

## Supplemental Figure 1: Alignment of HetN-like proteins

MAST-10914-SCAD-B	0	-----	-----	-----	-----	-----
Cal-6303.p-Cal-6303-1520 (5.0d-28)	0	-----	-----	-----	-----	-----
Npun.p-NpF2349 (4.0d-29)	0	-----	-----	-----	-----	-----
N-7107.p-N-7107-0937 (1.0d-27)	0	-----	-----	-----	-----	-----
Ana-90.p-ana90-1712 (1.0d-28)	0	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-4545 (9.0d-28)	0	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-2353 (9.0d-27)	0	-----	-----	-----	-----	-----
Cyl-505.p-Cyl-505-0204 (2.0d-28)	0	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-2349 (6.0d-29)	0	-----	-----	-----	-----	-----
R7116-SCAD-C	0	-----	-----	-----	-----	-----
ter.p-Tery_3438 (2.0d-28)	0	-----	-----	-----	-----	-----
lyn.p-18106?21814 (1.0d-27)	0	-----	-----	-----	-----	-----
Amar.p-AM1_5632 (1.0d-26)	0	-----	-----	-----	-----	-----
cyr.p-c8801?2930 (1.0d-28)	0	-----	-----	-----	-----	-----
S6803.p-Slr0886 (4.0d-27)	0	-----	-----	-----	-----	-----
mae.p-MAE_33900 (3.0d-29)	0	-----	-----	-----	-----	-----
TeBP1.p-tlr1502 (5.0d-29)	0	-----	-----	-----	-----	-----
S7942.p-Synpcc7942_0684 (4.0d-26)	0	-----	-----	-----	-----	-----
syx.p-SynWH7803_1861 (7.0d-30)	0	-----	-----	-----	-----	-----
S7805.p-WH7805_13603 (5.0d-28)	0	-----	-----	-----	-----	-----
S9916.p-RS9916_33507 (8.0d-31)	0	-----	-----	-----	-----	-----
Ssp-RS9917.p-Ssp-RS9917-1614 (2.0d-29)	1	MWCWHPVNCW	WCLAARANCG	CCGICSVPPS	TWWKRWGARG	AADPCLRSRA
S9917.p-RS9917_09056 (3.0d-29)	0	-----	-----	-----	-----	-----
syg.p-sync_2137 (4.0d-29)	0	-----	-----	-----	-----	-----
P9313.p-PMT1333 (6.0d-29)	0	-----	-----	-----	-----	-----
pmf.p-P9303_06521 (1.0d-28)	1	-----	-----	-----	-----	-----MGPY
S107.p-BL107_09856 (2.0d-28)	1	-----	-----	-----	-----	-----LREKASDLY
S9902.p-Sync9902_1745 (4.0d-28)	0	-----	-----	-----	-----	-----
S9605.p-Sync9605_0617 (4.0d-27)	1	-----	-----	-----	-----	-----MSMAPY
S8102.p-SynW1852 (9.0d-28)	0	-----	-----	-----	-----	-----
syr.p-SynRCC307_0681 (2.0d-28)	0	-----	-----	-----	-----	-----
S5701.p-WH5701_07809 (1.0d-28)	0	-----	-----	-----	-----	-----
pmn.p-PMN2A_1785 (5.0d-28)	0	-----	-----	-----	-----	-----
pme.p-NATL1_05081 (1.0d-27)	0	-----	-----	-----	-----	-----
pmz.p-p9211?06582 (1.0d-27)	0	-----	-----	-----	-----	-----

PRO1375.p-Pro0452	(7.0d-27)	0	-----	-----	-----	-----	-----
Gvi.p-glr3506	(5.0d-28)	0	-----	-----	-----	-----	-----
pmb.p-P9601_05091	(9.0d-28)	0	-----	-----	-----	-----	-----
pmi.p-PMT9312_0453	(1.0d-27)	0	-----	-----	-----	-----	-----
pmg.p-P9301_04781	(1.0d-27)	0	-----	-----	-----	-----	-----
PMED4.p-PMM0453	(9.0d-28)	0	-----	-----	-----	-----	-----
pmc.p-P9515_05161	(2.0d-27)	0	-----	-----	-----	-----	-----
Npun.p-NpR0578	(6.0d-27)	0	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-0303	(5.0d-26)	0	-----	-----	-----	-----	-----
Npun.p-NpF2231	(1.0d-26)	0	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-3400	(1.0d-26)	0	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-3225	(4.0d-28)	0	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-2459	(6.0d-26)	0	-----	-----	-----	-----	-----
Ana-90.p-ana90-1189	(1.0d-28)	0	-----	-----	-----	-----	-----
Cyl-505.p-Cyl-505-2036	(2.0d-32)	0	-----	-----	-----	-----	-----
A29413.p-Ava2536	(2.0d-28)	0	-----	-----	-----	-----	-----
A7120.p-Alr5286	(2.0d-28)	1	-----	-----	-----	-----	-----MTR
N-7524.p-N-7524-4179	(1.0d-27)	0	-----	-----	-----	-----	-----
MAST-10914-SCAD-C		0	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-1063	(4.0d-30)	0	-----	-----	-----	-----	-----
nod.p-n9414?21215	(5.0d-26)	0	-----	-----	-----	-----	-----
N-7107.p-N-7107-1008	(2.0d-29)	0	-----	-----	-----	-----	-----
M7126-SCAD-A		0	-----	-----	-----	-----	-----
R7116-SCAD-B		0	-----	-----	-----	-----a-----	-----
lyn.p-l8106?23630	(2.0d-26)	0	-----	-----	-----	-----	-----
Amar.p-AM1_5634	(3.0d-27)	0	-----	-----	-----	-----	-----
cyb.p-CYB_0189	(1.0d-27)	0	-----	-----	-----	-----	-----
cya.p-CYA_2793	(8.0d-26)	0	-----	-----	-----	-----	-----
M7126-SCAD-D		0	-----	-----	-----	-----	-----
cyb.p-CYB_0005	(4.0d-34)	0	-----	-----	-----	-----	-----
cya.p-CYA_0005	(2.0d-33)	0	-----	-----	-----	-----	-----
N-7107.p-N-7107-5182	(3.0d-28)	0	-----	-----	-----	-----	-----
Npun.p-NpR3707	(3.0d-27)	0	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-1205	(2.0d-26)	1	-----	-----	-----	-----MLNFK	STVTLSRYSI
R7116-SCAD-F		1	-----	-----	-----	-----	-----V
Npun.p-NpF0204	(3.0d-28)	0	-----	-----	-----	-----	-----
MAST-10914-SCAD-D		0	-----	-----	-----	-----	-----
Cal-6303.p-Cal-6303-3407	(1.0d-27)	0	-----	-----	-----	-----	-----
Ana-90.p-ana90-4359	(1.0d-27)	0	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-4762	(6.0d-27)	0	-----	-----	-----	-----	-----

Nsp-0708.p-Nsp-0708-3536	(2.0d-26)	0	-----	-----	-----	-----	-----
N-7107.p-N-7107-1296	(2.0d-26)	0	-----	-----	-----	-----	-----
Npun.p-NpR1019	(4.0d-26)	0	-----	-----	-----	-----	-----
N-7524.p-N-7524-4265	(1.0d-25)	0	-----	-----	-----	-----	-----
M7126-SCAD-E		0	-----	-----	-----	-----	-----
R7116-SCAD-E		0	-----	-----	-----	-----	-----
cyt.p-cce_3588	(3.0d-27)	0	-----	-----	-----	-----	-----
ctc.p-c0110?06289	(2.0d-26)	0	-----	-----	-----	-----	-----
cyr.p-c8801?0598	(2.0d-26)	0	-----	-----	-----	-----	-----
Amar.p-AM1_6363	(1.0d-30)	0	-----	-----	-----	-----	-----
Amar.p-AM1_0210	(1.0d-27)	0	-----	-----	-----	-----	-----
lyn.p-l8106?00785	(4.0d-31)	0	-----	-----	-----	-----	-----
ter.p-Tery_3453	(8.0d-31)	0	-----	-----	-----	-----	-----
A29413.p-Ava0943	(1.0d-30)	1	-----	-----	-----	-----	----MDLYSS
A7120.p-All2963	(5.0d-29)	1	-----	-----	-----	-----	----MDLYSS
Npun.p-NpR4797	(3.0d-30)	0	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-4424	(3.0d-30)	0	-----	-----	-----	-----	-----
MAST-10914-SCAD-E		0	-----	-----	-----	-----	-----
M7126-SCAD-C		0	-----	-----	-----	-----	-----
R7116-SCAD-D		0	-----	-----	-----	-----	-----
Npun.p-NpF0199	(2.0d-29)	1	-----	-----	-----M	NINYQNLPIF	TLFIIGALLS
A7120.p-Alr5358	(3.0d-156)	0	-----	-----	-----	-----	-----
A29413.p-Ava2596	(8.0d-151)	0	-----	-----	-----	-----	-----
N-7524.p-N-7524-5224	(2.0d-121)	0	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-1544	(2.0d-100)	0	-----	-----	-----	-----	-----
MAST-10914-SCAD-A		0	-----	-----	-----	-----	-----
N-7524.p-N-7524-5355	(2.0d-74)	0	-----	-----	-----	-----	-----
Npun.p-NpF3363	(2.0d-81)	0	-----	-----	-----	-----	-----
R7116-SCAD-A		0	-----	-----	-----	-----	-----
cyr.p-c8801?3820	(4.0d-26)	0	-----	-----	-----	-----	-----
A7120.p-All1418	(8.0d-26)	0	-----	-----	-----	-----	-----
consensus		1					

A7120.p-Alr1894	(1.0d-26)	1	----MAILSE	NLR---GQVA	VVTGASRGIG	RAIALELANY	GATVVVNYAS
A29413.p-Ava3764	(1.0d-26)	1	----MAILSE	NLR---GQVA	VVTGASRGIG	RAIALELANY	GATVVVNYAS
N-7524.p-N-7524-0010	(9.0d-30)	1	----MAILSE	NLK---GQVA	IVTGASRGIG	RAIALELSTY	GATVVVNYAS
M7126-SCAD-B		1	----MAVLSE	NLPNLQEKVA	IVTGASRGIG	RAIALELSQY	GASVVVNYAS
nod.p-n9414?22428	(4.0d-28)	1	----MKLLQ-	-----GQVA	IITGASRGIG	RAIALELATQ	GATIIIVNYAN
MAST-10914-SCAD-B		1	----MELLPD	NLQSLRGQVA	LVTGASRGIG	RAIAQELAKQ	GANVVVNYAS
Cal-6303.p-Cal-6303-1520	(5.0d-28)	1	----MELLPE	NLQTLRGQVA	IVTGASRGIG	RAIALELSKQ	GATLVVNYAA
Npun.p-NpF2349	(4.0d-29)	1	-----	-MTLLQGKVA	IVTGASRGIG	KAI AIELASQ	GAI VVNYAS
N-7107.p-N-7107-0937	(1.0d-27)	1	----MEVLPG	NLQSLK GKVA	IVTGGSRGIG	KAI AIELAKY	GASVAVNYAS
Ana-90.p-ana90-1712	(1.0d-28)	1	-----	-MSLLKDQVA	IVTGASRGIG	RAIAIQLASQ	GAKVVVNYAS
Acyl-7122.p-acyl-4545	(9.0d-28)	1	-----	-MTLLKDQVA	IVTGASRGIG	RAIALQLASQ	GAKVVVNYAS
Nsp-0708.p-Nsp-0708-2353	(9.0d-27)	1	-----	-MTLLHDQVA	IVTGASRGIG	RAITLQLASQ	GAKVVINYAN
Cyl-505.p-Cyl-505-0204	(2.0d-28)	1	-----	-MTSVKDQVA	IVTGASRGIG	RAIALQLAEK	GAKIVVNYAS
Cyl-7417.p-Cyl-7417-2349	(6.0d-29)	1	----MELMPE	NLQSLQNOVA	IITGASRGIG	RAIALELATQ	GAKVVINYAQ
R7116-SCAD-C		1	----MELMPE	NLQSLREQVA	VVTGASRGIG	RAIAQELAKL	GASVVVNYAS
ter.p-Tery_3438	(2.0d-28)	1	----MEALPE	TLQRLK GKVA	IVTGASRGIG	RATALALAME	GANVVVNYAK
lyn.p-l8106?21814	(1.0d-27)	1	----MDVLPE	TQQHLKEQVA	IVTGASRGIG	RAIAIALASL	GANIVVNYAS
Amar.p-AM1_5632	(1.0d-26)	1	-----	-MNSLQDKVA	IVTGASRGIG	RATALALAGE	GAKVAINYAN
cyr.p-c8801?2930	(1.0d-28)	1	-----	-MA DSQALSEQVA	IVTGASRGIG	KAI ALALASQ	GLKVVVNYAR
S6803.p-Slr0886	(4.0d-27)	1	-----	-MTALTAQVA	LVTGASRGIG	KATALALAAAT	GMKVVVNYAQ
mae.p-MAE_33900	(3.0d-29)	1	----MKLLPA	ECQHLDQKVA	IVTGASRGIG	KAI ALELASQ	GATVVVNYAK
TeBP1.p-tlr1502	(5.0d-29)	1	-----	---MSETAVA	IVTGASRGIG	RAIALELAKE	GATVVVNYAR
S7942.p-Synpcc7942_0684	(4.0d-26)	1	-----	-M TALPLTDRIA	LVTGASRGIG	RAIALELAAA	GAKVAVNYAS
syx.p-SynWH7803_1861	(7.0d-30)	1	-----	-MN PTRTLDGQTA	LVTGASRGIG	RAVALALAEK	GAEVVNYAS
S7805.p-WH7805_13603	(5.0d-28)	1	-----	-MN PTRTLDGQTA	LVTGASRGIG	RAVALALAEK	GAEVVNYAS
S9916.p-RS9916_33507	(8.0d-31)	1	-----	-MT THASLAGQTA	LVTGASRGIG	RAVAQALAEA	GAEVVNYAS
Ssp-RS9917.p-Ssp-RS9917-1614	(2.0d-29)	51	IDHRCRAAMT	TSAPMTGQTA	IVTGASRGIG	RCVALALADA	GAEVVNYAR
S9917.p-RS9917_09056	(3.0d-29)	1	-----	-MT TSAPMTGQTA	IVTGASRGIG	RCVALALADA	GAEVVNYAR
syg.p-sync_2137	(4.0d-29)	1	-----	-MS SSASLDGQTA	LVTGASRGIG	RAVALALAAE	GAEVVNYAS
P9313.p-PMT1333	(6.0d-29)	1	-----	-MT SPRPLTGQTA	LITGASRGIG	RAVALALAEA	GAEVVNYSS
pmf.p-P9303_06521	(1.0d-28)	5	DPARTNHAMT	SNPPLTGQTA	LITGASRGIG	RAVALALAEA	GAEVVNYSS
S107.p-BL107_09856	(2.0d-28)	10	DPSIFSSAMS	PTTSLAGQTA	LVTGGGRGIG	KAI ALALGEA	GAEVVNYSS
S9902.p-Syncc9902_1745	(4.0d-28)	1	-----	-MS PTTSLAGQTA	LVTGGGRGIG	KAI ALALGEA	GAEVVNYSS
S9605.p-Syncc9605_0617	(4.0d-27)	7	DPAINGALMS	PSASLAGQTA	LVTGGGRGIG	RAIALALGEA	GAEVVNYSS
S8102.p-SynW1852	(9.0d-28)	1	-----	-ML SSASLDGQTA	LVTGGGRGIG	KAI ALALAEA	GAEVVNYAN
syr.p-SynRCC307_0681	(2.0d-28)	1	-----	-MS SLAPLAGQIA	LVTGASRGIG	RAIALQLAEA	GAEVVNYAS
S5701.p-WH5701_07809	(1.0d-28)	1	-----	-MTGS AVAPLTGQVA	LVTGASRGIG	RAIALELAAS	GAEVVNYAA
pmn.p-PMN2A_1785	(5.0d-28)	1	-----	-MT LSKLLEGQTA	IVTGASRGIG	KAI AIFLAKE	GAEVIINYSS
pme.p-NATL1_05081	(1.0d-27)	1	-----	-MT LSKLLEGQTA	IVTGASRGIG	KAI AIFLAKE	GAEVIINYSS

pmz.p-p9211?06582 (1.0d-27)	1	-----MT	NQNLCCEGQTV	LVTGASRGIG	RAIALNLATT	GAEIVVNYAN
PRO1375.p-Pro0452 (7.0d-27)	1	-----MT	SSSLLIGQTA	IVTGASRGIG	KAIALNLAQA	GAEVVVNYAN
Gvi.p-glr3506 (5.0d-28)	1	-----	MTGLLTGKVA	LVTGAGRGIG	RACALALASE	GAHAVVNYSR
pmb.p-P9601_05091 (9.0d-28)	1	-----MS	NTDSLSGKVA	LITGASRGIG	KEIALELSRL	GAEVFINYSS
pmi.p-PMT9312_0453 (1.0d-27)	1	-----MS	NTALLSGKVA	LITGASRGIG	KEIALELSRL	GAEVFINYSS
pmg.p-P9301_04781 (1.0d-27)	1	-----MS	NTDSLSGKVA	LITGASRGIG	KEIALELSRF	GAEVFINYSS
PMED4.p-PMM0453 (9.0d-28)	1	-----MS	NTESLTGKVA	LITGASRGIG	KEIALELSNL	GAKVIINYSS
pmc.p-P9515_05161 (2.0d-27)	1	-----MS	NKESLTGKVA	LITGASRGIG	KEIALELSNL	GAEVIINYSS
Npun.p-NpR0578 (6.0d-27)	1	-----MTKN	ENGNYTGKVA	FVTGAANGIG	RATALAFARE	GANVVVADVS
Cyl-7417.p-Cyl-7417-0303 (5.0d-26)	1	-----	MDLQLQGKRV	LITGSTSGIG	EAIKALAKE	GARVVV-HGR
Npun.p-NpF2231 (1.0d-26)	1	-----	MSKQLENKVV	IVTGAGKGIG	RAIALAFAVE	GAHIVIADKS
Cyl-7417.p-Cyl-7417-3400 (1.0d-26)	1	-----	MSEQLIDKVA	IVTGAGKGIG	RAIALTFASE	GANVIIADKS
Acyl-7122.p-acyl-3225 (4.0d-28)	1	-----	-MSFEQKRRA	LITGASSGIG	KATALAFAKA	GIDVALVSRS
Nsp-0708.p-Nsp-0708-2459 (6.0d-26)	1	-----	-MSFDQKRRA	LITGASSGIG	KATALAFAKA	GIDVALVSRS
Ana-90.p-ana90-1189 (1.0d-28)	1	-----	-MNFEQKRRA	LITGASSGIG	KATALAFAKA	GIDVALVSRS
Cyl-505.p-Cyl-505-2036 (2.0d-32)	1	-----	-MSFEKKKRA	LITGASAGIG	KETAIAFAKE	GIDVALVSRS
A29413.p-Ava2536 (2.0d-28)	1	-----	-MSLEQKRRA	LITGASSGIG	KATALAFAKA	GIDVALVSRS
A7120.p-Alr5286 (2.0d-28)	4	ACKTAKKLGE	SMSLEQKRRA	LITGASSGIG	KATALAFAKA	GIDVALVSRS
N-7524.p-N-7524-4179 (1.0d-27)	1	-----	-MSLEQKRRA	LITGASSGIG	KATALAFAKA	GIDVALVSRS
MAST-10914-SCAD-C	1	-----LGD	SMSVEQKRRA	LITGASSGIG	KATALAFAKA	GIDVALVSRS
Cyl-7417.p-Cyl-7417-1063 (4.0d-30)	1	-----	-MSVEQKRRA	LITGASSGIG	KATALAFAKA	GIDVALVSRS
nod.p-n9414?21215 (5.0d-26)	1	-----	-MSLD-KRRA	LITGASSGIG	KATALAFAKA	GIDVALVSRS
N-7107.p-N-7107-1008 (2.0d-29)	1	-----	-MSSKQKQNA	LITGASSGIG	KATALAFAKA	GIDVALVSRS
M7126-SCAD-A	1	-----	-MSVEQKQQA	LITGASSGIG	KATALALAKA	GINVALVSRS
R7116-SCAD-B	1	-----	--MSELKKRA	LITGASSGIG	KQTALAFASS	GIDVALLGRS
lyn.p-l8106?23630 (2.0d-26)	1	-----	-MTSPIERRA	LITGASSGIG	KATALAFAKA	GIHVALVSRS
Amar.p-AM1_5634 (3.0d-27)	1	-----	-MTAQRKLRA	LITGASRGIG	RATAEFAAAS	NIDLVLVSRS
cyb.p-CYB_0189 (1.0d-27)	1	-----M	SFETKFPERA	LITGASRGIG	RAVALALARQ	GIAVALVARS
cya.p-CYA_2793 (8.0d-26)	1	-----M	SFETQFPERA	LITGASRGIG	KAVALLALARQ	GVAVALVARS
M7126-SCAD-D	1	-----	--MRLKNQVV	IITGASRGLG	RATALLFGKE	GAHIIAASRS
cyb.p-CYB_0005 (4.0d-34)	1	-----	-MPSLANQVV	LITGASAGIG	EAVALEAAKR	GARLVLAARR
cya.p-CYA_0005 (2.0d-33)	1	-----	-MLSLANQVV	LITGASAGIG	KAVALEAAKR	GARLVLAARR
N-7107.p-N-7107-5182 (3.0d-28)	1	-----	MTIKLNGKVA	IITGASSGIG	EATAIALAAE	GATVAIAARR
Npun.p-NpR3707 (3.0d-27)	1	-----	MTGKLKEQVA	IITGASAGIG	EATAIALAAE	GATVVIAARR
Acyl-7122.p-acyl-1205 (2.0d-26)	16	FKLINQWVFT	MAGKLDGKVA	IITGASSGIG	KGTAIALATE	GAKVVIAARR
R7116-SCAD-F	2	WIVNYQLTSS	PMTSIQNQIV	LITGASSGIG	ASCVKYFAEA	GAKLVLAARR
Npun.p-NpF0204 (3.0d-28)	1	-----MAI	SLKPLRNQVV	VITGASSGIG	LVTARMAAKQ	GAKLVLAARN
MAST-10914-SCAD-D	1	-----	--MNIQ GKTA	LVTGASRGIG	QAI AIELAKQ	GVKRLLLVAR
Cal-6303.p-Cal-6303-3407 (1.0d-27)	1	-----	--MDIQ GKTA	LVTGASRGIG	RAIAISLAKQ	KAKRLLLVAR
Ana-90.p-ana90-4359 (1.0d-27)	1	-----	--MKIQ GKVA	LITGASRGIG	KAI AIELAKQ	GMKRLLILVAR

Cyl-7417.p-Cyl-7417-4762	(6.0d-27)	1	-----	--MNIRGKVA	LITGASRGIG	RAIAFELAKL	GMKRLILVAR
Nsp-0708.p-Nsp-0708-3536	(2.0d-26)	1	-----	--MNIQGVKVA	LITGASRGIG	KAIALELAQQ	GVKRLILVAR
N-7107.p-N-7107-1296	(2.0d-26)	1	-----	--MKIQGNVA	LITGASRGIG	KAIALALAQQ	GMKKLILVAR
Npun.p-NpR1019	(4.0d-26)	1	-----	--MEIQGVKVA	LITGASRGIG	RAIALELAQV	GIKRLILVAR
N-7524.p-N-7524-4265	(1.0d-25)	1	-----	--MNLQGVKVA	LITGASRGIG	RAIAIELAQQ	GVQRLILVAR
M7126-SCAD-E		1	-----	--MKIQGVKVA	LITGASRGIG	RAIALELAQQ	GIKRVILLAR
R7116-SCAD-E		1	-----	---ME	VIMIIQGCTA	LITGASRGIG	RAIAIQLAHQ
cyt.p-cce_3588	(3.0d-27)	1	-----	---MKEV	FFMNIQGVKTA	LITGASRGIG	RAIALELARN
ctc.p-c0110?06289	(2.0d-26)	1	-----	---MEV	FFMNIQGVKTA	LVTGASRGIG	RAIALELAKN
cyr.p-c8801?0598	(2.0d-26)	1	-----	--MKLLGKTG	LITGASRGIG	RAITLELAHQ	GFKRLLLVAR
Amar.p-AM1_6363	(1.0d-30)	1	-----	--MKIQGVKTA	LITGASRGIG	RAIAKELAQQ	GMDKVILVAR
Amar.p-AM1_0210	(1.0d-27)	1	-----	--MRLKNKTA	LITGASRGIG	KAIALELAQQ	GIARLILVAR
lyn.p-l8106?00785	(4.0d-31)	1	-----	-----	MVSTV	LITGASQGS	KATALLFAQK
ter.p-Tery_3453	(8.0d-31)	1	-----	-----	MLPTV	LITGASQCG	RETALLFARK
A29413.p-Ava0943	(1.0d-30)	7		IFRCFCIVEA	QVNSYMTNTV	IITGASQIG	KATALLFARQ
A7120.p-A112963	(5.0d-29)	7		IFRCLCIVEA	QVNSYMTNTV	IITGASQIG	KATALLFARH
Npun.p-NpR4797	(3.0d-30)	1	-----	-----	MAPT	LITGASEGIG	KATALLFARQ
Cyl-7417.p-Cyl-7417-4424	(3.0d-30)	1	-----	-----	MAPT	LITGASQIG	KATALLFSRK
MAST-10914-SCAD-E		1	-----	-----	MAPT	LITGASQIG	KATSLLFARK
M7126-SCAD-C		1	-----	-----	MAPT	IITGASQIG	KATALLFAQQ
R7116-SCAD-D		1	-----	-----	MPSA	IITGGSQIG	KATALLFARK
Npun.p-NpF0199	(2.0d-29)	22		SLLLDLDRWWRD	RIYNLNGKTV	LITGGSRGLG	LVMARQLIQA
A7120.p-Alr5358	(3.0d-156)	1	-----	-----	MTTLTGKTV	LLTGASRGLG	VYIARALAKE
A29413.p-Ava2596	(8.0d-151)	1	-----	-----	MTTLTGKTV	LLTGASRGLG	VYIARALAKE
N-7524.p-N-7524-5224	(2.0d-121)	1	-----	-----	MTTLTGKTV	LLTGASRGLG	IHIARALAKE
Cyl-7417.p-Cyl-7417-1544	(2.0d-100)	1	-----	-----	MKILADKTV	LLTGASRGLG	VYIARVLARE
MAST-10914-SCAD-A		1	-----	-----	MKTIAGKTV	VLTGASGGIG	VFIARALARE
N-7524.p-N-7524-5355	(2.0d-74)	1	-----	-----	MKSIAGKTV	LLTGATGGIG	VFIARALAKE
Npun.p-NpF3363	(2.0d-81)	1	-----	-----	MTSIAGKTV	LLTGASRGIG	VFIARALAKE
R7116-SCAD-A		1		LLLMSNAQFR	PINNIEGKTV	ILTGASRGIG	AFIARELAKK
cyr.p-c8801?3820	(4.0d-26)	1	-----	-----	MTTKTA	LITGASFGIG	TAFQAELAAR
A7120.p-A111418	(8.0d-26)	1	----	MFRLET	PSMSFTNKTI	VLTGASAGIG	RMLAISLSQQ
consensus		51					DANLVLAARN

