

CX2_022WO_SL
SEQUENCE LISTING

<110> Gilson, Lynne
<111> Collier, Steven James
<112> Sukumaran, Joly
<113> Yeo, Wan Lin
<114> Alvizo, Oscar
<115> Teo, Ee Ling
<116> Wilson, Robert John
<117> Xu Junye

<120> Variant LovD Polypeptides and Their Uses

<130> 376247-043US (105191) {CX2-022}

<141> 2010-09-24

<160> 20

<210> 1

<211> 1242

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimized *Aspergillus terreus* lovD

<400> 1

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<210> 2

<211> 413

<212> PRT

<213> Artificial Sequence

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<223> Codon optimized *Aspergillus terreus* lovD

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Ala Val Ile Met Ala Arg Asp Cys Ser Gly Asn Leu Asn Tyr Thr Arg
           35           40           45
Cys Phe Gly Ala Arg Thr Val Arg Arg Asp Glu Cys Asn Gln Leu Pro
           50           55           60
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CX2_022WO_SL

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Val	Leu	Glu	Gly	Phe	Asp	Asp	Ala	Gly	Asn	Ala	Arg	Leu	Arg	125	130	135	140
Arg	Gly	Lys	Ile	Thr	Leu	Arg	His	Leu	Leu	Thr	His	Thr	Ser	145	150	155	160
Ser	Tyr	Val	Phe	Leu	His	Pro	Leu	Leu	Arg	Glu	Tyr	Met	Ala	165	170	175	180
His	Leu	Gln	Ser	Ala	Glu	Lys	Phe	Gly	Ile	Gln	Ser	Arg	Leu	185	190	195	200
Pro	Ala	Val	Asn	Asp	Pro	Gly	Ala	Glu	Trp	Ile	Tyr	Gly	Ala	205	210	215	220
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Gln	Thr	His	Arg	Asn	Ser	Ala	Asp	Gly	Arg	Leu	Arg	Tyr	Asp	285	290	295	300
Val	Tyr	Phe	Arg	Ala	Asp	Gly	Glu	Glu	Cys	Phe	Gly	Gly	Gln	305	310	315	320
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Pro	Ala	Leu	Glu	Pro	Arg	Leu	Glu	Glu	Gln	Met	Asn	Gln	His	365	370	375	380
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<210> 3
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> variant of IovD

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<212> PRT

<213> Artificial Sequence

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<223> Variant of IovD

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35      40      45
Cys Phe Gly Ala Arg Thr Val Arg Arg Asp Glu Cys Asn Gln Leu Pro
50      55      60
Pro Leu Gln Val Asp Thr Pro Cys Arg Leu Ala Ser Ala Thr Lys Leu
65      70      75      80
Leu Thr Thr Ile Met Ala Leu Gln Cys Met Glu Arg Gly Leu Val Asp
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Leu Asp Glu Thr Val Asp Arg Leu Leu Pro Asp Leu Ser Ala Met Pro
100      105      110
Val Leu Glu Gly Phe Asp Asp Ala Gly Asn Ala Arg Leu Arg Glu Arg
115      120      125
Arg Gly Lys Ile Thr Leu Arg His Leu Leu Thr His Thr Ser Gly Leu
130      135      140
Ser Tyr Val Phe Leu His Pro Leu Leu Arg Glu Tyr Met Ala Gln Gly
145      150      155      160
His Leu Gln Ser Ala Glu Lys Phe Gly Ile Gln Ser Arg Leu Ala Pro
165      170      175
Pro Ala Val Asn Asp Pro Gly Ala Glu Trp Ile Tyr Gly Ala Asn Leu
180      185      190
Asp Trp Ala Gly Lys Leu Val Glu Arg Ala Thr Gly Leu Asp Leu Glu
195      200      205
Gln Tyr Leu Gln Glu Asn Ile Cys Ala Pro Leu Gly Ile Thr Asp Met
210      215      220
Thr Phe Lys Leu Gln Gln Arg Pro Asp Met Leu Ala Arg Arg Ala Asp
225      230      235      240
Gln Thr His Arg Asn Ser Ala Asp Gly Arg Leu Arg Tyr Asp Asp Ser
245      250      255
Val Tyr Phe Arg Ala Asp Gly Glu Glu Cys Phe Gly Gly Gln Gly Val
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Phe Ser Gly Pro Gly Ser Tyr Met Lys Val Leu His Ser Leu Leu Lys
275      280      285
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290      295      300
Pro Ala Leu Glu Pro Arg Leu Glu Glu Gln Met Asn Gln His Met Asp
305      310      315      320
Ala Ser Pro His Ile Asn Tyr Gly Gly Pro Met Pro Met Val Leu Arg
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Arg Ser Phe Gly Leu Gly Gly Ile Ile Ala Leu Glu Asp Leu Asp Gly
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 <212> PRT
 <213> Artificial Sequence

