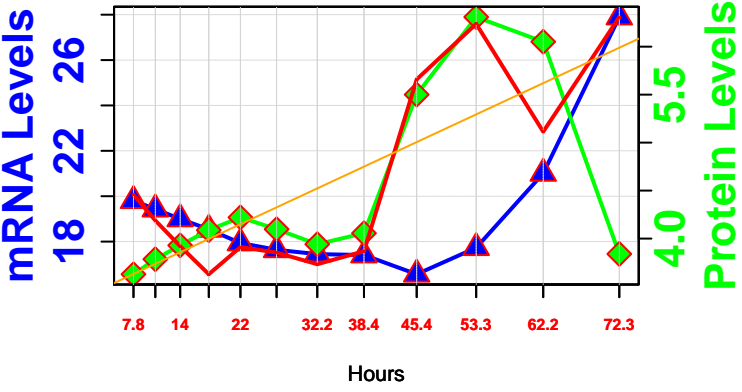


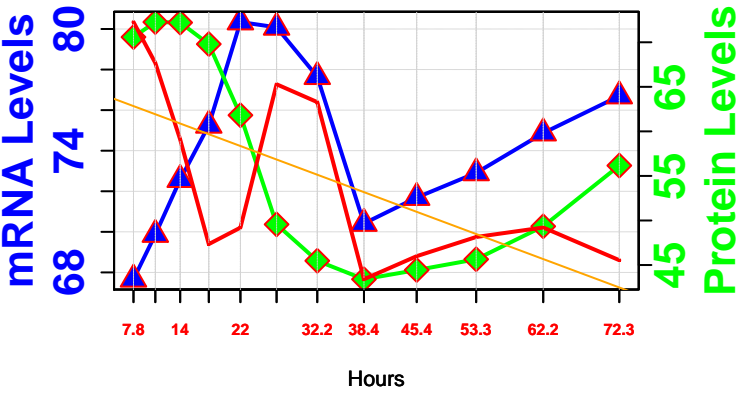
# heme biosynthesis

4 - HEM14 RLS: 36.78  
YER014W  
ORF

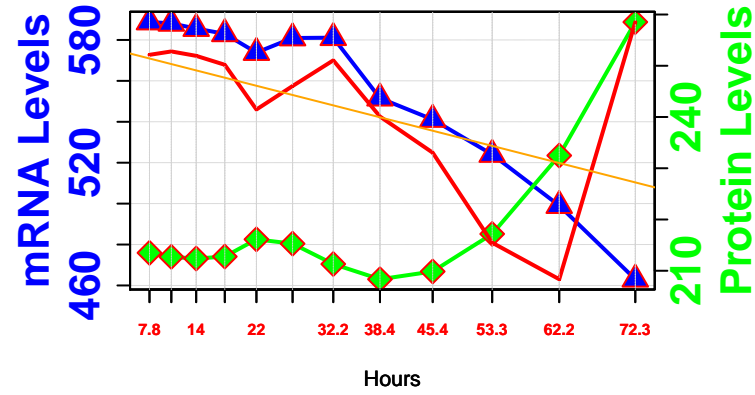


# salvage pathways of guanine, xanthine and their nucleosides

6 – XPT1 RLS: 36  
YJR133W  
ORF

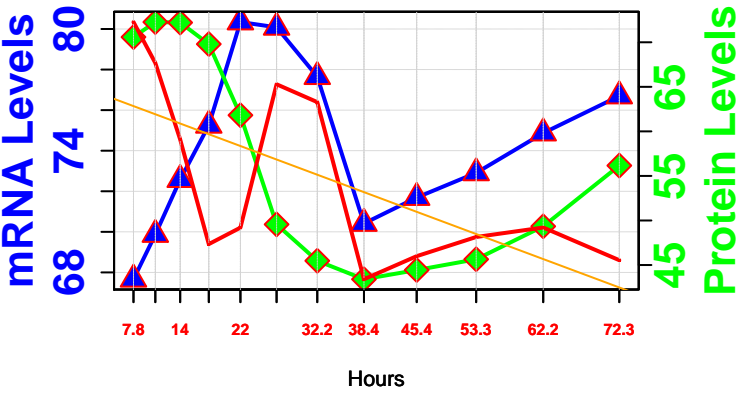


26 – HPT1 RLS: 33.6  
YDR399W  
ORF

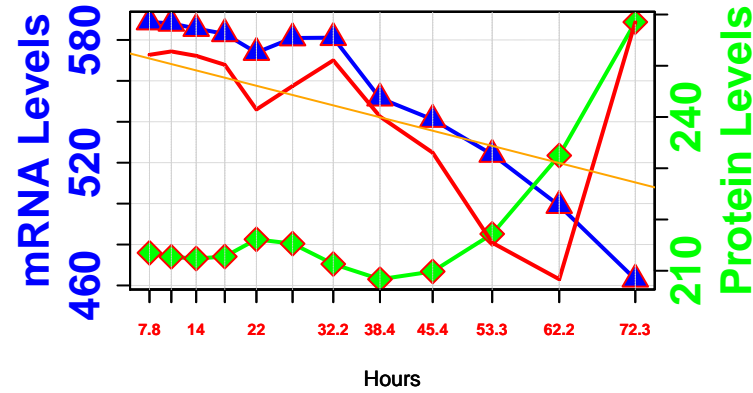


# salvage pathways of purines and their nucleosides

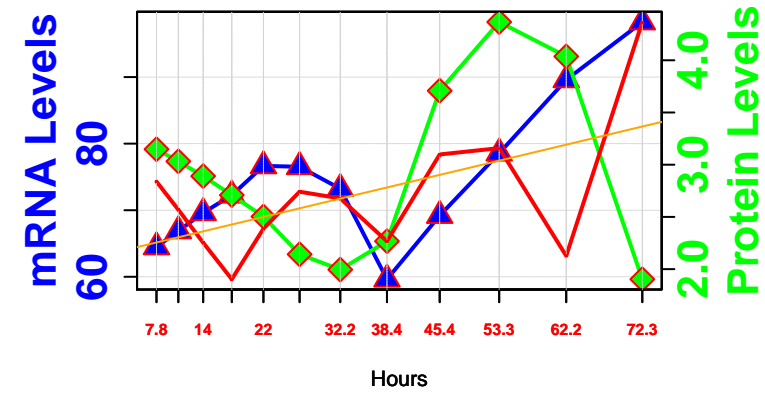
6 – XPT1 RLS: 36  
YJR133W  
ORF



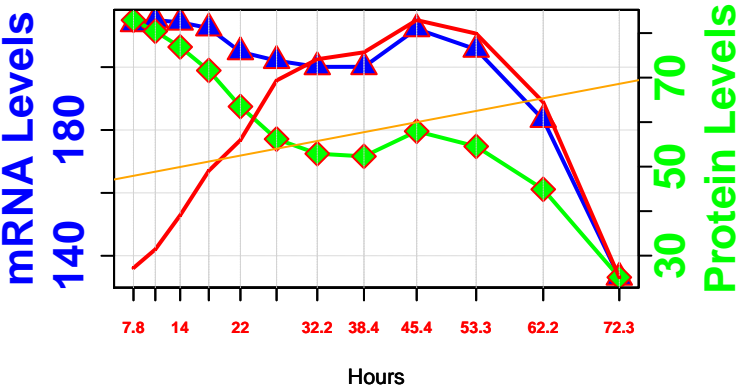
26 – HPT1 RLS: 33.6  
YDR399W  
ORF



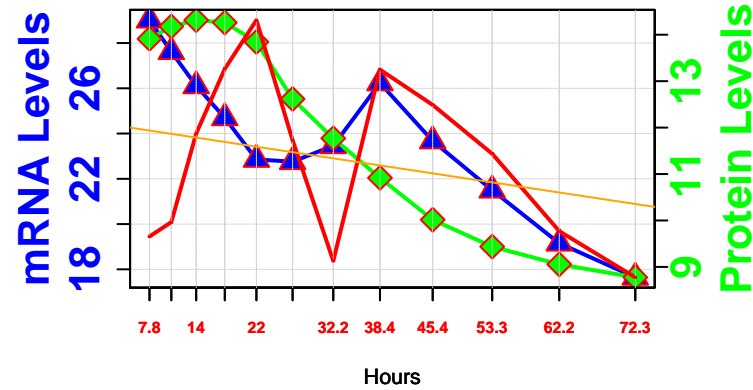
130 – APT2 RLS: 29.6  
YDR441C  
ORF



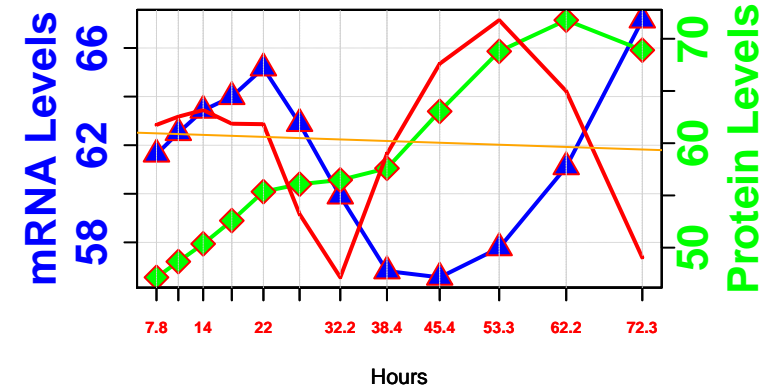
132 – APT1 RLS: 29.6  
YML022W  
ORF



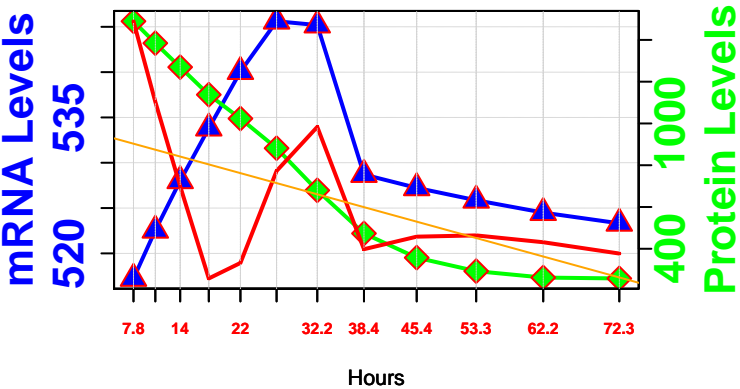
196 – AMD1 RLS: 28.07  
YML035C  
ORF



278 – PNP1 RLS: 26.4  
YLR209C  
ORF

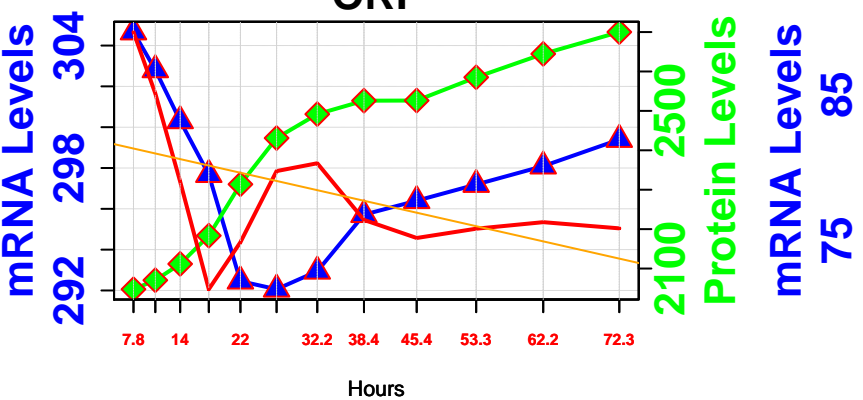


582 – ADO1 RLS: 18.6  
YJR105W  
ORF

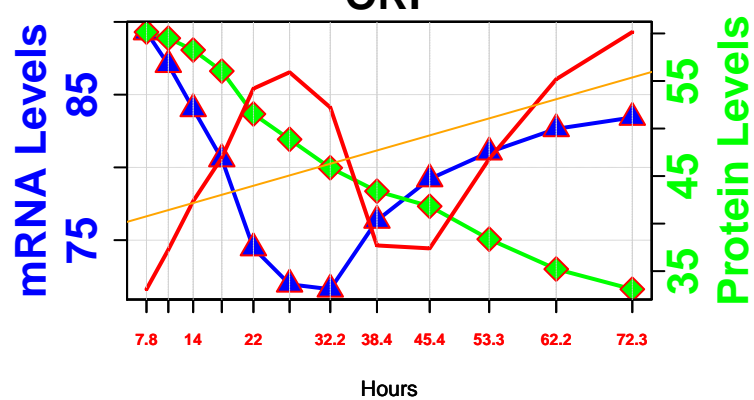


# tryptophan biosynthesis

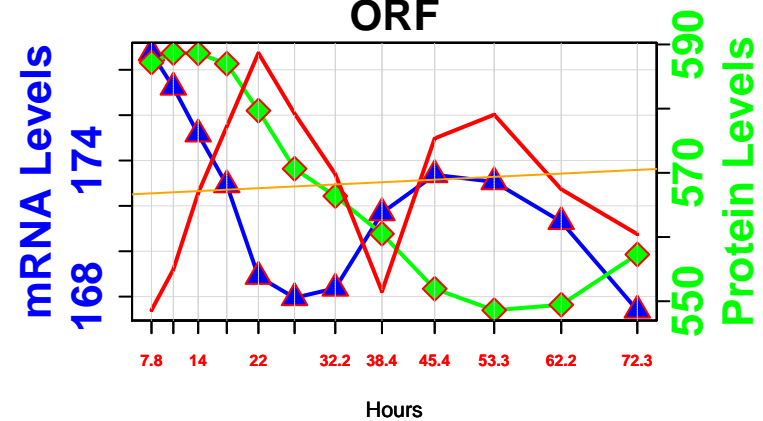
19 – TRP5 RLS: 34  
YGL026C  
ORF

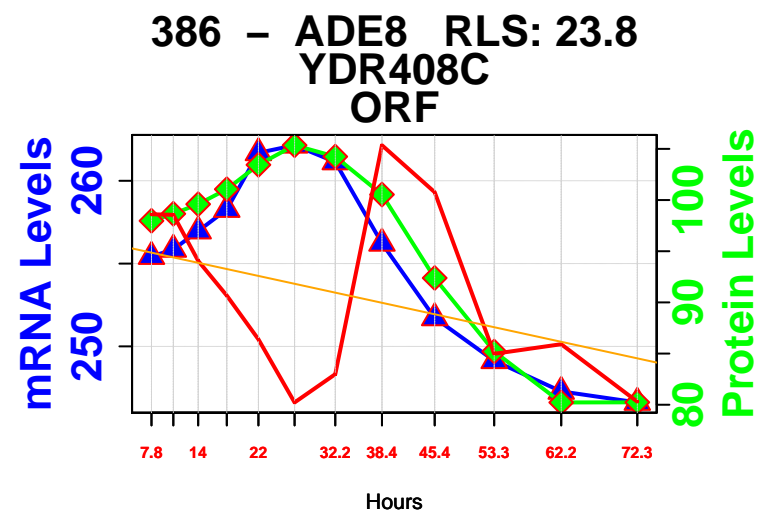
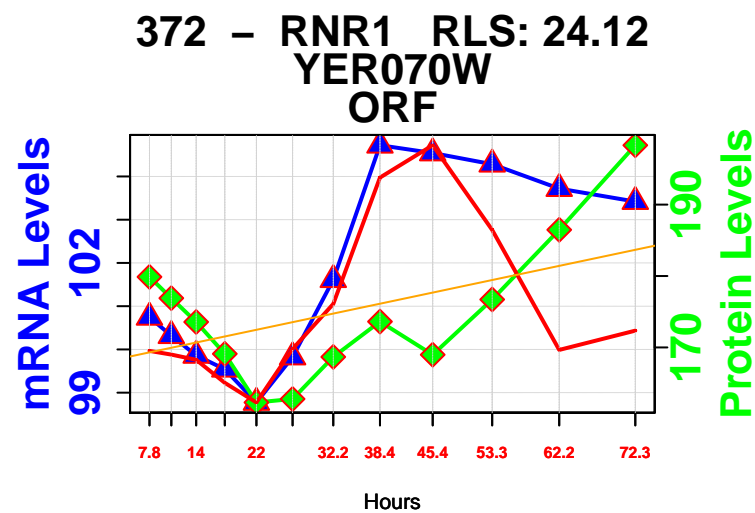
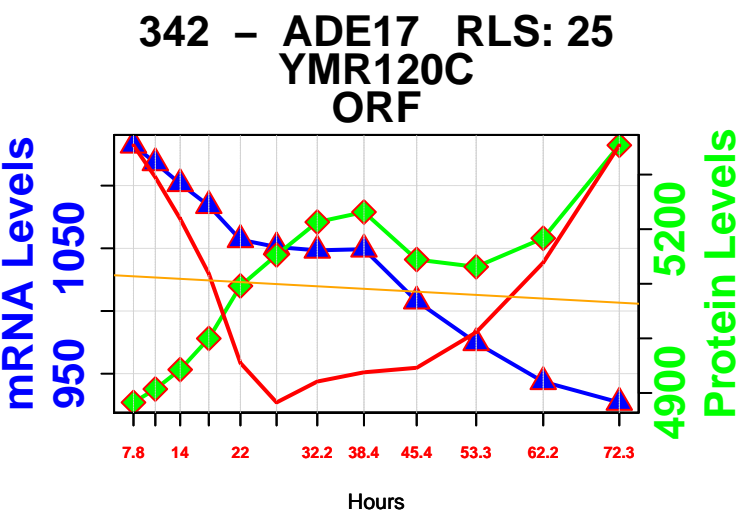
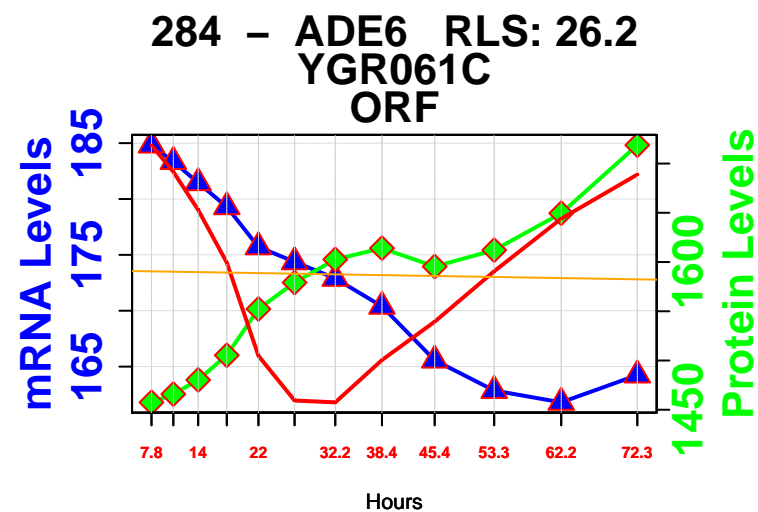
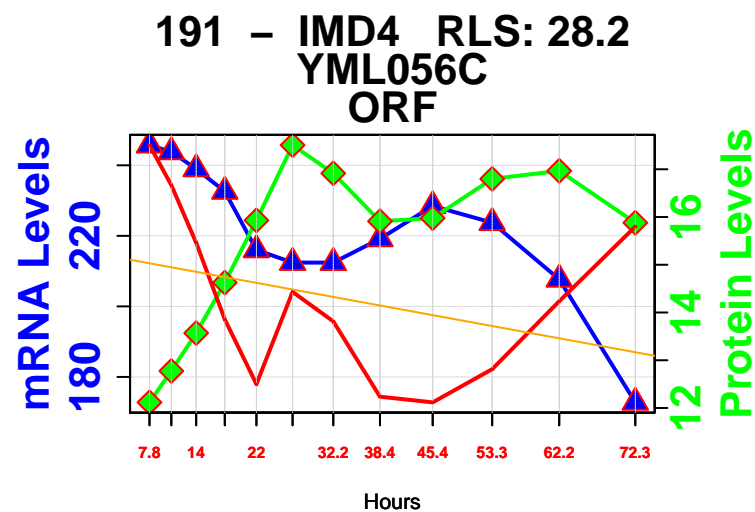
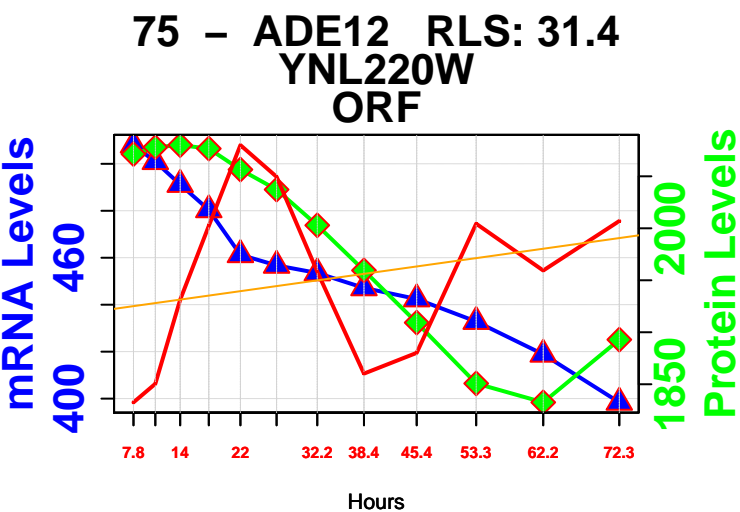
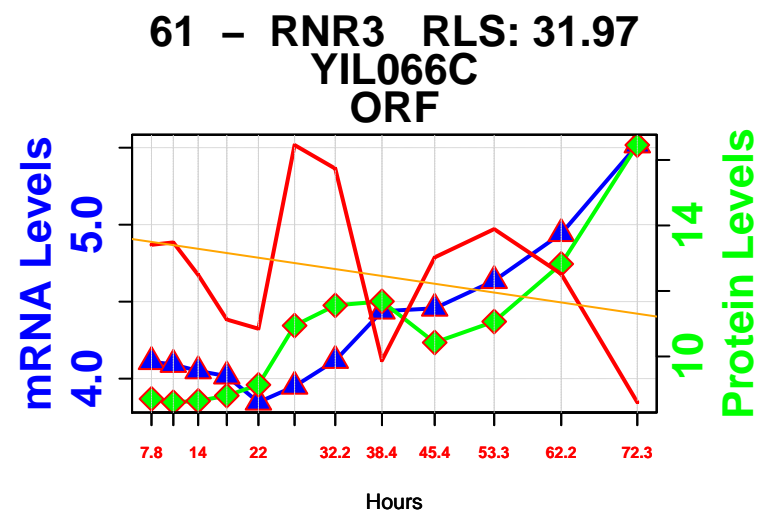
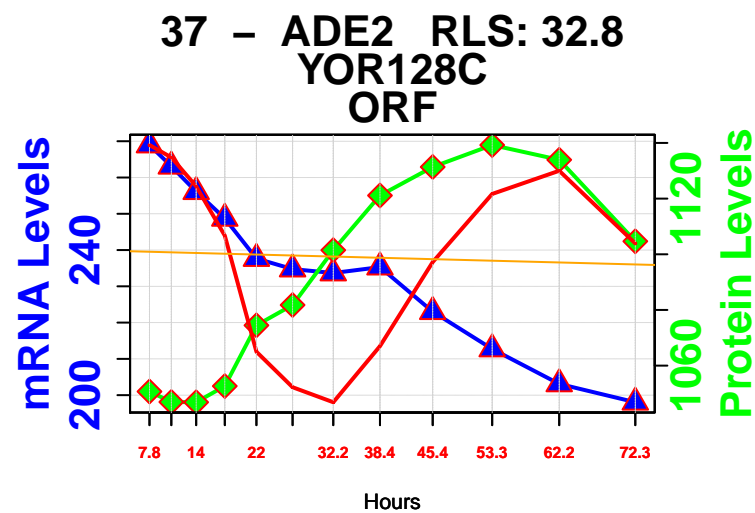
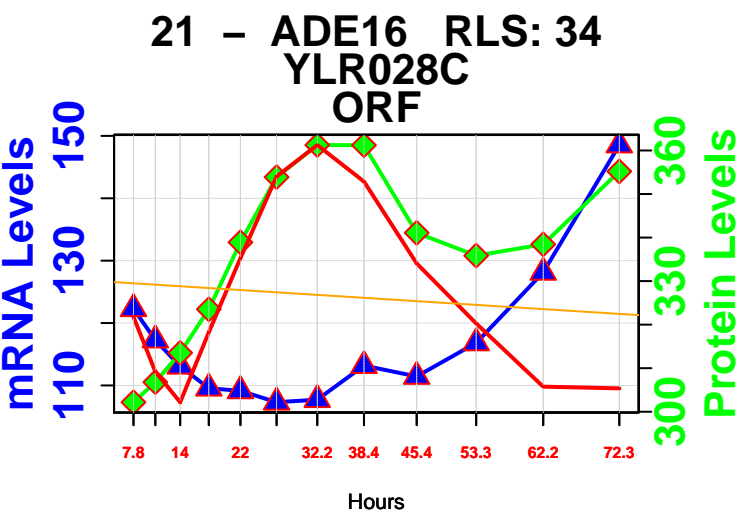


