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Supporting information for article:

Solution structure and assembly of β -amylase 2 from *Arabidopsis thaliana*

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Figure S1 Full length sequence alignment of BAM sequences from a charophyte green alga, various land plants, and a bacterium illustrating conservation of residues identified as important for the catalytic activity of Arabidopsis BAM2 (Monroe et al., 2018). Above the horizontal lines are BAM2-like sequences from the charophyte green alga, *Klebsormidium flaccidum* (kfl00081_0270), the nonvascular plants *Marchantia polymorpha* (OAE23062.1) and *Physcomitrella patens* (XP_024360526.1), the seedless vascular plant *Selaginella moellendorffii* (XP_024540821.1), the gymnosperm *Araucaria cunninghamii* (JAG96982.1), and the flowering plants *Erythranthe guttata* (XP_012843727.1), *Ricinus communis* (XP_002511858.1), *Fragaria vesca* (XP_004306786.1) and *Arabidopsis thaliana* (NP_191958.3). Below the horizontal lines are other catalytically active BAMs from Arabidopsis include BAM1 (NP_189034.1), BAM3 (NP_197368.1), BAM6 (NP_180788.2), and BAM5 (NP_567460.1) as well as BAM5 from sweet potato, *Ipomoea batatas* (XP_019180769.1) and a BAM from *Thermoanaerobacterium thermosulfurigenes* (P19584).

Kf_BAM2 1 MASRAAVLTS---NASCAALFQSVGALP--DVACKRVAQAVPARSSSQSRFEVQ-----
 Pp_BAM2 1 MSGL-QLLT^VGLVPAKSSEFVGCT---K--FSQCSNLR-LPESRSVQWGVFVSHS---WT
 Mp_BAM2 1 -----M^I---ALTPA---QSG---Q--ERKSRRGG-R-PRSLV-WQHFIVSGERTDK
 Sm_BAM2 1 MR-Q-ALLSQ---AAMDARFLCCP---V--ALLPRCHP-----K-----
 Ac_BAM2 1 -----MA---AASSFNLLRCP---N--YNISLRNS-K-TCK-RQFS--SV---KSQG
 Eg_BAM2 1 -----MA^I---NVSSPELLRRF---T--TLSTRNYA-S-PAFSVAAPLLSVN-SNCRS
 Rc_BAM2 1 -----M^I---AVSSHQLLHCP---S--PYYS-----T-ASKAQSF-LASIS-TFCCS
 Fv_BAM2 1 -----M^I---ALLSLQPFRCF---T--PRRP-----S-NVSKTTMPALSFS-PGLWG
 At_BAM2 1 -----M^I---AIR---LNHSV---I--PVSVK-LG-A-PTRVSARSSLPFS-VGDWR

 At_BAM1 1 -----MA^I-----NLSHQLGVLAGTPIKSGEMT---DS-----SLLSISPP----
 At_BAM3 1 -----ME^I-----TLNSSSSLIKRKDAKSSRNQ---BSSSNMTFAMKPP----
 At_BAM6 1 -----
 At_BAM5 1 -----
 Ib_BAM5 1 -----
 Tt_BAM 1 -----

 Kf_BAM2 50 -----TALERSGWKVAPVD---QS-----RISRMSEP-----VQNRGQ
 Pp_BAM2 50 HFSPAAISTSGQLREGSKRG-----R-----GVWCRAVEV-----E^KLPE---
 Mp_BAM2 39 SRRFNVCKSCGIDMVSRLGTMEKHI-----AFECEKADPD---GRV^KIQERLA
 Sm_BAM2 30 -----LAPAARS-----N-----HFVQA-----ITGR^KVSN--L
 Ac_BAM2 37 SFR---IKSVGLKSSSKK-----I-----HGCQ-SIVLA-LVEEK---G--E
 Eg_BAM2 43 IPK-----LCKLRESG-----VRSRA-IVGDTELKI--E
 Rc_BAM2 36 SSE---FNSCGFRASMVS-----FCTRSQNLA-VVRGK^K-QR---
 Fv_BAM2 37 SPE---FD-----SRRLR-VVGGG^KYRR---
 At_BAM2 37 GVS---TFS-G-----ARPLV--LAKV^KLRA--E