<220>
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 35 40 45
 Cys Phe Gly Ala Arg Thr Val Arg Arg Asp Glu Cys Asn Gln Leu Pro
 50 55 60
 Pro Leu Gln Val Asp Thr Pro Cys Arg Leu Ala Ser Ala Thr Lys Leu
 65 70 75 80
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 85 90 95
 Leu Asp Glu Thr Val Asp Arg Leu Leu Pro Asp Leu Ser Ala Met Pro
 100 105 110
 Val Leu Glu Gly Phe Asp Asp Ala Gly Asn Pro Arg Leu Arg Glu Arg
 115 120 125
 Arg Gly Lys Ile Thr Leu Arg His Leu Leu Thr His Thr Ser Gly Leu
 130 135 140
 Ser Tyr Val Phe Leu His Pro Leu Leu Arg Glu Tyr Met Ala Gln Gly
 145 150 155 160
 His Leu Gln Ser Ala Glu Lys Phe Gly Ile Gln Ser Arg Phe Ala Pro
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Gln	Tyr	Leu	Gln	Glu	Asn	Ile	Cys	Ala	Pro	Leu	Gly	Ile	Thr	Asp	Met
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Thr	Phe	Lys	Leu	Gln	Gln	Arg	Pro	Asp	Met	Leu	Ala	Arg	Arg	Ala	Asp
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Val	Tyr	Phe	Arg	Ala	Asp	Gly	Glu	Glu	Cys	Phe	Gly	Gly	Gln	Gly	Val
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Pro	Ala	Leu	Glu	Pro	Arg	Leu	Glu	Glu	Gln	Met	Asn	Gln	His	Met	Asp
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Ala	Ser	Pro	His	Ile	Asn	Tyr	Gly	Gly	Pro	Met	Pro	Met	Val	Leu	Arg
				325					330					335	
Arg	Ser	Phe	Gly	Leu	Gly	Gly	Ile	Ile	Ala	Leu	Glu	Asp	Leu	Asp	Gly
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Phe	Gln	Leu	Glu	Pro	Trp	Asn	Asp	Pro	Val	Cys	Arg	Asp	Leu	Thr	Arg
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Thr	Phe	Glu	His	Ala	Ile	Tyr	Ala	Gln	Tyr	Gln	Gln	Gly			
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 <213> Artificial Sequence

<220>
 <223> Variant of IovD

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<210> 8
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<220>

<223> Variant of IovD

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35      40      45
Cys Phe Gly Ala Arg Thr Val Arg Arg Asp Glu Cys Asn Gln Leu Pro
50      55      60
Pro Leu Gln Val Asp Thr Pro Cys Arg Leu Ala Ser Ala Thr Lys Leu
65      70      75      80
Leu Thr Thr Ile Met Ala Leu Gln Cys Met Glu Arg Gly Leu Val Asp
85      90      95
Leu Asp Glu Thr Val Asp Arg Leu Leu Pro Asp Leu Ser Ala Met Pro
100      105      110
Val Leu Glu Gly Phe Asp Asp Ala Gly Asn Pro Arg Leu Arg Glu Arg
115      120      125
Arg Gly Lys Ile Thr Leu Arg His Leu Leu Thr His Thr Ser Gly Leu
130      135      140
Ser Tyr Val Phe Leu His Pro Leu Leu Arg Glu Tyr Met Ala Gln Gly
145      150      155      160
His Leu Gln Ser Ala Glu Lys Phe Gly Ile Gln Ser Arg Phe Ala Pro
165      170      175
Pro Leu Val Asn Asp Pro Gly Ala Glu Trp Ile Tyr Gly Ala Ser Leu
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Asp Trp Ala Gly Lys Leu Val Glu Arg Ala Thr Gly Leu Asp Leu Glu
195      200      205
Gln Tyr Leu Gln Glu Asn Ile Cys Ala Pro Leu Gly Ile Thr Asp Met
210      215      220
Thr Phe Lys Leu Gln Gln Arg Pro Asp Met Leu Ala Arg Arg Ala Asp
225      230      235      240
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245      250      255
Val Tyr Phe Arg Ala Asp Gly Glu Glu Cys Phe Gly Gly Gln Gly Val
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275      280      285
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Pro Ala Leu Glu Pro Arg Leu Glu Glu Gln Met Asn Gln His Met Asp
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325      330      335
Arg Ser Phe Gly Leu Gly Gly Ile Ile Ala Leu Glu Asp Leu Asp Gly
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Glu Asn Trp Arg Arg Lys Gly Ser Met Thr Phe Gly Gly Gly Pro Asn
355      360      365
Ile Val Trp Gln Ile Asp Pro Lys Ala Gly Leu Cys Thr Leu Ala Phe
370      375      380
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<210> 9

