

Distribution of the 135 newly identified GOEs throughout the genomes
of the *Xylella fastidiosa* strains used in this study

Update: 17 October 2007

GOE #	Presumed Function	187b	56a	912c	Cv21	Fb7	36f
01	Plasmid encoded RepA protein	X	X		X		X
02	TrbL/VirB6 plasmid conjugal transfer protein	X	X	X	X	X	X
03	TrbL/VirB6 plasmid conjugal transfer protein		X	X			
04	TRAG protein	X				X	
05	CagE, TrbE, VirB component of type IV transporter system	X	X	X			X
06	CagE, TrbE, VirB component of type IV transporter system	X	X		X		
07	Probable conjugal transfer protein TraL	X	X	X		X	X
08	Phage-related integrase	X			X		X
09	Conjugal transfer protein TrbG/VirB9/CagX		X			X	X
10	CagE, TrbE, VirB component of type IV transporter system			X			X
11	Putative IS element transposase	X				X	
12	Conserved hypothetical protein			X	X		
13	Probable conjugal transfer protein TraL		X	X	X		X
14	Conjugation TrbL-like protein		X		X		
15	Conserved hypothetical protein		X	X			
16	Resolvase, N-terminal:Resolvase helix-turn-helix region		X		X		
17	Transcriptional regulator AbrB	X	X			X	
18	TRAG protein			X	X		X
19	Putative transposase TnA	X	X				
20	Helix-turn-helix motif	X	X	X	X	X	
21	No hit	X		X			
22	Adenylate kinase subfamily	X		X			X
23	Conserved hypothetical protein	X		X			
24	Plasmid-related exported protein			X		X	
25	Plasmid encoded RepA protein			X	X		
26	Lpx-Transferase hexapeptide repeat	X		X	X		
27	Conserved hypothetical protein			X	X		
28	No hit	X		X	X		
29	Helix-turn-helix motif:Peptidase S24, S26A and S26B			X			X
30	VirB8	X	X		X		
31	type IV secretory pathway, VirB3 family protein		X	X	X		
32	Type II secretion system protein E	X	X	X	X	X	X
33	Phage-related integrase			X			X
34	Phage-related integrase	X	X	X	X	X	
35	CagE, TrbE, VirB component of type IV transporter system	X	X	X		X	X
36	Plasmid encoded RepA protein	X		X			
37	CopG-like DNA-binding protein	X		X			
38	Type II secretion system protein E	X			X		X
39	No hit			X		X	
40	CagE, TrbE, VirB component of type IV transporter system	X	X	X	X	X	X

41	Type II secretion system protein E		X	X	X		X
42	Conjugal transfer protein TrbG/VirB9/CagX		X	X	X		
43	SpoVT/AbrB-like		X	X			
44	Conserved hypothetical protein				X		X
45	Methyltransferase, type III restriction-modification system	X	X			X	X
46	BRO, N-terminal			X		X	
47	Conserved hypothetical protein	X		X			
48	conjugation TrbI-like protein	X	X			X	X
49	No hit	X	X	X		X	
50	Conserved hypothetical protein	X	X	X		X	
51	Zonula occludens toxin	X		X			
52	Conserved hypothetical protein	X	X		X		
53	TRAG protein			X	X		
54	Conserved hypothetical protein			X	X		X
55	Conserved hypothetical protein			X	X		
56	Conserved hypothetical protein	X	X	X	X	X	X
57	No hit	X	X	X	X		X
58	No hit				X		X
59	Conserved hypothetical protein		X	X	X		X
60	Conserved hypothetical protein		X	X			X
61	Conserved hypothetical protein			X			X
62	Conserved hypothetical protein			X			X
63	Plasmid-related exported protein				X		X
64	Conserved hypothetical protein	X			X		
65	Plasmid-related exported protein	X	X				
66	Conjugation TrbI-like protein			X			X
67	Resolvase N-terminal domain	X		X			
68	Conserved hypothetical protein			X	X		
69	No hit			X	X		
70	Conserved hypothetical protein				X		X
71	Helix-turn-helix motif:Peptidase S24, S26A and S26B			X	X		
72	Conjugal transfer protein TrbG/VirB9/CagX	X		X			
73	TRAG protein		X				
74	RepB/MobA-like protein			X			
75	Conserved hypothetical protein			X			
76	Fimbrial protein pilin			X			
77	Putative transposase			X			
78	Conserved hypothetical protein			X			
79	No hit			X			
80	No hit			X			
81	No hit			X			
82	Filamentous phage Cf1c related protein			X			
83	Replication initiator-like protein			X			
84	No hit			X			
85	Conserved hypothetical protein			X			
86	Conserved hypothetical protein			X			
87	Conserved hypothetical protein			X			
88	Conserved hypothetical protein			X			
89	No hit			X			
90	No hit			X			
91	No hit			X			
92	Phage integrase			X			

93	Lpx-Acyl-[ACP]-UDP-N-acetylglucosamine			X			
94	VirB8			X			
95	ParB-like partition protein					X	
96	Conserved hypothetical protein					X	
97	Conjugal Transfer protein TrbA					X	
98	Type II secretion system protein E					X	
99	Relaxase/mobilization nuclease domain					X	
100	Helix-turn-helix motif:Peptidase S24, S26A and S26B					X	
101	Plasmid encoded RepA protein					X	
102	Conserved hypothetical protein					X	
103	Similar to Uncharacterized phage-associated protein					X	
104	No hit					X	
105	Conserved hypothetical protein					X	
106	Plasmid-related exported protein					X	
107	Putative plasmid conjugal transfer protein - TraJ					X	
108	Relaxase/mobilization nuclease domain					X	
109	No hit					X	
110	Conserved hypothetical protein					X	
111	Conserved hypothetical protein						X
112	Conserved hypothetical protein						X
113	Phage/plasmid primase P4, C-terminal						X
114	No hit						X
115	No hit						X
116	Helix-turn-helix motif:Peptidase S24, S26A and S26B	X					
117	No hit	X					
118	Methyltransferase, type III restriction-modification system	X					
119	No hit	X					
120	Peptidase S24, S26A and S26B		X				
121	No hit		X				
122	Conserved hypothetical protein		X				
123	No hit		X				
124	Helix-turn-helix motif:Peptidase S24, S26A and S26B		X				
125	TRAG protein		X				
126	Type I restriction system specificity protein				X		
127	Conserved hypothetical protein				X		
128	Conserved hypothetical protein				X		
129	Phage integrase				X		
130	Conserved hypothetical protein				X		
131	Conserved hypothetical protein				X		
132	Conserved hypothetical protein				X		
133	Conjugation TrbI-like protein				X		
134	No hit				X		
135	Conserved hypothetical protein				X		

GOE #01

SSH33_56a
SSH40_Cv21
SSH21_187b
SSH16_36f

[return to main table](#)

MFLGAGCWRGVRRDRVPRPRPRYSVVAAEVHGETPAITEAPGKENKSEHKKITAQESRLI 60
-----LI 2
-----LI 2

SSH33_56a	-----	
SSH40_Cv21	KTAAEIAMERPGDDDDRAYMHSIMCQVGLPRSKVEGNSFERVSGAAALLIEAGKLWDGKRF	120
SSH21_187b	KTAAEIAMERPGDDDDRAYMHSIMCQVGLPRSKVEGNSFERVSGAAALLIEAGKLWDGKRF	62
SSH16_36f	KTAAEIAMERPGDDDDRAYMHSIMCQVGLPRSKVEGNSFERVSGAAALLIEAGKLWDGKRF	62

SSH33_56a	-----MPRLILAWMNTYAVRCNTPVIPIGDSASEFLKILGKTPNGGVRGAFTTFFK	51
SSH40_Cv21	VQQSIPYGPMPRLILAWMNTYAVRCNTPVIPIGDSASEFLKILGKTPNGGVRGAFTTFFK	180
SSH21_187b	VQQSIPYGPMPRLILAWMNTYAVRCNTPVIPIGDSASEFLKILGKTPNGGVRGAFTTFFK	122
SSH16_36f	VQQSIPYGPMPRLILAWMNTYAVRCNTPVIPIGDSASEFLKILGKTPNGGVRGAFTTFFK	122

SSH33_56a	QIQALSACRMTLGFNTNGHAHTYEGKPIKHFDAWLSGKEEQRLWPGBTVTFSDDDYYQTLK	111
SSH40_Cv21	QIQALSACRMTLGFNTNGHAHTYEGKPIKHFDAWLSGKEEQRLWPGBTVTFSDDDYYQTLK	240
SSH21_187b	QIQALSACRMTLGFNTNGHAHTYEGKPIKHFDAWLSGKEEQRLWPGBTVTFSDDDYYPTLK	182
SSH16_36f	QIQALSACRMTLGFNTNGHAHTYEGKPIKHFDAWLSGKEEQRLRPG--TCPGGRSNSVV	180
	***** * .. :	

SSH33_56a	LHAVPLDLRAYMELKRPRPRPRYFERPPGVLDVSM	148
SSH40_Cv21	LHAVPLDLRAYMELKRPRPRPRNGCLYMGRTTPIPH-	276
SSH21_187b	LHAVPLDLRAYIAWS----RPRYFM----EIESITA-	210
SSH16_36f	AAEVP-ELHKNAEKCD-----NIRNLMTH	203
	** :*: . :	

GOE #02

[return to main table](#)

SSH18_36f	---MDESAPITWLIDEINKIVSSGADAAASAIATTVTPLASICFGIYILLICLNYMRGAE	57
SSH15_Cv21	---MDESAPITWLIDEINKIVSSGADAAASAIATTVTPLASICFGIYILLICLNYMRGAE	57
SSH02_56a	---MDESAPITWLIDEINKIVSSGADAAASAIATTVTPLASICFGIYILLICLNYMRGAE	57
SSH16_187b	---MDESAPITWLIDEINKIVSSGADAAASAIATTVTPLASICFGIYILLICLNYMRGAE	57
SSH28_Fb7	---MDESAPITWLIDEINKIVSSGADAAASAIATTVTPLASICFGIYILLICLNYMRGAE	57
SSH57_912c	---MDESAPITWLIDEINKIVSSGADAAASAIATTVTPLASICFGIYILLICLNYMRGAE	57
SSH22_912c	MDEMDESAPITWLIGEINKIVSSGADAAASTIATTITPLVSICFGIYILLICVNYMRGAE	60
	*****.*****:***:***.*****:*****	

SSH18_36f	TEPVIDFGIRCAGFAVIIIGLGLNAANYTSLVIPLVTGVGSDLASAISSGGHANVGTLDQLA	117
SSH15_Cv21	TEPVIDFGIRCAGFAVIIIGLGLNAANYTSLVIPLVTGVGSDLASAISSGGHANAGTLDQLA	117
SSH02_56a	TEPVIDFGIRCAGFAVIIIGLGLNAANYTSLVIPLVTGVGSDLASAISSGGHANAGTLDQLA	117
SSH16_187b	TEPVIDFGIRCAGFAVIIIGLGLNAANYTSLVIPLVTGVGSDLASAISSGGHANAGTLDQLA	117
SSH28_Fb7	TEPVIDFGIRCAGFAVIIIGLGLNAANYTSLVIPLVTGVGSDLASAISSGGHANAGTLDQLA	117
SSH57_912c	TEPVIDFGIRCAGFAVIIIGLGLNAANYTSLVIPLVTGVGSDLASAISSGGHANAGTLDQLA	117
SSH22_912c	TEPVIDFGIRCAGFAVIGLGLNAANYTSLVIMVTGIGSDLASAISSGSANAGTLDQLA	120
	*****:*****:***:***** ** *	

SSH18_36f	LHYFNILDESYQSVKALKFPGSVGAMLIYGLKAIFILVGLIPFLVAATLCLIVADVGSVM	177
SSH15_Cv21	LHYFNILDESYQSVKALKFPGSVGAMLIYGLKAIFILVGLIPFLVAATLCLIVADVGSVM	177
SSH02_56a	LHYFNILDESYQSAQALKFPGSVGAMLIYGLKAIFILVGLIPFPAAG-----FRA	167
SSH16_187b	LHYFNILDESYQSVKALKFPGSVGAMLIYGLKAIFILVGLIPFLVAATLCLIVADVGSVM	177
SSH28_Fb7	LHYFNILDESYQSVKALKFPGSVGAMLIYGLKAIFILVGLIPFLVAATLCLIVADVGSVM	177
SSH57_912c	LHYFNILDESYQSVKALKFPGSVGAMLIYGLKAIFILVGLIPFLVAATLCLIVADVGSVM	177
SSH22_912c	LHYLNILDKSYKSLEKIYFPSNVAPLIYAIKIFILVGLIPFRAAR-----AGTLS	173
	::***: * : : *..*..*:*:***** *	

SSH18_36f	VAMVGPMYFAFLIFPATRQYFSSWLNTAFSYALMPIFVAVIATISVGLSKQMFSANGTLN	237
SSH15_Cv21	VAMVGPMYFAFLIFPATRQYFSSWLNTAFSYALMPIFVAVIATISVGLSKQMFSANGTLR	237
SSH02_56a	AALAGTIRNLNCIH-----	181
SSH16_187b	VAMVGPMYAVSSQK-----	191
SSH28_Fb7	VAMVGPMYLGRDHAR-----	237
SSH57_912c	VAMVGPMYLGRDHAISS---DASVFLIMAQYGIQTSAAATLTERPPGQVRFYVGRQQLYN	234
SSH22_912c	LPMLAL-----	179
	.. .	

