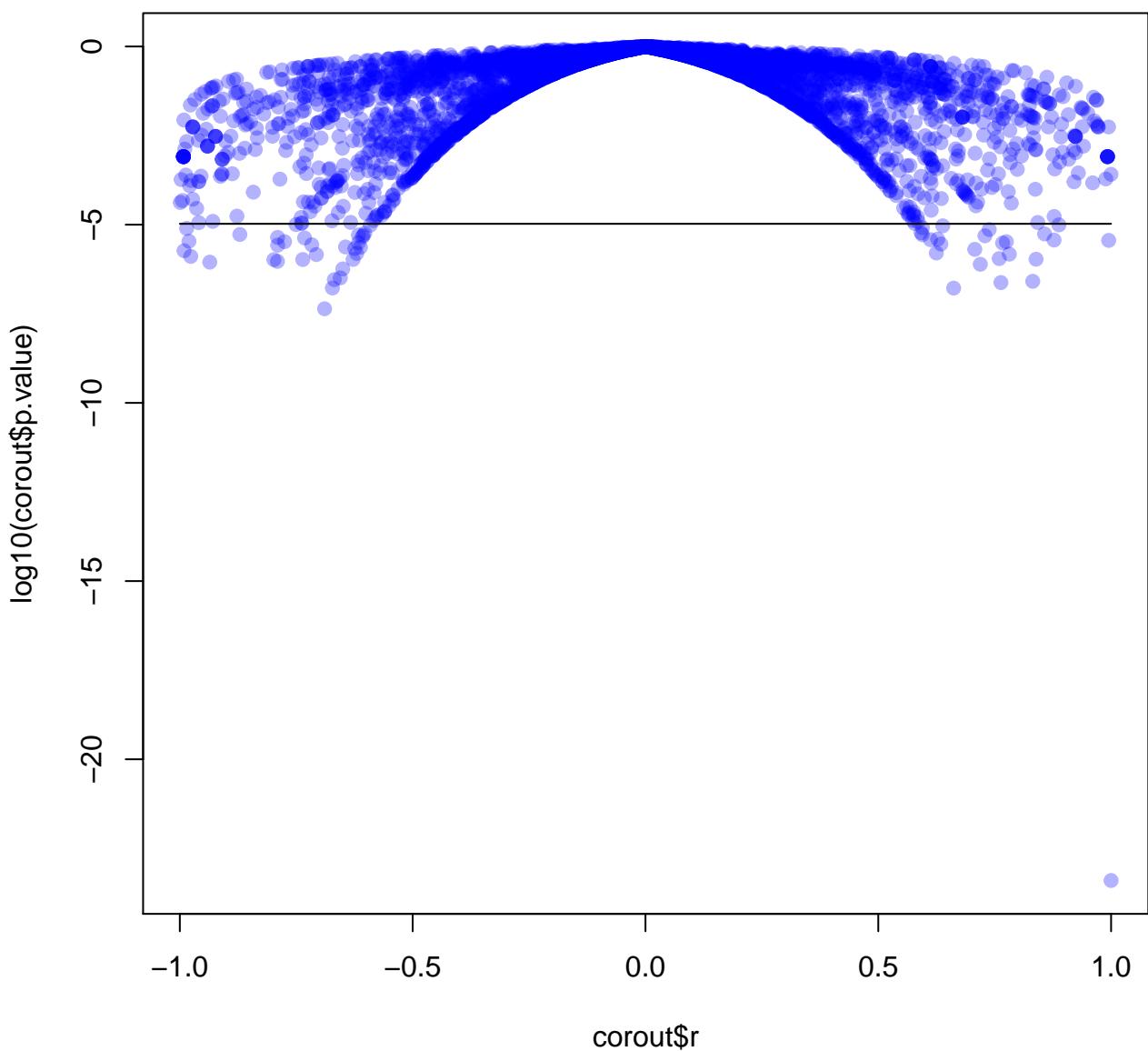
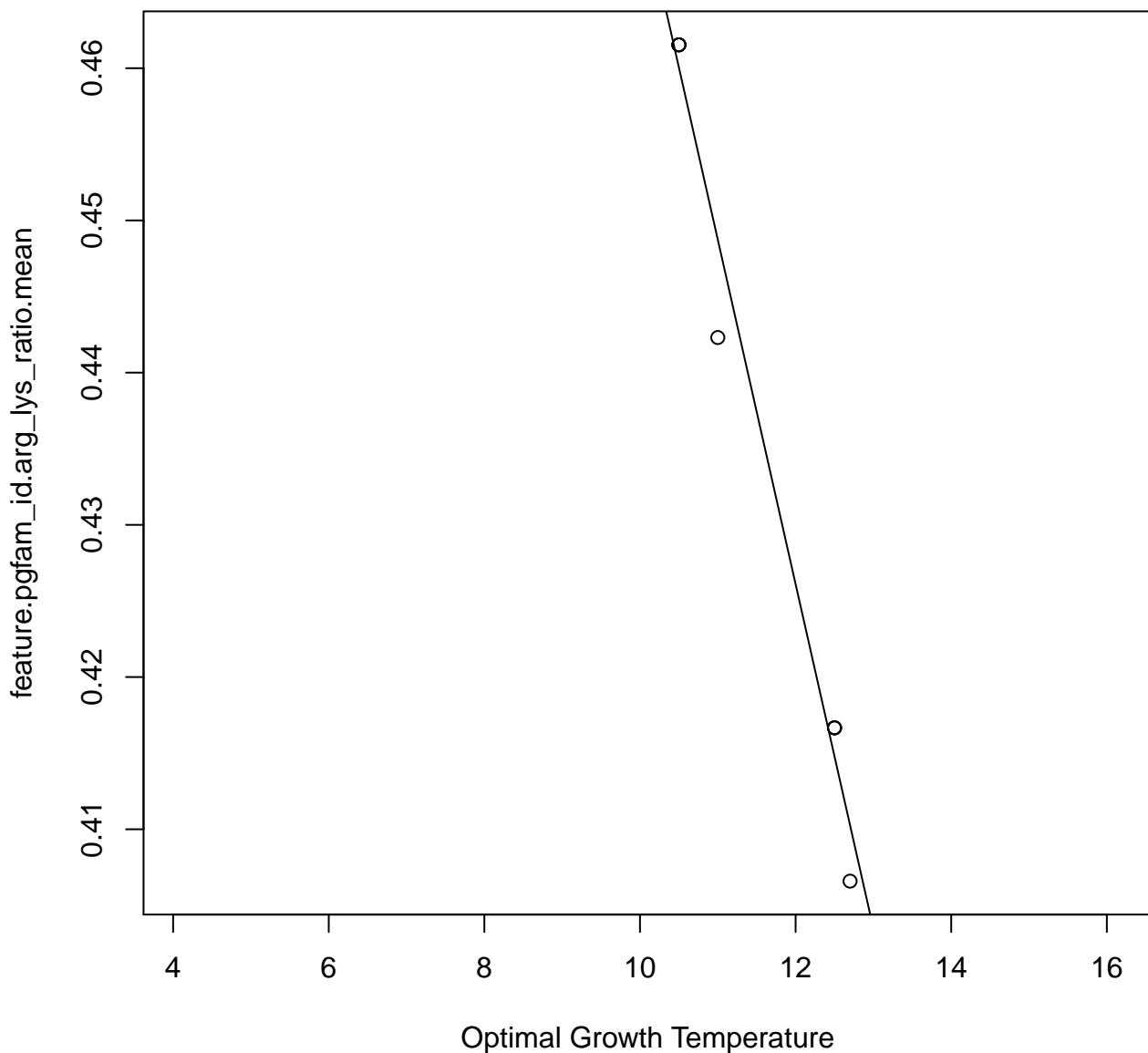


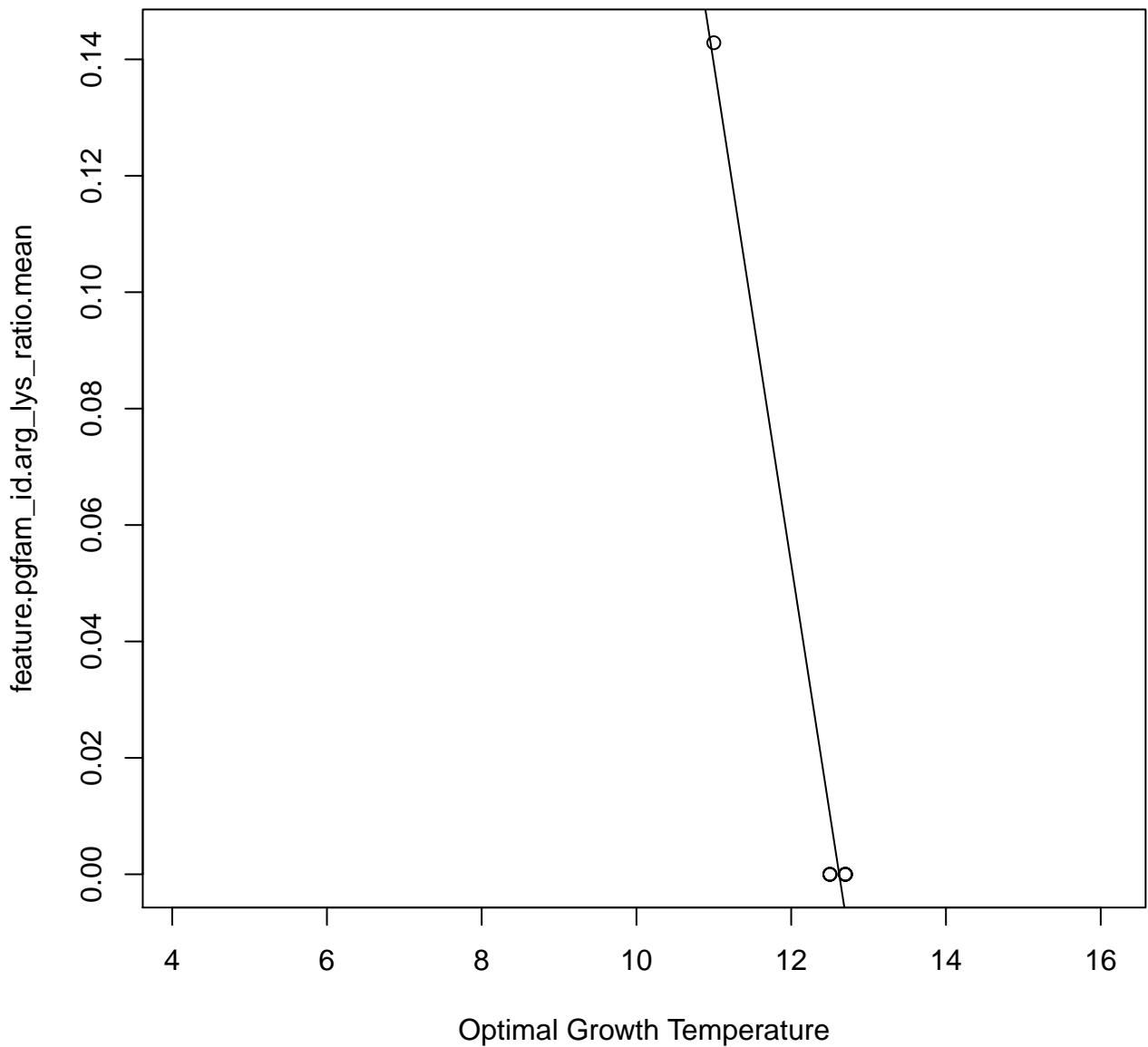
feature.pgfam_id.arg_lys_ratio.mean



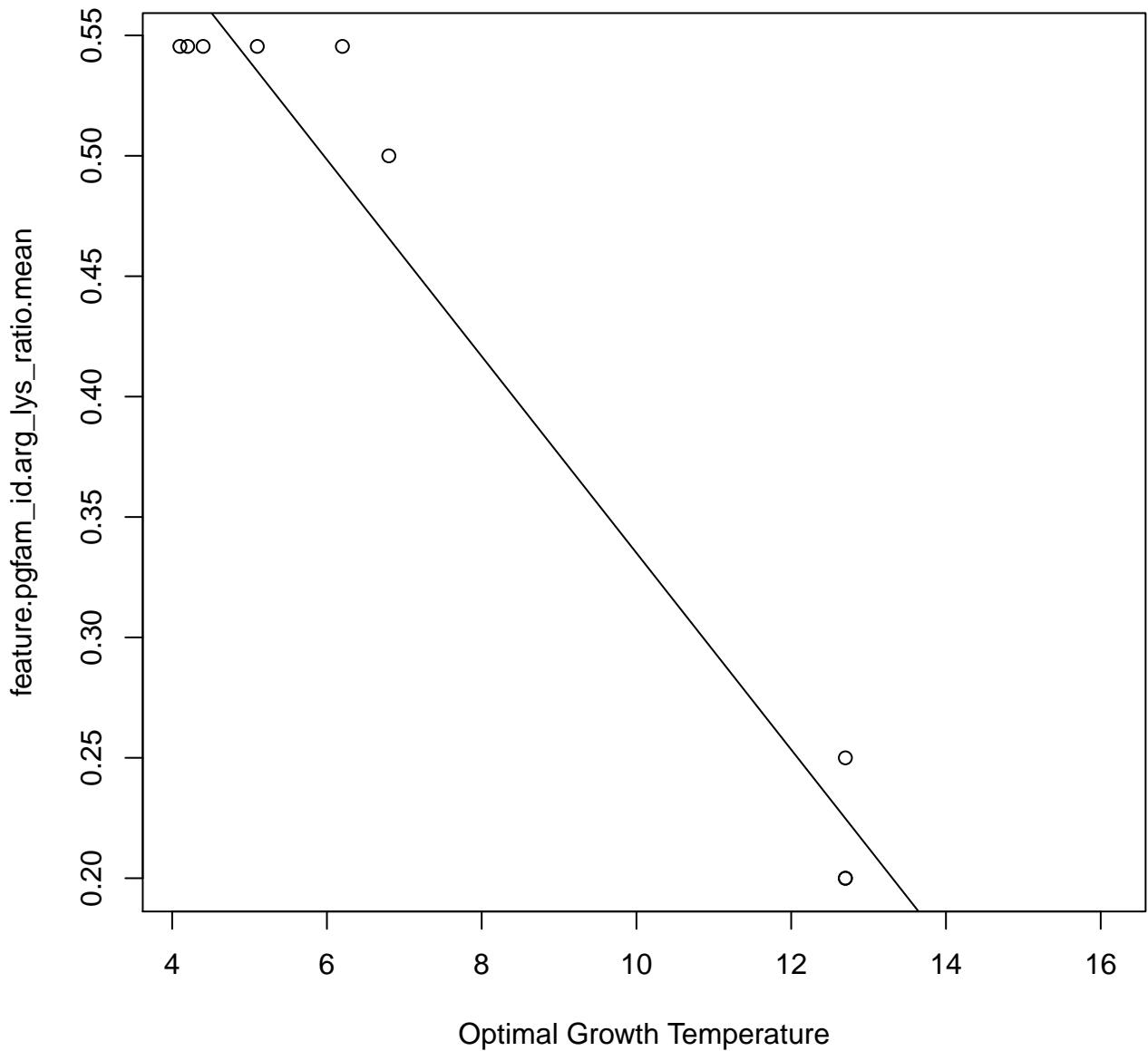
feature.pgfam_id.arg_lys_ratio.mean
PGF_01339224
hypothetical protein



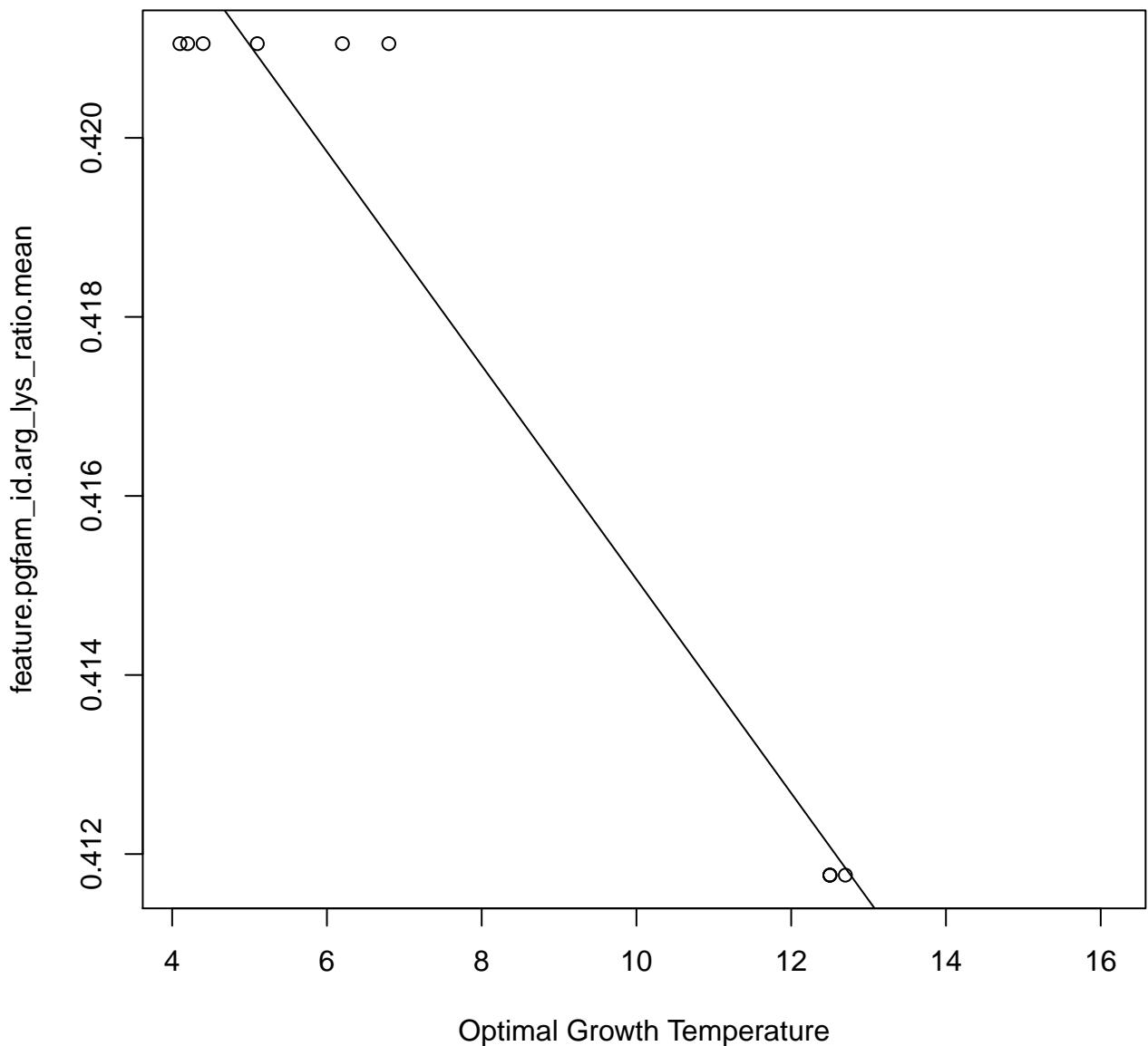
feature.pgfam_id.arg_lys_ratio.mean
PGF_00414476
uncharacterized conserved protein containing predicted Zn-ribbon like domain



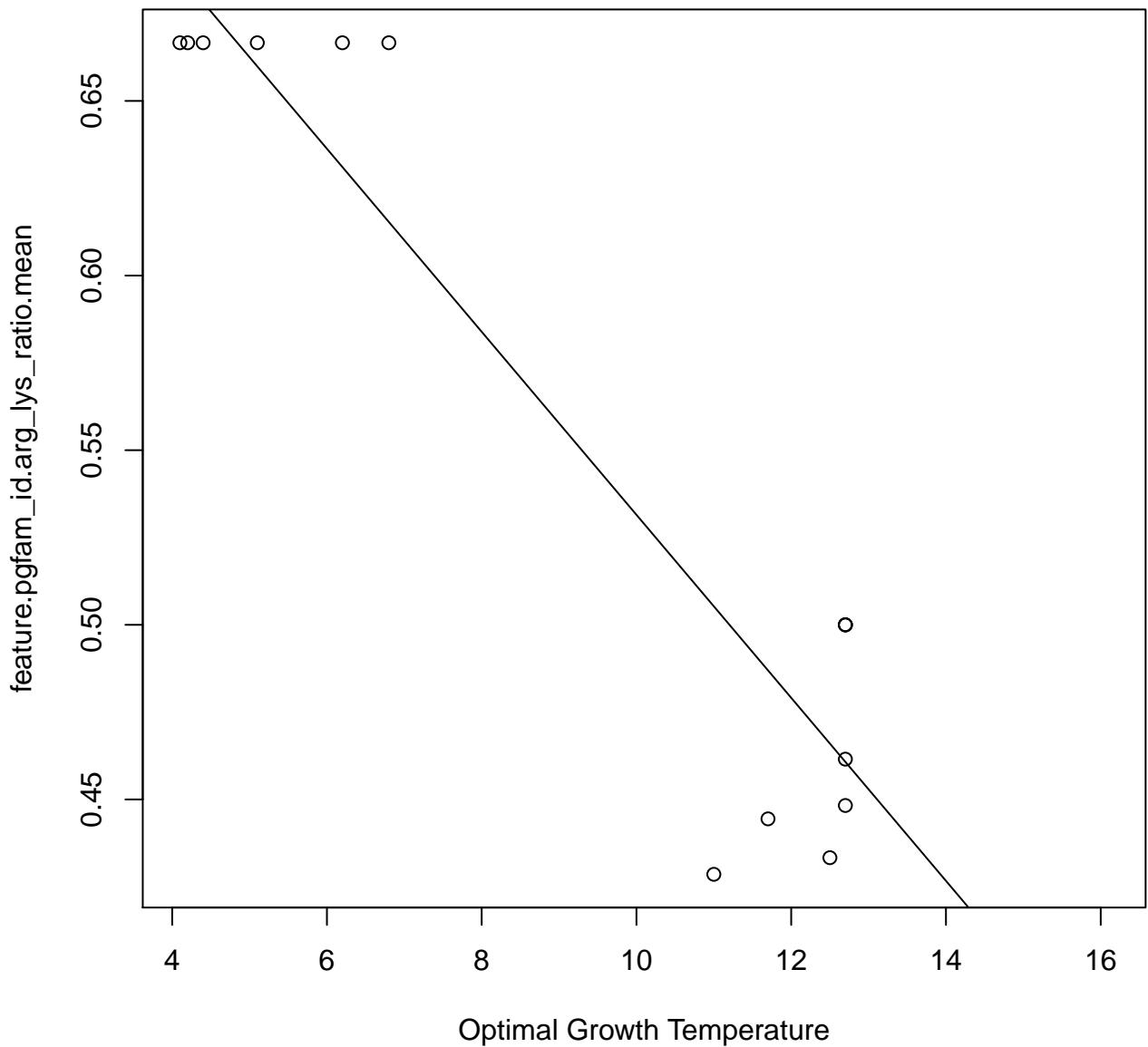
feature.pgfam_id.arg_lys_ratio.mean
PGF_01336811
hypothetical protein



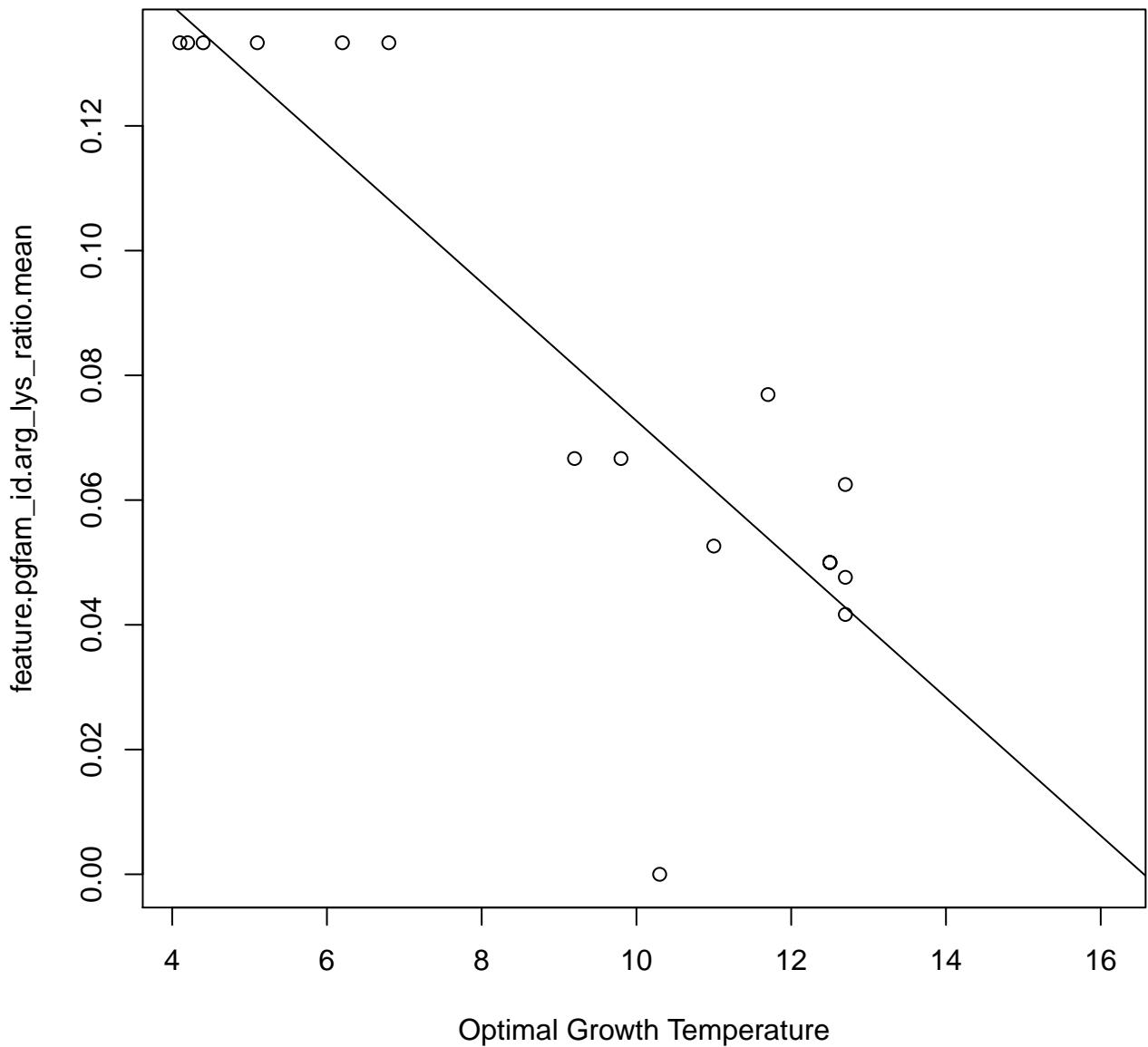
feature.pgfam_id.arg_lys_ratio.mean
PGF_01338043
hypothetical protein



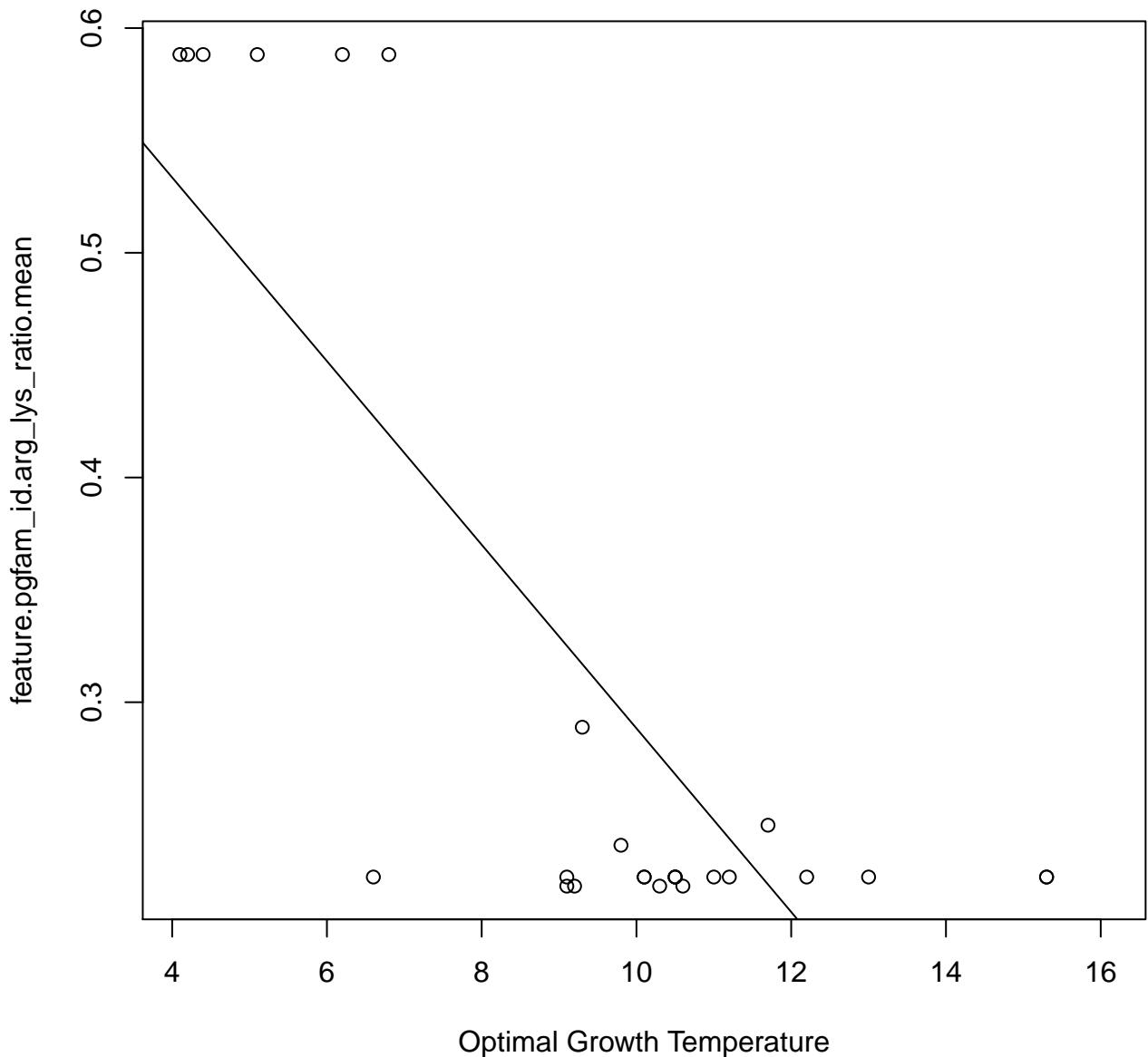
feature.pgfam_id.arg_lys_ratio.mean
PGF_12884992
Uncharacterized MFS-type transporter



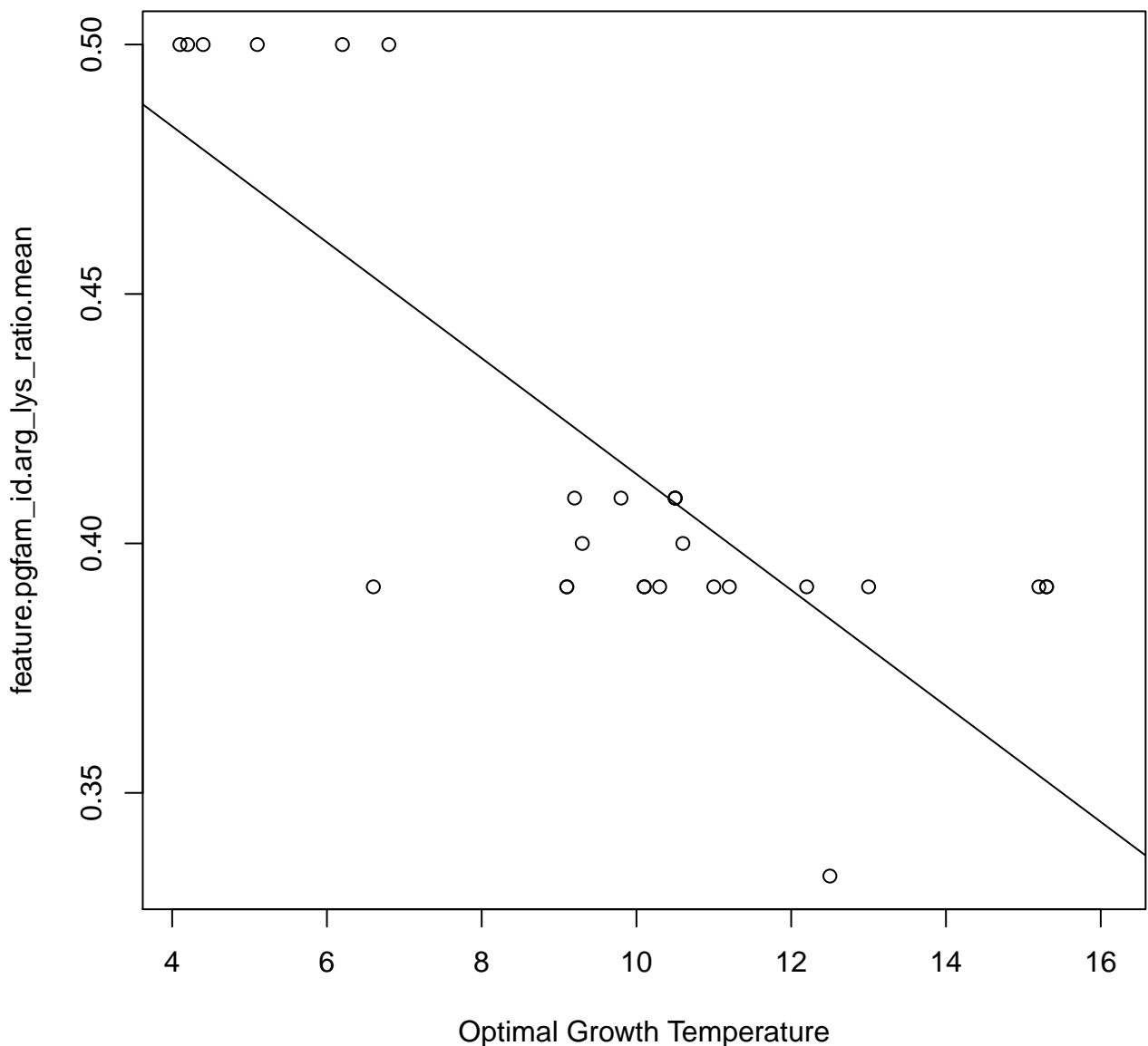
feature.pgfam_id.arg_lys_ratio.mean
PGF_00060323
Transforming growth factor-beta induced protein IG-H3 precursor



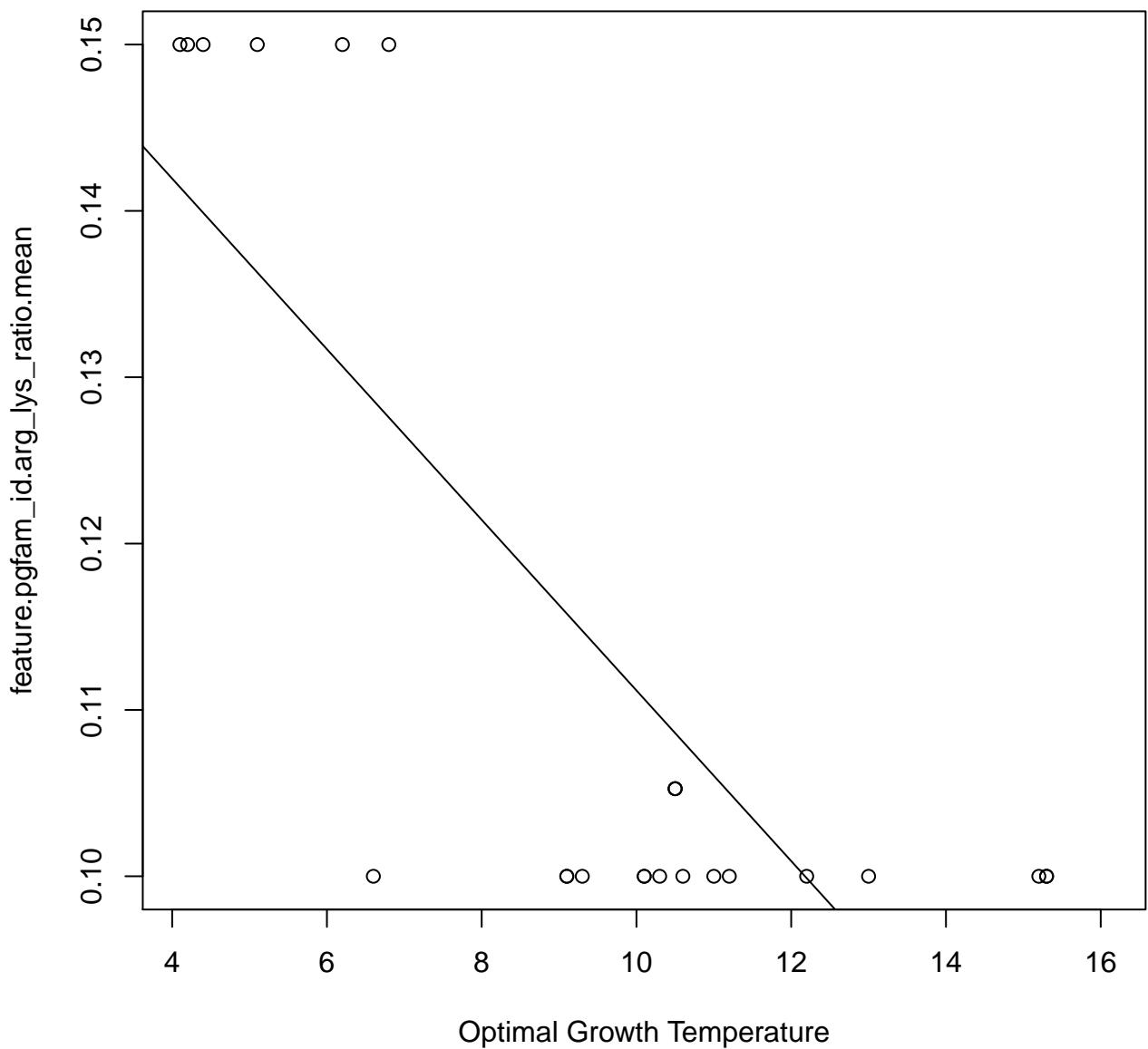
feature.pgfam_id.arg_lys_ratio.mean
PGF_03083319
Maltodextrin glucosidase (EC 3.2.1.20)



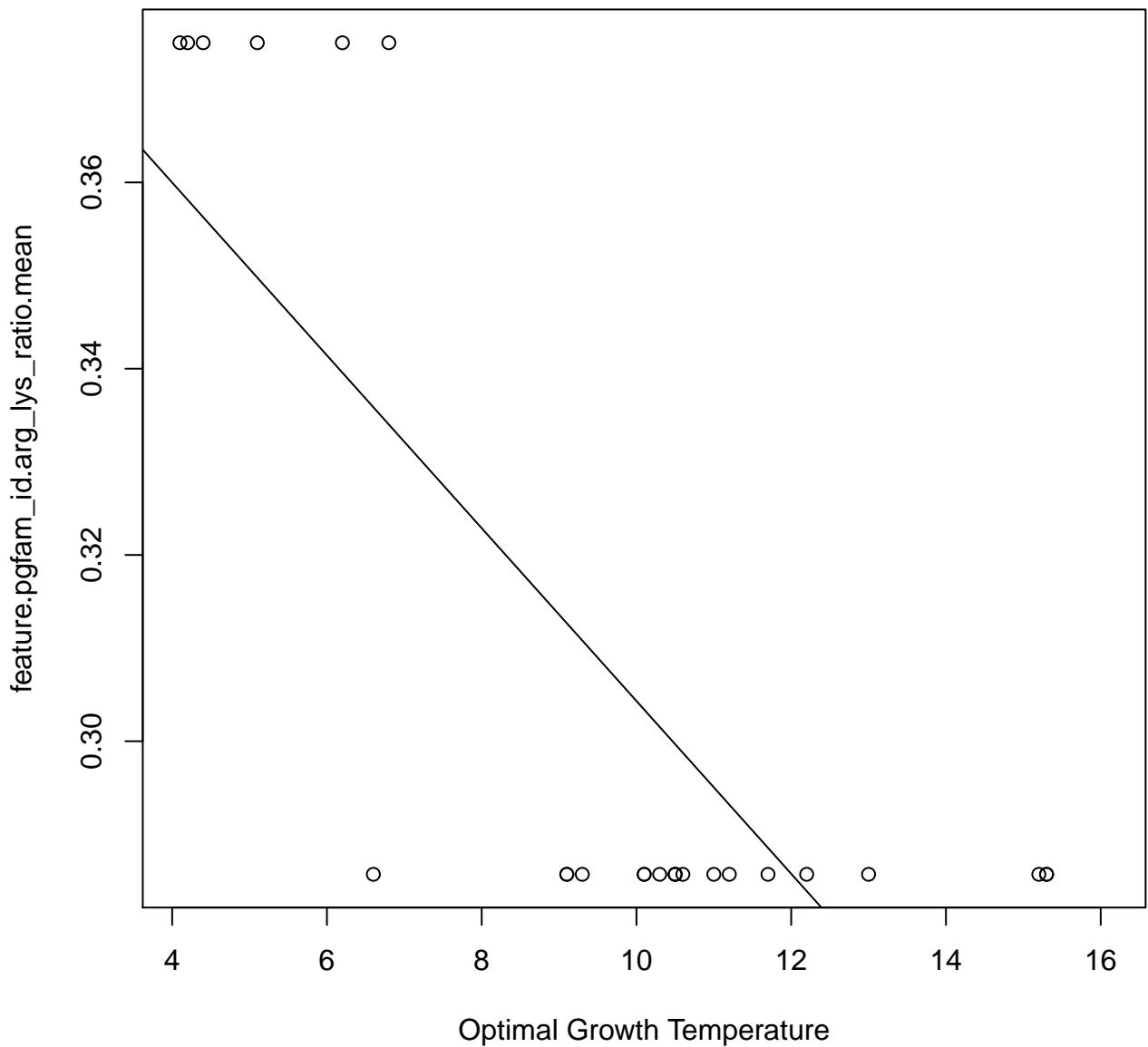
feature.pgfam_id.arg_lys_ratio.mean
PGF_06792096
hypothetical protein



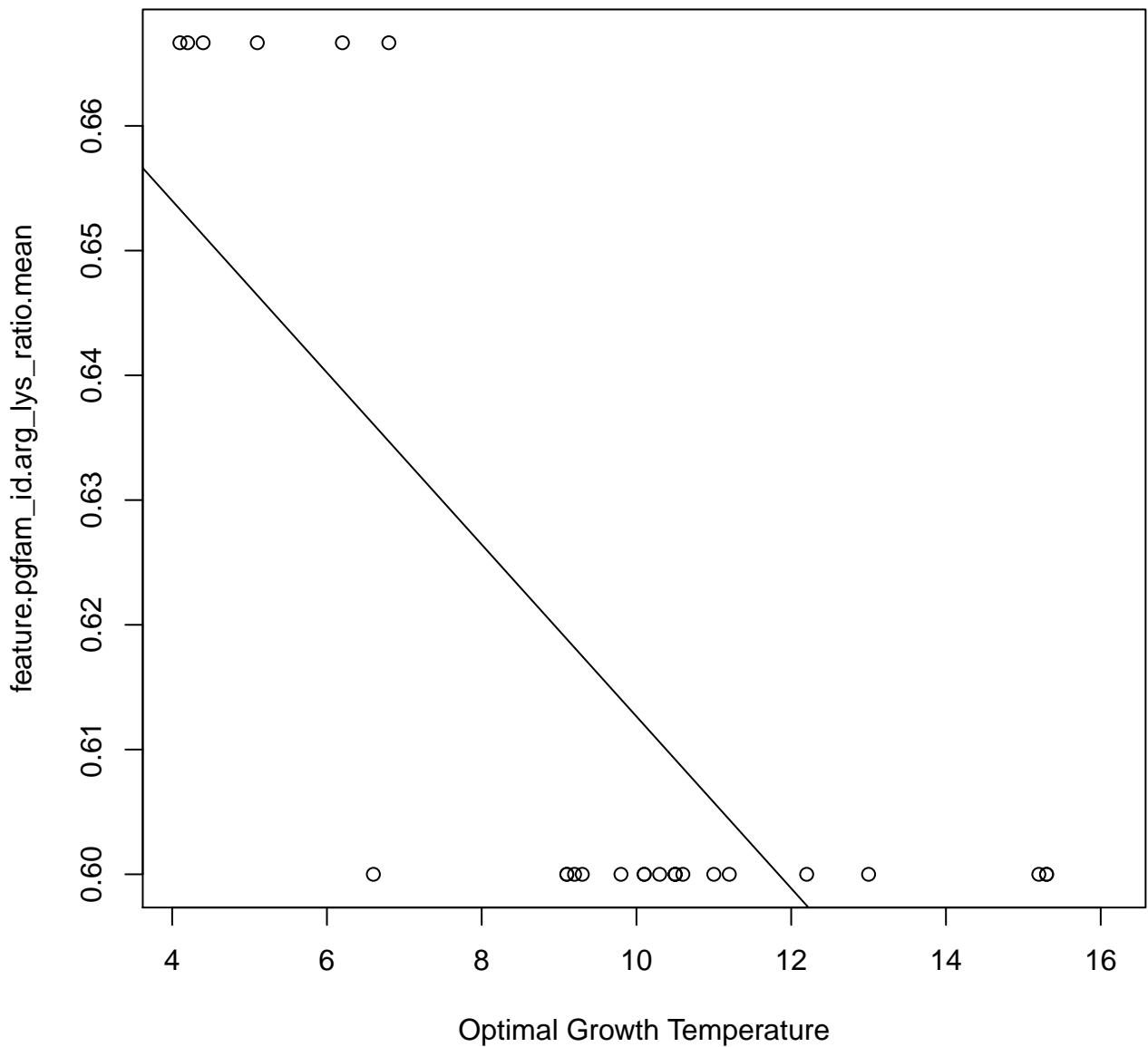
feature.pgfam_id.arg_lys_ratio.mean
PGF_10751741
Redoxin domain protein



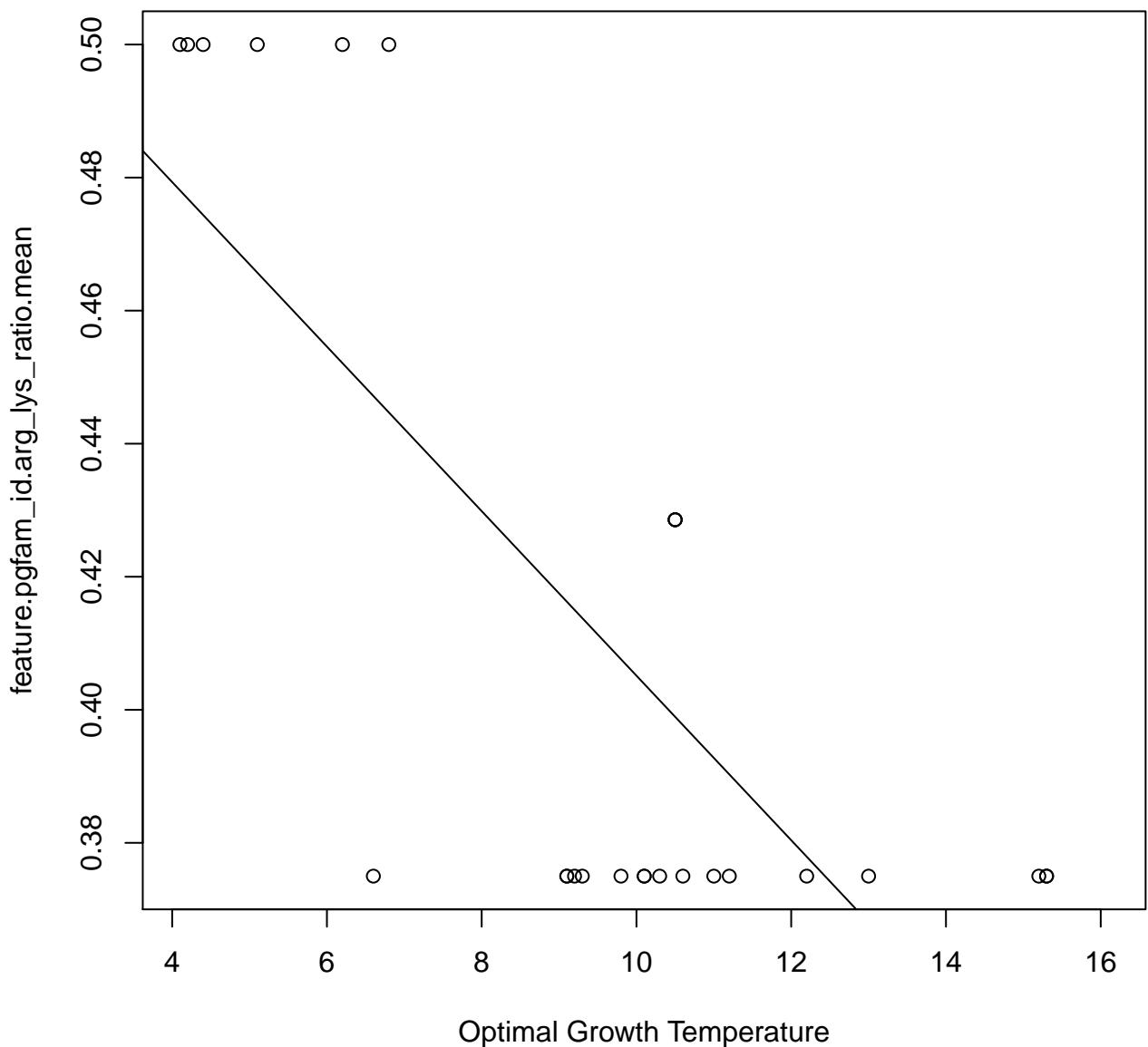
feature.pgfam_id.arg_lys_ratio.mean
PGF_10906072
hypothetical protein



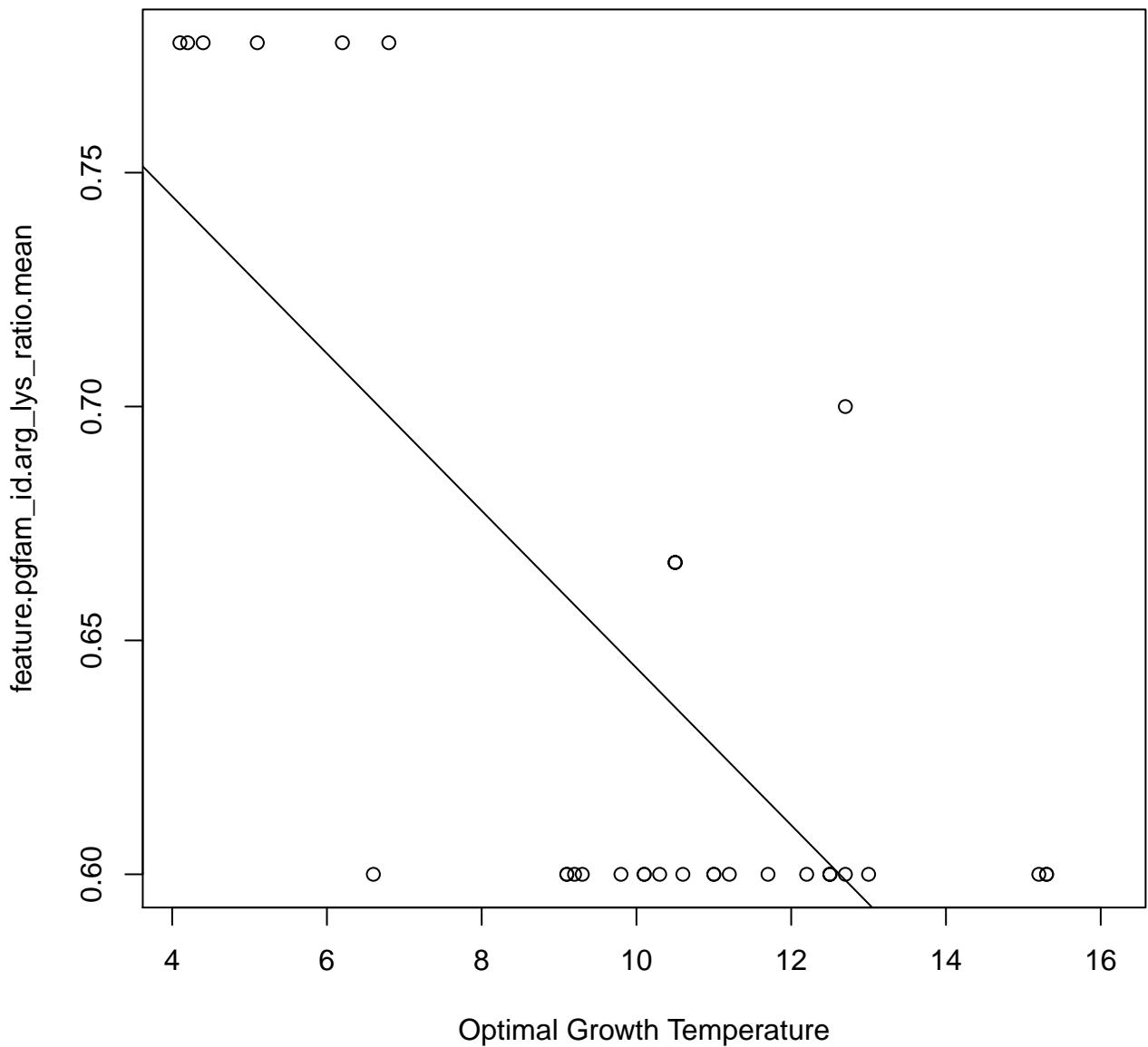
feature.pgfam_id.arg_lys_ratio.mean
PGF_12071964
hypothetical protein



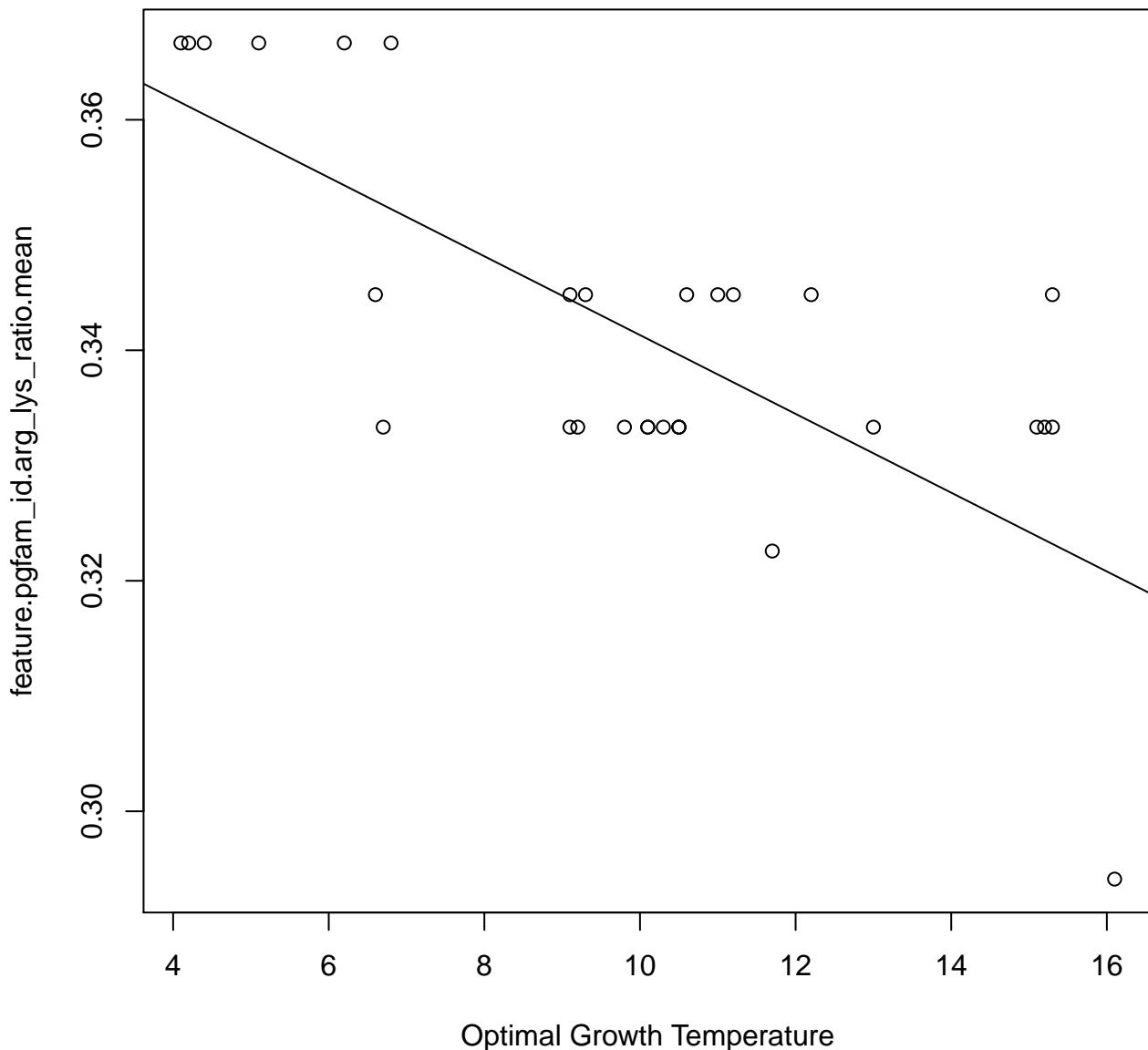
feature.pgfam_id.arg_lys_ratio.mean
PGF_11600935
hypothetical protein



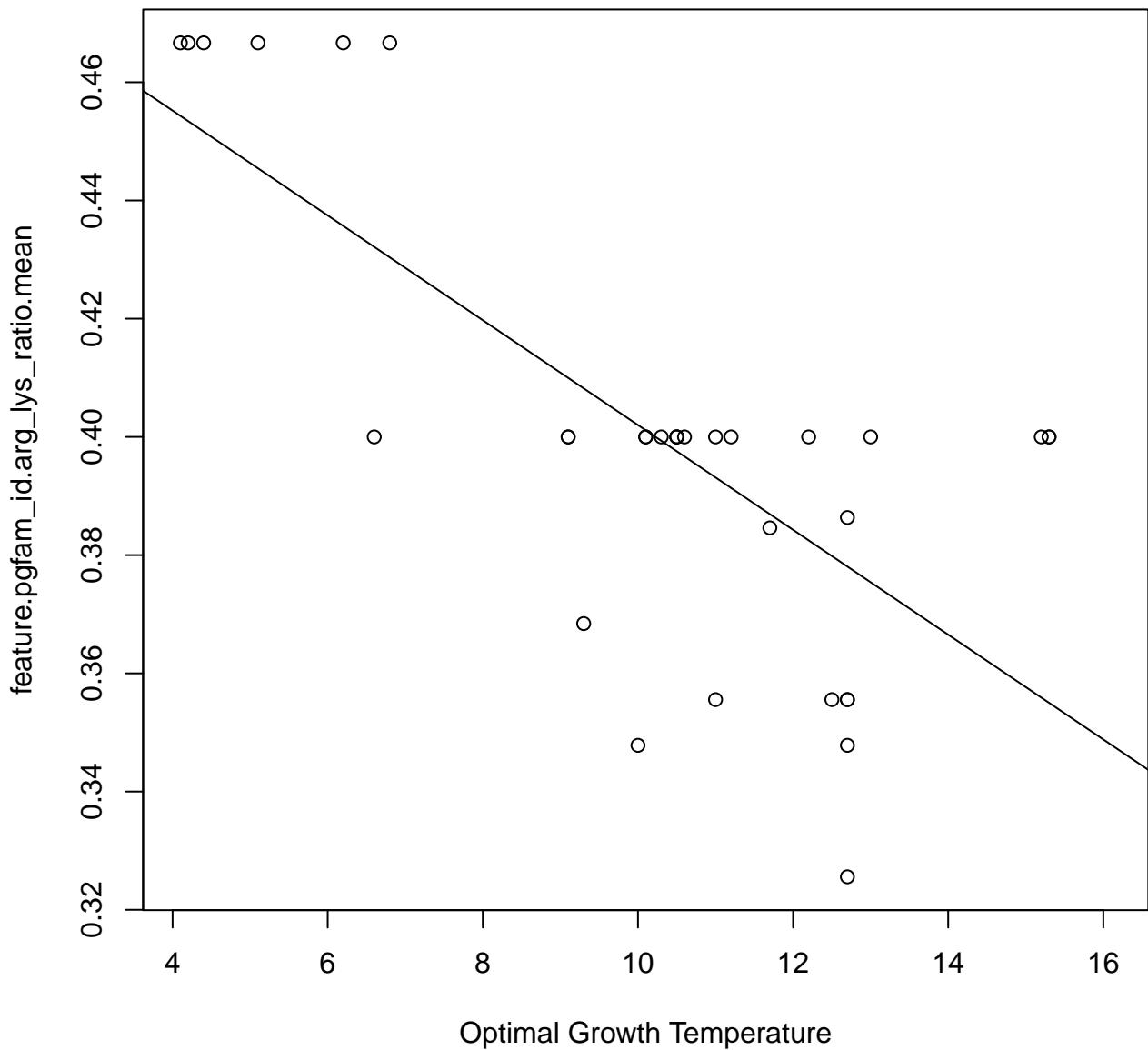
feature.pgfam_id.arg_lys_ratio.mean
PGF_00044582
Putative transmembrane protein



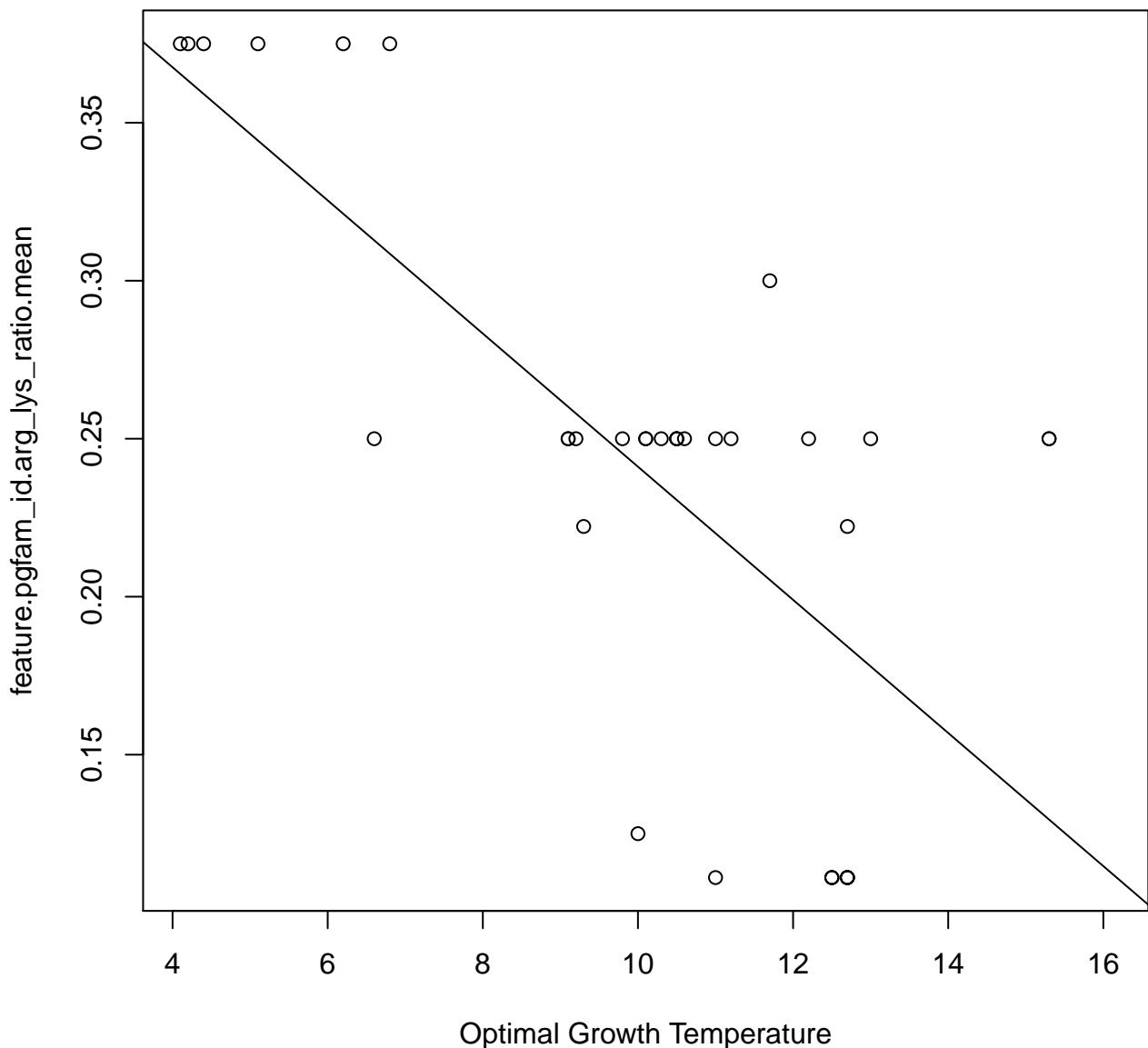
feature.pgfam_id.arg_lys_ratio.mean
PGF_00062002
Tryptophan 2,3-dioxygenase (EC 1.13.11.11)



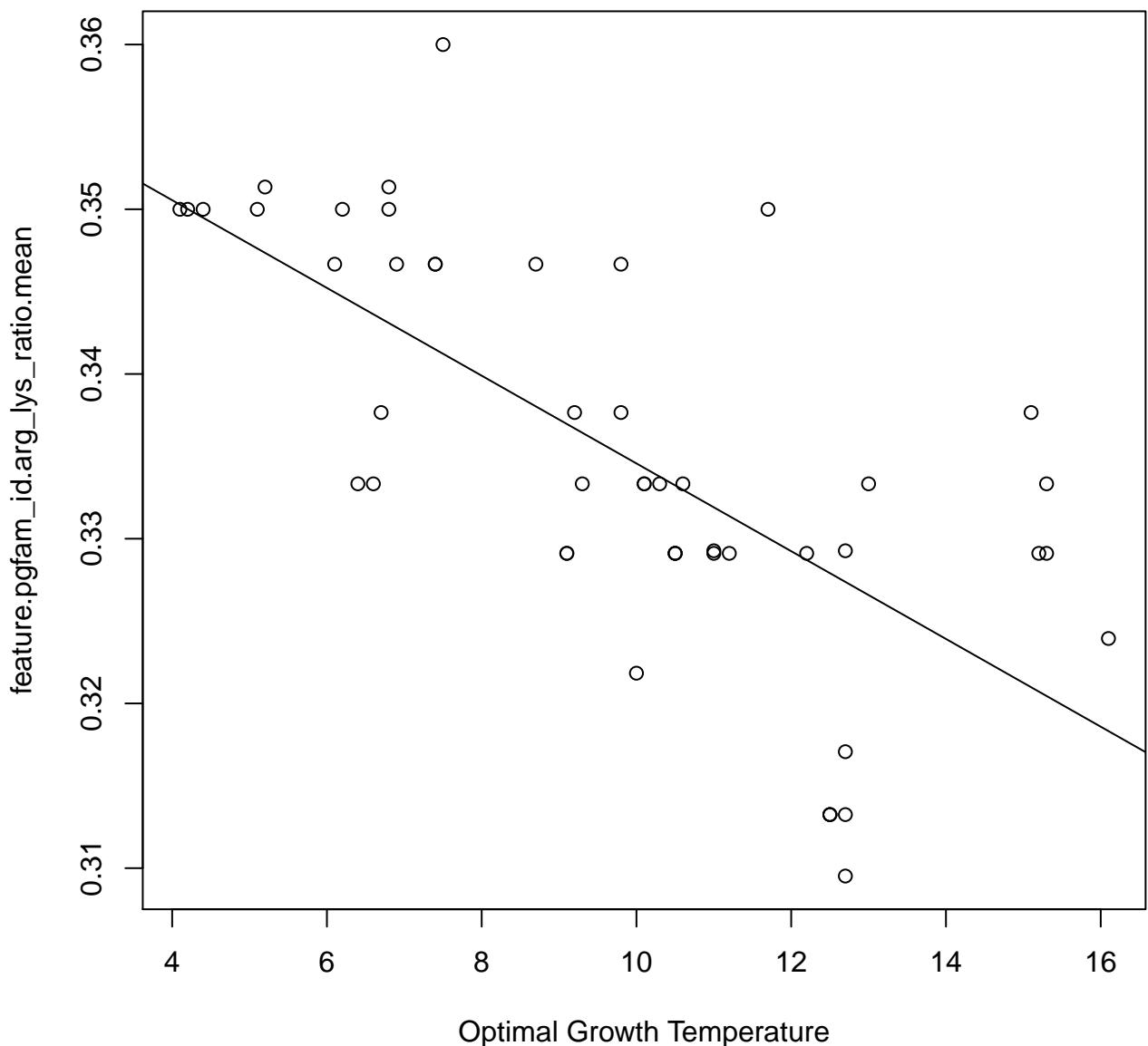
feature.pgfam_id.arg_lys_ratio.mean
PGF_12765299



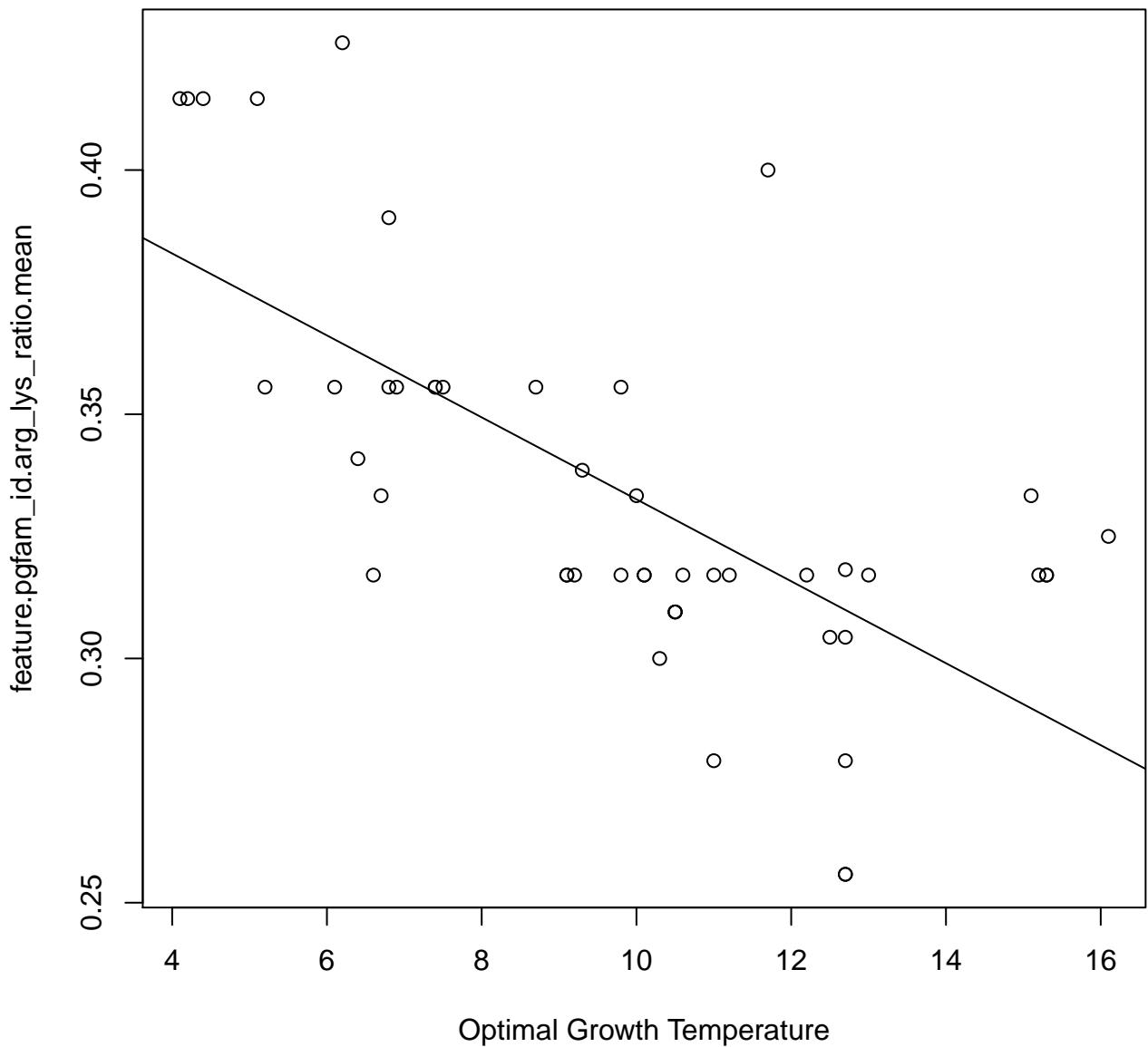
feature.pgfam_id.arg_lys_ratio.mean
PGF_01442793
Putative manganese efflux pump MntP



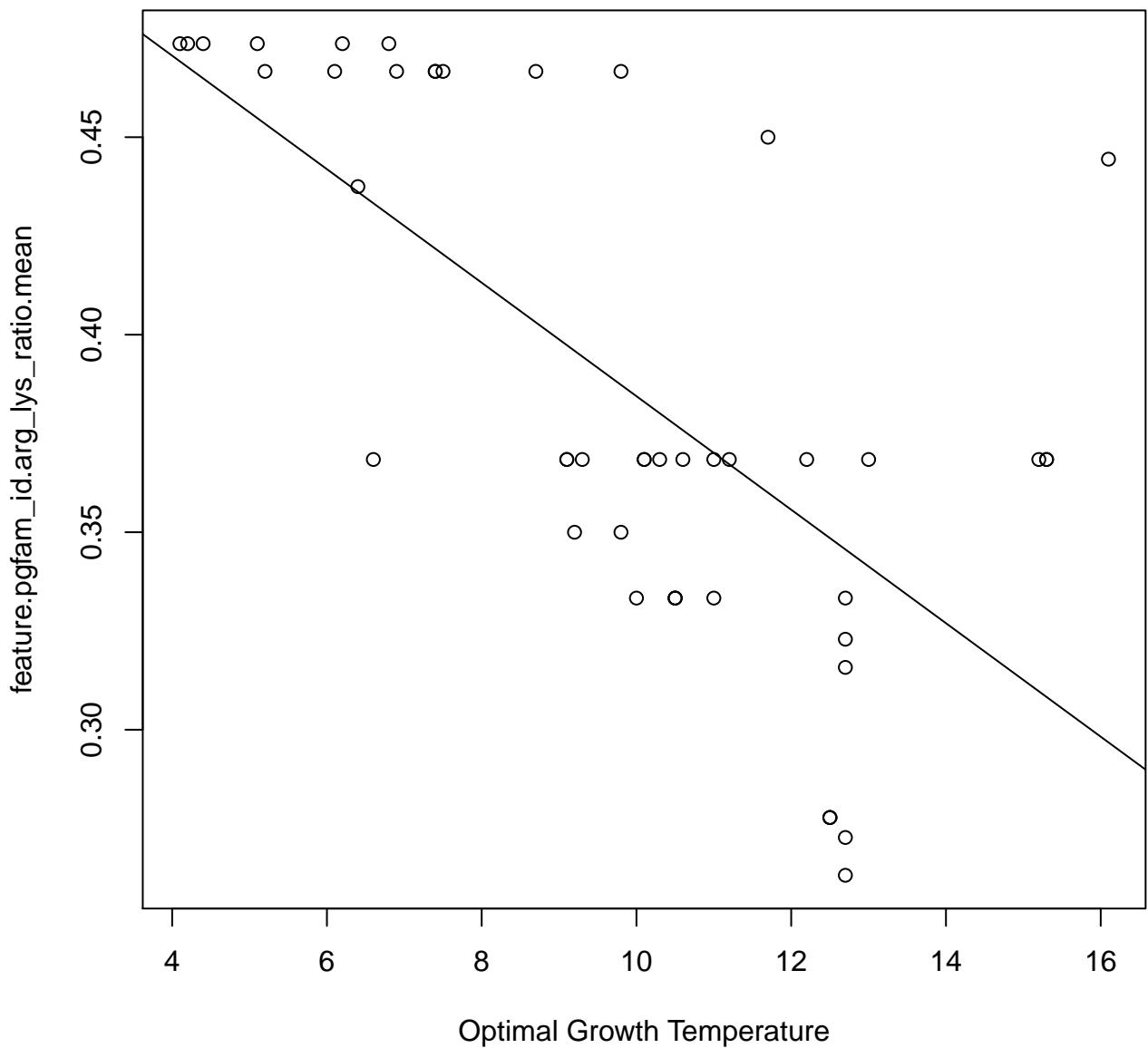
feature.pgfam_id.arg_lys_ratio.mean
PGF_00047484
Related to collagenase



