

Hs AMPD2 ----MRNRGQGLFRLRSLRFLHQSLPLGAGRRKGLDVAEPGSRCSRSDSPAVAAVVPAMASYPGSGKPKAKYPPFKRASLQASTAAPEARGLGAPPLQ
 At FAC1 MEPNIYQLAALAFGASFVAVSGFFMHFKALNLVLERGKERKENPDGEPQNTPLVRRRSQVRRKRVNDQYGRSPASLPDAPFTFDGGGGGGDGRSNGH
 Sc Amd1p ---MDNQATQRLNLDLSLEPAPSHDEQDGLVIDIDQRKIGDEQAGVVVDETPPLEQQDSHESLAADSRNANFSYHENQQLLENGTKQALDEHDSHSA
 Sc Yj1070p -----MQAVERRPSLLFDEYQNSVTKPNETKNEARVLSENDGDVSPSVLKQKEISVDMDMI SLPTFEFDRQM
 Sc Ybr284p -----MVQNNSEVFFVECDSEKESPSSTSPIR-----LDDLGDNAVSDQGLAFDGDVGTTSQARVNRNRA

Hs AMPD2 SARSLLPGPAPCLKHFLDLRLTSMGKCKEIAEELFTRSLAESELRSAPYEFPEESPIEQLEERRQRLERQISQDVKLEPDILLRAKQDFLTKDSDSLQL
 At FAC1 VYVDEIPPGLPRLHPTSEGRASVHGASSIRKTGSFVVRPISP-----KSPVASASAFESVEESDDDDNLTNSEGLDASYLQANGDNEMPADANE
 Sc Amd1p ILEQPSHSTNCSSSNIAMNKGHDSADHASQNSGGKP-----RTLSASAQHILPETLKSFAGAPVVKQVRTSASYKMGMLADDASQQF
 Sc Yj1070p VLGSPMFFDLEDEENKIDPLPSVSHHYGNGESDSFVSSYTP-----SNLKTGEETKDLFINPPELVSQMRKRYIAASKQDGI SNIKNDTEKW
 Sc Ybr284p QIFEDSNTDVLVHLDDLDMVP-----LNTKFDQM MEMGSPMAMP AETPPPVEPLKTKDLA

Hs AMPD2 YKEQGEQGGDRSLRERDVLEREFQRVTISGEEKCVPTDLLDAAKSVVVALFIREKYMALSLQSFCTTRRYLQQLAEKPLETRTYEQGPDTPVSADAP
 At FAC1 EQISMAASSMIRSHSVSGDLHGVPDPDIAADILRKEPEQETFFVRLNVPLEVPTDVEEAYKCLQECLELRKRYVQETVAPWEKEVISDPSPTKPNTEPF
 Sc Amd1p LDDPSSSELIDLYSKVAECRNLRAKYQTSVQNDQNPKNKPGWVYVPPPKPSYNSDTKTVPVTKNKPDAEVFDFTKCEIPGEDPDEFTLNDSDSYVH
 Sc Yj1070p FLYPKPLPKFWRFEEDKRFQDPSDSLNDGDSTGTGAAPPHRGGYYPSTFDHYHYTYSGLKKGKNIKVPYTGFEFDLEDYKQYIYHLSNQENTQN
 Sc Ybr284p YSSLAHLPSTVFFEQTHFRID-----RKCLLEMSKLRRLNYLTISKQDALSCPQLHSRVAGGYLKPVKEKLFGRHFLDLEESNT

Hs AMPD2 VHPPALEQHPYEHCEPSTMPGDGLGLRMVGRVHVHYTRREPDEHCSEVELPYDPLQEFVADVNVLMALIINGPKSFCYRRLQYLSKSKFMHVLNEMK
 At FAC1 AHYPQKSD-----HCFEMQDGVVHVFN-----KDAKEDLFPVADATAFFTDLHHVLKVI AAGNIRTLCHRRLLVLEQKFNHLHMLNADK
 Sc Amd1p RSG-----KTDELAIQIPTLRDYYLLEKMSISSDGPAKSFAYRRLQYLEARWNLYYLLNEYQ
 Sc Yj1070p PLSPYSKE-----ESLEEEFLTDVPTTFQEFRRDFAYIIELIQSHKFNESRKRLLSYLLDKFELFQYLNLSKK
 Sc Ybr284p VNLQDQNY-----MTELFNSQINIPTKFEFREDFEWCLKIIRDRSLSRFSEKRLQYLVNKKFPVQHLHSKE

