

Consensus

Identity

1. SRF019_MK014483_PVBV
2. NP_569153.1_CMBV
3. ACE76864.1_CMBV
4. YP_009130664.1_TaBV
5. YP_009140788_GRBaV:
6. YP_006273075.1_FBaV-1
7. ANK58542.1_FBaV-1
8. ATV81254.1_Grape
9. YP_001036293.1_DBSNV
10. ATW01249.1_DBSNV
11. AHG32725.1_DBSNV
12. YP_009002585.1_HBV
13. YP_009113237.2_MBV-1
14. ATZ69526.1_CSSV
15. ATZ69522.1_CSSV
16. YP_003208050.1_PVBV
17. YP_009229919.1_BVF
18. YP_009408594.1_Jujude
19. YP_610965.1_DrMV
20. ABR01170.1_Lucky
21. YP_009121747.1_YNMov
22. YP_009345075_CCYVB
23. ASG91874.1_CCYVB
24. AVT44083.1_CaYMV
25. API68654.1_CaYMV
26. YP_009259698.1_CaYMV
27. YP_003284237.1_ScBV
28. YP_009116631.1_RYNV
29. AEE39279.1_GVBaV
30. AEE39276.1_GVBaV
31. AIY62341.1_GVCV
32. AVA17853.1_BLRD
33. YP_002321513.1_BsCVBV
34. YP_009041481.1_PYMAVO
35. YP_009352866.1_WBV

RLLERLERMGYSQNPLOHWAKNQICCKLEIIDPNRFINDKPLKHVTPAMEKQFHKHTEALLKIGV
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 GLIQDLKAQGYIGEEPMPKYWAKNQVVCCHLDIKNPDMVIEDRPLKHVTPQMEESFRKHVEALLKIGA
 KLIQELKDMGYIGDDPMKYWSSNKITCQLEIKNPDLTIEDRPLKHISPQMEASYRRHTEAVLKLGT
 PLIEEFQ EAGY IGEN PLOHW EKNQVLCQLD IKN PDFI IEDR PLKSVTPQMKESFKRHVKALLDLKV
 PLLEELK EAGF IGEN PLOHWKKNQ ILCQLD IKN PDFI IEDR PLKNLT PQMKESFKKH IKVLLDLGV
 PLLEELK EAGF IGEN PLOHWKKNQ ILCQLD IKN PDFI IEDR PLKNLT SQMKESFKKH IKVLLDLGV
 ALINQLK EAGY IGEN PLOHW EKNRNVVCQLD IKN PDFI IEDK PLKHLTPSMKESFRRHTEALLKLGV
 QVFOELKAAGYIGDDPLKFWSKNQVVCCELNIINPDLTIQDKPLKHVTPAMEETFRKHIDALLKLV
 QVLQELKQAGYIGDDPLKFWSKNQVTCELNIINPDLTIQDKPLKHVTPAMSETFRKHIDALLKLV
 QVLQELKQAGYIGDDPLKFWSKNQVTCELNIINPDLTIQDKPLKHVTPAMSETFRKHIDALLKLV
 PLMKELKDQGYIGENPMKHWARNKVL CYLD IKN PDMV IEDK PIKHVTPQMEESFRKH IKGLLELKV
 PLIEELK EQGT VGEN PLOHWERNRVHCYLD IKN PDLT VQDK PLDQITPVQK EMYKKH IDALLQIGV
 GVIEELKQQGF IGEN PLOHWSKNRVTCYLD IKN PDLT VEDK PLDNVTP TQK EQYKRHV DALLKLV
 GVIEELKQQGF IGEN PLOHWSKNRVTCYLD IKN PDLT VEDK PLDNVTP TQK EQYKRHV DALLKLV
 GLIGRLRNLGFIGENPVKHWARNQVKCRLEIINPDLTIQDKPLKHVTPQMEAQFKRHTDALLQLGV
 PLLERLKEQGYVGEEMPMPRHWSKNQVKCKLEIINPDITIQDKPMKHVTPAMKDQFQKHTQALLKLV
 GTLDRLKEQGYIGDN PLOHWEKNQLKCHID IIN PDIT IQDPPLKHVTPALKETFQKHIDALLKLV
 KIVQRLLQQN - I SDD PLKFWAKNKVTCQLEIINPDLTIQDKPLKHVTPLMEQQFKRHVEALLQLKV
 KIVQRLLQQN - I SDD PLKFWAKNKVTCQLEIINPDLTIQDKPLKHVTPLMEQQFKRHVEALLQLKV
 PILKELKQQGXIGEEPPLKHWRKNGETCKLDIINPDITVQDKPLKHVTPALEASFQKXIEALLKLV
 KALQQMEELNFIGPNPQIHWAKNRVVCCKID IIN PDLT IEDR PLKHITPEMKAQFSRHTEALLKLV
 QLMERLKDQGF IGEN PMQHWAKNK ILCRLD IKN PDLI IEDK PIKHLTPAMEKQFQKHVKALLD IGV
 QLFRSLKEAGYIGEEPPLKHWSQNQIKCRLEIKNPDMVIEDRPLKHVTPKLEKEDMQKHIDQLLKLKV
 QLFRNLKEAGYIGEEPPLKHWSQNQIKCRLEIKNPDMVIEDRPLKHVTPKLEKEDMQKHIDQLLKLKV
 QLFKELKENGVMGEEPPLKHWRKNQIKCKLEIKNPDLI IEDR PLKHVTPKMKEDMAKHVNQLLKLGV
 SIFRRLKELGYIGEEPPLKHWRKNQVKCSLEIKNPDMVIEDRPLKHVTPKMKEQMKKHVDKLELKV
 RLLQELREQGYIGEEPMPRHWAKNGIKCKLD IKN PDIVISSKPPDSVSKETKAQYQRHIDALLKIGV
 RLLAELKEQGFIGNDPMLHWAKNQVKCKLD IIN PDIT IQGKPPSTATPEIKDQRYQRHIDALLSIGV
 RLLAELKEQGFIGNDPMLHWAKNQVKCKLD IIN PDIT IQGKPPSTATPEIKDQRYQRHIDALLSIGV
 KLLAELKEQGYIGEEPPLKHWSKNKVRCKLD IIN PDIT IEAKPPGHLTLEDKVKYQKHIDALLDLGV
 PLMEELKAQGF IGEK PLOHWSLNR IQCKLD IIN PHLT IECRPLKHVTPAMKDQFKRHTDQLLKLGV
 STIEDLKAQGVIGDAPLQLWERNQVKCKLEV IN PDIT ISDKPLKHVSIGLQKQFQNLDP LKMGV
 PILKDLMAQGYIGEDPVRHWVKNQVICRLD IIN PDIT IQSQPLKHVTVEMERSFQTHVDGLLKLKV
 PILADLKAQGF IGEDPVKHWKKNQVICCKLEIINPDIT IQAQLKHVTAEMEKSFKTQVDGLLKLKV

