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HSA.009223.2.ACOX1      : -----MNF-----D-----LRERDSASFNPELLTHILDGSPKTRRRREIENMILNPDF-QHEDLNFLTSSQRYEVAVRKSAIMVKKMREFGIA : 80
MUS.001258827.1.ACOX1  : -----MNF-----D-----LRERAAATFNPELLTHILDGSPENRRRREIENILNPDF-QHEDYNFLTSSQRYEVAVKKSATMVKKMREFGIA : 80
CF.64869.12.ACOX1      : -----MAAAKMSVNF-----D-----LAKERRKATFDVEQLTYIYLKERIKRRKRYLEDLAVNDPVIKECKPWAFCSREEQYEMGLKKHHIAKQIKLLGIT : 89
CF.11051.3.1.ACOX1     : -----MASAGTGTTAVNF-----D-----LAKERNRNSFHVENLTNFIYHSPERVRRRRYMQNIALQEPALKDMKPWAFRTREEENELSLCKQLHVLKQKELGIT : 91
CF.17615.31.ACOX1      : -----MAVAVNF-----D-----LERERQNAFDRETLTDFLYGSAQKQRRRYLKQNVFSDPEYQTMKSRVFCNREELYALHLQYINMRQIQEKLHIT : 85
CF.3421.13.ACOX1       : -----MAARGRVTVNA-----D-----LAKERASATFDVENLTDFIDGVAATKRRKRYLQDLAINDPELKNKSPWAVMTREEQYETALRKHYIMTKRLEEMGIT : 89
PY.8373.9.ACOX1        : -----MASAGTGKMTVNF-----D-----IAKERNRNSGFHVENLTNFIYHSPERVRRRRYMQNIALQDPVMKDSKPWAFRTREEEYELSLRKQLHVLQKQDLGIT : 91
PY.9399.9.ACOX1        : -----MAARGRVTVNA-----D-----LAKERASATFDVENLTDFIDGVAATKRRKRYLQDLAINDPELKNKSPWAVMTRKEQYETALRKHYIMAKRLEEMGIT : 89
PY.11121.10.ACOX1     : -----MNVNF-----D-----LAKERSKATFDVEQLTYVLYLKERTERKRYLENLAVNDPVIKECKPWAFCSREEQYEMALKKKHHIAKQIKLLGIT : 83
PY.5547.59.ACOX1       : -----MASAVNF-----D-----LERERKRAFDRETLTNFIYHSAQKQRRRYLKNAVFSDEYQAMKSRVFCNREELYALHLQYISFRRIQENLIT : 85
HSA.003491.1.ACOX2     : MGSPVHRVSLGDTWSRQMH-----D-----IESERMQSFDVERLTNILDGAQNTALRRKVESIIHSYEF-SCKDNYFMTQNERYKAAMRAFHRIIARRLGWL : 97
MUS.001155139.1.ACOX2 : MGNPGDRVSLGETWSREVH-----D-----IDSERHSPSFSVERLTNILDGIPNTELRRRVESLIQRDPVF-NLKHLYFMTDELYEDAVOKRFHLEKLAWSLGWS : 97
CF.52871.92.ACOX2      : ----MANEVMAGMGSTAINF-----D-----IARERLKASFDPVELTHVLDGKERTRARKLENLFLSDPLF-CLRDNIYLTSDLSYATMARSVKFLRLKQDKWS : 93
PY.716361.21.ACOX2     : ----MANEVMAGMESNAINF-----D-----IARERLKATFDPLELTHIFDGKERTRARKLENLFLSDPLF-CLRDNIYLTSDLSYATMARSVKFLRLKQDKWS : 93
HSA.015254.ACOX3       : -----MASTVEGGDTALF-----EFPGRGLDAYRARASFSWKELALFTE-EGMLRFRKTIFFSALENDPLF-ARSPGADLSLEKYRELNFLR----CKRIFEYDFL : 91