 At_BAM1 34 -----SARMMTPKAMNRNYKAHG---TDPSPMPSPILGAT^RADL--S
 At_BAM3 39 -----TYQFQ-----AKN--S
 At_BAM6 1 -----MTSVLGMNPNLINGRNLHKGSSI FVQDKE-----TKK^RVQWRLS
 At_BAM5 1 -----
 Ib_BAM5 1 -----
 Tt_BAM 1 -----MIGAFKRLGQKLF-----L--T

 Kf_BAM2 80 QAHVGIAPETLQAVEAVTASKDQNGKAEGEQIE^RERCFAG^SEYV^PIYVMLPLNT^VDES^NQ^L
 Pp_BAM2 85 -V-----DGTSTLKDL-EIEE^VT--EDLQPTV^RERDFT^GT^PN^IP^IYVMLPL^GT^IGHD^NK^V
 Mp_BAM2 85 VKSAQIIGHAAKRVKKE-GRRK^IF--EVHERDF^RERDFA^GT^IY^PIYVMLPL^NT^IDEN^NE^V
 Sm_BAM2 52 ASH-KMVS---RSSTSS-TAAAV^EEEMTKEEKE^RERDFA^GT^PV^VIYVMLPL^GI^SES^NE^L
 Ac_BAM2 69 K-----EDEKTDDSLQ-EREK^VQE--FPLKVP^RERDFA^GT^PV^VYVMLPL^GT^IDOQC^L
 Eg_BAM2 69 EEDASLLGDDNSAEASS-VHKP^VDE--IIQKVQ^RERDFT^GT^PV^VIYVMLPL^GI^NMDC^L
 Rc_BAM2 68 -TDND--SLIDNSVDSI-DDNQ^VSD--IPVEVY^RERDFT^GT^AV^VPVYVMLPL^GV^INMNC^E
 Fv_BAM2 56 -LAVV--SAEGSVENV-GDEQ^VAE--VAQIVQ^RERDFT^GT^PV^VIYVMLPL^GV^INMNSE^V
 At_BAM2 58 STEED--RVPIDDDDDSD--TDQL^VDE--EIVHFE^RERDFA^GT^AC^VPVYVMLPL^GV^IDMNSE^V

 At_BAM1 71 VACKAFAVENGIG-----TIEEQR--TYREGGIGGKKEGGG^VPV^VFV^MPL^DS^VTMG^NT^V
 At_BAM3 48 VKEMKF^THEKTFTPEGE-TLEKWE--KLH-VLSYPH^SKNDAS^VPV^VFV^MPL^DT^VTMSG^H
 At_BAM6 41 IKEGSLRTHQATAS-SA-TEPKAT--EFNT^TTYE^DKML^NV^VPVYVML^QLG^VITND^NV^L
 At_BAM5 1 -----MATN^NE^KLLLN^VPVYVML^{PL}GV^VNVEN^VF

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Ib_BAM5      1  -----MAPIPGVMPIGNYVPLIYVMLPLGVVNAENVF
Tt_BAM       16 LLTASL-----IFASSIVTANASIAPNFKVVFVVGPLEKVTDF---