43 – TRP4 RLS: 32.4  
YDR354W  
ORF



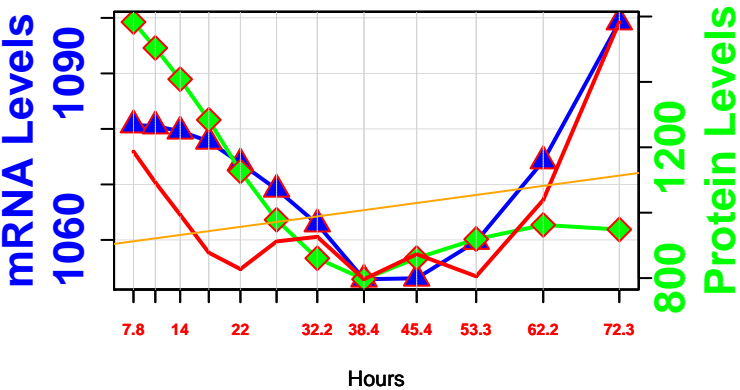
165 – TRP2 RLS: 28.6  
YER090W  
ORF



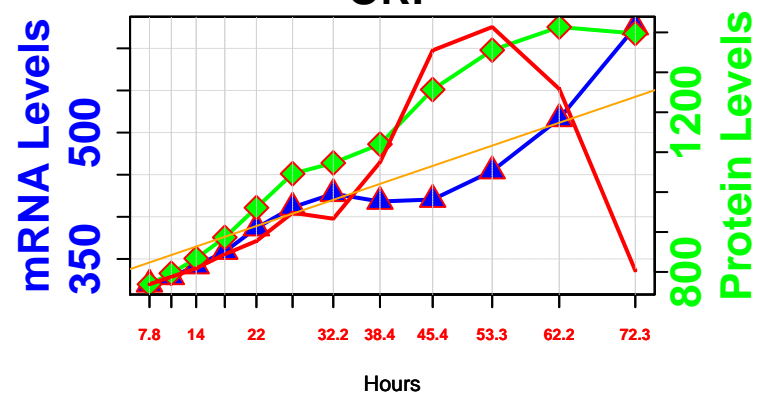


# de novo biosynthesis of purine nucleotides

587 – ADK1 RLS: 18.2  
YDR226W  
ORF

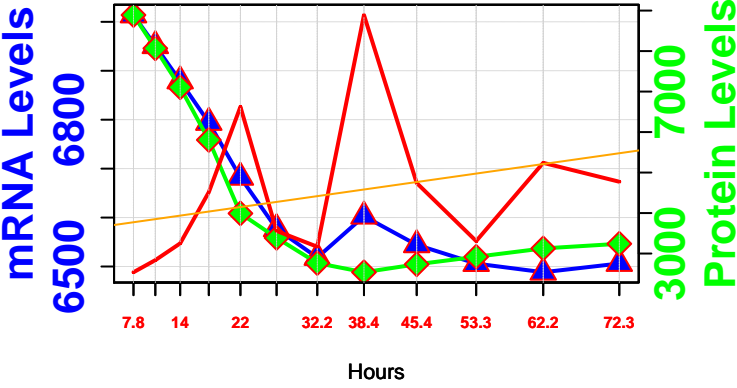


667 – RNR4 RLS: 6.2  
YGR180C  
ORF

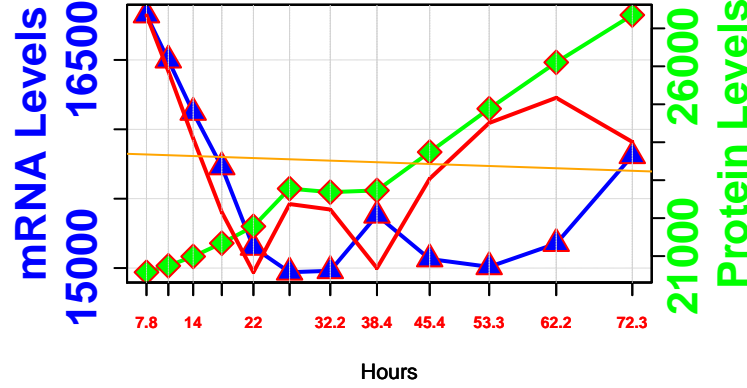


# glycolysis

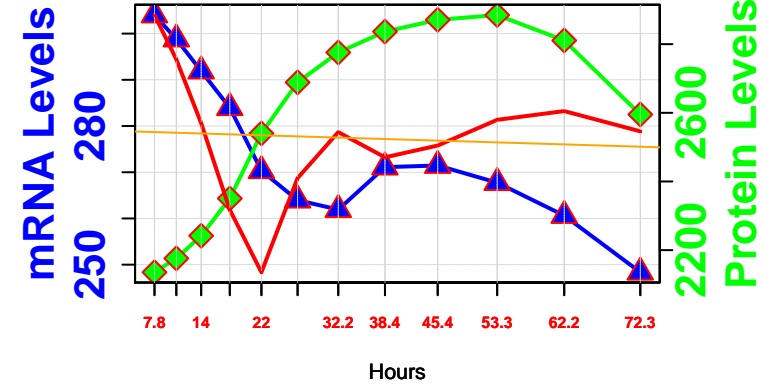
24 – TPI1 RLS: 33.9  
YDR050C  
ORF



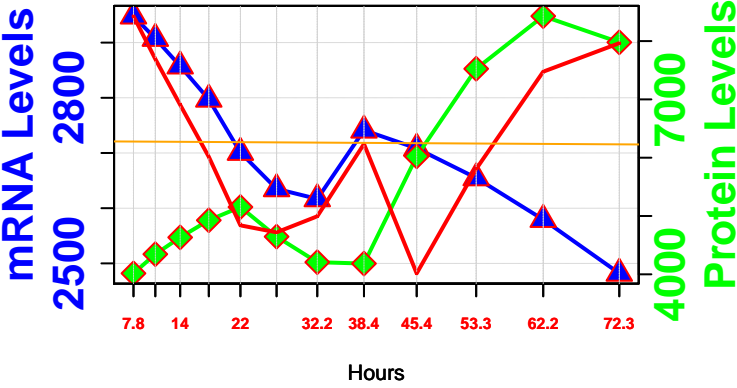
98 – TDH3 RLS: 30.57  
YGR192C  
ORF



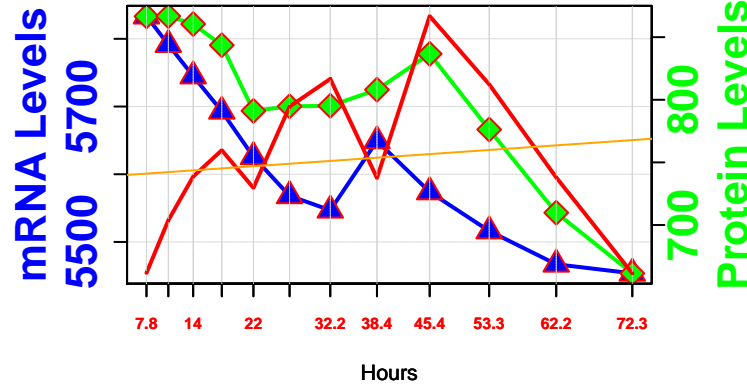
192 – PFK2 RLS: 28.2  
YMR205C  
ORF



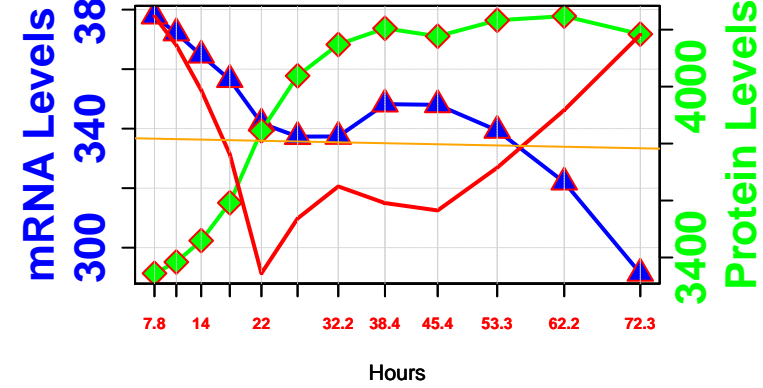
255 – ENO1 RLS: 27.04  
YGR254W  
ORF



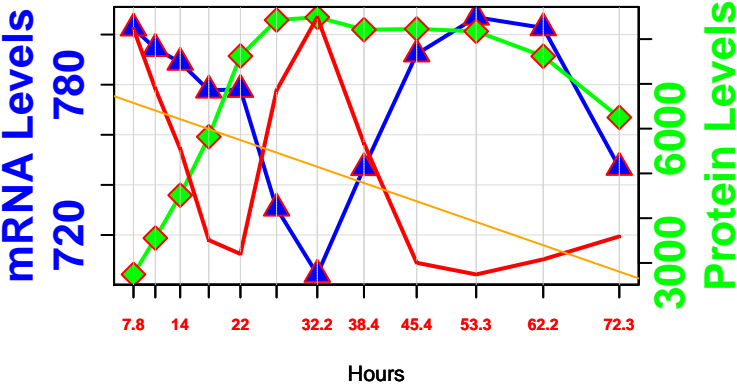
267 – TDH2 RLS: 26.69  
YJR009C  
ORF



269 – PFK1 RLS: 26.63  
YGR240C  
ORF

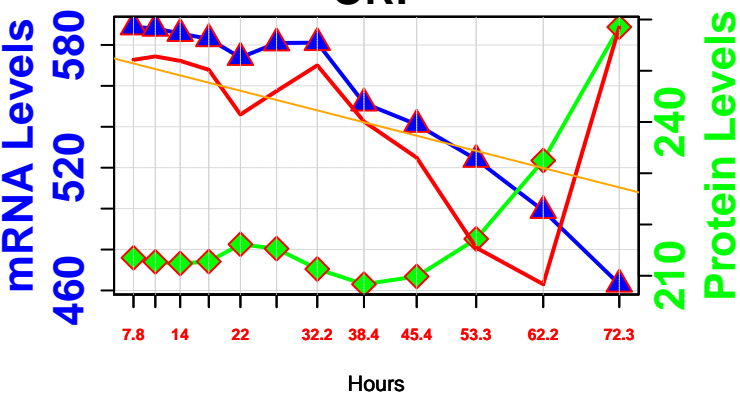


352 – TDH1 RLS: 24.6  
YJL052W  
ORF

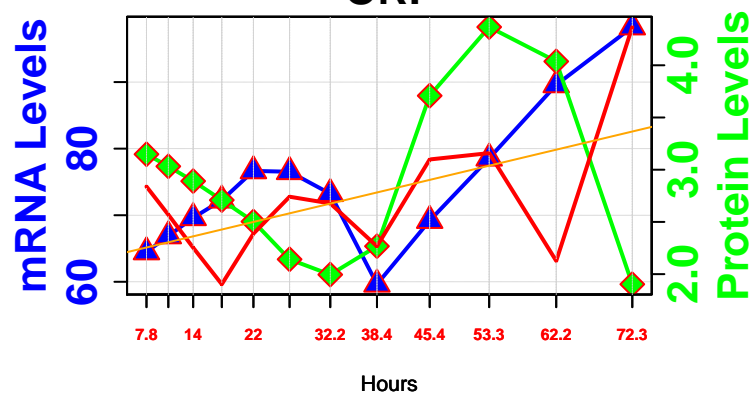


# salvage pathways of adenine, hypoxanthine and their nucleosides

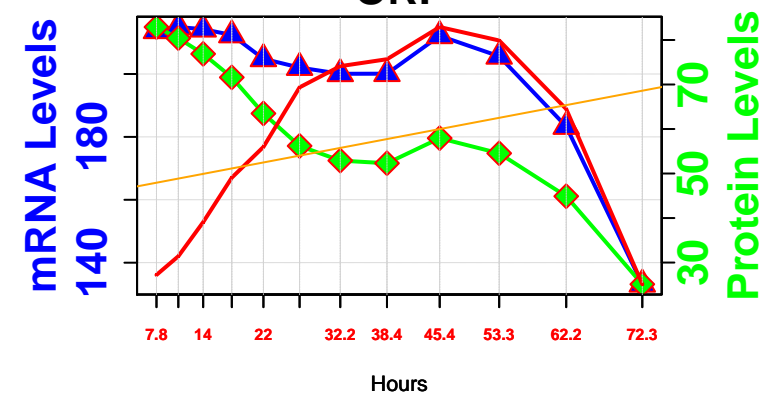
26 – HPT1 RLS: 33.6  
YDR399W  
ORF



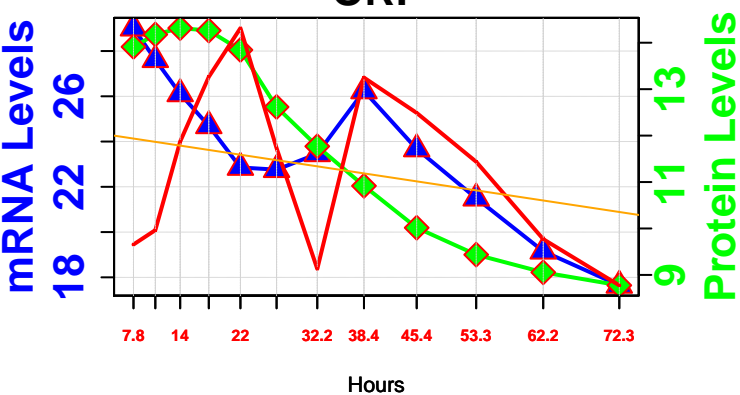
130 – APT2 RLS: 29.6  
YDR441C  
ORF



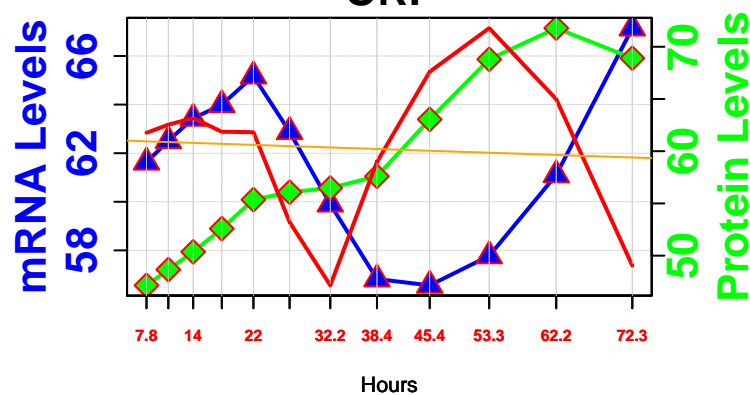
132 – APT1 RLS: 29.6  
YML022W  
ORF



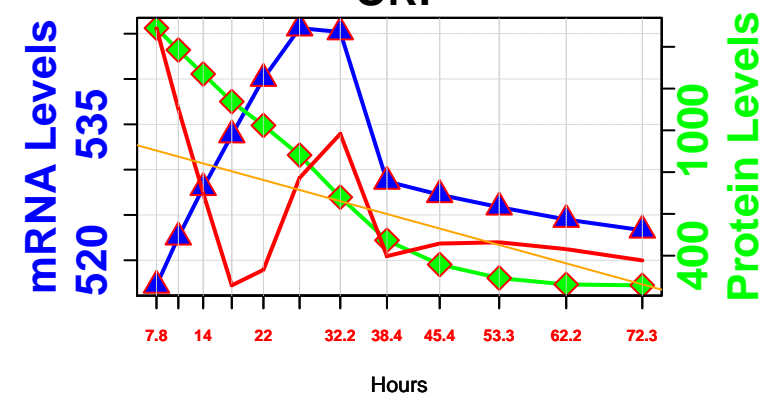
196 – AMD1 RLS: 28.07  
YML035C  
ORF



278 – PNP1 RLS: 26.4  
YLR209C  
ORF



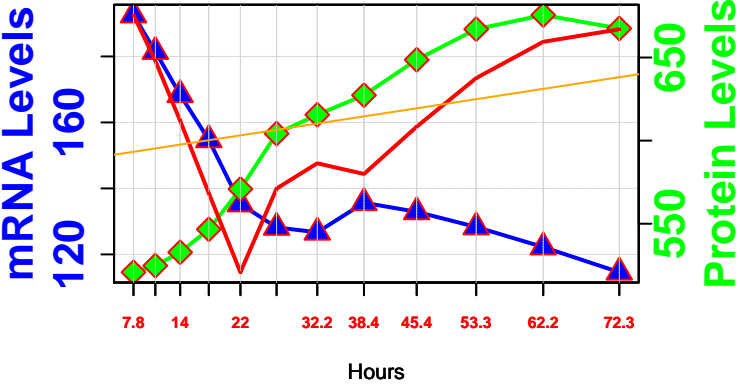
582 – ADO1 RLS: 18.6  
YJR105W  
ORF



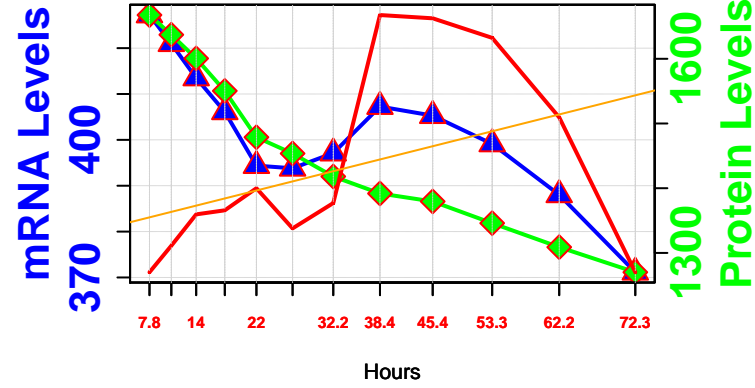


# serine biosynthesis from 3-phosphoglycerate

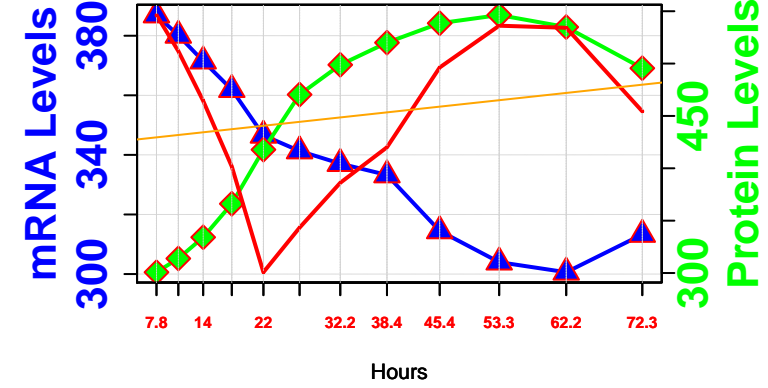
28 – SER33 RLS: 33.4  
YIL074C  
ORF



428 – SER1 RLS: 23.2  
YOR184W  
ORF

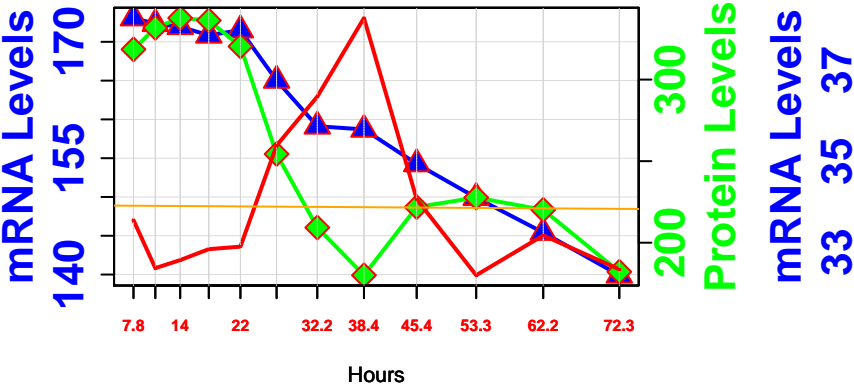


444 – SER3 RLS: 22.8  
YER081W  
ORF

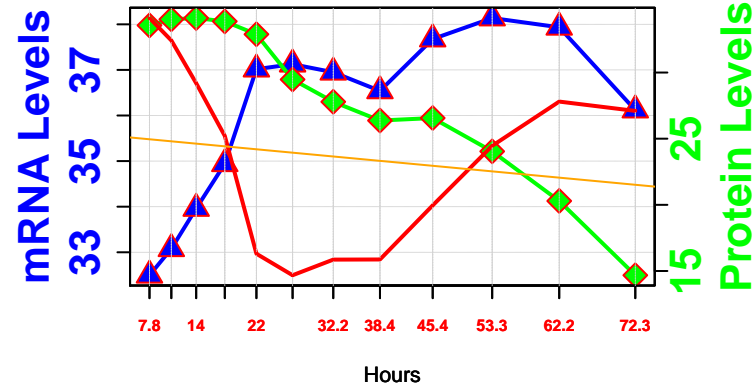


# tryptophan degradation via kynurenine

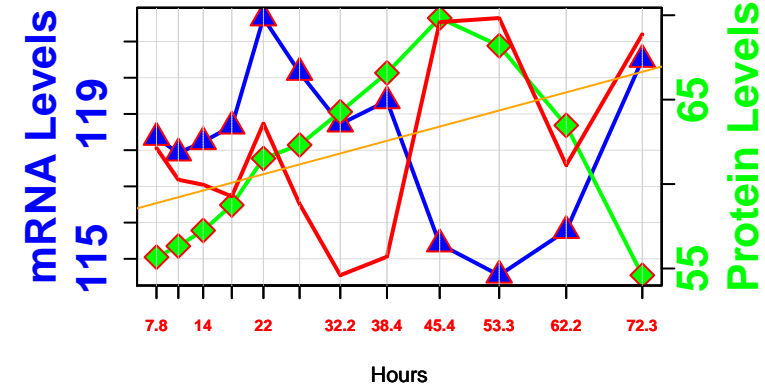
33 – BNA1 RLS: 33  
YJR025C  
ORF



39 – BNA4 RLS: 32.6  
YBL098W  
ORF

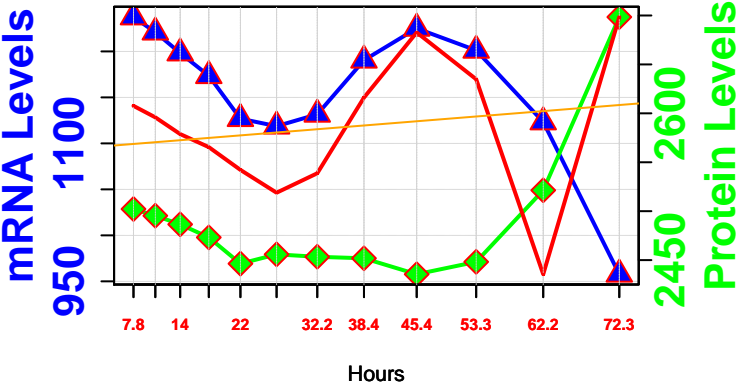


415 – BNA6 RLS: 23.4  
YFR047C  
ORF

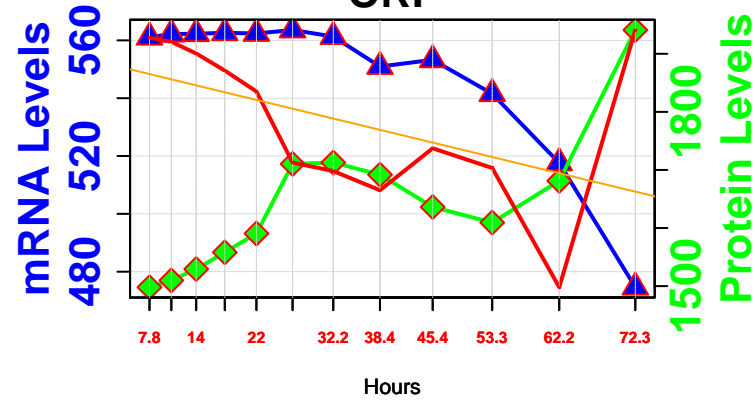


# S-adenosylmethionine biosynthesis

34 – SAM1 RLS: 32.96  
YLR180W  
ORF

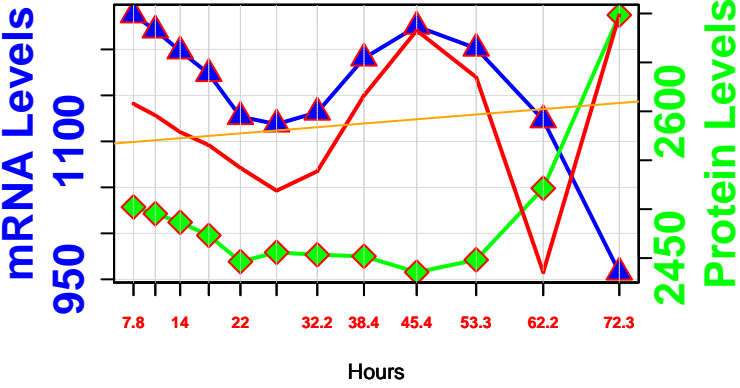


387 – SAM2 RLS: 23.8  
YDR502C  
ORF

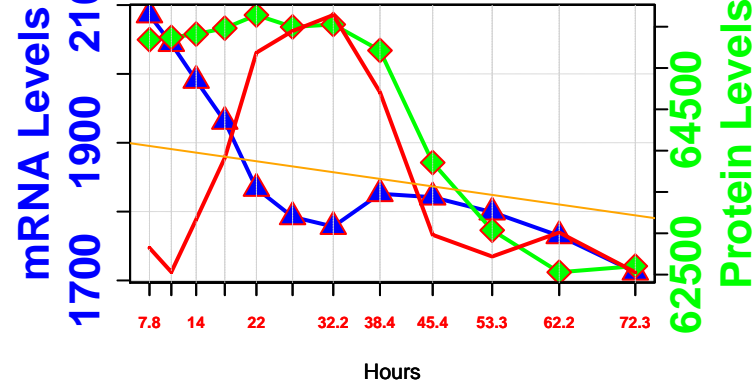


# S-adenosylmethionine cycle

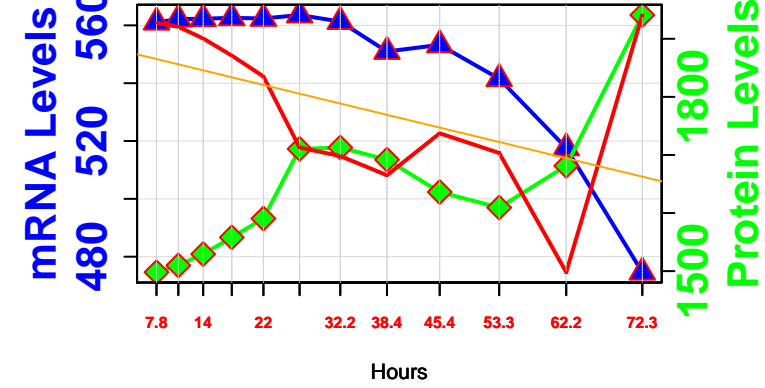
34 – SAM1 RLS: 32.96  
YLR180W  
ORF



312 – MET6 RLS: 25.74  
YER091C  
ORF

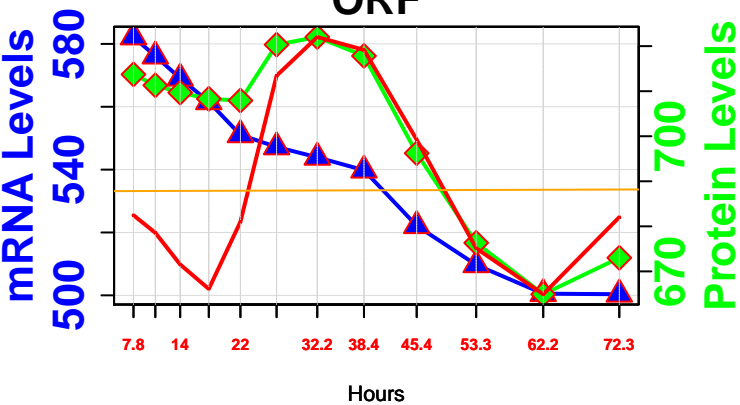


387 – SAM2 RLS: 23.8  
YDR502C  
ORF

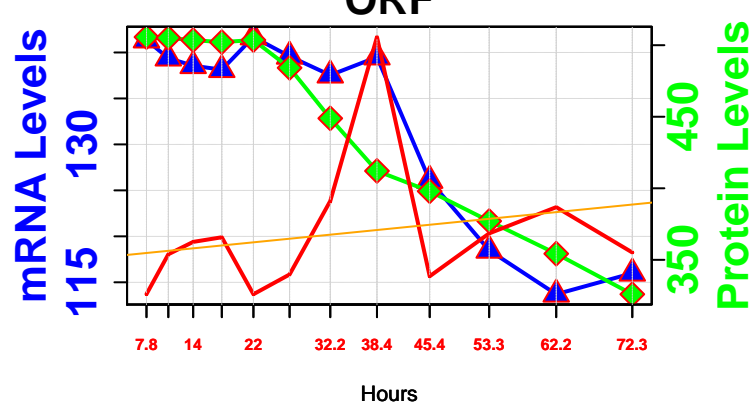


# folate biosynthesis

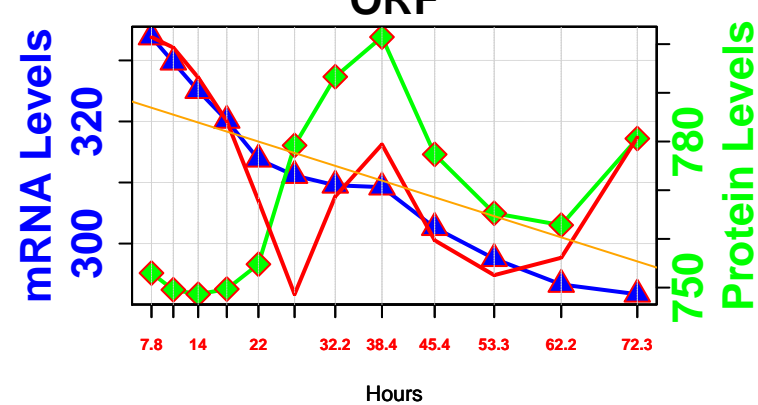
36 - GCV1 RLS: 32.8  
YDR019C  
ORF



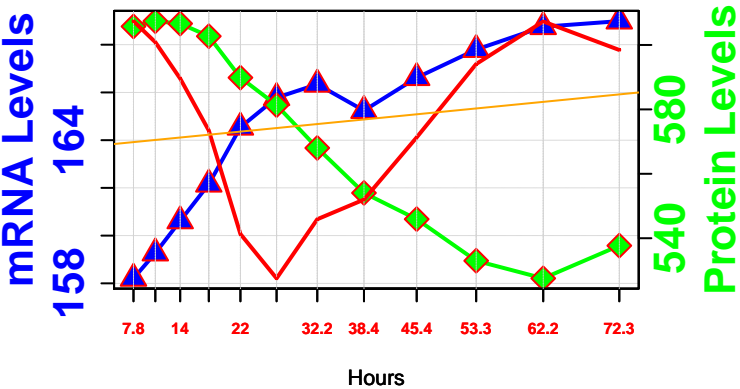
93 - LPD1 RLS: 30.69  
YFL018C  
ORF



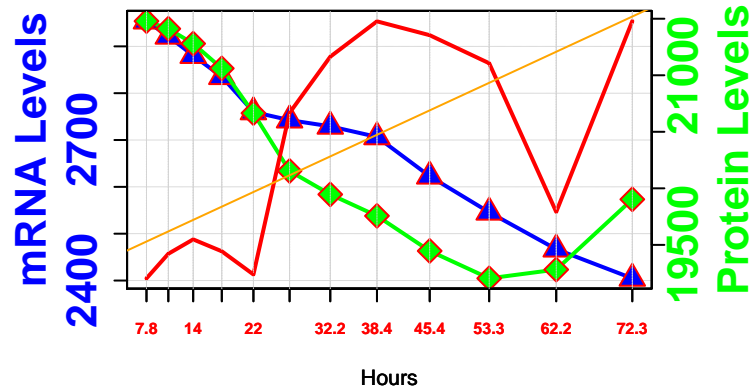
109 - GCV2 RLS: 30.36  
YMR189W  
ORF



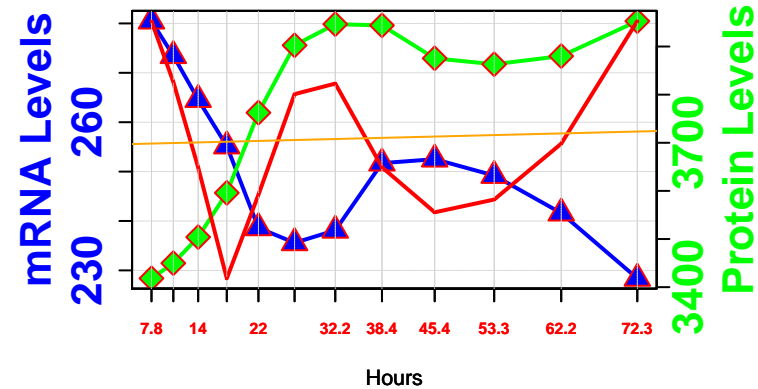
170 - SHM1 RLS: 28.53  
YBR263W  
ORF



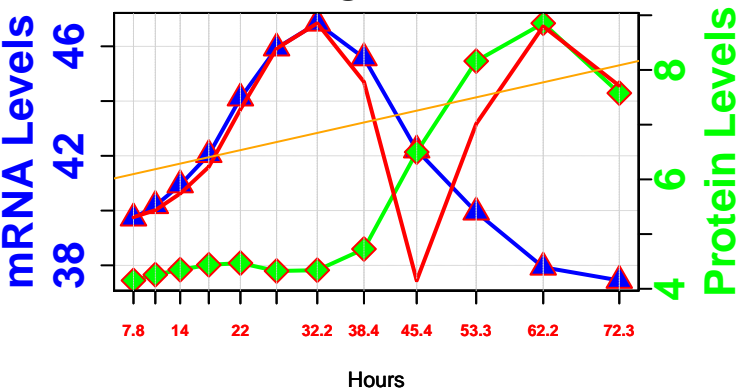
182 - SHM2 RLS: 28.28  
YLR058C  
ORF



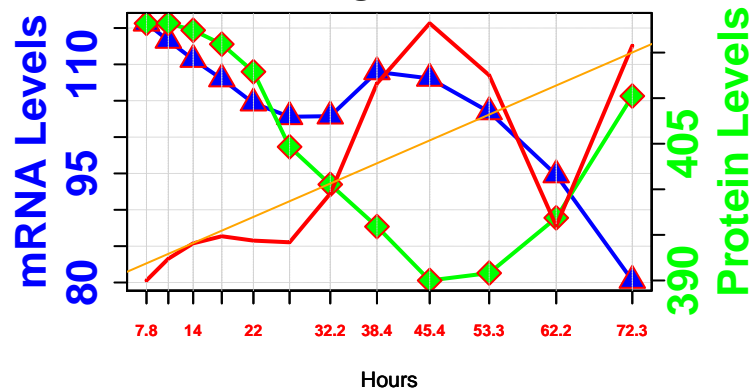
327 - ADE3 RLS: 25.4  
YGR204W  
ORF



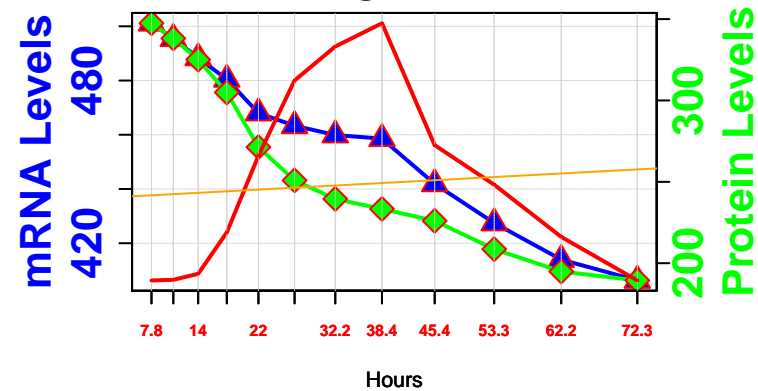
370 - MET12 RLS: 24.2  
YPL023C  
ORF



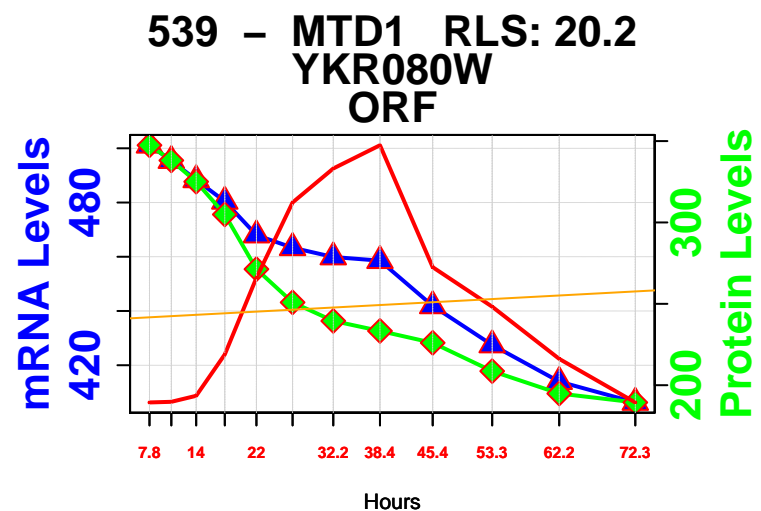
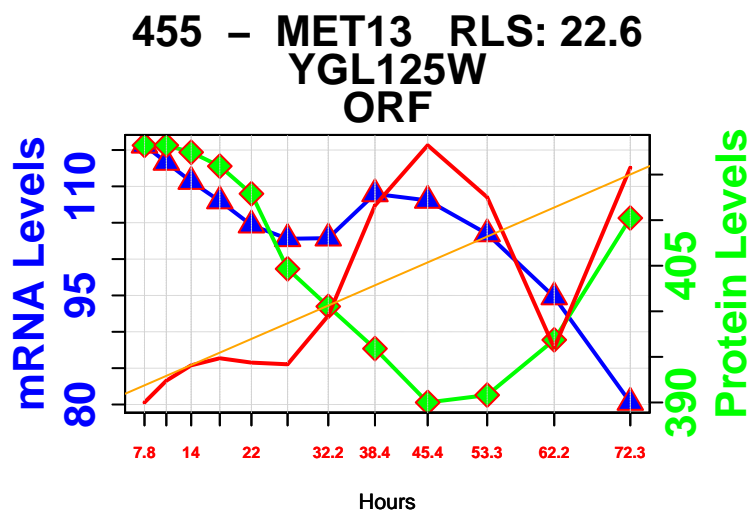
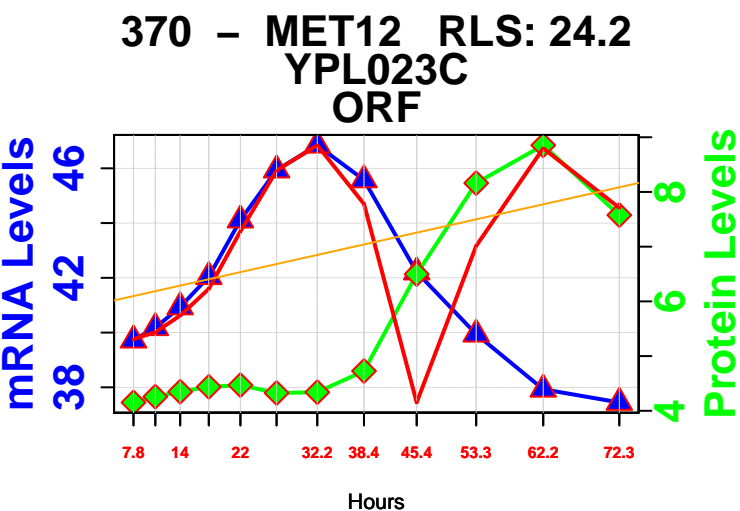
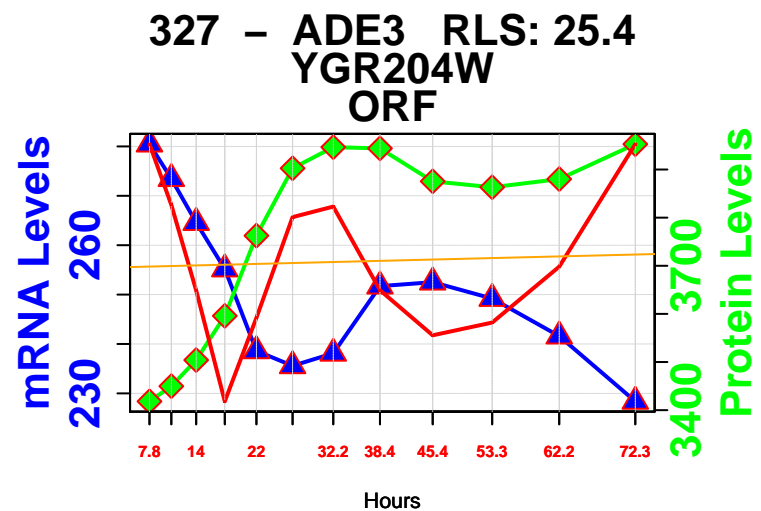
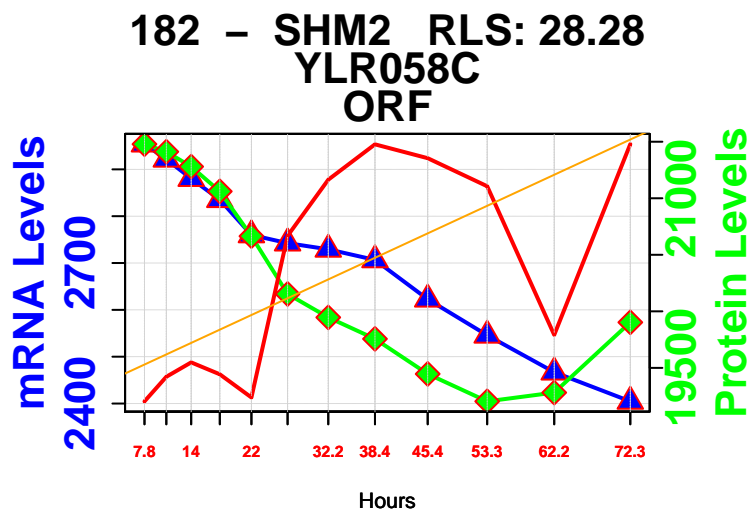
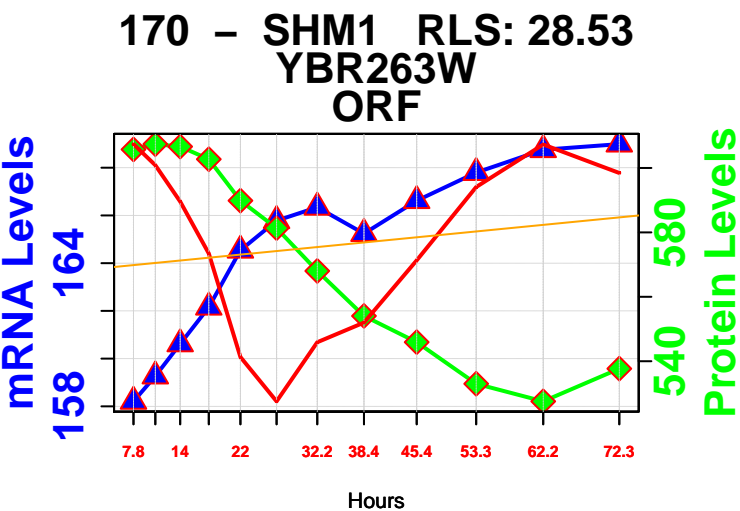
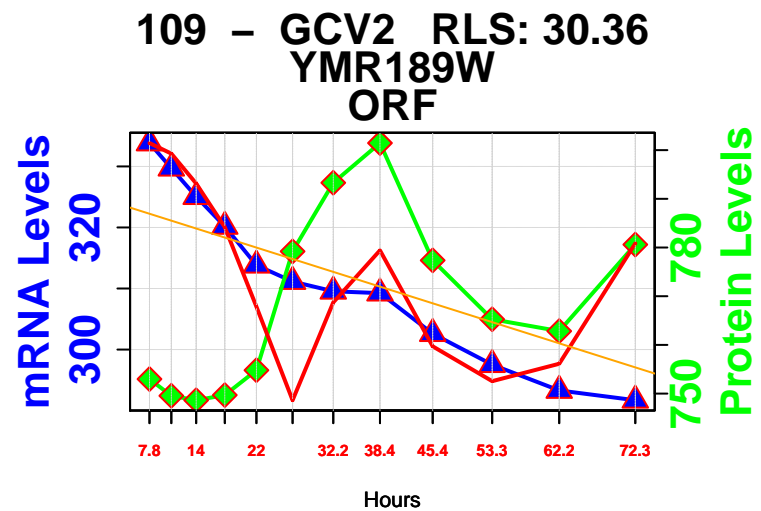
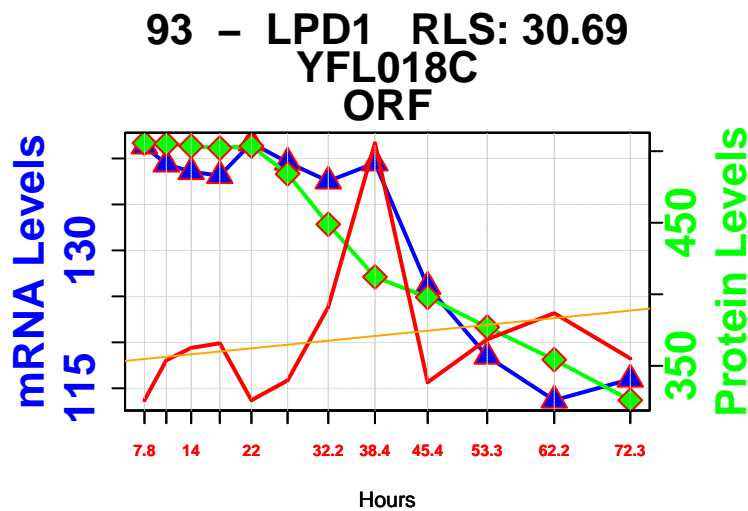
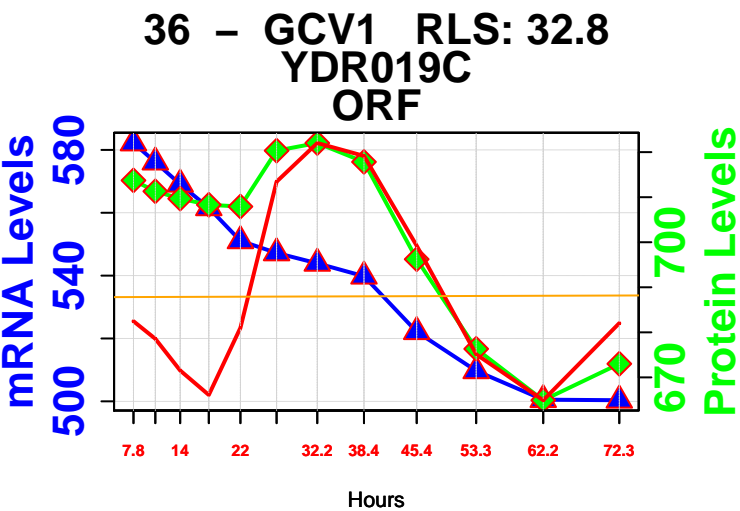
455 - MET13 RLS: 22.6  
YGL125W  
ORF



