

MULTIPLE SEQUENCE ALIGNMENT RESULTS

ACONITATE HYDRATASE

CLUSTAL 0(1.2.4) multiple sequence alignment

eco:b0118	MLEEYRKHVAERAEGIAPKPLDANQMAALVELLKNPAGEEEFLLDLLTNRVPPGVDEA	60
eco:b0771	-	0
sce:YLR304C	-	0
dme:Dmel(CG4706	-	0
dme:Dmel(CG9244	-	0
cel:CELE_F54H12.1	-	0
mmu:11429	-	0
hsa:50	-	0
eco:b1276	-	0
cel:CELE_ZK455.1	-	0
mmu:11428	-	0
hsa:48	-	0
dme:Dmel(CG4900	-	0
dme:Dmel(CG6342	-	0
eco:b0118	AYVKAGFLAAIAKGEAKSPLLTPEKAIELLGTMQGGYNIHPLIDALDDAKLAPIAAKALS	120
eco:b0771	-	0
sce:YLR304C	-	0
dme:Dmel(CG4706	-	0
dme:Dmel(CG9244	-	0
cel:CELE_F54H12.1	-	0
mmu:11429	-	0
hsa:50	-	0
eco:b1276	-	0
cel:CELE_ZK455.1	-	0
mmu:11428	-	0
hsa:48	-	0
dme:Dmel(CG4900	-	0
dme:Dmel(CG6342	-	0

eco:b0118	HTLLMFDNFYDVEEKAKAGNEYAKQVMQS WADA EWF LNRP ALAEKLT VTVFKV TGETNTD	180
eco:b0771	- - - - -	0
sce:YLR304C	- - - - -	0
dme:Dmel(CG4706	- - - - -	0
dme:Dmel(CG9244	- - - - -	0
cel:CELE_F54H12.1	- - - - -	0
mmu:11429	- - - - -	0
hsa:50	- - - - -	0
eco:b1276	- - - - -	0
cel:CELE_ZK455.1	- - - - -	0
mmu:11428	- - - - -	0
hsa:48	- - - - -	0
dme:Dmel(CG4900	- - - - -	0
dme:Dmel(CG6342	- - - - -	0

eco:b0118	DLSPAPDAWSRPDIPLHALAMLKNAREGIEPDQPGVVGPIKQIEALQQKGFP ALAYVG DVV	240
eco:b0771	- - - - -	0
sce:YLR304C	- - - - -	0
dme:Dmel(CG4706	- - - - -	0
dme:Dmel(CG9244	- - - - -	0
cel:CELE_F54H12.1	- - - - -	0
mmu:11429	- - - - -	0
hsa:50	- - - - -	0
eco:b1276	- - - - -	0
cel:CELE_ZK455.1	- - - - -	0
mmu:11428	- - - - -	0
hsa:48	- - - - -	0
dme:Dmel(CG4900	- - - - -	0
dme:Dmel(CG6342	- - - - -	0

eco:b0118	GTGSSRKSATNSVLWFMGDDIPHVPNKRGGGLCLGGKIAPIFFNTMEDAGALPIEVDSN	300
eco:b0771	-----	0
sce:YLR304C	-----MLSARSAIK-----RPIVRGLA-TVSN	21
dme:Dmel(CG4706	-----MAQRTHRYICLA-----GSMVRNFH-TAR	23
dme:Dmel(CG9244	-----MAARLMNAQ-AQVCRLGKHVASE-----ATVVRQFH-ASC	33
cel:CELE_F54H12.1	-----M-NSLLRLSH-----LAGPAHYRALHSS	22
mmu:11429	-----MAP-YS-----LLVTRLQK-----ALGVRQYH-VASV	25
hsa:50	-----MAP-YS-----LLVTRLQK-----ALGVRQYH-VASV	25
eco:b1276	-----MS-----S-TLREASKDT	12
cel:CELE_ZK455.1	----------MAFNNLIRN	9
mmu:11428	----------MKNPFAHLAEP	11
hsa:48	----------MSNPF AHLAEP	11
dme:Dmel(CG4900	-----MS-----GSGANPFAQFQES	15
dme:Dmel(CG6342	----------MSGANPFAQFEKT	13

eco:b0118	LNMGDVIDVYPYKGEVRNHETGELLATFELKTDVLIDEVRAGGRIPPLIIGRGLTTKAREA	360
eco:b0771	-----MIKLSE-----KGVF LASNEIIAE-----	20
sce:YLR304C	LTRDSKV-----QNLLED-----HSFINYKQN VETLDIVRK-----	53
dme:Dmel(CG4706	FPRCDKVA-----MSNFDT-----GIPLPYKKLRENLD CIKG-----	55
dme:Dmel(CG9244	Y-TASKVA-----LSKFDS-----DVYLPYEKLNKRLEVVRG-----	64
cel:CELE_F54H12.1	SSIWSKVA-----ISKFEP-----KSYLPYEKLSQTVKIVKD-----	54
mmu:11429	LCQRAKVA-----MSHFEP-----SEYI RYD LLEKNINIVRK-----	57
hsa:50	LCQRAKVA-----MSHFEP-----NEYI HYD LLEKNINIVRK-----	57
eco:b1276	LQAKDKTY-----HYYSLPL-----AAKSLGDITRLPKSLKVLE-----	47
cel:CELE_ZK455.1	LAIGDNVY-----KYFDLNG-----LN-DARYNELPISIKYLLE-----	42
mmu:11428	LDAAQPGK-----RFFNLNK-----LE-DSRYGRLPFSIRVLLE-----	44
hsa:48	LDPVQPGK-----KFFNLNK-----LE-DSRYGRLPFSIRVLLE-----	44
dme:Dmel(CG4900	FTQDG NVY-----KYFDLPS-----I-DSKY ESLPFSIRVLLE-----	47
dme:Dmel(CG6342	FSQAGTTY-----KYFDLAS-----I-DSKY DQLPYSIRVLLE-----	45

eco:b0118	LGLPHSDVFRQAKDVAESDRGFSLAQKMVRACGVKGIRPGAYCEPKMTSVGSQDTTGPM	420
eco:b0771	---EHFTGEIKKEAKKGTIAWSILSSHN-----TSGNMDKLKIKFDSLASHDITFVG	70
sce:YLR304C	---RLNRPFYAEKILYGHLDDPHGQDI-----QRGVSYLRLRPDRVACQDATAQM	101
dme:Dmel(CG4706)	---RLGGPLTLSEKVLVLYSHLDQPDQE-----ERGKSYLRLRPDRVALQDATAQM	103
dme:Dmel(CG9244)	---RLNRPLTLSEKVLVLYSHLDDPANQDI-----VRGTSYLRRLRPDRVAMQDATAQM	112
cel:CELE_F54H12.1	---RLKRPLTLSEKILYGHLDQPKTQDI-----ERGVSYLRLRPDRVAMQDATAQM	102
mmu:11429	---RLNRPLTLSEKIVYGHLDDPANQEI-----ERGKTYLRLRPDRVAMQDATAQM	105
hsa:50	---RLNRPLTLSEKIVYGHLDDPASQEI-----ERGKSYLRLRPDRVAMQDATAQM	105
eco:b1276	NLLRWQDGNSVTEEDIHALAGWLKNA-----HADREIAYRPARVLMQDFTGVP	95
cel:CELE_ZK455.1	AAVRHCDEFHVLLKKDVETILDWKNSQ-----RNQAEIPFKPARVILQDFTGVP	90
mmu:11428	AAVRNCDEFLVKKNDIENILNWNVMQ-----HKNIEVPFKPARVILQDFTGVP	92
hsa:48	AAIRNCDEFLVKKQDIENILHWNVQT-----HKNIEVPFKPARVILQDFTGVP	92
dme:Dmel(CG4900)	SAVRNCDFNFHVLEKDVSQISLGWTPSLKQ-----ETSDVEVSFKPARVILQDFTGVP	98
dme:Dmel(CG6342)	SAVRNCDFNFILEKDVSQISLGWSPALKQ-----GSNDVEVSFKPARVILQDFTGVP	96

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eco:b0118	TRDELKDLAC--LGFSADLVMQSFCHTAAYPKPVDVNTHTL-----	460
eco:b0771	IVQTAKASGM-----ER-----FPLPYVLTNCNSL-CAVGG-----	101
sce:YLR304C	AILQFMSAGL-----P-----QVAKPVTVHCDHLIQAQVGGEKD-----LKRA	139
dme:Dmel(CG4706)	TLLQFISSGL-----K-----KVAVPSTVHCDHLIEAQISGDKD-----LARA	141
dme:Dmel(CG9244)	ALLQFISSGL-----K-----KVAVPSTVHCDHLIEAQIGGPKD-----LARA	150
cel:CELE_F54H12.1	AMLQFISSGL-----P-----KTAVPSTIHCDHLIEAQKGGAQD-----LARA	140
mmu:11429	AMLQFISSGL-----P-----KVAVPSTIHCDDHLIEAQVGGEKD-----LRRA	143
hsa:50	AMLQFISSGL-----S-----KVAVPSTIHCDDHLIEAQVGGEKD-----LRRA	143
eco:b1276	AVVDLAAMREAVKRLGGDT-----AKVNPLSPVLDVIDHSVTDRFGDDEAFEENVRL	149
cel:CELE_ZK455.1	AVVDLAAMRDADVQNMADP-----AKINPVCVPVLDVIDHSVQVDHYGNLEALAKNQSIE	144
mmu:11428	AVVDFAAMRDADVKKLGGNP-----EKINPVCVPADLVIDHSIqvDFNRRADSLQKNQDLE	146
hsa:48	AVVDFAAMRDADVKKLGGDP-----EKINPVCVPADLVIDHSIqvDFNRRADSLQKNQDLE	146
dme:Dmel(CG4900)	AVVDFAAMRDADVRELGGNP-----EKINPICPADLVIDHSVQVDFVRSSDALTKNESLE	152
dme:Dmel(CG6342)	AVVDFAAMRDADVLDLGGDP-----EKINPICPADLVIDHSVQVDFARAPDATALAKNQSLE	150

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eco:b0118	-PDFIM-----NRGGVSLRPGDGVIHSWLNRML-----	LPDT	491
eco:b0771	-TINGDDHVFGLS-AAQRYGGIFVPPHIAVIHQYMREMM-----	AGGGK	143
sce:YLR304C	IDLNKEVYDFLASATA-KYNMNGFWKPGSGIIHQIVLENY-----	AFPGA	182
dme:Dmel(CG4706)	KDLNKEVYDFLSSACA-KYNLGFWKPGSGIIHQIILENY-----	AFPGL	184
dme:Dmel(CG9244)	KDLNKEVYDFLASTCA-KYGLGFWKPGSGIIHQIILENY-----	AFPGL	193
cel:CELE_F54H12.1	KDLNKEVFNFNLATAGS-KYGVGFWKPGSGIIHQIILENY-----	AFPGL	183
mmu:11429	KDINQEYVNFLATAGA-KYGVGFWRPGSGIIHQIILENY-----	AYPGV	186
hsa:50	KDINQEYVNFLATAGA-KYGVGFWKPGSGIIHQIILENY-----	AYPGV	186
eco:b1276	MERNHERYVFLWKQKQAFSRFSVVPPGTGICHQVNLEYLGKAVWSEL--QDGEWIAYPD-	206	
cel:CELE_ZK455.1	FERNRERFNFLWKWSKAFDNLLIVPPGSGIVHQVNLEYLARTVFVGKD-----GVLYPD-	198	
mmu:11428	FERNKERFEFLWKWSQAFCNMRIIPPGSGIIHQVNLEYLARVVFQDQG-----CYYPD-	199	
hsa:48	FERNRERFEFLWKWSQAFHNMRIIPPGSGIIHQVNLEYLARVVFQDQG-----YYYPD-	199	
dme:Dmel(CG4900)	FQRNKERFTFLWKWAGARAFDNMLIVPPGSGIVHQVNLEYLARVVFESDSSADGSKILYPD-	211	
dme:Dmel(CG6342)	FERNKERFTFLWKWAKAFNNMLIVPPGSGIVHQVNLEYLARVVFENDA-TDGSKILYPD-	208	
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eco:b0118	VGTGGDSHTRFPIGISFP---AGSGLVFAAAATGVMPLDMPESVLVRFKGKMQPGITLRD	548	
eco:b0771	MILGSDSHTR-YGALGTMAVGEGGGEELVKQLLNDTWDIDYPGVVAVHLTGPAPYVGPQD	202	
sce:YLR304C	LIIGTDSHTPNAGGLGQLAIGVGGADAVDVMAGRPWEKLAKPILGVKLTGKMGWTSPKD	242	
dme:Dmel(CG4706)	LMI GTDSHTPNGGLGGLCICVGCGADAVDVMANIPWEKLCPVIGCHLTGKISGWTSPKD	244	
dme:Dmel(CG9244)	LMI GTDSHTPNGGLGGLCICVGCGADAVDVMA_DIPWEKLCPVIGVNLTGKISGWTSPKD	253	
cel:CELE_F54H12.1	LLIGTDSHTPNGGLGGLCICVGCGADAVDVMA_DIPWEKLCPVIGIKLTGKLNWTSAKD	243	
mmu:11429	LLIGTDSHTPNGGLGGLCICVGCGADAVDVMA_GIPWEKLCPVIGVKTGSLSGWTSPKD	246	
hsa:50	LLIGTDSHTPNGGLGGLCICVGCGADAVDVMA_GIPWEKLCPVIGVKTGSLSGWSSPKD	246	
eco:b1276	TLVGTDSHTTMINGLGVLGWGVGGIEAEAAAMLGQPVSMLIPDVFGFKLTGKLRGITATD	266	
cel:CELE_ZK455.1	SVVGTDSHTTMINGLGVLGWGVGGIEAEAVMLGQPISMVLPQVIGYKLMGKPHPLVTSTD	258	
mmu:11428	SLVGTDSHTTMINGLGVLGWGVGGIEAEAVMLGQPISMVLPQVIGYRLMGKPHPLVTSTD	259	
hsa:48	SLVGTDSHTTMINGLGVLGWGVGGIEAEAVMLGQPISMVLPQVIGYRLEGKLGPLATSTD	259	
dme:Dmel(CG4900)	SVVGTDSHTTMINGLGVLGWGVGGIEAEAVMLGQSISMLLPEVIGYKLEGKLSPLVTSTD	271	
dme:Dmel(CG6342)	SVVGTDSHTTMINGLGVLGWGVGGIEAEAVMLGQSISMLLPEVIGYKLEGKLSPLVTSTD	268	
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eco:b0118	LVHAIPLYAIKQGLLTVEKKGKKNIFSGRILEIEGL--PDLKVEQAFELTDASAERSAAG	606				
eco:b0771	VALAIIGAVFKNGY-----VKNKVMEFVGPGVSALSTDF-----RNSV	240				
sce:YLR304C	IILKLAGITTVKGG-----TGKIVEYFGDGVDTFSATG-----MGTI	279				
dme:Dmel(CG4706)	VILKVAEILT.VKGG-----TGAIVEYHGPGVESISCTG-----MATI	281				
dme:Dmel(CG9244)	VILKVADILTVKGG-----TGAIIEYHGKGVDISCTG-----MATI	290				
cel:CELE_F54H12.1	VILKVADILTVKGG-----TGAIIVEYFGPGVDSISATG-----MGTI	280				
mmu:11429	VILKVAGILT.VKGG-----TGAIVEYHGPGVDSISCTG-----MATI	283				
hsa:50	VILKVAGILT.VKGG-----TGAIVEYHGPGVDSISCTG-----MATI	283				
eco:b1276	LVLTVTQMLRKHGV-----VGKFVEFYGDGLDSLPLAD-----RATI	303				
cel:CELE_ZK455.1	LVLTITKNLRDLGV-----VGKFVEFFGTGVASLSIAD-----RATI	295				
mmu:11428	IVLTTIKHLRQVGV-----VGKFVEFFGPVGVAQLSIAD-----RATI	296				
hsa:48	IVLTTIKHLRQVGV-----VGKFVEFFGPVGVAQLSIAD-----RATI	296				
dme:Dmel(CG4900)	LVLTTIKHLRQLGV-----VGKFVEFYGPVVAELSIAD-----RATI	308				
dme:Dmel(CG6342)	LVLTTIKHLRQLGV-----VGKFVEFYGPVVAELSIAD-----RATI	305				
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eco:b0118	CTIKLNKEPIIEYLNSNIVLLKWMIAEGYGRRTLERRIQGMKWLA---NPELLEADA	662				
eco:b0771	DVMTTETTCISSLVWQTDEEVHNWLALHGRGQDYCQ-----L-----NPQP	280				
sce:YLR304C	CNMGAEIGATTSVFPFNKSIMEYLEATGRGKIAD-----FAKLY-----HKDLLSADK	327				
dme:Dmel(CG4706)	TNMGAEIGATTISIFPFNERMVTYL RATGRGAIAD-----EATKN-----KDLLVPDE	328				
dme:Dmel(CG9244)	CNMGAEIGATTSLFPFNQRMADYLKSTGRAGIAS-----EAQKY-----QAKILSADK	338				
cel:CELE_F54H12.1	CNMGAEIGATTSVFPYNESMYKYLEATGRKEIAE-----EARKY-----KDLLTADD	327				
mmu:11429	CNMGAEIGATTSVFPYNHMRMKKYL SKTGRTDIAN-----LAEEF-----KDHLVPDP	330				
hsa:50	CNMGAEIGATTSVFPYNHMRMKKYL SKTGRREDIAN-----LADEF-----KDHLVPDP	330				
eco:b1276	ANMSPEYGATCGFFPIDAVTL DYMRLSGRSEDQVE-----LVEKYAKA QGMWRN---PGD	355				
cel:CELE_ZK455.1	ANMCPEYGATIGFFPVDSRTIDYL TQTGRD TDY TQ-----RVEQYLKS VGMFVNFTDDSY	350				
mmu:11428	ANMCPEYGATAAFFPVDEVSIA YLL QTGREEDKV K-----HIQKYLQAVGMFRDFNDTSQ	351				
hsa:48	ANMCPEYGATAAFFPVDEVSITYLVQTGRDEEKLK-----YIKKYLQAVGMFRDFNDPSQ	351				
dme:Dmel(CG4900)	SNMCPEYGATVGYFPIDENTLSYMRQTNRSEKKID-----IIRKYLKATRQLRDYSLVDQ	363				
dme:Dmel(CG6342)	SNMCPEYGATVGYFPIDENTLG YMKQTNRSEKKID-----IIRQYLKATQQLRN YADAAQ	360				
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eco:b0118	DAEYAAVIDIDLADIKEPILCAPNDPDDARPLSAVQGEKI-----	702
eco:b0771	MAYYDGCISVDLSAIK-PMIALPFHPSNVYEIDTLNQNLTDLRE-IEIESERVAHGKAK	338
sce:YLR304C	DAEYDEVVEIDLNTLE-PYINGPFTPDLATPVSKMKEVAVA-----	367
dme:Dmel(CG4706)	GCKYDKVIEINLDTLE-PLVNGPFTPDLAHPISKLGQNSEK-----	368
dme:Dmel(CG9244)	NCEYDELIEINLDTLE-PHVNGPFTPDLGHPISKLGENSKK-----	378
cel:CELE_F54H12.1	GANYDQIIIEINLDTLT-PHVNGPFTPDLASSIDKLGENAKK-----	367
mmu:11429	GCQYDQVIEINLNELK-PHINGPFTPDLAHPVADVGTVAEK-----	370
hsa:50	GCHYDQLIEINLSELK-PHINGPFTPDLAHPVAEVGKVAEK-----	370
eco:b1276	EPIFTSTLELDMNDVE-ASLAGPKRPQDRVALPDVPKAFAASNELEVNA-----THKD	407
cel:CELE_ZK455.1	RPTYTTTLKLDLGSVV-PSVSGPKRPHDRVELASLAQDFSKGLTDKISFKAFGLKPEDAT	409
mmu:11428	DPDFTQVVELDLKTVV-PCCSGPKRPQDKVAVSEMKKDFESCLGAKQGFKGQVAPDRHN	410
hsa:48	DPDFTQVVELDLKTVV-PCCSGPKRPQDKVAVSDMKDFESCLGAKQGFKGQVAPEHHN	410
dme:Dmel(CG4900)	DPQYTESTVLDLSTVV-TSVSGPKRPHDRVSVSSMCEDFKSCLISPVGFKGFAIPPSALA	422
dme:Dmel(CG6342)	DPKFTQSITLDLSTVV-TSVSGPKRPHDRVSVDMPEDFKSCLSSPVGFKGFAIAPEAQ	419
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eco:b0118	-----DEVFIGSCMTNIGHF--RAAGKLLD-AHKGQLP---TRL	735
eco:b0771	LSLLDKV-----ENGRLKVQQGIIAGCSGGNYENVIAANALRGQSCGNNDT----FSL	387
sce:YLR304C	-----NNWP-----LDVRVGLIGSCTNSSYEDM-SRSASIVKDAAHGLKSK--TIF	411
dme:Dmel(CG4706)	-----NGYP-----MEIKVSLIGSCTNSSYEDM-GRCASIANDALGHGLKSC--VPF	412
dme:Dmel(CG9244)	-----NGYP-----MDIRVGLIGSCTNSSYEDM-GRCASIAKDAMSHGLKSK--IPF	422
cel:CELE_F54H12.1	-----NGWP-----LDVKVSLIGSCTNSSYEDM-TRAASIAKQALDKGLKAK--TIF	411
mmu:11429	-----EGWP-----LDIRVGLIGSCTNSSYEDM-GRSAAVAKQALAHGLKCK--SQF	414
hsa:50	-----EGWP-----LDIRVGLIGSCTNSSYEDM-GRSAAVAKQALAHGLKCK--SQF	414
eco:b1276	RQPVDYVMNGHQYQLPDGAVVIAAITSCTNTSNPSVLMAGLLAKKAVTLGLKRQPWKA	467
cel:CELE_ZK455.1	KSVT-ITNHGRTAELTHGSVVIAAITSCTNTSNPSVMLAAGLVAKKAVEGLGNVQPYVKT	468
mmu:11428	DRKTFLYSN-SEFTLAHGSVVIAAITSCTNTSNPSVMLGAGLLAKKAVEAGLSVKPYIKT	469
hsa:48	DHKTFIYDN-TEFTLAHGSVVIAAITSCTNTSNPSVMLGAGLLAKKAVDAGLNVMPYIKT	469
dme:Dmel(CG4900)	ASGEFWDDGKSYKIGHGSVVIAAITSCTNTSNPSVMLGAGLLAKNAVQKGLSILPYIKT	482
dme:Dmel(CG6342)	AFGEFWDDGKTYKLHHGSVVIAAITSCTNTSNPSVMLGAGLLAKKAVEKGLSILPYIKT	479

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eco:b0118	WVAPPTRMDAALTEEGYYSVFGKSGARIEIPGCSLCMGNQARAVADG-----AT	784
eco:b0771	AVYPSSQPVFMDLAKKGVADLIGAGAIIRTAFCGPCFGAGDTPIN-----NG--L	436
sce:YLR304C	TVTPGSEQIRATIERDGQLETKEFGGIVLANACGPCIGQWDRD--IKKGDKN---T	464
dme:Dmel(CG4706)	NVTPGSEQVRATIARDGIIDVLEKFGGTVLANACGPCIGQWDRKD--VKMGEKN---T	465
dme:Dmel(CG9244)	NVTPGSEQIRATIERDGISEVFDKFGGTVLANACGPCIGQWDRKD--VKKGDKN---T	475
cel:CELE_F54H12.1	TITPGSEQVRATIERDGLSKIFADFGGMVLANACGPCIGQWDRQD--VKKGEKN---T	464
mmu:11429	TITPGSEQIRATIERDGYAQILRDVGGIVLANACGPCIGQWDRKD--IKKGEKN---T	467
hsa:50	TITPGSEQIRATIERDGYAQILRDLGGIVLANACGPCIGQWDRKD--IKKGEKN---T	467
eco:b1276	SLAPGSKVSDYLAKAKLTPYLDELGFNLVGYGCTTCIGNSGPLDPPIETAIKSDLTVG	527
cel:CELE_ZK455.1	SLSPGSGVVTKYLEASGLLPYLEKIGFNIAGYGCMTCIGNSGPLDEPVTKAIEENNLLVVA	528
mmu:11428	SLSPGSGVVYYLRESGVMPYLSQLGFDVVGYGCMTCIGNSGPLPEPVVEAITQGDLVAV	529
hsa:48	SLSPGSGVVYYLQESGVMPYLSQLGFDIVGYGCMTCIGNSGPLPEPVVEAITQGDLVAV	529
dme:Dmel(CG4900)	SLSPGSGVVYYLRESGVIPYLEQLGFDIVGYGCMTCIGNSGPLDENVVNTIEKNGLVCC	542
dme:Dmel(CG6342)	SLSPGSGVVYYLKESGVIPYLEKLGF DIVGYGCMTCIGNSGPLEENVVNTIEKNGLVCA	539
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eco:b0118	VVSTSTRNFPNRRLGTGAN--VFLASAEELAAVALIGKLPTPEEY-----	826
eco:b0771	SIRHTTRNFPNREGSKPAN-GQMSAVALMDARSIAATAA--NGGYLT----SASELD	486
sce:YLR304C	IVSSYNRNFTSRNDGNPQTHAFVASPELVTAFAIAGRQLDFNPMTDELT-GTDGKTFKLKE	523
dme:Dmel(CG4706)	IVTSYRNFTGRNDANPATHCFVTSPEMATALAIAGRLDFNPMTDELT-GTDGKTFKLKE	524
dme:Dmel(CG9244)	IVTSYRNFTGRNDANPATHCFVTSPELVTAISIAGRQLDFNPMTDELT-GADGKKFKLKA	534
cel:CELE_F54H12.1	IVTSYRNFTGRNDANPATHGFVTSPEITTAMAISIAGRQLDFNPMTDELT-AADGSKFKLQA	523
mmu:11429	IVTSYRNFTGRNDANPETHAFVTSPEIVTALAIAGTLKFNPETDFLT-GKDGGKKFKLEA	526
hsa:50	IVTSYRNFTGRNDANPETHAFVTSPEIVTALAIAGTLKFNPETDFLT-GTDGKKFRLEA	526
eco:b1276	AVLSGNRNFEGRIRHPLVKT-NWLASPPLVVAYALAGNMNINLASEPIGHDRKDPVYLKD	586
cel:CELE_ZK455.1	GVLSGNRNFEGRIRHPHVRA-NYLASPPLVLYSIIGNVNVDING-VLAVTPDGKEIRLAD	586
mmu:11428	GVLSGNRNFEGRVHPNTRA-NYLASPPLVIAYAIAGTVRIDFEKEPLGVNAQGRQVFLKD	588
hsa:48	GVLSGNRNFEGRVHPNTRA-NYLASPPLVIAYAIAGTIRIDFEKEPLGVNAKGQQVFLKD	588
dme:Dmel(CG4900)	GVLSGNRNFEGRIRHPNTRA-NYLASPPLVIAYAIAGRVIDDFEIEPLGVDSNGKEVFLRD	601
dme:Dmel(CG6342)	GVLSGNRNFEGRIRHPNTRA-NYLASPPLVIAYAIAGRVIDDFEKEPLGVVDANGKNVFLQD	598
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eco:b0118	-QTYVAQVDKTA CWDNVPEYAF	-QYT-EKADGVIFQTA-	864 517
eco:b0771	-DVTPYKNRVYQGFVKGATQ	-QP	517
sce:YLR304C	P--HGDGLPQRG	-Y-DAGENTYQAPPADRSTVEVKVSPTSDRLQLLK	566
dme:Dmel(CG4706)	P--HGEELPSKG	-F-DPGEDTYQAPPAKADDIKVNVDPKSDRLQLLE	567
dme:Dmel(CG9244)	P--FGDELPAKG	-F-DPGQDTYTAPPPSGENVKAVDPKSTRLQLLE	577
cel:CELE_F54H12.1	P--TGLDLPPKG	-Y-DPGEDTFQAPSG--SGQVDVSPSSDRLQLLS	563
mmu:11429	P--DADELPRTS	-F-DPGQDTYQHPPKDSSGQRVDVSPSTSQRQLLE	569
hsa:50	P--DADELPKGE	-F-DPGQDTYQHPPKDSSGQHVVDVSPSTSQRQLLE	569
eco:b1276	IWPSAQEIARAVE-QVSTEMFRKEYAEVFEGTAEWKGINVTRS	-DTYGWQEDSTYIRLSP	644
cel:CELE_ZK455.1	IWPTRKEVAKFEEEFVKPQFFREVYANIELGSTEWQQLECPAV	-KLYPWDDASTYIKKP	645
mmu:11428	IWPTRDEIQAVERQHQVIPGMFKEVYQKIEVTVNKSWNALAPSE	-KLYAWNPKSTYIKSPP	647
hsa:48	IWPTRDEIQAVERQYVIPGMFKEVYQKIEVTVNESWNALATPSD	-KLFFWNSKSTYIKSPP	647
dme:Dmel(CG4900)	IWPTRSEIQEVEHKHVIPAMFQEVSYSKIQLGSRDWQTLEVSDS	-KLYPWSEISTYIKLPP	660
dme:Dmel(CG6342)	IWPTRSEIQEVENKHVIPAMFQEVSYSKIELGSQDWQTLQVSEG	-KLFSWSADSTYIKRPP	657

