

347 921.ST25 Sequence Listing
SEQUENCE LISTING

<110> Metabolic Explorer

<120> Recombinant Enzyme with Altered Feedback Sensitivity

<130> 347 921

<150> PCT/IB2004/001901

<151> 2004-05-12

<160> 34

<170> PatentIn version 3.1

<210> 1

<211> 930

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(930)

<223> Homoserine transsuccinylase

<400> 1

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Met	Pro	Ile	Arg	Val	Pro	Asp	Glu	Leu	Pro	Ala	Val	Asn	Phe	Leu	Arg	
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gaa	gaa	aac	gtc	ttt	gtg	atg	aca	act	tct	cgt	gcg	tct	ggt	cag	gaa	96
Glu	Glu	Asn	Val	Phe	Val	Met	Thr	Thr	Ser	Arg	Ala	Ser	Gly	Gln	Glu	
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att	cgt	cca	ctt	aag	gtt	ctg	atc	ctt	aac	ctg	atg	ccg	aag	aag	att	144
Ile	Arg	Pro	Leu	Lys	Val	Leu	Ile	Leu	Asn	Leu	Met	Pro	Lys	Lys	Ile	
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gaa	act	gaa	aat	cag	ttt	ctg	cgc	ctg	ctt	tca	aac	tca	cct	ttg	cag	192
Glu	Thr	Glu	Asn	Gln	Phe	Leu	Arg	Leu	Leu	Ser	Asn	Ser	Pro	Leu	Gln	
	50					55					60					

gtc	gat	att	cag	ctg	ttg	cgc	atc	gat	tcc	cgt	gaa	tcg	cgc	aac	acg	240
Val	Asp	Ile	Gln	Leu	Leu	Arg	Ile	Asp	Ser	Arg	Glu	Ser	Arg	Asn	Thr	
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ccc	gca	gag	cat	ctg	aac	aac	ttc	tac	tgt	aac	ttt	gaa	gat	att	cag	288
Pro	Ala	Glu	His	Leu	Asn	Asn	Phe	Tyr	Cys	Asn	Phe	Glu	Asp	Ile	Gln	
				85					90					95		

gat	cag	aac	ttt	gac	ggt	ttg	att	gta	act	ggt	gcg	ccg	ctg	ggc	ctg	336
Asp	Gln	Asn	Phe	Asp	Gly	Leu	Ile	Val	Thr	Gly	Ala	Pro	Leu	Gly	Leu	
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gtg	gag	ttt	aat	gat	gtc	gct	tac	tgg	ccg	cag	atc	aaa	cag	gtg	ctg	384
Val	Glu	Phe	Asn	Asp	Val	Ala	Tyr	Trp	Pro	Gln	Ile	Lys	Gln	Val	Leu	
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gag	tgg	tcg	aaa	gat	cac	gtc	acc	tcg	acg	ctg	ttt	gtc	tgc	tgg	gcg	432
Glu	Trp	Ser	Lys	Asp	His	Val	Thr	Ser	Thr	Leu	Phe	Val	Cys	Trp	Ala	
	130					135					140					

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gta cag gcc gcg ctc aat atc ctc tac ggc att cct aag caa act cgc Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg 145 150 155 160	480
acc gaa aaa ctc tct ggc gtt tac gag cat cat att ctc cat cct cat Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His 165 170 175	528
gcg ctt ctg acg cgt ggc ttt gat gat tca ttc ctg gca ccg cat tcg Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser 180 185 190	576
cgc tat gct gac ttt ccg gca gcg ttg att cgt gat tac acc gat ctg Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu 195 200 205	624
gaa att ctg gca gag acg gaa gaa ggg gat gca tat ctg ttt gcc agt Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr 220 Leu Phe Ala Ser 210 215	672
aaa gat aag cgc att gcc ttt gtg acg ggc cat ccc gaa tat gat gcg Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala 225 230 235 240	720
caa acg ctg gcg cag gaa ttt ttc cgc gat gtg gaa gcc gga cta gac Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp 245 250 255	768
ccg gat gta ccg tat aac tat ttc ccg cac aat gat ccg caa aat aca Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr 260 265 270	816
ccg cga gcg agc tgg cgt agt cac ggt aat tta ctg ttt acc aac tgg Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp 275 280 285	864
ctc aac tat tac gtc tac cag atc acg cca tac gat cta cgg cac atg Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met 290 295 300	912
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gac aaa att gct gac caa att tct gat gcc gtt tta gac gcg atc ctc Asp Lys Ile Ala Asp Gln Ile Ser Asp Ala Val Leu Asp Ala Ile Leu 20 25 30	96