SSH18_36f	D-----ISFTSAATTLFERPPGQVFRCSRRCSRMVQK	269
SSH15_Cv21	DRGRGKAVFLASMGNTLLFLKQVGAMASSLSAGGINVSMPGSANTLRHAAQAARLGAK	297
SSH02_56a	-----	
SSH16_187b	-----ATRLSVPSYP	201
SSH28_Fb7	-----RLANLVFS	277
SSH57_912c	TR-----KGKAAGRSAFRFLT	250
SSH22_912c	-----	

SSH18_36f	HC-----	271
SSH15_Cv21	GIQQGGRTAINAGKAAGRWAENKFNSIRKAG	328
SSH02_56a	-----	
SSH16_187b	AKRPCHASQ-----	210
SSH28_Fb7	SLFSIIPP-----	285
SSH57_912c	SRHSRVGA-----	258
SSH22_912c	-----	

GOE #03

[return to main table](#)

SSH74_912c	MPIFVAVIATISVGLSKQMFSANGTLNDISFKAVFLASMGNTLLFLLKQVGAMASSLSA	60
SSH01_56a	MPIFVAVIATISVRLSKQMFSANGTLNDISFKAVFLASMGNTLLFLLKQVGAMASSLSA	60
SSH23_912c	MPIFVAVIATISVGLSKAMLSTNGTLDNISFRSVFLASMGNTLLFLLRQVGAMASSLSA	60
	***** ** *:*:***::***::*****:*****	
SSH74_912c	GGINVSMPGSANTLRHAAQAARLGAKGFE--RPPGQVPPSMLARLLVDGQRTNLIRSGK	117
SSH01_56a	GGINVSMPGSANTLRHAAQAARLGAKGIQQGGRTSAATTLAWSRPRYENDPRWTNATGA	120
SSH23_912c	GGINVSMPGSANTLRNAAEATKLGAAILQQ--GGRASINAGKAAGRWAQNTFNSIRKAG-	117
	*****:***:***:***: . : : *	
SSH74_912c	QAKL-----	121
SSH01_56a	VVQLEGLQECWPTKPISTATTDHDCCLRKGK	153
SSH23_912c	-----	

GOE #04

[return to main table](#)

SSH35_187b	MNKKKIAIAVLVLLLLAMVSVLVMLYMSSGLLVKYLNLGDLTPHLSLPLDLAKFGTKKEK	60
SSH25_Fb7	MNKKKIAIAVLVLLLLAMVSVLVMLYMSSGLLVKYLNLGDLTPHLSLPLDLAKFGTKKEK	60

SSH35_187b	GFGIIAMVVSVGLPVMLFGIIGYAALAPKKRELHGSARFATRELVKSGLLQSDKPDQY	120
SSH25_Fb7	GFGIIAMVVSVGLPVMLFGIIGYAALAPKKRELHGSARLATRRRLVQSGLLPSDKP----	116
	*****:***:***:***:***	
SSH35_187b	PSILVGKQDKDFLFFRQQQFMFLAAPTRSGKGVGIVIPNLLHYRDSVVVLDIKGENFEIT	180
SSH25_Fb7	-----	
SSH35_187b	SGFRASVVAEVRKD	195
SSH25_Fb7	-----	

GOE #05

[return to main table](#)

SSH36_56a	MNLIIAVAAAAAPAMRPLPTATGYRFDSVVRPARAAASNSRGRGGRERLRAAARAGLEEM	60
SSH15_36f	-----	
SSH12_187b	-----L	1
SSH50_912c	-----	
SSH36_56a	QIIVTQTLASYECEVLSDYDHNGHQFSQFYEFIAIYLYNGFWERVPVTSPLPLFQVVQTSAL	120
SSH15_36f	-----VVQTSAL	7
SSH12_187b	QSDLIVLIPSQPVDTLAWSRPR-----YLYNGFWERVPVTSPLPLFQVVQTSAL	49
SSH50_912c	-----	
SSH36_56a	HHGYKLETRFPNGGNRYSAFFDLKDFPEPTTRGKFNPLLELPFPFVMCLSFTEINTADS	180
SSH15_36f	HHGYKLETRFPNGGNRYSAFFDLKDFPEPTTRGKFNPLLELPFPFVMCLSFTEINTADS	67
SSH12_187b	HHGYKLETRFPNGGNRYSAFFDLKDFPEPTTRGKFNPLLELPFPFVMCLSFTEINTADS	109
SSH50_912c	-----	
SSH36_56a	IRLINQALNKMESAGDEATEQMKDMDFGKGAIMAGEVYFGELHGALAVYLPG----	236
SSH15_36f	IRLINQALNKMESAGDEATEQMKDMDFGKGAIMAGEVYFGELHGALAVYLGRDHAIASR	127
SSH12_187b	IRLINQALNKMESAGDEATEQMKDMDFGKGAIMAGEVYFGELHGALAVYLPG-----R	162
SSH50_912c	-----MESAGDEATEQMKDMDFGKGAIMAGEVYGETSAATTLFE-----R	41
	*****:***:***:***:***	
SSH36_56a	PKIGALRL-----	244
SSH15_36f	PRY-MVRLPRSRKHLARKTNQSIKKLPKKNP	158
SSH12_187b	PLIRAAARAGTGQNQP--TPNQWRNCSP----	188
SSH50_912c	PPGQVQ-----	47

*

GOE #06

[return to main table](#)

SSH17_Cv21	MAFILKAKGLPFEMTSDNVLENQYDELNGLFSLAKSTGSRLAVWAHIDHYAKTLKSNYE	60
SSH36_187b	-----	
SSH37_56a	-----	
SSH17_Cv21	FSYEWIRLFTEKYMARFEGESIFENSFYLTFILKPGMNSLEECIRELEEMQIIVTQTLA	120
SSH36_187b	-----	
SSH37_56a	-----	
SSH17_Cv21	SYECEVLSIYDHNGHQFSQFYEFIAYLYNGFWERVPVTSIPLFQVVQTSALHHGYKLLT	180
SSH36_187b	-----	
SSH37_56a	-----	
SSH17_Cv21	RFPNGGNRYSAFFDLPPGQVKDFPEPTTRGKFNPILLELPFPFVMCLSFTEINTADSIRLI	240
SSH36_187b	-----	
SSH37_56a	-----	
SSH17_Cv21	NQALNKMESAGDEATEQMKDMDFGKGAIMAGEVYFGELHGALAVYGKTEKQAENRGATAL	300
SSH36_187b	-----	
SSH37_56a	-----	
SSH17_Cv21	ASLSGSCATRFVPATISAPETFFSMFPGNVKRRPRPMPKTTRNFLGLFSMNTYNSGKQYG	360
SSH36_187b	-----MNTYNSGKQYG	11
SSH37_56a	-----MPKTTRNFLGLFSMNTYNSGKQYG	24

SSH17_Cv21	NPVGDGSAIMPLQTPAHGVYHLNFHYSPDLDSHGKGVAGHLLITGATGVGKTTVQTVAL	420
SSH36_187b	NPVGDGSAIMPLQTPAHGVYHLNFHYSPDLDSHGKGVAGHLLITGATGVGKTTVQTVAL	71
SSH37_56a	NPVGDGSAIMPLQTPAHGVYHLNFHYSPDLDSHGKGVAGHLLITGATGVGKTTVQTVAL	84

SSH17_Cv21	TFCSRWGNKLFVAVDKDGSMRGFIEAVGGTYFRLASGEPTGL-----PRRPR-	467
SSH36_187b	TFCSRWGNKLFVAVDKDGSMRGFIEAVGGTYLR-----PRPR---	107
SSH37_56a	TFCSRWGNKLFVAVDKDGSMRGFIEAVGGTYFRLASGELTGYSDRDHANPAARPD	139
	*****:*	*.*

GOE #07

[return to main table](#)

SSH07_56a	-----	
SSH23_36f	-----LKIY-----PTEKVSEL-----	12
SSH30_187b	-----VYLP-----	4
SSH20_Fb7	-----	
SSH04_912c	MPKTTRNFLGLFSMNTYNSGKQYGNPVGDGSAIMPLQTPAHGVYHLNFHYSPDLDSHGE	60
SSH07_56a	-----	
SSH23_36f	-----AKTLAESPALPLKFISH-----SETIAKFERPPGQVPLSNYLI	50
SSH30_187b	-----GRPLEHAPG--RHGRG-----NSVVA-----AEVPLSNYLI	33
SSH20_Fb7	-----	
SSH04_912c	KVAGHLLITGATGVGKTTVQTVALTFCSRWGNKTCPGGRSNSSGRPARSSSFVPLSNYLI	120
SSH07_56a	-----MLKESGRNVFIHSVLTGGQALMDTLAGFKSLAEQADTNNIVWLNEYFGAIEAN	54
SSH23_36f	ENNAISMLKESGRNVFIHSVLTGGQALMDTLAGFKSLAEQADTNNIVWLNEYFGAIEAN	110
SSH30_187b	ENNAISMLKESGRNVFIHSVLTGGQALMDTLAGFKSLAEQADTNNIVWLNEYFGAIEAN	93
SSH20_Fb7	-----MLKESGRNVFIHSVLTGGQALMDTLAGFKSLAEQADTNNIVWLNEYFGAIEAN	54
SSH04_912c	ENNAISMLKESGRNVFIHSVLTGGQALMDTLAGFKSLAEQADTNNIVWLNEYFGAIEAN	180

SSH07_56a	GKTFTMKVYTENAHKVRGIVPRP-RPR-YVRKGYGSDGIKKAYVFERPSGQVLTSL	109
SSH23_36f	GKTFTMKVYTENAHKVRGIVPRP-RPR-YVRKGYGSDGIKKAYVFERPPGQVLTSL	165
SSH30_187b	GKTFTMKVYTENAHKVRGIVPRP-RPR-YVRKGYGSDGIKKAYV-----	137
SSH20_Fb7	GKTFTMKVYTENAHKVRGIVPRP-RPR-YVRKGYGSDGIKKAYVFRSSERY-----	104
SSH04_912c	GKTFTMKVYTENAHKVRGIVRIIGRNQDTFGKDMEVMASKKTYVFRSSERY-----	232

***** * : . * . . ** : ***

GOE #08

[return to main table](#)

```
SSH01_187b -----MEARSGAHERGTIGHVITHYLRSTDFQQLAPRTQED 36
SSH31_Cv21 VLEIPRKAVAVAGPSALLSDLHSIMEARSGAHERGTIGHVITHYLRSTDFQQLAPRTQED 60
SSH10_36f -----MEARSGAHERGTIGHVITHYLRSTDFQQLAPRTQED 36
*****

SSH01_187b YHRQVEIVRSYKTTMGMTLDRHLIARMSPAI IQRIVEKIAVGNGEIKGKPTKANHLFRFL 96
SSH31_Cv21 YHRQVEIVRSYKTTMGMTLDRHLIARMSPAI IQRIVEKIAVGNGEIKGKPTKANHLFRFL 120
SSH10_36f YHRQVEIVRSYKTTMGMTLDRHLIARMSPAI IQRIVEKIAVGNGEIKGKPTKANHLFRFL 96
*****

SSH01_187b RLVFSWGIRHGHCMNDNPAKGVRQAPERKRDMPTLEAF AAILQFATRGRGLKAHTAGSVP 156
SSH31_Cv21 RLVFSWGIRHGHCMNDNPAKGVRQAPERKRDMPTLEAF AAILQFATRGRGLKAHTAGSVP 180
SSH10_36f RLVFSWGIRHGHCMNDNPAKGVRQAPERKRDMPTLEAF AAILQFATRGRGLKAHTAGSVP 156
*****

SSH01_187b RYIAPLMYLGRDHAIPA AAVAAGSVRSRSDSLRAGCPLTHNSFSLSLICPHCYGEDVW 216
SSH31_Cv21 RYIAPLMYLP-----GRPLEMLNC----- 199
SSH10_36f RYIAPLSSGRP-----ARYDATVAS--RQTLRQLPDVTELAG-----RA 193
*****
          . *      : .

SSH01_187b VSILDTVNTVGILIDSE 233
SSH31_Cv21 -----
SSH10_36f MPKLQRSNDGNSL---- 206
```

GOE #09

[return to main table](#)

```
SSH19_36f -----
SSH30_56a -----
SSH29_Fb7 MIRWICIRTPGRMAAGLAWSRPRYVLEIPRKAVAVAGPSALLSDLHSIMEARSGAHERGT 60

SSH19_36f -----
SSH30_56a -----
SSH29_Fb7 IGHVITHYLRSTDFQQLAPRTQEDYHRQVEIVRSYKTTMGMTLDRHLIARMSPAI IQRIV 120

SSH19_36f -----
SSH30_56a -----VFFKALPDG 9
SSH29_Fb7 EKIAVGNGEIKGKPTKANHLFRFLRLVFSWGIRHGHCM AARFRAAARAGLPVFFKVLDPDG 180

SSH19_36f ----LNSNIDPEHKQTVVLHEVIRTVRARLGDQVIEI INRAYKLPKFNETGTSVPGAVRA 56
SSH30_56a TEALLNSNIDPEHKQTVVLHEVIRTVRARLGDQVIEI INRAYKLPKFNETGTSVPGAVRA 69
SSH29_Fb7 TEALLNSNIDPEHKQTVVLHEVIRTVRARLGDQVIEI INRAYKLPKFNETGTSVPGAVRA 240
*****

SSH19_36f DRDI 60
SSH30_56a DRDI 73
SSH29_Fb7 DRDI 244
*****
```

GOE #10

[return to main table](#)

```
SSH04_36f LFDVSVVAAEVLAMDAADF KYLEA AKAQAGTHPDQWVPVYKALRKKGRENVTQPVTVKE 59
SSH28_912c ---MADDIAVLAMDAADF KYLEA AKAQAGTHPDQWVPVYKALRKKGRENVTQPVTVKE 55
          *****
          .
```

GOE #11

[return to main table](#)

```
SSH31_187b -----MVGLDAGVTKLATLS DGTVYHPVNSFKAN 29
SSH13_Fb7 VTYGHIAWSRPRYVSIQTEYEVADPVHNAESMVGLDAGVTKLATLS DGTVYHPVNSFKAN 60
*****

SSH31_187b QRKLAILQRQLSRKVKFSTNWQKQKRKI QNLHSHIANIRRDYLHKL TSEISKNHAMIVIE 89
SSH13_Fb7 QRKLAILQRQLSRKVKFSTNWQKQKRKI QNLHSHIANIRRDYLHKL TSEISKNHAMIVIE 120
*****

SSH31_187b DLKVSNMRSRAKGTCPGGRSTMG---ESMLPAVWPRDSSVGP AEVLATTAIRCDDLFLLL 146
```

SSH13_Fb7 DLKVSNMRSASIERPPGQVLKIGLIRVAQLTSVR-AAARAGTTDRQRNCITATNSYRQK 179
***** ** .:* :*.* :.*.: .*. : :

SSH31_187b HERLM- 151
SSH13_Fb7 RYKSKQ 185

GOE #12

[return to main table](#)

SSH15_912c -----MHFIKNYDARQITKMISE 18
SSH23_Cv21 LKIYPTEKVSSELAKTLAESPALPLKFISHSETIAKTSKHIRDMHFIKNYDARQITKMISE 60

SSH15_912c NGIKITLKEIKSILQNKKEKKSQ 40
SSH23_Cv21 NGIKITLKEIKRILQNKKEKKSQ 82

GOE #13

[return to main table](#)

