

>NFS1 (cysteine desulfurase) Contig23289 (complete), 431 aa, 2450  
MKNRNSSSITHRGALLRKGWPRAPSAAPIRLSSGAARMASSVPSATQGG  
SVYLDMQATTPVDPRVLDAMLVYTEAYGNPHSRTHHYGWETQDLVEDAR  
EKVARLIGADAKEVFTSGATESNNAAIKGVARFYGEKRKHIIITVTEHK  
CVLDSRCVLEAGEGVRGDPVAGGEERGAGRGQARGGDEARHGAGERDGG  
QRDRGHPARRRDRAAVPAAGRVLPLLSISGHKLYGPKGVGALYVRRKPRV  
RLHPIISGGGQERGLRSGTVPTPLVVGLGKACEVALEEMERDGAWVKHLF  
HRLYDGIARVPEVYLNGLDERRYHGHLNLSIFAYVEGESLLMALKEVALS  
SGSACTSASLEPSYVLRALGVSEDMHTSLRFGIGRFTTTEREVDHAIELC  
AKHVDRLEMSPLWEMVKEGVDISKIQWTOH

>ISD11 Contig7577 NOT DETECTED, 83 aa, 53C  
MASRPQALRVYRQLMRNGRQYNDYMRREYIQRRVRDEFKANKTMSDAEQI  
DKCLDKARHELEVVKRQAIISRLYNHGKLIIEV

>ISD11 Contig21283 (complete), 74 aa, 238C  
MSSRLRLVAPPTRRQVLGLYKEMVVASRSFKHSDPQWFLARVRQEFYKTN  
REPAERIKWFEKGQQLIRNKECIL

>Isu1 Contig20119 NOT DETECTED, 161 aa, F34  
MLRTRTRAVFGSATLASHNGGSRMAGGAQRLYHERVIDHYENPRNVGSLD  
KNATDVGTGLVGAPACGDMVKLQIEVKDGIKIVNAVFKTFGCGSAIASSL  
ATEWVKGKSLDEAKVIKNSQIAKHLALPPVKLHCSMLAEDAIAKSAISDYE  
KKQKAKQEAQQ

>Isa1 homolog (IscA1) Contig2426 NOT DETECTED, 130 aa, 4C1  
MSVAGTVRVVRKPLTSRFAAKAPITLTPAAVSRHLHSLMGGSKDKYEGIRL  
DVKSRGCGGNSFTLDYAEKKERTDEVVEADAGVKVVFVGSKALLHVIGTEM  
DYVEDDLQSGVFVFNPNQAKSTCGCGESFTL

>Iron-sulfur assembly protein (IscA2) Contig20123 (complete), 245 aa, 1B94  
MARTPTSAASFMRGYSALALPARTLHTSLPAALRSSAMNRVAVPSTSASS  
GPSCTTVPSLGRVRSRCVPSALSIGTRFVPASSTSRRTASAAAAPLQDLH  
PQTHPMAPSASTFDTTPVSLILDATASATRAVPSTQTILLSDRAKKKLRGL  
TSKREGGAILRVEVQSGGCSGFSYKFTVEDRPLTEEDILIEEEGARVVVD  
DVSLPLINGATLDWDEKLIKSKFQMLANPHSAGECGCKYSFTPKD

>Iba57 homolog Contig13880 (likely complete ... could in introns/gaps)  
MMSRAGRLRAWYRSTEVVRGAVVGKRGIIHHAAPLWLVAREAPPLEQPAPP  
PLGWWVGEVGGRAIVEVRGRDAARFLQGLTTNDLLAAAATS RAGREEGRY  
TAFLLTPTGRLLADALVCQLPPGQQQQQGEQTFLLVECDARAAPGLVVH  
LRRYRLRAHVDITPPAQRPAADEWAVGAVLTRGHVQSSSSSSSGGGSGE  
ATPSPRDSSLQCLRSHAPSLPCFADPRTAAMGIRVYHRRSSSFAPPPGLA  
EASAKYRLHRLHRAVPEGIDELEPNVAVPLECNLDALNGVSYDKGCYL  
QELTSRVHHTGVIRFVSSLDLIDRSLPSLATTNIASDKTELFLVGADGTPER  
RQVGRLCGGV  
EAGLGFALLRLQHTTAVLTPSTTTAPFFLAKPLWPPPYPLP