Kf_BAM2     140 HNPEQLKDFEALK-SVGVGVMCDVWVGIVEVERECPGQYDWRGYQELFKRISGAGLKLQV
Pp_BAM2     135 TNPDDLQKFNALK-TAEVDGVMVDCWVGIVEGKEPQHVDWSGYRQLFTVVRDCGLKLQV
Mp_BAM2     142 SDPEFLKYDLRALK-SVNVGVMVDCWVGIVEGKAPQHYNWNWGYRQLFNTVREAGLKLQV
Sm_BAM2     107 VNPEGLRRDLQALK-SVNVGVMVDCWVGIVED-TPOKYNWSAYRELFTVRESDLKLQV
Ac_BAM2     120 VDPESLQKYLITLK-SANVDGVMVDCWVGIVEGQSPQKYNWSGYRELFDIVCRTKLKLQV
Eg_BAM2     126 VDPDELINHLRVLK-SINVDGVMVDCWVGIVEANAPQYNNWSGYRKLQFIVRDLNLKLQV
Rc_BAM2     122 VDPEGLWNGLKILK-SANVDGVMIDCWVGIVEGNAPQVYDWSGYRKLQFIVNELKLKLQV
Fv_BAM2     110 VEPEVLMQDLRALK-SVGVGVMVDCWVGIVEAHNPQSYNWSGYKKLQFIVRDLNLKLQV
At_BAM2     113 VEPEELLDQLRITLK-SVNVGVMVDCWVGIVESHTPQVYNWSGYKKLQFQMIRELGLKLQV
At_BAM1     124 NRRKAKASLQALK-SAGVEGIMIDVWVGIVEKESPGTYNWSGYNELLELAKLGLKLVQA
At_BAM3     104 NKPRAMNASLMALK-GAGVVGVMVDVWVGIVEKDGPMNWNWEGYAEILIQMVQKHGLKLQV
At_BAM6     96  ENEESLKKQLKLLK-QSQVDGVMVDVWVGIVESKCPKQYDWSAYRNLFATVQSFGLKLQA
At_BAM5     32  ADPETLETQLKRLKEEAGVDGVMVDVWVGIVESKCPKQYDWTAYKTLFQLIARLGLKLQA
Ib_BAM5     32  PDKEKVEGELKQVK-AAGCDGVMVDVWVGIEAKAPKQYDWSAYTELFQIVKCGLKLQA
Tt_BAM       53  ---NAFKDQLITLK-NNGVYGLITTDIWWGYVENAGENQEDWSYKTYADTVRAAGLKWVP

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Kf_BAM2 199 VMSFHQCGGNVGDDTDIPIEPWVHEIAKONPDIFFTNRKGERNPECLSWGDKERVLKGR
 Pp_BAM2 194 VMSFHQCGGNVGDDVYIPIEQWVLDIGKDNPDIFFTDKSGVVNPECLTWGDKVRVLRGR
 Mp_BAM2 201 VMSFHQCGGNVGDDTNIPIESWVLDIGKKNPDIFFTDRQGVNPECLSWGDKERVLGR
 Sm_BAM2 165 VMSFHQCGGNVGDDVNIPKFWVLEIGKENPDIFFTDKHCHRNPECLTWGDKERVLKSR
 Ac_BAM2 179 VMSLHECGGNVGDDANITTEKWILOIGEDNPDIFFMREGORNKECLTWGDKERVLGR
 Eg_BAM2 185 VMSFHECGGNVGDDVHIPIEPWVTEIGGKNPDIFFMDDRRQNRRECLTWGDKERVLGR
 Rc_BAM2 181 VMSFHECGGNVGDDVHIPIEPHWVTEIGQTNPDIFYFTDREGRRNTECLTWGDKERVLKGR
 Fv_BAM2 169 VMSFHECGGNVGDDVHIPIEPYVWTEIGQKNPDIFYFTNREGQRIVECLTWGDKERVLKGR
 At_BAM2 172 VMSFHECGGNVGDDVHIQIPEWVREIGQSNDPDIFYFTDSAGRNTTECLTWGDKQVLRGR
 At_BAM1 183 VMSFHQCGGNVGDSVTIPIEQWVVEEVDKDPDLAYTDQWGRNHEYISLGADTLPLKGR
 At_BAM3 163 VMSFHQCGGNVGDSVCSIPKFWVLEEISKNDPDIFYTDKSGRRNPEYISLGCDSVPVLRGR
 At_BAM6 155 IMSFHRCGGNIGDDVNIPKFWVLEIGDSNDPDIFYTNKSGNRNKECLSLSDNLSLFRGR
 At_BAM5 92 IMSFHQCGGNVGDIIVTIPIEQWVRDVGDNNDPDIFYTNKSGTRDIEYLSIGVDNLPVIFAGR
 Ib_BAM5 91 IMSFHQCGGNVGDAVFIPIEQWVLEIGDKNDPDIFYTNRAGNRNKEYLSLGDVNRQLFQGR
 Tt_BAM 109 IMSTHACGNVGDTVNIPIESWVWTKDTQ-DNVOYKDEAGNWDNDAVSP-----WYSC-