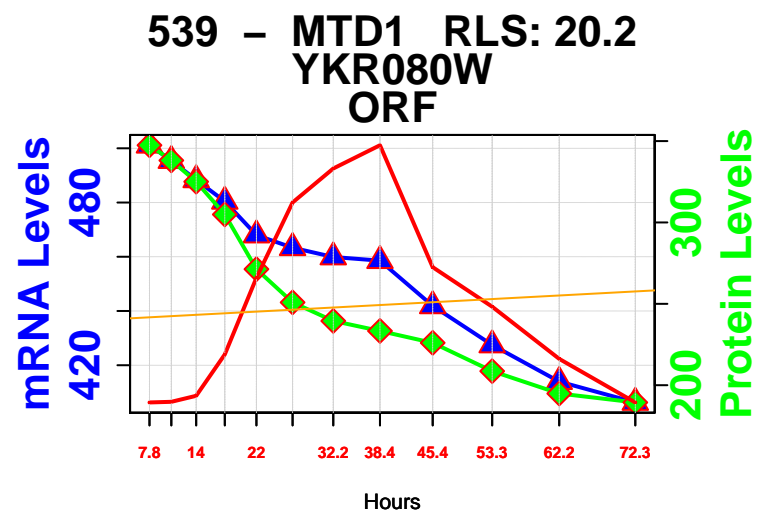
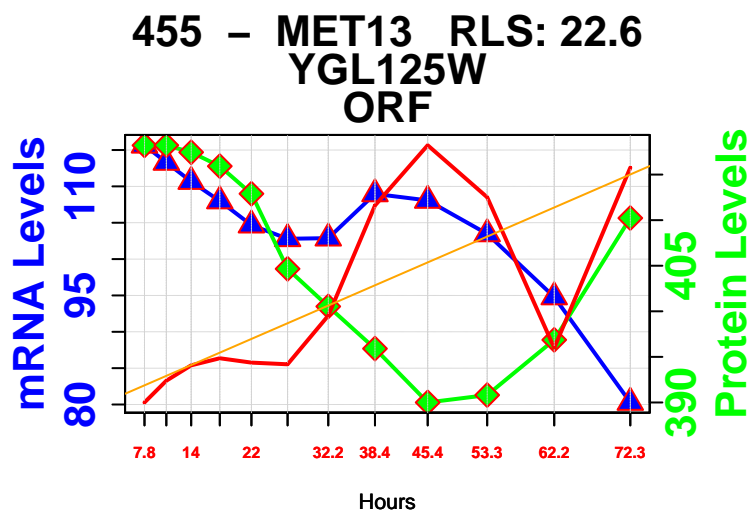
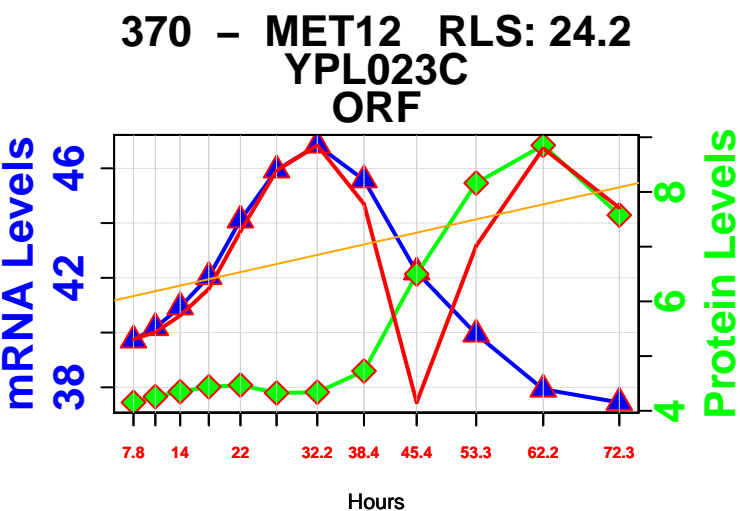
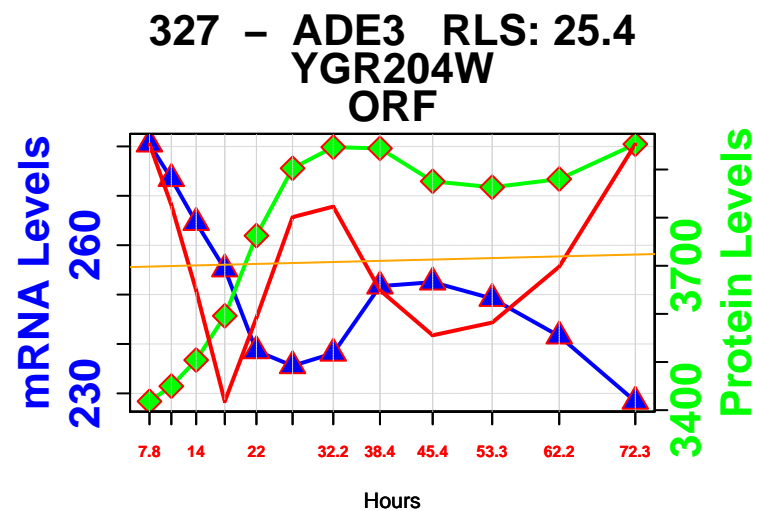
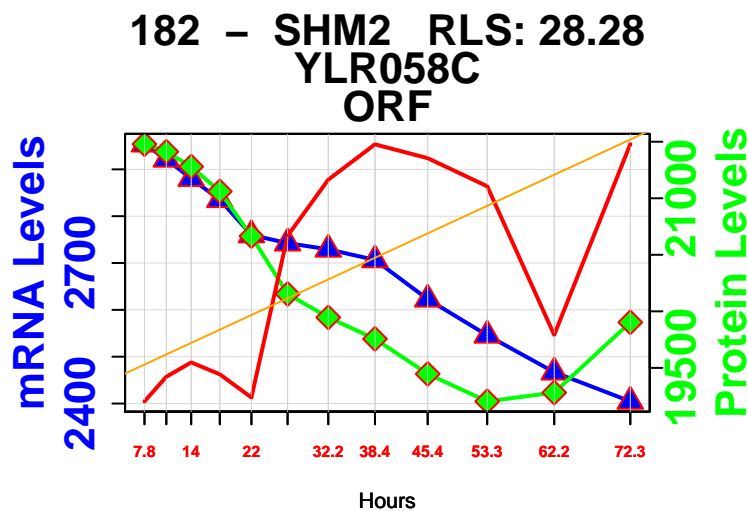
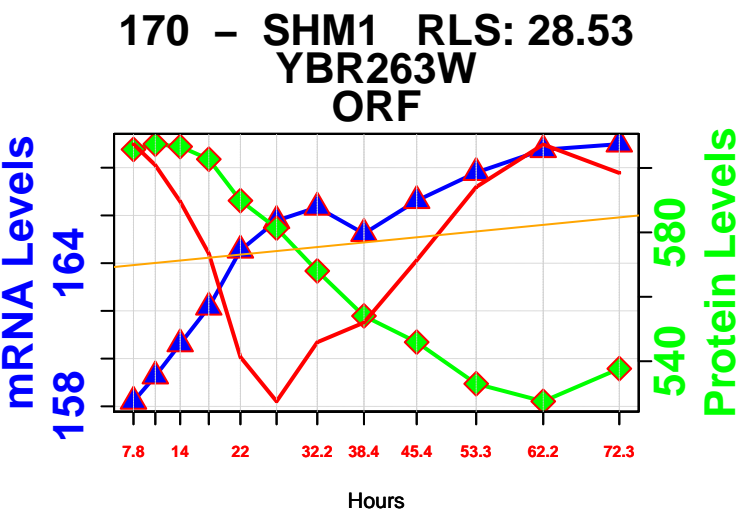
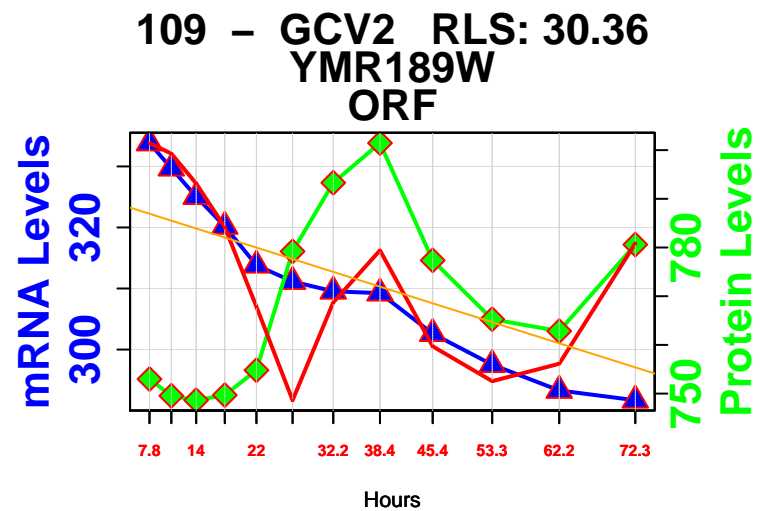
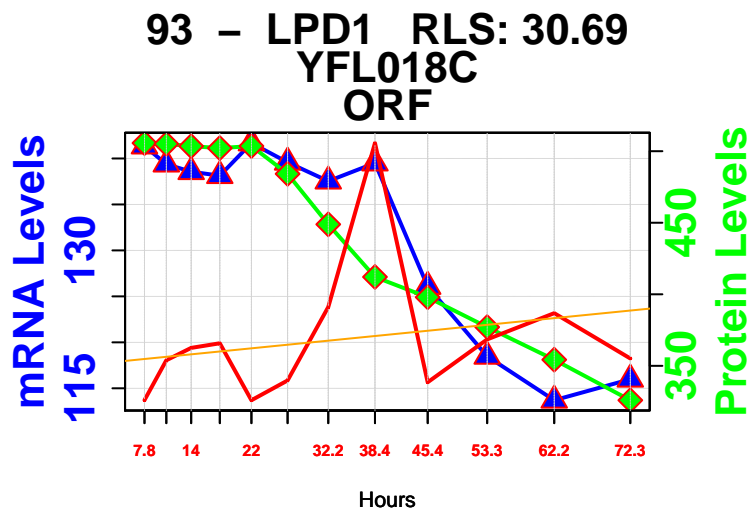
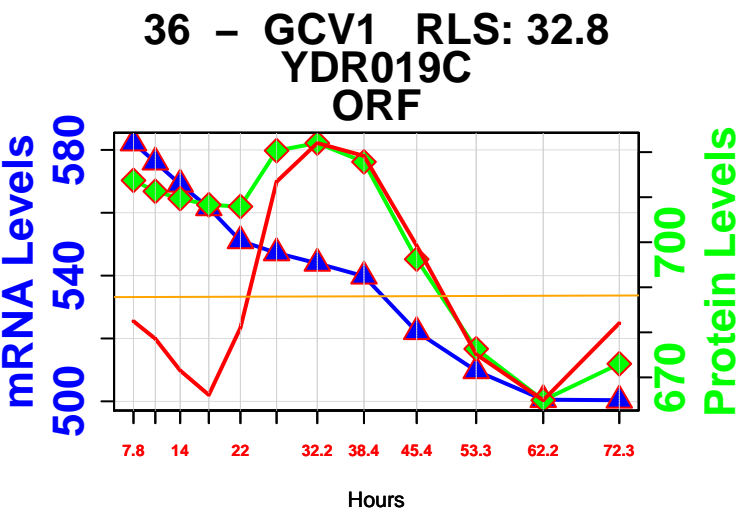
539 - MTD1 RLS: 20.2  
YKR080W  
ORF



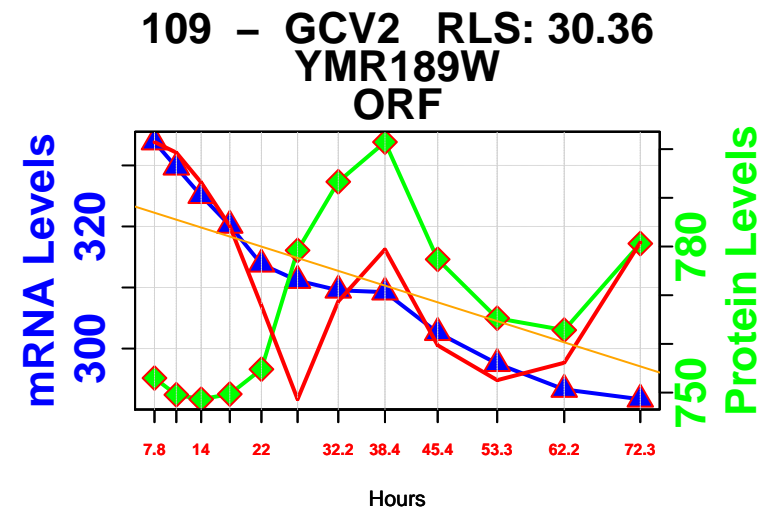
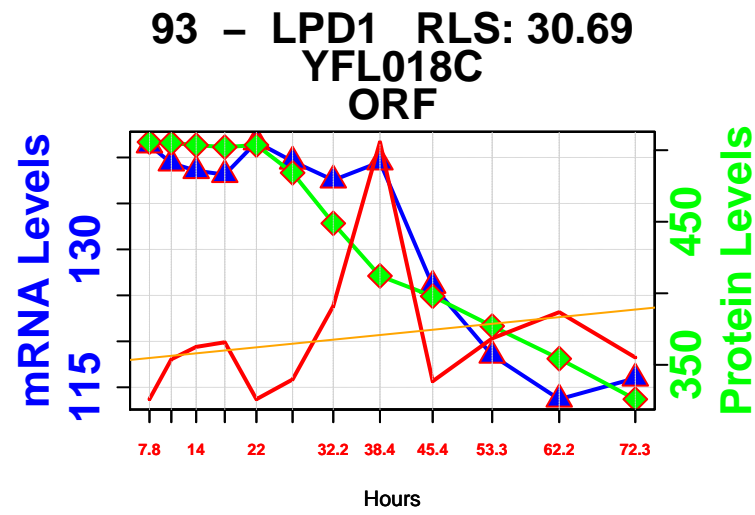
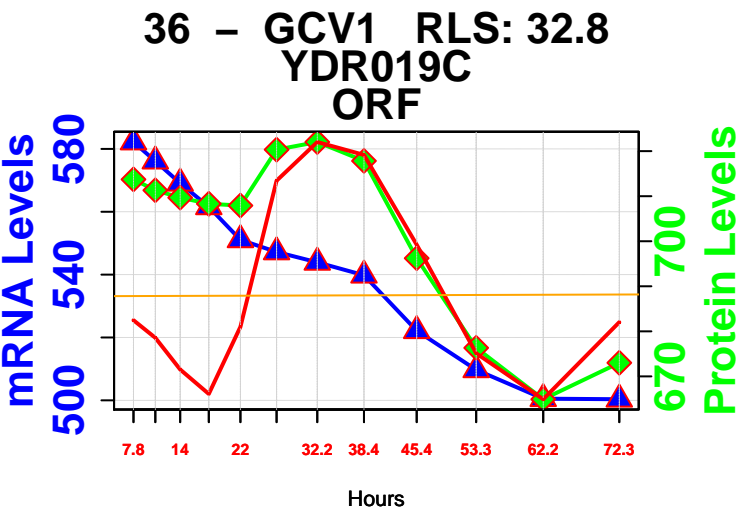
# folate interconversions