	70	80	90	100	110	120	130
Consensus	IRPSKSRHRTTAMIVNSGTTVDPKTGKVKGKERMFVFNKRLNDNTHKDQYSLPGINTILKRVGNS						
Identity							
1. SRF019_MK014483_PVBV	IRASSSPHRTMAMIVYSGTTIDPVTGEQKQGKERMFVFNKRLNDNTHKDQYSLPGINTILKRVGCA						
2. NP_569153.1_CMBV	IRPSKSRHRTTAIIIVNSGTSIDPITGKVKGKERMFVFNKRLNDLTKNDQYSLPGIQTILQRLKGS						
3. ACE76864.1_CMBV	IRPSKSRHRTTAIIIVNSGTSIDPITGKVKGKERMFVFNKRLNDLTKNDQYSLPGIQTILQRLKGS						
4. YP_009130664.1_TaBV	IRPSKSKHRTTAIIIVNSGTTIDPITGKVRGKERMFVFNKRLNDNTHKDQYSLPGINTIIQKVGNS						
5. YP_009140788_GRBaV:	IRPSKSRHRTTAMLVNSGTTVDPKTGKVKGKERMFVFNKRLNDITHKDQYSLPGINTILKRIGNS						
6. YP_006273075.1_FBaV-1	IRASKSRHRTTAMLVNSGTTVDPKTGKEIKRKERMFVFNKRLNDITHKDQYSLPGINTILKRVGNS						
7. ANK58542.1_FBaV-1	IRASKSRHRTTAMLVNSGTTVDPKTGKEIKGKERMFVFNKRLNDITHKDQYSLPGINTILKRVGNS						
8. ATV81254.1_Grape	IRPSKSRHRTTAMIVQSGTAVD PVTGKETRGKERMFVFNKRLNDLTKNDQYSLPGISTIMKRVGNS						
9. YP_001036293.1_DBSNV	IRASKSRHRTTAFIVYSGTTVD PVTGKENKGKERMFVFNKRLNDNTEKDQYSLPGINTILKRVGQS						
10. ATW01249.1_DBSNV	IRESKSRHRTTAFIVYSGTTVD PSTGKEQKQGKERMFVFNKRLNDNTEKDQYSLPGINTILKRVGQS						
11. AHG32725.1_DBSNV	IRESKSRHRTTAFIVYSGTTVD PTTGKEQKQGKERMFVFNKRLNDNTEKDQYSLPGINTILKRVGQS						
12. YP_009002585.1_HBV	IRPSTSKHRTTAFIVNSGTSVD PVTGKETGKERMFVFNKRLNDLTKNDQYSLPGINTIMKRVGHA						
13. YP_009113237.2_MBV-1	IRRSNSRHRTNAFIVHSGTTVD PRTGEEFKGKERMFVFNKRLNDLTKNDQYSLPGIQGI IARVGRA						
14. ATZ69526.1_CSSV	IRESTSRHRTNAFIVNSGTTID PVTGEEKKGKERMFVFNKRLNDLTKNDQYSLPGIQSILARIGPA						
15. ATZ69522.1_CSSV	IRESTSRHRTNAFIVNSGTTID PVTGEEKKGKERMFVFNKRLNDLTKNDQYSLPGIQSILARIGQA						
16. YP_003208050.1_PVBV	IRPSKSRHRTMAMIVQSGTTVD PATGKETRGKERMFVFNKRLNDNTHKDQYSLPGINTILKRVGTS						
17. YP_009229919.1_BVF	IRPSKSRHRTMAMIVYSGTSVD EKTGKVKGKERMFVFNKRLNDNTEKDQYSLPGINTILQRVGKS						
