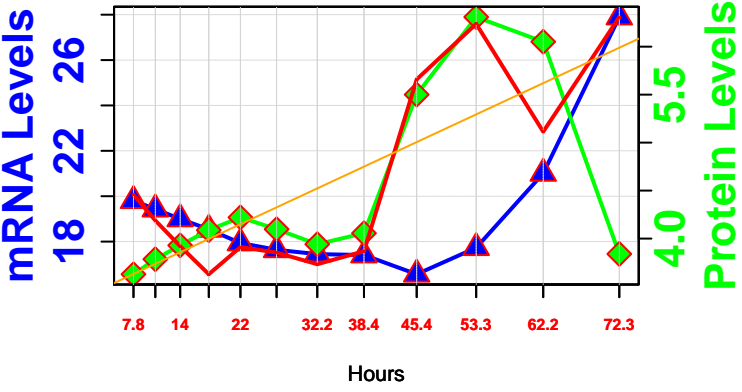


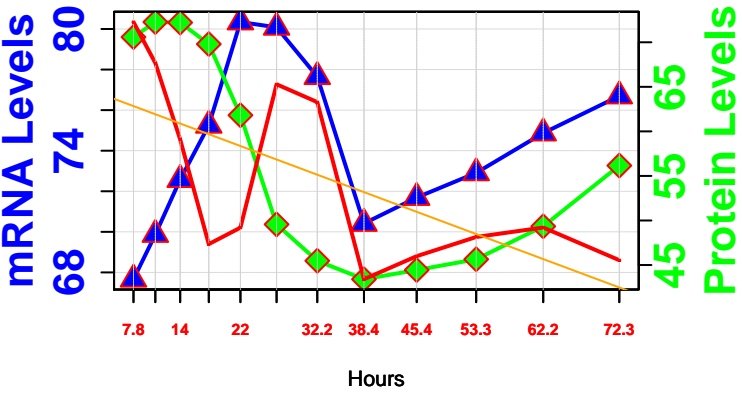
heme biosynthesis

4 - HEM14 RLS: 36.78
YER014W
ORF

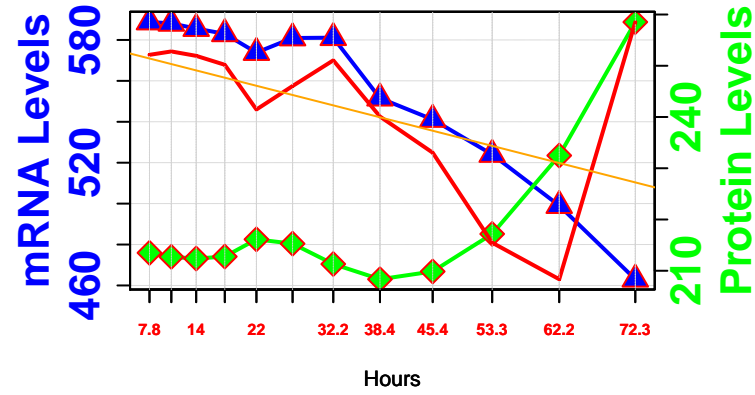


salvage pathways of guanine, xanthine and their nucleosides

6 – XPT1 RLS: 36
YJR133W
ORF

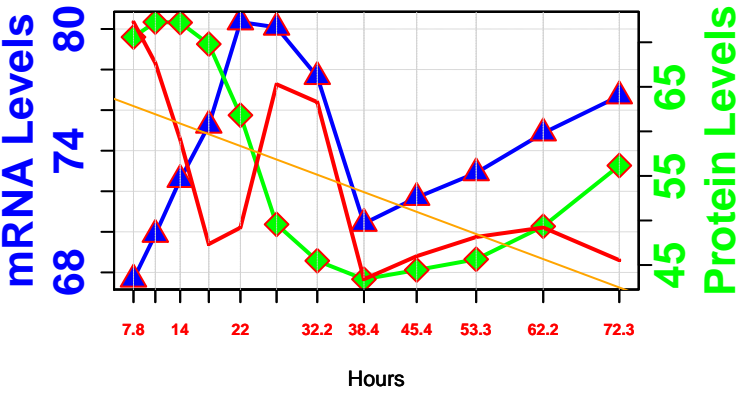


26 – HPT1 RLS: 33.6
YDR399W
ORF

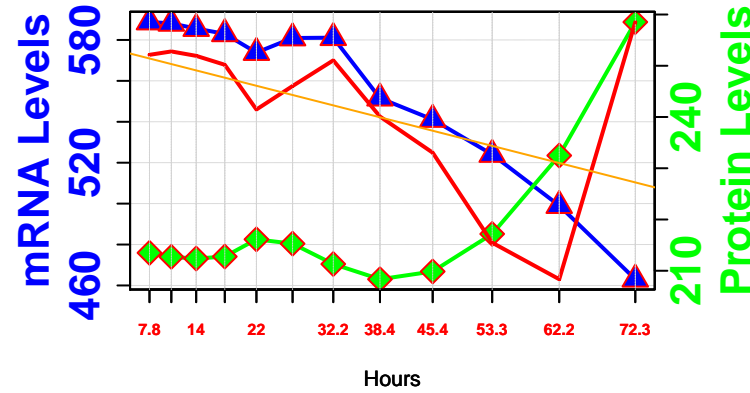


salvage pathways of purines and their nucleosides

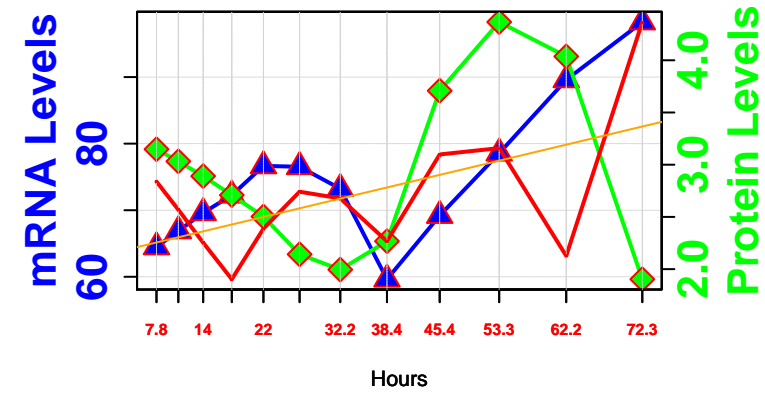
6 - XPT1 RLS: 36
YJR133W
ORF



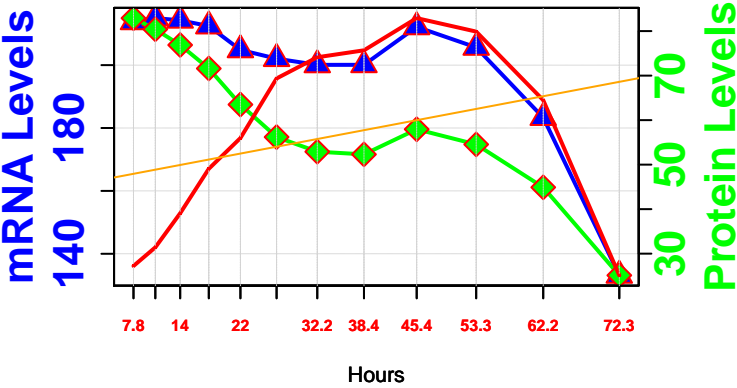
26 - HPT1 RLS: 33.6
YDR399W
ORF



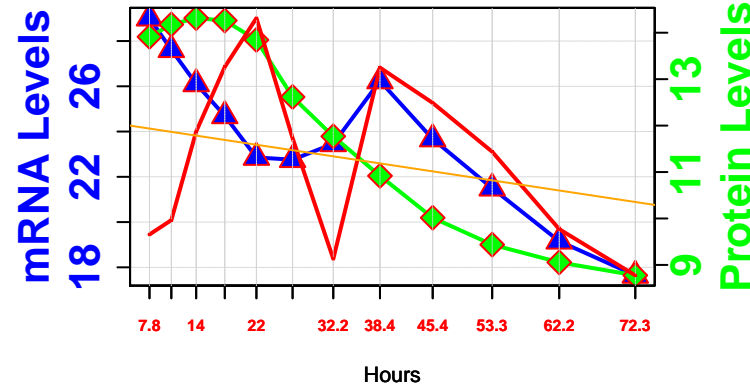
130 - APT2 RLS: 29.6
YDR441C
ORF



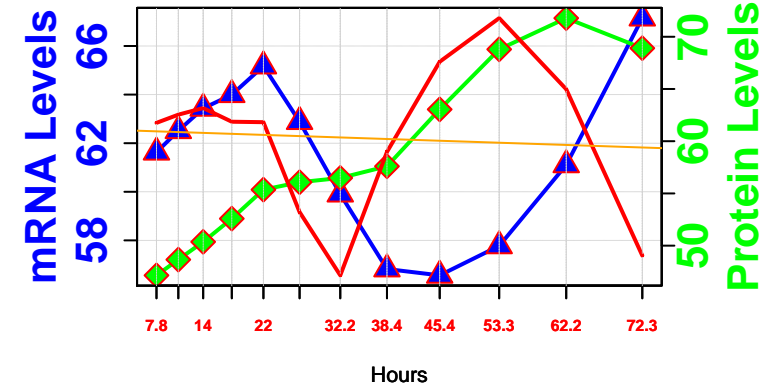
132 - APT1 RLS: 29.6
YML022W
ORF



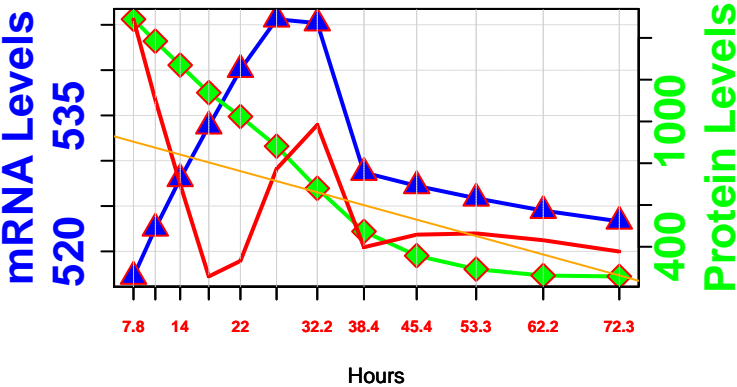
196 - AMD1 RLS: 28.07
YML035C
ORF



278 - PNP1 RLS: 26.4
YLR209C
ORF

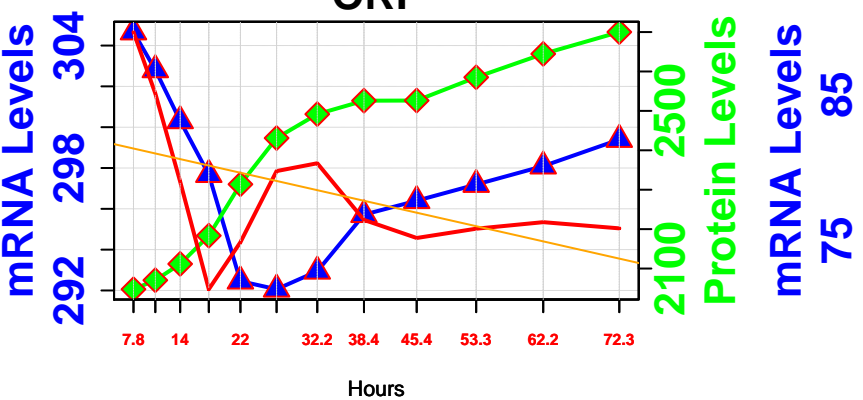


582 - ADO1 RLS: 18.6
YJR105W
ORF

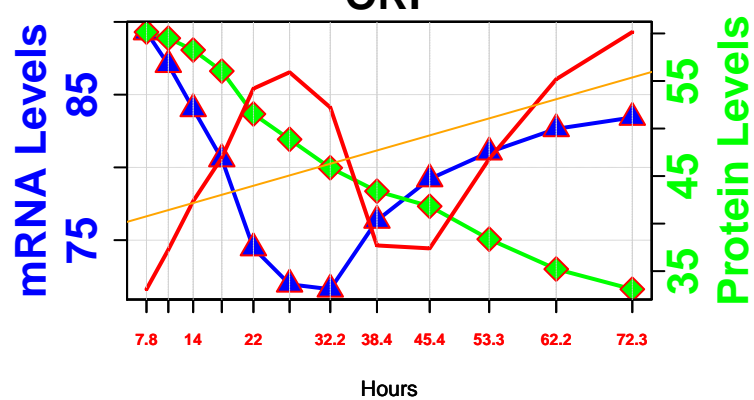


tryptophan biosynthesis

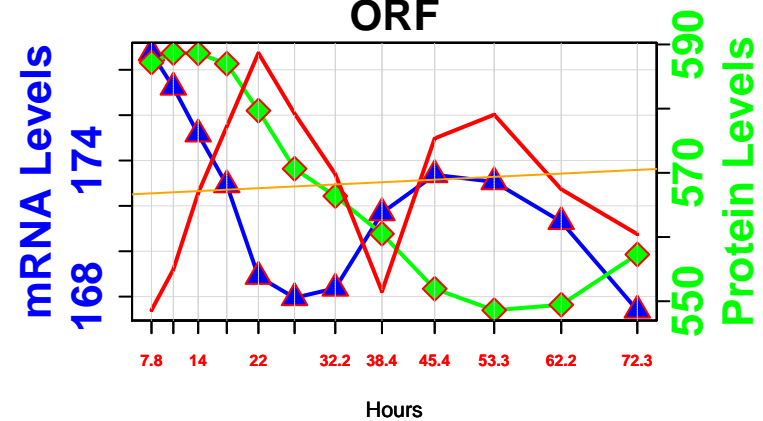
19 – TRP5 RLS: 34
YGL026C
ORF

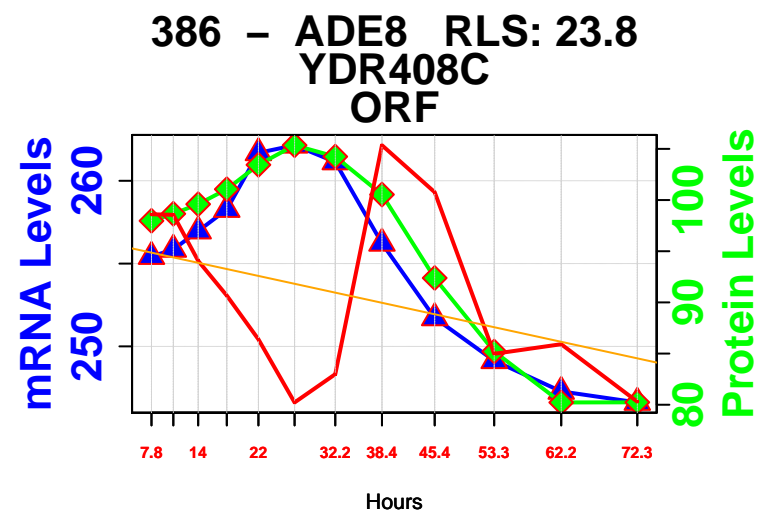
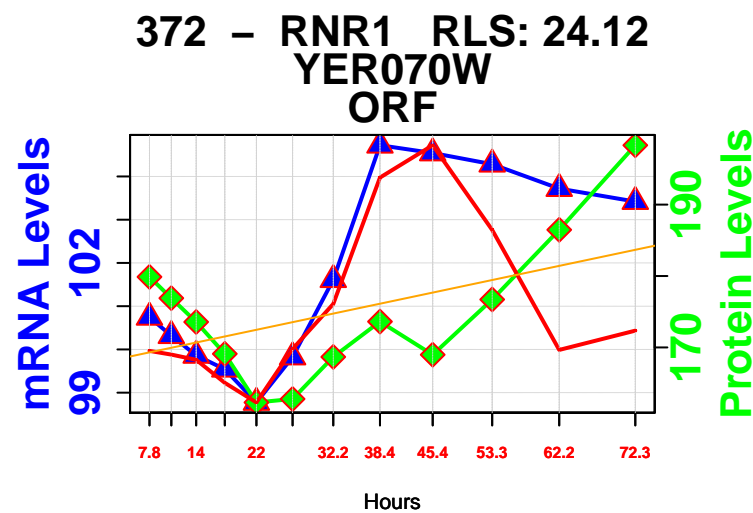
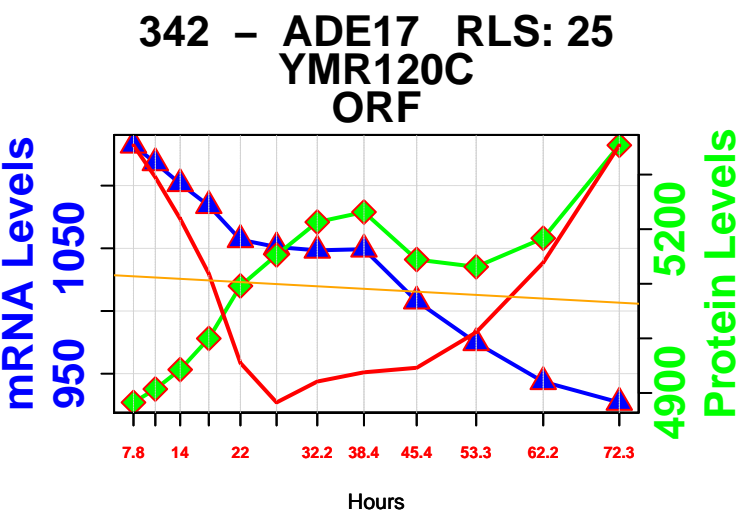
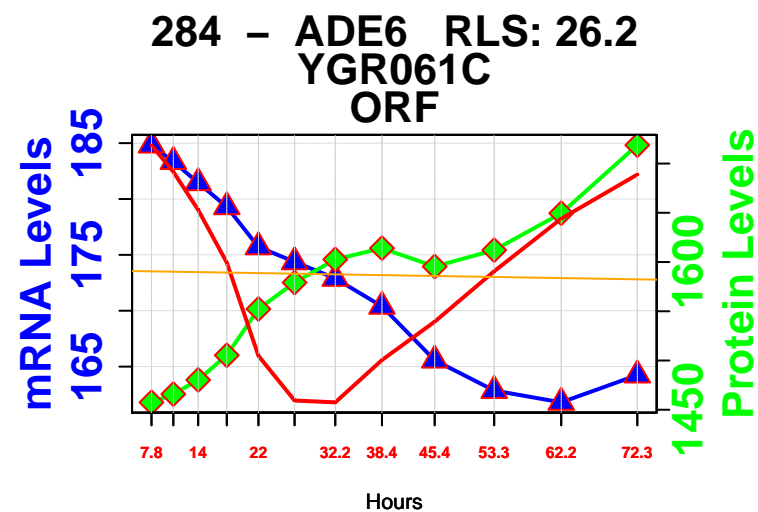
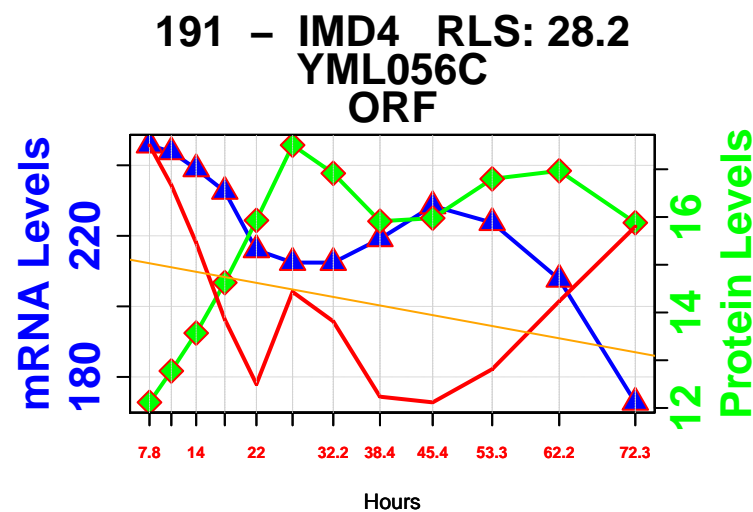
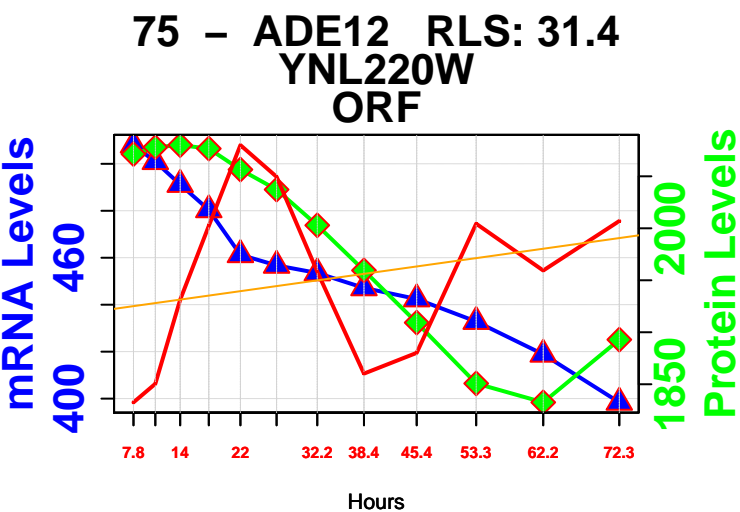
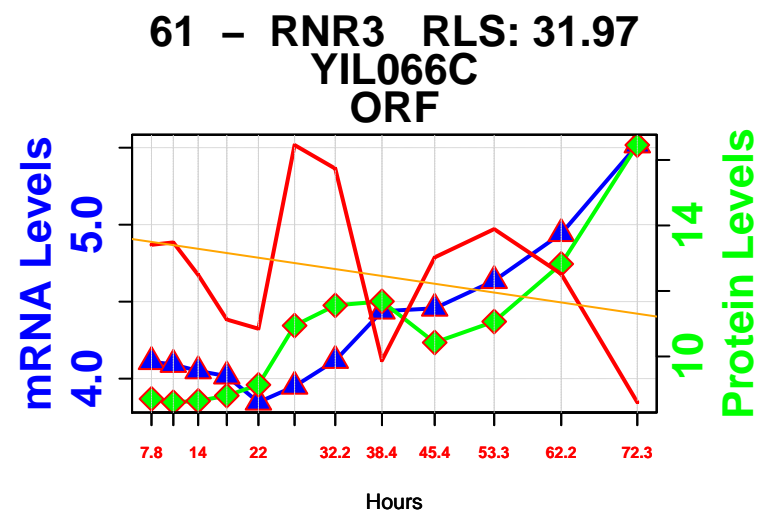
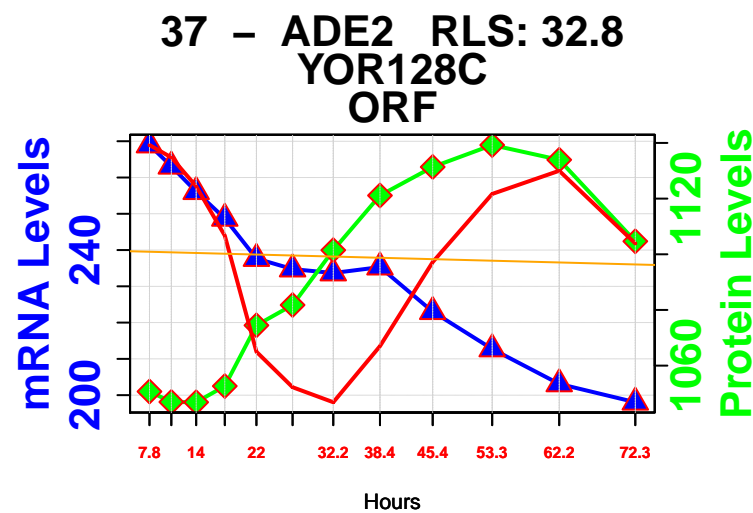
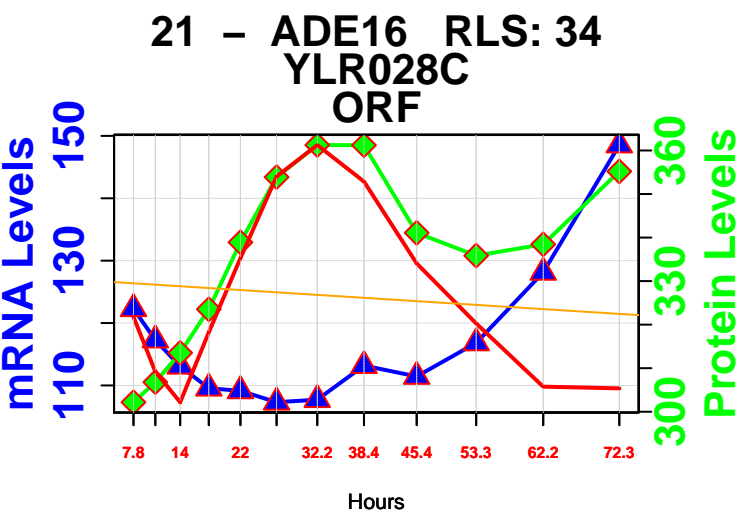


