

	1	10	20	30	40	50
MdoICE1_MD09G1003800	..MLFPM	SSGA	AMG	CDED.....	DAA	SWTRNSTTTHNNNNNEAEPRRNDQDSSLGASF
AthICE1_AT3G26744	MGLDGN	NGGGV	WLN	GGGGEREE..	NE	EGSWGRNQE.....DGS
AthICE2_AT1G12860	.....M	NSDG	VWLD	GSGESPEVNNG	EAA	SWVRNP.....

	60	70	80	90	100
MdoICE1_MD09G1003800	SNFKSML	EGDWY	MNNVLSNPAQDLH.....	AE	SSAQASETTLAPLQPTDSSASCS
AthICE1_AT3G26744	SQFKPML	EGDWT	SSNQPHQDQLQMLQNPDFRYFGG	EPFNPNDNLL	L..QHSIDSSSSCS
AthICE2_AT1G12860	.....D	EDWE	NNPPPPQ.....	HTNQNDFRFGG	EPLNPSENLLLLQQSIDSSSSS

	110	120	130	140	150
MdoICE1_MD09G1003800	PS.PA	FSLD	PSQP.....	PQQFL	PPKSCFSSLLNVVC.SNPPFDNSFDL
AthICE1_AT3G26744	PS.QA	FSLD	PSQ.....	QNQFL	STNNKGCLLNVPPSSANPPFDNAFE
AthICE2_AT1G12860	PLLHE	FTLDA	AASQQQQQQQQQ	QSF	LATKACIVSLLNVPTINNNTF..DDFGFDSGLFLG

	160	170	180	190	200
MdoICE1_MD09G1003800	SFQGNQPSNSSVLM	GF	FTALN	SHAQMGTPELS	SSAE
AthICE1_AT3G26744	QIH.....	APISM	MGFGSLT	..QLGNRDL	SV
AthICE2_AT1G12860	QFHGN.HQSPNS	MN	FTGLN	.....H	SV

	210	220	230	240	250
MdoICE1_MD09G1003800	..GFEGFDGSAG.AQLL	NRAKL	.....	LFPPM	GAQPTLFQKR
AthICE1_AT3G26744	PLELEGFGSPANGGFVGN	NRAKV	LKPLEV	LASS	GAQPTLFQKR
AthICE2_AT1G12860	...NSSGSCGLSPLFS	NRAKV	LKPLQV	MASS	GSQPTLFQKR

	260	270	280	290	300	310
MdoICE1_MD09G1003800	GPRYGGLESLEKK	RKRNE	EGE	...MEEGS	LDVSG	SLNYDSDDF
AthICE1_AT3G26744	GM.....	RRFSD	DDMD	..ETG	IEVSG	SLNYESDEIN
AthICE2_AT1G12860	SE.....	MKKS	SYRE	IDDTSTGI	IDIS	SLNYESDHN

↑  
a

	320	330	340	350	360	370
MdoICE1_MD09G1003800	NSNANSTVTGVEGGDR	KGKKKG	LPAKNLMAERRRRKKL	NDRLYMLRSVVPKISKMDRASI		
AthICE1_AT3G26744	.....ESVQIGGGG	KGKKKG	LPAKNLMAERRRRKKL	NDRLYMLRSVVPKISKMDRASI		
AthICE2_AT1G12860	.....NNN	KGKKKG	LPAKNLMAERRRRKKL	NDRLYMLRSVVPKISKMDRASI		

Helix-loop-helix DNA-binding domain

	380	390	400	410	420	430
MdoICE1_MD09G1003800	LGDAIDY	LKELLQ	RINDLHNELES	APP	GSLP	ASTSEHPLTPTPTSTL
AthICE1_AT3G26744	LGDAIDY	LKELLQ	RINDLHNELES	TTP	GSLP	PTPTSTL
AthICE2_AT1G12860	LGDAIDY	LKELLQ	RINDLHNELES	TTP	.....SSSL	HPLTPTPTQTL

↑  
b

	440	450	460	470	480	490
MdoICE1_MD09G1003800	L.SPK.	TQPK	VEVRV	REGRTVNIHMFCS	RRPGLLL	STMRALDNL
AthICE1_AT3G26744	LPSPK	GQAR	VEVRV	LREGRAVNIHMFCS	RRPGLLL	ATMKALDNL
AthICE2_AT1G12860	LPSPK	GQAR	VEVRV	LREGRTVNIHMFCS	RRPGLLL	STMRALDNL

↑  
c

	500	510	520
MdoICE1_MD09G1003800	LDVFRAEQ	CREN.QF	LPEQIKAVILDSACF
AthICE1_AT3G26744	LDVFRAEQ	QEGQEI	LPDOIKAVILDTAGY
AthICE2_AT1G12860	LDVFRAEQ	QEDHDV	LPEQIKAVILDTAGY