Supplementary Information

for

Viral AlkB proteins repair RNA damage by oxidative demethylation

Erwin van den Born[1], Marina V. Omelchenko[2], Anders Bekkelund[1], Vibeke Leihne[1], Eugene V. Koonin[2], Valerian V. Dolja[3], and Pål Ø. Falnes[1,4*]

[1]Department of Molecular Biosciences, University of Oslo, P.O. Box 1041 Blindern, N-0316 Oslo, Norway

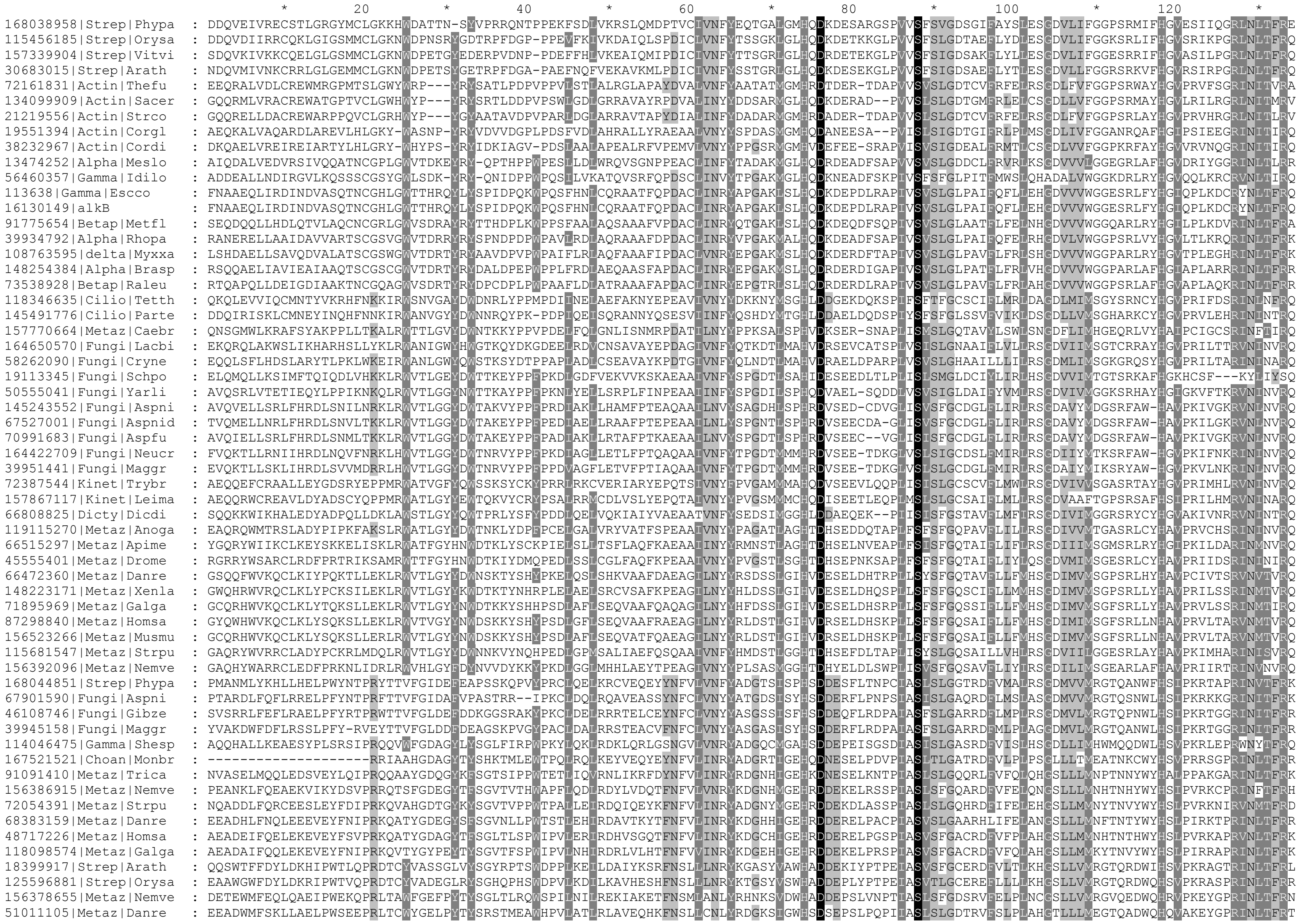
[2]National Center for Biotechnology Information, National Institutes of Health, Bethesda, Maryland 20894, USA

[3]Department of Botany and Plant Pathology and Center for Genome Research and Biocomputing, Oregon State University, Corvallis, OR 97331, USA

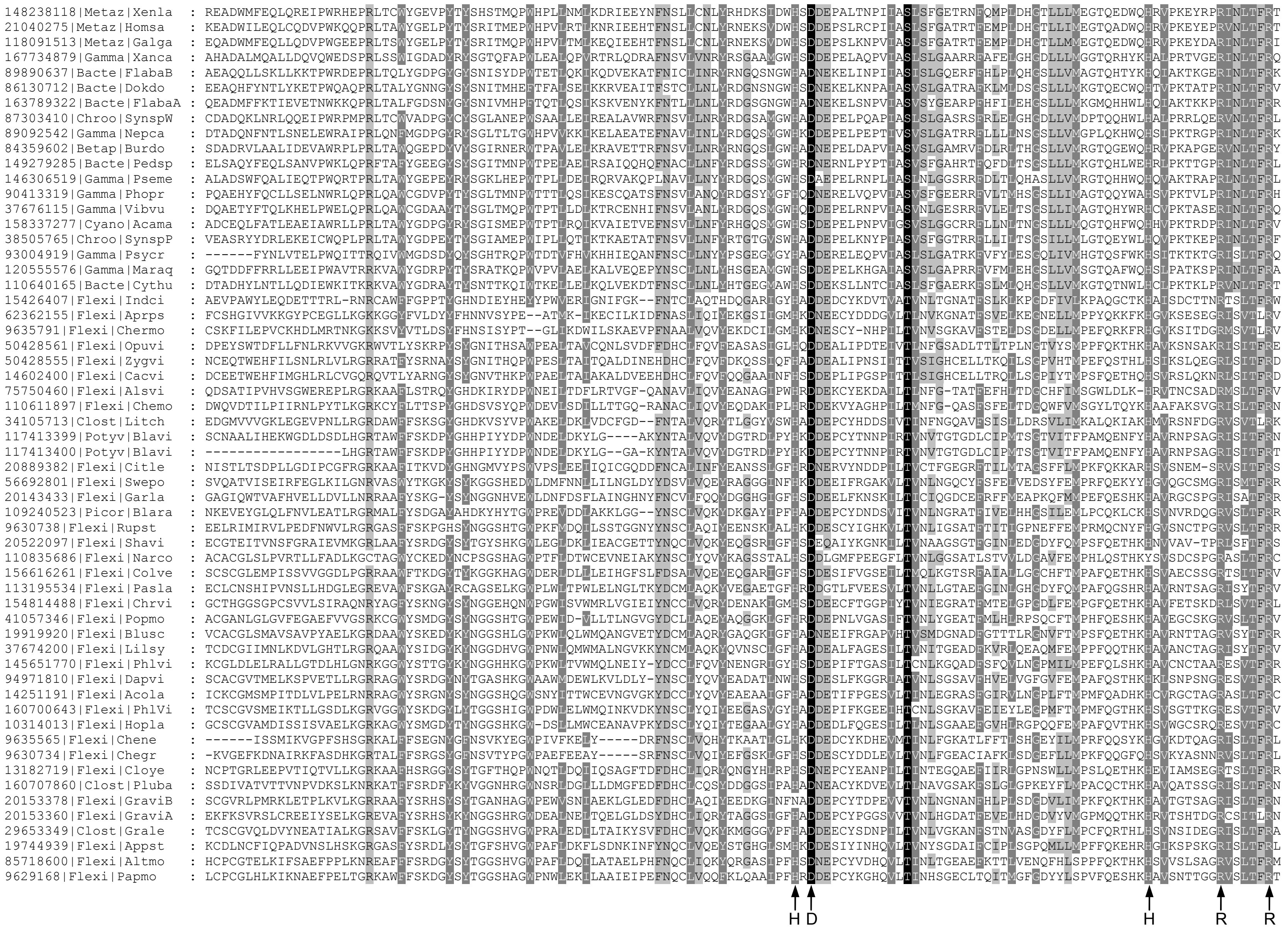
[4]Centre for Molecular Biology and Neuroscience, Rikshospitalet-Radiumhospitalet HF, University of Oslo, Oslo, Norway

*Corresponding author. Tel: +47–22854840; fax: +47–22854443. E-mail: pal.falnes@imbv.uio.no