MUS.109646.2.ACOX3     : -----MGSLPEEKDSALWS-----DTPKGPLSAYRARASFSNGELLFWD-QQDVHFKKTIFFSTLENDFLF-ARSYGADLPLEKLRLEINFLR----CKRVFEYGF : 91
CF.57427.4.ACOX3       : MGDQRVKVQAAAGTQGGLEDVAVVPDSENMPKDLSDIELLKPPPGPLDVYRQASFDWKKMRLFMD-EEIIRYNMWTTLKEKDFLF-SQPMVTE-TVEKQRESTFYR----CKRLEFEYNFL : 117
PY.11077.9.ACOX3       : MGDRRVKVFQASSGTQEGLEDVAVVPGSENMPKDLSDIELLKPPPGPLDVYRQASFDWKKMRLFMD-EEIVRYKNMWTTLKEKDFLF-SQPMVTE-TVEKQRESTFYR----CKRLEFEYNFL : 117

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Fatty acyl CoA oxidase domain

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HSA.009223.2.ACOX1      : DPDEIMWFKKLHLVNFVEPVG-----LNYSMFIPTLLNQTTAQKEKWLL-----SSKGLQIITYAQTEMGHGTHLRGLETTATYDPKTOEFILENSPTVTSIKWWPGGLGKTSNHAI : 188
MUS.001258827.1.ACOX1  : DPDEIMWFKKLHVMNFVEPVG-----LNYSMFIPTLLNQTTAQKEKWMH-----PSQELQIITYAQTEMGHGTHLRGLETTATYDPKTOEFILENSPTVTSIKWWPGGLGKTSNHAI : 188
CF.64869.12.ACOX1      : DDWDKFFYTEAAACHENSPIG-----LHTAMFLPLTRKQASEDQKKKFLS-----LAENMTIITYAQTELGHGCTFIRGLETTATYDPKTOEFILENSPTVTSIKWYWPNGNLGKTVNFCM : 197
CF.11051.3.1.ACOX1     : EEFDKYYYNEAVAPNENNVPG-----LHFGMFIPTIEKHTEEQKKKFVQ-----PAKDLKILCTYVQTELGHGCTFIRGLETTATFDPKTOEFILENSPTVTSIKWYWPNGNLGKTVNFCI : 199
CF.17615.31.ACOX1      : DNEELFIIRQALGPNEYAYLG-----VHGFMIPTIQKLTTEEQKKRWLP-----LAKNLEIITYAQTELGHGCTFIRGLETTATYDPKTOEFILENSPTVTSIKWYWPNGNLGKTVNFCI : 193
CF.3421.13.ACOX1       : NKDKLTYKEWVSLKHYPPTL-----VPHNRLLRKLESYVQCNAHKWIESFRSSSTQQVTLDECSRT-----FVRGLETTATYEPKTRFEVFLNSPTLTSIKWYWPNGNLGKTVNFCI : 197
PY.8373.9.ACOX1        : DEFDKYYNEATAPNENNVPG-----LHFGMFIPTIEKHTEEQKKKFVQ-----PAKDLKIICTYVQTELGHGCTFIRGLETTATFDPKTOEFILENSPTVTSIKWYWPNGNLGKTVNFCI : 199
PY.9399.9.ACOX1        : DERDKLNYKEAGANHESSPIG-----VHLSMFLPLTRKQASTEDQRRKFLP-----LAEKLAIIITYAQTELGHGCTFVRGLETTATYDAKTRFEVFLNSPTLTSIKWYWPNGNLGKTVNFCI : 197
PY.11121.10.ACOX1     : DEWDQYFYTEAAACHENSPIG-----LHSSMFLPLTRKQASEDQKKKFLP-----LAENMTIITYAQTELGHGCTFIRGLETTATYDPKTOEFILENSPTVTSIKWYWPNGNLGKTVNFCI : 191
PY.5547.59.ACOX1       : DQEECFIIRQAIGPNYYAIG-----VHGFMIPTIQKLTTEEQKKRWLP-----LAENLTIIITYAQTELGHGCTFIRGLETTATYDPKTOEFILENSPTVTSIKWYWPNGNLGKTVNFCI : 193