.:\*\*.\* \*\*

A7120.p-Alr1894	(1.0d-26)	44	SSTAADDEVVA	EITGAG--GE	AVALKADVSQ	VEQVDNLING	AIDKFK--RI
A29413.p-Ava3764	(1.0d-26)	44	SSTAADDEVVA	EITGAG--GE	AVALQADVSQ	VDQVDNLIDG	AIDKFK--HI
N-7524.p-N-7524-0010	(9.0d-30)	44	SSGAADNLVA	EITGAG--GE	AIALQADVSQ	ADQVDALINA	VMDKFK--RV
M7126-SCAD-B		47	SSGAADSLVA	EISGAG--GE	AIAIQADVSQ	AEQVDALFNT	VIDKFK--RV
nod.p-n9414?22428	(4.0d-28)	40	YSGAAESVVA	DIIADG--GQ	AIALQADVSQ	AQQVDTLIST	VMEKFK--RI
MAST-10914-SCAD-B		47	SNHAAEEVVD	TITKAG--GS	AIALQADVSQ	VSQVEALVNT	VMEKFN--RV
Cal-6303.p-Cal-6303-1520	(5.0d-28)	47	SSSAADAVVD	TITQAG--GN	AVALQADVSK	TEEVDALINA	VMEKFK--RV
Npun.p-NpF2349	(4.0d-29)	40	SSAAAEAVVT	EITAVG--GQ	AIAIQADVSK	GDQVDALVNA	VMEKFS--RV
N-7107.p-N-7107-0937	(1.0d-27)	47	SSTAADDEVVT	DITAVG--GQ	AIALQADVSQ	ADQVEGLINA	TTEKFG--RV
Ana-90.p-ana90-1712	(1.0d-28)	40	SSTAADDEVVA	EITAAG--GE	AIALQADVSQ	ENQVDTLIKT	TLEKFK--RV
Acyl-7122.p-acyl-4545	(9.0d-28)	40	SSAAAEVVA	EIIANG--GD	AFALKADVSQ	PDQVDTLINT	TVEKYK--RV
Nsp-0708.p-Nsp-0708-2353	(9.0d-27)	40	SSAAADQLVA	KITAKG--GD	AITLQADVSQ	SDQVDTLINT	TLEKFK--RI
Cyl-505.p-Cyl-505-0204	(2.0d-28)	40	SSTAAEKVVS	EIIALG--GE	AIALQADVSQ	AGQVEDMVNK	TLETFN--RI
Cyl-7417.p-Cyl-7417-2349	(6.0d-29)	47	SSAAADKVVV	EITAAG--GI	AIALQADVSQ	VDQVDALVKL	VTDKFK--RI
R7116-SCAD-C		47	SSKAADDELVA	EITAAG--GS	AIALQADVSS	SEEVDKLINT	VLEKFK--KI
ter.p-Tery_3438	(2.0d-28)	47	SSDTAEVVA	EIVAAG--GN	GLALQADVSQ	VEEVDNLIKE	VMEKWS--RV
lyn.p-l8106?21814	(1.0d-27)	47	SSGAADELVE	EITNSG--GN	AIALCADVSQ	AEQVDTLINT	VMEKWG--RV
Amar.p-AM1_5632	(1.0d-26)	40	SSGAADAVVA	EITGQG--GE	ALALQANVAE	ADQVDTLFKT	VLDKWG--RA
cyr.p-c8801?2930	(1.0d-28)	43	SSSAAEELVQ	AIINSG--GE	AIAVQGDVSK	TEEVDTLIQT	TLDKFG--RI
S6803.p-Slr0886	(4.0d-27)	40	SSTAADAVVA	EIIANG--GE	AIAVQANVAN	ADEVDQLIKT	TLDKFS--RI
mae.p-MAE_33900	(3.0d-29)	47	SSSAADAVVE	EITAAG--GK	AIALQADVAK	SEEVDNLVDS	TKEKFG--HI
TeBP1.p-tlr1502	(5.0d-29)	38	SAAEALEVQ	RIEQQG--GT	AIAIAADVSV	PEQVDTLVAK	TVETYG--RV
S7942.p-Synpcc7942_0684	(4.0d-26)	42	SAGAADEVVA	AIAAAG--GE	AFAVKADVSQ	ESEVEALFAA	VIERWG--RL
syx.p-SynWH7803_1861	(7.0d-30)	43	SPDAADAVVK	EIESGG--GK	AYALQADVGD	EEAVDALIKT	VLERSG--RI
S7805.p-WH7805_13603	(5.0d-28)	43	SPDAAEAVVK	EIESMG--QK	GYALQADVGD	EDAVDALIKT	VLERSG--RI
S9916.p-RS9916_33507	(8.0d-31)	43	SPDAAESVVN	EITAAG--GK	AYALQANVAD	EDAVDGLIKT	VLERSG--RI
Ssp-RS9917.p-Ssp-RS9917-1614	(2.0d-29)	101	SAAEADEVVA	EILEAG--GQ	AYALKADVAE	EHAVEAMVKT	ALERSG--RI
S9917.p-RS9917_09056	(3.0d-29)	43	SAAEADEVVA	EILEAG--GQ	AYALKADVAE	EHAVEAMVKT	ALERSG--RI
syg.p-sync_2137	(4.0d-29)	43	SSDAAEAVVA	EIQAKG--GS	AYALQADVAD	EASVDDLIKT	VLKRSE--RI
P9313.p-PMT1333	(6.0d-29)	43	SADAAEEVVQ	AITSNG--GS	AYAIKANVAE	EDAVDQLIKT	VLERSS--RL
pmf.p-P9303_06521	(1.0d-28)	55	SADAAEEVVK	AITSNG--GS	AYAIKANVAE	EDAVDQLIKT	VLERSS--SL
S107.p-BL107_09856	(2.0d-28)	60	SAAAADDEVVT	AIEALG--GK	AYALQANVSV	ESDVDGLIKA	VLDRSG--RI
S9902.p-Syncc9902_1745	(4.0d-28)	43	SAAAADDEVVA	AIEALG--GK	AYALQANVSL	ESDVDGLIKT	VLERSG--RI
S9605.p-Syncc9605_0617	(4.0d-27)	57	SAAAADDEVVA	AITTAG--GK	AYALQASVSV	ETEVDGLIKT	VLERSG--RL
S8102.p-SynW1852	(9.0d-28)	43	SAGAADEVVA	SINAAG--GK	AYALKANVSI	EEEVDGLIKA	VLERSG--RL
syr.p-SynRCC307_0681	(2.0d-28)	43	SADAAEQVVS	AITAAG--GS	AYALKADVSQ	EDQVEQLMAA	VLEKSG--RI
S5701.p-WH5701_07809	(1.0d-28)	45	SADAAEAVVA	AITAAG--GR	AWSHRADVSQ	EADVEAMVKQ	VLERSG--RL
pmn.p-PMN2A_1785	(5.0d-28)	43	SLENANKVVS	EINSFG--GK	AYPLQADISN	ENSVNELIKT	VLEKNN--KI
pme.p-NATL1_05081	(1.0d-27)	43	SLENANKVVS	EINSFG--GK	AYPLQADISN	ENSVNLIKT	VLEKNN--KI

pmz.p-p9211?06582 (1.0d-27)	43 SAESAKDVVQ AITASG--GK AYSLQANVAD EESVNDLIKK VLERSG--RI
PRO1375.p-Pro0452 (7.0d-27)	43 SATKAEVVVS LIKSTG--GK AYALQANVAD ESSVNELVDT VLEKSD--HI
Gvi.p-glr3506 (5.0d-28)	41 SEEAQQVVA AIEAAG--GQ AVALKADVAD PEQVERLFAD LLAKYG--RL
pmb.p-P9601_05091 (9.0d-28)	43 SDEKAEVVVN SIKNSG--GK AHKLFKFDVSR EDSVSSAFEE IIKING--SI
pmi.p-PMT9312_0453 (1.0d-27)	43 SDEKAEVVVN SIKNSG--GK AHKLFKFDVSK EDSVSSAFEE IIKING--SI
pmg.p-P9301_04781 (1.0d-27)	43 SDEKAEVVVN SIKNSG--GK AHKLFKFDVSR EDSVSSAFEE IIKVNG--SI
PMED4.p-PMM0453 (9.0d-28)	43 SDEKAEVVVN LIKESG--GK VHKLKFDVSK EESVSKAFEE IIKING--AI
pmc.p-P9515_05161 (2.0d-27)	43 SDEKAEVVLN LIKGLG--GK VHKLKFDVSK EESVSQAFEE IIKING--SI
Npun.p-NpR0578 (6.0d-27)	45 -EQGNQETVR LIEDLG--GR VLAVKCDVTR TEDVTAALSK TIETFG--RL
Cyl-7417.p-Cyl-7417-0303 (5.0d-26)	40 NEKEANRVAQ EIAANG--GK GFVAIGDLAT DTGADESVDK ALSILG--AI
Npun.p-NpF2231 (1.0d-26)	41 -EELASLSAD AIKAIG--GK AIALITDVTQ EQSVADMVEQ TLVSFG--KI
Cyl-7417.p-Cyl-7417-3400 (1.0d-26)	41 -PELAIETAD AIKILG--RN ALAIPIDVTH EQAVADMVLQ TLTTFG--KI
Acyl-7122.p-acyl-3225 (4.0d-28)	40 EDKLA-VAQ TAIEIG--VE AKAFVVDLAS VSQVKAKIQA IAHEFG--DI
Nsp-0708.p-Nsp-0708-2459 (6.0d-26)	40 QDKLER-VAA AAKEIG--VE AKAFVVDLSC VSQVQAKIQA IPHEFG--DI
Ana-90.p-ana90-1189 (1.0d-28)	40 QDKLES-VAK AAQELG--VE AKAFVVDLAE VTQVKSIIQI IADEFG--NI
Cyl-505.p-Cyl-505-2036 (2.0d-32)	40 QDKLQGVVA AAKAAG--VE AKAFVVDLSC VSQVKAKIQA IADEFG--DI
A29413.p-Ava2536 (2.0d-28)	40 GDKLTP-VVE ATKQTG--VV AKAYTVDLAD VSQVEAKIQA IAIDFG--DI
A7120.p-Alr5286 (2.0d-28)	54 LDKLTP-VVE ATKQTG--VV AKAYTVDLAD VSQVEAKIQA IAIDFG--DI
N-7524.p-N-7524-4179 (1.0d-27)	40 LDKLET-VAQ ATKNTG--VA AKVYAVDLAD VSQVEAKMQA IASDFG--DI
MAST-10914-SCAD-C	44 VDKLTA-VCE AVSHTG--VE AKAYEVDLAC VAQVQEKMQA IALNFG--DI
Cyl-7417.p-Cyl-7417-1063 (4.0d-30)	40 VDKLEA-VAA AARLTG--VE ATAFVVDLAN VSQVQAKIQA IAIEFG--DI
nod.p-n9414?21215 (5.0d-26)	39 LDKLET-VAQ AARHTG--VV AKAYAVDLAN ITQVKAIEIA IALDFG--GI
N-7107.p-N-7107-1008 (2.0d-29)	40 LDKLEA-VAT AAKQTG--VE AKAYTLDLAD LPQVEAKINA IAQDFG--NI
M7126-SCAD-A	40 LDKLAA-VTT AAHTG--VK AQAYAVDLAC IEQVKENIQA IAHDFFG--HI
R7116-SCAD-B	39 EQKLAA-VEN AVKKG--VN AKTYVVDLAN VSQVQENMRQ IVLDFG--NI
lyn.p-l8106?23630 (2.0d-26)	40 HETLET-IAQ QARASG--VE ANAYALDLAK VEQVHEQIDT IAAAFG--PI
Amar.p-AM1_5634 (3.0d-27)	40 QAQLDE-LAQ TLQEQG--VE VRGVAIINLSE VGQVKSQISQ LLDQVG--SI
cyb.p-CYB_0189 (1.0d-27)	42 QPDLLA-VQA QIQAQG--GK AAVFPMDLAD LAALPQQLQA LLDQVG--VC
cya.p-CYA_2793 (8.0d-26)	42 HPDLLG-VQA EIQAAG--GK AEFVPIIDLAD LRALPQRLQA LLDQVG--VC
M7126-SCAD-D	39 SSEIEQ-IAQ QIRDAG--GS AQAI PADITD PIQVLNLFQR VDEYYG--KI
cyb.p-CYB_0005 (4.0d-34)	40 EGLLRN-VKD LVESRG--AE ALVVPTDMAD TAQVEALAQK ALDHFV--RV
cya.p-CYA_0005 (2.0d-33)	40 EELLQN-VKD LVEKQG--TE ALVVPTDMAD TAQVEALAQK ALDRFV--RV
N-7107.p-N-7107-5182 (3.0d-28)	41 GDRLEA-LAK HIAAIG--GK ALPIVTDITD ETQANNLIHK TNAQLG--QV
Npun.p-NpR3707 (3.0d-27)	41 GDRIQA-LAE RIEASG--GK ALPIVTDVTD ENQVNHLVAK ANVELG--RV
Acyl-7122.p-acyl-1205 (2.0d-26)	66 GDRLQA-VAK YITDNG--GQ ALSVIADITD EAQAKNLVQK ANAEFG--QV
R7116-SCAD-F	52 LERLQQ-LVE NLKLPS--EN FHLLLEDVRN RSAVE SAVSN LPSEWS--NI
Npun.p-NpF0204 (3.0d-28)	44 EDALRQ-LVD EIRAKG--GQ AIYVVADVGQ EEDVNRIAER AIAEFG--GF
MAST-10914-SCAD-D	39 DTTRLG EVAT EIEMLG--VE VVTLPLDLSQ VVEVNIAIAQ AWRDHG--PI
Cal-6303.p-Cal-6303-3407 (1.0d-27)	39 NRQSLAEVAA EIEELG--TE AVILPLDLTQ IVEVNIAIAQ AWRDYG--AI
Ana-90.p-ana90-4359 (1.0d-27)	39 DRQKLAEVAA QIEALG--VE TTIMALDLTH SINVNIAIAQ LWRSYG--PI



Cyl-7417.p-Cyl-7417-4762	(6.0d-27)	39	DRQKLAEVAQ	QIEAMG--VE	TTVLALDLAN	PVNINIAIAQ	LWRHDG--PI
Nsp-0708.p-Nsp-0708-3536	(2.0d-26)	39	DHHKLAQVAQ	EIEEIG--TE	TIIIALDLTQ	SVNVNIAIAQ	LWRNYG--PV
N-7107.p-N-7107-1296	(2.0d-26)	39	DRQKLTEVAE	EIEALG--TE	AVIMTLDLTR	ATEVNIAVAQ	LWRNHG--PI
Npun.p-NpR1019	(4.0d-26)	39	DRQKLVEVAN	EIEAMG--TE	TAIVPLDLTQ	TIEVNIAVAQ	LWRNFG--QI
N-7524.p-N-7524-4265	(1.0d-25)	39	DRQKLREVAE	EIEAMG--VQ	ATTLAIDLTO	ATEVNIAIAQ	LWRSYG--PI
M7126-SCAD-E		39	DQRKLTQVAK	EIEAMG--TQ	ATIVAVDLTQ	AVELNIAVAQ	IWRNYG--PI
R7116-SCAD-E		43	SRDKLAEVAK	VVEAMG--VE	AIIMPLDLTK	PVVFVNVAQAQ	LWRSYG--AI
cyt.p-cce_3588	(3.0d-27)	45	NENKLLDVSA	DIKGFQ--VE	VIIPLDLTK	VAVVNKTISQ	AWRNHG--PI
ctc.p-c0110?06289	(2.0d-26)	44	NEHRLINLSA	DMEPLG--VE	VIIPLDLTD	VVAVNTAIAQ	AWRNHG--PI
cyr.p-c8801?0598	(2.0d-26)	39	DAKQLTAVAA	EVEAMG--VD	VVIIALDLTQ	LTAVNIAISQ	AWRDYG--PI
Amar.p-AM1_6363	(1.0d-30)	39	NQARLQEVAT	EIEAIG--TQ	AVVLPLDLTQ	TVEVNIAIAQ	TWKQHG--PI
Amar.p-AM1_0210	(1.0d-27)	39	QQCCLKHLTR	EIHQLAPEVD	VVVISLDTQ	TGQIKQFIPQ	ALSDFG--PI
lyn.p-l8106?00785	(4.0d-31)	36	FERLET-AAN	EVRSLG-GSA	-FAIATDVGE	VQQVQELVEK	ALEVYQ--NI
ter.p-Tery_3453	(8.0d-31)	36	LDRLAT-TAN	EVRETG-KSA	-LAIPTDVTD	AKQVEYLVKK	AIELYE--KI
A29413.p-Ava0943	(1.0d-30)	57	PDRLEA-IAT	EIRELG-QEA	-IAIPTDVKD	ATQVNNMIQK	AIAHFG--QV
A7120.p-A112963	(5.0d-29)	57	LDRLEA-IAT	EIREMG-QQA	-IAISTDVKD	ATQVNNMMQK	AIAHFG--QV
Npun.p-NpR4797	(3.0d-30)	36	ADRLEA-LAQ	EVQSIG-CPA	PLTITCDVTD	SSQVNALVQK	ALGNYG--YI
Cyl-7417.p-Cyl-7417-4424	(3.0d-30)	36	TERLEA-TAQ	EVQSLG-LAA	PLTVTCDVTN	PSQVEMLVQK	ALEHYG--YI
MAST-10914-SCAD-E		36	LDRLES-VAQ	EVQSLG-RPA	PLTISCDVTD	PSQVNSLVEK	ALDHYG--YI
M7126-SCAD-C		36	ANNLEA-LAQ	QIQSLG-LKT	PLTFACDVKD	PSQVQTMTQK	AWEQYN--YI
R7116-SCAD-D		35	LETLEA-TAA	EIRAIG-TKV	-LAVPCDVSQ	EAEVNNLIPK	ALEYFG--SI
Npun.p-NpF0199	(2.0d-29)	72	PEELER-SRI	ELEQRG-GEV	-LAVPCDVTD	KTQVEQMVQQ	VRDRFG--AI
A7120.p-Alr5358	(3.0d-156)	40	QSGLAQ-TCN	AVKAAG--GK	AIAIPFDVRN	TSQLSALVQQ	AQDIVG--PI
A29413.p-Ava2596	(8.0d-151)	40	QSGLAQ-TCN	VVKAAG--GK	AIAIPFDVRN	ISQLSALVQQ	AQDIVG--PI
N-7524.p-N-7524-5224	(2.0d-121)	40	RSGLEQ-TCH	AVNAAG--GR	AIAIPFDITK	VGELSALTQQ	VQSTVG--PV
Cyl-7417.p-Cyl-7417-1544	(2.0d-100)	40	KSGLDK-TSD	EVTALG--GK	FIGFTFDLKK	VEELPILVQQ	INKVVG--PV
MAST-10914-SCAD-A		40	KESLEK-ISA	EVEIAG--GR	GISIPFDISK	VEELSVLVQQ	IHELAG--PI
N-7524.p-N-7524-5355	(2.0d-74)	40	EEKLNQ-ICA	EVDALG--GK	GISIAFDISN	LEELPDLVDK	INQFAG--QI
Npun.p-NpF3363	(2.0d-81)	40	HQQLDN-LTT	ELKALG--CN	FIPFTCDISN	LSELPILLNK	INQIVG--DV
R7116-SCAD-A		51	QEGLDK-ICN	EINDLG--GK	GIGINFNISK	VERIPELVYE	IKQLTGSFQV
cyr.p-c8801?3820	(4.0d-26)	37	QDKLYQLAET	LKQETA--IE	VEVIVQDLVQ	PGATKAVYDR	VQEKGL--TV
A7120.p-A111418	(8.0d-26)	47	QEALQQTMTA	CTNYPG---K	VIAVHTDVTQ	AEACQQLIER	AIATFG--QI
consensus		101					

A7120.p-Alr1894	(1.0d-26)	90	DILVNNAGIT	-RDTLLLRMK	PEDWQAVIDL	NLTGVFLCTR	AVSKMLKQ-
A29413.p-Ava3764	(1.0d-26)	90	DILVNNAGIT	-RDTLLLRMK	PEDWQAVIDL	NLTGVFLCTR	AVSKMLKQ-
N-7524.p-N-7524-0010	(9.0d-30)	90	DILVNNAGIT	-RDTLLLRMK	LEDWQAVIDL	NLTGVFLCTR	SVSKIMLKQ-
M7126-SCAD-B		93	DILVNNAGIT	-RDTLLLRMK	PEDWQAVIDL	NLTGVFLCTR	AASKIMLKQ-
nod.p-n9414?22428	(4.0d-28)	86	DILVNNAGIT	-RDTLLLRMK	PEDWQAVIDL	NLTGVFLCTR	AVSKIMLKQ-
MAST-10914-SCAD-B		93	DILVNNAGIT	-RDTLLLRMK	PEDWQAVIDL	NLTGVFLCTR	AVSKIMLKQ-
Cal-6303.p-Cal-6303-1520	(5.0d-28)	93	DILVNNAGIT	-RDTLLLRMK	QEDWQAVIDL	NLTGVFLCTR	AASKIMLKQ-
Npun.p-NpF2349	(4.0d-29)	86	DILVNNAGIT	-RDTLLLRMK	PEDWQAVIDL	NLTGVFLCTR	AVSKIMLKQ-
N-7107.p-N-7107-0937	(1.0d-27)	93	DILVNNAGIT	-RDTLLLRMK	PEEWQAVIDL	NLTGVFLCTR	AVSKIMLKQ-
Ana-90.p-ana90-1712	(1.0d-28)	86	DILVNNAGIT	-RDTLLLRMK	LEEWQAVIDL	NLTGVFLCTR	VVSKIMLKQ-
Acyl-7122.p-acyl-4545	(9.0d-28)	86	DILVNNAGIT	-RDTLLLRMK	LEDWQAVIDL	NLTGVFLCTR	LVSKIMLKQ-
Nsp-0708.p-Nsp-0708-2353	(9.0d-27)	86	DILVNNAGIT	-RDTLLLRMK	LEEWQAVIDL	NLTGVFLCTR	AVSKTMLRQ-
Cyl-505.p-Cyl-505-0204	(2.0d-28)	86	DILVNNAGIT	-RDTLLLRMK	LEDWQAVIDL	NLTGVFLCTR	AVSKIMLKQ-
Cyl-7417.p-Cyl-7417-2349	(6.0d-29)	93	DILVNNAGIT	-RDALLLRMK	LEEWQAVIDL	NLTGVFLCTR	AVSKIMLKQ-
R7116-SCAD-C		93	DILVNNAGIT	-RDTLLLRMK	PEDWQAVINL	NLTGVFLCTR	AVSKGMLKQ-
ter.p-Tery_3438	(2.0d-28)	93	DILVNNAGIT	-RDTLLLRMK	LEDWQSVIDL	NLTGVFLCTR	AVSKIMLKQ-
lyn.p-l8106?21814	(1.0d-27)	93	DILVNNAGIT	-RDTLLLRMK	PEEWQAVIDL	NLTGVFLCTR	AVSKIMLKQ-
Amar.p-AM1_5632	(1.0d-26)	86	DILVNNAGIT	-RDTLLLRMK	PEDWQAVINL	NLTGVFLCTR	AVSKVMLKQ-
cyr.p-c8801?2930	(1.0d-28)	89	DILVNNAGIT	-RDTLLLRMK	LEQWQEVIDL	NLTGVFLCTR	AVTKTMLKQ-
S6803.p-Slr0886	(4.0d-27)	86	DILVNNAGIT	-RDTLLLRMK	LEDWQAVIDL	NLTGVFLCTR	AVSKMLKQ-
mae.p-MAE_33900	(3.0d-29)	93	DILVNNAGIT	-RDTLLLRMK	LEDWQAVIDL	NLTGVFLCTR	AVSKMLKQ-
TeBP1.p-tlr1502	(5.0d-29)	84	DILVNNAGIT	-RDTLLLRMS	LEDWQAVINL	NLTGVFLCTR	AVSKMLKQ-
S7942.p-Synpcc7942_0684	(4.0d-26)	88	DILVNNAGIT	-RDTLLLRMK	RDDWQSVIDL	NLTGVFLCTR	AAAKIMLKQ-
syx.p-SynWH7803_1861	(7.0d-30)	89	DILVNNAGIT	-RDGLLMRMK	AADWNAVINL	NLTGVFLCTR	AVTRPMLKQ-
S7805.p-WH7805_13603	(5.0d-28)	89	DILVNNAGIT	-RDGLLMRMK	STDWNAVINL	NLTGVFLCTR	AVTRPMLKQ-
S9916.p-RS9916_33507	(8.0d-31)	89	DILVNNAGIT	-RDGLLMRMK	TADWQSVIDL	NLTGVFLCTR	AVTRPMLKQ-
Ssp-RS9917.p-Ssp-RS9917-1614	(2.0d-29)	147	DILVNNAGIT	-RDGLLMRMK	TDDWQAVINL	NLTGVFLCTR	AVTRTMLKQ-
S9917.p-RS9917_09056	(3.0d-29)	89	DILVNNAGIT	-RDGLLMRMK	TDDWQAVINL	NLTGVFLCTR	AVTRTMLKQ-
syg.p-sync_2137	(4.0d-29)	89	DILVNNAGIT	-RDGLLMRMK	TEDWQAVINL	NLTGVFLCTR	AVTRPMLKQ-
P9313.p-PMT1333	(6.0d-29)	89	DILVNNAGIT	-RDGLLMRMK	TEDWQAVVNL	NLTGVFLCTR	AVARTMLKQ-
pmf.p-P9303_06521	(1.0d-28)	101	DILVNNAGIT	-RDGLLMRMK	TEDWQAVVNL	NLTGVFLCTR	AVARTMLKQ-
S107.p-BL107_09856	(2.0d-28)	106	DILVNNAGIT	-RDGLLMRMK	TDDWQSVIDL	NLTGVFLCTR	AIARPMLKQ-
S9902.p-Syncc9902_1745	(4.0d-28)	89	DILVNNAGIT	-RDGLLMRMK	TDDWQSVIDL	NLTGVFLCTR	AIARPMLKQ-
S9605.p-Syncc9605_0617	(4.0d-27)	103	DILVNNAGIT	-RDGLLMRMK	TDDWQSVIDL	NLTGVFLCTR	AVSRPMLKQ-
S8102.p-SynW1852	(9.0d-28)	89	DILVNNAGIT	-RDGLLMRMK	TSDWQAVIDL	NLTGVFLCTR	AVARPMLKQ-
syr.p-SynRCC307_0681	(2.0d-28)	89	DILVNNAGIT	-RDGLLMRMK	TPDWQAVLDL	NLTGVFLCTR	AVTRTMLKQ-
S5701.p-WH5701_07809	(1.0d-28)	91	DILVNNAGIT	-RDGLLMRMK	TADWQSVIDL	NLTGVFLCTR	AVCRTMLKA-
pmn.p-PMN2A_1785	(5.0d-28)	89	DILVNNAGIT	-KDGLLRMK	TDDWQKVLDL	NLTGVFLCTR	AVSRQMLKQ-
pme.p-NATL1_05081	(1.0d-27)	89	DILVNNAGIT	-KDGLLRMK	TDDWQKVLDL	NLTGVFLCTR	AVSRQMLKQ-