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<212> DNA

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acctttgagc acgcgatcta tgcacagtat caacagggct aa 1242

```

<210> 10

<211> 413

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of IovD

<400> 10

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

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Arg Asp Gly Leu Leu Leu Gln Pro Gln Thr Val Asp Leu Met Phe Gln
290          295          300
Pro Ala Leu Glu Pro Arg Leu Glu Glu Gln Met Asn Gln His Met Asp
305          310          315          320
Ala Ser Pro His Ile Asn Tyr Gly Gly Pro Met Pro Met Val Leu Arg
          325          330          335
Arg Ser Phe Gly Leu Gly Gly Ile Ile Ala Leu Glu Asp Leu Asp Gly
          340          345          350
Glu Asn Trp Arg Arg Lys Gly Ser Met Thr Phe Gly Gly Gly Pro Asn
          355          360          365
Ile Val Trp Gln Ile Asp Pro Lys Ala Gly Leu Cys Thr Leu Ala Phe
          370          375          380
Phe Gln Leu Glu Pro Trp Asn Asp Pro Val Cys Arg Asp Leu Thr Arg
          385          390          395          400
Thr Phe Glu His Ala Ile Tyr Ala Gln Tyr Gln Gln Gly
          405          410

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<210> 11
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of IovD

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<400> 11
atgggttcta tcattgatgc ggctgtggcc gcggaacccgg tggttctgat ggaaacggct 60
ttccgtaaaag cggttgaaag ccgccagatt ccgggtgctg ttattatggc gcgtgattgt 120
agtggtaacc tgaactacac tcgctgtttc ggcgcacgca ctgtgctgcg cgacgagtgc 180
aatcaattac caccgctgca ggtggataca ccatgtcgtc tggcaagcgc tactaaatta 240
ctgaccacga ttatggcact gcagtgcatt gaacgcggcc tggtagactt ggatgaaact 300
gttgaccgcc tgctgccgga cctgagcgcg atgccgggtg tggaggctt tgatgatgcc 360
ggcaacccgc gtctgcgcga acgccgtggt aaaattacgt tacgccatct gctgacacac 420
accagcggtc tgctgtacgt cttcctgcat ccgctgctgc gcgagtatgt tgcccagggt 480
catttgaga gcgctgagaa gtttggcatt cagaatcgtt ttgcgccgcc attagttaat 540
gatccaggcg cggaatggat ttatggcgtt tctatcgact gggcaggcaa attagtggaa 600
cgcgcaacgg gcttggacct ggaacagtag ttgcaggaga acatttgcgc gccgctgggc 660
atcactgata tgacgttcaa actgcagcag cgtccggata tgctggcacg tcgtgccgac 720
cagaccacc gcaactccag cgatggtaaa ctgcgctatg atgactctgt gtattttcgc 780
gcggacggtg aagagtgttt cgggggccag ggcgtgttca gcagtccagg cagttacatg 840
aaggttctgc actctctgct gaaacgtgac ggcctgttgc tgcagccaga aaccgtggat 900
ctgatgttcc agccggcgct ggaaccgcgc ttggaagaac aaatgaacca gcatatggac 960
gcgtcgccgc acatcaacta tggcggtcca atgcctatgg tcctgcgtcg cagcttcggc 1020
ctgggtggtg tcattgcact ggaggatctg gatggtgaga actggcgctc taaaggctcg 1080
