

>Lys20/Lys21 homocitrate synthase Contig17695 (and 124) (complete) 356 aa, E82

MNRTTALRNPIFNACSASRRAASVTSSVARSQ LPSVIATRRDFSKITAKK
HVSNVTNFKIIESTLREGEQFANAFFTTDKKLEIATLLDDFGVEYIELTS
PAASAQSLHDCQKVAALPLRKS KTLTHIRCTMEDAKLAIESGVDGIDLVF
GTSSVLRREFSHGKDIEYI IDQATKVINYVKDAGKEVRFSSSEDSFRSDIVD
LLKIYSSVNKLKVDRVGIADTVGVASPLQVMEMVKTIRGVVDCDIEFHAH
NDTGCAIANSFVALEHGVTHTIDTSILGIGERNGITPLGGFVARMYSVDRE
YVKNKYNLKLLRELENLVADCVSVQVPFNYYITGYTAFTHKAGIHAKGHP
QQPRDL

>LYS7 ----- NOT DETECTED, 237 aa, 9D6

MEGTQOSEKLRTGVKAQLNVMETCQSCVEGITTALKAVPGVTVLDVLDLDR
GEVELLTQRVPVEKLLRILRETGRSASLQGLGGEQQLGSAVSQLEPADG
SKEGPHATVRFVAQVALDRCLVEAILDGFPPGEYDLAVHEFGDLSAERSV
GDVFGRHPGYADKPAGEIGRIAVGQNGEGTIMADNKQLKVWDIIIGRSVVA
RPASPGGARGVAFGVIARSAGVRENPKKICRCDPDF

>Lys4 homoaconitase Contig12386 (incomplete ... internal gaps) Lys4, 661 aa, 2509

MKRFFGFLRCLHLRQCPRIRLGARRYSV PGLQLPHFRSRLAATTESRRED
CTKICCTLPPLVLCIQRMGNSFHSLIASFLFDECKVDAGGREVQSLDFVT
IRPRHVMTHDNTSAVIKKFKSIAASVKDREVRVANPRQPVTLDHNIQDR
SDANLNKYKQIQEFADKYGIDAYPAGRIGHQVMCEEYAFPGTMVVASD
SHSNMYGGLGCLGTPILPEYATGKDIIITL CGLFNKDEVLNHAVEFVGEV
VGRLTIDDRLTIANMTTEWGALAENVLAADRSAFYAKELVLDLSTVRPHV
SGPNHVKVMHSDMMERRGIKVS KAYIVSCTNSRVQDLSAAANVLRGKKV
AEGVELYIAAASSEVESDSAKRGDWQALIDAGAIPLPPGCGPCIGLGAGL
LKAGEVGISATNRNFKGRMGSR EADVYLASPEVVAASALAGI IKAPGGPG
ANGLTAQGSVKVNSKDTQDSGEGETVAAILPGFVEKLEGELVFCHQDNINT
DGIYPGKYTYNEDISPQQQAEVSMENYDPAFTKKARKGDLVSGYNFGTG
SSREQAATCLKHYGISLVLAGSFSE TYKRNAFNNGYL VIEVPELV DYLKQ
KAASDKGTNELTQRTGLKAVLDFKSSVLSVDGRKFAFPVGAQAQEI VLA
GGLEQWVEKKL

>Lys12 homo-isocitrate dehydrogenase Contig6170 (complete) Lys12, 400 aa, 1DA

MNRCGARASLGLCRQRLASSPTAAARLYSSATVKIEKTGEPVKVALIPSD
GVGKEVVPEARRVLEAVEPHLPFAFSWVPLHAGWETFQQQGVSLPKETIE
GLKGC DGALFGAVSSPSHKVEGYSSPIIGMRKALDLYANLRPVISAPIKT
SRPDIDMLIVRENTECLYVKKERMENGPQGRVAIADRVI SEYASTRIAQM
AFSQAERRAAVRAGSKRPARVTVVHKS NVLSVTDGLFRECALEVAKKYPH
IEVEEQLVDSMVYKMILDPQRYDVV VAPNLYGDILSDAAAALVGGLGLAP
SANVSDSFALCEPVHGSAPDIAGKGIVNPLATIRAAALLLRHLRGP HADA
AAQMGDVIEEAVNRALAAAGPLTPDMGGKASTTQVTD AVIEHLKSLLLNKH