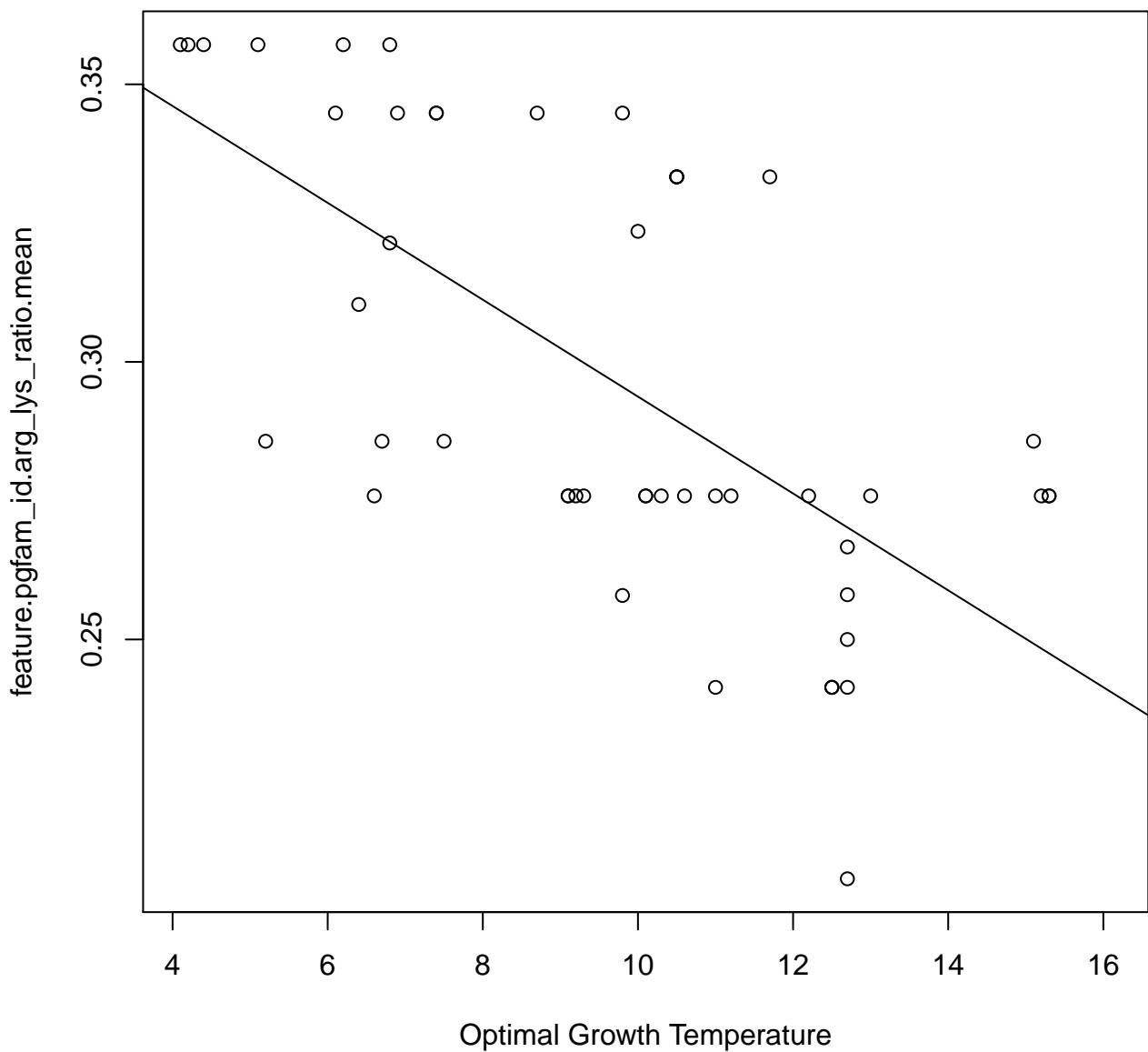
feature.pgfam_id.arg_lys_ratio.mean
PGF_06606669
Alanine transaminase (EC 2.6.1.2)



feature.pgfam_id.arg_lys_ratio.mean
PGF_00035421
Potential queD like 2



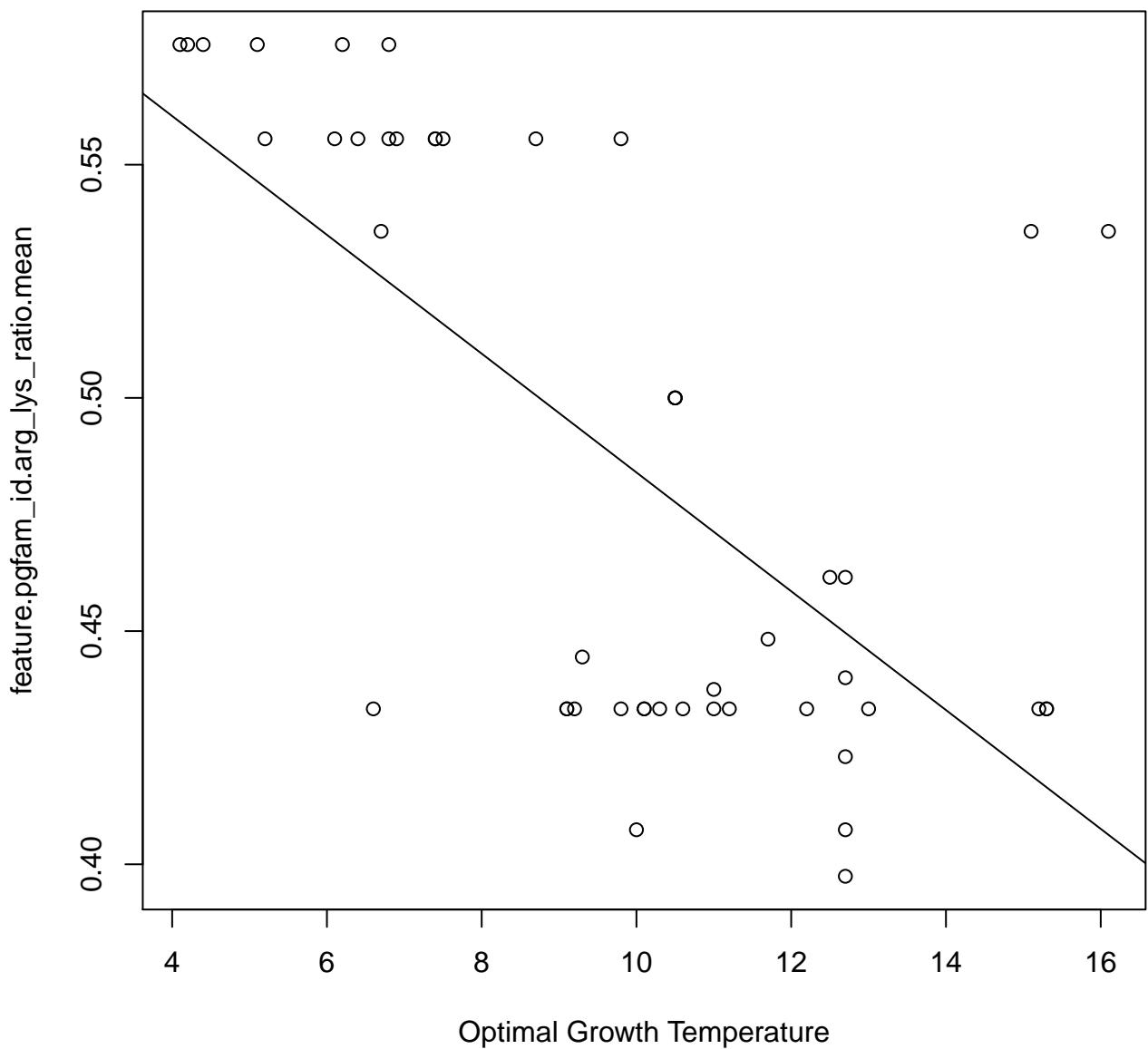
feature.pgfam_id.arg_lys_ratio.mean
PGF_00343871
hypothetical protein



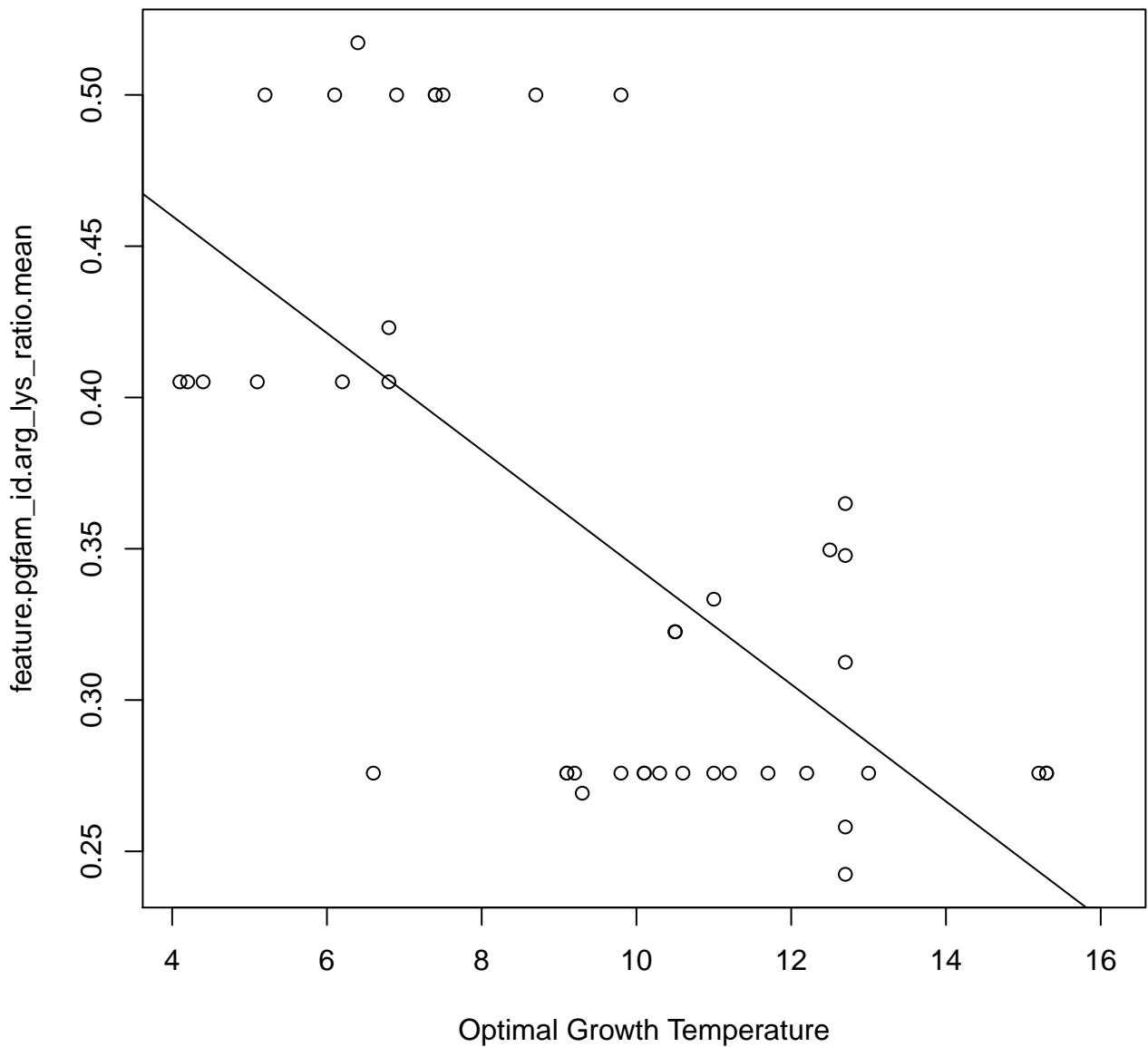
feature.pgfam_id.arg_lys_ratio.mean

PGF_06747785

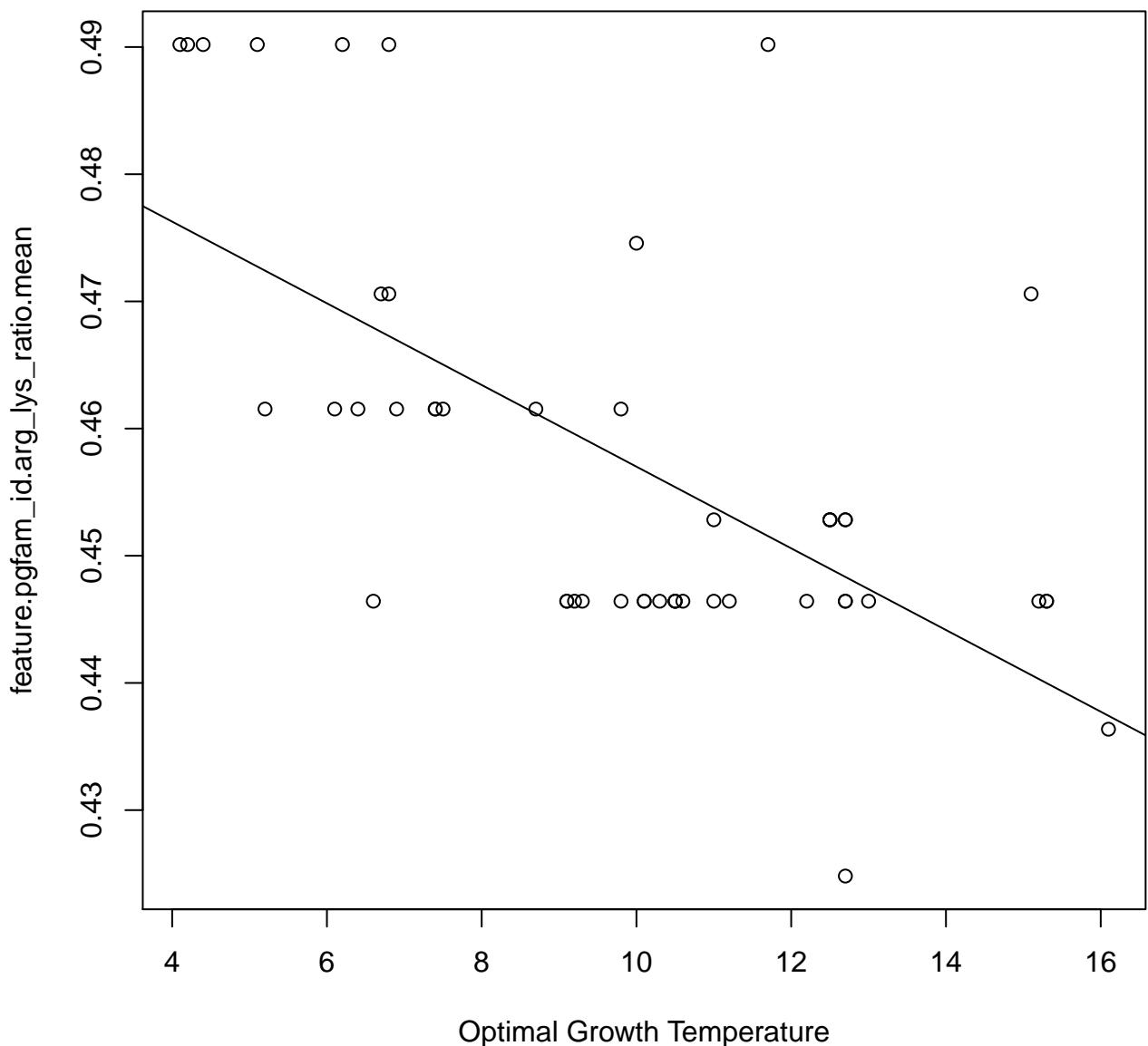
AmpG permease



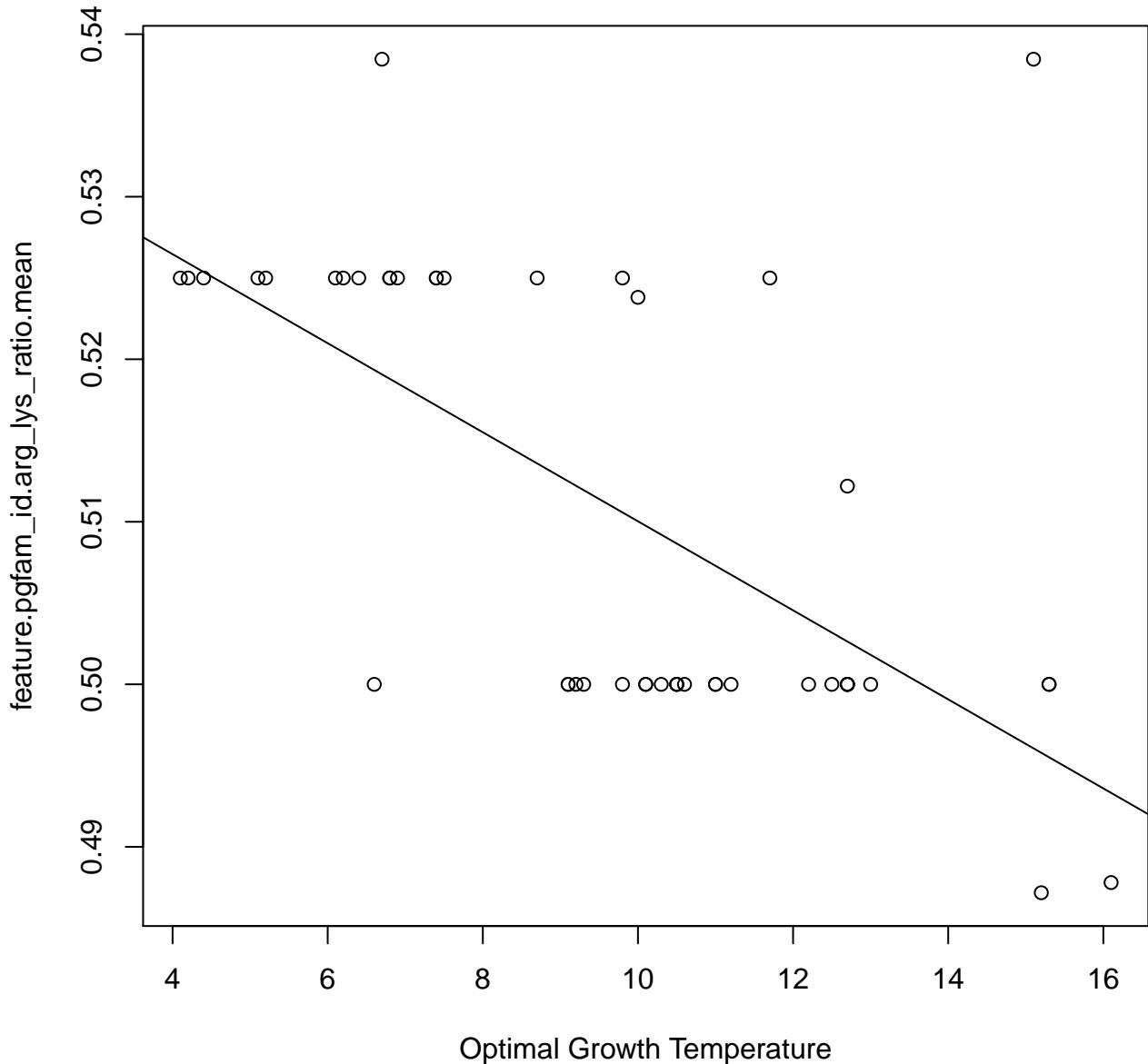
feature.pgfam_id.arg_lys_ratio.mean
PGF_12669666
FIG006045: Sigma factor, ECF subfamily



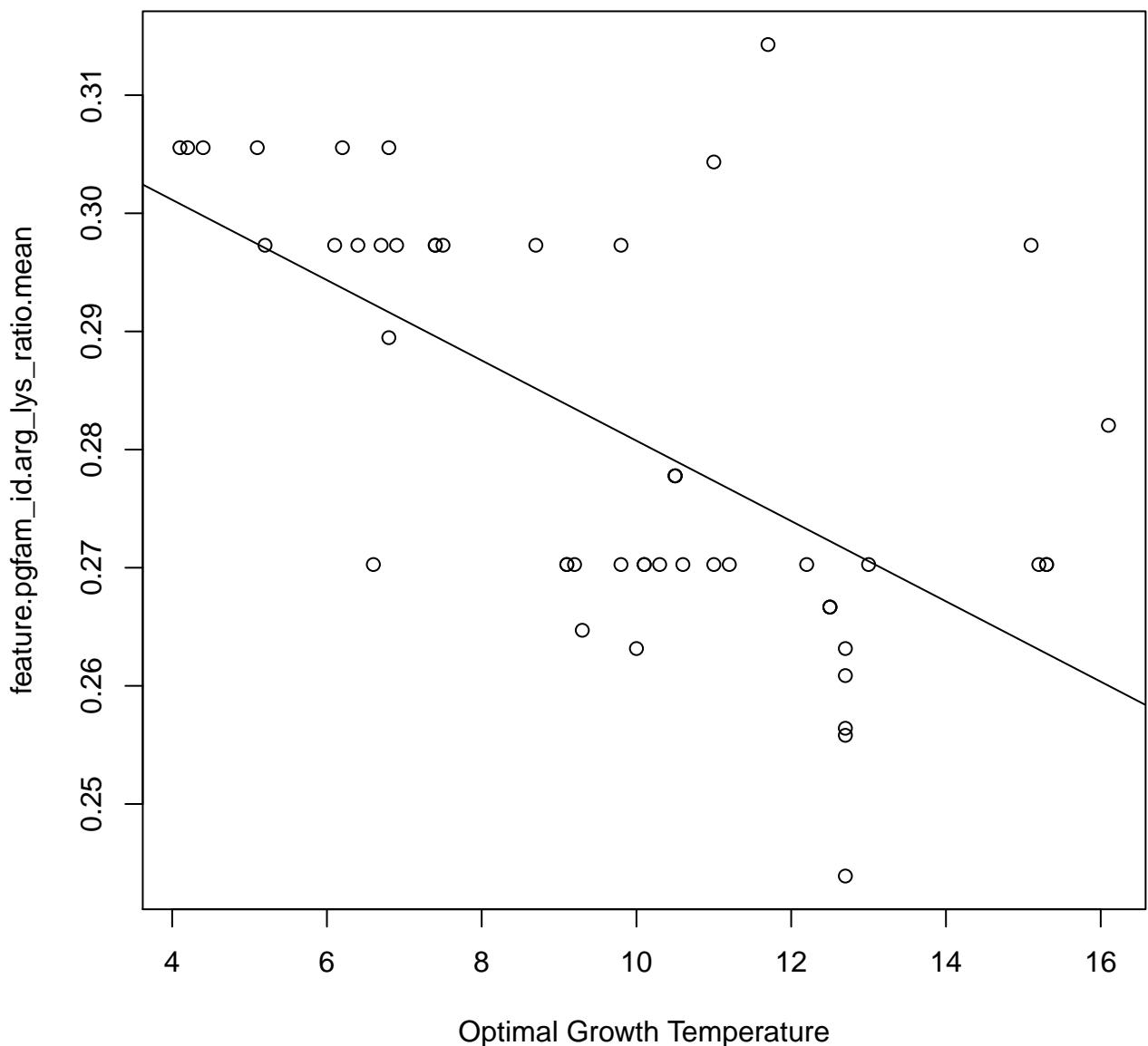
feature.pgfam_id.arg_lys_ratio.mean
PGF_00015709
Isocitrate lyase (EC 4.1.3.1)



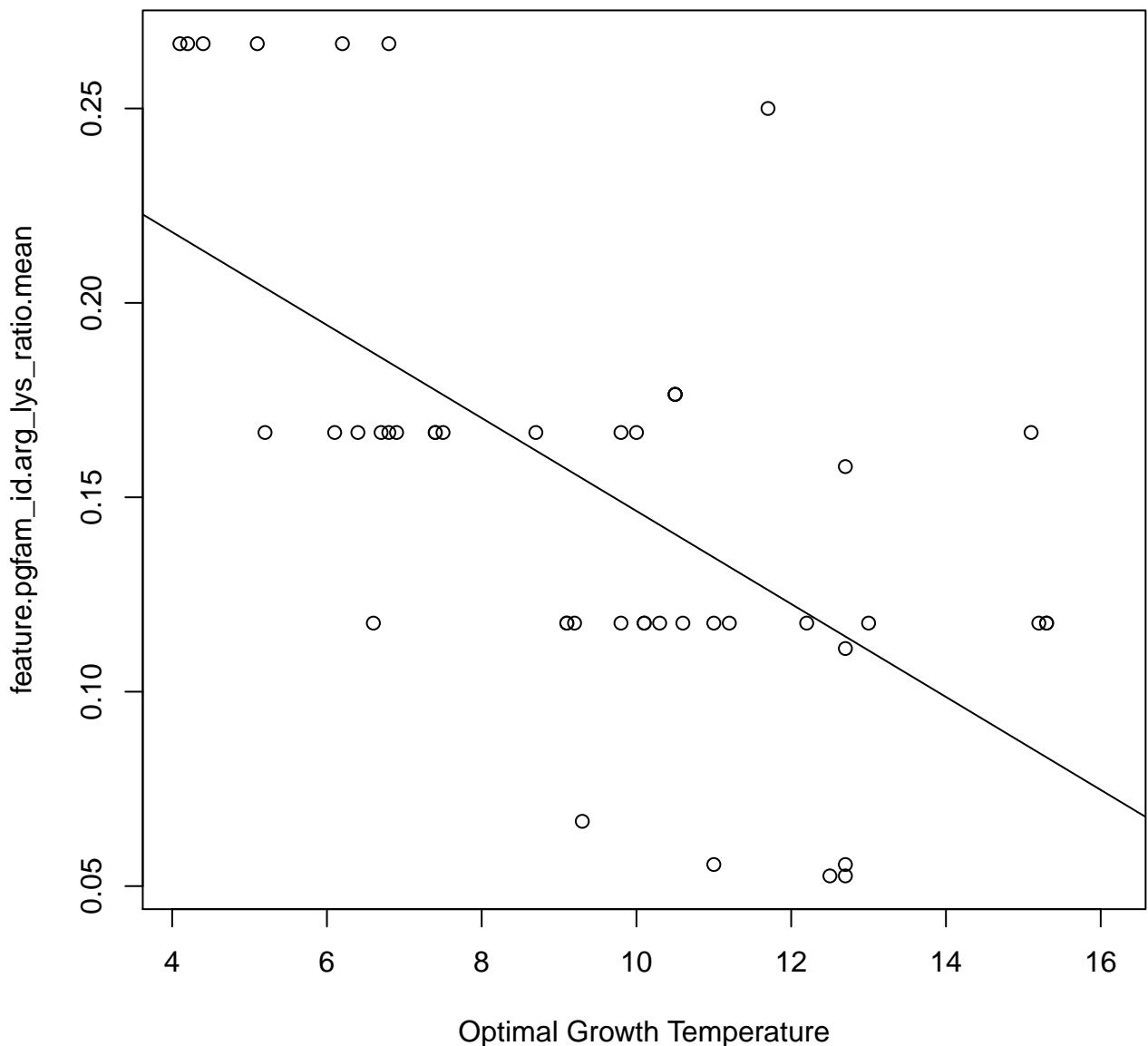
feature.pgfam_id.arg_lys_ratio.mean
PGF_06473395
DNA polymerase III beta subunit (EC 2.7.7.7)



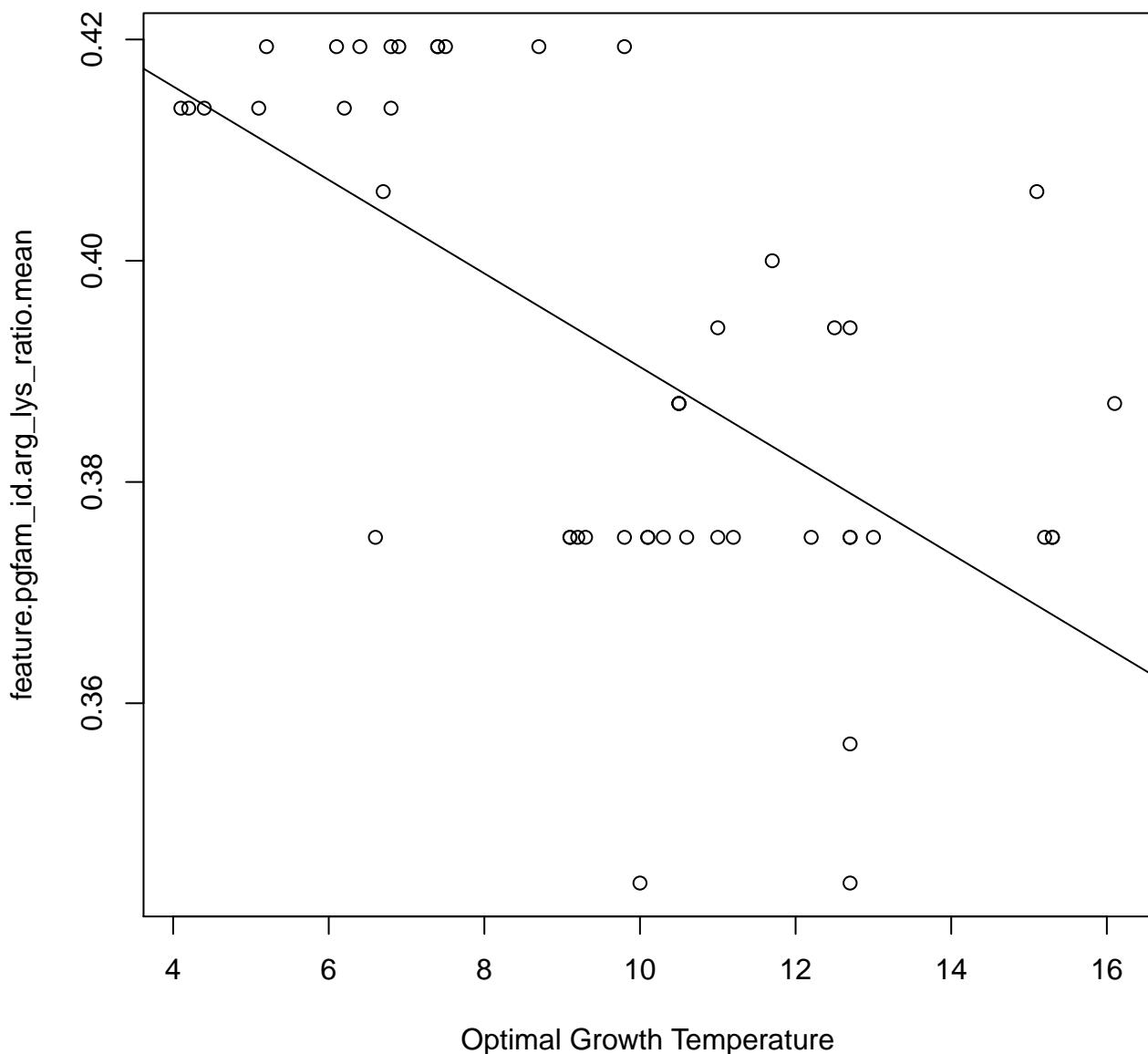
feature.pgfam_id.arg_lys_ratio.mean
PGF_01336369
hypothetical protein



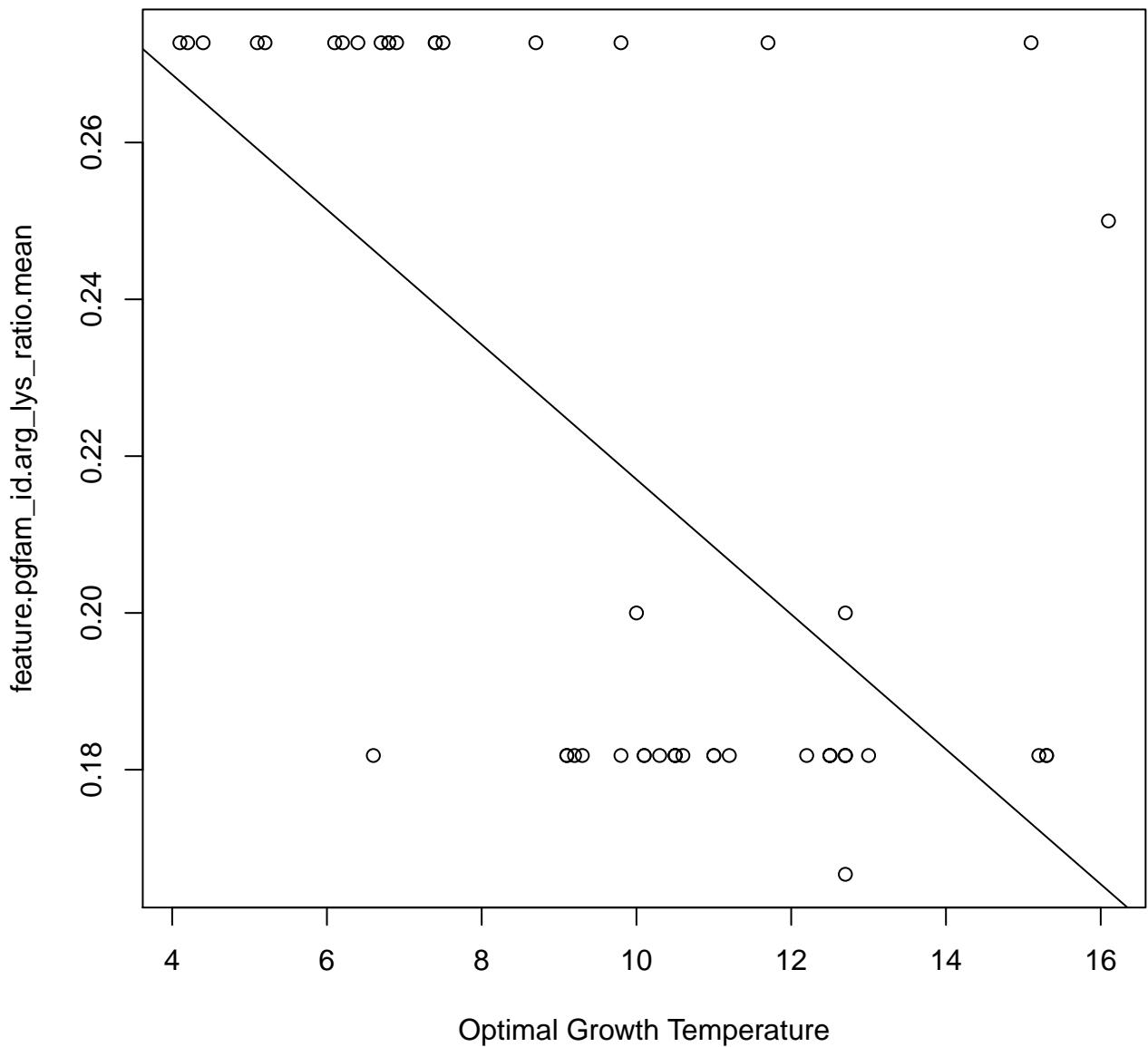
feature.pgfam_id.arg_lys_ratio.mean
PGF_08252890
hypothetical protein



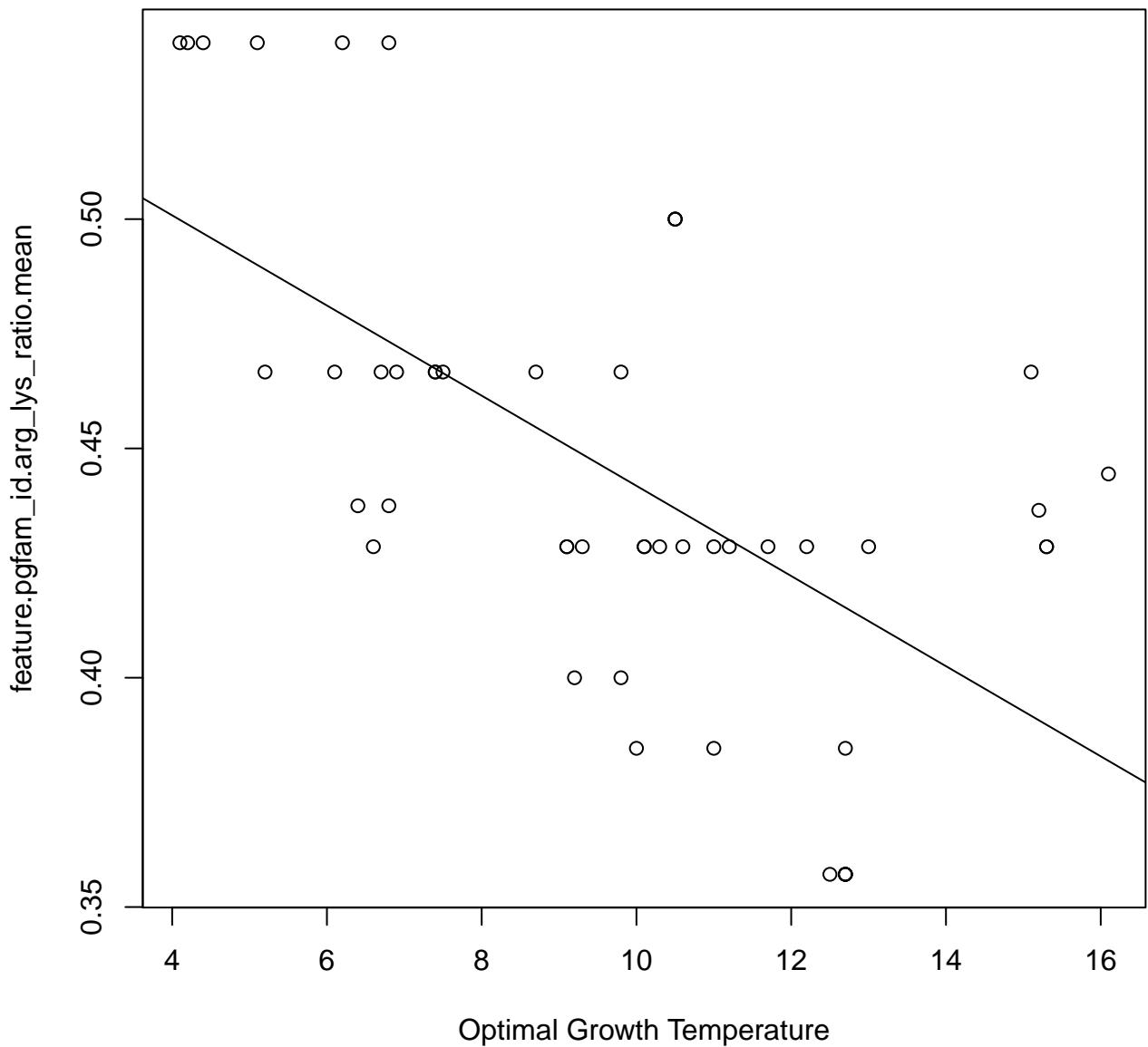
feature.pgfam_id.arg_lys_ratio.mean
PGF_03237586
L-threonine 3-dehydrogenase (EC 1.1.1.103)



feature.pgfam_id.arg_lys_ratio.mean
PGF_02744871
Flagellar hook–basal body complex protein FliE



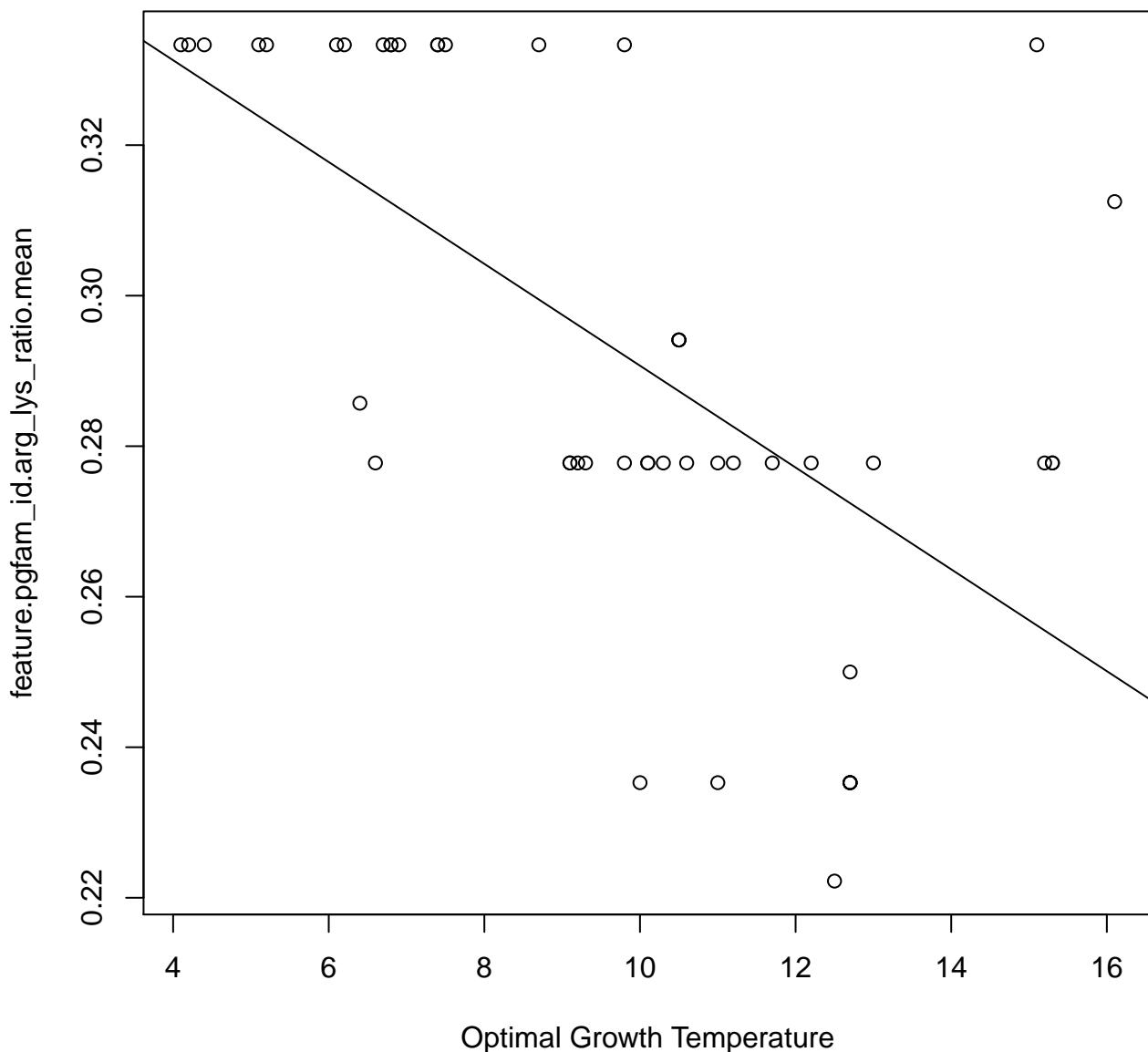
feature.pgfam_id.arg_lys_ratio.mean
PGF_09375481
Uncharacterized protein YfgD, not an arsenate reductase



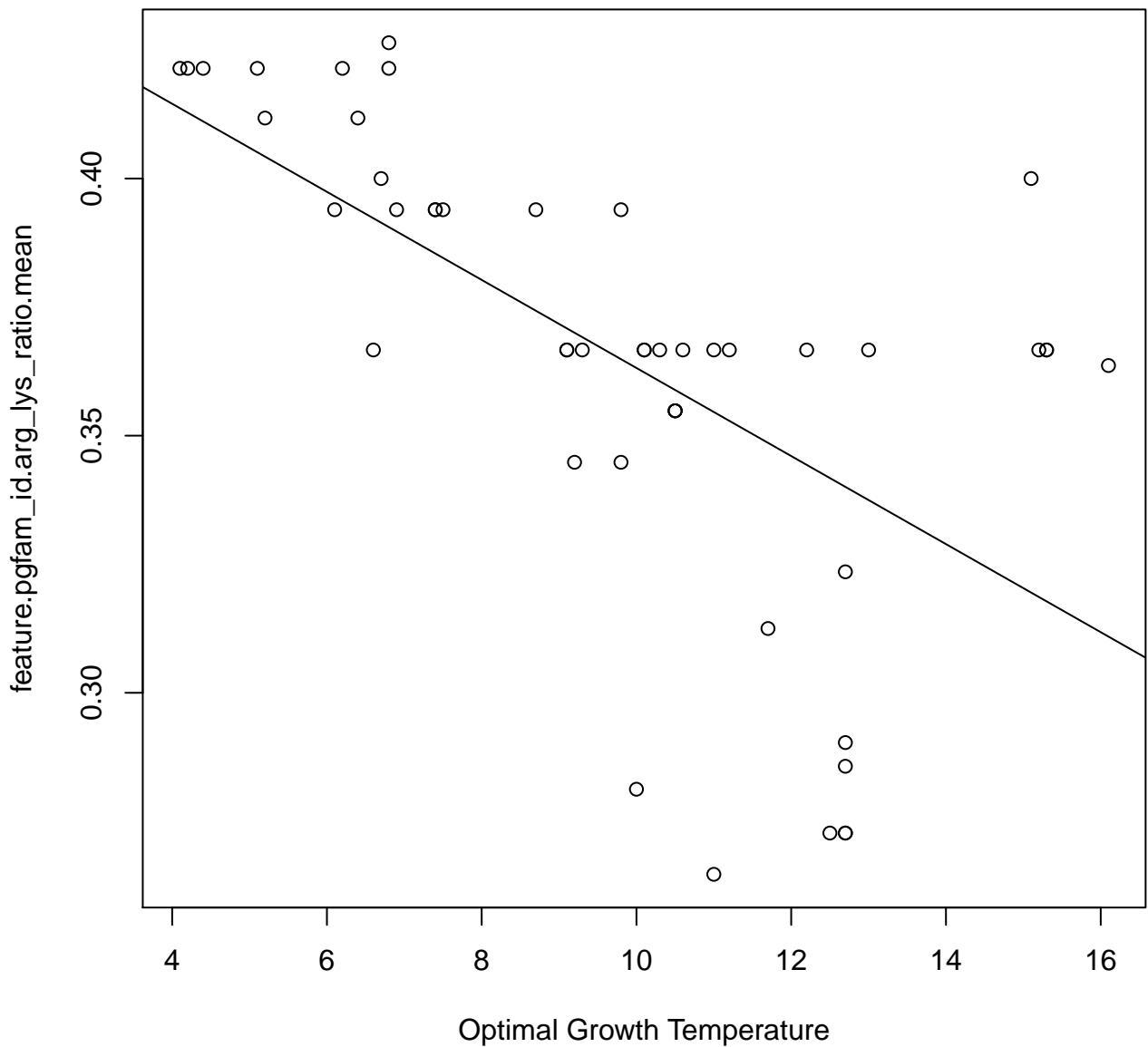
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PGF_02658061

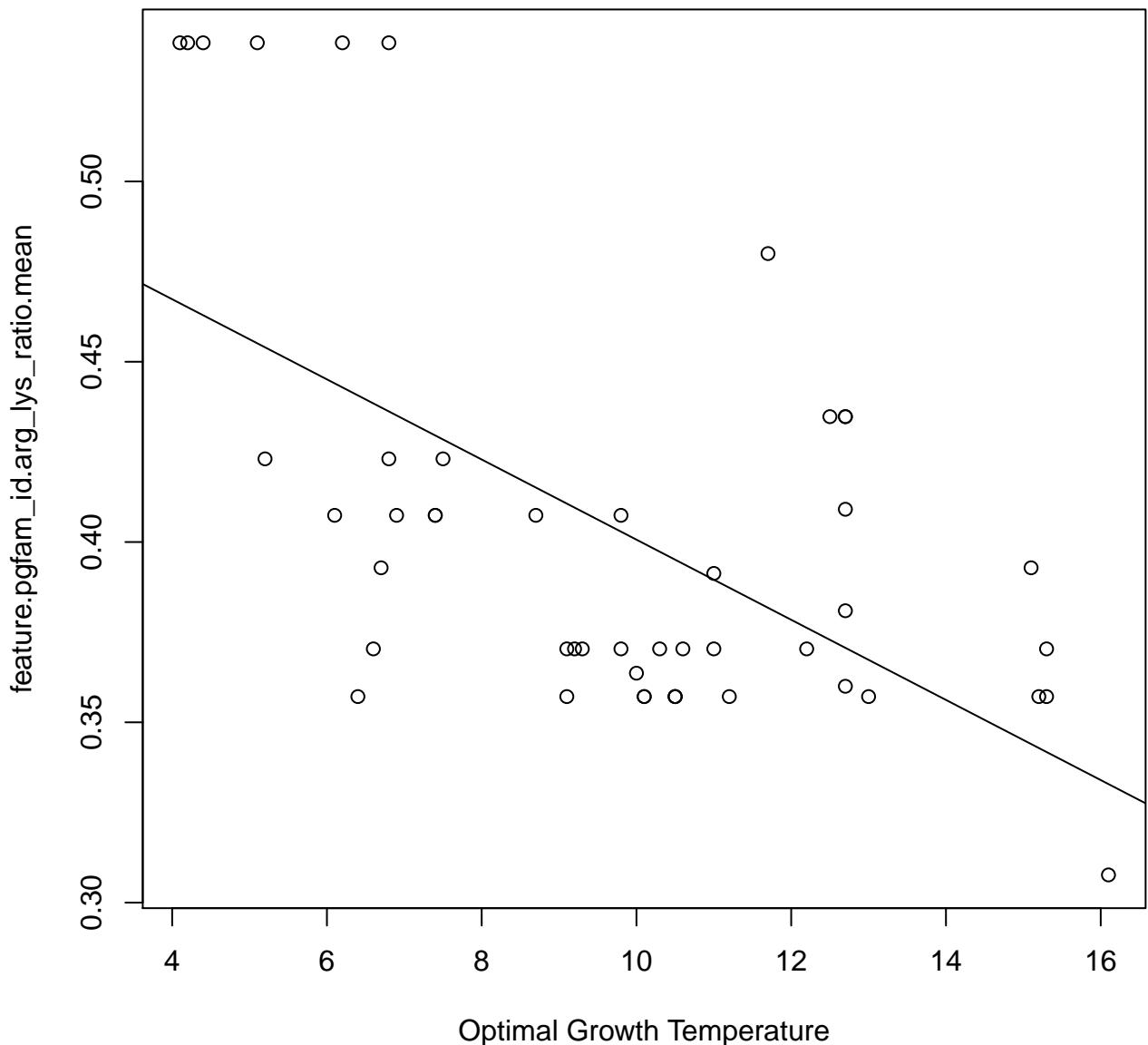
Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)



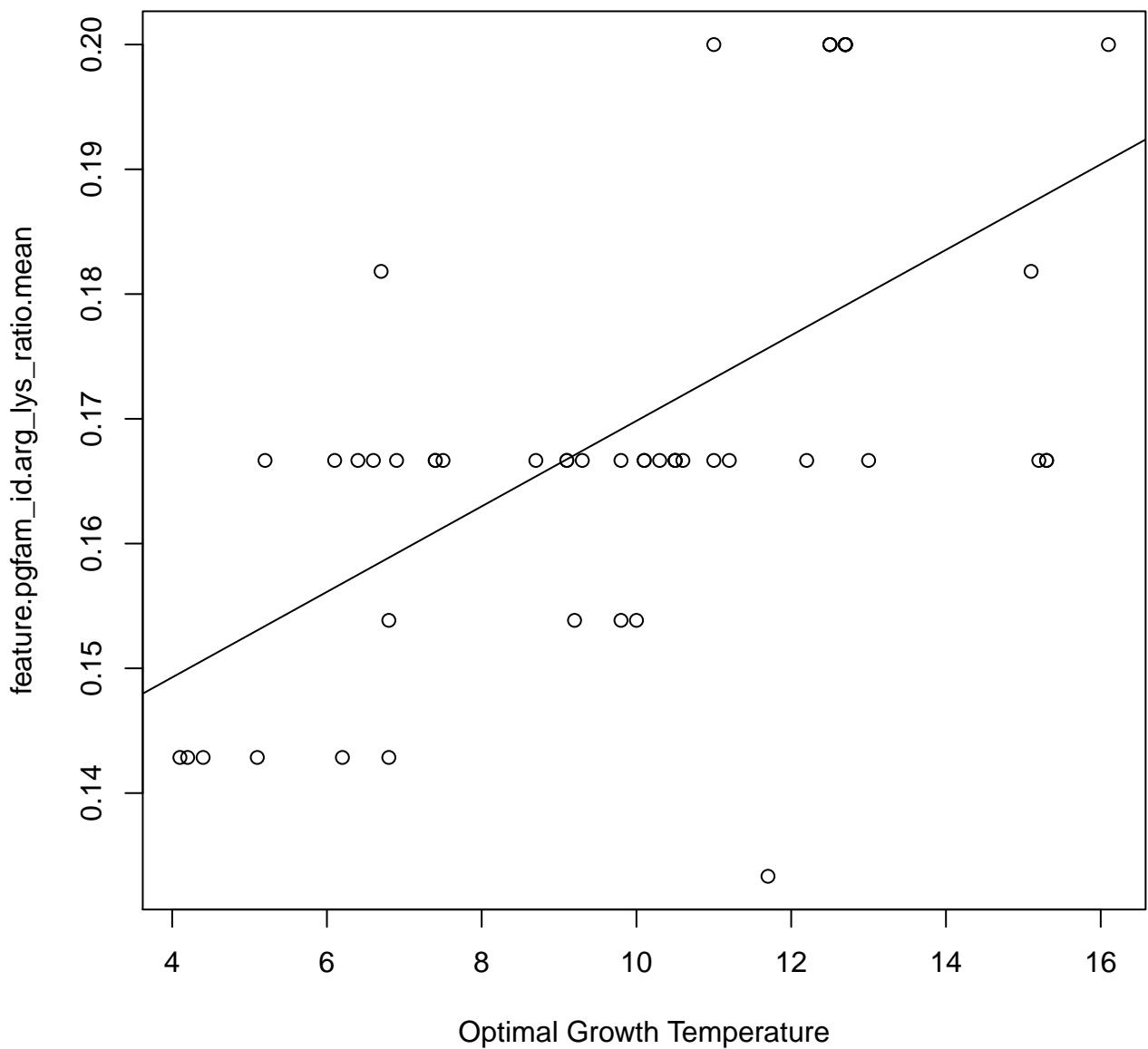
feature.pgfam_id.arg_lys_ratio.mean
PGF_10414515
Nucleoside triphosphate pyrophosphohydrolase MazG (EC 3.6.1.8)



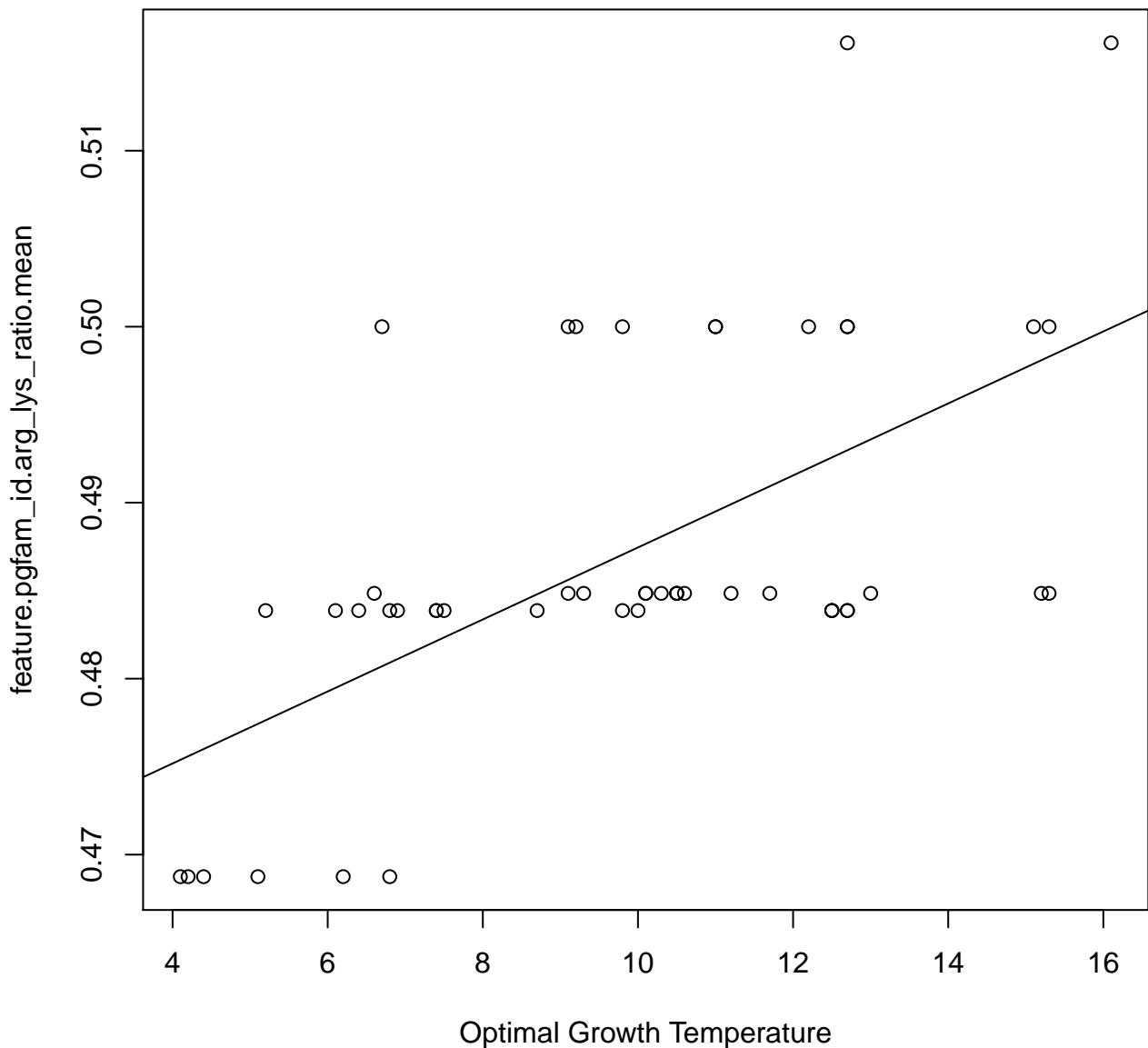
feature.pgfam_id.arg_lys_ratio.mean
PGF_00523822
Pantoate--beta-alanine ligase (EC 6.3.2.1)



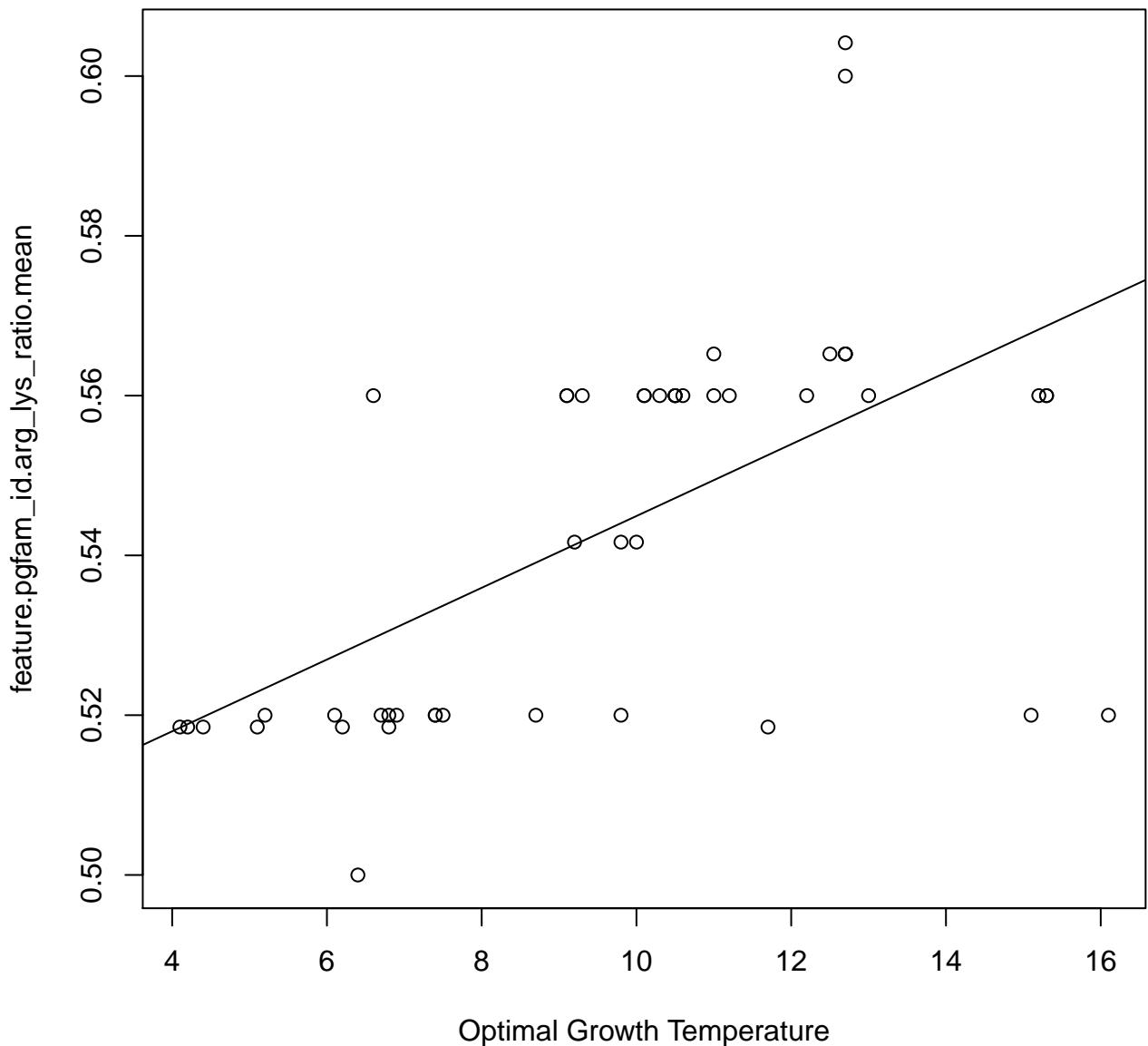
feature.pgfam_id.arg_lys_ratio.mean
PGF_00059675
Antioxidant, AhpC/Tsa family



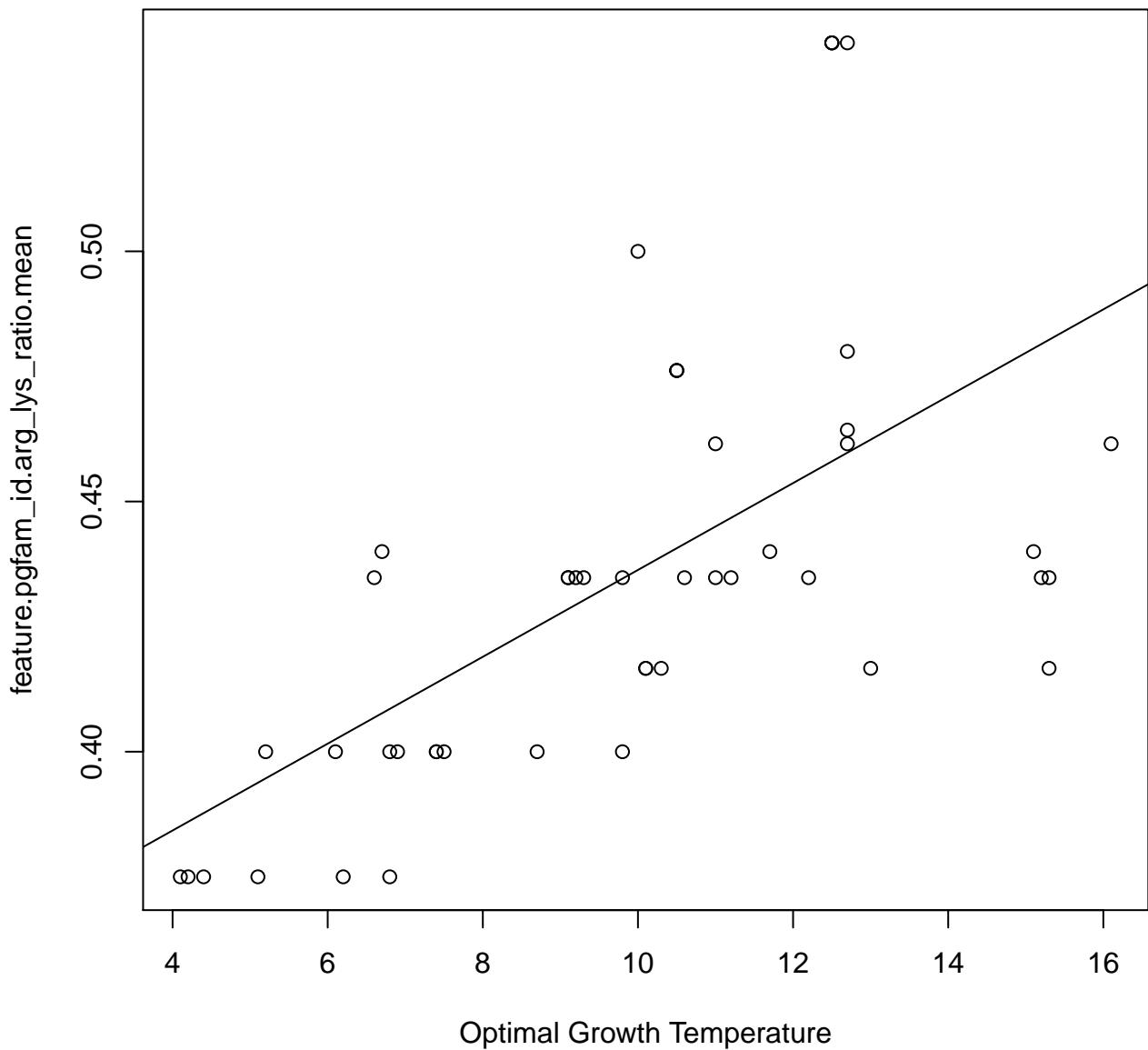
feature.pgfam_id.arg_lys_ratio.mean
PGF_00413295
tRNA pseudouridine(55) synthase (EC 5.4.99.25)



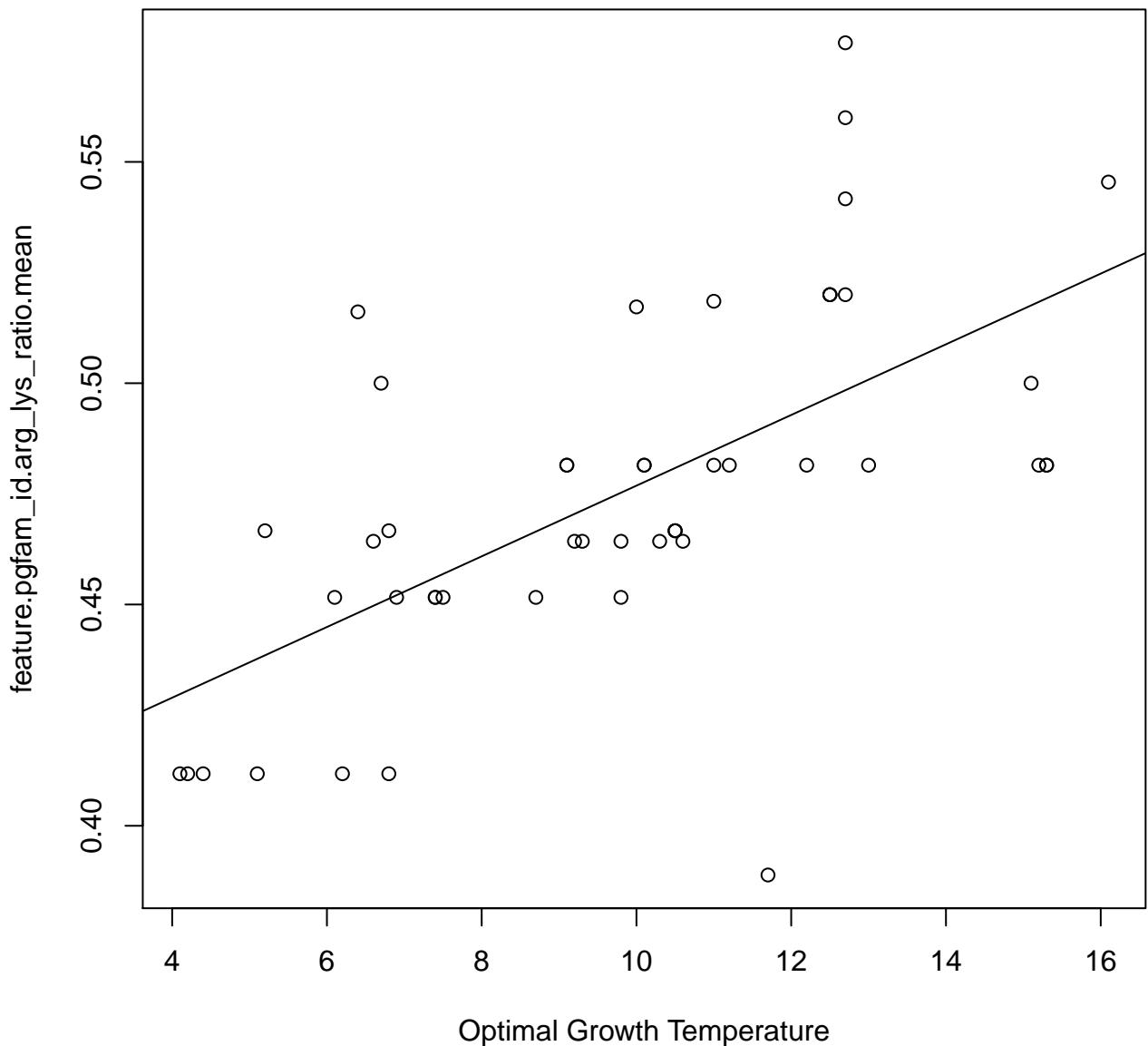
feature.pgfam_id.arg_lys_ratio.mean
PGF_10697445
Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8)



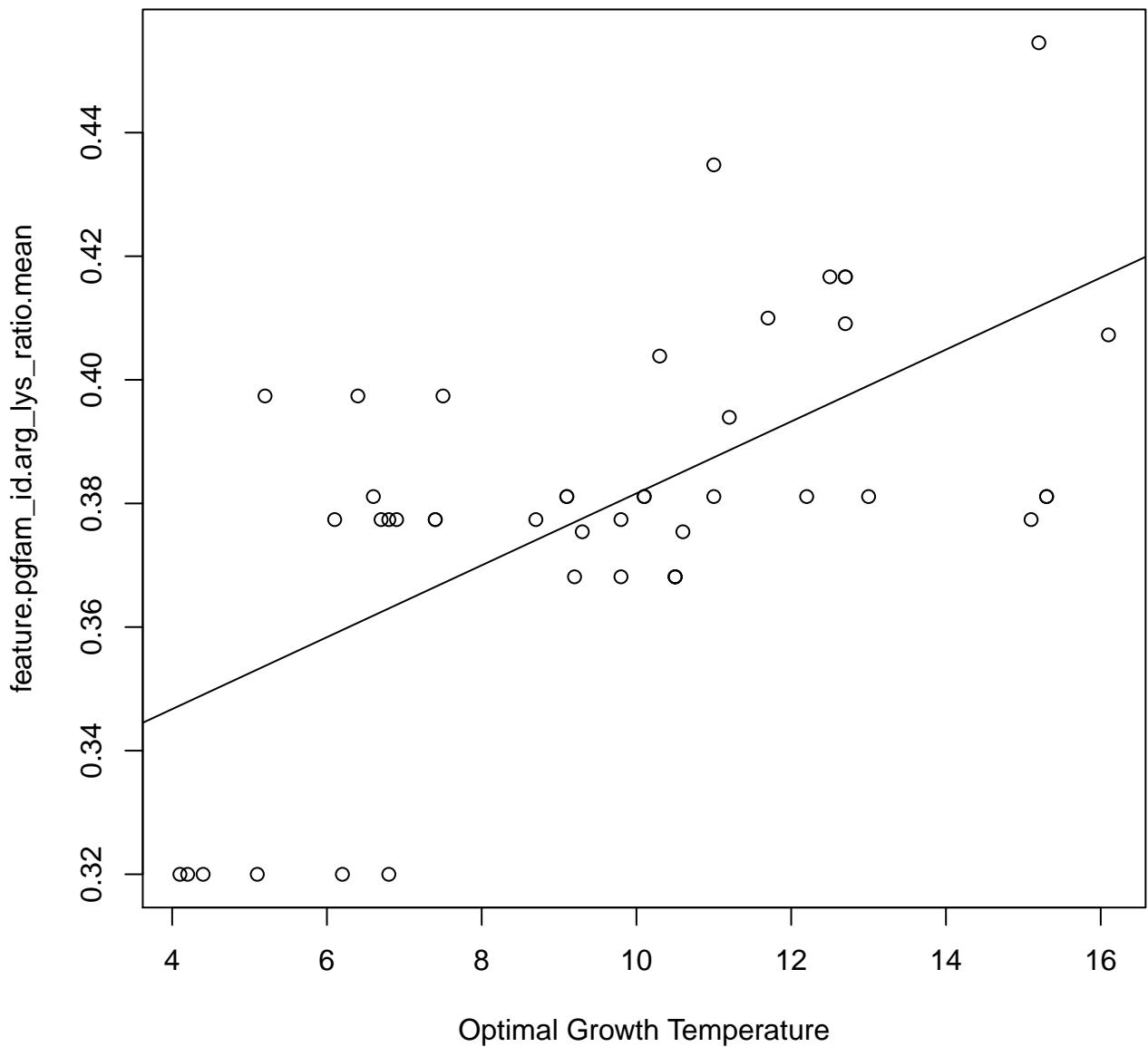
feature.pgfam_id.arg_lys_ratio.mean
PGF_01737958
2-haloalkanoic acid dehalogenase (EC 3.8.1.2)



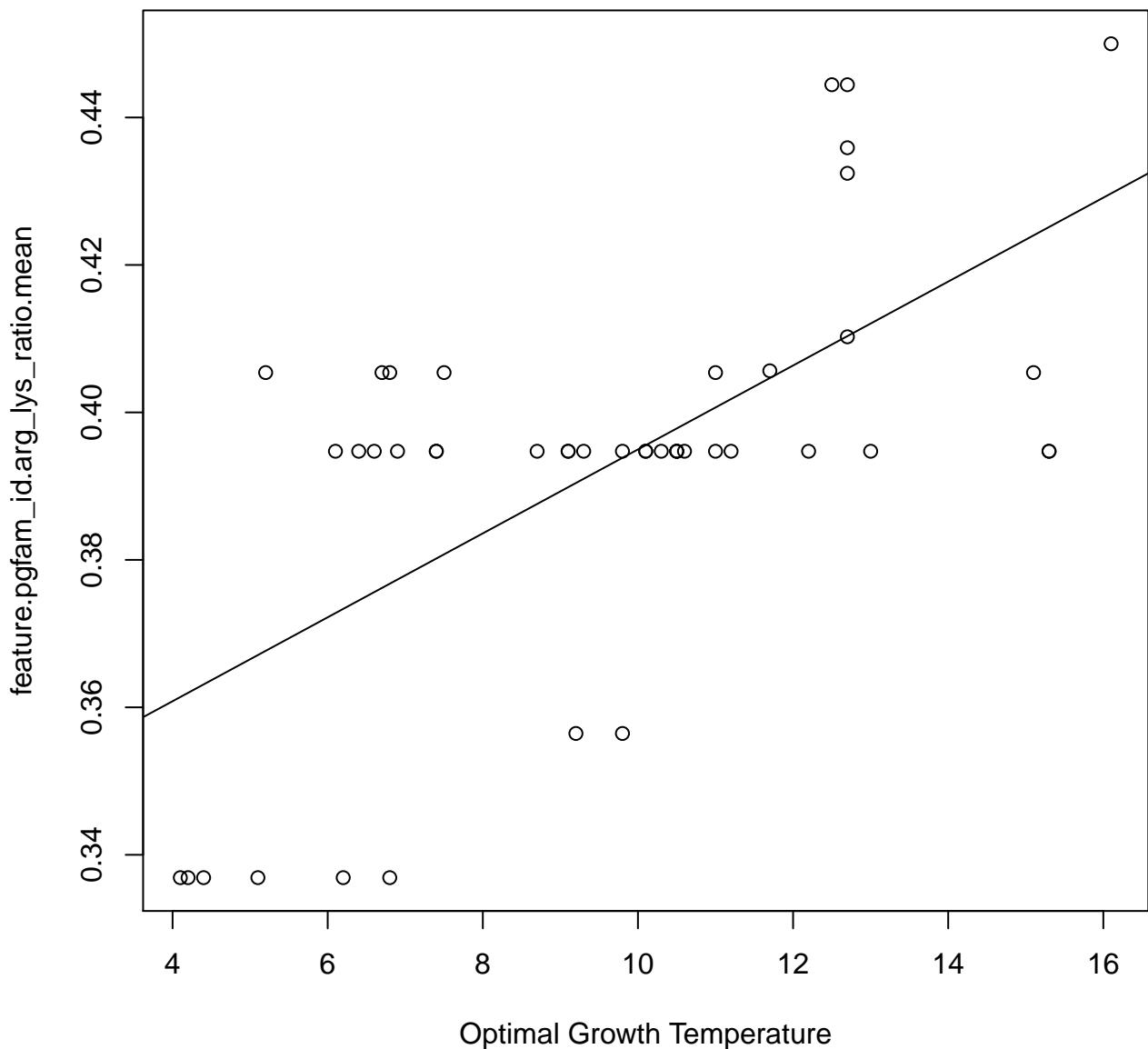
feature.pgfam_id.arg_lys_ratio.mean
PGF_01782190
3-deoxy-D-manno-octulose-4-acid kinase (EC 2.7.1.166)



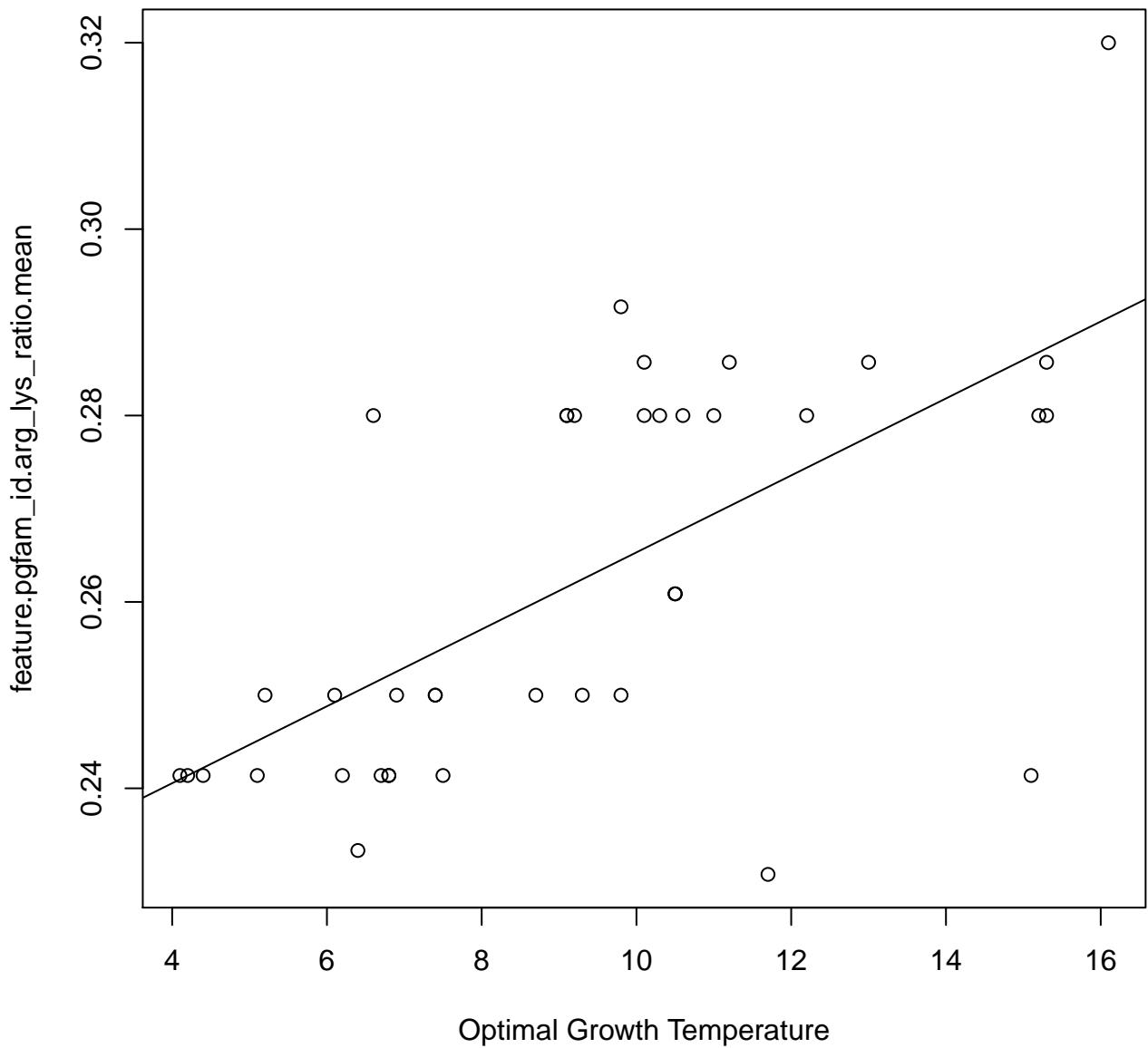
feature.pgfam_id.arg_lys_ratio.mean
PGF_07370053
RNA polymerase sigma-70 factor



