The Putative Arthritogenic Cationic 19-Kilodalton Antigen of Yersinia enterocolitica Is a Urease β-Subunit

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The gene coding for a putative 19-kDa arthritogenic antigen of Yersinia enterocolitica O:3 (A. K. H. Mertz et al., J. Clin. Invest. 87:632-642, 1991) was cloned and sequenced after amplification of part of the gene by the polymerase chain reaction using degenerate primers, inferred from the amino acid sequence. The deduced amino acid sequence of the antigen showed similarity to small subunits of ureases from several different organisms, including the jack bean urease. Screening of a genomic library of Y. enterocolitica O:3 with a 19-kDa-antigen-specific DNA probe allowed recombinant clones containing the entire urease operon to be obtained. These clones expressed urease activity in Escherichia coli.

Yersinia enterocolitica serotype O:3 strains cause infections accompanied by enterocolitis and mesenterial lymphadenitis (26). Patients with certain HLA types, especially those positive for HLA-B27, quite often develop postinfectious symptoms, such as reactive arthritis, erythema nodosum, and uveitis (26). Despite intensive efforts in many laboratories to identify the bacterial arthritogenic factor(s), only minimal progress has been made. A putative bacterial arthritogen is lipopolysaccharide, which has been found in synovial fluid cells of affected joints (9). Another putative arthritogen is a cationic 19-kDa antigen derived from Y. enterocolitica O:3, which when injected intra-articularly into preimmunized rats triggered joint inflammation (16). In this study, we further characterized the 19-kDa antigen and identified it as a small β -subunit of urease.

MATERIALS AND METHODS

Bacterial strains and plasmids. A Y. enterocolitica serotype O:3 strain isolated from a case of enteritis (Freiburg strain 10543) was used as a source for purifying the 19-kDa antigen (16). Y. enterocolitica O:3 strain 6471/76-c (23) was used for the construction of the genomic library (1). The cloning vector in the library was pBR322 (5). Recombinant plasmids isolated from this library are shown in Fig. 2. Bacteriophage M13mp18 (17) was used as a vector in singlestranded sequencing. Escherichia coli C600 (2) and JM103 (17) were used as host strains for the genomic library and M13mp18, respectively.

Construction of the genomic library. The genomic library has been described earlier (1). Briefly, the genomic DNA of 6471/76-c was partially digested with restriction endonuclease *Sau*3AI, and fragments larger than 6 kb were isolated by preparative electrophoresis. These fragments were ligated to plasmid pBR322, which was opened with restriction endonuclease *Bam*HI.

PCR. Polymerase chain reaction (PCR) was performed by using degenerate oligonucleotide combinations Pr5 and Pr3 (see Results). Amplification was carried out in a reaction

mixture containing 20 ng of Y. enterocolitica genomic DNA, 300 pmol of each oligonucleotide combination, 200 μ M each deoxynucleoside triphosphate, and 2.5 U of Taq polymerase (Boehringer GmbH, Mannheim, Germany) in 10 mM Tris-HCl-1.5 mM MgCl₂-50 mM KCl plus 1 mg of gelatin per ml in a reaction volume of 100 μ l at pH 8.3 at 20°C. Amplification for 30 cycles was carried out under the following conditions: denaturation at 94°C for 45 s, annealing at 35°C for 1 min, and extension at 72°C for 2 min.

Purification of the 19-kDa antigen. Purification of the 19-kDa antigen has been described in detail earlier (16). *Y. enterocolitica* O:3 strain 10543 was grown in brain heart infusion medium at 30°C. Fifty grams of washed cells was disrupted in a Braun homogenizer, and after DNase treatment, the ribosomal pellet was obtained by differential centrifugation. This pellet was acid extracted, and the soluble fraction was dialyzed to neutrality. Further purification was performed on a fast protein liquid chromatography system (Pharmacia-LKB, Uppsala, Sweden) using a mono-S cation exchanger and a sodium chloride salt gradient (0.15 to 2.0 M); a highly purified fraction eluted at 0.3 M NaCl in low quantities was employed in this study.

Amino-terminal sequence determination of the 19-kDa antigen and its tryptic peptides. Two hundred micrograms of protein was digested with 4 μ g of sequencing-grade trypsin for 4 h at 37°C in 300 μ l of phosphate-buffered saline (PBS) buffer, adjusted to pH 8.0. The fragments were separated on a reversed-phase high-pressure liquid chromatography (HPLC) column (PEP-S; Pharmacia) by 0.1% trifluoroacetic acid-acetonitrile gradient elution as described earlier (22). Peptides were sequenced in a pulsed-liquid gas-phase sequencer with on-line identification of the amino acid derivatives (models 477A and 120A; Applied Biosystems, Foster City, Calif.) according to the manufacturer's instructions. The N-terminal sequence on 60 μ g of the whole protein was determined in the same way.

SDS-PAGE and immunoblotting. A total cell lysate of bacteria was prepared by sonicating about 200 mg of bacteria (wet weight) in 1 ml of PBS containing a protease inhibitor. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) was performed as described previously (3) by using a 4% stacking gel and a 12.6% separating gel. The

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Peptide	Sequence ^a	Positions in deduced sequence ^b		
NH ₂ terminus	STKTNSTKAT SEKTDSLKTN RGTKSSAGYS EQNTPLGGxI LAD	2-44 (C)		
Peak 7	AAAYGK + GFK ^c	88–93, 159–161		
Peak 8	TDSLK	15-19		
Peak 12	ALEFDR	82-87		
Peak 15	LNISSTTAIR	95-104		
Peak 20	NTGDRPIQVG SxF	62–74 (H)		
Peak 27	FEPGDET	105–111		
Peak 31	QTLYGFNNLV DGx1TGx2GVVP Nx3x4R	122-145 (W. E. S. E)		
Peak 32	SSAGYSEQNT PLGGxILADT PITFN	26–50 (C)		

TABLE 1. Amino acid sequences of proteolytic fragments and of the amino terminus of the intact protein

^a x, an unidentified amino acid residue.

^b See Fig. 4. Amino acids represented by "x" under "Sequence" are identified in parentheses, as deduced from the DNA sequence.

^c Peak 7 was interpreted in the first analysis as AFAYGK, but reanalysis after availability of the nucleotide sequencing data revealed that this peak contained the two peptides AAAYGK and GFK.

separated bands were transferred to an Immobilon membrane (Millipore, Molsheim, France) by electrotransfer. The membrane was blocked with 10% skim milk in PBS and incubated first with rabbit antiserum to the 19-kDa antigen diluted 1:5,000 (16) and, after washing, with peroxidaseconjugated goat anti-rabbit antibodies (Dianova) at a 1:4,000 dilution. Finally, the bound peroxidase was detected by incubating the blot in substrate solution containing diaminobenzidine (Sigma, St. Louis, Mo.).

Antiserum to the 19-kDa polypeptide was raised in rabbits by repeated immunization with purified antigen (see above) in Freund's complete adjuvant; a panel of mouse monoclonal antibodies was also produced. Titer and specificity of the antibodies were tested by Ouchterlony's diffusion test and in immunoblot. In the latter case, SDS-PAGE gels were run under both native and reducing conditions; this switched the antigen from a 38-kDa thiol-linked dimer to the 19-kDa monomeric form, providing a further specificity control. The antibodies obtained could be absorbed with the antigenic fraction (16).

DNA techniques. Isolation of DNA, restriction digestions, colony hybridizations, labelling of probes, and autoradiography, etc., were performed by using standard techniques (3). DNA sequencing was performed on single- and double-stranded templates by the dideoxy chain termination method using the Sequenase version 2.0 kit (United States Biochemicals), as recommended by the supplier. Primers for sequencing and for PCR were synthesized by using the PCR-Mate DNA synthesizer (Applied Biosystems).

Computer analysis. The DNA sequences were handled by the GENEUS (11) and Genetics Computer Group (University of Wisconsin) (7) program packages. Data bank searches for homologous polypeptides were performed by the TFASTA program (15). The amino acid sequences were aligned by using the GAP and LINEUP programs, and the consensus sequence was generated by the PRETTY program.

Nucleotide sequence accession number. The nucleotide sequence of the urease operon genes yeuA, yeuB, and yeuC of Y. enterocolitica O:3 has been submitted to the EMBL, GenBank, and DDBJ nucleotide sequence data bases under accession number Z18865.

RESULTS

Amino acid sequence determination for the 19-kDa protein and its tryptic fragments. The 19-kDa protein was sequenced from its N terminus to the 43rd residue. Tryptic peptides generated from the whole protein were separated by reversed-phase HPLC and subjected to Edman degradation. Table 1 shows the sequences obtained and a comparison with the DNA-deduced primary structure (see below). These results agreed completely.

PCR cloning. On the basis of the determined amino acid sequence of the amino terminus and the peak 31 fragment, two degenerate oligonucleotide combinations were constructed. Degenerate oligonucleotide Pr5 corresponds to amino acids 2 to 10 of the amino-terminal sequence, and Pr3 corresponds to the amino acids present in the peak 31 fragment (Table 1). The codon usage in the published sequences of Y. enterocolitica was used as a guideline in selecting the bases for wobble positions. Taking into account the 19-kDa size of the intact protein (150 to 180 amino acids), the anticipated length of the amplified PCR product could be at most 500 bp (in case the peak 31 fragment is located close to the carboxy terminus of the protein). Accordingly, if the peak 31 fragment is located closer to the amino terminus of the protein, the PCR product would be shorter. Thus, any PCR product shorter than 500 bp could be considered representative. Chromosomal DNA of Y. enterocolitica O:3 6471/76-c was used as a template, and upon amplification under conditions given in Materials and Methods, several fragments of different sizes, among which a fragment of about 400 bp was dominant, were obtained. This fragment was purified from a preparative agarose gel and cloned into M13mp18, and its DNA sequence was determined (Fig. 1). One of the reading frames was open throughout the length of the fragment and some of the sequenced peptides as well as the amino-terminal amino acid sequence could be identified from this open reading frame (Fig. 1 and Table 1).

The 400-bp fragment was used as a probe to screen the genomic library of Y. *enterocolitica* O:3 previously cloned into pBR322 (1). Nine positive clones were identified. The recombinant plasmids of the clones were shown to carry six different overlapping inserts of Y. *enterocolitica* DNA, ranging in size between 3 and 13.5 kb. The restriction maps of these plasmids are shown in Fig. 2.

Nucleotide sequence. The recombinant plasmid of one of the recovered clones, p19kd-107, was used as a template to determine the DNA sequence outside the sequenced 400-bp PCR-amplified fragment. The whole sequence is shown in Fig. 1.

It is interesting that the degenerate primers, constructed to generate the 400-bp fragment by PCR, had significant homology to the actual sequence only in their 3' ends and that

L T P R E V E K L M I Y T L S D V A F

yeuA MQ

P N S E R P D K L E A I R R A A E R G F K S S K * 841 tcccaatagcgaacgtccggataagctaggggctattcgtcgtgcggctgaacgtggcttcaaatcgtctaaatgacaccttatctcactaaaaattatcgaaattcgcatacgtgtaat M P Q I S R Q E Y A G L F G P T T G D K I R L G D T N L F M Q I E K D L R G Y G 1081 ATGCCTCAAATTTCTCGGCAAGAATACGCGGGGTCTATTTGGCCCAACGACTGGCGATAAAATCCGGTTTGGGTGACACCAATCTATTTATGCAAATCGAAAAAGACCTGCGTGGATATGGT S P F R V I K A D V G I R D G K I V G I G K S G N P G V M D G V T P G L V V G V 1321 Agcccgttatgggttatcaaagccgacgtcggtatccgtgatggtaaaattgttggtagtaggtaaagtggcaacccaggcgtgatggacggagttacacctggacggggtggtgggggggt S T D A I S G E H L I L T A A G I D T H I H L I S P Q Q A Y H A L S N G V A T F 1441 Agtaccatgccattccggtgaacatttgattctcactgccgccggtattgatactcatattcacttaatttctccacaacaggcttaccatgcgctctcttaatggcgtggcgactttc F G G G I G P T D G T N G T T V T P G P W N I R Q M L R S V E G L P V N V G I L 1561 TTTGGCGGTGGGATTGGCCCAACTGATGGCACCAACGGGACGACAGTCACCCCCGGCCCGTGGAACATTCGCCAGATGCTGCGCTCAGTGAAGGGCTGCCGGTCAACGTGGGTATTCTG MADEMDIQVSVHTDSLNECGYVEDTIDAFEGRTIHT FHTE 1801 Atggcggatgatattcaggtttccggtacataccgacagtttgaacgatgtggtagacaccattgatgccgctcgaaggccgcaccatccacactttccacaccg WVPRFFGAKPKMVIKGGMINCCAAAGCGGAAACCTAAGATGGTTATCAAAGGGGGGCATGATCAGGGGGGGCAATGGGGGGGATGGGCGGCATGACCCCAACCCGGACGCCGCGGTGTTCTATCGT PMFGAMGKTMQDTCVTFVSQAALDDGVKEKAGLDRQVIAV 2521 CCAATGTTTGGCGCAATGGGTAAAACCATGCAAGACACCTGCGTCACCTTCGTTTCTCAGGCCGGGCTGAAAGAGAAAAGCCGGGCTGGATGATGGCGGGGTGAAAGAGAAAGCCGGGCTGGATCGCCAGGTTATTGCGGTT K N C R T I S K H D L V R N D Q T P N I B V D P B T F A V K V D G V H A T C B P 2641 AAAAACTGCCGTACCATCTCTAAACATGACCTGGTGGCGCAATGACCAAACACCCAAACATGGAGGGATCCTGAAACCTTTGCGGTGAAAGTGGATGGCGTACATGCCACCGGTACCATGACCC

2881 GGCGACCAACAATGGTCGGGATGCGTGGCATAGAAACGGATTTCATTACTGTGGGCAACTGCTTTTGCCAAAAATACAGGCAAGGAGTCTATACATGATTTTGATA 2986

FIG. 1. Nucleotide sequence of the urease operon genes yeuA, yeuB, and yeuC of Y. enterocolitica O:3. The positions and sequences of the degenerate primer combinations, Pr3 and Pr5, deduced from amino acid sequences, are indicated. Note that none of the degenerate primer combinations perfectly matched the genomic sequence. The sequences of the oligonucleotide pair incorporated into the cloned and sequenced PCR product (see text) are given closest to the genomic sequence. Amino acid sequences of the open reading frames are given by the one-letter code; stop codons are indicated (*). The ribosomal binding sequences (sd) and SphI and ClaI restriction sites are also indicated.

identity in a sequence as short as 8 nucleotides had been sufficient for initiation of amplification.

peptide fragments shown in Table 1 could be tracked to this open reading frame. The calculated size of the polypeptide was 17.9 kDa, with a high pI of 10.2.

An open reading frame which could code for a 164-aminoacid polypeptide was identified (Fig. 1). All the sequenced

A second open reading frame was identified upstream of



FIG. 2. Recombinant-DNA plasmids positive for the 19-kDa antigen probe. pBR322 DNA in the plasmids is shown as a shaded box, and the *Y. enterocolitica* DNA is shown as a solid line. Restriction enzymes: E, *Eco*RI; H, *Hind*III; S, *Sph*I; C, *Cla*I. Urease expression and the 19-kDa antigen expression of the clones carrying these plasmids are shown on the right. Only the *Eco*RI site of pBR322 is shown to indicate its orientation. The arrow above the p19kd-48 map indicates the position and the 5'-to-3' direction of the pBR322-specific primer used to determine the direction and location of the open reading frames shown by a thick line and arrow at the top.

the one described above. This frame had a coding capacity for 102 amino acids. The calculated size of the polypeptide was 11.3 kDa, with a pI of 5.95. An *SphI* restriction site was found between the open reading frames. The *SphI* site was mapped in plasmid p19kd-48 as shown in Fig. 2. In PCR analysis, using p19kd-48 as a template and Pr6 or Pr7 (positions 746 to 763 and 493 to 473, respectively, in Fig. 1) together with a pBR322-specific primer (arrow above the p19kd-48 map in Fig. 2), a 2.3-kb amplified product was obtained with the Pr6-containing PCR mixture while nothing was amplified in the Pr7-containing PCR mixture (data not shown). On the basis of this information, we could map the open reading frames and their directions as shown in Fig. 2.

A third open reading frame was identified downstream of the 19-kDa open reading frame. This open reading frame had a coding capacity for 573 amino acids. The calculated size of the polypeptide was 61.5 kDa, with a pI of 6.33.