HSA.003491.1.ACOX2     : EDGRELGYA-YRALS GDVALN-----IH-RVEVRALRSLSEEQIAKWDP-----LCKNQIATITYAQTELGHGCTYQGLETTATYDAATOEFILENSPTVTSIKWYWPNGNLGKTVNFCI : 203
MUS.001155139.1.ACOX2 : EDGPERIYAD-RVLAGYNNLN-----LH-GIAMNAIRSLSEEQIAKWGO-----LGKNFOIITITYAQTELGHGCTYQGLETTATYDATOEFILENSPTVTSIKWYWPNGNLGKTVNFCI : 203
CF.52871.92.ACOX2      : EDDLHVA---LRIIRDQNCIT-----LHHSMFLPALERLASDEQKARWLP-----LARRYNMVITYAQTELGHGCTNLMELETTATYDKSTDEEVLSTPKLSSIKWWPGSLGKTSNHAI : 198
PY.716361.21.ACOX2     : EDDLILLA---LRLIRDQNCIS-----LHHSMFLPALERLASDQKARWLP-----LARRYHMYITYAQTELGHGCTNLMELETTATYDKATDEEVLSTPKLSSIKWWPGSLGKTSNHAI : 198
HSA.015254.ACOX3       : SVEDMFK-SPLKVPALIQCLGMDSSSLAAYKYLHLSLVGSAVYSSSE-RHLYTIO-----KIFRMEIFGCFALTELSHGCSNTKAMRTTAHYDPTOEFILENSPTVTSIKWYWPNGNLGKTVNFCI : 208
MUS.109646.2.ACOX3     : KVEELLK-NPLKILVLINCLGMDWSLANKCVLHMLVEGTTVFVSSE-KHFHYLE-----KIYSLIEFCFALTELSHGCSNTKAMRTTAHYDPTOEFILENSPTVTSIKWYWPNGNLGKTVNFCI : 208
CF.57427.4.ACOX3       : SEEALFD-NPLKHKILTCLGMYNWSLGAKYQLDVENTGGTVQATSA-RHADIVE-----KIKNFYEYFCFALTELSHGCSNTKAMRTTATYDLKTEEFILQTPDFEATKIWSGNYGKTMATHAV : 234
PY.11077.9.ACOX3       : SEDALFD-NPLKHKILTCLGMYNWSLGAKYQLDVENTGGTVQATSA-RHGDIIVE-----KIKSFEYFCFALTELSHGCSNTKAMRTTATYDPKTEEFVLQTPDFEATKIWSGNYGKTMATHAV : 234

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HSA.009223.2.ACOX1      : VLAQLIT-KKCYGLHAFVPIREIGTHKPLPGITVGDIGPKFGYDEIDNGYIKMDNHRIPRENMLMKYAAQKPDGTYVKPLS--NK---LTYGTVFVRSFLV-GEAARA-SKACTIAIRYSA : 305
MUS.001258827.1.ACOX1  : VLAQLIT-RGEYGLHAFVPIREIGTHKPLPGITVGDIGPKFGYEEMDNGYIKMDNHRIPRENMLMKYAAQKPDGTYVKPLS--NK---LTYGTVFVRSFLV-GSAAQS-SKACTIAIRYSA : 305
CF.64869.12.ACOX1      : IMAQLYT-KKCYGVHAFVPIREIGTHKPLPGITVGDIGPKFGYGTNDNGYIRLNNVRIPRDHMLMRYSKVLEDGTYVKPPN--SR---LSYGSMTLVRAAIV-GDSSRG-LAQACTIAIRYSA : 314
CF.11051.3.1.ACOX1     : IMAQLYS-QCKCQGPMPHFLPLRDLNTHQSLPGVELGDIGPKFGYAAANDNGYIRLNNLRIPRDHMLMRYSKVLEDGTYVKPPN--SK---LSYGSVMIRASIV-GFSSRA-LAQACVIAVRYSA : 316
CF.17615.31.ACOX1      : IMAVLNT-QCKNHGLSFVPIRDLKTHESLPGVEVGDIGPKFGFNENDNGYIRLNNVRIPRDHMLMRYAKVLEDGTYVKPPN--AQ---SNLGPVVVRVLLSGEILPILOKACVIAVRYSA : 312
