

SEQUENCE LISTING

<110> Sanofi-Aventis Deutschland GmbH

<120> Method for reducing misincorporation of non-canonical branched-chain amino acids

<130> DE2018-069

<150> EP 18 214 562.3

<151> 2018-12-20

<160> 46

<170> BiSSAP 1.3.6

<210> 1

<211> 1572

<212> DNA

<213> Escherichia coli

<220>

<223> leuA, 2-isopropylmalate synthase

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<213> Escherichia coli

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<223> leuA, 2-isopropylmalate synthase

<400> 2

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Leu Ala Leu Glu Arg Met Gly Val Asp Val Met Glu Val Gly Phe Pro
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 <223> ilvC, ketol-acid reductoisomerase

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<211> 491

<212> PRT

<213> Escherichia coli

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<223> ilvC, ketol-acid reductoisomerase

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<211> 1644

<212> DNA

<213> Escherichia coli

<220>

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<210> 6
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<213> Escherichia coli

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Asn Glu Val Thr Phe Pro His Ala Glu Val Glu Gln Ala Arg Gln Met
180       185       190
Leu Ala Lys Ala Gln Lys Pro Met Leu Tyr Val Gly Gly Gly Val Gly
195       200       205
Met Ala Gln Ala Val Pro Ala Leu Arg Glu Phe Leu Ala Ala Thr Lys
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Tyr Pro Tyr Tyr Leu Gly Met Leu Gly Met His Gly Thr Lys Ala Ala

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<212> DNA

<213> Escherichia coli

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<223> Native gene ilvM

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1          5          10          15
Leu Glu Arg Val Leu Arg Val Val Arg His Arg Gly Phe His Val Cys
20          25          30
Ser Met Asn Met Ala Ala Ala Ser Asp Ala Gln Asn Ile Asn Ile Glu
35          40          45
Leu Thr Val Ala Ser Pro Arg Ser Val Asp Leu Leu Phe Ser Gln Leu
50          55          60
Asn Lys Leu Val Asp Val Ala His Val Ala Ile Cys Gln Ser Thr Thr
65          70          75          80
Thr Ser Gln Gln Ile Arg Ala
85

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<210> 9
 <211> 933
 <212> DNA
 <213> Escherichia coli

<220>
 <223> thrB, homoserine kinase

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<400> 9
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ggggcgggcg tgacacctgt tgatggtgca ttgctcggag atgtagtcac gggtgaggcg      120
gcagagacat tcagtctcaa caacctcgga cgctttgccg ataagctgcc gtcagaacca      180

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cgggaaaata tcgtttatca gtgctgggag cgtttttgcc aggaactggg taagcaaatt	240
ccagtggcga tgacctgga aaagaatatg ccgatcggtt cgggcttagg ctccagtgcc	300
tgttcgggtg tcgcggcgct gatggcgatg aatgaacact gcggcaagcc gcttaatgac	360
actcgtttgc tggctttgat gggcgagctg gaaggccgta tctccggcag cattcattac	420
gacaacgtgg caccgtgttt tctcgggtgt atgcagttga tgatcgaaga aaacgacatc	480
atcagccagc aagtgccagg gtttgatgag tggctgtggg tgctggcgta tccggggatt	540
aaagtctcga cggcagaagc cagggctatt ttaccggcgc agtatcgccg ccaggattgc	600
attgcgcacg ggcgacatct ggcaggcttc attcacgcct gctattccccg tcagcctgag	660
cttgccgcga agctgatgaa agatgttatc gctgaaccct accgtgaacg gttactgcca	720
ggcttccggc aggcgcggca ggcggtcgcg gaaatcggcg cggtagcgag cggtatctcc	780
ggctccggcc cgaccttggt cgctctgtgt gacaagccgg aaaccgcca gcgcgttgcc	840
gactggttgg gtaagaacta cctgcaaaat caggaagggt ttgttcatat ttgccggctg	900
gatacggcgg gcgcacgagt actggaaaac taa	933

<210> 10
 <211> 310
 <212> PRT
 <213> Escherichia coli

<220>
 <223> thrB, homoserine kinase

<400> 10

Met	Val	Lys	Val	Tyr	Ala	Pro	Ala	Ser	Ser	Ala	Asn	Met	Ser	Val	Gly
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Phe	Asp	Val	Leu	Gly	Ala	Ala	Val	Thr	Pro	Val	Asp	Gly	Ala	Leu	Leu
			20					25					30		
Gly	Asp	Val	Val	Thr	Val	Glu	Ala	Ala	Glu	Thr	Phe	Ser	Leu	Asn	Asn
			35				40					45			
Leu	Gly	Arg	Phe	Ala	Asp	Lys	Leu	Pro	Ser	Glu	Pro	Arg	Glu	Asn	Ile
		50				55				60					
Val	Tyr	Gln	Cys	Trp	Glu	Arg	Phe	Cys	Gln	Glu	Leu	Gly	Lys	Gln	Ile
65				70					75					80	
Pro	Val	Ala	Met	Thr	Leu	Glu	Lys	Asn	Met	Pro	Ile	Gly	Ser	Gly	Leu
			85					90					95		
Gly	Ser	Ser	Ala	Cys	Ser	Val	Val	Ala	Ala	Leu	Met	Ala	Met	Asn	Glu

			100					105					110				
His	Cys	Gly	Lys	Pro	Leu	Asn	Asp	Thr	Arg	Leu	Leu	Ala	Leu	Met	Gly		
		115					120					125					
Glu	Leu	Glu	Gly	Arg	Ile	Ser	Gly	Ser	Ile	His	Tyr	Asp	Asn	Val	Ala		
		130				135					140						
Pro	Cys	Phe	Leu	Gly	Gly	Met	Gln	Leu	Met	Ile	Glu	Glu	Asn	Asp	Ile		
145				150					155						160		
Ile	Ser	Gln	Gln	Val	Pro	Gly	Phe	Asp	Glu	Trp	Leu	Trp	Val	Leu	Ala		
			165					170							175		
Tyr	Pro	Gly	Ile	Lys	Val	Ser	Thr	Ala	Glu	Ala	Arg	Ala	Ile	Leu	Pro		
		180					185					190					
Ala	Gln	Tyr	Arg	Arg	Gln	Asp	Cys	Ile	Ala	His	Gly	Arg	His	Leu	Ala		
		195				200					205						
Gly	Phe	Ile	His	Ala	Cys	Tyr	Ser	Arg	Gln	Pro	Glu	Leu	Ala	Ala	Lys		
		210				215					220						
Leu	Met	Lys	Asp	Val	Ile	Ala	Glu	Pro	Tyr	Arg	Glu	Arg	Leu	Leu	Pro		
225				230					235						240		
Gly	Phe	Arg	Gln	Ala	Arg	Gln	Ala	Val	Ala	Glu	Ile	Gly	Ala	Val	Ala		
			245					250						255			
Ser	Gly	Ile	Ser	Gly	Ser	Gly	Pro	Thr	Leu	Phe	Ala	Leu	Cys	Asp	Lys		
		260					265						270				
Pro	Glu	Thr	Ala	Gln	Arg	Val	Ala	Asp	Trp	Leu	Gly	Lys	Asn	Tyr	Leu		
		275				280						285					
Gln	Asn	Gln	Glu	Gly	Phe	Val	His	Ile	Cys	Arg	Leu	Asp	Thr	Ala	Gly		
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Ala	Arg	Val	Leu	Glu	Asn												
305					310												

<210> 11

<211> 1545

<212> DNA

<213> Escherichia coli

<220>

<223> Native gene ilvA, L-threonine dehydratase

<400> 11

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tcgtcgcgtc ttgataacgt cattctggtg aagcgcgaag atcgccagcc agtcacagc	180
tttaagctgc gcggcgcata cgccatgatg gcgggcctga cggaagaaca gaaagcgcac	240
ggcgtgatca ctgcttctgc gggtaaccac gcgcagggcg tcgctgtttc ttctgcgcgg	300
ttaggcgtga aggccctgat cgttatgcca accgccaccg ccgacatcaa agtcgacgcg	360

gtgcgcggct tcggcggcga agtgctgctc cacggcgcga actttgatga agcgaaagcc	420
aaagcgatcg aactgtcaca gcagcagggg ttcacctggg tgccgccgtt cgaccatccg	480
atggtgattg ccgggcaagg cacgctggcg ctggaactgc tccagcagga cgcccatctc	540
gaccgcgtat ttgtgccagt cggcggcggc ggtctggctg ctggcgtggc ggtgctgac	600
aaacaactga tgccgcaaat caaagtgatc gccgtagaag cggaagactc cgcctgcctg	660
aaagcagcgc tggatgcggg tcatccggtt gatctgccgc gcgtagggct atttgctgaa	720
ggcgtagcgg taaaacgcat cggtgacgaa accttccgtt tatgccagga gtatctcgac	780
gacatcatca ccgtcgatag cgatgcgatc tgtgcggcga tgaaggattt attcgaagat	840
gtgcgcgcgg tggcggaacc ctctggcgcg ctggcgctgg cgggaatgaa aaaatatatc	900
gccctgcaca acattcgcgg cgaacggctg gcgcatattc tttccggtgc caacgtgaac	960
ttccacggcc tgcgctacgt ctcagaacgc tgcgaactgg gcgaacagcg tgaagcgttg	1020
ttggcgggtga ccattccgga agaaaaaggc agcttcctca aattctgcca actgcttggc	1080
gggcgttcgg tcaccgagtt caactaccgt tttgccgatg caaaaaacgc ctgcatcttt	1140
gtcgggtgtgc gcctgagccg cggcctcgaa gagcgcaaag aaattttgca gatgctcaac	1200
gacggcggct acagcgtggt tgatctctcc gacgacgaaa tggcgaagct acacgtgcgc	1260
tatatggtcg gcggacgtcc atcgcatccg ttgcaggaaac gcctctacag cttcgaattc	1320
ccggaatcac cgggcgcgct gctgcgcttc ctcaacacgc tgggtacgta ctggaacatt	1380
tccttgttcc actatcgcag ccatggcacc gactacgggc gcgtactggc ggcgttcgaa	1440
cttggcgacc atgaaccgga tttcgaaacc cggctgaatg agctgggcta cgattgccac	1500
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<210> 12