atgacgtttg gtggcggtcc aaacattgtt tggcagattg acccgaaagc gggctctgtg 1140
actttagtct ttttcagct ggaaccgtgg aacgacccgg tgtgtcgtga cctgactcgc 1200
acctttgagc acgcgatcta tgcacagtat caacagggtc aa 1242

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<210> 12
 <211> 413
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of IovD

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<400> 12
Met Gly Ser Ile Ile Asp Ala Ala Val Ala Ala Asp Pro Val Val Leu
1          5          10          15
Met Glu Thr Ala Phe Arg Lys Ala Val Glu Ser Arg Gln Ile Pro Gly
          20          25          30
Ala Val Ile Met Ala Arg Asp Cys Ser Gly Asn Leu Asn Tyr Thr Arg
          35          40          45
Cys Phe Gly Ala Arg Thr Val Arg Arg Asp Glu Cys Asn Gln Leu Pro
          50          55          60
Pro Leu Gln Val Asp Thr Pro Cys Arg Leu Ala Ser Ala Thr Lys Leu
          65          70          75          80

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

<210> 13
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of IovD

<400> 13

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ttccgtaaag	cggttgaaag	ccgccagatt	ccgggtgctg	ttattatggc	gcgtgattgt	120
agtggctcgtc	tgaactacac	tcgctgtttc	ggcgacgca	ctgtgcgtcg	cgacgagtgc	180
aatcaattac	caccgctgca	ggtggataca	ccatgtcgtc	tggcaagcgc	tactaaatta	240
ctgaccacga	ttatggcact	gcagtgcatt	gaacgcggcc	tggtagactt	ggatgaaact	300
ggtgaccgcc	tgctgccgga	cctgagcgcg	atgccggtgc	tggaaggctt	tgatgatgcc	360
ggcaaccgcg	gtctgcgcga	acgccgtggt	aaaattacgt	tacgccatct	gctgacacac	420
accagcggtc	tgctgtacgt	cttcctgcatt	ccgctgctgc	gcgagtatgt	tgcccagggt	480
catttgcagg	gcgctgagaa	gtttggcatt	cagaatcggt	ttgcgccgcc	attagttaat	540
gatccaggcg	cggaatggat	ttatggcgct	ggcatcgact	gggcaggcaa	attagtggaa	600
cgcgcaacgg	gcttggacct	ggaacagtac	ttgcaggaga	acatttgcgc	gccgctgggc	660
atcactgata	tgacgttcaa	actgcagcag	cgctccgata	tgctggcacg	tcgtgccgac	720
atgacccacc	gcaactccag	cgatggtaaa	ctgcgctatg	atgactctgt	gtattttcgc	780
gcggacggtg	aagagtgttt	cggggggccag	ggcgtgttca	gcagtccagg	cagttacatg	840

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aaggttctgc actctctgct gaaacgtgac ggcctgttgc tgcagccaga aaccgtggat 900
ctgatgttcc agccggcgct ggaaccgcgc ttggaagaac aaatgaacca gcatatggac 960
gcgtcgccgc acatcaacta tggcgggtcca atgcctatgg tcctgcgtcg cagcttcggc 1020
ctgggtggta tcattgcact ggaggatctg gatgggtgaga actggcgctcg taaaggctcg 1080
atgacgtttg gtggcggtcc aaacattatt tggcagattg acccgaaagc gggctctgtg 1140
acttttagtct ttttccagct ggaaccgtgg aacgacccgg tgtgtcgtga cctgactcgc 1200
acctttgaga aagcgatcta tgcacagtat caacagggct aa 1242

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<210> 14
 <211> 413
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of IovD

