Supplementary material

Fig. S1. Map of genes and other genomic features of *T.cruzi* scaffolds containing *masp* genes. The maps show the position and orientation of the genes. Colored arrows below the central line represent genes oriented 5' → 3' left to right, and above in the reverse direction. *T. cruzi* specific genes correspond to genes not present in *T. brucei* or *L. major* genomes. Other genes correspond to *T. cruzi* genes also present in *T. brucei* and/or *L. major* genomes. The scaffold identifier is the Genbank accession number.

Fig S2: Histogram showing the variability in protein length of MASP members. The protein length of all 771 MASP members containing both N- and C-terminal conserved domains was analyzed.

Fig. S3: Example of a chimeric TcMUCII/MASP sequence. Alignment of the cDNA clone 66 [Genbank Acc.# EU825839], the contig (Genbank acc.# AAHK01000303) containing the chimeric gene Tc00.1047053508219.50 and the whole genome shotgun reads TCHKU21TF and TCJTB48TR. The TCHKU21TF read is shown as the reverse complement sequence. The predicted amino acid sequence in shown on the top of each alignment block and the conserved nucleotide positions are indicated by asterisks on the bottom of each alignment block. Gray shaded and non-shaded nucleotides correspond to the TcMUCII and MASP sequences, respectively. The TcMUCII conserved N-terminal sequence is shown within a gray box while the MASP C-terminal conserved region, within a black box. The coding region is shown in upper case and the 5′ flanking region and the 3′ UTR MASP sequences are shown in lower case. The predicted signal peptide is in bold and underlined and the predicted GPI-anchor addition site is in bold, italic and underlined.

Table S1: Repetitive domains derived from the central region of the MASP proteins.

Table S2: MASP proteins containing the Mucin-like glycoprotein Pfam domain (PF01456).

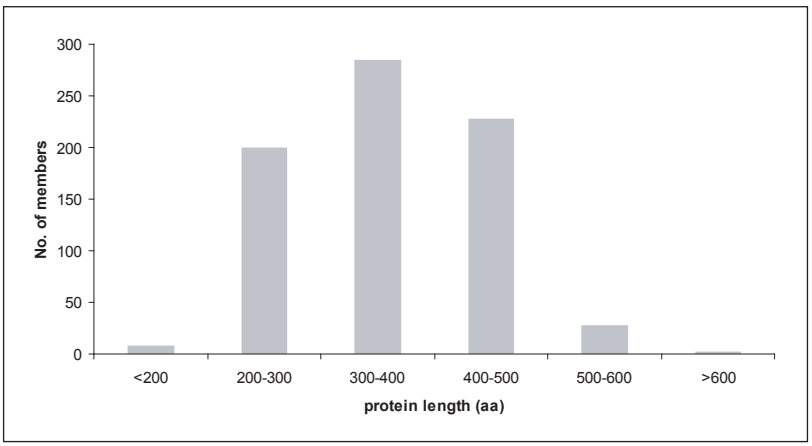
Table S3: MASP and mucin TcMUC aminoacid composition.

Table S4: MASP cDNA annotation.

File S1: MASP subgroups.

T. cruzi scaffold NW_001849576
T. cruzi scaffold NW_001849575
T. cruzi scaffold NW_001849551
T. cruzi scaffold NW_001849526
T. cruzi scaffold NW_001849571
MASP
TcMUCs
gp85/TS
GP63, DGF-1,SAP
RHS
Syntaxin
EF-1 gamma
Other T. cruzi specific genes
Other genes
DIRE, SIRE, VIPER, L1Tc, NARTc
Pseudogenes
Contig break

Bartholomeu et al. Figure S2



```
                                                    M  M  T  T  C  R  L  L  C  A  L  L  V  L  A  L  C  C  C  P  20
cDNA_66      GCTCCACATCACTGAACGACCACACTCACGATGATGACGACGTGCCGTCTGCTGTGCGCCCTGCTGGTGCTCGCCCTGTGCTGCTGCCCG 90
Cg_7643      GCTCCACATCACTGAACGACCACACTCACGATGATGACGACGTGCCGTCTGCTGTGCGCCCTGCTGGTGCTCGCCCTGTGCTGCTGCCCG 90
TCHKU21TF_RC             GAACGACCACACTCACGATGATGACGACGTGCCGTCTGCTGTGCGCCCTGCTGGTGCTCGCCCTGTGCTGCTGCCCG 77
                         *****************************************************************************

              S  V  C  A  A  D  T  Q  E  A  V  H  E  P  S  K  N  T  T  T  N  T  K  S  Q  A  P  T  I  T  50
cDNA_66      TCCGTGTGCGCCGCAGACACTCAGGAGGCTGTTCATGAACCTTCGAAGAACACGACGACGAACACTAAATCACAGGCACCCACAATAACA 180
Cg_7643      TCCGTGTGCGCCGCAGACACTCAGGAGGCTGTTCATGAACCTTCGAAGAACACGACGACGAACACTAAATCACAGGCACCCACAATAACA 180
TCHKU21TF_RC TCCGTGTGCGCCGCAGACACTCAGGAGGCTGTTCATGAACCTTCGAAGAACACGACGACGAACACTAAATCACAGGCACCCACAATAACA 167
             ******************************************************************************************

              Q  T  K  A  G  E  Q  S  S  T  E  Q  G  T  E  G  S  P  E  E  V  T  T  G  K  E  N  V  D  T  80
cDNA_66      CAAACAAAAGCAGGAGAGCAGTCCTCCACTGAACAGGGCACAGAAGGTAGTCCAGACACAGAGGAGGTTACAACCGGAAAAGAGAACGTG 270
Cg_7643      CAAACAAAAGCAGGAGAGCAGTCCTCCACTGAACAGGGCACAGAAGGTAGTCCAGACACAGAGGAGGTTACAACCGGAAAAGAGAACGTG 270
TCHKU21TF_RC CAAACAAAAGCAGGAGAGCAGTCCTCCACTGAACAGGGCACAGAAGGTAGTCCAGACACAGAGGAGGTTACAACCGGAAAAGAGAACGTG 257
             ******************************************************************************************

              Q  N  T  V  E  T  G  I  P  S  R  S  S  S  A  A  S  K  P  P  I  K  Q  T  T  P  I  L  A  Q  110
cDNA_66      CAGAATACTGTCGAGACGGGAATTCCTTCCAGGTCGTCGTCTGCCGCCAGCAAGCCACCCATAAAACAAACAACGCCAATATTAGCACAA 360
Cg_7643      CAGAATACTGTCGAGACGGGAATTCCTTCCAGGTCGTCGTCTGCCGCCAGCAAGCCACCCATAAAACAAACAACGCCAATATTAGCACAA 360
TCHKU21TF_RC CAGAATACTGTCGAGACGGGAATTCCTTCCAGGTCGTCGTCTGCCGCCAGCAAGCCACCCATAAAACAAACAACGCCAATATTAGCACAA 347
             ******************************************************************************************

              S  P  A  V  P  S  P  E  R  L  A  A  A  T  S  E  E  K  S  T  A  P  S  F  S  A  G  E  G  S  140
cDNA_66      TCACCGGCAGTGCCATCACCAGAACGATTAGCAGCAGCAACATCAGAAGAAAAATCAACAGCACCGAGTTTTTCAGCAGGAGAAGGAAGC 450
Cg_7643      TCACCGGCAGTGCCATCACCAGAACGATTAGCAGCAGCAACATCAGAAGAAAAATCAACAGCACCGAGTTTTTCAGCAGGAGAAGGAAGC 450
TCHKU21TF_RC TCACCGGCAGTGCCATCACCAGAACGATTAGCAGCAGCAACATCAGAAGAAAAATCAACAGCACCGAGTTTTTCAGCAGGAGAAGGAAGC 437
             ******************************************************************************************

              R  T  A  T  N  V  A  Q  N  S  K  E  E  K  N  E  K  L  P  S  E  N  E  T  E  S  K  A  V  E  170
cDNA_66      CGTACAGCAACAAACGTCGCACAGAACTCAAAGGAAGAAAAGAATGAAAAAATTGCCGTCAGAAAACGAAACGGAGTCCAAAGCGGTGGAA 540
Cg_7643      CGTACAGCAACAAACGTCGCACAGAACTCAAAGGAAGAAAAGAATGAAAAAATTGCCGTCAGAAAACGAAACGGAGTCCAAAGCGGTGGAA 540
TCHKU21TF_RC CGTACAGCAACAAACGTCGCACAGAACT                                                               465
             ****************************

              Q  P  S  G  N  D  V  A  E  Q  D  S  P  A  R  T  T  A  S  P  I  P  A  S  G  S  A  D  A  Q  200
cDNA_66      CAGCCTTCAGGGAATGATGTGGCAGAGCAAGACAGTCCAGCGCGAACAACAGCATCACCCATCCCCGCAAGTGGCAGTGCCGATGCCCAG 630
Cg_7643      CAGCCTTCAGGGAATGATGTGGCAGAGCAAGACAGTCCAGCGCGAACAACAGCATCACCCATCCCCGCAAGTGGCAGTGCCGATGCCCAG 630
TCJTB48TR                   GATGTGGCAGAGCAAGACAGTCCAGCGCGAACAACAGCATCACCCATCCCCGCAAGTGGCAGTGCCGATGCCCAG  75
                            ****************************************************************************

              R  N  E  D  A  D  N  S  N  A  Q  V  L  K  S  E  G  T  H  E  N  S  E  T  G  Y  T  N  L  A  230
cDNA_66      AGAAATGAGGACGCGGATAATAGTAATGCTCAAGTGCTTAAATCCGAAGGAACACATGAGAACTCCGAAACTGGTTATACAAACCTTGCT 720
Cg_7643      AGAAATGAGGACGCGGATAATAGTAATGCTCAAGTGCTTAAATCCGAAGGAACACATGAGAACTCCGAAACTGGTTATACAAACCTTGCT 720
TCJTB48TR    AGAAATGAGGACGCGGATAATAGTAATGCTCAAGTGCTTAAATCCGAAGGAACACATGAGAACTCCGAAACTGGTTATACAAACCTTGCT 165
             ******************************************************************************************

              S  T  A  G  D  A  A  T  Q  T  E  K  A  P  A  D  A  K  T  N  D  T  V  T  P  G  D  S  D  G  260
cDNA_66      TCTACAGCCGGTGATGCAGCAACACAAACAGAAAAAGCACCCGCCGACGCCAAAACAAATGATACGGTGACACCTGGCGACAGTGACGGC 810
Cg_7643      TCTACAGCCGGTGATGCAGCAACACAAACAGAAAAAGCACCCGCCGACGCCAAAACAAATGATACGGTGACACCTGGCGACAGTGACGGC 810
TCJTB48TR    TCTACAGCCGGTGATGCAGCAACACAAACAGAAAAAGCACCCGCCGACGCCAAAACAAATGATACGGTGACACCTGGCGACAGTGACGGC 255
             ******************************************************************************************

              C  T  E  V  S  H  T  T  S  P  L  L  L  L  L  V  A  C  A  A  A  A  V  V  A  A  *            287
cDNA_66      TGCACCGAGGTCTCCCACACCACCTCCCCTCTTTTGCTTCTTCTTGTTGCGTGTGCGGCTGCTGCTGTGGTGGCCGCGTGAgggtgaggg 900
Cg_7643      TGCACCGAGGTCTCCCACACCACCTCCCCTCTTTTGCTTCTTCTTGTTGCGTGTGCGGCTGCTGCTGTGGTGGCCGCGTGAgggtgaggg 900
TCJTB48TR    TGCACCGAGGTCTCCCACACCACCTCCCCTCTTTTGCTTCTTCTTGTTGCGTGTGCGGCTGCTGCTGTGGTGGCCGCGTGAgggtgaggg 345
             ******************************************************************************************

cDNA_66      agagagagccgtgcaccgcccggcacacacacttctttccttcttcttcttctgtgtgtgtgtcccct-gtgcatggacttttctgccct 989
Cg_7643      agagagagccgtgcaccgcccg-cacacacact-ctt-ccttct-ct-ct-ctgtgtgtgtgtcccttg--catggact--ctcgccct 980
TCJTB48TR    agagagagccgtgcaccgcccg-cacacacact-ctt-ccttct-ct-ct-ctgtgtgtgtgtcccttg--catggact--ctcgccct 425
             ********************** ********** *** ****** ** ** ***************** *  ********  ********

cDNA_66      caccttcaccccacgagggcacacacaatgtgcccattgtaataataatgcatgcacacccatgcaggcccgttggtgctctcttttgca 1079
Cg_7643      cacct-caccccacgagg-cacacacaatgtgcccattgta-ta-ta-tgcatgcacacccatgcaggcccgttggtgctctcttttgca 1065
TCJTB48TR    cacct-caccccacgagg-cacacacaatgtgcccattgta-ta-ta-tgcatgcacacccatgcaggcccgttggtgctctcttttgca  510
             ***** ************ ********************* ** ** ****************************************

cDNA_66      cgacacgcacccgctgccgtcctgcctggctgcatggaccggagcacccgtaactgtttctgttttgtttttattgcacttgaggtgggc 1169
Cg_7643      cgacacgcacc-gctgccgtcctgcctggctgcatggac-ggagcacc-gtaactgtttctgttttgtttttattgca-ttgag-tgggc 1150
TCJTB48TR    cgacacgcacc-gctgccgtcctgcctggctgcatggac-ggagcacc-gtaactgtttctgttttgtttttattgca-ttgag-tgggc  595
             *********** *************************** ******** ***************************** ***** *****

cDNA_66      gatcttcttcttcttcttctccctgtgtgtgtgtgttttgctttaccgggagcacatgaggaggtgtgtgtgcgcttgtcgtcccaccgc 1259
Cg_7643      gatct-ct-ct-ct-ct-ctccctgtgtgtgtgtgttttgctttac-gggagca-atgag-ag-tgtgtgtgcgcttgtcgtcccac-gc 1230
TCJTB48TR    gatct-ct-ct-ct-ct-ctccctgtgtgtgtgtgttttgctttac-gggagca-atgag-ag-tgtgtgtgcgcttgtcgtcccac-gc  675
             ***** ** ** ** ** ************************** ******* ***** ** ********************** **
```

Table 1: Repetitive domains derived from the central region of the MASP proteins

MOTIF	NUMBER OF BLOCKS	NUMBER OF OCCURRENCE
E	5-14, 16, 23	183
G	5-9, 11	90
A	5-7	87
P	5-9, 11	66
S	5-8	41
D	5-11	23
Q	5-7, 9	17
T	5-7	14
AEAA	2	8
AAEA	2	7
NDDV	2	6
AAAE	2-3	5
AIPG	2	5
AAAEA	2	4
GGGGSGS	2	4
GSRG	2	4
AAAAE	2	3
AAAEK	2	3
AGP	3-4	3
EEKR	2	3
GGGS	2	3
K	5-7	3
KAEE	2	3
AAE	3	2
AAEAE	2	2
AAG	3	2
AAKA	2	2
AATKAKA	2	2
AKAAAEA	2	2
APA	3	2
DT	4	2
EEED	2	2
EK	4	2
GGKD	2	2
KKEE	2	2
PPAP	2	2
V	6	2
AAAKAA	2	1
AAAT	2	1
AAATAAE	2	1
AAEAAKA	2	1
AAEEAKA	2	1
AAEKA	2	1
AAKAA	2	1
AAKAAA	2	1
AAKAAAE	2	1
AAKEAEA	2	1
AAKEAET	2	1
AAPPA	2	1
AAPPAP	2	1
AEEA	2	1
AGGGSG	2	1
AIPGA	2	1
AKAAAEK	2	1
APPA	3	1
APPV	2	1
ATATAA	2	1
AVE	3	1
DEKE	2	1
DGTP	2	1
EAAA	2	1
EAAE	2	1
EAAK	2	1
EAAS	2	1
EDEG	2	1
EEDEEE	4	1
EEEDEEEE	4	1
EEEED	2	1
EEEEEED	2	1
EEEEEEG	2	1
EEEEV	3	1
EEGEED	2	1
EENDTK	2	1
EEVE	2	1
ENED	2	1
GAAGP	2	1
GE	5	1
GEGAGS	2	1
GGGE	2	1
GGGSGG	2	1
GGSP	2	1
GLGAA	2	1
GPADPA	2	1
GSGGSS	2	1
GVG	3	1
KASE	2	1
KEDE	2	1
L	6	1
PADPAG	3	1
PPAA	2	1
PQ	4	1
QEQQ	2	1
QP	4	1
QQAA	2	1
QQKQ	2	1
QSPL	2	1
R	6	1
SGGG	2	1
TA	4	1
TATPT	2	1
TGESP	2	1
TKAKAASEA	2	1
WDG	2	1

Table S2. MASP proteins containing the Mucin-like glycoprotein Pfam domain (PF01456)

locus_id	annotation	Pfam expect value*	chimera
Tc00.1047053503587.10	mucin-associated surface protein (MASP), putative	3.30E-07	yes
Tc00.1047053503609.60	mucin-associated surface protein (MASP), putative	0.00012	yes
Tc00.1047053511089.90	mucin-associated surface protein (MASP), putative	3.60E-06	yes
Tc00.1047053511197.60	mucin-associated surface protein (MASP), putative	3.80E-05	no
Tc00.1047053511591.10	mucin-associated surface protein (MASP), putative	1.70E-06	yes
Tc00.1047053511603.500	mucin-associated surface protein (MASP), putative	1.70E-11	yes
Tc00.1047053506067.260	mucin-associated surface protein (MASP), putative	8.70E-09	yes
Tc00.1047053506279.160	mucin-associated surface protein (MASP, pseudogene), putative	9.90E-05	yes
Tc00.1047053506909.90	mucin-associated surface protein (MASP, pseudogene), putative	2.20E-06	yes
Tc00.1047053506969.10	mucin-associated surface protein (MASP, pseudogene), putative	0.00021	no
Tc00.1047053506993.180	mucin-associated surface protein (MASP), putative	6.50E-05	yes
Tc00.1047053507071.380	mucin-associated surface protein (MASP, pseudogene), putative	1.10E-09	yes
Tc00.1047053508359.80	mucin-associated surface protein (MASP), putative	6.00E-06	yes
Tc00.1047053508435.70	mucin-associated surface protein (MASP), putative	4.10E-05	yes
Tc00.1047053510363.70	mucin-associated surface protein (MASP), putative	1.30E-06	yes
Tc00.1047053510363.80	mucin-associated surface protein (MASP), putative	4.70E-06	yes
Tc00.1047053510693.150	mucin-associated surface protein (MASP), putative	1.90E-05	yes
Tc00.1047053511233.130	mucin-associated surface protein (MASP), putative	4.80E-08	yes

*Pfam expect value for T. cruzi mucins (eg. Tc00.1047053511625.100) is ~1.0E-50

Table S3. Comparative amino acid composition of T. cruzi MASP and mucins

Amino acid	Amino acid frequency (% ± SD)					
	TcMuc I n=54	TcMUC II n=582	TcMUC III n=2	TcSMUG S n=10	TcSMUG L n=7	MASP n=771
Ala	10.9 ± 2.7	11.0 ± 1.9	20.5 ± 1.5	13.7 ± 2.3	15.4 ± 1.4	12.1 ± 4.6
Cys	5.1 ± 1.1	3.3 ± 1.0	6.5 ± 0	5.3 ± 1.3	5.3 ± 0.7	1.6 ± 0.6
Asp	1.1 ± 0.8	3.8 ± 1.4	1.1 ± 0	3.2 ± 1.0	2.7 ± 0.4	5.8 ± 1.3
Glu	2.8 ± 1.2	6.2 ± 1.8	4.3 ± 0	2.9 ± 0.6	2.7 ± 0.4	9.8 ± 3.1
Phe	0.3 ± 0.4	0.2 ± 0.4	0.6 ± 0.8	1.6 ± 1.1	1.9 ± 0.6	0.5 ± 0.5
Gly	2.6 ± 1.1	7.0 ± 2.2	8.6 ± 0	6.2 ± 1.4	5.3 ± 0.7	10 ± 2.9
His	0.3 ± 1.1	0.7 ± 0.8	0	0.3 ± 0.7	0	1.6 ± 0.8
Ile	1.6 ± 1.7	1.4 ± 0.8	0.6 ± 0.8	0.3 ± 0.6	0	1.6 ± 0.7
Lys	2.4 ± 1.4	3.8 ± 1.4	2.7 ± 0.7	3.3 ± 0.9	5.9 ± 0.5	5.1 ± 1.9
Leu	8.9 ± 1.5	7.7 ± 1.3	12.9 ± 0	8.4 ± 0.9	8.5 ± 1.5	5.6 ± 1.0
Met	2.0 ± 1.0	1.5 ± 0.6	1.1 ± 0	1.6 ± 0.3	1.8 ± 0.2	1.6 ± 0.6
Asn	1.2 ± 0.9	3.3 ± 1.3	3.8 ± 0.8	2.2 ± 0.8	2.8 ± 0.3	4.6 ± 1.1
Pro	8.3 ± 1.7	7.8 ± 1.7	6.0 ± 0.8	5.3 ± 0.8	5.6 ± 0.2	7.0 ± 2.0
Gln	1.4 ± 2.3	3.4 ± 1.3	0.6 ± 0.8	3.3 ± 1.5	2.7 ± 0.4	4.2 ± 1.6
Arg	3.4 ± 3.0	3.1 ± 1.7	1.1 ± 0	2.4 ± 1.8	2.7 ± 0.4	2.5 ± 1.0
Ser	7.8 ± 2.7	10.8 ± 2.1	16.1 ± 0	4.7 ± 1.8	5.1 ± 0.6	9.7 ± 2.5
Thr	33.5 ± 7.7	18.0 ± 3.8	9.7 ± 1.6	25.8 ± 8.0	21.7 ± 6.2	9.1 ± 1.8
Val	4.3 ± 1.5	5.5 ± 1.7	1.1 ± 0	7.2 ± 1.9	7.3 ± 0.5	6.4 ± 1.3
Trp	0.7 ± 0.3	0.5 ± 0.4	1.1 ± 0	0.9 ± 0.3	0.9 ± 0.1	0.4 ± 0.2
Tyr	1.0 ± 0.4	0.5 ± 0.3	1.1 ± 0	0.8 ± 0.2	0.9 ± 0.1	0.4 ± 0.5
Total	~100	~100	~100	~100	~100	~100
Thr+Ser+Pro	49.6 ± 6.1	36.7 ±3.9	31.7 ± 2.3	35.8 ± 8.4	32.4 ± 6.6	25.8 ± 4.3

Table S4. MASP cDNA annotation

cDNA Clone	Genbank Acc. No.	Best hit	Annotation	Conserved domains	MASP subgroup
Clone_01	EU825796	Tc00.1047053504587.30	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S008
Clone_30	EU825819	Tc00.1047053504587.30	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S008
Clone_35	EU825822	Tc00.1047053504587.30	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S008
Clone_38	EU825824	Tc00.1047053504587.30	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S008
Clone_52	EU825833	Tc00.1047053504587.30	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S008
Clone_63	EU825836	Tc00.1047053504587.30	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S008
Clone_46	EU825828	Tc00.1047053506615.100	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S008
Clone_27	EU825817	Tc00.1047053507803.10	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S010
Clone_60	EU825834	Tc00.1047053511259.220	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S012
Clone_73	EU825845	Tc00.1047053506321.50	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S025
Clone_04	EU825799	Tc00.1047053509979.350	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S030
Clone_75	EU825846	Tc00.1047053506799.130	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S043
Clone_48	EU825830	Tc00.1047053510279.140	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S049
Clone_72	EU825844	Tc00.1047053506245.270	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S061
Clone_37	EU825823	Tc00.1047053508305.50	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S067
Clone_64	EU825837	Tc00.1047053508541.110	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S068
Clone_02	EU825797	Tc00.1047053510025.260	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S074
Clone_79	EU825847	Tc00.1047053508165.30	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S080
Clone_69	EU825842	Tc00.1047053511173.100	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S099
Clone_29	EU825818	Tc00.1047053508125.140	mucin-associated surface protein (MASP), putative	MASP N- and C-terminal domains	S100
Clone_41	EU825826	Tc00.1047053506285.110	mucin-associated surface protein (MASP, pseudogene), putative	MASP C-terminal domain and reconstituted N-terminal domain	NULL
Clone_47	EU825829	T+C1c00.1047053509897.124	mucin-associated surface protein (MASP, pseudogene), putative	MASP N-terminal domain and reconstituted C-terminal domain	NULL
Clone_19	EU825809	Tc00.1047053510547.14	mucin-associated surface protein (MASP, pseudogene), putative	MASP N-terminal domain and reconstituted C-terminal domain	NULL
Clone_18	EU825808	Tc00.1047053510583.114	mucin-associated surface protein (MASP, pseudogene), putative	MASP N- and C-terminal conserved domains, stop codon in frame	NULL
Clone_65	EU825838	Tc00.1047053511605.5	mucin-associated surface protein (MASP, pseudogene), putative	5' partial gene, only MASP C-terminal domain in other frame	NULL
Clone_15	EU825806	Tc00.1047053509751.28	mucin-associated surface protein (MASP, pseudogene), putative	MASP C-terminal domain, unknown N-terminal domain	NULL
Clone_23	EU825813	Tc00.1047053509751.28	mucin-associated surface protein (MASP, pseudogene), putative	MASP C-terminal domain, unknown N-terminal domain	NULL
Clone_14	EU825805	Tc00.1047053509325.10	mucin-associated surface protein (MASP), putative	MASP C-terminal domain, unknown N-terminal domain	NULL
Clone_20	EU825810	Tc00.1047053507859.15	hypothetical protein	MASP C-terminal like	NULL
Clone_22	EU825812	Tc00.1047053507859.15	hypothetical protein	MASP C-terminal like	NULL
Clone_67	EU825840	Tc00.1047053507859.15	hypothetical protein	MASP C-terminal like	NULL
Clone_32	EU825821	Tc00.1047053509521.7	hypothetical protein	MASP C-terminal like in other frame	NULL
Clone_21	EU825811	Tc00.1047053509521.7	hypothetical protein	MASP C-terminal like in other frame	NULL
Clone_50	EU825831	Tc00.1047053508049.40	hypothetical protein, conserved	MASP C-terminal like	NULL
Clone_66	EU825839	Tc00.1047053508219.50	mucin TcMUCII, putative	TcMUCII N-terminal domains and MASP C-terminal domain MASP	NULL
Clone_12	EU825804	Tc00.1047053413893.10	trans-sialidase (pseudogene), putative	MASP 3'UTR	NULL
Clone_03	EU825798	Unknown	MASP unknown	Only MASP C-terminal domain	NULL
Clone_05	EU825800	Unknown	MASP unknown	Only MASP C-terminal domain	NULL
Clone_09	EU825802	Unknown	MASP unknown	Only MASP C-terminal domain	NULL
Clone_17	EU825807	Unknown	MASP unknown	Only MASP C-terminal domain	NULL
Clone_25	EU825815	Unknown	MASP unknown	Only MASP C-terminal domain	NULL
Clone_44	EU825827	Unknown	MASP unknown	Only MASP C-terminal domain	NULL
Clone_51	EU825832	Unknown	MASP unknown	Only MASP C-terminal domain	NULL
Clone_61	EU825835	Unknown	MASP unknown	Only MASP C-terminal domain	NULL
Clone_68	EU825841	Unknown	MASP unknown	Only MASP C-terminal domain	NULL
Clone_71	EU825843	Unknown	MASP unknown	Only MASP C-terminal domain	NULL
Clone_10	EU825803	Unknown	MASP unknown	Only MASP C-terminal domain	NULL
Clone_31	EU825820	Unknown	MASP unknown	Only MASP C-terminal domain	NULL
Clone_06	EU825801	NULL	NULL	NULL	NULL
Clone_24	EU825814	NULL	NULL	NULL	NULL
Clone_26	EU825816	NULL	NULL	NULL	NULL
Clone_40	EU825825	NULL	NULL	NULL	NULL

File S1. MASP subgroups

Meme motifs identified in the 771 MASP proteins containing both N- and C-terminal conserved domains
Motif: 1 code: A size: 15 RVLLVCALCVLWCGA
Motif: 2 code: C size: 15 STAVSHTTSPLLLLL
Motif: 3 code: D size: 8 CAAAAAVV
Motif: 4 code: E size: 15 TAQTNDTATTGDSDG
Motif: 5 code: F size: 21 AGTAEEKQNENKDANPKETPV
Motif: 6 code: G size: 41 VDNNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLPI
Motif: 7 code: H size: 21 QQHQQHEHPAENGEESAKDKN
Motif: 8 code: I size: 50
KKEEADTGTTEGISAGGQEQPSLSSGAEGASNITNPNSTQTTGDDDPAAD
Motif: 9 code: K size: 29 RPNSKEPHDDLETGNTNVAPTASEAAPQT
Motif: 10 code: L size: 26 DDGVSLKADCGLLSTRMALIKAVEAA
Motif: 11 code: M size: 21 VFGHAMDDYCSEGGGNGLRHT
Motif: 12 code: N size: 20 SAGEYLVLNWRALLRRECAE
Motif: 13 code: P size: 43
KICIHKAMKEVCDAFYNKTSGETHDPEVERICTYYAGIPDEPV
Motif: 14 code: Q size: 50
EVSRRTGGRANASAVEECVRQGMDGVRAVVDGRRRWRRQRFAVAAAAAGD
Motif: 15 code: R size: 50
VRSDTGTEGTPTTNHPNRPSTEGATPPGTTSDGEAASANKYDTVSQSAGS
Motif: 16 code: S size: 50
DGVDSREQDGEDTTSEGKKNVPSPETAATPQSHRDKGSEGTGEDTKATTV
Motif: 17 code: T size: 21 EEEEEEEEEEEKQEESDExQV
Motif: 18 code: V size: 29 TPPSPSANGDAANNEADKSTEEGIPNNDP
Motif: 19 code: W size: 29 AGSSGGTAGSSGSNPSNTTGDSSTGDQTP
Motif: 20 code: Y size: 29 QHGHDTDTEDSMKNAATGSPAETTASSIS

>Tc00.1047053416605.10|S104|ANP-VF-CD|10
MAMMMAGRVLLVCALCVLWCGASVVLSAAGGFTSDRSDTAENMVLLWYPETNKTCKENSTKGGILDESA
FKSCMHKSMKEICEVYYNMASTDSDDPEAEEICKKYTGDPVEAAESSTPQDKLSPGAETPVAAPTPETS
KGGAAEMGSTPGIPAGDSPANPTEGSQSTSDANDTANSEAEKGITEVMPKNAPESNATGKEEEKRNERN
HNNTKTTPLDADAMQRITSSADSDSSTAVSHATSPLLPPLLLVVACAAAAAVVAA*
>Tc00.1047053457979.10|S043|AG-----CD|27
MAMMMTGRVLLVCALCVLWCGAGGVYARDLDNRALGGCMASGVLGMNASYEPNGCNEYMPTPPLRSALP
IPAIQAEDGQVRDTPSGPGSGGGGGDKGARDPAGGGDGHAASGPVAGPTADPPAGVLDPTGPGGNDDSS
GATGLPGAAVSSVGPSSLPGPANSNAASVGLPAGSENSNTGCGEVSDCGSQGNLEKATVEKEDFTVSKA
QKPPATQNTKSKDNEENPAEASSTESENTEPQQEIKTPVDESDSTSTDASTAVAARSTSAGSQEEATAS
SSNGSHSPLQGEVFTGTDTPENAPSPAAAETEKRQGENVTTPGDSDSSPAASHTTSPLLLVVVACAAAA
AVVAA*
>Tc00.1047053503429.30|S012|A----REC-|10
MMMTGRVLLVCALCVLWCGADEIYAEGDLEGPPAALSPGLAPSSPGDVGSLDNTGSLAGHGVGVGRSEP
LENAVSGGDVSEDLLNSNNDDEESCSADEESGCGSEDGHRRQENRDEVAEDEVRIIPQTDQSEITPKGP
QIPAREDNAAQLQQKQPPQGVHRTSAAHERAQDASELRTPLSKNLSQQKTGAVSSQFAIHTPTDNEEGK
IPSPPPKSGSDTSNSPEQLVAAKKERGNQREGADDSPTESKEDKNPPATTRKTDAENTHSSVSSSAADT
TPKPDAVTEENPPATDSSRTSSEDAEQLTAIPNPEDASDSTENAATQSAGSANKTNDTAKTAESDSDSS
TAVSHTTSPLLLLLLVPAAAAAVVAA*
>Tc00.1047053503491.19|S043|AG-----CD|27
MMMTGRVLLVCALCVLWCGAGRVYARNPDNNSLGGCIASGGFGRKKSFLSNGSIKNLSTPLLLSASFIS
AIQAEAREEVPSAGVTNLPLSGSTGLSPAFSDLGTSSPRPTVPVPGADVSAHVPAIPGRVPATPGPAGH
GHGPVGPGLRAAIPGVDVPSDGPGAIPAVSGVRAADAPTPGVAVRSDGAAAFSGLGAAGLGAAGPGPLR
DPAFPGPDANIRGSVAPGHGTPITGAAGPGAAAFSSLGAAIHDAADPGAAIPGAIPGPSSVRGAAVHGP
AGPSDGPAGTDHVPAFSGLVPAGPGAGHSVGGGSKPPDSRSVVISSSQGGNGKTAPVSVLSDEQIASPK
EVLAQKETGSEGTSSPEGQPTVSSNNEKQRNNSASAGGHSLGHDAAGDELQDSLEEQKKNDHSQTNETK
KSSGDQNTESQSSGGALSEVSNTTTHGIKTQQPKTNSANEKNYSQNTDASHTTSPLLLLFVVACAAAAA
VVAA*
>Tc00.1047053503503.40|S033|A---V--CD|9
MAMMITGRVLLVCALCVLWCGAGGGGCTEGQLPVVVSPVNPASGAGVTHNPADHTVPGGAGKHSAEQTQ
LNNVEGSASRKVSLEAPLQPVSTTQQTPSSSEPTDSLTNSQSSGGKRQDVQHEGPPGEPETSLNQEENK
DVSNGNQQSIDPPSHSGNDDVVSSNSEERTEDTPRSTEIIVAVPSEEGQERENVTPSLEQPRETSTAAP
AITTQTSSMRPTDVGESNTVKMSDAAPQSTGTANTNDTTTKIANSDGSTAVSHTTSPLLLFLVVACAAA
AAVVAA*

>Tc00.1047053503519.30|S082|A---YKEC-|17
MAMMMTGRVLLVCALCVLWCGAGGGCDDTPQASPSDSGGTVVGTGAGQSGEADNAVCGVGPSGSSSGSG
VKSMVSASFSACTLSPPNPVDGDVLQGGKGTTATLSMDSSEKSVKPQSAEPPAPAQPNLDRQEASTSNA
ENHSPIKPHTAGNEVVSGGATGKENTQRAAVTGGPSSDTRSTTLQAAPQEQPKTELIIVPAGKELQIST
EEMHQTSPSEAQKLLLGQETPSKDDAEDQNTEGTAASDSVKDEAASSLVETTAPPISTSGGADTKSVAS
EDADNAQQPNHKEAHKDPEPQNTSPAFTTTEALPQTAIPLTTAPTNDNTTPGDSDSSTAVSHTTSPPLL
LLVVACAAAAVVAA*
>Tc00.1047053503533.40|S099|AML-VFECD|25
MAMMTGRVLLVCALCVLWCGAVFGHAMEDYCGEGGGNGLRHTSNGGDDGVSLKADCVLLSTRMALIKAV
EAADGQGLSGDPLETSQDSSPGKKLDDKTSGGGTPGLGGGVAGPAIAAAAALEPGESGRGEPKRELEVA
DTAGEEHANDRMKGSERNPENLKNGQSSSFSSGSPVTLGGEGLASEKNSKAAEPSEDGLKVTKLSQQKA
EGDKENKNDTILIGVRENPEKNTEIQTAPPPPANNGKSGPEDTVRMQQLQQVLDGIESNYNSQTKSVAS
IAANQHNEPSADNAESTPPSATANGDAANNEADNSTEEGIPKNDPAADGAGTAEGKQNENKDANPKETP
VTAAAMKTTTATTGDSDSSTAVSHTISPLLLLLLVVACAAAAAMVAA*
>Tc00.1047053503585.10|S008|A-----ECD|43
MAMMMTGRVLLVCALCVLWCGAGGGYAWPYKECKSDDKSCLNHGQHKSVYNSSIRSWFLGETDSTSTGL
LGSSTGSTGSGGEVSRNGAGGTTNSATDPQKGGAQSSLTPSQHASASSGDSSRSKESSEKTEETPGPVS
TSDNDGDGGPNTANQAHLTGSEKRDSGHQTEYGDTDPNLPLEDSKDGEGTHSSPTPPPANKANVPQVTA
EGEKAPAVLTRQEESEGNPEAEPENEQHSSASGVSVPQPEAAQQSETEDDNTTEKTPDEAAAPKNGTAT
TGDSDGSTAVSHTTSHLLLLLVVACAAAAAVVAA*
>Tc00.1047053503645.10|S099|AML-VFECD|25
MAMMTGRVLLVCALCVLWCGAVFGHAMEDYCSEGGGDGLRHASNGGDDGVSLKADCGLLSTRMALIKAV
EAVEAVEEGLSGVPDPSQDTEESSPNNKLDDNTQSTGAAGLGGGVAGPATAAAGAAGLPPNPKGSDKKG
QQGKQEELGPAVGRKAGNKEDRNDGKATGPKLQTVDQPSPSSSLPGSPGARNGEEHKLENTSESDEPSD
DSPEDDEGDRLSQSDSREEKAEELVKQNELNTENTSNEAPALTAAPAEEAEAKTAIPTTSLHGHSSAED
SGDVQQLQQPQDGIESNDSQTKTAATIAANQHNEPSADHAESGLPSPTANGDASNNEADNSTEDGISNN
GPAADGAGTREKKQNENKDANPKETPVEATATKTTTATTGDSDGSTAVSHTTSPLFLLLVVACAAAAAV
VAV*
>Tc00.1047053503645.40|S061|A--TIFECD|52
MTMTGRVLLVCALCVLWCGAGGGGCSETTPGSPGSSGTPPVNDNDSKSDNNSTGGAGEGVQTGKQAVPQ
APAPPASGLPEVPARPSQGTQSGGASETPSTKKDSMVQNTEVKKKEEEEEEHGGNEEEEEKQEEEEEEK
RQEEEEDGTEEEETKKEEAGTGTTEVTSAGGQEQPNLSPGAAGASNKTNPNSTQTTGDDDPAADGAGTP
EGKQNENKDANPKETPVEATAMKTTTATTGDSDGSTAVPHTTSPLLLLLFACAAAAAVVAA*
>Tc00.1047053503665.30|S072|A---VFEC-|6
MAMMMTGRVLLVVCALCVLWCGAAMVMAEANVDKSTEMKKDESFESSELVAGIVSAEQHVTQDSVREVS
ENGKQSLGAQTGNGINQDNGGIIASPASTVRGEEEEEEGETEEIEELTSSIEGEETSQLTLTQEGVPPP
SEPLTTTLNGNPAGTLNATPAKGQSSSDDGSAQEEGLKSPTLKAPAAPAAPAAAAEATTTQTKDENPFL
ADDPLVQHVEASQHDMESRSASRKEGSIPTTVTKTDGPTEVNAESTPTSPSASKGAITNDADEGNEEGI
PKHDQAPDGEATKEAQQGENKEENANKTATLEAAAITNDTATIGDSDGSTAVSHSTSPLLLLLVVACAS
AAAVVAA*
>Tc00.1047053503699.19|S043|AG-----CD|27
MAMMMTGRVLLVCALCVLWCGVCGVYARNPDNNSLGGYMASGGFGRNKSFLSTGASKNLSTPPLLSASF
ISAIQAEAREGEVSSPGVTDSPLSGATGLSPAFSGLGPAVPGPGPGFVHGHVHGPAGPGDGAAAFSGLG
AAGPDPVRGPAFSGPDANIFGAPVPGNGPAAIPGAPVPGHGPAAIPGAPVPGNGPAFSGLGAAVPGDGA
AAFSGRGAAIADAAIPGAAGPVRGVDAPIPGPAVPGDGPAFSGLGAAGPGTADPAAIPGSAVLGHGAIP
GSISDAAIPGPAGPGGGPALSGLGAAFSGAGHSVAGGSEPPNSRSVVISSNQGGNGKTTPISVSSDEQI
VSSQEVLAQKETGSQHTSLPEEQPTVSSNNEKQRNNFASAGGRSLGHNAAGHELQDSLEEQNKNEHSQT
NETKKSSGDQITESQRSGKEISEVSNTKTHGIKTQQPKTNPVNEKNYSQSTDASHTTSPLLLLVVACAA
AAAVVAA*
>Tc00.1047053503717.20|S089|AG---KECD|6
MAMMMAGRVLLVCALCVLWCGACGVYARDRDNSAVGGCMASGVLDTRRLYMPRRCNKTAVTLPLRHVFP
ISAVGASTDGQVSGKIDGGLFPIPAPALPPAPNTPKAPEAPTSHGVSQPAVGVHSGDGTPSLHIPNVDS
SVGGGSGQSGNSNGSVVSVMEPPSTVVVISPSSVSPEVDGLQNKDGPPSNLKLGSPAISVESGKILVGH
NGETEKDSTPDDGPESSRIQEETESRATTEEARGSEAGQSGVGTNGPSNVLSTESQQQNRETTVTETKP
PPPSPGKQIPAVSLPPGVDAPAALSPGPQASSPEPSRAAEDPEEEKRILPATTASHNSKGETHKASSLR
TETVSAAPKPPSPDVVLEQNSEGTVTKDAMKTDAYTDGPAATSESSISTSDSGVVQDKTEEEDDNEQRR
EAKGPHNDPHAGNTNDAPTASVTAAETVKTITTQTNTTSKSGDSDGSTTASHTTSPLLLLLFVVACAAA
AAVVAA*
>Tc00.1047053503761.40|S002|A---S-ECD|19
MAMMMTGRVLLLCGLCVLWCGVCGGLADEETAGSGSGDELPPESQGVETSPQDPQGSQNRAPGGKENIT
PERIEEADDDDDDDDDDGETKAEEERSTERQSVQEGAAAPDPVSREENLSDSGQEKNQAILSAEDVSLS
GSRESNANPTQTEFEEKKDSEKNPPAVEDALTTGNGGNTLPGGVARGNFPSSPEDGVDSRKQDGEETTS
ENKKNVPSPTTAVTPQSHREEGSEGTGEDTKATTVTANKTDTTNTQNSDSSTAVSHTTSPLLLLLVVAC
AAAAAVVAA*

>Tc00.1047053503771.90|S087|AG--YKEC-|7
MAMMMTGRVLLVCALCVLWCGACGVYARNRENKALDGCTASGEFGKKKLYLSSGCNKTALTLSLRSVLP
IVAAEVSVDENDYDQTVIGPALVSSEEPSILPPAALSDVSVAPGVGGVGGVGGGGESGASNLGSPGSGG
GSQLGGVSSKATPSGVLPTPLPHTPQTGEGLQPSGVKPSTPSRDPQTTITQSGEIKTPSSTTPPKVEAL
VEGPKPEAERQVANTHEEANSQVTGVNANENSTDKRATREETPPIVLPIDSTPPVKLTTPPPLPTPEVS
QPKASPPVTVSETGESSTTRDLSQEPKTQTNENSPSQNKTEPEALKELSGDAETEQQDQDKDASNMVKA
AVIGRHAETTSSSISTNDSDDAQSTGDENNDKAERPSPKETSNHTAHNTNDAPTSTEAAPPTAKTATII
QTNDTATKGDSDGSTAVSHTTSPLLLLVVVACAAAVVVAA*
>Tc00.1047053503783.80|S123|ANQ-V--CD|3
MAMMMTGRVLLVCALCVLWCGIDGVAETEEPVIGVVPGVDEYLVVEWRSQLRSECAEKAGRRTGGRANP
SAVEECVRQGMEGLRTFVDGRRRWRRQQFAVAADDDGSGNDGRNSVSSQKAVSVTGTVLPDDPKLKSPI
APGPVLADTTTGGGNLLIPAGSLETAKNKNGEPSKETDKGEKPTVENRSHEGTNGDEQVDNAAIGNPNE
DPENKKGETLQFGEEIVKNEENEVKNGLEEINTETDEENRNKAAEDPEGDDEVTVLSSGGQYNEEGERQ
TEKDSGSNKKGNEVNGGGATDGISAVVPLVLQPASPVDVTDRRNLEKKNDGDTGGKRDAGRTQTQEAAV
PSQAEKLAAELITEEEAAETETGTPGKKTQPEDAGKEQTTVGAKSNPETPAAAKEANNKKEVPKEEEDS
GKATTNENFDKKRTAGKDNAHNEAETTMQENENEVEKAEGTQAEAEGNEEQTGKKDFADKDLKLNGTAI
NADSDGGTAVSHFTTSPLLLLFACAAAAAVVAA*
>Tc00.1047053503827.20|S061|A--TIFECD|52
MMMTGRVLLVCALCVLWCGGCGGGCSETISPAPPDSPSDGNPQKEGEATDVTGKGDQSGQSEASRGKSP
ASELPAAPAKSLQETQSGGGAPDSANTTTDKNNPNTEGKKEEKEEDEAEEEEDEEEEVEVEEDEEKQQE
EEGNQEADGGDVTKEEEEEGKGEENGANEKGETKKEAVTGTTEGISAGGQKQPILSSGAAGASNITNPN
STQTTGGDDPAADGAGTAEGKQNENKDANPKETPVEATATKNTTATTGDGDGSTAVSHTTSPLLLLLVV
VVCAAAAAVVAA*
>Tc00.1047053503827.60|S082|A---YKEC-|17
MAMVMAGRVLLVCALCVLWCGAAEVSVTDGDVVAGGPVALGDPGVGGQSPLVNKGDGGSGGSKGDSSHE
SKSESLVAASGEESPALLLDEDEGRNPAEEHLRVEKEDSKGKQEESQSPPQGASPTEVNPEEALDSLPQ
ERSLDAPEKGVITNGGGGGTANGVKDDTDQNAGLSPNNSDPTALVEPEVKQVVTPQPITTGPSPAMTVS
AEETNPTASTGPQHATETTSTTSPSHSKKVPEATEKTSGNVEPNQQREETDQPDSMNNGTTSHPAETAA
SSTIGSDGAQNKEGKVDNGIQRPDRKEPQDGLEDRNTDDASTASETEPKSAKTDITQKNATSKSGDSDG
STAVSHTTSPLLLLVFACAAAVVAA*
>Tc00.1047053503849.40|S100|AML-VFEC-|15
MAMLMAGRVLLVCALCVLWCGAVFGHAMEDYCSEGGGNGLRHTSNGGDDGVSLKADCGLLSTRMALINA
VEAAEAGEKPSRPDPPQDTEESLPDNKLGNNANGTGAPDSGGGSVSVQPAGIPPTPKGSDKEEKGKKPE
VEDTSGEKVAGDQEQKDGTTTGPQLQRADQLSSSSSGSSDTEGVKRPSSKENSEISESSDNPPQEEGEK
DLGSASDSHEEEAEEKETEGDQKNAGNQAPTEKRGDAAKHTEIQKATTEPNGQSSPEALEGVKQSEEVQ
SEKDSKNNPQTKSVDSIAANQQNGPSADHGESGLPSPTANGDAANNEADNSTEDGIPNSDPAADGAGTR
EEKQNENKDANPKETPVTAAAMKTTTATTGDSDGSTAVSHTTSPLLLLLVVACAAAVVAA*
>Tc00.1047053503859.40|S091|AG--YKECD|14
MAMMMTGRVLLVCALCVLWCGAGWVYAGDVENNAGEGFMASGVLGVNRLRVPSVCGKVAITLPSRMVSF
ITAAEASTNDDASGIIGGNPDSPSGAAAAGSVSGGAGGAGGSGGGGGTSGGSGNSAGGSDGNRDTTEDP
KGVGGGSLQSPPSVDPNSSRIPNEVGESQNTEASLSPEETISPEAAAESGPTASPGNTPPKVETADKSK
PKEEEKELSVTQAAAPISVNGNASTGEQNPHNDVGKVDHSSNQTPPPVLPSAVTSPAPSKEPALPATEP
SPSDGSIPAPNVPQNAKDQEQKTSVLTIKMESNAPEIPSEDNVVQQQGQNTTTEELMETSSRVSQAETT
TTSIYTSGTGEAQSTADADDAQRPNPSESQNDLEGTDIINYPTASEAAPQTAETATTAHKNDTAAPGDS
DGSTAVSHTTFPLLLLLLVACAAAAAVVAA*
>Tc00.1047053503875.30|S025|A------C-|17
MAMMMTGRVLLVCALCVVWCGTSGGRCDEEKETTPANLSGAPSSGESPPTESKALSPASGSPSLISKPK
EDEKSKHLPAKESSEAKEGSSSEGNVVNGDEALQEEPSGNLSESEEEEGLPKEQKEEKKTHVIQDGEQN
RNQPTSHEPSPHQPPSAESHAGSTSASVGGVKDSLDSPLPGVISSPHGDGDRGTTGSTLSNPQSTSPKE
VLSTEETGAQRHSLSNEKAAKGDIVGSIATPGSEGPSFLEEQKTKDLESETHQTAGSSEDLNTESQGSA
KAQLELVNVIKPEPQTSHGIKTPETEGNDSHNTDISKNLPDAQETEHVQEKNNENPASSPVKAQRTSTA
THEEAPASHPNGIPSPLQKETFTGMKTTEDVQPPEAAATNKPQTGDKSKDVNSDGGTAVSHTTSPLLLL
LVAAAAAAVVAA*
>Tc00.1047053503947.20|S061|A--TIFECD|52
MMMMTGRVLLVCALCVLWCGACGGERAEATPGSPGNASREEKPQSEGEPVGGAGNDVKKGEQKVTQGAA
LKAPESHESPANSPQAPPPEGGASVTASTTTENKGKNAQEGEKGENEEKEDEDEEDEVEEEEEEEEQEE
EDEDEEEEDGAKENGETEEETATGTTEETSAGSQEKPSSSSAAEGASNITNPNSTQTTGDDDPAADGAG
TAEGKQNENKDANPKETPVTATAMKTTTATTGDSDGSTAVSHTTSPPLLLLVFACAAAAAVVTA*
>Tc00.1047053503973.80|S033|A---V--CD|9
MAMMSGRVLLVCALCVLWCGAGGRCDEEGTAGHGVQPGVSASGGSGAPDNASGQTASGVAVKPSAEQTQ
LRKAEDSAPGSPQSQADLQNQSSTIQRTPSSSENAVPSTHSKPSGEQMQDLPEEVPPGKPEILSSQEEG
KNETIANQQSIDPPSHSGNNDVVGRNSGERTDDTPSSTEIIDAAPSEEVQEREKVTPSLEQPQETSTAA
PAITTQTTSMTPPKDGENSSVKMSDASPHSTVTVTQTNHTATITQNSDSSTAVFHCTSPLLLLLVVACA
AAAAVVAA*

>Tc00.1047053503973.120|S025|A------C-|17
MAMMTGRVLLVCALCVLWCGAGGRCDEEMEAAAGGAGGGIAGKGAVEPAGTSTPAADSSSLTKGLPRVN
QSKETRGVKPLEVKEVNADQQDVVPGVEDEDGIPSEQLEETVNAGPGKENTKTQLKNVGQEVRQPPEAQ
FNLPQQPQPQTPASEKGEGAGENNKGGAGQPSLGVQDIGNEDSKALGKGDLLKSPGKESESSEQVQTTV
QKTVPPEHKTQNEVLTSEQKTNESQSTDTSNNLPETQKENKEYPASTKGTAQSTSIGSQEQEAEPSTSE
EPSPFEEQQFTGTNTTEDARTPDAAATEKSQSVNKETAGESDGSTAVSHTTSPLLLLLFVACAAAVVAA
*
>Tc00.1047053503973.150|S070|A--TIFEC-|13
MMMTMTGRVLLVCALCVLWCGAGGGGCSETPSVISGNASDENTQKEKEMTVVGGEEGEQESKQAAPQAT
SSPTGSGLRGVPVNPPQTTQPGGEASDPANTTKDNKDQNKKDKKEEKEEKKENQDEEEDDKNEEEGKDE
DKDDVKEEDGEEEKKEEDEEEDYISTTMGMSAGNQEQPILSSRVEEASNKTKPQSTQTTGDKDPTTDGA
GTQEEKQNENKETNPKEKAVEATAMKTTAATTGDSDGSTAVSHTTSPLLLPLLVACAAAVVAA*
>Tc00.1047053503973.190|S080|A---YKECD|24
MAMTTGRVLLVCALCVLWCVAGGRCDGEDTVLVVVSPGGRSNDGQSGPGPAPPSPPGIGTSGPGSIVPE
SEGSQEIIAGTYSEGSGEKNYKDEDGEEESVAEDGENSRNHERLSEQPTQQEVSHEETPEEKGLKERLK
EKDVYPPGEEVIKGAQQSQSQQPPPQQLQVQITAPAGRGGTTAATGPARPPAPAEPSSMDGSRTIEPTD
SRSPSQESHDKSPLLTKTESSAPVPPLKDAFPEQHGQETTTPDSVMSAPAGRQARNTAPSTSTNDSGEA
QSEADGSDAQRPNPNESHDESDSGKTKVPTTLSEAAPQATETVAATQTNHTKTIGDSDDSTAASHTASP
LLLLLVACAAAAAVVAA*
>Tc00.1047053503973.280|S121|ANQ----CD|9
MAMMTGRVLLACALCMLWWGLFGIAADGAGGVPDGSAGEYLFPRWRAQLRSECAEEVGRRTGGGVNDPA
VEECVRRRTDGVRAVVDGRGHWRPQQFVVVATSAGDTSDDYKDPGSLPEGQSGSVAQLTDQQPLKPAPS
TVPGSADNATEKNKPTNPAQPLATGEKINGELIEIKSDDEGTKGKSEDEGEEVEENGDEADGNAGSGTS
DGSREQGKQKAGTGQGASGGTAKENVNVVAGSNLAEGAAASPPVVSVNVENPKSVELIRDDVGGRRQTR
EKTVQEPPAVKLKENVPAELISTEDAAEGEKQKTEEKAEEAETKEEQKNAAEKSKEETPTAPEKKTKEE
QKDKEVQHIRSKNEEKETDGAQPPATKEADVEKTAAFKNTHMNNINKPGDSDGSTAVSHTTSPLLLLLV
VACAAAAAVVAA*
>Tc00.1047053503977.30|S034|A---H--C-|4
MAMMMTGRVLLVCALCVLWCSAGGGRCGEEIAKDPVGANDAPGNLGEDETEKAEPAALGHGDLGLNPET
TKDVSQGGPSEKPLGGTGGGAVENDEGLLSSGRGDEFKSPSPEEEPPETDDPGKRIEEEEVELRQRRNE
EKKLENQPQLQVPVAQQEQSALPQPPQSMQQPSPPQEQPRQQKQQPPHEHPADNEQESKKNKNAVFANK
TENAQDSDGSTAVTHITFPVLLLLLLVAAAAAVVAA*
>Tc00.1047053504031.30|S051|A--TS-EC-|2
MAMMMTGRVLLVCALCVLWCGADGGECSEPTPVPPASQSEDRNTPKSEKETIGGAGGGGQSGQLEALQA
AGLSVQEEKKAETPLRTGTQLAPGTADAEKKGKEQTREVGDVGEKKDEEQEKKEEEEEEDGIEQVEEEE
EEEDEEEVSEENDEGAGAEDGEKTRTEGQGDQEVTIALDQNSGEKNLSGSEQQTRQSIVSAGEIPPPGS
RESSANPTQTKIEEKKETDKSAPAAENTLTTVNGENTVPAGVPGGNPSPPPEDGVDSREQDGEVTTSEG
EKNVPPPATAATPQSHQEKGSEGTGEDTKATTVTANTTDTTNAQNSDGITAVPHTTSPLLLLLFVACAA
AAAAVVAA*
>Tc00.1047053504039.130|S121|ANQ----CD|9
MAMMMTGRVLLVCALCVLWCGVFGIVADGACGGDADGSAVEYSLSRWRAQLRSECAEEVGRRTGGGANA
SAVEECLRQGTDGVRAVVDGRSRWRRQQFAVAAAADGDSGGNVKEEKTKTLSKELHQQPQDSNVAAPGM
NESPGRAHEPSSIGEGGAGSEESQSSLPEVPHEMQNSLLESQKVLGGVGRKAESTVNGPTGHESAADGS
GHIESPEIGVTGDPEKESSQKGSPKITASSQGAGTGEAPQPPTRAGGGTQKDPGIKNPETAETPGEQIT
QTAEQGTPQGGQVPKVQQIVSEPANKQSKVEQEVDSITTPVNAPGVTPQQEKEEDAENEGTADEDEAEE
EIETQEDIAWRPLTPIRKKSSHSISSLHGSAASFSQEEKPTTQVISENLPISETVLEEGGRQHGDTATP
HNVNSSNAPSSVTEPDTATTTKTMIATHNASNLNWDGVKPFTEEKEKRDETPNLNSASEGTKNTPANSE
VPTTATEHAKDITNTTPPADSDGSTAVSHTTSPLLLLVVVACAAAAAVVAA*
>Tc00.1047053504039.160|S061|A--TIFECD|52
MMMMTGRLLLLFALCVLCCGVCGGGCSEAAPASPVTGVSGDGNNPEGKNNTTVGGVGAVDQTGQQAASQ
AAASSSVQNAPGAEAESAQQTGAQALGTANATTENNNDTTKTGENEKTNHDTVEDDDEEEKKEEEEEEE
EDEEEEEEDDGNEEEDGGEEKKQEEKDDTSTTKRISEGGQEEPILSSGVEEASNKTKPQSTQTTGDKDP
AADGAGTQEEKQNGNKEANPKETPVESTVMKTTTPTTGDSDGSTTVSHTTSPLLLLLVACAAAAAVVAA
*
>Tc00.1047053504039.180|S001|A---H-ECD|18
MAMMMTGRVLLVCALCVLWCVAADGAVGVVSGGDDNSLKELFIPVARLQERQEQRAAGATADAKAAAEA
AETAVAKATAAKVAAEAAAKAKAAAAETASKATAAKAAAEAAKAAAEAAAEAAAEAAAKAKTSAETDET
AATKVTAAAEAEAKAAAASEAAKAAATQATATAEAATKAKAAAEKAAKEAATAAAAEAVTATAAAEAEA
KAAAASEAAEAAATQATATAEAATKAKAAAEKAKEEAEKAKAAEKAKEAVTATAAAEAATAAKAAAEAA
KEEAEKAAAATQEAAKTTAAAKEEAEKAAETAAAEAEAAEAEAKAAAEAAKAAEAKAKEAAETAAAESL
RGTTVGEEAKTATHDQDNSVEHHSEEKQELLQEHEPERQEKEQHEKQQHQQREHSAGNGEESPKEKIAN
GTNATAITDDSDGITAVPHTTSPLLLLLLVVCAAAAAVVAA*
>Tc00.1047053504039.200|S008|A-----ECD|43
MAMMMTGRVLLVCALCVLWCGAAVEAEGDDVTEPQDEPSRASQSASEGGHEEEPDIRNPVGEVLNTSEG

PLVARDLTKVSPQKTSFKQPPRDNGGAAGKEEKVEVKKVGDEETRSDGEEPPKDHSEGTQERDGPKENE
RNPSPTPAEKMLTSGDKTAEHAGRAGQAIRAPQSPESDGTRPSGSSVGGSKRGESSNLDNSASDGGKQS
AVDGLGSGGGTVLDPNGGGGSSGRGGGSSRGDSSVSPLSTAGISSSSALDAPFVQSTQPSEKGLQSETM
SLGTALPNEQPKERSGSKAKQGSSTSEEAAESLDDSGDAVEKEKEKGDIGPKATTSLSSTTSYPPVTRT
TPRSSEKPSPTKTEVQAGKETSTENVTITKRNDTATPGDSDGSTAVSHTTSPLLLLLFACAAAAVVVAA
*
>Tc00.1047053504039.230|S002|A---S-ECD|19
MAMMMTGRVLLVCALCVLWCGAGGGFADEEKAAGSESGGELPPASNPVVTPPVGSQGLQNGVTVVTEEV
SPISSPPQGGDADGDDEDEEMEDGETEEKEGKRTAGQSGQGGTVAPDPGSREEILIGSENEKNQSILSA
EDVSPSNSRESIANPTQTEFEEEKNTDENKPAVEDALKTGNGENTLPGGGNLPSSPEDGVDSRKQDGEE
TTSENKKNLPLPATAATPQSHRDKGSEGTGEDTKATTVTANKTDTTNTQNSDSSTAVFHTTSPLLLLLN
ACAAAAAVVAA*
>Tc00.1047053504081.40|S047|A--TS-ECD|8
MAMMMTGRVLLVCALCVLWCGAGGRCDGGKTAGLGSAEHLLESQELEKSPQFTQGIRDGTGGVKEKVLS
TSSEDEDKEDASEENEHEETEDGEKKSIERQGDQGGTVASDPNSGEKNLIGSGQENNPAIVPAGGISPS
GSQESNANPSQPEVDEKKETEKSLPAVENAHTPGNRENTLPGGVAGGNPPSPPEDGVASREHDGEETTS
EEKKDVPPPETAATPQSHQDKGSEGNGEDTKATTVTANTTDTTSTQNSDGSTAVSHTTSPLFLLLVVAC
AAAAAVVAA*
>Tc00.1047053504081.50|S008|A-----ECD|43
MAMTMTGRVLLVCALCVLWCGAAVVESVANDVVDGGVKEGPLGGSRSDSGDEKAGNPELSKPVDEGLGS
AGHSLDTRSGTNVSEQGNLVKEPPTGNVGKEEVEGKGLGTQRNEVHEQQVEAEGEEITVTHKSQTKDKG
TLPQSTPPTPALMQGSPRTPGQPKENSQKSTGQSPTLKLPPAKSPSQASGVGEADGGSVGIEGTGRNVS
GGSLVGASETSLVTGEAIKDPKGSEGPVSGPPSGGASSSTISNNGDASRNNGGAPSTQDTKSLKNNEQS
GPTISSGNAPLNRETPETSTPDAKQHSSETQENETSRVADGDANYRAAGQSAVGTKGSSGVSTTAKNAP
TPPTATVTGAPAEKPTAERSPPPADSTTGEGLAATTTAQTNDTTKSGDSDSSTAVSHSTSPLLLLLVAC
AAAAAVVAA*
>Tc00.1047053504081.90|S073|A-L-YKECD|2
MAMMMAGRVLLVCALCVLWCGAGGRCEEEGTAVPESGGKLLTHTHNGGNDGLRLKADFGLISTRMGLIK
AVAAGDDGGDGAGNDSLENEDKSPQGGVLAGTKDNEAPGAGGGNGAAGAVNGQLPAAGQKGIENKNVDP
GRNAATDSQDQNNDHLSSSSGSTPSRSGEKPSSTGTSEMTQLPKDTVTKLDADLQDKRESSEGIKAEET
EEEERQKIKAHTGSRESKNNGGETTPPLPTSSDEESPISDQENSQNSKKVKNEATLSESKTASEAPAPP
SKDATQGQHSHDTDTEDPTKNAATGSPVEPTTSSTSKSGSGDHVQNKVDEDDAQSSEEQHDGIETGNTN
VVPTLSERASQTPETATDARTNDTTTPGDSDGSTAVSHTTSPFLLFVTCAAAAAVVAA*
>Tc00.1047053504081.170|S002|A---S-ECD|19
MAMMMTCRVLLVCALCVLWCGVGGVCTEEEETAGRGSGADLPLESKEIVISPEGPQGLQGGAPGGEENL
TPVVIQEADDDDDDEETKAEKEKSNEMQSVQEVAIAPGPDSREKNLSGSDQEMHQAIISAEDISPSSSQ
ESKTNPTQTEFEKKTTDENTPAAGNALTTVNGEQTLPAEGNLPSPPEDSVDSRKQDGEDTTSEDKKNVP
SPETAATPQSHRDKGSEGTGEDTKATTVTANTTDTTNTQNSDGSTAASHTTPPLLLLLVVACAAAAAVV
AA*
>Tc00.1047053504081.350|S004|A---V-ECD|18
MAMMMAGRVLLVCALCVVWCGAGGRCDEGGTGGTPPGANPASGAGTTGNAAGQTAPGEAEGFSAQQPQL
EKVGDSPSGGSRSQVDLQLQSPTIQLTPSGAEHTAPSTHSKPSGEQMQDLPDEGPPGKPGISPSQEEGK
NKTIVNQQSNGPPSHSSNNDFVSRNSEERTEDNSGSTETLVAAPSEEGQERENVTPSLEQPQETSTAAP
TVTTQTISTKPSEENKSNTVKMSAASPQSTVTANTTDTTNTQNSDGSTAASHTTSSLLLLLVVACVAAA
AVVAA*
>Tc00.1047053504081.400|S080|A---YKECD|24
MAMMAGRVLLVCALCVLWCGAGGRCDGEDTALVVASPGGRSNDGKSGPGPAPPSPLAIRTSGPGSIVPE
SEGSQEIIAGTYSEGSGEKNYQDEDGEEESVAEDGENSRHHERLSEQPTQQEVSHEETPEGKGLKERLE
EKDVYPPGEEVIKGAQQSQSQQPPPQQLQVQITAPAGREGTTAATGPARPPAPAEPSSRDGSRTIEPTD
SRSPSQESHDKSPLLTKTESSAPEPPLKDAFPEQHGQETTTPDSVMSASAGRQARITAPSTSTSDSGEA
QSEADGNDAQRPNPNESHDESDSGKTKVPTTLSEAAPQATETVAATQTNHTKTIGDSDSSTAVPRTTSP
LLLLLVVACAAAAAVVAA*
>Tc00.1047053504081.460|S009|A----KECD|5
MAMMMTGRVLLVCALCVLWCGAGGGDAEMNDESLVGSQHVSGVGEKSPTGLPESGERVPDSAGHSLGIN
NGINSSLQEGTGTGTTTDRVGKKEEEDNDDDDLEEAEEERSKEKEDTAQTRKSKTSSKEVAATIPTVSG
LSESDGGSPSGVDGVGSSESSDGSEDLNLEVPGPVVNSPPPLSNAAAGGLQNTDGALSPQKNNFPETGV
HSGTTPLAPSLPKSQAPAITQPKAEEQSSTEQDTEDSPDTGEVTTGKKNVQNTVETGIPSRSLSAASKP
PVQQPTPLLAPSPAVPSPGRSAPAPSEKKSTAPSFSAGEGSRRAPNVAQNSKEEKNEKLPSETETESKA
VEQPSGNDVAEQDSPARTTASPIPASGSADAQRNEDADNSNAQVLKSEGTHENSETGYINLASTAGDAA
TQTEKPLADAKTNDTATRGDSDGSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053504081.490|S002|A---S-ECD|19
MAMMTGRVLLVCALCVLWCGAGCGRCEEEGTAVPESDADLPLASKQLENSPQDTQGLNGGVPGANVNVP
PASPEPREGEDDVDDDDSEETEAQEEIIEGQSGQGGTAAIGSDSMEENLIGSEKKTGQSIVPAKDIPHS
GSQESNANPTQKEIEKKDSGKNTPAVGNALTTRNGENTLPAEGNPPSSPKSSDDSRKQDGEDTTSEEEE

NVPPPETAATPQSHRDKGTEGTVEDTKATTVTANTRDTTSTQNSDGSTAVSHTTSPLLLLLLVSCAAAA
AVVAA*
>Tc00.1047053504081.530|S032|A---H--CD|8
MAMMMTGRVLLVCALCVLWCGAAGAAADSSEKMADPSSSERSQALRNGLSEPTDGKKSVEHKSCSVEPV
SDANTAECTKAKSNNLDAISTDPLSPSHAPSNQDPQTGLQPVVPPTGPVQANQPSPGHVKGVVEEVREE
DDEAKRKKELEEQNKQQNQESHENPSSREKPSVLKGDQAVGQEATLQGDSAQQGRKHQEEAPVQIQQEK
DVQHRGLSQHDQQLQSHEEGQEGRHPDEEQPQLPKVQKEKIATASPTGPNLTQQSPPQVKLHGMQQEGS
AASSSERLKEKIPSVSTESKSNGTIDPPSPKASEGEGGAAAALQAEEEDEKFRKDAEFFETAVTEDHHH
EQPTENEGETTKEKPAVVKNNTAITNDSGSDGSTAASHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053504081.420|S001|A---H-ECD|18
MAMMMTGRVLLVCALCVLWCVPADGDIVVVSGGDDNILKELFIPVARLRLRQEKRAAEAIADAKAAAET
AAKAAKAATEATKTAAVKAEEAEAAAEAAAKAAEAAEAAAEEAKAAATEAAKAVDTEEKARAAAAAAES
AATKATTASKAATKAKAAAEEAKAAAEAAAAKAEEAEAKAAAEAAATATEAAEAAKAAAEAAAEAAATA
TEAAEAAATAANAATAAAKAAEEKDEAEEAAKEAAKEAAAAKIIAASAAKAAKEAAEKAEKAKAAAETA
EAKAAAAAEAAAAEKAKAAATEADAKATAAKTAEAAAEALRGTTVGEEKGKTAIHDQDNSVEHHSGEKQ
ELLQEQEPERQEKEQHEKQQHQQREHSARNTEESAKDNTANGTNATAITDDTDSSTAVSHTTSPLLLLL
VFACAAAAAVVAA*
>Tc00.1047053504155.80|S082|A---YKEC-|17
MALMMTGRVLLVCALCVLWCGAGGGYAEDVDVVFGHPGTRGERGGGAVGQSPPAGGSNGGSGGSKADSP
HGSESEPLDSTSDEESSSLDIDQELDPNPPEEHVLQKEVDPIGKQDHSESGPQDALPPDANGTVTLDSD
AQLQLSDTKKKQTEVLTNVGGGEIADGEKDSTGRSNGLSPNKSDPPALLEPRIKEVSQPTEPSPPPANL
SPAPQELPTAVSPAERPPAIAVSAGETNPTASTGSRNATETTTTTSPSHSKTAPEAAETPSGNGEPNQK
IQDTDTPDSMKDGPTSLPAETVVSSVSKSGIGGAHNKEDKVDDGAQRPNTKEPQDGPEDGNTNDAPTST
EAAPQKALTATITQTNVTATKGDSDGGTAVSHTTSPLLLLLVVACAAAVVAA*
>Tc00.1047053504155.160|S066|A---VFECD|8
MAMMMTGRVLLVCALCVLWCGVCAVGVSMADDSENTDVSQGSAKGPPSEPAGRNNGKQESSDQVSQGLQ
KVGEPLDSKKEAVGNQRKDPKIETPTTDKSMDDKGEAEKEQIRGSAGEESGELLEEREAPLDGQGGEGQ
ARQAGNGSAKVGGHSSATTPSEGERPGTGESSPPGSLLPPASTQGNGAAIPASLQGAPAATMKTNEKPV
ENPRAEPEKEKLSSEDDVPEQTSQGVNDGVEPNNDSQKKENVSVTLKERNGESDGDSESTQTRPLAVGD
ASNMDAERGTEIGLPKNNPTANNAVTEGAKRGDNKHSTRKETPVKATAITNDTARTGDSDGSTAVPHTT
SPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053504155.230|S010|A----RECD|22
MAMMMTGRVLLVCALCVLWCGAGRCQEALLVSQSEVPGAIEGDGGQPRGSSGFKMPESHAPGSEASVRE
VQQEQDPSPPREETQLGTKGGNMVEKAKEKGAAKDAGKEGELDGKTIELKKPEDKLTSVEGQQLNNNEG
LHPTTLNGPNGVETTTPSREILSVREDQQDLSSSLLPPLHNTSPGGTPPSTPAAGRADTKSHENDIGKK
NSQQSVVGDIGQNNDTGEKAVDSTGEEEGSRLSVATVEEMSETTKKSDSGGTATTTAVGTDIGTEETPP
TNHPSKPSTEGATTPGTTSDGEAASTNKYDTVSQNAGSTTAATTNATTGDTAKKGDSDSSTAVPHTTSP
LLLLLVACAAAAAVVAA*
>Tc00.1047053504197.20|S025|A------C-|17
MMMTGRVLLVCALCVLWCGAGGRCDEEVVEIPVGGGKVAVGSTGTSTPGSDSLDPTKGLPKVNQSTEKS
EGKSLEGKEVKNDQLFVAPGVEGEDRSPSEQLEERLKNAPEQGKTKPEIQNKEQEVGQPPKSQLNVLQQ
PQPQPPSAPQPHTPASERGEGVGENSKGGEGQSSLGVENSGNEDPENPREEDLLKSPGTKSESSEQVQT
TVPDTVPPEHKTQNEVLTPEQKTNESQSTDTSTNLPETQKENKEYSASTESTAQSTSTGSQEQETEPST
SEEPSPFEEEHSTGTKTSEDARTPDAAATEKRQTGDNEKVGDSDSSTAVSHTTSPLLLLLLVACAAAVV
AA*
>Tc00.1047053504201.40|S082|A---YKEC-|17
MAMMTDRALLVCALCVLWCGAAVVAVGDVIGEVGIKEESSKALQVDSQAREAGKRDVSGPEAVVPRLHE
QQGKNARKNDDSAIQPTRQFKVEEDRDHSEEEEEKENEGSLEGTVKDGEVLPSPAEGQPTSNEPPPPPA
SGGSRNGVISGGGSKLGEGSNGGEGPTLNSSSSSGDGKPPAVDSSGSGGGTGSVPGGKGIGGGGTPGVE
SLKFPVSGVALPPSTPAAGSASSAQNLEPSERSGWPEPTASLRIAPLNVDARKESKPKDEPQTFSAHGE
AERHVTDEETSKKEAEESAVEGKRLFNLPHTASSTPAGPAVRLPEGSQVQGNRDEGEGLPPEATKSETS
TGQKHGTSQSQNESRGTKFPSKNEVAVKHGHVTVPSDSMTNASANSQGLTTAPSISTSGSEDAQSTVDG
NTDDDQRPNKKKAHNNPEDDNANVAPTFSETAPETDTIQKNATSKVDDSDGSTAVSHTTSPLLLLLVAS
AATAVVAA*
>Tc00.1047053504201.50|S025|A------C-|17
MAMMMTGRVLLVCALCVFWCGAGGRCAEEKADEVLVAEPGPSLSGGGDSPTKQSKNSSPVPGPLVLPPK
QQKDDKSEHLHAKESLESEEEVPLKTQEGENKTQVPQDGVQNGNQSIPQEQSPHQALPPHQPPSVGSDA
VSPGGSSVGSSSSGVISSPHGGGDKGTTDIILSNAPSSSPKGVLPAEEAETEHHSLPNENAAERGNVGR
AAAQGNEDPFPLEERRTQDGKSEAHQTEESSKDLNKQPQGNGKIQNGSPNADTPQLQTPHGRKTPETKG
NNSHNTDISTNLPDAQEPKYVKESNNENPASTPVKTQGTSTGIQEEAPASHPNGIPSLQQENFTGMKTT
ENVQPPEVAATNKLQTGDKSKDVNSDGSTGVSRTTSPLLLLLVVCAAAAAAAAAVVAA*
>Tc00.1047053504239.30|S009|A----KECD|5
MAMMMTGRVLLVCALCVLWCGAGGSFANEERTGLGSGAESLLESQELETSPQVTQGIRDGTGGVKGQVP
SKPPEDEVEEDEDEDNDDDEGAGTDEEEEERSKEKEDAQQTRKSKSSSKEVATTIPTASGLSEAGGGSP

SGVDGVGSSESSDGSEDLNLEVSGPVVNFPPLLPNAAAGGGLQDTDGALSSQKNNFSETGVHSGTTPPA
PSLPKSQAPAITKPEAEEQSSTEQDTEDSPDTEEVTTGKENVQNTVETGIPSRSSSAASKPPVQLTTPI
LTQSPAVALPERSALAPSEKKSTAPSFSAGEGSRRATNVAQNSKEEKNEKLPSENETESKAVEQPSGDD
LAEQDSPARTTAAPIPASGSSADAQRNADADNRNAQALKYEGTQKNSETGYKNLASTTGDAATQTEKAL
ADAKANDTATPGDSDGSTAVSHTTSPLLLFLVVACAAAAVVVAA*
>Tc00.1047053504239.110|S004|A---V-ECD|18
MAMMMTGRVLLVCALCVLWCGVGGGGCTEGQLPDVGPPVNPASGAGVTHNPVDHTVPDGAGKHSAEQTQ
LNNVEGSASREVSLEAPLQPVSTTQQTPSSSEPTDSLTNSQSSGGKRQDVQHEGPPGRPGTSPSQEDNT
KVSNGNQQSIDPPSPSGNDDVVSSNSGERTEDTPGSTETFDAAPSEEGQERENVTPFLEQPRETSTAAP
AVTTQTSSTTPTDVGESSTVKMSEASPQSTGTANTNDTTTKIGDSDGSTAAFHTTSPLLLLIVVACAAA
AAVVAA*
>Tc00.1047053504239.220|S015|A---H-EC-|9
MAMMMTGRVLLVCALCVLWSVAADGAVGVVSGGDDNSLKELFIPVARLKVRQEQRAAEATADAKAAAEA
AETAEKAKAEAEAASEAAEKAKAAAEEAAVKTTAAVEASAKAAEAAAKAKTLAETAETATEAADAKAAA
ETAEKAKAEAEAASEAASEAAEEAAGKTTAAAEASAKAAEAAAKAKTLAETAETATEAAEKAAAKATAA
SEAAEKAKAAAAEAAAKTAAAEAAAAEAKTSAETAKMATANAATAAAKAETETEKAAAAAAKEATTKAK
AAEAAKDEAAKAAATAKTAAEEASAKAAEAAAKAKAAAEAAETAKASAGKAAEEAAKAAAEAAATAAEA
AAEAKTSAETANTETAAAKAKAETEKAAAAATEADAKTTAAKTAEAAAEALRGTTVREEEVKTAIHDQD
KSVEHHSEEKQELLQEEGTERQEKEQHEKQQHQQREHSAGNGEESPKEKTANGTNATAITDDSDGSTAV
SHTTSPLLLLFFFACAAATAVVAA*
>Tc00.1047053504239.290|S002|A---S-ECD|19
MAMMMTGRVLLVCALCVLWCGAGGRSDGEDTAGSGIGGESPLSSQELETPPQVTQDLRRGAGGLKEELP
PAPSEDEVEEDEDEDNDDDGAGTDEAERTERQGDQEVAVTSDPNSGEKNLIGSRRKNHQPIVSAGDISH
SGSREPNANPTQKEVEEKKDETDENTPAVENALTTGNGEHTLPVGIAGGNPPPPPEDDVDSREQDGEDT
TSGGKKKVQSPETAAAPQSHRDKGSEGNGEDTKATTVTANTTDTTNTQNSDGSTAVSHTTSPLLLLLLV
ACAAAAAVVPA*
>Tc00.1047053504239.350|S099|AML-VFECD|25
MAMMMTGRVLLVCALCVLWCGAVFGRAMNDYCSEGGGNGLMHKSNGGNGGVSLKADCGLLSTRMALINA
VEAADEGGLSGDAGSSQKSKESLQDKTLSDDTEGDAALVSGGVVADPPPPPAAAPLQNPGGRNTGEEGK
QEELGTKGNEADDKSRSEPGPQKPKTEQSTSSASGGPGTQSDVELALEDTSESNESSNDAPKQEDAGET
ELTKLSDEEPEKGKSNMALTETNDSQAKQKEIQLPTPTTLPTTRVDEHSSPGDTVTKQQLQKPQSEMEP
NNNSQTKSVVTITADQHNEPSADHAGSRPPSPTANGDAANHEADKTTEDGIPNNDPAADGAVTREEKQN
ENKEVNPKETPAESTVIKTTTATTGDSDGSTAVSHTTSPLLLLLFFACAAAAAVVTA*
>Tc00.1047053504239.420|S004|A---V-ECD|18
MAMMMSGRVLLVCALCVLWCGAGGGGCTEGQLPDVGPLVNSESGGVITGNPTGHTVPDGAGKHSAEQTQ
LNNVEGSTSREVSLEAPLQPVSTTQQTPSSSEPTDSLTNSQSSGGKRQDVQHEDPPGRPGTSLNQEENK
DVSNGNQQSIDPPSPSGNDDVVSSNSGERTEDTPGSTETFDAAPSEEGQERENVTPFLEQPRETSTAAP
AVTTQTSSTTPTDVGESSTVKMSEASPQSTGTANTNDTTTKIGDSDGSTAAFHTTSPLLLLIVVACAAA
AAVVAA*
>Tc00.1047053504249.30|S043|AG-----CD|27
MMMTMTGRVLLVCALCVLWCVAGGVYARDVDNNAQGVCMASGVVVKNCSQMPSGCDKTTITVPLRSVLP
ITAVEASTENNVSGSTDGNQDSTSDINPGVVDGTDGEGTVQAGGSKTAGDSRGGGDAGSSGSSKGSEGL
DSEPLPSGGGGTGDSPPSSSTDVTSSTRSGGGMDSTGNALSSVGNKTPEVVQPEKAANAALPQHPTSQE
QETMKSTPGTQSQTPSLAAGQDVGDGVTDGEGQGSSREKTKENEDLKAPGTEVIFESPGPKLHGSGGNE
SELPNATLQETKTQKQGKTLEKENNDSQSGGAPKNSSNKHERNDRREGSSKATTSTAGTAQSTSTGSQE
QAAASSSVGTPTPDQEEKFTGKKRTESTQPPDAAGTGKPSSGDKANIADSDGSTAVYHTTSPLLLLLVV
ACAAAAAVVAA*
>Tc00.1047053504261.40|S002|A---S-ECD|19
MAMMTGRVLLVCALCVLWCGACSGRFGGEETVGLGSDGPLPKSTQLETSPLISQDIKDNAPVVKGNLPS
ALSTPREERDDVEGDGDDGEGTKDEGEKTRTERQGSEGGTAAIVLDSREEILSGNEQENHQSIVPAEGI
SSSNSQESNANPLQTEVEEKKETDKNTPTVENTPTPVDGENTLPPGVAEGNRPPPPEDGVDSREQDGED
TTSEGEKNVPSPETAATPQDHRDEGSEETGEGTKATTVTANTTDTTNTQNSDGSTAVSHTTSPLLLLLV
VACAAAAAVVAA*
>Tc00.1047053506133.140|S061|A--TIFECD|52
MAMMMTGRVLLVCALCVLWCGACCGGRAETSLPDSSGTTSSEGNDSESDKNSIGGAGGVDQSGKPAQSQ
AAGLSVQGATGVAAENAIKTEAQVSSTADAEKKKEEETQRAEDVVEKKGKEQEPKGEEEEEEIEQGEGE
GEEERREEDKDEEEQEEKSNGQKEEQEETKKGEAVTGTIGGMSAGTEEQPSLSSGAAGASNKTNPNSTP
TTGDDDSTADGAGTAEGKQNENKDANPKEAPVTAAATKNTTATSGDSDGSTAVSHTTSPLLLLVACAAA
AAVVAA*
>Tc00.1047053506133.54|S016|A-----EC-|10
MAMMTGRVLLVCALCVLWCGAGGGYAWPYKECESDKESCLNHSQHKSVYNSSIRSRYLGETDSTSTGLL
GSSTGSTGSGGDVSRNGAGGTTNSATDSQKGGAQSSLTPSQHASASSGDSSRSKESSEKTEETPGPAPT
SDNDGDGGPNTANQAHLTGGEKLDSGHQTEDGETDPNLPPEDSKDGEDTHSSPTPPPANKANLPNVTAE
GEKAPAVLTRQEESDGNPEAEPENEQHSSASGVSVPQPEVAQQGETEDDNTTEKTPDEAAAPKNGTATL

