

Correction

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Primary structure of the *Streptomyces* R61 extracellular DD-peptidase. 1. Cloning into *Streptomyces lividans* and nucleotide sequence of the gene, by C. Duez, C. Piron-Fraipont, B. Joris, J. Dusart, M. S. Urdea, J. A. Martial, J.-M. Frère and J.-M. Ghuysen.

Page 515, Fig. 5. The correct sequence for the *Streptomyces* R61 extracellular DD-peptidase is shown.

GTC	GAC	ACC	CTG	CTC	ACC	ACC	GCG	GCC	CAG	GCG	CAC	AGC	GAC	GAC	ATG	GTC	GCC	GCG	GCC	TTC	TAC	TCC	CAC	ACC	TCC	CCC	GAC	GGC	AGC	90	
CAG	TGC	CGG	GGA	CCG	GGC	GCG	GCG	GCG	GGC	TCC	GAG	GCG	GCG	ACC	ATC	GGG	GAG	AAC	ATC	GCC	TGC	GGC	CAG	CGC	TCC	CCC	GCC	GAG	GTC	180	
GTC	GCG	GCG	TGG	ATG	AAC	AGC	CCG	GGC	CAC	GCC	GCC	AAC	ATC	CTC	AAG	CCC	GAT	TTC	ACC	CAC	ATA	GGC	ATC	GGC	TTC	GCG	GGC	GGC	GGC	270	
TCG	GCC	GGG	CCG	ACG	TAC	TGG	ACG	CAG	CTT	TTC	GGC	CCG	CTG	AAG	GAT	CTT	TTC	GCG	TTT	GGC	CTT	GCG	TAC	ATG	CAA	CCC	ATC	TGC	CCC	360	
GTC	CTG	GCG	GTA	GAG	ATG	GTG	CCG	GCG	TTC	CGA	TCC	GCG	CGG	TAC	ACA	GAG	GGA	ACT	CGG	GAG	AAG	AAT	CAG	Met	Val	Ser	Gly	Thr	Val	450	
Gly	Arg	Gly	Thr	Ala	Leu	Gly	Ala	Val	Leu	Leu	Ala	Leu	Leu	Ala	Val	Pro	Ala	Gln	Ala	Gly	Thr	Ala	Ala	Ala	Ala	Asp	Leu	Pro	Ala	540	
GGC	AGA	GGT	ACG	GCG	CTG	GGC	GCG	GTG	CTG	TTG	GCC	CTC	CTC	GCA	GTC	CCC	GCA	CAG	GCC	GGC	ACC	GCC	GCG	GCC	CGG	GAT	CTG	CCG	GCA		
Pro	Asp	Asp	Thr	Gly	Leu	Gln	Ala	Val	Leu	His	Thr	Ala	Leu	Ser	20	Gln	Gly	Ala	Pro	Gly	Ala	Met	Val	Arg	Val	Asp	Asp	Asn	Gly	Thr	630
CCC	GAC	GAC	ACC	GGT	CTG	CAG	GCG	GTG	CTG	CAC	ACG	GCC	CTT	TCC	CAG	GGA	GCC	CCC	GGT	GCG	ATG	GTG	CGG	GTC	GAC	GAC	AAC	GGC	ACG		
Ile	His	Gln	Leu	Ser	Glu	Gly	Val	Ala	Asp	Arg	Ala	Thr	Gly	Arg	50	Ala	Ile	Thr	Thr	Thr	Asp	Arg	Phe	Arg	Val	Gly	Ser	Val	Thr	Lys	720
ATC	CAC	CAG	TTG	TGC	GAG	GGA	GTC	GCC	GAC	CGG	GCC	ACC	GGG	CGT	GCG	ATC	ACC	ACG	ACC	GAC	CGG	TTC	GCG	ATC	GGC	AGC	GTC	ACC	AAG		
Ser	Phe	Ser	Ala	Val	Val	Leu	Leu	Gln	Leu	Val	Asp	Glu	Gly	Lys	80	Leu	Asp	Leu	Asp	Ala	Ser	Val	Asn	Thr	Tyr	Leu	Pro	Gly	Leu	Leu	810
AGC	TTC	TCC	GCC	GTG	GTC	CTG	CTG	CAA	CTG	GTG	GAC	GAG	GGC	AAG	CTC	GAC	CTG	GAC	GCT	TGC	GTG	AAC	ACC	TAT	CTG	CCC	GGG	CTG	CTG		
Pro	Asp	Asp	Arg	Ile	Thr	Val	Arg	Gln	Val	Met	Ser	His	Arg	Ser	110	Gly	Leu	Tyr	Asp	Tyr	Thr	Asn	Asp	Met	Phe	Ala	Gln	Thr	Val	Pro	900
CCC	GAC	GAC	CCG	ATC	ACC	GTG	CGT	CAG	GTG	ATG	AGC	CAC	CGC	AGT	GGG	CTG	TAC	GAC	TAC	ACC	AAC	GAC	ATG	TTC	GCG	CAG	ACG	GTC	CCG		
Gly	Phe	Glu	Ser	Val	Arg	Asn	Lys	Val	Phe	Ser	Tyr	Gln	Asp	Leu	140	Ile	Thr	Leu	Ser	Leu	Lys	His	Gly	Val	Thr	Asn	Ala	Pro	Gly	Ala	990
GGC	TTC	GAG	TCC	GTC	GCG	AAC	AAG	GTC	TTC	AGC	TAC	CAG	GAC	CTG	ATC	ACC	CTG	TCC	CTC	AAG	CAC	GGG	GTC	ACC	AAC	GCA	CCG	GGC	GCG		