Figure S1



```
                                  *         20         *         40         *         60         *         80         *        100         *        120         *
168038958|Strep|Phypa  : DDQVEIVRECSTLGRGYMCLGKKHWDATTN-SYVPRRQNTPPEKFSDLVKRSLQMDPTVCIVNFYEQTGALGMHQDKDESARGSPVVSFSVGDSGIFAYSLESGDVLIFGGPSRMIFHGVESIIQGRLNLTFRE
115456185|Strep|Orysa  : DDQVDIIRRCQKLGIGSMMCLGKNWDPNSRYGDTRPFDGP-PPEVFKIVKDAIQLSPDICLVNFYTSSGKLGLHQDKDETKKGLPVVSFSLGDTAEFLYDLESGDVLIFGGKSRLIFHGVSRIKPGRLNLTFRQ
157339904|Strep|Vitvi  : SDQVKIVKKCQELGLGSMMCLGKNWDPETGYEDERPVDNP-PDEFFHLVKEAIQMIPDICIVNFYTTSGRLGLHQDRDETEKGLPVVSFSIGDSAKFLYLLESGDVLIFGGESRRIFHGVASILPGRLNLTFRQ
30683015|Strep|Arath   : NDQVMIVNKCRRLGLGEMMCLGKNWDPETSYGETRPFDGA-PAEFNQFVEKAVKMLPDICIVNFYSSTGRLGLHQDKDESEKGLPVVSFSIGDSAEFLYTLESGDVLLFGGRSRKVFHGVRSIRPGRLNLTFRQ
72161831|Actin|Thefu   : EEQRALVDLCREWMRGPMTSLGWYWRP---YRYSATLPDPVPPVLSTLALRGLAPAYDVALVNFYAATATMGMHRDTDER-TDAPVVSVSLGDTCVFRFELRSGDLFVFGGPSRWAYHGVPRVFSGRINITVRA
134099909|Actin|Sacer  : GQQRMLVRACREWATGPTVCLGWHWYP---YRYSRTLDDPVPSWLGDLGRRAVAYRPDVALINYYDDSARMGLHQDKDERAD--PVVSLSLGDTGMFRLELCSGDLLVFGGPSRMAYHGVLRILRGRLNITMRV
21219556|Actin|Strco   : GQQRELLDACREWARPPQVCLGRHWYP---YGYAATAVDPVPARLDGLARRAVTAPYDIALINFYDADARMGMHRDADER-TDAPVVSLSLGDTCVFRFELRSGDLFVFGGPSRLAYHGVPRVHRGRLNITLRV
19551394|Actin|Corgl   : AEQKALVAQARDLAREVLHLGKY-WASNP-YRYVDVVDGPLPDSFVDLAHRALLYRAEAALVNYYSPDASMGMHQDANEESA--PVISLSIGDTGIFRLPLMSGDLIVFGGANRQAFHGIPSIEEGRINITIRQ
38232967|Actin|Cordi   : DKQAELVREIREIARTYLHLGRY-WHYPS-YRYIDKIAGV-PDSLAALAPEALRFVPEMVLVNYYPPGSRMGMHVDEFEE-SRAPVISVSIGDEALFRMTLCSGDLVVFGGPKRFAYHGVVRVNQGRINITIRQ
13474252|Alpha|Meslo   : AIQDALVEDVRSIVQQATNCGPLGWVTDKEYRY-QPTHPPWPESLLDLWRQVSGNPPEACLINFYTADAKMGLHQDRDEADFSAPVVSVSLGDDCLFRVRLKSGDVVVLGGEGRLAFHGVDRIYGGRINLTLRR
56460357|Gamma|Idilo   : ADDEALLNDIRGVLKQSSSCGSYGWLSDK-YRY-QNIDPPWPQSILVKATQVSRFQPDSCLINVYTPGAKMGLHQDKNEADFSKPIVSFSFGLPITFMWSLQHADALVWGGKDRLRYHGVQQLKRCRVNLTIRQ
113638|Gamma|Escco     : FNAAEQLIRDINDVASQTNCGHLGWTTHRQYLYSPIDPQKWPQSFHNLCQRAATFQPDACLINRYAPGAKLSLHQDKDEPDLRAPIVSVSLGLPAIFQFLLEHGDVVVWGGESRLFYHGIQPLKDCRYNLTFRQ
16130149|alkB          : FNAAEQLIRDINDVASQTNCGHLGWTTHRQYLYSPIDPQKWPQSFHNLCQRAATFQPDACLINRYAPGAKLSLHQDKDEPDLRAPIVSVSLGLPAIFQFLLEHGDVVVWGGESRLFYHGIQPLKDCRYNLTFRQ
91775654|Betap|Metfl   : SEQDQQLLHDLQTVLAQCNCGRLGWVSDRAYRYTTHDPLKWPPSFAALAQSAAAFVPDACLINRYQTGAKLSLHQDKDEQDFSQPIVSVSLGLAATFLFELNHGDVVVWGGQARLRYHGILPLKDVRINLTFRA
39934792|Alpha|Rhopa   : RANERELLAAIDAVVARTSCGSVGWVTDRRYRYSPNDPDPWPAVLRDLAQRAAAFDPDACLINRYVPGAKMALHQDKDEADFSAPIVSVSLGLPAIFQFELRHGDVLVWGGPSRLVYHGVLTLKRQRINLTFRK
108763595|delta|Myxxa  : LSHDAELLSAVQDVALATSCGSWGWVTDRTYRYAAVDPVPWPAIFLRLAQFAAAFIPDACLVNRYEPGAKMSLHQDKDERDFTAPIVSVSLGLPAVFLFRLSHGDVVVWGGPARLRYHGVTPLEGHRINLTFRK
148254384|Alpha|Brasp  : RSQQAELIAVIEAIAAQTSCGSCGWVTDRTYRYDALDPEPWPPLFRDLAEQAASFAPDACLINRYEPGAKMSLHQDRDERDIGAPIVSVSLGLPATFLFRLVHGDVVVWGGPARLAFHGIAPLARRRINLTFRR
73538928|Betap|Raleu   : RTQAPQLLDEIGDIAAKTNCGQAGWVSDRTYRYDPCDPLPWPAAFLDLATRAAAFAPDACLINRYEPGTRLSLHQDRDERDLRAPIVSVSLGLPAVFLFRLAHGDVVVWGGPSRLAFHGVAPLAQKRINLTFRR
118346635|Cilio|Tetth  : QKQLEVVIQCMNTYVKRHFNKKIRWSNVGAYDWDNRLYPPMPDIINELAEFAKNYEPEAVIVNYYDKKNYMSGHLDDGEKDQKSPIFSFTFGCSCIFLMRLDAGDLMIMSGYSRNCYHGVPRIFDSRINLNFRQ
145491776|Cilio|Parte  : DDQIRISKLCMNEYINQHFNNKIRWANVGYYDWNNRQYPK-PDPIQEISQRANNYQSESVIINFYQSHDYMTGHLDDAELDQDSPIYSFSFGLSSVFVIKLDSGDLLVMSGHARKCYHGVPRVLEHRININTRQ
157770664|Metaz|Caebr  : QNSGMWLKRAFSYAKPPLLTKALRWTTLGVYDWNTKKYPPVPDELFQLGNLISNMRPDATILNYYPPKSALSPHVDKSER-SNAPLISMSLGQTAVYLSWLSNGDFLIMHGEQRLVYHAIPCIGCSRINFTIRQ
164650570|Fungi|Lacbi  : EKQRQLAKWSLIKHARHSLLYKLRWANIGWYHWGTKQYDKGDEELRDVCNSAVAYEPDAGIVNFYQTKDTLMAHVDRSEVCATSPLVSISLGNAAIFLVLLRSGDVIIMSGTCRRAYHGVPRILTTRVNINVRQ
58262090|Fungi|Cryne   : EQQLSFLHDSLARYTLPKLWKEIRWANLGWYQWSTKSYDTPPAPLADLCSEAVAYKPDTGIVNFYQLNDTLMAHVDRAELDPARPLVSVSLGHAAILLLILRSGDMLIMSGKGRQSYHGVPRILTARININARQ
19113345|Fungi|Schpo   : ELQMQLLKSIMFTQIQDLVHKKLRWVTLGEYDWTTKEYPPFPKDLGDFVEKVVKSKAEAAIVNFYSPGDTLSAHIDESEEDLTLPLISLSMGLDCIYLIRLHSGDVVIMTGTSRKAFHGKHCSF---KYLIYSQ
50555041|Fungi|Yarli   : AVQSRLVTETIEQYLPPIKNKQLRWVTLGGYNWTTKAYPPFPKNLYELLSRPLFINPEAAIINFYSPGDILSPHQDVAEL-SQDDLVSVSIGLDAIFYVMLRSGDVIVMGGKSRHAYHGIGKVFTKRVNINVRQ
145243552|Fungi|Aspni  : AVQVELLSRLFHRDLSNILNRKLRWVTLGGYDWTAKVYPPFPRDIAKLLHAMFPTEAQAAILNVYSAGDHLSPHRDVSED-CDVGLISVSFGCDGLFLIRLRSGDAVYMDGSRFAW-HAVPKIVGKRVNLNVRQ
67527001|Fungi|Aspnid  : TVQMELLNRLFHRDLSNVLTKKLRWVTLGGYDWTAKEYPPFPEDIAELLRAAFPTEPEAAILNLYSPGNTLSPHRDVSEECDA-GLISVSFGCDGLFLIRLRSGDAVYMDGSRFAW-HAVPKILGKRVNLNVRQ
70991683|Fungi|Aspfu   : AVQIELLSRLFHRDLSNMLTKKLRWVTLGGYDWTAKEYPPFPADIAKLLRTAFPTKAEAAILNVYSPGDTLSPHRDVSEEC--VGLISISFGCDGLFLIRLRSGDAVYMDGSRFAW-HAVPKIVGKRVNLNVRQ
164422709|Fungi|Neucr  : FVQKTLLRNIIHRDLNQVFNRKLHWVTLGGYDWTNRVYPPFPKDIAGLLETLFPTQAQAAIVNFYTPGDTMMMHRDVSEE-TDKGLVSLSIGCDSLFMIRLRSGDIIYMTKSRFAW-HGVPKIFNKRININVRQ
39951441|Fungi|Maggr   : EVQKTLLSKLIHRDLSVVMDRRLHWVTLGGYDWTNRVYPPFPPDVAGFLETVFPTIAQAAIVNFYTPGDTMMMHRDVSEE-TDKGLVSLSLGCDGLFMIRLRSGDAIYMIKSRYAW-HGVPKVLNKRINLNVRQ
72387544|Kinet|Trybr   : AEQQEFCRAALLEYGDSRYEPPMRWATVGFYQWSSKSYCKYPRRLRKCVERIARYEPQTSIVNYFPVGAMMMAHQDVSEEVLQQPLISISLGCSCVFLMWLRSGDVIVVSGASRTAYHGVPRIMHLRVNINVRQ
157867117|Kinet|Leima  : AEQQRWCREAVLDYADSCYQPPMRWATLGYYEWTQKVYCRYPSALRRMCDLVSLYEPQTAIVNYYPVGSMMMCHQDISEETLEQPLMSLSLGCSAIFLMLLRSGDVAAFTGPSRSAFHSIPRILHMRVNINARQ
66808825|Dicty|Dicdi   : SQQKKWIKHALEDYADPQLLDKLAWSTLGYYQWTPRLYSFYPDDLQELVQKIAIYVAEAATVNFYSEDSIMGGHLDDAEQEK--PIISISFGSTAVFLMFIRSGDIVIMGGRSRYCYHGVAKIVNRRVNINTRQ
119115270|Metaz|Anoga  : EAQRQWMTRSLADYPIPKFAKSLRWATLGYYDWTNKLYDPFPCELGALVRYVATFSPEAAIVNYYPAGATLAGHTDHSEDDQTAPLFSFSFGQPAVFLILLRSGDIVVMTGASRLCYHAVPRVCHSRININVRQ
66515297|Metaz|Apime   : YGQRYWIIKCLKEYSKKELISKLRWATFGYHNWDTKLYSCKPIELSLLTSFLAQFKAEAAIINYYRMNSTLAGHTDHSELNVEAPLFSISFGQTAIFLIFLRSGDIIIMSGMSRLRYHGIPKILDARINMNVRQ
45555401|Metaz|Drome   : RGRRYWSARCLRDFPRTRIKSAMRWTTFGYHNWDTKIYDMQPEDLSSLCGLFAQFKPEAAIVNYYPVGSTLSGHTDHSEPNKSAPLFSFSFGQTAIFLIYLQSGDVMIMSGESRLCYHAVPRIIDSRININIRQ
66472360|Metaz|Danre   : GSQQFWVKQCLKIYPQKTLLEKLRWVTLGYYDWNSKTYSHYPKELQSLSHKVAAFDAEAGILNYYRSDSSLGIHVDESELDHTRPLLSYSFGQTAVFLLFMHSGDIMVMSGPSRLHYHAVPCIVTSRVNVTVRQ
148223171|Metaz|Xenla  : GWQHRWVRQCLKLYPCKSILEKLRWVTLGYYKWDTKTYNHRPLELAELSRCVSAFKPEAGILNYYHLDSSLGIHVDESELDHQSPLLSFSFGQSCIFLLMMHSGDIMVMSGPSRLLYHAVPRILSSRINMTVRQ