The recombinant plasmids were analyzed by immunoblotting with antiserum specific for the 19-kDa antigen (Fig. 3). All of the plasmids expressed a 19-kDa antigen, immunologically identical to the Y. enterocolitica 19-kDa antigen (Fig. 3, lanes 1 to 3 and 5), as revealed by using polyclonal rabbit and monoclonal mouse antibodies to the 19-kDa polypeptide. The host strain of the recombinant plasmids, E. coli C600, was negative (Fig. 3, lane 4).

The 19-kDa protein is a urease subunit. The amino acid sequences of the three open reading frames, deduced from the nucleotide sequence, were compared with the Gen-EMBL nucleotide data base by using the TFASTA program of the Genetics Computer Group program package (7, 15). Several high scores were obtained. All of these turned out to be subunits of ureases (4, 6, 13, 14, 19–21, 24, 25). Alignments of the complete amino acid sequences of the 19-kDa antigen and the polypeptides of the upstream and downstream open reading frames with the urease subunits are shown in Fig. 4.

These findings led us to search for urease activity in the clones identified from the Y. enterocolitica O:3 genomic library. The clone carrying the largest plasmid, p19kd-15, was clearly positive for urease activity, as tested by using Christensen's urea agar (Fig. 2). On the basis of these results, the structural gene of the 19-kDa antigen was designated yeuB, the upstream gene was designated yeuA, and the downstream gene was designated yeuC (for Y. enterocolitica urease).



FIG. 3. Expression of the 19-kDa antigen by Y. enterocolitica O:3 strain 10543 and E. coli strains. Bacterial samples were separated by SDS-PAGE and transferred to a nitrocellulose membrane. Immunodetection was performed with a rabbit anti-19-kDa-antigen antiserum and total cell lysates as antigens. Lane 1, E. coli C600/ p19kd-48; lane 2, E. coli C600/p19kd-107; lane 3, E. coli C600/p19kd-15; lane 4, E. coli C600; lane 5, Y. enterocolitica 10543; lane M, molecular weight markers.

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Y. ent Yeuk (1) H. pyl Hpuk (1) H. pyl Urek (1) H. pyl Urek (1) Kl. ser Urek (1) L. fer gamma (1) P. mír Urek (1) P. vul gamma (1) Jack bean (1) Consensus	MQLTPREVER MLLTPREIDS MLLTPREIDS MLLTPREDS MLLTPREDS MLLTPREDS MLLSIREQR MLLSIREQR MLLSIREVER * *000* * MLLSIREVER 1	LMIYTISdVA IMLhyAGelA LMLhyAGelA LLLFTAelVA MMISLAGmIA LLLFTAGIVA LLLFTAGIVA LLLFTAGIVA LLLFTAGIVA LGLhnAGYIA O O *	fKRkpkARGL kKRkekGi EFRkakGi EFRkdRGL EFRkdRGL EFRLAkGL FFRLAkGL RFRLAKGL QRRLARGV **	KLNYPEAVSI KLNYVEAVAL KLNYVEAVAL KLNYPESVAL KLNYPESVAL KLNYPESVAL KLNYSETVAL CNYVEEVAL C**0 * *00 kLNYPEAVAL	ItvtaNEGAR ISahIMEGAR ISafIMEGAR ISafIMEGAR IScaIMEGAR IScaIMEGAR IscaIMEGAR ItasqIMEYAR * 0* ** IsimEgAR	DG.KSVEDVM FGKKTAAELM GGKKTAAELM DG.KSVASLM DG.KTVGELM EG.KTVAQLM EG.KTVAQLM DGEKTVAQLM * 00 0* dG-KTVAELM	kEaskVLTkD qEGRT1LkpD qEGRT1LkpD gEGRhVLTrE nEGaTWLTrE sEGRTVLTaE geaReVLTaE qeaReVLraD clGqhlLgrr co • -egrtvLt-d	dVMDGVaDLI dVMDGVasMI dVMEGVasMI QVMEGVPEMI dVMEGVPEMI QVMEGVPEMI QVMEGVPEMI QVMEGVPEMI QVLgaVPhL1 *0 00 00 qVmegvpEmi	pnVQVEAIFt hEVgIEAmFP pDIQVEATFP pDIQVEATFP kDVQVECTFP kDIQVECTFP dIQVECTFP naVQVEATFP naVQVEATFP oo* *0 -dvqvEatFP	DGsrLVTVHD DGTKLVTVHt DGTKLVTVHt DGTKLITVTD DGTKLITVTD DGTKLVSIHS DGTKLVSIHD DGTKLVSVHD DGTKLVTVHD	PIR. PIe. PIe. PII. PIT. PIV. PIV. PIY. PIY. PIY. PIS. ** PI 104	(102) (101) (101) (100) (100) (100) (101) (101)
В												
Y. ent YeuB (1) H. pyl Hpul (102) H. pyl UreA (102) Kl. aer UreB (1) L. fer beta (1) P. mir UreB (1) P. vul beta (1) H. ure beta (1)	mstktnstka	. tsektdslkt	nrgtkesagy	aeqntpl0gc angkLVPGE1 angkLVPGE1 MIPGE2 MVPGE2 MIPGE1 MIPGE1	iLadtpIT flkned.IT flkned.IT hvkpgIa kLqpdk.Vp rvnaalgdie rvngalgdie	FNEnkpvtkV iNEGkkAVsV iNEGkkAVsV LNtGRatczV YNVGyDdIs1 LNaGREtkII LNaGREtkII	KVrNtGDRPI KVppvGDRPV KVkNvGDRPV VVeNhGDRPI KVkNvGDRPV QVaNhGDRPV QVaNhGDRPV	QVGSHFHFFE QIGSHFHFFE QIGSHFHFFE QVGSHYHF2E QVGSHYHF2E QVGSHYHF7E QVGSHYHF7E QVGSHYHF7E	aN. rALeFD. VN. rcLdFD. VN. rcLdFD. aNeggLqFD. VN. eALrFa. VN. eALrFa.	Rag Rek Rek Rgg Rsg Rsg		
Jack bean (102)	rengel	qealfgsllp	vpsldkfaet	kednrIPGEi 0*0	lcedec1T	LNIGRRAVII * 0	KVtskGDRPI 0 0 ****	QVGSHYHFIE *0**0 *0 *	VN.pyLtFD. * 0 *0	Rrk		
Consensus	1			mipGei	-1it	lNegreav-v	kv-n-GDRPv	QvGSbyHffE	vNal-Fd-	R 100		
Y. ent YeuB H. pyl BpuA H. pyl DreA Kl. ser UreB L. fer Deta P. mir DreB P. vul Deta U. ure Deta Jack Dean	AyGKRLMIss tfGKRLdIas AaGyRLMIPA AwGKLLdIPA tlGfRLMIPA tlGfRLMIPA AyGGRFdIPs AyGMRLMIA AyGRRMINEA	ttairfegd Gtavrfegg Gtavrfegg Gtavrfegg Gtairfegg Gtairfegg Gtairfegg Gtairfegg Gtairfegg Otavrfegg	EteV.pLIpF EKSV.ELIdi EKSV.ELIdi EKSV.ELIdi KReV.ELVAF ERLV.KLIDF CRLV.ELVAF KKSV.SVIdL CKSV.LUSi * 0	GGRqtlYGFN GGDRTIFGFN GGDRTIFGFN aGhRaVFGFr GGRRIVFGFN dGRReIYGFh VGCRwslrck eGnkvIrGgN	nLVDOwtgeg aLVDruadnE aLVDruadnE geVmGpLevn nkVnGwLdvd gkVmGkLesE rLs aiaDGpvnet	vvpnserpdk sKkialhrak sKkialhrak de kkadtyngyp kK nK nleaamhavr	leairraaer ergFhgaksd ergFhgaksd leksypeek srgfgheeek	gfkesk dnyvktike dnyvktike dapegftke	(164) (238) (106) (124) (108) (108) (121) (264)			
Consensus	a-GETINIDA 101	gravRIEpG-	er-v-ell-f	gowr-11gfn	-ivag-1e	-x		179				

FIG. 4. Alignment of the Y. enterocolitica O:3 urease γ - (A), β - (B), and α - (C) subunit amino acid sequences with the corresponding subunit sequences of different organisms. The polypeptides were aligned by using the GAP program, such that all sequences were "gapped" against each other to obtain maximal fitting. The gapped sequences were then lined up, and the consensus peptide was created by the PRETTY program. A consensus was created whenever four or more sequences had the same or similar amino acids at a particular position. Positions at which the consensus threshold was not reached are shown by dashes. In the sequences, amino acids identical or similar to those in the consensus are in uppercase letters; others are lowercase. Positions occupied by the same amino acid in sequences are indicated by uppercase letters in the consensus sequence and by asterisks above the letters. Positions occupied by the same amino acid in seven of the nine sequences are marked by circles above the consensus sequence. Gaps are shown by dots. Amino acid sequences are as follows: small and large subunits of two *Helicobacter pylori* (*H. pyl*) ureases (HpuB, HpuA, and UreA; accession [acc.] numbers for the nucleotide sequences, M60398, X57132, and X17079), *Klebsiella aerogenes* (Kl. aer) urease α -, β -, and γ -subunits (UreC, UreB, and UreA; acc. no. M36068), *Lactobacillus fermentum* (*L. fer*) urease α -, β -, and γ -subunits (acc. no. D10605), *Proteus mirabilis* (*P. mir*) urease α -, β -, and γ -subunits (acc. no. X51816), *Ureaplasma urealyticum* (*U. ure*) urease α -, β -, and γ -subunits (acc. no. M65260). The first and last positions of each sequence used in the comparison are indicated in parentheses. Note that the *H. pylori* small subunit and the jack bean urease sequences continue from panel A to panel B; the latter also continues to panel C.

DISCUSSION

This article describes the molecular cloning, sequencing, and identification of a cationic 19-kDa antigen isolated from Y. enterocolitica. The antigen was identified as a β -subunit of the Y. enterocolitica urease. Two lines of evidence support this conclusion. First, the amino acid sequence similarities to other urease small subunits are convincing (Fig. 4). Second, recombinant plasmids carrying and expressing the gene of the 19-kDa antigen conferred urease activity to urease-negative E. coli strains. Likewise, the size of the insert in the urease-positive clones is in accordance with the known sizes of urease operons of other bacteria. Bacterial ureases are usually large composite structures of two or three different subunits, designated α -, β -, and γ -subunits (4, 14, 19). In addition to the genes for the subunits, the urease operons contain genes coding for accessory and regulatory proteins (13, 14, 20). The accessory proteins are required to assemble the holoenzyme, which needs nickel ions for activity (20). Thus, the sizes of the urease operons are usually between 5 and 10 kb. In this study, the urease activity was expressed only by the recombinant plasmids containing the largest Y. enterocolitica DNA insert, i.e., 13.4 kb (p19kd-15), but not by p19kd-63, which contained a 9.2-kb insert. On the basis of the data obtained in this study and assuming that yeuA is the first gene in the operon, the minimal size of the operon would be over 6 kb (Fig. 2). No apparent promoter motifs were detected upstream of the yeuA gene. Most probably, expression of the 19-kDa antigen by an E. coli strain carrying plasmid p19kd-48 was made possible by the tetracycline resistance gene promoter of pBR322. Further work will be needed to elucidate the structure of the Y. enterocolitica urease operon.

Comparison of the amino acid sequences of the Y. enterocolitica urease subunits with other corresponding sequences revealed that the γ -subunit is highly conserved. Identities ranged between 51 and 60%, and similarities ranged between 67 and 80%. In addition, the lengths of the polypeptides are constant, ranging between 100 and 102 amino acid residues. The β -subunit seems to be less conserved, with the lengths of the polypeptide chains ranging between 106 and 164 amino acid residues. Likewise, the identities and similarities be-