eco:b0118	-V-	-	865
eco:b0771	LIYGPNIKDWP ELGALT	DNIVLK CSKILDEV TTTDEL IPSGETSS	-YRSNP 568
sce:YLR304C	PFK-PWDGKDAKDM	-PILIKAVGK CTTDHISAGPW LK	-YRGHL 607
dme:Dmel(CG4706)	PFE-KWDGKD YIDL	-MVL LIKIGK CTTDHISAGPW LK	-YRGHL 608
dme:Dmel(CG9244)	PFD-KWNGQDL TDL	-TVL IKVKGK CTTDHISAGPW LK	-YRGHL 618
cel:CELE_F54H12.1	PFD-KWDGKD LEDL	-KIL IKVTGK CTTDHISAGPW LK	-YRGHL 604
mmu:11429	PFD-KWDGKD LEDL	-QIL IKVKGK CTTDHISAGPW LK	-FRGHL 610
hsa:50	PFD-KWDGKD LEDL	-QIL IKVKGK CTTDHISAGPW LK	-FRGHL 610
eco:b1276	FFDEM QATPAP VEDI HGA	-RILA MLGDS VTTDHIS PAGSI KPD SPAGRY LQGR GVE	699
cel:CELE_ZK455.1	FFDGMTSEL PSQSD IVNA	-HVLLNL GDS VTTDHIS PAGSI KTS SPAAR FLAG RGVT	700
mmu:11428	FFESLTLDL QPPP KSIV DVA	-YVLLNL GDS VTTDHIS PAGNI ARN SPAARY LTNR GLT	702
hsa:48	FFENLTLDL QPPP KSIV DVA	-YVLLNL GDS VTTDHIS PAGNI ARN SPAARY LTNR GLT	702
dme:Dmel(CG4900)	FFEGMT RALPKL KGIE KA	-RCL LLL GDS VTTDHIS PAGSI ARK SPAARY LSEL GLT	715
dme:Dmel(CG6342)	FFEGMT RDLPLK LQS IQKA	-RCL LFL GDS VTTDHIS PAGSI ART SPAAR FLSER NIT	712

eco:b0118	-	865
eco:b0771	IGLAEFTLSRRDPGY-VSRS-KATAELENQRLAGNVSELTEVFARIKQIAGQEHDPLQ-	625
sce:YLR304C	ENISNNYM-----IGAINAENKKANC-----VKNVYTGEYKGVPDT	643
dme:Dmel(CG4706	DNISNNMF-----IGATNAENNEMNK-----VKNQKTGSFDAVPAV	644
dme:Dmel(CG9244	DNISNNMF-----IGATNYENNEMNN-----IKNQRNGSWGGVPDV	654
cel:CELE_F54H12.1	DNISNNLF-----LTAINADNGEMNK-----VKNQVTGEYGAVPAT	640
mmu:11429	DNISNNLL-----IGAINIENGKANS-----VRNAVQTQEFGPVPDT	646
hsa:50	DNISNNLL-----IGAINIENGKANS-----VRNAVQTQEFGPVPDT	646
eco:b1276	RKDFNSYGSRRGNHEVMMRGTFANIRIRNEMVPGVEGG-----MTRHLPSDSDVVSIYDA	753
cel:CELE_ZK455.1	PRDFNTYGARRGNDEIMARGTFANIRLVNKLASK-VGP-----ITLHVPSGEELDIFDA	753
mmu:11428	PREFNSYGSRRGNDAIMARGTFANIRLLNKFLNK-QAP-----QTVHLPSGETLDVFDA	755
hsa:48	PREFNSYGSRRGNDAVMARGTFANIRLLNRFLNK-QAP-----QTIHLPSGEILDVFDA	755
dme:Dmel(CG4900	PRDFNSYGSRRGNDAVMARGTFANIRLVNKLASK-TGP-----STLHVPSGEEMDIFDA	768
dme:Dmel(CG6342	PRDFNSYGSRRGNDAIMSRGTFANIRLVNKLVEK-TGP-----RTVHIPSQEELDIFDA	765

eco:b0118	-	865
eco:b0771	-TEI-GSMVYAVKPGDGSAREQAACQRVIGGLANIAEEYATKRYRSNVINWGML	678
sce:YLR304C	ARDYRDQGIKWVVGDENFGEGSSREHAALEPRHLGGFAIITKSFAR-IHETNLKKQGLL	702
dme:Dmel(CG4706	ARDYKANKIKWCAVGEENYGEKGSSREHAALEPRHLGGVIIIVKSFAR-IHETNLKKQGLL	703
dme:Dmel(CG9244	ARDYKANGIKWAVGDENYGEKGSSREHAALEPRHLGGRAIIVKSFAR-IHETNLKKQGLL	713
cel:CELE_F54H12.1	ARKYKADGVRVWAIGDENYGEKGSSREHAALEPRHLGGRAIIVKSFAR-IHETNLKKQGLL	699
mmu:11429	ARYYKKHGIRWVVGDENYGEKGSSREHAALEPRHLGGRAIITKSFAR-IHETNLKKQGLL	705
hsa:50	ARYYKKHGIRWVVGDENYGEKGSSREHAALEPRHLGGRAIITKSFAR-IHETNLKKQGLL	705
eco:b1276	AMRYKQEQTPLAVIAGKEYGSGSSRDWAAKGPRLLGIRVIAESFER-IHRSNLIGMGIL	812
cel:CELE_ZK455.1	AQKYKDAGIPAIILAGKEYGCGSSRDWAAKGPFLQGVKAVIAESFER-IHRSNLIGMGII	812
mmu:11428	AERYQQAGLPLIVLAGKEYGSGSSRDWAAKGPFLLGIKAVLAESYER-IHRSNLVGMGVI	814
hsa:48	AERYQQAGLPLIVLAGKEYGAGSSRDWAAKGPFLLGIKAVLAESYER-IHRSNLVGMGVI	814
dme:Dmel(CG4900	AERYASEGTPVLVVGKDYGSGSSRDWAAKGPFLLGIKAVIAESYER-IHRSNLVGMGII	827
dme:Dmel(CG6342	AERYREEGTPVLVVGKDYGSGSSRDWAAKGPFLLGKVAVIAESYER-IHRSNLVGMGII	824

eco:b0118		865
eco:b0771	PLQMAEVPTFEVGD-----YIYIPGIKAALDNPGTTFKGYVIHEDAPVTEITLYMESLTA	733
sce:YLR304C	PLNFKNPADYDKIN--PDDRIDILGLAE--LAPGKPVTMRVHPKNGKPWDAVLTHFT-ND	757
dme:Dmel(CG4706	ALTFANPGDYDKVQ--PSSKISILNLKD--LAPGKPVDAEIKN-NGSSDKIQLNHTL-NE	757
dme:Dmel(CG9244	PLTFANPADYDKIQ--PTSKISLLNLKS--LAPGKPVDAEIKN-GDKVERIKLNHTL-ND	767
cel:CELE_F54H12.1	PLTFANPADYDKID--PSDNVSIVGLSS--FAPGKPLTAIFKKTNGSKVEVTLNHTF-NE	754
mmu:11429	PLTFADPSDYNKIH--PVDKLTIQGLKD--FAPGKPLKCVIKHPNGTQETILLNHTF-NE	760
hsa:50	PLTFADPADYNIKIH--PVDKLTIQGLKD--FTPGBKLCIIKHPNGTQETILLNHTF-NE	760
eco:b1276	PLEFPQGVTRKTLGLTGEEKIDIGDLQN--LQPGATVPVTLTRADGSQEVVPCRCRDTA	870
cel:CELE_ZK455.1	PFQYQAGQNADSLGLTGKEQFSIGVPDD--LKPGQLIDVNVSN---GSVFQVICRFDTE	866
mmu:11428	PLEYLPGETADSLGLTGRERYTINIPED--LKPRMTVQIKLDT--GKTFQAVMRFDTD	868
hsa:48	PLEYLPGENADALGLTGQERYTIIIPEN--LKPQMKVQVKLDT--GKTFQAVMRFDTD	868
dme:Dmel(CG4900	PLQFLPGQSADTLKLSGREVYNIVLPEG-ELKGPGQRIQVD-AD--GNVFETTLRFDTE	881
dme:Dmel(CG6342	PLQFLPGQSACETLNLTGREVYNIALPES-GLKPGQKIQVE-AD--GTVFETILRFDTE	878

eco:b0118	-----	865
eco:b0771	EEREIIKAGSSLINFNRQM-----	753
sce:YLR304C	EQIEWFKAGSALNMRKELAKGGDKK-----	778
dme:Dmel(CG4706	LQIQWFQAGSALNLMKELAAKGGDKK-----	783
dme:Dmel(CG9244	LQIGWFKAGSALNRMKELAQ-----	787
cel:CELE_F54H12.1	QQIEWFKAGSALNRMKEVFAKSK-----	777
mmu:11429	TQIEWFRAGSALNRMKELQQ-----	780
hsa:50	TQIEWFRAGSALNRMKELQQ-----	780
eco:b1276	TELTYYQNDGILHYVIRNMLK-----	891
cel:CELE_ZK455.1	VELTYYRNNGGILQYMIRKLIQ-----	887
mmu:11428	VELTYFHNGGILNYMIRKMAQ-----	889
hsa:48	VELTYFLNGGILNYMIRKMAK-----	889
dme:Dmel(CG4900	VDIRTYYKNGGILNYMIRKMLD-----	902
dme:Dmel(CG6342	VDIRTYYKNGGILNYMIRKMLS-----	899

```

#
#
# Percent Identity Matrix - created by Clustal2.1
#
#
1: eco_b0118      100.00   19.91   22.04   20.54   20.12   18.83   19.83   19.21   20.44   21.89   20.20   21.00   20.36   21.23
2: eco_b0771      19.91   100.00   23.46   23.64   22.89   23.16   24.51   24.81   20.61   21.55   20.39   20.11   20.58   21.54
3: sce_YLR304C    22.04   23.46   100.00   63.61   66.67   67.36   66.93   66.54   26.52   26.90   29.48   28.95   28.68   26.91
4: dme_Dmel(CG4706) 20.54   23.64   63.61   100.00   79.12   71.50   69.43   69.43   25.83   28.70   28.23   28.23   28.76   27.51
5: dme_Dmel(CG9244) 20.12   22.89   66.67   79.12   100.00   73.38   72.46   72.46   26.26   27.81   28.40   27.47   28.01   27.95
6: cel_CELE_F54H12.1 18.83   23.16   67.36   71.50   73.38   100.00   73.22   73.22   26.69   28.07   28.27   28.13   29.67   28.74
7: mmu_11429      19.83   24.51   66.93   69.43   72.46   73.22   100.00   96.79   27.98   28.30   28.36   28.10   28.17   27.38
8: hsa_50          19.21   24.81   66.54   69.43   72.46   73.22   96.79   100.00   27.59   28.44   28.63   27.96   28.44   27.51
9: eco_b1276      20.44   20.61   26.52   25.83   26.26   26.69   27.98   27.59   100.00   52.69   51.77   51.77   52.49   52.61
10: cel_CELE_ZK455.1 21.89   21.55   26.90   28.70   27.81   28.07   28.30   28.44   52.69   100.00   63.28   63.05   64.29   64.86
11: mmu_11428      20.20   20.39   29.48   28.23   28.40   28.27   28.36   28.63   51.77   63.28   100.00   93.36   68.66   69.00
12: hsa_48          21.00   20.11   28.95   28.23   27.47   28.13   28.10   27.96   51.77   63.05   93.36   100.00   67.87   68.32
13: dme_Dmel(CG4900) 20.36   20.58   28.68   28.76   28.01   29.67   28.17   28.44   52.49   64.29   68.66   67.87   100.00   87.54
14: dme_Dmel(CG6342) 21.23   21.54   26.91   27.51   27.95   28.74   27.38   27.51   52.61   64.86   69.00   68.32   87.54   100.00

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CITRATE LYASE

CLUSTAL O(1.2.4) multiple sequence alignment

cel:CELE_B0365.1	MSAKAVSELSGKEVLYKYFESTGIVSAPHAFH-VKAGDKFSDVAAKYEWLAQDNKGVIKP	59
cel:CELE_D1005.1	MSAKAVSELSGKEVLYKYFEPSGLLSAPHAFH-VKAGENFDEIANKYEWLARDNKGVIKP	59
dme:Dmel(CG8322)	MSAKAITEASGKDILNRHLNTHGAGAACATCRFSTVNSTTDWSKLAVDHPWLLTT-PLVCKP	59
mmu:104112	MSAKAISEQTGKELLYKYICTTSAIQNRFKYARVTPD TDWAHLLQDH PWLLSQ-SLVVKP	59
hsa:47	MSAKAISEQTGKELLYKFICTTSAIQNRFKYARVTPD TDWARLLQDH PWLLSQ-NLVVKP	59
	*****: : * : * : * . . : * . . : . : ** * **	
cel:CELE_B0365.1	DQLIKRRGKLGLVKIGSP-KELEAWFGKTANSYVKVGQTEGRHLHTFIVEPFCAHTENEEM	118
cel:CELE_D1005.1	DQLIKRRGKLGLVKIGTP-QELKAWEKTGDSYVRVGQTEGRHLHTFIVEPFCAHTEKDEM	118
dme:Dmel(CG8322)	DQLIKRRGKLGLIGVKKNFEQVKQWIGERLNKDQKIGNAVGKLRNFIIEPFVPHDAEEM	119
mmu:104112	DQLIKRRGKLGLVGVNLSLDGVKSWLKPRLGHEATVGKAKGFLKNFLIEPFVPHSQAEFF	119
hsa:47	DQLIKRRGKLGLVGVNLTLDGVKSWLKPRLGQEATVGKATGFLKNFLIEPFVPHSQAEFF	119
	*****: : . . : * : . : * : * : . : * : *** * : : : * :	
cel:CELE_B0365.1	YIAIYSERC RDVIMFYEQGGVDIGDVEEKARSVHVPVQLDDNAMSISERELGVLLGPCSD	178
cel:CELE_D1005.1	YIAIYSERFRDVIMFYEQGGVDIGDVEEKARTSVPVQLNENAMTPSDEELTLLGPLKD	178
dme:Dmel(CG8322)	YVCIYSHRAADTILFYHQGGVDIGDVKDAKAVKLDVPVNSSLSLADVSK-LLKEVKDAGT	178
mmu:104112	YVCIYATREGDYVLFHHEGGVDVGVDAKAQKLLGVDEKLNTEDIKRH-LLVHAP-EDK	177
hsa:47	YVCIYATREGDYVLFHHEGGVDVGVDAKAQKLLGVDEKLNPEDIKKH-LLVHAP-EDK	177
	* : . : * : * : * : : * : : * : : * : : * : : * :	

cel:CELE_B0365.1	KDDIRKFVRSLYEAYKALHFTYLEINPFVLTNGKIHI LDLAAKLDEASFLCSDKWSGRN	238
cel:CELE_D1005.1	SDIVRRFVVELYKAYKDLHFTYLEINPFVLLNNQIHVL DLAARLDETANFLCADWKWSRL	238
dme:Dmel(CG8322)	KERIAKFVSALYTTYVDLYFTYLEINPLVVTADNL YILDLAAKLDSTADFIGCRPKWG---	235
mmu:104112	KEVLASFISGLFNFYEDLYFTYLEINPLVVT KDGVYILDLAAKVDATA DYICKVKWG---	234
hsa:47	KEILASFISGLFNFYEDLYFTYLEINPLVVT KDGVYVLDLAAKVDATA DYICKVKWG---	234
	. : *: *: * *:*****: * . :*****: * **. :* **	
cel:CELE_B0365.1	ASARIAPTLFPAPFGRDLTSEEQYISDM DAKTGASLKL TILNRKGRVWTMVAGGGASVV	298
cel:CELE_D1005.1	TPYGGPNHVEFPAPFGRDLTSEEQYISEMD AKTGASLKL TILNRKGRVWTMVAGGGASVV	298
dme:Dmel(CG8322)	-----EIDYPPP FGRDAYPEEAYIADL DAKSGASLKL TILNRNGRIWTMVAGGGASVI	288
mmu:104112	-----DIEFPPP FGREAYPEEAYIADL DAKSGASLKL TLLNPKGRIWTMVAGGGASVV	287
hsa:47	-----DIEFPPP FGREAYPEEAYIADL DAKSGASLKL TLLNPKGRIWTMVAGGGASVV	287
	:*: * **: ** * :* :*****: * :* :*****: *	
cel:CELE_B0365.1	FTDTVCDLGGSELANYGEYSGDPSEA QTYEYAKTIL SVMTEGAPR PDGVLIIGGSIAN	358
cel:CELE_D1005.1	FTDTVCDLGGASELANYGEYSGDPSE SQTYEYAKT LLSVMTEG TPRPDGKVLIIGGSIAN	358
dme:Dmel(CG8322)	YSDTICDLGGASELANYGEYSGAP SEQQT YEYAKT ILNLM TSSPKHPDG KVLIITGGGIAN	348
mmu:104112	YSDTICDLGGVNE LANYGEYSGAP SEQQT DYAKT ILSLMTR-EKH PEGKILII GGSIAN	346
hsa:47	YSDTICDLGGVNE LANYGEYSGAP SEQQT DYAKT ILSLMTR-EKH PDGKILII GGSIAN	346
	:*:***** .*****: *** * :* :* :* .:*** :* :* :* :* .:***	

cel:CELE_B0365.1	FTNVAKTFGGIVRAFETFIDKLKEHNVSIYVRRGGPNYQEGLRRVKDAATKLEIPIYVFG	418
cel:CELE_D1005.1	FTNVAKTFGGIVRAFETFVSKLKEHKVTIFVRRGGPNYQEGLRRIKDAATKLELPIHVFG	418
dme:Dmel(CG8322)	FTNVAATFQGIITALREFQPKLVEHNVSIFVRRAGPNYQEGLRKMRDFGSTLGIPLVFG	408
mmu:104112	FTNVAATFKGIVRAIRDYQGPLKEHEVTIFVRRGGPNYQEGLRVMGEVGKTTGIPIHVFG	406
hsa:47	FTNVAATFKGIVRAIRDYQGPLKEHEVTIFVRRGGPNYQEGLRVMGEVGKTTGIPIHVFG	406
	***** * *: *.. : * *;*:***,***** : : ... :*;***	
cel:CELE_B0365.1	PETHMTAIVGAALGLKPMPTVPTAPQTTGQFLLSPERNAGTER-----P	463
cel:CELE_D1005.1	PETHMTAIVGAALGVKPMPTVPTAPQTTGQFLLSPERNNTGGTER-----A	463
dme:Dmel(CG8322)	PETHMTAICGMALGKRPIPQTASVEFSTANFLLPGGQQAQADLKAASDASEALGSGSALS	468
mmu:104112	TETHMTAIVGMALGHRPIPQPPATAHTANFLLNASGSTSTPAPSRTA-SFSESRADEVA	465
hsa:47	TETHMTAIVGMALGHRPIPQPPATAHTANFLLNASGSTSTPAPSRTA-SFSESRADEVA	465
	***** * *** :*:* . .:*** ..	
cel:CELE_B0365.1	PASPAP-----NTSTIEHPLAKRH----PLHQSLFENDTKAIIWGQQHKAIQGMLDFD	512
cel:CELE_D1005.1	PPSPAA-----NATPTEHPLTTAQQNKLKSFRGLFEDDTKAIIWGQQAKAIQGMLDFD	516
dme:Dmel(CG8322)	PTAAKPIKLPPISADEADSAGISGAQRNGSSLNRKFFSNTTKAIIVWGMQQRAVQSMLDFD	528
mmu:104112	PAKKA---KPAMPQ-----GKSATLFSRHTKAIIVWGMQTRAVQGMLDFD	506
hsa:47	PAKKA---KPAMPQDS-----VPSPRLQGKSTTLFSRHTKAIIVWGMQTRAVQGMLDFD	516
	* :*. ****:*** * :*;*.*****	

cel:CELE_B0365.1	FVCRRHSPSVVASTYPFTGDNKQKYYFGQKEILIPAYKSMAKAFASHPDATVMVTFASMR	572
cel:CELE_D1005.1	YVCRRSSPSVVASTYPFTGDNKQKYYFGQKEILIPAYKSMAKAFATHPDASIMVTFASMR	576
dme:Dmel(CG8322)	FICRRDEPSVVAMVYPFTGDKHQKYYWGHKEILIPVYKKMSDAIHKHKEVDVMVNFAASMR	588
mmu:104112	YVCSRDEPSVAAMVYPFTGDHKQKFYWHGKEILIPFKNMADAMKKHPEVDVLINFAASLR	566
hsa:47	YVCSRDEPSVAAMVYPFTGDHKQKFYWHGKEILIPFKNMADAMRKHPEVDVLINFAASLR ::* * .****.* .*****:***:*:*****.:.**:.*: .* :. :****:*	576
cel:CELE_B0365.1	SVFETVLEALQFTQIKVIAIIAEGVPENQTRKLLKIAEDKGVTLIGPATVGGIKPGCFKI	632
cel:CELE_D1005.1	SVFETVLEALEFPQIKVIAIIAEGVPENQTRKLLKIAHDRGVTLVGPATVGGIKPGCFKI	636
dme:Dmel(CG8322)	SAYESTLEVLEFPQIRTVAIIAEGIPENMTRKLIIEADKKGVAIIGPATVGGVKPGCFKI	648
mmu:104112	SAYDSTMETMNYAQIRTIAIIAEGIPEALTRKLICKADQKGVTIIGPATVGGIKPGCFKI	626
hsa:47	SAYDSTMETMNYAQIRTIAIIAEGIPEALTRKLICKADQKGVTIIGPATVGGIKPGCFKI *.:.:.*.::: **.:*****:*** ****: *..:***:*****:*****	636
cel:CELE_B0365.1	GNTGGMMDNILASKLYRPGSVAYVSRSGGMSNELNNIISQNTNGVYEGIAIGGDRYPGST	692
cel:CELE_D1005.1	GNTGGMMDNILASKLYRPGSVAYVSRSGGMSNELNNIISQNTNGVYEGIAIGGDRYPGST	696
dme:Dmel(CG8322)	GNTGGMLDNILHSKLYRPGSVAYVSRSGGMSNELNNIISKATDGVIEGIAIGGDRYPGST	708
mmu:104112	GNTGGMLDNILASKLYRPGSVAYVSRSGGMSNELNNIISRTTDGVYEGVAIGGDRYPGST	686
hsa:47	GNTGGMLDNILASKLYRPGSVAYVSRSGGMSNELNNIISRTTDGVYEGVAIGGDRYPGST *****:**** *****:*****:*****: *:*** **:*****	696

cel:CELE_B0365.1	YTDHVMRYQHDDRVKMIVLLGEVGGIEEYRIVELLKEKKITKPLIAWCIGTCADHITSEV	752
cel:CELE_D1005.1	YTDHVIRYQNDDRVKMIVLLGEVGGVEEYKIVDLLQKKVTKPLVAWCIGTCADHITSEV	756
dme:Dmel(CG8322)	FMDHILRYQADPETKLIVLLGEVGGTEEYDVCAALKDGRITKPLVAWCIGTCASMFTSEV	768
mmu:104112	FMDHVLRYQDTPGVKMIVVLGEIGGTEEYKICRGRIKEGRLTKPVVCWCIGTCATMFSSEV	746
hsa:47	FMDHVLRYQDTPGVKMIVVLGEIGGTEEYKICRGRIKEGRLTKPIVCWCIGTCATMFSSEV	756
	: *:**** .*:****:*** *** : :*: :****:***** :****	
cel:CELE_B0365.1	QFGHAGASANGQGETAACNTALRTAGALVPDSFDDLGNKIRQTYEELLRLEIIVPQPEV	812
cel:CELE_D1005.1	QFGHAGASANALGETAACNAALRASGALVPESFDDLGNKIRQTYDELVSQQIIVPQPEV	816
dme:Dmel(CG8322)	QFGHAGSCANSRETATAKNKGLRDAGAYVPDSFDLGEELIHVVYGELVKTGRVVPKEEV	828
mmu:104112	QFGHAGACANQASETAVAKNQALKEAGVFVPRSFDELGEIIQSVDLVAKGAIIVPAQEV	806
hsa:47	QFGHAGACANQASETAVAKNQALKEAGVFVPRSFDELGEIIQSVDLVANGVIVPAQEV	816
	*****:.* *.* .*: :*. ** *** **: *: .* :*: :** **	
cel:CELE_B0365.1	PPPAVPMDYAWARELGLIRKPASFMTSICDERGEELNYAGVPITKVLESDMGIGGVVLGLL	872
cel:CELE_D1005.1	PPPAVPMDYAWARELGLIRKPASFMTSICDERGEELNYAGVPITKVLESDMGIGGVVLGLL	876
dme:Dmel(CG8322)	PPPTVPMDYSWARELGLIRKPASFMTSICDERGQELIYAGMPISEVLSKDVGIGGVISLL	888
mmu:104112	PPPTVPMDYSWARELGLIRKPASFMTSICDERGQELIYAGMPITEVFKEEMGIGGVVLGLL	866
hsa:47	PPPTVPMDYSWARELGLIRKPASFMTSICDERGQELIYAGMPITEVFKEEMGIGGVVLGLL	876
	:**:*****:*****:*****:*** ***:***:***:***:*****:***	

cel:CELE_B0365.1	WFQKRLPPHANKFIEICLMLTADHGP AVSGA HNTIVCARAGKDL I SSL T GLL T IGDRFG	932
cel:CELE_D1005.1	WFQKRLPPHANKFIEICLMLTADHGP AVSGA HNTIVCARAGKDL I SSL T GLL T IGDRFG	936
dme:Dmel(CG8322)	WFQRCLPSYVCKFFEMCLMVTADHGP AVSGA HNTIVCARAGKDL I VSSVVSGLL T GDRFG	948
mmu:104112	WFQRRLPKYSCQFIEMCLMVTADHGP AVSGA HNTIIICARAGKDL I VSSL T GLL T IGDRFG	926
hsa:47	WFQKRLPKYSCQFIEMCLMVTADHGP AVSGA HNTIIICARAGKDL I VSSL T GLL T IGDRFG	936
	*****: ** : :*:***:*****:*****:*****:*****:***.*****	
cel:CELE_B0365.1	GALDGAARQFSEAFDQGW SPN QFVGEMRK R GTHIMGIGHRV KSINN PDKRVEILKRFALN	992
cel:CELE_D1005.1	GALDGAARQFSEAFDQGW SAN QFVSEMRKK G KHIMGIGHRV KSINN PDKRVEILKRFAMD	996
dme:Dmel(CG8322)	GALDGSARQFSEAYDTNLHPMEFVN KMRKEG KLILGIGHRV KSINN P D V R V K I I KEFVLE	1008
mmu:104112	GALDAAAKMFSKA FD SGIIPMEFVN KMKKEG KLIMGIGHRV KSINN P D M R V Q I L KDFVKQ	986
hsa:47	GALDAAAKMFSKA FD SGIIPMEFVN KMKKEG KLIMGIGHRV KSINN P D M R V Q I L KDYVRQ	996
	****.**: **:***:*. . .:*.**:*. *. *:*****:***** **:***:*. . :	
cel:CELE_B0365.1	KKEFAQETPLLDYALEVEKITTAKKP NL LNV D GAI IA IIFVDILRN S GMFTTA E AQEVIE	1052
cel:CELE_D1005.1	KKEFAQETPLFEYALEVEKITTAKKP NL LNV D GAI IA IILFVDILRHSGMFTK Q EAEETIE	1056
dme:Dmel(CG8322)	N---FPACPLL K YALEVEKITTNNKP NL LNV D GVIATAFV D MLRN S GSFT T EEAQ EY IN	1065
mmu:104112	H---FPATPLLDYALEVEKITT SK KP NL LNV D GFIGVA F V D MLRN C GSFTREEADEYVD	1043
hsa:47	H---FPATPLLDYALEVEKITT SK KP NL LNV D GLIGVA F V D MLRN C GSFTREEADEYID	1053
	: ***.*****:*****:*. .:***:*. * ** ***:***::	

cel:CELE_B0365.1	IGALNGMFVLGRSIGFIGHYLDQSRLKQGLYRHPWDDISYIMPERNL---	1099
cel:CELE_D1005.1	IGSLNGLFVLGRSIGFIGHYLDQSRLKQGLYRHPWDDISYIMPESNLVKF	1106
dme:Dmel(CG8322	VGAISNSLFVLGRSIGFIGHYMDQKRLKQGLYRHPWDDISYVIPEQYN---	1112
mmu:104112	IGALNGIFVLGRSMGFIGHYLDQKRLKQGLYRHPWDDISYVLPEHMSM--	1091
hsa:47	IGALNGIFVLGRSMGFIGHYLDQKRLKQGLYRHPWDDISYVLPEHMSM--	1101

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```
#  
#  
# Percent Identity Matrix - created by Clustal2.1  
#  
#  
  
1: cel_CELE_B0365.1 100.00 87.35 63.19 62.68 62.42  
2: cel_CELE_D1005.1 87.35 100.00 61.40 61.50 61.20  
3: dme_Dmel(CG8322 63.19 61.40 100.00 70.00 69.45  
4: mmu_104112 62.68 61.50 70.00 100.00 98.08  
5: hsa_47 62.42 61.20 69.45 98.08 100.00
```

