



ALB01044.1	MD - KSS IANKIEAYLGAKSDDSKIDQSLKADPSEVQY YGSGGDGYLLRKNICKITVNHSDSGTNDPCDRKELSYGDI DEWKCAI ILSKVSEKPEVNFVPPRRQRMCIKNLENLKF DKIRDKHAFLADVLL	129
ALB01053.1	MD - KSS IANKIEAYLGAKSDDSKIDQSLKADPSEVQY YGSGGDGYLLRKNICKITVNHSDSGTNDPCDRKELSYGDI DEWKCAI ILSKVSEKPEVNFVPPRRQRMCIKNLENLKF DKIRDKHAFLADVLL	129
ETW56275.1	MDSTSTIANKIEAYLGAKSDDSKIDELLKADPSEVQY YRSGGDGYLLKNNICKITVNHSDSGTNDPCDSIPPPYGDNDQWKCAI ILSKVSEKPEVNFVPPRRQHMCIKNLEKLVNVDKIRDKHAFLADVLL	130
ALB01048.1	MDSTSTIANKIEAYLGAKSNDKIDQSLKADPSEVQY YGSGGDGYLLKNNICKITVNHSDSGKYDPCDRKELSYGDI DEWKCCQNSSDGSSEKPEVNFVPPRRQHMCIKNLENLKF DKIRDKHAFLADVLL	130
ALB01041.1	MDSTSTIGDKIEEYLGAKSDESNI EQSLKADPSKVQY YGSGGDGYLLKNNICKITVNHSDSGKYEPCDSIPPPYGDNDQWKCENLYKVEKPEVNFVPPRRQRMCIKNLEKLVNVDKIRDKHAFLADVLL	130
ALB01039.1	MDSTSTIGDKIEEYLGAKSDESNI EQSLKADPSKVQY YGSGGDGYLLKNNICKITVNHSDSGKYEPCDSIPPPYGDNDQWKCENLYKVEKPEVNFVPPRRQRMCIKNLEKLVNVDKIRDKHAFLADVLL	130
ALB01056.1	MDSTSTIANKIEAYLGAKSDESNI DQSLKADPSEVQY YRSGGDGYLLKNNICKITVNHSDSGKYDPCDRKELSYGDI DEWKCAI ILSKVSEKPEVNFVPPRRQRMCIKNLEKLVNVDKIRDKHAFLADVLL	130
KNC35427.1	MDSTSTIANKIEAYLGAKSDDSKIDELLKADPSEVEY YRSGGDGYLLKNNICKITVNHSDSGKYDPCCKKLPYGDNDQWKCENLYKASENNKNI FVPPRRQRMCIKNLENLKF DKIRDKHAFLADVLL	130
ALB01046.1	MDSTSTIANKIEAYLKEKSNESKIDQSLKADPSEVQY YGSGGDGYLLKNNICKITVNHSDSGTNDPCENKLLPYGDNDQWKCENLYKASEKPEVICVPPRRQRMCIKNLEKLVNVEKIRDKHAFLADVLL	130
ALB01037.1	MDSTSTIANKIEAYLGAKSDESNI DQSLKADPSEVQY YRSGGDGYLLKNNICKITVNHSDSGTNDPCDSIPPPYGDNDQWKCENLYKASEKPEVICVPPRRQRMCIKNLEKLVNVDKIRDKHAFLADVLL	130
ALB01055.1	MDSKTTTIAEKIEAYLEKKSNDKIDQSLKADPSEVQY YRSGGDGYLLKNNICKITVNHSDSGKYDPCDRKELSYGDNQWKCQNSSDGSSEKPEVICVPPRRQRMCIKNLENLKF DKIRDKHAFLADVLL	130
AAQ73924.1	MD - KSSIGDKIEAYLEKKSDESIEQSLKADPSEVEY YRSGGDGYLLRKNICKITVNHSDSGKYEPCDRKELSYGDI DEWKCCQNSSDGSSEKPEVICVPPRRQRMCIKNLENLKF DKIRDNNAFLADVLL	129
ALB01042.1	MD - KSSIGDKIEEYLKESNDKIDQSLKADPSEVQY YGSGGDGYLLKNNICKITVNHSDSGKYEPCDSIPPPYGDNDQWKCENLSKVSEKPEVICVPPRRQRMCIKNLENLKF DKIRDKHAFLADVLL	129
AJD77410.1	MDSKTTTIAEKIEEYLKESNDKIDQSLKADPSEVQY YGSGGDGYLLKNNICKITVNHSDSGTNDPCCKKLLPYGDNDQWKCENLKFASGNHKNICVPPRRQHMCIKNLENLKF DKIRDKHAFLADVLL	130
EWC75615.1	MDSTSTIGDKIEEYLKESDESNI DQSLKADPSKVQY YGSGGDGYLLKNNICKITVNHSDSGKYEPCDSIPPPYGDNDQWKCENLYKASGNHKNIFVPPRRQHMCIKNLEKLVNVEKIRDKHAFLADVLL	130
ALB01054.1	MDSTSTIAEKIEAYLGAKSNEPNIDQSLKADPSKVQY YRSGGDGYLLKNNICKITVNHSDSGKQNEP - YGTNQTWKCAI ILSKVSEKPEVNFVPPRRQRMCIKNLEKLVNVDKIRDKHAFLADVLL	129
ALB01057.1	MDSTSTIANKIEAYLEKKSNDKIDQSLKADPSEVQY YGSGGDGYLLKNNICKITVNHSDSGTNDPCDSIPPPYGDIDEWKCAI ILSKVSEKPEVNFVPPRRQRMCIKNLEKLVNVDKIRDKHAFLADVLL	130
ALB01040.1	MDSTSTIGDKIEEYLKESDESNI DQSLKADPSEVQY YGSGGDGYLLKNNICKITVNHSDSGTNDPCDSIPPPYGDNDQWKCENLKFASGNHKNICVPPRRQHMCIKNLEKLVNVDKIRDKHAFLADVLL	130
ETW41644.1	MDSTSTIGDKIEAYLGAKSDDSKIDQSLKADPSEVQY YRSGGDGYLLKNNICKITVNHSDSGTNDPCDRIPPPYDNDQWKCENLSKVSEKPEVICVPPRRQRMCIKNLEKLVNVDKIRDKHAFLADVLL	130
ALB01043.1	MDSTSTIGDKIEEYLKESDESNI DQSLKADPSEVQY YGSGGDGYLLKNNICKITVNHSDSGTNDPCDSIPPPYGDNDQWKCENLKFASGNHKNICVPPRRQHMCIKNLEKLVNVDKIRDKHAFLADVLL	130
EUT82883.1	MD - KSSIGDKIEAYLEKKSDESNI EQSLKADPSEVQY YGSGGDGYLLRKNICKITVNHSDSGTNDPCDRKELSYGDI DEWKCAI ILSKVSEKPEVNFVPPRRQRMCIKNLENLKF DKIRDKHAFLADVLL	129
ALB01038.1	MD - KSSIGDKIEAYLEKKSDESNI DQSLKADPSEVQY YRSGGDGYLLRKNICKITVNHSDSGTNDPCDSIPPPYGDNDQWKCQNSSDGSSEKPEVICVPPRRQRMCIKNLENLKF DKIRDKHAFLADVLL	129
ALB01058.1	MD - KSSIGDKIEAYLEKKSDESNI DQSLKADPSEVQY YRSGGDGYLLRKNICKITVNHSDSGTNDPCDSIPPPYGDNDQWKCQNSSDGSSEKPEVICVPPRRQRMCIKNLENLNFVERIRDKHAFLADVLL	129
ALB01059.1	MDSTSTIADKIEAYLGAKSDESNI EQSLKADPSEVQY YGSGGDGYLLKNNICKITVNHSDSGTNDPCCKKLLPYGDNDQWKCQNSSDGSSEKPEVICVPPRRQRMCIKNLENLKF DKIRDKHAFLADVLL	130
KNG76633.1	MDSKTTTIAEKIEAYLGAKSDDSKIDQSLKADPSEVQY YGSGGDGYLLKNNICKITVNHSDSGTNDPCCKKLLPYGDNDQWKCENLYKASENNKNI FVPPRRQRMCIKNLEKLVNVEKIRDKHAFLADVLL	130
ALB01051.1	MDSTSTIGDKIEEYLGAKSDESNI EQSLKADPSEVQY YGSGGDGYLLKNNICKITVNHSDSGKYEPCDSIPPPYGDNDQWKCENLYKVEKPEVNFVPPRRQRMCIKNLEKLVNVEKIRDKHAFLADVLL	130
ALB01049.1	MD - KSSIGDKIEEYLKESDDSKIDELLKADPSEVQY YRSGGDGYLLKNNICKITVNHSDSGKYDPCDRIPPPYDNDQWKCENLYKASENNKNI FVPPRRQRMCIKNLENLKF DKIRDKHAFLADVLL	129
EWC75604.1	MD - KSSIGDKIEAYLEKKSDESNI DQSLKADPSEVQY YRSGGDGYLLRKNICKITVNHSDSGTNDPCDSIPPPYGDNDQWKCENLSKVSEKPEVICVPPRRQRMCIKNLEKLVNVEKIRDKHAFLADVLL	129
ALB01045.1	MD - KSS IANKIEAYLKEKSDSKIDQSLKADPSEVQY YGSGGDGYLLKNNICKITVNHSDSGTNDPCCKKLLPYGDNDQWKCENLSKVSEKPEVICVPPRRQRMCIKNLEKLVNVEKIRDKHAFLADVLL	129
ALB01047.1	MDSKTTTIAEKIEEYLKESNDKIDQSLKADPSEVQY YGSGGDGYLLKNNICKITVNHSDSGKYEPCDSIPPPYGDNDQWKCENLKFASGNHKNICVPPRRQHMCIKNLEKLVNVDKIRDKHAFLADVLL	130
7G8.pro	MD - KSSIGDKIEEYLKESDDSKIDELLKADPSEVEY YRSGGDGYLLKNNICKITVNHSDSGKYEPCDRIPPPYGDNDQWKCQNLKASENNKNIFVPPRRQRMCIKNLENLNFVERIRDKHAFLADVLL	129
124_8.pro	MDSTSTIANKIEAYLKEKSNESNI DQSLKADPSEIDY YNFGGDGYLLRKNICKITVNHSDSGTNDPCDRKELSYGDNQWKCQNSSDGSSEKPEVICVPPRRQRMCIKNLEKLVNVDKIRDKHAFLADVLL	130
indo.pro	MDSKTTTIAEKIEAYLGAKSNDKIDQSLKADPSEVQY YRSGGDGYLLKNNICKITVNHSDSGTNDPCDRKELSYGDI DEWKCEENLYKASENNKNI FVPPRRQRMCIKNLEKLVNVDKIRDKHAFLADVLL	130
KMWII.pro	MD - KSSIGDKIEAYLEKKSNDKIDQSLKADPSEVQY YRSGGDGYLLKNNICKITVNHSDSGTNDPCDRKELSYGDI DEWKCEENLYKASENNKNI FVPPRRERLCTYNLEKLVNVEKIRDKHAFLADVLL	129
M24.pro	MDSKTTIADKIEAYLGAKSDDSKIDQSLKADPSEVQY YGSGGDGYLLKNNICKITVNHSDSGTNDPCCKKLLPYGDNDQWKCENLYKASENNKNI FVPPRRQRMCIKNLENLKF DKIRDKHAFLADVLL	130
MTS1.pro	MDSKTTTIAEKIEAYLVAKSDDSKIDELLKADPSEIDY YNFGGDGYLLKNNICKITVNHSDSGKYEPCDSIPPPYGDNDQWKCQNSSDGSSEKPEVICVPPRRQRMCIKNLENLKF DKIRDNNAFLADVLL	130
P13.pro	MDSTSTIADKIEAYLKEKSNDSKIDQSLKADPSEVQY YGSGGDGYLLKNNICKITVNHSDSGTNDPCDRKLLPYGDNDQWKCQNSSDGSSEKPEVICVPPRRQRMCIKNLENLNFVERIRDKHAFLADVLL	130
T2C6.pro	MDSKTTIADKIEAYLKEKSDSKIDQSLKADPSEVQY YRSGGDGYLLKNNICKITVNHSDSGKYDPCDRKELSYGDI DEWKCAI ILSKVSEKPEVNFVPPRRQRMCIKNLENLNFVERIRDKHAFLADVLL	130
VL_S.pro	MDSKTTTIAEKIEAYLKEKSNESDI DQSLKADPSEVEY YRSGGDGYLLRKNICKITVNHSDSGMYEPCDRKELSYGDI DEWKCEENLKFASGNHKNICVPPRRQHMCIKNLEKLVNVEKIRDNNAFLADVLL	130
WR80.pro	MDSKTTTIAEKIEAYLKEKSNESNI EQSLKADPSEVQY YGSGGDGYLLKNNICKITVNHSDSGTNDPCDRIPPPYDNDQWKCQNSSDGSSEKPEVICVPPRRQRMCIKNLEKLVNVEKIRDKHAFLADVLL	130
PFL0030cexon1+2.pro	MD - KSS IANKIEAYLGAKSDDSKIDQSLKADPSEVQY YGSGGDGYLLRKNICKITVNHSDSGTNDPCDRIPPPYGDNDQWKCQNSSDGSSEKPEVICVPPRRQRMCIKNLEKLVNVDKIRDKHAFLADVLL	129
A4PFL0030c exon1+2.pro	MDSTSTIANKIEAYLGAKSDDSKIDELLKADPSEVEY YRSGGDGYLLKNNICKITVNHSDSGKYDPCCKKLPYDNDQWKCQNSSDGSSEKPEVICVPPRRERLCTYNLENLKF DKIRDNNAFLADVLL	130
Newdd2var2CSAsequence.pro	MD - KSSIGDKIEAYLEKKSDESIEQSLKADPSEVEY YRSGGDGYLLRKNICKITVNHSDSGKYEPCDRKELSYGDI DEWKCCQNSSDGSSEKPEVICVPPRRQRMCIKNLENLKF DKIRDKHAFLADVLL	129
McPFL0030c.pro	MDSTSTIANKIEAYLGAKSDDSKIDELLKADPSEVQY YRSGGDGYLLKNNICKITVNHSDSGTNDPCDSIPPPYGDNDQWKCQNSSDGSSEKPEVICVPPRRQRMCIKNLEKLVNVDKIRDKHAFLADVLL	130
HB3-1var2CSA.pro	MDSTSTIGDKIEAYLGAKSNDKIDQSLKADPSKVQY YGSGGDGYLLKNNICKITVNHSDSGTNDPCCKKELSYGDNQWKCQNSSDGSSENNKNI FVPPRRQRMCIKNLEKLVNVDKIRDKHAFLADVLL	130
HB3-2var2CSA.pro	MDSKTTTIAEKIEEYLKESNDKIDQSLKADPSEIDY YNFGGDGYLLKNNICKITVNHSDSGTNDPCCKKLLPYGDNDQWKCENLKFASGNHKNICVPPRRQHMCIKNLEKLVNVEKIRDKHAFLADVLL	130



ALB01044.1	TARNEGEKIVQNHDPDTSNVCVALERSFADLADIIRGTD---QWKGTN---SNLEQNLKQMFAKIREKDS	TLKNNYSKKDQNYTKLREDWWT	TNRQKVVEVITCGARSNDLLIKRRWTTSGK	SNGENK	252
ALB01053.1	TARNEGEKIVQNHDPDTSNVCVALERSFADLADIIRGTD---QWKGTN---SNLEQNLKQMFAKIREKDS	TLKNNYSKKDQNYTKLREDWWT	TNRQKVVEVITCGARSNDLLIKRRWTTSGK	SNGENK	252
ETW56275.1	TARKEGERIVQNHDPDTSNVCVALERSFADLADIIRGTD---LWKGTN---SNLEKNLQMFKNILEKGSTI	QSNYSKD-QNYRKLREDWWT	TNRQKVVEVITCGARSNDLLIKRGWTTSGK	SNGDNK	252