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Y. ent YeuC	(1)	. MpqISRqEY	AglfGPTTGD	KIRLGDTALF	mqIEKDLrgY	GEESVYGGGK	sLRDGMGann	hltrdng	gyLefsh	ngrhyccspi	TV1KAD.VG1
H. pyl HpuB	(1)	. MKKISREBY	AsmygPttgd	KVRLGDTDLi	ABVENDYTIY	GEELKFOGGK	tLREGMsQS.	nnPSkEe	LDLIITN	ALIVDYT	GIYKAD.IGI
H. pyl UreB	(1)	.MKKISRKEY	VSMYGPTTGD	KVRLGDTDLI	ABVENDYTIY	GEELKFGGGK	tLREGMsQS.	nnPSkE	LDLIITN	ALIVDYT	GIYKAD.IGI
Kl. aer UreC	(1)	.MsnISRqaY	ADMFGPTVGD	KVRLaDTELW	IEVEDDLTTY	GEEVKFGGGK	VirDGMGQg.	QmlaADC	VDLV1TN	ALIVDhw	GIVKAD.IGV
L. fer alfa	(1)	msfdmdheqF	Asfygpttgd	SVRLGDTDLF	AKIEKDLTvh	GqEslFGGGK	VLRDGMGvSa	tetrAEn	pmvaDLIIsd	AIIIDWT	GIYKAD.1GI
P. mir UreB	(1)	.MKtISRqaY	ADMFGPTTGD	rlRLaDTELF	1BIEKDFTTY	GEEVEFGGGE	VIRDGMGQS.	QVVSAEC	VDV11TN	AIIIDYW	GIVKAD. IGI
P. vul alfa	(1)	.MKtISRqaY	ADMFGPTTGD	rlRLaDTELF	1BIEqDFTTY	GEEVKFGGGK	VIRDGMGQS.	QVVSAEC	vDvlitn	AIIIDhw	GIVKAD.1GI
<i>U. ure</i> alfa	(1)	.MfKISRknY	SDLYGITTGD	sVRLGDTnLW	VEKULTTY	GRESVFGGGK	tLREGMGmns	tmkldDklgn	aevMDLVITN	ALIIDYT	GIYKADDIGI
Jack bean	(271)	fntfIhRkEY	AnkYGPTTGD	KIRLGDTELL	ABIEKDYalY	GDECVFGGGK	VIRDGMGQSc	ghPpAis	LDEVITN	AVIIDYT	GI1KAD.IG
		0 000 0	0 *0*0**	** ** *	* * 0 0	*0* 0****	*0**0		0 000	0 00	00 *** 0*0
Consensus		-mkkisr-ey	admyGpTtGD	kvRLgDT-Lf	aeiEkDltty	GeE-kfGGGK	vlRdGMgqs-	q-psaec	ldl-itn	ali-dyt	g1-KAD-1G1
		101									1
Y. ent YeuC		rDGKIVGIGK	sGNPgVmDGV	tpgLVVGvsT	DalsGELLI	TAAGIDTHIH	LISPQQAYDA	Langvatrig	GGIGPEdGTN	GTTVTPGPWN	1 TQALFSVE
H. pyl HpuB		KDGKIAGIGK	GONEDEODGV	knnLsVGPaT	BALAGEGLIV	TAGGIDTHIH	FISPOOLPCA	FASGVTTMIG	GGTGPAGGTN	ATTITPGERN	LAPALIAAS
H. pyl UreB		KDGKIAGIGK	GONEDRODGV	KNNLSVGPAT	BALAGEGLIV	TAGGIDTHIH	FISPOOLPCA	FASGVITALG	GGTGPAGGTN	ATTITFGIRM	LARMINABI
KI. Aer Urec		KDGFITAIGK	AGNYDIODIV		BVIABBGRIV	TAGGIDTHIA	WICPQQAGEA	LABOTTEN	GOTOPAROTA	ATTCIPUT WY	themioavor
L. Fer alla		TOGRITAIGK	GGNPDVBD NV	DFIVGast	RAISGEGHIV	TAGGIDIHVH	IICPSIAGAA	Langittic	GOTOPALOTI	arcurdany	MURNIGAVDI
P. mir ures		KDGF1VG1GK	AGNPDVOpnV	DivigPgT	EVVAGEGRIV	TAGGIDTHIH	FICFQQAQEG	LUSGVITFIG	CONGPUTATIN	ATTVIPOLWA	Mh BMLe AvDI
P. VUI ALLA		ADGFICGIGK	AGAPDVODIV	DIVIGPGT	BVVAGBGKII	TAGGVDTHIA	FICFQQAGES	LACOTOR	COmorradomia	ATTVITCINA	L icLObeDo
U. Ure alla		KEGRIASIGK	SGNPHICDGV		EVBAGEGELY	TAGGIDTAVA	TIGPGLVPVA	Laggittvic	COTODA COTT	ATTVSFGHSG	W-1WI Oct DI
Jack Dean		ADGITABIGK	AGRIPDIMIGV	remailigant	BVIAGEGLIV	TAGAIDCAVA	IICFULVYER	1820111040	44040 44	ALLCIPBEUL	01 0
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Consensus		KOGKIAGIGK	acubavdadv	aivvop-i	eviagegilv	TAGGIDCHIH	LTCLddabea	1-sover-1g	Gocopa-orn	actvergpwn	
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W		AUL		Boad Services			DeMDTON-I	mpet Margaret	WOMTAL SACT		000479777-
I. ent Yeud		LPVNVG1LGK	GNSYGTGPLI	SURIAGVVGY	AVHEDWGAT&	HALTASLIMA	PermitőAsAH	TDELNECGIV	SUTIOALOGK	TTATE ATEGA	GOOMAPDIII
H. DYI HDUB		YSENIGPLAK	GNASDGASLA	DUIBAGAIGL	ALHEDWGCTP	SAIDDALdVA	DRYDVQVAIH	TUTLNEAGCV	BUTMAALAGR	THATIATSGA	GOODAFUIII
H. DYL UTOB		YSMNIGFLAK	GNASIDASLA	DULEAGAIGF	ALHEDWGCTP	SALINALOVA	DRYDVQVAIH	TUTLAKAGCV	SUTMAALAGE	THETE STAR	GOGRAPDIII
KI. Aer Urec		LPVNIGLLGK	GNVSQPDALR	EQVAAGVIGL	KIHEDWGATP	AALDCALTVA	DemDIQVAIH	SDTLINESGFV	RUTIANIGOR	TINTFHTEGA	GGGHAPDIIC
L. fer alfa		aPINyGLMak	GegSrPElig	EQIEAGCaal	KEHEDWGATa	AgIENsiaaA	DRYDVQYAVH	TDSLNEGGFV	ENTINAINGE	TVHTFHTEGA	GGGHAPDIM
P. mir UreB		LPINVGLFGK	GCVSQPEALR	EQICAGAIGL	KIHEDWGATP	MAIDNCLDVA	DemDVQVAIH	SDTLNEGGPY	BETVRALAGR	VIHVFHTEGA	GGGHAPDVII
P. VUI ALIA		LPINVGLPGK	GCVSQPEALR	EQIEAGAIGL	KIHEDWGATP	MALINCLEVA	DERDVQVAIH	SDTLMEGGFY	BETVKALAGR	VINVENTEGA	GGGERFDVII
U. Ure alla		LPINAGPLAK	Gqg.meDp11	BOIVAGACGL	KIHEDWGANF	NAIDIALTVA	EKCDVAVAIH	TOTLNEAGEV	RATIAAMKGR	TIQUEIQEVI	vvanigitie
Jack Dean		LPINIGFEGK	GSSSRPDeLA	BIIRAGAMGL	KIHEDWGSTP	AAIDNCLTIA	RUNDIGINIH	TUTLNEAGEV	BABLAALKGR	TIATIABLOA	GGGERPDIII
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Consensus		TDINAG-IQK	Guvsqp-air	ediesesiği	KIHEDWGaCD	aaldhaltvA	d-mnAdvaru	CDCLINEAGIV	BOCIANIAGE	cincincega	gggnaparri
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W		301		No			-		600000N00	WORLD- Parto	man-Mr.eR(
r. ent reuc		VASQPNVLPS	STAPTIPIGV	NEGARIFDAL	MVCHILIPIV	PADVSFABSR	VRDeTIAABI	VLHDMGVISH	LSSDSUARGR	VGENWLRVING	TAHAAAASA
H. pyl HpuB		VAGEDNILPA	STNFTIPFTV	NTOAKHRDML	MVCHHLDRSI	KEDVQFADSR	IRDOTIAABD	TURDWOILST	CSSDSQANGR	VGEVICKTWQ	TAGAIAKEIG
H. PYL UTEB		VAGEDNILIPA	STAPTIPFTV	NTOASHRDRL	AVCHHLDRSI	KEDVQFADSK	INDOLIVARD	CLEDROITSI	CASDSUMMER	VGEVICKING	TAURIANOIC
KI. aer Urec		acanphilips	STNPTIPITI	NTIDERLONL	WACHHEDDAT	ABDVAFABSR	IRTOTIAAED	VLHDLGAISI	tsspsgangr	VGEVILLRIWQ	VAREARVOR
L. IOT ALLA		VAGQUNVLPS	STUPTIPICK	NTIDEIFYNC	MVCHNLNPKI	PUDVAFAESR	IRRETOAAED	VLQDMGAISE	MESDAUANGR	VGEVALACHO	TABARAKAVRO
P. MIF UTEB		SVGEPHILPA	STRPTEPITI	NTYDERLORL	AVCHALDPSI	PEDVAFABOR	IRIGIIAARD	TURDWOATSV	NGGDGOLNOR	VGEVILLATING	-AHRARIOR
P. Vul alta		SULIKPNILPA	STNPTEPITI	NEVUKHLIJMU	MACHHUDESI	PEDVAFAESK	LATOTIAAAU		MAAUAUA MINA	A COPPA A MUKUMO	CARARAUTOR
		and and by TT D1	amand pump			DEPUTATION	TRANSTAND	1 TIDWON TOT	MCCD+11W-D	TOWNER	-> HTML +OF
U. ure alra		svkyahILPA	STNPTIPYTV	NTIABHLDML	MVCHHLnPkV	PEDVAFADSR	IRSQTIANED	1LHDMGAISI	MSSDt1AMeR	IGEVVtRsWQ	mAHKMKaQf
Jack bean		svkyahILPA VcGikNVLPs	STNPTIPYTV STNPTrPLTs	NTIAEHLDML NTIDEHLDML	MVCHHLnPkV MVCHHLDreI	PEDVAFADSR PEDLAFALSR	IRSQTIAAED IRKKTIAAED	1LHDMGAISI VLnDiGAISI	MSSDtlAMeR issDsQAMGR	IGEVVtRsWQ VGEVIsRTWQ	MAHEMEAQTO
Jack bean		svkyahILPA VcGikNVLPs 0 **	STNPTIPYTV STNPTrPLTs **0** * 0	NTIAEHLDML NTIDEHLDML *0 *0 0*0	MVCHHLnPkV MVCHHLDreI ****0* 0	PEDVAFADSR PEDIAFALSR 0*0 ** **	IRSQTIAAED IRKKTIAAED O* *0***0	1LHDMGAISI VLnDiGAISI *0*0* *	MSSDtlAMeR issDsQAMGR 0**00**0*	IGEVVtRsWQ VGEVIsRTWQ 0**0 * 0*	mAHKMKaQf(TAdKMKaQt(0 00*
Jack bean Consensus		svkyahILPA VcGikNVLPs O ** vagepniLPa	STNPTiPYTV STNPTrPLTs **0** * 0 STnPT-Pytv	NTIAEHLDML NTIDEHLDML *0 *0 0*0 NtidEhldMl	MVCHHLnPkV MVCHHLDreI ****0* 0 MVCHhLdpsi	PEDVAFADSR PEDLAFALSR 0*0 ** ** peDvaFAeSR	IRSQTIAAED IRARTIAAED 0* *0***0 iRTiaaed	1LHDMGAISI VLnDiGAISI *0*0* * vLhDmGaiSi	MSSDtlAMeR issDsQAMGR 0**00**0* msSDsqAMgR	IGEVVtRsWQ VGEVIsRTWQ O**0 * O* VGEVIlRtwQ	mAHKMKaQf(TAdKMKaQt(0 00* tahkmK-gr(
Jack bean Consensus		svkyahiLPA VcGikNVLPs 0 ** vagepniLPa	STNPTIPYTV STNPTrPLTs **0** * 0 STnPT-Pytv	NTIABHLDML NTIDBHLDML *0 *0 0*0 NtidBhldMl	MVCHHLnPkV MVCHHLDreI ****0* 0 MVCHhLdpsi	PEDVAFADSR PEDIAFALSR 0*0 ** ** peDvaFAeSR	IRSQTIAABD IR&RTIAABD O* *O***O IRTIAABd	lLHDMGAISI VLnDiGAISI *0*0* * VLhDmGaiSi	MSSDtlAMeR issDsQAMGR o**00**0* msSDsqAMgR	IGBVVtRsWQ VGEVISRTWQ O**O * O* VGEVILRtwQ	mAHKMKaQfC TAdKMKaQtC 0 00* tahkmK-qrC
Jack bean Consensus		svkyahilPA VcGikNVLPs 0 ** vagepnilPa 401	STNPTIPITV STNPTrPLTs **0** * 0 STnPT-Pytv	NTIABHLDML NTIDBHLDML *0 *0 0*0 NtidBhldMl	MVCHHLnPkV MVCHHLDreI ****0* 0 MVCHhLdpsi	PEDVAFADSR PEDLAFAbSR 0*0 ** ** peDvaFAeSR	IRSQTIAABD IRKKTIAABD O* *O***O IRTIAABd	LLHDMGAISI VLnDiGAISI *0*0* * VLhDmGaiSi	MSSDtlAMeR iSSDSQAMGR o**00**0* msSDsqAMgR	IGEVVtRsWQ VGEVISRTWQ O**O * O* VGEVILRtwQ	mAHKMKaQfC TAdKMKaQtC o oo* tahkmK-grC 500 FGAMGKtmcT
Jack bean Consensus Y. ent YeuC		svkyahilPA VcGikNVLPs 0 ** vagepnilPa 401 klpeDapgND	STNPTIPITV STNPTrPLTs **0** * 0 STnPT-Pytv NFRVVRYVAK	NTIAEHLDML NTIDEHLDML *0 *0 0*0 NtidEhldMl iTINPAIAGG	MVCHHLnPkV MVCHHLDrei ****0* 0 MVCHhLdpsi VSHvIGSVEV	PEDVAFADSR PEDIAFALSR 0*0 ** ** peDvaFAeSR GKMADLVLWv GKvADLVLWv	IRSQTIAABD IRKKTIAABD O* *O***O IRTIAABd PrFFGaKPKM PapPGUKPpm	LLHDMGAISI VLnDiGAISI *0*0* * VLhDmGaiSi VIKGGMINWA	MSSDtlAMeR 1SSDSQAMGR 0**00**0* msSDsqAMgR aMGDPNAS1P cMGDaNAS1P	IGEVVtRsWQ VGEVISRTWQ O**O * O* VGEVILRtwQ TPQPVfYRPM TPQPVfYRPM	mAHKMKaQf(TAdKMKaQt(0 00* tahkmK-qr(500 FGAMGKtmqI FahbGKAKYI
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pvl UraB		svkyahILPA VcGikNVLPs 0 ** vagepniLPa 401 kLpeDapgND rLKeEkGDND rLKeEkGDND	STNPTiPYTV STNPTrPLTs **0** * 0 STnPT-Pytv NFRVvRYVAK NFRIKRY1sK NFFIKRY1sk	NTIABHLDML NTIDBHLDML *0 *0 0*0 NtidBhldMl iTINPAIAGG YTINPAIAHG YTINPAIAHG	WVCHHLnPkV MVCHHLDreI ****0* O MVCHhLdpsi VSHvIGSVEV ISeYVGSVEV ISeYVGSVEV	PEDVAFADSR PEDLAFAbSR 0*0 ** ** peDvaFAeSR GRMADLVLWv GRVADLVLWs GRVADLVLWs	IRSQTIAABD IRKKTIAABD O* *O***O IRTIAABd PrFFGakPkM PAFFGVKPnM PAFFGVKPnM	LLHDMGAISI VLnDiGAISI *0*0* * VLhDmGaiSi VIKGGMInWA IIKGGFIAls	MSSDtlAMeR issDsQAMGR o**00**0* msSDsQAMgR aMGDPNASIP gMGDaNASIP gMGDaNASIP	IGEVVTRSWQ VGEVISRTWQ O**O * O* VGEVIIRTWQ TPQPVfYRPM TPQPVyYReM TPQPVyYReM	mAHKMKaQf(TAdKMKaQt(0 00+ tahkmK-qr(500 FGAMGKtmqI FahhGKAKYI FahhGKAKYI
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB Kl. ser UreC		svkyahILPA VcGikNVLPs 0 ** vagepniLPa 401 kLpeDapgND rLKeEkGDND rLKEEKGDND	STNPTIPYTV STNPTIPYTS **0** * 0 STNPT-Pytv NFRVVRYVAK MFRIKRY1sK NFRIKRY1sk	NTIABHLDML NTIDEHLDML *0 *0 0*0 NtidBhldMl iTINPAIAQG YTINPAIAHG YTINPAIAHG	WYCHHLDPkV MYCHHLDreI ****0* O MYCHHLdpsi VSHvIGSVEV ISeYVGSVEV ISeYVGSVEV ISeYVGSVEV	PEDVAFADSR PEDIAFAbSR O*O ** ** peDvaFAeSR GRMADLVLWv GRVADLVLWs GRVADLVLWs GRLADLVVWs	IReqTIAAED IREKTIAAED O* *0***0 IRTIAAEd PrffGakPkm PAFFGVKPam PAFFGVKPat	LHDMGAISI VLnDiGAISI *0*0* * vLhDmGaiSi VIKGGMInWA IIKGGfIAIs VIKGGMIAIA	MSSDtlAMeR issDsQAMGR 0**00**0* msSDsQAMgR aMGDPNASIP QMGDaNASIP QMGDaNASIP PMGDiNASIP	IGEVVLRSWQ VGEVISRTWQ O**O * O* VGEVIIRTWQ TPQPVfYRPM TPQPVyYReM TPQPVyYReM	mAHKMKaQfC TAdKMKaQtC O OO* tahkmK-qrC 500 FGAMGKtmqI FahhGKAKYI FahhGKAKYI FGALGsArbh
Jack bean Consensus Y. ent YeuC H. pyl EpuB H. pyl UreB Kl. ser UreC L. fer alfa		svkyahilPA VcGikNVLPs o ** vagepnilPa 401 kLpeDapgND rLKeEkGDND aLaeEtGDND aLaeEtGDND	STNPT1PYTV STNPT1PLTS **0** * 0 STNPT-Pytv NFRVXRYVAK MFRIKRY1SK NFRIKRY1SK NFRIKRY1SK NFRIKRY1SK	NTIABHLDML NTIDEHLDML *0 *0 0*0 NtidBhldMl iTINPAIAGG YTINPAIAHG YTINPAIAHG YTINPAIAHG	WVCHHLnPkV MVCHHLDreI ****0* 0 MVCHhLdpsi VSHvIGSVEV ISEYVGSVEV ISEYVGSVEV ISEYVGSVEV ISEYVGSVEV ISEYVGSVEV	PEDVAFADSR PEDIAFAbSR 0*0 ** ** peDvaFAeSR GKNADLVLWv GKVADLVLWs GKVADLVLWs GKLADLVLWs	IRAGTIAAED IRKKTIAAED O**0**0 IRTIAAEd Prffgarpim Paffgvrpim Paffgvrpim Paffgvrpim Paffgvrpim	LHDMGAISI VLDDGAISI *O*O* VLDDGAISI *O*O* VLDDGAISI VIKGGMINWA IIKGGFIAIs VIKGGMIAIA VIKGGMIAYA	MSSDtlAMeR iSSDSQAMGR 0**00**0 msSDsqAMgR aMGDPNASIP QMGDaNASIP PMGDiNASIP PMGDiNASIP	IGEVVLRSWQ VGEVISRTWQ 0**0 * 0* VGEVISRTWQ TPQPVfYRPM TPQPVyYReM TPQPVyYReM TPQPVhYRPM TPePVlRFL	mAHKMKaQfG TAAKMKaQtG 0 00* tahkmK-qrG 500 FGAMGKTmqI FahhGKAKYI FahhGKAKYI FGALGSATHI YGASGATHI
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB Kl. ser UreC L. fer alfa P. mir UreB		svkyahlLPA VcGikNVLPs o ** vagepniLPa 401 kLpeDapgND rLKeEkGDND pLdgDSkydD pLdgDSkydD pLdgDSkydD	STNPTIPYTV STNPTIPLTS **0** * 0 STNPT-Pytv NFRIKRYISK NFRIKRYISK NFRIKRYISK NMRIKRYISK NMRIKRYISK	NTIGEHLDML NTIDEHLDML *0 *0 0*0 NtidEhldMl ITINPAIAG YTINPAIAHG YTINPAIAHG YTINPAICNG YTINPAIAHG	WVCHHLDPkV MVCHHLDreI ****0* 0 MVCHhLdpsi VSHVIGSVEV ISeYVGSVEV ISeYVGSVEV ISeYVGSUEV ISHVQSIEV ISHVQSIEV	PEDVAFADSR PEDLAFAbSR 0*0 ** ** peDvaFAeSR GKNADLVLWv GKVADLVLWs GKLADLVLWs GKLADLVLWs GKLADLVLWs	IRSGTIAAED IRKKTIAAED O* *0**0 IRTIAAEd PAFFGVKPAM PAFFGVKPAM PAFFGVKPAL PAFFGVKPAL	LHDMGAISI VLnDiGAISI *0*0* * VLhDmGaiSi VIKGGMInWA IIKGGFIAIs IIKGGFIAIs VIKGGMIAIA VIKGGMIAIA	MSSDtlAMeR isSDSQAMGR o**00**0* msSDsQAMGR aNGDPNASIP QMGDaNASIP QMGDaNASIP iaGDPssSIP iaGDPssSIP	IGEVVLRSWQ VGEVISRTWQ O**0 * O* VGEVISRTWQ TPQPVYRAM TPQPVYRAM TPQPVYRAM TPQPVLRFM TPOPVLRFM	mAHKNKaQfG TAdKNKaQtC O OO* tahkmK-qrG FGAMGKTmqI FGAMGKAKYI FGALGSArbH YGALGSArbH YGALGSArbH