pmz.p-p9211?06582 (1.0d-27)	89 DALINNAGIT -KDGLLMRMR TEDWQSVINL NLTGVFLCTR AVARPMLKQ-
PRO1375.p-Pro0452 (7.0d-27)	89 DILINNAGIT -KDGLLMRMK TEDWQSVLNL NLTGVFLCTK AVSRSMKQ-
Gvi.p-glr3506 (5.0d-28)	87 DALVNNAGIT -RDGLILRMS LEDWNDVVSL NLTGTFLCLK AASRIMLKQ-
pmb.p-P9601_05091 (9.0d-28)	89 DILINNAGIT -RDGLLMRMK SEQWDDVLNT NLKGVFLCTK YASKFMMKK-
pmi.p-PMT9312_0453 (1.0d-27)	89 DILINNAGIT -RDGLLMRMK SEQWDDVLNT NLKGVFLCTK YASKFMMKK-
pmg.p-P9301_04781 (1.0d-27)	89 DILINNAGIT -RDGLLMRMK SEQWDDVLNT NLKGVFLCTK YASKFMMKK-
PMED4.p-PMM0453 (9.0d-28)	89 DILVNNAGIT -RDGLLMRMK SEQWDDVLNT NLKGVFLCTK YASKFMIKK-
pmc.p-P9515_05161 (2.0d-27)	89 DILINNAGIT -RDGLLMRMK SEQWDDVLNT NLKGVFLCTK YASKFMLKK-
Npun.p-NpR0578 (6.0d-27)	90 DFAFNAGVE QKKAATAELE EAEDRIVNT DLRSVFLCLK HEIPLMLKQ-
Cyl-7417.p-Cyl-7417-0303 (5.0d-26)	86 DILVNTGTY -FMSGWMNST SSQWVDLYNI NVVSMVRTIQ LLIPRMREL-
Npun.p-NpF2231 (1.0d-26)	86 DILVANAGIQ -RRYFVADLP LAEFQAILDV NLLGVFLTSK AVLPFYYSR-
Cyl-7417.p-Cyl-7417-3400 (1.0d-26)	86 DILVTNAGIQ -RRYFVADLP RAEFQAMLVD NLLGAFFCCQ AVLPNFYNO-
Acyl-7122.p-acyl-3225 (4.0d-28)	85 DILVNNAGMG -YTANLSETP LEDWQQVINL NLTSAFQCMM GILPEMRQR-
Nsp-0708.p-Nsp-0708-2459 (6.0d-26)	85 DILVNNAGMG -YTANLSETP LEDWQQVINL NLTSVFACIM GTLPGMRQR-
Ana-90.p-ana90-1189 (1.0d-28)	85 NILINNAGIT -YTGNLSETP LEDWQQVINL NLTSVFQCMM GILPRMRQR-
Cyl-505.p-Cyl-505-2036 (2.0d-32)	85 DILVNNAGMG -YTGNLSDTS LEDWRRVIDL NLTSVFQCTM GILPRMRQR-
A29413.p-Ava2536 (2.0d-28)	85 DILVNNAGVA -YTATLSETP LADWQQVINL NLTSVFECIK GILPRMRAR-
A7120.p-Alr5286 (2.0d-28)	99 DILVNNAGVA -YTATLSETP LADWQQVINL NLTGVFECIK GILPTMRDR-
N-7524.p-N-7524-4179 (1.0d-27)	85 DILVNNAGIG -YTGILRETT LEDWQQVINL NLTSVFQCIQ GILPGMLAR-
MAST-10914-SCAD-C	89 DILVNNAGMG -YTATLSETP LSDWQQVIEL NLTSVFQSIM GILPRMRER-
Cyl-7417.p-Cyl-7417-1063 (4.0d-30)	85 DILVNNAGMA -YTATLSETP LEEWQQVINL NLTSVFQCIN GILPTMRHR-
nod.p-n9414?21215 (5.0d-26)	84 DILVNNAGIA -YTANLSETP LEDWQKVINL NLTSVFQCLM GILPGMRSR-
N-7107.p-N-7107-1008 (2.0d-29)	85 DILVNNAGIG -YTANLIDTS LEDWQKVINI NLTSVFECIK GILPGMRDR-
M7126-SCAD-A	85 DILVNSAGIA -YTANLSEIP LEDWQQVLNL NLTSVFECIM GILPGMRDR-
R7116-SCAD-B	84 DILVNNAGMG -YTATLSQTP LSDWQQVIDL NLTSVFECIK GILPSMREQ-
lyn.p-l8106?23630 (2.0d-26)	85 DILVNNAGIG -YTSPLVSTP LTEWQQVLDL NLTSVFQCVQ GVLPGMRER-
Amar.p-AM1_5634 (3.0d-27)	85 DILINNAGMG -YTGELIDMP LADWQRVLGL NVTSVFECVQ AVLPGMRSQ-
cyb.p-CYB_0189 (1.0d-27)	87 DVLVNNAGMA -HVGPLATLP LSDWQRVIDL NLTA AFLCAQ AVLPGMRRQ-
cya.p-CYA_2793 (8.0d-26)	87 DVLVNNAGIA -HVGPLATLS LSDWQRVIDL NLTA AFLCAQ AVLPAMRRQ-
M7126-SCAD-D	84 DILINNAGIG -LFGPVEELT DEALEQMLAV NVKGTVYCSQ AAFKRMKQA-
cyb.p-CYB_0005 (4.0d-34)	85 DILVNNAGYG Q-MGPVEEVD VAAMRRQFEV NVFGLHALTR ALLPQMRER-
cya.p-CYA_0005 (2.0d-33)	85 DILVNNAGYG Q-MGPVEEVD VAAMRRQFEV NVFGLHALTR ALLPQMRER-
N-7107.p-N-7107-5182 (3.0d-28)	86 DILVNNAGVA L-TGNIDGGN TSDWRRMFDV NVFGVLYTTH AVLPKFKAQ-
Npun.p-NpR3707 (3.0d-27)	86 DILVNNAGIA L-LGTIEAGN SSDWRRSFDI NVLGLLYATH AVLPPLLKQ-
Acyl-7122.p-acyl-1205 (2.0d-26)	111 DILVNNAGIS F-PGRIENAD PANWRKMIDI NVLALMYTTY TVLPKFKAQ-
R7116-SCAD-F	97 DILINNAGLS RGLNKLYEGS YQDWEEMIDT NVKGLLYLTR CVVPGMVER-
Npun.p-NpF0204 (3.0d-28)	89 DTWVNNAGVS I-FGRCMDVS IPDMKRMFDT NFWGVVYGSR AAVNHFKQRK
MAST-10914-SCAD-D	85 DLLINCAGVA -HQT PFLNSR LPNVQTEIAV NLIGMYTITR IVARRMVVQ-
Cal-6303.p-Cal-6303-3407 (1.0d-27)	85 HLLINCAGVA -HQTAFLESK LSDVQEELET NLIGMYSITR LIARRMVTQ-
Ana-90.p-ana90-4359 (1.0d-27)	85 HLLVNCAGVA -HQNSFLQSK LPQLQEELSV NLMGMYTLTN LIAKRMVVSQ-

Cyl-7417.p-Cyl-7417-4762 (6.0d-27)	85 DLLVNCAGVA -YQNSFLQSK LPQVQEELSV NLMGMYTLTS LIARRMASQ-
Nsp-0708.p-Nsp-0708-3536 (2.0d-26)	85 HILVNCAGVA -YQNSFLQSK LPQVQEELSV NLLGMYNLTS LIARRMVSQ-
N-7107.p-N-7107-1296 (2.0d-26)	85 HLLVNCAGVA -YQTSFLRSK LFQVQEELSV NLLGMYTLTS LIARRMASQ-
Npun.p-NpR1019 (4.0d-26)	85 HLLVNCAGVA -YQSSFLQSK MPQVQEELSV NLLGMYNLTS LIARRMVSQ-
N-7524.p-N-7524-4265 (1.0d-25)	85 HLLINCAGVA -YQNSFLRSK LPQLQEELSV NLLGMYTLTS LIAKRMASQ-
M7126-SCAD-E	85 HLLVNCAGVA -YQNSFLQCK LPQVQEEISV NLMGMYTLTS LIARRMATQ-
R7116-SCAD-E	89 DMLVNCAGVA -HQNSFLKTK LPQVQEELSL NFMGTYTMTH IVARRMAKR-
cyt.p-cce_3588 (3.0d-27)	91 DILVNCAGVA -HQTPFLHTN FSQVQAEELSV NLMATYQMTR LIAKRMAYR-
ctc.p-c0110?06289 (2.0d-26)	90 DLLVNCAGVA -HQTSFLRAS LSQVQAEELSV NLMATYQMTR LIARRMAYR-
cyr.p-c8801?0598 (2.0d-26)	85 DLLVNCAGVA -HQTSFLKAQ LSQVQNELNL NLMGTYAITR LVARRMAQR-
Amar.p-AM1_6363 (1.0d-30)	85 HLLVNCAGVA -HQAPFLQTK LPKVQEELSL NLMGIYSMTQ VLARRMASK-
Amar.p-AM1_0210 (1.0d-27)	87 DLLVNNAGVA -HQASFLSST IEEFEAEIRL NLCGTFAITR LIAQHMVKH-
lyn.p-l8106?00785 (4.0d-31)	81 DVLVNNAGIC -LTGSMAKTT LEDWQQLMNT NFWGYVHTIN ALLPHFIER-
ter.p-Tery_3453 (8.0d-31)	81 DVLVNNAGIC -LTGGIEYTT LEDFQQLMNI NFFGYVNTIK ALLPHFLSR-
A29413.p-Ava0943 (1.0d-30)	102 DVLINNAGIF -CLGSVENFS LEDRHQIIDT NLWGYIHTIY AILPYFLQR-
A7120.p-A112963 (5.0d-29)	102 DVLINNAGIF -CLGSVENFS LEDWHQIIDT NLWGYIHTIH AILPHFLQR-
Npun.p-NpR4797 (3.0d-30)	82 DVLINNAGIF -ASGPVEQFS LSDWHQIIDT NLWGYIHTIN AILPHFLQR-
Cyl-7417.p-Cyl-7417-4424 (3.0d-30)	82 DVLVNNAGIF -ASGPVEQFS LSDWHQVIDT NLWGYIHTIQ ALLPHFLQR-
MAST-10914-SCAD-E	82 DVLINNAGVF -AEGPVDGFS LNDWHQVIDL NLWGYIHTIH ALLPHFLQR-
M7126-SCAD-C	82 DLLINNAGIF -ASGPVENFS LSDWHDVIDT NLWGYIHTIN AILPHFLQR-
R7116-SCAD-D	80 DVLINNAGVC -MTGPIENTS LDDWHRVIDV NLWGYIHTIH ALLPHFLVR-
Npun.p-NpF0199 (2.0d-29)	117 DILINNAGVD -FVGPMDLMT VEDYDDAMKL HFWAPLYASY AVLPQMRER-
A7120.p-Alr5358 (3.0d-156)	85 DVLINNAGIE -INGTFANYS LAEIQSIFNT NLLAAMELTR LLLPSMMER-
A29413.p-Ava2596 (8.0d-151)	85 DVLINNAGIE -INAAFANYS LAEIQSIFNT NLLAVMELTR LLLPSMMER-
N-7524.p-N-7524-5224 (2.0d-121)	85 DILINNAGIE -IISAFANYS LAEIHVSFNT NLLATMELTR LLLPNMMER-
Cyl-7417.p-Cyl-7417-1544 (2.0d-100)	85 DVLINNSGIE -LYRAFADYS LEDLQSVLTT NLLSAIELTR LLLPSMLER-
MAST-10914-SCAD-A	85 DILINNAIE -KYRPFQNYT LEDIQSILTT NLVAPMELSR LILPSMVDR-
N-7524.p-N-7524-5355 (2.0d-74)	85 DILINNAIE -KYRNFQDYT LEDIQSILTT NLISGMELTR LIMPSMIAR-
Npun.p-NpF3363 (2.0d-81)	85 DILINNAGIE -IYRSFPDYS LAEMQSVIST NLLAAMELSR LLLPNMLVQ-
R7116-SCAD-A	98 DILINNAGIE -IYRAFHHYS LKDIQLVLSV NLLAAIELSR LVLPMMLDK-
cyr.p-c8801?3820 (4.0d-26)	83 DLLINNAGFG -DYGAFTERD LSRQVEMIQI NVVALVELTH LFLPMQOQK-
A7120.p-A111418 (8.0d-26)	92 DILINNAGIG MLTRFDEVTD ISIFEQVMOA NYLGAVYCTH YALPYLKAS-
consensus	151 . . . :

A7120.p-Alr1894	(1.0d-26)	138	-RSGRIINIT	SVAGQMGNPG	QANYSAAKAG	VIGFTKTVAK	ELASR--GIT
A29413.p-Ava3764	(1.0d-26)	138	-RSGRIINIT	SVAGQMGNPG	QANYSAAKAG	VIGFTKTVAK	ELASR--GIT
N-7524.p-N-7524-0010	(9.0d-30)	138	-RSGRIINIS	SVAGQMGNPG	QANYSAAKAG	VIGFTKTVAK	ELASR--GIT
M7126-SCAD-B		141	-RSGRIINIA	SVAGQMGNPG	QANYSAAKAG	VIGFTKTVAK	ELASR--GIT
nod.p-n9414?22428	(4.0d-28)	134	-RSGRIINIA	SVAGQMGNPG	QANYSAAKAG	VIGFTKTVAK	ELASR--GIT
MAST-10914-SCAD-B		141	-RSGRIINIT	SVAGQMGNPG	QANYSAAKAG	VIGFTKTIAK	ELASR--GIT
Cal-6303.p-Cal-6303-1520	(5.0d-28)	141	-RSGRIINIT	SVAGQMGNPG	QANYSAAKAG	VIGFTKSVAK	ELAPR--GIT
Npun.p-NpF2349	(4.0d-29)	134	-RSGRIINIT	SVAGQMGNPG	QSNYSAAKAG	VIGFTKSVAK	ELATR--GIT
N-7107.p-N-7107-0937	(1.0d-27)	141	-RFGRIINIA	SVAGQMGNPG	QANYSAAKAG	VIGFTKTVAK	ELATR--GIT
Ana-90.p-ana90-1712	(1.0d-28)	134	-RSGRIINIA	SVAGQMGNPG	QANYSAAKAG	VIGFTKTVAK	ELSSR--GIT
Acyl-7122.p-acyl-4545	(9.0d-28)	134	-RSGRIINIA	SVAGQMGNPG	QANYSAAKAG	VIGFTKTVAK	ELASR--GIT
Nsp-0708.p-Nsp-0708-2353	(9.0d-27)	134	-RSGRIINIS	SVAGQMGNPG	QANYSAAKAG	VIGFTKTVAK	ELASR--GIT
Cyl-505.p-Cyl-505-0204	(2.0d-28)	134	-RSGRIINIS	SVAGQMGNPG	QANYSAAKAG	VIGFTKTVAK	ELASR--GIT
Cyl-7417.p-Cyl-7417-2349	(6.0d-29)	141	-RSGRIINIA	SVAGQMGNPG	QANYSAAKAG	VIGFTKTVAK	ELASR--GIT
R7116-SCAD-C		141	-RSGRIINIA	SVAGQMGNPG	QANYSAAKAG	VIGLTKTLAK	EFASR--GIT
ter.p-Tery_3438	(2.0d-28)	141	-KSGRIINVA	SVSGQMGNPG	QANYSAAKAG	VIGFTKTVAK	ELANR--GIT
lyn.p-l8106?21814	(1.0d-27)	141	-RSGRIINIA	SVAGQMGNPG	QANYSAAKAG	VIGFTKTVAK	ELASR--GIT
Amar.p-AM1_5632	(1.0d-26)	134	-RSGRIINIA	SVAGQMGNPG	QANYSAAKAG	VIGFTKTVAK	EMASR--GVT
cyr.p-c8801?2930	(1.0d-28)	137	-KSGRIINIT	SVSGLMGNPG	QANYSAAKAG	VIGLTKTVAK	ELASR--GVT
S6803.p-Slr0886	(4.0d-27)	134	-KSGRIINIT	SVAGMMGNPG	QANYSAAKAG	VIGFTKTVAK	ELASR--GVT
mae.p-MAE_33900	(3.0d-29)	141	-KSGRIINIT	SVSGLMGNPG	QSNYSAAKAG	VIGLTKTLAK	EFASR--GIT
TeBP1.p-tlr1502	(5.0d-29)	132	-KRGRINIA	SVAGQMGNPG	QANYSAAKAG	VIGFSKTVAK	ELASR--GIT
S7942.p-Synpcc7942_0684	(4.0d-26)	136	-RSGRIINIA	SVVGEMGNPG	QANYSAAKAG	VIGLTKTVAK	ELASR--GIT
syx.p-SynWH7803_1861	(7.0d-30)	137	-KSGRIINIT	SVVGLMGNAG	QANYAAAKAG	VVGLTRSAK	EMASR--GIT
S7805.p-WH7805_13603	(5.0d-28)	137	-KSGRIINIT	SVVGLMGNAG	QANYAAAKAG	VVGLTRSAK	EMASR--GIT
S9916.p-RS9916_33507	(8.0d-31)	137	-KSGRIINIT	SVVGLMGNAG	QANYAAAKAG	VVGLTRSAK	EMASR--GIT
Ssp-RS9917.p-Ssp-RS9917-1614	(2.0d-29)	195	-KSGRIINIT	SVVGLMGNAG	QANYAAAKAG	VVGLTRSAK	EMASR--GIT
S9917.p-RS9917_09056	(3.0d-29)	137	-KSGRIINIT	SVVGLMGNAG	QANYAAAKAG	VVGLTRSAK	EMASR--GIT
syg.p-sync_2137	(4.0d-29)	137	-RSGRIINIT	SVVGLMGNAG	QANYAAAKAG	VVGLTRSSAK	EMASR--GIT
P9313.p-PMT1333	(6.0d-29)	137	-KSGRIINIT	SVVGLMGNAG	QANYAAAKAG	VVGLTKSTAK	EVASR--GIT
pmf.p-P9303_06521	(1.0d-28)	149	-KSGRIINIT	SVVGLMGNAG	QANYAAAKAG	VVGLTKSTAK	EFASR--GIT
S107.p-BL107_09856	(2.0d-28)	154	-KSGRIINIT	SVVGLMGNAG	QANYAAAKAG	VIGLTRSTAK	ELASR--GIT
S9902.p-Syncc9902_1745	(4.0d-28)	137	-KSGRIINIT	SVVGLMGNAG	QANYAAAKAG	VIGLTRSTAK	ELASR--GIT
S9605.p-Syncc9605_0617	(4.0d-27)	151	-KSGRIINIT	SVVGLMGNAG	QANYAAAKAG	VIGLTRSTAK	ELASR--GIT
S8102.p-SynW1852	(9.0d-28)	137	-KSGRIINIT	SVVGLMGNAG	QANYAAAKAG	VIGLTKSTAK	ELASR--GIT
syr.p-SynRCC307_0681	(2.0d-28)	137	-KQGRINIA	SVVGLMGNAG	QANYAAAKAG	VIGFTKSTAR	ELASR--GIT
S5701.p-WH5701_07809	(1.0d-28)	139	-RSGRIINIT	SVVGLMGNPG	QANYSAAKAG	VIGFTRSTAA	ELASR--GVT
pmn.p-PMN2A_1785	(5.0d-28)	137	-KKGRINIA	SVVGLMGNPG	QANYSAAKAG	VVGLTQSAK	EFASR--GIT
pme.p-NATL1_05081	(1.0d-27)	137	-KKGRINIA	SVVGLMGNPG	QANYSAAKAG	VVGLTQSAK	EFASR--GIT

pmz.p-p9211?06582 (1.0d-27)	137	-KTGRIVNIT	SVVGLMGNAG	QANYAAAKAG	VVGLTKSTAK	EFASR--GIT
PRO1375.p-Pro0452 (7.0d-27)	137	-RKGRINIIT	SVVGLMGNAG	QANYASAKAG	VIGFTKSAAK	EFASR--GIT
Gvi.p-glr3506 (5.0d-28)	135	-RSGRVVNIS	STSGVAGNAG	QANYSAAKAG	VLGLTRSAAR	ELGSR--GIT
pmb.p-P9601_05091 (9.0d-28)	137	-RSGSIVNIS	SVVGIIGNPG	QANYSAAKAG	VIGFTKTCAK	EFASR--GIN
pmi.p-PMT9312_0453 (1.0d-27)	137	-RSGSIVNIS	SVVGIIGNPG	QANYSAAKAG	VIGFTKTCAK	EFASR--GIN
pmg.p-P9301_04781 (1.0d-27)	137	-RSGSIVNIS	SVVGIIGNPG	QANYSAAKAG	VIGFTKTCAK	EFASR--GIN
PMED4.p-PMM0453 (9.0d-28)	137	-RSGKIINIS	SIVGIIGNPG	QANYSAAKAG	VIGFTKTCAK	EFASR--GIN
pmc.p-P9515_05161 (2.0d-27)	137	-RSGKIINIS	SIVGIIGNPG	QANYSAAKAG	VIGFTKTCAK	EFASR--GIN
Npun.p-NpR0578 (6.0d-27)	139	-GGGAIVNTS	SGAGVIGIKG	GAAYTAAKHG	VIGLTKAAAL	DYASQ--NIR
Cyl-7417.p-Cyl-7417-0303 (5.0d-26)	134	-GWGRIINMA	SSVATQPTP-	MADYSATKAA	ILNLTVSLAK	ELAGT--GIT
Npun.p-NpF2231 (1.0d-26)	134	-QEGNIILIA	SDSGKHGYSY	NAAYCASKFA	VVGFMEALAD	EAKHY--QVR
Cyl-7417.p-Cyl-7417-3400 (1.0d-26)	134	-RQGNIIILIA	SDSGKLGAY	NSAYCASKFA	VLGFMEALAD	EARAY--KVR
Acyl-7122.p-acyl-3225 (4.0d-28)	133	-GTGTIINVA	SIAAKQAFAG	WGAYCVSKAG	LLALSQTLAQ	EERVH--GIR
Nsp-0708.p-Nsp-0708-2459 (6.0d-26)	133	-GQGTIINIA	SIAAKQAFAG	WGAYCVSKAG	LLALSQTLAI	EERSH--GIR
Ana-90.p-ana90-1189 (1.0d-28)	133	-GQGTIINIA	SIAGKQAFPG	WGAYCVSKAG	LLFLSQTLAQ	EERAN--GIR
Cyl-505.p-Cyl-505-2036 (2.0d-32)	133	-GQGTIINIA	SIAAKQAFAG	WGVYCVSKAG	LLALSQTLAQ	EERVH--GIR
A29413.p-Ava2536 (2.0d-28)	133	-HTGTIINVS	SIAAKQSFPH	WGVYSVSKAG	LMALSQTLAQ	EERVH--GIR
A7120.p-Alr5286 (2.0d-28)	147	-HTGTIINVS	SIAAKQSFPH	WGVYSVSKAG	LMALSQTLAQ	EERVH--GIR
N-7524.p-N-7524-4179 (1.0d-27)	133	-GAGTIINVA	SIAAKQAFPN	WGAYCVSKAG	LLALAQTLAQ	EERTH--GIR
MAST-10914-SCAD-C	137	-GAGTIINLT	SIAGKQAFAN	WGAYSVSKAG	LIALSQTLAQ	EERVH--GIR
Cyl-7417.p-Cyl-7417-1063 (4.0d-30)	133	-GIGTIINVT	SIAGKQPFPG	WGAYSASKAG	LMALSLALAQ	EERAN--GIR
nod.p-n9414?21215 (5.0d-26)	132	-HTGTIINVA	SIAAKQPFPG	WGVYSVSKAG	VMALSQTLAQ	EERAH--GIR
N-7107.p-N-7107-1008 (2.0d-29)	133	-GTGTIINVA	SIAAKQTFAG	WGAYCVSKAG	LLALSQTLAQ	EERAH--GIR
M7126-SCAD-A	133	-GRGTIINVA	SIAGKQAFPG	WGAYSVSKAG	LISLSQTLAQ	EERVH--GIR
R7116-SCAD-B	132	-NRGTIINVA	SIAGKQAFAN	WGAYSVSKAG	VIALSQALAQ	EERNN--GIR
lyn.p-l8106?23630 (2.0d-26)	133	-ASGTIVNVV	SIAGQQVFPD	WGAYCVSKFG	LMALSKAFAA	EERQN--GIR
Amar.p-AM1_5634 (3.0d-27)	133	-QQGTIINIV	SIAGQQAFPO	WGAYCASKFA	LMGFTKSLAQ	EERPH--GIR
cyb.p-CYB_0189 (1.0d-27)	135	-RCGTIVNVI	SIAGKRAFPN	WGAYCASKFG	LMGFSQALAE	EERQH--GIR
cya.p-CYA_2793 (8.0d-26)	135	-RCGTIVNII	SIAGKRAFPN	WGAYCASKFG	LLGFSQALAA	EERQH--GIR
M7126-SCAD-D	132	-RSGIINIL	STASKVGRAN	ESGYTASKWA	QAGFTESLKA	EAKPF--GIR
cyb.p-CYB_0005 (4.0d-34)	133	-GSGRILNLS	SVAGQMSMPF	SGVYNATKFA	VEALSDALRV	EVAPF--GIK
cya.p-CYA_0005 (2.0d-33)	133	-GSGRILNLS	SVAGQMSMPF	SGVYSATKFA	VEALSDALRV	EVAPF--GIK
N-7107.p-N-7107-5182 (3.0d-28)	134	-GSGHIVNIS	SVAGRIARAG	VGIYNATKWG	VNAFSESLRQ	EVLKD--NIR
Npun.p-NpR3707 (3.0d-27)	134	-KSGHIVNIS	SVAGRIARAG	VGIVYNATKWG	VNALSEALRQ	EVHKD--NIR
Acyl-7122.p-acyl-1205 (2.0d-26)	159	-KSGHIVNIS	SVAGRIARAG	MGAYNVTKWG	VNAFSEALRQ	EVYQD--NIR
R7116-SCAD-F	146	-DRGHVVNIG	SIAGHQTPG	GNVYCATKAA	VKAISEGLKQ	DLLGT--PVR
Npun.p-NpF0204 (3.0d-28)	138	SGSGALINVG	SFLGDRAVAV	QSTYSASKHA	LHGWDALRT	ELEAEGAPVS
MAST-10914-SCAD-D	133	-GSGTIVNVS	SLMGKIAAPT	MATYSATKFA	IVGFTQALRG	ELAAH--NIR
Cal-6303.p-Cal-6303-3407 (1.0d-27)	133	-HQGVIVNVS	SLMGKVAAPT	MATYSATKFA	IVGFTQALRG	ELASH--NIR
Ana-90.p-ana90-4359 (1.0d-27)	133	-RQGIIVNVS	SLMGKVAAPT	MATYSATKFA	IVGFTQALRQ	ELAQH--NVR