ALB01048.1	TARNEGERIVQNHDPDTSNVCVALERSFADLADIIRGTD---QWKGTN---SNLEKNLQMFAKIREKDS	TLKNNYSK-DQNYTKLREDWWT	TNRQKVVEVITCGARSNDLLIKRRWTTSGK	SNGENK	252
ALB01041.1	TARNEGERIVQNHDPDTSNVCNALERSFADIADIIIRGRDENKCETKSPN---NVEELIKNFFGKNYRSNEEYKRYQND	DENYKLLREAWWNNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGENK	256	
ALB01039.1	TARNEGERIVQNHDPDTSNVCNALERSFADIADIIIRGRDENKCETKSPN---NVEELIKNFFGKNYRSNEEYKRYQND	DENYKLLREAWWNNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGENK	256	
ALB01056.1	TARNEGERIVQNHDPDTSNVCVALERSFADLADIIRGRDENKCETKSPN---NVEELIKNFFGKNYRSNEEYKRYQND	DPKYTKLREAWWNNRQKVVEVITCSARSNDLLIKRGWTTSGK	SNGENK	256	
KNC35427.1	TARNEGERIVQNHDPDTSNVCVALERSFADIADIIIRGRDGNKCETKSPN---NVEELIKKFFFKNYRSNEEYKRYQND	DENYKLLREAWWNNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGDNK	256	
ALB01046.1	TARNEGEKIVQNHDPDTSNVCVALERSFADLADIIRGTD---LWKGTN---SNLEKNLQMFKNILEKDS	TLKNNYSNDDENYKLLREAWWNNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGENK	253	
ALB01037.1	TARNEGERIVQNHDPDTSNVCVALERSFADLADIIRGRDENKCETKSPN---NVEELIKNFFGKNYRSNEEYKRYQND	DPKYTKLREAWWNNRQKVVEVITCGARSNDLLIKRGWTTSGK	SNGDNK	256	
ALB01055.1	TARNEGERIILYHPDTSNVCNALERSFADIADIIIRGTD---LWKGTN---SNLEKNLQMFAKILEKDS	TLKNNYSKKDQNYRKLREDWWT	TNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGENK	253
AAQ73924.1	TARNEGERIVQNHDPDTSNVCVALERSFADLADIIRGTDQWKGTN-----KFEPLKQMFAKIRENDKVLQDKY	PNDDPKYTKLREDWWT	TNRQKVVEVITCSARSNDLLIKLGWTTSGK	SEGDNK	251
ALB01042.1	TARNEGERIILYHPDTSNVCNALERSFADIADIIIRGTD---QWKGTN---SNLEQNLKQMFAKIRENDKVLQDKY	PNDDENYKLLREDWWT	TNRQKVVEVITCGARSNDLLIKRGWTTSGK	SNGENK	252
ADJ77410.1	TARNEGERIVQNHDPDTSNVCVALERSFADLADIIRGRDENKCETKSTN---NVEELIKNFFGKNYRSNEEYKRYQND	DPKYTKLREAWWNNRQKVVEVITCGARSNDLLIKRRWTTSGK	SNGENK	256	
EWC75615.1	TARNEGERIVQNHDPDTSNVCVALERSFADLADIIRGTD---QLKGSN---ILEQNLRRMFKNILEKDV	LQDKYQNDDENYKLLREDWWT	TNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGENK	252
ALB01054.1	TARNEGEKIVQNHDPDTSNVCVALERSFADLADIIRGTD---LWKGTN---SNLEKNLQMFKNILEKDS	TLKNNYSNDDENYKLLREAWWNNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGENK	252	
ALB01057.1	TARNEGERIVQNHDPDTSNVCNALERSFADIADIIIRGTDQWKGTN---S---NLEKNLQMFARILEKDS	TLKNNYSKDK-NYRKLREDWWT	TNRQKVVEVITCSARSNDLLIKRGWTTSGK	SDRKN	252
ALB01040.1	TARNEGERIVQNHDPDTSNVCNALERSFADIADIIIRGTD---LWKGTN---SNLEQNLRRMFAKIRENDKVLQDKY	PK-DQNYTKLREDWWT	TNRQKVVEVITCGARSNDLLIKRGWTTSGK	SNGENK	252
ETW41644.1	TARNEGERIILYHPDTSNVCVALERSFADLADIIRGTDLWKGTN---S---NLEQNLQMFAKILEKDV	LQDKYPK-QNYTKLREDWWT	TNRQKVVEVITCGARSNDLLIKRRWTTSGK	SNGDNK	252
ALB01043.1	TARNEGERIVQNHDPDTSNVCNALERSFADIADIIIRGTD---LWKGTN---SNLEQNLRRMFAKIRENDKVLQDKY	PK-DQNYTKLREDWWT	TNRQKVVEVITCGARSNDLLIKRGWTTSGK	SNGENK	252
EUT82883.1	TARNEGEKIVQNHDPDTSNVCVALERSFADLADIIRGTD---QWKGTN---SNLEQNLKQMFAKILEKDS	TLKNNYSKKDQNYTKLRESWWT	TNRQKVVEVITCGARSNDLLIKRRWTTSGK	SNGENK	252
ALB01038.1	TARNEGERIVQNHDPDTSNVCVALERSFADIADIIIRGRDGNKCETKSPN---NVEELIKKFFGKNYRSNEEYKRYQND	DPKYTKLREDWWT	TNRQKVVEVITCSARSNDLLIKRGWTTSGK	SNGENK	255
ALB01058.1	TARNEGERIVQNHDPDTSNVCVALERSFADIADIIIRGRDGNKCETKSPN---NVEELIKKFFGKNYRSNEEYKRYQND	DPKYTKLREDWWT	TNRQKVVEVITCSARSNDLLIKRGWTTSGK	SNGENK	255
ALB01059.1	TARNEGERIVQNHDPDTSNVCVALERSFADIADIIIRGTD---QLKGSN---ILEQNLKQMFKNILEKDS	TLKNNYSNDDENYKLLREAWWNNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGENK	252	
KMG76633.1	TARNEGEKIVQNHDPDTSNVCVALERSFADIADIIIRGTD---QWKGTN---SNLEQNLKQMFAKILEKDS	TLKNNYSKKDQNYTKLREDWWT	TNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGENK	253
ALB01051.1	TARNEGERIILYHPDTSNVCVALERSFADLADIIRGRD---GNKCETKSTNNVEELIKKFFGKNYRSNEEYKRYQND	DPKYTKLREDWWT	TNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGENK	256
ALB01049.1	TARNEGERIILYHPDTSNVCIALERSFADLADIIRGRD---GNKCETKSTNNVEELIKKFFGKNYRSNEEYKRYQND	DPKYTKLREDWWT	TNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGDNK	255
EWC75604.1	TARNEGEKIVQNHDPDTSNVCVALERSFADIADIIIRGTD---LWKGTN---SNLEQNLQMFKNILEKGSTI	QSNYSKDK-NYRKLREAWWNNRQKVVEVITCGARSNDLLIKRRWTTSGK	SNGDNK	251	
ALB01045.1	TARNEGEKIVQNHDPDTSNVCVALERSFADLADIIRGTD---QWKGTN---SNLEQNLRRMFAKILEKDS	TLKNNYSKKDQNYTKLREAWWNNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGENK	252	
ALB01047.1	TARNEGERIVQNHDPDTSNVCVALERSFADLADIIRGRD---ENKCETKSTNNVEELIKNFFGKNYRSNEEYKRYQND	DPKYTKLREAWWNNRQKVVEVITCGARSNDLLIKRRWTTSGK	SNGDNK	256	
7g8.pro	TARNEGERIVQNHDPDTSNVCIALERSFADIADIIIRGRDGNKCETKSTN---NVEELIKKFFGKNYRSNEEYKRYQND	DPKYTKLREDWWT	TNRQKVVEVITCGARSNDLLIKRGWTTSGK	SEGENK	255
124_8.pro	TARNEGEKIVQNHDPDTSNVCVALERSFADIADIIIRGTD---LWKGTN---SNLEKNLQMFAKILEKDV	LQDKYPNDDENYKLLREDWWT	TNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGENK	253
kimdo.pro	TARNEGERIILYHPDTSNVCVALERSFADLADIIRGTD---QWKGTN---SNLEKNLQMFAKIRENDKVLQDKY	PNDDENYKLLREDWWT	TNRQKVVEVITCSARSNDLLIKRRWTTSGK	SEGENK	253
KMWII.pro	TARNEGERIVQNHDPDTSNVCVALERSFADLADIIRGTD---LWKGTN---KFEPLYKQMFAKILEKDS	TLKNNYSKDKPKYTKLREDWWT	TNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGENK	251
M24.pro	TARNEGEKIVQNHDPDTSNVCVALERSFADIADIIIRGTD---QWKGTN---SNLEQNLKQMFAKIREKDS	TLKNNYSK-DQNYRKLREDWWT	TNRQKVVEVITCGARSNDLLIKRRWTTSGK	SNGENK	252
MTS1.pro	TARNEGERIVQNHDPDTSNVCIALERSFADLADIIRGRDGNKCETKSPN---NVEELIKKFFFKNYRSNEEYKRYQND	DPKYTKLREDWWT	TNRQKVVEVITCGARSNDLLIKRGWTTSGK	SNGENK	256
p13.pro	TARNEGERIILYHPDTSNVCVALERSFADLADIIRGTDQWKGTN---S---NLEQNLQMFKNILEKDV	LQDKYQNDDENYKLLRESWWT	TNRQKVVEVITCSARSNDLLIKRGWTTSGK	SEGENK	253
T2C6.pro	TARNEGERIVQNHDPDTSNVCVALERSFADLADIIRGTD---QWKGTN---SNLEKNLQMFAKIRENDKVLQDKY	PNDDENYKLLREDWWT	TNRQKVVEVITCGARNNDLLIKRRWTTSGK	SNGENK	253
V1_S.pro	TARNEGERIILYHPDTSNVCNALERSFADLADIIRGRDENKCETKSPN---NVEELIKNFFGKNYRSNEEYKRYQND	DPKYTKLREAWWNNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGDNK	256	
WR80.pro	TARNEGERIVQNHDPDTSNVCVALERSFADIADIIIRGTD---LWKGTN---SNLEQNLKQMFAKILEKDV	LQDKYPK-NYTKLREAWWNNRQKVVEVITCSARSNDLLIKRRWTTSGK	SNGDNK	252	
PFL0030cexon1+2.pro	TARNEGERIVQNHDPDTSNVCNALERSFADIADIIIRGTD---LWKGTN---SNLEQNLKQMFAKIRENDKVLQDKY	PK-DQNYRKLREDWWT	TNRQKVVEVITCGARSNDLLIKRGWTTSGK	SNGDNK	251
A4PFL0030c exon1+2.pro	TARNEGEKIVQNHDPDTSNVCNALERSFADLADIIRGTD---QWKGTN---SNLEKNLQMFAKIRENDKVLQDKY	PK-DQYTKLREAWWNNRQKVVEVITCGARSNDLLIKRGWTTSGK	SDRKN	252	
Newdd2var2CSAsequence.pro	TARNEGERIVQNHDPDTSNVCVALERSFADLADIIRGTDQWKGTN-----KFEPLKQMFAKIRENDKVLQDKY	PNDDPKYTKLREDWWT	TNRQKVVEVITCGARSNDLLIKLGWTTSGK	SEGDNK	251
McPFL0030c.pro	TARKEGERIVQNHDPDTSNVCNALERSFADIADIIIRGTD---LWKGTN---SNLEKNLQMFKNILEKGSTI	QSNYSKDK-QNYRKLREDWWT	TNRQKVVEVITCGARSNDLLIKRGWTTSGK	SNGDNK	252
HB3-1var2CSA.pro	TARNEGERIILYHPDTSNVCVALERSFADIADIIIRGTD---QLKGSN---ILEQNLKQMFAKIREKDV	LQDKYPNDDENYKLLREDWWT	TNRQKVVEVITCSARSNDLLIKRRWTTSGK	SEGENK	252
HB3-2var2CSA.pro	TARNEGERIVQNHDPDTSNVCVALERSFADLADIIRGRDENKCETKSTN---NVEELIKNFFGKNYRSNEEYKRYQND	DPKYTKLREAWWNNRQKVVEVITCGARSNDLLIKRRWTTSGK	SNGDNK	256	



ALB01044.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDGMRHREECTREDDKCKEGTSCYNMCKEKHTTKYCECVKKWKTEWENQKNK-YKDLYQQ-ENETSQ--KNTSRYDDYVKEFFKFKG 378
ALB01053.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDGMRHREECTREDDKCKEGTSCYNMCKEKHTTKYCECVKKWKTEWENQKNK-YKDLYQQ-ENETSQ--KNTSRYDDYVKEFFKFKG 378
ETW56275.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDLYREKQNLIDDMERHREECTRKNVDSKEGTSCYCTCKDKCKKCYCECVKKWKTEWENQKNK-YKDLYKDKRKKSS-AKHASRYDDYVKDFPFKLE 380
ALB01048.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDDMERHREECTSEDHKCKEGTSCYCTCKDKCKKCYCECVKKWKTEWENQKNK-YTELYEQ-ENETSSSSKKKSRYDDYVKDFPFKLE 380
