Supplementary Data File 2. Phylogenies of developmentally essential genes annotated with domain architectures and developmental expression profiles

Phylogenies of 385 *DD* DEG with their closest homologs in the Dictyostelids *DP*, *DL*, *PP* and *DF*, the unicellular amoebozoa *PhyP*, *AC* and *EH* and outside of Amoebozoa were prepared by Bayesian inference as outlined in Methods. Bayesian posterior probabilities of tree nodes are indicated by coloured dots. The trees are annotated with the protein domain architectures of the genes as determined by SMART[1], using simplified diagrams to allow size-reduction. PFAM[2] or SCOP[3] domains are represented by rectangles, filled with colour gradients starting from black or tan on the left side, respectively.

Developmental transcriptional profiles were retrieved for *DD* (DDBa, DDBb) and *DP* (DPUa, DPUb) from a replicate time course[4] and for *DF* and *PP* from two separate experiments, which were analysed using either the Roche 454 (DFAa, PPLa) or Illumina platforms (DFAb, PPLb). For *DL* a single experiment, analysed using the Illumina platform (DLA) was used. Due to differences in the duration of development between species, the profiles were stage-matched rather than time matched. These stage are vegetative (t0 for *DD*, *DP*), early aggregate (t4), completed aggregate (t8), tipped mound (t12), slug (t16), early culmination (t20), mature fruiting body (t24). The *DD* and *DP* experiments also contain transcript reads for purified prestalk (pst) and prespore cells (psp), while the *PP* 454 series contains reads from purified spore- and stalk cells.

For time series, normalized reads were expressed as percentage of the highest read count of the series and presented as yellow to red heatmaps. For (pre)stalk and (pre)spore isolates reads are expressed as percentage of the summed reads of both isolates, and presented as white to green heatmaps. Names of species or kingdoms (for non-Amoebozoa) are colour-coded, as indicated at the top of the figure. Genes are alphabetically ordered and can be found at the following page numbers:

Gene name	**page**	**Gene name**	**page**
aa-al	1	grp-ip	12
am-bz	2	kc-mhc	13
ca-cm	3	mhk-myoB	14
cn-co	4	myoG-pad	15
cp-cy	5	pak-pkg	16
dga-DG1039	6	pl-pte	17
DG1040-DG1122	7	ptp-ri	18
DG2033-dn	8	ro-snf	19
do-fr p9 fu-gefB	10	snp-sv	20
gefL-grl	11	ta-tsg	21
		tsu-zi	22

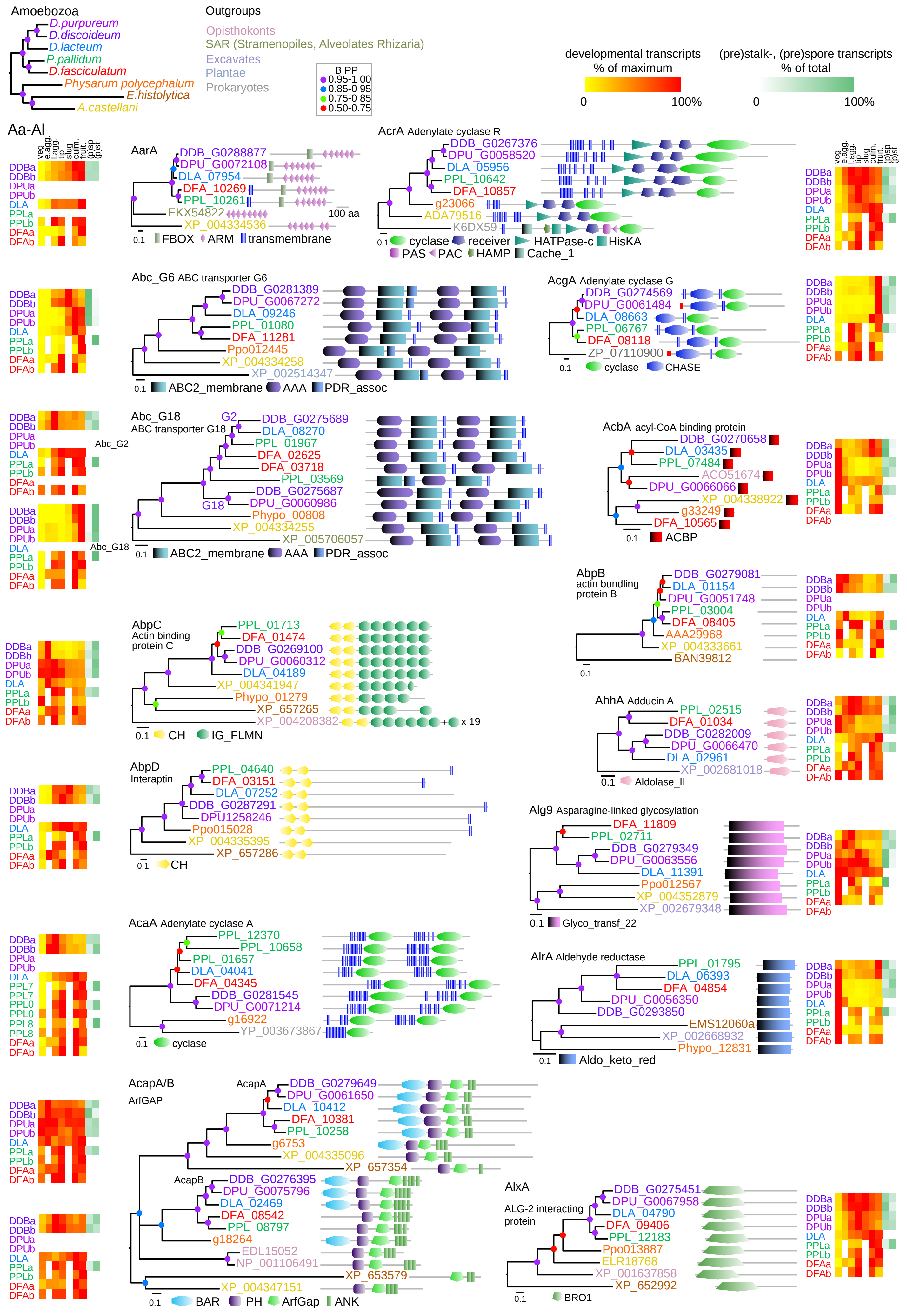
References

1 Schultz, J., Milpetz, F., Bork, P. & Ponting, C. P. SMART, a simple modular architecture research tool: identification of signaling domains. *Proc. Natl. Acad. Sci. USA* **95**, 5857-5864. (1998).

2 Bateman, A. *et al.* The Pfam protein families database. *Nucleic Acids Res.* **28**, 263-266. (2000).

3 Murzin, A. G., Brenner, S. E., Hubbard, T. & Chothia, C. SCOP: a structural classification of proteins database for the investigation of sequences and structures. *J Mol Biol* **247**, 536-540 (1995).

4 Parikh, A. *et al.* Conserved developmental transcriptomes in evolutionarily divergent species. *Genome Biol* **11**, R35, doi:gb-2010-11-3-r35 (2010).


Amoebozoa
D.purpureum
D.discoideum
D.lacteum
P.pallidum
D.fasciculatum
Physarum polycephalum
E.histolytica
A.castellani
Outgroups
Opisthokonts
SAR (Stramenopiles, Alveolates Rhizaria)
Excavates
Plantae
Prokaryotes
B PP
0.95-1 00
0.85-0 95
0.75-0 85
0.50-0.75
developmental transcripts
% of maximum
0
100%
(pre)stalk-, (pre)spore transcripts
% of total
0
100%
Aa-Al
veg
e.agg.
l.agg.
tip
slug
culm.
fruit.
(p)sp
(p)st
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
AarA
DDB_G0288877
DPU_G0072108
DLA_07954
DFA_10269
PPL_10261
EKX54822
XP_004334536
100 aa
0.1
FBOX
ARM
transmembrane
AcrA Adenylate cyclase R
DDB_G0267376
DPU_G0058520
DLA_05956
PPL_10642
DFA_10857
g23066
ADA79516
K6DX59
cyclase
receiver
HATPase-c
HisKA
PAS
PAC
HAMP
Cache_1
Abc_G6 ABC transporter G6
DDB_G0281389
DPU_G0067272
DLA_09246
PPL_01080
DFA_11281
Ppo012445
XP_004334258
XP_002514347
ABC2_membrane
AAA
PDR_assoc
AcgA Adenylate cyclase G
DDB_G0274569
DPU_G0061484
DLA_08663
PPL_06767
DFA_08118
ZP_07110900
cyclase
CHASE
Abc_G18
ABC transporter G18
G2
G18
DDB_G0275689
DLA_08270
PPL_01967
DFA_02625
DFA_03718
PPL_03569
DDB_G0275687
DPU_G0060986
Phypo_00808
XP_004334255
XP_005706057
Abc_G2
Abc_G18
AcbA acyl-CoA binding protein
DDB_G0270658
DLA_03435
PPL_07484
ACO51674
DPU_G0066066
XP_004338922
g33249
DFA_10565
ACBP
AbpB
actin bundling
protein B
DDB_G0279081
DLA_01154
DPU_G0051748
PPL_03004
DFA_08405
AAA29968
XP_004333661
BAN39812
AbpC
Actin binding
protein C
PPL_01713
DFA_01474
DDB_G0269100
DPU_G0060312
DLA_04189
XP_004341947
Phypo_01279
XP_657265
XP_004208382
+ x 19
CH
IG_FLMN
AhhA Adducin A
PPL_02515
DFA_01034
DDB_G0282009
DPU_G0066470
DLA_02961
XP_002681018
Aldolase_II
AbpD
Interaptin
PPL_04640
DFA_03151
DLA_07252
DDB_G0287291
DPU1258246
Ppo015028
XP_004335395
XP_657286
CH
Alg9 Asparagine-linked glycosylation
DFA_11809
PPL_02711
DDB_G0279349
DPU_G0063556
DLA_11391
Ppo012567
XP_004352879
XP_002679348
Glyco_transf_22
AcaA Adenylate cyclase A
PPL_12370
PPL_10658
PPL_01657
DLA_04041
DFA_04345
DDB_G0281545
DPU_G0071214
g16922
YP_003673867
cyclase
PPL7
PPL0
PPL8
AlrA Aldehyde reductase
PPL_01795
DLA_06393
DFA_04854
DPU_G0056350
DDB_G0293850
EMS12060a
XP_002668932
Phypo_12831
Aldo_keto_red
AcapA/B
ArfGAP
AcapA
DDB_G0279649
DPU_G0061650
DLA_10412
DFA_10381
PPL_10258
g6753
XP_004335096
XP_657354
AcapB
DDB_G0276395
DPU_G0075796
DLA_02469
DFA_08542
PPL_08797
g18264
EDL15052
NP_001106491
XP_653579
XP_004347151
BAR
PH
ArfGap
ANK
AlxA
ALG-2 interacting
protein
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DPU_G0067958
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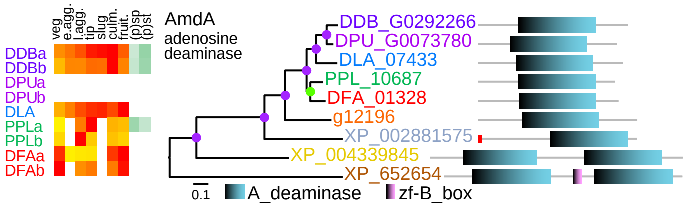
BRO1

AmdA-B


veg
e.agg.
l.agg.
tip
slug
culm.
fruit.
(p)sp
(p)st
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
AmdA
adenosine
deaminase
DDB_G0292266
DPU_G0073780
DLA_07433
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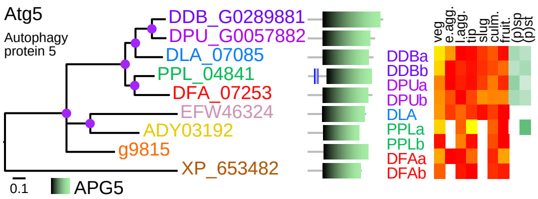
zf-B_box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protein 5
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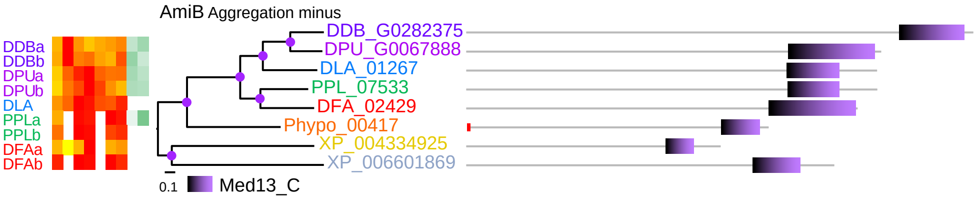
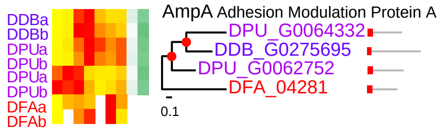
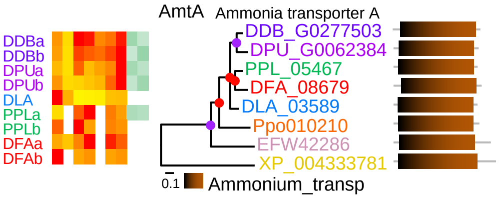
PPL_04841
DFA_07253
EFW46324
ADY03192
g9815
XP_653482
0.1
APG5
veg
e.agg.
l.agg.
tip
slug
culm.
fruit.
(p)sp
(p)st
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb


AmiB Aggregation minus
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
DDB_G0282375
DPU_G0067888
DLA_01267
PPL_07533
DFA_02429
Phypo_00417
XP_004334925
XP_006601869
0.1
Med13_C


DDBa
DDBb
DPUa
DPUb
DPUa
DPUb
DFAa
DFAb
AmpA Adhesion Modulation Protein A
DPU_G0064332
DDB_G0275695
DPU_G0062752
DFA_04281
0.1


AmtA Ammonia transporter A
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
DDB_G0277503
DPU_G0062384
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DFA_08679
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Ppo010210
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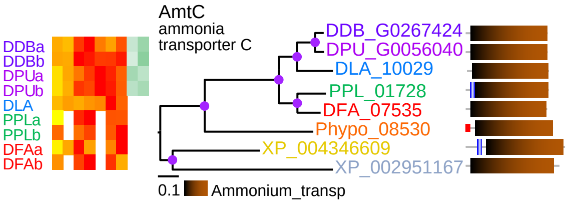
Ammonium_transp


AmtC
ammonia
transporter C
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
DDB_G0267424
DPU_G0056040
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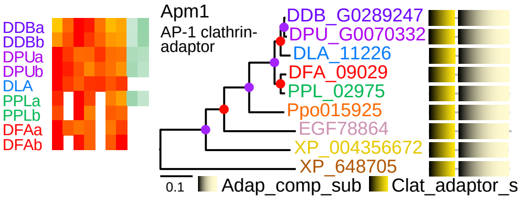
Ammonium_transp


Apm1
AP-1 clathrin-
adaptor
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
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DPU_G0070332
DLA_11226
DFA_09029
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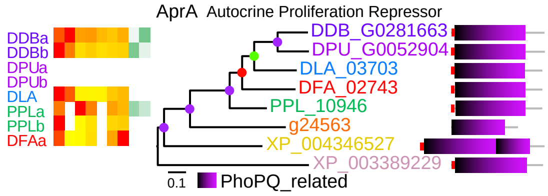
Adap_comp_sub
Clat_adaptor_s


AprA Autocrine Proliferation Repressor
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DDB_G0281663
DPU_G0052904
DLA_03703
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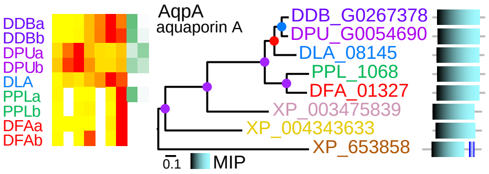
AqpA
aquaporin A
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
DDB_G0267378
DPU_G0054690
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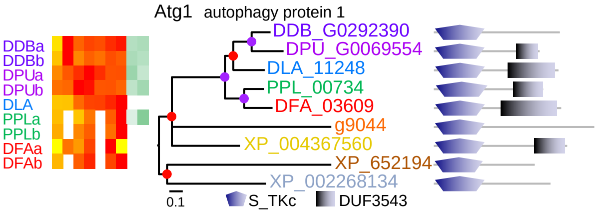
0.1
MIP


Atg1 autophagy protein 1
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
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DPU_G0069554
DLA_11248
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S_TKc
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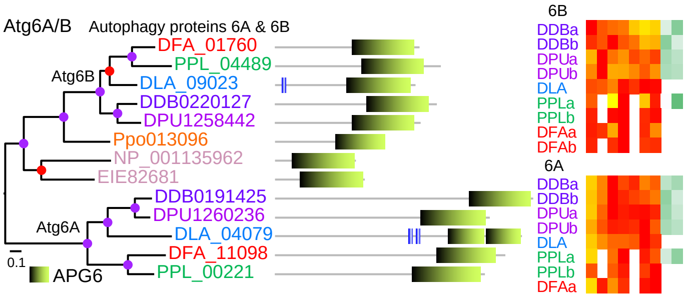
Atg6A/B Autophagy proteins 6A & 6B
Atg6B
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Ppo013096
NP_001135962
EIE82681
Atg6A
DDB0191425
DPU1260236
DLA_04079
DFA_11098
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0.1
APG6
6B
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
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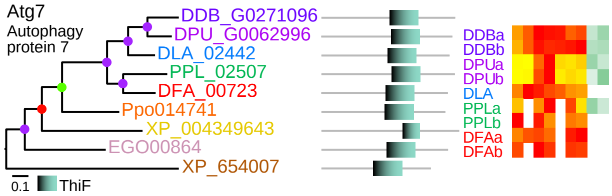
PPLa
PPLb
DFAa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Autophagy
protein 7
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DPU_G0062996
DLA_02442
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XP_004349643
EGO00864
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DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
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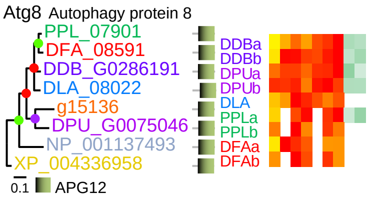
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PPL_07901
DFA_08591
DDB_G0286191
DLA_08022
g15136
DPU_G0075046
NP_001137493
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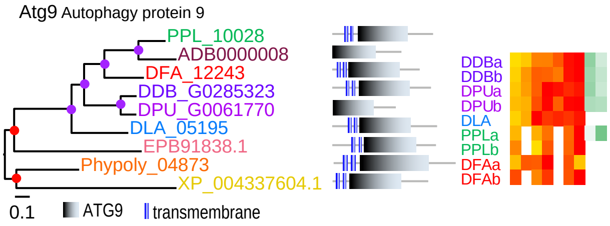
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DPU_G0061770
DLA_05195
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Phypoly_04873
XP_004337604.1
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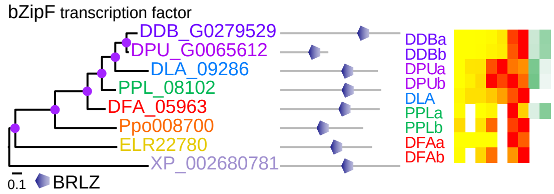
B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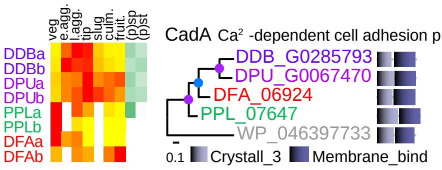
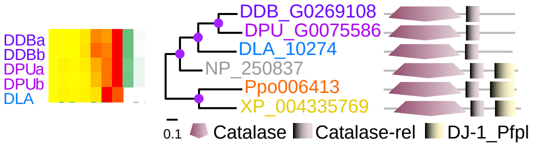
0.1
BRLZ
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb

Ca-Cm

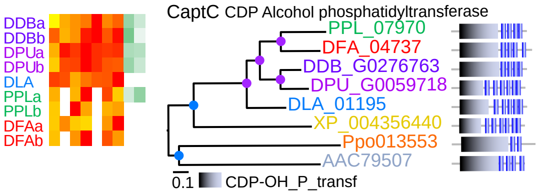
CadA Ca^{2} -dependent cell adhesion protein 1



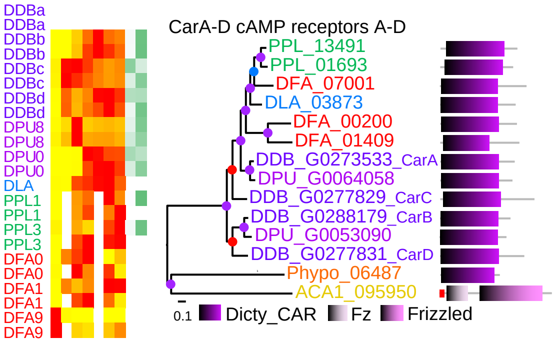
CatB Catalase B



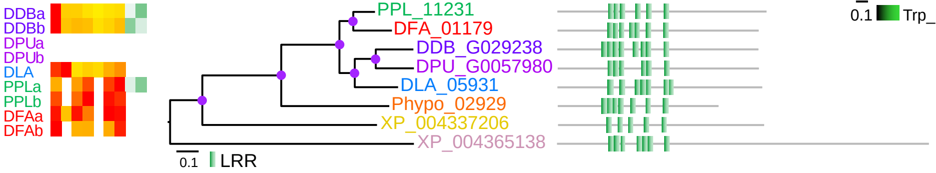
CaptC CDP Alcohol phosphatidyltransferase