DDSDGSTAVSHTTSHLLLLLVFACAAAAVVAA*
>Tc00.1047053506133.61|S015|A---H-EC-|9
MAMMMTGRVLLVCALCVLWCGAADGAVVFSGGDDSILKELFFPVTRLLLRQEQRAAEAAADAQAAAETA
AKAAAATKAATEATKRAAEKAKEAEAAAEAAKAAAEAAATAVKAVDAEAKAKAAAAATESAATKAKAAA
EAAKAAAEAAAKAAAAAAKAEEAEAEAKAAAEAAAKAREAAEAAKAAAVAAAGAAAEAANAATLAAKSA
AKASAEAEKAAAQDETEEAAAEAAAATLAATSAAKEAAEKAAKAKAAAETAEAKATAAEKAAAEKAKAA
ANKAETAAEALRGTTVGEEEVKTAIHSQDNSVEHHSGEKQELLQEEEPERQEKEQHEKQQHQQHEHSAG
NGEKSAKDETANGTNATAIKNDSDSSTAVSHTTSPLLPLLLVACAAVTAVVAA*
>Tc00.1047053506139.10|S087|AG--YKEC-|7
MAMMMTGRVLLVCALCVLWCGAGGVYARDHDSNGLVGSMSSGVLGANLPHMPSGSDKNAFMLPMRSVLP
ITVAEALNENDVSVPAEEDVDLSLNAGYPHAAANGGGGRIGNTTGSHAGGSKTSGGGIGSPGAGAVGVQ
GEGAQRSGGGVDPNGSGHSTLETLGREANGKGGDQSGVRTEENSRNPPAELSSSVQSKPPLTPPEPAGV
PQIQHAPQLLPQKAPETAEASPSPAVSAVDRGTPESRDSQISGKETKKHSTSEAKTEPQITEKFLNGGL
TEENGQEATRPNLAKNAVTDTPTKTTAPSLSTSGTGDVQTTTDTVDNGAQRPNTKEPQDGLEDGNTNVP
PRASGAAPQTALTATITQKNHTKTIGDSDGGTAVPHTTSPLLLLLLLVACAAAVVAA*
>Tc00.1047053506139.40|S024|A--T-R-C-|1
MAMMMTGRVLLVCALCVLWCGAGGGFGEEAPTVSVPDLPTADTVAQGITEMTGDAGNGGPQDGKEKLQG
ETKPEVNVNNSENPAGTPSGVNAEEEEDDKEETEEEEEIRDEHNVETEPRKDQGEEAEDGPGVPNARPV
ASAQQHLQPAPSTGSKSPSGSLETTLQATQTGLQQSADTPNNLPTGNNKINKETGRKTASDKTAEETSP
SSLREGVVDIQKDAEGNNEKHQNNPHLPATAATLQVHQQDGKLDTINETILSGETNNENIQQNDSSSKS
VKAVQSDAGTEGNPTANELSRPSIEDATPISKTHDFNKDSDSTENVASETAGSVTAPNTDSKPGGTAMP
GDSDSSTAVSHTTSPLLLLLVACAAAAVVAA*
>Tc00.1047053506139.70|S066|A---VFECD|8
MAMTMTGRVLLVCALCVLWCGVCAMEVSKADDSENTDVSQGPAKGSPSEPAGRNNGKQESSDQVSQGLQ
NVGEPLDSKKEAAGNQRKDPKIETPTADKSMDHKGEAEKEQIGGSAEESGELLEERKAPLDGQGGEGQA
RQAGNGSAKVGGHSSATTPSEGERPGTGEPSPPASLLPPASTQGNGAAPPASLQGAPAATMKTNEKPVE
NPRAEPEKEKLSSEDDVPEQTSQGVNDGVEPNNDSQKKENVSVALKERNGESDGDSESTQPRHLAVGNA
SNIDAERGTEIGLPKNNPTANSAVTEGAKRGDNKHGNRKETPVEAAAITNDTARTGDSDGSTAVSHTTS
PLLLLVVACAAAAAVVAA*
>Tc00.1047053506139.110|S072|A---VFEC-|6
MAMMMAGRVLLVCALCVLWCGAAAASSAAGREDVVTEEDEQTRTTEVLPSGGKNKSQVTSVEESTGKKA
GNVKTPENSQAAILSTTNGPSDKKQEDEKKKKEKEGDTKDGEDEGKGEEEREKIEKPPTLPPPSGQTST
PTTNGNSAGTSNETRAKEMPSTDRDSTQEQVLKSPAAPTAATPKAKNENPGSADAVLVQQVQKVQSGLE
SGTESRKEESVLTKNKQQDGTFDSHAESTPTSRSSEKSVAASNGPDKATEDEISNKNTAGVDAVPEAAK
DDGNKDDNKKETPIKTTDIANGTAPTGDSDSSTAVPHTTSPLLLLLLVACAAAAAAVAA*
>Tc00.1047053506139.160|S100|AML-VFEC-|15
MAMTMTGRVLLVCALCVLWCGGVFGRAMDDYCSEGGGSGLMHTSNGGDDGVAIKANCGLLSTRMRLINA
VEAADEGGLNGDAGSSQDNPKVSLQDKKLSGNKEGDAAHISGGGVIADPPLPPAAAPLQKPGGRNTGEE
GKQEELDKKGNEAGDKSRSEPAPQKTKSEQSTSSASGGPGTQSDVEPGLEDTSESNESSDDALKQEDAG
ETELTKLSDGEPEKGKSNTALTETSDIQAKQKETQLPTLPTAQVDEHSSPGDTVTTQQLQKPQSEMDPK
NNSQTKNVATITANQHNEPSADHAGSTPPSPTANGDAANNETDKTTEDGIPNNDPAADGTGTAEGKQNE
NMNANPKETPVEAAAMKTTTAKAGDSDGSTAVSHTTSPFLLLLLLVACAAAVVAA*
>Tc00.1047053506277.10|S025|A------C-|17
MAMMMAGRVLLVCALCVLWCGAGGRCDGDEVSSSALSGPRGGVDGPQSSSKSVAGVSEDARQLLYAQNG
KNENQGRGSVIEPSLDDVYEEEDEGEETETRETPPPAGGGIKAPSASAGPGVIPTSGSSSPSGVDSSSR
IGGGTGPTVSTSSNTVGKASKEDMALQEKESQHTQLGDGEAAGTHNNGSQQNSSAPPPTGGQNDNDAVT
LSADGLRTLGVQIAVKGDLEASRSEEPSDGPSTNLPESGRAPPESSQAAAAPEHTPQHKVMTSVKEETE
RMNMNASANLPGAPKRSNEDPASTATTMQSTSTGGQEGEATPSSNGIPKIQEEKLTGNNTTENVQPSDT
AETERLQSVNTSNVGDSDGSTTVSHTASPLLLLLVVASAAAVVAA*
>Tc00.1047053506309.30|S085|AG--YK-C-|2
MAMMMTGRVLLVCALCVLWCGACGVYARDRDSNELVGSMSSGVLGANLPHMPSGSDKNAVMLPTRSVLP
ITVAEALNENDVSVTTEEDADLSLNTGSLHAAANGGTGGIGNTIDSHAGGSKTSGGEIGSPGAGAVGVQ
GEGAQRSGGGGDPNGSGHSTLETLGREASGKGGDQSGVRTEENSRNPPAELSPSVHSKPPLTPPEPAGV
PQIQNAPQVLPQKTPQTAEASPSPVVSAEDRGTPESRDSQISSEETKKHSTSETKTESQVKEKFSNGGL
TEEDGQEATTPNLAKNAVTETPTKTTASSLSTSGTGDVQTTTDTVDNGAQRPNTKEPQDGFEDGNTKVP
PRASGAAPQTAKTATITQKNDTATSTQNSDGSTAVSHTTSPLLLLLVVACASAAAVVAA*
>Tc00.1047053506309.40|S010|A----RECD|22
MAMMMTSRVLLACALCVLWCGVSVANGDTGNDREHSGQGDVGIFSHSSSSVVGHGDNGVVTDGNFQGSG
SHSPGFAPNGGKTSLTGVVEGVGLKSSKDALTPAEEGRGGMQGQQELVPKVSHQPEAGTTGKSHHNAPE
QLPNARTELGNGGGATAEGDEVKTTVKDAQLGRSSTNDSHPPAADRGLKEQEGTVRKATSTVALTPAVG
RETPPKADPKEDSPKEKAASSAGVTQDSPTVSQQQTHSSSSSQSGIDPTYTPGEGRDAEEIFNNNQPSG
GVVLKEGAQHETVAGSEKPTIPAANTRNTIGTTIYGDSNSSTATITALRSDAGTEGTPTTNHLNRPSTE
GATPPETNSDGEAVSANKYDTVSQSTGSTTAQTTNAKPGDTAKPGDSDCGTAVSHTTSPLLLLLVVACA
AAAAVAAA*

>Tc00.1047053506309.70|S100|AML-VFEC-|15
MMTGRVLLACALCVLWCGAAFGHAMEDYCSEGGGNGLRHTSNGGDDGVSLKADCGLISTRMGLINAVEA
GDDGIDENGNAVLENKDKSQHGSVLAGTGGNETPGQKGVKGAAGAGLPPSPSGPGGSDTEEQRQPEQLD
TKGKEAGGKRDEKGGKATESQQQRADQSSSSGSDGPQGGKEPALKEKSESTESSVDTPTQEDEVEAEET
NVSEEETGGDEENNNNVALTVTSESQAKLKGTQTATPPTLPTTQVNERSRTEDLGHVQQPKGVQSDIES
NSNSQTEGAAPITANQHNEPSADHAGSRPLSPTANGDAANNDSDKSTEEGIPNNDPAADGAGTAEEKQN
ENKESNPKETSVEATAMKNTTVTTGDSDGSTAVSHTTSPLLPLVFVACAAAVVAA*
>Tc00.1047053506309.140|S100|AML-VFEC-|15
MAMMMTGRVLLVCALCVLWCGAVFGHAMDDYCSEGGGNGLRHTSNGGDDGVSLKADCGLLSTRMGLIRA
VEAVEAGQELSGPDPPQDNSKVSSSDKKVRSGAPGSKGGSVAAAAAAIPPTPGGSGTGGQVVKPEGLDA
NGGKEADHKEDRNDSTATGPQLQSVDQSSSSSSSSGSPGTQSGEEHNLENTSKSDESSDDSAEDDESDP
LSQSDSREERAEEEPEKNELNTENTSHEAPTLTTAPAEEAEIQATIPTTPLHGHSGAEDSGEVQQLQQP
QDGIESNNHSQTKSVATIAANQKNEPPGGHAESRPPSPTANGDAANNESETSTEEGIPNNDPAADAPGT
AEEKQNENKDANPKETPVEATAMKTTTATTGDSDGSTAVSHTTSPLLPLLVVACSAAAAVVAA*
>Tc00.1047053506601.40|S008|A-----ECD|43
MAMMMSGRVLLVCALCVLWCGVGGVCAEEQEAGTLLLPPGPVHDDQEEVLSEIGRMKPSDTDEQVTVDG
VGDREDSKHLSGHVPSVDAKDVTPAGIGGAGNGAVEEVAPEENESLQNSCDEDGEMSEGCVQVQGSDDF
PGSEGGHVDRGRQQDDRNPPLPLSDQTSSEEINSPLPAEGKPKNRRPVPRQLPVEEEQTDPVNIRPQEE
AATLESEAVRNVASSHSQESAAELANGTLPAHARVTEAEDRSKHIVDPHKDAAEKQKKPAHTTGKSKST
AASGDAHKTTASPAAVDNEAAIKKAKSPGDASSLTSISDNSLNNDTEQNNARDTSDEASHSTENAATHS
AGIPRETITTAKTDDTATQEDSNSDGSNVKMGEAAPQTAGTAQPNDTATTGESDGSTAVSHTTSPLLLL
LLVVACAAAAAVVAA*
>Tc00.1047053506759.20|S061|A--TIFECD|52
MMMVTGRLLLLCALCVLWCGVCGGGCSEAAPALPGTEPEDNKRKGENNTTDNVGGGGPTGQPAVTQPAA
GSVPVSGIEAESALQPAAQALQPAAKASGTANATTENNKNTTKKEDKADNEELKDEEKEDEEEEEGEEE
EDEVEVYDGKEKKEETEEEKKEEEKDDTSTTERISEGGQEEPILSSRVEEASNKTKPQSTQTTGDKDPA
ADGAVTQEEKQNENKEANPKETPVAATVMKTTTAKTGDSDGSTAVSHTTFPLLLLLVACAAAAAMVAA*
>Tc00.1047053506759.40|S064|A--T-KECD|5
MAMMMTGRVLLVCALCVLWCGAGGRCDGGETAGSGSGGGPPPESKEIETSPQVKQELKDEARSVKGKKP
PTSSEDEVEEDEKEDNDDDDDDEPEEEKEKSKEKEDAQQTRKSKSSSKEVAPLTIPKASGLSEAGGGSP
SGVDGVGSSESSGGSEDLNLEVSAPVVNFPPLLPNAAAGGLQNTDGALSSQKNNFSETGVHSGTTPPAP
SLPKSQAPAITKPEAEEQSSTEQDTEDSPDTEEVTTGKENVQNTVETGIPSRSSSAASKPPVQLTTPIL
TQSPAVALPERSALAPSEKKSTAPSFSAGEGSRRATNVAQNSKEEKNEKLPSENETESKAVEQPSGDDL
AEQDSPARTTASPIPASGSAEAQRNADADNSNAQALKYEGTNKNSETGYTNLASTAGDAATQTEKALAD
AKANDTVTPGDGDGSTAVSHTTSPLLLLLFVTCAAAAVVVAA*
>Tc00.1047053506759.80|S059|A-TTIFECD|4
MMMVTGRLLLLCALCVLWCGVCGGGCSEAAPEAQLIESEDNKRKGENTTIDGVGEVDRLGQPAASQSAE
SVPVSGSEEESASNPSPALQPAAKASEVANATTENNKNTTKKEGEADNDEELKDEEKEEDEEEEEDEEE
EEDEEEEEDEEEEGEEVEEKKEEGEEVEEEVELDDGKEEEGEEEEKDDTSTTKGILAGGQEEPILSSRV
EEASNKTKPQSTQTTGDKDPAADGAVTQEEKQNENKEANPKETPVEATVIKTTTATPGDSDGSTAVSHN
TSPLSLLLFVACAAAAAVVAA*
>Tc00.1047053506759.170|S008|A-----ECD|43
MAMMMTGRVLLVCALCVLWCGAGGRCEDLGTFSSEPVVDNPVNAPGSKKGSDLPKSNDNEDPKTLGEGQ
NCDSLNLPENEICTNDSTKSSKCTEGPEDALVSPLDPVGQGEHHEVQNSGSSGSSEKDKTRKDQDSQVR
LHDGETLSREPATLKDPQITMPAEHSSSPSPSKGTHETVSSTDISGVGDGTVQRDNMQNTLNGNDGSES
RASQLDSASGNTQTSVDEETSSNGGAPQVSTAADTDSAGSTTKALNTADTKKENSGGGDSSLAASPAVG
TNTATTTTSATQDASEYNKDGVKLSTEEVEQNASKTNPTANSGSTETAAANSEVPTAASNATNKKSNTE
TTADSDSSTAVSHTTSPLLLLLLVACAAAAVVVAA*
>Tc00.1047053506801.40|S043|AG-----CD|27
MMAMMMTGRVLLVCALCVLWCVAGGVYARDLDNNAQEGCMASGVLGMNASYVPNGCNKYMPMPPLRSAL
PIPAIQAEDEQLTDVSQDGTNSTSVNAPESGSGVGSGGSPGPAASPGSPTGAGGPAAAAAAAGPAGPAG
PAAAAPAAPNVVPGAAAAGGGPNGPAGVTGGNAGSSGATDVLGAAVSSDVPSSLPADSENSNADCGEEA
SDCGNQEKLEKTKVENQELEASKTQKTPATQNTKSKDNEENSTEASSTELQNTETQQEIKPPVDENDTT
STDASTAVAAQSTSAGIQEEATESSSDGSHSPLQGEVFTGTDTPENAPSPAAAEAEKRQGENVTKDGDS
DSTTAVSHTTSPLLLLVACAAAAVVVAA*
>Tc00.1047053506813.29|S043|AG-----CD|27
MAMMMTGRVLLVCALCVLWCGAGGVYARNPDNNSLGGYMASRGFGRNTSFLSNGSIKNLSTPLLLSASF
ISAMQAEAREGKVSSARVTDSHLSGATGLVPAFSDLGASSPRPTVPGHGAAVPVPGSVRGPDAPIPGVA
VPSPGPSGPGLRAAGHGLGASVPSPAVPGAAAAIPGHGPAGPDHVPGAIPGHGPAVPVPGPGPVPGPAV
PGPGSVRGPDAPIPGVAVPSPGPSGPGLRAAGHGLGASVPSPAVSGVGAAIPGHGPAAHGHGPGAIPGH
GPVRVPDAIPGASVPGNGPVVPGPAFSGLDAAGHGRDAAIPGPGSARGPALSGLGAAGPGHVPVGPDHG
PAIPGHGPAGPGAGHSVGGGSEPPDSRSVVTSSSQGGNGKTAPVSVSSDEQIVSSKEVSAQKETGSQDT
SSPEGQPTVSSNTEKQRNNSASAGGHSLGHDAAGDELQDSLEEQKKNDHSQTNETKKSPGDQNTESQSS
GGALSEVSNTTTHGIKTQEPKTNSANEKNYSQNTDASHSTSPLLLLLVVACAAAAAVVAA*

>Tc00.1047053506877.20|S133|ANQ---ECD|6
MAMMMTGRVLLVCALCVLWCGLPGVAADGVDVVSDGSGDEDLLLQWRAWLRRESAEEVSRRTGGGANAS
AVEECVRQGMDGLRAVVDGHRRWRHQRIVVAAAAGNGDVITDKDGQARNNEVSPPEIKDEKPVASGKES
TDATRGKDQTTQNPSAAIVSRKKLISEKKQEGGERMTEKEDGDNEDEEVEDEAKIRETTPVVPPPAAAG
GGIKPPSGASGPAAPGAILTSRSSSGVVSSSRIGDEGSTVGISPNAVGKPSRQDKVPEAKESQHAQPHD
GVAADTLNNGSEQNGSAPTTGQNDNEVATVGAGGSRSSREQITVKGGSEASRTDESSADPNTKLQENEK
TPLKPSQAAATETKTSHEVLTSVKEETNSKSTDASANLPDAPKSSEEHPASAATTMQSTSTAIQEAAAT
PSSNRIPPLHEETTTGTNITENAQPPKETPVETTTMKNTTATTGDSDGSTAVSHTTSPLLLLLVVACAA
AAAMVAA*
>Tc00.1047053506877.60|S061|A--TIFECD|52
MMMTGRVLLVCALCVLWCGACGGGCSEAPSSDAPASSDNASSEKKPQREEEAVVVTGEGVKNGEEAAPK
GTASPASGLPAAVAAIQTGTQLSPQPEGGGTSETASTTTDNNNTNTEGKKEEKEEEEDEDDKKKEERET
KEEKKDKEKEEEKIKEDDADATKGMPAGGEEPPSLSSGAEEAANQTNLKSTQTTGDDDPAADVTGTREG
KRNENKDANPKERPVEATAMKTTTATTGDSDGSTAVSHTTSPPLLLLLVACAAAAAVVAA*
>Tc00.1047053506939.50|S030|A------CD|31
MAMMMTGRVLLVCALCVLWCGAWLCDAMQTSSSAPHRENAKETMTPEEVTVAIEKLTKEVLESIRLSCR
MSFITSVNATLPAHNDTEVEKCVNKTAVEISGVTSRGRPAAATTDANFASPLPSSSSAASALQGQAQGS
PGAAPETVKPPQTDPVNNEQLSEAPASTGGGPGGGGELADRSSRTPTDDAKTHEARPARNATSTPTATQ
GYSEKSPANTTRTRETNETDDTDGSTAVSHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053506939.110|S004|A---V-ECD|18
MAMMMTGRVLLVCALCVLWCGGGGSCDVEVLPAVEPLVNPASGSGVTGNASGHTVTGEAEVVSLQQSRL
DNAGNSAAGSPQLQAALEPESPTEQPQSDPEHTVPSTHSQSSGEGRQDGAPDGQPGKPGISPSQEDNKD
VSIENQQSNDPPSHSGNDDVVSRNSGERTEDDSRRTETLVAAPSEEGQEPENVTPSLEQPRETSTAAPA
VTTQTTSITLPEENASNTVKMNDASPHSTVTANTNHTVTPAENDGSTAVAHTTSPLLIVACAAAAAVVA
A*
>Tc00.1047053506939.180|S080|A---YKECD|24
MAMVMTGRVLLVCALCVLWCGAGGGYAEGVDVAFGGPGAFGEGGGGAGGQSPPADGSRGGSRGSKADGS
HLGESDASDSASDDISLAPSPALDVVPTLSEEPLPQEEEESERKQKHPQTGPQVASTPKVSGREAIDPD
SQKQLPDKSKTESITNVGGGETADGGKGNNAHNSGLSSNKSDPPALLEARITKVSLPTEPSQPPADLSP
PPHELPTVPSPTGLAPAMAISAGETNPTASTGSQNTTETTSTTSPSNAKAEREATEKTSGNVAPNQNRH
DTDTPGLMKGTTTSRPAETAVPSVSKSGSDGAQNKEGKVDNGAQRTNSKEPQDGPEDGNTDDAPTANET
SSQTATTAITTQTNDTTTTGDSDGSTAVSHTTSPLLLLLLFACAAAAAMVAA*
>Tc00.1047053506951.60|S008|A-----ECD|43
MAMMMTGRVLLLVCALCVLWCGAGGVLASASDVAAGGSGTSGERGGGDKSSLADGSHGGSGGSNGDSSH
ESESEPSDSASNEKSSNLQVDENEDPNSSGQPLQQGKEGSKGKQDHLQSAPQNGSPHKVNGTETLGSDA
QVQLSATPNAELNTNVADGEIANGGRGNTGHNAGLSPYSSDSSAPPVPQVNDVVPPAEPSPAMTVPAGE
TNPTASKDLQNITETTSTTPPSHSKTASEAPENPSGNGAPKQHREETDPPDLKDAPTSHTAQSTASPIS
TSGSSGAQSEADADDDDPQRPNPEGPQNDGTEAGDTHGPSAASDAAPQAAKAIAAQTNGTVTPGDSDGS
TAVSHSTSPLLLLVVVVCAAAAAVVAA*
>Tc00.1047053506973.20|S134|ANQ-H-ECD|1
MAMMMTGRVLLVCALCVLWWGFSGVVADGAGGGDGSAGEDLRALWLTRLRRECAEEVIRRTGGRTNASA
VEECVYQGLESLRAVVDGRRRWRHQRYAVAAVEGVVDGKGNIGQSDDRLKVSSPSVQGLQEGSGLPGVV
GGPPNLPAREDTLKLSGDAISPDGLKVNAGADPAKITASQRPKEDSTAAGTRNHSPPGPSPTTSSKAEN
ALLLTNSEGQKTEIKVEPKDQTLSVGEEGLRNQEGQSPQGKEHQPTVEIKASDIPTERPLEGGEHDVDS
QEEDREDKVVAGRKQTGDGGHEVSNEKVLRVPVEPKANLTEIEQEVTRTHTGEHLVRDAEAAEKEKQRE
QGADGQNEKNEKGPVTRKEQREQEENQLPHQQEQQEKEGTLSASPAGLETTQRSLSTVQPEGIQEELLQ
QQHQQHEHPAESGEESAKDKNAIRTNATANKDDSDSSTAASHSTSPLLPLLVVACAAAAAVVAA*
>Tc00.1047053506973.30|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCGAGGVYARDILKNAQGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASDGEGASQHANNSGSNANNSGSGGGGGSAAGPGASVGAGVSGEGDSGGGSGGGGGSGGAGGDS
GSADGAGGPFASPPGPPPAPLGGPSAASAPGVDSSAGSSDGTAESSGSHPTNTTGDSSTGDQSSAAAAA
NDSSPPEGPAGTTSGAGHTRQEEEEEEEEDHEKQQQSDEAQVQQHQRHERPAENGEESAKDKNALRTNA
TANKDDSDSSTAASHATSPLLPLLVVACAAAAAVVAA*
>Tc00.1047053506995.70|S083|A---YK-C-|4
MAMMTGRVLLVCALCVLWCGAGGSCEEEAGAPVSGGVPPPAAKELETAGQGTKNLKVGSPDIEGKVIPA
PSPPTEEAEDEDSDEEEETAEETEKDKKGEKEKNKLHPQTHESQNNEGAPPPPPTIPSGGPAPSSTAGE
GGPLPDQENLQKLNKAKKENTPSRSKTDSEAPEPPPGDATQGQHNHDTDTKDSTKNAAAGSPAETTTTS
STSTSGSGDHAQNKADEVDAQSSEEQHESLEIGNSNVVPPLSERAPKTARTTTDAQTNGTVTKVGESDG
STAVSHTTSPLLLLLLVACAAAAVAA*
>Tc00.1047053507067.60|S025|A------C-|17
MAMMAGRVLLVCALCVLWCGAGGGCDEEVVEAAAGGLLGTAGKGTVETSGTSTPGPDGSDLPKGLPKVN
QPTETSTGKSLEVNKVNVDQQDVAPGVGDEEDGSPSDHLEEPLKDDPEKGKTKPELQNKGQEGREPPQL
QVTVPQQPQPPLQQSQPPSAPQPQPSASEKGEVVGENNKGGEGQLSLGVEHKGSAAPEAPRKEDLLEGS
GKESENNEPVQTTVPNKVPPEHKTQNGMLTPEQKTNESQGTDTSMNLPEIKKENKEYSASTKSTAPSTS

TGSQEQEAEPSTSEEPSPFEEEQSTVTKKTEDARTPDAAATEKRQNGANEKDGDSDSSTAVSDTTSPLL
LLLLVVACAAAAVVAA*
>Tc00.1047053507867.10|S017|A---S-EC-|13
MMTGRVLLVCALCVLWCGAGGRCNEGLAEGRAGVSGSDVEPPPAPTPLVTSPQDTQSLHGRVSGVKEKL
SPASSTPTEEEDDDDEEDDSDEAEAQEGSIEGQGGKGGTAASEPGSGEKNLSGSKKETGQAIVSAEGIS
HSGSRESNANPTQTEVEEKKNTDKNTPAVENAITTGNGENTLPAGIAGGNLPSLPEDSVDSHEQDGEDA
TSEGKKNVPLPETAATPQSHQENGSEGTVEDTKATTVTSNTTDTTNTQNSDSSTAVSHATSPLLVLLVV
ACAAAPAVVAA*
>Tc00.1047053507937.50|S061|A--TIFECD|52
MAMMTGRVLLVCALCVLWCGACCGGCSEKPPVPPASPSSKDKDPPEVEETTGLAAGDDQSGKQKAPQAA
APTAPESQEVPAKSSQAPQPEGIVSETTNTTKDNNDQKEEGGKKGEKEKGAEEEEEEEEEEEDGAKENG
ETKKEEAVTGTTEGTSAGGQEQRSLSSGAEGASNITNPNSTQTTGDDDPAADVAGTAEGKQSENEDANP
KETPLTAAAMKNGTATPGDSDSSTAVSHTTSPLLLLLVAACAAAAAVVAA*
>Tc00.1047053508013.110|S058|A-TTIFEC-|2
MMAMMMTGRVLLVCALCVLWCGAGGGGCSETPQAPQDIKSGNGNNHQSVNNNAGGAGESGQSGEPVESQ
AAGLSVTELPGAGAATKLPGAETPTAGTEKKNEETGQEKEEEDDKQQEEEKTKKDEKVVDKKEEEAEED
DEEDKDDDVKDEEEEEEQKKKKDDNGATKKLSAGSEEQPLLPSGAEGASNNTKSKGTQTPDDDDPAADG
AGTREEKQNENKEANPKETPVEATATKNTTATTGDSDGSTAVFHTTSPLLLLLFVVAAAAVVAA*
>Tc00.1047053508151.20|S038|AG-----C-|7
MMAMMMTGRVLLVCALCVLWCGAGGVYARDVDNNAQGVCMTSGGFGKKKSYLSSGCDKNAPTLSLRSVL
PIPAIQAEDSEEVASSKGKGGKNPTSGVVEAADIAAGVGGGGSGGGSGVKSAGQGGGGSSEAGSVPAAG
LSPGAGLSPAAGGPASGGGSSPDRIVGTETSVSLSSPLQSESEKKVLRRDEAKDQSHQLPNGKAAGTPV
AETQSRGSDKTRGQDVGDTSTLGFKQERSSEEPEKKDGDSYTLQTVKSPEDPNKELQEKGKALPELSNA
PLPEPKTDHPKTNPEKEKKGSQNTSASTDSPAKQEGNNEDPVSTSDAAESVSTGSQEQAAATSSNDSSS
PLQKETSVEKTTVENSQPSDTAQTEKRQSVNKEKVGDSDSSSALSHTTSPLLLLLLVACAAASAVVAA*
>Tc00.1047053508157.20|S090|AG--YK-CD|3
MALMMTGRVLLVCALCVLWCGTPGVDATNHENNAVGVCMTSGGFGGKMSYLSSGCDKTDVGLAMRSILP
ITAAEASDDEVVSNTADINSQSSQNSNADTAGGGGSGGSGGIVNNFGDDREGVRGHSDSRSHDDLSSSS
ILNEVVDSNALSGPIPAKSRKSPEKDPKSEEMSTRPLLPELVVQEDTITKAHDQLSHTIEKAGNQVVGG
GAAGEGVKQRDMGTTGPSSNQPAPPAPQEITQTPADPPGKGGLPAPTESRNKKDQPLENLPLTTKTESE
ALETSLGDQLPERKRHEEAPADLMKDAVTDNPGKTTATSISTIDSGDAHEKEGKDDDTDERPTSKEHNS
SPETGNTNDAPTASEAEPQRAETTATTVAKKNDTTPGERESSNAVSHTTSPLLLLLLVACAAAAAVVAA
*
>Tc00.1047053508227.20|S017|A---S-EC-|13
MAMMMTGRVLLVCALCVLWCGASGRCDGEDTAVSGSGGESPLASKGIETSPQGTQELRRGAGGVEGNVP
STSSEDEVEEDEDYDDDDKGTEDGEGKRTERQSVQGGKAAQDPDSREKNLGGSDQEIHQSIAPAGDISH
SDTQESNAIPTQTEIEEKKEIEENTPAVENALKTVNGEHTLPGGIAGGNPSSSPEDSVDSREKDGEDPK
SGGRKNDPPPETAATPQSHRDKGSGRTGEDKKATTVESTANTNHTTTPGDSDGSTAVSHTTSPLLLLLL
VACAAAAAAVVAP*
>Tc00.1047053508227.40|S034|A---H--C-|4
MAMMMTGRVLLVCALCVLWCGAGGGRCDEEIAKDPVGANDTPGNFGEDETEKAEPAALGHGDLGLKPEP
PKEVSQGGPSEKPLGGTGGDDVENDEGVLSSGRGDEFKSPSPEEEPPETDDPGKSREEEEVELRQRRNE
EKKLENQPQLQVPVAQEEHGTLPLSLPHTQSQQSHQTTQQQQPQPQILQQEGGLPHEKGSEKGTQELDK
LKEDTQHTELQNKVKEEKTTQELKNEKKGREHQPQLQVPVEQQEQSALTQPPQSMQQPSPPQEQTRQQK
QQPPHEHPADNEQESKKDKNAVFANKTENAQDSDGSTAVTHTTSPLLLLLLLVAAAAALVAA*
>Tc00.1047053508327.10|S099|AML-VFECD|25
MAMMMTGRVLLVCALCVLWRGAVFGHAMEDYCSEGGGNGLRHTSNGGDDGVSLKTECVLLSTRMALIKA
VEAAEAGEDELSGAPAPSQDKSKVSSPDNTEDGGATGLGSGVVAVQAAAIQPKPEGSGTGGQEGKSTVV
NTKGKEGDNKNGTAADSKKPKPDQSSSSSGGPGPLVGEEPLSEHSKTSEFSGIQLKEQGKDLRSKPHSH
EEVVEETSESEQEGTGEGKYEKINDKAPAVIRENPLEQKEMQTATSPTQVNGQSGTEDNVPMQQLQQPQ
SGMNQSNNSQTRSVAPTTANQHNDPSAVHMETRPPSPTANRDAANIVSDKSTEDSNQKNDLAADGAGTA
EEKQNENKDANPKETPVEATAMKTTTATTGDSDGSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053508433.10|S046|A--TV-ECD|3
MAMMTGRVLLVCALCVLRCGAAAMASAPDVAAASPAAGKGGPEEDHSLGAQTGNSTNEQSVVVISPPES
PLGTEEEEEEEVETVQKEKLESKTKEEETPKLTSPQVGEGPPAPVTTRKNEKPAETSDATPGKGQSSSG
DVSTRPELHKKPSEEQPSSTAPQAPAPAAAAQIKNESTTSADVVSGQQIKEESQHDMQSEGTSGKEENV
PTTVTKKDGPTESNAESTPTTPSASKDAITNDDEKSNEEEIPKHDQTPDGETMNEASQVGNNEGNTTKT
QTVEAAAITNNTATPGDSDGSIAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053508433.30|S059|A-TTIFECD|4
MAMTMTGRVLLVCALCVLWCGAGGGGCSEPTQDPQDITSGNGNNHQSVNNSTGGGGEVGLSGESAESQA
AGLSVTELPGAGAATNLPGAQTPPTAGTGNNSEDTGQENEEEDGKQQEEDKKKEDEMEVDKKEEEAEED
DEEDKDDDVKDEEEDEEHRKMKDDAGATKKLSADSEEQPILTFPAEEASNKTKSKGTQTPDDDDPAADA
AGTAEGKQNENKDANPKETPATAAAMKTTTATTGDSDGSTAVSHTTSPPLLLLVVACAAAAAVVAA*
>Tc00.1047053508433.90|S061|A--TIFECD|52

MMTMTGRVLLVCALCVLWCGVFGGGCSEAPSPALPGSASDGNPQKEGKATDVAGGVQSSQQAELQETPV
PPASGSQELPARPSPAPQPGGGAPDSANTTTEKNNPNTESKKEEKDRKKEEEDNEAEGEEDEEEEEEEE
EEGEVEVEVEKEEDDTKEKEETGKEKEAVTSTTEVISAGTEEQPILSSGAAGASNITNPNSTPTTGDDD
PAADGAGTAEGKQNENKEADPKETPVEATATKTTTATTGDSDSSTAVSHTTSPLLLLLLVVACAAAAAV
AA*
>Tc00.1047053508433.180|S003|A---Y-ECD|2
MAMMTGRVLLVCALCVLWCGGGGGYAEDVDVAVGGPGTFGEGGGGAGGQSPPADGSRGGSRGSKADGSH
LGESDASDSASDDISLAPSPALDVFPTLSEMPLPQEEEESEAKQKHPQTGPQVASTPKVSGREAIDSDS
QKQLPDKSKTESITNVGGGETADGGKENNAQNNGLSSNKSDPQPLLEPGIPKVSLPTEPSQPPADLSLP
PHELPTVPSPTGLAPATAVSAGETTPTASTGSQNTRETTSTKSPSNAKAEREAQEKPSGNVAPNQNRHY
TDTPGSMKGATTSRPAETAVPSLSKSGSGGAQNKEDKVDNGAQRTNSKEPQDGPEDDTSDAPTANETPS
QTPEKATTQTNDTTTPGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053508433.220|S099|AML-VFECD|25
MAMMMTGRVLLVCALCVLWCGAVLGHAMEDYCGEGGGNGLRQTSNGDDDGVSLKADCGLLSIRMALIKA
VEAGEKGLSDTAPPQDNSKASSPENKVGNNTKSTGAPDSKGGSVAGEPAEAAPTPGESDTEEKVVKPEG
LDANGGKKADGKRDRNDGTATGPQHQRADQPSSSSSSGSSGTESAKQPLVKENSERNETLDDPPQEEEK
DRGSESDSHEEEAEELEKKEDKKNASNQAPTETLGGLTKHTEIHTATTEPNGQSSPQALGDVEQPEEVQ
RDIESNNNSQTKSVASIAANQQNEPSADHGESGSPSPTANGDAANNDSDNSTEDGIPNSDPAADVAETR
EKQNENKDANPKETPVEATAMKNTTATAGDSDGSTAVSHTTSPLLLLVVFACAAAAAVVAA*
>Tc00.1047053509547.40|S012|A----REC-|10
MAMMTGRVLLVCALCVLWCVAGRCQETLLVSHSDVPGAIEGDGGQPQGSSGFKTPESHAPGSEASVREV
QQEQDPSPPREETHLGTKGGNKVEKAKEKGAAKDAGKEGEVDGKTIELKKPEDKLTSVEGQQLNNNEGL
QPTTLNGPHGVETTTPSRDSLPAREDQQDLSSSLLPPLHNTSPGGTPPSTPAAGRADTKSHENDIGKKN
SQQSVVGEIGQNNDTGEKAVDSTGEEEGSRLSVATAEEMSETTTKSDSGGTATTTAVGTDIGTEETPPT
NHPSKPSTEGATPPGTTSDGEAASTNKYDTVSQNAGSTTAATTNATTGDTAKRGDSDSSTAVSHTTSPL
LLLVVVACAAAAATVVAA*
>Tc00.1047053509867.20|S043|AG-----CD|27
MAMMTGRVLLVCALCVLWCGAGGVYARNPDNNSLGGYMASRGFGRNTSFLSNGSIKNLSTPLLLSASFI
SAMQAEAHEEVPSAGVTNLPLSGAAGLSPAFSGPAAAGPGPIPGPAIPVPGSVRGPGAIPDVALPSPGP
SGPGLRAAGPDHVPGAIPGRGPAGPDQVPGAIPGRGPAGPDQVPGAIPGRGPAIPVRGPGAIPGVAVPS
NGPAFSGLDAAGHGRDAAIPGPAGPGAAIPGAIPGRGSVRGAAVHGPAGPGLGPAIPGHGPAGPDPAFS
GLVPAVPGAGHSVGGGSEPPDSRSVVISSSQGGNGKTAPVSVSSDEQIASSKEVLAQKETGSQGTSSPE
GQPTVSSNNEKQRNNSASAGGHSLGHDAAGDALQDSLEEQKKNDHSQTNATKKSSGDQNTESQSSGGAL
SEVSNTTTHGIKTQQPKTNPANEKNYSQNTDASHTTSPLLLLLAVACAAAAAVVAA*
>Tc00.1047053509867.60|S043|AG-----CD|27
MMTGRVLLVCALCVLWCGAGGVYARDIGNNSQGVCMVLGGFGKKTSHLASGCDKNAPTLSLRPALPIAA
IQAEDTEEGAGSDITAVGGGGGGSGVNSARQDGAGSSQAGSVPGAGLPPPAGASGVGGNPSGSVTPGGD
SSPDRSVGTGTSASLSSTSQGESEKKVLQGDEAKDQSHQLPNGRAPDTPVFETQSRGSDATRGQDVGDN
STLSGKEQRSSEEPEKKDGDSDTIQTVNSPGDPNKESQEKGKALPELSNAPLPKPKTDHPKMNPEKEKN
GRQKTSASTDSPAKQEGNSEDPVSTSDTAEGVSTGSQEQTAATSSNDSFSPLQKETSTEKTPVENSQPS
HTAQTEKRQSVNKEKIGDSDGSTAVSHTTSPLLLLLLVVACAAAAAVVVAA*
>Tc00.1047053509977.30|S008|A-----ECD|43
MAMMMTGRVLLVCALSVLWCGAGGGYAWDFGRENESLRKKHYGANGTYCRLNSSLFFCNEKRNASELEE
TVSQKSTVQREEGSDQPKAGDSSGGQDHGSEKNGSDRSIGNSGTTELKNPGERETTPTQPSTGAENLPK
PAAPGEPEAPGTTTELQPPQQSPLQSPLPAGGTPPPTTATPTADGSSGGQDNSSEKNGSNDSEKTDAGP
QESQPPNGNVTETPTPATVTAAQTSATRTPDESDGSTAASHTTSPLLLFLVACAAAAAVVAA*
>Tc00.1047053509977.80|S008|A-----ECD|43
MAMMMAGRVLLVCALSVLWCGACGGYAWDFNDESVNEYYYGANGTYCRLNRSFPFCEEKRNASKRKEAA
LQKSTAQSGTGSGLQAPQPLNGNVTATPTTATPTAGGSSGGQDNSSEKNGSNDSEKTDAGPQESQPPQG
NVTETPTPATVTAAQTSATRTPDESDGSTAASHSTSPLLLFLVACAAAAAVVAA*
>Tc00.1047053510039.30|S008|A-----ECD|43
MAMMMTGRVLLVCVLCALWCGAGGGYAWDFGSESLNEHYYGANGAFCKILPKMYSCELRINASKLQEAA
SQKNNTQSGTGTGQPNAGGSSGRQDQTLEESGSGQPEGTAGEGTQASQPPGEGGTETPTPLSSPPTATA
TATAAQTSATRTPDESDGSTAASHSTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053510085.60|S080|A---YKECD|24
MMMTGRVLLVCALCVLWCGAGGGFGDEEEGTALVVVSPGGRSNDGKGGPGSVPPSPPGTGTSGPRSIVP
ESQGSQERIAGTSSEEREEKNYQNKDEEEESVAEDGENSRHQKRLSEQPTQKEESHEETPEEKGPKKRI
EEEKDVPPPGEEGIKGTQQSQSQQPPPKQLQVQITAPAGRGGPTAPTGPARPPAPAETSSMDGSQTIEP
TDSRNPSQSTHDKSPLQTKTESSAPDPPLKMAFPAQHGEETTTPDSVMNASAGSQARNTAPSTSTSGSG
EAQSEAAGNDAQRRNPNKSHDDSDSRKNKVSTTLSEAAPQATETVAAAQTNHTKTTGDSDGSTAAFHTT
SPLLLLLLVACAAAAAVVAA*
>Tc00.1047053510107.30|S049|A--T--ECD|5
MMAMMMTGRVLLVCALCVLWYGAGGCAEESAGGVLPGASGGGAKSLQGSQPIVPEVLKNSDLKASDIND
KTEETLIKVSLAEQEEISDDDDEGEDEEEGPSPPTPPKGGGVQPQANNGKLKKANESEPQKENQRHVEV

ERQNPSEKETVVDEAEGTNEKEAIGLQPQQQKIPVREQDTRNGEGNQPTQGNEEQTIVEEITPHNPTED
HSSGEHKGSDGSKEMEEGEEGGVEGYEGRNERHRDQVREEAVHAAGTPKLNSTDIQQEVQRTHAGETPT
GIKQKAEEEKDDETEAEREQQKKQHQGNPTDKKQEFTSGANATNKINTTPGDSDGSTAVSHTTSPLLFL
LLVACAAAAVVVAA*
>Tc00.1047053510193.10|S030|A------CD|31
MAMMMTGRVLLVCALCVLWCSAYCICTEEESVSLSRSGIGDSRTGSGVSGENGVKTDKTRTMRTASEGD
SHPSERDVSDGGSFDQATPDKSMCKEKNDGSTVKPLTTDGEVLVDSQETVATHLKGTDTDLADPNINQN
HKNPKAIDGIDTQLPDAPAAPKAQPSPPTVPTANKTVNSKEELTAEETPEHSRATRNPNEGSETKNPTD
QALKPDAGGIDTLASEDASSPSIDDAATSEATANTARVGSPIASLNNTDGKNEGSGDGDSPTPSPSAAE
PETITTAKPTTRDVSHPNKNGIVTFTGEKNAPTTNPKSATEGKETADVESDSSTAVSHTASPLLLLLVV
ACAAAAAVVAA*
>Tc00.1047053510199.30|S030|A------CD|31
MAMMTGRVLLVCALCVLWCGVCAVVVSAADSGIADASDGHLLHNGSGGGVGGSSPSEAGRPGGTEDAMG
KISNVNGSDSAGSVVSGNNLLFSGGGEGGVSDVSKLKLPPVEEGPNDIKNQPQALSGVALPPGVDSTGT
SKPDAEKPSSINKSSKGDRTDDVVDISLKKKEELTDVNKEEKTVLPPNDSESPAPTELGAEEGLKGKPA
SGVASLPAKGEEGLPETGQGEGSPRSEAASSAGKQQDSPTVSQQQTHFSLSPSQNEIVPTPSLGKGRAA
EDISKNIPPSGNAVQKEGAQHETVAGGEKPTTPAANTRNTIGKTLPGDSDGSLTTTFSAGPVASRRSTQ
VSGDAINTDGLNFDVSSDNVAHNNMTAKVENATGSKETVATNSGKSTTVPETFTDKAIGTVTTGDNDGS
TAVSHTTSPLLLLLVIACAAAAAVVAA*
>Tc00.1047053510205.20|S010|A----RECD|22
MAMMMTGRVLLVCALCVLWCGVGGGCEEVPGVSPSGVSGDLEREGGDSQDSSRSEPPGTKKSAPETPAP
KVQQQEVISPPPNDPPAGSEDGAGGDEEGKAREEGAKDAGKENRGVATSKEVKNPENHQMSVKDPQLRN
NEGLQSPSLNGTHGVGTITTSLSGSLTVNTNQQDLSSPLQPPLPNSPPHAIPSSTSAAGPDNEKRHENG
NGTKNSQQSVVGDIQEKNGTGVKAVASTSGEENSRLSVTTLEEMGDATKKGDSNSSTAATVALRSDAGT
EGTPPTNHPNQPSTEGATQPETNSDGEAVSANKYDTVSQSAGSTTAQTTNAKTGDTAKPVDSDGGTAVS
HTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053510205.50|S061|A--TIFECD|52
MMMTGRLLLVCALCVLWCGAGGGGCSETPQDPPGGASQGGNNPDGRKNTTNGAGGGVKSSVPAKPQLSA
ESVTDLSVAAAGADVSAAQQHGKQASDTEEEKTKNKNERNDEKDKHEDDEKDDDEEEEYEYEEEEIDED
DKNKEEGKRKKKKKIRRRRRRKSKKMIPTPQKGMSAGSEEPTIISSGAEGASNNTKSKGTQTPDDDDPA
ADGAGTREEKRNENKEANPKETPVEATATKNTTATTGDSDSSTAVSHTTSPLLPLLLVVACAAAAAVVA
A*
>Tc00.1047053510213.70|S099|AML-VFECD|25
MAMMMTGRVLLVCALCVLWCGAVFGHAMDDYCSEGGGNGLRHTSNGDDGVSLKAECGLLSARMALIKAV
EAAEGKQELSGPDPPQDKSRVSSPDNKLGNNTQSTGAPGAGGGGVGGQPAAVTPKPGGSDTEEQVGELG
VMDTNNGKVAGDEEQKDGNEADSQQQSVDQLTSSSSSSGSSGTEGVKQPSSRANSKSKETLDELPQEEE
EEDLPSESDSREEEAEEQETEEDKKNDKMVHKSPTETPGGPTNNAEIQTATTQVNGDSIPETLEDVQQP
EEFQGEKDSNNNSQTKSAASIAANQHNEPSADHGESGPPSPTANGDAANNDSDKSTEDGIPNSDPVSDA
PGTAEEKQNENKESNPKETPVTATAMKNTTATTGDSDGSTAISHTTSPLLLLLVAACAAAAAVVAA*
>Tc00.1047053510213.39|S043|AG-----CD|27
MMAMMMTSRVLLVCALCVLWCGVCGVYARNPDNNSLGGYMASGGFGRNKSFLSTGSIKNLSTPLLLSAS
FISAIQAEAREEVSSTRVTNSPLSGATGFGTVPHAPVPAIPGAAVPGHFADAIPGPSPVRVPGAIPGAA
VSAHAAAAFSGPGAAAPGNAADAIPGPGPSPAFSGPVRGAAVPGHGTAGPGAVRGAAGHGHGTAIPGAA
IPGAAIPGYGAAGPGPGAAGHGHGPAAIPGSPVPGHGPGATPGSLRGPAVPGDDAAVPAFSGLGDAVAE
AGPGAAAVFSSLGAAVPGHAAGPAGAGAAAAFSDPGDAIPGPGPFRGPAFSGLGAVGPGAAAAFSGGGH
SVLGGSEPPDSRPVVISSNEGGNGKTTPVSVSSDEQIVSPQEVLAQKETGSQHTSSPEGQPTVSSNNEK
KRNNFASAGGRSIGHDAAGDELQDSLEEQKKNDHSQTNETKKSPGDQITGSQRNGKELSEVSNTTTHGV
KTQQPKTNSVNEKNYSQNTDASHTTSPLLLLLVVACAAAAAVVAV*
>Tc00.1047053510269.20|S135|ANQTTTTC-|1
MAMMMTGRVLLVCALCVLWCGAAVAVPAADVSVGGDGSAGEYLLLQWRTRLRTECAEKVGRRTGGRANA
SAVEECVRRVMESLHAVVDGRSRWKRQLSAVAAAAAAAPVSPPAAPAEGGGKENPNTGKGDKKKINVLL
PLEKKNETLATSGKASTDKPTAVASEQTSLNPAPAIVPPTRETSDQGKHNGEKRKEEEEEEEEKDGESE
NEEEDAEDTEEEEEEKEEVDGEGDKEEKEGDEGGEKDDTDGVEEEEKEDTEEEDEDEAEEVEEEEEGGE
KDDSEEEEENHKEEDEQEDAEEGEKAEEREEDEKKNKKNNEDREEEDEEEKEEREEDKEEESEKNTKKE
EDEEDEEKVDDDALEGMPAGGQEKRNSTSGPEGAPNKTKTEGTQTPGDSDGSPAAFHTTSPLLLLVVAC
AAAAAAAVVAA*
>Tc00.1047053510269.50|S046|A--TV-ECD|3
MAMMMTGRVLLVCALCVLWCGAAAANGEEDAEKKKVENSWGSVPDADVGSAGLQVMPASIKEGPENAKE
SLGAQTGNSTNQQSVVVTSPPESSLRAEEQAEEEEEEEEVKTVQKEKLESTTEEEETPKLTLPQEGERP
PAPATTRKEEKPAETSNATPGEGQSSSDDVLPRPELHKTPSKEQPSSTALQAPASAAAAEIKNENTTSA
DVVSGQQIREESQHDMESESASGKEEAVPTTVTKKDGPTESNAESTPTSPSASKDAITNDDEKSNEEEI
PKHHQEHDGETMNEASQVENNEVNTKKTSTVEAAAITNNTATIGDSDGSTAFSHTTSPLLLLLVVACAA
AAAVVAA*
>Tc00.1047053510369.10|S061|A--TIFECD|52

MMMVTGRLLLLCALCVLWCGVCGGGCSEAAPALPGTEPEDNKRKGENNTTDNVGGGGPTGQPAVTQPAA
GSVPVSGIEAESALQPAAKASGTANATTENNKNTTKKEDKADNEELKDEEKEDEEEEEGEEEEDEVEVD
DGKKKKEETEEEKKQEEKDDTSTTERISEGGQEDPILSSRVEEASNKTKPQSTQTTGDKDPAADGAVTQ
EEKQNENKEANPKETPVAATVIKTTTATTGDSDGSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053510373.10|S025|A------C-|17
MAMMMTGRVLLVCALCVLWCGAGGGECTEVVKAPADGAGSGSEPLVQSQELGTSPQGSQELKDGAPVVK
KEAPPAPPTPSYEEDDDDEDNDGKGDGDGQEDESPSEHLEETVEDAAGKEKTKTQLQNKEQEVRQPPKS
QVHVPQQPQSQTQLQPQPHTPASEEGEGVGENNAGGAGQPSLGVENKGNADSRALGKGDSLRGPGKESE
SSEPVQTTVPNTVPPEHKTKNEMLTPEQKTNESQSTDTSTNLPELQKENKEYPASTEGAVQSTSTGIQE
QEAEPSTSEEPSRFEEEHSTGTKTTEDARTPDAAATEKRQTGDNEKVGDSDGSTAVSHTSSPLLLLLVA
CAAAVVAA*
>Tc00.1047053510373.60|S119|ANQFVFECD|2
MAMMMTGRVLLVCALCVLWCGIDGVAETEEPGIDVAPGVDEYLVVEWRAQLRRECAEEVSRRTGGRANV
SAVEECLREGMESLHAVVDGRRRWRPQRYALVAENPEDGPPEVISVGAPPPLPGQKTQGSLQELSLGDP
EKLSEGGAGRGTGLGSEQLQPEELPVTKQNESEVEGELIRDENNSELEKKVLVDSDLTKYQTMNVPEIQ
PEAVGLLLLSRDGRAAGIPGGDSSELSSEVSRLSEASGTGGDDQQKNTPGKEKQAATPPQPVPVPHSKP
SGSAGTVPGEGGRLEDLLPETPVKETAPAAPSSRESFHTASLPAKEDTESTKPADVLLKQGNIPTTDAT
QNATTEVQGETTSSSSAADDDNALTNDADEGNAENSNDVSASRAAVTDEKQQREREDGNEKERAPAATP
QVKNEDLGSADVVSVQQVQKTQSGLESGNESRKEDSVLTTNKQRDGTSDSHAESTPTSRSSAKSVGASN
GPDKATEEEISNTNTARVDAVPEAAQDDGNKDDNKKETPIKTTAIANDTTLTADSDSSTAVSHTTSPLF
LLLVACAAAAAVVAA*
>Tc00.1047053510373.90|S079|A--TYKECD|5
MAMMMTGRVLLVCALCVLWCGAGGRCDEEGPAVPAGGAGPPPGSKELGTLPQDTQELKVGSQDIKVKVP
PAPSPSLEEDEDEDSNPNEEEETTEDTEEEEEEKIKAQNETHEGKNNEGASIPPPPPIPSGDPTAERGN
PQNPKKVTNEATPSGPKMEFEAPEPPSGDATQGQHRHDTDTEDSTKNAAAGSPAEKTTTSSTSTSGSGD
HVQNKAEENDAQSSEGQHDSLETGNTNVVPTLSEEAPQTPKTITAARINGTATPDDSDGSTAVSHTTSP
LLLLLLVACAAAAAVVAA*
>Tc00.1047053510375.10|S047|A--TS-ECD|8
MAMMMTGRVLLVCALCVLWCGAGGGFANEERTGLGSGGGPPLESQELEKSPQVTQGIRDGTGGVKGQVP
SKPPGDEVEDEDEDDEDEEDDSEENEHEETEDGEKKSIERQSDQGGTVASDPNSGEKNLIGGGQENHQP
IVSAEGISLSGSQESNANPTQTKIEGNKSADKNSPSAEKALTTVNGENTLLGGVAGGNPPPPPEDGADS
REHDGEDTTSEEKKDVPPPETAATPQGHQDEGSEGTEEDTKATTVTANTTDTTNTQNSDGSTAVSHTTS
PLLLLIVVACAAAAAVVAA*
>Tc00.1047053510489.20|S061|A--TIFECD|52
MMTMTGRVLLVCALCVLWCGAGGGGRAQAASPDTTSSEEKPQNVNDTTGVVGAGEGDKNDKQAAPKAPA
APTTSGLQGAPASPSPATESGGASETPGAANDSKHQKEDEKEDEEDEEGEEEEEEEEEDEEEEDDTKEV
EGTGEEEAVTSTTGEISAGGQEQPNLSSGAAGASNITNPNSTQTTGDDVSAADGAGTPEGKQNENKDAN
PKETPVEAAVMKTTTATTGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053510629.10|S043|AG-----CD|27
MAMMMAGRVLLVCALCVLWCGAGGVYARDTLNNSPGVCMVPGGFGKKTSYLASGCNKNSPTLSLRPALP
IAVIQAEDTEEDAGSDITPGGGGGGSGLNSARQDGSGSSQTDSVPGAGLLPPAGVSGVGGNPSGSVTPG
GDSSPDRSVGTGTSASLSSTLQGESGKKVLQRDEAKDQNHQLPNGKAPDTPVVETQSRGSDTTRGQDVG
GASTLSGKEQRSSEEPEKKDGDSDIPQTVNTPEDQNKELQEKGKALLELSNGSLPEPKTDHPKTNPEKE
KNGGQNTSASTDSPAKQEGNSEDPVSNSDTAESVSTGSQEQSATTSSNEGSSPIQKETSTEKNTVENSQ
PSDTAQTEKRQSVNKEKVGDSDSSTAVSHATSSLLLLLLVVACAAAAAVVAA*
>Tc00.1047053510629.30|S097|AGWTH-ECD|44
MAMTMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGFHMPDGCNETAITVPLRSVLP
ITVVEASAGKGGSAGATGASGGPGPGDAGGSGGTQKNSNSSETSDAGVPRGGDSDGGSAAGEKGGSGGG
GSGTSTDGHGTGSVSSGLSAVPAPAPAAPPSAPGHSGGPSAPTDAPGVDPSAGSSGGTAVPPGSNPSNT
TGVSSTGDQSSAAEANDTSPAEGPTGTTSGTGHTRQEEEEEEEENERQQSDEAQVQQQQQHEHPAESGEE
SAKNKSALRTNATANTGDSDGSTAVSHATSPLLPLVVVACAAAAAVVAA*
>Tc00.1047053510629.70|S086|AG---KEC-|3
MAMTMAGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNETAITVPFRSALP
ITAVEASTGESVSDSTDIYPDSLSVPPSPPPVTGLPEALKAPKAPQDPPESDVGQTGVGNRLSLVPNDD
SSGGGGFEENGNSNKSGVSASEFSTVVGASRSSIPPEVGGSENKSGAPPNLKLESPETNEPRERILVET
NKDTQKVSKLEENPESSRKKEKANIRGTSEEAGKNEAGRSGVEAHGPSSVLSADGQLQHQGTTVTMTQP
PPPSPEQQTSAVSPSPGVDTPAARSREAGDPEEGRGIPPARKASHNSTDEKHKAPPLRSEKESAAPKPP
SADGVLEQNSEDTTTKEAIKMDAHTDGPAATSEQSTSASESGVVKRNESEDGDNAQRPEPKGQHNDPDA
VNTKAAPTASEAASYTAKTVPAQKNDTVTYGDIDGGTAVSHTTSPLFSLVVVACAVAAAVVTA*
>Tc00.1047053510629.150|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCVASGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASNGRDDALATTNNSNSSGTFNAGASPGGGSSTGSVGGPAAGGAGAAGASGSGSSGAGGDSSGS
AGAVPGAPAGTGASAGGQGTDSVPPAAAPAGGPGASVGAGGSGAGGGGGSSVSGGSGGTPTGGHVTGGI
SSGSSEGLSDPSVATVVDPPAGSSDGTAGSSGSNQSNTTGESQTGDQTPAAEANNSSLPEGLAGTTSGT

GHTRQEEEEEEDHEKQQQSDEAQVQQHQQHEHPAEIGEESAKDKNALRTNATANTGDSDGSTAVSHTTS
PLLLLLVVACAAAAAVVAA*
>Tc00.1047053510629.310|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASDGGNDALVMQNNSNSSKTSDAGASTAGSSTGSAGGPGPGGAGAAGAPGGGSAAGEGAGSAGS
SAPAASPSAVSPAVTAGPPGVDSSAGSSGGTAGSSGTNPSNTTGESSTGNQTPAAAAAHNSSLPEGPAG
TTSGTEHKGREEEEEEEEEKQQQSDETQVQQQQHEHPAESGEESAKDKNALRTNATANTGDSDGSTAVS
HATSPLLPLLLVVACAAAAAVVAA*
>Tc00.1047053510629.350|S097|AGWTH-ECD|44
MAMMMTGRVPLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
IAAVEASTEEDNAVATPNNSNSSKTSDAGASGSAVTGPGGVAGVSAASSGAVAPPSVGGPGAPVGGSSV
GGPAGASPGGSGTSTGSTQNNSNSSENLESGAFPGGGSSGSGGSSRTPTGDQGTGDVSSSAGAAGAPGG
GGGGGGGVSPTGGQVTGGTSAAVPGATVVDTSAGSSGGEAGSSGTNPSNTTGDSSTGDQSSAAAAHNSS
PPEIPAGKTSGTEHKGREEEEENEKQQKSDETQVQQHQQHEHPAESGEESAKDKNALRTNATADTGDSD
GSTAVSHATSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053510697.40|S067|A---IFEC-|4
MMMTGRVLLVCALCVLWCGAGGDGRAEATLPAPPVPPVTPPEDNTQKEENTVGAAAEVGQSGQKSALEE
KSPKASGSPEVQASQSPAPKSRGEALEKAGAGTDNKDQETEGEKKKDDEEEEVTKKEKAEQESEELEEE
RRGERDEEEEKSNDKKEGEEKKKEKAVTGTAEGTSAAGQKQPSLSSGAAGASNITNTNRTQTTGDGDST
ADAAGTREGKQNENKEANPKERPVEATATKNTTATTGDSDGSTAVSHTTFPLLLFVVVVACAAAAVVAA
*
>Tc00.1047053510697.60|S100|AML-VFEC-|15
MAMMMTGRVLLVCALCVLWCGAAFGHAMEDYCGEGGGNGLRHTSNGGDDGVSLKADCGLLSTRMALIKA
VEAAEAGEESSGDPDQSQDTGESLPHNKLNDNTRGTAEPGLGGGGVAGQTAEAAVTLEPGGSDTGGQQV
RQPKVVEANGKEGETANDTKSGSASNSEELKTVESSSSSGSPGPEEGEELPSKKTSKSDESSDGTPTQE
EDARNHRITSHSREAGAEEHEVKKENTIHEAPTETRGTPANDTEIQTATPPPLPATMNGHSSTEDLRPI
QLLQRVQDDHAESGPPSPTANGDAANNEADNSTEDGIPSNDPVADGAGTRKEKQNENKDANPKETPVTA
TAIKTTTATTGDSDGSTAVSHTTSPLLLPLLVACAAASAVVAA*
>Tc00.1047053510697.80|S008|A-----ECD|43
MAMMTGRVLLVCALCVLWCGAAVLVSAAGDVVDGDGRGVRGESLPEGAQHAVLLPSSPDSSVALKEGTS
PLQKRVEKVPALAKQSSEEDNEAGDQVVEDVTVPIEGQQQRQENAQEMYGVETPGVLIIKKEAPQAREG
ERNLTAAPMEGSPTTPGPQAPKPKLQPPPTPAILRPEAGEERPSPPQASGVGEADGGPVGIEGTGRNVS
GGGSLVGASDASRVTGEATKDPKGSEGPVSGPPSGGASSSPISNDGDASRKNGGAPSTQDTTSLKNNEQ
SRPTTSSGNAPLNRETPERSTPDAKQHSSETQENETSRLPDGDANYSAAGQSAVGTKGSSGVSTTASNA
PTTPLPQLPAPPVPTVSTVTGAPAEKPTAEQSPPPADSTTGEGLAATTTAQTNDTATPGDSDGSTAVSH
TTSPLLLLVFACAAAAAVVAA*
>Tc00.1047053510697.130|S061|A--TIFECD|52
MMMTMTGRVLLVCALCVLWCGAGGGVRAETPQGFSGNPSEKGTKNDNATSVRAGKGDQSGQKAEPQETS
PTGSGSPEAAPGPSPAPKPGGEASDPTNTTTESTDQKQEEKKEQKNEEAKDGEEDEEEEEEEEEEGEEE
EEEGEEEDGAKENGETKKEETDTGTTERTLAGGQEQPSLSSAAEGASNITNPNSTPTTGDGDSAADGAG
TAEGKQNENKDANPKETPVTATAMKNTTATTGDSDGSTAVSHTTFPLLLLLVVACAAAAAVVAA*
>Tc00.1047053510701.10|S070|A--TIFEC-|13
MAMMMTGRALLVCALCVLWCGAGGGGRAEAAPPAPSGSTPEKSTKKDNATVVDAEGGVQNDKQAAPQAP
ALTAPGLQGEEAEAPARPSQQPGGASKAANTTTDNTDHNTDDEKREEEQQEEEDEEEDEEGEEEEQDEE
DGTKEEETKKEKVVASTTGEMSAVSREQPSLSSGTARASNITDSNSTQTTGNDVSAADAAGTAEGKQNE
NKDANPKETPATVAAMKTTTAATGDSDSSTAVSHTTSPLLLLLVVACAAAVAA*
>Tc00.1047053510705.10|S099|AML-VFECD|25
MAMMMTGRALLVCALCVLWCGAVFGYAMEDYCGEGGGNGLRHTSNGGDDGVSLKADCGLLSTRMALIKA
VEAADGKGLSGDPLETSQDSSPGKKLDDKTSGGGTPGLGGGVAGPATAAAAALEPGESGRGEPNRELEV
ADTTGEENANDRRKGAERNPENLKNGQSSSFSSGSPVTLGGEGRASEKNSKAAEPSEDGPKVTKLSQQK
AEGDKGNKNDTILIGVHENPEKNTEIQTAPPPPANNGKSSPEDTVRMQQLQQVLDGIGSNNNSQTNSIA
SIAVNKHNEPSGAHAESGPPSPTANGDAVNNEADNSTEDGMPNNGPAADGAGTREKQNENKDANPKETP
VTAAAMKTTTATTGDSDGSTAVSHTTSPLFLLLVFACAAAAAVVAA*
>Tc00.1047053510709.60|S047|A--TS-ECD|8
MAMMMTGRVLLVCALCVLWCGAAVEAEGDGSGGSAELLPESQEPEKSPEGTQDFGHEAGGLKEELTPTS
ADEDDEDDDDYEGAEAEEEKQIEGQSGEKGNAAPDPVSGEKKLIGTEQQTRQSIVSAEDTPLSGNRESN
AILTQTKIEGTKDSDKNPPAVENPLTTVNREQTLHAEGNLPPLPEVDDSREHDGKDTTSEDKKNVQPPE
TAATPTSHRDKGSEGTGDDTNATTVTANTTDTTNTQNSDSSTAVSHTTSPLLLLLLLVACAAAAAVVAA
*
>Tc00.1047053510807.50|S012|A----REC-|10
MAMMMTGRVLLVCALCVLWCGFSLVSADSGDDRENSGQGVVGSVGQPSPVGGHGDNGVGTDGSSVSGGS
HLPGSAPTGGKPSLPGVGDGVGLTESKDALTLAKEGHEVVRDQHELVPQVSHHTDAGAGGKSDLSAPEQ
SPNAKTELENGGGVCGDDAATAEGEVITTVNEEQLGGSSTSDSHPPAADRGAKEQEGTVEQAASTAALT
PVVGRETTPKGDTEEDSPEDKAATGAGVTQDIPAVSQQQTNSSSTSTTGNGPTSTLGKGRAAEDISNNN

ERSGKALLQEGAEHETVAGSQSQAIPAATARNTLGTTVSGGSDNSTTITTAVRSDTGTKGTPTSNHPNR
QSIEGATSPGTNSDGEAASAKNYDTVPQSAGSTAAPTTNNKKNDAASHGDSDGSTAVSHTTSPLSLLLV
VVACAAAAAVLTT*
>Tc00.1047053510915.10|S008|A-----ECD|43
MAMMMTGRVLLVCALCVLWCGAGGGYALFFNDEVHAYYYGANGTYCKAFPTIFCSKTTEVTSQQNAAGG
SVTGGNAESGEQENAQSIAGLGGEGSGEASDEGSAGRLAHGSEGSGSGRLKEDEGKAEELNQPGGAPPS
PPATPPAPTGPINLPKSAEPGEPATSGVTTEVQSAQQPPPQSQLPAEEAPPTAAPIADGSSGGQEQTSE
KNGSDQSEGATGTQLQKPGEGGTETSTPTVTAAHSADGQDNSSEESHLDQSEGTAGEGTHASQPPGEGG
TETPTPTPATVTAAQTSATRTPDDSDGSTAASHTTSPLFLFLLACAAAAAVVAA*
>Tc00.1047053510917.9|S061|A--TIFECD|52
MAMTMTGRVLLVCALCVLWCGAGGGGCSEPTQVPQDITSGNGNNHQSVNNSTGGAGEVGLSGKSAESQA
AGLSVTELPGAGAATNLPGAQTSPTAGAGKNSEETGQEKEEEDEKQQEKEKRKEDEIEVAKREEEAEED
DEEDKDDDVIDEEEDEEQKKKKDDAGATKGISAGSQEQPILSSGAAGASNITNPNSTQTTGDDDPAADG
AGAAEGKQNENKDANPKETPFEATARKNTTSTTGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511083.30|S043|AG-----CD|27
MAMMMTGRVLLVCALCVLWCGAGGVYARNPDSNSLGGHMASRGFGRNTSFLSNGSIKNLSTPLLLSASF
ISAMQAEAREEVSSPGVTNLPLSGATVLSPAFSGLGASSPRPTVPGHGTPIPGAAFPGTSGAGPIPDVA
VPSPGPSVLPGHVPAITGPTSHGPGAAAFSGLGAAIPGAADPGAAIPGAIPGPGSVRGAAVHGHVPAIT
GRTGAGPGHAAGPAPGPGSVRGPGAIPGAAAFSGLGAAGPGAAGPGPLRDPAFPGPDANIPVSVLPGHG
TPITGAAGPGAAAFSGPGAAIPGAIPGPGSVRGPALSGLVPAVPGAGHSVGGGSELPDSRSVVTSSSQG
GNGKIAPVSVSSDEQIASPEEVLAQKETGSQGTSSPEGQPTVSSNTEKQRNNSASAGGHSLGHDAAGDE
LQDSLEEQQKNDHSQTNETKKSPGDQNTESQSSGGALSEVSNTTTHGIKTQEPKTNSVNEKNYSQNTDA
SHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511089.10|S097|AGWTH-ECD|44
MTMAGRVLLVCALCVLWCVAGGVYARDVDINALGGCVASGVLGENGSHMPDGCNKTTITMPLRSVLPIT
AVEASTEKDNAVAKQNDSNSIGTSNIGASPGGGSGDGDSSGSAGAVPGAPGGTGASGEGGSAGGGGSGG
GSTGDHGTGGVSSGPSVSAAPSAVSPAAPAPPPVSPSGPPAPAVYSSAAPGVNSSTGRSGGTAGSSGSN
SSNTTGESSTGDQTPAAAAHISSPPERPEGTTSGTGHKGQEKEEEEEEEKRQQSDEAQVQQHQQHEHPA
ESGEESAKDKNALRTNATANTGDSDSSTAVSHTTSPLLLLLVLLACAAAAAVVAA*
>Tc00.1047053511089.30|S061|A--TIFECD|52
MMMTGRVLLVCALCVLWCGVCGGGQAEATPAPPPDKSTKNDNATTGVAEGGGQNSKPAELQEAPAAKAP
EPQKASARPSPAPKSGSEVSETASTTKGSNGQKTEGEKKEEEGEGEEEEEEEKQEEEDDTKEVEGTRKE
EAVTSTTGEISAGTEEQPSLSSGAEGASNITNPNSTPTTGDDDPAADGAGTAEGKQNENKDANPKEAPI
EATATKTTTATTGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511089.130|S061|A--TIFECD|52
MMMTGRVLLVCALCVLWCCAGGGGCSEAAPVVPGTGVTGNGNNPESKNNTTDGVGGDGQTGQKAVTQPA
AGSVQKVPGTEAESAPKPGAQVSGTAEETIEKKDTTKKEDEDEEEGKDEDKEEGEEDDGGEEKKEKEED
DTSTTEGKSAIGQEEPISPSGTVKASNKTQPQSTQTTGDKDQAADGAGTQEEKKNENKEANPKETTVEA
TAMKTTTATTGDSDGSTAVSHTKSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511089.140|S059|A-TTIFECD|4
MMMMTGRVLLVCALCVLWCGACGGGCSELTPAPPDSSGIPSENNTQKNATVVVTGGGGRSGEQAPPKVT
ATTTSEPQKAPARPSPAPQPGSEVSETVIATKDNNNTNTKGKKEEKEEEDEEEEEEEDEEEEEEEDEEE
EEEEDEEEEEEEEGEPKEEKSNDKKEGEEKKHEDAVTGTTEGMSAGGEEPPIISYGVEEAANQTNLKST
QKTGDDDPAADGAGTGEGKQNENKDANPKETPVEAAAMKTTTATTGDSDSSTTASHATSPLLLLLVVAC
AAAAAVVAA*
>Tc00.1047053511089.19|S061|A--TIFECD|52
MMMMTGRVLLVCALCVLWCGAGGGGCSEKPQVSQDITPVNDNDSKNGNDSRSGAGGDGQNGKQAESQQT
PAPPASGSQGAAPKASPSPASQSEGGGAPETASTKKGSKRQKTEGEKKEEEREEEEEEEEEEEKQEEED
DKKEEETKKEEDDADATEVTSAGGEEQPNLSSGAARASNITNPNSTQTTGDDDPAADGAGTREEKPDEN
KDANPKGTPVEATAMKTTTATTGDSDGSTAVSHTTSPLLLLLLVACAAAAAVVAARE*
>Tc00.1047053511091.9|S043|AG-----CD|27
MAMMMTGRVLLVCALCVLWCGAGDVYAGDLDNRALGGCMASGVLGMNASYVPNGCNEYMPTPPLRSALP
IPAIQAEDGQVRDTAPGSGSGVGEGGGSPGALSPAGAAASGSAPAPVAPVAPAGPVADPTADPPGGSAA
TGPAAAPGSPVSVPGPVAGPGGNAGSSPGVHAPPHIDDTVITSSDLSSTREGSREEALQQKETESHDPS
SSKGLTQEALPDVQQSQISTSENIKTGCGEEASNCEDEQSVEKATLGKKDLTVAKAQKPPATQNTKSKD
NEENSTEASSTESENTEPQQEIKTPVDESDSTSTDASTAVAARSTSAGSQEEATASSSNGSHSPLQGEV
FTGTDTPENAPSPAAAETEKRQGENVTTPGDSDSSPAASHTTSPLLLVVVACAAAAAVVAA*
>Tc00.1047053511197.60|S008|A-----ECD|43
MMAMMMTGRVLLVYALCVLWCGAAMVVVAEGSDGIKEITDKLPRGSQSASQVGHAEDPNIPKPNDGVLN
TSEKPSDAQELNNAIPQKGSVEQPSTDNDGMEVKEGKLEEKEPENAEPRRNGKEQSQDASEGTRGRKAL
MEAQGDPSPKTSADEMPTSEEATGPGKEQTPGQEGETGQAVKPPQSLPATSPPASDRGQPGGSSGADSS
VGGPKGVGGSNLKISASDGVNQSAVDSLGSAGGSSGGDGGSSRGDSLGSPLSTAGTSLSSALDTPSTQD
SQSSEGARHSEKMSLGTAVPNEQPKERSESKAKQGSSTSEEAAEIPDGGGDAIGNEKEKRDVGLKSTTS
PTPDTSNPPVKQTTPRASSAEPSPTTEVQAGEETSKDNVTTAKGNNTATPGDIDGSTAVSHFTTSPLLL

LLACAAAAAVVAA*
>Tc00.1047053511377.30|S032|A---H--CD|8
MMAMMMTGRVLLVCALCVLWCGAGGICEEQVKVVDGGARGGGNVLLVKENGATATLMPSEQTGVLQVEE
KAPNKRAADSSSEEEDKEEEDDDDDDDEPEEGSKEEAEEIIIEDGKGGKETVKEHQSQGEEAAGRSVST
KGITRNSNQQTLHTPLSTEHNPSPDSLGLNPESPQKNLSKNDDSAKNQQTEDSTPGEEDKSKLSEGVPE
PGAGKGNSGPEPGKPTEIHEPTGLSSASSGDAQETKHVVNEPPNASPGPLGGVTTGSHTDVKTGTEVHP
PPPQEHHSAAVAAEKEGSIMEDAAIQRGGYERPQEKLPEAATAAPPEGLRTSAVRSSEKTEDVTDENEE
IGEENAEDETKKQQEQIQLPQQPQQFGEKGQQQQQQEEQPHGYPTDDGEVPKKDKNAVGTNNSDGGTAV
SHATSPLLPPLVLVVVCAAAAAVVAA*
>Tc00.1047053511595.30|S062|A--TVFECD|5
MTMMMTGRVLLVCALCVLCCGAAMVMAEANVDKGTEMKKDESFDSSELISGIVGAEQHVTQDSVREGSE
NGNQSLGAQTGNGINQDNGVIIASPASTVRGEEEEEEEEEEEEEEEEEEEEEEEGESVDAEGETEEIEE
LKGPIEGEETSQLTLPQEGVLLPSEPLKTTLNGNPAGTLNATPAKGQPRSDDGSAQEEGLKLPTLQAPA
APAAPAAAAAAAEATTTQTKDENPSSADDPSVQHVEASQHDMELRSALRKEGTIPTTVTKTDGPTEVNA
ESTPTSPSASKGAITNDADEGNEEGIQKHDQAPDGEATKEAQQGENKEENTNKTATLEAAAITNDTATH
GDSDGSTAVSCTTFPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053511597.40|S111|ANP-V--CD|2
MTMMMTGRVLLVCALCVLWCGVSVVMAEAGGGDAEENMVLTWYPETKKGCENQSTKEGKLNKSAFKSCM
HESMKEICDAYYSEMPSTSREPAAVEICNNYTGDPEKADDASKSQDKSPHDAVTPEAVTTPETAKVDAA
EMGSTPGVPAGDSPANPTEGPHSTSAATDTANSEAEKDGKKVTLKNAPESNATRKEEVEEGEKNHNSAK
ETPVDADTMKNVTTTAGNDGSTAVSHTTSPLLFLLVVVACAAAAAVVAA*
>Tc00.1047053511603.30|S033|A---V--CD|9
MAMMMTGRVLLVCALCVLWCSAGCRCDEEEDTALVGDLPANSESGSGGPEKDTDHTVPGGAENPSAQQS
QLNKVRGSPAGISSLEAPSEVESKKKQTQSDPEHTDLLSPSKSSGEQRQDGTPEGPPEEPETSPNQEYN
KDVSIVNQQNIDPPSPSGNDDVVSHNSGERTEDTPSSTEIIDAAPSEEGEKRENVTPSLEQPLETSTAA
PAITTQTSSTTPTDVGESNTVKMSEASPKSTGTSQTDHTTTKIANSDGSTAVSHTTSPLLLLLVVACAA
AAAVVAA*
>Tc00.1047053511603.80|S013|A---V-EC-|8
MAMMMTGRVLLVCALCVLWCGVGGGFCEEALEEAPLVGSSLDSTGVGVSENATGHTVPGDAGVLSAEQK
QLNPLGDPPLQAALQTESPTEQTHSSPEHKDSLPPSTQLQEERQGGPDEGILEEPGASLSQEDKKHTSI
GDQQRNDPPPASSNNDVVSNNSEESTEDTPSSTEIIDAAPSEEGQENENVTPYLEQPRETSTAAPAIAT
QTISMTPPDQSESNTVKMSEASPQSTAATQTNHTTTPAENDGSTAVSHTTSPLLLLLLPVACASAAAVV
AA*
>Tc00.1047053511603.100|S091|AG--YKECD|14
MMAMVMTGRVLLVCALCVLWCGAGWVYAREFENNAVGGCMASGVLGENGFHMPSGCAKTVLALPLRSTL
PVTAAGVPTSEEESEKNFSNPNLKPLSPPVSGGSQGVSGGSGGAGQSGGADNNAVVGGVVGPSGSSSGG
VVNFLVSDSFSAATPSPSNPVGADGLQGSKGTTSTVSMDAPETGVKSQSARPPAPAQTNLDRQEVSITN
AETQSSIKPHAAGNQIVNGDETGREIERKAAVTGGPPSNQQPTPLQPVQQEQPTTDSHTRQKEERDSEE
APSPPPSPSPTNSTEGIPATRELQISTEKKKQTSPSETQKELVGQEKPSKGDAAEHNTKGTTKSDSVKD
AVASGSEETTASPISTSGGADAQNEVSKDGDNAQRTNHKETHKHPEPDNTNPAPTANNTQPQTALTLST
VQTNDTATPGDSDGSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053511603.160|S082|A---YKEC-|17
MIAMMMAGRVLLLVCALCVLWCGAGGIVADDAVRAELEKENKSDSLRADPPIDEADTQEPQDLGRQLSD
KENGLMVAQEGMIATQQDGLALKSSTNPLELEEDKDEDEEKEDGKGKGKAEKDKRSMEQTETQKSLMKD
GETSKLTSAPGTPSTLIPPERGGQKTPSETPPGPPTNGKPAEETGPPASTGSQNATETTSTTSLPNAET
APEVQEKPLGNGEPSQNRQDTDQPDSMNNATTSRPAETPAPLVSTSGSDGTQKKEEKVDNGDQRPNRKE
TQDGLEDRNTSDAPTSTEAAPPTAETVNNYQTNDTATKGNSDGSTAVSHTTSPLLLLLVVACAAAAAAA
VMAA*
>Tc00.1047053511603.190|S002|A---S-ECD|19
MAMMMTGRVLLVCALCVLWCGAGGRCEAGVGVGAQQDGGKSPPESKGLETSSQGTQDLKGGAADAKENS
PPLPTEEDHEDVDDDSEEGDDDDGGTEDEEEEKVRGQSGQEGTVALGSDSTEKKLIGSGKQTELSISSA
ESISPSGSRELNVNHTQTEFEGKKETDKNTPAVESALTTGNGENTLPAEIVDGNPSPPPPQVGIHSREQ
DGEGTTSEGQKNDPLPETAATPKSHHDKGSEGTGEDTKATTVTANTTDTTNTQNSDGSTAVSHTTSPLL
LLLVVACAAAAAVVAA*
>Tc00.1047053511603.250|S080|A---YKECD|24
MTMMMTGRVLLVCALCALWCGAGSRCDEEEDTALVVGPPGSRSNDGKGGPGSAPPSLPGTGTSVPRSIL
PESEVPQERIAGTSSEERGEKNYKNEDGEEEDVDEDGENSRHHERLSEQPTQKEESQEETPEEKELKKG
LEEEKDVHQPGEEGIKGAQQSQSQQPPPQQLQVKITAPAGRGGPTAPTGPARPPAPAEPSSMDGSQTIE
PTDSRNPSQESHDKSLLQTKKESSAPDPSLKDAFPEQHGQETTTPDSVMNASAGSQARITAPSTSTSGS
GEAQSKADGNDAQRPNPNKSHDDSDAGKTKVSTTLSEAAPQTTETVAATQTNHTKTIGDNDGSTAVSHT
TFPLLLLLLPVACAAAAAVVAA*
>Tc00.1047053511603.300|S030|A------CD|31
MAMMMTGRVLLVCALCVLWCSAGGCAENDAEVVEIPAGGKGAVGSTGTSAPGPGVSVLRIDVPNVNQSK
ETSAVKSFEGNEVKTDQQDFPSREDEKDGSPSEQLEEPVEDATEKAKIEPPLQNVGQEGREPQQSQLQV

NLPQKAQPQPQQSQPLPPSAPQPHTPASEEGKGVGENNTGGEGQSPLGVQDIGNEDAEAPRKEDLLNGP
GKESESSEEVQTKGPKTVTPKHKTQNEMLTPEQKKNESQSTDTSTNLPQLQKENKEYPASREDTAQSTS
TGSEEKEAEPSTSEETSPFEEEQSTGTKTTEDAQTPDAAATEKKKPGDNEKVGDRDGSTAVSHTTSPLL
LPVACAAAAAVVVAA*
>Tc00.1047053511603.320|S002|A---S-ECD|19
MMAMMMTGRVLLVCALCVLWCGAGGRCEAGVGVGAQQDGGKSPPESKGLETSSQGTQDLKGGAADAKEN
SPPLPTEEDDEDVDDDSEEGDDDDGGTEDEEEEKVRGQSVQEGKVALGSDSTEKKLIGSEKQTELSISS
AGSISPSGSRELNVNLTQTEVEGKKETDKNTPAVEGALTTGNGENTLPAGIVEGNPSPPPPQDGVGSRE
QDDEGTTSEGQKNDPLPETAATPKSHHDKGSEGTGEDTKATTVTANTTDTTNTQNSDGSTAVSHSTSPL
LLLVACAAAAAVVAA*
>Tc00.1047053511603.380|S025|A------C-|17
MAMMMTGRVLPVCALCVLCCGLLSADAGDDDVSGDHGTLGGSGVGADGRPSVPVGSDVSTGGTKDECSL
GSGGGSPVSASTPCKSLLSDAENPGGEVFNDNKKGLSRVEGNSNVEQDPPQPGSHVVSTAEVLAPGQSN
SEAQEQSSGKLRTEEGRNNGDGGTTVKEEVTGVKSRDTADLSPNDSRPPKAARPVTGEEKGTEKQAASK
ASLTPEEERGTSAATDQKVDLPKEEAASSAGATKNRSPVGQQQTEASSPSTSGSTSTLTPQKEPAEELH
SNNNQPPGDAAPTEGTQHETLPGDKTQTEPATTNNKPIDATPTGDSESSPTAPPAGESDAATTTTTNNH
DPRSLNNNGNNTFTEEVDQKEATRKPKNAPESTDTAAANSEASATAINISTNTTNKTTTGDSSTAVSHT
TSPLSLLLVVACAAAVVAA*
>Tc00.1047053511605.20|S021|A---SR-CD|1
MAMTMTGRVLLVCALCVLWCGAGGRCDEETAARGSDAEPPLASKPETPESGIPGTQPQVKRDNEEAKRP
MGEGSLEGSEDNVVAKTEDLSEDDEGSKEEGNEETQRKKLNGRQEEHEENGPASGLDTSNGSSIESQLQ
TLQTNSSTGSSPPSSSLKAILDLTQTGIKENGVSVTNSPTDEETLEKDTRDNAPHGGLAKVTLPPPLED
SAAASGISAEYKKDEGQKDANLHSTAATVQDSQDDTTKNTKKETIPTAITTDTETTQHNDSSPAELTAP
QSDAGVESTPSTNYSRHSSTEDAARLSETNDAEDASGSTETADSKIAETEKAPLATANTTDTTTNDSDG
DSSTAVSHTTFPLLLLLPVACAAAAAVVAA*
>Tc00.1047053511605.80|S030|A------CD|31
MTMMMTGRVLLLVCALCVLCCGLVSADAGDDDVSGGHGTLGGSGVGADGRPSVPVGSDVSTGGTKDECS
LGSGGGSPVSASTPCKSLLSDAENPGGEVFNDTTKGLSRVEGNSNVEQDPPQPGSHVVSTAEVLAPGQS
NSEAQEQSSGKLRTEEGSNNGDGGTTVKEEVTGVESRDTADLSPNDSHPPKAARPVTGEEKGTEKQGAS
KASLTPEEERGTSAATDQKVDSPKEEAASSAGATKNRSPVGQQQTEASSPSTSGSTSTLTPEKEPAEEL
HSNNNQPPGDAAPTEGTQHETLPGDKTQTEPATTNNKPIDAAPTGDSESSPTAPPAGESDAATTTTTNN
HDARSLNNNGNNTFTEELDQKAATTKPKSAPESTDTAAANSEASATAINISTNTTNKTTTGDSSTAVSH
TTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511609.30|S112|ANP-V-ECD|4
MAMMAGRVLLVCALCVLWCGGAAVVSSMPDVTGRENVPHGYLVVNWEKLLKNECATDKKYINEDGTVNE
SAVKDCVRDAMRLVCNFFCRKISGEPDDSEGGRICEEYVGSQDEAGQSSHVITPAEAKTLQAPRSELEE
LGKTPGETPKPLSGGPATEDEAAKPTGGPPTPPVEAQHNREENVPVLHPEDDPGTTESNSDSEEDDSAS
TTDKQEGVTPDGHDKSTPTLPSTATDTVKNEADRVNTEGTQKPATESNAEGKEVEESDEKKYDNTKRIP
AEAAATTNNTAMPADSDGSTSAVSHTTSPLLLLLLLVVACAAAAAVVAA*
>Tc00.1047053511611.20|S110|ANP---ECD|3
MAMMMTGRVLLLVCALCVLWCCGAAVVSSMPDVTGRENVPHGYLVVNWETLLKNECATDEKYINKDGTV
NESAVKDCIRDAMRVVCNVFCRKISGEPDDSEGERICEEYVGSRDEAGQSSHVITPAEAETLQAPMSDL
EELGKTPGETPKPLSGGPATEGEAAKTTGGPPTPPVEAQHNREGNVPVLHPEDDPGTTESNSDSEEDDS
ASTTDKQEGVTPDGHDKSTPTLLSTATDTVKHEADRVNTEGTQKPATESNAEGKEVEESDEKTYDNTKK
IPAEAAATTNNTAMPGDGDGSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053511667.50|S128|ANQ--KECD|1
MAMMTGRVLLACALCVLWCGAAVVASAADGAEGDGGAGEYLIFRWRAHLRRKCVEKVNRRTGGCANASA
VEECVRQWMDGVRAVADGRRRWGRHRYAVAAADGPFENDSTPESSLQGQIGSGAGVTGGQRLEPSLRSD
TGISDKATAEEETLTRPPEAPELVKNRTEEIINDQEKEKEKKKSAEEGNEDEVNDNGEDDNASTESPGD
DYDEEEEDLEAGTNKKEGRDGDVVGDNSLDDHAIVQLAAPVDVERQERSLTLNNGRSGGKGGAGETRVP
EGAGLQGAEKESAKLTHETGADLMETEGLKEGADQTDAGKQQAIDEAKSNEAAPPATREEMKKEALKEA
KKATANEDVIRKETTEKGKNGAERGNGESSDKAGKEEKENEERKVEEANNEPQDGSETANTDVALTVGE
AAPQALVTATVAQANDTGTPGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511787.10|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCGAGGVYARDVDTNAVGGCMASGVLGENGSHMPEGCNKTAITVPLRSVLP
ITAVEASAGEDVSPAAGPSAPPTGGQGTGVISSGSSAFPPAPPAAPPSAAPVVDSSVGSGDGKAESSGS
HPSNTTGDSSTGDQTPAAAAANNSSPPEIPAGATSGTEHTRQEEEEEEDHEKQQQSDETQVQQHQQHEH
PAEGGEESAKDKNALRTNATANTGDSDSSTAASHATSFLLPLLVVVACAAAAAVVAA*
>Tc00.1047053511839.20|S084|A---YK-CD|3
MAMMTDRVLLVCALCVLWCGAAVVAVGDVIGEVGIKDESSKALQVDSQAREAGKRDVSGPEAVVPRLHE
QQGKNARKNDDSAIQPTRQVKVEEEDRDHSEEEEEKENEGSLEGTVKDGEVLPSQAEGQPRSNEPPPPP
ASGGSRNGVISGGGSKLGESSNGGEGPTLNSSSSSGDGKPPAVDGSGSGGGTGSVPGGKGIGGGGGGTP
GVESLKFPVSGVALPPSTPAAGSASSAQNLESSERSGWPEPTVSLRIAPLNVDARKESKPKDEPQTFSA
QGEAERQVTDEETSKKEAKESVVEGKRLFNLPHNASSTPAGPAVRLPEGSQVQGNRDEGGGLPPEATKS