18. YP_009408594.1_Jujude	IRESSSRHRTMAMIVKSGTTVD PITGQEQKQGKERMFVFNKRLNDNTYKDQYSLPGINTILKRVGNS						
19. YP_610965.1_DrMV	IRPSKSRHRTMAMIGNSGTSVD PTTGKVKGKERMFVFNKRLNDNTHKDQYSLPGINTIIQKIGRA						
20. ABR01170.1_Lucky	IRPSKSRHRTMAMIGNSGTSVD PTTGKVKGKERMFVFNKRLNDNTHKDQYSLPGINTIIQKIGRA						
21. YP_009121747.1_YNMov	IRPSKSRHRTMAMIVNSGTTVD PATGKETGKXRMVFNKRLNDNTYKDXYSLPGINTLLKRIGNA						
22. YP_009345075_CCYVB	IRKSSSRHRTNAMIVRSGTSVD PKTGFRHGKERMFVFDYRKLNDNTHKDQYSLPGINTIIKLVGNS						
23. ASG91874.1_CCYVB	IRSSKSKHRTTAFIVEESGTV IDPVT KKT IHGKERMFVFNKRLNDNTEKDQYSLPGIQTILKRVGNK						
24. AVT44083.1_CaYMV	IRPSASKHRTTAMLVESGTEVD PKTGLEKKGKQRLVFNKRLNDNTEKDQYSLPGINTIIQRVIGRS						
25. API68654.1_CaYMV	IRPSASKHRTTAMLVESGTEVD PKTGLEKKGKQRLVFNKRLNDNTEKDQYSLPGINTIIQRVIGRS						
26. YP_009259698.1_CaYMV	IRPSNSKHRTTAMLVESGTEVD PKTGEKRGKQRLVFNKRLNDNTEKDQYSLPGINTIIQRVIGRS						
27. YP_003284237.1_ScBV	IRPSTSKHRTTAMIVESGTE IDPKTGQEKRGKERLVFNKRLNDNTEKDQYSLPGINTIIQRVIGRS						
28. YP_009116631.1_RYNV	IQPSKSKHRTAAFITHSGTSID PITKKVRGKERMFVFDYRSLNDNTHKDQYTLPGINTIIISAIGNA						
29. AEE39279.1_GVBaV	IRPSKSRHRTAAFITYSGTSVD PKTGEEIRGKERMFVFDYRALNNNTHKDQYTLPGINSIVAAVUNA						
30. AEE39276.1_GVBaV	IRPSKSRHRTAAFITYSGTSVD PKTGEEIRGKERMFVFDYRALNNNTHKDQYTLPGINSIVAAVUNA						
31. AIY62341.1_GVCV	IRPSKSRHRSAAFIVA SGT SVD PKTGKETRGKERMFVIDYRMLNDNCHKDQYSLPGITSI IKSLGQA						
32. AVA17853.1_BLRD	IRPSSSRHRTMAIIVQSGTSID PKTGKVRGKERMFVLDYRSLNDNTHKDQYSLPGINTIVQRVIGNA						
33. YP_002321513.1_BsCVBV	IRPSTSRHRTMAMIINSGTTVD PVTGEEKRGKERMFVFNKRLNDNTYRDPYSLPGINTIIQKVGRS						
34. YP_009041481.1_PYMAVO	IRPSKSRHRTLAILVKSGTSID PLTGKVKGKERMFVYDYRQLNNNTHKDQYSLPGINTIIQKVGRA						
35. YP_009352866.1_WBV	IRPSKSRHRTLAILVKSGTSID PLTGKVKGKERMFVYDYRQLNNNTHKDQYSLPGINTIIQKVGRA						