43 – TRP4 RLS: 32.4
YDR354W
ORF



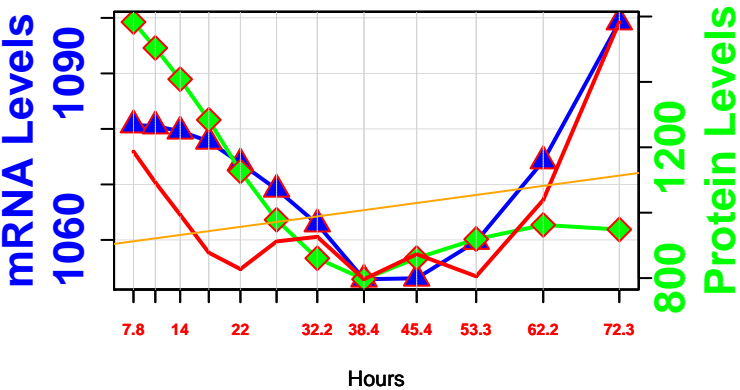
165 – TRP2 RLS: 28.6
YER090W
ORF



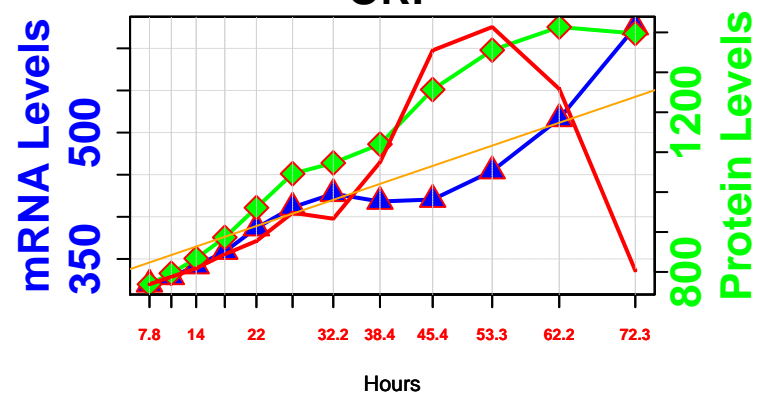


de novo biosynthesis of purine nucleotides

587 – ADK1 RLS: 18.2
YDR226W
ORF

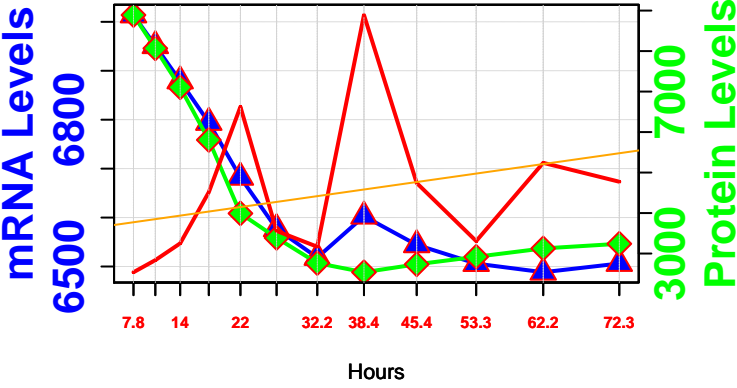


667 – RNR4 RLS: 6.2
YGR180C
ORF

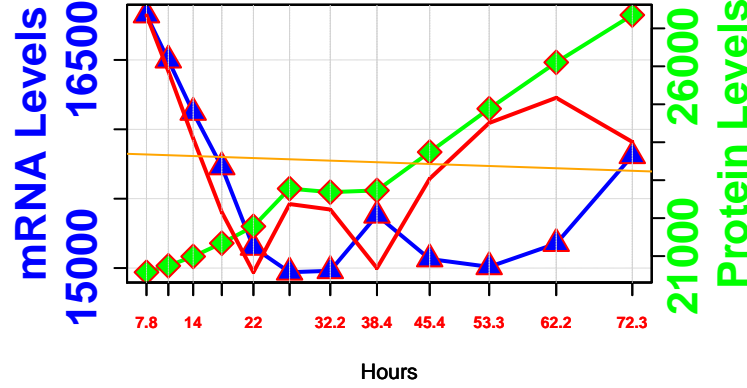


glycolysis

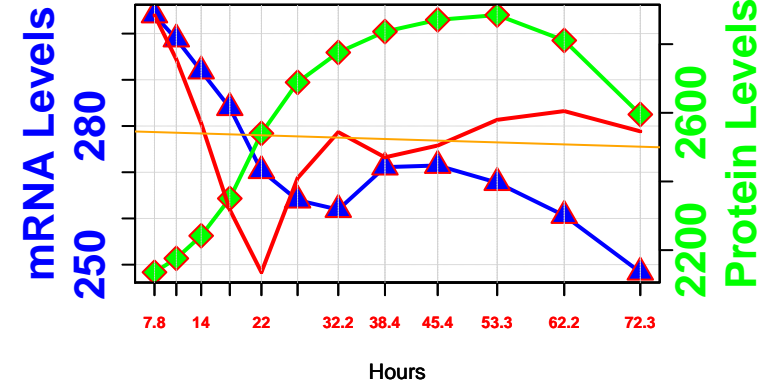
24 – TPI1 RLS: 33.9
YDR050C
ORF



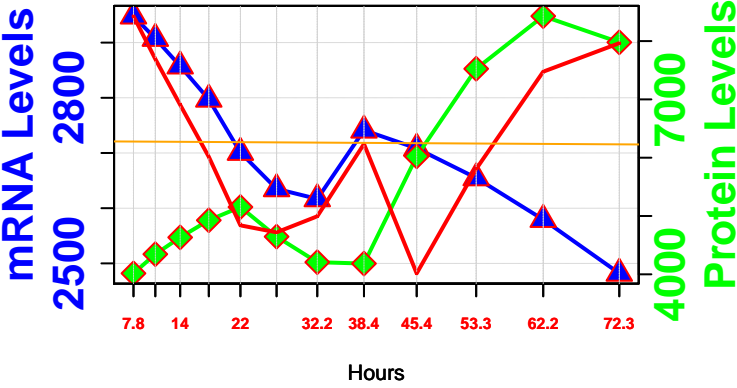
98 – TDH3 RLS: 30.57
YGR192C
ORF



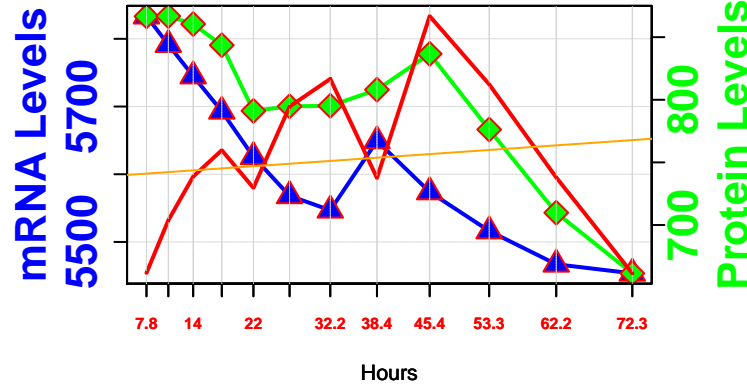
192 – PFK2 RLS: 28.2
YMR205C
ORF



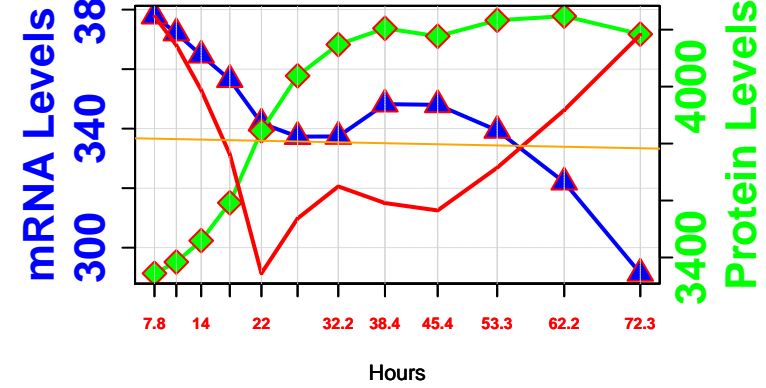
255 – ENO1 RLS: 27.04
YGR254W
ORF



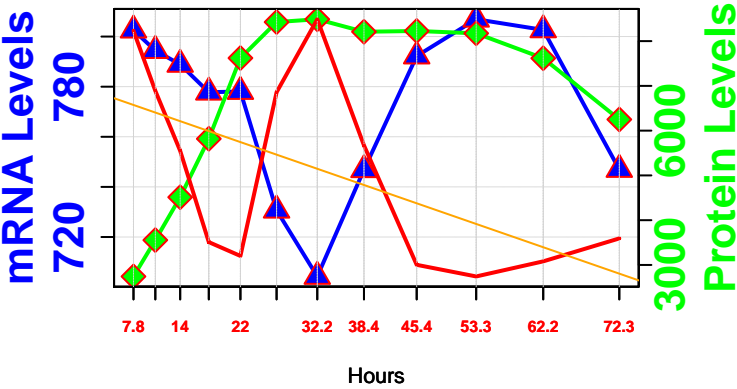
267 – TDH2 RLS: 26.69
YJR009C
ORF



269 – PFK1 RLS: 26.63
YGR240C
ORF

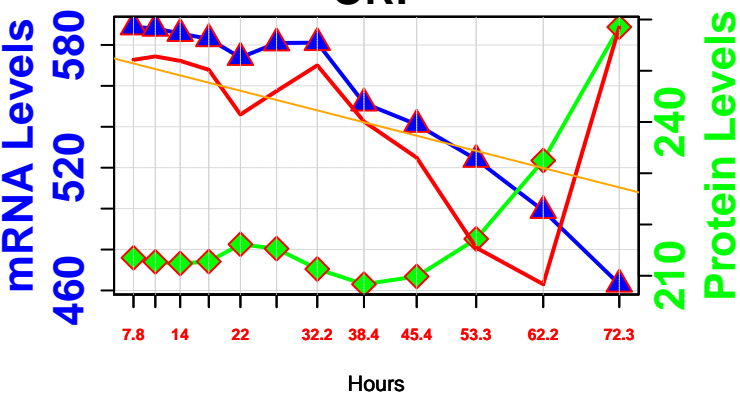


352 – TDH1 RLS: 24.6
YJL052W
ORF

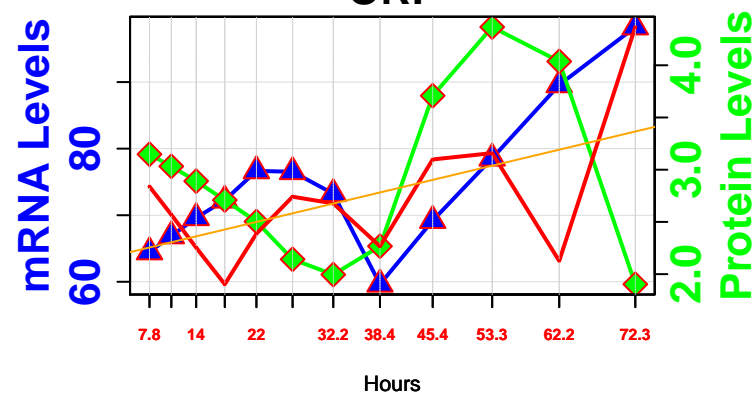


salvage pathways of adenine, hypoxanthine and their nucleosides

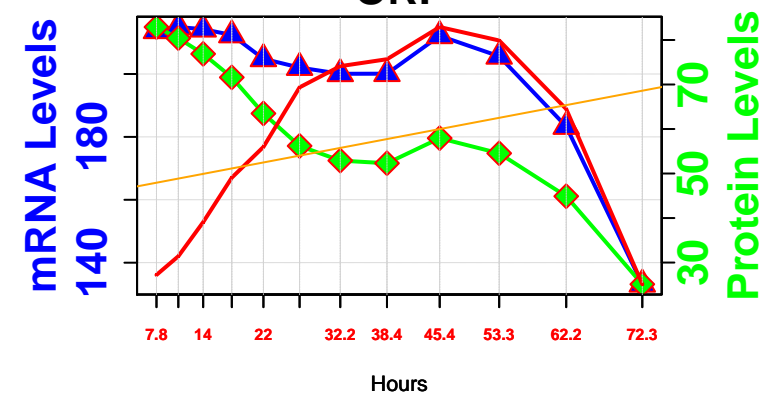
26 – HPT1 RLS: 33.6
YDR399W
ORF



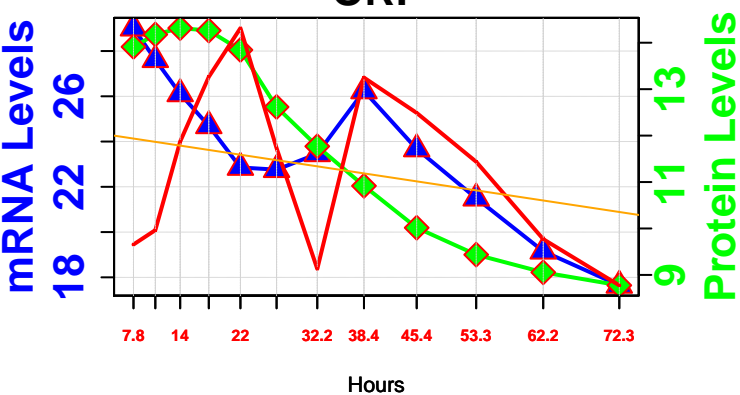
130 – APT2 RLS: 29.6
YDR441C
ORF



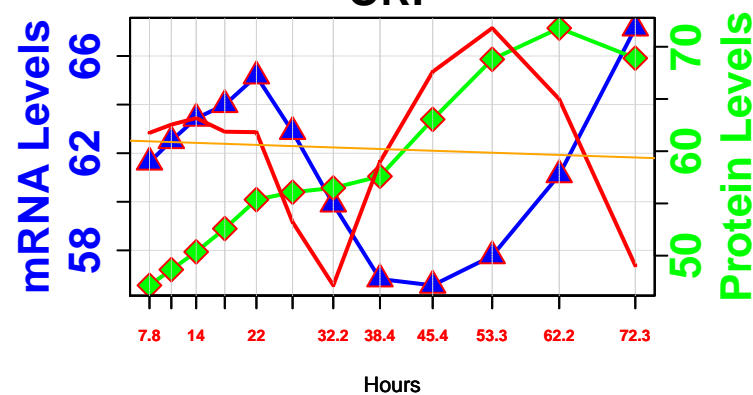
132 – APT1 RLS: 29.6
YML022W
ORF



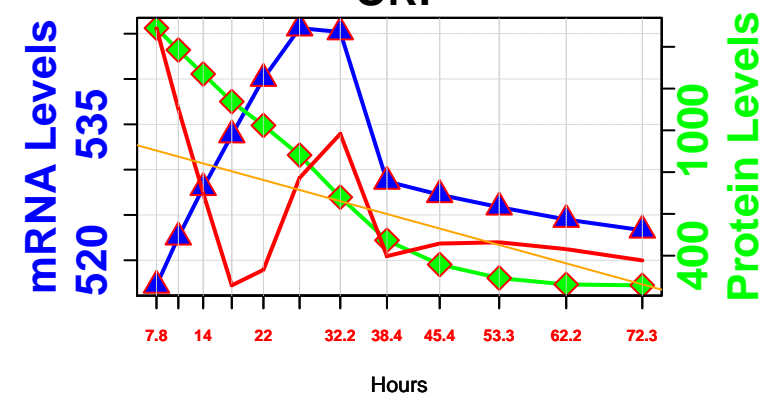
196 – AMD1 RLS: 28.07
YML035C
ORF



278 – PNP1 RLS: 26.4
YLR209C
ORF

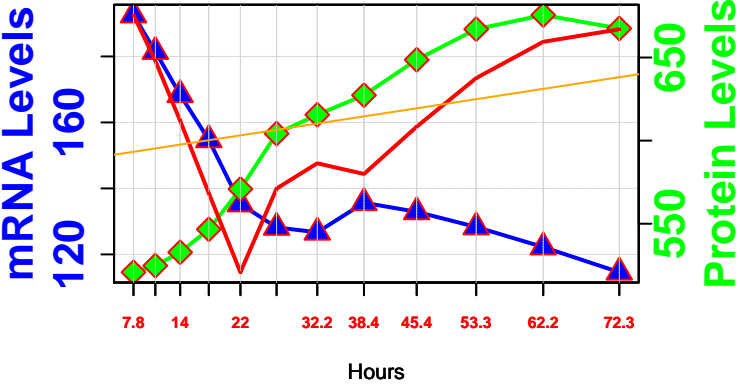


582 – ADO1 RLS: 18.6
YJR105W
ORF

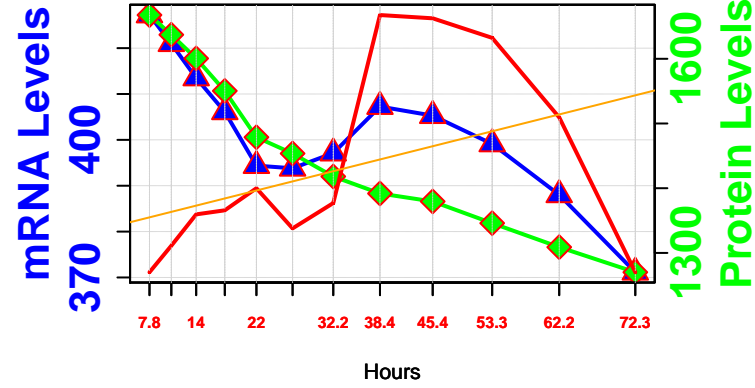


serine biosynthesis from 3-phosphoglycerate

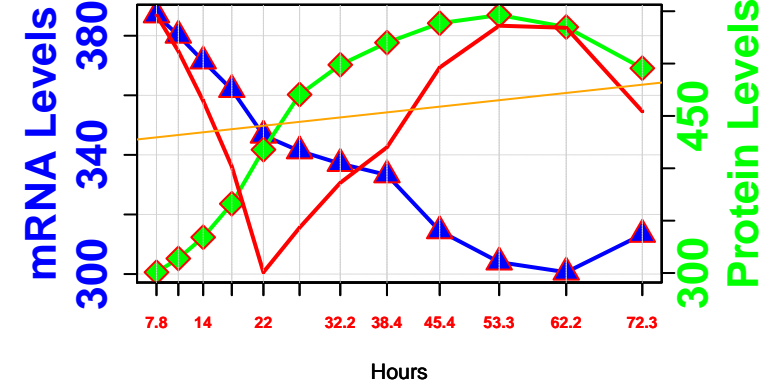
28 – SER33 RLS: 33.4
YIL074C
ORF



428 – SER1 RLS: 23.2
YOR184W
ORF

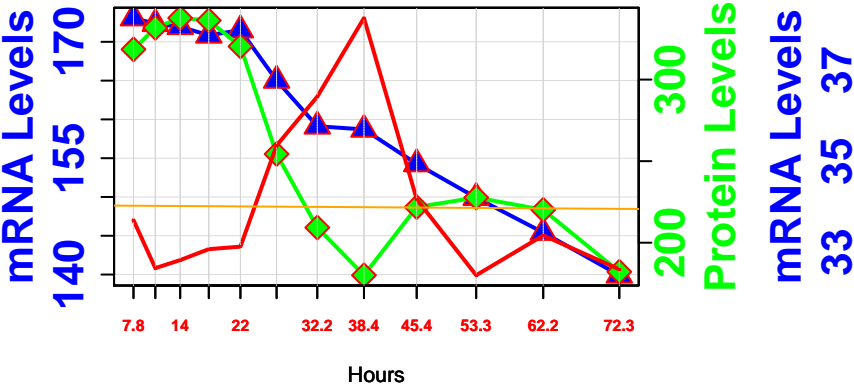


444 – SER3 RLS: 22.8
YER081W
ORF

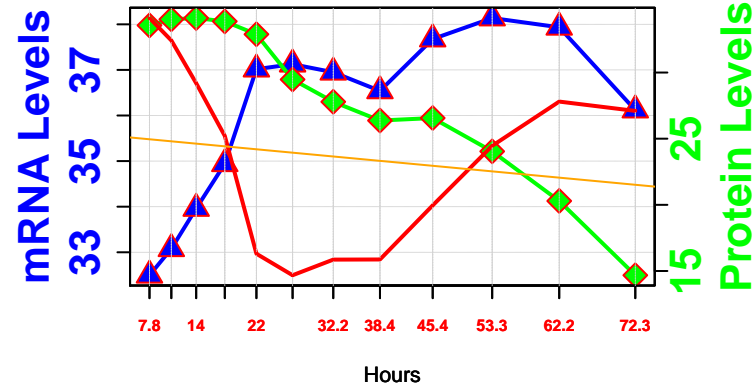


tryptophan degradation via kynurenine

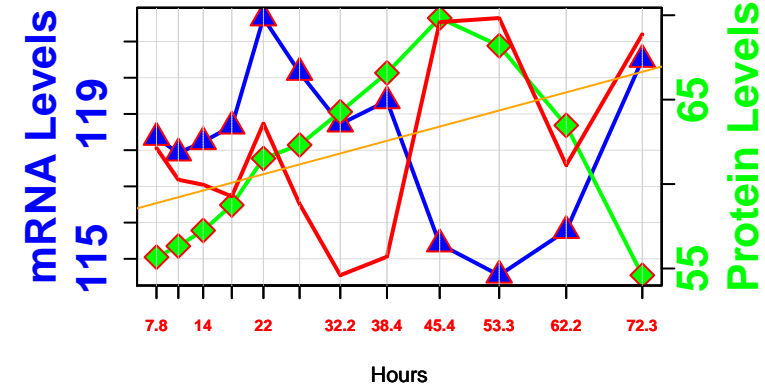
33 – BNA1 RLS: 33
YJR025C
ORF



39 – BNA4 RLS: 32.6
YBL098W
ORF

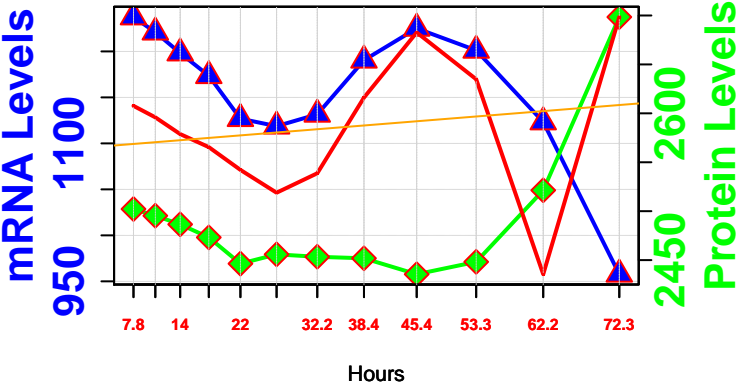


415 – BNA6 RLS: 23.4
YFR047C
ORF

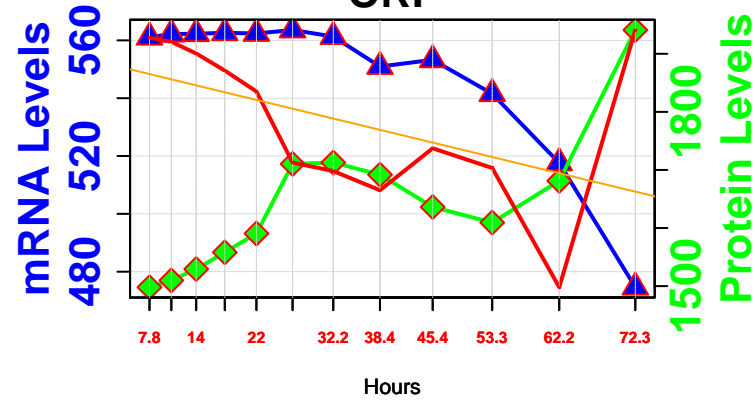


S-adenosylmethionine biosynthesis

34 – SAM1 RLS: 32.96
YLR180W
ORF

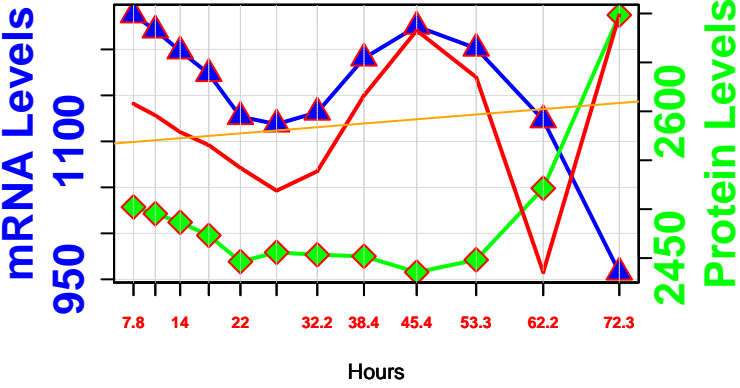


387 – SAM2 RLS: 23.8
YDR502C
ORF

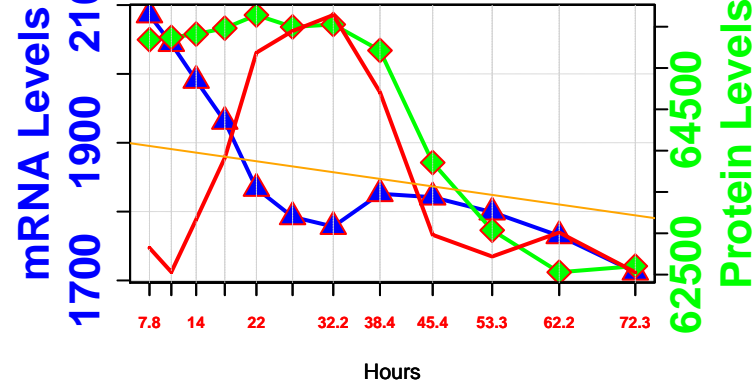


S-adenosylmethionine cycle

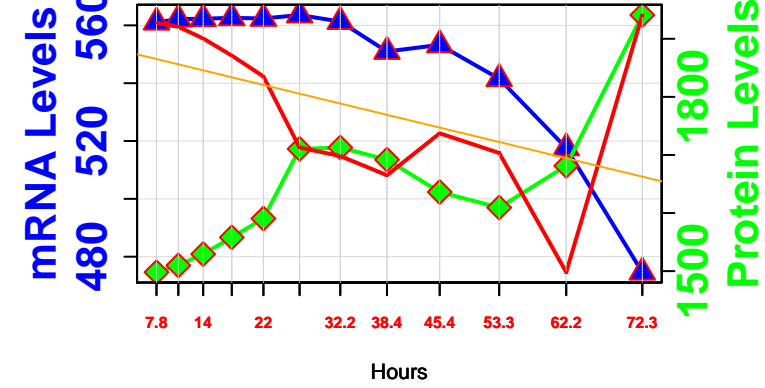
34 – SAM1 RLS: 32.96
YLR180W
ORF



312 – MET6 RLS: 25.74
YER091C
ORF

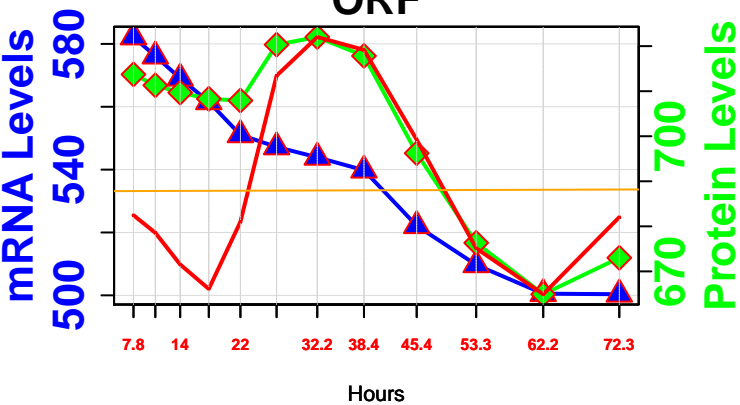


387 – SAM2 RLS: 23.8
YDR502C
ORF

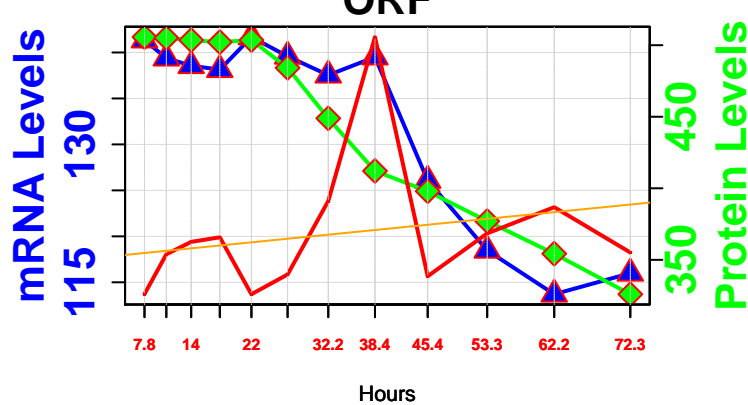


folate biosynthesis

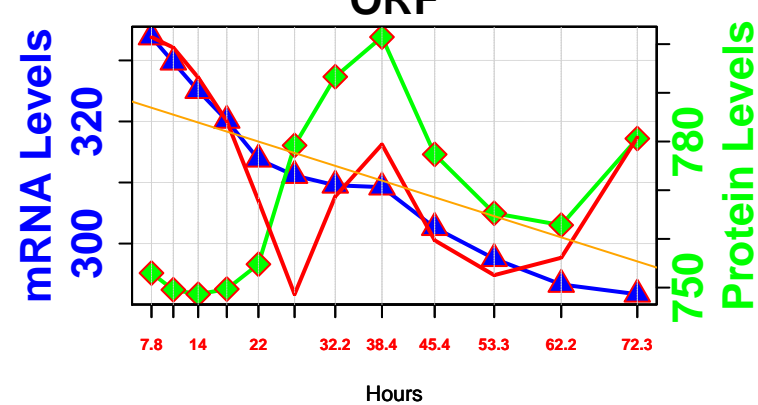
36 - GCV1 RLS: 32.8
YDR019C
ORF



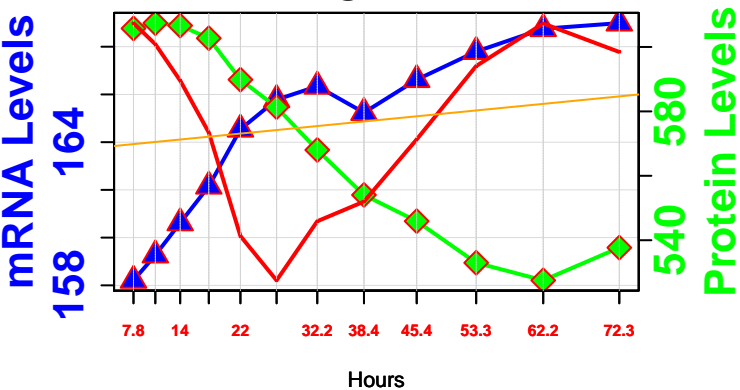
93 - LPD1 RLS: 30.69
YFL018C
ORF



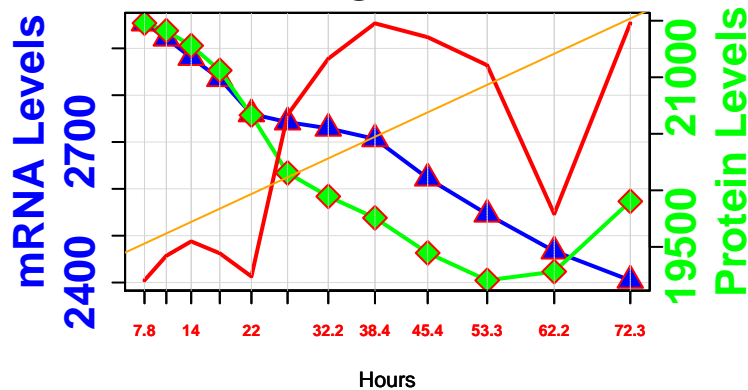
109 - GCV2 RLS: 30.36
YMR189W
ORF



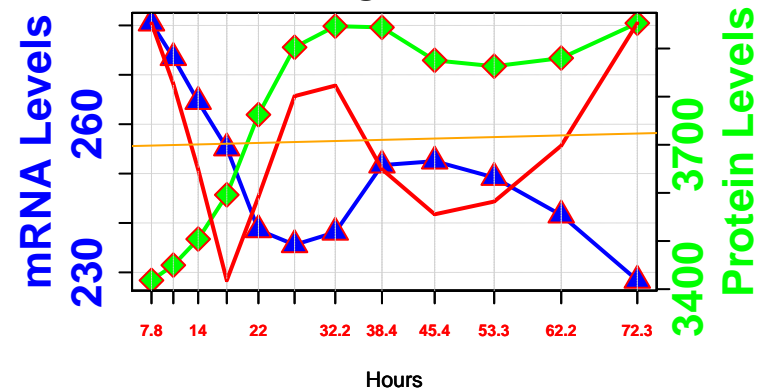
170 - SHM1 RLS: 28.53
YBR263W
ORF



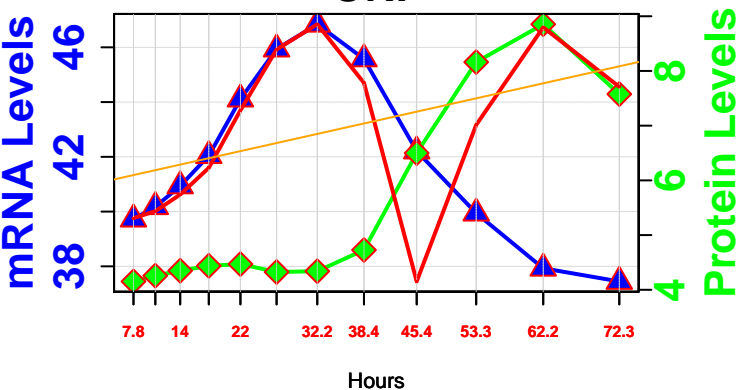
182 - SHM2 RLS: 28.28
YLR058C
ORF



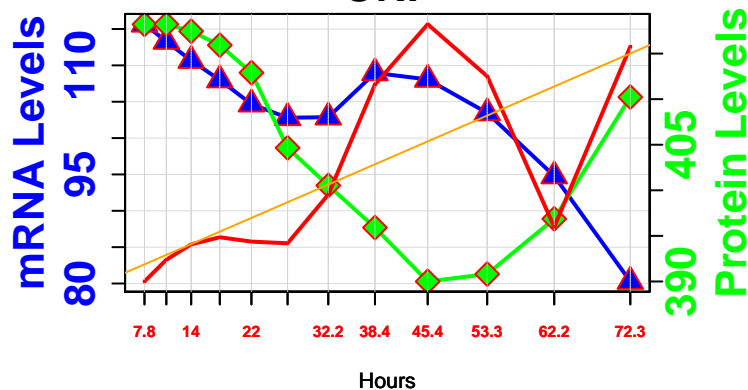
327 - ADE3 RLS: 25.4
YGR204W
ORF



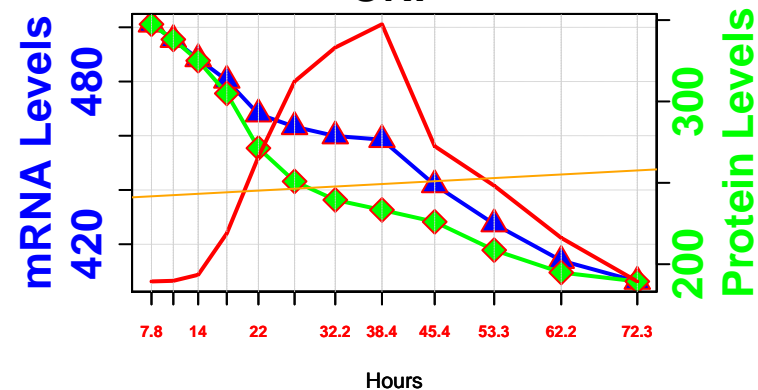
370 - MET12 RLS: 24.2
YPL023C
ORF



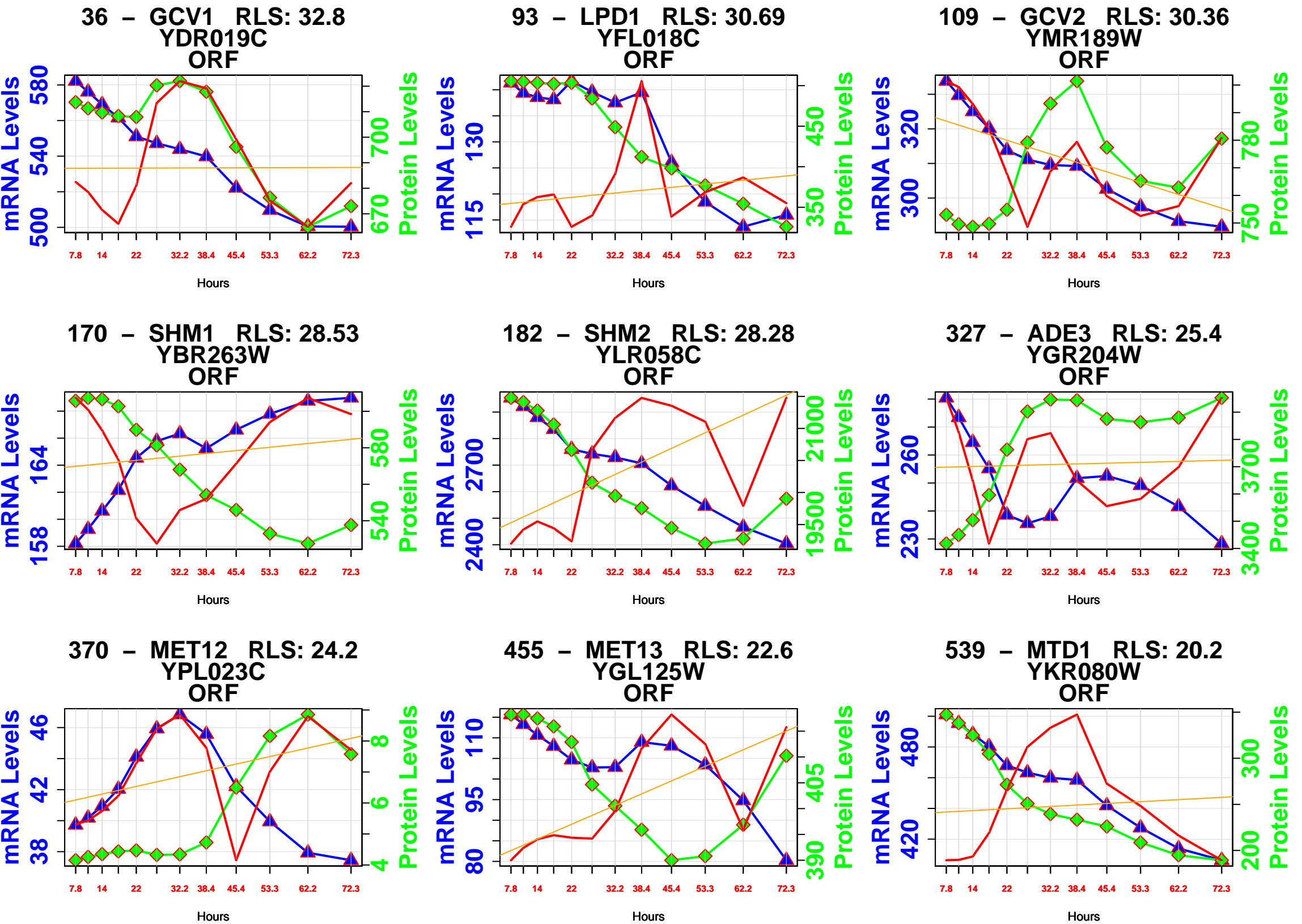
455 - MET13 RLS: 22.6
YGL125W
ORF



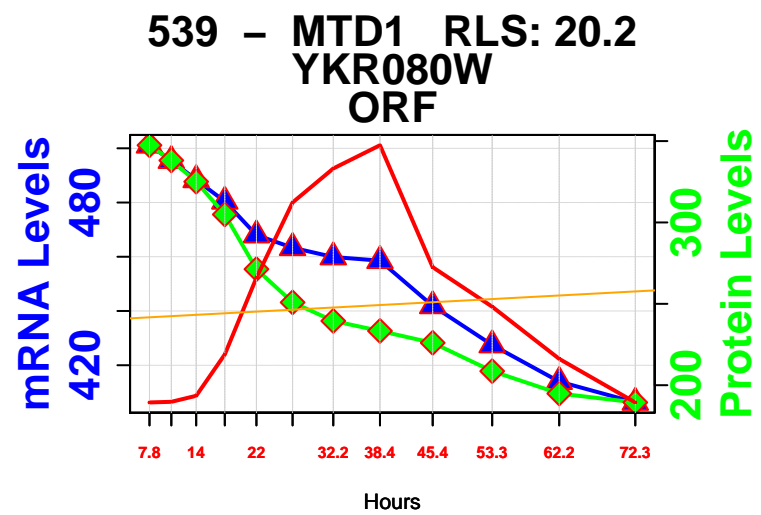
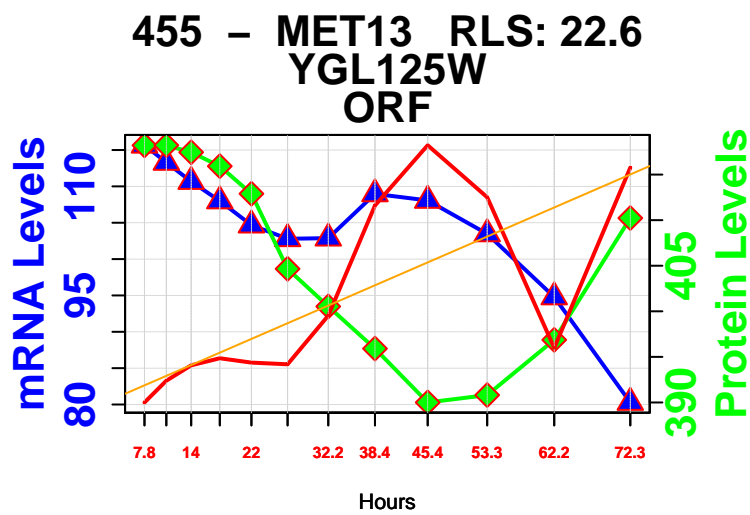
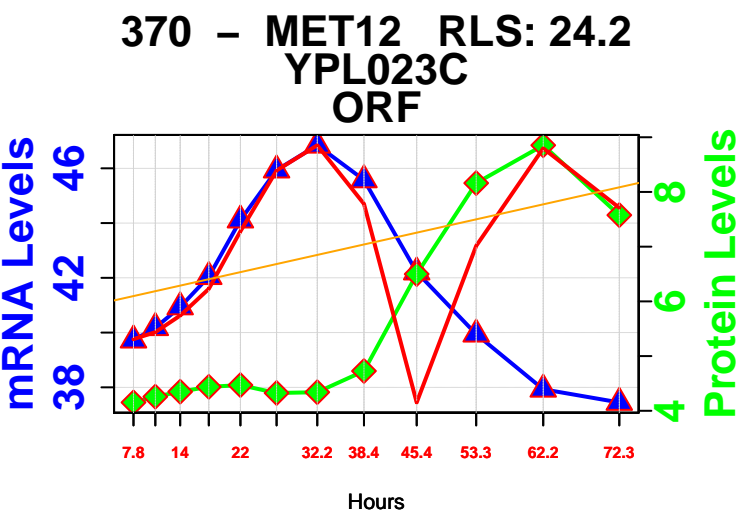
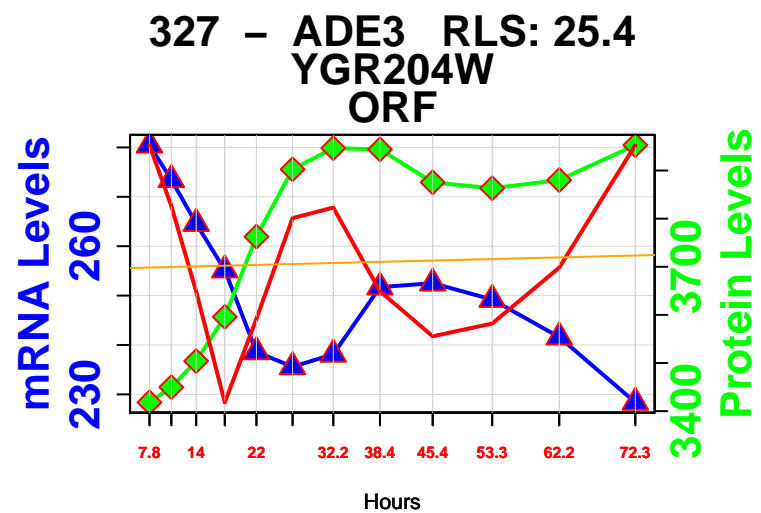
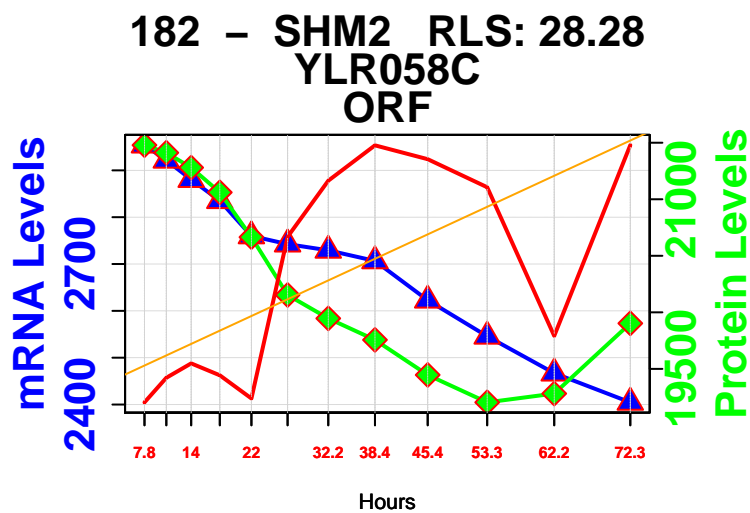
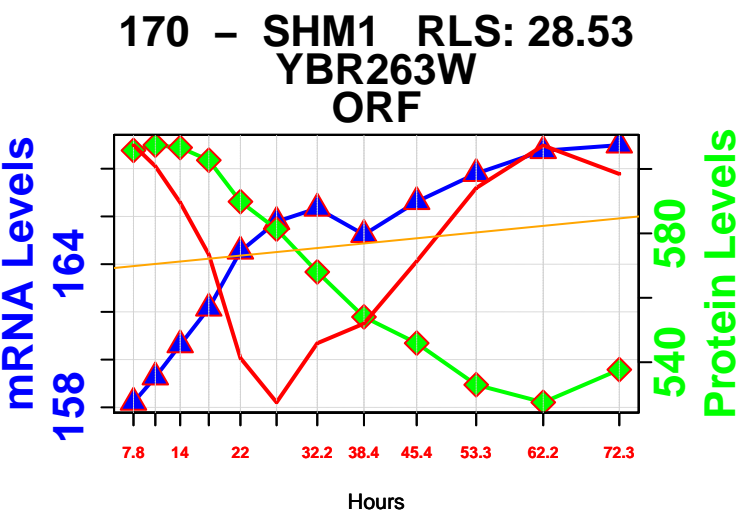
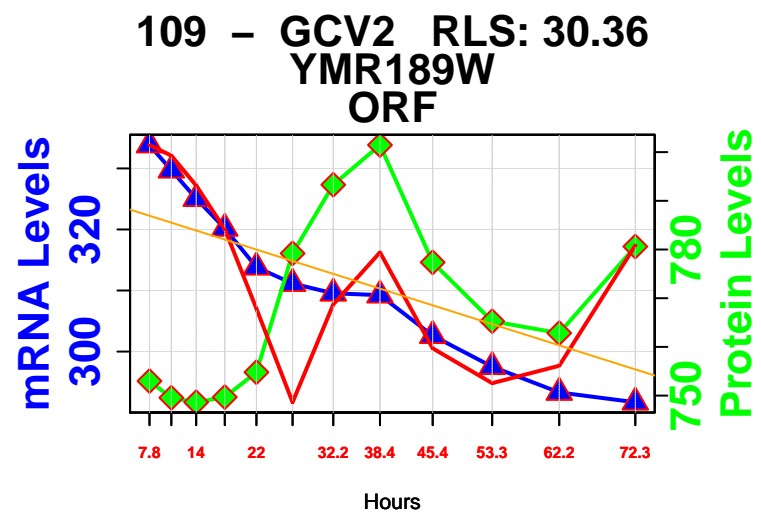
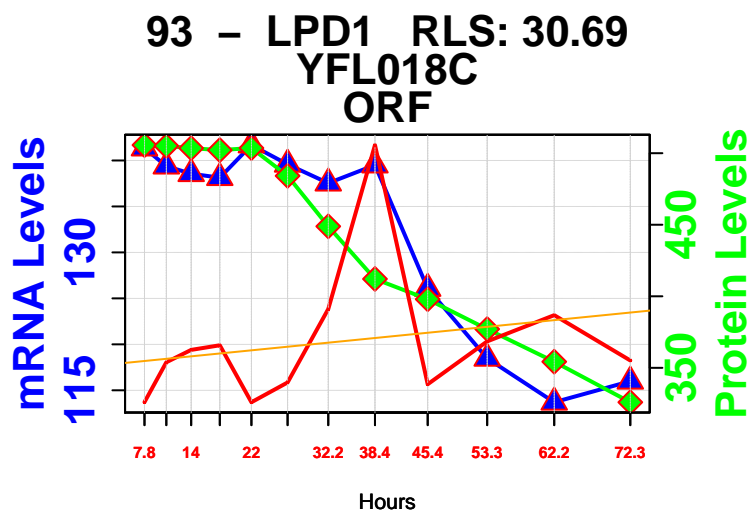
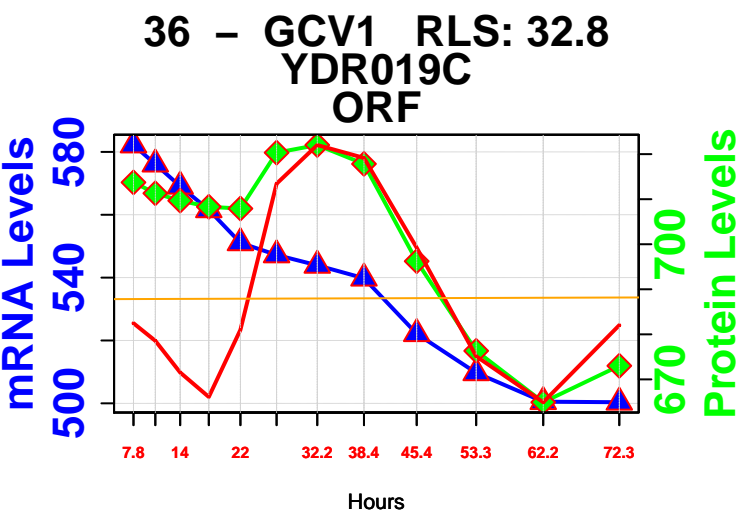
539 - MTD1 RLS: 20.2
YKR080W
ORF