# folate transformations



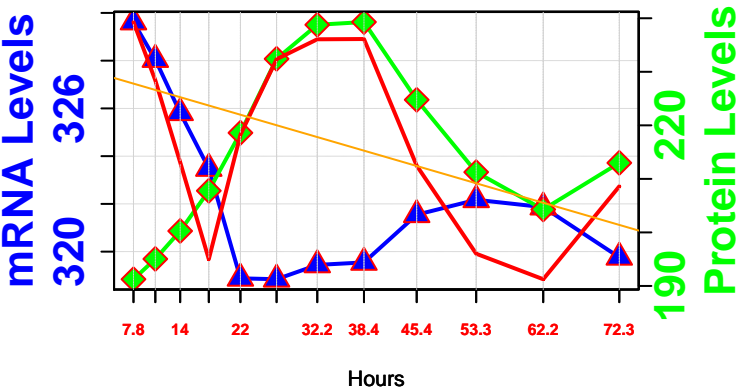
# glycine cleavage complex



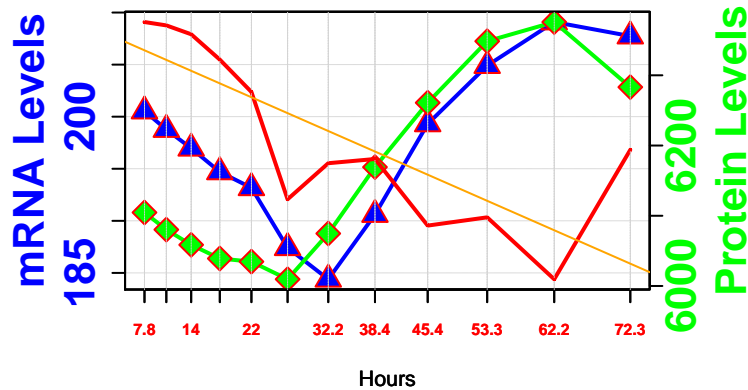


# de novo biosynthesis of pyrimidine ribonucleotides

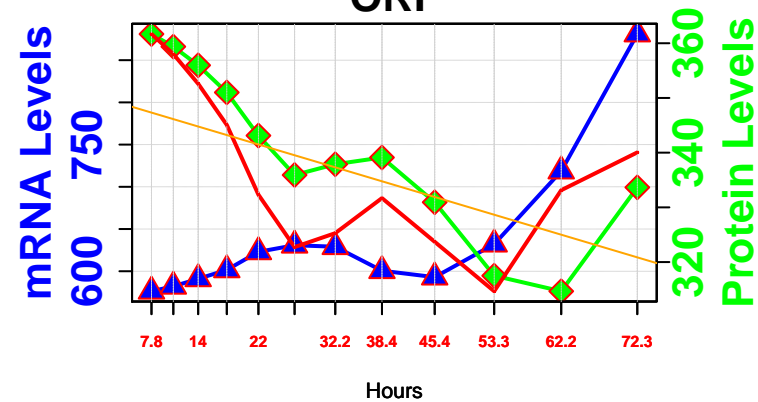
52 - URA5 RLS: 32.2  
YML106W  
ORF



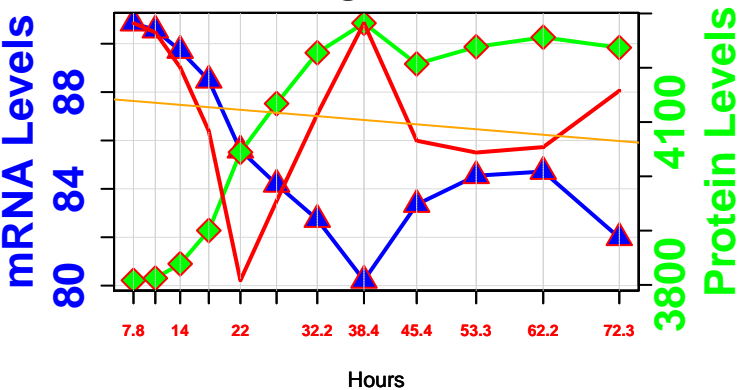
250 - CPA2 RLS: 27.16  
YJR109C  
ORF



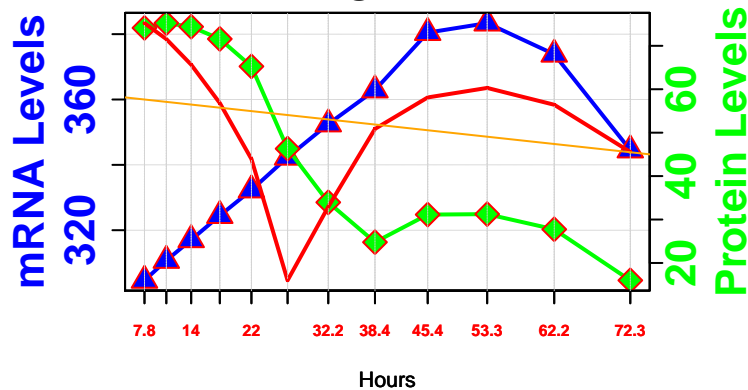
429 - CPA1 RLS: 23.2  
YOR303W  
ORF



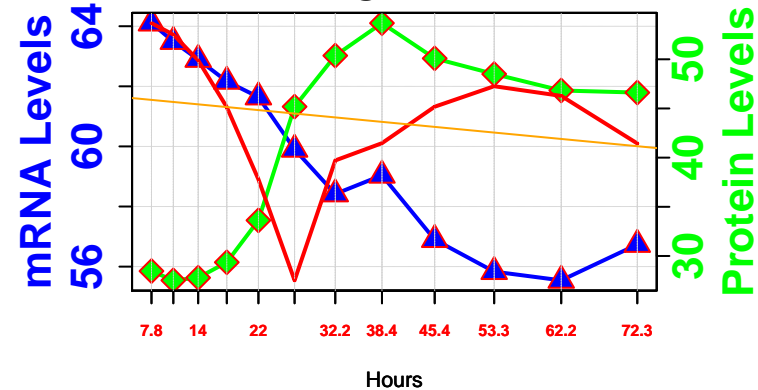
464 - URA2 RLS: 22.54  
YJL130C  
ORF



525 - URA1 RLS: 20.79  
YKL216W  
ORF

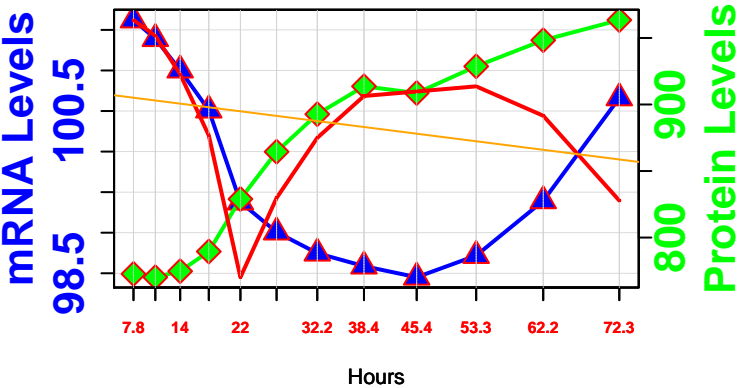


526 - URA8 RLS: 20.75  
YJR103W  
ORF

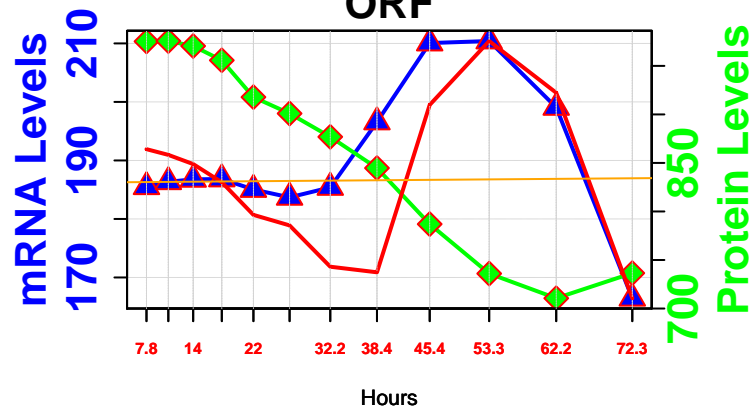


# lysine biosynthesis

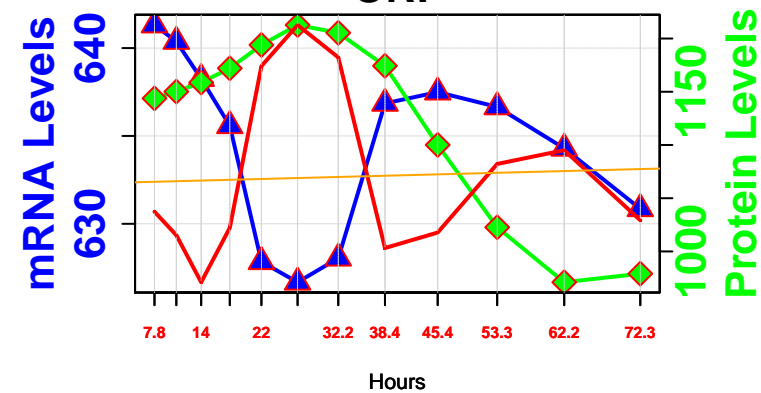
57 - LYS2 RLS: 32  
YBR115C  
ORF



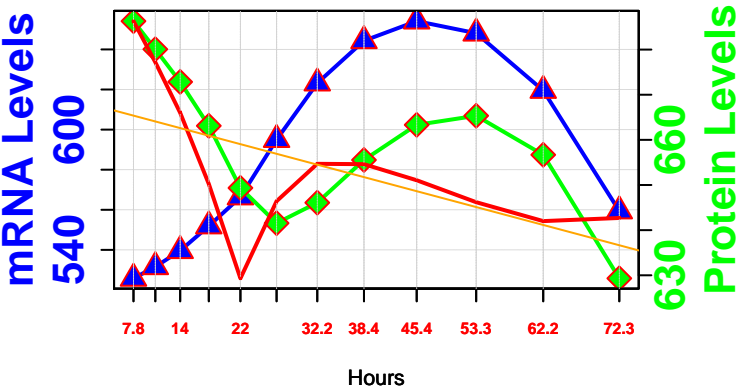
107 - LYS4 RLS: 30.39  
YDR234W  
ORF



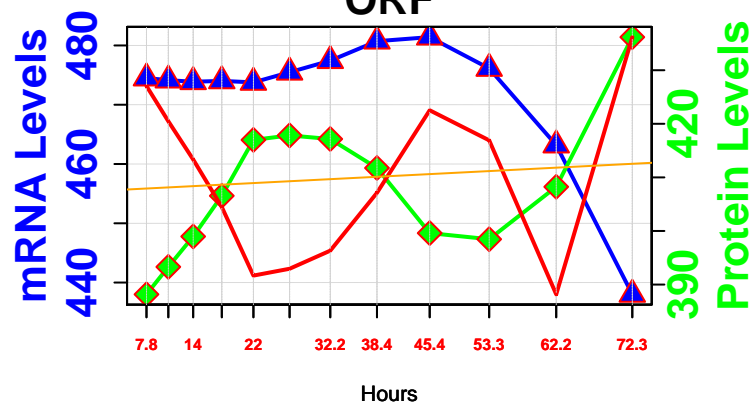
260 - LYS12 RLS: 26.91  
YIL094C  
ORF



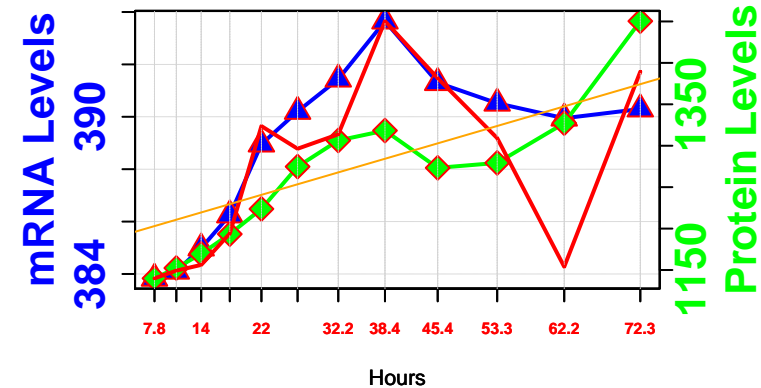
374 - LYS20 RLS: 24  
YDL182W  
ORF



495 - LYS21 RLS: 21.4  
YDL131W  
ORF

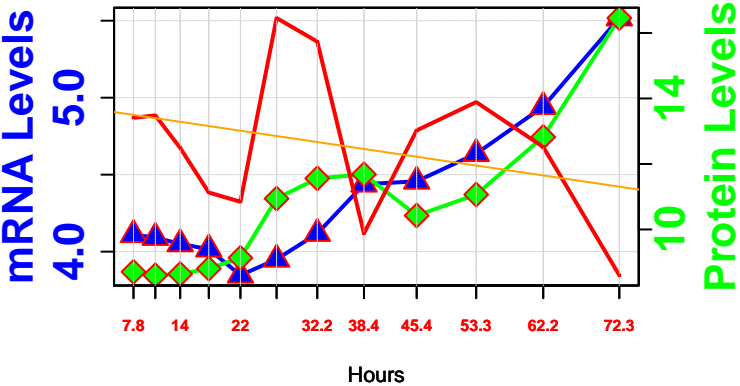


555 - LYS1 RLS: 19.6  
YIR034C  
ORF

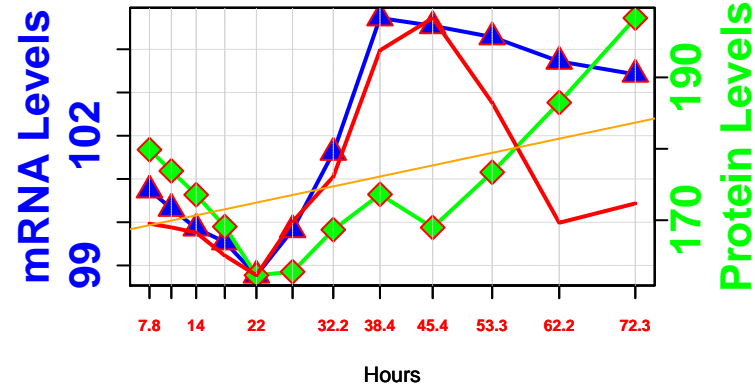


# de novo biosynthesis of pyrimidine deoxyribonucleotides

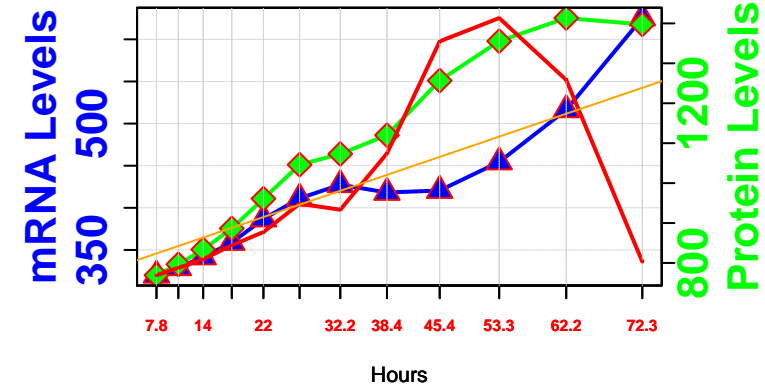
61 – RNR3 RLS: 31.97  
YIL066C  
ORF



372 – RNR1 RLS: 24.12  
YER070W  
ORF

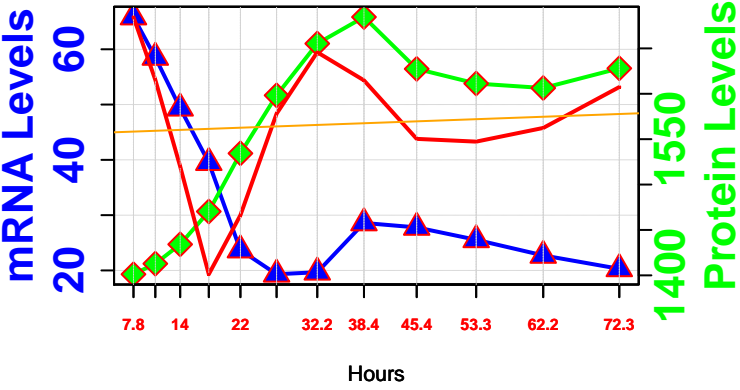


667 – RNR4 RLS: 6.2  
YGR180C  
ORF

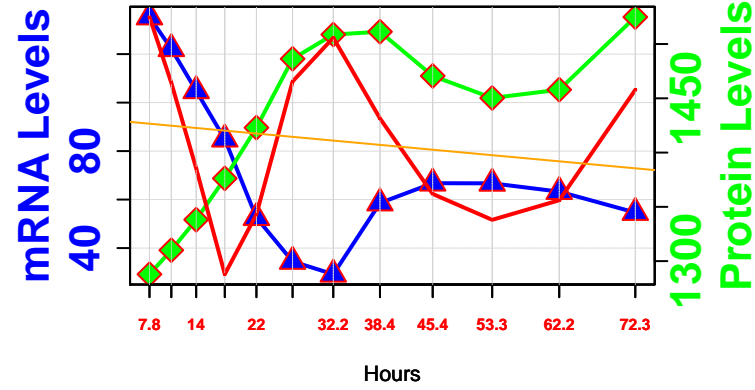


# sulfate assimilation pathway

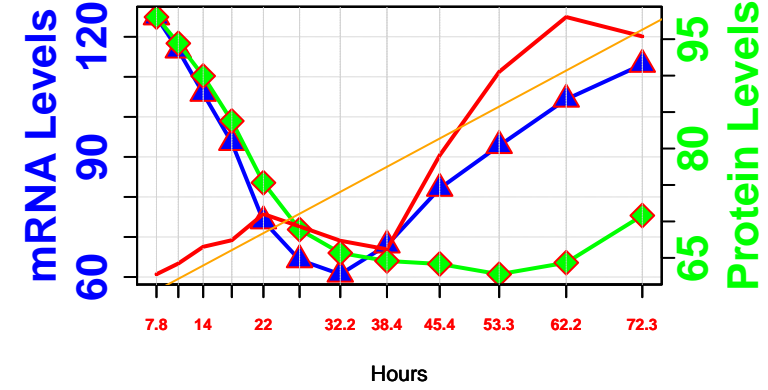
68 – MET10 RLS: 31.58  
YFR030W  
ORF



71 – MET3 RLS: 31.51  
YJR010W  
ORF

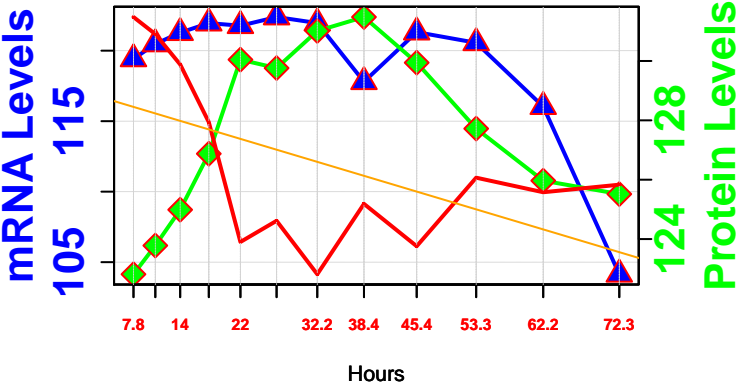


126 – MET16 RLS: 29.74  
YPR167C  
ORF

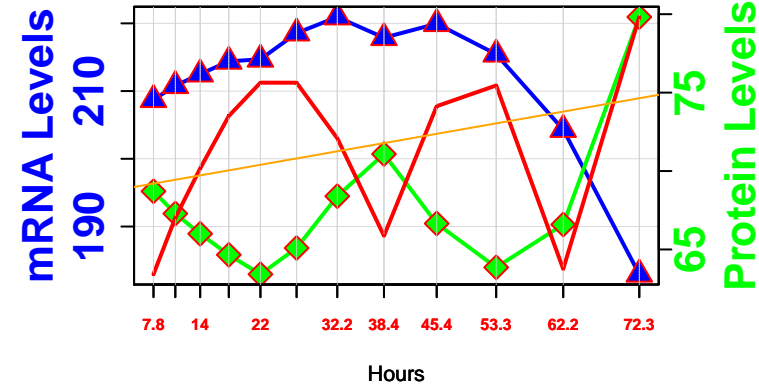


# superpathway of histidine, purine, and pyrimidine biosynthesis

76 – PRS5 RLS: 31.4  
YOL061W  
ORF

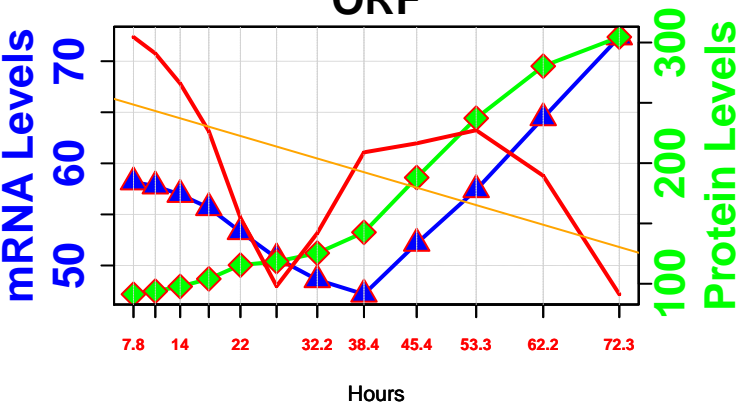


189 – PRS3 RLS: 28.2  
YHL011C  
ORF

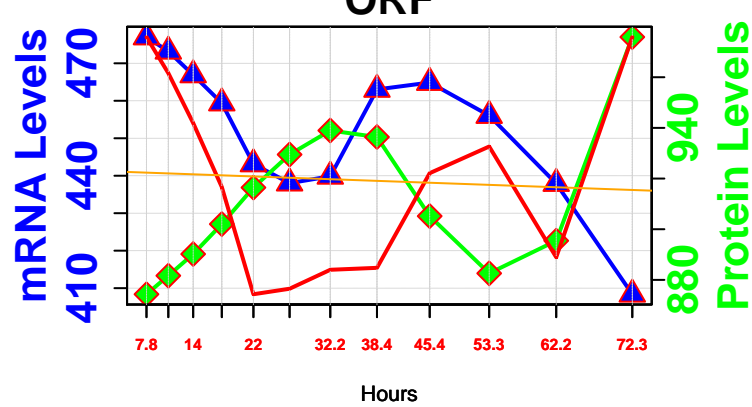


# ethanol degradation

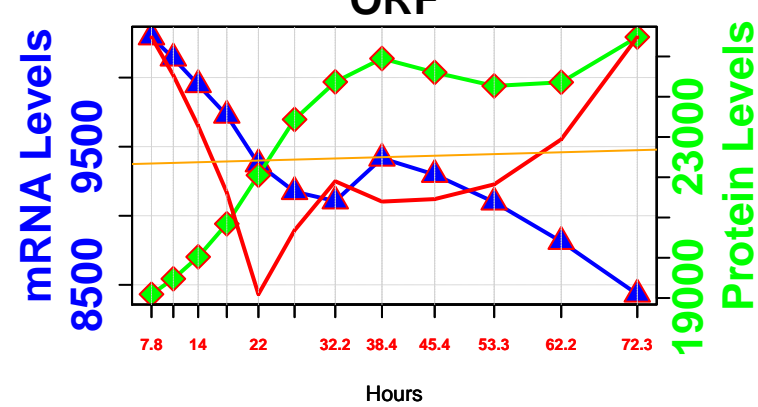
78 – ADH4 RLS: 31.34  
YGL256W  
ORF



296 – ADH3 RLS: 25.94  
YMR083W  
ORF

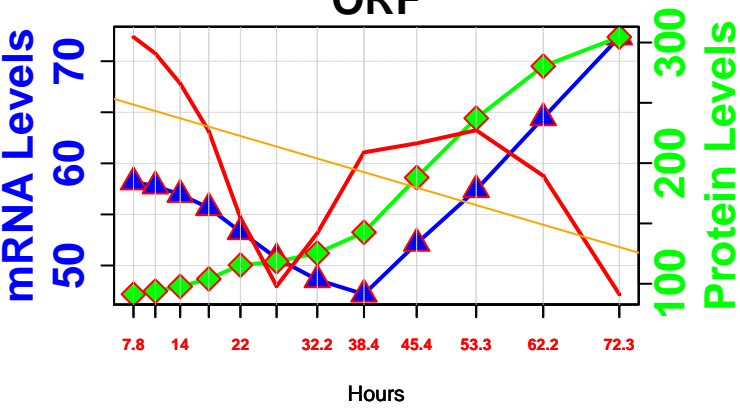


660 – ADH1 RLS: 7.83  
YOL086C  
ORF

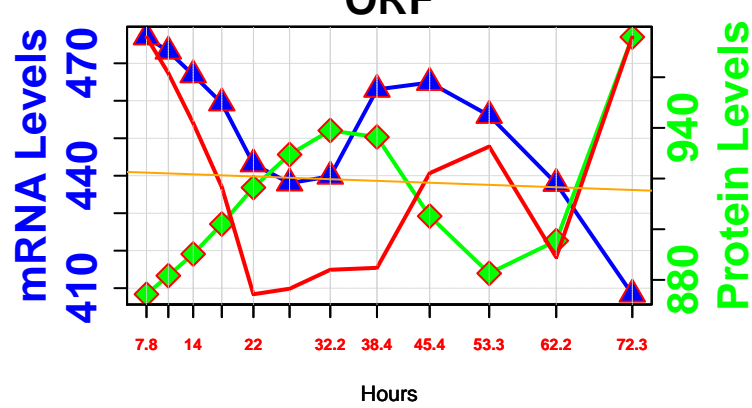


# isoleucine degradation

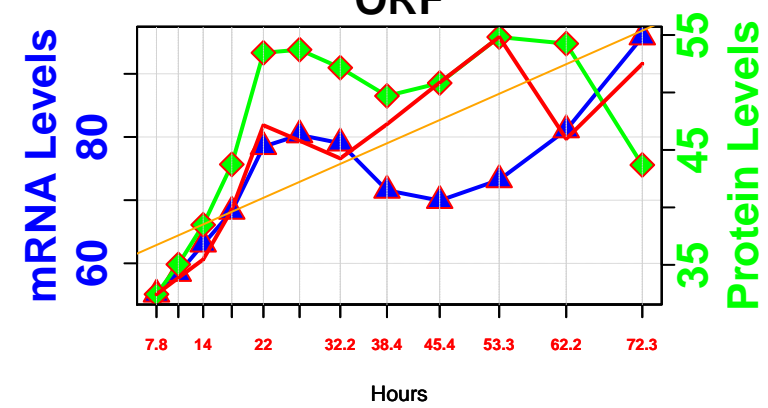
78 – ADH4 RLS: 31.34  
YGL256W  
ORF



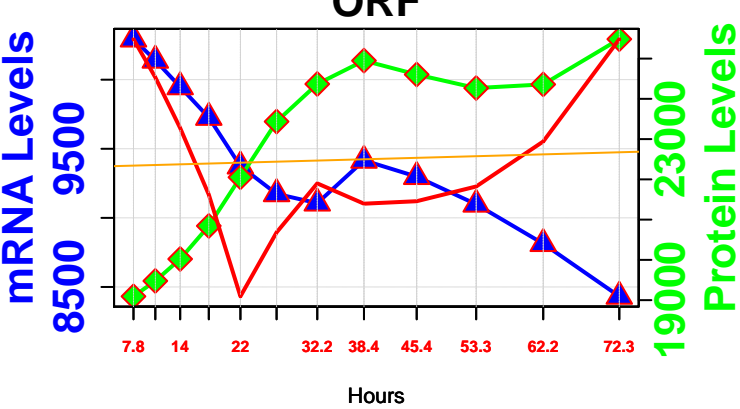
296 – ADH3 RLS: 25.94  
YMR083W  
ORF



302 – SFA1 RLS: 25.8  
YDL168W  
ORF

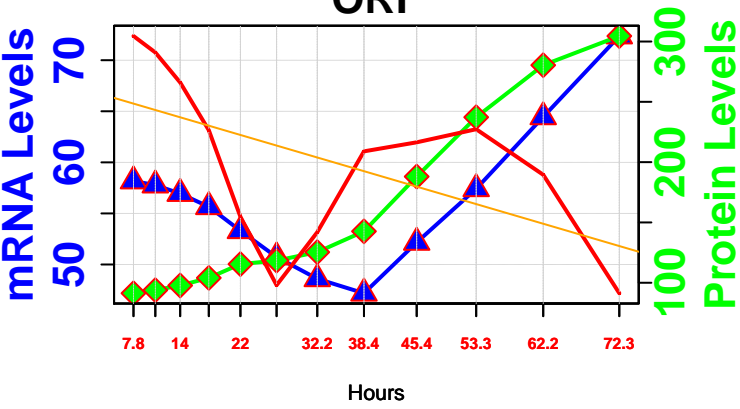


660 – ADH1 RLS: 7.83  
YOL086C  
ORF

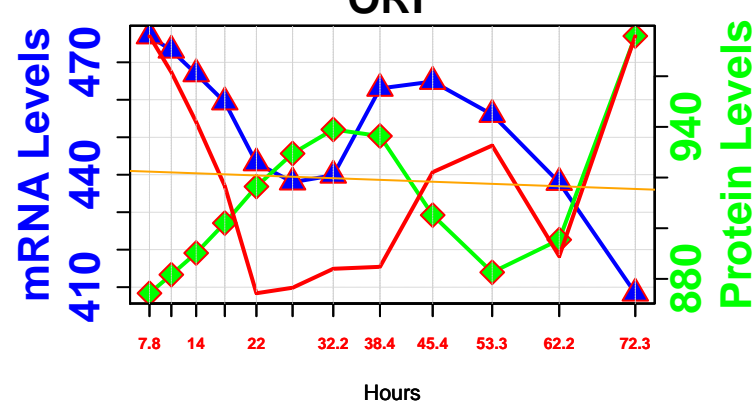


# leucine degradation

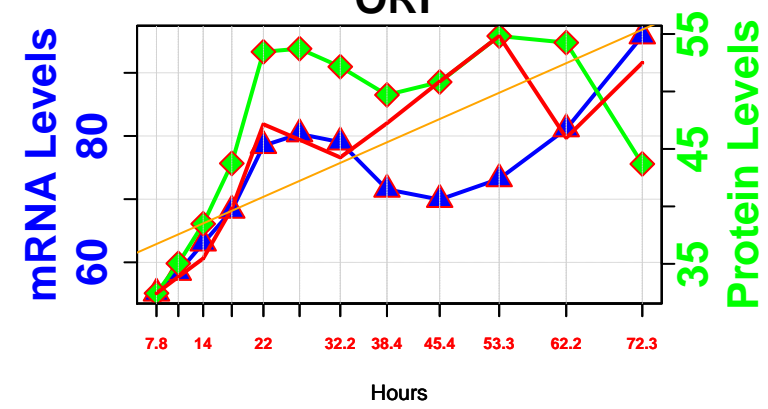
78 – ADH4 RLS: 31.34  
YGL256W  
ORF



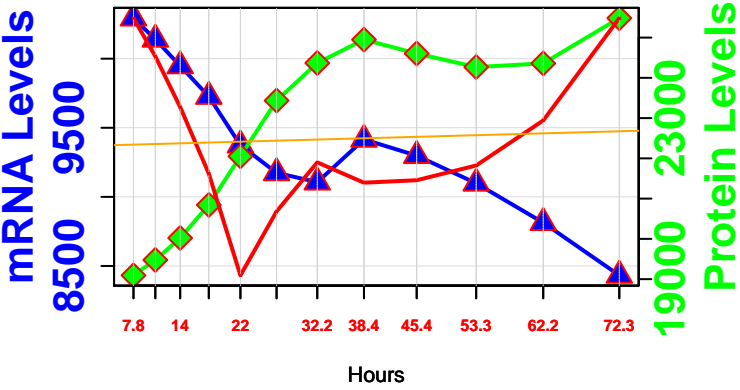
296 – ADH3 RLS: 25.94  
YMR083W  
ORF



302 – SFA1 RLS: 25.8  
YDL168W  
ORF



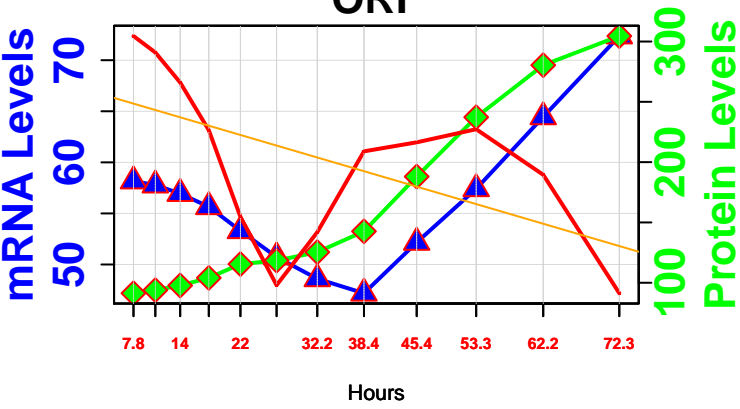
660 – ADH1 RLS: 7.83  
YOL086C  
ORF



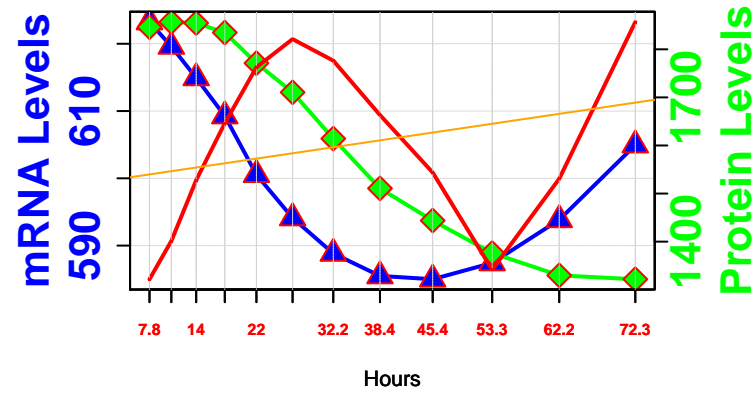


# phenylalanine degradation

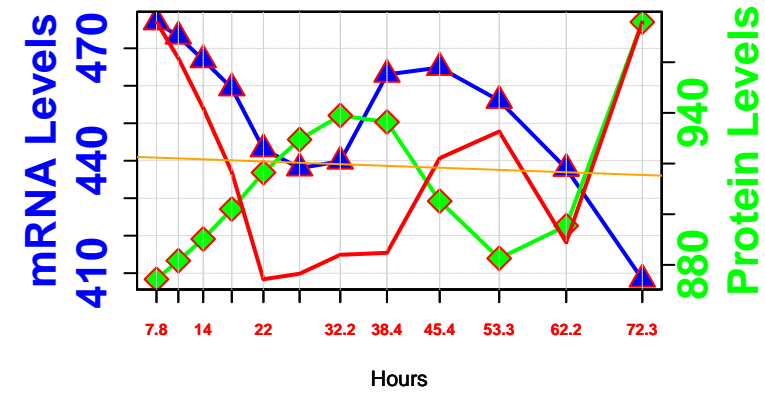
78 – ADH4 RLS: 31.34  
YGL256W  
ORF



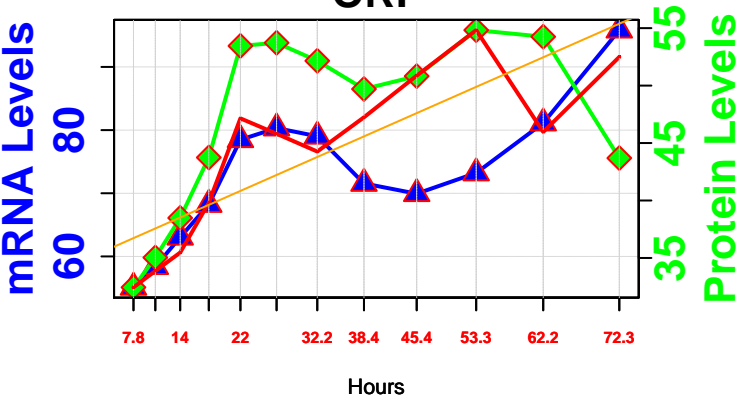
206 – ARO8 RLS: 27.94  
YGL202W  
ORF



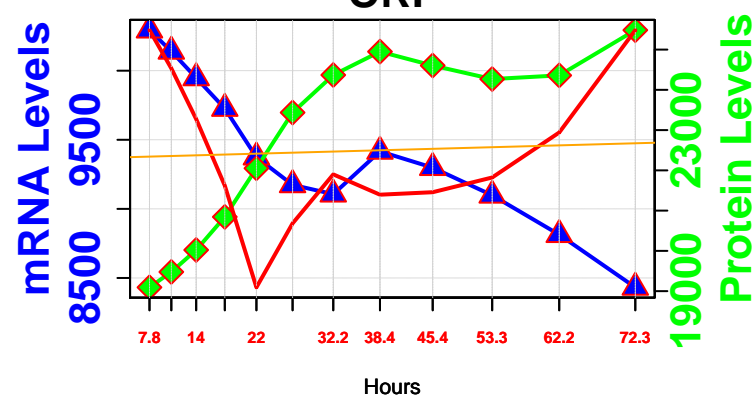
296 – ADH3 RLS: 25.94  
YMR083W  
ORF



302 – SFA1 RLS: 25.8  
YDL168W  
ORF

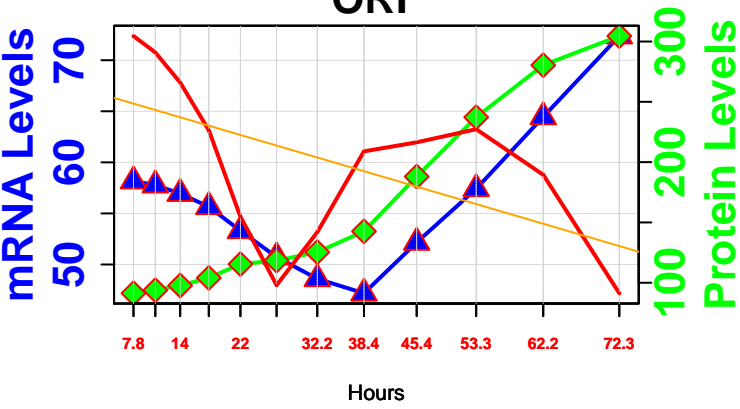


660 – ADH1 RLS: 7.83  
YOL086C  
ORF

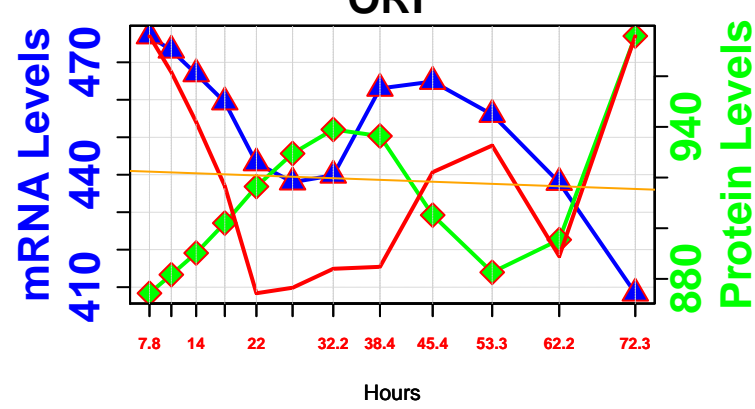


# superpathway of glucose fermentation

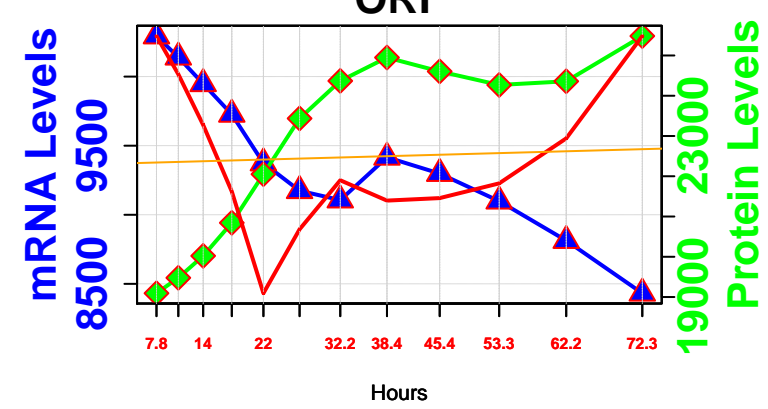
78 – ADH4 RLS: 31.34  
YGL256W  
ORF



296 – ADH3 RLS: 25.94  
YMR083W  
ORF

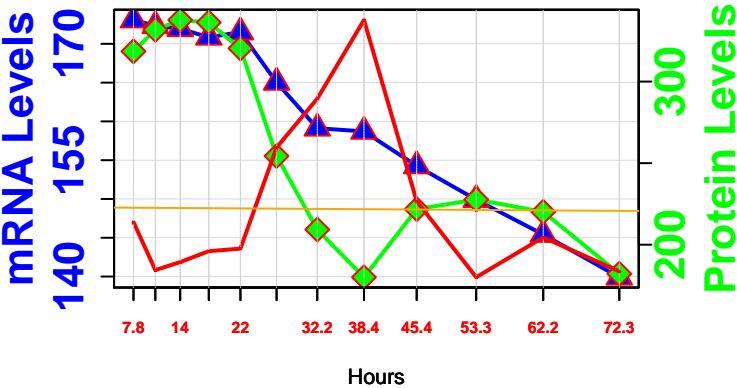


660 – ADH1 RLS: 7.83  
YOL086C  