Jack bean Jack bean Consensus Y. ent YeuC H. pyl BpuB H. pyl UreB Kl. aer UreC L. fer alfa P. mir UreB P. vul alfa		svkyahiLPA VcGikNVLPs o** vagepniLPa 401 rLKeEkGDND rLKeEkGDND rLKeEKGDND pLdgDSkydD tLagDSaDND rLagDSaDND	STNPT1PYTV STNPT1PYTV STNPT1PLTs STDPT-Pytv MFRIKRY1sK MFRIKRY1sK MRRIKRY1AK MRRIKRY1AK MRRIKRY1AK	NTIGEHLDML NTIDEHLDML *0 *0 0*0 NtidEhldMl iTINPAIAHG YTINPAIAHG YTINPAICHG YTINPAICHG YTINPAICHG YTINPAIAHG	WVCHHLnPkV MVCHHLDrei ****0* NVCHLdpsi VSHvIGSVEV ISeYVGSVEV ISeYVGSVEV ISEYVGSIEV ISHVGSIEV ISHVGSIEV ISHVGSIEV	PEDVAFADSR PEDIAFAbSR O*O ** ** peDvaFAeSR GKWADLVLWy GKVADLVLWS GKVADLVLWS GKLADLVVWS GKLADLVVWS GKLADIVLWD	IRQTIAAED IRKTIAAED O**0**0 IRTIAAEd PIFFGAKPAM PAFFGVKPAM PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL	LHDMGAISI VILDIGAISI *O*O* * VLDDmGaiSi IIKGGfIAls IIKGGfIAls VIKGGMIXIA VIKGGMIXIA UIKGGMVYIA	MSSDtlAMeR iSSDSQAMGR o**oo**o* msSDsQAMGR aMGDPNASIP QMGDaNASIP QMGDaNASIP iaGDPssSIP PMGDiNASIP PMGDiNAaIP	IGEVVLRSWQ VGEVISRTWQ 0**0 * 0* VGEVIIRTWQ TPQPVYRPM TPQPVYRPM TPQPVIRPM TPoPVleRfL TPQPVhyRPM	mAHKMKaQfd TAAKMKaQtd O OO* tahkmK-qrd 500 FGAMGKtmqI FahhGKAKYI FahhGKAKYI YGAcGAXVh YGAcGGRAVh YacLGKAKYG
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB KI. der UreC L. for alfa P. mir UreB P. vul alfa		svkyahilPA vcGikNVLPs 0 ** vagepnilPa 401 kLpeDapgND rLKeEKGDND rLKeEKGDND pLdgDSkydD tLagDSaDND sLagDtaEND sLkgDSafND	STNPTIPYTV STNPTIPYTV STNPTIPYTV STNPTIPYTV NFRIKRYISK NFRIKRYISK NARIKRYISK NARIKRYISK NARIKRYISK NARIKRYISK	NTIABHLDML NTIDBHLDML *0 *0 A*0 NtidBhldMl TINPAIAHG TTINPAIAHG TTINPAIAHG TTINPAIAHG TTINPAIAHG TTINPAIAHG	MVCHHLDPkV MVCHHLDrei ****0 MVCHhLdpsi USHVIGSVEV ISHVGSVEV ISHVGSVEV ISHVGSIEV ISHVGSIEV ISHVGSIEK IAHEVGSIEK IAHEVGSIEV	PEDVAFADSR PEDLAFAbSR O*O ** ** peDvaFAeSR GKVADLVLW* GKVADLVLW* GKVADLVLW* GKVADLVLW* GKVADLVLWB GKLADIVLWD GKLADIVLWD GKLADIVLWD	IRSQTIAAED IRACTIAAED O* ****0 IRTIAAEd PAFFGVKPAM PAFFGVKPAM PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL	LHDMGAISI VLnDIGAISI *0*0* * vLhDmGaiSi IIKGGfIAIs IIKGGfIAIs VIKnGMILYG IIKGGMVIYA IMKGGMVIYA	MSSDtlAMeR issDsQAMGR o*too*to msSDsQAMGR QMGDaNASIP QMGDaNASIP PMGDiNASIP PMGDiNAAIP PMGDiNAAIP PMGDINAAIP	IGEVVLRSWQ VGEVISRTWQ O**0 * 0* VGEVIIRtwQ TPQPVfYRPM TPQPVyYReM TPQPVhYRPM TPOPVLRFL TPQPVhYRPM TPQPVhYRPM	mAHKMKaQfG TAAKMKAQtC O OO' tahkmK-qrG FGAMGKtmqT FahhGKAKYT FahhGKAKYT FGAhGKAKYG YacLGKAKYG YacLGKAKYG FGLVGTALta
Jack bean Consensus H. pyl HpuB H. pyl HpuB H. pyl UreB Kl. aer UreC L. for alfa P. wil alfa U. ure alfa Jack bean		svkyahiLPA vcGikNVLPs o ** vagepniLPa 401 klpeDapgND rLKeBkGDND rLKeBkGDND pldgDSkydD tLagDSaDND sLagDtaEND aLKgDSefND DLKcDSaDND	STNPTIPITV STNPTIPITS STNPTIPITS STNPT-Pytv MFRIKRYISK MFRIKRYISK MARIKRYISK MARIKRYISK MARIKRYISK KOPCKRYISK KOPCKRYISK	NTIAEHLDML NTIDEHLDML *0 *0 n*0 NtidebldMl iTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG	NVCHLLPkV NVCHLLPkV NVCHLDpsi VSEvIGSVEV ISaVVGSVEV IsaEvGSVEV IsaEvGSVEV IsAEvGSVEV IsAEvGSIEk IaEvGSIEk IdaEvGSIEk IdaEvGSUEK	PEDVAPADSR PEDLAPADSR PEDLAPADSR O*O ** ** peDvaPAeSR GKNADLVLWy GKLADLVLWS GKLADLVLWS GKLADLVLWG GKLADLVLWG GKLADLVLWG GKLADLVWG	IRSQTIAABD IRKTIAABD O* *0**0 IRTIAABd PAFFGVKPAM PAFFGVKPAM PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGKRPAM PAFFGKRPAM	LHDMGAISI VLnDIGAISI *0*0* * vLhDmGaiSi UIKGGfIAIs IIKGGfIAIs UIKGGMITAIA VIKGGMITAIA VIKGGMITYG IIKGGMVYYA VVKMGVIARC	MSSDtlAMeR issDsQAMGR o**oo**o* msSDsqAMgR aMGDPNASIP qMGDaNASIP qMGDINASIP PMGDINASIP PMGDINAAIP PMGDINAAIP YaGDPNASIP	IGEVVIRSWQ VGEVISRTWQ O**0 * 0* VGEVIIRTWQ TPQPVYYReM TPQPVYRPM TPQPVARPM TPQPVARPM TPQPVARPM TCPVIRPM TCPVIRPM	mAHKMKaQfC TAdKMKaQfC 0 00* tahkmX-qrC 500 FGAMGKtmqI FahbGXAXI FGALGSATH YGALGSATH YGALGSATH YacLGKAXY YacLGKAXY YacLGKAXY YGLLGKAGA
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB KI. eer UreC L. fer alfa P. mir UreB P. vul alfa Jack bean		svkyahilpa vcGinVLPs o** vagepnilPa 401 klpeDapgND rLKsEkcOND rLKsEkcOND rLKsEkcOND slagDtaEND slagDtaEND slagDtaEND slagDtaEND * o*	STNPT1PJTV STNPTTPLDTS STNPT-Pytv NFRVvRYVAK NFRIKRY1SK NFRIKRY1SK NNRIKRYIAK NNRIKRYIAK NNRIKRYIAK NNRIKRYIAK NNRIKRYIAK NSTLRYIAK NSTLRYIAK	NTIBEHLDNL NTIBEHLDNL *0 *0 *0 *0 Ntidehldml itinpalag ytimpalahg ytimpalahg ytimpalahg ytimpalahg ytimpalahg ytimpalahg ytimpalahg	NVCHHLDPKV NVCHHLDPSI ONVCHLDpsi VSHVIGSVEV IS&YVGSVEV IS&YVGSVEV IS&YVGSVEV IAHEVGSIEK IAHEVGSIEK IAHEVGSIEK IAHEVGSIEV O O** *0	PEDVAPADSR PEDLAPADSR O*O *** peDvaPAeSR GRVADLVLWS GRVADLVLWS GRVADLVLWS GRVADLVLWS GRVADLVLWS GRVADLAIWD GRLADIVLWD GRLADIVLWD GRLADIVAWE GRLADLVWW	IRSGTIAAED IRKATIAAED IRKATIAAED O* 0***0 IRTIAAEd PAFFGVKPAM PAFFGVKPAM PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGKRPM ****	LLHDMGAISI VLnDIGAISI *0*0* * VLhDmGaiSi VIKOGMInWA IIKOGFIAIs VIKOGMIAIS VIKOGMVAYA VVKNGVAVA 0*0*	MSSDtlamer issbsgamer msSDsgamer msSDsgamer gmodanasip gmodanasip gmodanasip gmodanasip pmodinasip pmodinaaip pmodinaaip ymodinaaip staoppessip pmodinaaip staoppessip ymodinaaip staoppensip staoppensip staoppensip staoppensip staoppensip	IGEVVLRSMQ VGEVISRTWQ VGEVISRTWQ TPQPVIRPM TPQPVJRAM TPQPVJRAM TPQPVJRAM TPQPVLRFL TPQPVLRFL TPQPVLRAPM TPQPVLRAPM TPQPVLRAPM TPQPVLRAPM TPQPVLRAPM	mAHKMKaQf(TAdKMKAQC(0 00° tahkmK-qr(500 FGAMGKtmqT PahbGRAKTI PahbGRAKTI PahbGRAKTI PGALGSAKY YGCLGRAKYQ YacLGRAKYQ YacLGRAKYQ YGCLGRAKYQ ************************************
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB Kl. aer UreC L. fer alfa P. mir UreB P. vul alfa Jack bean Consensus		svkyahiLPA vcGiNVLPs o** vagepniLPa 401 kLpeDagND rLKeBKGDND rLKeBKGDND pLdgDSkydD sLagDSaDND sLagDSaDND sLagDSaDND sLCDSSDND * O*	STNPTIPTTY STNPTIPLTS **0** 0 STNPT-Pytv NFRVKRYJSK NFRVKRYJSK NFRVKRYJSK NNRIKRYJSK NNRIKRYJSK NNRIKRYJSK NDRIKRYJSK O 0 0** 0*	NTIAEHLDNL NTIDEHLDNL ***********************************	NVCHHLDPkV NVCHHLDPsi VSHVIGSVEV IS&IVGSVEV IS&IVGSVEV IS&IVGSVEV IS&IVGSIEV IS&IVGSIEV IAHEVGSIEK IAHEVGSIEK IAHEVGSIEK IS&IVGSVEV 0 0***0	PEDVAPADSR PEDIAPADSR O'O *** peDvaPASSR GRWADLVLWV GRVADLVLWS GRVADLVLWS GRLADLVWWS GRLADLVWWS GRLADIVLWD GRLADIVLWD GRLADIVLWD SRLADIVLWH ***** 0*	IRsqTIAAED IRktIAAED IRktIAAED IRkTIAAEd PIFFGAKPhM PAFFGVKPhM PAFFGVKPhM PAFFGVKPhL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL	1LHDMGAISI VLnDiGAISI *0°0° * VLhDmGaiSi VIKOGMINWA IIKGGTIAIs IIKOGMVYA IIKOGMVYA IIKOGMVYA VVKMGVIAKO VVKMGVIAKO VVKGGNVAWA 0°0*	MSSDtlamer issbsonmgr msSDsonmgr amgdpnasip gmgdanasip gmgdanasip gmgdinasip pmgdinasip ymgdinasip ** 0000*	IGBVVLRAW VGEVISTWQ VGEVISTWQ TPOPVJRAM TPOPVJRAM TPOPVJRAM TPOPVJRAM TPOPVJRAM TPOPVJRAM TPOPVJRAM TPOPVJRAM TPOPVJRAM TCOPVJRAM TCOPVJRAM	mAHRMRAG(TAdKMKAQtC 000° tahkmK-qr(5000 FahbGKAKMG PahbGKAKM PahbGKAKM PahbGKAKM YGALGKAKM YGCJCKAKM YGCJCKAKM YGCJCKAKM YGCJCKAKM YGCJCKAKM YGCJCKAKM
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB KI. ser UreC L. for alfa P. wil alfa Jack bean Consensus		svkyahilpa o** vagepnilpa 401 klpedapgND rlkeäkGDND rlkeäkGDND pldgDSkydD tlagDSaDND pldgDSkydD tlagDSaDND pldgDSkydD rlkeDSSDDD plkcDSSDD * o*	STNPT:PTTY STNPT:PLTY STNPT:PLTY STNPT-Pyty NFRVVRYVAK NFRIKRYISK NFRIKRYISK NFRIKRYISK NARIKRYIAK NARIKRYIAK NARIKRYIAK NARIKRYIAK NFRIKRYISK SO O 0** 0* nfrikryisk	NTIBEHLDNL NTIDEHLDNL *0 *0 *0 *0 Ntidehldni itinpalaqg ytimpalaqg ytimpaleg ytimpaleg ytimpalag ytimpalag ytimpalag ytimpalag ytimpalag	NVCHLLPKV NVCHLLPKV NVCHLLDPSI VSHVIGSVEV IS&YVGSVEV IS&YVGSVEV IS&YVGSVEV IS&YVGSVEV IS&YVGSVEV fSQTVGSVEV 0 0**00 isbyvGSiEv	PEDVAPADSR PEDLAPADSR O*O **** peDvaPADSR GRMADLVLWV GRVADLVLWS GRVADLVLWS GRVADLVLWS GRLADLVLWD GRLADLVLWD GRLADLVWD GRLADLVWD CRLADLVWD	IRSQTIAAED IRKATIAAED IRKATIAAED O* 0***0 IRTIAAEd PAFFGVKPAM PAFFGVKPAM PAFFGVKPAM PAFFGVKPAL PAFFGVKPAM PAFFGVKPAM PAFFGVKPAM	LEDNGAISI VLDDIGAISI *0*0* * VLDDMGaISI VIKOGMINWA IIKOGFIAIs VIKOGMIAIS VIKOGMIAIS IIKOGMVIYA VIKOGWIAYA VVKMGVIARC VIKOGWAWA 0*0* VIKOGWAWA	MSSDtlaner issbognar msSDsgangr msSDsgangr gMGDansIP gMGDansIP pMGDinsIP iagDPssSIP PMGDinsIP iagDPssSIP PMGDINAIP vaGDPNSIP ** 0000* pmGDpnsiP	IGEVVIRANG VGEVIRRING 0*0 * 0* VGEVIRRING TPOPVYRAN TPOPVYRAN TPOPVYRAN TPOPVARRI TPOPVARRI TPOPVARRN TPOPVARRN TPOPVARRN TPOPVARRN TPOPVARRN O ** 0 0 TPQPV-yRpm	mAHKMKaQf(TAdKMKAQC(0 00° tahkmK-qr(500 FahbGKAKT FahbGKAKT FahbGKAKT YGALGKAKY FGLYGASILs YGALGKAKY FGLYGISLS YGLLGKAKY FGLYGISLS YGLLGKAKY
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB XI. aer UreC L. fer alfa P. mir UreB P. vul alfa Jack bean Consensus		svkyahiLPA vcGiNVLPs o** vagepniLPa 401 kLpaDapgND rLKaEkGDND rLKaEkGDND pLdgDSkydD sLagDSaDND aLKgDSsCND pLKcDSsDND * o* -Lk-dsgdnD 501	STNPFIPTTY STNPFIPTS STNPT-Pytv NFRVvRTVAK NFRIKRIISK NFRIKRIISK NFRIKRIISK NMRIKRIIAK NMRIKRIIAK NMRIKRIIAK NMRIKRIIAK NFRIRRIAK	NTISEHLDNI NTIDEHLDNI ************************************	NVCHHLDPkV NVCHHLDPsi VSHVIGSVEV ISelVGSVEV ISelVGSVEV ISelVGSVEV ISAEVGSIEV ISAEVGSIEV ISAEVGSIEV ISAEVGSIEV ISAEVGSIEV 0 0***0 ishyvGSiEV	PEDVAFADSR PEDLAFADSR O'O ** ** peDvaFAGSR GRWADLVLWY GRVADLVLWS GRVADLVLWS GRLADLVLWS GRLADLVLWS GRLADLVLWG GRLADLVLWG GRLADLVWK **** O* GRLADLVLWG	IRSGTIAAED IRSGTIAAED IRKKTIAAED O* 0***0 IRTIAAEd PAFFGVKPAM PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAR PAFFGVKPAM	LEDMGAISI VLADIGAISI *0°0° * vLADMGAISI VIKOGMIAWA IIKOGMIAWA VIKOGTAIS IIKOGMVYA IIKOGMVYA VIKOGWIAWA 0°0* viKOGMVAWA	MSSDtlamer issbsonmgr o*to*to msSDsgamgr gmodanasip gmodanasip gmodanasip gmodinasip pmodinasip pmodinasip et occos statisticasi statisticasi gmodanasip statisticasi statisti	IGBVVERAWG VGEVISTWO O*0 * 0* VGEVISTRWO TPOPVYTRM TPOPVYTRM TPOPVYTRM TPOPVYTRM TPOPVIRM TPOPVIRM TPOPVIRM TPOPVIRM TPOPVIRM TPOPVIRM TPOPVIRM TPOPVIRM	mAHRMRAGIC TAdRMKAQLC 0 00° tahkmK-qrc 5000 PahbGKAKT PahbGKAKT PahbGKAKT YGALGKAKY YacLGKAKY YacLGKAKY YacLGKAKY YacLGKAKY GGYGTSILS YGLLGKAG GGO fgalGkaky 600
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB Kl. aer UreC L. for alfa P. wil alfa J. ure alfa Jack bean Consensus Y. ent YeuC		svkyahilpa o** vagepnilpa 401 klpedapgND rlkeikGDND rlkeikGDND pldgDSkydD slagDtaEND pldgDSkydD tlagDSaDND rlkcDSSDND * o* -lk-dsgdnD 501	STNPTIPTTY STNPTIPTTS STNPTTPTPTP STNPT-Pytv NFRVKRYLSK NFRVKRYLSK NFRVKRYLSK NMRIKRYLSK NMRIKRYLSK NMRIKRYLSK NMRIKRYLSK DAGERYLSK O O O** O* nfrikRYLSK LDdGVKEKAG	NTIBEHLDNL NTIDEHLDNL *0 *0 *0 *0 NtidEhldMl iTINPATAHG YTINPATAHG YTINPATHG YTINPATHG YTINPATHG YTINPATHG YTINPATHG O*****00 * YTINPATAHG UTINPATHAG O*****0 *	NVCHHLDPKU NVCHHLDPKU NVCHHLDPSI VSHVIGSVEV IS&IVGSVEV IS&IVGSVEV IS&IVGSVEV IS&IVGSIEV IS&IVGSIEV IS&IVGSIEV IS&IVGSIEV 0 0** *0 isbyvGSIEV CRtIsKhDLV	PEDVAFADSR PEDLAFADSR O*O ** ** peDvaFASSR GRNADLVLWW GRVADLVLWW GRVADLVLWW GRLADLVLWW GRLADLVLWW GRLADLVLWW GRLADLVLWW GRLADLVWW ***** O* GRLADLVWW ***** O*	IRsqTIARD IRkTIARD O* 0***0 IR-TIARD PIFFGARPAM PAFFGVRPAM PAFFGVRPAM PAFFGVRPAM PAFFGVRPAM PAFFGVRPAM PAFFGVRPAM ****** PaFFGVRPAM	LEDNGAISI VLADIGAISI *0*0* * VLADMGAISI VIKOGMINWA IIKOGIIAI VIKOGMIAIA VIKOGMVYA VIKOGWVYA VIKOGWVAYA O*0* VIKOGWVAWA O*0* D	MSSDtlaner issbsgange msSDsgange msSDsgange gmgdansip gmgdansip gmgdinsip iagdpessip Pmgdinaip Pmgdinaip yagdpnsip stationaip yagdinsip ** 0000*	IGBVVLRAWO VGEVISTWQ VGEVISTWQ TPQPVfYRPM TPQPVyTReM TPQPVyTReM TPQPVYRPM TPQPVLRPM TPQPVLRPM TCQPVLRPM TCQPVLRPM *0 ** * 0 TPQPV-yRPm Gvha	mARKKaQf(TAdKNKaQtG 0 00° tahkmK-qr 500 PahloKAKI PahloKAKI PahloKAKI PahloKAKI YacLoKAKYQ YacLoKAKYQ YacLoKAKYQ YacLoKAKYQ SGLGKAKYG 600 CGEPidKakYG