SSH08_56a -----
SSH05_912c -----
SSH46_Cv21 MLKESGRNVFIHSLVTGGQALMDTLAGFKSLAEQADTNNIVIWLNEYFGAIEANGKTFTE 60
SSH24_36f -----

SSH08_56a -----MAKQRIKTVQ 10
SSH05_912c -----MAKQRIKTVQ 10
SSH46_Cv21 MKVYTENAHKVRGIVRIERNQDTFGKDMEVMASKKLTSEVLSGTDFTLMAKQRIKTVQ 120
SSH24_36f -----MAKQRIKTVQ 10

SSH08_56a RELNEQLDAIGF 22
SSH05_912c RELNEQLDAIGF 22
SSH46_Cv21 RELNEQLDAIGF 132
SSH24_36f RELNEQLDAIGF 22

GOE #14

[return to main table](#)

SSH14_56a LKPELASNNASLESDLIEKKKAEIKKKQEEQQAQIKAEQAQARIQAETLAAANAAR 60
SSH34_Cv21 LKPELASNNASLESDLIEKKKAEIKKKQEEQQAQIKAEQAQARIQAETLAAANAAR 60

SSH14_56a AQGDSAQVQQGNQPPRPPTPMERKMAGSVLLENTGAKPKTDAPLSENTSSSEKEQQQRE 120
SSH34_Cv21 AQGDSAQVQQGNQPPRPPTPMERKMAGSVLLENTGAKPKTDAPLSENTSSSEKEQQQRE 120

SSH14_56a VQARMAAMGMNQGGVQQLTPVGQSEGTDGLAGRLKPTVLQARLAAKLPNLDYLLKRGTTI 180
SSH34_Cv21 VQARMAAMCMNQGGVQQLTPVDQSEVTDLAGRLKHTVLQARFGCKAA----- 168
***** :.*.* ** ***** :.*.*

SSH14_56a PCALKTGIDTTLPFVILAWSRPRYPAYTQWCKESGVYALSKVRFLGELERCVPKFGKKVT 240
SSH34_Cv21 -----

SSH14_56a KETVGAGKRREFTVIQGIELTAADL 265
SSH34_Cv21 -----

GOE #15

[return to main table](#)

SSH41_56a MPVFIAQLLTGLFSLKTKLGYFIMAAFWVLGINWGSYHFVITPIVKQIYIYMDNVGVAE 60
912c26 -----LAAFAYHDCVRESGDQDYINRIERPPRQVIYIYMDNVGVAE 41
. * .*. : : * : *****

SSH41_56a GSLGEMAMSGLAILNFDRAVSMIISAYVARFAVLNGRLYLFKRFGGATPGAAP 113
912c26 GSLGEMAMSGLAILNFDRAVSMIISAYVARFAVLNGRLYLFKRFGGATPGAAP 94

GOE #16

[return to main table](#)

SSH28_Cv21 MSTLTVTARGQVTRKEVLQHLGIKPGERIELDLLPDGRFERPPGQVLTVWRLDRLGRSM 60
SSH19_56a -----M 1
*

SSH28_Cv21 TELVAIVNDLASRGVTFESLTHEIDTSSASGKF AFHLFSALAEFERNTIKERTRAGLAAA 120
SSH19_56a TELVAIVNDLVSRGVTFESLTHEIDTSSASGKF AFHLFSALAEFERNTIKERTRAGLAAA 61
*****.
SSH28_Cv21 RARGRMGGRPAKVTPKAKREM KALYTSQEVSVKDICTRYNITRSTFYRVVLERDYTANGK 180
SSH19_56a RARGRMGGRPAKVTPKAKREM KALYTSQEVSVKDICTRYNITRSTFYRVVLERDYTANGK 121
*****.
SSH28_Cv21 A 181
SSH19_56a A 122
*

GOE #17

[return to main table](#)

SSH18_56a MSTLTVTARGQVTFRKEVLQHLGIKPGERIE LDLLPDGRAELKAAQPKAHSRNAGVPLAA 60
SSH14_Fb7 MSTLTVTARGQVTFRKEALQHLGIKPGERIE LDLLPDGRAERGRGLAWIIQPLTTPRV 60
SSH34_Fb7 MSTLTVTARGQVTFRKEVLQHLGIKPGERIE LDLLPDGRAACSRPLGRGD----- 50
SSH28_187b MSTLTVTARGQVTFRKEVLQHLGIKPGERIE LDLLPDGRAELKAAQPKGSFQELRGFLKG 60
*****.
SSH18_56a EIRAAARAGTPTSLSMSRPVTKRSPIK- 87
SSH14_Fb7 KTM LPAHQVAARFRAAARAGTT----- 82
SSH34_Fb7 -----
SSH28_187b KTN GARLSIEEINDAIAEAGTLAGSGDA 88

GOE #18

[return to main table](#)

SSH20_912c -----VVARAG-----LYDETGAQTMLTNMALQVAYAPRDD 31
SSH09_36f MTEEGIFVVVAWSRPRYNMRLLLIFQSKSQIKDRKLYDETGAQTMLTNMALQVAYAPRDD 60
SSH35_Cv21 ----MRLLLIFQSK-----SQIKDRKLYDETGAQTMLTNMALQVAYAPRDD 42
:: : *****
SSH20_912c DDAKDYSEMIGYMTEKGLSKSRQLGLKSGRSESESDQRRAVLLPQEVKAIGQFKEIISME 91
SSH09_36f DDAKDYSEMIGYMTEKGLSKSRQLGLKSGRSESESDQRRAVLLPQEVKAIGQFKEIISME 120
SSH35_Cv21 DDAKDYSEMIGYMTEKGLSKSRQLGLKSGRSESESDQRRAVLLPQEVKAIGQFKEIISME 102

SSH20_912c NMAPALVDKIFWYQEP IFQARANLPHDPDPDQSDLVNTIEPDLGRDHANPA-----AKR 145
SSH09_36f NMAPALVDKIFWYQEP IFQARANLPHDPDPDQSDLVNTIEPAPPSPTLDFA-----ERP 174
SSH35_Cv21 NMAPALVDKIFWYQEP IFQARANLPHDPDPDQSDLVNTIEPAPPSPTLDFA GAIIEEQALP 162
***** : *
SSH20_912c PGACRAFE-----RPPGQVSRTRDRDRST----- 168
SSH09_36f PGQVRARNPQKGCGRGRTVCTTFRSAFHGSKVWRP 210
SSH35_Cv21 TGATFEVG-FSPKRNALEVVM SFVLGARLNYWWLHT 197
.* * * :

GOE #19

[return to main table](#)

SSH19_56a --MHVHLVFV---AKYR-----RKVFDLDAIEKLRSYFASVCVDFDVELVEMDGEC 46
SSH20_187b VIAGVSPCTCPGGRSKSRGQG GREHGRKVFDLDAIEKLRSYFASVCVDFDVELVEMDGEC 60
* : * *****
SSH19_56a DHVHLLINYPKLAISNLVNSLKGVS S RLLRRDRPDIALHYYYKGVLWTPSYFASSCGGA 106
SSH20_187b DHVHLLINYPKLAISNLVNSLKGVS S RLLRRDRPDIALHYYYKGVLWTPSYFASSCGGA 120

SSH19_56a PISIIRQYIQQQQTPS 122
SSH20_187b PISIIRQYIQQQQTPS 136

GOE #20

[return to main table](#)

SSH46_187b MSEKMTVSCGNVFEDLGFPDPDEAAAMLARETLLIALEKELRKRGKKQQLADELGVPRT 60
SSH43_Cv21 MSEKMTVSCGNVFEDLGFPDPDEAAAMLARETLLIALEKELRKRGKKQQLADELGVPRT 60
SSH39_56a MSEKMTVSCGNVFEDLGFPDPDEAAAMLARETLLIALEKELRKRGKKQQLADELGVPRT 60
SSH60_912c MSEKMTVSCGNVFEDLGFPDPDEAAAMLARETLLIALEKELRKRGKKQQLADELGVPRT 60
SSH41_Fb7 MSEKMTVSCGNVFEDLGFPDPDEAAAMLARETLLIALSFNHR-----LLFSLSVVAAE 52
***** : * * .*. * :.
SSH46_187b ISEVMHLKTRDFSVDKLVSL LHRAGNSSGRPGRYKLAHPSVKTPAKSDSLKPELASNNAS 120

SSH43_Cv21	ISEVMHLKTDRFSVDKLVSLLRHAGNSGGR-GR-----GTSGS	97
SSH39_56a	ISEVMHLKTDRFSVDKLVSLLRHAGKRVEIRVR-----	93
SSH60_912c	ISEVMHPQTDRFSVDKLVSLLRHAVERPPGQVLLY-----FLAIA	100
SSH41_Fb7	VHGVC-----	57
	: *	

SSH46_187b	LESDLIEKKKAEIKKKQEEEEQAQIKATEEAAQAQARIQAETLAAANAAKRAQGDQAQVQQQ	180
SSH43_Cv21	FE-----	99
SSH39_56a	-----	
SSH60_912c	L-----	101
SSH41_Fb7	-----	

SSH46_187b	GNQPPRPPTPMERKMAGSVLLENTGAKPKTDAPLSENTSSSEKEQQQREVQARMAAMGMN	240
SSH43_Cv21	-----	
SSH39_56a	-----	
SSH60_912c	-----	
SSH41_Fb7	-----	

SSH46_187b	QGGVQQLTPVGQSEGTDGLAGRLKPTVLQARLAAKLPNLDYLLKRGTTSVVAAEVHQLQR	300
SSH43_Cv21	-----	
SSH39_56a	-----	
SSH60_912c	-----	
SSH41_Fb7	-----	

SSH46_187b	SWT	303
SSH43_Cv21	---	
SSH39_56a	---	
SSH60_912c	---	
SSH41_Fb7	---	

GOE #21 [return to main table](#)

SSH55_912c	MNSEIQVSLRVDWKANSQVATKENAFSRFVTELVEVFSLGIGHSGSARCTCPGGRSNAAR	60
SSH26_187b	MNSEIQVSLRVDWKANSQVATKENAFSRFVTELVEVFSLGIGHSGSARCTCPGGRSNSVV	60
	*****:	
SSH55_912c	A-----	61
SSH26_187b	AAEVQEKR	68
	*	

GOE #22 [return to main table](#)

SSH28_36f	VLVERIAGRAQAESREDDTPDAVRKRLQVYNDCTAPVIGFYQQRGILAWARPRYLYKIDG	60
SSH52_912c	-----	
SSH06_187b	-----	

SSH28_36f	LADWAKKPEILAAFPYVGQITEDAGKKEQQHGVKLTSVGWEAKGLDN	107
SSH52_912c	LADWAKKPEILAAFPYVGQITEDAGKKEQQHGVKLTSVGWEAKGLDN	47
SSH06_187b	LADWAKKPEILAAFPYVGQITEDAGKKEQQHGVKLTSVGWEAKGPDN	47
	*****	**

GOE #23 [return to main table](#)

SSH51_912c	VPRRITQTYTEVDGKFYAKDSNRVMFEDKGEKLATSTTNKDAVADMVAYAKAKQWDSLKL	60
SSH42_187b	VPRRITQTYTEVDGKFYAKDSNRVMFEDKGEKLATSTTNKDAVADMVAYAKAKQWDSLKL	60

SSH51_912c	SGSQEFRREAWLQAESQGIKTQGYTPKQTDLAALETLRQERSTNSITPLQERKTERQAST	120
SSH42_187b	SGSQEFRREAWLQAESQGIKTQGYTPKQTDLAALETLRQERSTNSITPLQERKTERPPST	120
	*****	**

SSH51_912c	SAATTL-----	126
SSH42_187b	AAAPRHDNMKNQAAMHVEASKFIATNMQALQNQPNMADKSVEDLTKLAYWRGIVAENKL	180
	: **.	

SSH51_912c	-----	
SSH42_187b	QPKAVQDEAIARFDKQAADPQFLKRLNQETEPKIHDRTTERVQQQRDTHEQSL	232

GOE #24

[return to main table](#)

```
SSH18_Fb7 -----
SSH29_912c MSFTGILKKTRVPISAFVFIFAGTAYAQTFQVYDAANISTSIQNHVESIAKWKQQFEQLK 60

SSH18_Fb7 -----VTVLSDVKKTSAYATERSKYPTSG 24
SSH29_912c QQIDQHQQYEAITGSRGMGALLDNSALKASLPSDWKQVLSVKKTSAYATERSKYPTSG 120
*****

SSH18_Fb7 NLQKTNAMYDVIASQDVIMSDLYSKANRRNLNLIQSLTAQIDSANDPAAKADL-ANRLINE 83
SSH29_912c NLQKTNAMYDVIASQDVIMSDLYSKANRRNLNLIQSLTAQIDSANDPAAKDLPGATTLNE 180
*****

SSH18_Fb7 QNAIQANQNLVTILQAKQKQGLEIASQAAVEELSCKEFKRSGC 126
SSH29_912c QNAIQANQNLVTILQAKQKQGLEIASQAAVEELSCKEFKRSGC 223
*****
```

GOE #25

[return to main table](#)

```
SSH41_Cv21 -----VLYWSNLR 8
SSH18_912c VTLETSAAATLSPGRVRSTCVHIWPGQVSALAMDVYIWAAQRLYRIEGRPVVLYWSNLR 60
*****

SSH41_Cv21 NQFGQEYTGKEADKNFKKKFLPALRAMLAVYPEARIKQVTGGIMLIASPPPIPFKPS 65
SSH18_912c NQFGQEYTGKEADKNFKKKFLPALRAMLAVYPEARIKQVTGGIMLIASPPPIPFKPS 117
*****
```

