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pdb = X-ray
pdb = template complex structure
pdb = NMR structure

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[illegible]

Protein = no catalytic Cys

NM_003336 01_UBE2A
NM_003337 02_UBE2B
NM_007019 03_UBE2C
NM_003338 04_UBE2D1
NM_003339 05_UBE2D2
NM_003340 06_UBE2D3
NM_015983 07_UBE2D4
NM_003341 08_UBE2E1
NM_152653 09_UBE2E2
NM_006357 10_UBE2E3
NM_003342 11_UBE2G1
NM_003343 12_UBE2G2
NM_003344 13_UBE2H
NM_003345 14_UBE2I
NM_003347 15_UBE2L3 1fbv
NM_004223 16_UBE2L6
NM_003969 17_UBE2M
NM_003348 18_UBE2N 2c2v
NM_021988 19_UBE2V1
NM_003350 20_UBE2V2
NM_014501 21_UBE2S
NM_004359 22_CDC34
NM_005339 23_HIP2
NM_017811 24_UBE2R2
NM_016021 25_UBE2J1
NM_058167 26_UBE2J2
NM_018299 27_UBE2W
NM_018314 28_UEV3
NM_023079 29_UBE2Z
NM_022476 29_FTS
NM_022066 30_UBE2O
NM_017582 31_UBE2Q
NM_014176 32_UBE2T
NM_080678 32_UBE2F
NM_016252 33_BIRC6
NM_152489 34_UBE2U
NM_173469 35_UBE2Q2
NM_006292 36_TSG101