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB KI. eer UreC L. fer alfa P. mir UreB P. vul alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB		svkyahiLPA vcGiNVLPs o** vagepniLPa 401 tLsabagoND rLKaBKGDND pL&BKGDND pL&BKGDND pL&GDSkydD pL&GDSkydD pL&CDSeDND pL&CDSeDND pL&CDSeDND pL&CDSeDND pL&CDSeDND pL&CDSeDND 501 ToVTFVSQAA aniTFVSQAA	STNPTIPTTY STNPTIPLTY STNPTIPLTY STNPT-Pytv NFRVvRTVAK NFRIKRYIAK NFRIKRYIAK NMRIKRYIAK NMRIKRYIAK NMRIKRYIAK NMRIKRYIAK DIGVKEKAG UDGVKEKAG	NTISEHLDNI NTIDEHLDNI NTIDEHLDNI ITINPAIAAG YTINPAIAAG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG LDTQVisVKN LDTQVisVKN	NVCHHLDPkU NVCHHLDPsI ****0 NVCHLLdpsi VSHVIGSVBV IS@YVGSVBV IS@YVGSVEV IS@YVGSVEV IS@YVGSIEV IS@YVGSIEV CRLISKDLV CRLISKDLV	PEDVAPADSR PEDIAPADSR O'O ** ** peDvaFASSR GRMADLVLWY GRVADLVLWS GRVADLVLWS GRLADLVLWS GRLADLVWWS GRLADLVWW GRLADIVLWG GRLADIVLWG GRLADIVLWG GRLADIVLWG GRLADIVLWG GRLADIVLWG GRLADIVLWG GRLADIVLWG	IRsqTIAAED IRkTIAAED IRkTIAAED IRKTIAAED PIFFGAKPkm PAFFGVKPAM PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL VDPeTFaVKV VDseTFAVKV	LEDMGAISI VLADIGAISI *0°0° * vLhDmGaiSi VIKOGMINWA IIKOGFIAIs IIKOGMYAYA IIKOGMYAYA IIKOGMYAYA VIKAGMYAYA VIKAGMYAYA O*0* vIKGFMIaya D	MSSDtlamer issbsgamge msSDsgamge msSDsgamge mgDpnAslp gmgDanAsip pmgDinAsip pmgDinAsip PmgDinAsip PmgDinAsip pmgDpnAsip isgDpPasip ** 0000*	IGEVVIRANO VGEVIRTNO O*0 * O* VGEVIRTNO TPOPVJRAN TPOPVJRAN TPOPVJRAN TPOPVJRAN TPOPVJRAPURATL TPOPVJRAPURAT TPOPVJRAPURAT TPOPVJRAPU TPOPVJRAPU TPOPVJRAPU TPOPVJRAPU TPOPVJRAPU COVA COVA COVA COVA COVA COVA COVA	mAHRMRAGIG TAdRMKAQLG 000° tahkmK-qr(500 PGAMGKImqI PahbGRAKI PGALGSANH YGALGSANH YGALGSANH YGALGSANY YacLGRAXG YacLGRAXG YGLGRAXG GGO TCBPIdTaab 600 TCBPIdTaab
Jack bean Consensus H. pyl HpuB H. pyl HpuB H. pyl UreB Kl. aer UreC L. for alfa P. wil alfa J. ure alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB		svkyahilpa vcGinvUps o** vagepnilpa 401 klpeDagND rlkeBkGDND rlkeBkGDND rlkeBkGDND rlagDsaDND slagDtaBND	STNPTIPTTY STNPTIPTTY STNPTTPTPTY STNPTTPTY STNPT-Pytv NFRURRYISK NFRURRYISK NNRIKRYISK NNRIKRYISK NNRIKRYISK NNRIKRYISK NDRIKRYISK DOCKRYSK DOCKRYSK DOCKRYSK DOCKRYSK DOCKRYSK DOCKRYSK DOCKRYSK DOCKRYSK DOCKRYSK STNPTIPTTY STNPTIPTTY STNPTIPTTY STNPTIPTTY STNPTIPTTY STNPTIPTTY STNPTIPTTY STNPTIPTY STNPT	NTIBEHLDNL NTIDEHLDNL ***********************************	NVCHHLDPkU NVCHHLDPkU NVCHHLDPsi VSHVIGSVEV IS&IVGSVEV IS&IVGSVEV IS&IVGSVEV IS&IVGSIEV IAHEVGSIEK IAHEVGSIEK IAHEVGSIEK IAHEVGSIEK O O** *0 IsbyvGSIEV CRLITKLDNG CRLITKLDNG	PEDVAFADSR PEDIAFADSR PEDIAFADSR GRWADLVLWV GRVADLVLWS GRVADLVLWS GRLADLVLWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS CRLADVS CRL	IRSQTIAAED IRSQTIAAED IRKKTIAAED O* 0***0 IRTIAAEd PAFFGVKPAM PAFFGVKPAM PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAM ****** PaFFGVKPAM	LEDNGAISI VLADIGAISI *0°0° * VLADMGAISI VIKOGMIAWA IIKOGTAIS IIKOGMVYA IIKOGMVYA VIKOGWAYA VVKMGVIAWA 0°0° VIKOGWAWA 0°0°	MSSDtlamer issbsonmer msSDsonmer msSDsgamer gmodanasip gmodanasip gmodanasip gmodinasip iaddpssslp Pmodinaip Pmodinaip ** 0000* pmodpnasip	IGEVULRAWU VGEVILRTWQ VGEVILRTWQ TPQPVJYRAM TPQPVJYRAM TPQPVJYRAM TPQPVJRAM TPQPVJRAM TPQPVJRAM TPQPVJRAM TOPVJRAM TOPVJRAM TOPVJRAM TOPVJRAM TOPVJRAM TOPVJRAM	mAHRMKaQTC TAdKMKaQtC 0 00° tahkmK-qrt 5000 PahhGKAKMT PahhGKAKMT PahhGKAKMT PahhGKAKMT YacLGKAKX YacLGKAKX YacLGKAKX YacLGKAKX YacLGKAKX YacLGKAKX YacLGKAKX YacLGKAKX YacLGKAKX GalGkakyC fgalGkakyC 600 TCEPidTaab Tlnqpik skPAnkvsI
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB KI. ser UreC L. for alfa P. wul alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB KI. ser UreC		svkyahiLPA vagepniLPa 401 kLeeDapgND rLKaEKGDND plagestgDND plagestgDND slagetgDND slagetgDAEND slagetaEND plkcosseND * 0* -Lk-dsgdnD 501 TcVTFVSQAA anITTVSQAA anITTVSQAA	STNPT:PITV STNPT:PITV STNPT:PITV STNPT:PITV STNPT-PytV NFR:VRYIAK NFR:KRYIAK NFR:KRYIAK NMR:KRYIAK NMR:KRYIAK NMR:KRYIAK NMR:KRYIAK NMR:KRYIAK NMR:KRYIAK NFR:KRYIAK NFR:KRYIAK DdGVKEkaG yDk0:KEsLG yDk0:KEsLG	NTISEHLDML NTIDEHLDML NTIDEHLDML *0 *0 0*0 Ntidehldml itinpalaq ytinpalag yt	NVCHHLDPkV NVCHHLDPsi VSHVIGSVBV ISeYUGSVBV ISeYUGSVBV ISeYUGSVBV ISHVGSIBV ISHVGSIBV ISHVGSIBV ISHVGSIBV CRLISKHDLV CRLISKHDLV CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ	PEDVAPADSR PEDLAPADSR O*O ** ** peDvaFASSR GRMADLVLWY GRVADLVLWS GRVADLVLWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS FNDQTPn.IE fNDCTaE.IE	IRsqTIAAED IRkTIAAED IRkTIAAED IRKTIAAED IRKTIAAEd PIFFGAKPkM PAFFGVKPAM PAFFGVKPAM PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL VDPeTFAVKV VDPeTFAVKV VDPGTYLVTV	LEDMGAISI VLADIGAISI *0*0* * vLhDmGaiSi VIKOGMIAWA IIKOGFIAIs VIKOGMIAIS VIKOGMIAIS VIKOGMIAIS VIKOGMVAYA O*0* VIKOGMVAWA 0*0* VIKOGMVAWA 0*0* D	MSSDtlamer issdsgamer mssdsgamer amgdpnasip gmgdanasip pmgdinasip pmgdinasip pmgdinasip pmgdinasip addessi pmgdpnasip stadpensip stadpensip stadpensip stadpensip stadpensip stadpensip stadpensip stadpensip stadpensip	IGEVVIRANO VGEVIRTNO O**0 * O* VGEVIRTNO TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TOOTON TPOPVIRAN COVA COVA COVA COVA COVA COVA COVA COVA	mAHKMKAGÍ TAARMKAGÍ TAARMKAGÍ SOO° tahkmK-qr SOO PGAMGKImqI PahbGRAXI PGAMGKAXI PGAMGRAXI YGAGGRAVAI YGAGGRAVAI YGCLGRAXG YGCLGRAXG YGCLGRAXG SOO fgalGkakyG 600 TSEPAdKaSI TInqpik TsEPAAvuE
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB Kl. der UreC L. for alfa P. wil alfa J. ure alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB Kl. der UreB Kl. der UreB L. for alfa		svkyahiLPA vGGiNVLPs o** vagepniLPa 401 kLepdagMD rLKeBkGDND rLKeBkGDND rLagDSaDND sLagDtaIND sLagDtaIND sLagDtaIND sLagDtaIND sLagDtaIND slagD	STNPTIPITY STNPTIPITS STNPTPILS **0** 0 STnPT-Pytv NFRVKRYJAK NFRIKRYJAK NFRIKRYJAK NMRIKRYJAK NMRIKRYJAK NMRIKRYJAK NMRIKRYJAK IDGGVKEKAG JDGGVKEKAG GDGGIKEALG aanGVAELG	NTIBEHLDNL NTIDEHLDNL ***********************************	NVCHHLDPkV NVCHHLDPsi VSHVIGSVEV ISelVGSVEV ISelVGSVEV ISelVGSVEV ISEVGSVEV ISEVGSIEV ISEVGSIEV ISEVGSIEV ISEVGSIEV ISEVGSIEV CRIITKLDMQ CRUITKLDMQ CRUITKLDMQ CRUITKLDMQ CRUITKLDMQ	PEDVAFADSR PEDLAFADSR PEDLAFADSR O'O ** ** peDvaFAGSR GKWADLVLWY GKVADLVLWY GKVADLVLWS GKLADLVLWS GKLADLVLWG GKLADLVLWG GKLADLVLWG GKLADLVLWG GKLADLVLWG FINDTTE.IE fNDTTE.IE fNDTTE.IE INDTTE.IE	IRSGTIANED IRSGTIANED IRKKTIANED O* 0***0 IRTIANEd PAFFGVKPhM PAFFGVKPhM PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAK ***** PaFFGVKPAM VDPeTFAVKV VDPeTFAVKV VDPeTFAVVFV VDPGTFAVVFV VDPGTFAVVFV	LEDNGAISI VLDDIGAISI *0°0° * vLbDmGaiSi VIKOGMINWA IIKOGTIAIs VIKOGTIAIs VIKOGMIASI IIKOGMVYA IIKOGMVYA VIKOGMVAYA 0°0° VIKOGMIASA 0°0° VIKOGMIASA 0°0°	MSSDtlamer issbsonmar msSDsonmar	IGBVVIRAWI VGEVIRTWQ VGEVIRTWQ TPQPVJRAM TPQPVJRAM TPQPVJRAM TPQPVJRAM TPQPVJRAM TPQPVJRAM TPQPVJRAM TPQPVJRAM TPQPVJRAM CoPVIRAM TPQPVJRAM TCPVIRAM CoPVIRAM CoPVIRAM COVAL C	mAHRMR.aGf TAdKMKaQtG 0 00° tahkmK-qr 5000 PahloKAKMT PahloKAKMT PahloKAKMT PahloKAKMT YGLGGAKMT YacLGKAKT YacLGKAKT YacLGKAKT GtyGrSt SglQkakYC 600 TCEPIdTaah Tlnqpik TsEPAhkVeI TsEPAdvLPP
Jack bean Consensus H. pr/ HpuB H. pr/ HpuB H. pr/ UreB KI. aer UreC L. for alfa Jack bean Consensus Y. ent YeuC H. pr/ HpuB H. pr/ UreB KI. aer UreC L. for alfa P. mir UreB		svkyahiLPA vGGLNVLPs o** vagepniLPa 401 tLseDsapND rLKsEKGDND rLseKGDND pLdgDSkydD tLsgDSsLND sLsgDSsLND sLsgDSsLND sLsgDSsLND * o* -Lk-dsgdnD 501 TcVTFVSQAA aniTFVSQAA aniTFVSQAA aniTFVSQAA SciTTISQA TcVTFVSQAA	STNPT:PTTV STNPT:PLTV STNPT:PLTV STNPT:PLTV STNPT-PytV NFR:VXRYIAK NFR:KRYIAK NFR:KRYIAK NMR:KRYIAK NMR:KRYIAK NMR:KRYIAK NMR:KRYIAK NMR:KRYIAK NFR:KRYAK NFR:KRYAK N	NTISEHLDML NTIDEHLDML *0 *0 0*0 Ntigelidmi itinpaiaqg ytinpaiaqg ytinpaiag ytinpaiag ytinpaiag ytinpaiag ytinpaiag ytinpaiag ytinpaiag ytinpaiag utinpaiag ytinpaiag utinpaiag ytinpaiag utinpaiag utinpaiag ytinpaiag utinpaiag ytinpaiag utinpaiag ytinpaiag utinpaiag ytinpaiag ytinpaiag utinpaiag ytinpaiag utinpaiag ytinpaiag ytinpaiag utinpaiag y	NVCHHLDFkV NVCHHLDFsi VSHVIGSVEV ISeYVGSVEV ISeYVGSVEV ISeYVGSVEV ISeYVGSVEV ISHVGSIEV ISHVGSIEV ISHVGSIEV ISHVGSIEV CRUITKLDMQ CRUITKLDMQ CRUITKLDMQ CRUITKLDMQ CRUITKLDMQ CRUITKLDMQ CRUITKLDMQ	PEDVAPADSR PEDLAPADSR O*O ** ** peDvaPADSR GKMADLVLWY GKVADLVLWS GKVADLVLWS GKLADLVLWS GKLADLVLWS GKLADLVWW GKLADLVWW GKLADLVWW TNDQTPn.IE fNDtTaE.IE fNDtTaE.IE fNDtTaE.IE hNslyPs.IE	IRsqTIAABD IRkKTIAABD IRkKTIAABD O* 0***0 IRTIAABd PAFFGVRPAM PAFFGVRPAM PAFFGVRPAM PAFFGVRPAL PAFFGVRPAL PAFFGVRPAL PAFFGVRPAL PAFFGVRPATRVIV VnseTINVIV VnseTINVIV VnseTINVIV VnseTINVIV VnseTINVIV	LEDMGAISI VLADIGAISI *0*0* * vLhDmGaiSi VIKOGMINWA IIKOGFIAIs VIKOGFIAIs VIKOGMIAIA VIROGMIAIA VIROGMIAIA VIROGMIAIA VIKOGMIAWA 0*0* VIKGKMIAWA D D D D D	MSSDtlamer issdsgamer mssdsgamer amgdpnasip gmgdanasip pmgdnasip pmgdinasip pmgdinasip pmgdinasip ssip pmgdinasip ssip pmgdpnasip ** 0000*	IGEVVIRANG VGEVIRTNO O**0 * O* VGEVIRTNO TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN TPOPVIRAN OTPAPVIRAN OTPAPVIRAN OTPAPVIRAN OTPAPVIRAN OTPAPVIRAN	mAHKMKAGÍ TAdRHKAGLÓ 000* tahkmK-qr 500 PGAMGKtmq PahbGRAKT PGAMGKAKT PGALGSANH YacLGRAKY YacLGRAKY YacLGRAKY YacLGRAKY FGLGRAgg *00 fgalGkaky 600 CEPIdTaab Tlnqpik TsEPANkVEP TCBAATLEP
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB RI. eer UreC L. fer alfa P. wil alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB RI. eer UreC L. fer alfa P. wil alfa		svkyahiLPA vcGiNVLPs o** vagepniLPa 401 kLpaDapgND rLKaEkGDND rLKaEkGDND pLdgDSkydD pLdgDSkydD pLKcDSsDND sLagDSsCND pLKcDSsDND 501 ToVTFVSQAA criTFVSQAA criTFVSQAA criTFVSQAA criTFVSQAA TSmlFmSkAg	STNPFIPTTV STNPFIPTTS STNPTPLTS **O** O STnPT-Pytv NFRVvRTVAK NFRIKRYISK NFRIKRYISK NNRIKRYISK NNRIKRYISK NNRIKRYISK NNRIKRYISK NNRIKRYISK NNRIKRYISK NNRIKRYISK NNRIKRYISK NNRIKRYISK STOPS NGIKESG STOPS S	NTIBEHLDNI NTIDEHLDNI "O *0 *0 *0 NTIDEHLDNI ITINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG UTINPALAG UTINPALAG UTINPALAG UTINPALAG UTINPALAG UTINPALAG LDrQViaVKN LBrQVLPVKN LBrQVLPVKN LBrQVLPVKN LASILGVVKG LAKTLEVVN LKalIGTVG	NVCHHLDPkU NVCHHLDPsI VSEVIGSVEV ISeYVGSVEV ISeYVGSVEV ISeYVGSVEV ISeYVGSVEV ISEVGSIEV ISEVGSIEV fSqTVGSIEV fSqTVGSIEV CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLSMI	PEDVAPADSR PEDLAPADSR PEDLAPADSR O*O ** ** peDvaFASSR GRWADLVLWS GRVADLVLWS GRVADLVLWS GRLADLVLWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS GRLADLVWS INDCTAH.IE INDCTAH.IE INNCTAH.IE bNSTVPE.IE	ΙR&QTIAAED IR&QTIAAED IR&KTIAAED IR&KTIAAED PAFFOVEPAM PAFFOVEPAM PAFFOVEPAM PAFFOVEPA PAFFOVEPAL PAFFOVEPAL PAFFOVEPAL VDPOTPAVKV VDAOTYAVV VDAOTYAVV VDAOTYAVI IDPOTYIVE	LEDMGAISI VLADIGAISI *0°0° * vLhDmGaiSi VIKOGMINWA IIKOGTIAIS IIKOGYIAIS IIKOGWVYA IIKOGMVYA VIKOGWVYA VIKOGWVAWA 0°0° VIKOGWVAWA 0°0° UKOGWVAWA 0°0°	MSSDtlamer issbsonmar msSDsonmar	IGEVVIRANG VGEVIRTNO O*0 * 0* VGEVIRTNO TPOPVJRAN TPOPVJRAN TPOPVJRAN TPOPVJRAN TPOVIRTPO TPOPVJRAN TPOPVJRAN TPOPVJRAN TPOPVJRAN TPOPVJRAN O*0 *0 TPOPVJRAN COVA O*0 *0 TPOPVJRAN COVA O*0 *0 TPOPVJRAN TPOPVJRAN COVA O*0 *0 TPOPVJRAN TPOPVJRAN TPOPVJRAN TPOPVJRAN TPOPVJRAN TPOPVJRAN TPOPVJRAN TPOPVJRAN TPOPVJRAN	mAHRMRAGIC TAdRMKAQLO 000° tahkmK-qr(5000 PahbGKAKT PahbGKAKT PahbGKAKT PahbGKAKT YacLGKAXQ YacLGKAXQ YacLGKAXQ YacLGKAXQ GCO fgalGkakyd fgalGkakyd CCEPidTaab fgalGkakyd TSEPAdvLPB TSEPAdvLPB TCDaApLEI VCEPATELPB
