

zma_100272900	MRPSLMRSTSQLRRR..SYSSASGQPERKVAILGAGGGIGQPLSILMLNPLVSSLSLYDIACITPGVAADVSHI	73
hsa_4191	MLSALARPASALRRSFTSFQNNAKVAVIGASGGIGQPLSILLNNSPLVSRLLDYDIATPGVAADLSHI	71
cel_CELF_F20H11.3	MSLEAKTLVCAANSGLRFSVSRHSSQAPKVALIGAGGGIGQPLGILLKQDPLVAHLIDYDVVNTPGVAADLSHI	75
sly_778285	MRTSMKSIIVRRSSTAGASYVSRGFSASGAPERKVAVIGAGGGIGQPLSILMLNPLVSSLSLYDIACITPGVAADVSHI	80
ath_A1g53240	...MFRSMLVRSSASAKQAVIRESFSSGSVPERKVAILGAGGGIGQPLAILMLNPLVSSLSLYDIATPGVAADVCHI	76
nta_107791114	MTISMIRSVRRTSTSGASRITRRQFSSEFAPERKVAILGAGGGIGQPLSILMLNPLVSSLSLYDIACITPGVAADVSHI	80
gmx_606509	MMKP SMLRSLHSAATRGASHIFRRGYASEFVPERKVAVIGAGGGIGQPLSILMLNPLVSSLSLYDIACITPGVAADLSHI	80
mmu_17448	MLSALARPAGAALRESFSTSFQNNAKVAVIGASGGIGQPLSILLNNSPLVSRLLDYDIATPGVAADLSHI	71
osa_Os01g0649100	MRPSLMRSASQVLRRRRGYSASGQPERKVAILGAGGGIGQPLSILMLNPLVSSLSLYDIACITPGVAADVSHI	74
dme_Dmel_CG7998	MLKQVTKQIALQGVRTFSVGGQNNYKVTVCGAGGGIGQPLSILLKQNPVLDLIDYDIATPGVAADLSHI	71
consensus	kv ga ggigqpl ll k plv l lyd tpgvaad hi	
zma_100272900	NSPALVKGFMDEQLGEALEGSDVVITIPAGVPRKPGMTRDDIFNINACIVKNLSTATAKYCPALVNMISNPVNSTVPIA	153
hsa_4191	ETKAAVKGYLSPEDLPCLKGCDDVVITIPAGVPRKPGMTRDDIFNINATIVETLIAACAQHCPEAMICVFANPVNSTIPIT	151
cel_CELF_F20H11.3	DSNAKVTATHTPEKELIYAEVENADVIITIPAGVPRKPGMTRDDIFNINACIVRDLFAVIAKASPKALIAITNPVNSTVPIA	155
sly_778285	NIRSEVAGFAEEOLGQALEGADVITIPAGVPRKPGMTRDDIFNINACIVKSLCTATAKYCPALVNMISNPVNSTVPIA	160
ath_A1g53240	NIRSEVVGGMDDNNAKALEGADVITIPAGVPRKPGMTRDDIFNINACIVKNLCTATAKYCPALVNMISNPVNSTVPIA	156
nta_107791114	NIRSEVAGFAEEOLGQALEGSDVVITIPAGVPRKPGMTRDDIFNINACIVKSLCTATAKYCPALVNMISNPVNSTVPIA	160
gmx_606509	NIRSEVVGQDEDELKALEGADVITIPAGVPRKPGMTRDDIFNINACIVKSLCTATAKYCPALVNMISNPVNSTVPIA	160
mmu_17448	ETKANVKGYLSPEDLPCLKGCDDVVITIPAGVPRKPGMTRDDIFNINATIVETLIAACAQHCPEAMICVFANPVNSTIPIT	151
osa_Os01g0649100	NAPAQVKGFMDDQLGEALEGSDIVITIPAGVPRKPGMTRDDIFNINACIVKNLCTATAKYCPALVNMISNPVNSTVPIA	154
dme_Dmel_CG7998	DTKSKTAGFICADQLGDSLKGSDDVVITIPAGVPRKPGMTRDDIFNINACIITKDISNSIAKNCPALVAILNPVNICVPIA	151
consensus	g l d ipagvprkpgmtrddifn na i a p a i npvn pi	
zma_100272900	AEVFKKAGHYDEKKIFGVTTIDVVRKTFYAGKANLPVTDVNVPVVGGHACITILPLFSCATATNALSDEDIKALTERT	233
hsa_4191	AEVFKKHGVYNNPKIFGVTTIDVVRANTFVAELKIDLPARVNVPVVGGHACITILPLISCTEKVD.FPQDQLTALTERT	230
cel_CELF_F20H11.3	SEVLKKAQVYDPKRVFGVTTIDVVRSCAFVSEIKGHDASKTVVPVGGHACITILPLISGVKISTK.FSEEEISRLTERT	234
sly_778285	AEVFKKAGHYDEKKIFGVTTIDVVRKTFYAGKAKNVVAEVLNVVGGHACITILPLFSCATKAN.LSDEEIVALTERT	239
ath_A1g53240	AEVFKKAGHYDEKKIFGVTTIDVVRKTFYAGKANVPVVAEVLNVVGGHACITILPLFSCATPOAN.LSSDILTALTERT	235
nta_107791114	AEVFKKAGHYDEKRLFGVTTIDVVRKTFYAGKAKNVSDVIVPVGGHACITILPLISCATKAN.LSDEEIVALTERT	239