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gaa Glu	cag Gln	gat Asp 35	ccg Pro	aaa Lys	gca Ala	cgc Arg	gtt Val 40	gct Ala	tgc Cys	gaa Glu	acc Thr	tac Tyr 45	gta Val	aaa Lys	acc Thr	144
ggc Gly	atg Met 50	gtt Val	tta Leu	gtt Val	ggc Gly	ggc Gly 55	gaa Glu	atc Ile	acc Thr	acc Thr	agc Ser 60	gcc Ala	tgg Trp	gta Val	gac Asp	192
atc Ile 65	gaa Glu	gag Glu	atc Ile	acc Thr	cgt Arg 70	aac Asn	acc Thr	gtt Val	cgc Arg	gaa Glu 75	att Ile	ggc Gly	tat Tyr	gtg Val	cat His 80	240
tcc Ser	gac Asp	atg Met	ggc Gly	ttt Phe 85	gac Asp	gct Ala	aac Asn	tcc Ser	tgt Cys 90	gcg Ala	gtt Val	ctg Leu	agc Ser	gct Ala 95	atc Ile	288
ggc Gly	aaa Lys	cag Gln	tct Ser 100	cct Pro	gac Asp	atc Ile	aac Asn	cag Gln 105	ggc Gly	gtt Val	gac Asp	cgt Arg	gcc Ala 110	gat Asp	ccg Pro	336
ctg Leu	gaa Glu	cag Gln 115	ggc Gly	gcg Ala	ggt Gly	gac Asp	cag Gln 120	ggt Gly	ctg Leu	atg Met	ttt Phe	ggc Gly 125	tac Tyr	gca Ala	act Thr	384
aat Asn	gaa Glu 130	acc Thr	gac Asp	gtg Val	ctg Leu	atg Met 135	cca Pro	gca Ala	cct Pro	atc Ile	acc Thr 140	tat Tyr	gca Ala	cac His	cgt Arg	432
ctg Leu 145	gta Val	cag Gln	cgt Arg	cag Gln	gct Ala 150	gaa Glu	gtg Val	cgt Arg	aaa Lys	aac Asn 155	ggc Gly	act Thr	ctg Leu	ccg Pro	tgg Trp 160	480
ctg Leu	cgc Arg	ccg Pro	gac Asp	gcg Ala 165	aaa Lys	agc Ser	cag Gln	gtg Val	act Thr 170	ttt Phe	cag Gln	tat Tyr	gac Asp	gac Asp 175	ggc Gly	528
aaa Lys	atc Ile	gtt Val 180	ggt Gly	atc Ile	gat Asp	gct Ala	gtc Val	gtg Val 185	ctt Leu	tcc Ser	act Thr	cag Gln	cac His 190	tct Ser	gaa Glu	576
gag Glu	atc Ile	gac Asp 195	cag Gln	aaa Lys	tcg Ser	ctg Leu	caa Gln 200	gaa Glu	gcg Ala	gta Val	atg Met	gaa Glu 205	gag Glu	atc Ile	atc Ile	624
aag Lys	cca Pro 210	att Ile	ctg Leu	ccc Pro	gct Ala	gaa Glu 215	tgg Trp	ctg Leu	act Thr	tct Ser	gcc Ala 220	acc Thr	aaa Lys	ttc Phe	ttc Phe	672
atc Ile 225	aac Asn	ccg Pro	acc Thr	ggt Gly	cgt Arg 230	ttc Phe	gtt Val	atc Ile	ggt Gly	ggc Gly 235	cca Pro	atg Met	ggt Gly	gac Asp	tgc Cys 240	720
ggt Gly	ctg Leu	act Thr	ggt Gly	cgt Arg 245	aaa Lys	att Ile	atc Ile	gtt Val	gat Asp 250	acc Thr	tac Tyr	ggc Gly	ggc Gly	atg Met 255	gcg Ala	768
cgt Arg	cac His	ggt Gly	ggc Gly 260	ggt Gly	gca Ala	ttc Phe	tct Ser	ggt Gly 265	aaa Lys	gat Asp	cca Pro	tca Ser	aaa Lys 270	gtg Val	gac Asp	816
cgt Arg	tcc Ser	gca Ala 275	gcc Ala	tac Tyr	gca Ala	gca Ala	cgt Arg 280	tat Tyr	gtc Val	gcg Ala	aaa Lys	aac Asn 285	atc Ile	gtt Val	gct Ala	864
gct Ala	ggc Gly 290	ctg Leu	gcc Ala	gat Asp	cgt Arg	tgt Cys 295	gaa Glu	att Ile	cag Gln	gtt Val	tcc Ser 300	tac Tyr	gca Ala	atc Ile	ggc Gly	912
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Val	Ala	Glu	Pro	Thr	Ser	Ile	Met	Val	Glu	Thr	Phe	Gly	Thr	Glu	Lys	
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Val	Pro	Ser	Glu	Gln	Leu	Thr	Leu	Leu	Val	Arg	Glu	Phe	Phe	Asp	Leu	
			325					330						335		
cgc	cca	tac	ggt	ctg	att	cag	atg	ctg	gat	ctg	ctg	cac	ccg	atc	tac	1056
Arg	Pro	Tyr	Gly	Leu	Ile	Gln	Met	Leu	Asp	Leu	Leu	His	Pro	Ile	Tyr	
			340					345					350			
aaa	gaa	acc	gca	gca	tac	ggt	cac	ttt	ggt	cgt	gaa	cat	ttc	ccg	tgg	1104
Lys	Glu	Thr	Ala	Ala	Tyr	Gly	His	Phe	Gly	Arg	Glu	His	Phe	Pro	Trp	
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gaa	aaa	acc	gac	aaa	gcg	cag	ctg	ctg	cgc	gat	gct	gcc	ggg	ctg	aag	1152
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