Jack bean Consensus H. pyl HpuB H. pyl UreB Kl. aer UreC L. for alfa J. ure alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl TreB Kl. aer UreC L. for alfa P. mir UreB H. pyl TreB H. pyl TreB H. pyl TreB J. for alfa J. ure alfa		svkyahilpa vcGinvLPs o** vagepniLPa 401 klpeDagND rLKeBKGDND rLKeBKGDND blagDSaDND slagDtABND slagDtABND pLGDSSYDD rLCDSSDND * o* -Lk-dsgdnD 501 fcvTFVSQAA anITFVSQAA criTFVSQAA rcvTFVSQAA TSmIFmSKAg TSmiFmSKAg	STNPT:PTTV STNPT:PLTV STNPT:PLTV STNPT:PTV STNPT-PytV NFR:VRYIAK NFR:KRYAK NFR:KR	NTIBEHLDNL NTIBEHLDNL ***********************************	NVCHHLDPkV NVCHHLDPsi VSHVIGSVEV IS&IVGSVEV IS&IVGSVEV IS&IVGSVEV IS&IVGSVEV IS&IVGSIEV IS&IVGSIEV IS&IVGSIEV IS&IVGSIEV O O***0 CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKASMI CRWITKASMI	PEDVAPADSR PEDLAPADSR O*O ** ** peDvaPADSR GRMADLVLWV GRVADLVLWV GRVADLVLWS GRVADLVLWS GRLADIVLWD GRLADIVLWD GRLADIVLWD GRLADIVLWD GRLADIVLWD FNDGTPD.IE fNDCTAH.IE fNDCTAH.IE fNDCTAH.IE hNslQPD.II INNTYPE.IE NNSTYPE.IE	IRSGTIABD IRSGTIABD IRKTIABD O* 0***0 iRTIABd PAFFGVKPAM PAFFGVKPAM PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAM ***** PaFFGVKPAM ***** PaFFGVKPAM ****** PaFFGVKPAM ******	LEBDMGAISI VLnDiGAISI *0°0° * vLhDmGaiSi VIKOGMINWA IIKOGTAIS IIKOGMVYA IIKOGMVYA VIKOGWAYA VVKMGVIARG D	MSSDtlaner issbsonmer msSDsonmer msSDsgamgr gmodannsip gmodannsip gmodannsip gmodannsip modinnaip Pmodinnaip Pmodinnaip ** 0000* pmodpnasip ** 0000* gmaclakkl	IGEVVIRANG VGEVIRRING O*O * O* VGEVIRRING TPOPVYRAN TPOPVYRAN TPOPVYRAN TPOPVHRPN TPOPVHRPN TPOPVHRPN TPOPVHRPN TPOPVHRPN TPOPVHRPN TPOPVHRPN TPOPVHRPN TPOPVHRPN TPOPVHRPN TPOPVHRPN TPOPVHRPN TPOPVHRPN TOGVURANG TPOPVHRPN TOGVURANG TPOPVHRPN TOGVURANG TPOPVHRPN TOGVURANG TPOPVHRPN TOGVURANG TPOPVHRPN TOGVURANG TPOPVHRPN TOGVURANG TPOPVHRPN TPOP	mAHKNKAGC TAARMKAGLC 000* tahkmK-qr 500 PGAMGKtmq PahbGRAXT PGADGRAXT PGADGRAXT PGADGRAXT YGLGRAXY YacLGRAXY YacLGRAXY YacLGRAXY TGLGRAY YacLGRAXY TGLGRAY TacLGRAXY TSLPANKUS TSLPANKUS TSLPANKUS TSLPANKUS TSLPANKUS TSLPANKUS TCLBAJTLEP VCEPATELP VCEPATELPS
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB KI. aer UreC L. for alfa P. wil alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB KI. aer UreC L. for alfa P. wil alfa D. ure alfa Jack bean		svkyahiLPA vGGiNVLPs o** vagepniLPa 401 kLpaDapgND rLKaEKGDND rLKaEKGDND pLAGDSkydD pLAGDSkydD pLAGDSkydD pLAGDSkydD pLCDSsDND sLagDSsDND sLagDSsDND sLagDsScND pLK-dsgdnD 501 TCVTTVSQAA aniTFVSQAA TCVTTVSQAA TCVTTVSQAA TCVTTVSQAA TSmIFmSLAg TSvsFvSkaA	STNPTIPTTY STNPTIPTTY STNPTPLTS STNPT-Pytv NFRVvRTVAK NFRIKRYISK NFRIKRYISK NMRIKRYISK NMRIKRYISK NMRIKRYISK NMRIKRYISK DGGVKEkaG yDkGIKELG yDkGIKELG JDAGVDELG IBAGVDELG IBAGVDELG IBAGVDELG IBAGVDELG	NTIBEHLDNI NTIDEHLDNI NTIDEHLDNI ITINPALAQG YTINPALAQG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG LDrQViaVKN LErQVLPVKN LERQVLPVKN LESQVLPVKN LESQULPVKN LAGLIGTVG LAGLIGTVG LEGLLFVKN LAGLIGTVG LEGLLFVKN LAGLIGTVG	NVCHHLDFkV NVCHHLDFkV NVCHHLDFsi VSEVIGSVEV ISeYVGSVEV ISeYVGSVEV ISEVVGSVEV ISEVVGSVEV ISEVVGSIEV ISEVGSIEV CRUISKDLV CRUISKDV CRUSKDV CRUSK	PEDVAPADSR PEDIAPADSR PEDIAPADSR O'0 ** ** peDvaFASSR GRMADLVLW* GRVADLVLW* GRVADLVLW* GRLADLVLW* GRLADLVLW* GRLADLVLW* GRLADLVW* GRLADLVW* GRLADLVW* GRLADLVW* GRLADLVW* GRLADLVW* GRLADLVW* GRLADLVW* SKIADLVW* GRLADVW* GRLADVW* GR	IRsqTIAAED IRktIAAED IRktIAAED IRktIAAED PrffGaKPkm PAFFGVKPam PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL VDPGTFAVKV VDsGTIAVfU VDsGTIAVfU IDPQTYdVKI IDPQTYdVKI IDPQTYdVKI IDPQTYdVKI IDPQTYdVKI IDPQTYdVKI	LEDMGAISI VLADIGAISI *0*0* * vLhhmGaiSi VIKOGMINWA IIKOGFIAIs IIKOGMYAYA IIKOGMYAYA VIKAGMYAYA VIKAGMYAYA D	MSSDtlamer issbsgamer msSDsgamer	IGEVVIRAMO VGEVIRTMO O*0 * 0* VGEVIRTMO TPOPVJRAM TPOPVJRAM TPOPVJRAM TPOPVJRAM TPOPVJRAPM TPOPVJRAPM TPOPVJRAPM TPOPVJRAPM TPOPVJRAPM TPOPVJRAPM *0 ** 0 TPQPV-yRpm Gvha GKu GKL GKL	mAHRMGAGT TAdKMKAGLC 000° tahkmK-qrt 500 PGAMGKImqT PahbGRANT PGALGSANH YGALGSANH YGALGSANH YGALGSANY YacLGKANY YacLGKANY YacLGKANY YGCJGKANY FGYGYSILS YGLJGKANY FGYGYSILS YGLJGKANY FGYGYSILS YGLJGKANY FGYGALGKANY TCBPIdTaab TSBPAdvLP TCDaApTLPI YCEPATELP aCTENTSSI CVSATTYPI
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Jack bean Consensus H. pyl HpuB H. pyl HpuB H. pyl UreB Kl. eer UreC L. for alfa P. wil alfa J. ure alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB Kl. eer UreC L. for alfa P. wil alfa J. ure alfa Jack bean Consensus		svkyahiLPA vcGiNVLPs o** vagepniLPa 401 kLpaDapyhD rLKaEkGDND rLKaEkGDND rLAGDSkydD sLagDsaND sLagDsaND sLagDsaND sLagDsaND sLagDsaND sLagDsaND sLagDsaND sLagDsaND sLagDsaND sl	STNPTIPITY STNPTIPITY STNPTPILS **0***0 STnPT-Pytv NFRVxRYIAK NFRIKRYIAK NFRIKRYIAK NMRIKRYIAK NMRIKRYIAK NMRIKRYIAK NMRIKRYIAK NMRIKRYIAK NMRIKRYIAK DOGWYERAG YDKOIKEAG YDKOIKEAG YDKOIKEAG JDAGVYERAG IBAGVYERLG IBAGVYERLG IBAGVYERLG IBAGVYERLG 0 0 0 -d-gvks-1g	NTIBEHLDML NTIDEHLDML NTIDEHLDML ITINPALAQG YTINPALAQG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG C****C0 * YTINPALAG C****C0 * C****C0 * C***C0 * C****C0 * C****C0 * C****C0 * C***C0 * C***	NVCHHLDPkV NVCHHLDPkV NVCHHLDPsi VSHVIGSVEV IS@IVGSVEV IS@IVGSVEV IS@IVGSIEV IS@IVGSIEV IS@IVGSIEV IS@IVGSIEV fSQIVGSIEV fSQIVGSIEV CRLIT&LDMQ CRLIT&CRLIT	PEDVAPADSR PEDLAPADSR PEDLAPADSR O*O ** ** peDvaFAeSR GKNADLVLWS GKVADLVLWS GKLADLVLWS GKLADLVLWS GKLADLVWS GKLADLVWS GKLADLVWW CKLADLVWW CKLADLVWW FNDQTPn.IE FNDTTAH.IE FNDTTAH.IE FNDTTAH.IE INNTTFKIE NNSTYPH.IE WNSATPN.IE INNSTFKIE NNSTYPH.IE	IRSQTIANED IRSQTIANED IRKTIANED O* 0***0 IRTIANEd PAFFGVKPAM PAFFGVKPAM PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAM ***** PaFFGVKPAM ***** PaFFGVKPAM ****** PaFFGVKPAM ************************************	LHEDMGAISI VLmDiGAISI *0°0° * vLhDmGaiSi VIKOGMINWA IIKOGIIAIS IIKOGVIAIS VIKOGWAYA VIKOGWAYA VVKNGVAYA VVKNGVAYA 0°0° VIKOGWAYA D	MSSDtlamer isSDsQAMGR o**06**0 msSDsQAMGR oMGDPNASIP gMGDaNASIP gMGDaNASIP gMGDANASIP MGDINASIP **0000* pmGDPNASIP **0000* pmGDPNASIP **0000* gmGDPnasiP **0000* pmGDPnasiP	IGBVVIRAWI VGEVIRTWO O*0 * 0* VGEVIRTWO TPOPVJRAM TPOPVJRAM TPOPVJRAM TPOPVJRAM TPOPVJRAM TPOPVJRAM TPOPVJRAM TPOPVJRAM TPOPVJRAM O** * 0 TPOPVJRAM * 0 TPOPV	mAHRMRAGIC TAdKMKAQCG 000° tahkmK-qr 500 GAMGKImqI PahhGKAKT PahhGKAKT PahhGKAKT YacLGKAKY YacLGKAKY YacLGKAKY YacLGKAKY YacLGKAKY GGUGTAL YGLGKAKY GGUGTAL YGLGKAKY GGUGTAL SC TSEPAJ TSEPAJ TSEPAJ COST TSEPAJ TSEPAJ COST C
Jack bean Consensus H. pr/ HpuB H. pr/ HpuB H. pr/ HpuB KI. aer UreC L. for alfa Jack bean Consensus Y. ent YeuC H. pr/ HpuB H. Jack bean Consensus		vkyahiLPA vagepniLPa 401 kLeabapgND rLKaEKGDND pldgDSkydD sLagDSaDND sLagDSaDND sLagDSaDND sLagDSaDND sLagDSaDND sLagDSaDND sLagDSaDND sLagDSaDND sLagDSaDND sLagDSaDND sLagDSaDND sLagDSaDND sLagDSaDND sLagDSaDND sLagDSaDND sciffvSQAA aniTTVSQAA aniTTVSQAA aniTTVSQAA sciffvSQAa sciffvSqAa s° 0 ts-tfvSqAa 601	STNPT:PTTV STNPT:PITV STNPT:PITV STNPT:PITV STNPT:Pytv NFR:VRT:SK NFR:KRT:SK NFR:SK NFR:KRT:SK NFR:	NTIZHLDML NTIDHLDML NTIDHLDML *0 *0 *0 *0 NtidBhldMl iTINPAIAAG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG YTINPAIAHG LBCQVLPVAN LBCQVLPVAN LBCQVLPVAN LBCQVLPVAN LBCQVLPVAN LBCQLPVAN LBCQLPVAN LCCLPVA	NVCHHLDPkV NVCHHLDPkV NVCHLDPsi VSHVIGSVBV ISeYVGSVBV ISeYVGSVBV ISHVGSIBV ISHVGSIBV ISHVGSIBV ISHVGSIBV CRLISKHDLV CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRITKLAMM	PEDVAPADSR PEDLAPADSR O*O ** ** peDvaPASR GKWADLVLWY GKVADLVLWS GKVADLVLWS GKLADLVLWS GKLADLVLWS GKLADLVLWS GKLADLVLWG GKLADLVLWG GKLADLVLWG GKLADLVLWG GKLADLVLWG GKLADLVLWG FNDQTPn.IE fNDCTAE.IE fNDCTAE.IE fNDCTAE.IE fNDCTAE.IE bNslQPD.IL lNNTVPKIE bNslVPE.IE bNslVPE.IE bNslVPE.IE bNslVPE.IE bNslVPE.IE	IRsqTIAABD IRsqTIAABD IRkKTIAABD O* 0***0 IRTIAABd PAFFGVKPAM PAFFGVKPAM PAFFGVKPAM PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL IBPGTYIVKA UDPGTFGVVV UDPGTYGVKL IBPGTYIVKA UDPGTFGAVV UDPGFFGAVV UDPGFFGAVV UDPGFFGAVV UDFGFFGA	LEDMGAISI VLADIGAISI *0°0° * vLhDmGaiSi VIKOGMIAWA IIKOGFIAIs VIKOGMIAIA VIKAGMIAIA VIKAGMIAIA VIKAGMIAIA O*0° VIKGGMIAWA D	MSSDtlamer isSDsQnMGR 0*00*0*0 msSDsQAMGR aMGDPNASIP GMGDaNASIP PMGDINASIP PMGDINASIP PMGDINASIP MGDINASIP MGDINASIP diGDPNSSIP diGDPNSSIP **0000* pmGDPNSSIP **0000*	IGEVVIRAMO VGEVIRTMO O**0 * O* VGEVIRTMO TPOPVJTRAM TPOPVJTRAM TPOPVJTRAM TPOPVJTRAM TPOPVJTRAM TPOPVJRAPM TPOPVJRAPM TPOPVJRAPM TPOPVJRAPM ************************************	mAHKMKAGÍ TAARMKAGÍ TAARMKAGÍ OO° tahkmK-qr Solo PGAMGKImgI PahbGRAKT PGALGSANHY YacLGRAKY YacLGRAKY YacLGRAKY YacLGRAKY FGLYGRAL FGLYGRAKY GO TGEPIdTAG SO TGEPIdTAG TSEPAALY TSEPAAVLP TCEPATELP VCEPATELP VCEPATELP SCTENTES
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB Ri. der UreC L. fer alfa P. wil alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB RI. der UreC L. fer alfa P. wil alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB RI. der UreB RI. der UreB VI alfa Jack bean Consensus Y. ent YeuC		svkrahiLPA vGGiNVLPs o** vagepniLPa 401 kLpaDapyND rLKaEkGDND rLKaEkGDND pLdgDSkydD sLagDSaDND sLagDSaDND sLagDSaDND slagDSefND pLKcDSsDND tovTTVSQAA criTFVSQAA CriT	STNPTIPTTY STNPTIPTTY STNPTTPLTS **O** O STNPT-Pytv NFRVKRYLSK NFRIKRYLSK NFRIKRYLSK NNRIKRYLAK NNRIKRYLAK NNRIKRYLAK NNRIKRYLAK NNRIKRYLAK NNRIKRYLAK NNRIKRYLAK NNRIKRYLAK NNRIKRYLAK NNRIKRYLAK SQDGRYKRAG JDGVYERLG IBaGVYERLG IBaGVYERLG IBaGVYERLG IBaGVYERLG IBaGVYERLG IBaGVYERLG IBaGVYERLG IBAGVYERLG IBAGVYERLG IBAGVYERLG IBAGVYERLG IBAGVYERLG IBAGVYERLG IBAGVYERLG IBAGVYERLG	NTIBEHLDNL NTIDEHLDNL NTIDEHLDNL ITINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG LBrQVLAVKN LBrQVLPVKN LBrQVLPVKN LBrQVLPVKN LASILGYVG LASILGYVG LASILGYVG LASILGYVG LASILGYVG LASILGYVG S. LogylpVKN LASILGYVG LASILGYVG S. LogylpVKN LASILGYVG S. LogylpVKN S. S. S	NVCHHLDPkU NVCHHLDPkU NVCHHLDPsi VSHVIGSVBV IS@YVGSVBV IS@YVGSVBV IS@YVGSIBV IS@YVGSIBV fSQTVGSIBV fSQTVGSIBV fSQTVGSIBV CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ CRLITKLDMQ O CRLITKLDMQ O CRLITKLDMQ	PEDVAPADSR PEDIAPADSR PEDIAPADSR O*O ** ** peDvaFAeSR GRWADLVLWS GRVADLVLWS GRVADLVLWS GRLADLVWS GRLADLVWS GRLADLVWG GRLADLVWG GRLADLVWG GRLADLVWG GRLADLVWG GRLADLVWG FNDCTAH.IE FNDCTAH.IE FNDCTAH.IE HNSTYPE.IE WNeaTPA.IE INSTYPE.IE WNeaTPA.IE INSTYPE.IE VNeaTPA.IE	IRsqTIAHED IRkTIAHED IRKTIAHED IRKTIAHED FIFFGAKPHM PAFFGVKPAM PAFFGVKPAM PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL VDPeTFAVKV VnseTYhVfV VnseTYhVfV VnseTYhVfV VnseTYhVfV VDPGTYAVKI DPGTYAVKI DDGCTYAVKI DDGCTYAVKI VDPGTFAVKV VDPGTYAVKI VDPGTYAVKI VDPGTYAVKI	LEDNGAISI VLADIGAISI *000* *000* VLADMGAISI VIKOGMIAWA IIKOGIIAIS IIKOGMVIA VIKOGIIAIS VIKOGMVAYA VIKOGMVAYA O00* VIKOGMVAWA 00* VIKOGMVAWA 00* VIKOGMVA VIKOGMVA VIKOGMVA VIKOGMVA VIKOGMVA VIKOGMVA VIKOGMVA VIKOGMVA VIKOGMVA VIKOGMVA VIKOGMVA VIKOGMVA VIKOGMVA VIKOGMVA VIKOGMVA VIKOGMVA VIKOGMVA VIKOGMVA VIKOVA VI	MSSDtlamer issbsonmar msSDsonmar msSDsonmar qMGDanasIP qMGDanasIP qMGDanasIP pMGDinasIP PMGDinasIP PMGDinasIP e*0000* pmGDpnasIP digDpnasIP mGDpnasIP gmGDpnasIP mGDpnasIP	IGBVVIRAWI VGEVIRTWO O*0 * 0* VGEVIRTWO TPOPVJYRAW TPOPVJYRAW TPOPVJYRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW O*0 *0 TPOPVJRAW O*0 *0 TPOPVJRAW O*0 *0 TPOPVJRAW O*0 *0 TPOPVJRAW O*0 *0 TPOPVJRAW O*0 *0 TPOPVJRAW O*0 *0 TPOPVJRAW O*0 *0 TPOPVJRAW O*0 TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW O*0 *0 TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW TPOPVJRAW O*0 *0 O TPOPVJRAW COVA CALLON	mAHRMGAGT TAdKMKQLCG 000° tahkmK-qr 500 GAMGKImqI PahbGKAKT PahbGKAKT PahbGKAKT YacLGKAXQ YacLGKAXQ YacLGKAXQ YacLGKAXQ YacLGKAXQ GGO TCEPidTaab fgalGkakyd fgalGkakyd CCEPidTaab fgalGkakyd TCEPidTaab TSEPAAVLPB TCDaApTLPI VCEPATELPB aCrtsnrssi CvsaATTVPI tcepattlpm
Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB Kl. aer UreC L. for alfa J. ure alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB Kl. aer UreC L. for alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB		svkyahiLPA vGGLNVLPs o** vagepniLPa 401 tLseDsapND rLKsEKGDND pldgDSkydD pldgDSkydD rLagDSaDND slagDsseND pldgDSkydD slagDsseND pldgDSkydD slagDsseND pldgDSkydD slagDsseND pldgDSkydD slagDsseND pldgDSkydD slagDsseND slagDsseND slagDsseND slagDsseND so so so so so tsvFVSQAA aniTYVSQAA aniTYVSQAA aniTYVSQAA aniTYVSQAA aniTYVSQAA aniTYVSQAA aniTYVSQAA sniTYVSQAA sniTYVSQAA sniTYVSQA so so tsvFVSLA ssa tsvFVSLA so so so so so so so so so so so so so	STNPT:PITV STNPT:PITV STNPT:PITV STNPT:PITV STNPT:PITV NFR:VXRYIAK NFR:VXRXX	NTISHLDML NTIDHLDML NTIDHLDML *0 *0 *0 *0 NtidBhldMl ITINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG LDrQViaVKN LBrQVLFVKN LBrQULFVKN LBrQULFVKN LBrGVLFVKN LBSLJGVVG LDRIGFVG LGXIGFVG LBKGLLFVKN LASIJGFVG LSKGLLFVKN LASIJGFVG SC SS) (573) (559)	NVCHHLDPkV NVCHHLDPkV NVCHHLDPsi VSHVIGSVBV ISeVVGSVBV ISeVVGSVBV ISeVVGSVBV ISHVGSIBV ISHVGSIBV ISHVGSIBV CRUISIBV CRUISIBV CRUISIBV CRUISIBV CRUITKLDMQ CRUITKLDMQ CRUITKLDMQ CRUITKLDMQ CRUITKLDMQ CRUITKLDMQ CRUITKLDMQ CRUITKLDMQ CRITKLAMM	PEDVAPADSR PEDLAPADSR O*O ** ** peDvaPASR GKMADLVLWY GKVADLVLWS GKLADLVLWS GKLADLVLWS GKLADLVWS GKLADLVWS GKLADLVWS GKLADLVWS GKLADLVWS GKLADLVWS GKLADLVWS TNDQTPn.IE fNDtTaH.IE fNDtTaH.IE fNDtTAH.IE hNsTVPH.IE hNsTVPH.IE hNsTVPH.IE hNsTVPH.IE hNSTVPH.IE NSTPH.IE	IRsqTIAAED IRsqTIAAED IRkKTIAAED O* 0***0 IRTIAAEd PAFFGVKPDM PAFFGVKPDM PAFFGVKPDM PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL VDPeTFAVKV VDsGTISVTV UDSGTISVTV UDSGTYGVTV UDSGTYGVKL IBPGTYIVKA IBPGTYIVKA UDPestVKA OO O Vdpqty-vkv	LEDMGAISI VLADIGAISI *0*0* * vLhDmGaiSi VIKOGMIANA IIKOGFIAIs VIKOGHIAIS VIKOGMIAIA VIROGHIAIS VIKOGMIAIA VIROGMIAIA VIKOGMIANA 0*0* VIKGKMIANA D	MSSDtlamer issDsQAMGR or*oo**0* msSDsQAMGR aMGDPNASIP GMGDaNASIP PMGDINASIP PMGDINASIP PMGDINASIP PMGDINASIP MGDINASIP MGDINASIP ** 0000* pmGDPNASIP ** 0000*	IGEVVIRANG VGEVIRTNO O**0 * O* VGEVIRTNO TPOPVYRAN TPOPVYRAN TPOPVYRAN TPOPVARTN TPOPV	mAHKMKAGÍ TAARMKAQL OOO* tahkmK-qr 500 PGAMGKtmq PahbGKAKT PGALGARAKY YacLGKAKY YacLGKAKY YacLGKAKY YacLGKAKY YacLGKAKY YacLGKAKY GGOGTAVA YacLGKAKY TGBAIGKAKY SGLGKAG SGLGKAKY TGBAIGKAKY TGBAIGKAKY CCEPAIGAN TINQDIK TSEPAAVLP TCBAATLEP VCEPATELP VCEPATELPS CFSATELPS CFSATELPS
Jack bean Consensus H. pyl HpuB H. pyl UreB Kl. 4er UreC L. fer alfa P. wil alfa J. ure alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB Kl. 4er UreC L. fer alfa P. wil alfa U. ure alfa Jack bean Consensus X. ent YeuC L. fer alfa P. wil alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB Y. ent YeuC H. pyl HpuB		svkyahiLPA vGGiNVLPs o** vagepniLPa 401 kLpaDapgND rLKaEKGDND rLKaEKGDND pLdgDSkydD pLdgDSkydD sLagDSaDND sLagDSaDND sLagDSaDND pLtoSsDND rCvTTVSQAA aniTFVSQAA critFVSQAA critFVSQAA SsiFWSKAA SsiFWSKAA SisFVSKAA o*o ts-tfvSqaa 601 nQRYFFg AQIssiF	STNPF1PTTV STNPF1PTTV STNPTPLTS **O** O STnPT-Pytv NFRVvRTVAK NFRIKRY1sK NFRIKRY1sK NFRIKRY1SK NMRIKRYTAK NMRIKRYTAK NMRIKRYTAK O O O O O O O O O O O O O O O O O O O	NTIBEHLDNI NTIDEHLDNI NTIDEHLDNI ITINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG YTINPALAG O*****0 ****0 *****0 *****0 *****0 *****0 *****0 ****0 *****0 ****0 ****0 ****0 *****0 ****0 ****0 ****0 ****0 ****0 *****0 *****0 *****0 ****0 *****0 *****0 *****0 *****0 *****0 *****0 *****0 *****0 *****0 *****0 *****0 ******	NVCHHLDFkV NVCHHLDFkV NVCHHLDFsi VSEVIGSVEV ISeTVGSVEV ISeTVGSVEV ISETVGSVEV ISETVGSVEV ISETVGSVEV ISETVGSVEV ISETVGSVEV CRUISEN CRUISENDLV CRUISENDLV CRUISENDLV CRUITENDMC CRUITENDMC CRUITENDMC CRUITENDMC CRUITENDMC CRUITENDMC CRUITENDMC CRUITENDMC	PEDVAPADSR PEDIAPADSR PEDIAPADSR O'0 ** ** peDvaFAeSR GKMADLVLW* GKVADLVLW* GKVADLVLW* GKLADLVLW* GKLADLVW* GKLADVW* GKLADVW* GKLADVW* GKLADV	IRsqTIAABD IRktIAABD IRktIAABD IRktIAABD PAFFGVKPAM PAFFGVKPAM PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL VDPGTFAVKV VDsGTIAVfV VDsGTIAVfV VDsGTIAVfV VDgQTYGVXL IDPQTIAVKL IDPQTIAVKL IDPQTIAVKL ODGOTGAUV VDPGTF4VKV VDGGTYGVXV	LEBDMGAISI VLADDIGAISI *0*0* * vLhhmGaiSi VIKOGMINWA IIKOGTIAIs IIKOGMIAIS VIKOGMIAIS VIKOGMIAIS VIKOGMIAIS VIKOGMIAIS VIKOGMIAIS 0*0* VIGGTMIAS D	MSSDtlamer issbsgamgr msSDsgamgr msSDsgamgr MGDanasip MGDanasip MGDanasip MGDinasip MGDinasip MGDinasip MGDinasip MGDINAsi MGDPNASIP dioDPNASIP dioDPNASIP dioDPNASIP dioDPNASIP dioDPNASIP dioDPNASIP	IGBVVIRAWO VGEVIARTWO O*0 * 0* VGEVIARTWO TPOPVJYRAW TPOPVJYRAW TPOPVJYRAW TPOPVHYRAW TPOPVHYRAW TPOPVHYRAW TPOPVHYRAW TPOPVHYRAW TPOPVHYRAW TPOPVHYRAW TPOPVHYRAW TPOPVHYRAW TPOPVHYRAW TPOPVHYRAW TPOPVHYRAW TPOPVHYRAW TOOVHY O TPOPVHYRAW COVALOVAL COVA	mAHRMGAOT TAdKMKAQCO 0 00° tahkmK-qrt 500 PahboKAKT PahboKAKT PahboKAKT PahboKAKT PahboKAKT PahboKAKT PahboKAKT PahboKAKT PGALGSANG YacLOKANG YacLOKANG TCEPidTaab fgalGkakyd 600 TCEPidTaab fgalGkakyd 600 TCEPidTaab TCEPidTaab TCDaApTLPI vCEPATeLPB aCrtsnrssi cvsaATTVPI tcepattlpm
Jack bean Consensus H. pyl HpuB H. pyl UreB Kl. aer UreC L. for alfa P. wil alfa J. ure alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB Rl. aer UreC L. for alfa P. wil alfa U. ure alfa P. mir UreB Rl. aer UreC L. for alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB Kl. aer UreC		svkyahiLPA vagepniLPa 401 klpeDapgND rLKaEKGDND pldgDSkydD slagDtaEND pldgDSkydD slagDtaEND pldgDSkydD slagDtaEND pldgDSkydD slagDtaEND pldgDSkydD slagDtaEND pldgDSkydD slagDtaEND pldgDSkydD slagDtaEND pldgDSkydD slagDtaEND pldgDSkydD slagDtaEND slagDtaEND slagDtaEND slagDtaEND slagDtaEND so so so so so tartFVSQAA o * 0 ts-tfvSqaa 601 nQRYFFg AQRYFFg	STNPT:PTTV STNPT:PLTV STNPT:PLTV STNPT:PJtV STNPT:PytV NFR:VXRYJAK NFR:KRYJAK NFR:KRYJAK NFR:KRYJAK NMR:KRYJAK NMR:KRYJAK NMR:KRYJAK NMR:KRYJAK NMR:KRYJAK NMR:KRYJAK NMR:KRYJAK NMR:KRYJAK NMR:KRYJAK NMR:KRYJAK NMR:KRYJAK NFR:VXR NFR:VXR NFR:VXR NMR:KRYJAK NMR:KRYJAK NMR:KRYJAK NMR:KRYJAK NMR:KRYJAK STR NMR:KRYJAK NMR:	NTIZEHLDML NTIDEHLDML NTIDEHLDML *0 *0 0*0 NtIGEHLGMI ITINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG YTINFAIAG LECVLFYKN LECVLFYKN LESGILGYVG LAKILGYVA LAKIYGAYAN LAKIYGAYA LAKIYGAYA LAKYYAY LONGYIGYYA LAKIYGAYA LAKYYAY LONGYIGYYA LAKYYAY LONGYIGYYA LAKYYAY LONGYIGYYA LAKYYAY LONGYIGYYA	NVCHHLDPkV NVCHHLDPkV NVCHHLDPsi VSHVIGSVEV IS*VVGSVEV IS*VVGSVEV IS*VVGSVEV IAHEVGSIEV IAHEVGSIEV IAHEVGSIEV IAHEVGSIEV CRLTEKLDMQ CRLTEKLDMQ CRLTEKLDMQ CRLTEKLDMQ CRLTEKLDMQ CRLTEKLDMQ CRLTEKLDMQ CRLTEKLDMQ CRLTEKLDMQ CRLTEKLDMQ CRLTEKLDMQ	PEDVAPADSR PEDLAPADSR O*O ** ** peDvaPADSR GKMADLVLWV GKVADLVLWS GKVADLVLWS GKVADLVLWS GKLADIVLWD GKLADIV	IRsqTAABD IRk/TIAABD O* 0***0 IR-TIAABd PIFFGaKPkM PAFFGVKPhM PAFFGVKPhM PAFFGVKPhL PAFFGVKPhL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL PAFFGVKPAL VDP0TFaVKV Vn02T1VfV VD02T1VfV VD02T1VfV VD02T1VfX LBPQT1VKA LBPQT1VKA 00 VDPQTFdaXV	LEBDMGAISI VLmDiGAISI *0*0* * vLhDmGaiSi VIKOGMINWA IIKOGTIAIs VIKOGMIASI VIKOGMIASI VIKOGMIASI VIKOGMIASI VIKOGMIASI D	MSSDtlamer isSDSQAMGR o**00**0 msSDsqAMGR qMQDaNASIP qMQDaNASIP qMQDaNASIP qMQDaNASIP mADINASIP MADINASIP **0000* pmGDPNASIP ** 0000* pmGDpnasiP ** 0000* gpgaelakkl	IGEVVIRANG VGEVIRRING 0*0 * 0* VGEVIRRING TPOPVYRAN TPOPVYRAN TPOPVYRAN TPOPVHRPN TPOP	mAHKMKAGT TAARMKAQL OOO* tahkmK-qr 500 PGAMGKtmq PahbGRAKT PGADGRAKT PGADGRAKT PGADGRAKT YGLGGRAKY YGLGGRAKY YGLGKAKY YGLGKAKY YGLGKAKY YGLGKAKY TGDAGRAKY TCDAAGT TIngpik TSKPANKVSI TCDAAGTLEP VCEPATELP VCEPATELP VCEPATELPS SCYSATTVPI tcopattlps
Jack bean Consensus H. pyl HpuB H. pyl HpuB H. pyl UreB KI. aer UreC L. fer alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl HpuB H. pyl HpuB H. pyl UreB KI. aer UreC L. fer alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB A. ure alfa Jack bean Consensus Y. ent YeuC H. pyl HpuB H. pyl UreB KI. aer UreC L. fer alfa		svkyahiLPA vcGikNVLPs o** vagepniLPa 401 tLagDsapND rLKsEKGDND rLKsEKGDND rLKsEKGDND pLdgDSkydD sLagDsaDND sLagDsaDND sLagDsseND pLKcDseND slagDseND rcvTFVSQAA aniTFVSQAA aniTFVSQAA cvTFVSQAA cvTFVSQAA TSmIPmSLAg TSwIPmSLAg TSwIPmSLAg cvfvfsqaa 601 nQRYFFg AQIFsiF AQIFsiF AQIFsiF	STNPT1PITY STNPT1PITY STNPT1PITY STNPT1PITY STNPT-Pytv NFRVARYIAK NFRITKRISK NFRITKRISK NFRITKRISK NFRITKRISK NMRITKRIAK NMRITKRIAK NMRITKRIAK NMRITKRIAK NMRITKRIAK NFRITKRIK NFRITKRIK NFRITKRIK NFRITKRIK NFRITKRIK NFRIT	NTI = EHLDNI NTI = EHLDNI NTI DEHLDNI NTI DEHLDNI ITINPAIAG YTINPAIAHG LBCYULWYWN LAGIGT YG SC SC SC SC SC SC SC SC SC SC SC SC SC	NVCHHLDFkV NVCHHLDFkV NVCHHLDFsi VSEVIGSVEV ISeYVGSVEV ISeYVGSVEV ISeYVGSVEV ISEVVGSIEV ISEVVGSIEV ISEVVGSIEV CRUISKDLV CRUSKDLV CRUSKDV C	PEDVAPADSR PEDIAPADSR PEDIAPADSR ONO ** ** peDvaFASSR GRWADLVLWS GRVADLVLWS GRLADLVLWS GRLADLVLWS GRLADLVLWS GRLADLVWS GRVG GRVG GRVG GRVG GRVG GRVG GRVG GRV	IRsqTIAABD IRktIAABD IRktIAABD IRktIAABD IRkTIAABD PAFFOVRPAN PAFFOVRPAN PAFFOVRPAN PAFFOVRPAN PAFFOVRPAN PAFFOVRPAN PAFFOVRPAN PAFFOVRPAN PAFFOVRPAN PAFFOVRPAN PAFFOVRPAN PAFFOVRPAN PAFFOVRPAN IDPOTYAVAN IDPOTYAVAN IDPOTYAVAN IDPOTYAVAN IDPOTYAVAN IDPOTYAVAN IDPOTYAVAN IDPOTYAVAN IDPOTYAVAN IDPOTYAVAN	LEDMGAISI VLADIGAISI *0*0* * vLhDmGaiSi VIKOGMINWA IIKOGFIA1s IIKOGMYAISI VIKOGMYAIN VIKOGMYAIAC VIKOGMYAIAC VIKOGMYAWA 0*0* vIKGKMIAIA D	MSSDtlaMeR isSDsQAMGR ottossQAMGR msSDsQAMGR msQAMGR	IGEVVIRANO VGEVIRTNO VGEVIRTNO TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TPOPVJTRAN TOGVL CONTON TPOPVJTRAN TOGVL CONTON TPOPVJTRAN TOGVL CONTON TPOPVJTRAN TOGVL TPOPVJTRAN T	nAHKNKAGÍ TAdKMKAGÍ O 00° tahkmK-qr Solo PGAMGKImqI PahbGRAKT PGADGRAKT PGADGRAKT YGLGGRAKY YacLGRAKY YacLGRAKY YacLGRAKY FGLYGTalts YGLJGRAKY FGLYGTSIts YGLJGRAKY FGLYGTSIts YGLJGRAKY FGLYGTSIts YGLJGRAKY FGLYGTSITS YGLJGRAKY FGLYGTSITS YGLJGRAKY YGLJGRAY YGL
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FIG. 4-Continued.