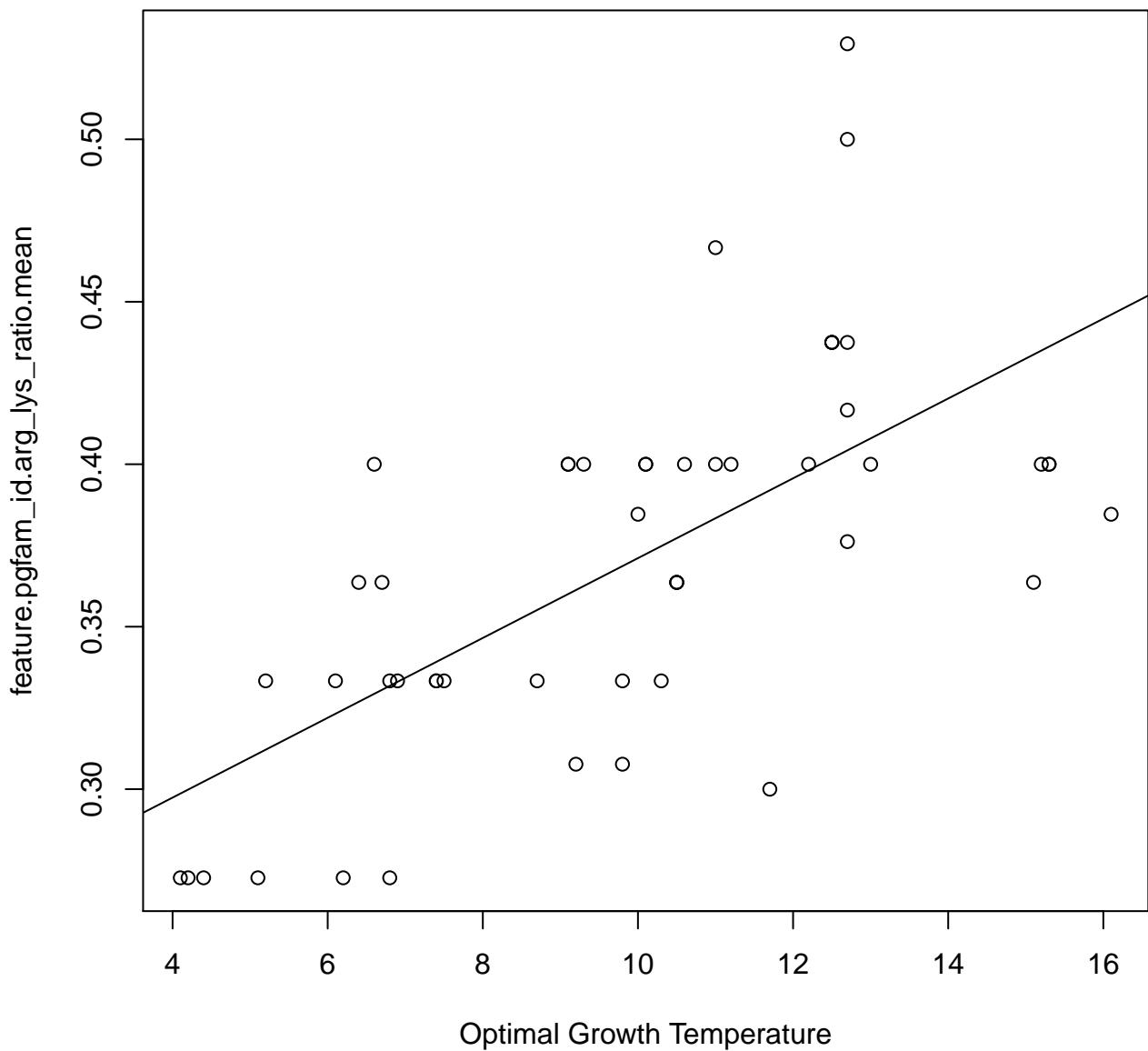
feature.pgfam_id.arg_lys_ratio.mean
PGF_02820072
aminotransferase, Class III pyridoxal-phosphate dependent



feature.pgfam_id.arg_lys_ratio.mean
PGF_00049322
S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50), eukaryotic



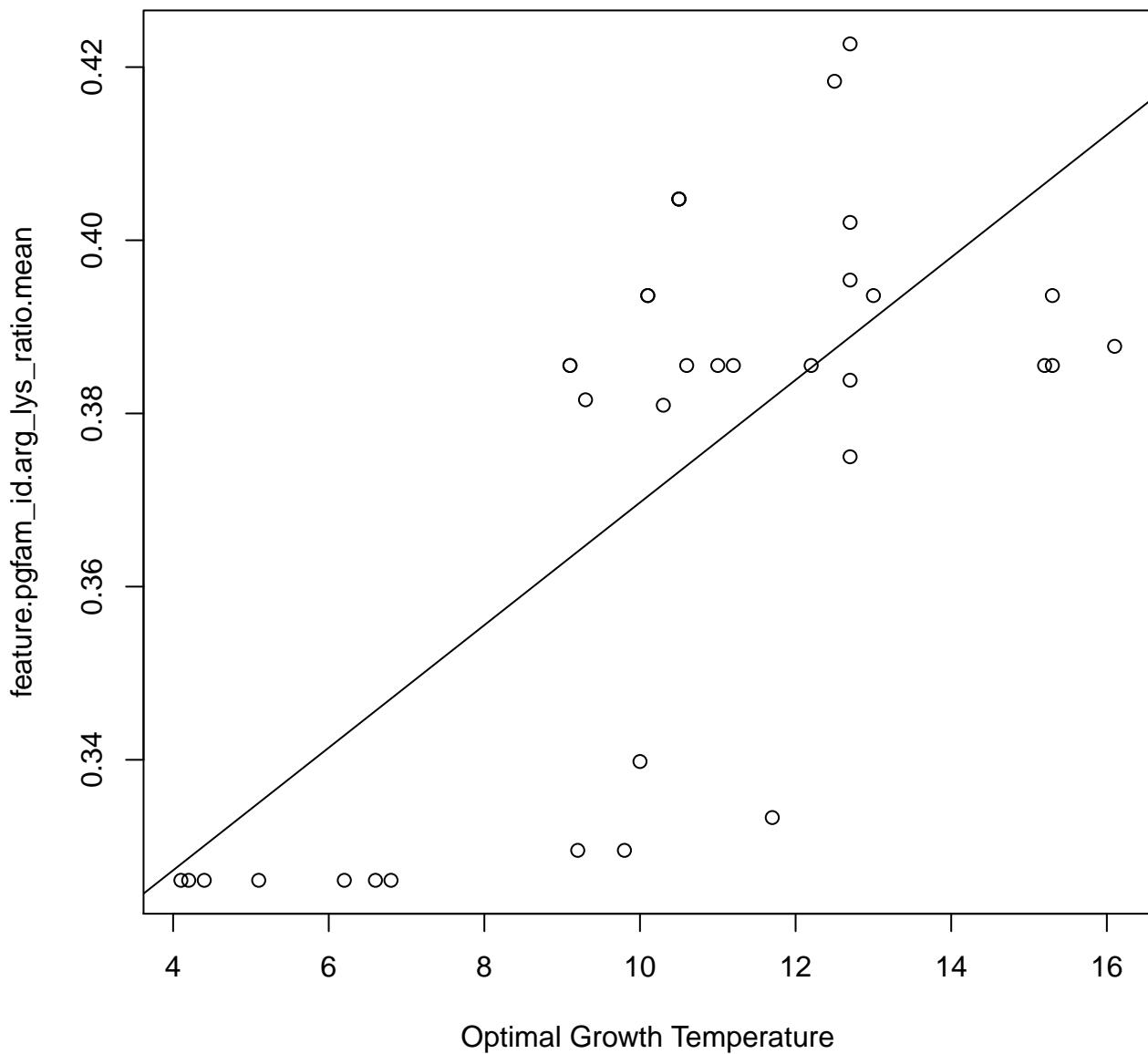
feature.pgfam_id.arg_lys_ratio.mean
PGF_00018430
MSHA pilin protein MshB



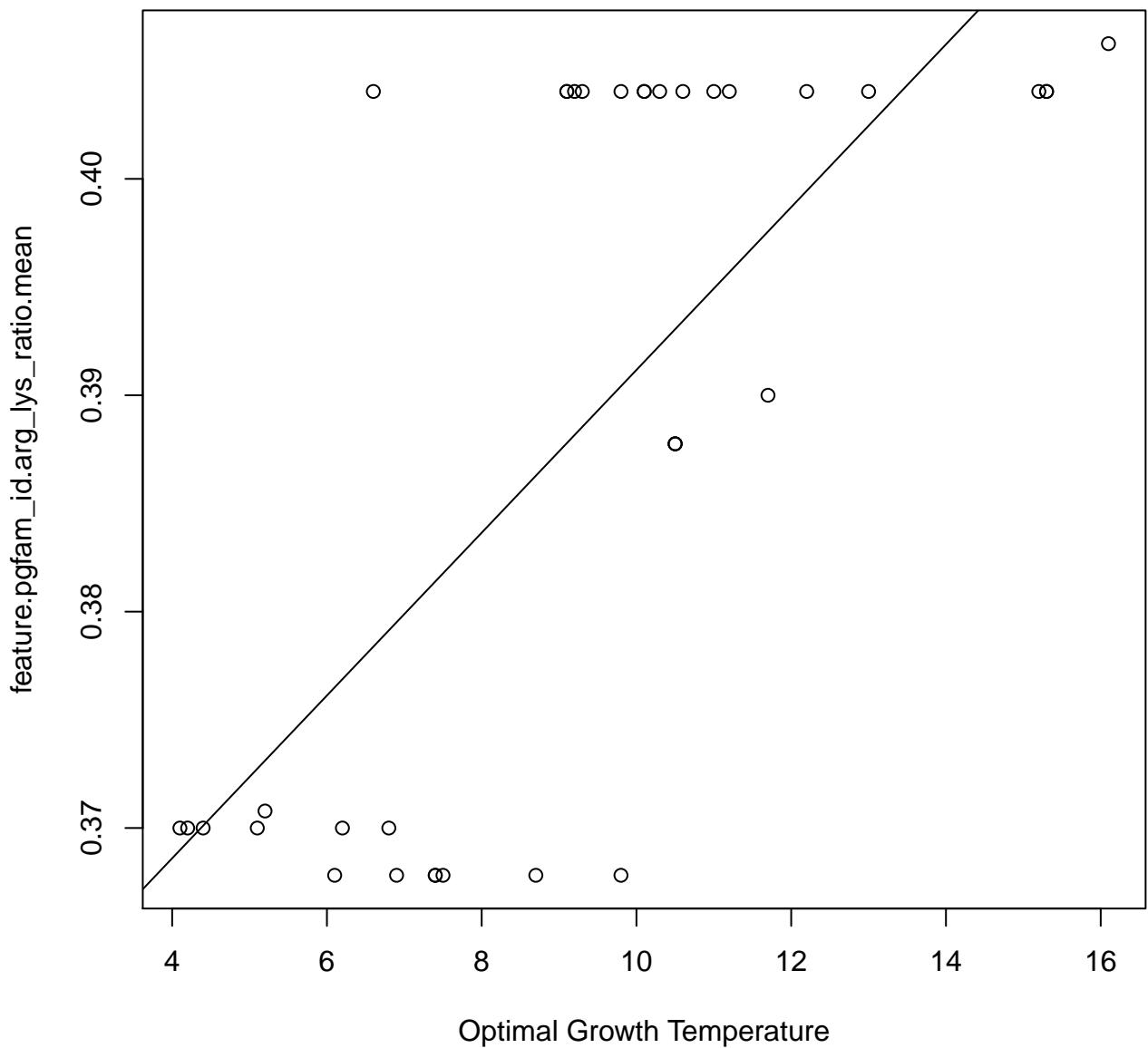
feature.pgfam_id.arg_lys_ratio.mean

PGF_12728693

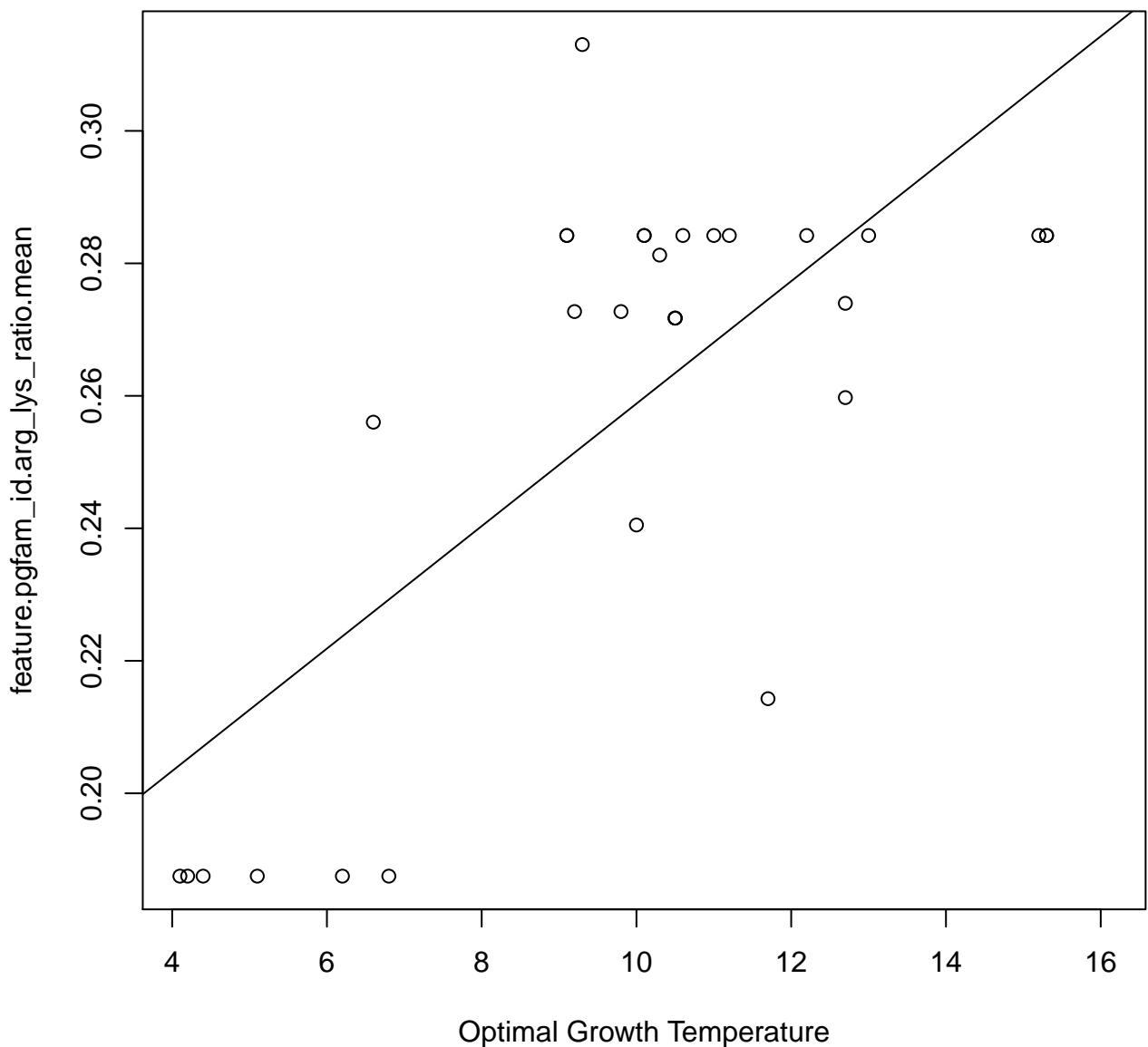
Two-component system sensor histidine kinase/response regulator hybrid



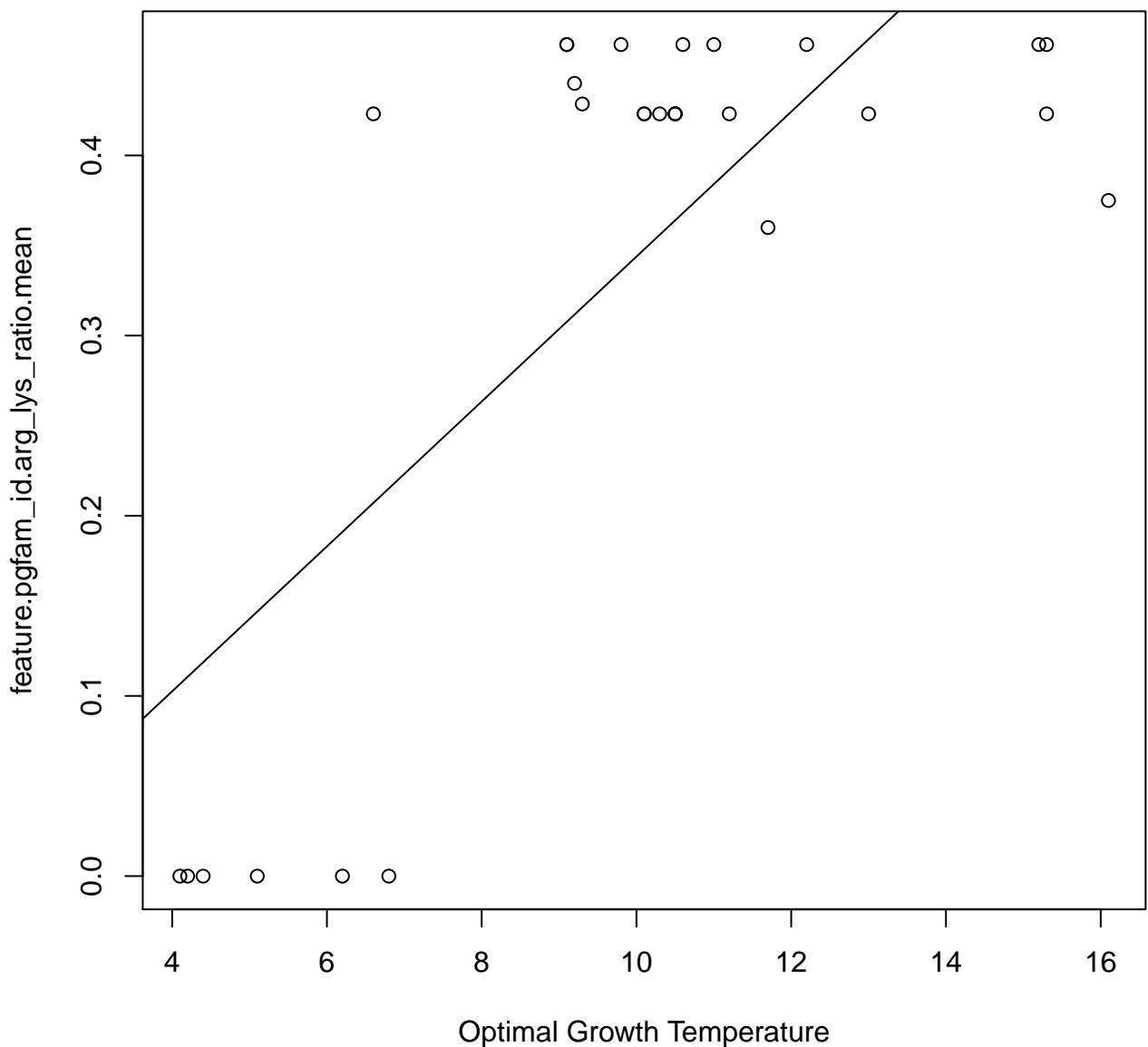
feature.pgfam_id.arg_lys_ratio.mean
PGF_10437481
hypothetical protein



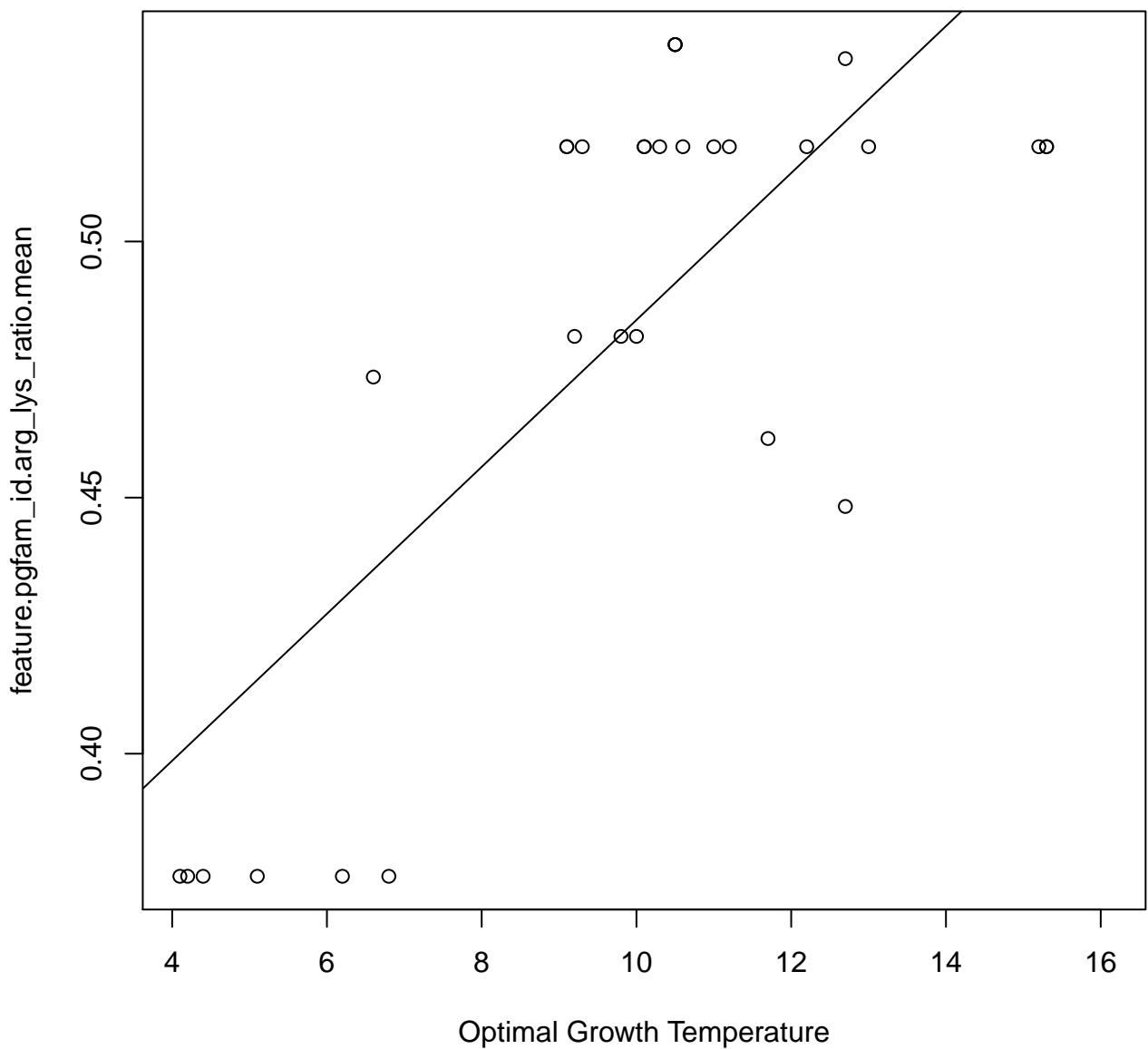
feature.pgfam_id.arg_lys_ratio.mean
PGF_01336773
hypothetical protein



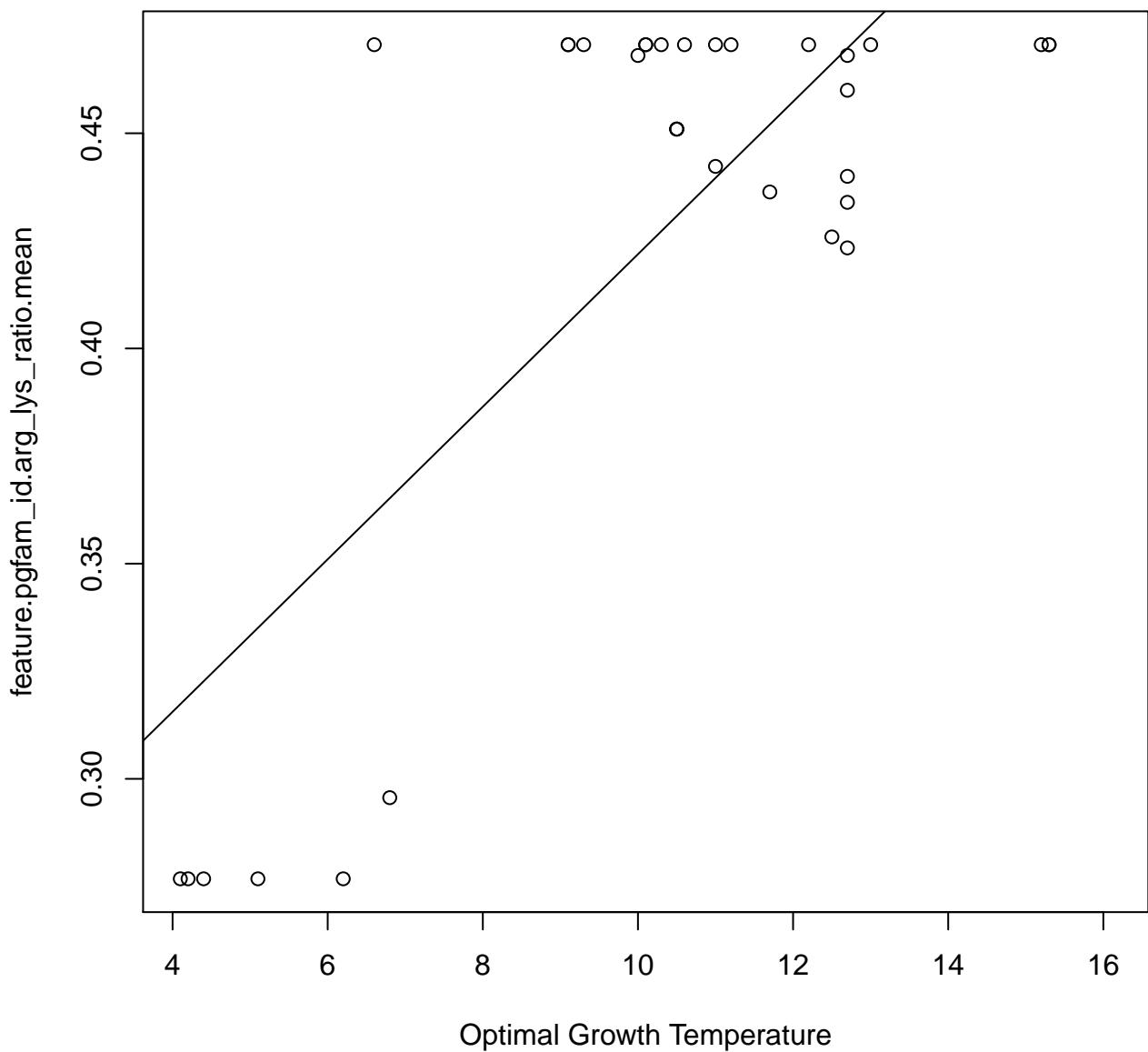
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PGF_06202619
hypothetical protein



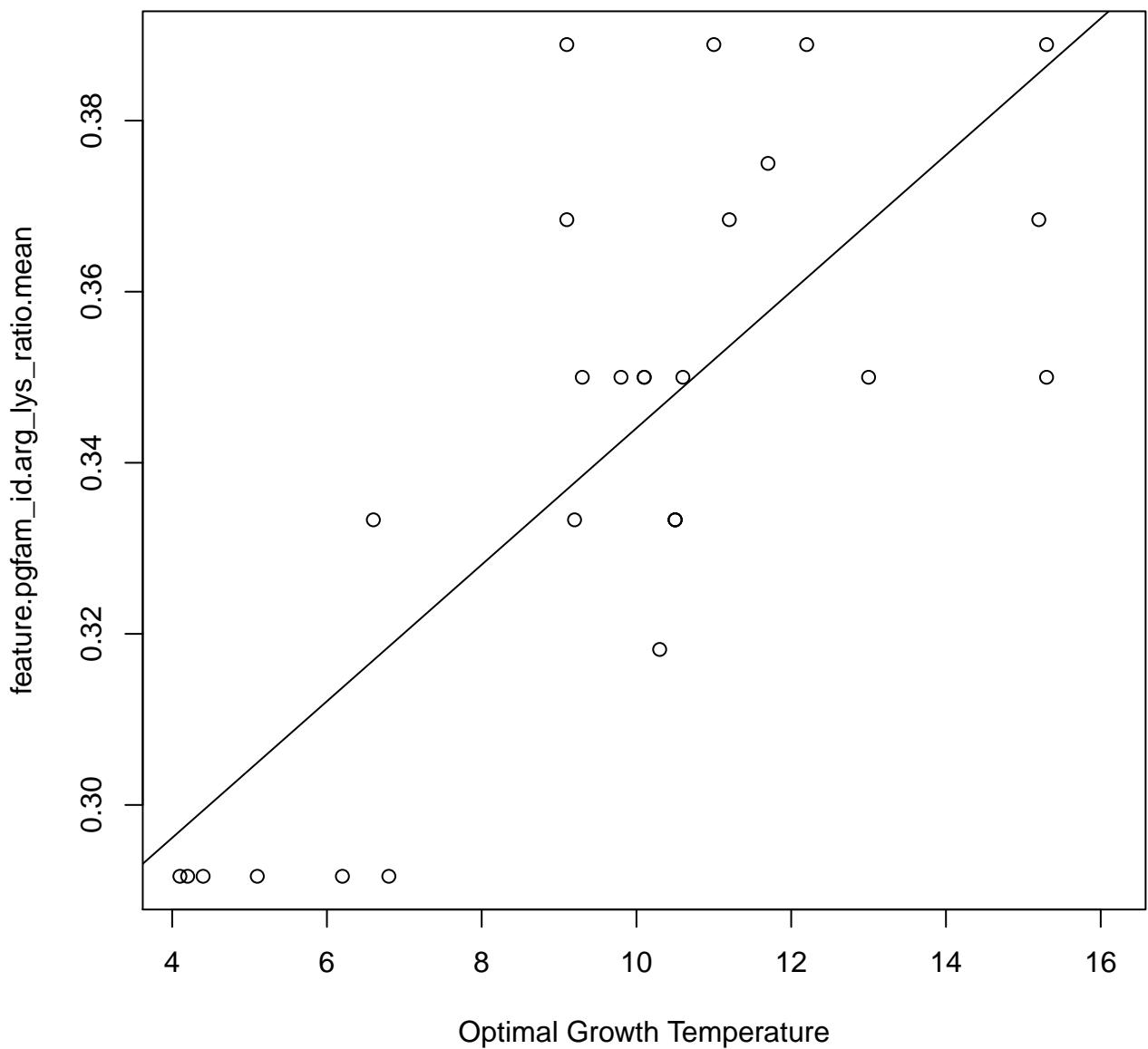
feature.pgfam_id.arg_lys_ratio.mean
PGF_01481272
Chemotaxis protein CheD



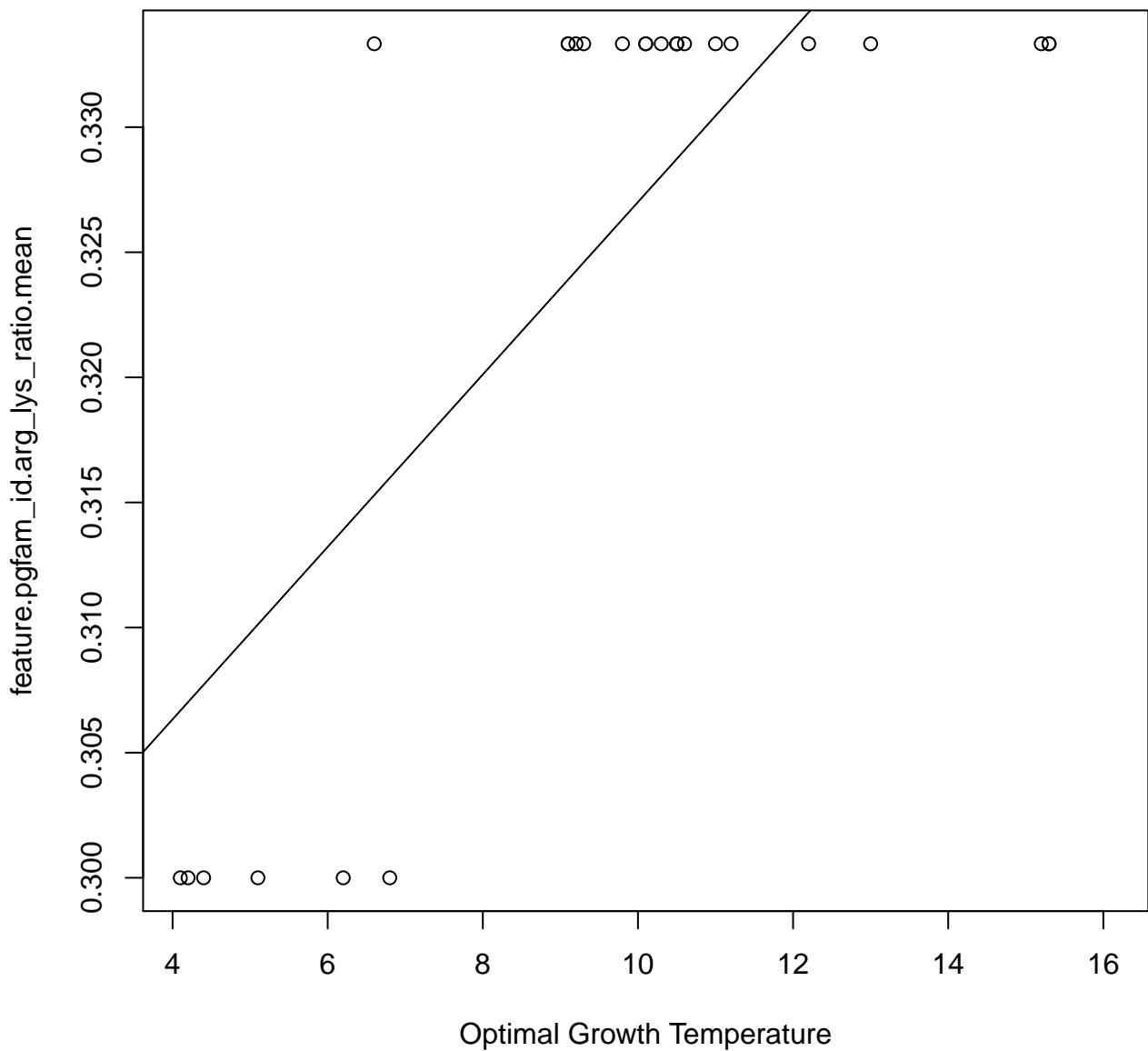
feature.pgfam_id.arg_lys_ratio.mean
PGF_02105064
Uncharacterized protease YegQ



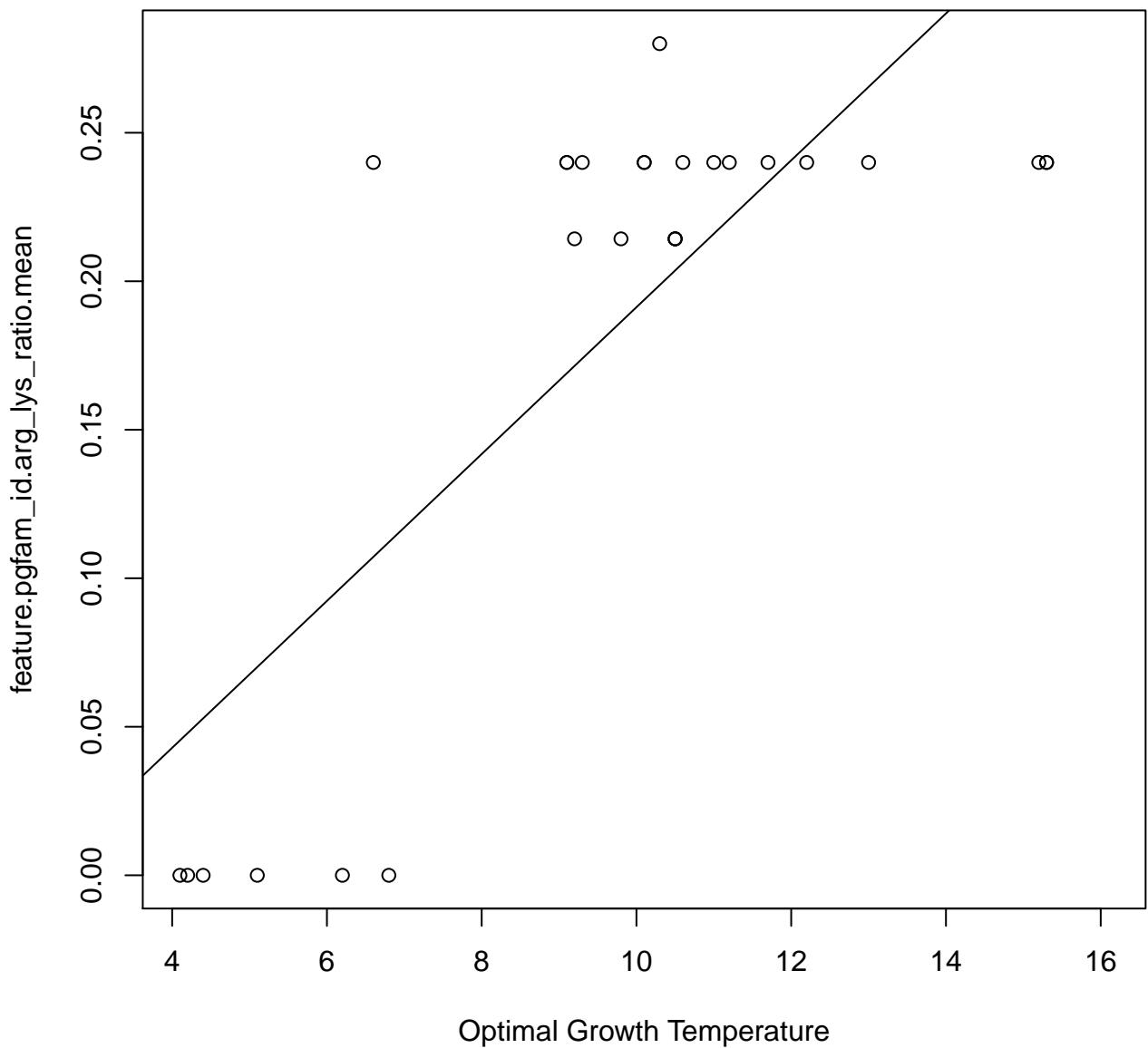
feature.pgfam_id.arg_lys_ratio.mean
PGF_11569208
hypothetical protein



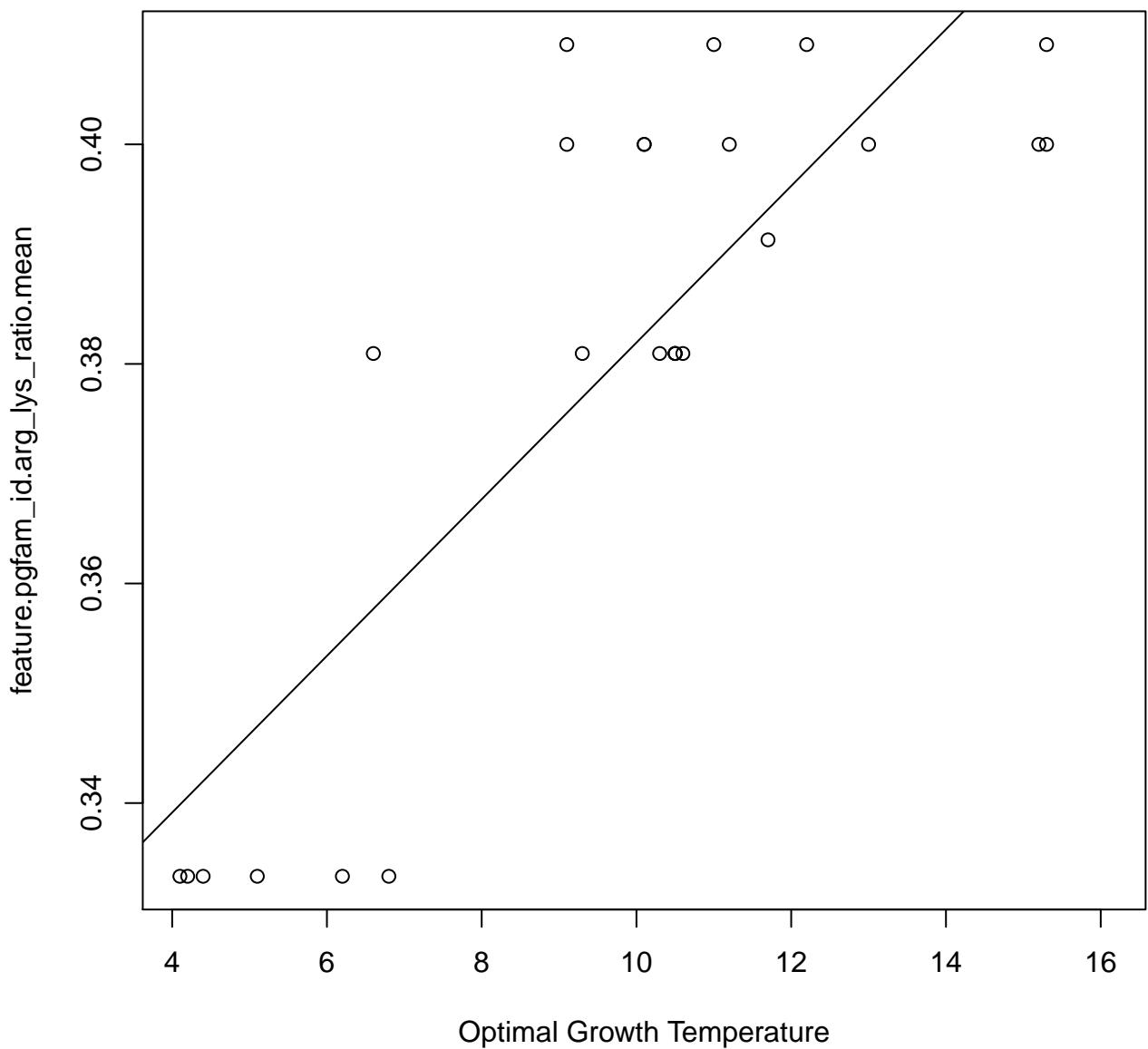
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PGF_12237460
hypothetical protein



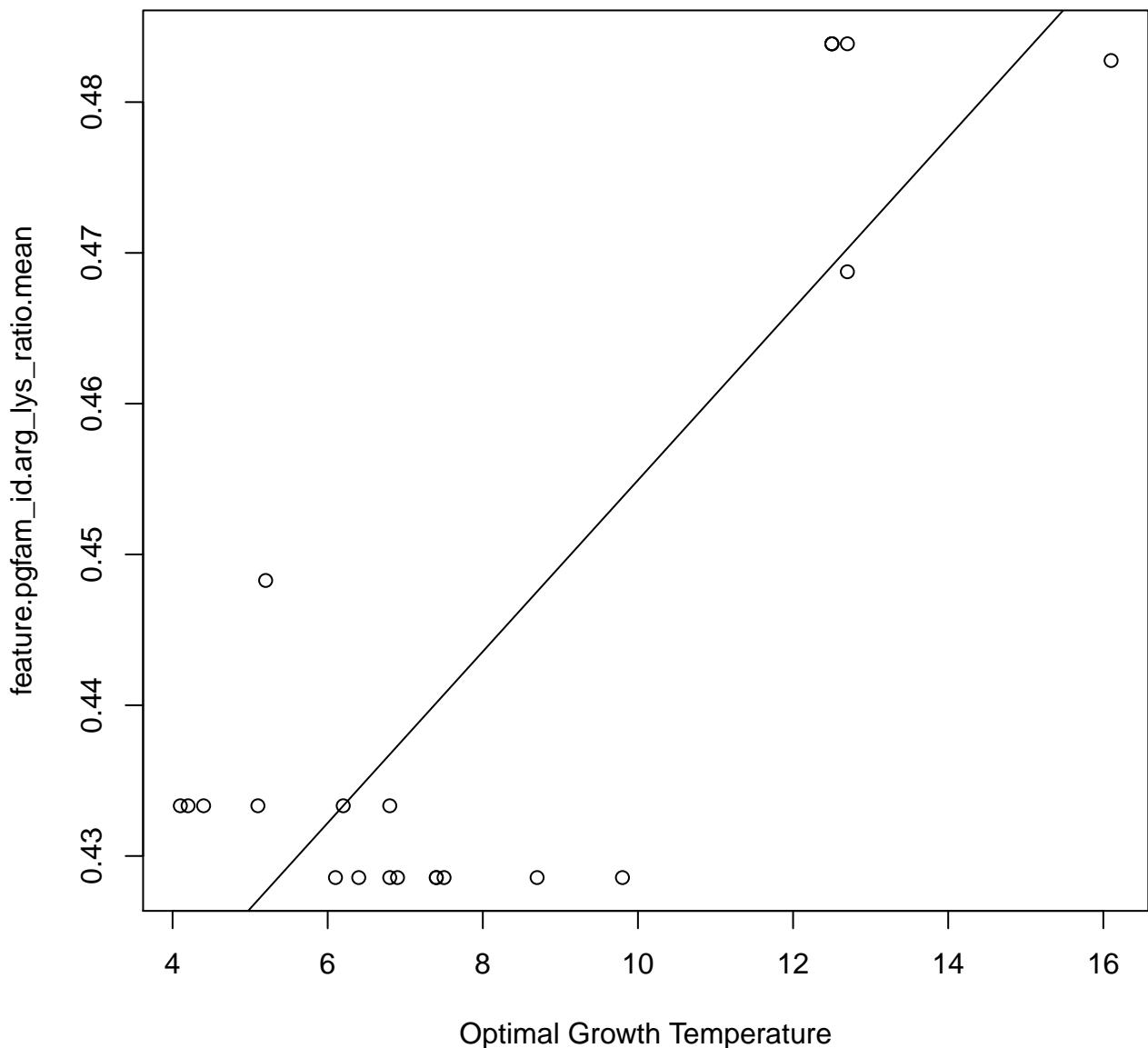
feature.pgfam_id.arg_lys_ratio.mean
PGF_11018774
hypothetical protein



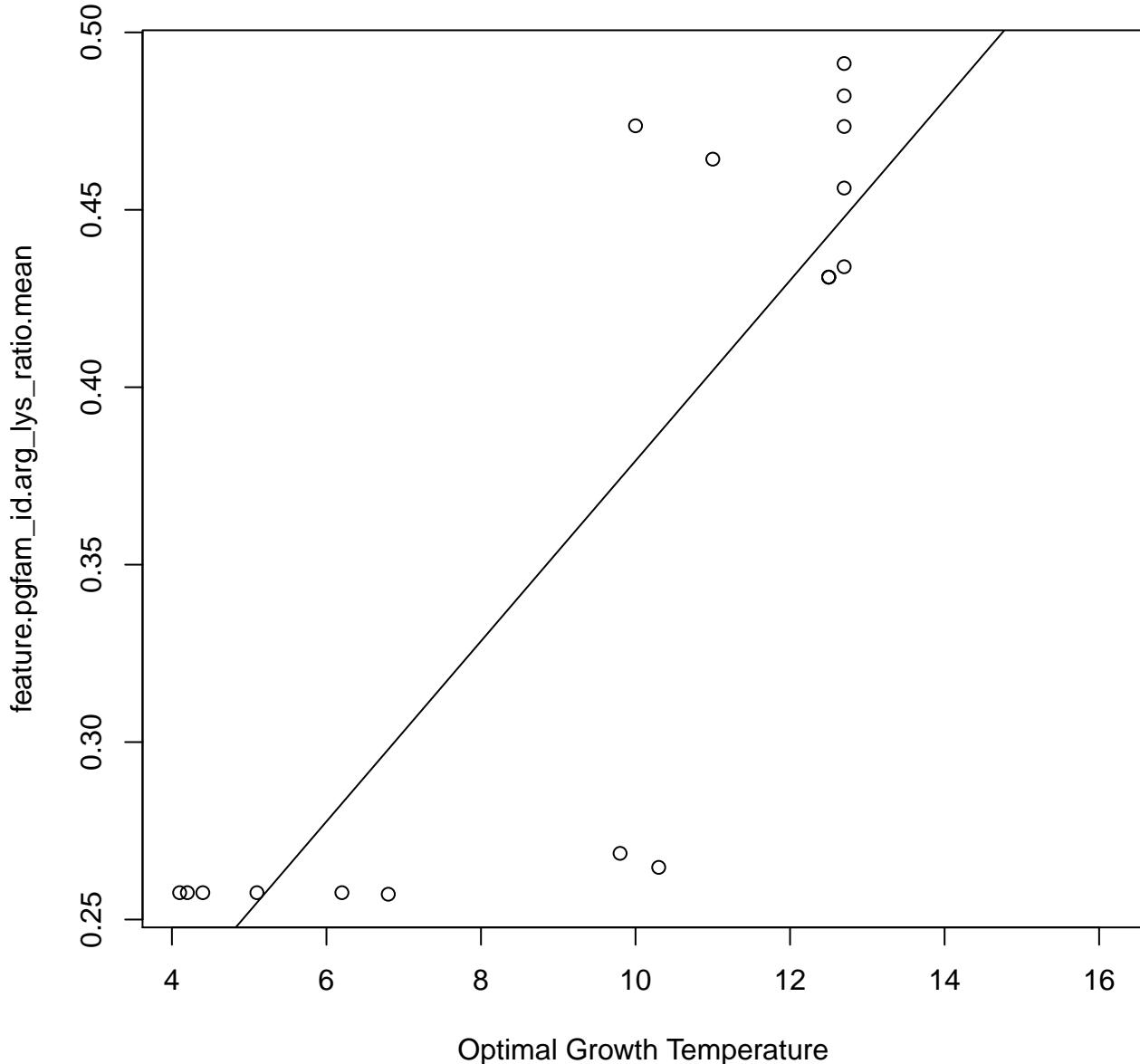
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PGF_08025863
hypothetical protein



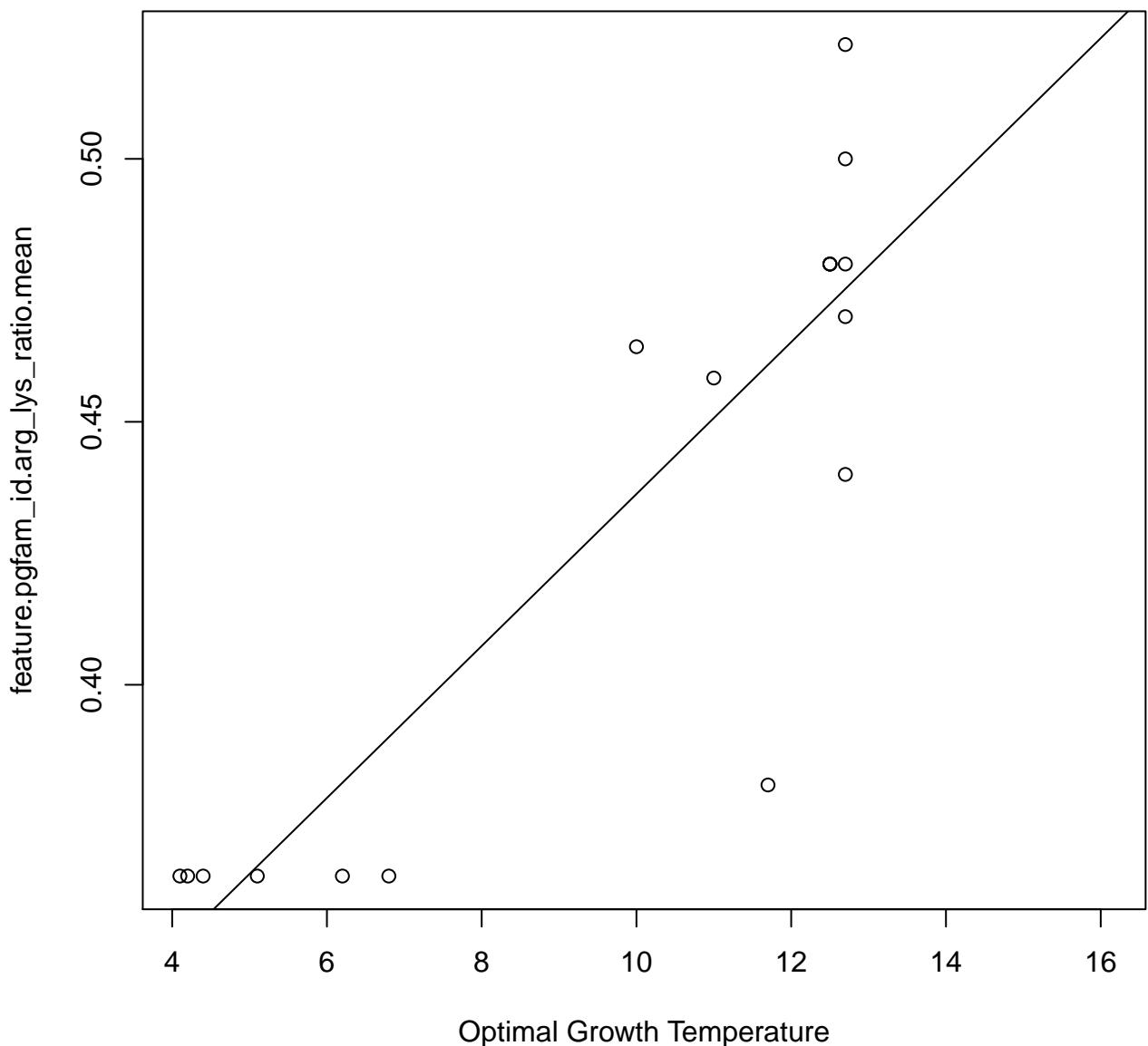
feature.pgfam_id.arg_lys_ratio.mean
PGF_02732386
Glucose/mannose:H⁺ symporter GlcP



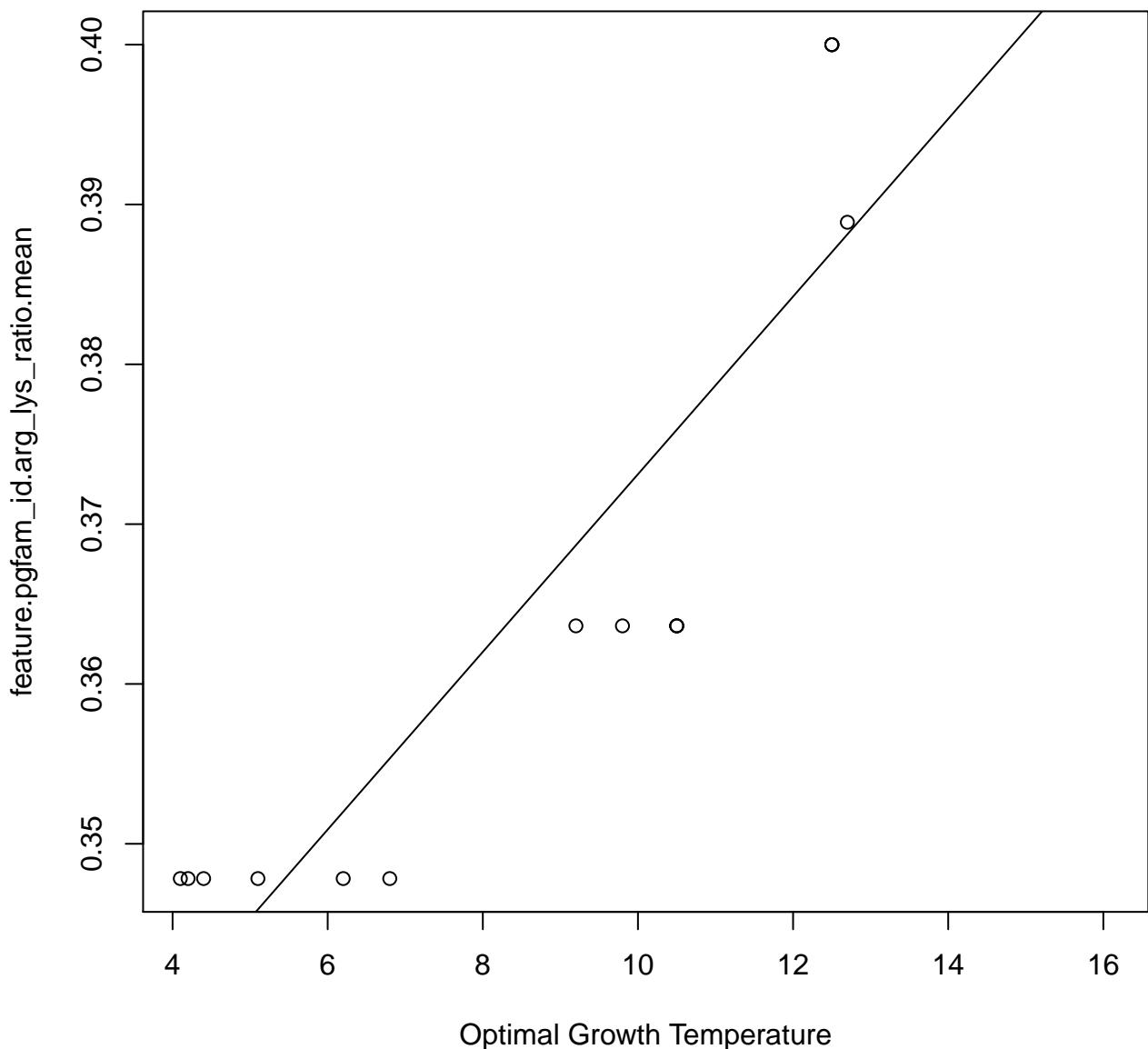
feature.pgfam_id.arg_lys_ratio.mean
PGF_00018516
Macrolide-specific ABC-type efflux carrier (TC 3.A.1.122.1)



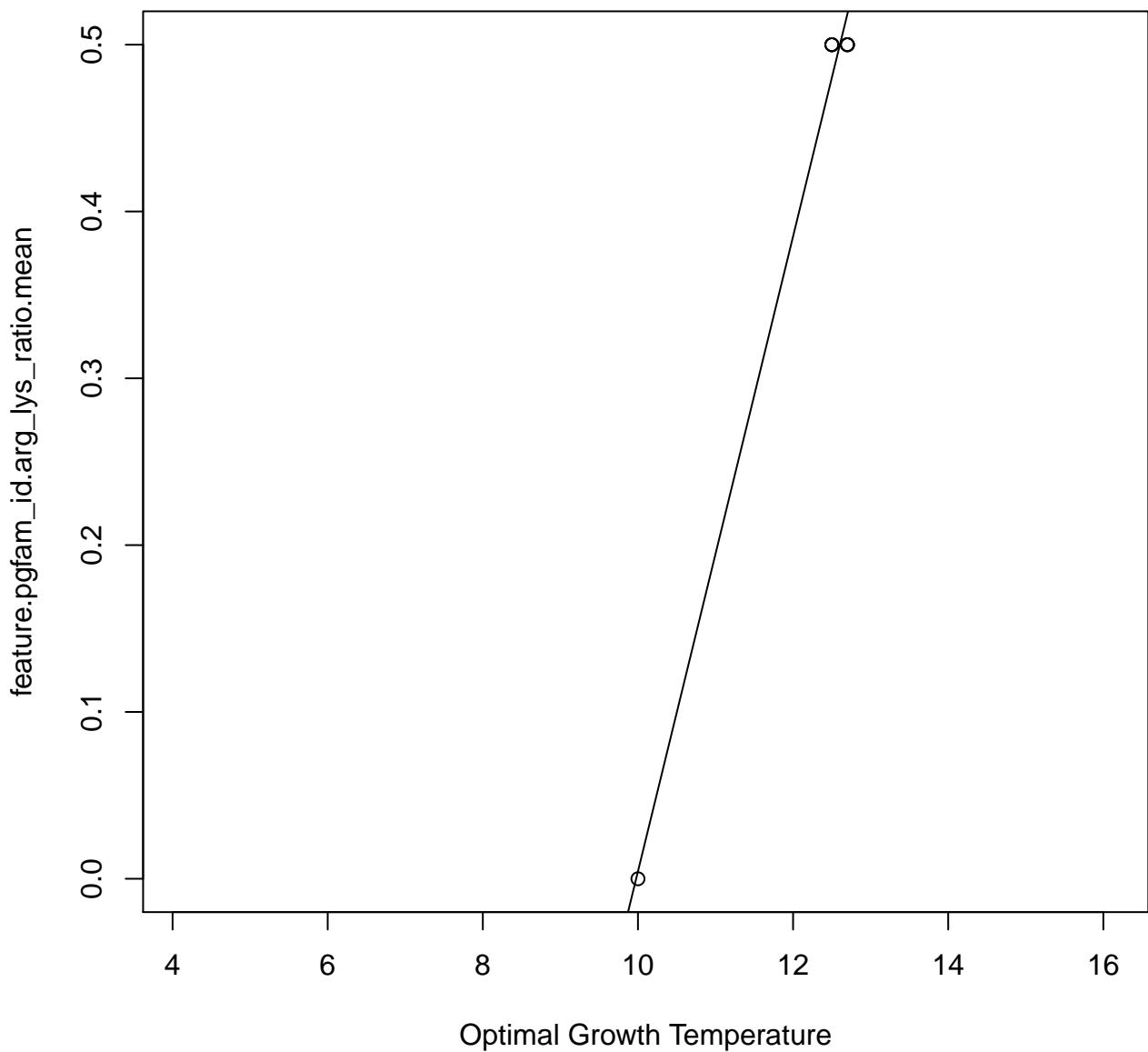
feature.pgfam_id.arg_lys_ratio.mean
PGF_00425647
FHA domain protein



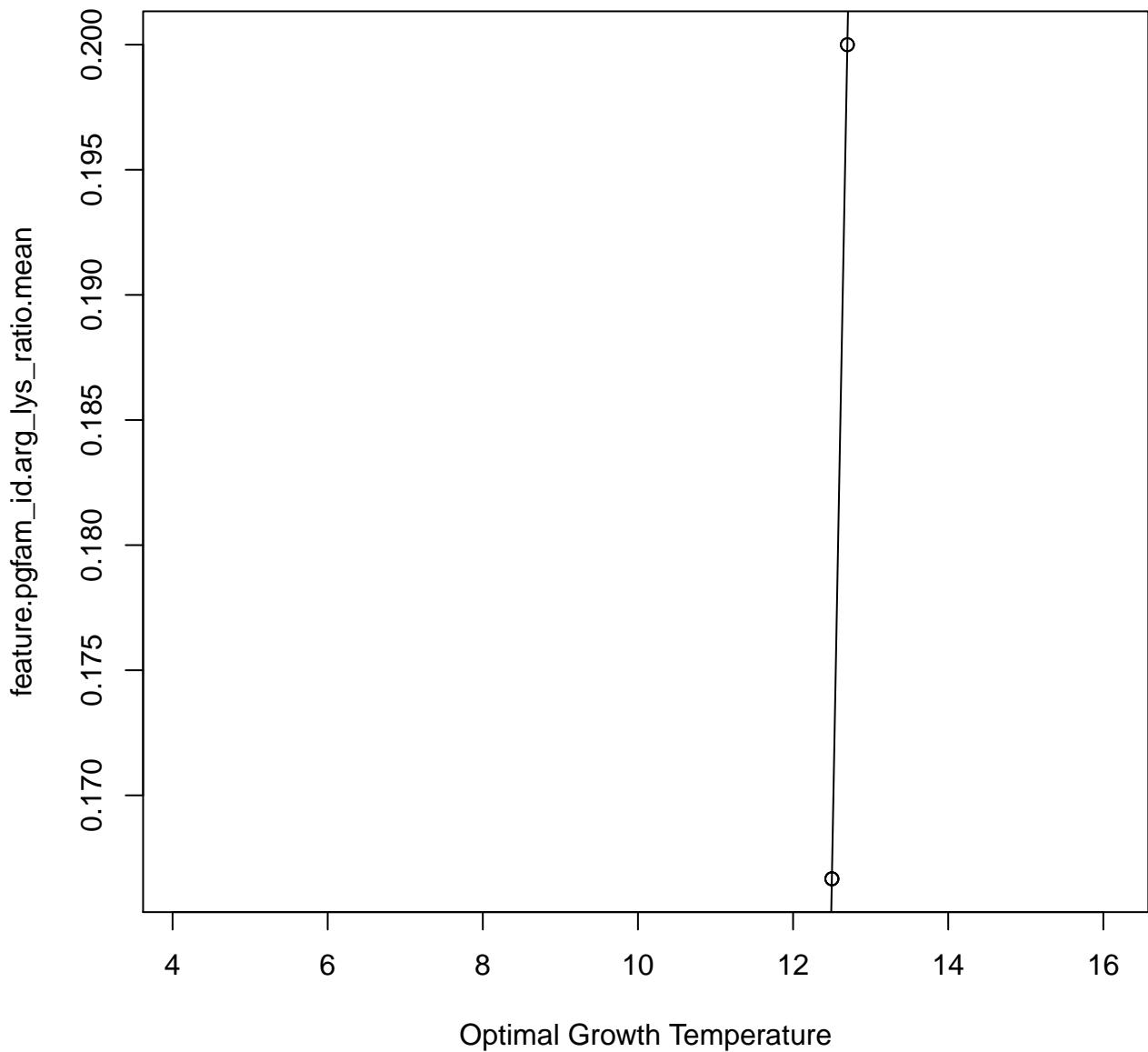
feature.pgfam_id.arg_lys_ratio.mean
PGF_01338042
hypothetical protein



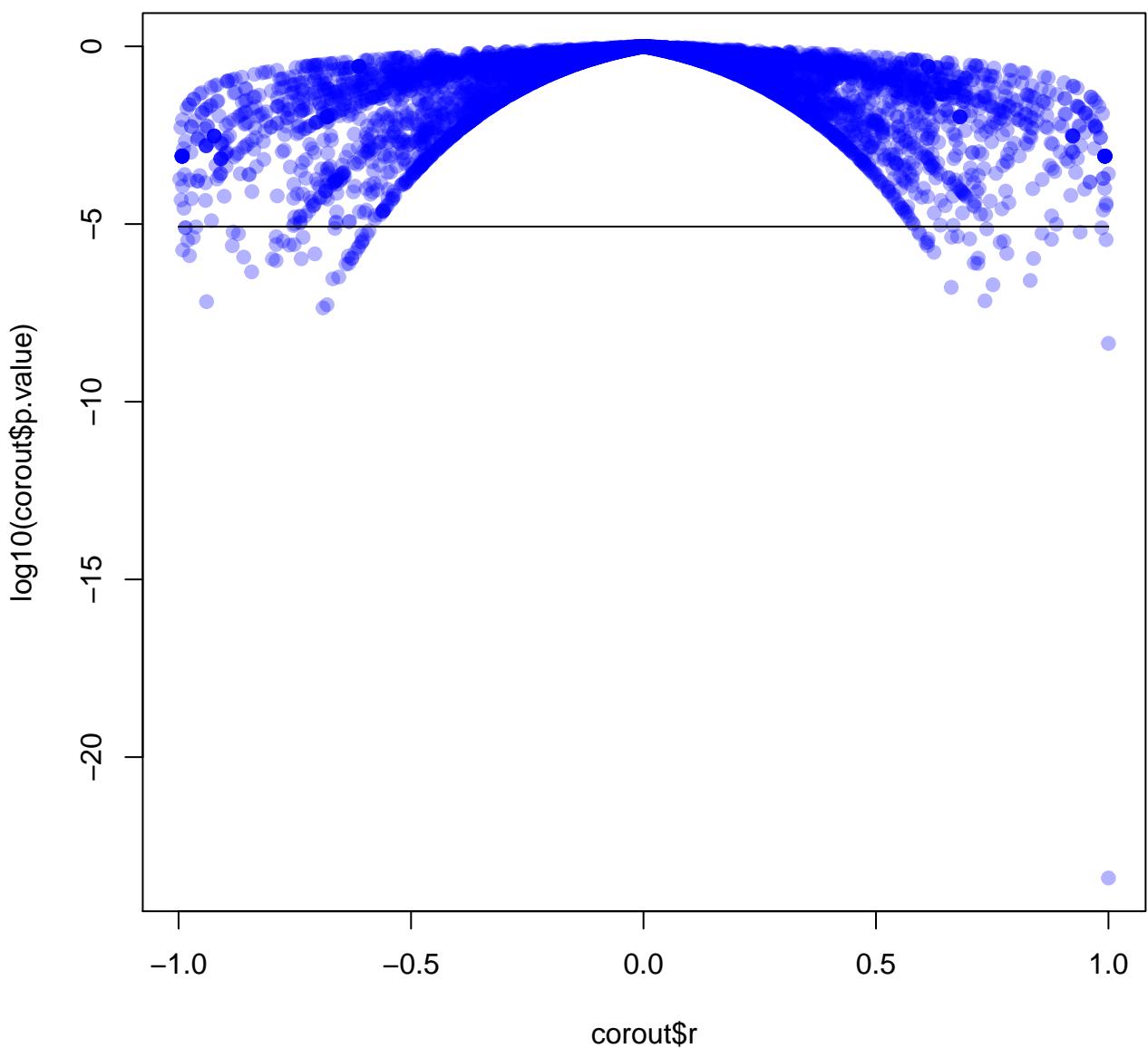
feature.pgfam_id.arg_lys_ratio.mean
PGF_01337096
hypothetical protein



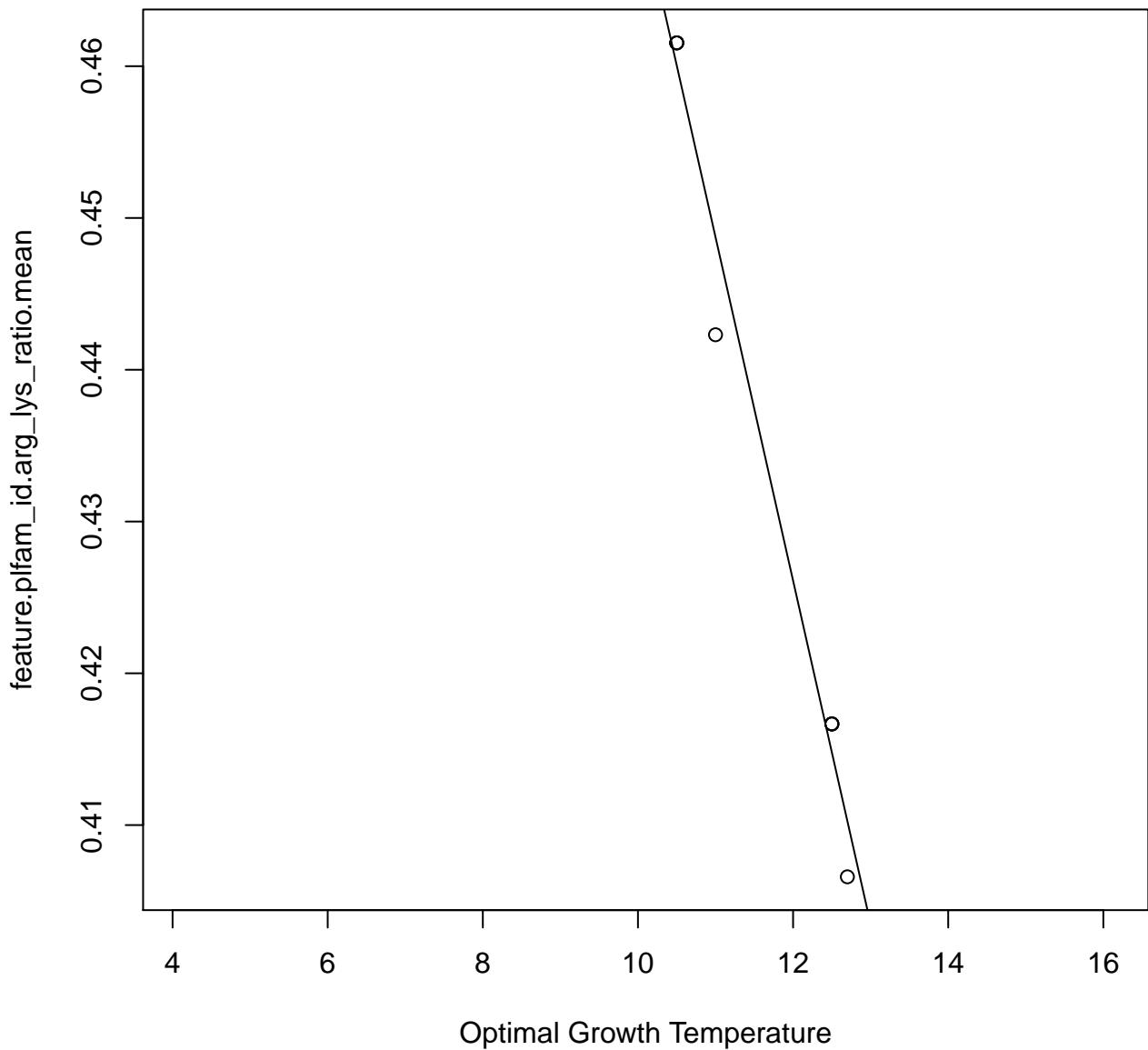
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PGF_01338035
hypothetical protein



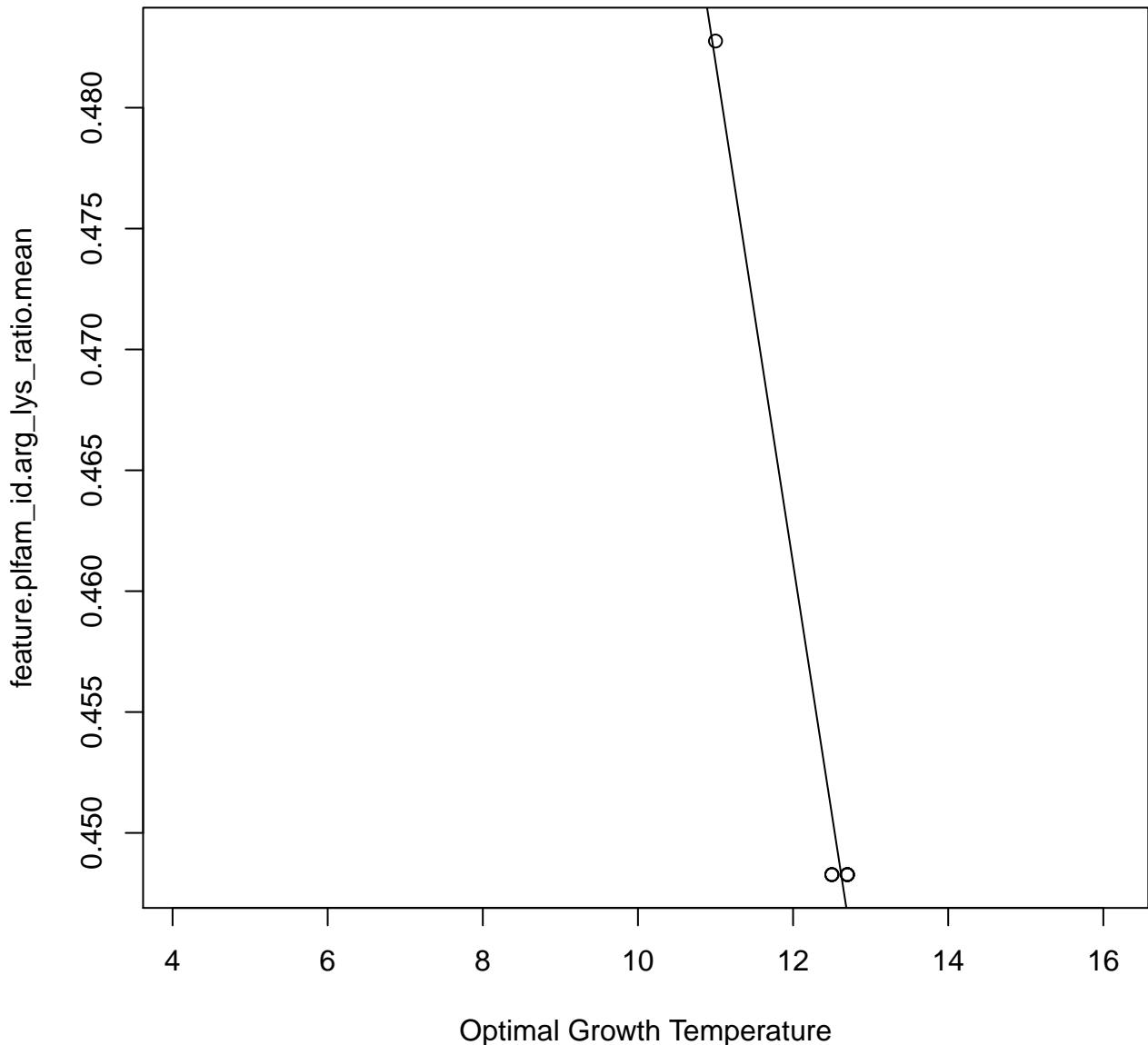
feature.plfam_id.arg_lys_ratio.mean



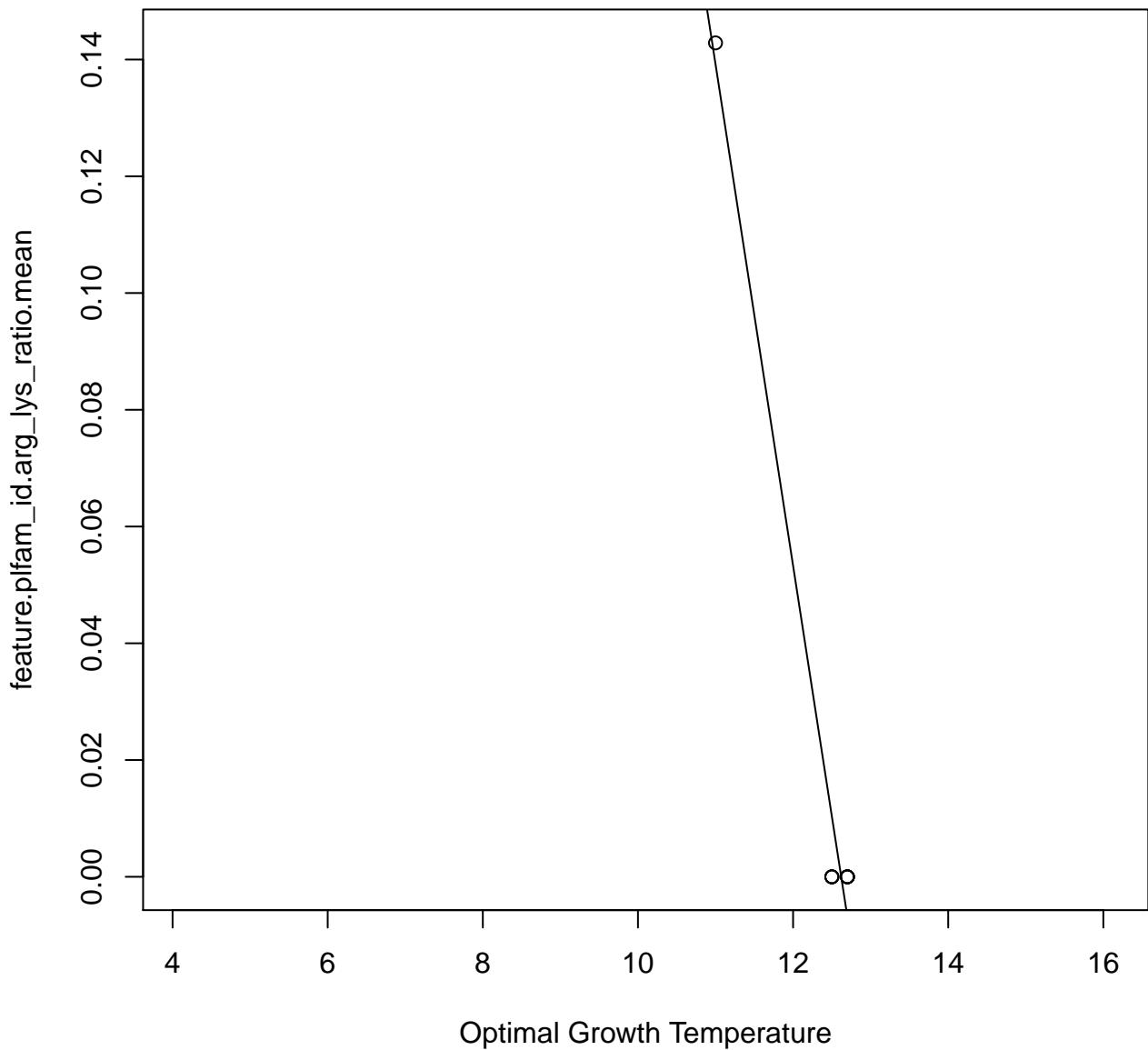
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00009489
hypothetical protein