CITRATE SYNTHASE

CLUSTAL 0(1.2.4) multiple sequence alignment

eco:b0720	-----	-MADTKAKLTLNGDT---A	15
sce:YPR001W	-MVQRLLPG--AHICRRSF-----N-SSAIKSSALTLEALENVIPKKR		41
dme:Dmel(CG14740)	-----MQKTNNY---KSFKIFFKNVPFRSYPDCKNGKGSGLKAKLAKKIPIER		45
sce:YCR005C	-----MTVVPYL-----NSNRN-----VASYLQSNSSQEKTLEKFSEIYPIHA		38
sce:YNR001C	MSAILSTTSKSFLSRGSTRQCQNMQKALFA--LLNARHYSSASEQTLKERFAEIIPIKA		57
cel:CELE_T20G5.2	-MSLSGMAIRRLITKGVIPV-----C-----QVAPLSTS AEGSTNLKEVL SKKIPAHN		47
dme:Dmel(CG3861)	-MSLYRISA-RKLSEAQKLP-----N-----VGAYVRMIAADGKSLRDVLAAKVPSEQ		46
mmu:71832	-MALLTAAA-WFLG-TKNPP-----C-----LVLAARHASASSTNLKDVLRLNLIKEQ		45
mmu:12974	-MALLTAAT-RLLG-AKNSS-----C-----LVLAARHASASSTNLKDVL SNLIPKEQ		45
hsa:1431	-MALLTAAA-RLLG-TKNAS-----C-----LVLAARHASASSTNLKDILADLIPKEQ		45
		: : :	
eco:b0720	VELDVLKGTLGQDVDIRTLGSKG VFTDPGFTSTASCESKITFIDGDEGILLHRGF PID		75
sce:YPR001W	DAVKKL KACYGSTFVGPITI-----SSV LGGMRGNQSMFWQGTS LDPEHGIKF-QGLTIE		95
dme:Dmel(CG14740)	EKFLGIKCLHGKKIIGQISV-----NSV IGGMRGLPLLF CETSSL DKNKG IYY-RGKLLK		99
sce:YCR005C	QDVRQFVK EHGKT KISDVLL-----EQV YGGMRGIPGSV WEGSVLD PEEGIRF-RGRTIA		92
sce:YNR001C	EEIKKF KK EHGKT VIGEVLL-----EQAYGGMRGIKGLV WEGSVLD PEEGIRF-RGRTIP		111
cel:CELE_T20G5.2	AKVKSFRTEHGSTVVQNVNI-----DMI YGGMRSMKG MV TETSVLD PEEGIRF-RGYSIP		101
dme:Dmel(CG3861)	ERVKNFRKQHGATKMGETTI-----DM MYGGMRGIKALV TETSVLD ADEGIRF-RGLSIP		100
mmu:71832	ARIKTFRKKHGKT VVGQITV-----DM MYGGMRGMKGLV YETSVLD PDEGIRF-RGYSIP		99
mmu:12974	ARIKTFKQQHGKT VVGQITV-----DM MYGGMRGMKGLV YETSVLD PDEGIRF-RGYSIP		99
hsa:1431	ARIKTFRQQHGKT VVGQITV-----DM MYGGMRGMKGLV YETSVLD PDEGIRF-RGFSIP		99
	. : * : : * : . * : : : * : .** : * : :		

eco:b0720	QL-----ATDSNY-LEVCYILLNGEKPTQEQQYDEFKTTVTRHT-MIHEQITRLFHA	124
sce:YPR001W	ECQNRLPNTGIDGDNFLPESMLWLLMTGGVPTFQQAASFRKELAIRGRKLPHYTEKVLS	155
dme:Dmel(CG14740)	DVCAKLPRVQEQTQEGTPEGCFLLTSGSMPTKKEAQEVTLNEWLKRG-SVPRYCLRMIDS	158
sce:YCR005C	DIQKDLPK-AKGSSQPLPEALFWLLL TGEVPTQAQVENLSADLMSRS-ELPSHVVQLLDN	150
sce:YNR001C	EIQRELPK-AEGSTEPLPEALFWLLL TGEIPTDAQVKALSADLAARS-EIPEHVIQLLDN	169
cel:CELE_T20G5.2	ECQKLLPK-AKGGEEPLPEAIWWLLCTGDVPSEAQTAAITKEWNARA-DLPTHVVRLMDN	159
dme:Dmel(CG3861)	ECQKVLPA-ADGGTEPLPEGLFWLLL TGEVPTKSQVQQLSREWAERA-ALPQHVVTMLNN	158
mmu:71832	ECQKLLPK-AKGGEEPLPEGLFWLLVTGQMPTEEQVSWLSQEWVKRA-ALPSHVVTMLDN	157
mmu:12974	ECQKMLPK-AKGGEEPLPEGLFWLLVTGQMPTEEQVSWLSREWAKRA-ALPSHVVTMLDN	157
hsa:1431	ECQKLLPK-AKGGEEPLPEGLFWLLVTGHIPTEEQVSWLSKEWAKRA-ALPSHVVTMLDN	157
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eco:b0720	FRRDSHPMMAVMCGITGALAA-----FYHDSL DV--NNPRHREIAFRLLSKMPTMAAMC	176
sce:YPR001W	LPKDMHPMTQLAIGLASMNKGSLFATNYQKGLIGKMEFWKDTLEDSLNLIASLPLLTGRI	215
dme:Dmel(CG14740)	MDKRVHPMAQLCAAACLNPQSQFVEAYTKGA-RRADYWKS YEDSMNLIAMLPTVAAAI	217
sce:YCR005C	LPKDLHPMAQFSIAVTALES ESKFAKAYAQGI-SKQDYWSYTFEDSLDLLGKL PVIAAKI	209
sce:YNR001C	LPKDLHPMAQFSIAVTALES ESKFAKAYAQGV-SKKEYWSYTFEDSLDLLGKL PVIASKI	228
cel:CELE_T20G5.2	FPDNLHPMAQFIAAIAALNNESKFAGAYARGV-AKASYWEYAYEDSMDLLAKLPTVAAII	218
dme:Dmel(CG3861)	MPTTLHPMSQFAAVTALNHDSKFAKAYSDGV-HKS KYWEVYEDSMDLIAKLPCVAAATI	217
mmu:71832	FPTKLHPMSQLSAAITVLNNE SNFARAYAQGM-NRTKYWELTYEDCMDLLAKLPCVAAKI	216
mmu:12974	FPTNLHPMSQLSAAITALNSESNFARAYAEGM-NRAKYWELIYEDCMDLIAKLPCVAAKI	216
hsa:1431	FPTNLHPMSQLSAAVTALNSESNFARAYAQGI-SRTKYWELIYEDSMDLIAKLPCVAAKI	216
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	***: : : * : * : . : :	

eco:b0720	YK--YSIGQPFVYPRNDLSYAGNFLNMMFSTP-----CEPY-EVNPILERAMDRILIL	226
sce:YPR001W	YSNITNEGHPLGQYSEEVDWCTNICSLLGMTNGTNSSNTCNLTSQQSLDFINLMRLYTGI	275
dme:Dmel(CG14740)	YSNVFRDGEGRREVNYEEDWSGNFCRMLGLPE-----KDFVDLMRLYMIL	262
sce:YCR005C	YRNVFKDGGK-MGEVDPNADYAKNLVNLIGSKD-----EDFVDLMRLYLTI	253
sce:YNR001C	YRNVFKDGGK-ITSTDPNADYGKNLAQLLGYEN-----KDFIDLMRLYLTI	272
cel:CELE_T20G5.2	YRNLYRDGSAVSVIDPKKDWSANFSSMLGYDD-----PLFAELMRLYLVI	263
dme:Dmel(CG3861)	YCNTYRGKGSRSIDSSLWSANFVKMLGYDN-----APFTELMRLYLTI	262
mmu:71832	YRNLYREDRNIEAIDSKLDWSHNFTNMLGYTD-----PQFTELMRLYLTI	261
mmu:12974	YRNLYREGSSIGAIDSRLDWSHNFTNMLGYTD-----PQFTELMRLYLTI	261
hsa:1431	YRNLYREGSGIGAIDSNLDSHNFVNMLGYTD-----HQFTELTRLYLTI	261
	* . . : * : :: : :	

eco:b0720	HADHEQ-NASTSTVRTAGSSGANPFACIAAGIASLWGPAHGGANEAAALKMLEEISSV---	282
sce:YPR001W	HVDHEGGNVSAHTTHLVGSALSDPYLSYSSGIMGLAGPLHGLAAQEVRFLIEMNSNISS	335
dme:Dmel(CG14740)	HADHESGNVSAHACHLVGTALSDPFLFSASMCGLAGPLHGLANQEVLVWLTKLRKAIGD	322
sce:YCR005C	HSDHEGGNVSAHTSHLVGSALSSPYLSASGLNGLAGPLHGRANQEVLWLFALKEEVND	313
sce:YNR001C	HSDHEGGNVSAHTSHLVGSALSSPYLSLAAGLNGLAGPLHGRANQEVLWLFKLREEVKG	332
cel:CELE_T20G5.2	HSDHEGGNVSAHTSHLVGSALSDPYLSFSAAMAGLAGPLHGLANQEVLVFLNKIVGEIGF	323
dme:Dmel(CG3861)	HSDHEGGNVSAHTVHLVGSALSDPYLSFAAGLNGLAGPLHGLANQEVLVWLRLQKEAGN	322
mmu:71832	HSDHEGGNVSAHTSHLVGSALSDPYLSFAAALNGLAGPLHGLANQEVLVWLTKLQKEVGE	321
mmu:12974	HSDHEGGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTKLQKEVGK	321
hsa:1431	HSDHEGGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTKLQKEVGK	321
	* *** *.*: : : .*:: :.*: . : . : . * ** * * : : * : :	

eco:b0720	----KHIPEFVRRAKDKNDSFRLMGFGRVYKNYDPRATVMRETCHVLKELGTKDDLLE	338
sce:YPR001W	IAREQEIKDYLWK--ILNSNRVIPGYGHAVLRKPDPRTAMLEFAQKRPIEFEND-KNVL	392
dme:Dmel(CG14740)	DPSDEELKKFIDD--TLKGGQVIPGYGHAVLRKTDPRTQNEFAMKH---CKDD-PGVK	376
sce:YCR005C	DYSKDTIEKYLWD--TLNSGRVIPGYGHAVLRKTDPRTYMAQRKFAMDH---FPDY-ELFK	367
sce:YNR001C	DYSKETIEKYLWD--TLNAGRVVPGYGHAVLRKTDPRTAQREFALKH---FPDY-ELFK	386
cel:CELE_T20G5.2	NYTEEQLKEWVWK--HLKSGQVVPGYGHAVLRKTDPRTYECQREFALKH---LPND-DLFK	377
dme:Dmel(CG3861)	NPSEEQLKEYIWK--TLKSGQVVPGYGHAVLRKTDPRTYCQREFALKH---LPED-ETFQ	376
mmu:71832	DASDEKLKNYIWN--TLNSGRVVPGYGHAVLRKTDPRTYSCQREFALKH---LPKD-PMFK	375
mmu:12974	DVSDEKLRDYIWN--TLNSGRVVPGYGHAVLRKTDPRTYSCQREFALKH---LPKD-PMFK	375
hsa:1431	DVSDEKLRDYIWN--TLNSGRVVPGYGHAVLRKTDPRTYCQREFALKH---LPND-PMFK	375

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eco:b0720	VAMELENIALN--DPYFIEKKLYPNVDYSGIILKAMGIPS-SMFTVIFAMARTVGWIAH	395
sce:YPR001W	LMQKLAEIAPKVLLEHGKSKNPFPNVDSASGILFYHYGIRELLFFTVIFGCSRAMGPLTQ	452
dme:Dmel(CG14740)	LVTRLWKIIPEVLKKLNKVANPYPNVDAHSGVLLQHYCLKEKFYTVLFGVSRALGVLSQ	436
sce:YCR005C	LVSSIYEVAPGVLTEHGKTKNPWPNVDAHSGVLLQYYGLKESSFYTVLFGVSRAFGILAQ	427
sce:YNR001C	LVSTIYEVAPGVLTKHGKTKNPWPNVDSHSGVLLQYYGLTEASFYTVLFGVARAIGVLPQ	446
cel:CELE_T20G5.2	LVSTLYKITPGILLEQGKAKNPWPNVDSHSGVLLQYFGMTEMSFYTVLFGVSRALGCLSQ	437
dme:Dmel(CG3861)	LVSKIYKVVPPILTETGKVKNPWPNVDAHSGVLLQYYGMKEMNYYTVLFGVSRALGVLAS	436
mmu:71832	LVGQLYKIVPDILLEQGKAKNPWPNVDAHSGVLLQYYGMREMNYYTVLFGVSRALGVLSQ	435
mmu:12974	LVAQLYKIVPNILLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQ	435
hsa:1431	LVAQLYKIVPNVLLLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQ	435

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eco:b0720	WSEMHSDGMKiarprqlytgyeKrdfks-DIKR-----	427
sce:YPR001W	LVWDRILGLPIERPkslnleglealtkasvnkl-----	486
dme:Dmel(CG14740)	LIWSRALGAPIERPksfssieickfineadkkagkknnkkc	478
sce:YCR005C	LITDRAIGASIERPKSystekykelvknieskl-----	460
sce:YNR001C	LIIDRAVGAPIERPksfsteKYkelvkkieskn-----	479
cel:CELE_T20G5.2	LIWARGMGLPLERPksHstdgliklalaakk-----	468
dme:Dmel(CG3861)	LVWDRALGLPIERPksfstdllvkmvQk-----	464
mmu:71832	LIWSRALGFPLERPksmstdalmkfvnsesg-----	466
mmu:12974	LIWSRALGFPLERPksmstdglmkfvdsk-----	464
hsa:1431	LIWSRALGFPLERPksmsteGLMKFVDSKSG-----	466

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```
#
#
# Percent Identity Matrix - created by Clustal2.1
#
#
1: eco_b0720      100.00   22.97   21.87   24.88   25.86   24.69   23.57   23.95   25.06   24.69
2: sce_YPR001W    22.97  100.00   41.27   44.74   45.79   45.30   44.37   43.74   45.03   45.49
3: dme_Dmel(CG14740)  21.87   41.27  100.00   45.27   45.47   48.46   50.77   51.21   51.66   51.65
4: sce_YCR005C     24.88   44.74   45.27 100.00   78.48   54.75   57.68   56.42   57.11   57.96
5: sce_YNR001C     25.86   45.79   45.47   78.48 100.00   55.46   58.96   58.06   58.32   59.78
6: cel_CELE_T20G5.2  24.69   45.30   48.46   54.75   55.46 100.00   64.22   67.17   68.32   67.17
7: dme_Dmel(CG3861)  23.57   44.37   50.77   57.68   58.96   64.22 100.00   69.55   70.19   70.41
8: mmu_71832        23.95   43.74   51.21   56.42   58.06   67.17   69.55 100.00   91.81   89.91
9: mmu_12974        25.06   45.03   51.66   57.11   58.32   68.32   70.19   91.81 100.00   94.40
10: hsa_1431         24.69   45.49   51.65   57.96   59.78   67.17   70.41   89.91   94.40 100.00
```

**ACETYLTRANSFERASE
COMPONENT OF PYRUVATE
DEHYDROGENASE**

CLUSTAL 0(1.2.4) multiple sequence alignment

eco:b0115	-----MA-----IEIKVVDIGADEVEITEILVKVGD-----	26
cel:CELE_C30H6.7	-----	0
sce:YNL071W	-----	0
dme:Dmel(CG5261)	-----	0
cel:CELE_F23B12.5	-----	0
mmu:235339	MWRVCARRARS A VPRDGFRARWA ALKE GPGAPCGSPRIGPA A VR CGSGIP RY-GVRSLCG	59
hsa:1737	MWRVCARRA QNVA PWAG LEARWT ALQE VP GT PRV TSRS GPAPARRNSVTTGYGGVRALCG	60
eco:b0115	-----KVEAEQSLITVEGDK-----ASMEVPSPQAGIVKEIKVSVGDKTQ	66
cel:CELE_C30H6.7	-----	0
sce:YNL071W	-----	0
dme:Dmel(CG5261)	-----	0
cel:CELE_F23B12.5	-----	0
mmu:235339	WSSGSGTVPRNRL RQLLGSPSRRSYSLPPHQKVPLPSLSPTMQAGTIARWEKKEGEKIS	119
hsa:1737	WTPSSGATPRNRL LQLLGSPGRRYYSLPPHQKVPLPSLSPTMQAGTIARWEKKEGDKIN	120
eco:b0115	TGALIMIFDSADGAADAAPAQAEEKKEAAPAAAPAAAAAKDVNVPDIGSDEVEVTEILVK	126
cel:CELE_C30H6.7	-----	0
sce:YNL071W	-----	0
dme:Dmel(CG5261)	-----	0
cel:CELE_F23B12.5	-----	0
mmu:235339	EGDLIAEVETDKA-----TVGFESLEEC-----	142
hsa:1737	EGDLIAEVETDKA-----TVGFESLEEC-----	143

eco:b0115	VGDKVEAEQSLITVEGDKASMEVPAPFAGTVKEIK-----VNVGDKVSTGSL-IMVF--	177
cel:CELE_C30H6.7	-----	0
sce:YNL071W	-----MSAF--	4
dme:Dmel(CG5261)	MLRSLATTRNELGALRSVLLRSNNATYVRRS-TGNVVVRALSS	42
cel:CELE_F23B12.5	MSKFPVPLRTIGGLRPSTTAISAANIGFT-Q-SSRALST	38
mmu:235339	YMAKILVPE-GTRDVPVGSIICITVEKP-Q-DIEAFKN	177
hsa:1737	YMAKILVAE-GTRDVPIGAIICITVGKP-E-DIEAFKN	178
eco:b0115	-----EVAGEAGAAAPAAKQEAAAPAAAAPAPAAGVKE	208
cel:CELE_C30H6.7	-----	0
sce:YNL071W	-VRVV-PRISSSVLTRLRLQLRCYASYPEHTIIGMPALSPTMT	47
dme:Dmel(CG5261)	QLINSRKLQSIRSKLNNTSQSPV-TWS-YNFARAYANLPEHIRVPLPALSPPTME	93
cel:CELE_F23B12.5	GAAAKS-SGLVGQV-ARQYPNAAAFSIKQVRLYSSGNLPKHNRVALPALSPPTME	90
mmu:235339	YTLDLA-AAAAPQAAPAAAPAPAAAAPSASAPGSSYPTHMQIVLPALSPPTMT	230
hsa:1737	YTLDSS-AAPTPQAAPAPTPAATASPPTPSAQAPGSSYPPHMQVLLPALSPPTMT	231
eco:b0115	VNVPDIGGDEVTEVMVKVGDKVAAEQSLITVEGDKASMEVPAPFAGVVKELKVNVGDK	268
cel:CELE_C30H6.7	-----	0
sce:YNL071W	-QGNLAAWTKKEGDQLSPGEVIAEIETDKAQMDFEFQEDGYLAKILVPEGTK	98
dme:Dmel(CG5261)	RGSIVSWEKKVGEKLSEGDLCEIETDKATMGFETPEEGFLAKILIQQGKT	144
cel:CELE_F23B12.5	LGTVVSWQKKEGDQLSEGDLCEIETDKATMGFETPEEGYLAKILIQEFSK	141
mmu:235339	MGTVQRWEKKVGEKLSEGDLAELIETDKATIGFEVQEEGYLAKILVPEGTR	281
hsa:1737	MGTVQRWEKKVGEKLSEGDLAELIETDKATIGFEVQEEGYLAKILVPEGTR	282

eco:b0115	V-KTGSLIMIF-EVEGAAPAA-----APAKQEAAAPAPAACKAEA-PAAAPAA	312
cel:CELE_C30H6.7	-----ML	2
sce:YNL071W	DIPVNKPIAVYVEDKADVPFKDFKLEDGSDSKTSTKAQ---PAEPQAEEKQEAPAEET	155
dme:Dmel(CG5261)	DVPVGQLLCIIVPDQGSVAAFANFKDDGAAAAPAAPAAPAPAPA---AAAAPPSSPPA	201
cel:CELE_F23B12.5	DVPIGKLLCIIVDNEADVAAFKDFKDDGASSGGSAPAAEKAPEPAKPAASSQPSPPAQMY	201
mmu:235339	DVPLGAPLCIIVEKQEDIAAFADYRPTEVTSLKP-----QAAPPAPPPVAAVPPTPQPVA	336
hsa:1737	DVPLGTPLCIIVEKEADISAFADYRPTEVTDLKP-----QVPPPTPPPVAAVPPTPQPLA	337
eco:b0115	----KAEGKSEFAENDAYVHATPLIRRLAREFGVNLAKVKGTRKGRI-LREDVQAYVKE	367
cel:CELE_C30H6.7	AGSQA--LRHLSTAAQNQGACGPAVKLLLIQYGLENRKIDGTGPKNKNILKGDMVKIVEA	60
sce:YNL071W	KTSAPEAKKSDVAAPQGRIFASPLAKTIALEKGISLKDVGHTGPRGRI-TKADIESYLEK	214
dme:Dmel(CG5261)	AAPAAAAPPPAPAAAAPAAA-----G-----Q	222
cel:CELE_F23B12.5	QAPSVPKSAPIPHSSSGRVSASPFAKKLAAENGDLGVSQSGPGGRI-LASDLSQAPAK	260
mmu:235339	PTPSA-----APAGPKGRVFVSPLAKLAAEKGIDLTVQVKGTPPEGRI-IKKDIDSFVPS	390
hsa:1737	PTPSAP-CPATPAGPKGRVFVSPLAKLAVEKGIDLTVQVKGTPDGRI-TKKDIDSFVPS	395
eco:b0115	AIKRAEAA-----PAAT-GGGIPGMLPWPKVDFSKFGEIEEVELGRIQKISGANLSRN	419
cel:CELE_C30H6.7	EKLKPVAH-HAHAPKETHIENKSIEKKSDIFGANNRSLRHQDIPLSNIRATIAKRLTAS	119
sce:YNL071W	SSKQSSQTSGAAAATPAAAT--S---STTAGSAPSPSSTASYEDVPISTMRSIIGERLLQS	270
dme:Dmel(CG5261)	KAA-----AKPAAA-----AP---AKAPRAAGARYEDIPVTNMRAVIKRLLES	263
cel:CELE_F23B12.5	GA-----TSTTTQAVSGQDYTDIPLSNMRKTIAKRLTES	294
mmu:235339	KAA-----PAAAAA-----MAPPGPRVAPAPAGVFTDIPISNIRRVIACQRLMQS	434
hsa:1737	KVA-----PAPAAV-----VPPTGPGMAPVPTGVFTDIPISNIRRVIACQRLMQS	439

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eco:b0115	WVMIPHVT HFDKTDITEA FRQQNEEAAKR--KLDVKITPVVFIMKAVAAA EQMPRF	477
cel:CELE_C30H6.7	KQQIPHEYQGV DVR I DDILALRQKLKKS-----GTAVSLNDFI I KAALALRSVPTV	171
sce:YNL071W	TQGIPSYIVSSKISISKLLKLQLS NAT AND-----KYKLSINDLLVKAITVAAKRVPDA	325
dme:Dmel(CG5261)	KTQLPHYYVTVQCQVDKLLKFRAKV NKKY EK----QGARVSVNDFI I KAVALASLKVP <i>E</i> A	319
cel:CELE_F23B12.5	KSTIPHYYLTSEIQLDTLLQVREKLNGLLAKGTSGQATKISINDFI I KASALACQRVPEA	354
mmu:235339	KQTIPHYYLSVDVNMGEVLLVRKELNKMLEG-----KGKISVNDFI I KASALACLKVP <i>E</i> A	489
hsa:1737	KQTIPHYYLSIDVNMGEVLLVRKELNKILEG-----RSKISVNDFI I KASALACLKVP <i>E</i> A	494

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eco:b0115	NSSLSEDGQRLTLKKYINIGVAVDTPNGLVVVFKDVNKKGII E LSRELMTISKARDGK	537
cel:CELE_C30H6.7	NVRWTPEGI---GLGSV D ISVAVATPTGLITPIVENSDILGVLA S SKV K ELSGLARESK	228
sce:YNL071W	NAYWLPNENVIRKFKNVDVS V AVATPTGLL T PIVKNC E AKGLSQISNEIKELVKRARINK	385
dme:Dmel(CG5261)	NSAWMD--TVIRKYDDVDVS V AVSTD K GLITPIVNADRGVLEISKDV K ALA A KARDNK	377
cel:CELE_F23B12.5	NSYWMD--SFIRENHHV D VS V AVSTPAGLITPIFNAHKG L ATIAS E IVELAQ R AREGK	412
mmu:235339	NSSWMD--TVIRQNHHVV D VS V AVSTPAGLITPIFNAH I KGETIASDV V SLASKAREGK	547
hsa:1737	NSSWMD--TVIRQNHHVV D VS V AVSTPAGLITPIFNAH I KGVETIANDV V SLATKAREGK	552

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eco:b0115	LTAGEMQGGCFTISSIGGLT-THFAPIVNAPEVAILGVSKSAMEPVW---NGKEFVPRL	593
cel:CELE_C30H6.7	LKPQQFQGGSFTISNLGMFGSVTNFTAII NPP QCAILTIGGTRSEVVS V --DGQLETQK	285
sce:YNL071W	LAPEEFQGGTICISNMGMNNAVNMFTSI NPP QSTILAIATVERVAVEDAAAENGFSFDN	445
dme:Dmel(CG5261)	LQPHEFQGGTISVSNLGMFGV-NQFAAVINPPQSCILAIGTTKQLVADPDSLKGFKEVN	436
cel:CELE_F23B12.5	LQPHEFQGGTFTVSNLGMFGSVSDFTAII NPP QSCILAIGGASDKLVPD-E-AEGYKKIK	470
mmu:235339	LQPHEFQGGTFTISNLGMFGI-KNFSAIINPPQACILAIGASEDKLIPA-DNEKGFDVAS	605
hsa:1737	LQPHEFQGGTFTISNLGMFGI-KNFSAIINPPQACILAIGASEDKLVPA-DNEKGFDVAS	610

* : : *** : : * . : . *: : : *: ** : . : :

eco:b0115	MLPISLSFDHRVIDGADGARFITIINNTLSDIRRLVM-----	630
cel:CELE_C30H6.7	LMGVNLCFDGRAISEECAKRFLLFSESLSDPELLIAEPLSPELDFDFSRLL-----	337
sce:YNL071W	QVTITGTFDHRTIDGAKGAEFMKELKTVIENPLEMLL-----	482
dme:Dmel(CG5261)	MLTVTLSADHRVVVDGAVAARWLQHFRDYMEDPSNMVL-----	473
cel:CELE_F23B12.5	TMKVTLSCDHRHTVDGAVGAVWLRFKEFLEKPHTMLL-----	507
mmu:235339	VMSVTLSCDHRVVVDGAVGAQWLAEFKKYLEKPITMLL-----	642
hsa:1737	MMSVTLSCDHRVVVDGAVGAQWLAEFRKYLEKPITMLL-----	647

: :. * *.: . :: : : .. ::