<211> 514

<212> PRT

<213> Escherichia coli

<220>

<223> Native protein product ilvA, L-threonine dehydratase

<400> 12

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Leu	Arg	Ala	Val	Leu	Arg	Ala	Pro	Val	Tyr	Glu	Ala	Ala	Gln	Val	Thr
			20					25					30		
Pro	Leu	Gln	Lys	Met	Glu	Lys	Leu	Ser	Ser	Arg	Leu	Asp	Asn	Val	Ile
		35					40					45			
Leu	Val	Lys	Arg	Glu	Asp	Arg	Gln	Pro	Val	His	Ser	Phe	Lys	Leu	Arg
	50					55					60				
Gly	Ala	Tyr	Ala	Met	Met	Ala	Gly	Leu	Thr	Glu	Glu	Gln	Lys	Ala	His
65					70					75					80
Gly	Val	Ile	Thr	Ala	Ser	Ala	Gly	Asn	His	Ala	Gln	Gly	Val	Ala	Phe
				85					90					95	
Ser	Ser	Ala	Arg	Leu	Gly	Val	Lys	Ala	Leu	Ile	Val	Met	Pro	Thr	Ala
		100						105					110		
Thr	Ala	Asp	Ile	Lys	Val	Asp	Ala	Val	Arg	Gly	Phe	Gly	Gly	Glu	Val
		115					120					125			
Leu	Leu	His	Gly	Ala	Asn	Phe	Asp	Glu	Ala	Lys	Ala	Lys	Ala	Ile	Glu
	130					135					140				
Leu	Ser	Gln	Gln	Gln	Gly	Phe	Thr	Trp	Val	Pro	Pro	Phe	Asp	His	Pro
145					150					155					160
Met	Val	Ile	Ala	Gly	Gln	Gly	Thr	Leu	Ala	Leu	Glu	Leu	Leu	Gln	Gln
				165					170					175	
Asp	Ala	His	Leu	Asp	Arg	Val	Phe	Val	Pro	Val	Gly	Gly	Gly	Gly	Leu
		180						185					190		
Ala	Ala	Gly	Val	Ala	Val	Leu	Ile	Lys	Gln	Leu	Met	Pro	Gln	Ile	Lys
		195					200					205			
Val	Ile	Ala	Val	Glu	Ala	Glu	Asp	Ser	Ala	Cys	Leu	Lys	Ala	Ala	Leu
	210					215					220				
Asp	Ala	Gly	His	Pro	Val	Asp	Leu	Pro	Arg	Val	Gly	Leu	Phe	Ala	Glu
225					230					235					240
Gly	Val	Ala	Val	Lys	Arg	Ile	Gly	Asp	Glu	Thr	Phe	Arg	Leu	Cys	Gln
				245					250					255	
Glu	Tyr	Leu	Asp	Asp	Ile	Ile	Thr	Val	Asp	Ser	Asp	Ala	Ile	Cys	Ala
		260						265					270		
Ala	Met	Lys	Asp	Leu	Phe	Glu	Asp	Val	Arg	Ala	Val	Ala	Glu	Pro	Ser
	275						280					285			
Gly	Ala	Leu	Ala	Leu	Ala	Gly	Met	Lys	Lys	Tyr	Ile	Ala	Leu	His	Asn
	290					295					300				
Ile	Arg	Gly	Glu	Arg	Leu	Ala	His	Ile	Leu	Ser	Gly	Ala	Asn	Val	Asn
305					310					315					320
Phe	His	Gly	Leu	Arg	Tyr	Val	Ser	Glu	Arg	Cys	Glu	Leu	Gly	Glu	Gln
				325					330					335	
Arg	Glu	Ala	Leu	Leu	Ala	Val	Thr	Ile	Pro	Glu	Glu	Lys	Gly	Ser	Phe
		340						345					350		
Leu	Lys	Phe	Cys	Gln	Leu	Leu	Gly	Gly	Arg	Ser	Val	Thr	Glu	Phe	Asn
	355						360					365			
Tyr	Arg	Phe	Ala	Asp	Ala	Lys	Asn	Ala	Cys	Ile	Phe	Val	Gly	Val	Arg
	370					375					380				
Leu	Ser	Arg	Gly	Leu	Glu	Glu	Arg	Lys	Glu	Ile	Leu	Gln	Met	Leu	Asn

385		390		395		400									
Asp	Gly	Gly	Tyr	Ser	Val	Val	Asp	Leu	Ser	Asp	Asp	Glu	Met	Ala	Lys
		405						410						415	
Leu	His	Val	Arg	Tyr	Met	Val	Gly	Gly	Arg	Pro	Ser	His	Pro	Leu	Gln
		420						425						430	
Glu	Arg	Leu	Tyr	Ser	Phe	Glu	Phe	Pro	Glu	Ser	Pro	Gly	Ala	Leu	Leu
		435						440						445	
Arg	Phe	Leu	Asn	Thr	Leu	Gly	Thr	Tyr	Trp	Asn	Ile	Ser	Leu	Phe	His
		450						455						460	
Tyr	Arg	Ser	His	Gly	Thr	Asp	Tyr	Gly	Arg	Val	Leu	Ala	Ala	Phe	Glu
465								470						475	
Leu	Gly	Asp	His	Glu	Pro	Asp	Phe	Glu	Thr	Arg	Leu	Asn	Glu	Leu	Gly
				485						490				495	
Tyr	Asp	Cys	His	Asp	Glu	Thr	Asn	Asn	Pro	Ala	Phe	Arg	Phe	Phe	Leu
			500					505						510	
Ala	Gly														

<210> 13
 <211> 1725
 <212> DNA
 <213> Escherichia coli

<220>
 <223> ilvI, AHAS Iso III, large subunit

<400> 13
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 ggtggtattg atcatgtatt agttcgtcat gagcaggcgg cggtgcatat ggccgatggc 180
 ctggcgcgcg cgaccgggga agtcggcgtc gtgctggtaa cgtcgggtcc aggggcgacc 240
 aatgcgatta ctggcatcgc caccgcttat atggattcca ttccattagt tgcctttcc 300
 gggcaggtag cgacctcgtt gataggttac gatgcctttc aggagtgcga catggtgggg 360
 atttcgcgac cggtgggttaa acacagtttt ctgggttaagc aaacggaaga cattccgcag 420
 gtgctgaaaa aggctttctg gctggcgga agtggtcgcc caggaccagt agtcgttgat 480
 ttaccgaaag atattcttaa tccggcgaac aaattaccct atgtctggcc ggagtcggtc 540
 agtatgcgtt cttacaatcc cactactacc ggacataaag ggcaaattaa gcgtgctctg 600
 caaacgctgg tagcggcaaa aaaaccgggt gtctacgtag gcggtggggc aatcacggcg 660

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ggctgccatc agcagttgaa agaaacgggtg gaggcgttga atctgcccgt tgtttgctca      720
ttgatggggc tgggggcggt tccggcaacg catcgtcagg cactgggcat gctgggaatg      780
cacggtacct acgaagccaa tatgacgatg cataacgcgg atgtgatttt cgccgtcggg      840
gtacgatttg atgaccgaac gacgaacaat ctggcaaagt actgccccaa tgccactgtt      900
ctgcatatcg atattgatcc tactttccatt tctaaaaccg tgactgcgga tatcccgatt      960
gtgggggatg ctcgccaggt cctcgaacaa atgcttgaac tcttgtcgca agaatccgcc     1020
catcaaccac tggatgagat ccgcgactgg tggcagcaaa ttgaacagtg gcgcgctcgt     1080
cagtcctga aatatgacac tcacagtga aagattaaac cgcaggcggg gatcgagact     1140
ctttggcggg tgacgaaggg agacgcttac gtgacgtccg atgtcgggca gcaccagatg     1200
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ctacccgatt tcgtccgtct ggcggaagcc tatgggcatg tcgggatcca gattttctcat     1560
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gtgtttgttg atgttaccgt cgatggcagc gagcacgtct acccgatgca gattcgcggg      1680
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<210> 14
<211> 574
<212> PRT
<213> Escherichia coli

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<220>
<223> ilvI, AHAS Iso III, large subunit

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<400> 14
Met Glu Met Leu Ser Gly Ala Glu Met Val Val Arg Ser Leu Ile Asp
1           5           10          15
Gln Gly Val Lys Gln Val Phe Gly Tyr Pro Gly Gly Ala Val Leu Asp