>Aro8 alpha-aminoadipate aminotransferase Contig13167 (and 6207) (complete) Aro8, 434 aa, CEF

MQRALASSGASRITDYEPFLSVTSKRRQPSPIRSLQPLLELPGMISLGGG
MPNTSFFPIKGV DVHLTDGTTLP IQGVMNAALQYSSSYGVTEFVWELKD
YQTRHHPPYASRKDWHVCVTNGSS DANAKAFEMLIDPDDYVLVENPTY S
GSLAGLRPLGCRVLGVETDHSGLSPTHLSLLDSWPVDRPKPKVLYVIPT
GQNPSGATLPEERRREIYGIAQOHNLI ILEDDPYFHLQLDKQDDEPLKS
FLSMDVDGRVVRFD SFSKI ISSGFRIGWATGPAPLIERIQLHQQASTLHV
SGLSQVLLTLLKNWGEEGFKRHIAMVQEGYRQRDLFCKLAEKHLTGLA
EWHPPSAGMFVWFKALGVRST EKMIKERALA QVLLVPGVAFTPNGEES S
FVRASFSTASPDDMEALRRFAALLHEERNAHQ

>LYS2 ----> NOT DETECTED, PROBABLY NOT MITOCHONDRIAL (incomplete/incorrect), g9161.t1

MEAKVKEANALFLQ GKHS PAVALYTA AIEAGSPTATLLCNRGAA YLRGL
YRKCLADCEAALRLQPADPRPYLLK GKALVGMNKSADAEAAWRAGLDKAD
GAADV ELLQLQQLNPPVAAPAIATAPAASSEPKPAVITNGEAKATIT T
PSPQASAVPRAAEPAGKTKSPAPAQQPKKEAKSPPTAAAVAAAANPNDLAE
ASAMVAARGLVQHSGNTTLD EKIAMGYLHVNTGNFPQA IKLFNVLVNL Y
PKLVAAAYLGRGTAYALS GHLSTAVEEF SAAIKIDDTCMEAWKRRGQSRAA
MGQDAEAVLDL TRAAELAPKDADIYHQRLIYFKLRNYGRAAE DFRRATA
ADAMSKLSWNHLGLCLNALGRPMEAIQAHKRALELDPAFREALANIGQAY
KDYGNLSLKAEKYFAKGLKVD PNYMHAFHLRGLARFGAGDHRGALSDF TAA
LRVDDKHKDSRLMRGIVLHGLGRF REAVADYDVLVREKPDHVAWYNRQIA