>Yah1 (ferredoxin) Contig18230 (complete), 171 aa, 17F3  
MMKRTTTLVTGRRFAGLQSPVVPFAWAGRQATSSSASTLRSARLYSADA  
DSKKTIVHVTFDKDGTEIPLEAPVGKSVLELAHDNKIDLEGACEASLACS  
TCHVILDKEYYDKLPAPVEEEDMLDLAFGLTETSRLGCQIIISPELEGI  
RLKLPPATRNMVDGYKPPHH

>Arh1 (Ferredoxin reductase) (sequence may contain mistakes ... N-terminus uncertain) NOT  
DETECTED, 507 aa, 31B  
MKVWRRGIRTSMALREVGGMGVPTSRHLKVCVVGSGPGGFYAVEALQRM  
AEEAKAKGQAPEMALDVDIYERQAVPYGLVRFVGPDPHPEVKAVQHRYDA  
FMADPRLRFVGNVSIQSTNSISQSSSSGAAALSVEELLGAYDGVVLAAGA  
QRDRPLGIEGEDLPGVYSAREFVAVYNGDPAMRSRQFELSSSREAVVIGQ  
GNVALDVARVLLHEPGQLASTDMPEYAVDALRRSQIDTVHIVGRRGPAQA  
SFTNKEVREILNLPVQCHFLPSGVLALNEASKAETAKERGKKRMIDLFA  
ATEKKAGETKGEKPKNLYFHLLSPLRFLANEKGHVSGIELARNELQGEA  
GNQKAVPTHEKETLECDVVFKSIGYKSEPLEGVPFDHHRGVVNEHGRVV  
RPDGSTVPGLYVSGWMMKRGPSGVIGTNRMDAETVASMWADLAATRPGEK  
PGWRAIQDKLRERQVAVVDWKQWKAIEDEEHRRGQVLGKEREKFTSVP  
EMLDVAFKQ

>Yfh1 frataxin Contig119 (likely complete), 124 aa, F65

MFGSARHARHLATSAEPPSAGEFAKAAEETLEDLQDRLEEAGLDEDLDIS  
YSDGVLTIIRLGDKGTYVINKQTPNRQLWFSPIGPKRFDYVATEGKWL  
TREREPLHQLLYAELEQLTGVSL

>Nful (NifU) Contig10864 (complete), 279 aa, 21D1  
MQAALKRAFARTSPRFLPAASLARGRGGSTLWSTTTLTSSARGEGRSWRWT  
AGGARSMFIQTENTPNPDSLKFPVDPGNVLESMTDFPDARSSLSSPLAK  
SLFTVTGVQVFFGNDFITVTKKPDVEWHEIKAQIFANIMDFYASGESV  
SEQQDTSNTTILPTDSETVAMIKELLEVRIRPSVQEDGGDIEYKGFDEEA  
GVVYLKMGVSCSGCPSSSVTLKSGIERMLMHWIKEVTGVVAVESDDELDR  
LTKQEFKLEKKGEEGKGGDDTAKESTVA

>glutaredoxin protein Contig25663 (complete), 186 aa, 2272  
MQKATSSLAMRGAVRSTAQRRLFSTALNRSRSVVTSRAALLSLRSVSSPC  
SYAPIAPRQQRWYTTDDNKEVGEVATDSVQDAIKKVSEYPCVVMKGT  
PDAPQCGFSNATIKALNTVGAHYEAFDVLQSAELRDGIKKFTDWPPTIPQV  
FIGGEFVGGCDITLQHLRSGELTTLLEKAKALKSQ

>glutaredoxin E80POFO01EPD8X (and 10896) (complete), 240 aa, 197C  
MMSSATRRSAQYSFLLASARSSFAGRIVTASNRRSAPLISTSSSAPSFI  
SISSRRHLYSTEAESPAAAVETAPEAAAAEKESITQEQEEVKQESLAE  
FLERIEKEDQAKIDAALKAFESGNAIDEHISLLGMKKYKCVVMYGD  
APADGQGYAVIKQLQORDHALFKTFDLNKYPLLKEGLIKHKGSYVRGEDI  
PQVYILGRPFGLREVMDSVATGQLEARLRLTRSQRHYA

