

Figure 2 - Figure Supplement 1

DSB-1 orthologs: [ST]Q in **magenta**, **similarity** and **identity** shown in green. SQ positions in DSB-1 shown in black/magenta.

CELEG.F08G5.1a	---MFPELQTLQWPIIRYKQLRGSGN---QEGKDIRVMEVNSRKLTVIHGVEPIETVYCNMEVSRYPSLKMKNTNLFVIVN	77
CBRIG.CBG03330	---MNSQNSHRGWSLLKYKEIKRSG---REVYNDVRVLLDEPKRIITVFRGMEELERIYCNMEVSKFPCCLKMKGPQLYVMVN	76
CDOUG.g17475.t1	---MYEQSSNLEWPIIRYKIKRER---REEHLNVRRAILVEPRRAIKVCGIEELEHIYLNMDVSKYPSLKMKGDLLYVLVN	76
CINOP.Sp34_40243400.	MSVLYHKGSIHNNWQIIKYKPIRRCG---REEHTDVRVLEESSKCLTVCGSEELDSIYCNMEVSKYPALKMKDTPQLYVAVN	79
CKAMA.g1992.t1	---MDSQNSTRSWKILKYQLKREN---REYDDVALEDESKRLVMTCKREELQIYYNMDVKRPSLKMKGAQLYVMVN	76
CLATE_recon_pmc	---MQHHNSCPQWPILKYKEIKRSG---REEVNNVRLLDDSKRVISVYIGNVEIEHIYCNMEVAKYPCLKMKGSHLYALVN	76
CNIGO.Cni-dsb-1.1	---MNSQNSHRGWPLLYKYKEIKRSG---REEYNDVRVLLDEPKRIITVYRGMEELERIYCNMEVSKFP---MKGPQLYVLVN	73
CREMA.FL82_03726	---MQHHNSCHQWSILKYKEIKRSG---REEYNNVRVLLDASKRLISVYIGNVEIEHIYCNMEVAKYPCLKMKSTHLYALVN	76
CSINI.Csp5_scaffold_	---MNSQNSCRQWPISIKYKEIKRNG---RTEYQNLRLVLLNESKRIIEVFKGAELEHIYCNMEVNKYPFLKMKGLQLYVMFN	76
CTRIB.g22712.t1	---MDCQPSGRQWPIIKYKQVKRSG---REEYQNVRMFLDESKRTLIVFHGTEELELVYLRMEVNRYPMLKMRGPQLYVMVN	76
CZANZ.g5350.t1	---MDSQNSCKKWLIVNYKEIKRSG---RVENQGLFVLLNESKRIILAVYQRTEELEHYVYCNMKKSKYPCLKMKGPQLYVMVN	76
CELEG.F08G5.1a	NQAQGFRLTLRGEDREN---LSTVRKFAIYIETPVKDHLNRSSTNT---DVMYNSVEKRKG---GSSSQPTSF ¹³⁷ SQ ¹⁴³ CDIDI	150
CBRIG.CBG03330	AQ ¹³⁷ QGFRLTFRDKDRNQ---MSTIRRIAYIETPEKNHLNKTFTNT---GNWGTGSGKKKNA---FTSS ¹³⁷ QPVSSSDR---PV	147
CDOUG.g17475.t1	KQGQGFRLTFHSKDRSS---MTAMRKVCYIETPEKNHNMRSFTNT---AMWAADVAQKKGS---ISF ¹³⁷ QVPNSYHYAPTCL	151
CINOP.Sp34_40243400.	NQ ¹³⁷ QGFRLTFERYDKAQ---LSIIRKIAIYIETPVKNHNMRSFTNT---DRWCTNVGK ¹³⁷ TQIT---SSSSHPISE ¹³⁷ Q---PSLT	152
CKAMA.g1992.t1	GQRQGFRLTFRDQDRQG---LEHVRNLTFIETPEKLEPSRMDWRT---NEWTSETVKTANTSFHLSSSQ ¹³⁷ QSTR---L	148
CLATE_recon_pmc	RQ ¹³⁷ QGFVRTFSAEHKAQ---MSTIRRIAYIETPEKNHNMRTFTRTGSDRWGRS---ADNNTT---ISSSQ ¹³⁷ PITPSEH-RVSR	151
CNIGO.Cni-dsb-1.1	TL ¹³⁷ QGFRLTFRDEDK ¹³⁷ Q---MSTIRRIAYIETPEKNHLNKTFTNT---GNWGTGSGKKKPT---FTSSQ ¹³⁷ PVLSDDR---PV	144
CREMA.FL82_03726	RE ¹³⁷ QGFVRTFSAEQKAQ---MSTIRRIAYIETPEKNHNMRTFTRTG-NRWGRS---ADNNTT---ISSSQ ¹³⁷ PITPSEH-RDPRT	150