GOE #26

[return to main table](#)

```
SSH64_912c --MKIVSLAPEVPRPRPRYFNRYFSEIAPAKNWINPDGIVGGIVATSADIHPSAWILRNT 58
SSH30_Cv21 LYLGRDHAIARAAARAGTGIFNYRFSEIAPAKNWINPDGIVGGIVATSADIHPSAWILRNT 60
SSH37_187b ---LAAEIRAAARAGTGIFNYRFSEIAPAKNWINPDGIVGGIVATSADIHPSAWILRNT 56
..*. . *****

SSH64_912c VIYPDVIIGKRVYIGHKTTIKQCAIINEDTHITDSCRIGVCASIGGRSNIGSHSDINDAV 118
SSH30_Cv21 VIYPDVIIGKRVYIGHKTTIKQCAIINEDTHITDSCRIGVCASIGGRSNIGSHSDINDAV 120
SSH37_187b VIYPDVIIGKRVYIGHKTTIKQCAIINEDTHITDSCRIGVCASIGGRSNIGSHSDINDAV 116
*****

SSH64_912c SIGESVSIGDFVKIFNNAVLGKNARIRDTVLI GEHVTIGAEIIVDHKAKIEHGASIGERA 178
SSH30_Cv21 SIGESVSIGDFVKIFNNAVLGKNARIRDTVLI GEHVTIGAEIIVNHKAKIEHGASIGERA 180
SSH37_187b SIGESVSIGDFVKIFNNAVLGKNARIRDTVLI GEHVTIGAEIIVNHKAKIEHGASIGERA 176
*****:*****

SSH64_912c VIECYVPRPRPRYSV---VAAEV----- 198
SSH30_Cv21 VIECYVPRPRPRYSV---VAAEVLQRAS-----FDVI-----NHVR 214
SSH37_187b VIECYVPRPRPRYHAPGRMAAGFRAAARAGTFVASWGWLFSLIGVPMILFVKI ICTNDDK 236
***** . : ** .

SSH64_912c -----
SSH30_Cv21 STYSLAKPAKWKAYHQTSWPMWQ--KLSPSSNFLGKFRPLQPFQ--SVF- 261
SSH37_187b AIRILMLEVKWSLLKALNGNAKYHGGTMAIAPTTYGRKLKNVKRYFKKTVCG 288
```

GOE #27

[return to main table](#)

```
SSH47_Cv21 -----MNKLDENAATLAHDARYAQHTRSELAKAAYFRGFHEKAS 39
SSH12_912c LICACSRPRPGGRYHAIRAAARAGLDENAATLVHDARYAQHTRSELAKAAYFRGFHEKAS 60
*****.*****

SSH47_Cv21 EFKGIAPDFSKYDATVASRQTLRQLPDVTELAGRAMPKLQRSNDGNSL 87
SSH12_912c EFKGIAPDFSKYDATVASRQTLRQLPDVTELAGRAMPKLQRSNDGNSL 108
*****
```

GOE #28

[return to main table](#)

```
SSH06_Cv21 -----VAAEV- YEVALEVLGQSRQPFMQAIYEEKQKSVPSQVFI RYCENRLAALDE 51
SSH01_912c MLDLGINSVDAAEV- YEVALEVLGQSRQPFMQAIYEEKQKSVPSQVFI RYCENRLAALDE 59
SSH49_187b ---MLDLGINSGISYEVLEVLGQSRQPFMQAIYEEKQKSVLSQVFI RYCENRLAALDE 57
: :.: *****

SSH06_Cv21 IQETLQPTDLATIERILTKGDLVFKVQ 78
```

SSH01_912c IQETLQPTDLATIERILTKGDLVFKVQ 86
SSH49_187b IQETLQPTDLATIERILTKGDLVFKVQ 84

GOE #29

[return to main table](#)

SSH54_912c MATAGTTLAGICRRYRQNLTTAPELLVPRPRPRYSVVAAEVLRIVSDNQDKDSEGRRIYQ 60
SSH33_36f -----VVAAEVLRIVSDNQDKDSEGRRIYQ 25

SSH54_912c DEVVPPKEMGTVCVLGRVIMKIGDGGL 87
SSH33_36f DEVVPPKEMDTVCVLGRVIMKIGDGGL 52

GOE #30

[return to main table](#)

SSH19_187b -----MIEWGRASTSFIPITALQCTCQGGRSKSRGQAAGSMVRAAAR----- 41
SSH24_56a -----LVRAAAR----- 7
SSH14_Cv21 MSTKEQAPVLNKLARLPQTFVEAAVDFEKSKIEEIKRSRKIAWIIASVATVICSVSILAF 60
:: :.*

SSH19_187b -----AGTGATTVLRSVRDTKDHYDEVVSVVAAESQYVRTCEGYDWF 83
SSH24_56a -----AGT-----CEGYDWF 17
SSH14_Cv21 LVALLTRSEPEPTILQVDKSTGATTVLRSVRDTKDHYDEVVKY-WLAQYVRTCEGYDWF 119
.* *****

SSH19_187b TINDQFNACKLMSDGDVAKEYDSKVDAPGSPLKVLADKGKIVVGIVSIAFLGDTAQVRFT 143
SSH24_56a TINDQFNACKLMSDGDVAKEYDSKVDAPGSPLKVLADKGKIVVGIVSIAFLGDTAQVPRP 77
SSH14_Cv21 TINDQFNACKLMSDGDVAKEYDSKVDAPGSPLKVLADKGKIVVGIVSIAFLGDTAQVRFT 179

SSH19_187b TEKLSASGENLDNSPVRKWIATIAFQFKPGLMTEQQRLINPLGFKVATYRVDPEVIQ 200
SSH24_56a RPR----- 80
SSH14_Cv21 TEKLSASGENLDNSPVRKWIATIAFQFKPGLMTEQQRLINPLGFKVATYRVDPEVIQ 236

GOE #31

[return to main table](#)

SSH18_Cv21 -----
SSH35_912c -----
SSH05_56a VGVGAIAQAIQQVKYLQQQLTQMKNQLDSMNGDRGMAGLLSGQNRNYLPTDWSAMNMLN 60

SSH18_Cv21 -----
SSH35_912c -----
SSH05_56a SGGGGSFGSLASAAQQIKQAQSVLSSSDLSRLSPQMQQYLDQVRNVASQQALGQQAYAT 120

SSH18_Cv21 -----MTDEQS-----PEEYISYNGLGRSP-----M 21
SSH35_912c -----MTDEQS-----PEEYISYNGLGRSP-----M 21
SSH05_56a ASQQRVNLQTLTNQISSAIDPKAVWDLQARIQSEQLQLQNDQSRLPSTQLTQAQSVATS 180
: * : * : *

SSH18_Cv21 IWGIPYMAGLAI---MCLSLGGLLLGTFVASWGWLFSLIGVPMILFVKIICTNDDKAIR 78
SSH35_912c IWGIPYMAGLAI---MCLSLGGLLLGTFVASWGWLFSLIGVPMILFVKIICTNDDKAIR 78
SSH05_56a KWPTNYVRKPAVPRPLAAGFRAAARAGTFVASWGWLFSLIGVPMILFVKIICTNDDKAIR 240
* * : * : : . * : *

SSH18_Cv21 ILMLEVKWSLLKALNGNAKYHGGTMAIAPTTYGRKLKNVR--AAARAGKKTVCG--- 130
SSH35_912c ILMLEVKWSLLKALNGNAKYHGGTMAIAPTTYGRKLKNVKRYFTCPGGRSNSSGRPGR 136
SSH05_56a ILMLEVKWSLLKALNGNAKYHGGTMAIAPTTYGRKLKNVK----RYFKKTVCG--- 289
***** : . . *

GOE #32

[return to main table](#)

SSH10_Fb7 MRMKPDHIFITELRGDETDWYLMALKSGHSGSVTSIHANDCRGALYKIGSYIKQSEVGQT 60
SSH35_56a MRMKPDHIFITELRGDETDWYLMALKSGHSGSVTSIHANDCRGALYKIGSYIKQSEVGQT 60
SSH37_36f MRMKPDHIFITELRGDETDWYLMALKSGHSGSVTSIHANDCRGALYKIGSYIKQSEVGQT 60
SSH29_187b MRMKPDHIFITELRGDETDWYLMALKSGHSGSVTSIHANDCRGALYKIGSYIKQSEVGQT 60
SSH47_912c MRMKPDHIFITELRGDETDWYLMALKSGHSGSVTSIHANDCRGALYKIGSYIKQSEVGQT 60
SSH08_Cv21 -----MALKSGHSGSVTSIHANDCRGALYKIGSYIKQSEVGQT 38

SSH10_Fb7	LDFNYIMQEVITTTIDVVVFEEKTHLKELYLGRDHVIRAAARAGTSG-----	106
SSH35_56a	LDFNYIMQEVITTTIDVVVFEEKTHLKELYLR-----PR-----	93
SSH37_36f	LDFNYIMQEVITTTIDVVVFEEKTHLKELYLGRDHAIIRAAARAGTVAGKEPRNSIAASGYR	120
SSH29_187b	LDFNYIMQEVITTTIDVVVFEEKTHLKELYLGRDHAIPAAVAAGS-----	104
SSH47_912c	LDFNYIMQEVITTTIDVVVFEEKTHLKELYLGRDHAKRHSSTFEE-----	104
SSH08_Cv21	LDFNYIMQEVITTTIDVVVFERPPGQNCTLTP-----	70
	*****: . :: *	

SSH10_Fb7	-----	
SSH35_56a	-----	
SSH37_36f	IRQSRGFFVPVRFHGGRTDKKPRKGEEVRLSGCRFLASRLLRVRLETSPRGHLDQPGD	180
SSH29_187b	-----	
SSH47_912c	-----	
SSH08_Cv21	-----	

SSH10_Fb7	-----	
SSH35_56a	-----	
SSH37_36f	IFMSQSIIPDFHSHAVRVVMRDGNPWFVATDVMGALDYAATSNPARVTEHIPSEWKGVN	240
SSH29_187b	-----	
SSH47_912c	-----	
SSH08_Cv21	-----	

SSH10_Fb7	-----WPVANLRV--	114
SSH35_56a	-----	
SSH37_36f	PIHTLGGEQKLLCLAEPGLYLPGLRAAARAGTFC	274
SSH29_187b	-----RAAARAGTE-	113
SSH47_912c	-----PPQFLE---	110
SSH08_Cv21	-----	

GOE #33

[return to main table](#)

SSH66_912c	MTLTEANATEHGILSNRRKRSRDNITRWTPLRQAWAELLAHRAAVLKRNCPLPQRLHPQD	60
SSH03_36f	MTLTEANATEHGILSNRRKRSRDNITRWTPLRQAWAELLAHRAAVLKRNCPLPQRLHPQD	60

SSH66_912c	RYLVLAESGHLLTKSGLDTAWQRLMALAIQEKVILDKQRFTLHGKIKHRGITDSTCPGGRS	120
SSH03_36f	RYLVLAESGHLLTKSGLDTAWQRLMALAIQEKVILDKQRFTLHGKIKHRGITDSTA----	115
	*****.	
SSH66_912c	KGRYSRYGAWTALAEA	136
SSH03_36f	-----	

GOE #34

[return to main table](#)

SSH72_912c	MTLTEANATEHGILSNRRKRSRDNITRWTPLRQAWAELLAHRAAVLKRNCPLPQRLHPQD	60
SSH03_36f	MTLTEANATEHGILSNRRKRSRDNITRWTPLRQAWAELLAHRAAVLKRNCPLPQRLHPQD	60

SSH72_912c	RYLVLAESGHLLTKSGLDTAWQRLMALAIQEKVILDKQRFTLHGKIKHRGITDSTCPGGRS	120
SSH03_36f	RYLVLAESGHLLTKSGLDTAWQRLMALAIQEKVILDKQRFTLHGKIKHRGITDSTA----	115
	*****.	
SSH72_912c	KGRYSRYGAWTALAEA	136
SSH03_36f	-----	
SSH72_912c	MTLTEANATEHGILSNRRKRSRDNITRWTPLRQAWAELLAHRAAVLKRNCPLPQRLHPQD	60
SSH03_36f	MTLTEANATEHGILSNRRKRSRDNITRWTPLRQAWAELLAHRAAVLKRNCPLPQRLHPQD	60

SSH72_912c	RYLVLAESGHLLTKSGLDTAWQRLMALAIQEKVILDKQRFTLHGKIKHRGITDSTCPGGRS	120
SSH03_36f	RYLVLAESGHLLTKSGLDTAWQRLMALAIQEKVILDKQRFTLHGKIKHRGITDSTA----	115
	*****.	
SSH72_912c	KGRYSRYGAWTALAEA	136
SSH03_36f	-----	

GOE #35

[return to main table](#)

SSH38_187b	-----	
SSH06_56a	-----	
SSH49_912c	MILFVKIICTNDKAIIRILMLEVKSLLKALNGNAKYHGGTMAIAPTTYGRKLSNVAAE	60

SSH16_Fb7 -----MATLNITAEQWRLQQLTVVN-----SKMLSAI 28
SSH07_36f -----MATLNITAEQWRLQQLTVVN-----SKMLSAI 28

SSH38_187b -----MAFILKAKGLPFEMTSDNVLENQYDELNGLF 31
SSH06_56a -----MAFILKAKGLPFEMTSDNVLENQYDELNGLF 31
SSH49_912c VKKQFAGEEQLPPYNYHVRDTIVSLEDGRMAFILKAKGLPFEMTSDNVLENQYDELNGLF 120
SSH16_Fb7 LKKQFAGEEQLPPYNYHVRDTIVSLEDGRMAFILKAKGLPFEMTSDNVLENQYDELNGLF 88
SSH07_36f LKKQFAGEEQLPPYNYHVRDTIVSLEDGRMAFILKAKGLPFEMTSDNVLENQYDELNGLF 88

SSH38_187b LSLAKSTGSRLAVWAHIDHYAKTLKSNYEFSYEWIR---LFTEKYLGR----- 76
SSH06_56a LSLAKSTGSRLAVWAHIDHYAKTLKSNYEFSYEWIR---LFTEKYLGR----- 76
SSH49_912c LSLAKSTGSRLAVWAHIDHYAKTLKSNYEFSYEWIR---LFTEKYMARFEGESIFENSFY 177
SSH16_Fb7 LSLAKSTGSRLAVWAHIDHYAKTLKSNYEFSYEWIRPGRHGRGISGR----- 136
SSH07_36f LSLAKSTGSRLAVWAHIDHYAKTLKSNYEFSYEWIR---LFTSVVAAE----- 133
***** . .

