```
                                   10        20        30        40        50        60        70
AmMYBl1 translated   MGR..SPCCVKEGMNRGAWTSMEDKILIEYIKAHGEGRWRNLPKRAGKKRCGKSCRLRWLNYLRPDIKRGNITPD   73
AmMYBl1 v2.1         MGR..SPCCVKEGMNRGAWTSMEDKILIEYIKAHGEGRWRNLPKRA............................   44
AmMYBl1 v1.0         MGR..SPCCVKEGMNRGAWTSMEDKILIEYIKAHGEGRWRNLPKRAGLKRCGKSCRLRWLNYLRPDIKRGNITPD   73
Bvg229400 crae       MGR..SPCCAKEGLNKGAWTAMEDKILIDYIKTHGEGRWRNLPKRAGLKRCGKSCRLRWLNYLRPDIKRGNITPD   73
TT2 AT5G35550.1      MGKRATTSVRREELNRGAWTDHEDKILRDYITTHGEGKWSTLPNQAGLKRCGKSCRLRWKNYLRPGIKRGNISSD   75
consensus            !!*  ******!**!*!!!!**!!!!!**!!**!!!!*!**!!**!****************************

                                80        90       100       110       120       130       140
AmMYBl1 translated   EEELILRLHKLLGNRYSLLAGRLPGRTDNEIKNYWNTNLSKRLNATNDQATNHNSKKSQNDSTKKRKKSSIMDTP  148
AmMYBl1 v2.1         ......................................................................................   44
AmMYBl1 v1.0         EEELILRLHKLLGNRWSLIAGRLP..............................................   97
Bvg229400 crae       EEELIIRLHKLLGNRWSLIAGRLPGRTDNEIKNYWNTNLSKRLNQCNNQAPN...TLTTYHKKLQKDQKNKKPIS  145
TT2 AT5G35550.1      EEELIIRLHNLLGNRWSLIAGRLPGRTDNEIKNHWNSNLRKRLPKTQTKQPK.....................RI  129
consensus            ******************************* ***** ***    *

                     150       160       170       180       190       200       210
AmMYBl1 translated   KPFNVQAIQSNVVRTRGVQCTKAFINPQPQPQPQPQPQPQPVYTNNI..ILSDNHN.......YSWTRLDEEYNKMS  214
AmMYBl1 v2.1         ......................................VYTNNI..ILSDNHN.......YSWTRLDEEYNKMS   71
AmMYBl1 v1.0         ......................................VYTNNI..ILSDNHN.......YSWTRLDEEYNKMS  124
Bvg229400 crae       IDQHKQTLESNVVRTKAVRCTKVFITPEPQPQ....QHILHANNITDVAAANHSSMVYNEDDSSLGLDEDYN.LS  215
TT2 AT5G35550.1      KHSTNNENNVCVIRTKAIRCSKTLLFSDLS.........LQKKSSTSPLPLKEQEMDQGGSSLMGDLEFDFDRIH  195
consensus                 *      ******* ***   *              ******  *******       *****!********

                          220       230       240       250       260       270       280
AmMYBl1 translated   SDFMMENNVNMGDFKLISELLTTDLMDICDFGNESMSGGSDLSSNSENDPFIFSQELLEDWLGDNQLI   282
AmMYBl1 v2.1         SDFMMENNVNMGDFKLISELLTTDLMDICDFGNESMSGGSDLSSNSENDPFIFSQELLEDWLGDNQLI   139
AmMYBl1 v1.0         SDFMMENNVNMGDFKLISELLTTDLMDICDFGNESMSGGSDLSSNSENDPFIFSQELLEDWLGDNQLI   192
Bvg229400 crae       SDFMMED.FNMGDFNLISELLTTNYSDVCDFSTECSNNASDLSPNSPEQPFVFSQELLEDWLGDQQVM   282
TT2 AT5G35550.1      SEFHFPD...LMDFDGLDCGNVTSLVSSNEILGELVPAQGNLDLNRPFTSCHHRGDD.EDWLRDFTC.   258
consensus            !*!*********!!********!**********!*******!**!*************!!!!*!****
```

X non conserved

X similar

X $\geq$ 50% conserved