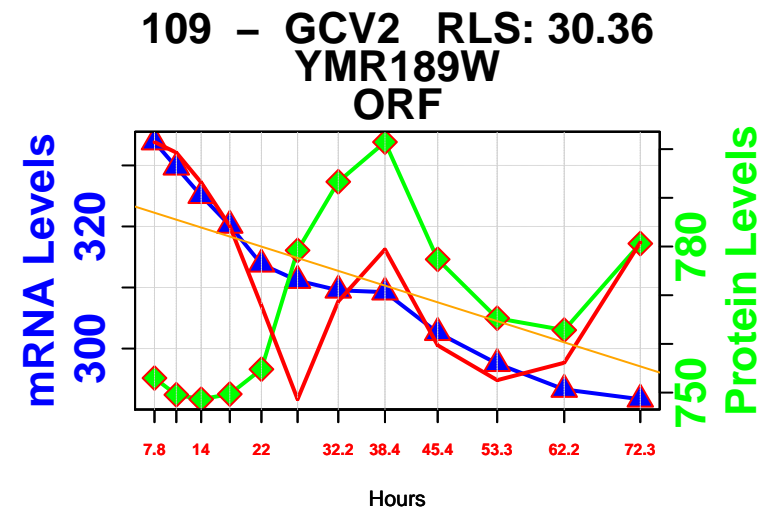
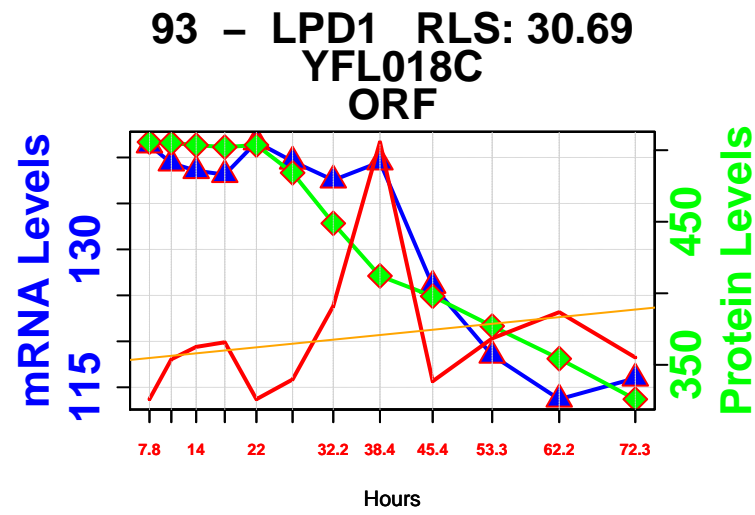
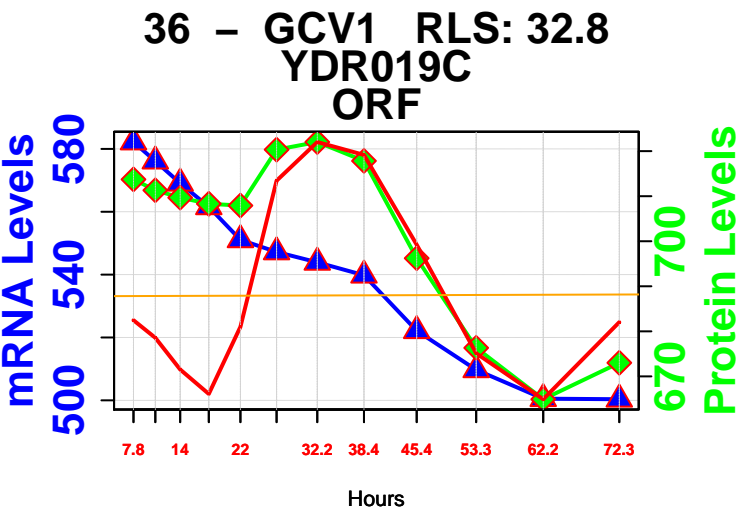
folate interconversions