Hs AMPD2 ELAAQKKVPHRDFYNIKRVDTTHIASSCMNQKHLRLFKRAMKRHLEEVHVE--QGREQTLREVFE SMNLTAYDLSVDTLDVHADRNTPHRFDKFNKY
 At FAC1 EFLAOKSAPHRDFYNIKRVDTTHVHSACMNQKHLRLFKSKLRKEPEVVI FR--DGTYLTLREVFE SLDLTGYDLNVDLVDVHADKSTFHRFDKFNKY
 Sc Amd1p ETSVSKRNPHRDFYNIKRVDTTHVHSACMNQKHLRLFKKHLRHSKDEKVI FR--DGKLLTLDEVFRSLHLTGYDLSIDTLDMHAHKDTPHRFDKFNKY
 Sc Yj1070p EILANKNVYRDFYNSRKVDRLDLSLGCISQRLSEYIWEKINLEPERIYQDPESTRKSLRDI FQFGCSSNQPIAIGLKLIDDEFLDWYRNIYLDY
 Sc Ybr284p EMRQSKKVPHKDFYNIKRVDTTHVHSACMNQKHLRLFKKHLRHSKDEKVI FR--DGKLLTLDEVFRSLHLTGYDLSIDTLDMHAHKDTPHRFDKFNKY

Hs AMPD2 NPIG-----ESVLEEIFIKTDNRVSGKYFAHIIKEVMSD--LEESKYQNAELRLSIYGRSRDE-----WDKLARWAVMHRVHSPNVRWL
 At FAC1 NPCG-----QSRLREIFLKDNLIQGRFLGEITKQVFS--LEASKYQMAEYRISYIGRKMSE-----WDQLASWIVNNDLYSENVVWL
 Sc Amd1p NPIG-----ESLREIFLKTNNYIKCTYLADITKQVIFD--LENSKYQNCYRISVYGRSLDE-----WDKLASWIVDNKVISHNVRWL
 Sc Yj1070p HLTNPKVAKLVG---KEMRFYLLAKVLEFDNPIEGEYLAEIFIKYVIHILEKSKYLAQVSVNFPYSSGED-----WYKFKSQWLLRKLVSYNIRWN
 Sc Ybr284p HLVNDEMEIHTGSHGQLRYYLIAKTFLEFDNYINGEYLAELLLKFLIKQOESKYQLCQLSVDFQFYLYHDNSVDNWNMVFANWLNHYNIFSNNIRWN

Hs AMPD2 VQVPRFLFDVYRTKQLANFQEMLENIPLPLFEATVHPASHP-----ELHLFLEHV DGFDSVDES--KPNHVFNLESPLPEAWVEE--DNPPYAYLYL
 At FAC1 IQLPRLYNIYKDMGIVTSFQNILDNIFIPLEFEATVDPDPSHP-----QLHVFLKQVVGFDLVDDES--KPE--RRPTKHMPTAQWNTNA--FNPAFSYVY
 Sc Amd1p VQIPRLYDIYKKTGIVQSFQDICKNLPQPLFEVTKNPQSHP-----KLHVFLQRVIGFDSVDES--K--VDRRFRHKYKPSLWEAP--QNPYSYLYL
 Sc Yj1070p IQIARIFPKLFKENVVSNFQEFLDLIFNPLFTLEKEQLPIDSSVNTDIIIGLQFFLSNVCSMDLVIKESDEYWKFEFTDMNCKPKFWTAQGDNPVVAHYMY
 Sc Ybr284p IRISRIPELYHTGKVKNFQEYLNLIKPLFNAENYLHKS LG-----PILLLKFLSVSSIDL CIQD TDNYIWKNF TAVSCLPKDWTSGGDNPTISQYMY