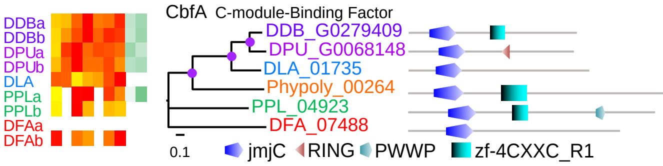
CarA-D cAMP receptors A-D



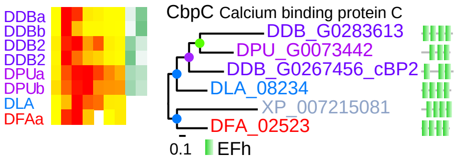
Carmil Capping protein, Arp2/3 and myosin I linker



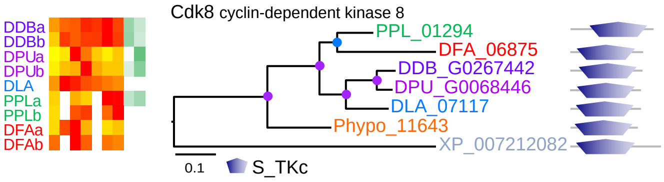
CbfA C-module-Binding Factor



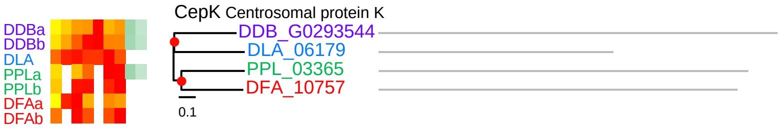
CbpC Calcium binding protein C



Cdk8 cyclin-dependent kinase 8



CepK Centrosomal protein K



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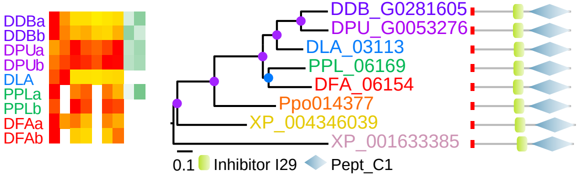

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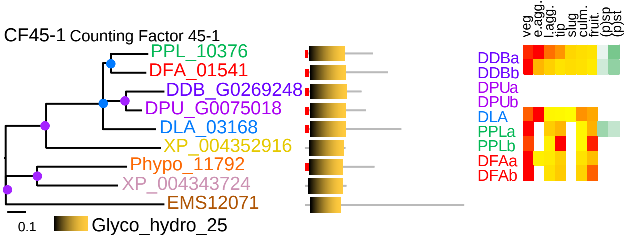
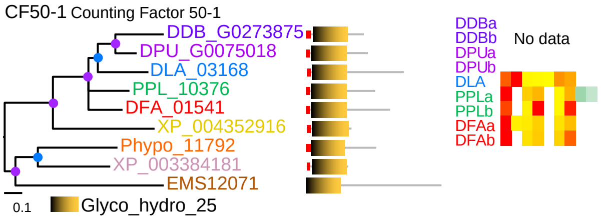
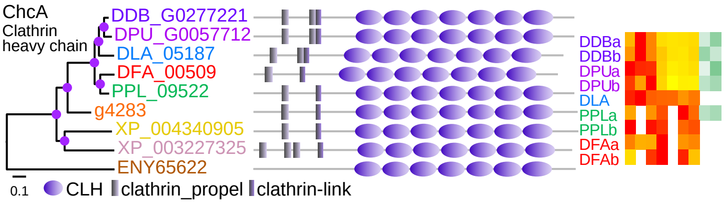


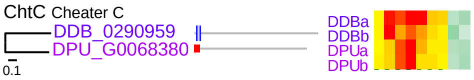
CF50-1 Counting Factor 50-1



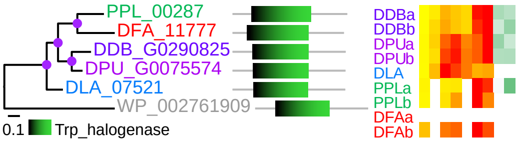
ChcA Clathrin heavy chain



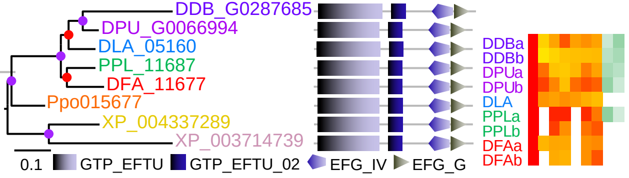
ChtC Cheater C



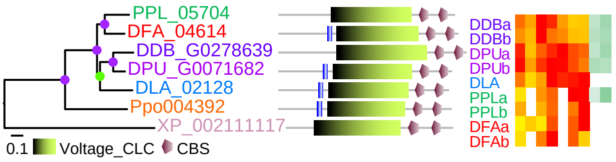
ChlA chlorinase A



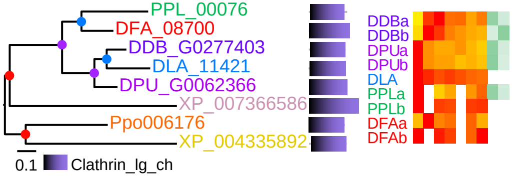
CinC Elongation Factor 2



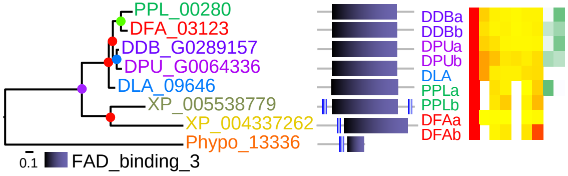
ClcD chloride channel C



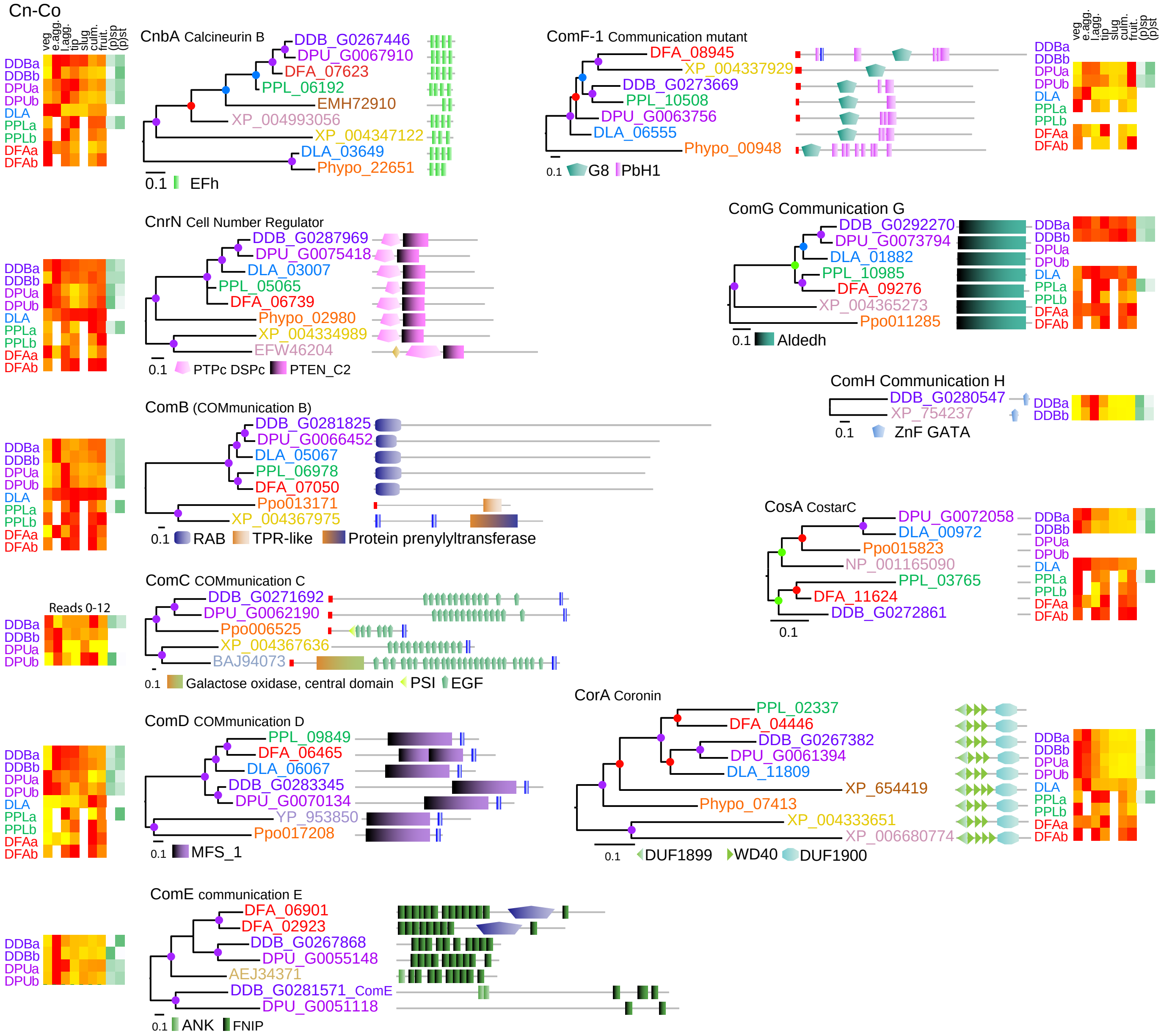
Clc clathrin light chain



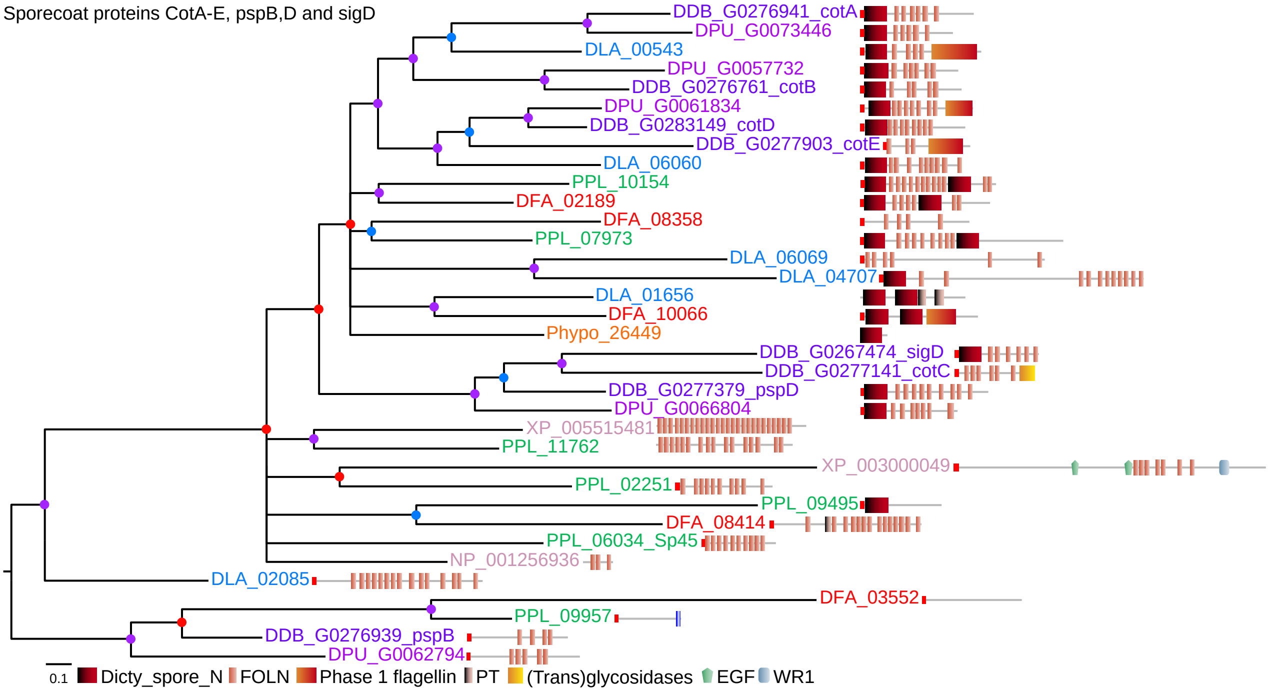
CmfB Conditioned medium factor receptor



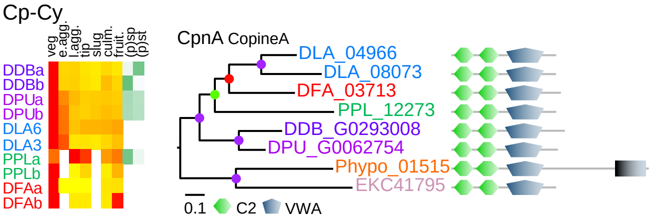
Cn-Co

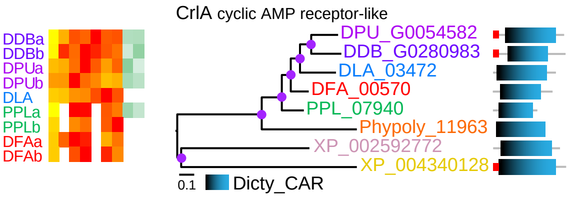


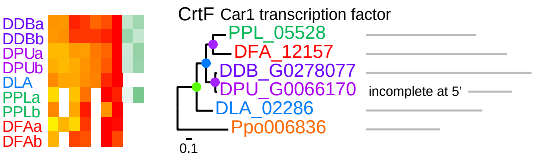
Sporecoat proteins CotA-E, pspB,D and sigD

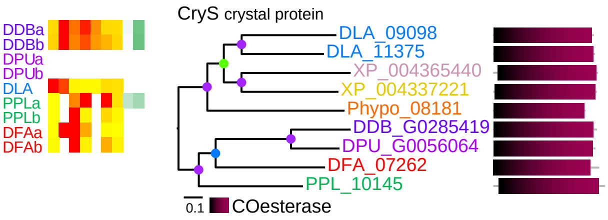


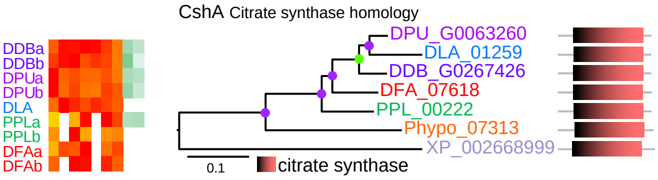
Cp-Cy

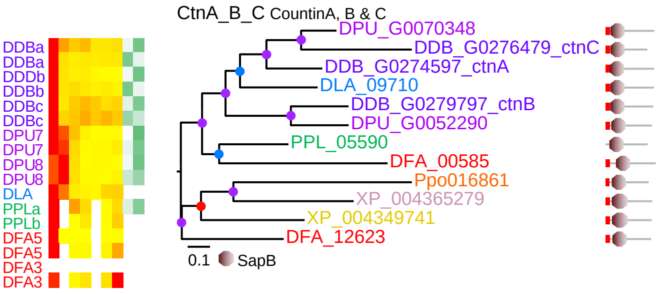

CpnA CopineA
veg
e.agg.
l.agg.
tip
slug
culm.
fruit.
(p)sp
(p)st
DDBa
DDBb
DPUa
DPUb
DLA6
DLA3
PPLa
PPLb
DFAa
DFAb
DLA_04966
DLA_08073
DFA_03713
PPL_12273
DDB_G0293008
DPU_G0062754
Phypo_01515
EKC41795
0.1
C2
VWA

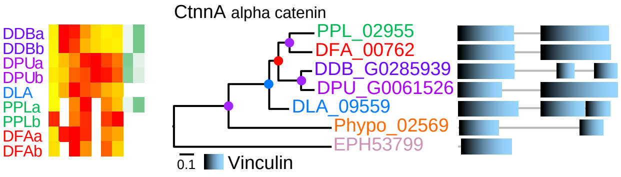

CrlA cyclic AMP receptor-like
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
DPU_G0054582
DDB_G0280983
DLA_03472
DFA_00570
PPL_07940
Phypoly_11963
XP_002592772
XP_004340128
0.1
Dicty_CAR

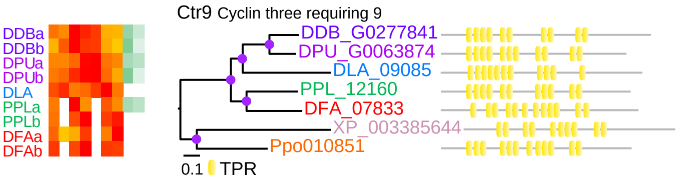

CrtF Car1 transcription factor
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
PPL_05528
DFA_12157
DDB_G0278077
DPU_G0066170
incomplete at 5'
DLA_02286
Ppo006836
0.1

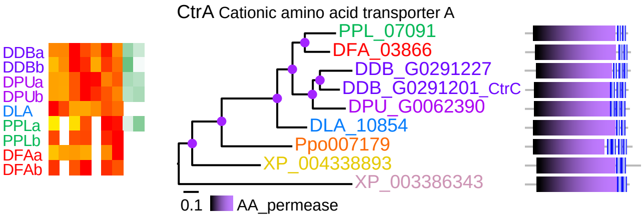

CryS crystal protein
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
DLA_09098
DLA_11375
XP_004365440
XP_004337221
Phypo_08181
DDB_G0285419
DPU_G0056064
DFA_07262
PPL_10145
0.1
COesterase

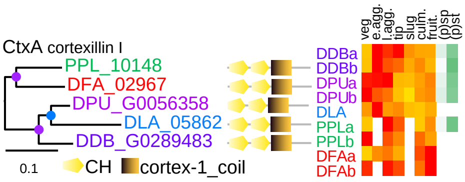

CshA Citrate synthase homology
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
DPU_G0063260
DLA_01259
DDB_G0267426
DFA_07618
PPL_00222
Phypo_07313
XP_002668999
0.1
citrate synthase

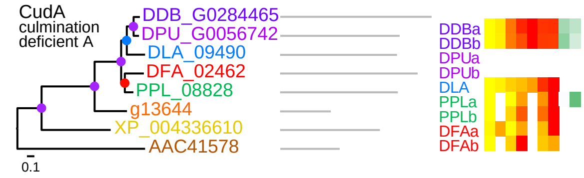

CtnA_B_C CountinA, B & C
DDBa
DDBa
DDDb
DDBb
DDBc
DDBc
DPU7
DPU7
DPU8
DPU8
DLA
PPLa
PPLb
DFA5
DFA5
DFA3
DFA3
DPU_G0070348
DDB_G0276479_ctnC
DDB_G0274597_ctnA
DLA_09710
DDB_G0279797_ctnB
DPU_G0052290
PPL_05590
DFA_00585
Ppo016861
XP_004365279
XP_004349741
DFA_12623
0.1
SapB


CtnnA alpha catenin
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
PPL_02955
DFA_00762
DDB_G0285939
DPU_G0061526
DLA_09559
Phypo_02569
EPH53799
0.1
Vinculin

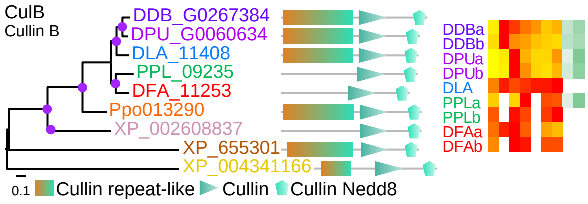

Ctr9 Cyclin three requiring 9
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
DDB_G0277841
DPU_G0063874
DLA_09085
PPL_12160
DFA_07833
XP_003385644
Ppo010851
0.1
TPR

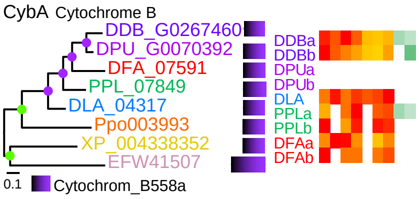

CtrA Cationic amino acid transporter A
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
PPL_07091
DFA_03866
DDB_G0291227
DDB_G0291201_CtrC
DPU_G0062390
DLA_10854
Ppo007179
XP_004338893
XP_003386343
0.1
AA_permease


CtxA cortexillin I
veg
e.agg.
l.agg.
tip
slug
culm.
fruit.
(p)sp
(p)st
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
PPL_10148
DFA_02967
DPU_G0056358
DLA_05862
DDB_G0289483
0.1
CH
cortex-1_coil


CudA culmination deficient A
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
DDB_G0284465
DPU_G0056742
DLA_09490
DFA_02462
PPL_08828
g13644
XP_004336610
AAC41578
0.1

