI <mark>S</mark> LS	FKKRS	STNTKKI	P <mark>n</mark> nis	C <mark>SLQ</mark>	:	57
Ι	:											:	-
J	:	MATSATTA <mark>S</mark>	NTWINTK	L <mark>AS</mark> SS	YSSPFKDI	SLNSN	<mark>s</mark> ns	<mark>I</mark> TLNK	K <mark>K</mark> NS <mark>T</mark> SF	k <mark>n</mark> ris	C <mark>SLQ</mark>	:	56
Κ	:	MASSISSSSP	K <mark>T</mark> LL <mark>NT</mark> T	' <mark>lps</mark> p-		P <mark>T</mark> SS <mark>S</mark>	-P <mark>T</mark> TS	IAI	- <mark>KK</mark> KP	- <mark>N</mark> API	'T <mark>SLQ</mark>	:	46
L	:	MAATS <mark>S</mark>	SI <mark>W</mark> AVT-	KPK	IS	- <mark>S</mark> SDN'	TLNWP	NKTQÇ	ΩI <mark>K</mark> S <mark>S</mark> Lζ	2LP <mark>L</mark> I	JD <mark>S</mark> PK	:	45
М	:	MAAT <mark>S</mark>	NTWINTK	LPS <mark>SC</mark>	SSLKG-AS	C <mark>S</mark> PQ <mark>T</mark>	PS <mark>S</mark> FT	IRS-N	I <mark>KR</mark> RSNY	(<mark>n</mark> kik	(C <mark>SLQ</mark>	:	52
Ν	:	MAAT <mark>S</mark>	NTWINTK	LPS SC	SSLKG-AS	C <mark>S</mark> PQ <mark>T</mark>	PS <mark>S</mark> FT	IRS-N	I <mark>KR</mark> RSNY	(<mark>n</mark> kik	(C <mark>SLQ</mark>	:	52
0	:	MAAT <mark>S</mark>	NTWINTK	LPS SC	SSLKG-AS	C <mark>S</mark> PQ <mark>T</mark>	PS <mark>S</mark> FT	IRS-N	I <mark>KR</mark> RSNY	(<mark>n</mark> kik	(C <mark>SLQ</mark>	:	52
Ρ	:	MASSAA <mark>T</mark>	NSWINTT	' <mark>lps</mark> sc	SS-PFKDI	N <mark>S</mark> TS <mark>S</mark>	-P <mark>T</mark> TS	ITI	J <mark>KK</mark> R <mark>S</mark> SI	P <mark>N</mark> T <mark>I</mark> I	C <mark>SLQ</mark>	:	52
				•							_		
А	:	T-LHFPKQYQP	TSTSTST	ATTTT	PTPIKTTI	'I	-TTTT	PPREI	NPLSD	TNQPI	'bők <mark>m</mark>	:	102
В	:	T-IHFPKQYHP	TSTSTPT	TTV	PTPIKTTS	'T'	TTTTT	PSREI	NPLSS	CNQPI	'bők <mark>m</mark>	:	102
C	:	T-LHFPKQYHF	TSTPTPT	PTTTI	PTPIKTTS	TSTST	TTTTT	PSREI	'NPLSA'	ľNQPI	JPQKW	:	106
D	:	T-LHFPKQLQF	T T T	TTTTT	KPSTKSIE	°T			F	KENKI	'AND <mark>W</mark>	:	89
E	:	KSST <mark>K</mark> TCQL	QKKI <mark>I</mark> SE	PKESN	TKPFSREN	IK				LSK	(P-Q <mark>w</mark>	:	/9
F,	:											:	105
G	:	T-LHYPKQYQP	TSTSTT	T	PIPIKPIII	T. — — — — .	1.1.1.1.1.1	PHREI	'KPLSD'I	ĽKQPE	PQKW	:	105
H				/	DIDITIOTZATATE	- D			TITIDI	ZOTIOT			100
	:	.ITHF. <mark>bk</mark> ðaðf	PSCPTT	K'I''I''I''I'	PTKGKNNK	(P			HHPF	KQHSE	°QKN <mark>W</mark>	:	100
II	:		PSCPTTI		PTKGKNNK	(P)			HHPP	KQHSE	QKN <mark>W</mark> 	:	100
I J V	:	TTLPFPKQYQF	PSCPTTT KPKPKPT	K111111 TTTTT	PTKGKNNK IIPTKETK 	(P) (P)	 	 	HHPF SETKPF	KQHSE KQQQF 7	QKNW NQKW	::	100 - 106
I J K L	::	T-LHFPKQYQF TTLPFPKQYQF T-LHFPKQYPF	PSCPTT KPKPKPT TTT		PTKGKNNK IIPTKETK KETK PKDNGKRS	(P) (P) (T)		 -NPPE	HHPF SETKPF 	(QHSE (QQQF <i>P</i> 	QKNW NQKW AEKW	::	100 - 106 69 84
I J K L M	::	T-LHFPKQYQF TTLPFPKQYQF T-LHFPKQYPF KTTPLPKKTSV	PSCPTT KPKPKPT TTT VPKEVRK	KTTTTT TTTTTT PILTQ	PTKGKNNF IIPTKETF KETF PKDNGKRS PTKENKT2	(P (P) (T) (L)	 	 -NPPE 	HHPP SETKPP 	(QHSE (QQQK R KSQ	PQKNW NQKW AEKW PFQW	::	100 - 106 69 84 92
I J K L M	:::::::::::::::::::::::::::::::::::::::	T-LHFPKQYQF TTLPFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF	PSCPTT KPKPKPT TTT VPKEVRK TTT	KTTTTT TTTTTT PPILTQ TTKPK	PTKGKNNF IIPTKETF KETF PKDNGKRS PTKENKTA PTKENKTA	(P (P) (T) (ST) (ST)				(QHSE (QQQF KSQ [TAAE	°QKN₩ MQK₩ AEK₩ PFQ₩ PVKDL	::	100 - 106 69 84 92 92
I J K L M N O	::	T-LHFPKQYQF TTLPFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF	PSCPTT KPKPKPT TTT VPKEVRK TTT TTT	KTTTTT TTTTTT PILTQ TTKPK TTKPK	PTKGKNNN IIPTKETK KETK PKDNGKRS PTKENKTA PTKENKTA PTKENKTA	(P (P (T (ST (ST) (ST)		 -NPPE 		(QHSE (QQQF KSQ (TAAE (TAAE (TAAE)	YQKNW NQKW AEKW YFQW YKDL YVKDL	::	100 - 106 69 84 92 92 88
I J K L M O P		T-LHFPKQYQF TTLPFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF	PSCPTT KPKPKP TTT VPKEVRK TTT TTT PSTTTT	KTTTTT TTTTTT PILTQ TTKPK TTKPK TTKPK	PTKGKNNN KETK IIPTKETK PKDNGKRS PTKENKTA PTKENKTA PTKENKTA TKTHC	(P (T) (ST) (ST) (ST) (ST) (P)				KQHSE KQQQF KSQ FTAAE FTAAE FTAAE STKPT	YQKNW NQKW AEKW YFQW YKDL YVKDL YVKDW PORW	: : : : : : : : : : : : : : : : : : : :	100 - 106 69 84 92 92 88 89
I J K L M O P		T-LHFPKQYQF TTLPFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF	PSCPTT KPKPKP TTT VPKEVRK TTT TTT PSTTTTT	KTTTTT TTTTTT PILTQ TTKPK TTKPK	PTKGKNNN KETK KETK PKDNGKRS PTKENKTA PTKENKTA PTKENKTA TKTHÇ	(P (T) (T) (ST) (ST				KQHSE KQQQF FTAAE FTAAE FTAAE DTKPI	PQKNW AEKW PFQW VKDL VKDL VKDL PQRW	:::::::::::::::::::::::::::::::::::::::	100 - 106 69 84 92 92 88 89
I J K L M O P		T-LHFPKQYQF TTLPFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LPFPKQYQF	PSCPTT KPKPKP TTT VPKEVRK TTT PSTTTT	KTTTT TTTTTT PILTQ TTKPK TTKPK TTKPK	PTKGKNNN KETK KETK PKDNGKRS PTKENKTA PTKENKTA PTKENKTA TKTHQ	(P (T) (ST) (ST) (ST) (ST) (S)		 		(QHSE (QQQF 	PQKNW NQKW NAEKW PFQW PVKDL PVKDL PVKDW PQRW		100 - 106 69 84 92 92 88 89
I J K L M N O P A		T-LHFPKQYQF T-LHFPKQYQF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LPFPKQYQF	PSCPTT KPKPKP TTT VPKEVRK TTT TTT PSTTTTT	TTTTT TTTTT TTTTT TTKPK TTKPK TTKPK	PTKGKNNN KETK PTKENKTA PTKENKTA PTKENKTA PTKENKTA TKTHQ KHPLPKTA	IP IP II II III III III IIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	 	 		(QHSE (QQQF FTAAE TTAAE TTAAE DTKPI	YQKNW AEKW PFQW YVKDL YVKDL YVKDW PQRW		100 - 106 69 84 92 92 88 89 161
I J K L M N O P A B		T-LHFPKQYQF T-LHFPKQYQF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LPFPKQYQF	PSCPTT KPKPKPKPT TTT VPKEVRK TTT PSTTTTT PSTTTTT	KTTTT TTTTT TTTTT TTKPK TTKPK TTKPK SHER VSHER	PTKGKNNP KETP PKDNGKRS PTKENKTA PTKENKTA PTKENKTA TKTHQ KHPLPKTA KHPLPKTA	IP IP II II III IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	 IAGNF IAGNF			(QHSE (QQQF KSQ TTAAE TTAAE TTAAE DTKPI QG <mark>LP</mark> (QG <mark>LP</mark> (YQKNW AAEKW YPFQW YVKDL YVKDU YVKDW YQRW VGKI		100 - 106 69 84 92 92 88 89 161 161
I J K L M N O P A B C		T-LHFPKQYQF T-LHFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LFFPKQYQF NFLQKAAATAI NFLQKAAATAI	PSCPTT KPKPKPKP TTT VPKEVRK TTT PSTTTT PSTTTTT DLVETAI	KTTTT TTTTT TTTTT TTKPK TTKPK TTKPK VSHER VSHER	PTKGKNNN KETK IIPTKETK PKDNGKRS PTKENKTA PTKENKTA PTKENKTA KHPLPKTA KHPLPKTA KHPLPKTA	IP IP II II III IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		 		(QHSE (QQQF FTAAE TTAAE TTAAE TTAAE DTKPI QGLP(QGLP(QGLP(YQKNW AEKW PFQW YVKDL YVKDL YVKDW PQRW VGKI VGKI		100 - 106 69 84 92 92 88 89 161 161
I J K L M N O P A B C D		T-LHFPKQYQF T-LHFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LPFPKQYQF NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NLIQKAASMAI	PSCPTT KPKPKP TTT VPKEVRK TTT PSTTTT PSTTTTT DLVETAI DLVETAI DLVETAI DLVETAI DFAESAI	KTTTT TTTTT PILTQ TTKPK TTKPK TTKPK TTKPK VSHER VSHER ASHER	PTKGKNNN KETK IIPTKETK PKDNGKRS PTKENKTA PTKENKTA PTKENKTA CHPLPKTA KHPLPKTA KHPLPKTA KHPLPKTA	IP IP IP II II III III III IIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		 	EHAAD EHAAD EHAAD EHAAD EHAAD EHAYD EHAYD	(QHSE (QQQF KSC TTAAE TTAAE TTAAE DTKPI QGLPV QGLPV QGLPV QNLPI	PQKNW PQKNW PFQW PFQW PVKDL PVKDL PQRW PQRW VGKI AGKI		100 - 106 69 84 92 92 88 89 161 161 165 148
I J K L M N O P A B C D E		T-LHFPKQYQF T-LHFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LPFPKQYQF NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI	PSCPTT KPKPKPT TTT VPKEVRK TTT PSTTTT PSTTTTT DLVETAI DLVETAI DFAESAI DMVEKVI	KTTTT TTTTT TTTTT TTKPK TTKPK TTKPK TTKPK SHER VSHER ASHER NTREC	PTKGKNNN 	IP IP II II III III IIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	IAGNF IAGNF IAGNF IAGNF IAGNF			(QHSE (QQQF 	YQKNW AEKW AEKW YFQW YKDL YKDL YKDU YCKI YQKI YGKI AGKI YGAI		100 - 106 69 84 92 92 88 89 161 161 165 148 138
I J K L M N O P A B C D E F		T-LHFPKQYQF T-LHFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LFFPKQYQF NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NLIQKAAAMAI NLIQKAAAMAI	PSCPTT KPKPKPKP TTT VPKEVRK TTT PSTTTT PSTTTTT DLVETAI DLVETAI DFAESAI DFAESAI	KTTTT TTTTT TTTTT TTKPK TTKPK TTKPK TTKPK VSHER VSHER ASHER NTREC VKLFY	PTKGKNNN KETK IIPTKETK PKDNGKRS PTKENKTA PTKENKTA PTKENKTA PTKENKTA KHPLPKTA KHPLPKTA KHPLPKTA KHPLPKTA CSSLPHH-	IP IP IP II III IIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		 		(QHSE (QQQF FTAAE TTAAE TTAAE TTAAE TTAAE TTAAE TTAAE QGLP QGLP QGLP QGLP QGLP (QLP (CLT)	YQKNW AEKW AEKW YFQW YKDL YKDL YKDW PQRW YGKI AGKI AGKI YGKI AGKL YGAI		100 - 106 69 84 92 92 88 89 161 161 165 148 138 71