	140	150	160	170	180	190
Consensus	K I Y S K F D L K S G F H Q V A M H P E S I P W T A F W V P D G - L Y E W L V M P F G L K N A P A V F Q R K M D N C F K G T E E F I					
Identity						
1. SRF019_MK014483_PVBV	K I Y S K F D L K S G F H Q V A M H P E S I P W T A F W V P P G Q L Y E W L V M P F G L K N A P A V F Q R K M N Q C F Q G C E N F V					
2. NP_569153.1_CMBV	T I F S K F D L K S G F H Q V A M H P D S I E W T A F W V P S G - L Y E W L V M P F G L K N A P A I F Q R K M D H C F K G T E A F I					
3. ACE76864.1_CMBV	T I F S K F D L K S G F H Q V A M H P D S V E W T A F W V P S G - L Y E W L V M P F G L K N A P A V F Q R K M D H C F K G T E A F I					
4. YP_009130664.1_TaBV	K I Y S K F D L K S G F H Q V A M H P Y S I E W T A F W V P Q G - L Y E W L A M P F G L K N A P A V F Q R K M D N C F K G T E N F I					
5. YP_009140788_GRBaV:	K I F S K F D L K S G F H Q V A M H P D S I E W T A F W V P D G - L Y E W L V M P F G L K N A P S I F Q R K M D E C F N G T E E F I					
6. YP_006273075.1_FBaV-1	K I F S K F D L K S G F H Q V A M H P D S I E W T A F W V P D G - L Y E W L V M P F G L K N A P S V F Q R K M D E C F K G T E D F I					
7. ANK58542.1_FBaV-1	T I F S K F D L K S G F H Q V A M H P D S I E W T A F W V P D G - L Y E W L V M P F G L K N A P S V F Q R K M D E C F K G T E D F I					
8. ATV81254.1_Grape	R I Y S K F D L K S G F H Q V A M H P D S I E W T A F W V P D G - L Y E W L V M P F G L K N A P A V F Q R K M D H C F K G T E D F I					
9. YP_001036293.1_DBSNV	K I Y S K F D L K S G F H Q V A M A P Q S V E W T A F L A P G G - L Y E W L V M P F G L K N A P A V F Q R K M D N V F R G T E E F I					
10. ATW01249.1_DBSNV	K I Y S K F D L K S G F H Q V A M A P Q S I E W T A F L V P G G - L Y E W L V M P F G L K N A P A V F Q R K M D H V F R G T E D F I					
11. AHG32725.1_DBSNV	K I Y S K F D L K S G F H Q V A M A P Q S I E W T A F L V P G G - L Y E W L V M P F G L K N A P A V F Q R K M D H V F R G T E D F I					
12. YP_009002585.1_HBV	K I Y S K F D L K S G F H Q V A M H P E S I K W T A F W V P D G - L Y E W L V M P F G L K N A P A V F Q R K M D N V F K G T E A F I					
13. YP_009113237.2_MBV-1	K I F S K F D L K S G F H Q V A M H P E S I P W T A F W V P Q G - L Y E W L V M P F G L K N A P A I F Q R K M D N C F M G T E E F I					
14. ATZ69526.1_CSSV	K I Y S K F D L K S G F H Q I A M H P E S I P W T A F W V P Q G - L Y E W L V M P F G I K N A P A I F Q R K M D H C F A G M E E F I					
15. ATZ69522.1_CSSV	K I Y S K F D L K S G F H Q I A M H P E S I P W T A F W V P Q G - L Y E W L V M P F G I K N A P A I F Q R K M D H C F A G M E E F I					
16. YP_003208050.1_PVBV	K V Y S K F D L K S G F H Q V A M D E E S I P W T A F C V P G G - L Y E W L V M P F G L K N A P S V F Q R K M D D C F K G T E A F I					
17. YP_009229919.1_BVF	K I Y S K F D L K S G F H Q V A M D E E S I P W T A F I T P E G - L Y E W L V M P F G L K N A P A I F Q R K M D N C F R G T E E F I					