<400> 14

Met	Gly	Ser	Ile	Ile	Asp	Ala	Ala	Val	Ala	Ala	Asp	Pro	Val	Val	Leu
1			5					10					15		
Met	Glu	Thr	Ala	Phe	Arg	Lys	Ala	Val	Glu	Ser	Arg	Gln	Ile	Pro	Gly
			20					25					30		
Ala	Val	Ile	Met	Ala	Arg	Asp	Cys	Ser	Gly	Arg	Leu	Asn	Tyr	Thr	Arg
		35					40					45			
Cys	Phe	Gly	Ala	Arg	Thr	Val	Arg	Arg	Asp	Glu	Cys	Asn	Gln	Leu	Pro
	50					55					60				
Pro	Leu	Gln	Val	Asp	Thr	Pro	Cys	Arg	Leu	Ala	Ser	Ala	Thr	Lys	Leu
65					70					75				80	
Leu	Thr	Thr	Ile	Met	Ala	Leu	Gln	Cys	Met	Glu	Arg	Gly	Leu	Val	Asp
			85					90					95		
Leu	Asp	Glu	Thr	Val	Asp	Arg	Leu	Leu	Pro	Asp	Leu	Ser	Ala	Met	Pro
			100					105					110		
Val	Leu	Glu	Gly	Phe	Asp	Asp	Ala	Gly	Asn	Pro	Arg	Leu	Arg	Glu	Arg
		115					120					125			
Arg	Gly	Lys	Ile	Thr	Leu	Arg	His	Leu	Leu	Thr	His	Thr	Ser	Gly	Leu
	130					135					140				
Ser	Tyr	Val	Phe	Leu	His	Pro	Leu	Leu	Arg	Glu	Tyr	Val	Ala	Gln	Gly
145					150					155					160
His	Leu	Gln	Gly	Ala	Glu	Lys	Phe	Gly	Ile	Gln	Asn	Arg	Phe	Ala	Pro
			165						170				175		
Pro	Leu	Val	Asn	Asp	Pro	Gly	Ala	Glu	Trp	Ile	Tyr	Gly	Ala	Gly	Ile
		180						185					190		
Asp	Trp	Ala	Gly	Lys	Leu	Val	Glu	Arg	Ala	Thr	Gly	Leu	Asp	Leu	Glu
	195						200					205			
Gln	Tyr	Leu	Gln	Glu	Asn	Ile	Cys	Ala	Pro	Leu	Gly	Ile	Thr	Asp	Met
	210					215					220				
Thr	Phe	Lys	Leu	Gln	Gln	Arg	Pro	Asp	Met	Leu	Ala	Arg	Arg	Ala	Asp
225					230					235				240	
Met	Thr	His	Arg	Asn	Ser	Ser	Asp	Gly	Lys	Leu	Arg	Tyr	Asp	Asp	Ser
			245						250					255	
Val	Tyr	Phe	Arg	Ala	Asp	Gly	Glu	Glu	Cys	Phe	Gly	Gly	Gln	Gly	Val
		260						265					270		
Phe	Ser	Ser	Pro	Gly	Ser	Tyr	Met	Lys	Val	Leu	His	Ser	Leu	Leu	Lys
		275					280					285			
Arg	Asp	Gly	Leu	Leu	Leu	Gln	Pro	Glu	Thr	Val	Asp	Leu	Met	Phe	Gln
	290					295					300				
Pro	Ala	Leu	Glu	Pro	Arg	Leu	Glu	Glu	Gln	Met	Asn	Gln	His	Met	Asp
					310					315					320
Ala	Ser	Pro	His	Ile	Asn	Tyr	Gly	Gly	Pro	Met	Pro	Met	Val	Leu	Arg
			325						330					335	
Arg	Ser	Phe	Gly	Leu	Gly	Gly	Ile	Ile	Ala	Leu	Glu	Asp	Leu	Asp	Gly
		340					345						350		
Glu	Asn	Trp	Arg	Arg	Lys	Gly	Ser	Met	Thr	Phe	Gly	Gly	Gly	Pro	Asn
		355					360					365			
Ile	Ile	Trp	Gln	Ile	Asp	Pro	Lys	Ala	Gly	Leu	Cys	Thr	Leu	Val	Phe
	370					375					380				
Phe	Gln	Leu	Glu	Pro	Trp	Asn	Asp	Pro	Val	Cys	Arg	Asp	Leu	Thr	Arg
385					390					395					400

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Thr Phe Glu Lys Ala Ile Tyr Ala Gln Tyr Gln Gln Gly
 405 410

<210> 15
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of IovD

<400> 15
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 ttccgtaaag cggttgaaag ccgccagatt ccgggtgctg ttattatggc gcgtgattgt 120
 agcggctgct tgaactacac tcgctgtttc ggcgacgca ctgtgcgtcg cgacgagtgc 180