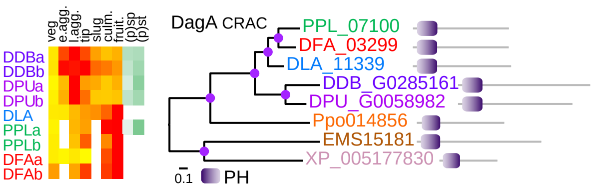

CulA cullin A
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
DDB_G0291972
DPU_G0052096
DLA_02694
PPL_02733
DFA_09462
Phypo_02629
ESA00289
XP_004368147
EMS13271
0.1
Cullin
Cullin Nedd8


CulB Cullin B
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
DDB_G0267384
DPU_G0060634
DLA_11408
PPL_09235
DFA_11253
Ppo013290
XP_002608837
XP_655301
XP_004341166
0.1
Cullin repeat-like
Cullin
Cullin Nedd8

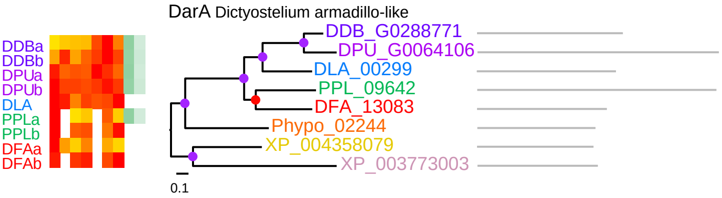

CybA Cytochrome B
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
DDB_G0267460
DPU_G0070392
DFA_07591
PPL_07849
DLA_04317
Ppo003993
XP_004338352
EFW41507
0.1
Cytochrom_B558a

Da-DG1039

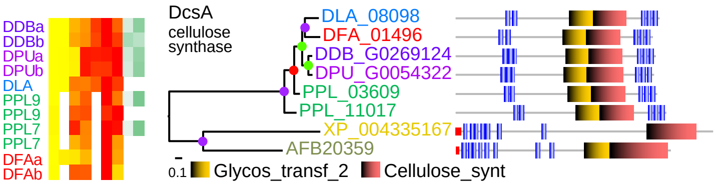
DagA CRAC



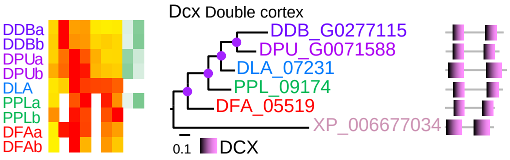
DarA Dictyostelium armadillo-like



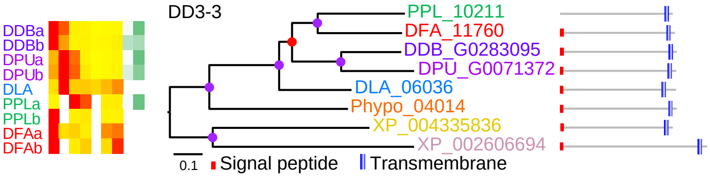
DcsA cellulose synthase



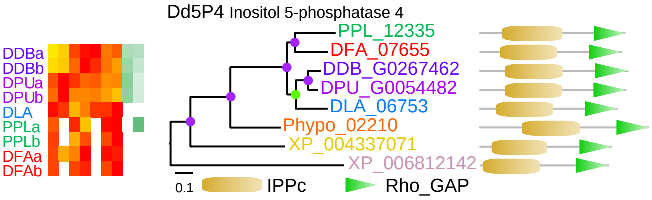
Dcx Double cortex



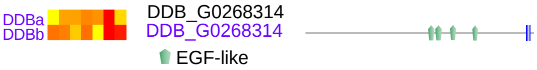
DD3-3



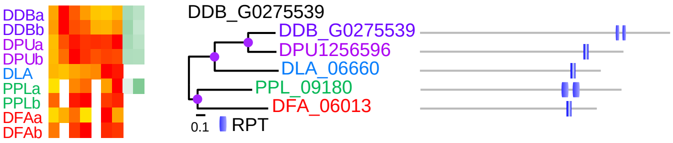
Dd5P4 Inositol 5-phosphatase 4



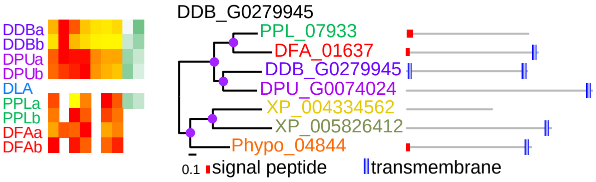
DDB_G0268314



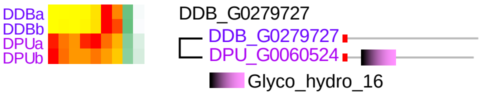
DDB_G0275539



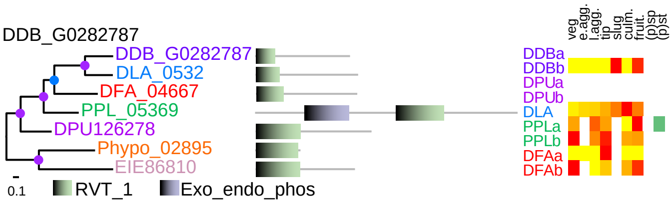
DDB_G0279945



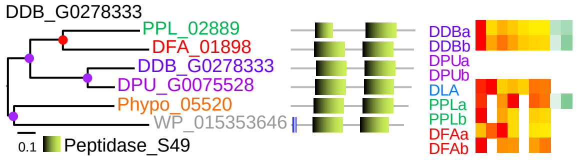
DDB_G0279727



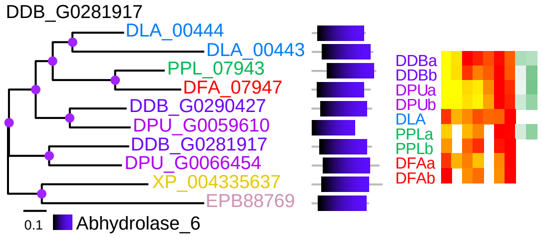
DDB_G0282787



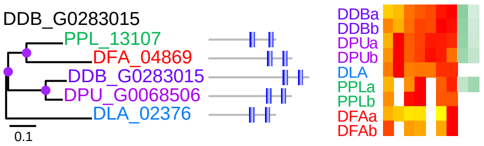
DDB_G0278333



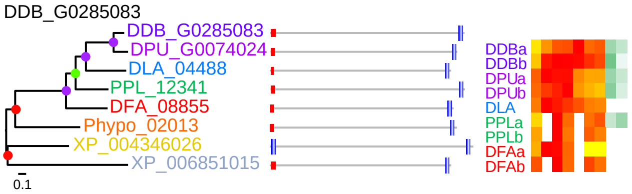
DDB_G0281917



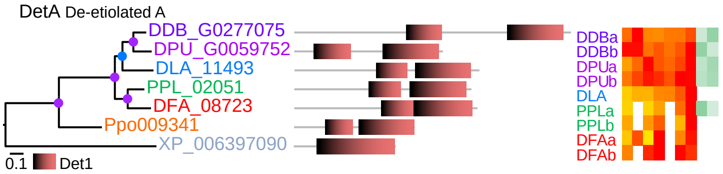
DDB_G0283015



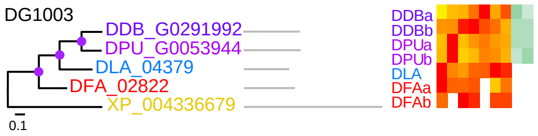
DDB_G0285083



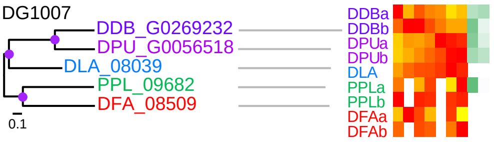
DetA De-etiolated A



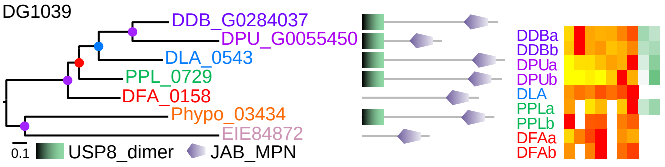
DG1003



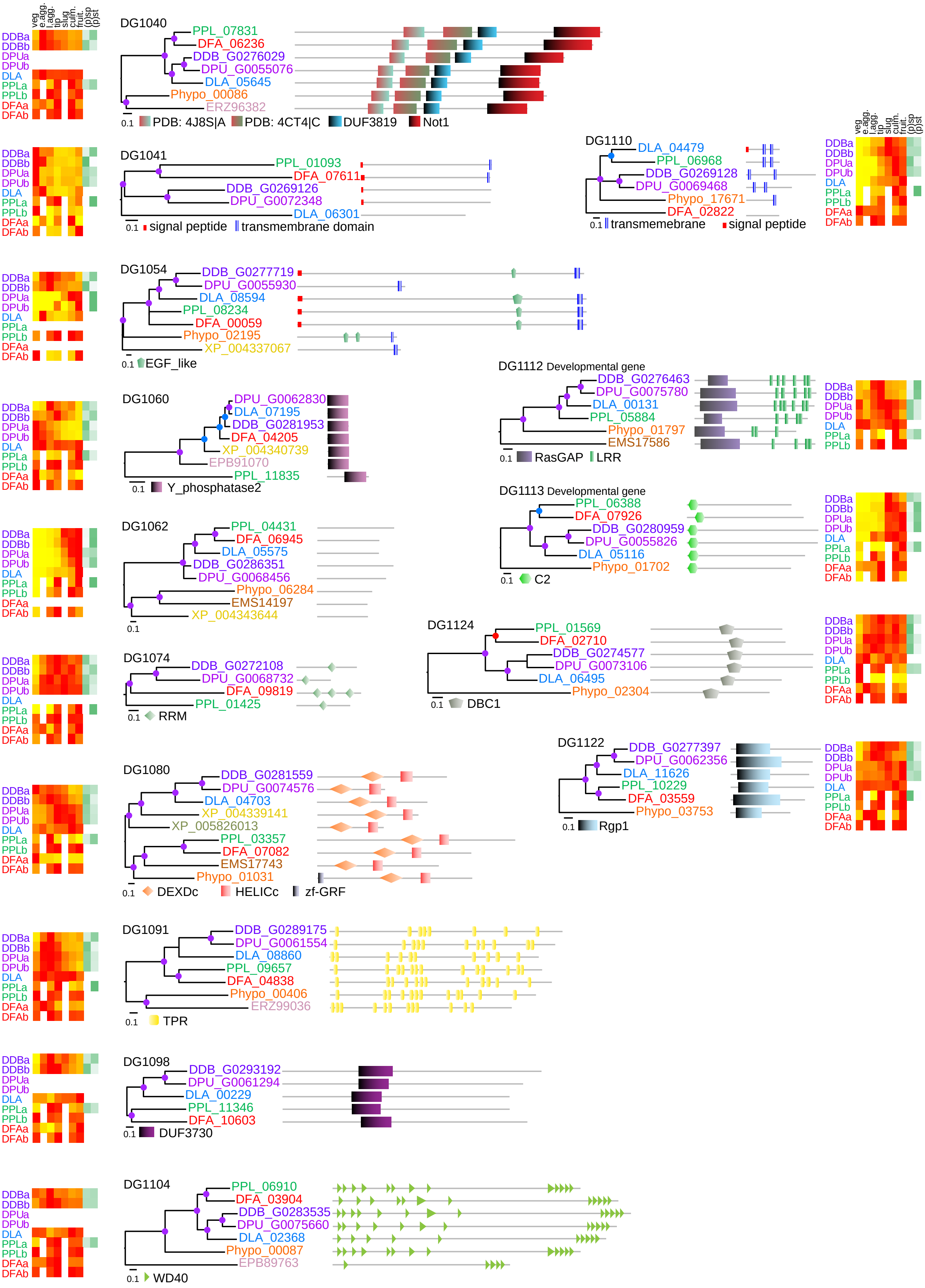
DG1007



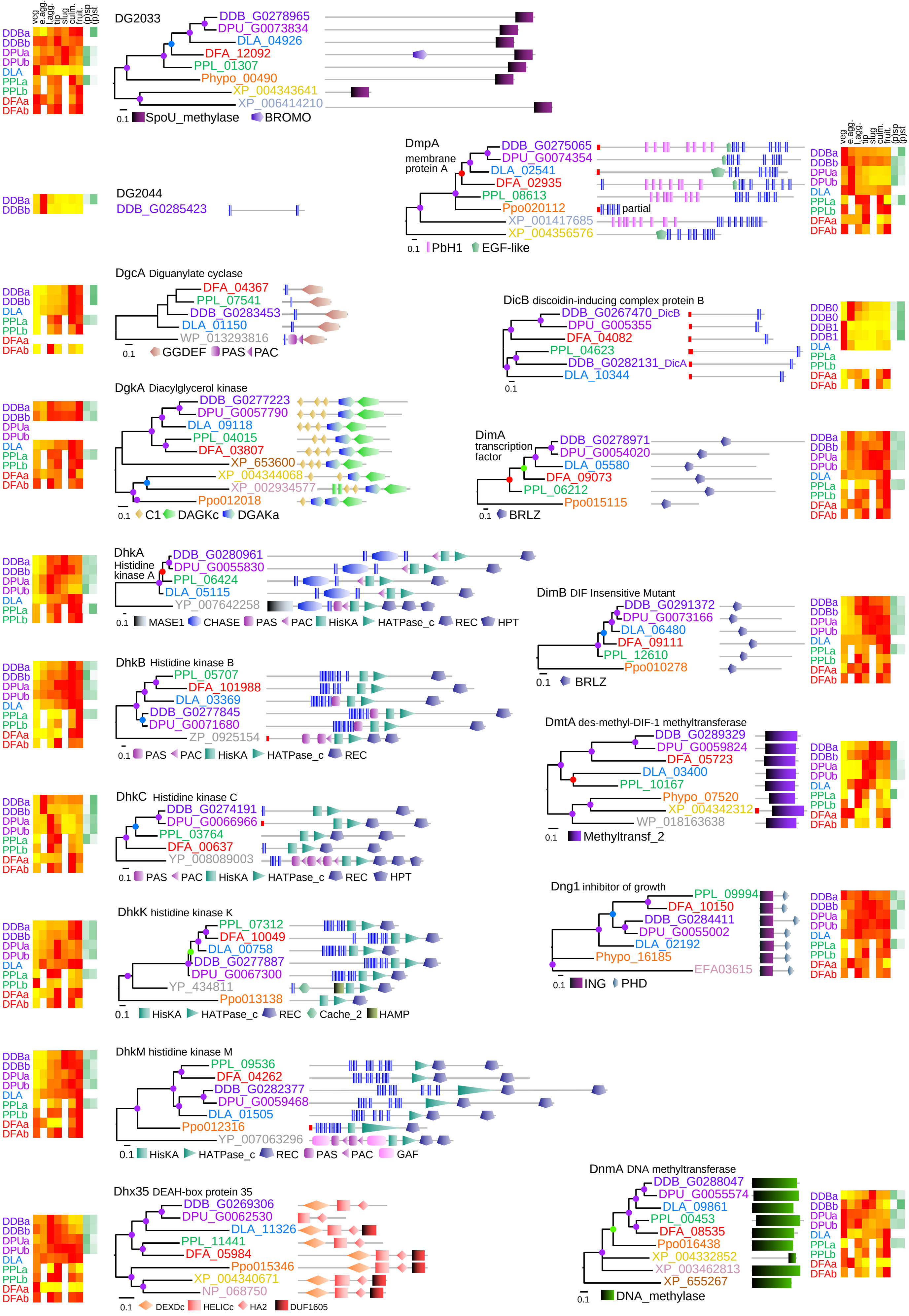
DG1039



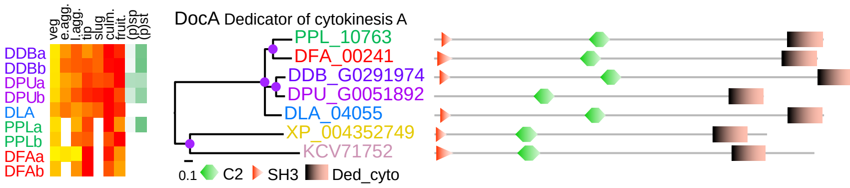
DG1040-DG1122



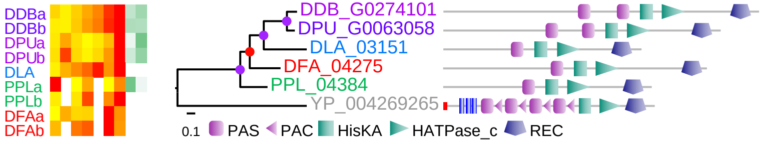
DG2033-Dn


veg
e.agg.
l.agg.
tip
slug
culm.
fruit.
(p)sp
(p)st
DG2033
DDB_G0278965
DPU_G0073834
DLA_04926
DFA_12092
PPL_01307
Phypo_00490
XP_004343641
XP_006414210
0.1
SpoU_methylase
BROMO
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
DG2044
DDB_G0285423
DmpA
membrane protein A
DDB_G0275065
DPU_G0074354
DLA_02541
DFA_02935
PPL_08613
Ppo020112
partial
XP_001417685
XP_004356576
PbH1
EGF-like
DgcA Diguanylate cyclase
DFA_04367
PPL_07541
DDB_G0283453
DLA_01150
WP_013293816
GGDEF
PAS
PAC
DicB discoidin-inducing complex protein B
DDB_G0267470_DicB
DPU_G005355
DFA_04082
PPL_04623
DDB_G0282131_DicA
DLA_10344
DDB0
DDB1
DgkA Diacylglycerol kinase
DDB_G0277223
DPU_G0057790
DLA_09118
PPL_04015
DFA_03807
XP_653600
XP_004344068
XP_002934577
Ppo012018
C1
DAGKc
DGAKa
DimA
transcription factor
DDB_G0278971
DPU_G0054020
DLA_05580
DFA_09073
PPL_06212
Ppo015115
BRLZ
DhkA
Histidine kinase A
DDB_G0280961
DPU_G0055830
PPL_06424
DLA_05115
YP_007642258
MASE1
CHASE
HisKA
HATPase_c
REC
HPT
DimB DIF Insensitive Mutant
DDB_G0291372
DPU_G0073166
DLA_06480
DFA_09111
PPL_12610
Ppo010278
DhkB Histidine kinase B
PPL_05707
DFA_101988
DLA_03369
DDB_G0277845
DPU_G0071680
ZP_0925154
DmtA des-methyl-DIF-1 methyltransferase
DDB_G0289329
DPU_G0059824
DFA_05723
DLA_03400
PPL_10167
Phypo_07520
XP_004342312
WP_018163638
Methyltransf_2
DhkC Histidine kinase C
DDB_G0274191
DPU_G0066966
PPL_03764
DFA_00637
YP_008089003
Dng1 inhibitor of growth
PPL_09994
DFA_10150
DDB_G0284411
DPU_G0055002
DLA_02192
Phypo_16185
EFA03615
ING
PHD
DhkK histidine kinase K
PPL_07312
DFA_10049
DLA_00758
DDB_G0277887
DPU_G0067300
YP_434811
Ppo013138
Cache_2
HAMP
DhkM histidine kinase M
PPL_09536
DFA_04262
DDB_G0282377
DPU_G0059468
DLA_01505
Ppo012316
YP_007063296
GAF
DnmA DNA methyltransferase
DDB_G0288047
DPU_G0055574
DLA_09861
PPL_00453
DFA_08535
Ppo016438
XP_004332852
XP_003462813
XP_655267
DNA_methylase
Dhx35 DEAH-box protein 35
DDB_G0269306
DPU_G0062530
DLA_11326
PPL_11441
DFA_05984
Ppo015346
XP_004340671
NP_068750
DEXDc
HELICc
HA2
DUF1605

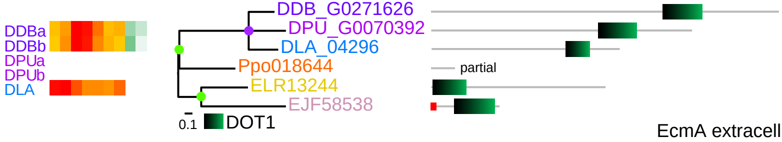
DocA Dedicator of cytokinesis A



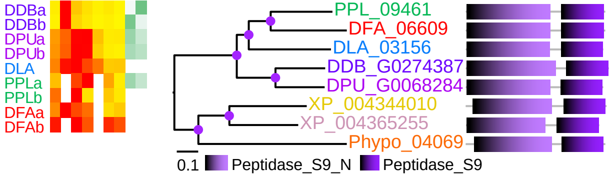
DokA osmosensing histidine kinase A



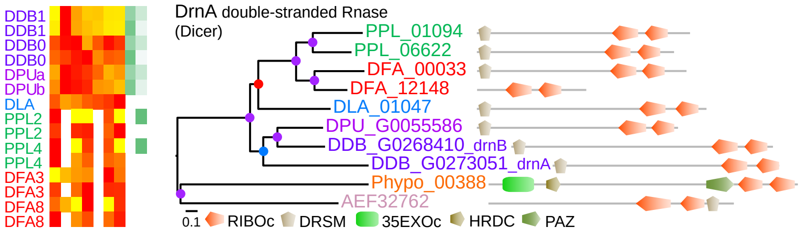
DotA histone methyltransferase



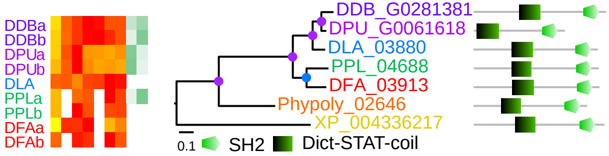
Dpo Prolyl oligopeptidase



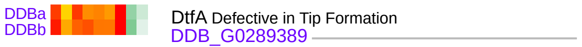
DrnA double-stranded Rnase (Dicer)