tween the sequences range between 33 and 52% and between 51 and 67%, respectively. Comparison of the amino acid sequences of the α -subunit (Fig. 4C) suggests that it is also highly conserved. The length is about 570 amino acid residues, and the identities and similarities between the sequences range between 48 and 57% and between 68 and 75%, respectively.

The regularity of occurrence of lysine residues in the N terminus of the 19-kDa antigen (positions 4, 9, 17, 19, and 25, etc.) is a striking structural feature, reminiscent of many DNA-binding proteins. It explains the polypeptide's high affinity for polyanionic molecules, like nucleic acids, and accounts for its occurrence in the ribosomal pellet as well as for the marked tendency for aggregation with other proteins

(16). Under the conditions employed for preparation, the polypeptide was obtained as a thiol-linked dimer (a single cysteine residue at position 40 was found), usually complexed with other molecules (16). The cellular distribution of the urease or the 19-kDa antigen was not examined; it is likely to be cytoplasmic, as this appears to be the case with all other urease-positive enteric bacteria studied to date (18). The antigen may be released from living cells and, in addition, be set free following cellular degradation.

In humans, arthritis following Y. enterocolitica O:3 infection is closely linked with the HLA-B27 antigen. No homologies between the B27 sequence and the 19-kDa antigen were seen. However, we found a panel of nine possible nonapeptides with the HLA-B27-specific anchor residue arginine at position P2. Of these, nonapeptide RRAA ERGFK, the nine residues in positions 153 to 161, should be ranked at the top because of the large consensus in sequence pattern to the peptide motifs fitting to the binding cleft of the HLA-B27 molecule (12, 15b). On the basis of structural studies, this nonapeptide would bind excellently to HLA-B27 (15a). Thus, the 19-KDa antigen could function as a source of an arthritogenic or immunogenic peptide to be presented to cytotoxic T lymphocytes. The relevance of this finding to Y. enterocolitica-induced reactive arthritis remains to be elucidated.

The β -subunit of the Y. enterocolitica O:3 urease, the 19-kDa cationic antigen, described here, attracted our attention because it has arthritogenic potential in rats (16). Antibody to the 19-kDa peptide is found in humans (16) and may prove to be a useful marker of Yersinia infection. As occurs with some other cationic antigens, intra-articular challenge of preimmunized rats induces a chronic destructive joint lesion (8, 16, 28); however, it is the first bacterial product reported to have this ability. Whether the β -subunit, as an antigen, plays a role in the induction of human and experimental Yersinia-reactive arthritides (10, 26, 27) remains to be determined.

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