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Ile	Tyr	Asp	Ala	Leu	His	Thr	Val	Gly	Gly	Ile	Asp	His	Val	Leu	Val		
		35					40					45					
Arg	His	Glu	Gln	Ala	Ala	Val	His	Met	Ala	Asp	Gly	Leu	Ala	Arg	Ala		
		50				55					60						
Thr	Gly	Glu	Val	Gly	Val	Val	Leu	Val	Thr	Ser	Gly	Pro	Gly	Ala	Thr		
65					70					75					80		
Asn	Ala	Ile	Thr	Gly	Ile	Ala	Thr	Ala	Tyr	Met	Asp	Ser	Ile	Pro	Leu		
				85					90					95			
Val	Val	Leu	Ser	Gly	Gln	Val	Ala	Thr	Ser	Leu	Ile	Gly	Tyr	Asp	Ala		
			100					105					110				
Phe	Gln	Glu	Cys	Asp	Met	Val	Gly	Ile	Ser	Arg	Pro	Val	Val	Lys	His		
		115					120					125					
Ser	Phe	Leu	Val	Lys	Gln	Thr	Glu	Asp	Ile	Pro	Gln	Val	Leu	Lys	Lys		
	130					135					140						
Ala	Phe	Trp	Leu	Ala	Ala	Ser	Gly	Arg	Pro	Gly	Pro	Val	Val	Val	Asp		
145				150						155					160		
Leu	Pro	Lys	Asp	Ile	Leu	Asn	Pro	Ala	Asn	Lys	Leu	Pro	Tyr	Val	Trp		
				165					170					175			
Pro	Glu	Ser	Val	Ser	Met	Arg	Ser	Tyr	Asn	Pro	Thr	Thr	Thr	Gly	His		
			180					185					190				
Lys	Gly	Gln	Ile	Lys	Arg	Ala	Leu	Gln	Thr	Leu	Val	Ala	Ala	Lys	Lys		
	195						200					205					
Pro	Val	Val	Tyr	Val	Gly	Gly	Gly	Ala	Ile	Thr	Ala	Gly	Cys	His	Gln		
	210				215						220						
Gln	Leu	Lys	Glu	Thr	Val	Glu	Ala	Leu	Asn	Leu	Pro	Val	Val	Cys	Ser		
225					230					235					240		
Leu	Met	Gly	Leu	Gly	Ala	Phe	Pro	Ala	Thr	His	Arg	Gln	Ala	Leu	Gly		
				245					250					255			
Met	Leu	Gly	Met	His	Gly	Thr	Tyr	Glu	Ala	Asn	Met	Thr	Met	His	Asn		
			260					265					270				
Ala	Asp	Val	Ile	Phe	Ala	Val	Gly	Val	Arg	Phe	Asp	Asp	Arg	Thr	Thr		
	275						280					285					
Asn	Asn	Leu	Ala	Lys	Tyr	Cys	Pro	Asn	Ala	Thr	Val	Leu	His	Ile	Asp		
	290					295					300						
Ile	Asp	Pro	Thr	Ser	Ile	Ser	Lys	Thr	Val	Thr	Ala	Asp	Ile	Pro	Ile		
305					310					315					320		
Val	Gly	Asp	Ala	Arg	Gln	Val	Leu	Glu	Gln	Met	Leu	Glu	Leu	Leu	Ser		
				325					330					335			
Gln	Glu	Ser	Ala	His	Gln	Pro	Leu	Asp	Glu	Ile	Arg	Asp	Trp	Trp	Gln		
			340					345					350				
Gln	Ile	Glu	Gln	Trp	Arg	Ala	Arg	Gln	Cys	Leu	Lys	Tyr	Asp	Thr	His		
	355						360					365					
Ser	Glu	Lys	Ile	Lys	Pro	Gln	Ala	Val	Ile	Glu	Thr	Leu	Trp	Arg	Leu		
	370					375					380						
Thr	Lys	Gly	Asp	Ala	Tyr	Val	Thr	Ser	Asp	Val	Gly	Gln	His	Gln	Met		
385					390					395					400		
Phe	Ala	Ala	Leu	Tyr	Tyr	Pro	Phe	Asp	Lys	Pro	Arg	Arg	Trp	Ile	Asn		
				405					410					415			
Ser	Gly	Gly	Leu	Gly	Thr	Met	Gly	Phe	Gly	Leu	Pro	Ala	Ala	Leu	Gly		

			420					425				430				
Val	Lys	Met	Ala	Leu	Pro	Glu	Glu	Thr	Val	Val	Cys	Val	Thr	Gly	Asp	
		435						440				445				
Gly	Ser	Ile	Gln	Met	Asn	Ile	Gln	Glu	Leu	Ser	Thr	Ala	Leu	Gln	Tyr	
		450					455					460				
Glu	Leu	Pro	Val	Leu	Val	Val	Asn	Leu	Asn	Asn	Arg	Tyr	Leu	Gly	Met	
465						470					475				480	
Val	Lys	Gln	Trp	Gln	Asp	Met	Ile	Tyr	Ser	Gly	Arg	His	Ser	Gln	Ser	
				485					490					495		
Tyr	Met	Gln	Ser	Leu	Pro	Asp	Phe	Val	Arg	Leu	Ala	Glu	Ala	Tyr	Gly	
			500					505					510			
His	Val	Gly	Ile	Gln	Ile	Ser	His	Pro	His	Glu	Leu	Glu	Ser	Lys	Leu	
		515					520					525				
Ser	Glu	Ala	Leu	Glu	Gln	Val	Arg	Asn	Asn	Arg	Leu	Val	Phe	Val	Asp	
		530				535					540					
Val	Thr	Val	Asp	Gly	Ser	Glu	His	Val	Tyr	Pro	Met	Gln	Ile	Arg	Gly	
545					550					555					560	
Gly	Gly	Met	Asp	Glu	Met	Trp	Leu	Ser	Lys	Thr	Glu	Arg	Thr			
			565						570							

<210> 15

<211> 492

<212> DNA

<213> Escherichia coli

<220>

<223> ilvH, AHAS Iso III, small subunit

<400> 15

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ccgacattat cgcgtatgac catccagacc gtgggcatg aaaaagtact tgagcagatc	180
gaaaagcaat tacacaaact ggatgatgtc ttgcgcgtga gtgagttggg gcagggcgcg	240
catgttgagc gggaaatcat gctggtgaaa attcaggcca gcggttacgg gcgtgacgaa	300
gtgaaacgta atacggaaat attccgtggg caaattatcg atgtcacacc ctcgctttat	360
accgttcaat tagcaggcac cagcggtaag cttgatgcat ttttagcatc gattcgcgat	420
gtggcgaaaa ttgtggaggt tgctcgctct ggtgtggtcg gactttcgcg cggcgataaa	480
ataatgcgtt ga	492

<210> 16

<211> 163
 <212> PRT
 <213> Escherichia coli

<220>
 <223> ilvH, AHAS Iso III, small subunit

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 20 25 30
 Leu Thr Val Ala Pro Thr Asp Asp Pro Thr Leu Ser Arg Met Thr Ile
 35 40 45
 Gln Thr Val Gly Asp Glu Lys Val Leu Glu Gln Ile Glu Lys Gln Leu
 50 55 60
 His Lys Leu Val Asp Val Leu Arg Val Ser Glu Leu Gly Gln Gly Ala
 65 70 75 80
 His Val Glu Arg Glu Ile Met Leu Val Lys Ile Gln Ala Ser Gly Tyr
 85 90 95
 Gly Arg Asp Glu Val Lys Arg Asn Thr Glu Ile Phe Arg Gly Gln Ile
 100 105 110
 Ile Asp Val Thr Pro Ser Leu Tyr Thr Val Gln Leu Ala Gly Thr Ser
 115 120 125
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 Ile Met Arg

<210> 17
 <211> 2463
 <212> DNA
 <213> Escherichia coli

<220>
 <223> thrA, aspartate kinase and homoserine dehydrogenase, bifunctional

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<210> 18
<211> 820
<212> PRT
<213> Escherichia coli

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<220>
<223> thrA, aspartate kinase and homoserine dehydrogenase, bifunctional

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35     40     45
Ala Met Ile Glu Lys Thr Ile Ser Gly Gln Asp Ala Leu Pro Asn Ile
50     55     60
Ser Asp Ala Glu Arg Ile Phe Ala Glu Leu Leu Thr Gly Leu Ala Ala
65     70     75     80
Ala Gln Pro Gly Phe Pro Leu Ala Gln Leu Lys Thr Phe Val Asp Gln
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Glu Phe Ala Gln Ile Lys His Val Leu His Gly Ile Ser Leu Leu Gly

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Arg	Asp	Glu	Gly	Lys	Val	Leu	Arg	Tyr	Val	Gly	Asn	Ile	Asp	Glu	Asp		
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785					790					795					800		
Val	Thr	Ala	Ala	Gly	Val	Phe	Ala	Asp	Leu	Leu	Arg	Thr	Leu	Ser	Trp		
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<210> 19

<211> 285

<212> DNA

<213> Escherichia coli

<220>

<223> araBAD promoter

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aagccatgac aaaaacgcgt aacaaaagtg tctataatca cggcagaaaa gtccacattg 180
attatttgca cggcgtcaca ctttgctatg ccatagcatt tttatccata agattagcgg 240
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<210> 20
<211> 879
<212> DNA
<213> Escherichia coli

<220>
<223> Gene araC

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accacccgga tgcctatcgc caccgtcggg cgcaatgttg gttttgacga tcaactctat 780
ttctcgcggg tattttaaaaa atgcaccggg gccagcccga gcgagttccg tgccggttgt 840

gaagaaaaag tgaatgatgt agccgtcaag ttgtcataa 879

<210> 21

<211> 81

<212> DNA

<213> Escherichia coli

<220>

<223> Pm promoter

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<210> 22

<211> 1135

<212> DNA

<213> Escherichia coli

<220>

<223> XylS promoter and gene xylS

<400> 22

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gcaatggggg taacccgtat acgcatcacg tcgagatgca ttttcatcga cttggcgctt 120

ttctacatca caccaagcag cccacattaa aataagagaa ccgtgaacta tggatttttg 180

cttattgaac gagaaaagtc agatcttcgt ccacgccgag ccctatgcag tctccgatta 240

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<210> 23

<211> 1689

<212> DNA

<213> Escherichia coli

<220>

<223> ilvB, AHAS Iso I, large subunit

<400> 23

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caggcttcat tgcaaggaaat catcaatcgc cctggcccgg cgctgatcca tgtgcgcatt	1620
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<210> 24
 <211> 562
 <212> PRT
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<220>
 <223> ilvB, AHAS Iso I, large subunit