ORF

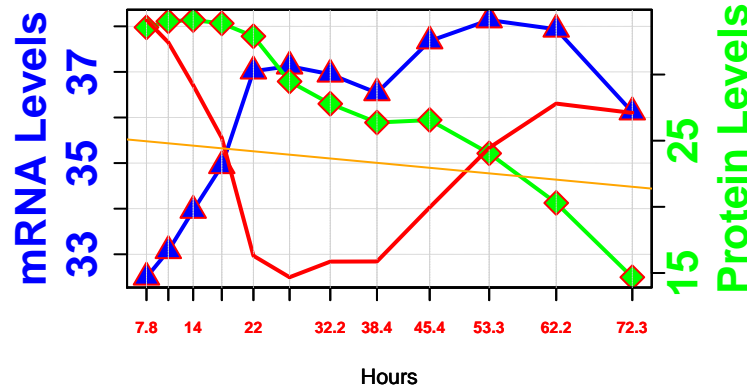


# tryptophan degradation

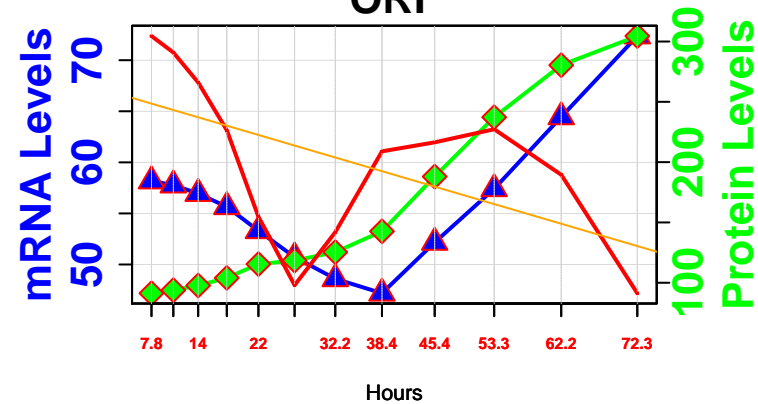
33 – BNA1 RLS: 33  
YJR025C  
ORF



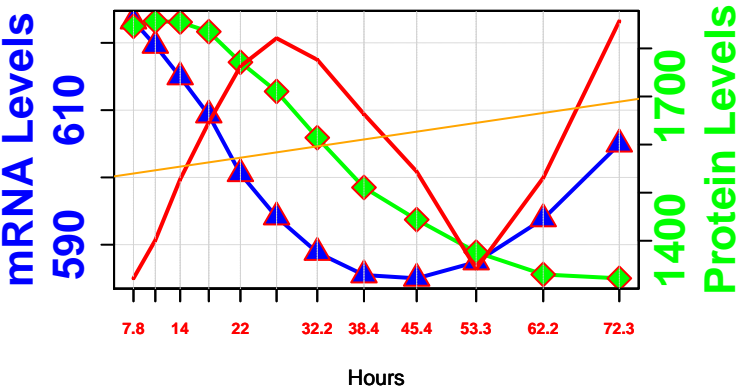
39 – BNA4 RLS: 32.6  
YBL098W  
ORF



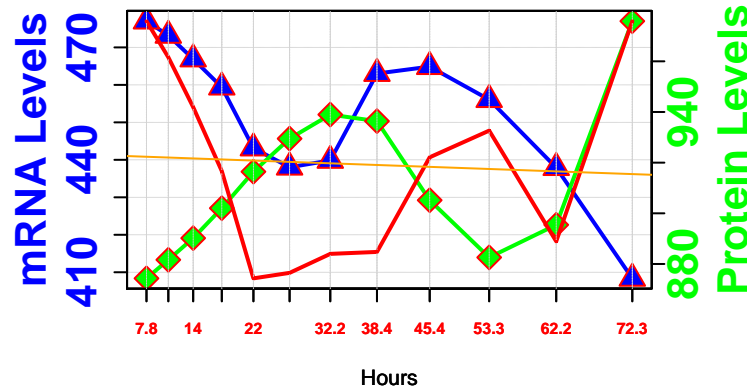
78 – ADH4 RLS: 31.34  
YGL256W  
ORF



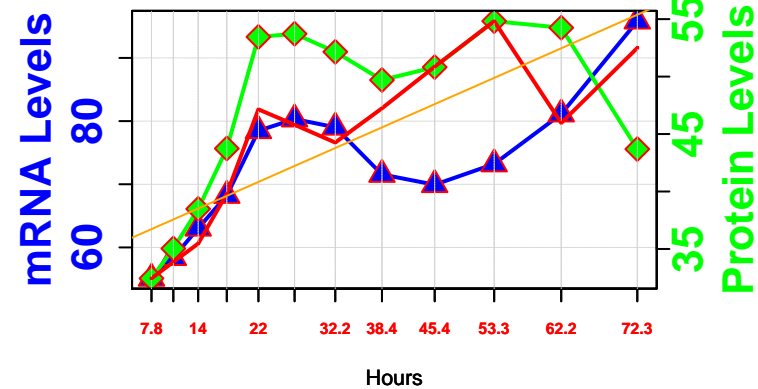
206 – ARO8 RLS: 27.94  
YGL202W  
ORF



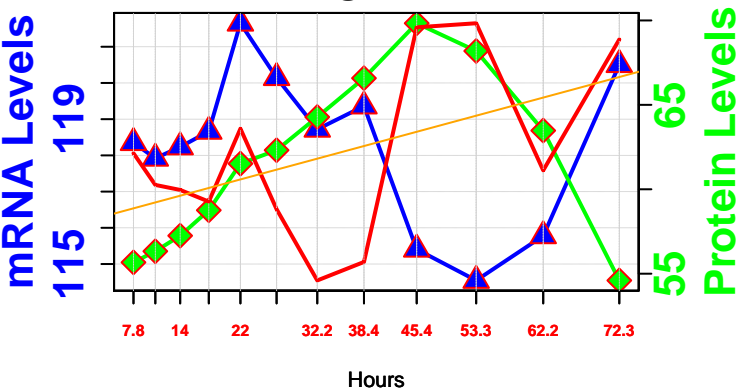
296 – ADH3 RLS: 25.94  
YMR083W  
ORF



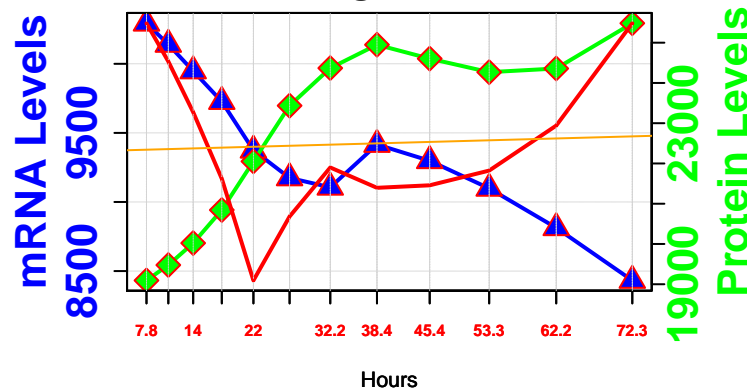
302 – SFA1 RLS: 25.8  
YDL168W  
ORF



415 – BNA6 RLS: 23.4  
YFR047C  
ORF

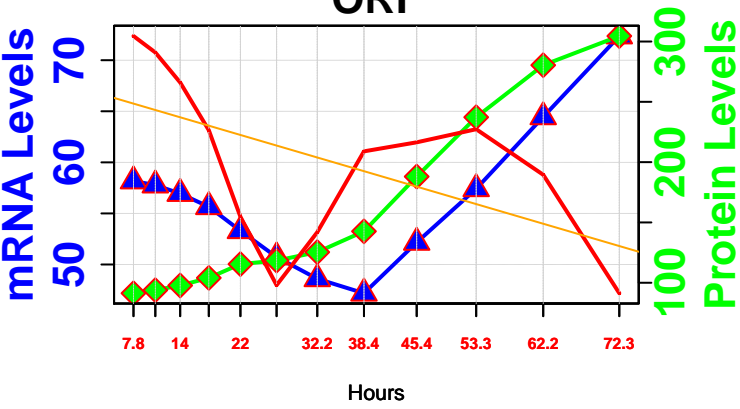


660 – ADH1 RLS: 7.83  
YOL086C  
ORF

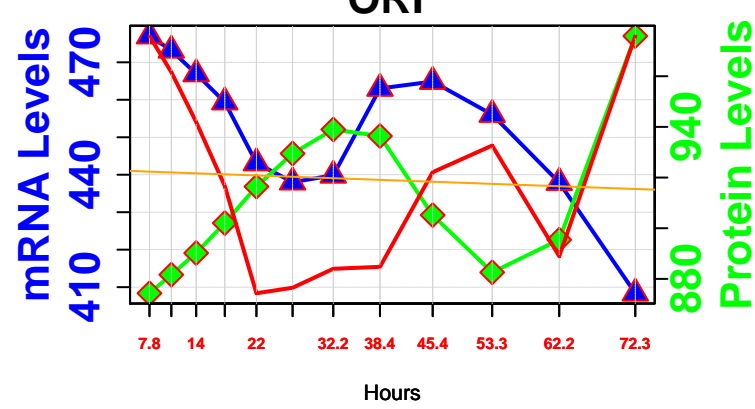


# valine degradation

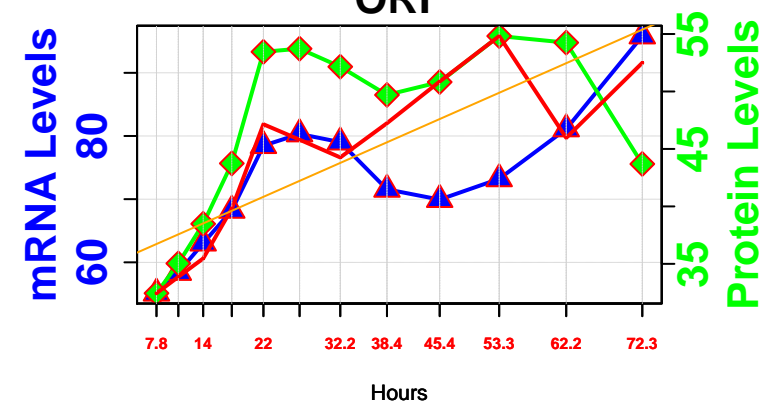
78 – ADH4 RLS: 31.34  
YGL256W  
ORF



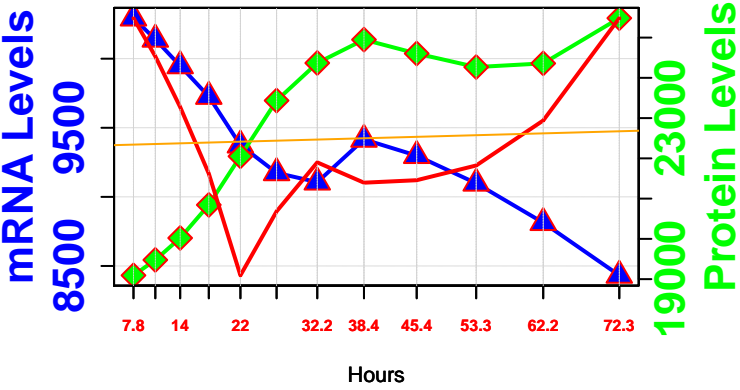
296 – ADH3 RLS: 25.94  
YMR083W  
ORF



302 – SFA1 RLS: 25.8  
YDL168W  
ORF

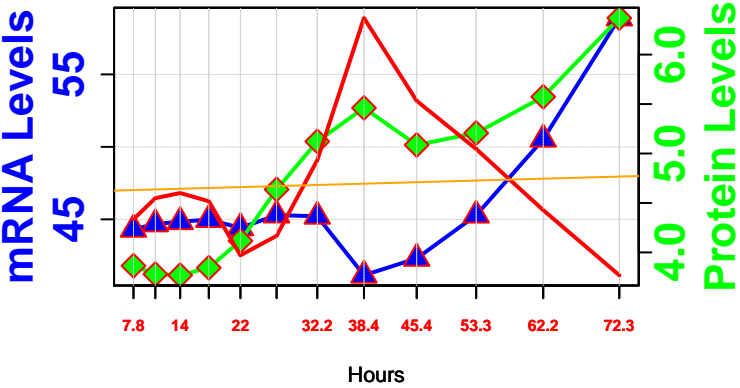


660 – ADH1 RLS: 7.83  
YOL086C  
ORF

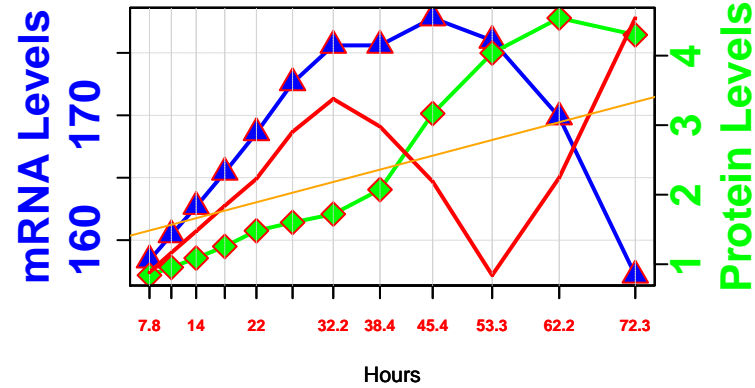


# diphthamide biosynthesis

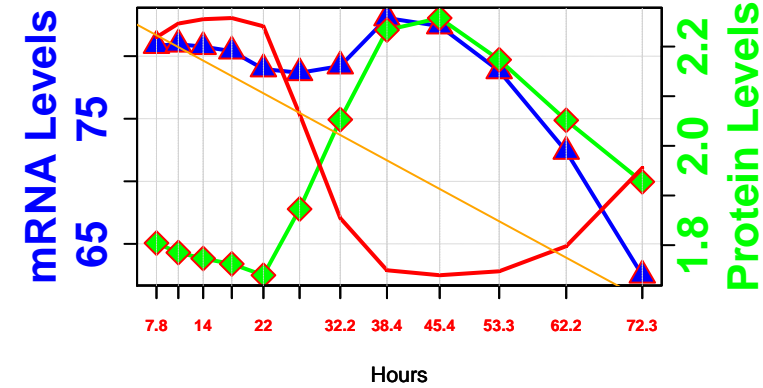
85 – DPH1 RLS: 31  
YIL103W  
ORF



498 – DPH5 RLS: 21.4  
YLR172C  
ORF

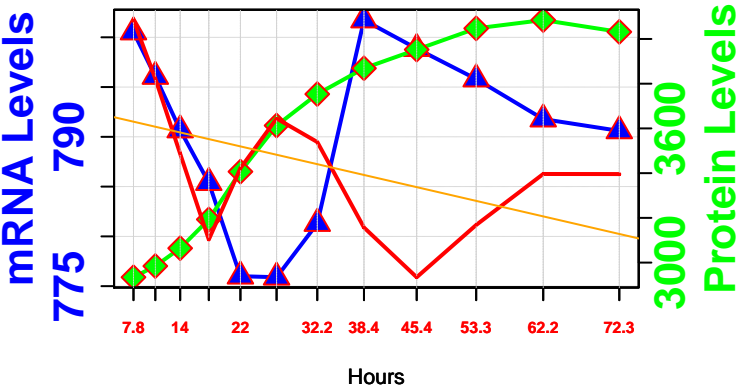


609 – DPH2 RLS: 17  
YKL191W  
ORF

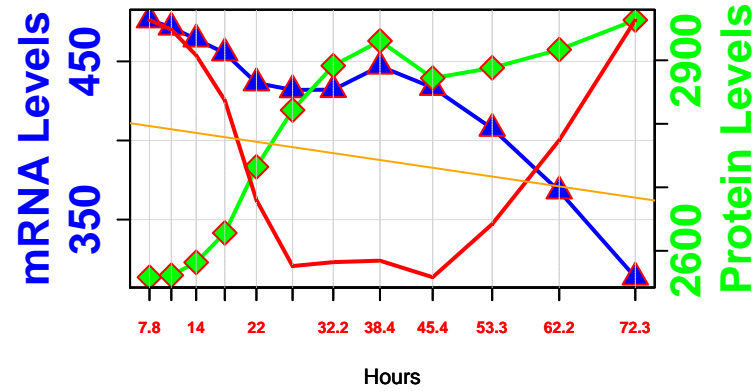


# oxidative branch of the pentose phosphate pathway

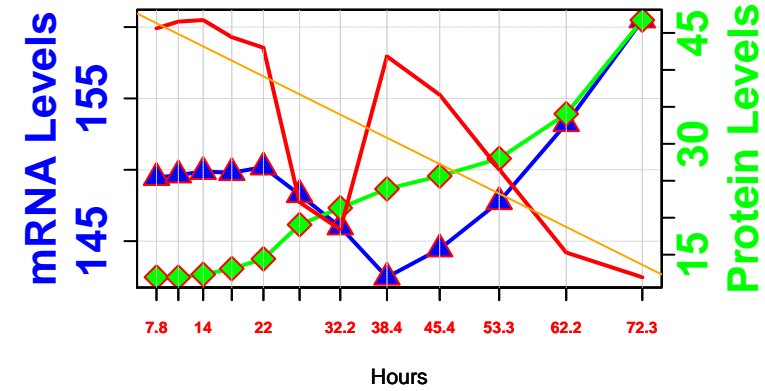
86 – GND1 RLS: 30.92  
YHR183W  
ORF



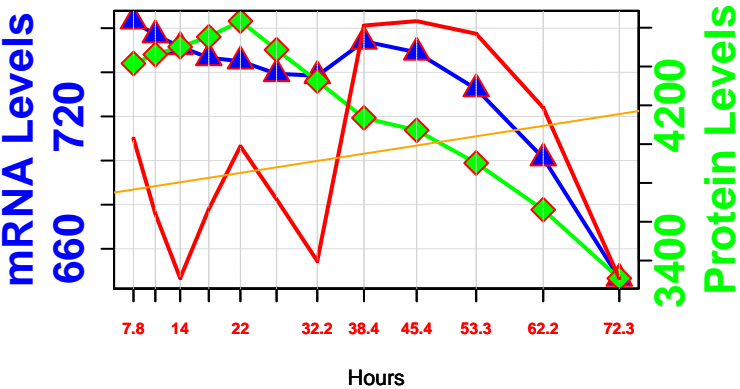
92 – TKL1 RLS: 30.76  
YPR074C  
ORF



156 – RPE1 RLS: 28.84  
YJL121C  
ORF

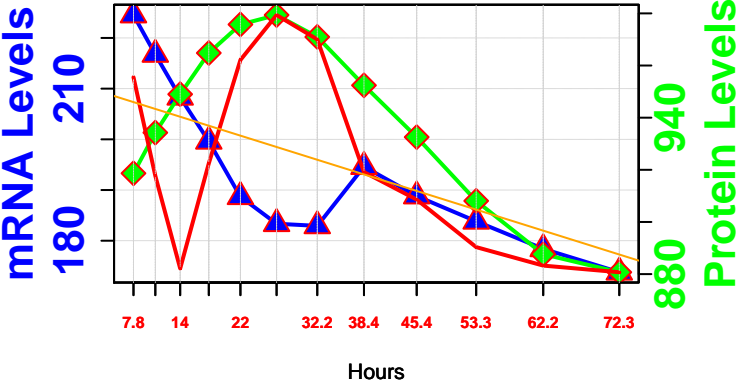


281 – TAL1 RLS: 26.34  
YLR354C  
ORF

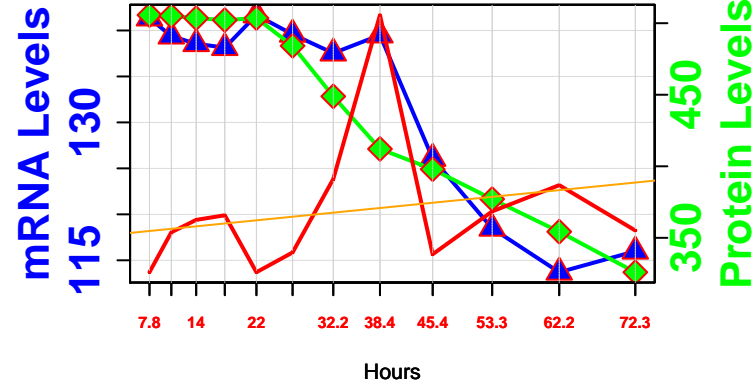


# TCA cycle, aerobic respiration

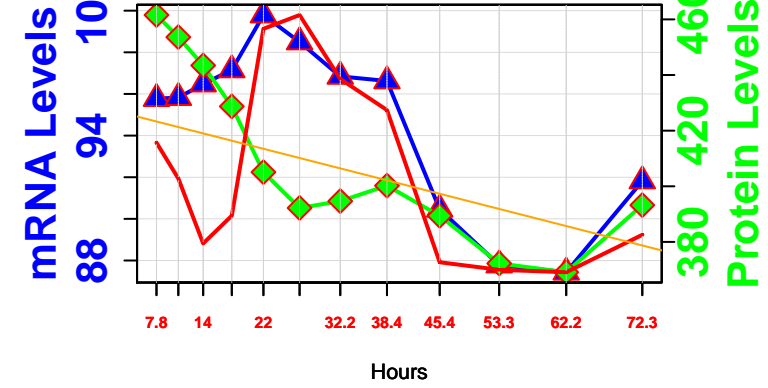
87 – IDH2 RLS: 30.84  
YOR136W  
ORF



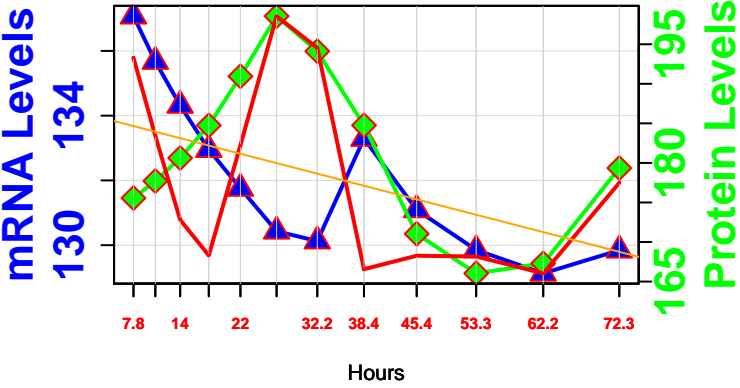
93 – LPD1 RLS: 30.69  
YFL018C  
ORF



111 – FUM1 RLS: 30.28  
YPL262W  
ORF

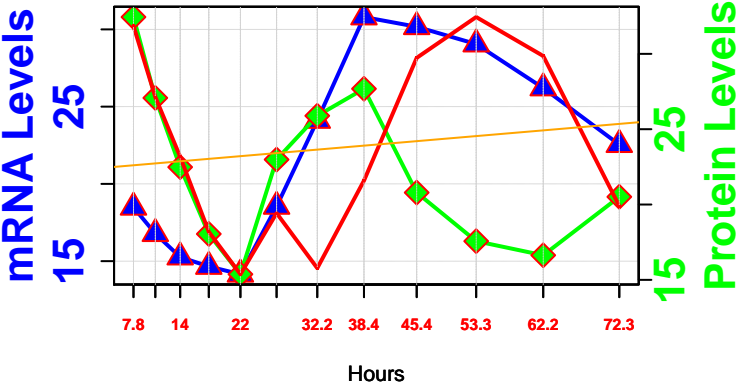


264 – PYC2 RLS: 26.75  
YBR218C  
ORF

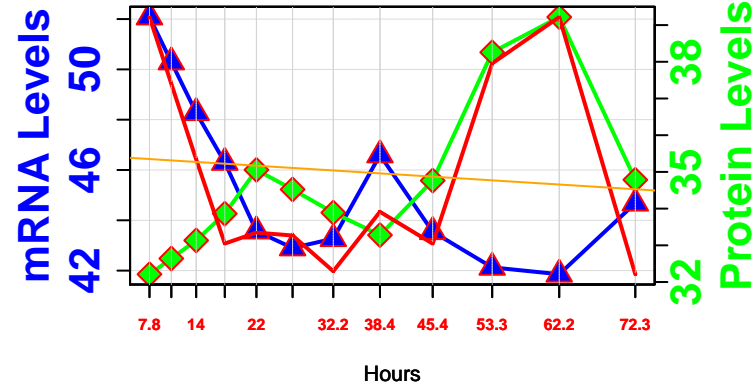


# glutathione biosynthesis

88 – GSH1 RLS: 30.83  
YJL101C  
ORF



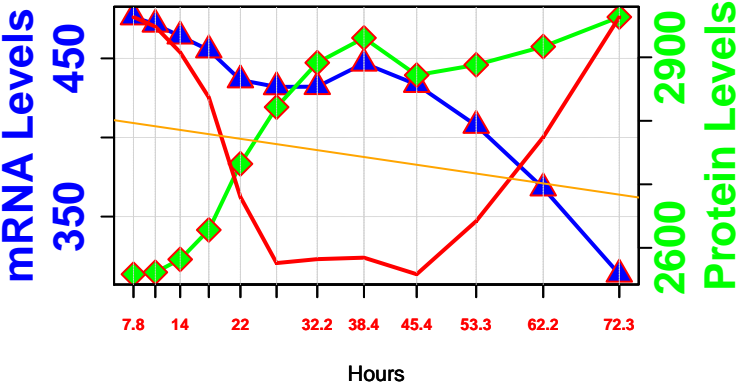
344 – GSH2 RLS: 24.87  
YOL049W  
ORF



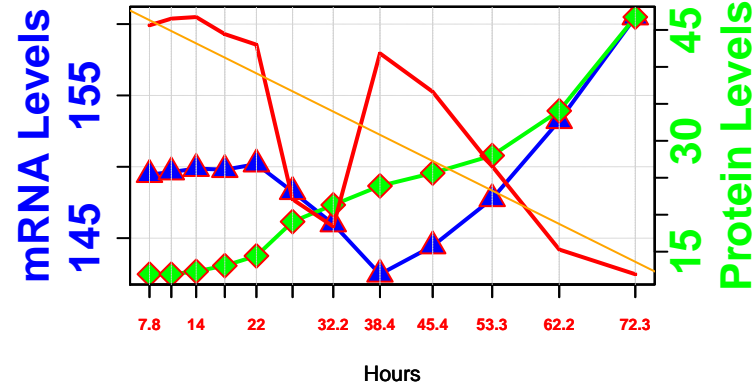


# non-oxidative branch of the pentose phosphate pathway

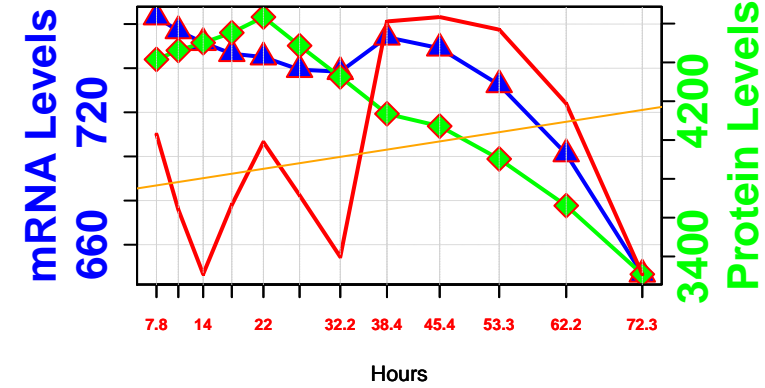
92 - TKL1 RLS: 30.76  
YPR074C  
ORF



156 - RPE1 RLS: 28.84  
YJL121C  
ORF

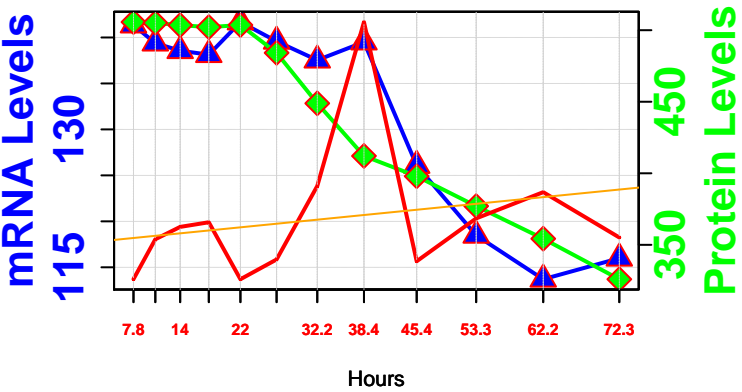


281 - TAL1 RLS: 26.34  
YLR354C  
ORF



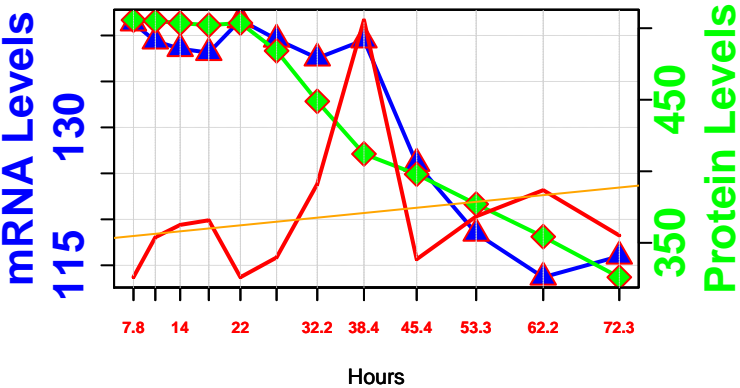
# 2-ketoglutarate dehydrogenase complex

93 - LPD1 RLS: 30.69  
YFL018C  
ORF

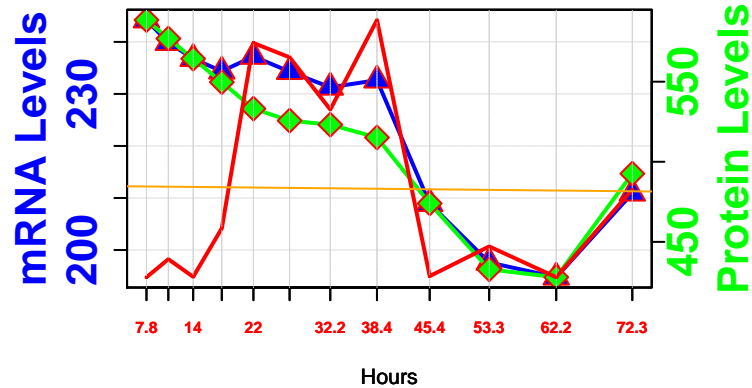


arginate dehydratase (serine)

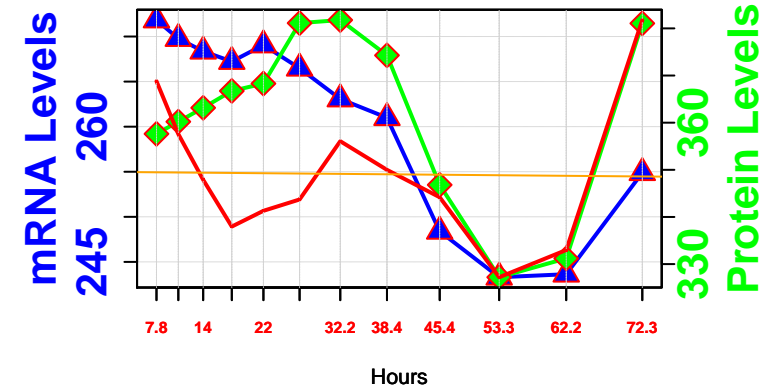
93 - LPD1 RLS: 30.69  
YFL018C  
ORF



613 - PDA1 RLS: 16.71  
YER178W  
ORF

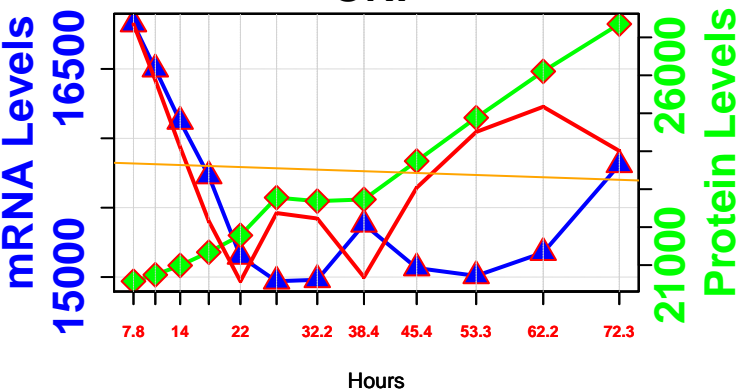


644 - PDB1 RLS: 12.77  
YBR221C  
ORF

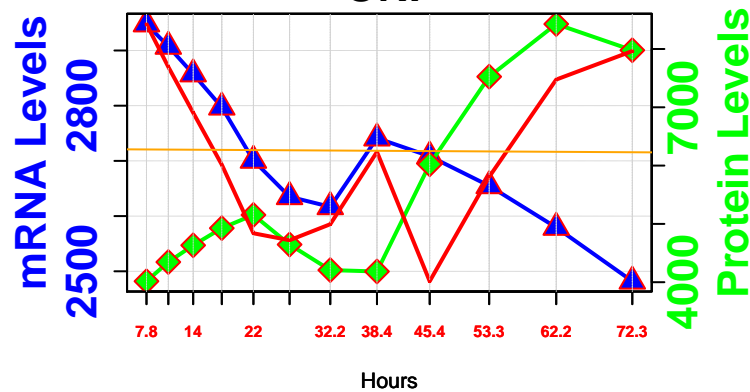


# gluconeogenesis

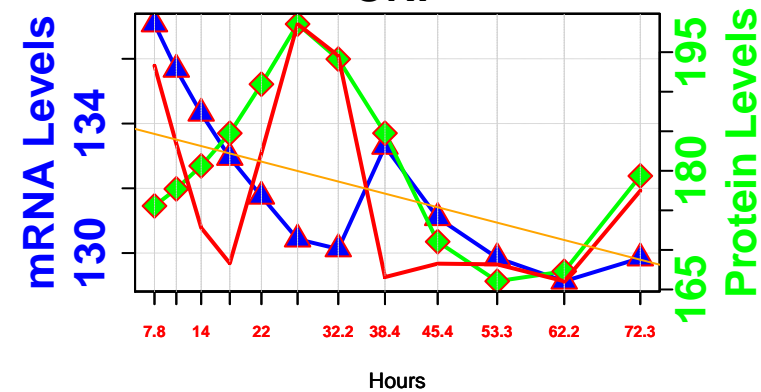
98 – TDH3 RLS: 30.57  
YGR192C  
ORF



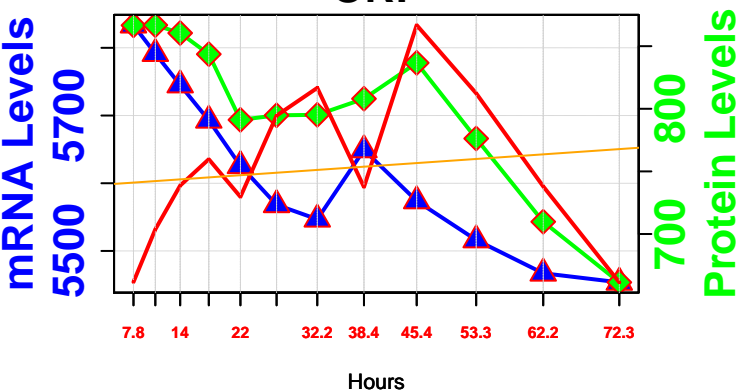
255 – ENO1 RLS: 27.04  
YGR254W  
ORF



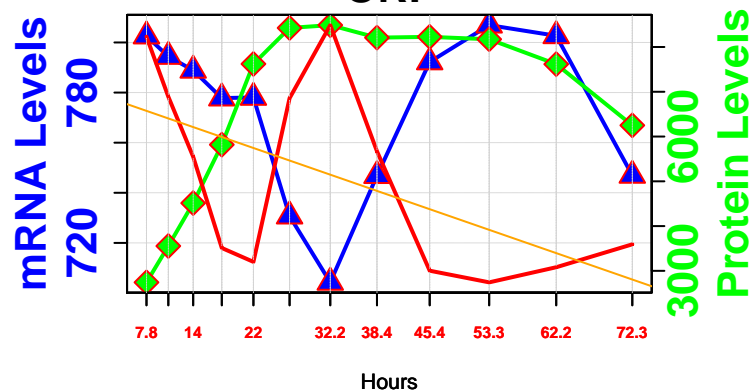
264 – PYC2 RLS: 26.75  
YBR218C  
ORF



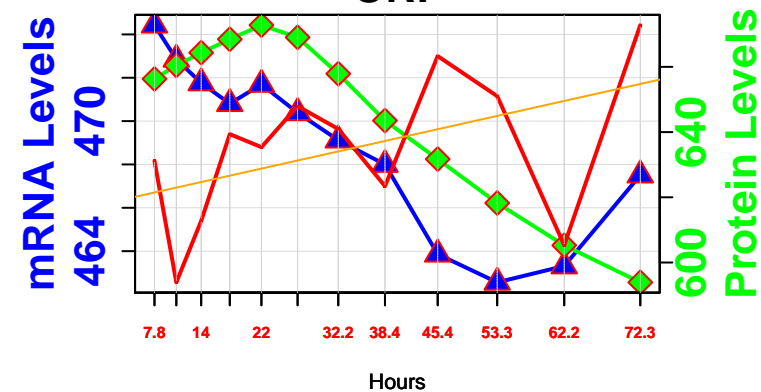
267 – TDH2 RLS: 26.69  
YJR009C  
ORF



352 – TDH1 RLS: 24.6  
YJL052W  
ORF

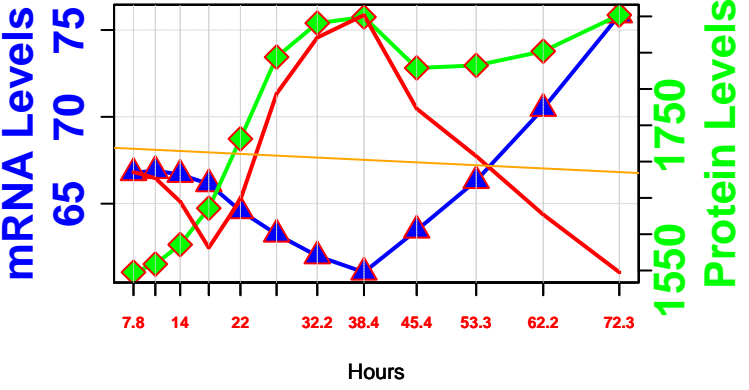


469 – MAE1 RLS: 22.31  
YKL029C  
ORF



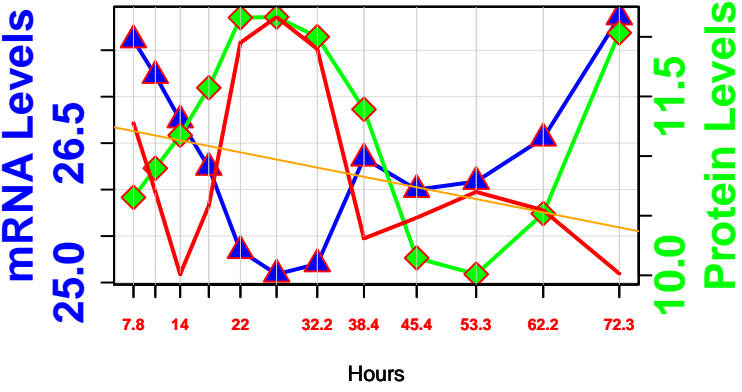
phosphatite biosynthesis (Kennedy pathway)

114 – GLT1 RLS: 30.25  
YDL171C  
ORF



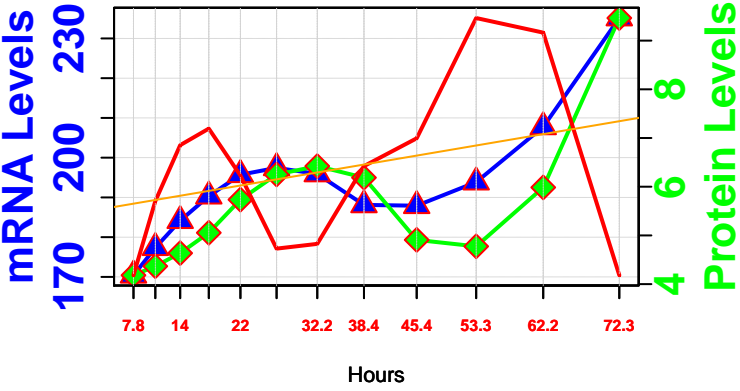
# lipid-linked oligosaccharide biosynthesis