I J K L M N O P A B C D E F G		T-LHFPKQYQF T-LHFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LPFPKQYQF NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NPIQKVAAAAI KPSNGFTSKAV	PSCPTTI KPKPKPRPI TTT VPKEVRK TTT PSTTTTI PSTTTTI DLVETAI DLVETAI DFAESAI DMVEKVI ULLEKII	KTTTT TTTTT TTTTT TTKPK TTKPK TTKPK TTKPK SHER VSHER ASHER NTREC VKLFY VSHES	PTKGKNNN KETK IIPTKETK PKDNGKRS PTKENKTA PTKENKTA PTKENKTA PTKENKTA CHPLPKTA KHPLPKTA KHPLPKTA CSLPHH- KHPLPKTA	IP IP IP II II		 		(QHSE (QQQF 	PQKNW AEKW PFQW PVKDL VKDL VKDW PQRW VGKI AGKI TGAI QGHL VGKI		100 - 106 69 84 92 88 89 161 161 165 148 138 71 164
I J K L M N O P A B C D E F G H		T-LHFPKQYQF T-LHFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LPFPKQYQF NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NPIQKVAAAAI KPSNGFTSKAV NFLQKAAATGI NFLQMAAAKAI	PSCPTT KPKPKPT TTT VPKEVRK TTT 	KTTTT TTTTT TTTTT TTKPK TTKPK TTKPK TTKPK SHER ASHER ASHER NTREC VKLFY VSHES VSHER	PTKGKNNN KETN IIPTKETK PKDNGKRS PTKENKTA PTKENKTA PTKENKTA PTKENKTA CHPLPKTA KHPLPKTA KHPLPKTA CSLPHH- KHPLPKTA KHPLPKTA	IP IP IP II II II III III IIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF			(QHSE (QQQF KSQ TTAAE TTAAE TTAAE TTAAE TTAAE TTAAE QGLP QGLP QGLP QGLP QGLP QGLP QGLP QGLP	YQKNW AEKW PFQW YKDL YKDL YKDW PQRW VGKI VGKI AGKI YGKI YGKI YGKI		100 - 106 69 84 92 92 88 89 161 165 148 138 71 164 159
I J K L M N O P A B C D E F G H I		T-LHFPKQYQF T-LHFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LFFPKQYQF MFLQKAAATAI NFLQKAAATAI NFLQKAAATAI KPSNGFTSKAV NFLQKAAATGI NFLQMAAAKAI KTAAAAI	PSCPTTI KPKPKPKPI TTT VPKEVRK TTI TTI PSTTTTI PSTTTTI DLVETAI DLVETAI DFAESAI DFAESAI DMVEKVI DLLEKII DMVETAI DLVETII DMVETAI	KTTTT TTTTT TTTTT TTKPK TTKPK TTKPK TTKPK K SHER NSHER VSHER VSHER VKLFY VSHES VSHER	PTKGKNNN KETK IIPTKETK PKDNGKRS PTKENKTA PTKENKTA PTKENKTA PTKENKTA COMPLENTA KHPLENTA KHPLENTA COMPLENTA KHPLENTA COMPLENTA COMPLENTA	IP IP IP II II III IIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF			(QHSE (QQQF KSQ TTAAE TTAAE TTAAE TTAAE TTAAE QGLP QGLP QGLP QGLP QGLP QGLP QGLP QGLP	PQKNW AEKW PFQW PVKDL VKDL VKDW PQRW VGKI VGKI AGKL VGKI QGHL VGKI TGSV		100 - 106 69 84 92 88 89 161 161 165 148 138 71 164 159 55
IIJKLMNOP ABCDEFGHIJ		T-LHFPKQYQF T-LHFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LPFPKQYQF NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NFIQKVAAAAI KPSNGFTSKAV NFLQKAAATGI NFLQMAAAKAI KTAAAAI	PSCPTTI KPKPKPR TTT VPKEVRK TTI TTI PSTTTTI PSTTTTI DLVETAI DLVETAI DLVETAI DMVEKVI DLLEKII DMVEKII DMVETAI DVETAI DVETAI	KTTTT TTTTT TTTTT TTKPK TTKPK TTKPK TTKPK TTKPK K SHER ASHER ASHER NTREC VKLFY VSHES VSHER NSFES I TQER	PTKGKNNN KETK IIPTKETK PKDNGKRS PTKENKTA PTKENKTA PTKENKTA PTKENKTA CHPLPKTA KHPLPKTA CONSLPHH- KHPLPKTA KHPLPKTA SQLPKTA KHPLPKTA	IP IP IP II	IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF	 		(QHSE (QQQF 	PQKNW PQKNW AEKW PFQW PVKDL PVKDL PVKDW PQRW VGKI VGKI VGKI VGKI VGKI TGKI TGKI		100 - 106 69 84 92 88 89 161 165 148 138 71 164 159 55 165
IIJKLMNOP ABCDEFGHIJK		T-LHFPKQYQF T-LHFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LPFPKQYQF NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NFLQMAAAKAI KTAAAAI NLFQKAAATAI	PSCPTTI KPKPKPKPI TTT VPKEVRK TTI PSTTTTI PSTTTTI DLVETAI DFAESAI DMVEKVI DLLEKII DMVEKAI DLVETTI DLVETTI DVETTI	KTTTT TTTTT TTTTT TTTTT TTKPK TTKPK TTKPK TTKPK TTKPK SHER VSHER ASHER NTREC VKLFY VSHER NSFES ITQER VSHER	PTKGKNNN KETK IIPTKETK PKDNGKRS PTKENKTA PTKENKTA PTKENKTA PTKENKTA CHPLPKTA KHPLPKTA KHPLPKTA CSLPHH- KHPLPKTA SQLPKTA KHPLPKTA QTPLPKTA	IP IP IP II II II II III III	I AGNF I AGNF			(QHSE (QQQF (QQQF 	PQKNW AEKW PFQW VKDL VKDL VKDW PQRW VGKI VGKI AGKI VGKI TGSV TGKI TGSV TGKI		100 - 106 69 84 92 92 88 89 161 165 148 138 71 164 159 55 128
IIJKLMNOP ABCDEFGHIJKL		T-LHFPKQYQF T-LHFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LFFPKQYQF T-LFFPKQYQF NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NFLQKAAATGI NFLQMAAAKAI KTAAAAI NLFQKAAATAI NLFQKAAATAI	PSCPTTI KPKPKPR TTT VPKEVRK TTT PSTTTTT PSTTTTT DLVETAI DLVETAI DLVETAI DLVETAI DMVEKAI DMVETAI DMVETAI DMVETAI DMVETAI DMVETAI	KTTTT TTTTT TTTTT TTKPK TTKPK TTKPK TTKPK K SHER VSHER NTREC VKLFY VSHES VSHER NSFES ITQER VSHER NSFES	PTKGKNNN KETN IIPTKETN PKDNGKRS PTKENKTA PTKENKTA PTKENKTA PTKENKTA COMPLENTA KHPLENTA KHPLENTA KHPLENTA KHPLENTA KHPLENTA SEQOLENTA KHPLENTA SEQOLENTA SEMPLENTA	IP IP IP II	IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF			(QHSE (QQQF 	PQKNW AEKW PFQW PVKDL PVKDL PVKDW PQRW VGKI VGKI VGKI VGKI VGKI VGKI TGSV TGKI TGSV TGKI		100 - 106 69 84 92 92 88 89 161 161 165 148 138 71 164 159 55 128 143
IIJKLMNOP ABCDEFGHIJKLM		T-LHFPKQYQF T-LHFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LFPFKQYQF NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NFLQKAAATGI NFLQMAAAKAI KTAAAAI NFLQKAAATAI NLFQKAAATAI NLFQKAAATAI NLFQKAAATAI	PSCPTTI KPKPKPRPI TTT VPKEVRK TTT PSTTTTI PSTTTTTI DLVETAI DLVETAI DLVETAI DAVEKVI DLLEKII DMVEKAI DLVETTI DMVEKAI DLVETTI DMVEKAI DFVETTI DMVEKAI	KTTTT TTTTT TTTTT TTTTT TTKPK TTKPK TTKPK TTKPK TTKPK SHER VSHER NTREC VSHER NSHES VSHER NSFES ITQER NSHES NSHES ASHER	PTKGKNNN KETK IIPTKETK PKDNGKRS PTKENKTA PTKENKTA PTKENKTA PTKENKTA CHPLPKTA KHPLPKTA CHPLPKTA CHPLPKTA CHPLPKTA CHPLPKTA CHPLPKTA CHPLPKTA CHPLPKTA CHPLPKTA CHPLPKTA	IP IP IP II				<pre><qhse </qhse </pre>	PQKNW PQKNW AEKW PFQW PVKDL PVKDL PVKDW PQRW VGKI VGKI VGKI VGKI TGAI TGKI TGKI AGKI AGKI		100 - 106 69 84 92 88 89 161 165 148 138 71 164 159 55 128 143 151
IIJKLMNOP ABCDEFGHIJKLMN		T-LHFPKQYQF T-LHFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LPFPKQYQF NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NFLQMAAAKAI KTAAAAI NLFQKAAATAI NLFQKAAATAI NLFQKAAATAI NLFQKAAATAI NLFQKAAATAI NLFQKAAATAI	PSCPTTI KPKPKPKPI TTT VPKEVRK TTI PSTTTTI PSTTTTI DLVETAI DLVETAI DFAESAI DWVEKAI DLLEKII DVETTI DVETTI DVETTI DVETAI DVETAI DFVETTI DWVEKAI DFAESAI	KTTTT TTTTT TTTTT TTTTT TTKPK TTKPK TTKPK TTKPK TTKPK SHER VSHER ASHER NTREC VKLFY VSHES VSHER NSFES ITQER NSFES ITQER NSHES ASHER ASHER	PTKGKNNN KETK IIPTKETK PKDNGKRS PTKENKTA PTKENKTA PTKENKTA PTKENKTA CHPLPKTA KHPLPKTA KHPLPKTA CHPLPKTA KHPLPKTA CULPKTA CHPLPKTA QHPLPKTA QHPLPKTA	IP IP IP II	IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF		HHPP PSETKPP 	<pre><qhse <qqqk <qqqk <p <p <p <p <p <p < < < < < < < < < <</p </p </p </p </p </p </qqqk </qqqk </qhse </pre>	PQKNW AEKW PFQW PVKDL VKDL VKDW PQRW VGKI VGKI AGKI TGAI TGAI TGKI TGKI TGKI AGKI AGKI AGKI		100 - 106 69 84 92 88 89 161 161 165 148 138 71 164 159 55 165 128 143 151 151
IIJKLMNOP ABCDEFGHIJKLMNO		T-LHFPKQYQF T-LHFPKQYQF T-LHFPKQYPF KTTPLPKKTSV T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LHFPKQLQF T-LPFPKQYQF T-LPFPKQYQF NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NFLQKAAATAI NFLQMAAAKAI KTAAAAI NLFQKAAATAI NLFQKAAATAI NLFQKAAATAI NLFQKAAATAI NLFQKAAATAI NLFQKAAATAI NLFQKAAATAI	PSCPTTI KPKPKPRPI TTT VPKEVRK TTT PSTTTTI PSTTTTI DLVETAI DLVETAI DLVETAI DKVETAI DMVEKAI DLVETTI DMVETAI DFVETTI DMVEKAI DFVETTI DMVEKAI DFAESAI DFAESAI DFAESAI	KTTTT TTTTT TTTTT TTTTT TTKPK TTKPK TTKPK TTKPK SHER VSHER ASHER NTREC VKLFY VSHES VSHES ITQER NSFES ITQER NSFES ASHER ASHER ASHER	PTKGKNNN KETN IIPTKETN PKDNGKRS PTKENKTA PTKENKTA PTKENKTA PTKENKTA PTKENKTA COMPLENTA COMPLENTA COMPLENTA CHELENTA CHELENTA CHELENTA CHELENTA CHELENTA CHELENTA CHELENTA CHELENTA CHELENTA CHELENTA CHELENTA CHELENTA	IP IP IP II II II III III IIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF IAGNF		HHPP SETKPP 	<pre><qhse <qqqf <</qqqf </qhse </pre>	PQKNW AEKW PFQW PVKDL VKDL VKDW PQRW VGKI VGKI VGKI VGKI VGKI VGKI TGSV TGKI TGSV TGKI AGKI AGKI AGKL AGXX		100 - 106 69 84 92 92 88 89 161 161 165 148 138 71 164 159 55 128 143 151 151 147