```

#
#
# Percent Identity Matrix - created by Clustal2.1
#
#
 1: eco_b0115      100.00   25.65   26.79   28.26   26.62   28.79   27.77
 2: cel_CELE_C30H6.7    25.65 100.00   31.86   41.60   41.16   39.00   38.94
 3: sce_YNL071W      26.79   31.86 100.00   41.53   42.98   43.86   43.26
 4: dme_Dmel(CG5261)    28.26   41.60   41.53 100.00   52.97   49.12   48.68
 5: cel_CELE_F23B12.5    26.62   41.16   42.98   52.97 100.00   54.00   53.56
 6: mmu_235339        28.79   39.00   43.86   49.12   54.00 100.00   86.14
 7: hsa_1737          27.77   38.94   43.26   48.68   53.56   86.14 100.00

```

**SUCCINYLTRANSFERASE
COMPONENT OF 2-OXOGLUTARATE
DEHYDROGENASE**

CLUSTAL 0(1.2.4) multiple sequence alignment

sce:YDR148C	-----MLS RAT RTAAKSLVKS KVAR NVMAAS---FVKR--HASTL	37
eco:b0727	-----	0
dme:Dmel(CG5214)	MTGIISIVTRRLPQTLGMRALRSNE--VKRCIRQYSRLVACAAQQQQ-LL--RQDGSNR	54
cel:CELE_W02F12.5	-----MLGRRAVS--VHRFLSRAARQS VTAASSA-----QPSLQA	33
mmu:78920	-----MLS RS-----RCVSRAFSRSLSAFQKGNCPLGRRSLPGVSL	36
hsa:1743	-----MLS RS-----RCVSRAFSRSLSAFQKGNCPLGRRSLPGVSL	36

sce:YDR148C	FKQANKVESLGSIYLSGKKISVAANPFSITSNRFKSTSIEVPPMAESLTE GSLKEYTKNV	97
eco:b0727	-----MSSVDILVPDLPE SVADATVATWHKKP	27
dme:Dmel(CG5214)	CQE-----AT-RLLTWQGIHTT-SSLWSEQTVNVPPFADSIAEGD-IKF TCKV	99
cel:CELE_W02F12.5	KTS L-----LEPLVQNV-RITSSANFHMSAVRMSDVTVEGP AFAESISEG D-IRWLKQK	86
mmu:78920	CRGPGYPDNRKMVINS G-SVFRVRFFQTTAVCKNDVITVQTPAFAESVTEGD-VRWEKAV	94
hsa:1743	CQGPGYPNSRKVVIN-N-SVFSVRFFRTTAVCKDDLTVKTPAFAESVTEGD-VRWEKAV	93
	. : * : : * : : .	

sce:YDR148C	GDFIKEDELLATIETDKIDIEVN SPVSGT VTKLNFKPEDTVT VGEELAQ VEPGE APAEGS	157
eco:b0727	GDAVVRDEV LVEIETDKVVLEV PAPASADGILD AVLEDEGTTVTSRQILGRLREGNSAGKET	87
dme:Dmel(CG5214)	GDSFAADEAVMEIETDKTTVAVPAP FSGT LTDILVKDGDTV KPGQALFKIKPGAA PAKAA	159
cel:CELE_W02F12.5	GDHVNEDELVAEIEIETDKTSVEVPAP QAGTIVEFLVEDGAKVTA KQKL YKLQPGAGGGSSS	146
mmu:78920	GDAVAEDEVVCEIEIETDKTSVQV PSPANGII EALLVPDGGKVEGGTPLFTLRKTGA A-----	150
hsa:1743	GDTVAEDEVVCEIEIETDKTSVQV PSPANGVIE ALLVPDGGKVEGGTPLFTLRKTGA A-----	149
	** . ** : ***** : * : * : . . * * : .	

sce:YDR148C	GESKPEPTEQAEPSQG--VAARENNSSEETASKKEAAPKK-----EA----AP	198
eco:b0727	SAKSEEKASTPAQRQQASLEEQNNDALSPAIRRLLAEHNLDA SAIKGTGVGGRLTREDVE	147
dme:Dmel(CG5214)	APAAAAPAPAAP---KAAPAPA-----AAPKPAPP-----PPAAGA----PK	193
cel:CELE_W02F12.5	APAKEEPKSAPAKEEKS SKPAPAKE--DSKPAVTAAPP-----KPVSGD----IP	189
mmu:78920	-PAKAKPAETP-----APAHK--A-EPAAP-AAPP-----PPA-AP----VL	182
hsa:1743	-PAKAKPAEAP-----AAAAP--K-AEPTA-AAVP-----PPA-AP----IP	181

sce:YDR148C	KKEVTEPKKADQPK-----KTVSKAQEPPVASNSFTPFPRTETRVKMNRMLRIA E	249
eco:b0727	KHLAKAPAKE-----SAPA-----AAAPAAQPALAARSEKRVPMTRLRKVAE	190
dme:Dmel(CG5214)	PPPPPPP KAAPR PPP PPP P VAALK PAVAQ VKVPPAD GSRQILGTRSE QRVKMNRMRLKIAA	253
cel:CELE_W02F12.5	KSAPPVARPP STPSS STPVGA VPVT-RVV VPKGVD PSHAIT GARDEV RVKANRM RMRMRIAQ	248
mmu:78920	TQM PPVPSP-SQPPSS KPVS AIKPT-AAPPLAE AGAAKGLRSEHRE KMNRMRQRIAQ	237
hsa:1743	TQM PPVPSP-SQPPSG KPVS AVKPT-VAPPLAE PGAGKGLRSEHRE KMNRMRQRIAQ	236

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sce:YDR148C	RLKESQNTAASLTTFNEVDMSALMEMRKL YKDEIIKKTGT KFGFMGLFSKACTLAA KDIP	309
eco:b0727	RLLEAKNSTAML TTFNEVN MKPIMDLR KQYGEAF EKRHGIRLG FMSFYVKAV VEALKRYP	250
dme:Dmel(CG5214)	RLKDAQNT CAML TTFNEVDMSYAMDFRK QNLDAFT KKYGI KFGFMSI FAKASAYAL QDQP	313
cel:CELE_W02F12.5	RLKDAQNTY AML TTFNEIDMSS LIEMRKT YQKDFV AKHGVL GMMSPF VRAAYAL QESP	308
mmu:78920	RLKEAQNT CAML TTFNEIDMSNI QEMR RARHK DAFLKK HNLL KGFM SAFVK ASA FALQE QP	297
hsa:1743	RLKEAQNT CAML TTFNEIDMSNI QEMR RARHK EAFLKK HNLL KGFM SAFVK ASA FALQE QP	296

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sce:YDR148C	AVNGAIEG--DQIVYRDYTDISVAVATPKGLVTPVVRNAESLSVLDIENEIVRLSHKARD	367
eco:b0727	EVNASIDG--DDVVYHNYFDVSMAVSTPRGLVTPVLRDVDTLGMADIEKKIKELAVKGRD	308
dme:Dmel(CG5214)	VVNAVIDG--TDIVYRDYVDISVAVATPRGLVVPVIRNVEGMNYADIEIALAGLADKARR	371
cel:CELE_W02F12.5	VVNAVLDE--NEIVYRHFVDISVAVATPKGLVVPVLRNVESMNYAQIELELANLGVKARD	366
mmu:78920	VVNAVIDDATKEVVYRDYIDISVAVATPRGLVVPVIRNVETMNYADIERTINELGEKARK	357
hsa:1743	VVNAVIDDTTKEVVYRDYIDISVAVATPRGLVVPVIRNVEAMNFADIERTITELGEKARK	356

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sce:YDR148C	GKLTLLEDGTGGFTISNGGVFGSLYGTPIINSPPQTAVLGLHGVKERPVTVNGQIVSRPMM	427
eco:b0727	GKLTVEDLTGGNFTITNGGVFGSLMSTPIINPPQSAILGMHAIKDRPMANQVEILPMM	368
dme:Dmel(CG5214)	DAITVEDMDGGTFTISNGGVFGSLMGTPIINPPQSAILGMHGIFERPIAVKGEVKIRPMM	431
cel:CELE_W02F12.5	GKLAVEDMEGGTFTISNGGVFGSMFGTPIINPPQSAILGMHGVFDRVVPVNGKPEIRPIM	426
mmu:78920	NELAIEDMDGGTFTISNGGVFGSLFGTPIINPPQSAILGMHAIFDRPVAVGGKVEVRPMM	417
hsa:1743	NELAIEDMDGGTFTISNGGVFGSLFGTPIINPPQSAILGMHGIFDRPVAAIGGKVEVRPMM	416

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sce:YDR148C	YLALTYDHRLLDGREAVTFLKTVKELIEDPRKMLLW-	463
eco:b0727	YLALSYDHRLIDGRESVGFLVTIKELLEDPTRLLL DV	405
dme:Dmel(CG5214)	YIALTYDHRIIDGREAVLFLRKIKA AVENPAIIVAGL	468
cel:CELE_W02F12.5	QIALTYDHRLIDGREAVTFLKKIKTAVEDPRIMFMNL	463
mmu:78920	YVALTYDHRLIDGREAVTFLRKIKA AVEDPRVLLLDL	454
hsa:1743	YVALTYDHRLIDGREAVTFLRKIKA AVEDPRVLLLDL	453

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```
#  
#  
# Percent Identity Matrix - created by Clustal2.1  
#  
#  
  
1: sce_YDR148C      100.00   43.57   45.24   44.49   45.96   45.37  
2: eco_b0727        43.57   100.00   46.30   43.67   50.40   47.17  
3: dme_Dmel(CG5214) 45.24   46.30   100.00   52.69   57.44   56.18  
4: cel_CELE_W02F12.5 44.49   43.67   52.69   100.00   57.63   57.53  
5: mmu_78920        45.96   50.40   57.44   57.63   100.00   91.39  
6: hsa_1743         45.37   47.17   56.18   57.53   91.39   100.00
```

DIHYDROLIPOYL DEHYDROGENASE

CLUSTAL 0(1.2.4) multiple sequence alignment

eco:b0116	-----MSTEIKTQVVVLGAGPAGYSAAFRC	25
sce:YFL018C	-MLRI-----RSLLNNKRAF-SSTVRTL-TINKSHDVIIIGGGPAGYVAAIKA	45
mmu:13382	MQSWSRVYRSLAKKGHFNRISHGLQGVSSVPLRTYADQPIADVTVIIGSGPGGYVAAIKS	60
hsa:1738	MQSWSRVYCSLAKRGHFNRISHGLQQLSAVPLRTYADQPIDADVTVIIGSGPGGYVAAIKA	60
cel:CELE_llc1.3	-----MSLSRTTQL--PFAKRQFFQVLARNY-SNTQDADLVVIGGGPGGYVAAIKA	48
dme:Dmel(CG7430	MQFTLRHVVSAYAKTPL---RTNAAILGALNARCY-SSTHEADIVVIGSGPGGYVAAIKA	56
	. : .:.*.*.** * *:.	

eco:b0116	ADLGLETVIVERYNTLGGVCLNVGCIPS KALLHVAKVIEEA--KALAEHGIVF-GEPKTD	82
sce:YFL018C	AQLGFNTACVEKRGKLG GTCLNVGCIPS KALLNNSHLFHQ MHT-EAQKRGIDVN GDIKIN	104
mmu:13382	AQLGFKTV CIEKNETLGGTCLNVGCIPS KALLNNSHYYHMAHGKDFASRGIEI-PEVRLN	119
hsa:1738	AQLGFKTV CIEKNETLGGTCLNVGCIPS KALLNNSHYYHMAHGKDFASRGIEI-SEVRLN	119
cel:CELE_llc1.3	AQLGMKTV CVEKNATLGGTCLNVGCIPS KALLNNSHYLHMAQH-DFAARGIDC-T-ASLN	105
dme:Dmel(CG7430	AQMGMKTV SVEKEATLGGTCLNVGCIPS KALLNNSHYYHMAHSGDLEKRGISC-GSVSLD	115
	: :: . :* .***,*****: : : . . : ** : :	

eco:b0116	IDKIRTWKEKVINQLTGGLAGMAKGRKV VVNGLKFTGAN TLEVEGENGKT-----V	135
sce:YFL018C	VANFQKAKDDAVKQLTGGIELLFKKNKV TYYKGNGSFEDET KIRVTPVDGLEGTVKEDHI	164
mmu:13382	LEKMMEQKHS AVKALTGGIAHLFKQN KV VHVNGFGKITGK NQVTATKADGST-----QV	173
hsa:1738	LDKMMEQKSTAVKALTGGIAHLFKQN KV VHVNGY GKITGK NQVTATKADGGT-----QV	173
cel:CELE_llc1.3	LPKMMEQKSNSVQQLTGGIKQLFKANKV GHVEGFATIVGPNTVQAKKNDGSV-----ET	159
dme:Dmel(CG7430	LEKLMGQKSNAV KALTGGIAMLFKKNKV TQLTGFGTIVNPNEEVKKSDGST-----ET	169
	: : * : : ****: : * .** * : *	

eco:b0116	INF DN AIIAAGSRPIQLPFIPHE DPRIWDSTD AELKEVPERLLVMGGGIIGLEMGTVYH	195
sce:YFL018C	LDVKNII VATGSEVTPFP GIEIDEEKIVSSTGALSLKEIPKRLTII GGGIIGLEMGSVYS	224
mmu:13382	IDTKN ILVATGSEVTPFP GITID ETDIVSSTGALSLKKVPEKL VVIGAGVIGVELGSVWQ	233
hsa:1738	IDTKN I LIA TGSEVTPFP GITID ETDIVSSTGALSLKKVPEKM VVIGAGVIGVELGSVWQ	233
cel:CELE_llc1.3	INARNILIASGSEVTPFP GITID EKQIVSSTGALSLQVPKM VVIGAGVIGLELGSVWQ	219
dme:Dmel(CG7430)	VKT KN ILIATGSEVTPFP GIEIDEEVIVSSTGALKAKVPKHLVVIGAGVIGLELGSVWS	229
	.. * :**:**. :* * :: * .**.*. * :*: : :*.*:***:***:*	
eco:b0116	ALGSQ IDVVEMFDQVIP -AADKD IVKVFTKRIS -KKFNLML ETKVTA VEAKEDGIYVTM-	252
sce:YFL018C	RLG SKVTVVEF QPQIG -ASMDGEVAKATQKFLKKQGLDFKLSTKVISA KRND KNVVEIV	283
mmu:13382	RLG ADVT AV EFLGHVGGIGIDME ISKNFQRILQ RQGFKFKLNTKVTGATKKSDGK-IDVS	292
hsa:1738	RLG ADVT AV EFLGHVGGVGIDME ISKNFQRILQKQGFKFKLNTKVTGATKKSDGK-IDVS	292
cel:CELE_llc1.3	RLGA EVT AV EFLGHVGGMGIDGEVSKNFQRSLTKQGFKFLLNTKVM GASQN-GST-ITVE	277
dme:Dmel(CG7430)	RLGA EVT AIEFMDTIGGVGIDNEVSKTFQKVLTQGLKFKLGTKVTAASRS-GDN-VTVS	287
	.: .: * : . * : * : : : : * * : :	
eco:b0116	-EG-KKAPAE PQR YDAVLVAI GRVPNGKNLDAGKAGVEVDDRGFIRVDKQLRTNVPHIFA	310
sce:YFL018C	VEDTKTNKQENLEAEVLLVAVGRRPYIAGLGA EKIGLEVDKRGRLVIDDQFNSKFPHIKV	343
mmu:13382	VEAASGGKAEVITCDVLLCIGRRPFTQNLG LEE LGIELDPKGRIPVN NRFQT KIPNIYA	352
hsa:1738	IEAASGGKAEVITCDVLLCIGRRPFTK NLG LEE LGIELDPRGRIPVNTRFQT KIPNIYA	352
cel:CELE_llc1.3	VEGAKDGKKQTLECDTLLVSVGRRPYTEGLGLSNVQIDLDNRGRVPVNERFQT KVP SIFA	337
dme:Dmel(CG7430)	VENAKSGEKEEIQCDALLVSVGRRPYTEGLGLEAVGIVKDDRGRI PVNATFQT VVP NIYA	347
	* . : .: **. :** * .*. : * :* : : : . * * .	

eco:b0116	IGDIVGQPMALAHKGVHEGHVAEVIAGKKHYFDPKVIPSIAYTEPEVAWGLTEKEAKEK	370
sce:YFL018C	VGDVTFGPMLAHKAEEEGIAAVEMLKTHGHVNYYNNIPSVMYSHPEVAWVGKTEEQLKEA	403
mmu:13382	IGDVVAGPMLAHKAEDEGIICVEGMAGGAHVIDYNCVPSVIYTHPEVAWVGKSEEQLKEE	412
hsa:1738	IGDVVAGPMLAHKAEDEGIICVEGMAGGAHVIDYNCVPSVIYTHPEVAWVGKSEEQLKEE	412
cel:CELE_LLC1.3	IGDVIEGPMLAHKAEDEGILCVEGIAGGPVHIDYNCVPSVYTHPEVAWVGKAEEQLQE	397
dme:Dmel(CG7430)	IGDCIHGPMLAHKAEDEGLITIEGINGGHVHIDYNCVPSVYTHPEVAWVGKSEEQLQE	407
	:** * *****. .** * : .: : :**: *:.***** :*: *:	
eco:b0116	GISYETATFPWAASGRAIASDCADGMTKLIFDKESHRVIGGAIVGTNNGELLGEIGLAIE	430
sce:YFL018C	GIDYKIGKFPFAANSRAKTNQDTEGVKILIDSSTERILGAHIIGPNAGEMIAEAGLALE	463
mmu:13382	GIEFKIGKFPFAANSRAKTNAADTGMVKILGHKSTDRLVLAGHILGPGAGEMVNEAALALE	472
hsa:1738	GIEYKVGKFPFAANSRAKTNAADTGMVKILGQKSTDRLVLAGHILGPGAGEMVNEAALALE	472
cel:CELE_LLC1.3	GVAYKIGKFPFVANSRAKTNNQEGFVKVLADKQTDRMLGVHIIGPNAGEMIAEATLAME	457
dme:Dmel(CG7430)	GVAYKVGKFPFLANSRAKTNNTDGFVKVLADQATDKILGTHIIGPGAGELINEAVLAME	467
	*: : : ..**: *..** :. :*:.*: .. :.::* *;* ..**: * * **	
eco:b0116	MGCDAEDIALTIHAHPTLHESVGLAAE--VFEGSITDLPNPKAKKK	474
sce:YFL018C	YGASAEDVARVCHAHPTLSEAFKEANMAAYD-KAIHC-----	499
mmu:13382	YGASCEDIARVCHAHPTLSEAFREANLAAF GKPINF-----	509
hsa:1738	YGASCEDIARVCHAHPTLSEAFREANLAASF GKSIINF-----	509
cel:CELE_LLC1.3	YGASAEDVARVCHPHPTLSEAFREANLAAYCGKAINNV-----	495
dme:Dmel(CG7430)	YGAAAEDVARVCHAHPTCSEALREANVAAAFGKPINF-----	504
	*. .**:*. * *** *:. *	*

```
|#  
|#  
# Percent Identity Matrix - created by Clustal2.1  
#  
#  
  
1: eco_b0116      100.00    39.91    42.03    43.10    38.61    39.61  
2: sce_YFL018C     39.91   100.00    55.80    55.60    57.88    57.08  
3: mmu_13382       42.03    55.80   100.00    94.89    69.23    66.87  
4: hsa_1738        43.10    55.60    94.89   100.00    70.04    67.06  
5: cel_CELE_LLC1.3  38.61    57.88    69.23    70.04   100.00    71.26  
6: dme_Dmel_CG7430  39.61    57.08    66.87    67.06    71.26   100.00
```

FUMARATE HYDRATASE

CLUSTAL O(1.2.4) multiple sequence alignment

eco:b2929		-MA	2
eco:b1612		-MSNKPFHYQAPFPLK-----K	16
eco:b4122		-MSNKPFIYQAPFPMG-----K	16
eco:b1675		-MGNRTKEDEL	10
eco:b1611		-MNT	3
dme:Dmel(CG31874		-MSFDQKE-IFSLMYKLARLIVPD	22
sce:YPL262W		-MLRFTNCSCKTFVKSSYKLNIRRMNS	27
cel:CELE_H14A12.2	MSAVSMLQGEM-LA	-RGGAVIARGASLATAR-----NFSRTTVPMAK	40
mmu:14194	-----MYRALRLLARSRLLL	RVPSSAGAAV-----SGEATTLPRCA-----PNVARMASQNS	46
hsa:2271	-----MYRALRLLARSRPLVR	AAPAAALASAPGLGGAAPSFWP-----PNAARMASQNS	49
dme:Dmel(CG6140		-----MSSTKKVE	8
dme:Dmel(CG4094	MVLPLLQRS-TL	-RGVQQMTKPWA-----AIGSLRLASQE	33
dme:Dmel(CG4095	-----MLKQNNGLHLARRNLWVVC	SGLRAKDCDSG-----GKGGKGKENGK	41
eco:b2929	TLTEDDV	-EQLDAQDNLFNSFMKTAHTILLQGIRQ	36
eco:b1612	DDTEYYLLTSEHVS	VSEFEGQEILKVAPEALTLLARQAFHDASF-MLRPAHQQQVADILR	75
eco:b4122	DNTEYYLLTSDYVS	VADFGETILKVEPEALTLLAQAFHDASF-MLRPAHQKQVAAILH	75
eco:b1675	YREMCRVVVGKV	VLEMRD-----LGQ-----EPKH-IVIAGVLR	42
eco:b1611	VRSEKDSMGAIDV	PADKLWGAQTQR-----SLEHFRIS--TEKMPTS LIHALALT K	52
dme:Dmel(CG31874	TRVEYDSMGAHV	IPLDRMFGPQTMR-----SLMKFP IGGV VEERMP RPLIKALGIVK	73
sce:YPL262W	FRTETDAFGEIHVP	ADKYWGAQTQR-----SFQNFKIGGARERMPPLPLVHAFGVLK	78
cel:CELE_H14A12.2	IRKERDTFGEI	VPADKY YGAQTAR-----SQMNFKIGGPEERMPIPVIHAFGILK	91
mmu:14194	FRVEFDTFGE	LKVPTDKY YGAQTVR-----STMNFKIGGATERMPIPVIQAFGILK	97
hsa:2271	FRIEYDTFGE	LKV PNDK Y YGAQTVR-----STMNFKIGGVTERMP TPV IKA FGILK	100
dme:Dmel(CG6140	TRQESDTLGPME	VPM DR Y YGAQTMR-----CLINFRIGEEERMPRQIIQAMGILK	59
dme:Dmel(CG4094	FRVESDTFGE	LKV PADK Y YGAQTMR-----SQINFP IGGATERMPKPV VQAMGILK	84
dme:Dmel(CG4095	FRTEKDTFGE	LKV PADKLYGAQTMR-----SKLN FPIGDIGERMPMPV I QAMGILK	92
		: :	

eco:b2929	FLPSLFVDNDEE-IVEYAVKPLLAQSGPLD-DIDVALRLIYALGKMDKWLYADITHFSQ-	93
eco:b1612	DPE--ASENDKYVALQFLRNSDIAAKGVLPCTQDTGTAI--VGKKGQRVWTGGGDEAAL	131
eco:b4122	DPE--ASENDKYVALQFLRNSEIAAKGVLPCTQDTGTAI--VGKKGQRVWTGGGDEETL	131
eco:b1675	TAL--A-----	46
eco:b1611	RAA--AKVNEDLGLLSEEKA----SAIRQADEVLAGQHD--DEFPLAIWQTGSGTQSN	103
dme:Dmel(CG31874	KSA--AETNKIH-CLEEHLC----DAISKACDDVISGKLYDEEHFPLVIWQDGSGEHTN	125
sce:YPL262W	KSA--AIVNESLGGLDPKIS----KAIQQAADEVASGKLD--DHFPLVVFQTGSGTQSN	129
cel:CELE_H14A12.2	CAA--ALVNTEF-GLDKKLA----DAISQAADEVVDGKLD--EHFPLVTWQTGSGTQSN	141
mmu:14194	RAA--AEVNQEY-GLDPKIA----SAIMKAADEVAEGKLN--DHFPLVVWQTGSGTQTN	147
hsa:2271	RAA--AEVNQDY-GLDPKIA----NAIMKAADEVAEGKLN--DHFPLVVWQTGSGTQTN	150
dme:Dmel(CG6140	KAA--AETNQEF-GLDPKLS----TAISNAADDVISGKLYDEGHFPLPIWQTGSGTQSN	111
dme:Dmel(CG4094	KAA--AEVNKEF-GLDSKVS----EAISKAADDVISGKLYD-DHFPLVIWQTGSGTQSN	135
dme:Dmel(CG4095	KAC--AEVNKDY-GLDGKVS----DAVSCACDDVISGKLYKQGHFPLVIWQTGSGTQTN	144

eco:b2929	----FWHYLNEQDETPGFADDMTWDFISNV-----	NS	121
eco:b1612	ARGVYNTYIE--DNLRYSQNAPLDMYKEVNTGTNLPAQIDLAYAVDGDEYKFLCIAKGGG		188
eco:b4122	SKGVYNTYIE--DNLRYSQNAALDMYKEVNTGTNLPAQIDLAYAVDGDEYKFLCVAKGGG		188
eco:b1675	-----		46
eco:b1611	MN--MNEVLA----NRASELL-----GGV		121
dme:Dmel(CG31874	MN--VNEVIC----NRAIEIL-----GGQ		143
sce:YPL262W	MN--ANEVIS----NRAIEIL-----GGK		147
cel:CELE_H14A12.2	MN--VNEVIS----NRAIEIL-----GGE		159
mmu:14194	MN--VNEVIS----NRAIEML-----GGE		165
hsa:2271	MN--VNEVIS----NRAIEML-----GGE		168
dme:Dmel(CG6140	MN--SNEVIG----NRAIELL-----GGR		129
dme:Dmel(CG4094	MN--VNEVIS----NRAIELL-----GGK		153
dme:Dmel(CG4095	MN--TNEVIS----NAAIKMM-----GGE		162

eco:b2929	ITRNAMLYDALK----AMKFADFSVWSEARFSGMVKTALTAVTTTLK-ELTP-----	169
eco:b1612	SANKTYLYQETKALLTPGKLKNYLVEKMRTLGTAAACPPYHIAFVIGGT---SAETNLKT	244
eco:b4122	SANKTYLYQETKALLTPGKLKNFLVEKMRTLGTAAACPPYHIAFVIGGT---SAETNLKT	244
eco:b1675	-----NKRIQRSELEKQAME-----TVIN-----	65
eco:b1611	RGM-----ERKVHPNNDVNSQSSNDVFP----TAMHVAALLALRKQLIPQLKLTQ	169
dme:Dmel(CG31874	MGS-----KEPVDPNEHVNMAQSSHDTFS----TAVRIAVAMQLQETLYPSLRTFID	191
sce:YPL262W	IGS-----K-QVHPNNHCNQSQSSNDTFP----TVMHIAASLQIQNELIPELTNLKN	194
cel:CELE_H14A12.2	LGS-----KKPVHPNDHVNVMSQSSNDTFP----TAMHIAVGREVNRSRLLPALKLRT	207
mmu:14194	LGS-----KKPVHPNDHVNVKSQSSNDTFP----TAMHIAAAEVHKVLLPGLQKLHD	213
hsa:2271	LGS-----KIPVHPNDHVNVKSQSSNDTFP----TAMHIAAAIEVHEVLLPGLQKLHD	216
dme:Dmel(CG6140	IGT-----KDPVHPNDHVNVKSQSSNDTFP----SAIHIAVATALTKDLRPAVTALRD	177
dme:Dmel(CG4094	LGS-----KTPVHPNDHVNVKSQSSNDTFP----TAIHISVALELNNNLKPAIKTLHD	201
dme:Dmel(CG4095	LGS-----KKPVHPNDHVNVKSQSSNDTFP----TAIHISVGMELNERLVPAVTHLRD	210
. : . :		
eco:b2929	-----	169
eco:b1612	VKLASAKYYDELPTEGNEHGQAFRDVELEKELLIEAQNLGLGAQFGGKYFAHDI-----	298
eco:b4122	VKLASAHHYDELPTEGNEHGQAFRDVQLEQELLEEAQKLGLGAQFGGKYFAHDI-----	298
eco:b1675	-----	65
eco:b1611	TLNEKSRAFADIV-----KIGRTHLQDATPLTLGQEISGWAMLEHNLKIE	216
dme:Dmel(CG31874	LLGKKSNDWMIDL-----KIGRTHLMDAVPLSLGQEFSGYQQQLVNGRTRLD	238
sce:YPL262W	ALEAKSKEFDHIV-----KIGRTHLQDATPLTLGQEFSGYVQQVENGIQRVA	241
cel:CELE_H14A12.2	ALHNKAEEFKDII-----KIGRTHHTQDAVPLTLGQEFSAYVTQLDNSIARVE	254
mmu:14194	ALSAKSKEFAQVI-----KIGRTHHTQDAVPLTLGQEFSGYVQQVQYAMVRIK	260
hsa:2271	ALDAKSKEFAQII-----KIGRTHHTQDAVPLTLGQEFSGYVQQVKYAMTRIK	263
dme:Dmel(CG6140	SLQAKSNEWKDII-----KIGRTHHTQDAVPLTLGQEFSGYAQQLTNGLQRID	224
dme:Dmel(CG4094	ALRAKSEEFKDII-----KIGRTHHTMDAVPLTLGQEFSGYAQQLAYAQRERID	248
dme:Dmel(CG4095	ALKSKSDEFKDII-----KIGRTHLMDAVPLTLGQEFSGYTQQLTNGLERIK	257