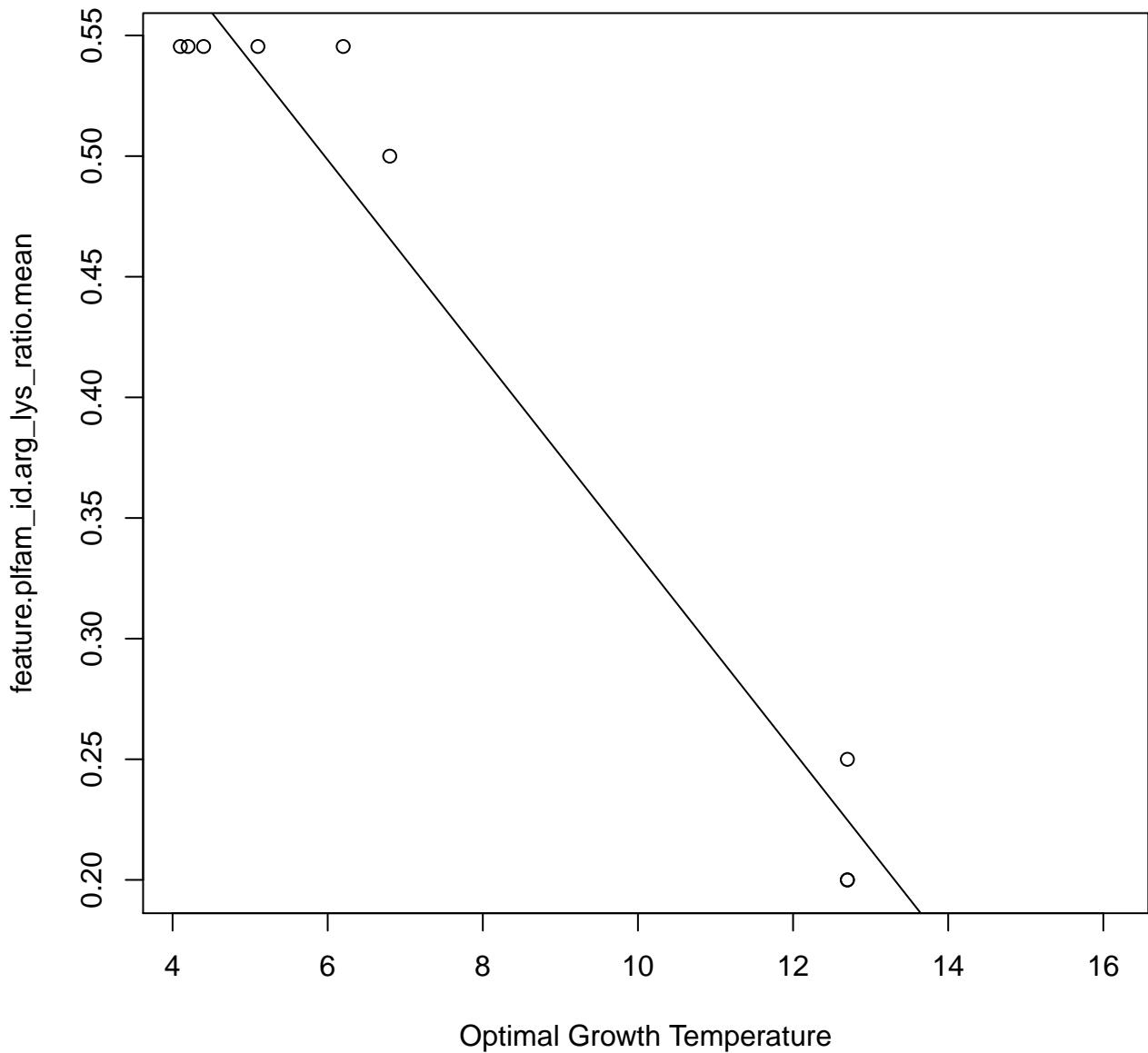
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00003137
Two-component transcriptional response regulator, LuxR family



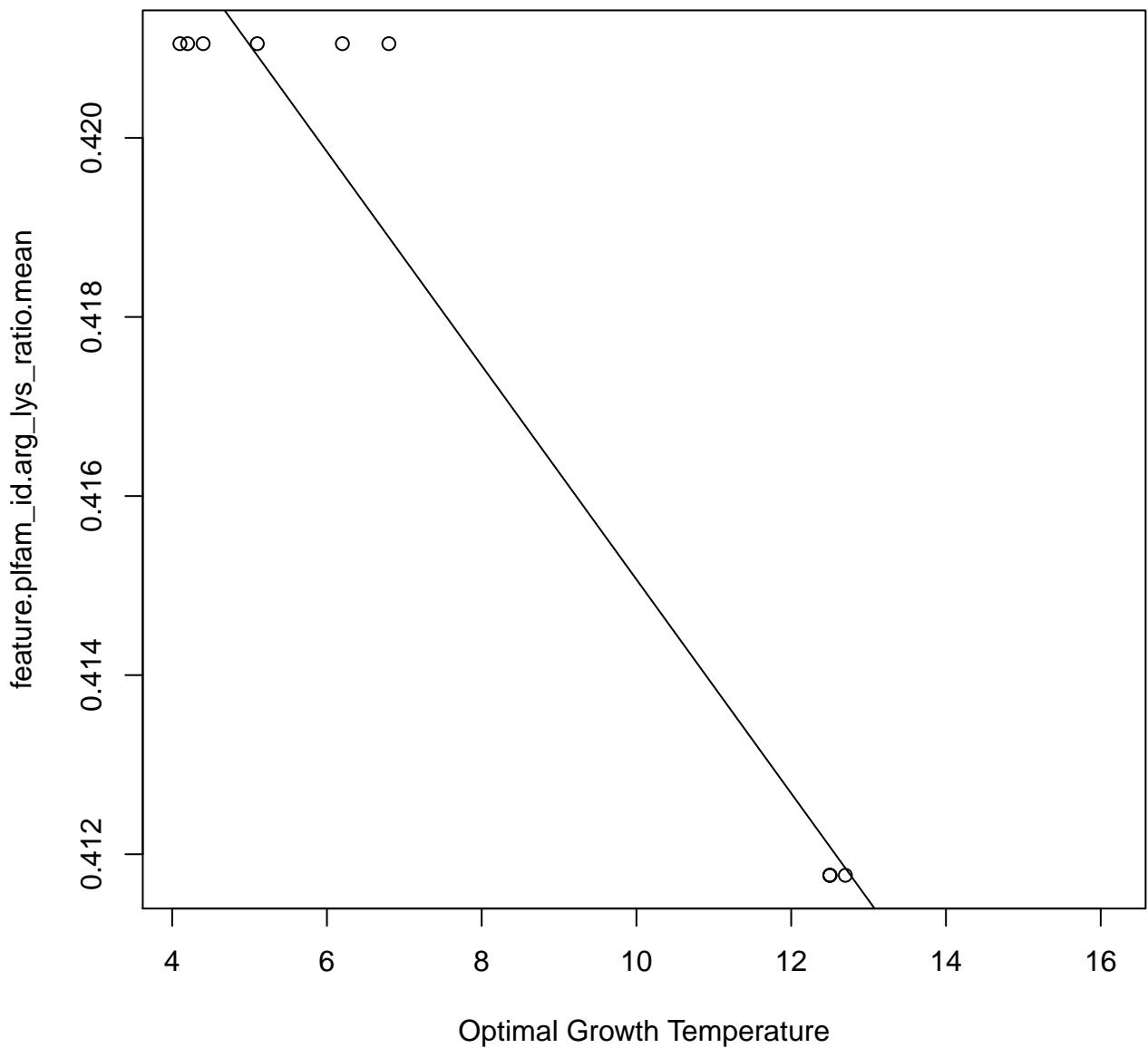
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00004147
uncharacterized conserved protein containing predicted Zn-ribbon like domain



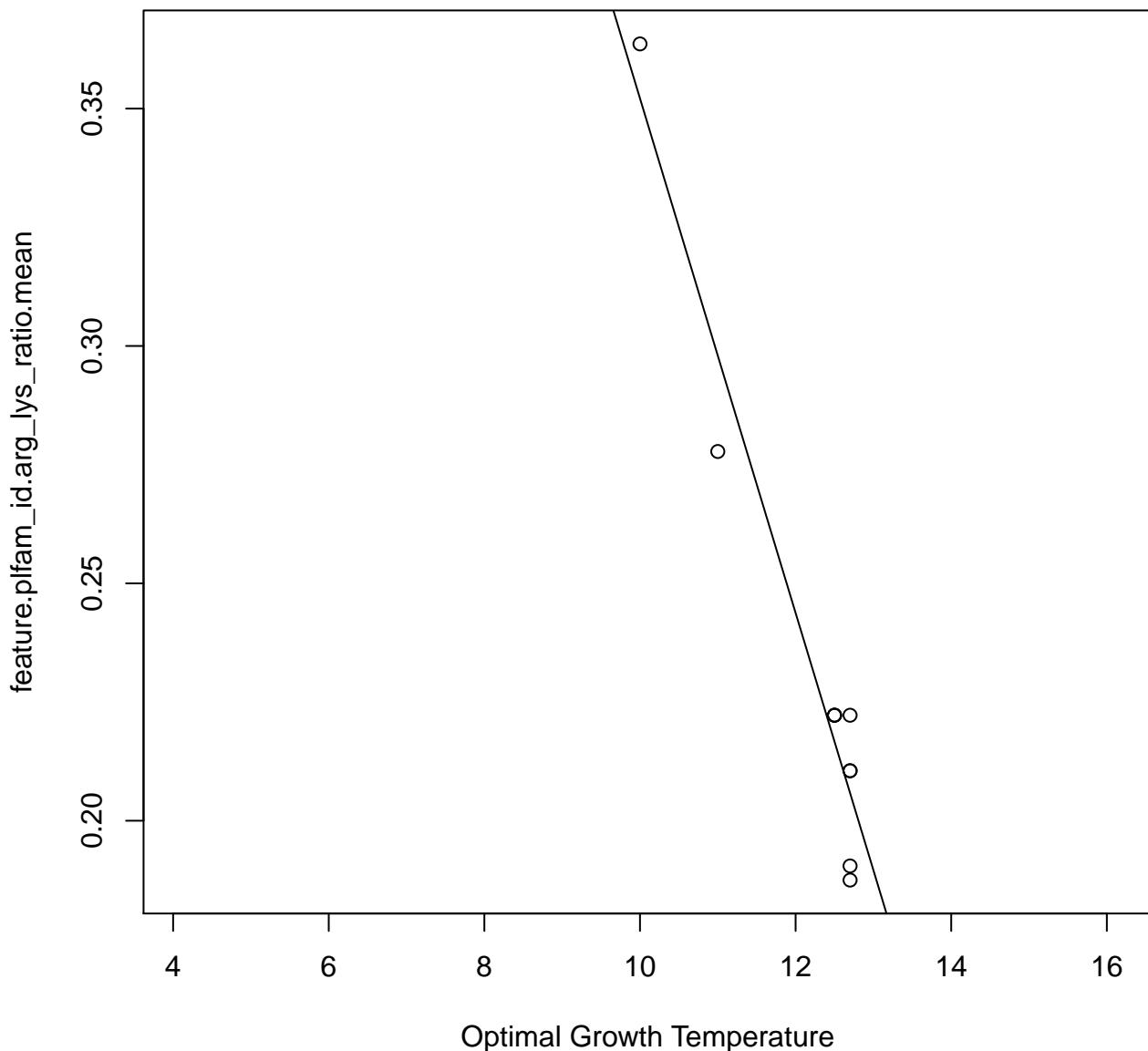
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00003941
hypothetical protein



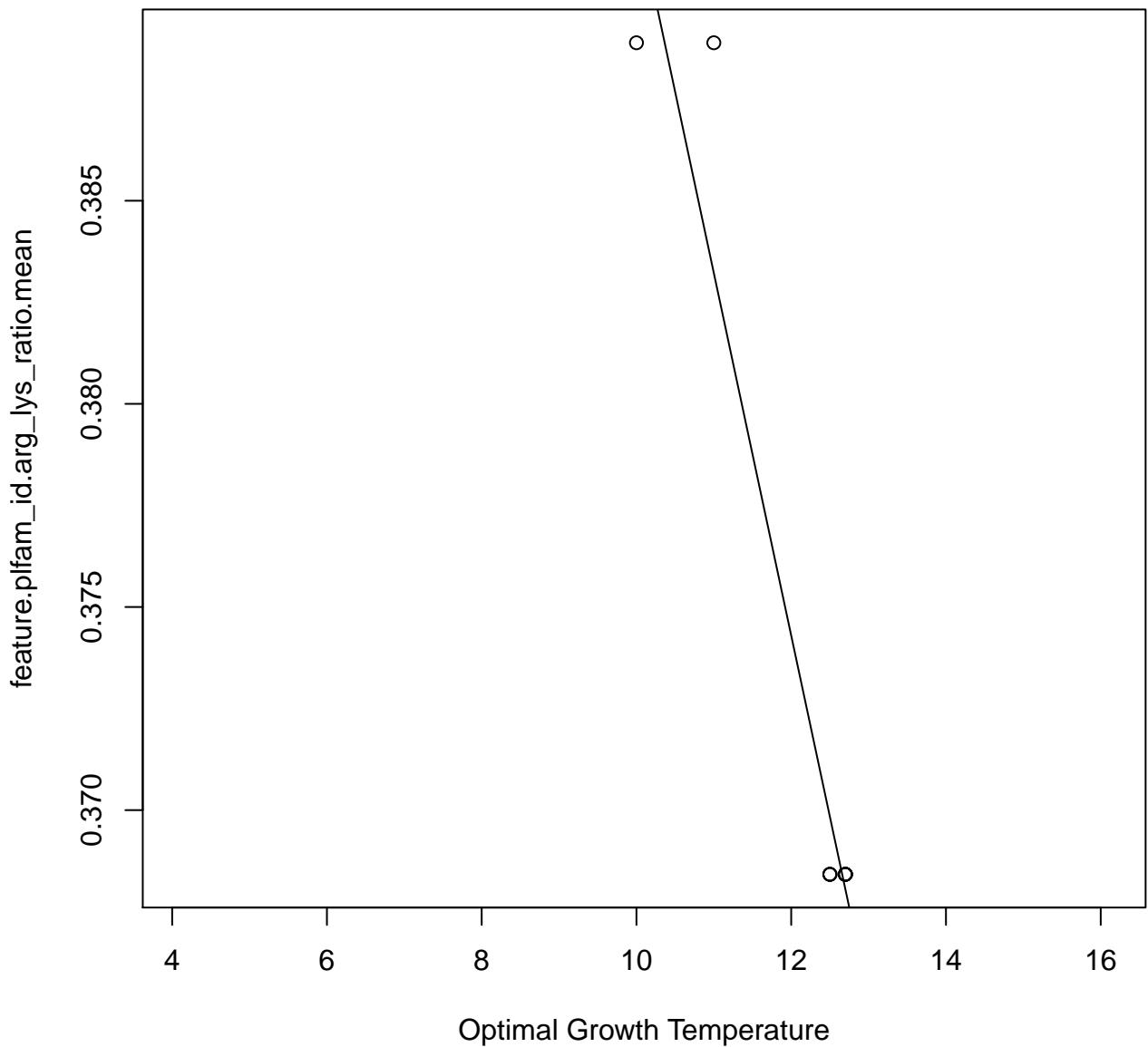
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00007839
hypothetical protein



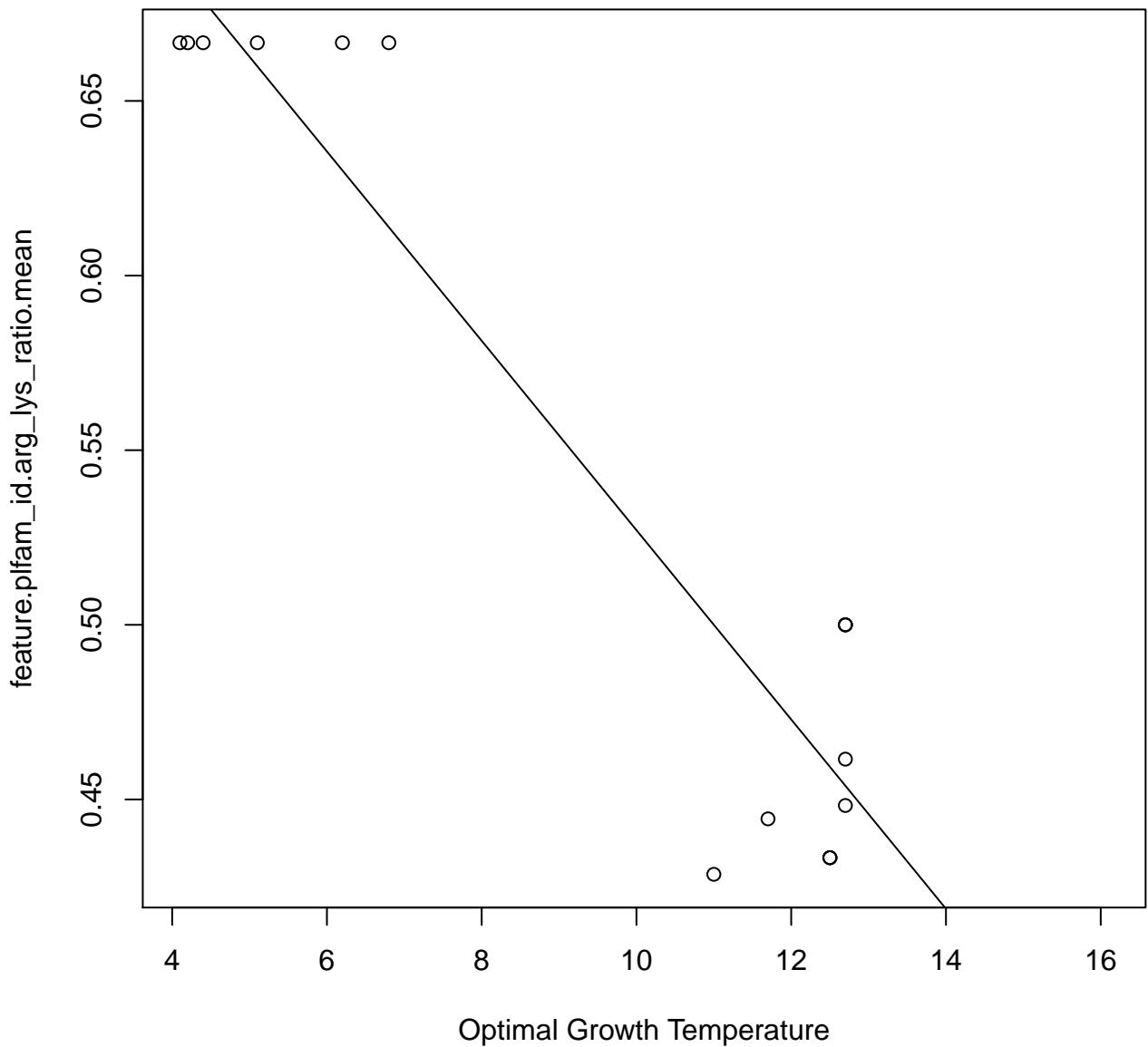
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001877
Outer membrane lipoprotein carrier protein LolA



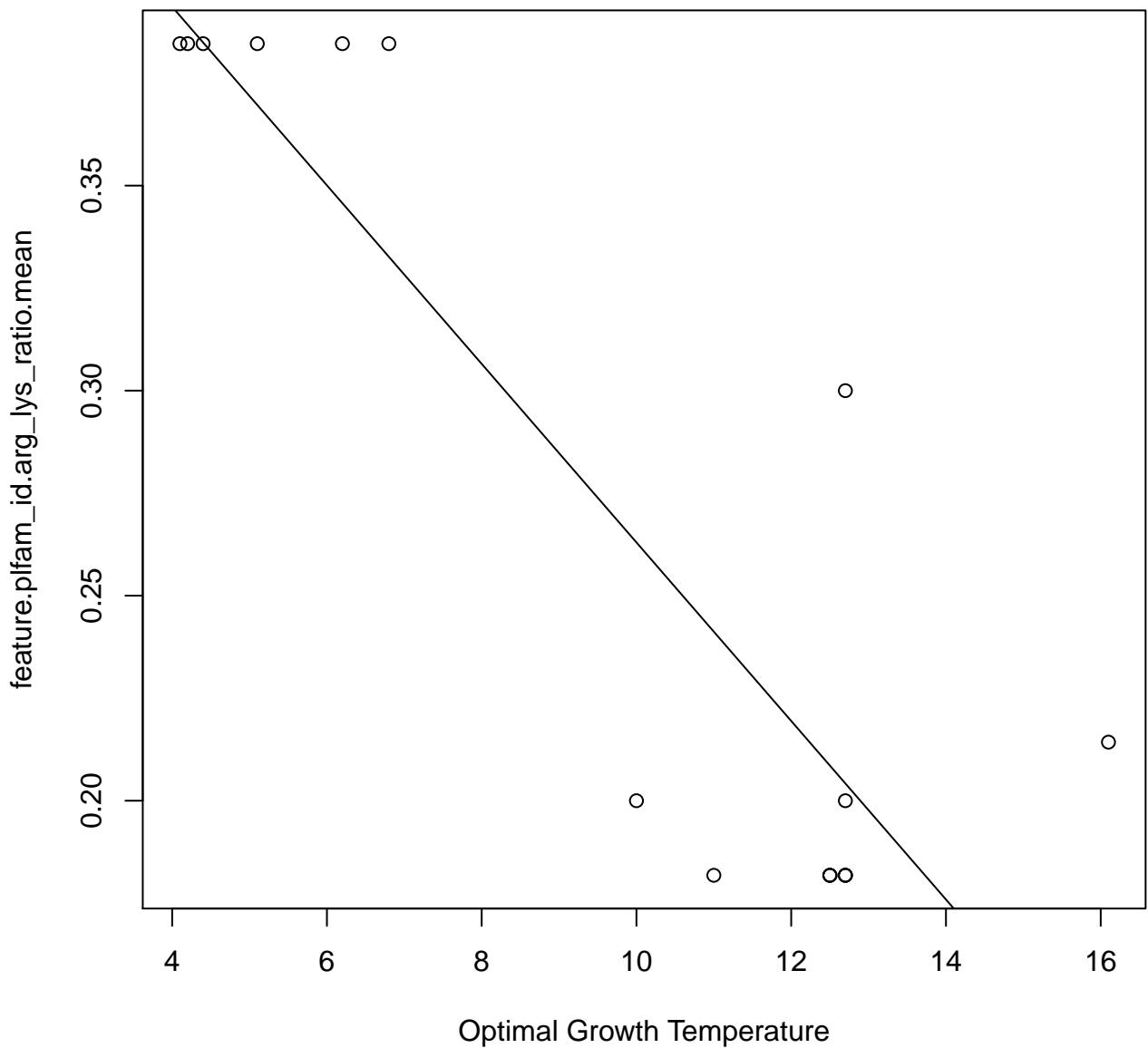
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001345
hypothetical protein



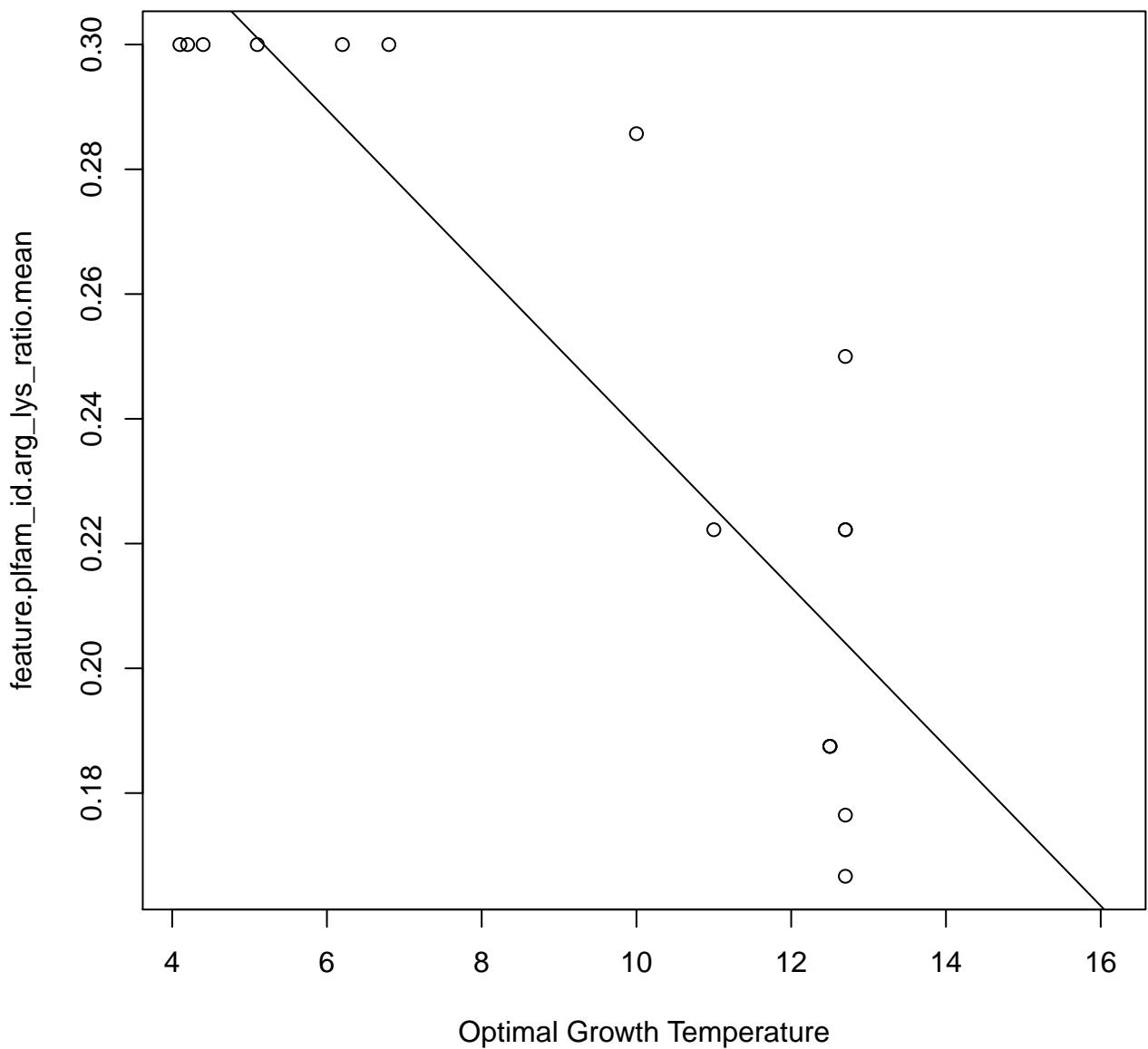
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PLF_28228_00002761
Uncharacterized MFS-type transporter



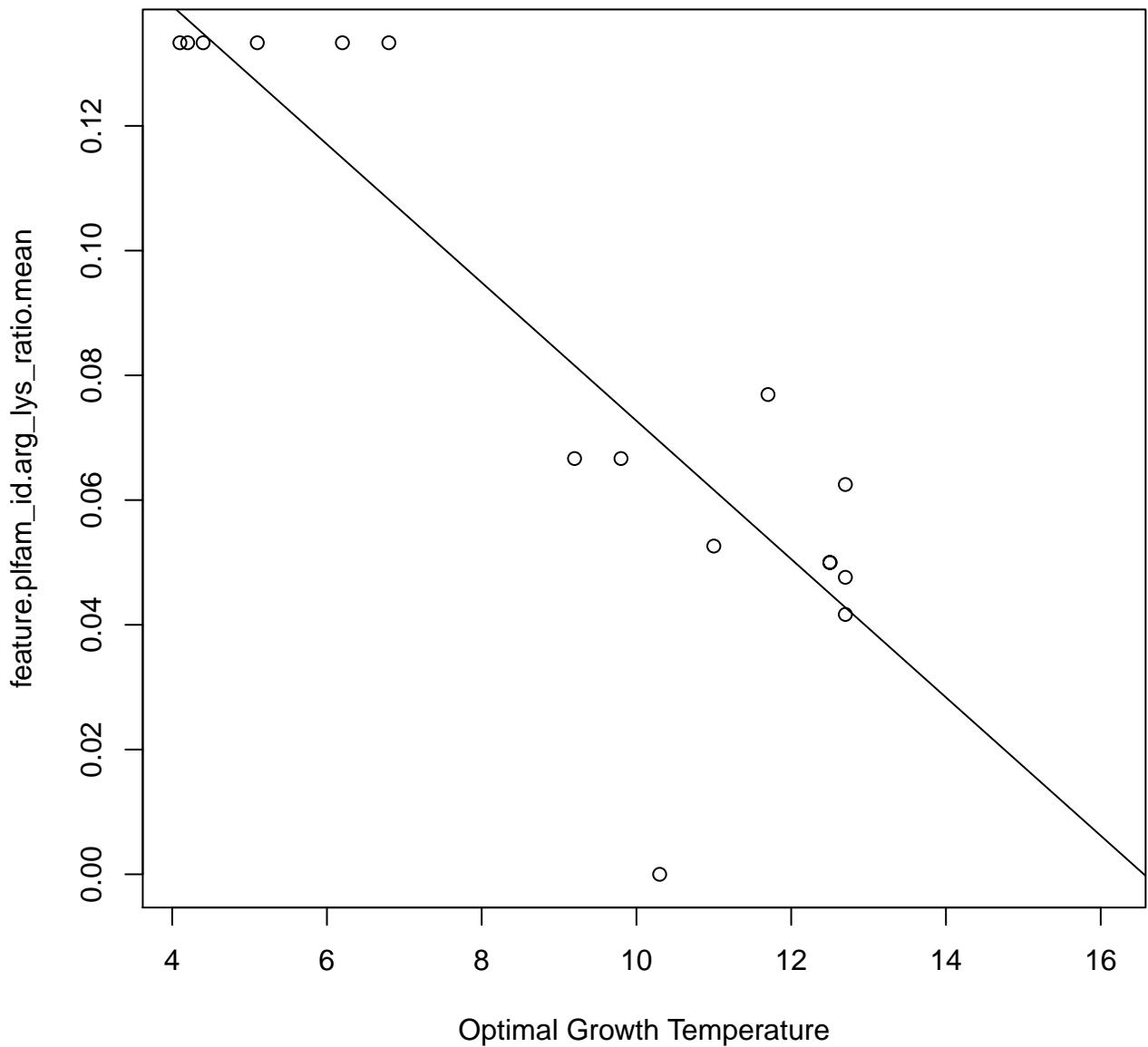
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001519
GcvR-like protein



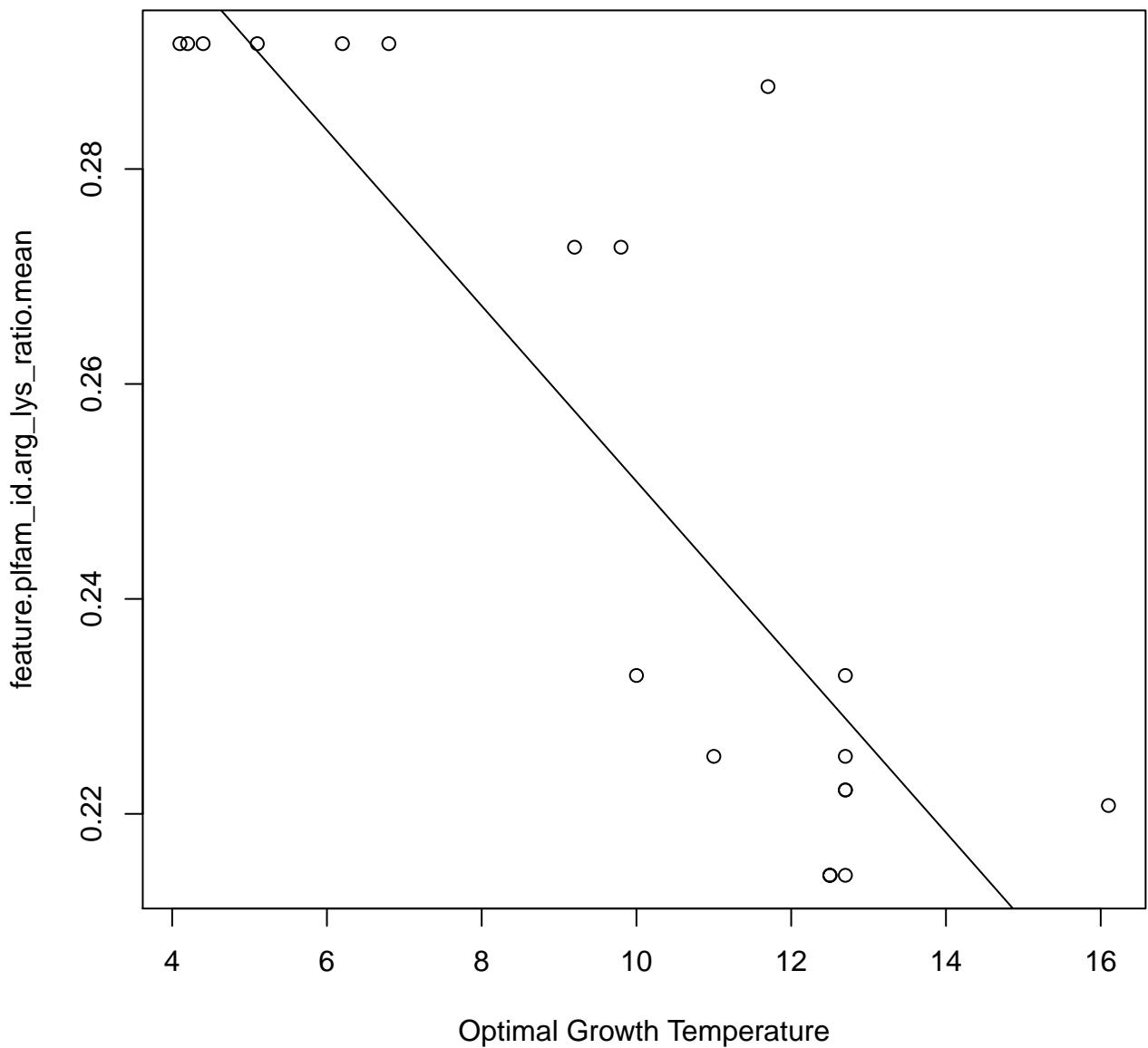
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001794
Outer membrane beta-barrel assembly protein BamE



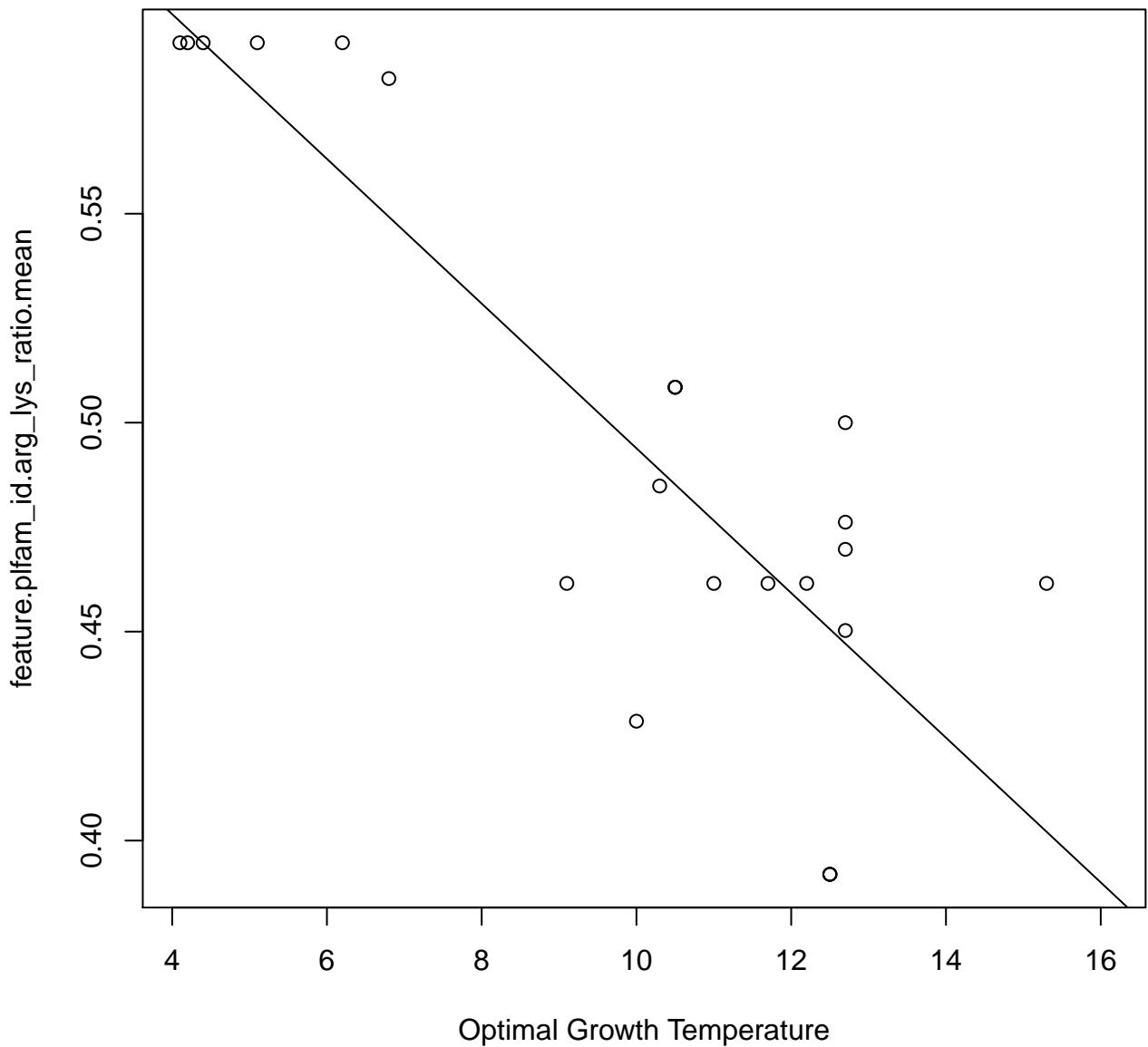
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002857
Transforming growth factor-beta induced protein IG-H3 precursor



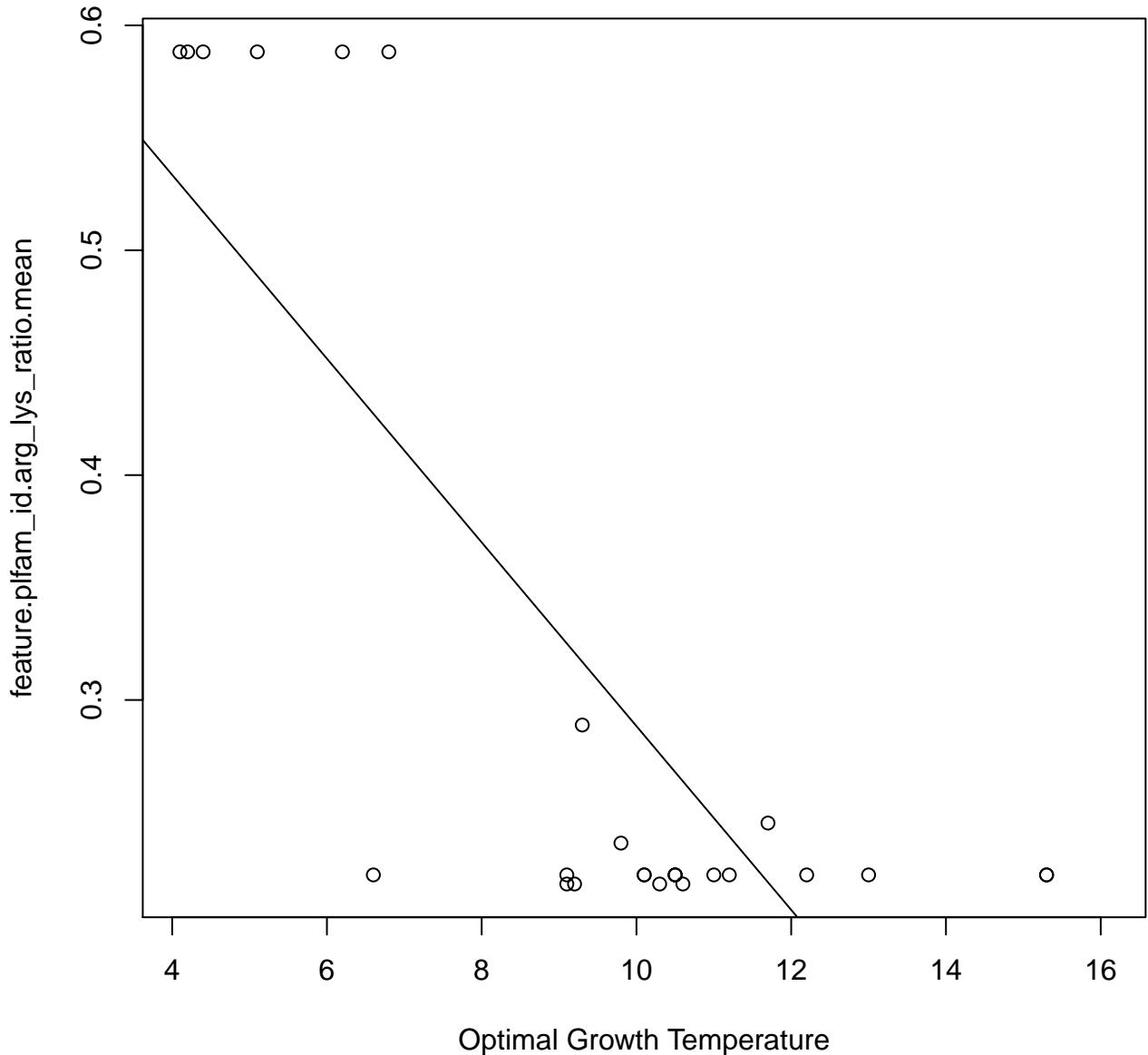
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PLF_28228_00001859
GGDEF domain protein



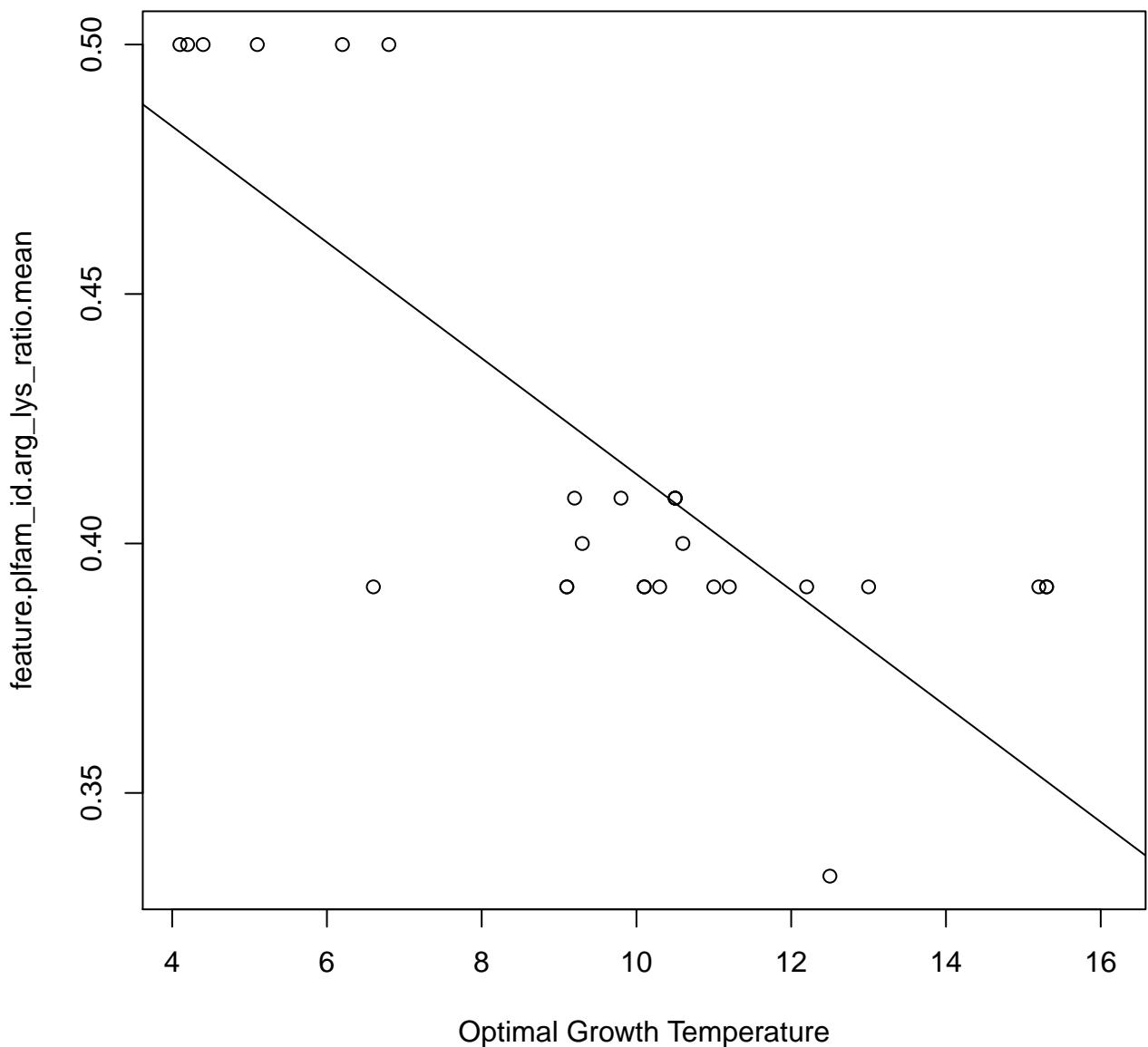
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001912
Phage integrase



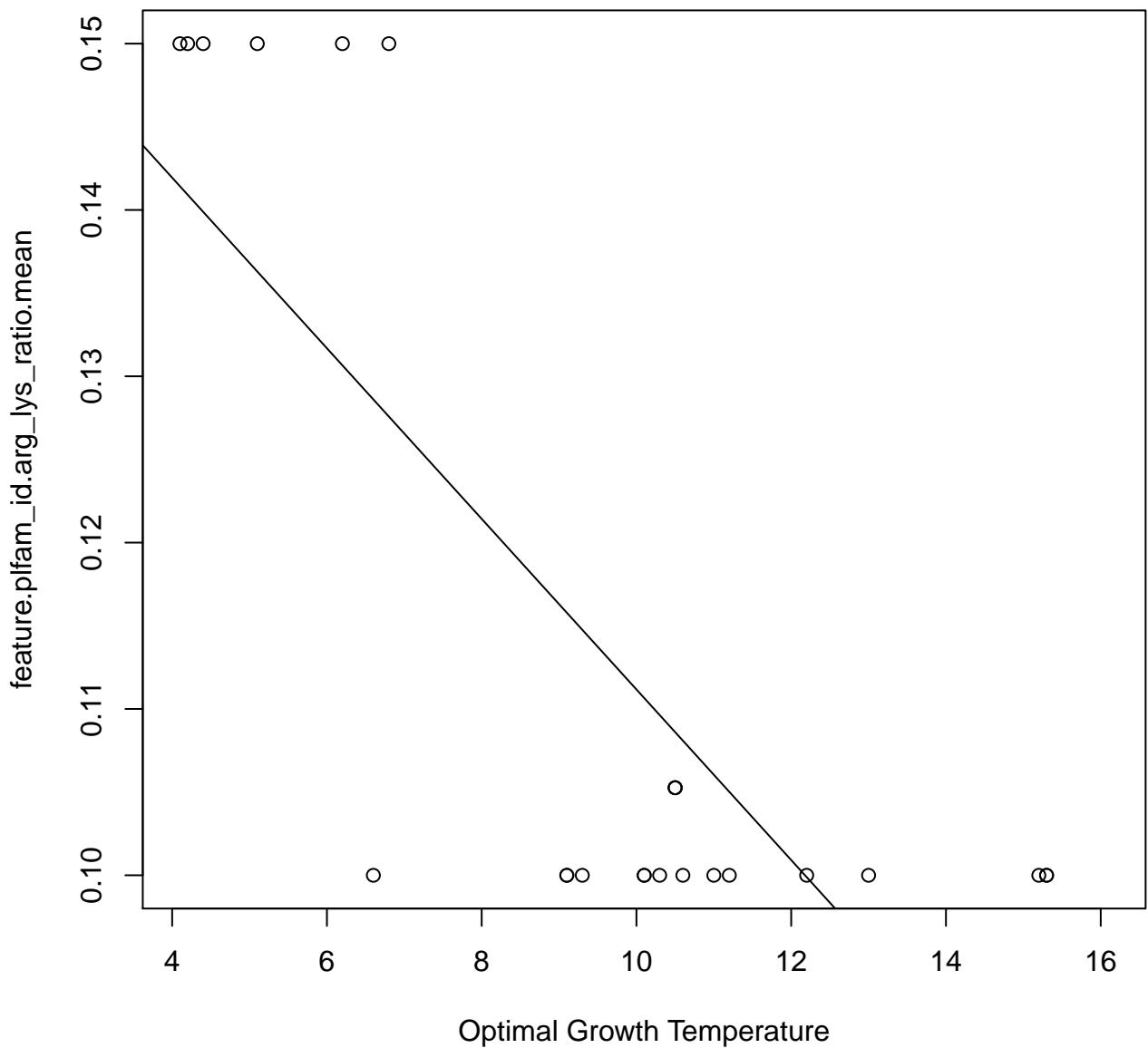
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00017455
Maltodextrin glucosidase (EC 3.2.1.20)



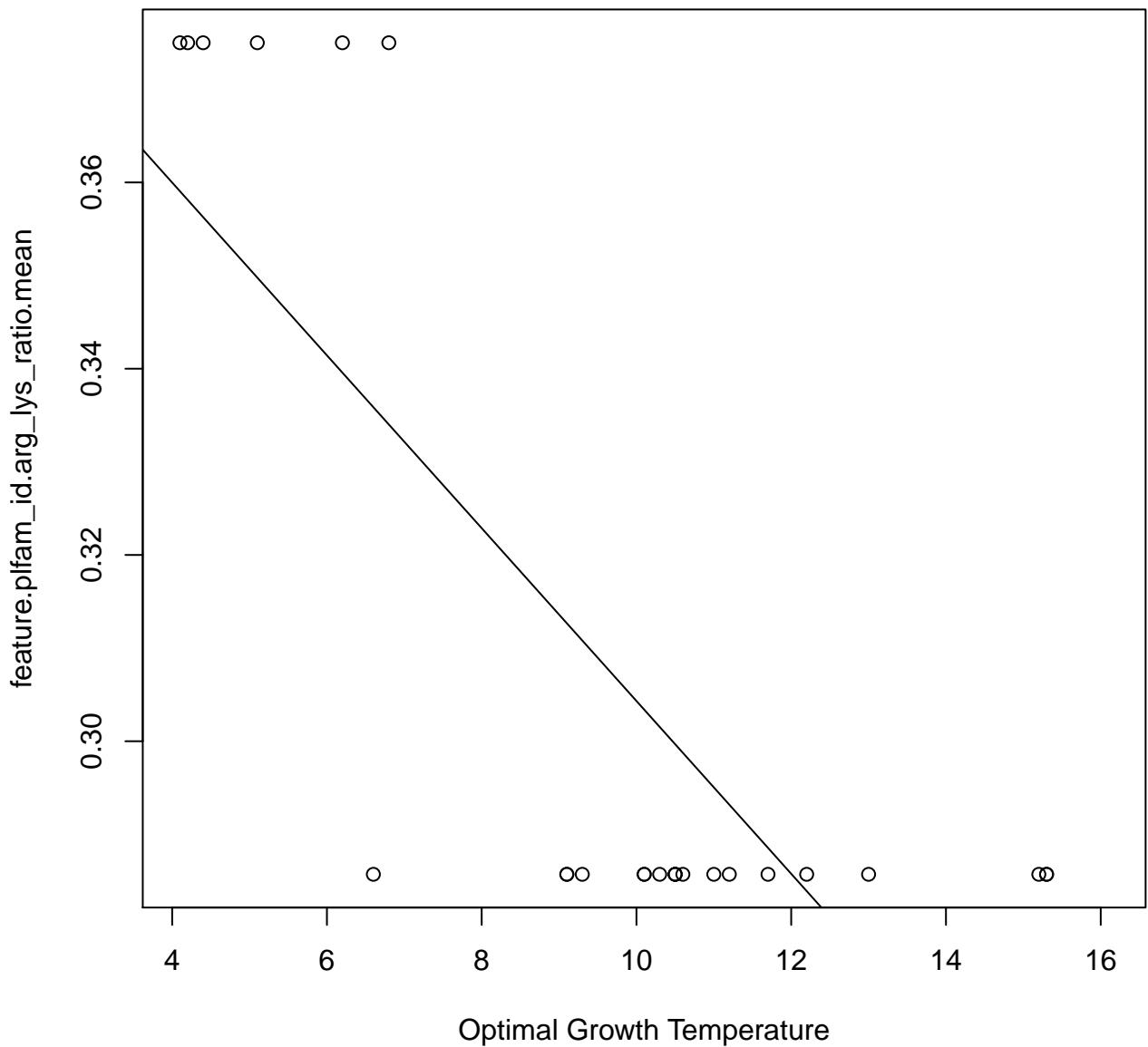
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PLF_28228_00014070
hypothetical protein



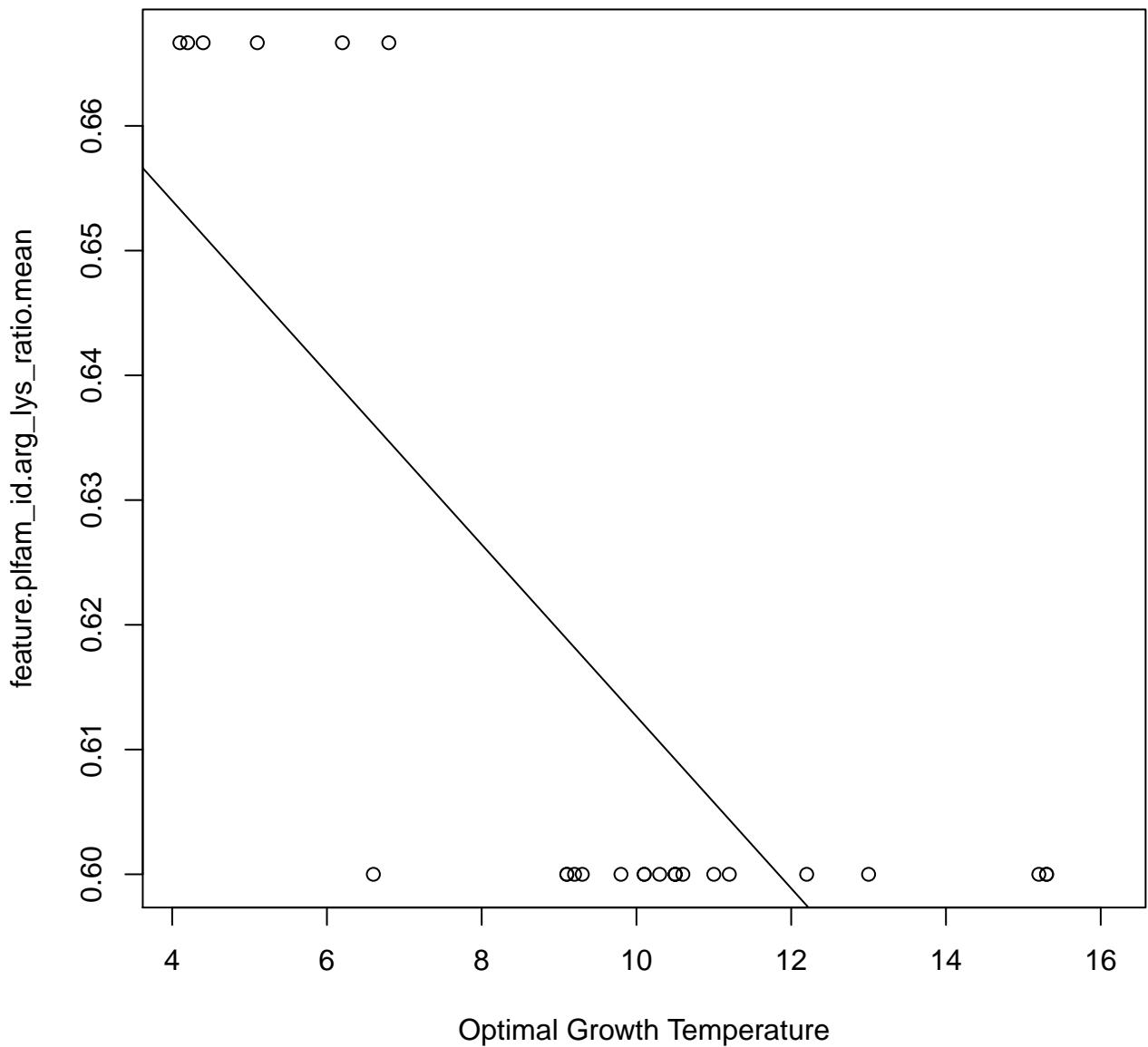
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PLF_28228_00030467
Redoxin domain protein



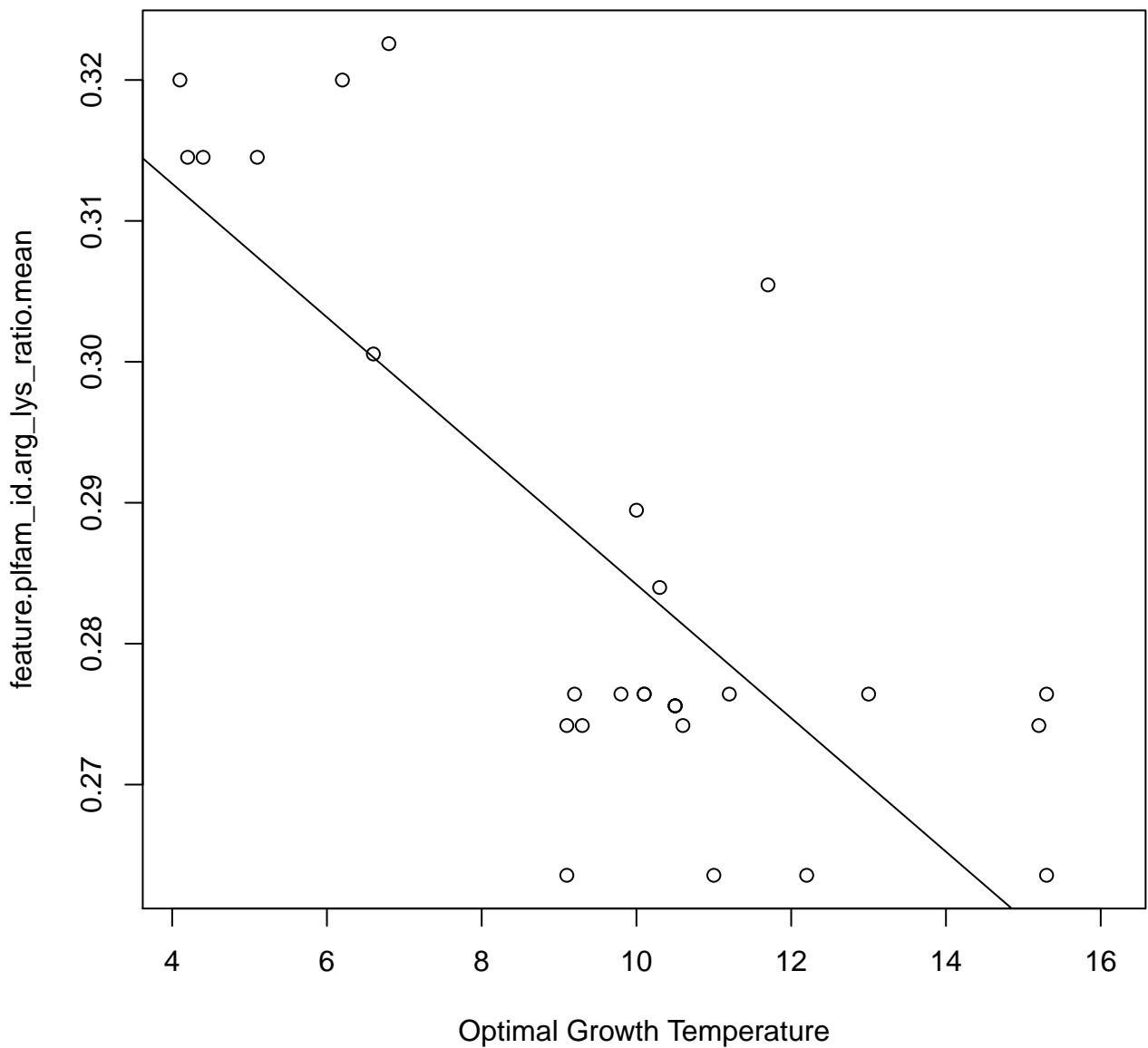
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PLF_28228_00029549
hypothetical protein



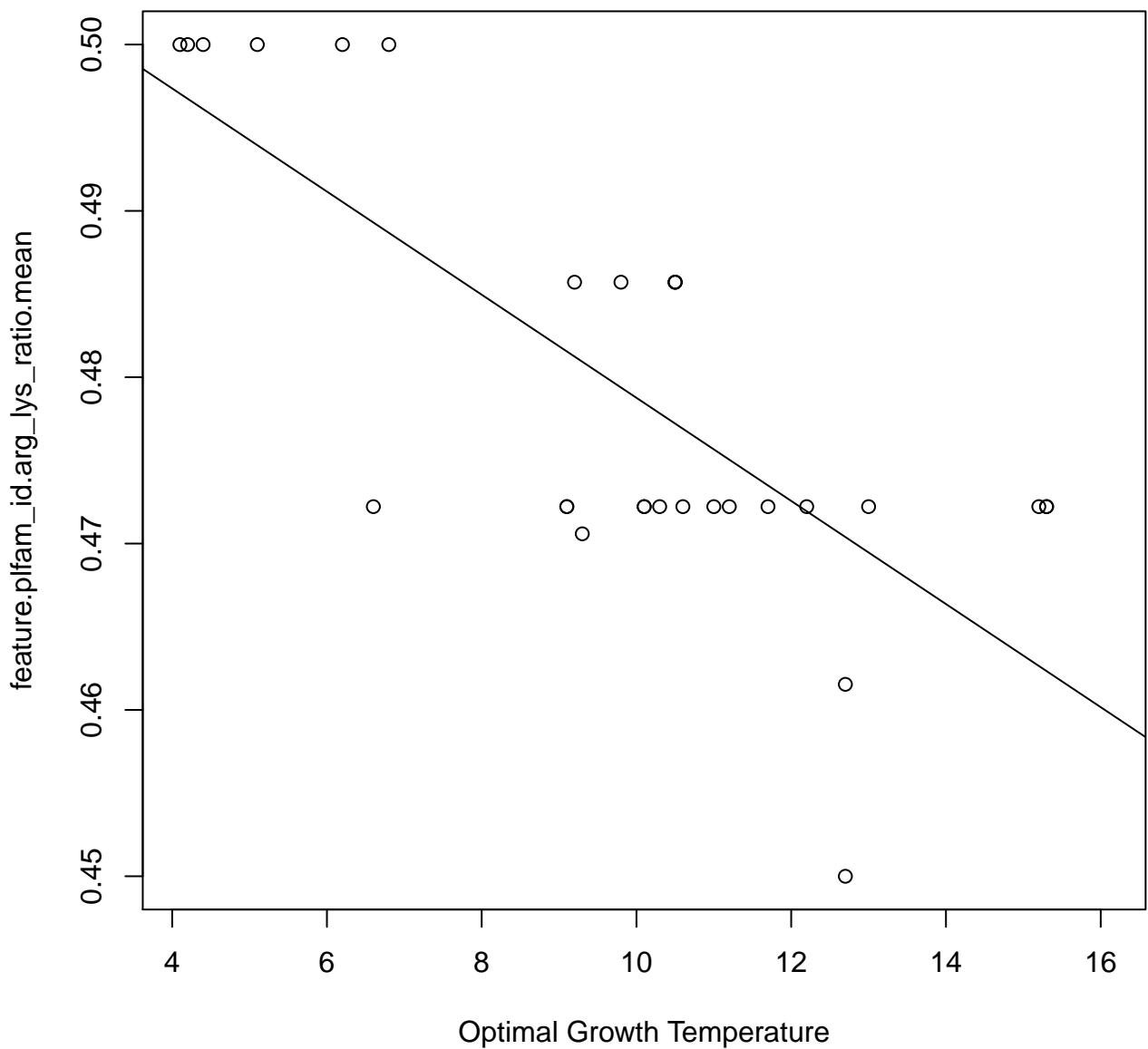
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PLF_28228_00029369
hypothetical protein



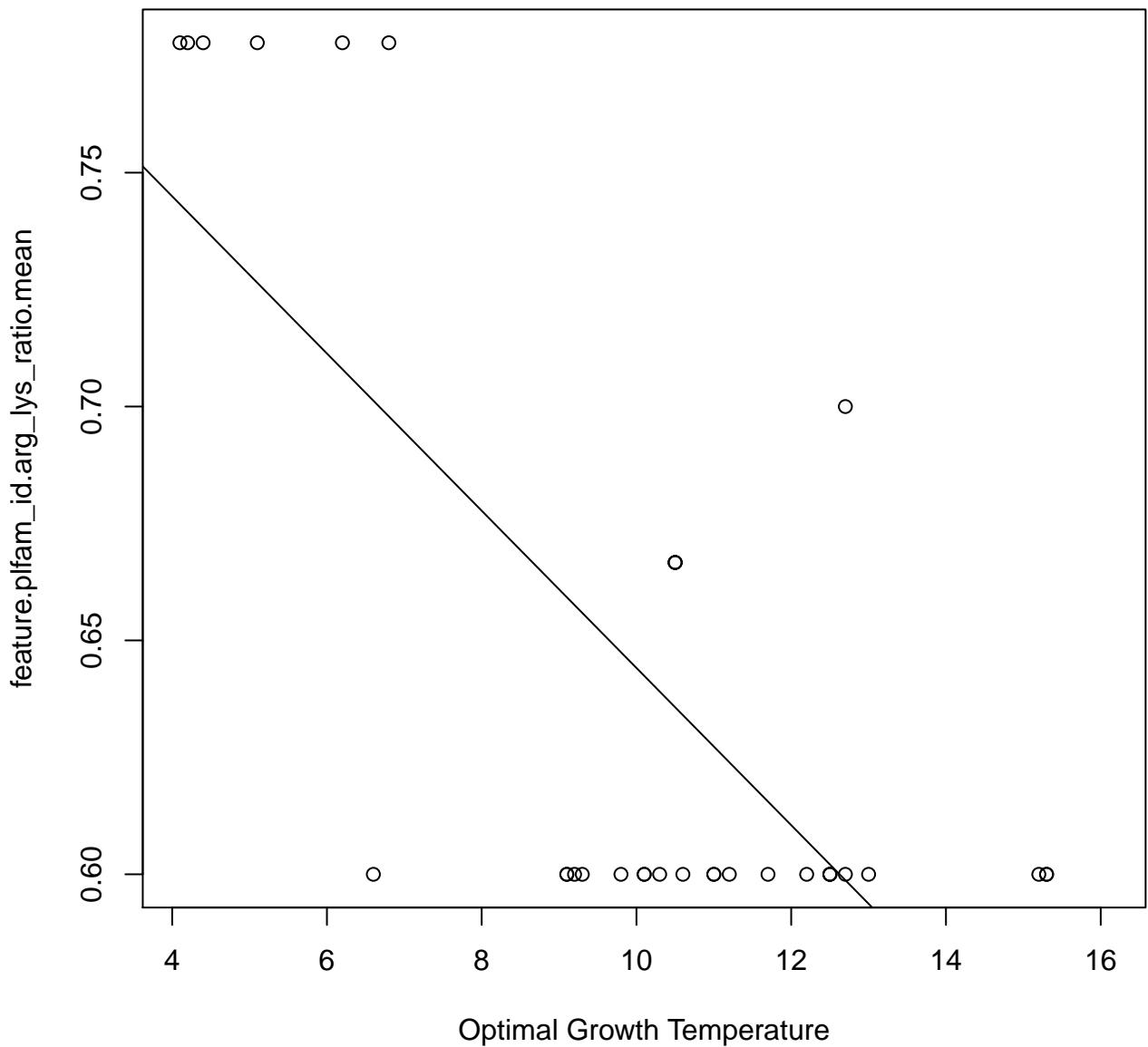
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PLF_28228_00015154
hypothetical protein



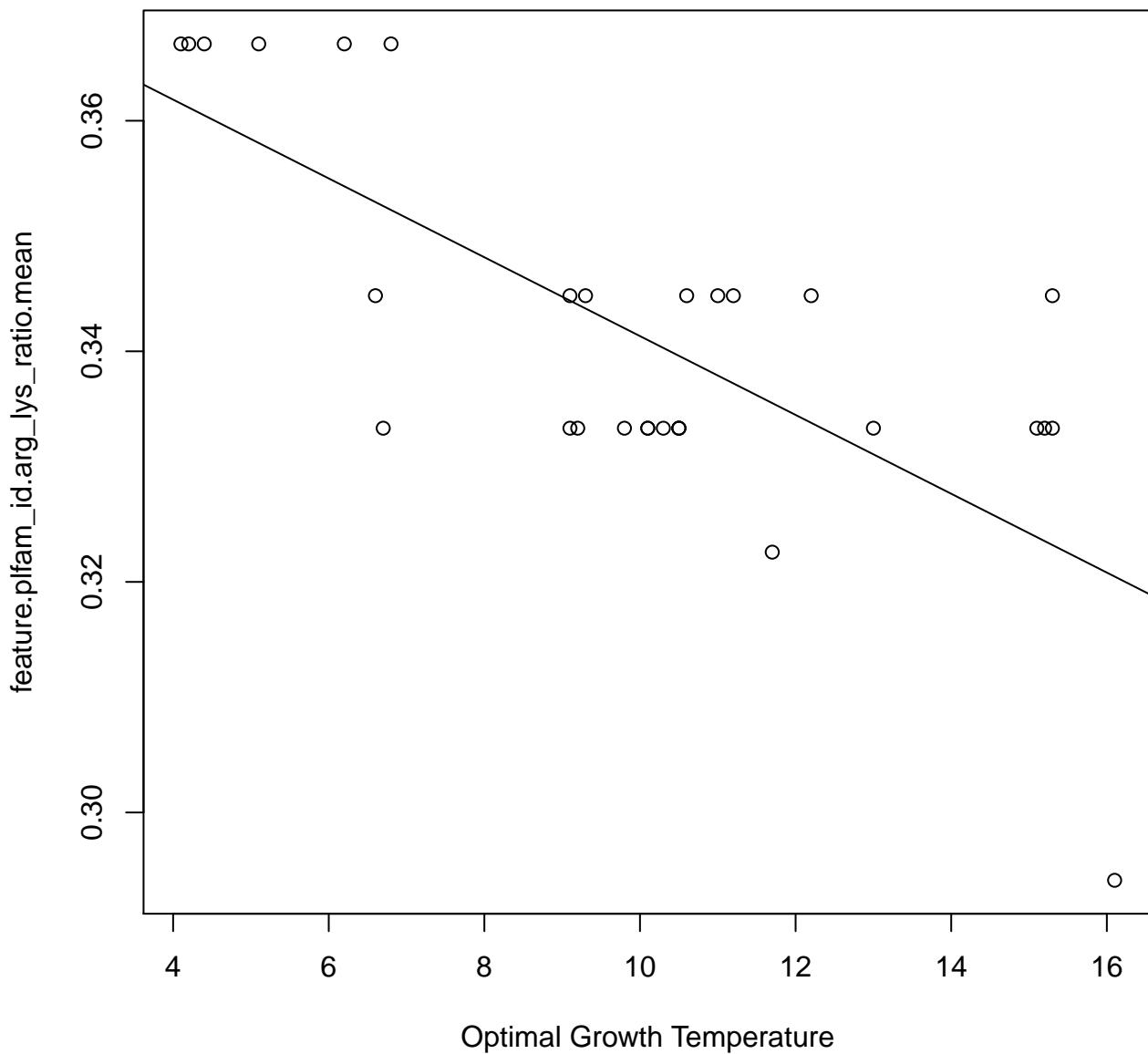
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hypothetical protein



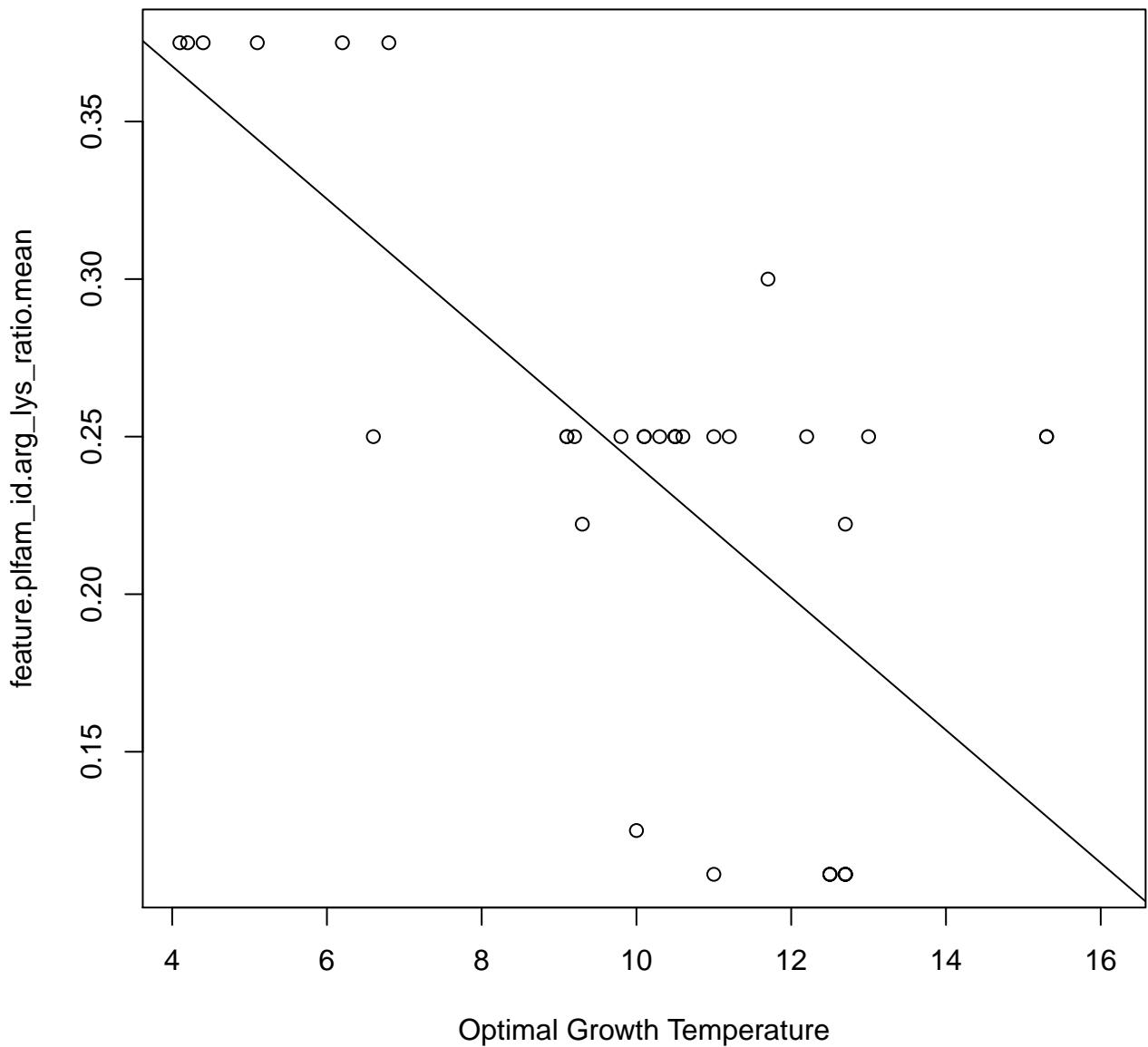
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00003600
Putative transmembrane protein