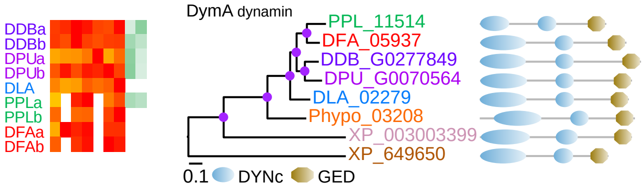
DstA signal transducer and activator of transcription A



DtfA Defective in Tip Formation

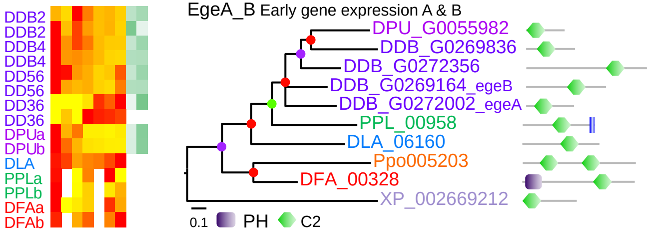


DymA dynamin

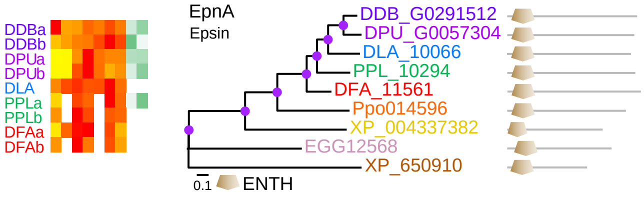


E

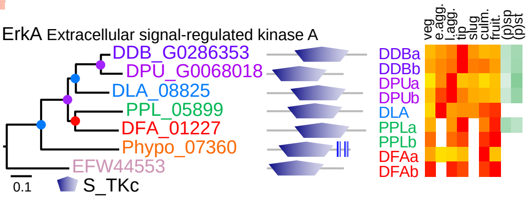
EgeA_B Early gene expression A & B



EpnA Epsin

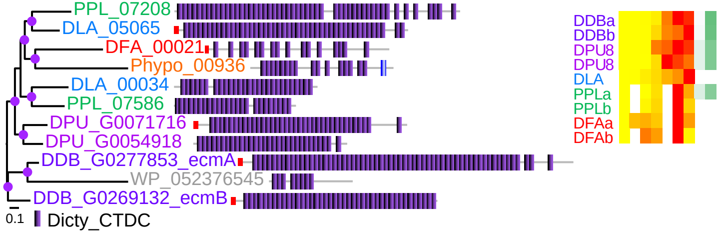


ErkA Extracellular signal-regulated kinase A



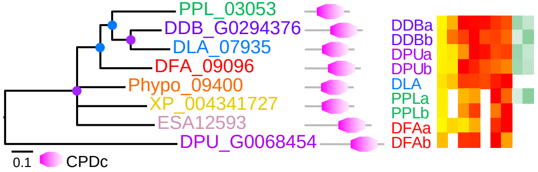
ErkB Extracellular signal-regulated kinase B

EcmA extracellular matrix protein A

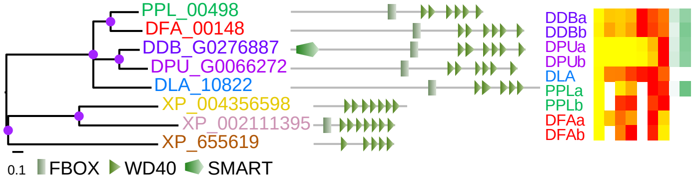


F

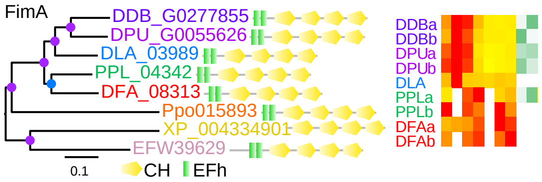
FcpA putative CTD phosphatase



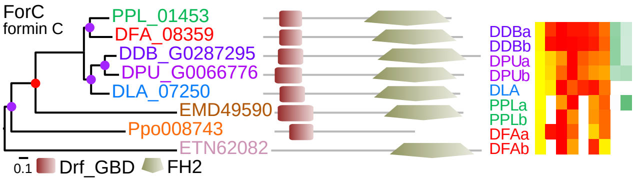
FbxA E3 ubiquitin ligase component



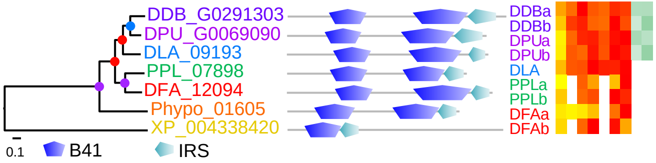
FimA



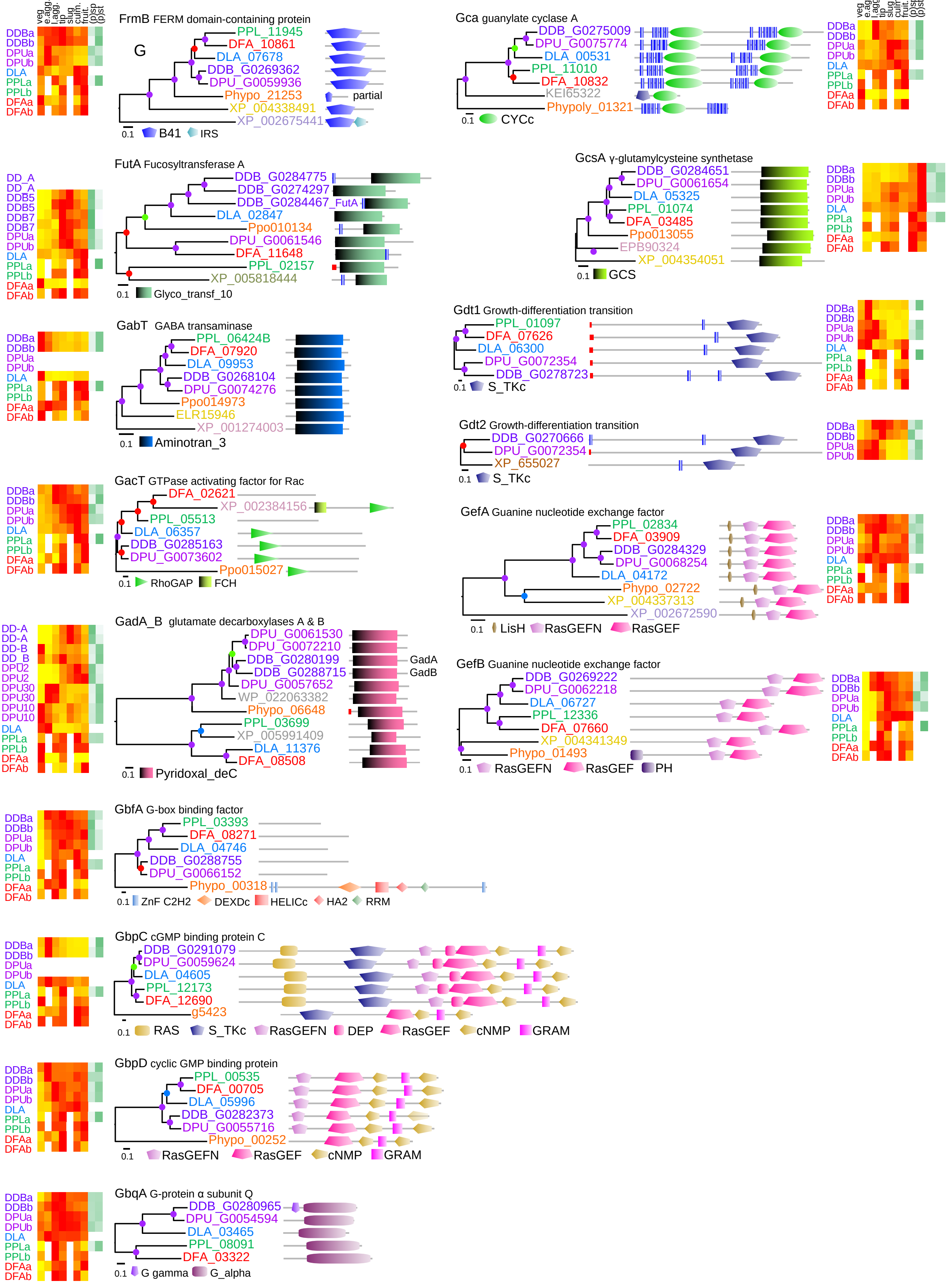
ForC formin C

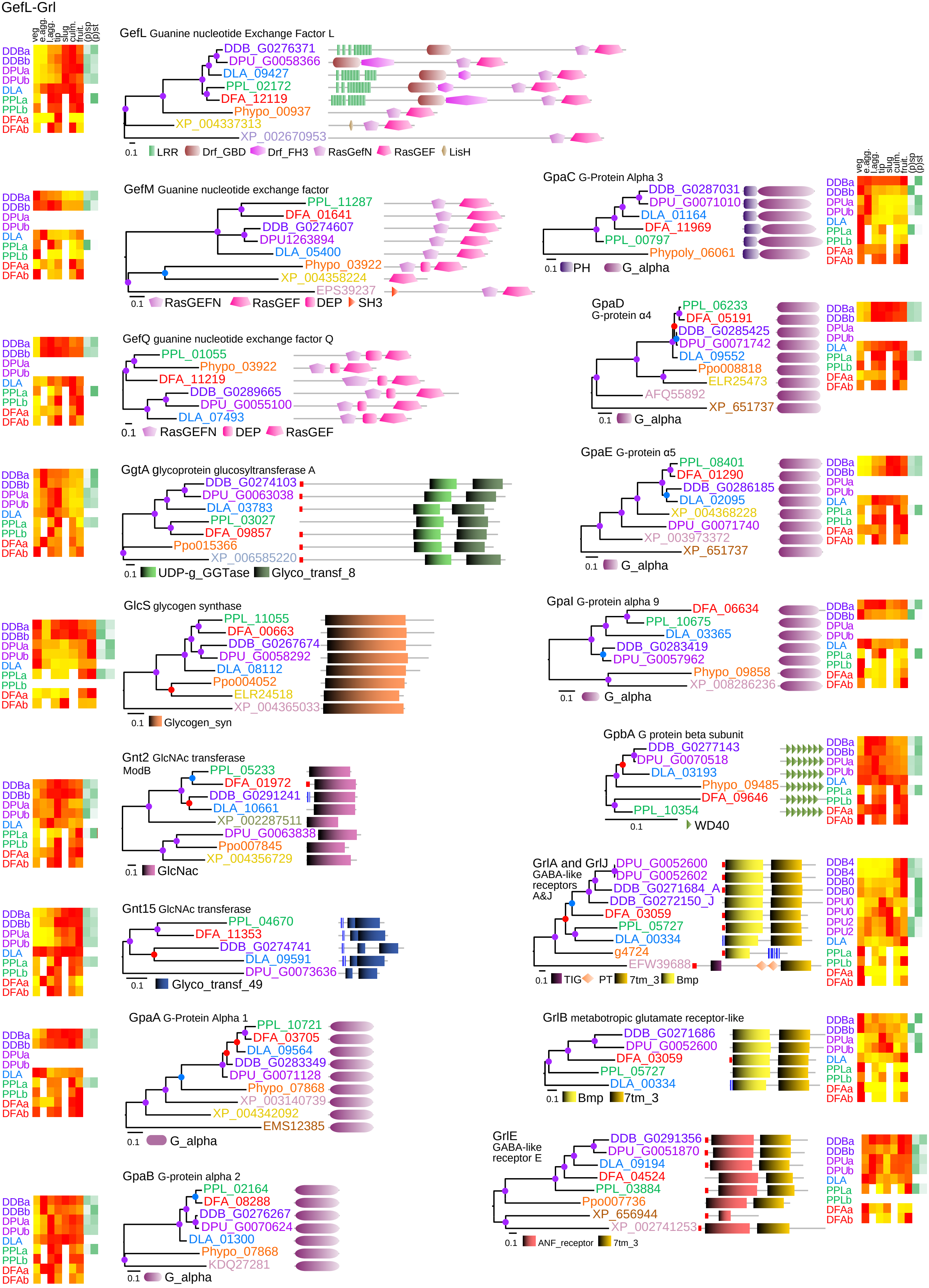


FrmA 4.1 ezrin, radixin, moesin domain



Fu-GefB


veg
e.agg.
l.agg.
tip
slug
culm.
fruit.
(p)sp
(p)st
FrmB FERM domain-containing protein
G
PPL_11945
DFA_10861
DLA_07678
DDB_G0269362
DPU_G0059936
Phypo_21253
partial
XP_004338491
XP_002675441
0.1
B41
IRS
Gca guanylate cyclase A
DDB_G0275009
DPU_G0075774
DLA_00531
PPL_11010
DFA_10832
KEI65322
Phypoly_01321
CYCc
FutA Fucosyltransferase A
DDB_G0284775
DDB_G0274297
DDB_G0284467_FutA
DLA_02847
Ppo010134
DPU_G0061546
DFA_11648
PPL_02157
XP_005818444
Glyco_transf_10
GcsA γ-glutamylcysteine synthetase
DDB_G0284651
DPU_G0061654
DLA_05325
PPL_01074
DFA_03485
Ppo013055
EPB90324
XP_004354051
GCS
GabT GABA transaminase
PPL_06424B
DFA_07920
DLA_09953
DDB_G0268104
DPU_G0074276
Ppo014973
ELR15946
XP_001274003
Aminotran_3
Gdt1 Growth-differentiation transition
PPL_01097
DFA_07626
DLA_06300
DPU_G0072354
DDB_G0278723
S_TKc
Gdt2 Growth-differentiation transition
DDB_G0270666
DPU_G0072354
XP_655027
S_TKc
GacT GTPase activating factor for Rac
DFA_02621
XP_002384156
PPL_05513
DLA_06357
DDB_G0285163
DPU_G0073602
Ppo015027
RhoGAP
FCH
GefA Guanine nucleotide exchange factor
PPL_02834
DFA_03909
DDB_G0284329
DPU_G0068254
DLA_04172
Phypo_02722
XP_004337313
XP_002672590
LisH
RasGEFN
RasGEF
GadA_B glutamate decarboxylases A & B
DPU_G0061530
DPU_G0072210
DDB_G0280199
DDB_G0288715
DPU_G0057652
WP_022063382
Phypo_06648
PPL_03699
XP_005991409
DLA_11376
DFA_08508
GadA
GadB
Pyridoxal_deC
GefB Guanine nucleotide exchange factor
DDB_G0269222
DPU_G0062218
DLA_06727
PPL_12336
DFA_07660
XP_004341349
Phypo_01493
RasGEFN
RasGEF
PH
GbfA G-box binding factor
PPL_03393
DFA_08271
DLA_04746
DDB_G0288755
DPU_G0066152
Phypo_00318
ZnF C2H2
DEXDc
HELICc
HA2
RRM
GbpC cGMP binding protein C
DDB_G0291079
DPU_G0059624
DLA_04605
PPL_12173
DFA_12690
g5423
RAS
S_TKc
RasGEFN
DEP
RasGEF
cNMP
GRAM
GbpD cyclic GMP binding protein
PPL_00535
DFA_00705
DLA_05996
DDB_G0282373
DPU_G0055716
Phypo_00252
RasGEFN
RasGEF
cNMP
GRAM
GbqA G-protein α subunit Q
DDB_G0280965
DPU_G0054594
DLA_03465
PPL_08091
DFA_03322
G gamma
G_alpha
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
DD_A
DDB5
DDB7
DD-A
DD-B
DD_B
DPU2
DPU30
DPU10


GefL-Grl
veg
e.agg.
l.agg.
tip
slug
culm.
fruit.
(p)sp
(p)st
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
GefL Guanine nucleotide Exchange Factor L
DDB_G0276371
DPU_G0058366
DLA_09427
PPL_02172
DFA_12119
Phypo_00937
XP_004337313
XP_002670953
0.1
LRR
Drf_GBD
Drf_FH3
RasGefN
RasGEF
LisH
GefM Guanine nucleotide exchange factor
PPL_11287
DFA_01641
DDB_G0274607
DPU1263894
DLA_05400
Phypo_03922
XP_004358224
EPS39237
0.1
RasGEFN
RasGEF
DEP
SH3
GefQ guanine nucleotide exchange factor Q
PPL_01055
Phypo_03922
DFA_11219
DDB_G0289665
DPU_G0055100
DLA_07493
0.1
RasGEFN
DEP
RasGEF
GgtA glycoprotein glucosyltransferase A
DDB_G0274103
DPU_G0063038
DLA_03783
PPL_03027
DFA_09857
Ppo015366
XP_006585220
0.1
UDP-g_GGTase
Glyco_transf_8
GlcS glycogen synthase
PPL_11055
DFA_00663
DDB_G0267674
DPU_G0058292
DLA_08112
Ppo004052
ELR24518
XP_004365033
0.1
Glycogen_syn
Gnt2 GlcNAc transferase
ModB
PPL_05233
DFA_01972
DDB_G0291241
DLA_10661
XP_002287511
DPU_G0063838
Ppo007845
XP_004356729
0.1
GlcNac
Gnt15 GlcNAc transferase
PPL_04670
DFA_11353
DDB_G0274741
DLA_09591
DPU_G0073636
0.1
Glyco_transf_49
GpaA G-Protein Alpha 1
PPL_10721
DFA_03705
DLA_09564
DDB_G0283349
DPU_G0071128
Phypo_07868
XP_003140739
XP_004342092
EMS12385
0.1
G_alpha
GpaB G-protein alpha 2
PPL_02164
DFA_08288
DDB_G0276267
DPU_G0070624
DLA_01300
Phypo_07868
KDQ27281
0.1
G_alpha
GpaC G-Protein Alpha 3
DDB_G0287031
DPU_G0071010
DLA_01164
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Phypoly_06061
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PH
G_alpha
GpaD
G-protein α4
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DLA_09552
Ppo008818
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AFQ55892
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GpaE G-protein α5
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DDB_G0286185
DLA_02095
XP_004368228
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XP_003973372
XP_651737
0.1
G_alpha
GpaI G-protein alpha 9
DFA_06634
PPL_10675
DLA_03365
DDB_G0283419
DPU_G0057962
Phypo_09858
XP_008286236
0.1
G_alpha
GpbA G protein beta subunit
DDB_G0277143
DPU_G0070518
DLA_03193
Phypo_09485
DFA_09646
PPL_10354
0.1
WD40
GrlA and GrlJ
GABA-like
receptors
A&J
DPU_G0052600
DPU_G0052602
DDB_G0271684_A
DDB_G0272150_J
DFA_03059
PPL_05727
DLA_00334
g4724
EFW39688
0.1
TIG
PT
7tm_3
Bmp
DDB4
DDB4
DDB0
DDB0
DPU0
DPU0
DPU2
DPU2
DLA
PPLa
PPLb
DFAa
DFAb
GrlB metabotropic glutamate receptor-like
DDB_G0271686
DPU_G0052600
DFA_03059
PPL_05727
DLA_00334
0.1
Bmp
7tm_3
GrlE
GABA-like
receptor E
DDB_G0291356
DPU_G0051870
DLA_09194
DFA_04524
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XP_656944
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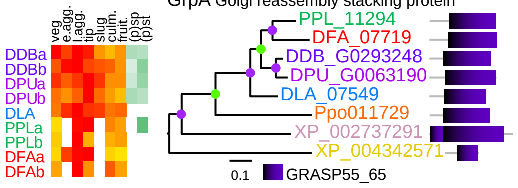
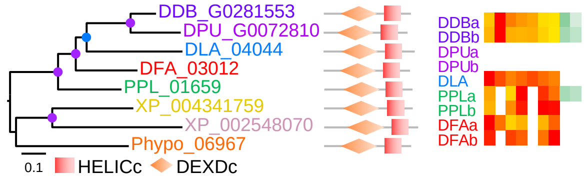
0.1
ANF_receptor
7tm_3