ALB01041.1 LELFRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDLYREKQNLIDDMERHREECTREDDKCKEVTSYCNMCKDKCKKCYCECVKKWKSEWENQKNK-YKDLYQQNKNETSSSSKNSRYDDYVKDFPFKLE 385
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KNC35427.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDDMERHREECTRKNVDSKEGTSCYCTCKDKCKKCYCECVKKWKTEWENQKNK-YNDLYQQE-NETS SSKKKSRYDDYVKEFFKFKG 384
ALB01046.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDDMERHREECTSEDHKCKEVTSYCTNCKEKCKKYCECVKKWKSEWKNQENK-YKELYEQ-ENKTS SSKKKSRYDDYVKDFPFKLE-E 380
ALB01037.1 LELCRKCGHYEGKVPPTKLDYVPPQLRWLWTEWIEDLYREKQNLIDDMERHREECTSEDHKCKEVTSYCTNCKEKCKKYCECVKKWKTEWENQKNK-YTELYEQ-ENETS--QKNTSRYDNYVKEFFKFKG 382
ALB01055.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDDMERHREECTREDDKCKEVTSYCNMCKEKHTTKYCECVKKWKSEWKNQENK-YKDLYEQNKNETSSSSKNTSRYDDYVKEFFKLE-E 381
AAQ73924.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDGMRHREECTRKNVDSKEGTSCYCTNCKEKCKKYCEVFNKWKSEWENQKNK-YNDLYQQE-NKTS SSKKKSRYDDYVKEFFKFKG 379
ALB01042.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDDMERHREECTREYDKCKEGAS YCNMCKDKCKKCYCECVKKWKSEWENQKNK-YKDLYQQNKNETSSSSKNTSRYDNYVKEFFKLE 381
ADJ77410.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDDMERHREECTSEDHKCKEVTSYCTNCKEKCKKYCECVKKWKSEWENQKNK-YTELYEQNKNETSSSSKNTSRYDDYVKEFFKLE 385
EWC75615.1 LELFRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDLYREKQNLIDDMERHREECTREYDKCKEGTSCYCTNCKEKCKKYCECVFNKWKSEWENLKNK-YKELYEQ-ENKTS SSKKKSRYDDYVKEFFKFKG 380
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ETW41644.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDLYREKQNLIDDMERHREECTSEDDKCKEGTSCYCTNCKEKHTTKYCECVKKWKTEWENQKNK-YKDLYQQE-NETS SSKKKSRYDDYVKEFFKFKG 380
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EUT82883.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDLYREKQNLIDGMRHREECTREDDKCKEVTSYCNMCKDKCKKCYCECVKKWKTEWENQKNK-YKDLYQQNKNETSSSSKNTSRYDDYVKEFFKLE 381
ALB01038.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDLYREKQNLIDDMERHREECTSEDHKCKEVTSYCTNCKEKCKKYCECVKKWKSEWENQKNK-YKDLYQQ-ENETS SSKKKSRYDDYVKDFPFKFKG 383
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ALB01059.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDLYREKQNLIDGMRHREECTSQDDKSNEGTSCYCTNCKEKCKKYCECVKKWKTEWENQKNK-YNDLYQQKNETSSSSKKSRYDDYVKEFFKLE 381
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ALB01049.1 LELFRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDRLEENCKKYKGNVNCVNGTENSACKDQCVCYCTFIRNRKNHWEQKCKKYYKSLYQDVGSSDSSSLYVPSVDDNVKFEFFKFKG 385
EWC75604.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDRLEYYCEKCNQKGNVNCVNGTENSACKDQYVKYCTFIRNRKNHWEQKCKKYYKSLYQDVGSSDSSSLYVPSVDDNVKFEFFKFKG 380
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ALB01047.1 LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDRLEYYCEKCNQKGNVNCVNGTENSACKDQCVCYCTFIRNRKNHWEQKCKKYYKSLYQDVGSSDSSSLYVPSVDDNVDFLQKFKG 385
7G8.pro LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDLYREKQNLIDDMERHREECTSEDHKCKEGTSCYCNMCKDKCKKCYCECVKKWKSEWENQKNK-YKDLYQQ-ENETS SSKKKSRYDDYVKEFFKFKLE 383
124_8.pro LELCRKCGHYEGKVPPTKLDYVPPQLRWLWTEWIEDLYREKQNLIDDMERHREECTREYDKCKEVTSYCNMCKEKCKKYCECVKKWKTEWENQENK-YNDLYKDK-KRKKSSAKHASRYDNYVKEFFKFKG 381
indo.pro LELCRKCGHYEGKVPPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDDMERHREECTSEDHKCKEVTSYCTNCKEKHTTKYCECVKKWKSEWENQKNK-YTELYEQ-ENETS SSKKKSRYDDYVKEFFKFKG 381
KMWII.pro LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDLYREKQNLIDDMERHREECTRKYVESKGVTSYCNMCKDKCKKCYCECVKKWKTEWENQKNK-YNDLYQQE-NETS SSKKKSRYDDYVKDFPFKFKG 379
M24.pro LELFRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDGMRHREECTSEDDKCKEVTSYCNMCKDKCKKCYCECVKKWKTEWENQKNK-YKDLYEQNKNETSSSSKKSRYDDYVKEFFKFKG 381
MTS1.pro LELCRKCGHYEGKVPPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDDMERHREECTSEDDKCKEGTSCYCNMCKDKCKKCYCECVKKWKSEWENQKNK-YKDLYQQ-ENETS SSKKKSRYDDYVKEFFKFKG 384
p13.pro LELCRKCGHYEGKVPPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDDMERHREECTRKYVESKGVTSYCNMCKEKHTTKYCECVKKWKTEWENQKNK-YKDLYEQNKNETSSSPKKKSRYDDYVKEFFKFKLE 382
T2C6.pro LELFRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDLYREKQNLIDDMERHREECTREDDKCKEGTSCYCTNCKEKCKKYCECVKKWKSEWENQKNK-YKDLYEQNKNETSSSSKKSRYDNYVKEFFKLE 382
V1_S.pro LELFRKCGHYEGKVPPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDDMERHREECTREDDKCKEGTSCYCTNCKEKHTTKYCEVFNKWKSEWENQKNK-YTELYEQ--NKNTS QKNTSRYDDYVKEFFKFKG 383
WR80.pro LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDDMERHREECTRKYVESKGVTSYCNMCKEKHTTKYCECVKKWKTEWENQKNK-YKDLYEQNKNETSSSPKKKSRYDDYVKEFFKFKLE 381
PFL0030cexon1+2.pro LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDDMERHREECTSEDHKCKEGTSCYCTNCKEKCKKYCECVKKWKSEWENQKNK-YTELYQQNKNETS--KNTSRYDDYVKDFPFKLE 378
A4PFL0030c exon1+2.pro FELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDDMERHREECTREDDKCKEGTSCYCTNCKEKCKKYCECVKKWKTEWENQKNK-YKDLYQQ--NKNTS QKNTSRYDDYVKDFPFKLE 379
Newdd2var2CSAsequence.pro LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDFYREKQNLIDGMRHREECTRKNVDSKEGTSCYCTNCKEKCKKYCEVFNKWKSEWENQKNK-YNDLYQQE-NETS SSKKKSRYDDYVKEFFKFKG 379
McPFL0030c.pro LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDLYREKQNLIDDMERHREECTRKNVDSKEGTSCYCTNCKEKCKKYCECVKKWKTEWENQKNK-YKDLYKDKRKKSS-AKHASRYDDYVKDFPFKLE 380
HB3-1var2CSA.pro LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDLYREKQNLIDDMERHREECTRKNVDSKEGTSCYCNMCKEKHTTKYCECVKKWKSEWENQKNK-YTELYEQ--ENETS QKNTSRYDDYVKDFPFKFKG 378
HB3-2var2CSA.pro LELCRKCGHYEEKVPTKLDYVPPQLRWLWTEWIEDLYREKQNLIDDMERHREECTRKNVDSKEGTSCYCNMCKEKHTTKYCECVKKWKSEWENQKNK-YTELYEQ--ENETS QKNTSRYDDYVKDFPFKFKG 382



ALB01044.1	DNYKSLDDYIKGDPYSKEYVTKLSFILNSSDANTSSEKIQKNNDEVNCNNESEISSVEQAQTSDESSNKTCTHSS--IKANKKKECKDVKLVGVRENDKDLRVCVIEHTSLSGVENCXQDLLGILQENCS	507
ALB01053.1	DNYKSLDDYIKGDPYSKEYVTKLSFILNSSDANTSSEKIQKNNDEVNCNNESEISSVEQAQTSDESSNKTCTHSS--IKANKKKECKDVKLVGVRENDKDLRVCVIEHTSLSGVENCXQDLLGILQENCS	507
ETW56275.1	ANYKSLDDYIKGDPYFAEYATKLSFILNSSDANTSSEGETANHNDEACNPNSEISSVEHAQTSDESSNKTCTHSS--IKANKKKECKDVKLVGVRENDKDLRVCVIEHTSLSGVENCXQDLLGILQENCS	509
ALB01048.1	ANYKSLDNYIKGDPYSKEYVTKLSFILNSSDANTSSEKIQKNNDEVNCNPNSEISSVEQAQTSDESSNKTCTHSS--IGANKKKECKDVKLVGINNNDKVLKICVIEDDSLGRVENCXQDLLGILQENCS	509
ALB01041.1	N-YSSLDDYIKDDPYSAQVYTKLSFILNPSDENTENASETPSKYYDEVCPNPNSEISSVEHAQTSDESSSQKACNTHSS--IKTNKKKVECKHVKLVGVRENDKDLKICVIEHTSLSGVENCXQDLLGILQENCS	513
ALB01039.1	N-YSSLDDYIKDDPYSAQVYTKLSFILNPSDENTENASETPSKYYDEVCPNPNSEISSVEHAQTSDESSSQKACNTHSS--IKTNKKKVECKHVKLVGVRENDKDLKICVIEHTSLSGVENCXQDLLGILQENCS	513
ALB01056.1	NGYSSANSYVKNPYSAEYATKLSFILNSSDANTSSEGETANHNDEVNCNNESEISSVELAPISGPPSNKTCTHSS--IKTNKKKVECKHVKLVGREKDKDLKICVIEDTSLSGVENCXQDLLGILQENCS	513
KNC35427.1	DNYSSLDDYIKGDPYFAEYATKLSFILNPSDENTENASETPSKYYDEACNPNSEISSVEQAQTSDESSNKTCTHSS--IKTNKKKVECKDVKLVGVRENDKDLKICVIEDTSLSGVENCXQDLLGILQENCS	513
ALB01046.1	ANYKSLDNYIKGDPYFAEYATKLSFILNPSDANTSSEGETANHNDEVNCNPNSEISSVEQAQTSDESSNKTCTHSS--IKTNKKKVECKDVKLVGINNNDKDLKICVIEDTSLSGVENCXQDLLGILQENCS	509
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ALB01055.1	ANYKSLDNYIKGDPYFAEYATKLSFILNPSDANTSSEGETANHNDEVNCNPNSEISSVQQAQTSDESSNKTCTHSS--IGANKKKECKDVKLVGVRENDKDLKICVIEHTSLSGVENCXQDLLGILQENCS	510
AAQ73924.1	DNYKSLDNYIKGDPYFAEYATKLSFILNPSDANTSSEGETANHNDEVNCNNESEISSVQQAQTSDESSNKTCTHSS--IKTNKKKVECKDVKLVGINNNDKDLKICVIEDTSLSGVENCXQDLLGILQENCS	508