SSH38_187b -DHAIRAAALAGLAVLMAHARQMLIMTVSPMMS----- 108
SSH06_56a -DHAT----- 80
SSH49_912c LTFILKPGMNDSLEECIRELEEMQIIVTQTLASYECEVLSDYHNGHQFSQFYEFIAYLY 237
SSH16_Fb7 -----PGRYPAYTQWCKESGVYALSKVRFLGE----- 163
SSH07_36f -----VWQYQIWSSTVLKEY----- 147

SSH38_187b RTLRRRIKI-----KTRIKIRGRLE----- 130
SSH06_56a ---GRRISS-----GRPGRYLYRIIL----- 98
SSH49_912c NGFWERVVPTSLPLFQVVQTSALHHGYKLETRFPNGGNRYSAFFDLPRPRPRYTGKIQP 297
SSH16_Fb7 --LERCVPKFR-----NKRVARVTDGKRRE----- 186
SSH07_36f --LAGCF----- 152
.

SSH38_187b ---VSDAMCRPSVPVIR--- 144
SSH06_56a -----
SSH49_912c PVRVTVSFCHVLVIYIHQYG 317
SSH16_Fb7 -LVVIQIGLIDAGI----- 200
SSH07_36f --AVTDQI----- 158

GOE #36

[return to main table](#)

SSH68_912c MPQSTKENNKRYKPSSGADVALSKLRKLTGTHLIHTSSLIHLNKQAPTQNDQVPRPRPRY 60
SSH10_187b MPQSTKENNKRYKPSSGADVALSKLRKLTGTHLIHTSSLIHLNKQAPTQNDQVPRPRPRY 60

SSH68_912c S-----SGRPGRYTVHPEHVASRHKITN----- 84
SSH10_187b SVVAAEVFDLLMRWAFLCDGWKQEKAKKSKPQPQNLLQKKYPNIISALNI 113
* . : . : * : : : * . *

GOE #37

[return to main table](#)

SSH27_187b MVSVSLRPLDEVTRQLENLAALTGRSKTFYMVAEIREHIDDEDLYLAECELEAIRSGKS 60
SSH27_187b QTVPRPRPRYMLPAAWPRDSAARASQLGSPVPHQGA 95

GOE #38

[return to main table](#)

SSH40_187b MTIRKPSSSRFSLTDYADSGRLRPVLAGLSDEIQPWEAELLQLVQKGFVRFFELAVEHR 60
SSH29_36f MTIRKPSSSRFSLTDYADSGRLRPVLAGLSDEIQPWEAELLQLVQKGFVRFFELAVEHR 60
SSH37_Cv21 MTIRKPSSSRFSLTDYADSGRLRPVLAGLSDEIQPWEAELLQLVQKGFVRFFELAVEHR 60

SSH40_187b LNIIVTVGGTSGKTTFSKCLIDLYPTSCRLFTIEDAHELTPKHPNSVPRPRPR----- 114
SSH29_36f LNIIVTVGGTSGKTTFSKCLIDLYPTSCRLFTIEDAHELTPKHPNSVPRPRPRYSSGRP 120
SSH37_Cv21 LNIIVTVGGTSGKTTFSKCLIDLYPTSCRLFTIEDAHELTPKHPNS-----YS----- 109

SSH40_187b -----
SSH29_36f GRYRCVRHHLDEFVRQFRWALNSRAEWLREQRVRAETLTDIQRARFYYLQKLAFGGKV 180
SSH37_Cv21 -----VVAAEVL-----AGQWR----- 122

SSH40_187b -----
SSH29_36f NQHFGFVTCGTSAAATTLFERPPGVPTIFLISL 213
SSH37_Cv21 --TYGFKPLPTSR----YAAKP-----QLSL 142

GOE #39

[return to main table](#)

SSH26_Fb7 MPSMVFPFGFFVKLFSILLSACLIVIRVFAPARLIFAASFWSLIPDL-GRDHAKYTNTPIHQ 59
SSH43_912c MPSMVFPFGFFVKLFSILLSACLIVIRVFAPARLIFAASFWSLIPDLPGRPLAN----PVAM 56
***** * : * :

SSH26_Fb7 YTNTPIHQYTNTPIHQYTNTPIHQYTNTR 88
SSH43_912c AVERPPGQV----- 65
. : * *

GOE #40

[return to main table](#)

SSH32_56a -----VGA 3
SSH38_Cv21 -----VGA 3
SSH09_Fb7 -----VGA 3
SSH08_187b VSTCPGGRSNHAPGRLLAAG-LAWSRPRYFRLASGEPTGLNPFQLPDTPQNRNFLYDLVGA 59
SSH21_36f -----MRGFIEAVGG-TYFRLASGEPTGLNPFQLPDTPQNRNFLYDLVGA 44

SSH32_56a CGRKVGQESTAEDTKDIKQAVDNVFAMPFKLRRFGVLLQSI PDHGENCLARRLADWCYGE 63
SSH38_Cv21 CGRKVGQESTAEDTRDIKQAVDNVFAMPFKLRRFGVLLQSI PDHGENCLARRLADWCYGE 63
SSH09_Fb7 CGRKVGQESTAEDTKDIKQAVDNVFAMPFKLRRFGVLLQSI PDHGENCLARRLADWCYGE 63
SSH08_187b CGRKVGQESTAEDTKDIKQAVDNVFAMPFKLRRFGVLLQSI PDHGENCLARRLADWCYGE 119
SSH21_36f CGRKVGQESTAEDTKDIKQAVDNVFAMPFKLRRFGVLLQSI PDHGENCLARRLADWCYGE 104
***** : ***** *

SSH32_56a IEGRYAYALDNPQNNFDWENLKRVGFDVSDFLVAGHPATEP-ILAYLFHLKTLMQRDGEL 122
SSH38_Cv21 IEGRYAYALDNPQNNFDWENLKRVGFDVSDFLVAGHPATEP-ILAYLFHLKTLMQRDGEL 122
SSH09_Fb7 IEGRYAYALDNPQNNFDWENLKRVGFDVSDFLVAGHPATEP-ILAYLFHLKTLMQRDGEL 122
SSH08_187b IEGRYAYALDNPQNNFDWENLKRVGFDVSDFLVAGHPATEP-ILAYLFHLKTLMQRDGEL 178
SSH21_36f IEGRYAYALDNPQNNFDWENLKRVGFDVSDFLVAGHPATEP-ILAYLFHLKTLMQRDGEL 163
***** * . ***** : . : *****

SSH32_56a LATVVEEFWLPLQYPTTADQILDSLKTGRRRGEFILLVSQSPEDVIKSPLLPAVLQQTPT 182
SSH38_Cv21 LATVVEEFWLPLQYPTTADQILDSLKTGRRRGEFILLVSQSPEDVIKSPLLPAVLQQTPT 182
SSH09_Fb7 LATVVEEFWLPLQYPTTADQILDSLKTGRRRGEFILLVSQSPEDVIKSPLLPAVLQQTPT 182
SSH08_187b LATVVEEFWLPLQYPTTADQILDSLKTGRRRGEFILLVSQSPEDVIKSPLLPAVLQQTPT 238
SSH21_36f LATVVEEFWLPLQYPTTADQILDSLKTGRR----- 193

SSH32_56a KIFLNPDAEYTTDPGGGYSRFTQIKEFQKLKKLGLQSRMFIVKQGSQSSLVKLNLSGMA 242
SSH38_Cv21 KIFLNPDAEYTTDPGGGYSRFTQIKEFQKLKKLGLQSRMFIVKQGSQSSLVKLNLSGMA 242
SSH09_Fb7 KIFLNPDAEYTTDPGGGYSRFTQIKEFQKLKKLGLQSRMFIVKQGSQSSLVKLNLSGMA 242
SSH08_187b KIFLNPDAEYTTDPGGGYSRFTQIKEFQKLKKLGLQSRMFIVKQGSQSSLVKLNLSGMA 298
SSH21_36f -----

SSH32_56a DDIAVPRPRRY----- 254
SSH38_Cv21 DDIAVPRQ----- 250
SSH09_Fb7 DDIAVVAE----- 251
SSH08_187b DDIAVPGRAAATDTSRLAITLAWSRPRYNQPQLQEIIY 335
SSH21_36f -----

GOE #41

[return to main table](#)

SSH29_56a MSLTLLNDVPQKQVSQVDRSLSVRELMRKYGISEALMANITEFAINRPGSYWVEDAAGWR 60
SSH12_36f MSLTLLNDVPQKQVSQVDRSLSVRELMRKYGISEALMANITEFAINRPGSYWVEDAAGWR 60
SSH32_Cv21 -----MANITEFAINRPGSYWVEDAAGWR 24
SSH24_912c -----MRKYGISEALMANITEFAINRPGSYWVEDAAGWR 34

SSH29_56a EVPNESLSLSHLQGLATATAVFNQKKLDRDNPIASLTLPDGERCQVVPR----- 109
SSH12_36f EVPNESLSLSHLQGLATATAVFNQKKLDRDNPIASLTLPDGERCQVVPARAAAR---IAW 117
SSH32_Cv21 EVPNESLSLSHLQGLATATAVFNQKKLDRDNPIASLTLPDGERCQVVPR----- 73
SSH24_912c EVPNESLSLSHLQGLATAIAWSTGRGLDRDNPIASLTLPDGERCQVVLPACENGTVSMT 94
***** * : *****

SSH29_56a PRPR----- 113

SSH12_36f	SRPRYSKQFRAAARAGTSSSGAVVR-FWRYLRHIPASVVPVAVAIRKKKTACHKADSSALS	176
SSH32_Cv21	PRPR-----	77
SSH24_912c	IRKPSSSRFSLTDYADSGRLRPVLAGLSDEIQWEAEELLQLVQKGDVFRFFETSGRTSLE	154
	*	

SSH29_56a	-----	
SSH12_36f	A-DIPRTPIIS--TVLVTF-	191
SSH32_Cv21	-----	
SSH24_912c	HRDGGRHRVRENDVLKVPD	173

GOE #42

[return to main table](#)

SSH25_56a	MKKLPVLLLACVTHFAYANDPRI RTEIYDKSSVYNLHTQIGRASLIQ-LEADESLEISPS	59
SSH13_Cv21	MKKLPVLLLACVTHFAYANDPRI RTEIYDKSSVYNLHTQIGRASLIQ-LEADESLEISPS	59
SSH76_912c	MKKLPVLLLACVTHFAYANDPRI RTEIYDKSSVYNLHTQIGRASLIQTCPGDESLEISPS	60
	*****	*****

SSH25_56a	SLLGIGDAKAWDLG-----VLRGR-----	R 79
SSH13_Cv21	SLLGIGDAKAWDLGVRGNNIVLPRP-----	R 85
SSH76_912c	SLLGIGDAKAWDLGVRGNNIVLKPTQKMPQTNVIVVTNKRTYSFELLATAKDSMPTYILR	120
	*****	**

SSH25_56a	HLFSTASSDDQ-----HGADY-----	95
SSH13_Cv21	PRYSVVAEVRKRLRLHPLQIVIWPF-----	110
SSH76_912c	FRYPDTEASKADLGRDHATDNCRSPRRKNDHQYRLLLAW	159
	:. . :.	* :

GOE #43

[return to main table](#)

SSH13_912c	MHTTNLRKVGGSIMLAVPPAFLDQLHLEV GATVGLAVTDGRLVIEPVLHPQYLPGRPLDS	60
SSH28_56a	MHTTNLRKVGGSIMLAVPPAFLDQLHLEV GATVGLAVTDGRLVIEPVLHPQYLG RDHATS	60
	*****	*

SSH13_912c	VVAAEVYLFATPNRTP IYKNINI	84
SSH28_56a	VVAAEVHR--KRGR-----	72
	*****:	. . *

GOE #44

[return to main table](#)

SSH05_187b	-----LRSRT-----SAATTL-----	11
SSH11_Cv21	MPRRSL-----SFFHSA-----NVQRTFNPLVAG-----SIPARPTKLGREH--	A 39
SSH11_36f	MHTTNLRKVGGSIMLAVPPAFLDQLHLEV GATVGLAVTDGRLVIEPVLHPQYLG RDHAIA	60
	: : .	.. *.

SSH05_187b	FERPPGQVRPTNP AEAKISETKAKTLETWSQVVRNLEVTGQTDLAKSVMALMRDADKSTS	71
SSH11_Cv21	FERPPGQVRPTNP AEAKISETKAKTLETWSQVVRNLEVTGQTDLAKSVMALMRDADKSTS	99
SSH11_36f	WSRPRSGVRPTNP AEAKISETKAKTLETWSQVVRNLEVTGQTDLAKSVMALMRDADKSTS	120
	:.*. *	*****

SSH05_187b	SRTQELFDLAKSSH SKDKGIEQEL	95
SSH11_Cv21	SRTQELFDLAKSSH SKDKGIEQEL	123
SSH11_36f	SRTQELFDLAKSSH SKDKGIEQEL	144

GOE #45

[return to main table](#)

SSH13_56a	MYWRISKEKFAELDADNRIWWGKDGNNTPRLKRFLNEVKQGIVPQTLWTYSNVGHTQDAK	60
SSH22_187b	MYWRISKEKFAELDADNRIWWGKDGNNTPRLKRFLNEVKQGIVPQTLWTYSNVGHTQDAK	60
SSH31_36f	MYWRISKEKFAELDADNRIWWGKDGNNTPRLKRFLNEVKQGIVPQTLWTYSNVGHTQDAK	60
SSH07_Fb7	MYWRISKEKFAELDADNRIWWGKDGNNTPRLKRFLNEVKQGIVPQTLWTYSNVGHTQDAK	60
	*****	*****

SSH13_56a	KQLLDVLQFESSDVFSTPKPV-----	PARA-FERPPGQVQAGSSI 100
SSH22_187b	KQLLDVLQFESSDVFSTPKPV-----	PARASVVAEVLLEALSKG 101
SSH31_36f	KQLLDVLQFESSDVFSTPNSS-----	GRPGRYVADTVRHGLTLP 101
SSH07_Fb7	KQLLDVLQFESSDVFSTPIAWSRPRYIRQHLRELEERLNFQVRQEVILAE LKAKGYKT	120
	*****	. . .

SSH13_56a	CEDTR-----	105
SSH22_187b	LSQLRARPV TW-----	112
SSH31_36f	LRSACC-----	107
SSH07_Fb7	LKGFRNLLYRARIRAAQNPEKFQTKVEQKNEKEDAQLLAKKSENKKEEVSKNPLKKKAGF	180

SSH13_56a -----
SSH22_187b -----
SSH31_36f -----
SSH07_Fb7 DFKGTNSFDESDLI 194

GOE #46

[return to main table](#)

SSH58_912c MSQSIIPDFHSHAVRVVMDGNPWFVATDVMGALDYAATSNPARVTEHIPGEWIRVNPI 60
SSH38_Fb7 -----MIDGEAWFVAKDVM DALDYAETSNPARVTEHIPAEWVCVNPI 42
* *. : . ****. *. : ***** : ** : ****

SSH58_912c HTLGGEQKLLCLAEPLYLGRDHAIAWSRPRIYIHFHADDYFHGEHSGGYP 110
SSH38_Fb7 HTNA----- 46
** .