ETSTGQKHGTSQSQNESRGTKFPSKNEVAVQHGHVTVPSDSMTNASANSQGVTTAPSISTSGSEDAQST
VDGNTDDDQRPNKKKAHNNPEDDNTNVAPTFSETAQQTPETVTVVQTNDTTPGDSDGIKAASQTTSPLL
LLLLVVCAAAAAVVAARE*
>Tc00.1047053511839.30|S017|A---S-EC-|13
MAMMMTGRVLLVCALCVLWCGAGGRCDEGEAAGRVSGDELPQGSKSLVTPRVGSQGLQNGVTVVKEEVS
PISSPPQDGDADGDEGDDGGDDEETEAEEEESTEGRGGKGGTAAIGSDSRKENLSGSGQEKNQSIAPSG
GISPSGGQESNANPTQPEVEEKKEPDKNTPAENALTTVNREQTLSAGVAGGNPSPPPEDGVDSREQDGK
DTTSEGGKKVPSPETAATPQSHREEGSEGTGEDRKATTATANTTDTTSTQNSDGSTAVSHTTSPLLPLL
LACAAVAAVVAA*
>Tc00.1047053511849.30|S009|A----KECD|5
MAMMVPGRVLLVCALCVLWCGLTGVSADGAAGGHVTLGENVLEIVGGQSTSSLAIPGAKGASTGGVLVG
GEHPTSDSGTPGDVSFLPGSDDGSVSDSSEEDSALTKDSPRELKGKAQSVSLVVSPPKVKEIVSPESNK
QGIVLPAPAESENHNAGGVGAISNREIRDNGGHANASSNDSDPVLPSLSPKVQLPAISQAPGIPPPPSL
GQQTSTVTILQEVETPAARSRETSVSSKEISRHAEDPAEGKKGIPPAPTHSQNSTDEKHKTSLLQIGTE
SAAPKPLSPDGVLEQNSEGTATKDAMKTDVDTGSPAATSESSISTSEIVAVQNKTDEKDGNEQQPEPKG
LHNDPDAGNTNFAPTAGGTAAETVKTITAQNNATSNSVDSDGSTAVSHTTFPLLLLLVACAAAAAVVAA
*
>Tc00.1047053511877.20|S014|A---Y-EC-|1
MVMMMTGRVLLVCALCVLWCGAGGVVNGVGGIDGLSEVPSSGVPSSSSSNPNGNDLSKTLSNTPSIQNG
ESSEKGEPSGKKSPGPVSPSGQTGEVSKLEEKLRASDTQEEAETSVAGKDTTKAERTQSDMKTDGSSNT
LSTAAKSKVQSPPPPPPPVKPPTAEEQQPNTAPKDPRTATEEKYEMPTSATKTNPDTPKTSLKDGMADR
HGHDATTTVLVKNAATGNSAERKSPSISTNDSDDAQSTGDENNDDDPRPNHKETGDHKAANTKVGSTPS
ETATQTVKTETVTVAQKNDTATSGDSEGSPAASHTTSPLLLLLVVAAAAAAAVVAA*
>Tc00.1047053504587.30|S008|A-----ECD|43
MAMMMAGRVLLVCALCVLWCGACGGYAWDFNGNESLNEQHYGANGTYCRLNSSFPFCEEKRNASKLKEA
ALKASNAQSGTGSGQPNADGSSGGRDNSSEKNDSDESEETDEGPQESQPPNGNVTETPTPATVTSAQTS
ATRTPDESDGSTAVSHTTSPLLLFLVACAAAAAVVAV*
>Tc00.1047053504655.9|S030|A------CD|31
MAMMMTGRVLLVCALCVLWCGAGGVYAWDLSSDAALHKKHYGANGTYCRLNSSLFFCKEKGDASKGEET
VSQASTAQSGTGSGQPNAGGSSGGQDHGSEKNGSDELEKTEEGTQASQQPNGNVTETPTTATVTAAQTS
AMRTPDESDGSPAASHTTSPLLLFLVACAAAAAVVAA*
>Tc00.1047053504769.20|S008|A-----ECD|43
MAMMMAGRVLLVCALCVLWCGACGGYAWDFNGNESLNEQHYGANGTYCRLNSSLFLCKEKRNASELEET
TSQKSNTQSGTGSDELNAGDSSEGQDNSSEGNDLRGSGRSKEDEGKKELKNSVEGETTPTQPSTVSEDL
PKPAAPGGPEAPGTETELQPPQQSPPQSPLPAGGTPTPTPTADGSSGGRDNSSEKNGLDESEKTDAGPQ
ESQPPQGNVTETPTPATVTAAQTGATRTPDESDGSTAAFHSTSPLLLFLVACAAAAAVVAA*
>Tc00.1047053504787.30|S004|A---V-ECD|18
MAMMMTGRVLLVCALCVLWCGAGGRCDEALPVVVSAVNPASGGVVTDNAAGQTAPGEAEGLSAHQPQLE
SVGGSPSGGSRSQADLQPQSPTIQLTHSGAENTVPSTTSKPLGEKMQNVPDEGPPGEPGILSSQEEAIK
KTIVNQQSNDPPSHSINNDVVSRNSGERTEGNSRRAETLFAAHSEEGQEREKVTPSLEQPHETSTAAPA
ITTQTISMTPPDESEINTVKISEASPQSTGTAQTNHTATPGDSDSSTAVSHNFSPLLLLVVACVAAAAV
VAA*
>Tc00.1047053505023.40|S012|A----REC-|10
MAMMMAGRVLLVCALCVLWCGAGGGCEEGEVAVVAGSPGNVSVVTPNSQLELPLLEGQASNIQSPKVGK
ELPTVAGVSSEITEKNNAGGGGGENEELQERQRQGQAGGIRHDGQDGAHKEEDRQEEQEETKKKRVKDQ
NSHESDPVKLAELPLNQIKDSPSHSSNDVEKSDKKISGIATPLGNGDQLQDALRPLPNASTTLSTEENT
SFYSTGSGGDDNSHEKNNDANNAPQSSSTGIEQQDTEPHGKSITFTDSGEASKLPVTTVTKTSDTVAAG
GTPSAAMALQHNTGMEDIPATPDSSQPSTGGAEQPSATPDREEASDSTENGISQSAGSATEAMTTAKTN
DTTTPVDSDSSTAVSHTTSSLLLLLHAAAAAVVAA*
>Tc00.1047053505025.70|S025|A------C-|17
MAMMMTGRVLLVCALCVLWCGADGGECTEVVKAPAGGAGGGSGGKSAVETAENSTSGPDTSDSPIDVSK
VNQSTEASGGKSLEGNGVNVDQQDVVPGVEEEDGSPSGRLEETVVNDPGKENTERPLQNVGKEGIQQPQ
LQLNLSKQPQPPPQQSQPLSPSAPQPHTSASEEGEGVGENNTGGEGQPSLGAQDIGNEDSKNHRKEDLL
ESSGIKSQSSEQAQTTVPKTVPPEHKTQNEELTPEKKTNESQSTDTSTNLPKQQKENKEYPASTEGTAQ
STSTGSQEQEAEPSTSEEPSPFEEEQSTGTKTNEDARTPDAAATEKRQTGDNEKVGDSDGSTAVSHTTS
PLLLLLVAAAAAAVVSA*
>Tc00.1047053505025.90|S082|A---YKEC-|17
MAMMMTGRVLLVCALCVLWCGTSGGRCDEDVRVTEEKKKSSGDLQPVTPVAAAGKQHGEPINQDSDLVR
QPLVKDLEGPSPKHQTDDKVLGVVDNEDDGTDKEKEERDKAQEGAPDGQTQEEEVPPPPSPLSPAPLQS
PPPPAASDGTQPGGGPGADSSGGGSNGSGSSIGGGGSNLETLAVNCGNQSAFGSLGYGGETGSFSGGAG
KGGVDIGSPRGDFSDSSLSADGTFLSPAPDAPSSQGTQSSANVERSKTMPAGLPLPNVNAPKGPESKAG
SLPPNTQEKAKCSDANGGAAGNKAKQSDVETEDPSSSFANTGDQTVEKTLLLPQTPAVLLPVPSAELSP
EVPPVTPVQANPDGEGGLPTAPRASEASKREMQNKASSPNKTGSESPDRPSKDGMQEQKDKVTTQLNTT
KKASAGGLAETTAKSISANENGDVQNKEDEDDARQPKPNRPQDDAEAGNTNVAPTVSEAALQTAETVTT

SRKNDTAPPEDSDGSTAAFHTTSPLLLLLLVFACAAAAALEAA*
>Tc00.1047053505025.130|S105|ANP--F-C-|4
MAMMMTGRVLLACALCVLWCGAGGCFANEAEASANGAASKTTPADKIILNWYELTHEECETDNTKNGTV
NVPAMKRCINFAMKGICDTFYNKTPSEIHGPDVKDMCTYYAAIPDEPVELPTPQGPPSDSAVSNTTSNE
GTPKNAPESDVAGRGEGKEDEKEHGNTKKKAVETAAVQNITKTTDSDGSTAVSHTTSPLLLLLLVAAAA
AAAVVAA*
>Tc00.1047053505297.60|S039|AG----EC-|2
MAMMMTGRVLLVCALCVLWCGAGGVYARDIDNKALGDCMTSGVLVTNCSHVPSGCDKTAPKPPFRSALP
ITVLQADASEGKDLTSQGDNLNSSESSGTGAPGKASENPGGIPGTDDSSGGGSSGAGGKEARREAEGMN
EASSGKQVTNEKEVLSPAGGGSAPDPNGTHNSPETNAVNSASENEPESNSLERSSEDGEAGQQDEEADA
QGTQETEVRQGTAASPVSTSGSGGAQSEADADVDDPQRPNPEGPQNDGTEAGDTHGPTAVSDAAPQAAK
AITAQTNGTVTPGDSDGSTAVSHTTSPLLLLLVVACAAAAVVAA*
>Tc00.1047053408547.10|S030|A------CD|31
MAMMMTGRVLLVCALCVLWCGGGVFAEDPAPDAGVSGHSASIVGGLQEITQNGPSLLGEPSSETVTPKV
EGGAPLGSAVELPGRSEQEVDALEGEDLSDKSLDKEISKDKNAQLSSGPPADNNSSPTGVGNAGGSGLP
SSGASGDLTDSTDDRAGGAGNVGHIKPPAELTPPHPPEPNSKGGRAPPAVPNLNTSGSQGKIAAQGQPS
AKQETSLATQPQVSGMRPPPQDEKQSGGEIENSPEPGEAPATSDTTLVTSSGTEGQIPQSSSPRSGSDN
VTHQSEQHPEAPLGNTQQDDAAVADEERRRGETGGIPTDSHRGPEAAAATNANAKVAPPTEGSDGSTAV
SHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053505949.20|S008|A-----ECD|43
MMMAGRVLLVCALCVLWCGAAVVVSSAGDVVDGGVKVGPLGDSQSGSRDEKAAKPELSRSVDEKLGSAG
HLLDTRSGTNVSEQGNLVKEPPAGNVGKEGVQEEGKELPVTHTSRTKDKVTVPQSLPSPPAEDPPAKSP
SQASMQGSPTTPGQPQENSQKSTGQPPTLQAQPPSSPAASAEGEADGDPVGASDTSRVTGDKNKDSKGS
GGPISGPPSGDASSSPISNDGDASRNNGGAPSTQDTTSLKNNEQSGPTTSSGSAPLNRETPERSTPDAK
QHSSETQENETSRLPDGDAAHSAAGQSAMGTKGSSGVSTTASNAPTTPQPQRPAPPVPPTATVTGAPAE
KPTAERLPPPGDSTPGEGLAATTKAQANDTVTPGDSDGSTSVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053505949.80|S074|AML-YKECD|9
MAMMMTGRVLLVCALCVLWCGNGFGDARDDRYNEGGRNFLTHTHNGGNDRLRLKADRGLISTRMGLIKA
VAAEDDSEGGTTNALLEEKTAAGGISAGSGGDAAPVPKEMEGAAGAGTPFLPSGPGMPGTGAETGQSLM
AGQEGNEKNNLDPKKKEATDSKDKTNDELSSPSGSTPSPPGEKLSSTGTDDINQLPKGKVTELGVERQD
NRESDEAIEKEDGEKNTEEEEKQKIKAQTESRESKNNAGEKPPSLPAPPPPPPTTPSGGPAPSISEGEG
SPPTELKNSQNQKKVTNEATPSESKTDSEATQSSSGVATQGRHSHDTDTEDLMKNAATGSPAETTTTSS
TSTSGSGDHVQNREDKDDAQISEEQHDSLETGNTNGVPTLSEAEPQTPATVTAAQKNYTTAPGDSDGST
AASHTTSPLLLLLVFACAAAAAVVAA*
>Tc00.1047053506001.50|S008|A-----ECD|43
MAMMMTGRVLLVCALCVLWCGAAMVVVAEGSDGINEITDKLSRGSQSASQVGHAEDPKILKPNDGVSNT
SEKPLDAQELSNVSPQKGCVEQSSIFHGGMEVKEEKLEEKEPENAEPRRNGKEQSQDAPEGTRGRKGLM
EAQGDPSPKTPAEEMPTIEEATGPAKEQAPGQGGETGQAAKPPQSLPATSPPASDRGQPGGSSGADRSV
GGSKRGEGSNLKISASDGVNQSAVGSLGSGGGSSGGDGGSSRGDSLGSFLSAAGTSLSSALDTPSTQDT
QSSEGVRHSEKMPLGTAVPNKQPKERSEPKAKQGTSTSEEAAESQDDSGDAVEKEKEKRDVGLKSTISP
TPNTSNPPVTQTTPRASSAEPSPTTTEVQVGGETSKDNVTITKRNDTATPGDSDGSTAVSHATSPLLPL
LIACAAAAAVVAA*
>Tc00.1047053506001.14|S097|AGWTH-ECD|44
MAMMMAGRVLLVCALCVLWCGAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVLLRSILP
ITVVEASDGKAGALATKNDSNSSEASDAGVNGSGSAAVPGAGDSDVGERAPAAADGGGSGTSTGNHGTG
SVSSGSSEGPSDPPAAPGVDSSAGSSDGKAGSPGTNPSNTTGDSPTGNQTPAAAEANDTSPPERLAGTT
SGTEQKGKEKEEEEENEKQQQSDETQVQQHQQHEHPAENGEESAKDKTALRTNATANTGDSDGSTAASH
TTSPLFLLLLLVVCAAAAAVVAA*
>Tc00.1047053506067.70|S099|AML-VFECD|25
MAMMAGRVLLVCALCVLWCGAVFGHAMEDYGSEGGGNGLRHTSNGGDDGVSLKADCVLLSTRMALIKAV
EAEEAGDEPSRPDHLQDTGESSPNNTEGSAAAGPGGQPAGLLPKPEGSDTEGQQGEPEGLDLNGGKETE
DRNVPKDVKATGSQHQSVESSSSPSSSSGSPGTKSGNDGNLENTSESDESSDETPTEEKRDHRSKSDSP
DVEAEEEPKKTGDKKNASNEAPTETRGSPANNTEIQTATPPPPPAPMNGHSSFEDLPPMQPLQRVQDDN
AESRPPSPMANGDAANNEADNSTEEGIPRNHPAADGAGTRREKQNENKEANPKETTVTANTTDTTNTQN
SDGSTAASHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053506067.140|S061|A--TIFECD|52
MMTTGRVLLVCALCVLWCGVCGGERAEAAPGSSDNASSEEKPQSDKGETTGVAGGGGQKSEQAVPKAPA
SSKAPELPEVQTNSPQATQPEGGEAPETVNPTTGKKDQKEDDKKEKTDEAEAEDDEEEEEEEEKEEDDT
EEKGETMKEGAGTGTTEVISAGTEEQRSLSSGAEGASNITNPNGTQTTGDDDPAADAAGTAEGKQNENK
DANPKEAPFEAKSMKNTTATTGDSDGSTAVSHATSPLLLLLVVVACAAAAAVVAA*
>Tc00.1047053506067.240|S032|A---H--CD|8
MVMTMAGRVLLVCALCVLWCGAAGGAVGVSGGEDNTLKELFIPVARLQERSEQRAAEATADAKATAEMA
AKAAAVAEAAAEAAAKAKIAKEEAKSATAKAEEAKAAAEAVATAAEALRGTAVGEEEVKTAIHDHDNSV
EHHSGEKQELLQEEPERQEKEQHAKQQHQQREHSARNGEESAKDETANSTNATAIKDDNDGSTAVSHTT

SPLLLLLLVACAAAAAVVAA*
>Tc00.1047053506067.290|S099|AML-VFECD|25
MAMMVTGRVLLVCALCVLCCGAGGVVYAMADRCSEGNGNLLTHMNNAESDAVFPTAECSLLSTQMGLIR
AVEAGDEEGAELGGTVTSEKPKQLLSGTTSKGNDEVLTPVPPAPLPTAKLSDHVEKEKPLKTVDSNGIG
DTRDPSGGKATESQRQSVGQSSSGSTVTQPGKDHNLNNPSESDASSNFAPTDDSDANIPPNVPERGVGA
LGKVNEDEDKTKKSKQAVQEDAGEHKKKNKNDNSPTGTLENAAKLEKIPQATSPSLINAPAEVALETIA
KKEGDSTQARVNGQSSPEDTVPVQQLQLPQSDMKSNSNSQTEGIASITANSQNETSDGHAETKPPPTAN
GNFANNEADNSTEDGIPNSDPAVDVAKTRDEQNENKDANPKETPVTATAMKNTTATTGDSDGSTAVSHT
TSPLLLLVFVACAAAAAVVAA*
>Tc00.1047053506067.169|S061|A--TIFECD|52
MAMMMTGRVLLVCALCVLWCGVCCGEPSGPPSSPSKDKESQDDEVTTAVAGKGGQSGGPAAPQAAAPTA
LQSQGAAPGLSQAPPSGSEASGTASPTKESNDQKSKSTETSDEQDEEDEDEEEEEEEEEEKEDAVEEQE
ENGAKEEETRKGEAVTANTEVISAGSQEQPILSSGAEGASNITNPNSTQTTGGDHPAADGAGTAEGKQN
ENKDANPKETPVEATATKNTTATTGDGDGSTAVSHTTSPLLLLLVVVVCAAAAAVVAA*
>Tc00.1047053506101.10|S125|A-Q----CD|2
MMMTGRVLLVCALCVLWCGLSGIAADGAGGADGSAVEYSIAGRRSQLRRGCAEEVSRRTGGANASAVEE
CVREGMDGVRAVVDGRRRWRRQQFAVAAAADVDSDDKSGEGGNDKLKGLSSSDQRLQAGQDPDEGQEPK
NSLEEKKTLETSRDLKITGEQNVSTDDDRPKQTGSQESTGGLPKGEKDTRSPQPPQPPPPAESLQPPPR
QPSPGTNTLHSEETHLPIRVEKHSRPQDGGPAQETGMLQTKGSTKQEKGASSLQSPESVSHLGPESTTL
LSTSTESSDIAASMVEKSGANNPKPPAASVTQRDSNGDNGPAALPASNTELLSQELPSAGIVAKTNDDG
DDSSPAAPTAERTTAGTRSTQASGDASDLERANKDDVNSDVVHNSKTAEFEAASGDRDTEADKDERYTT
VPENATNKTSNTETTADSAGSTAVSHTTSPLLLLLVVACAAAAAVAA*
>Tc00.1047053506131.30|S088|AG---K-CD|1
MAMMNGRVLLVCALCVLWCVAGGAVASNLGNNAVGGCMASWVLNTNKSYTPSGCEKTALTLPLRSVLSI
TAVEASTDPLVTGTAENKSDLAPSSGADFGGAGSPPGRGGEGGGGRDDGAGGPGGVGGASGSQARGSKA
SVGGGGGSNGGSKARVDGSLKSPSPVLGDGGSSPGAPTGSAGSDGSKGFIFGSFSSGGRSQPDVGSPGG
DASLSAPVAGGNSPPFITDESDALEKTGAAASTKGRKPQEAGEQSEANRARNELPELSAPAESTPEAQE
DFPSKQEKPENEAAGRAATGNEKRRIDAEAQGPSTVMSTASTPPLPPPAPATVGEERPTAQTDSQNLTE
ERTKTPPSPNKKEPEETEPTSGDGVAEQQGQGTVLPDLKGGTTGSPAEVTASSISTSGSSDGRSRADEN
DDNSRGPNPGGLNNDPEASHTNVAPTASETKPPTAKAAATARTDGTASAGGSDGSTAVSHITSPLFLLL
LVVACAAAAAVAA*
>Tc00.1047053506131.110|S061|A--TIFECD|52
MAMTTGRVLLVCALCVLWCGACGGGRAEATPAPSDTTPDEESQKGKAVVVTEGVQNGEKKAPQAAAPMT
SGLQGAPAEAAQAPQPGGVSFEKAEAAKDNNNQKGEKTEEKEDEEEEEEDDTEEDGETMKEADTGTTEV
ISAGGQEQRSLSSGVEEAENKTNPNSTTTTGDGDSAADGAGTAEGKQNENKDANPKETPVTATATKPTT
ATTGDNDGSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053506131.140|S030|A------CD|31
MTGRVLLVCALRVLWCGAGGRCDDEVVEAAAGGLIGTAGKGTVETSGTSTPGLDGSDLTKGLPKVNQPT
ETSTGKSLEVNKVNADQQDVAPGVGVEEDGSPSDHLEEPLKDDPEKGETKPEIQNKGQEGREPPQLQVT
VPQQPQPPLQQSQTQLQLQLQPSASEKGEGVGKNNKGGEGQLSLGVENKGNAAPEAPRKEDLLEGSGKE
SESSEQVQTTVPNTVPPEHKTQNGMLTPEQKTNESQGTDTSTNLPELQKENKEYSASTKGTAQSTSTGS
QEQEAEPSTSEEPSPFEEEHSTGTKKTKDARTTDAAATEKRQTGANEKVGDSDGSTAVSHTTSPLLLLL
VVACAAAAAVVAA*
>Tc00.1047053506131.190|S017|A---S-EC-|13
MAMMMTGRVLLVCALCVLWCGAAVEAEGDGSGGSAELLPKSQEPEKSPEDTQDFGHEAGGLKEELTPTS
ADEDDEDDDDGEGAEDEEEKQIEGPSGEKGNAAPDPVSGEKKLIGTEQQTRQSIVSAENTPLSGNRESN
AILTQTKIEGTKDSDKNPPAVENPLTTVNREQTLHAEGNLPPPQEGDDSREHDGKDTTNEDKKNVQPPE
TAATPTSHRDKGSEGTGDDTKATTVTANTTDTTKTQNSDSSTAVSHTTSPLLLLLVFACAAAAAAVVAA
*
>Tc00.1047053506131.84|S060|A--TIF-CD|1
MMMTGRVLLVCALCVLWCGVCGGGRAETIPGSSGSSGTPSGKEKLQNDKDTVVVTGEVDQKSEQEVTQA
AATTGSGSQKAEANPPQTTQPEGGASETTSPSSEKKDQKEDDQKEKTDEAEEEEDEDDEEEEEEEEEEK
EEDDTEEKGETMKEGAGTSTTEVISAGGQEQRSLSSAAEEAENKTNPNSTQTTGDDDPAADGAGTAEGK
QNENKDANPKETPVEATAMKNTTATGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053506173.60|S080|A---YKECD|24
MAMMMTGRVLLVCVLCVLWCGAGGGCAAGEDAEDDGSVRGGKGLSINPENVISAPGALGAPKPHAGVGQ
EEPLTPKEVPPQTTEEIPEDDAEDEGENSSEEENNSGRINDSTKRIRVEEKKETPAKESLPVKDSHSPQ
VQEGLKEKDNTEPKTRKEKKKEEGPPPPVSTAQPTTLATTQTPEVKLPGRKTPHVAPEGDASQKGLNDA
QTLTHQKHENSSSQTETTAEPPEDPSEGIVAEQQGQATATENLTENAPATNQEETTASSNSTSSGDEAR
STADENTANAQRPNPNESHDDLEGSDTHPAPTAGEAAPQTGGTITTANTTDTATPGDSDSSTAVSHTTS
PLLLLLFVACAAAAAVVAA*
>Tc00.1047053506187.50|S061|A--TIFECD|52
MMTTGRVLLVCALCVLWCGVCGGEPAETSRGSSGNASGKMNSTKNDDDSKDAAGEGDKSGEHAASQETP
ALPAPELPGTPQAAASKASGSPGTEEKASPSPAKQSEGGEASETVSTTTDNNNKNTENKEKEEKEEEEE

EEEHGENGAKGKEETEKEEAVASTTEVTSAGGQEQRSLSSGAAGASNITNPNSTPTTGDDDPAADGAGT
AEGKQNENKDANPKETPVTATAMKTTTATTGDSDGSTAVSHTTSPLLLLLVFACAAAAAVVAA*
>Tc00.1047053506245.200|S131|ANQ---EC-|3
MAMMMTGRVLLVCAVCVLWCGLSGIATDGVGGGDGSADEDLLLQWRAWLRRECAEEVSRRTGGRENASV
VEECVHQGMDGVRAVVDGRRRWRRQRIVVAAAAAGNGDVSTDKDGQARNKEVSPPEIKDEKPVASGQES
TDATRGKDQTTQNTSAAIVSLKKLISGKKKQEEGERMTEKEDGDNEDEEVEDEAKIRETTPVVPPPTAA
AGGGIKPPSGASGPAAPGAILTSRSSSGVDSSSRIGDEGSTVGISPNAVGKPSRQDKVPEAEESQHAQR
HDGVAADTLNNGPEQNGSAPTTGQNENEVATLGAGGSRSSREQITVKGGSEASRTDESSADPNTKLQEN
EKTPLKPSQAAATEPKTQHEVLTSVKEETKSKSTDASANLPDAPKSSEEHPASAATTMQSTSTGSQEAA
ATPSSNRISSLHEETTTGNNITENAQPPKETPVEGTAMKTTTATTGDSDGSTAASHTTSPPLLLLLVVA
SAAAAAVVAA*
>Tc00.1047053506245.270|S061|A--TIFECD|52
MMMMMMIMAGRVLLVCALCVLWCSACSGGRSEKPQVPPASSSVYENGPKTDNSRGGAGGGPQSGQLAEL
QPEGVLVRGATGVGTATQPDAQVSPGAPDAERRNPDQTQESGDVVGTDDEQEPKEEEEEDYGIEQVEDE
EEEEEQEEEKIEQENEKREEESRGEEKKDEEEKRDGKKEEEEEKKEDAATGTTEEMPARTEEQPSLSSG
AAGASNITNTNSTPTTGDDDPAADGAGTAEGKQNENKDANPKETPFEATAMKTTTTTTGDSDGSTAVSH
TTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053506267.70|S030|A------CD|31
MMAMMMTGRVLLVCALCVLWCGAAVVVSSAGGDGDGGVKEGPLGGSKSDSRDEKAAKPELSKSVDEGLG
SADHSLDTRSGNNVNEQGNLANEPPTENVGKKGVQEEGNELPVTHISRTKDKVTLPQTSPPPTPAGEEP
QATSPSQASGVGEGDGGPVGIEGTGRNVSDGSLVGASDTSRVTGDKNKDPKGSEGPVSGPPSGGASSSP
ISNDGDASRNNGGAPSTQDTTSLKNNEQSRPTTSSGNAPLNRETPERSTPDAQRHSSDTQENETGQTAD
GDAAPSAAGQSAMGTKGSSGVSTTTSNAPTTPQPQLPAPPVPPTATVTGAPAEKPTAERLPPPADSTPG
ESLAATTTAQTKGTATPGDSDSSALSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053506267.80|S043|AG-----CD|27
MAMMMTGRVLLVCALCVLWCGAGGVYARDTLNNAQGVCMVPGGFGKKTSYLASGCDKNAPTLSLRPALP
IPAIQAEDSEEDAGPDITPGGGGGGSGVNSAGQGAPGSSQAGSVPGAGFPPPAGASGGGGNPSGPVTPG
GDSSPDPRVGTETSVSLSSTSQSESEKKVLQGDEAKDQSHQLPNERAADTPVVETQSWGSDTTRGQDVG
DTSTLVFKQERSSEEPEKKDGDSDTLQTVNSPEDPNKELQEKEKALPELSNAPLPEPKTDHPKTNPEKE
KNGRQNTSASTDSPAKQEGNNEDPVSTSDAAESVSTGSQEQAAATSSNDSSSPLQKETSVEKTTVENSQ
PSDTAQTEKRQSVNKEKVGDSDGSSAVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053506267.90|S061|A--TIFECD|52
MMMMTGRMLLLFALCVLWCGAGGGGCSETAPASPGTPSDKNTEKDENTVVGGVGAVDQTGQQAASQAAA
SSSVQNARGAEAESAQQTGAQALGTANATTENNNDTTKTGENEKTNQDTNEDDDEEEEEDEEEDEEEEE
EMEEEEEEDDGNEEEDGGEEKKQEEKDDTSTTKRISAGGQEEPILSSRVEEASNKTKPQSTQTTGDKDP
AADGAGTQEEKQNENKEANPKETPVAATVIKTTTATTGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVA
A*
>Tc00.1047053506269.10|S080|A---YKECD|24
MAMMMTGRVLLVCGLCVLWCGAGGRCEDVVKAPERGGESPQTKPETPDSGILGTQPKVTIDNEEDEDSD
ANEKEELEEEKAEKIKAPTQTHEGKKNEGASLPPPPPIPSGGPTAERGNPQNPRKVKNEATPSGSKKDS
EAPEPPSGVATQGQHSHDTETEDSTKNAATGSPAEPTSSSTSTSGSGDHVHNKADKDDAQSSEGQHDSL
ETGNTNVVPTLSETAPQTAKTTTAARINGTATPGDSDGSTAVSHTISPLLLLLLFVACAAAAAVVAA*
>Tc00.1047053506269.40|S001|A---H-ECD|18
MAMMMTSRVLLVCALCVLWCVAADGAVGVVSGGDDNSLKELFIPVARLQERQEQRATGATADAKAAAEA
AETAVAKATAAKVAAEAAAKAKAAATETASKAKAAAEAAAEAAAKAKTSAETDETAAKKVTVAAEAEAK
AAAASEAAKAAATQATATAEAATKAKAAAEKAAKEAATAAAAEAVTATAAAEAAAEAVTATAAAEAAAA
VAAAATQEAAKATTKAAEAAKAAAEAAKEEAEKAKKEAEKAAEEAKAKAATAATAAAAAAAEAAKATEA
AKEEAEKAAETAAAEAEAAEAEAKAAAEAAKAAEAKAKEAAEKAAAAAESLRVTTVGEEAKTATHDQDN
SVEHHSEEKQELLQEQEPERQEKEQHEKQQHQQREHSAGNGEESPKEKTANGTNATAIKDDSDGSTAVS
HTTSLLLLLLLVACAAAAAVVAA*
>Tc00.1047053506289.120|S038|AG-----C-|7
MMAMMTGRVLLVCALCVLWCGAGGVYARDLDNKALGGCMASGVLGMNTSYVPNGCNKYMPTPPLRSALP
ILAIQAEVGQVSVTPPDSGSGGGGGGSPGAAAPVPGGAAAPSGPAVPGVPAVPNAGDSVPGPAAGGGPP
AAPATDSPRPAAGRESDSLVPSSPRDISSQSDDTVITSSDLSNTHSGSREEVLQQEETETHNPSPSKGL
AQEALPDVQQPQTSASENSKTGCDAEASNCGSQGKLGKATMEKQDLEESNTAESPPTKHKESNGNEENP
TEASSTESQNTEAQQEIKTPVDESDSTGTDASIAVAAQSTSAGSQEEATESSSNGSHSPLQGEVFTGTD
TPENAPSPGAAETEKRQGENVTKDGDSDSSPAASHTTSPLLLVVACAAAVVAA*
>Tc00.1047053506289.150|S038|AG-----C-|7
MMAMMTGRVLLVCALCVLWCGAGGVYARDLDNKALGGCMASGVLGMNASYVPNGCNKYMPTPPLRSALP
IPAIQAEVGQVSVTPPDSGSGGGGGGSPGAPPVPGGAAAPSGPAVPGVPAVPNAGDSSGSEGDSPRPAA
GDLHSQSDDAVITSSDLSNTHSGSREEVLQQEETETHNPSPSKGLKQEALPDVQQPQTSASENSKTGCD
AEASNCGSQGKLGKATMEKQDLEESKTQESPPTKHKESNGNEENPTEASSTESQNTETQQEIKTPVDES
DSTGTDASIAVAAQSTSAGSQEEATESSSNGSHSPLQGEVFTGTDTPENAPSPGAAETEKRQGENVTKD
GDSDSSTAASHTTSPLLLLLVACAAAVVAA*

>Tc00.1047053506291.10|S043|AG-----CD|27
MMAMMMTGRVLLVCALCVLWCGAGGVYARDLDNKALGGCMASGVLGMNASYVPNGCNKYMPTPPLRSAL
PIPAIPAEVGQVSVTPPDSGSGGGGGGSPGAAAPTAGPPGGDVSRVPAAVAGDPVPNAGDPVPATDSPR
PAAGRESDSLVPSSPRDISSQSDDTVITSSDLSNTHSGSREEVLQQEETETHNPSPSKGLAQEALPDVQ
QSQTSASENSNTGCDAEASNCGSEGKLENTKAEKEDSEAPKTQESPPTQHKESNGNEENPTEASSTESQ
NTKAQQEIKPPVDESDSTSTDASIAVAAQSTSAGSQEEATESSSNGSHSPLQGEVFTGTDTPEDAPSPG
AAETEKRQGENVTKDGDSDSSTAASHTTSPLLLLVVCAAAAAVAA*
>Tc00.1047053506321.20|S061|A--TIFECD|52
MAMMTGRVLLVCALCVLWCGVCGGGLAETTQGLLDTASEESESPKKNKDTGGSAGTDGPTAETKAPQAA
DRGSKEQEGTVEQAAASVPGVTGAGAGMETAPQPGREATESAKGTRGNKEETKKEEESEKELEEGEEEE
EEKKEEEREKEKKEEDDTDAKKGISADSQEQRSLPSGAEGASNQTKPKSAQTTDVNDPAAEGAGKRKEK
QNENKEANPKKTPVEATAMKTTTATPGDSDSSTAVPHTTSPLLLLLVFACAAAAAVVAA*
>Tc00.1047053506321.50|S025|A------C-|17
MAMMMSGRVLLVCALCVLWCGAGGGYGLPAGYCADGGLDDVKPAKGMDDEVVLMKRECVPSTAFRGVVT
AVLAGEDSDLNSPGAGVGTSGKRNSDAEESPVVDAESGLTPSGSGAASTASSPAVADKDGASRAPVLGA
VGPNQQPAVVSGGQDDSSYGGREEKEREDAVSAGCGEEPSSPKVCPQPRLVGVELTPRAMEEKRGQKDN
ASVTNNQSEGTQQEDGVPHVPETRASVQTPPAPAPEEGHPENATQPFGASEEHATAPSSSLTRDASNGD
SQRQIPQPQTTTGTKQTVPVLQGVPEGVQEDQKNVEDGKKTNQVDSTGSAHNAEHDSAAETHELLTASS
NTRSSGAPGKEPASKSLSGNLRSSTAGAAEQAKAPAQGGAEEKKAPEEKEISEESPPTAAEVDAPGGPS
DPPPKPLPQSALPSSKEVQDTMQSTEDPQTKGIEPTTDARQNALTEGQAETTSPSSPADDAAANDADES
NAEIANDGSAVHAGVPEEEENQEQVDGSDKQTSFISTAKKYNTTIEDSDGSTVVSHATSPLLLFVACAG
AAAVVAA*
>Tc00.1047053506321.120|S083|A---YK-C-|4
MAGRVLLVCALCVLWCGAGGGYAEDVDVVSGDPGTRGERGGGTVGQTPPADGSNGGSGGSKADIPHGSE
SEPLDSASDEESSSLDIDQEVGPNPPEENVPQKEVDHIRKQDHSESGPQEALPPDVNGTVTLDSDAQLQ
LSDTKKNKKKTKVLTDVVGGEIADGGKDSTGRNNGLSPNKNYPQPLLKQRIKQVLPPKEPSPPPADISP
APQEVPTVVSPTERSPAITVSAGETNPTASTDSQNTTETTTMTSPSNAETAPEAEEKPLGNGEPSQNRK
DTDTPDSMNDSNTSRPAETAASSVSKSGSGGAQNKEDKVDNGAQRPNSREPQDGIEGGNTNNTPTSTET
APQKAETVNNYQTNDTSKSRDSDSSNVVSHATSPLLLLLLVVVCAAAAAAVVAA*
>Tc00.1047053506321.140|S061|A--TIFECD|52
MAMMTGRVLLVCALCVLWCGVCGGGLAETTQGLLDTASEESESPKKNKDTGGSAGTDGPTAETKAPQAA
DRGSKEQEGTVEQAAASVPGVTGAGAGMETAPQPGREATESAKGTRGNKEETKKEEESEKELEEGEEEE
EEKKEEEREKEKKEEDDTDAKKGISADSQEQRSLPSGAEGASNQTKPKSAQKTDVNDPAAEGAGKRKEKQ
NGNKEANPKKTPVEATAMKTTTATPGDSDSSTAVSHTTSPLLLLLFVACAAAAAVVAA*
>Tc00.1047053506321.200|S091|AG--YKECD|14
MSMMMTGRVLLVCALCVLWCGAGWVYAKELDNNAVGGCMGSGVLGENGFHMPSGCAKTVLALPLRSTLP
VTAAGVPTSEEESEKNFSNPDLKPLSPPVSGGSQGVSGGSGGAGQSGGADNNAFVVGVAGASGSSSGGV
VNSLVSDSFSAATPSPSNPVGADGLQGSKGTTSTLSMDAPETGVKSQSARPPAPAQTNLDRQEVSITNA
ETQSSIKPHAAGNQIVNGDETGREIEHRAAVTGGTPSNQQPTPLQPVQQEQPTTDSHTRQKEERDSEEA
PSPPPSPSPTNSTEGIPATRELQISTEKKKQTSPSETQKELVGQEKPSKGDAAEHNTKGTTTLDSVKDA
VASGSEETTASPISTSGGADAQNEVSKDGDNAQRTNHKETHKHPGPDNTNPAPTANNTKPQTALTFSTV
PTNDTATPGDSDGSTAVYHTTSPLLLLLFLACAAAAAMVAA*
>Tc00.1047053506335.50|S091|AG--YKECD|14
MAMMMTGRVLLVCALCVLWCGAGGVDASNLENNAQGGCMVSGGLGAKTSYSVRGCNKTVLTRPLRSAFF
INAIQAEAKEVKDISEEGDNLKLGSIPQPPAPPPAPETPPPPDASDSDGIGRSELGADGQTGGGGGGSS
GISNGDEDSTLKVPVPDDKSSSPIPNAGDGLKNTGDSSVTQKNNPSGTDEPSKKPLNVPAQPTVQTPEA
LDPDQNENTPNTQGEISVEARGKGASGGGAGESDVNSKGSSSVSTAKSNPTGKTTPSVPSAGETPTITA
TPNDSENPTGKNDSTAASGTELDSEATKKSSKDDAAEQHSQERDKADLVKSANTGHPAYTAASSISTYG
KGDAQGKANENGDDPERHDSKGTHDALEADNTNVAPTASEAAPEAVNTTEKNDTAPTGDSDSSTAVSHT
TSPLLLLLLVACAAAAAVVTA*
>Tc00.1047053506335.100|S026|A--T---C-|2
MAMMMTGRVLLVCALCVLWCVTGGTCDEDELPQASLLGASGSDGKSSLEPPIIAQGGSPNSVLEPISAK
ETRAETDEGGPSREESSADEEEEEEITLPPGGGGGKSQAADGKLKIINESEPKNENQRQVEGGTQNQSE
KETEANGQMKVTKQNANGSGPQPQHQEIPLQEENKKSGELQQPSQGKEQQTNVEDIAPRNPAGDHSSGE
HNGNDGSSEVEEEEGEEGAEGHERHRAREREEAAHVSGAPKVNSTDIQQEVQRTHAGETPTGNKERAGE
EKDDETEEEREEQKKQHQENPPGKEQETVTGANTTNQLNTMPGDSDGSTAVSHTTSPLLLLLPLLVACA
AAAVVTA*
>Tc00.1047053506339.40|S038|AG-----C-|7
MAMMMTGRVLLVCALCVLWCGAGGVYARNPDNNSLGGFMASRGFGRNKSFLSNGSIKNLSTPLLLSASF
ISAIQAEAHEEVSSAGVTDSHLSGATGFGTVPHVSGPAIPVPGSVRGPGAIPDVAVPVRAGHGPGLGAA
IPGHGPAGPDDVPAIPVPRPVRGPGAIPGAPFSSTDVTDLVPAFSGLGAATPGPAGPGLRAAIPGPAGH
GPVGPGHGAAIPGHGPAGPDPAFSGLVPAVPGAGHSVGGGSELPDSRSVVTSSSQGGNGKTTPVSVSSD
EQIASPEEVLAQKETGSQGTSSPEGQPTVSSNNEKQRNNSVSAGGHSLGHDAAGDELQDSLEEQQKNDH
SQTNETKKSSGDQNTESQHSGKTLSKVSNTTTHGIKTQLPMTNSVNEKNYSQNTDASHTTSPLLLLLVV

ACAAVVAA*
>Tc00.1047053506361.50|S100|AML-VFEC-|15
MAMMMTGRVLLVCALCVLWCGAVFGHAMEDYCGEGGGDGLRHTSNGGDDGVSLKADCVLLSTRMALIKA
VEAAEAGEDELSGPETSQDAEETLQDNTERSAAAGPGRDVVAIPPPTTPPKPEESGTKGQQGKPGVLGP
NDGEHTDSKNNRSEPHLEKPRTDQSSSSSGSLDPESAKELSLKKENKSDESSDETLTEEEEEHINKSDS
RELVPKKQLNEIQELRKGKMSHEAPTETHGRPANDAEIQTTTPPPPPATMNGHSSTEDLPPVQPLQRVQ
DDHEESGPPSPTANGDAANNEADNSTEEGIPNSDQAADGAGTAEGKQNENKDANPKETPVTAAAMKNTT
ATTGDSDGSTAVSHTTSPLLLLLLVVACGAAVVAV*
>Tc00.1047053506409.30|S018|A--SERECD|3
MAMMAGRVLLVCALCVLWCGAGGRCDEEGTAARGSGGGPPLASKQPETPRVGSQDVKNGVTVAKENVIP
TPPLPIDGDAEVDEDEDDDDDDNDNDADGEEEDNETGESKEKSTEGQINKEGKVPPDSDSREKNLIGSR
QEKGQSIVPAGDISHSKSQESNANSTQTEVEGKKDADKRPPSAENVLTTVNGENTLPEGIAGGNPPSPP
EDSVASREKDGEDTTSEDEKNVPSPESAATPQSHRDEVSEGTGEDTKATTVTTNTTDTTNKQNSDGSTA
AATVVQPEDGVESDPANNDLSPPSTEVAAQLSMTPDAEGASNNEENTDTQIAGNPNVTIATATQTNDTA
KPTDSDGSTVASHTTSPLLLLLFVACAAAAAVVAA*
>Tc00.1047053506409.90|S022|A----R-C-|4
MAMMTGRVLLVCALCVLWCVFSSVSADAGDDCGDSGQGVVGTVGQPSSPVGGHGDNGVVTDGSSLSSGS
HLPGSAPTGGKPPLPGVGVGVGLNESKDALTLAQEGREVVQDQHELVPQVSHHTDAGTGGKGDLNAPEQ
SPNAKTELEDGGGVCGDDAAAAEGEVKTTVNEGQLGGSSTSDSHPPAADRGSREQEGRVEQAASTAALT
PVVGRETPPKGDTNEDSPGDKAATGAGITQDIPAVSQQQTHSSSTSTTGNGLTSTLGKGRAAEDISSNN
ERSGKALLQEGAEHETVAGSQSQTIPAATARNTLGTTVSGDSDNSTTITTAVRSDTGTEGTPTSNHPNR
QSIEGATSPGMNSDGEAESAKKYDTVSQSAGSSTAPTTNNKTRDTASHGNSDSTVVSHTTSPLLLLLLV
ACAAAAVVAA*
>Tc00.1047053506423.10|S095|AGWTH-EC-|7
MAMMMTGRVLLVCALCVLWCGAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITMPLRSVLP
ITAVEASAGTDNTAVVIPNDSHSSGTSNAGASGGSAGPGAPDVGGGGDSGGEGSSGPGASPPVPAAPAP
GPSGGASSGDSGDGGNSGGGGGGAAGASGGGGGGGSGSGGGGSGSSTDDHATGSVPSSSSLASPAAPAA
PGDGSAGGHDTGGVSSGSSVPAHPPSPGPFGAPSPGVDSSAGSSGGKAGSSGSHPTNTTGDSSTGDQTP
AAAAANNSSPPEIPAGTTSGTGHTRQEEEEEEEEEDHEKQHQSDETQVQQHQQHEHPAESGEESAKDKN
ALRTNATANTGDSDSSTAVSHATSPLFPLLLVVVCAATTAVLAA*
>Tc00.1047053506453.30|S008|A-----ECD|43
MAMVMAGRVLLVCALCVLWCGAGGGYTWPYKECESDDKSCFNHSQHKSVYNSSIRSRYLGETDSTSTGL
LGSSTGSTGNGGDVSRNGAGGTTNSVTDSQKGGAQSSLTPSQHASASSGDSSRSKDSSEKTEETPGPVS
TSDNDGDGGPNTANQAHLTGGEKLDSGHQTEDGDTDPNLPIGDSKDGEGTHSSPTPPPTNKANVPRVTA
EGEKAPAVLTRQEESEGNPEAEPENEQRSSANGVSVPQPEAAQQGETEDDNTTEKTPDEAAAPKNGTAM
PGDNDGRTAVSHSASPLLLLVVACAAAAAVVAA*
>Tc00.1047053506459.10|S019|A---SRECD|1
MAMMMAGRVLLVCALCVLWCGAGGGFGEETAGRGSGADLPLESKGLVTSPESSQGLQGGAPGGEGNLTP
VVIHEADDDDDNGKTKAEKEKINERQSVQGGTIAIGSDSREKILSGSGKKTGQPILSAKGISPSGSLES
NANPTQPEVEGTNTEENTPAAGNPLTTVNGEQTVPEGVAGVNLPSPPEEGVDSHEQSGEDTTSEGEKNV
PSPETTATPQSHRDEGSEGTGEDTKATTVTPNTTDATNTQSSDDSTAAAAAVQPEDGMESNPAKNDLSP
PSTEVAIQLSTAPDAEGASNSEENTKSQSAGNPNVTIATATQTNHTTKPGDSDGSTAVSHTTSPLLLLL
VVACAAAAAVVAA*
>Tc00.1047053506459.130|S033|A---V--CD|9
MAMMMTGRVLLVCALCVLWCGAGGGGCTEKLAASAEITVDSASGGVVPDTATSHTAPGGAGDVSAKELQ
LNPVKGSASGSPPLQDALKLEPLTEQPHSDQENTDPPPHSKSFQEERRDGTPENSPGESGALPSQEDTK
HASIESPEINNPPPYSTNNNTVSRNSEERTEDNSGSTETLDAAPSEEGQEREKVTSSLEQPRETSTAAP
TVTTQTTSMTPPKDSESRSVKMSDASPHSTVTVTQTNHTATITQNSDSSTAASPTISPLLLLLVVACAA
AAAVVAA*
>Tc00.1047053506459.149|S001|A---H-ECD|18
MAMMMTGRVLLVCALCVLWCGAADGDVGVVSGGDDNILKELFIPVARLQLRKEGGAAEAAADAEAAAEE
AEAAAEATKKAAAKAKEAEAAAEAAKAAAEAAAAAAKAEESEAKAKAAAAATESAKAAAKAKEAEAAAE
VAKAAAIKAKTAAEAAAAKAEEVEAKAAAEAAAKAAAEATQAAKAAAEAAATATEAAEAAEEAAEAAAT
AANAATPAGAKAKAEEAAEAAATSTLVATSAAKAADEAAEKAAKAKAAAETAEAAAAAATSTLVATSAA
KAADEAAEKAAKAKAAAETAEAAAAAAAEAAAAEKAATEADAKAAAEKKAEAAAEALRGTAVGEKEVKT
ATHDQDNSVEHHSEEKQEILKEEERQEKEQHEKQQHQQREHSARNGEESAKHKTANGTNATAIKDDTDG
STAASHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053506499.40|S077|AML-YK-CD|1
MAMMMTGRVLLVCALCVLWCVTVFGIAMDNRCVEDDGNVLTHTHNGGNDRVRLKADFGLISTRMGLIKV
VEAGEREGEDLESVDAPLDSVGGKSPSSLLAGSEDNEAPGAGGGQGAAGAGAASLPSGPGVPGTGDENR
QSLMAGQKGNEKKNLDPDSKEPKESQDQTTDQLSSSSGSTSSLPREKPSSTGTSDINQLPTDTETKGDV
DPRNNSGDDEERDEEETGREKEENKLQPETQERGNNAEVPQSLPAPPSGGPAPTKPSGGPASSLSESEG
SPPTEPKNSQNPKKVTKENTPSESKMESKATQPPSGDATQGRHSHDTDTEDSTKNAAAGSPAEPTTSSS
STSGSGDHVQNKADKDDAQSSEEQHDSLETGNTNVVPTLSETAPQTPIKTPANTTYTVNAQNSDGSTAV

SHTTSPLLLLLLLAACAAAAAVAA*
>Tc00.1047053506499.80|S033|A---V--CD|9
MAMMMTGRVLLVCALCVLWCGAGGGGCTEGQLPVVEPPVNPASGAGVIHNPADHTVPGGAGKHSAEQTQ
LNNVEGSASREVSLEAPLQPVSTTQQTPSSSEPTDSLSHSQSSGGKRQDVQHEGPPGEPETSLNQEENK
NVSNGNQQSIDQPSPSGNDDVVSSNSEERTEGTPSSTEIIDAAPLEEWQERENVTPSLEQPRETSTAAP
AITTQTSSTTPTDVSESNTVKMSDAAPQSTGTANTNDTTTKIANSDGSTAVSHTTSPLLLLVVACAAAA
AVVAA*
>Tc00.1047053506499.140|S079|A--TYKECD|5
MAMMMTGRVLLVCALCVLWCGAGGRCDEGEAAVHGVPPDVPASGTEDGLGGTRNAAPAPESQIQSSGEE
QQHKSREGRPALPEGSSEEEEEEEEETVEDENLDEVTERGEEGRHEDGQNANERDGSQTSEVFTKQEET
PPPSTPAAPAEEGNQNASPQAPSVDSHGGGGTDRIEGSILKAPSSGVALQHAGDASTNQKNKSLETGKH
AENTITGGPVPSQVKAPKESINDAENHSVTGEDTASNQVVSRGTTEYEAQQRALATQDRSSVSFPDSEK
KWHTTPQETPTTQVPPSATEPSSRGGQLPTATTDSQTPNAQEHKKLLLPKKKTEYNAPEHPSGDTVAEQ
QGQATATENLTENAPATNQAETTASPNSTSGGGEARSTADENTANAQRPNPKEPHEDLEGIGTHPVPTA
SEAAPQTAGTATTANTTDTAAPGDSDGSTAVSHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053506499.160|S030|A------CD|31
MAMMMAGRVLLVCALCVLWCGDGGRCDEEAGGPAGGAGGGSGGKGAVGSTETSAPGPDASDPPKDVPKA
NQSTETSTGKSLEVNEVNAEQQDVAPGMEDEKKKNPSDHLEEPLKDDQGNEKTKTQLQNKEQELRQPPQ
AQVNIPQQPQSQTQLQPQPHTPALEEGEGVGENNAGGAGQSSLGVENIGNEDSRALGKGDSLKGPGKES
ESSEPVQTTVPKTVPPEHKTQNEELTPEQKTNQSQSTDKSTNLPELQKENKEYPASTEGAAQSTSTGTQ
EQEAEPSTSEETSPFEEEHSTGTKTTEDAQTPDAAATEKRQTGDNEKLGDSDGSTAVSHTTSTLLLLLF
VACAAAAAVVAA*
>Tc00.1047053506499.210|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCGAGGVYARDGENNALGGCMTSEVLGACFFHMSSGCNKTAITVPLRSTLP
ITAVEASAEGETPVAGLNDSGSNEDSIAGAPAGAAASPSGPSGGSDGKNEPSGPLSLDVDSSAGSSNGE
AGSRGSTSSNAVGEPPRENPSPDVAAAAHNPPPPGGVAGTTPGNKGEKEEEKEKEKEKELDEEHKRNHG
QENQSRLANQSEGEIGREGERLHKKTKVPKEEKEQIQVVEHSIENQGTLHEPGKEPQEIKRENEQSKHQ
NEELKGGQEKENPLQAIQQNSDAEEEMKKNRQQGQRPQEVTAPLASSSGSEATRKSQSPVPPEALHKKE
LTDGLREQLEEETPLAATQSKSHGTTDPQSSPASAIAGEAAVTHDADEENATGRNDDEPIETVFADDHQ
QHEHPENIQKEPAKDKNAVITNGTATPGDSDSSTAASHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053506501.10|S009|A----KECD|5
MAMMMTGRVLLVCALCVLWCGAGGGVTEINDESLGGSQLLSGVGEEAPKGLSEPGERGSDSAGHPLNKN
NGNNSNLQEGTVTGTTADRVGKEEEVDDNDDLEEAEEEERSKEKEDKAQTGKSKSSSKEVAPLTIPKAS
GLGEAGGGSPSGVDGVGSSESSDGSEDLNLEAPGLVVNFPPSLPNAAAGGLQNTDGALSPQKNNFSETG
VHSGTTPPAPSLPKSQAPAMPKPEAEEQSSTEQDTEDSPDTEEVTTGKDNVQNTVETGIPSRSSSAASK
PPVQQATPILTQPPAAPSPERSALAPSEKKSTAPSFSAGEGSRRATNVAQNSKEEKNEKLPSENETESK
AVEQPSGDDLAEQDSPARTTASPIPASGGADAQRNADADNRNAQALKYEGTHKNSETGYTNPASTIGDA
ATQTEKALADAKANDTATPGNSDGSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053506501.110|S111|ANP-V--CD|2
MAMMMTGRVLLVCALCVLWCSSVVQAADGFISDGSDEIGEMVLTWHNEFNRTCNEQSTKEGILDESAFK
SCMRVRMKEVCGSDDDGMSSTSHEPEAEEICKKYAGNTEEHVESSTPLTEPSHDAETQVATPNSETLKG
GAAEMESTPGAPAGDSPANPTEGPKSTSPATDTANSEAEKDGKEVMPKNAPESNATRKGEGEEKHSNTK
ETTVDADAMQNNTTAENDGSTAVSHTTSPLLPLLVACAAAAAVVAA*
>Tc00.1047053506501.220|S008|A-----ECD|43
MAMMMTGRVLLVCALCVLWCGAAVQAEGDGVTEPQDEPSRGSQSASRGGHEEKLNIRIPVGGVLNTSEE
PLDAQDLMRDSPQKNSVKQPPTDNGGAAGKEEKVEAKKAEDKVTGSDGEEQPKDHSDETQESDGPKENG
RNPSPTPADKMLTSGDKTAEHAGQTGQAIRAPQSPETDGTRPGGSSRGDSSVSPLSTAGISSSSAIDAP
FVQSTQPSEKGPQSEAMSLGTALPNEQPKERSESKANQGSFTSEEAAESLDDSGDAVEKEKEKGDVGPK
ATTSLSSTTSYPPVTQTTPRPSSAEPSPTTTELQAGEETSTENVTITKRNDTATPGDSDSSTAVSHTTS
PLLLLLVVACAAAAAVVAA*
>Tc00.1047053506501.240|S104|ANP-VF-CD|10
MAMMMTGRVLLVCALCVLWCSSAVQAADGLISDGSLEGENMVLTWYPVNNKTCEERSTNGGKLDESAFK
SCMHELMNEVCEAYYSMKSSESHVTEADSICGKYTGDPSEEDVQTSTPQEQPSPEVETPVASQTPETSK
VEAAEMGSPPGVPAGDSPANPTEGPQSTSDATDTANNEAEKSSTEVMPKNAPESNATRKEEEKRNEKNH
SNTKETPVDAEAKKNNTKTTDSDGSTAVSHTTSPLLPLLVACAAAAAVVAA*
>Tc00.1047053506501.290|S030|A------CD|31
MAMMMTGRVLLVCALCVLWCGAGGSCNEEKADEFCNNTYFGVLTLLANKSDEELKEKYCKNEDDKAKCV
NTLKNNIADALENEKKNKDNGADREPNVAHGAGVSVGSSKTKSSTAAGADNAGMSSPLPLSLKVEGDVD
DKVHSPAGGAGPQPHFDDGRRETERSHHSEAEGSNQHGVGVQGKKIHNKDEEKPQAGLKSTEAREGTDG
APAPSQDPPNTAESHEDKSRRVAAPDTTPALNTSPGSNREQTSQSPSPSGSETSGSSDNEVPEKNSINT
QMSGAPLKDEEQHRESTAGNKDSTTVESAAVQSNTTTPGDNDSSTAVTHTTSPPLLLLLVACAAAAAVV
AA*
>Tc00.1047053506501.350|S105|ANP--F-C-|4
MAMMMTGSVLLVCALCVLWCGAGGGFAKEAEASANGVASKTTPADRIILNWHVLMKEECATENTKNGTV

NVPAMKRCIQVAMKGICDTFYNKTPSEIHDPEVKGMCTYYAAIPDEPDEPPTPQGPPPDSAVSNTTSNE
GTPKNAPESDDAGREGKEDEKEHGNTKQKAVESAAMKHITETADSDGSTAVFHTTFPLLLLLLVACAAA
AALVAA*
>Tc00.1047053506501.380|S067|A---IFEC-|4
MATMMAGRVLLVCALCVLWCGAGDGGCSEAAPTLPGTGVTDNGNNLESKNNTTDGVGGGGPIGQQAASP
AAAGSVPVPGAEAESAPKTGAQALGPAEETIKKNKKTENGENEEGNQDADEEDEGEDEEEVEEKVEEEV
DDGKEEEEEEEKKKQEEKDDTSTTKRISAVGQEEPILSSRVEEASNKTKPQSTQTTGDKDPAADGAVTQE
EKQNENKEVNPKETPVEATVMKTTTATTGESDGSTTVSHATSPLLLLLLVACAAAAAAAVVAA*
>Tc00.1047053506599.50|S001|A---H-ECD|18
MAMMMTGRVLLVCALCVLWCGTSGAAADGDVVVSGGDDNSLKELFIPVARLQERQEQRAAGATADAKAA
AEAAETAVAKATVAKAAAEAAAAEAVKVAAEAAKAAAATQEAATAATAAAEAATAAKAAAEAATAAEAV
AEAAEEAKAAAEEAKAAAEKAKAAAEKAKEEAEKATEEEKAKAATAKAAAEAAAAKAAEAAAEAAKATA
AAEKAAETAAAEAVAAEAAAFAAAEAAEAKAKEAAEKAKEEAEKATEEEKAKAATAKTAAEAAAAESLR
VTTVGEEEVKTAIHDQDNSVVHHSGEKQELLQEQEPEPQEKEQHEKRQHQQREHSAGNGDEAANDNTAN
GTNATAIKDDSDGSTAVPHTTSPLLLFVAFAAAAAVVAA*
>Tc00.1047053506599.80|S008|A-----ECD|43
MAMMMNGRVLLVYALCVLWCGAAVVESVVDGVVDGGVKEGLLGDSQSGSRDEKAAKPELSKSADENLGS
ADHSLDTRSGNNVNEQGNLVNEPPTENVGKKGVEGEGKELPVTHISRTKDKVTLPQTSPPPTPAGEEPQ
ATSPSQASGVDEGDGGPVGIEGTDRNVSDGSLVGASDGSRGTRDKKKDPKGSEGRISGPPSGGASSSPI
SNDGDASRKNGGAPSTRGTTSLKNNEQSGPTTSSRHAALNRETPERSTPDAQRHSSDTQENETGQTADG
DAAHSAAGQSAMGTKGSSGVSTTASNAPTTPQPQLPAPPVPTTATVTGAPAEKPTAERLPPPADSTPKE
SLAAKTTAQTNDTATPGDSDGITAVLHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053506599.100|S068|A---IFECD|10
MMMMTGRLLLLCALCVLWCGAGAGGCSEAAPASPDTPSDKNTEKDEKTVVGGVGEVDQTGQQAASQAAA
SVPVSGTEEESELQTGAKASGTAEETIEKNKKMENGENEKANQDADEEDEGEKEETEEEKKQEKDDTST
TKRISAGGQEEPILSSRVEEASNKTKPQSTQTTGDKDPAADGAVTQEEKQNENKEVNPKETPVAATVIK
TTTAATGDSDGSTAVPHTTSPLLLLLFVACAAAAAVVAA*
>Tc00.1047053506599.150|S080|A---YKECD|24
MAMMMTGRVLLVCALCVLWCGAGGRCDEEGTAVPGSGAGGPPPASEGIGMPPQDTKNLEFGPQDIDSKA
SPESSPRIEEAEDEESDGEEETAEETEEEKEENIKALTDTHESHKNEGAPQSLSAPPPPPPPPPLPPSG
GPAPSSTAVEGGPTAEKENLQKVTKKDLEAPEPPSGDATQGQHSHDTDTEDSTKNAATGSPAEPTTSST
STIGSGDHVQNKADKDDAQSSEGQHDSLETGNTNVVPTLSETGPQTAKTISTANTTDTTNTQNSDGSTA
VSHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053506599.170|S008|A-----ECD|43
MMAMMMNGRVLLVYALCVLWCGAAVMESVVDDVVDGGVKEGPLGDSQSDSRDEKAAKPELFESVDEGVG
SADHSLDTRSGTSVNEQGNLVKEPQTGNVGKKGVEGEGLGTQRNEVHEQQVEEEVKELTVKQKSQTKDK
VTVPQSLPPTPAGTITSPPPPTASMQESPRTPGQPQENSQKSAGQPPKLQVQPPSSPAASAEGEADGGL
VGASDTSRVTGDKNKDPKESEGRVSGPPSGGASSSPISNNGDASRNNGGAPSTQDTTSLKNNEQSGPTT
SSGNAPLNRETPERSTPDAQRHSSDTQENETGQTADGDAAHSAAGQSAMGTKDSSGVSTTASNAPTTPQ
PQLPAPPVPPTATVTGAPAEKPTAERLPPPADSTPGEGLAATTTAQTNDTATPGDSDGSTTVSHTTSPL
LLLLLVACAAAAAVVAA*
>Tc00.1047053506599.210|S061|A--TIFECD|52
MMMVTGRLLLLCALCVLWCGAGGGGCSEAAPEAQLIESEDNKRKGDNTTTDGVGEVDRLGQPAASQAAE
SVPVSGAEEESASNPSPAKQSAAKASEVANATTENNKNTTKKEDKADNEELKDEEKEDEEEEEGEEEED
EVEVDDGKEETEEEKKEEEKDDTSTTKRISEGGQEEPTLSSRVEEASNKTKPQSTQTTGDKDPAADGAV
TQEEKQNENKEANPKETPVEATVMKTTTATTGDSEGSTAVSHSTFPLLLLLVACAAAAAVVAA*
>Tc00.1047053506599.240|S064|A--T-KECD|5
MVMMMTGRVLLVCALCVLWCGAGGRCDGGETAGSGSGGGPPPESKQLETSPQVKQELKDEARSIKVKKP
PTSSEDEAEEDEEDNDDDDDDDEEPEEEKEKSKEKEDAQQTRKSKSSSKEVAPLTIPKASGLGEAGGGS
PSGVDGVGSSESSGGSEDLNLEASGPVVNFPPPLPNAAAGGLQNTDGALSSQKNNFSETGVHSGTTPPA
PSLPKSQAPAMPKPEAEEQSSTEQDTEDSPDTEEVTTGKENVQNTVETGIPSRSSSAASKPPVQQTTPL
LTQSPAAPSPERSALAPSEKKSTAPSFSAGEGSRRATNVAQNSKEEKNEKLPSENETDSKAVEQPSGDD
LAEQDSPARTTASPIPASGSADARRNADADNSNAQALKYEGTNKNSETGYTNLASTTGDAATQTEKALA
DAKTNNTVTPGNSDSSTAVSHTTPPLLPLLVVVACAAAAAVVAA*
>Tc00.1047053506599.310|S043|AG-----CD|27
MAMMMTGRVLLVCALCVLWCGAGGVYARDTLNNAQGVCMVPGGFGKKTSYLASGCDKNAPTLSLRPALP
IPAIQAEDSEEDAGPDITPGGDDGGSGVNSAGQGAPGSSQAGSVPGAGFPPPAGASGGGGNPSGPVTPG
GDSSPDPRVGTETSVSLSSTSQSESEKKVLQGDEAKDQSHQLPNERAADTPVVETQSRGSDTTRGQDVG
DTSTLVFKQERSSEEPEKKDGDSDTLQTVNSPEDPNKELQEKEKASPELSNAPLPEPKTDHPKTNPEKE
KNGRQNTSASTDSPAKQEGNNEDPVSTSDAAEGISTGSQEQAAATSSNDSSSPLQKETSVEKTTVENSQ
PSDTAQTEKRQSVNKEKVGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053506599.330|S001|A---H-ECD|18
MAMMMTGRVLLVCALCVLWCGTSGAAADGDVVVSGGDDNSLKELFIPVARLQEREEKRAAGAAETAVAK
ATAEAAAKAKAAATETATAATAAAEAAAKAKTSAETAETAATKVTGVAEAEAKAAAASEAAKAAAKKAT

AAAEAATKAKAAAEKAAEEAATAAAAETVTATAAAAAEAATAAAATQEAATEAAEAAKAAAAAKGAAEE
AKEAAKKAAEEAKAKAKEAAEAEAEKAAAATQEAAKATAAAEAAAAAAAVAAAEAAKATEAAKAEAKKA
AAATQEAAKATAAAKEEAEKAAETAAEAAEAAEEAAAAESLRGTTVGEEAKTATHDQDNSVEHHSEEKQ
ELLQEHEPERQEKEQHEKQQHQQREHSAGNGEESPKEKTANGTNATAIKDDSDGSTAVSHTTSFLLLLL
VACAAAAAVVAA*
>Tc00.1047053506599.390|S008|A-----ECD|43
MMAMMMTGRVLLVCALCVLWCGAAVMESVVDDVVDGGVKEGPLGDSQSDSRDEKAAKPELFESVDEGLG
PADHSLDTRSGNNVNEQGNLVNEPQTENVGKEGVEGEGLGTQRNEVHEQQVEEEGEELTVKQKSQTKDK
VTVPQSLPPTPAGTITSPPPPTAPMQGSPTTPGQPQENSQKSTGQPPKLQVPPPPPAASAEGEADGGLV
GASDTSRVTGDKNKDPKESEGPVSGPPSGGASSSPISNNGDASRNNGGAPSTQDTTSLKNNEQSRPTAS
SGNAPLNRETPEKSTPDAQRHSSDTQENETGQTADGDAAHSAAGQSAMGTKGSSGVSTTASNAPTTPQP
QLPAPPVPPTATVTGAPAEKPTAERLPPPADSTPKESLAAKTTAQTNDTTKPSDSDGSTAVSRTTSPLL
LLLLVVACAAAAAVVAA*
>Tc00.1047053506599.420|S117|ANP-VFECD|7
MAMMMTGRVLLVCALCVVWCGLSGIAADGAGGVYVSEFEYLFLNWEELLKNECEAENSNETNLSLKELA
VNCCVYRAMHELCKDVYSKLFMETEFSNVEGVCKKYAAKPDEVKCPKQQTQPSPVTENSVKVSVPKALG
NEGDLGKTPEEAPLADPPAKPTKGPPSSPVGGQPANADDVPVPKSEESSVSTKSTNDSTEGDTDKITDT
DQEETSTSKAESATPKPTVASNNDDSNETDTDTGEEVPNNAPESDGAETQEEKQDENKEANPKETPVEA
TATKTTTATTGNSDGGTAVSHTTSPLLLLLFACAAAAAVVAA*
>Tc00.1047053506609.70|S080|A---YKECD|24
MMAMMMAGRVLLVCALCVLWCGAGCGVFADQDEELSTESPGGRSSGGDPLETQELEKPVLHGADSEIQS
PVVEQPQLNHPQDLRGAATESLGEGVEEVENEVEDDDDEKGRGKGKDGKDTRTTEKAEKQKSLTKDRGT
LQLTSQPERGITPAPPRESLQVEGEEGPPASGGDSRPRKPAATPSAPELLLTLTSIEGQGQGTPSETPP
GPTTTTTNGKPAGEASPTASTGSQTATETTSTTSPSNAKVALGAAEKPLGNRVPNQQKEETETPDSMKD
APTSHPAETKATSISTTGSGGAQKNEDKVDNGDQRPNSKEPQDGLEDGNTDDAPTASEVEPQTPETDTT
QKNATSKSGDSDGSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053506611.10|S087|AG--YKEC-|7
MAVIMTGRVLLVCALCVLWCGSSRIAASGVYASGVEDGARGGCMVSGVLGTNWSYTPSGCNKTVPMTAL
RSVFSVVAAEASTEQEDSETDTVLDSPSGDGPDSGLGSPVGSGAVDGSKVIDGELGNSAVVPPDTRVAV
ASPPPSAPETDASRLPEVTSSTKKHNSSEKLVHLKTKTPAGTPPLSNQASKESLPTVKPESPTTSDSTV
TVKGTDQISEEKLAVLQGPSTVNAGEDGKKAVTEIKPNTTTNTPDAAPTLSSEGDVTEQHGKDTDSSNF
MNNANTGSSAETTASSFSKSGGIDAPKNESEDEGDAQRPNSKEPQEKPEDSNTNDALTENETAPQTEKP
FGSAQTNDTSKSGDNDGSTAVSHAISPLLLLLLVVACAAVAAVVVA*
>Tc00.1047053506611.40|S066|A---VFECD|8
MAMMMAGRVLLVCALCVLWCGAAAVMCDGGAEMQGVEGSGGSQHVSGDPDGRGGQGETEVPFPPESDTV
IKSLGVGDGRDPKQLNGVVVTPPTNPDRKEEEREKEKSKEEKVVAEQTENTVIPKEDEKISQLKSMSED
EGETAPLAAEETPPASTGVTSTAQNGNSPEDLTAIPGKERVLPEDHSDQPQGGKNPADGLAAKMSREKG
EAPEAPPSPLAKNEKHEVDLKATTNNEKDSLENGVSVKKTEVLLEDKEVTSNLRKEGLASTTGNQESDP
SNSHAESTPPSNSGASNASNDDADTDTNEEILNNDSAAGGAATEGAHQGENKEDNTKETTPLRSAAMIN
ETAPTGDSDGSTAVSHTTSPLLLLLLVVVACAAAAAVVAA*
>Tc00.1047053506613.50|S055|A--T---CD|5
MAMLTGRVLLVCALCVLWCGAGGVYAEDDAGVTSPGASASDGKSFQEPPPIVHGGSHNSVLTASDVNEQ
TDETDKEVLLTKEVAGSDEVPQTSEEIPPPSPSPKKSKGGGGPPQEDDLNLEKVDENVMQPEKQRRVEE
GLETLGDGEAGVTKQNEGIGVQSQDHETPVQEEDTINGEGHQQTHGKDQQTNVEDIPPRKSAGDYSSGE
HKGNDGSNEKEEKEGEEGVEGRERHRAQEREEAAHVSGAPKVNSTDIQQEVQRTHAGETPTGIKQKAGE
EKDDEAEEEREEQKKQNQENPPGKVQETITGANATNQINTMPGDSDGSTAVSHATSPLFLHLVVVACAA
AAAVVAA*
>Tc00.1047053506615.100|S008|A-----ECD|43
MAMMMTGRVLLVCALCVLWCGAGGGYAWDFGSDGESLNEYYYGAYGVYCNASLNATFCEEKRKAIKLKE
AALQKNTARSGEGSGQPNAGGSSGRQAHGSEESGSGQSEGTAGEGTPELNKPGEGGTETPTPLSSPPPT
ATVTAAQTSATRTPDESDGSPAASHTTSPLLLFLIVCAAAAAVVAA*
>Tc00.1047053506667.10|S104|ANP-VF-CD|10
MAMMMTGRVLLVCALCVLWCCAAVVVSSAPDATRAQSVWPEYLFLNWHELLRNECEVENPYEKNVGLKK
LAVNCCVHDAMKKLCSDFYGTTVMENKDPKVDGICKNYGGEAADADKCSELEAKLSSAAAASVKVSDRE
APEDKEVLGKKSEEKPKAPPEEAPTPLAGRPLSDLPEKPTKVSPSPPLKGQPTNAEEVPVPNSEEGSVN
TEPTKDSEEGDTDTDTDTEQDEPSNSQAESTTPTPTVASDNDDNETDKSTGEDTPNNAPESDVARTEEN
QDKNKDNKPKETPVEVAGIKTATVTSGDADGSTAVSHITSPLFLLLVVACAAAAAVVAA*
>Tc00.1047053506667.40|S002|A---S-ECD|19
MMTGRVLLVCALCVLWCGAGSRCDEGEAAGRVSGAELLPGSKPLVTPRVGSQGLQNGVTVVKEEVSPIS
SLPQDGNADGDEGGEGDDGGDDDDKETEAEEESIEGRGGKGGTVAIGSDSREENLIGSENEKNQSIASA
GGISPSGSQESNANPTQPEVEEKKEPDKNPPVENTLTPGNGENTLPRGGNLPSPPEDGVASREQDGEDT
TSEGKKNVSPPATAATPHRHRDKGSEGTAKDTNATTVNANTTDTTSTQNSDSSTAVSHTTSPLLLLLLV
VACAAAAVVVAA*
>Tc00.1047053506667.80|S002|A---S-ECD|19

MAMMMTGRVLLVCALCVLWCSAGSRCDEGEAAGRVSGAELLPGSKPLVTPRVGSQGLQNGVTVVKEEVS
PISSLPQDGNAGGDEGGEGDDGGDDEDKETEAEEESIEGRGGKGGTVAIGSDSREENLIGSENEKNQSI
ASAGGILPSGSQESNANPTQPEVEEKKEPDKNPPVENTLTPGNGENTLLEGIAGGIPPSPPEDGVDSRE
KDGEDTTSEGKKNVSPPATAATPHGHREKGSEGTGEDTKATTVTANTTDTTSTQNSDGSTAVSHTTSPL
LLLLVVACAAAAAVVAA*
>Tc00.1047053506667.120|S089|AG---KECD|6
MMAMMMTGRVLLVCALCVLWCGAGRVYARDVNNNLLSGCMASGILGKKKSFLSSGCDKNAPTVSLHLAL
PITAVEASTGESVSDSTDIYPDSLSVPPSPPPVTGLPEALKAPKAPQDPPESDVGQTGVGNPSSLVPND
DSSGGGGSEENGNSNKSGVSASEFSTVVGASRSSIPPEVGGSENKSGAPSDLKLESPETNEPPERILVE
TNKDTQKVPKLEENPESSHKKEKANIRGTSEEAGKNEAGRSGVEAHGPSSVLSADSQLQQQGTTVTVTQ
PPPPSPEQQTSAVSPSPGVDTPAARSREAGDPEEGKGIPPTRTASHNSTDEKHKAPPLQSEKESAAPKP
PSADGVLEQNSEDTTTKEAIKMDADTDGPAASSESSISTSDSGVFQDKTEEEDENEQRPEAKGPHNDPH
AVNTNDAPTASEVEPQTPETDTTQTNATSTSGDIDGSTAVSHTTSPLFLLLIVVACAAAAAVVAA*
>Tc00.1047053506671.10|S020|A---HR-CD|2
MAMMMTGRVLLVCALCVLWCGAGGGAAEEPGGVAEPDVVPLGSTQQQITGGSQREDKGAKEEQGQGRDT
NNGDEQPIKKEEADEQQSQEQIQTQQDAQALKGNATPQPAGKSSEEGEIDDDSDVQNEIKVLDDGKRNE
ERVQSQEEVARDEDASTVNLNDSQQETSGGIRTGDLRGKSRQEGEKEGDDGGKKEREKHQEENKRKPQE
QNEMLQQKQQQKQQQDQGREHSEYNQKESTKDKNGVGTNQTAITHNSDSSTAATAALRSDAGKEDTPTT
NHPNRPSTEGATPPEKTSDGEAASANKYDTVPQSAGSTTAPTTNAKVGDTAKPVDNDGSSAFSHTTSPL
LLLLFVVACAAAAAVVAA*
>Tc00.1047053506671.90|S090|AG--YK-CD|3
MMAMMMTGRVLLVCALCVLWCGAGGVYARDTPNNAQGGCMASGGLGAKTSYLVRGCNKTVLTRPLRSAF
FINAIQAEAKDVKDISEERDNLKLDSIPQPPALPPAPETPGAPPPPPDASDSDGIGRSELGADSQTGGG
GGGGGGSSGISNGGEDSTLKVPVPDDKSSSPIPSAGDGLKNTGDSSVTQKNNSSGTDEPSKKTLNVPAL
PTVQTPEALDTDQNKNTPNTQGEISVEARGKGASGGDAGENDVNSKDSSSVSTANSKPTGKTTPSVPST
GETPTITATPKDSKNPTGKNDNTAASGTETDSEATKTSSKDDAAEQHSQERDKADLVKSANTGHPAYTA
ASSIPTYGNGDAQGTVNENGDDPERHDPKRTHDELEADNTNVGPTASEAAPEAVNSTEKKDTAPTGDSD
GSTAVSHTTSPLLLLLVVSCAAAAAVVAA*
>Tc00.1047053506703.20|S099|AML-VFECD|25
MAMMMTGRVLLVCALCVLWCGAVFGHAMDDYCSEGGGNGLRHTSNGGDDGVSLKADCGLLATRMALIKA
VEAEAGQDELSGGPGLSQDTKEKLDDTSVGTNTVGSAAAGLGGSIVAGQTAALPPTPGGSDTGGQEEKP
EGLDANGGKEADHKEDRNDSTATGPQHQSVDQSSSFSSSSGSPGTQNGEEHNLEDNSKSDESSDDSPED
DESDPLSQSDSREEKAEEEPEKNELNTENTSHEAPALTTAPAEEAEIQTAIPTTPLHGHSGAEDSGEVQ
QLQQPQDGIESNSNSQTKSAASITANQHNEPSGDHAESRPPPSTANGDAANNEADKSTEEGIPNNDPAA
DGAGTAEEKQNENEASNPKETPVEATATKNTTATTGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053506703.50|S073|A-L-YKECD|2
MTMMMTGRVLLVCALCVLWCWCGGFADEAGASAGGGNGLGYTSNGVNDGSSKADCGLFFTSMGLLKAVE
AGDDNLPLTDKVSSEIKEVSDLVVSQKGVDGGPLAGAKEGNGAAGAVTSPPGPGVSEANEGERHLEVLG
PKGDDELTRVSASGEASNSQNQTAHQPVLLSDSSDTRPGEVLPLSNSDSALIYKDPLKKGDVDSRDATV
GDTQKVEELKEENKEEEELKEFKDRAESETRKEGKKEEGTPTKISTAQPTALERAQRPVVKLNGGKSPD
AVPEGDASQTESEDAQALTHQQHESSSSQTETKSEAPEPPATDGVPPQQVQDTVTKDSMENATATNQAE
TTVSPNYTSGSGEVRSTADGNDPQRPNPNEPHDVLEGVDTNDAPTLSEAAPQTEETAAAARINGTATPG
DSDGSTAVSHATSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053506703.110|S061|A--TIFECD|52
MAMMMTGRVLLVCALCVLWCGAGGGGCSEPTPDLLGTQSEDRKTPKSEKETIGGAGGNGLTGKPAASQE
TSSPVQIVMGAGAGAATNSSPALKPGKQQASAILTPKTENNNEKTKEKGTREEEDEIQEEEEEDDEEED
EHKEIDKNDENKEEGETKEEKEADDKAEKHEEKKKEDAGTGTTEGMSAGGQEQPISPSGAEGASNNTNL
KSTKTAGDDDPAADGAGTREEKQNENKESNPKETSVEATATKTTTATTGDSDSSTAVPHTTSPLLLLLV
VVACAAAAAVVAA*
>Tc00.1047053506703.140|S099|AML-VFECD|25
MAMMMTGRVLLVCALCVLWCGAVFAHAMDDYCSEGGGNGLRHTCNGGDDGVSLRADCGLLATRMALIKA
VEAEAGQDELSGGPGLSQDTKEKLDDTSVGTNTVGSAAAGLGGSIVAGQTAALPPTPGGSDTGGQVVKP
EGLDANGGKEADHKEDRNDSTATGPQHQSVDQSSSSSSSSGSPGTQNGEEHNLENTSKSDESSDDSPKD
DESDRLSQSDSREEKAEELVKKKNELNTENTSHEAPTLTTAPAEEAEIQAAIPTTPLHSHSGAEDSGEV
QQLQQPQDGIESNKHSQTKSAASITANQHNEPPADHAESRPPSPTANGDAANNESEKSTEEGIPNNDPA
ADGAGTAEEKQNENKEANPKETSVEATATKTTTATPGDSDGSTAVSHTTSPLALVFVCAAAAAVVAA*
>Tc00.1047053506741.60|S099|AML-VFECD|25
MAMMMAGRVLLVCALCVLWCGAAFGHAMDDYCSEGGGNGLRHTSNGGDDGVSLKADCGLLATRMALIKA
VEAAEAGQGLSGDTKPQGNLKEPLPNNTEGSPAPGAGGSGVAVQPPPAVTLEHEGSDTGGQQVTLPNVV
DTNGGKKGDDKNGSELEPEEIGAGQSSSSSSGGAGTLGGKGLPSKQTSKSNEPSNGTPTQEEDAGNHRI
TPHSRDAEAEEEHEVKKENVSHEAPTETRGSPANDAGIQTATPSPPPATMNGPSSTEDLPPVQAPQRVQ
DDHAESRPPSHTANGDAANNDSDKSTEERMPSNDPAADGAGTAEGKQNENKEANPKETPVEATATKNTT
ATTGDSDGSTAVSHTTSPLLLLPVIACAAAAAVVAA*
>Tc00.1047053506741.90|S050|A--TH-EC-|2

MAMMMAGRVLLVCALCVLWCGAGGCAENDGGVAGSLEERGIAKDDEISKGLSSSGPILQEGQDQRAAAS
GGGGEGGGGSTDSLGVKDASFSEKGKKIPQKQEVKVGSHPNQPTGDEYGSNDLTEVGADTRNQTPPKST
TQSPTGLPPPPPPPLPEEAAEEAEEDPNNSVEHHPGEDQQLLQEEVTEHGQNNQNQLIQKQHDSKQLQM
QPETDEEKKRLEEQRQHQEELRDQQQKQKEQHEENIKEEKGQEQQQEQQHENQQQKDEIKDQQDQQHEH
SAEKEEESIKDKNAVGTNSTANTEDSDGSTAVSHTTSPLLFLLLVLVAAAAAVVAA*
>Tc00.1047053506741.120|S099|AML-VFECD|25
MAMMMAGRVLLACALCVLWCGAIFGHAMDDYCSEGGGNGLRHTSNGGDDGVSLKADCGLLATRMALIKA
VEAGDDGIDENGNAVLENKDKSQHGSVLAGTGGNETPGQKGVKGAAGAGLPPSPSGPGGSDTEEQRQPE
QLDTKGKEAGGKRDEKGGKATESQQQRADQSSSSGSDGPQGGKEPNLKEKSESTESSVDTPTQEDEVEA
EETSVSEEETGGDEENNNNVALTVTSESQAKLKGTQTATPPTLPTTQVNERSRTEDLGHVQLPKGVQSD
IESNYNSQTEGAAPITANQHNEPSADHAGSRPLSPTANGDAANNDSDKSTEEGIPNSDPAADGAGTAEE
KQNENKESNPKETPVTATAMKTTTATTGDSDSSTAVSQTTSPLLPLLVVACAAAAAVVAA*
>Tc00.1047053506741.140|S099|AML-VFECD|25
MMIGRVLLVCALCVLWCGAVFGHAMDDYCSEGGGNGLRHTSNGGDDGVSLKADCGLLSARMALIKAVEA
AEAGQDEQELSGDTKPQGSLKKPLPNNTEGSPAPGAGGSDVAVQPPAAVTLEHEGSDTGGQQVTLPNVV
DTNGGKKGDDKNGSELEPEEIGAGQSSSSSSGGAGTLGGKGLPSKQTSKSNEPSNGTPTQEEDAGNHRI
TPHSRDAEAEEEHEVKKENLSHEAPTETRGSPANDAGIQTATPSPPPATMNEPSSTEDLPPVQALQRVQ
DDHAESRPPSHTANGDAANNEADNSTEEGIPNNDPAADGAGTAEGKQNENKEANPKETPVEATATKNTT
ATTGDSDGGTAVSHTTSPLLLLPVIACAAAAAVVVA*
>Tc00.1047053506751.100|S047|A--TS-ECD|8
MAMMMAGRVLLVCALCVLLCGAGGRCDEEERAALGSDGGPPPGSAEPGTPRKETQELKDGAPGVIETAS
PPSSKPTGEDKDDDDEDDDDDDDDEETEAEGESIEGQSNKGGTALPDPGSGERNLSDSGQETGRANVPA
GSIPPSGSQLSNANSTQTEVEEKKDSGKNPPAVENPLTTVNGENTLPGDIAGVTPPPPPEDGVDSRKQD
GKDTTSVGEKNIPPPETTATPQSHRDEGSEGTGEDTKATTVTANTTDTTNKQNSDGSTAVSHTTSPLLP
LLVACAAAAAVVAA*
>Tc00.1047053506757.50|S103|ANP--F-CD|11
MAMMMTGRVLLVCALCVLWCGVGGGFADKVVEAPAGVVASKRTDEENLILNWYFLIREECANESTTGGK
LNVTAERICIHKVMKGVCDAFYDKTPGVTHDRDVEFICTYYATIPEEPVEPPTPQGPPSDSAVSSTTSN
EGTPKNAPESDDAGRGEGKEDEKEHGNTKQTPVETAAVENDTKTTDSDGSTAVSHATSPLLLLLLVVCA
AAAAVVAA*
>Tc00.1047053506757.150|S002|A---S-ECD|19
MAMMMTGRVLLVCALCVLWCSAGGVCTDEEETAGRGSGADLLLGSKGVETSPQDTQGSQNRAPGGEEKL
TPVVIEEADEDDDNDDDDEDEHDGETKAEKENITERQSVQEGTVAIGSDSREKNLSGSERKTVQPIVSP
EGISPSDNQESKTNPTQPEDEGNKDTDENTPAVGNALTTVNGEHTLPEGIAGGNSPPAPEEGVDSRKKD
GEDATSEGEKNVPLPATAATPQSHRNKGSEGTGKDTKATTVTANTTDTTNTQNSDGSTAVSHNTSPLLL
LLVVACAAAAAVVAA*
>Tc00.1047053506763.30|S061|A--TIFECD|52
MMMVTGRLLLLCALCVLWCGVCGGGCSEAALEAQLIESEDNKRKDENTTTDDVGEGGPTGQPAVTQPAA
GSVPVSGIEAESALQPAAKASGTANATTEKEDKADNEELKEEEGEEEEEEEEEEVDEDDEEKKEVTEEE
KKQEEKDDTSTTKRISAVGQEEPILSSRVEEASNKTKPQSTQTTGDKDPAADGAVTQEEKQNENKEVNP
KETPVESTVTKTTTATTGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053506763.50|S082|A---YKEC-|17
MAMMMTGRVLLVCALCVLWCGAGGRCDEEGPALPAGGGVPPPGSKELGTLPQDTQELKVGAKDIKVKVP
PAPSPSLEEDEDEDSNPNEEEETTEDTEEEKEEKIKAPTKTHEGKKNEGASLPPSPPLPPSGGPTAERE
NPKNQKKITNEATPSGPKMESEAPEPPSGDATQGQHSHDTDTEDSTKNAATGSPAEPTTTSTSASGSGD
HFQNKADKDDAQSSEGQHDSLETGNTNVVPTLSETAPQTAKTTTAAQTNDTATPADSDSSTAASHTTSP
LLLLLFVACAAAAVVAA*
>Tc00.1047053506763.130|S123|ANQ-V--CD|3
MAMMMTGRVLLVCALCVLWCGLSGIAAYDADGADGSAVEYSLSRWRAQLRRGCAVEVSRRTGGGANASA
VEECVGRGMDGVRAVVDGRSRWRRQQFAVAAAAVDGDVDSGEVDINSVSSPEDQSGTGAGSREESQAKP
PVVSEPGQADTTPGGENPPKPAESLETAKGKSGGTSKEKDKEERPTVETKGPNSTDDNKQVDNAAIGNS
NGGREEKNGVTLQVQDEVVKPKEEKQEPQKELEEKEKQKAQGNKQDEPEDPGEDAEDTEDSADGTDHKE
GEGQKEGDAGSSKKGKELNLGGDTDGTSPDVPAVLQPAPPVEVTDPQSIEKTNDDETGGKRDAGRTQTQ
EAAGPSQAENLTAELSTEENAAETETGTPGKKTQPEDAGKEQTTVGAKSNLETPAAEREAQNREEVLKD
EEGSEKATTNENFDGRQTAVKDNTHNEAEKTSQKNENEVDKAEETTAEVKEKEDTTERKTVAAKGPNLN
GTAATPADSDGSTAVSHTTSPLLLLLLVAFAAAAAVVAA*
>Tc00.1047053506763.150|S079|A--TYKECD|5
MAMMMTGRVLLVCALCVLWCGAGGRCDEGEAAVHGVPPDVSASGTEGGLGGTRNAAPAPDSQIQSSGEE
QQHKSREGRPALPEGSSEEEEEEEETVEDENLEEVTERGEEGRHEDGQDANERDGSQTSGVLTKQKETP
SPSTPAAPAEEGNQNASPQAPSVDSHGGGGTDRIEGSILKAPSSGVALQHAGDASTNQKNKSLETGKHS
ENTITGGPVPSQVKAPKESIKDAENHSVTGEDTASNQVVGRGTTEYEAQQRALATQDRSSVSFPDSEKK
WQTTPQETPKTQVPPSATEPSSREGQPPTATTDSQTPNAQEHKRLLLPKKTEYNAPEHHSEDILAEQQG
QATATENLTENAPATNQAEKTASPNSTSGGGEARSTADENTANAQRPNPNESHEDLEGSDTHPAPTASE
AAPQTAIKPTANTTDTATPAENDSSTAFSHTTSPLLLLLLVVACAAAAAVVAA*