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AJD77410.1	ANYSSLDDYIKDDPYFAEYATKLSFILNPSDANTSSEGETANHNDEVNCNPNSEISSVEQAQTSDESSNKTCTHSS--IKANKKKECKDVKLVGVRENDKDLKICVIEDTSLSGVENCXQDLLGILQENCS	514
EW75615.1	NGYSSANSYVKNPYSAEYATKLSFILNPSDANTSSEKIQKNNDEVNCNNESEISSVQQAQTSDESSSQKACI THSF--IGANKKKECKDVKLVGINNNDKDLKICVIEHTSLSGVENCXQDLLGILQENCS	509
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ETW41644.1	DNYSSLDNYIKGDPYFAEYATKLSFILNSSDANTSSEKIQKNNDEVNCNNESEISSVEQAQTSDESSNKTCTHSS--IKANKKKECKDVKLVGINNNDKDLKICVIEDTSLSGVENCXQDLLGILQENCS	509
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EUT82883.1	ANYSSLDNYIKGDPYSKEYVTKLSFILNPSDANTSSEKIQKNNDEVNCNPNSEISSVEHAQTSVLLSQKAYITHSS--IKTNKKKVECKHVKLVGVRENDKDLKICVIEDTSLSGVENCXQDLLGILQENCS	510
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ALB01059.1	N-YLSDDDYIKDDPYSAEYKLLKFD----NTNAFKESITCNKNVCCSCGNEKLIISEGSSSSSFPGTSSSYQSSIITSNKRKECKQIKFSGNKNMNMNINICSTQDEKLL--VK--LELLKSFCDTCD	501
KNG76633.1	NGYSSANSYIKNPNYSAEYKLLKFD----GPDAFIESPTYNNVCCSTPEKSAKTIDGSSSSSFPGTSSSYQSSIITSNKRKECKQIKFSGNKNMNMNINICSTQDNNLL--VE--FQELLSFCNISG	502
ALB01051.1	DNYSSLDDYIKGDPYSSDGGKLLIFD----NTNAFIESPTYNNVCCSTPEKSAKTIDGSSSSSFPGTSSSYQSSIITSNKRKECAQIKFSGNKNMNMNINICSTQDNNLL--VE--FQELLSKGFCDTCD	505
ALB01049.1	NGYSSANSYVKNPNYSAEYKLLKFD----GPDAFIESPTYNNVCCSTPEKSAKTIDGSSSSSFPGTSSSYQSSIITSNKRKECKQIKFSGNKNMNMNINICSTQDEKLL--VK--LELLKSFCDTCD	505
EW75604.1	NGYSSANSYIKNPNYSAEYKLLIFD----NTNAFKESITFNKNVCCSCGNEKLIISEGSSSSRFPGTSSSYQSSIITSNKRKECKQIKFSGNKNMNMNINICSTQDEKLL--VK--LELLKSFCDTCD	500
ALB01045.1	NGYSSANSYVKNPNYSSEDGKLLKFD----NTNAFKESITCNKNVCCSCGNEKLIISEGSSSSSFPGTSSSYQSSIITSNKRKECAQIKFSGNKNMNMNINICSTQDNNLL--VK--LELLKSFCDTCD	500
ALB01047.1	NEYSSANSYVKNPNYSSEDGKLLKFD----NTNAFKESITCNKNVCCSCGNEKLIISEGSSSSSFPGTSSSYQSSIITSNKRKECKQIKFSGNKNMNMNINICSTQDNNLL--VK--LELLKSFCDTCD	505
7G8.pro	ANYSSLDNYIKDDPYSAEYVTKLSFILNPSDANTSSEKIQKNNDEVNCNPNSEISSVEQAQTSDESSNKTCTHSS--IKANKKKECKDVKLVGVRENDKDLKICVIEDTSLSGVENCXQDLLGILQENCS	512
124_8.pro	NGYSSANSYVKNPYSKEYVTKLSFILNPSDANTSSEGETANHNDEVNCNPNSEISSVQQAQTSDESSNKTCTHSS--IGANKKKECKDVKLVGVRENDKDLKICVIEDDSLGRVENCXQDLLGILQENCS	510
indo.pro	DNYKSLDDYIKGDPYSAEYVTKLSFILNPSDANTSSEKIQKNNDEVNCNNESEISSVQQAQTSDESSNKTCTHSS--IKANKKKECKDVKLVGVRENDKDLRVCVIEHTSLSGVENCXQDLLGILQENCS	510
KMWII.pro	DNYKSLDDYIKGDPYSAEYVTKLSFILNPSDANTSSEGETANHNDEVNCNPNSEISSVQQAQTSDESSNKTCTHSS--IGANKKKECKDVKLVGVRENDKDLRVCVIEHTSLSGVENCXQDLLGILQENCS	508
M24.pro	DNYKSLDDYIKGDPYFAEYATKLSFILNSSDANTSSEGETANHNDEVNCNPNSEISSVQQAQTSDESSNKTCTHSS--IKANKKKECKDVKLVGINNNDKDLRVCVIEHTSLSGVENCXQDLLGILQENCS	510
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p13.pro	ANYKSLDDYIKDDPYSAEYATKLSFILNPSDANTSSEGETANHNDEVNCNNESEISSVELAPISDSSNKTCTHSS--IGANKKKECKDVKLVGVRENDKDLKICVIEDTSLSGVENCXQDLLGILQENCS	511
T2C6.pro	ANYKSLDNYIKGDPYSKEYVTKLSFILNPSDANTSSEKIQKNNDEVNCNPNSEISSVEQAQTSDESSNKTCTHSS--IKANKKKECKDVKLVGVRENDKDLKICVIEHTSLSGVENCXQDLLGILQENCS	511
V1_S.pro	DNYKSLDDYIKDDPYSAEYVTKLSFILNPSDANTSSEKIQKNNDEVNCNNESEISSVQQAQTSDESSNKTCTHSS--IKANKKKECKDVKLVGINNNDKDLRVCVIEHTSLSGVENCXQDLLGILQENCS	512
WR80.pro	NEYSSANSYIKNPNYSSEDGKLLIFD----NTNAFIESPTYNNVCCSTPEKSAKTIDGSSSSSFPGTSSSYQSSIITSNKRKECKQIKFSGNKNMNMNINICSPDEKLL--VK--LELLKSFCDTCD	501
PFL0030cexon1+2.pro	N-YSSLDNYIKGDPYFAEYATKLSFILNSSDANTSSEKIQKNNDEVNCNNESEISSVEQAQTSDESSNKTCTHSS--IKANKKKECKDVKLVGVRENDKDLRVCVIEHTSLSGVENCXQDLLGILQENCS	506
A4PFL0030c exon1+2.pro	N-YSSLDNYIKGDPYFAEYATKLSFILNPSDANTSSEGETANHNDEVNCNPNSEISSVQQAQTSDESSNKTCTHSS--IKTNKKKVECKDVKLVGVRENDKDLKICVIEDTSLSGVENCXQDLLGILQENCS	507
Newdd2var2CSAsequence.pro	DNYKSLDNYIKGDPYFAEYATKLSFILNSSDANTSSETPSKYYDEVCPNPNSEISSVQQAQTSDESSNKTCTHSS--IKTNKKKVECKDVKLVGINNNDKDLRVCVIEHTSLSGVENCXQDLLGILQENCS	508
McPFL0030c.pro	ANYKSLDDYIKGDPYFAEYATKLSFILNSSDANTSSEGETANHNDEVNCNNESEISSVEHAQTSDESSNKTCTHSS--IKANKKKECKHVKLVGVRENDKDLRVCVIEHTSLSGVENCXQDLLGILQENCS	509
HB3-1var2CSA.pro	NGYSSANSYVKNPYSAEYVTKLSFILNSSDANTSSETPSKYYDEVCPNPNSEISSVQQAQTSDESSNKTCTHSS--IKTNKKKVECKDVKLVGINNNDKDLRVCVIEHTSLSGVENCXQDLLGILQENCS	507
HB3-2var2CSA.pro	NEYSSANSYVKNPNYSAEYVTKLSFILNSSDANTSSETPSKYYDEVCPNPNSEISSVQQAQTSDESSNKTCTHSS--IKTNKKKVECKDVKLVGINNNDKDLRVCVIEHTSLSGVENCXQDLLGILQENCS	511



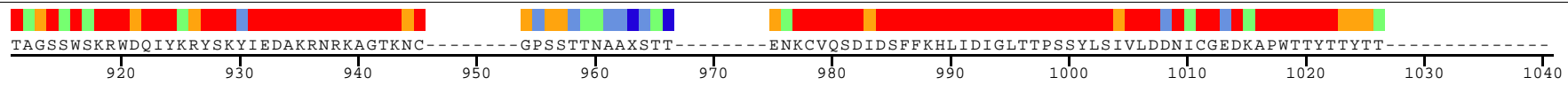
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D-NKSGSSSSNGSCNKNKQEAACEKNL-EKVLASLTNICYKCDKCKSEQSKNNKNKIWKSSSGKEGGLQKEYANTI GLP PRT QSLCLV-VCLDEK-GKKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKPS-- 632
D-NKSGSSSSNGSCDNKNEEACEKNL-EKVFASLTNICYKCEKCKSEQSKNNKNKIWKSSSGKEGGLQKEYANTI GLP PRT QSLCLV-VCLDEK-GKKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKPSHE 636
D-NKSGSSSSNGSCDNKQEAACEKNL-EKVLASLTNICYKCDKCKSEQSKNNNIWIWRKSSSGKEGGLQKEYANTI GLP PRT QSLCLV-VCLDEK-GKKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKPS-- 634
D-NKRRSSSSNGSCDNKNQDECEKNL-EKVLASLTNICYKCDKCKSGTSTVN-NKIWKKYSVKEGGLQKEYANTI ALP PRT QSLYL--VCLHEK-EGKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKIS-- 636
D-NKRRSSSSNGSCDNKNQDECEKNL-EKVLASLTNICYKCDKCKSGTSTVN-NKIWKKYSVKEGGLQKEYANTI ALP PRT QSLYL--VCLHEK-EGKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKIS-- 636
D-NIRGSSSSNGSCDNKNEEACEKNL-EKVFASLTNICYKCDKCKSGTSTVN-NKIWKKYSVKEGGLQKEYANTI ALP PRT QSLCLV-VCLDEK-EGKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKTYY-- 638
D-NKRGSSSSNGSCDNKNEEACEKNL-DEALASLTNICYKCEKCKSGTSTVN-KKWTRKSSGNEEGLQKEYANTI GLP PRT QSLCL--VCLHEK-EGKTKH-KTISTNSELLKKEWIIAAPHGEGKNLKTSH-- 636
D-NKRESSSSNGSCNKNQDECEKQKL-DEALASLTNICYKCEKCKSGTSTVN-KKIWKSSGNEEGLQKEYANTI GLS PRT QSLCL--VCLHEK-EGKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKPS-- 633
D-NKRESSSSNGSCDNKNEEACEKNL-EKVFASLTNICYKCDKCKSEQSKNNKNKIWKSSSGNGEGLQKEYANTI GLP PRT HSLY LGNLRKLEN-VCEDEVKIDNFDTKEKFLAGCLIAAPHGEGKNLKTSS-- 637
DKNQSGSSSSNGSCDNKNEEACEKNL-DEALASLTNICYKCEKCKSEQSKNNKIWTRKFPNGEGLQKEYANTI GLS PRT QLLYL--VCLHEK-GKKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKR-- 635
D-NKRGSSSSNGSCDNKNEEACEKNL-EKVFASLTNICYKCDKCKSGTSTVN-KKIWKSSGNEEGLQKEYANTI GLP PRT QSLCL--VCLHEK-EGKTKH-KTISTNSELLKKEWIIAAPHGEGKNLKTSH-- 631
D-NKRESSSSNGSCNKNQDECEKQKL-EKVFASLTNICYKCEKCKSGTSTVN-SKKIWKSSGNGEGLQKEYANTI GLP PRT QSLCLV-VCLDEK-GKKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKT-- 634
D-NKRGSSSSNGSCDNKNEEACEKNL-DEALASLTNICYKCDKCKSGTSTVN-KKIWKSSGKEGGLQKEYANTI GLP PRT QSLCLV-VCLHEK-EGKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKP-- 639
DKNQSGSSSSNGSCDNKNEEACEKNL-EKVLASLTNICYKCDKCKSGTSTVN-KKIWKSSGKEGGLQKEYANTI ALP PRT QSLCL--VCLHEK-EGKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKR-- 634
D-NKRESSSSNGSCNKNQDECEKQKL-DEALASLTNICYKCDKCKSGTSTVN-KKIWKSSGKEGGLQKEYANTI ALP PRT QSLCLV-VCLDEK-GKKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKTSH-- 635
D-NKSGSSSSNGSCDNKNEEACEKNL-EKVFASLTNICYKCEKCKSEQSKNNKNKIWKSSSGNGEGLQKEYANTI GLP PRT HSLY LGNLRKLEN-VCEDEVKIDNFDTKEKFLAGCLIAAPHGEGKNLKTYY-- 637
D-NKRESSSSNGSCNKNQEAACEKNL-DEALASLTNICYKCEKCKSGTSTVN-KKIWKSSGDEKGLQKEYANTI GLP PRT HSLY LGNLRKLEN-VCEDEVKIDNFDTKEKFLAGCLIAAPHGEGKNLKR-- 633
D-NKRGSSSSNGSCDNKNEEACEKNL-EKVLASLTNICYKCDKCKSGTSTVN-KKIWKSSGKEGGLQKEYANTI GLP PRT QSLCL--VCLHEK-EGKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKTSH-- 633
D-NKRESSSSNGSCNKNQEAACEKNL-DEALASLTNICYKCEKCKSGTSTVN-KKIWKSSGDEEGLQKEYANTI GLP PRT HSLY LGNLRKLEN-VCEDEVKIDNFDTKEKFLAGCLIAAPHGEGKNLKR-- 633
D-NKRRSSSSNGSCDNKNQDECEKNL-EKVLASLTNICYKCDKCKSGTSTVN-NKIWKKYSVKEGGLQKEYANTI GLP PRT QSLY LGNLRKLEN-VCEDEVKIDNFDTKEKFLAGCLIAAPHGEGKNLKTYY-- 636