А	:	PKCIDGVYVRNGANPLYEPVAGHHFFDGDGMVHAVKFT-NGAASYACRFTETQRLSQEKS	:	220
В	:	PKCIDGVYVRNGANPLYEPVAGHHFFDGDGMVHAVKFT-NGSASYACRFTETQRLTQEKS	:	220
С	:	PKCIDGVYVRNGANPLYEPVAGHHFFDGDGMVHAVKFT-NGSASYSCRFTETQRLTQEKS	:	224
D	:	PECIDGVYVRNGANPMYEPLAGHHLFDGDGMVHALKFH-NGSASYSCRFTETNRLVQEKS	:	207
Е	:	PECIRGVYVRNGANPLYEPVAGHHFFDGDGMIHAVQFNSDG <mark>SASY</mark> SCRFTETNRFVQERA	:	198
F	:	PDCLNGEFVRVGPNPKFSPVAGYHWFDGDGMIHGLRIK-DGKASYVSRFVKTSRFKQEEY	:	130
G	:	PKCIDGVYVRNGANPLYEPVAGHHFFDGDGMVHAVKFT-NGAASYACRFTETQRLAQEKS	:	223
Η	:	PKCIEGVYVRNGANPLYEPSAGHHLFDGDGMVHAVRFK-DGSASYACRFTETQRLVQEKE	:	218
Ι	:	PDCIRGVYVRNGANPLYEPVAGHHFFDGDGMIHAVQFDSDGSVSYSCRFTQTNRFVQERA	:	115
J	:	PKCIDGVYLRNGANPHYEPVAGHHFFDGDGMVHAVKFT-NGSVSYSCRFTETHRLAQEKA	:	224
Κ	:	PKCIDGVYVRNGANPLYEPLAGHHFFDGDGMVHAVKFH-NG <mark>SASY</mark> AXXXXXXRLAQEKA	:	187
L	:	PECIRGVYVRNGANPLYEPIAGHHFFDGDGMIHSVQFNNDG <mark>SASY</mark> SCRFTETNRFVQEKK	:	203
М	:	PECIDGVYVRNGANPMYEPLAGHHLFDGDGMVHAVKFH-NGSASYSCRFTETNRLVQEKS	:	210
Ν	:	PECIDGVYVRNGANPMYEPLAGHHLFDGDGMVHAVKFH-NGSASYSCRFTETNRLVQEKS	:	210
0	:	-XX <mark>IDGVYVRNGANPMYEPLAGH</mark> HLFDGDGMVH <mark>AVKF</mark> H-NG <mark>SASY</mark> SCRFTETNRLVQEKS	:	205
Ρ	:	PKCIEGVYVRNGANPLYEPVAGHHFFDGDGMVHAVKFK-DGSASYACRFTETQRLVQEKA	:	207
А	:	LGRPVFPKAIGELHGHSGIARLLLFYARGLFGLVDGSQGMGVANAGLVYFNNHLLAMSED	:	280
В	:	LGRPVFPKAIGELHGHSGIARLLLFYARGLFGLVDGSHGMGVANAGLVYFNNHLLAMSED	:	280
С	:	LGRPVFPKAIGELHGHSGIARLLLFYARGLFGLVDGSHGMGVANAGLVYFNNHLLAMSED	:	284
D	:	LGKPVFPKAIGELHGHSGIARLLLFYARGLFGLVDGKNGMGVANAGLVYFNNHLLAMSED	:	267
Ε	:	LGRPIFPKAIGELHGHTGIGRLLLFYSRALFGLLDQTNGIGVANAGVVYFNNRLLAMSED	:	258
F	:	FNGSKFMK-IGDLKGLFGLLMVNMQMLRAKLKILDVSYGHGTANTALVYHHQKLLALSEG	:	189
G	:	LGRPVFPKAIGELHGHSGIARLLLFYARSLFQLVDGSHGMGVANAGLVYFNNHLLAMSED	:	283
Η	:	LGKPVFPKAIGELHGHSGIARLLLFYARGLFGLVDGNNGMGVANAGLVYFNNHLLAMSED	:	278
Ι	:	LGRPIFPKAIGELHGHSGIARLMLFYSRALCGLLDQTHGIGVANAGVVYFNDRLLAMSED	:	175
J	:	LGRPVFPKAIGELHGHSGIARLMLYYARSLFNLVDGSHGMGVANAGLVYFNNRLLAMSED	:	284
Κ	:	LGRPIFPKAIGELHGHSGIARLLLFYARSLFGLVDGSHGMGVANAGLVYFNNRLLAMSED	:	247
L	:	LGRPIFPKAIGELHGHSGIARLLLFYSRALFGLLDQTNGIGVANAGVVFFNNRLLAMSED	:	263
М	:	LGKPVFPKAIGELHGHSGIARLLLFYARGLFGIVDGKNGMGVANAGLVYFNNRLLAMSED	:	270
Ν	:	LGKPVFPKAIGELHGHSGIARLLLFYARGLFGIVDGKNGMGVANAGLVYFNNRLLAMSED	:	270
0	:	LGKPVFPKAIGELHGHSGIARLLLFYARGLFGLVDGKNGMGVANAGLVYFNNRLLAMSED	:	265
Ρ	:	LGRPVFPKAIGELHGHSGIARLLLFYARSLFGLLDGTHGMGVANAGLVYFNNHLLAMSED	:	267
_				
A	:	DLPYHVRITPNGDLTTVGRYDFNGQLNSTMIAHPKLDPVDGDLHALSYDVIQKPYLKYFR	:	340
В	:	DLPYHVRITPNGDLTTVGRYDFNGQLNSTMIAHPKLDPVDGDLHALSYDVIQKPYLKYFR	:	340
C	:	DLPYHVRITPNGDLSTVGRYDFNGQLNSTMIAHPKLDPVHGDLHALSYDVIQKPYLKYFR	:	344
D	:	DLPYHVRVTPSGDLKTVGRYDFNGQLKSTMIAHPKVDPVSGELFALSYDVVSKPYLKYFK	:	327
E	:	DVPYQVRVTPSGDLKTVGRYDFNGQLKSTMIAHPKVDPVSGEMFALSYDVVKRPYLKYFW	:	318
F.	:	DKPYAIRVFEDGDLQTLGMLDYDKRLGHNFTAHPKVDPFTGEMFTFGYSHT-APYVTYRV	:	248
G	:	DLPYHVRITSNGDLTTVGRYDFNGQLNSTMIAHPKLDPVNGDLHALSYDVVQKPYLKYFR	:	343
H	:	DLPYHVHVTENGDLKTVGRYNFEEQLKSTMIAHPKVDPVTGDLHALSYDVVKKPYLKYFS	:	338
1 -	:	DLPYQVKVTPSGDLTTVGRYDFNGQLSSTMIAHPKVDPVSGEMFGLSYDVVKKPYLKYFW	:	235
J	:	DIPYQIRVTPNGDLTTVCRYDFNNQLKSTMIAHPKVDPIDNNLYALSYDVIQKPYLKYFR	:	344
K -	:	DLPYHLRITPNGDLTTVGRYNFNSQLTSTMIAHPKLDPSTGHLHALSYDVVHRPYLKYFR	:	307
L	:	DLPYQVRVTPSGDLKTVGRYNF <mark>N</mark> GELKSTMIAHPKVDPVSGEMFALSYDVVKRPYLKYFW	:	323
М	:	DLPYHVRVTPNGDLKTVGRYDFNGQLKSTMIAHPKVDPVSGELFALSYDVISKPYLKYFK	:	330
Ν	:	DLPYHVRVTPNGDLKTVGRYDFNGQLKSTMIAHPKVDPVSGELFALSYDVISKPYLKYFK	:	330
0	:	DLPYHVRVTPNGDLKTVGRYDFNGQLKSTMIAHPKVDPVSGELFALSYDVVSKPYLKYFK	:	325
Ρ	:	DLPYHIHVTTNGDLTTVGRYDFNGQLKNTMIAHPKVDPVDGDLYALSYDVVQKPYLKYFR	:	327