folate transformations

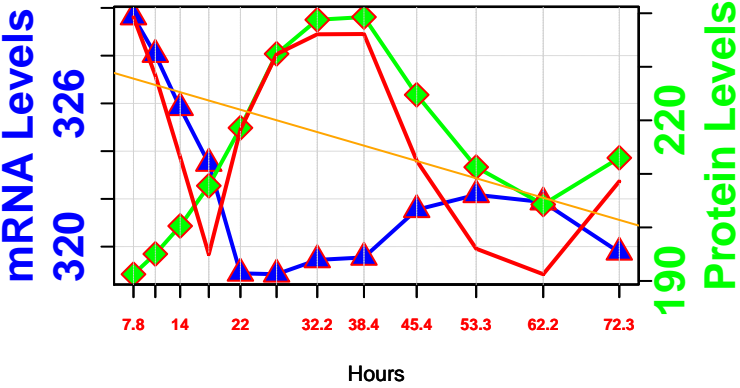


glycine cleavage complex

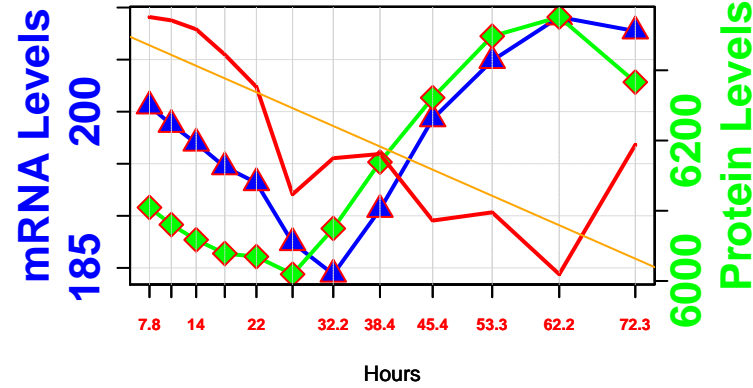


de novo biosynthesis of pyrimidine ribonucleotides

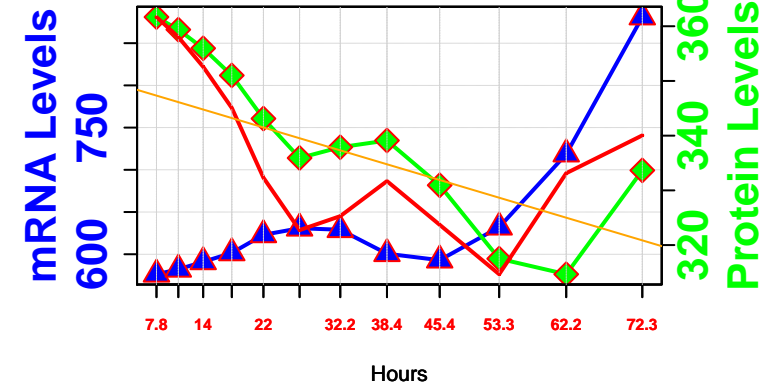
52 - URA5 RLS: 32.2
YML106W
ORF



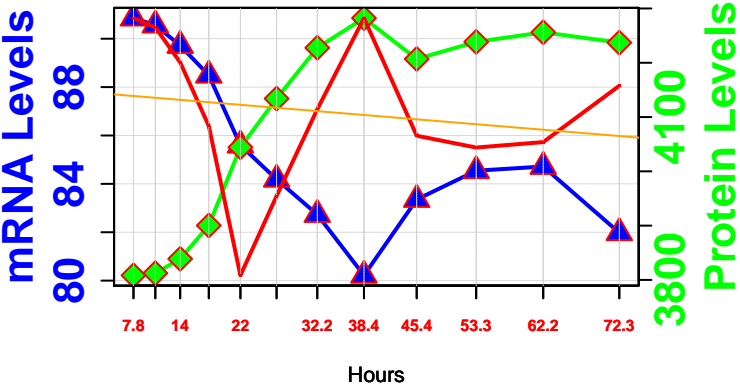
250 - CPA2 RLS: 27.16
YJR109C
ORF



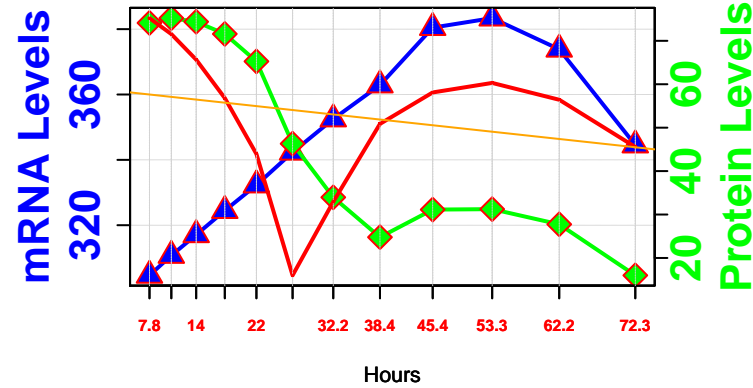
429 - CPA1 RLS: 23.2
YOR303W
ORF



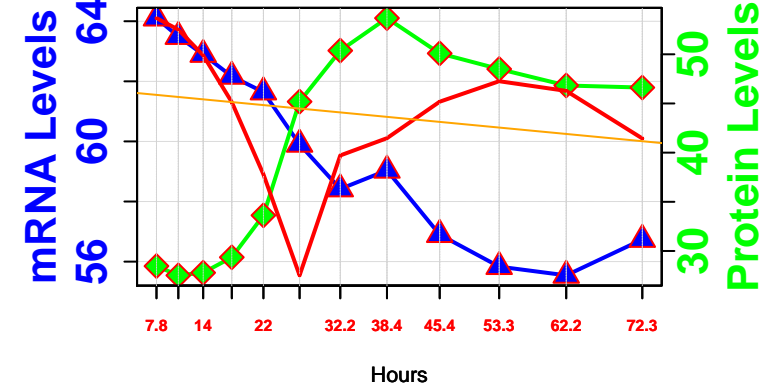
464 - URA2 RLS: 22.54
YJL130C
ORF



525 - URA1 RLS: 20.79
YKL216W
ORF

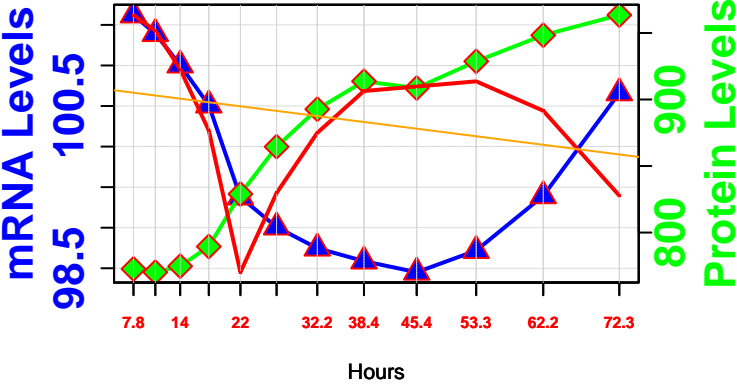


526 - URA8 RLS: 20.75
YJR103W
ORF

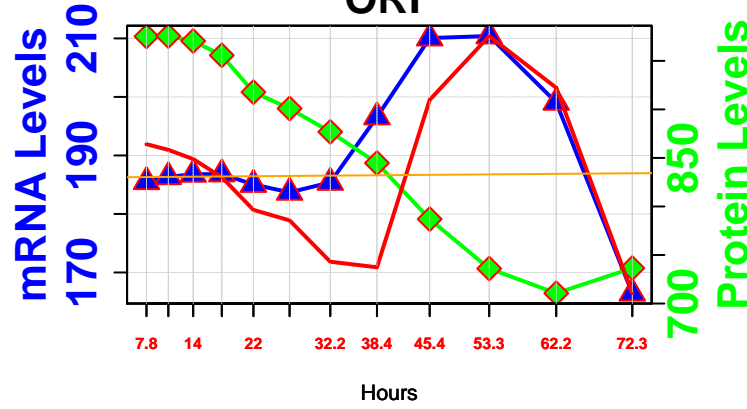


lysine biosynthesis

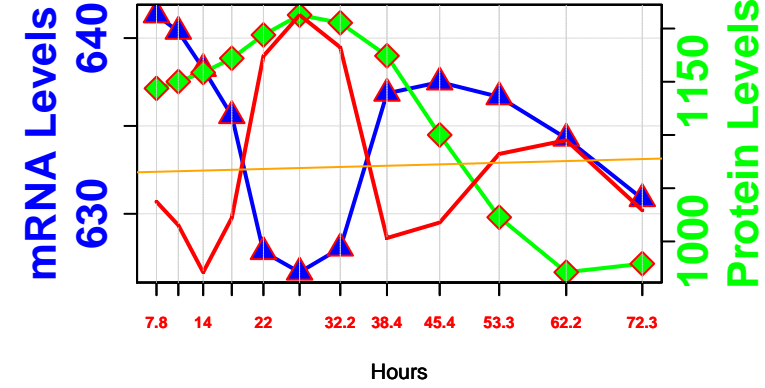
57 - LYS2 RLS: 32
YBR115C
ORF



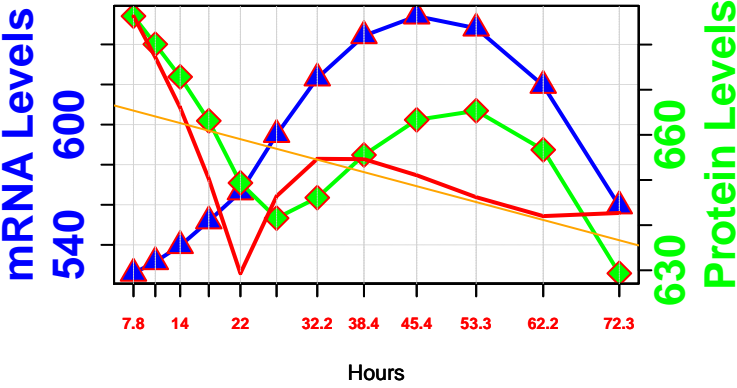
107 - LYS4 RLS: 30.39
YDR234W
ORF



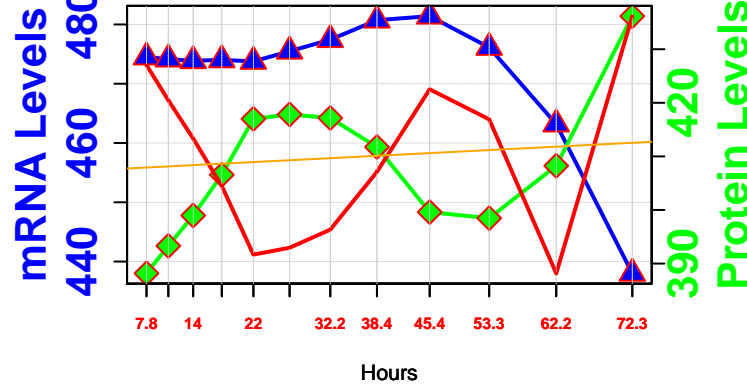
260 - LYS12 RLS: 26.91
YIL094C
ORF



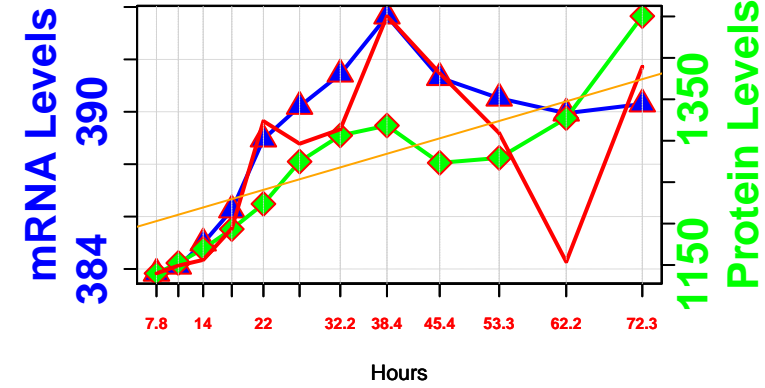
374 - LYS20 RLS: 24
YDL182W
ORF



495 - LYS21 RLS: 21.4
YDL131W
ORF

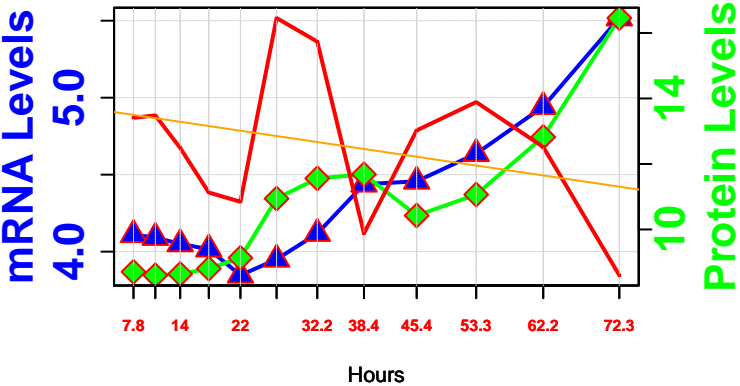


555 - LYS1 RLS: 19.6
YIR034C
ORF

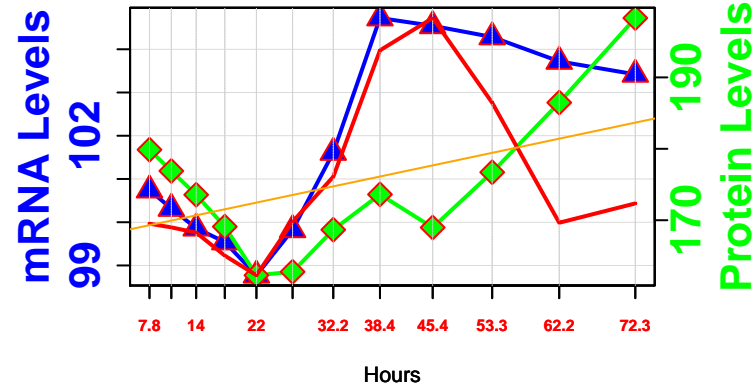


de novo biosynthesis of pyrimidine deoxyribonucleotides

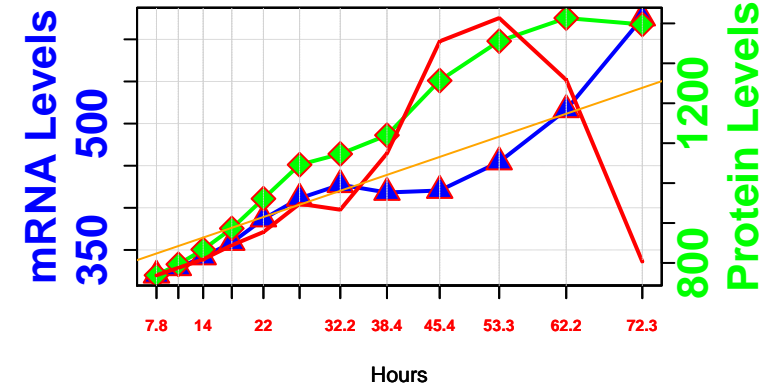
61 – RNR3 RLS: 31.97
YIL066C
ORF



372 – RNR1 RLS: 24.12
YER070W
ORF

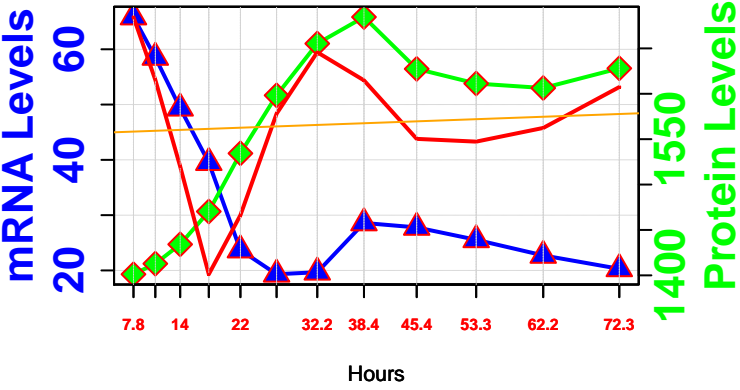


667 – RNR4 RLS: 6.2
YGR180C
ORF

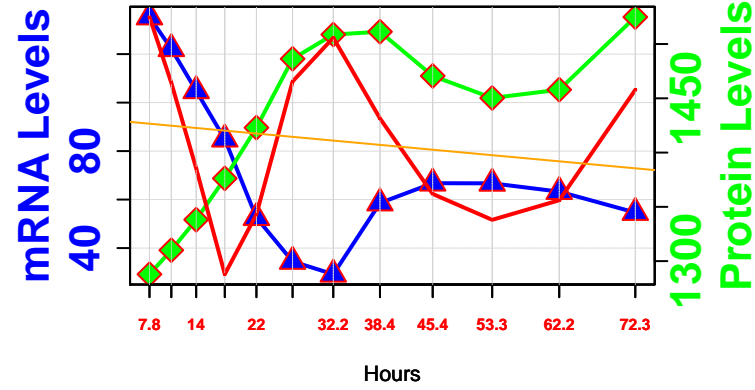


sulfate assimilation pathway

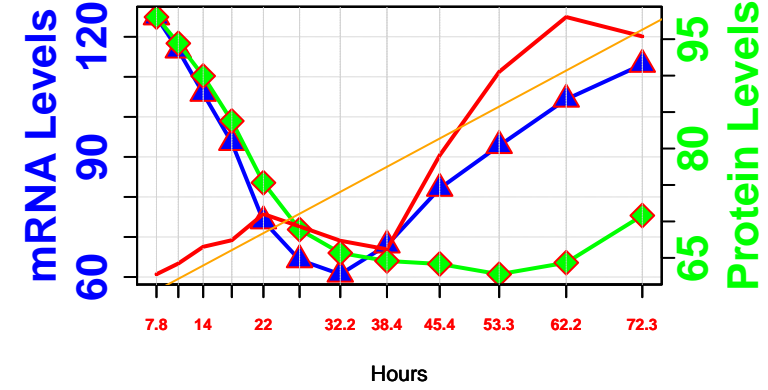
68 – MET10 RLS: 31.58
YFR030W
ORF



71 – MET3 RLS: 31.51
YJR010W
ORF

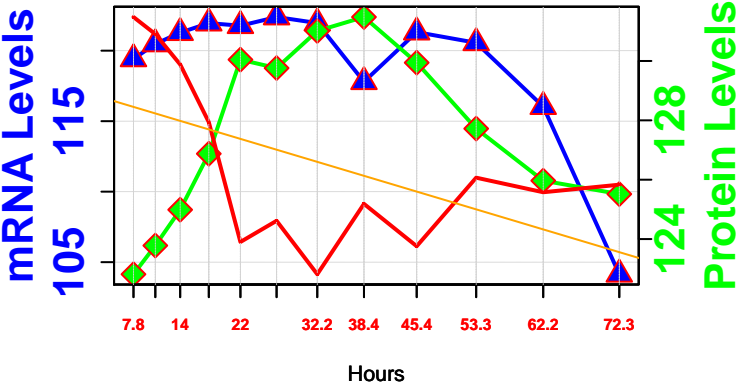


126 – MET16 RLS: 29.74
YPR167C
ORF

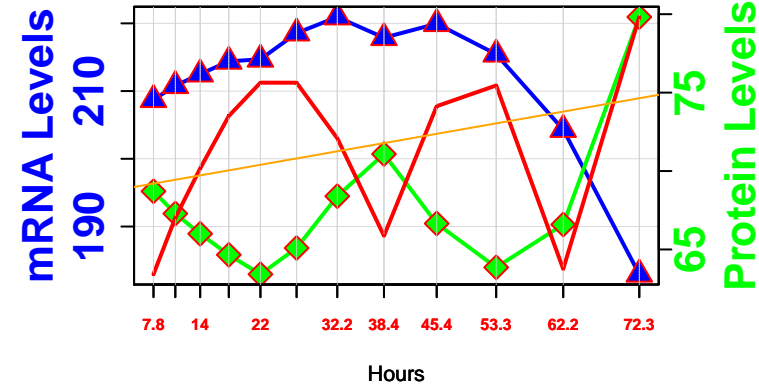


superpathway of histidine, purine, and pyrimidine biosynthesis

76 – PRS5 RLS: 31.4
YOL061W
ORF

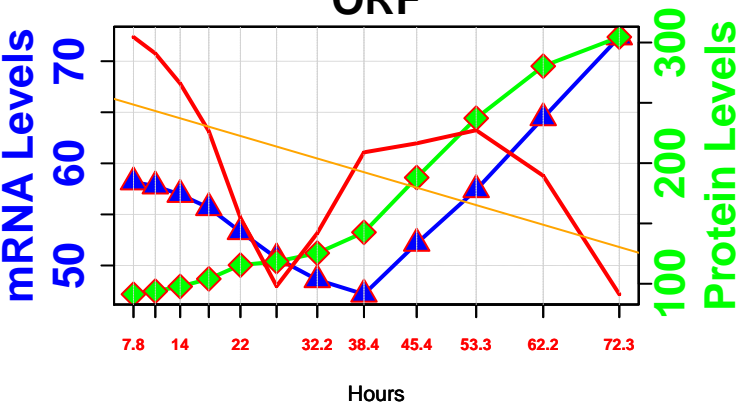


189 – PRS3 RLS: 28.2
YHL011C
ORF

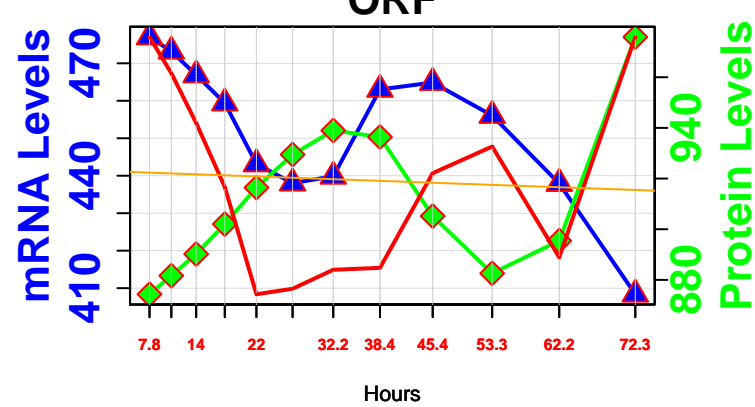


ethanol degradation

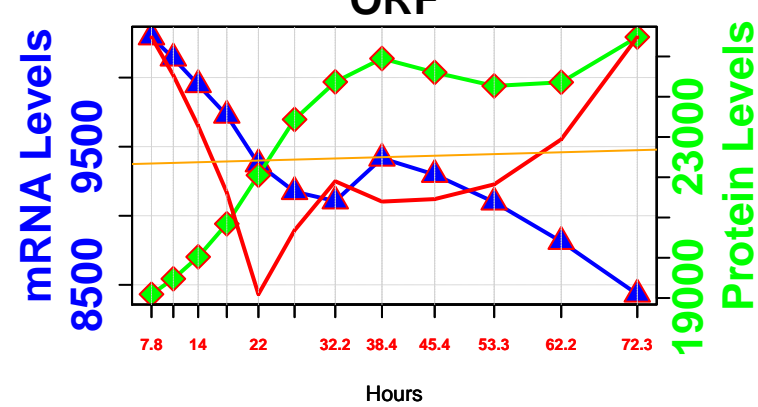
78 – ADH4 RLS: 31.34
YGL256W
ORF



296 – ADH3 RLS: 25.94
YMR083W
ORF

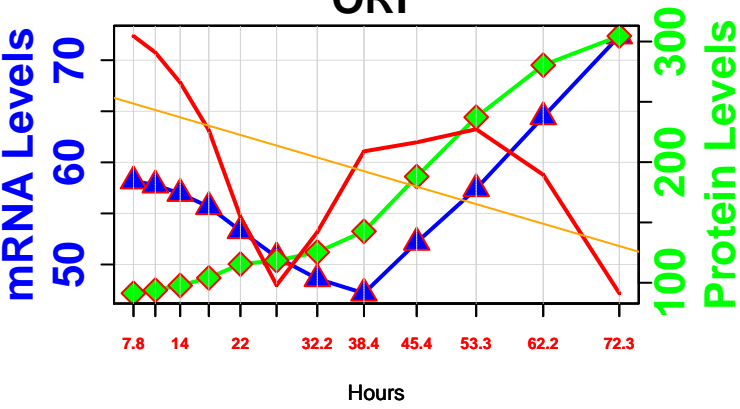


660 – ADH1 RLS: 7.83
YOL086C
ORF

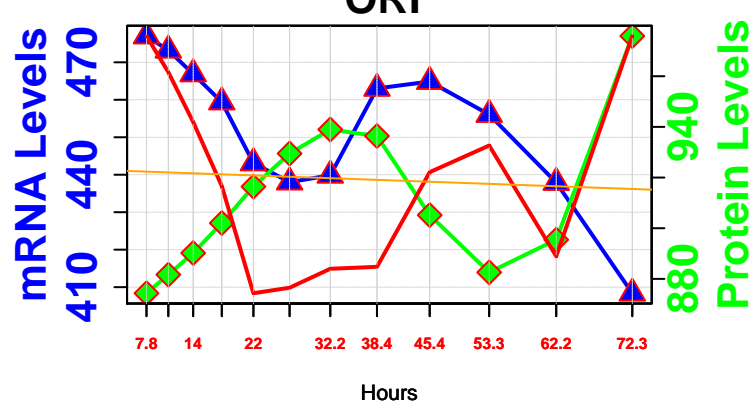


isoleucine degradation

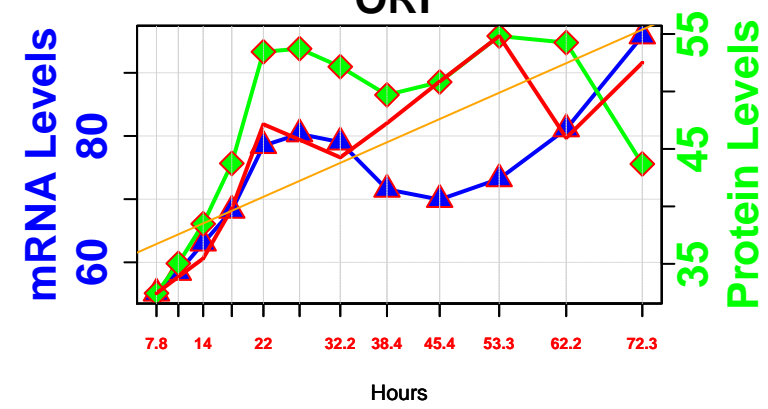
78 – ADH4 RLS: 31.34
YGL256W
ORF



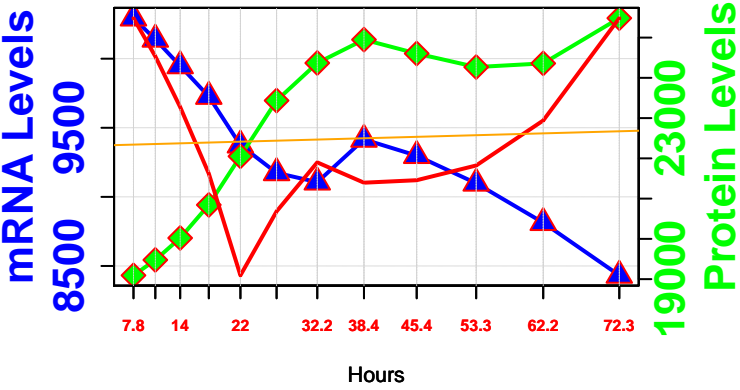
296 – ADH3 RLS: 25.94
YMR083W
ORF



302 – SFA1 RLS: 25.8
YDL168W
ORF

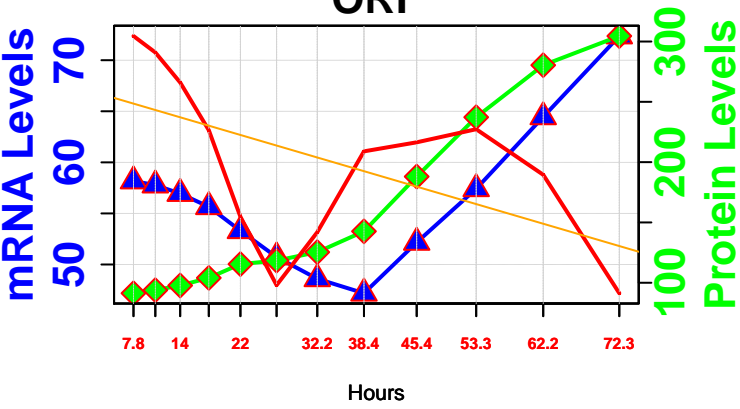


660 – ADH1 RLS: 7.83
YOL086C
ORF

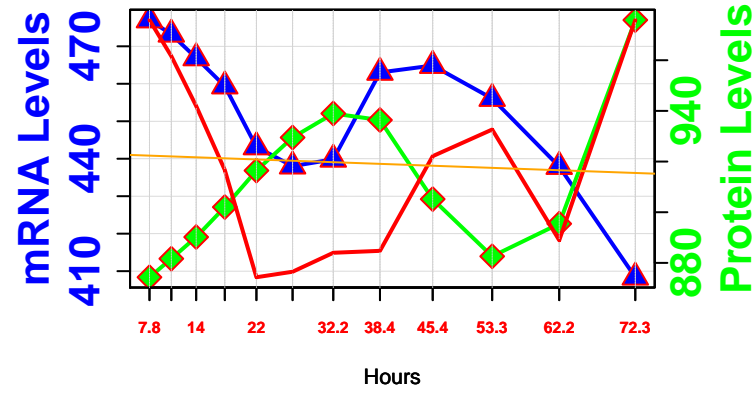


leucine degradation

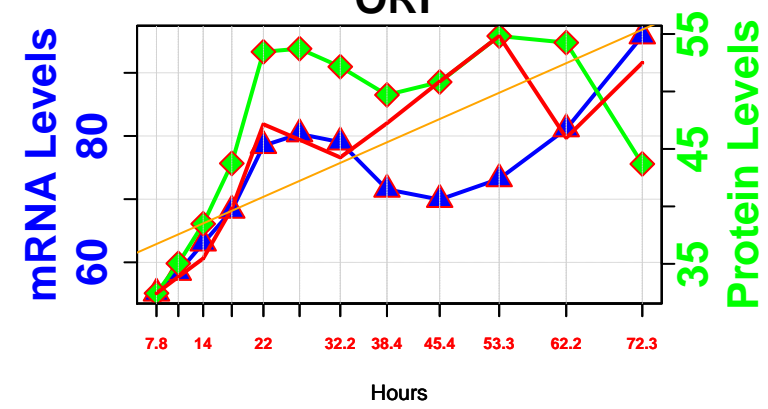
78 – ADH4 RLS: 31.34
YGL256W
ORF



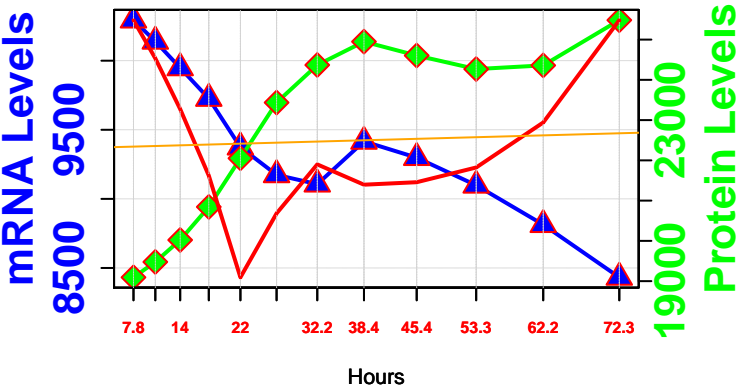
296 – ADH3 RLS: 25.94
YMR083W
ORF



302 – SFA1 RLS: 25.8
YDL168W
ORF

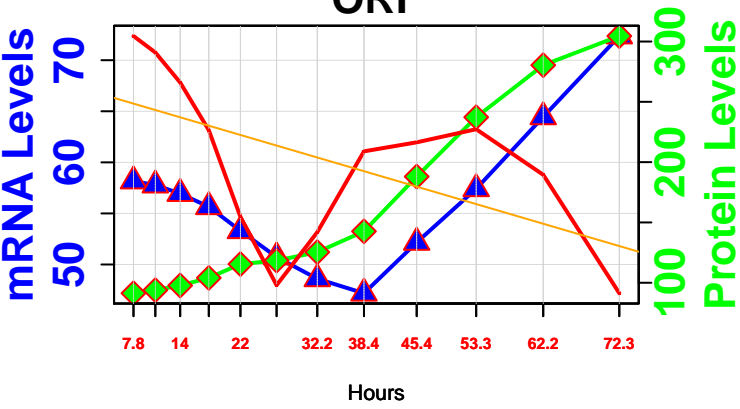


660 – ADH1 RLS: 7.83
YOL086C
ORF

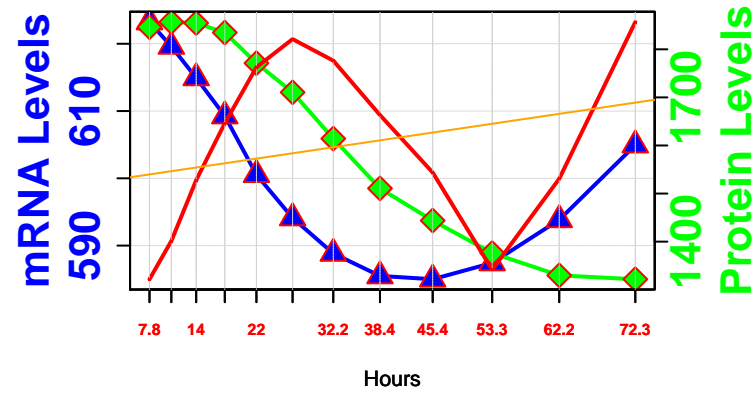


phenylalanine degradation

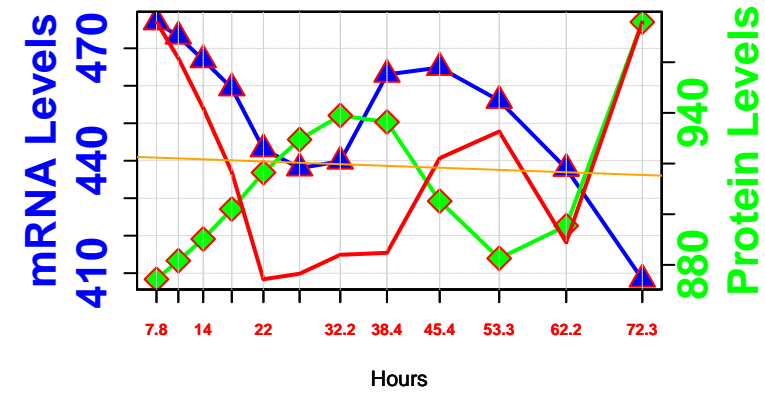
78 – ADH4 RLS: 31.34
YGL256W
ORF



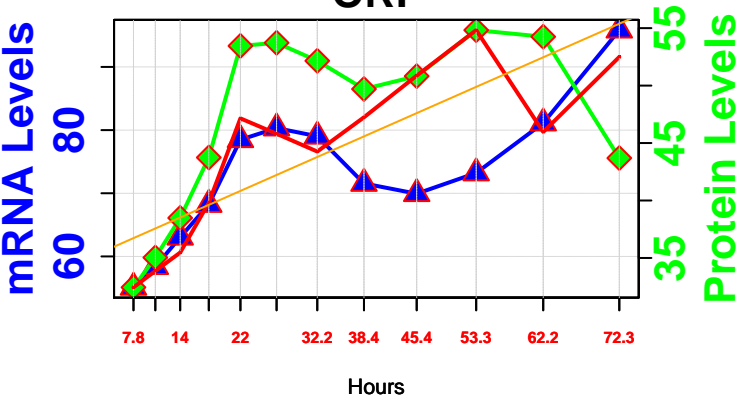
206 – ARO8 RLS: 27.94
YGL202W
ORF



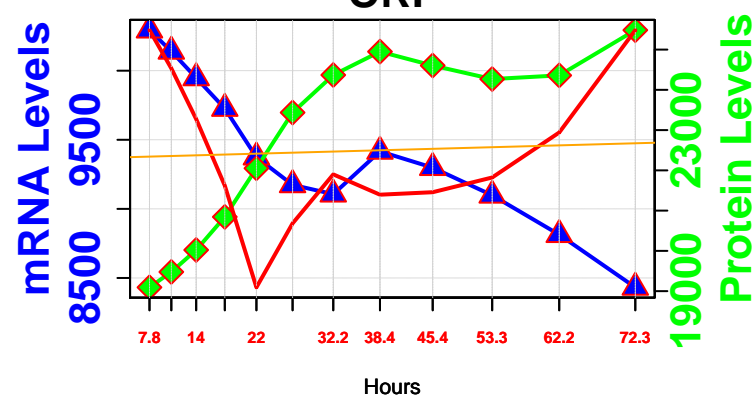
296 – ADH3 RLS: 25.94
YMR083W
ORF



302 – SFA1 RLS: 25.8
YDL168W
ORF

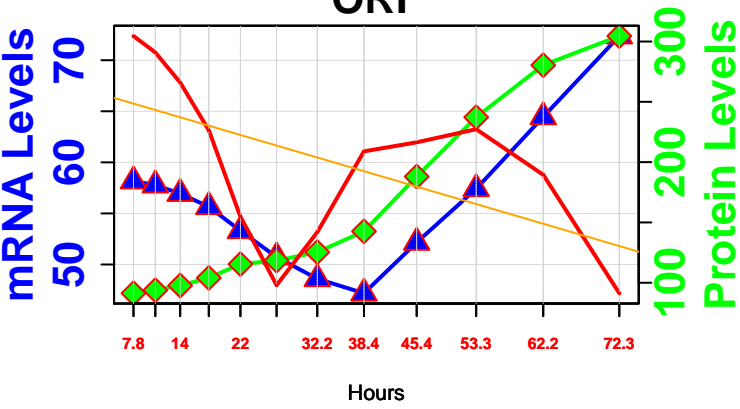


660 – ADH1 RLS: 7.83
YOL086C
ORF

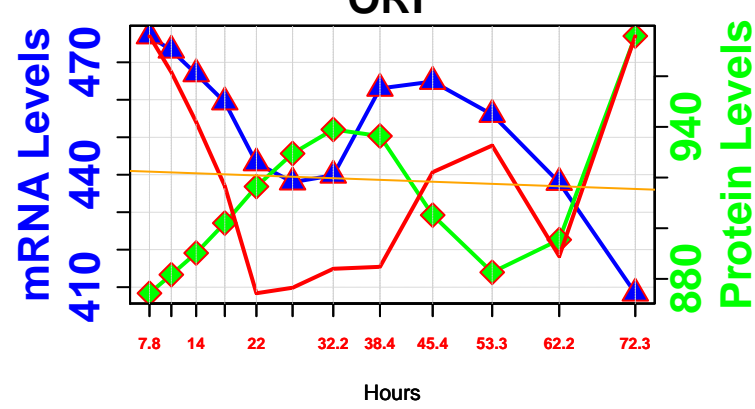


superpathway of glucose fermentation

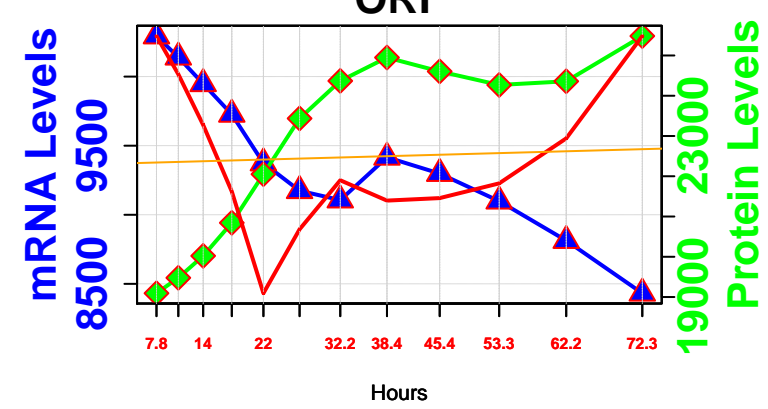
78 – ADH4 RLS: 31.34
YGL256W
ORF



296 – ADH3 RLS: 25.94
YMR083W
ORF

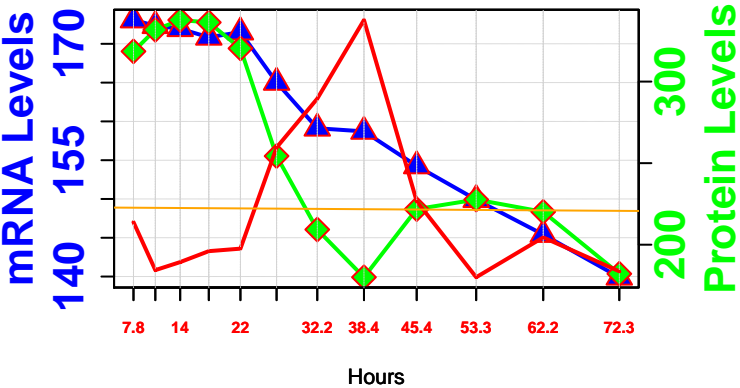


660 – ADH1 RLS: 7.83
YOL086C
ORF