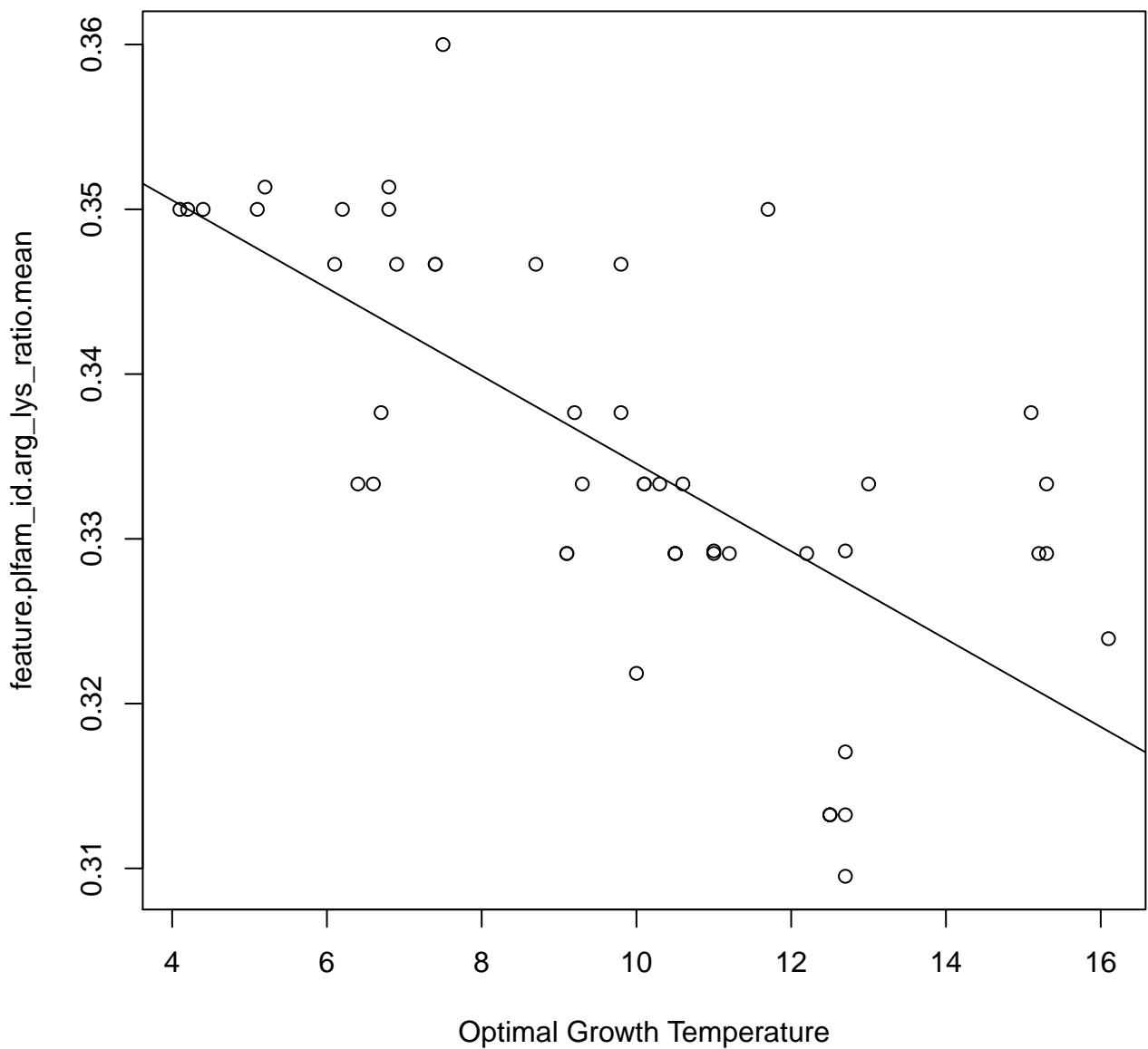
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00016853
Tryptophan 2,3-dioxygenase (EC 1.13.11.11)



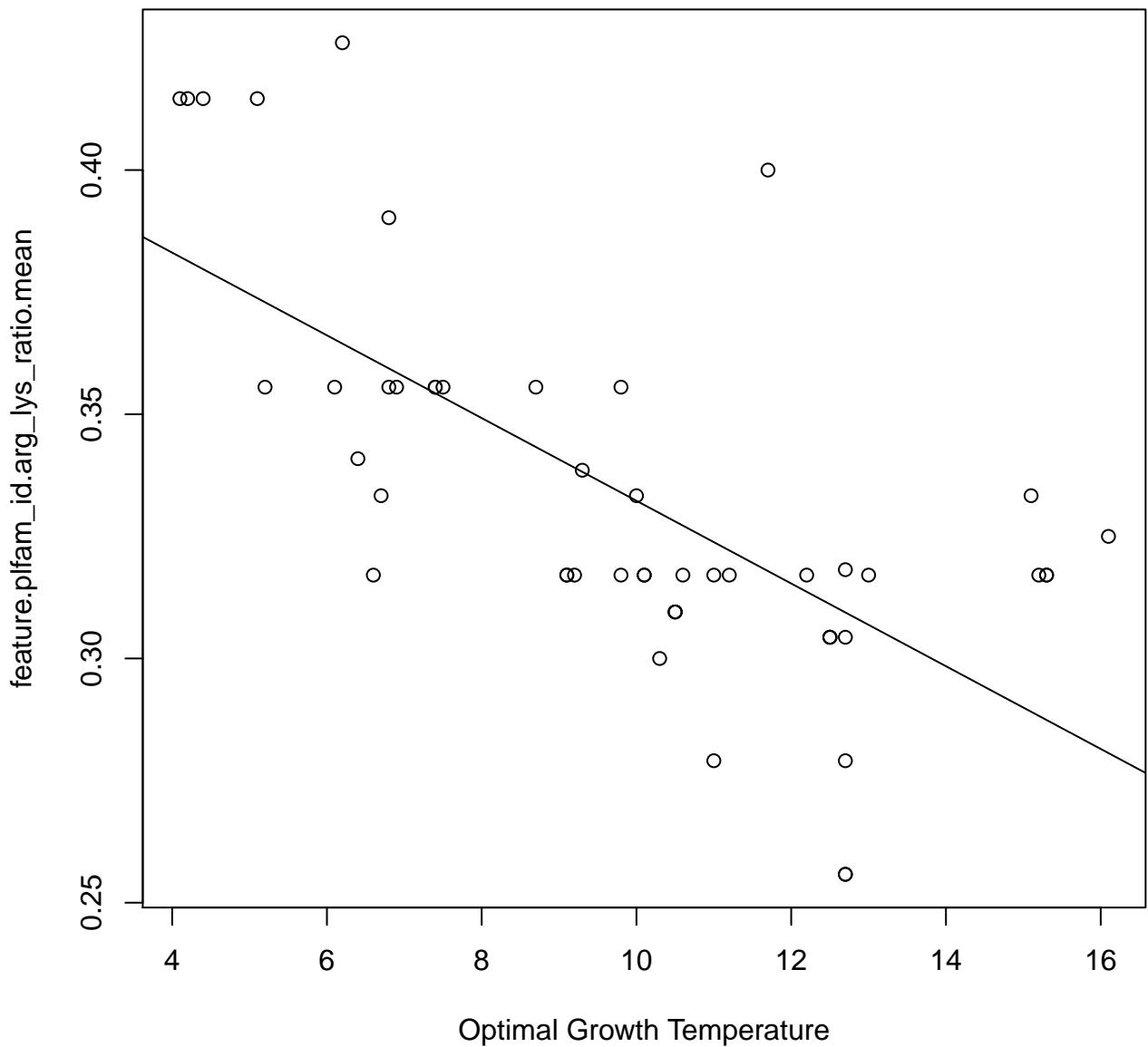
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PLF_28228_00000991
Putative manganese efflux pump MntP



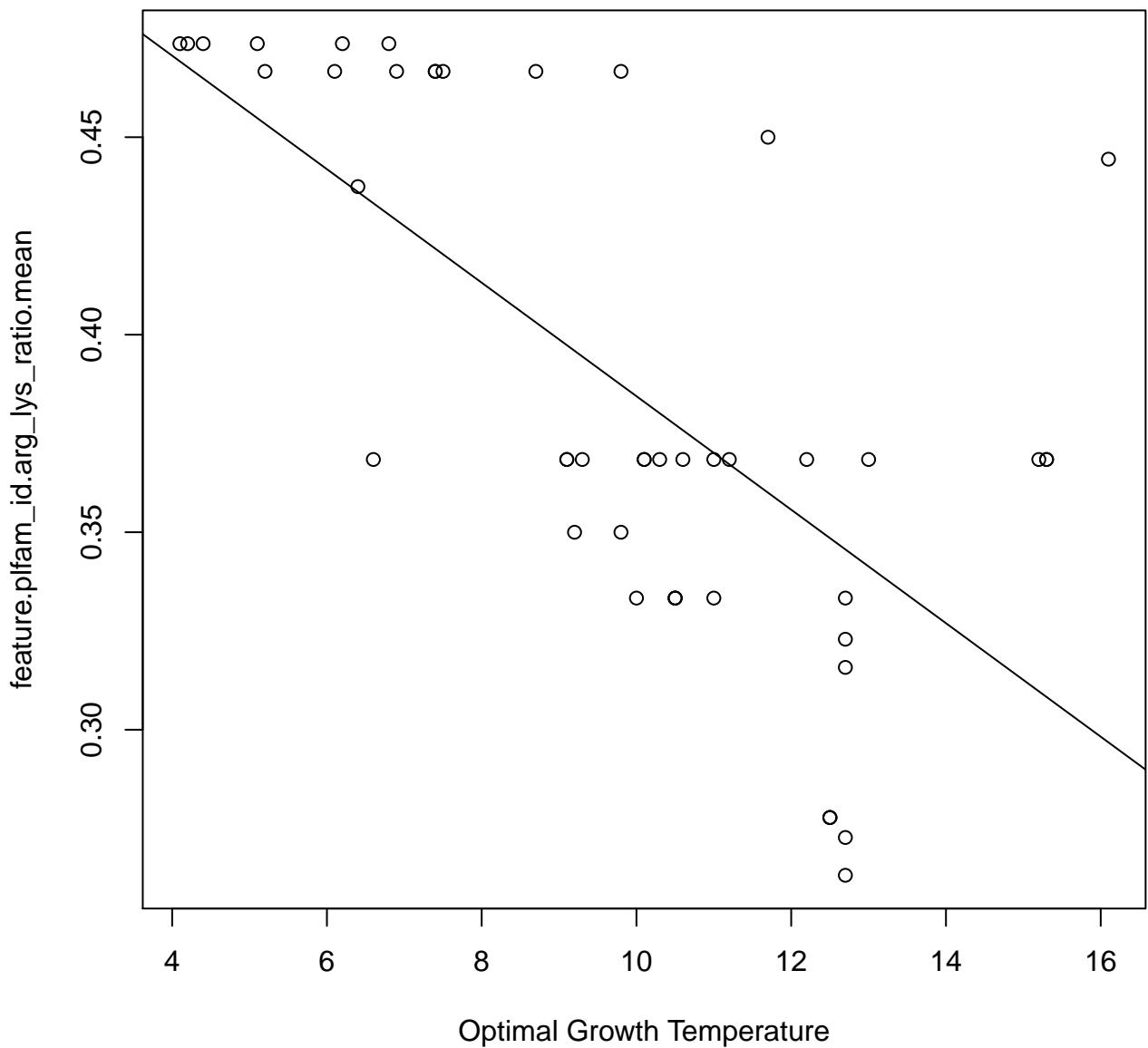
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002008
Related to collagenase



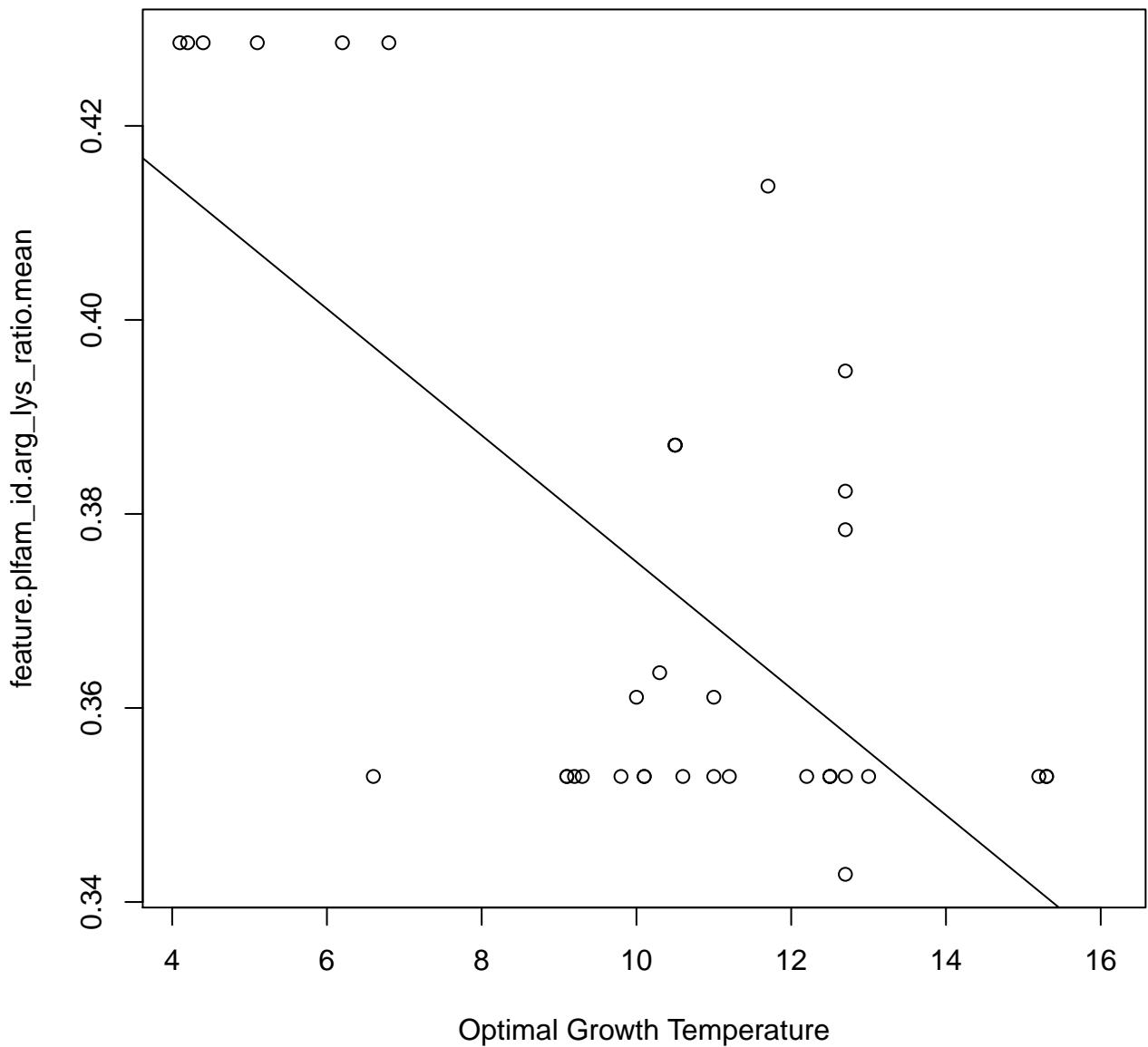
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000740
Alanine transaminase (EC 2.6.1.2)



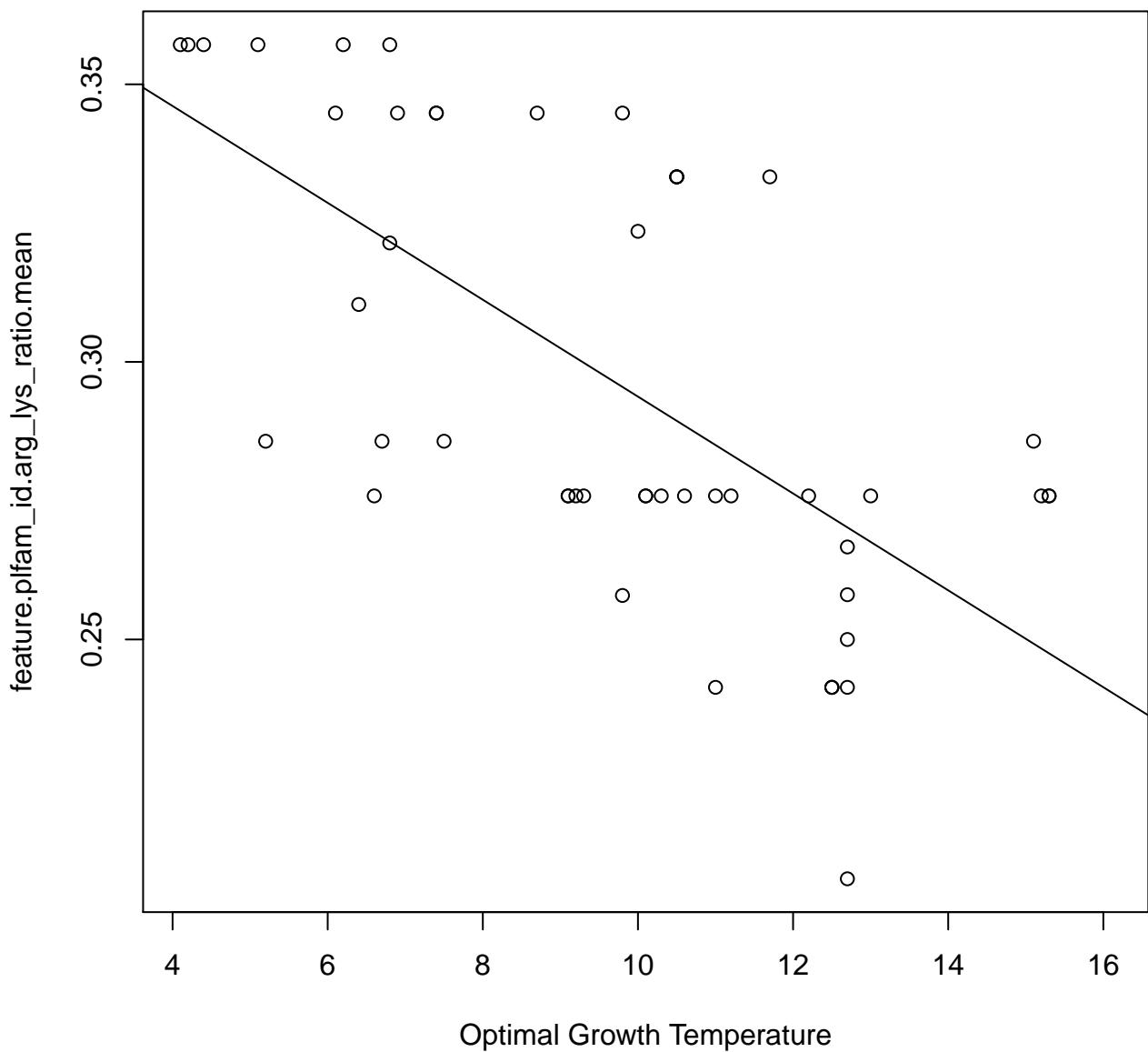
feature.plfam_id.arg_lyc_ratio.mean
PLF_28228_00001927
Potential queD like 2



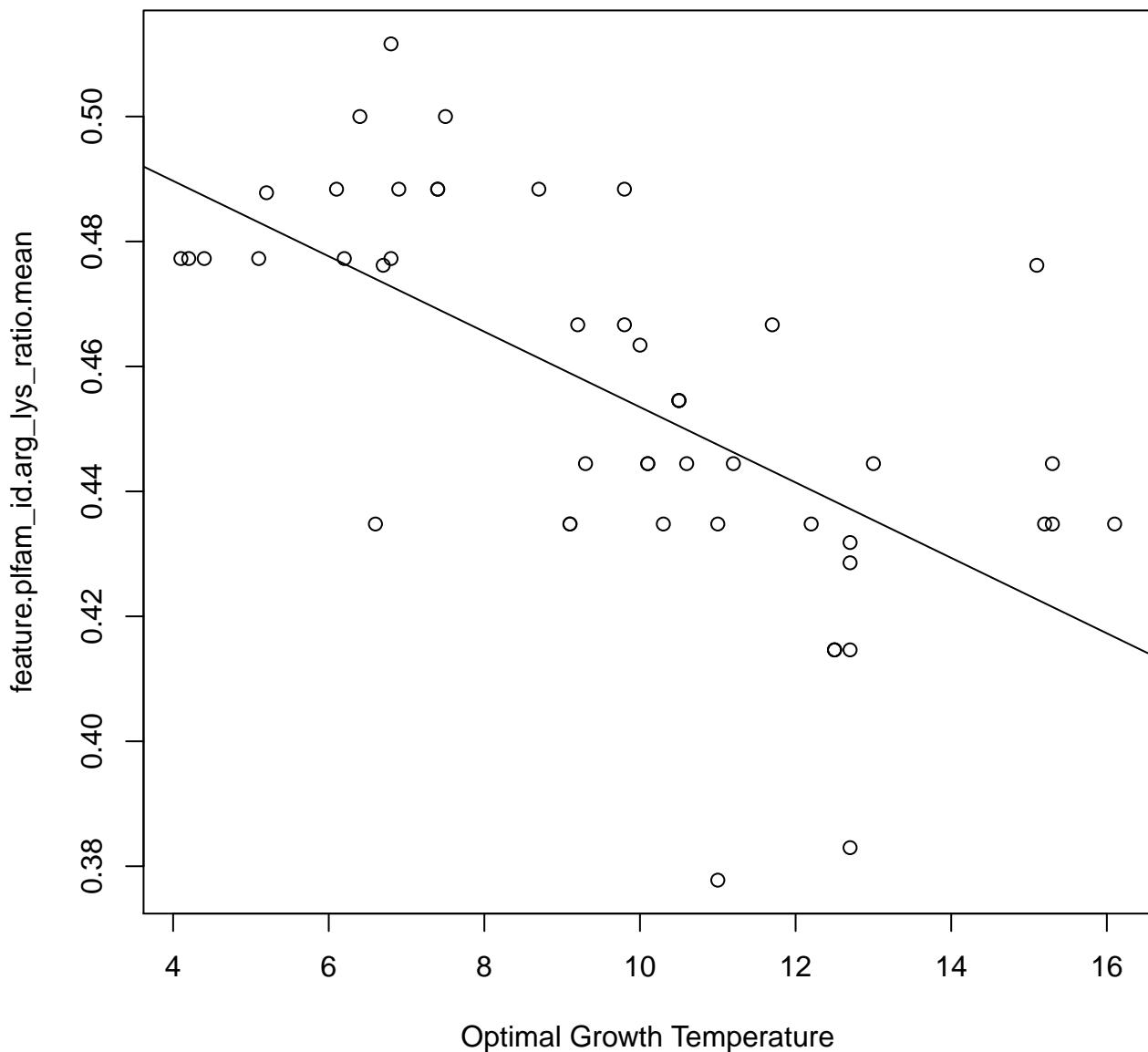
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001203
Cell division coordinator CpoB



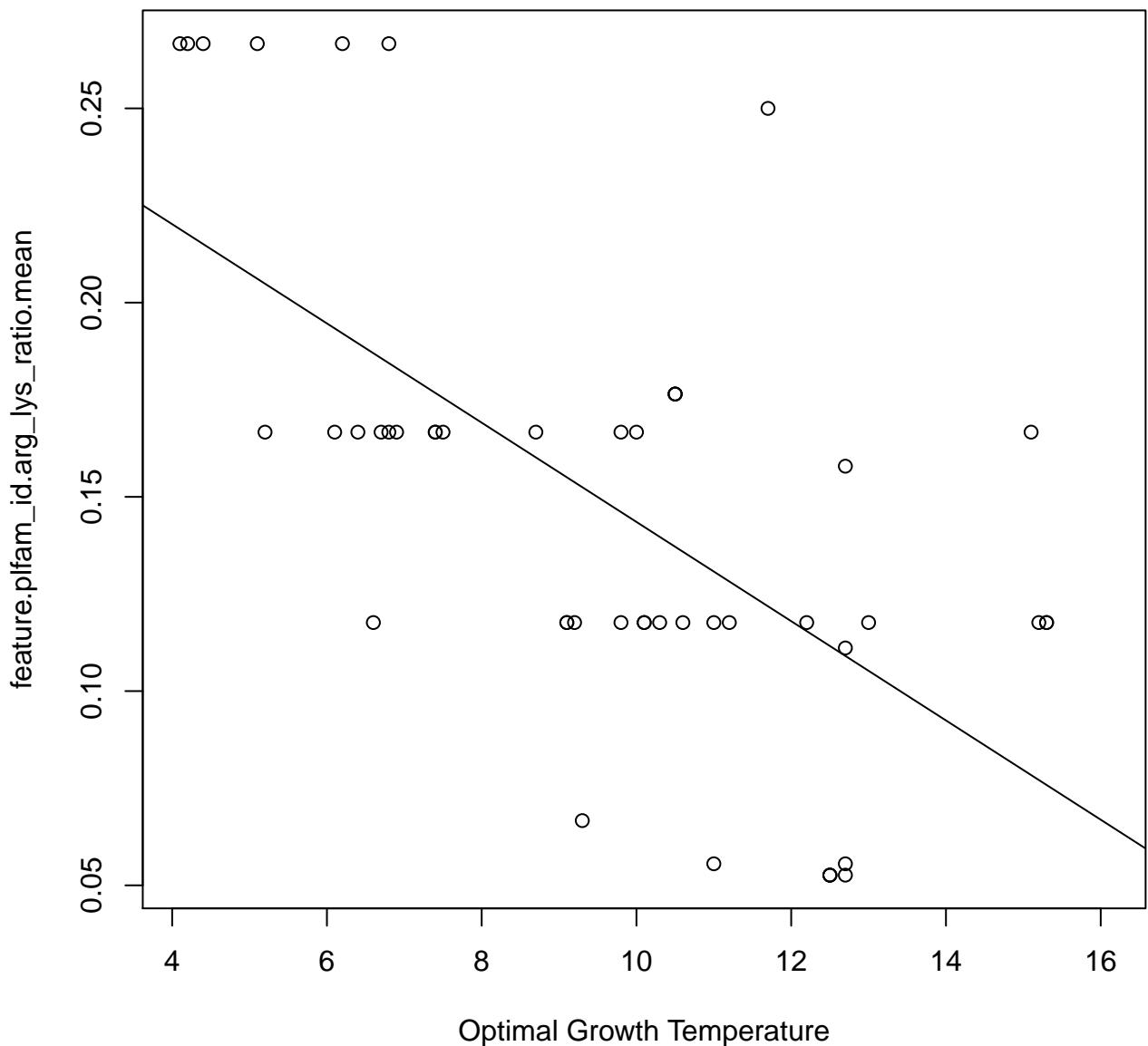
feature.plfam_id.arg_lyc_ratio.mean
PLF_28228_00001366
hypothetical protein



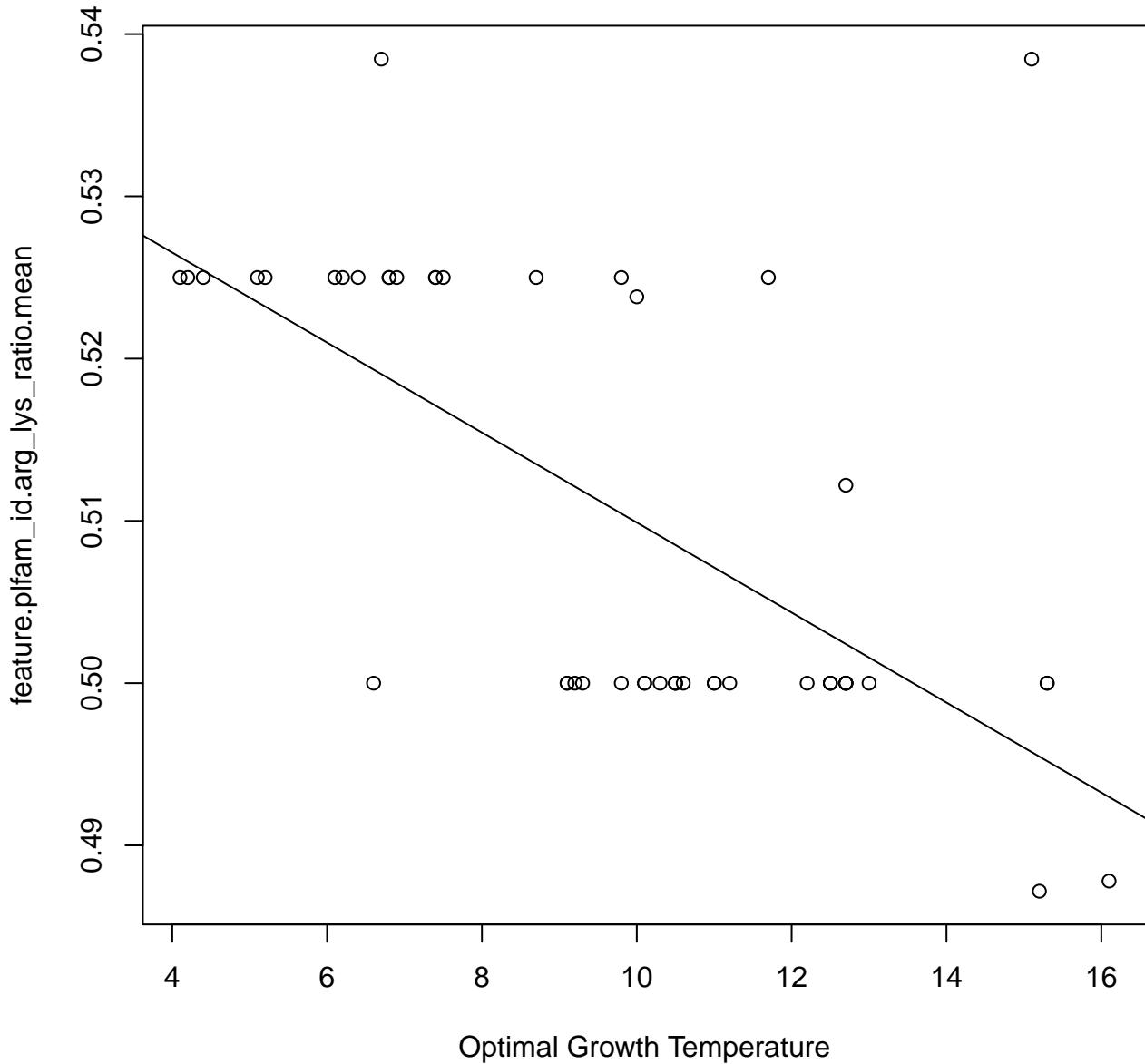
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000141
RND efflux system, membrane fusion protein



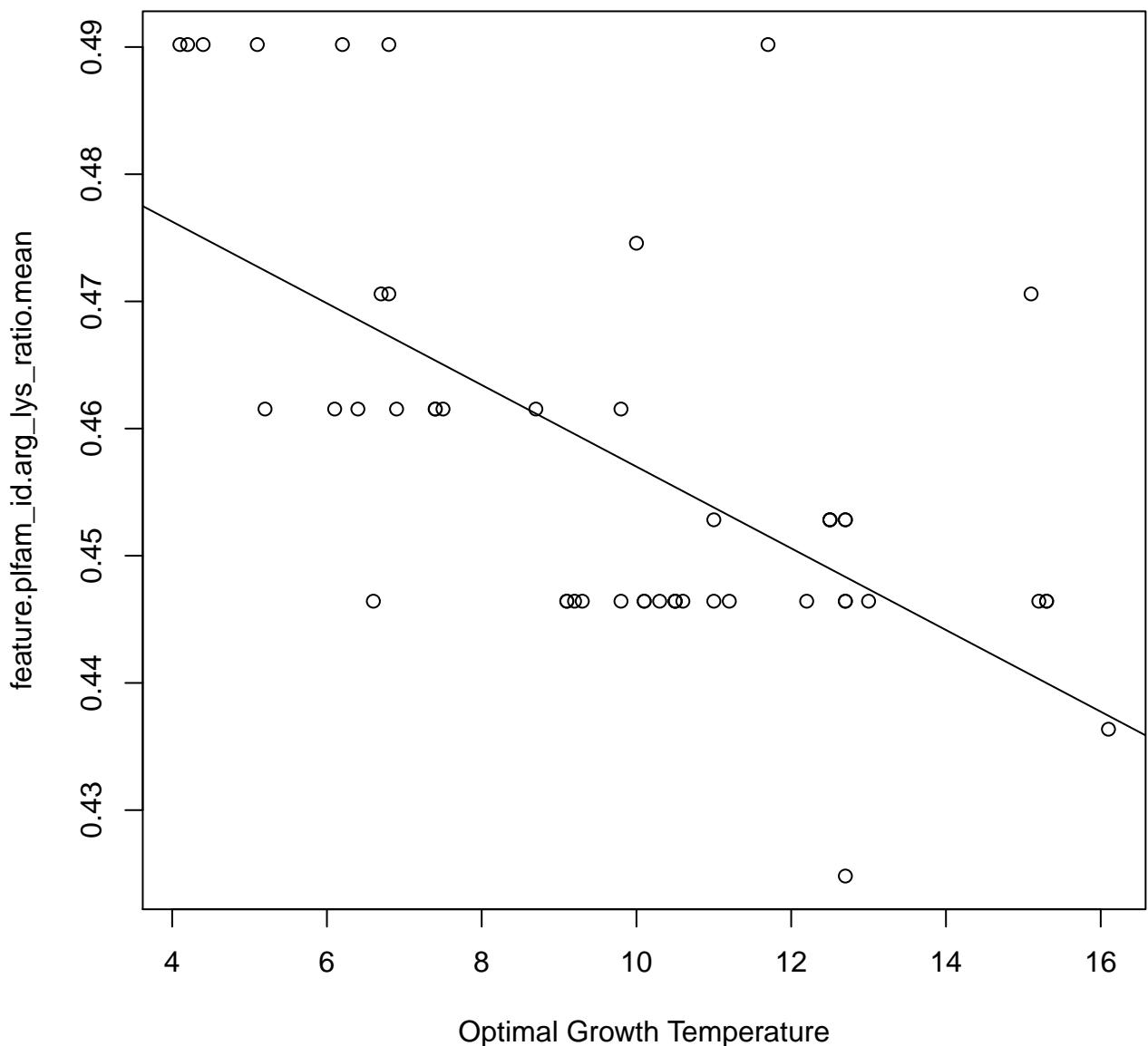
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002406
hypothetical protein



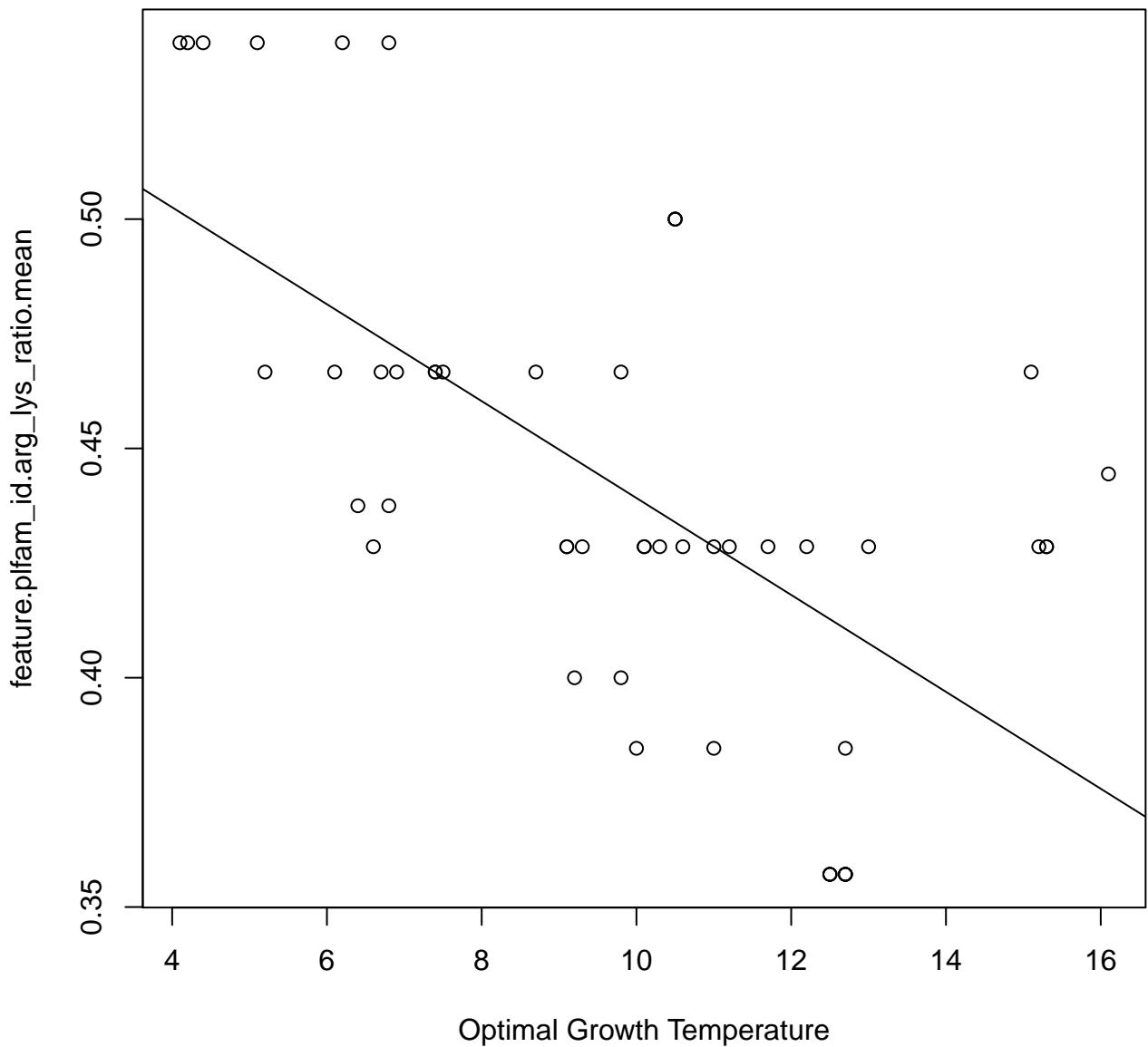
feature.plfam_id.arg_lyso_ratio.mean
PLF_28228_00000461
DNA polymerase III beta subunit (EC 2.7.7.7)



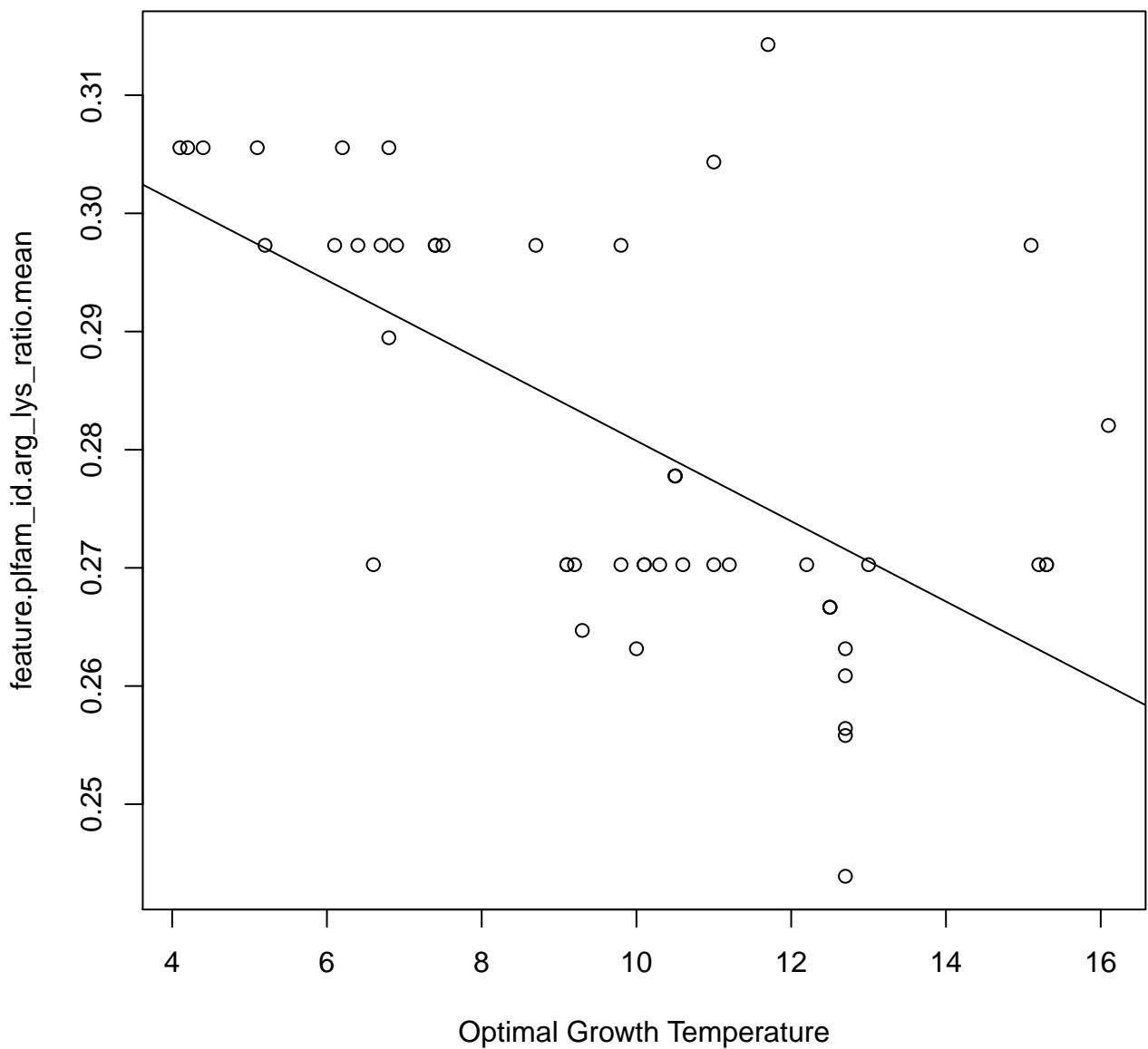
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000537
Isocitrate lyase (EC 4.1.3.1)



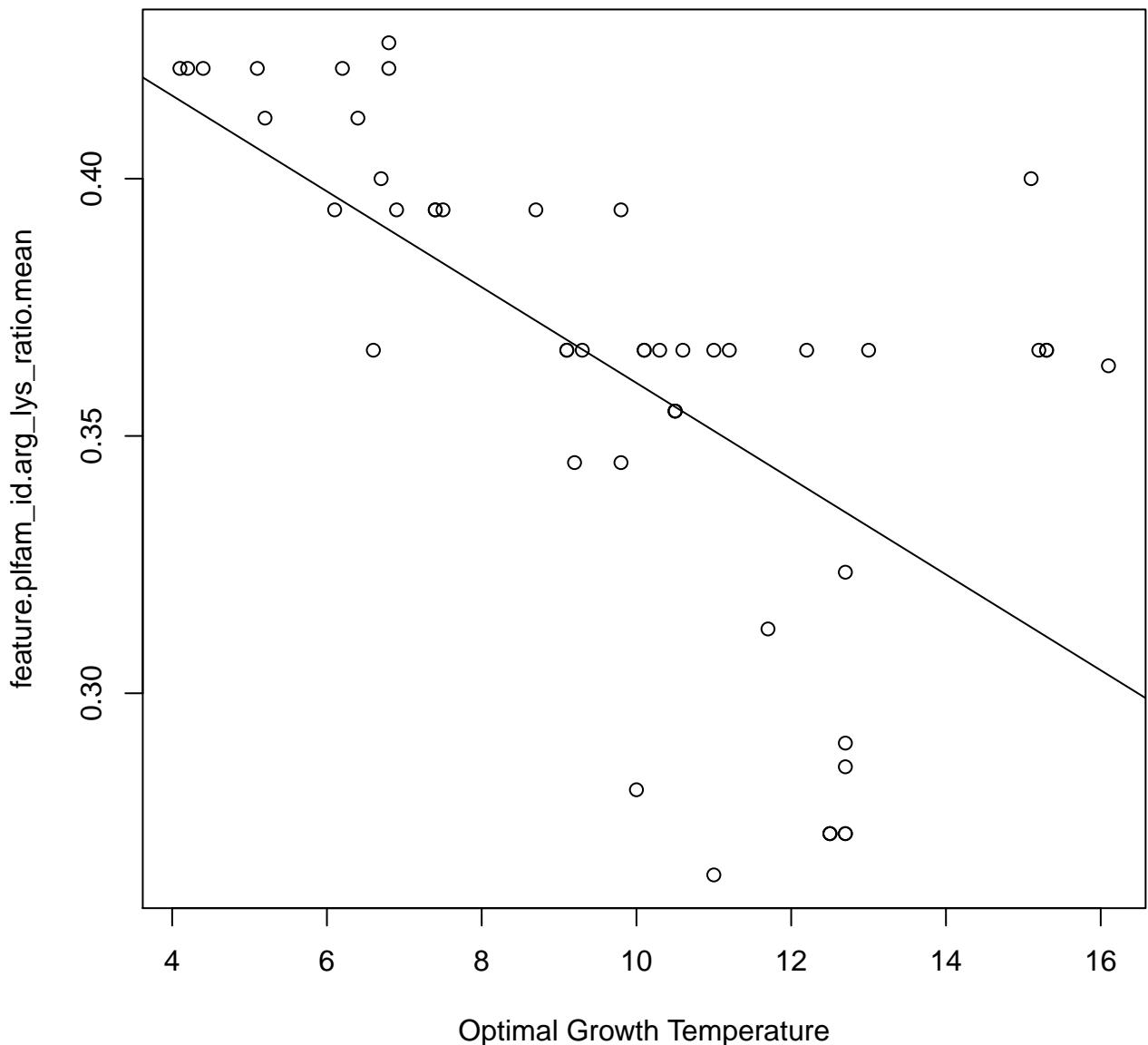
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002875
Uncharacterized protein YfgD, not an arsenate reductase



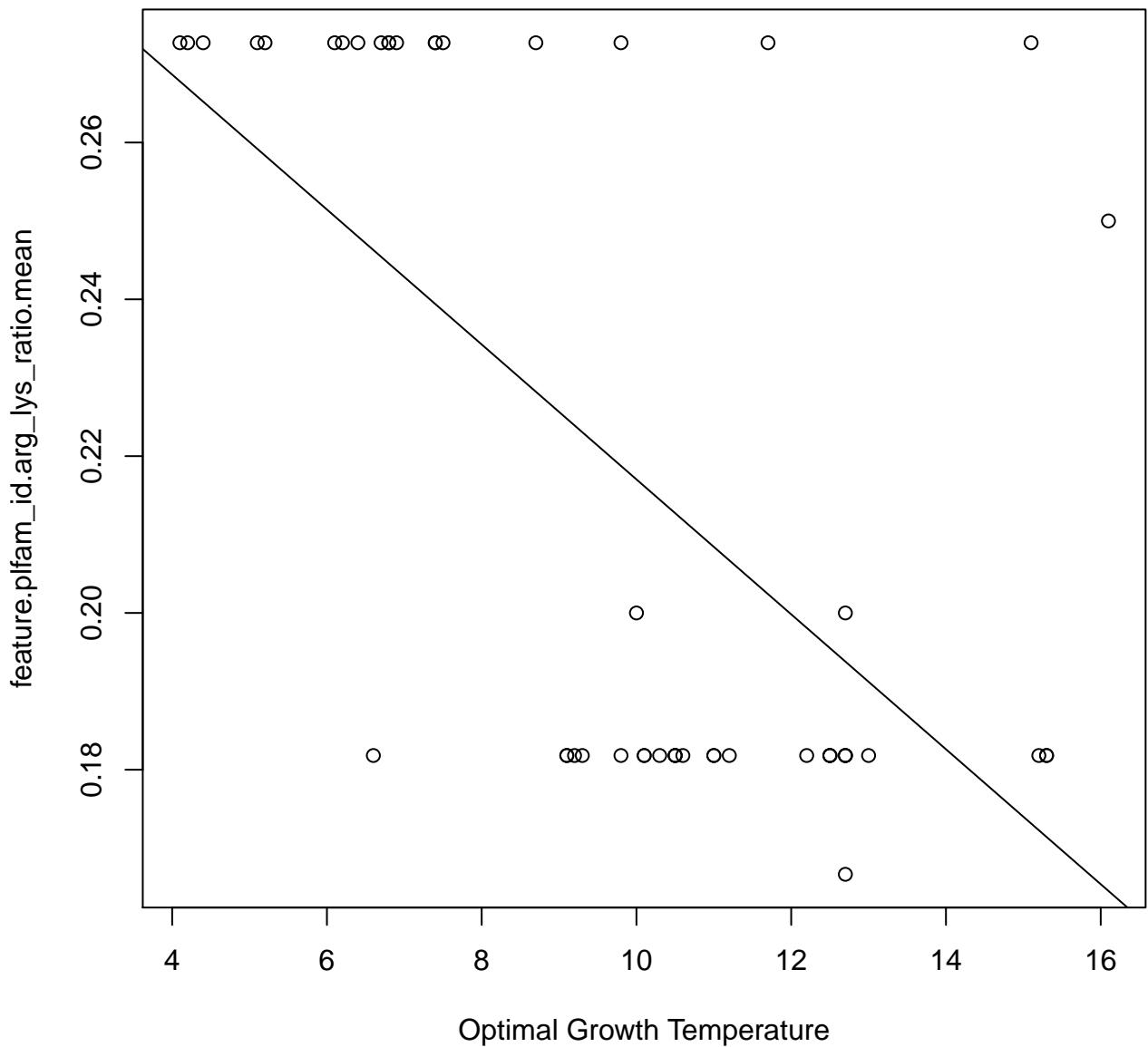
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002251
hypothetical protein



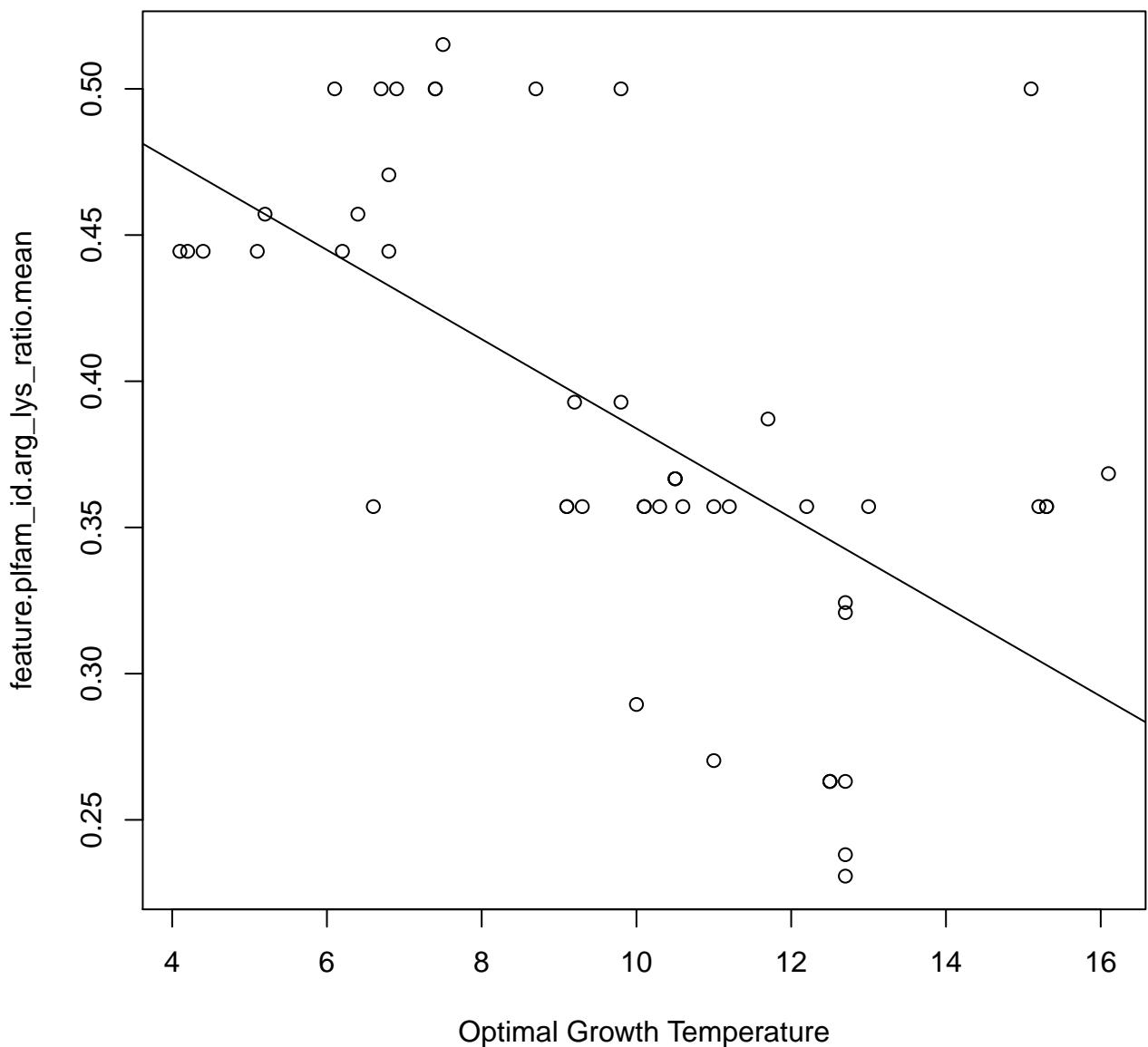
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000670
Nucleoside triphosphate pyrophosphohydrolase MazG (EC 3.6.1.8)



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001841
Flagellar hook-basal body complex protein FliE



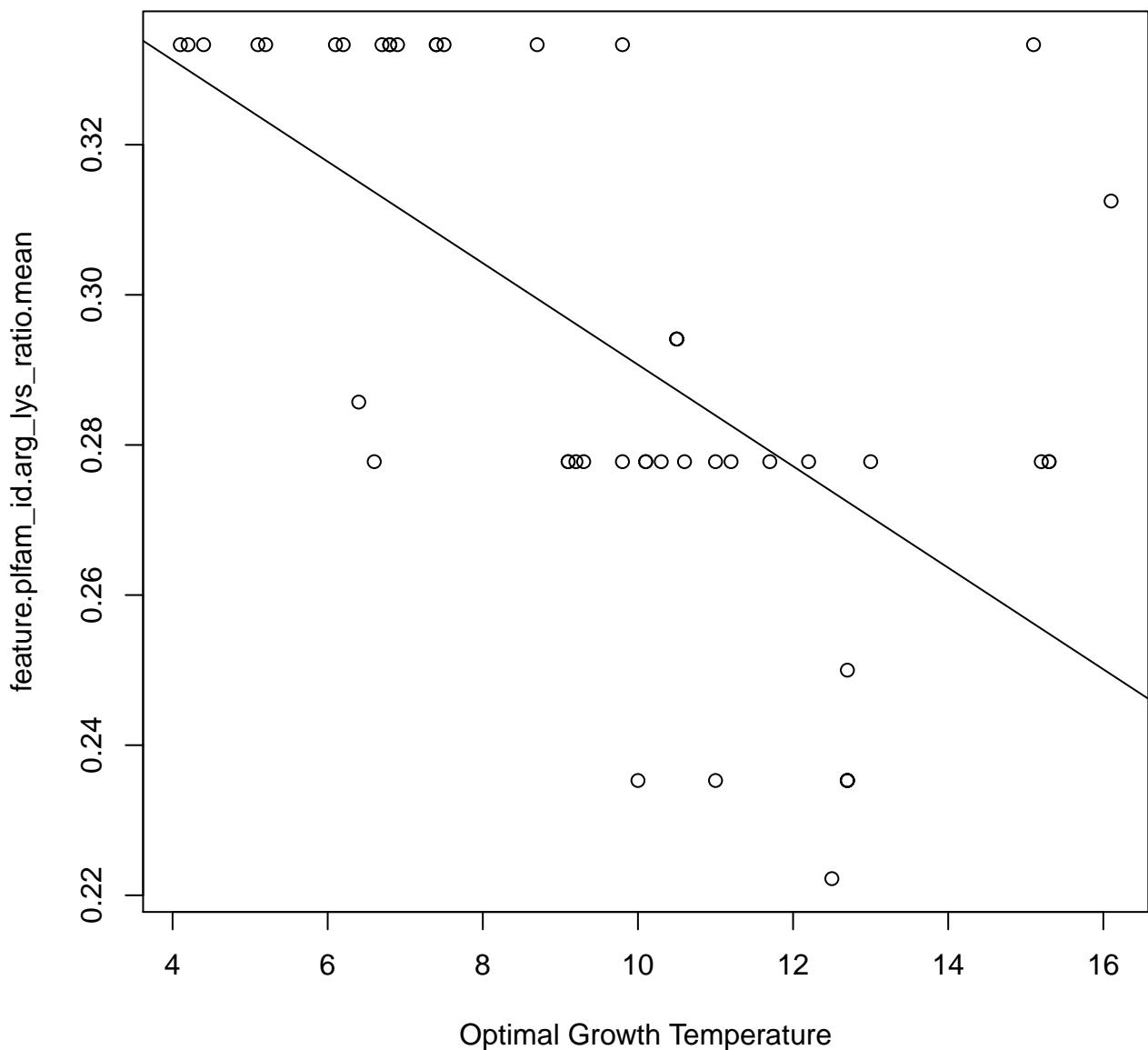
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001134
Septum-associated rare lipoprotein A



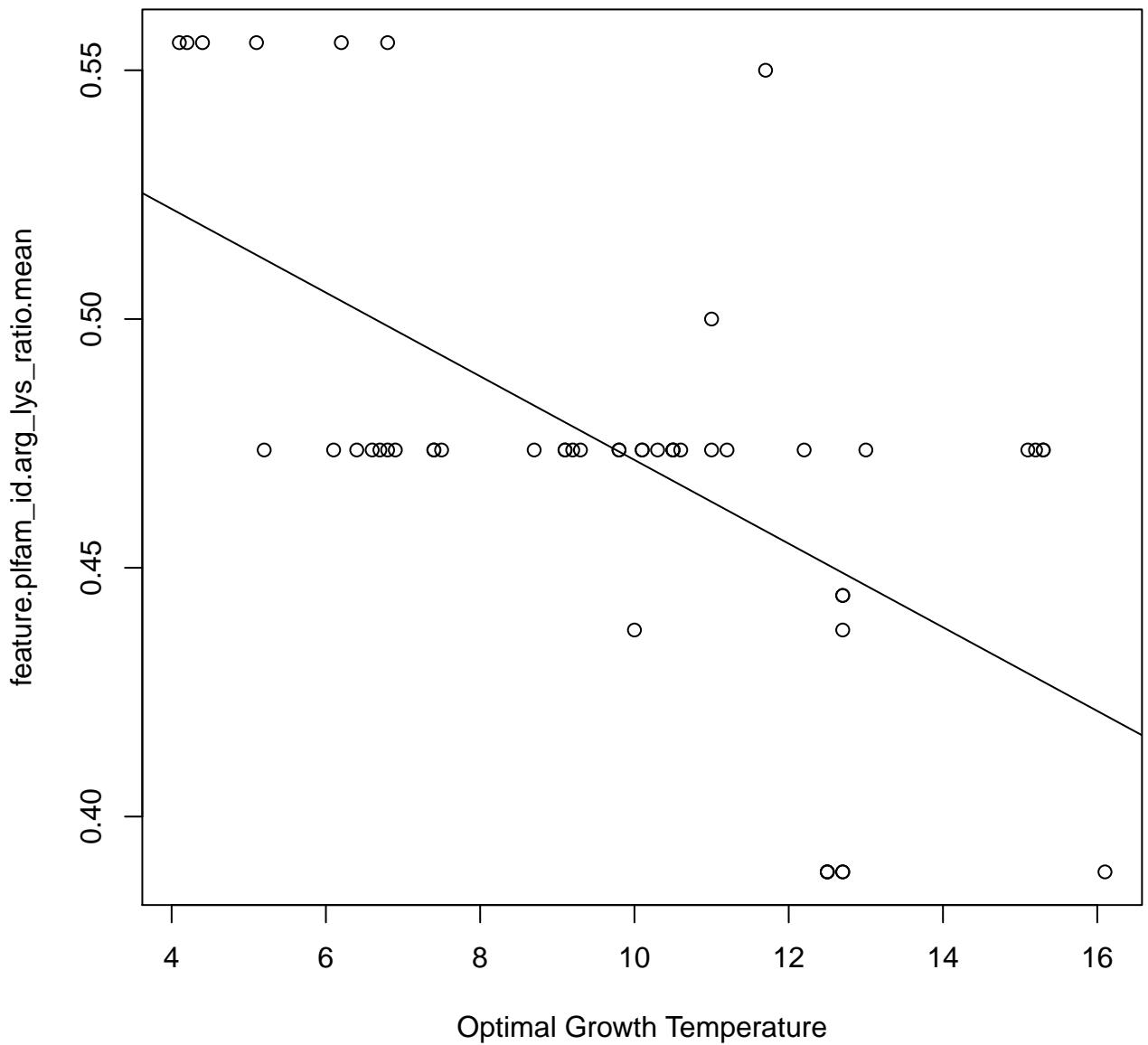
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PLF_28228_00028265

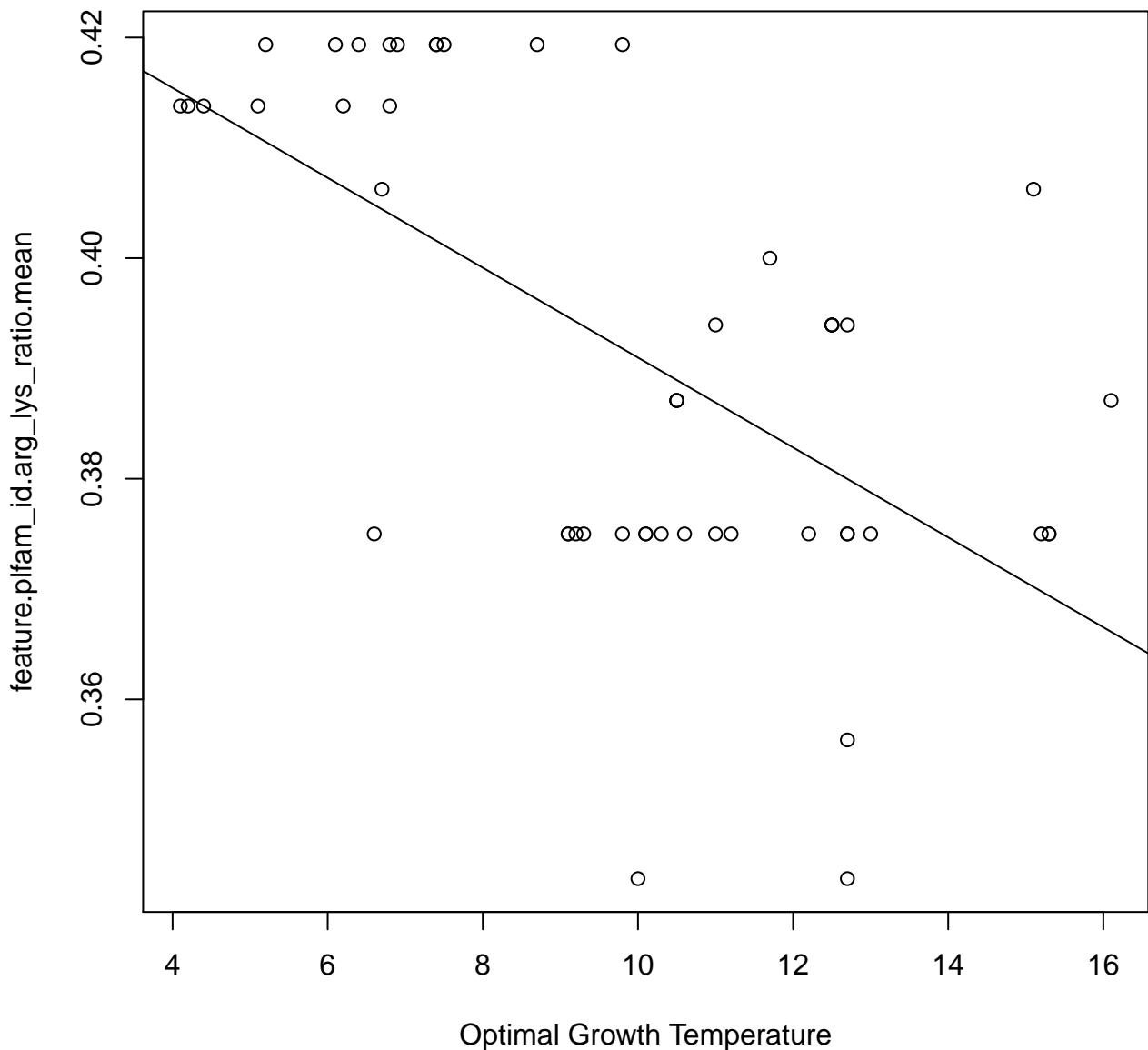
Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)



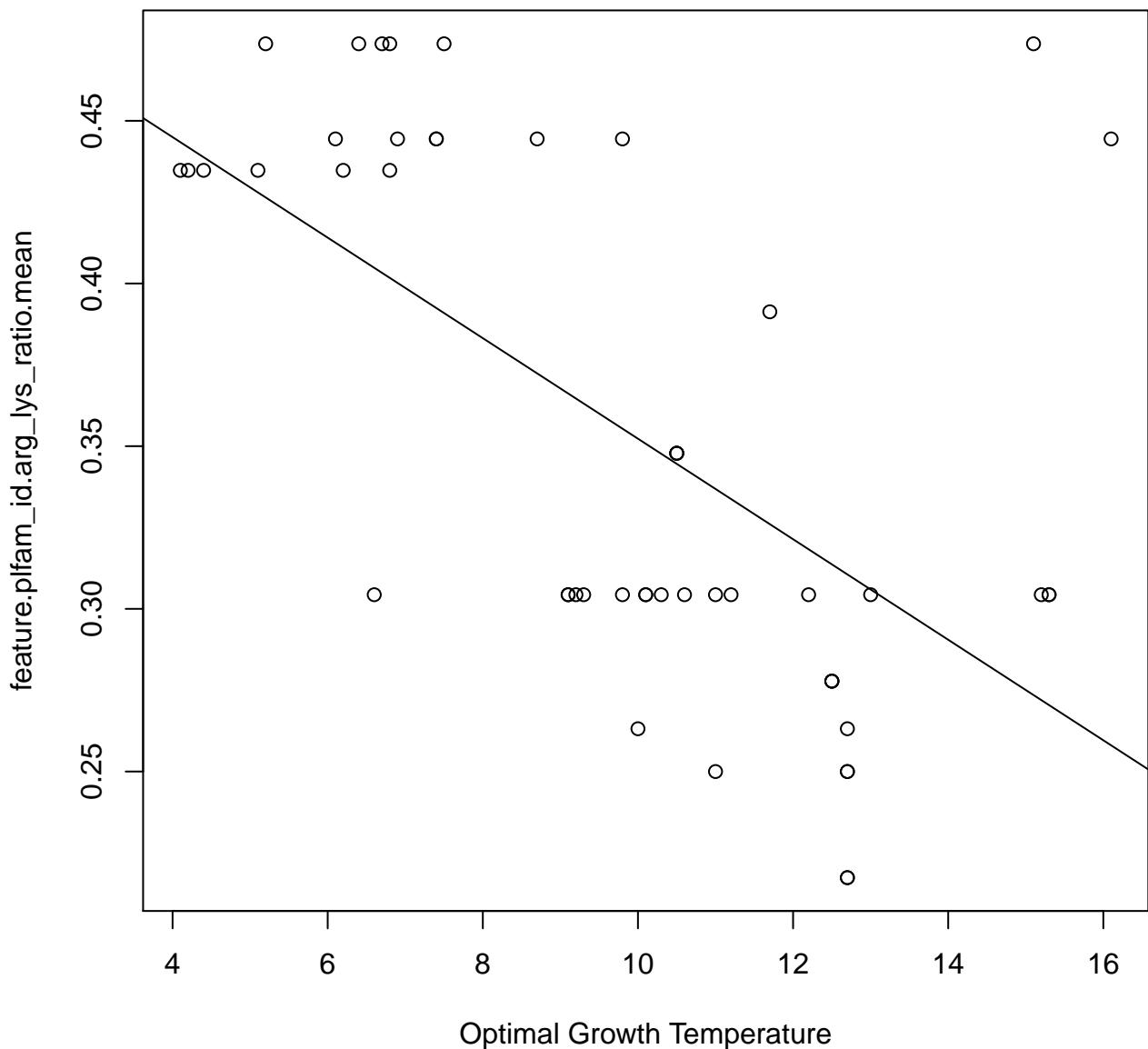
feature.plfam_id.arg_lyc_ratio.mean
PLF_28228_00000522
Inner membrane protein YrbG, predicted calcium/sodium:proton antiporter



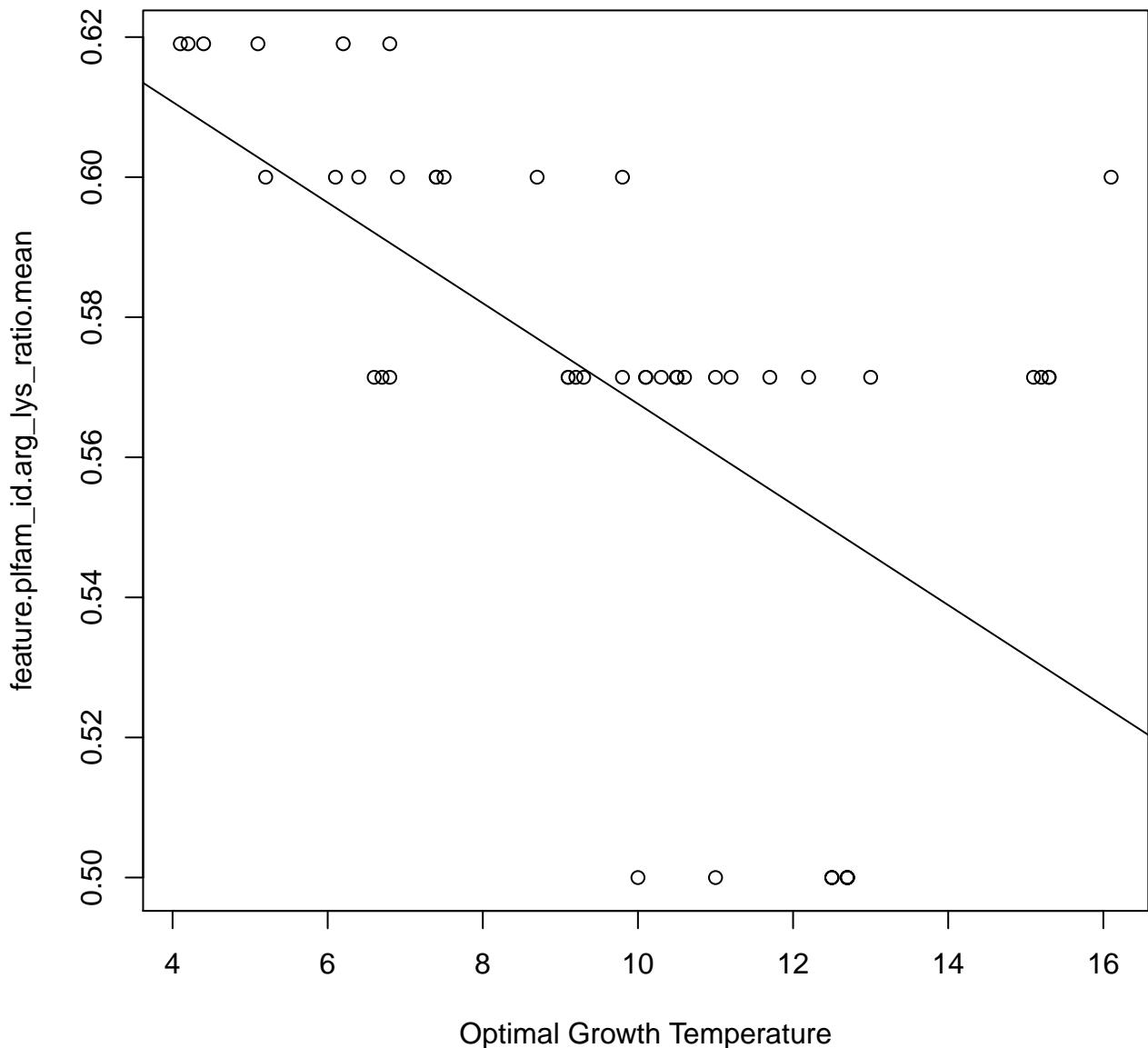
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000809
L-threonine 3-dehydrogenase (EC 1.1.1.103)



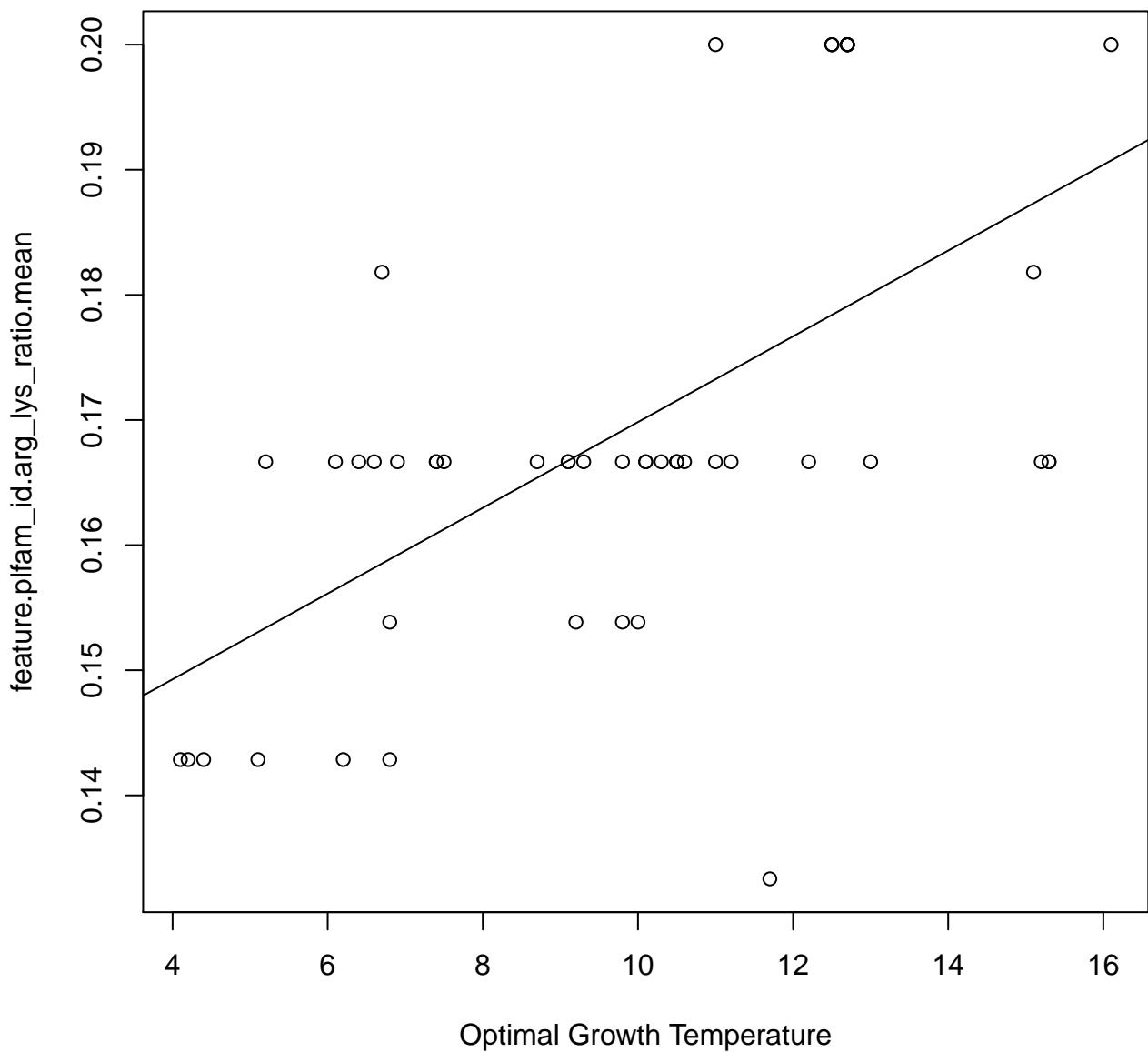
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000224
33 kDa chaperonin HsIO



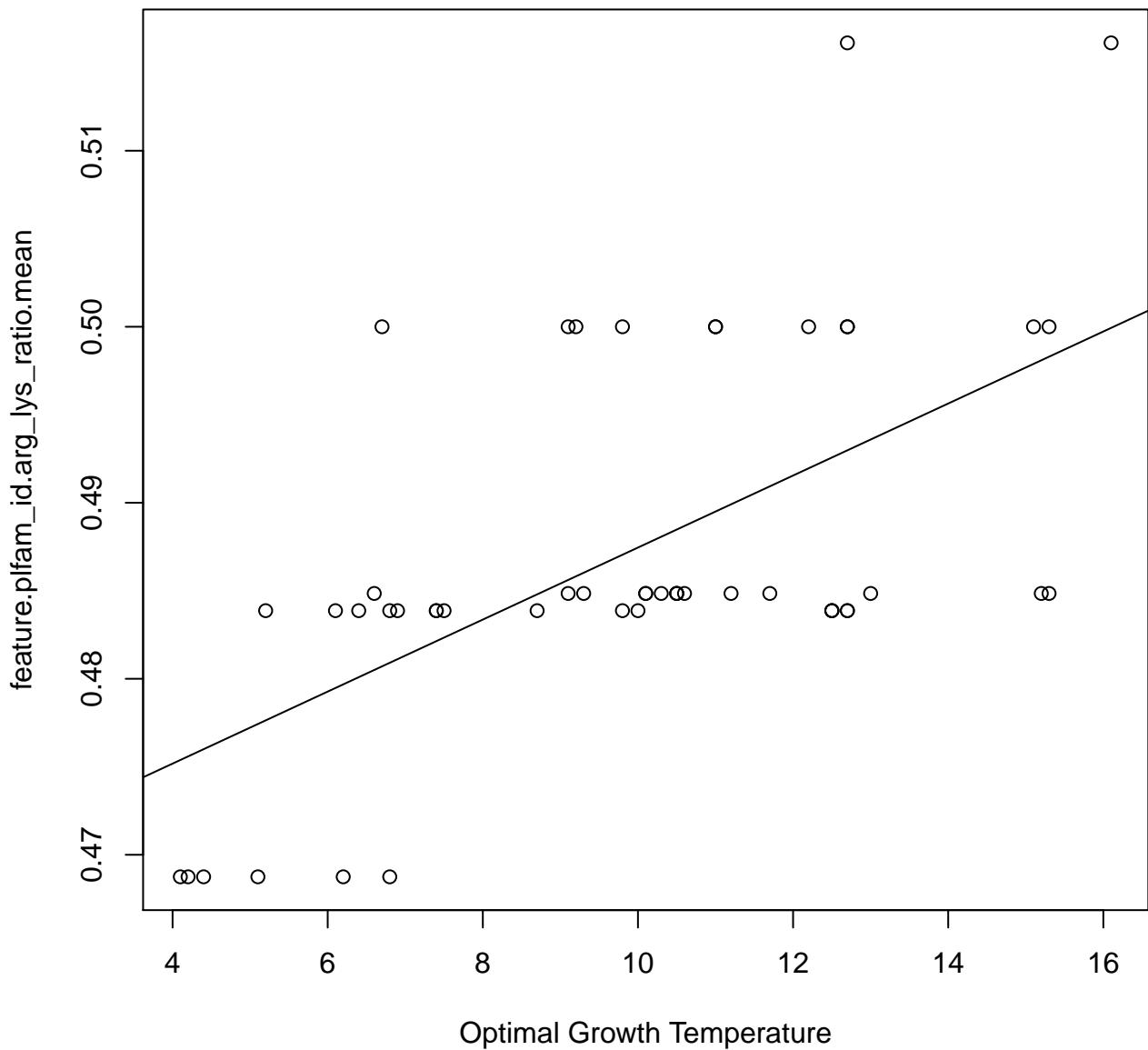
feature.plfam_id.arg_lys_ratio.mean
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23S rRNA (pseudouridine(1915)-N(3))-methyltransferase (EC 2.1.1.177)