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Met	Ala	Cys	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Leu	Val	Thr	Ala	Ile	Ala
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Gly	Ile	Ser	Ile	Pro	Ile	Thr	Lys	His	Asn	Tyr	Leu	Val	Arg	His	Ile
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Glu	Glu	Leu	Pro	Gln	Val	Met	Ser	Asp	Ala	Phe	Arg	Ile	Ala	Gln	Ser
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Gly	Arg	Pro	Gly	Pro	Val	Trp	Ile	Asp	Ile	Pro	Lys	Asp	Val	Gln	Thr
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Val	Ala	Ile	Gln	Ala	Asp	Val	Asp	Asp	Val	Leu	Ala	Gln	Leu	Ile	Pro
				325				330						335	
Leu	Val	Glu	Ala	Gln	Pro	Arg	Ala	Glu	Trp	His	Gln	Leu	Val	Ala	Asp
			340					345					350		
Leu	Gln	Arg	Glu	Phe	Pro	Cys	Pro	Ile	Pro	Lys	Ala	Cys	Asp	Pro	Leu
		355					360					365			
Ser	His	Tyr	Gly	Leu	Ile	Asn	Ala	Val	Ala	Ala	Cys	Val	Asp	Asp	Asn
	370					375					380				
Ala	Ile	Ile	Thr	Thr	Asp	Val	Gly	Gln	His	Gln	Met	Trp	Thr	Ala	Gln
385					390					395					400
Ala	Tyr	Pro	Leu	Asn	Arg	Pro	Arg	Gln	Trp	Leu	Thr	Ser	Gly	Gly	Leu
				405				410						415	
Gly	Thr	Met	Gly	Phe	Gly	Leu	Pro	Ala	Ala	Ile	Gly	Ala	Ala	Leu	Ala

			420					425					430				
Asn	Pro	Asp	Arg	Lys	Val	Leu	Cys	Phe	Ser	Gly	Asp	Gly	Ser	Leu	Met		
		435					440					445					
Met	Asn	Ile	Gln	Glu	Met	Ala	Thr	Ala	Ser	Glu	Asn	Gln	Leu	Asp	Val		
	450					455					460						
Lys	Ile	Ile	Leu	Met	Asn	Asn	Glu	Ala	Leu	Gly	Leu	Val	His	Gln	Gln		
465					470					475					480		
Gln	Ser	Leu	Phe	Tyr	Glu	Gln	Gly	Val	Phe	Ala	Ala	Thr	Tyr	Pro	Gly		
			485					490					495				
Lys	Ile	Asn	Phe	Met	Gln	Ile	Ala	Ala	Gly	Phe	Gly	Leu	Glu	Thr	Cys		
		500					505					510					
Asp	Leu	Asn	Asn	Glu	Ala	Asp	Pro	Gln	Ala	Ser	Leu	Gln	Glu	Ile	Ile		
	515						520					525					
Asn	Arg	Pro	Gly	Pro	Ala	Leu	Ile	His	Val	Arg	Ile	Asp	Ala	Glu	Glu		
	530					535					540						
Lys	Val	Tyr	Pro	Met	Val	Pro	Pro	Gly	Ala	Ala	Asn	Thr	Glu	Met	Val		
545					550					555					560		
Gly	Glu																

<210> 25
 <211> 291
 <212> DNA
 <213> Escherichia coli

<220>
 <223> ilvN, AHAS Iso I, small subunit

<400> 25	
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gtaatgaccc acgtttgtgg cctttttgcc cgccgcgctt ttaacgttga aggcattctt	120
tgtctgccga ttcaggacag cgacaaaagc catatctggc tactgggtcaa tgacgaccag	180
cgtctggagc agatgataag ccaaatcgat aagctggaag atgtcgtgaa agtcgagcgt	240
aatcagtccg atccgacgat gttaacaag atcgcggtgt tttttcagta a	291

<210> 26
 <211> 96
 <212> PRT
 <213> Escherichia coli

<220>
 <223> ilvN, AHAS Iso I, small subunit

<400> 26

Met	Gln	Asn	Thr	Thr	His	Asp	Asn	Val	Ile	Leu	Glu	Leu	Thr	Val	Arg
1				5					10					15	
Asn	His	Pro	Gly	Val	Met	Thr	His	Val	Cys	Gly	Leu	Phe	Ala	Arg	Arg
			20					25					30		
Ala	Phe	Asn	Val	Glu	Gly	Ile	Leu	Cys	Leu	Pro	Ile	Gln	Asp	Ser	Asp
		35					40					45			
Lys	Ser	His	Ile	Trp	Leu	Leu	Val	Asn	Asp	Asp	Gln	Arg	Leu	Glu	Gln
	50					55					60				
Met	Ile	Ser	Gln	Ile	Asp	Lys	Leu	Glu	Asp	Val	Val	Lys	Val	Gln	Arg
65					70				75					80	
Asn	Gln	Ser	Asp	Pro	Thr	Met	Phe	Asn	Lys	Ile	Ala	Val	Phe	Phe	Gln
				85					90					95	

<210> 27

<211> 1647

<212> DNA

<213> *Shigella boydii*

<220>

<223> AHAS II, large subunit

<400> 27

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ggttatccgg gtggcgcaat tatgccggtt tacgatgcat tgtatgacgg cggcgtggag	120
cacttgctgt gccgacatga gcagggtgcg gcaatggcgg ctatcggtta tgcccgtgct	180
accggcaaaa ctggcgtatg tatcgccacg tctgggtccgg gcgcaaccaa cctgataacc	240
gggcttgctg acgcactgtt agattctatc cctgttggtt ccatcaccgg tcaagtgtcc	300
gcaccgttta tcggcactga tgcatttcag gaagtggatg tcctgggatt gtcgttagcc	360
tgtaccaagc acagctttct ggtgcagtcg ctggaagagt tgccgcgcat tatggctgaa	420
gcattcgacg ttgccagctc aggtcgtcct ggtccggttc tggtcgatat cccaaaagat	480
atccagctag ccagcggatga cctggaaccg tggttcacca ccgttgaaaa cgaagtgact	540
ttcccacatg ccgaagttga gcaagcgcgc cagatgctgg caaaagcgca aaaaccgatg	600
ctgtacgttg gtgggtggcgt gggatatggcg caggcagttc ctgctttacg agaatttctc	660
gctaccacaa aaatgcctgc cacctgcacg ctgaaagggc tgggcgcagt tgaagcagat	720

tatccgtact atctgggcat gctgggaatg catggcacca aagcggcgaa cttcgcggtg	780
caggagtgcg acttgctgat cgccgtgggt gcacgttttg atgaccgggt gaccggcaaa	840
ctgaacacct tcgcaccaca cgccagcggt atccatatgg atatcgaccc ggcagaaatg	900
aacaagctgc gtcaggcaca tgtggcatta caaggtgatt taaatgctct gttaccagaa	960
ttacagcagc cgttaaatat caatgactgg cagcaatact gcgcgcagct gcgtgatgaa	1020
catgcctggc gttacgacca tcccggcgac gctatctacg cgccgttggt gttaaaacaa	1080
ctgtcggatc gtaaacctgc ggattgcgtc gtgaccacag atgtggggca gcaccagatg	1140
tgggctgcgc aacacatcgc ccacactcgc ccggaaaatt tcatcacctc cagcggctta	1200
ggcactatgg gttttggttt accagcggcg gttggcgcac aagtcgcgcg accgaacgat	1260
accgtcgtct gtatctccgg tgacggctct ttcatgatga atgtgcaaga gctgggcacc	1320
gtaaaacgca agcagttacc gttgaaaatc gtcttactcg ataaccaacg gttagggatg	1380
gttcgacaat ggcagcaact gttttttcag gaacgataca gcgaaaccac ctttactgat	1440
aaccccgatt tcctcatggt agccagcgcc ttcggcatcc ctggccaaca catcacccgt	1500
aaagaccagg ttgaagcggc actcgacacc atgctgaaca gtgatgggcc atacctgctt	1560
catgtctcaa tcgacgaact tgagaacgtc tggccgctgg tgccgcctgg cgccagtaat	1620
tcagaaatgt tggagaaatt atcatga	1647

<210> 28

<211> 548

<212> PRT

<213> *Shigella boydii*

<220>

<223> AHAS II, large subunit

<400> 28

Met	Asn	Gly	Ala	Gln	Trp	Val	Val	His	Ala	Leu	Arg	Ala	Gln	Gly	Val
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Asn	Thr	Val	Phe	Gly	Tyr	Pro	Gly	Gly	Ala	Ile	Met	Pro	Val	Tyr	Asp
			20				25						30		
Ala	Leu	Tyr	Asp	Gly	Gly	Val	Glu	His	Leu	Leu	Cys	Arg	His	Glu	Gln
		35				40					45				
Gly	Ala	Ala	Met	Ala	Ala	Ile	Gly	Tyr	Ala	Arg	Ala	Thr	Gly	Lys	Thr

