

SEQUENCE LISTING

<110> DSM IP Assets B.V.

<120> MUTANT PENICILLIN G ACYLASES

<130> 26942-WO-PCT

<140>

<141>

<160> 1

<170> PatentIn Ver. 2.1

<210> 1

<211> 846

<212> PRT

<213> Escherichia coli

<400> 1

Met	Lys	Asn	Arg	Asn	Arg	Met	Ile	Val	Asn	Cys	Val	Thr	Ala	Ser	Leu	1	5	10	15
Met	Tyr	Tyr	Trp	Ser	Leu	Pro	Ala	Leu	Ala	Glu	Gln	Ser	Ser	Ser	Glu	20	25	30	
Ile	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala	Asn	35	40	45	
Asp	Thr	Trp	His	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	Asp	50	55	60	
Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr	Val	65	70	75	80
Ala	Glu	Val	Leu	Gly	Lys	Asp	Phe	Val	Lys	Phe	Asp	Lys	Asp	Ile	Arg	85	90	95	
Arg	Asn	Tyr	Trp	Pro	Asp	Ala	Ile	Arg	Ala	Gln	Ile	Ala	Ala	Leu	Ser	100	105	110	
Pro	Glu	Asp	Met	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn	Ala	115	120	125	
Trp	Ile	Asp	Lys	Val	Asn	Thr	Asn	Pro	Glu	Thr	Leu	Leu	Pro	Lys	Gln	130	135	140	
Phe	Asn	Thr	Phe	Gly	Phe	Thr	Pro	Lys	Arg	Trp	Glu	Pro	Phe	Asp	Val	145	150	155	160
Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser	Thr	165	170	175	
Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys	Tyr	180	185	190	

Gly	Val	Ser	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu	Val
		195					200					205			
Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Val	Gln	Glu	Ser	Asn	Tyr	Pro
	210					215					220				
Leu	Lys	Phe	Asn	Gln	Gln	Asn	Ser	Gln	Thr	Ala	Ala	Leu	Leu	Pro	Arg
225					230					235					240
Tyr	Asp	Leu	Pro	Ala	Pro	Met	Leu	Asp	Arg	Pro	Ala	Lys	Gly	Ala	Asp
				245					250					255	
Gly	Ala	Leu	Leu	Ala	Leu	Thr	Ala	Gly	Lys	Asn	Arg	Glu	Thr	Ile	Ala
			260					265					270		
Ala	Gln	Phe	Ala	Gln	Gly	Gly	Ala	Asn	Gly	Leu	Ala	Gly	Tyr	Pro	Thr
		275					280					285			
Thr	Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Ser	Lys	Ala	Gln	Asp	Ala	Lys
	290					295					300				
Ala	Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Tyr	Ala	Pro	Ala	Tyr
305					310					315					320
Thr	Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn
				325					330					335	
Thr	Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Val	Ile
			340					345					350		
Ser	Trp	Gly	Ser	Thr	Ala	Gly	Phe	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala
		355					360					365			
Glu	Arg	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Leu	His	Asn	Gly	Lys
	370					375					380				
Trp	Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Thr	Val	Lys	Asn	Gly
385					390					395					400
Gln	Ala	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Val	His	Gly	Asn	Ile	Leu
				405					410					415	
Gln	Thr	Asp	Gln	Thr	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ser	Arg	Ala	Trp
			420					425					430		
Asp	Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys
		435					440					445			
Ala	Lys	Asn	Trp	Gln	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu
						455					460				
Thr	Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val
465					470					475					480
His	Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Ser	Gly	His	Asp	Pro	Arg	Leu
				485					490					495	

Pro	Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Pro	Phe	
			500					505					510			
Glu	Met	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	
		515					520					525				
Trp	Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	
	530					535					540					
Phe	Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Arg	Leu	Leu	
545					550					555					560	
Glu	Gln	Lys	Pro	Arg	Leu	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	
				565					570					575		
Gln	Thr	Ser	Arg	Gln	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Thr	Leu	
			580					585					590			
Gln	Ala	Ala	Thr	Ser	Gly	Leu	Thr	Gln	Ser	Asp	Pro	Arg	Arg	Gln	Leu	
		595						600				605				
Val	Glu	Thr	Leu	Thr	Arg	Trp	Asp	Gly	Ile	Asn	Leu	Leu	Asn	Asp	Asp	
	610					615					620					
Gly	Lys	Thr	Trp	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Val	Trp	Leu	
625					630					635					640	
Thr	Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Met	Pro	Phe	
				645					650					655		
Asp	Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	
			660					665					670			
Thr	Gly	Ser	Leu	Asn	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	
		675					680					685				
Val	Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Ala	
	690					695					700					
Gly	Lys	Pro	Gln	Gln	Glu	Val	Val	Leu	Ala	Ala	Leu	Glu	Asp	Thr	Trp	
705					710					715					720	
Glu	Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asn	Val	Ser	Asn	Trp	Lys	Thr	
				725					730					735		
Pro	Ala	Met	Ala	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	
			740					745					750			
Gln	Ala	Ala	Ala	Glu	Glu	Thr	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	
		755					760					765				
Gly	Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Thr	Ser	Asp	Arg	
	770					775					780					
Pro	Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	
785					790					795					800	

Ala	Pro	Asp	Gly	Thr	Val	Asp	Lys	His	Tyr	Glu	Asp	Gln	Leu	Lys	Met
				805					810					815	
Tyr	Glu	Asn	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Lys	Gln	Asp	Val
			820					825					830		
Glu	Ala	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	His	Val	Gln	Arg		
		835					840					845			