Hs AMPD2 YTFANMAMNHLRQRGFHTFVLRPFCGEAGP-----IHHLVS AFMLAEN--ISHGLLLRKAPVLYLYL LAOIGIAMSPLS-----
 At FAC1 YCYANLYVNLKRESKGMTITLRFPSGEAGD-----IDLAAATFLLTCHS--IAHGINLRKSPVLYLYL LAOIGIAMSPLS-----
 Sc Amd1p YLYSNVASLNRQAKRGFTLVLRFPCGEAGD-----PEHLVSAYLLAHG--ISHGILLRKVPVQYLYL LDOVGIAMSPLS-----
 Sc Yj1070p YIYKSLAKNFLRSQNLQNTITLRYNCSPLSS--RTSQFGVDLYFTDQVESLVNLLCNGGLLQVEPLWDATMIOYLYLFOIPILAAAPLSSVSLNSQ
 Sc Ybr284p YVYVNLTKLNHRIQALHQNTFTLRSSCSPTSMNRSTSQFSNTLNFTEHTAILNLFLLACGGFLNAENLWNAPPVSLVLYLYLFOIPIMVVAPLN-----

Hs AMPD2 -----NNSLFLSYHRNPLPEYLSRGLMVSLSLTDDEPLQFH--FTKEPLMEEYSIATQVWKLSSCDMCELARNSVLM
 At FAC1 -----NNSLFLDYHRNPFVFFLRGLNVSLSLTDDEPLQIH--LTKPELVEEYSIAASVWKL SACLCEIARNVYQ
 Sc Amd1p -----NNALFLTYDKNPFPRYFKRGLNVSLSLTDDEPLQFS--YTREPLIEEYSVAAQIYKLSNVMCELARNSVLQ
 Sc Yj1070p KSTFLKNKNVLEHLDYKQETAKINPSRDI TVGEQRSYETNPFMKMFKMGLKISLSKSLYNSSYTLEPLIEEYSVAASIYLLNPTDLCELSRTSLS
 Sc Ybr284p --SIVDSKPTMQEQAPTG-----LVLEPSKYKKNPFMKMFKMGLKISLSSESILYNSSYTKEPIIEEYSVAASIYLRHSADLCELLRNSVIT

Hs AMPD2 SGFSHKVKS HWLGPNYTKE-----GPEGNDIRRTNVDPDIRVGYRYETLCEELALITQAVQSEMLETIPEEAGITMSPGPQ
 At FAC1 SGFSHALKSHWIKDYKYR-----GPDGNDIHKTNVPHIRVEFRDTIWKEEMQVYVYLGKAVISDEVVP-----
 Sc Amd1p SGWEAQIKKHWIKDFDKS-----GVEGNDVVRTNVDPDIRINRYRDTLSTLELNVHNFANFKRTIEEK-----
 Sc Yj1070p SGYEGWYKAHWIYGVVKKAPYFEENVGGIDNWDYTDARTS IKNVPMIRRRYRKETLDQEWNFVRDHFGVINSIW-----
 Sc Ybr284p SGFSSTLKNKWLGVSLASHDYFVENTGFVDKWDYCKPNTSLEHNVPDIRRQYRSSTLAGEWRLIIA-----

FIGURE S1.—Sequence comparison of AMP deaminase homologs. Sequences of human AMP deaminase isoform 2 (AMPD2, NP_004028), *Arabidopsis thaliana* FAC1 (NP_850294) and yeast Amd1p (NP_013677), Yj1070p (NP_012465) and Ybr284p (NP_009843) were aligned using ClustalW. Residues involved in all five proteins are highlighted in yellow. Dashes indicate the gaps created for alignment. The four histidine residues involved in zinc binding and the SL(S/N)TDDP motif highly conserved in adenosine deaminases are highlighted in red.