	50					55				60					
Gly 65	Val	Cys	Ile	Ala	Thr 70	Ser	Gly	Pro	Gly	Ala 75	Thr	Asn	Leu	Ile	Thr 80
Gly	Leu	Ala	Asp	Ala 85	Leu	Leu	Asp	Ser	Ile 90	Pro	Val	Val	Ala	Ile 95	Thr
Gly	Gln	Val	Ser 100	Ala	Pro	Phe	Ile	Gly 105	Thr	Asp	Ala	Phe	Gln	Glu	Val
Asp	Val	Leu 115	Gly	Leu	Ser	Leu	Ala 120	Cys	Thr	Lys	His	Ser 125	Phe	Leu	Val
Gln	Ser 130	Leu	Glu	Glu	Leu	Pro	Arg 135	Ile	Met	Ala	Glu	Ala	Phe	Asp	Val
Ala 145	Ser	Ser	Gly	Arg	Pro	Gly	Pro	Val	Leu	Val	Asp	Ile	Pro	Lys	Asp 160
Ile	Gln	Leu	Ala	Ser 165	Gly	Asp	Leu	Glu	Pro	Trp	Phe	Thr	Thr	Val	Glu
Asn	Glu	Val	Thr 180	Phe	Pro	His	Ala	Glu 185	Val	Glu	Gln	Ala	Arg	Gln	Met
Leu	Ala	Lys 195	Ala	Gln	Lys	Pro	Met	Leu 200	Tyr	Val	Gly	Gly	Gly	Val	Gly
Met	Ala 210	Gln	Ala	Val	Pro	Ala	Leu	Arg 215	Glu	Phe	Leu	Ala	Thr	Thr	Lys
Met 225	Pro	Ala	Thr	Cys	Thr	Leu	Lys	Gly	Leu	Gly	Ala	Val	Glu	Ala	Asp 240
Tyr	Pro	Tyr	Tyr	Leu 245	Gly	Met	Leu	Gly	Met	His	Gly	Thr	Lys	Ala	Ala
Asn	Phe	Ala	Val 260	Gln	Glu	Cys	Asp	Leu	Leu	Ile	Ala	Val	Gly	Ala	Arg
Phe	Asp	Asp 275	Arg	Val	Thr	Gly	Lys	Leu	Asn	Thr	Phe	Ala	Pro	His	Ala
Ser	Val	Ile	His	Met	Asp	Ile 295	Asp	Pro	Ala	Glu	Met	Asn	Lys	Leu	Arg
Gln 305	Ala	His	Val	Ala	Leu	Gln	Gly	Asp	Leu	Asn	Ala	Leu	Leu	Pro	Glu
Leu	Gln	Gln	Pro	Leu 325	Asn	Ile	Asn	Asp	Trp	Gln	Gln	Tyr	Cys	Ala	Gln
Leu	Arg	Asp	Glu 340	His	Ala	Trp	Arg	Tyr	Asp	His	Pro	Gly	Asp	Ala	Ile
Tyr	Ala	Pro 355	Leu	Leu	Leu	Lys	Gln	Leu	Ser	Asp	Arg	Lys	Pro	Ala	Asp
Cys	Val	Val	Thr	Thr	Asp	Val 375	Gly	Gln	His	Gln	Met	Trp	Ala	Ala	Gln
His 385	Ile	Ala	His	Thr	Arg	Pro	Glu	Asn	Phe	Ile	Thr	Ser	Ser	Gly	Leu
Gly	Thr	Met	Gly	Phe 405	Gly	Leu	Pro	Ala	Ala	Val	Gly	Ala	Gln	Val	Ala
Arg	Pro	Asn	Asp 420	Thr	Val	Val	Cys	Ile	Ser	Gly	Asp	Gly	Ser	Phe	Met
Met	Asn	Val	Gln	Glu	Leu	Gly	Thr	Val	Lys	Arg	Lys	Gln	Leu	Pro	Leu
Lys	Ile	Val	Leu	Leu	Asp	Asn	Gln	Arg	Leu	Gly	Met	Val	Arg	Gln	Trp

450		455		460
Gln Gln Leu Phe Phe Gln Glu Arg Tyr Ser Glu Thr Thr Leu Thr Asp				
465		470		480
Asn Pro Asp Phe Leu Met Leu Ala Ser Ala Phe Gly Ile Pro Gly Gln				
	485		490	495
His Ile Thr Arg Lys Asp Gln Val Glu Ala Ala Leu Asp Thr Met Leu				
	500		505	510
Asn Ser Asp Gly Pro Tyr Leu Leu His Val Ser Ile Asp Glu Leu Glu				
	515		520	525
Asn Val Trp Pro Leu Val Pro Pro Gly Ala Ser Asn Ser Glu Met Leu				
	530		535	540
Glu Lys Leu Ser				
545				

<210> 29
 <211> 264
 <212> DNA
 <213> Shigella boydii

<220>
 <223> AHAS II, small subunit

<400> 29
 atgatgcaat atcaggtcaa tgtatcggct cgcttcaatc cggaaacctt agaacgtgtt 60
 ttacgcgtgg tgcgtcatcg tggtttccac gtctgctcaa tgaatatggc cgccgccagc 120
 gatgcacaaa atataaatat cgaattgacc gttgccagcc cacggtcggt cgacttactg 180
 tttagtcagt taaataaaact ggtggacgtc gcacacgttg ccatctgcca gagcacaacc 240
 acatcacaac aaatccgcgc ctga 264

<210> 30
 <211> 87
 <212> PRT
 <213> Shigella boydii

<220>
 <223> AHAS II, small subunit

<400> 30
 Met Met Gln Tyr Gln Val Asn Val Ser Ala Arg Phe Asn Pro Glu Thr
 1 5 10 15
 Leu Glu Arg Val Leu Arg Val Val Arg His Arg Gly Phe His Val Cys
 20 25 30
 Ser Met Asn Met Ala Ala Ala Ser Asp Ala Gln Asn Ile Asn Ile Glu


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ttgcagcgcc cgctgaatat cgccgcctgg cagcagcagg tggcgggtact gaaagctgag 1020
cacgcctgtc gctacgatca ccccggccag ccgatctacg cgccattgtt cttgcgccag 1080
ctgtccgccc gcaagccggc caacagcgtg gtgaccaccg acgtggggcca gcatcagatg 1140
tggagcgcgc agcacatgac gttcgaacgc ccggagaatt tcatcacctc cagcggcctc 1200
ggcaccatgg ggttcggcgt gccggcggcg gtggggggccc agatcgcgcg cccgcaagat 1260
acggtgatct gcgtctcggg cgatggctcc ttcgatgatga acgtacagga gctgggcacc 1320
atcaagcgta aacagctgcc gctcaagatc gtgctgctgg acaaccaacg cctcggaatg 1380
gtgcgtcagt ggcagcagct gttcttcgac ggccgctaca gcgaaaccaa cctgtccgat 1440
aaccccgact tcctgatgct ggccgccgcc ttcggcattc ccggccagcg catcagccgc 1500
aaggatcagg tggaggacgc gctcgaggcg ctgttcaaca ccgaaggccc ttatctgctg 1560
caggtctcta tcgacgaact cgaaaacgtc tggccgctgg tgccgccggg cgccggcaac 1620
gaaaccatgt tggaggaaat atcatga 1647

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<210> 32

<211> 548

<212> PRT

<213> *Serratia marcescens*

<220>

<223> AHAS II, large subunit

<400> 32

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Met Asn Gly Ala Gln Trp Val Val Gln Ala Leu Arg Ala Gln Gly Val
1      5      10     15
Asp Thr Val Phe Gly Tyr Pro Gly Gly Ala Ile Met Pro Val Tyr Asp
20     25     30
Ala Leu Tyr Asp Gly Gly Val Glu His Leu Leu Cys Arg His Glu Gln
35     40     45
Gly Ala Ala Met Ala Ala Ile Gly Tyr Ala Arg Ala Thr Gly Lys Val
50     55     60
Gly Val Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Ile Thr
65     70     75     80
Gly Leu Ala Asp Ala Leu Leu Asp Ser Val Pro Val Val Ala Ile Thr
85     90     95
Gly Gln Val Gly Ser Ala Leu Ile Gly Thr Asp Ala Phe Gln Glu Ile
100    105    110
Asp Val Leu Gly Leu Ser Leu Ala Cys Thr Lys His Ser Phe Leu Val

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		115					120				125				
Glu	Ser	Leu	Asp	Ala	Leu	Pro	Gly	Ile	Met	Ala	Glu	Ala	Phe	Ala	Ile
	130					135					140				
Ala	Ala	Gly	Gly	Arg	Pro	Gly	Pro	Val	Leu	Ile	Asp	Ile	Pro	Lys	Asp
145					150					155					160
Ile	Gln	Leu	Ala	Gln	Gly	Asp	Leu	His	Pro	His	Leu	Met	Pro	Val	Asp
				165					170					175	
Glu	Ala	Pro	Ala	Phe	Pro	Ala	Ala	Ala	Leu	Ala	Glu	Ala	Ala	Glu	Leu
			180					185					190		
Leu	Ala	Gln	Ala	Gln	Lys	Pro	Met	Leu	Tyr	Val	Gly	Gly	Gly	Val	Gly
		195					200					205			
Met	Ala	Gln	Ala	Val	Pro	Ala	Leu	Arg	Glu	Phe	Ile	Ala	Val	Thr	Arg
	210					215					220				
Met	Pro	Asn	Val	Ala	Thr	Leu	Lys	Gly	Leu	Gly	Ala	Pro	Asp	Ala	Gln
225					230						235				240
Asp	Pro	Leu	Tyr	Leu	Gly	Met	Leu	Gly	Met	His	Gly	Thr	Lys	Ala	Ala
				245					250					255	
Asn	Leu	Ala	Val	Gln	Ala	Cys	Asp	Leu	Leu	Ile	Ala	Val	Gly	Ala	Arg
		260					265						270		
Phe	Asp	Asp	Arg	Val	Thr	Gly	Lys	Leu	Asn	Ala	Phe	Ala	Pro	His	Ala
		275					280					285			
Lys	Val	Ile	His	Met	Asp	Ile	Asp	Pro	Ala	Glu	Met	Ser	Lys	Leu	Arg
	290				295						300				
Gln	Ala	His	Val	Ala	Leu	Gln	Gly	Asp	Leu	Lys	Ala	Leu	Leu	Pro	Ala
305					310					315					320
Leu	Gln	Arg	Pro	Leu	Asn	Ile	Ala	Ala	Trp	Gln	Gln	Gln	Val	Ala	Val
				325				330						335	
Leu	Lys	Ala	Glu	His	Ala	Cys	Arg	Tyr	Asp	His	Pro	Gly	Gln	Pro	Ile
		340						345					350		
Tyr	Ala	Pro	Leu	Phe	Leu	Arg	Gln	Leu	Ser	Ala	Arg	Lys	Pro	Ala	Asn
		355					360					365			
Ser	Val	Val	Thr	Thr	Asp	Val	Gly	Gln	His	Gln	Met	Trp	Ser	Ala	Gln
	370					375					380				
His	Met	Thr	Phe	Glu	Arg	Pro	Glu	Asn	Phe	Ile	Thr	Ser	Ser	Gly	Leu
385					390					395					400
Gly	Thr	Met	Gly	Phe	Gly	Val	Pro	Ala	Ala	Val	Gly	Ala	Gln	Ile	Ala
				405					410					415	
Arg	Pro	Gln	Asp	Thr	Val	Ile	Cys	Val	Ser	Gly	Asp	Gly	Ser	Phe	Met
			420					425					430		
Met	Asn	Val	Gln	Glu	Leu	Gly	Thr	Ile	Lys	Arg	Lys	Gln	Leu	Pro	Leu
		435					440					445			
Lys	Ile	Val	Leu	Leu	Asp	Asn	Gln	Arg	Leu	Gly	Met	Val	Arg	Gln	Trp
	450					455					460				
Gln	Gln	Leu	Phe	Phe	Asp	Gly	Arg	Tyr	Ser	Glu	Thr	Asn	Leu	Ser	Asp

