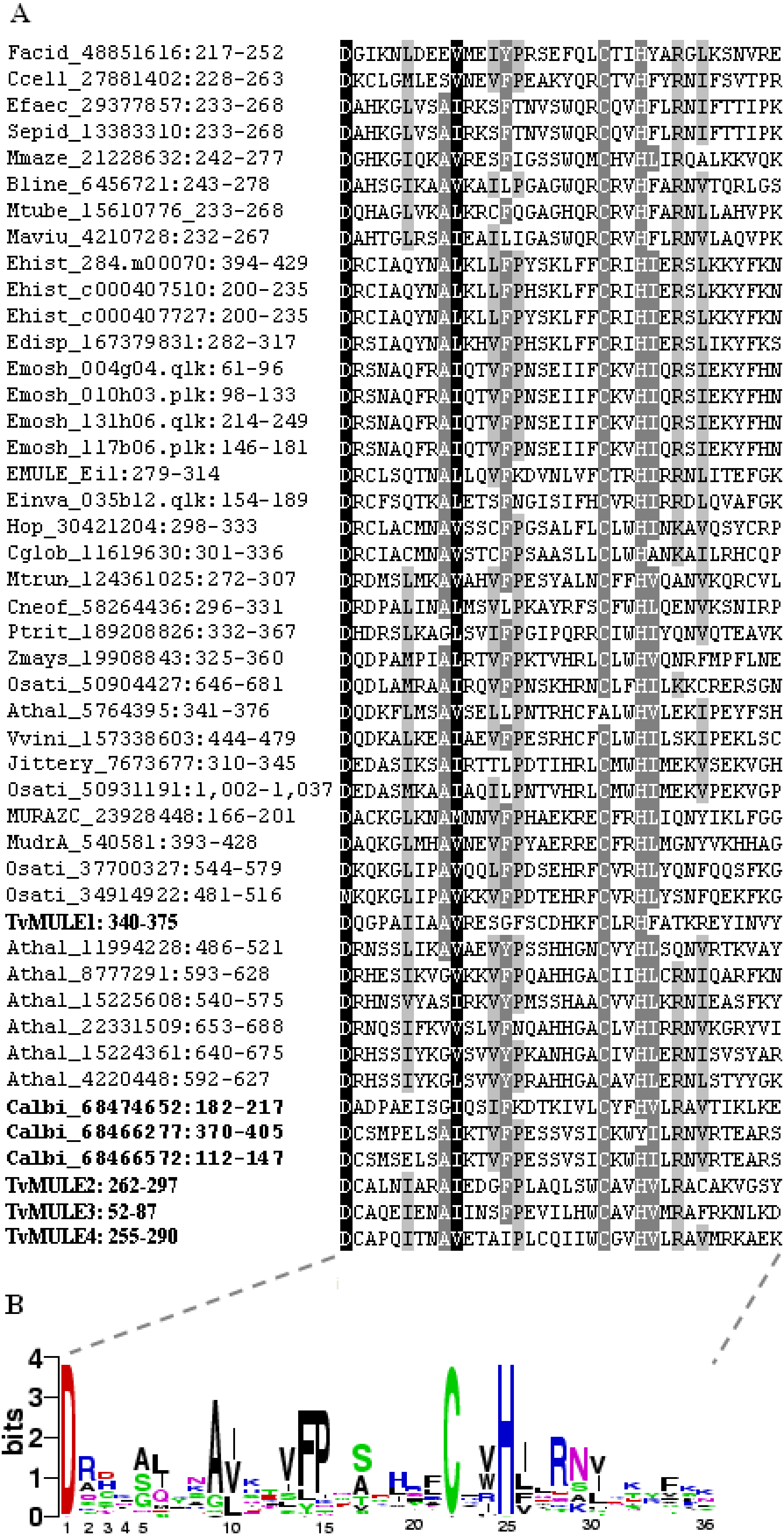

Facid_48851616:217-252	DGIKNLDEEVMEIYPRSEFQLCTIHYARGLKSNVRE
Ccell_27881402:228-263	DKCLGMLESVNEVFPEAKYQRCTVHFYRNIFSVTPR
Efaec_29377857:233-268	DAHKGLVSAIRKSFTNVSWQRCQVHFLRNIFTTIPK
Sepid_13383310:233-268	DAHKGLVSAIRKSFTNVSWQRCQVHFLRNIFTTIPK
Mmaze_21228632:242-277	DGHKGIQKAVRESFIGSSWQMCHVHLIRQALKKVQK
Bline_6456721:243-278	DAHSGIKAAVKAILPGAGWQRCRVHFARNVTQRLGS
Mtube_15610776_233-268	DQHAGLVKALKRCFQGAGHQRCRVHFARNLLAHVPK
Maviu_4210728:232-267	DAHTGLRSAIEAILIGASWQRCRVHFLRNVLAQVPK
Ehist_284.m00070:394-429	DRCIAQYNALKLLFPYSKLFFCRIHIERSLKKYFKN
Ehist_c000407510:200-235	DRCIAQYNALKLLFPHSKLFFCRIHIERSLKKYFKN
Ehist_c000407727:200-235	DRCIAQYNALKLLFPYSKLFFCRIHIERSLKKYFKN
Edisp_167379831:282-317	DRSIAQYNALKHVFPHSKLFFCRIHIERSLIKYFKS
Emosh_004g04.qlk:61-96	DRSNAQFRAIQTVFPNSEIIFCKVHIQRSIEKYFHN
Emosh_010h03.plk:98-133	DRSNAQFRAIQTVFPNSEIIFCKVHIQRSIEKYFHN
Emosh_131h06.qlk:214-249	DRSNAQFRAIQTVFPNSEIIFCKVHIQRSIEKYFHN
Emosh_117b06.plk:146-181	DRSNAQFRAIQTVFPNSEIIFCKVHIQRSIEKYFHN
EMULE_Eil:279-314	DRCLSQTNALLQVFKDVNLVFCTRHIRRNLITEFGK
Einva_035b12.qlk:154-189	DRCFSQTKALETSFNGISIFHCVRHIRRDLQVAFGK
Hop_30421204:298-333	DRCLACMNAVSSCFPGSALFLCLWHINKAVQSYCRP
Cglob_11619630:301-336	DRCIACMNAVSTCFPSAASLLCLWHANKAILRHCQP
Mtrun_124361025:272-307	DRDMSLMKAVAHVFPESYALNCFFHVQANVKQRCVL
Cneof_58264436:296-331	DRDPALINALMSVLPKAYRFSCFWHLQENVKSNIRP