71895969|Metaz|Galga   : GCQRHWVKQCLKLYTQKSLLEKLRWVTLGYYNWDTKKYSHHPSDLAFLSEQVAAFQAQAGILNYYHFDSSLGIHVDESELDHSRPLLSFSFGQSSIFLLFMHSGDIMVMSGFSRLLYHAVPRVLSSRINMTIRQ
87298840|Metaz|Homsa   : GYQWHWVKQCLKLYSQKSLLEKLRWVTVGYYNWDSKKYSHYPSDLGFLSEQVAAFRAEAGILNYYRLDSTLGIHVDRSELDHSKPLLSFSFGQSAIFLLFMHSGDIMIMSGFSRLLNHAVPRVLTARVNMTVRQ
156523266|Metaz|Musmu  : GCQRHWVKQCLKLYSQKSLLERLRWVTLGYYNWDSKKYSHYPSDLAFLSEQVATFQAEAGILNYYRLDSTLGIHVDRSELDHSKPLLSFSFGQSAIFLLFMHSGDIMVMSGFSRLLNHAVPRVLTARVNMTVRQ
115681547|Metaz|Strpu  : GAQRYWVRRCLADYPCKRLMDQLRWVTLGYYDWNNKVYNQHPEDLGPMSALIAEFQSQAAIVNFYHMDSTLGGHTDHSEFDLTAPLISYSLGQSAILLVHLRSGDVIILGGESRLAYHAVPKIMHARINISVRQ
156392096|Metaz|Nemve  : GAQHYWARRCLEDFPRKNLIDRLRWVHLGYFDYNVVDYKKYPKDLGGLMHHLAEYTPEAGIVNYYPLSASMGGHTDHYELDLSWPLISVSFGQSAVFLIYIRSGDILIMSGEARLAFHAVPRIIRTRINVNVRQ
168044851|Strep|Phypa  : PMANMLYKHLLHELPWYNTPRYTTVFGIDEFEAPSSKQPVYPRCLQELKRCVEQEYYNFVLVNFYADGTSISPHSDDESFLTNPCIASLSLGGTRDFVMALRSGDMVVMRGTQANWFHSIPKRTAPRINVTFRK
67901590|Fungi|Aspni   : PTARDLFQFLRRELPFYNTPRFTTVFGIDAFVPASTRR--IPKCLDQLRQAVEASSYNFCLVNYYATGDSISYHSDDERFLPNPSIASISLGAQRDFLMSLASGDMVVMRGTQSNWLHSIPKRKKGRINITFRK
46108746|Fungi|Gibze   : SVSRRLFEFLRAELPFYRTPRWTTVFGLDEFDDKGGSRAKYPKCLDELRRRTELCEYNFCLVNYYASGSSISFHSDDEQFLRDPAIASFSLGARRDFLMPLRSGDMVLMRGTQPNWLHSIPKRTGGRINITFRR
39945158|Fungi|Maggr   : YVAKDWFDFLRSSLPFY-RVEYTTVFGLDDFDEAGSKPVGYPACLDALRRSTEACVFNFCLVNYYASGASISYHSDDERFLRDPAIASFSLGARRDFMLPLAGGDMVLMRGTQANWLHSIPKRTGGRINITFRR
114046475|Gamma|Shesp  : AQQHALLKEAESYPLSRSIPRQQVWFGDAGYLYSGLFIRPWPKYLQKLRDKLQRLGSNGVLVNRYADGQCMGAHSDDEPEISGSDIASISLGASRDFVISLHSGDLLIMHWMQQDWLHSVPKRLEPRWNYTFRQ
167521521|Choan|Monbr  : --------------------RRIAAHGDAGYTYSHKTMLEWTPQLRQLKEYVEQYEYNFVLINRYADGRTIGEHQDNESELPDVPIASLTLGATRDFVLPLPSGLLLTMEATNKCWYHSVPRRSGPRINLTFRR
91091410|Metaz|Trica   : NVASELMQQLEDSVEYLQIPRQQAAYGDQGYKFSGTSIPPWTETLIQVRNLIKRFDYNFVLINRYRDGNHIGEHKDNESELKNTPIASLSLGQQRLFVFQLQHGSLLLMNPTNNYWYHALPPAKGARINLTFRK
156386915|Metaz|Nemve  : PEANKLFQEAEKVIKYDSVPRRQTSFGDEGYTFSGVTVTHWAPFLQDLRDYLVDQTFNFVLVNRYKDGNHMGEHRDDEKELRSSPIASLSFGQARDFVFELQNGSLLLMNHTNHYWYHSIPVRKCPRINFTFRH
72054391|Metaz|Strpu   : NQADDLFQRCEESLEYFDIPRKQVAHGDTGYKYSGVTVPPWTPALLEIRDQIQEYKFNFVLINRYADGNYMGEHRDDEKDLASSPIASLSLGQHRDFIFELEHGSLLMMNYTNVYWYHSLPVRKNIRVNMTFRD
68383159|Metaz|Danre   : EEADHLFNQLEEEVEYFNIPRKQATYGDEGYSFSGVNLLPWTSTLEHIRDAVTKYTFNFVLINRYKDGHHIGEHRDDERELPACPIASVSLGAARHLIFELANGSLLLMNFTNTYWYHSLPIRKTPRINLTFRR
48717226|Metaz|Homsa   : AEADEIFQELEKEVEYFSVPRKQATYGDAGYTFSGLTLSPWIPVLERIRDHVSGQTFNFVLINRYKDGCHIGEHRDDERELPGSPIASVSFGACRDFVFPLAHGSLLMMNHTNTHWYHSLPVRKAPRVNLTFRK
118098574|Metaz|Galga  : AEADAIFQQLEKEVEYFNIPRKQVTYGYPEYTYSGVTFSPWIPVLNHIRDRLVLHTFNFVVINRYKDGEHIGEHRDDEKELPRSPIASVSFGACRDFVFQLAHGSLLMMKYTNVYWYHSLPIRRAPRINLTFRK
18399917|Strep|Arath   : QQSWTFFDYLDKHIPWTLQPRDTCYVASSGLVYSGYRPTSWDPPLKEILDAIYKSRFNSLLLNRYKGASYVAWHADDEKIYPTPEIASVSFGCERDFVLTLKHGSLLVMRGTQRDWIHSVPKRAGTRINLTFRL
125596881|Strep|Orysa  : EAAWGWFDYLDKRIPWTVQPRDTCYVADEGLRYSGHQPHSWDPVLKDILKAVHESHFNSLLLNRYKTGSYVSWHADDEPLYPTPEIASVTLGCEREFLLLLKHGSLLVMRGTQRDWQHSVPKRASPRINLTFRR
156378655|Metaz|Nemve  : DETEWMFEQLQAEIPWEKQPRLTAWFGEFPYTYSGLTLRQWSPILNILREKIAKETFNSMLANLYRHNKSVDWHADDEPSLVNPTIASLSFGDSRVFELPLNCGSLLVMRGVQEDWQHRVPKEYGPRINLTFRN
51011105|Metaz|Danre   : EEADWMFSKLLAELPWSEEPRLTCWYGELPYTYSRSTMEAWHPVLATLRLAVEQHKFNSLLCNLYRDGKSIGWHSDSEPSLPQPIIASLSLGDTRVFSLPLAHGTLLLMEGTQADWQHQVAKEYGPRINLTFRT
```



```
148238118|Metaz|Xenla  : READWMFEQLQREIPWRHEPRLTCWYGEVPYTYSHSTMQPWHPLLNMLKDRIEEYNFNSLLCNLYRHDKSIDWHSDDEPALTNPIIASLSFGETRNFQMPLDHGTLLLMEGTQEDWQHRVPKEYRPRINLTFRT
21040275|Metaz|Homsa   : KEADWILEQLCQDVPWKQQPRLTAWYGELPYTYSRITMEPWHPVLRTLKNRIEEHTFNSLLCNLYRNEKSVDWHSDDEPSLRCPIIASLSFGATRTFEMPLDHGTLLIMEGTQADWQHRVPKEYEPRVNLTFRT
118091513|Metaz|Galga  : EQADWMFEQLLQDVPWGEEPRLTSWYGELPYTYSRITMQPWHPVLTMLKEQIEEHTFNSLLCNLYRNEKSVDWHSDDEPSLKNPVIASLSFGATRTFEMPLDHGTLLMMEGTQEDWQHRVPKEYDARINLTFRI
167734879|Gamma|Xanca  : AHADALMQALLDQVQWEDSPRLSSWIGDADYRYSGTQFAPWLEALQPVRTRLQDRAFNSVLVNRYRSGAAMGWHSDDEPELAQPVIASLSLGAARRFAFELGHGDLLLMGGTQRHYKHALPRTVGERINLTFRQ
89890637|Bacte|FlabaB  : AEAQQLLSKLLKKTPWRDEPRLTQLYGDPGYGYSNISYDPWTETLQKIKQDVEKATFNICLINRYRNGQSNGWHADNEKELINPIIASISLGQERFFHLPLQHGSLLVMAGTQHTYKHQIAKTKGERINLTFRK
86130712|Bacte|Dokdo   : EEAQHFYNTLYKETPWQAQPRLTALYGNNGYSYSNITMHEFTFALSEIKKRVEAITFSTCLLNLYRDGNSNGWHSDNEKELKNPAIASVSLGATRAFKLMLDSGSLLLMKGTQECWQHTVPKTATPRINLTFRV
163789322|Bacte|FlabaA : QEADMFFKTIEVETNWKKQPRLTALFGDSNYGYSNIVMHPFTQTLQSIKSKVENYKFNTLLLNLYRDGSGNGWHADNEKELSNPVIASVSYGEARPFHFILEHGSLLLMKGMQHHWLHQIAKTKKPRINLTFRR
87303410|Chroo|SynspW  : CDADQKLNRLQQEIPWRPMPRLTCWVADPGYCYSGLANEPWSAALLEIREALAVWRFNSVLLNRYRDGSAMGWHADDEPELPQAPIASLSLGASRSFRLELGHGDLLVMDPTQQHWLHALPRRLQERVNLTFRL
89092542|Gamma|Nepca   : DTADQNFNTLSNELEWRAIPRLQNFMGDPGYRYSGLTLTGWHPVVKKIKELAEATEFNAVLINLYRDGQSMGWHKDDEPELPEPTIVSVSLGATRRFLLLLNSGSLLVMGPLQKHWQHSIPKTRGPRINLTFRK
84359602|Betap|Burdo   : SDADRVLAALIDEVAWRPLPRLTAWQGEPDYVYSGIRNERWTPAVLELKRAVETTRFNSVLLNRYRNGQSLGWHADNEPELDAPVIASVSLGAMRVFDLRLTHGSLLVMRGTQGEWQHRVPKAPGERVNLTFRY
149279285|Bacte|Pedsp  : ELSAQYFEQLSANVPWKLQPRFTAFYGEEGYSYSGITMNPWTPELAEIRSAIQQHQFNACLLNFYRDGSSMGWHRDNERNLPYPTIASVSFGAHRTFQFDLTSGSLLLMKGTQHLWEHRLPKTTGPRINLTFRL
146306519|Gamma|Pseme  : ALADSWFQALIEQTPWQRTPRLTAWYGEPEYRYSGKLHEPWTPLLDEIRQRVAKQPLNAVLLNYYRDGQSMGWHSDAEPELRNPLIASLNLGGSRRFDLTLQHASLLVMRGTQHHWQHQVAKTRAPRLNLTFRL
90413319|Gamma|Phopr   : PQAEHYFQCLLSELNWRLQPRLQAWCGDVPYTYSGLTMNPWTTTLQSIKESCQATSFNSVLANQYRDGSYMGFHQDNERELVQPVIASVSFGEERRFVLTMHSGSLLIMAGTQQYWAHSVPKTVLPRINLTFRH
37676115|Gamma|Vibvu   : DQAETYFTQLKHELPWELQPRLQAWCGDAAYTYSGLTMQPWTPTLLDLKTRCENHIFNSVLANLYRDGQSMGWHQDDEPELRNPVIASVNLGESRRFVLELTSGSLLIMAGTQHYWRHCVPKTASERINLTFRQ
158337277|Cyano|Acama  : ADCEQLFATLEAEIAWRLLPRLTAWYGDPGYRYSGISMEPWTPTLRQIKVAIETVEFNSVLLNFYRHGQSMGWHSDDEPELPNPVIGSVSLGGCRRFLLNLTNGSLLLMQGTQHFWQHHVPKTRDPRINLTFRV
38505765|Chroo|SynspP  : VEASRYYDRLEKEICWQPLPRLTAWYGDPEYTYSGIAMEPWIPLLQTIKTKAETATFNSVLLNFYRTGTGVSWHADDEPELKNYPIASVSFGGTRRFLLILTSGSILLMLGTQEYWLHQVPKTKEPRINLTFRF
93004919|Gamma|Psycr   : ------FYNLVTELPWQITTRQIVWMGDSDYQYSGHTRQPWTDTVFHVKHHIEQANFNSCLLNYYPSGEGMGYHADDERELEQPVIASLSLGATRKFVFYLESGQLIVMHGTQSFWKHSITKTKTGRISLTFRQ
120555576|Gamma|Maraq  : GQTDDFFRRLLEEIPWAVTRRKVAWYGDRPYTYSRATKQPWVPVLAELKALVEQEPYNSCLLNLYHSGEAMGWHSDDEPELKHGAIASVSLGAPRRFVFMLEHGSLLVMSGTQAFWQHSLPATKSPRINLTFRA
110640165|Bacte|Cythu  : DTADHYLNTLLQDIEWKITKRKVAWYGDRAYTYSNTTKQIWTKELLELKQLVEKDTFNSCLLNLYHTGEGMAWHSDDEKSLLNTCIASLSFGAERKFSLMLQHGSLLVMKGTQTNWLHCLPKTKLPRVNLTFRT