CF.3421.13.ACOX1       : VMAQLYT-NCKCYGMHTFLPLRDLRTHRSPLGIELCDIGPKFGYSSNDNGYIRLNNVRIPRENMLMRYAAQVLEDGTYVKPSN-AK---ISYGTMTLIRVGIV-TNVSRC-LAQACVIAVRYSA : 314
PY.8373.9.ACOX1        : LMAQLYS-QCKCQGPMPHFLPLRDLNTHQSLPGVELGDIGPKFGFNANDNGYIRLNNVRIPRENMLMRYSKVLEDGTYVKPPN--SK---LSYGSVMIRASIV-GAVSRA-LAQACVIAVRYSA : 316
PY.9399.9.ACOX1        : VMAQLYT-NCKCYGMHTFLPLRDLNTHQSLPGIELGDIGPKFGYGSNDNGYIRLNNVRIPRENMLMRYAAQVLEDGTYVKPPN-AK---ISYGTMTLIRVGIV-TNVSRC-LAQACVIAVRYSA : 314
PY.11121.10.ACOX1     : IMAQLYT-KKCKGIGITFLPLRDLQTHQSLPGIELCDIGPKFGYGTNDNGYIRLNNVRIPRDYMLMRYSKVLEDGTYVKPPN--SR---LSYGSMTLIRAAIV-GDSSRG-LAQACTIAIRYSA : 308
PY.5547.59.ACOX1       : IMAVLNT-QCKNHGLSFVPIRDLKTHKSLPGVEVGDIGPKFGFNENDNGYIRLNNVRIPRDHMLMRYAKVAEDGAFTVSTNEGSR---LTYGTVLFRVAMIV-SGTSTV-LGMACTVIAVRYSA : 312
HSA.003491.1.ACOX2     : VQAQLIC-SGARRGMAHAFVPIRSLQDHTPLPGIIGDIGPKMDFDQTLNNGYIRLNNVRIPRDHMLMRYAKVAEDGAFTVSTNEGSR---LTYGTVLFRVAMIV-SGTSTV-LGMACTVIAVRYSA : 312
MUS.001155139.1.ACOX2 : VLAHLIC-LGARRGMAHAFVPIRSLQDHTPLPGITVGDIGPKMDFFNENDNGYIRLNNVRIPRENMLMRYAAQVLEDGTYVKPLS--AQ---SNLGPVVVRVLLSGEILPILOKACVIAVRYSA : 321
CF.52871.92.ACOX2      : VLAQLVVDNKKC-GMFFFMVQIRSLMDHTPMPGKIKGVIGQKMGNYNDNGYIRLNNVRIPRENMLMKNAQVTRTEKFLTSGP--NK---ANATMIYVRVMTL-SWSFGAICAAATAIRYSS : 315
PY.716361.21.ACOX2     : VLAQLVVDSSKKC-GMFFFMVQIRSLMDHTPMPGKIKGVIGQKMGNYNDNGYIRLNNVRIPRENMLMKNAQVTRTEKFLTSGP--NK---ANATMIYVRVMTL-SWSFGAICAAATAIRYSS : 315
HSA.015254.ACOX3       : VFAKLCVPGDQCCHGLSFLVQIRDPKLLPMPGVMVGDIGKKLQNGLNGFAMFHKVVRPQSLNLFMGDVTPEGTYYSPFKDVQRQFGASLGSLSGGSIVSII-SMVSVN-KLVAIAIRYSA : 331
MUS.109646.2.ACOX3     : VFAQLYMPDQCCHGLSFLVQIRDPKLLPMPGVMVGDIGKKLQNGLNGFAMFHKVVRPQSLNLFMGDVTPEGTYYSPFKDVQRQFGASLGSLSGGSIVSII-SMVSVN-KLVAIAIRYSA : 331
CF.57427.4.ACOX3       : TYAQLYTPDNCCHGLSFLVQIRDPKLLPMPGVMVGDIGKKLQNGLNGFAMFNNYHIRETLNRTGDKADGIYVTPYKDPKSRFGASLGSLSGGSIVSII-SMVSVN-KLVAIAIRYSA : 357
PY.11077.9.ACOX3       : VYAQLYTPDNCCHGLSFLVQIRDPKLLPMPGVMVGDIGKKLQNGLNGFAMFNGYHIRETLNRTGDKADGIYVTPYKDPKSRFGASLGSLSGGSIVSII-SMVSVN-KLVAIAIRYSA : 357

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[illegible]

