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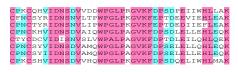
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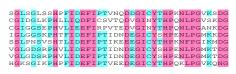
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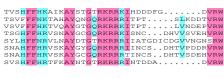
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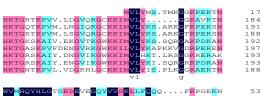
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CONSENSUS

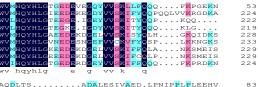
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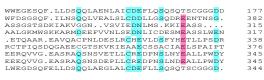


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ENPDEGE SSSGVRGGETTPKTNTPTPSLVD
250
ETGNADES DAFAARVGEKTPK SNTPQ PCRLKN
KTDVVVES DASVAKINPRTPMTDPPQRRRLNN
265
ETETACEEP EAPASVIGEKTPKTTPQPRHPKS
262
ETETAYEEP GAPASVIGEKTPKTTPQPRHPKN
262
AQELTT SDDLESMAAESNLPDFTTLFTDKHV
255

		ETITDQGKETSEINNEDNAVEDVAHM	121
Ą	SDYVTPSDYVSAH	EVSLAETSEVMCMEDEVQSIQPNHER	304
3	VDEDEIAFD	DSKMVL	270
3	VAGDEEAFD	LKMF	265
3	PCETENYDPILE	QDEEE	280
3	SCNTGQHTPTQE <mark>D</mark>	QGEEECGTSKMKTEAAECSACFAESS	305
3	PCETQQNISIVQ <mark>D</mark>	QLLLDSEGE	285
3	PCETEQSIFILQ	QLLLDGEDE	285
3	TVQEVVHNP	PEHNLYQLNRNCEINIEETVVLPPSVK	291

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DSYAEGLENIQE	
DPFFEELDSIPE	
SNIPAWCAG.	
PAIPTSDA.PVRTPMTDRPQPRRLNNSRCNTR	
PTMPAWCAVA	
PTMPAWCAVA	
TTKDGDNLQSQDQK	



		LEECQRLDPSDGTNLEL	217
		LEECQKIVL.DPSNIEL	421
IPNHGNVDYG.S	GNFS	VSDLENAEL	339
		ISDLENADL	344
		LPDLYNVDL	367
		LLDLDNTLPFTET	412
PILSQCRNEMLDGN	NGYG	LPDHHNVDL	373
		LPDLHNVDL	373
EPRETKPCLAAYAH	SAEDFKKD	LEECQRLEPTDNTNLEL	384

EN.	AS	EFR	L	SQII	E F	١.	sQ	D	SF	TTZ	V	AGGKVID	246
												GTGKTD	449
GT	LΡ			DLLS	SF	Α	SE	D	SI	MN.	. V	LGWF	361
GT	PΡ			DFL?	ΓI	Α	SQ	E	SI	LN.	. V	IGWL	366
GT	PΡ	DFQ	L	ADL	QΕ	G	so	E	sI	GN.	v	LDSI	393
PS	GG	GIS	L	DDI	. F	G	PL	D	SI	GA.	v	PDGFL	438
GT	PP	DLQ	L	ADF	QΕ	G	SQ	E	SI	GS.	v	LDRI	399
GT	PΡ	DLQ	L	ADF	QΕ	G	SQ	E	SI	GS.	. V	LDRI	399
DN	TD	EFR	L	SQII	ΞF		so	D	SF	MT.	v	AAEKITD	412
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0 '	Name	Pro-aa	Gene ID	Protein entry
8	OsNAC02	393	Os02g0594800	Q6ZI65_ORYSJ
5 7	Zem-NAC	438	Zm00014a_036995	A0A3L6FRI6_MAIZE
7	ANAC044	412	Zm00001e022870	B6TBS0_MAIZE
7	NAC1	399	NAC1	C0PGC9_MAIZE
7	NAC2	399	ZEAMMB73_Zm00001d037315	A0A1D6LWF7

Name	Pro-aa	Gene ID	Protein entry
OsNAC06	246	Os06g0267500	Q5Z9V2_ORYSJ
AtSOG1	499	At1g26390	A0A178WLI1
ARATH_NAC085	361	At5g13980	A0A178UA43
NAC_44	366	At3g00730	A0A178VDA1

## S4 Fig. The homologous analysis of NAC in plant

- **(A)** The homologous analysis of NAC proteins with amino acid sequence alignment in the rice, maize and Arabidopsis by using DNAMAN 7.0.
- (B) The Uniprot accession of 9 genes in homologous analysis. (https://www.uniprot.org/). OsNAC06 (Os06g0267500) has simple protein constructure and contains only 246 aa, which was highly homologous to *AtSOG1*. Its N-terminal region with 0 45aa was a strictly conserved region of NAM domain.