15426407|Flexi|Indci   : AEVPAWYLEQDETTTRL-RNRCAWFFGPPTYGHNDIEYHEYYPWVERIGNIFGK--FNTCLAQTHDQGARIGYHADDEDCYKDVTVATVNLTGNATFSLKLKPGDFIVLKPAQGCTKHAISDCTTNRTSLTFRW
62362155|Flexi|Aprps   : FCSHGIVVKKGYPCEGLLKGKKGGYFVLDYYFHNNVSYPE--ATMK-IKECILKIDFNASLIQIYEKGSIIGMHKDNEECYDDDGVLTLNVKGNATFSVELKEGNELLMPPYQKKFKHGVKSESEGRISVTLRV
9635791|Flexi|Chermo   : CSKFILEPVCKHDLMRTNKGKKSVYVTLDSYFHNSISYPT--GLIKDWILSKAEVPFNAALVQVYEKDCILGMHKDNESCY-NHPILTVNVSGKAVFSTELDSGDELLMPEFQRKFRHGVKSITDGRMSVTLRV
50428561|Flexi|Opuvi   : DPEYSWTDFLLFNLRKVVGKRWVTLYSKRPYSYGNITHSAWPEALTAVCQNLSVDFFDHCLFQVFEASASIGLHQDDEALIPDTEIVTLNFGSADLTTLTPLNGTVYSMPPFQKTHKHAVKSNSAKRISITFRE
50428555|Flexi|Zygvi   : NCEQTWEHFILSNLRLVLRGRRATFYSRNAYSYGNITHQPWPESLTAITQALDINEHDHCLFQVFDKQSSIQFHADDEALIPNSIITTVSIGHCELLTKQILSGPVHTMPEFQSTHLHSIKSLQEGRLSITFRD
14602400|Flexi|Cacvi   : DCEETWEHFIMGHLRLCVGQRQVTLYARNGYSYGNVTHKPWPAELTAIAKALDVEEHDHCLFQVFQQGAAINFHSDDEPLIPGSPITTLSIGHCELLTRQLLSGPIYTMPSFQETHQHSVRSLQKNRLSITFRD
75750460|Flexi|Alsvi   : QDSATIPVHVSGWEREPLRGRKAAFLSTRQYGHDKIRYDPWNEILTDFLRTVGF-QANAVLIQVYEANAGIPWHRDDEKCYEKDAILTLNFG-TATFEFHLTDGCHFIMSGWLDLK-HRVTNCSADRMSLTFRV
110611897|Flexi|Chemo  : DWQVDTILPIIRNLPYTLKGRKCYFLTTSPYGHDSVSYQPWDEVLSDILLTTGQ-RANACLIQVYEQDAKIPLHRDDEKVYAGHPILTMNFG-QASFSFELTDGQWFVMSGYLTQYKHAAFAKSVGRISLTFRN
34105713|Clost|Litch   : EDGMVVVGKLEGEVPNLLRGRDAWFFSKSGYGHDKVSYVPWAKELDKLVDCFGD--FNTALVQRYTLGGYVSWHADDEPCYHDDSIVTINFNGQAVFSISLLDRSVLIMKALQKIAKHMVRSNFDGRVSVTLRK
117413399|Potyv|Blavi  : SCNAALIHEKWGDLDSDLHGRTAWFFSKDPYGHHPIYYDPWNDELDKYLG----AKYNTALVQVYDGTRDLPYHKDDEPCYTNNPIRTVNVTGTGDLCIPMTSGTVITFPAMQENFYHAVRNPSAGRISITFRN
117413400|Potyv|Blavi  : -----------------LHGRTAWFFSKDPYGHHPIYYDPWNDELDKYLG--GA-KYNTALVQVYDGTRDLPYHKDDEPCYTNNPIRTVNVTGTGDLCIPMTSGTVITFPAMQENFYHAVRNPSAGRISITFRT
20889382|Flexi|Citle   : NISTLTSDPLLGDIPCGFRGRKAAFITKVDYGHNGMVYPSWVPSLEEIIQICGQDDFNCALINFYEANSSLGFHRDNERVYNDDPILTVCTFGEGRFTILMTAGSFFLMPKFQKKARHSVSNEM-SRVSITFRS
56692801|Flexi|Swepo   : SVQATVISEIRFEGLKILGNRVASWYTKGKYSYKGGSHEDWLDMFNNLLILNGLDYYDSVLVQEYRAGGGINFHKDDEEIFRGAKVLTVNLNGQCYFSFELVEDSYFEMPRFQEKYYHGVQGCSMGRISMTFRR
20143433|Flexi|Garla   : GAGIQWTVAFHVELLDVLLNRRAAFYSKG-YSYNGGNHVEWLDNFDSFLAINGHNYFNCVLFQQYDGGHGIGFHSDDEELFKNSKILTICIQGDCEFRFFMEAPKQFMMPEFQESHKHAVRGCSPGRISATFRR
109240523|Picor|Blara  : NKEVEYGLQLFNVLEATLRGRMALFYSDGAYAHDKYHYTGWPREVDDLAKKLGG--YNSCLVQKYDKGAYIPFHADDEPCYDNDSVITVNLNGRATFIVELHHGSILEMLPCQKLCKHSVNVRDQGRVSLTFRR
9630738|Flexi|Rupst    : EELRIMIRVLPEDFNWVLRGRGASFFSKPGHSYNGGSHTGWPKFMDQILSSTGGNYYNSCLAQIYEENSKLALHKDDESCYIGHKVLTVNLIGSATFTITIGPNEFFEMPRMQCNYFHGVSNCTPGRVSLTFRR
20522097|Flexi|Shavi   : ECGTEITVNSFGRAIEVMKGRLAAFYSRDGYSYTGYSHKGWLEGLDKLIEACGETTYNQCLVQKYEQGSRIGFHSDEQAIYKGNKILTVNAAGSGTFGINLEDGDYFQMPSFQETHKHNVVAV-TPRLSFTFRS
110835686|Flexi|Narco  : ACACGLSLPVRTLLFADLKGCTAGWYCKEDYNCPSGSHAGWPTFLDTWCEVNEIAKYNSCLYQVYKAGSSTALHSDDLGMFPEEGFLTVNLGGSATLSTVVLDGAVFEMPHLQSTHKYSVSDCSPGRASLTFRC
156616261|Flexi|Colve  : SCSCGLEMPISSVVGGDLPGRRAAWFTKDGYTYKGGKHAGWDERLDLLLEIHGFSLFDSALVQEYEQGARIGFHSDDESIFVGSEILTMQLKGTSRFAIALLGGCHFTMPAFQETHKHSVAECSSGRTSITFRV
113195534|Flexi|Pasla  : ECLCNSHIPVNSLLHDGLEGREVAWFSKGAYRCAGSELKGWPLWLTPWLELNGLTKYDCMLAQKYVEGAETGFHRDDGTLFVEESVLTVNLLGTAEFGINLGHGDYFQMPAFQGSHRHAVRNTSAGRISYTFRV
154814488|Flexi|Chrvi  : GCTHGGSGPCSVVLSIRAQNRYAGFYSKNGYSYNGGEHQNWPGWISVWMRLVGIEIYNCCLVQRYDENAKIGMHSDDEECFTGGPIYTVNIEGRATFMTELGPGDLFEMPGFQETHKHAVFETSKDRLSVTFRL
41057346|Flexi|Popmo   : ACGANLGLGVFEGAEFVVGSRKCGWYSMDGYSYNGGSHTGWPEWID-VLLTLNGVGYDCLLAQEYAQGGKLGFHRDDEPNLVGASIFTVNLYGEATFMLHLRPSQCFTMPHFQESHKHAVEGCSKGRVSLTFRV
19919920|Flexi|Blusc   : VCACGLSMAVSAVPYAELKGRDAAWYSKEDYKYNGGSHLGWPKWLQLWMQANGVETYDCMLAQRYGAQGKIGFHADNEEIFRGAPVHTVSMDGNADFGTTTLRGNVFTMPSFQETHKHAVRNTTAGRVSYTFRR
37674200|Flexi|Lilsy   : TCDCGIIMNLKDVLGHTLRGRQAAWYSIDGYKYNGGDHVGWPNWLQMWMALNGVKKYNCMLAQKYQVNSCLGFHADDEALFAGESILTVNITGEADFKVRLQEAQMFEMPPFQQTHKHAVANCTAGRISYTFRV
145651770|Flexi|Phlvi  : KCGLDLELRALLGTDLHLGNRKGGWYSTTGYKYNGGHHKGWPKWLTVWMQLNEIY-YDCCLFQVYNENGRIGYHSDDEPIFTGASILTCNLKGQADFSFQVLNGPMILMPEFQLSHKHAVCNCTAARESVTFRR
94971810|Flexi|Dapvi   : SCACGVTMELKSPVETLLRGRRAGWYSRDGYNYTGASHKGWAAWMDEWLKVLDLY-YNSCLYQVYEADATLNWHSDDESLFKGGRIATVNLSGSAVFHVELVGFGVFEMPAFQSTHKHKLSNPSNGRESVTFRR
14251191|Flexi|Acola   : ICKCGMSMPITDLVLPELRNRRAGWYSRGNYSYNGGSHQGWSNYITTWCEVNGVGKYDCCLYQVYEAEAAIGFHADDETIFPGESVLTINLEGRASFGIRVLNGPLFTMPMFQADHKHCVRGCTAGRASLTFRC
160700643|Flexi|PhlVi  : TCSCGVSMEIKTLLGSDLKGRVGGWYSKDGYLYTGGSHIGWPDWLELWMQINKVDKYNSCLYQIYEEGASVGYHADDEPIFKGEEIHTCNLSGKAVFEIEYLEGPMFTMPMFQGTHKHSVSGTTKGRESVTFRV
10314013|Flexi|Hopla   : GCSCGVAMDISSISVAELKGRKAGWYSMGDYTYNGGSHKGW-DSLLMWCEANAVPKYDSCLYQIYTEGAALGYHADDEDLFQGESILTLNLSGAAEFGVHLRGPQQFEMPAFQVTHKHSVWGCSRQRESVTFRC
9635565|Flexi|Chene    : ------ISSMIKVGPFSHSGRKALFFSEGNYGFNSVKYEGWPIVFKELY-----DRFNSCLVQHYTKAATLGLHKDDEDCYKDHEVMTINLFGKATLFFTLSHGEYILMPRFQQSYKHGVKDTQAGRISLTFRL
9630734|Flexi|Chegr    : -KVGEFKDNAIRKFASDHKGRTALFFSRGSYGFNSVTYPGWPAEFEEAY-----SRFNSCLVQIYEFGSKLGFHSDDESCYDDLEVLTVNLFGEACIAFKLSDGEFLLMPKFQQGFQHSVKYASNNRVSLTFRL
13182719|Flexi|Cloye   : NCPTGRLEEPVTIQTVLLKGRKAAFHSRGGYSYTGFTHQPWNQTLDQIIQSAGFTDFDHCLIQRYQNGYHLRPHSDNEPCYEANPILTINTEGQAEFIIRLGPNSWLLMPSLQETHKHEVIAMSEGRTSLTFRR
160707860|Clost|Pluba  : SSDIVATVTTVNPVDKSLKNRKATFFSRDFYKYVGGNHRGWNSRLDGLLLDMGFEDFDHCLCQSYDDGGSIPAHADNEACYKDVEVLTLNAVGSAKFSLGLGPKEYFLMPACQCTHKHAVQATSSGRISLTFRN
20153378|Flexi|GraviB  : SCGVRLPMRKLETPLKVLKGRRAAFYSRHSYSYTGANHAGWPEWVSNIAEKLGLEDFDHCLAQIYEEDKGINFNADDEPCYTDPEVVTVNLNGNANFHLPLSDGDVLIMPKFQKTHKHAVTGTSAGRISLTFRN
20153360|Flexi|GraviA  : EKFKSVRSLCREEIYSELKGREVAFYSRHSYKYNGGSHRGWDEALNELTQELGLDSYDHCLIQRYTAGGSIGFHADDEPCYPGGSVVTVNLHGDATFEVELHDGDVYVMGPMQQTHKHRVTSHTDGRCSITLRN
29653349|Clost|Grale   : TCSCGVQLDVYNEATIALKGRSAVFFSKLGYTYNGGSHVGWPRALEDILTAIKYSVFDHCLVQKYKMGGGVPFHADDEECYSDNPILTVNLVGKANFSTNVASGDYFLMPCFQRTHLHSVNSIDEGRISLTFRA
19744939|Flexi|Appst   : KCDLNCFIQPADVNSLHSKGRGASFYSRDLYSYTGFSHVGWPAFLDKFLSDNKINFYNQCLVQEYSTGHGLSMHKDDESIYINHQVLTVNYSGDAIFCIPLSGPQMLLMPFFQKEHRHGIKSPSKGRISLTFRL
85718600|Flexi|Altmo   : HCPCGTELKIFSAEFPPLKNREAFFFSRDGYSYTGGSHVGWPAFLDQILATAELPHFNQCLIQKYQRGASIPFHSDNEPCYVDHQVLTINLTGEAEFKTTLVENQFHLSPPFQKTHKHSVVSLSAGRVSLTFRM
9629168|Flexi|Papmo    : LCPCGLHLKIKNAEFPELTGRKAWFFSKDGYSYTGGSHAGWPNWLEKILAAIEIPEFNQCLVQQFKLQAAIPFHRDDEPCYKGHQVLTINHSGECLTQITMGFGDYYLSPVFQESHKHAVSNTTGGRVSLTFRT
```