LWTHHHLDTVAHFNIDRVLNAYFKEAWCKRRLDPATLTSYTSQPPINNAI
ADVALNDELRSSEHAKLLIRAAVDIGKKIQLNCPGYLANQRQORACGFAL
ELAQTLLRRVWAGEETQLSGKASSLTDQPHTFAWRDLYDIPIRWRQFSEPN
DPVWVVDLLSPEQFAEGFGSHTPMVTGQTYVVRYSPMAPRAIRIMREQLQ
QSPLVSQELRHKLTRDNLDCCKTLHEAVQHDFVWVTPCHSLARPNRIMEGT
RLTIQRSPEPEGYEFSIRTPGTPNRWQEYNAEMAHNYRLLQEEASKPHRDL
SKLTELVLHMAFYWYFNFMPLSRGTAAGVGLVTVHAMFLALGFEMESGLPQG
LQPDWEGILTARPSDFVKCLRSAWIDAACRPTTTLDALPLVAQVCPTLRH
MVLALNAANRKMVGRHIWLRAEASATRPSRGDSANLETDRRTPLVPGDAR
LLIEAGYLVTVRSEQRVFPDAEYGAVGCTLVEAGAWREAPKDALVVGIR
APQGLSVDCAGLERVHMYFGHAYKGGQGAHRLAPFVRGGGLLLDLEFVN
DPVTGARLTSFGPSAGI IATAAAVLRVGMVAVPEDLLHRVEGVSLIAHIK
ALLQLATTFAKKAPRAVI I GPRGRVGSKAVEMAGELGIEVALWGREQTVG
EGPFPALLDFDILINAI SLGTEMVGPVFTHEAIRRGDRRLAVVVDVACDV
SNPNNPLPIYDRTTTTFERPALRVLDGDATKDLPLLDVIAIPTLPALVPSL
SSADFSAQRLRPLLLRLDALEADPVSRTAAFDLHSAWLRPASVDSVGE
SVEGILPVVLSFAQEREAKRPARPPVVLALHAPADVTPAQFQAALMGLVA
RHAALRTCFRHVAEDGHKKLVAFVKHAKQIDVASLLQVVPTGDAHELVTQ
QQAVTFDLEKTEGPLFRVVLRLGSDSGERPVVVIAADRLVADAHSLHLIA
RELLQASEPKPETTPYTNALWQRRLHELADDEDVATQEAGYWREQVITYW
RERLTLRPPTIQLPNDRPRPAVPDWRGAEQLTLEPALWSRVAALAAQLA
GPTASHSIRADPILGGSIAI I TAAWVLSRWAGEEDVAAACFAFRPLPHT
VGPLARPLPLRCHVHSKLSFSPSLFANLIETLSQAVHHQDAAAESFTAEG
EDVSPISFVLPGAMPTIAHQQAEGHLHLLAPLSPYDLSFHLQATPSSQVE
ATVLFNQGLYHPERARELIRQIRSLLSQVVELDETALAKAGLDYSLVTE
FGRSVLPVPDADLDTTWEGPIHFFLTKHAQSGPDLPAISYNNQVVYKQL
EERSNRVAHYLLQONVGREQPVVIYGHRS PAVVVAIILAALKAGAAYSMVD
PKYPASRI IDCVTVAKARAWLQISEAGSPPAEVQEFGLTGLACQAQVFN
EPSEFENLYGGFSVAPPEVDVGPNDVAIVTFTSGSTGLPKGVMGRHLPLT
HFYPMATRFGIGEGDRFSLCSGIAHDPLQDIFTPIFFGAQIYIPLLEDD
IGTPGALAKWFAEQQINVACLTPAMGQLLITVEDDSFKIDSLRAVFFVGD
LLIKRDVARLRMAPRAQI INMYGSTETQRSVGYWVVP SDEEVRPMKEVM
PCGEGMKDVQLLIINEAGQLAGVGEVAEIVVRS PHLARGYVGLDAETRAK
FLPNPLGKGLEWDRAVRTGDLGRYNTKGEVECSGRADDQVKIRGFRIELG
EVNAALAQHPLVKENVTVLRTDRAGDKHLVSIYVPASRAAAAATDDTPAT
THAHQLEKDCRDFLRTRLPOYMPRRVIVLRALPLTPNGKINRQGLPDPF
QEPEAEAEKQGADSESDIVRVLS DTERGLLEIFAKLLGASPLKIQLDDDF
FELGGHSLLATQAI FHSI SOKLHVHLPINLLFQSPTITALAKHVDRIKQLG
SSRVEAESTENMAHAQALDAAVRFVAPAAESAAAALPASPTNVFITGAT
GFVGAFLVREVMQORTNGRVLCVLRADSPKHALARLEASLKAHAVWRDEWL
ERLVLVPGDLARPLGLDEAQFLELARSVDAILHNGAFLHWHLPYKYGARP
RQRPWARENHYCYIVRSQVLRRLACSSGRAEPTPVHVMSTTSVYEATEV
HKLPRVGELELDHWRGIGGGYPQSKWVADKMAQIARSERGIVTSIYRPAY
IVGDTTHGLWNTDDFLCRLIKGCIQLGAPELDGDIAADMTVPDYVAHAV
VALMFKPASLGRFTFNI INPAGPLPFRRLFEAIAAFGYPVQVVPYAEWRRR
LVEATNSGEENALSALLAHFGEDWAASQHGPIYERPNADAFADVKDAPP
AAISDELLWRYFTYFIHCGFLPAPPKQPSNALAIDWERISEGVQSLTLLT
RTNRS

>LYS9 ---- NOT DETECTED, PROBABLY NOT MITOCHONDRIAL (this is more similar to yeast Lys9), 453
aa, 1FF0