 aatcaattac caccgctgca ggtggataca ccattgctgc tggcaagcgc tactaaatta 240
 ctgaccacga ttatggcact gcagtgcatt gaacgcggcc tggtagactt ggatgaaact 300
 gttgaccgcc tgctgccgga cctgagcgcg atgccgggtg tggaggctt tgatgatgcc 360
 ggcaaccgca gtcctgcgca acgcccgtgt aaaattacgt tacgccatct gctgacacac 420
 accagcggtc tgcctgactg cttcctgcat ccgctgctgc gcgagtatgt tgcccagggt 480
 catttgcagg gcgctgagaa gtttggcatt cagaatcgtt ttgcgccgcc attagttaat 540
 gatccaggcg cggaatggat ttatggcgct ggcatcgact gggcaggcaa attagtggaa 600
 cgcgcaacgg gcttggacct ggaacagtac ttgcaggaga acatttgcgc gccgctgggc 660
 atcactgata tgacgttcaa actgcagcag cgcccggata tgctggcagc tcgtgccgac 720
 atgacccacc gcaactccag cgatggtaaa ctgcgctatg atgacacggt gtattttcgc 780
 gttgacggtg aagagtgttt cgggggcccag ggcgtgttca gcagtccagg cagttacatg 840
 aagggttctg actctctgct gaaacgtgac ggcctgttgc tgcagccagg gaccgtggat 900
 ctgatgttcc agccggcgct ggaaccgcgc ttggaagaac aaatgaacca gcatatggac 960
 gcgtcgccgc acatcaacta tggcgggtcca atgcctatgg tcctgcgtcg cagcttcggc 1020
 ctgggttgga tcattgcact ggaggatctg gatggtgaga actggcgtcg taaaggctcg 1080
 atgacgtttg gtggcggtcc aaacattatt tggcagattg acccgaaagc gggctctgtg 1140
 actttagtct ttttccagct ggaaccgtgg agtgaccggt tgtgtcgtga cctgactcgc 1200
 acctttgaga aagcgatcta tgcacagtat caacagggtc aa 1242

<210> 16
 <211> 413
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of IovD

<400> 16
 Met Gly Ser Ile Ile Asp Ala Ala Val Ala Ala Asp Pro Val Val Leu
 1 5 10 15
 Met Glu Thr Ala Phe Arg Lys Ala Val Glu Ser Arg Gln Ile Pro Gly
 20 25 30
 Ala Val Ile Met Ala Arg Asp Cys Ser Gly Arg Leu Asn Tyr Thr Arg
 35 40 45
 Cys Phe Gly Ala Arg Thr Val Arg Arg Asp Glu Cys Asn Gln Leu Pro
 50 55 60
 Pro Leu Gln Val Asp Thr Pro Cys Arg Leu Ala Ser Ala Thr Lys Leu
 65 70 75 80
 Leu Thr Thr Ile Met Ala Leu Gln Cys Met Glu Arg Gly Leu Val Asp
 85 90 95
 Leu Asp Glu Thr Val Asp Arg Leu Leu Pro Asp Leu Ser Ala Met Pro
 100 105 110
 Val Leu Glu Gly Phe Asp Asp Ala Gly Asn Pro Arg Leu Arg Glu Arg
 115 120 125
 Arg Gly Lys Ile Thr Leu Arg His Leu Leu Thr His Thr Ser Gly Leu
 130 135 140
 Ser Tyr Val Phe Leu His Pro Leu Leu Arg Glu Tyr Val Ala Gln Gly
 145 150 155 160
 His Leu Gln Gly Ala Glu Lys Phe Gly Ile Gln Asn Arg Phe Ala Pro
 165 170 175
 Pro Leu Val Asn Asp Pro Gly Ala Glu Trp Ile Tyr Gly Ala Gly Ile

CX2_022wo_SL

Asp	Trp	Ala	180	Gly	Lys	Leu	Val	Glu	185	Arg	Ala	Thr	Gly	Leu	190	Asp	Leu	Glu
		195						200						205				
Gln	Tyr	Leu	Gln	Glu	Asn	Ile	Cys	Ala	Pro	Leu	Gly	Ile	Thr	Asp	Met			
	210				215						220							
Thr	Phe	Lys	Leu	Gln	Gln	Arg	Pro	Asp	Met	Leu	Ala	Arg	Arg	Ala	Asp			
225				230						235					240			
Met	Thr	His	Arg	Asn	Ser	Ser	Asp	Gly	Lys	Leu	Arg	Tyr	Asp	Asp	Thr			
			245						250					255				