Grp-Ip

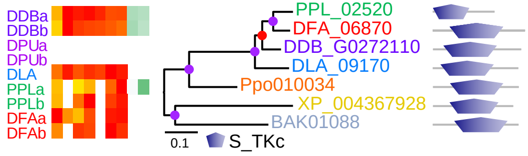
GrpA Golgi reassembly stacking protein



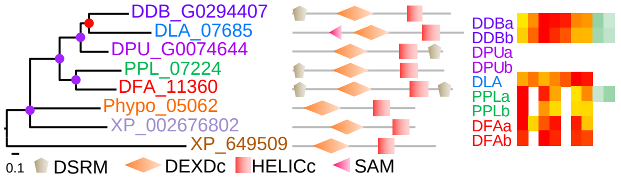
HelC DEAD-box RNA helicase



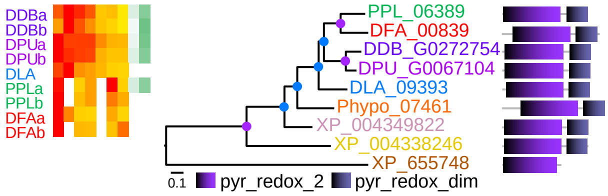
GsKA glycogen synthase kinase A



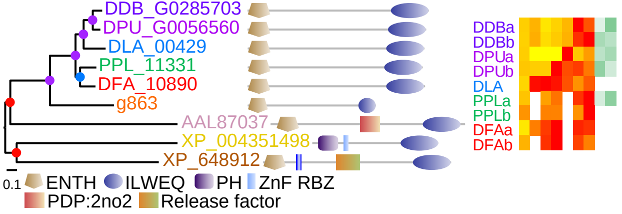
HelF RNA helicase F



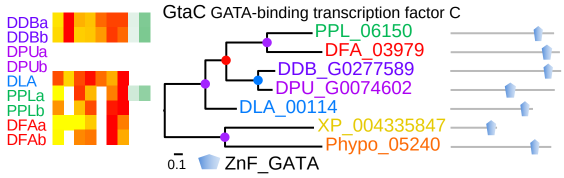
Gsr Gluthathione-SH Reductase



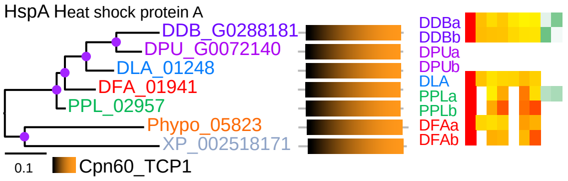
HipA clathrin-associated protein Hip1r



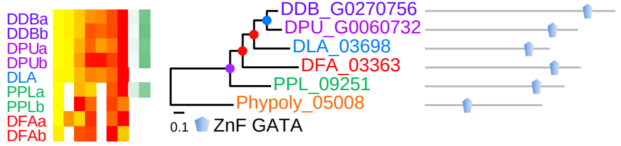
GtaC GATA-binding transcription factor C



HspA Heat shock protein A

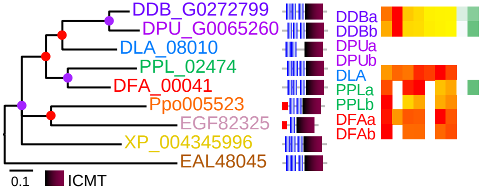


GtaG Gata G

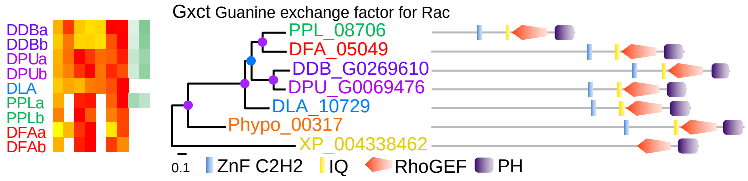


I

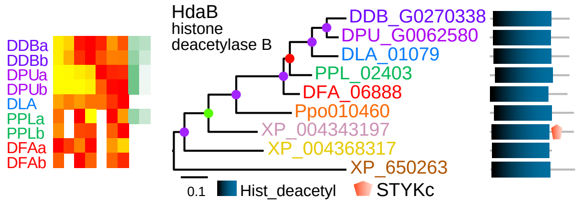
IcmA isoprenylcysteine methyltransferase



Gxct Guanine exchange factor for Rac

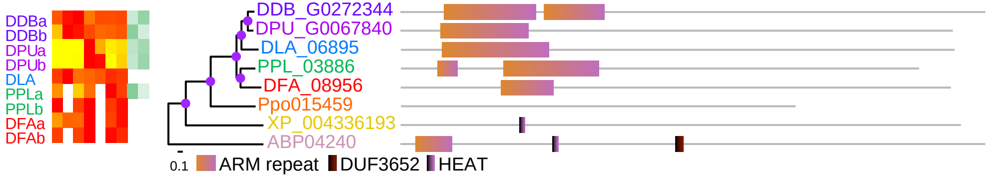


HdaB
histone
deacetylase B

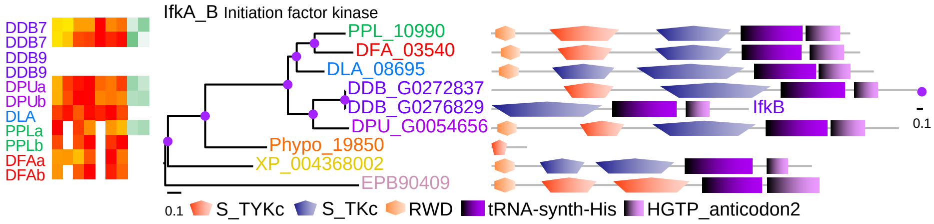


Ino1 inositol-3-phosphate synthase

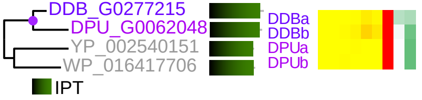
Htt huntingtin



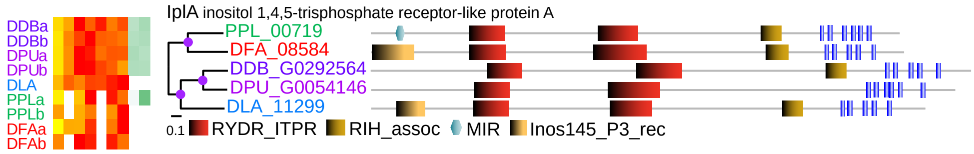
IfkA_B Initiation factor kinase



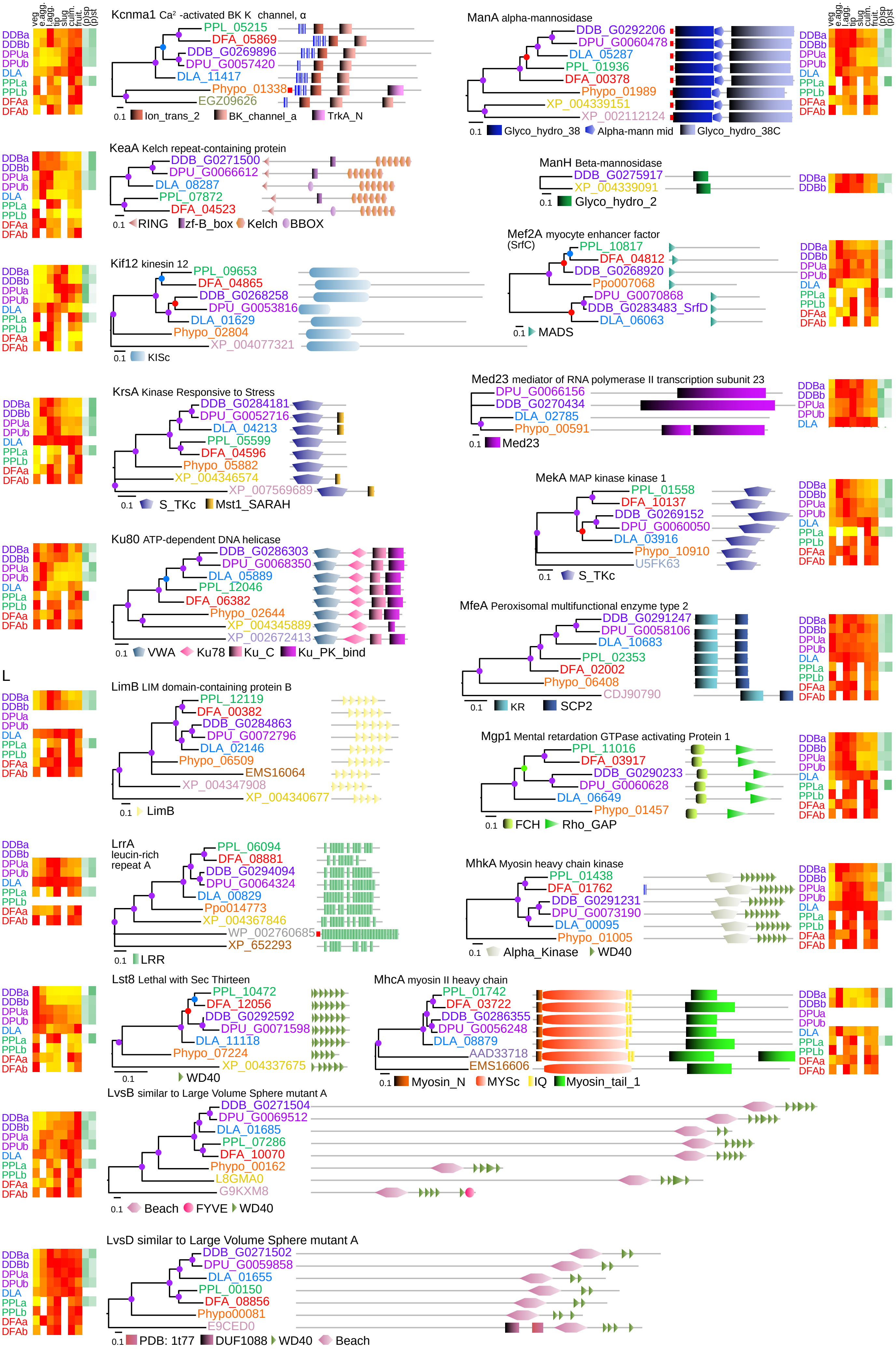
iptA isopentenyltransferase



IplA inositol 1,4,5-trisphosphate receptor-like protein A



Kc-MhkA


veg
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l.agg.
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slug
culm.
fruit.
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(p)st
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
Kcnma1 Ca2 -activated BK K channel, α
PPL_05215
DFA_05869
DDB_G0269896
DPU_G0057420
DLA_11417
Phypo_01338
EGZ09626
0.1
Ion_trans_2
BK_channel_a
TrkA_N
KeaA Kelch repeat-containing protein
DDB_G0271500
DPU_G0066612
DLA_08287
PPL_07872
DFA_04523
0.1
RING
zf-B_box
Kelch
BBOX
Kif12 kinesin 12
PPL_09653
DFA_04865
DDB_G0268258
DPU_G0053816
DLA_01629
Phypo_02804
XP_004077321
0.1
KISc
KrsA Kinase Responsive to Stress
DDB_G0284181
DPU_G0052716
DLA_04213
PPL_05599
DFA_04596
Phypo_05882
XP_004346574
XP_007569689
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S_TKc
Mst1_SARAH
Ku80 ATP-dependent DNA helicase
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DPU_G0068350
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DFA_06382
Phypo_02644
XP_004345889
XP_002672413
0.1
VWA
Ku78
Ku_C
Ku_PK_bind
L
LimB LIM domain-containing protein B
PPL_12119
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leucin-rich
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LRR
Lst8 Lethal with Sec Thirteen
PPL_10472
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DPU_G0071598
DLA_11118
Phypo_07224
XP_004337675
0.1
WD40
LvsB similar to Large Volume Sphere mutant A
DDB_G0271504
DPU_G0069512
DLA_01685
PPL_07286
DFA_10070
Phypo_00162
L8GMA0
G9KXM8
0.1
Beach
FYVE
WD40
LvsD similar to Large Volume Sphere mutant A
DDB_G0271502
DPU_G0059858
DLA_01655
PPL_00150
DFA_08856
Phypo00081
E9CED0
0.1
PDB: 1t77
DUF1088
WD40
Beach
M
ManA alpha-mannosidase
DDB_G0292206
DPU_G0060478
DLA_05287
PPL_01936
DFA_00378
Phypo_01989
XP_004339151
XP_002112124
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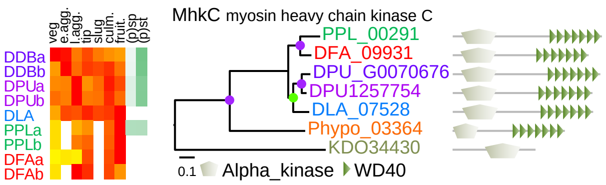
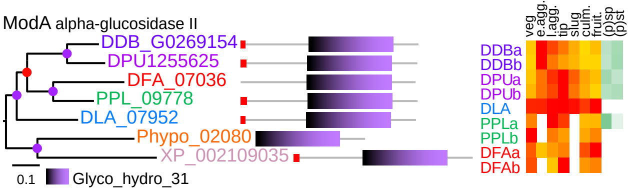
Glyco_hydro_38
Alpha-mann mid
Glyco_hydro_38C
ManH Beta-mannosidase
DDB_G0275917
XP_004339091
0.1
Glyco_hydro_2
Mef2A myocyte enhancer factor
(SrfC)
PPL_10817
DFA_04812
DDB_G0268920
Ppo007068
DPU_G0070868
DDB_G0283483_SrfD
DLA_06063
0.1
MADS
Med23 mediator of RNA polymerase II transcription subunit 23
DPU_G0066156
DDB_G0270434
DLA_02785
Phypo_00591
0.1
Med23
MekA MAP kinase kinase 1
PPL_01558
DFA_10137
DDB_G0269152
DPU_G0060050
DLA_03916
Phypo_10910
U5FK63
0.1
S_TKc
MfeA Peroxisomal multifunctional enzyme type 2
DDB_G0291247
DPU_G0058106
DLA_10683
PPL_02353
DFA_02002
Phypo_06408
CDJ90790
0.1
KR
SCP2
Mgp1 Mental retardation GTPase activating Protein 1
PPL_11016
DFA_03917
DDB_G0290233
DPU_G0060628
DLA_06649
Phypo_01457
0.1
FCH
Rho_GAP
MhkA Myosin heavy chain kinase
PPL_01438
DFA_01762
DDB_G0291231
DPU_G0073190
DLA_00095
Phypo_01005
0.1
Alpha_Kinase
WD40
MhcA myosin II heavy chain
PPL_01742
DFA_03722
DDB_G0286355
DPU_G0056248
DLA_08879
AAD33718
EMS16606
0.1
Myosin_N
MYSc
IQ
Myosin_tail_1

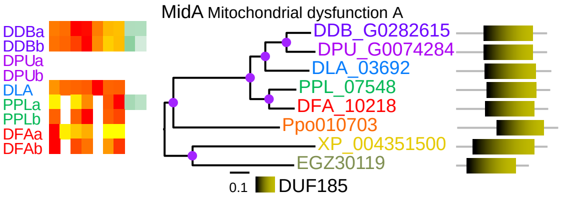
MhkC myosin heavy chain kinase C



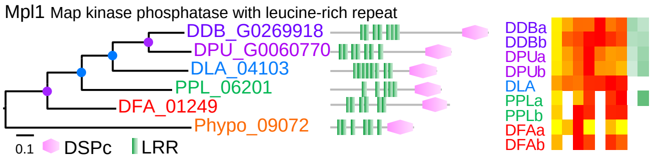
ModA alpha-glucosidase II



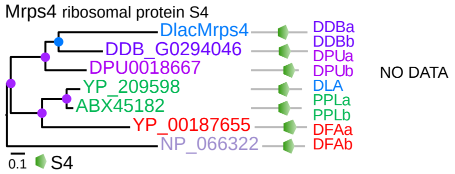
MidA Mitochondrial dysfunction A



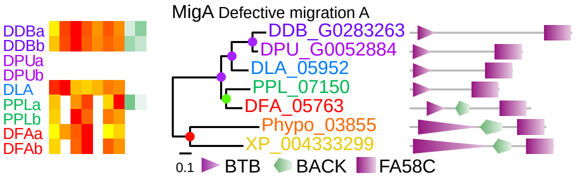
Mpl1 Map kinase phosphatase with leucine-rich repeat



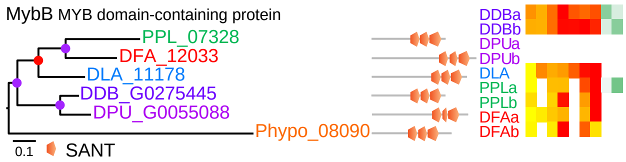
Mrps4 ribosomal protein S4



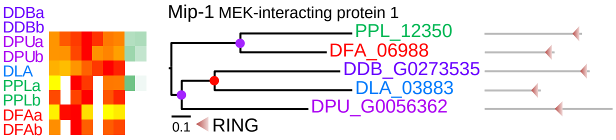
MigA Defective migration A



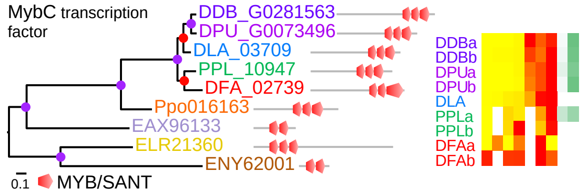
MybB MYB domain-containing protein



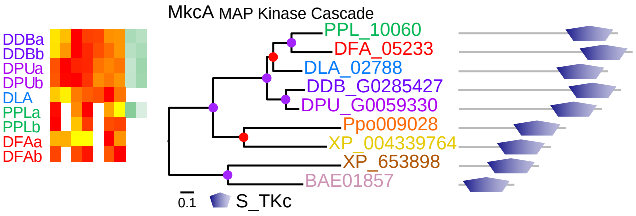
Mip-1 MEK-interacting protein 1



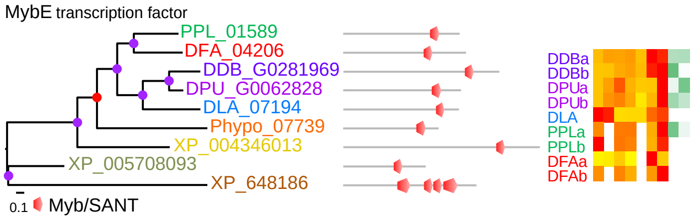
MybC transcription factor



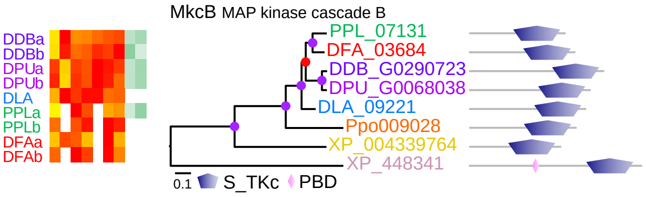
MkcA MAP Kinase Cascade



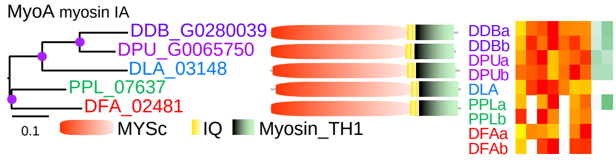
MybE transcription factor



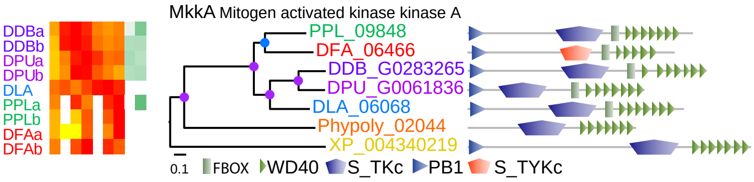
MkcB MAP kinase cascade B



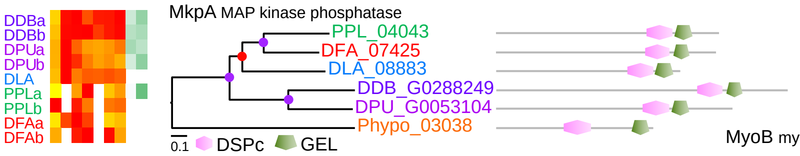
MyoA myosin IA



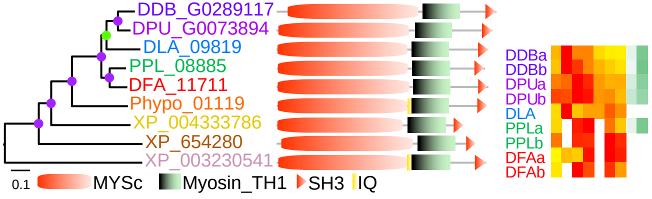
MkkA Mitogen activated kinase kinase A



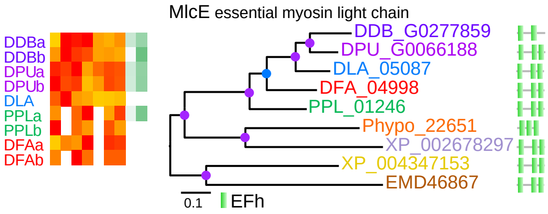
MkpA MAP kinase phosphatase



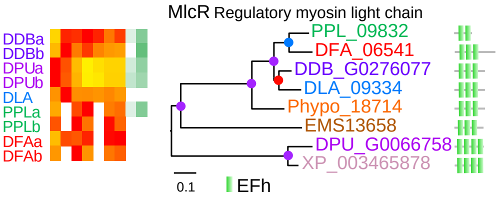
MyoB myosin IB



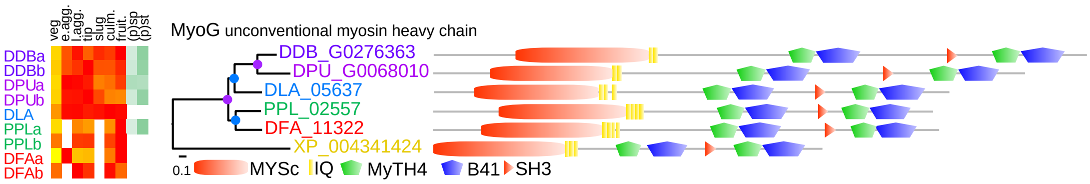
MlcE essential myosin light chain

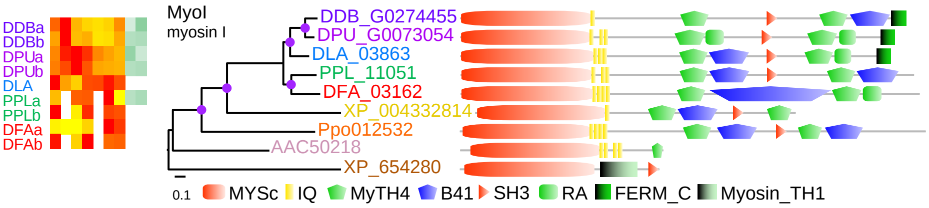


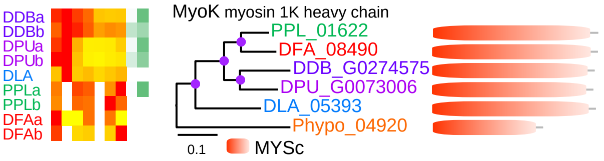
MlcR Regulatory myosin light chain

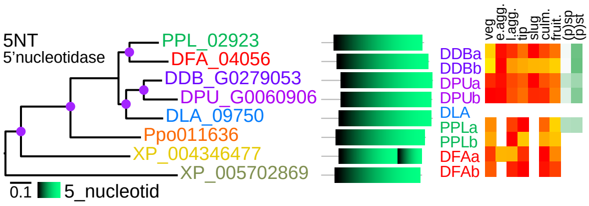


MyoG-Pad

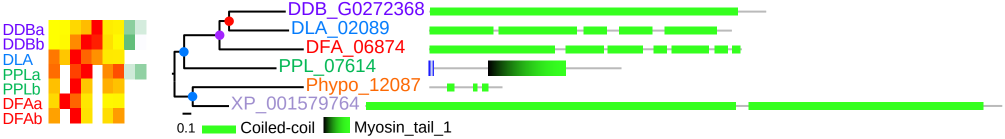

veg
e.agg.
l.agg.
tip
slug
culm.
fruit.
(p)sp
(p)st
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
MyoG unconventional myosin heavy chain
DDB_G0276363
DPU_G0068010
DLA_05637
PPL_02557
DFA_11322
XP_004341424
0.1
MYSc
IQ
MyTH4
B41
SH3