>Tc00.1047053506763.260|S001|A---H-ECD|18
MAMMMTGRVLLVCALCVLWCSAADGDVVVSGGEDNNLKELFIPVARLQERQEQGAAGATADAKAAAEAA
AKAAAAAEVATEAAERAKIAIEATKTATAKAEETAKAAAEAAATAAEAKAAVEAATKAVETEAKAKAAA
EAAESAATKATTATEAAERAKIATEEAKTATATASAGKAAEEAAKAAAEAAATAAEAKTSAERAKTATA
NAATAAAKAKTETEKAAAAAKAAEEAAKDEATAKAAAEEAAKAAAAAKDEAKVATEAAKTAATAKAAEA
EKAAATATAAAEAETAKAKAAAEEAAKAAAAAKAAAEAAAKAAAAAKAAAAANDEAAKAAAAAAEKAAT
ATATASAETAKAKAAAEKAKATATAETKATAGKTAEAAAEALRGTTVGEKEVQTAIHDQDNSVEHHSEE
KQELPKEEEHELQEKEQHEKQQHQQREHSAGNGEESPKEKTANGTNATAIKDDSDGSTVVSHTTSPLLL
LLVVACAAAAAVVAA*
>Tc00.1047053506763.280|S097|AGWTH-ECD|44
MAMMMAGRVLLVCALCVLWCGAGGVYARDGENNALGGCMASEVLGACFFHMSSGCNKTAITVPLRSTLP
ITAVEASAEGETPVAGLNDSGSSEDSIAVVPVTVGVAGAPAGAAASPSGPSGGSDGKNEPSGPLSLDVD
SSAGSSNGEAGSRGSTSSNAVGEPPRENPSPDVAAAAHNPPPPGGVAGTTPGNKVEKEEEKEKEKEKEL
DEEHKRNHGQENQSRLANQSEGEIGREGERLHKKTKVPKEEKEQIQVVEHSIENQGTLHEPGKEPQEIK
RENEQSKHQNEELKGGQEKENPLQAIQQNSDAEEEMNKNRQQGQRPQEVTAPLASSSGSEATRKSQSPV
PPEALHKKELTDGLREQLEEETPLAATQSKSHGTTDPQSSPASAIAGEAAVTHDADEENATGRNDDEPI
ETVFADDHQQHEHPENIQKEPAKDKNAVITNGTATPGGGDGSTAFSHTTSPLLLLLFFACAAAAAVVAA
*
>Tc00.1047053506763.330|S004|A---V-ECD|18
MAMMMTGRVLLVCALCVLWCGAGGVCTDEVVPVDDAPVISASGGSGAADKDTGRTVPGGAENLSAQQSQ
LQKVGDSSPGISSLEAASGIESTKQQTQSDHKYKDPVTPSQSSGERRQDEQHEGPPGKPGASLGQEERK
HALDGVPERNDPPPASSNNNTVSSNSEERTEDTPSSTEIIVAVPSEEGQERENVTPSLEQPRETSTAAP
AITTQTSSTTTPTDVSESNTVKMSDASPKSTRTAQTNHTATPGDSDSCTAVSHTTSPLLLLLVACAAAA
VVVAA*
>Tc00.1047053506765.50|S103|ANP--F-CD|11
MAMMMTGRVLLVCALCVLWCGVGGGFANEVVEAPAGVVASKRTDEENLILNWYFLIREECANESTTGGK
LNVTAERICIHKVMKGVCDAFYDKKSGVTHDRDVEFICTYYATIPEEPVEPPTPQGPPPHSAVSSTTSN
EGTPKNAPESDDAGRGEGKEDEKEHGNTKEKAVETAAVENDTKTTDSDGSTAASHTTSPLLLLLLVACA
AAAAVVAA*
>Tc00.1047053506765.74|S027|A-P-V--C-|1
MMMTGRALLVCALCVLWCGAAVEAEGDGSGVGSGDADGNMVLIWYIDANETCKKKNTQGEKLDKSAFKS
CVNAAMKEICYDYYNETPSESRDFESDEICNNYIGDSEETIDTSTPLTEPSHDAEKPVATPTPETSKVE
AAEMGSPPGVPAGDSPANPTEGPQSTLAANDTANSEAEKDGKEVMPKNAPESNASRKEEGEKKHSNTKE
KPLEAEAKKNITMTADSDGSTAVSHTTSPLLLLVVAYAATAAVVAA*
>Tc00.1047053506767.40|S104|ANP-VF-CD|10
MAMMTGRVLLVCALCVLWCSSAVQAADGLISDGSLEGENMVLTWYPVNSKTCEERSTNGGKLDELAFKS
CMHELMNEVCEAYYSMKSSESHVTEADSICGKYTGDPSEEDVQTPTPQEQPSPEVETPVASQTPETSKV
EAAEMGSPPGVPAGDSPANPTEGPQSTSDATDTANNEAEKSSTEVMPKNAPESNATRKEEEKRNEKNHS
NTKETPVDAEAKKNNTKTTDSDSSTAVSHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053506767.70|S072|A---VFEC-|6
MAMMMTGRVLLVCALCVLWCGDEGRCDEEVVPVGKGNASTDNDDQKRTAEVPAPRKSIALPVNSGQESA
VSTLRNEQTPQISESAIVLPKQITSDQKQEDEDAKDGKDGKEERDAREDPRPPPPPGETPTTINGNSAG
TLNEKTEKELPSADDGSNQEHVLKSPAAESAPAPASQVKNENPGSANLDTVQDVQDVQNAQRGRESDGE
SRKEDNALTTNKQQDGKSNSHAESTPTSGSSAKRVAASNGPDKATEEEISNKNTARVDAVPEAAEDDGN
KDDNKKELPIKTTSIANDTTLTGNSDGSTAVFHTTSPLLLLLVACAAAVVAA*
>Tc00.1047053506767.110|S002|A---S-ECD|19
MAMMMTGRVLLVCALCVLWSGAGGRCDVGEAAGLRSAELPPAPAPLEKSPEGPKGLQGGVPGVKENVTP
ASSIPTEEEHDYEEDDSDDDEEVEDTENGETEEEEEKRKEGQSNKGGTVAPDPNSGEKNLIGSEKETGQ
SISSAGSISPSGSRESNANLTQPEVEEKKETEKNTPAVENPPTTVNGENTLLGGIAGGNLPSPSEEGVD
SREKDGKDTTSEGEKNVPPPATAATPQGHRDKGSEGTEEDTKATTVTANTTDTTNTQNSDSSTAASHTT
SPLLLLLVVACAAAAVVVAA*
>Tc00.1047053506767.140|S080|A---YKECD|24
MAMVMTGRVLLVFALCVLWCSAGGGCDGEETAARGSGDGPPPESQELGTPRQETQDLKVGSPDVNGKVP
PESSPHIEEAGGEDSDDDENGEEKDKKGENEKNKVQLQTHEGKNNEGAPQSSPAPPPPPIPSGGPTAEK
ESSQKVTKAKKENTPSGSKMESEAPEPPSGDATQGQHRHDTDTEDSTKNAATGSPAEPTTSSTSTSGSG
DHVQNKAEENDAQSSEGQHDGLETGNTNVVPTLSEAAPQTAKTTTATQTNHTTNTENSDGSTAVSHTTS
PLLLLLVVACAAAAAVVAA*
>Tc00.1047053506767.230|S004|A---V-ECD|18
MAMMMSGRVLLVCALCVLWCGAGGVCTDEVVPVDEPPVISASGGSGAADKDTGRTVPGGAENLSAQQSK
LQKVGDSSPGISSLEAASEIESTKEQTQSDHEHKDPVTPSQSSGEQRQDEQHEGPPGKPGASLGQEERK
HALDGVPERNDPPPVSSNNNTVSSNSEERTEDTPRSTEIIVAAPSDEGQEDENATPSLEQPRETSTAAP
AITTQTSSTTPTDVSESNTVKMSDASQQTAKTTTAAQTNHTATPGDNDSSTAASHTASPLLLLLLVACA
AAAAVVAA*
>Tc00.1047053506767.240|S103|ANP--F-CD|11

MAMMMTGRVLLVCALCVLWCGVGGGFANEVVEAPAGVVASKRTDEENLILNWYFLIREECANESTTGGK
LNVTAERICIHKVMKGVCDAFYDKKSGVTHDRDVEFICTYYATIPEEPVEPPTPQGPPPHSAVSSTTSN
EGTPKNAPESDDAGRGEGKEDEKEHGNTKEKAVETAAVENDTKTTDSDGSTAASHTTSPLLLLLLVACA
AAAAVVAA*
>Tc00.1047053506767.340|S074|AML-YKECD|9
MAMMVTGRVLLMCALCVLWCLTVFGDARDNRCVEGDGNVLTRTHNGGNNGLRLKADCGLISTRMGLIKA
VAAGEREEELESVDAPLDSVGGTSPGSLLAVTEGNAAPGAGGVEGAAGAATPSLPVSGPGVSGTGDEGG
QLPVAGQEGNEKNNLDPGSKEPKESQDQNTDQLSSPSGSTSTRSDEKLSSTGTDDLTPLSKDTETELGA
DRQDNRESNEAIEEEDGEKDKGKKQEKNILQPETQEVQNNGGGTPPPSLPALPLPLPPSGVPAPSSTAG
EGSPPTEPKNSQNSKKIKNEATPSGPTMESKATQPPSGDATQGQHSHDTDTEDSTKNATTGSPAEPTSS
STSTSGSGDHFQNKADKNDAQSSEGQHDSLETGNTNVVPTLSETAPQTAKTTNTAQTNDTATPGDSDGS
TAVSHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053506767.400|S004|A---V-ECD|18
MAMMMTGRVLLVCALCVLWCGAGGRSDGGKTPGSESGPSIRGVDEVSESANGQTASGEAGNPTVQQTQL
NNVGGPSLGAPPLQADLPPESTVQQTQIDTEPTDSLSHSQSLGEERQGGSSDGSSGKPAASPSREDREN
ESIGDQPRNDPPSSSINNDVVSSNSEERTEDTPRRAEIIDAAPSEEGQERENVTPSLEQPRETSTAAPA
VTIQTSSMTTSDDGALDTVKMSDASLQSTGTANTNVTTTPAENDSSTAVSHTTSPLLLLIVVVACAAAA
AVVAA*
>Tc00.1047053506769.30|S079|A--TYKECD|5
MAMMMSGRVLLVCALCVLWCGAGGSCDEGEAAVHGVPPDVPASGAEDGLGGTRNAAPAPDSQIQSSGEE
QQHKSREGRPALPEGSSEEEEEEEETVEDENLDEVTERGEERRHEDGQNANERDGSQTSGVFTKRKETP
SPSTPAAPAEEGNQNASPQAPSVDSHGGGGTDRIEGSILKAPSSGVALQHAGDASTNQKNKSLETGKHA
ENTITGGPVPSQVKAPKESINDAENHSVTGEDTASNQVVGRGTTEYEAQQRALATQDRSGVSFPDSETK
WQTTPQETPKTQVPPSATEPSSREGQPPTATTDSQTPNAQEHKKLLLPKKTEYNAPEHPSEDILAEQQG
QATATENLTENAPATNQAETTASPNSTSGGGEARSTADENTANAQRPNPKEPHEDLEGSDTHPAPTASE
AAPQTAIKPTANTTDTATPAENDSSTAFSHTTSPLLLLLFLVVACAAAAAVAA*
>Tc00.1047053506769.80|S037|A---S--CD|2
MAMMMTGRVLLVCALCVLWCGAGGRCDEDKAGSGIDAELPPAPVPLETSQQDPQDLKNGVPGVKGTASL
ASFPPKDGDADGETEDQEESKEGQSSEKGNVALGSDSRERNLIGSGQETGQSIAPAGDISPSGSKESKA
NPTQTEIEGNKSADKNSPSAEKALTTVNGENTLPGEIAEGNLPSPPEEDVASREQDGEDTTSEGEKNVP
PPETAATPQSHRDKGSEGTGEDAKATTVTANTTDTKTKIADSDGSTAVSNTTSPLLLLLVVACAAAAAV
VAA*
>Tc00.1047053506769.120|S068|A---IFECD|10
MMMVTGRLLLLCALCVLWCGAGGGGCSEAAPEAPGTGVSGDGNNSEGKHNTIDGVGAVGPTGQQAASQP
AAPSPVPVPGTEEESALQPAAEASGTAEETTKKGEADNELKEEDDDEGEDEVEEEVEVEVDDGKEEEGE
EEEKVGTSTTKRISEGGQEEPILSSRVEEASNKTKPQSTQTTGDKDPAADGAVTQEEKQNENKEANPKE
TPVESTVMKTTTATTGESDGSTAVSHNTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053506781.19|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLF
ITAVEASTGTGDAVATTNNSNSRENSNAASSPDGSVSAVGPGPGASAPPSVGGPGASGSGSAVGGPAGA
SPGGGSSGAVPGASGEGDSDGGGGVSPTGGQGTGGTSGAPPAAPPVPFSTAGPAAPGVDSSAGGSDGTA
GSSGTNSSNTTGDSSTGNQSSAAAANDTSPAERPTGTTSGTGHTRQEEEEEEDHVMRQQRDEAQVQQNQ
QHEHPAESGEESAKDKNALRTNATANTGDSDGSTAVSHATSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053506781.39|S097|AGWTH-ECD|44
MAMMMAGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASTGESDAVATKNNSHSRENSNTGGTGSAAGGPGGSDASAPPSGPAGVGASGSGSAGGAGAAGA
PAAAGGGSSESSTGGHGTGDVSSGSYASPSALPPSGPPAPAVPPAPDATVVDTSAGSSGGTAGSSGSNS
YNTTGDSSTGDQSSAAEANDSSPPEGTAGTTSGTGHKGQEKEEEEENEQQQSDEAQVQQHQQHEHPAEN
GEESAKDKNALRTNATANTGDSDGSTAVSHATSPLLPLLLLVACAAAAAVVAA*
>Tc00.1047053506783.39|S097|AGWTH-ECD|44
MAMTMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGMLGENGSHMPDGCNKTAITVRLRSVLP
IAAVEAANEEVSDTSQHANNSGSDTNTGSGGEGGGSAAGAGGPSASPAPPPTGGTEGSVGAGDSSVSGG
SSGNSTGGHVTGGVSSDSSESPSGLPADSPGVDPSASSSGGTAGSPGTNPSNTTGDSSTGDQTSAASAA
AHNSSLPEGPAGTTSGTGQKEEEEEEEENEQQQSDETQVQQHQQHEHPAESGEESAKDKNALLTNATA
NTGDSDGSTAVSHATSPLLPLLLGVACAAAAAVVAA*
>Tc00.1047053506785.14|S097|AGWTH-ECD|44
MAMTMAGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASAGEGSPDGGAGAAGASGDRGATGDTSGSGGPSASPAPPAAAAPGGSPGGGAPGGSGTSTGGH
GTGGIPPAGSPTVPAAPGVDSSAGSSGGTAGSSGSNPSNTTGDSSTEDQSYAAAEANDTSLPEGQVGTT
SGTGHTRQEEEEEEEEENEKQQQSDEAQVQQHQQHEHPAENGEESAKDKNALRTNATANTGDSDSSTAV
SHTTSPLLPLLLVACAAAAAVVAA*
>Tc00.1047053506789.50|S097|AGWTH-ECD|44
MAMTMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVRLRSVLP
ITAVEAANEEVSNTSQHANNSGSDTNTGSGGGEGGSSAAGAGGPSASPAPPPTGGTEGSVGAGDSSVSG

GSSGNSTGGHVTGGVSSDSSESPSDPPAAPGVDSSARSSGGTAGSSGNNPSNTTGDSQTEDQSPAAAAP
TNDSSLPEGPVGTTSGTGHTRKEEDEEENEMQQQSDETQVQQHQQHEHPAESGEESAKDKNALRTNATA
NTGDSDGSTAFSHTASPLLPLLLVVACAAAAAVVAA*
>Tc00.1047053506799.50|S043|AG-----CD|27
MMAMMLTGRVLLVCALCVLWCGAGGVYARDLDNKALGGCVASGVLGMNTSYVPNGCNKYMPMPPLRSAL
PIPAIQAEVEQVSVTTQDGTNSTSDTAPESGSGVGSGGSPGPTAPAAGPNVVPGAGGPAVSGAAGPAPP
APGGVPGPTGPAGVTGGPGGNTGSSGATDVLGAAVSSDGPSSFPAANSNAVSLGLPAGSEKSNAGCGEE
ASDCGSQEKLEKSKVENQELEESKTQKPPATQNTKSKDNEENSTEASSTELQNTETQQEIKPPVDENDT
TSTDASTAVAAQSTSAGSQEEATESSSDGSHSPLQGEVFTGTDTPENAPSPAAAEAEKRQGENVTKDGD
SDSSTAVFHSTSPLLLLVACAAAAVVVAA*
>Tc00.1047053506799.130|S043|AG-----CD|27
MMAMMMTGRVLLVCALCVLWCGAGGVYARDLDNKALGGCMASGVLGMNTSYVPNGCNKYMPMPPLRSAL
PIPAIQAEVQQLTDVSQDDIKLSSDTAPESGSGVGSGGSPGPAASPTGAVPGAGVPAATGPAGPAAAAG
GGPTGVTDPAAAAPGGGGGGPAGVTGSSGSAVSSVVPSLPADSENSKTGCGEEASDCGSQEKLEKSKVE
NQDLEKSNTAELPATQNTKSKDNEEDSTEASSTELQNTETQQETKPPVDENDTTSTDASTAVAAQSTSA
GSQEEATESSSDGSHSPLRGEVFTGTDTPKNAPSPAAAEAEKRQGENVTKDGDSGSTTAVSHTTSPLLL
LVACAAAAVVVAA*
>Tc00.1047053506879.10|S114|ANP-VFEC-|3
MALMMTGRVLLVCALCVLWCGLSGIAVNDAGGVSDGSEFEYLFLNWEELLKNECEAEYSNETNLSLKDL
AVNCCLHHDMHELCEDLYSRLFMETEFPNVGGVCKKYAEKTDEVKCRKQQTQPPPAAENSVKVSVPKAL
GKEGDLGETPKEAPLADPPAKPTKGPPSSPVGGQPTNADDVPTPKSEERPVTTRPTKDSTEGNTDTITD
TDQEETSTSEAESAAPTPTVASDNDDDNETDKGTGEEVPNNAPESDDAGRKEKQDENKEANPKETPVES
TATKTTTPTTPGDSDGSTAISHTTSPPLLLLLLVVVACAAAVVVA*
>Tc00.1047053506879.60|S015|A---H-EC-|9
MAMMMTGRVLLVCALCVLWCGAADGAVGVVSGGDDNILREVFIPVARLQESQEKRTSGATADAKGAAAE
TATKAKKAAEAESLPVTTVGEEEVKTTINDQDNSVEHHSGQKKELLKEEEPENREKEQHEKQRHQQRDH
SARKGEEYAKDKTANGTNATAVKDDSDSSTAVSHTTSPLLLLLVVACAAAVVVA*
>Tc00.1047053506911.20|S010|A----RECD|22
MMTGRLLLVCALWVLWCGVSGIAADDAGGGDVFVSCGDNKKLEETELSFPVIPGVEPQAPEVKEESPTR
RSDDVLEEKGEVVAERDEADGGGVGVDGEKVKTVQKGRGEGVSEGDAPAEAELHSTDDETLRRPSPNGA
KGGEKTVPSDDTPPEGRVQQRQEDPPGLLQSEPGDPASGRGVPPESTEHKPLASGSPSSETETTGIQKV
STPTHAGESPRVTEKDVVATEHEREDKEGPVSNPIKVADVRLPEPQELRSQSLDGTQRVETGVRPINSS
PEDQNKQRVLLNLSQGESANDPPETTPQSSSTGGHRVENSRTNGDGAKNTEGSAAGEKKDDKKGLEKDV
VPTISEGKIQPPVTAAASTSETAIDGDSKGSSTAATALRSDDDTEGNPAKNGLRQPSSERTAEHSTTPD
SEDASDSAEKAASQNAGIPTTKAIATAKTNDTASHGDSDGSTAVSHTTSSLLLLLLVACAAAAAVVAA*
>Tc00.1047053506955.70|S061|A--TIFECD|52
MMMMTGRVLLVCALCVLWCGVCGGGCSEATPPGSPTSRGTPLEKSTQNDNATKAVAAGVDRNGQQKVPE
APAPPGSESQELSPGPSQATQPGGGEASQMTSAKIDTEGQKEEEKTDEKEEKEEKDEAEEDEEDEEEEE
EEEEEEEEEGEEGEEEETDDQEDDRREDGEDDKKQEEEKKKEEAVTGTTEVISAGGGEQPSLSSGAEGA
SNTTNPNSTPKTGDDDPAADGAGTAAGKQNENKDVNPKETPVTAAATKNTTATTGDSDGSTAVSHTTSP
LLLLLIVACAAAAAVVAA*
>Tc00.1047053506955.150|S099|AML-VFECD|25
MAMMMAGRVLLVCALCVLWCGAVFGHAMEDYCGEGGGNGLSNGGDDGVSLKADCGLLSTRMGLIRAVEA
EEAGSGLSVPDSSGNSKDKALEGDTNGSEAVGSGDVGVAGQAAAPAAPTFGGSGTEEQVRELEVVGTSD
GNVAGAKKDHEDVNEVDSKHQRAEQLSSSSSSGSSETEGVKQPVVKENSKSSETSDSPPQEEEKDPRSK
PDSREGEAEEKETEEDKKNASNQAPTETPGGLTKHTEIQTATTEPNGQSSPEALEGVKQSEEVQGKKDS
NHNSQTKSVDSIAANQQKEPSADHGESGPPSPTANGDAANNDFDKSTEDGIPSSDPAADVAEKRKEKQN
ENKDANPKETPVTAAAMKTTTATTGDSDGSTAVSHTTSPLLLLLPVVACAAAAAVVAA*
>Tc00.1047053506955.99|S058|A-TTIFEC-|2
MMTMTGRVLLVCALCVLWCGACGGERSETTPGSSGNPSENDPKKEKVAVVGAEGGDESGKPAAPQAPAS
PTGSGSPEAAPGPSPATKPEGEASVTASPTTENKGGNTEGKKEEEEEEKQQEDEEEEVEEEEDEEEEEE
EEGEEGEEEDDTRENEEEETKKEGAITGTTEGISAGGGEQPSSSSAAEGASNITNPNSTPTTGDDDPAA
DGAGTREEKQSENKDANPKETPVTAAAMKTGTATPGDSDGSTAVSHTTSPLLLLLIVAFVAAAAVAA*
>Tc00.1047053506955.212|S061|A--TIFECD|52
MAMMTGRVLLVCALCVLWCGACGGGRAEVTSPASSPSKDKESQEVEVTTAVAGKVGQSGQPESPQETPP
TTLQSQKAPANSSQAPQPEGGPSKKEDEAMDNTGLNTEDEKEEEDDEQHEEEDEDEEEEEEEEEKEDGG
EKKEENDTKGKEETKKQAATSTTEGTSAGTEEQPSLSFAAAGASNITNPNITQTTGDGDPAADGAGTAE
GKQNENKDANPKETPVTAAAVKTTTATTGDSDGSTAVSHTTSPLLLLLVFACAAAAAVVAA*
>Tc00.1047053506955.244|S061|A--TIFECD|52
MAMMTGRVPLVCALCVLWCGVCCGEPSEPPSSASASPGTTPEKKPQNQEEVVGGAAGDDQSGQPESPKE
TPSPTRSELPAGGPRPPQAQQSGGEASVTSSTTTDSKVQKQEEKKEQKNEEAKDEDEDEDDEEEEEKEE
EEEDEEDEDEVEETGKEEAATGTTEGTSAGTEEQPSLSSGAEGASNITNPNSTPTTGDDDPAADGAGTA
EEKQNENKETNPKETPVTAAAMKTTTATTGDSDGSTAVSHTTSPLLLLLVFACAAAAAVVAA*
>Tc00.1047053506965.20|S110|ANP---ECD|3

MMAMMMTGRVLLVCALCVLWCCGAAVVSSIPDVTGRENVPHGYLVVNWETLLKNECATDKKYINKDGTV
NESAVKDCIRDAMRVVCNVFCRKILGEPDDSEGERICEEYVGSRDEAGQSSHVITPAEAKTLQAPRSEL
VELGKTPGETPKPLSGGPATEDEAAKPTGGPPTPPVEAQHNREENVPVLHPEDDPGTTESNSDSEEDDS
ASTTDNQESVTPDGHDKSTPTLLSTATDTVKKEADRVNTKGTQKPATESNAERKEVEESDEKTYDNTKK
IPAEAAATTNNTAMPGDSDSSTAVPHTTSPLLLLFIVACAAAAAVVAA*
>Tc00.1047053506965.70|S098|AML-VF-CD|2
MAMMTTGRVLLVCALCVLWCGAVFGRAMDDYCSEGGGSGLMHTSNGGDDGVSLKANCGLLSTRMALINA
VEAADEGGLSGDAGSSQDNSKESLQDKTLSDNAEGGAALVSGGGVVADPPPPPPAAPLQKPGGRNTGEE
GKQEELDKKGNEADDKSRSEPGPQKPKTEQSSSSASGGPGTQSDVEPALEDTSESNESLDDALKQEDAG
ETEVTKLSDGEPEKGKGNMALTETNDSQAKQKEIQLPTPPTLPTTQVDEHSSPGDTVNKQQLQKPQSEM
DPKNNSQKKSVITITADQHNEPSADHAGSRPPSPTANGDAANNEADKSTEDGTPNNDPAADGAETREEK
KNENMNANPKETPVEATVIKNPTKTTTDSDSDGSTAVSHTTSPLLLLLVVACAAAAVVVAA*
>Tc00.1047053506965.100|S110|ANP---ECD|3
MAMMMTGRVLLVCALCVLWCCGAAVVSSIPDVTGRENVPHGYLVVNWETLLKNECATDKKYINEDGTVN
ESAVKDCIRDAMRVVCKVFCRKILGEPDDSEGERICEEYVGSRDEAGQSSHVITPAEAETLQAPRSELE
ELEKTPGETPKPLSGGPATEGEAAKTTGGPPTPPVEAQHNREGNVPVLHPEDDPGTTESNSDSEEDDSA
STTDNQESVTPDGHDKSTPTLLSTATDTVKNEADRVNTEGTQKPATESNAERKEVEESDEKKYDNTKTI
PAEAAATTNNTAMPGDSDGSTAVSHTTSPLLLLLLLVVACAAAAAVVAA*
>Tc00.1047053506965.130|S091|AG--YKECD|14
MMMTGRVLLVCALCVLWCGAGWVYAREFENSALGGCMASGALGASWYHMPSGCDKAALTPPLRSALPIP
AIKAEASEDDVPLREEDDSISTSGAVVGTAMPGESDGAGLVIQSGPPAGGVAPTTPSGGSSTQNMESQR
AVQHLEPTDPAASVLLKVEVPGEPMPIAEESLSNTQDRPEIRVTGEDNTEREKLRSAVDTGDRFSDQPK
EPTPPLKTTPQLQPTTPVPPPSSKASTTELSSGEGNPQAATTDTQTPTPTIGKTTTSETATDYKAPKTP
SKDDEAEQHSKERVPSDLMKNTANGHPADTTASSIPTIGSGDVQRNADKNGNDAQRPDTKGTHNDPAAV
NTNDTLTASVAAPQTTERLADAKTNHTVTPGNSEGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053506965.140|S030|A------CD|31
MMAMMMTGRVLLLVCALCVLWCGAGGCAENDAEVVEIPAGGKGAVGSTGTSVPGPGVSVLRIDVPNVNQ
SKETSAVKSFEGNEVKTDQQDVVNGVEDEKNNNSSEHLEETMEDGPGKERTEPPLQNVGQEEIQPPQLQ
VNLPQKAQPQPQQSQPLPPSAPQPHISASEEGKGVGENNTGGEGQPSLGVQDIGNAAPKNPRKEDLLEG
PGKESESSEQVQTTVPNTVTPEHKTQNEMLTPEQKTNEGQSTDTSTNIPELQKENKKYPAFAEVTAQST
STGSQEKEAEPSTSEEPSPLEEEQSTGTKTNEDARTPDAAATEKRQNGDNEKVGDSDGSTAVSHTTSPL
LLLLVVCAAAAAVVAA*
>Tc00.1047053506965.180|S013|A---V-EC-|8
MAMMTGRVLLVCALCVLWCGSGGRCEEEVVPVADLPANSESGSGGPEKDTDHTVPGGAENLSAQQSQLN
KVRGSPPGISSLEAPSEVESKKKHTQSDPEHTDLLSPSKSSGEQRQDGTPDGTPGRLATSHSQEDRKHP
SIEGPERNGPPSSSSNNNTVGRKSEERTEDTPSSTEIIVAAPSEEGQERENVAASLEQPEGNSTAAPAI
TTQTISTTPTDDGTVDTVRMSDAAEQSTGTAQTNHTMTPGDSDSSTAVSHTTSPLLLLLVVACAAAAAV
LAA*
>Tc00.1047053506967.50|S015|A---H-EC-|9
MSMMMAGRVLLVCALCVLWCCGGGGYAEDDADVVSGGGPGTGKGEKNSEELSSPVPGLPERQEELAGGA
AGRAAGGRGSAGSQELKDNVVPNTDRHAPNEEQGANLDVDPPNPTTDQNKSEDSMKAGAGTINQTAPPP
AGPPPPPPPPPPPVPPVPPSLPEAEGVKLTKTPEKQDSPVDHHSTQHRTVPQKKELEQQEQNTQGQIIK
EQHESERIQVQQEKEKEEQRSEEQLEQREHLEEEIRDQQKKKKQEQQEEEHEEPQEEHEDSIKQGKEQD
QQQQQQHENAAENSEEPTKNETAVGTNATTSTGDSDGSTAVSHTTSPLLLLLVVACAAAVVAA*
>Tc00.1047053506967.70|S031|A---Y--CD|1
MAMMMAGRVLLVCALCVLWCGAGGGYAEDVDVAVGGPGTFGEGGGGAGGQSPPADGSRGGSRGSKADGS
HLGEGDASDSASDDISLALSPELDVVPTLSEEPLPQEEEESEGKQKHPQTGPQDASTPKVNGRETIDPD
PQKQLSDKSKTESITNVGGGETADGGKENNAHNNGLSSNKSDPQPLLEPRIKKVSLPTEPSPPPAELSP
APPELPTVPSPTGLAPATTVSAGETNPTPSTGSQNTTGTTSKTSTSNAKTKREAQEKSSGNVAPNQNRQ
DTDTPDSMRGATTSRPAETAVPSVSKIGSGGTQNKEDKVDNGAQRPNTREPQYGLEDDTDDAHTASETE
LQTPGTATTQNNASSKSGGTDSSTAASHTTSPLLLLLLLVACAAAAAVVAA*
>Tc00.1047053506967.100|S016|A-----EC-|10
MAMMMTGRVLLVCALCVLWCGAGGGFCEGALEDEFCSKSYVEALSLLANKTDDEIKEKYCKQDDEKTTC
LKTLRSNIADALKKEKTKEDSAAHRESDISRDTGASVGSSRAKSSKAAGANTAVLSPPLPLNVIGGVDA
QIHGSAGGAGHQQHSDDVRSEAEQRNHPESGRCSEGQAALGECSHVPAADAAAEGSHQHRVDVQGKKIH
KKEEHTPEAGLKSAEAREGTEEAPATPQDPTNTAESHEDKSQRVAAPATIPAENALSGSSQEQTSQSSS
PSGSETTGSLDNEVPEETSINTQMSGAPFNGEGKHRESTAGNEGTTKVGSAAVQSNTATPGDSDSSTEV
SHTTSPLLLLLAVACAAAAVVAA*
>Tc00.1047053506971.60|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCGAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITMPLRSVLP
ITAVEASAGEDVSPAAGPSAPPTGGQGTGVISSGSSAFPPAPPAAPPAAPPAAPPSAAPVVDSSVGSSG
GEAESSGSHPTNTTGDSSTGDQTPAAAAANDSSPPEIPAGTTSGTGHTRQEEEEEGEDHEKQHQSDETQ
VQQHQQHEHPVESGEESAKDKNALLTNATANTGDSDGSTAVSHATSPLLPLLVVACAAAAAVVAA*
>Tc00.1047053507063.340|S025|A------C-|17

MAMMADRVLLVCALCVLWCGAGGGYGLPAGYCADGGLDNAKPAKGMDGEVVLMKRDCVTSTAFRGVVTA
VPAAEDGDLNSPGAGVGTGGKRNSDAEEPPVVDAESGLTSSGSGAASTASSPAVADKDGASRAPVLGAV
GPKQQPAVVSGGQDDSSSGGREEKESEEAGSESCGEEPSSPKVCPQPRLVGVELTPRAMEERRGQKDNA
SVANNQSEEKQQEDGVPHVPETRASVQTLPAPAPAEGHPEDATGPFGASEEHATAPSSSLTRDALNGDS
QRQTPQPQTTTGIKQTVPVIQGLSEGVQENQKNVEDGKKRKQVDSTGSAHNAEHDSAAETHELSTASSN
TRSSEAPGNEPASKSLSGNLRSSTAGAAEQAKAPAQGGAEQKTAPEEKEISEELPPTAAEVEVRGGPSA
PPPKPLPQSALPSSKEVPDTMQSTEDPQTKGIEPAKDARQNAITEGQAETTSPSSPVDDAAANDADKSN
AEIPNDGSAVHAGVPEEEERQEQVEESHKQTSFTSTAKKFNTTIQDSDGSTAVSHTTSPLLILIFVAYA
AAAVVAA*
>Tc00.1047053507065.60|S099|AML-VFECD|25
MAMMMTGRVLLVCALCVLWCGAAFGHAMEDYCGEGGGNGLRHTSNGGDDGVSLKADCVLLSTRMALIKA
VEAADGQGLSGDPLETSQDSSPGKKLDDKTSGGGTPGLGGGVAGPATAAAAALEPGESGRGEPKRELEV
ADTAGEEHANDRMKGSERNPENLKNGQSSSFSSGSPVTLGGEGLASEKNSKAAEPSEDGPKVTKLSQQK
AEGDKENKNDTILIGVRENPEKNTEIQTAPPPPATNGKSSPEDTVRMQQLQQVLDGIESNNNSQTNSIA
SIASNQHNEPSADHGESGPPSPTANGDAANNEADNSTEDGMPNNGPAADGAETREKQNENKDANPKETT
VTAAAMKTATPTTGDSDGSTAVSHTTSPLLLLLVVVCAAAAAVVAA*
>Tc00.1047053507069.10|S061|A--TIFECD|52
MVMMTGRVLLVCALCVLWCGAGGGGRAETTPVVPGNASDGSTQKEEAVGGAGGGGQNDQSEALQAAEGV
SVQGATGTVVALQTGTQLAPKTADAEKKGKDQTQDVEDVVVKKGKEQEPKEEEEDNGIEQEEEEREEEE
EEEKKHEDAVTGTTNGTSAGSQKQPSFSSGAEGASNNTNPKSTQTAGDDDPAADVSGTAEGKQNENKEA
NPKETPVEATAMKTTTATTGDSDSSTAVSHTTSPLLLLLVVACAAAAAVVTA*
>Tc00.1047053507069.150|S061|A--TIFECD|52
MAMMMTGRVLLVCALCVLWCGAVFGRAKATPASPPSKDNSPKNNNNSTGVAAGVDPNGQQKAPQEKSPA
SESPESPAEATPAPQSGGGAPDSANTTTDSKDPNTQEKMEEKEEKEKNEETEENEDEEEGEEEEEQDDR
KQDGGDDKKEKEQGTMKEEADTGTTEETSAGGQEQPILSSGAARASNITKPNSTQTTGDDDSAADVAGT
AEGKQNENKEAIPKETPVTVTAMKNTTATTGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053507069.180|S070|A--TIFEC-|13
MAMMTGRVLLVCALCVLWCVAGGGGCSETTQEPSGGASQGGKNTDGTKNTANGAGGGVKSSATAKSQLS
AESVTELKVEAAGADTSATQQHEKQASETEEEKMKKKNERTDEKEKKEYDEEDDDQEEEEEHEDEEIDE
GEGDEKKEESEMKEEKKDEKEEEKIKEDDADARKGMSAGGEEPPIISSAAEEAANQTNLKSTQTTGDGD
STADVAKTREEKQNENKDANPKETPIKTTAIANGTAPTGDSDGSTAVSHTTSPLLLLLVVACAAAVVVA
*
>Tc00.1047053507069.220|S070|A--TIFEC-|13
MAMMTGRVLLVCALCVLWCGAGGGGRAETPRPAPSGTTPEKSTKNDNATVVDAEGGVKSGKQEELQAPT
PTGSELQAAPAKSLQITEPGGEASETTSATKDNNDQNKKDKKKEEKEEENDRREDGKDDKKEKEEIKKE
KVVTGTAEEMSADSEEPRSLSSGAARASNKTNPNSTTTTGDDDPAADGAGTAEGKRNENKEADPKETPV
EATAMNTATATTGDGDGSTAVSHTTSPLLLLLVAWAAAAAAAVVAA*
>Tc00.1047053507069.94|S038|AG-----C-|7
MAMMMTGRVLLVCALCVLWCGAGGIHARNPDNNSLGGYMASRGFGRNKSFLSNGSIKNLSTPLLLSASF
ISAMQAEAHEEVPSAGVTDSPLSGGTGLSPAFSGPDTAIARPTVPGHVPGAAIPVADFSARVPAFSGLG
SAGPVHGPVSGADAIPVAAVHGHGAGPGHGAAAFSGLGAAGPGAIPGPAPVRGPTFSVPDANIFGAPVP
GNGPAAIPGAPVSGHVPGAIPGAPVPGNGPAAIPGAPVSGHVPGAIPGAPVPGNGPAAIPGAPVSSHGP
GAAAFSGLGAAIHGAADPGAAIHGAIPGPGSVRGAAVHVPVGPDHGPALSGLVPAVPGAGHSVGGGSEP
PDSRSVVISSSQGGNGKTAPVSVSSDEQIASPEEVLPQKETGSQGTSSPEGQPTVSSNTEKQRNNSASA
GGHSLGHDAAGDELQDSLEEQQKNDHSQTNETKKSSGDQITESQRSGGALSKVSNTTTHGIKTQLPKTN
SANEKNYSQNTDASHTTSPLLLLVVVACAAAVVAA*
>Tc00.1047053507071.20|S118|ANP-VFE-D|3
MAMMMTGRVLLVCALCVLWCGAATVVSTAPDATRAQSVWPEYLFLNWHELFRNECKVENPYENEDLKGL
AVNCCVRDAMRELCSSFYGKTVMENKDPNVEGICKEYAGKPDDVADCPKPQTNLSPAAVTLVKVSVPEA
PKDKEKELRKQSEEAPKAPPEEAPTPLARTPLTNSPANPTNVSPSPPLKGQPANEEEVPVPNSEEGSLS
TGPINDSEEGDTDTVTDTEQDEPSNSQAEPTTPTPTVASDNGDNETDKGTGEDTPNNTPEPDVAGTEEK
QDEDKNNKPKERTLQVAGIKTTTATTGDSDGVKATSPLLLLVVACAAAAAVVAA*
>Tc00.1047053507071.100|S120|ANQTIFECD|1
MTMMMTGRVLLVCALCVLWCGVCGLPGIAADGVGGGDGSAGEDLLLQWRAWLRRECAEQVSRRTGGGAN
VSAVEECVRQGMESLHAVTDGRSRWRRQRIAAAAAADGAGNEKFIAGAISQEGRSGKDNVLSSVKQLES
PANSGKETAGRSETGATLQNIAETRARGETEKEDLISDKTNSEKEENEENEKKKNAKQSEREDDEENDE
EEDGSEEAEVKDEKETKEEGGKGDEANEGKKRKKKENDTGTTKEISAGSEEQPILSSGVEELANQTNPK
STQTTGDDDPAADGAGTAEGKQNENKEANPKETPLEATATKNTTATTGDSDGSTAVSHTTSPLLLLLVV
VACAAAAAVVAA*
>Tc00.1047053507071.120|S070|A--TIFEC-|13
MLMMMTGRVLLVCALCVLWCGAGGGGRAETSSPGSSVKASDGSTQKEEAVVGAGEGDQNGEPAASQEKP
APTTSGLPAAVAATRTGTQAPGKANAEKKNQTENGEEEENVAKKKDEDKERKGEEVEEEKAEQENEERE
EERREEEEDEEEEKRNDKKEEEQKKKEDAATGTTGAISAGGQEQPNLSSGAEGASNKTNPNSTTTTGDD
DPAADVAGTAEGKQNENKDANPKETPVEATAMNTATATTGDSDGSTAVSHTTSPLLLLLVACAAAVVAA

*
>Tc00.1047053507071.140|S068|A---IFECD|10
MLMMMTGRVLLVCALCVLWCGACGGGCSETSSPGSSVKASDGSTQKEEAVVGAGEGDQNGEPAEPQEKP
APKASESQGAVPGPSLAPKSGEASDPASKTTDNNDQNAQGGKKGEKDEKQEQEDEEENNGANEEEVTMK
ENAVTSTTEVISAGGQEQRILSSGAAGASNKTKPNSTTTTGDDDPAADGAGTAEGKQNENKGANPKETP
LTAAVMKTTTATTGDSDSSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053507071.180|S126|ANQ----C-|2
MAMMTGRVLLVCALCVLWWGLSGVAADGAGVVSDGSLDEDLILHWRTRLRRKCAEEVSRRTGGSANASA
VEKCVHQGMDGLRAVVDGRRRWRHQWYAVVAVEGVDDGKGNNGQSNDRPKGSSPSVQGLQEGSGLPGVE
GGSLNPPAREDTLKLSGDAISPEGLKVNAGADPAKITASQRPKEDSTAAGTRNHPPPGPSPPTSPKEEN
AVLLTNLKGTKTEIEIEPKDQALPVGEQGLHNQEGQSPQGKEHQPTVEPKASDIPTERPLEGGEHAVDS
QEEDRKNKVVAGRKQTGDGGHEVSNENVVRVPVEPKVNSTEIEQEVTRTHTGEHLVGDAEAAEKEKQRE
QRADGQNEKNEKGPVTRTQQREQEENQLPHQQEQQEKQGILPASPAGLETTQRSLSTVQPEGLHEEQQQ
NHSSYQNDFTNDKNIVRTNATANTDATDGSTAASPTTSPLLLLLLVVASAAMVAA*
>Tc00.1047053507071.240|S002|A---S-ECD|19
MAMMTGRVLLVCALCVLWCGAAVEAEGDGSDGSAELLLESQEPEKSPEGTQDFVHEAGGLKEELTPKSA
DEDDEDDDDGEGSEDEEEKQIEGPSGEKGNAAPDPVSGEKKLIGTEQQARQSIVSAEDIPLSDNRESNA
ILTQTKIEGTKDSDNNPPAVENPLTTVNREQTLHAEGNLPPPQEGDDSREHDGKDTTSEDKKNVQPPET
AATPQSHRDKGSEGTGDDTKATTVTANTTDTTNTQNRDGSTAVSHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053507071.310|S013|A---V-EC-|8
MAMTMTGRVLLLCALCVLWCGAGGRCDVEVVRVADSPANSESGSVAPDKDTDHTVHGGAGVVSGEQSQK
QKVGGHPLVAPQLQAVLQPESTVQQTLFDTEPTDSLSHSQSLQEERQGGSPDGSSGRPAASHSQEDRKN
ESIGDQQRKDPPSPAINNDVVSRKSEELTEDTPRRTEIIDAAHSEERQEPENVTPSLEQTRETSTAAPA
ITTQTISMQPPEENASSTVKMSDASPQPTGTANTNHTTTPGDSDGSTAVSHTTSPPLLLLVFVACAAAA
VVAA*
>Tc00.1047053507071.349|S008|A-----ECD|43
MMMTGRVLLVCALCVLWCGAGGGYAWPYKECKSDNESCLNDGQHKSVYNSSILSRFLGETDSTSTGLLG
SSTGSTGSGGDVSRNGAGGTTISATDSQKGGAQSSLTPSQHASASPGDSSRSKESSEKTEETPGPASTS
DNDGDGGPNTANQAHLTGGEKRDSGHQTEDGDTDPNLPLEDSKDGEDTHSSPTPPPANKANVPNVTAEG
EKVPAVLTRQEESEGNPEAEPENEQHSSANGVSVPQPEAAQQGETEDDNTTEKTPDEAAAPKNGTATLD
DSDGNTAVSHTASPLLLVVACAAAAAVVAA*
>Tc00.1047053507091.80|S121|ANQ----CD|9
MMAMVMTDRVLLVCALCVLWCGVSVVAADVAGGGDGGADEYFVLRWHAQLRRECAEAFGRRTEGGANAS
AVEDCVRRGMDGVRAFGDGRRVWRRQRSAVVAGDDTTDDDSTRGSSSEVQTETETGSLDGRPLKPSVKP
IPGEVTDGQDSGKISEASVPTINGTGENLDGDEEEGDVSQDESQEDRDGEDEAVDAAVGNGGSESSHTE
HEEEKERVKEEKAGSTTNEREGDENNAAGRRPPQGTAASRPALPVDVSNPQNPVLGQDGAGGEKAGAVP
VVLPQAAGLREAERAPAKLTPGGGAAGKETEKQNGTAEQVAAKEVQTAVEDSSAEAAAAGKDSKGEKEE
ENVSEAAKEESHGNVDEEAAGKNGGNATKKLQKEATDEAKTKKRNEQKEAENANNTKEEPDEEEVKKAA
QEEEAADKEKMGAARIPTKTNMTTPENSDGGTAVSHTTSPLVLLLLVACAAAAAVVAA*
>Tc00.1047053507091.120|S131|ANQ---EC-|3
MMAMRMTGCVLLVCALCVLWRGVSVVAADVAGGAGGSADEYFVLRWRAQLRRECAEAFGRRTEGGANAS
AVEECVRRGMDGVRAVVDGRSRWRRQHSAVVAAAADGEVDDKSGEGSDGTLKGLSSSDQMSQAGKNPEE
RRELTGSLEVTNTLEGSEDSQITGELNVSSDVDRPKQTGSQEPTVGQPEDEEGTRNLQLPPPPPPPAEP
LPPIPRQPPPGTNTLQSEKTHPQIRAEKHSKPQDGGHSHETKMLQTKGSTKHEEGASSLQSPESVSHLS
REKTTPLSTSTDSSGVAGSTVENSGANNPKPPAASVTQHDSKGDTGSAALPANNTELQSEEIPNAGIIA
TTYDDGDDSSPAAPTAERTTAGTRSTQASGDASDLERANNDDVNDDVAHNDKTAEFEAASGGKDTEADN
NERYTTVPENAANKTINTEITADSDGSTAFSHTTSPLLLLLVACAAALVAA*
>Tc00.1047053507163.40|S017|A---S-EC-|13
MAMRMTGRVLLVCALCVLWCGAGGRCDAGVGVGAQQDGGKSPPESKGLETSSQGTQDLKGGAADAKENS
PSTPTEEDDEDVDDDIEESDDDDGGTEDEGEENVRGQSGQEGTVALGSGSTENKLIGSWKQTELSISSA
ESISPSGSRELNVNLTQTEVEGKKETDKNTPAVESALTTISGENTLPAGIVEGNPSPPPPQDGIHSREQ
DGEGTTSEGKKNVPLPETAATPQSHHDKGSEGTGEDTKATTVTANTTDTTNTQNSDGSTAVFHTTSPLL
LLVVVACAAAAVVAA*
>Tc00.1047053507231.30|S129|ANQT-KECD|2
MAMMMTGRVLLVCALCVLWCGAAVVVSAADGAEEDGSAGEYLISRWRAYLRRECVEKVSRRTGGRANAS
AVEECVCQGMDGARAVADGRRRWGRHRYAVAAADGPFENDSTPESSLQGQTGSGAGLTGGRRLEPSLNP
DTGISDKATAEEETLTRHPEAPELVKNRTEEILKEQEKEKEKKKSAEEENEDEGNDNGEDDNASTESSG
DDHDEEEEEEEDVEAGTNKKEGRDGGDVDGDNSLDDHAIVQLAAPVYVERQERSLTLNNGGAKGKGGAG
ETRVPEGAGLQGAEKESAKLTHETGADLMETEGLKEGADQSGAGNQQAIDESKSNEAAPPATQEEMKKE
APKEAKKATANENVIRKETTEKGKNGAERGKGESSDRAGKEKKENEERKVEEANNEPQDGSETANTDVA
LTVGEAAPQTAEPVTVAQANDTGTPGDSDSSTAVSHTTSLPLLLVVACVAAAAVVAA*
>Tc00.1047053507237.20|S002|A---S-ECD|19
MAMMTGRVLLVCALCVLWCGVGGRCEAGVGVGAQQDGGKSPPESKGLETSSKGTQDLKGGAAGAKENSL
STPTEEDDEDVDDDIEEGDDDDGGAVDEEEENVRGQSGQEGTVALGPGSSEKKLIGSEKQTELSISSAE

STSPSGSRELNVNLTQTEVEGKKETDKNTPAVENPLTTVNGENTLPAGIVEGNPSPPPPQDGVGSREQD
GEGTTSEGQKNVPLPESAATPQSHHDKGSEGTGEDTKATTVTANTTDTTNTQNSDGSTAVSHTTSPLLL
LVVVACAAAAAVVAA*
>Tc00.1047053507237.80|S002|A---S-ECD|19
MMAMMTGRVLLVCALCVLWCGVGGRCEAGVGVGAQQDGGKSPPESKGLETSSKGTQDLKGGAAGAKENS
LSTPTEEDDEDVDDDIEEGDDDDGGAVDEEEENVRGQSGQEGTVALGPGSSEKKLIGSEKQTELSISSA
ESTSPSGSRELNVNLTQTEVEGKKETDKNTPAVENPLTTVNGENTLPAGIVEGNPSPPPPQDGVGSREQ
DGEGTTSESQKNVPLPESAATPQSHQDKGSEGTGEDTKATTVTANTTDTTNTQNSDGSTAVSHTTSPLL
LLLVVACAAAAAVVAA*
>Tc00.1047053507237.100|S112|ANP-V-ECD|4
MAMMTGRVLLVCALCVLWCCGAAVVSSIPDVTGRENVPHGYLVVNWEKLLKNECATDKKYINEDGTVNE
SAVKDCIRDAMRVVCKVFCRKISGEPDDSEGERICEEYVGSRDEAGQSSHVITPAEAETLQAPRSELEE
LEKTPEETPKPLSGGPATEDEAAKPTGGPPTPPVEAQHNREGNVPVLHPEDDPGTTESNSDSEEDDSAS
TTDKQEGVTPDGHDKSTPTLLSTATDTVKNEADRLNTEGTQKPATESNAEGKEVEESDEKKYDNTKKIP
AEAAATTNNTAMPADSDGGTAVSHTTSPLLLLLLVVVACAAAAAVVAA*
>Tc00.1047053507237.120|S015|A---H-EC-|9
MAMMMTGRVLLLVCALCVLWCGAGGCAENDAGGLGEDENTELKGIASDGLQRDSHDSETGKKQLTEPKA
AEEPLIAPGGDHIDKQGSSVVQLKADRDGRREEVEPTGNVNGSQKNSKDALDTHQTEITEVRTKVEGTP
PSPPEGGGGPTQTKSPEISRAPVQSPEQLFPPAAHAGEKSLRAPTALSPITSVQPPLLPKGKGETDGVQ
PGPEDKSNEPKVKVEPQVHGNEGQHQSTQHHEVPQEKELEAQEQDTQNQIINEQHESERLQVQQEKEKE
KQRSEEELEKREHLHEEEREGEHLQEEIRHQEKKQEQQEEKHEEPQEEHEEIIKQGKEQDQQQQHQQHE
NAAKNSEEPTKNETAVGTNDTASTGDSDCSNAVSHTTSPLLLLLLVVACAAAAVVAA*
>Tc00.1047053507237.170|S109|ANP-V-EC-|1
MAMMAGRVLLVCALCVLWCCGAAVVSSIPDVTGRENVPHGYLVVNWEKLLKNECATDKKYINEDGTVNE
SAVKDCIRDAMRVVCKVFCRKILGEPDDSEGERICEEYVGSRDEAGQSSHVITPAEAETLQAPRSELEE
LEKTPGETPKATIGRTSTEDEAAKPTGGPPTPPVEAQDNREENVPVLHPEDDPGTTESNSDSEEDDSAS
TTDNQESVTPDGHDKSTPTLPSTATDNVKNEADRVNTEGTQKPATESNAERKEVEESDEKKYDNTKKIP
AEAAATTNNTVMPGESYGSTAVPHTTSPLLLLLLVVACFTAAVVAA*
>Tc00.1047053507237.190|S091|AG--YKECD|14
MMAMMMTGRVLLVCALCVLWCGAGWVYAREFESNALGGCMASGALGASWYHMPSGCDKAALTPPLRSAL
PIPAIKAEASEDDVPLREEDDSISTSGAVVGTAMPGESDGAALVIQSGPPAGGVAPTTPSGGSSTQNME
SQRAVQHLEPTDPAASVLPKVEVPGEPMPIAEESLSNTQDRPEIRVTGEDNTEREKLRSAVDTGDRFSD
QPKEPTPPLKTTPQLQPTTPVPPPSSKASTTELSSGEGNPQAATTDTQTPTPTIGKTTTSETATDYKAP
KTPSKDDEAEQHSKERVPSDLMKNTANGHPADTTASSIPTIGSGDVQRNADKNGNDAQRPDTKGTHNDP
AAVNTNDTLTASVAAPQTTERLADAKTNHTVTPGDSDGGTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053507237.220|S053|AG-TH-ECD|1
MAMVMTGRVLLVCGLCVLWCGAGGFYARDVDSNAVGGCTTSGELGTGLSHVSSGCNKPGITAPLRSTLP
VTAVEASGEEINSVTMQNDLGSSEISNAAGPGPAGLADAAGAAGAGVPGGGGGTSLGGGGTDEIPSGSS
GGKNEPAPPPPLETENEALRVTTVGEDEAKKAPQNHDNSVEHQSGQNQEHLHEEEREGEHLQEEIRDQQ
KKQEQQEEEHEESIKQEKEQEEKQHQQHENAAENSEEPTKNETAVGTNATASTGDSDGSTSAVSHTTSP
LLLLLLVVCAAAAAVVAA*
>Tc00.1047053507237.270|S017|A---S-EC-|13
MAMMMTGRVLLVCALCVLCCGVGGRCEAGVGVGAQQDGGTSPPESKGLETSSQDSQDLKDKAPVVKGEV
PPASPGINAEEEDDDDDDDGEGDGDGQENGGVEVEEKPIGRQGGQGGTAALGSDSRETNLSGSEQENHQ
AIVSAEGISHSDSRESKAILTQPEFEEKNDSDKNTTAVENPLTTVNGENTLPAGVAGGNPPPPKDGVGS
REQDGEDTTSEGQKNVPLPESAATPQSHQDKGSEGTGEDTKATTVTANTTDTTNTQTSDGITAVSHTTS
PLLLLLLVACTAAAAVVVAA*
>Tc00.1047053507237.340|S016|A-----EC-|10
MAMMMTGRVLLVCALCVLWCGAGGGFCEGALEDEFCSKSYVEALSLLANKTDDEIKEKYCKQDDEKTTC
LKTLRSNIADALKKEKTKEDSAAHRESDISRDTGASVGSSRAKSSKAAGANTAVLSPPLPLNVIGGVDA
QIHGSAGGAGQQQHSDDVRSEAEQRNHPESGRCSEGQAALGECSHVPAGDAAAEGSHQHRVDVQDKKIH
KKEERTPEAGLKSAESREGTEEAPATPQDPTNTAESHEDKSQRVAAPATIPAENALSGSSQEQTSQSSS
PSGSETTGSLDNEVPEETSINTQMSGAPFNGEGKHRESTAGNEDTTKVVSAAVQSNTATPGDSDSTTEV
SHTTSPLLLLLLLVVACAAAAVVAA*
>Tc00.1047053507295.20|S102|AML-VF-C-|1
MAMMTGHLLLVGAICVLWCGAVFGHAMDDYCSEGGGNGLRHTSNSGNEGVSIKADCGLLSARVGLINAV
EAGEKDGEGLSGGTGPLGKTKETLQDNKLENKTLGKEATGSGGGGVAVQPPAALPLGSGGSDTEEQRQS
EELDTKGKEAGGKGDEKGGKATESQQKRADQPSSSGSDGPQGDKEPNLKEKSESTESSVDTPTQEDEVE
TEETNVSEEETGVDEENNNNVALTVTSESQVKLKEIQLPTPPTLPTTQVNERSRTEDSGHVQQPKGVQS
DIESNHNSQTEGAAPITANQHNEPSADHAGSRPPSPTANGDAANNEADKSTEVSTPNNDPAADGTGTRE
EKQNENREANPKESVPATNATTAATGDSDSSTAVSHTTSPLLLLLFVACAAAASAVVAA*
>Tc00.1047053507295.50|S008|A-----ECD|43
MVMMSGHLLLVGAICVLWCGLSGVAADDAGDVGSLEENGTGKDENELKGISSPGLSVPKGKEKPAAAAL
GGGGAPDSQGGKDTSMSEEGENILQEHGVNLYVDLPKTNEDENENKGLTDAGLDTRNQAAPPTPLPGTS

GESPEPPLLPAVKGPPASPGVSSQEPPTQASTKLTVPVQPAELNTAGSVTPVQSQGGPETMQPTQEPPK
VSSIPDTGTQKDSLTEDRAEKTLSPAGTNDTTDDHSEEEIVEESPGDAAESGVVLTEGNESETPGSGSK
ETKTSHTKFEESNAVTPGNGESSPTAPPAGESDAATTTTPNNHDARSLNNNGDNTFTEELDQKAATTKP
KSAPESTDTAAANSEASTTAITISTNTKNKTTTGDSDSSTAVSHTTSPFLLLLFVACAAAAAVVAA*
>Tc00.1047053507357.90|S117|ANP-VFECD|7
MAMMMTGRVLLVCTLCVLWCGVFGIAVNDAGGVSDGSEFEYLFLNWKELLKNECEAENSNEKNLSSKNL
AVNCCVHRAMHELCKGVYSNLFMETEFPNVEGVCKKYAEKPDEVKCPKQQTQLSPVTENSVKVSVPEAL
GNEGDLGKTPEEAPLADPPAKPTKGPLSSPVGGQPANADDVPVPNSEKSPVSTKSTNDSREGDTETITD
TDQEETSTSEAESATPTPPVASDNDDSNEKDTDTGEEVPNNAPESDGAETQEEKQDENKEANPKETPGE
ATATKTTTPMTGNSDGGTAVSHSTSPLLLLVVACAAAAAVVAA*
>Tc00.1047053507429.20|S089|AG---KECD|6
MAMVMTGRVLLVCALCVLWCGAGRVDASNLENNAVGGCMASGVLNTNKSYTPSGCDKTALTLPLRSVVS
ITAVEASTDPLVTGTAENKSDLAPTSGADFGGAGSPPGRGGEGGGGRNDDAGGPGGVGGASGSQARGRK
SSGGGGGGSNGGSKARFGGSLKSPASDVKSPSPVLGDGGSSPGAPTGSVGSDGSKGFILGSFSSGGRSQ
PDVGSPGGDASLSAPVAGGNSPPSITDESDALEKTGAAASTKGRKPQEAGEQSEANRARNELPKLSAPA
ESTPEAQEDSPSKQEKPESEAAGRAATGDEKRRSDAEAQGPSTVISTASSPPLPPPAPATVGEERPTAV
AVPAGGSPTAQTGSQTLTEERTKTSPSPNKKEPEETEPTSGDGVAEQQGQGTVLPDLKGGPTGSPAEVT
ASSNSTSGSGDGQSKADENEYNSEGPNPRGPHNDPEASHTNVAPTASETNPRTAKAAATARTDGTATPG
SSDGSTAVSHTTSPLFVVACAAAAAVVAA*
>Tc00.1047053507437.10|S012|A----REC-|10
MAMMMAGRVLLVCALCVLWCGAGGGCEEGEVAVVAGSPGNVSVVTPNSQLELPLLEGQASNIQSPKVGK
ELPTVAGVSSEITEKNNAGGGGGENEELQERQRQGQAGGIRHDGQDGAHKEEDRQEEQEETKKKRVKDQ
NSHESDPVKLAELPLNQIKDSPSHSSNDVEKSDKKISGIATPLGNGDQLQDALRPLPNASTTLSTEENT
SFYSTGSGGDDNSHEKNNDANNAPQSSSTGIEQQDTEPHGKSITFTDSGEASKLPVTTVTKTSDTVAAG
GTPSAAMALQHNTGMEDIPATPDSSQPSTGGAEQPSATPDREEASDSTENGISQSAGSATEAMTTAKTN
DTTTPVDSDSSTAVSHTTSSLLLLLHAAAAAVVAA*
>Tc00.1047053507487.20|S080|A---YKECD|24
MAMMMTGRVLLVCVLCVLWCGAGGGGCDDTPQALLSGSGGGTVVGTGVGQSGGADNALFASETNGESEG
HRLEGTDFGQINSSPRGGTVGLENKLAVIPAGSPVTRNQLLSNEALSLQSPPSPKPSAPELQDLPEGPA
VSGGSQGGGADNAVGGVVGPSGSSSGSGVKSMVSASFSAGTLSPPNPVDGDVLQGGKGTTATLSMDSSE
ESFKSQSAEPPAPAQPNLDRQEASTSNAENHSSIKPHTAGNQVVNGGATGKENKQRAAVTGGPSSVTQS
TTLQPAPQEQPKTELIIVPAGKERTTDPHSREKEERDSKKAPPPPPANSAGGTPAAKDLQISTEEMHQT
SPSETQKELLGQETPSKDDAEDQNTEGTATSDSVKDEAASSLVETTASPISTSGGADTKSVASKDADNA
QQPNHKETHKDPEPQNTNPAFTATEALPQTAIPLTTAPTDDKTTPGDSDGSTAVSHTTSPLLLLLVVAC
AAAAAVVAA*
>Tc00.1047053507523.60|S013|A---V-EC-|8
MAMMMTGRVLLVCVLCVLWCGAGGSCDVEVPPAVEPLVHPASGSGVNGNASGHTVTGEAEVVSLQQSRL
DNVGNSAAGYPQLQAALEPESPTEQPQSDPEHMVPSTHSQSSGEGRQDGTPDGQPGKPGISPSQEDNKD
VSIENQQSNDPPSHSGNDDVVSRNSGERTEDDSRRAETLVVAPSEEGQEPENVTPSLEQPLETSTAAPA
VTTQTTSITLPEENESNTVKMNDAAPHSTVTANTNHTVTPAENDSSTAVSHATSPLLLLVVVVACAAAV
VVA*
>Tc00.1047053507523.80|S070|A--TIFEC-|13
MAMTMTGRVLLVCALCVLWCGAGGGGCAEAPSSAPPGSSPDKNPQNENDTTRGAAEGDQNGEQAAPQVP
TSPTNSESQGVPANPPHTIQPEGASETTSTTKGSKDQNAQEGKKGEKEEKEKDDEDEAEEEKEVEVEED
EEEEGETKKGGVVASTTEVTSAVSQEQPSFSSGAAGASNITNPNSTQTTGDDDPAADVSGTREAKQNEN
KDANPKETPVEATAMKNTTATTGDSDGSTAVSHTTSPLLLLLVVACAAAVVAA*
>Tc00.1047053507687.70|S103|ANP--F-CD|11
MAMMMTGRVLLVCALCVLWCGAGGGFANEAETSANGVASKTTPADKIILNWYELTQEDCATDNTKNGTV
NVPAMKSCINFAMKGICDTFYNKTPSEIHGPEVKDMCTYYAAIPDEPVEPPTPQGPPSDLAVSNTTSNE
GTPKNAPEFDVAERREGKEDEKEHGNTKEKAVETAAVKSSTKTTDSDGSTAVSHTTSPLLLLLVVACAA
AAAVVAT*
>Tc00.1047053507699.130|S010|A----RECD|22
MAMMMTGRVLLVCALCVLWCAADGGCEEASAGFQSDASGDLVGEGVDSQDSPRPETPGSHTAGPETPLP
NVQGQALSPPPEVTVSGTEGAAEEEKARRNEDVKLVEKEKEGDGTSQEVKEPENKLISVKHRQSHDNEG
LQPPSLNGTHEAETITPSEDSLQVNKDKQELPSPLQLPLPNSAADGNPSSTSAAGRGDEKSHENGNGTR
NSQQSVAEDIEQNKDAGEKVVAPTGGEEDSRLPVMTVEEMRGATTKGNSGSSTTAATAMQSDTGTEGTP
TNNHPNRLSIDSDTPPGTISDGEAASANKYDTVSQSAGSTTAPTTNAKTGETAMPGDSDGSTAVSHTTS
PLLLLLVACAAAAAVVAA*
>Tc00.1047053507747.170|S017|A---S-EC-|13
MAMRMTGRVLLVCALCVLWCGTGGRCDEEGTAGSGIGGRPPPESKQLETSPEGPQGLKVEVPGGEENVT
PASSPPTEEKDDDENDGEENDEGAERKAEEEKSTEMQNVQEGTDAIGSGSREKNLGGSRLEKNQAIVSA
EGISHSGSQESNANSTQTEFEGKKDADENTPAAEITLTTGNGENTVPRGIAGVNLPSPPEEGVDSREQD
SEDTTSEGEKNVQSPETAATPQSHRDKGSEGTGEDTKATTVTANTTDTTNTQNSDGSTAVSHTTSPLLL
LLVACAAAVVVTA*

>Tc00.1047053507803.10|S010|A----RECD|22
MAMMMSGRVLLVCALCVLWCGADEIYAEGDLEGPLAALSPGLAPSSPGDVGSLDNTGSLAGHGVGVGRS
EPLENAVSGGDVSEDLLNSNNDDEESCSADEESGCGSEDGHRRQENRDEVAEDEVRIMPQNDQSEITPK
GPQIPAREDNAAQLQQKQPPQGVHLTSAAHERAQDASELRTPLSKNLSQQKTGAVSSQFAIHTPTDNEE
GKIPSPPPKSGSDTSNSPEQLVAAKKERGNQREGADDSPTESKEDKNPPATTRKTDAENTHSSVSSSAA
DTTPKPDAVTEENPPATDSSRTSSEDAEQLTAIPNPDDASDSTENAATQSAESANKTNDTAKTAESDSD
SSTAVSHTTSPLLLLVFACAAAAAVVAA*
>Tc00.1047053507833.10|S070|A--TIFEC-|13
MTMMMTGRVLLVCALCVLWCGAGGGGCSEPTQVSQDITSVNENGPKTDNDSSGGAGGGGKNGQSAQSQP
AGVSVQGANEVGAALRTGTQAPETADAEKKNQTEKGKDSMVQNTDDEKKQVEENGANEEKEDRNKEEED
EEVEEDEEGEEEEEREEKEEDGTKGKEETMKGADTSTTEVISAGNEEQPSLSSGAARASNTTNTNSTQT
TGDDHPAADGAGTAEGKQNENKDANPKETPVTAAAMKNTTATTGDSDGSTAVSHTTSPLLLLLLVVACG
AAVVAV*
>Tc00.1047053507859.60|S095|AGWTH-EC-|7
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDTNALGVCITSGVLGENGSHMPDGCNKTVITMPLRSVLP
ITAVEASAGEGASPSASAGAAGASGASSGAVDTGGDSDAGGGGGTSAGGQGSGGIPPAPAPPPGPSGGG
GGNSSGSAPVHPPSPPGPPPAVSPGALPPAAPAVDSSASSSGGEAGSSGSNPTKTTGDSSTGDQSSAAA
AANDSSPPEGPAGTTSGAEHTRQEEEEKEEEGEDHEKQQQSDEAQVQQHQQHEHPAENGEESAKDTNAL
RTNATANTGDSDGSTAASHATSPLLLLPLVVAAAATTAVVVAA*
>Tc00.1047053507953.40|S004|A---V-ECD|18
MAMMMTGRVLLVCALCVLWCGAGGRSDGGKTAGSESGLSNRGGDEDSESASGQTASGEAGNPTVQQMQL
NNVGGHPLVAPPLQADLPPESTTQQTPSSSEHTDSLSHSQSLQEERQGGSPDGSSGEPETSPSQEDRKN
ESIGDQPRNDPPSSSSNNDVVSSNSEERTEDTPRSTEIIVAVPSEEGQERENVTPSLEQPRETSTAAPA
ITTQTSSMTTSDDGESNTVKMSDASLQPTGTANTNVTTTPAENDSSTAVSHTTSPLLLLLVVACAAAAV
VVAA*
>Tc00.1047053507955.20|S001|A---H-ECD|18
MAMMMTGRVLLVCALCVLWSVVADGDVGVVSGGDDNSLKELFIPVARLQERPEQRAAGATADAKAAAAA
KASAEAAERAKIATAKASAEKAAAAATEADAKTTAAKTAEAAAEALRGTTIREQEVKTAIHDQDNSVEH
HSGEKQELLQEQEPERQEKEQHEKQQHQQREHSAGNGEESPKEKTANGTNASAITDDSDGSTAVSHNTS
LLLLLLVVVACAAAAAVVAA*
>Tc00.1047053507957.10|S064|A--T-KECD|5
MAMMMTGRVLLVCALCVLWCGAGGGVTEINDESLGGSQLLSGVGEEAPKGLSEPGERGSDSPGHPLNKN
NGNNSNLQEGTVTGTTADRVGKEEEVDDNDDLEEAEEEERSKEKEDAQQTRKSKRSSKEVATTIPTASG
LSEAGGGSPSGVDGVGSSESSDGSEDLNLEAPGLVVNFPPSLPNAAAGGLQDTDGALSPQKNNFSETGV
HSGTTPPAPSLPKSQAPAITKPEAEEQSSTEQDTEDSPDTEEVTTGKDNVQNTVETGIPSRSSSAASKP
PVQQTTPILTQPPAAPSPERSALAPSEKKSTAPSFSAGEGSRRATNVAQNSKEEKNEKLPSENETESKA
VEQPSGDDLAEQDSPARTTASPIPASGGADAQRNADADNRNAQALKYEGTHKNSETGYTNPASTIGDAA
TQTEKALADAKANDTATPGNSDGSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053507957.150|S074|AML-YKECD|9
MAMMMTGRVLLVCALCVLWCLTVFGAARDNRCVEGDGNVLTHTHNGGNNGLRLKADFGLISTRMGLIKA
VEAGEREGEELESLDAPLDSVGGKSPSSLLAGSGDNEAPGAGGGQGAAGAGAASLPSGPGVPGTGDENR
QSLMAGQKGNEKNNLDPGSKEPRESQDQTTDQLSSSSGSTSTRSGENPSSMGTSGVKQLPRDTETKGDV
DPRNNSGDDEEREDEKTGREKQKNKAQTGSRESKNNGGETTPPLLPSSEGEESPLPDQENSQNPKKITN
EATPSGPTMESKAPEQPSGDATQGQHSHDTDTEDSTKNAATGSPAEPTTSSTSTSGSGDHVQNKADKDD
AQSSEEQHDSLETGNTNVVPALSEAAPQTAKTTTANTTYTVNAQNSDGSTAVSHTTSPLLLLLLVACAA
AAAVAIVWV*
>Tc00.1047053507957.160|S017|A---S-EC-|13
MAMMMTGRVLLVCAFCVLWCGAGGRCDEAEDTAVSGIGGESPLASKGIETSPEDTQELRRGAGGVEGNV
PSTSSEDEVEEGEDDDDDKGGEDGEGKRTERQSVQEGTAAPEPGSRENNISGSDQEKNQSIAPAGDISP
SGSRESNANPSQPEFEKKNDTGKNPSAVENPLTTVNGENRLPGGIAGGIPPPPPEDGVNSREQDGEDTM
SEGEKNVPSPETAATPQSHRDKGSEGTGEDTKATTVTANTTDTTNTQNSDGSTAVSHTTSPLLLLLFVA
CAAAAAAAVAA*
>Tc00.1047053507957.200|S001|A---H-ECD|18
MAMMMTGRVLLVCALCVLWCVAADGAVGVVSGGDDNSLKELFIPVARLKVRQEQRAAEATADAKAAAEA
AEAAEKAKAEAEAASEAAEKAKAAAEEAAVKTTAAVEASAKAAEAAAKAKTLAETAETATEAADAKAAA
ETAEKAKAEAEAASEAAEEAAVKTTAAAEASAKAAEAAAKAKTLAETAETATEAAEKAAAKATAASEAA
EKAKAAAAEAAAKTAAAEAAAAEAKTSAETAKMATANAATAAAKAKAETEKAAAAAAKEATTKAKAAEA
AKDEAAKAAAAKAAEEATAAKDEAAKAAATAKTAAEEASAKAAEAAAKAKAAAEAAETAKASAGKAAEE
AAKAAAEAAATAAEAAAEAKTSAETAKTATANTETAAAKAKAETEKAAAAATEADAKTTAAKTAEAVAE
ALRGTTVGEEEVKTAIHDQDNSVEHHSGEKQELLQEQEPERQEKEQHEKQQHQQREHSAGNGEESPKEK
TANGTNATPITDDSDGSTAVSHTTAPLLLLLFVAFAAAAAVVAA*
>Tc00.1047053507957.220|S078|A--TYKEC-|2
MAMMTGRVLLVCALCVLCCGAGGRCDEGEAAVHGVPPDVPASGTEDGLGGKRNAAPAPDSQIQSSGEEQ
QHKSREGRPALPEGSSEEEEEEEETVEDENLDEVTERREERRHEDGQDANERDGSQTSGVLTKQKETPS

PSTPAAPAEEGNQHASPQAPSVDSHGGGRTDRIEGSILKAPSSGVALQHAGDASTNQKNRSLETGKHAE
NTITGGPVPSQVKAPKESINDAENHSVTGEDTASNQVVGRGTTEYEAQQRALATQDRSSVSFPDSETKW
HTTPQETPKTQVPPSATEPSSREGQPPTATTDSQTPNAQEHKKLLLPKKTEYNAPEHTSEDIVAEQQGQ
ATATENLTENAPATNQAETTASPNSTSGSGEARSTADENTANAQRPNPKEPHEDLEGSDTHPAPTASEA
APQTAIKPTTANTTDTAAPGDSDGSTAVSHTTFPLLLLLVVAAAAAAVVAA*
>Tc00.1047053507957.240|S112|ANP-V-ECD|4
MAMMTGRVLLVCALCVLWCCGAAVVSSIPDVTGRKNVPHGYLVVNWEKLLKNECATDKKYINEDGTVNE
SAVKDCIRDAMRVVCNVFCRKNSGEPDDSEGERICEEYVGSRDEAGQSSHLITPAEAKTLKAPRSELEE
LGKTPGETPKPLSGGPATEDEAAKTTGGPPTPPVEAQHNREENVPVLHPEDEPGTTESNSDSEEDDSAS
TKDNQESVTPDGHDKSTPTLPSTATDTVKNEADRINTEGTQKPATESNAERKEIEESDEKIYENTKKIP
AEAAAATHNTVMPGDSDGSTAASNTTSPLLILLLVACAAAAAVVAA*
>Tc00.1047053507957.280|S004|A---V-ECD|18
MMMTGRLLLVCALCVLWCGAGGGGCTEDTAGSESGLSNRGSDEVSEGASGHTASGGAGNPSAEQTRLRK
VEGSAPGSPQLQADLKPQSPTIQAPSPSSSEHTDSLSHSQSSGEERQDETPEGPPGEPETSLNQEENKD
VSIENQQNIDHPSPSGNDDVVSSNSEERTEGTPSSTEIIVAAPSEEGQERENVTRSLEQPQETSTAAPA
ITTQTSSTTTSDVGESNTVKMSDAAPQSTGTAQTNDTTMPAENDSSTAVSHTTSPPLLFLVVACAAAAA
VVVAA*
>Tc00.1047053507957.300|S105|ANP--F-C-|4
MAMMMTGRVLLVCALCVLWCGAGGGFAKEAEASANGVSSKTTPADRIILNWHVLMKEECATENTKNGTV
NVPAMKRCIQVAMKGICDTFYNKTPSEIHDPEVKGMCTYYAAIPDEPDEPPTPQGPPPDSAVSNTTSNE
GTPKNAPESDDAGRGEGKEDEKEHGNTKQKAVESAAMKHITKTADSDGRTAVTHITFPLLLLLLVAAAA
ALVAA*
>Tc00.1047053507957.320|S068|A---IFECD|10
MMMMTGRLLLLCALCVLWCGAGGGGCSEADLALPGTGLTDNGNNSEGKNNTTDGVGGGGPIGQPAASQP
AAPSSVPVSETKAESALKTGAKASETAEETIEKNKKTENGGNGEANQDADEEDEGEDEGEDEEGEEVEL
GDGKEEKKETEEEKKQEEKDDTRTTKRISAGGQEEPILSSRVEEASNKTKPQSTQTTGDKDPAADGAVT
QEEKQNGNKEANPKETPVESTVMKTTAATTGDSDGSTAVPHTTSPLLLLLLLVACAAAAAVVAA*
>Tc00.1047053507957.179|S001|A---H-ECD|18
MAMMMTGRVLLVCALCVLWSVAADGDVVVSGGEDNSLKELFIPVARLQERQEQRAVEATADAKAAAEAA
EASAEAAERAKIATAEAKAAAEAAAAAAAEAAKAAATAAKAVDTEAKAKAAAAAAESAATKATTASEAA
TKAKAAASAAKAATEAAAAKAEAAAAAKAEEAEAAAEAAKAAAKAAATAAETAATAAEAATEAKTSAET
AKAATAKAKTEAEKAAALKDDAEKAAAAKAAAEAAAAEATAAAEKAATAASKATAAAEKAATATSKAKA
SAETAKAKAAAAAEKAAAEKAKAAAEKEAEEAAEKEAETAKEGAKAASTEADAKATAEEALRGTTVRAE
EVKTATHDQDNSVEHHSGEKQELLKEQEPERQEKEQHEKQQHQQREHSAGNGDEAAKEKTANGTNATAI
TDDSDGSNAVSHSTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053507959.80|S034|A---H--C-|4
MTMMMTGRVLLVCALCVLWCGAAGAAADVSEERVDLSSSERSQMLQNVLSEPTDGKESLEHNSCLERLG
SDVNTAECTKAKTNNSDAISTDPLSPSHAPSNPNPEKGLQPVAPPTGPVQAHQPNLMHVKGVVEEVREE
DEEGKRKKELEEQNKHQNQESHENPSSREKPSVLKGNQPVGQEATLQGDSAQQGRKHQEEAPVQIQQEK
DVQHRELSQHDQLLQGHQEGQEGRRPDEEQPQILKAQKEKVATASSTGPNLTQQSPPHMKINGLQQEGS
AASSSEQLKEEIPSVSTESKSNGTIDPPSPQASEGEGGAPAALQTQEEDANIRQVVEFSETAAREEDHQ
HEHPPDNYGETTKEKPAVVTNNTANKNGGDSDGSTAVSHTTSPLLLLLVVVACTAAAAVVAA*
>Tc00.1047053507959.110|S008|A-----ECD|43
MAMMMTGRVLLVCALCVLWCGAGGGFGEGDDVTELQDEPSRGSQSASKGGHEEKLNIRNPVGGVLNTSG
GPLVAQDLMKDSPQQNSVKQPPRNNGGAAGKEEKVEVKKVGDKVTGSDGEEPPKDHSEGTQESDGPKEN
ERNPSPTPAEKMLTSGDKTAEHAGQAGQAIRPPQSPESDGTRPGGSSREDSSVSPLSTAGISSSSAIDA
PFVQSTQPSEKGPQSEAMSLGTALPNEQPKERSGSKAKQGSSTSEEAAESPDDSGDAVEKEKEKGDIGP
KATTSLSSTTSNPLVTQTTPRSSSTEPSPTETELQAGEETSTENVTITKRNDTAATGDSDSSTAASHTT
FPLLLLVVACAAAAAVVAA*
>Tc00.1047053507959.170|S130|ANQT--ECD|2
MAMMMTGRVLLVCALCVLWCGVFGIAADDAGGADGSAVEYLLSRWRAQLRRGCAVEVSRRTGGGANASA
VEECVGRGMDGVRAVVDGRSRWAHQRSVIVATSAGDNSDDYKVPGSLPEGQSGSVAQLPVQQPLKPAPS
SVPGSTDNATEKNKPTNPAQPLATGENINGELIEVKRDDEVKKEESEEEEGEEVEETDDEEDDNAGSGT
SDGSQEQGKQKAGTGQGASGGTGKENGNVVAGSKLAEGAAASPPVVSVDVENPKSVELTRDDVGGKRQT
HEKTVQEPPAVKLRENVPAELISTEDAAEGEKQKAEEKAEEAETNEEQKTTAKKLREETPTAPEKKTKE
EQKDKEVQHIQSKNEEKETDGAEPTAEKEADVEKTAAFKNINMNNITKPGDSDGSTAVSHTTSPLLLLL
VVVACAAAAAVVAA*
>Tc00.1047053507959.210|S010|A----RECD|22
MAMMMTGRVLLVCALCVLWCGAGGGCTEGGETPVESKLGNTASGAEVLQAKPETAESGIPGTQPQVPID
NEEAKRLIGEGSLEGSEDNVVADTEDLSEDDEGGEEEGNEETQRKKLNGRQEEHEEKGPASGLDTSNGS
SIESQLQTLQTNSSTGSSPPSSSLKAIPDPTQTGIKENGVSVTNPPTGEETLKEDTRDNVPHGGLAKLT
LPPPPEHSAAASGIFAEYKKDEGQQDANLHSTATTVQDSQDDTTKNTKKETIPTAIKTDTETTQHNDSS
PAELTAPQSDAGVESTPSTNYSRHSSTEDAARLSETNDAEDALGSTENADSKIAETEKAPLATANTTDT
TNTQNGDGSTAASHTTSPLLLLLLVVACAAAAAVVAA*