Val	Tyr	Phe	Arg	Val	Asp	Gly	Glu	Glu	Cys	Phe	Gly	Gly	Gln	Gly	Val			
			260					265					270					
Phe	Ser	Ser	Pro	Gly	Ser	Tyr	Met	Lys	Val	Leu	His	Ser	Leu	Leu	Lys			
		275					280					285						
Arg	Asp	Gly	Leu	Leu	Leu	Gln	Pro	Gly	Thr	Val	Asp	Leu	Met	Phe	Gln			
	290					295					300							
Pro	Ala	Leu	Glu	Pro	Arg	Leu	Glu	Glu	Gln	Met	Asn	Gln	His	Met	Asp			
305					310					315					320			
Ala	Ser	Pro	His	Ile	Asn	Tyr	Gly	Gly	Pro	Met	Pro	Met	Val	Leu	Arg			
			325						330					335				
Arg	Ser	Phe	Gly	Leu	Gly	Gly	Ile	Ile	Ala	Leu	Glu	Asp	Leu	Asp	Gly			
			340					345					350					
Glu	Asn	Trp	Arg	Arg	Lys	Gly	Ser	Met	Thr	Phe	Gly	Gly	Gly	Pro	Asn			
		355						360				365						
Ile	Ile	Trp	Gln	Ile	Asp	Pro	Lys	Ala	Gly	Leu	Cys	Thr	Leu	Val	Phe			
	370					375					380							
Phe	Gln	Leu	Glu	Pro	Trp	Ser	Asp	Pro	Val	Cys	Arg	Asp	Leu	Thr	Arg			
385					390					395					400			
Thr	Phe	Glu	Lys	Ala	Ile	Tyr	Ala	Gln	Tyr	Gln	Gln	Gly						
			405					410										

<210> 17
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Iovd

<400> 17
 atgggttcta acattgatgc ggctgtggcc gcggaacccgg tggttctgat ggaaacggct 60
 ttccgtaaaag cgggtgaaag ctctcagatt ccgggtgctg ttattatggc gcgtgattgt 120
 agcggtcgtc tgaactacac tcgctgtttc ggcgcacgca ctgtgcgtcg cgacgagtgc 180
 aatcaattac caccgctgca ggtggataca ccatgtcgtc tggcaagcgc tactaaatta 240
 ctgaccacga ttatggcact gcagtgcatt gaacgcggcc tggtagactt ggatgaaact 300
 gttgaccgcc tgctgccgga cctgagcgcg atgccggtgc tggaaaggctt tgatgatgcc 360
 ggcaacccgc gtctgcgcga acgccgtggg aaaattacgt tacgccatct gctgacacac 420
 accagcggtc tgcgtacgt ctccctgcat ccgctgctgc gcgagtatgt tgcccagggt 480
 catttgcagg gcgctgagaa gtttggcatt cagaatcggt ttgcgccgcc attagttaat 540
 gatccaggcg cggaatggat ttatggcgct ggcctcgact gggcaggcaa attagtggaa 600
 cgcgcaacgg gcttggacct ggaacagtag ttgcaggaga acatttgcgc gccgctgggc 660
 atcactgata tgacgttcaa actgcagcag cgcccggata tgctggcacg tcgtgccgac 720
 atgacccacc gcaactccag cgatggtaaa ctgcgctatg atgacacggg gtattttcgc 780
 catgacggtg aagagtgttt cggggggccag ggcgtgttca gcagtccagg cagttacatg 840
 aagggttctgc actctctgct gaaacgtgac ggcctgttgc tgcagccagg gaccgtggat 900
 ctgatgttcc agccggcgct ggaaccgcgt ttggaagaac aaatgaacca gcatatggac 960
 gcgtcgccgc acatcaacta tggcgggtcca atgcctatgg tcctgcgtcg cagcttcggc 1020
 ctgggtggtg tcattgcact ggaggatctg gatggtgaga actggcgtcg taaaggctcg 1080
 atgacgtttg gtggcggtcc aaacattatt tggcagattg acccgaaagc gggctctgtg 1140
 acttttagtct ttttccagct ggaaccgtgg agtgacccgg tgtgtcgtga cctgactcgc 1200
 acctttgaga aagcgatcta tgcacagtat caacagggct aa 1242

<210> 18
 <211> 413
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of IovD

<400> 18

Met Gly Ser Asn Ile Asp Ala Ala Val Ala Ala Asp Pro Val Val Leu