eco:b2929	-----	169
eco:b1612	-----RVIRLPRHGASC _P VGMGVSCSADRNIKAKINRQGIWIEKLEHNPGKYIPEELRKAG	354
eco:b4122	-----RVIRLPRHGASC _P VGMGVSCSADRNIKAKINREGIWIEKLEHNPGQYIPQELRQAG	354
eco:b1675	-----	65
eco:b1611	YSLPHVAELALGGTAV--GTGLNT-----	238
dme:Dmel(CG31874	CAMCRLYQLPMGGTSV--GTKVDT-----	260
sce:YPL262W	HSLKTLSSLFLAQGGTAV--GTGLNT-----	263
cel:CELE_H14A12.2	STLPRLYQLAAGGTAV--GTGLNT-----	276
mmu:14194	AAMPRIYELAAGGTAV--GTGLNT-----	282
hsa:2271	AAMPRIYELAAGGTAV--GTGLNT-----	285
dme:Dmel(CG6140	AVLPRVYQLALGGTAV--GTGLNT-----	246
dme:Dmel(CG4094	ACLPRVYELALGGTAV--GTGLNT-----	270
dme:Dmel(CG4095	GCLPRVYELALGGTAV--GTGLNT-----	279

eco:b2929	-----	169
eco:b1612	EGEA _R VRVDLNRP _M K _E I _L AQLSQY _P V _S TRL _L N _G T _I I _V GRDI--AHAKLK--ERMDNGE	408
eco:b4122	EGEA _V K _D LNRP _M K _E I _L AQLSQY _P V _S TRL _L T _G T _I I _V GRDI--AHAKLK--ELIDAGK	408
eco:b1675	-----	65
eco:b1611	-----HPEYARRVADELAVITCAPFVTAPNKFEALATCDALVQAHGALKGLAASLMKIAN	293
dme:Dmel(CG31874	-----KAEYSAQC _I KRIAELTFLPFVESP _N FES _I SACDCLVELHGELNTIAASVMKIAN	315
sce:YPL262W	-----KPGFDVKIAEQISKETGLKFQTAPNKFEALAAHDAIVECSGALNTLACSLFKIAQ	318
cel:CELE_H14A12.2	-----RKGFAEKVAATVSEL _T GLPFVTAPNKFEALAAHDALVEVHGALNTVAVSFMKIGN	331
mmu:14194	-----RIGFAEKVAAKVAALTGLPFVTAPNKFEALAAHDALVELSGAMNTAACSLMKIAN	337
hsa:2271	-----RIGFAEKVAAKVAALTGLPFVTAPNKFEALAAHDALVELSGAMNTTACSLMKIAN	340
dme:Dmel(CG6140	-----RRGFAEKCVKRIAQLSGLPFVVAPNFFEALACRDAMVEVHGALNVLAWSLMKVTN	301
dme:Dmel(CG4094	-----RKGFAEKCAAKIAELTSLPFVTAPNKFEALAAARDAMVEVHGVLNTIAVSLMKIAN	325
dme:Dmel(CG4095	-----RKGFAEKVAKRIS _E LTCLPFVSAPNKFEALAAARDAMVEVHGVLNTIAVSLMKIAN	334

eco:b2929			169
eco:b1612	GLPQYIKDHPIYYAGPAKTPEGYASGSLGPTTAGRMDSYVDQLQAQQGSIMILAKGNRSQ		468
eco:b4122	ELPQYIKDHPIYYAGPAKTPAGYPGSGSLGPTTAGRMDSYVDLLQSHGGSIMILAKGNRSQ		468
eco:b1675			65
eco:b1611	-DVRWLASGPRCGIGEISIPENE	PGSSIMPGKVNP T Q	329
dme:Dmel(CG31874	-DIRFLGSGPRCGFGEMLPENE	PGSSIMPGKVNP T Q	351
sce:YPL262W	-DIRYLGSGPRCGYHEMLPENE	PGSSIMPGKVNP T Q	354
cel:CELE_H14A12.2	-DIRFLGSGPRCGLGEMLPENE	PGSSIMPGKVNP T Q	367
mmu:14194	-DIRFLGSGPRSGLGEMLPENE	PGSSIMPGKVNP T Q	373
hsa:2271	-DIRFLGSGPRSGLGEMLPENE	PGSSIMPGKVNP T Q	376
dme:Dmel(CG6140	-DIRFLGSGPRCGLGEMLPENE	PGSSIMPGKVNP T Q	337
dme:Dmel(CG4094	-DIRFLGSGPRCGLGEMLPENE	PGSSIMPGKVNP T Q	361
dme:Dmel(CG4095	-DIRLLGSGPRCGLGEMLPENE	PGSSIMPGKVNP T Q	370

eco:b2929			169
eco:b1612	QVTDAKKHGGFYLGSI GGPAAVLAQGSIKS LEC VEY PELGMEAIW KIEVED FPAFILVD		528
eco:b4122	QVTDAKHGGFYLGSI GGPAAVLAQGSIKH LECVAYPELGMEAIW KIEVED FPAFILVD		528
eco:b1675			65
eco:b1611	C-----EALTMLCCQVMGN NDVAINMGGASGN FELNVFRPMVIHN F	LQSVRLLA	377
dme:Dmel(CG31874	C-----EAMSMICAQVMGNHV AVVSMGGSSGH FQLNTFMPMIASNV	LRSITLLG	399
sce:YPL262W	N-----EALTQVCVQVMGNNAITFAGSQ GQFELNVFKPVMIANL	LNSIRLIT	402
cel:CELE_H14A12.2	C-----EAITMVAAQVMGNHV AVSVGGNSGH FELNVFKPLIVRN V	LQSTRLLA	415
mmu:14194	C-----EAITMVAAQVMGNHV AVTVGGNSGH FELNVFKPMMIKNV	LHSARLLG	421
hsa:2271	C-----EAITMVAAQVMGNHV AVTVGGNSGH FELNVFKPMMIKNV	LHSARLLG	424
dme:Dmel(CG6140	C-----EAMTMICAQVMGNHV AVSVGGANGH FELNVFKPLIASNV	LRSIKLLA	385
dme:Dmel(CG4094	C-----ESLTMLS AQVMGNQVAVTIGGSNGH FELNVFKPLIVSN V	LRSIRLLS	409
dme:Dmel(CG4095	C-----ESMTMLCAQVMGNQV AVTIGGSNGH FELNVFKPLVVSN V	LRSIRLLA	418

eco:b2929		169
eco:b1612	DKGNDFQQIQLTQCTRCVK	548
eco:b4122	DKGNDFQQIVNKQCANCTK	548
eco:b1675	-----ALVK-----	69
eco:b1611	DG-----MESFNKHCAVGIEPNRERINQLLNESLMLVTALNTHIGYDKAACIAAKAH	429
dme:Dmel(CG31874	DG-----MKSFCTNCLEGIEPNRSKIGSIVKESLMLVTALSPHIGYERSAAIAAKAH	451
sce:YPL262W	DA-----AYSFRVHCVEGIKANEPRIHELLTKSLMLVTALNPKIGYDAASKVAKNAH	454
cel:CELE_H14A12.2	DS-----AVSFTDHCVDGIVANKDNIAKIMRESLMLVTALNPHIGYDNAAKIAKTAH	467
mmu:14194	DA-----SVSFTDNCVVGIQANTERINKLMNESLMLVTALNPHIGYDKAAKIAKTAH	473
hsa:2271	DA-----SVSFTENCVVGIQANTERINKLMNESLMLVTALNPHIGYDKAAKIAKTAH	476
dme:Dmel(CG6140	DG-----CISFNCNCVKGIKPNEKEKLAKIVNESLMLVTALNPHIGYDKSAQIAAKAH	437
dme:Dmel(CG4094	DG-----SRTFTANCVNGIQANRENIAKIMNESLMLVTALNPHIGYDKAAKIAKTAH	461
dme:Dmel(CG4095	DG-----SMTFSKNCVEGLQANKERIDKIMNESLMLVTALNPHIGYDKAALIAKTAH	470

eco:b2929	-----	169
eco:b1612	-----	548
eco:b4122	-----	548
eco:b1675	-----	69
eco:b1611	KEGLTLKAAALALGYLSEAEFD SWVRPEQMVGSMKAGR	467
dme:Dmel(CG31874	HNGTTLQEAILDGI-QREDFREWVQPSKMLGPE-----	484
sce:YPL262W	KKGITLKESAELGVLTEKEFDEWVVPEHMLGPK-----	488
cel:CELE_H14A12.2	KNGTTLVQEAVKLGILTEEQFAQWVKPENMLGPK-----	501
mmu:14194	KNGSTLKETAIELGYLTAEQFDEWVKPKDMLGPK-----	507
hsa:2271	KNGSTLKETAIELGYLTAEQFDEWVKPKDMLGPK-----	510
dme:Dmel(CG6140	KNGTTLKVEALNAGI-SEKDFNEWVRPEKMLGPS-----	470
dme:Dmel(CG4094	KNGTTLKEEAINLGYLTEQQFNDWVRPEQMLGPK-----	495
dme:Dmel(CG4095	KNKTTTLKEEALKTGI-TEEQFKEWVNPKEMLGPK-----	503

```

#
#
# Percent Identity Matrix - created by Clustal2.1
#
#


 1: eco_b2929      100.00   16.56   17.83   14.58   12.03   16.79   12.59   14.07   14.07   12.59   18.25   15.44   16.79
 2: eco_b1612      16.56   100.00   89.96   11.67   15.89   18.64   19.16   19.14   18.67   18.93   20.60   18.93   21.01
 3: eco_b4122      17.83   89.96   100.00   11.67   15.89   18.64   18.64   18.60   18.40   18.67   20.60   18.93   20.48
 4: eco_b1675      14.58   11.67   11.67   100.00   16.39   17.39   20.29   18.84   20.29   20.29   20.90   20.29   23.19
 5: eco_b1611      12.03   15.89   15.89   16.39   100.00   50.54   58.44   58.66   60.17   60.39   58.13   60.17   57.70
 6: dme_Dmel(CG31874) 16.79   18.64   18.64   17.39   50.54   100.00   50.10   57.93   56.60   57.44   63.62   60.67   59.29
 7: sce_YPL262W     12.59   19.16   18.64   20.29   58.44   50.10   100.00   63.73   65.49   65.07   59.10   62.37   60.83
 8: cel_CELE_H14A12.2 14.07   19.14   18.60   18.84   58.66   57.93   63.73   100.00   73.43   72.18   69.44   74.33   71.25
 9: mmu_14194       14.07   18.67   18.40   20.29   60.17   56.60   65.49   73.43   100.00   93.29   67.31   73.48   68.86
10: hsa_2271        12.59   18.93   18.67   20.29   60.39   57.44   65.07   72.18   93.29   100.00   66.88   72.67   68.46
11: dme_Dmel(CG6140) 18.25   20.60   20.60   20.90   58.13   63.62   59.10   69.44   67.31   66.88   100.00   75.69   72.34
12: dme_Dmel(CG4094) 15.44   18.93   18.93   20.29   60.17   60.67   62.37   74.33   73.48   72.67   75.69   100.00   78.14
13: dme_Dmel(CG4095) 16.79   21.01   20.48   23.19   57.70   59.29   60.83   71.25   68.86   68.46   72.34   78.14   100.00

```

ISOCITRATE DEHYDROGENASE

CLUSTAL O(1.2.4) multiple sequence alignment

sce:YDL066W		0
sce:YLR174W		0
sce:YNL009W		0
cel:CELE_C34F6.8		0
mmu:269951		0
hsa:3418		0
dme:Dmel(CG7176		0
cel:CELE_F59B8.2		0
mmu:15926		0
hsa:3417		0
eco:b1136		0
dme:Dmel(CG3483		0
sce:YOR136W		0
dme:Dmel(CG32026	MSGNWFKWTA LHGRPRTVGLNTNGRILRLLD AVVRFRQPFYESWRRRRR LEDIEKREIP	60
mmu:67834		0
hsa:3419		0
cel:CELE_F43G9.1		0
dme:Dmel(CG12233		0
cel:CELE_C37E2.1		0
dme:Dmel(CG6439		0
mmu:170718		0
hsa:3420		0
sce:YNL037C		0
mmu:243996		0
mmu:15929		0
hsa:3421		0
dme:Dmel(CG5028		0
cel:CELE_C30F12.7		0
cel:CELE_F35G12.2		0

sce:YDL066W	-	0
sce:YLR174W	-	0
sce:YNL009W	-	0
cel:CELE_C34F6.8	-	0
mmu:269951	-	0
hsa:3418	-	0
dme:Dmel(CG7176	-	0
cel:CELE_F59B8.2	-	0
mmu:15926	-	0
hsa:3417	-	0
eco:b1136	-	0
dme:Dmel(CG3483	-	0
sce:Y0R136W	-	0
dme:Dmel(CG32026	VRQQVPRIRHNRCPGAKENPCRKMPSVLPGKGEVLVPSRIQPPRNSMGFSVIRLFGSSTN	120
mmu:67834	-	0
hsa:3419	-	0
cel:CELE_F43G9.1	-	0
dme:Dmel(CG12233	-	0
cel:CELE_C37E2.1	-	0
dme:Dmel(CG6439	-	0
mmu:170718	-	0
hsa:3420	-	0
sce:YNL037C	-	0
mmu:243996	-	0
mmu:15929	-	0
hsa:3421	-	0
dme:Dmel(CG5028	-	0
cel:CELE_C30F12.7	-	0
cel:CELE_F35G12.2	-	0

sce:YDL066W		0
sce:YLR174W		0
sce:YNL009W		0
cel:CELE_C34F6.8		0
mmu:269951		0
hsa:3418		0
dme:Dmel(CG7176		0
cel:CELE_F59B8.2		0
mmu:15926		0
hsa:3417		0
eco:b1136		0
dme:Dmel(CG3483		0
sce:YOR136W		0
dme:Dmel(CG32026	DGGSGEPPENREGKLIKFTVGSRIAKPKTGKIEISKGPLGFETTKLPVQESLPQSDYLS	180
mmu:67834		0
hsa:3419		0
cel:CELE_F43G9.1		0
dme:Dmel(CG12233		0
cel:CELE_C37E2.1		0
dme:Dmel(CG6439		0
mmu:170718		0
hsa:3420		0
sce:YNL037C		0
mmu:243996		0
mmu:15929		0
hsa:3421		0
dme:Dmel(CG5028		0
cel:CELE_C30F12.7		0
cel:CELE_F35G12.2		0

sce:YDL066W	-	0
sce:YLR174W	-	0
sce:YNL009W	-	0
cel:CELE_C34F6.8	-	0
mmu:269951	-	0
hsa:3418	-	0
dme:Dmel(CG7176	-	0
cel:CELE_F59B8.2	-	0
mmu:15926	-	0
hsa:3417	-	0
eco:b1136	-	0
dme:Dmel(CG3483	-	0
sce:YOR136W	-	0
dme:Dmel(CG32026	GLSKKSPDKDTTPDTSTTQASDRSGKEGNEEKIKDDIPRSFSEYIIHWDS ESKNPSGIQS	240
mmu:67834	-	0
hsa:3419	-	0
cel:CELE_F43G9.1	-	0
dme:Dmel(CG12233	-	0
cel:CELE_C37E2.1	-	0
dme:Dmel(CG6439	-	0
mmu:170718	-	0
hsa:3420	-	0
sce:YNL037C	-	0
mmu:243996	-	0
mmu:15929	-	0
hsa:3421	-	0
dme:Dmel(CG5028	-	0
cel:CELE_C30F12.7	-	0
cel:CELE_F35G12.2	-	0

sce:YDL066W		0
sce:YLR174W		0
sce:YNL009W		0
cel:CELE_C34F6.8		0
mmu:269951		0
hsa:3418		0
dme:Dmel(CG7176)		0
cel:CELE_F59B8.2		0
mmu:15926		0
hsa:3417		0
eco:b1136		0
dme:Dmel(CG3483)	-MNTLR-	5
sce:Y0R136W		0
dme:Dmel(CG32026)	QQPERCESAGNPPSGGKPPTKPPTGPSTPSGPSNPSRPPSRKDNNPFSGMGSEPPKKPL	300
mmu:67834		0
hsa:3419		0
cel:CELE_F43G9.1		0
dme:Dmel(CG12233)		0
cel:CELE_C37E2.1		0
dme:Dmel(CG6439)		0
mmu:170718		0
hsa:3420		0
sce:YNL037C		0
mmu:243996		0
mmu:15929		0
hsa:3421		0
dme:Dmel(CG5028)		0
cel:CELE_C30F12.7		0
cel:CELE_F35G12.2		0

sce:YDL066W				0
sce:YLR174W				0
sce:YNL009W				0
cel:CELE_C34F6.8				0
mmu:269951		- MAGYLRA	- VSSL - CRASGSAR	19
hsa:3418		- MAGYLRV	- VRSL - CRASGSRP	19
dme:Dmel(CG7176	MFALRRTAAMMT	SVHRQPHLSQA	VFRANFA - ISAADPKT	38
cel:CELE_F59B8.2		- MRPFL	- A - C	7
mmu:15926				0
hsa:3417				0
eco:b1136				0
dme:Dmel(CG3483		- KLNSLPPFRS VGGAYRLFAGKDQKKDSAGQ - KT		37
sce:Y0R136W		MLRNTFFRNTS	- RRF	14
dme:Dmel(CG32026	GSKPPSKLPPRSTSPKKPPTGSTPPQKPTKSSKPPN		- KPPAGPGKKSASK - PP	351
mmu:67834		MAGSAWVS	- KVSRLLGA	16
hsa:3419		MAGPAWIS	- KVSRLLGA	16
cel:CELE_F43G9.1			- ML	2
dme:Dmel(CG12233	- MAARFIQ		- KILNQLGLIAARD - AP	22
cel:CELE_C37E2.1		MLSRTVSSL SRV	- APQTLGAV	20
dme:Dmel(CG6439		MSMLART	- VGRTFMQA	15
mmu:170718		MAALSNVRWLTRAVLAAR	- NSGAWRGL	26
hsa:3420		MAALSGVRWLTRALVSAG	- NPGAWRGL	26
sce:YNL037C			- ML - NRTI	6
mmu:243996		MLAVTS-CSMKTVLQ	- YAVFLGHSREVVCEL	29
mmu:15929		MAL - KVAIAA-GGAAKAML	- KPTLLCRPWEVLAAH	32
hsa:3421		MAL - KVATVA-GSAAKAVL	- GPALLCRPWEVLGAH	32
dme:Dmel(CG5028		MAL - RLTQRLLQTQTPFLT	- RGYPULLVTKEKTEDVAH	35
cel:CELE_C30F12.7	MFS - K		- LPIQAVRG - A	13
cel:CELE_F35G12.2	MSS -	NVLGHTLRSSKNVVQ - KAFVATSPNS	- D	29

sce:YDL066W	-----MSMLSRRLFSTSRLAA-	FSKIKVKQPVVLDGDEMTRIIWDKIKKKLI	47
sce:YLR174W	-----	MTKIKVANPIVEMDGDEQTRIIWHLIRDKLV	31
sce:YNL009W	-----	MSKIKVVHPIVEMDGDEQTRVIWKLKEKLI	31
cel:CELE_C34F6.8	----MLSRLTSRNVLARNVATAATQE-	RQKIKVDNPVVLDGDEMTRIIWKEIKNKLI	54
mmu:269951	-----TWAPAALT-VP--SWPEQPR-RHYA-	EKRIKVEKPVVEMDGDEMTRIIWQFIKEKLI	71
hsa:3418	-----AWAPAALT-AP--TSQEQPR-RHYA-	DKRIKVAKPVVEMDGDEMTRIIWQFIKEKLI	71
dme:Dmel(CG7176	HKISMDNERMSAVS--EHSSVVC-SPEQ-	MAQKIKAGPVVLDGDEMTRIIWDSIKSQLI	94
cel:CELE_F59B8.2	--SSLA-----RH--VFRGFPT-TNAM-	AAQKIQGGDIVEMQGDEMTRIIWDLIKEKLI	55
mmu:15926	-----	MSRKIQGGSVVEMQGDEMTRIIWELIKEKLI	31
hsa:3417	-----	MSKKISGGSVVEMQGDEMTRIIWELIKEKLI	31
eco:b1136	-----MESK-VV-VPA-QGKKITL---	QNGKLNVPENPIIPYIEGDGIGVDVTAMLKVVD	50
dme:Dmel(CG3483	RQPEKPPQ-DK-QKS-KGASGKAKS-AGSTD	SACKTTKVTLINGEGVGRELMDAVQEVIC	93
sce:YOR136W	-----LAT-VK-QPS-IGR-YTG-----	KPNPSTGKYTVSFIEGDGIGPEISKVKIFS	60
dme:Dmel(CG32026	TAS--KPP-VK-SPA-GGQQQKGAGGKSGKAS	GEPFRVITLMPGDGIGPEISMAVIKILE	406
mmu:67834	-----	FHNT-KQVTRGFAGGVQTVTLIPGDGIGPEISASVMKIFD	55
hsa:3419	-----	FHNP-KQVTRGFAGGVQTVTLIPGDGIGPEISAAVMKIFD	55
cel:CELE_F43G9.1	-----GKC-IK-K-----	ASSTVGQSIRYSSGDVRRVTLIPGDGIGPEISASVQKIFE	48
dme:Dmel(CG12233	AVTA-TPA-VS-Q-----	VNATPAASRSYS-SGTKKVTLIPGDGIGPEISAAVQKIFT	71
cel:CELE_C37E2.1	-----NAA-S-----	SRQYSITAPRPPTELNQKLKVTIIPGDGVGPELIYTVQDIVK	66
dme:Dmel(CG6439	-----AAA-R-----	SLHTTSTLRATDNYGANRTTCLIPGDGVGPVELVYSLQEVFK	61
mmu:170718	-----GTS-T-----	AHAASQSQAQDVRVEGAFPVTMLPGDGVGPPELMHAVKEVFK	71
hsa:3420	-----STS-A-----	AAHAASRSQAEDVRVEGSSFPVTMLPGDGVGPPELMHAVKEVFK	72
sce:YNL037C	-----AKR-T-----	LATAAQAAERTLPKKYGRFTVTLIPGDGVGKEITDSVRTIFE	52
mmu:243996	-----VTS-F-----	RSFCSHCAVPPSPKYGGRHTVAMIPGDGIGPELMVHVKKIFR	75
mmu:15929	-----VAP-R-----	RSISSLQQTIPPSAKYGGGRHTVTMIPGDGIGPEMLHVKSVFR	78
hsa:3421	-----EVP-S-----	RNIFSEQTIPPSAKYGGGRHTVTMIPGDGIGPEMLHVKSVFR	78
dme:Dmel(CG5028	-----TKS-A-----	LQKKVTGTDIPSQYGGGRHVTMLPGGGIGPELMGYVREIFR	81
cel:CELE_C30F12.7	-----ASA-I-----	RTHQIPGHRLPLAKYGGGRHTVCALPGDGIGPEMIAHIRNIFS	59
cel:CELE_F35G12.2	-----MLR-F-----	RSPVLTQNTTKLARYGGGRHNVTVLPGDGIGPEMLHHVERILS	75

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sce:YDL066W	LPYL-----DVDLKYYDLSVESR--DATSDKITQDAEAIKKYGVGIKCATITPDEAR	98
sce:YLR174W	LPYL-----DVDLKYYDLSVEYR--DQTNDQVTVDSATATLKYGVAVKCATITPDEAR	82
sce:YNL009W	LPYL-----DVDLKYYDLSIWER--DRTNDQVTKDSSYATLKYGVAVKCATITPDEAR	82
cel:CELE_C34F6.8	LPYL-----DL DIKYYDLGLEYR--DETNDQVTIDAHAILEHSGVGIKCATITPDEAR	105
mmu:269951	LPHV-----DVQLKYFDLGLPNR--DQTNDQVTIDSALATQKYSVAVKCATITPDEAR	122
hsa:3418	LPHV-----DIQLKYFDLGLPNR--DQTDDQVTIDSALATQKYSVAVKCATITPDEAR	122
dme:Dmel(CG7176	LPFL-----DIELHTYDLGIENR--DKTEDQVTIDCAEAIKKYNVGIKCATITPDEKR	145
cel:CELE_F59B8.2	LPYV-----DLNVHFFDLGIEHR--DATDDQVTIDAANATLKYNVAVKCATITPDEAR	106
mmu:15926	LPYV-----ELDLHSYDLGIENR--DATNDQVTKDAAEAIKKYNVGVKCATITPDEKR	82
hsa:3417	FPYV-----ELDLHSYDLGIENR--DATNDQVTKDAAEAIKKHNVGVKCATITPDEKR	82
eco:b1136	AAVEKAYKGGERKISWMEIYTGEKSTQVYGQDVWLPAETLDLIREYRAIKGPLTPVG--	108
dme:Dmel(CG3483	AVKA-----PIEWDVHDEFKAKD--S---DDVSPEVLKSLRANKVGIGKGPVDSRHW--	139
sce:YOR136W	AANV-----PIEWESCDVSPIFV--NGLTTIPDPAVQSITKNLVALKGPLATPIG--	108
dme:Dmel(CG32026	AAKT-----PLIFEPVDVTPVLN--SQGMTSVPEQVIESMNRTKVLKGPLMTPVG--	455
mmu:67834	AAKA-----PIQWEERNVTAIQG--PGGKWMIPPEAKESMDKNMGLKGPLKTPIA--	104
hsa:3419	AAKA-----PIQWEERNVTAIQG--PGGKWMIPSEAKESMDKNMGLKGPLKTPIA--	104
cel:CELE_F43G9.1	AADA-----PIAWDPDVTPVKG--RDGVFRIPSRCIELMHANKVGLKGPLETPIG--	97
dme:Dmel(CG12233	AANV-----PIEWEAVDVTPVRG--PDGKFGIPQAIDSNTNKIGLKGPLMTPVG--	120
cel:CELE_C37E2.1	QTGI-----PIEFEEIFLSEVHY--TRS-SSIENAVESIGRNNNVALKGAIIESAV--	114
dme:Dmel(CG6439	AASV-----PVDFECYFLSEINP--VL--SAKLEDVVASIQKNKVCIKGVLAT-PD--	107
mmu:170718	AAA V-----PVEFKEHHLSEVQN--MAS-EEKLEQVLSSMKENKVAIIGKIYT-PM--	118
hsa:3420	AAA V-----PVEFQEHHLSEVQN--MAS-EEKLEQVLSSMKENKVAIIGKIHT-PM--	119
sce:YNL037C	AENI-----PIDWETINIKQTD--H-KEGVYEAESLKRKNIGLKGWLWHTPAD--	97
mmu:243996	SNCV-----PVDFEEVWVTSTS--N-EEEINNALMAIRRNRVALKGNIATNHN--	120
mmu:15929	HACV-----PVDFEEVHVSSNA--D-EEDIRNAIMAIRRNVALKGNIETNHN--	123
hsa:3421	HACV-----PVDFEEVHVSSNA--D-EEDIRNAIMAIRRNVALKGNIETNHN--	123
dme:Dmel(CG5028	YCGA-----PIDFEVIDIDPSTE--G-NDDLDYAITSIKRNGVALKGNIETKSQ--	127
cel:CELE_C30F12.7	FCHA-----PVNFEEVQVSSL--L-DGDMDAAMLAIERNGVAIKGNIETKHD--	104
cel:CELE_F35G12.2	AVQA-----PVDFEVNLTSKED--A-SEDLAEAITAIKRNGVALKGNIETKFD--	121