D-----KNQKCKSEQSKNNKNKIWKSSSGKEGGLQKEYANTI GLP PRT QSLY LGNLRKLEN-VCKGVTDIDNFDTKEKFLAGCLIAAPHGEGKNLKTYY-- 605
D-----KNQKCKSEQSKNNKNKIWKSSSGKEGGLQKEYANTI GLP PRT QSLY LGNLRKLEN-VCKGVTDIDNFDTKEKFLAGCLIAAPHGEGKNLKTYY-- 605
I--GIG--VEVVCENNCEEQYKLLPCLKCTVLCNECNKTRCKPLKKEQEKWIWKSSSGKEGGLQKEYANTI ALP PRT QSLCLVCLHEKE--KTQELKNIRTNSELLKKEWIIAAPHGEGKNLKTYY-- 624
V--NTGG-VEVVCENNCEEQYKLLPCLKCTILTCCKENKTRCKPLKKEQEKWIWKSSSGKEGGLQKEYANTI GLP PRT QSLCLVCLHEKEG-KTQELKNIS--TNSELLKKEWIIAAPHGEGKNLKTSH-- 626
T--DIG--VEVVCENNCEEQYKLLPCLKCTVLCNECNKTRCKPLKKEQEKWIWKSSSGKEGGLQKEYANTI GLP PRT QSLCLVCLHEKE--GKTQHKTISTNSELLKKEWIIAAPHGEGKNLKTYY-- 627
T--DIG--VEVVCENNCEEQYKLLPCLKCTILTCCKENKTRCKPLKKEQEKWIWKSSSGNEKGLQKEYANTI GLP PRT QSLCLVCLHEKE--GKTQHKTISTNSELLKKEWIIAAPHGEGKNLKTYY-- 627
V--NTGG-VEVVCENNCEEQYKLLPCLKCTILTCCKENKTRCKPLKKEQEKWIWKSSSGNEKGLQKEYANTI GLP PRT QSLY LGNLRKLEN-VCLHEK-EGKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKR-- 623
T--GIG--VEVVCENNCEEQYKLLPCLKCTVLCNECNKTRCKPLKKEQEKWIWKSSSGKEGGLQKEYANTI GLP PRT QSLY LGNLRKLEN-VSKGVTDIDNFDTKEKFLAGCLIAAPHGEGKNLKTSH-- 625
T--DIG--VEVVCENNCEEQYKLLPCLKCTVLCNECNKTVFKNLKQEQEKWIWKSSSGNEKGLQKEYANTI GLP PRT QSLY LGNLRKLEN-VCKGVTDIDNFDTKEKFLAGCLIAAPHGEGKNLKTYY-- 630
D-NKRGSSSSNGSCDNKNQDECEKQKL-DEALASLTNICYKCDKCKSGTSTVN-KKIWKSSSGNEKGLQKEYANTI GLP PRT QSLY LGNLRKLEN-VSKGVTDIYDTKEKFLAGCLIAAPHGEGKNLKTSS-- 637
D-NKSGSSSSNGSCNKNQDECEKQKL-DEALASLTNICYKCDKCKSGTSTVN-KKIWKSSSGNEKGLQKEYANTI GLP PRT QSLY LGNLRKLEN-VCKGVTDIDNFDTKEKFLAGCLIAAPHGEGKNLKISN-- 636
DKNQSGSSSSNGSCDNKNEEACEKNL-EKVLASLTNICYKCDKCKSGTSTVN-SKKIWKSSSGKEGGLQKEYANTI GLP PRT QSLCLV-VCLDEK-EGKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKPS-- 635
D-NKRGSSSSNGSCDNKNEEACEKNL-EKVFASLTNICYKCDKCKSGTSTVN-KKIWKSSSGNEKGLQKEYANTI GLP PRT HSLY LGNLRKLEN-VCEDEVKIDNFDTKEKFLAGCLIAAPHGEGKNLKIS-- 634
D-NKSGSSSSNGSCNKNQEAACEKNL-EKVLASLTNICYKCDKCKSGTSTVN-KKIWKSSSGNEKGLQKEYANTI GLP PRT HSLY LGNLRKLEN-VCEDEVKIDNFDTKEKFLAGCLIAAPHGEGKNLKR-- 636
D-NKRGSSSSNGSCDNKNEEACEKNL-DEALASLTNICYKCDKCKSGTSTVN-KKIWKSSSGNEKGLQKEYANTI GLP PRT QSLY LGNLRKLEN-VCKGVTDIDNFDTKEKFLAGCLIAAPHGEGKNLKTYY-- 640
D-NKSGSSSSNGSCDNKNEEACEKNL-ENVFASLTNICYKCDKCKSGTSTVN-KKIWKSSSGNEEGLQKEYANTI GLP PRT HSLY--VCLHEK-EGKTKH-KTISTNSELLKKEWIIAAPHGEGKNLKTSS-- 633
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D-NKRGSSSSNGSCDNKNEEACEKNL-DEALASLTNICYKCDKCKSGTSTVN-KKIWKSSSGNEEGLQKEYANTI GLP PRT QSLCL--VCLHEK-EGKTKH-KTISTNSELLKKEWIIAAPHGEGKNLKTSH-- 635
P--DIG--VEVVCENNCEEQYKLLPCLKCTILTCCKENKTRCKPLKKEQEKWIWKSSSGNEKGLQKEYANTI GLP PRT QSLY LGNLRKLEN-VCKGVTDIDNFDTKEKFLAGCLIAAPHGEGKNLKTSSP-- 626
D-NKSGSSSSNGSCNKNQEAACEKNL-EKVLASLTNICYKCDKCKSEQSKNNKNKIWKSSSGKEGGLQKEYANTI GLP PRT QSLCLV-VCLDEK-GKKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKPS-- 631
A4PFL0030c exon1+2.pro D-NKRGSSSSNGSCDNKNQDECEKQKL-EKVFASLTNICYKCDKCKSGTSTVN-KKIWKSSSGNEEGLQKEYANTI GLP PRT QSLY LGNLRKLEN-VCEDEVKIDNFDTKEKFLAGCLIAAPHGEGKNLKR-- 633
Newd2var2CSAsequence.pro D-NKRGSSSSNGSCDNKNEEACEKNL-EKVFASLTNICYKCEKCKSGTSTVN-KKIWKSSSGNEEGLQKEYANTI GLP PRT QSLCL--VCLHEK-EGKTKH-KTISTNSELLKKEWIIAAPHGEGKNLKTSH-- 631
McPFL0030c.pro D-NKSGSSSSNGSCDNKNEEACEKNL-EKVFASLTNICYKCEKCKSEQSKNNKNKIWKSSSGKEGGLQKEYANTI GLP PRT QSLCLV-VCLDEK-GKKTQELKNIRTNSELLKKEWIIAAPHGEGKNLKPSHE-- 636
HB3-1var2CSA.pro DKNQSGSSSSNGSCNKNQDECEKQKL-EKVFASLTNICYKCDKCKSGTSTVN-KKIWKSSSGNEEGLQKEYANTI GLP PRT QSLY LGNLRKLEN-VCKGVTDIYDTKEKFLAGCLIAAPHGEGKNLKTSH-- 634
HB3-2var2CSA.pro DKNQSGSSSSNGSCNKNQDECEKQKL-EKVFASLTNICYKCDKCKSGTSTVN-KKIWKSSSGNEEGLQKEYANTI GLP PRT QSLY LGNLRKLEN-VCKGVTDIDNFDTKEKFLAGCLIAAPHGEGKNLKTYY-- 638



ALB01044.1 -----HEKKNDDNGKKLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQKIFGKLFKRYIKKNNTAEQDTSYSSSDELRESWWTNKKYIWLAMKHGAGMNSTTCCGD-----GSVT- 741
ALB01053.1 -----HEKKNDDNGKKLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQKIFGKLFKRYIKKNNTAEQDTSYSSSDELRESWWTNKKYIWLAMKHGAGMNSTTCCGD-----GSVT- 741
ETW56275.1 KKNDDNGKKLCKDLKYSFADYGDLIKGTSIWDNEYTKDLELNLQKIFGKLFKRYIKKNIASDENTLYSSSDELRESWWTNKKYIWLAMKHGAE MNGTTCNAD-----GSVT- 751
ALB01048.1 -----LEKKKGDNNKSLCKDLKYSFADYGDLIKGTSIWDNEYTKNVELNLQNNFGKLFKRYIKKNIASDENTLYSSSDELRESWWTNKKYIWTAMKHGAGMNGTMCNAD-----GSVT- 743
ALB01041.1 -----PQNKNDNGKKLCKALKYSFADYGDLIKGTSIWDNDFTKDLELNLQKIFGKLFKRYIKKNISTEQDPTYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCGD-----GSVTG 745
ALB01039.1 -----PQNKNDNGKKLCKALKYSFADYGDLIKGTSIWDNDFTKDLELNLQKIFGKLFKRYIKKNISTEQDPTYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCGD-----GSVTG 745
ALB01056.1 -----PQNKNAENKKKLCKALKYSFADYGDLIKGTSIWDNDFTKDLELNLQKIFGKLFKRYIKKNNTIVENTSYSSSDELRESWWTNKKYIWTAMKHGAE MNGTMCNAD-----GSVTG 747
KNC35427.1 -----EKKNDNDGKKLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQKAFGKLFKRYIKKNNTAEQDTSYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCSSGSGDNGDSSITGSSDSGSTT- 759
ALB01046.1 -----HENKN--DNGKKLCKDLKYSFADYGDLIKGTSIWDNEYTKDLELNLQKIFGKLFKRYIKKNNTIVENTSYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCNAD-----GSVTG 741
ALB01037.1 -----HEKKKGDNGKKLCKDLKYSFADYGDLIKGTSIWDNEYTKDLELNLQKIFGKLFKRYIKKNNTIVENTSYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCNAD-----GSVT- 746
ALB01055.1 -----YLEKKKGDNNKSLCKDLKYSFADYGDLIKGTSIWDNDFTKDLELNLQKIFGKLFKRYIKKNNTAEQDPTYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCGD-----GSVTG 745
AAQ73924.1 -----EKKNDNDGKKLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQKIFGKLFKRYIKKNNTAEQDTSYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCSS-----GSVTG 733
ALB01042.1 -----YPQKNDDNNKSLCKDLKYSFADYGDLIKGTSIWDNDFTKDLELNLQKIFGKLFKRYIKKNNTIVENTSYSSSDELRESWWTNKKYIWTAMKHGAE MNGTMCNAD-----GSVTG 744
ADJ77410.1 -----EKKNAENKKKLCKALKYSFADYGDLIKGTSIWDNDFTKDLELNLQKIFGKLFKRYIKKNIASDENTLYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCSS-----GSVTG 742
EWC75615.1 -----HQNNNSGKKKLCKALKYSFADYGDLIKGTSIWDNDFTKNLELNLQKIFGKLFKRYIKKNISTEQHTSYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCGD-----GSVTG 743
ALB01054.1 KKNADNRKKNADNNKSLCKALKYSFADYGDLIKGTSIWDNEYTKDLELNLQNNFGKLFKRYIKKNNTAEQHTSYSSSDELRESWWTNKKYIWLAMKHGAE MNGTTCSS-----GSVT- 745
ALB01057.1 -----LEKKKGDNGKKLCKALKYSFADYGDLIKGTSIWDNEYTKDLELNLQKIFGKLFKRYIKKNNTAEQHTSYSSSDELRESWWTNKKYIWLAMKHGAE MNGTMCNAD-----GSVT- 746
ALB01040.1 -----PQNKNDNNKSLCKDLKYSFADYGDLIKGTSIWDNEYTKDLELNLQKAFGLFKGYIKKNNTAEQDTSYSSSDELRESWWTNKKYIWLAMKHGTTCSGTCNDNGD-----GSVT- 743
ETW41644.1 -----QKKNDDNGKKLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQKIFGKLFKRYIKKNNTIVENTSYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCSS--G-----GSVT- 737
ALB01043.1 -----PQNKNDNNKSLCKDLKYSFADYGDLIKGTSIWDNEYTKDLELNLQKAFGLFKGYIKKNNTAEQDTSYSSSDELRESWWTNKKYIWLAMKHGTTCSGSGDNGD-----GSVT- 743
EUT82883.1 -----LEKKNADNNKSLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQNNFGKLFKRYIKKNIASDENTLYSSSDELRESWWTNKKYIWLAMKHGAE MNG--TTCSSG-----SGDN- 745
ALB01038.1 -----PQNKNAENKKKLCKDLKYSFADYGDLIKGTSIWDNDFTKDLELNLQKAFGLFKRYIKKNISTEQHTLYSSSDELRESWWTNKKYIWTAMKHGAE MNIITCCGD-----GSVT- 714
ALB01058.1 -----PQNKNAENKKKLCKDLKYSFADYGDLIKGTSIWDNDFTKDLELNLQKAFGLFKRYIKKNISTEQHTLYSSSDELRESWWTNKKYIWTAMKHGAE MNIITCCGD-----GSVT- 714
ALB01059.1 -----PQNNNSGNKENLCKALKYSFADYGDLIKGTSIWDNDFTKDLELNLQKAFGLFKRYIKKNIASDENTSYSSSDELRESWWTNKKYIWLAMKHGAE MNGTTCG-----DGSVT- 733
KNG76633.1 -----Q--NNNSGNKENLCKALKYSFADYGDLIKGTSIWDNDFTKDLELNLQKIFGKLFKRYIKKNIASDENTSYSSSDELRESWWTNKKYIWLAMKHGAE MNGTTCSS-----GSVT- 728