B : SEPTIGATE POST DELASE PENANDERATE NETWARDON VERTITEMET AND UNDER 1: 399 C : DES DEVERTED DE DELASE PENANDERATE NETVATEDO VARENTE DELTEGEN V-EDANKET : 403 D : NANCET KE DUS DETES ALTEMENTENTEN VULLES DEVERTICENTERS FUN-EDANKET : 403 D : NANCET KE DUS DETES ALTEMENTENTEN VULLES DEVERTICENTERS FUN-EDANKET : 403 D : NANCET KE DUS DETES ALTEMENTENNE VLEDS DEVERTICENTERS FUN-EDANKET : 403 D : NANCET KE DUS DETES DEVENTIONED ATTENES (FUN DE) (FERTERITEGERV-FUNKET) SETES FUNCTIONES (************************************	А	:	FSPDGVKSPDVEIPLKEPTMMHDFAITENFVVVPDQQVVFKLTEMITGGSPVV-YDKNKT	:	399
C : SPECTRE D'ALENAL FEMALE FEMALES ATTENE VENUE D'AVENUE TENET TELEV - YENNET : 403 C : NACHTARK VE FEMALES ALEMANDS ATTENE VENUE VENUE CONVEXUE CONSENSUE - 2012 AT 100 PM PLANE ALEMANDS ATTENEND FEMALES AVENUE CONVEXUE CONSENSUE - 306 C : SALOV RE D'ALEMA FEMALES ALEMANDS ATTENEND FEMALES VENUE CONVEXUE CONVEXUE CONVEXUE SENTER : 307 C : SALOV RE D'ALEMAR ALEMANDS ATTENEND TENE VENUE OCUVEKUE SENTER SENTER : 307 C : SALOV RE D'ALEMAR ALEMANDS ATTENEND TENE VENUE OCUVEKUE SENTER SENTER : 307 C : SALOV RE D'ALEMAR ALEMANDS ATTENEND TENE VENUE OCUVEKUE SENTER SENTER : 307 C : SALOV RE D'ALEMAR ALEMANDS ATTENEND TENE VENUE OCUVEKUE SENTER SENTER : 307 C : SALOV RE D'ALEMAR ALEMANDS ATTENEND TENE VENUE OCUVEKUE SENTER SENTER : 307 C : SALOV RE D'ALEMAR ALEMANDS ATTENEND VENUE OCUVEKUE SENTR SEGTEV- PDAESKT : 362 C : SALOV RE D'ALEMAR ALEMANDS ATTENEND VENUE OCUVEKUE SENTR SEGTEV- PDAESKT : 362 C : SALOV RE D'ALEMAR ALEMANDS ATTENEND VENUE OCUVEKUE SENTR SEGTEV- PDAESKT : 382 C : SALOV RE D'ALEMAR ALEMANDS ATTENEND VENUE OCUVEKUE SENTR SEGTEV- PDAESKT : 382 C : SALOV RE SALOV DE HAMEDS ATTENEND VENUE OCUVEKUE SENTR SEGTEV- PDAESKT : 384 C : SRECTHER D'ALEMANDS ATTENEND VENUE OCUVEKUE SENTR SEGTEV- PDAESKT : 384 C : SRECTHER SALOV DE HAMEDS ATTENE VENUE OCUVEKUE SENTR SEGTEV- PDAESKT : 384 C : SRECTHER SALOV DE HAMEDS ATTENE VENUE OCUVEKUE SENTR SEGTEV- PDAESKT : 384 C : SRECTHER SALOV DE HAMEDS ATTENE VENUE OCUVEKUE SENTR SEGTEV- PDAESKT : 384 C : SRECTHER SALOV DE HAMEDS ATTENE VENUE OCUVEKUE SENTR SEGTEV- PDAESKT : 384 C : SRECTHER SALOV DE HAMEDS ATTENE VENUE OCUVEKUE SENTR SEGTEV- PDAESKT : 384 C : SRECTHER SALAVER SALOV DE HAMANDE PETER VENUE SETTENE VE	В	:	FSPNGVKSPDVEIPLKEPTMMHDFAITENFVVVPDQQVVFKLTEMITGGSPVV-YDKNKT	:	399
D INKEDITISKUM ZPERVETAMED ALTERNETVETEGOVER, GENERGESPU-FULEKU : 336 D SKADGTREPUNDER, KESTMENDER, ITERNETVETEGOVER, GENERGESPU-FULEKU : 307 F ISKEDTISKUM ZPERVETER, KESTMENDER, ITERNETVETEGOVER, GENERGESPU-FULEKU : 307 G SALGVISPENDER, KESTMENDER, ITERNEVVEDGOVER, ITERTITUM TOGSEVV-FULEKU : 307 F ISKEDTISKUM, HUDELLIKER, INNERTITER, EVENTPOCOVER, ISKED, INNEGSEVV-FULEKU : 337 F ISKEDTISKUM, DELEKER, INNERTITER, EVENTPOCOVER, ISKED, INNEGSEVV-FULEKU : 337 F ISKEDTISKUM, DELEKER, INNERTITER, EVENTPOCOVER, ISKED, INNEGSEVV-FULEKU : 336 F ISKEDTISKUM, DELEKER, INNERTITER, EVENTPOCOVER, ISKED, INNEGSEVV-FULEKU : 338 NENKETISKUM DELEKER, INNERTITER, EVENTPOCOVER, ISKED, INNEGSEVV-FULEKU : 338 NENKETISKUM DELEKER, VENMEDFALTER, EVENTPOCOVER, ISKED, INNEGSEVV-FULEKU : 338 NENKETISKUM DELEKER, VENMEDFALTER, EVENTPOCOVER, ISKED, INNEGSEVV-FULEKU : 338 SERGTIL, EXART ANADRATIDA POCTORE, INNARED PETERVVIGGOMER, ISSEVV-FULEKU : 338 SERGTIL, ISKEN, INNERVIDA POTORE, INNARED PETERVVIGGOMER, ISSEVV-FULEKU : 338 SERGTIL, ISKEN, INNERVIDA POTORE, INNARED PETERVVIGGOMER, ISSEVV-FULEKU : 338 SERGTIL, ISKEN, INNERVIDA POTORE, INNARED PETERVVIGGOMER, ISSEVV-FULEKU : 3384 SERGTIL, ISKEN, INNERVIDA POTORE, INNARED PETERVVIGGOMER, ISSEVV-FULEKU : 3384 SERGTIL, ISKEN, INNERVIDA POTORE, INNARED PETERVVIGGOMER, ISSET, INDEDE : 4459	С	:	FSPDGVKSPDVEIPLKEPTMMHDFAITENFVVVPDQQVVFKLTEMITGGSPVV-YDKNKT	:	403
E MARGETES POWEINUESATION NUMBER SUPPORT CONTRACT IN TOTAL AND A CONTRACT AND A CONTRA	D	:	FNKDGTKSKDVEIPLKVPTMMHDFAITENFVVVPDQQVVFKLGEMMKGGSPVV-YDKEKV	:	386
 F SARGERVOPEVERTISE FUNNINGENTER IVENTIGENUS PROCOVERIGENUS (* 306 F SARGVKE POVELELKERINNER ITER IVENTIGEN (* 1000) F SARGVKE POVELELKERINNER ITER IVENTIGEN (* 1000) F SARGVKE POVELELKERINNER ITER IVENTIGEN (* 1000) F KERGENSKERINGEN FURDER I DARE WUNDFANSEN INTELEDS (* 1000) F SARGVKE POVELE DARE WUNDFANSEN INTELEDS (* 1000) F SARGVKE POVELE DARE WUNDFANSEN INTELEDS (* 1000) F SARGVKE POVELE DORTMUNDFANSEN INTELEDS (* 1000) F SARGVKE POVELE DORTMUNDFANTEN HUV I PDOGVVERIGEMURGES V * 10000000000000000000000000000000000	Е	:	FKA <mark>DGTKS</mark> PD <mark>VEI</mark> NLESATMMHDFAITENNIVIPDSQVVFKLQEMIG <mark>GG</mark> SPVV-FDKEKT	:	377
G : SALGVISEPWEIELKE ZUMHDELITE NEUVIEGOUVEKUTTMIT GOSTU - YDENY : 402 H : NIKBGUKH HUVEIELKE A ENNELEZIER VIEGU VIEGOUVEKUS ENVERGES V - YDEKY : 397 I : KNEGTKAAND ELIKE A ENNELEZIER VIEGU VIEGOUVEKUS ENVERGES V - YDEKY : 294 J : DSN VIEGEN ELEDOPTAMETALTE HEVVIEGOUVEKUS ENUEGES V - YDEKY : 294 J : DSN VIEGEN ELEDOPTAMETALTE HEVVIEGOUVEKUS ENUEGES V - YDEKY : 366 L : GSNGTHEPUN ELEDAPT WHEPAITE HEVVIEGOUVEKUS ENUEGES V - YDEKY : 399 N : NIKBGINGEN U DELKVIENNELEZIEN VUEGOUVEKUS ENUEGES V - YDEKY : 389 N : NIKBGINGEN U DELKVIENNELEZIEN VUEGOUVEKUS ENUEGES V - YDEKY : 389 N : NIKBGINGEN U VIEGU ELEVTENNELEZIEN VUEGOUVEKUS ENUEGES V - YDEKY : 389 N : NIKBGINGEN U VIEGU ELEVTENNELEZIEN VUEGOUVEKUS ENUEGOS V - YDEKY : 389 N : NIKBGINGEN U VIEGU ELEVTENNELEZIEN VUEGOUVEKUS ENUEGOS V - YDEKY : 384 P : JSS GVIEFUNGI ELEVTENDE DIT CELINAVED PERE VVIGGOUTPALS ENUEGE : 459 C : NIKBGINGEN U VIEGU ELEVTENDE VIEGU ELEVTIG SEMTRAGES V - YDEKY : 384 P : JSS GVIEFUNGEN U VIEGU ELEVTENDE VIEGU ELEVTIG SEMTRAGES V - YDEKY : 386 A : SPOTLHKNAK NANARNI DA POTCEFELINAVED PERE VVIGGOUTPALS ENUEGE : 459 C : SPOTLHKNAK NANARNI DA POTCEFELINAVED PERE VVIGGOUTPALS ENUEGE : 459 C : SPOTLHKNAK NANARNI DA POTCEFELINAVED PERE VVIGGOUTPALS ENUEGE : 459 C : SPOTLHKNAK NANARNI DA POTCEFELINAVED PERE VVIGGOUTPALS ENUEGE : 459 C : SPOTLHKNAK NANARNI DA POTCEFELINAVED PERE VVIGGOUTPALS ENUEGE : 459 C : SPOTLHKNAK NANARNI DA POTCEFELINAVED PERE VVIGGOUTPALS ENUEGE : 462 C : SPOTLHKNAK NANARNI DA POTCEFELINAVED PETE VVIGGOUTPALS ENUEGE : 462 C : SPOTLHKNAK SANARNI DA POTCEFELINAVED PETE VVIGGOUTPALS ENUEGE : 462 C : SPOTLHKNAK SANARNI DA POTCEFELINAVED PETE VVIGGOUTPALS ENUEGE : 463 C : SROULPANK SANAR DA POTCEFELINAVED PETE VVIGGOUTPALS ENUEGE : 464 C : SROULPANK SANAR DA POTCEFELINAVED PETE VVIGGOUTPALS ENUEGE : 464 C : SROULPANK SANAR DA POTCEFELINAVESE ETDIVVIGGOUTPALS ENUEGE : 464 C : SROULPANK SANAR DA POTCEFELINAVESE ETDIVVIGGOUTPALS ENUEGE : 464 C : SROULPANK SANAR DA POTCEFELINAVESE ETDIVVIGGOUTPALS ENUEGE : 464 C : SROULPANK SANAR DA POTC	F	:	ISK <mark>DG</mark> FMQDP <mark>VPITISDP</mark> VMMHDFAITE <mark>NY</mark> SIFMDLPLYFRPK <mark>EMVK</mark> NKTLIFSFDSTKK	:	308
H : INKEGLKSHOVE JELKER MANDER ITEREVET POOLVEKE SERVREGGEVET - UTKERV : 397 I : RKPGUKSPOLELERETMINER ITEREVET POOLVEKE SERVREGGEVET - UTKERV : 403 K : SPRGVKSPOLELERETMINER ITEREVET POOLVEKE SERVREGGEVET - UTKERV : 366 L : RCSGUKSPOLELERETMINER ITEREVET POOLVEKE SERVREGGEVET - UTKERV : 389 M : NNKGUKSPOLELERETMINDER ITENEVET POOLVEKE GEMREGGEVET - UTKERV : 389 N : NNKGUKSPOLELERETMINDER ITENEVET POOLVEKE GEMREGGEVET - UTKERV : 389 N : NNKGUKSPOLELERETMINDER ITENEVET POOLVEKE GEMREGGEVET - UTKERV : 389 N : NNKGUKSPOLELERETMINDER ITENEVETVPEOLVEREGEMREGSEVET - UTKERV : 389 N : NNKGUKSPOLELERETMINDER ITENEVETVPEOLVEREGEMREGSEVET - UTKERV : 389 N : NNKGUKSPOLELERETMINDER ITENEVETVPEOLVEREGEMREGSEVET - UTKERV : 386 A : SPEGULSKNKDAMEN DAE DECCEH LINAWEEPETEEVVUESCOMPAD I FNECEE : 459 B : SREGULSKNKDANARMI DAE DECCEH LINAWEEPETEEVVUESCOMPAD I FNECEE : 453 C : SREGULSKNKDAMEN DAE DECCEH LINAWEEPETEEVVUESCOMPAD I FNECEE : 453 C : SREGULSKNKDANARMI DAE DECCEH LINAWEEPETEEVVUESCOMPAD I FNECEE : 453 C : SREGULSKNKDAMEN DAE DECCEH LINAWEEPETEEVVUESCOMPAD I FNECEE : 453 C : SREGULSKNKDANARMI DAE DECCEH LINAWEEPETEEVVUESCOMPAD I FNECEE : 453 C : SREGULSKNKDANARMI DAE DECCEH LINAWEEPETEEVVUESCOMPAD I FNECEE :	G	:	FSADGVKSPDVEIPLKEPTMMHDFAITENFVVVPDQQVVFKLTEMITGGSPVV-YDKNKT	:	402
I : RYPOTKSANDCHIDAETMUNDEMSENTITEDS.WITKGCENTRGSEV - TWEEKY : 294 J : DSROVKSPDUE PLAEPTMUNDEMSENTITEDS.WITKGCENTRGSEV - TWEEKY : 203 K : RSPROVKSPDUE PLAEPTMUNDEATEN HVUTPDOUVPKUESENTRGSEV - TWEEKY : 382 K : RSPROVKSPDUE IN EAPTMUNDEATEN HVUTPDOUVPKUESENTRGSEV - TWEEKY : 383 K : RSPROVKSPDUE IN EAPTMUNDEATEN HVUTPDOUVPKUESENTRGSEV - TWEEKY : 389 C : NKCGTKSKMOD PLAVEMANDEATEN HVUTPDOUVFKUESENTRGSEV - TWEEKY : 389 C : SRFGTLHKNAKANANKWIDAEDCECEH LNNAWEEPETEEVVVIGSCMTPADSTENECE : 459 C : SRFGTLHKNAKANANKWIDAEDCECEH LNNAWEEPETEEVVVIGSCMTPADSTENECE : 463 D : SRFGTLHKNAKANANKWIDAEDCECEH LNNAWEEPETEEVVVIGSCMTPADSTENECE : 463 C : SRFGTLHKNAKANANKWIDAEDCECEH LNNAWEEPETEEVVVIGSCMTPADSTENECE : 463 C : SRFGTLHKNAKANANKWIDAEDCECEH LNNAWEEPETETEVVIGSCMTPADSTENECE : 463 C : SRFGTLHKNAKANANKWIDAECETEH UNAMEEPETETEVVIGSCMTPADSTENECE : 463 C : SRFGTLHKNAKANANKWIDAECETEH UNAMEEPETETEVVIGSCMTPADSTENECE : 463 C : SRFGTLHKNAKANANKWIDAECETEH UNAMEEPETETEVVIGSCMTPADSTENECE : 463 C : SRFGTLHKNAKANANKUDAECETEH UNAMEEPETETEVVIGSCMTPADSTENECE : 463 C : SRFGTLHKNAKANANKUDAECETEH UNAMEEPETETEVVIGSCMTPADSTENECE : 464 C : SRFGTLHKNAKANANKUDAECETEH UNAMEEPETETEVVIGSCMTPADSTENECE : 463 C : SRFGTLHKNAKANANKUDAECETEH UNAMEEPETTETEVVIGSCMTPADSTENECE : 464 C : SRFGTLHKNAKANANKUDAECETEH UNAMEEPETTETEVVIGSCMTPADSTENECE : 464 C : SRFGTLHKNAKANANKUDAECETEH UNAMEEPETTETVVIGSCMTPADSTENECE : 466 C : SRFGTLHKNAKANANKUDAECETEH UNAMEEPETTETVVIGSCMTPADSTENECE C : SRFGTLHKNAKANANKUNDAECETEH UNAM	Η	:	FNKEGL <mark>KS</mark> HD <mark>VEIELKEATMMHDFAITERFVVIPDQQVVFKLSEMVRGGSPVI-YDKEK</mark> V	:	397