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sce:YDL066W	VKEFNLHKMWKSPNGTIRNILGGTVFREPIVIPRLVPRW----	EKPIIIIGRHAHGDQ	154
sce:YLR174W	VEEFHLKKMWKSPNGTIRNILGGTVFREPIIIIPRLVPGW----	EKPIIIIGRHAHGDQ	138
sce:YNL009W	MKEFNLKEMWKSPNGTIRNILGGTVFREPIIIIPRLVPHW----	EKPIIIIGRHAHGDQ	138
cel:CELE_C34F6.8	IKEFNLKKMWLSPNGTIRNILGGTVFREPILCKNIPRLVPGW----	TQPIТИGRHAHGDQ	161
mmu:269951	VEEFKLKKMWKSPNGTIRNILGGTVFREPIICKNIPRLVPGW----	TKPITIGRHAHGDQ	178
hsa:3418	VEEFKLKKMWKSPNGTIRNILGGTVFREPIICKNIPRLVPGW----	TKPITIGRHAHGDQ	178
dme:Dmel(CG7176)	VEEFNLKKMWKSPNGTIRNILGGTVFREAIICKNIPRLVTGW----	QKPIVIGRHAHADQ	201
cel:CELE_F59B8.2	VEEFKLKKMWKSPNGTIRNILGGTVFREPIIVKNVPRLVNTW----	SKPIIIIGRHAHADQ	162
mmu:15926	VEEFKLKQMWKSPNGTIRNILGGTVFREAIICKNIPRLVTGW----	VKPIIIIGRHAYGDQ	138
hsa:3417	VEEFKLQMWKSPNGTIRNILGGTVFREAIICKNIPRLVSGW----	VKPIIIIGRHAYGDQ	138
eco:b1136	-----GGIRSLNVALRQELD--LYICLRPVRYQQTPSPVKHPELTDMVIFRENSEDI		159
dme:Dmel(CG3483)	-----QRQIRKQFA--QFAYVSLCSHIEGLDSP--YG-DFDVVIIRDQMEGD		181
sce:YOR136W	-----KGHRSLNLTLLRKTFG--LFANVRPAKSIEGFKTT--YE-NVDLVLIRENTEGE		156
dme:Dmel(CG32026)	-----TGFRSLNLTLLRQLFN--LYANIRPCRSLPGVETV--YG-DVDIVTIRENTEGE		503
mmu:67834	-----AGHPSMNLLLRLKTFD--LYANVRPCVSIEGYKTP--YT-DVNIVTIRENTEGE		152
hsa:3419	-----AGHPSMNLLLRLKTFD--LYANVRPCVSIEGYKTP--YT-DVNIVTIRENTEGE		152
cel:CELE_F43G9.1	-----KGHRSLNLAURKEFS--LYANVRPCRSLEGHKTL--YD-NVDVVTIRENTEGE		145
dme:Dmel(CG12233)	-----KGHRSLNLAURKEFN--LYANVRPCRSLEGYKTL--YD-DVDVVTIRENTEGE		168
cel:CELE_C37E2.1	---LHTEGELQGLNMRLRRSLD--LFANVVHIKTLGIKTR--HGKQLDFVIVREQTEGE		167
dme:Dmel(CG6439)	---YSNVGDLQTLNMKLRNDLD--LYANVVHVRSLPGVKTR--HT-NIDTVIIREQTEGE		159
mmu:170718	---EYKGELASYDMQLRRKLD--LFANVVHVKSLSGPYKTR--HN-NLDLVIIREQTEGE		169
hsa:3420	---EYKGELASYDMRLRRKLD--LFANVVHVKSLSPGYMTR--HN-NLDLVIIREQTEGE		170
sce:YNL037C	---QT-GHGSLSNVALRKQLD--IYANVALFKSLKGVKTR--IP-DIDLIVIRENTEGE		146
mmu:243996	---LPARYKSHNTKFRTILD--LYASVVHFKTFPGVMTR--HK-DIDILVVRENTEGE		170
mmu:15929	---LPPSHKSRNNILRTSLD--LYANVIHCKSLPGVVTR--HK-DIDILIVRENTEGE		173
hsa:3421	---LPPSHKSRNNILRTSLD--LYANVIHCKSLPGVVTR--HK-DIDILIVRENTEGE		173
dme:Dmel(CG5028)	---SL-TEVSRNVAIRNELD--LYVNVVHCKSYPGIPAR--HH-DIDVVLIRQNTDGE		176
cel:CELE_C30F12.7	---DP-QFNSRNVELRTKLD--LYANILHCVTIPTVPTR--HS-GIDIVLIRENTEGE		153
cel:CELE_F35G12.2	---NP-SFVSRNLELRRQLN--LYANVLHCSTIPTVPSR--HT-GIDMVIIRENTEGE		170

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sce:YDL066W	YKATDTLIP---	GPGSLELVYKPSDPTTAQPQTLKVYDYKG-SGVAMAMYNTDESIEGFA	210
sce:YLR174W	YKATDVIP---	EEGELRLVYKSKGTH--DVLKVFDYPHEGGVAMMMYNTTDSIEGFA	193
sce:YNL009W	YRATDIKIK---	KAGKLRLQFSSDDGKE--NIDLKVYEFPKSGGIAMAMFNTNDISKGFA	193
cel:CELE_C34F6.8	YKCTDLVIP---	SGSTLQLLVNKPDSK--D-VHNVYDFKKSGGVGLAMYNTDESIKGFA	215
mmu:269951	YKATDFVVD---	RAGTFKLVFTPDKGSS--AKEWEVYNFP-AGGVGMGMYNTDESIKGFA	232
hsa:3418	YKATDFVAD---	RAGTFKMVFVTPDKGSG--VKEWEVYNFP-AGGVGMGMYNTDESIKGFA	232
dme:Dmel(CG7176	YKAVDYVVP---	GPGKLTWTKGTDGQ--VIDEVINDFK-GPGIALGMFNTDDSIVDFA	254
cel:CELE_F59B8.2	YKATDFVVP---	GAGKLEIKFVSADGTQ--TIQETVFDLK-GPGVSLSMYNTDDSIRDFA	216
mmu:15926	YRATDFVVP---	GPGKVEITYTPKDGTQ--KVTYMVHDFEEGGGVAMGMYNQDKSIEDFA	193
hsa:3417	YRATDFVVP---	GPGKVEITYTPSDGTQ--KVTYLVHNFEEGGGVAMGMYNQDKSIEDFA	193
eco:b1136	YAGIEWKADSADAEEKVIKFLRE-----	EMGVKKIRFPEHCIGIKPCS-EEGTKRLV	210
dme:Dmel(CG3483	YSGIEHLVV---	PGVMQ-----TIKVST-TAGAARIA	209
sce:Y0R136W	YSGIEHIVC---	PGVVQ-----SIKLIT-RDASERVI	184
dme:Dmel(CG32026	YSGIEHTLV---	NGVVQ-----SIKLIT-RNASLRVA	531
mmu:67834	YSGIEHVIV---	DGVVQ-----SIKLIT-EEASKRIA	180
hsa:3419	YSGIEHVIV---	DGVVQ-----SIKLIT-EGASKRIA	180
cel:CELE_F43G9.1	YSGIEHEIV---	PGVVQ-----SIKLIT-ETASRNVA	173
dme:Dmel(CG12233	YSGIEHEIV---	DGVVQ-----SIKLIT-EEASKRVA	196
cel:CELE_C37E2.1	YSSLEHELV---	PGVIE-----CLKIST-RTKAERIA	195
dme:Dmel(CG6439	YSALEHESV---	PGIVE-----CLKIIT-AKKSMRRA	187
mmu:170718	YSSLEHESA---	KGVIE-----CLKIVT-RTKSQRIA	197
hsa:3420	YSSLEHESA---	RGVIE-----CLKIVT-RAKSQRIA	198
sce:YNL037C	FSGLEHESV---	PGVVE-----SLKVMT-RPKTERIA	174
mmu:243996	YTNLLEHESV---	KGVVE-----SLKIVT-KTKSVRIA	198
mmu:15929	YSSLEHESV---	AGVVE-----SLKIIT-KAKSLRIA	201
hsa:3421	YSSLEHESV---	AGVVE-----SLKIIT-KAKSLRIA	201
dme:Dmel(CG5028	YAMLEHESV---	PGIVE-----SMKVVT-VENAERVA	204
cel:CELE_C30F12.7	YSGLEHEAV---	PGIVE-----SIKIVT-REKIERIS	181
cel:CELE_F35G12.2	YSGNEHEAVNAPHPRVVE-----	SLKVVT-REKSEQIT	202

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sce:YDL066W	HSSFKLAI DKKLN -LFLST KNTILKKYDGRF KDIFQE VYEAQYKS KF E-----	257
sce:YLR174W	KASFELAIER KLP -LYST TNTILKKYDGRKF KDVF EAMYARSYKE KF F-----	240
sce:YNL009W	KASFELALKR KLP -LFFTT KNTILKKNYDNQFKQIF DNL FDKEYKE KF F-----	240
cel:CELE_C34F6.8	HSCFQYALMK QWP -LYLST KNTILKKYDGRF KDIFQD IYEKKYEAD FK F-----	262
mmu:269951	HSCFQYSI QKKWP -LYLST KNTILKAYDGRF KDIFQE IFDKHYKTDF D F-----	279
hsa:3418	HSCFQYAI QKKWP -LYMST KNTILKAYDGRF KDIFQE IFDKHYKTDF D F-----	279
dme:Dmel(CG7176	HASF KYALDR K LP -LYMST KNTILKKYDGRF KDIFEDLYNK QYKKEYE-----	301
cel:CELE_F59B8.2	HASF KYALQR K FP -LYLST KNTILKKYDGRF KDIFAEIYP-EYEAEFK -----	262
mmu:15926	HSSFQ MALSKG WP-LYLST KNTILKKYDGRF KDIFQE IYDKKYKSQF E -----	240
hsa:3417	HSSFQ MALSKG WP-LYLST KNTILKKYDGRF KDIFQE IYDKQYKSQF E -----	240
eco:b1136	RAAIEYAI ANDRSVT L VHKGNIMKFTEGA F KD WG YQLAREEFGGELIDGGPWLKVKNPN -----	270
dme:Dmel(CG3483	EFVFNYAV KNKRKRIT VAH KANIMRMTDG N FLEAMRAEADKHVD -----	253
sce:YOR136W	RYAF EYARAIGPRVIVV H KSTIQRLADGLFVN AKELS-KEYP -----	227
dme:Dmel(CG32026	EYTFQYALAM KRKKV TAVA ESQVMRMSDGLFLRCVREMA -AKY KSKM -----	577
mmu:67834	EFAFEYARNNHRSNV TAVHKANIMRMSDGLFLQKC REVA-ENCK -----	223
hsa:3419	EFAFEYARNNHRSNV TAVHKANIMRMSDGLFLQKC REVA-ESCK -----	223
cel:CELE_F43G9.1	SFAFEYARQN GRKVV TAV HKANIMRMRQSDGLFLSIC REQA-ALYP -----	216
dme:Dmel(CG12233	EYAFQYAKNNRKK KVTVV H KANIMRMSDGLFLRCVRDMA -QKFP -----	239
cel:CELE_C37E2.1	KFAFDYAT KTGRKKV TAV HKANIMKLG D GLFLRTCE GVA-KQYP -----	238
dme:Dmel(CG6439	KFAFDYAT KNQRKKV TAV HKANIMKLG D GLFLRSCEE V-S-RLYP -----	230
mmu:170718	KFAFDYAT KKGRSKV TAV HKANIMKLG D GLFLQCCEE VA-ELYP -----	240
hsa:3420	KFAFDYAT KKGRGKV TAV HKANIMKLG D GLFLQCCEE VA-ELYP -----	241
sce:YNL037C	RFAFD FAKKYNRKSV TAV HKANIMKLG D GLFRNIITEIGQ KEYP -----	218
mmu:243996	DYAF KLAKQMGRKKV T VVKANIMKLG D GLFLQCCKDVA -AHYP -----	241
mmu:15929	EYAF KLAEQESGRKKV TAV HKANIMKLG D GLFLQCCEE VA-AHYP -----	244
hsa:3421	EYAF KLAEQESGRKKV TAV HKANIMKLG D GLFLQCCEE VA-ARYP -----	244
dme:Dmel(CG5028	RYAFEFARQNNRKK VTTIHKANIMKLSDGLF L EVA NRVH-KDYP -----	247
cel:CELE_C30F12.7	RMAFEYAKANGRKK VTA V HKANIQKLG D GLFLKVVRDMS -EDYK -----	224
cel:CELE_F35G12.2	RFAFQFAKKYGRKK VTA V HKANIQKLG D GLFLKVATDIA KA E YP -----	246

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sce:YDL066W	-QLGIHYEHRLIDDMVAQMIKSKGFF--IMALKNYDGDVQSDIVAQGF-GSLGLMTSIL	312
sce:YLR174W	-SLGIWYEHRLIDDMVAQMLKSKGYY--IIAMKNYDGDVESDIVAQGF-GSLGLMTSVL	295
sce:YNL009W	-ALKITYEHRLIDDMVAQMLKSKGFF--IIAMKNYDGDVQSDIVAQGF-GSLGLMTSIL	295
cel:CELE_C34F6.8	-NNKIWYEHRLIDDMVAQMLKSKGFF--VWACKNYDGDVQSDIVAQGY-GSLGLMSSVL	317
mmu:269951	-KNKIWYEHRLIDDMVAQVLKSSGGF--VWACKNYDGDVQSDILAQGF-GSLGLMTSVL	334
hsa:3418	-KNKIWYEHRLIDDMVAQVLKSSGGF--VWACKNYDGDVQSDILAQGF-GSLGLMTSVL	334
dme:Dmel(CG7176	-AAGIWIYEHRLIDDMVAYAMKSEGGF--VWACKNYDGDVQSDSVAQGY-GSLGLMTSVL	356
cel:CELE_F59B8.2	-AAGIWIYEHRLIDDMVAQAMKSDGGF--VWACKNYDGDVQSDSVAQGY-GSLGLMTSVL	317
mmu:15926	-AQKICYEHRLIDDMVAQAMKSEGGF--IWACKNYDGDVQSDSVAQGY-GSLGMMTSVL	295
hsa:3417	-AQKIWYEHRLIDDMVAQAMKSEGGF--IWACKNYDGDVQSDSVAQGY-GSLGMMTSVL	295
eco:b1136	TGKEIVIKDVIADAFLQQILLRPAEYD--VIACMNLNGDYISDALAAQV-GGIGIAPGAN	327
dme:Dmel(CG3483	--DVLFEERYLDTCILKILLKPHKCD--VMVSSSMYGDVLRVIAAGGMM-GVPGICPGYS	307
sce:Y0R136W	--DLTLETELIDNSVLKVVTNPASYTDAVSVCNPILYGDILSDLNGLSAGSLGLTPSAN	284
dme:Dmel(CG32026	DQAGIKYEESTMVCLCNIVQDPKRYD--MLVLPNLYGDILSDTCAGLI-GGLGLTPSGN	634
mmu:67834	--DIKFNEYMLDTVCLNMVQDPSQFD--VLVMPNLYGDILSDLCAGLI-GGLGVTPSGN	277
hsa:3419	--DIKFNEYMLDTVCLNMVQDPSQFD--VLVMPNLYGDILSDLCAGLI-GGLGVTPSGN	277
cel:CELE_F43G9.1	--DIKFKEAYLDTVCLNMVQDPSQYD--VLVMPNLYGDILSDLCAGLV-GGLGVTPSGN	270
dme:Dmel(CG12233	--EIQFEEKYLDTVCLNMVQNPGKYD--VLVMPNLYGDILSDMCAGLV-GGLGLTPSGN	293
cel:CELE_C37E2.1	--KIQFESMIIDNTCMQLVSKPEQFD--VMVMPNLYGNIIDNLAAGLV-GGAGVVPGQS	292
dme:Dmel(CG6439	--RIQFEKMOVNDNTTMQMVSNPQNFQD--VMVTPNLYGAIVDNLASGLV-GGAGVVAGAS	284
mmu:170718	--KIKFETMIIDNCCMQLVQNPYQFD--VLVMPNLYGNIIDNLAAGLV-GGAGVVPGES	294
hsa:3420	--KIKFETMIIDNCCMQLVQNPYQFD--VLVMPNLYGNIIDNLAAGLV-GGAGVVPGES	295
sce:YNL037C	--DIDVSSIIVDNASMQAVAKPHQFD--VLVTPSMYGTILGNIGAALI-GGPGLVAGAN	272
mmu:243996	--QITLESMIIDNTTMQLVSKPQQFD--VMVMPNLYGNIINSICTGLV-GGSGIVPGAN	295
mmu:15929	--QITFDMSIVDNTTMQLVSRPQQFD--VMVMPNLYGNIIVNNVCAGLV-GGPGLVAGAN	298
hsa:3421	--QITFENMIVDNTTMQLVSRPQQFD--VMVMPNLYGNIIVNNVCAGLV-GGPGLVAGAN	298
dme:Dmel(CG5028	--ELEHNNMIIDNTCMQSVSNPHQFD--VMNMTNLGYTIVSNVLCGLM-GGAGLISGRN	301
cel:CELE_C30F12.7	--DIKFEAMIVDNASMQLVSKPQQFD--VMVMPNLYGNIISNIACGLV-GGPGLVSGMN	278
cel:CELE_F35G12.2	--DIEFNAMIVDNASMQLVSRPQQFD--VMLMPNLYGNIISNIACGLV-GGPGLVSGMN	300

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sce:YDL066W	VTPDG-KTFESEAAHGTVTRHYRKYQKGEETSTNSIASIFAWSRGLLKRGELDNTPALCK	371
sce:YLR174W	ITPDG-KTFESEAAHGTVTRHFRQHQGKETSTNSIASIFAWTRGIIQRGKLDNTPDVVK	354
sce:YNL009W	ITPDG-KTFESEAAHGTVTRHFRKHQRGEETSTNSIASIFAWTRAIQRGKLDNTDDVIK	354
cel:CELE_C34F6.8	MCPDG-KTIEAAAHGTVTRHYREHQKGNSTSTNPIASIFAWTRGLHHRGVLDNNEALKT	376
mmu:269951	VCPDG-KTIEAAAHGTVTRHYREHQKGRPTSTNPIASIFAWTRGLEHRGKLDGNQDLIR	393
hsa:3418	VCPDG-KTIEAAAHGTVTRHYREHQKGRPTSTNPIASIFAWTRGLEHRGKLDGNQDLIR	393
dme:Dmel(CG7176)	LCPDG-KTVEAAAHGTVTRHFRFYQQGKETSTNPIASIFAWTRGLLHRAKLDNNNEPLQ	415
cel:CELE_F59B8.2	VCPDG-KTVEAAAHGTVTRHYRMHQKGQETSTNPIASIFAWSRGLAHRATLDKNSALET	376
mmu:15926	ICPDG-KTVEAAAHGTVTRHYRMYQKGQETSTNPIASIFAWSRGLAHRAKLDNNTELSF	354
hsa:3417	VCPDG-KTVEAAAHGTVTRHYRMYQKGQETSTNPIASIFAWTRGLAHRAKLDNNKELAF	354
eco:b1136	IGDEC-ALFEA--THGTAPK-----YAGQDKVNPGSIIILSAEMMLRH-----GWTE	371
dme:Dmel(CG3483)	VSSLG-TVFDC--RMKACHA-----LAGKDLANPTGPLLSAALMLRH-----KMDK	351
sce:YOR136W	IGHKI-SIFE-----VHGSAPD-----IAGQDKANPTALLSSVMMNLNH-----GLTN	328
dme:Dmel(CG32026)	VGTNG-AIFES--VHGTAPE-----IAGKDLANPTALLSSVMMHLHYI-----GLHE	678
mmu:67834	IGANGVAIFES--VHGTAPE-----IAGKDMANPTALLSAVMMMLRH-----GLFD	322
hsa:3419	IGANGVAIFES--VHGTAPE-----IAGKDMANPTALLSAVMMMLRH-----GLFD	322
cel:CELE_F43G9.1	IGKGA-AVFES--VHGTAPE-----IAGQDKANPTALLSAVMMMLRYM-----NLPQ	314
dme:Dmel(CG12233)	MGLNG-ALFES--VHGTAPE-----IAGKDLANPTALLSAVMMMLRH-----ELNT	337
cel:CELE_C37E2.1	VGRDF-VIFEP-GSRHSFQE-----AMGRSIANPTAMILCAAANMLNHL-----HLDA	337
dme:Dmel(CG6439)	YSSES-VVFEP-GARHTFAE-----AVGKNVANPTAMLLCGVKLLRHI-----NLPT	329
mmu:170718	YSAEY-AVFET-GARHPFAQ-----AVGRNIANPTAMLLSATNMLRHL-----NLEY	339
hsa:3420	YSAEY-AVFET-GARHPFAQ-----AVGRNIANPTAMLLSASNMLRHL-----NLEY	340
sce:YNL037C	FGRDY-AVFEP-GSRHVGLD-----IKGQN VANPTAMILSSTLMLNHL-----GLNE	317
mmu:243996	YGDSY-AIFEM-GSKEIGKD-----LAHRNIANPVAMLLTSCIMLDYL-----DLQP	340
mmu:15929	YGHVY-AVFET-ATRNTGKS-----IANKNIANPTATLLASCMMLDHL-----KLHS	343
hsa:3421	YGHVY-AVFET-ATRNTGKS-----IANKNIANPTATLLASCMMLDHL-----KLHS	343
dme:Dmel(CG5028)	YGDHY-AIFEP-GTRNTGTA-----IAGKNIANPVAMISASIDMLNHL-----GHKE	346
cel:CELE_C30F12.7	LGDKY-AVFET-GTRNTGTS-----LAGKDIANPTAFIRASVDMRLRYL-----GCHY	323
cel:CELE_F35G12.2	IGEDY-AVFET-GTRNTGTT-----LAGKDLANPTAFIRAAVDMRLFL-----GLQS	345

sce:YDL066W	FANILESATLNTVQQDG-----IMTKDLALACG-----NNERSAYVTTEEFLDAVEKRLQ	421
sce:YLR174W	FGQILESATVNTVQEDG-----IMTKDLALILG-----KSERSAYVTTEEFLDAVESRLK	404
sce:YNL009W	FGNLLEKATLDTVQVGG-----KMTKDLALMLG-----KTNRSSYVTTEEFLIDEVAKRLQ	404
cel:CELE_C34F6.8	FSLTLEKACIDTVE-EG-----KMTKDLSCIHGTKK-GTEKGAYLITEDFLSAIDTAKMA	429
mmu:269951	FAQTLEKVCVQTVE-SG-----AMTKDLAGCIHGLSN-VKLNEHFLNTTDFLDTIKSNLD	446
hsa:3418	FAQMLEKVCVETVE-SG-----AMTKDLAGCIHGLSN-VKLNEHFLNTTDFLDTIKSNLD	446
dme:Dmel(CG7176	FADTLEQVCIDTIE-SG-----AMTKDLAICIKGN-INAVERRDYQETFEFINTLAKNLE	468
cel:CELE_F59B8.2	FANNLEAVCIETME-AG-----FLTKDLAICVKGGNASAVRTDYLNTFEFLDKLAENLA	430
mmu:15926	FAKALEDVCIETIE-AG-----FMTKDLAACIKGL--PNVQRSDYLNTFEFMDKLGGENLK	406
hsa:3417	FANALEEVSIETIE-AG-----FMTKDLAACIKGL--PNVQRSDYLNTFEFMDKLGGENLK	406
eco:b1136	AADLIVKGMEAGAINAKTVTYDFERLMDGAK-----LLKCSEFGDAAIENM-	416
dme:Dmel(CG3483	QADQVDCAIRKVKYKDTD-----IRTPDVGG-----KAKCSEFVKAVCDCL-	391
sce:YOR136W	HADQIQNAVLSIATSGP-----ENRTGDLAG-----TATTSSFTEAVIDKRL-	369
dme:Dmel(CG32026	HADKIEKAVLKTIRDDN-----IRTMDLGG-----KAKCSEYTDALIKNLK	719
mmu:67834	HAAKIEAACFATIKDGK-----SLTKDLGG-----NAKCSDFTEEICRRVK	363
hsa:3419	HAARIEAACFATIKDGK-----SLTKDLGG-----NAKCSDFTEEICRRVK	363
cel:CELE_F43G9.1	HAARIEKAVFDAIADGR-----AKTGDLAG-----TGTCSSFTADVCARVK	355
dme:Dmel(CG12233	YADKIERAAFETIKEGK-----YLTGDLGG-----RAKCSEFTNEICAKL-	377
cel:CELE_C37E2.1	WGNSLRQAVADVVKKEGK-----VRTRDLGG-----YATTVDFAADVIDKFR	378
dme:Dmel(CG6439	YGEIIQNAINKVLNDGK-----VRTKDLGG-----QSTTQDFTRAIILNMS	370
mmu:170718	HSSMIADAVKKVIKAGK-----VRTSDMGG-----YATCHDFTEAVITALS	380
hsa:3420	HSSMIADAVKKVIKVKGK-----VRTRDMGG-----YSTTTDFIKSVIGHLQ	381
sce:YNL037C	YATRISKAVHETIAEGK-----HTTRDIGG-----SSSTTDFTEIINKLS	358
mmu:243996	YATHIRSAVMASLQNKA-----VCTPDIGG-----QGNTASTVEYILHHMK	381
mmu:15929	YATSIRKAVLASMDNEN-----MHTPDIGG-----QGTTSQAIQDIIRHIR	384
hsa:3421	YATSIRKAVLASMDNEN-----MHTPDIGG-----QGTTSEAIQDVIRHIR	384
dme:Dmel(CG5028	HANVIQEAVYQTIVNDA-----IRTPDIGG-----TNSSTDVVENILKILS	387
cel:CELE_C30F12.7	HANIISDALWKALVEQR-----IHTADIGG-----NNASDVINATLQNIK	364
cel:CELE_F35G12.2	HADMISDSLFRTLVDKR-----IHTADIGG-----TSKSSELVQSVLDFIE	386

