

# Figure S1

num	.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....
features	.....G.GG.G.....
Consensus	.....R.....MS.EV.D.NPYSRIMAL.M.V.Y..IR.....VG.GGGVGS.VA.MLTRCGIG.L.L.DYD.VELANMNRLF..P..G..K..AA..TL..
worm_170587840	MSKNLSEQLDALHAKLLAIGTDLICVRSNVL-DTNASVCRPKIDVMSAEVDNSNPYSRIMALKMKGIVKNYDEIRKKTVLIVGGVGSVVAEMLTRCGIGKLILFDYDKVELANMNRLFYQPQHSGMSKVDAARNTLRE
corn_226529804	-MRERLVAMMM----PAAGASRSRKIKDMSAEVDDNNPYSRIMALKRMGVVNEYERIRDYSAVIQIGGGVSVAAEMLTRCGIGKLILFDYDKVELANMNRLFYQPQHSGMSKVDAARNTLRE
fly_194889595	---MPYAIDELQEIGNRTRLEPELIDSGG--VNNTRLGRDRVERMSAEVVDNSNPYSRIMALKRMNVNIDYERIRDYKAVAVGVVGGVSVTADMLTRCGIGKLILFDYDKVELANMNRLFPTNPQAGLSKVAAAGATLNF
tick_241622411	---MALAHSLEDVRLEAIEARLKW---AEGSNPNGKISQMSSEVVDNSNPYSRIMALKRMGVVNEYERIRDYKAVAVGVVGGVSVTADMLTRCGIGKLILFDYDKVELANMNRLFPTNPQAGLSKVAAAGATLNF
frog_148225200	---MEGLIEELRSVRELEELDRVRN---QEHGHRTKIEKMSAEVVDNSNPYSRIMALKRMGVVNEYERIRDYKAVAVGVVGGVSVTADMLTRCGIGKLILFDYDKVELANMNRLFPTNPQAGLSKVAAAGATLNF
chicken_48976121	---MAERVELLERVRELERELLELR---GGRASARARIEITMSPEVTDNSNPYSRIMALKRMGVVNEYERIRDYKAVAVGVVGGVSVTADMLTRCGIGKLILFDYDKVELANMNRLFPTNPQAGLSKVAAAGATLNF
mouse_227499242	---MADSVERLQRVVELEQELARELERSR---GGDHGHCGRTRIQEMSDVLDNSNPYSRIMALKRMGVVNEYERIRDYKAVAVGVVGGVSVTADMLTRCGIGKLILFDYDKVELANMNRLFPTNPQAGLSKVAAAGATLNF
rat_57527209	---MAESVERLQRVVELEQELARELERSR---GAEGHGCGRTRIQKMSDEVVDNSNPYSRIMALKRMGVVNEYERIRDYKAVAVGVVGGVSVTADMLTRCGIGKLILFDYDKVELANMNRLFPTNPQAGLSKVAAAGATLNF
cow_155371865	---MAESVERLQRVVELEQELARELERSR---GAGDHGHCGRTRIQKMSDEVVDNSNPYSRIMALKRMGVVNEYERIRDYKAVAVGVVGGVSVTADMLTRCGIGKLILFDYDKVELANMNRLFPTNPQAGLSKVAAAGATLNF
chimp_197102922	---MAESVERLQRVVELEQELARELERSR---GAGDHGHCGRTRIQKMSDEVVDNSNPYSRIMALKRMGVVNEYERIRDYKAVAVGVVGGVSVTADMLTRCGIGKLILFDYDKVELANMNRLFPTNPQAGLSKVAAAGATLNF
man_13376212	---MAESVERLQRVVELEQELARELERSR---GAGDHGHCGRTRIQKMSDEVVDNSNPYSRIMALKRMGVVNEYERIRDYKAVAVGVVGGVSVTADMLTRCGIGKLILFDYDKVELANMNRLFPTNPQAGLSKVAAAGATLNF
num	.....140.....150.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....
features	.....Z.Z.....^~~~~~^.....