J : DSNGVKSPOLE PLAEETMANDEA ITENE VVPDOUVERL GENIR GGEVV - YNKEKV : 403 K : SSPROVKSPOLE PLOOTMANDEA ITENE VVPDOUVERL GENIR GGEVV - YNKEKV : 362 M : NKKOTKSKUVDIPIKVETMANDEA ITENE VVPDOUVERL GEMARGGEVV - YNKEKV : 389 N : NKKOTKSKUVDIPIKVETMANDEA ITENE VVPDOUVERL GEMARGGEVV - YNKEKV : 389 N : NKKOTKSKUVDIPIKVETMANDEA ITENE VVPDOUVERL GEMARGGEVV - YNKEKV : 389 N : NKKOTKSKUVDIPIKVETMANDEA ITENE VVPDOUVERL GEMARGGEVV - YNKEKV : 389 N : NKKOTKSKUVDIPIKVETMANDEA ITENE VVPDOUVERL GEMARGGEVV - YNKEKV : 389 A : SRFGTIHKNAKDANARWIDAE DCECEH INVEDOUVERL SEMIRGGEVV - YNKEKV : 389 N : SNKOTKSKUVDIPIKVETMANDEA ITENE VVPDOUVERL SEMIRGGEVV - YNKEKV : 389 A : SRFGTIHKNAKDANARWIDAE DCECEH INVEDOUVERL SEMIRGGEVV - YNKEKV : 380 N : SNFGTIHKNAKDANARWIDAE DCECEH INVEDE ETEEVVVIGSCMTPADS I FNECE : 459 B : SRFGTIHKNAKDANARWIDAE DCECEH INVEDE ETEEVVVIGSCMTPADS I FNECE : 459 C : SRFGTIHKNAKDANARWIDAE DCECEH INVEDE ETEEVVVIGSCMTPADS I FNECE : 459 C : SRFGTIPKYNDGSCIGWUP DCECEH INVAEER KTDEVVIGSCMTPADS I FNECE : 449 C : SRFGTIPKYNDGSCIGWUP DCECEH INVAEER KTDEVVIGSCMTPADS I FNECE : 449 C : SRFGTIPKYNDGSCIGWUP DCECEH INVAEER KTDEVVIGSCMTPADS I FNECE : 449 C : SRFGTIPKYNDGSCIGWUP DCECEH INVAEER KTDEVVIGSCMTPADS I FNECE : 449 C : SRFGTIPKYNDGSCIGWUP DCECEH INVAEER KTDEVVIGSCMTPADS I FNECE : 449 C : SRFGTIPKYNDGSCIGWUP DCECEH INVAEER KTDEVVIGSCMTPADS I FNECE : 449 C : SRFGTIPKYNDGSCIGWUP DCECEH INVAEER KTDEVVVIGSCMTPADS I FNECE : 449 C : SRFGTIPKYNDGSCIGWUP DCECEH INVAEER KTDEVVVIGSCMTPADS I FNECE : 449 C : SRFGTIPKYNDGSCIGWUP DCECEH INVAEER KTDEVVVIGSCMTPADS I FNECE : 449 C : SRFGTIPKYNDGSCIGWUP DCECEH INVAEER KTDEVVVIGSCMTPADS I FNECE : 449 C : SRFGTIPKYNDGSCIGWUP DCECEH INVAEER KTDEVVVIGSCMTPADS I FNECE : 449 C : SRFGTIPKYNDGSCIGWUP DECECEH INVAEER KTDEVVVIGSCMTPADS I FNECE : 449 C : SRFGTIPKYNDGSCIGWUP DCECEH INVAEER KTDEVVVIGSCMTPADS I FNECE : 449 C : SRFGTIPKYNDGSCIGWUP DCECEH INVAEER KTDEVVVIGSCMTPADS I FNECE : 449 C : SRFGTIPKYNDGSCIGWUP C : SETENAR GENER KTDEVVVIGSCMTPADS I FNECE : 449 C : SRFGTIPKNAKDSDG	Ι	:	FKP <mark>DG</mark> T <mark>KS</mark> AD <mark>VDI</mark> HLDAPTMVHDFAMSENNIIIPDS <mark>QVVFK</mark> LQ <mark>EMIRGG</mark> SPVV-FDKSKT	:	294
 K. S. PSPKOVKSPECE PELOQPTIMHEDEALTEN, HVVLEDOGVVEKI, SENTBAGGEVV-YINSSKV. 366 L. GOSGUTKSPEVELINEADTMENDEALTEN, VVEDOGVVEKI, SENTBAGGEVV-YINSKKV. 389 N. ENKKOTKSKVDDERKVETMHEDEALTEN, VVEDOGVVEKI, GEMARGGEVV-YINSKV. 389 O. ENKKOTKSKVDDERKVETMHEDEALTEN, VVEDOGVVEKI, GEMARGGEVV-YINSKV. 389 O. ENKKOTKSKVDDERKVETMHEDEALTEN, VVEDOGVVEKI, SEMERGGIVV-YINSKV. 389 O. ENKKOTKSKVDDERKVETMHEDEALTEN, VVEDOGVVEKI, SEMERGGIVV-YINSKV. 389 O. ENKKOTKSKVDDERKVETMHEDEALTEN, VVEDOGVVEKI, SEMERGGIVV-YINSKV. 386 P. ESSOVSKVEPVELIPLKEPTMHEDEALTEN, VVEDOGVVEKI, SEMERGGIVV-YINSKV. 386 S. SREGLIEKNAKDANARWI, DABOCECEH, LINAMEBERTEEVVVIGSCHTEADS, ENECDE. 459 C. SREGLIEKNAKDANARWI, DABOCECEH, LINAMEBERTEEVVVIGSCHTEADS, ENECDE. 4463 D. SREGLIEKNAKDANARWI, DABOCECEH, LINAMEBERTEEVVVIGSCHTEADS, ENECDE. 4464 SREGLIEKNAKDANARWI, DABOCECEH, LINAMEBERTEVVVIGSCHTEADS, ENECDE. 4464 SREGUDERY KIDOSTRUEABECECEH, LINAMEBERDEVULTCRLENPILDVUGGAVKE. 368 G. SREGLIDKNA, SOKSVMUDABOCECEH, LINAMEBERDEVULTCRLENPILDVUGGAVKE. 368 G. SREGLIDKNA, SOKSVMUDABOCECEH, LINAMEBERDEVULTCRLENPILDVUGGAVKE. 368 G. SREGUDERY KKORANARWI, DABOCECH, LINAMEBERDEVULTCRLENPILDVUGGAVKE. 368 SREGUDERNA, SOKSVMUDABOCECH, LINAMEBERTEVUVUGSCHTEADS, ENECDE. 442 SREGUDERNA, SOAKSVMUDABOCECH, LINAMEBERTEVUVUGSCHTEADS, ENECDE. 442 SREGUDERNA, SOAKSVMUDABOCECH, LINAMEBERTEVUVUGSCHTEADS, ENECDE. 444 SREGUDERNA, SOAKSVMUDABOCECH, LINAMEBERTEVUVUGSCHTEADS, ENECDE. 444 SREGUDERNA, SOAKSVMUDABOCECH, LINAMEBERTEVUVUGSCHTEADS, ENECDE. 444 SREGUDERNA, SOAKSVMUDABOCECH, LINAMEBERTEVVVUGSCHTEADS, ENECDE. 449 SREGUDERNA, SOAKSVMUDABOCECH, LINAMEBERTEVVUGSCHTEADS, ENECDE	J	:	FDSNGVKSPDVEIPLAEPTMMHDFAITENFVVVPDQQVVFKLGEMIRGGSPVV-YNKEKV	:	403
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M : PNKbCTKSKDVDIP: KV PTMHHDFAITEN FVVVPDQ.VV FKLGEMARGGSFV-VDKEV : 389 N : PNKbCTKSKDVDIP: KV PTMHHDFAITEN FVVPDQ.VV FKLGEMARGGSFV-VDKEV : 384 P : PSSDCVKSPDVETP: KE PTMHHDFAITEN FVVPDQ.VVFKLGEMARGGSFV-VDKEV : 386 S : SRFGILHENAKCANAMENTDAPDCFCFHLNAWEPPTDEVVVIGSCMTPADSTFNECE : 459 B : SRFGILHENAKCANAMENTDAPDCFCFHLNAWEPPTDEVVVIGSCMTPADSTFNECE : 459 C : SRFGILDENARCANAMENTDAPDCFCFHLNAWEPPTDEVVVIGSCMTPADSTFNECE : 466 E : SRFGILDENARCANAMENTDAPDCFCFHLNAWEPPTDEVVVIGSCMTPADSTFNECE : 466 C : SRFGILDENARCANAMENTDAPDCFCFHLNAWEPPTDEVVVIGSCMTPADSTFNECE : 466 C : SRFGILDENARCANAMENTDAPDCFCFHLNAWEPPTDEVVVIGSCMTPADSTFNECE : 466 C : SRFGILDENARCANAMENTDAPDCFCFHLNAWEPPTDEVVVIGSCMTPADSTFNECE : 467 F : AREGUPYAKIDSCHRIEPECFCHLNAWEPPTDEVVVIGSCMTPADSTFNECE : 466 C : SRFGILDENARCANAMENTDAPDCFCFHLNAWEPPTDEVVVIGSCMTPADSTFNECE : 467 F : AREGUPYAKIDSCHRIEPECFCHLNAWEPPTDEVVVIGSCMTPADSTFNECE : 467 I : SRFGILDENARCANAMENTDAPDCFCFHLNAWEPPTDEVVIGSCMTPADSTFNECE : 463 C : SRFGILDENARCANAMENTDAPDCFCFHLNAWEPPTDEVVIGSCMTPADSTFNECE : 465 I : SRFGILDENASSGKSVMVVDAPDCFCFHLNAWEPSTDEVVIGSCMTPADSTFNECE : 465 I : SRFGILDENASSGKSVMVVDAPDCFCFHLNAWEPSTDEVVIGSCMTPADSTFNECE : 464 C : SRFGILPENARSSANDENDPDCFCFHLNAWEPSTDEVVIGSCMTPADSTFNECE : 464 C : SRFGILPENARSSANDENDPDCFCFHLNAWEPSTDEVVIGSCMTPADSTFNECE : 464 C : SRFGILPENARSSANDENDPDCFCFHLNAWEPSTDEVVIGSCMTPADSTFNECE : 444 F : SRFGILPENARSSANDENDPDCFCFHLNAWEPSTDEVVIGSCMTPADSTFNECE : 444 F : SRFGILDENARSSANDENDFFEFCFHLNAWEPSTDEVVIGSCMTPADSTFNECE : 444 F : SRFGILDENARTSDGERKIEAPECFCFHLNAWEPSTDEVVIGSCMTPADSTFNECE : 444 F : SRFGILDENARTSDGERKIEAPECFCF	L	:	<mark>F</mark> GS <mark>DGTKS</mark> P <mark>DVEI</mark> NLEA <mark>PT</mark> MMHDFAITE <mark>NYVIIPD</mark> S <mark>QVVFK</mark> LQEMIG <mark>GG</mark> SPVV-YDKEKK	:	382
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P : SREGILEKNARDASATKWIDAPECFCFHLWNAWEEPETNEVVVIGSCMTPADSIFNECEE : 446 A : SLKS B : SLKS C : SLKS C : SLKS P : NLKS VLSEIRLNLRTGQSTRPIISDAEQVNLEAGMVNR : 498 C : SLKS D : NLKS VLSEIRLNLRTGQSTRPIISDAEQVNLEAGMVNR : 502 D : NLKS P : KLDNFSN VLSEIRLNLRTGKSTRRAI IREEQVNLEAGMVNR : 485 E : NLTS VLSEIRLNLKTGKSTRRAI IREEQVNLEAGMVNR : 406 G : SLKS F : KLDNFSN VLSEIRLNLKTGKSTRRAIDETEQVNLEAGMVNR : 406 G : SLKS VLSEIRLNLKTGKSTRRAIDETEQVNLEAGMVNR : 501 H : NLKS VLSEIRLNLKTGKSTRRAIDETEQVNLEAGMVNR : 496 I : NLSS S : SLKS S	0	:	SRFGILDKNATDSDGIRWIEAPECFCFHLWNAWEEKETDEVVVIGSCMTPADSIFNECDE	:	444
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C : SLKSVLSEIRLNLKTGQSTRRPIISDAEQVNLEAGMVNR : 502 D : NLKSVLSEIRLNLKTGQSTRRPIISDAEQVNLEAGMVNR : 485 E : NLTSVLSEIRLNLKTGKSTRRAIIREEQVNLEAGMVNR : 476 F : KLDNFSN	B	:	SLKSVLSETRINI.BTCOSTREPTISDAEOVNLEACMVNR	•	498
D:NLKSD:NLKSF:KLDNFSNVLSEIRLNLKTGKSTRRAIIREEQVNLEAGMVNR: 485G:SLKSSIKS	С	•	SLKSVLSETRINI.RTGOSTRRPTISDAEOVNLEAGMVNR	•	502
E : NLTS VLSEIRLNRKTGISTRREILPTSQKMNLEAGMVNR : 476 F : KLDNFSN ELYEMRFNMKTGEASQKKLSAST 406 G : SLKS VLSEIRLNLRTGKSTRRPIISDAEQVNLEAGMVNR : 501 H : NLKS VLSEIRLNLKTGKSTRRAIMDETEQVNLEAGMVNR : 496 I : NLSS VLSEIRLNLKTGKSTRRAIMDETEQVNLEAGMVNR : 390 J : SLKS VLSEIRLNLKTGKSTRRAIIDESQHVNLEAGMVNR : 502 K : SLKXXXXXXXXXXXXXXXXXXXXXXXXXSEIRLNLATGDSTRRPIISQAQQLNLEAGMVNR : 486 L : NLTS DLSEIRLNLKTGKSTRKAIIDESQHVNLEAGMVNR : 481 M : NLKS VLSEIRLNLKTGKSTRKAIIREEQVNLEAGMVNR : 488 N : NLKS VLSEIRLNLKTGKSTRKAIIREEQVNLEAGMVNK : 488 O : NLKS VLSEIRLNLKTGKSTRKAIIREEQVNLEAGMVNK : 483 P : SLKS VLSEIRLNLKTGESTRPIIDEAQQVNLEAGMVNK : 485	D	•	NLKSVLSETRLNLKTGKSTRRATIREEGOVNLEAGMVNK	•	48.5
F : KLDNFSNELYEMRFNMKTGEASQKKLSASTVDFPRVNE : 406 G : SLKSVDFPRVNE : 501 H : NLKSVLSEIRLNLKTGKSTRRAIMDETEQVNLEAGMVNR : 496 I : NLSSVLSEIRLNLKTGKSTRRAIMDETEQVNLEAGMVNR : 496 J : SLKSVLSEIRLNLKTGKSTRRAIDETEQVNLEAGMVNR : 390 J : SLKSVLSEIRLNLKTGKSTRRAIDESQHVNLEAGMVNR : 502 K : SLKXXXXXXXXXXXXXXXXXSEIRLNLATGDSTRRPIISQAQQLNLEAGMVNR : 486 L : NLTSDLSEIRLNRKTGISTRREILSSSDKMNLEAGMVNR : 481 M : NLKS	E	•	NLTSVLSETRINRKTGISTRRETLPTSOKMNLEAGMVNR	•	476
G : SLKSVLSEIRLNLKTGKSTRRAIIDESQUNLEAGMVNR : 501 H : NLKSVLSEIRLNLKTGKSTRRAIMDETEQVNLEAGMVNR : 496 I : NLSSVLSEIRLNLKTGKSTRRAIIDESQHVNLEAGMVNR : 390 J : SLKSVLSEIRLNLKTGKSTRRAIIDESQHVNLEAGMVNR : 502 K : SLKXXXXXXXXXXXXXXXXXSEIRLNLATGDSTRRPIISQAQQLNLEAGMVNR : 486 L : NLTSDLSEIRLNRKTGISTRREILSSSDKMNLEAGMVNR : 481 M : NLKSVLSEIRLNLKTGKSTRKAIIREEQVNLEAGMVNK : 488 N : NLKSVLSEIRLNLKTGKSTRKAIIREEQVNLEAGMVNK : 488 P : SLKS	F	•	KLDNFSNWDFPRVNE		406
H : NLKS VLSEIRLNLKTGKSTRRAIMDETEQVNLEAGMVNR : 496 I : NLSS VLSEIRLNTVTGVSTRREIVSETNLEAGMVNR : 390 J : SLKS VLSEIRLNLKTGKSTRRAIIDESQHVNLEAGMVNR : 502 K : SLKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	G	•	SLKSVLSETRINLRTGKSTRPTISDAEOVNLEAGMVNR	•	501
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K : SLKXXXXXXXXXXXXXXXXXXXXXXXSEIRLNLATGDSTRRPIISQAQQLNLEAGMVNR : 486 L : NLTS M : NLKS VLSEIRLNLKTGKSTRKAIIREEQVNLEAGMVNK : 488 N : NLKS O : NLKS VLSEIRLNLKTGKSTRRAIIREEQVNLEAGMVNK : 483 P : SLKS	J	:	SLKSVLSEIRINLKTGKSTRRATIDESOHWILFAGWVIK	•	502
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N : NLKSVLSEIRLNLKTGKSTRKAIIREEQVNLEAGMVNK : 488 O : NLKSVLSEIRLNLKTGKSTRRAIIREEQVNLEAGMVNK : 483 P : SLKSVLSEIRLNLKTGESTRRPIIDEAQQVNLEAGMVNR : 485	M	:	NLKSVLSEIRLNLKTGKSTRKAIIREE <mark>E</mark> OVNLEAGMVNK	:	488
O : NLKSVLSEIRLNLKTGKSTRRAIIREEQVNLEAGMVNK : 483 P : SLKSVLSEIRLNLKTGESTRRPIIDEAQQVNLEAGMVNR : 485	N	:	NLKSZUNLEAGMVNK	:	488
P : SLKSVLSEIRLNLKTGESTRRPIIDEAQQVNLEAGMVNR : 485	0	:	NLKSZUNLEAGMVNK	:	483
	Ρ	:	S <mark>LKS</mark> INS <mark>EIRLNLKTG</mark> ESTRRPIIDEAQQVNLEAGMVNR	:	485