Kf_BAM2 259 TGLEVYDFMRSFRSAMDEFRSKGVITTEVEVGLGACGELRYPSPYPERHG-WKYPGIGEFQ
 Pp_BAM2 254 TALEVYDFMRSFRQEMDEFFMDKTIIEIEI-GLGACGELRYPSPYPERHG-WKYPGIGEFQ
 Mp_BAM2 261 TGLEIYDFMRSFRSQFDEFFEDGTIIEIEVGLGACGELRYPSPYPERHG-WKYPGIGEFQ
 Sm_BAM2 225 TGLEVYDFMRSFRQEFDFLQSGVIAEIEVGLGACGELRYPSPYVPRSG-WBYPGIGEFQ
 Ac_BAM2 239 TGLEVCFDFMRSFRMEFNDFEDGIITSEIEI-GLGPCGELRYPSPYPERHG-WKYPGIGQFQ
 Eg_BAM2 245 TALEVYDFMRSFRVEFDEFFEDGVITIEIEI-GLGPCGELRYPSPYPAKHG-WKYPGIGEFQ
 Rc_BAM2 241 TAVEVYDFMRSFRVEFDEFFEDGMITSEIEVGLGPCGELRYPSPYPAKHG-WBYPGIGEFQ
 Fv_BAM2 229 TAVEVYDFMRSFRVEFDEFFAEGITSEIEVGLGPCGELRYPSPYPAQHG-WKYPGIGEFQ
 At_BAM2 232 TALEVYDFMRSFRVEFDEFFEEKIIPETIEVGLGPCGELRYPSPYPAQFG-WKYPGIGEFQ
 At_BAM1 243 TPVQCYADFMRAFRDNFKHLL-GETTIVEIQVGMGPAGELRYPSPYPEQEGTWKYPGIGAFQ
 At_BAM3 223 TPIQVYSDFMRSFRFRFEGYI-GGVIAEIQVGMGPCGELRYPSPYSPESNCTWRFPGIGEFQ
 At_BAM6 215 TAVEVYRDYMSFRFRENMEDEIISCGVITIDIEVGLGPAGELRYPSPYSETQG-WBYPGIGEFQ
 At_BAM5 152 TAVQLYSDYMSFSENMAALIEAGGVIVDIEVGLGPAGELRYPSPYQSQGWBYPGIGEFQ
 Ib_BAM5 151 TALEVYRDFMRSFRDNMAEFLKGGDITVIEVCGGAAGELRYPSPYPERQG-WBYPGIGEFQ
 Tt_BAM 161 -LTQLYNEEYSSFASNFSSV--KDIITIKIYISGGPSGELRYPSPYNPSHG-WTYPGRGSLSQ