(6) RRLMRDFKRLQEDPPAGVSGAPSEN-----NIMVWNAV-IFGPEGTPFEDST- - - - -KLTIEFTEE-PNKPPTVR-VSKV
(6) RRLMRDFKRLQEDPPVGVSGAPSEN-----NIMQWNAV-IFGPEGTPFEDST- - - - -FKLVIEFSEE-PNKPPTVR-LSKV
(32) KRLQQELMTLMMSGDGKISAFPESD-----NLFKVVGT-IHGAAGTVYEDLR- - - - -KLSLEFSPSG-PYNATPVK-LTLP
(3) KRIQKELSDLRDPPAHCAGPVGD-----DLDFHWQAT-IMGPPDASVQGGV- - - - -FLTIVHFPTD-PFKPPKVA-TTRK
(3) KRIHKELNDLARDPPAQCAGPVGD-----DMFHWQAT-IMGPNDSPLYQGGV- - - - -FLTIVHFPTD-PFKPPKVA-TTRK
(3) KRINKELSDLARDPPAQCAGPVGD-----DMFHWQAT-IMGPNDSPLYQGGV- - - - -FLTIVHFPTD-PFKPPKVA-TTRK
(3) KRIQKELTDLRDPPAQCAGPVGD-----DLFHWQAT-IMGPNDSPLYQGGV- - - - -FLTIVHFPTD-PFKPPKVA-TTRK
(49) KRIQKELADITLDPPNCAGPKGD-----NIYEWST-ILGPPGSVYEGGV- - - - -FLDITFTPE-PFKPPKVT-RTIR
(57) KRIQKELAEITLDPPNCAGPKGD-----NIYEWST-ILGPPGSVYEGGV- - - - -FLDITFSPD-PFKPPKVT-RTIR
(63) KRIQKELAEITLDPPNCAGPKGD-----NIYEWST-ILGPPGSVYEGGV- - - - -FLDITFSSD-PFKPPKVT-RTIR
(19) LLRLRQLAELNKNPVEGFSAGLIDN-----DLYRWEVL-ITGPPDTLYEGGV- - - - -KAHLTFPKD-PLRPPKMK-ITEE
(6) KRLMAEYKQLTLNPPEGIVAGPMNEE-----NFFEWEAL-IMGPDTCFEFGV- - - - -PAISLFPDL-PLSPKMR-TCCE
(5) VKLIESKHVITLG-----GLNEFVVK-FYGPQGTPYEGGV- - - - -KVRVDLPDK-PFKSPSIG-MNKK
(19) SRLAQERKAWRKDHPPGFVAVPTKNPDGTM-NLMNWECA-IPGKKGTPEGGGL- - - - -FKLRMLFKDD-PSSPPKCK-EPPP
(4) RRLMKLEELIRKCGMKFNRIQVDEA-----NLLTWGG-LTVPDNPVYDGEA- - - - -FRIENFPAE-PFKPPKIT-ITTK
(6) MRVVKLEEDLQKPPPYLRNLSSDA-----NVLVWHA-LLLDQPPYHLKA- - - - -NLRISFPPE-PFKPPMK-ITTK
(31) LRHQKDINELNLPKCTDISFSDPD-----DLDLNFKL-VTCDEGFKYSK- - - - -VFSFKVGGQ-PHDDPKVKCETM
(5) RRIIKETQRLAEPVPGIKAEPPDES-----NARYFHVV-IAGPQDSPFEGST- - - - -KLELFLPEE-PMAAPKVR-MTKK
(37) FRLLLEELGEGQGVGDGTVSWGLEDDEDM-----TLTRMTGM-ITGPPRIIYENRI- - - - -SLKIECGPK-PEAPPFVR-VTKK
(12) FRLLLEELGEGQGVGDGTVSWGLEDDEDM-----TLTRMTGM-ITGPPRIIYENRI- - - - -SLKVECGPK-PEAPPFVR-VTKK
(10) IRLVYKEVTTLTADPPDGIKVFPNEE-----DLTDLQVT-IEGPEGTPYAGEL- - - - -RMKLLLGKD-PASPPKGY-LTKK
(10) KALLLELKGLEQEPVEGFRVTLVDEG-----DLYNWEVA-IFGPPNTIYEGGY- - - - -FKARLKFPID-PYSPPAFR-LTKK
(6) QRIRKREFKEVLKSEETSKNQIKVLDVE-----NFTELRGE-IAGPPDTPYEGK- - - - -QLEIKIPET-PFNPPKVR-ITKK
(10) KALMLELKSLEQEPVEGFRITLVDES-----DLYNWEVA-IFGPPNTIYEGGY- - - - -FKAIKFPID-PYSPPFR-LTKK
(13) KRLMKEAELKDPTDHYHAQPLED-----NLFHWHTF-VRGPPDSDVGGV- - - - -VHGRIVLPEE-PMKPPSIILLTA
(14) QRLKQDYLRIRIKKDPVPYICAEPLPS-----NILEWHYV-VRGPEMTPYEGGY- - - - -VHGKLIFFRE-PFKPPSIYMITP
(5) KRLQKELLALQNDPPPGMTLSEKSVQN-----SITQWIVD-MEGAPGTLYEGEK- - - - -QOLLFKSSR-PFDSPPVMTGEE
(18) DLTVEELRNVNWFPHFKYSMDTYVFKDSSQKD-LNFTGT-IPVMYQNTYNIP- - - - -IRFWILDS-PFAPHICFLKPT
-----MSIYKEPPPMGFVVPDVT-----DMTKIHAI-ITGPFDTIYEGGF- - - - -FLFVRCFPD-PHHPBRVKLFDI
(70) GPFYLEYSLAEFTLVVKQLPGVYVQPSYR-SALMWFG-VIFIRHGLYQDGV- - - - -KFTVYIPDN-PDGDPCRLVVVL
(955) STVRKEMALLATSLPEGIMVKTFED-----RMDLFSAL-IGKPTRTPYEDGL- - - - -FLFDIQLPNI-PAVPPHFC-LSQV
(253) DRLMKELRDIYRSQSFKGNYAVELVND-----SLYDWNVK-LKVDQDSALHNDQLILKEGEGADFILLNFSFKDN-PFDPPFVRVVSF
(4) SRLKRELHMLATEPPPGITCWDKQD-----QMDDLRQ-ILGAGNTPYEGKV- - - - -KLEVIIPER-PFEPQIR-LTLP
(x) -LLVKEVAELLEANLPCTKVHFPDPN-----KLHCFQLT-VTPDEGYVQGGK- - - - -QFETEVPPDA-NMVPPKVKCLTKK
(4547) RRLAQEAVTSTSLPLSSSSSVFVRCDEE-----RLDIMKVL-ITGPDTPYANGC- - - - -EFDVYFPQD-PSSPPLVNLETT
(6) LLLHRDFCDLKENNYKGTAKPVSE-----DMMEWEVE-IEGLQNSVYQGLV- - - - -QLTIHFTSE-NYAPPVVK-ITII
(206) DRLMKELRDIYRSQSYKTGIYSVELIND-----SLYDWHVK-LQKVDQDSPLHNDQLILKEGEGEYILLNFSFKDN-PFDPPFVRVVSF
(17) RDLTVRETIVNVTILYKDLKPVLSVYFND-----GSSRELNM-LTGTIPVYRGNT-----YNIPICLLWLDLT-PYNPPICFVKPK

Structure-based alignment - ALL structures: (second part)

pdb = X-ray

pdb = template complex structure

pdb = NMR structure

Secondary Structure

Consensus UBCc

1fbv UBC7 UBE2L3

2C2V UBC13 UBE2N

laHPNIs..sSp1CLsILp.....GpWSsbslpsllbtlltLLSc..PssssPhss-stpbapp.....spppappscbbsschsh.
 tttttttt
 IYHPNID-EKQVCLPVISA-----ENKPKATKTDQVIQSLIALVND-PQPEHLRADLAEEYSK-----DRKKCKNAEFTKKY
 IYHPNVD-KLGRICLDILK-----DKWSPALQIRTVLLSIQALLSA-PNPDDPLVNDV--AEQWKT-----NEAQAIETARAWTRLYAM