18. YP_009408594.1_Jujude	K I Y S K F D L K S G F H Q I A M E K E S I P W T A F I V P Q G - L Y E W L V M P F G L K N A P A L F Q R K M D N C F K G T E D F I					
19. YP_610965.1_DrMV	T V Y S K F D L K S G F H Q V A M S P E S I E W T A F I V L G G - L Y E W L V M P F G L K N A P A V F Q R K M D H C F A G T E K F I					
20. ABR01170.1_Lucky	T V Y S K F D L K S G F H Q V A M S P E S I E W T A F I V P G G - L Y E W L V M P F G - K N A P A V F Q R K M D H C F A G T E K F I					
21. YP_009121747.1_YNMov	K I F S K F D L K S G F H Q V A M E E E S I P W T A F L I P G G - L Y E W L V M P F G L K N A P A I F Q R K M D K C F K D T E E F I					
22. YP_009345075_CCYVB	K I Y S K F D L K S G F H Q V A M E E S S I P W T A F W V P D G - L Y E W L V M P F G L K N A P A I F Q R K M D N C F K G T E E F I					
23. ASG91874.1_CCYVB	K I F S K F D L K S G F H Q V A M A E E S I P W T A F W V P Q G - L Y E W L V M P F G L K N A P A V F Q R K M D Q C F K G T E E F I					
24. AVT44083.1_CaYMV	K I Y S K F D L K S G F H Q V A M E A E S I P W T A F W A I D G - L Y E W L V M P F G L K N A P A V F Q R K M D S C F R G T E E F I					
25. API68654.1_CaYMV	K I Y S K F D L K S G F H Q V A M E A E S I P W T A F W A I D G - L Y E W L V M P F G L K N A P A V F Q R K M D G C F K G T E E F I					
26. YP_009259698.1_CaYMV	R V Y S K F D L K S G F H Q V A M E E E S I P W T A F W A I D G - L Y E W L V M P F G L K N A P A C F Q R K M D N C F R G K E H F I					
27. YP_003284237.1_ScBV	K I Y S K F D L K S G F H Q V A M E E A S I P W T A F W A I D G - L Y E W L V M P F G L K N A P A V F Q R K M D N C F R G T E E F I					
28. YP_009116631.1_RYNV	K I F S K F D L K S G F H Q V L M D E E S I P W T A F V T P V G - F Y E W K V M P F G L A N A P A V F Q R K M D Q C F A G T S E F I					
29. AEE39279.1_GVBaV	K I Y S K F D L K A G F H Q V L M E E S S I P W T A F I T P V G - F Y E W L V M P F G I A N A P A V F Q R K M D N C F H K L R E F V					
30. AEE39276.1_GVBaV	K I Y S K F D L K A G F H Q V L M E E S S I P W T A F I T P V G - F Y E W L V M P F G I A N A P A V F Q R K M D N C F H K L R E F V					
31. AIY62341.1_GVCV	K I F S K F D L K S G F H Q V M E E E S I P W T A F I S P A G - L Y E W L V M P F G I Q N A P A I F Q R K M D E C F K G T E D F I					
32. AVA17853.1_BLRD	K V F S K F D L K S G F H Q V T M D E E S I P W T A F L T P D G - L Y E W L V M P F G L K N A P A V F Q R K M D N C F K G T E E F I					
33. YP_002321513.1_BsCVBV	K I Y S K F D L K S G F H Q V A M D P E S I P W T A F L T P Q G - L F E W L V M P F G L K N A P A I F Q R K M D N C F S R Y S D F I					
34. YP_009041481.1_PYMAV0	K V Y S K F D L K S G F H Q V A M D E A S I P W T A F L V P G G - L Y E W L V M P F G L R N A P A I F Q R K M D E V F A D L K E F V					
35. YP_009352866.1_WBV	K V Y S K F D L K S G F H Q V A M D E D S I P W T A F L V P G G - L Y E W L V M P F G L R N A P A I F Q R K M D E V F G D L K D F I					