>Tc00.1047053507959.260|S001|A---H-ECD|18
MAMMMTGRVLLVCALCVLWCGAGVVVTDGTGMDAQASVAQPGPSEPQITAGGNGENEGEKDVTKNEEHK
LSKQEKDDVEKKNQEQILPEEHDQALKNKAAEKPAGEPSEEIKIDVDSEVEEEISLVDGGTPKQDEKEL
GQEAVEVVLGKDDSPVNLTVSRQEGSGIHAEDLEGKSEHEGEKEGEQHVQHQEENKGKKQDKEDTEEND
QMLQQQDQGLEHTADKQKGSKKDEKAVGTADTARTGDSDSSTAVTHTTSPLLLLIVVACAAAAAVVAA*
>Tc00.1047053507959.280|S008|A-----ECD|43
MAMMMTGRVLLVCALCVLWCGAGGSCDEEKADEFCNNTYFGVLTLLANKSDEELKEKYCKKEDDKAKCV
NTLKNNIADALENEKKKKDNGADREPNVAHGAGVPVGSSKTKSSTAAGADNAGMSSPLPLSLKVEGDVD
AQIHNPAGGAGHQPHFDDGRREAERSHHSEAEGSNQHGVGVQGKTIHNKDEEKPQAGLKSTEAREGTDG
APAPSQDPPNTAESHEDKSRRVAAPDTTPALNTSPGSNREQTSQSPSPSGSETSGSSDNEGPEKNSINT
LMSGAPLKDEGQHRESTAGNEGATTVESAAVQSNTTTPGDSDSSTAVTHTTPPLLLLLVVACAAAAAVV
AA*
>Tc00.1047053507959.300|S082|A---YKEC-|17
MAMMMTGRVLLVCALCVLWCGAGGRCDEEETAARGSGGGPPPGSAELQTSPQDTQELKVGSPDIKVEVP
PESSPHIEVAGGEDSDDENGEEKDKKDENEKNKVQLQTHKGKNNEGVPPPPPPPPQPPAPPSGEPAPSS
TAGEGGPTAEKESSQKVTKAKNENTPSEFKTDSEAPEQPSGDATQGQHSHDTDTEDSTKNAATGSPAEP
TSSSTSTSGSGDHVQNKADEDDAQSSEEQHDSLETGNTNVVSTLSETAPQTAETITAAQTNHTATPGDS
DGSTAASHTTSPLLPLLVVACAAAAVVAA*
>Tc00.1047053507959.350|S032|A---H--CD|8
MAMMMTGRVLLVCALCVLWCGAAGAAADVSEERVDLSSSERSQMLQNVLSEPTDGKESLEHNSCLERLG
SDVNTAECTKAKTNNSDAISTDPLSPSHAPSNPNPEKGLQPVAPPTGPVQAHQPNPMHVKGVVEEVREE
DDEGKRKKELEEQNKQKNQEGHENPSSREKPSVIKANQPVGQEATLQGDSAQQGRKHQEEAPVQIQQEK
DVQHRELSQHDQLLQGHQEGQEGRRPDEEQPQILKAQKEKVATASSNGPNLTQQSPPHIKINGLQQEGS
AASSSEQLKEEIPSVSTESKSNVTIDPASPKASEGEGGAPAALETEEEDANIRQVVEFSETAAREEGHQ
HEHPPDNEKETTKEKPAVVTNNTANKNGGDSDGSTAVSHTTSPLLLLIVVACAAAAAVVAA*
>Tc00.1047053508011.110|S100|AML-VFEC-|15
MAMMMTGRVLLVCALCVLWCGAVFGHAMDDYCSEGGGNGLRHTSNGGDDGVSLKADCGLLATRMALIKA
VEASDAGQDELSGGPGPSQDTGEPLQNDTEGSAAPGPGRDVAGPAEAAIPPTPGGSGTGGQEEKPGVLG
PNDGEHTDNKKNTSETHLEKPRTNQSSSSSSSGSLDPEGAKGLSLKTKNKSDESSDETPTEDEEDHINK
SDSREVVLKEQINEIQEVRKGKIIHDAPTETRGSPANDAGIQTATPPPPPATMNGPSSTEDLPPVQPLQ
RVQYDKAESRPPSPTANGDAANNEADKNTKEDIPNSDPASDGTNTAEKKPDENKDANPKETPVEATAMK
NTAVNTGDSDSSTAVSHTTSSLLLLLLVVVAAAAAVVAA*
>Tc00.1047053508047.20|S049|A--T--ECD|5
MMAMMMTGRVLLVCALCVLWCGAGGCAEESAGGVLPGASGGGAKSLQGSQPIVPEVLKNSDLKASDIND
KTEETLIKVSLAEQEEISDDDDEGEDEEEGPSPPTPPKGGGVQPQANNGKLKKANESEPQKENQRHVEV
ERQNPSEKETVVDEAEGTNEKEAIGLQPQQQKIPVREQDTRNGEGNQPTQGNEEQTIVEEITPSNPAGD
YSPGEHKGSDGSKEMEEGEEGGVEGYEGRNERHRDQVREEAVHVSGTPKVNSTDIQQEVQRTHAGETPT
GIKQKAEEEKDDETEAEREQQKKQHQGNPTDKKQGFTSGANATNKINTTPGDSDGSTAVSHTTSPLLFL
LLVACAAAAVVVAA*
>Tc00.1047053508047.70|S098|AML-VF-CD|2
MAMMTGHLLLVGAICVLWCGAVFGHAMDDYCSEGGGNGLRHTSNSGNEGVSIKADCGLLSARVGLINAV
EAGEKDGEGLSGGTGPLGKTKETLQDNKLENKTLGKEATGSGGGGVAVQPPAALPLGSGGSDTEEQRQS
EELDTKGKEAGGKGDEKDGKTTESQQQRADQPSSSGSDGPQGGKEPNLKEKSESTESSVDTPTQEDEVE
TEETNVSEEETGGDEENNNNVALTVTSESQVKLKEIQLPTPPTLPTTQVNERSRTEDSGHVQQPKGVQS
DIESNHNSQTEGAAPITANQHNEPSADHAGSRPPSPTANGDAANNGADKSTEVSTPNNDPAADGTGTRE
EKQNENREANPKESVPATNATTAATGDSGSSTAISHTTSPLLLLLVVVACAAAAAVVAA*
>Tc00.1047053508081.30|S117|ANP-VFECD|7
MAMMMTGRVLLVCALCVLWCGAGGGAADDAGSAGEKLLSNWQKLLKSECETDNTSKTDGKLNESAVNCC
VHHAMRELCNDVYGKILNETEDSQVGGICKEYAGKPNDADKCPKPQTEPSPGTGATVGVSVPEGLGNEE
ELRKQSEEAPGAPPEDLDPKPTGLPASPPVEGSPDKAKDVRVPNSEEGSVSMEPIKDSAEGGIVPIADT
DHNEASNGQAESTTTTPPDASDNANNKTEKGTGENIPNNTNESDVAGTEGKTDENKDNNPNETALHVAG
IKTVTTTPGDSDGSTAVSHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053508081.50|S117|ANP-VFECD|7
MAMMMTGRALLVCALCVLWSGLSGIAADDAGSAGEKLLSNWQKLLKSECETDNTSKTDGKLNESAVNCC
VHHAMRELCNDVYGKILKETEDSQVGGICKEYAGKPNDADKCPKPQTEPSPGTGATVGISVPEGLGNEE
ELRKQSEEAPGAPPEDLDPKPTGLPASPPVEGSPDKAKDVRVPNSEEGSVSMEPTKDSAKGGIVPIADT
DHNEASNGQTESTTTTPPDASDNANKKTEKGTGENIPNNTNESDVAGTEGKTDENKDNNPNETALHVAG
MKTVTTTPGDSDGSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053508081.70|S117|ANP-VFECD|7
MAMMMTGRALLVCALCVLWCGAGGGAADDAGSAGEKLLSNWQKLLKSECETDNTSKTDGKLNESAVNCC
VHHAMRELCNDVYGKILKETEDSQVGGICKEYAGKPNDADKCPKPQTEPSPGTGATVGVSVPEGLGNEE
ELRKQSEEAPGAPPEDLDPKPTGLPASPPVEGSPDKAKDVRVPNSEEGSVSMEPTKDSAEGGIVPIADT
DHNEASNGQAESTTTTPPDASDNANNKTEKGTGENIPNNTNESDVAGTEGKTDENKDNNPNETTLHVAG
MKTVTTTTGDSDGSTAASHTTSPLLLLIVACAAAAAVVAA*

>Tc00.1047053508081.90|S117|ANP-VFECD|7
MAMMMTGRALLVCALCVLWCGAGGGAADDAGSAGENLLSNWQKLLKSECETDNTSKTDGKLNESAVNCC
VHHAMRELCNDVYGKILNETEDSQVGGICKEYAGKPNDADKCPKPQTEPSPGTGATVGVSVPEGLGNEE
ELRKQSEEAPGAPPEDLDPKPTGLPASPPVEGSPDKAKDVRVPNSEEGSVSMEPTKDSAEGGIVPIADT
DHNEASNGQAESTTTTPPDASDNANNKTEKGTGENIPNNTNESDVAGTEGKTDENKDNNPNETTLHVAG
IKTVTTTPGDSDGSTAASHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053508097.60|S012|A----REC-|10
MMAMLKTGRVLLVCALCVLWCGAGGGCKEVPAHPDSDASTDIERDRGQSQDLSLSETPESHTPGSETLV
TNVQQEEVLLPLLEFSQAGTEDVAGKEKARKEDVTKEIGKDEKVGETGKGIQKPEDELISVKGQQSHDK
EGLRPQLLNGPHGVGTATPSRGSLPVNKDQRELSNPLQPPLPNSSPHVIQSSTSAAGRGDDKSHENGNE
TKNSQQPVVGGIQEKNGTGVKAVASTSGEENSRLSVTTLEEMSDATKKGDSNSSTAATAALRSDAGTEG
TPTTNHPKQPSTEGATPPGTNSDGEAAPANKYDTVSQSAGSTTAPTTNATTGDTATPGHSDGSTAVSHT
TSPLLLLFVVACASAAAVVAA*
>Tc00.1047053508109.10|S045|A--TH-ECD|2
MAMMMTGRVLLVCALCVLWCGAAVVANGDTDDLGTGRDDKNAEHLSSSDLSLPVRQGETTAAAAGGGGG
GGGSTNSQEGKEASMPNTDIRVPQEQEVKLDAGPRKPTGNEYENKGPTEAGADTRNQPAPPPPLSLSEE
GEEDELKKAKQDQDSPVEHESTQNNKVLQKEEPGHELSTQNPLPQEQHTFKQLQVKQERGKEKQRSGQL
EQREHREELKDQQEIQEKQDEESIKHEEEQQQQKDEIQDQQHQQHEHPTENEEESAKDENAVRTNVTAN
KDDSDSSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053508109.30|S104|ANP-VF-CD|10
MAMMMTGRVLLVCALCVLWCGPAVVVSSAPDAARAQSVWPEYLFLNWQEMLRNECEVENPYEKNVGLKK
LAVNCCVHDAMRALCSAFYGTTVMENKDPKVEGICKEYAGKPDDVADCPKPQTNLSSAAVNSVKVSVPE
APKDEEEELRKTPEEVPTPLPGTPLADPPAKPTKVSPSPPLKGQPTNAEEVPVPNSEEGSVNTEPTKDS
EEEDTDTDTDTEQDEPSNSQAESTTPTPTVVSDNDDNETDKSTGEDTPNNAPESDVAGTEENQEENKKN
KPKERTLQVAGIKTATVTSGDADGSTAVSHTTSPLLLLLLVVVCAAAAAVVAA*
>Tc00.1047053508119.20|S030|A------CD|31
MAMMMTGRVLLVCALCVLWCGAWLCDAAETSSSALHRDNAEERMNPEEVTEAIEKLAEGVLYMIRESCR
MSFLTSKNATLPAHNDTEVEKCVNKTAVDISGVTSRGRPAAATADATLASPLPSSSSATSALQGQAQGS
PGAAPEPVKPPQTDPVNNEQLSETPASTGGGAGGDGELTGRSSRTPTDVAKTHEARPAGNATSTPTATQ
RDSERSPANTTRTRETNETDDSDGSTAASYTTSPLPLLLLVCAAAAAVVAA*
>Tc00.1047053508121.110|S025|A------C-|17
MAMMTGRVLLVCALCVLWCGVGGRCDEVADSGVAAGKGNGGRSAVEPAGNSEPVPDASDLRIDVLNVNQ
ATGTSTGKSLEGKKVNTDQQDVLSREDKKDGGPSENLEEPVEDAPGNEKTNLKLKKEEQEGIQPLQSQS
NVSPHPQPIPQQSQSQRQPQPQRERED EETKRQLQPPSAPQPHISASEKGEGVGENNTGGEGQSPLGVQ
DIGNEDPKAPRKGDLLEGPGTKSESSEQVQTTVPNTVTPEHKTQNEMLTPEQKTNESQSTDTSTNIPEL
QKENKEYPASTEATAQSTSTGSQEQEAEPSTSEEFSPFEEEESTGTKTTEDAQTPDAAATEKRQTGDNE
KVGDSDSSTAVSHTTSPLLLLLVVACAAAAAAVPRPA*
>Tc00.1047053508125.140|S100|AML-VFEC-|15
MAMMMTGRVLLVCALCVQWCGAVFGHAMDDYCSEGGGNGLRHTSNGGDDGVSLKADCGLLATRMALIKA
VEAAEAGQGLSGGPGLSQDTKEKLDDNSLGTNTVGSAAPGSGRGIVAGQPEASPPKLKGLDTEGQQGKP
EGLGLNGGKEVDKRDHTDGKTTEPQHQRVDQSSSSSSSGSPGSKSGNDGNSENTSERNESSDETLTEEE
NNLRSKSDSPEEKAEEEPKKTGDKKSLSHEAPTETRGSPANNAEIQTATPSLPPATMNGPSSTEDLPPV
QPLKRVQDDHAESRPPSPTANGDAANNEADKSTEDGIPNNDPAADGAGAREEKQNENKEANPKETPVEA
TAMKNTTATTGDSDSSTAVFHTTSPLLLLLVVACAAAAAAVAA*
>Tc00.1047053508143.80|S022|A----R-C-|4
MAMMMTGRVLLVCALCVLWCGVSVANGDTGNDLEHSGQGDVGIVSHSSSSVVGHGDNGVVTDGNFRGSG
SHSPGLAPNGGKTSPTGVVEGVGLKSSKDALTPAEEGRGGMQGQQELVPKVSHQPEAGTTGKSHHNAPE
QLPNAKTELGNGGGATAEGDKVKTTVKDGQLGGSSTNDSHSPAADRGLKEQEGTVRKAASTVALTPAVG
RETPPKADPKEDSPEDKAASSAGVTQDSPTVSQQQTHSSSSSQSGIDPTYTPGEGRDAEEIFNNNQPFG
GVVLKEGAQHETVAGSEKPTIPAANTRNIIGTTISGDSNSSTLTITALRSDAGTEGTPTTNHLNRPSTE
GATPPETNSDGEAVSANKYDTVSQSAGSKTAPTTNAKPVDTAKPVDSDGSIAVSYTTSSLLLLLVVACA
AAVVAA*
>Tc00.1047053508147.150|S008|A-----ECD|43
MAMMMTGRVLLLCALCVLWCTIGVVADGDTEEVLEDFVPPSRTDETQELQEELRSKGHSANDEQVDETQ
LQKPQKEGGGHQAEDPLQPVERSVRAKPQSEGPRVEETGNQIEQEQLLRGTQRSPKVENKTPTIPGDKP
QGGNGEGDVSNEKEKQKGKETISQIKEEVVAPGAGTPEAISIEDHQEASRNLAEKTLVENKDIAKENNV
KKEEKEKKSEQQELQLKQQDGKQVTLHGSPRGPAATQGSLAPVPPEGLQQKQISDGSTKQPEGEAPLIG
TESTSDGTTDPSLPSVSTGAGVAATSESDKREVKVSAIAESNETTANETDDQQERIGKKDRESAKGKTA
VGTNQTTNKDDSDSSTAVSQTTSPLLLLFIAACAAAAAVVAA*
>Tc00.1047053508161.10|S045|A--TH-ECD|2
MAMMMTGRVLLVCALCVLWCCLSVVANGDTDDLRNGRDEKNAEQLSSSDLSLPVRQGEPTAAAAGGGGG
GGSTNSQEGKDASMPITDISVPQEQEVKLDAGPHKPTGNEYENKGSTEAGADTRKQTVPPPLTHAPSPP
PEGPPLLSPSEEEEDELKKATQDQDSPVEHKSTQNNKVLEEEEPGHELNTQNLPPKEQHTSEQLQENQE
NGKEKQRSGQLEHREHREELKDQQQKQEKQHEESIKHEEEQQQQKDEIQDQQNQQHEHPTENEVESAKD

ENAFRTNVTANKDDGDGSNAVSHTTSPLLLFVVACAAAAAVVTA*
>Tc00.1047053508161.30|S055|A--T---CD|5
MAMMMTGRVLLVCALCVLWCGTPGGRCEEGETGETPPGASSSVVGKGSRESSPIGRGVSQISGLKASDI
KDGTEDSGDEQLLTEEEEEEEEEEIPPPTPPEGGGGGQPQAADEKLENVNGNGPKPENQRQVESGTQN
LSEKETVGDGEAAVTKQNEGSGPQPQDHPHPVQEEDTKSGEGHEPSQGKEQKTNVEATIPINPAGDHSS
GEHNGNDGSNEKEEEEGEEGVEGHERHRAQEREEAAHVSGAPKVNSTDIRQEVQHKNAGETPTGIKQRA
GEEKDDETEEEREKQKEQHQENPPGKVKETITGANATNQINTTPGDSDSSTAASHTTSPLLLLLVVACA
AAAAVVAA*
>Tc00.1047053508163.50|S048|A--T--EC-|1
MAMMMTGRVLLVCALCVLWCGAGGVHAEDDAGVTSPGASASDGKSFQEPPTIVNGGSHNSVLRASDVNE
QTDETDKEVLLTKEVAGSDEDEVPQTSAEEIPPPSASPKKSKGGGGTQQEDDLDLKRVNEIVLQPEKQR
REEEGLETVGDGEAAVTKLNEGSGPQPQDNPHPVQEEDTKSGEGHELTQGKDQQIKVEAKTPSNPAGDH
SSGEHNGNDGSNEREGGEEKDDERHRAQEREEAAHVSGAPKVNSTDIQQEVQHKNAGETPTGIKQRAGE
EKDDETEEEREKQKEQHQENPPGKEKETITGANTINQINTTPGDSDGSTAVYHTTSPLLLLLVVACAAA
AVVAA*
>Tc00.1047053508163.140|S082|A---YKEC-|17
MAMMMTGRVLLVCALCVLWCGVCGGSVDDLDVDGKAGGSSSGGEDTLGSPKPLPPEPDLSDSERNQPEH
QGNASPSRATGEVLGDDSVEEKKKDNDSNDDDDDSEESELPPPPAIGASGKEDTKKSLITLPQVSGVGG
SAGGGGGPSGNPNRSGDDVLSSSALISAPPPFISTGSNGSQTVIGVSSTQQMEYSKESANLLKKPAEDI
PSKVYPQEKPAPNAREVSSTQRVTTKSQVAGKDTTGKDEAQNGNVANNPSGKQTGQMALQKPQTQPIKV
TKDPISPLPPTEKSPAPTVKAEKEGPPATTGFQTSTEQKQEGSPSQTETQPKEMKQSSTDGGGKQKGKD
TVSSDSMTNAVTDTSAETKSSSISTSGSGIAQEKEVEDDDDPQRPNSKEPHKDPEAHNTNVAPTASENA
PQTVKTVTAQTKGTATPGDSDGSTAVYHTTSPLLLLLVACAAAVVAA*
>Tc00.1047053508163.230|S030|A------CD|31
MAMMMAGRVLLGCALCVLWCGAGGRCKEEAGSPAGGKGAVETTGASASGQDSSDLKKVLPKANQSTETP
AGKSLEGKEVNTDQLVVVPGVEDEEDGNPSEQLEEPVEDGPDQEKTKPKLQNKEQEVTQPSQAQVDLPQ
KAQPLLQQSQPLPPSAPQPHTPASEEGKGVGENNTGGEGQPSLGAQDIGNEDPKAPIKGNSLKDSGTKS
ENSEQVQTTVPKTVPPENKTQNEILTPKKKTNESESTDTSTNLTELPKENKEYPAFVEVTAQSTSTGSE
EQEAEPSTSEEPSPFEEQHSTGTKTTENARTPAAAATEKLQTGDNEKVGDSDGSTAVSHTTSPLLLLLL
LVVACAAAAAVVAA*
>Tc00.1047053508163.270|S124|ANQ-W--CD|1
MAMMMTGRVLLVCALCVLWCGIDGVAETEEPEIGIVPGVDEYLVVEWRSQLRRECAEEVSRRTGGRANA
STVEECVREGMEGLRAVVDGRRHWRHQRYAAAAAAVAAEEGDATPENDDQARNNEDLLPEKKDETPVTS
GQGLADATTVKERTPHNPAAAPVLTKNGASEHQKERGKETKNEEKAEDEEEETETRETTTPAGGGGIKA
PSVSAGPGVILTSGSSSPSGVDSSSSIGGETGPTISTSSNTVGKTSKEDMALQAKESQHAQLGDGEAAE
TLNDGSQQNSSAPSPTGDQNDNGAATLSADGLRSLGVQIAVKGDLEASRTEEPSDGPSTNLPESGRAPP
ESSQAAAAPEPTLQHKVITSIKEETESENMDASENLPGAPKRSNEDPASTATTMQSTSTGSQEGAATPS
TDGIPPLQEEKLIGNNTTENVQPSDTAGTERLKSVNTSKVGDSDGSTAVSHTTSPLLLLLLVVACAAAV
AVVAA*
>Tc00.1047053508163.320|S091|AG--YKECD|14
MAMMMTGCVLLVCALCVLWCGAGAVYARGTPNNAQGGSMASGGLGAKTSYLVRGCNKTVLTRPLRSAFF
INAIQAEAKDVKDISEERDNLNLDSIPQPPALPPAPETPPPPDASDSDGIGRSELGADSQTGGGGGGGG
GSSGISNGGEDSTLKVPVPDDKSSSPIPSAGDGLKNTGDSSVTQKNNSSGTDEPSKKTLNVPALPTVQT
PEALDTDQNKNTPNTQGEISVEARGKGASGGDAGENDVNSKDSSSVSTANSKPTGKTTPSVPSTGETPT
ITATPKDSKNPTGKNDNTAASGTETDSEATKTSSKDDAAEQYSQERDKADLVKSANTGHPAYTAASSIP
TYGNGDAQGTVNENGDDPERHDSKRTHDELEADNTNVAPTASEAAPEAVNSTEKNDTAPTGDSDGSTAI
SHTTSPHLLLLVVACAAAAAVVAA*
>Tc00.1047053508165.30|S080|A---YKECD|24
MAMMMTGRVLLLCALCVLWCGAGCGVFADQDEELSTESPGGRSSGGDPLETKELENPVPHGADSEIQSP
VVEQPQLNHPQDLRGAATESLGEGEGEGEGEEDDDDEKEDEKERGKGKDGKDTRTTEKTEKQKSLTKDR
GTLQLPSQPERGITPAPPGEALQVEEEEGPPASGGDSRPRQPAATPSAPELLLTLTSIEGQGQGTPSEI
PPGPKTTTTNGKPAGEASPTASTGSQTATETTSTTSPSNAKVALGAAEKHLGNRVPNQQKEKTEAPDSM
KDAPTSHPAETKATSISTTGSGGAQKNEDRVDNGDQRSNSKEPQDGHEDGNTDDAPTASEAEPQTPETD
TTQTNAKSKSGDSDGSTVVSQTTSPLLLLLFDVACAAAAAVVAA*
>Tc00.1047053508165.50|S037|A---S--CD|2
MAMMMTGRVLLLVCALCVLWCGAGGRCDEGVVESRAGVSGIGVDPLPASKGIGTSLQGVKDLKDEAGVK
GKKTPTSAQDEAEEDEEEDDDDDDADEDTKAVEEKSTERQGGQEVTVALDSNSREKNLSGSDHENHQAI
VSAEVIPPSGSRETNANSTQTRIEEGKDAEKSSPAVENTLTKGNGDKTLPAGIAGGNLSPPPEEGVDSR
KQDGKDTTSEDEKNVPSPETAATPQSHRDKGSEGTGDDTKATTATANTTGMTNTQNSDDSTAVSHTTSP
LLLLLVVACAAAAAVVAA*
>Tc00.1047053508165.110|S118|ANP-VFE-D|3
MAMMMAGRVLLVCALCVLWCGLCGIAANDTRAQSVWPEYLFLNWHELLRNECEVENAKGTNADLKELAV
KCCVHDAMREICSVFYGTTVMENKDPKVDGICKNYGGEPADADKCSELEAKLSPNAVTPVKVSDREAPK
DEEEELRKTLEEEPTPLPGTPLTNSPAKTTKISPSPPLKGKPTNAEEVPVPNSEEGSVNTEPANDSEEE

DTDTVTDTEQDEPSNSQAESTTPTPTVASDNDDNETDKSTGEDTPNNAPESDVARTEENQDKNKNNKPK
ETPVEVAGIKTATVTTGDSDGVKAASPLLLLLLVACAAAAAVVAA*
>Tc00.1047053508165.120|S054|AG-T---CD|1
MAMMMTGRVLLVCALCVLWCGAAGGVYASNLENNAVSRCMASGVLNTNKSYTPSGCEKTALTLPLRSVL
SITAAEALTDAEDLSPEDSQDSDSGVDTGSVGGADEGESNSQASGGKAGGGSKGDGVAESSESSGSGLS
ADRPGDGVGDSLGSAAPAATLASPIPKVNTSSNDRSGLPSNRKMDSSEAGKQPEATVGAGPKAPNIKPP
GNLEIKADEHSSPAKDTNEETGSTDLGKSKESSEERAKGTQSSSSSSSTTRILPQSPQSPAVAAGGKGL
TASAVHSPTPQAQTTPPASEEEGTPPSAPEGENSLGKEEDVEEEKEQKKQEQRQGVKQNEEHQEQLSQQ
QQEQKRQEPQQEKQEEKVIQQHHQQEQQKNEISAENEENHATNATVTGTNTTANKDDTDGSTAVSHTTS
PLLLLLVVACAAAAAVVAA*
>Tc00.1047053508165.150|S083|A---YK-C-|4
MAMMMTGRVLLVCALCVLWCGAAVVAEGDIGEVGIKDESSKALQVDSQAREAGKKDVRGPEAAVPRLQE
QQGKNARKNDGSAIQPTRQVKVEEEEKENEGSLEGTVKDGEILPSPAEGQPTSSEPPPPPAPGGSRNGV
ISGGGSKLGETSNGGEGPTLNSSSSSGDGKPPAVDSSGSGGGTGSVPGGKEIGGGGTPGVESSKFPVSG
VALPPSTPGAGSASSAQNLEPSERSGWPEPTVSPRTAPLNVDARKESKPKGEPQTFSAQGETERQVTDE
KTSKKEAEESAIEGKRLFNLPHTASSTPAGPAVRLPEGSQVQGNRDEGEGLPPEATKSETSTGQERRTS
QSQSESTELKFSSKDEVAVQHGHVTVPSDSMTNASTNSQGVTPAPSISTNGGDDAQSTVDGNNDDDQRP
NSKEAHNNPEDDNTNVAPKFSETAQQTPETVTVVQTNDTTSGDSDGIKAASHTTSLPLLLFLVACAAAS
AVVAA*
>Tc00.1047053508165.170|S030|A------CD|31
MAMMMTGRVLLVCALCVLWCGAGGRCAEEKADEFLVTEPGGSLSGGDSSPKQSRNSSPVPGSLVSPPKP
QKDDNSENLHAKESLEPEEGIPLKPQEGENKTQVPQDGVRNGNQSIPHEQSPNQALPPPPPHQPPSVGS
DAVSPGGSSVGGKDPLGSSSSGVISSPHGGGDRGTTGSILSNAPSSFPKGVLLAEEAETEHHSLPNENA
AERGNVGRAAAPGSEGPSPLEERRTQDGKSEAHQTEESSEDLNKQPQGNGKVQNESPNADTPRLQTPHG
GKPPETKGNNSHNTDISTNLPDAQEPEYVKENKNENPASIPDKAQGTSTGIQEEAPASHPNVSPSPLQQ
ENFSGMKTTENVQPPDAAATEKRQTGDNEKVGDSDGSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053508165.210|S008|A-----ECD|43
MAMMMTGRVLLVCALCVLWCGAGGRCDGDADFAEIKDEPSKASQSSSQGGHAGEKHMPNPIVGVVNTSN
ELLNEQDGKNGSPQTGSVEQPSTDNDGMEAEGEKAKGKKVEDAEPRRNGKEQSQDDSERTEEREALIEE
ERNTSPPTVANKLVTSEEGAGPAAGNAGPRVQAVKPPQLPASPQASDETQSGDSSVGGPKKDKGSNLNN
SASDSGNPSPVDSLFSGGGSSGLGGGSPQDDSSDSPLSAAVLSLSSPLGTPSVQDTQPSEKVRQSETIS
SETAFPNEQPKERSESEAKEGTFTSQEAAESPYGDGDATENEKEKRDVGLKSTTSPTPTTSDPPVKQTT
PRASSAEPSPTTEVQAEEETLKDNVTTAMRNDTAIPGDSDGSTAVSHTTSPLLLLLFLVACAAAAAVVA
A*
>Tc00.1047053508165.280|S121|ANQ----CD|9
MAMMMTGRVLLVCVLCALWCGIDGVAETEEPEIGIVPGVDEYLIVEWRSQLRRECAEDVSRRAGGRANA
STVEECVLEGMEGLRAVVDGRRRWRHQRYATAVAAEEGDATPENDDQAWNNEDLLLEKKDETPMTSGQG
LADATTVKERTPHNPAAAPLLTKNGNSEHQKERGKETKNEERAEDEEEETETRETTTPAGGGGIKAPSV
SAGPGVIPTLGSSSPGVDSSSRIGGETGPTVSTSANTVEKTSKEDMALQAKESQHAQLGDGEAAETLND
GSRQNSSAPPPTGGQNDNDAATLSPDGLRSLGVQIAVKGDLEASRTEEPSDGPSTNLPESGRAPPESSQ
AAAAPEPTLQHKVITPVKEETESENMDASANLPGAPKRSNEDPASTATTMQSTSTGSQEGAATPSSNGI
PPLQEEKLTGNNTTENVQPSDTAGTERLKSVNTSKDGDSDGSTAISHTTSPLLLVVACAAAAAVVTA*
>Tc00.1047053508165.300|S049|A--T--ECD|5
MAMMMTGRVLLVCALCVLWCGTPGGRCEEGGTGEALPVASSSVVGKSLQEPSPIGRGELHNPGLNASGI
TDQNEDSGDEQPLTEEEEEEACSDEDEDEPNPITSKLPSKPPGGGEGGGEVQPKDDDGKLEKVNGNGPQ
PQDHESPVQEEDTKSGEEKELTQEKDQQANVEAKTPSNPAGDYSPGEHKGNDGSNEKEEEEGEEGAEGH
ERHRAQEREEAAHVSGAPEVNSTDIQQEVQRTHAGETPTGIKQKAGEERDDETEEEREEQKGENQENPP
DKEKETITGANATNQINTTPGDSDGSTAASHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053508165.350|S071|A--TVFEC-|1
MIAMMMTGRVLLVCALCVLWCDVAAASAADGKGDTITKEDEKTRTTEVSPPGRKKESPVTSGQESAGNV
RTPQSYGVDIPLPNNLNLDQKQEGEIMTENEDDDEDEEENEEDAEMSENEEEGDEDTETREKQPPPGPP
PPPPSGQTSTPTINGNSAGTSNEARAKELPSSDKDSTQGQGLKSPAAESAPAATPQVKNEDPGSADVVS
VQQVQKAQSGLESGSESRKEDGVLTTNKQQDGTSDSHAESTPTSRSSAKSVAASNGPDKATEEEISNKN
TARVDEVPEAAQEDGNKDDNKKETPIKTTAIANGTAPTGDSDGSTAVSHTTSPLLLLLLVVACAAAAVV
AA*
>Tc00.1047053508165.410|S062|A--TVFECD|5
MMAMMMTGRVLLLVCALCVFCCGVGLTNGDTAMEMRIEENPQSTVPDPAVGNAKEQATQDLVMEGPENG
DPSLAAQTGNNTKQQKVVVETPPLIPVRTEEEEEEEVKTEESEEPRSLSEGREKSKLSSMPEGERPPPP
PPPPGTPSPLILNGNSAGNTNENSVEEIPSFDGGFTQGQGLKSPAAESAPAATPQVKNEDPGSADVVSV
QQVQKAQSGPESGSESRKEDGVLTTNKQQDGTSDSHAESTPTSRSSAKSVAASNGPDKATEEEISNKNT
ARVDEVPEAAQEDGNKDDNTKETPIKTTAIANGTAPTGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA
*
>Tc00.1047053508165.420|S049|A--T--ECD|5
MAMMMAGRVLLVYALCVLWCGTPGGRCDEDELPQASLVGASGSDGKSSLEPPIIAQGGSPNSVLESISV

KETRAETDEGRLSTEEEEEDEDENEGIPQPPSPPPPKNDEKLEKVNESEPQPENQRQVEGGTQNQSEKE
TETNGQEEVTKKKEEESELKPQDNQTPVQEEDTRNVGGHQPSQGKDQQIKVEAKTPSNPAGDYSPGEHN
GNDGSNEKEEEEGEEGVEGHERHRAQEREEAAHVSGAPEVNSTDIQQEVQRTHAGETPTGIKQKAGEER
DDETEEEREEQKGENQENPPGKEKETITGANATNQINTTPGDSDGSTAVSHTTSPLLLLLLVVACAAAA
AVVAA*
>Tc00.1047053508201.30|S030|A------CD|31
MAMMMTGRVLLVCALCVLWCGACGGYAWDFDNNSSLNEYYYGAYGVYCNASLNATFCEEKRNASKGEET
ALKTSTVQSENDGGQSSAGDSSGEQEQTLEESGSDRSIGNSGGQELKNPGEGEATPTEQSPSPTQPSTV
SEDLPKPAAPGGSEAPGTTTELQPPPQSPLPAGGTPTPTTATPIADGPSGGRDNSSEKNGSDDSEKTDA
GPQESQPPNGNVTETPTPATVTAAPTSATRTPDESDGSPAASHTTSPLLLFLLACAAAAAVVAA*
>Tc00.1047053508219.70|S103|ANP--F-CD|11
MAMMMTGRVLLVCALCVLWCGAGGGFADKVVEAAAGVVASNRTDEENLILNWYVLTQGECANESTTGGK
LNVTAERICMHKVMKEVCDAFYNKTSGVTHDRDVEFICTYYATIPEEPVEPPTPQGPPSHSAVSNATSD
EGTPKNAPESDVAGRGEGKEDDKEHGNTKQKAVETAAVESITRSTDSEVSTAVSHTISPLLLLLVACAA
AAAVVAA*
>Tc00.1047053508219.110|S121|ANQ----CD|9
MAMMMTGRVLLVCALCVLWCGVFGIAAEEVGGADGSAVEYSFAGRHVQLRRGCAEEVNRRTGGGANASA
VEECVRRGTDGVRAVVDGRSRWRRQQFAVAAAADGVGDSGDKSGEGSDVKLKVLSSSDQMLEAGQDPEE
GQEHTGSPEVTKTLETNKDSQKTEEQNVSPDGDRSKQPESQEPAVGQPEGEGNTRNPQPRQPPPGTNKL
QSEETHPPITAEKHSKSQDGRPAQETKVLQTKGSTKHEEGASSLHSSENVSHLSRESTTPLSTSTESSN
IAGSTVEKSGAKNSKTTAASVTQHDSEGDTGPAALPASTSELQSDEISNAGIIAATHRDGDDDSSPAAS
IAERPTAGTRSTKASGDASDLDQSNNDDVNDDVAHNGKTAEFEAASGTRDNKADNNERYTAVTENATNK
SSNTETTADSDSSTAVSHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053508221.30|S030|A------CD|31
MAMMMTGRVLLVCALCVLWCGVWLCDAAVVGSAAGGAGGESAGKGAVETTETSAPGPDTSDSSIDESKV
NQSPEKSAVKSLEVKEDAGQEDVVAGVGGETNKNTSGRLEKTVINDPGKEITEPPLQDVGQEEIQLPKS
QVNLPQQPQPPLQQLQPQPQPQPHTPASEEGKGVGENSKGGTGQPPLGVQDKGNEDSKALMKEDSLKSP
GEESENSEQFQTTVPNTVTAEHKTQNGMLTPEQKTNGSQSTDTSTNLPETQKENKEYPASTEGTAQSTS
TGSQEQESEPSTSEEPSPFEEEQSIGTNTTEDARTPDAATTEKRQTGDNEKVGDSDGSTAVSHTTSPLL
LLLVVACAAAAAVVAA*
>Tc00.1047053508221.150|S097|AGWTH-ECD|44
MAMMMTGRVLLVCVLCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGYNKTAITVLLRSVLP
ITAVEASAEKDNALVMQNISNSSGTFNAGASTAGDSVPGSDSPAGGFGAETPASAAGGGGGSSGGGGG
GGGGDSSTGVQGTDSVPSVPVPGATGVDSSASSSGGTAGSPGTNSSNTTGDSSTGDQTPAAEANDSSLP
EGPAGTTSGTEHTRQEKEEEGEEEEDHEKQQQSDETQVQQQQQHEHPAENGEESAKDKNALRTNATANT
GDSDSSTAVSHTTSPLLLLLVVVCAAAAAVVAA*
>Tc00.1047053508221.170|S061|A--TIFECD|52
MMTMTGRVLLVCALCVLWCGAGGGGCSEAPQRPPGSTSVKGNDSKGDNVTVGGTAGGGQNGKPAQSQAA
GVSVQGANEAAAEGRPAPQPGGGASENAEAAKGSNGQKEGKTEEKEDKEEDEEVEEDEEGKEEEEEEND
TEEEEETKKGEAVTGTTEVMSAGGREQPILSSGAEGASNNTNPNSTPTTGDDDPAADVAGTAEGKQNEN
KDANPKETPVEATAMKTTTAKTGDSDGSTAASHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053508221.210|S017|A---S-EC-|13
MAMMTGRVPLVCALCVLWCGAGGRCDEEERAVSGSGDGPPPGSAEHGTPRKETQELKVGAPGVIETASP
PSLKPTGEDKDDDDEDDAGGDEDDNETDETKEKRREGQSNKGGTVLPDTDSREENLTGSGQETGQPNVP
AGGISPSGSQLSNANPLRTEVEEKNDTDKRPPAVKNALTTVNGEQTLLGGIAGGNLPSPPEDGVDSRKQ
DGEDTTSEGKKNAPPPETAATPKSHRDEGPEGTGEDTKATTVTANTTDTTNTQNSDSSTAASHTTSPLL
LLLVVACAAAAVVAA*
>Tc00.1047053508221.420|S104|ANP-VF-CD|10
MAMMTGRVLLVCALCVLWCGAAVVVSSMPDANSVQSFWRENLIPRWHELLKNECEAEYSKETNLSLKDL
AVNCCLHHAMHELCKDLYSRLFKKTEFSNVEGVCKEYAEKPDEVKCRKRQTQPPPATDNSVKLSVPEAL
GKEGDLGKTPEEASLADPSAKPTKGPPSSPMGGQPANADDVPAPKSEERPVSTRPTNGSREGDTDTITD
TDQEEISTSEAESATPTPPVASDNDDSNETDKGTGEKVPNNAPESDGAGTEGKQDENKDANPKETPVEA
TAMKTDTTPGDSDSSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053508221.490|S061|A--TIFECD|52
MTMTGRVLLVCALCVLWCGACGGGRAETPSSDTPTSSGNASGKEKPQEEEAVVGAGGGGQSGEHAASQA
AAPTGSGLPAAPAEAAPQSGGVVSVTASTTTYNKVKKEEEEEKDDDEENEDEEHEEEEDDKKEKKETKK
VESVTATTEGTSAGGQEQPSSSSGAEGASNITNPNSTQTTGDDDPAADGAGTREEKQNENKDANPKETP
VTAAAMKTATATTGDSDGNTAASHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053508221.550|S133|ANQ---ECD|6
MAMMTGRVLLVCALCMLWWGLFGIAADGAGGADGSAVEYLFPRWRAQLRSECAEEVGRRTGGGVNDPAL
EECVRRRTDGVRAVVDGRGHWRPQQFVVVATSAGDTSDDYKDPGSLPEGQSGSVAQLTVQQPLKPAPSS
VPGSADNATEKNKPTNPAQPLATGEKINGELIEIKSDDEGTKGKSEDEGEKVEENDDEADGNAGSGTSD
GSQEQGKQKAGTGQGASGGTAKENVNVVAGSNLAEGAAASPPVVSVNVENPKSVELIRDDVGGRRQTRE
KTVQEPPAVKLKENVPAELISTEDAAEGEKQKTEEKAEEAETKEEQKNAAEKSKEETPTAPEKKTKEEQ

KDKEVQRVRSKNEEKETDGAEPPAKKEAEVEKTAAFKNIHMNNITKPGDSDGSTAVSHTTSPLLLLVVV
ACAAAAAVVAA*
>Tc00.1047053508221.580|S008|A-----ECD|43
MAMMTGRVLLVCALCVLWCGAGCGFCEGTLEDEFCNKSYVEALSLLANKTDDEIKKKYCKQEDEKATCL
KTLRSNIADALEKEKAKEDNAAHRESDISRDTGASVGSPTTKSSKAAGANTAVLSSPPPLNVEGGFDAQ
IHGSAGGAGHQQHSDDVRSEEEQRNHPESGRCSEGQDALGECSHVPAGDAAAEGSHQHSVDAQGKTIHK
KGEETTPTGLKSTEARDGTDGAPAPPQDPPNTTESHEDKSRRVAAPDTIPADNTSPGSNQEQTSQSSSP
SGSETTGSSDKEDREKNSKNAQISDTPLKDEEQHRESTAGSKDATTVESAAEQRNTTTPGDSDGSTAVS
HTTSPLLLVVVACAAAAAVVAA*
>Tc00.1047053508221.600|S125|A-Q----CD|2
MAMMMTGRVLLVCALCVLWCGFSGIAADGAGGVPDGSAGECLFSRWRAQLRRECAEVSRRTGGRANASA
VEECMRRRMDGVLAVVDGRRRWRRQRPAVAAAAENADELGTENTSSERNVLSGGNGSGSEDAHVRGGDL
HSESRDGVVRPEGATSEELNVNSNSHTEALPTKEIRQVIPESISPVSLPDSKEVEEDTASKDDKTQEIL
VTGEQQALQSSSSLGGNSPASDQGAELTAAENPQNGKKGEAEKEKNLSDKNVPTGSDPSATNSNDNAPT
KLQAETTLPSPPNANFSAKHHTDEGAAKTILDAIPLSGAAVTEENPTLRHTTDRPIQTTQVEATFAKPE
NNAAPRDSNSSSQISKGASSTSNESVTQNAVDKEVETTPDGTNNTASETNNSTKAPDNATNKINTVTLT
DGDSSTAASHTTSPLLLVVVACAAAAAVVAA*
>Tc00.1047053508221.660|S001|A---H-ECD|18
MAMMMAGRVLLVCALCVLWCGAGGRCEENGADVVSGGGPGTGNDDKNSEALRSPDLSSLERQEEGAGGA
AGGFADAQGGKDISTSSPGTNILKVEKVDLVVDPPNPIENQNKSKDSTKAGTGTTNQTAPPSKPQSPPP
AGPPPPPLPEAEGVKLTKTPEKQDSSVGHQSTQHHTVPQVKELKQQEQNTQNQIINEKHESQRLQVQEE
KEKQRSEEQLEQRERPHEEERDGEDLQEEIRDQQKKQEQQEEEHEEAQEEHVDSTKQEKEQDQQQQHQQ
HETFAKKSDGPIKNETAVGSNSTANTDDSDGSTAVAHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053508221.960|S061|A--TIFECD|52
MMVTGRLLLLCALCVLWCGACGGGCSEAALALPVTGESEDNKRKGENNTTDDVGGGGPTGQPAVTQPAA
GSVPVSGTEAESALQPAAQALQSVAKASGTANATTENNKNTTKKEDKTDNDELKNEEKEEEEEEEEEEE
EDEVEVDDGKEKKEETEEEKKEEEKDDTGTTERISERGQEEPISPSRVEEASNKTKPQRTQTTGDKDPA
ADGAGTQEEKQNENKEANPKKTPVEATAMKTTTPTTGDSDSSTAVSHSTSPLLLLPLLVACAAAAAVVA
A*
>Tc00.1047053508221.970|S065|A----FECD|1
MMMTMTGRVLLVCALCVLWCGTAGAAADGSEERADLSGIGGGSLPELKEIGKSPEEPQGKKDEAGDVKG
KKHPASSEDKEEDDADGDEEDYDVVDDLEEEEREEETVETAETEIPNDPTKEEASSPPQSKHEKAPAAA
PAEGIPTAQSPATPVQPTTQGQPPTAAPSPEDSPVPAALAATAAPKLTSSEQGNTPAAARKKDEKQSED
IDPAQESEQPDPQDVVLVQQSQGVHESKESNSNPRNPASASATANQRDATFNGRGEPAQTTSSTKSGFE
SNDDNSGTEEGITSDDPTADGAGKNDTKNSKNKHGNTKETPVEATAVKATTATTGDSDSSTAASHTTSP
LLLLLLVACAAAAAVVAA*
>Tc00.1047053508221.1010|S025|A------C-|17
MAMMMTGRVLLVCALCVLWCGATVVGSVANDVVDGGIKEGPLGGSQSDFRDEKAGKPELSESVDEGLGS
AGHSLDTRSGTNVSEQGNLVNEPPTGNVGKEEVEGEALGTQRNEVHEQQVEEEGKELTVKQKSQTKDKG
TLPQSTPPTTAGRITSPPPTPALMQGSPRTPGQPKENSQKSTGQPPKLQVPPAKSPSQASDLGEADAGP
VGIKGTGRNVIGGSLDKNKDPKGREGHISGPPSGGASLSPISNNGDASQMNGGAPSTQDTKSLKNNEQS
GPTTYSGNAPLNRETPETSTPDAKQHSSETQENETSRVADGDANYTAAGQSAVGTKGSSGVSTTASNAP
TTLQPQLPASPVPPTATVTGAPAEKPTAERSPPPADSTTGGNLAATTTAPTNDTTTKPGDSDSNTAVSH
TTSPLLLLLVVVACAAAVVAA*
>Tc00.1047053508221.894|S047|A--TS-ECD|8
MAMMMAGRVLLVCALCVLWCGAGGRCDGGETAGLGSAEHLPESQEPGTSPEGTQDLQDEAGGVVETAVP
STSSEDEDKEDASEENEHEETEDGEKKSIERQGDQGGTVASDPNSGEKNLIGSGQENNPAIVPAGGISP
SGSQESNANPSQPEVDEKKETEKSLPAVENAHTPGNRENTLPGGVAGGNPPSPPEDGVASREHDGEDTT
SGDKKNVPSPETAATPQSHRDKGSEGTGEDTKATTVTANTTDTTSTQNSDGSTAVSHTTSPLLLLLLVA
CAAAAAVVAA*
>Tc00.1047053508221.104|S097|AGWTH-ECD|44
MAMMMAGRVLLVCVLCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGYNKTAITVLLRSVLP
ITAVEASDGGDSAGGTQNSSNSSETSDAGASTASGPGAFAAGDSGSGDFDAGPGAPAAPGGGGSGTSAG
DHGAGSVSSGSSEGPSAPPVAPPVASPAPPGTSGGPSASVDATVVDTSAGRSGGTAGSPGTNPSNTIGD
SQTEDQTPAAEANDSSLPEGAAGTTSGTEHTRKEEEEEEEENEKQQQSDETQVQQQQQHEHPAESGEES
AKDKNALRTNATANTGDSDSSTAVSHTTSPLLLLLLVVVCAAAAAVVAA*
>Tc00.1047053508229.30|S002|A---S-ECD|19
MAMMMTGRVLLVCALCVLWCGAGGRCDGGETAGLRSDEPPPESQELEKSPQVTQDLQDEAGGVVETAVP
STTTRKDEEDGDDGDKGTEGEERTKGQGGQGGKAAPDPDSGERDLSGSGQQTHQSILSAGDISHSDSQE
SNANPTQTEVEGKNETDENTPAAENALTTVNGEHTLPAGIVEGNLPSPSKDSLASRKQDGEYTTSEGKE
NVPSPATAATLQSHRDKGSEGTGEDTKATTVTANTTDTTKPGDSDGSTAASHTTSPLLLLLFACAAAAA
VVAA*
>Tc00.1047053508243.10|S016|A-----EC-|10
MAMMMTGRVLLVCALCVLWCGLVSADAGGDDFSGGHGTLGGSGVGADGRPSVPVGGEVSTGGTKDECSL

GSGGGSPVSASPACKSLLSDAENPGGEAFNDTKKGLSRVEEDPDAEQDPPQPGSHVVSTAEVPAPGQPN
SEAQEQSSGTLRTEEGRNNGDGGTTAKEEVTGVESRGTADLYPNDSRPSKAARPVTGEEKGTEKQAASK
ASLTPAEGRGTSAATDQKVELPKEKAASSAGATKNRPPVGQQQTEPSSPFTSGSTSTLTPEKEPAEEVH
SNNNQPPGDAVPTEGTQHETLPGDKTQTEPATTNNKLIDAAPTGDSESSPTAPPAGESDAATTTTPNNH
DARSLNNNGNNAFTEEVDQKEAARKPKSAPHSIDTAAANSEASTAAVNISTNTKNKTTTGDSDSSTAVS
HTISPLLLLLVVACADAVVAA*
>Tc00.1047053508243.50|S126|ANQ----C-|2
MAMMMTGRVLLVCALCVLWCGAAVAVLSADGAGGGDGSAGEYLPLQWRTRFLTECAEEVGRRTGGRANA
SSVEECVRQVMESLHAAVDGRSRWRRQLSAVAVAAAAEGGGKENPNTVEDEKTSETLATSGKASTGKKT
AVASEQTSVNPAPAIVPPARETLVQGKHNETNAKEEKEEEGGEKDDSEEEEENHKEDDEEEDAEEGEKA
EEREEDKKGEESEKNTKEEEAKYGVEEDEEDKEKDDDNTSEGMPAVSQEKRNSTSGPEGAPNKTNTEGT
QTPGDIDGSTAVSHTTSPLLLLVVVSAAAAVVAA*
>Tc00.1047053508245.40|S017|A---S-EC-|13
MAMKMTGRVLLVCALCVLWCGAGGGFANDEKSGPGNRAELPLASQGPETAPQDSQGSQNRAPGEEENLT
SVLGEEADGDDVDREKKAEEEEITERQGSEGGTAAVGSDSSETNLSDSEQETGQPIVPAGSISPSNSQE
SNANLTQTEVEGKKEPDKNTTTVEGALTTVNGEHTLPAGIAEGNLPPPTEDSVDSREQDGEEATSEGKK
NASSPETAATPQRDREKGSEGTGGDTKATIVTANTTDTTSTQNSDSDSSTAVSHTTSPLLLLLVACAAA
VVAA*
>Tc00.1047053508245.70|S087|AG--YKEC-|7
MMTGRVLLVCALCVLWCGACGVYARELDNKNAVGDCMASGVLGANRLRVPSVCDKVAISLPSRMVSFIT
AAEASTNDDASDVVEGNPASPSGAAAAGSVSGGVGGAGGSRGGGVTSGGSGNSAGGSDGNRNTSEDPKG
GGGGFLQSPPSVDPHSPRIPNGVGESQNTEVSLSTEETISPEAAAEPGSTASPGDTPPKVETQDKSEPK
EEDKDPSFTQAAAPTSVNGKASTGERNQQNDVGKVDHSSNQTPPPAPPSAVTSPVLSKEPAPPGKEPSP
SNVSLPAPNVPQTTKGQEQKPSILTTKKESKTPEIPSEDNVLQQQGQNTTTEGLMENSSPGSQARNTEP
STSTSGTGEAQITADADNAQRPNPSESQDDLEGTDINNSPTADEAAPQSAITLTTAQKNETATVGDSDG
STAVSHTTSPLLLLLLLVACAAAVMAA*
>Tc00.1047053508247.80|S025|A------C-|17
MAMMMSGRVLLVCALCVLWCGLVSADAGGDDFSGGHGTLGGSGVGADGRPSLPVGGDISTGGTKDECSL
GSGGGSPVSASPACKSLLSDAENPGGKALNDTKKGLSRVEEDPDAEQDPPQPGSHVVSTAEVLAPGQPN
SEAQEQSSGKLRTEEGRNNGDGGTTAKEEVTGVESRDTADLSPNDSRPPKAARPVTGEEKGTEKQAASR
ASLTPAEGRGTSAATDQKVELPKEKAASSAGATNIRSPVGQQQTEPSSPFTSGSTSTLTPEKEPAGEVH
SNNNQPPGDAVPTEGTQHETLPGDKTQTEPATTNNKLIDAAPTGDSESSPTAPPAGESDAATTTTPNNH
DARSLKNNGNNTFTEEVDQMEAAIKPQSAPDGTDTAAANSEASTAAVNISTNTTNKTTTVDSDGSTAVS
HTTSPLLLLLVVACAAAAVVAA*
>Tc00.1047053508247.130|S108|ANP---EC-|1
MAMMTGRVLLVCALCVLWCGVSVVMASNVGGLAPHAEINVFFGRWYSLMMGDCENTSAFENGTVNESAV
EECKREAKKALCDFFYGDHSGEHDASHLHSICSPDVGSGGAVDQQAQEQILTLRETGNPAPPTTPQGLS
EESPDTPPTPASAGASSQAPPIQASTEPTVLAKQAEPNTAGSVPPKQSQGGAEAMRPPQEPPKVSSIHD
TATQRDPPTEDRAEQTLPPAKANDNSSDHSEEGTAEESTVDTPASGAVQTEGNESETPGSGLKKTKTPH
TTVEGSNIVKPGDSESSSTAPPAGESDAATTTTQNNHDARRLNSNGNNTFTEEVDQMEAAIKPQSAPDS
IDTAAANSEASTTAITISTNTTNKTTTGDSDSSTAVSHTTSPLLLLLVVACAAAAVVAA*
>Tc00.1047053508253.10|S082|A---YKEC-|17
MVMMMTGRVLLVCALCVLCCGAAVVVSAADGADGPEKEGKESAEDSGSESPDSQEELLGSSGSVDGRPE
SAGQLLDKKGGINSHQQVDSVIHPSTGDERRVEEKEKEKEGDKNVSGALENLKKDEETSPLPSNPPEGV
GILPPPIPPASNDGHVDGIPADGGIVGNVLLSPPSAGTSRQSPNPTVGDNLQNTGVASFNQENKSSGTG
KQLGPTTAGTTLPKVDVQKVSIPASEQQRDRSASQDAARNHFFGGGETENEADRSDVATEGPSKQTPGN
QTLPQIKTTPEPPTAPPSQERPHVKPQEELSPTPDVPAEGKSLPAPRVSRTPTEETHKTPLSETNTEPE
TKLQPLKDEVQEQNGSPTNQSHLLKNAATDRLAETTASSISKIGSDDAQRPSSNEPQDGSETANTDVAL
TVGEAAPQTAKPVTVAQANDTVTPGDSDSSTAVSHTTSPPLLLVVACVAAAVVAA*
>Tc00.1047053508261.50|S097|AGWTH-ECD|44
MAMMMAGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASNGRDTTVATPNNSHSSRTSNAGASTAGGSPGVPAPPAAAAPGGSPGGGAPGGSGTSTGGHGT
GGIPPAGSPAVPAAPGVDSSAGSSGGTAGSSGSNPSNTTGDSSTEDQSYAAAEANDTSLPEGQVGTTSG
TGHTRQEEEEEEEEENEKQQQSDETQVQQHQQHEHPAENGEESAKDKNALRTNATANTGDSDSSTAVSH
TTSPLLLLLVVVACAAAAAVVAA*
>Tc00.1047053508261.130|S095|AGWTH-EC-|7
MAMMMAGRVLLVCALCVLWCVAGGVYARDFDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASAGEGDALATKNNSHSSETSNAGASTAGSGGGDSSGSAGASGSGSAGAAGASGGSGTSTGGSG
SGGGGGVGPAGPSAGGQGNGGISPASSGPAVAPSDPPAGSPSAFAAPSGPAAAPGVNSSAGSSGGTAGS
PGSNPSNTTGESPTGNQSSAAAAPNDSSPAEGPEGTTSGTGHTRQEEEEEEENEKQQQSDEAQAQQHQQ
HEHPAENGEESAKDENALRTNATANTGDSDSSTAVSHTASPLLPLIVVVACAAASAVVAA*
>Tc00.1047053508289.9|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASTGEGSPDGGAGAAGASGDRGATGDTSGSGGPSASPAPPAAAAPGGSPGGGSGGGSGTSTGGT

QNNSNSSENLESGASGGGPAAGGGGGSGGGGGRTPTGGHGTGGIPPAPAAPPASPPAPASSPAPAAPGV
DSSASSSGGTAGSSGSNPSNTTGDSSTGDQSSAAAEAHNSSLPEGPEGTTSGTGHTRQEEEEENEKQQQ
SDETQVQQHQQHEHPAENGEESAKDKNALRTNATANTGDSDGSTAVSHTTSPLLPLLLVACAAAAAVVA
A*
>Tc00.1047053508293.80|S097|AGWTH-ECD|44
MAMTMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASAGKGDALAPKNNSNSSKTSDAGASAGDGSGGATGASGGPVPGSAGASGSGSAGAAGASGGSG
TSTGGSGSGGGGGGGPAGPSAGGQGNGGISPASSGPAVAPSDPPAGFPSAPGAPPPPAPPSGPAPAAPG
ADSSADRIGGTAGSSGTNSSNTTGDSPTGDQTPAAAAAHNSSLPEGPAGTTSGTGHTRQEEEESEKQQQ
SDEVQVQQHQQHEHPAENDEESAKDKNALRTNATANTGDSDSSTAVPHTTSPLLPLLVVVACAAAAAVV
AA*
>Tc00.1047053508293.140|S097|AGWTH-ECD|44
MAMTMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
IAAVEASDGKGGSAGGTQNDSNSSGTSDAGANGSAGASPADGVPAAAVPGASGTGSPRAGGGGGSGTAA
GGQGAGSVSSGPSAAPGGGGGVPSGGGGGGSAVGGPAGASPGVGGTSTGGTQNNTNSSENLESGASGGG
PAGGSGGTPTGGDSGGGSGGSSGSGGSSGTPTGDQGTGDVSSSGGGGGGGGGGVSPTGGQGTGGTSAA
VPGATVVDSSAGSSGGEAGSSGTNSSNTTGESSTGDQTSAAAAAHNSSLPEIPAGKTSDTGHTRKEEEE
MQQQSDETQVQQQQQHEHPAENGEESAKDKNALRANATANTGDSDGSTAVSHTASPLFLLLVVACAAAA
AVVAA*
>Tc00.1047053508295.40|S012|A----REC-|10
MAMMTGRVLLVCALCVLWCVFSSVSADARDDFEDSGQAVVGSVGQPSSPVAGHGDNGVVTDGSSLSSGS
HLPGSAPTGGKPPLPGVGEGVGLNESKDALTLAQEGREVVQDQHELVPQVSHHTDAGTGGKSDPNAPEQ
SPNAKTELEDGGGVCGDDAAAAEGEVKTTVNEGQLGGSSTSDSHPPAADRGSREQEGTVEQAASTAALT
PVVGRETPPKGDTKEDSPEDKAATGAGNTQDIPAVSQQQTHSSSTPTAGNGLTSTLGKGRAAEDISSNN
ERSGKALLQEGAEHETVAGSQSQTIPAATARNTLGTTVSGDSDNSTTITTAVRSDTGTEGTPTSNHPNR
QSIEGATSPGMNSDGEAASTKKYDTVSQSAGSSTAPTTNNKTRDTASHGNSDSSNAVSHTTSPLLLLVV
VACAAAPVAVVAGPA*
>Tc00.1047053508305.20|S099|AML-VFECD|25
MAMMMTGRVLLVCALCVLWCLSGFGAARDNRCGEGGGDVFTHAKKDGDDRVRLKADCGLLSTRMGLINA
VAAGDDGEDGSNNAVLEKTEKSLHSSVLAGPGDIAAPGAKGVEGAAGAGLPPSPSGPGGSGTGGEQRQS
EQLDTKGKGEGGKRDEKGGKAAESQQQRPDQSSSSGSDGPQGGKELALKEKSESTEPSVDTPTQEDEVE
TEETNVSEKEEPGGDEGKNNNVALTVTSESQAKLKKTQTATPPTTQVNERSRTEDLGYPQQPKGVQSDI
ESKYNSQTEDGVSIAANQQNEPSDDHGKSGIPSPTANGGAANNETDNSTEDGISNSDPAADATGTREGK
QNENKDANPKKTPVTAAAMKTTTATTGDSDGSTAVSHTTSHLLLLLVVFACAAAAAVVAA*
>Tc00.1047053508305.50|S067|A---IFEC-|4
MAMMTTGRVLLVCALCVLWCGAGGGGRAETPSSPSLETQPEKSTQKKEEVVAGDVDQSSKPVAPKEPTP
KASELPEKPANSLQPQQPGGASKAASPTTDSMVQNTEGKNEEEEEEGDDTKEKEETKKEEETVTSITGG
ISAGGQEQPSLSSAAEGASNITNPNSTQTTGDGDPAADGAGTAEGKQNENKDANPKETPVTAAAMKTTT
ATTGNSDGSTAVSHTTSPLLLLLLVVACAAAVVAA*
>Tc00.1047053508309.10|S061|A--TIFECD|52
MAMMTGRVLLVCALCVLCAGAGGGGCSEIPRAPWDTPPGNNTKNDNSTVVGAGEVVKSSAPAKSQLPAE
SVTDLRVVAAGADTSAAQQQEKQASEMQEKGEDGEEDNEEGEEEYEEEEIDEGEDDAKKEESETKEEKQ
DKEREEEKIKEDDADATNGMPAGGEEQPSLSSGAEEAANQKNLKSTQTNGDDDPAADVAGTAEGKQNEN
KDANPKETPVEATAMKNTTATTGDSDGSTAVSHTASPLLLLLVVACAAAAAVVAA*
>Tc00.1047053508313.30|S010|A----RECD|22
MMTGRVLLVCVLCVLWCGYSLVSADAGDDREHSGQGVAGSVGQPPSPVGGHGDNGVVTDGSSVSSGSHL
PGSAPTGGKPSLPGVGECVGLNESKDALTLAKEGHEVVRDQHELVPQVSHHTDAGTGGKSDLSAPEQSP
NAKTELENGGGVCGDDAATAEGEVITTVNEEQLGGSSTSDSHPPAADRGAKEQEGTVEQAASTAALTPV
VGRETPPKGDTEEDSPEDKAATGAGVTQDIPAVSQQQTHSSSTSTTGNGPTSALGKGRAAEDISNNNER
SGKALLQEGAEHETVAGSQSQAIPAATARNTLGTTVSGGSDNSTTITTAVRSDTGTEGTPTSNHPNRQS
IEGATSPGTNSDGEAASAKKYDTVPQSAGSTEAPTTDNKTRDTASHGDSDSSTAVSHTTSPLLLLLLLV
CAAAAAVVAA*
>Tc00.1047053508365.40|S010|A----RECD|22
MMAMMTGRVLLVCVLCVLWCVFSSVSADAGDDCEDSGQAVVGSVGQPSSPVAGHGDNGVVTDGSSLSSG
SHLPGSAPTGDKPPLPGVGVGVGLNESKDALTLAKEGREVVQDQHELVPQVSHHTDAGTGGKSDLNAPE
QSPNAKTELENGGGVCGDDAAAAEGEVKTTVNEGQLGGSSTSDSHPPAADRGSREQEGTVEQAASTAAL
TPVVGRETPLKGDTKEDSPGDKAATGAGITQDIPAVSQQQTHSSSTSTAGNGLTSTLGKGRTAEDISSN
NERSGKALLQEGAQHETVAGSQSQTIPAATARNTLGTTLPGDSDNSTTITTAVRSDTGTEGTPTSNHPN
RKSIEGATSPGMNSDGEAASAKKYDTVSQSAGSSTASTTNNKTRDTASHGNSDSSNAVSHTTSPLLLLV
VVACAAAAAVVAGPA*
>Tc00.1047053508365.160|S018|A--SERECD|3
MAMMAGRVLLVCALCVLWCGAGGRCDEEGTAARGSGGGPPLASKQPETPRVGSEGVKNGVTVAKENVIP
TPPLPIDGDAEVDEDEDDDDDDNDNDADGEEEDNETGESKEKSTEGQINKGGKVPPDSDSREKNLIGSR
QEKDQSIVPAGDISHSKSQESNANSTQTEVEGKKDADKRPPSAENALTTVNGENTLPEGIAGGNPPSPP

EDSVASREKDGEDTTSEDEKNVPSPESAATPQSHRDEVSEGTGEDTKATTVTTNTTDTTNKQNSDGSTA
AATVVQPEDGVESDPANNDLSPPSTEVAAQLSMTPDAEGASNNEENTDTQIAGNPNVTIATATQTNDTA
KPTDSDGSTVASHTTSPLLLLLFVACAAAAAVVAA*
>Tc00.1047053508365.200|S010|A----RECD|22
MAMRMTGRVLLVCALCVLWCVFSSVSADARDDCEDSGQAVVGSVGQPSSPVGGHGDNGVVTDGSSLSSG
SHLPGSAPTGGKPPLPGVGVGVGLNESKDALTLAQEGREVVQDQHELVPQVSHHTDAGTGGKSDPNAPE
QSPNAKTELENGGGVCGDDAAAAEGEVKTTVNEGQLGGSSTSDSHSPAADRGSREQEGTVEQAASTAAL
TPVVGRETPPKGDTKEDSPEDKAATGAGITQGIPAVSQQQTHSPSTSTTGNGLTSTLGKGRAAEDISSN
NERSGKALLQEGAQHETVAGSQSQTIPAATARNTLGTTLPGDSDNSTTITTAVRSDTGTEGTPTSNHPN
RQSIEGATSPGMNSDGEAASAKKYDTVSQSAGSSTAPTTNNKTRDTASHGNSDGSTAVSHTTSPLLLLV
VVTCAAAAAVVAA*
>Tc00.1047053508375.10|S006|A---REECD|1
MAMMMTGRVLLVCALCVLWCGVSVVAVPAADVSGGGDGGADVSGRQPKPPQLETTPSNIQDPKRPSANV
DEPMLEVAATSLEGTGGDDVEDGDGEDEEEGQLVRKDNEGIRAQEQHDEHDRQNDQHDGEKERNANDPK
SGKEGKTPGKDPAKETGLQSTPEDDSPSHLPNDARRGNTQEPRNASPPGNDDRKQDSLNVSQDAPIKFT
PDTILSSSSTGGNGADNSHENQREAKNAQQASAGVKQHDAESGEKSAAPTKGEGESQLPVTADEKTSNT
TIPGISVSSSAATTAVRSETSTESSRTISDLSPSSSEDDALPKNTPDGDDASHITEDVVSPIAGTPIPQ
QTAAQTNHTPTPDDSDSSTAAPPAGESDAATTTTPNNHDARSLNNNGNNTFTEEVDQKEATRKPKSAPE
STDTAAANSEASTTAINISTNTTNKTTTGDSDSSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053508389.50|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCGAGGVYARDVDTNAVGGCMASGVLGENGSHMPDGCNKTAITMTLRSVLP
ITAVEASAGTDNTVVIQNDSHSSGTSNAGASPGGHSAGGGGGTSAGGQGSGGISSGSSASPPVPSGGPP
APPAGSPPPAAPDPPAAPAVSPALTPATPGVDSSAGSSDGKAGSSGSHRTNTTGDSSTGDQTSAAAAAH
NPSPAEGSAGTTSGTEHTRQEEEEEEEEEDYEKQQQSDETQVQQHQQHERPAEGGEESAKDKNALRTNA
TANTGDSDSSTAVSHATSPLLPLLVVACAAAAAVVAA*
>Tc00.1047053508389.100|S132|ANQ-H-EC-|3
MAMMMTGRVLLVCALCVLWCGFSGIAADFVGSTNGSAGEYWVSWWITQLRRECAEEVIRRTGGRTNVSA
VEECVRQGMDGVRAVLDGRSRWRPQRSAVVVVVVAAEDGGDPVKNGDSSERSFSSEQSLQAGRVLPAGG
GGGSGSLPGGEGGTGNNPPPPHSPPTGPSLPTLPEKKASSSAAAEEEEEEGVKSDPKNNENNPGERLQD
RETPIDNQHTQNPEEIPPGKKLNEEHNKTKQPPQGDDQPPKVEEITPRKPVEEPPIEKEDVDEPDAGAA
ERNSIESHLEATRKHAEKPLAGSEHVDKENDDQKEEKEKKREEQEDAHVQQQNGKHDTLHGLPIEAGAT
QGSLANSPLEELQQKQTSAGSTKQLEGEAPLINADGTSNGNNDLSLPSVSARAGVAGAHEAAKGNAEVQ
NNAESTETAVNKKDDSNEHLTENDKESAKDKNALCTNATANTGDSDGSTAVSHATSPLLPPLLLVVACA
AAATVVAA*
>Tc00.1047053508389.130|S095|AGWTH-EC-|7
MAMMMTGRVLLVCALCVLWCGAGGVYARDVDTNALGGCMGSGVLGENGSHMPDGCNKTAITMPLRSVLP
ITAVEASAGTDNTAVVIQNDSHSSETFNAGASGGPAGPGAPDVGGGGDSGGEGSSGPGASPPVPAAPAP
GPSGGASSGDSGDGGNSGGGGGGAAGASGGGGGGGSGSGGGGSGSSTDDHATGSVPSSSSLASPPAPAA
PGDGSAGGHDTGGVSSGSSVPAHPPPAAPPAAAPPAAPVVDPSAGSSGGKAGSSGSHPTNTTGDSSTGD
QTSAAAAANDSSPAEGPAGTTSGTEHTRQEEEKEEEEEEDHEKQQQSDETQVQQHQRHEHPAENGEESA
KDKNALRTNATANTGDSDSSTAVSHATSPLLPPLLVVVACAATTAAVVAA*
>Tc00.1047053508389.154|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCSAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITMPLRSVLP
ITAVEASAGTDNTVVIPNDSHSSETSNAGASPAVSSAGGGGSGGGAGGSGSGVGSAGGGSGAGGGSGTS
AGDQGSGGISSGSSAALPAAPAVSPALPPSDPPVVDSSAGSSDGTAGSSDSNPSNTTGDSSTGDQTSAA
AAANDSSPAKIPAGTTSGTGHTRQEEEEGEEEDHEKQQQSDETQVQQHQQHEHPAENGEESAKGKNAIR
TNATANTGDSDGSAAASHSTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053508427.20|S061|A--TIFECD|52
MMTMTGRVLLVCALCVLWCGAGGGGRAEPTQVPPGTKSSEVSGSESDKNSKGAAGGGGRSDQSKVLKEK
SSSVQDATGVAAENAIKTEAQVSSTADAEKKKEDKTQVFEDVGEKKGKEQEPKGEEEEEIEQGEGEGEE
ERREEDKDEEEQEEKRNGQKEEEVEKKEDAGAGTTEGMSAGGREQPSLSSGAEGASNITNPNSTPTTGD
GDPAADAAGTREGKQNENKDANPKETPVTAAAMKTTTATTGDSDGSTAISHTASPLLLLLAVACAAAAA
VVAA*
>Tc00.1047053508427.40|S061|A--TIFECD|52
MAMMMTGRVLLVCALCVLWCGAGGGGCSETPQDPPGGASQGGNNLDGTKNTTNGAGGGVNSGATAKSQL
SAESVTDIMVAVAGADTSAAQQQEKQASEMQEKGEDGEEDNEEGEEEYEEEEIDEGEDDAKKEESETKE
EKQDKEREEEKIKEDDADATNGMPAGGEEQPSLSSGAEEAANQTNLKSTQTNGDDDPAADVAGTAEGKQ
NENKDANPKETPVEATAMKNTTATTGDSDGSTAVSHTASPLLLLLVVVACAAAAAVVAA*
>Tc00.1047053508453.10|S055|A--T---CD|5
MMMMAGRVLLVCALCVLWCGAGCCAEESAGGVLPGASGGGAGSLQGSQPIVPEALKNSDLKASDINDKT
EETPIKVPLAEQEEISDDDDEGEDEEEGPSPPTPTKGGGGVQPQANNGKLKKENESELQTENQRHVEVE
RQNPSEKETVDAGEAGVNQQNEGSRLKPQHQKIPVQEEDTRNVEGNQPTQEKEQQTNVEEITPHNPAGD
HSPGEHKGNDGSNEGEEKDGEEGVEDHEGHRDQVREEAAHVSGAPKVNSADIQQEVQRTHAGGTLTGIK
QKTGEEKDDETEEEREQQKEQNQENPPGKEQKTKTGANTTNQINTTPADSDSSTAVSHTTTSPLLLLFV

ACAAAAAVVAA*
>Tc00.1047053508493.110|S080|A---YKECD|24
MAMMMAGRVLLVCALCVLWCGAGGGGCDDTPQALLSGSGGGTVVGTGAGPSGGADNGLFASEPNGESEG
DRLERTDLGQINSSPRGGTVGLDNKLAVMPVGSPVTRNQVLSNEALSLQSPPSPKPSAPELQNLPEGPP
LSGGSQGGEADNAVGGVGPSGSSSGSGVKSMVSASFSACTLSPPNPVDWDVLQGGKGTTATLSMDSSEK
SVKSQSAEPPAPAQPNLDRQEASTSNAEDHSPIKPHTAGNQVVNGGATEKENTQRAAVTGGPSSDTQPT
TLQAAPQEQPKTELIIVPAGKERATDPRTREKEERDSKKAPPPPPPASSAGGTPAAKELQISTEEMHQT
SPSEAQKELLGQETPSKDDAEEQNTEGTAASDSVKDEAASSLVETTAPPISTSGGADTKSVASEDADNA
QQPNHKETHKDPEPQNTSPAFTATEALPQTAIPLTTAPTNDNTTPGDSDSSTAVSHTTSPPLLLLVVVA
CAAAAAVVAA*
>Tc00.1047053508501.80|S080|A---YKECD|24
MAMMMTGRVLLVCALCVLWCGAGGGGCDETTQASPSGSGGGTVVGTGAGPSGGADNGLVASEPNGESEG
DRLEGTDLGQINSSPRGGTVGLDNKLAVMPVGSPVTRNQVLSNEALSLQSPPSPKPSAPELQDLPEGPP
LSGGSQGGEADNAVGGVGPSGSSSGSGVKSMVSASFSACTLSPPNPVDWDVLQGGKGTTATLSMDSSEK
SVKSQSAEPPAPAQPNLDRQEASTSNAEDHSPVKPHTAGNQVVNGGATGKENTQRAAVTGGPSSDTQPT
TLQPAPQEQPKTELIIVPAGKERATDPRTREKEERDSKKAPRPPPPASSAGGTPAAKDLQISVEEMHQT
SPSETQKLLLGQETPSKDDAEDQNTEGTATSDSVKDEAASSLVETTAPPISTSGGADTKSVASEDADNA
QQPNHKEAHKDPEPQNTSPAFTATEALPQTAIPLTTAPTNDTTTPGDSDGSTAVSHTTSPPLLLLVVAC
AAAAAVVAA*
>Tc00.1047053508539.60|S061|A--TIFECD|52
MTMTGRVLLVCALCVLWCGVCGGGRAETPPPDSPDNTSDGNTQNEEGTVVGAGGGDQNDQQAAPQAAAP
TTSGLPAAAPSPSPAPQSGREASEKASTTTDNEDQNKEDKKNEEQKEEKKKEEEEEEEEVEKEVEENDT
KEENDTKEENEEETKKEEPVTGTTEGISAGGQEQPSLSSGAEGASNETNPNSTPTTGDDDPAADVSGTA
EGKQDENKESNAKETPVTATAMKTTTATTGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053508539.80|S099|AML-VFECD|25
MMMMTGRVLLVCALCVLWCGAVFGHAMDDYCSEGGGNGLRHTSNGGDDGVPLKADCGLLSTRMGLIKAV
EAAEAGQGLSVTLPPGEPKETSLDNNQGGGAPGLGGNDVGVGDQPAAAAAPTIGGSGTEEQDRGLEVVD
TNDGNVAGDKKDHEDVSEADSQQQTADQLSSSSSGSSGTEGVKEPALKENSESKETSDSRSQEEEDIRS
ESDGREGEAEELVKNEEEPKNDKMGHKSPTETPGGPTNKAELQTATTQVNGDSSPETLGDVQQPEEVQG
EKDSNNNSQTRSAATIAANQQNEPSADHGESGPPSPTANGDAANNDSDKSTEDGIPNSDPAADVAGVAE
EKQNENKESNPKETPVEATAMKTTTATTGDSDGSTAVSHATSPLLLLLLVACAAAAAVVTA*
>Tc00.1047053508539.110|S070|A--TIFEC-|13
MTMTGRVLLVCALCVLWCGAGGGGRAETTSPASPASPGNTSDGNTQNEGETTGVAGEVVQNGKPAAPQA
PAPTTSGLPAAPASPSPAPQSGGEASETASATTDNKGQNTEGKKKEEKKEEEEDKEEKEENKEEKEEDK
EEKKNEEEREPVTGTTEGISAGGQEQPSLSSGAEGASKITNPNSTQTTGDDDPAADVAGTAEGKQNENK
EPNPKETPVTATAMKTTTATTGDSDGSTAVSHTTSPLLLLLVVACAASAAVVAA*
>Tc00.1047053508539.160|S061|A--TIFECD|52
MAMMMTGRVLLVCALCVLWCGVCGGERAETTPDSPGNTSEKKPQNEEIVGATGGGDQSSKPAAPQEQAP
AASGLPAAPANSLQETHSGREASEKASETIEKKDQKEDKDKGEEGEEDEEGEEDEEEEDEDKEEEEEEE
EEEEKNDTNEKEEEEEAVTGTTEGISAGGQEQTSLSSGAEGASNKTNPNSTPTTGDDDPAADGAGTAEG
KQNENKESNPKETPVTATAMKTTTATTGDSDGSTAVSHTTSPLLLLLVAACAAAAAVVAA*
>Tc00.1047053508541.20|S070|A--TIFEC-|13
MMMMTGRVLLLCALCVLWCGVCGGGRAETTPPDSPDNTSHGNTQNEGETTRVAGGGEQSGQPEAQQAAA
PATSGLPAAPPNSLQTTQSGGEASEKPSETKEKKDQNKEDKKKEEEVVEEEEEEDEEERKKEEEETKKE
EPVTGTTEGISAGSEEQPSLSSGAEGSSNKTNPNSTPTTGDDDPAADGAGVAEGKQNENKEPNPKETPV
TATAMKTTTATTGDSDGSTAVSHTTSPLLFLLLVAFAATTTAVVAA*
>Tc00.1047053508541.90|S078|A--TYKEC-|2
MAMMMTGRVLLVCALCVLWCGVCGGGCDGGETAVPRSGAGGPPPGSAELGTPLQDTQELNVESPDINGK
VPSQSSPRIEKADDEDSDDEDREGKDKKDEKEKNKVQPEKDEGKKKEGPPPPPPPPPPPAPPPPPGGPA
PSSTAVEGGPTAEKENLQKVTKKDSEAPEAPSGDATQGQHSHDTDTEDSTKNAATGSPAEPTTTLSTSA
SGSGDHVQNKADEDDAQSSEEQHDSVETGNANDVPTLSEEAPQTAETITAARINVTTTPGDSDGSTAVS
HTTSPLLLLLVVACAAAAAVMAA*
>Tc00.1047053508541.110|S068|A---IFECD|10
MMMTGRVLLVCALCVLWCGVCGGGRAETTPAASPGNTSDGNTQNDSTGVAGGGVQNGQQAAQQAAAPTT
SELPGTPPSPSLAPQSGGKASEKASETIEKKDQNTEEKKKQEKKEEEEEKEEKEEEEPVTGTTEGISAG
GQEQPSLSSGAEGASNITNPNSTPTTGDDDPAADVAGTAEGKQNENKESNPKETPVESTAMKTTTATTG
DSDGSTAISHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053508541.130|S100|AML-VFEC-|15
MMVMASRVLLVCALCVLWCGAVFGHAMDDYCSEGGGNGLRHTSNGGDDGVSLKADCGLLSTRMGLIKAV
EAAEAGQGLSVTLQPGEPKETSLDNNQGGGAPGSGGNDVGVGGQPAPAPPAAPSIGGSGTEEQVGKLEV
VDTNDGNVAGDKKDHEDVNAADSQQQTADQLSSSSSSGSSGTEGVKEPALKENSESKETSDSRSQEEDD
LRSESDGREEEAEELVKNEEELKNDKMVHKSPTETPGGPTNKAEIQTATTQVNGHSSPETLGDVQQPEE
VQGEKDSNNNSQTKSAATITANQQNEPSADHGESGPPSPTANGDAANNDSDKSTEDGIPNSDPAADGAG
TAEEKQNENKESNPKETPVTATAMKTTTATTGDSDGSTAVSHTTSPLLLLVFACAAAVVAA*

>Tc00.1047053508613.74|S008|A-----ECD|43
MAMMMTGRVLLVCALCVLWCGAGGGYAWDLSDNETLHEKHYGANGTYCRLNSNYSFCEEKRNASKREQA
ASQAGDGAQRDNDSDQSSAGGSSGGQEQTSEKNVSDRSGGATGTQLQKPGEGGTETPTPTVTAAHSADG
QGNSSEESHLGQPEGTAGEGTQASQKPGEGGTETPTPATVTAAQTSATRTPDDSDSSTAASHTTSPLFL
FLLACAAAAAVVAA*
>Tc00.1047053508735.30|S016|A-----EC-|10
MAMMMTGRVLLACALCVLWCGAASANGSDAAETHEDPSRGLQSAPQLGPAKQPEETKPIEGVSNTAEQS
LDAQEVKNGNPPKGSVKQTPTQNGGMEENLKKGEGKKSEKDEKAEQELEGDQEQPLTRKDTTEDEKETT
PALPENKEPPPPPPAGAATPPASDGNHPGDSSKLRNSASDGDIQPAADRMHSGGGAGSIRNGGGGKQSG
QSGVSGGDHLPNPSSSSGSFPRPPTHDGKGAPQDPGEDSSPQNKKSLEKVVQSGASVDSALPKVDEVQK
SEPDPQQIRPEALVTVGGTGNEARREAEGMNEASSGKQVTNEKEVLSPPAGGSAPDPNGTHNSPETNAV
NSASENEPESNSLERPSGDGEAGQQDKEADTQGTQETEVTQGTAASPVSTSGSGGAQSEADADGDDPQR
PNPEGPQNDGTEAGDTHGPTAASDAAPQAAKAITAQTNGTVTPADSDGSTAVSHTTSPLLLLLVVACAA
AAVVAA*
>Tc00.1047053508745.20|S029|A---VF-CD|1
MAMMMTGRVLLVCALCVLWCGAAVLVSAAGDVVEMESEGSESLPSGRQDGDGRSHRESEDSVQQESETA
NESLGAGRGKSSERQDGVVSTQPRNSDRTVVETETEKSKSKEEKGNKEKMENIVTPKQDGKITELTSTP
EEDRKTASPPAEGAQTQEETPPGVTPPAQNGSSAGILTATPGKAMVIPEGNSKQSQGGKTPANGLAAEM
PSTKKGEAPEAIPSPPTKNEKPEGDSKAKTNAEKPSPEVIVSVQKTEILLDDEEVTSNQRNEGLASTTG
NQEGEQSDVHAESTLPSISAASNAANDDADTDTDKGIPNNDSAAGGAATEERHQYENKEDNTKETKPLR
SAANTSETLPPGDSDGSTAVSHTTSPLLPLLVVVACAAAAAVVAV*
>Tc00.1047053508759.10|S004|A---V-ECD|18
MMMTGRVLLVCALCVLWCGAGGRCDEVLPVAVSSVISASGVSGAPDNASGQTSSGVAGNPSAEQTQLNK
VGNSAPGSPQLQVDLQTQSPTIQQTHSGAENAISSTTSKPSGEQLQNVPDGVPPGEPEASLGQEEGKNE
TIANQQSNGPPSPSSNNDIVSRNSGERTEDTSRRAETLVAAPSEEAQQRENVTRSLEQPREASTAAPAV
TTQTIFMTLPKDGESSGVKMSEASPQSARTAQTNHTTTPGDSDGSTAVSHATSPLLLLLVVACAAAAAV
VAA*
>Tc00.1047053508759.40|S122|ANQT---CD|3
MAMMMTGRVLLVCALCVLWCGASGGDGSVDEYSFAGRRAWLRRECVEEVGRRTGGGANVSAVEECVHQG
MESLRAVVDGRRRWRRQQFAVAAAAENTEERVKINTSNEGEGLSGGNGVESEQAQLQVEDLRTASGDGG
VQPEGAPLEGSNANSVLQTKASPAKEAKQVIPASSSSMRLPSDQQEEEEVEEEEVEEEEVQEEDDNSGK
AGKAQELLGCGQQETLQSSSPPGGNPSASGQGTALTAADNKKNTQLEVAKEKVYLDESAPTEGNPSATK
PSDDKPTIRQAYTIPISPPSVNFSATLRGTTDRPIPPAQVEATTYETRNNAASHDSNSRTHISKGVGSD
STEGVAKNAVNTEVSTKTDGTNNAAPDSKESTKAPDSANNKIITATPISSDSSAAVSHATSPLLLLLVA
CAAAAAVVVAA*
>Tc00.1047053508759.60|S068|A---IFECD|10
MMMTMTGRVLLVCALCVLWCGAGGGGRAEAPQAPSDTPPGNNTKNENSTVVGAGGGVQNGEQAELQEKS
PKASRLPEVQAEASLPPAPKPEGEASETASTTKDRKGQKEEQKTEKKEEKEENEEGEEEEEEEEGETAT
GTTGEISAGGQEQPILSSGAAGASNITNPNSTQTTGDDDPAADGAGTREGKQNENKDANPKETPVTAAA
MKTTTAKSGDSDSSTAVSHTTSPLLLLLVVVACAAAAAVVAA*
>Tc00.1047053508761.30|S010|A----RECD|22
MMAMMMAGRVLLVCALCVLWCGAGCVFCEKVSPDGFCDKKSVELSSLANKTDEELKEKCCKNEDDETTC
VNTLKNNISDAMKNEKTKEDNAADRDPKVAHVSGVPVGSSTTKSSTAAGVNNAGVSPPITPPLKVEGDV
DAKVHSPAGGASHQPHSDDGRSEAERSHHSEAEGSNQHSVGVQGETIHKKEEKTPETGVNFTEARDGTD
GAPPPSQDPPNTTESHEDKSRRVTAPDTTPALNTSPGSNQEQTSQSSSPSGSDTTGSLDKEDPEKNSKN
AEIYDAPLKDEGQQRESTAGNEDATTVESAAEQSNTTAPRDSDGSTAAAAAVQPEDGMESNPAKNDLSP
PSTEVAAELSTAPDAEGASNSEENTNSQSVGNPNVTIATATQKNHTTKPGDSDGSTAVSHTTSPLLPLL
LVAFAAAAAVVAA*
>Tc00.1047053508761.70|S100|AML-VFEC-|15
MAMMAGRVLLVCALCVLWCGAVFGHATEGYCSEGGGSGLRHTSNGGDDGVSIKADCGLLSTRMGLINAV
EAADEGGLGGDAGSSQDKSKESLQDKKLSGNTEGDAALGSGGVVVADPPPPPAAAPLQKPGERNTGEEG
KQEELDKKGNEAEDKSRGEPGPPKPKPEQSSSSASGGPGTQSDVELALEVTSEGNKFSDDALKQEDAGK
TEVTKLSDGEPEKGKSNMALTETHDSQAEQKEAQLPKPPTLPTTQVNEHYSPGDTVAKQQLKKTQSEMD
PNTNSQTKSAVTITASQHNEPSADHAGSTTPSPAASGDAANNETDKTTEDGIPKNDSAADGEEKREEKR
NENMNANPRETPVEAAAMKPTKATTDDSDGSTAASHTTSPLFLVVACAAAVVAARE*
>Tc00.1047053508761.90|S010|A----RECD|22
MMTGRVLLVCALCVLWRGFSLVSAVTGDYREHSGQGVVGSVGQPPSPVGGHGDNGVVTDGSSLSGGSHL
PGSAPTGGKPSLPGVGEGVGLNESKDALTLAKEGHEVVRDQHELVPQVSHHTDAGTGGKSDLSAPEQSP
NAKTELENGGGVCGDDAATAEGEVITTVNEEQLGGSSTSGSHPPAADRGAKEQEGTVEQAASTAALTPV
VGRETTPKGDTEEDSPEDKAATGAGITQDIPAVSQQQTHPSSTSTTGNGPTSTLGKGRAAEDISNNNER
SGKALLQEGAEHETVAGSQSQAIPAATARNTLGTTVSGDSDNSTTITTAVRSDTGTEGTPTSNHPNRQS
IEGATSPGMNSDGEAASAKNYDTVPQSAGSTTAPTTNNKTRDTASHGDSDSSTAVSHTTSPLLLLLLVV
ACAAAAAVVAA*
>Tc00.1047053508761.270|S015|A---H-EC-|9