ALL E2 Sequences

Protein = no catalytic Cys

NM_003336	01_UBE2A	M-HPNVY-ADPSTICLDILQ-----NRWSTYDVSSILTSIQSLLDE--PNPNSPANSQAAQLYQE-----NKREYEKRVSAIVEQSWR (2)
NM_003337	02_UBE2B	M-HPNVY-ADPSTICLDILQ-----NRWSTYDVSSILTSIQSLLDE--PNPNSPANSQAAQLYQE-----NKREYEKRVSAIVEQSWN (2)
NM_007019	03_UBE2C	C-HPNVD-TQGNICLDILK-----EKWSALYDVRTILLSIQSLLEGE--PNIDSPLNTHAAELWKNPT----AFKKYLQETYSKQVTSQE (1)
NM_003338	04_UBE2D1	IYHPNIN-SNGSICLDILR-----SQWSPALTISKVLLSICSLLCD--PNPDDPLVPDIAQIYKS-----DKEKYNRHAREWTKYAM (x)
NM_003339	05_UBE2D2	IYHPNIN-SNGSICLDILR-----SQWSPALTISKVLLSICSLLCD--PNPDDPLVPEIARIYKT-----DREKYNRIAREWTKYAM (x)
NM_003340	06_UBE2D3	IYHPNIN-SNGSICLDILR-----SQWSPALTISKVLLSICSLLCD--PNPDDPLVPEIARIYKT-----DRDKYNRISREWTKYAM (x)
NM_015983	07_UBE2D4	IYHPNIN-SNGSICLDILR-----SQWSPALTISKVLLSICSLLCD--PNPDDPLVPEIAHTYKA-----DREKYNRLAREWTKYAM (x)
NM_003341	08_UBE2E1	IYHCNIN-SQGVICLDILK-----DNWSPALTISKVLLSICSLLCD--CNPADPLVGSIATQYMT-----NRAEYDRMARQWTKRYAT (x)
NM_152653	09_UBE2E2	IYHCNIN-SQGVICLDILK-----DNWSPALTISKVLLSICSLLCD--CNPADPLVGSIATQYMT-----NRAEYDRMARQWTKRYAT (x)
NM_006357	10_UBE2E3	IYHCNIN-SQGVICLDILK-----DNWSPALTISKVLLSICSLLCD--CNPADPLVGSIATQYLT-----NRAEYDRMARQWTKRYAT (x)
NM_003342	11_UBE2G1	IYHPNVD-KNGDVCSILH-(13)--ERWLPHTVETIMISVISMLAD--PNGDSPANVDAAKEWRED----RNGEYKRKVARCVRKSQE (4)
NM_003343	12_UBE2G2	M-HPNIY-PDGRVCSILH-(13)--ERWSPVQSVEKILLSVSMALAE--PNDESGANVDASKMWRDD----REQFYKIAKQIVQSLGL (x)
NM_003344	13_UBE2H	IFHPNIDEASGTVCLDVIN-----QDTALYDITNIFESFLPQLLAYPNPIDPLNGDAAMYLH-----RPEEYKQKIKEYIQYAT (33)
NM_003345	14_UBE2I	LFHPNVY-PSGTVCISILEED-----DKWRPAITIKQILLGTQELLE--PNIQDPAQAEAYTIYCO-----NRVEYEKRVSAIAKAFAP (1)
NM_003347	15_UBE2L3 1fbv	IYHPNID-EKQVCLPVISA-----ENKPKATKTDQVIQSLIALVND-PQPEHLRADLAEEYSK-----DRKKCKNAEFTKKYGE (5)
NM_004223	16_UBE2L6	IYHPNVD-ENGQICLPISSS-----ENKPKCTKTQVLEALNVLVNR--PNIREPLRMDLADLLTQ-----NPELFRKNAEFTLRFGV (4)
NM_003969	17_UBE2M	VYHPNVD-LEGNVCLNLR-----EDWKPVLTIINSITIGLYQLFLE--PNPEDPLNKEAAEVLQN-----NRRLEQNVQQRSMRGGYI (10)
NM_003348	18_UBE2N 2c2v	IYHPNVD-KLGRICLDILK-----DKWSPALQIRTVLLSIQALLSA--PNPDDPLANDVAEQWKT-----NEAQAIETARAWTRLYAM (3)
NM_021988	19_UBE2V1	INMNGVN-SSNGVVDPRASVL---AKWQNSYSIKVVLQELRRLMMSKENMKLPQPPEG-QCYSN-----