CSINI.Csp5_scaffold_	AS ¹³⁷ QGFVRTFCDGDKAQ---MATIRKVAIYIETPPKNHLNKTFTST---DNWGSAGKKNP---VTSSQ ¹³⁷ PVSSGR---H	145
CTRIB.g22712.t1	SS ¹³⁷ QGFRLTFRDGDRAQ---MATIRKMAIYIETPEKNHLNKTFTKI---DNWGSSTGKKKPI---VSSSQ ¹³⁷ PVIFSDP---H	146
CZANZ.g5350.t1	NQNQGFRLTFRDEDRSR---METIRRIAYIETPEKNHLNKTFTSI---DNWGANAGVKKTM---VTSSQ ¹³⁷ PVSYSG---CH	146
CELEG.F08G5.1a	GGSVKKS---AARNLSHTYSTNIGESS---RMPALTANEF ¹⁸⁶ FSQ ¹⁸⁶ VYVNPYRNPASSASTVSSSISGAYSVLHDDSPFSGFSPN	226
CBRIG.CBG03330	PSS ¹⁸⁶ TQRPAAARNLANSLQSDFFTNR---TTTSS ¹⁸⁶ FATPATFY ¹⁸⁶ SQ ¹⁸⁶ VHNPYSRPISSASSVSSSISALSSLNDDSPFFNF ¹⁸⁶ SS	225
CDOUG.g17475.t1	GSPQKKS---AARNLATSFKATTPERAQMSPYSHSHSPVNFY ¹⁸⁶ SQ ¹⁸⁶ VHNPYSRPISSASSVSSSISAFSSLNEEGPYLSYPOS	231
CINOP.Sp34_40243400.	ETSLKKA---AARNLAKNFVSTPEFYQNS---DSPS---SPSPFY ¹⁸⁶ SQ ¹⁸⁶ VDSSYPRESNASSVSSSISAYSSLNEDSPFSGF ¹⁸⁶ SW	227
CKAMA.g1992.t1	SPPRKSPA---ARNL ¹⁸⁶ QEMAMDYNNRY---KISKNEPDMRMSH ¹⁸⁶ SQ ¹⁸⁶ VYDIYSRPPSIASSISSSISGVGSSFFDDSP---KFSD	224
CLATE_recon_pmc	GFQS---TATRNLAQNFIPELYEGS---QLSSPAISPMSS ¹⁸⁶ FSQ ¹⁸⁶ VHNPYSRPISSASSISSSISVLSLNDGPPYNF ¹⁸⁶ SV	227
CNIGO.Cni-dsb-1.1	PSS ¹⁸⁶ TQRPAAARNLANSLQSDFFTNR---TTTSS ¹⁸⁶ FATPATFY ¹⁸⁶ SQ ¹⁸⁶ VHNPYSRPISSASSVSSSISALSSLHEDSPFFNF ¹⁸⁶ SS	222
CREMA.FL82_03726	GFHSMKT---AARNLAQNFIPELYEGS---QLSSPAISPMSS ¹⁸⁶ FSQ ¹⁸⁶ VHNPYSRPISSASSISSSISVLSLNDGPPYNF ¹⁸⁶ SV	228
CSINI.Csp5_scaffold_	ASAPRKPA---AARNLAQSFQSDFFTGNYHAPPSPVPPVTFY ¹⁸⁶ SQ ¹⁸⁶ IHPNPYSRPLSSASSISSTISVMSSLNDDSPFYF ¹⁸⁶ SG	225
CTRIB.g22712.t1	ASASRKPA---AARNLAQSFQSDFFAGINHRQPTAPLQATFY ¹⁸⁶ SQ ¹⁸⁶ THNPYTRPLSSASSISSSISAMSSLNDESPMYNF ¹⁸⁶ SC	226
CZANZ.g5350.t1	ASTSKKPA---AARNLAQSYQSDFFAENY---SQ ¹⁸⁶ PSTSAKTY ¹⁸⁶ SQ ¹⁸⁶ THNPYTRPLSSASSISSSISASISALTEDESPFFSY ¹⁸⁶ SK	223
CELEG.F08G5.1a	SN-HSLQ ²⁴⁸ FPCPSPSHSSSFSGF ²⁴⁸ SSSSHS ²⁴⁸ QLSSSPANAPSFDP ²⁴⁸ FHSP ²⁴⁸ PSANDIQIDQLNPVTVAPOIKQTADKCVQTDK	305
CBRIG.CBG03330	SRCSSYMSPPRDLIRSPYSGQVSD---GSSYANLVSH ²⁴⁸ SGNS ²⁴⁸ QHSS---DPF ²⁴⁸ TQ ²⁴⁸ FSPVTTYNKCVQTDG	292
CDOUG.g17475.t1	PR-NSCPSSYSPYRKSYPYSN ²⁴⁸ SGQSDPFQSYTTLSSPDPTCF SRLS-----DHL ²⁴⁸ QPSLVKSTENKSVQTD	298
CINOP.Sp34_40243400.	SSCSSFQSSC-SAIPATPSSVNSVSSGSHSSSLKLLL-----DPYSSKNPVVHTKNQYVQTEG	283
CKAMA.g1992.t1	SR-----PS ²⁴⁸ QSSVSS ²⁴⁸ QYTSL-----QQSS-----NQYSS ²⁴⁸ QNSCDVFDK---KTEI	264