MMTGRVLLVCALCVLWCSVSAVNGDESDENVDFSSGRSEAPQGGSSEVMDGREGLDHKSCSVEPGSEGN
TAECTKATTNDTDAISTNPSLPSHKSSDPNPQTGLQPPAPPTGAGQSHQTNPVQDAGVTRQVRQDVEEV
KTKKGLEEQNKQKNKESHEKQSSREDASVIKGNQLVGQEAALQGDPAQQERKQLEVEPGQPQHETDVQH
RGLSQHDHLLQGHEEVQEKRRRGEEQPQLPKAQKEKVPTASTTEPKSTPQSPPPVKPRGMQQEGSAASS
SDPLKREIPSVLTKSKPNETIDPPLPQSSAGEGGAAAALGADEEDAKIRKDAEFPESAATEEDHQHKHS
LKNDGEAKKEKTAFGTNNTAITNDSDSDSSTAGSHTSPLLLLLHVAAAAVVAGPA*
>Tc00.1047053508789.80|S100|AML-VFEC-|15
MAMMAGRVLLVCALCVLWCGAVFGHATEGYCSEGGGSGLRHTSNGGDDGVSIKADCGLLSTRMGLINAV
EAADEGGLGGDAGSSQDESKESLQDKKLSGNTEGDAALGSGGVVVADPPPPPAAAPLQKPGERNTGEEG
KQEELDKKGNEAEDKSRGEPGPPKPKPEQSSSSASGGPGTQSDVELALEVTSEGNKFSDDALKQENAGK
TEVTKLSDGEPEKGKSNTALTETHDSQAEQKETQPPKTTTLPTTQVNEHSSSGDTVTTQQLQKPQSEMD
PKNNSQTKSVVTITASEHNEPSADHAGSRPPSPAANGDAADNETDKTTEDGIPKNDSAADGEEKREEKR
NENMNANPKGTPVEAAAMKPTKATTDESDGSTAVSHTTSPLLLVLVVAAAVVAARE*
>Tc00.1047053508789.150|S011|A----KEC-|2
MAMMMTGLVLLACALCVLWCGAGVGYAEDVDVVSGDPGTRGERGGGDKSSLADGSHGGSGGSNGDSSHE
SESEPSDSASNEKSLNPQVDEDEDPNSSEQPLRQGKEGSKGKQDHSQSAPQNGSPHKVNGAETLDSAAQ
VQLSATPNAELNTNVADGEIASGGSGNTGHNTGLSPNSSDSSAPPVPPAMTVPAGDTNPTASKDLQNIK
ETTSTTPPSNSKTAAEAPQTPSGNGAPKQHRKESDTPDLKDAPASHTAESTAKSIYTMGSDGAQKNEEK
FDNGDQRSNRKETQDGLEDRNTDDAPTASETEPETATTQKNATPKFGDSDGSTAVSHTTSPLLLLTVAC
AAAAVVAA*
>Tc00.1047053508869.59|S001|A---H-ECD|18
MAMMMAGRVLLVCALCVLWSVPADGDIVVVSGGEDNILKELFIPVARLQLRREQGAAEATADAKAAAET
AAKEAEAAAEAAKAAAETAAEAAAEAAKAAAEATESAATNATTASEAATKAKAAATKAKAAAEATETAA
EAAEAAKAAATAAATATEAAEAAKAAADAAAEAAKAAAEAAAEAAEAGEAAVHADAAIILATSAAEAAK
EAAEKAAKAKAAAETAEAKAAAAAAEKAAATEADAKAAAAKTPEAAAEALRGTGVGEDEVKKATHDQDN
SVEHHSGEKQELIKEEERQEKEQHEKQQHQQRENSAGNGEESAKDNTANGTNATAIKDYSDSSTAVSHT
TSPLLLLLVACAAAAAVAVAALE*
>Tc00.1047053508871.40|S001|A---H-ECD|18
MAMMMAGRVLLVCALCVLWSVPADGDIGVVSGGEDNILKELFIPVARLQLIQEQGAAEATADAKAAAET
AAKEAEAAAEAAKAAAETAAEAAEAAAKAAEAAAEATESAATKAKAAAEEAKAVATKAKAATEEAKAAA
TKAKAAATAAEAAEAAKAAGKAAATATEAAEAAKAAAEAAKAAAEAAGEAAAEAEEAAAEADAAITVAK
SAVEAAKEAAEKAAKAKAAAETAEAKAAAAEAAAAEKAAATKADAKATAAKTPEAAAEALQYTGVGEEE
VKKATHDQDNSVEHHSGEKQELLQEEEPEREQEQHEKQQHQQREHSAGNDEESAKDKTANGTNATAIKE
DSDSSTAVSHTTSPLLLLLVSCAAAAAVVAA*
>Tc00.1047053508871.60|S103|ANP--F-CD|11
MAMMMTGRVLLVCALCVLWCGAGGGFANEAEASANGAASKTTPADEIILNWYELTHEECATDNTKNGTV
NVPAMKRCINFAMKGICDTFYNKTPSEIHGPEVKDMCTYYATIPDEPVESPTTQGPPPDSAVSNTTSNE
GTPKNAPEFDAAGRGEGKQDEKEHGNTKEKAVEAAAVKNITKNTDSDSDGSTAVSHTTSPLLLLLVACA
AAAAVVAA*
>Tc00.1047053508871.150|S032|A---H--CD|8
MAMMTGRVLLVCALCVLWCGAGGRCDEEIAKDPVGPSGAPGNLGKDGMEKADRSAVGHGELGLVPEPPK
DVSQGGPSERTLGGPGGDAVDKNKDVLISGKVDEFKSPSPEKQPPGTDDPAKSIEEEVELQQQRNDGKE
LENQPQLQVPVTQQEHGVLPLSLPHPQSQQSHQNTQQQQPQPQILRKEGGMPHEKGSEKGTQELDKLKE
ESQDTELQNKVKEEKMKQELKNEEKGGEHQPQLHVPVEQQEQSALPQPPQSMQQPSPPQEQPRQQKQQP
PHGNPADNEQESKTDKNAVGTNKTANGTATPADSDGSTAVSHTTSSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053508873.10|S055|A--T---CD|5
MMMMAGRVLLVCALCVLWCGAGCCAEESAGGVLPGASGGGAGSLQGSQPIVPEALKNSDLKASDINDKT
EETPIKVPLAEQEEISDDDDEGEDEEEGPSPPTPTKGGGGVQPQANNGKLKKENESELQTENQRHVEVE
RQNPSEKETVDDEAEGTNEKETIGLQPQHQKIPVQEEDTRNVEGNQPTQEKEQQTNVEEITPHNPAGDH
SPGEHKGNDGSNEGEEKDGEEGVEDHEGHRDQVREEAAHVSGAPKVNSADIQQEVQRTHAGGTLTGIKQ
KTGEEKDDETEEEREQQKEQNQENPPGKEQKTKTGANTTNQINTTPADSDSSTAVSHTTTSPLLLLFVA
CAAAAAVVAA*
>Tc00.1047053508873.30|S030|A------CD|31
MAMMTGRVLLVCALCVLWCGAGGRCEKVVVGSAAGGGGDVSGGKGAVKNTDTSTSGPDTSDSSIDVSKV
NQATEKSEVKSLEGNGDNVDQQDVVVSRVEGEKKKNSSEQLEEPMKDDLGKEKTNPEIKNKEQEGGQPP
QAQLNVQQQPQPQTQQSQTQLQQQPHAPASEEGKGVGENNTGGAGQPPLGVEDKGNEDSKALGKGDSLK
SPGKESENSERVQTTAPNTVTPEHETQNEMLTPEQKTNESQSTDTSTNLPELQKENKEYPASTEGTARS
TSTGSQEQEAEPSTSEEPSPFEEEQSTVTKTTEDARTPDAAATEKRQTVNNEKVGDSDSSTAVSHTTSP
LLPLLLVVACAAAAAVVAA*
>Tc00.1047053508873.160|S025|A------C-|17
MAMMMAGRVLLVCALCVLWCGAWLCDATQTSSSAPHRDNAEETMTPEEVTKAIEKLTEEVLESIRLSCR
MSFITSVNATLPAHNDTEVEKCVNKTAVGISGVTSRGRPAAATTDATFASPLPSSSSAASALQGQAQGS
PGAAPEPVKPPQTDPVNNEQLSEAPASTGGGPGGGGELADRSSRTPTDDAKTHEARPAGNATSTPTATQ
GDSEKSPANTTRTRETNETDDTDGSTAVSHTTSPLLLLLLVACAAVAVVAA*

>Tc00.1047053508873.210|S105|ANP--F-C-|4
MAMMTGRVLLVCALCVLWCGAGGGFADKVVEAAAGVVASNRTDEENLILNWYVLTQEECANESTTGGKL
NVTAERICMHKVMKGICNAFYNKTSGVTHDRDAKFICTYYATIPEEPVEPTTPQGPTSHSAVSNTTSDD
GAPKNAPESDVAGRGEGKDDYKEHGNTKQKAVETAAVENDTKTTDSDVSTAVSHTTSPLFLLVVACAAA
AAAVVHGLCDCVGRCIGVTNTSVWRVSVCWNDVRMTREGCCL*
>Tc00.1047053508873.250|S074|AML-YKECD|9
MAMMTGRVLLVCALCVLWCLTVFGDARDNRCVEDDGNVLTHTHNRGNEGLRLKADFGLISTRMGLIKAV
AAVDGGDGAGNDSLENKDKSPQGGVLAGTKDNEAPGAGGVQGAAGDENGQLPAAGREGNENKDVDSGIK
AATDSQDKTNDQLSSSSGSTPSRSGEKPSSTGTSEMTQLPKDTVTKLDADLQDKRESSEGIKAEETEEE
ERQKIKAHTGSSESKNNGGETTPPPLTSSDEESPISDQENSQNSKKVKNEATLSESKTASEAPAPPSKD
ATQGQHSHDTDTEDPTKNAAAGSPVEPTTSSTSASGSGDHVQNKADEDDTQSHEGQHDSLETGNNNVVP
TLSGTASQMPETATATQTNDTTTHGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053508873.450|S015|A---H-EC-|9
MAMMTGRVLLVCALCVLWCGAADGDVVVSGGEDNILKELFIPVARLQLRQEQGAAEAAADAEAAAETAA
KEAKAAAEAAKAAAETAAEAAKAAAEATESAAAAAAESEATKATTVSEAATKAKAAAEEAKAAETKAKA
ASEAATKAKAASEAATKAKAAATKAKAAAEAAATAAEAAEAAKAAATKAKAAAEAAKAVAEAAAEAEEA
AAQADAATLIAKSAAEVAKEAAEKAAKAKAAAETAEAKAAATTEADAKAAAAKTPEAAAEALRYTGVGE
EEVKTATHDQDNSVEHHSGEKQELIKEEEPERQENEQHEKQQHQQREHSAGNGEESAKDKTANGTNATA
IKEDSDGITAVAHATSPLLPLLLVACTAAAAVVAA*
>Tc00.1047053508873.460|S055|A--T---CD|5
MAMMTGRVLLVCALCVLWWGTPGGRCDEGGTGGTPPGASASDVVGNGSQESPPIAQGGSHTPGLEAPGI
KNKNEDPDDEQLLTEDEEEEEESSDEEDEDEDRDRRLQISGKEGIPTTPPPGGGGGGKSEAAGGKLEKV
NEDGPKPEKQHPVESAAQKTSEKETVDAGEAGVNQQNEGSRLKPQENPNPVQEEDTRNGEGHQQTQEKE
QQTNVEEITPHNPAGDHSPGEHNGNDGSKEMEEGEEGGVEDHERHRAQEREEAAHVSGAPKVNSADIQQ
EVQRTHAGGTLTGIKQKTGEEEDDETEEEREQQKEQNQENPPGKEQETKTGANATNQINTTPGDSDSST
AVSHTTSPLLLLLVVVACAAAAAVVAA*
>Tc00.1047053508873.580|S080|A---YKECD|24
MAMMMTGRVLLVCALCVLWCGAGGRCDGEDTALVVASPGGRSNDGQSGPGPAPPSPTGIRTSGPASIVP
ESEGSQKIIAGTYSEGRGEKNYQDEDGEEESVAEDGENSRHHEGLSEQPTQQEVSHEETPEGKGLKERL
EEKDVYPPGEEVIKGAQQSQSQQPPPQQLQVQITAPAGREGTTAATGPARPPAPAEPPSMDGSRTIEPT
DSRSPSQESHDKSPLLTKTESSAPDPPLKDAFPEQHGQETTTPDSVMSAPAGRQARIATPSTSTNDSGE
AQSKADGNDAQRPNPNESHDESDSGKTKVPTTLSEAATQATETVAATQTNHTKTIGDSDDSTAASHTTS
PLLLLLAVVSCAAAAAVVAA*
>Tc00.1047053508939.30|S043|AG-----CD|27
MAMMMTDRVLLVCALCVLWCGAGGICDEKAVGGCMASEVLGENGSNMPNGCDRTALMLSLRSVLPIIVA
EVSGEEDGPSKGGSGGGGGVNPGGKDGGKDGAAGAPASGGGGNSSGSVSPGGGSPHHPGAGTVTSGNPL
SRPQNASQTEVLRRDETENQSLSSPKGKAADTPVNGAQTKNPDNSVIALPDNLASKESSNKVKSESLTA
PGAAPKPSPEGPNTELQGKGKASPELSDAKLPEPKTEHQTTTSEEGKNRSQNTSASTDSPAKQGRNNED
PVSTSGTAESISTGSQEQAATTSSNESFSPLQEETSTETTNVENSRPSDTAQTEKRQNGGKEKAGDGDS
STAVSHSTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053508977.20|S133|ANQ---ECD|6
MMAMMMTGRVLLVCALCVLWRGVCVVAVPAADVAGGGDGGADEYFVLRWHAQLRRECAEAFGRRTGGRK
DVFTVDDCVRRGMDGVRAFGDGRSRWRRQHSAVVAAAADGEVDDKSGEGSGDTLKGLSSSDQMSQAGQN
QEERRELTGSLEVTNTLEGSEDSQITGEQNFSLDVDRPKQTGSQEPTVGQPEDEEGTRNLQLPPPPPPP
AEPLPPTPRQPPPGTNTLQSEKTNPQITAEKHSKPQDGGHSHETKMLQTKGSTKHEEGASSLQSPESVS
HLSREKTTPLSTSTDSSGVAGSTVENSGANNPKPPAASVTQHDSKGDIGSAALPANNTELQSEEIPNAG
IIATTYDDGDDSSPAAPTAERTTAGTRSTQASGDASDVERANNDDVNDDVAHNDKTAEFEAASGGKDTE
ADNNERYTSEPENATNKTINTETIADSDGSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053508977.50|S121|ANQ----CD|9
MMAMMMTGRVLLVCALCVLWRGVSVVAVPAADVAGGGDGGADEYFVLRWHAQLRRECAEAFGRRTEGRK
DVFAVDDCVRRGMDGVRAFGDGRRVWRRQRSAVVAGDDTTDDDSTRGSSSEVQTETETGSLDGRTPKPS
VKPIPGEVPDGQDSGKISEASVPTINGTGENLDGEEEEGDVSQDESQEDRDGEDEAVDAAVGNGGSETS
HTEHEEEKERVKEEKAGSTTNEREGDENNAAGRRPPQGSAASRPALPVDVSNPQNPVLGQDGAGGEKAG
AGPVVLPQAAGLREAERAPAKLTPGGGAAGKETEKQNGTAEQVAAKEVQTAVEDSSAEAAAAGKDSKGE
KEEENVSEAAKEESHGDVDEEAAGKNGGNATKKLQKEATDDEAKTKKRNEQKEAENANNTKEEPDEEEA
KKAAQEEAAADKENMASARIPTKINTTTPENSDGSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053508977.130|S121|ANQ----CD|9
MMAMMMTGRVLLVCALCVLWCGVSVVAVDVAGGGDGGADEYFVLRWHAQLRRECAKAFGRRTEGRKDVF
TVDDCVRRGMDGVRAFGDGRSRWRRQRFAVAAAVDGEVDDKSGEGSDGTLKGLSSSDQMSQAGQNPEER
REHAGSLEVTNTLEGSEDSQITGEQNVSSDGDRPKQTGSQEPTVGQPEDEEDTRNLQLPPPPPPPAEPL
PPIPRQPPPGTNTLQSEKTNPQITAEKHSKPQDGGHPHETKMLQTKGSTKHEEGASSLQSPESVSHLIR
EKTTPLSTSTDSSGVAGSTVENSGANNPKPPAASVTQHDPKGDIGSAALPASNTESQSEEIPNAGIIAT
TYDDGDDSSPAAPIAERTTAGTRSTQASGDASDVERANNDDVNDDVAHNDKTAEFEAASGGKDTEADNN
ERYTTVPENAVNKTINTEITADIDGSTAVSHTTSPLVLLLLVVACAAAAAVVAA*

>Tc00.1047053508979.60|S076|AML-YK-C-|1
MMTGRVLLVCALCVLWCLTGFGDARDNRCIEGDGNVLTHTHNGGNNGLRLKADFGLISTQIGLIKAVEA
GEREEESESDNDSLVKKDKTAPGSEPAVTGDNERRGTGVVQGVAGAGTPSLPASGPGVSRTGAETRQLP
VAVQEGNEKNNLDPKKKESKESQDQNTDQLPSPSGSSSTRSDEKLSSKVTSKITPLPKDTETESGADRQ
DKTGSEEAIEEEDGDEDKEQKQEKNTLQPEKQEGQNNGGGAPPVPAPPTGEESPTAEKESSQNITKVKK
ENTPSRSKTDSETTQPPPGDATQGQHSHDTDTKDSTKNAAAGSPAETTATSSTSTSGSGDHVQNKADED
DAQSSEEQHDSLETGNSNVVPPLSDTAPKTARTTTDAQTHGTVTKVGDSDGSTAVSHTTSPLLLLLTVA
CAAAVVAA*
>Tc00.1047053508999.70|S064|A--T-KECD|5
MAMMTGRVLLVCALCVLWCGACGGGAEMNDESLVGSQHVSGVSEKAPNGLPQPGERGPDSAGHSLNKNN
GDNSNLQEGTGTGTTTDRVGKEEEEEVVGNDDLEEEEEEKERSKEREDTPQAGKSESLSKEAAATIPAA
SGLSESGGGSPSGVDGVGPSESSEGSEDLNLEVPVPVVISPPSIPNAAAGGSQNADGALSPRKNNFPET
GVHSGKTPLAPSLPKSQASAMPKPKAEEQSSTEQDTEDSPDTEEVTTGKENVQNTVETGIPSSSSSTAS
KPPVQQTTPILTQSPAAPSPERSAPATSEEKSTAPSFSAGEGSRRATNVAQNSKEEKNEKLPSENETES
KAVEQPSGDDLAEQDSPVGTTASPIPASSSADAQKNADADNSNAQVLKSEGTNKNSETGYTNLASTAGD
AATQTEKALADAKANDTVTPGDSDGSTAVSHTTSPLLLLLLFACAAAAAVVAA*
>Tc00.1047053508999.80|S008|A-----ECD|43
MMAMTMTGRVLLVCALCVLWCGAGGVCDEGQEAGTLSPPPGSVHGDQGGVLSGIGRMKPSDIDGQVAVD
GGVRDREESKHLSSHVPLVDAKDVTPAGIGGAGNGAVEEVAPEENESLQNSCDEDGEMSEGCVKVQGSN
GFPGSGGGHVDRGRQQDDRNPPLPLSDQTSSEEINSPLPAEGKPKNRRPVSRQLPVEEEQTDPVNIRLQ
EEAATLESEAVRNVASSHSQESAAELANGTLPAHARVTEAEDRSKHIVDPHKDAAEKQKKPVHTTGKSK
STAASGDAHKTTASPAAVDNEAAIKKAKSPGDASSLTSISDNSSNNDTEQNNARDTSEEASHSTENAAT
HSAGIPRAPNTTAKTDDTATQEDSNSDGSNVKMGEAAPQTAGTAQPNDTATTGESDSSTAVSHTTSPLL
LLLLFACAAAAAVVAA*
>Tc00.1047053508999.150|S016|A-----EC-|10
MMAMTMTGRVLLVCALCVLWCGAGGVCDEGQEAGTLSPPPGSVHGDQGGVLSGIGRMKPSDIDGQVAVD
GGVRDREESKHLSSHVPLVDAKDVTPAGIGGAGNGAVEEVAPEENESLQNSCDEDGEMSEGCVKVQGSN
GFPGSGGGHVDRGRQQDDRNPPLPLSDQTSSEEINSPLPAEGKPKNRRPVSRQLPVEEEQTDPVNIRLQ
EEAATLESEAVRNVASSHSQESAAELANGTLPAHARVTEAEDRSKHIVDPHKDAAEKQKKPAHTTGKSK
STAASGDAHKTTASPAAVDNEAAIKKAKSPGDASSLTSISDNSSNNDTEQNNARDTSEEASHSTENAAT
HSAGIPRAPNTTVKTDDTATQEDSNSDGSNVKMGEAAPQTTGTAQANDTVTTGESDSSTAASHTTSPLL
LLLLVACTAAAAVVAA*
>Tc00.1047053509079.20|S004|A---V-ECD|18
MAMMMTGRVLLVCALCVLWCGAGGGGCTEGQLPDVGPPVISASGGVVPDTATSHTAPGGAGDVSAQQSQ
LNPVKDSASGSPPLQDALKHEPLTEQPQSDHENTDPPPHSKSLQEERRDGTPEDSPGELGALPSQENTM
HASIEGPELNNPPPYSSNNNTVSSNSEERTEDTPRSTEIIDAAPSDEGHERENAAPSLEQPQETSTAAP
AITTQTSSITPPDESGSNTVKMSEASPQSTGTTQTNHTATPGDSDGSTAASHSTSPLLLLLFVACAAAA
AVVSA*
>Tc00.1047053509081.20|S122|ANQT---CD|3
MAMMMTGRVLLVCALCVLWCGVFGIVAYGACGGDADGSAVEYSLLRWRAQLRSECAEEVSRRTGDGANA
SAVEECVRQGTDGVRAVVDGRGHWRPQQFVVVAAENAEELEHNHESSPQTLTGSVAQLPDQQPLESSPN
SVPGSAVITTGEGKPTSSAQPPGTPDKGSEGLIKKESDDEGTKEKSEEEEDEEVEETDEEEDDNAGSGT
SDGSQEQGKQKAGTGQRASGGTGKENGNVVAGNKLTEAAAASPPVVSVDVENPKSVELTRDDVGGKRQT
HEKTVQEPPAVKLRENVAAEIISTEDAAEGEKQKAEEKAEETETKEEQRTTAEKLKEETPTTPEKTTKE
EQKDKEVQHVQSKNEEKETDGAEPTAKKEADVEKTAAFKNINMNNITKPGESDSSTAVSHTTSPLLLLL
VACAAAAAVVAA*
>Tc00.1047053509081.110|S007|A--F-RECD|2
MAMMMTGRVLLVCALCVLWCGAAVVVSSEPDVDGTSGDSASRGGISLESPPTVLSPLPPVKSDFAEDEG
EGVSGKEEMERSSEEEGSAPVLDTKKSTPIKPQQEATHTLAGKTSEGMDGVAGVEGGGKEKKAEEKKDD
KSKEKPGSTLLTVSGSNLTGEQNPRVHPPGGTQESEVVNPLTDSSPGIGVQQQVSLGLLEGAPAKSTTD
ANPSSLSTGGRGFDNGEGREDGSGITELPAAREGQIEMEDGGRKVKSTTGVEKELQSPVNKAANTSETV
INGYRKSRPTAATALQSDDGSESNPATNGLNHSSSEGIAHLSTTPDPEDASEGTENATSQSAEIPTAPI
NTVKTNDTAIPGDSDGSTAIPHTTSHLLILLPVVACAAAAAVVAA*
>Tc00.1047053509081.150|S001|A---H-ECD|18
MAMMMTGRVLLVCALCVLWCGTSGGRCDDVKQKELLDQRSVSQLGEESQRASSESIDGGPEEAKQRLEK
QKGMDAGPQVNSGVQTPSESLSAKEEELTKKRDELSPKPHNENGVNPPPEHVANEQQENPARNNPIRRV
GESTNDPERKDSSKLPPPTSDPPVPTPLTPNITNETPPITTGNIAVGKGKGTDVENEDGKRNKTNEGKQ
QKIQTQQQQEQLLQVQQETLSASSTGPVEKESTPPPVAKQQELPPKEVTTDLKEQLRKEAPSAATHSKS
NGNNDPTLSSAPGDAAAVANHSADKNTATVHNDTESSETVVTEEDHQNEHTADNEGENMKNKNIVVTNH
TTSTQNSDSSTAIPHTTSPLLLLVVACAAAAAVVSA*
>Tc00.1047053509095.10|S091|AG--YKECD|14
MMMTGRVLLVCALCVLWCGAGWVYAREFENNALGGCMASGALGASWYHMPSGCDKAALTPPLRSALPIP
AIKAEASEDDVPLREEDDSISTSGAVVGTAMPGESDGAALVIQSGPPAGGVAPTTPSGGSSTQNMESQR
AVQHLEPTDPAASVLPKVEVPGEPMPIAEESLSNTQDRPEIRVTGEDNTEREKLRSAVDTGDRFSDQPK

EPTPPLKTTPQLQPTTPVPPPSSKASTTELSSGEGNPQAATTDTQTPTPTIGKTTTSETATDYKAPKTP
SKDDEAEQHSKERVPSDLMKNTANGHPADTTASSIPTIGSGDVQRNADKNGNDAQRPDTKGTHNDPAAV
NTNDTLTASVAAPQTTERLADAKTNHTVTPGNSDGGTAVSNTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053509115.30|S133|ANQ---ECD|6
MAMMMTGRVLLVCALCVLWCGVSVAAADVAGGGDGSADEYFVLRWHAQLRKECAEAVGRRTEDRKDAFT
VDDCVRRGMDGMSAFGDGRRVWRRQLSAVVAGDDITDDDSTRGSSSEVQAETDTGSLGGRPPKPPLESV
PGAVPDAQELGKLSEASGPTINGTGETLDGEGEEGDVSQDEGQDDKDGKDEVVDAAPGNGDSETSNKGH
EDEKERVKEEKAGSTTKEREGDENNAAGRGPAQGTTASRPASPVDVRNPQNSVLDQDGAGREKGGAGPV
VLPQAAGLREAEGVPAKLAPGGDAAGKETERQNGTAEQVAAKEVQTPVGDSSAEAAAAGKESKGEKEEE
NVSEAEKEKSHENVDEEAAGKNGGNATKKLQKEAMDETRLKKRNEQKEAENANNTKEEPDEEEVKKATQ
EEEAADKEKMVSARILTKINTTTPADSDGSTAVSHTTFPLLLLLVACAAAAAVVAA*
>Tc00.1047053509195.30|S097|AGWTH-ECD|44
MAMMMTGRVLLVCGLCVLWCGAGGVYARDVDTNALGGCMASGVLGENGSHMPDRCNKTAITVPLRSVLP
ITVVEASAGTDNTAVVIQKDLNSSETSNAGVTAAVSSASDAPDGGSGASPGAGAPAAAAAPTLPTGGQD
NGSIPPGPPAAPVVDPSAGSSGGEAGSSGSHPTNTTGDSSTGDQTPAAAAAHNSSPPEIPVETKSSTGH
TRQEEEEEEEEEDNEKQQQSDEAQVQQHQQHEHPAENGEESAKDKNALRTNATANAGDSDSSTAVSHAT
SPLLPLLLVVACAAAAAVVAA*
>Tc00.1047053509195.50|S104|ANP-VF-CD|10
MAMMMTGRVLLVCALCVLWCCGAVLTVVATDDFIIDENTEQKMVLLWYNIYNKECEEKNKENGSLNDSA
MKSCMRTSMKEICGVFYNDTSGETPDPESDRICKEYTGDPVEAAESSTPQDKPSPGAETPVAAPTPETS
KDEAEEMGLTPGIPAGDSPAKPTEGPPLPSAAIDAASNETQKGITEVMPKNAPESNATRKEEEEKRNER
NHNNTKTTPLDADAMQRITSSADSDSSTAVSHATSPFLLLLLLLVACAAAAAVVAA*
>Tc00.1047053509195.70|S043|AG-----CD|27
MAMMMTGRVLLVCALCVLWCGAGGVYARDILKNAQGGCVASGGFGKKRSYLWSGFDKDVPTPFLRSVLP
IPVIQAGDSEGVSSKENNGKNLILGDGVSGAEITAGVGRGGGGSDGRGGVNSAGEEGAGGSHAGSVPGA
GSSPPAGGPASGGGSSPDRSANTGTTVSLSSPLQREAQQEVLQSDEAKNQSRQLLDGKAPDTPVAETQS
RGSGPARGQGVDDTSTLSGKEQHSSEEPRKEDGDSDTLQTVDLAEDPNTKIEKKGKVLPELSKATLPEP
QDEHPTKTPEKEKKGSQNTSASTDSPAKQEGNNEDPVSTSDTAESVSTGSQEQAAATSSNESSSPLQKE
TSIEKTTVENSQPSDGAQTEKRQSGDKEKVGDTDGSTAVSHATSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053509217.90|S016|A-----EC-|10
MAMMMTGRVLLVCALCVLWCGAAMVVVAEVVNSSSEPAVEKSIIAPDPQKGNDLREITDVEGPKPLEDD
GIRDSATLPERETCKNDLTKSPMCNKGSEVVIDSPSVLVGPNEHHEAQDRGSPAPSEVDKTREKKEVQE
RPQDVETLPPDPATVKEPKITMPAEHSSSPSPPNATVTASSAEIPGGGGGTVQRDNMPNTSNDNDGSKS
RTAQPDSASGNTPVSADEDTSSNGGAPQVNTAADTDSAGSTTALSTTNTKKENNGDSGGSSLAASPAVW
NNTDTTTTTTTHDASKYKKDGVKLPTEDLEQNASKTNPDADSGTTETAAANSEVPTAANNATNITSNTE
TTADSDSSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053509287.110|S011|A----KEC-|2
MAMMMTGRVLLVSALCVLWCGAGGGYAEDVGVVSGDPGTRGERGGGDKSSLADGSHGGSGGSNGDSSHE
GESEPSDSASNEKSLNPQVDEDEDPNSSEQPLRQGKGGSKGKQDHSQSVPQNGSPHKVNGAETLGSAAQ
VQLSATPNAELNTNVADGEIANGGRGNTGHNTGLSPNSSDSSAPPVPPAMTVPTGDTNRTASKDLQNIN
ETTSMTPPSHSKTAAEALQTPSGNGAPKQHRKETDTPDLKDAPASHTAESTAKSIYTMGSDGAQKNEEK
FDNGDQRSNGKEPQDGLEDRNTDDAPTASETETETATTQKNATPKFGDSDGSTAVSHTTSPLLLLLVVA
CAAAAVVAA*
>Tc00.1047053509419.20|S012|A----REC-|10
MAMMMTGRVLLVCALCVLWCGVSVANGDTGNDLEHSGQGDVGIFSHSSSSVVGHGDNGVVTDGNFQGSG
SHSPGFAPNGGKTSLTGVVEGVGLKSSKDALTPAEEGRGGMQGQQELVPKVSHQPEAGTTGKSHHNAPE
QLPNAKTELGNGGGATAEGDEVKTTVKDAQLGRSSTNDSHPPAADRGLKEQEGTVRKATSTVALTPAVG
RETPPKADPKEDSPEEKAASSAGVTQDSPTVSQQQTHSSSSSQSGIDPTYTPGEGRDAEEIFNNNQPSG
WVVVKEGAQHETVAGSEKPTIPAANTRNTIGTTISGDSNSSTATITALRSDAGTEGTPTTNHLNRPSTE
GATPPETNSDGETVSANKYDTVSQSTGSTTAQTTNAKTGDTAKPGDSDCGTAVSHTTSPLLLLLVVACA
AAAAVMAA*
>Tc00.1047053509419.80|S061|A--TIFECD|52
MAMMMAGRVLLVCALCVLWCGAGGGGCSEPTPDLPGTQSEDRNTPKNEKETIGGAGGGGQSGKPAASQE
TSSPVQIEMGTGAGAATNSSPAPKPGKQQASAILTPKTENNNEKTKEEGTRSEEEENEDENEDENEEDE
EKEDGGEDHKDEKDKEKEEDYTGTTVGTSAEGQEQPSLSSGAEGASNKTNPNSTPTTGDGDPVADVSGA
AEGKPDENKEANPKETPVEATAMKNTTVNTGDSDGSTAVSHTTSPLLLLFVVVACAAAAAVVAA*
>Tc00.1047053509419.150|S100|AML-VFEC-|15
MAMMMTGRVLLVCALCVLWCGAVFGHAMDDYCSEGGGNGLRHTSNGGDDGVSLKANCGLLSTRMALIKA
VEAEDGQELSGPDSPQDKSKVSSPDNKLGNNTQSTGAPGAGGSIVGGQPAELPPKPGGSGTEEQVRKLE
VVDTSGEEVAGDKKDHEDGTATGPQHQSVDQLSSSSSSSGSSGTEGVKQPSLKENSEISETSNSRPQEE
EVLPSESDSPEEEADVTILSEQETEELVKKKEDKKNAINEAPTETHGNPTNNAEIQTAIPTTQVNGDSS
PETLEDVQQPEEVQGEKDSNNNSQTKSAVTIAANQHNETSADHGESGPPSPTVNGDAADNEADKSTEDG
TPNSDPASDAPGTAEGKQNENKDANPKETPVTATAMKTTTVTTGDSDGSTAVSHTTSPLLLLLLVACAA
AVVAA*

>Tc00.1047053509525.230|S010|A----RECD|22
MAMMTVRVLLVFVLCVLWCVFSSVSADAGDDCGDSGQAVVGSVGQPSSPVGGHGDNGVVTDGSSLSSGS
HLPGSAPTGGKPPLPGVGEGVGLNESKDALTLAKEGREVVQDQHELVPQVSHHTDAGTGGKGDLNAPEQ
SPNAKTELEDGGGVCGDDAAAAEGEVKTTVNEGQLGGSSTSDSHPPAADRGSREQEGTVEQAASTAALT
PVVGRETPPKGDTNEDSPEDKAATGAGITQDIPAVSQQQTHSSSTSTTGNGLTSTLGKGRAPEDISSNN
ERSGKALLQEGAEHETVAGSQSQTIPAATARNTLGTTLPGDSDNSTTITTAVRSDTGTEGTRTSNHPNR
QSIEGATSPGMNSDGEAASAKKYDTVSQSAGSSTAPTTNNKTRDTASHGNSDSSTAVSHTTFPLLLLVV
VACAAAAAVVTA*
>Tc00.1047053509525.240|S018|A--SERECD|3
MAMMTGRVLLVCALCVLWCGAGGRCDEEGTAARGSGGGPPLASKQPETPRVGSQDVKNGVTVAKENVIP
TLPLPIDGDAEVDEDEDDDDDDNDNDADGEEEDNETGESKEKSTEGQINKGGKVPPDSDSREKNLIGSR
QEKGQSIVPAGDISHSKSQESNANSTQTEVEGKKDADKRPPSAENVLTTVNGENTLPEGIAGGNPPSPP
EDSVASREKDGEDTTSEDEKNVPSPESAATPQSPRDEVSEGTGEDTKATTVTTNTTDTTNTQNIDGSTA
AATVVQPEDGVESDPANNDLSPPSTEVAAQLSMTPDAEGASNNEENTDTQSAGNPNVTIATATQTNNTA
KPSESDGSTAVSHTTSPLLLLLVVVCAAAAAVVAA*
>Tc00.1047053509525.390|S010|A----RECD|22
MAMMTGRVLLVCALCVLWCVFSSVSADARDDCEDSGQGVVGSVGQPSSPVAGHGDNGVVTDGSSLSSGS
HLPGSAPTGGKPPLPGVGEGVGLNESKDALTLAKEGREVVQDQHELVPQVSHHTDAGTGGKGDLNAPEQ
SPNAKTELEDGGGVCGDDAAAAEGEVKTTVNEGQLGGSSTSDSHPPAADRGSREQEGTVEQASSTAALT
PVVGRETPPKGDTNEDSPEDKAATGAGITQDIPAVSQQQTHSSSTSTTGNGLTSTLGKGRAPEDISSNN
ERSGKALLQEGAEHETVAGSQSQTIPAATARNTLGTTLSGDSDNSTTITTAVRSDTGTEGTPTSNHPNR
KSIEGATSPGMNFDGEAASTKKYDTVSQSAGSSTAPTTNNKTRDTASHGDRDSSNAVSHTTSPLLLLLL
VACAAAAAVVAGPA*
>Tc00.1047053509527.80|S010|A----RECD|22
MAMMTGRVLLVFVLCVLWCVFSSVSADAGDDCEDSGQAVVGSVGQTSSPVGGHGDNGVVTDGSSLSSGS
HLPGSAPTGGKPPLPGVGVGVGLNESKDALTLAKEGREVVQDQHELLPHVSHHTDAGTGGKSDPNAPEQ
SPNAKTELEDGGGVCGDDAAAAEGEVKTTVNEGQLGGSSTSDSHPPAADRGSREQEGTVEQAASTAALT
PVVGRETPPKGDTEEDSPEDNAATGAGITQDIPAVSQQQTHSSSTPTTGNGLTSTLGKGRAAEEISSNN
ERSGKALLQEGAQHETVAGSQSQTIPAATARNTLGTTLPGDSDNSTTITTAVRSDTGTEGTPTSNHPNR
KSIEGATSPGMNFDGEAASTKKYDTVSQSAGSSTAPTTNNKTRDTASHGDRDSSNAVSHTTSPLLLLLL
VACAAAAAVVAA*
>Tc00.1047053509545.10|S012|A----REC-|10
MAMMTGRVLLVCALCVLWCGVSGTNGDAGDDREHSGQGDVGIVSHSPSSVVGHGDNGAVTDGNSQGSGS
HSPGVAPNGGKTSPTGVVEGVDLKSSKDALAPAEEGRGGMQGQQELVPKVSHQPEVGTTGKSHHDAPEQ
LPNAKTELENGGGATAEGDEIKTTVKDGQLGRSSTNDSHPPAADRGLKEQEGTVRKAATTVALTPAVGR
ETPPKADPKEDSPEDKAASGAGVTQDSPTVSQQQTHSSSSQSGIDPTYTPGEGRDAEDIFNNEQPSGGV
VLKEGAQHETVAGIEKPTIPAANTRNIIGTTISGDSNSSTATTAAVRSDAGTEETPPTNHPSKPSTEGA
TPPGTTSDGEAASTNKYDTVSQNAGSTTAATTNATTGDTAKKGDSDSSTAVPHTTSSLLLLVVVACAAA
VVAA*
>Tc00.1047053509545.50|S005|A---S-E-D|1
MAMMMTGRVLLVCALCVLWCGAGGGFANDEKSGPGNRAELPLASQGPETAPQDSQGSQNRAPGEEENLT
SVLGEEADGDDVDREKKAEEEEITERQGSEGGTAAIGSDSRETNLSDSEQETGQPIVPAGSISPSNSQE
SNANLTQTEVEGKKEPDKNTTTVEGALTTVNGEHTLPAGIAEGNLPPPTEDSVDSREQDGEDATSEGKK
NASSPETAATPQRDREKGSEGTGGDTKATTVTANTTDTTSTQNSDGSTGEFCNRTDSICFVVCAAAAAV
VAA*
>Tc00.1047053509549.20|S047|A--TS-ECD|8
MAMMMTVRVLLVCTLCLLWCGTPGGRCEGEDTPGSGSDAQLDGAEILPESEEPVTSPESSQGLPHGVPG
VKENVPPAFPTPTDEEDDDEVDGEENEDEEKKTQEESIEGQGDKGGTGVIGSGSRENNLSGSGQEKNQE
ILSAEGISHSKSQKSNANPTQPEFEEKKEADKRTPSAENPLTTGNGEHTLPEGIAEGNPPSPPEGSVAS
RKQDGEDTKSEDKKNVPPPATAATPQRHRNKGSEGTGEDTKATTVAANKTDTTNTQNSDGSTAVSHTTS
PLLVLFLACAAAAAVVAA*
>Tc00.1047053509631.20|S087|AG--YKEC-|7
MAMMMTGRVLLVCGLCVLWCGAGGVYARGTLNNAVGGCMASGGFGGKMSYLSSGCDKTEVGLAMRSILL
ITTAEASDDEDVSNTVDTDSQSSQILNEGTAGGGGSGGSGGIVNNFGGDREDVRGHSDSLSPDDLSSSP
ILNDVVDSNTLSGTLSAKSRKSPEKDPKSEEISAGHLSPELKALEQTLPKAQEQSSHTIEKAVNQVVRG
APGEGVKQREMGTTGPSSNQPAPPPPQPQIITSPEVTQTPADPPEKGGLPAPTESRNKKDQPLENLPLP
TKTEPEALETSLGDKVPERKRHEKAPADLMKNAVTDNPGKTTATPISTTDSGDAHEKEGKDDDTDERPA
SKEHNISPETGNTNDALTASETEPQRAETTATTVAKKNDTTPGDSDGSTAVSHTTSPLLLLLLVPCAVA
AAVVAA*
>Tc00.1047053509631.80|S034|A---H--C-|4
MMMTGRVLLVCAFCVLWCTIGVVADGDTEEVLEDFVPPSRADETQELQEELRGKGHSANDEQVDETQEL
QEELRGKGHSANDEQVDETQELQEELRGKGHSANDEQVDETQLQKPQKEGGGHQAEDPLQPVERSVRAK
LQSEGPRVEETGNQIEQEQLLRGTQRNPNVENKTPTMPVDKPQGSDGEGDVSNEKEKQKVKETISQIKE
EVVAPGAGTPEAISIEGHQEASRNPAEKTLVENKDIAKENNVKKEEKEKKSEQQELQLKQKNGKQVTLH

GSPTGPAATQGSLAPVPPEGLQQKQISDGSTKQPEGEAPLIGTESTSDGTTDPPLPSVSTGAAVAATSE
SDKREVKVSAIAESNETTVNETDDQQERIGEKDEESAKGKTAFETNQTENIDDSDGSTAVSHTTSPLLL
LLFVVCAAAAVVAA*
>Tc00.1047053509657.30|S026|A--T---C-|2
MAMLTGRVLLVCALCVLWCGAGGAHAEDDAGVTSPGASASDGKSFQEPPPIVQGGSHNSVLTASDVNEQ
TDETDKEVLLTKEVAGSDEVPQTSGEEIPPPSPSPKKSKGGGGPPQEDDLNLEKVDENVMQPEKQRRVE
EGLETLGDGEAGVTKQNEGIGVQSQDHETPFQEEDTINGEGHQQTHGKDQQTNVEDIPPRKSAGDYSSG
EHKGNDGSNEKEEKEGEEGVEGRERHRTQEREEAAHVSGAPKVNSTDIQQEVQRTHAGETPTGIKQKAG
EEKDDETEEEREEQKKQNQENPPGKVQETITGANATNQLNTMPGDNDGSTAASHTTSPLFLLLLVVACA
AAAVVAA*
>Tc00.1047053509657.50|S087|AG--YKEC-|7
MAMVMTGRVLLVCVLCVLWCGSSRIAASGVYASGVEDGARGGCMVSGVLGTNLSYTPSGCNKTVPMTAL
RSVFSVVAAEASTEQEDSETDTVPDSPSGDGPDSVSGSPVGSVVIGGSKVVDSTLGRLNVVPPDTRVDV
APPPPPAPETDDSRLPEVSQSTEKHNSSEKLVDLKTKTPAGTPLLSNQASKESLPTVKPESSTTSDSTV
TVKGTDQISEEKLAVLQGPSTVNAGEDGKKAVTEIKPNTTTNTPDAAPTLPSEGDVTEQHGKDTDSSNF
MNNANTGSSAETTASSFSKSGGIDAPKNESEDEGDAQRPKSKEPQEKPEDSNTNDAPTENETAPQTEKP
FGSAQTNDTSKSGDSDGSTAVSHTTSPLLLLLVVVAAAAAAVVAA*
>Tc00.1047053509665.20|S016|A-----EC-|10
MAMMAGRVLLVCVLCVLWCGAAMVVVAEGSDGINEITDKLSRGSQSASQVGHAEDPKILKPNDGVSNTS
ENPLDAQELSNVSPQKVCVEQSSIFHGGMEVKEEKLEEKEPENAEPRRNGKEQSQDAPEGTRGRKGIME
AQGDPSPKTPAEEMPTSEEATGPAKEQTPGQEGETGQAAKPPQSLPATSPPASDRGQPGGSSGADRSVG
GSKRGEGSNLKISASDGVNQSAVGSLGSGGGTGLDPNGGGGSSGGDGGSSRGDSLGSFLSAAGTSLSSA
LDTPSTQDTQSSEGVRHSEKMPLGTAVPNKQPKERSEPKAKQGTSTSEEAAESQDDSGDAVEKEKEKRD
VGLKSTISPTPNTSNPPVTQTTPRASSAEPSPTTTEVQAVEETSKDNVTITKRNDTATPGDSDSSVAAF
HTTSPLLLLLTVVVCAAAAALVAA*
>Tc00.1047053509699.110|S002|A---S-ECD|19
MMMITGRVLLVCALCVLWCGAGGRCDGEDTAVSGIGGESPLASKGIEKSPQVTQDLRRGAGGLKEELPP
APSGDEDEDDEDDDDDDDDEGAGAEDEEEKPIGKQSVQGGTVLIGSGSRHKNLIGTEQQKGQSIAPAED
ISLFGSQESNANPTQTEVEEKNETDENTPAVENALTTGNGENTLPGGIAGGNPSPAHEEGVDSREQDGE
DTTSEGKKNVPSPETAATPQSHRNKGSEGTEEDTKATTVTANTTDTTNTQNSDGGTAVSHTTSPLLLLL
LVACAAAAAVVAA*
>Tc00.1047053509699.210|S113|ANP-VF-C-|1
MAMMTGRVLLVCALCVLWCDVVVPAAYGLVSDRSVVEEDMVLTWYPVFNETCRNKSTKEGMLDELAMKN
CMRTAMKDVCEAYYIEKSTKSHEPEADRICKKYAGDTEEVVQPSIPQTKESPDAEIQVAAATPETPKGG
AAGMGSKPGAPAGDSSANTTEGPESTSAATDTSINEAQKGGELAMPKNAPESDYAGRGEGEQGEEKHSN
TKETPAKAETMKNITTIAESDSSTAVSHTTSPLLLLLVVLRLLLLLR*
>Tc00.1047053509753.60|S106|ANP----C-|2
MAMMMTGRVLLVCALCVLWCGVSVVMASNVGGLAPHADINVFFGRWYSLMMGDCENTSAFENGTVNESA
VEECKREAKKALCDLFYGDHSGEHDASHLHSICSPDVGSGGAVDQQAQEQIPTLRETGNPAPPTTPQGL
SEESPDTPPTPASAGASSQAPPIQASSEPTVLAKQAEPNTAGSVPPKQSQGGPEAMRPPQEPPKVTSIH
DTATQRDSPTEDRAEQTLPPAKANDNSNDHNEEGTAEESTVDTPASGAVQTEGDESETPGSGLKKTKTP
HNTVEGSNTVKPGDSESSPAAPPAGESDTATTTRPNNHDARSLNKNGNNTFTEEVDQMEAAIKPKSAPD
SIDTAAANSEASTAAINISTNTTNKTNTVDSDGSTAVSHTISPLLLLVVACAAAAVAA*
>Tc00.1047053509753.70|S106|ANP----C-|2
MAMMMTGRVLLVCALCVLWCGVSVVMASNVGGLAPHADINVFFGRWYSLMMGDCENTSAFENGTVNESA
VEECKREAKKALCDLFYGDHSGEHDASHLHSICSPDVGSGGAVDQQAQEQIPTLRETGNPAPPTTPQGL
SEESPDTPPTPASAGASSQAPPIQASSEPTVLAKQAEPNTAGSVPPKQSQGGPEAMRPPQEPPKVTSIH
DTATQRDSPTEDRAEQTLPPAKANDNSNDHNEEGTAEESTVDTPASGAVQTEGDESETPGSGLKKTKTP
HNTVEGSNTVKPGDSESSPAAPPAGESDTATTTRPNNHDARSLNKNGNNTFTEEVDQMEAAIKPKSAPD
SIDTAAANSEASTAAINISTNTTNKTNTVDSDGSTAVSHTISPLLLLVVACAAAAVAA*
>Tc00.1047053509753.100|S082|A---YKEC-|17
MAMMTGRVLLVCALCVLWCGAGGGRGEGEATVVGPPGGRSNDGKGGPGPAPPSPPGTGTSGPLSIVPES
EGSQERIAGTSSEGSGEKNYKNEDGVEGDVDEDGENSIHHERPSEQPTQQEVSDEETPEGKGLKKRLEE
KDVHQPGEEEMKGTQQSQSQQPPPQQSQVQIKAPAERGGPTAPTGPARPPPPAEPSSMDGSRTTEPTDS
RNPSQESHDKSLLQTKTESSAPDPPLKDDFPEQHGQETTTPVSMLNASAGSQARITAPSTSTGGSGEAQ
IKVDEDDAQRPNPNESHENSDAGKTKVPTTFSEATTQATETVAATQTNHTKNIGDSDGGTAISHTTSPL
FLLLVVACAAAVVAA*
>Tc00.1047053509753.140|S082|A---YKEC-|17
MMMTGRVLLVCALCVLWCGAGGIVADDAVPAELEKENKSESLKDDPSVDKTDTHEPQEGMIATQQNGLA
LKSTTNPLELEEDMDEDEEKEDGKGKGKAEKDTRSTEQTETQKSLTKDGETSKLTSAPGTPSTPIPPER
EGQETPSETPPGPPTNGKPAEETGPPALTGSQNAAETTSTTSPSHSKTAPEAAETPSGNGEPNQHREDA
ETPDSMKDGPTSLPAETAVSSVSKSGIGGTQKREDKVDDSDQRPNTKEPQDGIEDGNTNVAPTFSETAQ
KTPETITVAKTNDTTTTGDSDGSTAVSHTTSPLLLLLVVAAAAAAAVVAA*
>Tc00.1047053509753.210|S080|A---YKECD|24

MAMMMTGRVLLVCALCVLWCGAGGGYAEDDDVVSGHPGTRGERGGGAVGQSPPAGGSNGGSGGSKADSP
HGSESEPLDSTSDEESSSLDTDQELDPNLPEEHVLQKEVDPIGKQDHSESGPQDALPPDANGTVTLDSD
AQLQLSDTKKKQTEVLTNVGGGEIADGGKDSTGRSNGLSPNKSDPPALLEPRIKEVSQPTEPSPPPANL
SPAPQELPTAVSPAERPPAIAASAGETNPTASTGSRNATETTTTTSPSHSKTAPEAAETPSGNGEPNQK
RQDTDTPDSMKDGPTSLPAETAVSSVSKSGIGGTQKKEDKVDDSDQRPNTKEPQDGIEDGNTNVAPTFS
ETAQKTPETITVAKTNDTTTTGDSDGSTAVSHTTSPLLLLLLLVVACAAAAAVVAA*
>Tc00.1047053509753.250|S072|A---VFEC-|6
MAMMMAGRVLLVCALCVLWCGAAMVMAEANVDKGTEMRKDEKLDSSQLVAGIVGAEQHVTQDSVKEGSE
NGNKFLSAQTGNGISQDNGVIMVSPASTVRGEEEEEEIEELKSSIESEEKSQLTFPQEGVPPPSEPLAT
TLNGNPGGTLNTTPAKGQSSSDDGSAQEEGLKLPTRKAPAAAAEATTQAKDENPSFADDPSVQHVEASQ
HDMESRSASRKEGTIPTTVTKTDGPTEVNAESTPTSPSASKSAITNDADKSHEEGIPKNDQAADGEAKK
EEQQDENKEENTNKTANAEAAAITNDTATIGDSDGSTAVSHTTSPFLLLLLLVVACAAAVVAA*
>Tc00.1047053509753.310|S066|A---VFECD|8
MAMMMTGRVLLVCALCVLWCGVCAVEVSMADDSENTDVSQGSAKGPPSELAGRNNGKQESSDQVSQGLQ
NVGEALNSKKEAAGNQRKDPKIETPTADKSMDDKGEAEKEQIGGSAGEESGELLEEREAPLDGQGGEGQ
ARQAGNGSAKVGGHSSATTPSGGERKGTGEPSPPGSLLPPASTQGNGAAPPASLQGAPAATMKTNEKTV
ENPRAEPEKEKLSSEDDVPEQTSQGVNDGVEPNNDSQKKENVSVALKEQNGESDGDSESTQPRHLAVDN
ASNMDAERGTEIGLPKNNPTANSAVTEGAKRGDNKHGNRKETPVEATAITNDTARTGDSDDSTAVSHTT
SPLLLLLLLVVACAAAAAVVAA*
>Tc00.1047053509753.194|S070|A--TIFEC-|13
MMMTGRVLLVCALCVLWCGACGGGCSEATSPGSPGTPSGNNTPNDNVTVGVTEGGVKNGKPEAPKAAAP
TGSGSPEASPPPAQQPKGGESGTPNAGMDNKGRNTEGKKKEDEEEEEKHVEEEEETDEQEDDRREDGED
DKKQEEERKKGEAVTGTTEVISAGGEEQRSLSSAAEGASNITNPNSTPTTGDDDPAADGAGTAEGKQNE
NKYANPKETPVTAAVMKTTTATTGDSDGSTAVFHTTSPLLLLLVACAAAVVAV*
>Tc00.1047053509755.40|S036|A---S--C-|1
MAMTMTGRVLLVCALCVLWCGAGGRCDDVVTAALGSGGSSPKSTQLETPPLDSQELKDEAPVVKEEVPP
ASPGIKAEEEEDKDDDDTGEGDGQEDGGAEGEEKPIERQDGQGGTVAPGSGYRETNLSGSEQENHQSIT
PAGGISHSGSQESKSNPTQTEVEEKNGKEENTPAVENPLTTGNGENTLPAGIVEGNPSPPPPKDSVDSR
EQDGEGTTSEGHKNVPPPETAATTQSHREKGSEGSGENTKATAVTTNTTDKTSTQNTDSSTAVSHTTSP
FLLLLVVAAAAAVVAA*
>Tc00.1047053509897.150|S080|A---YKECD|24
MAMVTGRVLLVCALCVLWCGAGGRCDEDVRVTEEKKESSGDLQPVTPVAGAGKQHAEPINQDSDLVRQP
LVKDLEVPSPKHQTDDKVFGVVDNEDDGTDKEKEERDKAQEGAPDGQTQEEEVLPPPSPLSPAPLQPPP
PPAASDGTQPGGGPGADSSGGGSNGSGSSIEGGGSNLETLALNGGSQSAFGSLGYGGETGSFSGGAGKG
GVDIGSPRGDFSDSSLSADGTFLSPALDAPSSQDTQSSENVERSKTMPAGLPLPNVNALKGPESKAGSL
PPNTQEKSKFSDASGGAAGNKAKQSDVETDDPSSSFANTGDQTVEKTLLLPQTPAVLLPVPSAELSPEV
PPVTPVQANPDGEGSLPTAPRASEASKRELQNKASSPNKTGSESPDRPSKDGMQKQKDKVTTQLNTTKK
ASAGGLAERTATSISANGNGDVQNKEDEDDARQPTPNRVQDDAEAGNTNVAPTVSEAAPQTVETVTTRK
RETNETGDSDGSTAVSHTTSPLFLLLVVACAAAAAVVAA*
>Tc00.1047053509905.180|S133|ANQ---ECD|6
MAMMTGRVLLVCALCVLWCGVSVVAADVAGGGDGGADEYFVLRWHAQLRRECAEAFGRRTEGRKDAFAV
DDCVRRGMDGVRAFGDGRRVWRRQRSAVVAGDDTTDDDSTRGSSSEVQAETDTDSLDGPLKPSVKPIPG
EVPDGQESGKLSEASEPTINGTGGNLDGEGEEGDVSQDERQDDNDVKDEVVDAAPGNGDSETSNKGHEE
EKERVKEEKAGSTTKEREGDENNAAGRGPAQGAAASRPPSPVDVSNPQNPVLDQDGAGGERGGAGPVVL
PQAAGLREAEGAPAKLAPGGDAAGKETERQNGTAEQVATKEVQTAVEDSSAEAAAAGKESKGEKEGENV
SEAEKEGSHGNVDEEAAGKNGGNATKKLQKEATDEAKTKKRNEKKEAENANNTKEEPDEEEVKKATQEE
EAADKENTTSARILTKINTATPDNSDGSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053509925.10|S040|AG----ECD|2
MAMMMTGRVLLVCVLCVLWCGAGGVYARDIDNKALGDCMTSGVLGTNCSRVPGGCDKTAPKLPFRSALP
ITVLQADAPEGEVPASEGGNSSESSGTGGSGGRSGGVDGMKSGQSGVSGGDNLSNPSSSSGGSSPRPPT
LDGKGAPQDPGEDPSPQGRKSPEKVVQSGTSVDSALLKREEVQKSEPDTQKIRAEALVTFGGTGNEARR
EAEDTDNTPSGPPVKTVTPQAEVLSPPAGGVPPASDDTHNSPENNAGNSASKNETKSNPLERPSEDGEA
GQQDKEADAQGAQETEGTQGTAASPISTSGSGGAQSEADADDDDPQRPNPEGPQNDGTEAGDTHGPSAA
SDAAPQAAKAIAAQTNGTVTPGDSDGSTAVSYSTSPLLLLVVVCAAAAAVVAA*
>Tc00.1047053509973.10|S008|A-----ECD|43
MAMMMAGRVLLVCALCVLWCGAGGGYAWDFNNESVNEYYYGANGTYCRLNSSIFSFCEEKRNASKRQEA
ALPKSTVQSGTGSDQSEAGDSSEGQDNSSEKNDTDDSKKTDAGPQESQPPNANVTETPTPATVTAAQTS
ATRTPDESDGSPAASHTTSPLLLFLIVCAAAAAVVAA*
>Tc00.1047053509973.70|S042|AM----ECD|1
MAMMMAGRVLLVCALCVLWCGACGGYAWDFNDTLNKYYYGANGTYCRLNSNFSFCNKKGDPSKGEEAAS
HKSNAQSGTGSDQSNADGSSGGQGRGSEGNDFRGPGGDSGTKELKNSVGGETTPTQQSPSATQPSTVSE
DLPKPAAPGGPEAPGTTTELQPPPQSPLPAGGTPTPTTATPTADGSSGGRDNSSEKNGSDESEETDEGP
QESQPPNANVTETPTPATVTAAQTSATRTPDESDGSTAASHTTSPLLLFLVACAAAAAVVAA*
>Tc00.1047053509975.30|S044|AM-----CD|2

MAMMMTGRVLLVCALCALWCGAGGGYAWDFNDTLHKYYYGANGTYCRLNFSFCNEKGDPSKLEETALKT
SNAQSEEGSGQPKAGGSSEGQGRGSEGSDLRGPGGDSGTKELKSPGGETTPTQQSPSATQPSTVSEDLP
KPAAPGGSEAPGTTTELQPPPQSPLPAGGTPTPTTATPTADGPSGGRDNSSEKNDTDDSKKTDAGPQES
QPPNGNETETPTPATVTSAQASATRTPDESDGSTAASHTTSPLLLFLVACAAAAAVVAA*
>Tc00.1047053509979.200|S008|A-----ECD|43
MAMMTTGRVLLVCALCVLWCGAGGGYAWDFVNEEMNEYYYGANGVYCKIFPKMYSCELKINASKLKEAA
LQKSTAQSGEGSGQSSAGGSSDGQEQTSEKNGSDQSEGDAGPQAPQPPGEGGTETTPATVTAAHSADGQ
DNSSEENHLGQPEGTAGEGTQASQPPGEGGTETPTPATVTAAQTSATRTPDDSDGSTAASHTTSPLFLF
LLACAAAAAVVAA*
>Tc00.1047053509979.270|S008|A-----ECD|43
MAMMMTGRVLLVCALCVLWCGAGGGYAWDFNNDSLNEYYYGANGTYCKIFPKMYSCELKINASKREKAA
SQAKATQSGEGSGQSSAGGSSGRQDQTLEEGGLDQSEGATGPQAPQPPGEGGTETPTPTVTAAHSADGQ
DNSSEESHLGQPEGTAGEGTQASQPPGEGGTETPTPATATVTAAQTSDTRTPDESDGSTAASHTTSPLF
LFLLACAAAAAVVAA*
>Tc00.1047053509979.350|S030|A------CD|31
MAMMMTGRVLLVCALCVLWCGACGGYAWFYKECGSGEESCINSNQYKGLYNSSFRSSFLGETNSASGKI
DSSTGSTGNGGDRARSGADGTKGSAGHAPSGGSESPPAPSQPASNTPGDRSASNEPSDTSEEDPDSAVT
LGSGGGGGPNTVVGTQLAVGGDLASDHQTPEDGDTDPDVSHAASEDGEDTHSPPTSPPDKKTEEPKVTK
EGEEGTKNTREEAPAVLTTKEESEGNPEAEPGNEQRSSANGVSEQQPEAAQQGETEDGNTTEKTPTPAT
VAAAQAGATRTPDESDGSTAASHTTSPLFLFLLACAAAAAVVAA*
>Tc00.1047053509979.174|S008|A-----ECD|43
MAMLMTGRVLLVCALCVLWCGAGGGDAWDFNNDSLNEYYYGAYGVYCNASLNATFCEEKRNASKREKAP
SQADDDSRRDNGSGQPNAGGSSGGQEQTSEKNGSDQSGGATGTQLQKPGEGGTETPTPTVTAAHSADGQ
DNSSEESHLGQPEGTAGEGTQASQPPGEGGTETPTPATVTAAQTSATRTPDESDGSTAASHTTSPLFLF
LLACAAAAAVVAA*
>Tc00.1047053510011.9|S015|A---H-EC-|9
MAMMMTGRVLLVCALCVLWSVVADGDVGVVSGGDDNSLKELFIPVARLQERPEQRAAGATADAKAAAAA
KASAEAAKTATANAATAAAKAKTEAAAASKAAASAEKAATAAAKAAASAEKAATATSKAKASAETAKAK
AAAAEKAAAGKEAEEAAEKATEEEKAKASTAEKAKAAATEADAKTTAAKTAEAAAEALRGTTVREQEVK
TAIHDQDNSVEHHSGEKQELLKEEEQERQEKEQHEKQQHQQREHSAGNGEESPKEKTANGTNASAITDD
SDGSTAASHTTSPLLLLLLVVACAAAVVAA*
>Tc00.1047053510013.40|S074|AML-YKECD|9
MAMMMTGRVLLVCALCVLWCVTVFGIAMDNRCVEDDGNVLTHTHNGGNDRLRLKADRGLISTRMGLIKA
IAAGDDSEDENGNAPLEEKTAPGGEPAGSGDNETPGPKGGNGAAGAATPTSPSEPGVPGAGAETGQLPA
AGQEGNENKNVDPNNKAATDSQDQTNDQLSSSSGSTSTPSGEKHPSTGTSDIKQLPTETLKNGVAGPRN
KSGDDGERDEEETRKEKEENKLQPETQERGNNAEVPQSLPAPPSGGPAPPPPPASAGEESPTAEKESLQ
KVTKAKNENTPSEFETDSEASEPPSGDTTQEQHSHDTDTEDSTKNAATGSPAETTSSSSSTSGSGDHVQ
NKADKDDAQSSEGQHDSLETGNTNVVPTLSEEAPQTATANTTDTATTGDSDGSTAVFHTTSPLLLLLVV
ACAAAAAVVAA*
>Tc00.1047053510013.70|S079|A--TYKECD|5
MAMMMTGRVLLVCALCVLWCGAGGCFANEERAGLGSGGEPLVQSQKLGTPRQETQDLKVGPTVVNGKMP
PASSTPTEEEVDDDDDDDDDNEEEETEEEKQKKIKAPTETHEGKNNEVSSLPPPPSGDPTAERENSHNS
KKITNEATPSGAAMESKAPEQPSGDATQGQHSHDTDTEDPTKNAATGSPAETATSSTSASGSGDHAQNK
ADEDDAQSSEEQHDSLDTGNTNVVPTLSEESPKTAERITTANTTDTATTGDSDGSTAVFHSTSPLLLLL
VVACAAAAAVVAP*
>Tc00.1047053510013.170|S001|A---H-ECD|18
MAMMMTGRVLLVCALCVLWSVAADGAVGVVSGGDDNSLKELFIPVARLQERPEQRAAEATADAKAAAAA
KASAEAAERAKIATEATKTATAKAEEAEAAAEALRGTTVREQEVKAAIHDQDNSVEHHSEEKQELLQEE
PERQEKEQHEKQQHQQHEHSAGNGDEPAKDNTANGTNASAITDDSDGSTALSHTTSLLLLLLVVVACAA
AAAVVAA*
>Tc00.1047053510013.230|S002|A---S-ECD|19
MAMMTGRVLLVCALCVLWCGAGGGGAEMNEEETAGLGSAEHLPESEAPEKSPEGTQDLKGAVPGVVETV
PSTTTRKDEEDDDDDDKGTEDEEEKPIGKQGDQEVTVTSYPNSGEKNSRGNEQQTRQSIVSAGDIPHSG
SQESNANPTQTKIEKKKETDENTSAVESPLKTVNREQTLPAGIVEGNPPSPPEEGVDSREQDGEDTMSE
DKKNVPPPDTAATSQGHQDEGSEGTGEDTKATTVTANTTDTTNTQNSDGSTAIPHTTSPLFLVVACAAA
AAVVAA*
>Tc00.1047053510013.260|S008|A-----ECD|43
MAMMMSGRVLLVCALCVLWCGAAVLVSAAGDVVDGDGRDVDSESLLESAESGMSLPSSPESRIKLKAVS
NPPPKDVEEAHTPAKESSGEEDEAEDEVTVKSEERQQQEDENALKVNERKTPELLVKQNETPQSREGER
SLTATPIKGSPTTPGPQAPTLQVQAPPPPPPAAAASADGEADGGPVGVEGPISGPPSGGASSSPISIDG
DASGNNGGALSTQDTTSLKNDEQSGPTTSSGNAPLNRETPERSTPDAQRHSSDTQENETSRLPDGDANY
SAVGQSAVGTKGSSGVSTTASNAPTTPQPQLPAPPVPPKATVTGAPAEKPTAERLPPPADSTPGEGLAT
TTTAQTNGTATPGDSDSSTAASHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053510013.290|S080|A---YKECD|24

MAMMMTGRVLLVCALCVLWCGAGGRCDEEGIAAPVSDGGPPPESKELGTPRQETQDLKVGSPDVNGKVP
PTSSTHIEKAEDEGIDDEDGEEKDKKDENEKNKVQPQTHKGKKNEGVPPPAPPSGGPAPSSTAGEGGPT
AEKESSQKVTKAKKENTPSEFETDSEAPEAPSGDATQGQHSHDTDTEDSTKNAATGSLAETTTTSSTST
SGSGDHVQNKADEDDAQSSEGQHDSIENGNTNVVPTLSETAPQTAGKATTAAQTNHTATPGDSDSSTAV
SHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053510013.310|S119|ANQFVFECD|2
MAMMMTGRVLLVCALCVLWSGIDGVAETEEPGIDVAPGVDEYLVVEWRAQLRRECAEEVSRRTGGRANV
SAVEECLREGMESLHAVVDGRRRWRPQRYALVAKDPEDGPPEVISVGAPPPLPGQKTQGSLQELSLGDP
EKLSEGGAGGGTGLGSEQMQPEELAVTKQNESEVEGELIRDENNSELEKKVLVDSDLTKSQTMNVPEIQ
PEAVGLLLPSRDGRAAGIPGGDSSELSSEVSRLSEASGTGGDDQQKNTPGKEKQAAAETQPVPVAHSKP
SGSAGTVPGEGGRLEDLLPQAPVKETAPAAPSPRESFHTASSPAKEGTESTQPADVLLKQGNIPTTDAT
QNATTEGQEETTSSSSAADDDNAVTNDADEGNEENSGDDSASRAAVPDEKQQREREDGNEKERAPAATP
QVKNEDLGSADVVSVQQEQKTQSGLESGNESRKEDSVLTTNKQQDGTSDSHAESTPTSRSSAKSVGASN
GPDKATEEEISNTNTARVDAVPEAAQDDGNKDDNKKETPVESTAIANDTTPTSDSDGSTAVSHTTSPLL
LLLLVVVACAAAAAVVAA*
>Tc00.1047053510015.30|S033|A---V--CD|9
MAMMMTGRVLLVCALCVLWCGLSGIAADGSGVVSGASSGGVVEAGGVPSVAVESIAFDAGGKDATSNEH
GTLSSEPVVQVDNSSSSNIGQDASNVLDPPVKDLKLTEEDPKVNADQLQSVLPADLPPKAEVEGSHHFN
APDPLPRAQGSKEVLNNDDGDVETLEKDGRKVDVKNDAIAGFSSNSNGDPTEAPRGPGAKEITVEQTAP
TAATPPAKGQVTSQATEQKEASPRKEATSSVVVTQKSSTVIQQPTKSSSPPTNGITPTPGNKLAGGDTF
QNDQQSDEQVPEEAAQNGTIAGEELKTKPETTTEKGPNSTDDNKQVDNAAIGNSNGGQEEKNGVTLQVQ
DEVVKPKEEKEVKKELEEKEKQKAQGNKQDEPEDLGEDAEDTEDSADGTDHKEGEGQKEGDAGSNKKGK
ELNGGGDTDGTPPDAPVVLQPAPPVEVTDPQSIEKTNDDDTGGKEDAGRTQTQEAAGPSQAENLTAELS
TEEVAAETETGTPGKKTQPEDAGKEQTTVGAKSNPETPAAETEAHNREEVPKEEEDSEKATTNENFDGR
QTAVNDNAHNEAENTRQENENELDKAEETTAEVKEKEETTERKTVAAKDPNLNSTAATDDSDGSTAVSH
TTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053510021.20|S047|A--TS-ECD|8
MAMMTGRVLLVCALFVLWCAAGGGGRCDGGETAGLGSAEHLPESEAPEKSPEGTQGIRDGTGGVKGQVP
SKPPEDEVEEDEDEDDEDEEEDSEENGDGAGAEYEEGKRTEGQGDQEVTVTSYPNSGEKNSRGNEQQTR
QSIVSAGDIPHSGSQESNANPTQTKIEKKKETDENTPAVESPLKTVNREQTLPAGIAGGNPSPAQEEGI
DSREQDGEDTTSEDKKNVPPPDTAATPQSHREEGSEGTEEDTKATTVTANTTDTTNTQNNDSSTAVSHT
TSPPLLLIVVACAAAAAVVAA*
>Tc00.1047053510021.50|S017|A---S-EC-|13
MAMMMTGRVLLVCALCVLWCGAGGRSDGGKTAGSGSGDGSPLESKELETSPQGTQGLHGRETGVKGNVP
PASSTPTEEEDDVDEVDSDNDVDEETEAEEGSIEGQSDKGGTAALDPGSGEKNLSGSGQEKNQSIAYTQ
GISLSDSQESNAISTQPEVEEKNETDENTPAVENALKRVNRESTVPAGGNLPPPPEEGVDSRKKDGEDT
TSEDKKNDPSPETADTPQSHRDEGSERTEEDTKATTVTANTNDTTNAQSSDGSTAVSHTTSPLFLLVAC
AAAVVAA*
>Tc00.1047053510021.130|S074|AML-YKECD|9
MAMMMTGRVLLVCALCVLWCVTVFGIARDDRCVEGDGNVLTHTHNGGNDRVRLKAGCGLISTRMGLINA
VAAGDGSEGGTSNAPLDSVGGTSPGSLLAGIGGNAAPGAGGGNGAAGAATPSLPVSGPGVSGTGDEGGQ
LPAADQKWNEKNKVNPGSNAAADPQEQTNDQLSSPSGSSPTRSGENPSSKDTDEINQLPKGTETKGDAD
RQDKNGSDEAVEEEDGDKDKGKKQEKNTLQPETQEGQHNGGGTPPPSLPALPLPLPPSGVPAPSSTTGE
GSPPTEPKNSQNQKKVTNEATPSGPKMESEAPEQPSGDATQGQHSHDTDTEDSTKNAAAGSPAEPTSSS
TSTSGSGDHFQNKADEDDAQSSEGQHDSLETGNTNVVPTLSETAPQTAKTITARINGTATPGDSDGSTA
VSHTTSPLLLLLVVACAAAAVVVAA*
>Tc00.1047053510025.100|S074|AML-YKECD|9
MAMMMTGRVLLVCALCVLWCVTVFGDARDNRCIEGDGNVLTHTHNGGNNGLRLKAGCGLISTRMGLINA
VAAGDGSEGGTSNAPLDSVGGTSPGAGGGNGAAGAATPTSPSGPGVSGAGDEGGQLPLAGQEENKKNKV
DPNSNAAAGPPDQTNDQLSSSSGSTPTRSGENPSSMGTDDLTPLSKDTETEGDADRQDNRESNEAVEEE
DGNKDKEKKQEKNTLQPETQEGQNNGGGTPPPPVPAPLPPTTPSGGPAPSSTAETENLQNENTPSEFET
DSEAPEQPSGDATQGQHSHDTDTEDPTKNAATGSPAEPTTFSSTSTSGSGDHVQNKADKDDAQSSEGQH
DSLETGNTNVVPTLSETAPQTAKTTTAAQKNGTTTPADSDSSTAVSHTTSPLLLLLLLVACAAAAAVAA
*
>Tc00.1047053510025.160|S091|AG--YKECD|14
MAMMMTGRVLLVCALCVLWCGAGWVYAGDVENNAGEGFMASGVLGVNRLRVPSVCGKVAITLPSRMVSF
ITAAEASTNDDASGIIGGNPDSPSGAGAAAGSVSGGAGGAGGSGGGGGTSGGSGNSAGGSDGNRDTTED
PTGVGGGSLQSPPSVDPNSSRIPNEVGESQNTEVSLSPEETISPEAAAESGPTASPGNTPPKVETADKS
KPKEEEKGLSVTQAAAPISVNGEASTGEQNQHNDVGKVDHSSNQTPPPVPPSAVTTPGLSKEPAPPATE
ASPSDGSLPAPNVPQTAKDQEQKTSVLTIKMESNAPEIPSEDNVVQQQGQNTTTEELMENSSRGSQAET
TTSSIYTSGTGEAQSTADADDAQRPNPSESQNDLEGSDTNNSSKTDEVAPQSAITLTTAQKNGTTTPGD
SDSSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053510025.180|S010|A----RECD|22
MAMMMTGRVLQVCALCVLWCGAGGRCTEGGETPVEGKLGNTASGAEVLQAKPETAESGIPGTQPQVPID

NEEAKRLIGEGSLEGSEDNVVADTEDLSEDDEGGEEEGNEETQRKKLNGRQEEHEEKGPASGLDTSNGS
SIESQLQTLQTNSSTGSSPPSSSLKAIPDPTQTGIKENGVSVTNPPTDEETLKEDTRDNVPHGGLAKLT
LPPPPEDSAAASGIFAEYKKDEGQQDANLHSTATTVQDSQDDTTKNTKKETIPTAIKTDTETTQHNDSS
PAELTAPQSDAGAESTPSTNYSGHSSTEDAARLSETNDAEDALGSTENADSKIAETEKAPLATANTTDT
TNTQNGDGSTAASHTTSPLLLLIVVACAAAAAVVAA*
>Tc00.1047053510025.220|S032|A---H--CD|8
MAMMMTGRVLLVCALCVLWCGAGVVVTDGTGMDAQASVAQPGPSEPQITAGGNGENEGEKDVTKNEEHK
LSKQEKDDVEKKNQEQILPEEHDQALTNKAAQKPAGEPLEEVKIDVDSEVEEEISLVDGGTPKEDEKEL
GQEAVEVVLGKDDSPVNLTVSRQETSGIHAEDPEGKSEQEGEKEGEQHVQHQEENKGKKQDKENTEENE
QMLQQQDQGLEHTADKQKGSKKDEKAVGTADTARTDDSDSSTAASHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053510025.260|S074|AML-YKECD|9
MAMMMTGRVLLVCALCVLWCLTVFGAARDNRCVEDDGNVLTHTHNGGNDRLRLKADFGLISTRTGLIKA
VEAGEREGEDLENGHDSLENEDKSPQGGEPAGIGGNEAPGAGGGQGAAGAGAPSLPVSGPGVPGAGGEN
RQLPVAGQEGNENKNVDPNNKEPRESQDQTNDQFSSSSGSTSTRSGEKPSSTGTSDINQLPRDTETKGD
VGPRNNSGDDGERDEEETGREKEENKLQPETQERGNNGEVPPPPPPLPPLPPSGGPASSLSESEGSSPT
EPKNSQNPKKVTNENTPSEFKTDSEAPEQPSGDATQGQHSHDTDTEDSTKNAAAGSPAEKTTSSSTSAS
GSGDHVHNKADEDDAQSSEGQHDSLETGNTKVVSKLSETAPQTAETITATQTNHTVTPGDSDSSAAVSH
TTSPLLLLLVACAAAAAVVAT*
>Tc00.1047053510037.10|S008|A-----ECD|43
MAMMTGRVLLVCALCVLWCGAGGGYAWDFGSDGESLNEYYYGAYGVYCNASLNATFCEEKRKAIKHKEA
ALQKNTAQSGTGTGQPNAGGSSGRQDQTLEESGLGQPEGTAGEGTPELNKPGEGGTETPTPLSSPPPTA
TVTAAQTSATRTPDESDGSTAASHSTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053510047.120|S038|AG-----C-|7
MAMMMTDRVLLVCALCVLWCGAGGICDEKAVGGCMASEVLGENGSNMPNGCDRTALMLSLRSVLPIIVA
EVSGEEDGPSKGGSGGGGGVNPGGKDGGKDGAAGAPASGGGGNSSGSVSPGGGSPHHPGAGTVTSGNPL
SRPQNASQTEVLRRDETENQSLSSPKGKAADTPVNGAQTKNPDNSVIALPDNLASKESSNKVKSESLTA
PGAAPKPSPEGPNTELQGKGKASPELSDAKLPEPKTEHQTTTSEEGKNRSQNTSASTDSPAKQGRNNED
PVSTSGTAESISTGSQEQAATTSSNESFSPLQEETSTETTNVENSRPSDTAQTEKQQNGGKEKAGDGDS
STAVPHTTSPLLLLLLVACAAAVVAA*
>Tc00.1047053510089.10|S016|A-----EC-|10
MAMMMTGRVLLVCALCVLWCGAGGGYAWPYKECEGDDKSCFSHSQYKSVYNSSIRSRYLGETDSTSTGL
FDSSTGSTGNGGDVSRNGADGTTNSVTDSHKGGAQSSLSPSQHASASSGDSSRSNESSEKTEETPGPAS
TSDNDGDGGPNTANQAHLTGGEKLDSGHQTEDGDTDPNLPLGDSKDGEGTHSSPTPPPANKENVPKVTA
EGEKAPAVLTRQEESEGNPEAEPENEQRSSANGVSVPQPEAAQQGETEDDNTTEKTPDEAAAAKNGTAT
PDDSDGSTAASHTTSPFLLLLLVVVCAAAAAVLAA*
>Tc00.1047053510105.310|S085|AG--YK-C-|2
MMAMMMTGRVLLVCALCVLWCGAGGVYAGGIDNNAVGDCMASEVLGRKTLNTPSGCDKAAPKLPFRSAL
PITALQADVSEEGEEKDLNSIGPSGTGDSSGGGGGGGKSGVSNSGTPGSGGGSQLGDDPSNAAPSGGPP
PPPPPEGTEGLKLSGGKTSTPSREPQTTIKQPGGIKTPSSTTPPSVKVLEEGPKPEAGRQVANPQEKSN
SQVTGVNANENNKDKRAMKEEKPSTVSSIESTPQVNLPTPPQPTPEVSPPTASPEAKLPATGESSPTRN
LSRDPTEQTNDNSQSQNETAPETLIQPSGDAETQQQNQESDTSNLLEITDDGSLAEKTSSSISKNDSDD
AQSTVDENNDNSQRPSPKETSDHKADNKNVASTPSERAQQTVKTATITQRNDTATNGGSDSSTAVSHTT
SPLSFLLLVVCAAAAALVAA*
>Tc00.1047053510157.10|S022|A----R-C-|4
MAMMMTGRVLLVCALCVLWCGAGGGCEEVPGVSTSGVSGDIEREGGDSQDSSRSEPPGPKKPAPETPAP
KVQQQEVISPPPKDPPAETEDGAGGDEEGKAREEGAKDAGKENRGGATSKEVKKPENHLTSVKDPQSRD
NEGLQSPSLNGTHGVGTITTSLSGSLTVNTNQQDLSSPLQPPLPNSSPHAIPSSTSAAGPDNEKRHENV
NGTKNSQLPVVGDIQEKNGTGVKAVASTGGGEDPRLTVTTLEEMGDATKKGDSNSSTAATAALRSETGT
EGIPTTNHPNRPSTEGATSPEKTSDGEAASANKYDTVPQSAGSTTAPTTNAKTGETTPVDSDGSTAVSH
TTSPLLLLVVAAAASVVTA*
>Tc00.1047053510163.30|S008|A-----ECD|43
MAMMMTGRVLLVCALCVLWCGAWLCDAAETSSSAPHRDNAEETTTPEEVTEAIEKLAEGVLDMIRVSCR
MSFITSVNATLPAHNDTEVEKCVNKTAVEISGVTPRGRPAAATTDATLASPLPSSSSATSALQGQAQGS
PGAAPEPVKPPQTDSVNTEQLSETPASTGGGELADRSSHTPTDVARTHEARPAGNATSTPTATRGDSEK
SPAITTRTRETNETGDSDGSTAVSHSTSPLLLFVACAAAAAVVAA*
>Tc00.1047053510189.40|S086|AG---KEC-|3
MAMMMAGRVLLVCALCVLWCGAGRVYARDVNNNLLSGCMASGILGKKKSFLSSGCDKNAPTVSLHLALP
ITAVEASTGESVSDSTDIYPDSLSVPPSPPPVTGLPEALKAPKAPQDPPESDVGQTGVGNPSSLVPNDD
SSGGGGSEENGNSNKSGVSASEFSTVVGASRSSIPPEVGGSENKSGAPSDLKLESPETNEPPERILVET
NKDTQKVPKLEENPESSHKKEKANIRGTSEEAGKNEAGRSGVEAHGPSSVLSTDSQLQQQGTTVTVTQP
PPPSPEQQTSAVSPSPGVDTPAARSREAGDPEEGKGIPPTRTASHKSTDEKHKAPPLRSEKESAATKPP
SADGVLEQNSEDTTTKEAIKMDADTDGPAASSESSISTSDSGVFQDKTEEEDENEQRPEAKGPHNDPHA
VNTNDAPTASDTEAQTVKTITTQTNATSTSGDSDSSTAVSHTTSPLLLLLVVCVAASAVVAA*
>Tc00.1047053510191.10|S080|A---YKECD|24

MMAMMMAGRVLLVCALCVLWCGAGCGVFADQDEELSTESPGGRSSGGDPLETQELEKPVLHGADSEIQS
PVVEQPQLNHPQDLRGAATESLGEGVEEVENEVEDDDDEKGRGKGKDGKDTRTTEKAEKQKSLTKDRGT
LQLTSQPERGITPAPPRESLQVEGEEGPPASGGDSRPRKPAATPSAPELLLTLTSIEGQGQGTPSETPP
GPTTTTTNGKPAGEASPTASTGSQTATETTSTTSPSNAKVALGAAEKPLGNRVPNQQKEETETPDSMKD
APTSHPAETKATSISTTGSGGAQKNEDKVDNGDQRPNSKEPQDGLEDGNTDDAPTASEVEPQTPETDTT
QKNATSKSGDSDGSTAVSQTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053510191.70|S050|A--TH-EC-|2
MAMMMTGRVLLVCALCVLWCGAAVVANGDTDDLGGGRDDKNAEHLSSSDLSLPVRQGETTAAAAGGGGG
GGSTSSQEGKEASMPNTDIRVPQEQEVKLDAGPRKPTGNEYENKGPTEAGADKRNQPAPPPPPLSLSEE
GEEDELKQATQDQDSPVEHESTQNNKVLQKEEPGHELSTQNPLPQEQHTFKKLQVKQERGKEKQRSGQL
EQREHREELKDQQEIQEKQDEESIKHEEEQQQQKDEIQDQQHQQHEHPTENEEESAKDENAVRTNVTAN
KDDSDGSNAVSHTTSPLLLFVVACAATTAVVTA*
>Tc00.1047053510197.20|S093|AGWTH--C-|1
MAMMAGRVLLVCALCVLWCGGVFGRAMDDYCSEGGCIASEVLGACFSQMSGGCNKTAITVPLRSTLPIT
AVEALAEGETPVAGLNDSGSSEDSVAVVPVSVGAAGAAASPSGPSGGSDGKNEPSGPPSLDVDSSADSS
NGEAGSRGSTSSNAVGDPPRENPSPDVAAAAHNSPLPGGVAGTTPGNKGEKEEEKEKKKELDEENKRNH
GQENQSRPANQSEGEIGREGERLHKKTKGPKGEKEQIQVVEHSIENQGTLHEPGKQPREIKRENDQSKH
QNEELKAGQEKENPLQAIKQNSDAEEEKEKKKRQDQRPQEVTAPLASSSGSEAKRKSQPPVPPEALHTK
ELTDDLREQLEEETPLVPAQSKSHGTTDPQSSPASAIAGGAAVTHDADEENATGRNDDEPTETVFTEDH
QQHEHPEDIQKQSAKDKNAVSTNDTATTSDRDGSTAVSHTASPLLLLLVVVVACGAAAVVAA*
>Tc00.1047053510197.190|S030|A------CD|31
MAMMVPGRVLLVCALCVLWCGAGGRCDGDEVSSSALSGPRGGVDGPQGSLKSVAGVSEDARQLLYAQNG
KNENQGRGSVIEPSLDDVYEEEDEGEETETRETPPPAGGGIKASSVSAGPGVIPTSGSSSLSGVDSSSR
ISGETGPTVSTSSNTVGKASKEDMALQEKESQHTQLGDGEAAGTHNNGSQQNSSAPPPTGGQNDNDAAT
LSADGLRTLGVQIAVKGDLEASRSEEPSDGPSTNLPEGGRAPPESSQAAAAPEHTPQHKVIMSVKEETE
RMNMNASANLPGAPKRSNEGPASTATTMQSTSTGGQEGAATPSSNGIPKIQEEKLTGNNTTENAQPSDT
AETEIRQSVNTSKVGDRDGSTAVSHTTSPLLLVVVVVACAAAAVVVAA*
>Tc00.1047053510201.20|S091|AG--YKECD|14
MAVMMTGRVLLVCVLCVLWCGSSRIAASGVYASGVEDSGRGGCMVSGVLGTNWSYTPSGCNKTVPMTAL
RSVFSVFAAEASTEQEDSETDTVPDSPSGDGPDSVSGSPVGSVVIGGSKVVDSTLGRLNVVPPDTRVAV
ASPPPSAPETDASLLHKVSQSTEKHNSSEKLVDLKTKTPAGTPPLSNQASKESLPTVKPESPTTSDSTV
TVKGTDQISEEKLAVLQGPSTVNAGEDGKKAVTEIKPNTTTNTPDAAPTLSSEGDVTEQHGKDTDSPNF
MNNANTGSSAETTASSFSKSGGIDAPKNESEDEGDAQRPKSKEPQEKPEDSNTNDAPTENETAPQTEKP
FGSAQTNDTSKIGDSDGSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053510207.40|S030|A------CD|31
MAMMMAGRVLLVCALCVLWCGVGGRCDEVADSGVAAGKGNGGSSAVEPAGNSEPVPDASDLRIDVLNVN
QATGTSTGKSLEGKKVNTDQQDVLSREDKKDGGPSENLEEPVEDAPGNEKTNLKLKKEEQEGIQPLQSQ
SNVSPHPQPIPQQSQSQRQPQPQREREDEETKRQLQPPSAPQPHISASEKGEGVGENNTGGEGQSPLGV
QDIGNEDPKAPRKGDLLEGPGTKSESSEQVQTTVPNTVTPEHKTQNEMLTPEQKTNESQSTDTSTNIPE
LQKENKEYPASTEATAQSTSTGSQEQEAEPSTSEEFSPFEEEQSTGTKTTEDAQTPDAAATEKRQTGDN
VKVGDSDSSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053510237.70|S017|A---S-EC-|13
MAMMMTGRVLLVCALCVLWCGAGGTCDAAVGVGAQLDGGKSPPESKGVETPSQGTQDLKGGAAGVKEDP
PPLPTEEDDEDVVDDSEEGDDGRAEGEEEEKVQGQSGQEGKVALGSESTGNKSSGSEKQTELSIESAGS
ISPSGSRELNVNLTQTEVEGRKETDKNTPAVENPLTTGIGESTLPAGIVEGNPSPPPPLDGIHSREEDG
EGTASEGQKNVPSPETAATPQSHHDKSSEGTGENTKATTVTANTTGTTSTQNSDSGTAVSHTTSPLLLL
LVVACAAAAVVAA*
>Tc00.1047053510237.120|S080|A---YKECD|24
MAMMMTGRELLVCALCVLWCGAGGRCDEEEDTALVVGPPGGLSNDGKGGPGPAPSSLPGTGTSGPRSIL
PESEVSQEIIAVKSPEGSGEKKNQNEDGEEESVAEDGENSKNQERLSEQPTQQEVSDEETPDEKRLEEE
KEKDVHQPGEEEMKRTQQSQSQQPPPQQSQVQITAPAERGGPTAPTGPARPPAPAEPSSMDGSRTTEPT
DSRNPSQESHDKSQLQTKTESSAPDPPLKDDFPEQHGQETTTPASMLNSSPGSQARITAPSTSTGGSGE
AQSKVDEDDAQRPNPNESHDNSDAGKTKVPTTLSEATTQSTETVAATQTNHTKTIGDSDSSTAVSHTTS
PLFLLLVVACAAAAAVVAA*
>Tc00.1047053510239.70|S004|A---V-ECD|18
MAMMMTGRVLLVCALCVLWCGVCTVAAADTGGVEMERAEGSESLPSGPSDGDGGKQESEGSVRQVSDTA
NESLVAVDGKNSKQQDGVVITTPTKPERTSGGTETEEIKRKEQKENPEIPNKDDKTTQLTSRPKEEEEP
SAERGKAQGAALPGASPGVPSRAQNGNSAEDLTATPGEERALLEDHSDQPQGGKTPADGLAAEMPSREK
GEARDAIPSPPAKNEKTEGGLRATTNTEKNNLENAASVQKTEILLDDEEATSNQRNEGLASTTGNQEGE
PSDVHAELTPPTISAASNAANEDADTDTDKGILNNDLAAGGGATEGAQQDEKKERAEETTPLKSVAMIN
ETATVGDSDSSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053510261.10|S030|A------CD|31
MMAGRVLLVCALCVLWCGAGGRCKEEAGSPAGGKGAVGTTGASASGQDSSDLKKGLPKANQSTETPAGK
SLEGKEVNTDQLVVVPGVEDEEDGNPSEQLEEPVEDGPDQEKTKPQLQNKEQEVRQPPESQVNVPPQPQ