А	:	NKL <mark>GRK</mark> TQ <mark>F</mark> A <mark>Y</mark> LALAEPWP <mark>KVSG</mark> FA <mark>KVDL</mark> LS <mark>GEVK-KYMYG</mark> EEK <mark>FG</mark> GE	:	545
В	:	NKL <mark>GRK</mark> TQ <mark>FAY</mark> LALAEPWP <mark>KVSG</mark> FA <mark>KVDL</mark> LS <mark>GE</mark> VK-KYMYGEEKFGGE	:	545
С	:	NKL <mark>GRK</mark> TQ <mark>FAY</mark> LALAEPWP <mark>KVSG</mark> FA <mark>KVDL</mark> LS <mark>GE</mark> VK-KYMYGEEKFGGE	:	549
D	:	NKL <mark>GRK</mark> SQ <mark>FAY</mark> LALAEPWP <mark>KVSG</mark> FA <mark>KVDL</mark> STG <mark>EVK-KYIYG</mark> DEKFGGE	:	532
Е	:	NKLGRKTQFAYLAIAEPWPKVSGFAKVDLFTGEVK-KFMYGDDKYGGE	:	523
F	:	SYT <mark>GRK</mark> QR <mark>YVY</mark> GTTLDSIA <mark>KVTG</mark> IIKF <mark>DL</mark> HAEPDSGKTKLEVG <mark>G</mark> NVQGLYDLGPG <mark>RFG</mark> SE	:	466
G	:	NKLGRKTQFAYLALAEPWPKVSGFAKVDLFSGEVQ-KYMYGEEKFGGE	:	548
Н	:	NKLGRKTQFAYLALAEPWPKVSGFAKVDLFSGEVK-EFIYGDKKFGGE	:	543
Ι	:	NKLGRKTQYAYLAIAEPWPKVSGFAKVDLFSGEVK-KFMYGENKYGGE	:	437
J	:	NKLGRKTQFAYLALAETWPKVSGFAKVDLFSGQVN-KYLYGDQRFGGE	:	549
Κ	:	NMLGRKTRFAYLALAEPWPKVSGFAKVDLFSGEVK-KFMYGDERFGGE	:	533
L	:	NKLGRKTQYAYLAIAEPWPKVSGFAKVDLFTGEVK-KFEYGDGTYGGE	:	528
М	:	NKLGRKTQFAYLALAEPWPKVSGFAKVDLSSGEVK-KYMYGGEKFGGE	:	535
Ν	:	NKL <mark>GRKTQ</mark> FAYLALAEPWPKVSGFAKVDLSSGEVK-KYMYGGEKFGGE	:	535
0	:	SKLGRKTQFAYLALAEPWPKVSGFAKVDLSSGEVK-KYMYGGEKFGGE	:	530
Ρ	:	NKL <mark>GRK</mark> TQ <mark>FAYLALAEPWPKVSG</mark> FAKV <mark>DL</mark> FSGEVK-KYLYGEERFGGE	:	532
A	:	PLFLPNG <mark>OKEDDGYILAFVHDEKEWKSELOIVNA</mark> ONLK <mark>LEASIKLPSRVPYGFH</mark>	:	599
В	:	PLFLPNGQEEDDGYILAFVHDEKEWKSELQIVNAQNLKLEASIKLPSRVPYGFH	:	599
С	:	PLFLPNGQEEDDGYILAFVHDEKEWKSELQIVNAKNLKLEASIKLPSRVPYGFH	:	603
D	:	PMFLPR-SPSSDREDDGYILAFVHDEKEWKSELQVVNAMTLELEATIELPSRVPYGFH	:	589
Е	:	PLFLPNHTNSSQSEDDGYILAFVHDEMNWTSELQIVNATNLDLVATVKLPSRVPYGFH	:	581
F	:	A <mark>VYVP</mark> RVPGTDSE <mark>EDDGYLIFFVHDE</mark> NTG <mark>K</mark> SF <mark>VHVIDA</mark> KR <mark>M</mark> SA <mark>E</mark> PV <mark>A</mark> VVELPQRVPYGFH	:	526
G	:	PLFLPNGEEEGDGYILAFVHDEKEWKSELQIVNAQNLKLEASIKLPSRVPYGFH	:	602
Н	:	PMFLPR-DPNSEREDDGYILTFVHDEKEWKSELQIVNAMSLKLEATIKLPSRVPYGFH	:	600
Ι	:	PLFVPNHVNS-AQEDDGYILTFVHDEMNWESKLQIVNAVNLELVATVDLPSRVPYGFH	:	494
J	:	PLFLPTLDSNSGREDDGYILTFVHDEKEWKSELQIVNAITLKLEASIKLPSRVPYGFH	:	607
Κ	:	PLFLPRDNGEGREEDDGYILAFVHDEKVWKSELQIVNAETLKLEASIKLPSRVPYGFH	:	591
L	:	PLFLPRDANS-EREDDGYILAFVHDEINWESELKIVNAMTLELVATVKLPSRVPYGFH	:	585
М	:	PMFLPR-SASSEREDDGYILAFVHDEKEWRSELQVVNAMTLELEATIELPSRVPYGFH	:	592
Ν	:	PMFLPR-SASSEREDDGYILAFVHDEKEWRSELQVVNAMTLELEATIELPSRVPYGFH	:	592
0	:	PMFLPR-SAWSEREDDGYILAFVHDEKEWRSELQVVNAMTLELEATIELPSRVPYGFH	:	587
Ρ	:	PLFLPR-DINSEREDDGYILAFVHDEKEWKSELQIVNAMNLKLEASIKLPSRVPYGFH	:	589
A	:	<mark>GTFI</mark> H <mark>SKDL</mark> RKQA : 612		
В	:	<mark>GTFI</mark> H <mark>SKD<mark>LRKQA</mark> : 612</mark>		
С	:	<mark>GTFI</mark> H <mark>SKD</mark> LR <mark>KQA</mark> : 616		