ALB01051.1 -----PQKKNADNGKKLCKALKYSFADYGDLIKGTSIWDNDFTKDLELNLQKIFGKLFKRYIKKNISTEQHTLYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCSS-----GSVT- 730
ALB01049.1 -----PQNKNDNNKSLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQKAFGLFKRYIKKNNTAEQHTSYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCSS-----GSVT- 730
EWC75604.1 -----PQNNNSGNKENLCKALEYSFADYGDLIKGTSIWDNDFTKNVELNLQKIFGKLFKRYIKKNISTEQDPTYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCSS-----GSVT- 726
ALB01045.1 -----E--NKNDDNGKKLCKDLKYSFADYGDLIKGTSIWDNEYTKDLELNLQKAFGLFKRYIKKNNTAEQDTSYSSSDELRESWWTNKKYIWLAMKHGAE MNGTTCGGDGS-----VTGSSDSGSTT- 742
ALB01047.1 -----P-----QNKKKLCKDLKYSFADYGDLIKGTSIWDNEYTKDLELNLQKAFGLFKRYIKKNISTEQHTLYSSSDELRESWWTNKKYIWTAMKHGAE MNGTMCN-----ADGSVT- 734
7G8.pro -----HEKKNDDNGKKLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQKAFGLFKRYIKKNISTAEQDTSYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCGGD-----SSGE- 747
124_8.pro -----KKNDDNGKKLCKDLKYSFADYGDLIKGTSIWDNEYTKDLELNLQKIFGKLFKRYIKKNIASDENTLYSSSDELRESWWTNKKYIWLAMKHGTTCSGSGDNGD-----GSVT- 745
indo.pro -----PEKKKGDNGKKLCKDLKYSFADYGDLIKGTSIWDNEYTKDLELNLQKIFGKLFKRYIKKNIASDENTLYSSSDELRESWWTNKKYIWLAMKHGAE MNGTMCNAD-----GSVT- 744
KMWII.pro -----EKKKGDNGKKLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQKAFGLFKRYIKKNIASDENTSYSSSDELRESWWTNKKYIWTAMKHGAE MNS--TMCNAD-----GSVT- 742
M24.pro -----PQNKNDNNKSLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQKIFGKLFKRYIKKNISTEQDPTYSSSDELRESWWTNKKYIWLAMKHGAE MNIITC--CGD-----GSVT- 745
M51.pro -----LEKKNDNDGKKLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQKAFGLFKRYIKKNNTAEQDTSYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCSS-----GSGD- 748
P13.pro -----HQNNNSGKKKLCKALKYSFADYGDLIKGTSIWDNDFTKDLELNLQKIFGKLFKRYIKKNIASDENTSYSSSDELRESWWTNKKYIWLAMKHGAE MNGTMCNAD-----GSVTG 742
T2C6.pro -----PQKKNDDNGKKLCKDLKYSFADYGDLIKGTSIWDNEYTKNVELNLQNNFGKLFKRYIKKNNTAEQDTSYSSSDELRESWWTNKKYIWLAMKHGAE MNGTTCGGD-----GSVT- 747
V1_S.pro -----EKKNDNDGKKLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQKAFGLFKRYIKKNNTAEQDTSYSSSDELRESWWTNKKYIWLAMKHGAE MNGTTCSS-----GSVT- 737
WR80.pro -----EKK--GENKRLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQNNFGKLFKRYIKKNISTEQHTSYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCSSG-----SGDNGDSSIT- 740
PFL0030cexon1+2.pro -----HEKKNDDNGKKLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQKIFGKLFKRYIKKNNTAEQDTSYSSSDELRESWWTNKKYIWLAMKHGAE MNGTTCGGD-----GSVT- 740
A4PFL0030c exon1+2.pro -----PQNKNSGNKENLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQNNFGKLFKRYIKKNNTAEQDTSYSSSDELRESWWTNKKYIWTAMKHGAE MNIITC--NAD-----GSVT- 742
Newdd2var2CSAsequence.pro -----EKKNDNDGKKLCKALEYSFADYGDLIKGTSIWDNEYTKDLELNLQKIFGKLFKRYIKKNNTAEQHTSYSSSDELRESWWTNKKYIWTAMKHGAE MNGTTCSS-----GSVT- 733
McPFL0030c.pro KKNDDNGKKNDNNKSLCKDLKYSFADYGDLIKGTSIWDNEYTKDLELNLQKIFGKLFKRYIKKNIASDENTLYSSSDELRESWWTNKKYIWLAMKHGAE MNGTTCNAD-----GSVT- 751
HB3-1var2CSA.pro -----EKKNDNDGKKLCKALEYSFADYGDLIKGTSIWDNDFTKDLELNLQKIFGKLFKRYIKKNNTAEQDTSYSSSDELRESWWTNKKYIWTAMKHGAE MNS--TTCSSGD-----GSVT- 742
HB3-2var2CSA.pro -----PQ---NKKLCKDLKYSFADYGDLIKGTSIWDNEYTKDLELNLQKAFGLFKRYIKKNISTEQHTLYSSSDELRESWWTNKKYIWLAMKHGAE MNS--TTCSSGD-----GSVT- 742



ALB01044.1	-----GSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQEKVKPVIENCKSKCKES-----GGTCNGECKTECKNKCEVYKFFIEECG---TAA---GG--	823
ALB01053.1	-----GSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQEKVKPVIENCKSKCKES-----GGTCNGECKTECKNKCEVYKFFIEELW---TAA---GG--	823
ETW56275.1	-----GSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQAKVKDVIENCKSKCKES-----GNCKCKTECKNKCEAYKFFIENCK---GG---DG--	828
ALB01048.1	-----GSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQEKVKPVIENCKSKCKNTSSKTKLGGTCNGECKTECKNKCEAYKFFIEEFR---TAA---GG--	831
ALB01041.1	SSDSGS-----TTCSGDNGSIS-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQENVNAVIENCKSKCKES-----GGTCNSDCEKKCKIECEKYKNFIEECNG-TAAG---G--	841
ALB01039.1	SSDSGS-----TTCSGDNGSIS-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQENVNAVIENCKSKCKES-----GGTCNSDCEKKCKIECEKYKNFIEECNG-TAAG---G--	841
ALB01056.1	SSDSGS-----TTCSGDNGSIS-----CDDMPTIDLIPQYLRFLQEWVEHFCKQRQEKVNAVITNCKSKCKES-----GGTCGSDCKTKCKGCEAYKFFIEKCN-TAAE---G--	843
KNC35427.1	-----CSGDNGSIS-----CDDIPTTDFIPQYLRFLQEWVEHFCEQRQAKVKDVIENCKSKCKES-----GGTCNGECKTKCKDECEKYKFFIEDCN---GG---DG--	844
ALB01046.1	SSDSGSTTCCGDGSVTGSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCEQRQAKVKDVIENCKSKCKNTSGERKIGDTCGSDCKTKCKNKCDAYKFFIDGTG---GGGSRPTG--	850
ALB01037.1	-----GSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCEQRQAKVNAVITNCKSKCKES-----GGTCGSDCKTKCKDECEKYKFFIEECR---TAA---G--	828
ALB01055.1	SSDSGSTTCCSGD---N-GS-I---S-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQAKVKDVIENCKSKCKES-----GGTCNSDCKTKCKGCEYKFFIEHCK---GVGG---TG--	841
AAQ73924.1	-----CSGD---S-----SNDMPTIDLIPQYLRFLQEWVEHFCKQRQEKVNAVIENCKSKCKES-----GGTCNSDCKTECKNKCEAYKFFIEDCK---GGV---TG--	815
ALB01042.1	SSDSGSTTCCSGD---NGSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQEKVNAVITNCKSKCKES-----GGTCNSDCKTECKNKCEAYKFFIEDCK---GGG---TG--	840
AJD77410.1	-----GSGD---S-----SNDIPTIDLIPQYLRFLQEWVEHFCEQRQAKVKPVIENCKSKCKNTSSKTKIGDTCGNDCKTECKNKCEYKFFIEECR---TAA---EG--	830
EWC75615.1	SSDSGSTTCCGDGSVTGSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCEQRQAKVKDVIENCKSKCKECGG---TCNGECKTECKNKCEAYKFFIEECN---GGG---GEG	846
ALB01054.1	-----GSGD---S-----SNDIPTTDFIPQYLRFLQEWVEHFCKQRQEKVNAVIENCKSKCKES-----GNKCKTECEKKCEAYKFFIEECN---GGAA---EG--	824
ALB01057.1	-----GSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCEQRQGVKVKHVMESCKSKCKNTSGERKIGGTCNGDCKTECKNKCDAYKFFIEECR---TAAE---G--	834
ALB01040.1	-----GSSD---SGSTTCSGDNGSIS-----CDDMPTIDLIPQYLRFLQEWVEHFCKQRQAKVKDVIENCKSKCKNTSGERIIIGTCGSDCKTKCKVACDAYKFFIEKC---GTAAD---G--	844
ETW41644.1	-----DNGD---S-----SNDIPTTDFIPQYLRFLQEWVEHFCEQRQGVKVKHVMESCKSKCKNTSSKTKLGGKCGNDCEKKCKDECEKYKFFIEECV---TAA---GG--	825
ALB01043.1	-----GSSD---SGSTTCSGDNGSIS-----CDDMPTIDLIPQYLRFLQEWVEHFCKQRQAKVKDVIENCKSKCKNTSGERIIIGTCGSDCKTKCKVACDAYKFFIEKC---GTAAD---G--	844
EUT82883.1	-----GS-I---S-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQAKVKDVIENCKSKCKES-----GNKCKTECKNKCEAYKFFIEEF---CTAAG---G--	822
ALB01038.1	-----GSGS---S-----CDDMPTTDFIPQYLRFLQEWVEHFCKQRQAKVNAVIENCKSKCKNTSSKTKLGGKCGSDCEKKCKVACDAYKFFIEECG---TAVG---G--	802
ALB01058.1	-----GSGS---S-----CDDMPTTDFIPQYLRFLQEWVEHFCKQRQAKVNAVIENCKSKCKNTSSKTKLGGKCGSDCEKKCKVACDAYKFFIEECG---TAGG---G--	802
ALB01059.1	-----GSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCEQRQEKVKHVMESCKSKCKE---GGTCGSDCEKKCK---AYKEFIEKCKG-QAAE---G--	812
KNG76633.1	-----CSGD---S-----SDDIPTIDLIPQYLRFLQEWVEHFCKQRQAKVNAVITNCKSKCKES-----GNKCKTECKTECKNKCEVYKFFIEKCG---TAA---G--	810
ALB01051.1	-----CSGD---SSS---GENQNTNSCDDIPTIDLIPQYLRFLQEWVEHFCEQRQGVKVKDVIENCKSKCKE---TCNGECKTECKTKCKGCEYKFFIEECG-KAAE---G--	826
ALB01049.1	-----CSGD---S-----SNDIPTTDFIPQYLRFLQEWVEHFCEQRQAKVKDVIENCKSKCKES-----GGTCGSDCEKKCKDECEKYKFFIEEFC---TAA---G--	812
EWC75604.1	-----CSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQEKVNAVITNCKSKCKNTSSKTKIGDTCNSDCEKKCKDECEKYKFFIEEAG---TAVG---G--	814
ALB01045.1	-----CCGD---GSV---TGSGSSCDDIPTIDLIPQYLRFLQEWVEHFCEQRQAKVKDVIENCKSKCKNTSGERKIGDTCGNDCEKKCKVACDAYKFFIEECR---TAAE---G--	838