120 – ALG12 RLS: 30.03  
YNR030W  
ORF

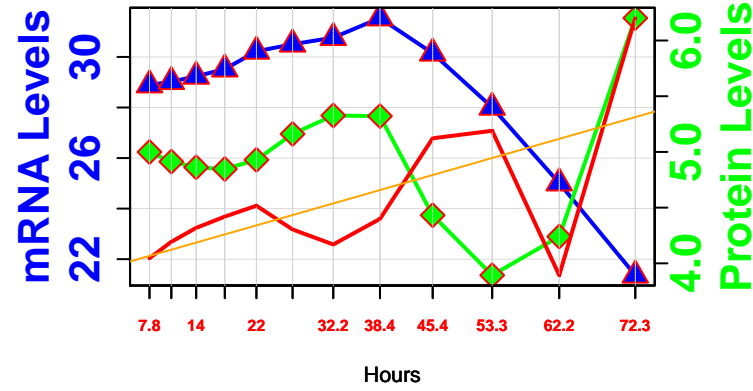


# sphingolipid metabolism

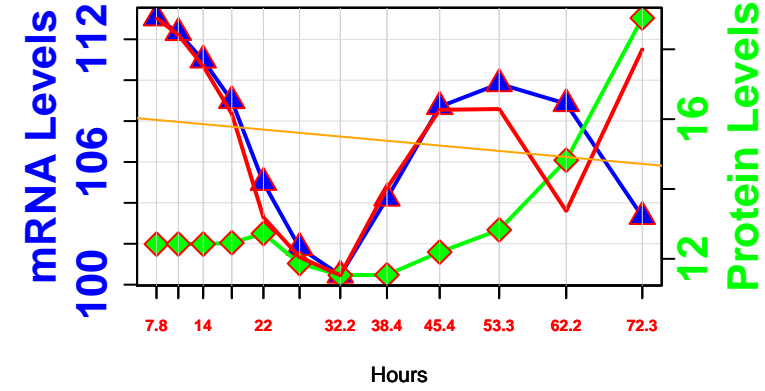
124 – SUR2 RLS: 29.8  
YDR297W  
ORF



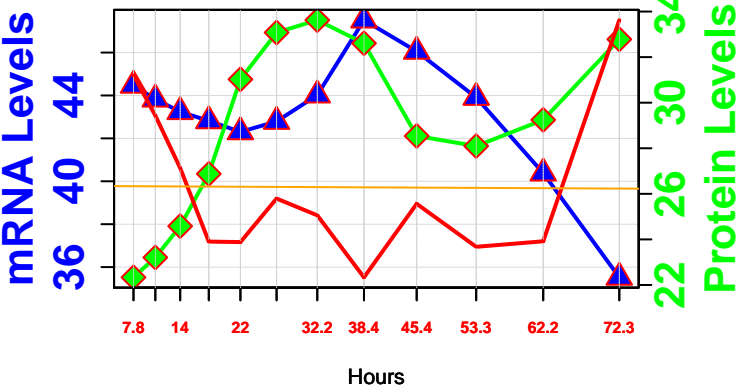
147 – LCB4 RLS: 29.14  
YOR171C  
ORF



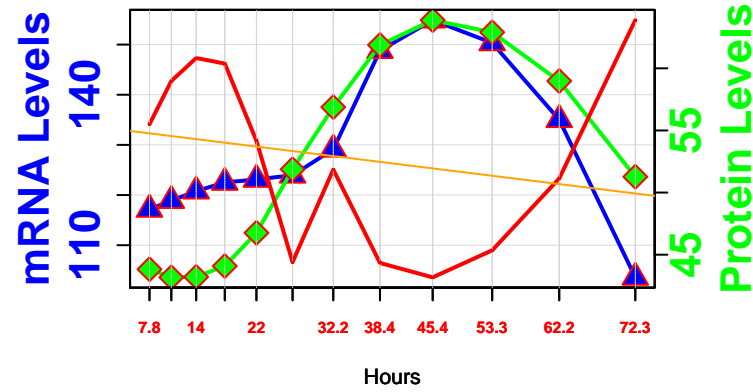
175 – LAC1 RLS: 28.42  
YKL008C  
ORF



465 – DPL1 RLS: 22.52  
YDR294C  
ORF

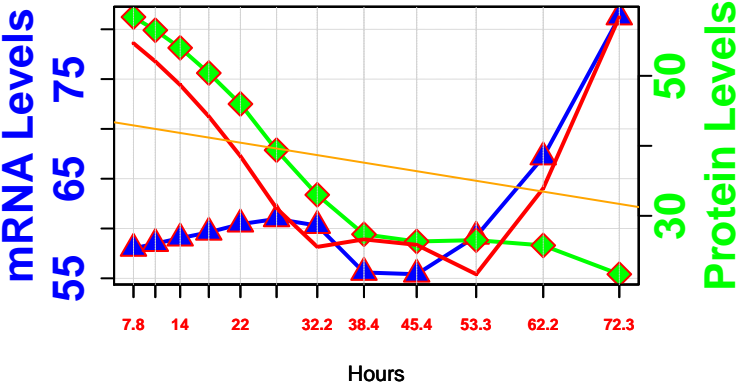


591 – SCS7 RLS: 18.2  
YMR272C  
ORF

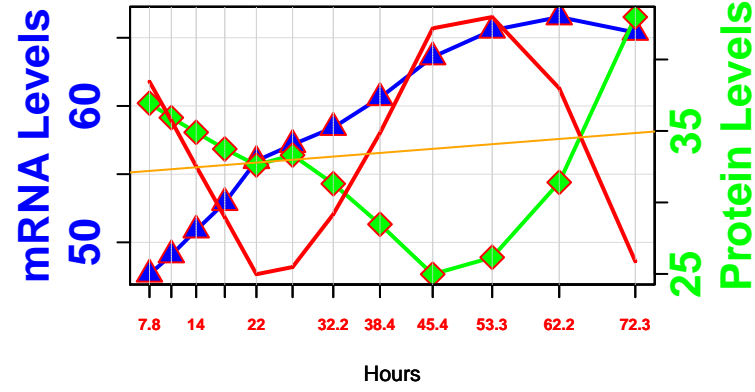


# allantoin degradation

152 – DAL3 RLS: 29  
YIR032C  
ORF



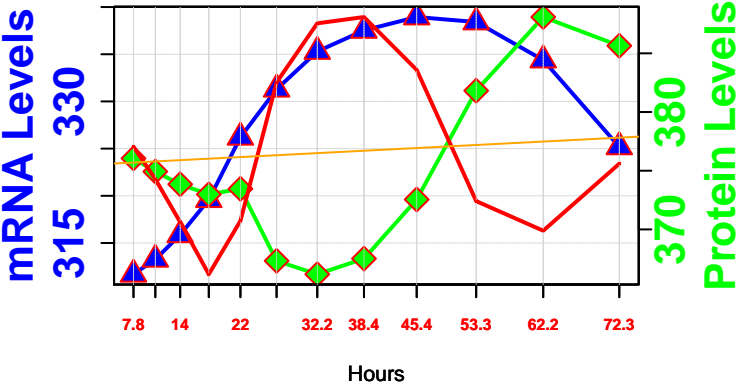
270 – DAL2 RLS: 26.6  
YIR029W  
ORF



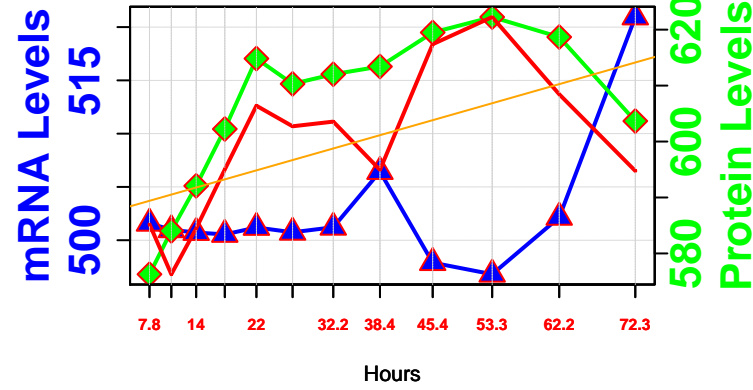


# asparagine biosynthesis

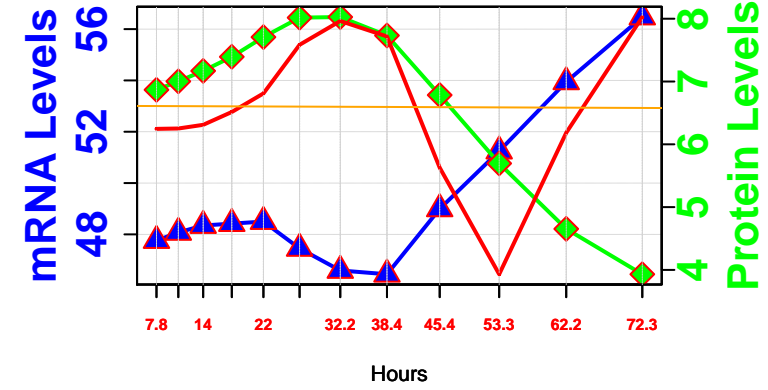
158 – ASN2 RLS: 28.8  
YGR124W  
ORF



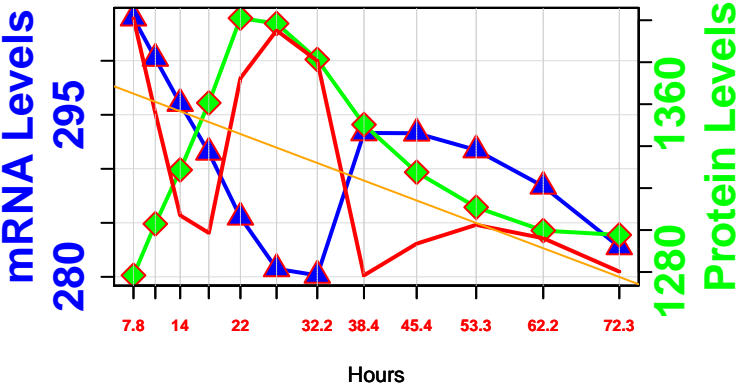
164 – ASN1 RLS: 28.69  
YPR145W  
ORF



283 – AAT1 RLS: 26.21  
YKL106W  
ORF

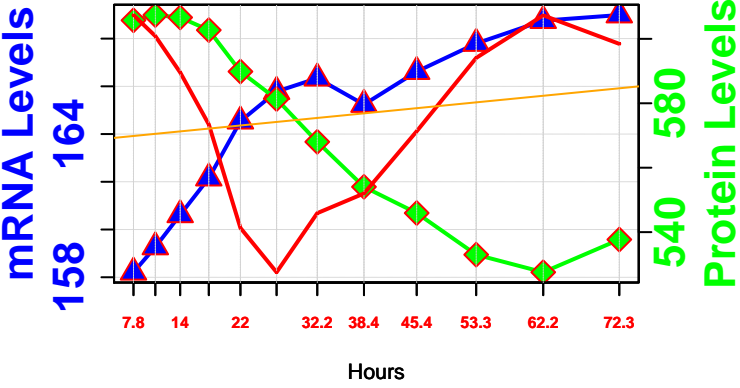


401 – AAT2 RLS: 23.6  
YLR027C  
ORF

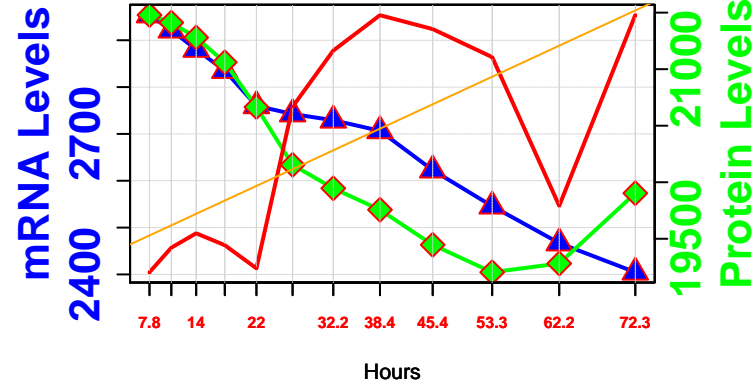


# folate polyglutamylation

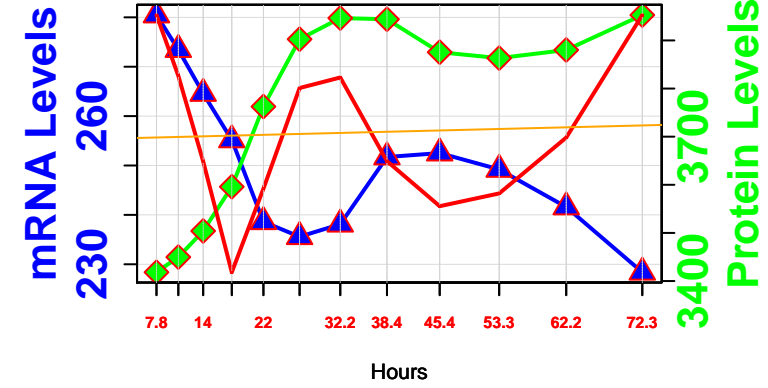
170 - SHM1 RLS: 28.53  
YBR263W  
ORF



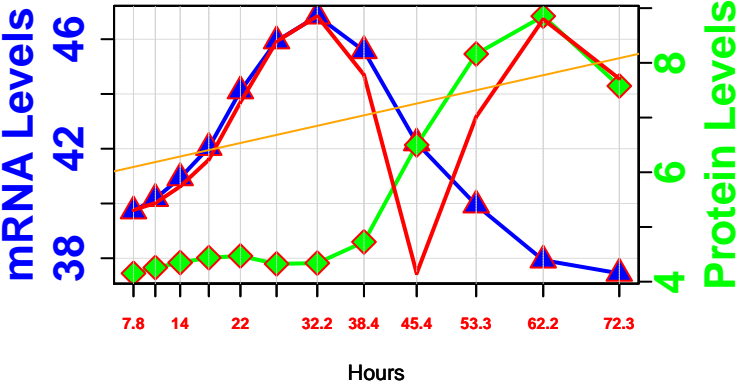
182 - SHM2 RLS: 28.28  
YLR058C  
ORF



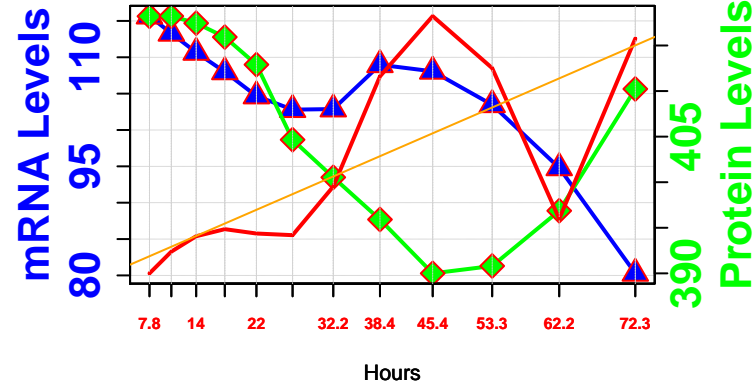
327 - ADE3 RLS: 25.4  
YGR204W  
ORF



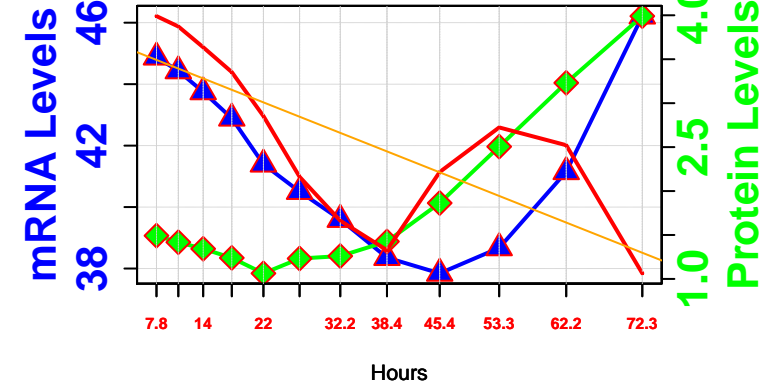
370 - MET12 RLS: 24.2  
YPL023C  
ORF



455 - MET13 RLS: 22.6  
YGL125W  
ORF

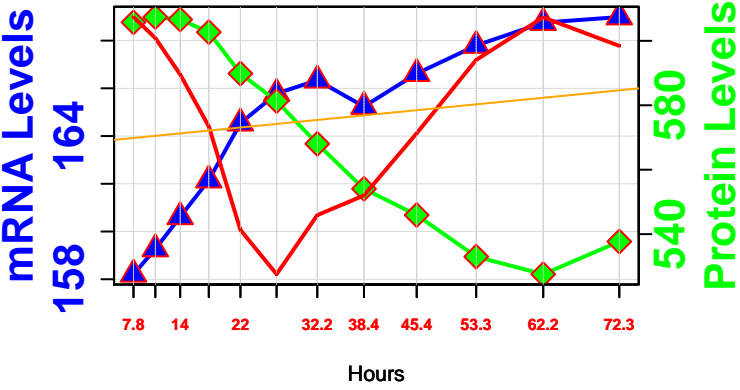


607 - MET7 RLS: 17.14  
YOR241W  
ORF

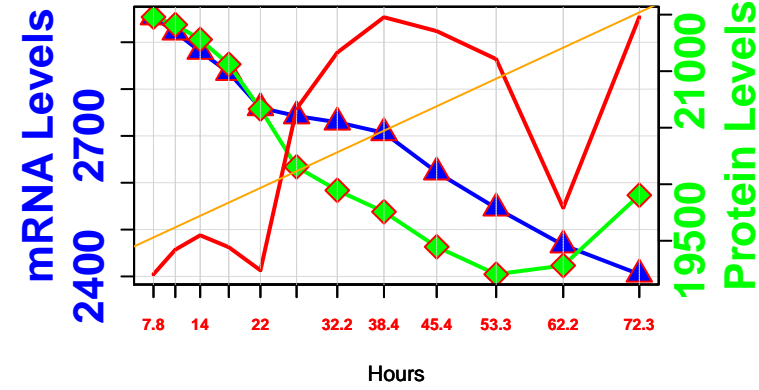


# glycine biosynthesis from serine

170 - SHM1 RLS: 28.53  
YBR263W  
ORF

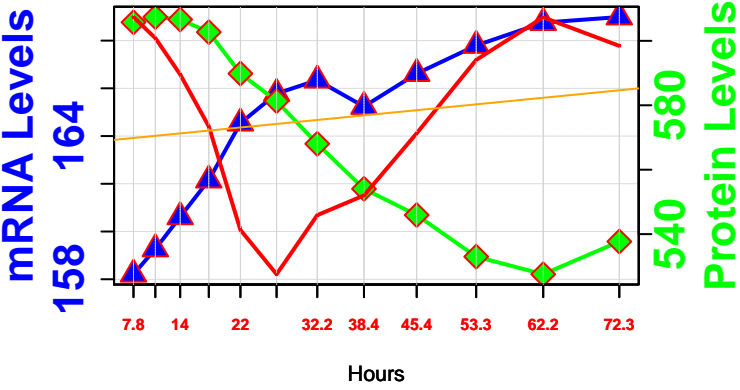


182 - SHM2 RLS: 28.28  
YLR058C  
ORF

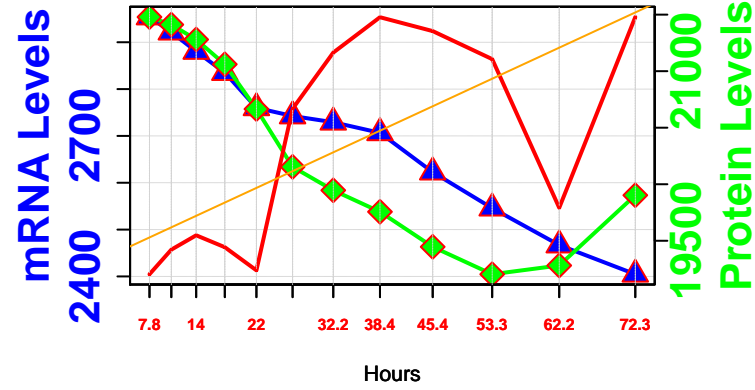


# serine biosynthesis from glyoxylate

170 - SHM1 RLS: 28.53  
YBR263W  
ORF

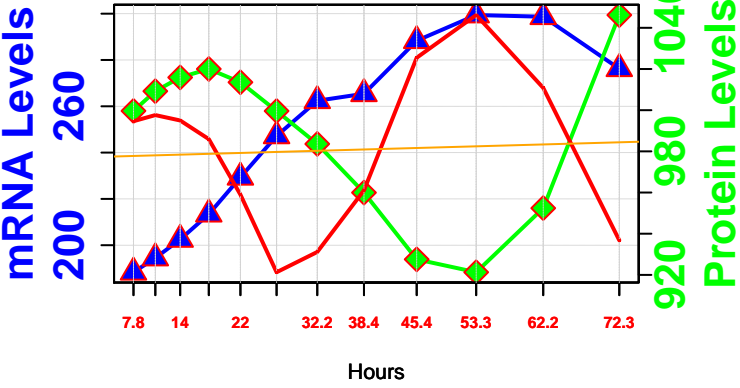


182 - SHM2 RLS: 28.28  
YLR058C  
ORF

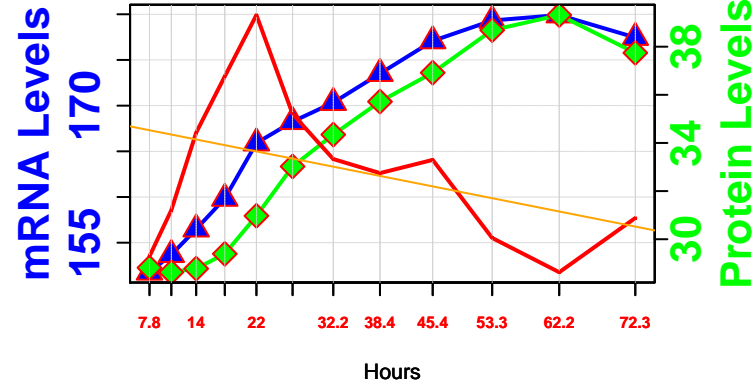


# ergosterol biosynthesis

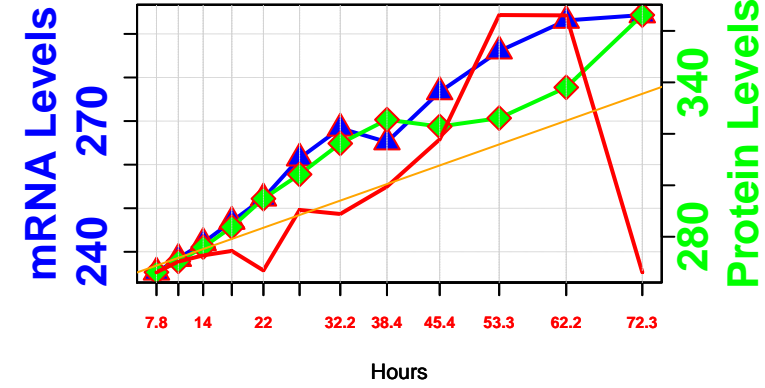
172 - ERG6 RLS: 28.53  
YML008C  
ORF



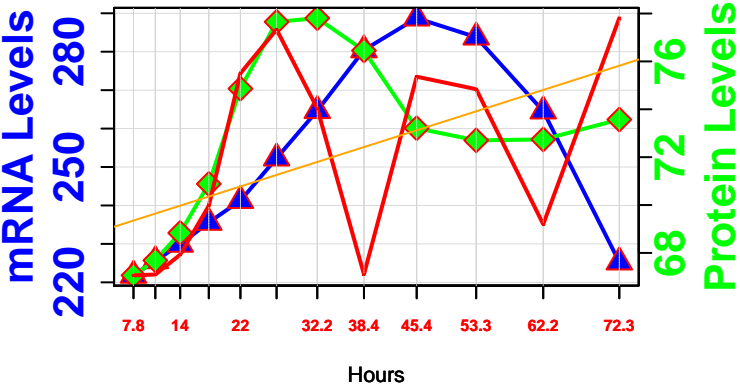
236 - ERG4 RLS: 27.42  
YGL012W  
ORF



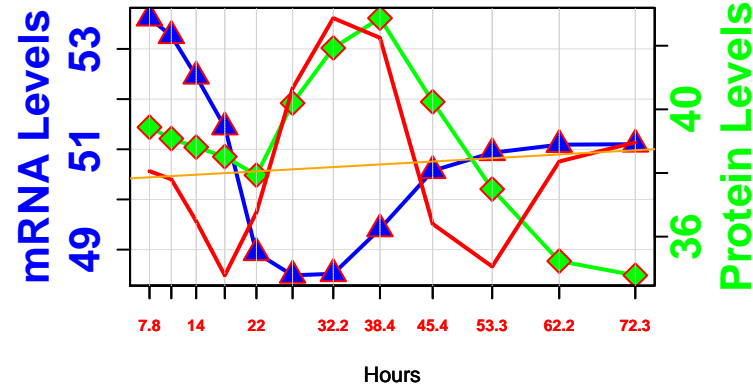
279 - ERG2 RLS: 26.4  
YMR202W  
ORF



286 - ERG3 RLS: 26.2  
YLR056W  
ORF

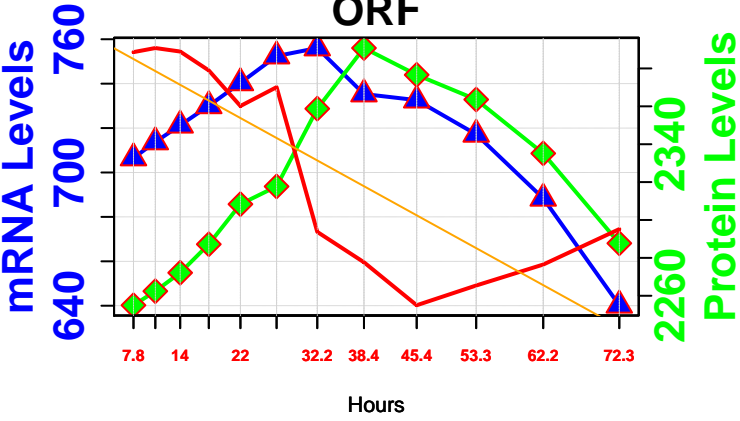


297 - ERG5 RLS: 25.93  
YMR015C  
ORF

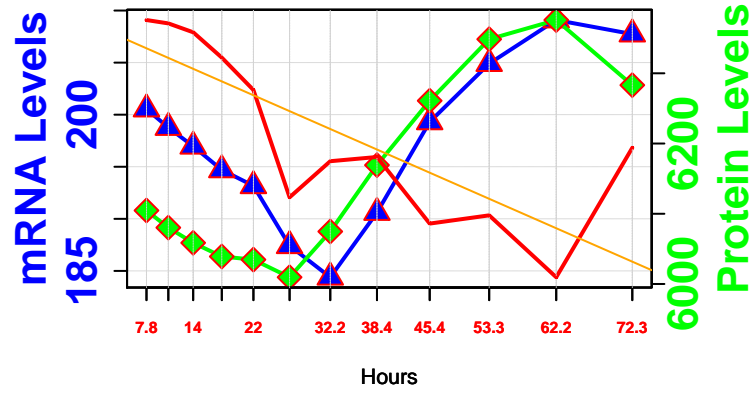


# arginine biosynthesis

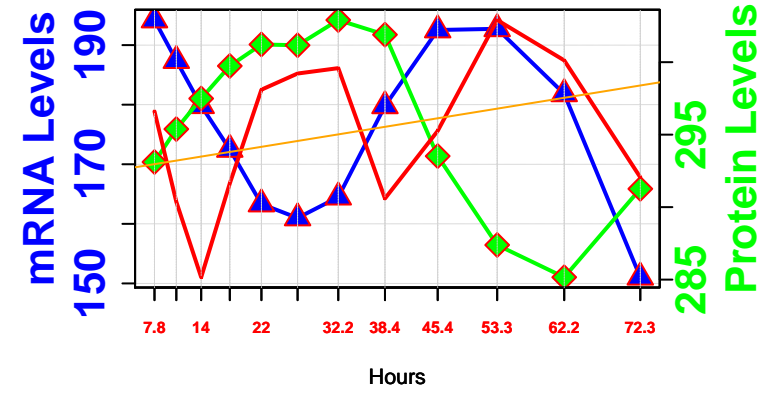
173 - ARG1 RLS: 28.5  
YOL058W  
ORF



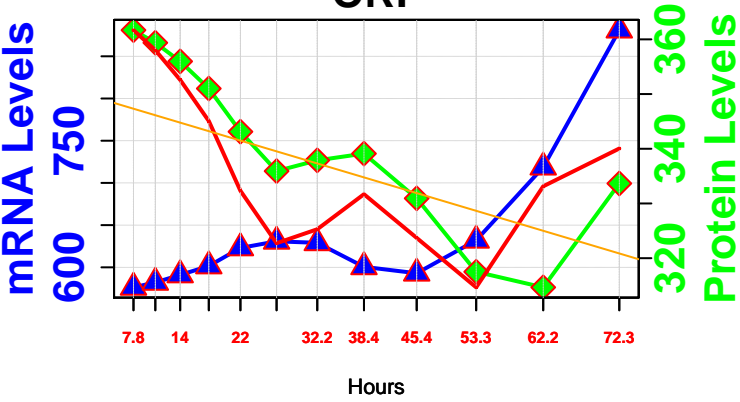
250 - CPA2 RLS: 27.16  
YJR109C  
ORF



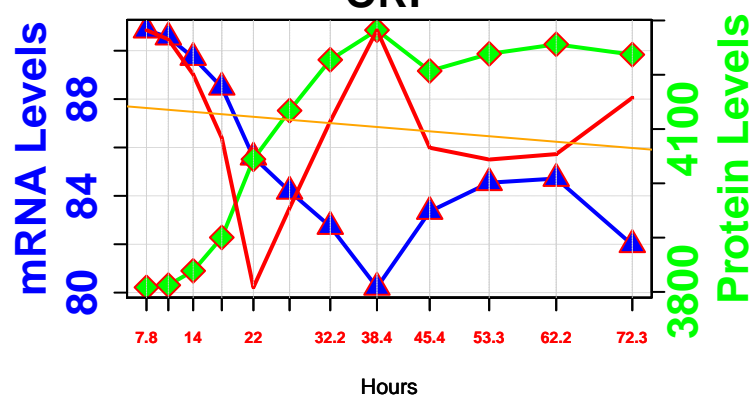
378 - ARG3 RLS: 24  
YJL088W  
ORF



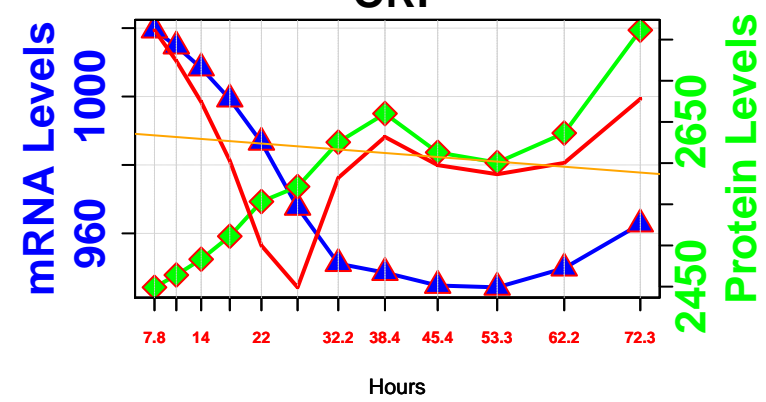
429 - CPA1 RLS: 23.2  
YOR303W  
ORF



464 - URA2 RLS: 22.54  
YJL130C  
ORF

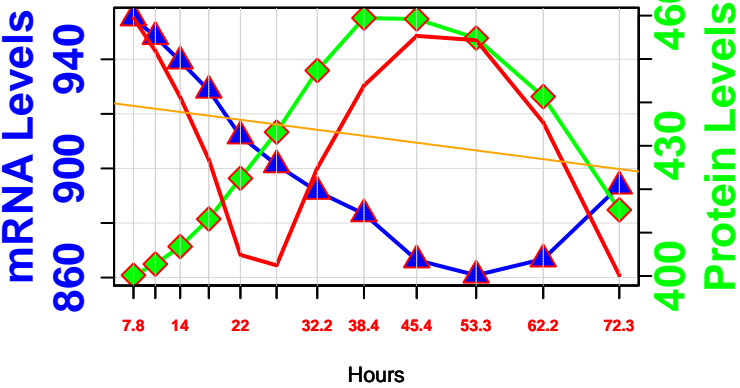


542 - ARG4 RLS: 20.03  
YHR018C  
ORF

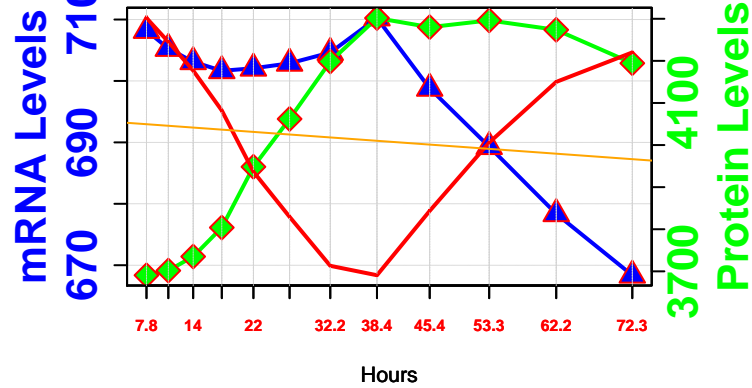


# histidine biosynthesis

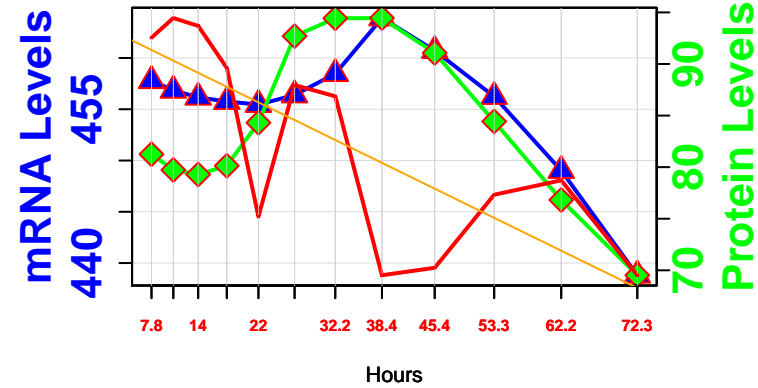
176 – HIS1 RLS: 28.4  
YER055C  
ORF



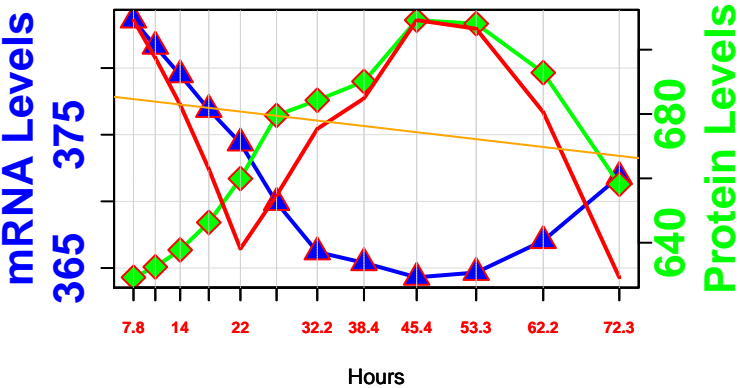
197 – HIS4 RLS: 28.05  
YCL030C  
ORF



449 – HIS3 RLS: 22.8  
YOR202W  
ORF

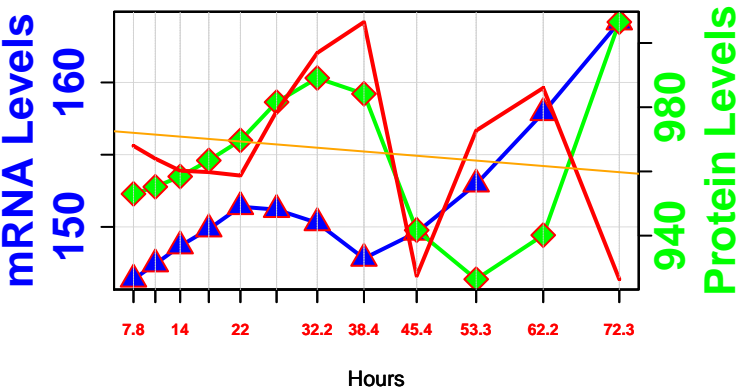


568 – HIS5 RLS: 19  
YIL116W  
ORF



# superpathway of glutamate biosynthesis

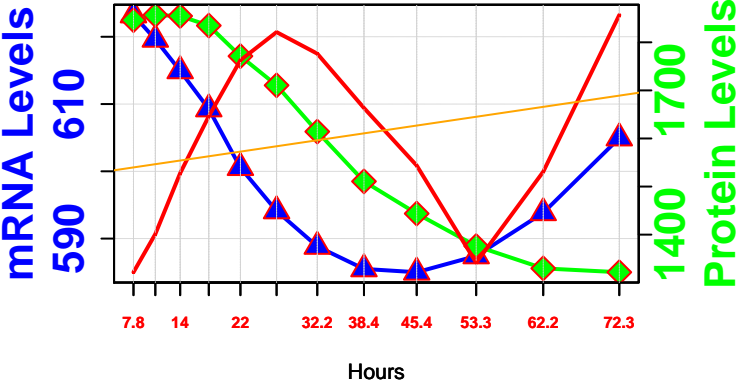
178 – IDP1 RLS: 28.38  
YDL066W  
ORF



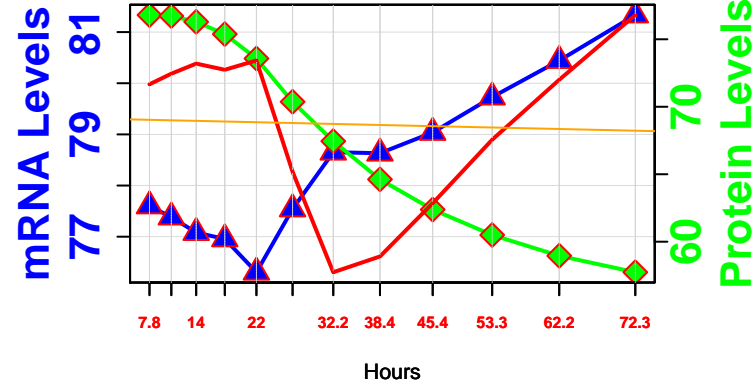


# methionine salvage pathway

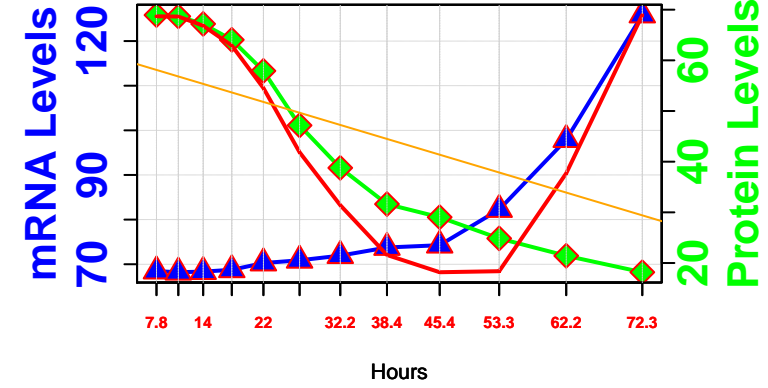
206 – ARO8 RLS: 27.94  
YGL202W  
ORF



430 – MRI1 RLS: 23.2  
YPR118W  
ORF

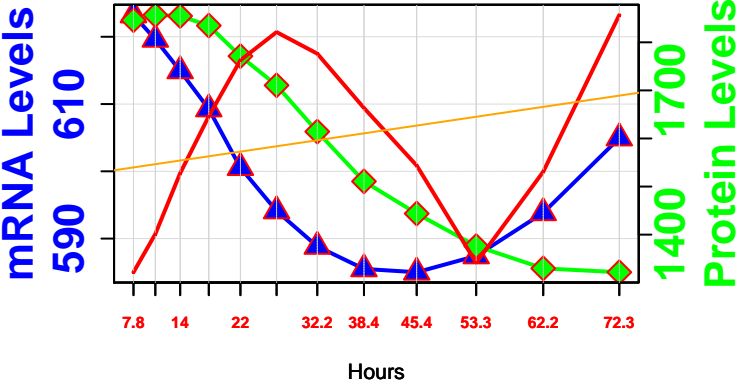


616 – UTR4 RLS: 16.6  
YEL038W  
ORF

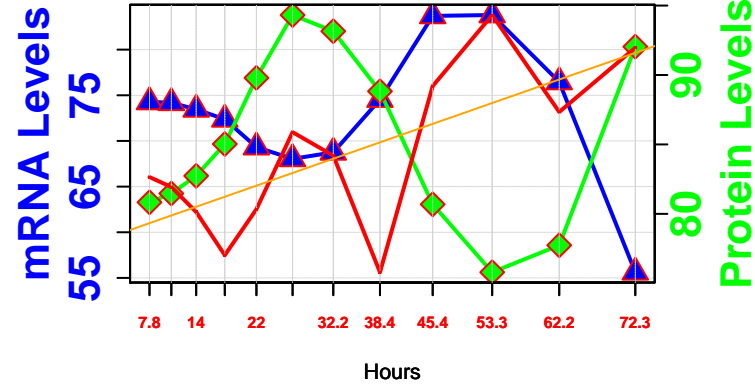


# phenylalanine biosynthesis

206 – ARO8 RLS: 27.94  
YGL202W  
ORF

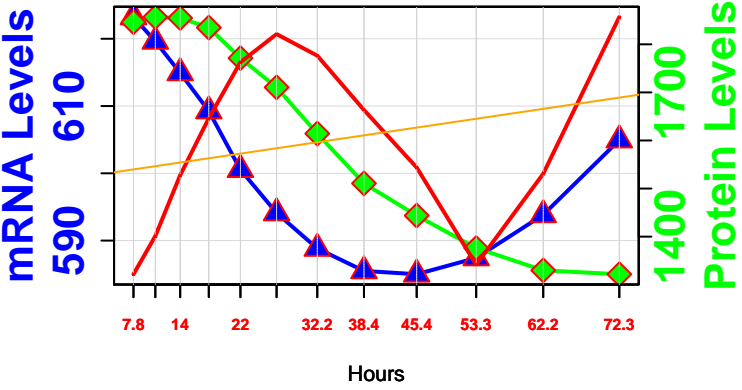


562 – ARO7 RLS: 19.4  
YPR060C  
ORF

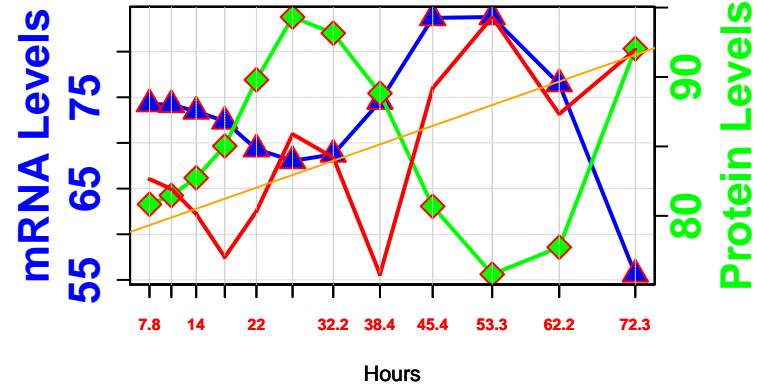


# tyrosine biosynthesis

206 – ARO8 RLS: 27.94  
YGL202W  
ORF

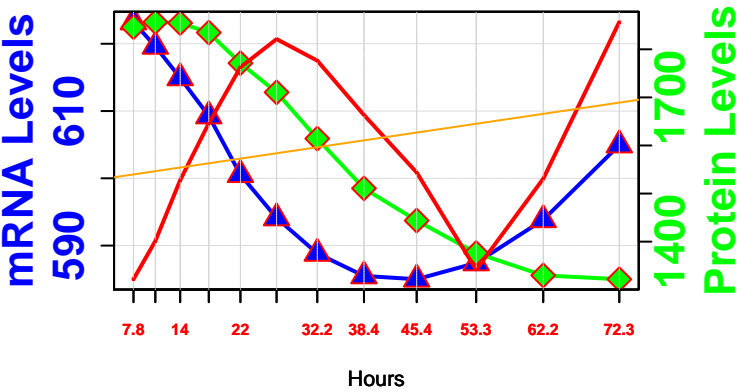


562 – ARO7 RLS: 19.4  
YPR060C  
ORF



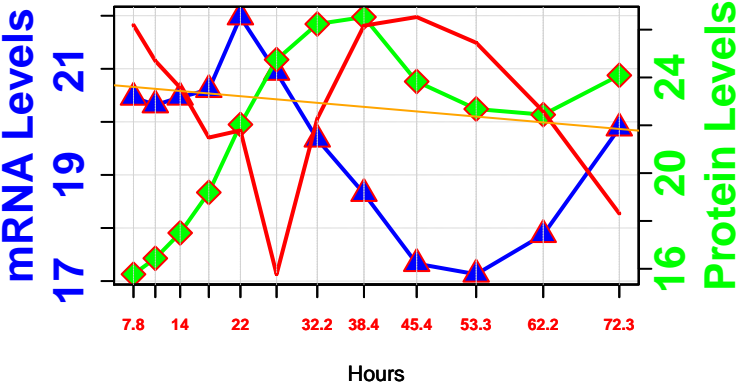