>glutaredoxin-like 25994 (bacterial-like), 136 aa, 904  
MVRLGCRGTNVATSSVLRGAASVRTLNRSASSLGARRGFASGVTPKVVE  
VYTTAWCPFCDRIRALLNSKGVQYKEIDVTSVAGAKDEMEKRTNGRRTVP  
QLFIDGEYIGDCDGHKLDAQGLLDAKLGLKERSTA

>Hsp70 Contig3529 (complete), 669 aa, EC4  
MLRRVAATRRAVSAASFLRSSWNAAPAAARLYSAKSGDHIIGIDLGTNS  
CVAIMEGSTPRVIENSEGERTTPSVVAFVKDDHGTNRLVGATAKRQAVTN  
PTNTFFAVKRLIGRDFNDPMTQKDLKMPYKIVRHSNGDAWLEDKSWGK  
SPSEISAFTLTKMKETAEGYLGTVKKAIVTPAYFNDSQRQATKDAGKI  
AGLQVERIINEPTAAALAYGLTNKGGETVAVYDLGGGTFDISILEISKEG  
VFEVKATNGDFTLGGEDFDNTLMQHLVGEFKAEGIDLSKDKLALQRLKE  
AAEKAKCELSSTVSTEINLPIITATAEGPKHLHIKLTARQFESLVDPLVQ  
RTIDPCKSCLKDAGLDKSDINNVLLVGGMTRMPKVQEVVKQFYGKQPSKG  
VNPDEAVAVGAAIQAGVLKGDVQQLLLLDVTPLSLGIETLGGVCTKLITR  
NTTIPTKKSQVFSTAADGQTEVEIKVLQGERHMANDNKTLGFSFILSGIPP  
APKGVQVEVTFDIDANGIVNVSARDKATGKEQAIRIQSSGGLSESEIDR  
MVKDAETHEEEDRKRKQTEARNHAESVIYDIEKNLNEFKEHVDQTEAER  
LREQITELRKTLESADHDQAIKSGADSLQRESLKAFESAYKQKASSNDSG  
SSSSTENKEDDTPDADIK

>Hsp70 Contig14215 (complete), 683 aa, 16FF  
MRATGRLNPMQGMFAFASLGGCRATAASSASALFNRSAMRSTFAGPVF  
SRRYTSTSDPLVMGIDLGTNSCVAVIENGKPRVIDNVDTGYNTTPSMVA  
FTKDKATGQOTMLVGDPAKRQCVLNPRGTVYGVKRLIGRRFDSEEVAKIK  
KHVPYEVKAAANTGDAAVSVGGKSYSPQIGAFILQCKESAETHVQGT  
ISKAVITVPAYFNDSQRQATKDAGAIAGLDVLRINEPTAASLAYGFSEE  
NSKERQRLAVFDLGGGTFDISILEIGDGMQVSTNGDFTLGGEDFDETV  
LQYLMNEFKKKEGVDLSKDVFAIQRLEGAEKAKKALDHMPNYEINLPII  
TRDKNFYSYSLTKEKFNELIKPLVDRTIKPCQSALKDAGLDKVDNVILVGG  
MTRTPAVIEKVKEVFGNPSKGVNPDEVVAMGAAIQGGVLSGKVNLSLILL  
DVTPLSLGVSVKGDLFSRIIKRNSSIPCSNTQTYTTAADGQRQVFDLLQ  
GEREIASANHLLGQVTLVMPAPKGIKIDVTFNIDVNGIVHVTAKDPVL  
NKVATVQIQANGLSQRDIDRMLKEAELQKERDQOIKELAEVKNEAETLI  
RSAETDYLHNDVVPEEDKETIRQAVSOLQOTAMDGNSDELKTIYASLKDTI  
LNVGAKLYQGGASSSSNDGHNHNNNQETKQ

>Jacl (Co-chaperone protein HscB) Contig22279 (likely complete ... N-terminus inferred by  
Genscan), 349 aa, 13BE  
MQRIRTSKMAATASSPSFSSLLPSSLPILSPAQMPPCCLMRAIGGSGAGR  
SAPCLMGSREIGHWAPLNRAQCYSALTSKPSPLFSSSSILSSTSRRFIRV  
RTASEADTASSTQHOPPSIEEDQASNCADCGHSTQOQHQQHQTHTAPGCG