Consensus	INPDV..E....NITT.....F.....V.LVLSCVDN.EARM..N.ACNE...W.ESGVSE..AVSGH.Q..PG..ACFAC.PFLVVA..E.TLK.EGVCAASLPTTM..AG.LVQN.LK.LL.FG
worm_170587840	INPDFETNNTTIVENQFLVDFR-KGKLGKVELVLCVDNFEARMTINTACNEQIWIWMSGVSENAVGHIQCMRPGYSAFCAPVPLVNASVLTPTMVAIAGFLVQNALKFLNFG
corn_226529804	INPDVLESYSLNNTTIVENQFLVDFR-KGKLGKVELVLCVDNFEARMTINTACNEQIWIWMSGVSENAVGHIQCMRPGYSAFCAPVPLVNASVLTPTMVAIAGFLVQNALKFLNFG
fly_194889595	INPDVLEIEMPNNTTIVENQFLVDFR-QGGRIAQQPVBLVLCVDNFEARMAINAACNERLNWFESENASHGIQFIRGDTACFACAPVPLVVAEINIDEKTLKREGVCAASLPTTMCIGKLILFDYDKVELANMNRLFQPHQAGLSKVAAAGATLNF
tick_241622411	INPDVFTYNNNTTIVENQFLVDFR-TGNI-QGGFPVBLVLCVDNFEARMAINTACNEQIWIWMSGVSENAVGHIQFIRGDTACFACAPVPLVVAEINIDEKTLKREGVCAASLPTTMCIGKLILFDYDKVELANMNRLFQPHQAGLSKVAAAGATLNF
frog_148225200	INPDVQFEVHNNTTITLDNFQHFMDRIS-KGGLKEGSFVBLVLCVDNFEARMAINTACNEQIWIWMSGVSENAVGHIQFIRGDTACFACAPVPLVVAEINIDEKTLKREGVCAASLPTTMCIGKLILFDYDKVELANMNRLFQPHQAGLSKVAAAGATLNF
chicken_48976121	INPDVQFEVHNNTTITLDNFQHFMDRIS-NGALEEGKPVBLVLCVDNFEARMAINTACNEQIWIWMSGVSENAVGHIQFIRGDTACFACAPVPLVVAEINIDEKTLKREGVCAASLPTTMCIGKLILFDYDKVELANMNRLFQPHQAGLSKVAAAGATLNF
mouse_227499242	INPDVLFEVHNNTTITVNFQHFMDRIS-NGGLEEGQFPVBLVLCVDNFEARMAINTACNEQIWIWMSGVSENAVGHIQFIRGDTACFACAPVPLVVAEINIDEKTLKREGVCAASLPTTMCIGKLILFDYDKVELANMNRLFQPHQAGLSKVAAAGATLNF
rat_57527209	INPDVLFEVHNNTTITVNFQHFMDRIS-NGGLEEGQFPVBLVLCVDNFEARMAINTACNEQIWIWMSGVSENAVGHIQFIRGDTACFACAPVPLVVAEINIDEKTLKREGVCAASLPTTMCIGKLILFDYDKVELANMNRLFQPHQAGLSKVAAAGATLNF
cow_155371865	INPDVLFEVHNNTTITVNFQHFMDRIS-NGGLEEGKPVBLVLCVDNFEARMAINTACNEQIWIWMSGVSENAVGHIQFIRGDTACFACAPVPLVVAEINIDEKTLKREGVCAASLPTTMCIGKLILFDYDKVELANMNRLFQPHQAGLSKVAAAGATLNF
chimp_197102922	INPDVLFEVHNNTTITVNFQHFMDRIS-NGGLEEGKPVBLVLCVDNFEARMAINTACNEQIWIWMSGVSENAVGHIQFIRGDTACFACAPVPLVVAEINIDEKTLKREGVCAASLPTTMCIGKLILFDYDKVELANMNRLFQPHQAGLSKVAAAGATLNF
man_13376212	INPDVLFEVHNNTTITVNFQHFMDRIS-NGGLEEGKPVBLVLCVDNFEARMAINTACNEQIWIWMSGVSENAVGHIQFIRGDTACFACAPVPLVVAEINIDEKTLKREGVCAASLPTTMCIGKLILFDYDKVELANMNRLFQPHQAGLSKVAAAGATLNF
num	.....280.....290.....300.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....
features	.....Z.Z.....