Figure S1. Alignment of representative sets of AlkB protein sequences from bacteria, eukaryotes, and viruses.

Actin = Actinobacteria; Alpha = Alphaproteobacteria; Bacte = Bacteroidetes; Betap = Betaproteobacteria; Choan = Choanoflagellida; Chroo = Chroococcales; Cilio = Ciliophora; Clost = Closteroviridae; Cyano = Cyanobacteria; Delta = Delta-epsilon_subdivisions; Dicty = Dictyosteliida; Flexi = Flexiviridae; Fungi = Fungi; Gamma = Gammaproteobacteria; Kinet = Kinetoplastida; Metaz = Metazoa; Picor = Picornavirales; Potyv = Potyviridae; Strep = Streptophyta.

Acama = Acaryochloris marina MBIC11017; Acola = Aconitum latent virus; Alsvi = Alstroemeria virus X; Altmo = Alternanthera mosaic virus; Anoga = Anopheles gambiae; Apime = Apis mellifera; Appst = Apple stem pitting virus; Aprps = Apricot pseudo-chlorotic leaf spot virus; Arath = Arabidopsis thaliana; Aspfu = Aspergillus fumigatus Af293; Aspnid = Aspergillus nidulans FGSC A4; Aspni = Aspergillus niger CBS 513-88; Blara = Black raspberry necrosis virus; Blavi = Blackberry virus Y; Blusc = Blueberry scorch virus; Brasp = Bradyrhizobium sp. BTAi1; Burdo = Burkholderia dolosa AUO158; Cacvi = Cactus virus X; Caebr = Caenorhabditis briggsae AF16; Chegr = Cherry green ring mottle virus; Chemo = Chenopodium mosaic virus X; Chermo = Cherry mottle leaf virus; Chene = Cherry necrotic rusty mottle virus; Chrvi = Chrysanthemum virus B; Citle = Citrus leaf blotch virus; Cloye = Clover yellow mosaic virus; Colve = Coleus vein necrosis virus; Cordi = Corynebacterium diphtheriae NCTC 13129; Corgl = Corynebacterium glutamicum ATCC 13032; Cryne = Cryptococcus neoformans; Cythu = Cytophaga hutchinsonii ATCC 33406; Danre = Danio rerio; Dapvi = Daphne virus S; Dicdi = Dictyostelium discoideum AX4; Dokdo = Dokdonia donghaensis MED134; Drome = Drosophila melanogaster; Escco = Escherichia coli K12; FlabaB = Flavobacteria bacterium BBFL7; FlabaA = Flavobacteriales bacterium ALC-1; Galga = Gallus gallus; Garla = Garlic latent virus; Gibze = Gibberella zeae PH-1; Grale = Grapevine leafroll-associated virus 3; GraviA = Grapevine virus A; GraviB = Grapevine virus B; Homsa = Homo sapiens; Hopla = Hop latent virus; Idilo = Idiomarina loihiensis L2TR; Indci = Indian citrus ringspot virus; Lacbi = Laccaria bicolor S238N-H82; Leima = Leishmania major strain Friedlin; Lilsy = Lily symptomless virus; Litch = Little cherry virus 2; Maggr = Magnaporthe grisea 70-15; Maraq = Marinobacter aquaeolei VT8; Meslo = Mesorhizobium loti MAFF303099; Metfl = Methylobacillus flagellatus KT; Monbr = Monosiga brevicollis MX1; Musmu = Mus musculus; Myxxa = Myxococcus xanthus DK 1622; Narco = Narcissus common latent virus; Nemve = Nematostella vectensis; Nepca = Neptuniibacter caesariensis; Neucr = Neurospora crassa OR74A; Opuvi = Opuntia virus X; Orysa = Oryza sativa Japonica Group; Papmo = Papaya mosaic virus; Parte = Paramecium tetraurelia; Pasla = Passiflora latent carlavirus; Pedsp = Pedobacter sp. BAL39; Phlvi = Phlox virus B; Phlvi = Phlox virus S; Phopr = Photobacterium profundum 3TCK; Phypa = Physcomitrella patens; Pluba = Plum bark necrosis and stem pitting-associated virus; Popmo = Poplar mosaic virus; Pseme = Pseudomonas mendocina ymp; Psycr = Psychrobacter cryohalolentis K5; Raleu = Ralstonia eutropha JMP134; Rhopa = Rhodopseudomonas palustris CGA009; Rupst = Rupestris stem pitting-associated virus; Sacer = Saccharopolyspora erythraea NRRL 2338; Schpo = Schizosaccharomyces pombe; Shavi = Shallot virus X; Shesp = Shewanella sp. MR-7; Strco = Streptomyces coelicolor ; Strpu = Strongylocentrotus purpuratus; Swepo = Sweet potato chlorotic fleck virus; SynspW = Synechococcus sp. WH