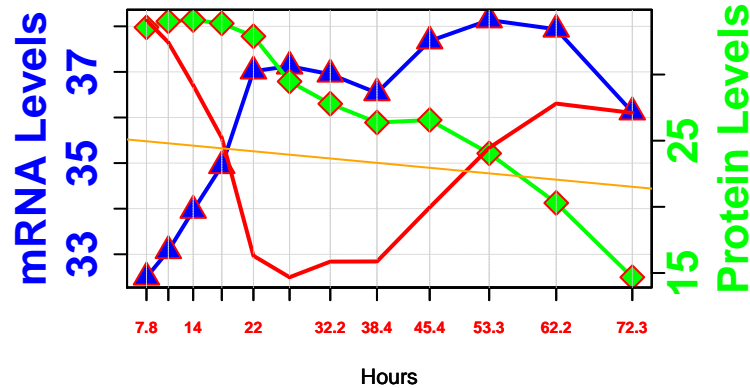


tryptophan degradation

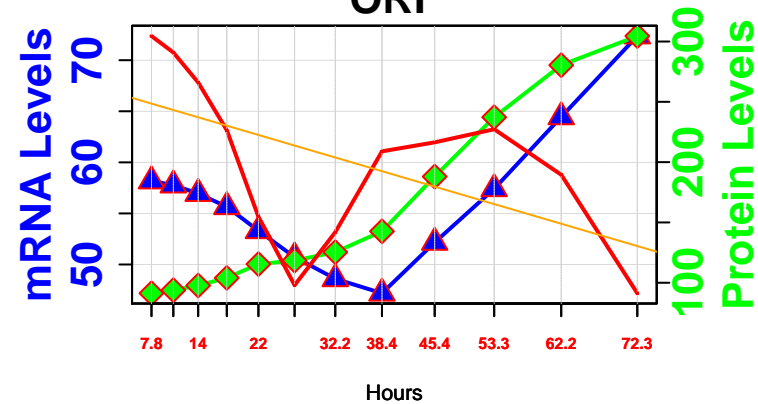
33 – BNA1 RLS: 33
YJR025C
ORF



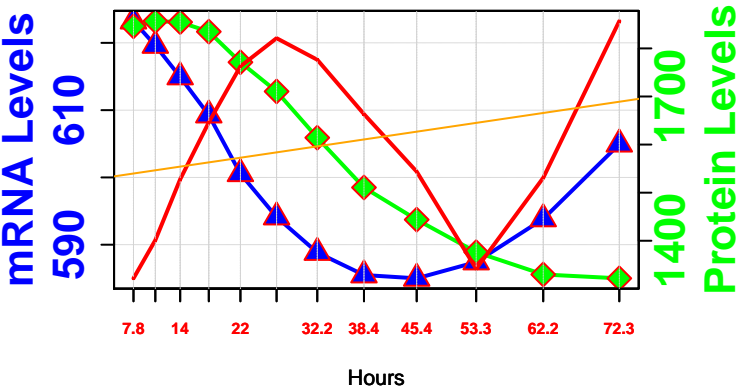
39 – BNA4 RLS: 32.6
YBL098W
ORF



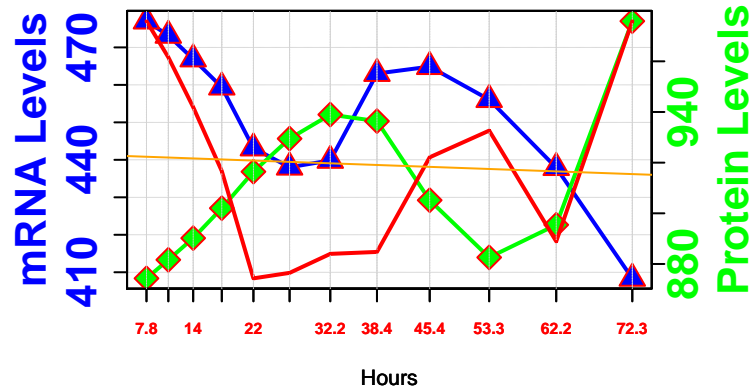
78 – ADH4 RLS: 31.34
YGL256W
ORF



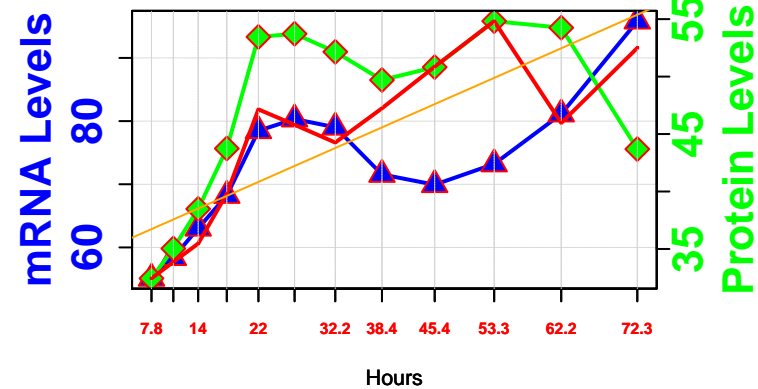
206 – ARO8 RLS: 27.94
YGL202W
ORF



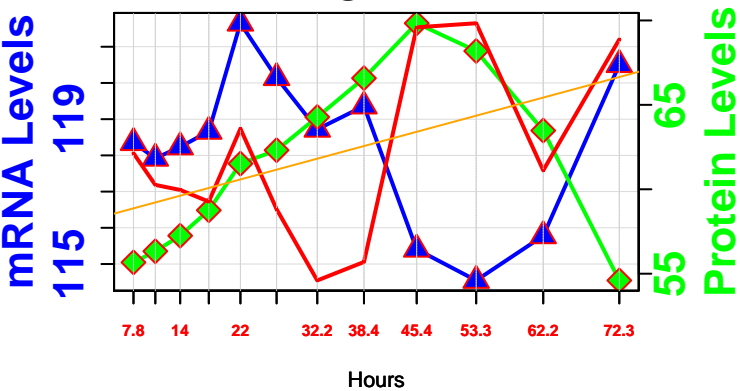
296 – ADH3 RLS: 25.94
YMR083W
ORF



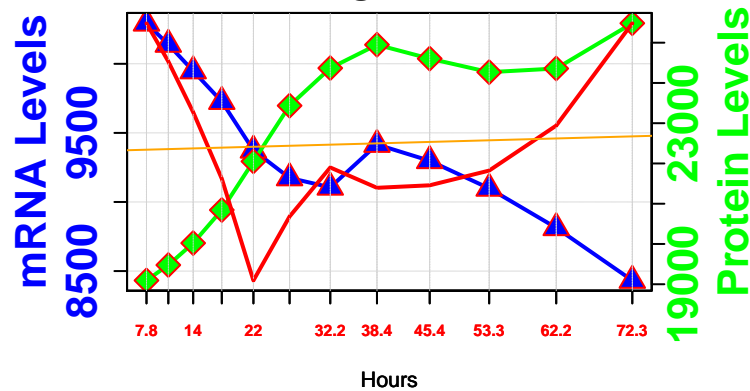
302 – SFA1 RLS: 25.8
YDL168W
ORF



415 – BNA6 RLS: 23.4
YFR047C
ORF

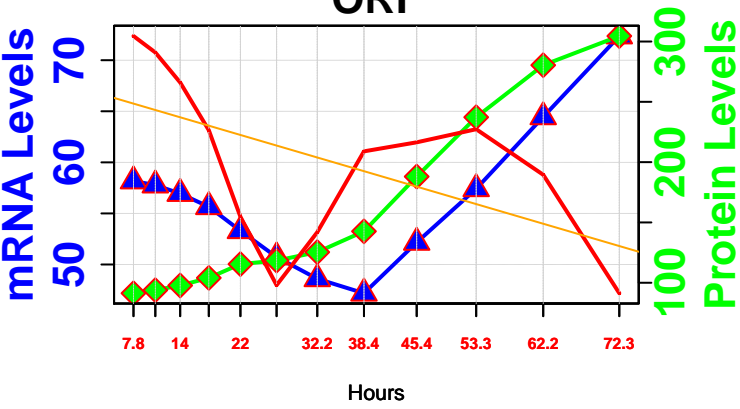


660 – ADH1 RLS: 7.83
YOL086C
ORF

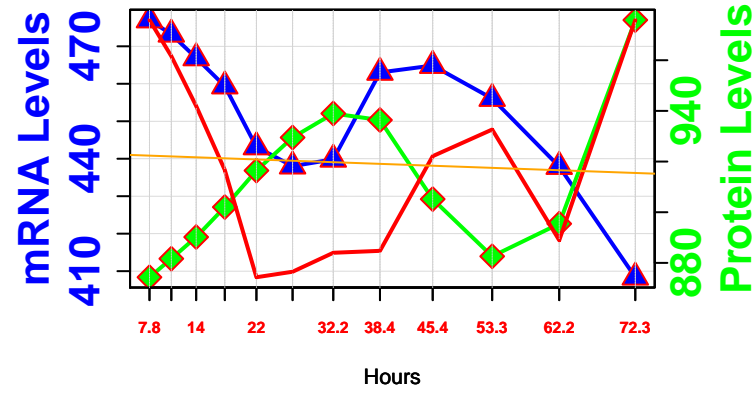


valine degradation

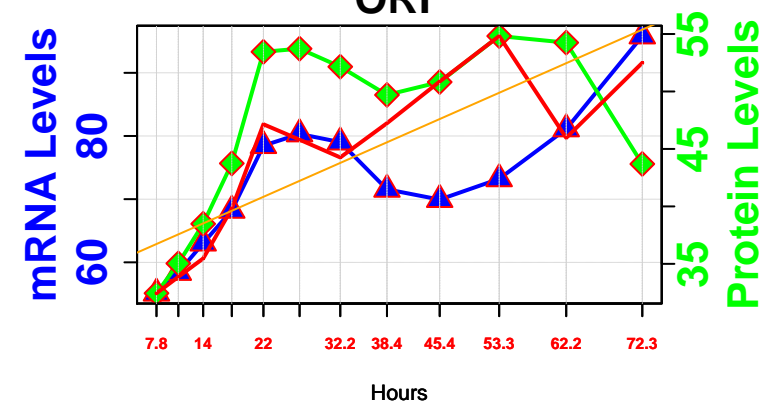
78 – ADH4 RLS: 31.34
YGL256W
ORF



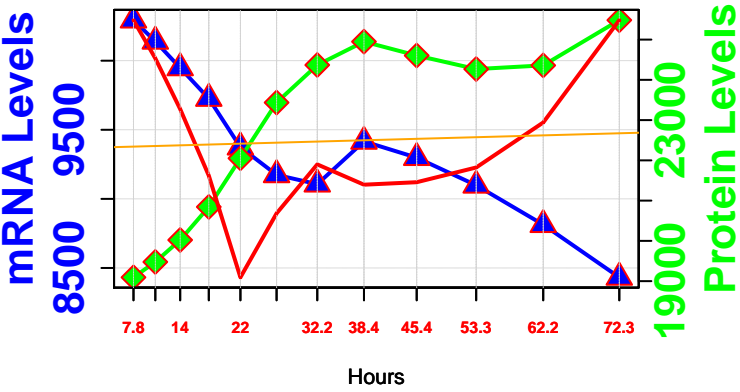
296 – ADH3 RLS: 25.94
YMR083W
ORF



302 – SFA1 RLS: 25.8
YDL168W
ORF

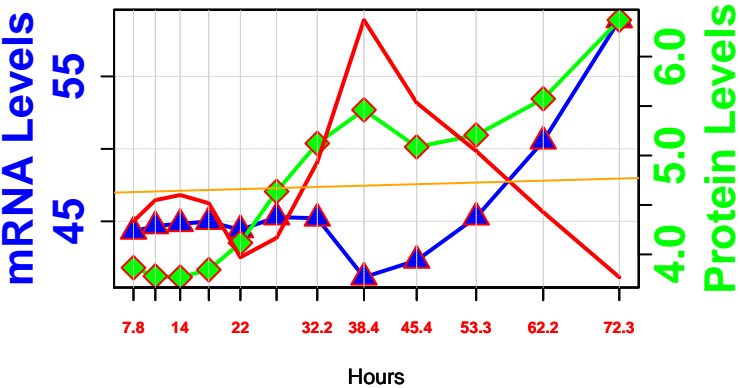


660 – ADH1 RLS: 7.83
YOL086C
ORF

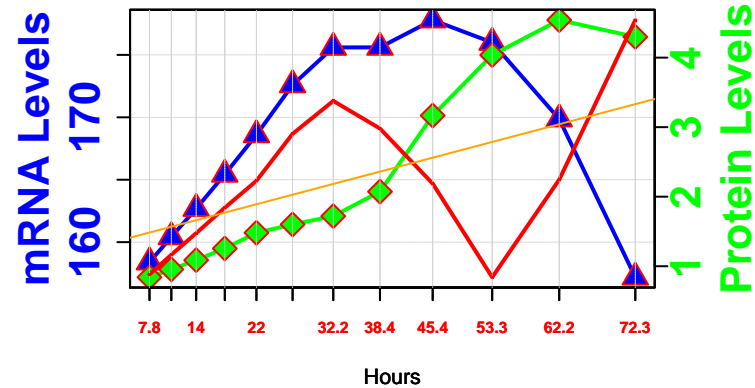


diphthamide biosynthesis

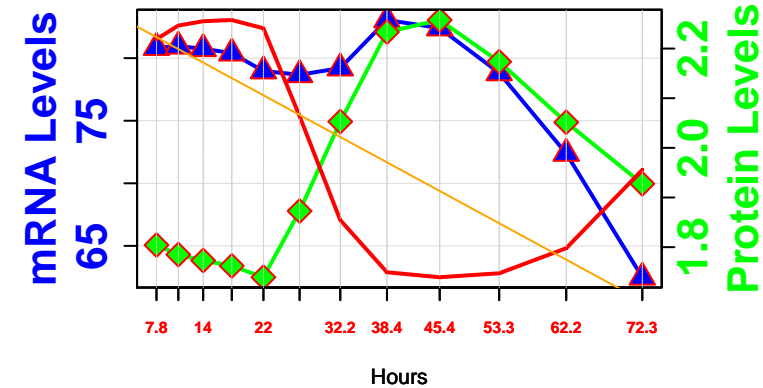
85 – DPH1 RLS: 31
YIL103W
ORF



498 – DPH5 RLS: 21.4
YLR172C
ORF

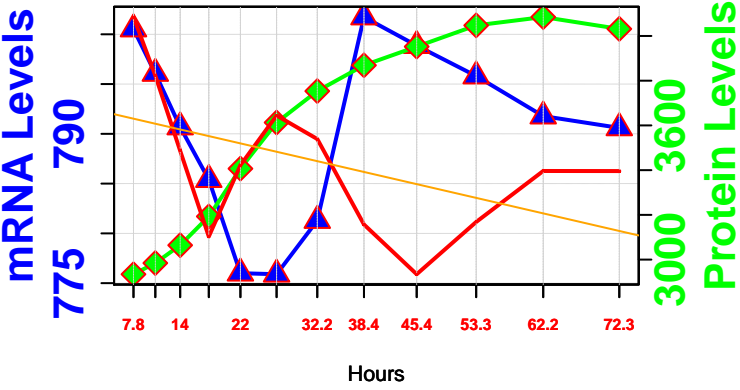


609 – DPH2 RLS: 17
YKL191W
ORF

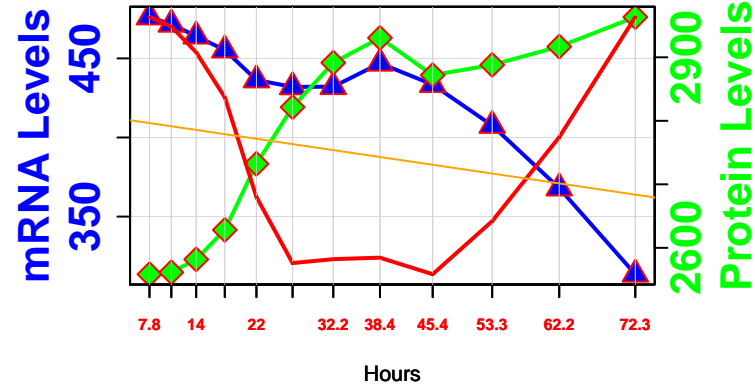


oxidative branch of the pentose phosphate pathway

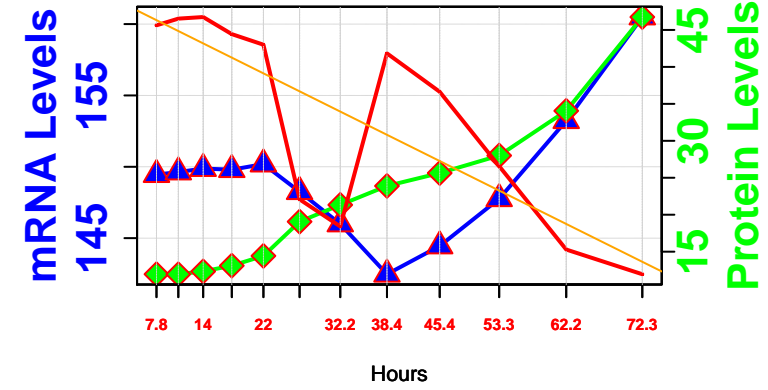
86 – GND1 RLS: 30.92
YHR183W
ORF



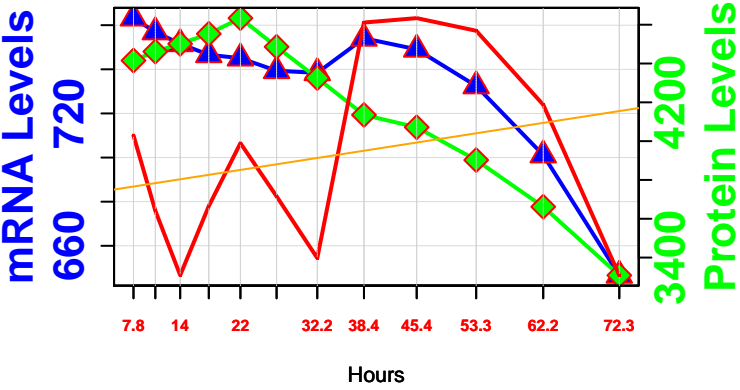
92 – TKL1 RLS: 30.76
YPR074C
ORF



156 – RPE1 RLS: 28.84
YJL121C
ORF

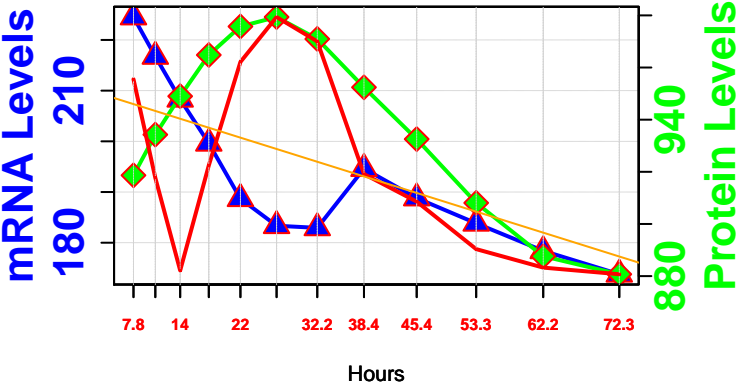


281 – TAL1 RLS: 26.34
YLR354C
ORF

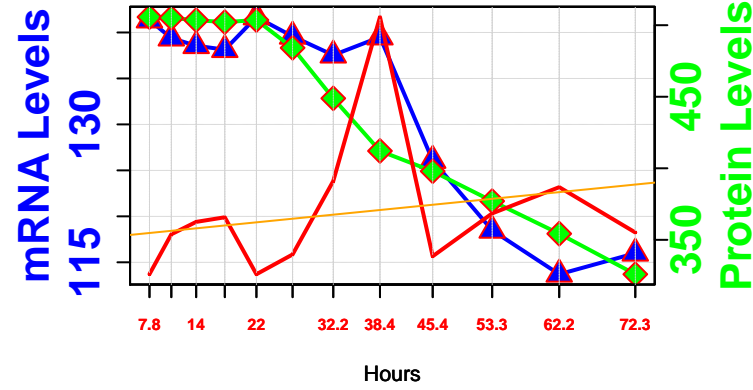


TCA cycle, aerobic respiration

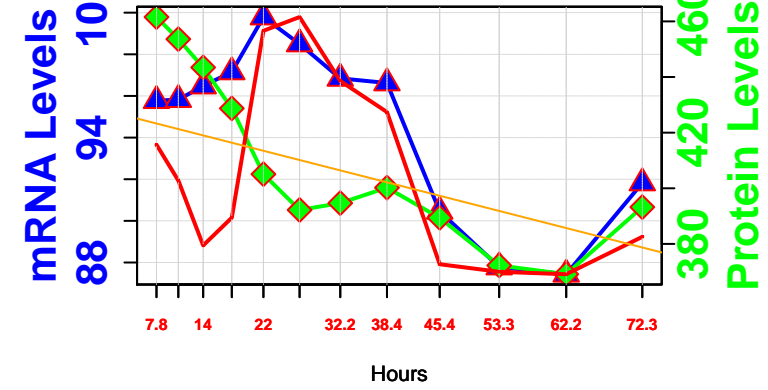
87 – IDH2 RLS: 30.84
YOR136W
ORF



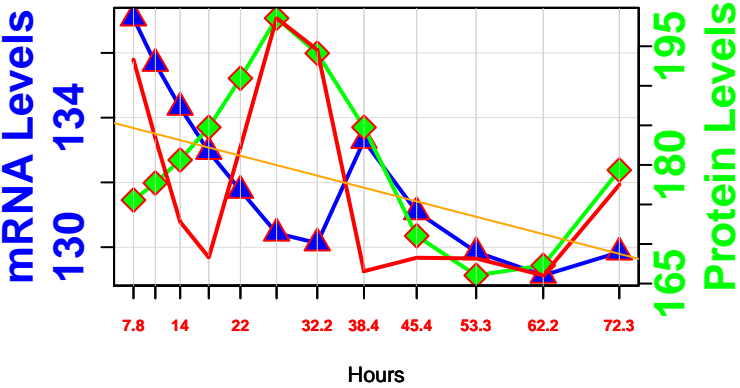
93 – LPD1 RLS: 30.69
YFL018C
ORF



111 – FUM1 RLS: 30.28
YPL262W
ORF

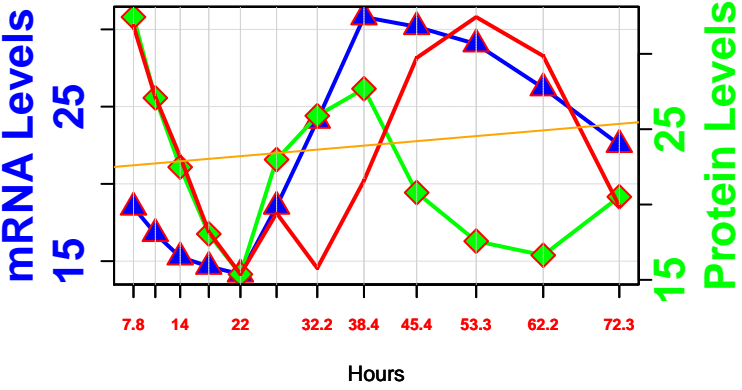


264 – PYC2 RLS: 26.75
YBR218C
ORF

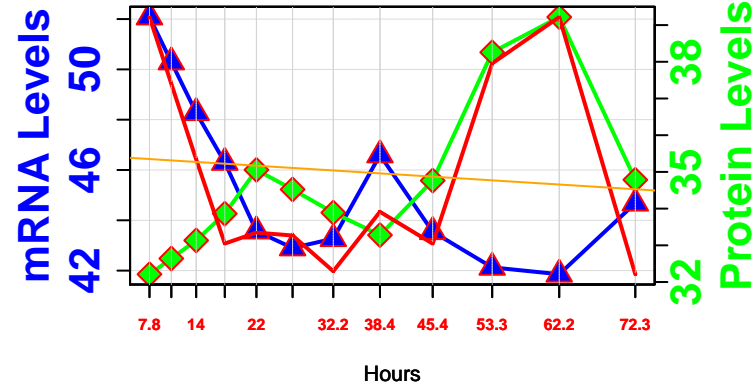


glutathione biosynthesis

88 – GSH1 RLS: 30.83
YJL101C
ORF

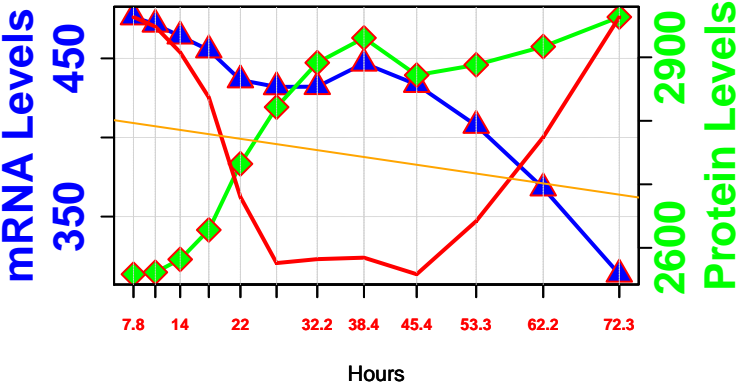


344 – GSH2 RLS: 24.87
YOL049W
ORF

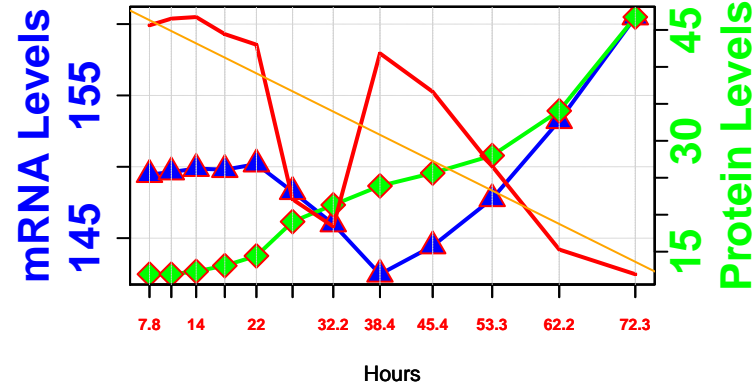


non-oxidative branch of the pentose phosphate pathway

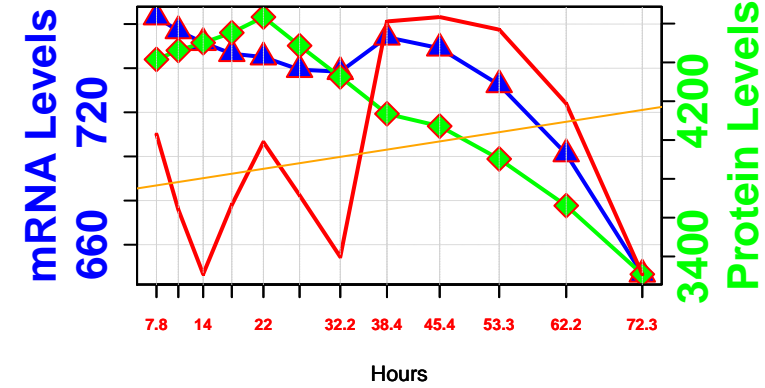
92 - TKL1 RLS: 30.76
YPR074C
ORF



156 - RPE1 RLS: 28.84
YJL121C
ORF

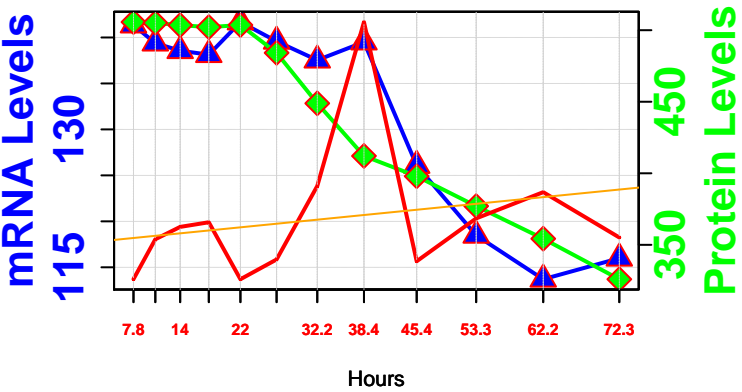


281 - TAL1 RLS: 26.34
YLR354C
ORF



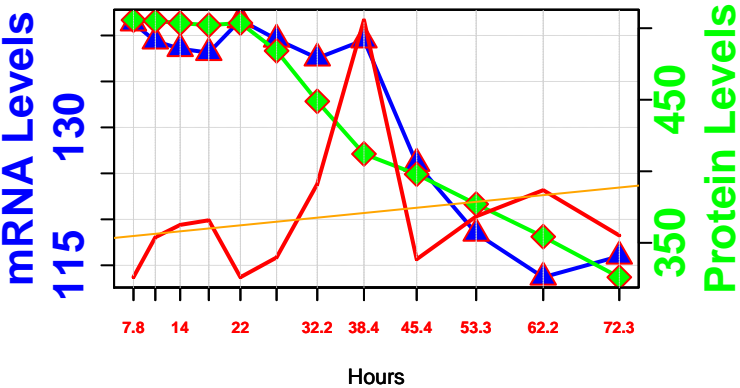
2-ketoglutarate dehydrogenase complex

93 - LPD1 RLS: 30.69
YFL018C
ORF

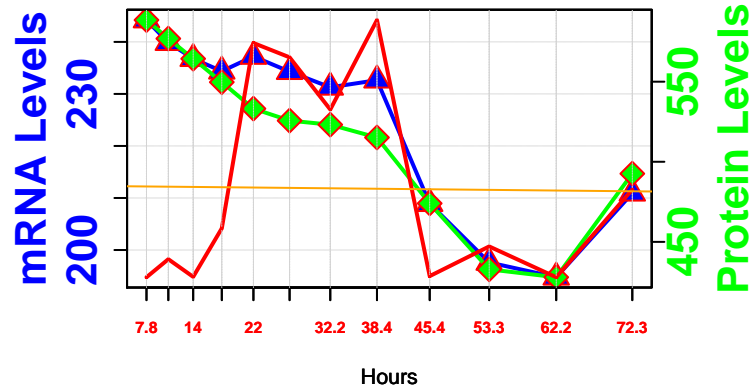


arginate dehydratase (serine)

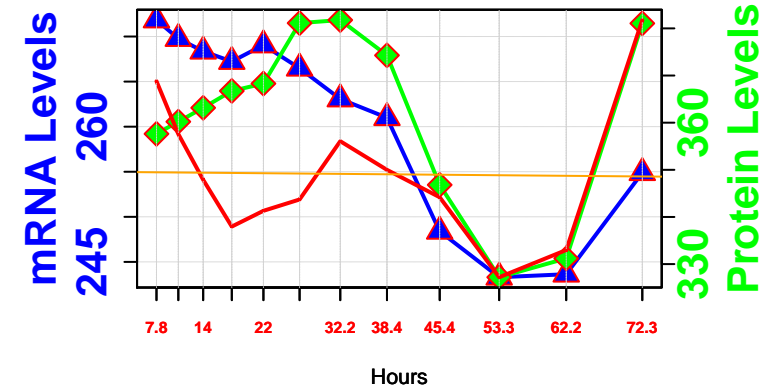
93 - LPD1 RLS: 30.69
YFL018C
ORF



613 - PDA1 RLS: 16.71
YER178W
ORF

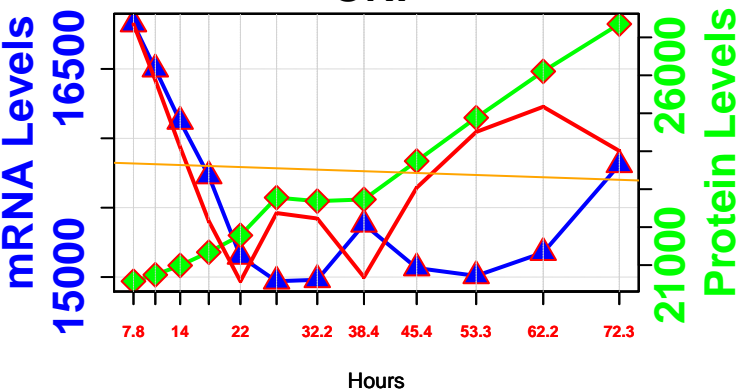


644 - PDB1 RLS: 12.77
YBR221C
ORF

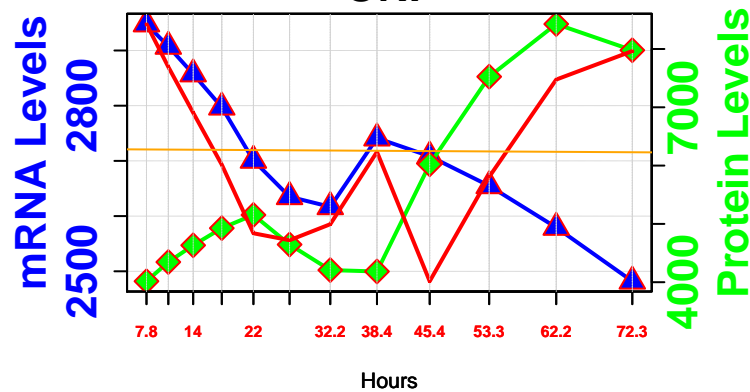


gluconeogenesis

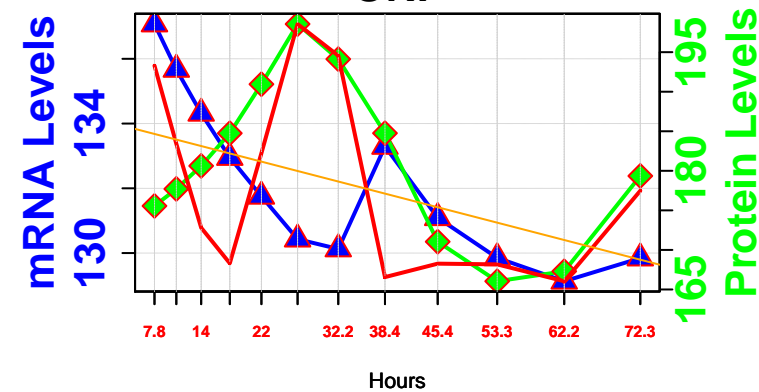
98 – TDH3 RLS: 30.57
YGR192C
ORF



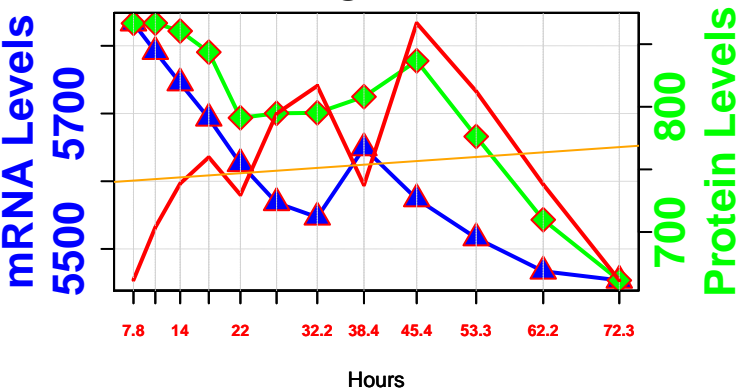
255 – ENO1 RLS: 27.04
YGR254W
ORF



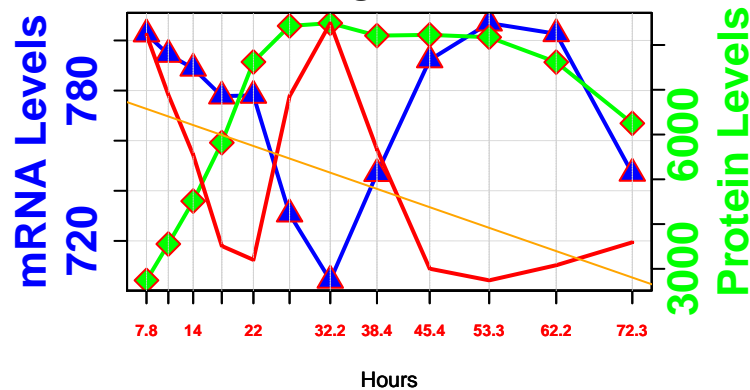
264 – PYC2 RLS: 26.75
YBR218C
ORF



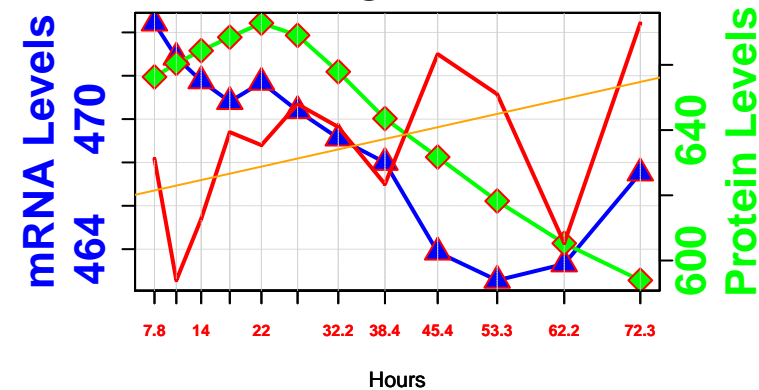
267 – TDH2 RLS: 26.69
YJR009C
ORF



352 – TDH1 RLS: 24.6
YJL052W
ORF

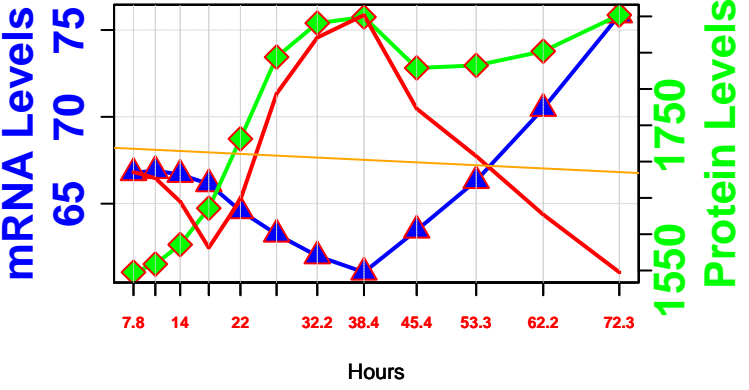


469 – MAE1 RLS: 22.31
YKL029C
ORF



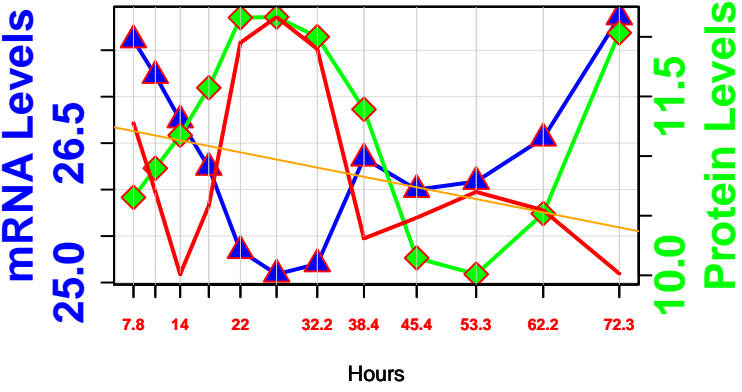
phosphatite biosynthesis (Kennedy pathway)

114 - GLT1 RLS: 30.25
YDL171C
ORF



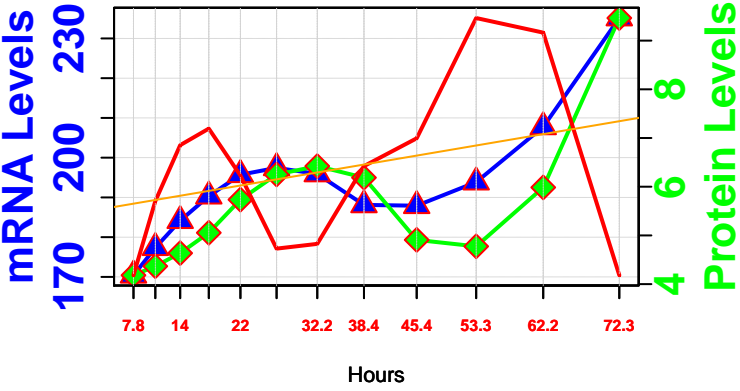
lipid-linked oligosaccharide biosynthesis