sce:YDL066W	KEIKSIE -----	428
sce:YLR174W	KEFEAAAL -----	412
sce:YNL009W	NMMLSSNEDKKGMCKL	420
cel:CELE_C34F6.8	ELMRQD -----	435
mmu:269951	RALGKQ -----	452
hsa:3418	RALGRO -----	452
dme:Dmel(CG7176	GALAKNAVAAK -----	479
cel:CELE_F59B8.2	KKQAH -----	435
mmu:15926	AKLAQAKL -----	414
hsa:3417	IKLAQAKL -----	414
eco:b1136	-----	416
dme:Dmel(CG3483	-----	391
sce:YOR136W	-----	369
dme:Dmel(CG32026	-----	719
mmu:67834	DLD -----	366
hsa:3419	DLD -----	366
cel:CELE_F43G9.1	DLE -----	358
dme:Dmel(CG12233	-----	377
cel:CELE_C37E2.1	I -----	379
dme:Dmel(CG6439	-----	370
mmu:170718	-----	380
hsa:3420	TKGS -----	385
sce:YNL037C	TM -----	360
mmu:243996	EQTS-GCHPNFFLQFT	396
mmu:15929	IING-RAVEA -----	393
hsa:3421	VING-RAVEA -----	393
dme:Dmel(CG5028	AKRVNWPHGNYFSQI-	402
cel:CELE_C30F12.7	VLMDENPKH -----	373
cel:CELE_F35G12.2	KELEDRNYRV -----	396

```

#
# Percent Identity Matrix - created by Clustal2.1
#
# 
1: sce_YDL066W    100.00   73.66   69.51   62.88   61.90   61.19   60.48   61.96   65.04   65.28   15.86   17.11   23.75   22.93   20.64   20.35   19.65   19.94   20.06   21.10   19.71   20.00   18.26   20.06   21.20   21.78   19.71   21.20   20.74
2: sce_YLR174W    73.66   100.00   75.49   60.29   63.24   62.75   60.15   61.08   61.31   60.83   17.45   16.00   22.59   20.94   17.51   17.80   17.51   18.07   19.17   18.15   17.86   17.06   15.22   16.47   17.94   18.82   17.30   20.00   18.66
3: sce_YNL009W    69.51   75.49   100.00   60.54   62.01   61.52   58.50   59.61   59.12   59.12   17.45   15.38   22.89   19.47   18.99   18.10   17.77   19.17   17.86   18.45   18.82   16.72   16.95   19.30   20.18   16.67   18.18   17.68
4: cel_CELE_C34F6.8 62.88   60.29   60.54   100.00   67.91   67.21   61.31   63.36   64.39   64.39   17.82   15.45   21.45   18.72   20.41   20.12   18.00   20.87   17.98   18.34   19.83   18.70   18.97   17.66   19.37   19.66   18.18   19.66   18.93
5: mmu_269951    61.90   63.24   62.01   67.91   100.00   95.13   59.11   64.43   68.78   68.54   18.88   16.07   22.48   20.16   19.65   19.36   17.38   19.66   17.78   18.70   18.64   18.66   17.95   17.31   19.23   18.96   18.36   19.21   17.36
6: hsa_3418    61.19   62.75   61.52   67.21   95.13   100.00   59.11   64.67   68.54   68.29   19.41   16.62   23.05   20.97   20.52   20.23   17.95   20.79   18.33   19.26   19.49   19.22   18.80   17.31   19.51   19.23   18.63   19.77   17.91
7: dme_Dmel(CG7176) 60.48   60.15   58.50   61.31   59.11   100.00   70.44   72.09   71.68   18.09   18.06   24.71   20.15   19.54   19.25   19.37   21.05   18.68   18.36   18.01   18.03   18.41   16.31   18.88   19.15   17.94   18.46   17.82
8: cel_CELE_F5988.2 61.96   61.08   59.61   63.36   64.43   64.67   70.44   100.00   76.53   75.79   18.60   15.03   23.68   20.89   18.71   18.71   16.81   19.24   18.13   19.08   18.16   18.47   18.02   17.90   19.60   20.17   18.41   17.92   18.08
9: mmu_15926    65.04   61.31   59.12   64.39   68.78   68.54   72.09   76.53   100.00   95.65   17.50   15.74   24.47   22.19   20.54   20.54   18.75   20.24   18.64   19.40   19.40   20.06   19.76   17.99   19.47   20.06   19.41   18.88   19.88
10: hsa_3417    65.28   60.83   59.12   64.39   68.54   68.29   71.60   75.79   95.65   100.00   17.22   16.36   23.87   21.89   19.64   19.64   18.15   19.64   19.23   19.10   18.81   18.88   20.06   17.99   19.76   20.06   19.71   19.17   19.30
11: eco_b1136    15.86   17.45   17.45   17.82   18.88   19.41   18.09   18.60   17.58   17.22   100.00   25.00   34.09   32.96   34.99   34.99   34.67   36.49   25.58   26.88   28.61   27.67   27.83   25.88   27.25   27.54   26.67   29.07   29.43
12: dme_Dmel(CG3483) 17.11   16.00   15.38   15.45   16.07   16.62   18.06   15.03   15.74   16.36   25.00   100.00   32.28   34.21   38.48   38.19   37.21   39.72   32.68   31.43   33.05   35.24   30.84   26.37   27.26   27.75   29.08   31.13
13: sce_YOR136W    23.75   22.59   22.89   21.45   22.48   23.05   24.71   23.60   24.47   23.87   34.09   32.28   100.00   49.86   54.13   53.85   56.77   54.37   36.83   38.92   37.36   36.13   42.82   36.47   38.75   39.03   37.78   38.55   36.93
14: dme_Dmel(CG32026) 22.03   20.94   19.47   18.72   20.16   20.97   20.15   20.89   22.19   21.89   32.96   34.21   49.86   100.00   57.46   57.18   59.15   60.64   33.06   34.52   35.11   34.75   37.57   33.96   38.20   38.90   33.86   38.83   37.10
15: mmu_67834    20.64   17.51   18.99   20.41   19.65   20.52   19.54   18.71   20.54   19.64   34.99   38.48   54.13   57.46   100.00   97.54   69.80   68.25   37.92   41.41   42.90   48.88   44.35   38.38   42.30   42.02   37.82   42.00   40.40
16: hsa_3419    20.35   17.80   18.99   20.12   19.36   20.23   19.25   18.71   20.54   19.64   34.99   38.19   53.85   57.18   97.54   100.00   69.80   67.97   37.92   41.13   43.18   41.16   44.35   38.38   42.30   42.02   37.25   42.00   40.11
17: cel_CELE_F43G9.1 19.65   17.51   18.10   18.00   17.38   17.95   19.37   16.81   18.75   18.15   34.67   37.21   56.77   59.15   69.80   69.80   100.00   69.41   38.81   40.86   42.17   49.40   43.18   37.78   42.61   42.61   37.78   40.00   40.74
18: dme_Dmel(CG12233) 19.94   18.07   17.77   20.87   19.66   20.79   21.05   19.24   20.24   19.64   36.49   39.72   54.37   60.64   68.25   67.97   69.41   100.00   38.72   39.55   39.78   38.67   44.57   37.40   41.83   41.83   39.34   39.60   40.00
19: cel_CELE_C37E2.1 20.06   19.17   19.17   17.99   17.78   18.33   18.68   18.13   18.64   19.23   25.50   32.68   36.83   33.06   37.92   37.92   38.81   38.72   100.00   55.43   57.53   57.22   44.92   45.43   45.97   46.24   39.41   43.42   42.43
20: dme_Dmel(CG6439) 21.18   18.15   17.86   18.34   18.76   19.26   18.36   19.08   19.40   19.18   26.88   31.43   38.92   34.52   41.41   41.13   40.86   39.55   55.43   100.00   58.70   57.99   47.01   43.68   48.63   48.00   40.66   45.63   42.94
21: mmu_170718    19.71   17.86   18.45   19.83   18.64   19.49   18.01   18.16   19.40   18.81   28.61   33.05   37.36   35.11   42.90   43.18   42.17   39.78   57.53   58.70   100.00   92.11   45.58   45.92   49.33   50.13   48.86   44.13   43.09
22: hsa_3420    20.00   17.06   18.82   18.70   18.66   19.22   18.03   18.47   20.06   18.88   27.67   33.24   36.13   34.75   40.88   41.16   40.40   38.67   57.22   57.99   92.11   100.00   45.48   45.84   49.47   50.53   48.85   43.53   43.85
23: sce_YNL037C 18.26   15.22   16.72   18.97   17.95   18.80   18.41   18.02   19.76   20.06   27.83   30.84   42.82   37.57   44.35   44.35   43.10   44.57   44.92   47.01   45.85   45.48   100.00   44.29   47.63   46.80   45.68   44.94   47.34
24: mmu_243996    20.06   16.47   16.95   17.66   17.31   17.31   16.31   17.90   17.99   25.89   26.37   36.47   33.96   38.38   38.38   37.78   37.40   45.43   43.68   45.92   45.84   44.29   100.00   64.62   63.85   45.18   49.05   47.26
25: mmu_15929    21.20   17.94   19.30   19.37   19.23   19.51   18.88   19.60   19.47   19.76   27.25   27.20   38.75   38.20   42.30   42.30   42.61   41.83   45.97   48.63   49.33   49.47   47.63   64.62   100.00   95.17   47.45   54.03   51.04
26: hsa_3421    21.78   18.82   20.18   19.66   18.96   19.23   19.15   20.17   20.06   27.54   27.75   39.03   38.99   42.02   42.02   42.61   41.83   46.24   48.08   50.13   56.53   46.80   63.85   95.17   100.00   47.45   54.57   51.81
27: dme_Dmel(CG5028) 19.71   17.30   16.67   18.18   18.36   18.63   17.94   18.41   19.41   19.71   26.67   29.08   37.78   33.86   37.82   37.25   37.78   39.34   39.41   40.66   40.86   40.85   45.68   45.18   47.45   47.45   100.00   51.74   48.08
28: cel_CELE_C30F12.7 21.20   20.00   18.18   19.66   19.21   19.77   18.46   17.92   18.88   19.17   29.07   28.08   38.55   38.83   42.00   42.00   40.00   39.60   43.42   45.63   44.13   43.53   44.94   49.05   54.03   54.57   51.74   100.00   64.34
29: cel_CELE_F35G12.2 20.74   18.66   17.68   18.93   17.36   17.91   17.82   18.08   19.88   19.30   29.43   31.13   36.93   37.10   40.40   40.11   40.74   40.00   42.43   42.94   43.09   43.85   47.34   47.26   51.04   51.81   48.08   64.34   100.00

```

MALATE DEHYDROGENASE

CLUSTAL 0(1.2.4) multiple sequence alignment

eco:b2210	MKKVTAMLFSMAVGLNA--VSMAAKAKA-SEEQETDV--LLIGGGIMSATLGTYLRELEP	55
cel:CELE_F46E10.10	-----MSAPLRLVLTGAAGQIG-Y SIVIRIADGTV	29
dme:Dmel(CG5362)	-----MAEPIRVVVVTGAAGQIA-Y SLLYMIARGEV	29
mmu:17449	-----MSEPIRVLVLTGAAGQIA-Y SLLYSIGNGSV	29
hsa:4190	-----MSEPIRVLVLTGAAGQIA-Y SLLYSIGNGSV	29
sce:YOL126C	-----MPHSVTPSIEQDSLKIAILGAAGGIG-Q SLSLLLKAQLQ	38
sce:YDL078C	-----MVKVAILGASGGVG-QPLSLLLKL-SP	25
dme:Dmel(CG10748)	-----MLLLTSLK-----SLAKPATWGVVVR TLKVAVV GAGGGIG-QPLSLLLRR-CP	46
sce:YKL085W	-----MLS-----RVAKRAFSS-TVANPYKVTVLGAGGGIG-QPLSLLLKL-NH	41
dme:Dmel(CG10749)	-----MFLASRLLSHVGNLPPKVQQLGYINRGLKVAVVGSVGGIG-QPLSLLLKH-NP	51
eco:b3236	-----MKVAVLGAAGGIG-QALALLLKQLP	25
cel:CELE_F20H11.3	-----MSLPAKTLVQAAANSGLRAVSVRHSSQAPKVALLGAAGGIG-QPLGLLLKQ-DP	52
dme:Dmel(CG7998)	-----MLKQVTKQLALQGVRTFSV-GQQNNYKVTVCGAAGGIG-QPLSLLLKQ-NP	48
mmu:17448	-----MLSALARPAGAACRRSFST-SAQNNAKVAVLGASGGIG-QPLSLLLKN-SP	48
hsa:4191	-----MLSALARPASAALRRSFST-SAQNNAKVAVLGASGGIG-QPLSLLLKN-SP	48

: * : : :

eco:b2210	E-----WSM----TMVERLEGVAQESSNGWNNAGTGHSAALMELNYTPQNADG	98
cel:CELE_F46E10.10	FG-----KEQPVELVLLDVPQCSNILEGVVFELQDCALPT-----LFSVVA---VTD	73
dme:Dmel(CG5362	FG-----KDQPIVLHLLDIPPMVGVLEGVVMEADCALPL-----LVEVVP---TTD	73
mmu:17449	FG-----KDQPIILVLLDITPMMGVLDGVLMELQDCALPL-----LQDVIA---TDK	73
hsa:4190	FG-----KDQPIILVLLDITPMMGVLDGVLMELQDCALPL-----LKDVIA---TDK	73
sce:YOL126C	YQLKESNRSVTHIHLALYDVNQE--AINGVTADLSHIDTPI-----SVSSHSP--AGG	87
sce:YDL078C	Y-----VSELALYDIR---AAEGIGKDLSHINTNS-----SCVGYDK---DS	61
dme:Dmel(CG10748	G-----IDEALHDLS---EMKGIAIDLISHISQTG-----KVIGFTG--EKE	83
sce:YKL085W	K-----VTDLRLYDLK---GAKGVATDLSHIPTNS-----VVKGFTPEEPDG	80
dme:Dmel(CG10749	Q-----ISTLSLYDIK---NTTGVGVDLSHINTR-----SVCPFEG--KNG	88
eco:b3236	S-----GSELSLYDIAP---VTPGVAADLSHIPTAV-----KIKGFSG--EDA	63
cel:CELE_F20H11.3	L-----VAHLALYDVV---NTPGVAADLSHIDSNA-----KVTAHTG--PKE	89
dme:Dmel(CG7998	L-----VTDLALYDIV---HTPGVAADLSHIDTKS-----KTAGFIG--ADQ	85
mmu:17448	L-----VSRLTLYDIA---HTPGVAADLSHIETRA-----NVKGYLG--PEQ	85
hsa:4191	L-----VSRLTLYDIA---HTPGVAADLSHIETKA-----AVKGYLG--PEQ	85

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eco:b2210	SISIEKAVAINEAFQISRQFWAHQVERGVLRTPRSINTVPHMSFVWGEDNVNFLRARYA	158
cel:CELE_F46E10.10	-----EKSAFTGID---YAFLVGAMPRRE-----	94
dme:Dmel(CG5362)	-----PAVGFKDVS---AAFLVGAMPRKE-----	94
mmu:17449	-----EEIAFKDLD---VAVLVGGSMPRRE-----	94
hsa:4190	-----EDVAFKDLD---VAILVGGSMPRRE-----	94
sce:YOL126C	-----IENCLHNAS---IVVIPAGVPRKP-----	108
sce:YDL078C	-----IENTLSNAQ---VVLIPAGVPRKP-----	82
dme:Dmel(CG10748)	-----LESAVSGAD---VVVVVAAGMPRLP-----	104
sce:YKL085W	-----LNNALKDTD---MVLIPAGVPRKP-----	101
dme:Dmel(CG10749)	-----LKKAMDKAD---IVVIPAGLPRKP-----	109
eco:b3236	-----T-PALEGAD---VVLISAGVARKP-----	83
cel:CELE_F20H11.3	-----LYAAVENAD---VIVVIPAGVPRKP-----	110
dme:Dmel(CG7998)	-----LGDSLKGSD---VVVIPAGVPRKP-----	106
mmu:17448	-----LPDCLKGCD---VVVIPAGVPRKP-----	106
hsa:4191	-----LPDCLKGCD---VVVIPAGVPRKP-----	106

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eco:b2210	ALQQSSLFRGM--RYSEDHAQIKEWAPLVMGRDPQQKVAATRTEIGTDVNYGEITRQLI	216
cel:CELE_F46E10.10	GMERKDLLAANVKIFKSQGKALAEYAKP-----	122
dme:Dmel(CG5362)	GMERKDLLSANVKIFRTQQQALDKFAKK-----	122
mmu:17449	GMERKDLLKANVKIFKSQGTALEKYAKK-----	122
hsa:4190	GMERKDLLKANVKIFKSQGAALDKYAKK-----	122
sce:YOL126C	GMTRDDLFNVNAGIIISQLGDSIAECCDL-----	136
sce:YDL078C	GLTRDDLFKMNAGIVKSLVTAVGKFAPN-----	110
dme:Dmel(CG10748)	GMQRDHLMANGNVAVKVATAISNASPR-----	132
sce:YKL085W	GMTRDDLFAINASIVRDLAAATAESAPN-----	129
dme:Dmel(CG10749)	GMKREDLVDVNASCVAFAASEVCPG-----	137
eco:b3236	GMDRSDFNFNVNAGIVKNLVQQVAKTCPK-----	111
cel:CELE_F20H11.3	GMTRDDLFNTNAGIVRDLAAVIAKASPK-----	138
dme:Dmel(CG7998)	GMTRDDLFNVNAGIIKDISNSIAKNCPK-----	134
mmu:17448	GMTRDDLFNTNATIVATLTAACAQHCPE-----	134
hsa:4191	GMTRDDLFNTNATIVATLTAACAQHCPE-----	134

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eco:b2210	ASLQKKSNFSLQLSSEVRALKRNDNTWTVTVADLKNGTAQNIRAKFVFIGAGGAALKLL	276
cel:CELE_F46E10.10	-----T-----	123
dme:Dmel(CG5362	-----D-----	123
mmu:17449	-----S-----	123
hsa:4190	-----S-----	123
sce:YOL126C	-----SK-----	138
sce:YDL078C	-----	110
dme:Dmel(CG10748	-----	132
sce:YKL085W	-----	129
dme:Dmel(CG10749	-----	137
eco:b3236	-----	111
cel:CELE_F20H11.3	-----	138
dme:Dmel(CG7998	-----	134
mmu:17448	-----	134
hsa:4191	-----	134

eco:b2210	QESGIPEAKDYAGFPVGGQFLVSENPDVVNHHLAKVYGKASVGAPPMSVP HIDTR-----	331
cel:CELE_F46E10.10	-----TKVIVVGNPANTNAFIAAKYAAAG-----KIPAKNFSAM	156
dme:Dmel(CG5362	-----VKVLVVGNPANTNALVCSSYA-P-----SIPRENFSAM	155
mmu:17449	-----VKVIVVGNPANTNCLTASKSA-P-----SIPKENFSCL	155
hsa:4190	-----VKVIVVGNPANTNCLTASKSA-P-----SIPKENFSCL	155
sce:YOL126C	-----VFVLVISNPVNSLVPVMVSNILK--NHPQSRNSGIERRIMGV	178
sce:YDL078C	-----ARILVISNPVNSLVPPIAVETLKK--MG-----KFKPGNVMGV	145
dme:Dmel(CG10748	-----AHLAFITNPVN MIVPAAA EVLMA--HG-----TFDSRRLFGI	167
sce:YKL085W	-----AAILVISNPVN STVPIVAQVLKN--KG-----VYNPKKLFGV	164
dme:Dmel(CG10749	-----AMLAFITNPIN VIVPIVATILKA--KG-----TYDPNRLFGV	172
eco:b3236	-----ACIGIITNPVN TTVAIAAEVLKK--AG-----VYDKNKLFGV	146
cel:CELE_F20H11.3	-----ALIAIIITNPVN STVPIASEVLKK--AG-----VYDPKRVFGV	173
dme:Dmel(CG7998	-----ALVAIITNPVN TCVPIAAEILKK--AG-----VYDPKRLFGV	169
mmu:17448	-----AMVCIIANPVNSTIPITAEVFKK--HG-----VYNPNKIFGV	169
hsa:4191	-----AMICVIANPVNSTIPITAEVFKK--HG-----VYNPNKIFGV	169

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eco:b2210	-VLDGKRVVLFGPF-ATFS-----	TKFLKNGLWDLMSSTTSNVMPMMHVGLD	378
cel:CELE_F46E10.10	TRL DHN RALA QLALKTGTT-----	IGNVKN VII WGN-----HSG-T	191
dme:Dmel(CG5362)	TRL DQN RAT SQIAA KLGVP-----	ISAVKN III WGN-----HSS-T	190
mmu:17449	TRL DHN RAKS QIA KLGVT-----	ADDVKN VII WGN-----HSS-T	190
hsa:4190	TRL DHN RAKA QIA KLGVT-----	ANDVKN VII WGN-----HSS-T	190
sce:YOL126C	TKL DIV RAST FLREINIESGL-----	TPRVNSMP-DVPVIGG-----HSGET	219
sce:YDL078C	TNL DLV RAETFLVDYLMLKNPKI GQE QDKTTMHR-KVT VIGG-----	HSGET	191
dme:Dmel(CG10748)	TTL DVVR SKK FIG DSMNIS-----	PDDV-NIPVIGG-----HAGIT	202
sce:YKL085W	TTL DSIRAARF ISEVENTD-----	PTQE-RVN VIGG-----HSGIT	199
dme:Dmel(CG10749)	TTL DVVR AQT FVA DIL NVD-----	PQKV-NIPVIGG-----HTGRT	207
eco:b3236	TTL DII RSNT FVA ELKGKQ-----	PGEV-EVPVIGG-----HSGVT	181
cel:CELE_F20H11.3	TTL DVVR SQAF VSEL KGHD-----	ASKT-VVPVVGG-----HAGIT	208
dme:Dmel(CG7998)	STL DVVR ARAF IGH ALGVD-----	PQTV-QIPVIGG-----HSGVT	204
mmu:17448	TTL DIV RANT FVA ELKG LD-----	PARV-NVPVIGG-----HAGKT	204
hsa:4191	TTL DIV RANT FVA ELKG LD-----	PARV-NVPVIGG-----HAGKT	204

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eco:b2210	NFDLVKYLVSQVMLSEEDRFEALKEYYPQAKKEDWRLWQAGQRVQIIKRDAEKGGVLRLG	438
cel:CELE_F46E10.10	QFPDVTHATVNKNGTETDA-----YAAVGDN AFLQGPFIAT-----VQKRG	232
dme:Dmel(CG5362	QYPDAGQAKVTANGTVKSV-----VDAINDNGYLQGSFVET-----VQKRG	231
mmu:17449	QYPDVNHAKVKLQGKEVGV-----YEALKDDSWLKGEFITT-----VQQRG	231
hsa:4190	QYPDVNHAKVKLQGKEVGV-----YEALKDDSWLKGEFVTT-----VQQRG	231
sce:YOL126C	IIPLFSQSNFLSRLNEDQ-----LKYLIHR-----VQYGG	249
sce:YDL078C	IIPIITDKSLVFQ-LDKQ-----YEHFIHR-----VQFGG	220
dme:Dmel(CG10748	ILPLISQCQPIYRCDLQE-----IQNLTHR-----IQEAG	232
sce:YKL085W	IIPLISQTNHKL-MSDDK-----RHELIHR-----IQFGG	228
dme:Dmel(CG10749	ILPILSQCDPPFKGTDKE-----REALIQR-----IQNAG	237
eco:b3236	ILPLLSQV-PGVSFTEQE-----VADLTKR-----IQNAG	210
cel:CELE_F20H11.3	IIPLLSQVKPSTKFSEEE-----ISKLTPR-----IQDAG	238
dme:Dmel(CG7998	ILPVLSQSQPLFKGNQDT-----IEKLTVR-----IQEAG	234
mmu:17448	IIPLISQCTPKVDFPQDQ-----LATLTGR-----IQEAG	234
hsa:4191	IIPLISQCTPKVDFPQDQ-----LTALTGR-----IQEAG	234

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eco:b2210	TEVVSDQQGTIAALLGASPGASTAAPIMLNLEKVFGRVSSPQWQATLKAIIVPSYGRKL	498
cel:CELE_F46E10.10	GVIIIEKRK-----LSSAMSAAK---AACDHIDWHFGTKAG----QFVSMAVPSDG---	276
dme:Dmel(CG5362)	AAVIAARK-----MSSAMSAAK---AACDHMHDDWWNGTAPG----QFVSMGVFSRG---	275
mmu:17449	AAVIKARK-----LSSAMSAAK---AIADHIDIRDIWFGTPEG----EFVSMGVISDG---	275
hsa:4190	AAVIKARK-----LSSAMSAAK---AICDHVRDIWFGTPEG----EFVSMGVISDG---	275
sce:YOL126C	DEVVVKAKNGKGSATLSMAHAGYK---CVVQFVSLLLGNIE-Q---IHGTYYVPLKDANN	301
sce:YDL078C	DEIVKAKQGAGSATLSMAFAGAK---FAEEVLRSFHNEKPET----ESLSAFVYLPGLKN	273
dme:Dmel(CG10748)	TEVVNAKAGKGSATLSMAYAGAT---FVNSSLRGIAGQD--G---LIECAFVASK----	279
sce:YKL085W	DEVVVKAKNGAGSATLSMAHAGAK---FANAVLSGFKGER--D---VIEPSFVDSPL---	276
dme:Dmel(CG10749)	TEVVNAKDGLGSATLSMAFAATQ---FVSSLIKGIKGSKDEC---IVECAYVESD----	286
eco:b3236	TEVVVEAKAGGGSATLSMGQAAAR---FGLSLVRALQGEQ--G---VVECAYVEGD----	257
cel:CELE_F20H11.3	TEVVNAKAGAGSATLSMALAGAR---FANALVRGIKGEK--N---V-QCAYVASDA---	285
dme:Dmel(CG7998)	TEVVVKAKAGAGSATLSMAYAGAR---FAGSLLKGLNGEK--N---VIECSYVQS-T---	281
mmu:17448	TEVVVKAKAGAGSATLSMAYAGAR---FVFSLVDAMNGKE--G---VWECSFVQS-K---	281
hsa:4191	TEVVVKAKAGAGSATLSMAYAGAR---FVFSLVDAMNGKE--G---VWECSFVKS-Q---	281

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eco:b2210	N---GD---VAATERELQYTSEVLGLNYDKPQAADSTPKPQLKPQPV-----QKE	542
cel:CELE_F46E10.10	-----SYGIPQGLIFSPVTIEGGEWKIVQGLSF---DDFAK-GKIAATTKELEE	322
dme:Dmel(CG5362)	-----SYDSPKDVIIFSPVEIKNKQWKIVSGLTL---SDFAK-TKLSVTGKELQE	321
mmu:17449	-----NSYGVPPDDLLYSFPVVVIKNKTWKFVEGLPI---NDFSR-EKMDLTAKELTE	322
hsa:4190	-----NSYGVPPDDLLYSFPVVVIKNKTWKFVEGLPI---NDFSR-EKMDLTAKELTE	322
sce:YOL126C	FPIAPGADQLLPLVDGADYFAIPLTITTGVSYVDYDIVNRMNDMERNQMLPICVSQKK	361
sce:YDL078C	----GKKAQQLVGDNSIEYFSLPIVLRNGSVVSI DTSVLEKLSPREE-QLVNTAVKELRK	328
dme:Dmel(CG10748)	-----LTDAPFFASPLELGKDGKIR--YIPLPQMSDYEK-EALEKLLPILRQ	323
sce:YKL085W	-----FKSEGIEFFASPVTLGPDGIEK--IHPIGELSSEEE-EMLQKCKETLKK	322
dme:Dmel(CG10749)	-----VTEAQFFATPLILGPQGVKE--NTGLPDLDDEER-KALNGMLPILKE	330
eco:b3236	-----GQYARFFSQPLLLGKNGVEE--RKSIGTLSAFEQ-NALEGMLDTLKK	301
cel:CELE_F20H11.3	-----VKGVEYFSTPVELGPNGVEK--ILGVGKVSAYEQ-KLIDASVPELNK	329
dme:Dmel(CG7998)	-----VTEATFFSTPLVLGKNGVQE--NLGLPKLNDYEK-KLLEAAIPELK	325
mmu:17448	-----ETECTYFSTPLLLGKKGLEK--NLGIGKITPFEE-KMIAEAIPELK	325
hsa:4191	-----ETECTYFSTPLLLGKKGIEK--NLGIGKVSSFEE-KMISDAIPELK	325

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eco:b2210	VADIAL-----	548
cel:CELE_F46E10.10	ERDDALKACDDANI-----	336
dme:Dmel(CG5362	EKDEALSVLDSNVSNL-----	337
mmu:17449	EKETAFEFLSSA-----	334
hsa:4190	EKESAFEFLSSA-----	334
sce:YOL126C	NIDKGLEFVASRSASS-----	377
sce:YDL078C	NIEKGKSFIELDSSKL-----	343
dme:Dmel(CG10748	NADEGVNFAKMILSGQSHSPIPAALP	349
sce:YKL085W	NIEKGVNFKVASK-----	334
dme:Dmel(CG10749	SIAKGIGLGEGMICSCA-----	347
eco:b3236	DIALGEEFVNK-----	312
cel:CELE_F20H11.3	NIAKGVAFKGN-----	341
dme:Dmel(CG7998	NIQKGIDFANA-----	336
mmu:17448	SIKKGEDFVKNMK-----	338
hsa:4191	SIKKGEDFVKTLK-----	338

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#
#
# Percent Identity Matrix - created by Clustal2.1
#
#



1: eco_b2210      100.00   15.82   14.53   15.15   15.49   19.30   19.80   21.26   19.93   19.93   21.07   20.66   18.54   18.87   18.87
2: cel_CELE_F46E10.10  15.82  100.00   60.60   60.36   60.36   21.18   22.98   19.93   21.57   21.10   22.74   21.38   22.44   21.64   21.31
3: dme_Dmel(CG5362)  14.53   60.36  100.00   65.47   66.37   21.74   21.68   20.52   21.97   20.71   21.48   21.12   23.18   21.05   21.71
4: mmu_17449       15.15   60.36   65.47  100.00   96.41   22.26   25.41   22.11   23.28   21.31   23.83   22.77   24.50   23.10   23.10
5: hsa_4190        15.49   60.36   66.37   96.41  100.00   21.63   24.43   20.79   23.28   20.33   24.16   23.43   24.50   23.43   23.43
6: sce_YOL126C     19.30   21.18   21.74   22.26   21.63  100.00   43.03   35.15   44.34   38.07   41.03   42.94   43.83   42.94   42.94
7: sce_YDL078C     19.80   22.98   21.68   25.41   24.43   43.03  100.00   36.51   49.68   39.12   41.88   45.19   45.98   44.73   45.37
8: dme_Dmel(CG10748) 21.26   19.93   20.52   22.11   20.79   35.15   36.51  100.00   45.12   50.00   46.45   47.60   49.39   44.28   44.88
9: sce_YKL085W     19.93   21.57   21.97   23.28   23.28   44.34   49.68   45.12  100.00   44.38   48.87   52.28   51.83   52.89   54.41
10: dme_Dmel(CG10749) 19.93   21.10   20.71   21.31   20.33   38.07   39.12   50.00   44.38  100.00   51.29   46.90   52.84   47.77   47.18
11: eco_b3236       21.07   22.74   21.48   23.83   24.16   41.03   41.88   46.45   48.87   51.29  100.00   57.61   57.93   58.58   58.58
12: cel_CELE_F20H11.3 20.66   21.38   21.12   22.77   23.43   42.94   45.19   47.60   52.28   46.90   57.61  100.00   60.00   55.95   56.55
13: dme_Dmel(CG7998) 18.54   22.44   23.18   24.50   24.50   43.83   45.98   49.39   51.83   52.84   57.93   60.00  100.00   59.82   59.23
14: mmu_17448       18.87   21.64   21.05   23.10   23.43   42.94   44.73   44.28   52.89   47.77   58.58   55.95   59.82  100.00   94.97
15: hsa_4191        18.87   21.31   21.71   23.10   23.43   42.94   45.37   44.88   54.41   47.18   58.58   56.55   59.23   94.97  100.00