Kf_BAM2 318 CYDKYMMAKLTKAAEA-----RNHADWA-HGPEPAGEYNSQPODTGFFR-DGGNFDSSY
 Pp_BAM2 313 CYDKYLLEDLTKAAEA-----RGHSHWT-KPFSNAGEYNSRPQDTEFFR-DGGDYDSY
 Mp_BAM2 320 VYDKYLQKSLTKAAVQ-----RGHGDWA-RAPDNAGEYNSRPQDTGFFR-DGGDYDSY
 Sm_BAM2 284 CYDKYLKSLKQAAEA-----RGHTEWG-CCPDNAGEYNSKQOETDFFR-DGGDYDSY
 Ac_BAM2 298 CYDKYLQKNLTKAAEA-----RGHPFWG-RCPDNAGHYNSRPQDTGFFC-DGGDYDSY
 Eg_BAM2 304 CYDKYLKSLKKAEEV-----RGHSFWG-EGPENAGTYNCKPOETKFFS-DGGDYDSY
 Rc_BAM2 300 CYDKYLKSLSKAAEA-----RGHSFWA-RCPDNAGFYNSAPHETGFFR-DGGDYDSY
 Fv_BAM2 288 CYDRYLMENLTKAAEV-----RGHSFWA-RAPDNAGSYNFRQDTGFFR-DGGDYDSY
 At_BAM2 291 CYDKYLNSLTKAAEV-----RGHSFWG-RCPDNTETYNSTPHGTGFFR-DGGDYDSY
 At_BAM1 302 CYDKYSLSLKAEEV-----YCKPEWVSTGPTDAGHYNNWPEDTQFFKKGCGGNWNSY
 At_BAM3 282 CYDKYMKSLQAYAES-----IGKINWVTSQPHDAGEYKNLPEDTEFFRRD-GTWNSEY
 At_BAM6 274 CYDKYLRSYEEVRR-----ICHPEWK--LPEPAGEYNSVPEGETEFFEYSNCTYLKEE
 At_BAM5 211 CYDKYLKDKFKAAAK-----AGHPEDW--LPEPAGEYNDKPEETGFFK-KDGTIVYSEK

Ib_BAM5 210 CYDKYMYADWKEAVKQ-----AGHADWE--MPGNAGTYNDTPDKTGFFK-PNGTYKTDK
Tt_BAM 217 CYSKAAITSFQNAAMKSKYGTIAAVNSAWETSLT-DFSQISPPTDGDNFFT---NGYKITY

Kf_BAM2 370 GRWFLKWYSQQLIEHGDRVLHIDAMVFEG-T--KIAAKVSGIHWYKT--ASHAAELCAG
Pp_BAM2 365 GRFFLKWYSQVLIQHGDRVLIFANLAFEG-V--KIAAKVSGIHWYKT--ASHAAELAAG
Mp_BAM2 372 GRFFLKWYSQVLIIEHGDNVLIANLAFEG-Y--KIAAKVSGIHWYKT--ASHAAELAAG
Sm_BAM2 336 GRFFLKWYSQVLIIEHGDRVLMIAKLAFAEG-F--HTASKVSGIHWYKT--ASHAAELAAG
Ac_BAM2 350 GRFFLRWYSQVLLDHGDRVLSIANLAFEG-T--RIAAKVSGIHWYKT--ASHAAELAAG
Eg_BAM2 356 GRFFLNWYSQVLIIDHGDRVLIFANLAFEG-T--PIAAKLSGIHWYKT--ASHAAELTAG
Rc_BAM2 352 GRFFLNWYSRVLIIDHGDRVLIFANLAFEG-T--CISAKVSGIHWYKT--ASHAAELTAG
Fv_BAM2 340 GRFFLNWYSNVLDVHGDRVLIFANLAFEG-T--SIAAKLSGIHWYKT--ASHAAELTAG
At_BAM2 343 GRFFLNWYSRVLIIDHGDRVLIFANLAFEG-T--CIAAKLSGIHWYKT--ASHAAELTAG
At_BAM1 356 GDFFLSWYSQMLLDHGERILSSAKSIFEN-MGVKISVKIAGIHWHYGT--RSHAPELTAG
At_BAM3 335 GKFFLEWYSQKLLIEHGQVLIISAKGIFQC-SGAKLSGKVAIHWHYNT--RSHAAELTAG
At_BAM6 326 GNFFLSWYSQKLLIIEHGQVLIIDVANKVFLG-CKLKIAAKVSGIHWYKT--ESHAAELTAG
At_BAM5 262 GKFFMTWYSQKLIIFHGQVLIIEGANKIFAC-LKVNLAAKVSGIHWLYNH--HSHAAELTAG
Ib_BAM5 261 GKFFLTWYSQNLIIIEHGQVLIIEQANKVFCV-FRVNLIAAKVSGIHWYNYH--VSHAAELTAG
Tt_BAM 273 GNDFLTWYSQSVLTNELANIASVAHSCFDPVFNVPICAKIAGVHWLYNSPTMPHAAEYCAG