515 520 525
 Asn Val Trp Pro Leu Val Pro Pro Gly Ala Gly Asn Glu Thr Met Leu
 530 535 540
 Glu Glu Ile Ser
 545

<210> 33
 <211> 258
 <212> DNA
 <213> *Serratia marcescens*

<220>
 <223> AHAS II, small subunit

<400> 33
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 aacgccgaca gcatcaatat cgaattgacc gttgccagcc cacgtccggt cgccctgttg 180
 tcattctcagt taagcaaact gctggacgtc tcctgcgtcg agatccagca gccaacatca 240
 caacaaatac gcgccctga 258

<210> 34
 <211> 85
 <212> PRT
 <213> *Serratia marcescens*

<220>
 <223> AHAS II, small subunit

<400> 34
 Met Met Gln His Gln Leu Ser Ile Gln Ala Arg Phe Arg Pro Glu Met
 1 5 10 15
 Leu Glu Arg Val Leu Arg Val Val Arg His Arg Gly Phe Gln Val Cys
 20 25 30
 Ala Met Asn Met Val Ser Pro Ala Asn Ala Asp Ser Ile Asn Ile Glu
 35 40 45
 Leu Thr Val Ala Ser Pro Arg Pro Val Ala Leu Leu Ser Ser Gln Leu
 50 55 60
 Ser Lys Leu Leu Asp Val Ser Cys Val Glu Ile Gln Gln Pro Thr Ser
 65 70 75 80
 Gln Gln Ile Arg Ala
 85

<210> 35
<211> 1725
<212> DNA
<213> *Shigella boydii*

<220>
<223> AHAS III, large subunit

<400> 35
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caagtattcg gttatcctgg aggcgcagtc cttgatattt acgatgcatt gcataccgtg 120
ggtggtatcg atcatgtttt agttcgtcat gagcaggcgg cagtgcatat ggccgatggg 180
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gtgctgaaaa aggctttctg gctggcggca agtggtcgtc ctggaccagt agtcgttgat 480
ttaccgaaag atattcttaa tccggcgaac aaattaccct atgtctggcc ggagtcggtc 540
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caaacgctgg tagtggcaaa aaaaccggtt gtctacgtag gcggtggggc aatcatggcg 660
ggctgccatc agcagttgaa agaaacgggtg gaggcgttga atctgcccgt tgtttcctca 720
ttgatggggc tgggggcggt tccggcaacg catcgtcagg cactgggcat gctgggaatg 780
cacggtacct acgaagcaa tatgacgatg cataacgcgg atgtgatttt cgccgtcggg 840
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catcaaccac tggatgagat ccgcgactgg tggcagcaaa ttgaacagtg gcgcgctcgt 1080
cagtgcctga aatatgacac tcacagtga aagattaaac cgcaggcggg gatcgagact 1140
ctttggcggg tgacgaaggg agacgcttac gtgacgtccg atgtcgggca gcaccagatg 1200

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accgtgggtt gcgtcactgg cgacggcagt attcagatga acattcagga actgtctacc 1380
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gtgtttgttg atgttaccgt cgatggcagt gagcacgtct acccgatgca gattcgcggg 1680
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<210> 36
 <211> 574
 <212> PRT
 <213> *Shigella boydii*

<220>
 <223> AHAS III, large subunit

<400> 36

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

				165				170					175			
Pro	Glu	Ser	Val	Ser	Met	Arg	Ser	Tyr	Asn	Pro	Thr	Thr	Thr	Gly	His	
			180					185					190			
Lys	Gly	Gln	Ile	Lys	Arg	Ala	Leu	Gln	Thr	Leu	Val	Val	Ala	Lys	Lys	
		195					200					205				
Pro	Val	Val	Tyr	Val	Gly	Gly	Gly	Ala	Ile	Met	Ala	Gly	Cys	His	Gln	
	210				215						220					
Gln	Leu	Lys	Glu	Thr	Val	Glu	Ala	Leu	Asn	Leu	Pro	Val	Val	Ser	Ser	
225				230						235					240	
Leu	Met	Gly	Leu	Gly	Ala	Phe	Pro	Ala	Thr	His	Arg	Gln	Ala	Leu	Gly	
			245						250					255		
Met	Leu	Gly	Met	His	Gly	Thr	Tyr	Glu	Ala	Asn	Met	Thr	Met	His	Asn	
			260					265					270			
Ala	Asp	Val	Ile	Phe	Ala	Val	Gly	Val	Arg	Phe	Asp	Asp	Arg	Thr	Thr	
	275						280					285				
Asn	Asn	Leu	Ala	Lys	Tyr	Cys	Pro	Asn	Ala	Thr	Val	Leu	His	Ile	Asp	
	290					295					300					
Ile	Asp	Pro	Thr	Ser	Ile	Ser	Lys	Thr	Val	Thr	Ala	Asp	Ile	Pro	Ile	
305				310						315					320	
Val	Gly	Asp	Ala	Arg	Gln	Val	Leu	Glu	Gln	Met	Leu	Glu	Leu	Leu	Ser	
			325						330					335		
Gln	Glu	Ser	Ala	His	Gln	Pro	Leu	Asp	Glu	Ile	Arg	Asp	Trp	Trp	Gln	
		340					345						350			
Gln	Ile	Glu	Gln	Trp	Arg	Ala	Arg	Gln	Cys	Leu	Lys	Tyr	Asp	Thr	His	
	355					360						365				
Ser	Glu	Lys	Ile	Lys	Pro	Gln	Ala	Val	Ile	Glu	Thr	Leu	Trp	Arg	Leu	
	370				375					380						
Thr	Lys	Gly	Asp	Ala	Tyr	Val	Thr	Ser	Asp	Val	Gly	Gln	His	Gln	Met	
385				390						395					400	
Phe	Ala	Ala	Leu	Tyr	Tyr	Pro	Phe	Asp	Lys	Pro	Arg	Arg	Trp	Ile	Asn	
			405					410						415		
Ser	Gly	Gly	Leu	Gly	Thr	Met	Gly	Phe	Gly	Leu	Pro	Ala	Ala	Leu	Gly	
		420					425						430			
Val	Lys	Met	Ala	Leu	Pro	Glu	Glu	Thr	Val	Val	Cys	Val	Thr	Gly	Asp	
	435					440						445				
Gly	Ser	Ile	Gln	Met	Asn	Ile	Gln	Glu	Leu	Ser	Thr	Ala	Leu	Gln	Tyr	
	450				455					460						
Glu	Leu	Pro	Val	Leu	Val	Val	Asn	Leu	Asn	Asn	Arg	Tyr	Leu	Gly	Met	
465				470					475					480		
Val	Lys	Gln	Trp	Gln	Asp	Met	Ile	Tyr	Ser	Gly	Arg	His	Ser	Gln	Ser	
			485					490						495		
Tyr	Met	Gln	Ser	Leu	Pro	Asp	Phe	Val	Arg	Leu	Ala	Glu	Ala	Tyr	Gly	
		500					505						510			
His	Val	Gly	Ile	Gln	Ile	Ser	His	Pro	His	Glu	Leu	Glu	Ser	Lys	Leu	
	515					520						525				
Ser	Glu	Ala	Leu	Glu	Gln	Val	Arg	Asn	Asn	Arg	Leu	Val	Phe	Val	Asp	
	530				535					540						
Val	Thr	Val	Asp	Gly	Ser	Glu	His	Val	Tyr	Pro	Met	Gln	Ile	Arg	Gly	
545				550						555					560	
Gly	Gly	Met	Asp	Glu	Met	Trp	Leu	Ser	Lys	Thr	Glu	Arg	Thr			

<210> 37

<211> 492

<212> DNA

<213> *Shigella boydii*

<220>

<223> AHAS III, small subunit

<400> 37

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ggcctttttt cccagcgagg ctacaacatt gaaagcctga ccgttgcgcc aaccgacgat      120
ccgacattat cgcgtatgac catccagacc gtgggcgatg aaaaagtact tgagcagatc      180
gaaaagcaat tacacaagct ggtc gatgtc ttgcgcgtga gtgagttggg gcagggcgcg      240
catgttgagc gggaaattat gctggtgaaa attcaggcca gcggttacgg gcgtgacgaa      300
gtgaaacgta atacggaaat attccgtggg caaattatcg atgtcacccc ctcgctttat      360
accgttcaat tagcaggcac cagcgataag cttgatgcat ttttagcatc gattcgcgag      420
gtggcgaaaa ttgtggaagt tgctcgctct ggtgtggctg gactttcgcg cggcgataaa      480
ataatgcgtt ga                                                                492

```

<210> 38

<211> 163

<212> PRT

<213> *Shigella boydii*

<220>

<223> AHAS III, small subunit

<400> 38