GOE #47

[return to main table](#)

SSH43_187b MKSIFALLAFMVSTVASAQQNELVRVENLSTVESTSAATTLRPPMAAGIAWSRPSIAI 60
SSH70_912c -----

SSH43_187b SITSSNALASVGGLGGLTRAKTAAENIKTGLYALVGVIAMIYLIYLGVMATFEKKSWADF 120
SSH70_912c -----MIYLIYLGVMATFEKKSWADF 21

SSH43_187b GWGVVYVSLVGGAVALGGWAWTLFA 145
SSH70_912c GWGVVYVSLVGGAVALGGWAWTLFA 46

GOE #48

[return to main table](#)

SSH20_36f MNKTIDFSNAGALPTLDGRTEVFGEPTSKAKSKTNVGKFLVLGLVLMMAFLFMVGGLLFYQ 60
SSH30_Fb7 MNKTIDFSNAGALPTLDGRTEVFGEPTSKAKSKTNVGKFLVLGLVLMMAFLFMVGGLLFYQ 60
SSH31_56a MNKTIDFSNAGALPTLDGRTEVFGEPTSKAKSKTNVGKFLVLGLVLMMAFLFMVGGLLFYQ 60
SSH48_187b -NKTIDFSNAGALPTLDGRTEVFGEPTSKAKSKTNVGKFLVLGLVLMMAFLFMVGGLLFYQ 59

SSH20_36f KYKTSAAATTLFERPPGQVSQRNRNGIPWQSAVASSPQEPPQQQLSNSFTKSTWKL TATH 120
SSH30_Fb7 KY----- 62
SSH31_56a KYKTSAAATLL-RAAARAGTR-----SPR----- 83
SSH48_187b KYKTSAAATL----- 69
**

SSH20_36f ALTSPTHVQVYYAMTATP 138
SSH30_Fb7 -----
SSH31_56a -----MIAT- 87
SSH48_187b -----

GOE #49

[return to main table](#)

SSH07_187b MKMYLRSLTLAFVLLPIMASAQTISEANVAKVKLKIVESEDRTGLKTITAKSCIHLNQS 60
SSH25_187b MKMYLRSLTLAFVLLPIMASAQTISEANVAKVKLKIVESEDRTGLKTITAKSCIHLNQS 60
SSH11_56a MKMYLRSLTLAFVLLPIMASAQTISEANVAKVKLKIVESEDRTGLKTITAKSCIHLNQS 60
SSH12_Fb7 -----

SSH07_187b GMLTDLYLCPAIASKPNQPLVMYARGDYTGYGWAFLTGQAQFLIDGKQYSAQGTARPEEK 120
SSH25_187b GMLTDLYLCPAIASKPNQPLVRYARGDYTGYGWAFLTGQAQFLIDGKQYSAQGTARPEEK 120
SSH11_56a GMLTDLYLCPAIASKPNQPPGMRYARGDYTGYGWAFLTGQAQFLIDGKQYSAQGTARPEEK 120
SSH12_Fb7 -----

SSH07_187b RVATCSGNVGCINKETARFSMTEELATAIANARDAEVRFVGRQGSVTGRNNAKHVAYFRE 180
SSH25_187b RVATCSGNVGCINKETARFSMTEELATAIANARDAEVRFVGRQGSVTGRNNAKHVAYFRE 180
SSH11_56a RVATCSGNVGCINKETARFSMTEELATAIANARDAEVRFVGRQGSVTGRNNAKHVAYFRE 180
SSH12_Fb7 -----MTEELATAIANARDAEVRFVGRQGSVTGRNNAKHVAYFRE 40

SSH07_187b MLRRYKTLGGVFESASTANEGTLEVNTSESENKVK 216
SSH25_187b MLRRYKTLGGVFESASTANEGTLEVNTSESENKVK 216

SSH11_56a MLRRYKTLGGVFESASTANEGTLEVNTSESENKVK 216
SSH12_Fb7 MLRRYKTLGGVFESASTANEGTLEVNTSESEQ--- 72
*****;

GOE #50

[return to main table](#)

SSH46_187b VPPQCSGDPVMCGQARIQWRIECSLRDVKIKGGTCDAPICTGEKCNAM EYASLLQWR 60
SSH40_56a -----MEYASLLQWR 11
SSH27_Fb7 -----MEYASLLQWR 11
SSH39_187b -----MCGQTRIQWRIECSLRDVKIKGGTCDAPICTGEKCNAM EYASLLQWR 50

SSH46_187b TACALEKGSAGAVLGGDNQGNADVGAIKDALTKDGTVDTGEEGDPGAFSD ESYGRE 120
SSH40_56a TACALEKGSAGAVLGGDNQGNADVGAIKDALTKDGTVDTGEEGDPGAFSD ESYGRE 71
SSH27_Fb7 TACALEKGSAGAVLGGDNQGNADVGAIKDALTKDGTVDTGEEGDPGAFSD ESYGRE 71
SSH39_187b TACALEKGSAGAVLGGDNQGNADVGAIKDALTKDGTVDTGEEGDPGAFSD ESYGRE 110

SSH46_187b GYPKVKIDDKGRGYSRVCPSIPINVFNGQIVISATPVCQFLQIGGKLV LIL----- 172
SSH40_56a GYPKVKIDDKGRGYSRVCPSIPINVFNGQIVISATPVCQFLQIGGKLV LIL----- 123
SSH27_Fb7 GYPKVKIDDKGRGYSRVCPSIPINVFNGQIVISATPVCQFLQIGGKLV LIL----- 123
SSH39_187b GYPKVKIDDKGRGYSRVCPSIPINVFNGQIVISATPVCQFLQIGGKLV LILDLD RDHAN 170

SSH46_187b -----AALACLRIMGGRLEG----- 187
SSH40_56a -----AALACLRIMGGRLEG----- 138
SSH27_Fb7 -----AALACLRIMGGRLEG----- 138
SSH39_187b LRGHGAGSMFERPLGQVPWSDFCILFRGNFQSRPLEKALQLLRIPSS GRPGRYCLLP AKM 230
* * * *

SSH46_187b ----
SSH40_56a ----
SSH27_Fb7 ----
SSH39_187b ARSA 234

GOE #51

[return to main table](#)

SSH02_912c VRGLIGQHTFIKRRFGTRWIDVWTWGEIDNVKSSSNRDLGEHVLRTLP SQVYGLYKSAE 60
SSH04_187b -----

SSH02_912c VHTIKARIPFKVYLLALLMVLVVVCVIVARTLRPSSFSRVLGTQAANGA ERARPEAPA 120
SSH04_187b -----VVAA-----EAPA 8
* : * *

SSH02_912c SHHPVGVENGDALRWETETAYAKDHLPRFASMPWTAPIYDSRPTADPQL ICMSGGEGLD 180
SSH04_187b SHHPVGVENGDALRWETETAYAKDHLPRFASMPWTAPIYDSRPTADPQL ICMSGGEGLD 68

SSH02_912c AQGM YKMSCTCYTEQGTLYEIPDGE CRRIARRGPVYNPYRERTQELG GASQGQVTALPS 240
SSH04_187b AQGM YKMSCTCYTEQGTLYEIPDGE CRRIARRGPVYNPYRERTQELG GASQGQVTALPS 128

SSH02_912c SRSTPGHVLVTSGHALP 257
SSH04_187b SRSTPGHVLVTSGHALP 145

GOE #52

[return to main table](#)

SSH17_187b -----MREAVMQFCQEEFANRRYVAALHDDTDHTHVHVCVGT RDIDRADEPRLSPR 51
SSH03_Cv21 MPPGTPEKAMREAVMQFCQEEFANRRYVAALHDDTDHTHVHVCVGT RDIDRADEPRLSPR 60
SSH04_56a -----MREDVMQFCQEEFGNRRYVAGLHDDTDHAHVHVCVGTQD IDRADEPRLSPR 51
* * * * * : * * * * *

SSH17_187b KADLFRWRQGFADKLRENGIDAAASERRHRFNHRKPENPVVRQIRADN PKSAVYNERRAK 111
SSH03_Cv21 KADLFRWRQGFADKLRENGIDAAASERRHRFNHRKPENPVVRQIRADN PKSAVYNERRAK 120
SSH04_56a KADLFRWRQGFADKLRENGIDAAASERRHRFNHRKPENPVVRQIRADN PKSAVYNERRAK 111

SSH17_187b EKALERAMKATARQEDAYVSPPLPRDPCPGGRSIRAAARAGTFTANDR -VVRNNNI ISN 170
SSH03_Cv21 EKALERAMKATARQEDAYVSPPLPRVPRPR----- 153
SSH04_56a EKALERAMKATARQEDAYVSPPLPRVP-KVYEALKSDLQAALK TARAGPPLGTSPYPLD 170

***** *

SSH17_187b A 171
SSH03_Cv21 -
SSH04_56a A 171

GOE #53

[return to main table](#)

SSH10_Cv21 -----
SSH32_912c MSFVLGAKTELLVAAYSFTSKDIAFALTEAKARGIDVRVVVDHAQNTDDQGGYKAVDYL 60

SSH10_Cv21 -----MHHKFMVADGLHVQLGSFNYTSSANLRNAETAVAFRNAPELASLYR 46
SSH32_912c SQGIPVFRCENYAAMHHKFMVADGLHVQLGSFNYTSSANLRNAETAVAFRNAPDRAAAR- 119
*****: *:

SSH10_Cv21 TEWLRLSTEPKASVETVMAVDRGLAILKEFGI 78
SSH32_912c ---AGLLQPPLP----- 128
* * .

GOE #54

[return to main table](#)

SSH27_36f -MKSIFAL-----LAFMVFSTVASAQQNELVRVENLS-TVESTTPQVPDIT 44
SSH63_912c --MGIYEIEWPPA-----RSFMVFSTVASAQQNELVRVENLS-TVESTTPQVPDIT 48
SSH21_Cv21 LSVNLADLGRDHASPGRVAILISTFMVFSTVASAQQNELVRVENLAWSRPSTTPQVPDIT 60
. : : *****: : *****

SSH27_36f GNVINIANKKLRHVTVEFNLYDEQNNLVGNAIDVVTNLEPNGKWKFKATTTTPYQRFKLT 104
SSH63_912c GNVINIANKKLRHVTVEFNLYDEQNNLVGNAIDVVTNLEPNGKWKFKATTTTPYQRFKLT 108
SSH21_Cv21 GNVINIANKKLRHVTVEFNLYDEQNNLVGNAIDVVTNLEPNGKWKFKATTTTPYQRFKLT 120

SSH27_36f NVEAY-----LE---- 111
SSH63_912c NVEDLGRDHAIVVRGAMEQRTD 130
SSH21_Cv21 NVEAY-----LE---- 127
*** :*

GOE #55

[return to main table](#)

SSH16_Cv21 MCALSVSEVSEVLGGNALTDSKISIGMDAGVFVGVMGFTSPMFLGAFAGAERLIGAAWGG 60
SSH42_912c MCALSVSEVSEVSEVLGGNALTDSKISIGMDAGVFVGVMGFTSPMFLGAFAGAERLIGAAWGG 60

SSH16_Cv21 GWMGTGTFIHKRFISMYPTIFYLGRDHANPAARRPGALAWSRPXYENDPRWTNATGAVVQL 120
SSH42_912c GWMGTGTFIHKRFISMYPTIFYLGRDHA-----IAWSRPR----- 94
*****: *****

SSH16_Cv21 EGLQECWPTKPISTATTDHDCCLRKGK 149
SSH42_912c -----

GOE #56

[return to main table](#)

SSH23187b MECTLFDKDQFVHIRINEKRDFTLPRKFFGSSFPKNVRPETILGGNNRPQHFDITIVITR
SSH39_36f MECTLFDKDQFVHIRINEKRDFTLPRKFFGSSFPKNVRPETILGGNNRPQHFDITIVITR
SSH10_56a MECTLFDKDQFVHIRINEKRDFTLPRKFFGSSFPKNVRPETILGGNNRPQHFDITIVITR
SSH08912c MECTLFDKDQFVHIRINEKRDFTLPRKFFGSSFPKNVRPETILGGNNRPQHFDITIVITR
SSH24_Fb7 MECTLFDKDQFVHIRINEKRDFTLPRKFFGSSFPKNVRPETILGGNNRPQHFDITIVITR
SSH44_Cv21 MECTLFDKDQFVHIRINEKRDFTLPRKFFGSSFPKNVRPETILGGNNRPQHFDITIVITR

GOE #57

[return to main table](#)

SSH24_187b MAAYPIIMLSIELVCSIFIKVQETFNATLPDENYKTAIEAALCLRIVSK
SSH22_36f MAAYPIIMLSIELVCSIFIKVQETFNATLPDENYKTAIEAALCLRIVSK
SSH16_56a MAAYPIIMLSIELVCSIFIKVQETFNATLPDENYKTAIEAALCLRIVSK
SSH22_Cv21 MAAYPIIMLSIELVCSIFIKVQETFNATLPDENYKTAIEAALCLRIVSK
SSH61_912c MAAYPIIMLSIELVCSIFIKVQETFNATLPDENYKTAIEAALCLRIVSK

GOE #58

[return to main table](#)

SSH22_36f MAAYPIIMLSIELVCSIFIKVQETFNATLPDENYKTAIEAALCLRIVSK
SSH22_Cv21 MAAYPIIMLSIELVCSIFIKVQETFNATLPDENYKTAIEAALCLRIVSK

GOE #59[return to main table](#)

SSH08_36f
SSH15_56a
SSH45_Cv21
SSH69_912c

VRQEVILAE LKAGYKTT LKGFRNLLYRARIRAAQNPEKFQTKVEQKNEKEDAQLLAKKS
VRQEVILAE LKAGYKTT LKGFRNLLYRARIRAAQNPEKFQTKVEQKNEKEDAQLLAKKS
VRQEVILAE LKAGYKTT LKGFRNLLYRARIRAAQNPEKFQTKVEQKNEKEDAQLLAKKS
VRQEVILAE LKAGYKTT LKGFRNLLYRARIRAAQNPEKFQTKVEQKNEKEDAQLLAKKS