120 – ALG12 RLS: 30.03
YNR030W
ORF

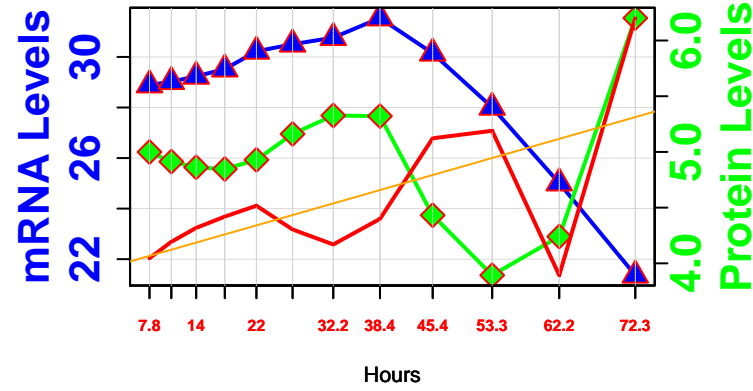


sphingolipid metabolism

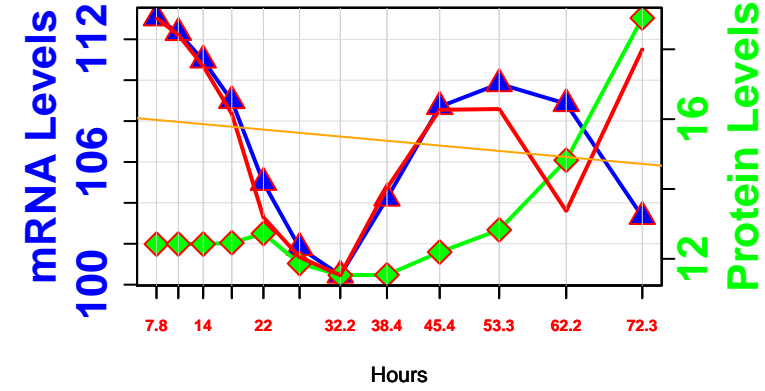
124 – SUR2 RLS: 29.8
YDR297W
ORF



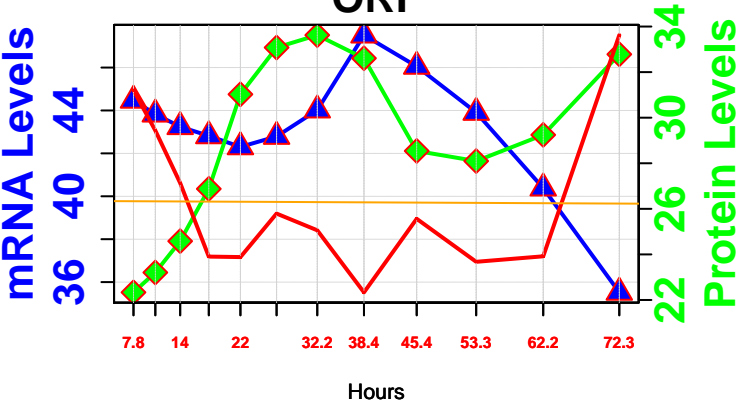
147 – LCB4 RLS: 29.14
YOR171C
ORF



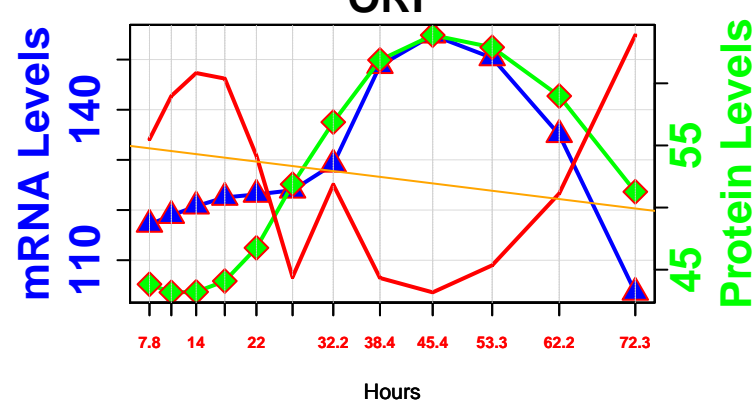
175 – LAC1 RLS: 28.42
YKL008C
ORF



465 – DPL1 RLS: 22.52
YDR294C
ORF

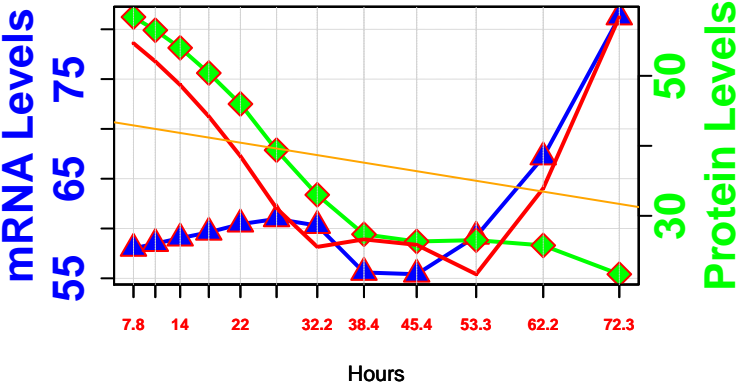


591 – SCS7 RLS: 18.2
YMR272C
ORF

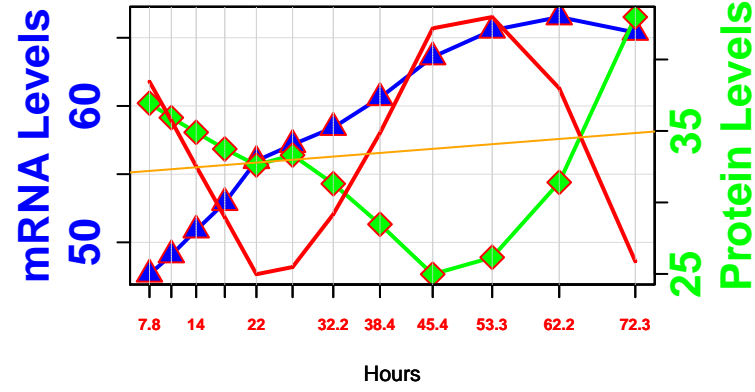


allantoin degradation

152 – DAL3 RLS: 29
YIR032C
ORF

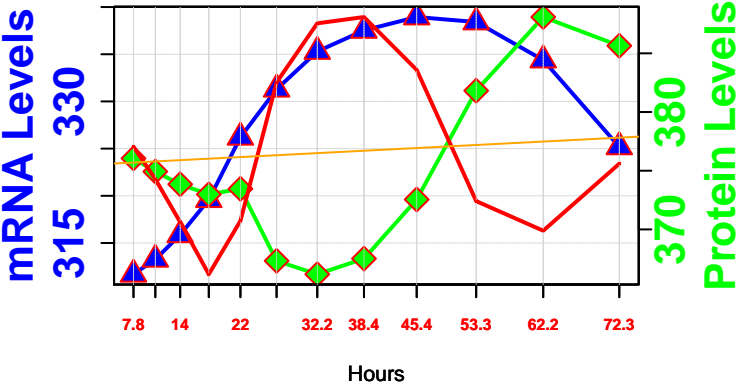


270 – DAL2 RLS: 26.6
YIR029W
ORF

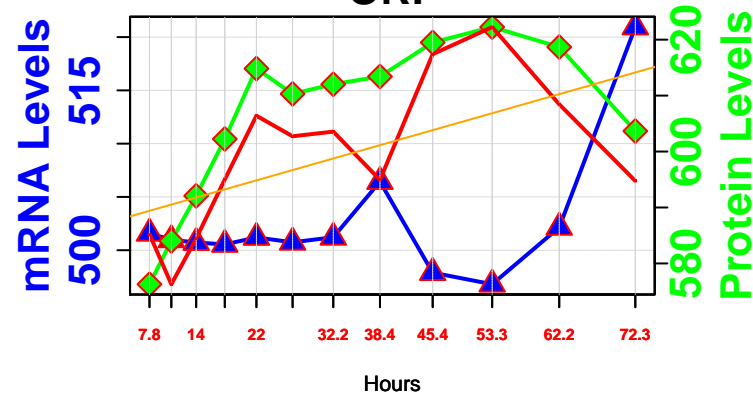


asparagine biosynthesis

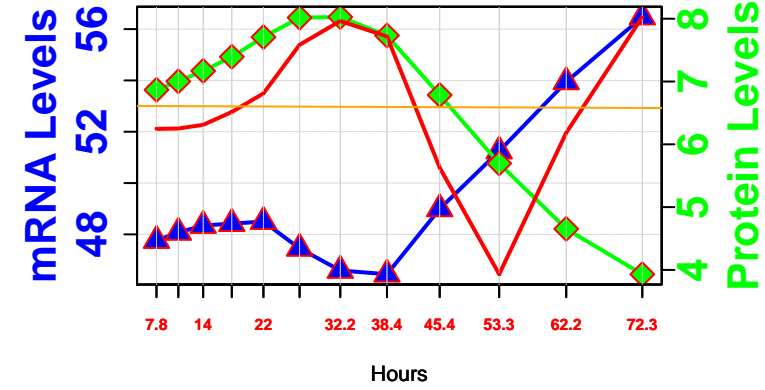
158 – ASN2 RLS: 28.8
YGR124W
ORF



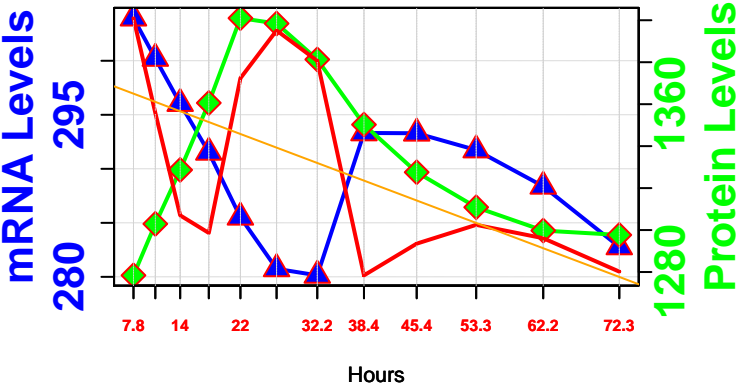
164 – ASN1 RLS: 28.69
YPR145W
ORF



283 – AAT1 RLS: 26.21
YKL106W
ORF

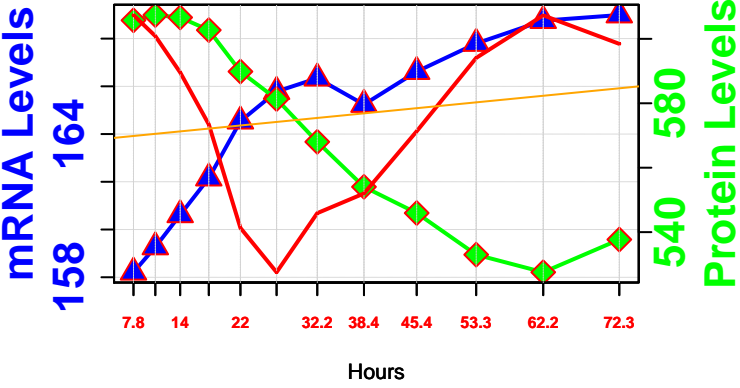


401 – AAT2 RLS: 23.6
YLR027C
ORF

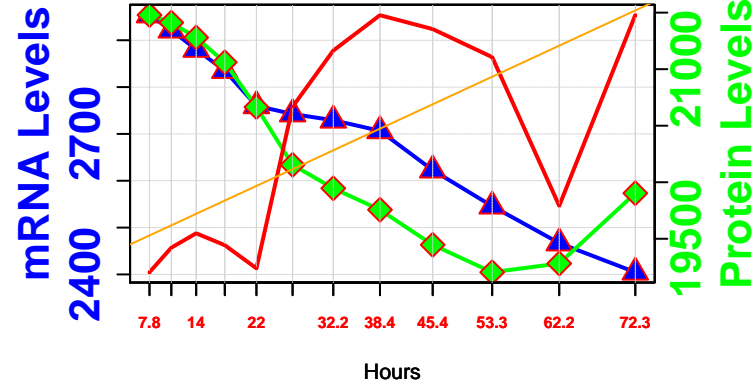


folate polyglutamylation

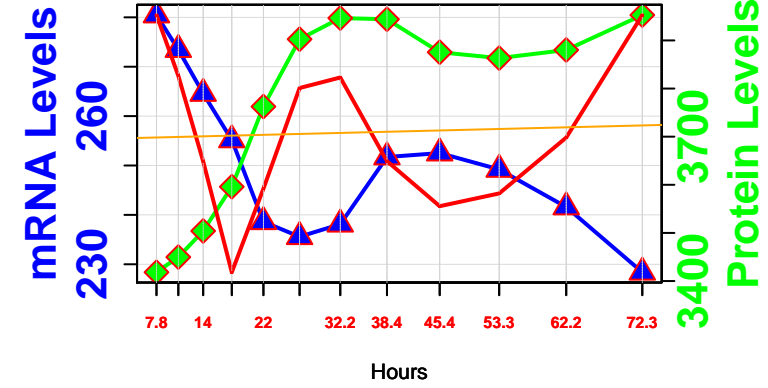
170 - SHM1 RLS: 28.53
YBR263W
ORF



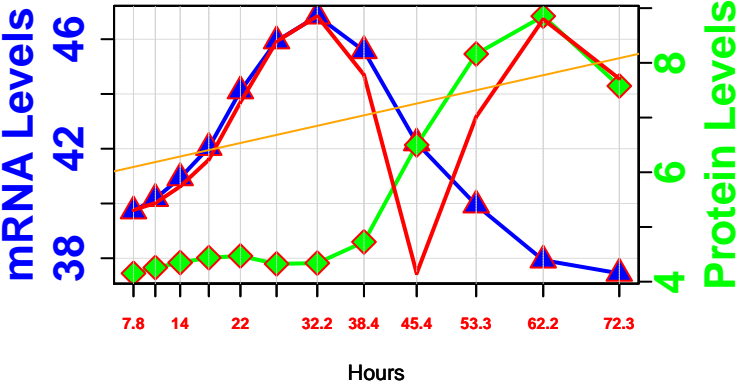
182 - SHM2 RLS: 28.28
YLR058C
ORF



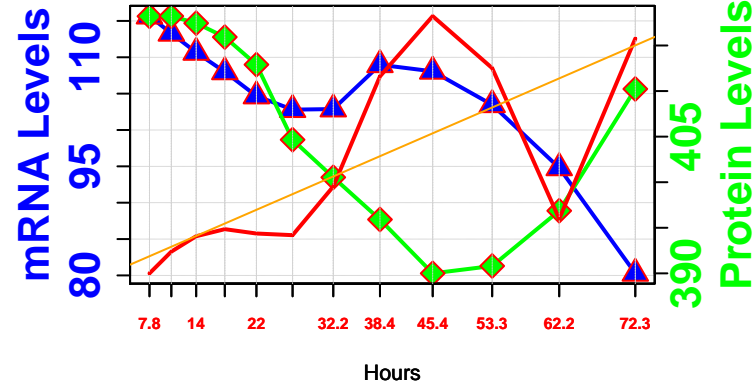
327 - ADE3 RLS: 25.4
YGR204W
ORF



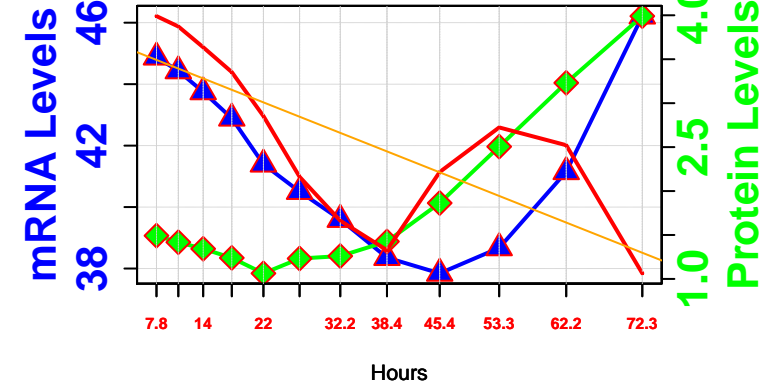
370 - MET12 RLS: 24.2
YPL023C
ORF



455 - MET13 RLS: 22.6
YGL125W
ORF

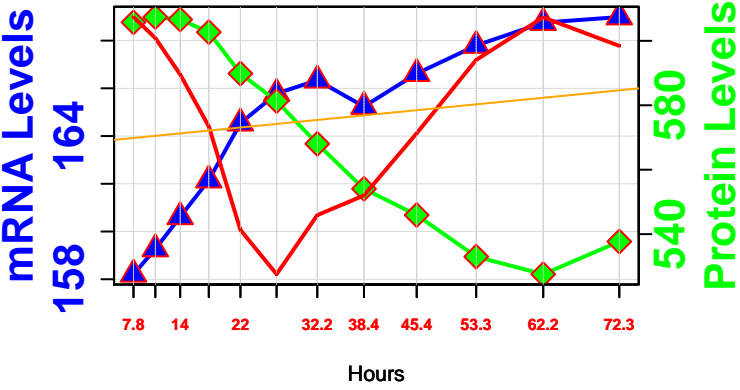


607 - MET7 RLS: 17.14
YOR241W
ORF

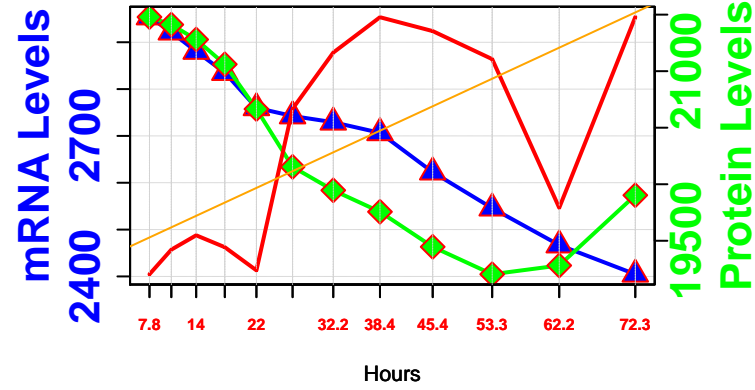


glycine biosynthesis from serine

170 – SHM1 RLS: 28.53
YBR263W
ORF

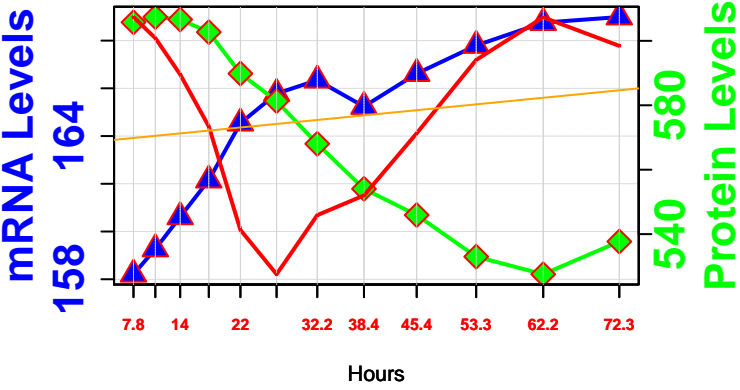


182 – SHM2 RLS: 28.28
YLR058C
ORF

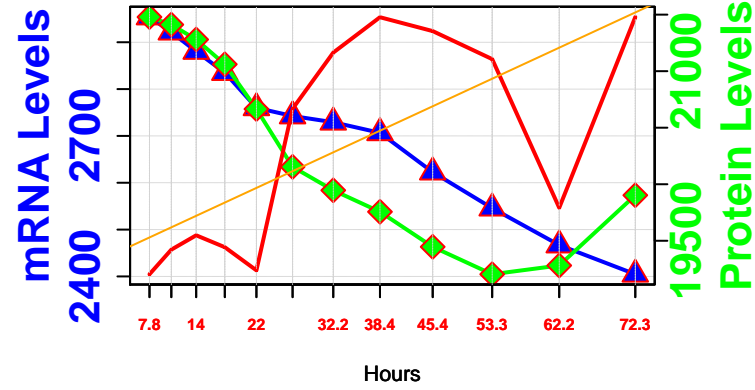


serine biosynthesis from glyoxylate

170 - SHM1 RLS: 28.53
YBR263W
ORF

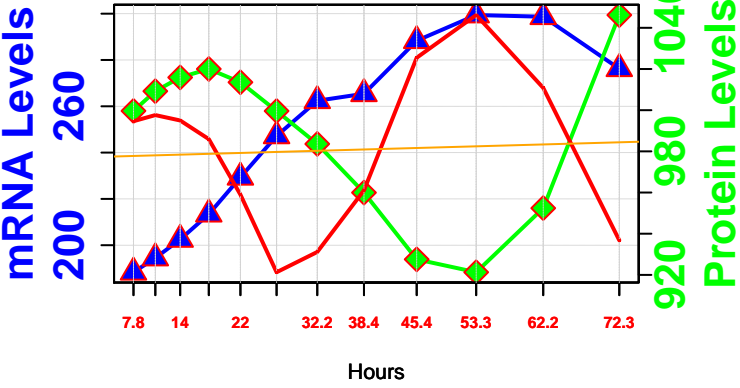


182 - SHM2 RLS: 28.28
YLR058C
ORF

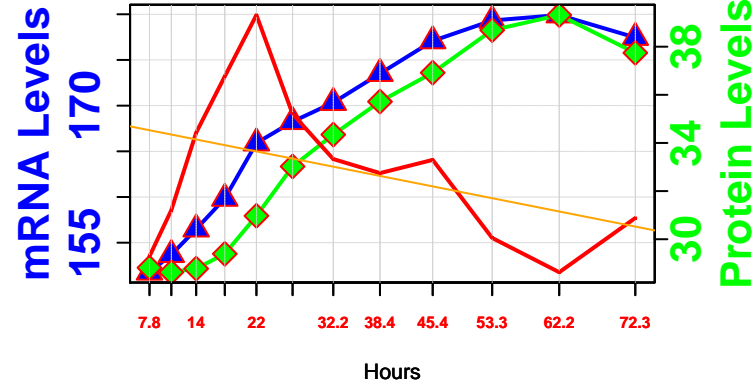


ergosterol biosynthesis

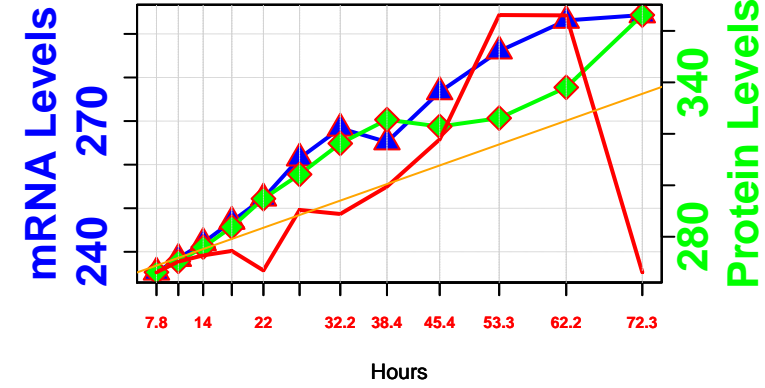
172 - ERG6 RLS: 28.53
YML008C
ORF



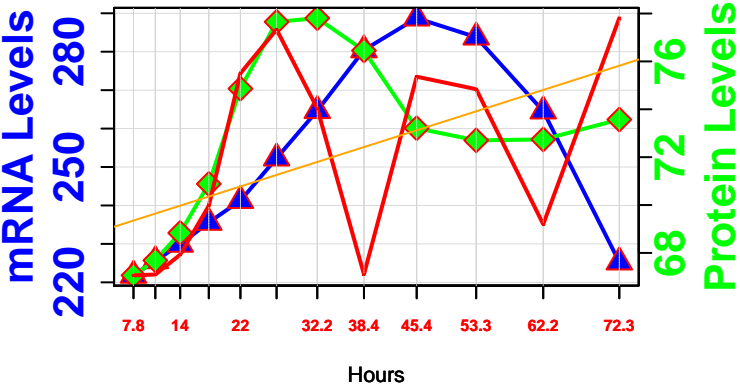
236 - ERG4 RLS: 27.42
YGL012W
ORF



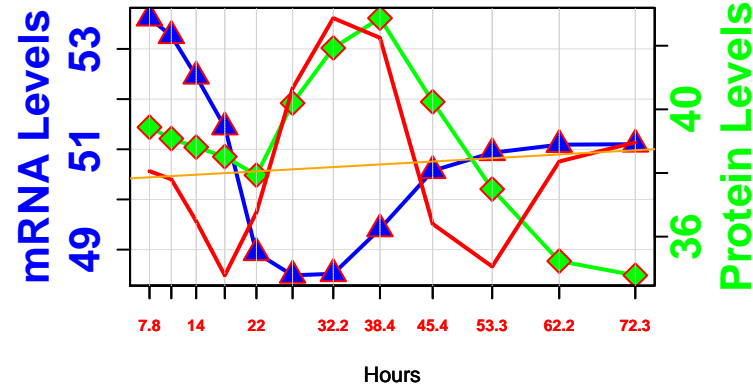
279 - ERG2 RLS: 26.4
YMR202W
ORF



286 - ERG3 RLS: 26.2
YLR056W
ORF

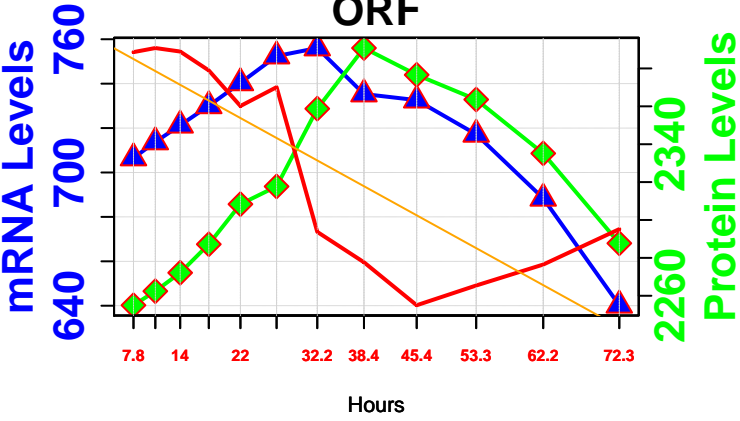


297 - ERG5 RLS: 25.93
YMR015C
ORF

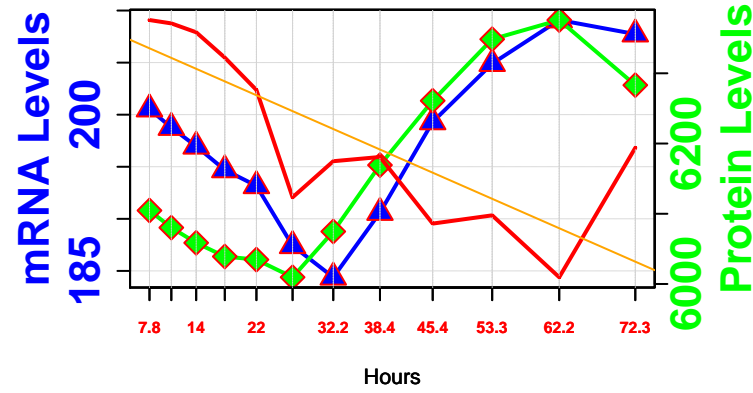


arginine biosynthesis

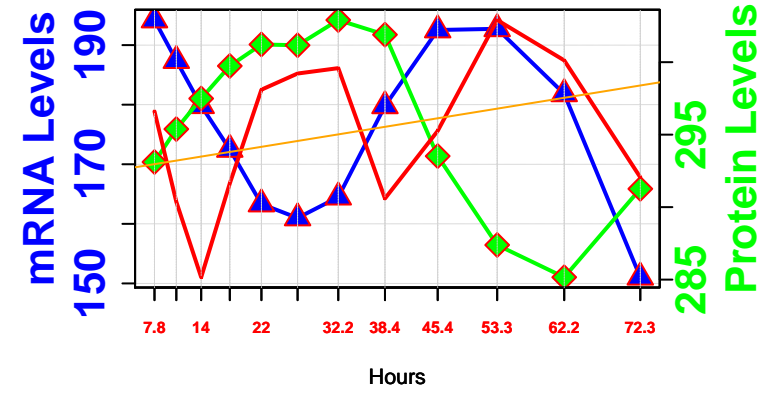
173 – ARG1 RLS: 28.5
YOL058W
ORF



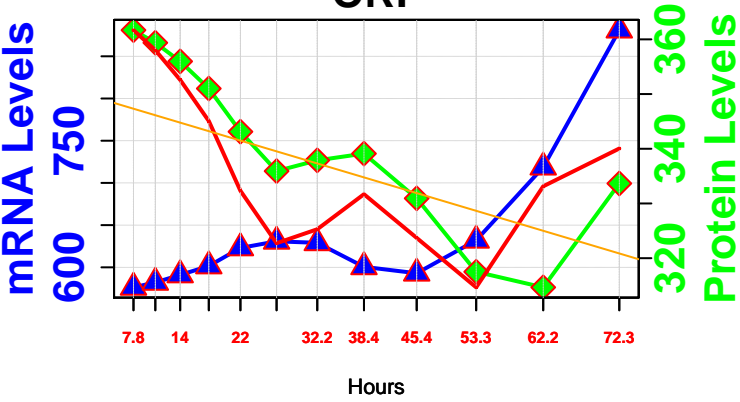
250 – CPA2 RLS: 27.16
YJR109C
ORF



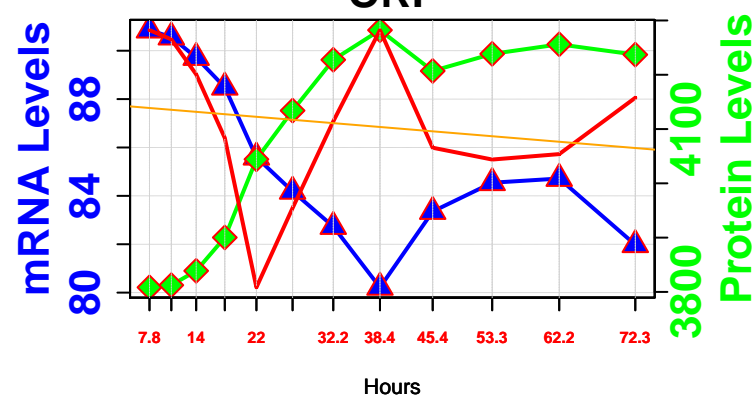
378 – ARG3 RLS: 24
YJL088W
ORF



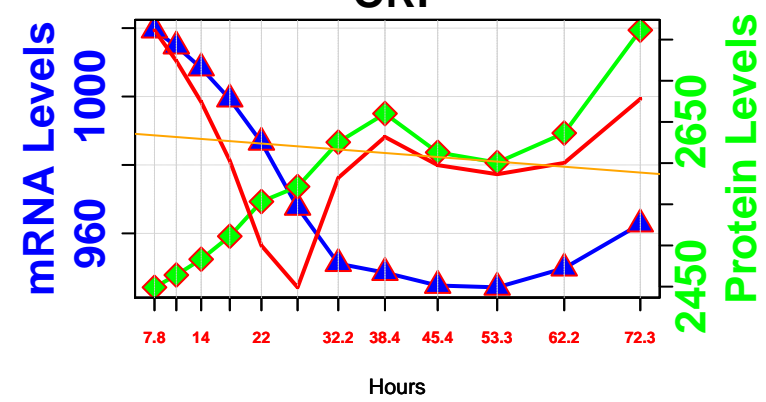
429 – CPA1 RLS: 23.2
YOR303W
ORF



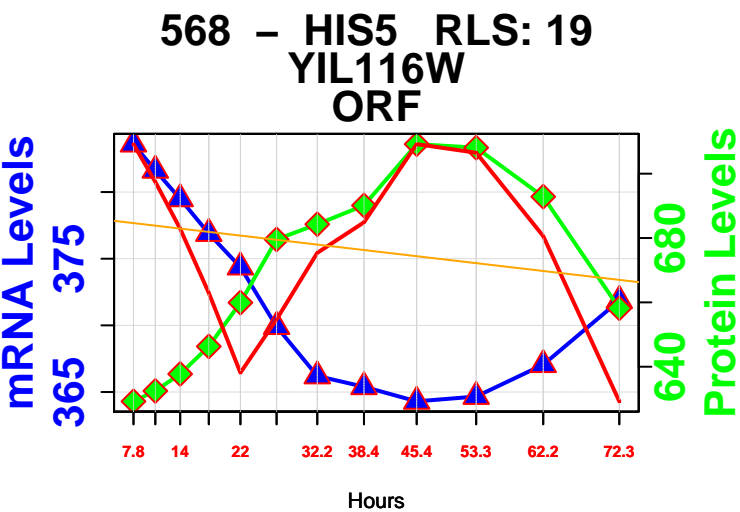
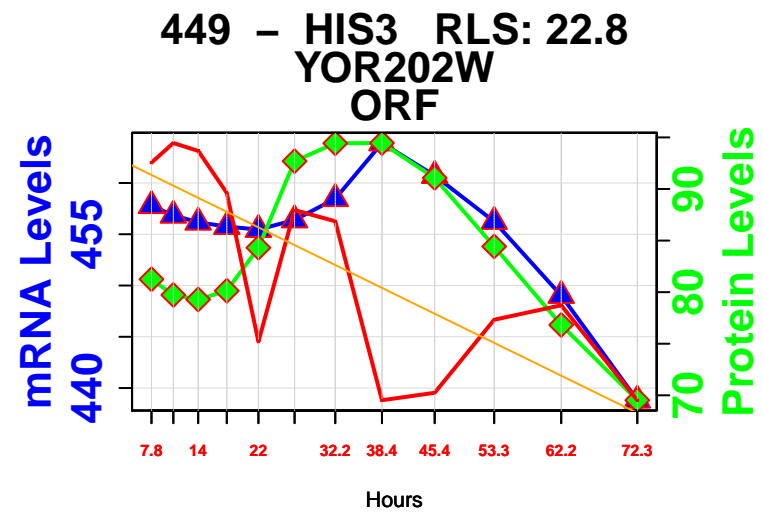
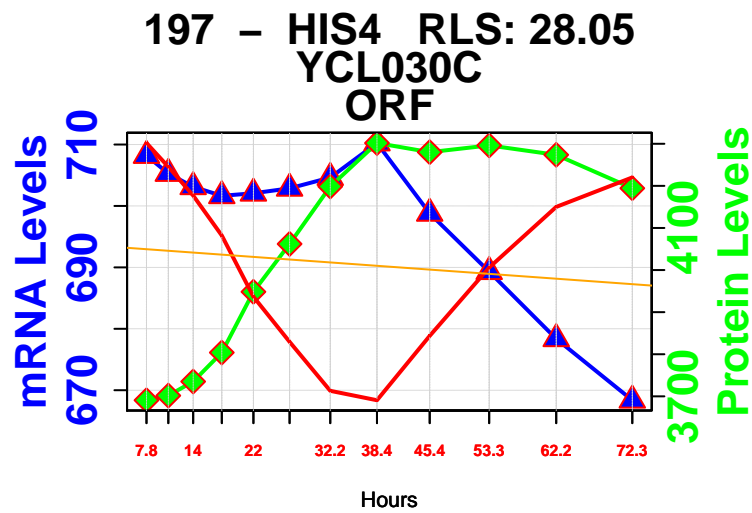
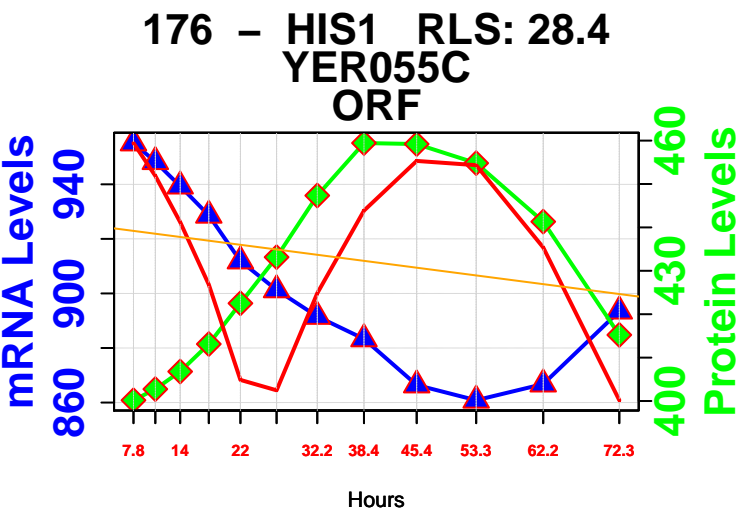
464 – URA2 RLS: 22.54
YJL130C
ORF