5701; SynspP = Synechocystis sp. PCC 6803; Tetth = Tetrahymena thermophila SB210; Thefu = Thermobifida fusca YX; Trica = Tribolium castaneum; Trybr = Trypanosoma brucei TREU927; Vibvu = Vibrio vulnificus YJ016; Vitvi = Vitis vinifera; Xanca = Xanthomonas campestris; Xenla = Xenopus laevis; Yarli = Yarrowia lipolytica CLIB122; Zygvi = Zygocactus virus

The arrows indicate key residues in the conserved $HXDX_nH$ and RX_5R motifs. Numbers represent Genbank Identifier (gi) numbers.

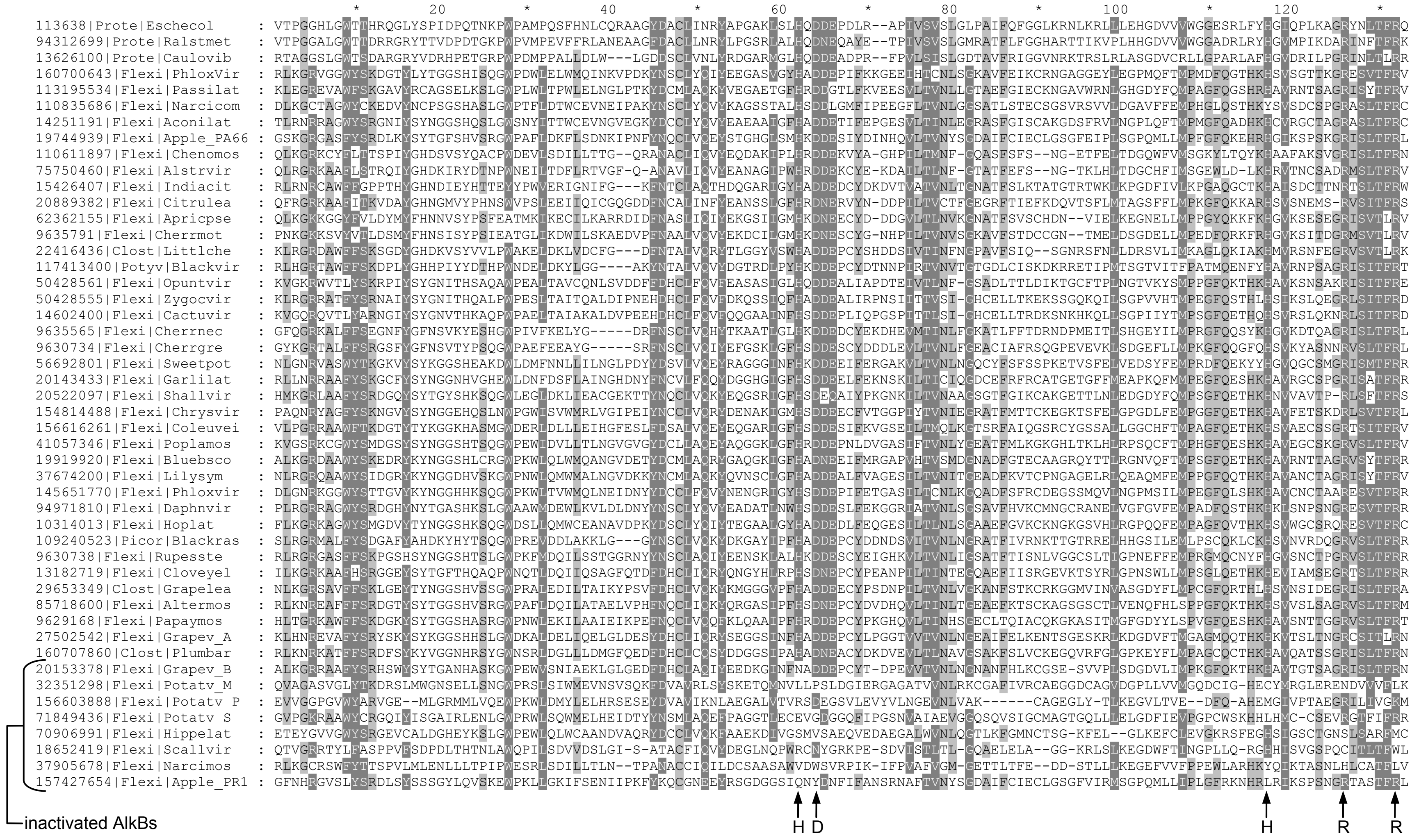
Figure S2


15426407|Flexi|Indian citrus ringspot virus
109240523|Picor|Black raspberry necrosis virus
34105713|Clost|Little cherry virus 2
117413399|Potyv|Blackberry virus Y
117413400|Potyv|Blackberry virus Y
50428561|Flexi|Opuntia virus X
50428555|Flexi|Zygocactus virus X
14602400|Flexi|Cactus virus X
56692801|Flexi|Sweet potato chlorotic fleck virus
20143433|Flexi|Garlic latent virus
41057346|Flexi|Poplar mosaic virus
110835686|Flexi|Narcissus common latent virus
14251191|Flexi|Aconitum latent virus
10314013|Flexi|Hop latent virus
94971810|Flexi|Daphne virus S
160700643|Flexi|Phlox Virus B
145651770|Flexi|Phlox virus S
113195534|Flexi|Passiflora latent carlavirus
19919920|Flexi|Blueberry scorch virus
37674200|Flexi|Lily symptomless virus
154814488|Flexi|Chrysanthemum virus B
156616261|Flexi|Coleus vein necrosis virus
20522097|Flexi|Shallot virus X
9630738|Flexi|Rupestris stem pitting-associated virus
29653349|Clost|Grapevine leafroll-associated virus 3
19744939|Flexi|Apple stem pitting virus
85718600|Flexi|Alternanthera mosaic virus
9629168|Flexi|Papaya mosaic virus
160707860|Clost|Plum bark necrosis and stem pitting-associated virus
20153378|Flexi|Grapevine virus B
20153360|Flexi|Grapevine virus A
13182719|Flexi|Clover yellow mosaic virus
62362155|Flexi|Apricot pseudo-chlorotic leaf spot virus
9635791|Flexi|Cherry mottle leaf virus
9635565|Flexi|Cherry necrotic rusty mottle virus
9630734|Flexi|Cherry green ring mottle virus
75750460|Flexi|Alstroemeria virus X
110611897|Flexi|Chenopodium mosaic virus X
20889382|Flexi|Citrus leaf blotch virus
168044851|Strep|Physcomitrella patens subsp. patens
67901590|Fungi|Aspergillus nidulans FGSC A4
46108746|Fungi|Gibberella zeae PH-1
39945158|Fungi|Magnaporthe grisea 70-15
114046475|Gamma|Shewanella sp- MR-7
167521521|Choan|Monosiga brevicollis MX1
91091410|Metaz|Tribolium castaneum
72054391|Metaz|Strongylocentrotus purpuratus
156386915|Metaz|Nematostella vectensis
68383159|Metaz|Danio rerio
48717226|Metaz|Homo sapiens
118098574|Metaz|Gallus gallus
18399917|Strep|Arabidopsis thaliana
125596881|Strep|Oryza sativa Japonica Group
87303410|Cyano|Synechococcus sp. WH 5701
149279285|Bacte|Pedobacter sp. BAL39
156378655|Metaz|Nematostella vectensis
51011105|Metaz|Danio rerio
148238118|Metaz|Xenopus laevis
21040275|Metaz|Homo sapiens
118091513|Metaz|Gallus gallus
89890637|Bacte|Flavobacteria bacterium BBFL7
86130712|Bacte|Dokdonia donghaensis MED134
163789322|Bacte|Flavobacteriales bacterium ALC-1
120555576|Gamma|Marinobacter aquaeolei VT8
110640165|Bacte|Cytophaga hutchinsonii ATCC 33406
84359602|Betap|Burkholderia dolosa AUO158
158337277|Cyano|Acaryochloris marina MBIC11017
38505765|Cyano|Synechocystis sp. PCC 6803
146306519|Gamma|Pseudomonas mendocina ymp
90413319|Gamma|Photobacterium profundum 3TCK
37676115|Gamma|Vibrio vulnificus YJ016
89092542|Gamma|Neptuniibacter caesariensis
167734879|Gamma|Xanthomonas campestris pv- campestris
93004919|Gamma|Psychrobacter cryohalolentis K5
118346635|Cilio|Tetrahymena thermophila SB210
145491776|Cilio|Paramecium tetraurelia strain d4-2
157770664|Metaz|Caenorhabditis briggsae AF16
66515297|Metaz|Apis mellifera
45555401|Metaz|Drosophila melanogaster
66472360|Metaz|Danio rerio
148223171|Metaz|Xenopus laevis
71895969|Metaz|Gallus gallus
87298840|Metaz|Homo sapiens
156523266|Metaz|Mus musculus
156392096|Metaz|Nematostella vectensis
115681547|Metaz|Strongylocentrotus purpuratus
119115270|Metaz|Anopheles gambiae str. PEST
164650570|Fungi|Laccaria bicolor S238N-H82
58262090|Fungi|Cryptococcus neoformans var- neoformans JEC21
72387544|Kinet|Trypanosoma brucei TREU927
157867117|Kinet|Leishmania major strain Friedlin
66808825|Dicty|Dictyostelium discoideum AX4
19113345|Fungi|Schizosaccharomyces pombe 972h-
50555041|Fungi|Yarrowia lipolytica CLIB122
145243552|Fungi|Aspergillus niger CBS 513-88
67527001|Fungi|Aspergillus nidulans FGSC A4
70991683|Fungi|Aspergillus fumigatus Af293
164422709|Fungi|Neurospora crassa OR74A
39951441|Fungi|Magnaporthe grisea 70-15
13474252|Alpha|Mesorhizobium loti MAFF303099
56460357|Gamma|Idiomarina loihiensis L2TR
alkB| Gamma|Escherichia coli
113638|Gamma|Escherichia coli K12
91775654|Betap|Methylobacillus flagellatus KT
39934792|Alpha|Rhodopseudomonas palustris CGA009
108763595|Delta|Myxococcus xanthus DK 1622
148254384|Alpha|Bradyrhizobium sp. BTAi1
73538928|Betap|Ralstonia eutropha JMP134
19551394|Actin|Corynebacterium glutamicum ATCC 13032
38232967|Actin|Corynebacterium diphtheriae NCTC 13129
72161831|Actin|Thermobifida fusca YX
21219556|Actin|Streptomyces coelicolor A3-2-
134099909|Actin|Saccharopolyspora erythraea NRRL 2338
115456185|Strep|Oryza sativa Japonica Group
30683015|Strep|Arabidopsis thaliana
157339904|Strep|Vitis vinifera
168038958|Strep|Physcomitrella patens subsp- patens
50