PLPQQSQTQLQLQPHTSASEEGKGVVENNKGGAGQSSLGVENIGNEDPENLGKEDSLDDPGKESENSEQ
VQTTVPNTVTPEHKTQNEMLTPEQKTNKSQSTDTFTNLPELQKENKEYPASTEVTAQSTSTGSQEQEAE
APTSEEPSPFEEQHSTGTKTSEDARTPDAAATEKRQTGDKEKVGDSDGITAVSHTTSPLLLLLPVACAA
AAAVVAA*
>Tc00.1047053510275.60|S020|A---HR-CD|2
MMAMMTGRALLVCALCVLWCGAFVSVAEGPGEVAEAGVEIPDSQQQMADGIQREEGGTKGKQLQGKDTQ
NEVEQVLKQGEDQERLKKKEEEGRENQEQISLQKNAQALEEKEKSTREPAGGSLEGRKIGDGSGGRQQI
TVEEVGKPNEEGVLKSEEKVEVVVGKDASGVNLTASQQETSGIHTGESPGQSQKEGGKEEDDRKDKERE
QHDQQQEENKRKLQEQNQMLQQQQQQKQQQDQGREHSENNQKESTKDKNGVGTNQTAITHNSDSSTAAT
AALRSDAGTEDTPTTNHPNRPSTEGATPPEKTSDGEAASANKYDTVPQSAGSTTAPTTNAKVGDTAKPV
DNDSSSAASHTTSPLLLLFVVACAAAAAVVAA*
>Tc00.1047053510275.190|S066|A---VFECD|8
MAMMMTGRVLLVCALCVLWCGAAASPAAENGDAVTEEDEKTRTTEVSPPGRKNESPLTSVEESTGTKTG
DVKTPQNSEAAILLTTKGTSDQKQEDEKNKKEKEEDPEHGEDEEEGDEETETREKTPGPPPPPPSGQTS
TPTINGNSAGTSNEARAKELPSSDKDSTQGQELKSPAAESAPAATPQVKNENPSSADFVSVQQVQKAQG
GLESGNESRKEDSALTTNKQQDGTSDSHAESTPTSRSSAKRVAASNGSDEATEEEISNKNTARVDAVPE
AAQEDGNKDDNTKETPIKTTAIANDTAPTGDSDSSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053510275.250|S072|A---VFEC-|6
MTMMMTGRVLLVCALCVLWCGVCAVEVSKADASENTNVFHVPAEGPQPESAGRNTGQQEPLEHVSQERQ
NAGKPLDPKNEATDDQKRDLEIETPTADELRGEKEEVHKEQIDGGAGREKRKEILEERKAPPDGRGSEG
GARQAGKGLAKVGVHSPATTPSGGERPGTSEPSPPESSLPAASTQEPGAAIPASLQEAPAATMKKKKEK
TVENPRAEPGKEKLSSEDDVSEQTSQRVNDGVEPNNELKNDENVSVLLIEQNGESDGNSESTQARPLAV
GDASNMGAEKGNEMGLQKNNPTDNGAVTEGAKRGENKHGNRKETSDTATITQTNETATNGDSDGSTAAF
HTTSPLLLLLLVACAAAAVVAA*
>Tc00.1047053510275.370|S136|A--TT-ECD|1
MAMMMTGRVLLVCALCVLWCGTPGGRCEEGGTGGTPPVASSSDVDESSQESSPIAQGGSHKPGLKASDV
KDGTEDSGDEQPSTEEEEEEEEEEEEEGSDEEDQDERLKTPGEGGGGGQSQAADEKLENVNESGPKPES
QRQVESGTQNQSEKETVGDGEAAVTKQNEGSGPQPQDHPHPVQEEDTKSGEGHQPSQGKEQQTNVEATI
PINLAGDHSSGEHNGNDGSNEKEKEGEEEKDDERHRAQEREEAAHVSGAPKVNSTDIQQEVQHKNAGET
PTGIKQRAGEEKDDETEEEREKQMEQHQENPPGKEKETITGANTINQINTTPGDSDGSTAVSHTTSPLL
LFVVACAAAAAVVTA*
>Tc00.1047053510275.400|S091|AG--YKECD|14
MAMMMTGRVLLVCALCVLWCGAGGVYARDVDNNALGGCVASEVLSTNWFHLSSGCEETALTPPLRSALP
ISAVEASTVEEVSSPCDGSCSRSAGDSVTGGGVGGLDGSLGGTGDVSRAGVSVVGSSGPREDCKENRGA
NLVSSLGGAPPTPISSDDASHSLNGELSTRTECHETVKHSESKKIAESKVKTPEMSTPLKEHHSNTEDT
EEKEVADEGPAEGEARQNAVVTKDSSSDVQAPLPLPQIQQSQPPGQETPVVTSLQDAKPPEKQSQATPI
LSTEEKSPKAAVTAIGEGDPPTTTHDLQSSTEENHKTLQSPATTTSETQGQHLKDGMAEQQGQDATTAD
LVKNAATGNPAGRTASSISTSGSGESQRKPAKENDDTQRPNRKKPQNGLEDVNTKDAPTATETAPQTAE
MVTNTQTNNTATVGDSDGSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053510279.60|S028|A---VF-C-|1
MAMMMTGRVLLVCALCVLWCGAAAVVSVADSGVAAEKGNASTGNDDQRRTGGVPASGKSIASPVNSGQE
SAVSTIRNEQTPQISEASIVLPKQITLDQKQEDEDAKDGKDGKEERETREDARPPPPPPPPPGPPQPPG
EPPTTINGNSAGTLNEKPAKELPIADDGSNQEQVLKSSAPAATTTAAASPLKAAATPQVKNEDLGSANL
DTVQQVQNAQRGLESDGESIKEDSAVTTNKQQDGTSDSHAESTPTSRSSAKSVAASNGPDKATEEEISN
KNTTADGEVKESAQEDGNKDDNQKETPIKTTAIANADDSDGSTAVSHTTSPLLLLLVVSCAAAAVVAA*
>Tc00.1047053510279.120|S066|A---VFECD|8
MAMMMTGRVLLVCALCVLWCGAAAASPAAEKGDAVTEEDEQKRNTEVLPPGRKNESPVTSVEESAGTTT
GGEETPQSYGVDIPLPNNLNLDQKQEGEKKKKEKEEGPEHGEDEEEGEEERETREKQPTPPPPPPPSGQ
TSTPTINGDSAGTSNEARAKELPSSDKDSTQEQVLKPPAAESAPAATPQVKNEDPGSADVVSVQQVQKA
QSGLESGSESIKEDSALTTNKQQDGTSDSHAESTPTSRSSAKSVAASNGPDEATEEEISNKNTARVDAV
PEAAQEDGNKDDNKKETPIKTTAIVNGTAPTGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053510279.140|S049|A--T--ECD|5
MAMMMTGRVLLVCALCVLWCGADGLAEEGSGTTPPGASSSDGERLQETPPVVPGVSKNSVLKAPEAKDK
KGELDKEILLKEEEAGSDEEDQDEDEDEGITPSGEEEIPPPPPGGGGGQSQAADEKLENVNESGPKPEN
QRQVESGTQNLSEKETVGAGEAAVTKQKEGSGPQPQDNPHPVQEEDTKSGEGHELTQEKEQQTNVEDMP
PRNSAGDHSSGEHNGSDGSNEKEKEGEEGVEGHERHRAQEREEAAHVSGAPKVNSTDIQQEVQRTHAGE
TPTGIKQRAGEEKDDETEEEREKQNQEDPPGKEQETITGANATNQINTTPGDSDGSTAVSHTTSPLLLL
LVVACAAAAAVVTA*
>Tc00.1047053510279.190|S084|A---YK-CD|3
MAMMMTGRVLLVCALCVLWCGAAVVAEGDIGEIGIKDESSKVLQVDSQAREAGKKDVRGPEAAVPRLHE
QQGKNARNNDGSAIQPTRQVKVEEEEKENEGSLEGMVKDGEILPSPAEGQPTSSEPLPPPAPGGSRNGV
ISGGGSKLGETSNGGEGPTLNSSSSSGDGKPPAVDSSGSGGGTGSVPGGKEIGGGGTPGVESSKFPVSG
VALPPSTPGAGSASSAQNLEPSERSGWPEPTVSPRTAPLNVDARKEPKPKGEPQTFSAQGETERQVTDE
KTSKKEAEESAIEGKRLFNLPHTASSTPAGPAVRLPEGSQVQGNRDEGEGLPPEATKSETSTGQERRTS

QSQSESTGPKFSSKDEVAVQHGHVTVPSDSMTNASTNSQGVTPAPSISTNGGDDAQSTVDGNNDDDQRP
NSKEAHNNPEDDNTNVAPKFSETAQQTPETVTVVQTYDTATKSNNDGIKAASHTTSPLLLLLLVVACAA
AAAVVAA*
>Tc00.1047053510279.210|S090|AG--YK-CD|3
MAMMMTGRVLLVCALCVLWCGAGGVYARDTPNNAQGGCMASGGLGAKTSYLVRGCNKTVLTRPLRSAFF
INAIQAEAKDVKDISEERDNLNLDSIPQPPALPPAPETPPPPDASDSDGIGRSELGAGSQTGGGGGGGG
GSSGISNGGEDSTLKVPVPDDKSSSPIPSAGGGLKNTGDSSVTQKNNSSGTDEPSKKTLNVPALPTVQT
PEALEPDQNENTPNTQGEISVEARGKGASGGDAGESDVNSKDSSSVSTANSKPTGKTTPSVPSTGKTPT
ITATPKDSENPTGKNDNTAASGTETDSEATKTSSKDDAAEQHSQERDKADLVKSANTGHPAYTAASSIP
TYGNGDAQGKANENGDDPERHDPKRTHDELEADNTNVGPTASEAAQEAVNSTEKKDTAPTGDSDGSTAV
SHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053510279.250|S104|ANP-VF-CD|10
MAMMMTGRVLLVCALCVLWCGAAAMESSLPGATTVQSAWPEDLFLKWHELLKNECKAKFKDGNFDESAV
NCCVHNAMKDLCYDVYGETVMENKDLKVEGICKEYAGKPDDVANCPKPQTSLSSAAVTSVKVSVPEVPG
REGNLRTPSEEEPTASAVAPPGASTAKPTDPPPSLPVEGQPDGADDMPVPNSEETSESMKPTKDLAEED
TVTTADTKQNEASNGQTEATKKTPPEASDNGDNETNKGTGEDIPNNAPESDVAGTEENQDKNKDNNPKE
TPVEVAGIKAATVNSGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053510279.310|S084|A---YK-CD|3
MAMMMTGRVLLVCALCVLWCGAAAVAEGDDIGEVGIKDESSKALQVDSQAREAGKKDVRGPEAAVPRLH
EKQGKNARNNDGSAIQPTRQVKVEEEEKENEGSLEGMVKDGEILPSPAEGQPTSSEPPPPPGAGGSRNG
VISGGGSKLGETSNGGEGPTLNSSSSSGDGKPPAVDSSGSGGGTGSVPGGKEIGGGGGTPGVESSKFPV
SGVALPPSTPGAGSASSAQNLEPSERSGWPEPTVSPRTAPLNVDARKEPKPKGEPQTFSAQGETERQVT
DEKTSKKEAEESAIEGKRLFNLPHTASSTPAGPAVRLPEGSQVQGNRDEGEGLPPEATKSETSTGQERR
TSQSQNESTEPKFSSKDEVAVQHGHVTVPSDSMTNASTNSQGVTPAPSISTNGSDDAQSTVDGNNDDDQ
RPNSKEAHNNPEDDNNNVAPKFSETAQQTPETVNFVQTYDTATKSNNDGSTAISHTTSPLLLVVACAAA
AAVVAA*
>Tc00.1047053510279.330|S086|AG---KEC-|3
MAMMMTGRVLLVCALCVLWCGACGVYARDRDNSAVGGCMASGVLDTRRLYMPRICNKTAVTQPLRRVFP
ISAVGASTDGQVSGTIDGGLVPIPAPPLPPAPNTPKAPEAPTSHGVSQPAVGVHSGDGTPSLHIPNVDS
SVGGGSGQSGNSGGTVVSVMEPPSTVVVISPSSVSPEVDGLQNKDGPPSNLKLGSPAISVESGKILVGH
NGETEKDSTPDDGPESSRIQKETESRATTEEARGSEAGQSGVGTNGPSNVLSTESQQQHRETTVTETKP
PPPSPGKQIPAVSLPPGVDTPAALSQGPQASSPEPSRAAEDPEEEKRILPATTASHNSKGKTHKASSLR
KETVSAAPKTPSPNVVLEQNSEGTVTKDAIKTDAYTDGPAATSESSISTSDSGVVQDKTEEEDDNEQRR
EAKGPHNDHHAGNTNDAPTASVTAAETVKTITTQTNTTSKSGDSDSSTAVSHSTSPLLLLVVACAAAAA
AVVAA*
>Tc00.1047053510359.380|S103|ANP--F-CD|11
MAMMMTGRVLLVCALCVLWCDAGGVCTDEVGVPASVVASKRTDEENLILNWYVLMKEECANESTTGGKL
NVTAERICMHKVMKEVCDAFYDKTSGVTHDRDVELICTYYATIPEEPVEPPTPQGPTSHSAVSNTTSDE
GTPKNAPESDVAGRGEGKDDDKEHGNTKQKAVETAAVESITRTTDSDVSTAVSHTTSHLLLLLLVVACA
AAAAVVAA*
>Tc00.1047053510359.460|S103|ANP--F-CD|11
MAMMMAGRVLLVCALCVLWCGVGCGFADKVVEAAAGVVASNRTDEENLILNWYVLTQGECANESTTGGK
LNVTAERICMHKVMKEVCDAFYNKTSGVTHDRDVEFICTYYATIPEEPVEPPTPQGPPPDSAVSNTTID
EGTPKNAPESDVAGRGEGKDDDKEHGNTKQKAVETAAVESITRSTDSDVSTEVSHTTSHLLLLLVVVAC
AAAAAVVAA*
>Tc00.1047053510359.520|S103|ANP--F-CD|11
MAMMMTGRVLLVCALCVLWCGVGCGFADKVVEAAAGVVASNRTDEENLILNWYVLTQEECANESTTGGK
LNVTAERICMHKVMKGVCDAFYNKTSGVTHDRDVEFICTYYATIPEEPVEPPTPQGPPSHSAVSNATSD
EGTPKNAPESDVAGRGEGKQDDKEHGNTKQKAVETAAVESITRTTVSDVSTAVSHTTSPLLLLLLFVAC
AAAAAVVAA*
>Tc00.1047053510359.550|S103|ANP--F-CD|11
MAMMMTGRVLLVCALCVLWCGVGCGFADKVVEAAAGVVASNRTDEENLILNWYVLTQEECANESTTGGK
LNVTAERICMHKVMKGVCDAFYNKTSGVTHDRDVEFICTYYATIPEEPVEPPTPQGPPSHSAVSNATSD
EGTPKNAPESDVAGRGEGKQDDKEHGNTKQKAVETAAVESITRTTDSDGSTAASHTTSHLLLLLLVVAC
AAAAAVVAA*
>Tc00.1047053510359.600|S103|ANP--F-CD|11
MAMMMTGRVLLVCALCVLWCGVGCGFADKVVEAAAGVVASNRTDEENLILNWYVLTQGECANESTTGGK
LNVTAERICMHKVMKEVCDAFYNKTSGVTHDRDVEFICTYYATIPEEPVEPPTPQGPPSHSAVSNATSD
EGTPKNAPESDVAGRGEGKEDDKEHGNTKQKAVETAAVESITRSTDSEVSTAVSHTTSPLLLLLVVACA
AAAAVVAA*
>Tc00.1047053510359.650|S104|ANP-VF-CD|10
MAMMMTGRVLLVCALCVLWCGAAVVVSSMPDANSVQSFWRENLIPRWHELLKNECEAEYSKETNLSLKD
LAVNCCLHHAMHELCKDLYPKLFKKTEFSNVEGVCKEYAAEPDEVKCPKRQTQPPPATDNSVKVSVPEA
LGKEGDLGETPEEAPLADLPAKPTKGPPSSPMGGQPTNADDVPAPKSEERPVSTRPTNDSREGDTDTIT

DTDQEETSTSEAESAAPTPPVASDNDDDNETDKGTGEKVPNNAPESDVAGTNEKKDENKDNNPKETPVQ
VAGIKTDTTPGDSDGSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053510361.30|S030|A------CD|31
MAMMMTGRVLLVCALCVLWCGAAVEAEGDDVTELQGEPSRVSQSPSKGGHEEEPDVRKPVGGVLNTSEE
PSDARDLTKVSPQKTSVKQTPRDNGGAAEKEGKVEAKKAGDEETRSDGEEQPKDHSDETQESDGPKENE
RSPSPTPTDKMLTSEDPAAKHAGQAGQAIRPPPSPESDGTRPSGSSRGDSSVSPLSTAGISSSSALDAP
LVQSTQPSEKGLQSETMSLGTALPNEQPKERSESKAKQGFSTSEEAAKSPDDSGDAVEKKKEKGDVGPK
ATTSLSSTTSNPPVTQTTPRPPSAEPSPTETELQAGEETSTENVTITKRNETTTPADTDGSTAASHTTS
PPLLLLVFACAAAAAVVAA*
>Tc00.1047053510361.110|S013|A---V-EC-|8
MAMMTGRVLLVCALCVLWFGAGGGGCTEGRLPVVGPLVNSESGDVVTDNAIGHTVPGGAGKLSAEQTQL
NNVEGSAPRKVSLEAPLQSVSTTQQTPSSSEHTDSLTNSQSLQEERQAGSPDGSSGRPAASPSQEDRKN
ESIGDQQRNNTPSPSSNNDVVSRKSEELIEDTPRRAEIIVAAPSEEGQEPENVTRSLEQPQETSTAAPA
ITTQTTSMTPSEENKSNTVKMSEAAPQSAGTTQTNHTATPGDSDGSTAAFHTTSPLLLLVVACAAAVVA
A*
>Tc00.1047053510361.190|S080|A---YKECD|24
MAMMMAGRVLLVCALCVLWCGAGGRCDEGETAVRGVPPDVSASGTEGELGGTKNAGPAPDSQIQSSGEE
QQHKSREGRPTLPEGSLEEEVEEETVENLDEVTERGEEGQRGDGQDANEPDGSQTSEVLTKQKETLPPS
TPAAPAGEGNQSASPQAQSVDSHVGGRTDRIEDSILGAPSSGVALQHAGDASTNQKNNSLETGKHTEKT
ITGGPVPFQTKTTKEPINDAEIHSVTGEDTASNQVVSRGTAEYEAQQRALATQDRSSVSFTESETKWQT
TPHEAPGTQVPPSATEPSSREGQPPTAKTDSQTPNAQEHKEILLPKKEYNAPERPSEDVVAEQQGQATA
TENSTENAPATNQAETTASSNSTSGSGEARIMADENTANAQRPNPNESHDDLEGSDAHPAPTASEAAPQ
STGTANANDTTKPGDSDGSTAVSHTASPLLLLLVVACAAAAAVVAA*
>Tc00.1047053510361.260|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCGAGGVYARDVDNSAVGGCMASGVLGTRRLYMPRCNKTAVTLPLRHVFPV
SAVGASTDGEGDSAGGRQNSSNSRETSDAGSPGGGPAAVTGPGSAGGPGGAGDSGASSGAGGSGTAAGG
HGGGVSSAGDQGTDSVSSGPSAVAPPPLPSADPGVDSPASSASPPAPPSGTPAGSGAPPPPATPSGPPD
ATVVDSSTSSSGGTAGSPGTNPSNTTGESPTGDQTPAAAAAHNSSLPEGPAGTTSGTGQKEKQEEEEEE
EEDHEKQQQSDEAQVQQQQQHEHPAENGEESAKDKTANGTNATANTGDNDSSTAVSHTTSPLLLLLVVV
ACAAAAAVVAA*
>Tc00.1047053510363.220|S069|A--T-FEC-|1
MAMMTGRVLLVCALCVLWCGVFGIAADGEVDVTREKDESLEGPLRGSRENEDGPQKSLGSVMQRSNTAN
QALSLENGVMVSQPEDPAKKQVPDEVETQKESEETEEEDYDVVDDDDDVEEEEREEEAVETAETEIPND
QTKEEASSPPQSKHKKGPTPAKGIPTTQSPATPVLPTTQGQPPTAAPSPEDSPVPAALAATAAPKLTSS
EQGNIPAAARKKDEKQSEVIDPAQESEQPGPQDFVLVQHSQGVHESKESNSNPRNPASASAAANQRDAT
FNGHGEPAQTTSSNKSVFEINDANSGTEEGISSDDPTADGAGKNDTKNSQNKHGNTKETPVEATAMKGA
AATTGDSDGSTAVSHTTSPLLLLLLVVVACAAAVVAA*
>Tc00.1047053510363.260|S016|A-----EC-|10
MAMMTGRVLLVCALCVLWCGGAVEAEGDVVTELQGEPSRVSQSPSKGDHEEEPDVRKPVGGVLNTSGEP
SDAQDLTKVSPQKTSVKQTPRDNVGAAGKEEPVEAKRVRDEETRSDGEEQPKDHSDETQESDGPKEDKR
NPSPTPTNKMLTSEDPAAKHAGQAGQAIRPPPSPVPDVTRPSGSSRGDSSVSPLSTAGFSSSSALDVPL
VQSKQPSEKGLQSEAMYLGTALPNEHPQERSESKAKRGFSTSEEVTESPDDSGDAVEKEKEKGNVGPKF
TTGLSSTTSNPPVTQTTPRSPSAEPSPTDTELQAGEETSTEHVTITKRNNTTTPGDSDSSTAVSHTTSL
LLLLLLVACAAAVVAA*
>Tc00.1047053510363.280|S064|A--T-KECD|5
MAMMMAGRVLLVCVLCVLWCGAGGGGAEMNDETLVDSQHLSGVGEKAPKGLPESGERGPDSAGHSLDKN
NGINSNLQEGTVTGTTTERVGKKKEEDVGDDDGLEEEEEEAETDDDDDDEEEKEKSKEKEDTPQAGKSE
SSSKEVAATIPTASGLSGVGGGSPSGVDDGGSNGSPNGIEDLNLEVPGPVVNSPSPLPNAAAGGLQNPD
GALPSQKNNFSETGVHSGTTLPAPSLPKPQAPAITQPKAEEQSSTEQDTEYSPDIEEVTTVKEKVQNTV
ETGIPSRASSAASKPPVQQPTPLLTQSPAAPSPERLAAATSEEKSIAPSFSAGEGSRTATNVAQNSKEE
KNEKLPSENETESKAVEQPSGNDVAEENSPARTTASPIPASGGADDQRNADADNSNARVLKSEGTHKNS
ETGYTNLASTAGDAATQTEKAPADAKTNDTTKPGDSDGSTAVSHTTSPLLLLLLVACAAAAAVASA*
>Tc00.1047053510363.320|S062|A--TVFECD|5
MMMTGRVLLVCALCVLWCGAGGGEPSETPSPAPPDTPHEKNPQKEEETFVGTGQGVKNDEPEIPQAPAP
KASESPVVSAESLQAQQSGGGASVTASATTDNKDQNAKEDKKEEEAKDDDEDEEEEEEEEEKEDRDSIP
DGREEETEVIISEQETEQDKKNAGNQAPTETPGGPTNNEEIKTATTQVNGQPSPEDLGDVKQSEEVQGE
KDSNHNPQTKSVASIAAKQQNEPSADHEESRPPSPTANGDAANKDFDKSTKDGIPSNHPAADVAGTAEG
KQNENKDANPKETPVTATAMKTARETTGESDGSTAVSHTTSPLLLLVLVACAAAAAVVAA*
>Tc00.1047053510371.10|S123|ANQ-V--CD|3
MAMMMTGRVLLVCALCVLWCGLSGIAAYDADGADGSAVEYSLSRWRAQLRRGCAVEVSRRTGGGANASA
VEECVGRGMDGVRAVVDGRSRWRRQQFAVAAAAVDGDVDSGEVDINSVSSPEDQSGTGAGSREESQVKP
PVVSEPGQADTTPGGENPPKPAESLETAKGKSGGTSKEKDKEERPTVETKGPNSTDDNKQVDNAAIGNS
NGGREEKNGVTLQVQDEVVKPKEEKQEPQKELEEKEKQKAQGNKKDDPEDPGEDAEDTEDSADGTDHKE
GEGQKEGDAGSNKKGKELNGGGDTDGTPPDAPVVLQPAPPVEVTDPQSIEKTNDDDTGGKEDAGRTQTQ

EAAGPSQAENLTAELSTEENAAETETGTPGKKTQPEDAGKEQTTVGAKSNQETPAAEREAQNREEVIKD
EEGSEKATTNENFDGRQTAVKDNAHNEAEKTSQKNENELDKAEETTAEVKEKEETTERKTVAAKGPNLN
STAATNDSDSSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053510371.50|S017|A---S-EC-|13
MAMMMTGRVLLVCALCVLWCGVGGSCDEGEAAGLGSDAELPPAPAPLEKTPQGPKGLQSGEPGVKENVT
PASSTPTEEEDDDEEVEDTENGESEEEEEKRKEGQSNKGETGAIGSGSREENLIGSEKETGESISSAGS
ISPSGSRESNANLTQPEVEEKKETEKNTPAVENPLKTVNGENTLPAGIAGGNSPPPPEDSVDSREQDGE
DTTSEGKENVPSPATTATPQSHRDKGSEGTGEVTKATTVTANTTDTTNTQNSDGSTAVSHTTSPLLLLL
LVACAAAAAEVAA*
>Tc00.1047053510371.70|S061|A--TIFECD|52
MMMVTGRLLLLCALCVLWCGACAGGCSEAAPTLPGTGVTDNGNNLEGKNNTTDGVGAVGPTGQQAASQP
AAGSVPVPGTEEESELRTGEQALQSAAKAAEVANDTTKKGEADKDNELKEEDDDDEDEVEEEEEEEEEE
EDDGNEEEYGGEEKKEEEKDDTSTTKGISAVGQEEPILSSRVEEASNKTKPQSTQTTGDKDPAADGAVT
QEEKQNENKEANPKETPVESTGMKTTTATTGDSDSSTAVSHTTSPLLLLLLFVACAAAAAVVAA*
>Tc00.1047053510371.100|S008|A-----ECD|43
MAMMMTGRVLLLCALCVLWCGAGCRCEDLVTISSEPAVDNPVNAPGSKKGSDLPKSNDNEDPKPLGEGQ
NRDSVNLPENEICKNDSTKSSKCTEGPEDALVPPLDPVGQGEHNEVQNSGSSGSSEKDKTRKDQDLQER
PHDVETLSREPATLKDPQITMPAEHSSSPSPPNATVTASSTDISGVGIGTVQRDNMQNTLNGNDGSESP
AAQPDSASGNTQTSVDEETSSNGGAPQVSTAADTDSAGYTTKALKNADTKKENSGESHNSLAASPAVGT
NTATTTTSATQDASEYNKDGVKLSTEDVEQNAFKTNPTANSGSTKTAAANSEVPTAASNATNKKSNTET
TADSDGSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053510371.120|S068|A---IFECD|10
MAMMMTGRVLLVCALCVLWCGAGAGGCSEAAPTLPGTGVTDNGNNPEGKNNTTDGVGGGGPIGQQAASQ
AAAPSSVPVPGAEAESAPKTGAQALGPAEETIKKNEKTENGENEEGNQDADEEDEGEDEEEVEEKVEEE
VDDGKEEEGEEEEKDGTSTTKRISEGGQEEPILSSRVEEASNKTKPQSTQTTGDKDPAADGAGTQEEKQ
NENKEANPKETPVESTVMKTTTATTGDSDGSTAVSHTTSPLFLLVACAAAAAVVAA*
>Tc00.1047053510377.100|S033|A---V--CD|9
MAMMMTGRVLLVCALCVLWCGAGGGGCSEALVPVAEITVDSASVGVVTDKDTDRTVPGELGNPSVEKKQ
LQNVEDSAPGSPQSQAGLDIELTKQQPHTDHKHTDPPPHSQSLQEERRDGIPEGSPGESAASLSQEDTK
HTSIVSPERNDPPSASSNNNTVSSNSEEGTEGTPSSTEIIVAAPSEDGQEDENVTPYLEQPQETSTAAP
AITTQTSSMTAPEENESNTVKMSDASPQTTVAANSNVATKPAENDGSTAVSHTTSPLLLLLVVVACAAA
AAVVAA*
>Tc00.1047053510377.200|S002|A---S-ECD|19
MAMMMTGRVLLVCAFCVLWCGAGGRCKGETAVLGSRAELPPAPLETSQKGPQELQSGEPGAKGTASLAS
PPPKDKDADENEDEGDEDDDADEDTDESKVRRTEGQSGEKANAASDPDSGEKNLIGSGQETGQSIAPAG
DISHSDSQETKANPTQTEIEEKNETDENTPAVEKALTPGNGENTLPGGIAGGNPPPPPEEGVDSREQDG
EDTTSEGEKNVQSPATAATPQSHREGGSEGTEEDTKAKTVTANTTDTANTQNNDGSTAASHITSPLLLF
FVVACAAAAAVVAA*
>Tc00.1047053510377.260|S112|ANP-V-ECD|4
MAMMMTGRVLLVCGLCVLWCCGAAVVSSIPDVTGRKNVPHGYLVVNWEKLLKNECATDEKYINEDGTVN
ESAVKDCIRDAMRVVCNVFCRKNSGEPDDSEGERICEEYVGSRDEAGQSSHLITPAEAKTLKAPRSELE
ELEKTPGETPKPLSGGPATEDEPAKTTGGPPTPPVEAQHNREENVPVLHPEDDPGTTESNSDSEEDDSA
STTDNQESVTPDGHDKSTPTLPSTATDTVKNEADRINTEGTQKPATESNAERKEVEESDEKTYDNTKKI
PAEAAATTNNTVMPGDSDGSPAVSHTTSPLFLVVLVVACAAAAAVVAA*
>Tc00.1047053510377.350|S009|A----KECD|5
MAMMMTGRVLLVCALCVLWCGAGGSFADEERAGLGSGGGPPPESQELETSPQVTQGIRDGTGGVKVKKP
PEDEVEEEEDEDNDDDEGAGTDEEEKEKSKEKEDAQQTRKSKSSSKEVAPLTIPKASGLGEAGGGSPSG
VDGVGSSESSDGSEDLNLEVSGPVVNSPPPLPNAAAGGLQNTDGALSPQKNNFSETGVHSGKTPPAPSL
PKSQAPAMPKPEAEEQSSTEQDTEDSPDTEEVTTGKENVQNTVETGIPSRSSSAASKPPVQQTTPLLTQ
SPAAPSPERSALAPSEKKSTPPSFSAGEGSRRATNVAQNSKEEKNEKLPSENETESKAVEQPSGDDLAE
QDSPARTTASPIPANSSADAQRNADADNGNAQALKYEGTNKNSETGYTNLASTAGDAATQTEKALADAK
TNNTVTPVESDGSTAVSHTTSPLLLLVACAAAAAVVAA*
>Tc00.1047053510377.390|S068|A---IFECD|10
MAMMMTGRVLLVCALCVLWCGAGDGGCSEAAPTLPGTGVSGDGNNLEGINNTTDGVGGGGPIGQQAASQ
PAAPSSVPVPGAEAESAPKTGAQALGPAEETIKKNEKTENGENEEGNQDADEEDEGEDEEEVEEKVEEE
VDDGKEEEGEEEEKDGTSTTKRISAVGQEEPILSSRVEEASNKTKPQSTQTTGDKDPAADGAVTQEEKQ
NGNKEANPKETPVESTVMKTTTATTGESDGSTAASHTTSSLLLLLLVACAAAAAVVAA*
>Tc00.1047053510377.430|S087|AG--YKEC-|7
MAMMMTGRVLLVCALCVLWCGAGWVYAGDVENNAGEGFMASGVLGVNRLRVPSVCGKVAITLPSRMVSF
ITAAEASTNDDASGIIGGNPDSPSGAGAAAGSVSGGAGGAGGSGGGGGTSGGSGNSAGGSDGNRDTTED
HPGVGGGSLQSPPSVDPNSSRIPNEVGESQNTEVSLSTEEAISPEAAAESGPTASPGNTPPKVETADKS
KPNEEEKELSVTQAAAPISVNGEASTGEQNQHNDVGKVDHSSNQTPPPVPPSAVTTPAPSKEPAPPATE
PSPSDGSIPAPNVPQNAKDQEQKTSVLTIKMESNAPEIPSEDNVVQQQGQNTTTEELMETSSRGSQAET
TTSSIYTSGTGEAQSTADADDAQRPNPSESQNDLEGSDTNNSSKTDEVAPQSAITLTTAQKNGTTTPGD

SDSSTAVSHTTSPLFLLLLVVAAAAAVVAA*
>Tc00.1047053510377.450|S047|A--TS-ECD|8
MAMMMVTGRLLLLCALCVLWCGAGGGFANEERAGLGSGGAESLLESQELEKSPQVTQGIRDGTGGVKEQ
VPSKPPEDEVEEDEDEDDEDEEDDSEENEHEETEDGEKKSIEGQSDQEGTVAPEPGSREKNLIGSGQEN
HQPIVSAEGISLSGSQESNANPTQPEVDEKKETKKSLPAVENAHTPVNGEHTLLGGVAGGNPPSPPEEG
VDSREHDGEDTTSEEKKDVPPPETAATPQSRQDKGSEGNGEDTKATTVTANTTDTKNTQNSDGSTAVSH
TTSPLLLLVVACAAAAAVVAA*
>Tc00.1047053510377.134|S001|A---H-ECD|18
MAMMMSGRVLLVCALCVLWSVAADGDVVVSGGEDNSLKELFIPVARLQERQEQRAVEATADAKAAAEAA
ETATAKAEEAEAAATEAKAAAETAAEAAKAAAEAAATAAEAAAAEAKTAATAAKAVDTEAKAKAAAAAA
ESAATKATTASEAATKAKATASAAKAATEAAAAKAAAAAAAKAEEAEAEAAAEAAKAAAKAAATAAEAA
ATAAEAATEAKTSAETAKTATAKAKTEAEKAAKATATATAAATATAAAEKAATAAAKAAASAEKAATAT
SKAKASAETAKAKAAAAEKAAAEKAKAAAGKEAEEAAEKATEEEKAKASTAKAAVKAAATEADAKATAG
KTAEAAAEALRGTTVREEEVKTATHDQDNSVEHHSGEKQELLQEKEPERQEKEQHEKQQHQQREHSAGN
GEESPKEKTANGTNATAITDDSDGSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053510387.40|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASAGTDNTVATTNNSNSSETSNAGSSPGGVTGSSSAGGTSGPAAVPGASGAGEGGAGVSGDGST
GDQGTGGPPAPAAAPPSPASPSGGPSVPAAAPGGDSSASGSDGEAGPSGTNSSSTTGDSPTGDQTPAAA
AAHNSSPPEGPEGTTSGTGHKGQEKEEEEEEEEENEKQQQSDEAQAQQHQQHEHPAENGEESAKDKTAL
RTNATANTGESDGSTAVSHTASPLLLLPLVVVVCAAAAAVVAA*
>Tc00.1047053510391.20|S133|ANQ---ECD|6
MAMTMTGRVLLVCALCVLWCGVFGIAADDAGGGDGSAGENLIALWLTRLRMECAEEVIRRKGSSANASA
VEECMRRGMDGVRAVLDGRRRWRRQQFAVAAADVARDVSDPESSSQGQSGSDDGLKDKVPLEPALEPPP
EKLDKAPGNGDALQTPAEIPGLPETRSEKMLNEKNEKEVKDDRDPVKRIGEGVSIDIDEEVDGAAEISD
ENPKHEDEEATNTRERNGGEGSLNNEDEISGNHHVSDDISTGLHVALPSVSHVNGKGTQSVEGTNGTVG
EKGLAGQTIVQQAEGSPAPEEPTVEFIQKEDTSKEAKEKGHQVGRGKEQTTIEEKSTEGAAAGNTAEDS
HVTEAQTPEQSETSNTNGNVEKAEEKKRDESTKNEEKSTKEKEREKNAVKSKNEEKEETKEERVADEKE
TTTVEKKMAAVQSLTKINTTTPGDSDSSTAASHTTSPLLLLLLVVVACAAAAAVVAA*
>Tc00.1047053510459.20|S132|ANQ-H-EC-|3
MAMMMTGRMPLVCALCVLWCGLAGIAADFVGSANGSAGEYWGSWWITQLRRECAEEVIRRTGGRTNVSA
VEECVRQGIDGVRAVLDGRRRWGPQRSAVVVVAAEDGEDPVKNGDSSERSFLSEQSSQAGRVLPSGGGG
SGILPGGEGGTGQNTPPPHSPSTGPSPPNLPEKQASAAEEEEEGVKSDPKDNENKPGESLKDRETPIDN
QNTQNPEETTTGKKLHEEDNKTKQLLQGDNQPPKVEEIAPRKPVEEPPREKEDVDEPDAGAAERNSIES
HLEATRNHAEKPLAGSEHFDKENYYQKEEKEKKREEQGDAHVQQQNGKHETLHGLPIEAGTTRGSLANP
PPEELQQKQTSAGSTKQLEGEVPLISAESKSNGNNDPSLPSVSTRAGVAATHEAAKGNAEVQNNAESTE
TAVNNKEDPNEHLTENDKESAKDKNALRANATANTGDSDGSTAVSHTTSPLLPLLLVVACAAAAVVAA*
>Tc00.1047053510463.90|S097|AGWTH-ECD|44
MAMTMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASDGKGASVETKNRSNSSENSDAGASTGSAGPGGGPGRDGGAGGSAASSGASGSVAPSGGASSG
AVVPGGGDSGASGSGSRGAGGPAGSSTGGGPAAGGAGAAGASGSGSAGGEVDGSGGTPASSAPGAPPSA
PGPSGGPSAPADATGVDPSAGSSDGEAGSSGTNPSNTTGDSSTGNQTPAAAAEANNSSLPGGPAGTTSG
TEHTQEKEEEEEEEEEENEKQQQSDETQVQQHQQHEHPAESGEESAKDKNALRTNATANTGDSDGSTAV
SHTTSPLLPLLLVVACAAAAAVVAA*
>Tc00.1047053510463.120|S097|AGWTH-ECD|44
MAMTMTGRVLLVCALCVLWCGAGGVYARDVDTNALGGCMALGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASDGKGASVETKNRSNSSENSDAGASTGSAGPGGGPGRDGGAGGSAASSGASGSVAPSGGASSG
AVVPGGGDSVASGSGSRGAGGPAGSSTGGGPAAGGAGAAGASGSGSAGGEVDGSGGTPASSAPGAPPSA
PGPSGGPSAPADATGVDPSAGSSDGEAGSSGTNPSNTTGDSSTGNQTPAAAAEANNSSLPGGPAGTTSG
TEHTQEKEEEEEEEEEENEKQQQSDETQVQQHQQHEHPAESGEESAKDKNALRTNATANTGDSDGSTAV
SHTTSPLLPLLLVACAAAAAVVAA*
>Tc00.1047053510463.140|S094|AGW-H-EC-|1
MAMTMTGRVLLVCALCVLWCGAGGVYARDVDTNALGGCMALGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASDGKGASVETKNRSNSSENSDAGASTGSAGPGGGPGRDGGAGGSAASSGASGSVAPSGGASSG
AVVPGGGDSGASGAVPGAPGVPGSGGGGGGSGTSAVGHGTGSVSSASVPGAPGGGSVAGEVDGSGGTPA
SSAPAAPPSAPGPSGGPSAPADATGVDPSARSSDGEAGSSGTNPSNTTGDSSTGNQTPAAAAAHNSSPP
EGLAGTTSGTGHTRKEEEEEEEENEKQQQSGEAQVQQQRHEHPAESGEESAKDKNALRTNATANTGDSD
SSTAVSHATSPLLPLLLVVACAAAAVVAA*
>Tc00.1047053510463.150|S095|AGWTH-EC-|7
MAMMMAGRVLLVCALCVLWCVAGGVYARDFDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
IAAVEASDEEGSVETKNNSHSSETSDVGASPGGAGAAGAPAAAGGTSAGGDSSGSAGAVPGAPGGTGAS
GVPGSGGGGGGSGTSAGGQGNSGISPASSGPAAPTGVNSSTGRSGEAGSSGSNSSNTTGESQTGDQTPA
PAAAHNSSLPEGPAGTTSGTGHTRQEEEESEKQQQSDEVQVQQHQQHEHPAENGEESAKDKNALRTNAT
ANTGDSDGSTAVSHTTSPLLLLLVVAYAAAAAVVAA*

>Tc00.1047053510463.200|S099|AML-VFECD|25
MAMMVTGRVLLVCALCVLWCGAVFGHATEDYCGEGGGNGLRHTSNGGDDGVSLKTDCGLLSSRMGLIKA
VEASDAGPELSVVPEQVEKSQDTENSSKDKTSRSGASVPDGDGFAGQPAPPKPGESGPGGQERESGVLD
PNVRKEAEERNGSLSESQKLRTDQSSTTGGPGTEDSEEPALEDTSERNGSSNIHLNEEDAGEAEVQEIS
EPEEPEKDKSNMALTETHDSQAKQKEAQLPTPPTLPTTQVDEHSSPGDTVAKQQLQKPQSEMGPNENSQ
STSVATITANQHNEPSADHAGSRPPSPTANGDAANHEADKTTEDGIPNNDPAADGAETREGKRNENKEA
NPKETPVDVTAMKTTTAKAGDSDGSSAVSHTTSPLLLLLLGVACAAAAAVVAA*
>Tc00.1047053510463.240|S032|A---H--CD|8
MAMTMTDRVLLVCALCVLWCVAGGICEEQVKVVDGGAPGGGSVVLVKANGVTATPMPSEQTGVLQVAEE
APNKRAADSSSEEEAKEEDGGDEPEEGSKEEAEEIIMEEGKGGKETDKENQSQREGAAGHPVAAKGIAG
NSNQTLHTPLSTEHNPSPDSPRLNLESPQNNLSKNNDSAKNQQTEGSRPGEEDKSKLSEGVPEPGPGKG
NSGPEPGKQTEIHEPTGLSSASSGDAQETKHAVNGPPNASPGPVGGVTTGSHTDVKTGTEVHPPPPQEH
PSPAVAAEKEDSIMEDVAIQRGGNERPQEKLPEAATAAPPEGLRTSAVRSSEKTEDVTDENEEIGEENA
EDETKQRQEQLQLPQQPQQSGEKGQQQQQQQQQEDQSHGYSTDDGEVPKKDKNDVGTNNSDGSTAVSHA
TSPLLPLLLVVACAAAAAVVAV*
>Tc00.1047053510465.140|S132|ANQ-H-EC-|3
MAMTMTGRVLLVCALCVLWCGLAGIAADFVGSANGSAGEYWGSWWITQLRRECAEEVIRRTGGRTNVSA
VEECVRQGIDGVRAVLDGRRRWGPQRSAVVVVAAEDGKDTVKNGDSSERSFLSEQSSQAGRVLPSGGGG
SGSLPGGEGGTGQNPPPPHSPSTGPSPPNLPEKQASAAEEEEGVKSDPKDNENKPGESLKGRETPIDNQ
NTQNPEETTTGKKLHDEGNKNKQLLQGDNQPLKVEEIAPRKPIEEPPREKEDVDEPDAGATERNSIESH
LEATRNHAEKPLAGSEHVDKENYDQKEEKEKKREEQGDAHVQQQNGKHETLHGLPIEAGTTRGSLANPP
PEELQQKQTSAGSTKQLEGEAPFINAESKSNGHNDLSLPSVPTRAGVAATHEAAKGNAEVQNNAESTET
AVNNKDDPNENLTENDKESAKDKNALRTNATANTGDSDGSTAVSHTTSPFLPPLLVVACAAAAVVAA*
>Tc00.1047053510465.74|S095|AGWTH-EC-|7
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSMLP
IAAVEASAGEGGSAGGRQNSSNSRETSDAGANGSAGGSPGGGPAGGPGGSGSPAGGSGAEAPASAAGGS
GGGDGSGGSGGTPTGGRGTGGIPSGPASGAPPPAPPLAPAAVVATPASGSGGTAGSSGTNSSNTTGDSS
TGDQTPAAAAANDTSPPEGPAATTSDTGLKGQEKEEEEEDHEKQQQSDETQVQQHQPHGYSTDDGEESA
KDKNALRTNATANTGDSDGSTAVSHTTSPLLLLLLVVACVAATAVVAA*
>Tc00.1047053510469.10|S097|AGWTH-ECD|44
MAMMVTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGGNGSHMPDGCNKTAITVPLRSVLP
ITAVEASAGEGDALATKNDSHSSETSNAGASTAGSGGGDSSGSAGASGSGSAGAAGASGGSGTSTGGSG
SGGGGGGGPAGPSAGGKGNGGISPASSGPAVAPSDPPAGSPSAPAAPPAPAPPSDTAAAPGVNSSAGSS
GGTAGSPGSNPSNTTGESPTGNQSSAAAAPNDSSPAEGPEGTTSGTGHTRQEEEEEEENEKQQQSDEAQ
AQQHQQHEHPAENGEESAKDENALRTNATANTGDSDSSTAVSHTTSPLLPLIVVACAAAAVVVAA*
>Tc00.1047053510475.100|S030|A------CD|31
MAMMTGRVLLVCALCVLWCGDEGVGSPAGGAGGLLGNGGKGAVETTDNSTSAPDSSDLTKGLPKVNQST
ETFTGKSLEVDEVNAEQQDVAPGVEDEDGSPSDHLEESLKDDPDQGKTKPEIQNKGQEGRQTPQSQVNV
PQQPQPLLHQSQPLPPSAPQPHTPASEKGEGVGENNTGGEGQPSLRVENKGNEDPENLGKEDSLNDPGT
KSQSSEQVQTTVPNTVPPEHKTQNGMLTPEQMTNESQSTDTSTNLPEIQKENKEYPASTEGTAQSTSNG
SQEQEAEPSTSEEPSPFEEEQSTGTKTTEDARTPDAAATEKSQTGDNEKVGDSDGSTAVSHTTSSFLLL
LLVVACAAAAAVVAA*
>Tc00.1047053510477.80|S010|A----RECD|22
MMTGRVLLVCALCVLWCGVSGIAADDAGDGDVVVSGGDNKKLEEQKLSSPVIPGMKPQAPEVKEESPTR
RSDDVLEETDEAVVERDEADRRGVGVDGEKVKTVQKGRGEGASEGDSATEAELHLTEDEILRLPSPNGA
KGGEKTIPSNDTPPEEKVQQKQEDPPSLLQSEPGDPASGRGVPPESTEHKPPASGNPSSETETTGIERV
STPTHVRESPRVTEKEVVSTEHEREDKEGSGGNPIKVTDVRLPEPQELRSKSLDGTQRVETGVRPINSL
PGDQNKQRVLVNLSQGESANDPPETTPQSSSTGGHRVENSRTNEDGAKNTEGSAAGEKKDDKKGLEKDV
VPTISEGKVQPPVTTAASTSETAIDGDSKGSPTAATALQSDDDTESNPAKNDLSQPSSERTEELSTTPD
PEDASEITENAAAEKAGIPTTKAIATAKTNDTVTPGGSDSSTALLHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053510477.100|S070|A--TIFEC-|13
MAMMAGRVLLVCVLCVLWCGAGGGGLAEKTQDRLDTASEESESPKKNKDTDGSAGTDGPTAKTKAPQAA
DRGSKEQEGTVEQAAASVPGVTGAGAGMETAPQPGREATESAKGTRGNKEETKKEEESEKELEEGEEEE
EEEKEREKEKKEEDDTDAKKGISADSQEQRSLPSGAEGASNQTKPKSAQTTDVNDPAAEGAGKRKEKQN
ENKEANPKKTPVEATAMKTTTATPGDSDSSTAASHTTSPLLLLLFVACAAVAAVVAA*
>Tc00.1047053510483.20|S099|AML-VFECD|25
MAMMMTGRVLLVCALCVLWCGAVFGHAMEDYCGEGGGNGLRHTSNGGDDGVSLKADCGLLSTRMASIKA
VEAAEGEQEMNVTAPLENLEDNKLGNNTKGSGVAGLEGNDGVAVQPPTKKPLNLGRSGAGEQEGMSRPV
DANDGKRTSHTHNQSVRDPEKLKTVESSSSSRSPGTEGIKIHKLENTSERNESYKKTPTEENNLFSKYD
CTELVLKEEPEKTADKKNASHEAPTETRGSQAKDAEIQTATPPPPPATMNGHSSTVNLRPIQLLQYVQD
DNAEFRTPSLMANGGAANNQADKSTEEGIPNSDPAADVAGTAEGKQNENKDANPKERPVEATAMKTTTA
TTGDSDGSTAASHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053510483.70|S004|A---V-ECD|18
MAMMMTGRVLLVCALCVLWCGAGGGGCSETTQDPPGGASQAGNNPASGSGVTGNASGHTVTGEAEVVSL

QQSRLDNVGNSAAGSPQLQAALEPESPTEQPQSDPEHTVPSTHSQSSGEGRQDGTPDGQPGKPGISPSQ
EDNKDVSIENQQSNDPPSHSGNDDVVSRNSGERTEDDSRRAETLVAAPSEEGQEPENVTPSLEQPLETS
TAAPTATTQTTSMQPPEENASSTVKMNDAAPHSTVTANTNHTVTPAENDSSTAVSHTTSPLLLLLLVAC
AAAAAVVAA*
>Tc00.1047053510483.120|S118|ANP-VFE-D|3
MATMMTGRVLLVCALCVLWCGAATVVSSAPDATRAQSFWREDLIQKWHELLKNECKVENPYENNEDLKE
LAVNCCVRDAMNELCSAFYGNTVMENKDANVEGICKVYAGKPDDVVNCPKPKTNLSPAAVTPVKVSDPE
APREKEEELRKTPEEAPKAPPEEAPTPLAGTPLTNSPANPTKVSPSPPLKGQPTNAEEVPVPNSEEGSV
NTGPTNDSEEEDTDTVADTEQDEPSNSQAEPATPTHTVASDNGDNETDKGTGEDTPNNTPEPDVAGTEE
NQEENKNNKPKERTLQVAGIKTTTATSGDSDGVKATPPLLLLVVACAAAAVVVAA*
>Tc00.1047053510483.180|S080|A---YKECD|24
MAMMMTGRVLLVCALCVLWCGAGSRCDEGEDTAIVVVSPVGRSNDGNGGPGPAPPSPTGIGTSGPLPMV
PESEVSQERIPGAYSEGRGEKNYQNEDGVQENVAEDVENSRNHERLSEQSTQKESQEETPEEEKEKDAY
PPAEEVVKGTQQSLSQKPPPQQLQVQTTAPTEGGGPTAPTGPARPPAPAEPSSRNGSRTIEPTDSRNPS
QESHDKSLLQTKTESSAPEPPLKDAFSEQHGQETTTPDSMLNASAGSQARNTAPSTSTSGSGEAESEAD
ENDAQRPNPNKSHDDSDSRKTKVSTTMSEATTQKTETIAAAQTNHTANTDDSDGSTAVSHTTSPLLLLL
LVACAAAAAVVTA*
>Tc00.1047053510483.220|S051|A--TS-EC-|2
MAMMTGRVLLVCALCVLWCGAGGCFANEESVGLGGGADLSLGSKGPETSLQVTQGLKDEAEGVKGKKNL
SSSEDEDEEDEEENDDDDDDDDGPGTDEEERTQGQSDQEVKVTSDPNSREKKLISTEQQTGQSIVSAGN
ISPSGSQESNAKPLQTEVEGKKETDKSRTAVENALRPGKAENTIPGGIAGGNIPSPPEDGVDSREHDGD
ETTSEDKKNDPPPETAATPQRHRDEGSEGTGEDTKATTVTSNTTDTTNTQNSDGSSGVSHTTSPLLPLL
VVACAAAAVVAA*
>Tc00.1047053510483.310|S089|AG---KECD|6
MAMMVTGRVLLVCALCVLWCGAGGVDASNLENNAVGGCMASGVLNTNKSYTPSGCDKTALTLPLRSVLS
ITAVEASTDPLVTGTAENKSDLAPSSGADFGCAGSPPGRGDEGGGGRDDGAGGPGGVGGASGSQARGSK
ASVGGGGGSNGGSKARVDGSLKSPASDVKSPSPVLGDGGSSPGAPTGSVGSDGSKGFILGSFSSGGRSQ
PDAGSPGGDASLSAPVAGGNSPPSITDESDALEKTGAAASTKGGKPQEAGEQSGANRARNELPKLSAPA
ESTPEAQEDCPSEQEKPESEAAGRAATGKEKRRIDAEAQGPSTVMSTASTPPLPPPAPATVGEQPTAVA
VPAGGSPTAQTDSQTLTEERTKTPPPPNKKETEETEPTSGDGVAEQQGQGTVLPDLKGGPTGSPAEVTA
SSISTSGSGDGRSRTDENDDNSRGPNPGGLHNDPESSHTNVAPTASETKPRTAKAAATARTDDTAKPGS
SDGSTAVSHTTSPLLLLLVVVACAAAAAVVAA*
>Tc00.1047053510483.154|S043|AG-----CD|27
MMMMMTGRVLLVCALCVLWCGAGRVYARNPDNNSLGGYMASRGFGRNTSFLSNGSIKNLSTPLLLSASF
ISAMQAEAREEVSSPGVTNLPLSGATGLSPAFSDRGASIPRPTVPGLRAAIPGVDVPSDGPGAIPAPVR
AADAPIPGVAVSSDGAAAFSSLGAAAAGPGPLRDPAFPGPDANIPGSVAPGHGTPIHGTAGPGAAAFSS
LGTPIHDAADPGAAIPGAIPGPGSARGAAGHRPVGPGHGPGIPGHGPAGAGDGPAFSGLVPAVPGAGHS
VGGGSEPPDSRSAVISSSQGGNGKTAPVSVSSDERIASPEEVLAQKETGSQGTSSPEGQPTVSSNTEKQ
RNNSASAGGHSLGHDAAGDELQDSLEEQQKNDHSQTNETKKSSGDQNTESQRSGGALSEVSNTTTHGIK
TQQPKTNSANEKNYSQNTDATHTTSPLLLLLLLVACAAAAAVVAA*
>Tc00.1047053510487.50|S013|A---V-EC-|8
MAMMMTGRVLLVCALCVLWCGAGGGGCSETTQDPPGGACQAGNNPASGSGVTGNASGHTVTGEAEVVSL
QQSRLDNVGNSAAGSPQLQAALEPESPTEQPQSDPEHTVPSTHSQSSGEGRQDGTPDGQPGKPGISPSQ
EDNKDVSIENQQSNDPPSHSGNDDVVSRNSGERTKDDSRRAETLVAAPSEEGQEPENVTPSLEQPLETS
TAAPTATTQTTSMQPPEENASSTVKMNDAAPHSTVTANTNHTVTPAENDSSTAVSHTISPLLPLLVVAC
AAAVVAA*
>Tc00.1047053510487.79|S043|AG-----CD|27
MMMMMTGRVLLVCALCVLWCGAGGVYARNPDNNSLGGYMASRGFGRNKSFLSNGSIKNLSTPLLLSASF
ISAIKAEAREGKVPSARVTDSHLSGAAGLSPAFSGPDAAIARPTVPGHVPGAAIPGADFSARVPAFSGL
GSAGPVHGPVSAADAIPGAAVHGHGAGPGHGAAAFSGLGAAGPGAIPGPAPVRGPTFSGPDANIFGAPV
PGHGPAAIPGAPVSGHGPGAIPGAPVPGHGPGAIPGAPVSGHGPGAIPGAPVPGHGPGAIPGAPVSGHG
PGAIRGSLRGSAVPGDDDAFSGLGDAIIAEAVPGAAAAFSGHAAAVPGHAAGPAGAGDGPAFSGLVPAV
PGAGHSVGGGSEPPDSRSVVISSSQGGNAKTAPVSVSSDEQIASPEEVLPQKETGSQGTSSPEGQPTVS
SNTEKQRNNSASAGSHSLGHDAAGDELQDSLEEQQKNDHSQTNETKKSSGDQNTESQRSGGALSEVSNT
TTHGIKTQQPKKNSVNEKNYSQNTDASHSTSPLLLLVVACAAAAAVVAA*
>Tc00.1047053510495.20|S038|AG-----C-|7
MAMMMTGRVLLVCALCVLWCGAGDVYAGDLDKRALGGCMASGVLGMNASYVPNGCNEYMPTPPLRSALP
IPAIQAEDGQVRDTAPGSGSGVGEGGGSPGALSPAGAAASGSAPAPVAPVAPAGPVADPTADPPGGSAA
TGPAAAPGSPVSVPGPVAGPGGNAGSSPGVHAPPHIDDTVITSSDLSSTREGSREEALQQKETESHDPS
SSKGLTQEALPDVQQPETSTSENSKTGCGEDVSDCEGQEKLGKTKMEKQVLEASKTQKPPPAQHKESKD
NEENSTEASSTESQNTEPQQEIKTPVDESDSTSTDASTAVAARSTSAGSQEEATASSSNGSHSPLQGEV
FTGTDTPENAPSPAAAETEKRQGENVTTPGDSDGSPAASHTTSPLLLVVVACAAAAAAVVAA*
>Tc00.1047053510497.50|S083|A---YK-C-|4
MAMMMTGRVLLVCALCVLWCGAGGRCDEERTAARGSGDESLPESRGIGTPREETQELQVGSPVIKVEVP

RESSPHIEEADGEDSDDENGDEKVKKDEKEKNKVQPQKHESKNNEGAPQSLPPPPTPTPSGHTTAEREK
PQNSKKVTNEATPSGSKMDSEATQPPSGDATQEQHSHDADTEDPTMNAATGSPAEPTVSSTSASGSGDH
VHNKADEDDAQSSEEQHDSLETGKTKVVPKLSEAAPQTATITAAQTNGTTTKVGDSDGSTAVSHTTSPP
LLLLVVACAAAAVVAA*
>Tc00.1047053510497.100|S099|AML-VFECD|25
MAMMMTGRVLLVCALCVLWCGAGGGHAMEDYCGEGGGNGLRHTSDGEDDGVSLKEYCGLLSTRMGLIKA
VEAADGEELSGDPLETSEESSPGKKLDDKTSGGGTPGLGGGVAGPATAAAAALEPGESGRGETKRELEV
AETAGEKRANDRRKGSERNPENLKNGQSSSFSSGSPVTLGGEGLASEKNSKAAEPSEDGLKVTKLSQQK
AEGEKENKNDTILTGVRENPEKNTEIQTAPPPPATNGKSSPEDTVRMQQLQQVLDGIESNNNSQTNSGT
EISDNQHNEPSADHGESGLPSPTTNGDAANNEADKSTEDGMPNNGTAADGAGTAEGRQNENKDANPKET
TVTAAAMKNKTVTSDDSDSSTAVSHTTSPLLLFVVVACAAAAAVVAA*
>Tc00.1047053510553.30|S101|A-L-VF-C-|1
MMMTGRVLLVGALCVLWCGLSGMALNDYCSEGGENGLRHTSNGGSDGVSLKVDCGLLSAPMGLIKAVEA
ADEEQELSDPGPRDRSEELSPDNTEDGGATGLGRDVVAIQAAAIPPKPEGPGTGRQEGKSTVVNTKGKE
EDNKKGTAADSKKLKPDQSSSSSGGSGPPVGEEPLSENSKSSKYSGIQLKEQGKDLRSKSHSHEEVVEE
TSESEQEGTEEDKYKKINDKAPAVIRENPVEQKEMQTSTSPTQVNGQSGTEDNVPMQQLQQPQSGMNQN
NNSQTTSVAPTTANQHNEPSAIHTETRPPSPTAKRDAANIVSDKSTEDSNQNNDLAADGAVTAEEKQNE
NDEESAKEKNGVGANSTANTDESDGSTAAIHSTSPLLLLFVSAAAAAVVAA*
>Tc00.1047053510557.60|S010|A----RECD|22
MAMMMTGRVLLVCALCVLWCGADGGCEEASAGFQSDASGDLVGEGVDSQDSPRPETPGSHTAGPETPLP
NVQGQALSPPPEVTVSGTEGAAEEEKARRNEDVKLVEKEKEGDGTSQEVKEPENKLISVKDRQSHDNEG
LQPPSLNGTHEDETITPSEDSLQVNKDKQELPSPLQLPLPNSAADGNPSSTSAAGRGDEKSRENGNGTR
NSQQSVAEDIEQNKDAGEKVVAPTGGEEDSRLPVMTVEEMRGATTKGNSGSSTTAATAMQSGTGTEGTP
TNNHPNRPSIDSDTPLGSISDGEAASANKYDTVSQSAGSTTAPTTNAKTGETAMPGDSDGSTAVSHTTS
PLLLLLVVACAAAAAVVVAA*
>Tc00.1047053510561.30|S023|A----R-CD|3
MAMVMTGRVLLVCALCVLWCGADGGCEEASAGFQSDASGDLVGEGVDSQDSPRPETPGSHTAGPETPLP
NVQGQALSPPPEVTVSGTEGAAEEEKARRNEDVKLVEKEKEGDGTSQEVKEPENKLISVKDRQSHDNEG
LQPPSLNGTHEAETITPSEDSLQVNKGKQDLPSPLQLPLPNSAADGNPSSTSAAGRGDEKSHENGNGTR
NSQQSVAEDIEQNKDAGEKVVAPTGGEEDSRLPVMTVEEMRGATTKGNSGSSTTAATAMQSDTGTEGTP
TNNHPNRPSIDGDTPLGSISDGEAASANKYDTVSQSAGSTTVPTTNAKTGETDMPGSSDGSTAVAHTTS
PLLLLVVACAAAAAVVTA*
>Tc00.1047053510561.50|S089|AG---KECD|6
MAMMMTGRVLLVCALCVLWCGAGGVDASNLENNAVGGCMASGVLNTNKSYTPSGCDKTALTLPLRSVVS
ITAVEASTDPLVSGTAENKSDLAPTSGADFGGAGSPPGRGGEGGGGRNDDAGGPGGVGGASGSQARGRK
ASGGGGGGGSNGGSKAHFGGSLKSPASDVKSPSPVLGDGGSSPGAPTGSAGSDGSKGFILGSFSSGGRS
QPDVGSPGGDASLSAPVAGGNSPPSITDESDALEKTGAAASTKGRKPQEAGEQSEANRARNELPKLSAP
AESTPEAQEDSPSKQEKPESEAAGRAATGDEKRRSDAEAQGPSTVISTASSPPLPPPAPATVREERATA
VAVPAGGSPTAQTDSQTLTEERTKTPPSPNKKEPEETEPTSGDGVAEQQGQGTVLTDLKGEPTGSPAEV
TASSISTSGSGDGQSKADGNDDNSKGPNPRGPHNDPEASHTNVAPTASETNPLTAKAAATARTDGTATP
GDSDGSTAVSHTTSPLLLLVVACAAAAAVVAA*
>Tc00.1047053510583.130|S061|A--TIFECD|52
MMMTGRVLLVCALCVLWCGACGGEPSEPPSPALPDTAPEKKPQKKEGEAVVGGVDQSSKEVAPKEPTPK
APELKEVTEKSLQENVPGGGASKAASPTTDSMVQNTEVKNEEEEDEEENDEEEELEEGEEEKEDGENED
EEHKEDDTKEKGDTKKEEAVTGIAEGTSAGGQEQPSLSFAAEGASNITNPNSTPTTGDDDPAADGAGTV
EGKQNENKDANPKETPVEATAMKTTTATTGESDGSTAASHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053510621.20|S057|A--TH--CD|1
MAMMMTGRVLLVCALCVLWCGAGGICEEQVKVVDGGARGGGNVLLVKENGATATLMPSEQTGVLRVEEK
APNKRAADSSSEEEDKEEEEDDDDDDDEPEEGSKEEAEEIIIEEGKGGKETVKEHQSQGEEAAGRSVAT
KGITRNSNQQTLHTPLSTEHNPSPDSVGLNLESPQKNLSKNDDSAKNQQTEDSTPGEEDKSKLSEGVPE
PGAGKGNSGPEPGKPTEIHEPTGLSSASSGDAQETKHVVNEPPNASPGPLGGVTTGSHTDVKTGTEVHP
PPPQEHHSPAVAAEKEGSIMEDAAIQRGRHERPQEKLPEAATAAPPEGLRTSAVRSSEKTEDVTDENEE
IGEENAEDETKKQQEQIQLPQQPQQFGEKGQQQQQQEEQPHGYPTDDGEVPKKDKNAVGTNNSDSSTAV
SHATSPLLPLVLVVVCAAAAAVVAA*
>Tc00.1047053510621.60|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCGAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITMPLRSVLP
ITAVEASAGTDNTAVVIPNDSHSSGTSNAGASGGSAGPGAPDVGGGGDSGGEGSSGPGASPPVPAAPAP
GPSGGASSGDSGDGGNSGGGGGGAAGASGGGGGGGSGSGGGGSGSSTDDHATGSVPSSSSLASPAAPAA
PGDGSAGGHDTGGVSSGSSVPAHPPSPGPFGAPSPGVDSSAGSSGGKAGSSGSHPTNTTGDSSTGDQTP
AAAAANNSSPPEIPAGTTSGTGHTRQEEEEEEEDHEKQHQSDETQVQQHQQHEHPAENGEESAKDKNAL
RTNATANTGDRDSSTAVSHATSPLFPLLLVVACAAAAAVVAA*
>Tc00.1047053510621.49|S104|ANP-VF-CD|10
MAMMMAGRVLLVCALCVLWCGASVVLSAAGGFTSDRSDTAKNMVLLWYPETNKTCKENSTKGGILDESA
FKSCMHESMKEICEVYYNMASTDSDDPEAEEICKKYTGDPVEAAESSTPQDKLSPGAETPVAAPTPETS

KGGAAEMGSTPGIPGGDSPANPTEGSQSTLAATDTANNELGNGTGGRVPAGAPEFDVAGTEKGNESEAK
DGTTKKTPVESVVMRGVTAPDDSDGSTAVSHATSPLLPPLLLVACAAAAAVVAA*
>Tc00.1047053510623.20|S008|A-----ECD|43
MAMMMAGRVLLVCALCVLWCVAGGICDEEAGGPAGGVVGNGGRSAVESSESSAPGPDASEPPNDVLNVN
QATGTSAVKSLEGKEVSTAQRDVLSRGKDKKDGSPSEHLEDPAEDAPENEKTKLKLKKEEQEGIVPLQS
QANVSPQPQPQPQQSQPPSSPQPHISSSEKGKGVGENTKGGAGQSSLAVENKGNNDPKAPRKEDSLNVP
GKESESSEQAQTKVPNTVPPEHKIKNEMLTPEQKTNEGQNTDTSTNLPETQKESKEYPASREGAVQSTL
TGGQEQEAEPSTSEEPSPFGEEQQSTGTKTTADARTPDAAAKDKNALRTNATANTGDSDGSTAVSHATS
PLLLLLVACAAAAAVVAV*
>Tc00.1047053510625.150|S097|AGWTH-ECD|44
MAMMMAGRVLLVCALCVLRCGAGGVYARDVDTNGLGGCMASGVLGENGSHMPDGCNKTAITVPLRSILP
ITAVEASEGESDALATKNDSHSKENPDAGVSGSTAGPGAPAAAGGGRGGGGDGPGSGTSTGGQGTGGIS
PASSAPAAPPPPAPPSGPAAALGADSSADRIGGTAGFSGTNSSNTTGDSPTGDQTPAAAAAHNSSLPEG
PTGTTSGTGHTRQEEEEEEEEEMQQQSDETQVQQHQQHEHPAENGEESAKDKNALRTNATADTGDSDGS
TAASHATSPLLPLLVVACAAAAAVVAA*
>Tc00.1047053510625.190|S096|AGW-H-ECD|1
MAMMMAGRVLLVCALCVLRCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEAAAEEDNAGGTRNNSNSSENLESGASTASSAVPGAPAGGGSSGTSAGGQGTGGVSSGSSEGPST
PAALPASSSGGTAGSSGNNSSNTTGDSPTGNQSSTAEAHNSSLPEIPAGTTSGTGHTRQEEEEEEENER
QQQSDETQVQQQEHEHPAESGEESAKDKNALRTNATANTGDSDGSTAVSHTTSPLLPLLVVVCAAAAAV
VAA*
>Tc00.1047053510625.19|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASDVTDNAGGKKNDPNSSGTSNAGVNGSDPAAVTGRGSGGVPGGESDASSGAGAPAAAGGGGSG
GSGTSAGGHATDSVPSDAPGPAAPPPANAAGHSGGPPATAPGVNSSAGSSDGTAGSSVTNPSNTTGESQ
TGDQSSAAAANNSSLPEGTEGTTSGTGQKEEEEEENEKQQQSDETQVQQQQQHEHPAESGEESAKDKNA
LRTNATANTGDSDGSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053510625.54|S097|AGWTH-ECD|44
MAMMAGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNETAITVPLRSVLPI
TAVEASDGGGSVEKQNDSHSSGTSDAGSSPGNGAAGASAGSPAASGDRGATGGGSDAGGGSSGSEGGGD
SSGSGGGGGRGISAGDQDAGGISSGPSHPASRVGSGLASPPTPGAPSVPSGGGGTPTGGHGTGSVSSVP
SAAPPAPAAPPAPFSAAGPAAPGVDSSTGSSGGTAGSPGSISSNTTGDSPTGDQSSAAAAANDSSPAEV
PARTTSGTGHTREEEEEEEEEEEENEKQQQSDEAQVQQHQQHEHPAESGEESAKDKTALRTNATANTGD
SDGSTAVSHTTSPLLLLVVVACAAAAAVVAA*
>Tc00.1047053510625.88|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASDGGDSASGTKKDSHSSEASDAGVNGSGSAGVPDGGPGPDGGAGGAGDSDAGPGAPVAPLGGA
SGGSGTSTGDHGTGSVSSGSSEGPSAPAVATVVDTSAGRSDGEAGSPGTNPSNTTGDSSTGNQTPAAAA
NETSPPEGAAGTTSGTGHTRQEKEEEEEEENEKQQQSDEAQVQQHQQHEHPAENGEESAKDKNVLRTNA
TANTGDSDSSSAVSHNTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053510625.109|S095|AGWTH-EC-|7
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAIEASTGKGDALAPKNNSNSSETSDAGGSGSGSTAGPAGPAAAGGGGSGTSTGGQGTGGIPSGSAGP
PPPATPAPPSGPPAALGAGAPAAGSGDGEAGSPGSNSSNTAGDSQTGVQTPAAAAAHNSTPAEGPTRTT
SGTGHKGQEEEEEEEEEEENEKQQQSGEAQVQQQQQHEHPAESGEESAKDKNALRTNATANTGDSDGSTA
VSHATSPLLPLLLVVVCAAAVVAA*
>Tc00.1047053510627.60|S089|AG---KECD|6
MAMMMTGRVLLVCALCVLWCGAGGVCARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSALP
ITAIEASTGESVSDSTDIYPDSLSVPPSPPPVTGLPEALKAPKAPQDPPESDVGQTGVGDRLSLVPNDD
SSGAGGGFEENGNSNKSGVSASEFSTVVGASRSSIPPEVGGSENKSGAPPNLKLESPETNELRERILVE
TNKDTQKVSKLEENPESSRKKEKANIRGTSEEAGKNEAGRSGVEAHGPSSVLSADGQLQRQGTTVTMTQ
PPPPSPEQQTSAVSPSPGVDTPAARSREAGDLEEGRGIPPARKASHNSTDEKRKAPPLRSEKESAAPKP
PSADGVLEQNSEDTTTKEAIKMDAHTDGPAATSEQSTSASESGVVKRNESEDGDNAQRPEPKGQHNDPD
AVNTKAAPTASEAASYTAKTVPARKNDTVTYGDSDSSTAVSHTTSPLLFLLLLVVACAAAAAVVAA*
>Tc00.1047053510627.80|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLRCVAGGVYARDVDTNALGGCMSSGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASDGGDSAGGVIQNNSNSRETSNAGGSPGGGPAGGPGGSGASSGDSSGAVAPAAAGGGDSSGGG
GGSGGQGSGTSAGGHGTGSVPSGPSPAPAAPLAAAAPPAAAPGGPSAPVDATPASGSDGEAGSPGTNPS
NTTGDSLTGDQTSAAVEANDTSPPEGPEGTTSGTGHTRQEEEEEEDHEQQQQSDEAQVQQHQQHEHPAE
SGEESAKDKNALRTNATANTGDSDGSTAASHATSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053510627.110|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASDGGDSASGTKKDSHSSEASDAGVNVSAGVPDGGPGPDGGAGGAGDSDAGPGAHVAPLGGASG
GSGTSTGDHGTGSVSSGSSEGPSAPAVATVVDTSAGRSDGEAGSPGTNPSNTTGDSSTGNQTPAAAANE

TSLPEGAAGTTSGTGHTRQEEEEEEEEENEKQQQSDEAQVQQHQRHEHPAESGEESAKDKNALRTNATA
NTGDSDSSTAASHATSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053510627.150|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCVAGGVHARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASAGKGGSAGATGASGGPGPGDAGGSGGTQKNSISSETSDAGGIQNNSHSMKTSDTGVPRGGDS
DGGSAAGEKGGSGGGGSGTSTDGHGTGSVSSGPSAVPAPAPAAPPSAPGHSGGPSAPTDATGVDPSASG
SDGEAGSSGTNSSNTTGESPTGESPTGDQTPAAAEANNSTPAEGPAGTTSGNGHKGQEKEEEEEKEEEN
ENQQQSDEAQVQQQEHEHPAENGEESAKDKNALCTNATANTGDSDGSTAVSHTTSPLFPLLVVACAAAA
AVVAA*
>Tc00.1047053510627.190|S097|AGWTH-ECD|44
MAMTMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASTGESVSPSGPAGVVASGSSPGSGSGASPAGGPAAGAGGPSLSPAPPAAGGGSPGGSPGGGGG
SGTSAGGQGTGGVSSGAPGAPAVPGVNSSAGRSGEAVPSGSNPSNTTGESSTGDQTPAAAAAHNPSPPE
GPTGTTSGTGHKGQEKKEEEEEEEENEKQQQSDETQVQQHQQHEHPAENGEESAKDKNALRTNATANTG
DSDGSTAVSHTTSLLPRLLFACAAAAAVVAA*
>Tc00.1047053510627.128|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGFHMPDGCNKTAFTVPLRSVLP
ITAVEASTGGGSVETRNRSNSSGTSNAGASNGSVSAGGPGPGGVAGGSAASSGDSSGAVAPPGASAGSS
PDGGSGGGVSSGSGGSSGTPTGDQGTGDVSSAGGGGGGGSGDGSTGGDGTGSVSSAPAAAPAPPPVSPA
GPAVALPSDAPPGVDPPAGSSDGKAGSPGSNLSDTTGDSQTGNQTPAAAAAHNSSPPEGPAGTTSGTGH
KGQEKKEEEEENEMQQQSDETQVQQHQRHEHPAESGEESAKDKNALRTNATANTGDSDGSTAASHATSS
LLPLLLVVACAAAAAVVAA*
>Tc00.1047053510693.130|S061|A--TIFECD|52
MMTMTGRVLLVCALCVLWCGVCGGGRAQAASPDTKSSEEKPQNEKDTTGVVGAGEGDQNDKEAAPQAAA
PTKSGLPAVAPSPSQATESGGASETPGAAKDSKHQKEDEKKEKEEEEDQDEEKEVDEEEEKEVEEEETE
GEEDEEVEEEEEDDTNEGKATKKEDADTSTTEGISAGNEEQPSLSSAAEGASNIANPNSTPTTGNGDPA
ADVAGTREEKQNENKDANPKETPVEATAMKTTTATTGDSDGSTAASHTTSPLLLLLLVACAAAAAVVAA
*
>Tc00.1047053510693.190|S116|ANP-VFE--|1
MAMVMTGRVLLVCALCVLWCGAATVVSSAPDATRAQSVWPEYLFLNWHELFRNECKVEKPYGNNEDLKE
LAVNCCVRDAMNELCSAFYGNTVMENKDANVEGICKEYAGKPDDVADCPKPKTNLSPAAVTLVKVSVPE
APKDNEEELRKTPEEAPTPLAGTPLTNSLAKPTKISPSPPLKGQPTNAEEVPVPNSEEGSLNTGPTNDS
EEGDTDTVTDTEQDEPSNSQADPTTTTPTVARDNGDNETDKGTGEDTTNNAPEPDVAGTEENQEENKTN
KPKERTLQVAGIKTTTVTSGESDGVKATSPLLLLLVVACAAAAVVAA*
>Tc00.1047053510693.230|S004|A---V-ECD|18
MMMTGRVLLVCALCVLWCGAGGRCDEVLPVAVSSVISASGVSGAPDNASGQTSSGVAGNPSAEQTQLNK
VGNSAPGSPQLQVDLQTQSPTIQQTHSGAENAISSTTSKPSGEQLQNVPDGVPAGEPEASLGQEEGKNE
TIANQQSNGPPSPSSNNDIVSRNSGERTEDTSRRAETLVAAPSEEAQQRENVTRSLEQPRETSTAAPAV
TTQTIFMTLPKDGESSGVKMSEASPQSARTAQTNHTTTPGDSDGSTAVSHTTSPLLLLVVACAAAAAVV
AA*
>Tc00.1047053510693.280|S099|AML-VFECD|25
MIMTTGRVLLVCALCVLWCGAVLGHAMEDYCGEGGGNGLRHTSNGGDDGVSLKADCGLLSTRMALIKAV
EAAEGEQEMNVTARPQDNSKASSPDSKVGNNTKSTGAPDSKGGSVAGEPAEAAPTPGESDTEGQVVKPE
GLDANGGKKADGKRDRNDGTATGPQQQRADQPSSSSSSGSSGTESAKQPLVKENSERNETLDDPPQEEE
EKDRGSESDSHEEEAEELEKKEDKKNASNQAPTGTLGGLTKHTEIHTATTEPNGQSSPQALGDVEKPEE
VQGEKDPKNNSQTKSVASIAANQQNETSADHGESGSPSPTANGDAANNDSDNSTEERMQSNHSAADGAG
TAEGKQNENKDANPKGTPVEATAMKTTTATTGDSDGSTAVSHTTSPLFLLLLVACAAAAAVVAA*
>Tc00.1047053510693.320|S010|A----RECD|22
MMMMTGRVLLVCALCVLWCGAGGGCEEVPGVSPSGVSGGIERERGDSEDSLRSEPPGAKKLAPETPPPK
VQQQEVISPPPKVPPVGSEDGAGGDKEGKAGEEGAKDVGKENRGDATSKEVKKPENHPKSVKSPQSREN
EGLQSPSLNGTHGVGTITSTSDSLTVNTNQQDLSSPLQPPLPNSSPHAIPSSTSAAGPDNEKSRENGNG
TKNSQMPVVGEIQERNGTCVKAVASTSGEENSRLSAKRVEEMSDATKKDNSESSTTATAALRSDAGTEG
TPTTNHPNQPSTEGATQPATTFDGEAASANKYDTVSQSAGYTTAPTTNAKTNDTARAGDSDGSTAVSHT
TSPLLLLLVVACAAAAAVVAT*
>Tc00.1047053510693.163|S032|A---H--CD|8
MAMTMTGRVLLVCALCVLWCGAADGDVVVSCGDDRILKELFIPVARLKARQEQGAAEAAADAKAAAETA
AKAAAATKAATEAAAKAKEAEAAAKEAETAAKEAETAAKEAEAAAKEAEAAAKAAKAVDTEEKAKAVAA
ATESAAKKATTASEAAAKAKAAAEEAKAAAEAAATATEEAKAAAEAAATATEAAEAAAEAAATATEAAK
AAEAAAEATAEAANAATAAAKASAEEAAEEAATATLIATSAAKAAEEAAEKAAKAKEAAETAEAKAAAA
EKAAATEADAKATAAKTAEAPATATEAAKALRGKAVGEEEVKTAVHDQDNSVEHHTGEKQELPKEEEPE
RQENEQHEKQQHQQREHSAGNGDESAKNKTANTTNATAIKDDSNSSTAVSHTTSPLLPLLVVVACAAAA
AVVAA*
>Tc00.1047053510699.80|S061|A--TIFECD|52
MAMMMTGRMLLVCALCVLWCGAGGGGCSETAPVVPGTGVTGNGNNPESKSNTTDGVGGDGQTGQKAVTQ