# tyrosine degradation

206 – ARO8 RLS: 27.94  
YGL202W  
ORF

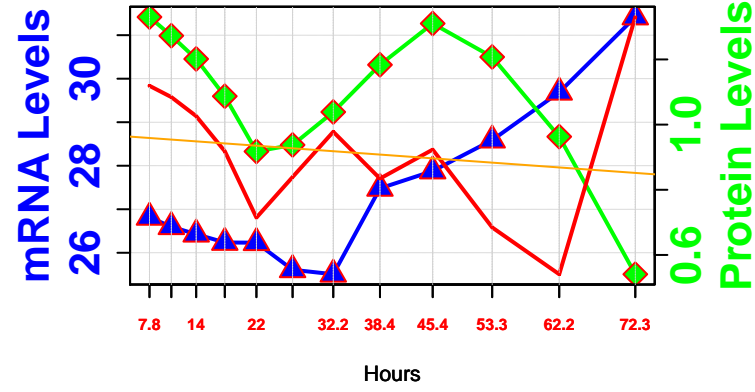


# mevalonate pathway

209 – HMG2 RLS: 27.91  
YLR450W  
ORF

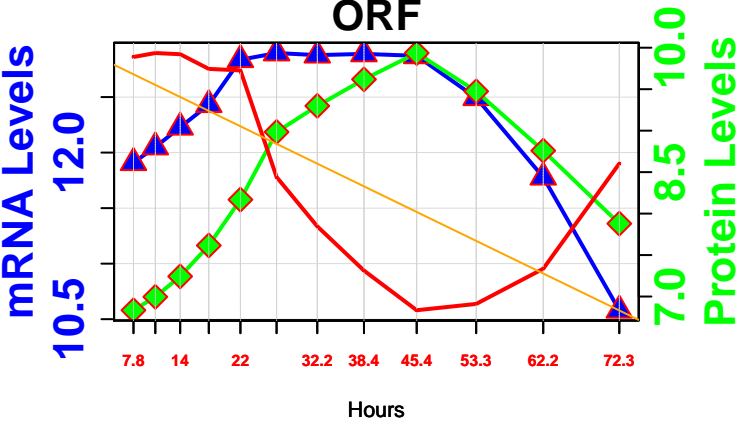


432 – HMG1 RLS: 23.08  
YML075C  
ORF

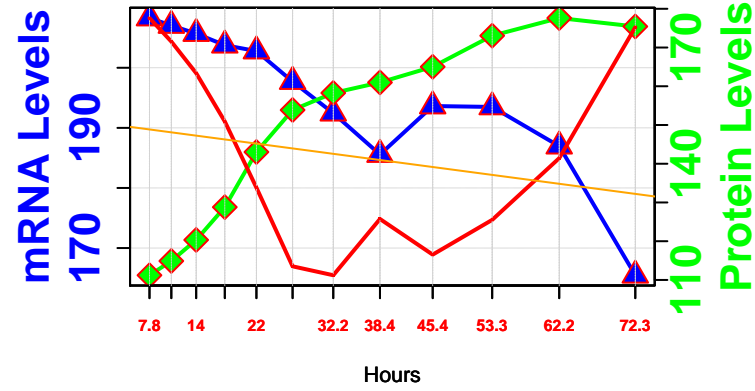


# fatty acid oxidation pathway

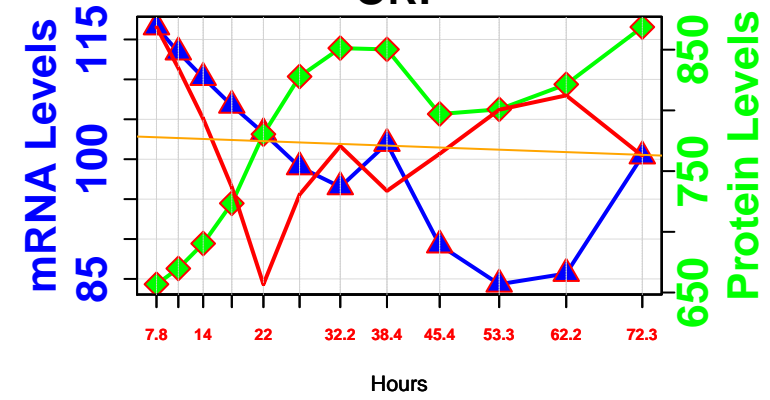
225 – FAA3 RLS: 27.6  
YIL009W  
ORF



262 – FAA4 RLS: 26.8  
YMR246W  
ORF

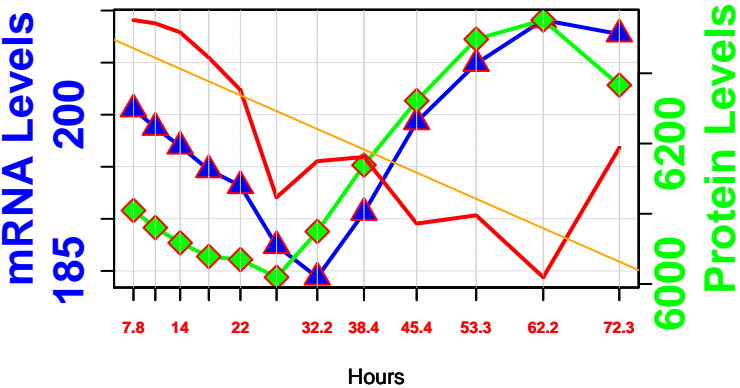


514 – FAA1 RLS: 21.2  
YOR317W  
ORF

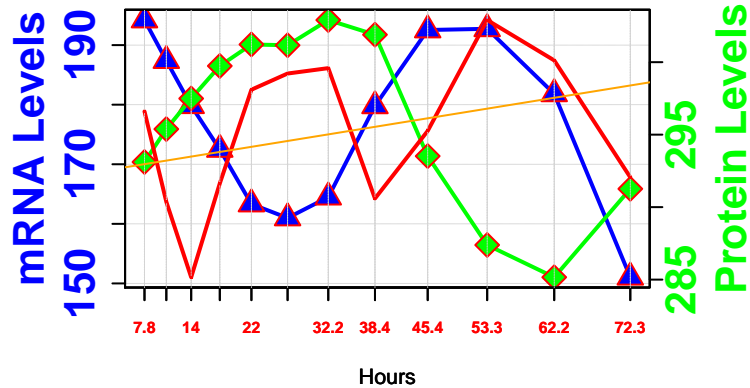


# citrulline biosynthesis

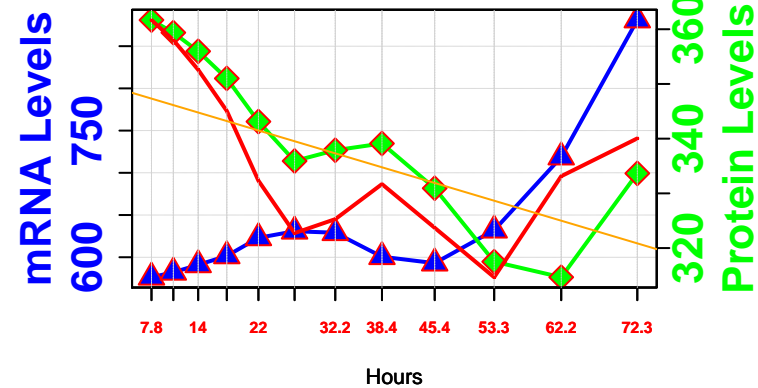
250 – CPA2 RLS: 27.16  
YJR109C  
ORF



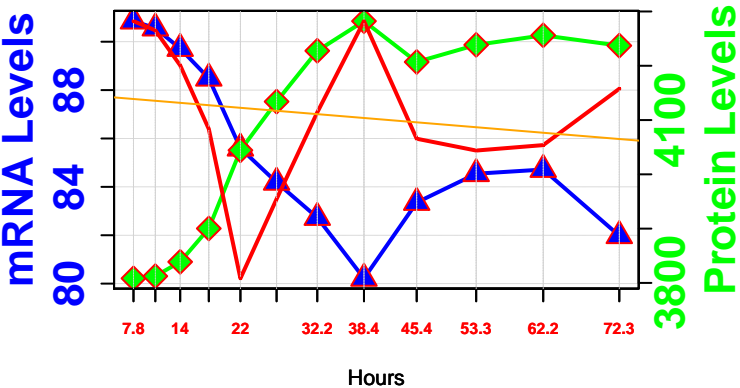
378 – ARG3 RLS: 24  
YJL088W  
ORF



429 – CPA1 RLS: 23.2  
YOR303W  
ORF

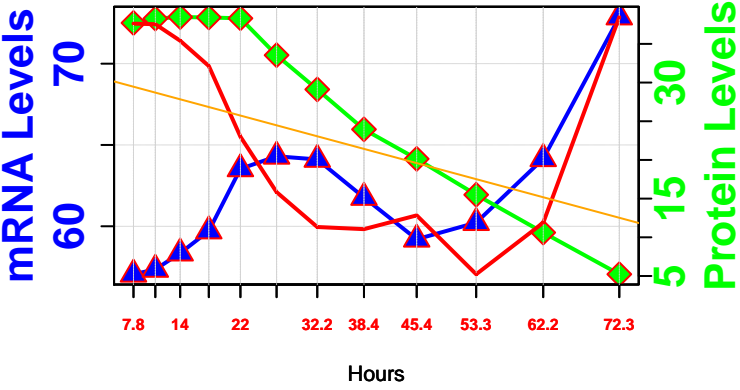


464 – URA2 RLS: 22.54  
YJL130C  
ORF

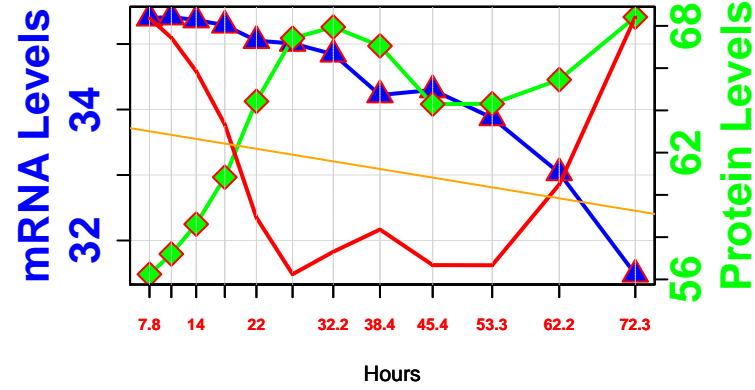


# inositol phosphate biosynthesis

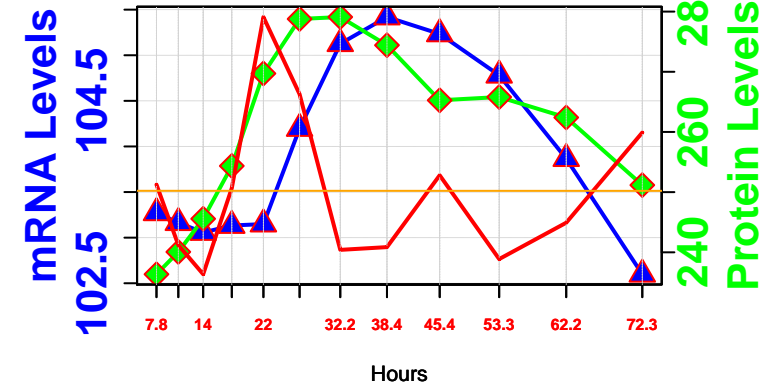
252 – DDP1 RLS: 27.11  
YOR163W  
ORF



273 – VIP1 RLS: 26.56  
YLR410W  
ORF



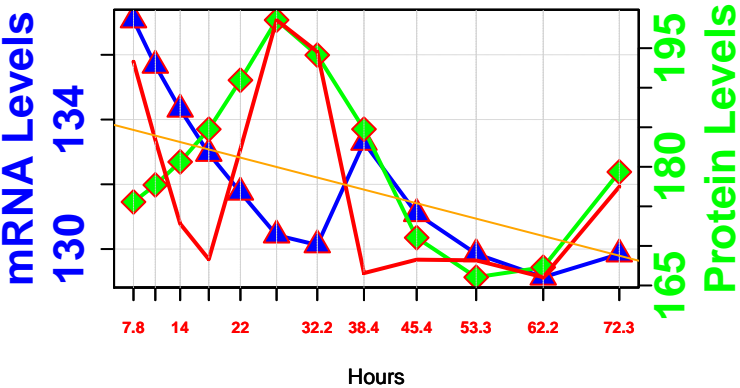
622 – SAC1 RLS: 15.89  
YKL212W  
ORF



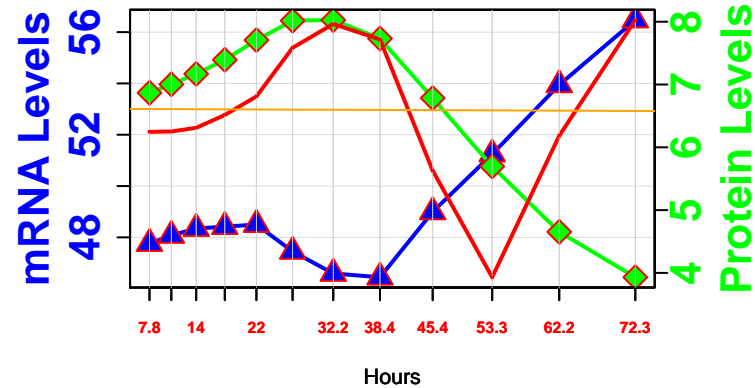


# aspartate biosynthesis

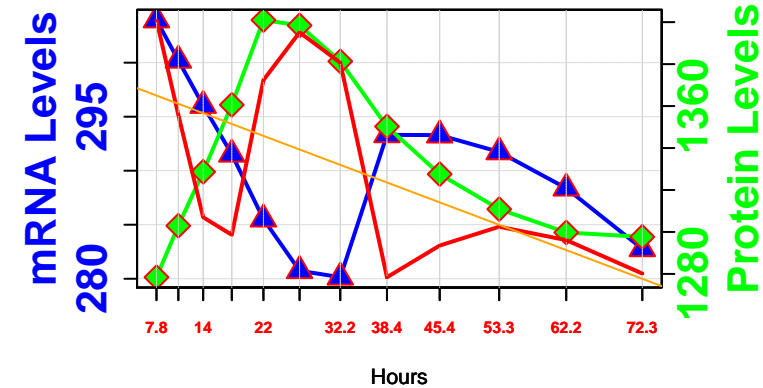
264 – PYC2 RLS: 26.75  
YBR218C  
ORF



283 – AAT1 RLS: 26.21  
YKL106W  
ORF

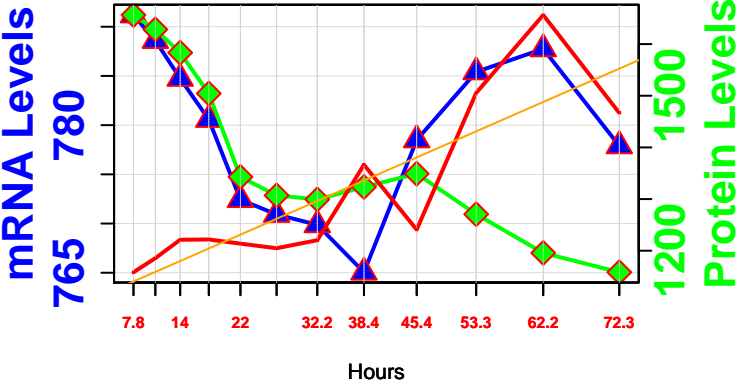


401 – AAT2 RLS: 23.6  
YLR027C  
ORF

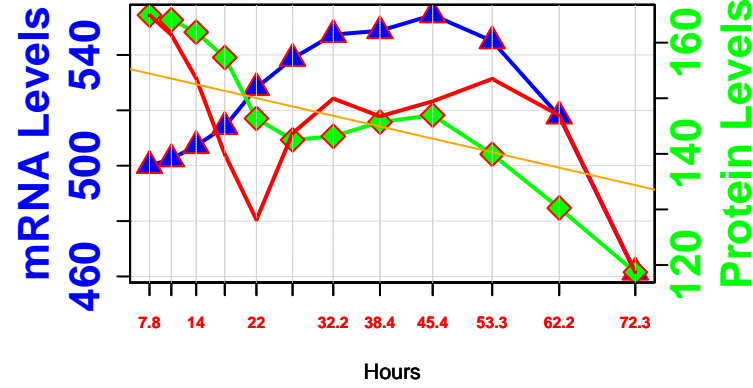


# chorismate biosynthesis

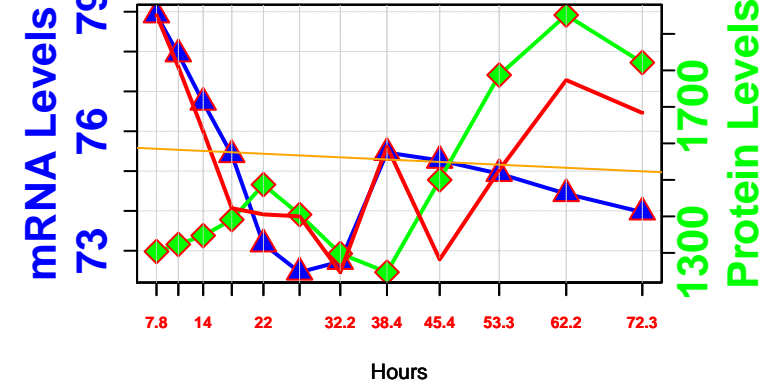
274 – ARO4 RLS: 26.53  
YBR249C  
ORF



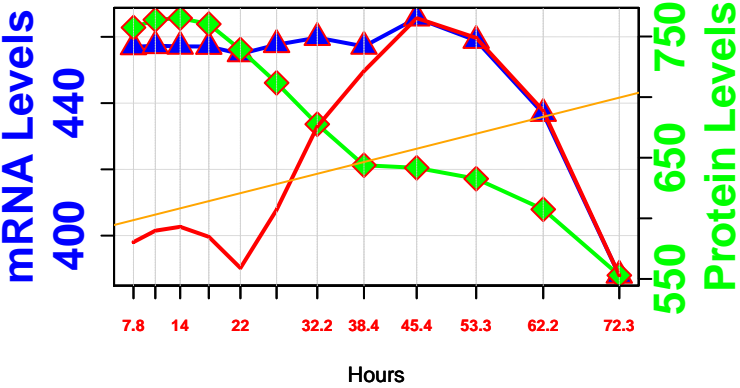
333 – ARO3 RLS: 25.2  
YDR035W  
ORF



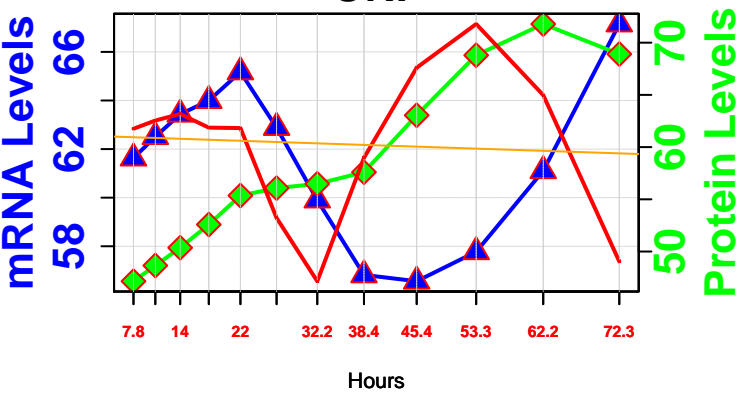
484 – ARO1 RLS: 21.8  
YDR127W  
ORF



648 – ARO2 RLS: 12  
YGL148W  
ORF

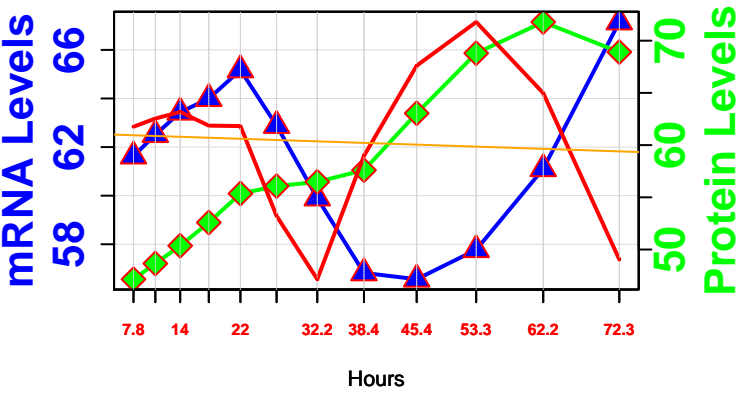


278 – PNP1 RLS: 26.4  
YLR209C  
ORF



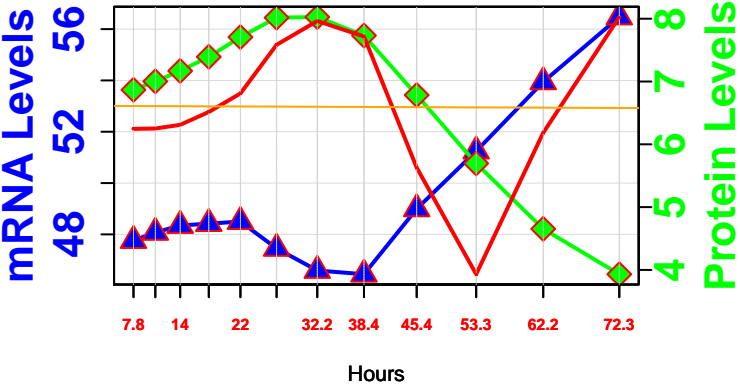
# nicotinate riboside salvage pathway II

278 – PNP1 RLS: 26.4  
YLR209C  
ORF

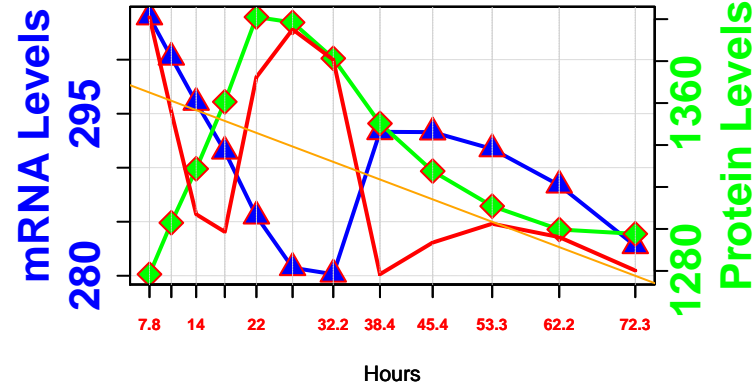


# asparagine degradation

283 – AAT1 RLS: 26.21  
YKL106W  
ORF

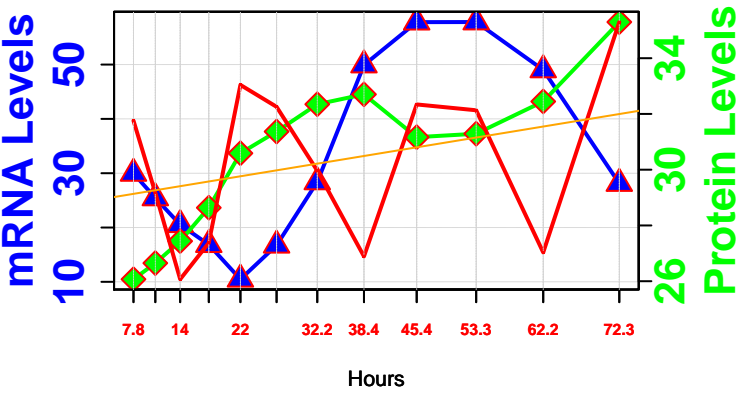


401 – AAT2 RLS: 23.6  
YLR027C  
ORF



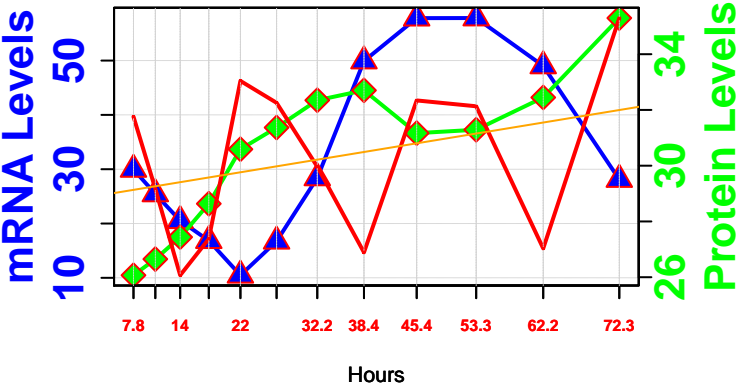
# homocysteine biosynthesis

288 – MET2 RLS: 26.2  
YNL277W  
ORF



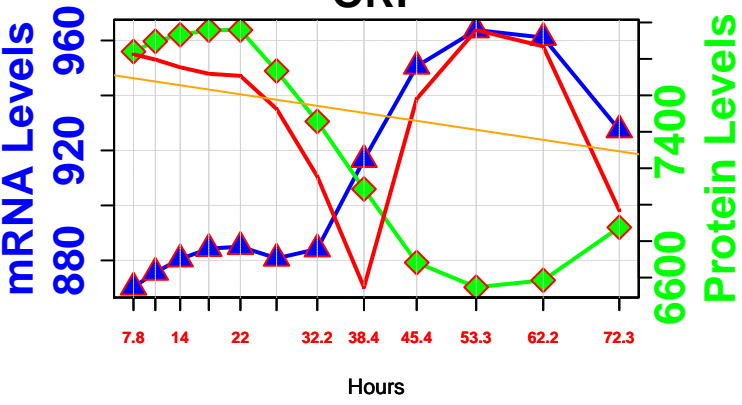
superpathway of sulfur amino acid biosynthesis

288 – MET2 RLS: 26.2  
YNL277W  
ORF



# formaldehyde oxidation (glutamine dependent)

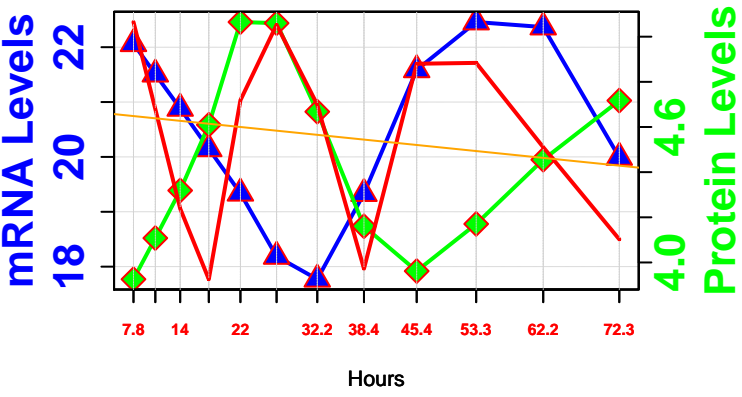
290 – GDH1 RLS: 26.13  
YOR375C  
ORF





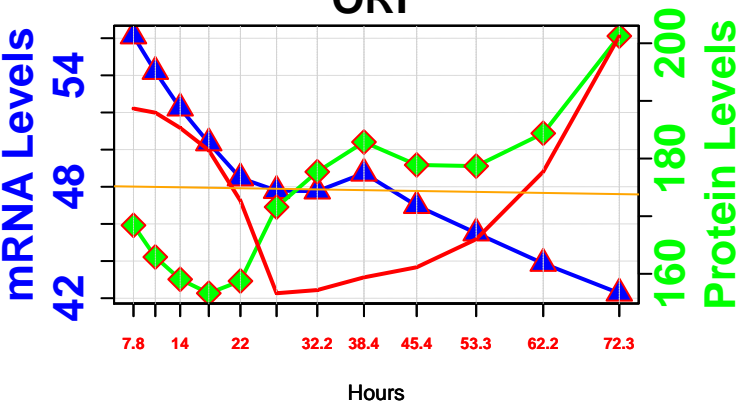
# thiamine biosynthesis

308 – THI6 RLS: 25.8  
YPL214C  
ORF



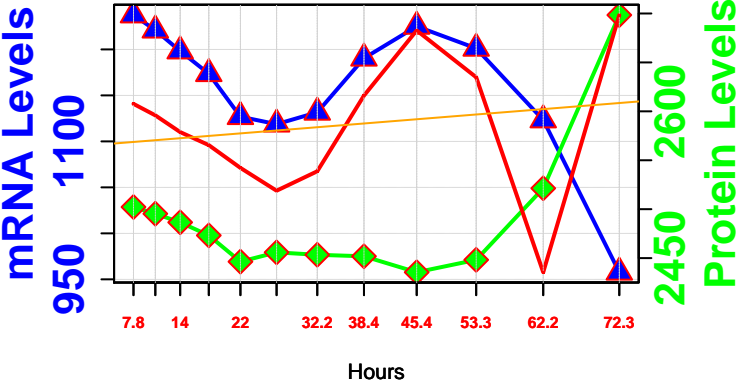
dehydro-D-arabinono-1,4-lactone biosynthesis

311 - ALO1 RLS: 25.76  
YML086C  
ORF

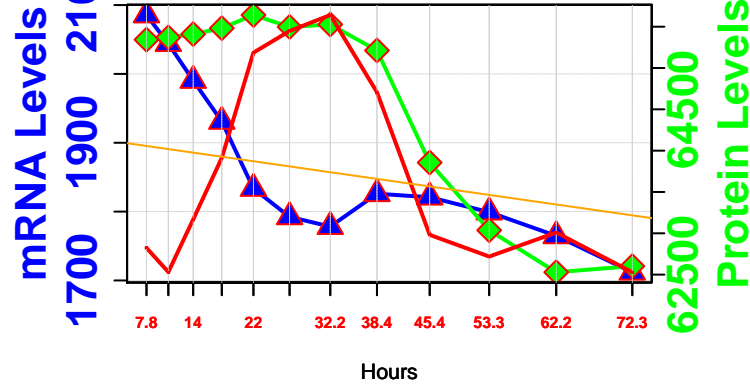


# methionine biosynthesis

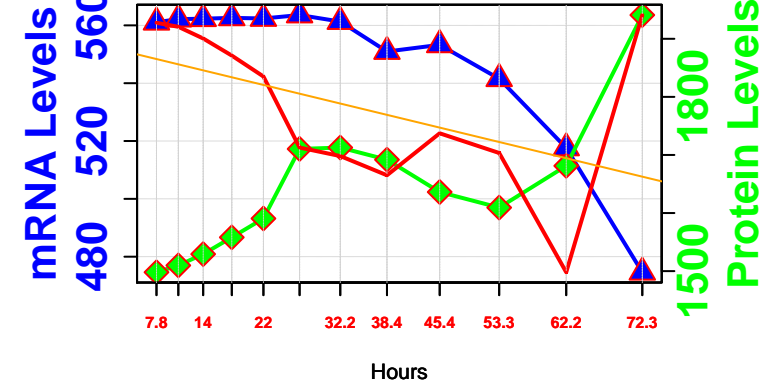
34 – SAM1 RLS: 32.96  
YLR180W  
ORF



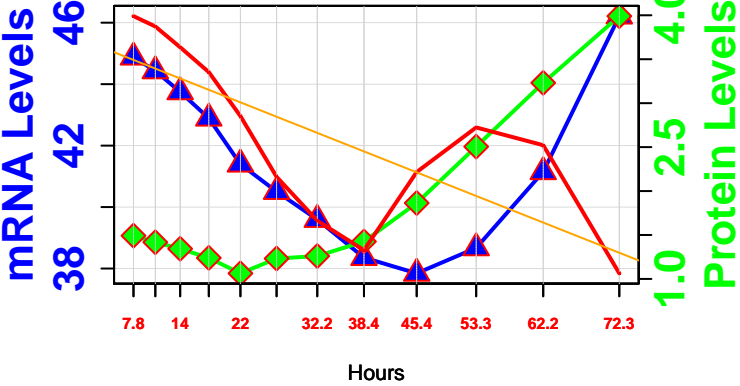
312 – MET6 RLS: 25.74  
YER091C  
ORF



387 – SAM2 RLS: 23.8  
YDR502C  
ORF

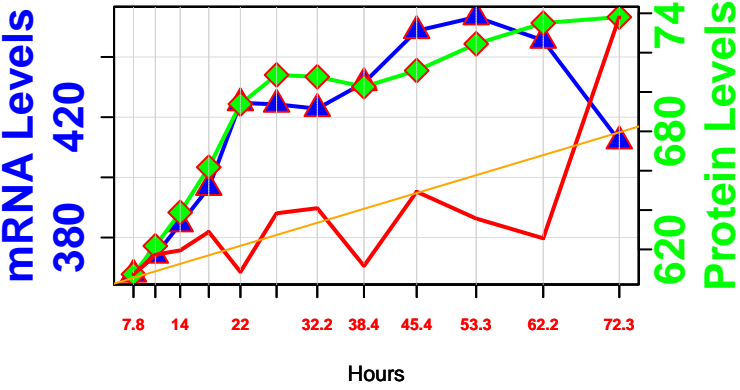


607 – MET7 RLS: 17.14  
YOR241W  
ORF

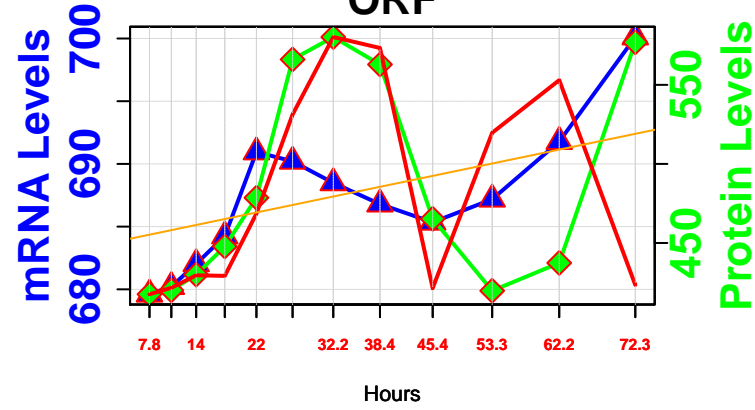


# leucine biosynthesis

329 – LEU4 RLS: 25.4  
YNL104C  
ORF

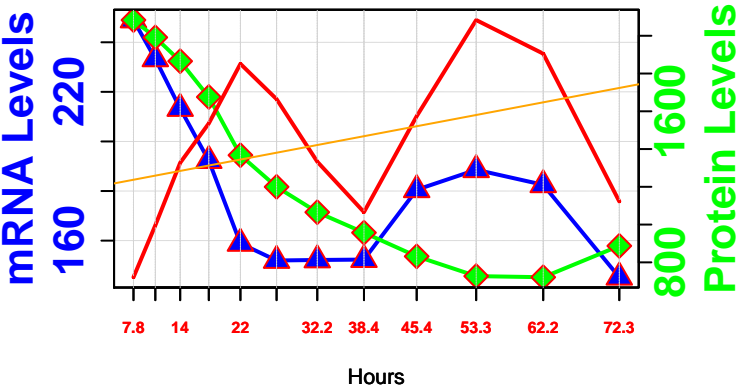


399 – ILV6 RLS: 23.6  
YCL009C  
ORF

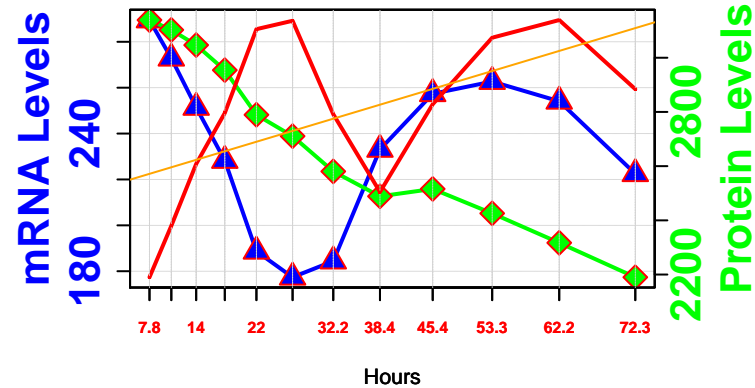


# cysteine biosynthesis from homocysteine

348 – CYS4 RLS: 24.67  
YGR155W  
ORF

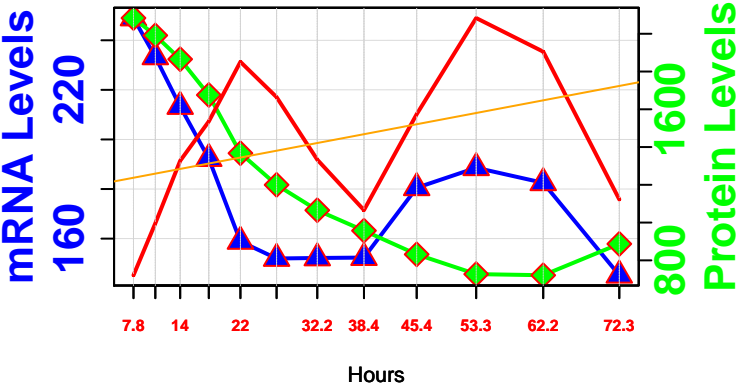


611 – CYS3 RLS: 16.83  
YAL012W  
ORF

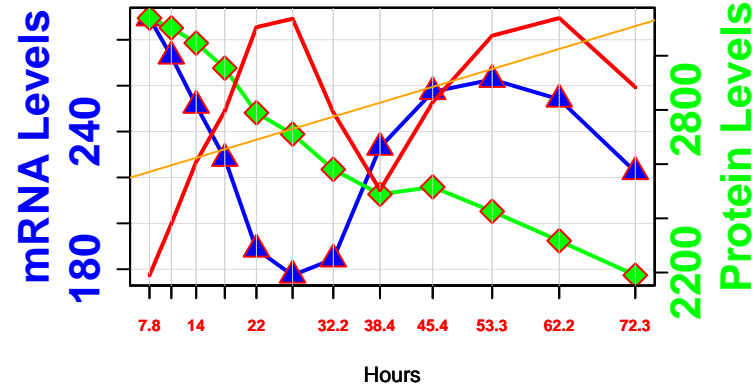


# cysteine biosynthesis/homocysteine degradation

348 – CYS4 RLS: 24.67  
YGR155W  
ORF

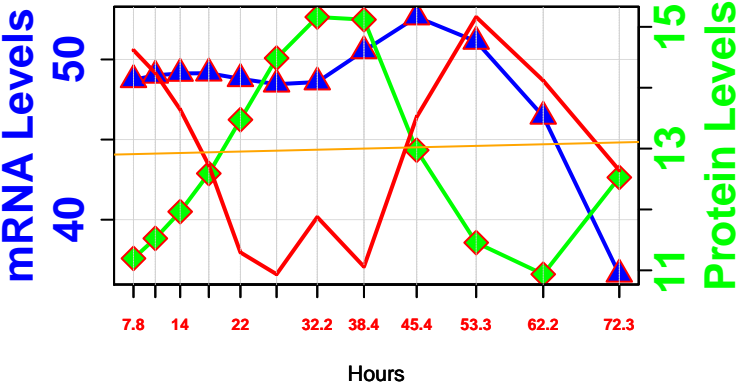


611 – CYS3 RLS: 16.83  
YAL012W  
ORF

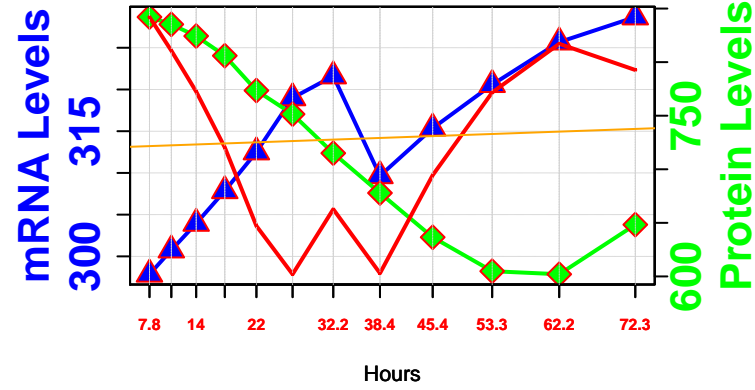


# spermidine and methylthioadenosine biosynthesis

361 – SPE2 RLS: 24.4  
YOL052C  
ORF

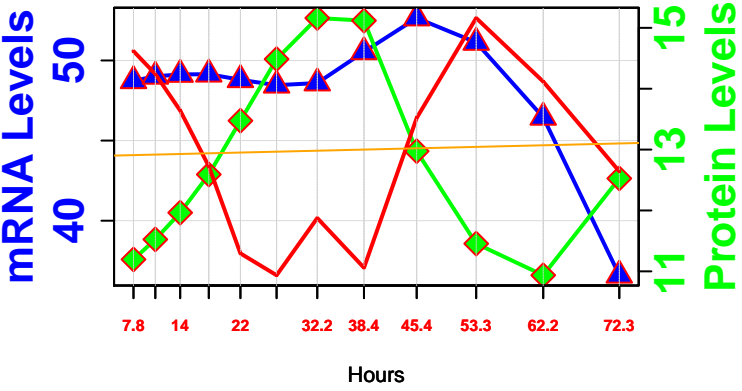


381 – SPE3 RLS: 24  
YPR069C  
ORF



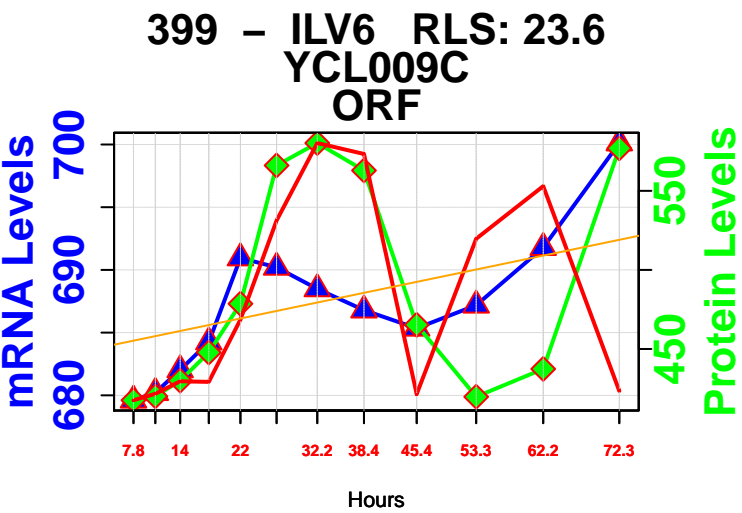
# spermine and methylthioadenosine biosynthesis