Figure S2. Phylogenetic tree constructed from the alignment shown in Fig. S1.

The scale bar represents the number of substitutions per 100 residues.

Figure S3



```
                                     *         20         *         40         *         60         *         80         *        100         *        120         *
113638|Prote|Eschecol     : VTPGGHLGWTTHRQGLYSPIDPQTNKPWPAMPQSFHNLCQRAAGYDACLINRYAPGAKLSLHQDDEPDLR--APIVSVSLGLPAIFQFGGLKRNLKRLLLEHGDVVVWGGESRLFYHGIQPLKAGRYNLTFRQ
94312699|Prote|Ralstmet   : VTPGGALGWTTDRRGRYTTVDPDTGKPWPVMPEVFFRLANEAAGFDACLLNRYLPGSRLALHQDNEQAYE--TPIVSVSLGMRATFLFGGHARTTIKVPLHHGDVVVWGGADRLRYHGVMPIKDARINFTFRK
13626100|Prote|Caulovib   : RTAGGSLGWTSDARGRYVDRHPETGRPWPDMPPALLDLW---LGDDSCLVNLYRDGARMGLHQDDEADPR--FPVLSISLGDTAVFRIGGVNRKTRSLRLASGDVCRLLGPARLAFHGVDRILPGRINLTLRR
160700643|Flexi|PhloxVir  : RLKGRVGGWYSKDGTYLYTGGSHISQGWPDWLELWMQINKVPDKYNSCLYQIYEEGASVGYHADDEPIFKKGEEIHTCNLSGKAVFEIKCRNGAGGEYLEGPMQFTMPMDFQGTHKHSVSGTTKGRESVTFRV
113195534|Flexi|Passilat  : KLEGREVAWFSKGAVYRCAGSELKSLGWPLWLTPWLELNGLPTKYDCMLAQKYVEGAETGFHRDDGTLFKVEESVLTVNLLGTAEFGIECKNGAVWRNLGHGDYFQMPAGFQGSHRHAVRNTSAGRISYTFRV
110835686|Flexi|Narcicom  : DLKGCTAGWYCKEDVYNCPSGSHASLGWPTFLDTWCEVNEIPAKYNSCLYQVYKAGSSTALHSDDLGMFIPEEGFLTVNLGGSATLSTECSGSVRSVVLDGAVFFEMPHGLQSTHKYSVSDCSPGRASLTFRC
14251191|Flexi|Aconilat   : TLRNRRAGWYSRGNIYSYNGGSHQSLGWSNYITTWCEVNGVEGKYDCCLYQVYEAEAAIGFHADDETIFEPGESVLTINLEGRASFGISCAKGDSFRVLNGPLQFTMPMGFQADHKHCVRGCTAGRASLTFRC
19744939|Flexi|Apple_PA66 : GSKGRGASFYSRDLKYSYTGFSHVSRGWPAFLDKFLSDNKIPNFYNQCLVQEYSTGHGLSMHKDDESIYDINHQVLTVNYSGDAIFCIECLGSGFEIPLSGPQMLLMPFGFQKEHRHGIKSPSKGRISLTFRL
110611897|Flexi|Chenomos  : QLKGRKCYFLTTSPIYGHDSVSYQACPWDEVLSDILLTTG--QRANACLIQVYEQDAKIPLHRDDEKVYA-GHPILTMNF-GQASFSFS--NG-ETFELTDGQWFVMSGKYLTQYKHAAFAKSVGRISLTFRN
75750460|Flexi|Alstrvir   : QLRGRKAAFLSTRQIYGHDKIRYDTNPWNEILTDFLRTVGF-Q-ANAVLIQVYEANAGIPWHRDDEKCYE-KDAILTLNF-GTATFEFS--NG-TKLHLTDGCHFIMSGEWLD-LKHRVTNCSADRMSLTFRV
15426407|Flexi|Indiacit   : RLRNRCAWFFGPPTHYGHNDIEYHTTEYYPWVERIGNIFG---KFNTCLAQTHDQGARIGYHADDEDCYDKDVTVATVNLTGNATFSLKTATGTRTWKLKPGDFIVLKPGAQGCTKHAISDCTTNRTSLTFRW
20889382|Flexi|Citrulea   : QFRGRKAAFITKVDAYGHNGMVYPHNSWVPSLEEIIQICGQGDDFNCALINFYEANSSLGFHRDNERVYN-DDPILTVCTFGEGRFTIEFKDQVTSFLMTAGSFFLMPKGFQKKARHSVSNEMS-RVSITFRS
62362155|Flexi|Apricpse   : QLKGKKGGYFVLDYMYFHNNVSYPSFEATMKIKECILKARRDIDFNASLIQIYEKGSIIGMHKDNEECYD-DDGVLTLNVKGNATFSVSCHDN--VIELKEGNELLMPPGYQKKFKHGVKSESEGRISVTLRV
9635791|Flexi|Chermot     : PNKGKKSVYVTLDSMYFHNSISYPSIEATGLIKDWILSKAEDVPFNAALVQVYEKDCILGMHKDNESCYG-NHPILTVNVSGKAVFSTDCCGN--TMELDSGDELLMPEDFQRKFRHGVKSITDGRMSVTLRV
22416436|Clost|Littlche   : KLRGRDAWFFSKSGDYGHDKVSYVVLPWAKELDKLVDCFG---DFNTALVQRYTLGGYVSWHADDEPCYSHDDSIVTINFNGPAVFSIQ--SGNRSFNLLDRSVLIMKAGLQKIAKHMVRSNFEGRVSVTLRK
117413400|Potyv|Blackvir  : RLHGRTAWFFSKDPLYGHHPIYYDTHPWNDELDKYLGG----AKYNTALVQVYDGTRDLPYHKDDEPCYDTNNPIRTVNVTGTGDLCISKDKRRETIPMTSGTVITFPATMQENFYHAVRNPSAGRISITFRT
50428561|Flexi|Opuntvir   : KVGKRWVTLYSKRPIYSYGNITHSAQAWPEALTAVCQNLSVDDFFDHCLFQVFEASASIGLHQDDEALIAPDTEIVTLNF-GSADLTTLDIKTGCFTPLNGTVKYSMPPGFQKTHKHAVKSNSAKRISITFRE
50428555|Flexi|Zygocvir   : KLRGRRATFYSRNAIYSYGNITHQALPWPESLTAITQALDIPNEHDHCLFQVFDKQSSIQFHADDEALIRPNSIITTVSI-GHCELLTKEKSSGQKQILSGPVVHTMPEGFQSTHLHSIKSLQEGRLSITFRD
14602400|Flexi|Cactuvir   : KVGQRQVTLYARNGIYSYGNVTHKAQPWPAELTAIAKALDVPEEHDHCLFQVFQQGAAINFHSDDEPLIQPGSPITTLSI-GHCELLTRDKSNKHKQLLSGPIIYTMPSGFQETHQHSVRSLQKNRLSITFRD
9635565|Flexi|Cherrnec    : GFQGRKALFFSEGNFYGFNSVKYESHGWPIVFKELYG-----DRFNSCLVQHYTKAATLGLHKDDEDCYEKDHEVMTINLFGKATLFFTDRNDPMEITLSHGEYILMPRGFQQSYKHGVKDTQAGRISLTFRL
9630734|Flexi|Cherrgre    : GYKGRTALFFSRGSFYGFNSVTYPSQGWPAEFEEAYG-----SRFNSCLVQIYEFGSKLGFHSDDESCYDDDLEVLTVNLFGEACIAFRSQGPEVEVKLSDGEFLLMPKGFQQGFQHSVKYASNNRVSLTFRL
56692801|Flexi|Sweetpot   : NLGNRVASWYTKGKVYSYKGGSHEAKDWLDMFNNLLILNGLPDYYDSVLVQEYRAGGGINFHKDDEEIFERGAKVLTVNLNGQCYFSFSSPKETVSFELVEDSYFEMPRDFQEKYYHGVQGCSMGRISMTFRR
20143433|Flexi|Garlilat   : RLLNRRAAFYSKGCFYSYNGGNHVGHEWLDNFDSFLAINGHDNYFNCVLFQQYDGGHGIGFHSDDEELFEKNSKILTICIQGDCEFRFRCATGETGFFMEAPKQFMMPEGFQESHKHAVRGCSPGRISATFRR
20522097|Flexi|Shallvir   : HMKGRLAAFYSRDGQYSYTGYSHKSQGWLEGLDKLIEACGEKTTYNQCLVQKYEQGSRIGFHSDEQAIYPKGNKILTVNAAGSGTFGIKCAKGETTLNLEDGDYFQMPSGFQETHKHNVVAVTP-RLSFTFRS
154814488|Flexi|Chrysvir  : PAQNRYAGFYSKNGVYSYNGGEHQSLNWPGWISVWMRLVGIPEIYNCCLVQRYDENAKIGMHSDDEECFVTGGPIYTVNIEGRATFMTTCKEGKTSFELGPGDLFEMPGGFQETHKHAVFETSKDRLSVTFRL
156616261|Flexi|Coleuvei  : VLPGRRAAWFTKDGTYTYKGGKHASMGWDERLDLLLEIHGFESLFDSALVQEYEQGARIGFHSDDESIFKVGSEILTMQLKGTSRFAIQGSRCYGSSALLGGCHFTMPAGFQETHKHSVAECSSGRTSITFRV
41057346|Flexi|Poplamos   : KVGSRKCGWYSMDGSYSYNGGSHTSQGWPEWIDVLLTLNGVGVGYDCLLAQEYAQGGKLGFHRDDEPNLDVGASIFTVNLYGEATFMLKGKGHLTKLHLRPSQCFTMPHGFQESHKHAVEGCSKGRVSLTFRV
19919920|Flexi|Bluebsco   : ALKGRDAAWYSKEDRYKYNGGSHLCRGWPKWLQLWMQANGVDETYDCMLAQRYGAQGKIGFHADNEEIFMRGAPVHTVSMDGNADFGTECAAGRQYTTLRGNVQFTMPSGFQETHKHAVRNTTAGRVSYTFRR
37674200|Flexi|Lilysym    : NLRGRQAAWYSIDGRYKYNGGDHVSKGWPNWLQMWMALNGVDKKYNCMLAQKYQVNSCLGFHADDEALFVAGESILTVNITGEADFKVTCPNGAGELRLQEAQMFEMPPGFQQTHKHAVANCTAGRISYTFRV
145651770|Flexi|Phloxvir  : DLGNRKGGWYSTTGVYKYNGGHHKSQGWPKWLTVWMQLNEIDNYYDCCLFQVYNENGRIGYHSDDEPIFETGASILTCNLKGQADFSFRCDEGSSMQVLNGPMSILMPEGFQLSHKHAVCNCTAARESVTFRR
94971810|Flexi|Daphnvir   : PLRGRRAGWYSRDGHYNYTGASHKSLGWAAWMDEWLKVLDLDNYYNSCLYQVYEADATLNWHSDDESLFEKGGRIATVNLSGSAVFHVKCMNGCRANELVGFGVFEMPADFQSTHKHKLSNPSNGRESVTFRR
10314013|Flexi|Hoplat     : FLKGRKAGWYSMGDVYTYNGGSHKSQGWDSLLQMWCEANAVDPKYDSCLYQIYTEGAALGYHADDEDLFEQGESILTLNLSGAAEFGVKCKNGKGSVHLRGPQQFEMPAGFQVTHKHSVWGCSRQRESVTFRC
109240523|Picor|Blackras  : SLRGRMALFYSDGAFYAHDKYHYTSQGWPREVDDLAKKLG---GYNSCLVQKYDKGAYIPFHADDEPCYDDNDSVITVNLNGRATFIVRNKTTGTRRELHHGSILEMLPSCQKLCKHSVNVRDQGRVSLTFRR
9630738|Flexi|Rupesste    : RLRGRGASFFSKPGSHSYNGGSHTSLGWPKFMDQILSSTGGRNYYNSCLAQIYEENSKLALHKDDESCYEIGHKVLTVNLIGSATFTISNLVGGCSLTIGPNEFFEMPRGMQCNYFHGVSNCTPGRVSLTFRR
13182719|Flexi|Cloveyel   : ILKGRKAAFHSRGGEYSYTGFTHQAQPWNQTLDQIIQSAGFQTDFDHCLIQRYQNGYHLRPHSDNEPCYPEANPILTINTEGQAEFIISRGEVKTSYRLGPNSWLLMPSGLQETHKHEVIAMSEGRTSLTFRR
29653349|Clost|Grapelea   : NLKGRSAVFFSKLGEYTYNGGSHVSSGWPRALEDILTAIKYPSVFDHCLVQKYKMGGGVPFHADDEECYPSDNPILTVNLVGKANFSTKCRKGGMVINVASGDYFLMPCGFQRTHLHSVNSIDEGRISLTFRA
85718600|Flexi|Altermos   : RLKNREAFFFSRDGTYSYTGGSHVSRGWPAFLDQILATAELVPHFNQCLIQKYQRGASIPFHSDNEPCYDVDHQVLTINLTGEAEFKTSCKAGSGSCTLVENQFHLSPPGFQKTHKHSVVSLSAGRVSLTFRM
9629168|Flexi|Papaymos    : HLTGRKAWFFSKDGKYSYTGGSHASRGWPNWLEKILAAIEIKPEFNQCLVQQFKLQAAIPFHRDDEPCYPKGHQVLTINHSGECLTQIACQKGKASITMGFGDYYLSPVGFQESHKHAVSNTTGGRVSLTFRT
27502542|Flexi|Grapev_A   : KLHNREVAFYSRYSKYSYKGGSHHSLGWDKALDELIQELGLDESYDHCLIQRYSEGGSINFHADDEPCYLPGGTVVTVNLNGEAIFELKENTSGESKRLKDGDVFTMGAGMQQTHKHKVTSLTNGRCSITLRN
160707860|Clost|Plumbar   : RLKNRKATFFSRDFSYKYVGGNHRSYGWNSRLDGLLLDMGFQEDFDHCLCQSYDDGGSIPAHADNEACYDKDVEVLTLNAVGSAKFSLVCKEGQVRFGLGPKEYFLMPAGCQCTHKHAVQATSSGRISLTFRN
20153378|Flexi|Grapev_B   : ALKGRRAAFYSRHSWYSYTGANHASKGWPEWVSNIAEKLGLGEDFDHCLAQIYEEDKGINFNADDEPCYT-DPEVVTVNLNGNANFHLKCGSE-SVVPLSDGDVLIMPKGFQKTHKHAVTGTSAGRISLTFRN
32351298|Flexi|Potatv_M   : QVAGASVGLYTKDRSLMWGNSELLSNGWPRSLSIWMEVNSVSQKFDVAVRLSYSKETQMNVLLPSLDGIERGAGATVVNLRKCGAFIVRCAEGGDCAGVDGPLLVVMGQDCIG-HECYMRGLERENDVVVFLK
156603888|Flexi|Potatv_P  : EVVGGPGVWYARVGE--MLGRMMLVQEWPKWLDMYLELHRSESEYDVAVIKNLAEGALVTVRSDEGSVLEVYVLNGEVNLVAK------CAGEGLY-TLKEGVLTVE--DFQ-AHEMGIVPTAEGRILIVGKM
71849436|Flexi|Potatv_S   : GVPGKRAAWYCRGQIYISGAIRLENLGWPRWLSQWMELHEIDTYYNSMLAQEFPAGGTLECEVGDGGQFIPGSNVAIAEVGGQSQVSIGCMAGTGQLLLELGDFIEVPGPCWSKHHLHMC-CSEVRGTFIFRR
70906991|Flexi|Hippelat   : ETEYGVVGWYSRGEVCALDGHEYKSLGWPEWLQLWCAANDVAQRYDCCLVQKFAAEKDIVGSMVSAEQVEDAEGALWVNLQGTLKFGMNCTSG-KFEL--GLKEFCLEVGKRSFEGHSIGSCTGNSLSARFMC
18652419|Flexi|Scallvir   : QTVGRRTYLFASPPVFSDPDLTHTNLAWQPILSDVVDSLGI-S-ATACFIQVYDEGLNQPWRCNYGRKPE-SDVISTLTL-GQAELELA--GG-KRLSLKEGDWFTINGPLLQ-RGHHISVGSPQCITLTFWL
37905678|Flexi|Narcimos   : RLKGCRSWFYTTSPVLMLENLLLTPIPWESRLSDILLTLN--TPANACCIQILDCSAASAWVDWSVRPIK-IFPVAFVGM-GETTLTFE--DD-STLLLKEGEFVVFPPEWLARHKYQIKTASNLHLCATFLV
157427654|Flexi|Apple_PR1 : GFNHRGVSLYSRDLSYSSSGYLQVSKEWPKLLGKIFSENIIPKFYKQCGNEEYRSGDGGSIQNYDNFIFANSRNAFTVNYSGDAIFCIECLGSGFVIRMSGPQMLLIPLGFRKNHRLRIKSPSNGRTASTFRL
```