200 210 220 230 240 250 260



Consensus
Identity

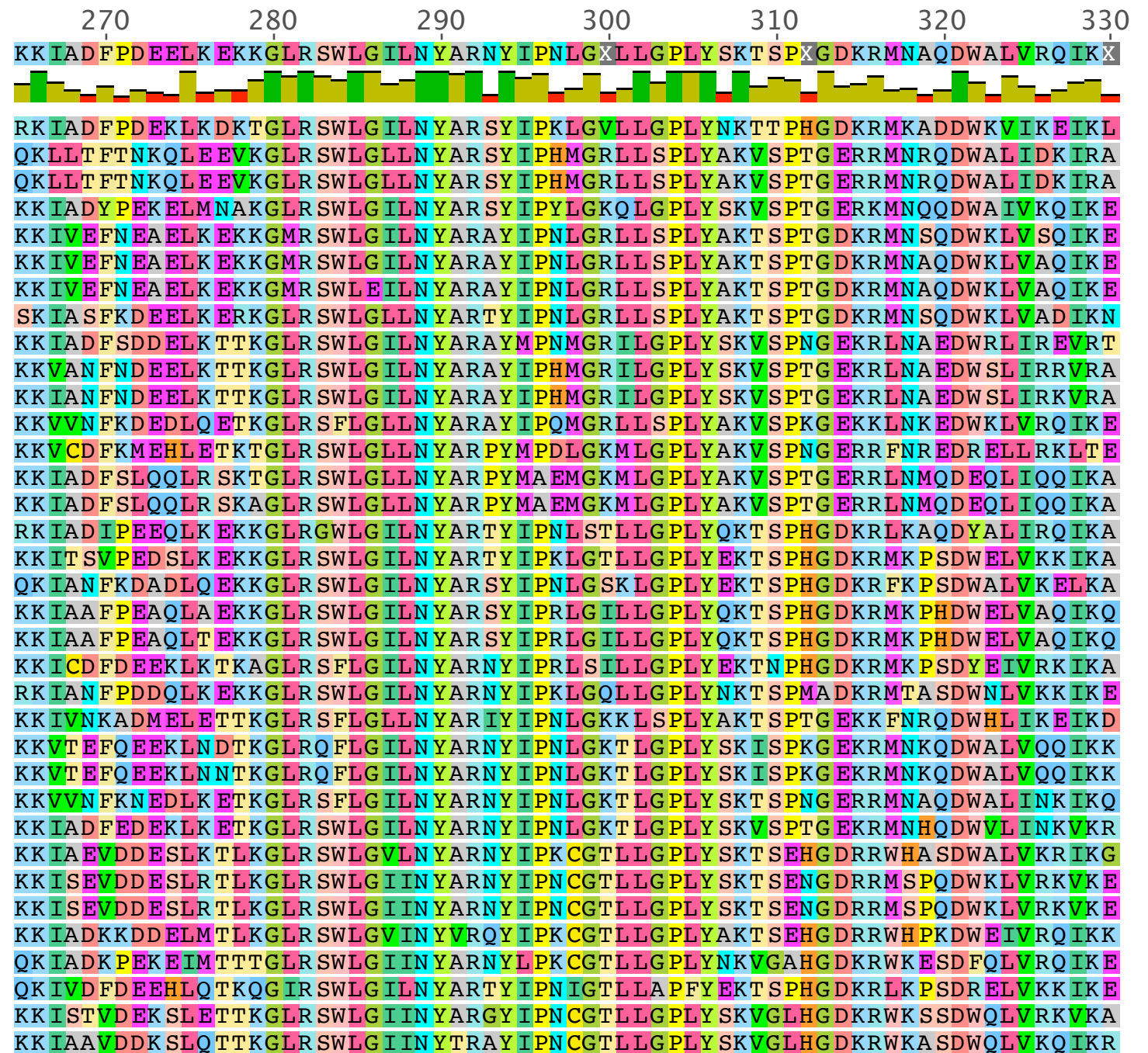
1. SRF019_MK014483_PVBV
2. NP_569153.1_CMBV
3. ACE76864.1_CMBV
4. YP_009130664.1_TaBV
5. YP_009140788_GRBaV:
6. YP_006273075.1_FBaV-1
7. ANK58542.1_FBaV-1
8. ATV81254.1_Grape
9. YP_001036293.1_DBSNV
10. ATW01249.1_DBSNV
11. AHG32725.1_DBSNV
12. YP_009002585.1_HBV
13. YP_009113237.2_MBV-1
14. ATZ69526.1_CSSV
15. ATZ69522.1_CSSV
16. YP_003208050.1_PVBV
17. YP_009229919.1_BVF
18. YP_009408594.1_Jujude
19. YP_610965.1_DrMV
20. ABR01170.1_Lucky
21. YP_009121747.1_YNMov
22. YP_009345075_CCYVB
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32. AVA17853.1_BLRD
33. YP_002321513.1_BsCVBV
34. YP_009041481.1_PYMAVO
35. YP_009352866.1_WBV