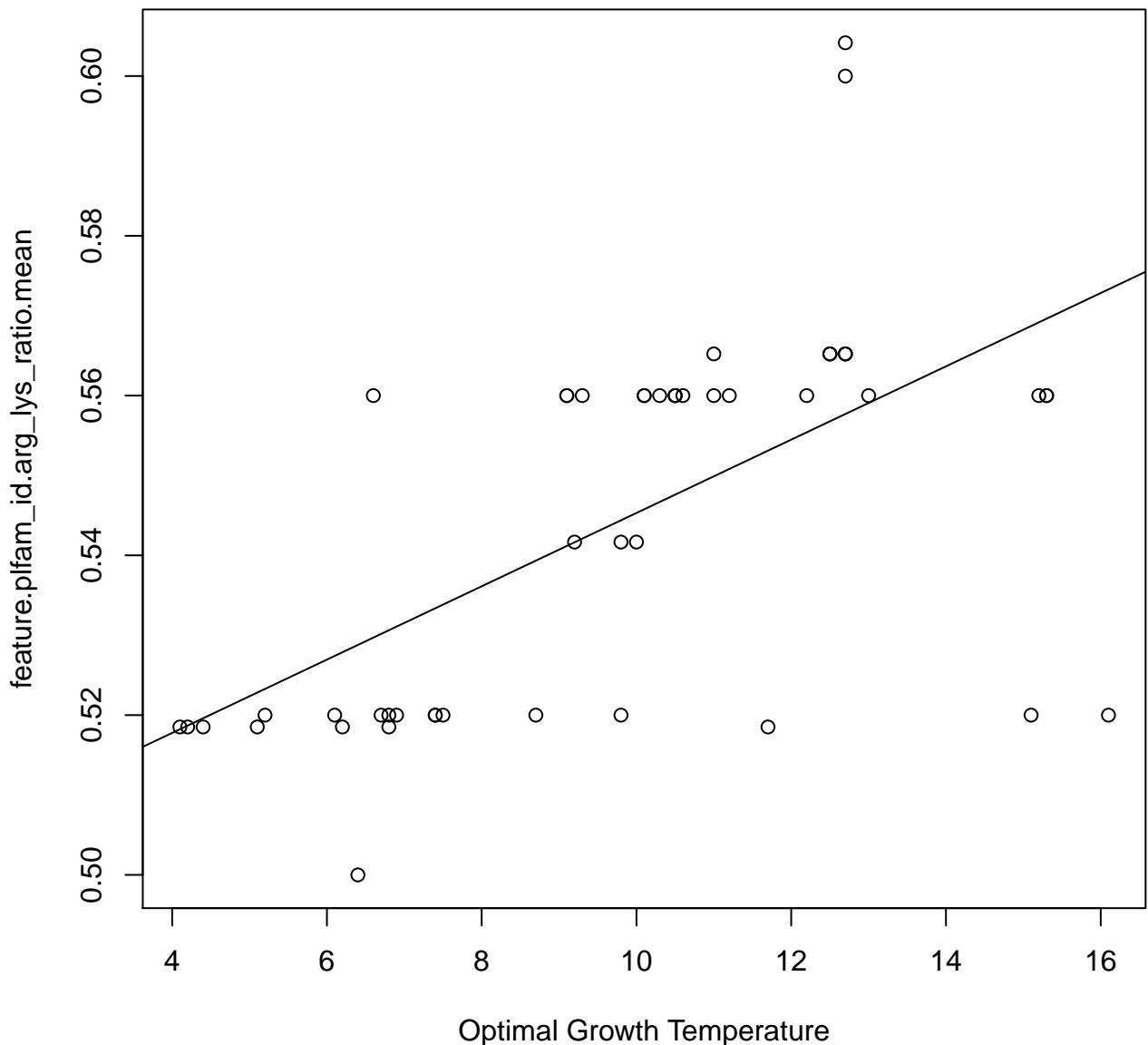
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000115
Antioxidant, AhpC/Tsa family



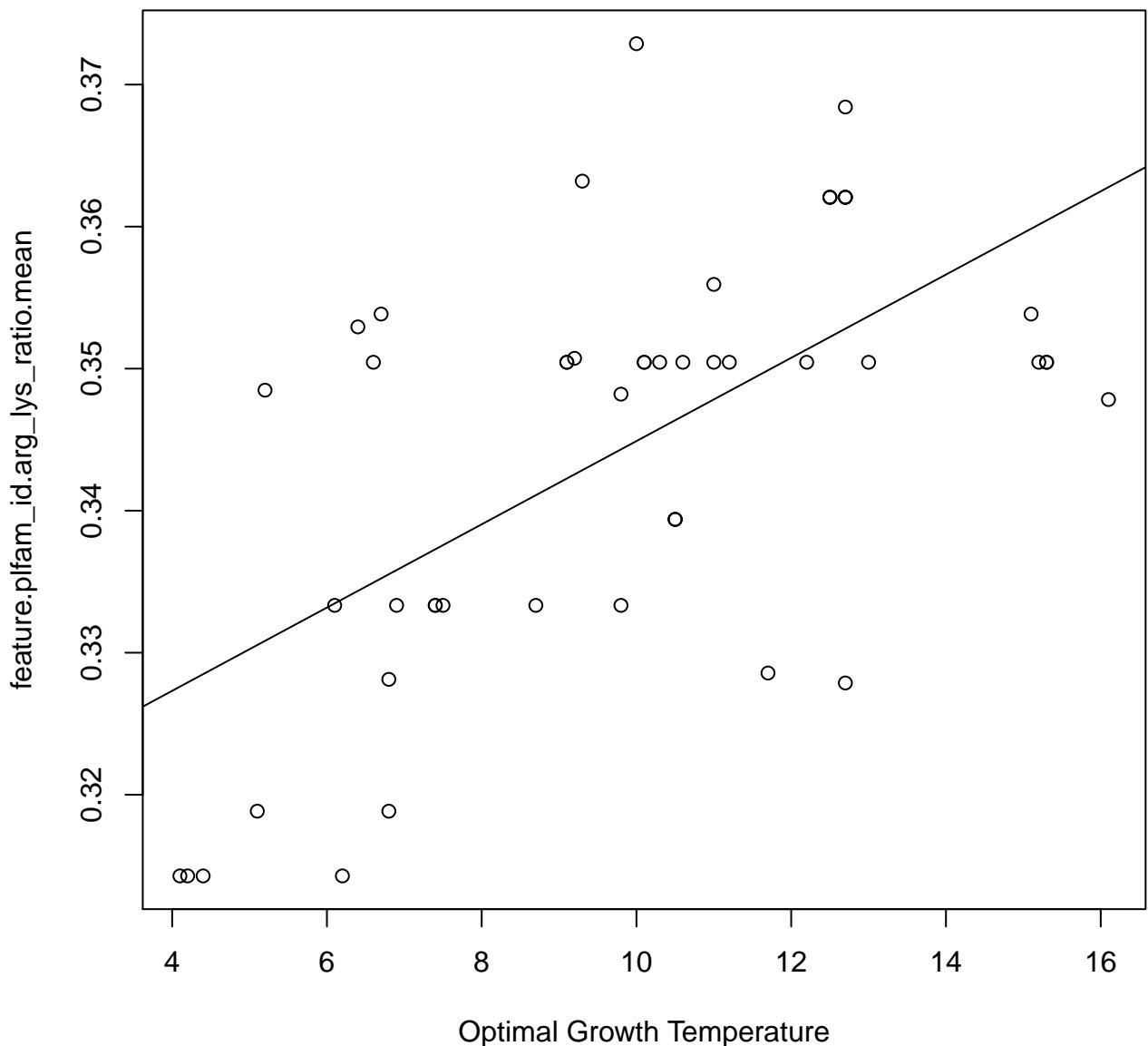
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001411
tRNA pseudouridine(55) synthase (EC 5.4.99.25)



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000955
Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8)



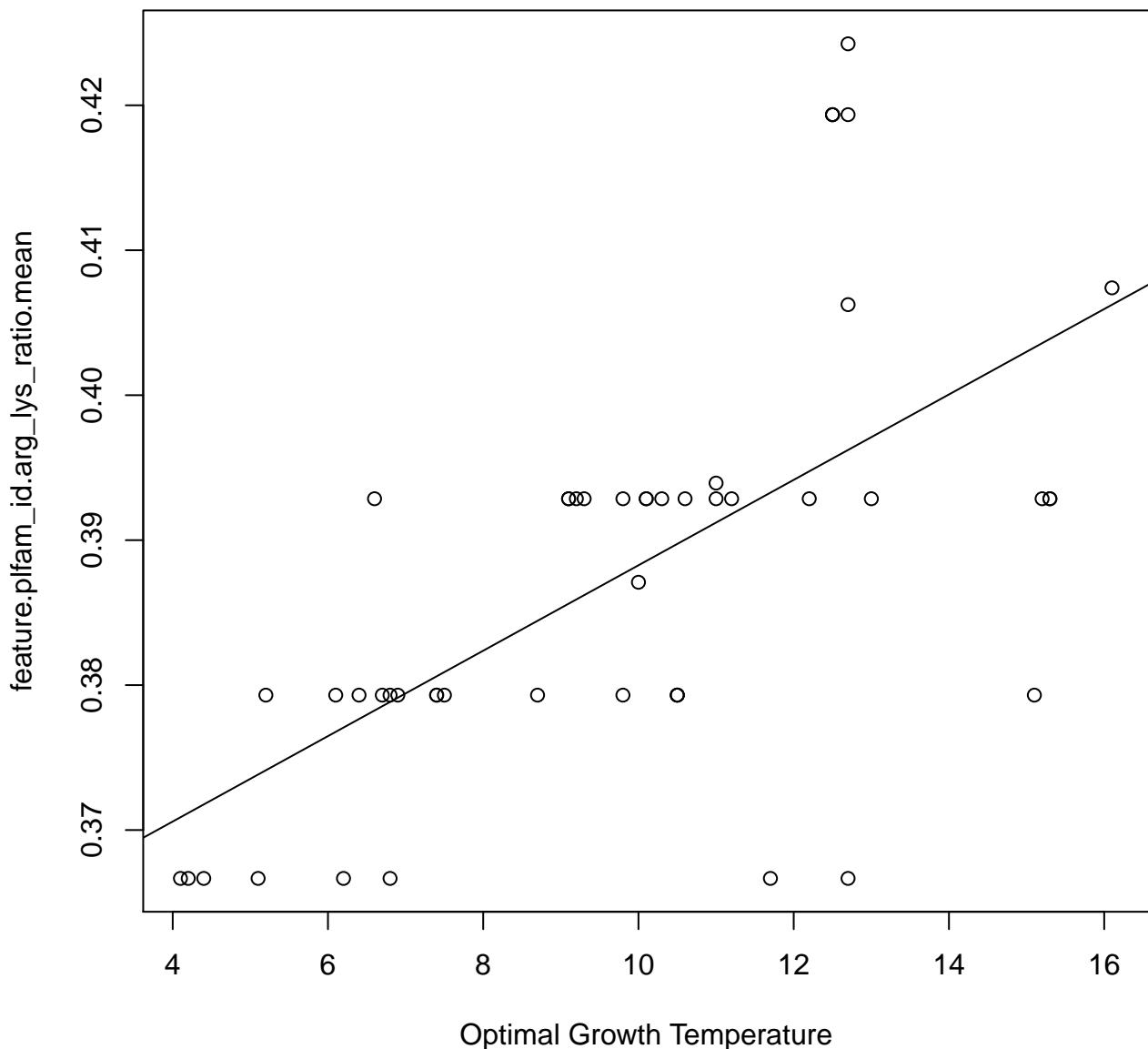
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PLF_28228_00000597
Malate synthase G (EC 2.3.3.9)



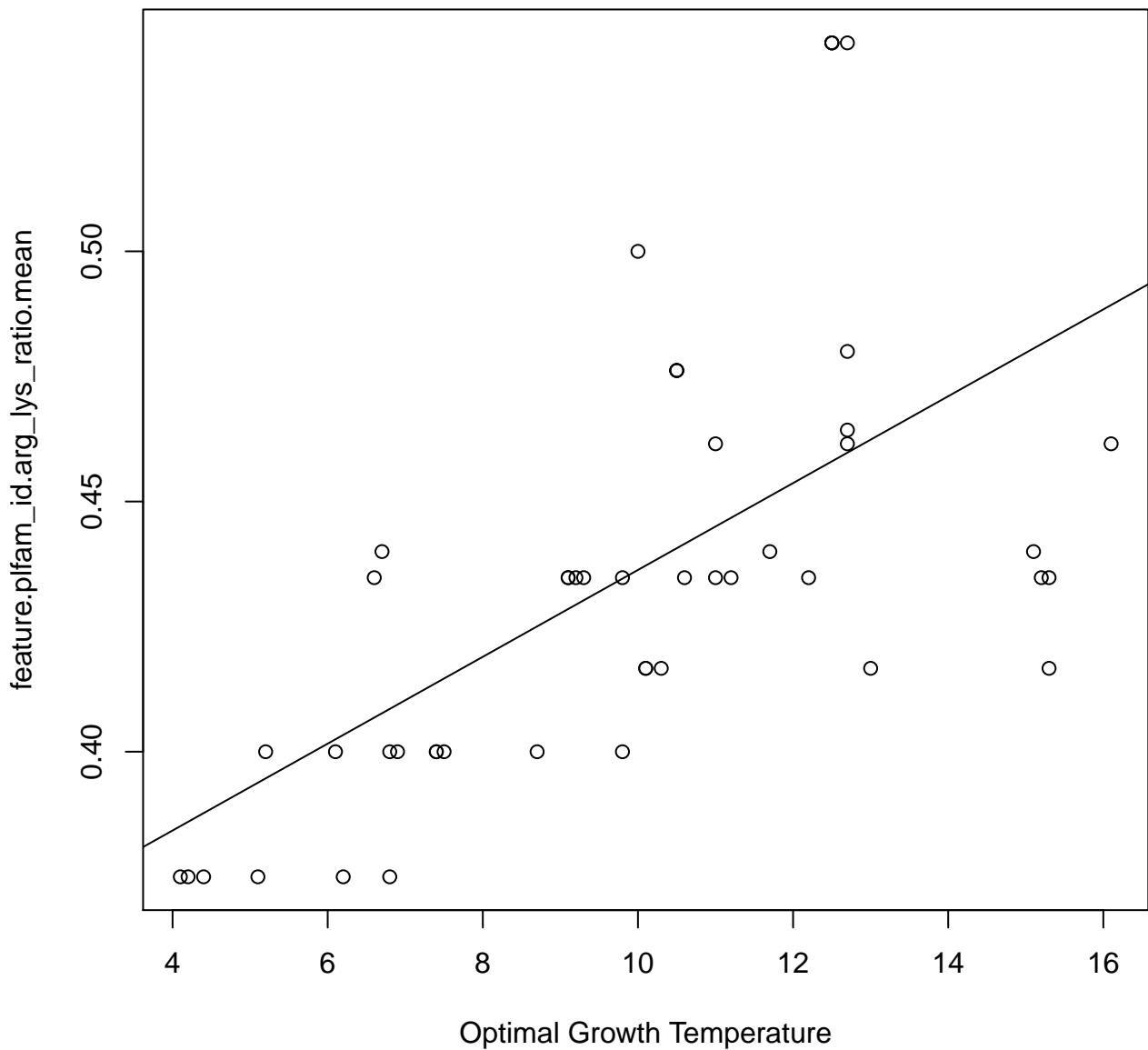
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PLF_28228_00000103

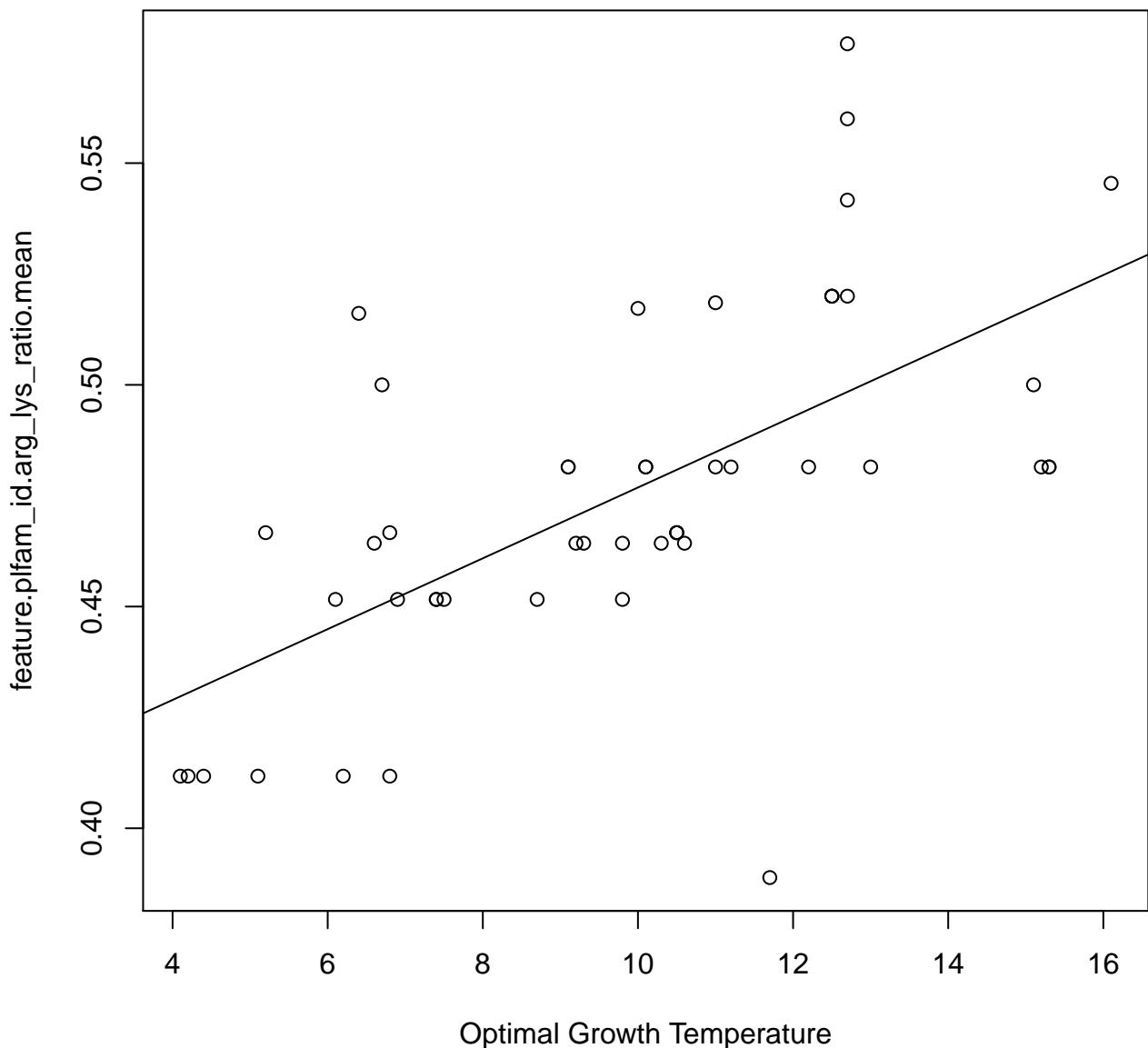
Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) / Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5)



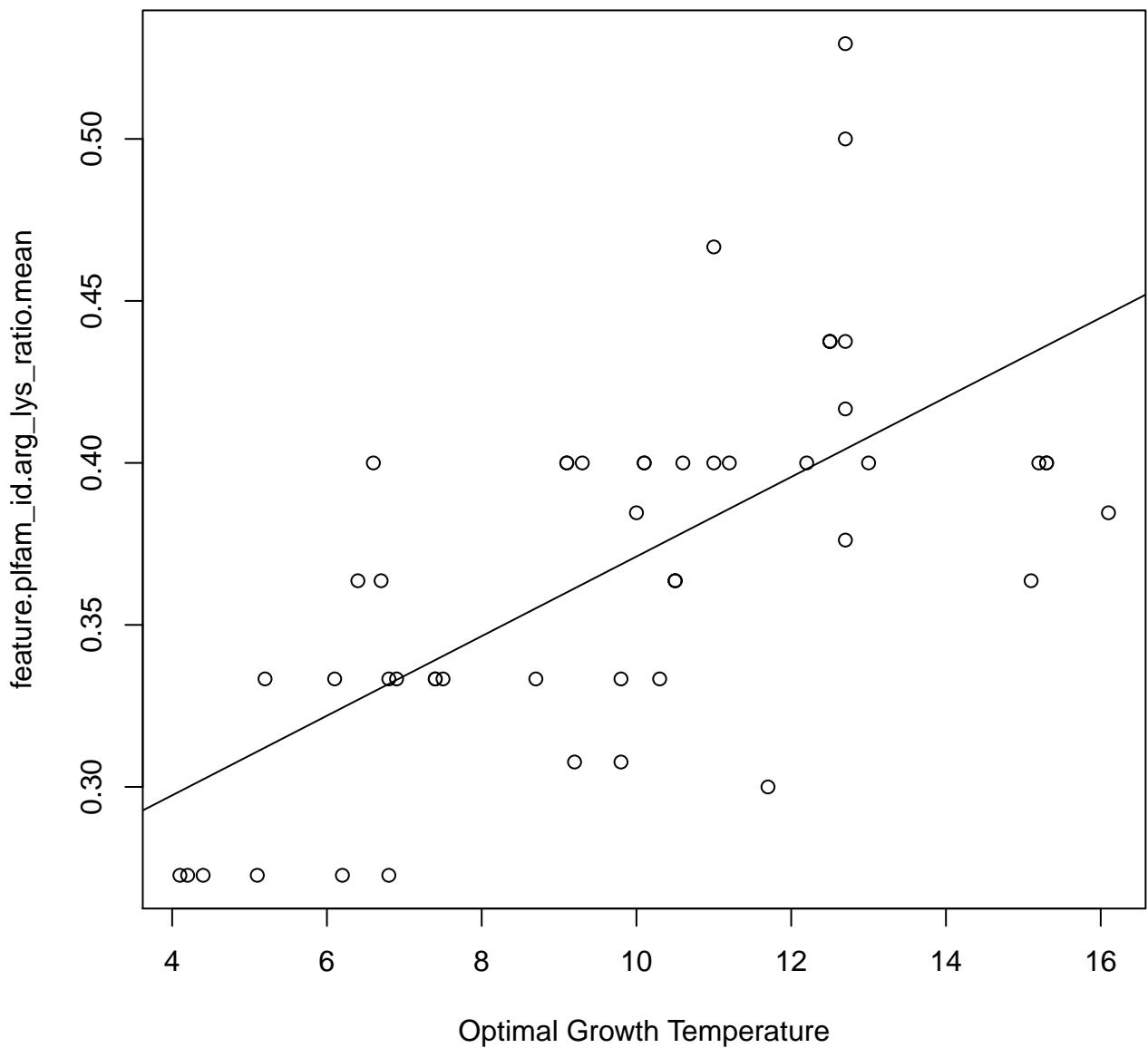
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000242
2-haloalkanoic acid dehalogenase (EC 3.8.1.2)



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00000268
3-deoxy-D-manno-octulose-2'-phosphate kinase (EC 2.7.1.166)



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001718
MSHA pilin protein MshB



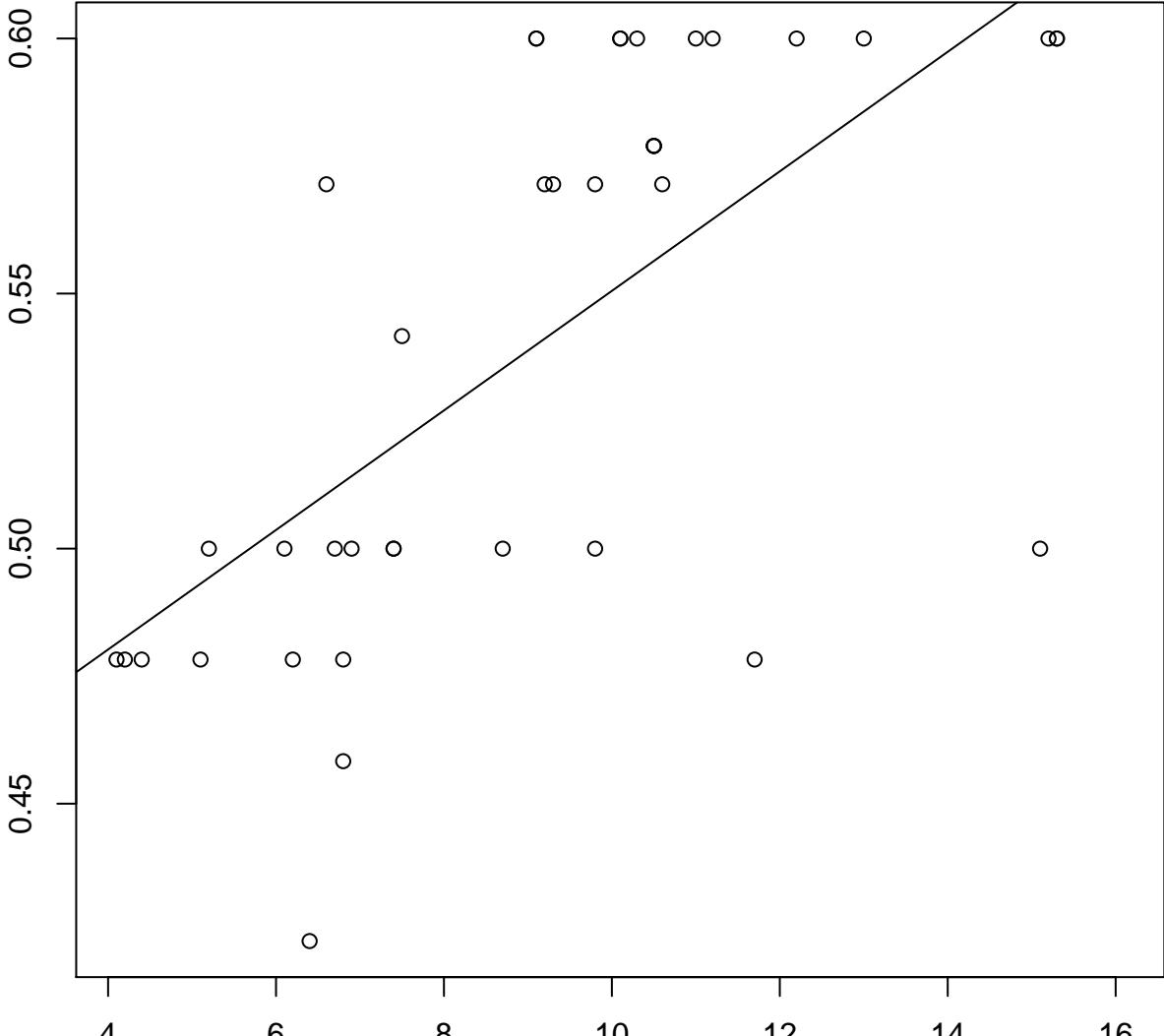
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PLF_28228_00006398

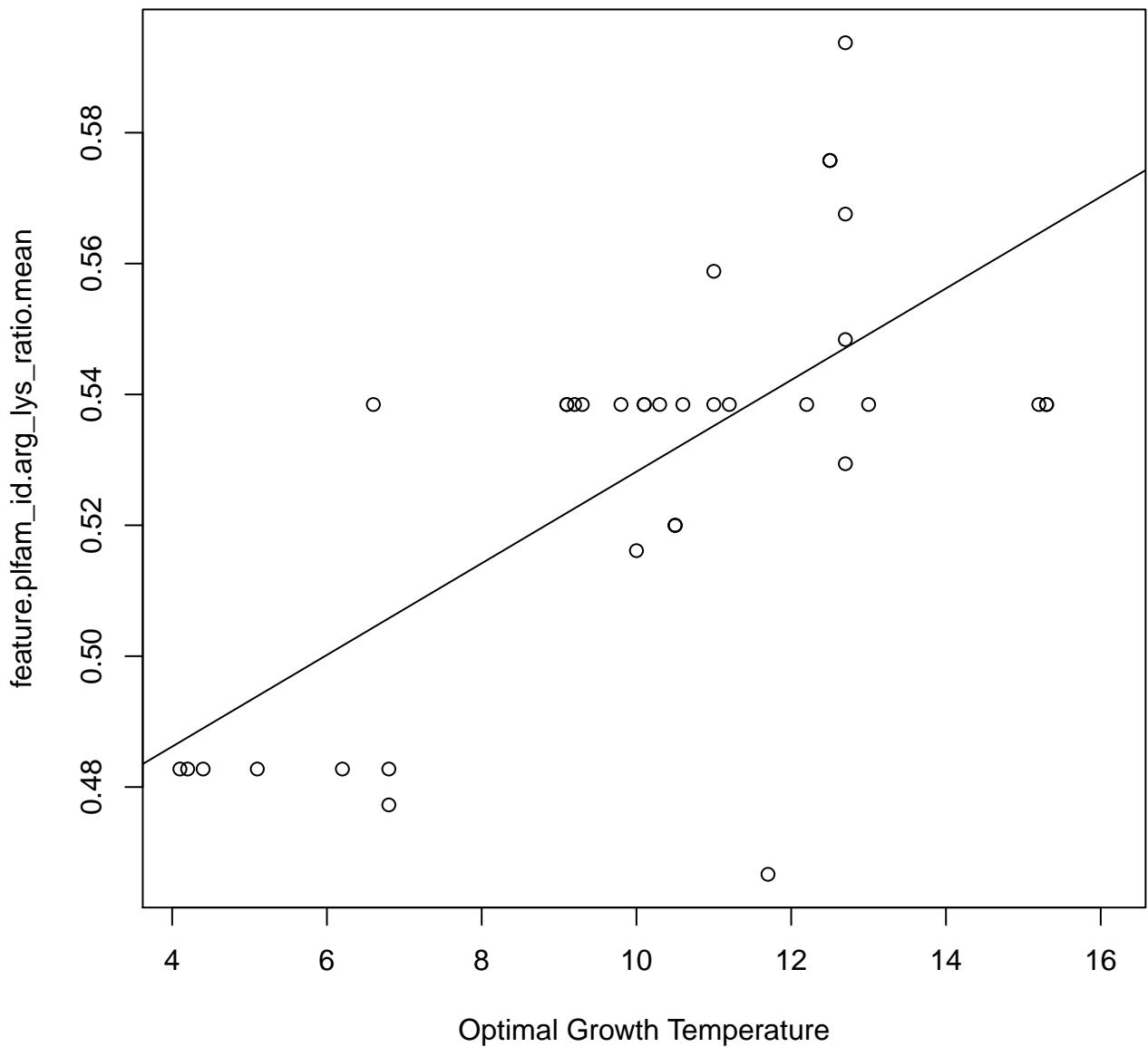
hypothetical protein

feature.plfam_id.arg_lys_ratio.mean

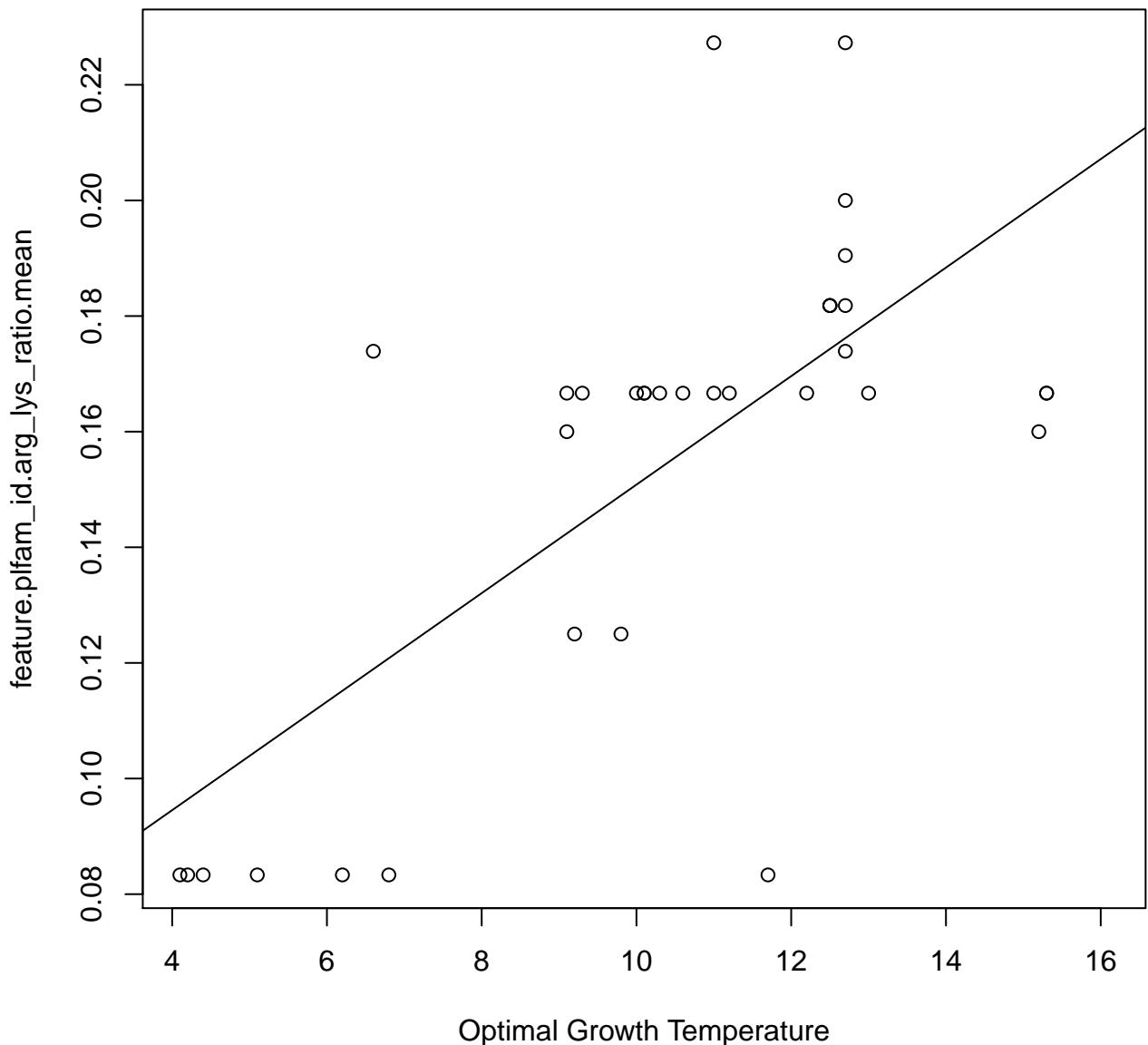
Optimal Growth Temperature



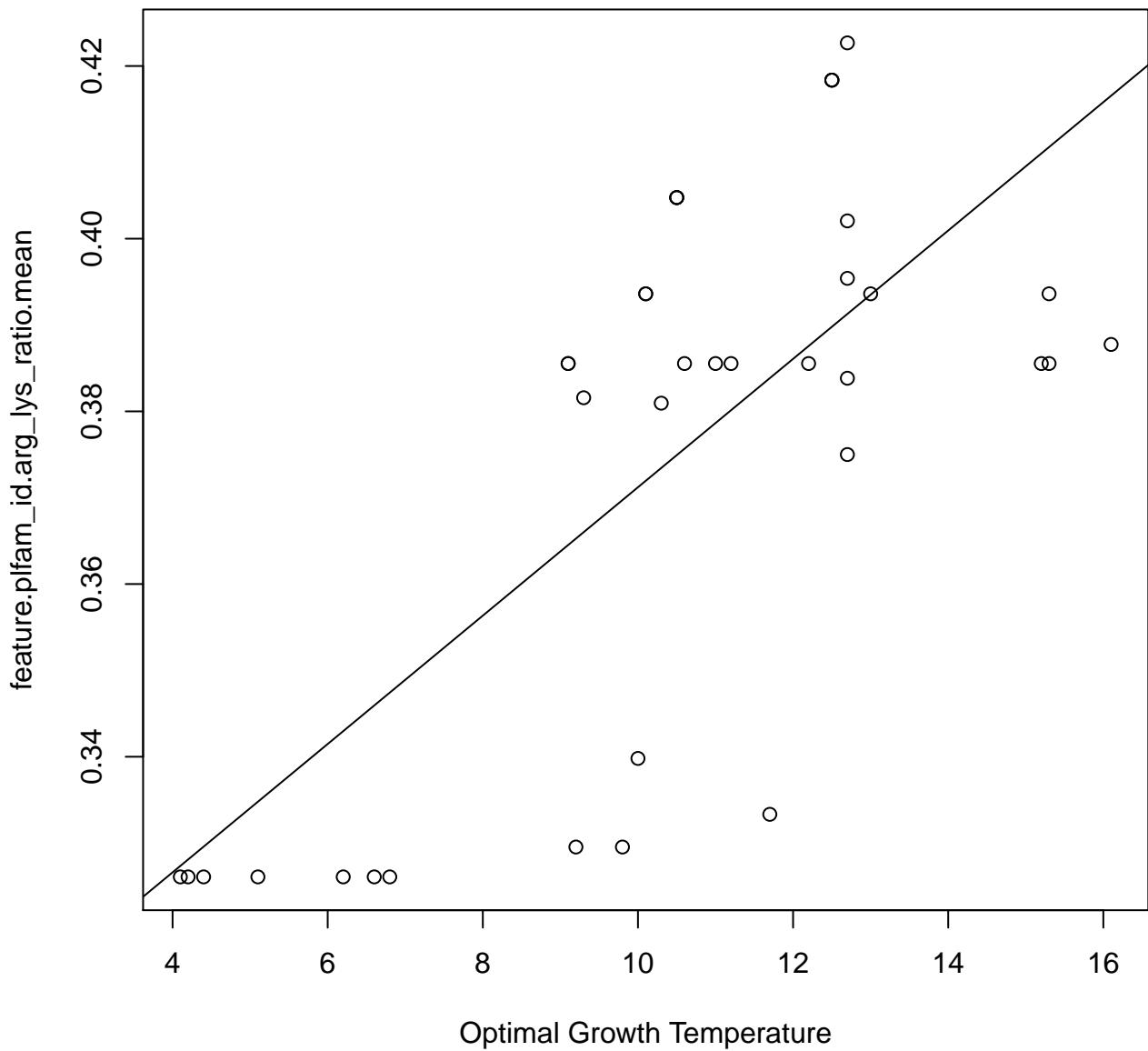
feature.plfam_id.arg_lyc_ratio.mean
PLF_28228_00001857
GGDEF domain protein



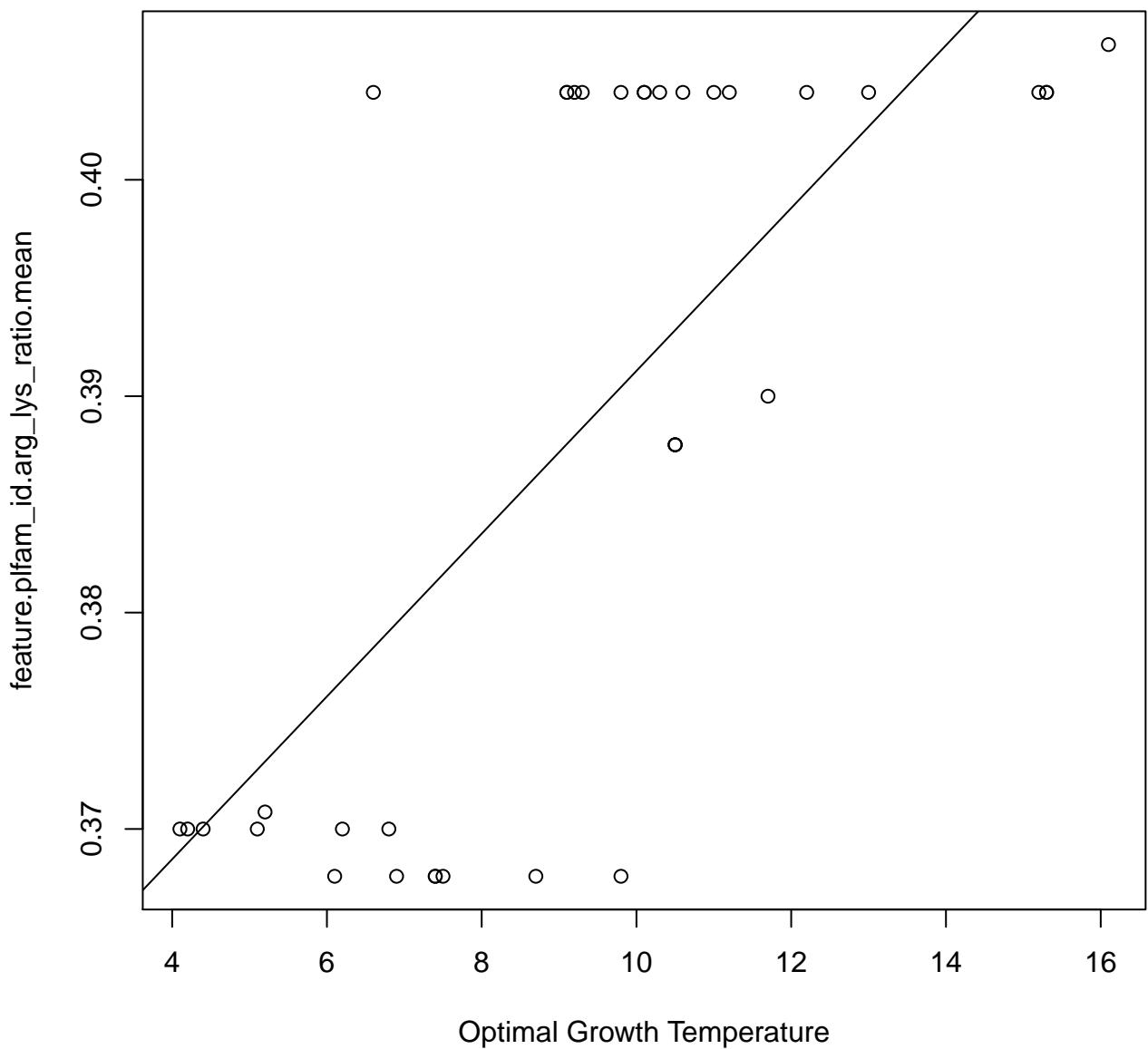
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PLF_28228_00000629
N-acetylglucosamine kinase of eukaryotic type (EC 2.7.1.59)



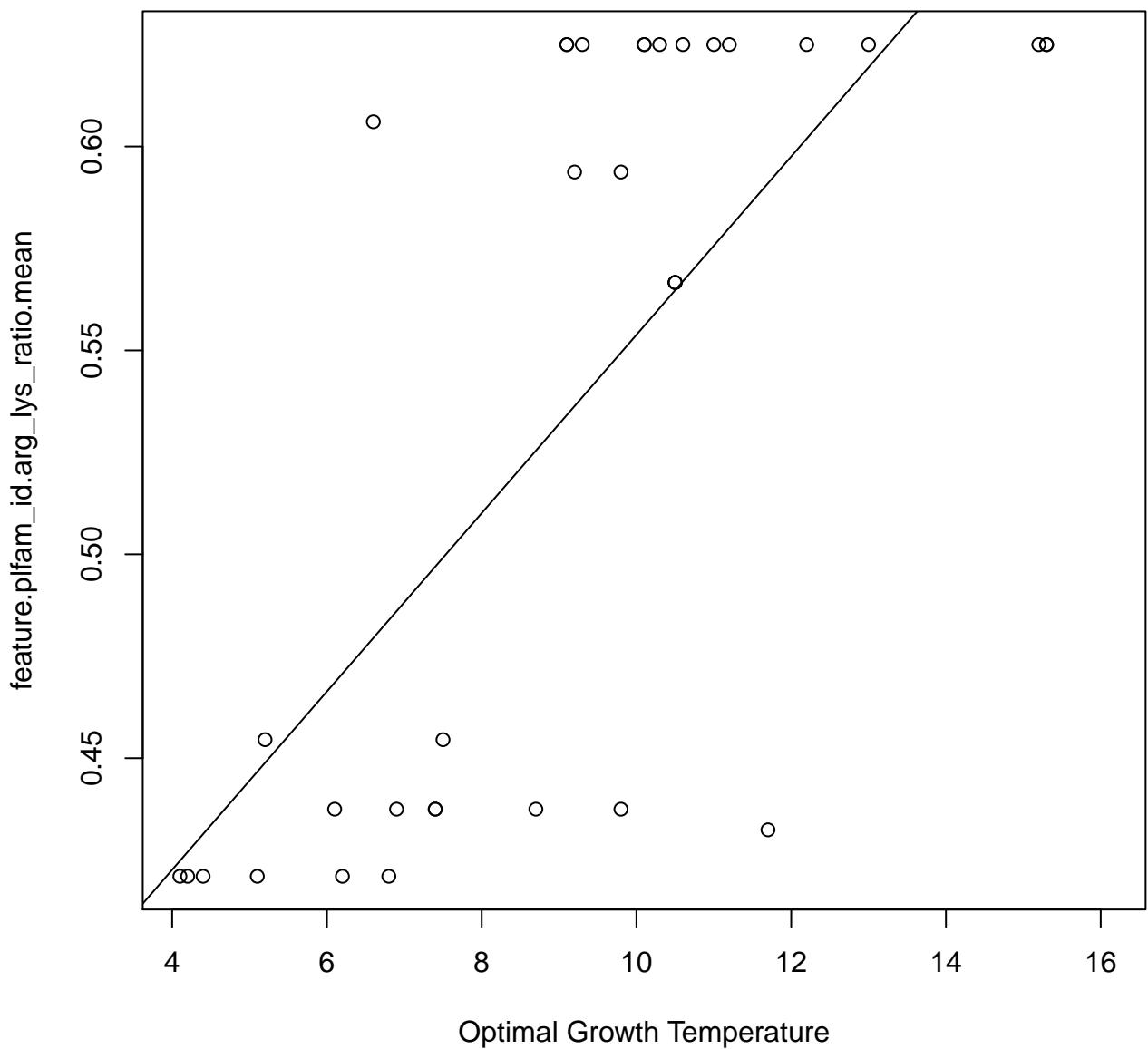
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00002160
Two-component system sensor histidine kinase/response regulator hybrid



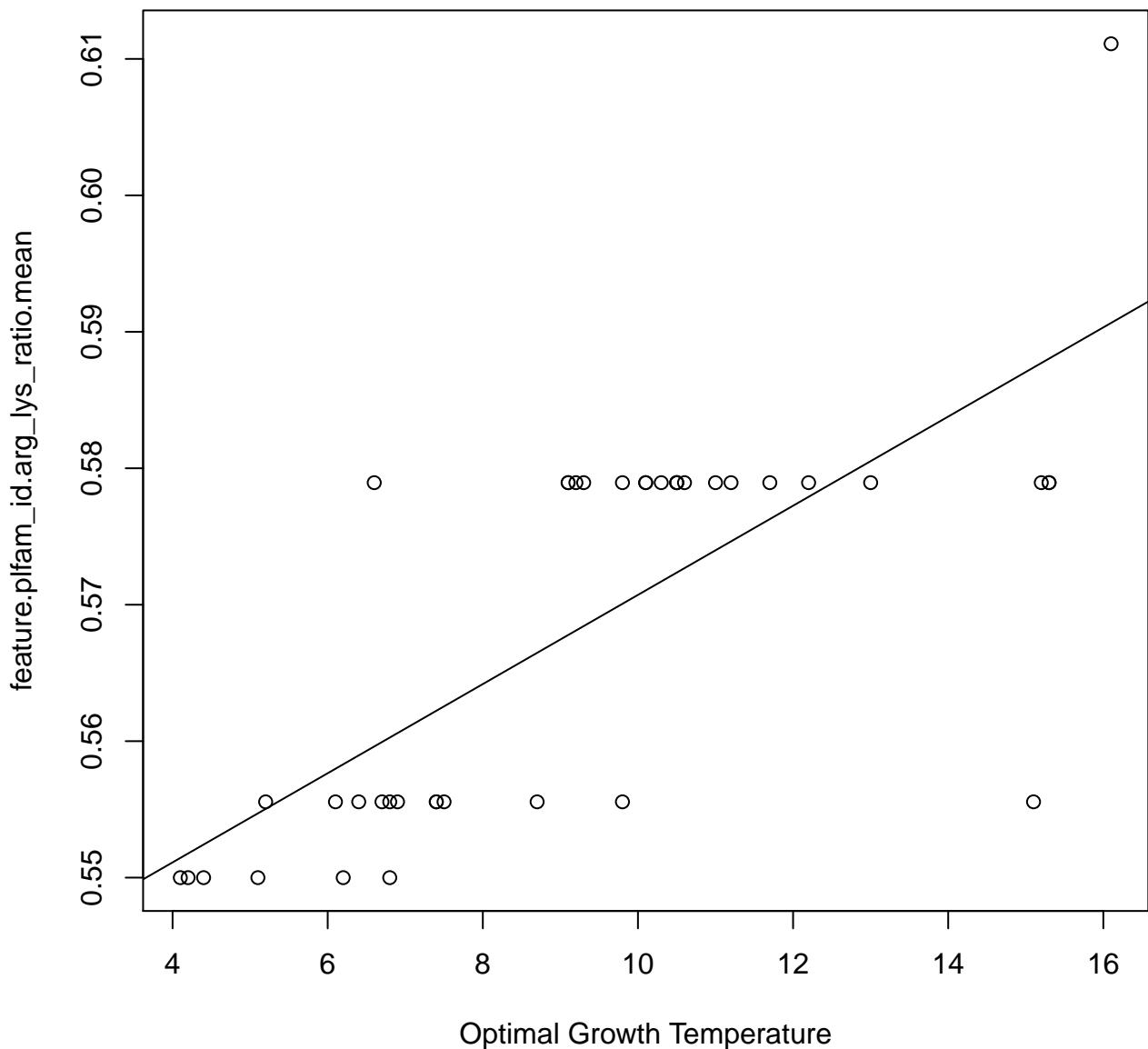
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hypothetical protein



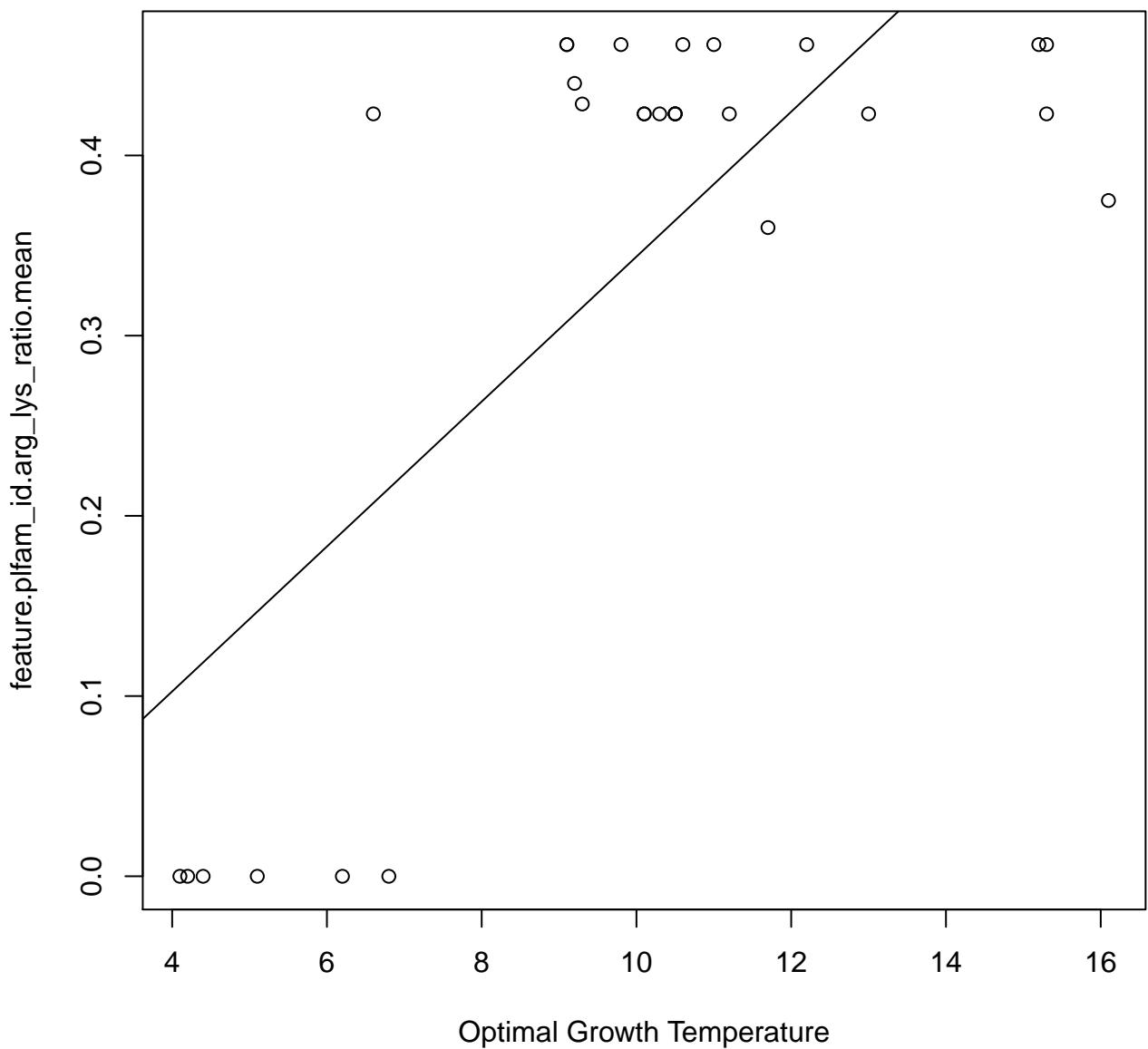
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PLF_28228_00013738
hypothetical protein



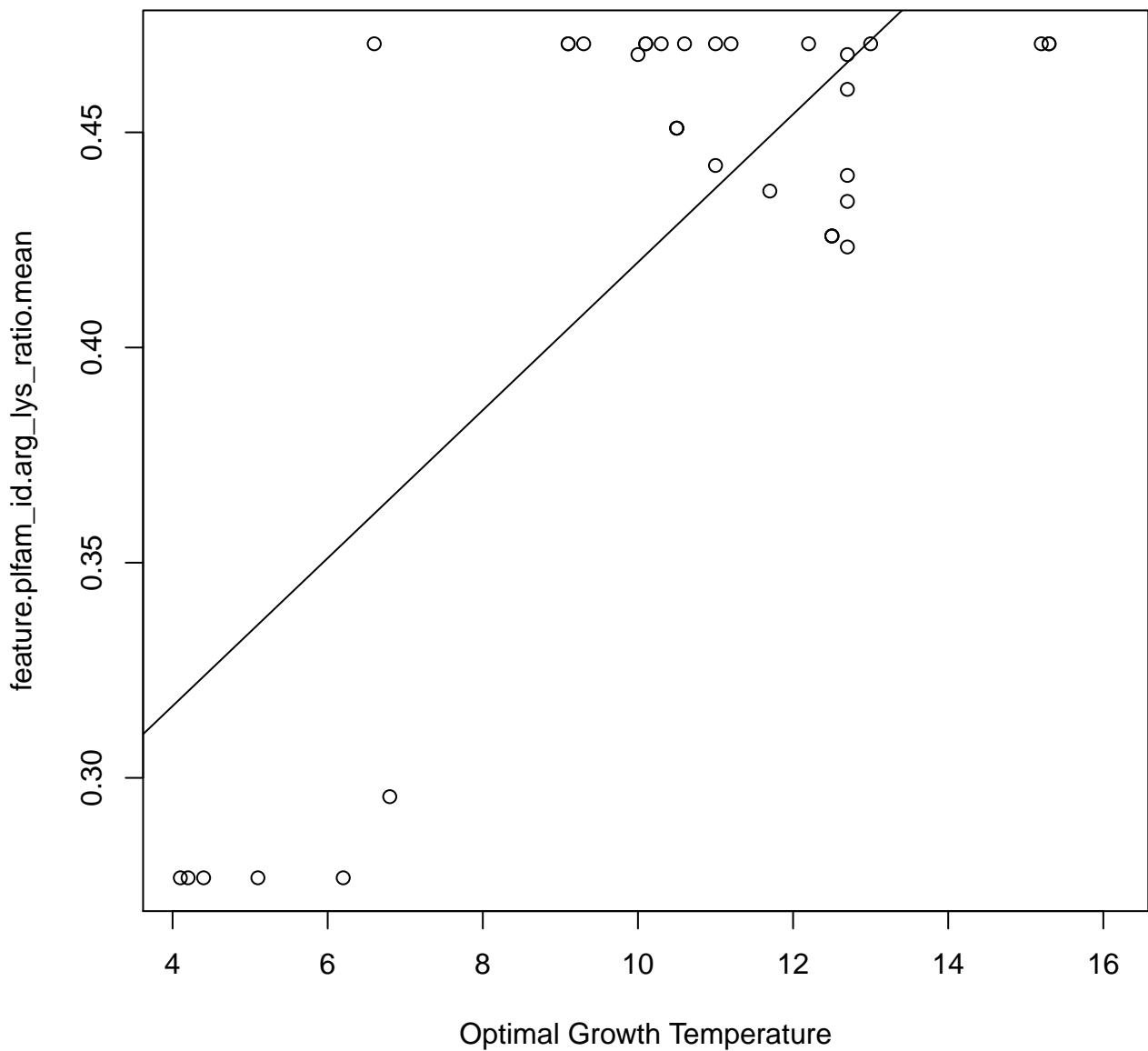
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PLF_28228_00014664
hypothetical protein



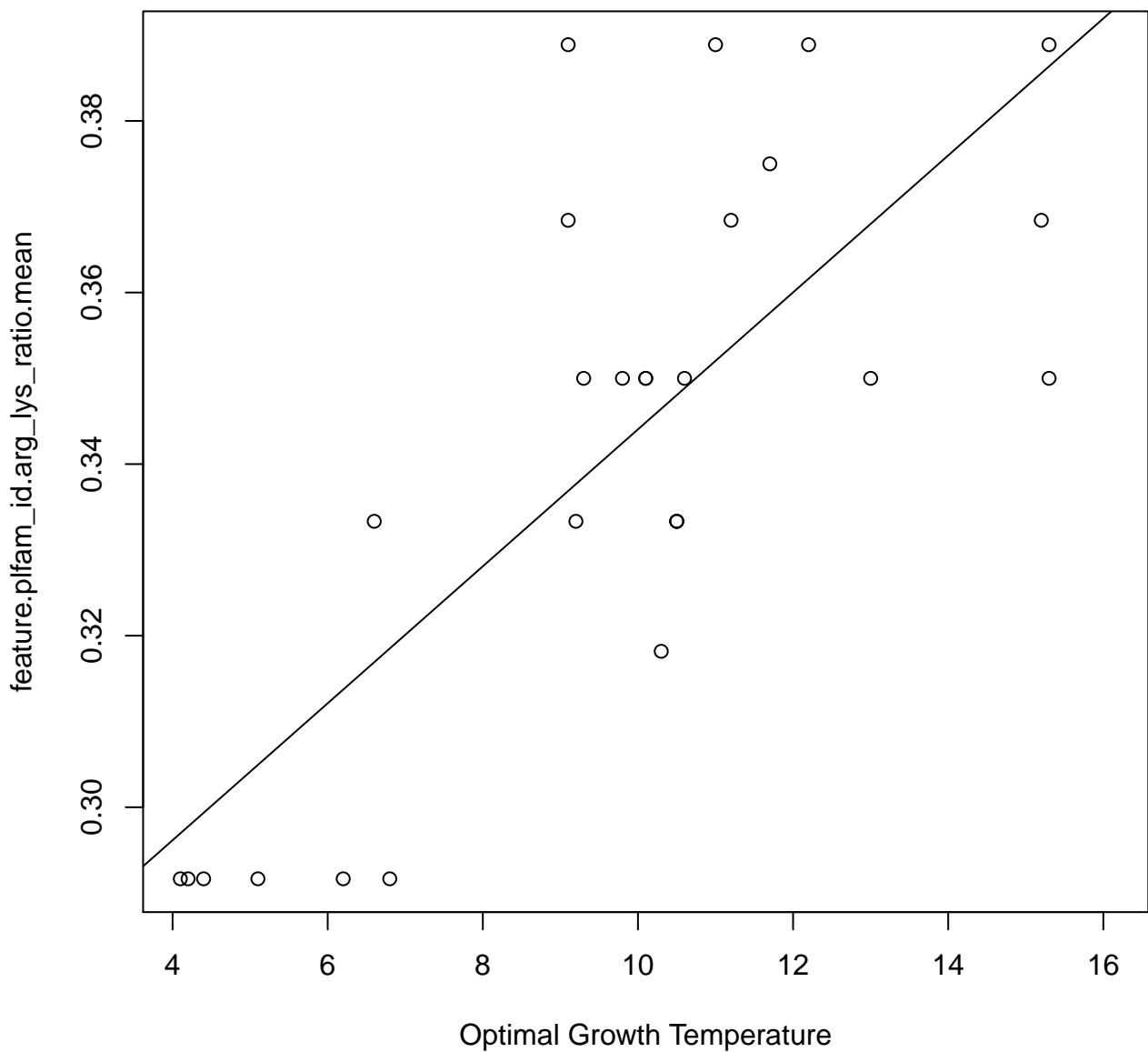
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PLF_28228_00021389
hypothetical protein



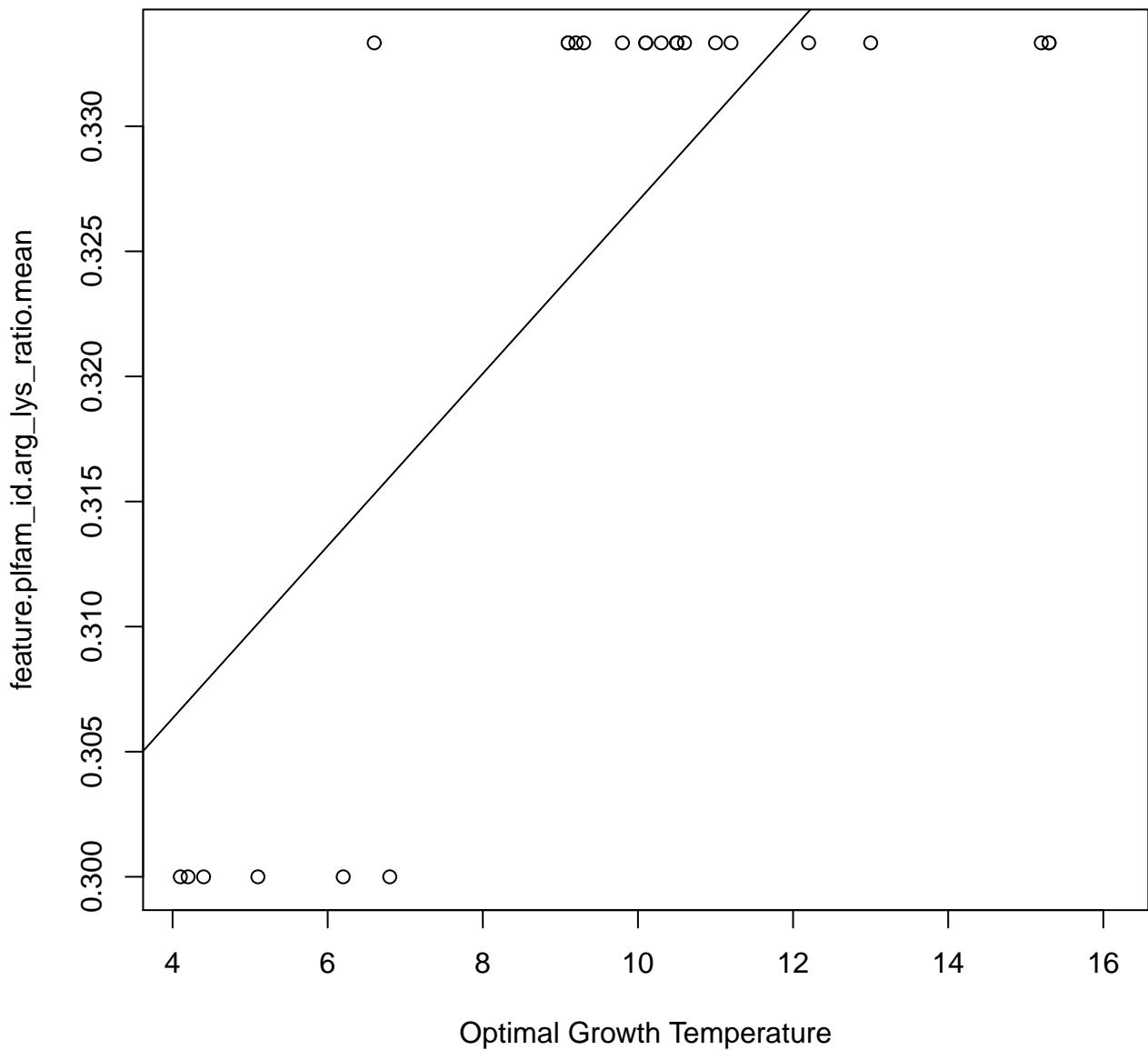
feature.plfam_id.arg_lys_ratio.mean
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Uncharacterized protease YegQ



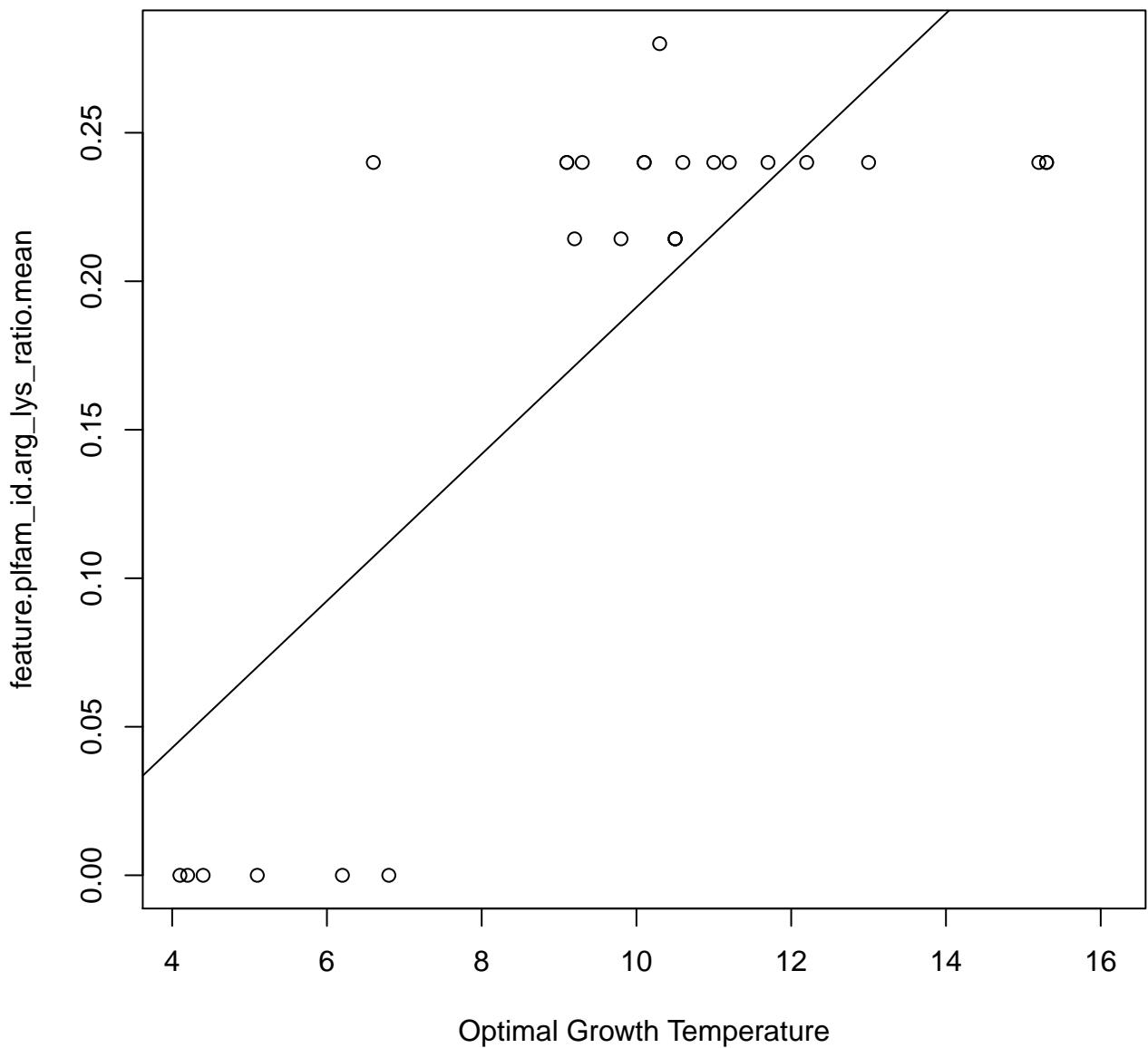
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hypothetical protein



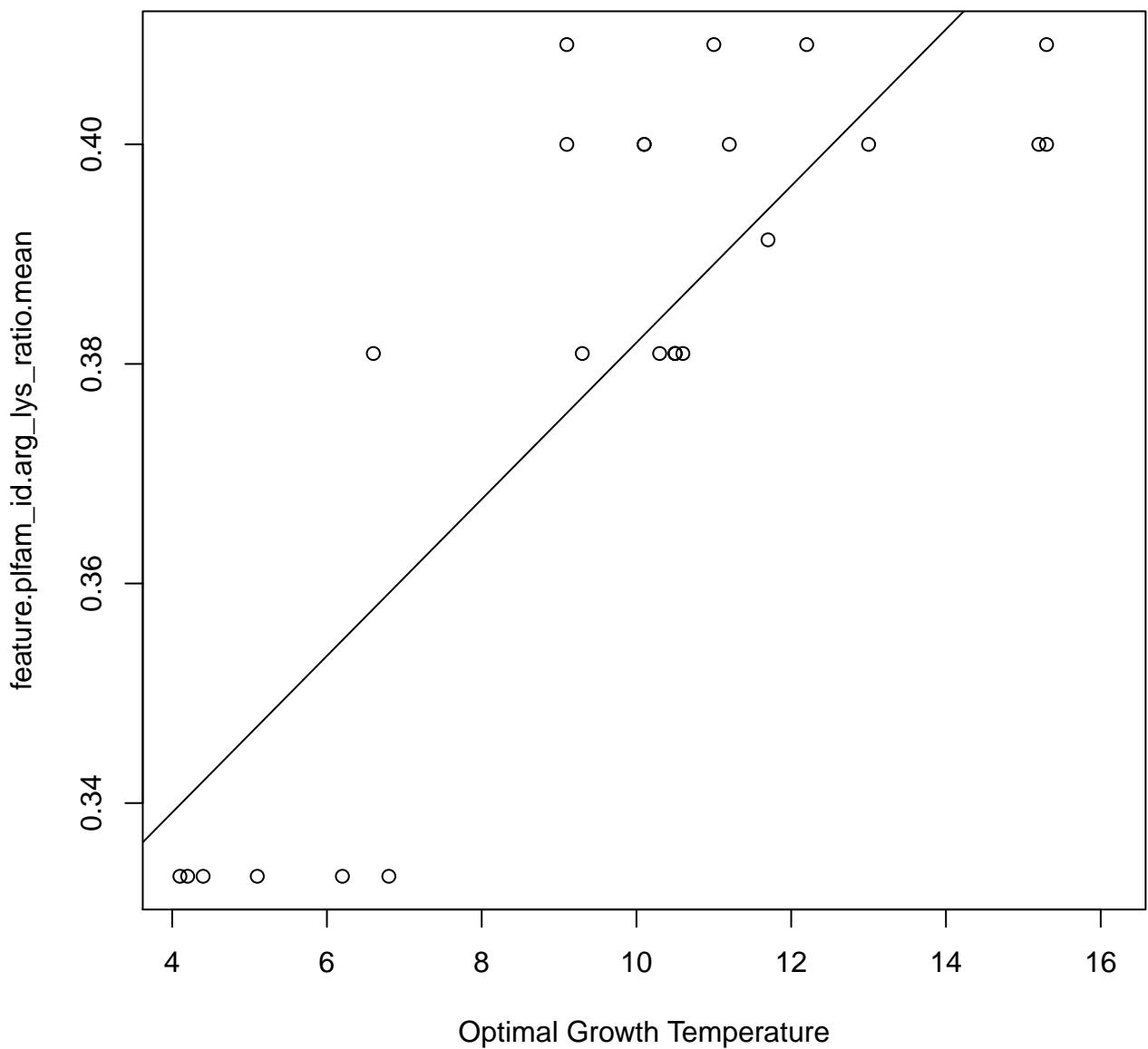
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hypothetical protein



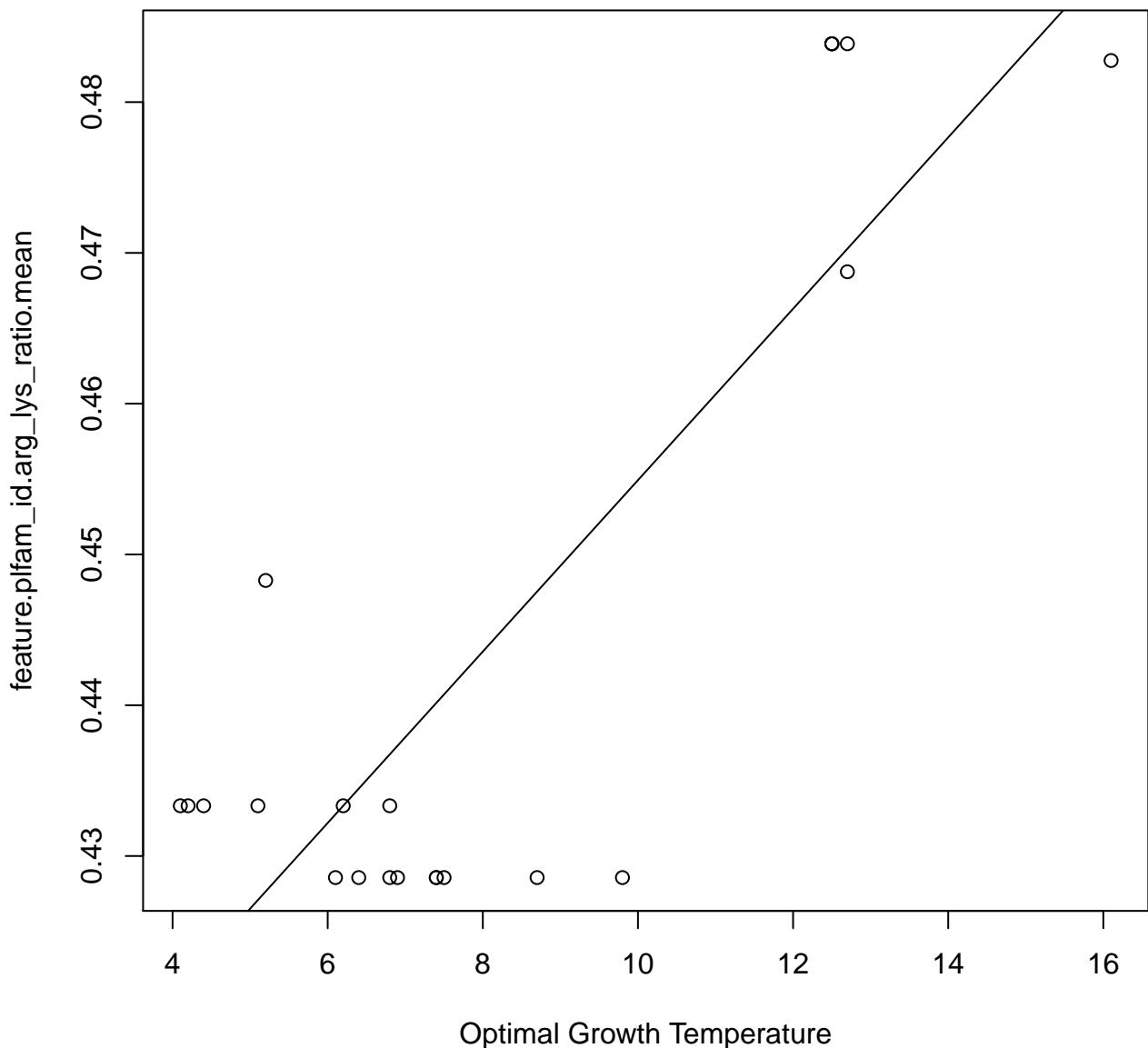
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00031426
hypothetical protein



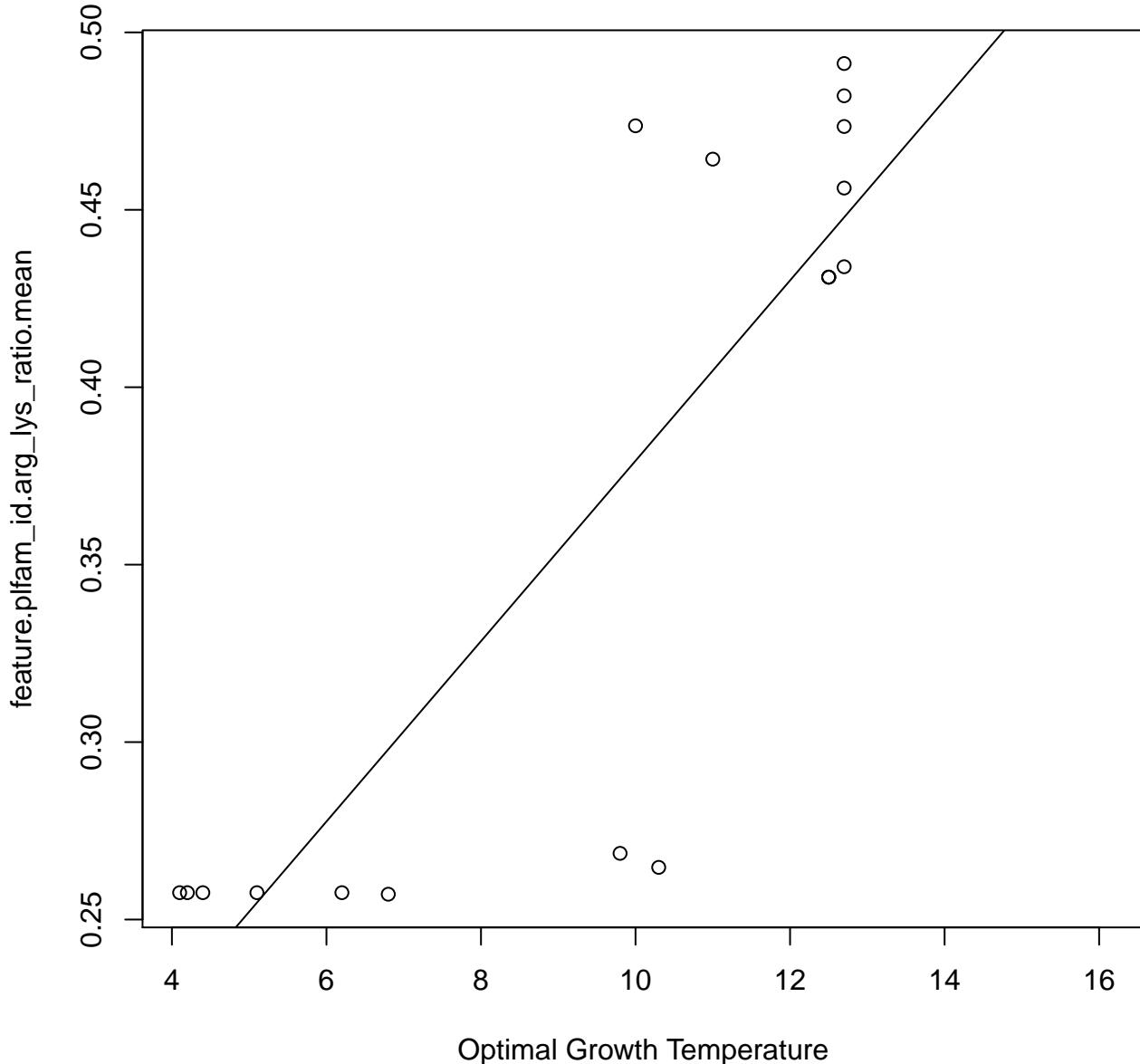
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hypothetical protein