Figure S3. Alignment of selected viral AlkB protein sequences.

Prote = Proteobacteria (as outgroup); Flexi = Flexiviridae; Clost = Closteroviridae; Potyv = Potyviridae; Picor = Picornavirales.

Eschecol = Escherichia coli K12; Ralstmet = Ralstonia metallidurans CH34; Caulovib = Caulobacter vibrioides; PhloxVir = Phlox Virus B; Passilat = Passiflora latent carlavirus; Narcicom = Narcissus common latent virus; Aconilat = Aconitum latent virus; Apple_PA66 = Apple stem pitting virus, isolate PA66; Chenomos = Chenopodium mosaic virus X; Alstrvir = Alstroemeria virus X; Indiacit = Indian citrus ringspot virus; Citrulea = Citrus leaf blotch virus; Apricpse = Apricot pseudo-chlorotic leaf spot virus; Cherrmot = Cherry mottle leaf virus; Littlche = Little cherry virus 2; Blackvir = Blackberry virus Y; Opuntvir = Opuntia virus X; Zygocvir = Zygocactus virus X; Cactuvir = Cactus virus X; Cherrnec = Cherry necrotic rusty mottle virus; Cherrgre = Cherry green ring mottle virus; Sweetpot = Sweet potato chlorotic fleck virus; Garlilat = Garlic latent virus; Shallvir = Shallot virus X; Chrysvir = Chrysanthemum virus B; Coleuvei = Coleus vein necrosis virus; Poplamos = Poplar mosaic virus; Bluebsco = Blueberry scorch virus; Lilysym = Lily symptomless virus; Phloxvir = Phlox virus S; Daphnvir = Daphne virus S; Hoplat = Hop latent virus; Blackras = Black raspberry necrosis virus; Rupesste = Rupestris stem pitting-associated virus; Cloveyel = Clover yellow mosaic virus; Grapelea = Grapevine leafroll-associated virus 3; Altermos = Alternanthera mosaic virus; Papaymos = Papaya mosaic virus; Grapev_A = Grapevine virus A; Plumbar = Plum bark necrosis and stem pitting-associated virus.

Viruses containing an inactivated AlkB form are indicated: Grapev_B = Grapevine virus B; Potatv_M = Potato virus M; Potatv_P = Potato Virus P; Potatv_S = Potato virus S; Hippelat = Hippeastrum latent virus; Scallvir = Scallion virus X; Narcimos = Narcissus mosaic virus strain New Zealand; Apple_PR1 = Apple stem pitting virus, isolate PR1.

The arrows indicate key residues in the conserved $HXDX_nH$ and RX_5R motifs. Numbers represent Genbank Identifier (gi) numbers.