С	:	GΤ	FΙ	Η	SK	D	L <mark>R</mark>	K	QA		:	616
D	:	GΤ	FΙ	Q	SK	D	<mark>L</mark> R	K	QA		:	602
Е	:	GΤ	FΙ	N.	AT	D	LQ	R	QA		:	594
F	:	AF	FV	Т	ΕD	Q	LQ	Ε	QA	KF	:	541
G	:	GΤ	FΙ	Η	SK	D	<mark>L</mark> R	K	QA		:	615
Η	:	GΤ	FΙ	Η	SK	E	L <mark></mark> K	Ν	QA		:	613
Ι	:	GΤ	FΙ	S.	AN	D	L	K	QA		:	507
J	:	GΤ	FΙ	Η	<mark>S</mark> N	D <mark>1</mark>	L <mark></mark> K	K	QA		:	620
Κ	:	GΤ	FΙ	Ν	<mark>S</mark> D	D	<mark>L</mark> R	K	QA		:	604
L	:	GΤ	FΙ	N.	A <mark>K</mark>	D	LM	Ά	QA		:	598
М	:	GΤ	FΙ	Q	SK	D	<mark>L</mark> R	K	QA		:	605
Ν	:	GΤ	FΙ	Q	SK	D	<mark>L</mark> R	K	QA		:	605
0	:	GΤ	FΙ	Q	SK	D	<mark>L</mark> R	K	QA		:	600
Ρ	:	GΤ	FΙ	Ρ	SK	E	L <mark>R</mark>	K	QA		:	602