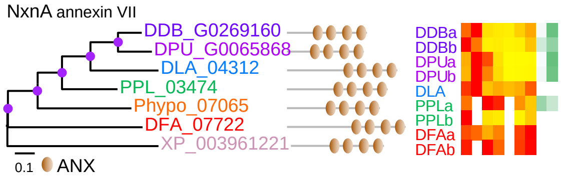

DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
MyoI
myosin I
DDB_G0274455
DPU_G0073054
DLA_03863
PPL_11051
DFA_03162
XP_004332814
Ppo012532
AAC50218
XP_654280
0.1
MYSc
IQ
MyTH4
B41
SH3
RA
FERM_C
Myosin_TH1

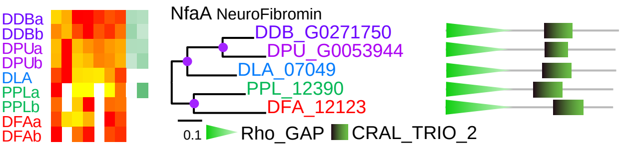

DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
MyoK myosin 1K heavy chain
PPL_01622
DFA_08490
DDB_G0274575
DPU_G0073006
DLA_05393
Phypo_04920
0.1
MYSc

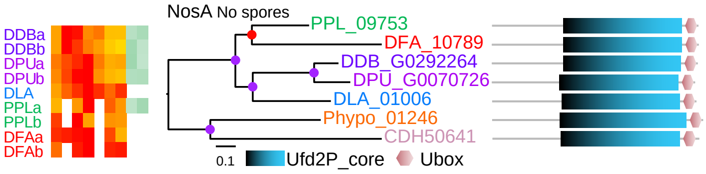

5NT
5'nucleotidase
PPL_02923
DFA_04056
DDB_G0279053
DPU_G0060906
DLA_09750
Ppo011636
XP_004346477
XP_005702869
0.1
5_nucleotid
veg
e.agg.
l.agg.
tip
slug
culm.
fruit.
(p)sp
(p)st
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb

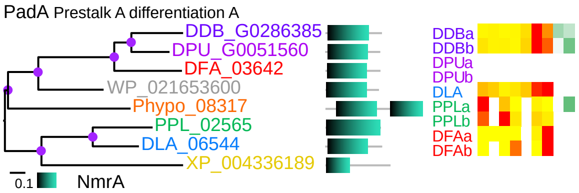
N

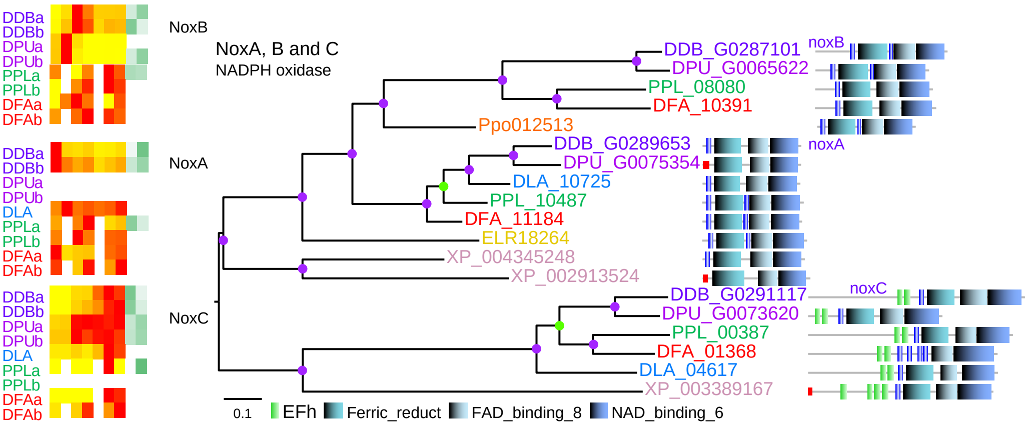

Ndm Negative director of macropinocytosis
DDBa
DDBb
DLA
PPLa
PPLb
DFAa
DFAb
DDB_G0272368
DLA_02089
DFA_06874
PPL_07614
Phypo_12087
XP_001579764
0.1
Coiled-coil
Myosin_tail_1

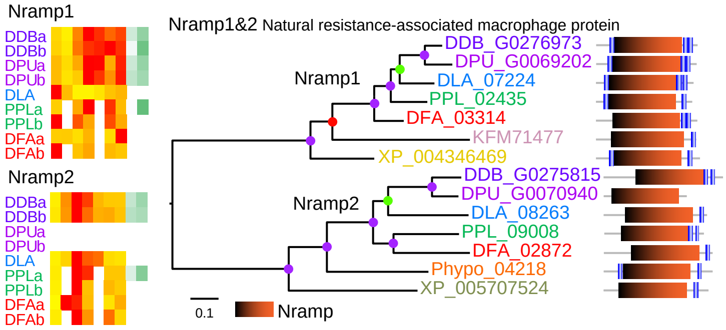

NxnA annexin VII
DDB_G0269160
DPU_G0065868
DLA_04312
PPL_03474
Phypo_07065
DFA_07722
XP_003961221
0.1
ANX
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb


DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
NfaA NeuroFibromin
DDB_G0271750
DPU_G0053944
DLA_07049
PPL_12390
DFA_12123
0.1
Rho_GAP
CRAL_TRIO_2


NosA No spores
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
PPL_09753
DFA_10789
DDB_G0292264
DPU_G0070726
DLA_01006
Phypo_01246
CDH50641
0.1
Ufd2P_core
Ubox

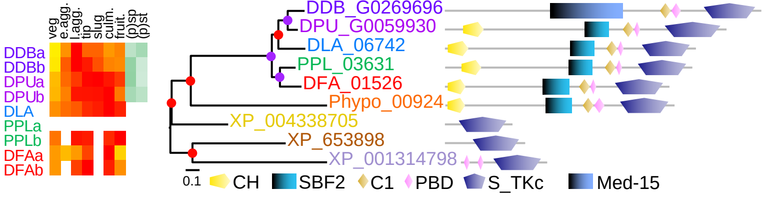

PadA Prestalk A differentiation A
DDB_G0286385
DPU_G0051560
DFA_03642
WP_021653600
Phypo_08317
PPL_02565
DLA_06544
XP_004336189
0.1
NmrA
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb


NoxB
NoxA
NoxC
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
NoxA, B and C
NADPH oxidase
DDB_G0287101
DPU_G0065622
PPL_08080
DFA_10391
Ppo012513
noxB
DDB_G0289653
DPU_G0075354
DLA_10725
PPL_10487
DFA_11184
ELR18264
XP_004345248
XP_002913524
noxA
DDB_G0291117
DPU_G0073620
PPL_00387
DFA_01368
DLA_04617
XP_003389167
noxC
0.1
EFh
Ferric_reduct
FAD_binding_8
NAD_binding_6

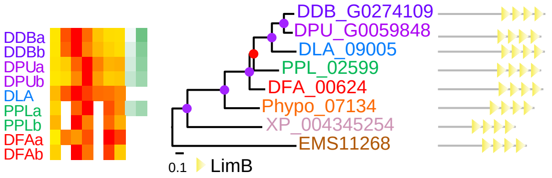

Nramp1
Nramp2
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
Nramp1&2 Natural resistance-associated macrophage protein
DDB_G0276973
DPU_G0069202
DLA_07224
PPL_02435
DFA_03314
KFM71477
XP_004346469
DDB_G0275815
DPU_G0070940
DLA_08263
PPL_09008
DFA_02872
Phypo_04218
XP_005707524
0.1
Nramp

Pak-Pkg

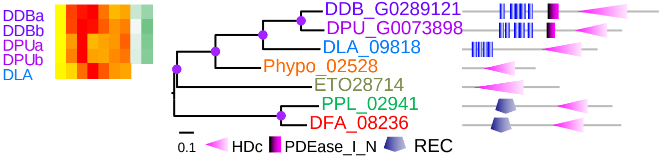
PakD P21-activated protein kinase



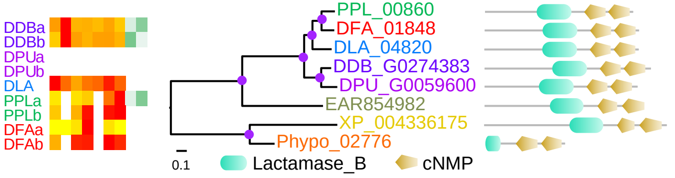
PaxB Paxillin B



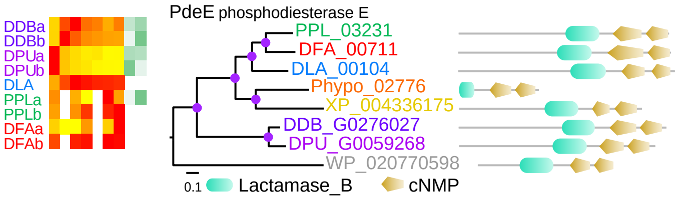
Pde4 cAMP phosphodiesterase 4



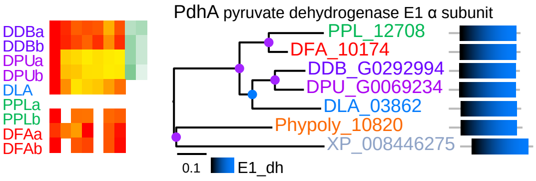
PdeD phosphodiesterase D



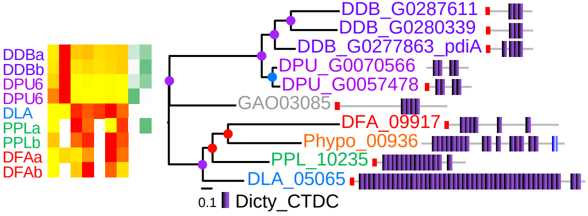
PdeE phosphodiesterase E



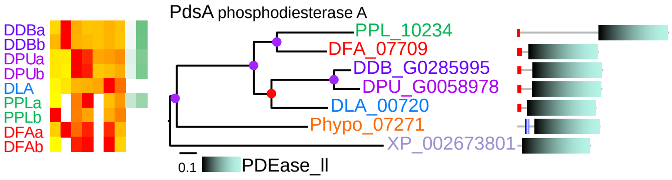
PdhA pyruvate dehydrogenase E1 α subunit