542 – ARG4 RLS: 20.03
YHR018C
ORF

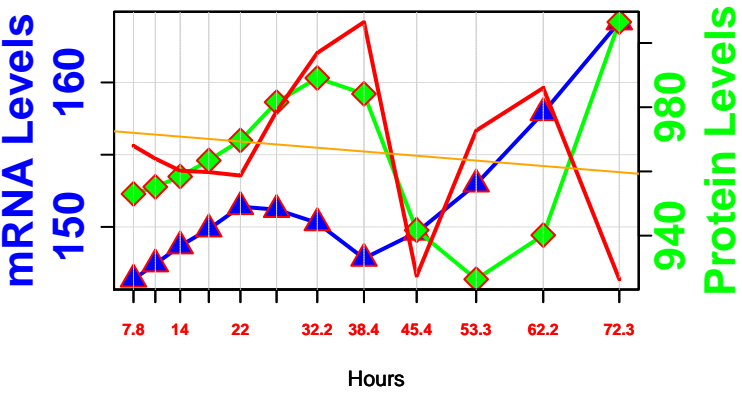


histidine biosynthesis



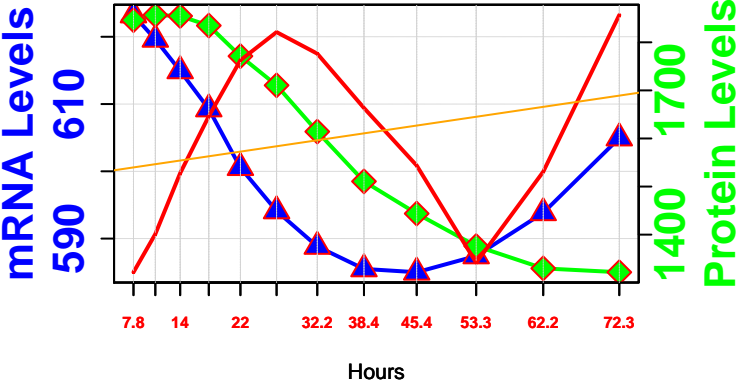
superpathway of glutamate biosynthesis

178 – IDP1 RLS: 28.38
YDL066W
ORF

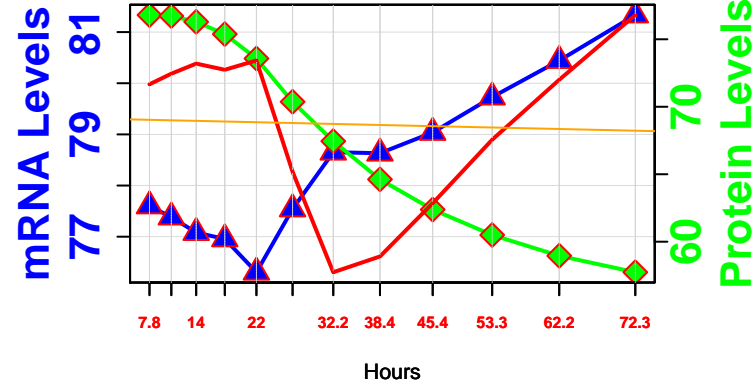


methionine salvage pathway

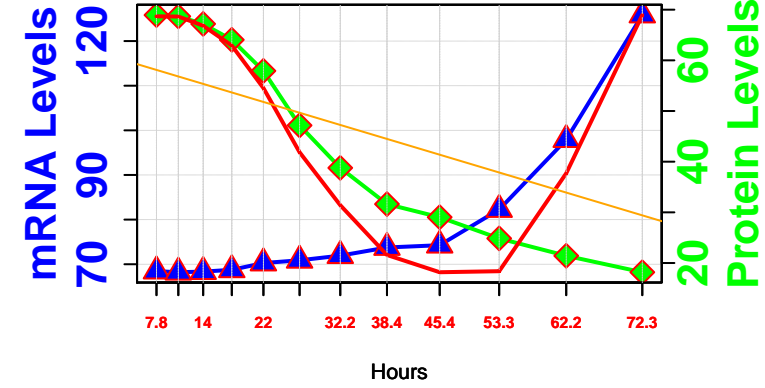
206 – ARO8 RLS: 27.94
YGL202W
ORF



430 – MRI1 RLS: 23.2
YPR118W
ORF

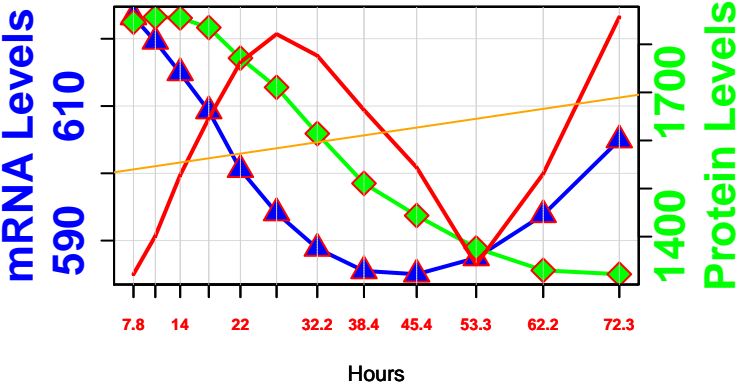


616 – UTR4 RLS: 16.6
YEL038W
ORF

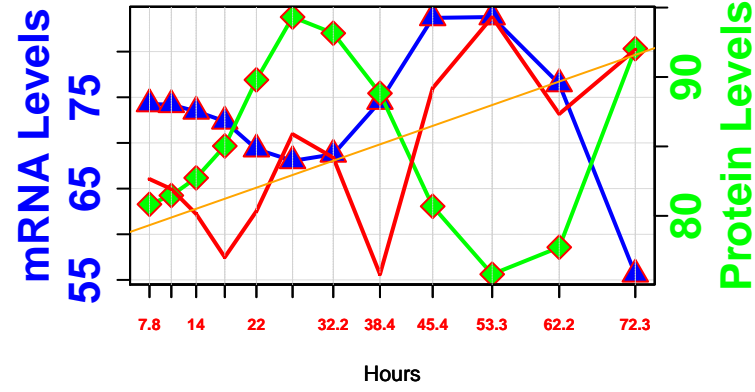


phenylalanine biosynthesis

206 – ARO8 RLS: 27.94
YGL202W
ORF

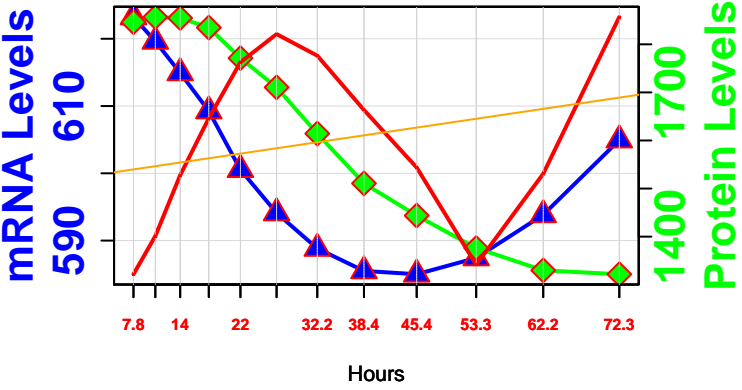


562 – ARO7 RLS: 19.4
YPR060C
ORF

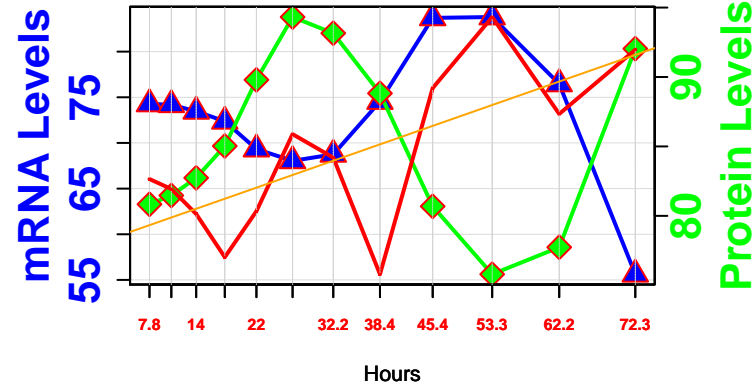


tyrosine biosynthesis

206 – ARO8 RLS: 27.94
YGL202W
ORF

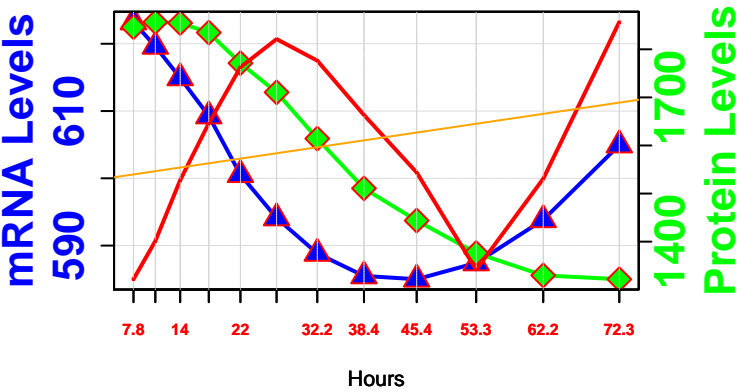


562 – ARO7 RLS: 19.4
YPR060C
ORF



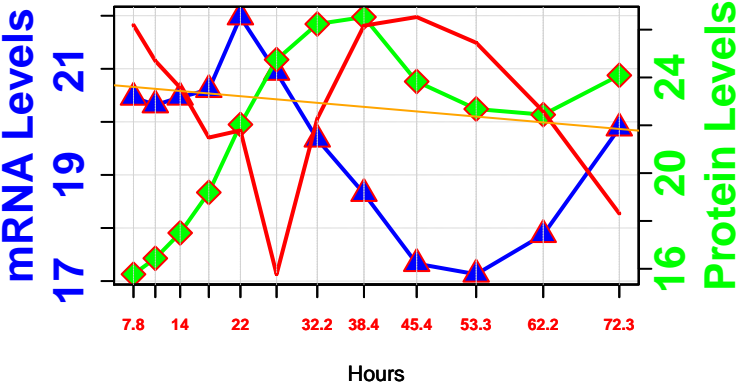
tyrosine degradation

206 – ARO8 RLS: 27.94
YGL202W
ORF

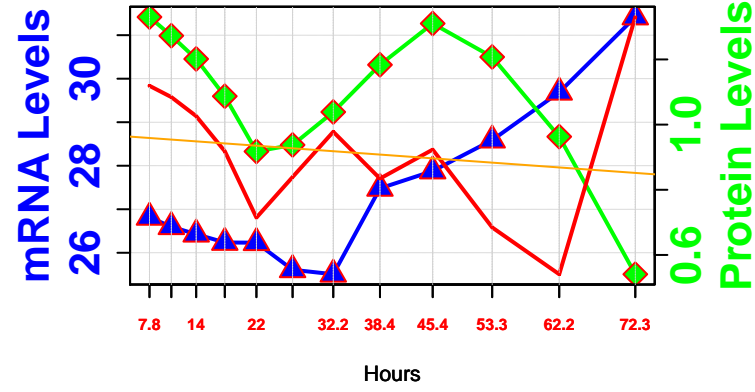


mevalonate pathway

209 – HMG2 RLS: 27.91
YLR450W
ORF

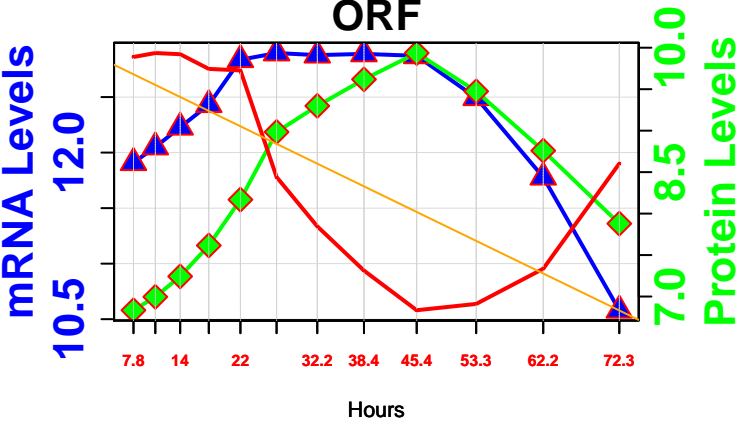


432 – HMG1 RLS: 23.08
YML075C
ORF

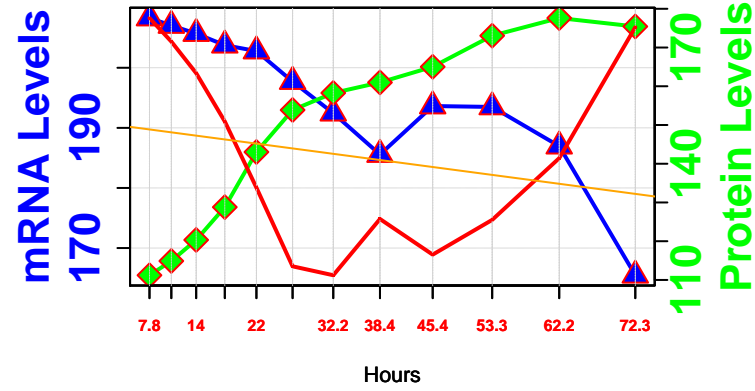


fatty acid oxidation pathway

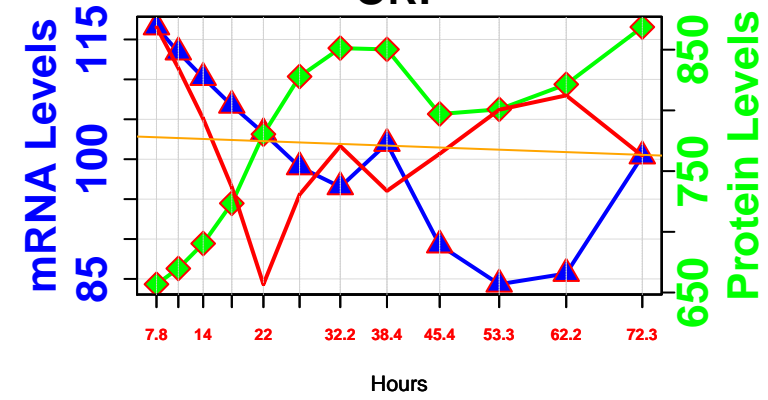
225 – FAA3 RLS: 27.6
YIL009W
ORF



262 – FAA4 RLS: 26.8
YMR246W
ORF

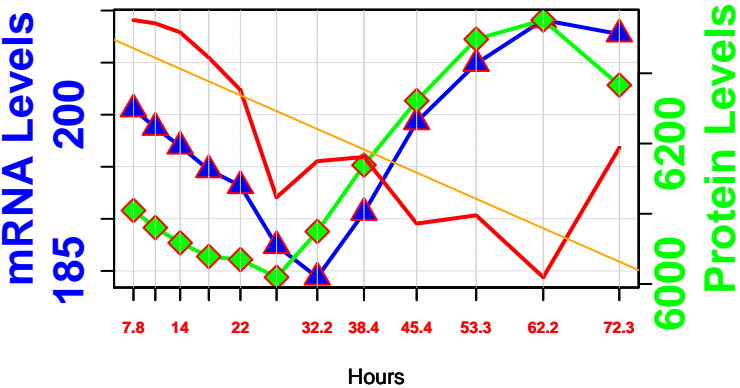


514 – FAA1 RLS: 21.2
YOR317W
ORF

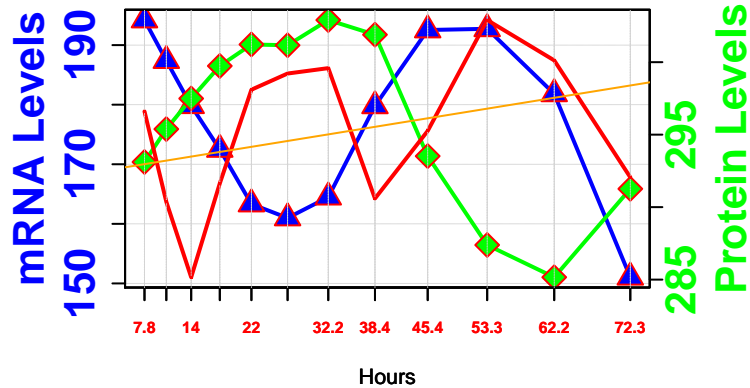


citrulline biosynthesis

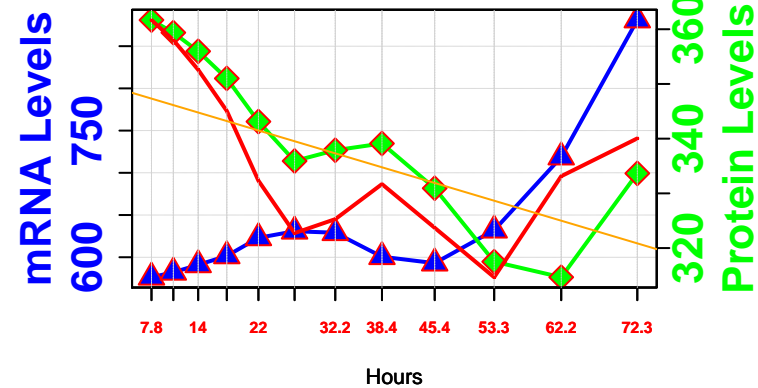
250 – CPA2 RLS: 27.16
YJR109C
ORF



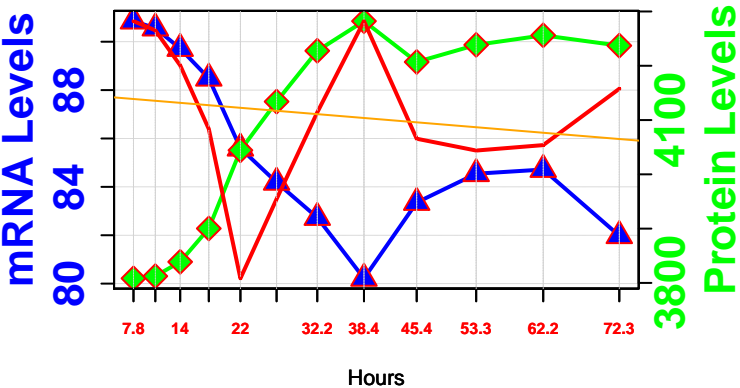
378 – ARG3 RLS: 24
YJL088W
ORF



429 – CPA1 RLS: 23.2
YOR303W
ORF

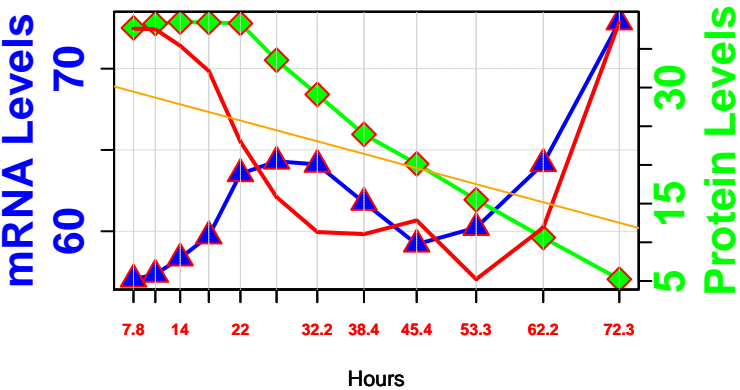


464 – URA2 RLS: 22.54
YJL130C
ORF

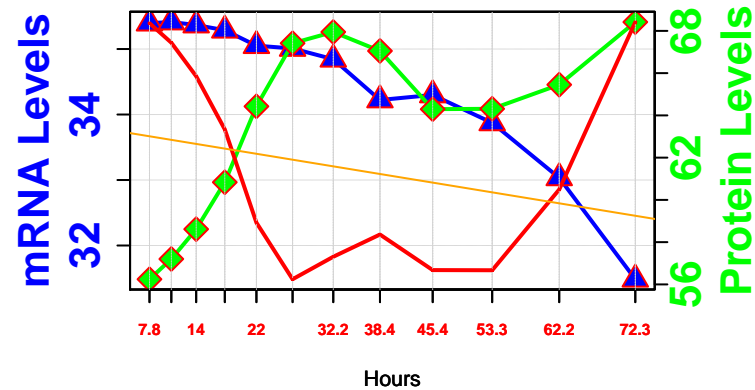


inositol phosphate biosynthesis

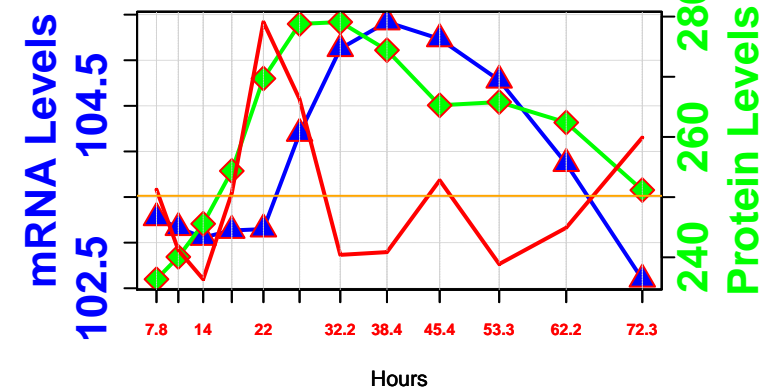
252 – DDP1 RLS: 27.11
YOR163W
ORF



273 – VIP1 RLS: 26.56
YLR410W
ORF

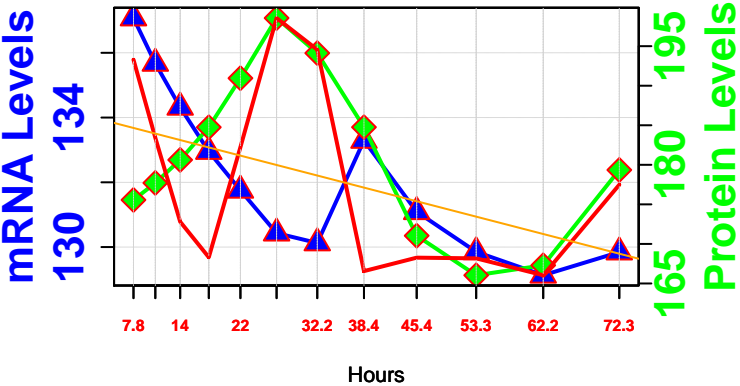


622 – SAC1 RLS: 15.89
YKL212W
ORF

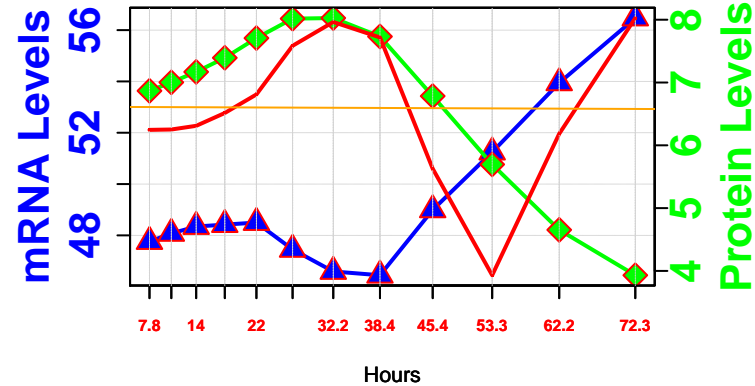


aspartate biosynthesis

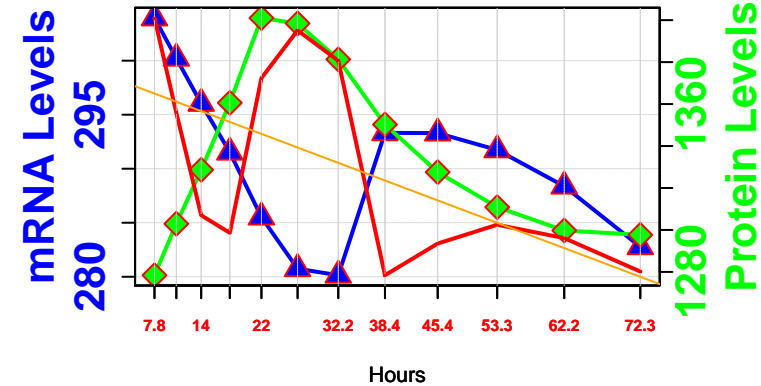
264 – PYC2 RLS: 26.75
YBR218C
ORF



283 – AAT1 RLS: 26.21
YKL106W
ORF

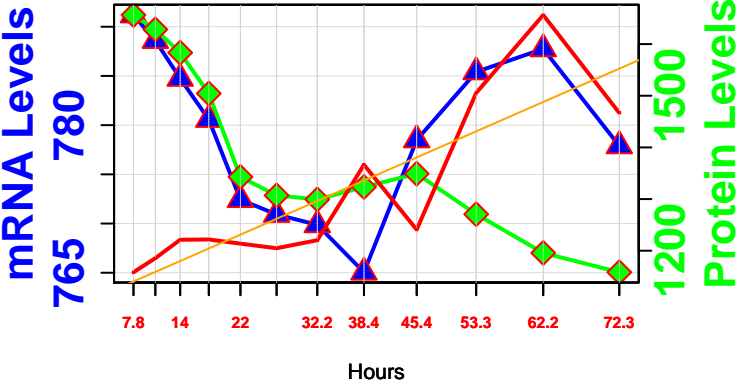


401 – AAT2 RLS: 23.6
YLR027C
ORF

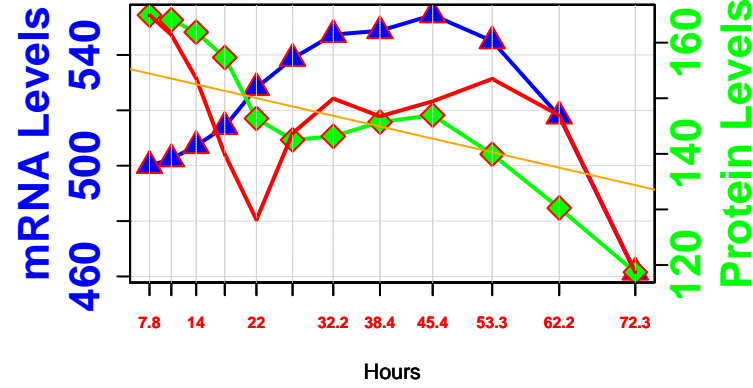


chorismate biosynthesis

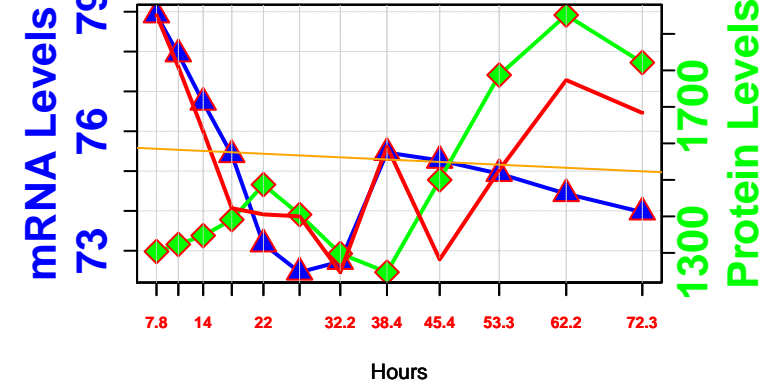
274 – ARO4 RLS: 26.53
YBR249C
ORF



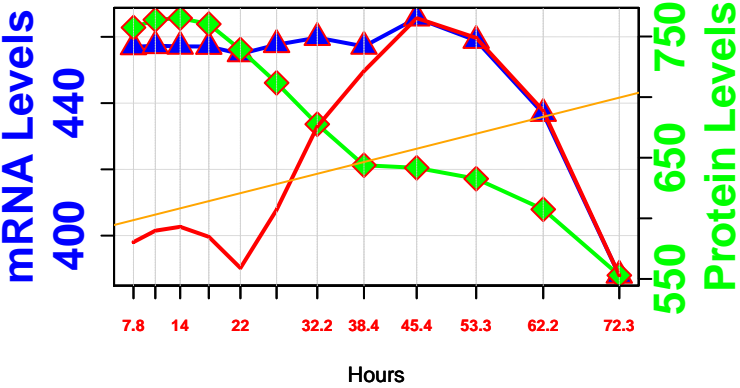
333 – ARO3 RLS: 25.2
YDR035W
ORF



484 – ARO1 RLS: 21.8
YDR127W
ORF

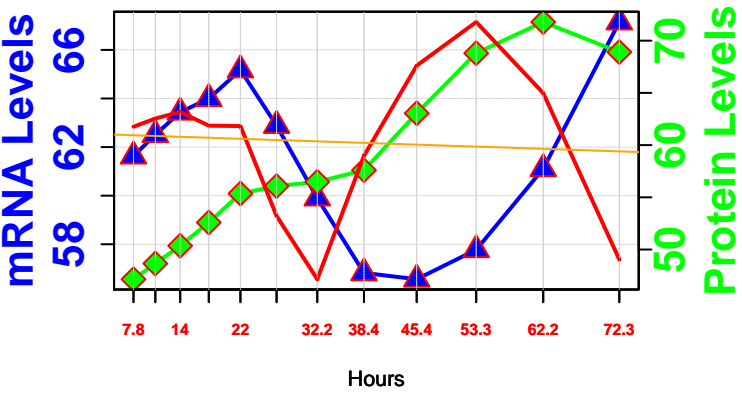


648 – ARO2 RLS: 12
YGL148W
ORF



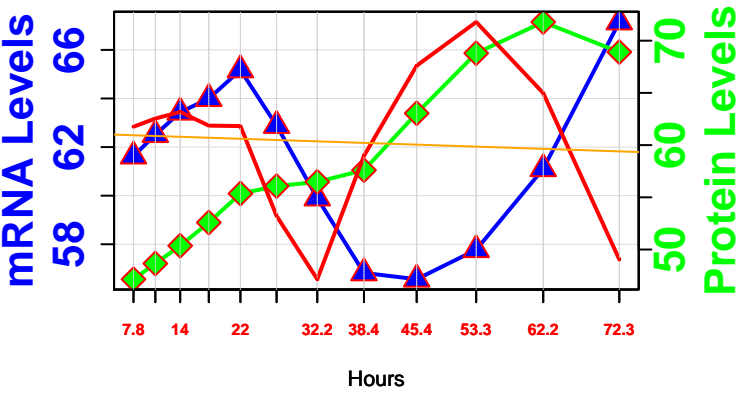
nicotinamide riboside salvage pathway II

278 – PNP1 RLS: 26.4
YLR209C
ORF



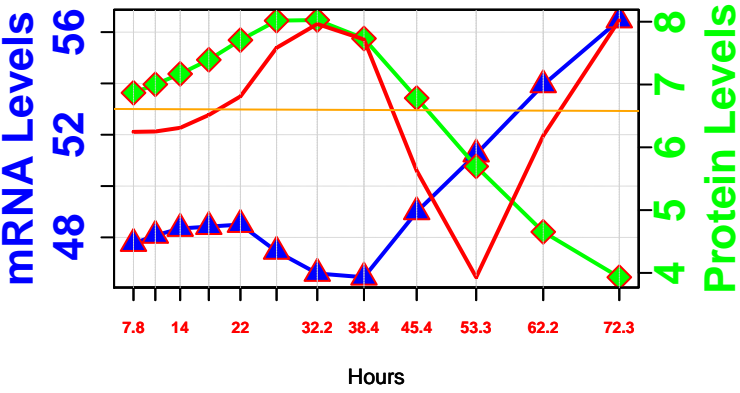
nicotinate riboside salvage pathway II

278 – PNP1 RLS: 26.4
YLR209C
ORF

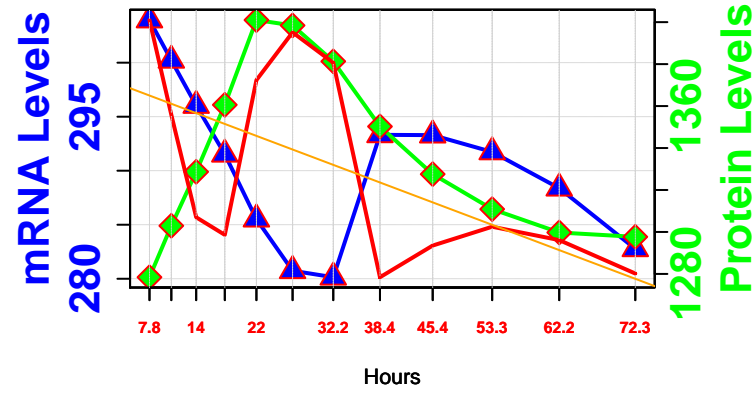


asparagine degradation

283 – AAT1 RLS: 26.21
YKL106W
ORF

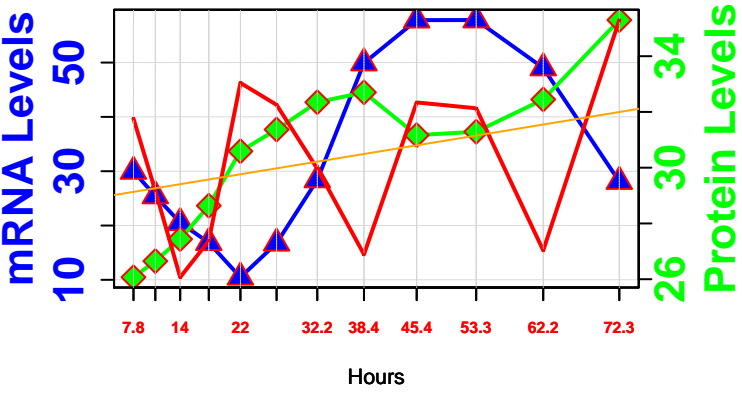


401 – AAT2 RLS: 23.6
YLR027C
ORF



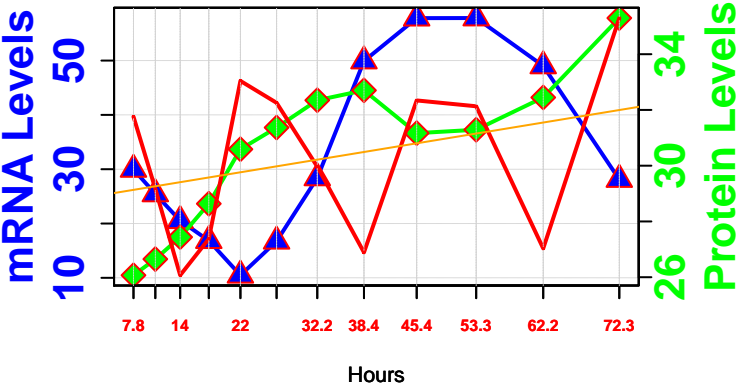
homocysteine biosynthesis

288 – MET2 RLS: 26.2
YNL277W
ORF



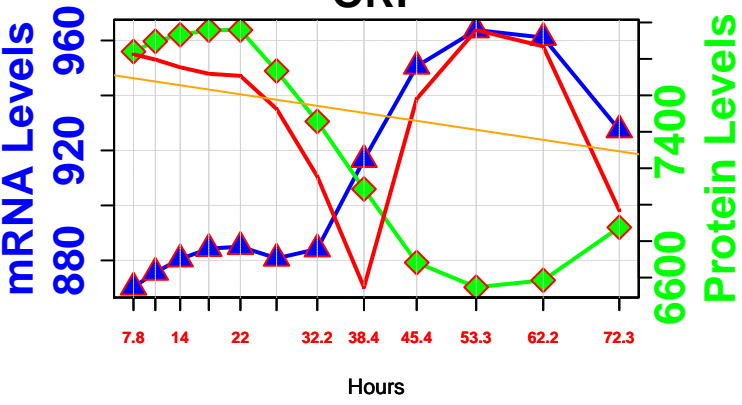
superpathway of sulfur amino acid biosynthesis

288 – MET2 RLS: 26.2
YNL277W
ORF



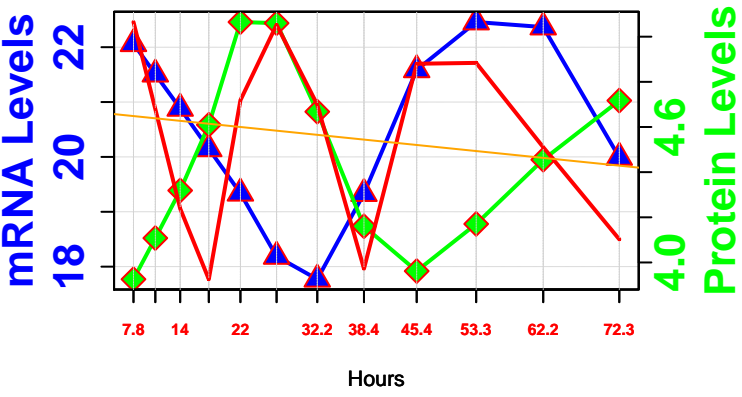
formaldehyde oxidation (glutamine dependent)

290 – GDH1_RLS: 26.13
YOR375C
ORF



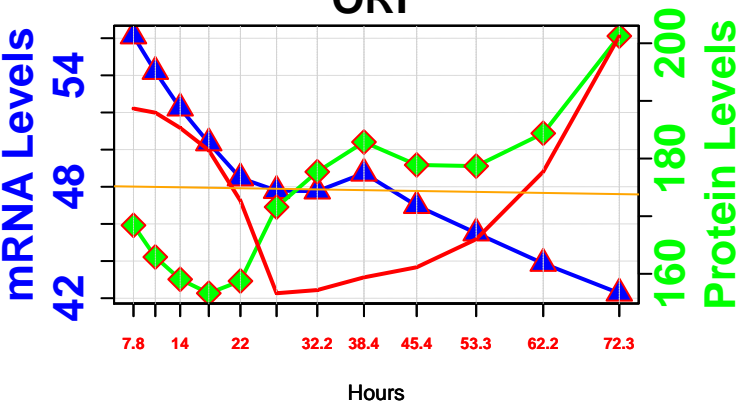
thiamine biosynthesis

308 – THI6 RLS: 25.8
YPL214C
ORF



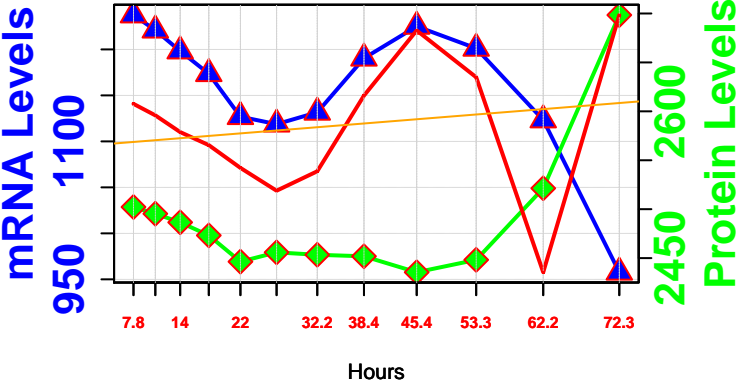
dehydro-D-arabinono-1,4-lactone biosynthesis