Cyl-7417.p-Cyl-7417-4762 (6.0d-27)	133	-RQGTIVNVS	SLMGKVAAPT	MATYSATKFA	IIGFTQALRQ	ELAAH--NIR
Nsp-0708.p-Nsp-0708-3536 (2.0d-26)	133	-REGTIVNVS	SLMGKVAAPT	MATYSATKFA	ILGFTQALRR	ELAEH--NIR
N-7107.p-N-7107-1296 (2.0d-26)	133	-RQGIIVNVS	SLMGKVAAPT	MATYSATKFA	ILGFTQALRQ	ELAEY--NIQ
Npun.p-NpR1019 (4.0d-26)	133	-RQGTIVNVS	SLMGKVAAPT	MATYSATKFA	ILGFTQALRR	ELAEH--NIR
N-7524.p-N-7524-4265 (1.0d-25)	133	-RQGTIIIVS	SLMGKVAAPT	MATYSATKFA	ILGFTQALRR	ELAEY--NIQ
M7126-SCAD-E	133	-KQGRIVNVS	SLMGKIAAPT	MATYSATKFA	ILGFTQALRR	ELAQH--NIQ
R7116-SCAD-E	137	-NQGTIVNVS	SLMGKVAAPT	MSTYSATKFA	ILGFTEALRR	ELAPH--NIK
cyt.p-cce_3588 (3.0d-27)	139	-QQGTIVNVS	SLMGKIAAPT	MATYSATKFA	LLGFTQALRG	ELAPY--NIR
ctc.p-c0110?06289 (2.0d-26)	138	-KQGTIVNVS	SLMGKIAAPT	MATYSATKFA	LLGFTQALRG	ELAPY--NIR
cyr.p-c8801?0598 (2.0d-26)	133	-QQGTIVNVS	SLMGKIAAPT	MATYSATKFA	LLGFTEALRG	ELAPY--NIR
Amar.p-AM1_6363 (1.0d-30)	133	-KEGRIVNVS	SLMGKIGAPT	MATYSATKFA	ILGFTQALRT	ELAAH--NIK
Amar.p-AM1_0210 (1.0d-27)	135	-RAGTIVNVS	SLMGKLAAPT	YSTYSATKFA	LLGMTQSLRM	ELASY--NVQ
lyn.p-l8106?00785 (4.0d-31)	129	-KKGTIVNVG	SVGGKMPLPD	MTAYCASKYA	VTGLTETLRL	ELDPK--GIN
ter.p-Tery_3453 (8.0d-31)	129	-KSGTIIINVG	SFGGKMPLPQ	MTAYCASKYA	VTGLTDTLRL	ELQSK--GIN
A29413.p-Ava0943 (1.0d-30)	150	-CAGTIVNVS	SIGGLEPIPY	HVPYTASKYA	ITGLTKSLHA	ELSPK--GIH
A7120.p-A112963 (5.0d-29)	150	-GAGTIVNVS	SIGGLEPIPY	HVPYTASKYA	ITGLTKSLHA	ELSPK--NIH
Npun.p-NpR4797 (3.0d-30)	130	-RSGTIVNLS	SIGGKVPSAY	LVPYCTSKFG	VTGLTESLQV	ELQPK--GIH
Cyl-7417.p-Cyl-7417-4424 (3.0d-30)	130	-GSGTIVNLS	SIGGKVPTAY	LVAYCTSKFG	VTGLTEALQA	ELQPK--GIH
MAST-10914-SCAD-E	130	-KSGTIVNLS	SIGGKVPTPY	VVYCTSKFA	VTGLTESLHA	ELQPK--GIH
M7126-SCAD-C	130	-GSGTIVNVS	SIGGKVPTPY	LVPYCTSKFA	VTGLTEALQT	ELKPK--GIH
R7116-SCAD-D	128	-SAGTIVNVG	SIGGKLPLPE	MTVYCTSKYA	ITGLTETLRL	ELKPK--NIH
Npun.p-NpF0199 (2.0d-29)	165	-HQGRIVNIS	SIGGKVVFPF	MLPYCASKFA	LTGLSEGMRA	ELAQE--GIS
A7120.p-Alr5358 (3.0d-156)	133	-GSGRIVNIA	SLAGKKGVAF	NSVYSASKAG	LIMWTDAMRQ	ELVGT--GVN
A29413.p-Ava2596 (8.0d-151)	133	-GSGRIVNIA	SLAGKKGVAF	NSVYSASKAG	LIMWTDAMRQ	ELVGT--GVN
N-7524.p-N-7524-5224 (2.0d-121)	133	-GSGRIVNIA	SLAGKKGIAF	NSIYSASKAS	LIMWTDAVRQ	ELAGS--GVH
Cyl-7417.p-Cyl-7417-1544 (2.0d-100)	133	-DSGHIVNIA	SLAGKKGVFY	NSIYSATKAG	LIWTDALRQ	ELAST--GMN
MAST-10914-SCAD-A	133	-NSGHIVNIS	SGSGKKGAPY	NSIYSASKAG	MIMWTDMSRQ	ELTNT--NVG
N-7524.p-N-7524-5355 (2.0d-74)	133	-NSGHIVNIA	SGSGKKGAPY	NSIYSASKAG	LIMWTDAVRQ	ELADT--KVN
Npun.p-NpF3363 (2.0d-81)	133	-NSGHIVNIA	SLAAKKGHPY	DSIYSASKAG	LLMWSDAVRQ	ELADT--GVE
R7116-SCAD-A	146	-ASGHIINIA	SLTGKKGLAY	DSIYSASKAG	LITWADALKQ	ELANT--NIK
cyr.p-c8801?3820 (4.0d-26)	131	-GSGGIINVA	SIAAFQPLPY	LSVYAATKAF	VLSLSEALWA	ENKDT--GVN
A7120.p-A111418 (8.0d-26)	141	--QQQLVAIS	SICGKTGVPT	RTGYVASKHA	MQGFFDTLRI	ELHST--GVD
consensus	201	* ::	* .	* :*	:	:

A7120.p-Alr1894	(1.0d-26)	185	VNAVAPGFIA	TDMTSNLK--	-----	-----	-----
A29413.p-Ava3764	(1.0d-26)	185	VNAVAPGFIA	TDMTSNLK--	-----	-----	-----
N-7524.p-N-7524-0010	(9.0d-30)	185	VNAIAPGFIA	TDMTSDLK--	-----	-----	-----
M7126-SCAD-B		188	VNAVAPGFIS	TDMTSNLSN-	-----	-----	-----
nod.p-n9414?22428	(4.0d-28)	181	VNAVAPGFIA	TDMTSSLSN-	-----	-----	-----
MAST-10914-SCAD-B		188	VNAVAPGFIA	TDMTSNLNN-	-----	-----	-----
Cal-6303.p-Cal-6303-1520	(5.0d-28)	188	VNAVAPGFIA	TDMTSNLGN-	-----	-----	-----
Npun.p-NpF2349	(4.0d-29)	181	VNAVAPGFIT	TDMTSDLNN-	-----	-----	-----
N-7107.p-N-7107-0937	(1.0d-27)	188	VNAVAPGFIT	TDMTSNLSN-	-----	-----	-----
Ana-90.p-ana90-1712	(1.0d-28)	181	VNAVAPGFIT	TDMTSDIK--	-----	-----	-----
Acyl-7122.p-acyl-4545	(9.0d-28)	181	VNAVAPGFIT	TDMTSDIK--	-----	-----	-----
Nsp-0708.p-Nsp-0708-2353	(9.0d-27)	181	VNAVAPGFIT	TDMTSNIA--	-----	-----	-----
Cyl-505.p-Cyl-505-0204	(2.0d-28)	181	VNAVAPGFIQ	TDMTSEIK--	-----	-----	-----
Cyl-7417.p-Cyl-7417-2349	(6.0d-29)	188	ANAVAPGFIT	TDMTNDLK--	-----	-----	-----
R7116-SCAD-C		188	VNAVSPGFIE	TDMTSELK--	-----	-----	-----
ter.p-Tery_3438	(2.0d-28)	188	ANVVAPGFIE	TDMTKDLKN-	-----	-----	-----
lyn.p-l8106?21814	(1.0d-27)	188	VNAVAPGFIE	TDMTKDLKN-	-----	-----	-----
Amar.p-AM1_5632	(1.0d-26)	181	VNAVAPGFIA	TDMTEGLG--	-----	-----	-----
cyr.p-c8801?2930	(1.0d-28)	184	VNAVAPGFIT	TDMTSDIK--	-----	-----	-----
S6803.p-Slr0886	(4.0d-27)	181	VNAVAPGFIA	TDMTENLN--	-----	-----	-----
mae.p-MAE_33900	(3.0d-29)	188	VNAVAPGFIE	TDMTHDLK--	-----	-----	-----
TeBP1.p-tlr1502	(5.0d-29)	179	VNAVAPGFIA	TEMTAELK--	-----	-----	-----
S7942.p-Synpcc7942_0684	(4.0d-26)	183	VNAVAPGFIA	TDMTSELA--	-----	-----	-----
syx.p-SynWH7803_1861	(7.0d-30)	184	VNAVAPGFIA	TDMTKDLD--	-----	-----	-----
S7805.p-WH7805_13603	(5.0d-28)	184	VNAVAPGFIA	TDMTKDLD--	-----	-----	-----
S9916.p-RS9916_33507	(8.0d-31)	184	VNAVAPGFIA	TDMTKDLD--	-----	-----	-----
Ssp-RS9917.p-Ssp-RS9917-1614	(2.0d-29)	242	VNAVAPGFIA	TDMTKDLD--	-----	-----	-----
S9917.p-RS9917_09056	(3.0d-29)	184	VNAVAPGFIA	TDMTKDLD--	-----	-----	-----
syg.p-sync_2137	(4.0d-29)	184	VNAVAPGFIA	TDMTKDLE--	-----	-----	-----
P9313.p-PMT1333	(6.0d-29)	184	VNAVAPGFIT	TDMTKELD--	-----	-----	-----
pmf.p-P9303_06521	(1.0d-28)	196	VNAVAPGFIT	TDMTKELD--	-----	-----	-----
S107.p-BL107_09856	(2.0d-28)	201	VNAVAPGFIA	TDMTKDLD--	-----	-----	-----
S9902.p-Sync9902_1745	(4.0d-28)	184	VNAVAPGFIA	TDMTKDLD--	-----	-----	-----
S9605.p-Sync9605_0617	(4.0d-27)	198	VNAVAPGFIA	TDMTKDLD--	-----	-----	-----
S8102.p-SynW1852	(9.0d-28)	184	VNAVAPGFIA	TDMTKDLD--	-----	-----	-----
syr.p-SynRCC307_0681	(2.0d-28)	184	VNAVAPGFIA	TDMTKDLA--	-----	-----	-----
S5701.p-WH5701_07809	(1.0d-28)	186	VNAVAPGFIA	SDMTKDLD--	-----	-----	-----
pmn.p-PMN2A_1785	(5.0d-28)	184	VNAVAPGFIS	TDMTKDLN--	-----	-----	-----
pme.p-NATL1_05081	(1.0d-27)	184	VNAVAPGFIS	TDMTKDLD--	-----	-----	-----



pmz.p-p9211?06582	(1.0d-27)	184	VNAVAPGFIE	TDMTKDLD--	-----	-----	-----
PRO1375.p-Pro0452	(7.0d-27)	184	VNAVAPGFIE	TDMTKELD--	-----	-----	-----
Gvi.p-glr3506	(5.0d-28)	182	VNAVAPGFIA	TDMTSALE--	-----	-----	-----
pmb.p-P9601_05091	(9.0d-28)	184	VNAIAPGFIE	TEMTEKLN--	-----	-----	-----
pmi.p-PMT9312_0453	(1.0d-27)	184	VNAIAPGFIE	TEMTEKLN--	-----	-----	-----
pmg.p-P9301_04781	(1.0d-27)	184	VNAIAPGFIE	TEMTEKLN--	-----	-----	-----
PMED4.p-PMM0453	(9.0d-28)	184	VNAIAPGFIE	TEMTEKLN--	-----	-----	-----
pmc.p-P9515_05161	(2.0d-27)	184	VNAIAPGFIE	TEMTEKLN--	-----	-----	-----
Npun.p-NpR0578	(6.0d-27)	186	INAVCPGYID	TSMMDRFTGG	T-----	-----	-----
Cyl-7417.p-Cyl-7417-0303	(5.0d-26)	180	VNAVSPGPIV	TPTLTEIMLQ	IGSMQGWGTD	-----	-----
Npun.p-NpF2231	(1.0d-26)	181	VNALCLAGVK	TDMGKELK--	-----	-----	-----
Cyl-7417.p-Cyl-7417-3400	(1.0d-26)	181	VNALCPAGVK	TDMGKTL--	-----	-----	-----
Acyl-7122.p-acyl-3225	(4.0d-28)	180	VTAICPGSVN	TEIWDTAT--	-----	-----	-----
Nsp-0708.p-Nsp-0708-2459	(6.0d-26)	180	VIAICPGSVN	TEIWDTET--	-----	-----	-----
Ana-90.p-ana90-1189	(1.0d-28)	180	VIAICPGSVN	TEIWDTPT--	-----	-----	-----
Cyl-505.p-Cyl-505-2036	(2.0d-32)	180	VSAICPGAVN	TEIWDTET--	-----	-----	-----
A29413.p-Ava2536	(2.0d-28)	180	VSAICPGAVN	TGLWDTET--	-----	-----	-----
A7120.p-Alr5286	(2.0d-28)	194	VTAICPGAVN	TGLWDTET--	-----	-----	-----
N-7524.p-N-7524-4179	(1.0d-27)	180	VTTICPGSVN	TGLWDTET--	-----	-----	-----
MAST-10914-SCAD-C		184	VIAICPGAVN	TELWDTET--	-----	-----	-----
Cyl-7417.p-Cyl-7417-1063	(4.0d-30)	180	VTAICPGAVN	TELWDTET--	-----	-----	-----
nod.p-n9414?21215	(5.0d-26)	179	VTAICPGAVN	TELWDTET--	-----	-----	-----
N-7107.p-N-7107-1008	(2.0d-29)	180	VTAICPGSVN	TEIWDTDT--	-----	-----	-----
M7126-SCAD-A		180	VTAVCPGAVN	TGLWDTET--	-----	-----	-----
R7116-SCAD-B		179	VTAICPGAVN	TEIWDTKT--	-----	-----	-----
lyn.p-l8106?23630	(2.0d-26)	180	VTAICPGAVN	TPLWDTET--	-----	-----	-----
Amar.p-AM1_5634	(3.0d-27)	180	VTAVCPGAVN	TPLWDTDT--	-----	-----	-----
cyb.p-CYB_0189	(1.0d-27)	182	VTSLCPGAVD	TSLWDTGT--	-----	-----	-----
cya.p-CYA_2793	(8.0d-26)	182	VTSLCLGAVD	TPLWDT---	-----	-----	-----
M7126-SCAD-D		179	VTSFCPGGMN	TAFWQTPD--	-----	-----	-----
cyb.p-CYB_0005	(4.0d-34)	180	VILIEPGPVA	TEFGRVAEET	FAAVVNP--	-----	-----
cya.p-CYA_0005	(2.0d-33)	180	VIVIEPGPVA	TEFGRVAEET	FAAVVNP--	-----	-----
N-7107.p-N-7107-5182	(3.0d-28)	181	VTIIEPGLVE	TEINNHVTD	VAKKN----	-----	-----
Npun.p-NpR3707	(3.0d-27)	181	VTIIEPGLVD	TEIDNQITDP	VAKQR-----	-----	-----
Acyl-7122.p-acyl-1205	(2.0d-26)	206	VTIIEPGLVE	TEIDQHITDI	VAKQE-----	-----	-----
R7116-SCAD-F		193	VSSVDPGLVE	TEFS-QVRFH	GDDEK-----	-----	-----
Npun.p-NpF0204	(3.0d-28)	188	VTLIHPGRID	TPYNEHARSY	MPKQPAHRGM	I-----	-----
MAST-10914-SCAD-D		180	VIALLPSTLD	TDMVRELQWF	R-----	-----	-----
Cal-6303.p-Cal-6303-3407	(1.0d-27)	180	VLGLLPSTLD	TDMVRDLKWF	R-----	-----	-----
Ana-90.p-ana90-4359	(1.0d-27)	180	VIALLPSTLE	TDMVRDLQSF	R-----	-----	-----

Cyl-7417.p-Cyl-7417-4762 (6.0d-27)	180	VIALLPRTLTD	TDMVRDLQLF	R-----	-----	-----
Nsp-0708.p-Nsp-0708-3536 (2.0d-26)	180	VVALLPRTLTD	TDMVRDLKLF	R-----	-----	-----
N-7107.p-N-7107-1296 (2.0d-26)	180	VKALLPSLTD	TDMVRDLQLF	R-----	-----	-----
Npun.p-NpR1019 (4.0d-26)	180	VIALLPSSLTD	TDMVRDLKLF	R-----	-----	-----
N-7524.p-N-7524-4265 (1.0d-25)	180	VKALLPSLTD	TDMVRDFKLF	R-----	-----	-----
M7126-SCAD-E	180	VQALLPRTLTD	TDMVRDFQNF	R-----	-----	-----
R7116-SCAD-E	184	VVSLLPRTLTD	TDMVRDLELY	R-----	-----	-----
cyt.p-cce_3588 (3.0d-27)	186	VVALLPSLTD	TDMVRGLDWF	R-----	-----	-----
ctc.p-c0110?06289 (2.0d-26)	185	VIALLPSSLTD	TDMIQGLDWF	R-----	-----	-----
cyr.p-c8801?0598 (2.0d-26)	180	VVALLPSLTD	TDMIADLEWF	R-----	-----	-----
Amar.p-AM1_6363 (1.0d-30)	180	VTALLPSLTE	TDMTRNTQRF	R-----	-----	-----
Amar.p-AM1_0210 (1.0d-27)	182	VVALLPRTLTE	TDMVQNTDKF	A-----	-----	-----
lyn.p-l8106?00785 (4.0d-31)	176	VCAVHPGVIN	SNFMERAQFR	GEN-----	-----	-----
ter.p-Tery_3453 (8.0d-31)	176	ISSVQPGVIN	SNFMERAKFR	GGD-----	-----	-----
A29413.p-Ava0943 (1.0d-30)	197	VSGIYPSFIS	TQLMERAIFR	GKD-----	-----	-----
A7120.p-A112963 (5.0d-29)	197	VSGIYPSFIS	TQLMERAIFR	GKD-----	-----	-----
Npun.p-NpR4797 (3.0d-30)	177	VCGIYPNLIK	STLMERAVFR	QGD-----	-----	-----
Cyl-7417.p-Cyl-7417-4424 (3.0d-30)	177	VCGIYPNLIK	SSLMERAIFR	GKD-----	-----	-----
MAST-10914-SCAD-E	177	VCGIYPNLIK	SSLMERAIFR	GSD-----	-----	-----
M7126-SCAD-C	177	VCGIYPNLIK	SSFMERAVFR	GKD-----	-----	-----
R7116-SCAD-D	175	VSAVHPSATN	SNFMERAQFR	GSS-----	-----	-----
Npun.p-NpF0199 (2.0d-29)	212	VTTVCPGLIR	TGAPENVIFK	GQHRKEYAWF	SISDSLPLLS	MSAEVVAYKT
A7120.p-Alr5358 (3.0d-156)	180	ISVVCPGYVS	QTGMTVDTRV	S-----	-----	-----
A29413.p-Ava2596 (8.0d-151)	180	ISVVCPGYVS	QTGMTVDTRV	S-----	-----	-----
N-7524.p-N-7524-5224 (2.0d-121)	180	ISAVCPGYVS	HTGMTVDPRV	P-----	-----	-----
Cyl-7417.p-Cyl-7417-1544 (2.0d-100)	180	ISVICPGYIS	ETGMTFDSRI	P-----	-----	-----
MAST-10914-SCAD-A	180	VSVVCPGYTS	AG-MFVNFGL	P-----	-----	-----
N-7524.p-N-7524-5355 (2.0d-74)	180	ISVVCPGYTA	AG-MFFAFGL	P-----	-----	-----
Npun.p-NpF3363 (2.0d-81)	180	ISTICPGYIA	EQGMLADTGI	P-----	-----	-----
R7116-SCAD-A	193	ISNICPESIS	EQASFADTGI	S-----	-----	-----
cyr.p-c8801?3820 (4.0d-26)	178	ILALCPGPTE	SNFFKVADFP	-----	-----	-----
A7120.p-A111418 (8.0d-26)	187	VLVVSPGFVA	TDIRQALGA	D-----	-----	-----
consensus	251	.	.			

A7120.p-Alr1894	(1.0d-26)	202	-----	-----	-----	-----	-----
A29413.p-Ava3764	(1.0d-26)	202	-----	-----	-----	-----	-----
N-7524.p-N-7524-0010	(9.0d-30)	202	-----	-----	-----	-----	-----
M7126-SCAD-B		206	-----	-----	-----	-----	-----
nod.p-n9414?22428	(4.0d-28)	199	-----	-----	-----	-----	-----
MAST-10914-SCAD-B		206	-----	-----	-----	-----	-----
Cal-6303.p-Cal-6303-1520	(5.0d-28)	206	-----	-----	-----	-----	-----
Npun.p-NpF2349	(4.0d-29)	199	-----	-----	-----	-----	-----
N-7107.p-N-7107-0937	(1.0d-27)	206	-----	-----	-----	-----	-----
Ana-90.p-ana90-1712	(1.0d-28)	198	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-4545	(9.0d-28)	198	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-2353	(9.0d-27)	198	-----	-----	-----	-----	-----
Cyl-505.p-Cyl-505-0204	(2.0d-28)	198	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-2349	(6.0d-29)	205	-----	-----	-----	-----	-----
R7116-SCAD-C		205	-----	-----	-----	-----	-----
ter.p-Tery_3438	(2.0d-28)	206	-----	-----	-----	-----	-----
lyn.p-l8106?21814	(1.0d-27)	206	-----	-----	-----	-----	-----
Amar.p-AM1_5632	(1.0d-26)	198	-----	-----	-----	-----	-----
cyr.p-c8801?2930	(1.0d-28)	201	-----	-----	-----	-----	-----
S6803.p-Slr0886	(4.0d-27)	198	-----	-----	-----	-----	-----
mae.p-MAE_33900	(3.0d-29)	205	-----	-----	-----	-----	-----
TeBP1.p-tlr1502	(5.0d-29)	196	-----	-----	-----	-----	-----
S7942.p-Synpcc7942_0684	(4.0d-26)	200	-----	-----	-----	-----	-----
syx.p-SynWH7803_1861	(7.0d-30)	201	-----	-----	-----	-----	-----
S7805.p-WH7805_13603	(5.0d-28)	201	-----	-----	-----	-----	-----
S9916.p-RS9916_33507	(8.0d-31)	201	-----	-----	-----	-----	-----
Ssp-RS9917.p-Ssp-RS9917-1614	(2.0d-29)	259	-----	-----	-----	-----	-----
S9917.p-RS9917_09056	(3.0d-29)	201	-----	-----	-----	-----	-----
syg.p-sync_2137	(4.0d-29)	201	-----	-----	-----	-----	-----
P9313.p-PMT1333	(6.0d-29)	201	-----	-----	-----	-----	-----
pmf.p-P9303_06521	(1.0d-28)	213	-----	-----	-----	-----	-----
S107.p-BL107_09856	(2.0d-28)	218	-----	-----	-----	-----	-----
S9902.p-Sync9902_1745	(4.0d-28)	201	-----	-----	-----	-----	-----
S9605.p-Sync9605_0617	(4.0d-27)	215	-----	-----	-----	-----	-----
S8102.p-SynW1852	(9.0d-28)	201	-----	-----	-----	-----	-----
syr.p-SynRCC307_0681	(2.0d-28)	201	-----	-----	-----	-----	-----
S5701.p-WH5701_07809	(1.0d-28)	203	-----	-----	-----	-----	-----
pmn.p-PMN2A_1785	(5.0d-28)	201	-----	-----	-----	-----	-----
pme.p-NATL1_05081	(1.0d-27)	201	-----	-----	-----	-----	-----

pmz.p-p9211?06582	(1.0d-27)	201	-----	-----	-----	-----	-----
PRO1375.p-Pro0452	(7.0d-27)	201	-----	-----	-----	-----	-----
Gvi.p-glr3506	(5.0d-28)	199	-----	-----	-----	-----	-----
pmb.p-P9601_05091	(9.0d-28)	201	-----	-----	-----	-----	-----
pmi.p-PMT9312_0453	(1.0d-27)	201	-----	-----	-----	-----	-----
pmg.p-P9301_04781	(1.0d-27)	201	-----	-----	-----	-----	-----
PMED4.p-PMM0453	(9.0d-28)	201	-----	-----	-----	-----	-----
pmc.p-P9515_05161	(2.0d-27)	201	-----	-----	-----	-----	-----
Npun.p-NpR0578	(6.0d-27)	206	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-0303	(5.0d-26)	209	-----	-----	-----	-----	-----
Npun.p-NpF2231	(1.0d-26)	198	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-3400	(1.0d-26)	198	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-3225	(4.0d-28)	197	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-2459	(6.0d-26)	197	-----	-----	-----	-----	-----
Ana-90.p-ana90-1189	(1.0d-28)	197	-----	-----	-----	-----	-----
Cyl-505.p-Cyl-505-2036	(2.0d-32)	197	-----	-----	-----	-----	-----
A29413.p-Ava2536	(2.0d-28)	197	-----	-----	-----	-----	-----
A7120.p-Alr5286	(2.0d-28)	211	-----	-----	-----	-----	-----
N-7524.p-N-7524-4179	(1.0d-27)	197	-----	-----	-----	-----	-----
MAST-10914-SCAD-C		201	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-1063	(4.0d-30)	197	-----	-----	-----	-----	-----
nod.p-n9414?21215	(5.0d-26)	196	-----	-----	-----	-----	-----
N-7107.p-N-7107-1008	(2.0d-29)	197	-----	-----	-----	-----	-----
M7126-SCAD-A		197	-----	-----	-----	-----	-----
R7116-SCAD-B		196	-----	-----	-----	-----	-----
lyn.p-18106?23630	(2.0d-26)	197	-----	-----	-----	-----	-----
Amar.p-AM1_5634	(3.0d-27)	197	-----	-----	-----	-----	-----
cyb.p-CYB_0189	(1.0d-27)	199	-----	-----	-----	-----	-----
cya.p-CYA_2793	(8.0d-26)	197	-----	-----	-----	-----	-----
M7126-SCAD-D		196	-----	-----	-----	-----	-----
cyb.p-CYB_0005	(4.0d-34)	207	-----	-----	-----	-----	-----
cya.p-CYA_0005	(2.0d-33)	207	-----	-----	-----	-----	-----
N-7107.p-N-7107-5182	(3.0d-28)	205	-----	-----	-----	-----	-----
Npun.p-NpR3707	(3.0d-27)	205	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-1205	(2.0d-26)	230	-----	-----	-----	-----	-----
R7116-SCAD-F		216	-----	-----	-----	-----	-----
Npun.p-NpF0204	(3.0d-28)	218	-----	-----	-----	-----	-----
MAST-10914-SCAD-D		200	-----	-----	-----	-----	-----
Cal-6303.p-Cal-6303-3407	(1.0d-27)	200	-----	-----	-----	-----	-----
Ana-90.p-ana90-4359	(1.0d-27)	200	-----	-----	-----	-----	-----

Cyl-7417.p-Cyl-7417-4762	(6.0d-27)	200	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-3536	(2.0d-26)	200	-----	-----	-----	-----	-----
N-7107.p-N-7107-1296	(2.0d-26)	200	-----	-----	-----	-----	-----
Npun.p-NpR1019	(4.0d-26)	200	-----	-----	-----	-----	-----
N-7524.p-N-7524-4265	(1.0d-25)	200	-----	-----	-----	-----	-----
M7126-SCAD-E		200	-----	-----	-----	-----	-----
R7116-SCAD-E		204	-----	-----	-----	-----	-----
cyt.p-cce_3588	(3.0d-27)	206	-----	-----	-----	-----	-----
ctc.p-c0110?06289	(2.0d-26)	205	-----	-----	-----	-----	-----
cyr.p-c8801?0598	(2.0d-26)	200	-----	-----	-----	-----	-----
Amar.p-AM1_6363	(1.0d-30)	200	-----	-----	-----	-----	-----
Amar.p-AM1_0210	(1.0d-27)	202	-----	-----	-----	-----	-----
lyn.p-l8106?00785	(4.0d-31)	198	-----	-----	-----	-----	-----
ter.p-Tery_3453	(8.0d-31)	198	-----	-----	-----	-----	-----
A29413.p-Ava0943	(1.0d-30)	219	-----	-----	-----	-----	-----
A7120.p-Al12963	(5.0d-29)	219	-----	-----	-----	-----	-----
Npun.p-NpR4797	(3.0d-30)	199	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-4424	(3.0d-30)	199	-----	-----	-----	-----	-----
MAST-10914-SCAD-E		199	-----	-----	-----	-----	-----
M7126-SCAD-C		199	-----	-----	-----	-----	-----
R7116-SCAD-D		197	-----	-----	-----	-----	-----
Npun.p-NpF0199	(2.0d-29)	262	IAALKRGDAE	IILSLPAQIA	TRFHGLFPGL	NTNLLTWVNW	LLPAASGGIG
A7120.p-Alr5358	(3.0d-156)	200	-----	-----	-----	-----	-----
A29413.p-Ava2596	(8.0d-151)	200	-----	-----	-----	-----	-----
N-7524.p-N-7524-5224	(2.0d-121)	200	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-1544	(2.0d-100)	200	-----	-----	-----	-----	-----
MAST-10914-SCAD-A		199	-----	-----	-----	-----	-----
N-7524.p-N-7524-5355	(2.0d-74)	199	-----	-----	-----	-----	-----
Npun.p-NpF3363	(2.0d-81)	200	-----	-----	-----	-----	-----
R7116-SCAD-A		213	-----	-----	-----	-----	-----
cyr.p-c8801?3820	(4.0d-26)	197	-----	-----	-----	-----	-----
A7120.p-Al11418	(8.0d-26)	207	-----	-----	-----	-----	-----
consensus		301	-----	-----	-----	-----	-----