SSH08_36f
SSH15_56a
SSH45_Cv21
SSH69_912c

ENKKEEVSKNPLKKKAGDFKGTNSFDES DLI
ENKKEEVSKNPLKKKAGDFKGTNSFDES DLI
ENKKEEVSKNPLKKKAGDFKGTNSFDES DLI
ENKKEEVSKNPLKKKAGDFKGTNSFDES DLI

GOE #60[return to main table](#)

SSH26_36f
SSH62_912c
SSH20_56a

MNKNQAAMHVEASKFIATNMQALQNQPNMADKSVEDLTKLAYWRGIVAEENKLQPKAVQD
MNKNQAAMHVEASKFIATNMQALQNQPNMADKSVEDLTKLAYWRGIVAEENKLQPKAVQD
MNKNQAAMHVEASKFIATNMQALQNQPNMADKSVEDLTKLAYWRGIVAEENKLQPKAVQD

SSH26_36f
SSH62_912c
SSH20_56a

EAIARFDKQAADPQFLKRLNQETEPKIHDRTERVQQRDTHEQSL
EAIARFDKQAADPQFLKRLNQETEPKIHDRTERVQQRDTHEQSL
EAIARFDKQAADPQFLKRLNQETEPKIHDRTERVQQRDTHEQSL

GOE #61[return to main table](#)

SSH33_187b
SSH32_36f

MLLNTNNIAVNRPAAEAGLEMLEAGGDFADGVIAYDGTWLGAE TFVSFDKKAVSLLTKHGHAA RLL
MLLNTNNIAVNRPAAEAGLEMLEAGGDFADGVIAYDGTWLGAE TFVSFDKKAVSLLTKHGHAA RLL

GOE #62[return to main table](#)

SSH25_36f
SSH06_912c

VNKRQLIAAIVEKSGIKLTEDDPAFLLV DNLNMMLEKQTSEAAKQLEAA TEKFNAVTT HN
VNKRQLIAAIVEKSGIKLTEDDPAFLLV DNLNMMLEKQTSEAAKQLEAA TEKFNAVTT HN

SSH25_36f
SSH06_912c

VDDFVSVANEALS-KFMQRTNEIKSSLD DLSKKLAQVANVTSTSSAHEVTKISHRSELLW
VDDFVSVANEALS-KFMQRTNEIKSSLD DLSKKLAQVANVTSTSSAHEVTKISHRSELLW

SSH25_36f
SSH06_912c

WLVP RPRPR
WLVP RPRPR

GOE #63[return to main table](#)

SSH05_36f
SSH39_Cv21

MSFTGILKKTRVPISAFVFIFAGTAYAQ LQVYDAANISTSIQNHVESIAKWKQ QFEQLKQ
MSFTGILKKTRVPISAFVFIFAGTAYAQ LQVYDAANISTSIQNHVESIAKWKQ QFEQLKQ

SSH05_36f
SSH39_Cv21

QIDQHQQQYEAITGSRGMGALLDNSALKASLPD WKQVLSDVKKTSAYATERSKYPTSGN
QIDQHQQQYEAITGSRGMGALLDNSALKASLPD WKQVLSDVKKTSAYATERSKYPTSGN

SSH05_36f
SSH39_Cv21

LQKTNAMEYDVASQDVIMSDLYSKANRR LNLIQSLTAQIDSANDPAAKADLANRLINEQN
LQKTNAMEYDVASQDVIMSDLYSKANRR LNLIQSLTAQIDSANDPAAKADLANRLINEQN

SSH05_36f
SSH39_Cv21

AIQANQNLVTILQAKQKQELEIASQA AVEELSCKEFKRSGC
AIQANQNLVTILQAKQKQELEIASQA AVEELSCKEFKRSGC

GOE #64[return to main table](#)

SSH07_187b
SSH29_Cv21

MSDSEMKIQANALMP ELVAELVALKQEAERFLSTQKIHTKVIYDVFDGAELLPETLARV
MSDSEMKIQANALMP ELVAELVALKQEAERFLSTQKIHTKVIYDVFDGAELLPETLARV

SSH07_187b

NNAVMIAHQMTANVQKRINALRGKLP EGYKDADGHFWNTNTFNLLRDTHKDFDQAVKIAK

SSH29_Cv21 NNAVMIHQMTANVQKRINALRGKLP EGYKDADGHFWNTNTFNLLRDTHKDFDQAVKIAK

SSH07_187b KISEWASVKIDGTSYSK
SSH29_Cv21 KISEWASVKIDGTSYSK

GOE #65

[return to main table](#)

SSH03_187b VVAEVLSDVKKTSAYATERSKYPTSGNLQKTNAMYDVIA SQDVIMSDLYSKANRRLNLI
SSH26_56a VVAEVLSDVKKTSAYATERSKYPTSGNLQKTNAMYDVIA SQDVIMSDLYSKANRRLNLI

SSH03_187b QSLTAQIDSANDPAAKADLANRLINEQNAIQANQNLVTILQAKQKQELEIASQA AVEELS
SSH26_56a QSLTAQIDSANDPAAKADLANRLINEQNAIQANQNLVTILQAKQKQELEIASQA AVEELS

SSH03_187b CKEFKRSGC
SSH26_56a CKEFKRSGC

GOE #66

[return to main table](#)

SSH13_36f VWTRIDNPNGVFANIDSPATDQMGYS GIPGYVDTHFWQRFGSAIMLSLIKDFSQAYSQ RV
SSH19_912c VWTRIDNPNGVFANIDSPATDQMGYS GIPGYVDTHFWQRFGSAIMLSLIKDFSQAYSQ RV

SSH13_36f ANRSNTGTTVIQPYANTTQATQDMGAEALRNSINIPPTLVVLPATAVNVMVARDV SFENV
912c_19 ANRSNTGTTVIQPYANTTQATQDMGAEALRNSINIPPTLVVLPATAVNVMVARDV SFENV

SSH13_36f FNLVE
SSH19_912c FNLVE

GOE #67

[return to main table](#)

SSH09_187b MTELVAIVNDLASRGVTFESL TEHIDTSSASGKFAFHLSALAEFERNTIKERTRAGLAA
SSH67_912c MTELVAIVNDLASRGVTFESL TEHIDTSSASGKFAFHLSALAEFERNTIKERTRAGLAA

SSH09_187b ARARGRMGGRPAKVTPKAKREMKALYTSQEVSVKDICTRYNITRSTFYRVVLERDY TANG
SSH67_912c ARARGRMGGRPAKVTPKAKREMKALYTSQEVSVKDICTRYNITRSTFYRVVLERDY TANG

SSH09_187b KA
SSH67_912c KA
**

GOE #68

[return to main table](#)

SSH34_912c MKHIFNNFLDKYHNVILAIAISITSSNALASVGGGLGGLTRAKTAAENIKTGLYALVG VIA
SSH19_Cv21 MKHIFNNFLDKYHNVILAIAISITSSNALASVGGGLGGLTRAKTAAENIKTGLYALVG VIA

SSH34_912c MIYLIYLGVM AFTEKKSWADFGWGVVYVSLVGGAV ALGGWAWTLFA
SSH19_Cv21 MIYLIYLGVM AFTEKKSWADFGWGVVYVSLVGGAV ALGGWAWTLFA

GOE #69

[return to main table](#)

SSH41_912c MKMRELSKVEIEQVSGASTSTTIWDDVVAATNGIWSGLVTATSNI FGGAVTATNNILGGT
SSH25_Cv21 MKMRELSKVEIEQVSGASTSTTIWDDVVAATNGIWSGLVTATSNI FGGAVTATNNILGGT

SSH41_912c AAGTNNIFNQFINSYFFRNYISISLFSNDSTVVDKKS
SSH25_Cv21 AAGTNNIFNQFINSYFFRNYISISLFSNDSTVVDKKS

GOE #70

[return to main table](#)

SSH02_36f MAILVHQRNEIFSKLKYFETSGDEAALERIQSELRSIDREISLISDTQNE DKYSIYNGNK
SSH24_Cv21 MAILVHQRNEIFSKLKYFETSGDEAALERIQSELRSIDREISLISDTQNE DKYSIYNGNK

SSH02_36f SSH24_Cv21	ESQQSKSEEITYKRWDIFKNFGLKGN ESQQSKSEEITYKRWDIFKNFGLKGN *****
GOE #71 SSH27_912c SSH01_Cv21	MIPVIQPGEVVLVDGTGIQSFDDGIYLINIGHGQQIKALQDRGDAVYVVSANPLYQPVPF MIPVIQPGEVVLVDGTGIQSFDDGIYLINIGHGQQIKALQDRGDAVYVVSANPLYQPVPF *****
SSH27_912c SSH01_Cv21	PSEFIGGKIYIKNKIERFN PSEFIGGKIYIKNKIERFN *****
GOE #72 SSH47_187b SSH77_912c	VFFKVLDPDGTALLNSNIDPEHKQTVVLHEVIRTVRARLGDQVIEIINRAYKLPKFNETG VFFKVLDPDGTALLNSNIDPEHKQTVVLHEVIRTVRARLGDQVIEIINRAYKLPKFNETG *****
SSH47_187b SSH77_912c	TSVPGAVRADRDI TSVPGAVRADRDI *****
GOE #73 SSH34_56a	*****
MNKKKIAIAVLVLLLLAMVSVLVMLYMSSGLLVKYLNLGDLTPHLSLPLDLAKFGTKKEKGFIIAMVSVGLPVMFLFGIIGYAALAPKKRE LHGSARFATRRELVKSGLLQSDKPDDQYPSILVGKQDKDFLFRGQQFMFLAAPTRSGKGVGIVIPNLLHYRDSVVVLDIKGENFEITSGFR AKCQGEVHKFAPDDENFQTACWNPLAYVRNDPRFRISDLMSITNILYPPSDDVWASTAERPVSWSGALHHGDV	
GOE #74 SSH03_912C	*****
VSHEGVLIILQTTEADTHFLDRRPRPRPRYSVVAEEVWNDKALLQNWREAEVHTNQALEQAGHSVRIDHRTLAEQGIERIPQIHIGPKVLEM ERRGIKTEIGGQALAEHKNKAITALQSDLETVRNERNHEDLPGRPLNSVVAEEVFAQWFMCPVRSCHYFST	
GOE #75 SSH06_912C	*****
VNKRQLIAAIVEKSGIKLTEDDPAFLLVLDNLMMLEKQTSEAAKQLEAATEKFNAVTTHNVDDFVSVANEALSKFMQRTNEIKSSLDDLKK LAQVANVTSTSSAHEVTKISHRSELLWWLVPRPRPR	
GOE #76 SSH09_912C	*****
MYQNYVARSQVTAGLAEITPGKVQAEILFSDAGTKTAITTPETIGLRTATTTRCSSIAVNLTPSAGTGTIVCTITGNSQVNGQTITWTRSDN TSGQGGTNNGGLWSCSTTVATTLSPTCTSTAKNG	
GOE #77 SSH011_912C	*****
MIVMKRLQAFKFQLRPNGQQRDMRRFAGACRFVFNRLALQNNENHEARNKYIPYTQMASWLIAWKSAPETQWLKESPSQPLQQSLKDLERG YRNFFQKRDLGRDHATEHVS	
GOE #78 SSH14_912C	*****
LSNEYSPDCAAAKECHQLTVGDYEDWHVPTLEEALSVIGADEFWYWGSGHVIWTCTPDLPGFERPPGQVLRSLIWLWLLWKISSKRMLYPAM YADAFSMMAMRPMAGNSSSSNRHWYKTSAAATLQLVHVQYKLLKKKIQKLTENVNIGRLHHHIDAHALFAHVAQIEDLPGRPLIRAAARA GLALLVWSEFRG	
GOE #79 SSH15_912C	*****
MHFIKNYDARQITKMISENGIKITLKEIKSILQNEKKSQ	
GOE #80 SSH16_912C	*****
LKPELASNNASLESDLIEKKAEIKKKQEEEAQAIKAEEDLPGHAPGRMAALASARPRSVDLTDMQS	

GOE #81[return to main table](#)

SSH21_912C

MLHFNAVGRTPFVERYKCALHDAIRAAARAGTRITQKRRKVRQYSQFNDALEGFPCEKYLGRDHAIICALLMGACTKEKVPSTSEYLGRTT
I**GOE #82**[return to main table](#)

SSH26_912C

MPISLLTGIPGGKTALMMERLVEESKRAERPLFAAGIDGLQPLATVLEDPRQWNAKDAEGNYLVPNGAMIFIDEAWKWFGLHDASRQPT
PHYVLETCPGGRSKPGQVFLQCRVCLVENGIYYQTKRF**GOE #83**[return to main table](#)

SSH30_912C

MDATEKQVANFAKVRTKIIEPAVKELTEKDGWIIQWVPVKAGRKVKALRFTFMRDPQGSLOF

GOE #84[return to main table](#)

SSH31_912C

MATKEERLKALELKQAQIKAQIQAIKARDTAQERKDDTRRKVLIGSVLKTSAATTL

GOE #85[return to main table](#)

SSH33_912C

MTTSRALRLGENPTSINVAPVGNACSSIAPAKSRVGEGLGRDHANAPGRMAAGLAWSRPRSPSTSTAKDIAVKERVDRMAILVHQNEIFS
KLKYFETSGDEAALERIQSELRSIDREISLISDTQNEDKYSIYNGNKESQQSKSEEIT**GOE #86**[return to main table](#)

SSH36_912C

LDDLISLRRQWTVDRERNFYLYEGGLTGNPAYEGVVYYCFYLYLNGTKFIVELDDEGGSLVFEDNPYVVWNKLVSIVMPHDQVSSLKRV
PPAAWDTDPAPQPLLQNYSLNQFISIFKEAVTVNGAGNSNRNIHHPIVVRFGF**GOE #87**[return to main table](#)

SSH39_912C

VIGDFMLTQEIDEICEMLGPFSLWGYIENAYATLPQQPDPAFEEERKKDFLFLIGKLLDEGRLKLAKKGKFMGTGTTEEQVEMFRKSFPA
SDEGMLLGAWFFADERPAGAVVVFKEGEGENGEYEWY**GOE #88**[return to main table](#)

SSH40_912C

MRSLPVATMPHDASMEARIVQLETIIPTLATKADVESLRADLPRPRPRYRAAARAGK

GOE #89[return to main table](#)