Kf_BAM2 425 FYNPHNRDGYAPIADMLARHNAAFNFTCVELITTAQEDSPEAMADPEGLVQVQLNSAWD
 Pp_BAM2 420 FYNPANRDGYAAIAQMLAKHGASFNFTCVELRTLAQAKGYPEAMADPEGLVQVQLNAAWD
 Mp_BAM2 427 FYNPSNRDGYAPIAEMLAKHKAALNFTCVELRTSSQEEGHPEAMADPEGLVQVQLNAAWD
 Sm_BAM2 391 FYNPCNRDGYVEIAEMFAKHDAALNFTCVELRTLAQEDDPEAMADPEGLVQVQLNAAWD
 Ac_BAM2 405 FYNPSNRDGYAAIAQMLKHKHDTALNFTCVELRTLAHEEGPEAMADPEGLVQVQLNAAWD
 Eg_BAM2 411 FYNPANRDGYAPIASVLLKKHETALNFTCVELRTMDQHEDDPEAMADPEGLVQVQLNAAWD
 Rc_BAM2 407 FYNPSNRDGYAPIAAMLNKHGVGLNFTCVEMRTLNQNEDEPEAMADPEGLVQVQLNAAWD
 Fv_BAM2 395 FYNPCNRDGYTPIAVMFKKHAALNFTCVELRTLNQHEDDPEAMADPEGLVQVQLNAAWD
 At_BAM2 398 FYNSSNRDGYGPIAAMFKKHDAALNFTCVELRTLDQHEDDPEAMADPEGLVQVQLNAAWD
 At_BAM1 413 YYNTRFRDGYLPIAQMALARHNAIFNFTCIEMRDHEQP---QDAI CAPEKLVNQVALATLA
 At_BAM3 392 YYNTRNHHDGYLPIAKMFNKHGVVLLNFTCIEMKDGEP---EHANCSPEGLVKQVQNATRO
 At_BAM6 383 YYNLKNRDGYRATAKIMRHHAILNFTCIEMKNTPEQP---AKAKSGPQELVQVQLSSGWR
 At_BAM5 319 YYNLFKRDGYRPIARMLSKHYGILNFTCIEMKDTDNT---AEASAPQELVQVQLSKAWK
 Ib_BAM5 318 FYNVAGRDGYRPIARMLARHHATLNFTCIEMRDSEQP---AEAKSAPQELVREVLNSGCK
 Tt_BAM 333 YYNY-----STLLDQFKASNLAMTFTCIEMDDSNAY--VSPYSAFMTLVHYVANLANN

Kf_BAM2 485 AGIPVASENALPCYDRQGYNKILENAKPRK-DPD---GRCLAFAFTYLRLNPTLMEEQNF-
 Pp_BAM2 480 AGISVASENALGCFDRQGYNKILENAKPEK-DPD---GRHLVAFTYLRLSDLEMLKEHNF-
 Mp_BAM2 487 SNISVASENALPCYDRDGYNKILENAKPLK-DPD---GRHLVAFTYLRLNPTLMEQSNL-
 Sm_BAM2 451 AGIYVASENALPCYDRDGYNKILENAKPSK-NPD---GRHISAFETYLRSLPVLMEEHNL-
 Ac_BAM2 465 AGIPVASENALPCFDRDGYNKILENAKPRN-DPD---GRHLEAFTYLRLSPTLMEKTNF-
 Eg_BAM2 471 VGIPVASENALPCYDREGYNKILENAKPFN-DPD---GRHLSAFTYLRLSPDLMEERNF-
 Rc_BAM2 467 ACIPVASENALPCYDREGYNKILENAKPLE-DPD---GRHLSVFTYLRLSAVLMERHNF-
 Fv_BAM2 455 ANIPVASENALNCHDREGYNKILENAKPRN-DPD---GRHLSAFTYLRLSPTLMEERNF-
 At_BAM2 458 ASIPVASENALPCYDREGYNKILENAKPLT-DPD---GRHLSCFETYLRRLNPTLMEQSNF-
 At_BAM1 470 AEVPLAAGENALPRYDDYHEQILLKASALNLDQNNEGEPREMCFAFTYLRLNPTLMEFQADNW-
 At_BAM3 449 AGTELAGENALERYDSSAFGQVVATN-----RSDSCNGLLAFTYLRLNKRLEFEGQNW-
 At_BAM6 440 EGIEVAGENALPRFDRNGYNQITLLNARPNGVNQDGKP--RWFQCFETYLRSLDKLNEPNF-
 At_BAM5 376 EGIEVAGENALETYGAKGYNQITLLNARPNGVNPNKPKLRMYCFETYLRSLDTPVQENNF-
 Ib_BAM5 375 EYIDVAGENALPRYDATAYNQITLLNVRPNGVNLNGPPKLMSCLETYLRLSDDLQTDNF-
 Tt_BAM 385 KGIVHNGENALAISNNN---QAYVN-----CANELTGYNFSCFTLLRLSNIVNSDGSVT