A7120.p-Alr1894	(1.0d-26)	203	-----	-----	-----	-SEGILQ---	YIPLGRYG--
A29413.p-Ava3764	(1.0d-26)	203	-----	-----	-----	-SEGILQ---	YIPLGRYG--
N-7524.p-N-7524-0010	(9.0d-30)	203	-----	-----	-----	-ADEILK---	YIPLGRYG--
M7126-SCAD-B		207	-----	-----	-----	-TEEILK---	YIPLGRYG--
nod.p-n9414?22428	(4.0d-28)	200	-----	-----	-----	-TEDILK---	YIPLGRYG--
MAST-10914-SCAD-B		207	-----	-----	-----	-TEEILK---	YIPLGRYG--
Cal-6303.p-Cal-6303-1520	(5.0d-28)	207	-----	-----	-----	-TEEIIK---	FIPLGRYG--
Npun.p-NpF2349	(4.0d-29)	200	-----	-----	-----	-PEDILK---	YIPLGRFG--
N-7107.p-N-7107-0937	(1.0d-27)	207	-----	-----	-----	-TEEILK---	FIPLGRYG--
Ana-90.p-ana90-1712	(1.0d-28)	199	-----	-----	-----	-ADGILQ---	YIPLGRFG--
Acyl-7122.p-acyl-4545	(9.0d-28)	199	-----	-----	-----	-ADNILQ---	FIPLGRYG--
Nsp-0708.p-Nsp-0708-2353	(9.0d-27)	199	-----	-----	-----	-AEGILQ---	YIPLGRFG--
Cyl-505.p-Cyl-505-0204	(2.0d-28)	199	-----	-----	-----	-AEGILQ---	YIPLGRFG--
Cyl-7417.p-Cyl-7417-2349	(6.0d-29)	206	-----	-----	-----	-ADEILN---	YIPLGRYG--
R7116-SCAD-C		206	-----	-----	-----	-SEEILK---	AIPLGRYG--
ter.p-Tery_3438	(2.0d-28)	207	-----	-----	-----	-SEEIIK---	FIPLGRYG--
lyn.p-l8106?21814	(1.0d-27)	207	-----	-----	-----	-TEEILK---	FIPLGRYG--
Amar.p-AM1_5632	(1.0d-26)	199	-----	-----	-----	-SEEIIK---	FIPLGRYG--
cyr.p-c8801?2930	(1.0d-28)	202	-----	-----	-----	-SEEIIK---	FIPLGRYG--
S6803.p-Slr0886	(4.0d-27)	199	-----	-----	-----	-AEPILQ---	FIPLARYG--
mae.p-MAE_33900	(3.0d-29)	206	-----	-----	-----	-ADEILK---	YIPLSRYG--
TeBP1.p-tlr1502	(5.0d-29)	197	-----	-----	-----	-AEDILK---	FIPLGRYG--
S7942.p-Syncpcc7942_0684	(4.0d-26)	201	-----	-----	-----	-AEKLE---	VIPLGRYG--
syx.p-SynWH7803_1861	(7.0d-30)	202	-----	-----	-----	-AEGILS---	AIPLGTFG--
S7805.p-WH7805_13603	(5.0d-28)	202	-----	-----	-----	-SEGILT---	AIPLGTFG--
S9916.p-RS9916_33507	(8.0d-31)	202	-----	-----	-----	-ADGILA---	AIPLGSFG--
Ssp-RS9917.p-Ssp-RS9917-1614	(2.0d-29)	260	-----	-----	-----	-AEGILA---	AIPLGRFG--
S9917.p-RS9917_09056	(3.0d-29)	202	-----	-----	-----	-AEGILA---	AIPLGRFG--
syg.p-sync_2137	(4.0d-29)	202	-----	-----	-----	-ADAILS---	AIPLGRFG--
P9313.p-PMT1333	(6.0d-29)	202	-----	-----	-----	-SEPILA---	AIPLGSFG--
pmf.p-P9303_06521	(1.0d-28)	214	-----	-----	-----	-SEPILA---	AIPLGSFG--
S107.p-BL107_09856	(2.0d-28)	219	-----	-----	-----	-ATAILK---	DIPLGTFG--
S9902.p-Sync9902_1745	(4.0d-28)	202	-----	-----	-----	-ATAILK---	DIPLGTFG--
S9605.p-Sync9605_0617	(4.0d-27)	216	-----	-----	-----	-AEAILK---	DIPLGTFG--
S8102.p-SynW1852	(9.0d-28)	202	-----	-----	-----	-ADAILK---	DIPLGQFG--
syr.p-SynRCC307_0681	(2.0d-28)	202	-----	-----	-----	-AEALLN---	AIPLGRYG--
S5701.p-WH5701_07809	(1.0d-28)	204	-----	-----	-----	-VERIQA---	AIPLGRLG--
pmn.p-PMN2A_1785	(5.0d-28)	202	-----	-----	-----	-SESILS---	AIPLGRFG--
pme.p-NATL1_05081	(1.0d-27)	202	-----	-----	-----	-SESILS---	AIPLGRFG--

pmz.p-p9211?06582	(1.0d-27)	202	-----	-----	-----	-SEQILS---	AIPLGEFG--
PRO1375.p-Pro0452	(7.0d-27)	202	-----	-----	-----	-AEPILS---	AIPLGHFG--
Gvi.p-glr3506	(5.0d-28)	200	-----	-----	-----	-LEPILA---	QVPLRRVG--
pmb.p-P9601_05091	(9.0d-28)	202	-----	-----	-----	-TEEILK---	VIPLGKLG--
pmi.p-PMT9312_0453	(1.0d-27)	202	-----	-----	-----	-TEEILK---	VIPLGKLG--
pmg.p-P9301_04781	(1.0d-27)	202	-----	-----	-----	-TEEILK---	VIPLGKLG--
PMED4.p-PMM0453	(9.0d-28)	202	-----	-----	-----	-NEEI IK---	AIPLGKLG--
pmc.p-P9515_05161	(2.0d-27)	202	-----	-----	-----	-NEEIVK---	AIPLGKLG--
Npun.p-NpR0578	(6.0d-27)	207	-----	-----	-----	PE GRQKVVS---	EEPIGRMG--
Cyl-7417.p-Cyl-7417-0303	(5.0d-26)	210	-----	-----	-----	LKQ IEQHLLKGM	SNPTGRLG--
Npun.p-NpF2231	(1.0d-26)	199	-----	-----	-----	--ETDGN---	CVNDTYFM--
Cyl-7417.p-Cyl-7417-3400	(1.0d-26)	199	-----	-----	-----	--EADGT---	PVNDSYFM--
Acyl-7122.p-acyl-3225	(4.0d-28)	198	-----	-----	-----	-VNADFD---	---RTKML--
Nsp-0708.p-Nsp-0708-2459	(6.0d-26)	198	-----	-----	-----	-VHVNFDF---	---RSKML--
Ana-90.p-ana90-1189	(1.0d-28)	198	-----	-----	-----	-VQANFD---	---RSQML--
Cyl-505.p-Cyl-505-2036	(2.0d-32)	198	-----	-----	-----	-VNANFD---	---RSKML--
A29413.p-Ava2536	(2.0d-28)	198	-----	-----	-----	-VKADFD---	---RSKML--
A7120.p-Alr5286	(2.0d-28)	212	-----	-----	-----	-VKADFD---	---RSKML--
N-7524.p-N-7524-4179	(1.0d-27)	198	-----	-----	-----	-VHADFD---	---RSQML--
MAST-10914-SCAD-C		202	-----	-----	-----	-VNANFD---	---RSKML--
Cyl-7417.p-Cyl-7417-1063	(4.0d-30)	198	-----	-----	-----	-VHANLD---	---RSKML--
nod.p-n9414?21215	(5.0d-26)	197	-----	-----	-----	-VQSDFD---	---RSKML--
N-7107.p-N-7107-1008	(2.0d-29)	198	-----	-----	-----	-VHANFD---	---RSKML--
M7126-SCAD-A		198	-----	-----	-----	-VNVNFD---	---RAKML--
R7116-SCAD-B		197	-----	-----	-----	-VNADFD---	---RSNML--
lyn.p-18106?23630	(2.0d-26)	198	-----	-----	-----	-VQADFD---	---RATML--
Amar.p-AM1_5634	(3.0d-27)	198	-----	-----	-----	-VDADFD---	---RSAML--
cyb.p-CYB_0189	(1.0d-27)	200	-----	-----	-----	-VGVNFD---	---RSKML--
cya.p-CYA_2793	(8.0d-26)	198	-----	-----	-----	-VQVDFD---	---RSKML--
M7126-SCAD-D		197	-----	-----	-----	-NQAHQQ---	---QAENFM--
cyb.p-CYB_0005	(4.0d-34)	208	-----	-----	-----	---GPYKA	ILDKTAELAS
cya.p-CYA_0005	(2.0d-33)	208	-----	-----	-----	---GPYKA	ILDKAAELAS
N-7107.p-N-7107-5182	(3.0d-28)	206	-----	-----	-----	---VEE	RLKAITPLQS
Npun.p-NpR3707	(3.0d-27)	206	-----	-----	-----	---IEE	RRKAITPLHS
Acyl-7122.p-acyl-1205	(2.0d-26)	231	-----	-----	-----	---IEA	RRKAIAPLQS
R7116-SCAD-F		217	-----	-----	-----	---AKK	VYQGLTPLTP
Npun.p-NpF0204	(3.0d-28)	219	-----	-----	-----	---YPPEA	VTEAILYAAE
MAST-10914-SCAD-D		201	-----	-----	-----	---WVL	PTTPQKVAQA
Cal-6303.p-Cal-6303-3407	(1.0d-27)	201	-----	-----	-----	---WIQ	PMTTEQVANA
Ana-90.p-ana90-4359	(1.0d-27)	201	-----	-----	-----	---GVI	PMTPEQVAQA

Cyl-7417.p-Cyl-7417-4762	(6.0d-27)	201	-----	-----	-----	-WVV	PMTPEKVAQV	LVTGLEKN--
Nsp-0708.p-Nsp-0708-3536	(2.0d-26)	201	-----	-----	-----	-GVT	PMTPOQVAQA	LMIGLQKD--
N-7107.p-N-7107-1296	(2.0d-26)	201	-----	-----	-----	-WVI	PMTPOQVAQA	LIVGLQND--
Npun.p-NpR1019	(4.0d-26)	201	-----	-----	-----	-WVI	PMTPOQVAKA	LVAGMQND--
N-7524.p-N-7524-4265	(1.0d-25)	201	-----	-----	-----	-WVI	PMTPOQVAKA	LVIGLEKD--
M7126-SCAD-E		201	-----	-----	-----	-WVI	PMTPOQVAQT	LITGLERD--
R7116-SCAD-E		205	-----	-----	-----	-GVI	PMSPEQVAQA	FIKGLQRD--
cyt.p-cce_3588	(3.0d-27)	207	-----	-----	-----	-FMK	PVSPKKVAQS	LIKGLQKD--
ctc.p-c0110?06289	(2.0d-26)	206	-----	-----	-----	-FVK	PVSPKKVAQS	LIKGLQKN--
cyr.p-c8801?0598	(2.0d-26)	201	-----	-----	-----	-WMK	PVSPKKVAQA	LVKGLQHN--
Amar.p-AM1_6363	(1.0d-30)	201	-----	-----	-----	-WVA	AMTPEKVAKV	LVNSLAKE--
Amar.p-AM1_0210	(1.0d-27)	203	-----	-----	-----	-WVI	ASSPSDVAKA	FVKGLRSG--
lyn.p-l8106?00785	(4.0d-31)	199	-----	-----	-----	-NSE	VENRRQQMQS	VLESSFVS--
ter.p-Tery_3453	(8.0d-31)	199	-----	-----	-----	-NSE	VENRRQQMNY	VLESNFVS--
A29413.p-Ava0943	(1.0d-30)	220	-----	-----	-----	-EEI	AQARTELVGK	AIQMPVLE--
A7120.p-A112963	(5.0d-29)	220	-----	-----	-----	-EEM	AQARTELVGK	AIQMPVLE--
Npun.p-NpR4797	(3.0d-30)	200	-----	-----	-----	-EQD	THTRRGQLEN	VLKNPVVE--
Cyl-7417.p-Cyl-7417-4424	(3.0d-30)	200	-----	-----	-----	-EEE	LQTRREQLNN	VLKNPVVE--
MAST-10914-SCAD-E		200	-----	-----	-----	-EHD	AQIRRDQLNT	VLKVPVME--
M7126-SCAD-C		200	-----	-----	-----	-EAD	LQTRREQLNT	ILKNPVVE--
R7116-SCAD-D		198	-----	-----	-----	-EQE	AEKRRNSMSS	FLESPAAS--
Npun.p-NpF0199	(2.0d-29)	312	TERALGKDSH	SFLSPSWLTY	LSNRAARRNN	TITRNEENGD	RADRQIVQPT	
A7120.p-Alr5358	(3.0d-156)	201	-----	-----	-----	-----	-----	APKLAGIS--
A29413.p-Ava2596	(8.0d-151)	201	-----	-----	-----	-----	-----	APKLAGIS--
N-7524.p-N-7524-5224	(2.0d-121)	201	-----	-----	-----	-----	-----	APKLAGVT--
Cyl-7417.p-Cyl-7417-1544	(2.0d-100)	201	-----	-----	-----	-----	-----	APRLAGVS--
MAST-10914-SCAD-A		200	-----	-----	-----	-----	-----	APSLARVH--
N-7524.p-N-7524-5355	(2.0d-74)	200	-----	-----	-----	-----	-----	APKLAKVS--
Npun.p-NpF3363	(2.0d-81)	201	-----	-----	-----	-----	-----	APSLSGTS--
R7116-SCAD-A		214	-----	-----	-----	-----	-----	TTLKA AIS--
cyr.p-c8801?3820	(4.0d-26)	198	-----	-----	-----	--ESFAG---	-KSNGLQTS-	
A7120.p-A111418	(8.0d-26)	208	-----	-----	-----	-GKPLGKSPR	DETQGNMS--	
consensus		351						



A7120.p-Alr1894	(1.0d-26)	217	-----	---QPEEIAG	MVRFLAADP-	-----	A	AAYITGQVFN
A29413.p-Ava3764	(1.0d-26)	217	-----	---QPEEIAG	MVRFLAADP-	-----	A	AAYITGQVFN
N-7524.p-N-7524-0010	(9.0d-30)	217	-----	---QPEEIAG	MVRFLAADP-	-----	A	AAYITGQVFN
M7126-SCAD-B		221	-----	---QPEEIAG	MVRFLAADP-	-----	A	AAYITGQVFN
nod.p-n9414?22428	(4.0d-28)	214	-----	---QPEEIAG	MVRFLAADP-	-----	A	AAYITGQVFN
MAST-10914-SCAD-B		221	-----	---QPEEVAG	MVRFLAADP-	-----	A	SAYITGQVFN
Cal-6303.p-Cal-6303-1520	(5.0d-28)	221	-----	---QPEEIAG	MVRFLASDS-	-----	A	AAYITGQVFN
Npun.p-NpF2349	(4.0d-29)	214	-----	---QPEEVAG	MVRFLAADP-	-----	A	ANYITGQVFN
N-7107.p-N-7107-0937	(1.0d-27)	221	-----	---QPEEVAG	MVRFLAADA-	-----	A	ANYITGQVFN
Ana-90.p-ana90-1712	(1.0d-28)	213	-----	---KPEEIAG	MVRFLASDP-	-----	A	AAYITGQVFN
Acyl-7122.p-acyl-4545	(9.0d-28)	213	-----	---QPEEIAG	MVRFLAADP-	-----	A	AAYITGQVFN
Nsp-0708.p-Nsp-0708-2353	(9.0d-27)	213	-----	---EPEDIAG	MVSFLAADP-	-----	A	AAYITGQVFN
Cyl-505.p-Cyl-505-0204	(2.0d-28)	213	-----	---KPEEIAG	MVSFLATDP-	-----	A	AAYITGQVFN
Cyl-7417.p-Cyl-7417-2349	(6.0d-29)	220	-----	---TPEEIAG	MVRFLAADP-	-----	A	AAYITGQVFN
R7116-SCAD-C		220	-----	---KPEEIAG	MVRFLAADT-	-----	A	AAYITGQVFN
ter.p-Tery_3438	(2.0d-28)	221	-----	---KPEEVAG	MIRFLAADD-	-----	A	ASYITAQVFN
lyn.p-l8106?21814	(1.0d-27)	221	-----	---QPQEVAG	MVRFLAADS-	-----	A	AAYITGQVFN
Amar.p-AM1_5632	(1.0d-26)	213	-----	---QPEEVAG	MIRFLAADP-	-----	A	SAYITGQVFN
cyr.p-c8801?2930	(1.0d-28)	216	-----	---MPEEVAG	MVRFLATDP-	-----	A	ASYITGQVFN
S6803.p-Slr0886	(4.0d-27)	213	-----	---QPEEVAG	TIRFLATDP-	-----	A	AAYITGQTFN
mae.p-MAE_33900	(3.0d-29)	220	-----	---KPEEVAG	MVRFLAADP-	-----	A	AIYISGQVFN
TeBP1.p-tlr1502	(5.0d-29)	211	-----	---EPTEVAG	MVRFLALDP-	-----	A	AAYITGQVFN
S7942.p-Syncpcc7942_0684	(4.0d-26)	215	-----	---EAAEVAG	VVRFLAADP-	-----	A	AAYITGQVIN
syx.p-SynWH7803_1861	(7.0d-30)	216	-----	---TPEQVAG	TVRFLAADP-	-----	A	AAYITGQVLQ
S7805.p-WH7805_13603	(5.0d-28)	216	-----	---TPEQVAG	AVRFLAADS-	-----	A	AAYITGQVLQ
S9916.p-RS9916_33507	(8.0d-31)	216	-----	---TPEHIAG	TVRFLAADP-	-----	A	AAYITGQVLQ
Ssp-RS9917.p-Ssp-RS9917-1614	(2.0d-29)	274	-----	---NPDQVAG	AVRFLAADP-	-----	A	AAYITGQVLQ
S9917.p-RS9917_09056	(3.0d-29)	216	-----	---NPDQVAG	AVRFLAADP-	-----	A	AAYITGQVLQ
syg.p-sync_2137	(4.0d-29)	216	-----	---SPDQVAG	AVRFLAADP-	-----	A	AAYITGQVLQ
P9313.p-PMT1333	(6.0d-29)	216	-----	---TPEQVAG	AVRFLVADP-	-----	A	AAYITGQVLQ
pmf.p-P9303_06521	(1.0d-28)	228	-----	---TPEQVAG	AVRFLAADP-	-----	A	AAYITGQVLQ
S107.p-BL107_09856	(2.0d-28)	233	-----	---TQEQQVAG	VVRFLAGDP-	-----	A	AAYITGQVLQ
S9902.p-Sync9902_1745	(4.0d-28)	216	-----	---TQEQQVAG	AVRFLAADP-	-----	A	AAYITGQVLQ
S9605.p-Sync9605_0617	(4.0d-27)	230	-----	---TQEQQVAG	AVRFLAADP-	-----	A	AAYITGQVLQ
S8102.p-SynW1852	(9.0d-28)	216	-----	---TQEQQVAG	AVRFLAADP-	-----	A	AAYITGQVLQ
syr.p-SynRCC307_0681	(2.0d-28)	216	-----	---EVDEVAG	AVRFLAADP-	-----	A	AAYITGQVLQ
S5701.p-WH5701_07809	(1.0d-28)	218	-----	---QPEDVAG	VVRFLAADP-	-----	A	AAYMTGQVLQ
pmn.p-PMN2A_1785	(5.0d-28)	216	-----	---NPEDVAG	AVKFLAADP-	-----	S	ASYITGQVIQ
pme.p-NATL1_05081	(1.0d-27)	216	-----	---NPEDVAG	AVRFLAADP-	-----	S	ASYITGQVIQ

pmz.p-p9211?06582	(1.0d-27)	216	-----	---SPEHIAG	TVRFLATDP-	-----	A	AAYITGQVLQ
PRO1375.p-Pro0452	(7.0d-27)	216	-----	---STEHVAG	TVRFLAADP-	-----	A	SSYITGQVLQ
Gvi.p-glr3506	(5.0d-28)	214	-----	---QPEEVAG	LVRFLCADP-	-----	A	AAYITGQVIT
pmb.p-P9601_05091	(9.0d-28)	216	-----	---SCTQIAN	LVSFLVSSN-	-----	A	GSYITGQTIS
pmi.p-PMT9312_0453	(1.0d-27)	216	-----	---SCTQIAN	LVSFLVSSN-	-----	A	GSYITGQTIS
pmg.p-P9301_04781	(1.0d-27)	216	-----	---SCTQIAN	LVSFLVSSD-	-----	A	GRYITGQTIS
PMED4.p-PMM0453	(9.0d-28)	216	-----	---SCSQIAN	LVSFLVSSN-	-----	A	GSYITGQTIS
pmc.p-P9515_05161	(2.0d-27)	216	-----	---SCSQIAD	LVSFLVSSN-	-----	A	GSYITGQTIS
Npun.p-NpR0578	(6.0d-27)	224	-----	---QPEEIAN	AVVWLCSD-	-----	A	SSFVVGHALI
Cyl-7417.p-Cyl-7417-0303	(5.0d-26)	231	-----	---TVEDVAH	LVTFLSSP-	-----	L	TSYINGANLR
Npun.p-NpF2231	(1.0d-26)	212	-----	---EPEEVAD	VALFLASH-	-----	Q	SRAIHGQAIN
Cyl-7417.p-Cyl-7417-3400	(1.0d-26)	212	-----	---EPEEVAD	VALFLASH-	-----	Q	SRAIHGQAIN
Acyl-7122.p-acyl-3225	(4.0d-28)	209	-----	---TPEIVAQ	TILHTVLLP-	-----	Q	QAVIEELTLM
Nsp-0708.p-Nsp-0708-2459	(6.0d-26)	209	-----	---IPEIVAQ	TILHTALLP-	-----	Q	QAVIEELTLI
Ana-90.p-ana90-1189	(1.0d-28)	209	-----	---TPEIVAT	TILHTVLLP-	-----	Q	EAVIQEELTIM
Cyl-505.p-Cyl-505-2036	(2.0d-32)	209	-----	---TAQTVAQ	TILHSALLH-	-----	Q	EAVIEELTLM
A29413.p-Ava2536	(2.0d-28)	209	-----	---TPEIVAQ	SILYTALLP-	-----	P	QAVIDELTLM
A7120.p-Alr5286	(2.0d-28)	223	-----	---TPEIVAQ	SILYTALLP-	-----	P	QAVIDELTLM
N-7524.p-N-7524-4179	(1.0d-27)	209	-----	---TPEIVAQ	SILHTALLP-	-----	P	QAVIDELILM
MAST-10914-SCAD-C		213	-----	---TPEIVAQ	SILHAALLP-	-----	Q	QAVIDELTIM
Cyl-7417.p-Cyl-7417-1063	(4.0d-30)	209	-----	---TPEVVAQ	SILHTVLLP-	-----	Q	QAVIEELILM
nod.p-n9414?21215	(5.0d-26)	208	-----	---TPEVVAQ	SILYTALLP-	-----	Q	QAVIDELTLM
N-7107.p-N-7107-1008	(2.0d-29)	209	-----	---TPEIVAQ	SILHTVLLP-	-----	P	QAVIDELILM
M7126-SCAD-A		209	-----	---TPEIVAE	SIVHTILLP-	-----	P	QAVIDELTIM
R7116-SCAD-B		208	-----	---TPEIVAQ	SILHTVLLP-	-----	K	QAVVDELTLM
lyn.p-18106?23630	(2.0d-26)	209	-----	---TPEIVAE	SILHVVMLP-	-----	Q	QAVIEELTLM
Amar.p-AM1_5634	(3.0d-27)	209	-----	---RPENVAQ	SILHIVQMP-	-----	Q	NAVIEELVLM
cyb.p-CYB_0189	(1.0d-27)	211	-----	---SPEWVAD	LITYIVRLP-	-----	T	GAVVEDLTFM
cya.p-CYA_2793	(8.0d-26)	209	-----	---SPEWVAD	LIAHIVRLP-	-----	K	GAVVEDLTLM
M7126-SCAD-D		209	-----	---NPYSIAE	LLLQIATVP-	-----	A	AINIDDIVIK
cyb.p-CYB_0005	(4.0d-34)	231	-----	---VEKVVEP	ILRAMTDPHP	SDRYTAFTGG		KVALGLMRLM
cya.p-CYA_0005	(2.0d-33)	231	-----	---VEKVVEP	ILRAMTDPHP	SDRYTAFTGG		KLALGLMRLM
N-7107.p-N-7107-5182	(3.0d-28)	219	-----	---EDIAAA	INYAVTQPH-	-----		YVNVNEILIR
Npun.p-NpR3707	(3.0d-27)	219	-----	---EDVAAA	IVYAVTQPS-	-----		HVNVNEILIR
Acyl-7122.p-acyl-1205	(2.0d-26)	244	-----	---EDIAAAA	IVYAVSQPQ-	-----		HVNVNEILIR
R7116-SCAD-F		230	-----	---DDIADV	VLFCVTRPS-	-----		HVNLSSEILLV
Npun.p-NpF0204	(3.0d-28)	242	-----	---GFQAKAL	AVLAGISPR-	-----	L	TDKLIELWAF
MAST-10914-SCAD-D		222	-----	---SPEILIG	WQSHLAVWCN	R-----	I	APWLLEKVLL
Cal-6303.p-Cal-6303-3407	(1.0d-27)	222	-----	---SPEILVG	WQSHLAVWCN	R-----	I	APWLLEKILL
Ana-90.p-ana90-4359	(1.0d-27)	222	-----	---TAEILVG	WQSHLAVLCQ	R-----	L	APWLLEIIMQ