HSA.009223.2.ACOX1	: TMMFQTARYFLMKSYD-QVHS	-----KLVCGMVS---	YLN	NDLPSQRIQPQQVAVWPTMVDINSPELSTE	AYKLRAARLVEIAAKNLQKE-VIHRKSKEV	WNLTSDVLVRA-SBAHCHYVV	: 536	
MUS.001258827.1.ACOX1	: TMMFQTARYFLMKIYD-QVQS	-----KLVCGMVS---	YLN	NDLPSQRIQPQQVAVWPTLIDNSLDLSTE	AYKLRAARLVEIAAKNLQQAQ-VSHRKSKEV	WNLTSDVLVRA-SBAHCHYVV	: 536	
CF.64869.12.ACOX1	: TMMFQTARYFLMKCFKFS-KVEN	-----EKLPGFVS---	YLS	T-----DLSVKSCKMSDVLSDCLVK	FEHRAARLVQVAARNIKRRLVVEE	QSQQEVWNNNTAQQLVWA-SBAHCHYVV	: 495	
CF.11051.3.1.ACOX1	: TMMFQTARYLLKCAL-MVQK	-----QRLPDLVA---	YLS	T-----DLSAKSCMTSDVALGCLVK	AYQHRAARLTKAATAAVQRY-TSE	KNPTDFNMASTQLSWA-ARAHCHQVV	: 538	
CF.17165.31.ACOX1	: TMMFQTARYFLMKCYN-QLKMK	-----KSLPSSFA---	YIT	D-----KLSGKSDLDNKLNFNSI	IEAYEHRAARLIKAAALNITFW-VKA	QKVPWDSNTKSSIHMVWA-AKASHCHLFV	: 534	
CF.3421.13.ACOX1	: TPLYQTARYLLKCFET-KVQK	-----EKLPGFVS---	YMG	T-----DLTIKSTIKSDVALESIVL	AYEHRAARMVRAAAMNIQGL-VRE	FTQPEWNNKSTAQQLVWA-TMAHCHYVV	: 536	
PY.8373.9.ACOX1	: SMMFQTARYLFECAM-MVQK	-----QRLPDLVS---	YLS	M-----DLSAKSCMTSDVALGCLVK	AYQHRAARLTNAATAVVQRH-INE	GKPTDFNMASTQTLTWA-ARAHCHQVV	: 538	
PY.9399.9.ACOX1	: TPLYQTARYLLKCFET-KVQK	-----EKLPGFVS---	YMG	T-----DLSIKSTIKSDVLSLLAY	EHRAARMVKAAMNIQGL-VQEF	FTQPEWNNKSTAQQLVWA-TMAHCHYVV	: 536	
PY.11121.10.ACOX1	: TMMFQTARYLLMKCFA-KVEN	-----EKLPGFVS---	YNT	T-----DLSAKSCMTSDVALDCLVK	AYEHRAARLVQVAARNIKRRLVVEE	QSQQEVWNNNTAQQLVWA-SBAHCHYVV	: 531	
PY.5547.59.ACOX1	: TMMFQTARYLLVKCYN-QMKMK	-----KSLPSSFA---	YIT	D-----NLSGKSDLDNKLNFDSI	IEAYEHRAARLIKAAALNITFW-MKA	KNKVPWDSNTKSSIQMVWA-AKASHCHLFV	: 534	
HSA.003491.1.ACOX2	: TPLYQVARYFLVKSYL-QTQMSPGSTPQRLSPSVA	-----YITAT---PD---	LAR	CPAQRAADFCEPLYTTAWHVAVAL	IKDSDVQHLOTLT-QTSDAQDHEWNNQT	TVHILQA-AKVHGYEYTV	: 552	
MUS.001155139.1.ACOX2	: TPLYQVARYFLMKSYL-QADTSPGSIPOKLPQSYM	-----YITAT---PR---	PAR	CPAQRAADFCEPVYTTAWHVAVAL	IKDSDVQHLOTLT-MRSDVQDHEWNNQT	TVHILQA-AKVHGYEYTV	: 552	
CF.52871.92.ACOX2	: TPLYQVARYLLKQIA-KALT	-----HQTGTGTE---	YLN	M---NEA---SYICPLQKVPDCRNTE	FLCEVYKKRAYSMVLKVAQALQD-MEAK	KEQAVYMNNNLQPLVRM-ATAHCHYLLAM	: 541	