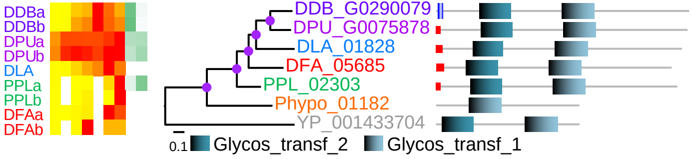
PdiA cAMP phosphodiesterase inhibitor



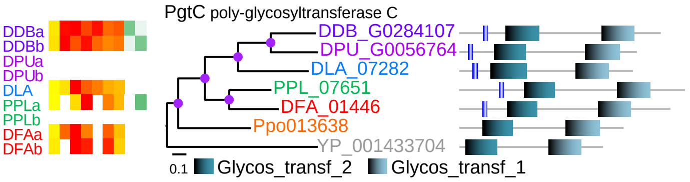
PdsA phosphodiesterase A



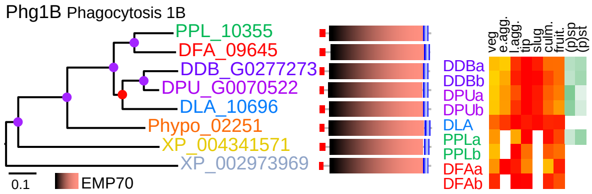
PgtB poly-glycosyltransferase B



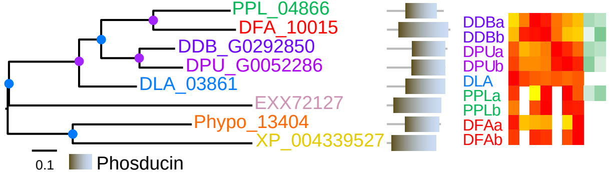
PgtC poly-glycosyltransferase C



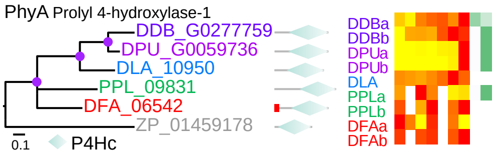
Phg1B Phagocytosis 1B



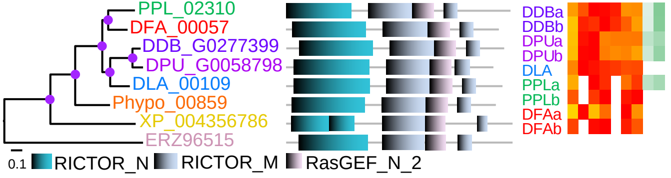
Phlp1 Phosducin-like protein 1



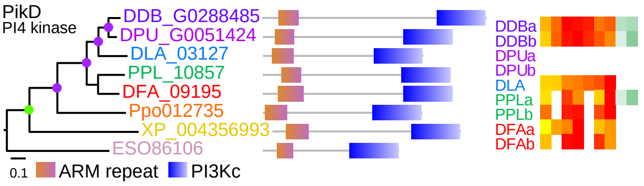
PhyA Prolyl 4-hydroxylase-1



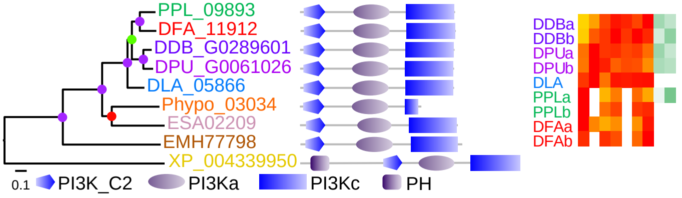
PiaA Pianissimo



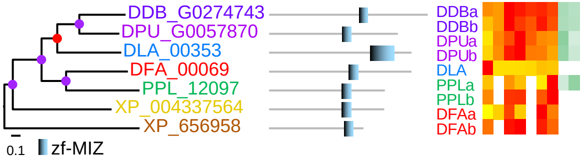
PikD
PI4 kinase



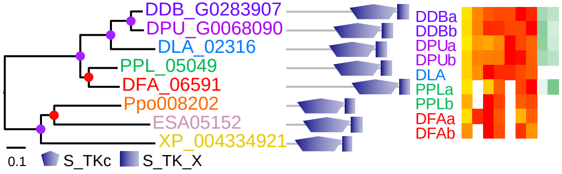
PikE Phosphatidylinositol Kinase E



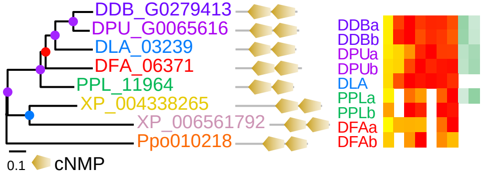
PisA Protein inhibitor of STAT



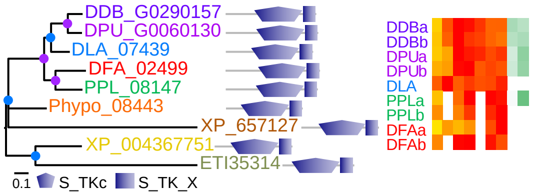
PKA-C PKA catalytic subunit

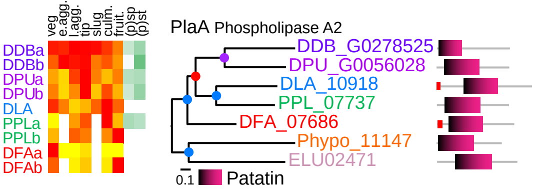


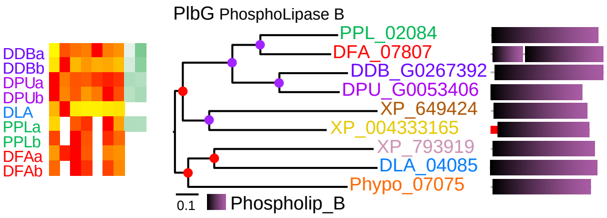
PKA-R PKA regulatory subunit

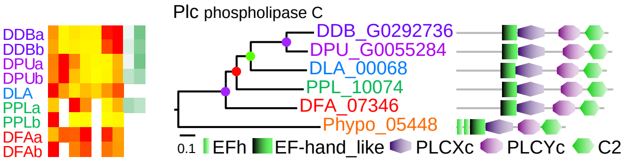


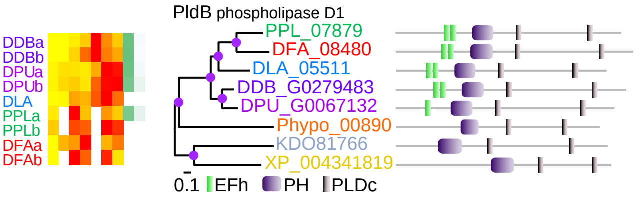
PkgB Protein kinase 2

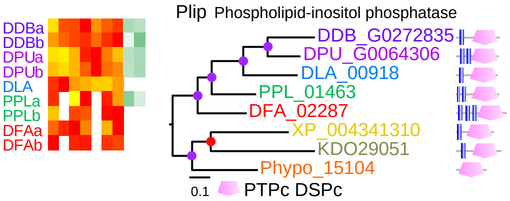


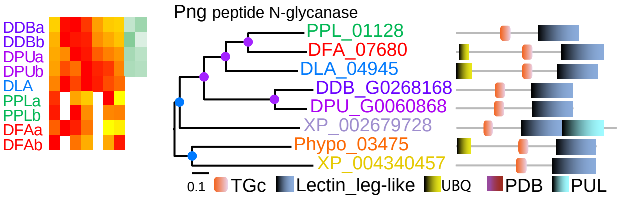

PlaA Phospholipase A2


PlbG PhosphoLipase B

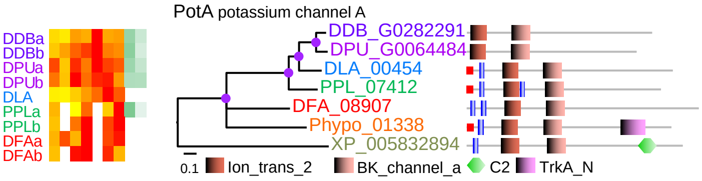

Plc phospholipase C

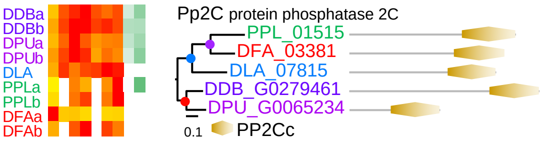

PldB phospholipase D1

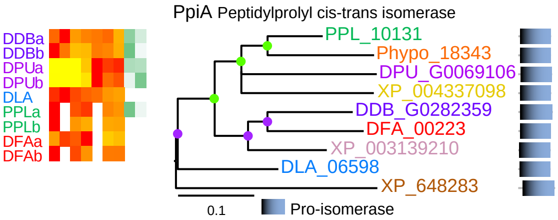

Plip Phospholipid-inositol phosphatase

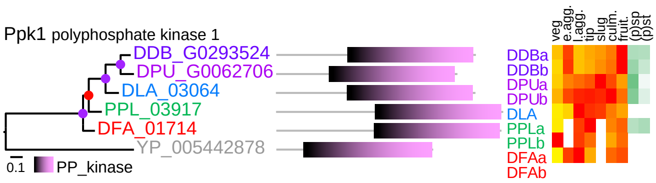

Png peptide N-glycanase

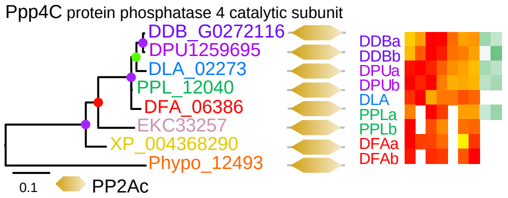

Pon A ponticulin

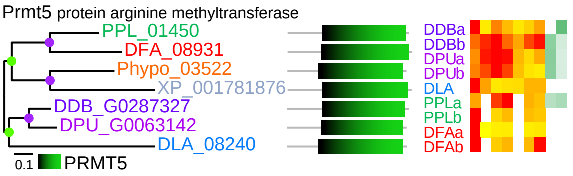

PotA potassium channel A

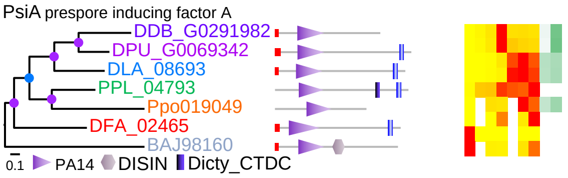

Pp2C protein phosphatase 2C

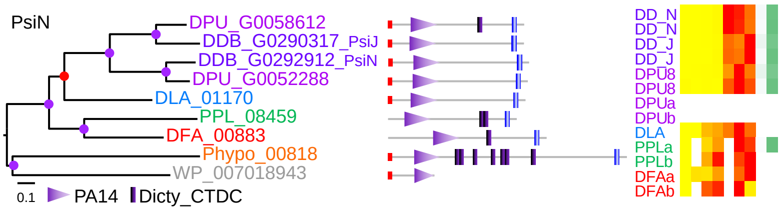

PpiA Peptidylprolyl cis-trans isomerase

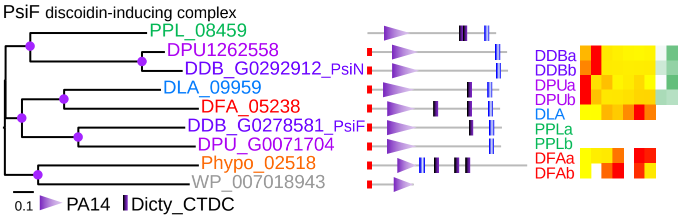

Ppk1 polyphosphate kinase 1


Ppp4C protein phosphatase 4 catalytic subunit

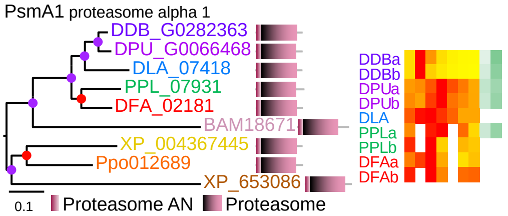

Prmt5 protein arginine methyltransferase

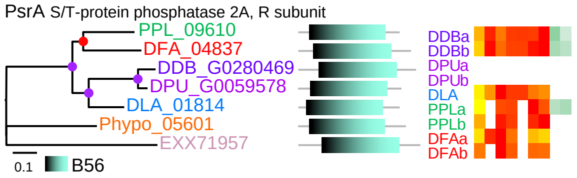

PsiA prespore inducing factor A

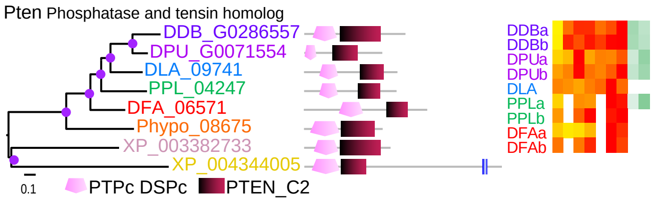

PsiN


PsiF discoidin-inducing complex


PslA PreSporeLess A

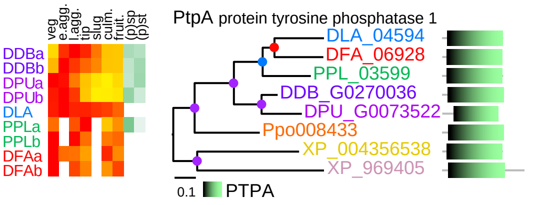

PsmA1 proteasome alpha 1


PsrA S/T-protein phosphatase 2A, R subunit

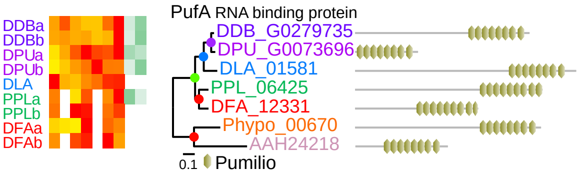

Pten Phosphatase and tensin homolog

Ptp-Rip

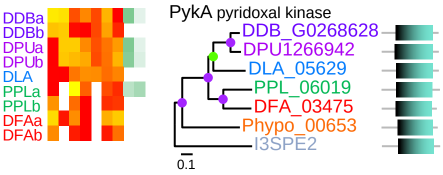
PtpA protein tyrosine phosphatase 1



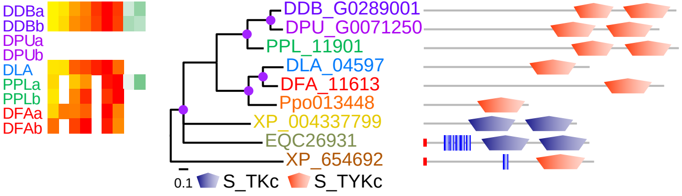
PufA RNA binding protein



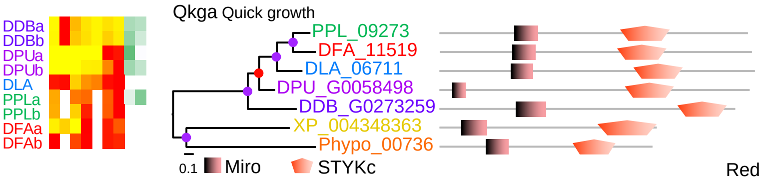
PykA pyridoxal kinase



Pyk3 protein tyrosine kinase 3

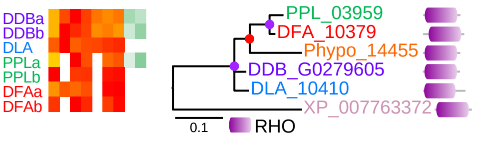


Qkga Quick growth

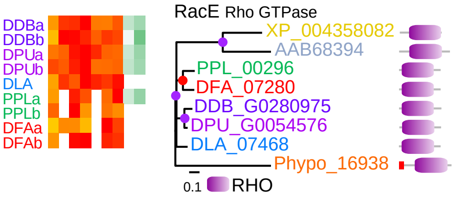


R

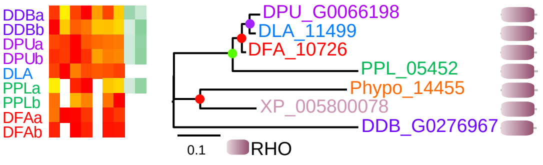
RacB RAs-related-C3 botulinum toxin substrate



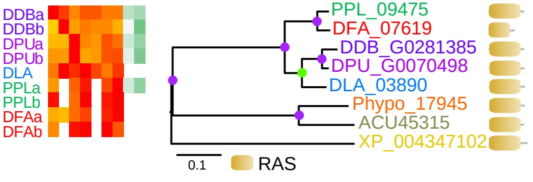
RacE Rho GTPase



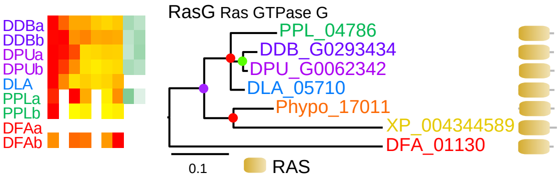
RacF2 Rho GTPase



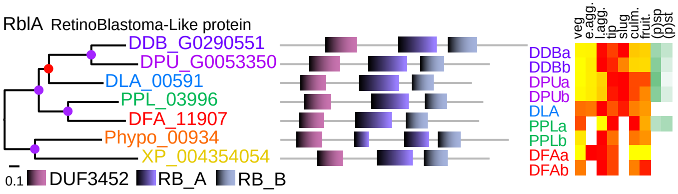
RasC Rat sarcoma



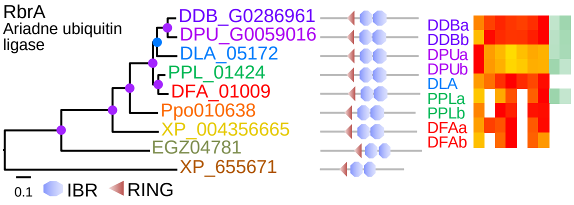
RasG Ras GTPase G



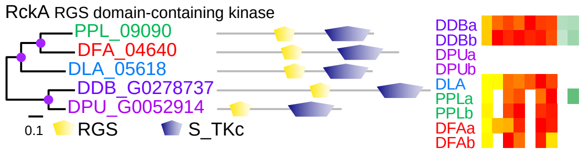
RblA RetinoBlastoma-Like protein



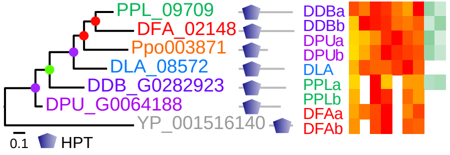
RbrA
Ariadne ubiquitin
ligase



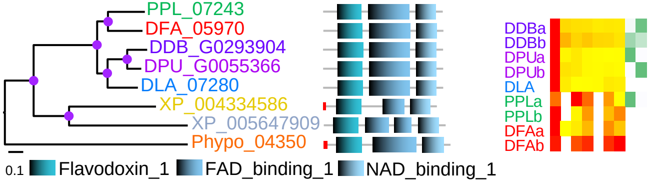
RckA RGS domain-containing kinase



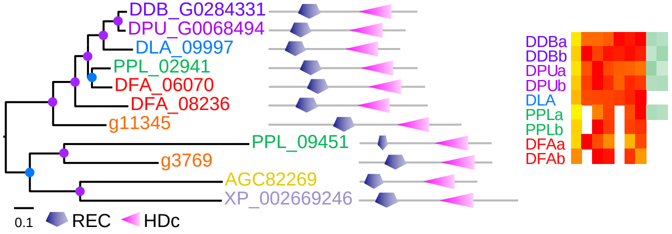
RdeA rapid development A



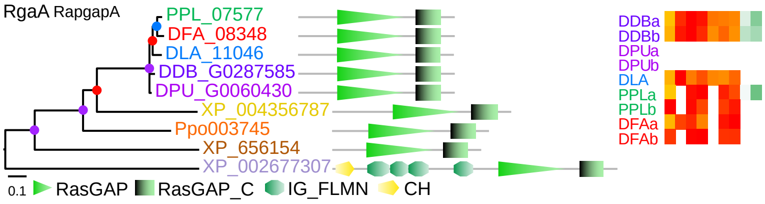
RedA NADPH-cytochrome-P450 oxidoreductase



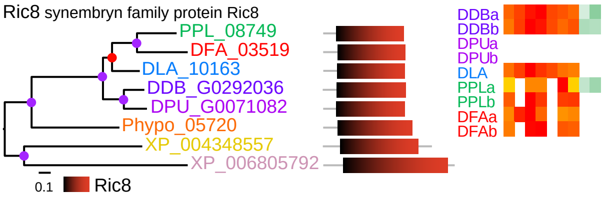
RegA cAMP phosphodiesterase



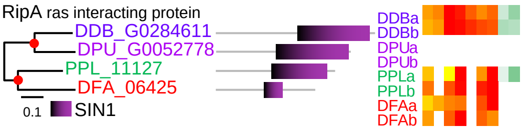
RgaA RapgapA



Ric8 synembryn family protein Ric8

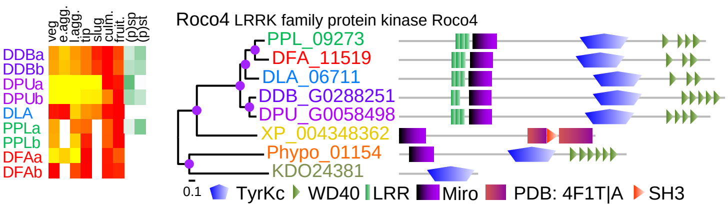


RipA ras interacting protein

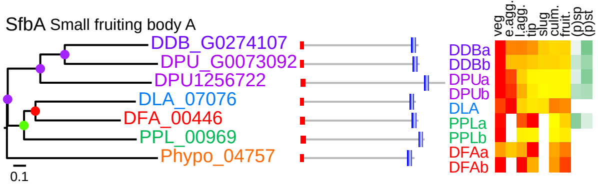


Roc-Snf

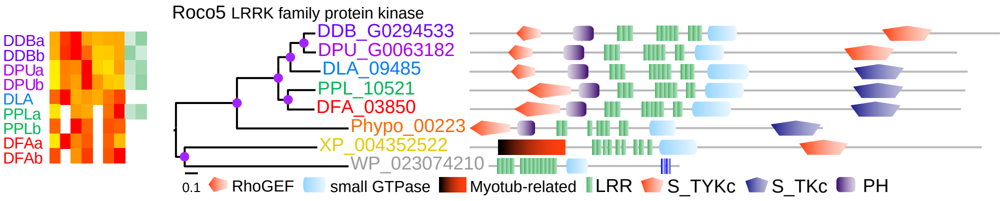
Roco4 LRRK family protein kinase Roco4



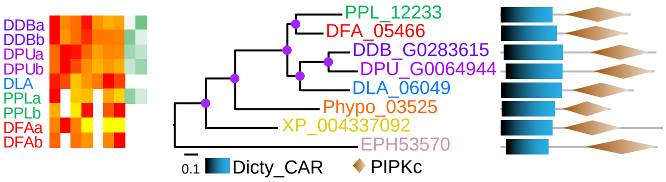
SfbA Small fruiting body A



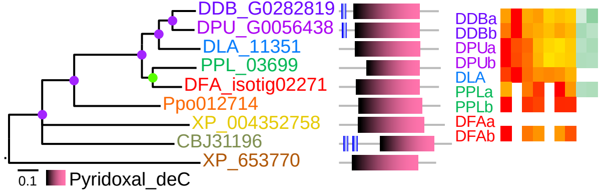
Roco5 LRRK family protein kinase



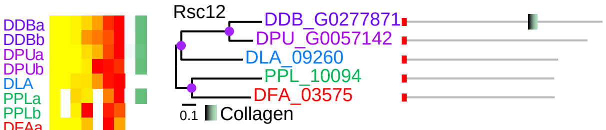
RpkA receptor phosphatidylinositol kinase A



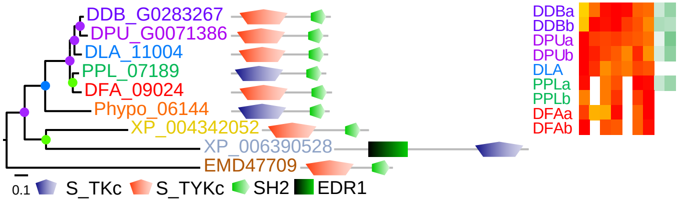
SglA sphingosine-1-phosphate lyase



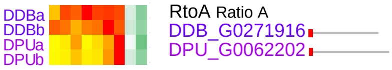
Rsc12



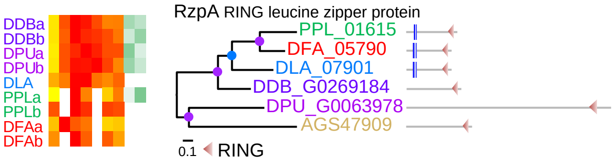
ShkA SH2 domain-containing kinase



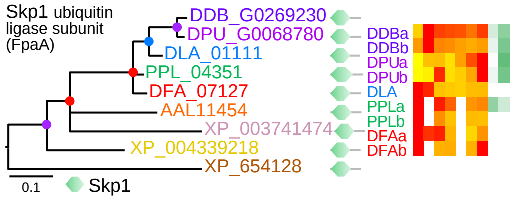
RtoA Ratio A



RzpA RING leucine zipper protein

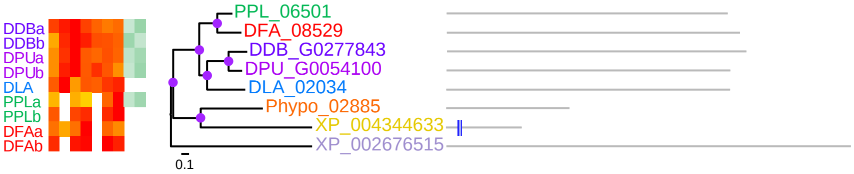


Skp1 ubiquitin ligase subunit (FpaA)

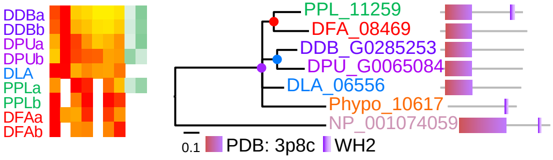


S

ScaA

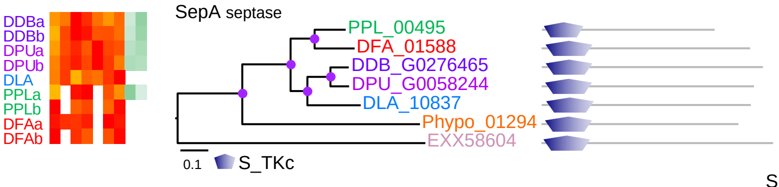


ScrA Suppressor of Car2

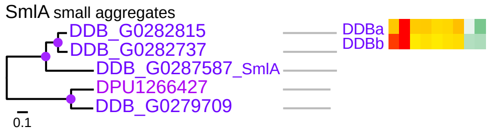


SmdA SET/MYND chromatin re-modelling

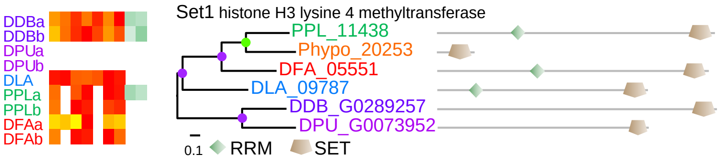
SepA septase



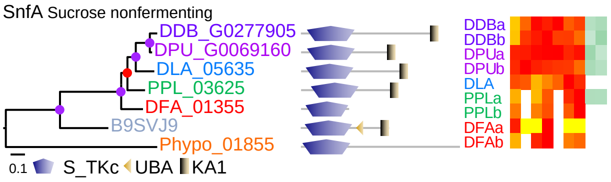
SmlA small aggregates



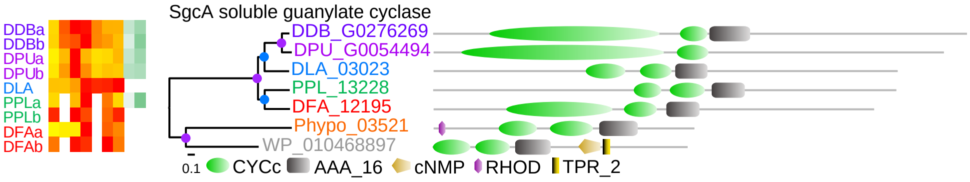
Set1 histone H3 lysine 4 methyltransferase