```

Met Arg Arg Ile Leu Ser Val Leu Leu Glu Asn Glu Ser Gly Ala Leu
1           5           10          15
Ser Arg Val Ile Gly Leu Phe Ser Gln Arg Gly Tyr Asn Ile Glu Ser
          20          25          30
Leu Thr Val Ala Pro Thr Asp Asp Pro Thr Leu Ser Arg Met Thr Ile
          35          40          45
Gln Thr Val Gly Asp Glu Lys Val Leu Glu Gln Ile Glu Lys Gln Leu
          50          55          60
His Lys Leu Val Asp Val Leu Arg Val Ser Glu Leu Gly Gln Gly Ala

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65		70		75		80									
His	Val	Glu	Arg	Glu	Ile	Met	Leu	Val	Lys	Ile	Gln	Ala	Ser	Gly	Tyr
		85							90					95	
Gly	Arg	Asp	Glu	Val	Lys	Arg	Asn	Thr	Glu	Ile	Phe	Arg	Gly	Gln	Ile
		100						105					110		
Ile	Asp	Val	Thr	Pro	Ser	Leu	Tyr	Thr	Val	Gln	Leu	Ala	Gly	Thr	Ser
		115					120					125			
Asp	Lys	Leu	Asp	Ala	Phe	Leu	Ala	Ser	Ile	Arg	Glu	Val	Ala	Lys	Ile
	130					135				140					
Val	Glu	Val	Ala	Arg	Ser	Gly	Val	Val	Gly	Leu	Ser	Arg	Gly	Asp	Lys
145					150				155					160	
Ile	Met	Arg													

<210> 39
 <211> 1719
 <212> DNA
 <213> *Serratia marcescens*

<220>
 <223> AHAS III, large subunit

<400> 39
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 catgtattcg gctaccccg gggggcggtg ctcgatatct acgacgccct gcatacggtc 120
 ggagggatcg atcatattct ggtgcgccac gagcaagggtg cgggtgcacat ggccgacggc 180
 tacgcgcgcg ccaccggcga agtgggcgtg gtgctgggtga cgtccggccc cggcgccacc 240
 aacgccatta ccggtatcgc taccgcttat atggactcga tcccgatggc cgtcctgtcg 300
 gggcagggtg ccagctcgct gatcggctac gacgcctttc aggagtgcga tatggtgggg 360
 atttctcggc cgggtggtgaa acacagcttc ctggtaaaac gcaccgaaga catcccggcg 420
 gtgttgaaga aggcctttta cctggcctcc agcggccgcc ccggcccggc ggtgatcgat 480
 ctgccgaaag acatcgtcgg cccggcggtg cggatgcctt atgcctaccc gcaggacgtg 540
 agcatgcgtt cttataaccc gacggtgcag ggccatcgcg ggcaaataca acgcgcgttg 600
 caaacatcc tggcggccaa gaagccgggtg atgtatgtcg gcggcggcgc gatcaacgcc 660
 ggttgcaag ccgaactgct ggcgttggcg gagcagctga acctgccggc gaccagcagc 720
 ctgatgggac tgggcgcttt ccccgccacc catcgccaga gtgtcggcat gctcggatatg 780

cacggcactt atgaagccaa caaaaccatg caccatgccg acgtgatctt cgcggtcggc 840
gtgcgttttcg acgatcgcac gaccaacaat ctggccaaat actgcccgga tgccaccgtg 900
ctgcatatcg atatcgatcc gacctcgatc tccaaaacgg tggatgccga tattccgatc 960
gtcggcgatg ccaaacaggt gttggtgcag atgctggagc tgttggcgca ggatgacaag 1020
gcgcaggatc acgatgcgtt gcgcgattgg tggcagtcta ttgaacagtg gcgcgcccgc 1080
gactgttttg ggtacgacaa aaacagcggc accatcaagc cgcaggcggg gatcgaaacc 1140
ctgcatcgcc tgaccaaagg cgatgcctat gtgacctccg acgtggggca gcaccagatg 1200
tttgccgcgc tctattaccc gttcgacaaa ccgcgccgtt ggatcaactc cggcggcctc 1260
ggcaccatgg gcttcggcct gccggcggca ttgggctga agctggcgct gccggaggaa 1320
accgtggtgt gcgtcaccgg cgacggcagc atccagatga acattcagga gctgtccacc 1380
gcgctgcaat ataacctgcc ggtggtggtg gtgaacctca acaaccgcta tctgggcatg 1440
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ctgccggact ttgtcaagct ggccgaggct tacggccatg tcggcatcgc catccgcacg 1560
ccggatgagc tggaaagcaa gctggcgcag gcgctggcgg aaaaagagcg gctggtgttc 1620
gtcgacgtga ccgtcgatga aaccgaacat gtttaccga tgcagatccg cggcgggaagc 1680
atggacgaaa tgtggcttag caaaacggag aggacctga 1719

<210> 40

<211> 572

<212> PRT

<213> *Serratia marcescens*

<220>

<223> AHAS III, largeV subunit

<400> 40

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Gln	Gly	Val	Lys	His	Val	Phe	Gly	Tyr	Pro	Gly	Gly	Ala	Val	Leu	Asp
			20					25					30		
Ile	Tyr	Asp	Ala	Leu	His	Thr	Val	Gly	Gly	Ile	Asp	His	Ile	Leu	Val
		35					40				45				
Arg	His	Glu	Gln	Gly	Ala	Val	His	Met	Ala	Asp	Gly	Tyr	Ala	Arg	Ala

50		55		60											
Thr	Gly	Glu	Val	Gly	Val	Val	Leu	Val	Thr	Ser	Gly	Pro	Gly	Ala	Thr
65				70						75					80
Asn	Ala	Ile	Thr	Gly	Ile	Ala	Thr	Ala	Tyr	Met	Asp	Ser	Ile	Pro	Met
				85					90					95	
Val	Val	Leu	Ser	Gly	Gln	Val	Pro	Ser	Ser	Leu	Ile	Gly	Tyr	Asp	Ala
			100					105				110			
Phe	Gln	Glu	Cys	Asp	Met	Val	Gly	Ile	Ser	Arg	Pro	Val	Val	Lys	His
		115					120					125			
Ser	Phe	Leu	Val	Lys	Arg	Thr	Glu	Asp	Ile	Pro	Ala	Val	Leu	Lys	Lys
	130					135					140				
Ala	Phe	Tyr	Leu	Ala	Ser	Ser	Gly	Arg	Pro	Gly	Pro	Val	Val	Ile	Asp
145				150						155					160
Leu	Pro	Lys	Asp	Ile	Val	Gly	Pro	Ala	Val	Arg	Met	Pro	Tyr	Ala	Tyr
			165					170						175	
Pro	Gln	Asp	Val	Ser	Met	Arg	Ser	Tyr	Asn	Pro	Thr	Val	Gln	Gly	His
		180						185					190		
Arg	Gly	Gln	Ile	Lys	Arg	Ala	Leu	Gln	Thr	Ile	Leu	Ala	Ala	Lys	Lys
	195						200					205			
Pro	Val	Met	Tyr	Val	Gly	Gly	Gly	Ala	Ile	Asn	Ala	Gly	Cys	Glu	Ala
	210				215						220				
Glu	Leu	Leu	Ala	Leu	Ala	Glu	Gln	Leu	Asn	Leu	Pro	Val	Thr	Ser	Ser
225				230						235					240
Leu	Met	Gly	Leu	Gly	Ala	Phe	Pro	Gly	Thr	His	Arg	Gln	Ser	Val	Gly
			245					250						255	
Met	Leu	Gly	Met	His	Gly	Thr	Tyr	Glu	Ala	Asn	Lys	Thr	Met	His	His
		260						265					270		
Ala	Asp	Val	Ile	Phe	Ala	Val	Gly	Val	Arg	Phe	Asp	Asp	Arg	Thr	Thr
	275						280					285			
Asn	Asn	Leu	Ala	Lys	Tyr	Cys	Pro	Asp	Ala	Thr	Val	Leu	His	Ile	Asp
	290				295						300				
Ile	Asp	Pro	Thr	Ser	Ile	Ser	Lys	Thr	Val	Asp	Ala	Asp	Ile	Pro	Ile
305				310						315					320
Val	Gly	Asp	Ala	Lys	Gln	Val	Leu	Val	Gln	Met	Leu	Glu	Leu	Leu	Ala
			325						330					335	
Gln	Asp	Asp	Lys	Ala	Gln	Asp	His	Asp	Ala	Leu	Arg	Asp	Trp	Trp	Gln
	340						345					350			
Ser	Ile	Glu	Gln	Trp	Arg	Ala	Arg	Asp	Cys	Leu	Gly	Tyr	Asp	Lys	Asn
	355					360					365				
Ser	Gly	Thr	Ile	Lys	Pro	Gln	Ala	Val	Ile	Glu	Thr	Leu	His	Arg	Leu
	370				375						380				
Thr	Lys	Gly	Asp	Ala	Tyr	Val	Thr	Ser	Asp	Val	Gly	Gln	His	Gln	Met
385				390						395					400
Phe	Ala	Ala	Leu	Tyr	Tyr	Pro	Phe	Asp	Lys	Pro	Arg	Arg	Trp	Ile	Asn
			405					410						415	
Ser	Gly	Gly	Leu	Gly	Thr	Met	Gly	Phe	Gly	Leu	Pro	Ala	Ala	Leu	Gly
		420					425					430			
Val	Lys	Leu	Ala	Leu	Pro	Glu	Glu	Thr	Val	Val	Cys	Val	Thr	Gly	Asp
	435					440						445			
Gly	Ser	Ile	Gln	Met	Asn	Ile	Gln	Glu	Leu	Ser	Thr	Ala	Leu	Gln	Tyr