ALB01047.1	-----GSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQEKVNAVINCKSKCKNTSSKTKLGGKCGSDCEKKCKIECEKYKFFIEEYV---TAVG---G--	822
7G8.pro	-----NQTN---S-----CDDIPTIDLIPQYLRFLQEWVEHFCEQRQAKVKDVIENCKSKCKNTSGERKIGGTCNGECKTECKNKCEAYKFFIEHC---KGGD---G--	834
124_8.pro	-----GSGS---S-----CDDMSTIDLIPQYLRFLQEWVEHFCKQRQEKVKDVIENCKSKCKNTSGERIIIGTCGSDCKTKCKGECDAYKNFIEE---CKRGD---G--	832
indo.pro	-----GSGS---S-----CDDMPTIDLIPQYLRFLQEWVEHFCKQRQEKVKPVIENCKSKCKNTSSERKIGGTCNSDCKTECKNKCEVYKFFIEDCK---GGDG---G--	830
KMWII.pro	-----GSGS---S-----CDDIPTTDFIPQYLRFLQEWVEHFCKQRQEKVNAVIENCKSKCKNTSGERKIGGTCNGECKTECKNKCEAYKFFIED---CKGGD---G--	829
M24.pro	-----GSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQEKVKDVIENCKSKCKNTSSKTKLGGTCNSDCEKKCKIECEKYKFFIEEC---RTAVG---G--	833
MTS1.pro	-----S-----SNDIPTTDFIPQYLRFLQEWVEHFCEQRQAKVKDVIENCKSKCKNTSGERKIGDTCNSDCEKKCKDECEKYKFFIEDCN---KGGD---G--	831
P13.pro	SSDSGS-----TTCSGDNGSIS-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQEKVKDVIENCKSKCKES-----GDTCSNDCCEKKCKNKCEAYKFFIEERR---TAAQ---G--	837
T2C6.pro	-----GSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQAKVKDVIENCKSKCKES-----GNKCKTECKNKCKDECEKYKFFIEACG---TAV---GGTG	830
V1_S.pro	-----CSGD---S-----SNDMPTIDLIPQYLRFLQEWVEHFCEQRQAKVKDVIENCKSKCKES-----GNKCKTECKTKCKDECEKYKFFIEDCN---GGG---TG--	819
WR80.pro	-----GSSD---SGSTTCSGDNGSIS-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQAKVNAVITNCKSKCKES-----GDTCSNDCCEKKCKIECEKYKFFIEECG---TAA---G--	835
PFL0030cexon1+2.pro	-----GSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQEKVKPVIENCKSKCKES-----GGTCNGECKTECKNKCEVYKFFIEDCK---GGD---G--	821
A4PFL0030c exon1+2.pro	-----GSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCEQRQAKVKDVIENCKSKCKES-----GNKCKTECKTKCKDECEKYKFFIEAC---GTAGG---IG--	826
Newdd2var2CSAsequence.pro	-----CSGD---S-----SNDMPTIDLIPQYLRFLQEWVEHFCKQRQEKVNAVIENCKSKCKES-----GGTCNSDCKTECKNKCEAYKFFIEDCK---GGG---TG--	815
McPFL0030c.pro	-----GSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQAKVKDVIENCKSKCKES-----GNKCKTECKNKCEAYKFFIENCK---GG---DG--	828
HB3-1var2CSA.pro	-----GSGS---S-----CDDMPTIDLIPQYLRFLQEWVEHFCKQRQEKVKDVIENCKSKCKE---DTCNGECKTECKTKCKGCEYKFFIEEC---NGTADG---G--	829
HB3-2var2CSA.pro	-----GSGS---S-----CDDIPTIDLIPQYLRFLQEWVEHFCKQRQEKVNAVIENCKSKCKE---DTCNGECKTECKCKIECEKYKFFIEEC---VTAVG---G--	828



ALB01044.1	TAGSPWSKRWDQIYKRYSKHIEDAKRNRKAGTKNC-----GPSSTTNAAEN-----KCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADKAPWTTYTTYTTT-----	920
ALB01053.1	TAGSPWSKRWDQIYKRYSKHIEDAKRNRKAGTKNC-----GPSSTTNAAEN-----KCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADKAPWTTYTTYTTT-----	920
ETW56275.1	TAGSSWVKRWDQIYMRYSKYIEDAKRNRKAGTKNC-----GPSSIITNVSASTD-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGDDKAPWTTYTTYTTYTT-----	936
ALB01048.1	TAGSPWSKRWDQIYKMYSKHIEDAKRNRKAGTKNC-----GITGTISGESSGATSGVTTTESKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDNAPWTTYTTYTTK-----	940
ALB01041.1	TSGSSWSKRWDQIYKRYSKYIEDAKRNRKAGTKNCGITTTGTISGESSGATSGVTTT-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDKAPWTTYTTYTT-----	949
ALB01039.1	TSGSSWSKRWDQIYKRYSKYIEDAKRNRKAGTKNCGITTTGTISGESSGATSGVTTT-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDKAPWTTYTTYTT-----	949
ALB01056.1	TSGSPWSKRWDQIYMRYSKYIEDAKRNRKAGTKNC-----GTSSGATSGVTTT-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADKAPWTTYTTYTT-----	943
KNC35427.1	TAGSSWVKRWDQIYKRYSKHIEDAKRNRKAGTKNC-----GPSSIITNAAASTD-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGDDKAPWTTYTTYTT-----	943
ALB01046.1	TAGSSWSKRWDQIYMRYSKYIEDAKRNRKAGTKSCGITTTGTISGESSGANGSVTTT-----ESKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDKAPWTTYTTYTT-----	959
ALB01037.1	TAGSSWSKRWDQIYKMYSKHIEDAKRNRKAGTKNCGITTTGTISGESSGANGSVTTT-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDKAPWTTYTTYTT-----	935
ALB01055.1	TAGSSWVKRWDQIYMRYSKYIEDAKRNRKAGTKSC-----GTSSGANGSVTTT-----ESKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGDDKAPWTTYTTYTT-----	941
AAQ73924.1	TAGSPWSKRWDQIYKRYSKHIEDAKRNRKAGTKNC-----GTSSTTNAASTD-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADKAPWTTYTTYTT-----	914
ALB01042.1	TAGSSWVKRWDQIYMRYSKYIEDAKRNRKAGTKSC-----GTSSGANGSVTTT-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADKAPWTTYTTYTTYTTYTT-----	946
AJD77410.1	TAGSSWVKRWDQIYKRYSKYIEDAKRNRKAGTKNC-----GPSSTTNAAEN-----KCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDNAPWTTYTTYTT-----	925
EWC7615.1	TSGSSWSKRWDQIYMRYSKYIEDAKRNRKAGTKNC-----GTSSTTNAAEN-----KCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDKAPWTTYTTYTT-----	942
ALB01054.1	TSGSSWSKRWDQIYMRYSKYIEDAKRNRKAGTKNC-----GPSSGANGSVTTT-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADNAPWTTYTTYTT-----	923
ALB01057.1	TAESSWSKRWDQIYKRYSKYIEDAKRNRKAGTKNCGITTTGTISGESSGANGSVTTT-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDNAPWTTYTTYTT-----	941
ALB01040.1	TAGSSWSKRWDQIYKMYSKHIEDAKRNRKAGTKNC-----GPSSTTNVSVSTD-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDKAPWTTYTTYTT-----	943
ETW41644.1	TAGSPWSKRWDQIYKRYSKYIEDAKRNRKAGTKNC-----GTSSTTNAASTA-----ESKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDKAPWTTYTTYTTYTTYTT-----	930
ALB01043.1	TAGSSWSKRWDQIYKMYSKHIEDAKRNRKAGTKNC-----GPSSTTNVSVSTD-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDKAPWTTYTTYTT-----	943
EUT82883.1	TSGSPWSKRWDQIYKMYSKYIEDAKRNRKAGTKNC-----GTSSTTST---A-----ESKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGDDKAPWTTYTTYTT-----	918
ALB01038.1	TAGSSWVKRWDQIYKRYSKHIEDAKRNRKAGTKNCGTSSSTTN-----AAASTA-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDKAPWTTYTTYTT-----	901
ALB01058.1	TAGSSWVKRWDQIYKRYSKHIEDAKRNRKAGTKNCGTSSSTTN-----AAASTA-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDKAPWTTYTTYTT-----	901
ALB01059.1	TSGSSWSKRWDQIYKRYSKYIEDAKRNRKAGTKNC-----GPSSTTNAASTT-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADKAPWTTYTTYTT-----	912
KNG76633.1	TAGSSWSKRWDQIYKRYSKHIEDAKRNRKAGTKNC-----GTSSTTN---AA-----ESKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGDDKAPWTTYTTYTT-----	906
ALB01051.1	TSGSSWVKRWDQIYKRYSKYIEDAKRNRKAGTKSC-----GTSSTTN---AA-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADNAPWTTYTTYTT-----	922
ALB01049.1	TSGSPWSKRWDQIYKRYSKDIEDAKRNRKAGTKNC-----GTS-----TA-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGDDKAPWTTYTTYTT-----	905
EWC75604.1	TAGSPWSKRWDQIYKRYSKHIEDAKRNRKAGTKNC-----GPSSTTNAASTD-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGDDKAPWTTYTTYTT-----	915
ALB01045.1	TAGSSWVKRWDQIYKRYSKYIEDAKRNRKAGTKNC-----GPSSTTN---AA-----ESKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDNAPWTTYTTYTT-----	935
ALB01047.1	TSGSPWSKRWDQIYKRYSKYIEDAKRNRKAGTKSC-----GTSSTTNAASTA-----ESKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADNAPWTTYTTYTT-----	923
7G8.pro	TAGSSWVKRWDQIYKRYSKHIEDAKRNRKAGTKNCGTSSST---A-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDKAPWTTYTT-----	922
124_8.pro	TAGSPWSKRWDQIYMRYSKYIEDAKRNRKAGTKNC-----GTSSTTNA---A-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGDDKAPWTTYTTYTT-----	928
indo.pro	TAGSSWSKRWDQIYKRYSKYIEDAKRNRKAGTKNC-----GPSSTTNAAEN-----KCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDNAPWTTYTTYTT-----	928
KMWII.pro	TAGSSWVKRWDQIYKRYSKHIEDAKRNRKAGTKSC-----GPSSIITNVSVD-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDNAPWTTYTTYTT-----	929
M24.pro	TAGSSWSKRWDQIYKMYSKHIEDAKRNRKAGTKNCGITTTGTISGESSGANGSVTTT-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGDDKAPWTTYTTYTTYTT-----	943
MTS1.pro	TAGSSWVKRWDQIYKRYSKHIEDAKRNRKAGTKNCGITTTGTISGESSGATSGVTTT-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDNAPWTTYTTYTT-----	937
p13.pro	TAESSWVKRWDQIYMRYSKYIEDAKRNRKAGTKSC-----GPSSTTNAASTA-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADNAPWTTYTTYTT-----	938
T2C6.pro	TAGSPWSKRWDQIYKRYSKHIEDAKRNRKAGTKNC-----GPSSTTNAAEN-----KCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADKAPWTTYTTYTT-----	927
V1_S.pro	TAGSSWVKRWDQIYKRYSKHIEDAKRNRKAGTKNC-----GPSSTTNAASTD-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGDDKAPWTTYTTYTT-----	918
WR80.pro	TAGSPWSKRWDQIYKRYSKYIEDAKRNRKAGTKNC-----GPSSTT---STA-----ESKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADKAPWTTYTTYTT-----	932
PFL0030cexon1+2.pro	TAGSSWVKRWDQIYKRYSKYIEDAKRNRKAGTKNC-----GPSSTTNAAEN-----KCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADKAPWTTYTTYTT-----	918
A4PFL0030c exon1+2.pro	TAGSPWSKRWDQIYKRYSKHIEDAKRNRKAGTKNC-----GTSSTTNAASTD-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADKAPWTTYTTYTT-----	926
Newdd2var2CSAsequence.pro	TAGSPWSKRWDQIYKRYSKHIEDAKRNRKAGTKNC-----GTSSTTNAASTD-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADKAPWTTYTTYTT-----	914
McPFL0030c.pro	TAGSSWVKRWDQIYMRYSKYIEDAKRNRKAGTKNC-----GPSSIITNVSASTD-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGDDKAPWTTYTTYTTYTTYTTYTTYTT-----	941
HB3-1var2CSA.pro	TSGSSWSKRWDQIYKRYSKYIEDAKRNRKAGTKNC-----GTSSTTNAASTT-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGEDKAPWTTYTTYTT-----	928
HB3-2var2CSA.pro	TSGSPWSKRWDQIYKRYSKYIEDAKRNRKAGTKNCGITTTGTISGESSGANGSVTTT-----ENKCVQSDIDSFFKHLIDIGLTTTPSSYLSIVLDDNICGADNAPWTTYTTYTTYTT-----	938



ALB01044.1	--EKC�KETDKSKSQSCNTAVVVVNVPSPLGNTPHGYKYACQCKIPTNEETCDDRKEYMNQWSSGSARTMVKR-GYKNDNYELCKYNGVDVKPTTVRSNSSKLD	1018
ALB01053.1	--EKC�KETDKSKSQSCNTAVVVVNVPSPLGNTPHGYKYACQCKIPTNEETCDDRKEYMNQWSSGSARTMVKR-GYKNDNYELCKYNGVDVKPTTVRSNSSKLD	1018
ETW56275.1	TTKNC DKERDKSKSQSCNTAVVVVNVPSPLGNTPHGYKYACECKTPSNKELCDDRKEYMNQWSSSGSAQTVRD-RSGKDYELTYNGVKETKLPKKLNSKLD	1036
ALB01048.1	--N-CDKEKDKSKSQSCNTAVVVVNVPSPLGNTPHGYKYACQCKIPTTEESCDDRKEYMNQWI IDNTKNPKGSGSTNNDYELTYNGVQIKQAAGRSSSTKLD	1038
ALB01041.1	--KNC DK EKDKSKSQSCNTAVVVVNVPSPLGNTPHGYKYACECKIPTTEETCDDRKEYMNQWSSSGSAQTVRD-RSGKDYELTYNGVKETKLPKKSSTKLD	1047
ALB01039.1	--KNC DK EKDKSKSQSCNTAVVVVNVPSPLGNTPHGYKYACECKIPTTEETCDDRKEYMNQWSSSGSAQTVRD-RSGKDYELTYNGVKETKLPKKSSTKLD	1047
ALB01056.1	--KNC DIQKDKSKLQCCNTAVVVVNVPSPLGNTPHGYKYACQCRTPSNKESDDRKEYMNQWSSCGSAQTVRG-RSTNNDYELTYNGVKETKPLGTLKNSKLN	1041
KNC35427.1	TTEKCNKERDKSKSQSSDILVVVVNVPSPLGNTPHGYKYACECKIPTTEETCDDRKEYMNQWISDTSKKQKGS GSKDYELTYNGVQIKQAAGRSSSTKLD	1044
ALB01046.1	--KNC DKDKKSKSQPINISVVVVNVPSPLGNTPHGYKYACECKIPTTEETCDDRKEYMNQWSRGSAGTVRG-RSTNNDYELTYNGVQIKQAAGTLNSPKLD	1057
ALB01037.1	TTKNC DK EKDKSKSQSCNTAVVVVNVPSPLGNTPHGYKYACQCKIPTNEETCDDRKEYMNQWSSSGSAQTVRG-RSTNNDYELTYNGVQIKPTTVRSSTKLD	1035
ALB01055.1	--KNC DKDKKTPK PQSSNTAVVVVNVPSPLGNTPHGYKYACQCKIPTTEETCDDRKEYMNQWSSSGSAQTVRG-RSTNNDYELTYNGVQIKQAAGTLNSKLD	1039
AAQ73924.1	TTKNC DIQKDKTPK SQSCDILVVVVNVPSPLGNTPHGYKYACECKIPTTEETCDDRKEYMNQWSSCGSAQTVRG-RSGKDYELTYNGVKETKPLGTLKNSKLD	1014
ALB01042.1	-TKNC DKDKKSKSQSCDILVVVVNVPSPLGNTPHGYKYACECKIPTNEETCDDRKEYMNQWISDTSKNPKGGRSTNNDYELTYNGVKETKPLGTLKNSKLN	1046
AJD77410.1	TTKNC DKDKKSKSQSCDILVVVVNVPSPLGNTPHGYKYACECKTPSNKQESDDRKEYMNQWISDNTKNPKGSGSKDYELTYNGVDVKPTTVRSSTKLD	1026
EWG75615.1	-TEKCNKETDKSKSQSCDILVVVVNVPSPLGNTPHGYKYACQCRTPSNKELCDDRKEYMNQWISDNTKNPKGSGSKDYELTYNGVQIKQAAGRSSSTKLD	1042
ALB01054.1	-TEKCNKETDKSKPQSCNTAVVVVNVPSPLGNTPHGYKYACQCRTPSNKELCDDRKEYMNQWSSSGSAQTVRD-RSGKDYELCKYNGVKETKLPKKSSTKLD	1022
ALB01057.1	TTKNC DIQKDKKSKSQSCNTAVVVVNVPSPLGNTPHGYKYACECKIPTTEESCDDRKEYMNQWSSCGSAQTVRG-RSTNNDYELTYNGVKETKPLGTLKNSKLN	1041
ALB01040.1	-TKNC DK EKDKSKSQSCNTAVVVVNVPSPLGNTPHGYKYACQCKIPTTEETCDDRKEYMNQWI IDTSKKQKGSSTNNDYELTYNGSEVKMSQKKLNSPKLD	1043
ETW41644.1	TTKNC DKDKKSKSQPINISVVVVNVPSPLGNTPHGYKYACQCKIPTTEESCDDRKEYMNQWISDTSKNPKGSRSTNNDYELTYNGVQIKQAAGRSSSTKLD	1031
ALB01043.1	-TKNC DK EKDKSKSQSCNTAVVVVNVPSPLGNTPHGYKYACQCKIPTTEETCDDRKEYMNQWI IDTSKKQKGSSTNNDYELTYNGSEVKMSQKKLNSPKLD	1043
EUT82883.1	-TKNC DKDKKSKSQSCNTAVVVVNVPSPLGNTPHGYKYACECKIPTTEESCDDRKEYMNQWISDTSKKQKGS GSKDYELTYNGVDVKPTTVRSSTKLD	1018
ALB01038.1	TTKNC DIQKDKSKSQSCDILVVVVNVPSPLGNTPHGYKYACQCKIPTTEESCDDRKEYMNQWSSCGSAQTVRG-RSGKDYELCKYNGVKETKLPKKLNSPKLD	1001
ALB01058.1	TTKNC DIQKDKSKSQSCDILVVVVNVPSPLGNTPHGYKYACQCKIPTTEESCDDRKEYMNQWSSCGSAQTVRG-RSGKDYELCKYNGVKETKLPKKLNSPKLD	1001
ALB01059.1	--EKC�KETDKSKSQSCDILVVVVNVPSPLGNTPHGYKYACQCRTPSNKELCDDRKEYMNQWSSSGSAQTVRDR-STNNDYELTYNGVQIKQATGTLKNSKLD	1010
KNG76633.1	--KNSDIQKKT PKSQSCNTAVVVVNVPSPLGNTPHGYKYACQCKIPTTEESCDDRKEYMNQWISDTSKKQKGSSTNNDYELTYNGVDVKPTTVRSSTKLD	1005
ALB01051.1	--KNC DIQKDKSKSQSCNTAVVVVNVPSPLGNTPHGYKYACECKTPSNKQESDDRKEYMNQWISDTSKNPKGGRSTNNDYELCKYNGVDVKPTTVRSSTKLD	1021
ALB01049.1	--KNC DKDKKSKLQCCNTAVVVVNVPSPLGNTPHGYKYACECKIPTTEESCDDRKEYMNQWSSSGSAQTVRDR-SGKDYELTYNGVDVKPTTVRSSTKLD	1003
EWG75604.1	--EKC�KERDKSKSQSCDILVVVVNVPSPLGNTPHGYKYACECKTPSNKQESDDRKEYMNQWISDNTKNPKGSGSKDYELCKYNGVKETKLPKKSSTKLD	1014
ALB01045.1	--KNC DIQKKT PKSQSCNTAVVVVNVPSPLGNTPHGYKYACECKIPTTEETCDDRKEYMNQWISDNTKNPKGSGSTNNDYELTYNGVKETKLPKKSSTKLD	1034
ALB01047.1	--KNC DKDKKSKSQSSNTAVVVVNVPSPLGNTPHGYKYACQCKIPTTEETCDDRKEYMNQWISDTSKKQKGSSTNNDYELTYNGVKETKPLGTLKNSKLD	1022
7G8.pro	TTKNC DIQKDKSKSQSSDILVVVVNVPSPLGNTPHGYKYACQCKIPTTEETCDDRKEYMNQWSSCGSARTMVKR-GYKNDNYELCKYNGVDVKPTTVRSSTKLD	1022
124_8.pro	--TEKCNKETDKSKSQSCNTAVVVVNVPSPLGNTPHGYKYACECKIPTTEETCDDRKEYMNQWISDTSKKPKGGRSTNNDYELTYNGVKETKLPKKSSTKLD	1028
indo.pro	--KNC DKDKKSKSQSCDILVVVVNVPSPLGNTPHGYKYACECKTPSNKQESDDRKEYMNQWISDNTKNPKGSGSKDYELTYNGVDVKPTTVRSSTKLD	1027
KMWII.pro	-TEKCNKDKKSKSQSCNTAVVVVNVPSPLGNTPHGYKYACQCKIPTTEETCDDRKEYMNQWISDTSKKQKGSSTNNDYELTYNGVKETKLPKKLNSPKLD	1029
M24.pro	TTEKCNKERDKSKSQSSNTAVVVVNVPSPLGNTPHGYKYACQCKIPTNEETCDDRKEYMNQWISDTSKNPKGSGSTNNDYELTYNGVKETKLPKKLNSPKLD	1044
MTS1.pro	TTEKCNKETDKSKSQSSNTAVVVVNVPSPLGNTPHGYKYACECKIPTTEETCDDRKEYMNQWSSCGSAQTVRD-RSGKDYELCKYNGVQIKQAAGTLKNSKLD	1037
P13.pro	--KNC DIKKTTPK PQSCDILVVVVNVPSPLGNTPHGYKYACQCRTPSNKQESDDRKEYMNQWSSSGSAQTVRG-RSTNNDYELTYNGVKETKLPKKLNSPKLD	1036
T2C6.pro	--ENCDIQKKT PKSQSCDILVVVVNVPSPLGNTPHGYKYACQCRTPSNKQESDDRKEYMNQWISDNTKNPKGSGSKDYELCKYNGVKETKPLGTLKNSKLD	1026
V1_S.pro	TTKNC DIQKDKSKSQPINISVVVVNVPSPLGNTPHGYKYACECKIPTTEESCDDRKEYMNQWSSCGSARTMVKR-GYKNDNYELCKYNGVDVKPTTVRSNSTKLD	1018
WR80.pro	--EKC�KERDKSKSQSSDILVVVVNVPSPLGNTPHGYKYACQCKIPTTEETCDDRKEYMNQWISDTSKNPKGSGSTNNDYELTYNGSEVKMSQKKLNSPKLD	1031
PFL0030cexon1+2.pro	--EKC�KETDKSKLQCCNTAVVVVNVPSPLGNTPHGYKYACQCKIPTNEETCDDRKEYMNQWSSCGSARTMVKR-GYKNDNYELCKYNGVDVKPTTVRSNSTKLD	1016
A4PFL0030c exon1+2.pro	-TEKCNKERDKSKSQSSDILVVVVNVPSPLGNTPHGYKYACQCKIPTNEETCDDRKEYMNQWSSCGSARTMVKR-GYKNDNYELCKYNGVDVKPTTVRSNSTKLD	1025
Newdd2var2CSAsequence.pro	TTKNC DIQKDKTPK SQSCDILVVVVNVPSPLGNTPHGYKYACECKIPTTEETCDDRKEYMNQWSSCGSAQTVRG-RSGKDYELTYNGVKETKPLGTLKNSKLD	1014
McPFL0030c.pro	TTKNC DKERDKSKSQSCNTAVVVVNVPSPLGNTPHGYKYACECKTPSNKELCDDRKEYMNQWSSSGSAQTVRD-RSGKDYELTYNGVKETKLPKKLNSKLD	1042
HB3-1var2CSA.pro	-TKNC DIQKKT PK PQSCDILVVVVNVPSPLGNTPHGYKYVCECKIPTTEETCDDRKEYMNQWISDTSKKQKGSSTNNDYELTYNGVQIKQAAGTLKNSKLD	1028
HB3-2var2CSA.pro	TTKNC DIKKT PK SQPINISVVVVNVPSPLGNTPHGYKYACQCKIPTTEESCDDRKEYMNQWISDTSKKQKGSSTNNDYELTYNGVKETKLPKKSSTKLD	1039