361 - SPE2 RLS: 24.4  
YOL052C  
ORF

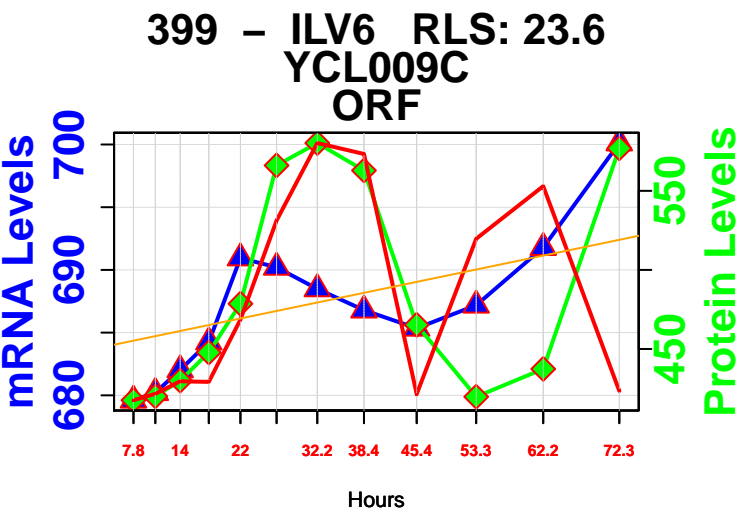




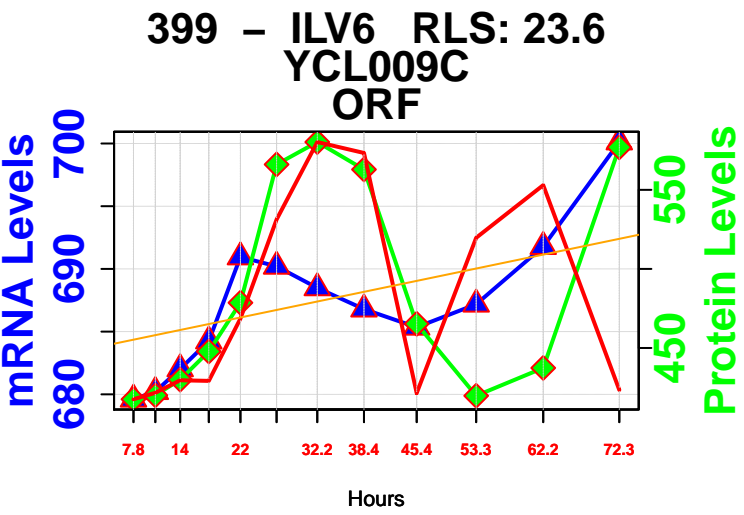
# acetoin biosynthesis



# isoleucine biosynthesis

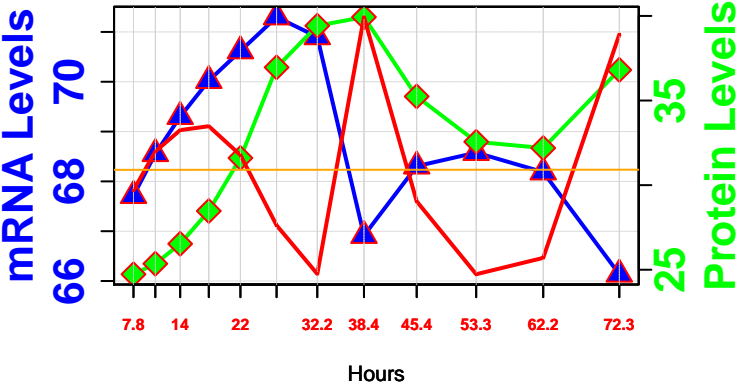


# valine biosynthesis

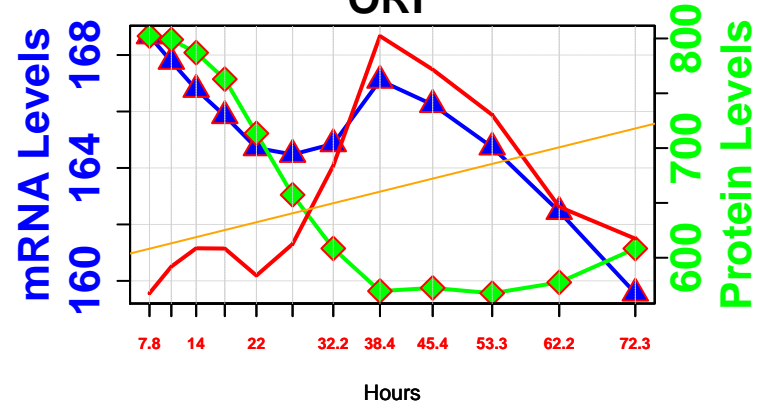


# proline biosynthesis

405 - PRO1 RLS: 23.58  
YDR300C  
ORF

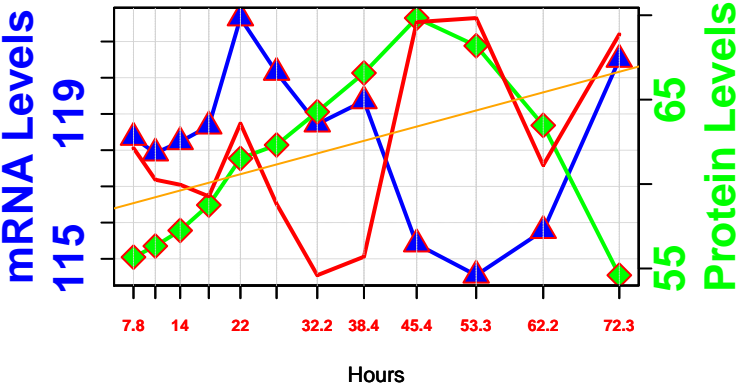


638 - PRO2 RLS: 13.68  
YOR323C  
ORF



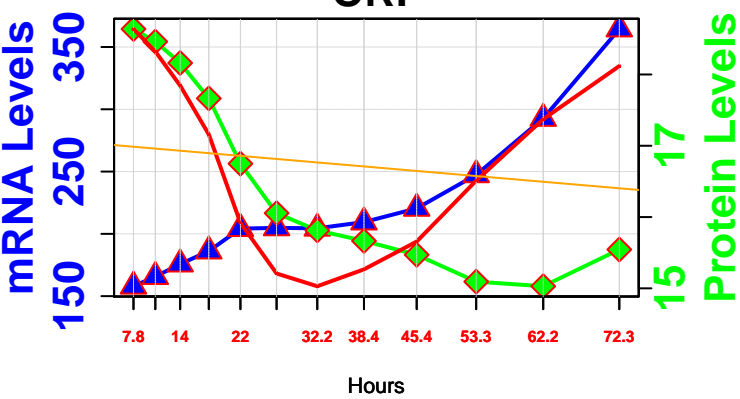
de novo NAD biosynthesis

415 – BNA6 RLS: 23.4  
YFR047C  
ORF

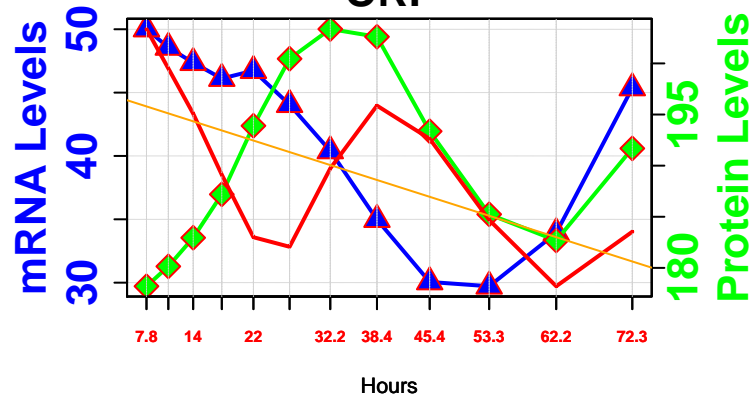


## proline utilization

418 – PUT1 RLS: 23.4  
YLR142W  
ORF

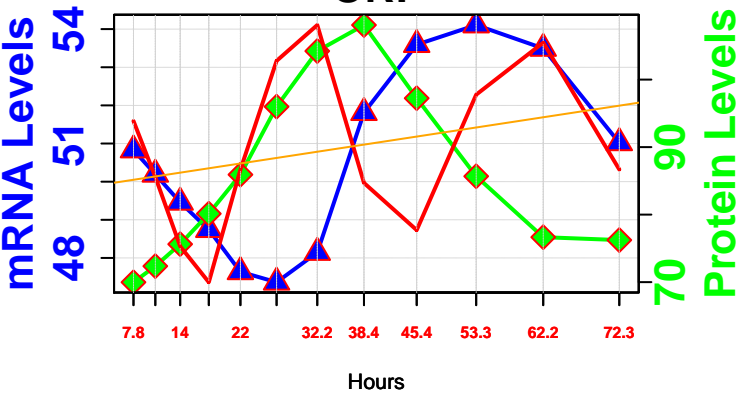


481 – PUT2 RLS: 22  
YHR037W  
ORF

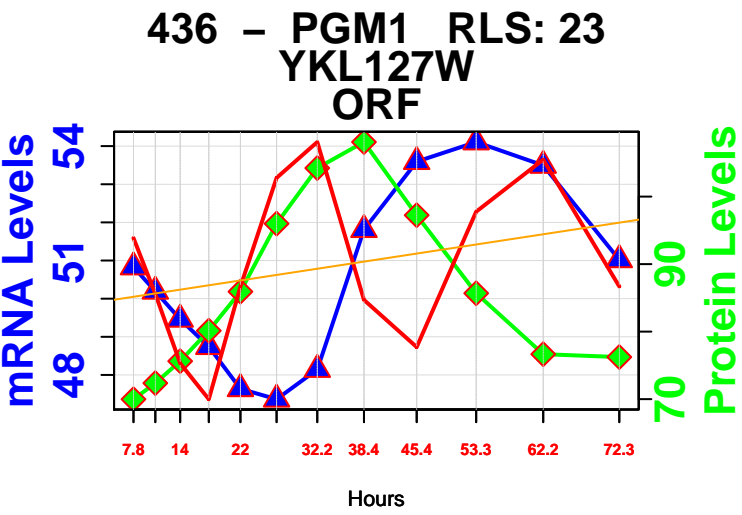


# dolichyl glucosyl phosphate biosynthesis

436 - PGM1 RLS: 23  
YKL127W  
ORF

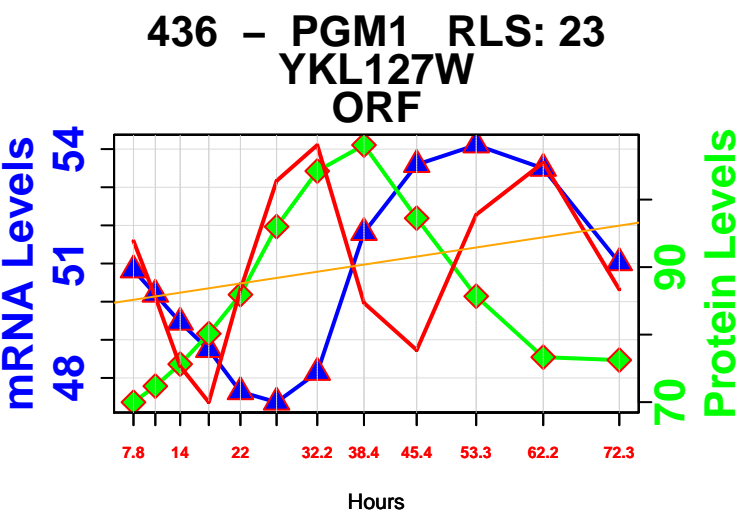


# galactose degradation



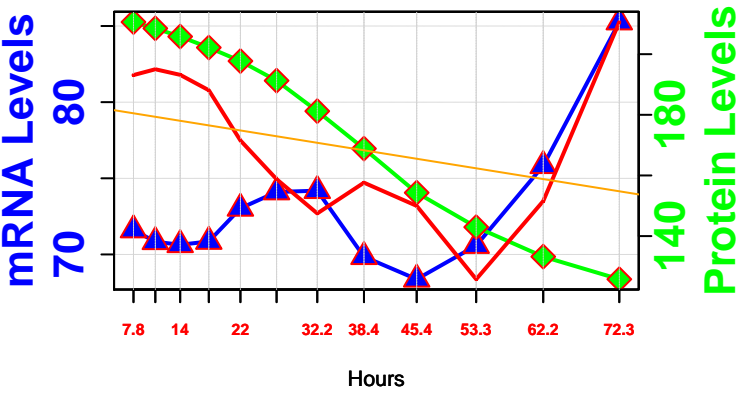


# glycogen biosynthesis



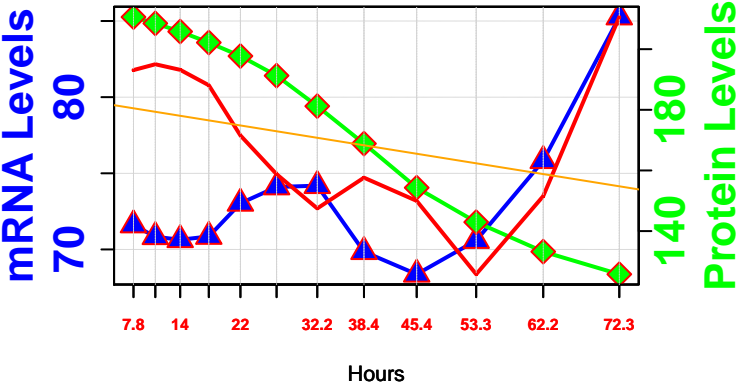
# glutathione-glutaredoxin redox reactions

441 - GLR1 RLS: 22.84  
YPL091W  
ORF



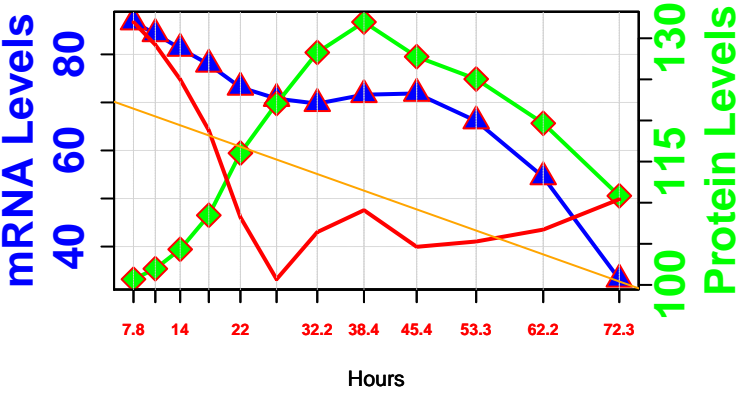
phosphatidylglycerol biosynthesis (triacylglycerols synthesis pathway)

441 - GLR1 RLS: 22.84  
YPL091W  
ORF



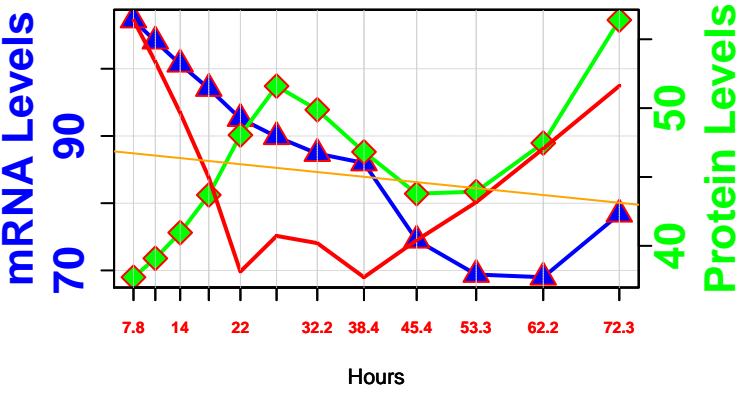
# triglyceride biosynthesis

442 – SLC1 RLS: 22.8  
YDL052C  
ORF



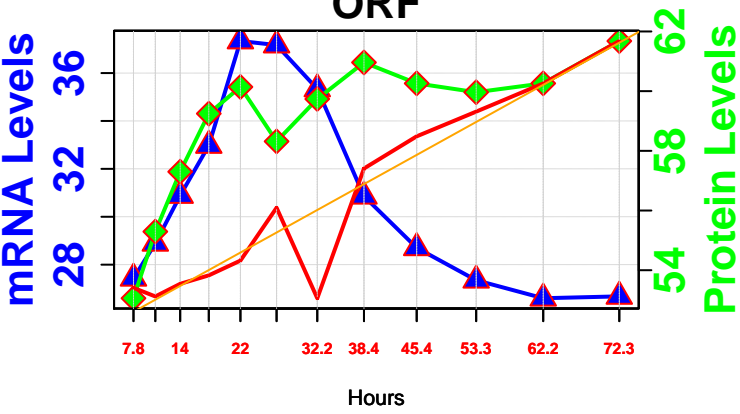
# ubiquinone biosynthesis from 4-hydroxybenzoate

488 – COQ5 RLS: 21.66  
YML110C  
ORF

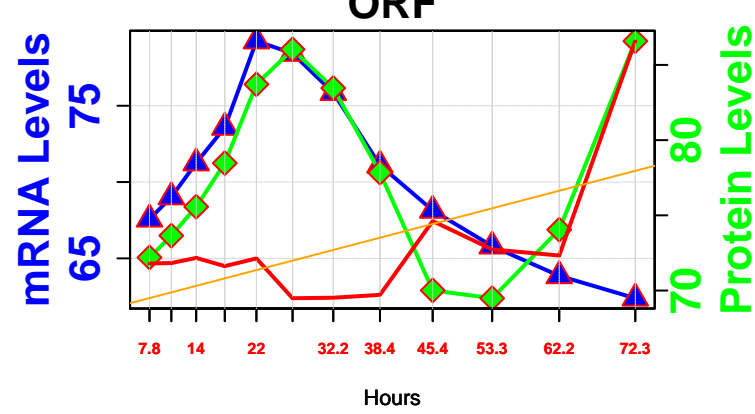


# phospholipid biosynthesis

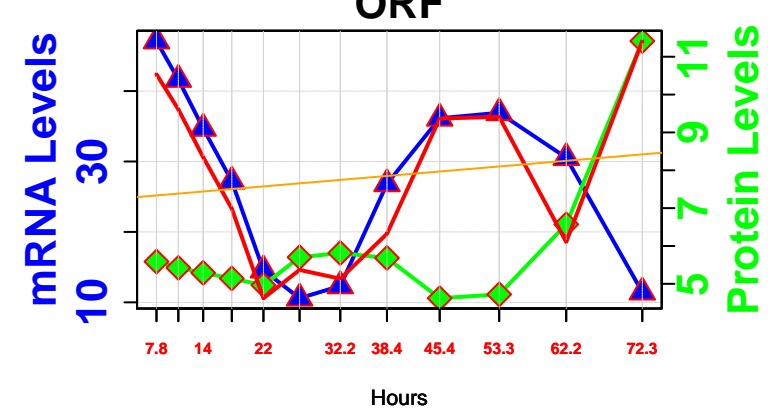
116 - CKI1 RLS: 30.2  
YLR133W  
ORF



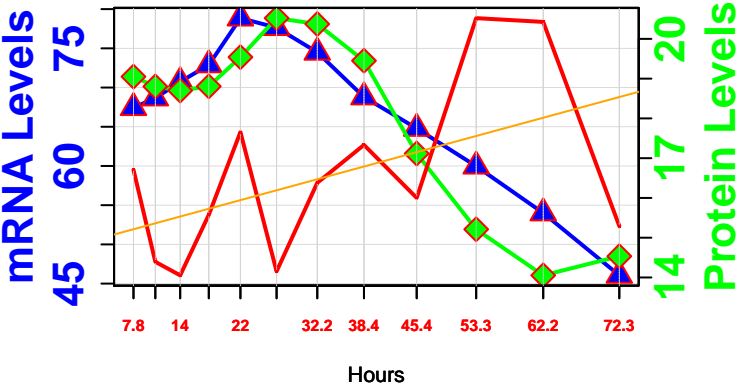
506 - CHO2 RLS: 21.2  
YGR157W  
ORF



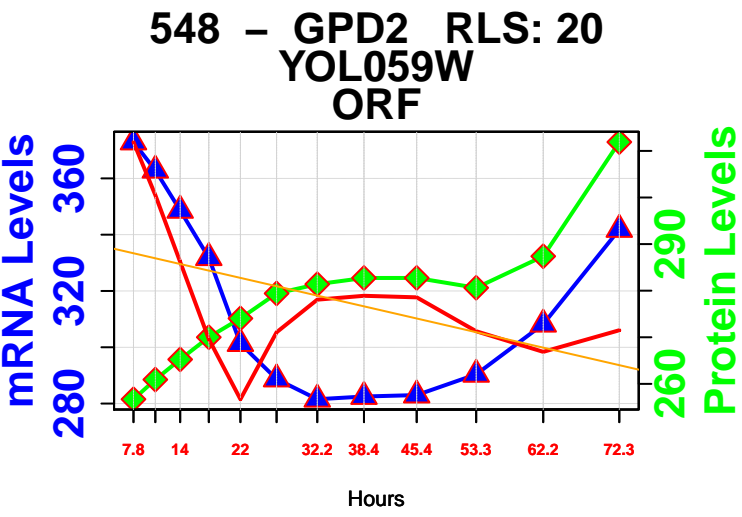
510 - PCT1 RLS: 21.2  
YGR202C  
ORF



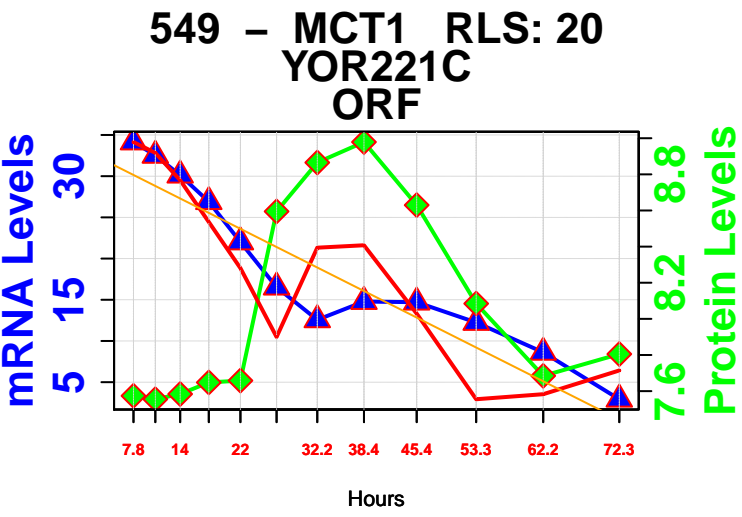
636 - PSD1 RLS: 13.93  
YNL169C  
ORF



# glycerol biosynthesis



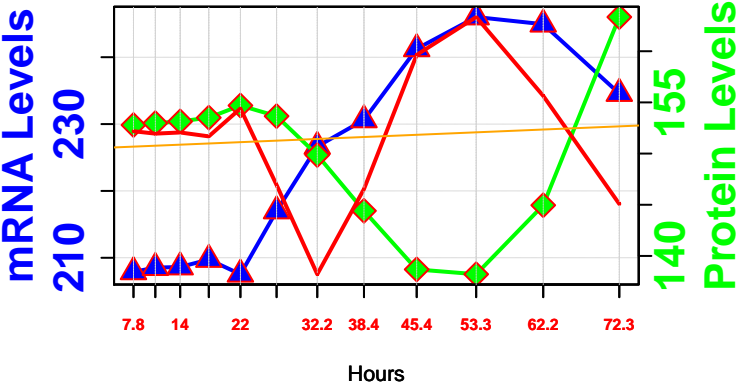
# fatty acid biosynthesis, initial steps



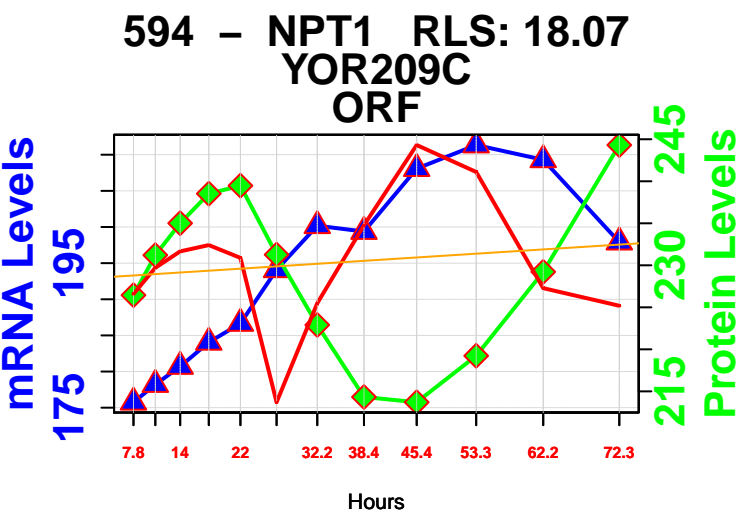


# glycine biosynthesis from threonine

579 – GLY1 RLS: 18.6  
YEL046C  
ORF

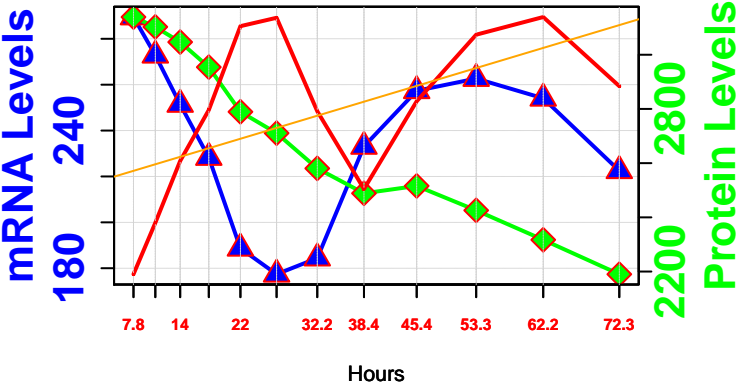


# NAD salvage pathway



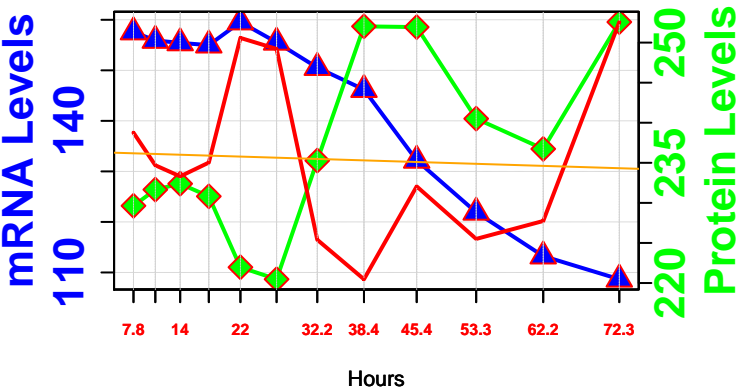
# threonine degradation

611 - CYS3 RLS: 16.83  
YAL012W  
ORF



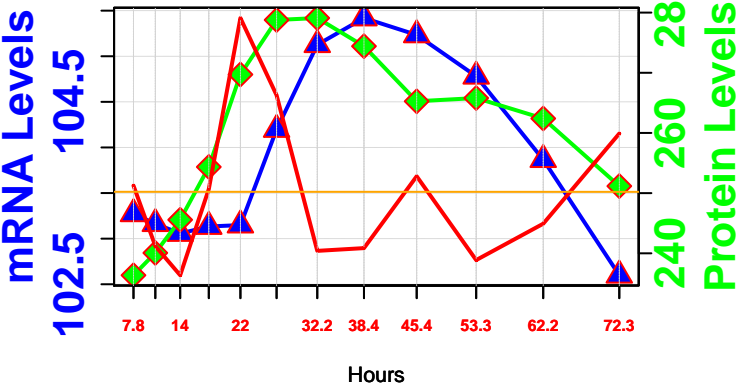
# pyridoxal 5'-phosphate salvage pathway

615 - PDX3 RLS: 16.6  
YBR035C  
ORF



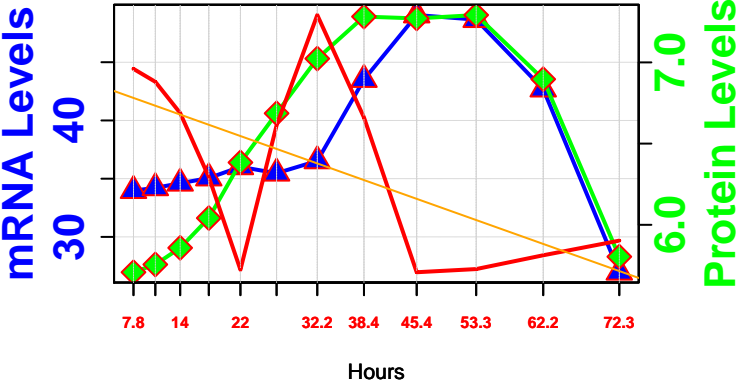
phosphatidylinositol phosphate biosynthesis

622 - SAC1 RLS: 15.89  
YKL212W  
ORF



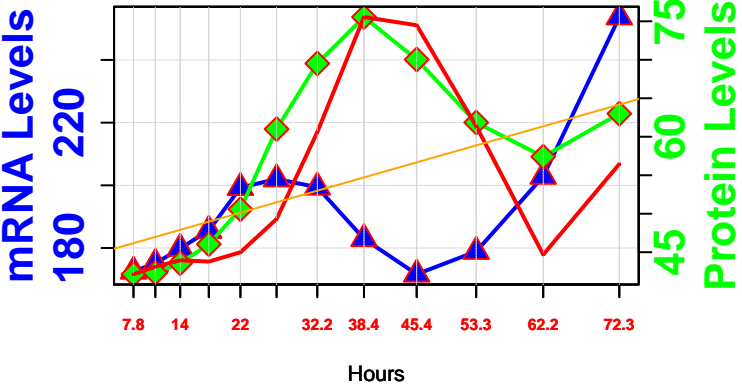
phospholipids degradation

642 - ISC1 RLS: 13.09  
YER019W  
ORF



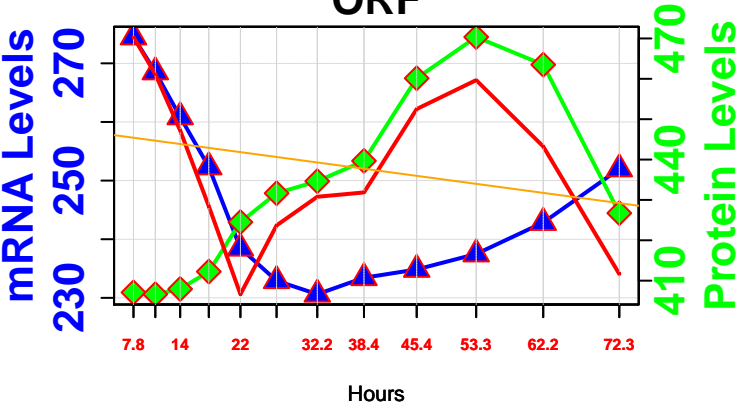
# riboflavin, FMN and FAD biosynthesis

647 – RIB4 RLS: 12.4  
YOL143C  
ORF

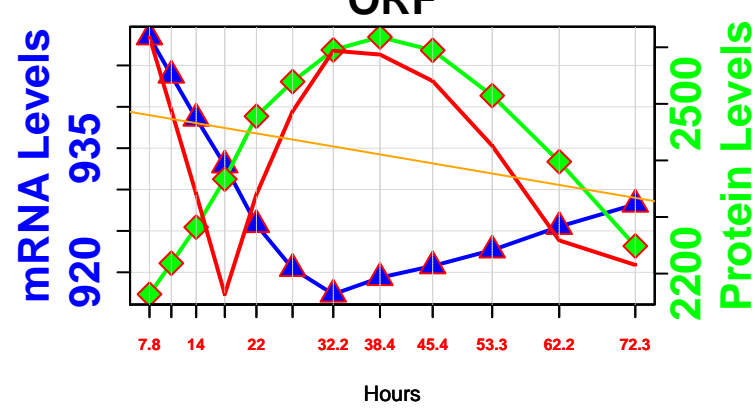


# homoserine biosynthesis

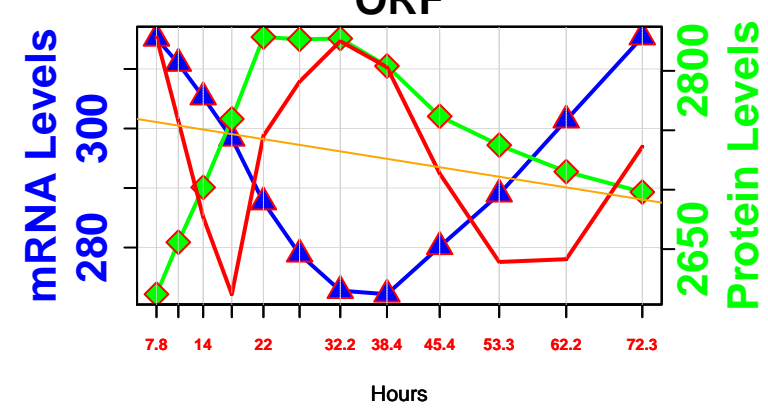
650 – HOM3 RLS: 11.79  
YER052C  
ORF



651 – HOM2 RLS: 11.68  
YDR158W  
ORF



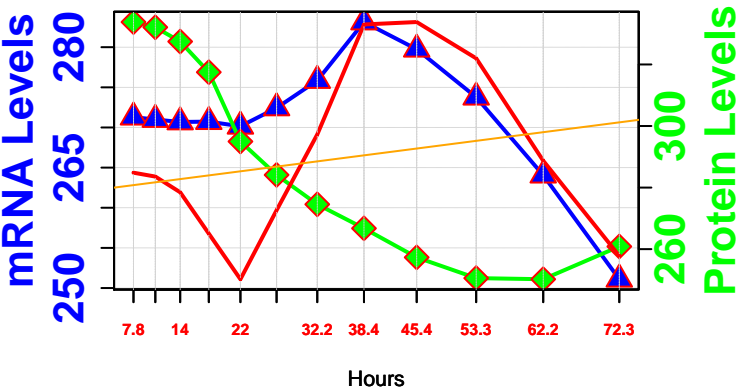
665 – HOM6 RLS: 6.76  
YJR139C  
ORF





# threonine biosynthesis

673 – THR1 RLS: 3.48  
YHR025W  
ORF



674 – THR4 RLS: 3.12  
YCR053W  
ORF