SSH53_912C

LKVVFIRRELVNLLTALCTEAGSNLEVLALDIQHDHRTVVEQVGNHDANALTRACRCQEHELLATEEQKILVLFYSYKNGWVLIIRFVRL

GOE #90[return to main table](#)

SSH65_912C

MYLPGRPLEPGQVPAFGRIGVDALVEVERCLAVFLGIAK

ORF91[return to main table](#)

SSH71_912C

VYWLWRRENITRRLKLQDIKQLFFCILCVSHIAVSPKRLRNALLDFIKKTFEPWRVITILSPPDSSGRPGRSQQIFLLISANTSQVAGLKL
PDLKDR***GOE #92**[return to main table](#)

SSH72_912C

MTQHGNKLASKDQAQRGVDMMNEFFGKSASVADITITRQEDFIKWLAEHGYTEGYCRRILGIGKSALNRSWKRGTEITQVPFVELPRIGEPP
HYASREQIVCLLNTDMPHEHIWAYFLIRLCTACRGDAARGLQRFQIDTDASVVAEVPRLYAMV**GOE #93**[return to main table](#)

SSH73_912C

VEARPHSIIIEADIIKEGAKIDEFSAISTGAVIGKKAYIGRNVSIGKNVSIGATQIYNSVEIGEDTTIGSNVVIYINCKIGKGVIIISDNVR
IGTDVEVYPHSSIANNIIVPDNAIVSGECPRPRPRYSSGRPGSRMH

GOE #94[return to main table](#)

SSH75_Fb7
MSTKEQAPVLNKLARLPQTFVEAAVDFEKSKEEIKRSRKIAWIIASVATVICSVSILAFVLALLTRSEPEPTILQVDKSTCPGGRSNCVPC
VTPKTTTMSSTSISGSSGRPGRYLRRLRLVHD

GOE #95[return to main table](#)

SSH01_Fb7
VTAYKKKPSEVGTWLKDEDQEITRGSVKLLREFLEEKMDQKETIDAEPEGNDQQWVDNDSANGKVVKAAKEVDPNKFERPPGQVLRTPCS
ISSDEASQ

GOE #96[return to main table](#)

SSH02_Fb7
MKHRVLVMNGQKIVQNEQTPGKWHTEHVDKAGLLKPGIYNIYAATVADKAKEHEGTIVHVDKQAIYQQIGKQFVKHECIDFYKIPEIGGVKR
IAYDQSTGRAQVDVASEKLAKKRSR

GOE #97[return to main table](#)

SSH05_Fb7
MEAIAEALKVPLTILLEYTDLDRNNLDMIDSRTQGLPPGYERVFVAVLPEHQAFIVKKWSKAAQKKLAGD

GOE #98[return to main table](#)

SSH06_Fb7
MQDEENHGSSVSARAIEKLRDDLGPVVMGALNDPETGEVLLKTFE

GOE #99[return to main table](#)

SSH08_Fb7
MDAISVVAEEVSSSGRPGRYLGLKPDNITKAGTVIYRVGSTAIRDDGDLNLSHGAGDYGVEAALRMAMYLGRDHATVKGSDEFKKRVVQIA
AAARLNISFDDEVLDRRKQLVSDAAVIVKLTDAMLSDKTAQFTQAQASRVGAFQEDALSEYDAAISRSINLANQEQINEQQRTRAKHYFVQ
RWSDRGGPNSRRDGHATRIRSGGNCQHDQSDILYDCL

GOE #100[return to main table](#)

SSH11_Fb7
MRMQLDNTALAVMAGLKSJVAAEVPPNEMETVQVLGRVIDRGGSGGL

GOE #101[return to main table](#)

SSH14_Fb7
MSKHEDFKGTKASMITLTKQEEKLLEAATAI

GOE #102[return to main table](#)

SSH15_Fb7
MDYYATEQPLPNDWKELYILTSAITAVEKAAVRKIIERFFTTIAEDGLHHNERVDKEIAKAQRRMVASRENGKKGGCPKKHKNPAGSENTVF
SEPKDNPAKTQPPPYSGVLRPRPR

GOE #103[return to main table](#)

SSH17_Fb7
MPYSPATIANANYFLQASKEGRALTPMQVFCLVYIAHGWHLGFRKEPLIDEVVEAWRHGFPVISSLYRKMKYGSGGITELLPVNPFWSWATASW
SNPVSKIDEKSAEILDSVWNGYGHFGGIQLSEMTHEKGSPPWQVWNGPKRKETGVINLTINDDLIQEFYEQIKAHKHGELYEKYRSNPDLG
RDHASIHQYSHRDGTE

GOE #104[return to main table](#)

SSH19_Fb7
MSISQVGLGLFRVWRGTSAAATTLHAPGRLAEEISVVAQVLRGRRHLFSTASSDDQHGADY

GOE #105[return to main table](#)

SSH23_Fb7
MIKVETRKPGEGMSFKSLGGPFAVSSVPVTDPAVLGNAYRKKRLLLASIRKLAKDLNLVKSKEFEDLDYEECGIEMYLERRYVARCIQEAHEY
MARFLGDIEGGVNV

GOE #106[return to main table](#)

SSH31_Fb7
MSFTGILKKTRVPISAFVFIFAGTAYAQLQVYDAANISTSIGNHVESIAKWKQQFEQLKQQIDQHQQYEAITGSRMGALLDNSALKASLP
SDWKQVPARASVVAEVLISAG

GOE #107[return to main table](#)

SSH32_Fb7
MGYEIQGILDHRRVHELAKVNGDLGRLGGLLKLWLNDARVVDFTPATIRNLLRKIEVTQDEIRAVMTQVVCK

GOE #108[return to main table](#)

SSH33_Fb7
VVAAEVLDAALEVQATQALNTRSEADKTYHLLISFREGENPAPEILEVIESRVCAALGYADYQQRVSVVHHTDNLHIHVAINKIHPKRYLPG
PHPLHELPAVWPPE

GOE #109[return to main table](#)

SSH37_Fb7
MDYFKMMAIQSKTAPEDFTLQTAIHALEDLLNEGKLTEKQIATLVGIGAIYREGFKQFQAGMHTNMFLSKFKNQE

GOE #110[return to main table](#)

SSH39_Fb7
MHESVQHCAHAPGRILAAGFRAAARAGTAAAPRHDMNKNQAAMHVEASKFIATNMQALQNQPNMADKSVEDLTCLAYWRGIVAENKLQPKAV
QDEAIARFDKQAADFPQLKRLNQETEPKIHDRTERVQQRDTHEQSL

GOE #111[return to main table](#)

SSH25_36f
VNKRQLIAAIVEKSGIKLTEDDPAFLLDNLMMLEKQTSEAAKQLEAATEKFNAVTTNHVDDFVSVANEALSKFMQRTNEIKSSLDDLSKK
LAQVANVTSTSSAHEVTKISHRSELLWW
LVPRPRPR

GOE #112[return to main table](#)

SSH32_36f
MLLNTNNIAVNRPAAEAGLEMLEAGGDFADGVIAYDGTWLGAEFTFVSFDKKAVSLLTKHGHAAARLL

GOE #113[return to main table](#)

SSH35_36f
LQRSKCLEKCPDVTGTVGTREEKRREDIKTKNNKIPDGILSASLDSEAPDIGEEHQNKKPPLSDRIPYLGRDHAIAWSRPRYPAYTQWCK
ESGVYALSKVRFLGELERCVPKFRNKRVARVDGKRRELVVIQIGLIDAGI

GOE #114[return to main table](#)

SSH36_36f
MLNFRFMVDDGFRADSHVLANENGISDTGILSKDGIVKNLDKVPDGYGFAYGNRIINVTMTTYI

GOE #115[return to main table](#)

SSH38_36f
VVFADFTGELVKVVPDIGNVRVQILDFFLLFPVCAELYFAA

GOE #116[return to main table](#)

SSH11_187b
MGESRVNLDYPDVIRSVEYTEAFIRSLIGFVPQKGRLPITGCGDSMIPVIQPGEVVLVDGTGQSFDGDGIYLINIGHGQQIKALQDRGDAV
YVVSANPLYQPVPFPSEGFIGGKIYIKNKIERFN

GOE #117[return to main table](#)

SSH18_187b
MWINLNISADTDVIRNNDADFADLAININNHITADGRVFSYFDVAVDLCRFTNRDVFANGDVAPNIGFFTDCACADRKGFINLGSFFNDVVR
LND

GOE #118[return to main table](#)

SSH22_187b
MYWRISKEKFAELDADNRIWWGKDGNNTPRLKRFLNEVKQGIVPQTLWTYSNVGHTQDAKKQLLDVLQFESSDVFSTPKPVPARASVVAEE
VLEALSKGLSQLRARPVTW

GOE #119[return to main table](#)

SSH32_187b
VQFERVRVADRSGEVLYDSDIQSNKQPNALEALAASRKLTDIKLAEITKAWSAVEAVARQRNASFAYLEAVSGHVQRLDDMQKERIHGHAMN
KLDENAATLVHDARYAQHTRSELAKAATLGPGRSNAIAWSRPRYRTQCWWCCCFA

GOE #120[return to main table](#)

SSH03_56a
MGDGYESDAPLEIIDYLEVKESWALLNLRPRPYDRVKIIIGRGNSNAPLINDGDLVFVDTSINSFIGEDIYVFVNWNGKALIKRLAVNLKTNTL
RIISANPDWVPARAAARTSVVAAEVPTSIVLNATRYTGKSDA

GOE #121[return to main table](#)

SSH12_56a
MPYPASRYAVMDSISIKYLGRDHANPSASSVVAAEVFQKYSQGSFMDKLHKVGLSCSVVAAEVQEKR

GOE #122[return to main table](#)

SSH21_56a
MALMRDADKSTSSRTQELFDLAKSSHSDKKGIEQEL

GOE #123[return to main table](#)

SSH22_56a
MKKLNVTLKIMCNTKLQHTQKQASRISYKNQNAIPPMRKIVDLKIVFPQYKLMF

GOE #124[return to main table](#)

SSH27_56a
METIGSRVRKEREQNINRSDFAKKTGIGYSTIAELERGGMQTTKLRLIADALGVSLRWLETGKGEKIEATTATKSIATEKISQHYIRVEH
LDAEAGMGESRVNLDPDVIRSVEYTEAFIRSLIGFVPARTAARKLAAIRAGSMITWSRPRY

GOE #125[return to main table](#)

SSH34_56a
MNKKKIAIAVLVLLLLAMVSVLVMLYMSSGLLVKYNLGDLTPHLSLPLDLAKFGTKKEKGFGIIAMVSVGLPVMFLGIIGYAALAPKKRE
LHGSARFATRRELVKSGLLQSDKPDDQYPSILVGKQDKDFLFRGQQFMFLAAPTRSGKGVGIVIPNLLHYRDSVVVLDIKGENFEITSGFR
AKCQGEVHKFAPDDENFQTACWNPLAYVRNDPRFRISDLMSITNILYPPSDDVWASTAERPVSWSGALHHGDV

GOE #126[return to main table](#)

SSH04_Cv21
MCASGVTRFNISKRFKVCIPIPSTAIQYEIVKVLDTFTTLEARRRQYQYRDALLRFGEGRDAATRVRWVTLGEIGSFIRGVGIQKSDFI
EFGAGCIHYGQIHTHYGTWADKTKSFIRSDFAARLRKANTGDLVMAALRAKMMHSSVVVAEVC

GOE #127[return to main table](#)

SSH05_Cv21
MVAVSLQSLCELWVLRSLRYGAARTDIAAALRMLLNTNNIAVNRPAEEAGLEMLEAGGDFADGVIAIDGTWLGAETFVSFDDKKAVALSLTKHG
HAARLL

GOE #128[return to main table](#)

SSH07_Cv21
MVDYKPLTDNEVRDTAVAYYTERQGKSLAKENPIIVLVGGQPGAGKSTASSMVKAETCPGGRSNSVVAAEVCVVMKHGITSWP

GOE #129[return to main table](#)

SSH12_Cv21
LALIRSILRRAFDIWLWIDRCPHISLFPEPTKRVRWLTPVQARSLLSELPLHQRAIVIFALATGLRQANVLKLRWGQVDLVRKVLRIADQA
KGRQAIRIPLSFHALQVLQAQRGQHHEWVFTYCGRPRIWVNTRAWHQALQRAGIQDFRWHDLRHTWASWHAQAGTPLYVLQDLGGWQSESMV
RRYAHLTPSHYSAYAEAVTEFLP

GOE #130[return to main table](#)

SSH20_Cv21
MKKAIGGAVAMTILLAGCGRKTDANEKNFGTAVGQYLDKKGDLCLNITKWPVDVNDMDLRLQKSMPTGTAGRMAALEAVGLAKSEYTEVQGT
GFDGKPTGVKFKVKRYALTDAAKPFERQQGVERVDLNGRTKETQTDLCWGKKALDKVVKWEGPMKFGDYHGRGRGTCTRTAWPIGRKSRKS
WQSPMSDKSRKMLARKSSSTA

GOE #131[return to main table](#)

SSH26_Cv21
MAGLRPVQIWWPDTRRPDFAEECRRQCLLVAQADSADTAIHQFMDEALADVDCWAE

GOE #132[return to main table](#)

SSH27_Cv21

VVAAEVNKSAGELLADLNKSAGELRADFEKAQKENRTWMLATAIGLFAGILGVGGFVVGSIKGSYQALPAQSPPIIIQVPAQALQPPPQAAK
QP

GOE #133

[return to main table](#)

SSH33_Cv21

LNAAQRSLANSNRSLQQGQERTFIVWTRIDNPNGVFANIDSPATDQMGYSGIPGYVDTHFWQRFGSAIMLSLIKDFSQAYSQRVANRSNTGT
TVIQPYANTTQATQDMGAEALRNSINIPPTLVVLPATAVNMVARDVSFENVFNLVE

GOE #134

[return to main table](#)

SSH36_Cv21

MQCVLPPIVPINNHAPRPIFNDDVCQAHMHGTEFFFNAAQQVQTGSTTGDKAEVLVNNLPTKR

GOE #135

[return to main table](#)

SSH45_Cv21

VRQEVILAEKAKGYKTTLKGFRLLYRARIRAAQNPEKFQTKVEQKNEKEDAQLLAKKSENKKEEVSKNPLKKAGFDKGTNSFDESDLI