NM_003350	20_UBE2V2	INMNGIN-NSSGMVDARSIPVL---AKWQNSYSIKVVLQELRRLMMSKENMKLPQPPEG-QTYNN-----
NM_014501	21_UBE2S	IFHPNVG-ANGETICVNLK-----RDTAELGIRHVLLTIKCLLIH--PNPESALNEEAGRLLE-----NYEEYAAARALLTEIHGG (65)
NM_004359	22_CDC34	M-HPNIY-ETGDVCSILH-(13)--ERNFTQNVRTILLSVISLLNE--PNTFSPANVDASVMYRKWKESGKDREYTDIIRKQVLGTKV (62)
NM_005339	23_HIP2	IYHPNIVSSVTGAICLDILK-----DQWAAAMTLRTVLLSIQALLAA--AEPDDPQDAVVANQYKQ-----NPMEYKQTAARLWAVYAG (46)
NM_017811	24_UBE2R2	M-HPNIY-ENGDVCSILH-(13)--ERNFTQNVRTILLSVISLLNE--PNTFSPANVDASVMYRKWRDSKGKDKEYAEIIRKQVSATKA (64)
NM_016021	25_UBE2J1	NGRFEVG---KKICLSISGHHP---ETWQPSWSTRTALLAIGFMPT--KGEGAIGSLDYTPERRALAK--KSQDFCCGCGSAMKDV (158)
NM_058167	26_UBE2J2	NGRFKCN---TRLCLSLTDFHP---DTWPAWSSTILTGILLSFMVE--KGPTLGSIET--SDFTKRQLAV-QSLAFNLKDKVFCFLF (99)
NM_018299	27_UBE2W	NIPVHPHY-SNGHICLSILT-----EDWSPALSVQSVCLSIISMLSSCKEKRRPDPNS--FYVRTCNKNPKTKWYHDDTC (x)
NM_018314	28_UBEV3	ANMGILVGKHVDAQGRILPYL---QNSHPKSVTVGLIKEMIAKFQEELPMYSLSSSDEARQVD-----LLAYIA (219)
NM_023079	29_UBE2Z	NNTVRNPNFY-RNCKVCLSLGTWTG--PAWSPAQSTSSVLSISQSLMTENPYHNEGFQEERHPGDS-----KNYNECIHETIRVAV (101)
NM_022476	29_ETS	---PVHQLDPTSGELDVKRAFA-(7)--HIVQLMYARVVFYKIDTASPLNEEAAVLYEKDIQLFKSVVDVSV--KVCTARLFDQPKIEDPYA (57)
NM_022066	30_UBE20	-CSGRLNPNLYD-NCKVCVSLGTWIGKGTERTSKSSLQVLISIQGLTLVNEPYNEAGFDSDRGLQEGY---ENSRCYNEMALIRVVQSMT (x)
NM_017582	31_UBE2Q	---VLSGGYVLGGGAICMELLTK-----QGSSAYSIESVIMQISATLVKGKARVQFGANKSQYSLTRAQ---QSYKSLVQIHEKNGWY (x)
NM_014176	32_UBE2T	---IYHPNIDS-AGRICLDVLKLPK--GAWRPSLNTATVLTSLQLMSE--PNPDDPLMADISSEFKY-----NKPALKNARQWTEKHAR (45)
NM_080678	32_UBE2F	---IYHPNITE-TGEICLSLREHSIDG-TGAPTRTLKDVVWGLNSLFTDLLNFDDPLNIEAAEHHLR-----DKEDFRNKVDYIKRYAR (x)
NM_016252	34_BIRC6	GGHSVRNPNLYN-DCKVCLSLNTHWRPEEKWNPQTSFLQVLVSVQSLILVAEPYFNEPGYERSRGTPSGTQ--SSREYDGNIRQATVKWAM (x)
NM_152489	35_UBE2U	---P-HPNVDPHTPQPCIDFLDNP-----EKWNTNYTSSILLALQVMSLN--PVLENPNL EAARILV--KDESLYRTILRLFNRLPLQM (73)
NM_173469	36_UBE2Q2	---VLSGGYVLGGGALCMELLTK-----QGSSAYSIESVIMQINATLVKGKARVQFGANK--NQYNLAR AQQSYNSIVQIHEKNGWY (x)
NM_006292	37_TSG101	SSMTIKTGKHDANGKIYLPYL-----HWKHPQSDLLGLIQVMIYVFGDEPPVFSRPIS-ASYPYQATGPPNTSYMPGMPGGISPYPS (88)