SDKFGSHPKCWSCDNFVKGIPLFCTCCQKVQPPSNYDFFELMGMPKRFAV  
DAGKLEKHYWALQRKLLHPDNFHTATTRERNYSEGVSSIINEAYHTLKHPN  
RRAKYLMQLKGVPLDETTGTITDPDLLMEVMEIRMRLDADDAELRALER  
ENKQRLDRCYEEVGHALDASDMDKCRDVAVRLQYFVKIEEEEIKRRKKVE

>Mge1 (Grpe co-chaperone) Contig881 (complete), 247 aa, 10A5

MRAAVRRLPNVASHSAASRGIFALNVPLRSRTLAIARPFSTEQNGEQKVE  
GEHPPAQQQAEGENKEQQQQEQDPQAAKIDELQNKVKDLEEQNKELNGNY  
LRSLADLDNMARIGKTNVENAKLYSIKSFAGMLEIADNLSRALESLEPEE  
KRGLPDVKVLFEGVAMTERVLQQVFARYGIKKFNPLNEKFDPTKSSALFE  
IQDPTKAPGTVAFAVQAPGYTLHDRLLRAAQVGVVAQPPDEPSSSDQA

>ATM1 homolog Contig14471 (and 26685, 6308) (incomplete due to internal gaps), 636 aa, A4

MLRASGAGVASAAQHGGWQKPAALRKQLPRGWAAKPAAPPAGTTPATK  
AAGPTKLGKLPDSGSGWAIMKSLSGYLWPKDNPAIKRRVLAVALLVGSK  
ILNVQVPFLFKEAVDLLNATTENVALVPIAILLAYGAARVGAAGFTELNRN  
VVFSKVAQSSIRQVACNTFLHLLSLDLRFHLSRQTGGLARAIDRGTRGIN  
FVLTSMVFNILPTILEIGLVCSILTYQYGAQFAALTAGTIGVYTAFTFGV  
TQWRTKFRKEMNAMESEASSKAIDSLINYETVKYFNNEKMEAERYDKYFA  
KYSAAASLKTNSLGMNLFQNFIFSAAITTAMILTAQGISAGSYTIGDLV  
MVNGLLFQLSLPLNFLTGYRELRQSFTDMETMFGLLSLNTDVKNEPGAT  
DLRVSKGEISFEGVGFYTPERTILNGATFNVPPGSSGSRYYFVHVTTLES  
LRKAIAVIPQDTVLFDNTIFYNIAAGRPTATREEVLEAARLARIDDAIRO  
MPMGYETVVGERGLKLSGGEKQRIAIARALLKDAPILLCDEATSSIDTAT  
EREVQQSLAQLTRGKTTLIIAHLSTVVDADVMMVMKGGNVVESGSHHQL  
IARNGLYAAMWRHQLEAAHHGNPTTATAPNQSTPA

>Erv1 Contig2125 (N-terminus inferred) (likely complete), 215 aa, 21B7

MEQFKKIKEKLQKEGDQLVVGGADEEDCGACKPRAGGLYGSDMRRRFRSQ  
QQAREQRSAQEQDGGTTSTDATATSAGTEEDASNENTTECYDSEGYWEKQ  
DAPDVIELGQAGWTLHLSMAAYPPKPSRQHQERMRSFLSLFPHLYPCKV  
CAKDFEETMDEIPPELESHDALSDWMCRAHNRVNQQLGKPLFPCERVRR  
WGPSNAFHTKEQDDSD

>mitoferrin (likely complete) NOT DETECTED Contig13335 (and 5394,17393)

MEFLVDEALEEELQOSSDPRVHLIAGACAGLMEHCGMFPIDTVKTHQQLA  
GSRTSIAATIRTIVAKNGVTGLFRGLPVVVAGSAPVHGVAFSIYEFCKRL  
LGADQPGHLLASSMSGVVATLAHDACLAPVDTLKQRLQFSARPYRGVWD  
CFGHILKSEGVSGFYRGYTTAAVMNLPHASIYYGAYESIKKLLKRATGKE  
YESNDPVTHMLAGAAGGCLAGGLTNPLDVGKTRLQVGTDAGKSYRGMVST  
LRTIYREDGWAGFTKIRPRMVFHSMASAAISWTTYEYIKHTLEPSFSSHS  
PPSSNKSGPS