 1 5 10 15
 Met Glu Thr Ala Phe Arg Lys Ala Val Glu Ser Ser Gln Ile Pro Gly
 20 25 30
 Ala Val Ile Met Ala Arg Asp Cys Ser Gly Arg Leu Asn Tyr Thr Arg
 35 40 45
 Cys Phe Gly Ala Arg Thr Val Arg Arg Asp Glu Cys Asn Gln Leu Pro
 50 55 60
 Pro Leu Gln Val Asp Thr Pro Cys Arg Leu Ala Ser Ala Thr Lys Leu
 65 70 75 80
 Leu Thr Thr Ile Met Ala Leu Gln Cys Met Glu Arg Gly Leu Val Asp
 85 90 95
 Leu Asp Glu Thr Val Asp Arg Leu Leu Pro Asp Leu Ser Ala Met Pro
 100 105 110
 Val Leu Glu Gly Phe Asp Asp Ala Gly Asn Pro Arg Leu Arg Glu Arg
 115 120 125
 Arg Gly Lys Ile Thr Leu Arg His Leu Leu Thr His Thr Ser Gly Leu
 130 135 140
 Ser Tyr Val Phe Leu His Pro Leu Leu Arg Glu Tyr Val Ala Gln Gly
 145 150 155 160
 His Leu Gln Gly Ala Glu Lys Phe Gly Ile Gln Asn Arg Phe Ala Pro
 165 170 175
 Pro Leu Val Asn Asp Pro Gly Ala Glu Trp Ile Tyr Gly Ala Gly Ile
 180 185 190
 Asp Trp Ala Gly Lys Leu Val Glu Arg Ala Thr Gly Leu Asp Leu Glu
 195 200 205
 Gln Tyr Leu Gln Glu Asn Ile Cys Ala Pro Leu Gly Ile Thr Asp Met
 210 215 220
 Thr Phe Lys Leu Gln Gln Arg Pro Asp Met Leu Ala Arg Arg Ala Asp
 225 230 235 240
 Met Thr His Arg Asn Ser Ser Asp Gly Lys Leu Arg Tyr Asp Asp Thr
 245 250 255
 Val Tyr Phe Arg His Asp Gly Glu Glu Cys Phe Gly Gly Gln Gly Val
 260 265 270
 Phe Ser Ser Pro Gly Ser Tyr Met Lys Val Leu His Ser Leu Leu Lys
 275 280 285
 Arg Asp Gly Leu Leu Leu Gln Pro Gly Thr Val Asp Leu Met Phe Gln
 290 295 300
 Pro Ala Leu Glu Pro Arg Leu Glu Glu Gln Met Asn Gln His Met Asp
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 Ala Ser Pro His Ile Asn Tyr Gly Gly Pro Met Pro Met Val Leu Arg
 325 330 335
 Arg Ser Phe Gly Leu Gly Gly Ile Ile Ala Leu Glu Asp Leu Asp Gly
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 Glu Asn Trp Arg Arg Lys Gly Ser Met Thr Phe Gly Gly Gly Pro Asn
 355 360 365
 Ile Ile Trp Gln Ile Asp Pro Lys Ala Gly Leu Cys Thr Leu Val Phe
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His Leu Gln Gly Ala Glu Lys Phe Gly Ile Gln Asn Arg Phe Ala Pro
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Pro Leu Val Asn Asp Pro Gly Ala Glu Trp Ile Tyr Gly Ala Gly Ile
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Asp Trp Ala Gly Lys Leu Val Glu Arg Ala Thr Gly Leu Asp Leu Glu
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Gln Tyr Leu Gln Glu Asn Ile Cys Ala Pro Leu Gly Ile Thr Asp Met
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Thr Phe Lys Leu Gln Gln Arg Pro Asp Met Leu Ala Arg Arg Ala Asp
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Val Tyr Phe Arg His Asp Gly Glu Glu Cys Phe Gly Gly Gln Gly Val
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				405					410								