

Nucleotide sequence for the *htpR* gene from *Citrobacter freundii*

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A homologous gene with the same chromosomal location (next to *livJ*) as the *E. coli* Heat Shock Regulatory Gene (*htpR*) (1,2) was sequenced from *Citrobacter freundii*. The two genes are identical at 89.6% of nucleotides and 94.4% of encoded amino acids. The figure shows the complete amino acid and nucleotide sequences for *C. freundii* and those residues that differ in *E. coli*.

-121 TGTGGATAAAATCACTGCTGATAAA -96

AGATTGAATGATATTCTCGTTGCTCATAAGCTCTGGCATGGTTGTTGCTATTGGTTTTAGCCAATGCGCCAGATGAAAAGATTGAGAGGATTGCA -1

ATG	ACC	AAA	GAA	ATG	CAA	G	ATA	G	GCT	TTA	G	GCC	CCT	A	GTT	GGT	AA	CTG	GAA	T	C	TAC	ATC	CGG	GCT	A	GC	AA	72
Met	Thr	Lys	Glu	Met	Gln	Asn	Leu	Ala	Leu	Ala	Leu	Ala	Pro	Val	Val	Gly	Asn	Leu	Glu	Asp	Ser	Tyr	Ile	Arg	Ala	Ala	Ala	Asn	24
	Ala	Asp	Lys			Ser																							
GCG	TGG	CCG	ATG	TTG	TCG	GCT	GAC	GAG	GAG	CGG	G	CTG	GCT	GAA	AAG	CTG	CAT	TAC	CAG	T	GCC	GAT	CTG	GAA	144				
Ala	Trp	Pro	Met	Leu	Ser	Ala	Asp	Glu	Glu	Arg	Ala	Leu	Ala	Glu	Lys	Leu	His	Tyr	CAG	Gln	Gly	Asp	Leu	Glu	48				
GCA	GCT	AAA	ACG	CTG	ATC	CTG	TCT	CAC	CTG	CG	TTT	GTT	GTT	CAT	A	GTT	GCT	CGT	AAT	TAT	GCC	GCC	TAT	GCC	216				
Ala	Ala	Lys	Thr	Leu	Ile	Leu	Ser	His	Leu	Arg	Phe	Val	Val	Val	His	Val	Ala	Arg	Asn	Tyr	Ala	Gly	Tyr	Gly	72				
CTG	CGC	CAG	GCG	GAT	TTG	ATT	CAG	GAA	GGT	AAT	ATC	GGC	CTG	ATG	AAA	GCC	GTG	CGC	CGT	TTC	AAC	CCA	GAA	288					
Leu	Arg	Gln	Ala	Asp	Ile	Ile	Gln	Glu	Gly	Asn	Ile	Gly	Leu	Met	Lys	Ala	Val	Arg	Arg	Phe	Asn	Pro	Glu	96					
	Pro																												
GTG	GGT	GTG	CGC	CTG	GTT	TCC	TTC	GCT	GTG	CAT	TGG	ATC	AAA	GCT	GAG	ATC	CAC	GAA	TAC	GTT	CTG	CGT	AAC	360					
Val	Gly	Val	Arg	Leu	Val	Ser	Phe	Ala	Val	His	Trp	Trp	Lys	Ala	Glu	Ile	His	Tyr	TAC	GTT	Leu	Arg	Asn	120					
TGG	CGT	ATC	GTT	AAA	GTC	GCC	ACC	ACT	Thr	Ala	Lys	Ala	Gln	Arg	AAG	CTG	TTC	TTT	AAC	CTG	CGT	AAA	ACC	AAG	CAG	432			
Trp	Arg	Ile	Val	Lys	Val	Ala	Ala	Thr	Thr	Lys	Gly	Gln	Arg	Lys	Leu	Phe	Phe	Phe	Asn	Leu	Arg	Lys	Thr	Lys	Gln	144			
CGT	CTG	GGC	TGG	TTT	AAC	CAG	GAC	GAA	GTT	GAA	ATG	G	GCT	C	T	GAG	CTG	GGT	G	TCC	AGC	AAA	GAC	ATG	504				
Arg	Leu	Gly	Trp	Phe	Asn	Gln	Asp	Glu	Val	Glu	Met	Val	Val	Ala	Arg	Glu	Leu	Gly	Val	Ser	Ser	Lys	Asp	Val	168				
CGC	GAA	ATG	GAA	TCC	CGT	ATG	GCG	GCG	CAG	GAC	ATG	ACG	TTT	Phe	Asp	Met	TCT	C	GAC	GAT	C	TCT	C	GAC	AGC	576			
Arg	Glu	Met	Glu	Ser	Arg	Met	Ala	Ala	Gln	Asp	Met	Thr	Phe	Asp	Leu	Met	Ser	Ser	Ser	Asp	Asp	Glu	Ser	Asp	Ser	192			
CAG	CCG	ATG	GCC	CCG	GTG	CTG	TAT	CTG	CAG	GAT	AAA	TCT	TCT	Asn	AAC	TTT	GCC	GAC	GGC	ATT	GAA	GAA	GAC	ATC	648				
Gln	Pro	Met	Ala	Pro	Val	Leu	Tyr	Leu	Gln	Asp	Lys	Ser	Ser	Asn	Phe	Phe	Ala	Asp	Gly	Ile	Glu	Glu	Asp	Asn	216				
TGG	GAA	GAT	CAG	GCC	GCG	AAC	CGT	G	AAA	CTT	ACC	CAC	GCA	ATG	GAA	GGT	CTG	GAC	GAG	CGT	AGC	CAG	GAC	ATC	720				
Trp	Glu	Asp	Gln	Ala	Ala	Asn	Lys	Arg	Ala	Leu	Thr	His	Ala	Met	Glu	Gly	Leu	Asp	Glu	Arg	Ser	Gln	Asp	Ile	Ile	240			
CGT	GCA	CGT	TGG	CTG	GAC	GAA	GAC	AAC	AAG	TCG	ACG	TTG	CAG	GAA	CTG	GCC	GAT	CGC	T	TAC	GGC	GTT	TCC	GCT	792				
Arg	Ala	Arg	Trp	Leu	Asp	Glu	Asp	Asn	Lys	Ser	Thr	Leu	Gln	Glu	Leu	Ala	Asp	Arg	Arg	Tyr	Gly	Val	Ser	Ala	264				
GAA	CGT	GTT	CGT	CAG	CTT	GAA	AAG	AAC	G	ATG	AAA	AAA	TTG	CGC	GCC	ATC	G	ATC	G	GAA	GCA	TAA	855						
Glu	Arg	Val	Arg	Gln	Leu	Glu	Lys	Asn	Ala	Met	Lys	Lys	Leu	Arg	Ala	Ile	Glu	Ala	Ile	Glu	Ala	Ter	285						
TCTTCCAGCGACCTGGAATGCTGATAAAACCCCTGGATGAAAATCCGGGGTTTTTGTGTTTTTATCTCTCCCCCTCTCTCGTACGTTTTATGCTTT	950																												
GTCATCAAGTTGTTATCTGTTTCATGTCAAATTTAGCTATTCCAAAATAAATAAAAAATCGGGTATGTTTTAGCAGAGTATGCTGCTAAAAGCAGCGGT	1045																												

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