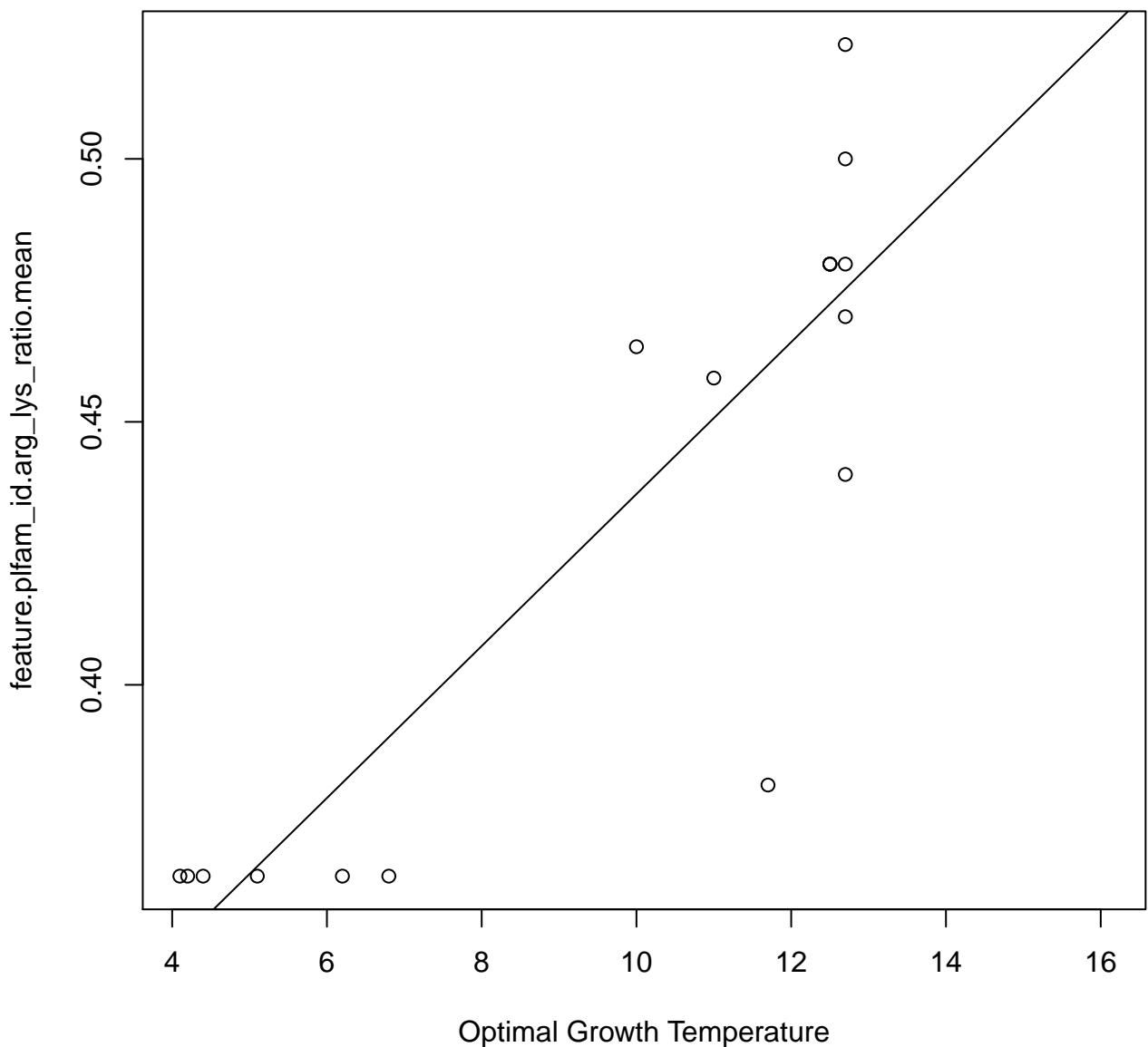
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00003471
Glucose/mannose:H⁺ symporter GlcP



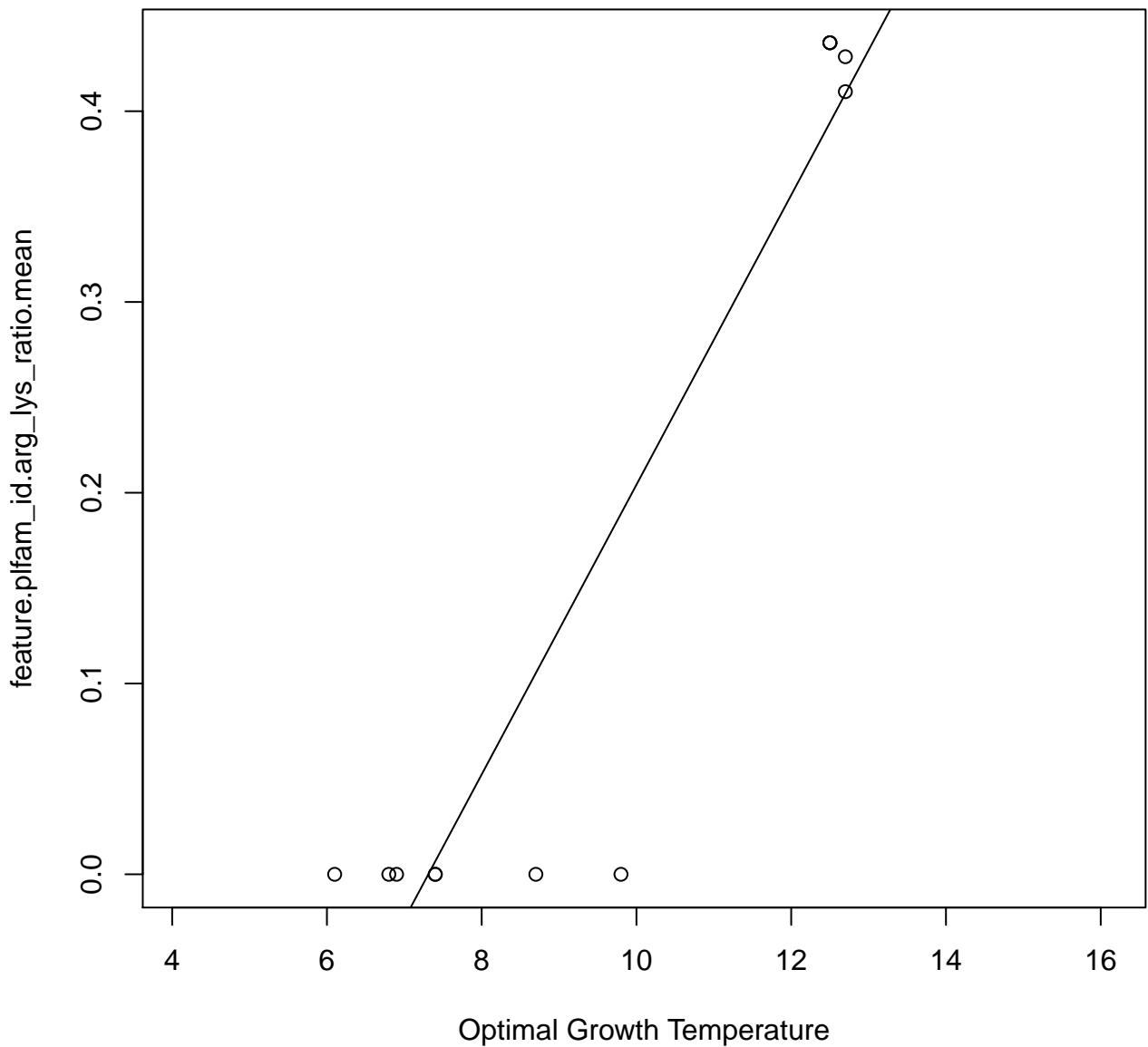
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001719
Macrolide-specific ABC-type efflux carrier (TC 3.A.1.122.1)



feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00001528
FHA domain protein



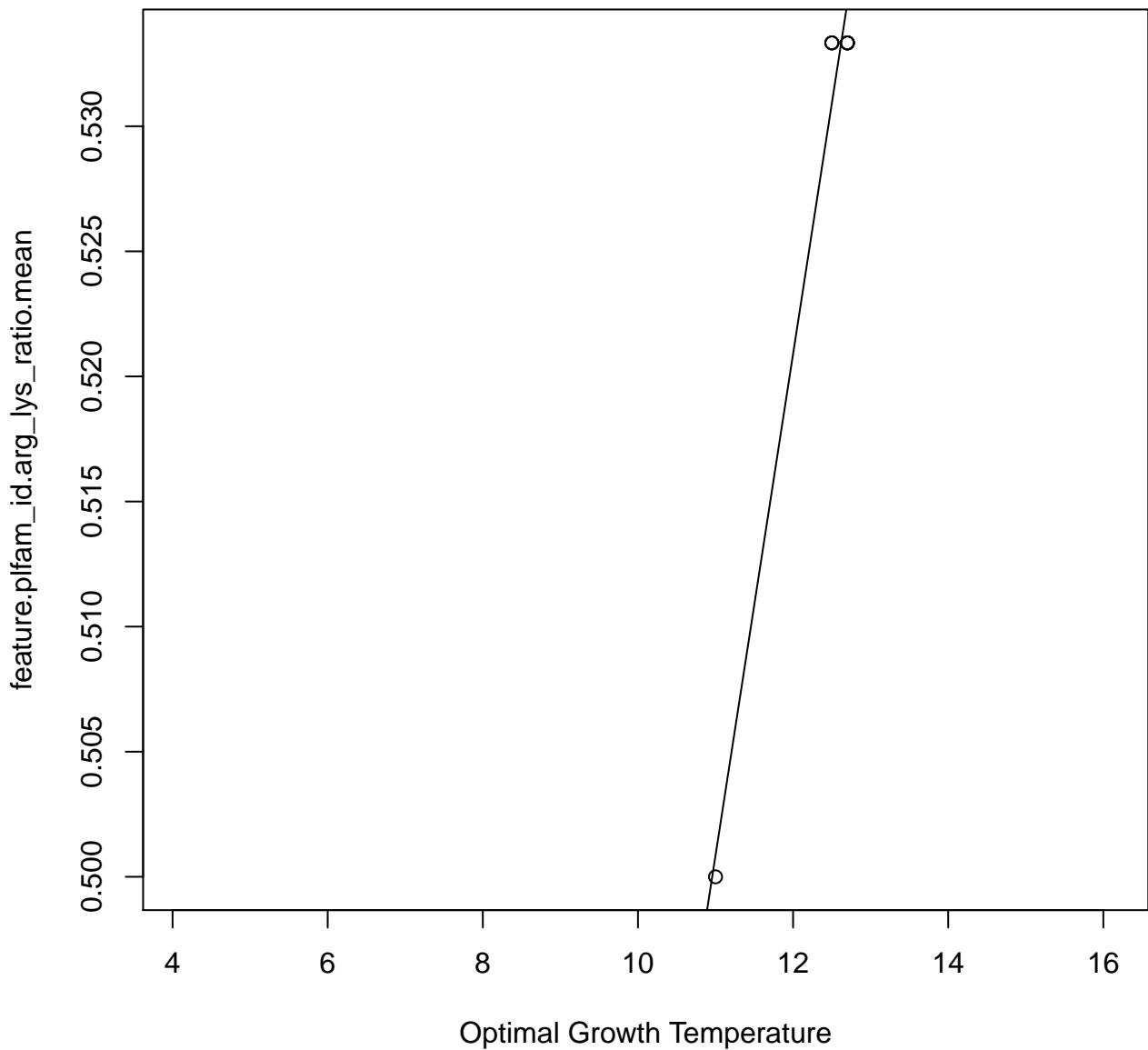
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00007748
EAL domain protein



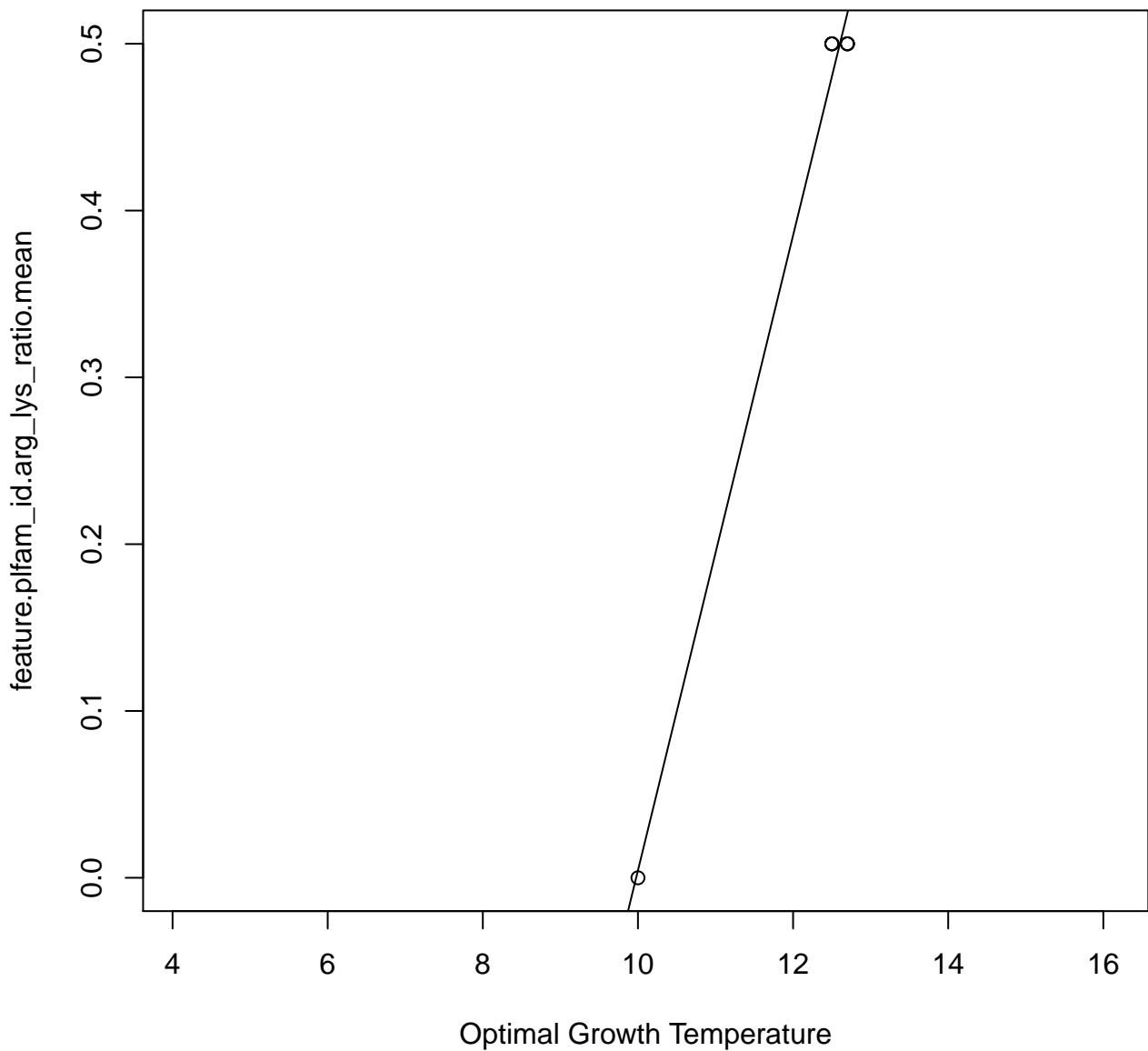
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PLF_28228_00003991

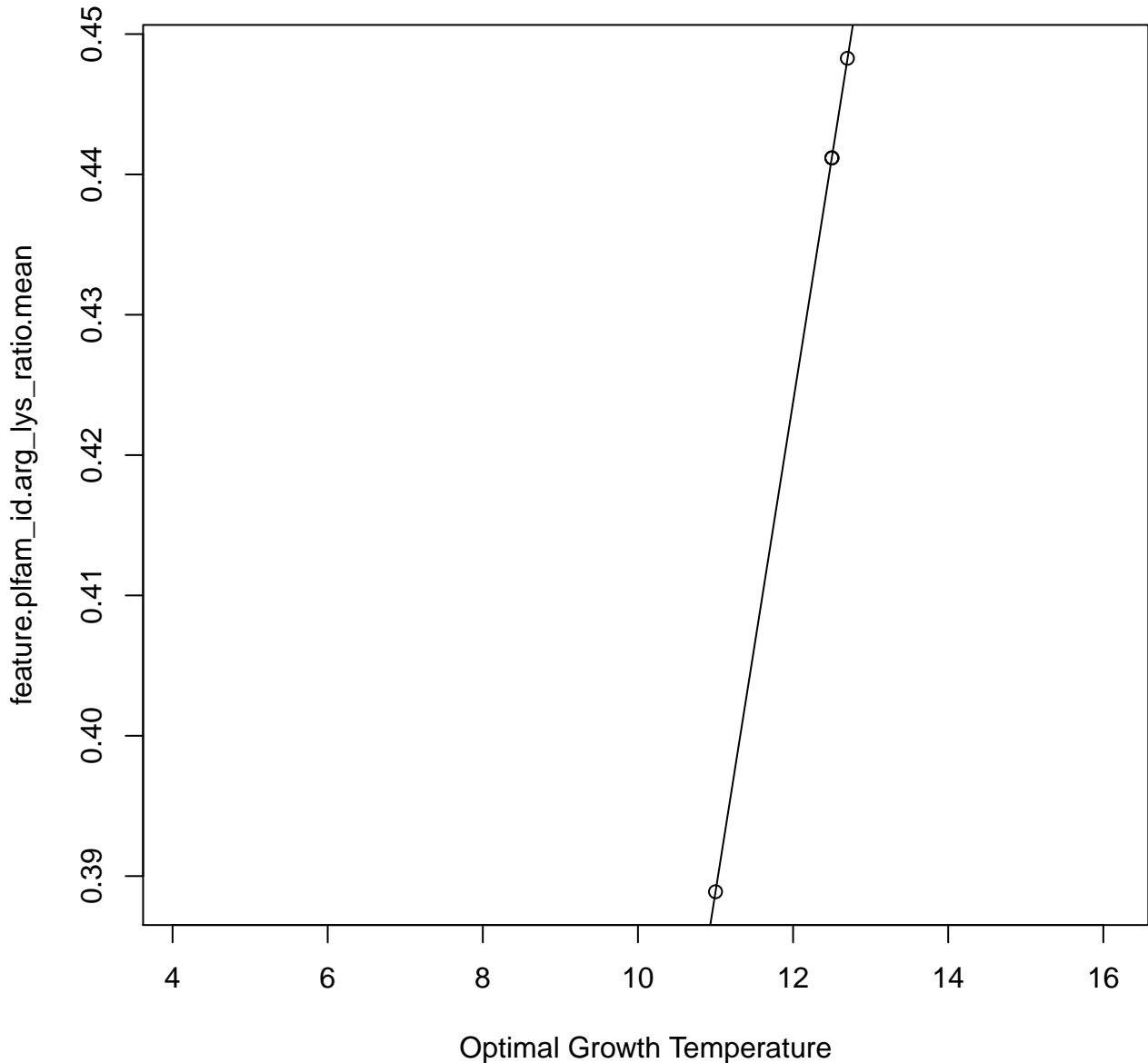
L-serine dehydratase, beta subunit (EC 4.3.1.17) / L-serine dehydratase, alpha subunit (EC 4.3.1.17)



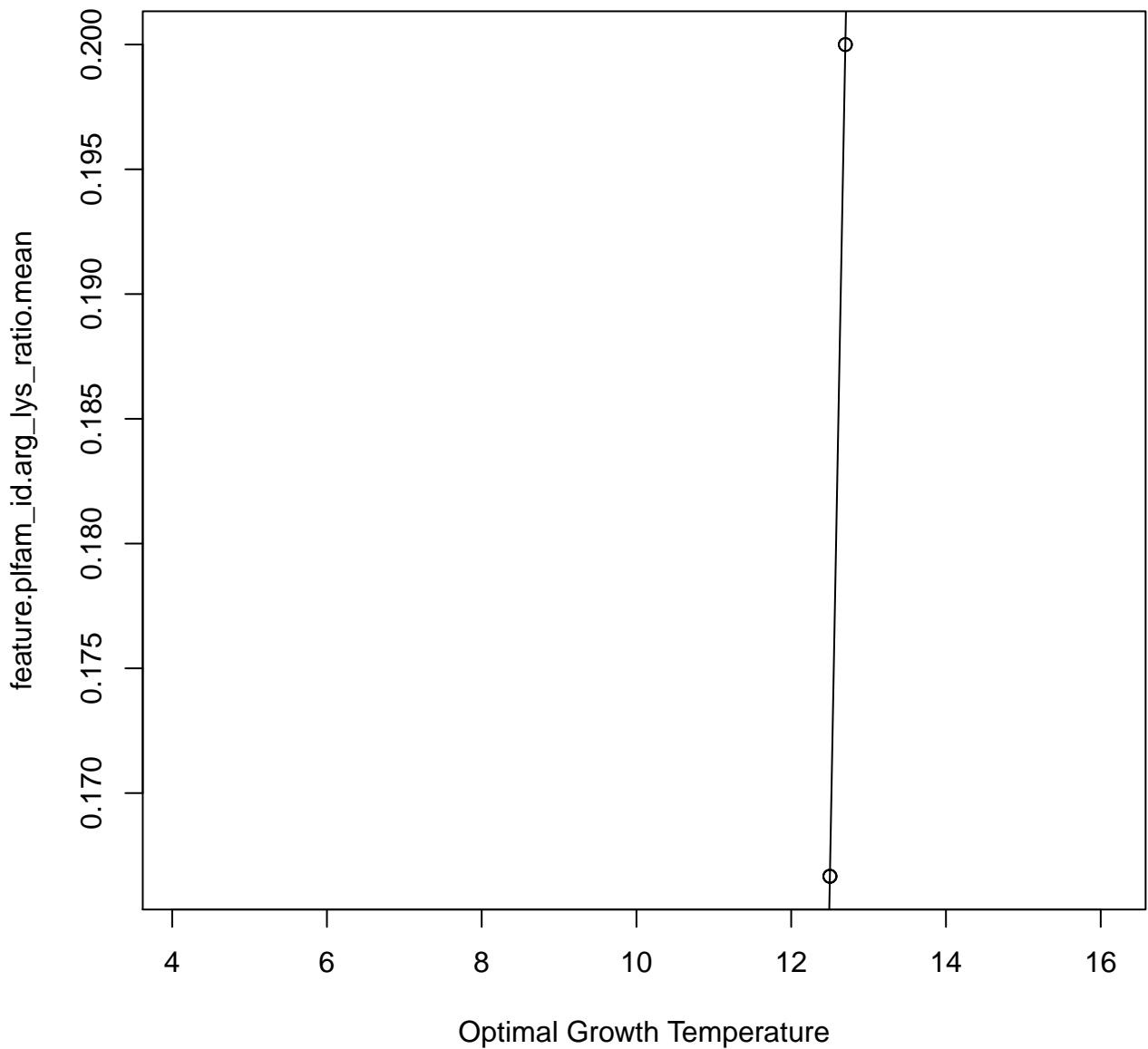
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00004382
hypothetical protein



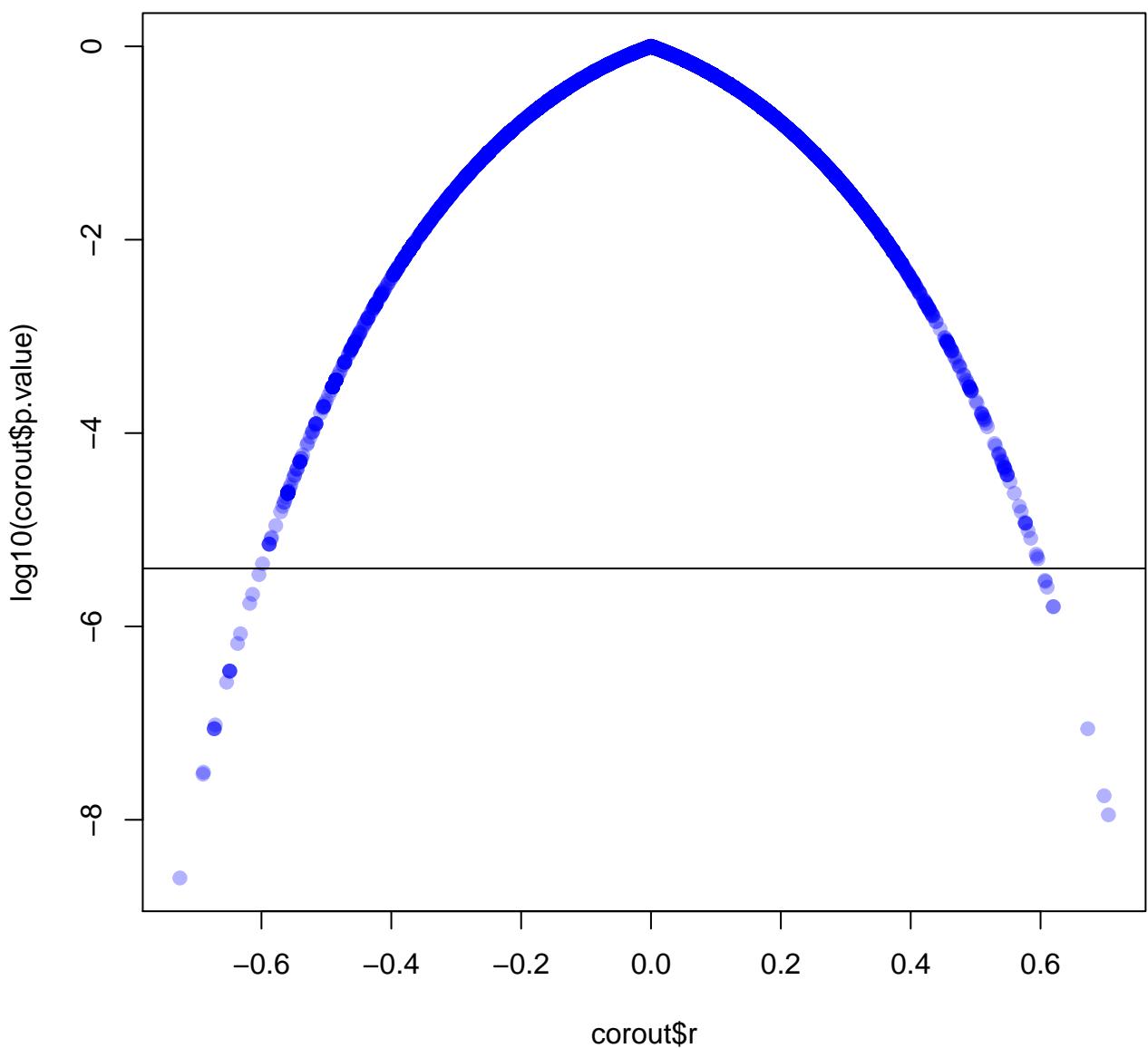
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PLF_28228_00007529
GGDEF domain protein



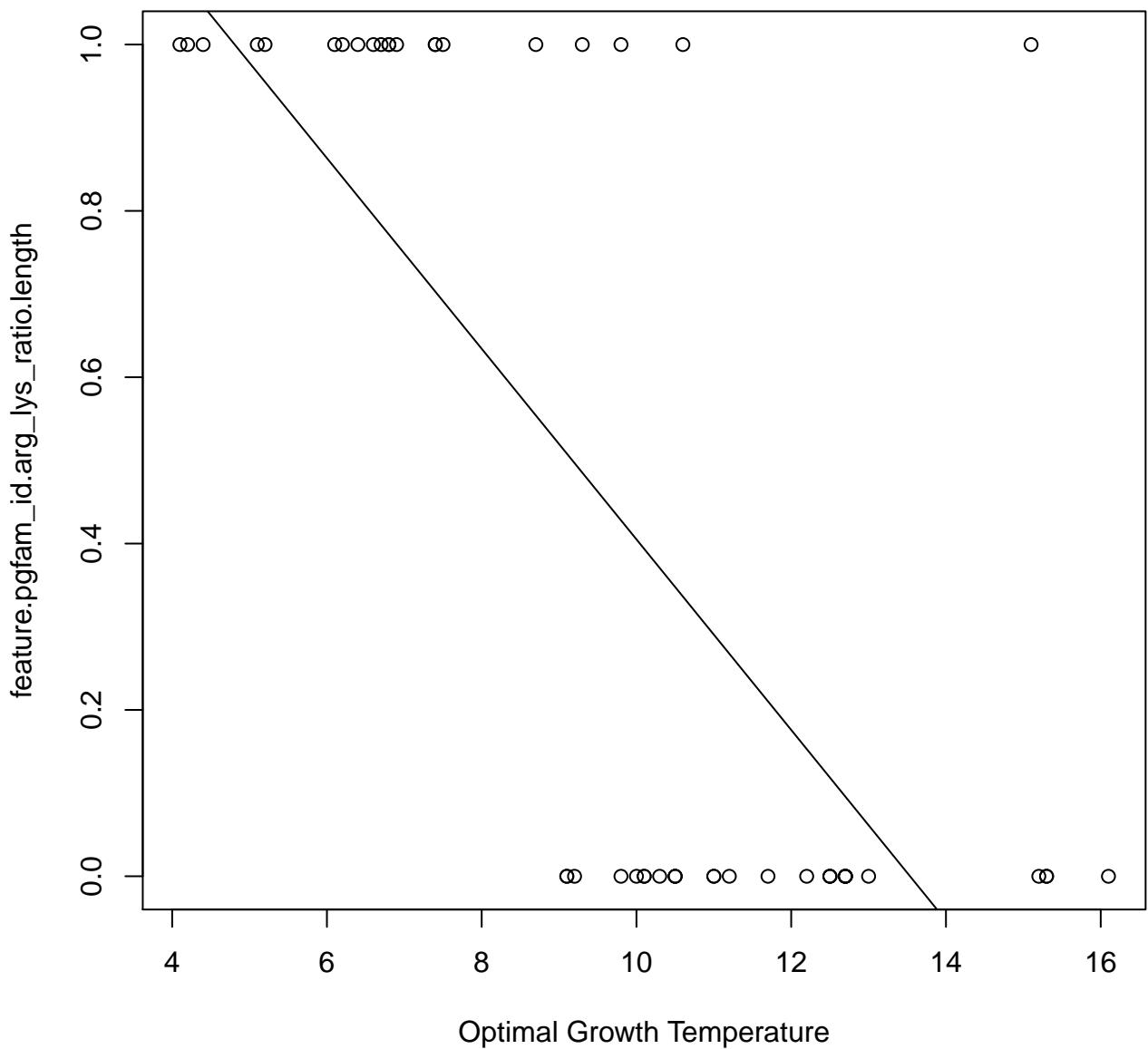
feature.plfam_id.arg_lys_ratio.mean
PLF_28228_00007816
hypothetical protein



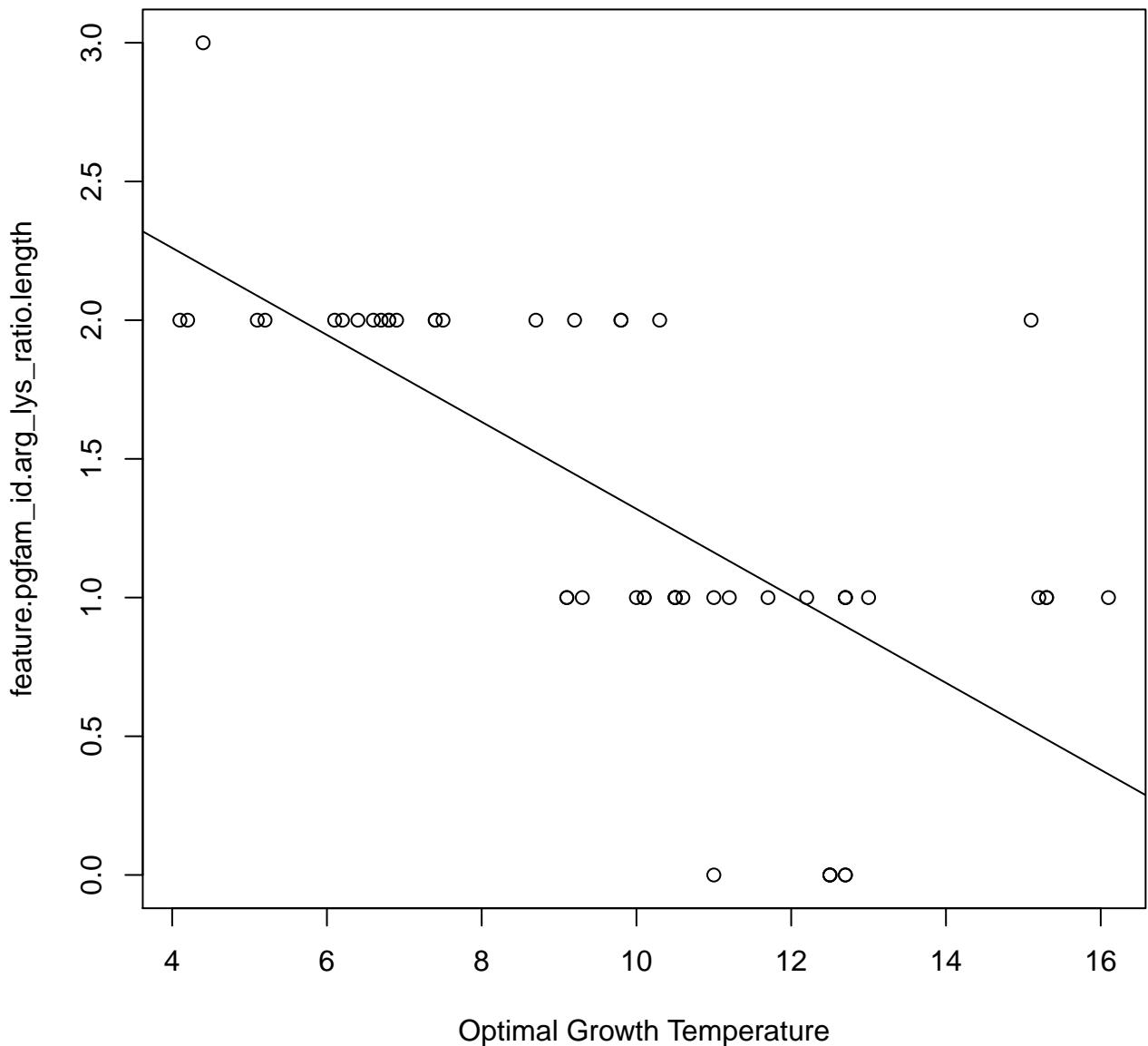
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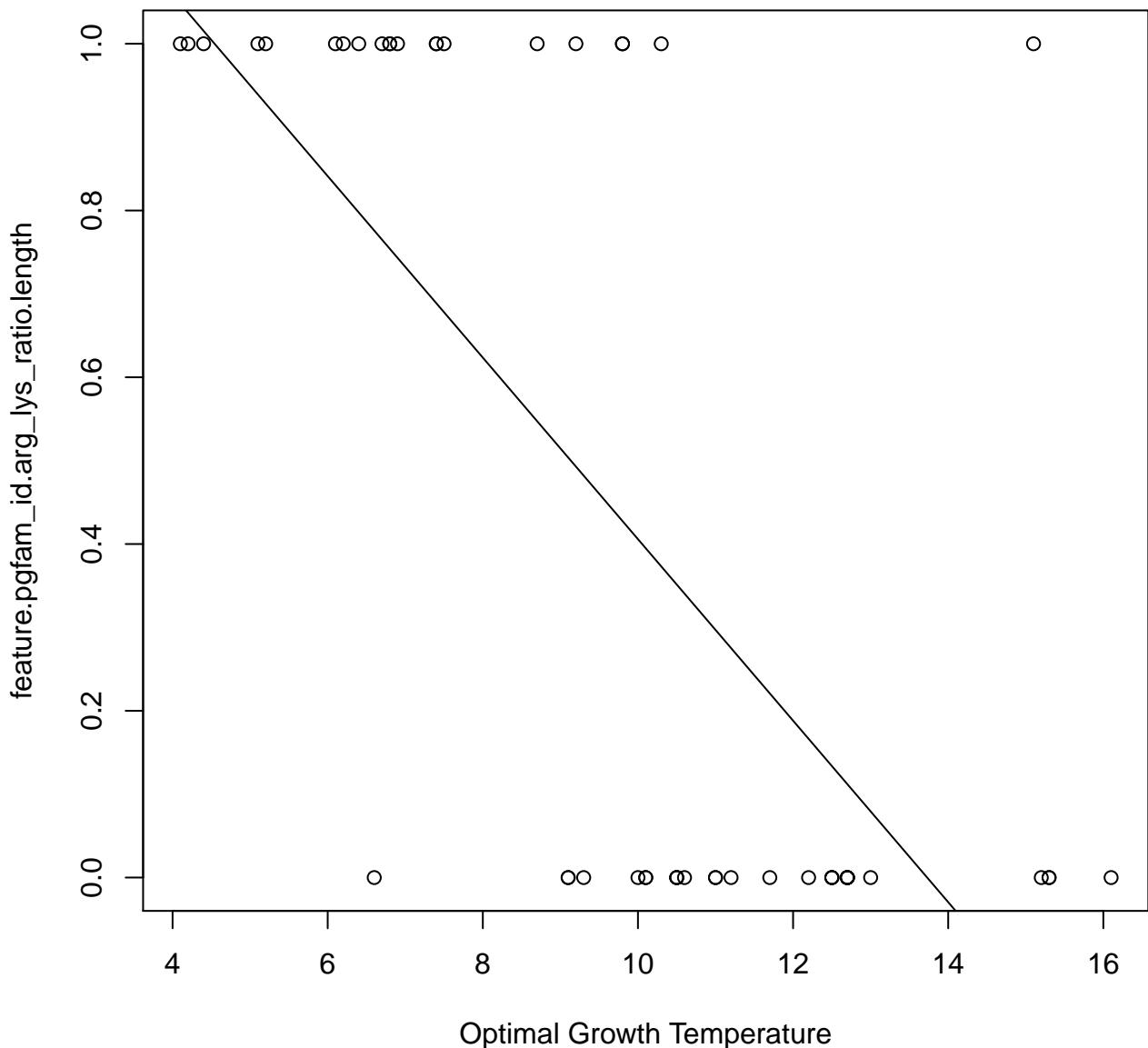
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PGF_07383941
hypothetical protein



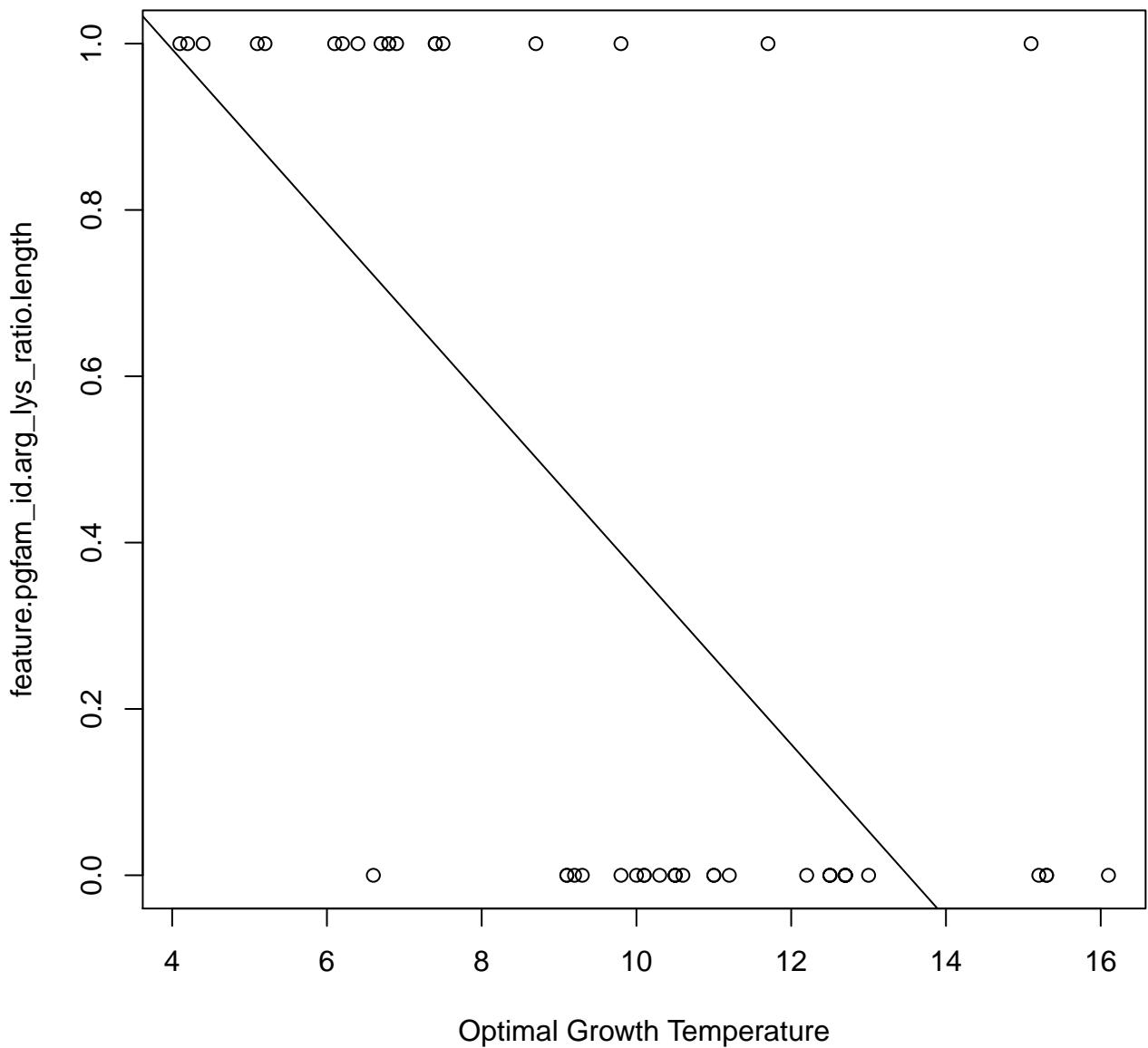
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Cysteine desulfurase (EC 2.8.1.7) => SufS



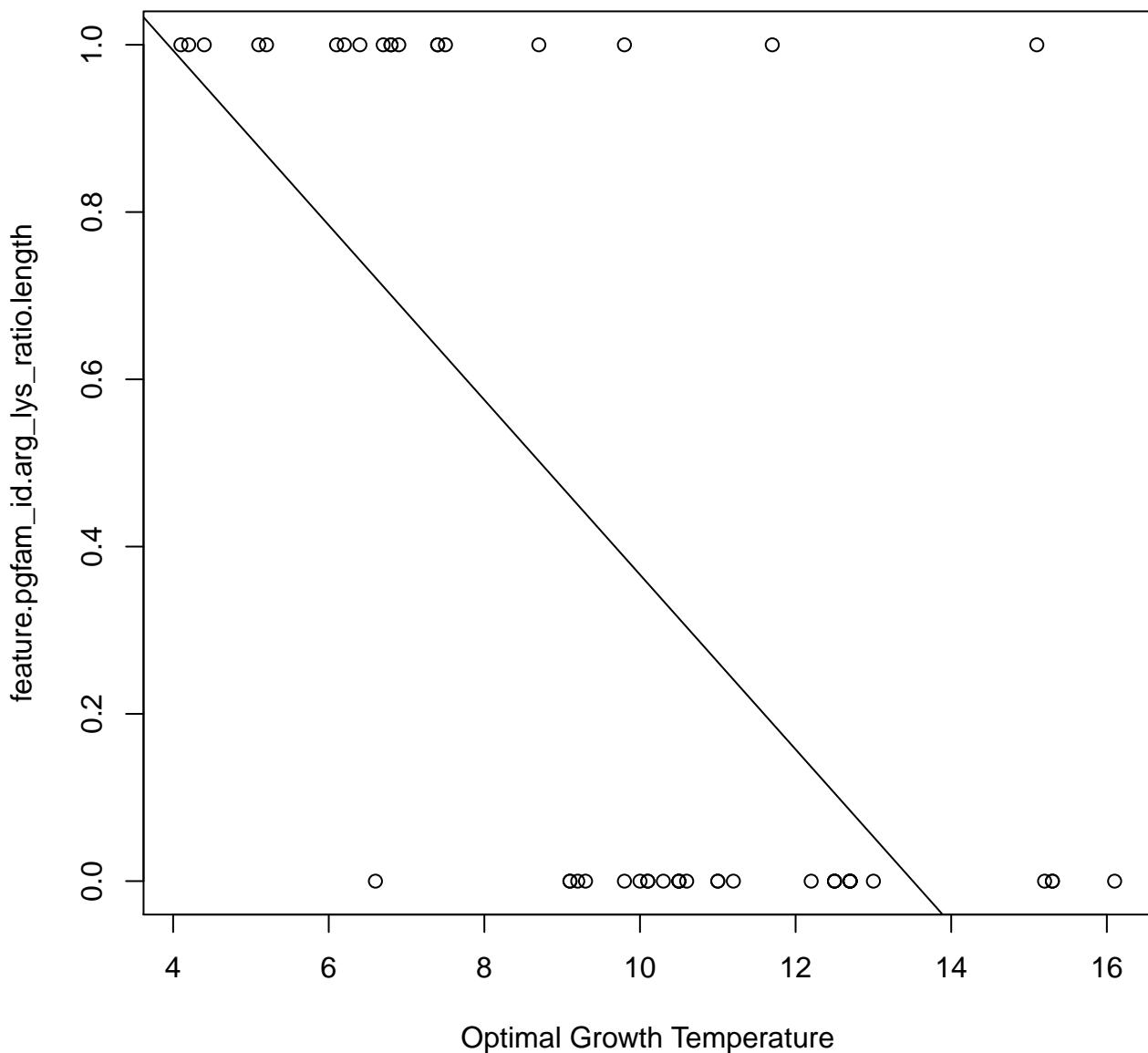
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PGF_00055099
Sulfur acceptor protein => iron-sulfur cluster assembly SuffE



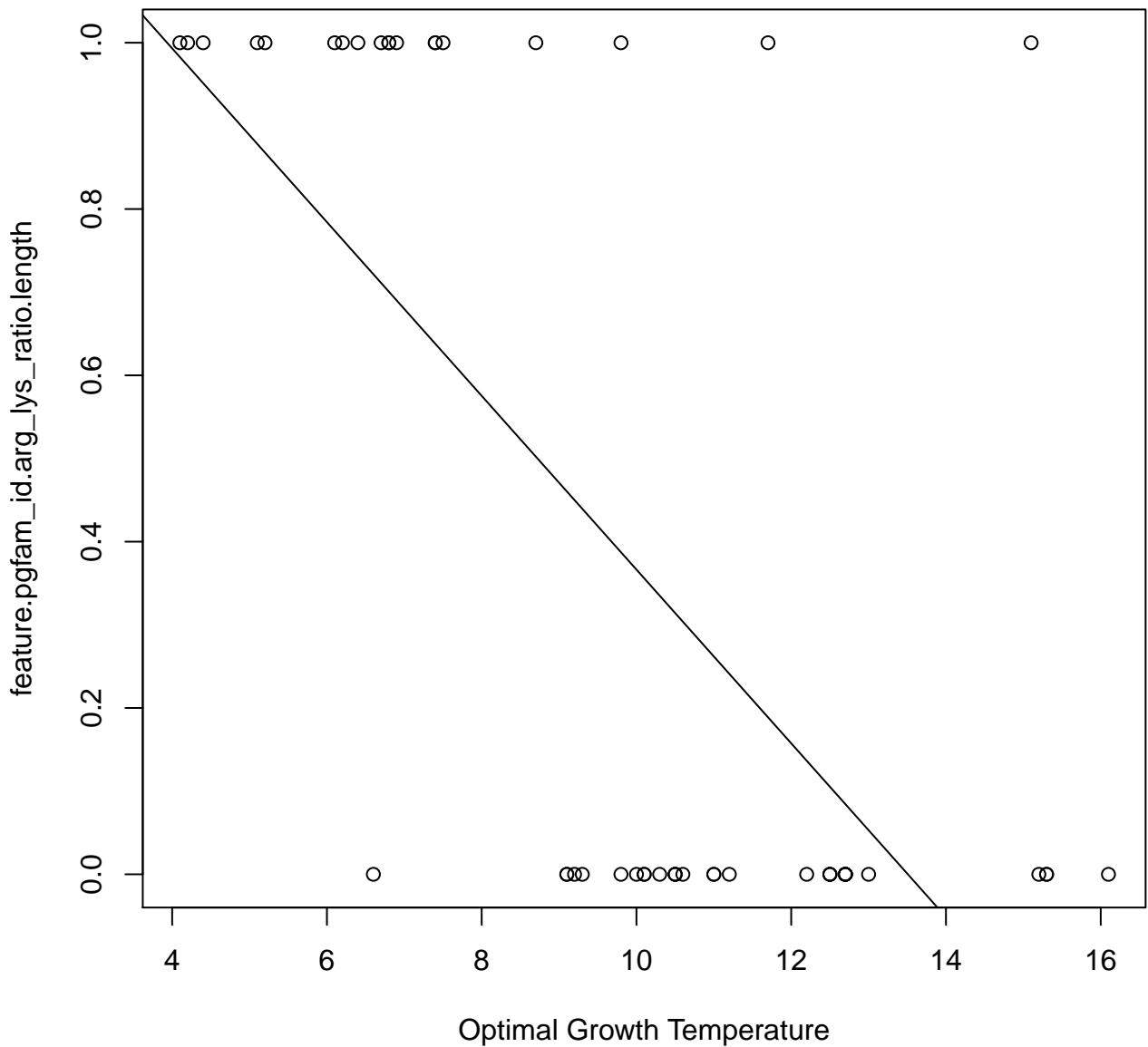
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PGF_00006186
Formate efflux transporter FocA



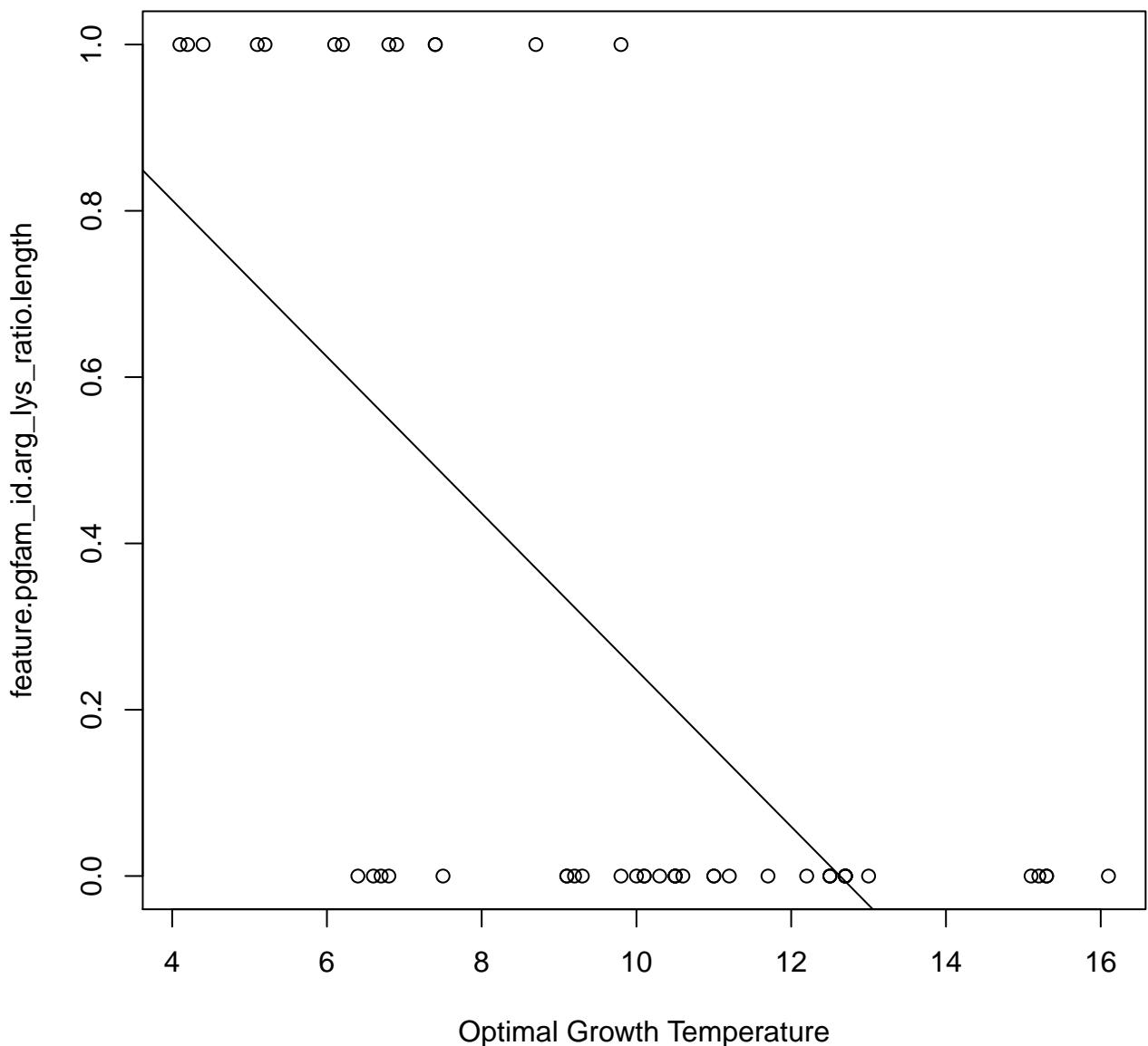
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Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)



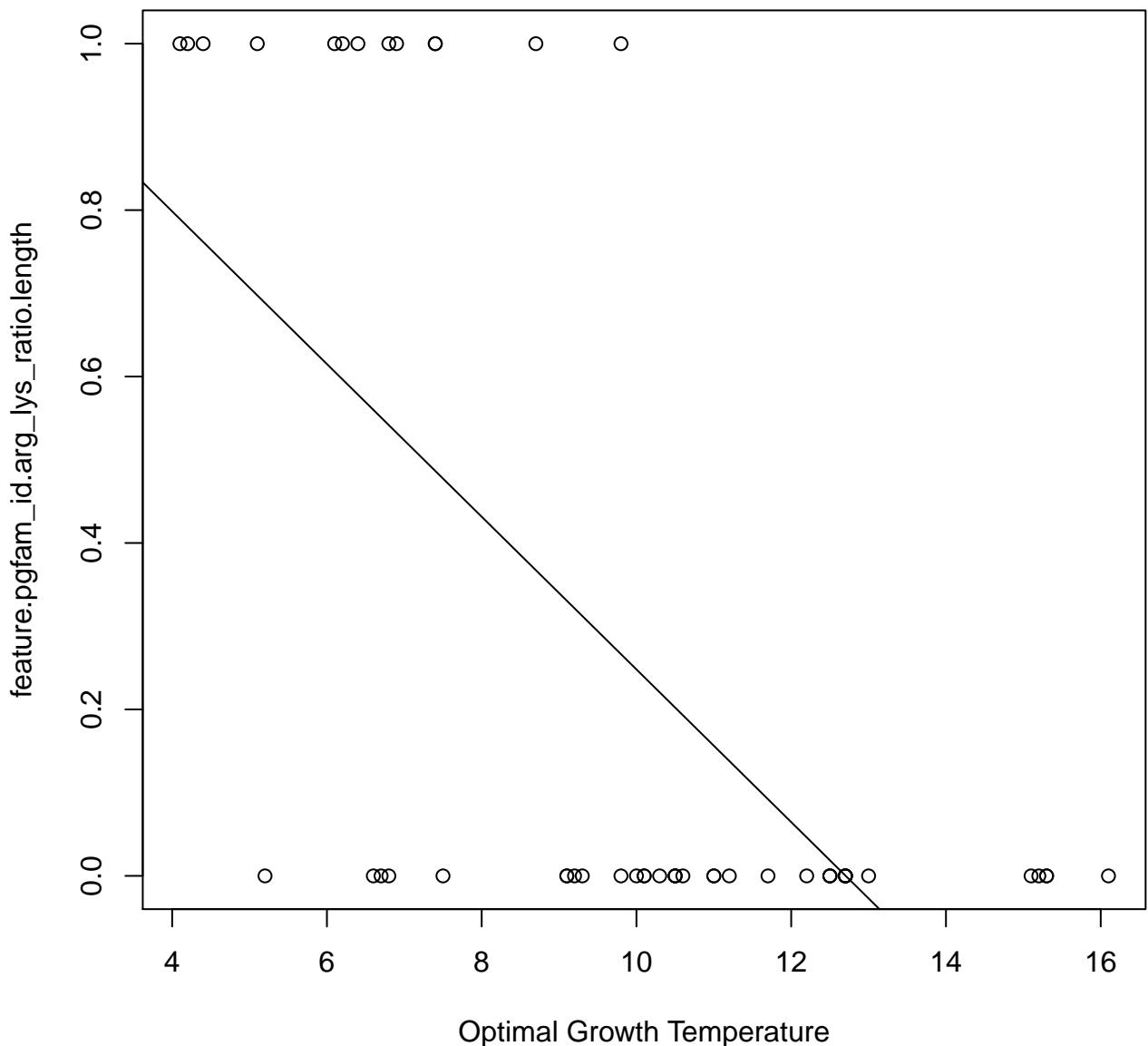
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PGF_01679161
hypothetical protein



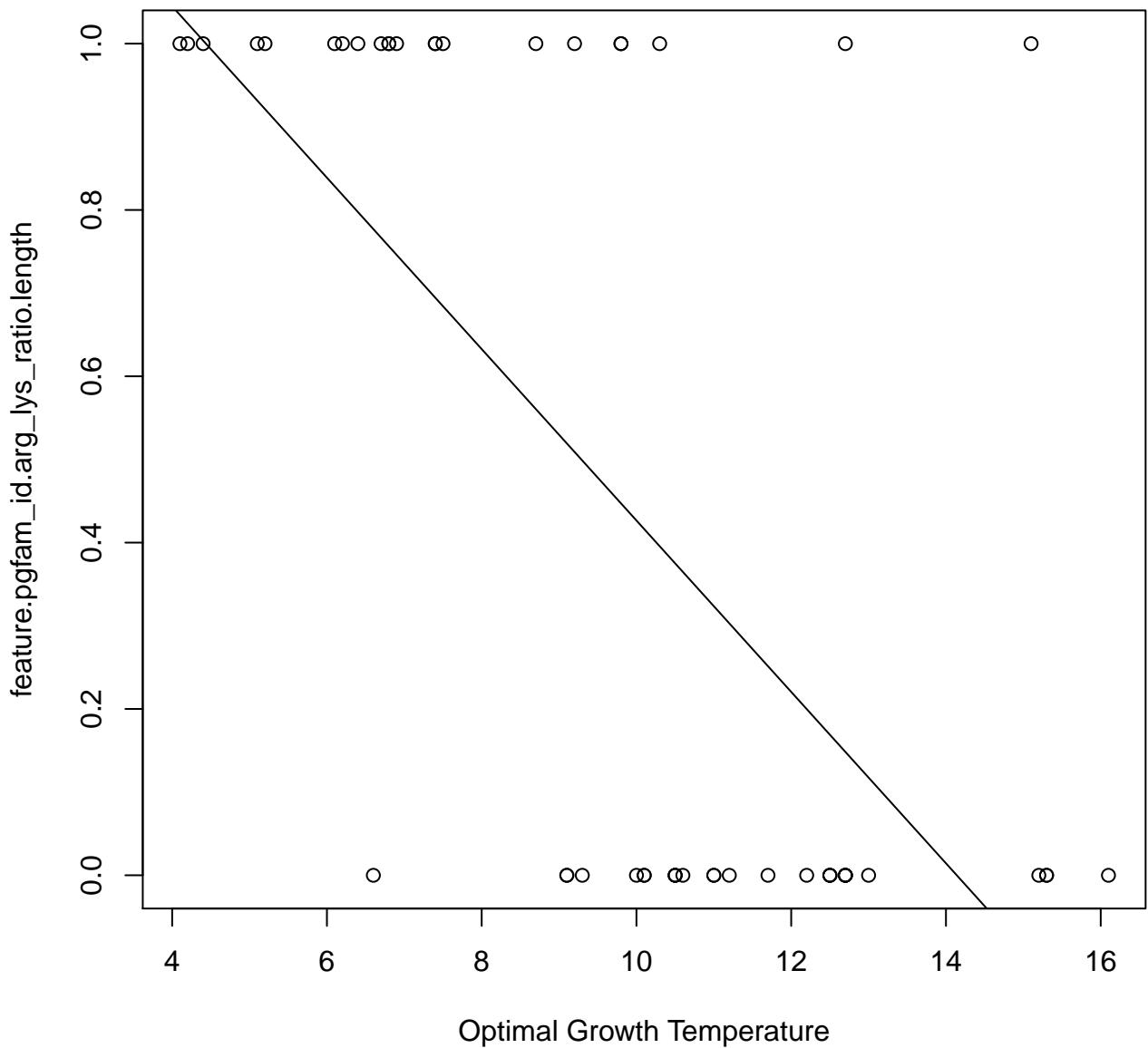
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PGF_05722284
hypothetical protein



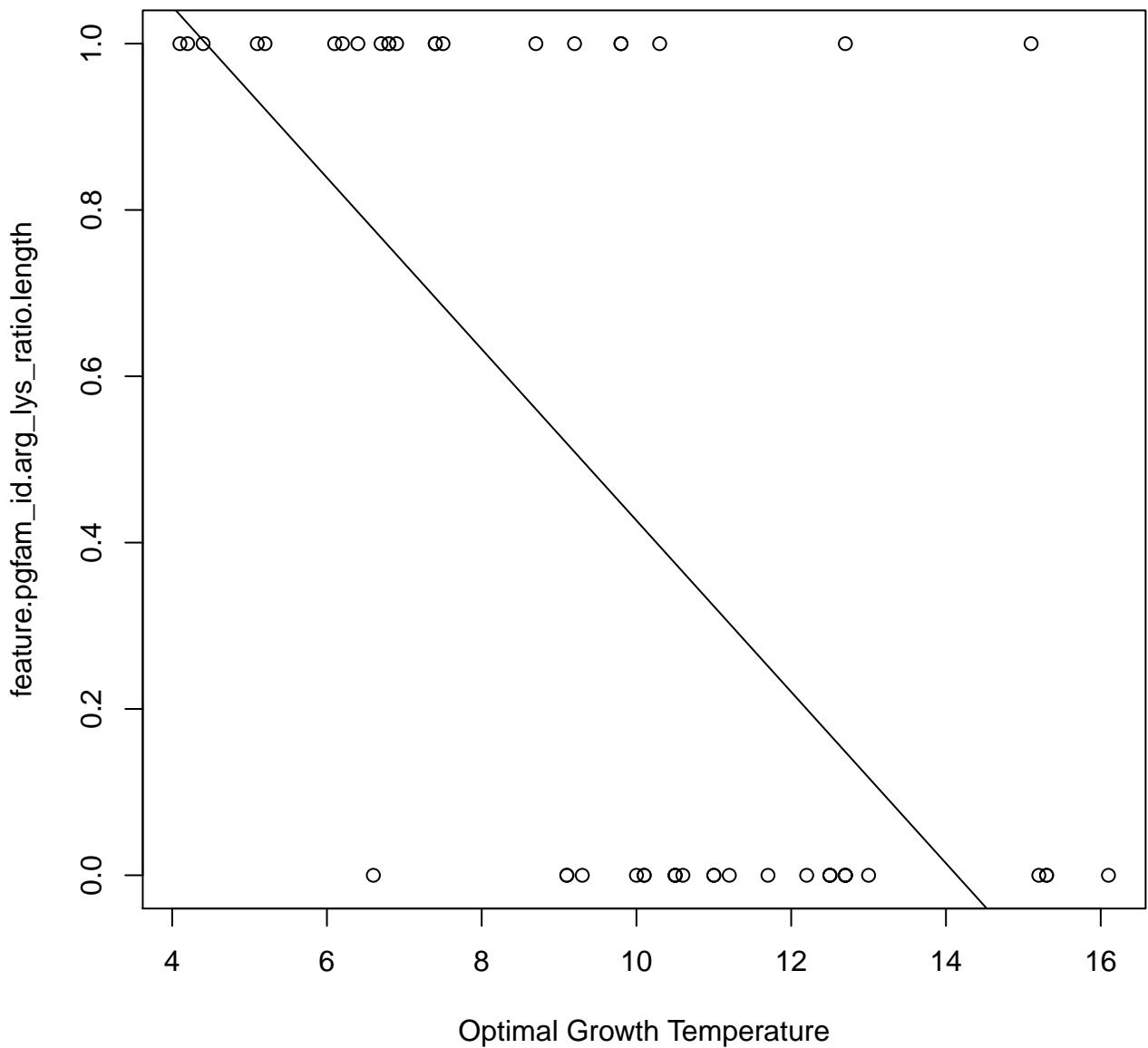
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Gluconate 2-dehydrogenase subunit 3 family protein



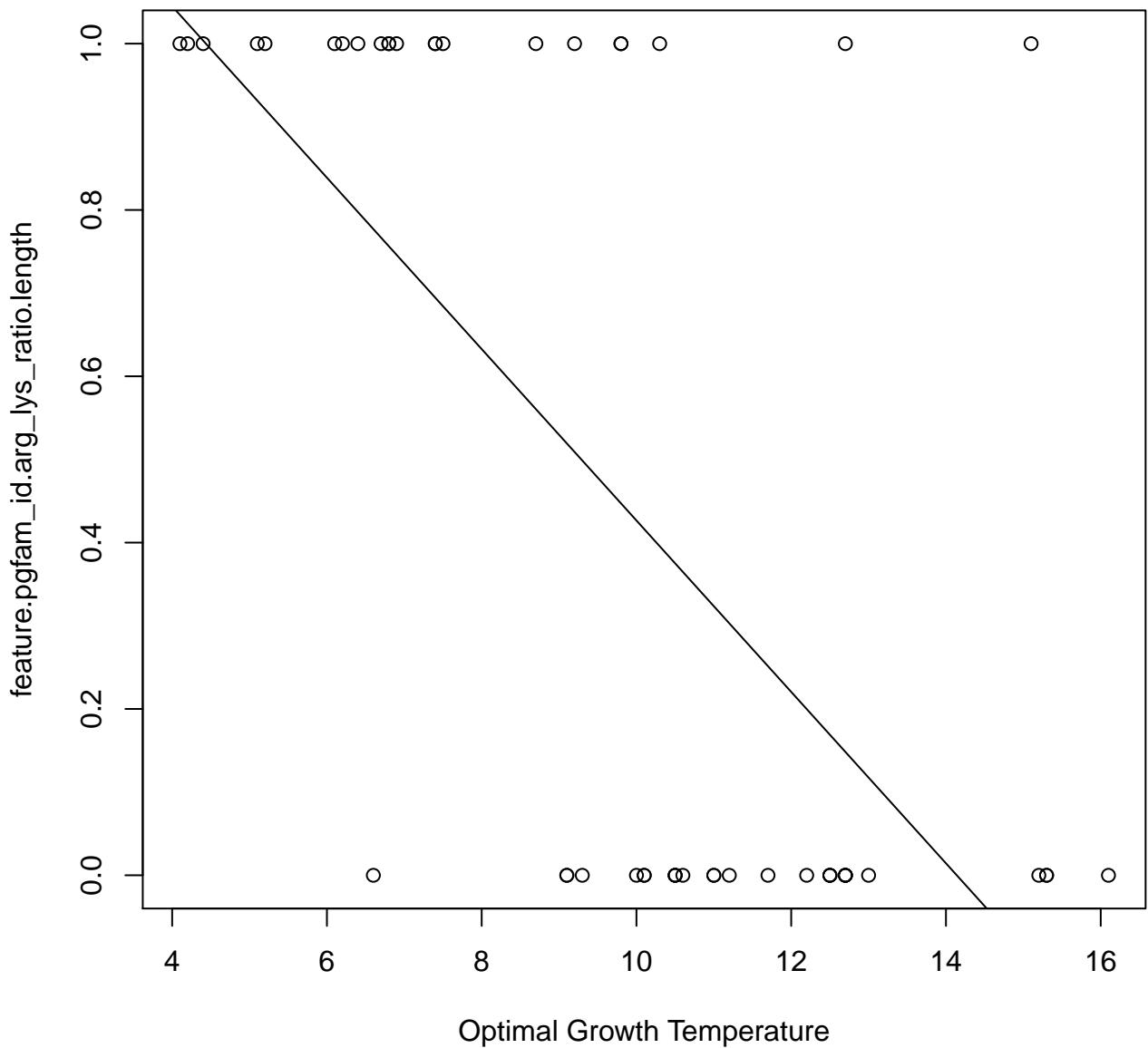
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PGF_00015510
Iron-sulfur cluster assembly ATPase protein SufC



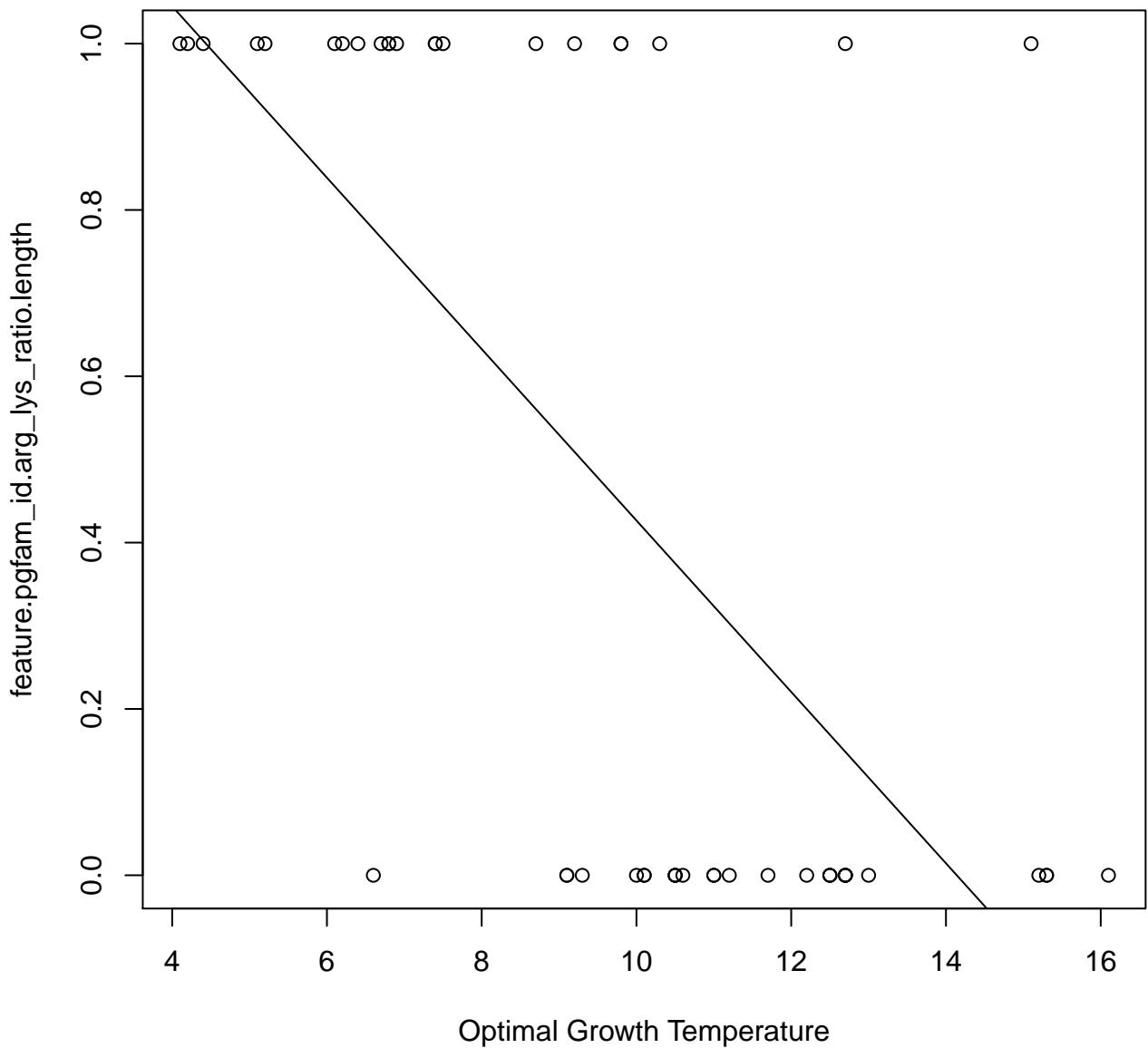
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Iron–sulfur cluster assembly protein SufB



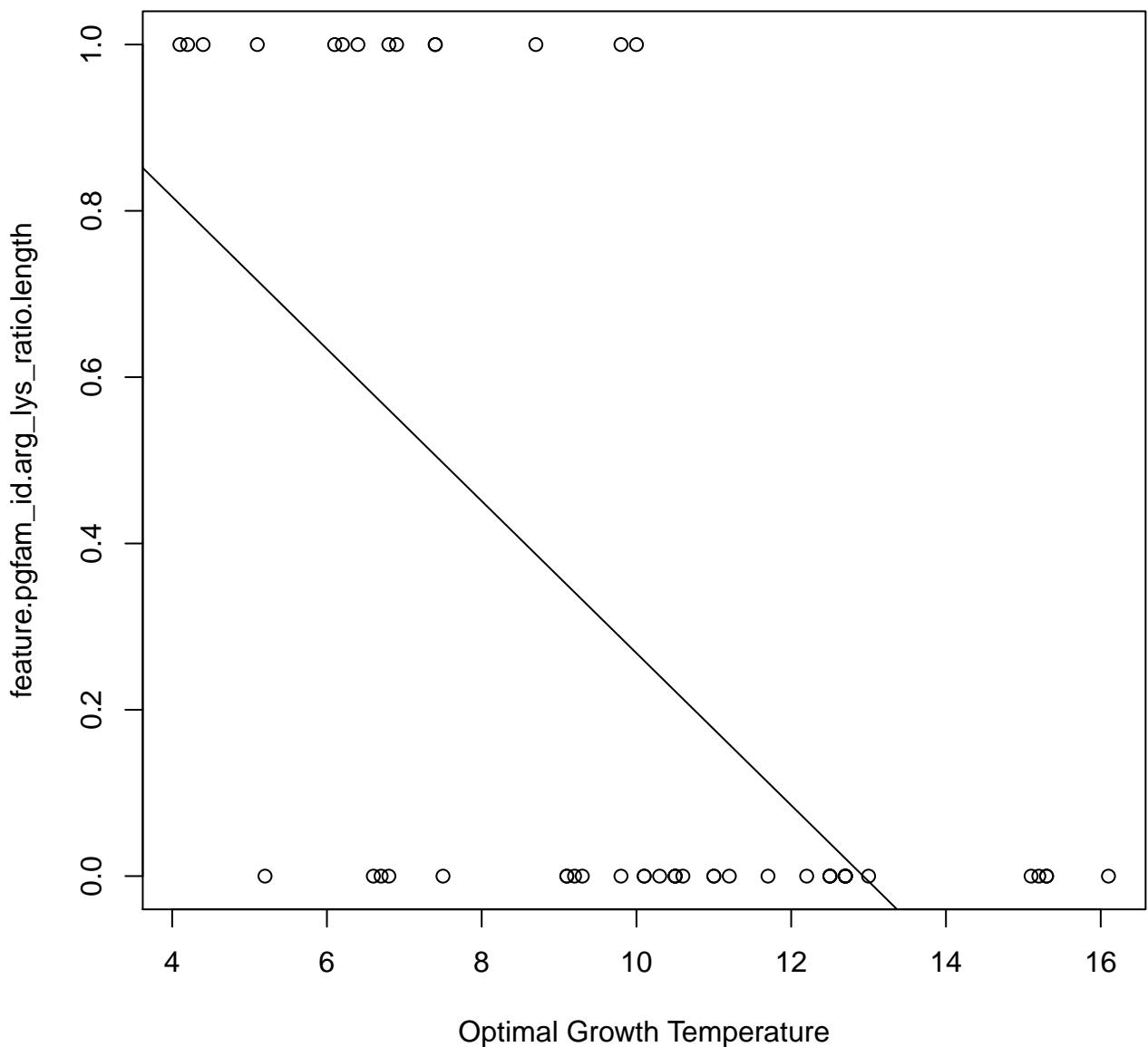
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Iron–sulfur cluster assembly protein SufD