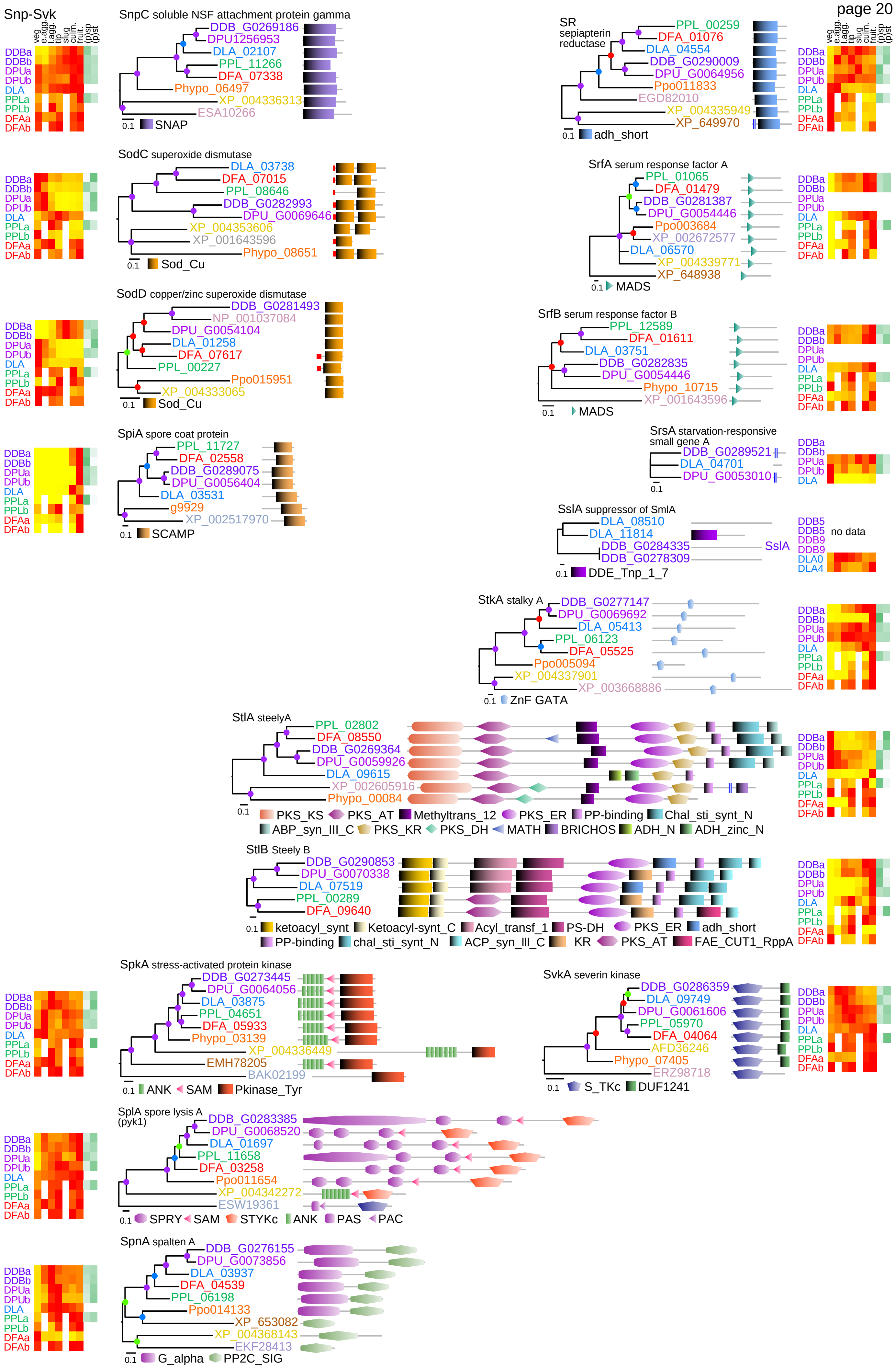


SnfA Sucrose nonfermenting



SgcA soluble guanylate cyclase




Snp-Svk
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e.agg.
l.agg.
tip
slug
culm.
fruit.
(p)sp
(p)st
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
SnpC soluble NSF attachment protein gamma
DDB_G0269186
DPU1256953
DLA_02107
PPL_11266
DFA_07338
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XP_004336313
ESA10266
0.1
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SR sepiapterin reductase
PPL_00259
DFA_01076
DLA_04554
DDB_G0290009
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EGD82010
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XP_649970
adh_short
SodC superoxide dismutase
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DFA_07015
PPL_08646
DDB_G0282993
DPU_G0069646
XP_004353606
XP_001643596
Phypo_08651
Sod_Cu
SrfA serum response factor A
PPL_01065
DFA_01479
DDB_G0281387
DPU_G0054446
Ppo003684
XP_002672577
DLA_06570
XP_004339771
XP_648938
MADS
SodD copper/zinc superoxide dismutase
DDB_G0281493
NP_001037084
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DLA_01258
DFA_07617
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Ppo015951
XP_004333065
Sod_Cu
SrfB serum response factor B
PPL_12589
DFA_01611
DLA_03751
DDB_G0282835
DPU_G0054446
Phypo_10715
XP_001643596
MADS
SpiA spore coat protein
PPL_11727
DFA_02558
DDB_G0289075
DPU_G0056404
DLA_03531
g9929
XP_002517970
SCAMP
SrsA starvation-responsive small gene A
DDB_G0289521
DLA_04701
DPU_G0053010
SslA suppressor of SmlA
DLA_08510
DLA_11814
DDB_G0284335
DDB_G0278309
SslA
DDE_Tnp_1_7
DDB5
DDB5
DDB9
DDB9
DLA0
DLA4
no data
StkA stalky A
DDB_G0277147
DPU_G0069692
DLA_05413
PPL_06123
DFA_05525
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XP_004337901
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ZnF GATA
StlA steelyA
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Phypo_00084
PKS_KS
PKS_AT
Methyltrans_12
PKS_ER
PP-binding
Chal_sti_synt_N
ABP_syn_III_C
PKS_KR
PKS_DH
MATH
BRICHOS
ADH_N
ADH_zinc_N
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Ketoacyl-synt_C
Acyl_transf_1
PS-DH
PKS_ER
adh_short
PP-binding
chal_sti_synt_N
ACP_syn_III_C
KR
PKS_AT
FAE_CUT1_RppA
SpkA stress-activated protein kinase
DDB_G0273445
DPU_G0064056
DLA_03875
PPL_04651
DFA_05933
Phypo_03139
XP_004336449
EMH78205
BAK02199
ANK
SAM
Pkinase_Tyr
SvkA severin kinase
DDB_G0286359
DLA_09749
DPU_G0061606
PPL_05970
DFA_04064
AFD36246
Phypo_07405
ERZ98718
S_TKc
DUF1241
SplA spore lysis A (pyk1)
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DFA_03258
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SPRY
SAM
STYKc
ANK
PAS
PAC
SpnA spalten A
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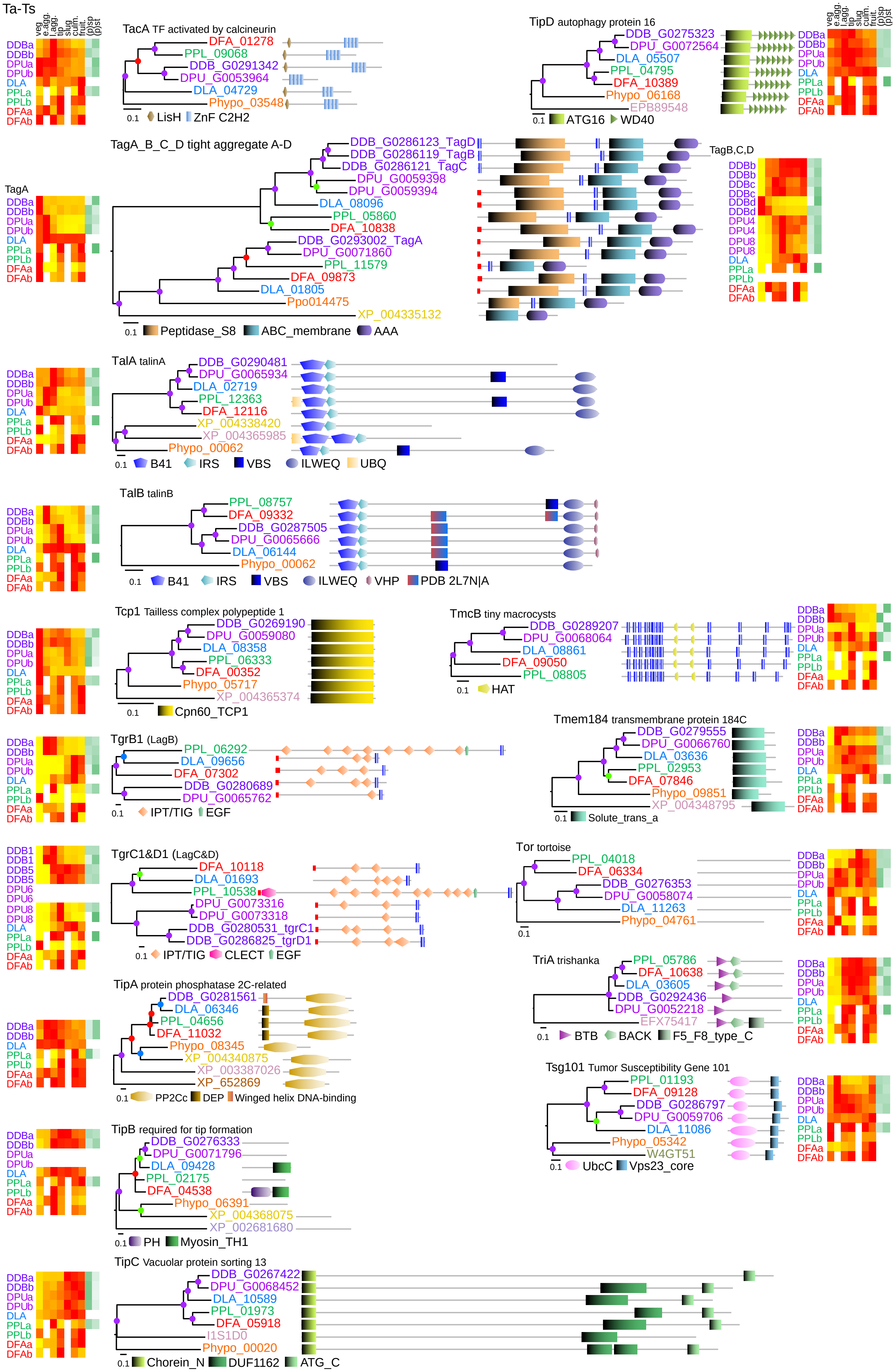
Ta-Ts
veg
e.agg.
l.agg.
tip
slug
culm.
fruit.
(p)sp
(p)st
DDBa DDBb DPUa DPUb DLA PPLa PPLb DFAa DFAb
TacA TF activated by calcineurin
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PPL_09068
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DPU_G0053964
DLA_04729
Phypo_03548
0.1
LisH
ZnF C2H2
TipD autophagy protein 16
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ATG16
WD40
TagA_B_C_D tight aggregate A-D
DDB_G0286123_TagD
DDB_G0286119_TagB
DDB_G0286121_TagC
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TalA talinA
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Phypo_00062
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IRS
VBS
ILWEQ
UBQ
TalB talinB
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DFA_09332
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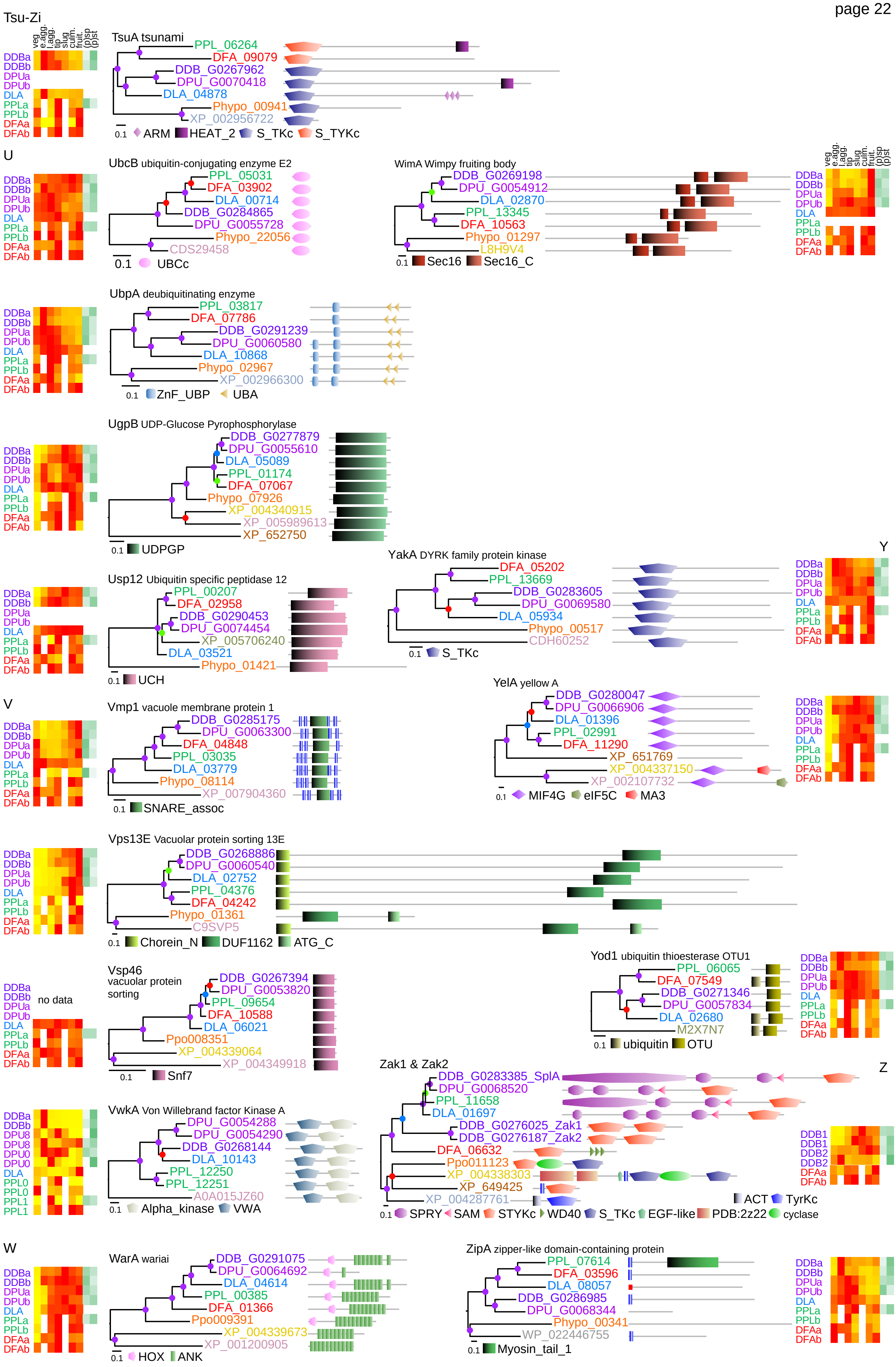
DPU_G0065666
DLA_06144
Phypo_00062
0.1
B41
IRS
VBS
ILWEQ
VHP
PDB 2L7N|A
Tcp1 Tailless complex polypeptide 1
DDB_G0269190
DPU_G0059080
DLA_08358
PPL_06333
DFA_00352
Phypo_05717
XP_004365374
0.1
Cpn60_TCP1
TmcB tiny macrocysts
DDB_G0289207
DPU_G0068064
DLA_08861
DFA_09050
PPL_08805
0.1
HAT
Tmem184 transmembrane protein 184C
DDB_G0279555
DPU_G0066760
DLA_03636
PPL_02953
DFA_07846
Phypo_09851
XP_004348795
0.1
Solute_trans_a
TgrB1 (LagB)
PPL_06292
DLA_09656
DFA_07302
DDB_G0280689
DPU_G0065762
0.1
IPT/TIG
EGF
TgrC1&D1 (LagC&D)
DDB1 DDB1 DDB5 DDB5 DPU6 DPU6 DPU8 DPU8 DLA PPLa PPLb DFAa DFAb
DFA_10118
DLA_01693
PPL_10538
DPU_G0073316
DPU_G0073318
DDB_G0280531_tgrC1
DDB_G0286825_tgrD1
0.1
IPT/TIG
CLECT
EGF
Tor tortoise
PPL_04018
DFA_06334
DDB_G0276353
DPU_G0058074
DLA_11263
Phypo_04761
0.1
TriA trishanka
PPL_05786
DFA_10638
DLA_03605
DDB_G0292436
DPU_G0052218
EFX75417
0.1
BTB
BACK
F5_F8_type_C
TipA protein phosphatase 2C-related
DDB_G0281561
DLA_06346
PPL_04656
DFA_11032
Phypo_08345
XP_004340875
XP_003387026
XP_652869
0.1
PP2Cc
DEP
Winged helix DNA-binding
Tsg101 Tumor Susceptibility Gene 101
PPL_01193
DFA_09128
DDB_G0286797
DPU_G0059706
DLA_11086
Phypo_05342
W4GT51
0.1
UbcC
Vps23_core
TipB required for tip formation
DDB_G0276333
DPU_G0071796
DLA_09428
PPL_02175
DFA_04538
Phypo_06391
XP_004368075
XP_002681680
0.1
PH
Myosin_TH1
TipC Vacuolar protein sorting 13
DDB_G0267422
DPU_G0068452
DLA_10589
PPL_01973
DFA_05918
I1S1D0
Phypo_00020
0.1
Chorein_N
DUF1162
ATG_C


Tsu-Zi
veg
e.agg.
l.agg.
tip
slug
culm.
fruit.
(p)sp
(p)st
DDBa
DDBb
DPUa
DPUb
DLA
PPLa
PPLb
DFAa
DFAb
TsuA tsunami
PPL_06264
DFA_09079
DDB_G0267962
DPU_G0070418
DLA_04878
Phypo_00941
XP_002956722
0.1
ARM
HEAT_2
S_TKc
S_TYKc
U
UbcB ubiquitin-conjugating enzyme E2
PPL_05031
DFA_03902
DLA_00714
DDB_G0284865
DPU_G0055728
Phypo_22056
CDS29458
0.1
UBCc
WimA Wimpy fruiting body
DDB_G0269198
DPU_G0054912
DLA_02870
PPL_13345
DFA_10563
Phypo_01297
L8H9V4
0.1
Sec16
Sec16_C
UbpA deubiquitinating enzyme
PPL_03817
DFA_07786
DDB_G0291239
DPU_G0060580
DLA_10868
Phypo_02967
XP_002966300
0.1
ZnF_UBP
UBA
UgpB UDP-Glucose Pyrophosphorylase
DDB_G0277879
DPU_G0055610
DLA_05089
PPL_01174
DFA_07067
Phypo_07926
XP_004340915
XP_005989613
XP_652750
0.1
UDPGP
Usp12 Ubiquitin specific peptidase 12
PPL_00207
DFA_02958
DDB_G0290453
DPU_G0074454
XP_005706240
DLA_03521
Phypo_01421
0.1
UCH
YakA DYRK family protein kinase
Y
DFA_05202
PPL_13669
DDB_G0283605
DPU_G0069580
DLA_05934
Phypo_00517
CDH60252
0.1
S_TKc
V
Vmp1 vacuole membrane protein 1
DDB_G0285175
DPU_G0063300
DFA_04848
PPL_03035
DLA_03779
Phypo_08114
XP_007904360
0.1
SNARE_assoc
YelA yellow A
DDB_G0280047
DPU_G0066906
DLA_01396
PPL_02991
DFA_11290
XP_651769
XP_004337150
XP_002107732
0.1
MIF4G
eIF5C
MA3
Vps13E Vacuolar protein sorting 13E
DDB_G0268886
DPU_G0060540
DLA_02752
PPL_04376
DFA_04242
Phypo_01361
C9SVP5
0.1
Chorein_N
DUF1162
ATG_C
Yod1 ubiquitin thioesterase OTU1
PPL_06065
DFA_07549
DDB_G0271346
DPU_G0057834
DLA_02680
M2X7N7
0.1
ubiquitin
OTU
no data
Vsp46
vacuolar protein
sorting
DDB_G0267394
DPU_G0053820
PPL_09654
DFA_10588
DLA_06021
Ppo008351
XP_004339064
XP_004349918
0.1
Snf7
Zak1 & Zak2
Z
DDB_G0283385_SplA
DPU_G0068520
PPL_11658
DLA_01697
DDB_G0276025_Zak1
DDB_G0276187_Zak2
DFA_06632
Ppo011123
XP_004338303
XP_649425
XP_004287761
0.1
SPRY
SAM
STYKc
WD40
S_TKc
EGF-like
PDB:2z22
ACT
TyrKc
cyclase
DDB1
DDB1
DDB2
DDB2
DFAa
DFAb
VwkA Von Willebrand factor Kinase A
DPU_G0054288
DPU_G0054290
DDB_G0268144
DLA_10143
PPL_12250
PPL_12251
A0A015JZ60
0.1
Alpha_kinase
VWA
DPU8
DPU8
DPU0
DPU0
DLA
PPL0
PPL0
PPL1
PPL1
W
WarA wariai
DDB_G0291075
DPU_G0064692
DLA_04614
PPL_00385
DFA_01366
Ppo009391
XP_004339673
XP_001200905
0.1
HOX
ANK
ZipA zipper-like domain-containing protein
PPL_07614
DFA_03596
DLA_08057
DDB_G0286985
DPU_G0068344
Phypo_00341
WP_022446755
0.1
Myosin_tail_1