Ptrit_189208826:332-367	DHDRSLKAGLSVIFPGIPQRRCIWHIYQNVQTEAVK
Zmays_19908843:325-360	DQDPAMPIALRTVFPKTVHRLCLWHVQNRFMPFLNE
Osati_50904427:646-681	DQDLAMRAAIRQVFPNSKHRNCLFHILKKCRERSGN
Athal_5764395:341-376	DQDKFLMSAVSELLPNTRHCFALWHVLEKIPEYFSH
Vvini_157338603:444-479	DQDKALKEAIAEVFPESRHCFCLWHILSKIPEKLSC
Jittery_7673677:310-345	DEDASIKSAIRTTLPDTIHRLCMWHIMEKVSEKVGH
Osati_50931191:1,002-1,037	DEDASMKAAIAQILPNTVHRLCMWHIMEKVPEKVGP
MURAZC_23928448:166-201	DACKGLKNAMNNVFPHAEKRECFRHLIQNYIKLFGG
MudrA_540581:393-428	DAQKGLMHAVNEVFPYAERRECFRHLMGNYVKHHAG
Osati_37700327:544-579	DKQKGLIPAVQQLFPDSEHRFCVRHLYQNFQQSFKG
Osati_34914922:481-516	NKQKGLIPAVKKVFPDTEHRFCVRHLYSNFQEKFKG
TvMULE1: 340-375	DQGPAIIAAVRESGFSCDHKFCLRHFATKREYINVY
Athal_11994228:486-521	DRNSSLIKAVAEVYPSSHHGNCVYHLSQNVRTKVAY
Athal_8777291:593-628	DRHESIKVGVKKVFPQAHHGACIIHLCRNIQARFKN
Athal_15225608:540-575	DRHNSVYASIRKVYPMSSHAACVVHLKRNIEASFKY
Athal_22331509:653-688	DRNQSIFKVVSLVFNQAHHGACLVHIRRNVKGRYVI
Athal_15224361:640-675	DRHSSIYKGVSVVYPKANHGACIVHLERNISVSYAR
Athal_4220448:592-627	DRHSSIYKGLSVVYPRAHHGACAVHLERNLSTYYGK
Calbi_68474652:182-217	DADPAEISGIQSIFKDTKIVLCYFHVLRAVTIKLKE
Calbi_68466277:370-405	DCSMPELSAIKTVFPESSVSICKWYILRNVRTEARS
Calbi_68466572:112-147	DCSMSELSAIKTVFPESSVSICKWHILRNVRTEARS
TvMULE2: 262-297	DCALNIARAIEDGFPLAQLSWCAVHVLRACAKVGSY
TvMULE3: 52-87	DCAQEIENAIINSFPEVILHWCAVHVMRAFRKNLKD
TvMULE4: 255-290	DCAPQITNAVETAIPLCQIIWCGVHVLRAVMRKAEK