

SEQUENCE PROTOCOL

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Degussa Aktiengesellschaft
(B) STREET: Weissfrauenstrasse 9
(C) TOWN: Frankfurt
(D) STATE: Hessen
(E) COUNTRY: Germany
(F) POSTCODE: 60311
(G) TELEPHONE: 06181593924
(H) TELEFAX: 06181594304

(A) NAME: University of Stuttgart
(B) STREET: Allmandring 31
(C) TOWN: Stuttgart
(E) COUNTRY: Germany
(F) POSTCODE: 70569
(G) TELEPHONE: 07116855156
(H) TELEFAX: 07116855164

(A) NAME: Boehringer Mannheim GmbH
(B) STREET: Sandhofer Strasse 116
(C) TOWN: Mannheim
(E) COUNTRY: Germany
(F) POSTCODE: 68298
(G) TELEPHONE: 06217594267
(H) TELEFAX: 06217594461

(ii) TITLE OF THE INVENTION: Recombinant L-N-carbamoylase from
Arthrobacter aureus, process for the preparation of
L-amino acids by means of this

(iii) NUMBER OF SEQUENCES: 1

(iv) COMPUTER-READABLE VERSION:

(A) DATA CARRIER: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) INFORMATION ON SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 1239 base pairs
(B) TYPE: Nucleotide
(C) STRAND FORM: single-stranded
(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: Genome DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) TYPE OF FRAGMENT: N-Terminus

(vi) ORIGINAL ORIGIN:

(A) ORGANISM: *Arthrobacter*(B) STRAIN: *aurescens*

5 (viii) POSITION IN THE GENOME:

(C) UNITS: bp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

10	GTGACCTGC AGAAAGCGCA AGCGGCGCGC ATTGAGAAAG AGATCCGGGA GCTCTCCCGG	60
	TTCTCGGCAG AAGGCCCCGG TGTACCCGG CTGACCTACA CTCCAGAGCA TGCCGCCGCG	120
	CGGGAAACGC TCATTGCGGC TATGAAAGCG GCCGCCTGA GCGTTCGTGA AGACGCACTC	180
15	GGAAACATCA TCGGCCGACG TGAAGGCACT GATCCGGAGC TTCCTGCGAT CGCGGTCGGT	240
	TCACACTTCG ATTCTGTCCG AAACGGCGGG ATGTTTGATG GCACTGCAGG CGTGGTGTGC	300
20	GCCCTTGAGG CTGCCCCGGT GATGCTGGAG AACGGCTACG TGAATCGGCA TCCATTTGAG	360
	TTCATCGCGA TCGTGGAGGA GGAAGGGGCC CGCTTCAGCA GTGGCATGTT GGGCGGCCGG	420
	GCCATTGCAG GGTGGTTCGC CGACAGGGAA CTGGACTCTT TGGTTGATGA GGATGGAGTG	480
25	TCCGTTAGGC AGGCGGCTAC TGCCTTCGGC TTGAAGCCGG GCGAACTGCA GGCTGCAGCC	540
	CGCTCCGCGG CGGACCTGCG TGCTTTTATC GAACTACACA TTGAACAAGG ACCGATCCTC	600
30	GAGCAGGAGC AAATAGAGAT CGGAGTTGTA ACCTCCATCG TTGGCGTTCG CGCATTCGCG	660
	GTTGCCGTCA AAGGCAGAAG CGACCACGCC GGCACAACCC CCATGCACCT GCGCCAGGAT	720
	GCGCTGGTAC CCGCCGCTCT CATGGTGAGG GAGGTCAACC GGTTCGTCAA CGAGATCGCC	780
35	GATGGCACAG TGGCTACCGT TGGCCACCTC ACAGTGGCCC CCGGTGGAGG CAACCAGGTC	840
	CCGGGGGAGG TGGACTTCAC ACTGGACCTG CGTTCTCCGC ATGAGGAGTC GCTCCGCGTG	900
40	CTGATCGACC GCATCTCGGT CATGGTCGGC GAGGTCGCCT CCCAGGCCGG TGTGGCTGCC	960
	GATGTGGATG AATTTTTCOA TCTCAGCCCG GTGCAGCTGG CTCCTACCAT GGTGGACGCC	1020
	GTTTCGGAAG CGGCCTCGGC CTTGCAGTTC ACACACCGGG ATATCAGCAG TGGGGCGGGC	1080
45	CACGACTCGA TGTTCATCGC CCAGGTCACG GACGTCGGAA TGGTTTTCGT TCCAAGCCGT	1140
	GCTGGCCGGA GCCACGTTC CGAAGAATGG ACCGATTTTC ATGACCTTCG CAAAGGAACT	1200
50	GAGGTTGTCC TCCGGGTAAT GAAGGCACTT GACCGGTAA	1239