gmx_606509	AEVFKKAGHYDEKKIFGVTTIDVVRKTFYAGKANVPVAGVNVPVVGGHACITILPLFSCATKAN.LDDVVIKALTERT	239
mmu_17448	AEVFKKHGVYNNPKIFGVTTIDVVRANTFVAELKIDLPARVNVPVVGGHACITILPLISCTEKVD.FPQDQLTALTERT	230
osa_Os01g0649100	AEVFKKAGHYDEKKIFGVTTIDVVRKTFYAGKANVPVTDVNVPVVGGHACITILPLFSCATATNALSDEDIKALTERT	234
dme_Dmel_CG7998	AEILKKAQVYDPKRVFGVTTIDVVRABFIGHALGVDPQTVCIPVGGHSVTTILPLVSCSQSLFK.GNQDTERTLTERT	230
consensus	e kk g y fgw ld vr f pv ggh g ti p sq p lt r	
zma_100272900	QDGGTEVVFAKAGKGSATLSMAYAGAFALACIKGLNGVPDVVECSFVQSVTTELPFAASKVRLGKNGVEEVLGIGELSD	313
hsa_4191	QDAGTEVVFAKAGKGSATLSMAYAGAFVFSILVDMNGKEGVVECSFVKSETECTYFSTPLILGKKGIEKNLGIGKVSS	310
cel_CELF_F20H11.3	QDAGTEVVFAKAGKGSATLSMAYAGAFANALVRGIKCEKNVQCAYVASDFVKGVYFSTPVLGPNCKEKLGVGKVSA	314
sly_778285	QDGGTEVVFAKAGKGSATLSMAYAGAFALACIKGLNGVPDVVECAFVQSVNTELPFAASKVRLGKNGVEEVLGIGPIND	319
ath_A1g53240	QDGGTEVVFAKAGKGSATLSMAYAGAFALACIKGLNGVPDVIECSYVQSTITELPFAASKVRLGKNGVEEVLGIGPLSD	315
nta_107791114	QDGGTEVVFAKAGKGSATLSMAYAGAFALACIKGLNGVPDVVECSFVQSVNTELPFAASKVRLGKNGVEEVLGIGPLSD	319
gmx_606509	QDGGTEVVFAKAGKGSATLSMAYAGAFALACIKGLNGVPDVVECSFVQSVTTELPFAASKVRLGKNGVEEVLGIGHISD	319
mmu_17448	QDAGTEVVFAKAGKGSATLSMAYAGAFVFSILVDMNGKEGVVECSFVQSETECTYFSTPLILGKKGIEKNLGIGKITP	310
osa_Os01g0649100	QDGGTEVVFAKAGKGSATLSMAYAGAFANALACIKGLNGVPDVVECSFVQSVTTELPFAASKVRLGKNGVEEVLGIGQLSD	314
dme_Dmel_CG7998	QDAGTEVVFAKAGKGSATLSMAYAGAFAGSLIKGLNGEKNVIECSYVQSVTTEATFSTPLVLCNKQWENLGIPKIND	310
consensus	q gtevv akag gsatlsma aga f g f lq g l	
zma_100272900	FEKEGIEIKSEKSSIEKGIKGSANDN.	340
hsa_4191	FEKEMISDAIPELKASIEKGEDVKTIK	338
cel_CELF_F20H11.3	YEKILIDASVPELNKNIEKGVASVKGN.	341
sly_778285	YEKQGIEAIKPELSSIEKGIKGAKEN.	346
ath_A1g53240	FEKEGIEAIKPELSSIEKGVKGAHQ..	341
nta_107791114	YEKKGIEALLPELSSIEKGIKGSANSN.	346
gmx_606509	FEQQGIESIKPELSSIEKGIKGAHQ..	345
mmu_17448	FEKEMIAEAIPELKASIEKGEDVKNMK	338
osa_Os01g0649100	FEKEGIENIKGELKASIEKGIKGSANA..	340
dme_Dmel_CG7998	YEKKILIEAIPELKKNIKGIKGSANA..	336
consensus	e el i kg f	

Supplementary information, Figure S10 Amino acid sequence alignments of SOM328.

Amino acid sequence alignments of SOM328 in *Arabidopsis thaliana* (ath), *Zea mays* (zma), *Solanum lycopersicum* (sly), *Nicotiana tabacum* (nta), *Glycine max* (gmx), *Oryza sativa* (osa), *Homo sapiens* (hsa), *Caenorhabditis elegans* (cel), *Mus musculus* (mmu), and *Drosophila melanogaster* (dme). The red line indicates the malate dehydrogenase domain. Dark blue and cyan shading indicate 100% and > 50% conserved amino acid residues, respectively. The red, green and purple triangles indicate the mutation sites of *som328*, *som2169* and *som2211*, respectively.