Cyl-7417.p-Cyl-7417-4762	(6.0d-27)	222	-----	---TPEILVG	WQSHLAVWCQ	R-----	L	SPWLLEQILQ
Nsp-0708.p-Nsp-0708-3536	(2.0d-26)	222	-----	---TSEILVG	WQSHLAVWSQ	N-----	F	APWLLEVVLLK
N-7107.p-N-7107-1296	(2.0d-26)	222	-----	---APEILVG	WQSHLAVWCQ	R-----	L	APWLLELILK
Npun.p-NpR1019	(4.0d-26)	222	-----	---SPEILVG	WQSHLAVLCQ	R-----	L	APWLLELILR
N-7524.p-N-7524-4265	(1.0d-25)	222	-----	---APEILVG	WQSHLAVWCQ	R-----	L	APGLLELLLK
M7126-SCAD-E		222	-----	---SPEILVG	WQTYLAVWCQ	R-----	F	TPWLLEWILN
R7116-SCAD-E		226	-----	---SSEILVG	WQSHLAILCQ	R-----	L	APWLLETVLK
cyt.p-cce_3588	(3.0d-27)	228	-----	---TPEILVG	WQSYLAVWGQ	R-----	L	APRLIEQFTI
ctc.p-c0110?06289	(2.0d-26)	227	-----	---KPEILVG	WQSYLAIWGQ	R-----	L	APRLTEQFTT
cyr.p-c8801?0598	(2.0d-26)	222	-----	---RREILVG	WQSHLAVWCQ	R-----	L	VPRLIEQISV
Amar.p-AM1_6363	(1.0d-30)	222	-----	---SPEILVG	WQSHLAVLGN	R-----	F	APRFLEWWLQ
Amar.p-AM1_0210	(1.0d-27)	224	-----	---KKEIIVG	WQSKIAIFAS	Y-----	I	APGFVERAMQ
lyn.p-l8106?00785	(4.0d-31)	220	-----	---QPEDIAK	AIWEAVNQKK	S----	ETVVG	LTSIATEAYR
ter.p-Tery_3453	(8.0d-31)	220	-----	---QPKDIAE	AIWNVYKNNQ	S----	EIVVG	PAVLATETYR
A29413.p-Ava0943	(1.0d-30)	241	-----	---KPEDVAK	AIWSAVKNKR	S----	DVVVG	SANFWKAAAYQ
A7120.p-A112963	(5.0d-29)	241	-----	---KPEDVAK	AIWSAVKEKR	S----	DVVVG	SANFWKAAAYQ
Npun.p-NpR4797	(3.0d-30)	221	-----	---KPEDVAN	AIWDAVKNKK	S----	EVMVG	SANLSQSILYR
Cyl-7417.p-Cyl-7417-4424	(3.0d-30)	221	-----	---KPEDVAN	AIWDAVNNQK	S----	EVMVG	SANFSQSILYR
MAST-10914-SCAD-E		221	-----	---KPEDVAN	AIWDAVKNQK	S----	EVMVG	SANVSQGFYR
M7126-SCAD-C		221	-----	---KPEDVAN	AIWDAVKNQK	S----	EVTVC	SANFSQALYR
R7116-SCAD-D		219	-----	---KPEDVAN	AVWDAVKHQK	D----	EVVVG	SGSFMSAAYK
Npun.p-NpF0199	(2.0d-29)	362	PQTTTEQPKI	QLIQPSQASP	EIQACFNDIQ	D----	TLGIP	WTPANWRAYA
A7120.p-Alr5358	(3.0d-156)	209	-----	---TPKSVAN	AVVKAIKNKT	TEVIVNQNP	I	TESLTKLMLA
A29413.p-Ava2596	(8.0d-151)	209	-----	---TPKSVAN	AVVKAIKKKT	SEVVVNQNP	I	TESLTKFMLA
N-7524.p-N-7524-5224	(2.0d-121)	209	-----	---TPKGIAN	AVMRAVGNP	AEIIVNQNP	I	TEGLTKLMLA
Cyl-7417.p-Cyl-7417-1544	(2.0d-100)	209	-----	---TPTEVAN	AVIKAIKQNE	AEVIVNESRI		TENLTKVMFA
MAST-10914-SCAD-A		208	-----	---RPLDVAI	AVIQAIKQNQ	GEVLLDG---	--	VLTRLLFS
N-7524.p-N-7524-5355	(2.0d-74)	208	-----	---QPTEVAI	AIIKAIKQNQ	PEVMLDG---	--	VLTRLLFS
Npun.p-NpF3363	(2.0d-81)	209	-----	---QPEAVAK	AVIQAIKKNQ	AEVIVNKDLI		TVGLTKILFA
R7116-SCAD-A		222	-----	---IPEKVAI	AVCYTLENNG	VEIVENGFL		TRNITKLKFA
cyr.p-c8801?3820	(4.0d-26)	211	-----	---AEEVVKD	ALKALENNQS	N-----	CV	TGGFANQLIV
A7120.p-A111418	(8.0d-26)	225	-----	---VDECVRQ	IIWAMERRKR	E-----	H	IMTLKGKVIP
consensus		401						

A7120.p-Alr1894	(1.0d-26)	244	VDGGM---VM	A-----	-----	-----	-----
A29413.p-Ava3764	(1.0d-26)	244	VDGGM---VM	A-----	-----	-----	-----
N-7524.p-N-7524-0010	(9.0d-30)	244	VDGGM---VM	-----	-----	-----	-----
M7126-SCAD-B		248	VDGGM---VM	A-----	-----	-----	-----
nod.p-n9414?22428	(4.0d-28)	241	VDGGM---VM	A-----	-----	-----	-----
MAST-10914-SCAD-B		248	VDGGM---VM	A-----	-----	-----	-----
Cal-6303.p-Cal-6303-1520	(5.0d-28)	248	VDGGM---VM	A-----	-----	-----	-----
Npun.p-NpF2349	(4.0d-29)	241	VDGGM---VM	A-----	-----	-----	-----
N-7107.p-N-7107-0937	(1.0d-27)	248	VDGGM---VM	-----	-----	-----	-----
Ana-90.p-ana90-1712	(1.0d-28)	240	VDGGM---VM	-----	-----	-----	-----
Acyl-7122.p-acyl-4545	(9.0d-28)	240	VDGGM---VM	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-2353	(9.0d-27)	240	VDGGM---VM	-----	-----	-----	-----
Cyl-505.p-Cyl-505-0204	(2.0d-28)	240	VDGGM---VI	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-2349	(6.0d-29)	247	VDGGM---VM	A-----	-----	-----	-----
R7116-SCAD-C		247	VDGGM---VM	A-----	-----	-----	-----
ter.p-Tery_3438	(2.0d-28)	248	VDGGF-----	-----	-----	-----	-----
lyn.p-l8106?21814	(1.0d-27)	248	VDGGM---VM	A-----	-----	-----	-----
Amar.p-AM1_5632	(1.0d-26)	240	VDGGM---VM	A-----	-----	-----	-----
cyr.p-c8801?2930	(1.0d-28)	243	VDGGM---VM	A-----	-----	-----	-----
S6803.p-Slr0886	(4.0d-27)	240	VDGGM---VM	F-----	-----	-----	-----
mae.p-MAE_33900	(3.0d-29)	247	VDGGM---VM	A-----	-----	-----	-----
TeBP1.p-tlr1502	(5.0d-29)	238	VDGGM---VM	A-----	-----	-----	-----
S7942.p-Synpcc7942_0684	(4.0d-26)	242	IDGGL---VM	A-----	-----	-----	-----
syx.p-SynWH7803_1861	(7.0d-30)	243	VDGGM---VM	G-----	-----	-----	-----
S7805.p-WH7805_13603	(5.0d-28)	243	VDGGM---VM	G-----	-----	-----	-----
S9916.p-RS9916_33507	(8.0d-31)	243	VDGGM---VM	G-----	-----	-----	-----
Ssp-RS9917.p-Ssp-RS9917-1614	(2.0d-29)	301	VDGGM---VM	G-----	-----	-----	-----
S9917.p-RS9917_09056	(3.0d-29)	243	VDGGM---VM	G-----	-----	-----	-----
syg.p-sync_2137	(4.0d-29)	243	VDGGM---VM	S-----	-----	-----	-----
P9313.p-PMT1333	(6.0d-29)	243	VDGGM---LM	G-----	-----	-----	-----
pmf.p-P9303_06521	(1.0d-28)	255	VDGGM---LM	G-----	-----	-----	-----
S107.p-BL107_09856	(2.0d-28)	260	VDGGM---VM	A-----	-----	-----	-----
S9902.p-Syncc9902_1745	(4.0d-28)	243	VDGGM---VM	A-----	-----	-----	-----
S9605.p-Syncc9605_0617	(4.0d-27)	257	VDGGM---VM	A-----	-----	-----	-----
S8102.p-SynW1852	(9.0d-28)	243	VDGGM---VM	A-----	-----	-----	-----
syr.p-SynRCC307_0681	(2.0d-28)	243	VDGGM---VM	A-----	-----	-----	-----
S5701.p-WH5701_07809	(1.0d-28)	245	VDGGL---VM	R-----	-----	-----	-----
pmn.p-PMN2A_1785	(5.0d-28)	243	VDGGM---VM	S-----	-----	-----	-----
pme.p-NATL1_05081	(1.0d-27)	243	VDGGM---VM	S-----	-----	-----	-----

pmz.p-p9211?06582	(1.0d-27)	243	VDGGM---LM	S-----	-----	-----	-----
PRO1375.p-Pro0452	(7.0d-27)	243	VDGGM---VM	S-----	-----	-----	-----
Gvi.p-glr3506	(5.0d-28)	241	IDGGM---VM	A-----	-----	-----	-----
pmb.p-P9601_05091	(9.0d-28)	243	IDGGM---SI	-----	-----	-----	-----
pmi.p-PMT9312_0453	(1.0d-27)	243	IDGGM---SI	-----	-----	-----	-----
pmg.p-P9301_04781	(1.0d-27)	243	IDGGM---SI	-----	-----	-----	-----
PMED4.p-PMM0453	(9.0d-28)	243	IDGGM---SI	-----	-----	-----	-----
pmc.p-P9515_05161	(2.0d-27)	243	IDGGM---SI	-----	-----	-----	-----
Npun.p-NpR0578	(6.0d-27)	250	IDGGQ---TV	Q-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-0303	(5.0d-26)	257	VDGAW---AS	SIN-----	-----	-----	-----
Npun.p-NpF2231	(1.0d-26)	238	VYGGVNYRLM	REAPLMTKPY	-----	-----	-----
Cyl-7417.p-Cyl-7417-3400	(1.0d-26)	238	VYGGVDYRLM	RG-----	-----	-----	-----
Acyl-7122.p-acyl-3225	(4.0d-28)	236	SNAGVL----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-2459	(6.0d-26)	236	SNAGVI----	-----	-----	-----	-----
Ana-90.p-ana90-1189	(1.0d-28)	236	SNAGVL----	-----	-----	-----	-----
Cyl-505.p-Cyl-505-2036	(2.0d-32)	236	SNAGVL----	-----	-----	-----	-----
A29413.p-Ava2536	(2.0d-28)	236	PSAGAL----	-----	-----	-----	-----
A7120.p-Alr5286	(2.0d-28)	250	PSAGAL----	-----	-----	-----	-----
N-7524.p-N-7524-4179	(1.0d-27)	236	PSAGAL----	-----	-----	-----	-----
MAST-10914-SCAD-C		240	PMAGAL----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-1063	(4.0d-30)	236	PNAGVL----	-----	-----	-----	-----
nod.p-n9414?21215	(5.0d-26)	235	PSAGAL----	-----	-----	-----	-----
N-7107.p-N-7107-1008	(2.0d-29)	236	PNTGTF----	-----	-----	-----	-----
M7126-SCAD-A		236	PSAGVL----	-----	-----	-----	-----
R7116-SCAD-B		235	PSAGVL----	-----	-----	-----	-----
lyn.p-l8106?23630	(2.0d-26)	236	PHGGAF----	-----	-----	-----	-----
Amar.p-AM1_5634	(3.0d-27)	236	PNAGTF----	-----	-----	-----	-----
cyb.p-CYB_0189	(1.0d-27)	238	PAVGAF----	-----	-----	-----	-----
cya.p-CYA_2793	(8.0d-26)	236	PAAGAF----	-----	-----	-----	-----
M7126-SCAD-D		236	RM-----	-----	-----	-----	-----
cyb.p-CYB_0005	(4.0d-34)	268	PAALADSMWR	RVYGLDGLGS	PGSA-----	-----	-----
cya.p-CYA_0005	(2.0d-33)	268	PAALADQMWR	RVYGLDALGS	PKSA-----	-----	-----
N-7107.p-N-7107-5182	(3.0d-28)	244	PTLQER----	-----	-----	-----	-----
Npun.p-NpR3707	(3.0d-27)	244	PTQQEH----	-----	-----	-----	-----
Acyl-7122.p-acyl-1205	(2.0d-26)	269	PTQQER----	-----	-----	-----	-----
R7116-SCAD-F		255	PVDQASATMV	NRK-----	-----	-----	-----
Npun.p-NpF0204	(3.0d-28)	269	PSQQSDRPSR	DREDSALYRA	GYGMHERGTH	QGWIRSGSLY	VKAEKHPVTT
MAST-10914-SCAD-D		251	MAAPQE----	-----	-RQLHYPRFR	DARGRT----	-----
Cal-6303.p-Cal-6303-3407	(1.0d-27)	251	ISAPLPP---	-----	VRRKYYQQLR	KA-----	-----
Ana-90.p-ana90-4359	(1.0d-27)	251	LATPKKPLPD	A-----A	G-----	-----	-----

Cyl-7417.p-Cyl-7417-4762 (6.0d-27)	251 FATPGRKQPQ E-----S LIQNFRAKIH RFGDWLLSGN MASFVFARKS
Nsp-0708.p-Nsp-0708-3536 (2.0d-26)	251 LAAP-RKQPQ I-----S LIKSLTAKIQ HFSNWLFSKN KVAFVSEK-
N-7107.p-N-7107-1296 (2.0d-26)	251 IATPP---KQ Q-----HVV EKPSLLSRIN RFCDSFFSRN MDSLLSPRKS
Npun.p-NpR1019 (4.0d-26)	251 IATPPVPRKQ QPAERLNKLI PKNFLNRIH RFGDLFLSRT -----
N-7524.p-N-7524-4265 (1.0d-25)	251 IAAPTAP--- -----KTL EQPSLFTKIQ RFGDFLFSAQ RLPFVFARKS
M7126-SCAD-E	251 LATP----- -----S TTNRLLSKFQ RLSDLLWSNN MTAFVSARKS
R7116-SCAD-E	255 LASP----- ----- --DSKAPKIQ EYYQRLVGSW -----
cyt.p-cce_3588 (3.0d-27)	257 MTAP----- ----- --LSQKPHSS NLNSFRLN-- -----
ctc.p-c0110?06289 (2.0d-26)	256 MAAP----- ----- --LSQKSRLS KLIPFWLS-- -----
cyr.p-c8801?0598 (2.0d-26)	251 MAAP----- ----- --LSRVPQVR PLESLLQTRS PF-----
Amar.p-AM1_6363 (1.0d-30)	251 LTAP----- ----- --RSEQPKKS IWSRGY---- -----
Amar.p-AM1_0210 (1.0d-27)	253 LSARLG---- ----- HRQSTRQTEF EFKDCCNAGP S-----
lyn.p-l8106?00785 (4.0d-31)	253 LFPGLMQFIM SQAQNQOK-- -----
ter.p-Tery_3453 (8.0d-31)	253 LFPGLTQFLM GKSVE----- -----
A29413.p-Ava0943 (1.0d-30)	274 LTPSLIQSLV RRVFGMEERK -----
A7120.p-A112963 (5.0d-29)	274 LTPSLIQSLV RRVFGMEERK -----
Npun.p-NpR4797 (3.0d-30)	254 LFPGLIKWVS RQGLKNQDN-----
Cyl-7417.p-Cyl-7417-4424 (3.0d-30)	254 LFPGLMKWVS RQTLKNQE-- -----
MAST-10914-SCAD-E	254 LFPGLLQWVS RQGLKNKDK-----
M7126-SCAD-C	254 LFPGLTKWLS RQALQNQDK-----
R7116-SCAD-D	252 FFPGLMQLAM QTSKQ-----
Npun.p-NpF0199 (2.0d-29)	408 MYPSVMQLFW QRLKPAMQTE AFLEDAIAIS EHVYRDINDW YQPGYQIEVE
A7120.p-Alr5358 (3.0d-156)	246 VGQISPTSVD RIYRWFVVD FNQKRAENRV KDGYPVAVESH RS-----
A29413.p-Ava2596 (8.0d-151)	246 IGQISPTSVD RIYRWLGVD FNQKRAENRV KDGYPVAVESH RS-----
N-7524.p-N-7524-5224 (2.0d-121)	246 MGQISPTAVD QLYQWLGIVN FNQIRAGNRA NLKCAAVG-- RA-----
Cyl-7417.p-Cyl-7417-1544 (2.0d-100)	246 IGQLYPQFLD AVYQWLDVVN LNQKRAKSFL KNRYQRVSK-----
MAST-10914-SCAD-A	240 NIQLFPNFGD AIYRWIGLTK LNRTCAENQM RDESSAQN-- -----
N-7524.p-N-7524-5355 (2.0d-74)	240 NIQLFPEFGD KIFNWIGVRQ LNKTRAEN-- -----
Npun.p-NpF3363 (2.0d-81)	246 LWQFFPKFGD AIYRRIGVIA LNKRRQTKN YSNSINLLHK -----
R7116-SCAD-A	259 FEEHLPRFGD DIKR-----S LHQPNSQ--- -----
cyr.p-c8801?3820 (4.0d-26)	241 NASRFVPREF LVNAVEKQFR A-----
A7120.p-A111418 (8.0d-26)	254 WAKLILPGFV DRIVAATIRK TTST-----
consensus	451

A7120.p-Alr1894	(1.0d-26)	251	-----	-----	-----	-----	-----
A29413.p-Ava3764	(1.0d-26)	251	-----	-----	-----	-----	-----
N-7524.p-N-7524-0010	(9.0d-30)	250	-----	-----	-----	-----	-----
M7126-SCAD-B		255	-----	-----	-----	-----	-----
nod.p-n9414?22428	(4.0d-28)	248	-----	-----	-----	-----	-----
MAST-10914-SCAD-B		255	-----	-----	-----	-----	-----
Cal-6303.p-Cal-6303-1520	(5.0d-28)	255	-----	-----	-----	-----	-----
Npun.p-NpF2349	(4.0d-29)	248	-----	-----	-----	-----	-----
N-7107.p-N-7107-0937	(1.0d-27)	254	-----	-----	-----	-----	-----
Ana-90.p-ana90-1712	(1.0d-28)	246	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-4545	(9.0d-28)	246	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-2353	(9.0d-27)	246	-----	-----	-----	-----	-----
Cyl-505.p-Cyl-505-0204	(2.0d-28)	246	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-2349	(6.0d-29)	254	-----	-----	-----	-----	-----
R7116-SCAD-C		254	-----	-----	-----	-----	-----
ter.p-Tery_3438	(2.0d-28)	252	-----	-----	-----	-----	-----
lyn.p-l8106?21814	(1.0d-27)	255	-----	-----	-----	-----	-----
Amar.p-AM1_5632	(1.0d-26)	247	-----	-----	-----	-----	-----
cyr.p-c8801?2930	(1.0d-28)	250	-----	-----	-----	-----	-----
S6803.p-Slr0886	(4.0d-27)	247	-----	-----	-----	-----	-----
mae.p-MAE_33900	(3.0d-29)	254	-----	-----	-----	-----	-----
TeBP1.p-tlr1502	(5.0d-29)	245	-----	-----	-----	-----	-----
S7942.p-Synpcc7942_0684	(4.0d-26)	249	-----	-----	-----	-----	-----
syx.p-SynWH7803_1861	(7.0d-30)	250	-----	-----	-----	-----	-----
S7805.p-WH7805_13603	(5.0d-28)	250	-----	-----	-----	-----	-----
S9916.p-RS9916_33507	(8.0d-31)	250	-----	-----	-----	-----	-----
Ssp-RS9917.p-Ssp-RS9917-1614	(2.0d-29)	308	-----	-----	-----	-----	-----
S9917.p-RS9917_09056	(3.0d-29)	250	-----	-----	-----	-----	-----
syg.p-sync_2137	(4.0d-29)	250	-----	-----	-----	-----	-----
P9313.p-PMT1333	(6.0d-29)	250	-----	-----	-----	-----	-----
pmf.p-P9303_06521	(1.0d-28)	262	-----	-----	-----	-----	-----
S107.p-BL107_09856	(2.0d-28)	267	-----	-----	-----	-----	-----
S9902.p-Sync9902_1745	(4.0d-28)	250	-----	-----	-----	-----	-----
S9605.p-Sync9605_0617	(4.0d-27)	264	-----	-----	-----	-----	-----
S8102.p-SynW1852	(9.0d-28)	250	-----	-----	-----	-----	-----
syr.p-SynRCC307_0681	(2.0d-28)	250	-----	-----	-----	-----	-----
S5701.p-WH5701_07809	(1.0d-28)	252	-----	-----	-----	-----	-----
pmn.p-PMN2A_1785	(5.0d-28)	250	-----	-----	-----	-----	-----
pme.p-NATL1_05081	(1.0d-27)	250	-----	-----	-----	-----	-----

pmz.p-p9211?06582	(1.0d-27)	250	-----	-----	-----	-----	-----
PRO1375.p-Pro0452	(7.0d-27)	250	-----	-----	-----	-----	-----
Gvi.p-glr3506	(5.0d-28)	248	-----	-----	-----	-----	-----
pmb.p-P9601_05091	(9.0d-28)	249	-----	-----	-----	-----	-----
pmi.p-PMT9312_0453	(1.0d-27)	249	-----	-----	-----	-----	-----
pmg.p-P9301_04781	(1.0d-27)	249	-----	-----	-----	-----	-----
PMED4.p-PMM0453	(9.0d-28)	249	-----	-----	-----	-----	-----
pmc.p-P9515_05161	(2.0d-27)	249	-----	-----	-----	-----	-----
Npun.p-NpR0578	(6.0d-27)	257	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-0303	(5.0d-26)	266	-----	-----	-----	-----	-----
Npun.p-NpF2231	(1.0d-26)	257	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-3400	(1.0d-26)	249	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-3225	(4.0d-28)	241	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-2459	(6.0d-26)	241	-----	-----	-----	-----	-----
Ana-90.p-ana90-1189	(1.0d-28)	241	-----	-----	-----	-----	-----
Cyl-505.p-Cyl-505-2036	(2.0d-32)	241	-----	-----	-----	-----	-----
A29413.p-Ava2536	(2.0d-28)	241	-----	-----	-----	-----	-----
A7120.p-Alr5286	(2.0d-28)	255	-----	-----	-----	-----	-----
N-7524.p-N-7524-4179	(1.0d-27)	241	-----	-----	-----	-----	-----
MAST-10914-SCAD-C		245	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-1063	(4.0d-30)	241	-----	-----	-----	-----	-----
nod.p-n9414?21215	(5.0d-26)	240	-----	-----	-----	-----	-----
N-7107.p-N-7107-1008	(2.0d-29)	241	-----	-----	-----	-----	-----
M7126-SCAD-A		241	-----	-----	-----	-----	-----
R7116-SCAD-B		240	-----	-----	-----	-----	-----
lyn.p-18106?23630	(2.0d-26)	241	-----	-----	-----	-----	-----
Amar.p-AM1_5634	(3.0d-27)	241	-----	-----	-----	-----	-----
cyb.p-CYB_0189	(1.0d-27)	243	-----	-----	-----	-----	-----
cya.p-CYA_2793	(8.0d-26)	241	-----	-----	-----	-----	-----
M7126-SCAD-D		237	-----	-----	-----	-----	-----
cyb.p-CYB_0005	(4.0d-34)	291	-----	-----	-----	-----	-----
cya.p-CYA_0005	(2.0d-33)	291	-----	-----	-----	-----	-----
N-7107.p-N-7107-5182	(3.0d-28)	249	-----	-----	-----	-----	-----
Npun.p-NpR3707	(3.0d-27)	249	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-1205	(2.0d-26)	274	-----	-----	-----	-----	-----
R7116-SCAD-F		267	-----	-----	-----	-----	-----
Npun.p-NpF0204	(3.0d-28)	319	TIIVVGLGTL	IWWFTSFAV-	-----	-----	-----
MAST-10914-SCAD-D		271	-----	-----	-----	-----	-----
Cal-6303.p-Cal-6303-3407	(1.0d-27)	269	-----	-----	-----	-----	-----
Ana-90.p-ana90-4359	(1.0d-27)	263	-----	-----	-----	-----	-----



Cyl-7417.p-Cyl-7417-4762	(6.0d-27)	292	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-3536	(2.0d-26)	290	-----	-----	-----	-----	-----
N-7107.p-N-7107-1296	(2.0d-26)	291	-----	-----	-----	-----	-----
Npun.p-NpR1019	(4.0d-26)	290	-----	-----	-----	-----	-----
N-7524.p-N-7524-4265	(1.0d-25)	290	-----	-----	-----	-----	-----
M7126-SCAD-E		285	-----	-----	-----	-----	-----
R7116-SCAD-E		276	-----	-----	-----	-----	-----
cyt.p-cce_3588	(3.0d-27)	276	-----	-----	-----	-----	-----
ctc.p-c0110?06289	(2.0d-26)	275	-----	-----	-----	-----	-----
cyr.p-c8801?0598	(2.0d-26)	274	-----	-----	-----	-----	-----
Amar.p-AM1_6363	(1.0d-30)	268	-----	-----	-----	-----	-----
Amar.p-AM1_0210	(1.0d-27)	279	-----	-----	-----	-----	-----
lyn.p-l8106?00785	(4.0d-31)	270	-----	-----	-----	-----	-----
ter.p-Tery_3453	(8.0d-31)	267	-----	-----	-----	-----	-----
A29413.p-Ava0943	(1.0d-30)	293	-----	-----	-----	-----	-----
A7120.p-Al12963	(5.0d-29)	293	-----	-----	-----	-----	-----
Npun.p-NpR4797	(3.0d-30)	272	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-4424	(3.0d-30)	271	-----	-----	-----	-----	-----
MAST-10914-SCAD-E		272	-----	-----	-----	-----	-----
M7126-SCAD-C		272	-----	-----	-----	-----	-----
R7116-SCAD-D		266	-----	-----	-----	-----	-----
Npun.p-NpF0199	(2.0d-29)	458	QAQQHHIRQE	LNAFIFGNPQ	LLIQQIALSK	TLAGEIVGQD	GSIDSRHGPN
A7120.p-Alr5358	(3.0d-156)	287	-----	-----	-----	-----	-----
A29413.p-Ava2596	(8.0d-151)	287	-----	-----	-----	-----	-----
N-7524.p-N-7524-5224	(2.0d-121)	285	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-1544	(2.0d-100)	284	-----	-----	-----	-----	-----
MAST-10914-SCAD-A		277	-----	-----	-----	-----	-----
N-7524.p-N-7524-5355	(2.0d-74)	267	-----	-----	-----	-----	-----
Npun.p-NpF3363	(2.0d-81)	285	-----	-----	-----	-----	-----
R7116-SCAD-A		280	-----	-----	-----	-----	-----
cyr.p-c8801?3820	(4.0d-26)	261	-----	-----	-----	-----	-----
A7120.p-Al11418	(8.0d-26)	277	-----	-----	-----	-----	-----
consensus		501	-----	-----	-----	-----	-----