Consensus	..S..LGYN..D.FP....PN..C..C..Q.E.....H..N.W.I.....G.....L.L.....
worm_170587840	EISYCLGYNALCDCFFPRHQM!LPNFSCEDRFCQQRQEECKQFVNENET----KGNEKTED-EITHEDNNNGIEVLDLESIGHTN----GCCSPGEGIGQFAYEAPIKEDTESKEQ---ISEMNLNSALMAEKL\$--
corn_226529804	QVSPLYGYNSLKDYPFAMEMRNPNCQCLNPACVHRQKEYMESPKARDAAAKTMEAEASTENECPVHLDNEWNISVLDG---EETTSIRNTPDILPEGLVRELFDADSYAGPAAPVSSAIADDDELDLQLDALNAS
fly_194889595	EVSDVYLGYNALQDPPTMOMKENQSQCDDSFCRRRQKEFREAKEAKPK----QEKAKKEEKEEIIHENEWGICLCLVSETEEDGKDRDPEATVPLGVLGVSVRLAYTVPAPOQIEEEP--TT-GTCSQSLDELMQAKNSL--
tick_241622411	TVSFLYLYGNALQDPPTMAMKPNPQCDDKYCRQKQEEFKLKEAKPK----QEVTVVVEEEBVHEDNDWIGIELVSEVSEEEELKAAS---GPVPDLPEGIKVAYTIPITPKP--TSGF--TVEDSEQSLDELMQAKNSL--
frog_148225200	TVSYYLGLYNAQMDPPTMAMKPNPQCDDKYCRQKQEEFKLKEAKPK----QEVIEHQEE-EIVHEDNDWIGIELVSEVSEEEELKAAS---GPVPDLPEGITVAYTIPKKEENLTAEE--TVAESEESLEDLMQAKNSL--
chicken_48976121	TVSFLYLYGNAMQDPPTMAMKPNPQCDDKYCRQKQEEFKKVAALPK----QEAEPQEEAEVHEDNEWGIELVSEVSEEEELKNS---GPVPLTPEGITVAYTIPKKEEDSETSEETVTAPPDDASLEDLMQAKNSL--
mouse_227499242	TVSFLYLYGNAMQDPPTMAMKPNPQCDDKYCRQKQEEFKKVAALPK----QEVATPQEEAEVHEDNEWGIELVSEVSEEEELKNS---GPVPLTPEGITVAYTIPKKEEDSETSEETVTAPPDDASLEDLMQAKNSL--
rat_57527209	TVSFLYLYGNAMQDPPTMAMKPNPQCDDKYCRQKQEEFKKVAALPK----QEVITQEEGIIHEDNEWGIELVSEVSEEEELKNS---GPVPLTPEGITVAYTIPKKEEDSETSEETVTAPPDDASLEDLMQAKNSL--
cow_155371865	TVSFLYLYGNAMQDPPTMAMKPNPQCDDKYCRQKQEEFKKVAALPK----QEVITQEEGIIHEDNEWGIELVSEVSEEEELKNS---GPVPLTPEGITVAYTIPKKEEDSETSEETVTAPPDDASLEDLMQAKNSL--
chimp_197102922	TVSFLYLYGNAMQDPPTMAMKPNPQCDDKYCRQKQEEFKKVAALPK----QEVITQEEGIIHEDNEWGIELVSEVSEEEELKNS---GPVPLTPEGITVAYTIPKKEEDSETSEETVTAPPDDASLEDLMQAKNSL--
man_13376212	TVSFLYLYGNAMQDPPTMAMKPNPQCDDKYCRQKQEEFKKVAALPK----QEVITQEEGIIHEDNEWGIELVSEVSEEEELKNS---GPVPLTPEGITVAYTIPKKEEDSETSEETVTAPPDDASLEDLMQAKNSL--

Supplementary Figure 1. Sequence alignment of UBA5. The number row corresponds to the human sequence. The NCBI GI number is included with species name. Strictly-conserved residues are shown in the Consensus line. Features include the glycine-rich motif (G), catalytic cysteine (\*), the Zinc-binding cystines (Z), and the crossover loop (^).