AVYIDDILVFSSENKKEHAKHLDIVLEIFFEKEGLIIAK EKMK IGTPEIEFLGATIFGQNR IKLQPHII
 AVYIDDILVFSKTEQDHEKHLQIMLAICQKNGLILSPTKMKIAQAEIEFLGAI IHKGLIKLQPHIV
 AVYIDDILVFSKTEKEHEEHLQIMLSICQRNGLILSPTKMKIAQAEIEFLGAI IHNGLIKLQPHIV
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 AVYIDDILVFSSEDEKSHAKHLRIMLGIICKRNGLVLSPTKMKIAVQEV EFLGAQIGNQK IKLQPHVI
 AVYIDDILVFSSENKDHAKHLKAMLEIICKRNGLVLSPSKMKIAVQEV EFLGAQIGNQR IRLQPHVI
 AVYIDDILVFSSENKDHAKHLKAMLEIICKRNGLVLSPSKMKIAVQEV EFLGAQIGNQR IRLQPHVI
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 AVYIDDILVFSSETEDDHVKHLRIMLDIICKRNGLVLSPTKMKIGTATVEFLGAVIGNRR IKLQPHII
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 AVYIDDILVFSQSSEEHIKHIRVMLEKCR ENGLVLSPTKMKIAQRKVEFLGAIL EAGR IQLQPHII
 VVYIDDILVFSQNEQDHERHIRAMLKICKENGLILSPSKMKIGQTKVEFLGAIIDK GK IRLQPNVI
 AVYIDDIIIFSET EKQHEEHLYKFI DRCKEHGLVLSPTKMKIGQRRIEFLGAV IDQGR IRLQPNII
 AVYIDDIIIFSET EKQHEEHLYKFI DRCKEHGLVLSPTKMKIGQRRIEFLGAV IDQGR IRLQPNII
 AVYIDDILVFSKN EEEHQKHLQKFL EIVEKEGLVLSPTKMKIAVPEVEFLGAIIGN STIKLQPHII
 AVYIDDILVFSSET EEQHAKHLQIMLEICEKNGLVLSANKMKIAVK EVEFLGAVICDRK IKLQPHII
 AVYIDDVLVFSNNEQDHRHLHVMLNICKQHGLILSPSKMKIAVPEVYFLGAVLGKQK LKLQPHII
 AVYIDDILIFSANDEEHVEHLKVFC AIVEKHGLILSSNKMQLGKREIDFLGATLGNRK IKLQAHII
 AVYIDYILIFSANDEEHVEHLKVFC AIVEKHGLILSSNKMQLGKGEIDFLGATLGNRK IKLQAHII
 AVYIDDILVYSN SEADHERHLKIMLGKQENGLVLSPTKMKIAVPEVEFLGAIIGNRK IKLQPHII
 AVYIDDILVFSQT EEEHVRHLQRFFQICQKHGLVLSKDKMAIAVPQIEFLGAIIGNRK IKLQPHII
 AVYIDDILVFSSETMAEHTKHIGIMLTICQENGLVLSPNKICLAQREIEFLGTIISQGMK LQPHVI
 AVYIDDILVFSSETPQQHVQH LRKFL EIVKKNGLVLSPTKMKIGVSQIDFLGATIGQSR IKLQPHII
 AVYIDDILVFSSETPQQHVQH LRKFL EIVKKNGLVLSPTKMKIGVSQIDFLGATIGQSR IKLQPHII
 AVYIDDILIFSENKEQH VQHLKEFLRIVKKEGLVLSPTKMKIGV PKVDFLGATIGESR IKLQPHII
 AVYIDDILIFSES PQQHVQH LKFKFMEICEKNGLVLSPTKMKIGVSQVDFLGATIGQSK IRLQPHII
 AVYIDDILVFSKTLKEHEKHL S IMLGICRDNGLVLSPSKMKLAATEIDFLGATIGDGR IKLQPHII
 AVYIDDILVFSN SLQEHESH LRQMLEVCRKNGLVLSPTKMKVAVTTVEFLGAIIGN GKIKLQPHIV
 AVYIDDILVFSN SLQEHESH LRQMLEVCRKNGLVLSPTKMKVAVTTVEFLGAIIGN GKIKLQPHIV
 AVYIDDILVFSN SIKHEHEKHLQ RMLSICKEHGLVLSPTKMKIAVPGIDFLGAHIRN SRVSLQPHII
 AVYIDDILVFSSENHKQHEGHLRKMLEIVRQNGLVLSPTKMKIACSEIDFLGATIGNSR IQLQPHIV
 AVYIDDILVFSSESERDHEKHLR VMLQVQENGLVLSPTKMKVAVKTIEFLGAILGNQ CVQLQPHII
 SVYIDDILVFSSETYE EHAHLKRMLQRCKK FGLVLSPTKMKIATR EIDFLGATIKDGR IKLQDHHI
 AVYIDDILVFSSETHEQHAQH IKRMLLRCKKHGLVLSPSKMKIAQKEIEFLGATLTGGQ IKLQDHIIV

Consensus

Identity

1. SRF019_MK014483_PVBV
2. NP_569153.1_CMBV
3. ACE76864.1_CMBV
4. YP_009130664.1_TaBV
5. YP_009140788_GRBaV:
6. YP_006273075.1_FBaV-1
7. ANK58542.1_FBaV-1
8. ATV81254.1_Grape
9. YP_001036293.1_DBSNV
10. ATW01249.1_DBSNV
11. AHG32725.1_DBSNV
12. YP_009002585.1_HBV
13. YP_009113237.2_MBV-1
14. ATZ69526.1_CSSV
15. ATZ69522.1_CSSV
16. YP_003208050.1_PVBV
17. YP_009229919.1_BVF
18. YP_009408594.1_Jujude
19. YP_610965.1_DrMV
20. ABR01170.1_Lucky
21. YP_009121747.1_YNMov
22. YP_009345075_CCYVB
23. ASG91874.1_CCYVB
24. AVT44083.1_CaYMV
25. API68654.1_CaYMV
26. YP_009259698.1_CaYMV
27. YP_003284237.1_ScBV
28. YP_009116631.1_RYNV
29. AEE39279.1_GVBaV
30. AEE39276.1_GVBaV
31. AIY62341.1_GVCV
32. AVA17853.1_BLRD
33. YP_002321513.1_BsCVBV
34. YP_009041481.1_PYMAV0
35. YP_009352866.1_WBV