A7120.p-Alr1894	(1.0d-26)	251	----	----	----	----	----
A29413.p-Ava3764	(1.0d-26)	251	----	----	----	----	----
N-7524.p-N-7524-0010	(9.0d-30)	250	----	----	----	----	----
M7126-SCAD-B		255	----	----	----	----	----
nod.p-n9414?22428	(4.0d-28)	248	----	----	----	----	----
MAST-10914-SCAD-B		255	----	----	----	----	----
Cal-6303.p-Cal-6303-1520	(5.0d-28)	255	----	----	----	----	----
Npun.p-NpF2349	(4.0d-29)	248	----	----	----	----	----
N-7107.p-N-7107-0937	(1.0d-27)	254	----	----	----	----	----
Ana-90.p-ana90-1712	(1.0d-28)	246	----	----	----	----	----
Acyl-7122.p-acyl-4545	(9.0d-28)	246	----	----	----	----	----
Nsp-0708.p-Nsp-0708-2353	(9.0d-27)	246	----	----	----	----	----
Cyl-505.p-Cyl-505-0204	(2.0d-28)	246	----	----	----	----	----
Cyl-7417.p-Cyl-7417-2349	(6.0d-29)	254	----	----	----	----	----
R7116-SCAD-C		254	----	----	----	----	----
ter.p-Tery_3438	(2.0d-28)	252	----	----	----	----	----
lyn.p-l8106?21814	(1.0d-27)	255	----	----	----	----	----
Amar.p-AM1_5632	(1.0d-26)	247	----	----	----	----	----
cyr.p-c8801?2930	(1.0d-28)	250	----	----	----	----	----
S6803.p-Slr0886	(4.0d-27)	247	----	----	----	----	----
mae.p-MAE_33900	(3.0d-29)	254	----	----	----	----	----
TeBP1.p-tlr1502	(5.0d-29)	245	----	----	----	----	----
S7942.p-Synpcc7942_0684	(4.0d-26)	249	----	----	----	----	----
syx.p-SynWH7803_1861	(7.0d-30)	250	----	----	----	----	----
S7805.p-WH7805_13603	(5.0d-28)	250	----	----	----	----	----
S9916.p-RS9916_33507	(8.0d-31)	250	----	----	----	----	----
Ssp-RS9917.p-Ssp-RS9917-1614	(2.0d-29)	308	----	----	----	----	----
S9917.p-RS9917_09056	(3.0d-29)	250	----	----	----	----	----
syg.p-sync_2137	(4.0d-29)	250	----	----	----	----	----
P9313.p-PMT1333	(6.0d-29)	250	----	----	----	----	----
pmf.p-P9303_06521	(1.0d-28)	262	----	----	----	----	----
S107.p-BL107_09856	(2.0d-28)	267	----	----	----	----	----
S9902.p-Syncc9902_1745	(4.0d-28)	250	----	----	----	----	----
S9605.p-Syncc9605_0617	(4.0d-27)	264	----	----	----	----	----
S8102.p-SynW1852	(9.0d-28)	250	----	----	----	----	----
syr.p-SynRCC307_0681	(2.0d-28)	250	----	----	----	----	----
S5701.p-WH5701_07809	(1.0d-28)	252	----	----	----	----	----
pmn.p-PMN2A_1785	(5.0d-28)	250	----	----	----	----	----
pme.p-NATL1_05081	(1.0d-27)	250	----	----	----	----	----

pmz.p-p9211?06582	(1.0d-27)	250	-----	-----	-----	-----	-----
PRO1375.p-Pro0452	(7.0d-27)	250	-----	-----	-----	-----	-----
Gvi.p-glr3506	(5.0d-28)	248	-----	-----	-----	-----	-----
pmb.p-P9601_05091	(9.0d-28)	249	-----	-----	-----	-----	-----
pmi.p-PMT9312_0453	(1.0d-27)	249	-----	-----	-----	-----	-----
pmg.p-P9301_04781	(1.0d-27)	249	-----	-----	-----	-----	-----
PMED4.p-PMM0453	(9.0d-28)	249	-----	-----	-----	-----	-----
pmc.p-P9515_05161	(2.0d-27)	249	-----	-----	-----	-----	-----
Npun.p-NpR0578	(6.0d-27)	257	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-0303	(5.0d-26)	266	-----	-----	-----	-----	-----
Npun.p-NpF2231	(1.0d-26)	257	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-3400	(1.0d-26)	249	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-3225	(4.0d-28)	241	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-2459	(6.0d-26)	241	-----	-----	-----	-----	-----
Ana-90.p-ana90-1189	(1.0d-28)	241	-----	-----	-----	-----	-----
Cyl-505.p-Cyl-505-2036	(2.0d-32)	241	-----	-----	-----	-----	-----
A29413.p-Ava2536	(2.0d-28)	241	-----	-----	-----	-----	-----
A7120.p-Alr5286	(2.0d-28)	255	-----	-----	-----	-----	-----
N-7524.p-N-7524-4179	(1.0d-27)	241	-----	-----	-----	-----	-----
MAST-10914-SCAD-C		245	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-1063	(4.0d-30)	241	-----	-----	-----	-----	-----
nod.p-n9414?21215	(5.0d-26)	240	-----	-----	-----	-----	-----
N-7107.p-N-7107-1008	(2.0d-29)	241	-----	-----	-----	-----	-----
M7126-SCAD-A		241	-----	-----	-----	-----	-----
R7116-SCAD-B		240	-----	-----	-----	-----	-----
lyn.p-18106?23630	(2.0d-26)	241	-----	-----	-----	-----	-----
Amar.p-AM1_5634	(3.0d-27)	241	-----	-----	-----	-----	-----
cyb.p-CYB_0189	(1.0d-27)	243	-----	-----	-----	-----	-----
cya.p-CYA_2793	(8.0d-26)	241	-----	-----	-----	-----	-----
M7126-SCAD-D		237	-----	-----	-----	-----	-----
cyb.p-CYB_0005	(4.0d-34)	291	-----	-----	-----	-----	-----
cya.p-CYA_0005	(2.0d-33)	291	-----	-----	-----	-----	-----
N-7107.p-N-7107-5182	(3.0d-28)	249	-----	-----	-----	-----	-----
Npun.p-NpR3707	(3.0d-27)	249	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-1205	(2.0d-26)	274	-----	-----	-----	-----	-----
R7116-SCAD-F		267	-----	-----	-----	-----	-----
Npun.p-NpF0204	(3.0d-28)	337	-----	-----	-----	-----	-----
MAST-10914-SCAD-D		271	-----	-----	-----	-----	-----
Cal-6303.p-Cal-6303-3407	(1.0d-27)	269	-----	-----	-----	-----	-----
Ana-90.p-ana90-4359	(1.0d-27)	263	-----	-----	-----	-----	-----

Cyl-7417.p-Cyl-7417-4762	(6.0d-27)	292	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-3536	(2.0d-26)	290	-----	-----	-----	-----	-----
N-7107.p-N-7107-1296	(2.0d-26)	291	-----	-----	-----	-----	-----
Npun.p-NpR1019	(4.0d-26)	290	-----	-----	-----	-----	-----
N-7524.p-N-7524-4265	(1.0d-25)	290	-----	-----	-----	-----	-----
M7126-SCAD-E		285	-----	-----	-----	-----	-----
R7116-SCAD-E		276	-----	-----	-----	-----	-----
cyt.p-cce_3588	(3.0d-27)	276	-----	-----	-----	-----	-----
ctc.p-c0110?06289	(2.0d-26)	275	-----	-----	-----	-----	-----
cyr.p-c8801?0598	(2.0d-26)	274	-----	-----	-----	-----	-----
Amar.p-AM1_6363	(1.0d-30)	268	-----	-----	-----	-----	-----
Amar.p-AM1_0210	(1.0d-27)	279	-----	-----	-----	-----	-----
lyn.p-l8106?00785	(4.0d-31)	270	-----	-----	-----	-----	-----
ter.p-Tery_3453	(8.0d-31)	267	-----	-----	-----	-----	-----
A29413.p-Ava0943	(1.0d-30)	293	-----	-----	-----	-----	-----
A7120.p-Al12963	(5.0d-29)	293	-----	-----	-----	-----	-----
Npun.p-NpR4797	(3.0d-30)	272	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-4424	(3.0d-30)	271	-----	-----	-----	-----	-----
MAST-10914-SCAD-E		272	-----	-----	-----	-----	-----
M7126-SCAD-C		272	-----	-----	-----	-----	-----
R7116-SCAD-D		266	-----	-----	-----	-----	-----
Npun.p-NpF0199	(2.0d-29)	508	AYRHHQIQLI	DEQSAQEISP	EMPQVYQDIK	QTLGVPIVNS	DYQALARWPA
A7120.p-Alr5358	(3.0d-156)	287	-----	-----	-----	-----	-----
A29413.p-Ava2596	(8.0d-151)	287	-----	-----	-----	-----	-----
N-7524.p-N-7524-5224	(2.0d-121)	285	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-1544	(2.0d-100)	284	-----	-----	-----	-----	-----
MAST-10914-SCAD-A		277	-----	-----	-----	-----	-----
N-7524.p-N-7524-5355	(2.0d-74)	267	-----	-----	-----	-----	-----
Npun.p-NpF3363	(2.0d-81)	285	-----	-----	-----	-----	-----
R7116-SCAD-A		280	-----	-----	-----	-----	-----
cyr.p-c8801?3820	(4.0d-26)	261	-----	-----	-----	-----	-----
A7120.p-Al11418	(8.0d-26)	277	-----	-----	-----	-----	-----
consensus		551	-----	-----	-----	-----	-----

A7120.p-Alr1894	(1.0d-26)	251	-----	-----	-----	-----	-----
A29413.p-Ava3764	(1.0d-26)	251	-----	-----	-----	-----	-----
N-7524.p-N-7524-0010	(9.0d-30)	250	-----	-----	-----	-----	-----
M7126-SCAD-B		255	-----	-----	-----	-----	-----
nod.p-n9414?22428	(4.0d-28)	248	-----	-----	-----	-----	-----
MAST-10914-SCAD-B		255	-----	-----	-----	-----	-----
Cal-6303.p-Cal-6303-1520	(5.0d-28)	255	-----	-----	-----	-----	-----
Npun.p-NpF2349	(4.0d-29)	248	-----	-----	-----	-----	-----
N-7107.p-N-7107-0937	(1.0d-27)	254	-----	-----	-----	-----	-----
Ana-90.p-ana90-1712	(1.0d-28)	246	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-4545	(9.0d-28)	246	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-2353	(9.0d-27)	246	-----	-----	-----	-----	-----
Cyl-505.p-Cyl-505-0204	(2.0d-28)	246	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-2349	(6.0d-29)	254	-----	-----	-----	-----	-----
R7116-SCAD-C		254	-----	-----	-----	-----	-----
ter.p-Tery_3438	(2.0d-28)	252	-----	-----	-----	-----	-----
lyn.p-l8106?21814	(1.0d-27)	255	-----	-----	-----	-----	-----
Amar.p-AM1_5632	(1.0d-26)	247	-----	-----	-----	-----	-----
cyr.p-c8801?2930	(1.0d-28)	250	-----	-----	-----	-----	-----
S6803.p-Slr0886	(4.0d-27)	247	-----	-----	-----	-----	-----
mae.p-MAE_33900	(3.0d-29)	254	-----	-----	-----	-----	-----
TeBP1.p-tlr1502	(5.0d-29)	245	-----	-----	-----	-----	-----
S7942.p-Synpcc7942_0684	(4.0d-26)	249	-----	-----	-----	-----	-----
syx.p-SynWH7803_1861	(7.0d-30)	250	-----	-----	-----	-----	-----
S7805.p-WH7805_13603	(5.0d-28)	250	-----	-----	-----	-----	-----
S9916.p-RS9916_33507	(8.0d-31)	250	-----	-----	-----	-----	-----
Ssp-RS9917.p-Ssp-RS9917-1614	(2.0d-29)	308	-----	-----	-----	-----	-----
S9917.p-RS9917_09056	(3.0d-29)	250	-----	-----	-----	-----	-----
syg.p-sync_2137	(4.0d-29)	250	-----	-----	-----	-----	-----
P9313.p-PMT1333	(6.0d-29)	250	-----	-----	-----	-----	-----
pmf.p-P9303_06521	(1.0d-28)	262	-----	-----	-----	-----	-----
S107.p-BL107_09856	(2.0d-28)	267	-----	-----	-----	-----	-----
S9902.p-Syncc9902_1745	(4.0d-28)	250	-----	-----	-----	-----	-----
S9605.p-Syncc9605_0617	(4.0d-27)	264	-----	-----	-----	-----	-----
S8102.p-SynW1852	(9.0d-28)	250	-----	-----	-----	-----	-----
syr.p-SynRCC307_0681	(2.0d-28)	250	-----	-----	-----	-----	-----
S5701.p-WH5701_07809	(1.0d-28)	252	-----	-----	-----	-----	-----
pmn.p-PMN2A_1785	(5.0d-28)	250	-----	-----	-----	-----	-----
pme.p-NATL1_05081	(1.0d-27)	250	-----	-----	-----	-----	-----

pmz.p-p9211?06582	(1.0d-27)	250	-----	-----	-----	-----	-----
PRO1375.p-Pro0452	(7.0d-27)	250	-----	-----	-----	-----	-----
Gvi.p-glr3506	(5.0d-28)	248	-----	-----	-----	-----	-----
pmb.p-P9601_05091	(9.0d-28)	249	-----	-----	-----	-----	-----
pmi.p-PMT9312_0453	(1.0d-27)	249	-----	-----	-----	-----	-----
pmg.p-P9301_04781	(1.0d-27)	249	-----	-----	-----	-----	-----
PMED4.p-PMM0453	(9.0d-28)	249	-----	-----	-----	-----	-----
pmc.p-P9515_05161	(2.0d-27)	249	-----	-----	-----	-----	-----
Npun.p-NpR0578	(6.0d-27)	257	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-0303	(5.0d-26)	266	-----	-----	-----	-----	-----
Npun.p-NpF2231	(1.0d-26)	257	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-3400	(1.0d-26)	249	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-3225	(4.0d-28)	241	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-2459	(6.0d-26)	241	-----	-----	-----	-----	-----
Ana-90.p-ana90-1189	(1.0d-28)	241	-----	-----	-----	-----	-----
Cyl-505.p-Cyl-505-2036	(2.0d-32)	241	-----	-----	-----	-----	-----
A29413.p-Ava2536	(2.0d-28)	241	-----	-----	-----	-----	-----
A7120.p-Alr5286	(2.0d-28)	255	-----	-----	-----	-----	-----
N-7524.p-N-7524-4179	(1.0d-27)	241	-----	-----	-----	-----	-----
MAST-10914-SCAD-C		245	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-1063	(4.0d-30)	241	-----	-----	-----	-----	-----
nod.p-n9414?21215	(5.0d-26)	240	-----	-----	-----	-----	-----
N-7107.p-N-7107-1008	(2.0d-29)	241	-----	-----	-----	-----	-----
M7126-SCAD-A		241	-----	-----	-----	-----	-----
R7116-SCAD-B		240	-----	-----	-----	-----	-----
lyn.p-18106?23630	(2.0d-26)	241	-----	-----	-----	-----	-----
Amar.p-AM1_5634	(3.0d-27)	241	-----	-----	-----	-----	-----
cyb.p-CYB_0189	(1.0d-27)	243	-----	-----	-----	-----	-----
cya.p-CYA_2793	(8.0d-26)	241	-----	-----	-----	-----	-----
M7126-SCAD-D		237	-----	-----	-----	-----	-----
cyb.p-CYB_0005	(4.0d-34)	291	-----	-----	-----	-----	-----
cya.p-CYA_0005	(2.0d-33)	291	-----	-----	-----	-----	-----
N-7107.p-N-7107-5182	(3.0d-28)	249	-----	-----	-----	-----	-----
Npun.p-NpR3707	(3.0d-27)	249	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-1205	(2.0d-26)	274	-----	-----	-----	-----	-----
R7116-SCAD-F		267	-----	-----	-----	-----	-----
Npun.p-NpF0204	(3.0d-28)	337	-----	-----	-----	-----	-----
MAST-10914-SCAD-D		271	-----	-----	-----	-----	-----
Cal-6303.p-Cal-6303-3407	(1.0d-27)	269	-----	-----	-----	-----	-----
Ana-90.p-ana90-4359	(1.0d-27)	263	-----	-----	-----	-----	-----

Cyl-7417.p-Cyl-7417-4762	(6.0d-27)	292	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-3536	(2.0d-26)	290	-----	-----	-----	-----	-----
N-7107.p-N-7107-1296	(2.0d-26)	291	-----	-----	-----	-----	-----
Npun.p-NpR1019	(4.0d-26)	290	-----	-----	-----	-----	-----
N-7524.p-N-7524-4265	(1.0d-25)	290	-----	-----	-----	-----	-----
M7126-SCAD-E		285	-----	-----	-----	-----	-----
R7116-SCAD-E		276	-----	-----	-----	-----	-----
cyt.p-cce_3588	(3.0d-27)	276	-----	-----	-----	-----	-----
ctc.p-c0110?06289	(2.0d-26)	275	-----	-----	-----	-----	-----
cyr.p-c8801?0598	(2.0d-26)	274	-----	-----	-----	-----	-----
Amar.p-AM1_6363	(1.0d-30)	268	-----	-----	-----	-----	-----
Amar.p-AM1_0210	(1.0d-27)	279	-----	-----	-----	-----	-----
lyn.p-l8106?00785	(4.0d-31)	270	-----	-----	-----	-----	-----
ter.p-Tery_3453	(8.0d-31)	267	-----	-----	-----	-----	-----
A29413.p-Ava0943	(1.0d-30)	293	-----	-----	-----	-----	-----
A7120.p-Al12963	(5.0d-29)	293	-----	-----	-----	-----	-----
Npun.p-NpR4797	(3.0d-30)	272	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-4424	(3.0d-30)	271	-----	-----	-----	-----	-----
MAST-10914-SCAD-E		272	-----	-----	-----	-----	-----
M7126-SCAD-C		272	-----	-----	-----	-----	-----
R7116-SCAD-D		266	-----	-----	-----	-----	-----
Npun.p-NpF0199	(2.0d-29)	558	FFLAAWS DIK	VWRERPEYQL	LVQDVVQKAE	EAASRLSPAV	WVGEREVEDI
A7120.p-Alr5358	(3.0d-156)	287	-----	-----	-----	-----	-----
A29413.p-Ava2596	(8.0d-151)	287	-----	-----	-----	-----	-----
N-7524.p-N-7524-5224	(2.0d-121)	285	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-1544	(2.0d-100)	284	-----	-----	-----	-----	-----
MAST-10914-SCAD-A		277	-----	-----	-----	-----	-----
N-7524.p-N-7524-5355	(2.0d-74)	267	-----	-----	-----	-----	-----
Npun.p-NpF3363	(2.0d-81)	285	-----	-----	-----	-----	-----
R7116-SCAD-A		280	-----	-----	-----	-----	-----
cyr.p-c8801?3820	(4.0d-26)	261	-----	-----	-----	-----	-----
A7120.p-Al11418	(8.0d-26)	277	-----	-----	-----	-----	-----
consensus		601	-----	-----	-----	-----	-----

A7120.p-Alr1894	(1.0d-26)	252	-----	-----	-----	-----	-----
A29413.p-Ava3764	(1.0d-26)	252	-----	-----	-----	-----	-----
N-7524.p-N-7524-0010	(9.0d-30)	251	-----	-----	-----	-----	-----
M7126-SCAD-B		256	-----	-----	-----	-----	-----
nod.p-n9414?22428	(4.0d-28)	249	-----	-----	-----	-----	-----
MAST-10914-SCAD-B		256	-----	-----	-----	-----	-----
Cal-6303.p-Cal-6303-1520	(5.0d-28)	256	-----	-----	-----	-----	-----
Npun.p-NpF2349	(4.0d-29)	249	-----	-----	-----	-----	-----
N-7107.p-N-7107-0937	(1.0d-27)	255	-----	-----	-----	-----	-----
Ana-90.p-ana90-1712	(1.0d-28)	247	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-4545	(9.0d-28)	247	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-2353	(9.0d-27)	247	-----	-----	-----	-----	-----
Cyl-505.p-Cyl-505-0204	(2.0d-28)	247	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-2349	(6.0d-29)	255	-----	-----	-----	-----	-----
R7116-SCAD-C		255	-----	-----	-----	-----	-----
ter.p-Tery_3438	(2.0d-28)	253	-----	-----	-----	-----	-----
lyn.p-l8106?21814	(1.0d-27)	256	-----	-----	-----	-----	-----
Amar.p-AM1_5632	(1.0d-26)	248	-----	-----	-----	-----	-----
cyr.p-c8801?2930	(1.0d-28)	251	-----	-----	-----	-----	-----
S6803.p-Slr0886	(4.0d-27)	248	-----	-----	-----	-----	-----
mae.p-MAE_33900	(3.0d-29)	255	-----	-----	-----	-----	-----
TeBP1.p-tlr1502	(5.0d-29)	246	-----	-----	-----	-----	-----
S7942.p-Syncpcc7942_0684	(4.0d-26)	250	-----	-----	-----	-----	-----
syx.p-SynWH7803_1861	(7.0d-30)	251	-----	-----	-----	-----	-----
S7805.p-WH7805_13603	(5.0d-28)	251	-----	-----	-----	-----	-----
S9916.p-RS9916_33507	(8.0d-31)	251	-----	-----	-----	-----	-----
Ssp-RS9917.p-Ssp-RS9917-1614	(2.0d-29)	309	-----	-----	-----	-----	-----
S9917.p-RS9917_09056	(3.0d-29)	251	-----	-----	-----	-----	-----
syg.p-sync_2137	(4.0d-29)	251	-----	-----	-----	-----	-----
P9313.p-PMT1333	(6.0d-29)	251	-----	-----	-----	-----	-----
pmf.p-P9303_06521	(1.0d-28)	263	-----	-----	-----	-----	-----
S107.p-BL107_09856	(2.0d-28)	268	-----	-----	-----	-----	-----
S9902.p-Sync9902_1745	(4.0d-28)	251	-----	-----	-----	-----	-----
S9605.p-Sync9605_0617	(4.0d-27)	265	-----	-----	-----	-----	-----
S8102.p-SynW1852	(9.0d-28)	251	-----	-----	-----	-----	-----
syr.p-SynRCC307_0681	(2.0d-28)	251	-----	-----	-----	-----	-----
S5701.p-WH5701_07809	(1.0d-28)	253	-----	-----	-----	-----	-----
pmn.p-PMN2A_1785	(5.0d-28)	251	-----	-----	-----	-----	-----
pme.p-NATL1_05081	(1.0d-27)	251	-----	-----	-----	-----	-----



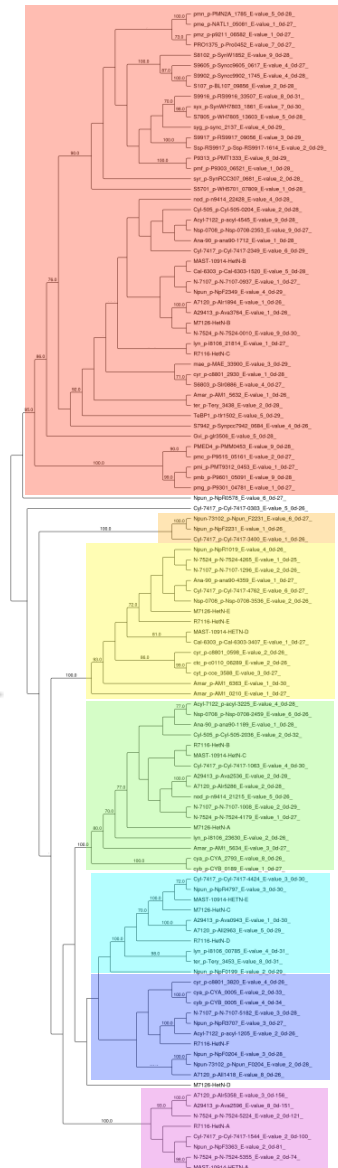
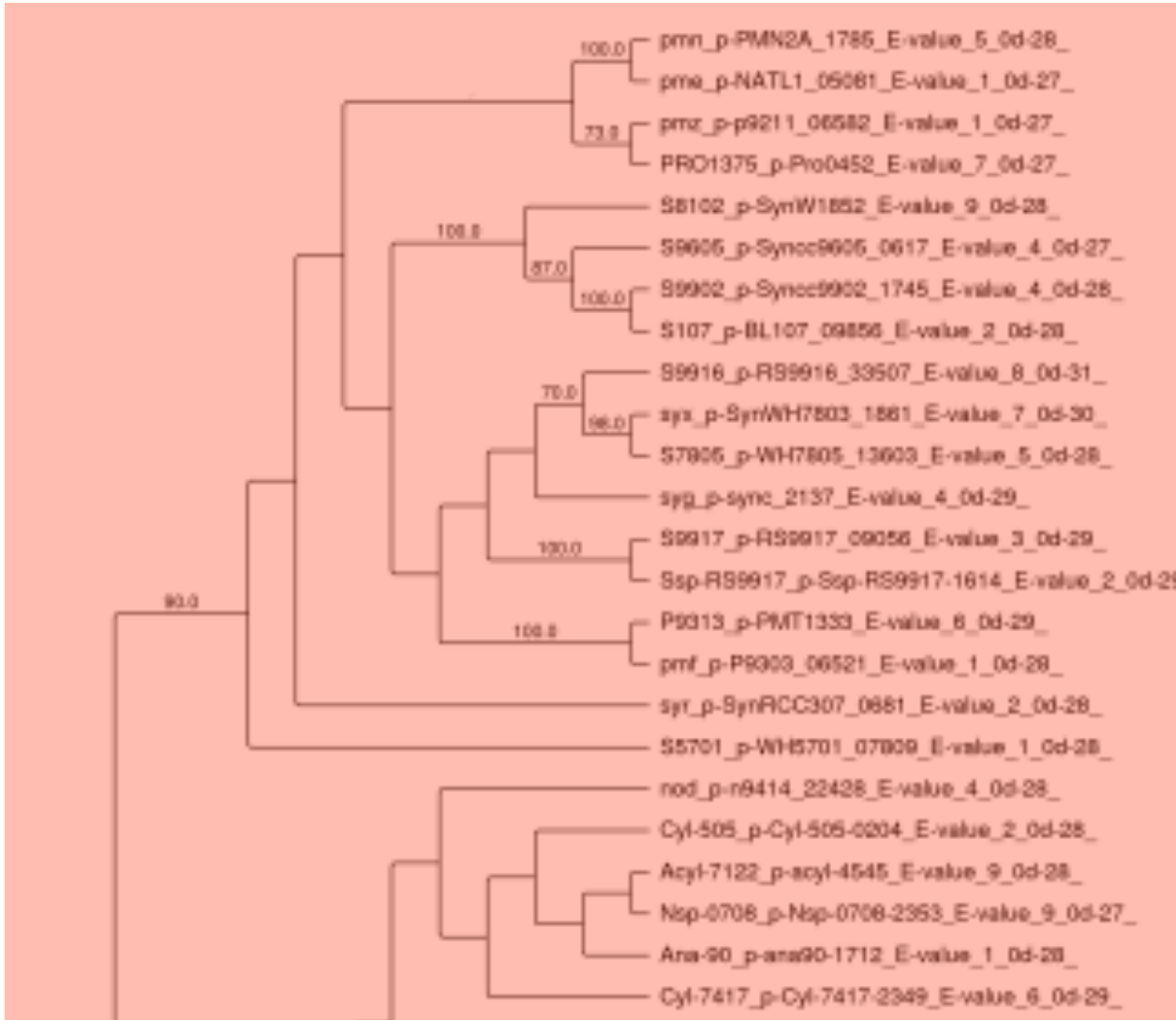
pmz.p-p9211?06582	(1.0d-27)	251	-----	-----	-----	-----	-----
PRO1375.p-Pro0452	(7.0d-27)	251	-----	-----	-----	-----	-----
Gvi.p-glr3506	(5.0d-28)	249	-----	-----	-----	-----	-----
pmb.p-P9601_05091	(9.0d-28)	250	-----	-----	-----	-----	-----
pmi.p-PMT9312_0453	(1.0d-27)	250	-----	-----	-----	-----	-----
pmg.p-P9301_04781	(1.0d-27)	250	-----	-----	-----	-----	-----
PMED4.p-PMM0453	(9.0d-28)	250	-----	-----	-----	-----	-----
pmc.p-P9515_05161	(2.0d-27)	250	-----	-----	-----	-----	-----
Npun.p-NpR0578	(6.0d-27)	258	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-0303	(5.0d-26)	267	-----	-----	-----	-----	-----
Npun.p-NpF2231	(1.0d-26)	258	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-3400	(1.0d-26)	250	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-3225	(4.0d-28)	242	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-2459	(6.0d-26)	242	-----	-----	-----	-----	-----
Ana-90.p-ana90-1189	(1.0d-28)	242	-----	-----	-----	-----	-----
Cyl-505.p-Cyl-505-2036	(2.0d-32)	242	-----	-----	-----	-----	-----
A29413.p-Ava2536	(2.0d-28)	242	-----	-----	-----	-----	-----
A7120.p-Alr5286	(2.0d-28)	256	-----	-----	-----	-----	-----
N-7524.p-N-7524-4179	(1.0d-27)	242	-----	-----	-----	-----	-----
MAST-10914-SCAD-C		246	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-1063	(4.0d-30)	242	-----	-----	-----	-----	-----
nod.p-n9414?21215	(5.0d-26)	241	-----	-----	-----	-----	-----
N-7107.p-N-7107-1008	(2.0d-29)	242	-----	-----	-----	-----	-----
M7126-SCAD-A		242	-----	-----	-----	-----	-----
R7116-SCAD-B		241	-----	-----	-----	-----	-----
lyn.p-18106?23630	(2.0d-26)	242	-----	-----	-----	-----	-----
Amar.p-AM1_5634	(3.0d-27)	242	-----	-----	-----	-----	-----
cyb.p-CYB_0189	(1.0d-27)	244	-----	-----	-----	-----	-----
cya.p-CYA_2793	(8.0d-26)	242	-----	-----	-----	-----	-----
M7126-SCAD-D		238	-----	-----	-----	-----	-----
cyb.p-CYB_0005	(4.0d-34)	292	-----	-----	-----	-----	-----
cya.p-CYA_0005	(2.0d-33)	292	-----	-----	-----	-----	-----
N-7107.p-N-7107-5182	(3.0d-28)	250	-----	-----	-----	-----	-----
Npun.p-NpR3707	(3.0d-27)	250	-----	-----	-----	-----	-----
Acyl-7122.p-acyl-1205	(2.0d-26)	275	-----	-----	-----	-----	-----
R7116-SCAD-F		268	-----	-----	-----	-----	-----
Npun.p-NpF0204	(3.0d-28)	338	-----	-----	-----	-----	-----
MAST-10914-SCAD-D		272	-----	-----	-----	-----	-----
Cal-6303.p-Cal-6303-3407	(1.0d-27)	270	-----	-----	-----	-----	-----
Ana-90.p-ana90-4359	(1.0d-27)	264	-----	-----	-----	-----	-----