Kf_BAM2 540 KEFARFVKRHHGAEVDDLNT-----
 Pp_BAM2 535 KEFSRFVKRHHGKPVESD-----
 Mp_BAM2 542 DEFALFVKRHHGKQTHFSS-----
 Sm_BAM2 506 HEFARFVKRHHGEGV-----
 Ac_BAM2 520 YEFERFVKRMHGEAVLDLQA-----
 Eg_BAM2 526 VEFEQFVKRMHGDVSPDLEHC---LEEEAR-----TVDEKT-----
 Rc_BAM2 522 IEFERFVKRMHGDLSLSPLLL---LGFSLY-----FLIQLTI-RM-----VCWHA
 Fv_BAM2 510 MEFERFVKRMHGEAATDLQIN---PNEENT-----ADSSANL-Q-----
 At_BAM2 513 KEFERFVKRMHGEAVPDLGLA---PGTQET-----NPE-----
 At_BAM1 529 GKFFVAFVKRMHGEGRDSDHRCREEVEREAHFVHVTQPLVQ-----EAAVALTH-----
 At_BAM3 501 QQLVEFVKRMHGEKGGHGRRLSKEDTTGSDLYVGFVKGKIAENV-EEAALV-----
 At_BAM6 497 STFKMFVKRMHGANQEYCSEPE---RYNHELLPLERSRNDESL-EMFMEETEPDFPPWLD
 At_BAM5 435 ELFKKLVKRMHADQDYCGDAA---KYGHEIVPLKTSNSQLTL-EDIADAAQPSGAFKWD

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Ib_BAM5 434 ELFKKFKMHADLDPSNAI-----SPAVLERSNSAISI-DELMEATKGSRPFPPWYD
Tt_BAM  436 SEMAPFVINIVTLT-----PNGTIPVTFITINNATYYGQNVYIVGSTSDLGNWNT

Kf_BAM2 -----
Pp_BAM2 -----
Mp_BAM2 -----
Sm_BAM2 -----
Ac_BAM2 -----
Eg_BAM2 -----
Rc_BAM2 563 MAYDIKICRCLEIPVYCSYLVCQLRFHFTLW--VHLHDRCGCVWVVSQS-----
Fv_BAM2 -----
At_BAM2 -----
At_BAM1 -----
At_BAM3 -----
At_BAM6 553 ET-DMSIR-----PFESVL-SLLRSTFL-----RKKS-----
At_BAM5 491 ET-DLKVD-----G-----
Ib_BAM5 486 VT-DMPVD-----GSNPF-----
Tt_BAM  486 -TYARGPASCPTYPTWTITL-NLLPGEQIQFKAVKIDSSGNVTWEGGSNHTYTVPTSGTG
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Kf_BAM2	-----
Pp_BAM2	-----
Mp_BAM2	-----
Sm_BAM2	-----
Ac_BAM2	-----
Eg_BAM2	-----
Rc_BAM2	-----
Fv_BAM2	-----
<u>At_BAM2</u>	<u>-----</u>
At_BAM1	-----
At_BAM3	-----
At_BAM6	-----
At_BAM5	-----
Ib_BAM5	-----
Tt_BAM	544 SVTITWQN