CLATE_recon_pmc	F-----	228
CNIGO.Cni-dsb-1.1	SSCSSYMSPPRDLIRSPYSGQVSDAHGSSFTNLVSH ²⁴⁸ SGNS ²⁴⁸ QHSS-----DLF ²⁴⁸ TQ ²⁴⁸ FSPVTTYNKCVQTDG	291
CREMA.FL82_03726	V-----	229
CSINI.Csp5_scaffold_	SSASSYQSL ²⁴⁸ TQSDHVKSPYSG ²⁴⁸ QVSDHYAPSHTMLACPPPLSL ²⁴⁸ SQQSS-----DPF ²⁴⁸ TQ ²⁴⁸ PSALMTDNKYVQTD	294
CTRIB.g22712.t1	SSSSSSFLPT---TPTLYSGSPASDQHAPSFNNLVSTSPLSW ²⁴⁸ SQQSP-----DPF ²⁴⁸ TQ ²⁴⁸ PSAVTSNNKSVQTD	291
CZANZ.g5350.t1	SCSSSYASG ²⁴⁸ QSDNMKSPYSG ²⁴⁸ QVSDIHAPSNTLVSTSPLSW ²⁴⁸ SQQSS-----DPF ²⁴⁸ TQ ²⁴⁸ SPSVMSKNKSVQTD	292
CELEG.F08G5.1a	QYVDER ³⁷⁵ FDD ³⁷⁵ AFLLRRYIKRVMMSDKMARLVGMM ³⁷⁵ SEIRKLPNDEFDAFYKKVKDHQRTAPSSSSKIGP ³⁷⁵ PA-----	375
CBRIG.CBG03330	SMIDNLAKD ³⁷⁵ IFIGKFLERMVSKSHVNLVRAM ³⁷⁵ REQIRKLPPGKLADFEKTKQTSSKDSALSSSI-QPS-----	361
CDOUG.g17475.t1	VLIDQLIQND ³⁷⁵ DEMNAFLMKTKSTKVNLVMT ³⁷⁵ SHIRSMDPKALDSLKRRTESYNNRITS ³⁷⁵ SQ ³⁷⁵ PSTRPP-----	368
CINOP.Sp34_40243400.	CSFDELLKNP ³⁷⁵ AFMEEYLERVKKSDELIRLVKLL ³⁷⁵ SIQKIPLSNFTEFKKAIQSLRQGGHIVPPSI-PL-----	351
CKAMA.g1992.t1	TGANFLLSN ³⁷⁵ SPQKIMKRKMMCPDFNLVKKM ³⁷⁵ VQIRMPAEKLEEFRRKTDPTRCNTFEASN---QPTISLFPKEVKD	341
CLATE_recon_pmc	-----IFFLHSRIHLCQITYALHSMALKARIRL ³⁷⁵ Q-----QSTRPVGYRGSSSNQH--QPA-----	277
CNIGO.Cni-dsb-1.1	DIIEKLAKD ³⁷⁵ IFIGKFLERMMSKPKHGNLVRAM ³⁷⁵ TQ ³⁷⁵ IRKLPPGKLADFEKTKPSSSIASVSSASI-QPN-----	360
CREMA.FL82_03726	-----PVLLPTRIHLHCQITYALHSMVLKARIRL ³⁷⁵ Q-----HSTRPVGYRGSSSNQH--QPA-----	278
CSINI.Csp5_scaffold_	NMIDRIVED ³⁷⁵ IFIGKFLERMKNKAKLAELVRTI ³⁷⁵ TQ ³⁷⁵ IRQLPADTFENFNKTTDPSCYRDTASS ³⁷⁵ SQ ³⁷⁵ -QPS-----	363
CTRIB.g22712.t1	NIMDRLAQD ³⁷⁵ IFIGKFLERMMSKPKLADLVRE ³⁷⁵ SHIRHLPSEKLEEFNKATNPSDNRDTPSYSL-QPS-----	360
CZANZ.g5350.t1	SMIDRLVED ³⁷⁵ IFIGKFLERLGKSPKANLVRAM ³⁷⁵ TQ ³⁷⁵ IRQLPAEDLVKFNKATNPSONYIASSSNYSL-QPS-----	361
CELEG.F08G5.1a	---IVQQTSDMEF-----	385
CBRIG.CBG03330	---MHHEKSDLEYDVVFENA	377
CDOUG.g17475.t1	---LVHLNSDSECDVFATT	384
CINOP.Sp34_40243400.	---VNHQSSLEN---TDN	364
CKAMA.g1992.t1	TTDVTNQTSDLEYDVFH--	358
CLATE_recon_pmc	---VTNQTSDLEYDVFH--	291
CNIGO.Cni-dsb-1.1	---MHHEKSDLEYDIFGDA	376
CREMA.FL82_03726	---VTNQTSDLEYDVFH--	292
CSINI.Csp5_scaffold_	---MSHOTSDLEYDLFANN	379
CTRIB.g22712.t1	---MTQ ³⁷⁵ QTSDEYDFVANI	376
CZANZ.g5350.t1	---LTQ ³⁷⁵ QTSDEYDVFANI	377