Cyl-7417.p-Cyl-7417-4762	(6.0d-27)	293	-----	-----	-----	-----	-----
Nsp-0708.p-Nsp-0708-3536	(2.0d-26)	291	-----	-----	-----	-----	-----
N-7107.p-N-7107-1296	(2.0d-26)	292	-----	-----	-----	-----	-----
Npun.p-NpR1019	(4.0d-26)	291	-----	-----	-----	-----	-----
N-7524.p-N-7524-4265	(1.0d-25)	291	-----	-----	-----	-----	-----
M7126-SCAD-E		286	-----	-----	-----	-----	-----
R7116-SCAD-E		277	-----	-----	-----	-----	-----
cyt.p-cce_3588	(3.0d-27)	277	-----	-----	-----	-----	-----
ctc.p-c0110?06289	(2.0d-26)	276	-----	-----	-----	-----	-----
cyr.p-c8801?0598	(2.0d-26)	275	-----	-----	-----	-----	-----
Amar.p-AM1_6363	(1.0d-30)	269	-----	-----	-----	-----	-----
Amar.p-AM1_0210	(1.0d-27)	280	-----	-----	-----	-----	-----
lyn.p-l8106?00785	(4.0d-31)	271	-----	-----	-----	-----	-----
ter.p-Tery_3453	(8.0d-31)	268	-----	-----	-----	-----	-----
A29413.p-Ava0943	(1.0d-30)	294	-----	-----	-----	-----	-----
A7120.p-Al12963	(5.0d-29)	294	-----	-----	-----	-----	-----
Npun.p-NpR4797	(3.0d-30)	273	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-4424	(3.0d-30)	272	-----	-----	-----	-----	-----
MAST-10914-SCAD-E		273	-----	-----	-----	-----	-----
M7126-SCAD-C		273	-----	-----	-----	-----	-----
R7116-SCAD-D		267	-----	-----	-----	-----	-----
Npun.p-NpF0199	(2.0d-29)	608	LDNPDNFEQI	QQMVQMFKDI	LPELIVQNAL	FHFGLRRVQS	VKGIGSSQL
A7120.p-Alr5358	(3.0d-156)	288	-----	-----	-----	-----	-----
A29413.p-Ava2596	(8.0d-151)	288	-----	-----	-----	-----	-----
N-7524.p-N-7524-5224	(2.0d-121)	286	-----	-----	-----	-----	-----
Cyl-7417.p-Cyl-7417-1544	(2.0d-100)	285	-----	-----	-----	-----	-----
MAST-10914-SCAD-A		278	-----	-----	-----	-----	-----
N-7524.p-N-7524-5355	(2.0d-74)	268	-----	-----	-----	-----	-----
Npun.p-NpF3363	(2.0d-81)	286	-----	-----	-----	-----	-----
R7116-SCAD-A		281	-----	-----	-----	-----	-----
cyr.p-c8801?3820	(4.0d-26)	262	-----	-----	-----	-----	-----
A7120.p-Al11418	(8.0d-26)	278	-----	-----	-----	-----	-----
consensus		651	-----	-----	-----	-----	-----

**Supplemental Fig. 1: Alignment of HetN-like proteins.** The sequences of proteins similar to HetN (Alr5358) with an E-value  $< 10^{25}$  were aligned, considering only positions without gaps, using Clustal. Names consist of an abbreviation of the organism (see Suppl. Table 1), a gene name, and the E-value of a Blast using HetN as the query. E-values for HetN-like proteins from *Mastigocladopsis repens* (MAST-10914) and *Rivularia* PCC 7116 (R7116) are not shown as they were found

by a separate Blast, and their E-values are not comparable to those of the other proteins. Proteins from these organisms were given unofficial names (SCAD, for Short Chain Alcohol Dehydrogenase). Red boxes highlight the RGSGR motif.

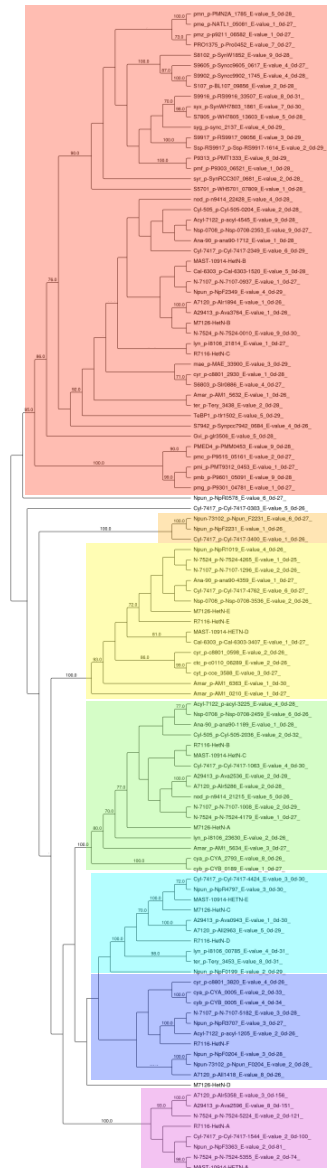
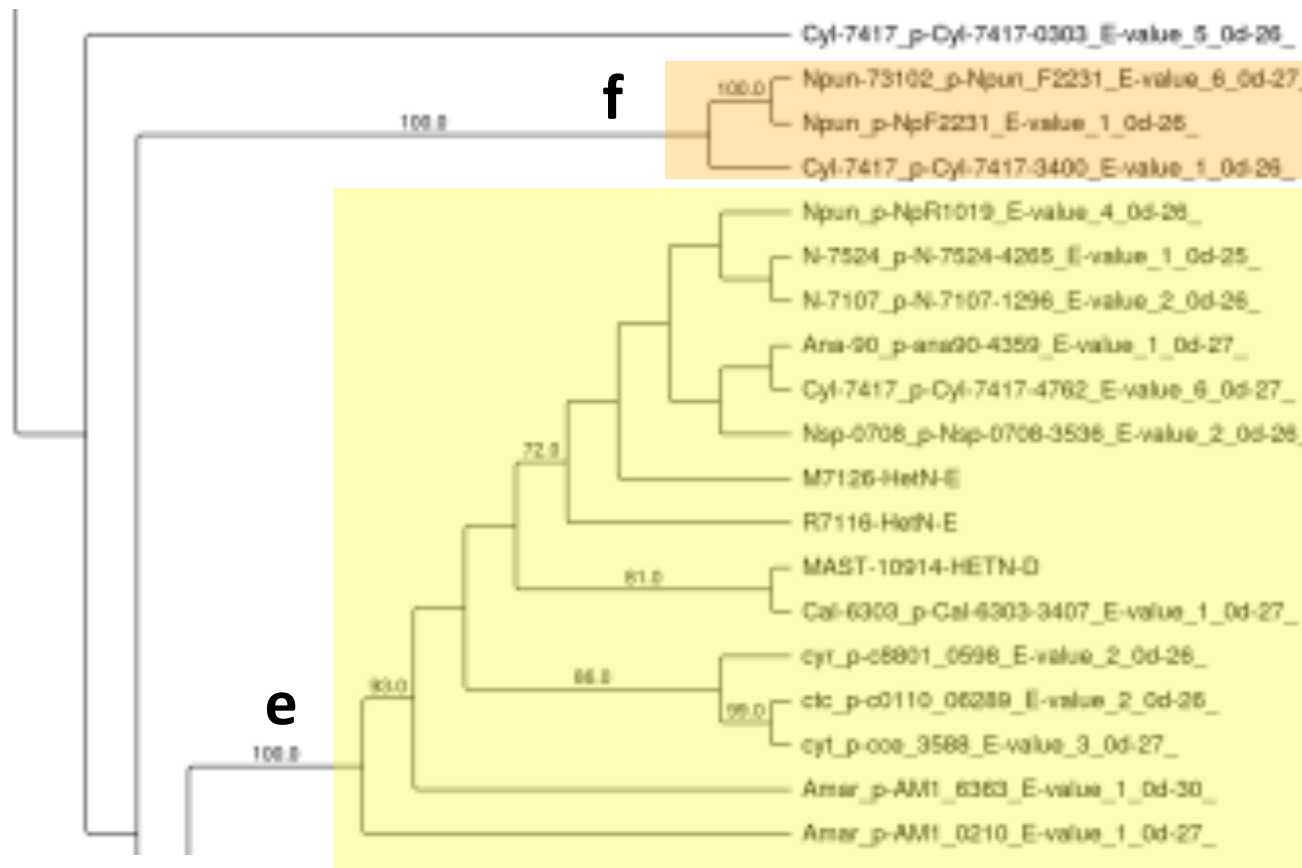
# Supplemental Figure 2: Phylogeny of HetN-like proteins



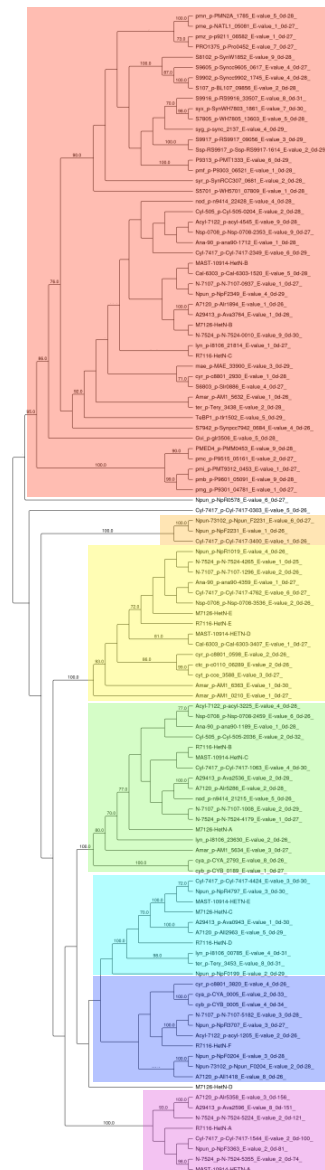
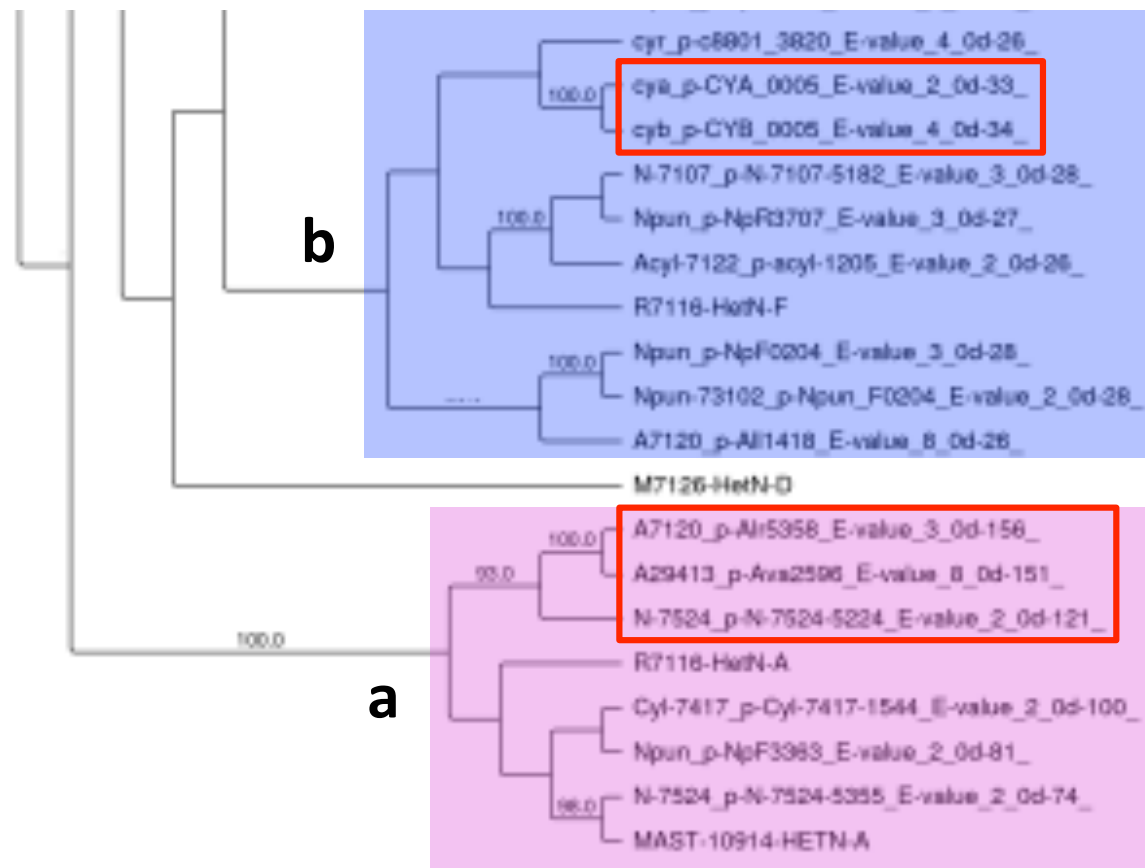
g  
f  
e  
d  
c  
b  
a

g





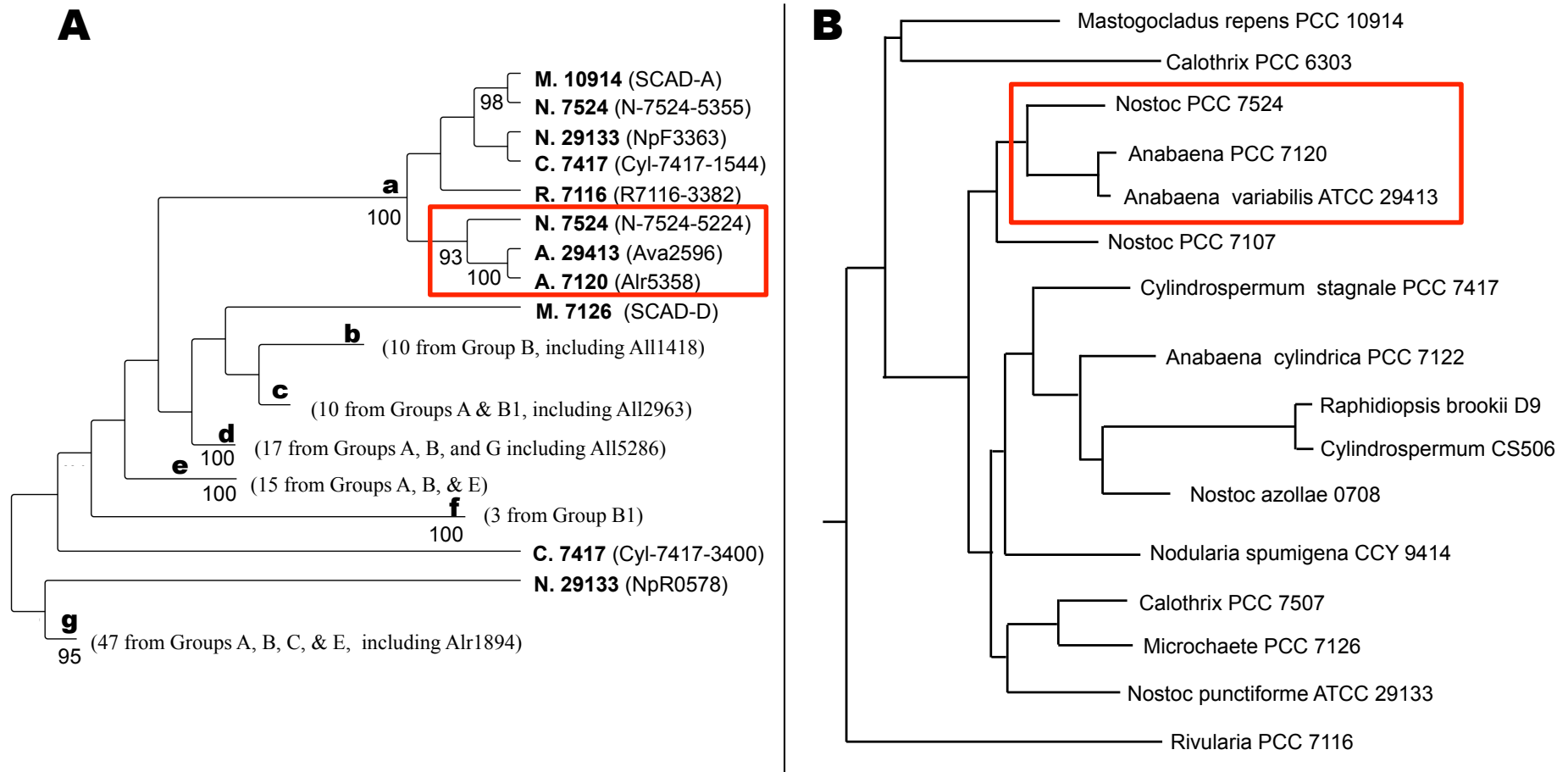




**Supplemental Fig. 2: Phylogeny of HetN-like proteins.** A neighbor-joining tree was made by Phylip from the alignment shown in Suppl. Fig. 1, with 100 bootstrap trials. Bootstrap values of at least 70 are shown. Names consist of an abbreviation of the organism (see Suppl. Table 1), a gene name, and the E-value of a Blast using HetN as the query. Red boxes highlight the proteins bearing the RGSGR motif.

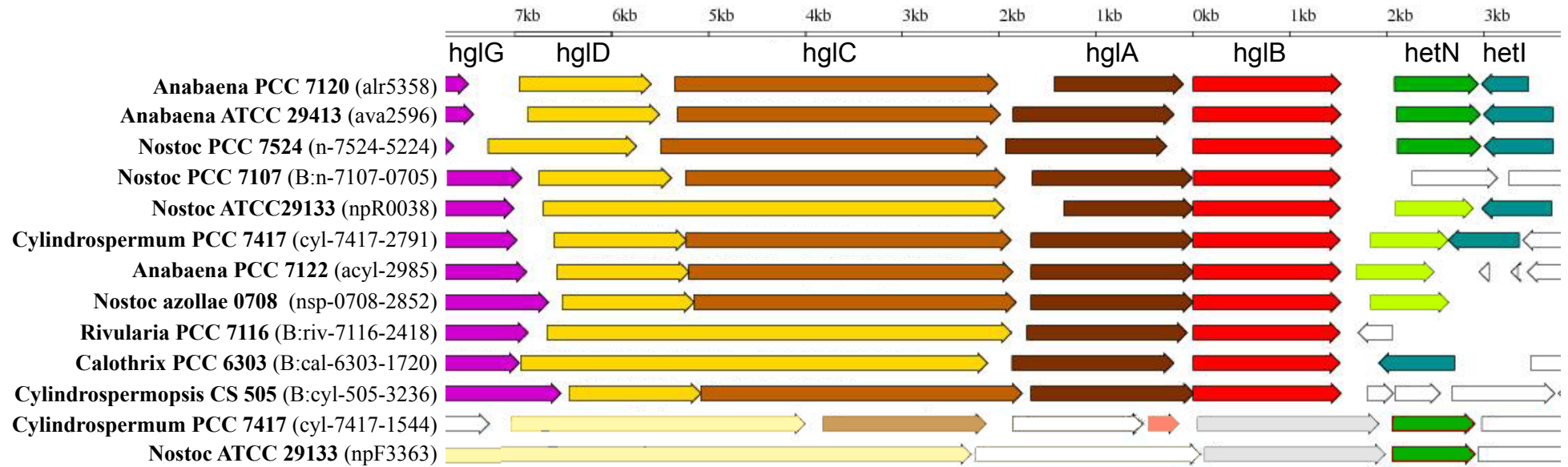


## Supplemental Figure 3: Phylogeny of HetN-like proteins



**Supplemental Fig. 3. Phylogeny of HetN-like proteins.** (A) Neighbor-joining tree of 111 cyanobacterial proteins similar to HetN, with E-values better than  $10^{-25}$ . The name of the organism is shown in bold and the name of the protein in parentheses. Clades have been collapsed to save space, except for the clade containing HetN (Alr5358) from Anabaena sp. strain PCC 7120. Bold lower case letters indicate the group, as defined by this tree. Groups with upper case letters refer to those defined by the organismal tree of Shih et al. (35). Numbers indicate bootstrap value for 100 trials. Red box surrounds proteins containing ERGSGR residues. The entire phylogeny is shown in Supplemental Fig. 1. (B) Organismal tree adapted from (35), showing the phylogenetic relationships amongst all the heterocyst-forming cyanobacteria used in this study. The red box surrounds the three cyanobacteria with HetN-like proteins containing ERGSGR residues.

## Supplemental Figure 4: Genetic context near genes encoding HetN-like proteins



**Supplemental Figure 4. Genetic context near genes encoding HetN-like proteins.** Genes represented in the same color are orthologous to a gene shown from *Anabaena* sp. strain PCC 7120, where two proteins are defined as orthologs if they are the best Blast hit of each other in their respective organisms, with E-values better than  $10^{-10}$ . Proteins with dimmer colors are similar but not orthologous to *Anabaena* proteins. The name of the organism is shown in bold and the name of the *hetN*-like gene is given in parenthesis. If the name is preceded by "B:", then it is the name of the *hglB*-like gene that is given.

**Supplemental Table 1: Genomes used in analysis of HetN-like proteins**

<b>Cyanobacterium</b>	<b>Nicknames/Aliases</b>	<b>Shih Group<sup>a</sup></b>	<b>Description<sup>b</sup></b>	<b>Genome-size</b>	<b>Contigs/Replicons</b>
<i>Acaryochloris marina</i> MBIC 11017	Amar	E	Unicellular	8361599	10
<i>Anabaena cylindrica</i> PCC 7122	Acyl-7122	B1	Linear, spaced heterocysts	7063285	7
<i>Anabaena</i> sp 90	Ana-90		Linear; spaced heterocysts?	5305675	5
<i>Anabaena</i> sp PCC 7120	A7120	B1	Linear; spaced heterocysts	7211789	7
<i>Anabaena variabilis</i> ATCC 29413	A29413	B1	Linear; spaced heterocysts	7105752	5
<i>Calothrix</i> PCC 6303	Cal-6303	B1	Linear; spaced/basal heterocysts	6960392	4
<i>Cyanothece</i> CCY0110	ctc		Unicellular	5880532	163
<i>Cyanothece</i> sp ATCC 51142	cyt	B2	Unicellular	5460377	6
<i>Cyanothece</i> sp PCC 8801	cyr	B2	Unicellular	4575961	29
<i>Cylindrospermopsis raciborskii</i> CS 505	Cyl-505	B1	Linear; terminal heterocysts	3879030	93
<i>Cylindrospermum stagnale</i> PCC7417	Cyl-7417, C.7417	B1	Linear; terminal heterocysts	7610589	4
<i>Gloeobacter violaceus</i> PCC 7421	gvi		Unicellular	4659019	1
<i>Lyngbya</i> sp PCC 8106	Lyn, CCY 9616	A	Filamentous	7037511	110
<i>Mastigocladopsis repens</i> PCC 10914	MAST-109014, M.10914	B1	branched; spaced heterocysts	6070411	1
<i>Microchaete</i> sp PCC 7126	M7126	B1	Linear; spaced/basal heterocysts	5207209	1
<i>Microcystis aeruginosa</i> NIES 843	mae	B2	Unicellular	5842795	1
<i>Nodularia spumigena</i> CCY 9414	nod	B1	Linear; spaced heterocysts	5316258	204
<i>Nostoc azollae</i> 0708	Nsp-0708	B1	Linear; spaced heterocysts	5486145	3
<i>Nostoc punctiforme</i> PCC 73102	Npun, N.29133	B1	Linear; spaced heterocysts	9059191	6
<i>Nostoc</i> sp PCC 7107	N-7107	B1	Linear; spaced heterocysts	6329823	1
<i>Nostoc</i> sp PCC 7524	N-7524, N.7524	B1	Linear; spaced heterocysts	6718869	3
<i>Prochlorococcus marinus</i> str MIT 9211	pmz	C1	Marine picoplankton	1839003	114
<i>Prochlorococcus marinus</i> str MIT 9312	pmi	C1	Marine picoplankton	1709204	1
<i>Prochlorococcus marinus</i> str MIT 9313	P9313	C1	Marine picoplankton	2410873	1
<i>Prochlorococcus marinus</i> str NATL1A	pme	C1	Marine picoplankton	1864731	1
<i>Prochlorococcus marinus</i> str NATL2A	pmn	C1	Marine picoplankton	1842899	1
<i>Prochlorococcus marinus</i> subsp <i>marinus</i> str CCMP1375	PRO1375, ss120	C1	Marine picoplankton	1751080	1
<i>Prochlorococcus marinus</i> subsp <i>pastoris</i> str CCMP1986	PMED4	C1	Marine picoplankton	1657990	1
<i>prochlorococcus marinus</i> as9601	pmb	C1	Marine picoplankton	1669886	1
<i>Prochlorococcus marinus</i> mit9301	pmg	C1	Marine picoplankton	1641879	1
<i>Prochlorococcus marinus</i> mit9303	pmf	C1	Marine picoplankton	2682675	1
<i>Prochlorococcus marinus</i> mit9515	pmc	C1	Marine picoplankton	1704176	1
<i>Rivularia</i> PCC 7116	R7116	B1	Linear; spaced/basal heterocysts	8728773	3

Synechococcus BL107	S107	C1	Marine picoplankton	2285034	1
Synechococcus CC9311	syg	C1	Marine picoplankton	2606748	1
Synechococcus elongatus PCC 7942	S7942	C2	Unicellular	2750104	3
Synechococcus RCC307	syr	C1	Marine picoplankton	2224914	1
Synechococcus sp CC9605	S9605	C1	Marine picoplankton	2510659	1
Synechococcus sp CC9902	S9902	C1	Marine picoplankton	2234828	1
Synechococcus sp JA 2 3B	cyb	G	Unicellular	3046682	1
Synechococcus sp JA 3 3Ab	cya	G	Unicellular	2932766	1
Synechococcus sp RS9916	S9916	C1	Marine picoplankton	2664873	1
Synechococcus sp RS9917	Ssp-RS9917	C1	Marine picoplankton	2584918	1
Synechococcus sp WH 5701	S5701	C1	Marine picoplankton	2860463	1
Synechococcus sp WH 7803	syx	C1	Marine picoplankton	2366980	1
Synechococcus sp WH 7805	S7805	C1	Marine picoplankton	2621166	1
Synechococcus sp WH 8102	S8102	C1	Marine picoplankton	2434428	1
Synechocystis sp PCC 6803	S6803	B2	Unicellular	3956956	8
Thermosynechococcus elongatus BP 1	TeBP1	D	Unicellular	2593857	1
Trichodesmium erythraeum IMS101	ter	A	Filamentous	7750108	1

<sup>a</sup> Groups are defined by Shih et al (2013)

<sup>b</sup> Description refers to the overall morphology of the cyanobacterium – either unicellular, linear filamentous, or branched filamentous – and the positions of heterocysts (if present).