PY.716361.21.ACOX2	: TPLYQVARYLLKQIA-KALT	-----HQTGTGTE---	YLN	M---NEA---SYICPLQKVPDCRNTE	FLCEVYKKRAYSMVLKVAQALQD-MEAK	KEQAVYMNNNLQPLVRM-ATAHCHYLLAM	: 541	
HSA.015254.ACOX3	: NILLQOTSNYLLGLLGHVQHD	-----AQFSPKSVDF---	DAY	PGIL---DYQFVESSVADLSDAVALA	YKWLVCYLRETYKLNQE-KRS	SDFEARNKQVSHGRPLALFYELTV	: 568	
MUS.109646.2.ACOX3	: NILLQOTSNYLLSLEPPLQD	-----AHFTSPLKTVDF---	EAY	PGIL---GQKFLGSSKADWMDS	AAPLAAAYRWLVCYLQBSHRRY	CQE-KKSRGSDFEARNNSQVYGC	RPLALAFMELTV	: 568
CF.57427.4.ACOX3	: NILLQOTSNYLLGLLESNIK	-----EINTPLKSVNF---	S	DLGGL---KTTFEARTVEDCFNPEV	SLRAYKWLGVRLVDSAEERLKEQ-QQA	KDAFSARNDSQAYYCRSLALAYEHTVL	: 594	
PY.11077.9.ACOX3	: NILLQOTSNYLLGLLESNIR	-----EINTPLKSVNF---	S	DLGGL---KTTFEARTVEDCFNPEV	SLRAYKWLGVRLVDSAEERLKEQ-QQA	KDAFSARNDSQAYYCRSLALAYEHTVL	: 594	

HSA.009223.2.ACOX1	:	KLFSEKLLK---IQ-DKAIQAVLRSLCLFYSLYGISQNAQDLOGSIMTEPI-TQVNRQVKELLTLISPAVALVDADFDFDVTLSVSLGRDGNVYENLFWEAKKSS--LNKAEVHESY-KH	: 652
MUS.001258827.1.ACOX1	:	KVEADKLPK---IQ-DRAVQAVLRNLCLFYSLYGISQKGGDELEGNITGAMQ-SQVNSRIELLETLVTPNAVALVDADFDFDVTLSVSLGRDGNVYENLFWEAKKSS--LNKTEVHESYKYH	: 653
CF.64869.12.ACOX1	:	KVEVMVTE---SNFDDQVNLVTSCKLYGVHGMENLCEIQDGYLSTSV-EDVTKGLMYLMAEIPDAVALVDADFDPDVLSSCLGRDGNVYALYKYYKSS--LNKTDVLTDSFYKY	: 613
CF.11051.3.1.ACOX1	:	KVEVMTMTE---AKIDDRTKAALTTLCKMYAVNGIMENLCEIQDQFFNADSV-DILTGKMMTLTLADVPDAVALVDADFDFHCKVLDSCLCRDGNVYALYKYYKSS--LNEKDVLDSSFHY	: 656
CF.17165.31.ACOX1	:	KTEFINVTS---ANLDPKVRSTALTTLCKRYAVNGMIENMQISQDGFLEDTI-NMLNRLTDLLEEVTNATFTVDAFEYHDNELHSCICGRDGOVYKALYNYKSS--LNDTDPVHSSFHKY	: 652
CF.3421.13.ACOX1	:	KTETATIFR---SLDDTKTKMTAALCKLYGVHGMVENLCEIQDGFMNASV-DVTRTKMLYLAETIPDAVALVDADFDPDVLSSCLGRDGOVYKALYNYKSS--LNKDKVLDSSFY	: 654
PY.8373.9.ACOX1	:	KVEVTTVTE---ANIDDRTKAALTTLCKMYAVNGIMENLCEIQDQFFNTDVS-DILTRKMMTLTLADVPDAVALVDADFDFHCKVLDSCLCRDGNVYALYKYYKSS--LNEKDVLDSSFHY	: 656
PY.9399.9.ACOX1	:	KTETATIFG---SNLDDQTKVMTAALCKLYGVHGMVENLCEIQDGFMNASV-DVTRTKMLYLAETIPDAVALVDADFDPDVLSSCLGRDGOVYKALYNYKSS--LNKDKVLDSSFY	: 654
PY.11121.10.ACOX1	:	KAEVAMVTE---SNLDDQVNLVTSCKLYGVHGMHLECEIQDGYLSTSV-EAVTGKMLMALKEIHNAVALVDADFDPDVLSSCLGRDGNVYALYKYYKSS--LNKQDVLDSEYKY	: 649