PAAGSVQKVPGTEAESAPKPGAQVSGTAEETIEKKDTTKKEDEDEEEGKDEDKEEGEEDDGGEEKKEKE
EDDTSTTEGKSAIGQEEPISPSGTVKASNKTQPQSTQTTSDKDQAADGAGTQEEKKNENKEANPKETTV
EATAMKTTTATTGDSDSSTAVSHTKSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053510699.89|S043|AG-----CD|27
MMMMTGRVLLVCALCVLCCGAGGVYARNPDNNSLGGYMASGGLGGNTSFLSNGSIKKLSTPLLLSASFI
SAIQAEAREGKVPSPGVTNSPLSGVAGLSPAFSGPAAAIPAPGPVPGPAIPVPGSVRGPDAPIPGVAVP
SPGPSGPGLRAAGHGLGASFPSPAVSGVGAAIPGRGPAGPDHVPGAIPGHGPADPGLGPAGHGHGPAIP
VRGPGAIPGVAVPGAPVPGNGPAFSGRDAAIPGPGPSPVIPGPGSAVHGPADPGAVIPGPGAAAAFSGH
GAGPGLGPAIPGHGPAGPDPAFSGLVPAVPGAGHSVGGGSKPPDSRSVVTSSSQGGSEKTAPVSVSSDE
RIASPEEVLAQKETGSQGTSSPEGQPTVSSNTEKQRNNSASAGGHSLGHDAAGDELQDSLQEQQKNDHS
QTNETKKSSGDQITESQSSGGALSEVSNKTTHGIKTQQPKTNSANEKNYSQNTDASHSTSPLLLLLVVA
CAAAAAVVTA*
>Tc00.1047053510713.110|S061|A--TIFECD|52
MTMMTGRVLLVCALCVLWCGVCGGGRAETSQDSPATPPEENTQKEENTVGVTGGGVQNGKPEVPQAAGV
SVQGANEAAARPSQAQQSGGGASVTSSTTKDNKGRNTEEGKKEEKEVEEEEDDRREDGKDDKKEKEETK
EEEAVTGTTEEISAGGQEQPSLSSGAAGASNITNPNSTPTTGDDDPAADVAGTAEGKQNENKDANPKET
PVEATKTTTATTGDSDGSTAVSHTSPLLLLLVVFACAAAAAVVAA*
>Tc00.1047053510713.130|S061|A--TIFECD|52
MAMMMTGRVLLVCALCVLWCGVCCGGRAETIPASPISPSDEKSQNGKAVVVAGEVGQNGEKKAPKETSS
PTRSELPAAAAKSLQETQPGGGASKAASTTTDNTDQNTEDKKKEEKGVEEKEDEEEEEEEEEDDRREDG
KDDKKQKEETKKEEAVASTTEEISAVSQEQPSSSSAAEGASNITNPNSTQTTGDDDPAADVAGKAEGKQ
NENKDANPKEAPVEATATKTTTATTGDSDGSTAVSHTASPLLLLLVVACAAAAAVVAA*
>Tc00.1047053510715.30|S046|A--TV-ECD|3
MAMMTGRVLLVCALCVLWCGLSGVAAHGEEDAEKKEDGSSGGPGPDADDGSAGLQAMQVPVKGGPERED
HSLGAQTGNSTNEQSVVVMSPPESSLGPEEEEEEEEVETVQKEKLESTTEEEETPKLTSSQEGEGPPAP
VTTRKNEKPAETSDATPGKGQSSSGDVSTRPELHKTPSEEQPSSTAPQAPAPAAAAQIKNESTTSADVV
SGQQIKEESQHDMQSEGASGKEENVPTTVTKKDGPTESNAESTPTPPSAYKDAITNDDEKSNEEVIPKH
DQTPDGETMNEASQVENNEGNTNKTQTVEAAAITNNTATPGDSDSSTAVSHTTSPLLLLLLVVACAAAA
AVVAA*
>Tc00.1047053510715.40|S070|A--TIFEC-|13
MMMMTGRVLLVCALCVLWCGAGGGGRAEAPSVISDTPSVKGNDSKGDNVTVGGAAGGGQNGKPAQSQAA
GVSVQGANEAAAEAAPAPQPGGVTSEKAEAAKGSNGQKEGKTEEKQDKEEEEEVEEDEEGKEEEEDDTE
EEEENGANEEEETKKGEAVTGTTEGTSAGGQVQPILSSGAEGASNNTNPNSTPTTGDDAPAADGAGTRE
GKQNENKDANPKETPVEATAIKNTTATTGDSDGSTAASLTTSPLLLLLLVVACAAAVVAA*
>Tc00.1047053510715.64|S097|AGWTH-ECD|44
MAMMTGPVLLVCALCVLWYVTGGVYARDVDTNALGGCMASGALGENGSHMPDGCNKTAITVPLRSVLLI
TAVEASTGRDSAGGTKNDSNSSGTSDAGASGAVAPPGGGPDGGAGAGGSAGASVPGGGGGGSSGAGVTG
SGSAGPGGGIPSDAGPPAPAVVAPPPVPPSAPAASPAVAPAAPVVDSSAGRSDGTAGSSGTNSSNTTGE
SQTGNQSSAAAAAHNSSLPETPTGTTSGTGHTRQEEEEEENEMQQQSDEAQVQQNQQHEHPAENGEESA
KDKNALRTNATANTGDSDGSTAVSHTTSPLLLLFFFVACAAAAAVVAA*
>Tc00.1047053510833.20|S068|A---IFECD|10
MAMMMTGRVLLVCALCVLWCGVCGGERAETTPASPGNTSGKNPQSKGETVVGAGGGEQNVQQTAPQAPA
SKASGLPAAEADAVPSPSPAPQPGGEASVTASATIEKKDQNKEDKKNEEKKEEVEEEEERKKEEEREPV
TGTTEGISAAGQEQPIVSSGAEGSSKITNPNSTPTTGDDDPAADAAGVAEGKQNENKESNAKETPVTAT
AMKTTTATTGDSDGSTAVSHTTSPLLLLLLVVACAAAAAVVAA*
>Tc00.1047053510921.30|S043|AG-----CD|27
MAMVMAGRVLLVCVLCVLCCGAGGVYARELDNKALGGYMALRGFGRNTSFLSNGSIKKLSTPLLLSASF
ISAMQAEAREEDVPSARVTDSPLSGATGLGTVPHVPGGPPAAEGKSLGPPSVSHSSRNTGGSSGNVGSV
PSTTQNKSPEEIPLQEQTGTEQNFLSPEKKAADEKIDGAQIQDYSSALRQGVDDAATLDGEGINSLEET
KNEKEDIKTPEAEESLEDPTKKLQGGETDPPASSTEKKPEPQPPHRTKNPATEENDSKNTDASTALPNT
GQEDNPKKRRTEGPLHEAGTVQSTSTGIQEQTPAAAPNENPSSLPKEQSTVTQTTTNAQPLDSVQTKKR
QSGDKKKLDNSDSSTAVSHTTSPLLLLLVVVCAAAAAVVAA*
>Tc00.1047053510933.20|S033|A---V--CD|9
MAMMLTGRVLLVCALSVLWCIAGGRCDEEEEAPLVGPPLNSTSVGVSENATGHTAPSDAGVLSAEQKQL
NPLGALPLQAALQPESPKEQTHSSPEHKDPLPPSTQLQEERQGGPDEGILKEPGASLSQEDKKHTSIGD
QQRNDPPPASSNKDVVSNNSEESTEDTSRSAEIIGGAPFEEVQERENVTLSLEQPRETSTAAPAITNQT
SSTTPPDQSESNTVKMSDATPQSIGTANTNDSTTKIDSSDSSTAVSHTTSPLLLLLLPVVACAAAAAVV
AA*
>Tc00.1047053510933.90|S080|A---YKECD|24
MAMMMTNRVLLVCALSVLWCGAAVVAVGDVIGEVGIKDESSKALQVDSQAREAGKRDVSGPEAVVPRLH
EQQGKNARKNDDSAIQPTRQFKVEEDRDHSEEEEEKENEGSLEGTVKDGEVLPSPAEGQPTSNEPPPPP
ASGGSRNGVISGGGSKLGEGSNGGEGPTLNSSSSSGDGKPPAVDSSGSGGGTGSVPGGKGIGGGGTPGV
ESLKFPVSGVALPPSTPAAGSASSAQNLEPSERSGWPEPTASLRIAPLNVDARKESKPKDEPQTFIAHG
EAERHVTDEETSKKEAEESAVEGKRLFNLPHNASSTPAGPAVRLPEGSQVQVNRDEGEGLPPEATKSET

STGQKHGTSQSQNESRGTKFSSKNEVAVKHGHVTVPSDSMTNASANSQGVTTAPSISTSGSEDAQSTVD
GNTDDDQRPNKKKAHNNPEDDNANVAPTFSETPPETDTIQKNGTSKVDDSDGSTAVSHSTSPLLLLLPV
VACAAAAAVVAA*
>Tc00.1047053510959.30|S023|A----R-CD|3
MAVMADRVLLVCALYVLWCGADGIYAEGDLEGPPAALSPGLAPSSPGDVGSLDNTGSLAEHGVGVGRIE
PLENAVSGGDVSEELLNSNNDDEESGCGSEDGHRRQENRDEVAEDEVLIIPQTDQSEITPKGPQIPARE
DNAAQLQQTQPPQGMHLTSTAHEGPQDASELRTPLSQNLSQQKTGTVSSKFAIHTPTDNEEGKIPSPPP
KSGSDTSNSPEQLFVAKPERGNQREGADDSPTDSKEDKNPPATTRKTDAKNTHSSVSSSATDTTPKPDA
VTEDNPPATDSSQKSSGDAEQLTAIPNPNEASDSTEDAASQSAGTATKTNDTAKPAESESDSSTAVSHT
TSPLSLLLLVACAAAAAVVAA*
>Tc00.1047053510961.10|S013|A---V-EC-|8
MAMMTGRVLLVCALYVLWCGAGGVGAEGQEAGTLSPPPGPVYDDQGGVLSGIGRMKPSDTDGQVTVDGV
RDRAESKHLSSRFPLVDAKDVTPDGIGGEGNGAVDEVAPEENESLQNSCDEDGERSEGCVQVQGGDGFP
GNEGGHVDRGRQQDDRNPLPPLSDQTSSEEINSPLPAERNPHNQRPVSRQAPVVVEKQTDPVSIRPQKE
AATLESEAVRNAANSHSQESAAELTNGTLPAHARVTEAEDRSKNVFDTHKDAAEKQKKPAHTTGKSESP
AASGDAHKATASTAAVDNEAAIKKAKSPGGASSPISISDNSNNDTEQNNARDTSEEASHSTENATTHSA
GIPRAPHTTAKTDDTTTQEDSNSDGGTVKMGEAAPQTAGTAQANDTATHDESDSSTAVSHTTSPLFLLL
LVACAAAAAAVAA*
>Tc00.1047053510961.30|S013|A---V-EC-|8
MAMMTGRVLLVCALYVLWCGAGGVGAEGQEAGTLSPPPGPVYDDQGGVLSGIGRMKPSDTDGQVTVDGV
RDRAESKHLSSRFPLVDAKDVTPDGIGGEGNGAVDEVAPEENESLQNSCDEDGERSEGCVQVQGGDGFP
GNEGGHVDRGRQQDDRNPLPPLSDQTSSEEINSPLPAERNPHNQRPVSRQAPVVVEKQTDPVSIRPQKE
AATLESEAVRNAANSHSQESAAELTNGTLPAHARVTEAEDRSKNVFDTHKDAAEKQKKPAHTTGKSESP
AASGDAHKATASTAAVDNEAAIKKAKSPGGASSPISISDNSNNDTEQNNARDTSEEASHSTENATTHSA
GIPRAPHTTAKTDDTTTQEDSNSDGGTVKMGEAAPQTAGTAQANDTATHDESDSSTAVSHTTSPLFLLL
LVACAAAAAAVAA*
>Tc00.1047053510979.10|S074|AML-YKECD|9
MAMMMTGRVLLVCVLCVLWCVTVFGDARDNRCVEGEKNFLTHTKNGGNDRVRLTADCELISTRMGLIKA
VEAGEREEESESDNAPLEKTEKSAPGTLLAVTEGNAAPGPKEGKGAAGAATPSPSGPGVPGTGDETRQL
TAAGQKGSENKNVDPNNKASNKSQDQHTDQLPSSPGSSSTRSDEKSSLTGTDEINQLPNDTETKGDASR
QDTNGSDEAIEKEDGEKEKEKKQEKNTLLPEKHEGQNNGGGKPPPVPAPPTGEESPIPDQENSQNPKKV
TNENKPSGSKTESKSTQPPLGDATQGQHSHNTDTEDSTKNVATGSPAETTTTSSTSTSGSCDHVQNKVD
EDDAQSSEEQHDVLETGNTNVVPTLSEAAPQTAGTATTAAQTNHTTKSGDGDGSTAASHITSPLLLLLT
VVACAAAAAVVAA*
>Tc00.1047053510979.50|S131|ANQ---EC-|3
MMTTTDRVLLVCALCVLWCCVAAVAVSAAGGAGGDGGAGEYLIAGRHAQLRRECAEEAGRRTGGRANPS
AVEECVRQGMDGVRTVVDGRRRWRRQQFAVAAADGGSGNDGRNSVSSQKAVSGTGTVLPDDPKLKSPVA
PGPILADTTTGGGNLLIPAGSLETAKDKNGEPSRETDKGEKATVENRSNEGTNGDEQVDNAAIGKPNED
PENKKGETLQVEERIVKTEEHEVKNGLEESNTETDEENRNKAAEDPEGDNEVTILSSGGQYNEEGERQT
EKDSGSIKKEKEVNGGGATDGISAVAPVALQPASPVDVTDRRNLEKKNDGDTGGNRDAGRTQTQESAGP
SQTEKLSAELVTEEEAAETETGAPGKKTQPEDAGKEQTTVGAKSNQETPVAAKEANNKKEVPREEEDAE
TAATNENFDKKRTSGKDNAHNGAETTRQENENEVEKAEGTHAEAEGNEEQTGKKNFADKDRKLNDTATP
GDSDSSVAAFHTTSPLLLLLTVVVCAAAAALVAA*
>Tc00.1047053511057.30|S100|AML-VFEC-|15
MMAMMMTGRVLLVCALCVLWCGAVFGRAMDDYCSEGGGNGLRHTSNGGDDGVSLKADCEVLSTRMALIK
AVEAADEQEMGVTGPSHDTGEPLQNDTKGSAAPGPGGGIVAGQPEASPPKPKGSGTEGQQGKPEGLDPN
GGKEVDKRDHTDGKTTEPQHQSVDQSSSSSSSSGSPGTQSGEEHNLENNSKSNEPSDDSPEDDESDPLS
QSDSREEKAEEEPKKTGDKKNLSHEAPTETRGSPANDAGIQTATPSPPPATMNGPSSTEDLPPVQAPQR
VQDDNAESRPPSHTANGDAANNEADNSTEERMPNNDPAADGAGTAEEKQNESKEANPKEKPVEATAMKN
DTATTGDSDGSTAAFHTTSPLLLLLVVACTAAAAVVAA*
>Tc00.1047053511077.60|S067|A---IFEC-|4
MAMMMTGRVLLVCALCVLWCGACCGGCSEIPPAPETGVSDDGKDSKIENKSVVSVGEDDQTGKPRVSET
AAPLVPEVPVAGVTQTQGAQASGTMEQNKKKTNENDEEEEESEEEAEDEAGEYKGNEMKEKEEDSKEAV
TSTTMGIPADGQEQQILSSGAEGASNITNPNSTQTTGDGDPAADGAGTAEGKQNENKDANPKETPVEAT
ATKTTTVTTGDSDGSTAVSHTTSPLLLLLLVACAAAVVAV*
>Tc00.1047053511077.110|S004|A---V-ECD|18
MMMTGRVLLVCALCVLWCGAGGRCDEVLPVAVSSVISASGVSGAPDNASGQTSSGVAGNPSAEQTQLNK
VGNSAPGSPQLQVDLQTQSPTIQQTHSGAENAISSTTSKPSGEQLQNVPDGVPPGEPEASLGQEEGKNE
TIANQQSNGPPSPSSNNDIVSRNSGERTEDTSRRAETLVAAPSEEAQQRENVTRSLEQPRETSTAAPAV
TTQTIFMTLPKDGESSGVKMSEASPQSARTAQTNHTTTPGDSDGSTAVSHATSPLLLLLVVACAAAAAV
VAA*
>Tc00.1047053511079.60|S100|AML-VFEC-|15
MAMMAGRVLLVCALCVLWCGAVFGHAMEDYGSEGGGNGLRHTSNGGDDGVSLKADCVLLSTRMALIKAV
EAADNGHVELSGVPDHLQDTGESSPNNTEGSAAAGPGGQPAGLLPKPEGSDTEGQQGEPEGLDPASGKK

TDGKSDRKDGTATGPQHQRADQSSSSSSPGSSGTEGVKRPSSRANSESNEALNHLPQEEKDLRGESDGR
EMEAEEEPKKTGDKKNANREAPTETRGSPANNTEIQTATPPPPPAPMNGHSSFEDLPPMQPLQRVQDDN
TESRPPSPTANADAANNDSEKSTENGMPNSDQASDAPGTAEEKQNENKDANPKETPVTATAMKTATATT
GDSDGSTAVSHATSPLLLLLVVMCAAAAVVAA*
>Tc00.1047053511081.10|S100|AML-VFEC-|15
MAMMMAGRVLLVCALCVLCCGAVFGHAMEDYCGEGGGNGLRHTSNGGDDGVSPKADCGLLSTRMALIKA
VEAAEAGEESSGVPDQPQDKSESSPNNKLGNNMQSTGVPGSGGSVAGQAPLGSGGSDTGGQERGSNVLG
PNEEKEAGRMDQKDGKGTGPHNEGAEQSSSSSGSPAPQSGEDHKLENTSESNESSDIQLKKEDAVEAEI
PKISEKEEPGGGKENENGKALTGIPDSQTKMKETKTVTPPPLLTKTAEEARITIGIPAGDSTPAETNGH
SKPEDTVNMQQLQQPQDGIESNNNSQTNSGTEISANQQNEPSADQAESTPLPTANGDAANNKAEKSTEE
GMPNNGPAADGAETREEKQDENKEANPKETPVEATAMKTTTATTGDSDGSTAVSHTTSPLLLLLLVACA
AAVVAA*
>Tc00.1047053511081.60|S061|A--TIFECD|52
MMMMMTGRVLLVCALCVLWCGAGGGGCSEPTQVSQDITSVNENGPKTDNDSSGGAGGGGKNGQSAQSQP
AGVSVQGANEVGAALRTGTQAPETADAEKKNQTEKGKDSMVQNTDDEKKQVEENGANEEKDDRNKEKED
EEVEGDEEGEEEEEREEKEEDGTKGKEETMKGADTSTTEVISAGNEEPPIISSGAARASNITNTNSTQT
TGDDDPAADGAGTAEGKQNENKDANPKETPVTAAAMKNTTATTGDSDSSTTASHTTSPLLLLLVVACAA
AAAVVAA*
>Tc00.1047053511099.190|S115|ANQ-VFEC-|1
MAMMTGRVLLVCVLCVLWCGAGGGDADGSAVEYSLLRWHAQLRRECAEEAGRRTGGEANASAVGECLRQ
GMDGVRAVVDGRRRWRPQRYALVAKDPEDGPTEAISVGSTLPLLVQETQGTLQGLALRDQAKSSKGGAG
GGTELGLEQPQPEEPSVTKYKELDVRRELMGDENRSVPERKALVGSDLKDSKAMKVPANQPEVDALSPS
SSDVRAADIPGGVSSDLSSEVSRSSEASGKGGGDQQKNTSVAAKTSAAAPSAKESFHTASSPAKEDTES
TQPADVLLKQGNIPTAGATQNVTTEGQEETTLSSFAADDDNAVTNDADEDNAENSGDDLASRAAVTDEK
QQHQREDGSEKETAPAATPQVKNEDPGSADVVSVQQVQKAQGGRESGSESRKEDSVLTTSKQKDGTYDS
HAESTPTSRLSEKSVAASNGPDEATEEEISNKNTAGVDAVPEAAQDDGNKDDGAKETPIKTTAIANDTT
PTGDSDSSTAVSHTTSPLLLLLVASAATAAAAVVAA*
>Tc00.1047053511099.220|S023|A----R-CD|3
MAMMTGRVLLVCALCVLWCGYPLVSAVTGEDREHSGQGVVGSVGQSSSPVGGHGDNGDVTDGSSVSGGS
HLPGSAPTGGKPSLPGVGESVGLNESRDALTLAKEGHEVVRDQHELVPHVSYHTDAGTGGKSDLSAPEQ
SPNAKTKLENGGGVCGDDAATAEGEVITTVNEEQLGVSSTSDSHPPAADRGAKEQEGTVEQAASTAALT
PVVGRETTPKGDTEEDSPEDKAATGAGITQDIPAVSQQQTHSSSTSTTGNGPTSALGKGGAAEDISNNN
ERSGKALLQEGAEHETVAGSQSQAIPAATARNTLGTTVSGDSDNSTTITTAVRSDTGTEGTPTSNHPNR
QSIEGATSPGMNSDGEAVLAKKYDTVPQSAGSTAAPTTNNKTRDTASHGNSGSSTVVSHTTSPLSLLLV
VVACAAAAAVVAGPA*
>Tc00.1047053511149.60|S022|A----R-C-|4
MTMMTGRVLLVCVLCVLWCGYPLVSAVTGEDREHSGQGVVGSVGQPSSPVGGHGDNGDVTDGSSVSSGS
HLPGSAPTGGKPSLPGVGEGVGLNESKDALTLAKEGREVVRDQHELVPQVSHHTDAGTGGKSDLSAPEQ
SPNAKTKLENGGGVCGDDAATAEGEVITTVNEEQLGVSSTSDSHPPAADRGAKEQEGTVEQAASTAALT
PVVGRETTPKGDTEEDSPEDKAATGAGITQDIPAVSQQQTHSSSTSTTGNGPNSTLGKGRAAEDISNNN
ERSGKALLQEGAEHETVAGSQSQAIPAATARNTLGTTVSGGSDNSTTITTAVRSDTGTEGTPTSNHPNR
QSIEGATSPGMNSDGEAVLAKKYDTVPQSAGSTAAPTTNNKTRDTASHGDSGSSTAVSHTTSPLSLLLL
VVVACAAAAAVMVAGPA*
>Tc00.1047053511171.90|S061|A--TIFECD|52
MMVTGRVLLVCALCVLWCGAGGGGCSETPQVPPASPPVNDSVPKNDNNSTGGAGGGRQSGQSKALQEKS
LPVQGATGAGVEKAIKPEAKVPETADAEKKNEDQTQGAEDVGKKKDEEQEPNEEEEEEEEEEKRNGKKE
EEEKKHEDAGTGTTEGMSTGSEEQPILSSGAEAASNKTNLKSTQITDDDDPAADAAGTRKEKQNENKEA
NPKETPVEATATKNTTAMSGDSDSSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511173.50|S081|A-L-YKEC-|1
MAMMTGRVLLVCALCVLWCWCGGFADEAGASAGGGNGLRHTSNGVNDGSSKADCGLFFTSMGLLKAVEA
GEDNLPLTDKVSSEIKEVSDLVFSQKGVDGGPLAGAKEGNGAAGAVTSPPGPGVSEANEGERYLEVLGP
KGDDELTRVSASGEASNSQNQTAHQPVLLSDSSDTRPGEVLPLSNSGSAPIYKDPLKKGDVDSRDATVG
DTQKVEELKEENKEEEELKEFKDRAESETRKEGKKEEGTPTKISTAQPTALERTQTPVVKLNVGKSPDA
VPEGDASQTESEDAQALTHQQHESSSSQTETKSEAPEPPATDGVPPQQVQDTVTKDSMENATATNQAET
TVSPNYTGGSGEAQSEADGNDAQRPNPNEPHDVLEGVDTNDAPTLSEAAPQTEETAAAARINGTATPGD
SDSSTAVSHATSPLLLLLVVACGAAAAVVAA*
>Tc00.1047053511173.100|S099|AML-VFECD|25
MAMMMAGRVLLVCALCVLWCGAVFGRAMDDYCSEGGGNGLRHTSNGGDDGVSLKADCGLLATRMALIKA
VEAAEAGQDELSGGPGLSQDTKEKLDDTSVGTNTVGSAAAGLGGSIVAGQTAALPPTPGGSGTGGQVVK
PEGLDANGGKEADHKEDRNDSTATGPQLQSVDQSSSSSSSSGSPGTQNGEEHNLENTSKSDESSDDSPE
DDESDPLSQSDSREEKAEEEPEKNELNTENTSHEAPTLTTAPAEEAEIQAAIPTTPLHSHSGAEDSGKV
QQLQQPQDGIESNKHSQTKSAASITANQHNEPPAGHAESRPLSPTANGDAANNESEKSTEEGIPNNDSP
ADGAGTREEKQNENEASNPKETPVEATATKTTTATTGDSDGGTAVSHATSPLLLLLVVACAAAAAVVAA
*

>Tc00.1047053511173.150|S010|A----RECD|22
MAMMMTGRVLLVCALCVLWCGACGGRCQEVLLVSQSDVPGEIEGERGHSQGSSGFKTPDSHTPDSETSV
RDVQQEQDPSPPREETQLGTKGGNKVGKAKEKDDAKEAGKEREVDGKIIEPKKPEDKLTPVEGQQLNNN
EGLQPTSLNGAHGAETIKSSRETLPVREDQQDLSSSLLPPLHNTSPGGTPPSTSAAGRVDTKSRENDIG
TKNSQQSVVGDIGQNKDTGEKAVASTDEEEGSRLSVTTVEGMSETTTKSDSGSTATTAAVRSDIGTEEI
LPTNHPSQPSTEGATPPGTTSDGEAASTNKYDTVSQNAGSTTAPTTNVTTTDTAKKGDSDGSTAISHTT
SPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511173.180|S003|A---Y-ECD|2
MAMMMAGRVLLVCALCVLWCGAGGGYAEDVDVAVGGPGTFGEGGGGAGGQSPPADGSRGGSRGSKADGS
HLGEGDASDSASDDISLALSPELDVVPTLSEEPLPQEEEESEGKQKHPQTGPQDASTPKVNGRETIDPD
PQKQLSDKSKTESITNVGGGETADGGKENNVHNNGLSSNKSDPQPLLEPRIKKVSLPTEPSPPPAELSP
APPELPTVPSPTGLAPATTVSAGETNPTPSTGSQNTTETTSKTSTSNAKTKREAQEKSSGNVAPNQNRQ
DTDTPDSMRGATTSRPAETAVPSVSKIGSGGTQNKEDKVDNGAQRTNRKEPQDGLEDDTDDAHTASETE
LQTPETATTQKNATSNSGDSDGSTAVSHTTSPLLLLLVVACAAAAAVAAA*
>Tc00.1047053511173.210|S010|A----RECD|22
MAMMMTGRVLLVCALCVLWCGAGRCQEVLLVSQSDVPGEIEGGRGHSQGSSGFKTPDSHTPDSETSVRD
VQQEQDPSPPREETLLGTKGGNKVEKAKEKDDAKEAGKEREVDGKIIEPKKPEDKLTSVEGQQLNNNEG
LQPTSLNGAHGAETIKSSRETLPVREDQQDLSSSLLPPLHNTSPGGTPPSTSAAGRVDTKSRENDIGTK
NSQQSVVGDIGQNNDTGEKAVASTGEEEGSRLSVTTVEEMSETTTKSDSGSTATTAAVRPDIGTEETLP
TNHPSQPSTEAATPPGTTSDREAASANKYDTVSQNAGSTTATTTNATTGDTAKKGDSDGSTAVSHTTSP
LLLLLVVACAAAAAVVAA*
>Tc00.1047053511173.270|S061|A--TIFECD|52
MMVTGRVLLVCALCVLWCGAGGGGCSEKAKVPSAPQDITPVNDNGPKNDNNSTGGAGGGRQSGQSKALQ
EKSLPDQGATGAGVEKAIKPEAKVPETADVEKKNEDQTQGAEDVGKKKDEEQEPNEEEEEEEEEEEQVE
EEGEEEEEEEKRNGKKEEEEKKHEDAGTGTTEGMSTGSEEQPNLSSGAEAASNKTNLKSTQITDDDDPA
ADAAGTRKEKQNENKEANPKETPVEATATKNTTAMSGDSDSSTAVSHTTSPLLLLLLVVACAAAAAVVA
A*
>Tc00.1047053511173.360|S061|A--TIFECD|52
MAMMMTGRVLLVCALCVLWCGGGGCSETTQDPPGGASQGGNNPDGRKNTTNGAGGGVKSSVPAEPQLPA
ESVTDLSLAAAGADVSAAQQSGKQASEMEEEKMKNKKERTDEKEKHEDDEEDDDEEEEEYEEEEIDEDD
KNKEEGETKEEKEDKEKEEKKIKEDDTDTTKGMSTGSEEPPIISSGVEGAANQTKLKSTQTPGDSDPAA
DGAVTREEKRNESKEANPKETPVEATATKNTTATTGDSDGSTAVSHTTSPPLLLLLVVACAAAAAVVAA
*
>Tc00.1047053511173.400|S070|A--TIFEC-|13
MAMMVTGRVLLVCALCVLWCGAGGGGCSETTPDLPGGASQGGNNPDSRTHTTNGAGGGVKSSVPAEPQL
PAESVTDLSLAAAGADVSAAQQSGKQASEMEEEKMKNKKERTDEKEKHEDDEEDDDEEEEEYEEEEIDE
DDKNKEEGETKEEKEDKEKEEKKIKEDDTDTTKGMSTGSEEPPIISSGVEGAANQTKLKSTQTPGDSDP
AADGAVTREEKRNESKEANPKETPVEATATKNTTATTGDSDGGTAVSHTTSPLLLLLVVACAAAASAVV
AA*
>Tc00.1047053511173.430|S130|ANQT--ECD|2
MAMMMTGRVLLVCVLCVPWCGLSGIAADGVGGGDGSADGELLLQWRNRLRRECAEEVSRRTGGSGNASA
VDECVRQAMESVRAVVDGRRRWRRQRIAVVAASAAAAAAGNGDVSTDKDGQARNKEVSPPEIKDEKPVA
SGQESTDATRRKDQTTQDPSAAIVSRKKLISDQKQEEDEDNEDEEAEEEAKIRETPPPVVPPVAAAGGG
GGIKPPSGASGPAGPGAILTSRSSSGVDSSSRIGGEGSTVSISPNAVGKPSKQDKVPEAKESQHAQPHD
GVAADTLNNGLEQNSSAPTTTGQNYNEVATLGAGGLRSSGEQITVKGGSEASRTDESSADPNTKLQESE
KTPLKSSQAAAKEPKTYHEVLTSVKEETKSKSTDASENLPDAAESINEHPASAATTMQSTSTGSQEAAV
TPSSNGIPPLHEETTTGTDTTENAQPPKETTVEATAMKNGTATTGDSDGSTAVSHTTSPLFLLLVVACA
AAAAVVAA*
>Tc00.1047053511173.460|S010|A----RECD|22
MAMMMTGRVLLVCALCVLWCGAGRCQEVLLVSQSDVPGEIEGERGHSQGSSGFKTPDSHTPDSETSVRD
VQQEQDPSPPREETLLGTKGGNKVEKAKEKDDAKDAGKEREVDGKIIEPKKPEDKLTPAEGQQLNNNEG
LQPTSLNGAHGAETIKSSRETLPVREEQQDLSSSLLPPLHNTSPHAIPPSTSAAGRVDTKSRENDIGTK
NSQQSVVGDIGQNNDTGEKAVASTGEEEGSRLSVTTVEGMSETTTKSDSGSTATTAAVRSDIGTEETLP
TNHPSQPSTEAATPPGTTSDGEAASTNKYDTVSQNAGSTTAPTTNATTGDTAKKGDSDGSTAVSHTTSP
LLLLLVVACAAAAAVVAA*
>Tc00.1047053511173.24|S043|AG-----CD|27
MAMMMTGRVLLVCALCVLWCGVCGVYARNPDNNSLGGYMASGGFGRNKSFLSTGSSKNLSTPPLLSASF
ISAIQAEAREGEVSSPGVTDSPLSGATGLSPAFSGLGSAVPGPGPGFVHGPAGPGDGAAAFSGRGAAGP
DPVRSPAFSGPDANIFGAPVPGHGPAAIPGAPFPGNGPAFSGLGAAGPGDGAAAFSGRGAAIADAAIPG
AAGPVRGVDAPIPGPAVPGDGPAFSGLGAAGPGHAAAIPGAAVPGTADPAAIPGSAVLGHGAIPGSISD
AAIPGPASPGDGAAAFSGRGAAIADAAIPGAAGPVRGVDAPIPGPAVPGDGPAFSGLGDAGPGHVAAIP
GAAVPGTADPAAIPGSAVLGHGAILGSISDAAIPGPAGAGAAAAFSSLGAAFSGAGHSVAGGSEPPNSR
SVVISSNQGGNGKTTPISVSSDEQIVPPQEVLAQKETGSQHTSSPEGQPTVSSNNEKQRNNFASAGGRS
LGHNAAGDELQDSLEEQKKNEHSQKNETKKSSGDQITESQSSGKEISEVSNTKAHGIKTQQPKKNPVNE

KNYSQNTDASHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053511173.64|S059|A-TTIFECD|4
MMTGRVLLVCALCVLWCGIAGGGGCSETPQVPQDIKSGNGNNHQSVNNNAGGAGEGGLSGKPVESQAAG
VSVTELPGAGAATKLPGAETSPTAGTEKKNEETGQEKEEENDKQEEEEKTKEDEKVVDKKEEEAEEDDE
EDKDDDVKDEEEEEEQKKKKDDNGATKKLSAVGQEQPLLPSGAEGASNNTKSKGTQTPDDDDPAADAAG
TREEKQNENKDANPKETPVEATATKNTTATTGDSDGSTAVSHTTSSLLLLLVVACAAAAAVVAA*
>Tc00.1047053511183.80|S114|ANP-VFEC-|3
MAMMAGRVLLVCALCVLWCGAAVVASSLPGATTVQSAWSEYMFLNWHELLKNECKAENATETNFDESAV
KCCVHNAMRDLCYDVYGKTVMENKDANVEGICKEYAGEPNHAGECPKQQQNPLPDAEATVGLSVPEVPG
KERSLRTPAAAPPGASTAKPTDPPPSLPVEGQHDGADDMPGPNSEETSESMKTTKDLAEEDIVTTADTK
QNEASNGQTEATTKTPPESSDDDDNETDKGTGEDTPNNAPESDVSETEENHDENKGNNSKETPVQVAGI
KTVTAKPDDSDSGTAVSHTTSSLLLLLHAAAAAVVAA*
>Tc00.1047053511183.260|S114|ANP-VFEC-|3
MAMMAGRVLLVCALCVLWCGAAVVASSLPGATTVQSAWSEYMFLNWHELLKNECKAENATETNFDESAV
KCCVHNAMRELCYDVYGKTVMENKDANVGVICKEYAGEPNHAGECPKQQQNPLPDAEATVGLSVPEVPG
KERSLRAPAAAPPGASTAKPTDPPPSLPVEGQHDGADDMPGPNSEETSESMKTTKDLAEEDIVTTADTK
QNEASNGQTEATTKTPPQASDDDDNETDKGTGEDTPNNAPESDVSETEENHDENKGNNSKETPVQVAGI
KTVTAKPGDTDGSTAVSHTTSPLLLLLVVACAAAVVAA*
>Tc00.1047053511183.280|S082|A---YKEC-|17
MAMMMAGRVLLVCALCVLWCGAADGDVVGPVTSGDPGGGQSPLADGSHGGSGGKKADISHESKSEPLVA
ASGEESPTVRIDPDGVSSLSEEHLRPEKRTSNGKQEESQSPPQDASPTKVNPAEALDFLPQERLLGTPE
KEVITNGGGGGTANGGKEDTDQNAGLSPDSSDSSVPPVPQVNHVLPPAEPSPAMTVSAEETNSPALTGS
QHATERTSTTSPSHSKTAPGAPEKSSGNGEPNQHREDSETPGSMKDGPTSHPAETPAPLVSTSGSDGAQ
KKEDKVDNSDQRPNNKEPQYGHEDGNTEDAPTANETAPQTAKTITTQKNVTSKPGDSDGSTAVSHITSP
LSLLFVVACAAAAVMAVPAWSVVR*
>Tc00.1047053511183.360|S062|A--TVFECD|5
MAMRMTGRVLLVCALCMLCCGVGLTNGDTAIEMRIEENPRSTVPDPAVGNAKEQATQDLVVEGPENGDP
SLAAQTGNNTKQQKVVVETPPLIPVRTQEEEEEEVKKEESEEPKSLSEDRETSKLLSMPEGERPPPPPP
GKPSPVIINGNSAGNTNEAREKELPSVDGGFTQRQVLKSPTAPTAATPQVKNEDLGSADVVSVQQVQKA
QSGRESGSESIKEDSVLTTSKQQDGTSDSHAESTPTIRSSAKSVAASNGPEKATEDEISNKNTAGVYAV
PEAAQADGNKDDNKKETPIKTTAIANGTASTGDNDSSTAASHTASPLFLLLVIACAAAAAVVAA*
>Tc00.1047053511183.530|S082|A---YKEC-|17
MAMMMTGRVLLVCALCVLWCGAADGDVVGPVTSGDPGGGQSPLADGSHGGSGGKKADISHESKSEPLVA
ASGEESPTVRIGPDGVSSLSEEHLRPEKRTSNGKQEESQSPPQDASPTKVNPAEALDFLPQERLLGTPE
KEVITNGGGGGTANGGKEDTDQNAGLSPDSSDSSVPPVPQVNHVLPPAEPSPAMTVSAEETNSPALTGS
QHATERTSTTSPSHSKTAPGAPEKSSGNGEPNQHREDSETPGSMKDGPTSHPAETPAPLVSTSGSDGAQ
KKEDKVDNSDQRPNNKEPQYGHEDGNTEDAPTANETAPQTAKTITTQKNVTSKPGDSDGSTAVSHITSP
LSLLFVVACAAAAVMAVPAWSVVR*
>Tc00.1047053511183.560|S117|ANP-VFECD|7
MAMMAGRVLLVCALCVLWCGAAVVASSLPGATTVQSAWSEYMFLNWHELLKNECKAENATETNFDESAV
KCCVHNAMRELCYDVYGKTVMENKDANVGVICKEYAGEPNHAGECPKQQQNPLPDAEATVGLSVPEVPG
KERSLRAPAAAPPGASTAKPTDPPPSLPVEGQHDGADDMPGPNSEETSESMKTTKDLAEEDIVTTADTK
QNEASNGQTEATTKTPPQASDDDDNETDKGTGEDTPNNAPESDVSETEENHDENKGNNSKETPVQVAGI
KTVTAKPDDSDGSTAVSHTTSPLSLLLLVVACAAAAAVVAA*
>Tc00.1047053511185.100|S025|A------C-|17
MAMMTGRVLLVCALCVLWCSAYCRCTEEESVSLSRSGIGDSRTGSGVSGENGVKTDKTKTMKTASEGDS
HPSERDVSDGGSFDQAPPDKSICKEKNDGSTVKPLTTDGEVLLDSQETIATHLKGMDTDLADPNINQNH
KNPKAIDGIDTQLPDAPAAPKAQPSPPTVPTANKTVNSKEELTAEETPEHSRATRNPNEGSETKNTTDQ
ALKPDAGGIDTLASEDASSPSIDDAATSEATANTARVGSPIASLNNTDGKNEGSRDGESPTPSPSAAEP
ETITTAKPTTHDVSHPNKNGTVTFTGEKNAPTTNPKSATEGKETADVESDSSTAVSHTTSPLLLLQLLI
VVARAAAAAVVAA*
>Tc00.1047053511185.120|S030|A------CD|31
MAMMRTGRVLLVCVLCVLWCGACGGYGRCTVGHCALAELDDAKFAKGMDGEVVLMKRDCVPTTALRGVV
TAVPAAGDSDELGSPDAGVGTSGKQKVDAEESAVVFAGSEPTPGGCGAVSTASSPASADTIAASSTPVS
GAGGAVGPKQQPAVVSGFQYDFSFGGREGKEGEEAGSAGRGEEPSVSSVCSQPPLVAVDLTICTVDQNK
EQNDNASFDTDHQMATQHEEGVPHVPGKRASVQTLPVPTPAGGQPGHATQPSEELEEHATAPNSGPTRD
ALNGDSQEQTPQPQTPTDNKQSLPVLQGLSEGVQENQNNMENIRKGNQVDSTGNTQNKEHDSAAATHEL
LTASINTRLSGAPGNESNTTLLSGTLRSSTAGTEEQAKAGSMPLRQPKPPEEKLISEELPPTATEVEAP
GGPSAPPPKSLPQSALPSSKKVPDTTQSTEDPQSKGVEPTTDARQNAITEGQAETTSPSSPADDAAAND
ADESNAEIANDGSAVNAGVPEEEPNQEQVDGSEKQTSFTSTAKKHNATIEDSDSSTAVSHTTSPLLPLL
LVVVACAAAAAVAAA*
>Tc00.1047053511213.60|S129|ANQT-KECD|2
MAMMMTGRVLLVCALCVLWCGAAVVVSAADGAEEDGSAGEYLISRWRAYLRRECVEKVSRRTGGRANAS
AVEECVCQGMDGARAVADGRRRWGRHRYAVAAADGPFENDSTPESSLQGQTGSGAGLTGGRRLEPSLNP

DTGISDKATAEEETLTRHPEAPELVKNRTEEILKEQEKEKEKKKSAEEENEDEGNDNGEDDNASTESSG
DDHDEEEEEEEDVEAGTNKKEGRDGGDVDGDNSLDDHAIVQLAAPVYVERQERSLTLNNGGAKGKGGAG
ETRVPEGAGLQGAEKESAKLPHETGADLMETEGLKEGADQSGAGNQQAIDESKSNEAAPPATQEEMKKE
PPKEAKKATANENVIKKETTEKGKNGAERGKGESSDRAGKEKKENEERKVEEANNEPQDGSETANTDVA
LTVGEAAPQTAKPVTVAQANDTVTPGDSDSSTAVSHTTSLPLLLLVACVAAAAVVAA*
>Tc00.1047053511221.50|S099|AML-VFECD|25
MAMMMTGRVLLVCALCVLWCGAGGVVYAMVDRCSEGNGNLLTQMNNAESDGVFPRADCSLLSTQMGLIR
AVEAGDKEGAELGGTVTSEKPKQLLSGTTSKGNDDVLTPGSPAPLPTPKVSDQVEQEKPLKTVDPNGID
DTRNPTSGKATESQRQSAGQSSSGSTVTQPGKDHNWNNPSESNASSTVKPTDDGGVNIPPNIPERGAGA
LEKVKEDEDETKKPKQAVQEEAGEHKENKNDNSPTGSLENAAKMKTIPQETSPSLTKAPAEVALKTIGK
TEGNSTQARVNGQSSPEDTVPVQQLQQPQSEMKSNNNSQTEGIAPIAANSQNEPSDGHAETKPPSPTEN
GNFASNEADKSTEDSTPKNDPAADGTGTREEKKNENKEANPKETVPATNATTGDTATPGDSDSSTAVSH
TTFPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511255.30|S033|A---V--CD|9
MAMMMTGRVLLVCALCVLWCGAGGRCEEEVVPVAEITVDSASGGVVTDKEIDRTVTGGAGNPSVEKTQP
QNVEDSAPGSPQSQAGSDIELTKQQPHTDQKNTDPPPHSKSLQEERRDGTSENSPGESATSLSQGDTKH
ASIESPERNNPPTVSSNDDVVSRKSEERTEDNSGSTETHVAAPSEEGQERENVTSSLEQPRETSTAAPN
VTTQTTSMTPPKDSESSSVKMSEASPQSTGTANTNQTATITQNSDGSTAASHTTSPPLLLLVVVVCAAA
AAVAA*
>Tc00.1047053511255.50|S063|A--T-FECD|1
MMMMMTGRVLLVCALCVLWCGTAGAAADGSEERADLSGIGGGSLPELKEIGKSPEEPQGKKDEAGDVKG
KKHPASSEDEEEDDADGDEEDYDVVDDDDDVEEEEREEETVETAETEIPNDPTKEEASSPPQSKHEKGP
AAAPAEGIPTTQSPATPVQPTTQGQPPTAAPSPEDSPVPAALAATVTPAVTPSEQGNTPAAARKKDEKQ
SEDIDPAQESEQPDPQDVVLVQHSQGVHESKESNNNPRNPASASATANQRDATFNGRGEPAQTTSSTKS
GFESNDDNSGTEEGISSDDPTADGAGKNDTKNSQNKHGNTKETPVEATAVKATTATTGESDGSTAVSHT
TSPLLLLVLVACAAAAAVVAA*
>Tc00.1047053511255.80|S030|A------CD|31
MAMMMTGRVLLVCALCVLWCGAAVVGSVANDVVDGGVKEGPLGGSRSDSGDEKAGKPELSKSVDEGLGS
AGHSLDTRSGTNVSEQGNLVNEPPTENVGKEGVEGEALGAQRNEVHAQQVEAEGEELAVKQKSQTKDKV
TVPQSLPPTPALMQGSQRTPRQPKENSKKSTGQPPKLQVPPAKSPSQASDLGEADAGPVGIEGTGRNVI
GGSRDKNKDPKGREGHISGPPSGGASSTISNNGDASQMNGGAPSTQDTKSLKNNEQSGPTASSGNAPLN
RETPETSTPDAKQHSSETQENETSQVADGDANYSTAGQSAVGTKGSSGVSTTASNAPTTPQPQLPAPPV
PPTATVTGAPAEKPTAERSPPPADSTTGGNLAATTTAPTNDTTTKPGDSDSNTAVSHTTSPLLLLLVVV
ACAAAAAVVAA*
>Tc00.1047053511255.130|S082|A---YKEC-|17
MMMMAGRVLLVCALCVLWCGAGGCAEGEDAEDDGFMSGGKGLPRNPENVISAPEALGAPKPHSGVREEE
SLIPEEVPPQTTEEISEDDAEDEEENSSEEEAKGGKINDSTKRMKDEEKKETPEEEPLPVKNSHSPQVQ
EELKEKDNTEPKTRNENKKEEGPPPPVSTAQPTTLATTQTPEIKLPGRKTPHEDPEGDASQKGLKDAPT
LTHQKNESSLSQAEKTAEPPEDPSQDIVAEQKGQATATENLTENAPATNQAETTASSNSTSGSGETRIT
ADENTANAQRPNPNESHDDLEGSDTHPAPTASEAAPQTAIKTATAHKNGTATPGDSDGSTAVSHTTSPL
LLLLVVFACAAAVAA*
>Tc00.1047053511255.200|S075|A-L-YK-CD|1
MAMMTGRVLLVCALCVLWCGAVGDARDNRCVEDDGNVLTHTHNGGNEGLRLKADFGLISTRMGLIKAVA
AVDGGDGAGNDSLENKDKSPQGGVLAGTKDNEAPGAGGVQGAAGAVNGQLPAAGQKGIENKNVDPGRNA
ATDSQDQNNDHLSSSSGSTPSRSGEKPSSTGTSEMTQLPKDTVTKLDADLQDKRESSEGIKAEETEEEE
RQKIKAHTGSSESKNNGGETTPPPLTSSDEESPISDQENSQNSKKVKNEATPSRSKTASEAPAPPSEDA
TQGQHSHDTDTEDPTKNAATGSPVEPTTPSTSASGSGDHVHNKVDEDDAQRHEGQHDSLETVNTNVVPT
LSERASQTPETATDARTNDTTTKVGDSDGSTAASRTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511255.280|S039|AG----EC-|2
MAMMMTGRVLLVCALCVLWCVAGGVYARDRDNNAVGGCVASGGFGAKTSYVKSGREKTALTLPLRSILP
IPAIQAEDEQEARESEEENTLGSVGTTGPGSVSGGGHGTVVPGVAGDSGGGPNLKSPSVDTPVTHGGGG
AGSTGGLSSTSQGNSQGVLPEVGPKPQQSSLLEEKVAAVAPTLVEPPKNSAPAGGESVENDAQSRADRQ
PRLDESTKGKLNLDPTEARALPGDTNQTLQGGEKAVPDVSKATEPEPKTQKETEPSEDKNDRHNTHAST
KSPDVPKGNNAKEGNNEDPAHTPVTPQSTSNGSQQLAAVSPSTGTPTSNEEKSTVAKETEDPQPSDTSQ
TEKRQTSGNGKVDDSDSSTTLSEAAPQTAITITAAQTNHTTTPGDSDGSSTAVSHTTSPLLLLLLVACA
AAVAIV*
>Tc00.1047053511255.330|S068|A---IFECD|10
MAMMMTGRVLLVCALCVLWCGAGGGCSEAAPESPATGVSGKDNNLEGRNNTTDGVGGGGQTGQQEASQT
AAASLVPVSGTAPNPLPAQQSAAKASEVANVTTEKNKDTTKKEGEADKHEKLKDEEEEVDDGKEEDGGE
EKKKQEEKDDTGTTKTKSAGGQEEPISPSRVEEASNKTKPQSTQKTGDKDPAADGAGTQEEKQKENKEA
NPKETPAEATAMKTTTATTGDSDGSTAVSHTTSPLLLLLVFACAAAAAVVAA*
>Tc00.1047053511255.360|S004|A---V-ECD|18
MAMMMTGRVLLVCALCVLWCIVAAVNGGAVAAMESEEESERLPSGRQDGDGRGHQESEDSVQQESETAN
ESLGAGKGKSPKKQDGVVSTQPINSDRTVIETETERGKSKEEGSKETTGRIVTPKRDEKITELTSTTEE

DRKKASPPAERAQTKDEITPGVTPPAKNENSAGILSATPGKAMVIPEGNSKQSEGGTNPANGLATAMPS
TKKGEAPEALTSQPTKNEKAEGDSTVRRNTEKPIPEVTASVQKTEILLDDEEVTSNQRNEDLASTTGNQ
EGEQSDFHAESTPKSISAASNAANDDADTDTDQGIPNNDSATGGAVTEGRHQDGKKEERAEEKTPLKSV
PIINDTATTGDSDGSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511255.540|S092|AGW-H--CD|1
MAMMMTGRVLLVCALCVLWCGAGGVYARDRDNKSLGGCIASGVLGENQFHLSSGFEKTVIKVPLRSTLP
IPAVESSTEDSIVSAVNDSGSSENSIPGDSGLAGAGTPGAGGPSGLPGAGGGGGSGSVVTGGTASGGDN
AGDVSSGPSGGVGGGKNDSAVPLSPSGVDSTPSSSDGEAGSPNSNSSNTVGESPREDQSPDATGTHNSS
PPDEPAEMTSSNEDARQEKEEKEQHEHPAENDEESAKDKNAVNKNTTENTENVDSSTSVSQNISPLLLL
FVVACVAAAAVVAA*
>Tc00.1047053511255.630|S030|A------CD|31
MAMMTTGRVLLVCTLCVLWCGAGGRCENSVTAPSESGVNNPIIAPVPTKGGDLPKSNKVEDSKPLEDDD
NHDPVNLPEQESCKNDSTKSPKCTEGPEVVIDSSLDPVGQGENNEVQNSGIPASSEKDMTLKDQELQER
LQDRETLSREPATVKEPKVTMSAEHSSLPSPSKANQETVSSADIYGVGIGTVQRDNMPNTLTGNDGSKS
RTAQPDSASINTQTSVDENTSSPETAPHVNTAADTDSAGSTTAALNTTNTKKENNADSGGSLAASPAVG
TNTATATTTTTQDASEFSKDGVKLSTDDVEQNAFKTNSDADSGTTETAAANSEVPTAANNATNITSNTE
TTADSDVSTAVSHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053511255.670|S030|A------CD|31
MAMTMTGRVLLLCALCVLWCGAWLCDATQTSSSAPHRDNAEETMTPEEVTKAIEKLTEEVLESIRLSCR
MSFITSVNATLPAHDDTEVEKCVNKTAVEISGVTSRGRPAAATTDANLASPLPSSSSAASALQGQAQGS
PGAAPESVKPPQTDPVNNEQLSEVPASTDGGAGGGGELADRSSRTPTDVARTHEARPAVNATSIPTATQ
GDSEKSPANTTRTRETNETGDTDGSTAVLHTTSPLLLLLLVACAAAAAVVAA*
>Tc00.1047053511255.690|S099|AML-VFECD|25
MAMMMTGRVLLVCALCVLWCGAVFGYAMEDYCSEGGGNGLRHTSNGGDDGVSLKSDCRLLSARMALIKA
VEAEEAGSGLSVTLPPGKPKETSLDNNQGGGAPGLGGDLGVEGQPEAAALQPTPGGSGTEEQVTELEVV
DPHDKNVAGDKKEQKDVNAGDSQHQRADQSSSSSSSSGSSGTENVKQPALKENSKSNEIPDKPPQEEEE
EEEKDLRSKSDGREEEAEEKETEEDKKKASNQAPTETPGGPTNKEEIQTATTETNGQPSPEALGDVKQS
EEVQDEKDSNNNSQTKSVDSIAANQPNEPSADHGESGPLSPTANGDAANNDSERSTQTTGDYGPAADVA
GTAEGKQNENKDVNPKETPVTATAMKTTTVTTGDSDGSTAASHTTSPLLLLLFVACAAAAAVVAA*
>Tc00.1047053511255.169|S041|AG--H-ECD|1
MAMMTGRVLLVCALCVLWCCAGSVYAGDRDNNAVGGCMASEVFGADLSHAPSGCNKPGITVLFRSTLPI
TAVVASDEEVTSVTMQNDLGSRENSNAAGPAGPAGPTGPADLADPADPAGPADPAGPADPAGPAGTAAA
GVPGAPGGGGGGGTSLGGGGTDEISSVSSGGENEPPPPLLKAENEAIRVPTVGEDEAKKAPQSHDNSVE
QHSGENQEHLHEEIRDQQKKQEQRQEQHENNINHEEGEEKQQQQEQHQQHDHSAKNSDGPTKNETTVGT
NATASTGDSDSSTAVFHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511257.90|S043|AG-----CD|27
MAMMMTGRVLLVCALCVLWCGAGDVYAGDLDNRALGGCMASGVLGMNASYVPNGCNEYMPTPPLRSALP
IPAIQAEDGQVRDTAPGSGSGVGEGGGSPGALSPAGAAASPGGSSGRESDSPASSSGYLSSQSDGAVMK
SSDLSTTHSGPQQEVLQQEATETHDPSLSKGLTQEALPDVQQSQISTSENIKTGCGEEASNCEDEQSVE
KATLGKKDLTVAKAQKPPATQNTKSKDNEEKPAEASSTESQNTEPQQEIKTPVDESDSTSTDAFTAVAT
RSTSAGSQEEATASSSNGSHSPLQGEVFTGTDTPENAPSPAAAETEKRQGENVTKDGDSDGSPAVSHTT
SPLLLVFACAAAAAVVAA*
>Tc00.1047053511259.180|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASDGGNDALVMQNYSNSRENLESGSDSGGAFGSNSAAGEGAGSGEGAGSGGTPAPAAPPPAPPA
GSSAPAVTASSPPGPAAPGVDPSAGSSGGTAGSSGTNSSNTTGDSQTGNHSSAAAAHNSSLPEGTEGTT
SGTGHTRQEEKEEEESEMQQKSDETQVQQQQQHEHPAENGEESSKDKNALRTNATANTGDSDGSTAVSH
TTSPLLLLPVACAAAAAVVAA*
>Tc00.1047053511259.220|S012|A----REC-|10
MMTGRVLLVCALCVLWCGFSLVSADTGDDREHSGQGVVGSVGQPSSPVGGHGDNGVVTDGSSLSSGSHL
PGSAPTGGKPSLPGVGECVGLTKSKDALTLAKEGHEFVRDQHELVPQVSHHTDAGTGGKSDLSAPEQSP
NAKTELENDDGVCGDDAAAAEGEVITTVNEEQLGGSSTSDSHPPAADRGAKEQEGTVEQAASTAALTPV
VGRETTPKGDTEEDSPEDKATTGAGITQDIPAAGQQQTHSSSTSTTGNGPTSTLGKGRAAEDISNNNER
SGKALLREGAEHETVAGSQSQAIPAATARNTLGTTLPGGSDNSTTITTAVRSDTGTEGTPTSNHPNRQS
IEGATSPGMNSDGEAASAKNYDTVPQNAGIPTTKAIATAKTNDAASHGDSDGSTAVSHTTSPLLLLLLP
VACAAAAVMAA*
>Tc00.1047053511373.30|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCGAGGVYARDVDTNALGGCMGSGVLGENGSHMPDGCNKTAITVPLRSVLP
ITAVEASDGKGASPSGSGAAGASGASPGASVAGGTGGGGDSGGAGGGSTGGHATGSVPSGSSAPPAAPA
PPAPAGGGGGISSGSSAAASPPSPPGPSAASGPPAPPAGSAPAAAPAVDSSAGSSGGEAGSSGSHPTNT
TGDSSTGDQTSAAAAANDSSPAEGRAGTTSSTEHTRQEEEEEEEEGEEEDHEKQQQSDEAQVQQHQQHE
HPAENGKESAKGKNAIRTNATANTGDSDGSTAVSHATSPLLPLLLVVVCAAAAAVVAA*
>Tc00.1047053511399.50|S121|ANQ----CD|9
MMAMMMTGRVLLVCALCVLWCGVSVVAADVAGGGDGGADEYFVLRWHAQLRRECAEAFGRRTEGRKDVF

TVDDCVRRGMDGVRAFGDGRRVWRRQRSAVVAGDDTTDDDSTRGSSSEVQTETETGSLDGRTPKPSVKP
IPGEVPDGQDSGTISEASVPTINGTGENLDGEEEEGDVSQDESQEDRDGEDEAVDAAVGNGGSETSHTE
HEEEKERVKEEKAGSTTNEREGDENNAAGRRPPQGTAASRPALPVDVSNPQNPVLGQDGAGGEKAGAGP
VVLPQAAGLREAERAPAKLTPGGGAAGKETEKQKGTAEQVAAKEVQTAVEDSSAEAAAAGKDSKGEKEE
ENVNEAAKEESHGNVDEEAAGKNGGNATKKLQKEPTDDEAKTKKRNEQKEAENANNTKEEPDEEEVKKA
AQEEEAADKEKMGAARIPTKINTTTPENSDGSTAVSHTTSPLVLLLLVVVCAAAAAVVAA*
>Tc00.1047053511401.100|S044|AM-----CD|2
MMAMMMTGRVLLVCALCVLWRGVSVVAADADDCVRRGMDGVRAFGDGHRVWRRQRSAVVAGDDTTDDDS
TRGSSSEVQTETETGSLDGRPPKPSVKSIPGEVPDGQDSGKISEASVPTINGTGENLDGDEEEGDVSQD
ESQEDRDGEDEAVDAAVGNGDRETSHTEHEEEKERVKEEKAGSTTNEREGDENNAAGRRPPQGSAASRP
ALPVDVSSPQNPVLGQDGAGGEKAGAGPVVLPQAAGLREAERAPAKLTPGGGAAGKETEKQNGTAEQVA
AKEVQTAVEDSSAEAAAAGKDYKGEKEEENVSEAAKEESHGNVDEEAAGKNGGNATKKLQKEPTDDEAK
TKKRNEQKEAENANNTKEEPDEEEVKKTAQEEAADKEKMGAARIPTKINTTTPENSDGSTSVSHTTSPL
LLLLVVVCAAAAAVVAA*
>Tc00.1047053511449.30|S008|A-----ECD|43
MVMTMTGRVLLVCALCVLWCGGTVLVLAAGDGDGDGRGVDSEPLLESAESAALLPSSPESRVELKVVSN
PPPKHVEEVHTPAKESSAEEEEAGEEEVTVKSEEGQQEDENSLQVNRRKTPELLINENETPQAREGEGS
LTAGALEESPTTPGPQAPTLQVPPPSPSQASVVGEGDGGLVGIGGTSRVTGEATKDPKGSEGPISGPPS
GGASSSTTSNDGDASRKNGGAPSTQDTTSLKNNEQSGPTTSSGNAPLNRGTPERSTPDAKRHFSETQEN
ETSRLPDGDANYSAAGQSAVGTKGSSGVSTTASNAPTTPLPQLPAPPVPTVSTVTGAPAEKPTAEQSPP
PADSTTGEGLAATTTAQTNDTATPGDRDGSTAVSHTTSPLLLLLVVVACAAAAAVVAA*
>Tc00.1047053511451.90|S080|A---YKECD|24
MAMMTGRVLLVCALCVLWCGTSGGRCDEDVRVTEEKKESSGDLQPVTPVAGAGKQHAEPINQDSDLVRQ
PLVKDLEGPLPKHQTDDKFLGVVDNEDDGTGKEKEEGDKAQEGAPDIHTQEEEEVSPPPSPLPPAPLQS
PPPAAASDETQPGGGTGADSSGGGSNGSGSSIGGGGSNLETLFLNGGSQSAFGSLGYDGETGSFSGGAG
KGGVDIGSPRGDFSDSSLSADGTFLSPALDAPSSQDTQSSENVERSKTMPAGLPLPNVNALKGPESKAG
SLPPNTQEKAKFSDAGGGAAGNKAKQSDVETDDPSSSFANTGSTTASSISRTIPRSATSNSCTGKSGQR
SLTTAPRTSEASKREMQNKASSPNKTGSESPDRPSKDGMQEQKDKVTTQLNTTKKASAGGLAETTATSI
SANPSGDVQNREDEDDARQPKPNRVQDDAEAGNTNVAPTVSEAAPQTLETVTTRKRETNETGDSDGSTA
VSHTTFPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511451.59|S043|AG-----CD|27
MAMMTGRVLLVCALCVLRCGAGGVYARNPDNNSLGGYMASRGFGRNKSFLSNGSIKNLSTPLLLSASFI
SAMQAEAREGKVPSAKVTDSHLSGATGRSPAFSGPDAAIARPTVPGHVPGAAIPGADFSAHVPAFSGLG
SAGPVHGPVSGADAIPGAAVHGHGAGPGHGAAAFSGLGAAGPGAIPGPAPVRGPTFSGPDANIFGAPVP
GNGPAAIPGAPVPGNGPAAIPGAPVPGNGPDAIPGAPVPGNGPAAIPGAPVPGNGPAAIPGAPVSGHGP
GAIPGAPVPGNGPAAIPGAPVSGHGPGAIPGAPVPGNGPAAIPGAPVPGHGPAAIPGAPVSGHGPGAIP
GAPVPGHGPGAIPGAPVSGHGPGAIRGSLRGSAVPGDDAAFSGHAAAVPGHAAGPAGAGDGPAFSGLVP
AVPGAGHSVGGGSEPPDSRSVVISSSQGGNGKTAPVSVSSDEQIVSSKEVLAQKETGSQGTSSPEGQPT
VSSNTEKQGNNSASAGSHSLGHDAAGDELQDSLEGQKKNDHSQTNETKKSSGGQNTESQSSGGALSEVS
NTTTHGIKTQQPKKNSVNEKNYSQNTDASHTTSPLLLLLVACAAAAAVVAA*
>Tc00.1047053511487.170|S001|A---H-ECD|18
MAMMTGRVLLVCVLCALWSVPADGDVVVSGGDDSILKELFIPVARLQLRQEQRAAEAAADAKAAAEAAA
KAGAAAKAATEAAEKAKAATAAAKAAKAAAKTAAAKAKEAEEAAEAAKAAAEAVDTEEKAKAEAAKATA
TSAATKSTTASEAAKEAKAAAEAAKAAAEAAAAKAEEAEAEAAVKAAAEAVATATEAAEAAKVAAEAAA
TAANAATAAAAADKDEAEEEDDEAAAAAAETAATATLIATSAAKEAAEKAEKAKAAAETAEAKAAAAEK
AAAEKAKAAATEADAKARAAKTAEAAAEALRGTAVGEEGGRTAIHDQDNSVEHHSGEKQELLQEEGPER
QEKEQHEEQQHQQHEHSARNGEESAKDNTANGTNATAITDDSDGSTAVSHTTSPLLPLLVVACAAAAAV
VAA*
>Tc00.1047053511553.10|S004|A---V-ECD|18
MAMMMTGRVLLVCALCVLWCGAGGVFADEVVPVVEPPVISASGGVVTDKDTGRTAPGGAGNPSVEKTEL
KKFEGSAPGISSLEAASEIESTKQQTQSDHEHKDPVTPSQSSGEQRQDEQNEDPPEEPGASLGQEERKH
ALGGVPERNNPPPASSNNNTVSSNSEERREDTSRSTEIIVAAPSDEGHERENVTPSLEQPLEASTAAPA
ITTQTSSITPPDESGSNTVKMSEASPQSTGTTQTNHTATPGDSDGSTAVSHTTSPLLLLLVACAAAAAV
VSAWE*
>Tc00.1047053511553.30|S122|ANQT---CD|3
MAMMMTGRVLLVCALCVLWCGVFGIVAYGACGGDADGSAVEYSLLRWRAQLRSECAEEVSRRTGDGANA
SAVEECVRQGTDGVRAVVDGRGHWRPQQFVVVAAENAEELEHNHESSPQTLTGSVAQLPDQQPLESSPN
SVPGSAVITTGEGKPTSSAQPPGTPDKGSEGLIKKESDDEGTKEKSEEEEDEEVEETDEEEDDNAGSGT
SDGSQEQGKQKAGTGQRASGGTGKENGNVVAGNKLTEAAAASPPVVSVDVENPKSVELTRDDVGGKRQT
HEKTVQEPPAVKLRENVAAEIISTEDAAEGEKQKAEEKAEETETKEEQRTTAEKLKEETPTTPEKTTKE
EQKDKEVQHVQSKNEEKETDGAEPTAKKEADVEKTAAFKNINMNNITKPGESDSSTAVSHTTSPLLLLL
VACAAAAAVVAA*
>Tc00.1047053511553.100|S007|A--F-RECD|2
MAMMMTGRVLLVCALCVLWCGAAVVVSSEPDVDGTSGDSASRGGISLESPPTVLSPLPPVKSDFAEDEG

EGVSGKEEMERSSEEEGSAPVLDTKKSTPIKPQQEATHTLAGKTSEGMDGVAGVEGGGKEKKAEEKKDD
KSKEKPGSTLLTVSGSNLTGEQNPRVHPPGGTQESEVVNPLTDSSPGIGVQQQVSLGLLEGAPAKSTTD
ANPSSLSTGGRGFDNGEGREDGSGITELPAAREGQIEMEDGGRKVKSTTGVEKELQSPVNKAANTSETV
INGYRKSRPTAATALQSDDGSESNPATNGLNHSSSEGIAHLSTTPDPEDASEGTENATSQSAEIPTAPI
NTVKTNDTAIPGDSDGSTAIPHTTSHLLILLPVVACAAAAAVVAA*
>Tc00.1047053511553.140|S082|A---YKEC-|17
MAMMMTGRVLLVCALCVLWCGTSGGRCDEDVRVTEEKKESSGDLQPVTPVAAAGKQHAEPINQDSDLVR
QPLVKDLEGPSPKHQTDDKVLGVVDNEDDVTDKEKEERDKAQEGAPDGQTQEEEEVPPPPSLLSPAPLQ
SPPPPAASDGTQPGGGPGADSSGGGSNGSGSSIGGGGSNLETLAHNGGNQSAFGSLGYGGETGSFSGGA
GKGGVDIGSPRGDFSDSSLSADGTFLSPAPDAPSSQGTQSSANVERSKTMPAGLPLPNVNAPKGPESKA
GSLPPNTQEKAKCSDANGGAAGNKAKQSDVETEDPSSSFANTGDQTVEKTLLLPQTPAVLLPVPSAELS
PEVPPVTPVQANPDGEGGLPTAPRASEASKREMQNKASSPNKTGSESPDRPSKDGMQEQKDKVTTQLNT
TKKASAGGLAETTAKSISANENGDVQNKEDEDDARQPKPNRPQDDAEAGNTNVAPTVSEAAIQTAETVT
TSRKNDTAPPEDSDGSTAAFHTTSPLLLLLLVFACAAAAAVEAA*
>Tc00.1047053511553.150|S025|A------C-|17
MAVMMTGRVLLVCALCVLWCGAGGGECTEVVKAPAGGAGGGSGGKSAVETAETSTSGPDTSDSPIDVSK
VNQSTEASGGKSLEGNGVNVDQQDVVPGVEEEDGSPSGRLEEIVVNDPGKENTERPLQNKEQEVRQLPQ
SQVHVPQQPQSPPQQSQPLSPSAPQPHTSASEEGKGVGENNTGGEGQPSLGAQDIGNEDSKNHRKEDPL
KSSGIKSQSSKQAQTTVPNTVPPEHKTQNEVLTQEKKTNESQSTDTSTNLPELQKENKEYPASTEGTAQ
STSTGSQEQEAEPSTSEEPSPFEEEQSTGTKTNEDARTPDAAATEKRQTGDNEKVGDSDGSTAIPHTTS
PLLLLVAAAAAAAAVVSA*
>Tc00.1047053511593.30|S066|A---VFECD|8
MAMMMTGRVLLVCALCVLWCGVCAVEVSKADDSETTDVSQGPAKGPLPGPAGRNTGQQESSGQVSQGLQ
NAEEPLDSKNEAVDNQRKDSKIETPTADKSMDDKGEAEKGQIGGGAGGEESGELLEERKAQPDGQGSEG
QARQAGNGSAKVGSHSSATTPSEGERQGTGEQSPPAPSLPAASTQGHGAAPPASLQGAPAATLKTNEKP
VENPRTEPEKEKLSSEDDVSEQTSQGVNDGVEPNNDSQKKENVSVALTEQNGESDGDSESTQPRHLAVG
DASNIDAERGTQIGLPKNNPTANGAVTEGAKRGENKHGNRKETSVEATAITNKTTTGDSDGSTAVSHTT
FPLLLLLLVACAAAAAVVAA*
>Tc00.1047053511593.60|S062|A--TVFECD|5
MAMMMTGRVLLVCALCVLWCGAVMVMAEANVDKGTEMKKDESFDSSELISGIVSAEQHVTQDSVREGSE
NGNQSLGAQTGNGINQDNVVIIASPASTVRGEEEEEEEEEEEEEEEEGESVDAEGETEEIEELKGPIEG
KETSQLTLPQEGVLLPSEPLTTTLNGNPAGTLNATPAKGQPRSDDGSAQEEGLKLPTLKAPAAPAAAAE
ATTTQTKDENPSSADDPSVQHVEASQHDMELRSASRKEGTIPTTVTKTDGPTEVNAESTPTSPSASKGA
ITNDADEGNEEGIQKHDQAPDGEATKEAQQGENKEENTNKTATLETAAITNDTATHGDSDGSTAVSHTT
FPLLLLLPVACAAAAAVVAA*
>Tc00.1047053511593.80|S072|A---VFEC-|6
MAMMMTGRVLLVCALCVLWCGVCAVEVSKADDSETTDVFHVPAKGPPPGPAGRNTGQQESSGQVSQGLQ
NAEEPLDSKNEAVDNQRKDPKIETPTADKSVDDKGEAEKGQIGGGAGGEESGELLEERKAQPDGQGSEG
QARQAGNGSAKVGSHSSATTPSEGERQGTGEQSPPAPLLPAASTQGHGAAPPASLQGAPAATLKTNEKP
VENPRTEPEKEKLSSEDDVSEQTSQGVNDGVEPNNDSQKKENVSVAPTEQNGESDGDSESTQPRHLAVG
DASNIDAERGTQIGLPKNNPTANGAVTEGAKRGENKHGNRKETSVEATAITNDTARTGDSDSSTAVSHT
TFPLLLLLLVACAAAAVVAA*
>Tc00.1047053511599.90|S107|ANP----CD|1
MMAMMMTGRVLLLVCALCVLWCGVSVVMASNVGGFALHADISVLFGRWYSLMMRDCESTSAFKNGTVNE
SAVGECKREAKKALCDFFYGDHSGEHDASHLHSICLPDVGTGGAVDQQAQEQISTLRETGKPAPPTTPQ
GLSEELPDPPPIPALEGTPASAGASSQAPPIQASTEPTVTAKQAEPNTAGSVPPTQSQGGPETMRPPQE
PPKLSSIPDTGTQRDPPTEDRAEQTLSPAKANDNSNDYNEEDTAEESTIDTPASGAVQKEGNESETPGS
GLKKTKTPHTTVEGSNTVKPGDGESSPTGPPAGESDAATTTTTNNHDPRSLNNNGNNTFTEEVDQKEAT
RKPKNAPDSTDTAAAKSEASATAINISTNTTKKTTTGDSSTAVSHTTFPLLLLLVACAAAAAVVAA*
>Tc00.1047053511599.120|S035|A---V--C-|1
MAMMMTGRVLLVCALCVLWCSAGCRCDEEEDTALVGDLPANSESGSGGPEKDTDHTVPGGAENPSAQQS
QLNKVRGSPPGISSLEAPSEVESKKRQTQSDPEHTDLLSPSKSSGEQRQDGTPERAPGRPETSPNQEDN
KDVSIVNQQNIDPPSPSGNDDVVSHNSGERTEDTPSSTEIIDAAPSEEVEKRENVIPSLEQPRGTSTAA
PAITTQTSSTTPTDVGESNTVKMSEASPKSTGTSQTDHTTTKIANSDGSTAVSHTTSPLLLLLLVCASA
AAVVAA*
>Tc00.1047053511607.40|S066|A---VFECD|8
MMAMMMTGRVLLVCALCVLWCGAAVVAAADTGGVEMEGAEGSESLPSGPSDGDEGGKQESEGSVRQVSD
TANESFVAVDGKNSKQQDGVVTTTPTKPERTDGGTETEEIKRKEQKENPEIPNKDDKTTQLTSRSEEKE
ETAPSPDEKEEPPAERGKTQGAALPGASPGVPSRAQNENSAENLTATPGEERVLPEDHSDQSQGGKTPA
DGLAAEMSSKEKGKAPEAPPSPLEKNEKPEGDLKATTNTEKNNLENLASVKKTESILEDKEATSNLQKE
GLASTTGNQESDPSDGYAESTPTSISAASNAAKDDADTDTDKGIPNNDSAAGVAATEGRHQDENKEDNR
KETTPLRSAAMINETATVGDSDGSTVVSHTTFPLLLLFVACAAAAAVVAA*
>Tc00.1047053511607.110|S091|AG--YKECD|14
MMMTGRVLLVCALCVLWCGAGWVYAREFENNALGGCMASGALGASWYHMPSGCDKAALTPPLRSALPIP

AIKAEASEDDVPLREEDDSISTSGAVVGTAMPGESDGAGLVIQSGPPAGGVAPTTPSGGSSTQNMESQR
AVQHLEPTDPAASVLLKVEVPGEPMPIAEESLSNTQDRPEIRVTGEDNTEREKLRSAVDTGDRFSDQPK
EPTPPLKTTPQLQPTTPVPPPSSKASTTELSSGEGNPQAATTDTQTPTPTIGKTTTSETATDYKAPKTP
SKDDEAEQHSKERVPSDLMKNTANGHPADTKASSIPTIGSGDVQRNADKNGNDAQRPDTKGTHKDPAAV
NTNDTLTASVAAPQTTERLADAKTNHTVTPGDSDSSTAVSHTTSPLLLLLLLVACAAAAAVVAA*
>Tc00.1047053511613.10|S052|AG-TH-EC-|1
MAMVMTGRVLLVCGLCALWCGAGGVYARDVDSNAVGGCTTSGELGTGLSHVSSGCNKPGITAPLRSTLP
VTAVEASGEEINSVTMQNNLGSSEISNAAGPGPAGPADAAGAAGAAGAGVPGGGGTSLGGGGTDEIPSG
SSGGKNEPAPPPLLETENEALRVTTVGEDEAKKAPQNHDNSVEHQSGQNQEHLHEEEREGEHLQEEIRD
QQKKQEQQEEEHEESIKQEKEQEEKQHQQHENYAKNSEEPTKNETAVGTNATASTGDSDGSTAVSHTTS
PLLLLLLVVVCAAAVVAA*
>Tc00.1047053511613.40|S091|AG--YKECD|14
MMAMMMTGRVLLVCALCVLWCGAGWVYAREFENNAVGGCMASGVLGMRTLYLSSGCNKTTPTLPLRSAF
FIDAIQAEERELKDISQESNSLGSVSIPPPPPLPAPETLEAPPPLGASVSEASGRSEVGPASQADGDGG
GGGSSRISHGDKHPILKVSGLVDKSTSSTTNDGDGLKNTDVESATQKDNSSGTDEQAGKALDLPILPTV
QNPEVLHSDKNKIPPNTQEATNVEARDNGASEGRTGESDVHAKDSSSVSSAKSKPTGKPSLPVQPTGQS
PPTAAGDTRNSTQTNEKTTTSGIGTDSEAPKPYSKNDVAEQYDEDRDPSDLIRGANTGHPTDTASSPIS
TSGNGDFQGMANENGDNPERHNPRETHDDPEVGNVNVGPKASQPAPETVKTVTAQTNDTVKPGDSDGST
AASHTTSPLLLLLLLVACAAAAAVVAA*
>Tc00.1047053511613.60|S091|AG--YKECD|14
MMMTGRVLLVCALCVLWCGAGWVYAREFENNALGGCMASGALGASWYHMPSGCDKAALTPPLRSALPIP
AIKAEASEDDVPLREEDDSISTSGAVVGTAMPGESDGAGLVIQSGPPAGGVAPTTPSGGSSTQNMESQR
AVQHLEPTDPAASVLPKVEVPGEPMPIAEESLSNTQDRPEIRVTGEDNTEREKLRSAVDTGDRFSDQPK
EPTPPLKTTPQLQPTTPVPPPSSKASTTELSSGEGNPQAATTDTQTPTPTIGKTTTSETATDYKAPKTP
SKDDEAEQHSKERVPSDLMKNTANGHPADTTASSIPTIGSGDVQRNADKNGNDAQRPDTKGTHNDPAAV
NTNDTLTASVAAPQTTERLADAKTNHTVTPGNSDGSTAVSNTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511613.80|S008|A-----ECD|43
MMAMMMTGRVLLVCALCVLWCGAGGGFCEGALEDEFCSKSYVEALSLLANKTDDEIKEKYCKQDDEKTT
CLKTLRSNIADALKKEKTKEDSAAHRESDISRDTGASVGSSRAKSSKAAGANTAVLSPPPPLNVIGGVD
AQIHGSAGGAGHQQHSDDVRSEAEQRNHPESGRCSEGQAALGECIHVPAGDAAAEGSRQHRVDVQGKKI
HKKEEHTPEAGLKSAEAREGTEEAPATPQDPTNTAESHEDKSQRVAAPATIPAENTSSGSSQEQTSQSS
SPSGSETTGSLDNEVPEETSINTQMSGAPFNGEGKHRESTAGNEDTTKVVSAAVQSNTATPGDSDGSTA
VSHSTSPLLLLLLLVVACAAAAAVVAA*
>Tc00.1047053511613.90|S015|A---H-EC-|9
MAMVMTGRVLLVCALCVLWCGAGGCAENDAGGLGEDENTELKGIASDGLQRDSHDSETGKKQLTEPKAA
EEPLIAPGGDHIDKQGSSVVQIKADRDGRREEVEPTGNVNGSQKNSKDALDTHQTEITEVRTKVEGTPP
SPPEGGGGPTQPKSPEISRAPVQSPEQLFPPAAHAGEKSLRAPTALSPITSVQPPLLPKGKGETDGVQP
GPEDKSNEPKVKVEPQVHGNEGQHQSTQHHEVPQEKELGAQEQNTQNQIINEQHESERLQVQQEKEKEK
QRSEEELEQREHLHEEEREGEHLQEEIRDQKKKQEQQEEKHEEPQEEHEDSIKQGKEQDQQKQHQQHEN
AAKNSEEPTKNETAVGTNDTASTGDSDCSNAVSHTTSPLLLLLVVACAAAVVAA*
>Tc00.1047053511613.110|S030|A------CD|31
MAMMMTGRVLPVCALCVLCCGLVSADAGDDDFSGGHGTLGGSGVGADGRPSVPVGSDVSTGGTKDECSL
GSGGGSPVSASPPCKSLLSDAENPGGEVFNDTKKVLSRVEGNSNVEQDPPQPRSHVVSTAEVLAPGQPN
SEAQEQSSGKLRTEEGRNNGDGGTTVKEEVTGVESRDTADLSPNDSRPPKAARPVTGEEKGTGKQAASK
ASLTPAEERGTSAATDQKVDSPKEEAASSAGATKNRSPVGQQQTEASSPSKRGSTSTLTPEKEPAEELH
SNNNQPPGDAAPTEGTQHETLPGEKMQTEPATTNNKPIDAAPTGDSESSPTAPPAGESDAATTTTTNNH
DARSLNNNGNNTFTEEVDQKEAARKPKSAPESTDTAAANSEASATAINISTNKTNKTTTGDSSTAVSHT
TSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511613.180|S030|A------CD|31
MAMMMTGRVLLVCVLCVLWCGAGVFAEDPSPDAGASGHSASIVGGLQEITQNGPSLLGEPSSETVTPKV
EGGAPLGSAVKFPGRSEQEVDALEGEDLSDKSFDKKISKDKNAQLSSGPPADNDSSPTGVGNAGGSGLP
SSGASGDLTDSTDDRAGGAGNVGHINPPAELTPPHPPEPNSKGGRAPPAVPNLNTSGSQGKIAAQGQPS
AKQETSLATQPQVSGMRPPPQDEKQSGGKIENSPEPGEAPATSDTTLVTSSGTEGQIPQSSSPRSGSDD
VTHQSEQHHVAPLGNTQQDDAAVADEERRRGETGGIPTDSHRGPEAAAANNANAKVAPPTEGSDGSTAV
SHTTSPLLLLLLVVCAAAAAVVAA*
>Tc00.1047053511625.90|S040|AG----ECD|2
MAMMMTGRVLLVCALCVLWCGAGGVYARDIDNNAVGDCMTSGVLGTNCSRVPSGCDKTAPKLPFWSALP
ITVLQADAPEGKELASQGGNLNSSESSGTGAPEKASENPDGIPGTDDSSSGGSFGGAGGNVARQEAEGT
DNTPSSPPVTPVTPQAKETKAKEVLSSSLPPPAGGSAPEPNGTHNLPGTNAGNSASENEPGSNSLERPS
EDGEAGQQDKEADTQGTQETEGTQGTAASPISTSGSSGAQIEADADDDDSQRPNPEGPQNDGTEAGDTH
GPSAVSDAAPQAAKAIAAQTNGTVTPGDSDSSTAVSHTTSPLLLLVACAAAAAVVAA*
>Tc00.1047053511645.10|S082|A---YKEC-|17
MMAMMMAGRVLLVCALCVLWCGAGGGGCDETPQALLSGSGGGTVVGTGAGPSGGADNGLFASEPNGESE
GDRLERTDLGQINSSPRGGTVGPDNNLAVMPVGSPVTRNQVLSNEALSLQSPPSPKPSAPELQDLPEGP

PLSGGSQGGEADNAVGGVGPSGSSSGSGVKSMVSASFSAGMLSPPNPVDGDVLQGGKGTTATLSMDSSE
KSVKSQSAEPPAPAQPNLDRQEASTSNAENHSPIKPHTAGNQVVNGGATGKENTQRAAVTGGPSSDTRP
TTLQPAPQEQPKTELIIVPAGKERATDPRTREKEERDSNKAPPPPASSAGGTPAAKELQISTEEMHQTS
PSETQKLLLGQETPSKDDAEDQNTEGTAASDSVKDEAASSLVETTASPISTSGGADTKSVASEDADNAQ
QPDHKEAHKDPEPQNTSPAFTATEALPQTAIPLTTAPTNDTTTPGDSDSSTAVPHTTSLLLLLLVACAA
ADAVVAA*
>Tc00.1047053511797.120|S008|A-----ECD|43
MMMTGRVLLVCALCVLWCGAGGRCDGDGSGITEPQDQPSKASQSLSQGGHAEQLEITNSIGGVVNNSNE
LLNGQDGKNGSPQTGSVKQPATDNDRMEAEEEKAKGKKVKDEEIKRDGKEKLQDDSEGTKEHEGPIEAK
RNTSPPTAANKLLTSEEEPVDPAAGHAGHTGQAVKPPQLPATPPLPAVGPQIPLKAASPQVSDETQPFG
SSVEGSKEGGGVDLKTPASDSGNPSSVVSLFSGGGTSGGGGGSPQGDSSDTPLSAGGTSLSSALDAPSV
QETQSPESVRHSETVSPGTAVPNEHPRERSESEAKKNFSTSQEAAKSPDDDGDATEKEKEKGDVGLKAT
TSPTPNTSSPPVTQTTPRASSEEPSPTTEVQAGEETSTENVTIAMRNATENTGDTDGSTAVSHFTSPLL
PLLLVVACAAAAAVVAA*
>Tc00.1047053511797.200|S043|AG-----CD|27
MMTGRVLLVCALCVLWCGAGGVYARDILKNAQGGCVASGGFGKKRSYLWSGFDKDVPTPFLRSVLPIPV
IQAGDSEGVSSKENNGKNLILGDGVSGAEITAGVGRGGGGSDGRGGVNSAGEEGAGGSHAGSVPGAGSS
PPAGGPASGGGSSPDRSANTGTTVSLSSPSQREAQQEVLQSDEAKDQSRQLLDGKAPDTPVAKTQSRGS
GPARGQGVEDTSTLSGKEQHSSEEPRKEDGDSDTLQTVDLAEDPNTKIEKKGKVLPELSNAPLPEPKTD
HPKTNPEKEKKGSQNTSASTDSPAKQEGNNEDPVSTSDTAESVSTGSQEQAAATSSNESSSPLQKETSI
EKTTVENSQPSDGAQTEKRQSGDKERVGDSDSSTAVSHATSPLLPLLLLVVCAAAAAVVAA*
>Tc00.1047053511797.167|S097|AGWTH-ECD|44
MAMMMTGRVLLVCALCVLWCVAGGVYARDVDTNALGGCMASGVLGENGSHMPDGCNKTAITMPLRSVLP
ITAVEASDGEDVSQQTNNSGSDTNTGSGGAAGASGGGGGGGSGSGGGGSGSSTDDHATGSVPSSSSLAS
PPAPAAPAVSPGDGSAGGHDTGGVSSGSSVPAPGPPSPPAPPEGPSDPPAAPVVDHSAGSSDGKAESSG
SNPSNTTGDSSTGDQTSAAAAAHNSSPAEIPAGTTSGTEHTRQEEEEEEEEEDHEKQQQSDEAQFQQHQ
QHEHPAENGEESAKDKNAIRTNATANTGDSDSSTAVSHTTSPLLLLLVVACAAAAAVVAA*
>Tc00.1047053511843.10|S056|A--TH--C-|1
MAMMMTGRVLLVCALCVLWCGLSVVANGGTDDLVSGRDEKNAEHLSSSDLSLPVRQGEPTAAGGGRGST
NSQEGKEASMSNTGIRLPQEQEVKLDAAPHKPTGNEYENKGPTEAGADTRNQPAPPPPPISLSEEEDDE
LTKATQDQDSPVEQESTQNNEILQEEPGHELNTQNPLPQEQHTSEQPQVKQEHGKEKQRSGQLEQREHR
EEPKDQQQKQEKQDEESIKHEEKQQQQKDEIQDQQHQQHEHPTENEEESAKDENVVRTNVTAAKGDSDD
SIAVSHTTSPLLPLLVACAAVAAVVAA*
>Tc00.1047053511875.80|S030|A------CD|31
MMTGRVLLVCALCVLWCGAGGGYGWAVGHCAVAELDDAKLAKGMDGEVVLMKRDCVPTTALRGVLTAVP
AAGDSDELGSPDAGVCTSGKQKVDAEESPVAFAGSEPTPSGSGAVPTASSPASADTIAASSTPVSGAGG
AVGPNQQPAVVSGCQDDSSSGGREGKEREEAGSAGCGEEPPVSSMCSQPPLVAVDLTICTADQNNEQND
NASFHTDQQMATQNEDEVPHVPGTRASVQTPPVPAPAGGQPGLATQPSEDLAEHATAPNSGLSRDASNG
DSQEQTPQPQTPTDTKQSLPVLQGLSEGVQENQNNMEDGKKRNQVDSSGNMRNKEHDSATEKLELLTAS
INTRPSGAPGNESDTKSLSGTLRSSTAGTEEQAKAGPMPLRQPKPPEEKVISEELPPTAAEVEAPGGPS
APPPKSLPQSALPSSKEVPDTTQSTEDPHTKGIEPTTDARQNAITEGQAETTSPSSSADDAAANDADES
NAEIANDGSVVHAGVPEEEPHQEQVDGSEKQTSFTSTAKKYNAAIEDNDGSPAASHTTSPLLLLLVVVC
AAAAAVVAA*
>Tc00.1047053511875.9|S127|ANQT---C-|1
MAMMMTGRVLLVCALCVLWCGAAVAVSAADVSVGGDGSAGEYLLLQWRTRLRTECAEEIGRMTGGRANA
SAVEECVRRVMESLHAVVDGRSRWKRQLSAVAAPAPVSPPAAPAAPAEGGGKENPNTVEVDKTRNNEVS
LPRQNNELLVNSGQATTESQKKLPHSETDIVPPSNETSDQGQHNGERRKEEEEEEENDGESEHEEEDAE
EGEKAEEREEDKEEEESEKNTKKEEGEEDEERVDDDALEGMPAGGQEKRNSTSGPEGAPNKTNTEGTQT
PGDSDGSTAVSHTTSPLLLLLVACAAAAAAVVAA*
>Tc00.1047053511921.140|S121|ANQ----CD|9
MAMMMTGRVLLVCALCVLWCGVSVVAADVAGGAGGSAVESLIAGRRAQLRRECAEAFGRRTGGGANISA
VEECVHRGMGGVRAVVDGRSRWRRQHSAVVAAVDSDDKIGEGSDGTLKGLSSSDQMPQAGQGGEEGQEH
TGSLEVTNKLEGNEDSQITGERNVSSDADRPKQTGSQVPAGGQPEDEEGTKSPQPPPPPPPAEPLPQLP
RQPPPGTNTLQSEETHPAITAEKHSKPQDGGHSHETKMPQTKGSTKHGEGASSLQSPEIVSHLSRESTT
PLSTSTGSSGVAGSTVENSGANNPTPPAASVTQHDSEGDTGPAAPPASNTELQSEEIPNAGIIATTYDD
VNDSSRAAPTAERTTAGTRSTQTSGDAGDLERANNDDANDDVAHNGKTVEFEAASGNRDTEADNDEKYT
TVPENATNNTINTEIPADSAGSTAVSHTTSPLLLLLVACAAAAAVVAA*