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OXOGLUTARATE DEHYDROGENASE

CLUSTAL 0(1.2.4) multiple sequence alignment

eco:b0726	-----	MQNSALKAWLD	11
sce:YIL125W	MLRFVSSQTCRYSSRGLLKTS-----	LLKNASTVKI-----VGRGLATTGT	41
cel:CELE_T22B11.5	MHRASLI--CRLASPSRINA---IRNASS-----	GKSHISASTLVQHRNQSVAAAVKH	48
dme:Dmel(CG33791	-----MNQCRLRSLARIRRSLTLGLRGTDQHVL--ARQALRTIQTTS-----	QRRGVHDL	48
dme:Dmel(CG11661	MHRAHTAFSLALSPMA-----HKNFAT-WLLKSSSSQQMAKVAAAVERTY--NSAAA		50
mmu:18293	-----MFHLRTCAAK-----LRPLTASQTVKTFSQNKPAAIRTFQQIRCY-SAPVAA		46
hsa:4967	-----MFHLRTCAAK-----LRPLTASQTVKTFSQNRPAAARTFQQIRCY-SAPVAA		46
mmu:239017	-----MSQLRLLPFR-----LGPRAT-----KLLATRAIPVFSGCRRSSGPPTTI		40
hsa:55753	-----MSQLRLLPSR-----LGVQAA-----RLLAAHDVPVFGWRSRSGPPATF		40

eco:b0726	SSYLSGANQSWEQLYEDFLTDPDSVDANWRSTFQQLPGTGVKP-DQFH-SQTREYFRR	69
sce:YIL125W	DNFLSTSNTAYIDEMYQAWQKDPSVHVSWDAYFKNMSNPKIPATKAFQAPPISNF-PQ	100
cel:CELE_T22B11.5	EPFLNGSSSIYIEQMYEAWLQDPSSVHTSVDAYFRNVEAGAGPG-QAFQAPPATAYAGAL	107
dme:Dmel(CG33791	DSFANGCSAAYIEGLYNWKKRNPSSVDESWNELSSNDWSSPKR-SPLQVSHSRKYRRPP	107
dme:Dmel(CG11661	EPFANGSTASYVEEMYNAWLDPPTSVHTSVDAYFRNSNYVSPPN-LAPVQA-----NT	102
mmu:18293	EPFLSGTSSNYVEEMYCAWLENPKSVHKSWDIFFRNTNAGAPPG-TAYQSP-----LS	98
hsa:4967	EPFLSGTSSNYVEEMYCAWLENPKSVHKSWDIFFRNTNAGAPPG-TAYQSP-----LP	98
mmu:239017	PRSRSGVSSSYVEEMYFAWLENPKSVHKSWDSFFQRASKEASVG-PAQPQL-----PA	92
hsa:55753	PSSKGGGGSSYMEEMYFAWLENPKSVHKSWDSFFREASEEAFSG-SAQPRP-----PS	92

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eco:b0726	AKD-----	ASRYSSTISDPDTNVKQVKVLQLINAYRFRGHQHANLDPLG	113
sce:YIL125W	-----GTEAAPLGTAMTGSVDENVSIHLKVQLLCRAYQVRGHLKAHDPLG		146
cel:CELE_T22B11.5	GVSP-A--AAQ-VTTSSAPATRLDTNASVQSISDHLKIQLLIRSYQTRGHNIAADLDPLG		162
dme:Dmel(CG33791)	VERIAVKARSGERTASGGASAAPAAPPSDWKNIDDHHVIQAIIRAYQSRGHLAADLDPLG		167
dme:Dmel(CG11661)	LPLT-----AF-NFGGAVAGAAPDSKTIDDHlavQAIIRSYQIRGHNIAHLDPLE		151
mmu:18293	LSRSSL-----ATMAHAQSLVEAQPNVDKLVEDHLAVQSLIRAYQIRGHHVAQLDPLG		151
hsa:4967	LSRGSL-----AAVAHAQSLVEAQPNVDKLVEDHLAVQSLIRAYQIRGHHVAQLDPLG		151
mmu:239017	-----VLQESRTSVSSCTKTSKLVEDHLAVQSLIRAYQIRGHHVAQLDPLG		138
hsa:55753	-----VVHESRSAVSSRTKTSKLVEDHLAVQSLIRAYQIRGHHVAQLDPLG		138

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eco:b0726	LWQQDKVA-----	DLDPSFHDLTEADFQETFNVGSF-----ASGKETMKG	155
sce:YIL125W	ISFGSNKNNPVPP-----	ELTLDYYGFSKHLDKEINLGPGILPRFARDGKSMSLKE	199
cel:CELE_T22B11.5	INSADL-DDTIPP-----	ELELSFYGLGERDLDRFLPPT---TFISE-KKSLTLRE	210
dme:Dmel(CG33791)	IVGPKK-RTSVDGTQRHAAREVLRQHFSYIFNDLNTVFKLPSS---	TMIGGDQEFLSLKE	223
dme:Dmel(CG11661)	INTPEL-PGNSST-----	KSIYANFSFGEQDMDRQFKLPST---TFIGGDEASLPLKE	200
mmu:18293	ILDADL-DSSVPADIIS--	STDKLGFYGLHESDLDKVFHLPTT---TFIGGQEPALPLRE	205
hsa:4967	ILDADL-DSSVPADIIS--	STDKLGFYGLDESLDKVFHLPTT---TFIGGQESALPLRE	205
mmu:239017	ILDADL-DSFVPSDLIT--	TIDKLAFYDLQEADLDKEFRLPTT---TFIGGPENTLSLRE	192
hsa:55753	ILDADL-DSFVPSDLIT--	TIDKLAFYDLQEADLDKEFQLPTT---TFIGGSENTLSLRE	192

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eco:b0726	LLEALKQTYCGPIGAEYMHITSTEERWIQQRIESG-RATFNSEEKKRFLSELTAAEGLE	214
sce:YIL125W	IVDHLEKLYCSSYGVQYTHIPSQKCDWLRRERIEIPEPYQYTVDQKRQILDRLTWATSFE	259
cel:CELE_T22B11.5	ILQRLKDIYCTSTGVEYMHNNLEQQDWIRRFEAPRVTELSHDQKKVLFKRLIRSTKFE	270
dme:Dmel(CG33791)	ILDRLERIYCGHIGVEQMITSLTKTNWLDRFEPKGGLDLTKEEKKLILERLTRLSTGFE	283
dme:Dmel(CG11661)	ILNRLENVYCNKIGVEFMFINSLEQCWNIRKRFETPGVLNFSPPEKRLILARLTRATGFE	260
mmu:18293	IIRRLEMAYCQHIGVEFMFINDLEQCQWIRQKFETPGIMQFTNEEKRTLLARLVRSTRFE	265
hsa:4967	IIRRLEMAYCQHIGVEFMFINDLEQCQWIRQKFETPGIMQFTNEEKRTLLARLVRSTRFE	265
mmu:239017	IIRRLESTYCQHIGLEFMFINDVEQCQWIRQKFETPGVMQFSVEEKRTLLARLVRSMRFE	252
hsa:55753	IIRRLENTYCQHIGLEFMFINDVEQCQWIRQKFETPGVMQFSSEEKRTLLARLVRSMRFE	252
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eco:b0726	RYLGAKFPGAKRFSLEGGDALIPMLKEMIRHAGNSGTREVVLGMAHRGRLNVLVNLGKK	274
sce:YIL125W	SFLSTKFPNDKRGLEGLESVVPGIKTLVDRSVELGVEDIVLGMAHRGRLNVLSNVVRKP	319
cel:CELE_T22B11.5	EFLAKKWPSEKRGLEGCEVLIPAMKQVIDSSSTLGVDVIGMPHRGRNLVLANVCRQP	330
dme:Dmel(CG33791)	NFLAKKSSEKRGLEGCDIMIPAIKEVVDRATDHGVESILIGMAHRGRLNVLANICRKP	343
dme:Dmel(CG11661)	AFLAKKYSSEKRGLEGCEIMIPALKEIIDVSTELGVESVIMGMMPHRGRNLNTLANVCRKP	320
mmu:18293	EFLQRKWSSSEKRGLEGCEVLIPALKTIIDMSSANGVDYVIMGMMPHRGRNLVLANVIRKE	325
hsa:4967	EFLQRKWSSSEKRGLEGCEVLIPALKTIIDKSSENGVDYVIMGMMPHRGRNLVLANVIRKE	325
mmu:239017	DFLARKWSSEKRGLEGCEVMIPALKTIIDKSSEMGIENVILGMMPHRGRNLVLANVIRKD	312
hsa:55753	DFLARKWSSEKRGLEGCEVMIPALKTIIDKSSEMGIENVILGMMPHRGRNLVLANVIRKD	312
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eco:b0726	PQDLFDEFAGKH--KEHLGTGDKYHMGFSSDF--QTDGLVHLALAFNPSHLEIVSPVV	330
sce:YIL125W	NESIFSEFKGSSARDDIEGSGDVKYHLGMNYQRPT-TSGKYVNLSLVANPSHLESQDPVV	378
cel:CELE_T22B11.5	LATILSQFS-TL-EPADEGSGDVKYHLGVCIERLNRSQKNVKIAVVANPSHLEAVDPVV	388
dme:Dmel(CG33791	ISDILSQFH-GL-QATDSGSGDVKYHLGVFQERLNQTNRMVRITVVANPSHLEHVNPVL	401
dme:Dmel(CG11661	LNQIFTQFA-GL-EAADDGSGDVKYHLGTYIERLNRTNKNIRLAVVANPSHLEAVDPVV	378
mmu:18293	LEQIFCQFDSKL-EAADEGSGDMKYHLGMYHRRINRVTDRNITLSLVANPSHLEAADPVV	384
hsa:4967	LEQIFCQFDSKL-EAADEGSGDVKYHLGMYHRRINRVTDRNITLSLVANPSHLEAADPVV	384
mmu:239017	LEQIFCQFDPKL-EAADEGSGDVKYHLGMYHERINRVTRNITLSLVANPSHLEAVDPVV	371
hsa:55753	LEQIFCQFDPKL-EAADEGSGDVKYHLGMYHERINRVTRNITLSLVANPSHLEAVDPVV	371

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eco:b0726	IGSVRARLDRLDEPS-SNKVLPITIHGDAAVTGQGVVQETLNMSKARGYEVGTVRIVIN	389
sce:YIL125W	LGRTRALLHAKNDLKEKTALKVLLHGDAAFAGQGVVYETMGFLTLPEYSTGGTIHVITN	438
cel:CELE_T22B11.5	MGKVRAEAFYAGDEK-CDRTMAILLHGDAAFAGQGVVLETFNLDLPSYTTHGAIHVNN	447
dme:Dmel(CG33791	LGKARAEMFQRGDTC-GSTVMPIIIHGDAASFSGQGVVYESMHLSDLPNYTTYGTIHIVSN	460
dme:Dmel(CG11661	QGKTRAEQFYRGDQE-GKKVMSILIHGDAAFCGQGVVYETMHLSDLPDYTTHGTIHVVNN	437
mmu:18293	MGKTKAEQFYCGDTE-GKKVMSILLHGDAAFAGQGVVYETFHLSDLPSYTTHGTVHVVNN	443
hsa:4967	MGKTKAEQFYCGDTE-GKKVMSILLHGDAAFAGQGVVYETFHLSDLPSYTTHGTVHVVNN	443
mmu:239017	QGKTKAEQFYRGDAQ-GRKVMSILVHGDAAFAGQGVVYETFHLSDLPSYTNGTVHVVNN	430
hsa:55753	QGKTKAEQFYRGDAQ-GKKVMSILVHGDAAFAGQGVVYETFHLSDLPSYTNGTVHVVNN	430

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eco:b0726	NQVGFTTSNPLDARSTPYCTDIGKMQAPIFHVNADDPEAVAFVTRLALDFRNTFKRDVF	449
sce:YIL125W	NQIGFTT-DPRFARSTPYPSDLAKAIDAPIFHVNANDVEAVTFIFNLAAEWRHKFHTDAI	497
cel:CELE_T22B11.5	NQIGFTT-DPRSSRSSPYCTDGRVVGCPIFHVNVDPEAVMHVCNVAAADWRKTFKKDVI	506
dme:Dmel(CG33791)	NQVGFTT-DPRFSRSSRYCTDVAKVVNAPILHVNADDPEACIQCARIAIDYRTRFKKDVV	519
dme:Dmel(CG11661)	NQIGFTT-DPRFSRSSPYCTDVARVVNAPIFHVNADDPEAVMHVCVAAEWRATFHKDCV	496
mmu:18293	NQIGFTT-DPRMARSSSPYPTDVARVVNAPIFHVNSDDPEAVMYVCKVAAEWRNTFKDVV	502
hsa:4967	NQIGFTT-DPRMARSSSPYPTDVARVVNAPIFHVNSDDPEAVMYVCKVAAEWRSTFHKDCV	502
mmu:239017	NQIGFTT-DPRMARSSSPYPTDVARVVNAPIFHVNADDPEAVIYVCSVAAEWRNTFNKDVV	489
hsa:55753	NQIGFTT-DPRMARSSSPYPTDVARVVNAPIFHVNADDPEAVIYVCSVAAEWRNTFNKDVV	489
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eco:b0726	IDLVCYRRHGHNEADEPSATQPLMYQKIKKHPTPRKIYADKLEQEKVATLEDATEMVNL	509
sce:YIL125W	IDVVGWRKHGHNETDQPSFTQPLMYKKIAKQKSVIDVYTEKLISEGTFSKKDIDEHKKWV	557
cel:CELE_T22B11.5	VDLVCYRRHGHNELDEPMFTQPLMYQRIKQTAKALEKYQEKILNEGVAEQYVKEELTKY	566
dme:Dmel(CG33791)	IDIVGYRRNGHNEADEPMFTQPLMYQRIKKLKPCQLYADKLIKEGVVTDSEFKAMVSSY	579
dme:Dmel(CG11661)	IDLVGYRRNGHNEIDEPMTQPLMYQKIRKHNCLDYADKLIAEGTVTAEEVKSVAAKY	556
mmu:18293	VDLVCYRRNGHNEIDEPMTQPLMYKQIRKQKPVLQKYAELLVSQGVVNQPEYEEEISKY	562
hsa:4967	VDLVCYRRNGHNEIDEPMTQPLMYKQIRKQKPVLQKYAELLVSQGVVNQPEYEEEISKY	562
mmu:239017	VDLVCYRRRGHNEIDEPMTQPLMYKQIHKQVPVLKKYADKLIAEGTVTLQEFEIIIAKY	549
hsa:55753	VDLVCYRRRGHNEIDEPMTQPLMYKQIHRQVPVLKKYADKLIAEGTVTLQEFEIIIAKY	549
	: *:.* *: * *****: * : . * : : : .	

eco:b0726	RDALDAGDCVVAEWRPMNMHSFTWSPYLNHEWDEEY-----	PNKVEMKRLQE	556
sce:YIL125W	WNLFEDAFEKAK-----DYV-PSQREWLTAAWEGFKSPKELATEILPHEPTNVPESTLKE		611
cel:CELE_T22B11.5	GSILEDAYENAQ-----KVTVRNRDWLDSWPDDFFKKRD----PLKLPSTGIEQENIEQ		617
dme:Dmel(CG33791)	EKICEDAWAKSK-----TIKTIKYSSWIDSPWPWGFFEGRD----RLKLCPTGISTDTLKT		630
dme:Dmel(CG11661)	ENICEEAFLAK-----TETHVKYKDWLDSWPWSGFFEGKD----PLKVAPTVKEETLIH		607
mmu:18293	DKICEEAFTRSK-----DEKILHIKHLDSPWPWGFFTLDGQP-RSMTCPSTGLEEDVLFH		616
hsa:4967	DKICEEAFARSK-----DEKILHIKHLDSPWPWGFFTLDGQP-RSMSCPSTGLTEDILTH		616
mmu:239017	DRICEEAYGRSK-----DKKILHIKHLDSPWPWGFFNVDGEP-KSMTCPPTGIPEEMLTH		603
hsa:55753	DRICEEAYGRSK-----DKKILHIKHLDSPWPWGFFNVDGEP-KSMTCPATGIPEDMLTH		603
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eco:b0726	LAKRISTVP---EAVEMQSRAVAKIYGDRQAMAAGEKLFDWGGAEALAYATLVDEGIPVRL		613
sce:YIL125W	LGKVLSSWP---EGFEVHKNLKRILKRGKSIETGEGIDWATGEALAFGTLVLDGQNVRV		668
cel:CELE_T22B11.5	IIGKFSQYP---EGFNLHRGLERTLKGQQML-KDNSLDWACGEALAFGSLIKEGIHVRL		673
dme:Dmel(CG33791)	IGNMFSTPPPPEHKFETHKGILRILAQRTQMV-QDKVADWSLGEAFAFGSLLKEGIHVRL		689
dme:Dmel(CG11661)	IGNRFSSPPPNAAEFVIHKGLLRVLAARKAMV-DEKVADWALGEAMAFGSLIKEGIHVRL		666
mmu:18293	IGKVASSVPV--ENFTIHGGLSRILKTRRELV-TNRTVDWALAEYMAFGSLLKEGIHVRL		673
hsa:4967	IGNVASSVPV--ENFTIHGGLSRILKTRGEMV-KNRTVDWALAEYMAFGSLLKEGIHIRL		673
mmu:239017	IGSVASSVPL--EDFKIHTGLSRILRGRADMT-KKRTVDWALAEYMAFGSLLKEGIHVRL		660
hsa:55753	IGSVASSVPL--EDFKIHTGLSRILRGRADMT-KNRTVDWALAEYMAFGSLLKEGIHVRL		660
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eco:b0726	SGEDSGRGTFFHRHAVIHNQSN-GSTYTPLQHIHNGQGAFRVWDSVLSEEAVLAFELYGYA	672
sce:YIL125W	SGEDVERGTFSQRHAVLHDQQS-EAIYTPLSTLNNEKADFTIANSSLSEYGVMGFELYGYS	727
cel:CELE_T22B11.5	SGQDVQRGTFSHRHHVLHDQKVDQKIYNPLNDLSEGQGEYTCNSSLSEYAVLGFEHGYS	733
dme:Dmel(CG33791	SGQDVERGTFSHRHHVLHHQSEDKVYNSLDHLYPDQAPYSVSNSSLSECABLGFEGHGS	749
dme:Dmel(CG11661	SGQDVERGTFSHRHHVLHHQLVDKATYNSLQHMYPDQAPYSVSNSSLSEYAVLGFEHGYS	726
mmu:18293	SGQDVERGTFSHRHHVLHDQNVDKRTCIPMNLWPNQAPYTVCNSSLSEYGVLGFEGLFA	733
hsa:4967	SGQDVERGTFSHRHHVLHDQNVDKRTCIPMNLWPNQAPYTVCNSSLSEYGVLGFEGLFA	733
mmu:239017	SGQDVERGTFSHRHHVLHDQEVDRTCVPMNLWPDQAPYTVCNSSLSEYGVLGFEGLGYA	720
hsa:55753	SGQDVERGTFSHRHHVLHDQEVDRTCVPMNLWPDQAPYTVCNSSLSEYGVLGFEGLGYA	720
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eco:b0726	TAEPRTLTIWEAQFGDFANGAQVVIDQFISSGEQKWGRMCGLVMLLPHYEGQGPHEHSSA	732
sce:YIL125W	LTSPDYLVWEAQFGDFANTAQVIIDQFIAGGEQWKQRSGLVLSLPHGYDGQGPHEHSSG	787
cel:CELE_T22B11.5	MVDPNSLVIWEAQFGDFNTAQCIIDQFISSGQSKWIRQSGLVMLLPHYEGMGPEHSSA	793
dme:Dmel(CG33791	MASPNALVMWEQFGDFCNTAQCIIDTFIASGETKWVRQSGVVMLLPHSMEGMGPEHSSG	809
dme:Dmel(CG11661	MTPNPNALVLWEAQFGDFNTAQSIIDQFISSGQSKWVRQSGLVMLLPHGMEGMGPEHSSC	786
mmu:18293	MASPNALVLWEAQFGDFNNMAQCIIDQFICPGQAKWVRQNGIVLLLPHGMEGMGPEHSSA	793
hsa:4967	MASPNALVLWEAQFGDFHNTAQCIIDQFICPGQAKWVRQNGIVLLLPHGMEGMGPEHSSA	793
mmu:239017	MASPNALVLWEAQFGDFHNTAQCIIDQFISTGQAKWVRHNGIVLLLPHGMEGMGPEHSSA	780
hsa:55753	MASPNALVLWEAQFGDFHNTAQCIIDQFISTGQAKWVRHNGIVLLLPHGMEGMGPEHSSA	780
	...* *.:**.***** * ** ;** **. *: ** : *: : ***. :* *****	

eco:b0726	RLE RLQLCAEQN -----MQCV PSTPAQVYHMLRRQALRGMR	770
sce:YIL125W	RLERFLQ LANEDPRYF --P---SEEKLQRQHQDCNFQVVYPTTPANLFHILRRQQH RQFR	842
cel:CELE_T22B11.5	RPERFLQ MCNEDDEIDLEKIAFEGT FEAQQLHDTNWIVANCTTPAN IYHLLRRQVTMPFR	853
dme:Dmel(CG33791)	RIERFLQ MSSDDPDVY --PDTCDADFVARQLMNVNWIVTNLSTPANLFHCLRRQVKMGFR	867
dme:Dmel(CG11661)	RVERFLQ MSSDDPDYF --PPE-SDEF GVRQLHDINWIVANCSTPANYYHILRRQIALPFR	843
mmu:18293	RPERFLQ MCNDDPDVL --PDLQEENFDINQLYDCN WIVVNCSTPGNFFHVLRRQILLPFR	851
hsa:4967	RPERFLQ MCNDDPDVL --PDLKEANFDINQLYDCN WIVVNCSTPGNFFHVLRRQILLPFR	851
mmu:239017	RPERFLQ MSNDDSDAY --PVF-TEDFEVSQ LYDCN WIVVNCSTPASYFHVLRRQILLPFR	837
hsa:55753	RPERFLQ MSNDDSDAY --PAF-TKDFEVSQ LYDCN WIVVNCSTPANYFHVLRRQILLPFR	837
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eco:b0726	RPLVVMSPKSLLRHPLAVSSLEELANGTFL-PAIGEI----DELDPKGVKRVVMCSGKVY	825
sce:YIL125W	KPLALFFSKQ LLRHPLARSSLSEFT TEGG-FQWIIE DIEHGKSIGT KEETKRLVLLSGQVY	901
cel:CELE_T22B11.5	KPAVFSPKSLLRHPMARSPVEDFQSGSNFQ RV PIE--TGAPSQNPPDV KR V F CTGKVY	911
dme:Dmel(CG33791)	KPLINFSPKSLLRHP LARSPFKDFNECSCF QRIIPD--KG PAGKQPDCVQ KL V FCSGKVY	925
dme:Dmel(CG11661)	KPLILCTPKSLLRHPEAKSPFSEMSEGSEFQ RIIPD --NGPAGQNPSNVKKVVFC SGR VY	901
mmu:18293	KPLIVFTP KSLLRHPEARTSFDEM LPGTHFQ RV PIE--NGPAAQDPHK V KRLLFCTGKVY	909
hsa:4967	KPLIIFTP KSLLRHPEARSSFDEM LPGTHFQ RV PIE--DGPAAQN PEN VKRLLFCTGKVY	909
mmu:239017	KPLIVFTP KSLLRHPDAKSSFDQM VSGTSFQ RLI PE--DGPAAH SPEQV QRLIFCTGKVY	895
hsa:55753	KPLIIFTP KSLLRHPEAKSSFDQM VSGTSFQ RV PIE--DGAAA RAPEQV QRLIFCTGKVY	895
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eco:b0726	YDLLEQRRKNN-QHDVAIVRIEQLYPFPHKAMQEVLQQFAHVVKDFVWCQEEPLNQGAWYC	884
sce:YIL125W	TALHKRRESLG-DKTTAFLKIEQLHPFPFAQLRDSLNSYPNLEIIVCQEEPLNMGSWAY	960
cel:CELE_T22B11.5	YDMVAARKHVGKENDVALVRVEQLSPFPYDLVQQECRKYQGA-EILWAQEEHKNMGAWSF	970
dme:Dmel(CG33791)	YDLVKERDDHEQVETVALVRVEQLCPFPYDLISQQLELYPKA-ELLWAQEEHKNMGAWSY	984
dme:Dmel(CG11661)	YDLTKTRREKQLEGEIAIVRVEQISPFPFDLVKEQANLYKNA-ELVWAQEEHKNQGSWTY	960
mmu:18293	YDLTRERKARNMEEEVAITRIEQLSPFPFDLLLKEAQKYPNA-ELAWCQEEHKNQGYYDY	968
hsa:4967	YDLTRERKARDMVGVQVAITRIEQLSPFPFDLLLKEVQKYPNA-ELAWCQEEHKNQGYYDY	968
mmu:239017	YDLVKERSSQGLEQQVAITRLEQISPFPFDLIMREAEKYSGA-ELVWCQEEHKNMGYYDY	954
hsa:55753	YDLVKERSSQDLEEKVAITRLEQISPFPFDLIKQEAEKYPGA-ELAWCQEEHKNMGYYDY	954

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eco:b0726	SQHHFREVI-----PFGASLRYAGRASPASPAVGYMSVHQKQQ-----QDLVNDALN	931
sce:YIL125W	TEPRLHTTLKETDKYKDFKVRYCGRNPSGAVAAGSKSLHLAEE-----DAFLKDVFQ	1012
cel:CELE_T22B11.5	VQPRINSLLS----IDGRATKYAGRPLSSSPATGNKFTHMSEQ-----KEMMSKVFG	1018
dme:Dmel(CG33791)	VQPRFDTALLKNE-NESRCVSYHGRPPSASPATGNKVQHYNEY-----KALITSIFG	1035
dme:Dmel(CG11661)	VQPRFLTAL-----NHSRDVSQSDEQSSSTNTTTTDHTNHESDTDSDSKSKPWLSRMFA	1015
mmu:18293	VKPRLRTTI-----DRAKPVWYAGRDPAAAPATGNKK--THLT-----ELQRFLDTAFD	1015
hsa:4967	VKPRLRTTI-----SRAKPVWYAGRDPAAAPATGNKK--THLT-----ELQRLLDTAFD	1015
mmu:239017	ISPRFMTLL-----GHSRPPIWYVGRDPAAAPATGNKN--AHLV-----SLRRFLDTAFN	1001
hsa:55753	ISPRFMTIL-----RRARPIWYVGRDPAAAPATGNRN--THLV-----SLKKFLDTAFN	1001

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eco:b0726	VE	933
sce:YIL125W	QS	1014
cel:CELE_T22B11.5	VPKSKEGFKA	1029
dme:Dmel(CG33791)	ELTPENKKRIEDRIKKQQAKAKA-DAQSKPSTKPPAAPPKGSSPPPGPAPRKPLISLPS	1094
dme:Dmel(CG11661)	APNSSTGGDPKDPAQTLGGDFNAAKHFDLKNVRHDFNRPA-GIAAAPGARIAK	1067
mmu:18293	L-----DAFKKFS	1023
hsa:4967	L-----DVFKNFS	1023
mmu:239017	L-----KAFEGKTF	1010
hsa:55753	L-----QAFEGKTF	1010

eco:b0726		933
sce:YIL125W		1014
cel:CELE_T22B11.5		1029
dme:Dmel(CG33791)	RPPRGKGQRSGSAPAPNLVDEDSAARNREPDA SAYDGASPSAWKRSGSAPAPSVVPRASA	1154
dme:Dmel(CG11661)	TGR-----KISYVGRACGASTATGSKAQ-----	1090
mmu:18293		1023
hsa:4967		1023
mmu:239017		1010
hsa:55753		1010

eco:b0726	-----	933
sce:YIL125W	-----	1014
cel:CELE_T22B11.5	-----	1029
dme:Dmel(CG33791)	SRSPSRKSPSPSHDGISPSTRQESLSKKKSGSAPAPPTSRGPFRAPSNTTEFIKRRPAK	1214
dme:Dmel(CG11661)	---HIRELNALLNDAIST---	1105
mmu:18293	-----	1023
hsa:4967	-----	1023
mmu:239017	-----	1010
hsa:55753	-----	1010

eco:b0726	-----	933
sce:YIL125W	-----	1014
cel:CELE_T22B11.5	-----	1029
dme:Dmel(CG33791)	DYGSRNETQSTPGESELDPTKPQP	1238
dme:Dmel(CG11661)	-----	1105
mmu:18293	-----	1023
hsa:4967	-----	1023
mmu:239017	-----	1010
hsa:55753	-----	1010

```
#  
#  
# Percent Identity Matrix - created by Clustal2.1  
#  
#  


|                      |        |        |        |        |        |        |        |        |        |
|----------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| 1: eco_b0726         | 100.00 | 39.93  | 41.91  | 40.91  | 39.98  | 39.80  | 39.47  | 40.99  | 40.77  |
| 2: sce_YIL125W       | 39.93  | 100.00 | 45.15  | 43.48  | 45.66  | 45.70  | 45.90  | 44.83  | 44.52  |
| 3: cel_CELE_T22B11.5 | 41.91  | 45.15  | 100.00 | 52.11  | 56.46  | 56.60  | 56.60  | 55.42  | 55.52  |
| 4: dme_Dmel(CG3)3791 | 40.91  | 43.48  | 52.11  | 100.00 | 57.56  | 51.88  | 52.48  | 53.35  | 53.15  |
| 5: dme_Dmel(CG1)1661 | 39.98  | 45.66  | 56.46  | 57.56  | 100.00 | 59.98  | 60.38  | 60.82  | 60.82  |
| 6: mmu_18293         | 39.80  | 45.70  | 56.60  | 51.88  | 59.98  | 100.00 | 95.89  | 75.89  | 76.29  |
| 7: hsa_4967          | 39.47  | 45.90  | 56.60  | 52.48  | 60.38  | 95.89  | 100.00 | 75.99  | 76.69  |
| 8: mmu_239017        | 40.99  | 44.83  | 55.42  | 53.35  | 60.82  | 75.89  | 75.99  | 100.00 | 93.17  |
| 9: hsa_55753         | 40.77  | 44.52  | 55.52  | 53.15  | 60.82  | 76.29  | 76.69  | 93.17  | 100.00 |


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