MSGSGKEVLVLGAGMVVRPLVPYLTQHGYRVVVASRTLAKAQHIVEGISG
AKAVECDVDTDEGKAILETLLPSADAVVSLLPYLLHPFLAKRALAHNKH
FTTSYVSPAMRELDEEAKAKNLVFINCEGVDPGTDHMSAMQIIDVKS
GKILSFTSYCGGLPAPDSNNNPLGYKFSWSARGVLLASTNNAIFLQDGEK
KEIQGKDLFDSFHLDIPELSSEFETYPNRNSLQYIDVYGITTTQTMIRG
TYRNKGWCPTVKKLGADLGLDLTERNFQGVTYAQALREMINSQAADKEA
LKSDVRAFLKLDASKEFVISTAEWLGLFEEEP IPAKIKTRLDALCHKMET
KMQYSAGERDMLLMKHTFIAEYPEGKKEKITCTLIDYGLPNGDSSMARTV
SLPVAISIRLVLEGGFTTPGLQIPIIKELYEPILQELEALEPSIKFVHHR
EAL

>Lys9 saccharopine dehydrogenase Contig9003 (and 1940, 8281, 12023, E80POFO01BQLBH) (likely complete) LYS9, 521 aa, 1B27

MFMRRLTRVSTSSAAPTGRITASALRGQVPCRRLLATSPDGDGIGALKAEEL
KAAEDRVATLKEAIVSHKDKPAKKSILVLGAGRSSSFLINYLLOAARERW
AVKVGDEDEHTARRKVQDHPDGTAFRFNINDTRQREEEIRRADVVSLLP
AFMHPVVAEECVKQGAHMVTASYSAAALAPFDEQARRAGVTILMECGLDPG
IDHMSAMEVIDAIKRDDGGQLTAFRSYTGGLVAPESDDNPWGYKFSWNPRN
VVVAGQGVCQYLQOGEYKYVYPYHQLFRRTDEIRVPGHGTFFEGYPNRDLSL
YRTIYGIPDCPTVLRGTLRKPGYCSAANNVQVQLGMTDDTYTIENADSLTY
RDFLNSFLPYRPHDTVELKLAHYLGLDINSPMQKIKWLGFMFGEQKISLK
SATPAQVLLQOILEKKWALQEGEKDMIVMYHHFVYTNKNGELKETKSSLVV
KGDGTDGTAMAKTVGLPLAVATRMVATEQVKGKTGVHVPTTPDLIYEPIL
RELEKDHGIIIFSHQHDVTHQA

>Lys1 saccharopine dehydrogenase (NAD+, L-lysine-forming) Lys1 Contig3474 (likely complete) LYS1, 435 aa, E3F

MQRAAAAGATSRLVVPLPHHARVFPPTSGACRRMLAISASTPSSSSSSSS
SSNASTTTTTTPEKHHFWLRAEAKKNERRSILLPEHVERLLLLLQAGHHVTV
ERSRLRCAPDAEYQRLLEPLVEEGSWKKAPRDAIILGLKELPEDDDPIK
HKHVYFAHVFKQNGAEKVLKRYAKGGGKLWDLEFLVDDK GARVAAFSGA
AGKVGMLAFVVAHQKLTGRPYSLPPLNTPYDSFAHMAHQMRELLDQAK
AKVGHDPVIVVGSRGRSGKGAVSFSESVGIKPTWEGREQTAKGGPFPEL
LNYDILINAIYLLPEVRLPAFITKGMIDHTPDRKLSVFSVDVSCDVTNPHS
VFPIYDHLTSFVHPTECVAEQPTPLEVIAIDHLPSLVPRESSKEFGDLIV
EHILQFDQTPVWSRALKLFDEKVPFLPPSPRAAA

>Lys1 Contig26880 ----- NOT DETECTED, PROBABLY NOT MITOCHONDRIAL (more similar to yeast Lys1)

MSAQKEVLHIRAEVKPQEERTAITPENAKKLIDSGRYTLHV
ERSPERIYKDDEYQQAGCTLVETGSWPKADPSAFIVGLKELPEEDTPLTHRHVFFGHCFK
QQNGWKELLHRFTSGKGTLLDLEFLVNEQGRRVAAF GRAAGLAGCAVGLMVWAQQQLHGF
DVPLSPIKSYPSVEALAREVAQSLAQVKQLTGKSPKVMVMGAKGRCGSGALYFLKEAGVE
GVTEWDMAETSRRGGPF AEIADHHIFVNCIYLMGAI PPVVTKEQLGAIQDRPLTVVVDVSC
DYTNPANPLPIYNEATTFLSPTVRVPLASGPLDVVVIDHLPSMIPRESSSDFSTDLLPSL
LELADFAAGQPAPVWDRALALFNQKVAEAAAQ