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- 30 (ii) TITEL OF THE INVENTION: Recombinant L-N-carbamoylase from
Arthrobacter aurescens, process for the preparation of
L-amino acids by means of this
- 35 (iii) NUMBER OF SEQUENCES: 1
- (iv) COMPUTER-READABLE VERSION:
- 40 (A) DATA CARRIER: Tape
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patentin Release #1.0, Version #1.30 (EPA)
- (2) INFORMATION ON SEQ ID NO: 1:
- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 amino acids
(B) TYPE: amino acid
(C) STRAND FORM: single-stranded
(D) TOPOLOGY: linear
- 50 (ii) TYPE OF MOLECULE: Peptide
- (iii) HYPOTHETICAL: NO
- 55 (v) TYPE OF FRAGMENT: N-Terminus
- (vi) ORIGINAL ORIGIN:
- 60 (A) ORGANISM: Arthrobacter
(B) STRAIN: aurescens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

	Met	Thr	Leu	Gln	Lys	Ala	Gln	Ala	Ala	Arg	Ile	Glu	Lys	Glu	Ile	Arg	
	1				5					10					15		
5	Glu	Leu	Ser	Arg	Phe	Ser	Ala	Glu	Gly	Pro	Gly	Val	Thr	Arg	Leu	Thr	
				20					25					30			
10	Tyr	Thr	Pro	Glu	His	Ala	Ala	Ala	Arg	Glu	Thr	Leu	Ile	Ala	Ala	Met	
			35					40					45				
	Lys	Ala	Ala	Ala	Leu	Ser	Val	Arg	Glu	Asp	Ala	Leu	Gly	Asn	Ile	Ile	
		50					55					60					
15	Gly	Arg	Arg	Glu	Gly	Thr	Asp	Pro	Glu	Leu	Pro	Ala	Ile	Ala	Val	Gly	
	65				70					75					80		
	Ser	His	Phe	Asp	Ser	Val	Arg	Asn	Gly	Gly	Met	Phe	Asp	Gly	Thr	Ala	
				85					90					95			
20	Gly	Val	Val	Cys	Ala	Leu	Glu	Ala	Ala	Arg	Val	Met	Leu	Glu	Asn	Gly	
				100				105					110				
25	Tyr	Val	Asn	Arg	His	Pro	Phe	Glu	Phe	Ile	Ala	Ile	Val	Glu	Glu	Glu	
		115					120					125					
	Gly	Ala	Arg	Phe	Ser	Ser	Gly	Met	Leu	Gly	Gly	Arg	Ala	Ile	Ala	Gly	
		130					135					140					
30	Leu	Val	Ala	Asp	Arg	Glu	Leu	Asp	Ser	Leu	Val	Asp	Glu	Asp	Gly	Val	
	145					150				155					160		
	Ser	Val	Arg	Gln	Ala	Ala	Thr	Ala	Phe	Gly	Leu	Lys	Pro	Gly	Glu	Leu	
				165				170						175			
35	Gln	Ala	Ala	Ala	Arg	Ser	Ala	Ala	Asp	Leu	Arg	Ala	Phe	Ile	Glu	Leu	
				180				185					190				
40	His	Ile	Glu	Gln	Gly	Pro	Ile	Leu	Glu	Gln	Glu	Gln	Ile	Glu	Ile	Gly	
		195					200					205					
	Val	Val	Thr	Ser	Ile	Val	Gly	Val	Arg	Ala	Leu	Arg	Val	Ala	Val	Lys	
		210				215					220						
45	Gly	Arg	Ser	Asp	His	Ala	Gly	Thr	Thr	Pro	Met	His	Leu	Arg	Gln	Asp	
	225				230					235					240		
	Ala	Leu	Val	Pro	Ala	Ala	Leu	Met	Val	Arg	Glu	Val	Asn	Arg	Phe	Val	
				245				250					255				
50	Asn	Glu	Ile	Ala	Asp	Gly	Thr	Val	Ala	Thr	Val	Gly	His	Leu	Thr	Val	
		260					265						270				
55	Ala	Pro	Gly	Gly	Gly	Asn	Gln	Val	Pro	Gly	Glu	Val	Asp	Phe	Thr	Leu	
		275					280					285					
	Asp	Leu	Arg	Ser	Pro	His	Glu	Glu	Ser	Leu	Arg	Val	Leu	Ile	Asp	Arg	
		290				295					300						
60	Ile	Ser	Val	Met	Val	Gly	Glu	Val	Ala	Ser	Gln	Ala	Gly	Val	Ala	Ala	
	305				310				315						320		
	Asp	Val	Asp	Glu	Phe	Phe	Asn	Leu	Ser	Pro	Val	Gln	Leu	Ala	Pro	Thr	
				325				330					335				
65	Met	Val	Asp	Ala	Val	Arg	Glu	Ala	Ala	Ser	Ala	Leu	Gln	Phe	Thr	His	
			340				345						350				
70	Arg	Asp	Ile	Ser	Ser	Gly	Ala	Gly	His	Asp	Ser	Met	Phe	Ile	Ala	Gln	
		355				360						365					

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Val Thr Asp Val Gly Met Val Phe Val Pro Ser Arg Ala Gly Arg Ser
370 375 380

5 His Val Pro Glu Glu Trp Thr Asp Phe Asp Asp Leu Arg Lys Gly Thr
385 390 395 400

Glu Val Val Leu Arg Val Met Lys Ala Leu Asp Arg
405 410

10