340 350 363

Consensus

QVQNLPDLELPPEDAYIIIETDGCMEGWGGVCK

Identity



1. SRF019_MK014483_PVBV

LVKQLPDLHIPPKDAYVVL ETDGCMEGWGGVCK

2. NP_569153.1_CMBV

QVQNLPAL ELPADCFIIIETDGCMDGWGGVCK

3. ACE76864.1_CMBV

QVQNLPAL ELPADCFIIIETDGCMDGWGGVCK

4. YP_009130664.1_TaBV

KVQNLPDLELPPPDCHIVL ETDGCMDGWGGVCK

5. YP_009140788_GRBaV:

EVQKLPDLEIIPPEDSFIILETDGCMTGWGGVCK

6. YP_006273075.1_FBaV-1

EVQKLPDLELPPEDCFIILETDGCMTGWGGICK

7. ANK58542.1_FBaV-1

EVQKLPDLELPPEDCFIILETDGCMTGWGGICK

8. ATV81254.1_Grape

LVQKLPDLEVPPESCIVL ETDGCMTGWGGICK

9. YP_001036293.1_DBSNV

TIRALPDLELPPADSFIVIEADGCMEGWGGVCK

10. ATW01249.1_DBSNV

IIQNLPDLEFPPEHSFIIIETDGCMDGWGGVCK

11. AHG32725.1_DBSNV

TIQNLPDLEFPPEHSFIII EADGCMDGWGGVCK

12. YP_009002585.1_HBV

QVQQLPDLELPPQECFIILETDGCMEGWGGVCK

13. YP_009113237.2_MBV-1

KIRNLPDLELPPPNAYIII ESDGCMTGWGGVCK

14. ATZ69526.1_CSSV

QIQNLPDLEIIPPEDAYIII ESDGCMEGWGGICK

15. ATZ69522.1_CSSV

QIQNLPDLEIIPPEDAYIII ESDGCMEGWGGICK

16. YP_003208050.1_PVBV

LVQNLPDLKIIPPADSYIVL ETDGCMEGWGGVCK

17. YP_009229919.1_BVF

QVQNLPDMEIIPPEKAHIVIETDGSMEGWGAVCK

18. YP_009408594.1_Jujude

QIQNLPDLEIAPASAYIVL ETDGSMTGWGGVCK

19. YP_610965.1_DrMV

MVQSLPDLEVPPKDSFIVL ETDGCMEGWGGICK

20. ABR01170.1_Lucky

MVQSLPDLEVPPKDSFIVL ETDGCMEGWGGICK

21. YP_009121747.1_YNMov

KVQQLPDLQIIPDDAYITIETDGCMDGWGGICK

22. YP_009345075_CCYVB

KVQALPDMELPPKDAFVIIETDGCTEGWGAVAK

23. ASG91874.1_CCYVB

MVQKLPNLAIPPAKCCIII ESDGCMEGWGAVCK

24. AVT44083.1_CaYMV

QVANLP EMELEPRRDVVVL ETDGCMDGWGGICK

25. API68654.1_CaYMV

QVANLP EMELEPRDAVMILETDGCMDGWGGICK

26. YP_009259698.1_CaYMV

QVQNLPDMELPPDNAVITL ETDGCMDGWGGVCK

27. YP_003284237.1_ScBV

QVKEL EDMELPPVEACIVL ETDGCMEGWGGVCK

28. YP_009116631.1_RYNV

LVQNLPDLKLPTEEAYMIIETDGCMEGWGGVCK

29. AEE39279.1_GVBaV

LVKSLPDLELPPAGAYVVIETDGCMEGWGGVCK

30. AEE39276.1_GVBaV

LVKSLPDLELPPAGAYVVIETDGCMEGWGGVCK

31. AIY62341.1_GVCV

MVQSLPDLELPPPHAVIII ESDGCMEGWGGICK

32. AVA17853.1_BLRD

MVQRLPALKLP PPGAYMVIETDGCMEGWGGICK

33. YP_002321513.1_BsCVBV

MVQHL PPLELPPPDAYIILETDGSMEGWGGICK

34. YP_009041481.1_PYMAVO

AVENLP ELEIIPPKNCHIII ETDGCMEGWGGVCK

35. YP_009352866.1_WBV

LVQIL PTL EIPPKDCHIII ETDGCMEGWGGICK