450		455		460
Asn Leu Pro Val Val Val Val Asn Leu Asn Asn Arg Tyr Leu Gly Met				
465		470		480
Val Lys Gln Trp Gln Asp Met Ile Tyr Ser Gly Arg His Ser Gln Ser				
	485		490	495
Tyr Met Asp Ser Leu Pro Asp Phe Val Lys Leu Ala Glu Ala Tyr Gly				
	500		505	510
His Val Gly Ile Ala Ile Arg Thr Pro Asp Glu Leu Glu Ser Lys Leu				
	515		520	525
Ala Gln Ala Leu Ala Glu Lys Glu Arg Leu Val Phe Val Asp Val Thr				
	530		535	540
Val Asp Glu Thr Glu His Val Tyr Pro Met Gln Ile Arg Gly Gly Ser				
545		550		560
Met Asp Glu Met Trp Leu Ser Lys Thr Glu Arg Thr				
	565		570	

<210> 41
 <211> 495
 <212> DNA
 <213> Serratia marcescens

<220>
 <223> AHAS III, small subunit

<400> 41	
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gtggggttgt tctcccagcg tggttataac attgagagcc tgaccggtggc gccgaccgac	120
gatccgacgc tgtcgcgtat gactatccag accgtcggcg acgagaaagt gctggagcag	180
attgagaagc agttgcacaa gctggtggac gtgctgcgcg tcagcgagct ggtgcagggc	240
gctcacgtcg agcgcgagat catgctggtg aaactgcagg ccagcggcta cggccgtgaa	300
gaggtgaagc gctgcgccga cttttccgc ggccagatcg tcgatgtgac ggcgacgttg	360
tatacgggtgc agttggccgg caccagcgat aaactggacg ctttcctgag tgcggtgcga	420
gacgtcgcgg agatcgtgga agtggcgcgt tccggcgtgg tcggcgtgtc gcgcggcgac	480
aaaatcatgc gctga	495

<210> 42
 <211> 164
 <212> PRT
 <213> Serratia marcescens

<220>

<223> AHAS III, small subunit

<400> 42

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

<210> 43

<211> 1725

<212> DNA

<213> Bacillus subtilis

<220>

<223> AHAS III, large subunit

<400> 43

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gcattaatgc tgattgaatc attaaaaaaa gagaaagtag aaatgatctt cggttatccg	120
ggcggggctg tgcttccgat ttacgataag ctatacaatt cagggttggt acatatcctt	180
ccccgtcacg aacaaggagc aattcatgca gcggagggat acgcaagggt ctccggaaaa	240
ccgggtgtcg tcattgccac gtcagggccg ggagcgacaa accttggttac aggccttgct	300
gatgccatga ttgattcatt gccgttagtc gtctttacag ggcaggtagc aacctctgta	360

atcgggagcg atgcatttca ggaagcagac attttaggga ttacgatgcc agtaacaaaa	420
cacagctacc aggttcgcca gccggaagat ctgccgcgca tcattaaaga agcgttccat	480
attgcaacaa ctggaagacc cggacctgta ttgattgata ttccgaaaga tntagcaaca	540
attgaaggag aattcagcta cgatcatgag atgaatctcc cgggatacca gccgacaaca	600
gagccgaatt atttgcagat ccgcaagctt gtggaagccg tgagcagtgc gaaaaaacg	660
gtgatcctgg cgggtgcggg cgtactgcac ggaaaagcgt cagaagaatt aaaaaattat	720
gctgaacagc agcaaatccc tgtggcacac acccttttgg ggctcggagg cttcccggct	780
gaccatccgc ttttcctagg gatggcggga atgcacggta cttatacagc caatatggcc	840
cttcatgaat gtgatctatt aatcagtatc ggcgcccgtt ttgatgaccg tgtcacagga	900
aacctgaaac actttgccag aaacgcaaag atagcccaca tcgatattga tccagctgaa	960
atcggaaaaa tcatgaaaac acagattcct gtagtcggag acagcaaaat tgtcctgcag	1020
gagctgatca aacaagacgg caaacaagc gattcaagcg aatggaaaaa acagctcgca	1080
gaatggaaaag aagagtatcc gctctggtat gtagataatg aagaagaagg ttttaaacct	1140
cagaaattga ttgaatatat tcatcaattt acaaaaggag aggccattgt cgcaacggat	1200
gtaggccagc atcaaatgtg gtcagcgcaa ttttatccgt tccaaaaagc agataaatgg	1260
gtcacgtcag gcggacttgg aacgatggga ttcggtcttc cggcggcgat cggcgcacag	1320
ctggccgaaa aagatgctac tgttgtcgcg gttgtcggag acggcggatt ccaaatacgc	1380
cttcaagaac tcgatgttat tcgcgaatta aatcttccgg tcaaggtagt gattttaaat	1440
aacgcttgtc tcggaatggc cagacagtgg caggaaattt tctatgaaga acgttattca	1500
gaatctaaat tcgcttctca gcctgacttc gtcaaatgtt ccgaagcata cggcattaaa	1560
ggcatcagaa tttcatcaga agcgggaagca aaggaaaagc tggaagaggc attaacatca	1620
agagaacctg ttgtcattga cgtgcggggt gccagcgaag aaaaagtatt cccgatggtg	1680
gctccgggga aagggtgca tgaaatggtg ggggtgaaac cttga	1725

<210> 44
 <211> 574
 <212> PRT

<213> Bacillus subtilis

<220>

<223> AHAS III, large subunit

<400> 44

Met	Gly	Thr	Asn	Val	Gln	Val	Asp	Ser	Ala	Ser	Ala	Glu	Cys	Thr	Gln
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Thr	Met	Ser	Gly	Ala	Leu	Met	Leu	Ile	Glu	Ser	Leu	Lys	Lys	Glu	Lys
			20				25					30			
Val	Glu	Met	Ile	Phe	Gly	Tyr	Pro	Gly	Gly	Ala	Val	Leu	Pro	Ile	Tyr
		35				40					45				
Asp	Lys	Leu	Tyr	Asn	Ser	Gly	Leu	Val	His	Ile	Leu	Pro	Arg	His	Glu
	50				55				60						
Gln	Gly	Ala	Ile	His	Ala	Ala	Glu	Gly	Tyr	Ala	Arg	Val	Ser	Gly	Lys
65				70					75					80	
Pro	Gly	Val	Val	Ile	Ala	Thr	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Leu	Val
			85					90					95		
Thr	Gly	Leu	Ala	Asp	Ala	Met	Ile	Asp	Ser	Leu	Pro	Leu	Val	Val	Phe
		100						105				110			
Thr	Gly	Gln	Val	Ala	Thr	Ser	Val	Ile	Gly	Ser	Asp	Ala	Phe	Gln	Glu
	115					120					125				
Ala	Asp	Ile	Leu	Gly	Ile	Thr	Met	Pro	Val	Thr	Lys	His	Ser	Tyr	Gln
	130				135					140					
Val	Arg	Gln	Pro	Glu	Asp	Leu	Pro	Arg	Ile	Ile	Lys	Glu	Ala	Phe	His
145				150					155					160	
Ile	Ala	Thr	Thr	Gly	Arg	Pro	Gly	Pro	Val	Leu	Ile	Asp	Ile	Pro	Lys
			165				170							175	
Asp	Val	Ala	Thr	Ile	Glu	Gly	Glu	Phe	Ser	Tyr	Asp	His	Glu	Met	Asn
	180						185					190			
Leu	Pro	Gly	Tyr	Gln	Pro	Thr	Thr	Glu	Pro	Asn	Tyr	Leu	Gln	Ile	Arg
	195					200						205			
Lys	Leu	Val	Glu	Ala	Val	Ser	Ser	Ala	Lys	Lys	Pro	Val	Ile	Leu	Ala
	210				215						220				
Gly	Ala	Gly	Val	Leu	His	Gly	Lys	Ala	Ser	Glu	Glu	Leu	Lys	Asn	Tyr
225				230						235				240	
Ala	Glu	Gln	Gln	Gln	Ile	Pro	Val	Ala	His	Thr	Leu	Leu	Gly	Leu	Gly
			245					250						255	
Gly	Phe	Pro	Ala	Asp	His	Pro	Leu	Phe	Leu	Gly	Met	Ala	Gly	Met	His
	260						265					270			
Gly	Thr	Tyr	Thr	Ala	Asn	Met	Ala	Leu	His	Glu	Cys	Asp	Leu	Leu	Ile
	275					280						285			
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			370					375					380				
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Ala	Asp	Lys	Trp	Val	Thr	Ser	Gly	Gly	Leu	Gly	Thr	Met	Gly	Phe	Gly		
			420					425					430				
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Glu	Ala	Lys	Glu	Lys	Leu	Glu	Glu	Ala	Leu	Thr	Ser	Arg	Glu	Pro	Val		
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tcgattgtcc agaggagct ggccttaatc aaggttgtct ccgcaccttc aacaagaaca	300

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 35 40 45
 Val Val His Val Glu Gly Glu Asn Asp Val Glu Gln Leu Thr Lys Gln
 50 55 60
 Leu Asn Lys Gln Ile Asp Val Leu Lys Val Thr Asp Ile Thr Asn Gln
 65 70 75 80
 Ser Ile Val Gln Arg Glu Leu Ala Leu Ile Lys Val Val Ser Ala Pro
 85 90 95
 Ser Thr Arg Thr Glu Ile Asn Gly Ile Ile Glu Pro Phe Arg Ala Ser
 100 105 110
 Val Val Asp Val Ser Arg Asp Ser Ile Val Val Gln Val Thr Gly Glu
 115 120 125
 Ser Asn Lys Ile Glu Ala Leu Ile Glu Leu Leu Lys Pro Tyr Gly Ile
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 Lys Glu Ile Ala Arg Thr Gly Thr Thr Ala Phe Ala Arg Gly Thr Gln
 145 150 155 160
 Gln Lys Ala Ser Ser Asn Lys Thr Ile Ser Ile Val
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