PY.5547.59.ACOX1	:	KTEINLVT---ANLDPKVRTALTTLCKRYAVNGMIENMQISQDGFLENETI-NMLNRLSALLEEVANAVAFVDAFEYHDNELHSCICGRDGOVYKALYNYKSS--LNDTDPVHSSFHKY	: 652
HSA.003491.1.ACOX2	:	KGEAEALK---LENEPAIQVLRKRDYHAHGLITNSGDLHDAFISGAV-DMARTAYLDLRLRLKDAILTDAFDFDQCNLSALCVGDNVERLRFWEAKKSS--TNQE-NPAYEY	: 669
MUS.001155139.1.ACOX2	:	RNEKAEVKE---LDNEPEIQVLRNLQDYLALGLITNSGDLHDGFLSGAV-DMARTAYLDLRLPLIKDAILTDAFDFSDHCLNSALCVGCHVYQRLFEWAKKSS--ANTQE-NPAYKY	: 669
CF.52871.92.ACOX2	:	AGYVEGLAS---VQLSPPAKKITNKKCCFVGHYIVTSLSGDLEAEAIGLEL-QWLQDLEIQLLAEIIPDAVTLVDALDFHDETSSAIGCDGRAYERLRYEALKKE--MNQTEVPDPAKEY	: 659
PY.716361.21.ACOX2	:	RSYIEGLAS---LQVSPPAKKLIDKCCFVGHYIVTSLSGDLEAEAIGLEL-LWLQELEQLLAEIIPDAVTLVDALDFHDETSSAIGCDGRAYERLRYEALKKE--MNQTEVPDPAKEY	: 659
HSA.015254.ACOX3	:	QREHEHVQ---PSVPPSLRAVLRGRSALYALWSLSRHAALYRGGYFSGEAGEVLESVALCSQKLDAAVLDVIAPDFVLDSPICRADGELYKNLNGAVLQESKVERASWPEFSVN	: 689
MUS.109646.2.ACOX3	:	QREHEHIHS---SGLSPSLRTVLGRSTLYGLWCLSQHMALLYRGGYISGETGRAMEDAILTLCQLKDDAVALVDVIAPDFVLSNPICAKDGLYKNLNGAVLQNGVLERAAWPEFSAN	: 689
CF.57427.4.ACOX3	:	DREHQLMTEGRNGDTPPELKPVLNKMCAFLGRWLEKHLSTLYCGGYIKGSNPPKIQEAILKLCYALKEAVSLVDAIAPDVFVNSPICLSDGQIYKNLYGAMIQGNALERPAAWKDFVDN	: 718
PY.11077.9.ACOX3	:	DREHQLMEGRNGDTPPELKPVLNKMCAFLGRWLEKHLSTLYCGGYIKGSNPPKIQEAILKLCYALKEAVSLVDAIAPDVFVNSPICLSDGQIYKNLYGAMIQGNALERPAAWKDFVDN	: 718

peroxisomal targeting signal

HSA.009223.2.ACOX1	: LKSLQ-----SKL	: 660
MUS.001258827.1.ACOX1	: LKFLQ-----SKL	: 661
CF.64869.12.ACOX1	: LKEMRGDTSTYPLRA--SKL	: 631
CF.11051.3.1.ACOX1	: IKEMREGQATSSLP---ARL	: 673
CF.17615.31.ACOX1	: LAFLKKKE-----SKL	: 662
CF.3421.13.ACOX1	: LRFLQGNMTTSTF---AKL	: 670
PY.8373.9.ACOX1	: IKELREGQATSSLP---SRL	: 673
PY.9399.9.ACOX1	: LRFLQGNTGTSSL---AKL	: 670
PY.11121.10.ACOX1	: LKEMRGDTSNSAHLPLRA--SKL	: 669
PY.5547.59.ACOX1	: LAFLKKKE-----SKL	: 662
HSA.003491.1.ACOX2	: IRELLQSWR-----SKL	: 681
MUS.001155139.1.ACOX2	: IRELMQSWK-----PKL	: 681
CF.52871.92.ACOX2	: LKHLIMEGAP-----SKL	: 672
PY.716361.21.ACOX2	: LKHLIMEGAQ-----SKL	: 672
HSA.015254.ACOX3	: -KEVIGSLK-----SKL	: 700
MUS.109646.2.ACOX3	: -KSVADRLK-----SQL	: 700
CF.57427.4.ACOX3	: -KEVVGSK-----SKL	: 728
PY.11077.9.ACOX3	: -KEVVGSK-----SKL	: 728