Ala	Tyr	Ser	Tyr	Ser	Asn	Thr	Asn	Phe	Val	Val	Ala	Gly	Met	Leu	170	Ile	Glu	Lys	Leu	Thr	Gly	His	Ser	Val	Ala	Thr	Glu	Tyr	Gln	Asn	1080
GCC	TAT	TCA	TAC	TCC	AAC	ACG	AAC	TTC	GTC	GTC	GCG	GGC	ATG	CTC	ATC	GAG	AAG	CTC	ACC	GGC	CAC	TCC	GTG	GCC	ACG	GAG	TAC	CAG	AAC		
Arg	Ile	Phe	Thr	Pro	Leu	Asn	Leu	Thr	Asp	Thr	Phe	Tyr	Val	His	200	Pro	Asp	Thr	Val	Ile	Pro	Gly	Thr	His	Ala	Asn	Gly	Tyr	Leu	Thr	1170
CGC	ATC	TTC	ACG	CCG	CTG	AAC	CTG	ACC	GAC	ACC	TTC	TAC	GTG	CAC	CCC	GAC	ACC	GTC	ATC	CCG	GGC	ACC	CAC	GCC	AAC	GGC	TAC	CTC	ACG		
Pro	Asp	Glu	Ala	Gly	Gly	Ala	Leu	Val	Asp	Ser	Thr	Glu	Gln	Thr	230	Val	Ser	Trp	Ala	Gln	Ser	Ala	Gly	Ala	Val	Ile	Ser	Ser	Thr	Gln	1260
CCG	GAC	GAG	GCC	GGT	GGG	GCC	CTG	GTC	GAC	TCC	ACC	GAG	CAG	ACG	GTG	TCG	TGG	GCG	CAG	AGC	GCG	GGC	GCG	GTC	ATC	TCC	AGC	ACG	CAG		
Asp	Leu	Asp	Thr	Phe	Phe	Ser	Ala	Leu	Met	Ser	Gly	Gln	Leu	Met	260	Ser	Ala	Ala	Gln	Leu	Ala	Gln	Met	Gln	Gln	Trp	Thr	Thr	Val	Asn	1350
GAC	CTG	GAC	ACG	TTC	TTC	TCC	GCG	TTG	ATG	AGC	GGG	CAG	CTC	ATG	TCC	GCC	GCG	CAG	CTC	GCG	CAG	ATG	CAG	TGG	ACG	ACG	GTC	AAC			
Ser	Thr	Gln	Gly	Tyr	Gly	Leu	Gly	Leu	Arg	Arg	Arg	Asp	Leu	Ser	290	Cys	Gly	Ile	Ser	Val	Tyr	Gly	His	Thr	Gly	Thr	Val	Gln	Gly	Tyr	1440
AGC	ACC	CAG	GGG	TAC	GGC	CTC	GGC	CTG	GCG	GCG	CGT	GAC	CTG	TCC	TGC	GGT	ATC	TCG	GTG	TAC	GGC	CAC	ACG	GGC	ACC	GTG	CAG	GGC	TAC		
Tyr	Thr	Tyr	Ala	Phe	Ala	Ser	Lys	Asp	Gly	Lys	Arg	Ser	Val	Thr	320	Ala	Leu	Ala	Asn	Thr	Ser	Asn	Asn	Val	Asn	Val	Leu	Asn	Thr	Met	1530
TAC	ACG	TAC	GCC	TTC	GCC	TCG	AAG	GAC	GGC	AAG	GCG	AGC	GTC	ACC	GCG	CTC	GCC	AAC	ACC	TCG	AAC	AAC	GTG	AAC	GTG	CTG	AAC	ACG	ATG		
Ala	Arg	Thr	Leu	Glu	Ser	Ala	Phe	Cys	Gly	Lys	Pro	Thr	Thr	Ala	350	Lys	Leu	Arg	Ser	Ala	Thr	Ser	Ser	Ala	Thr	Thr	Val	Glu	Arg	His	1620
GCC	GCG	ACG	CTG	GAA	TCC	GCG	TTC	TGC	GGC	AAG	CCG	ACG	ACC	GCG	AAG	CTG	GCG	AGC	GCG	ACC	TCC	TCG	GCG	ACC	ACC	ACC	GTG	GAG	GCG	CAC	
Glu	Asp	Ile	Ala	Pro	Gly	Ile	Ala	Arg	Asp	OP																					
GAG	GAC	ATC	GCG	CCG	GGT	ATC	GCC	GCG	GAC	TGA	GCG	GCG	AAG	GTG	CGG	CCG	GAC	CCA	CCC	GTG	CGG	CCG	ACC	CCT	GCG	CGG	ACA	GGA	CCT	1710	
GGG	CCG	GGC	TCA	TGA	CTT	CTT	CAG	GTC	GGA	CCG	GTA	G																	1822		

Fig. 5. Nucleotide sequence of the *Streptomyces* R61 DD-peptidase precursor-encoding gene and amino acid sequence of the expressed and excreted enzyme. The N-terminal alanine and C-terminal threonine of the mature, extracellular enzyme are in boxes. The processing sites are shown by vertical arrows. The putative ribosome binding site is underlined. The inverted repeats of the putative transcription termination signal are shown by horizontal arrows.