Fig. 3. The amino acid sequence of *KfNCED*₁ gene was aligned with amino acid sequence of *NCED*₁ from other plants. A: Vigna unguiculata, B: Vigna radiate, C: Vigna angularis, D: Stylosanthes, E: Spinacia oleracea, F: Pisum sativum, G: Phaseolus vulgaris, H: Lupinus angustifolius, I: Kalidium foliatum, J: Cicer arietinum, K: Cajanus cajan, L: Beta vulgaris, M: Arachis ipaensis, N: Arachis hypogaea, O: Arachis duranensis, P: Abrus precatorius



Fig. 4. Dendgrogram showing the relationships among the amino acid sequences of 9'-cis-epoxycarotenoid dioxygenase from K. *foliatum* (*KfNCED*₁) and other plants.



Fig. 5. Expression patterns of the $KfNCED_1$ genes after salinity stresses. Semi-quantitative RT-PCR analysis was carried out with specific primers using the RNA isolated from *K. foliatum* leaves subjected to salinity stress. 28*S rRNA* amplification was used as the internal control.



Fig. 6. ABA contents under different NaCl concentration (Average \pm standard deviation) The capital means significant differences at the 0.01 level, and the lower case letter means significant differences at the 0.05 level

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References

- Alzahrani, S.M., I.A. Alaraidh, H. Migdadi, S. Alghamdi, M.A. Khan and P. Ahmad. 2019. Physiological, Biochemical, and antioxidant properties of two genotypes of *Vicia faba* grown under salinity stress. *Pak. J. Bot.*, 51: 789-798.
- Aswath, C.R., S.H. Kim, S.Y. Mo and D.H. Kim. 2005. Transgenic plants of creeping bent grass harboring the stress-inducible gene, 9-cis-epoxycarotenoid dioxygenase, are highly tolerant to drought and NaCl Stress. *Plant Growth Regul.*, 47(2): 129-139.
- Bailey-Serres, J., S.C. Lee and E. Brinton. 2012. Waterproofing crops: effective flooding survival strategies. *Plant Physiol.*, 160(4): 1698-1709.
- Bang, S.W., S.H. Park, J.S. Jeong, Y.S. Kim, H. Jung, S.H. Ha and J.K. Kim. 2013. Characterization of the stressinducible *OsNCED*₃ promoter in different transgenic rice organs and over three homozygous generations. *Planta.*, 237(1): 211-224.
- Burbidge, A., T.M. Grieve, A. Jackson, A. Thompson, D.R. McCarty and I.B. Taylor. 1999. Characterization of the ABA-deficient tomato mutant notabilis and its relationship with maize Vp14. *Plant J.*, 17(4): 427-431.
- Chernys, J.T. and J.A. Zeevaart. 2000. Characterization of the 9'-cisepoxycarotenoid dioxygenase gene family and the regulation of abscisic acid biosynthesis in avocado. *Plant Physiol.*, 124(1): 343-353.
- Estrada-Melo, A.C., Chao, M.S. Reid and C.Z. Jiang. 2015. Overexpression of an ABA biosynthesis gene using a stress-inducible promoter enhances drought resistance in *petunia*. *Hort. Res.*, 2(1): 443-448.

- Hao, G.P., X.H. Zhang, Y.Q. Wang, Z.Y. Wu and C.L. Huang. 2009. Nucleotide Variation in the NCED₃ Region of Arabidopsis thaliana and its association study with Abscisic acid content under drought stress. J. Integr. Plant Biol., 51(2): 175-183.
- Hauser, F., R. Waadtl and J.I. Schroeder. 2011. Evolution of abscisic acid synthesis and signaling mechanisms. *Curr. Biol.*, 21(9): R346-R355.
- Hossain, M.S. and K.J. Dietz. 2016. Tuning of redox regulatory mechanisms, reactive oxygen species and redox homeostasis under salinity stress. *Front. Plant Sci.*, 7: 548.
- Hou, X., Y. Liang, X. He, Y. Shen and Z. Huang. 2013. A novel ABA responsive *TaSRHP* gene from wheat contributes to enhanced resistance to salt stress in *Arabidopsis thaliana*. *Plant Mol. Biol. Rep.*, 31(4): 791-801.
- Leng, P., B. Yuan and J. Giraudat. 2014. The role of abscisic acid in fruit ripening and responses to abiotic stress. J. Exp. Bot., 65(16): 4577-4588.
- Martínez-Andújar, C., M.I. Ordiz, Z. Huang, M. Nonogaki, R.N. Beachy and H. Nonogaki. 2011. Induction of 9'-cisepoxycarotenoid dioxygenase in *Arabidopsis thaliana* seeds enhances seed dormancy. *Proc. Natl. Acad. Sci.*, 108 (41): 17225-17229.
- Mehrotra, R., P. Bhalothia, P. Bansal, M.K. Basantani, V. Bharti and S. Mehrotra. 2014. Abscisic acid and abiotic stress tolerance-different tiers of regulation. J. Plant Physiol., 171(7): 486-496.
- Milborrow, B.V. 2001. The pathway of biosynthesis of abscisic acid in vascular plants: a review of the present state of knowledge of ABA biosynthesis. J. Exp. Bot., 52(359): 1145-1164.
- Nambara, E. and A. Marion-Poll. 2005. Abscisic acid biosynthesis and catabolism. *Ann. Rev. Plant Biol.*, 56(1): 165.
- Ng, L.M., K. Melcher, B.T. Teh and H.E. Xu. 2014. Abscisic acid perception and signaling: structural mechanisms and applications. *Acta Pharmacol. Sin.*, 35(5): 567-584.
- Qin, X. and J.A.D. Zeevaart. 2002. Overexpression of a 9-cisepoxycarotenoid dioxygenase gene in *Nicotiana plumbaginifolia* increases abscisic acid and phaseic acid

levels and enhances drought tolerance. *Plant Physiol.*, 128(2): 544-551.

- Ravindran, K.C., K. Venkatesa, V. Balakrishan, K.P. Chellappan and T. Balasubramanian. 2007. Restoration of saline land by halophytes for Indian soils. *Soil Biol. Biochem.*, 39(10): 2661-2664.
- Sah, S.K., K.R. Reddy and J. Li. 2016. Abscisic acid and abiotic stress tolerance in crop plants. *Front. Plant Sci.*, 7: 571.
- Schwartz, S.H., B.C. Tan, D.A. Gage, J.A. Zeevaart and D.R. McCarty. 1997. Specific oxidative cleavage of carotenoids by VP14 of maize. *Science.*, 276(5320): 1872-1874.
- Seiler, C., V.T. Harshavardhan, K. Rajesh, P.S. Reddy, M. Strickert, H. Rolletschek, U. Scholz, U. Wobus and N. Sreenivasulu. 2011. ABA biosynthesis and degradation contributing to ABA homeostasis during barley seed development under control and terminal drought-stress conditions. J. Exp. Bot., 62(8): 2615-2632.
- Seung, D., J.P.M. Risopatron, B. Jones and J. Marc. 2012. Circadian clock-dependent gating in ABA signalling networks. *Protoplasma.*, 249(3): 445-457.
- Tan, B.C., M. Leina, W.T. Dengy, L. Liu, Q.B. Li, K. Cline and D.R. McCarty. 2003. Molecular characterization of the Arabidopsis 9-cis epoxycarotenoid dioxygenase gene family. *Plant J.*, 35(1): 44-56.

- Teng, K., J. Li, L. Liu, Y. Han, Y. Du, J. Zhang, H.Z. Sun and Q.Z. Zhao. 2014. Exogenous ABA induces drought tolerance in upland rice: the role of chloroplast and ABA biosynthesisrelated gene expression on photosystem II during PEG stress. *Acta Physiol. Plantarum.*, 36(8): 2219-2227.
- Thompson, A.J., A.C. Jackson, R.A. Parker, D.R. Morpeth, A. Burbidge and I.B. Taylor. 2000. Abscisic acid biosynthesis in tomato: regulation of zeaxanthin epoxidase and 9-cisepoxycarotenoid dioxygenase mRNAs by light/dark cycles, water stress and abscisic acid. *Plant Mol. Biol.*, 42(6): 833-845.
- Wani, S.H. and S.K. Sah. 2014. Biotechnology and abiotic stress tolerance in rice. J. Rice Res., 2: 1000-1105.
- Xia, H., S. Wu and F. Ma. 2014. Cloning and expression of two 9'-cis-epoxycarotenoid dioxygenase genes during fruit development and under stress conditions from Malus. *Mol. Biol. Rep.*, 41(10): 6795-6802.
- Xu, P. and W. Cai. 2017. Functional characterization of the BnNCED₃ gene in Brassica napus. Plant Sci., 256: 16-24.
- Xu, Z.Y., D.H. Kim and I. Hwang. 2013. ABA homeostasis and signaling involving multiple subcellular compartments and multiple receptors. *Plant Cell Rep.*, 32(6): 807-813.
- Ye, N., G. Zhu, Y. Liu, Y. Li and J. Zhang. 2011. ABA controls H₂O₂ accumulation through the induction of *OsCATB* in rice leaves under water stress. *Plant Cell Physiol.*, 52(4): 689-698.

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