311 - ALO1 RLS: 25.76
YML086C
ORF

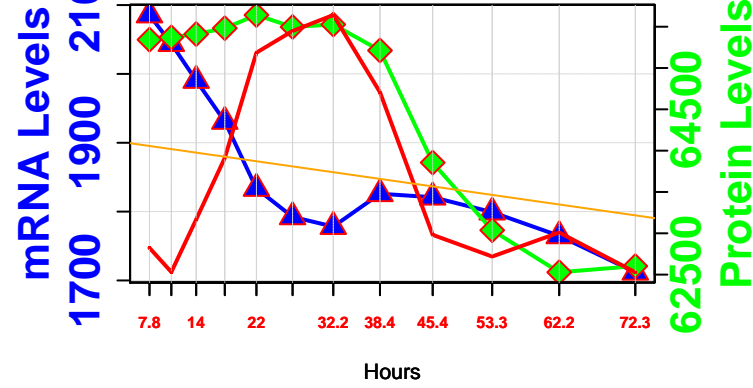


methionine biosynthesis

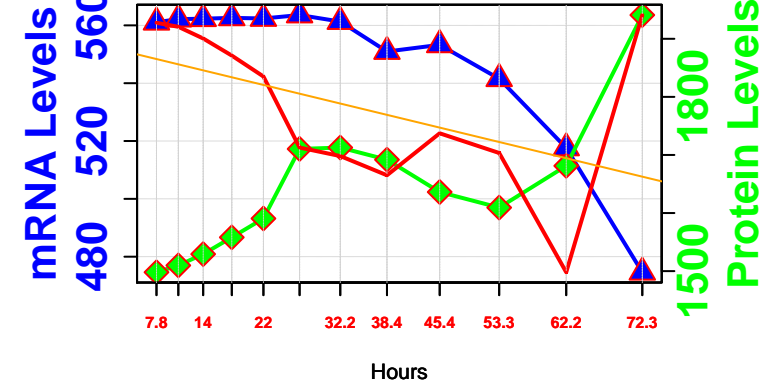
34 – SAM1 RLS: 32.96
YLR180W
ORF



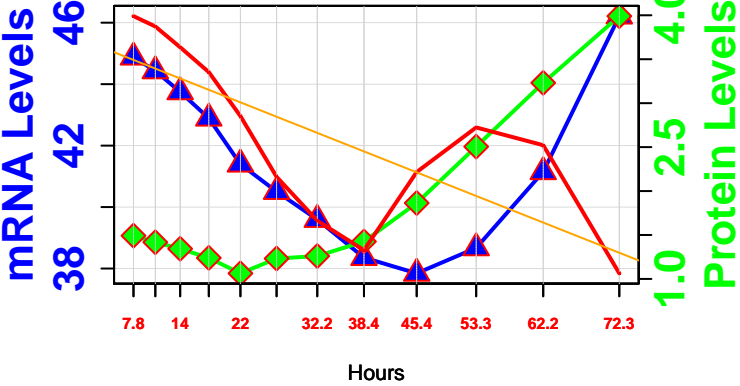
312 – MET6 RLS: 25.74
YER091C
ORF



387 – SAM2 RLS: 23.8
YDR502C
ORF

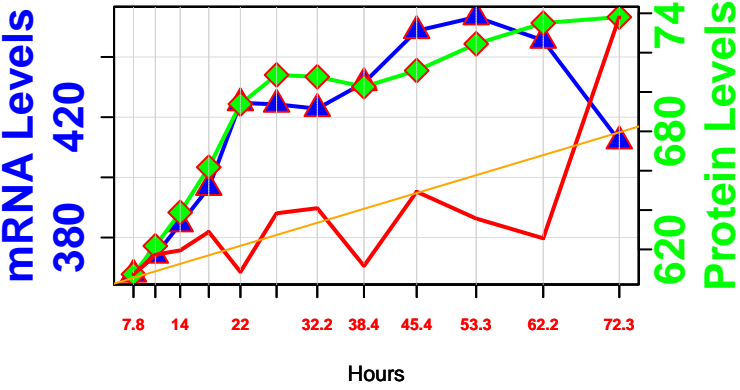


607 – MET7 RLS: 17.14
YOR241W
ORF

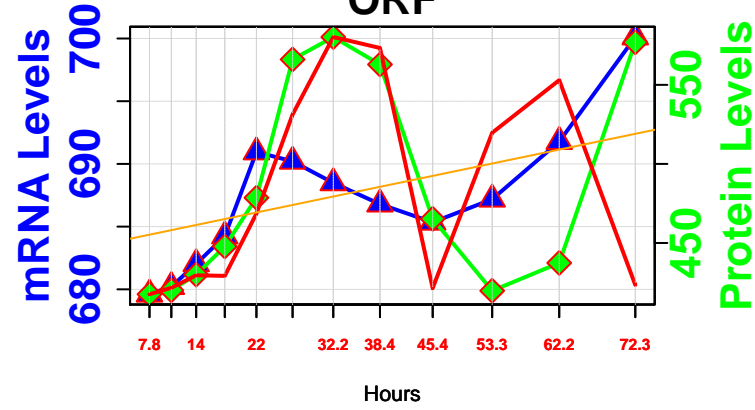


leucine biosynthesis

329 – LEU4 RLS: 25.4
YNL104C
ORF

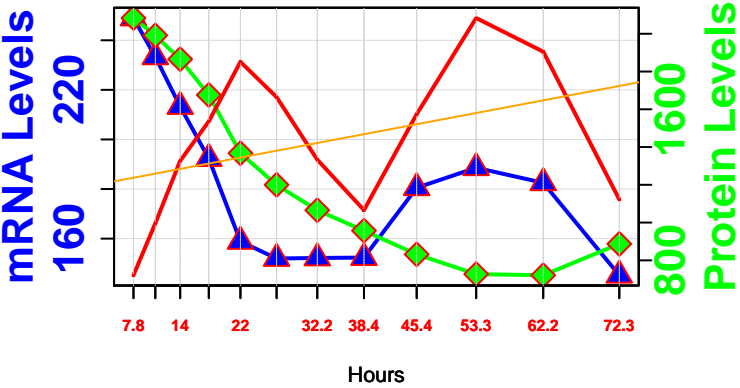


399 – ILV6 RLS: 23.6
YCL009C
ORF

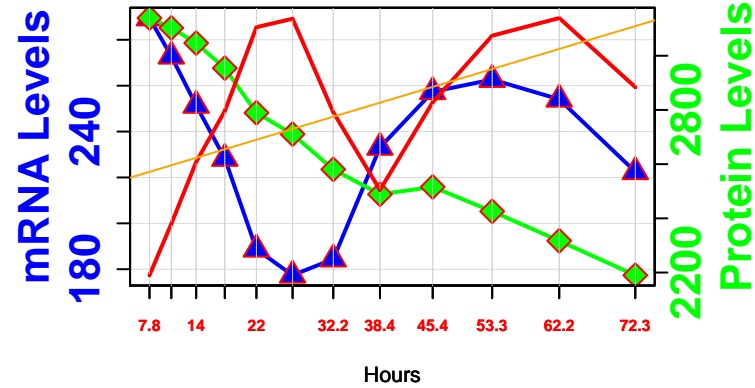


cysteine biosynthesis from homocysteine

348 – CYS4 RLS: 24.67
YGR155W
ORF

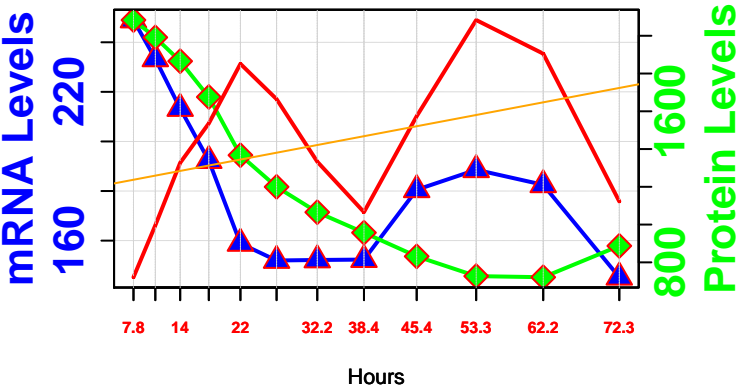


611 – CYS3 RLS: 16.83
YAL012W
ORF

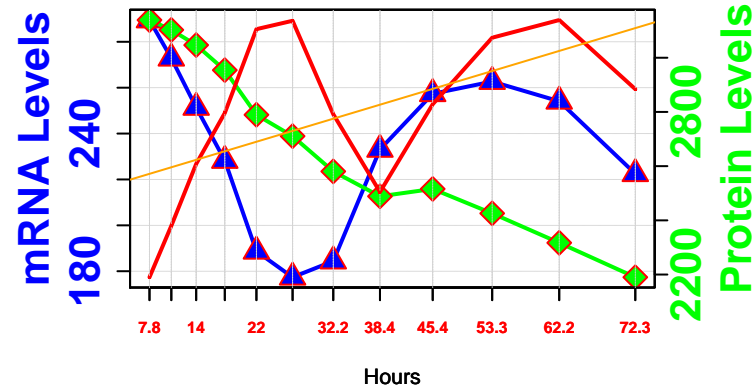


cysteine biosynthesis/homocysteine degradation

348 – CYS4 RLS: 24.67
YGR155W
ORF

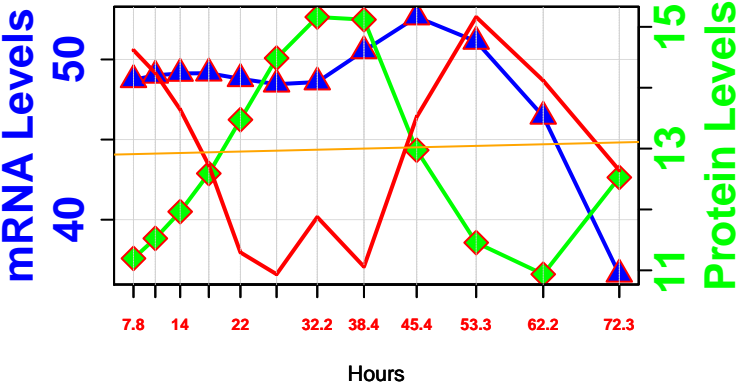


611 – CYS3 RLS: 16.83
YAL012W
ORF

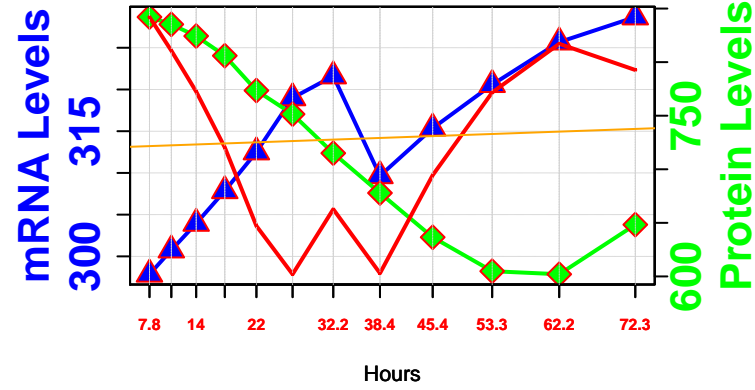


spermidine and methylthioadenosine biosynthesis

361 – SPE2 RLS: 24.4
YOL052C
ORF

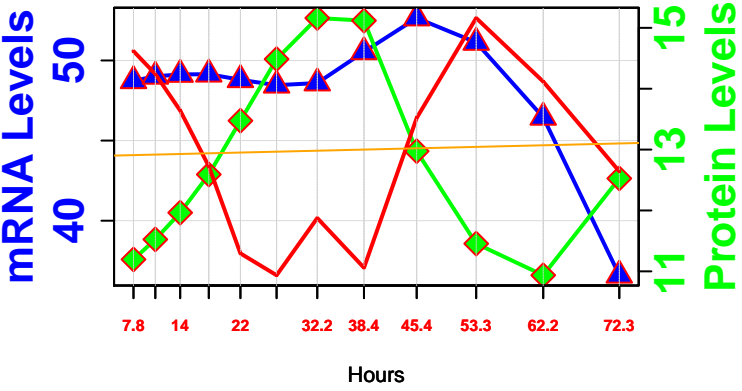


381 – SPE3 RLS: 24
YPR069C
ORF

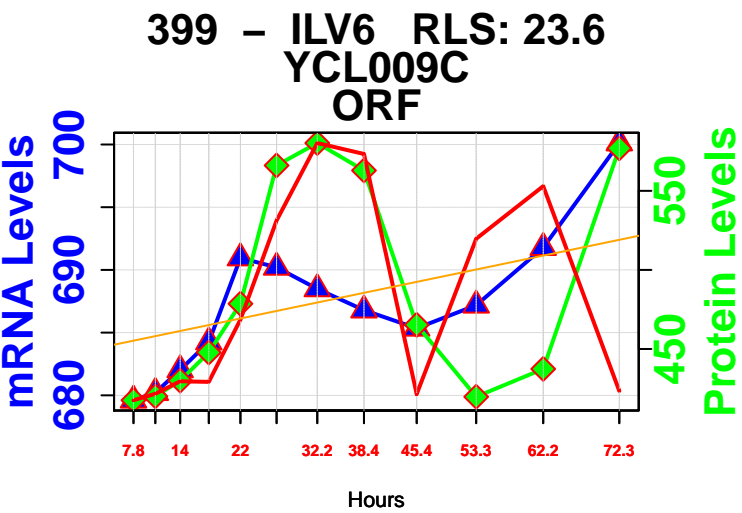


spermine and methylthioadenosine biosynthesis

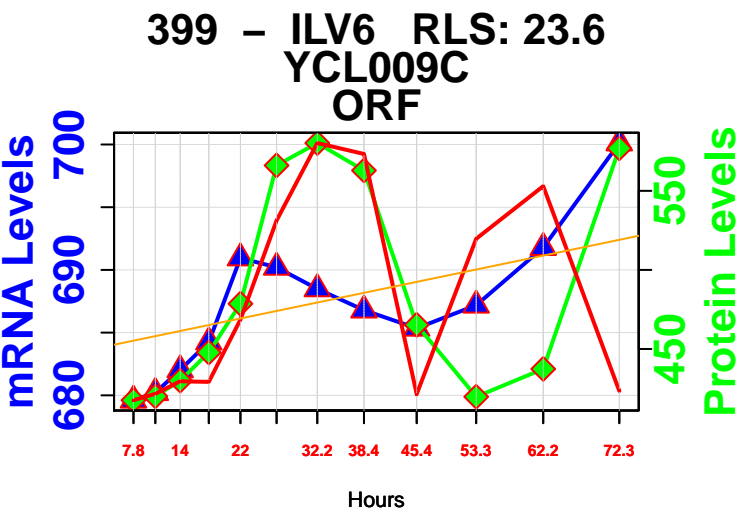
361 - SPE2 RLS: 24.4
YOL052C
ORF



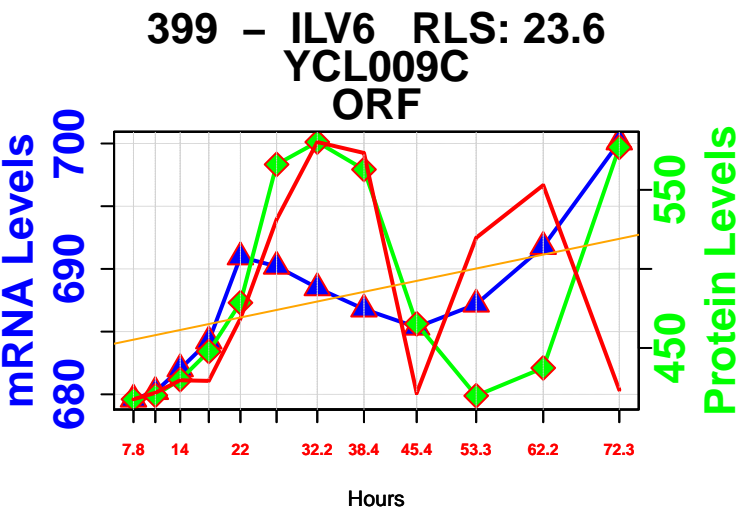
acetoin biosynthesis



isoleucine biosynthesis

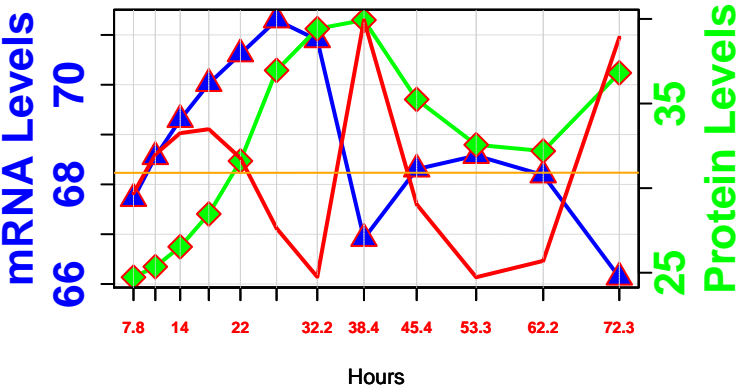


valine biosynthesis

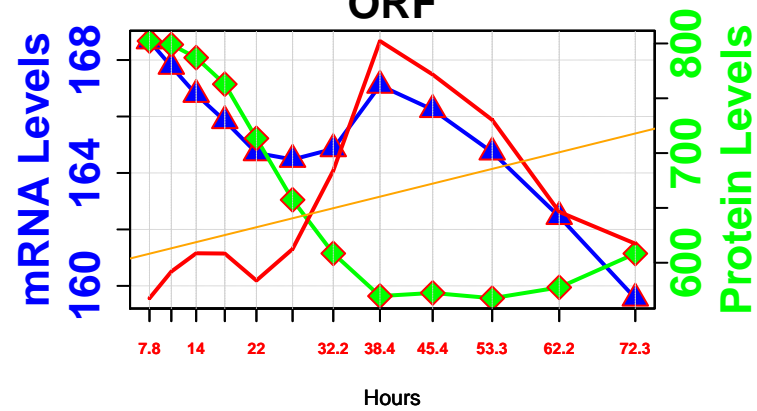


proline biosynthesis

405 - PRO1 RLS: 23.58
YDR300C
ORF

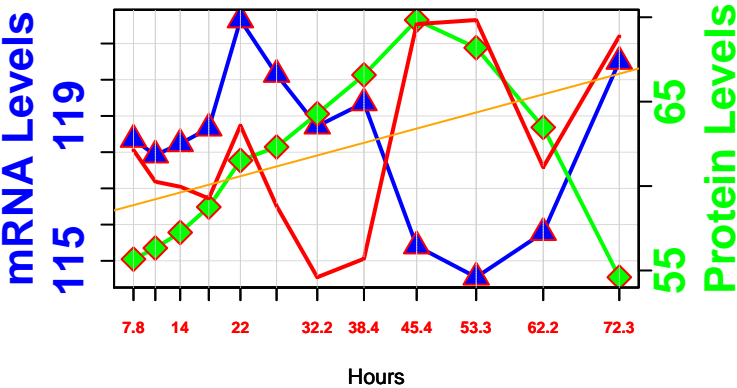


638 - PRO2 RLS: 13.68
YOR323C
ORF



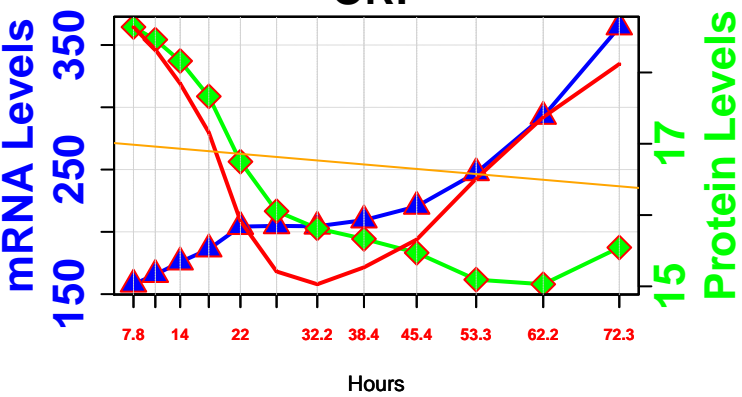
de novo NAD biosynthesis

415 – BNA6 RLS: 23.4
YFR047C
ORF

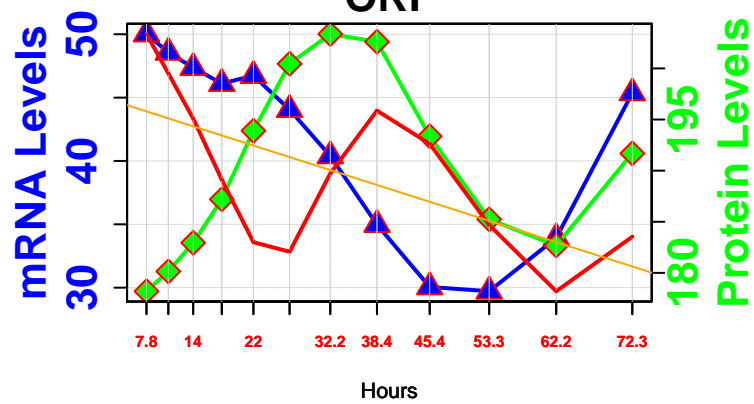


proline utilization

418 – PUT1 RLS: 23.4
YLR142W
ORF

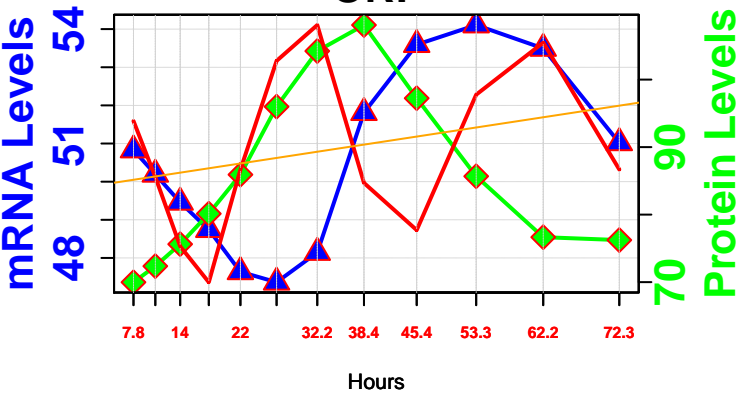


481 – PUT2 RLS: 22
YHR037W
ORF

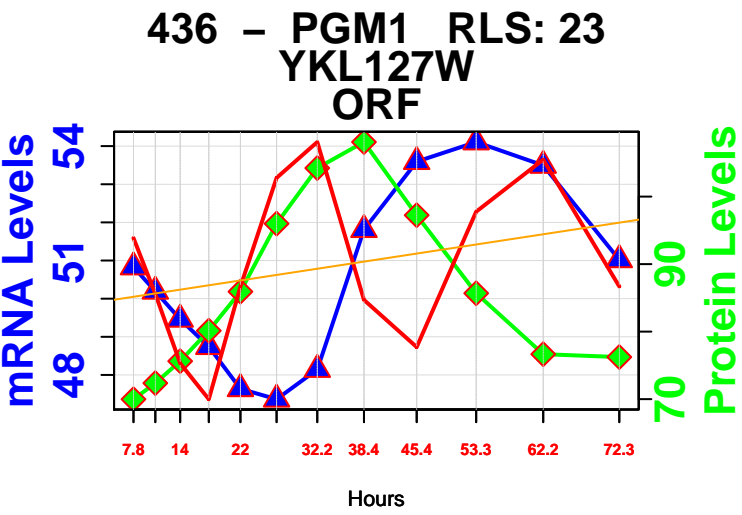


dolichyl glucosyl phosphate biosynthesis

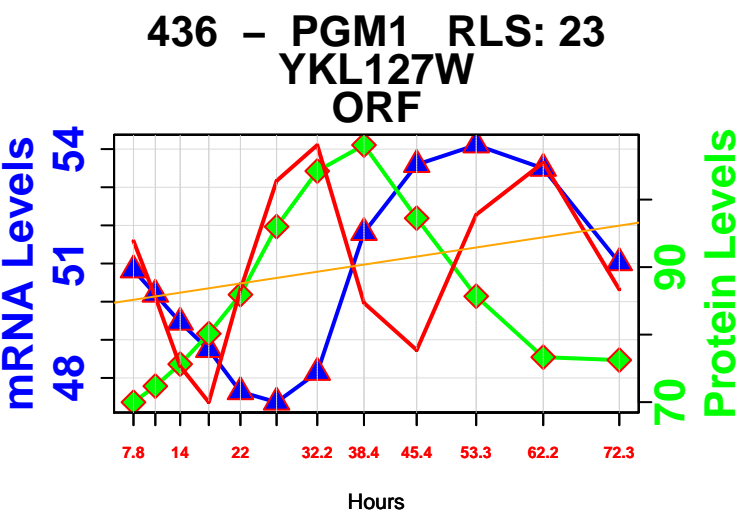
436 - PGM1 RLS: 23
YKL127W
ORF



galactose degradation

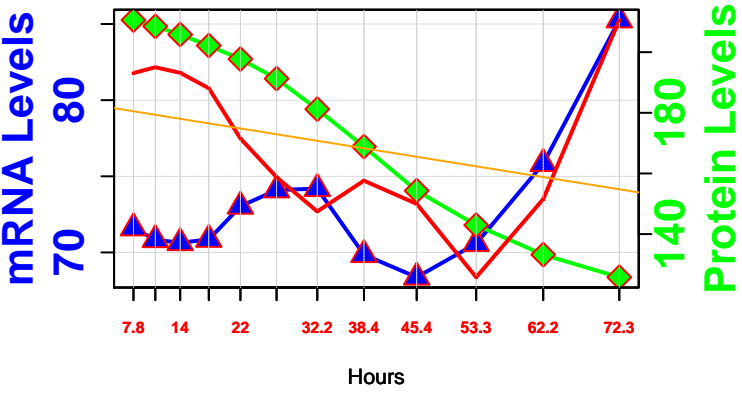


glycogen biosynthesis



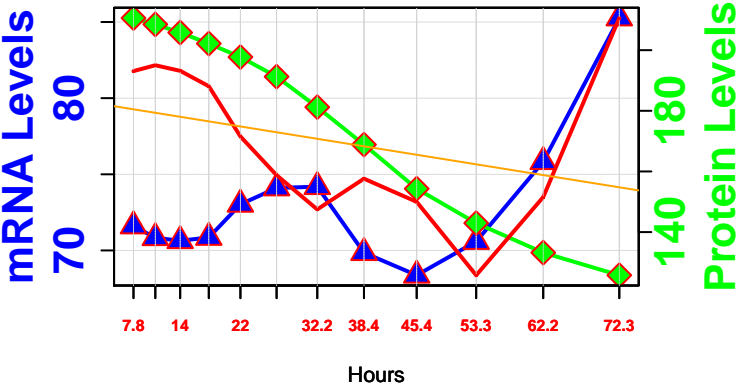
glutathione-glutaredoxin redox reactions

441 - GLR1 RLS: 22.84
YPL091W
ORF



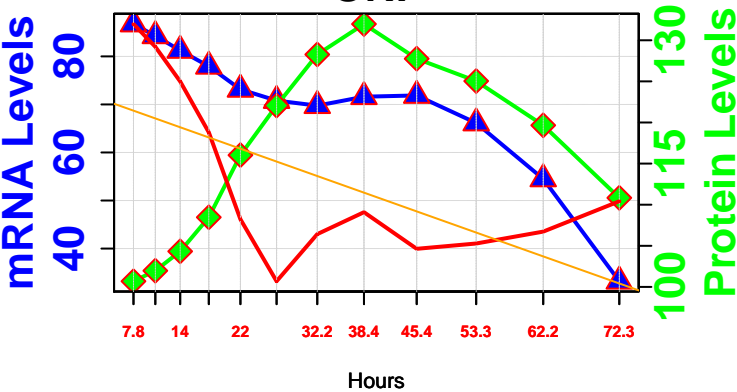
phosphatidylglycerol biosynthesis (triacylglycerols synthesis pathway)

441 - GLR1 RLS: 22.84
YPL091W
ORF



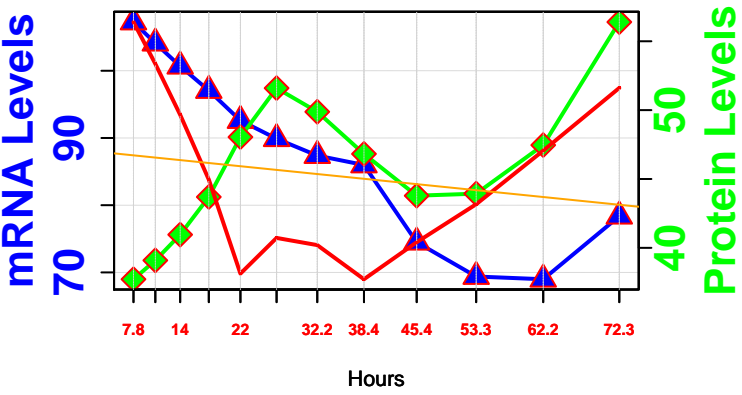
triglyceride biosynthesis

442 - SLC1 RLS: 22.8
YDL052C
ORF



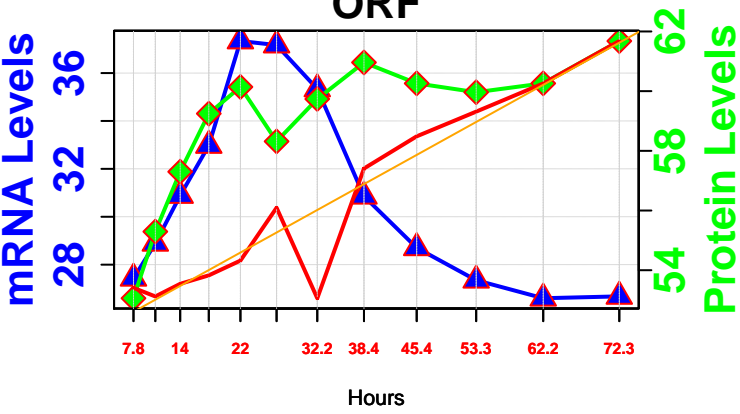
ubiquinone biosynthesis from 4-hydroxybenzoate

488 – COQ5 RLS: 21.66
YML110C
ORF

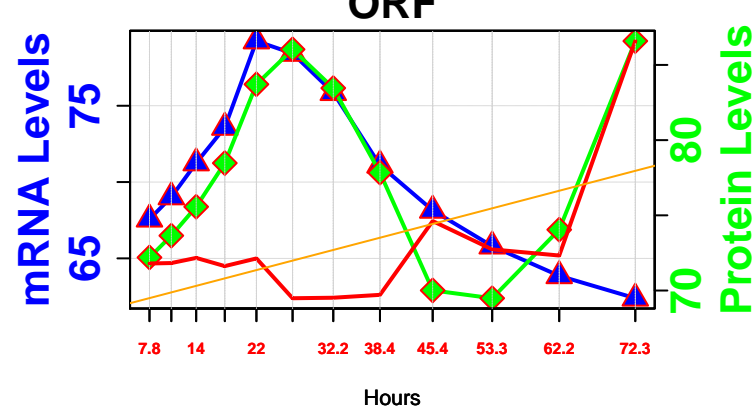


phospholipid biosynthesis

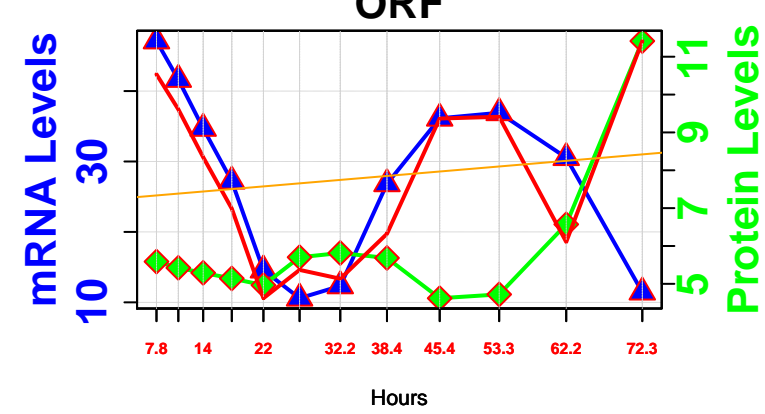
116 - CKI1 RLS: 30.2
YLR133W
ORF



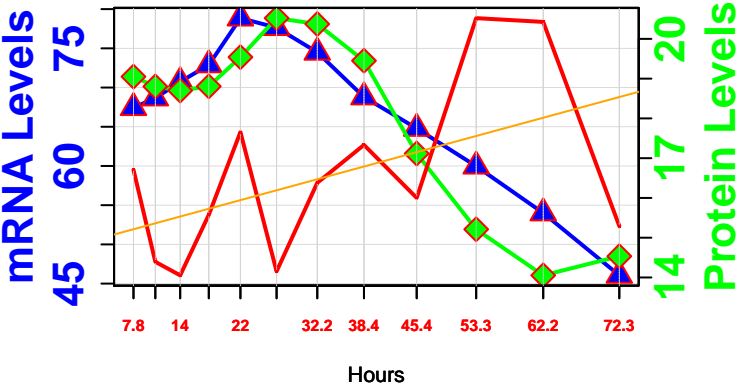
506 - CHO2 RLS: 21.2
YGR157W
ORF



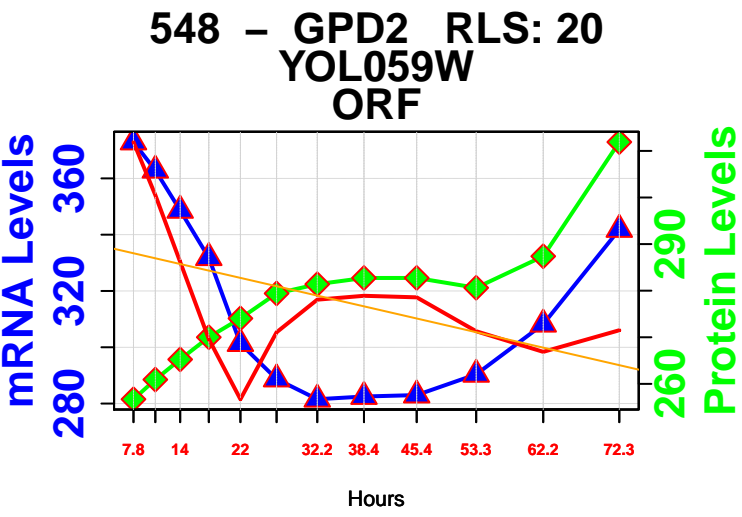
510 - PCT1 RLS: 21.2
YGR202C
ORF



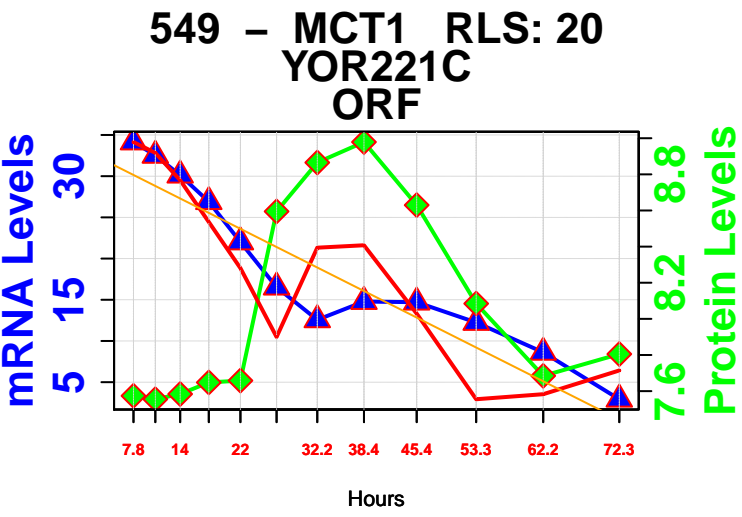
636 - PSD1 RLS: 13.93
YNL169C
ORF



glycerol biosynthesis

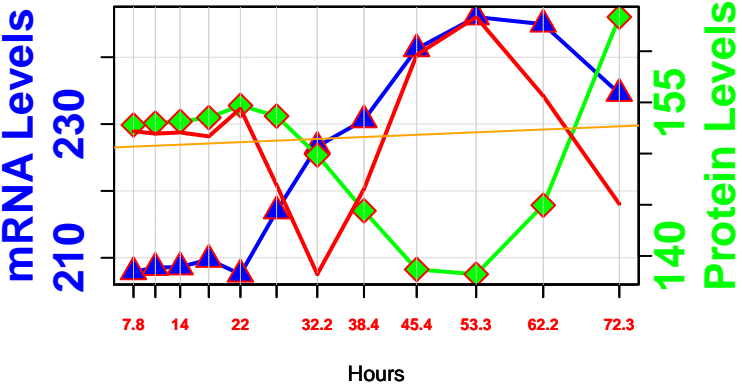


fatty acid biosynthesis, initial steps

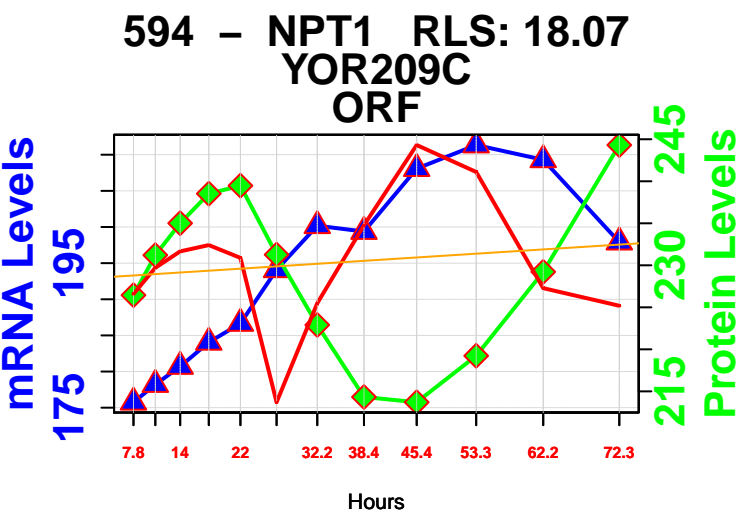


glycine biosynthesis from threonine

579 – GLY1 RLS: 18.6
YEL046C
ORF

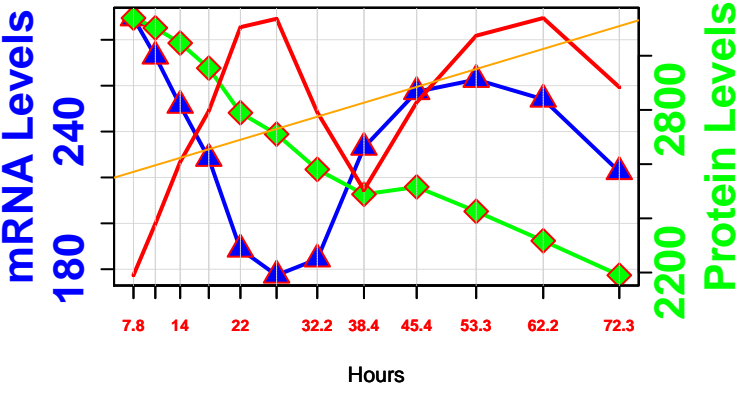


NAD salvage pathway



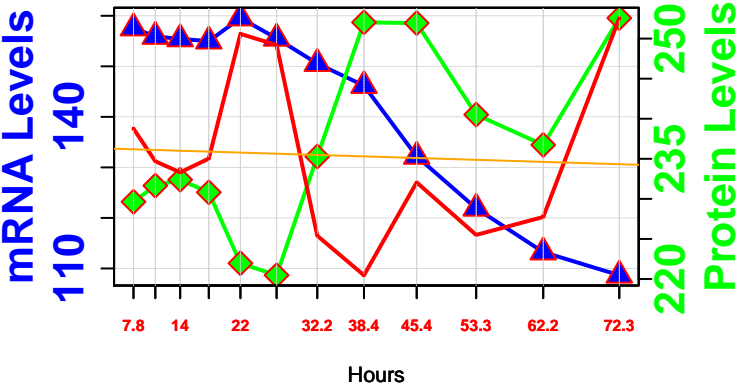
threonine degradation

611 - CYS3 RLS: 16.83
YAL012W
ORF



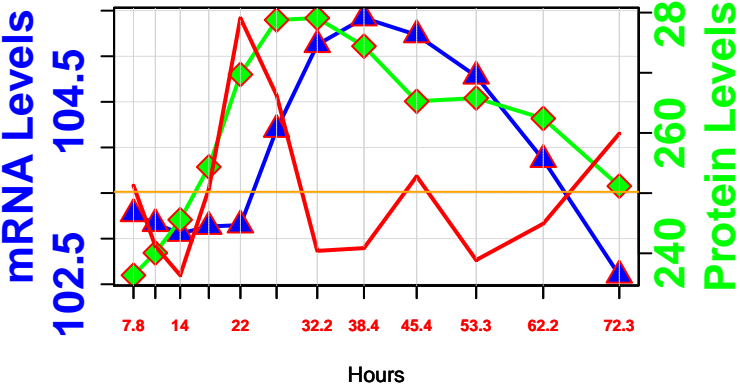
pyridoxal 5'-phosphate salvage pathway

615 - PDX3 RLS: 16.6
YBR035C
ORF



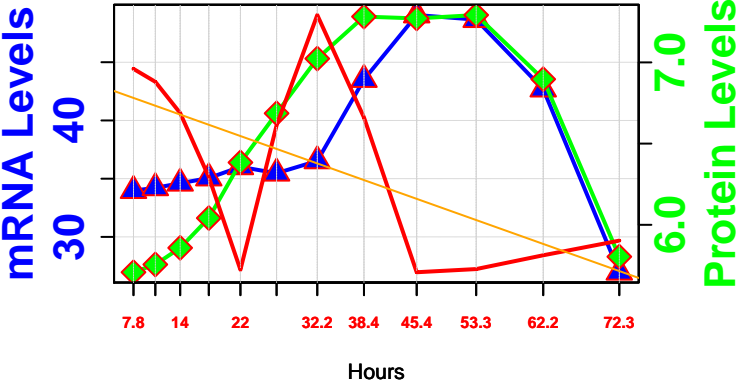
phosphatidylinositol phosphate biosynthesis

622 - SAC1 RLS: 15.89
YKL212W
ORF



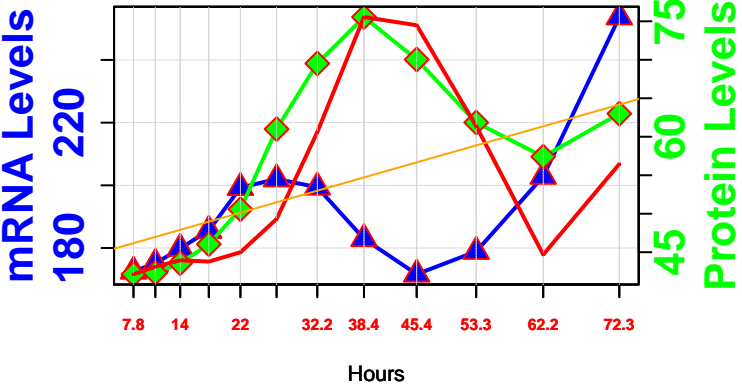
phospholipids degradation

642 - ISC1 RLS: 13.09
YER019W
ORF



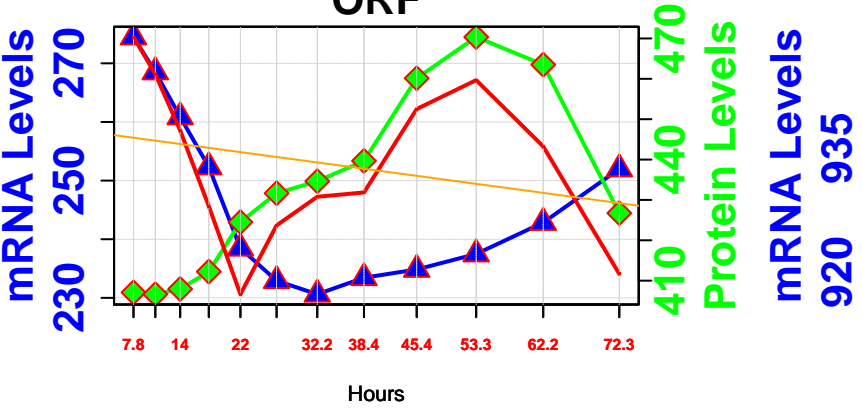
riboflavin, FMN and FAD biosynthesis

647 – RIB4 RLS: 12.4
YOL143C
ORF

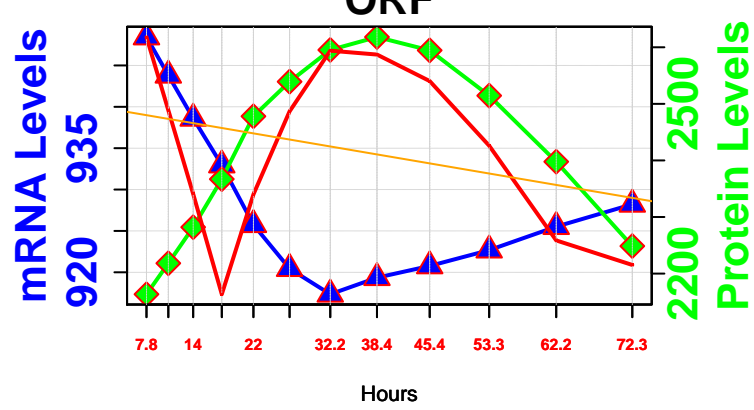


homoserine biosynthesis

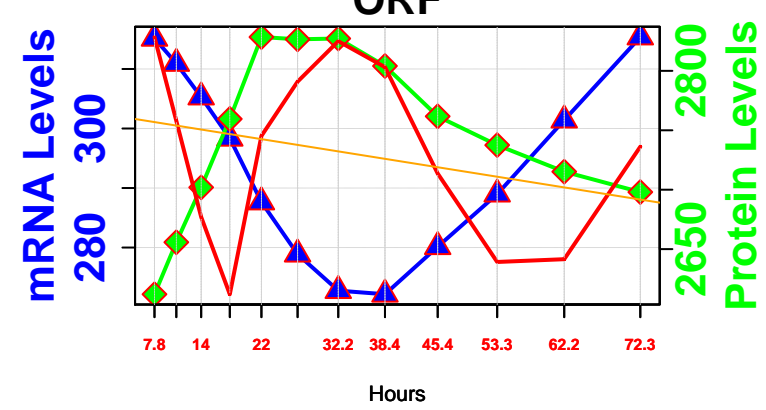
650 – HOM3 RLS: 11.79
YER052C
ORF



651 – HOM2 RLS: 11.68
YDR158W
ORF

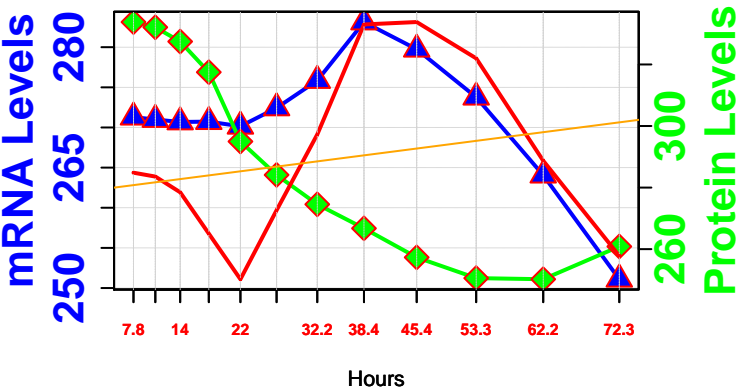


665 – HOM6 RLS: 6.76
YJR139C
ORF



threonine biosynthesis

673 – THR1 RLS: 3.48
YHR025W
ORF



674 – THR4 RLS: 3.12
YCR053W
ORF