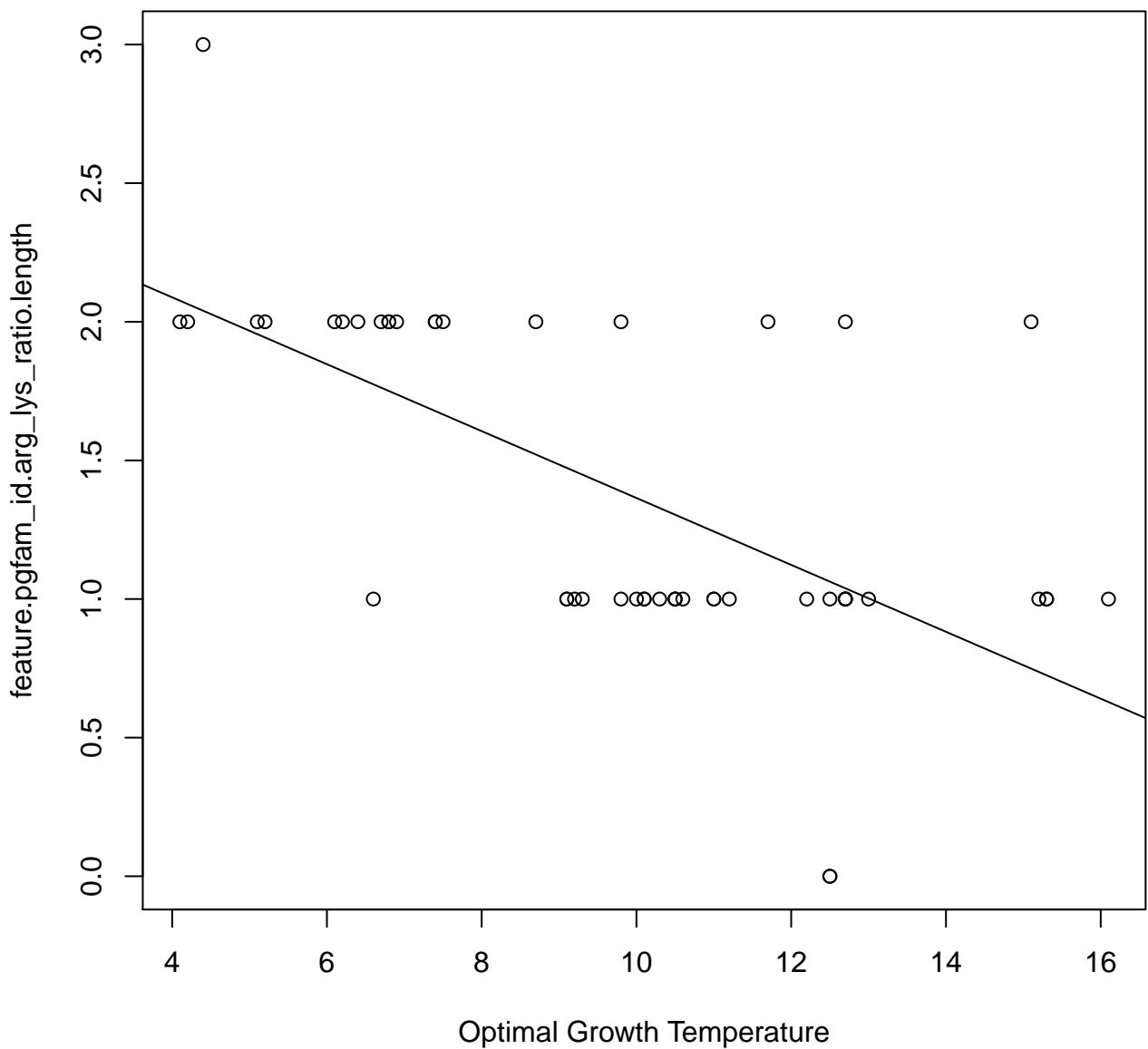
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PGF_06661068
PaaD-like protein (DUF59) involved in Fe-S cluster assembly



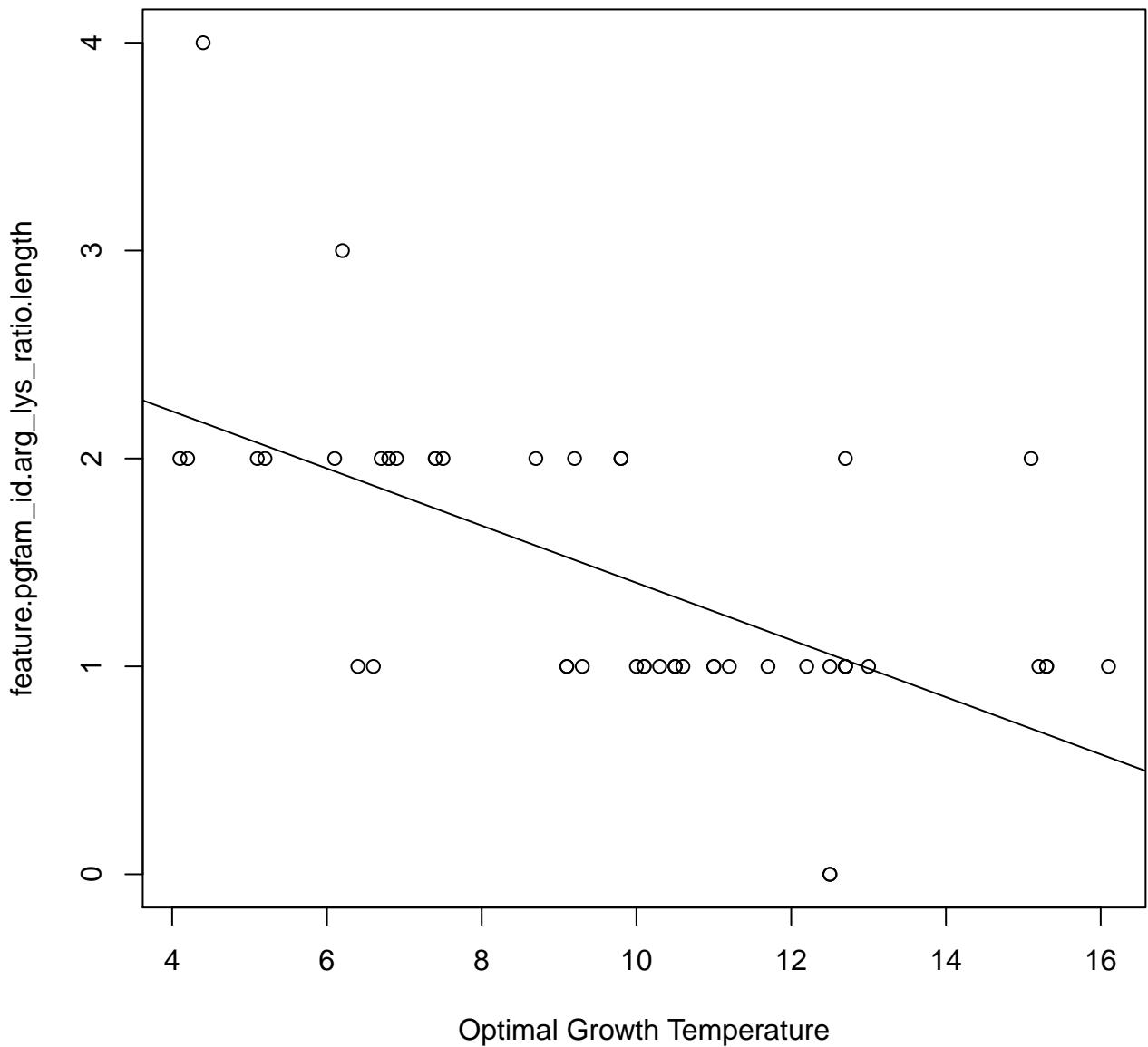
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PGF_03775681
YoeB toxin protein



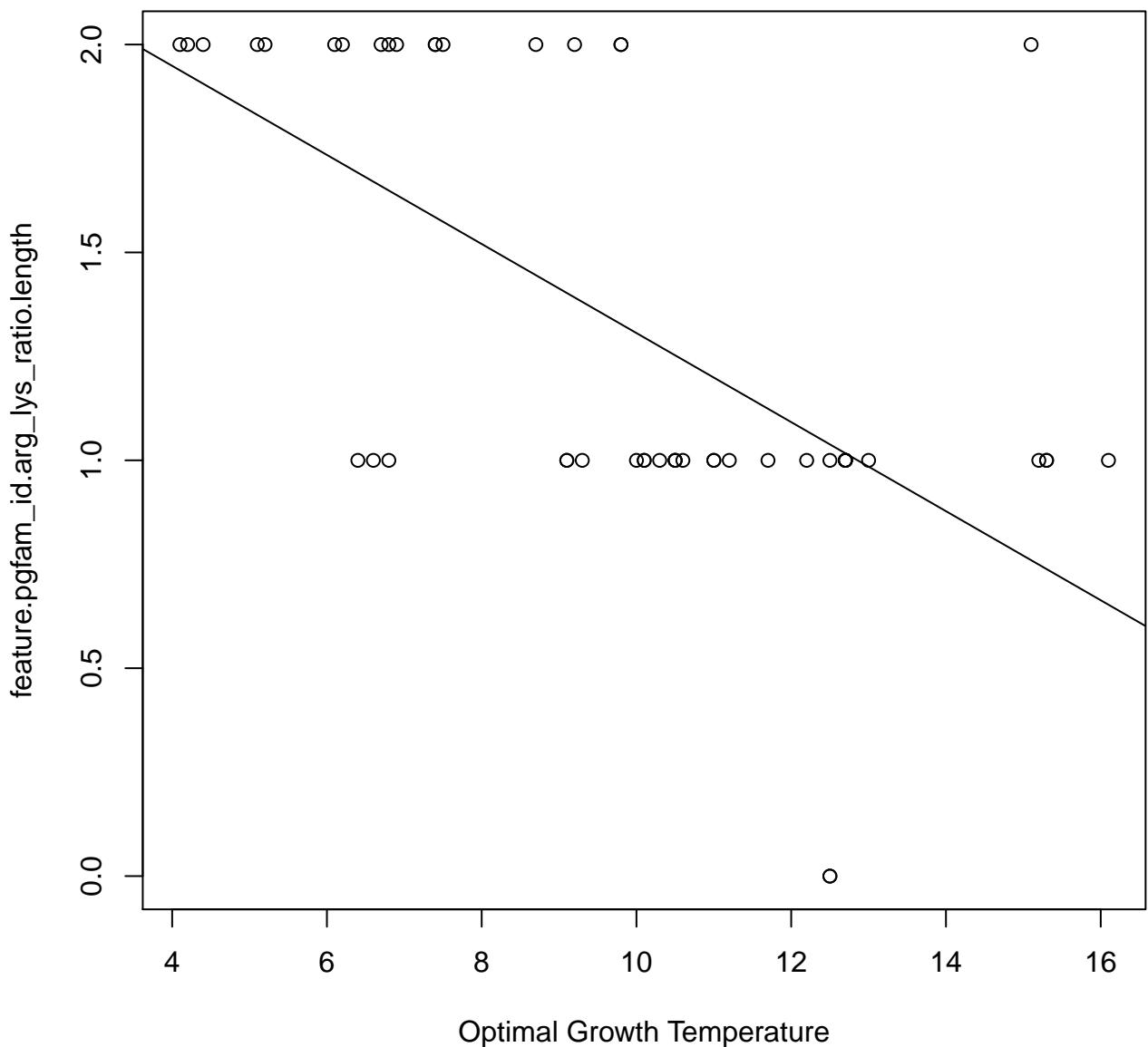
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PGF_10523783
Acetyl-CoA synthetase (EC 6.2.1.1)



feature.pgfam_id.arg_lys_ratio.length
PGF_05070366
Dihydroxy-acid dehydratase (EC 4.2.1.9)

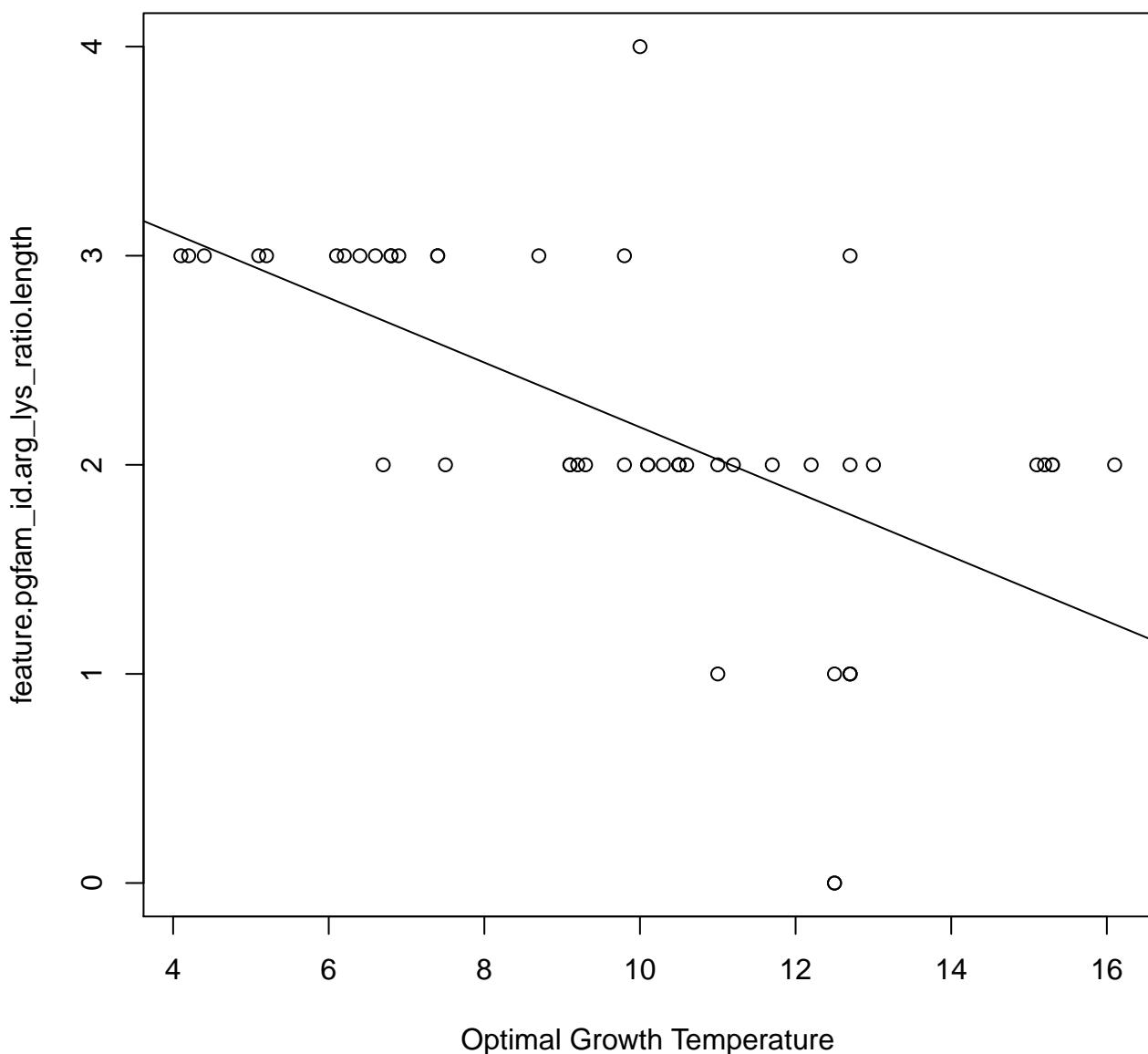


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PGF_00751789
hypothetical protein

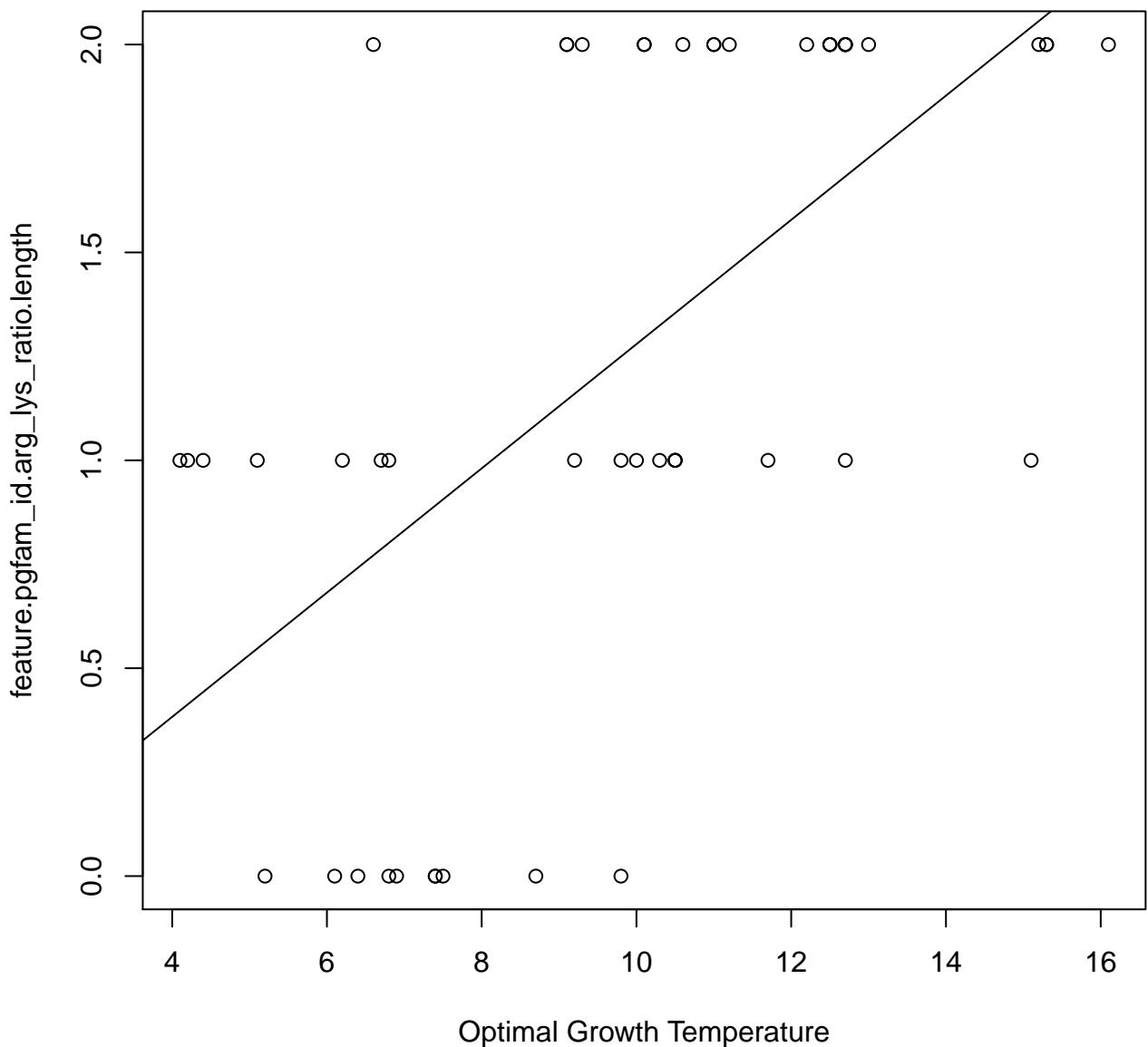


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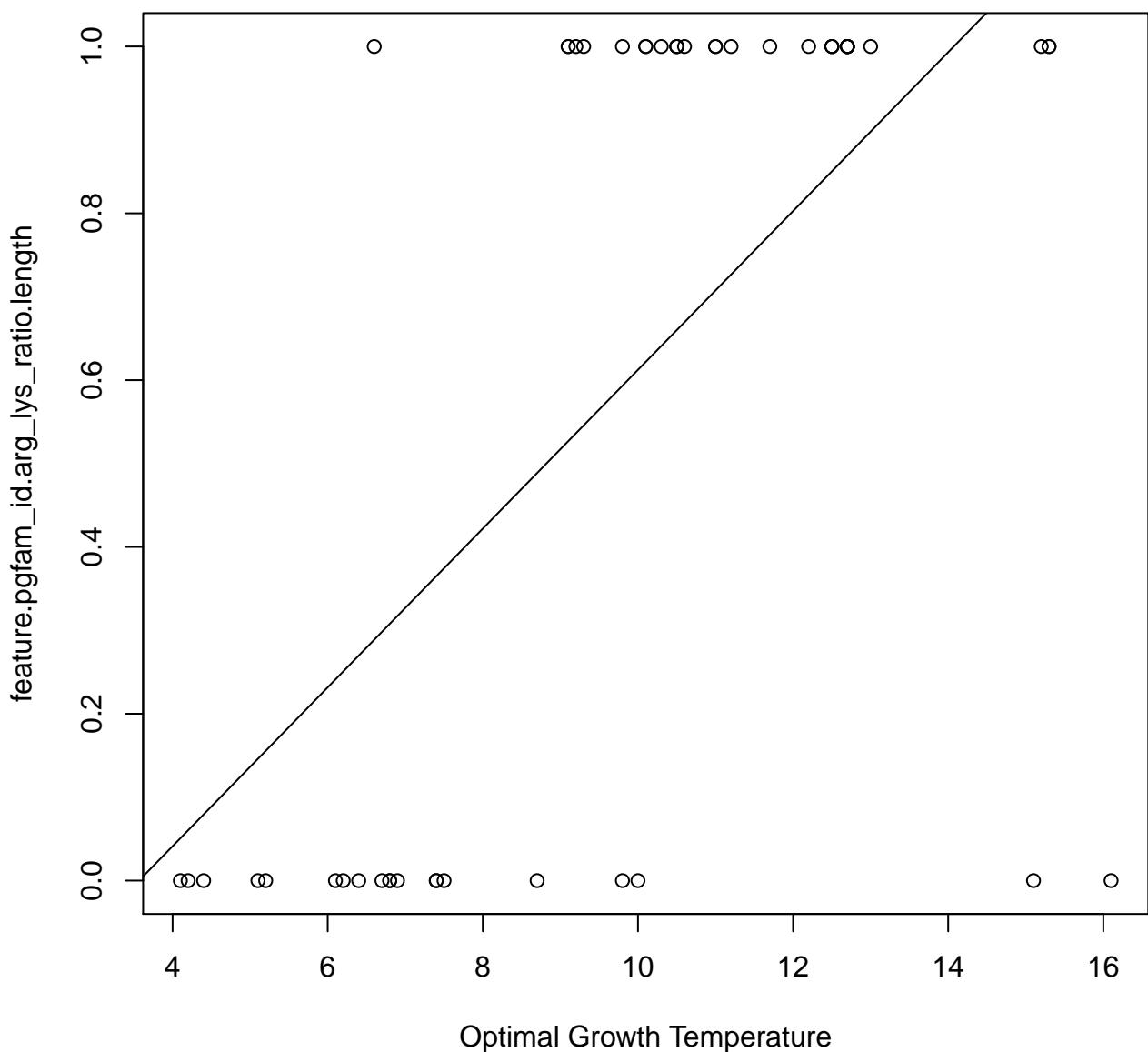
Chemotaxis regulator – transmits chemoreceptor signals to flagellar motor components CheY



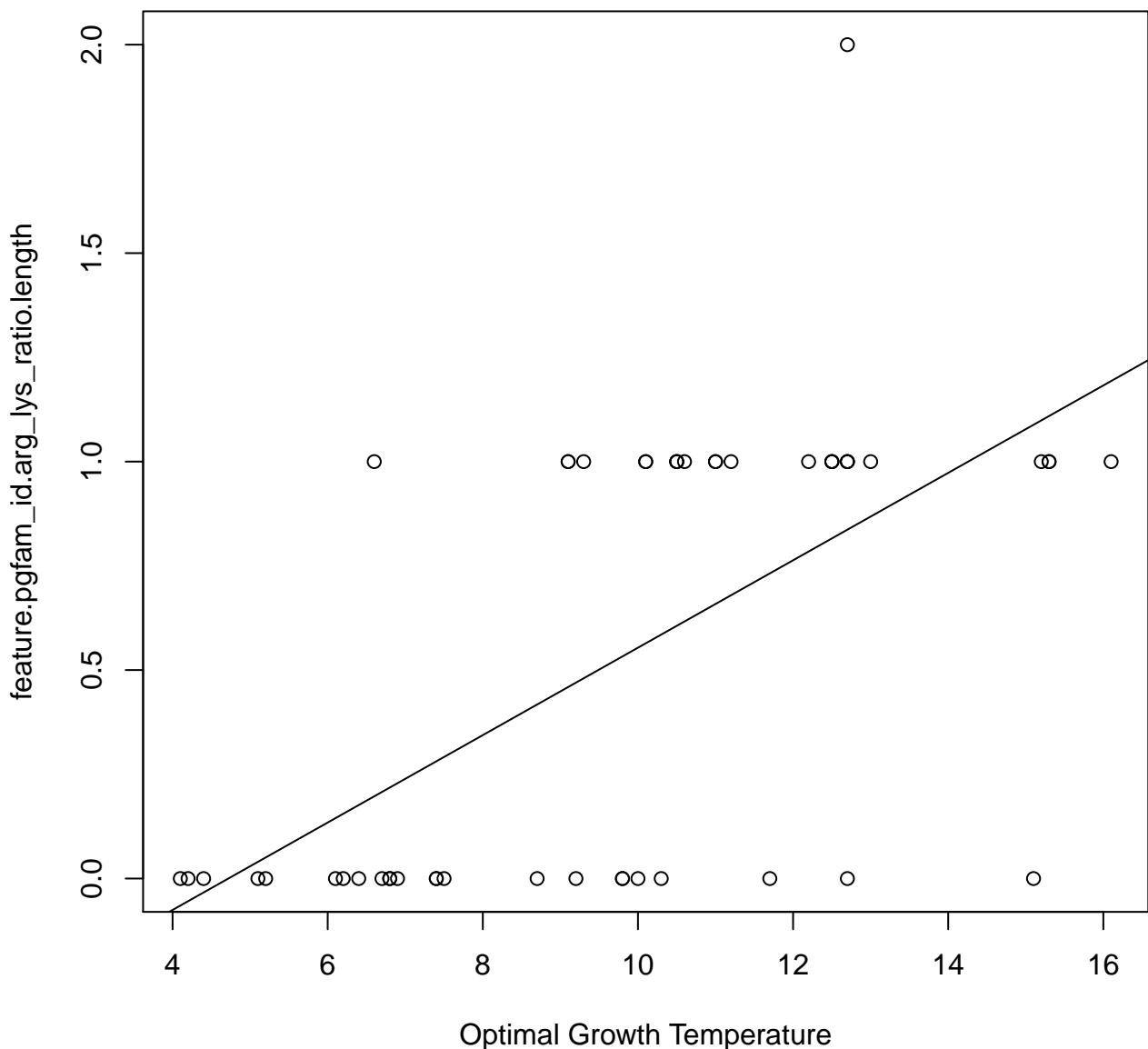
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Cytochrome c-type protein NapC



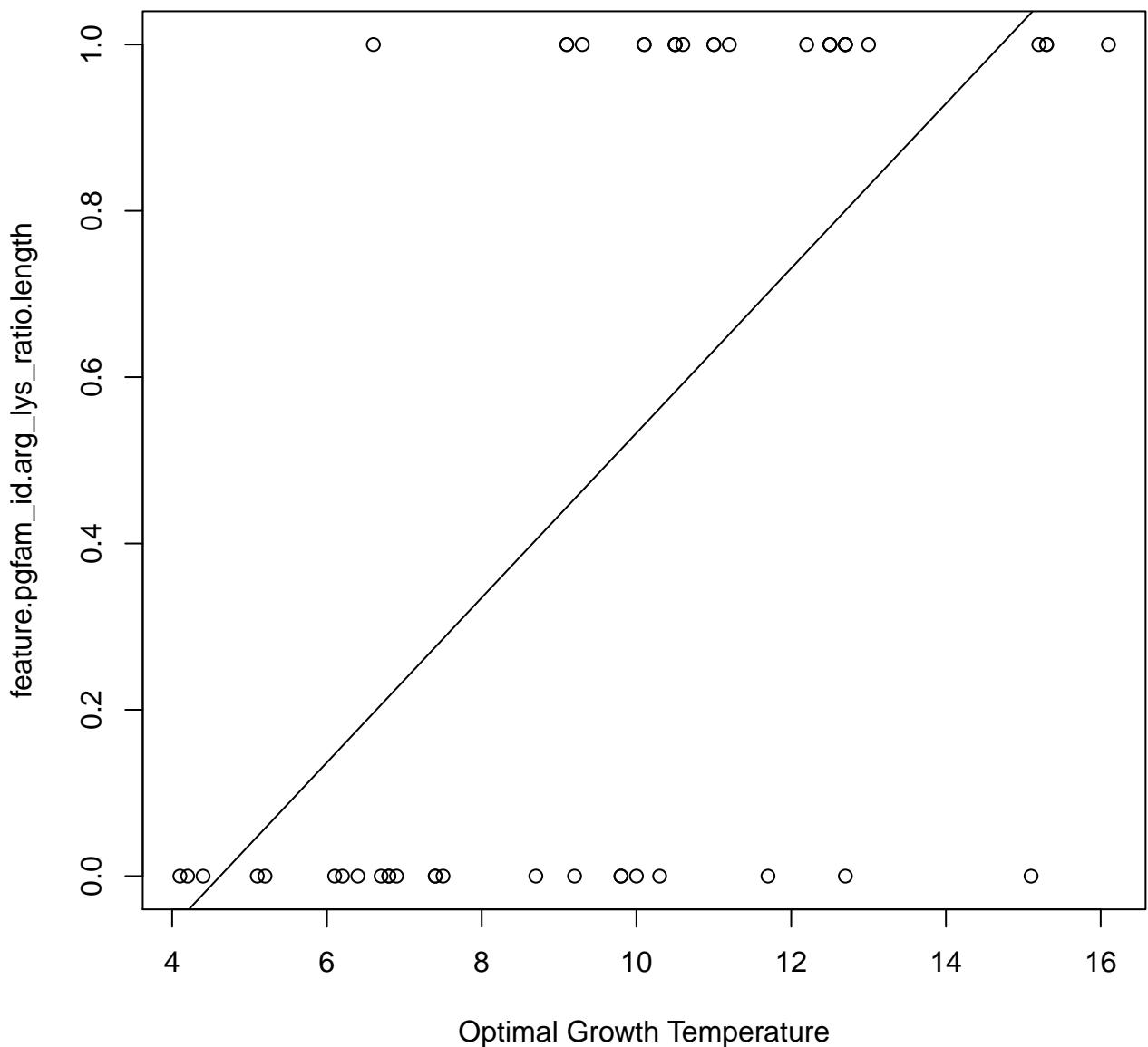
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PGF_01336627
hypothetical protein



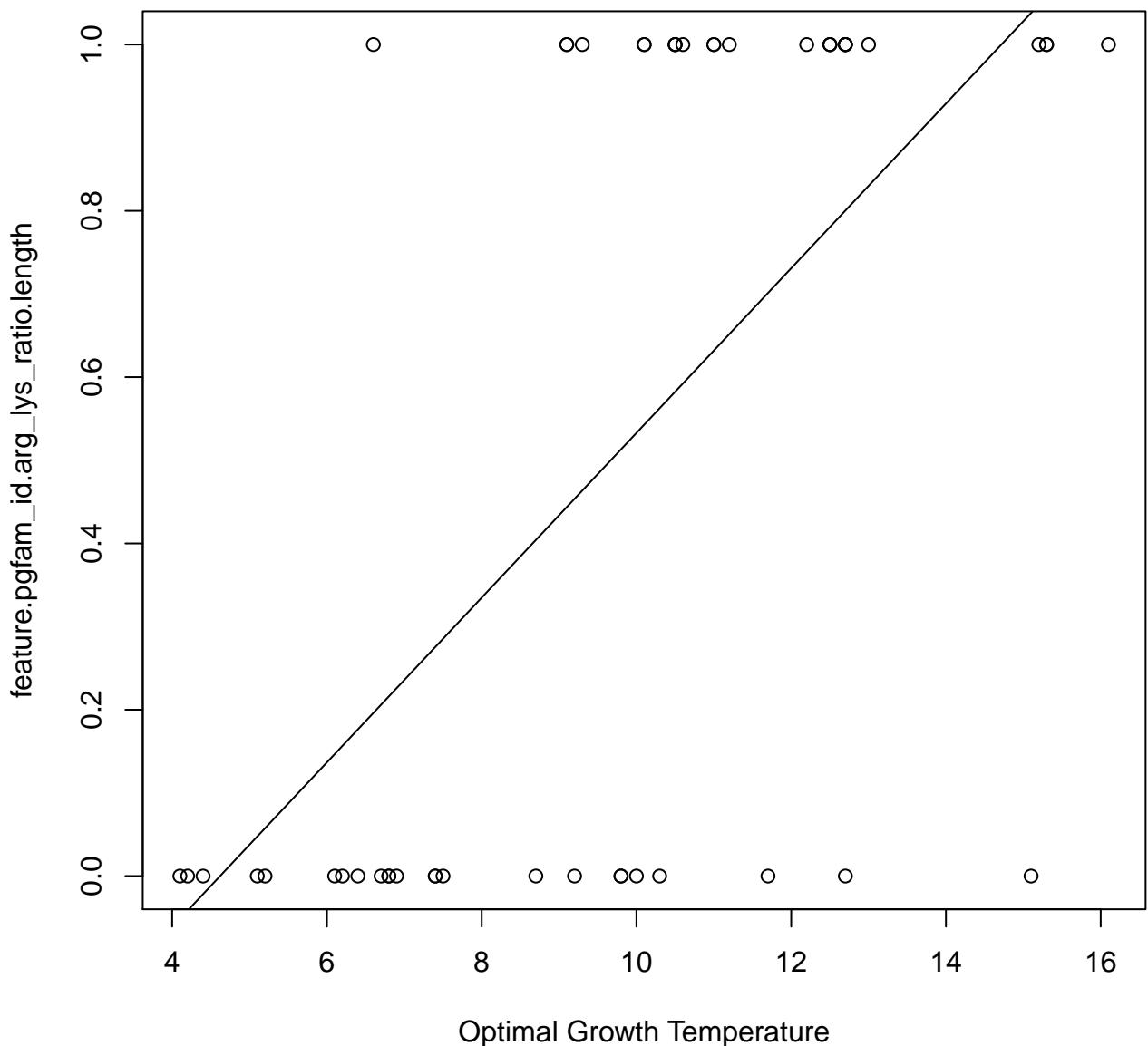
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Nitric oxide reductase activation protein NorQ



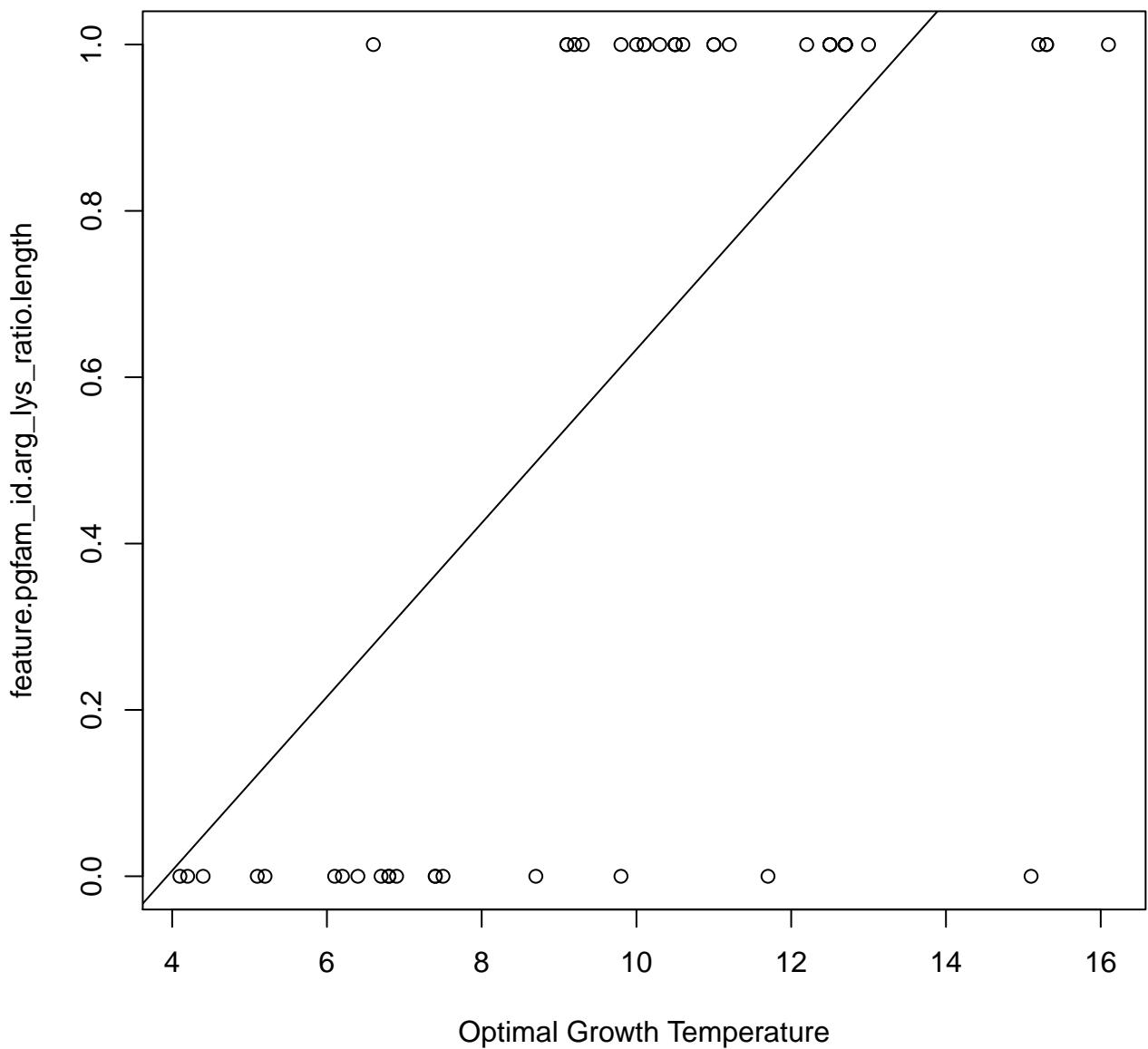
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Nitric oxide reductase activation protein NorF



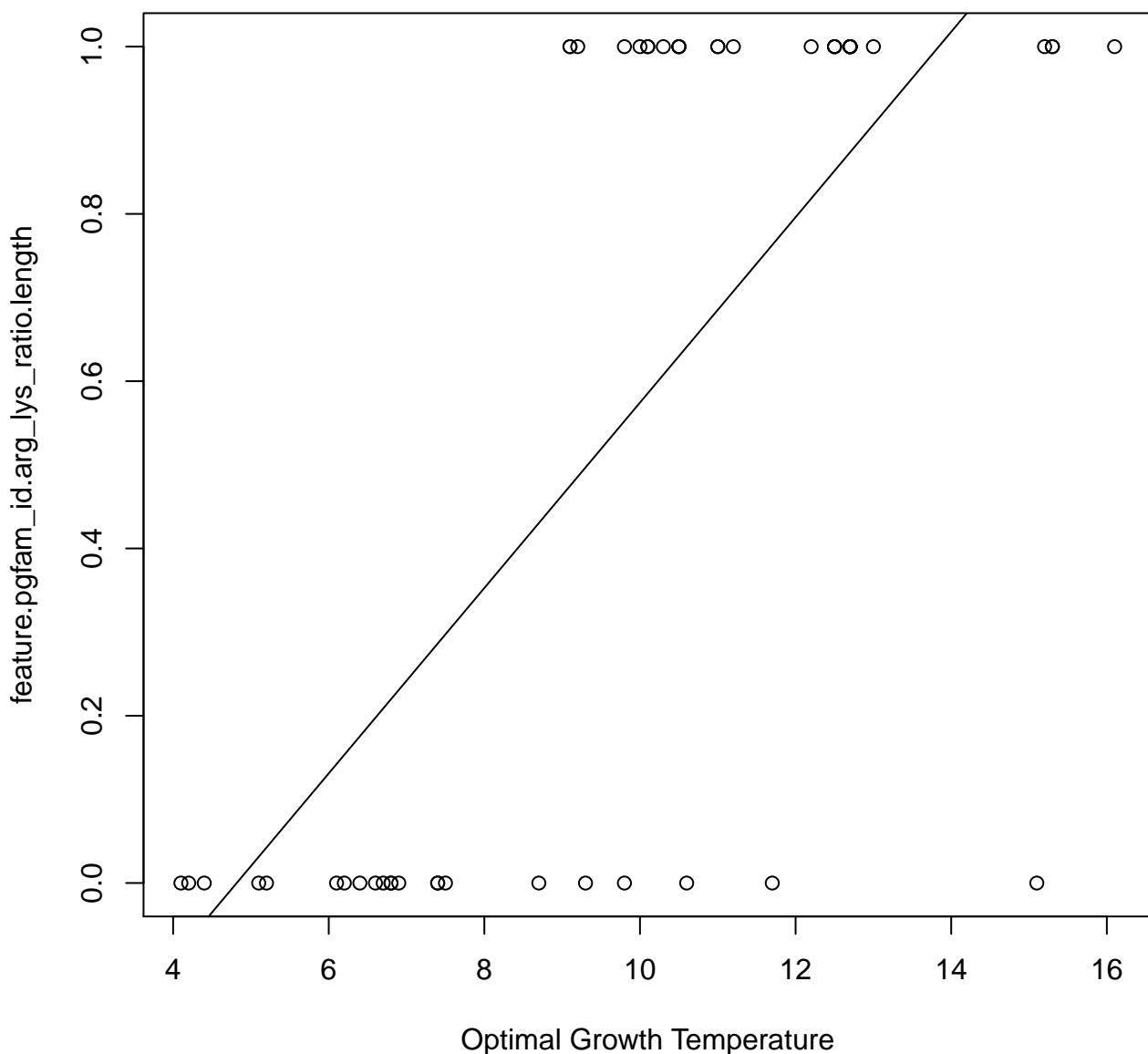
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Nitric-oxide reductase subunit C (EC 1.7.99.7)



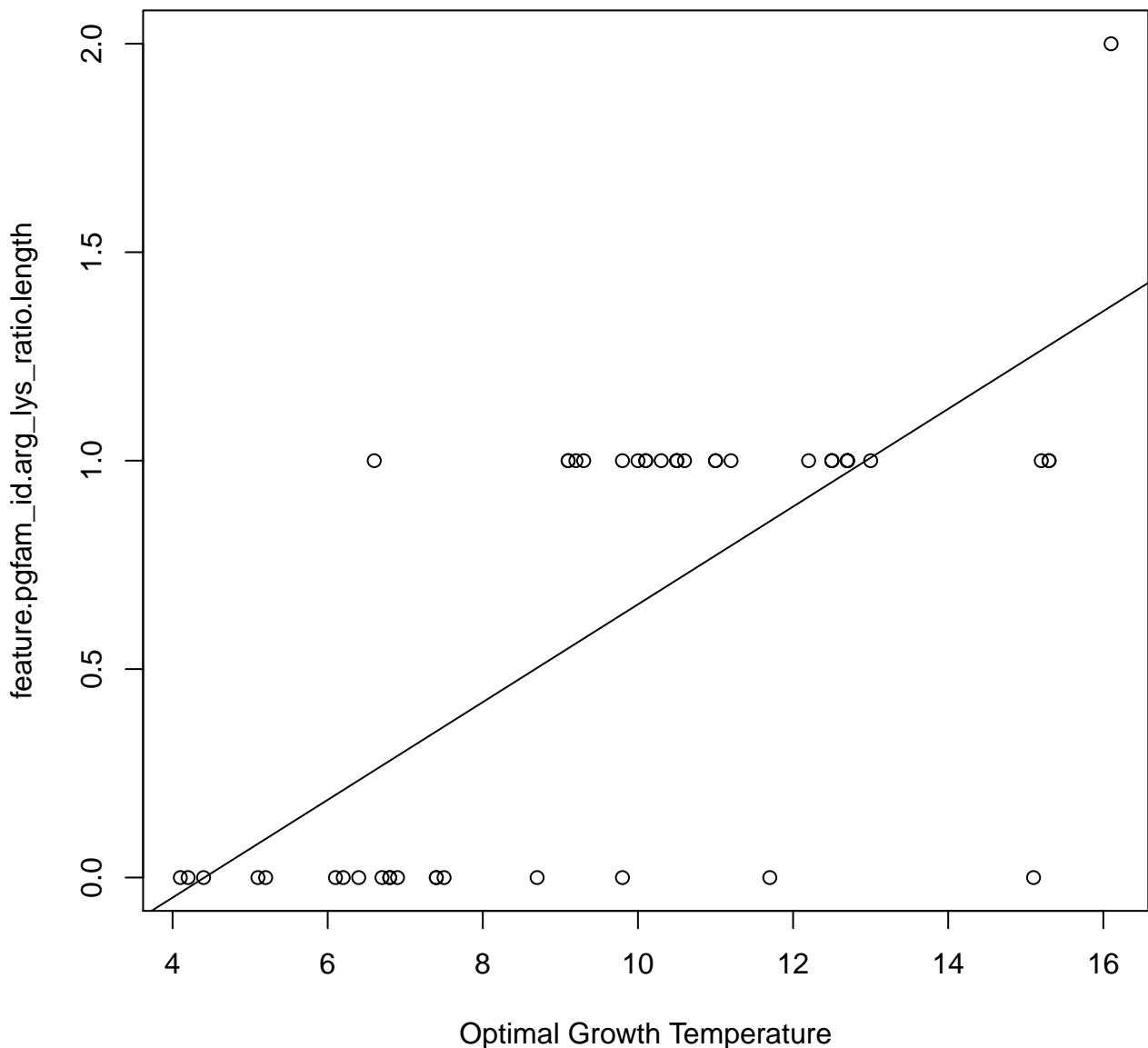
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Chorismate--pyruvate lyase (EC 4.1.3.40)



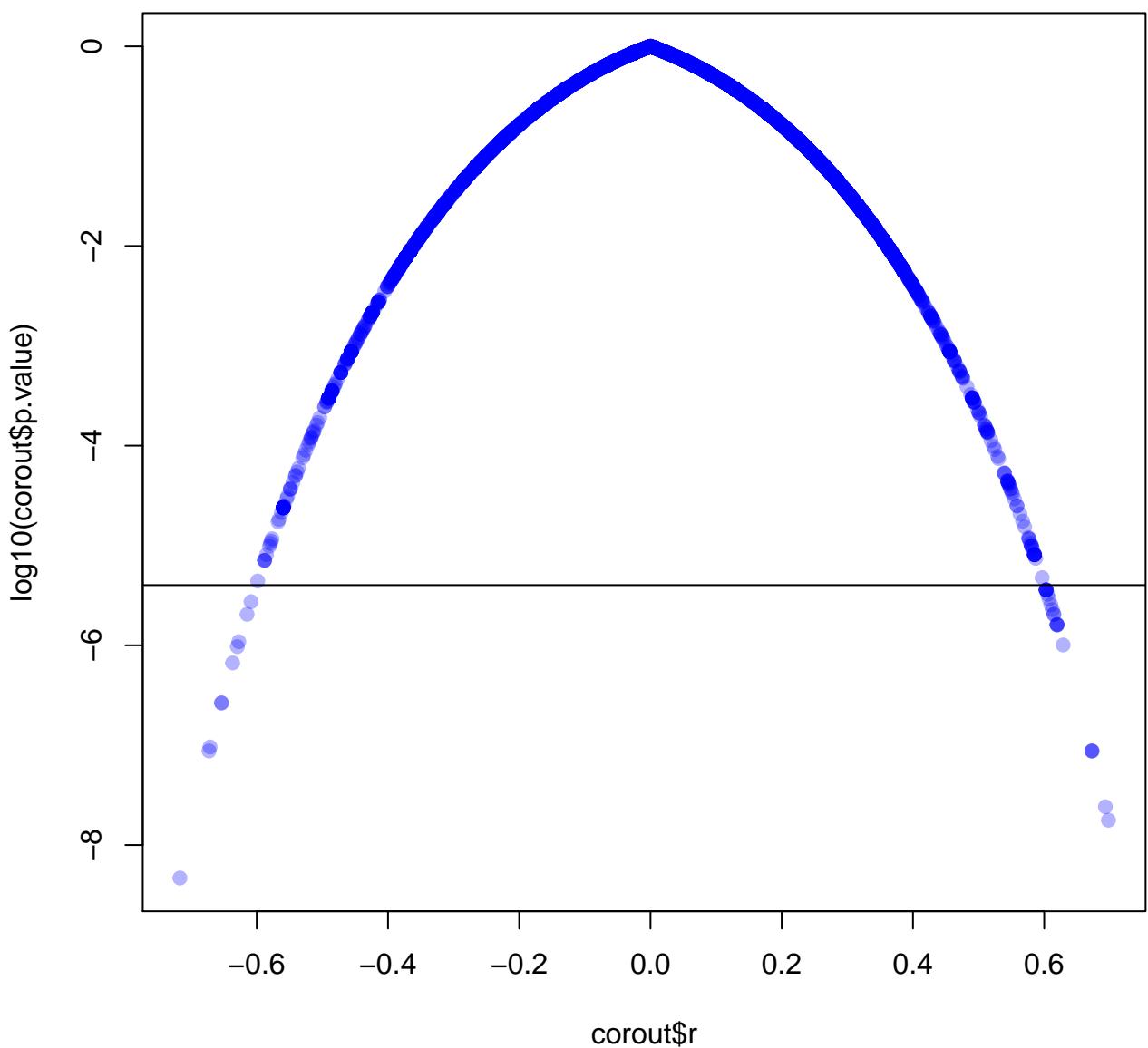
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PGF_01917480
General secretion pathway protein L



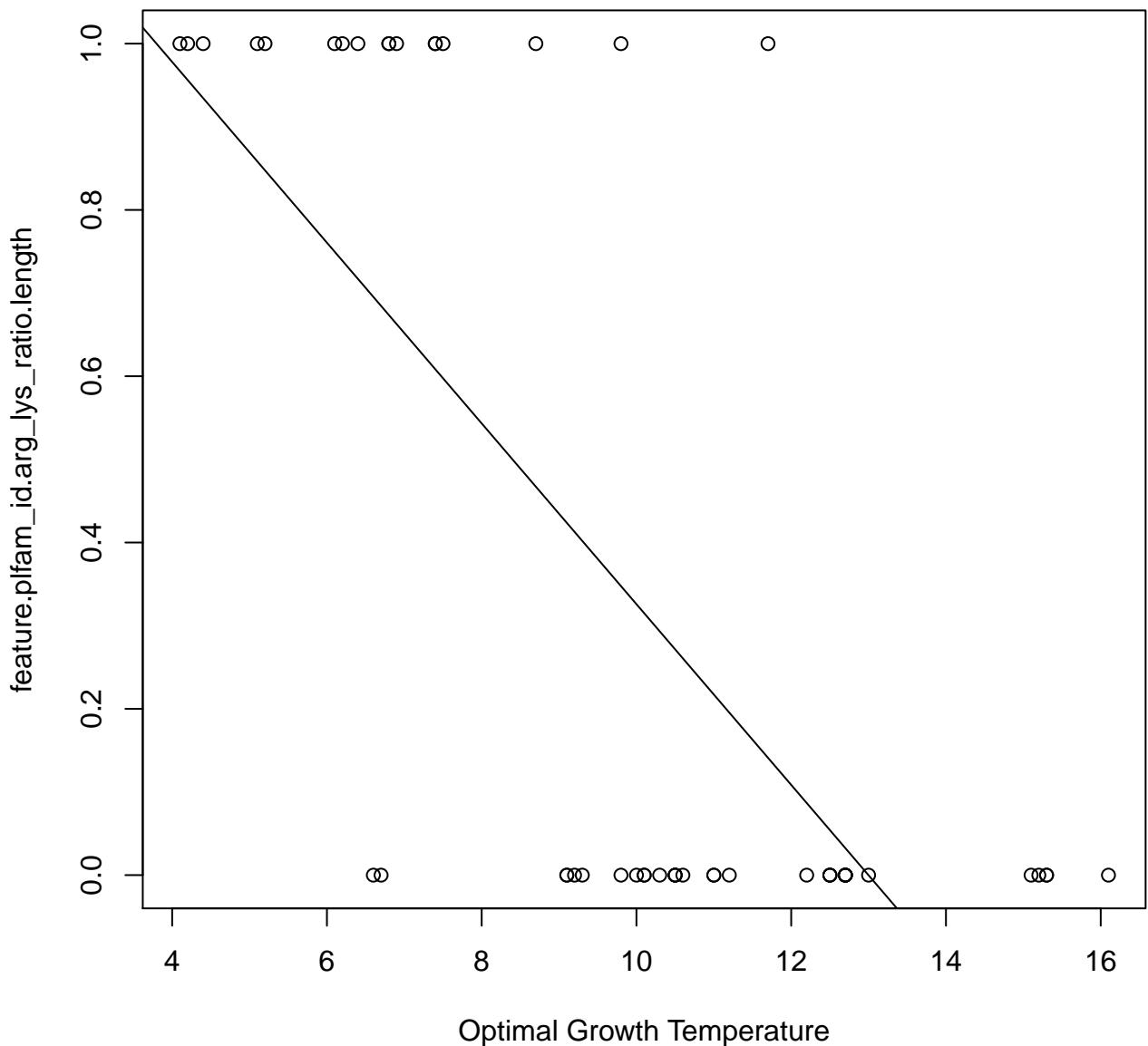
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PGF_03687279
Uncharacterized MFS-type transporter



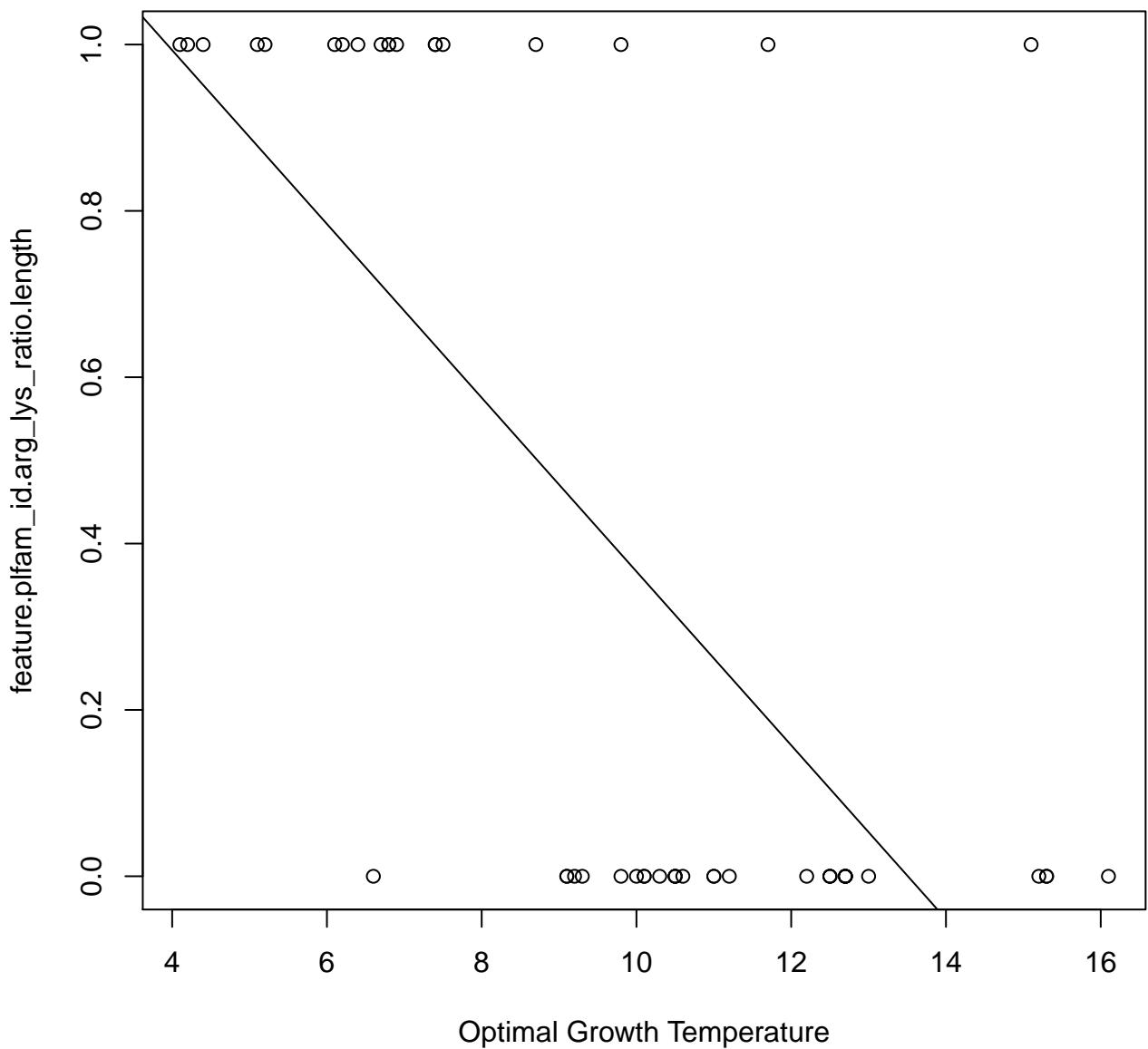
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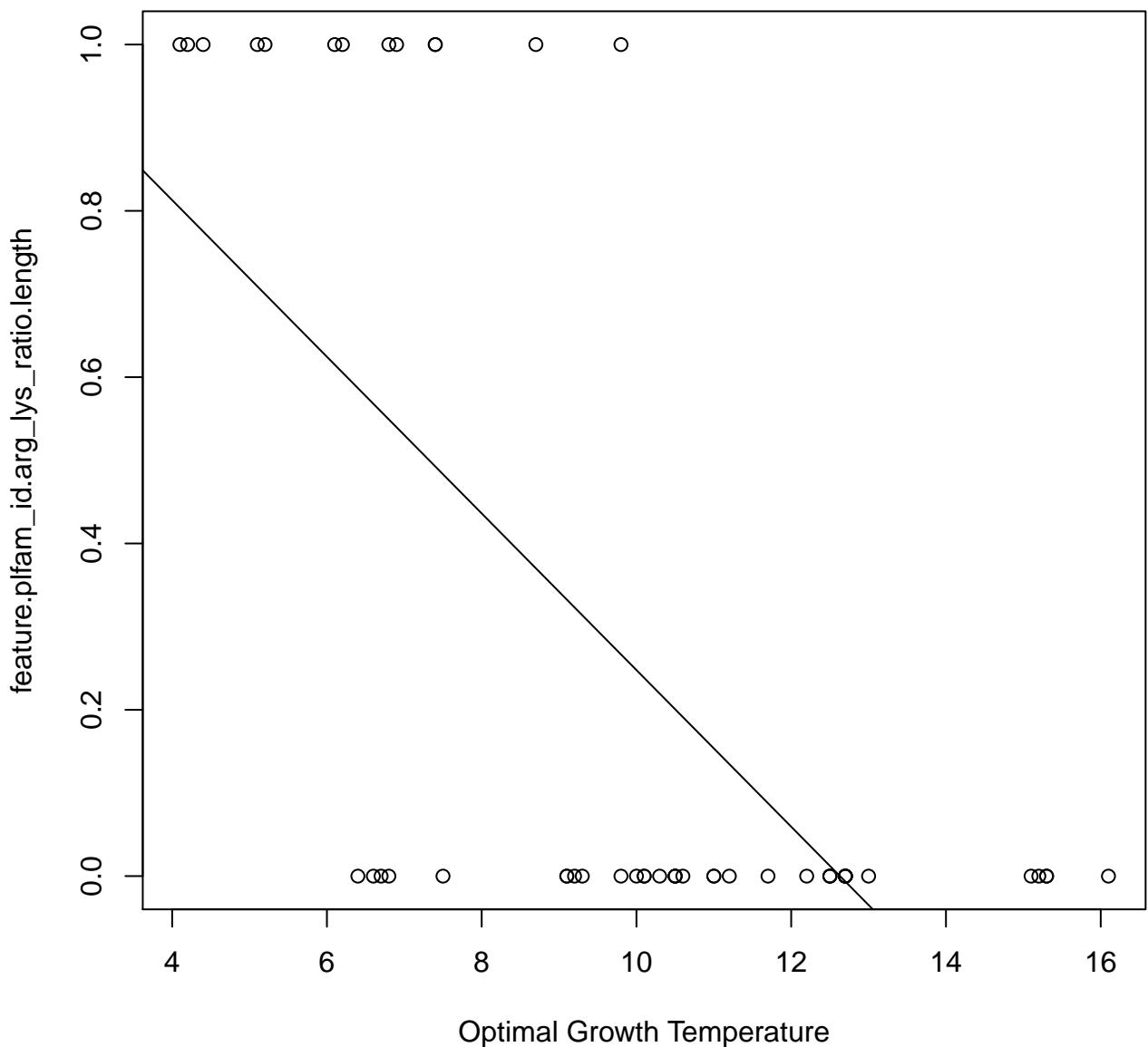
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Membrane-bound lytic murein transglycosylase C (EC 3.2.1.n1)



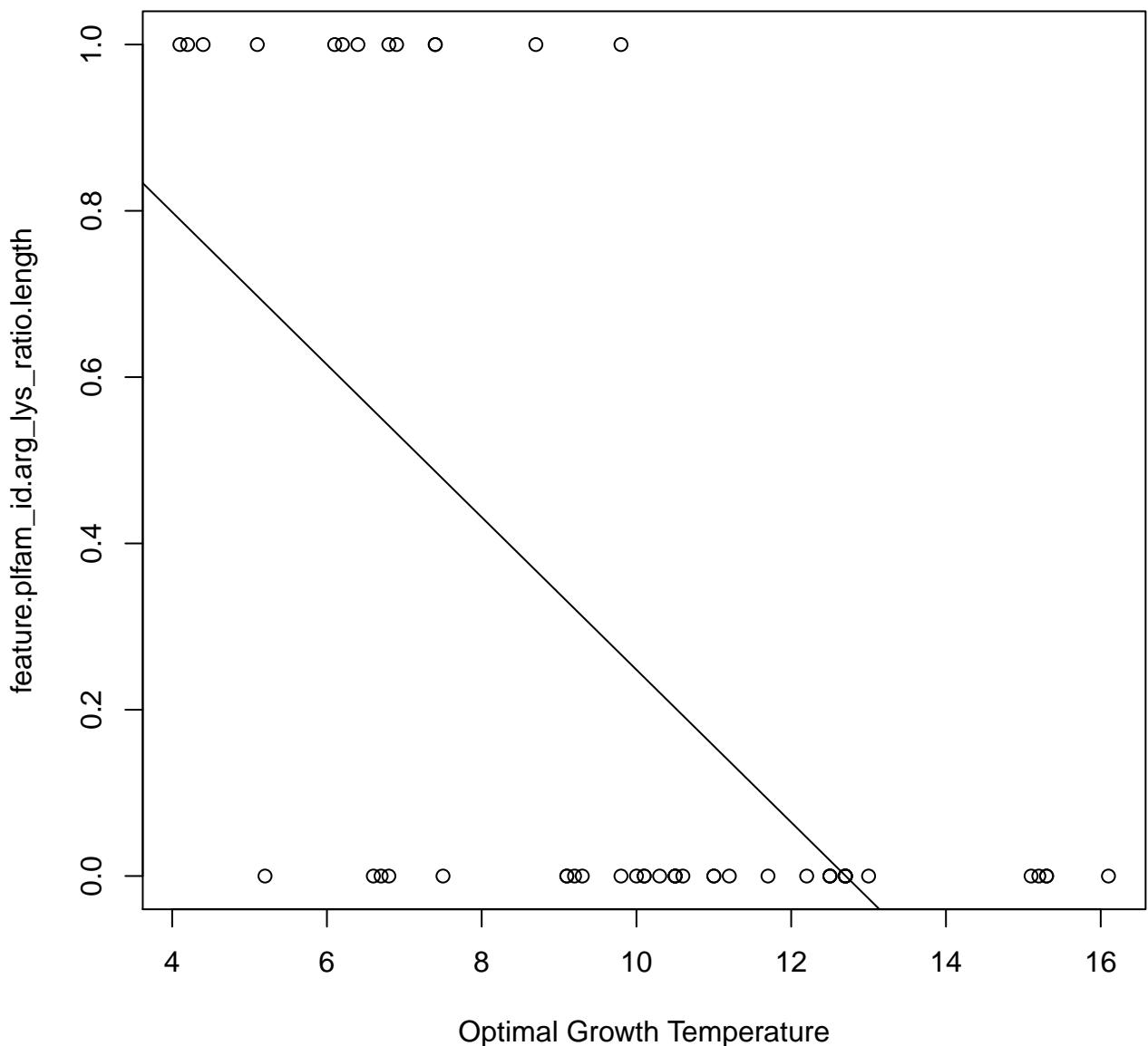
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hypothetical protein



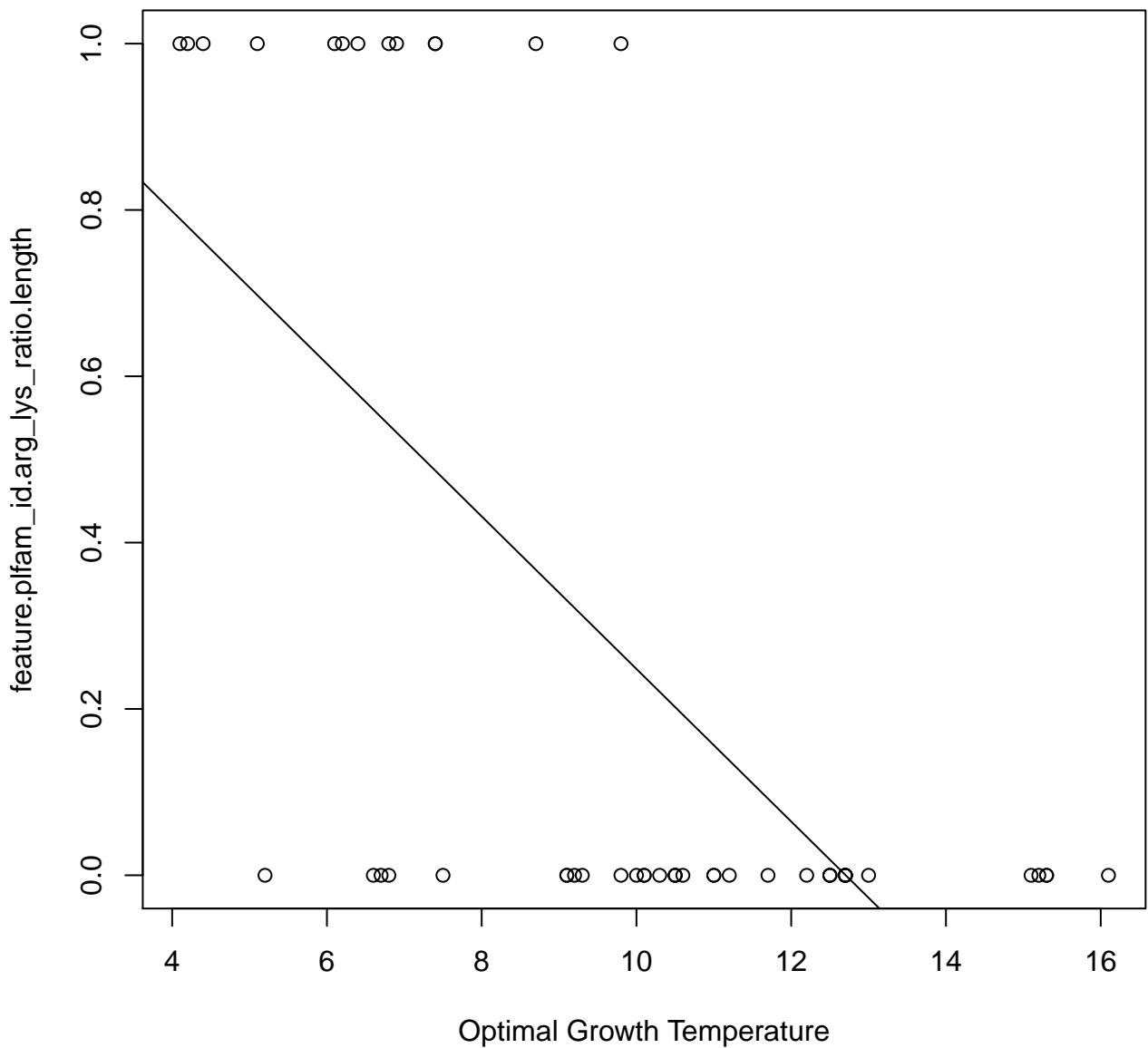
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hypothetical protein



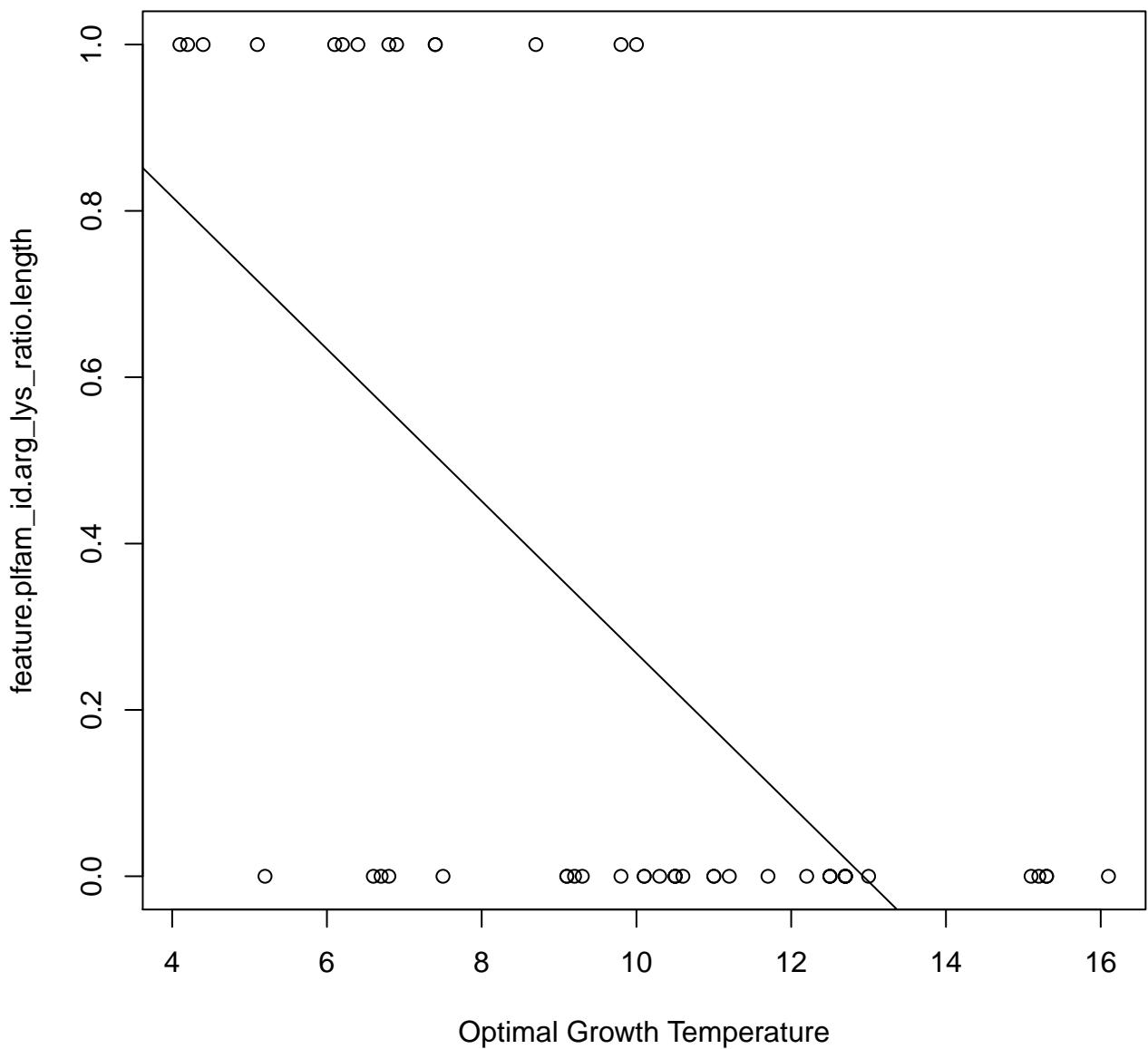
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Uncharacterized MFS-type transporter



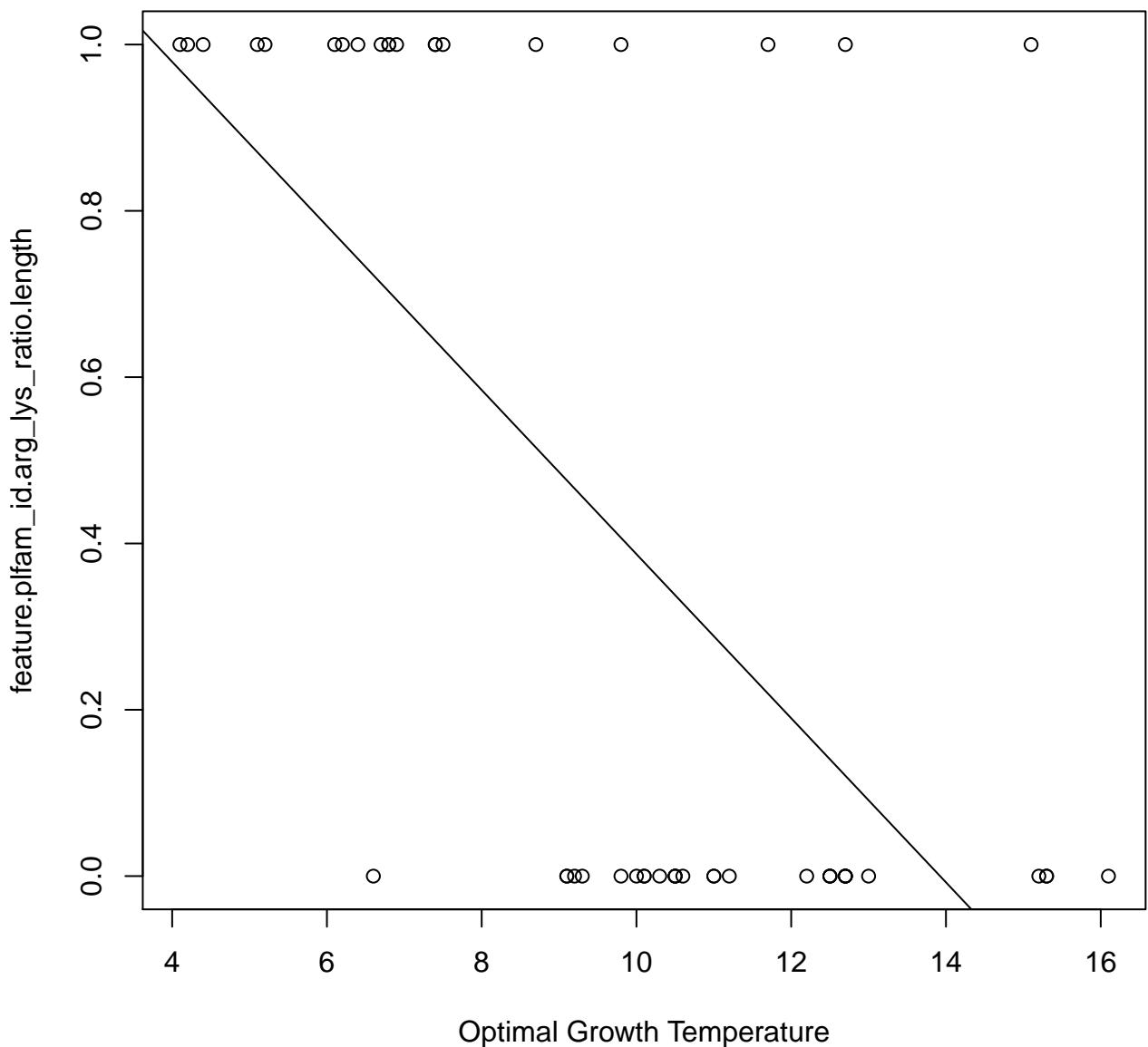
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Transcriptional regulator, AraC family



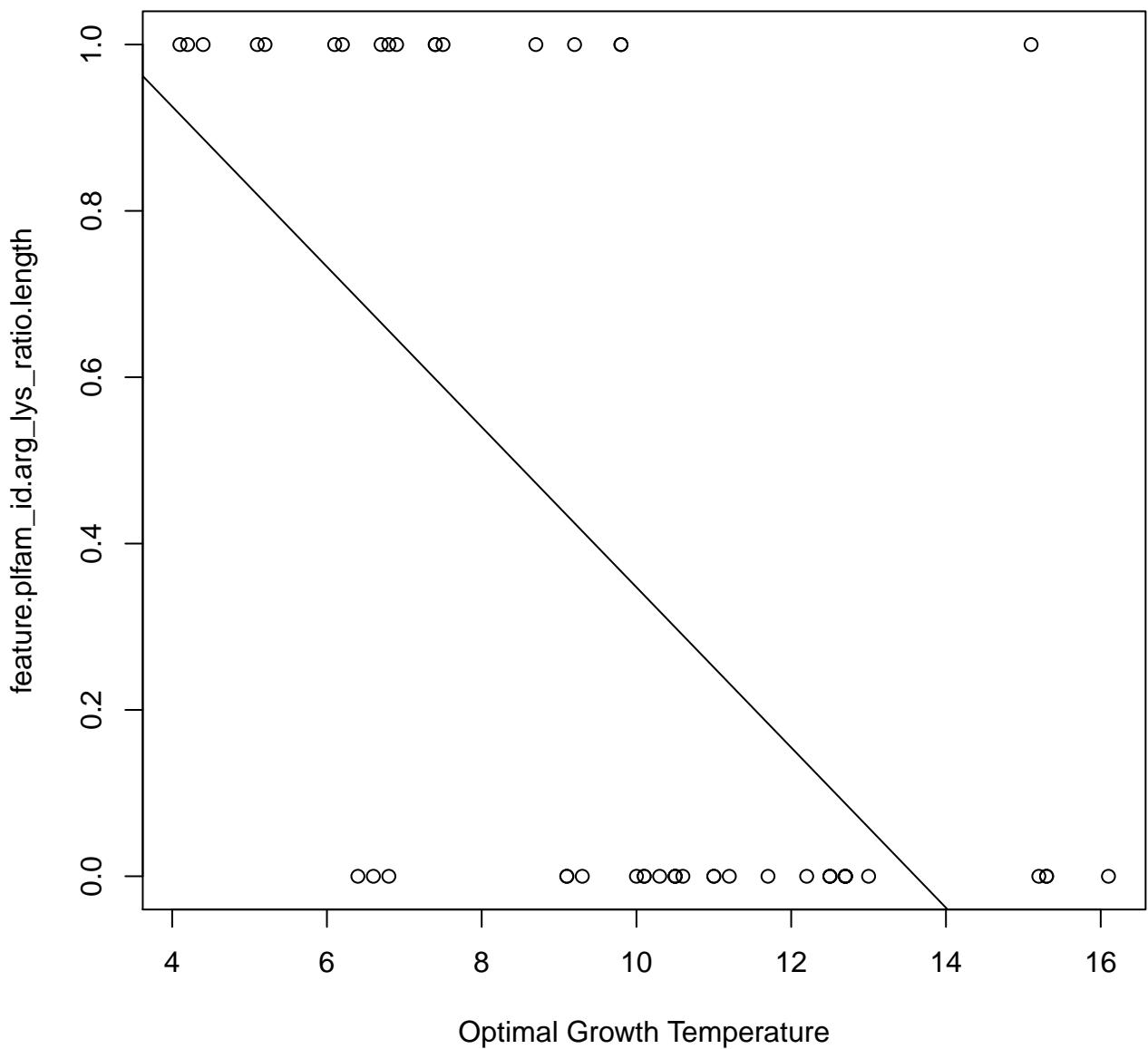
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YoeB toxin protein



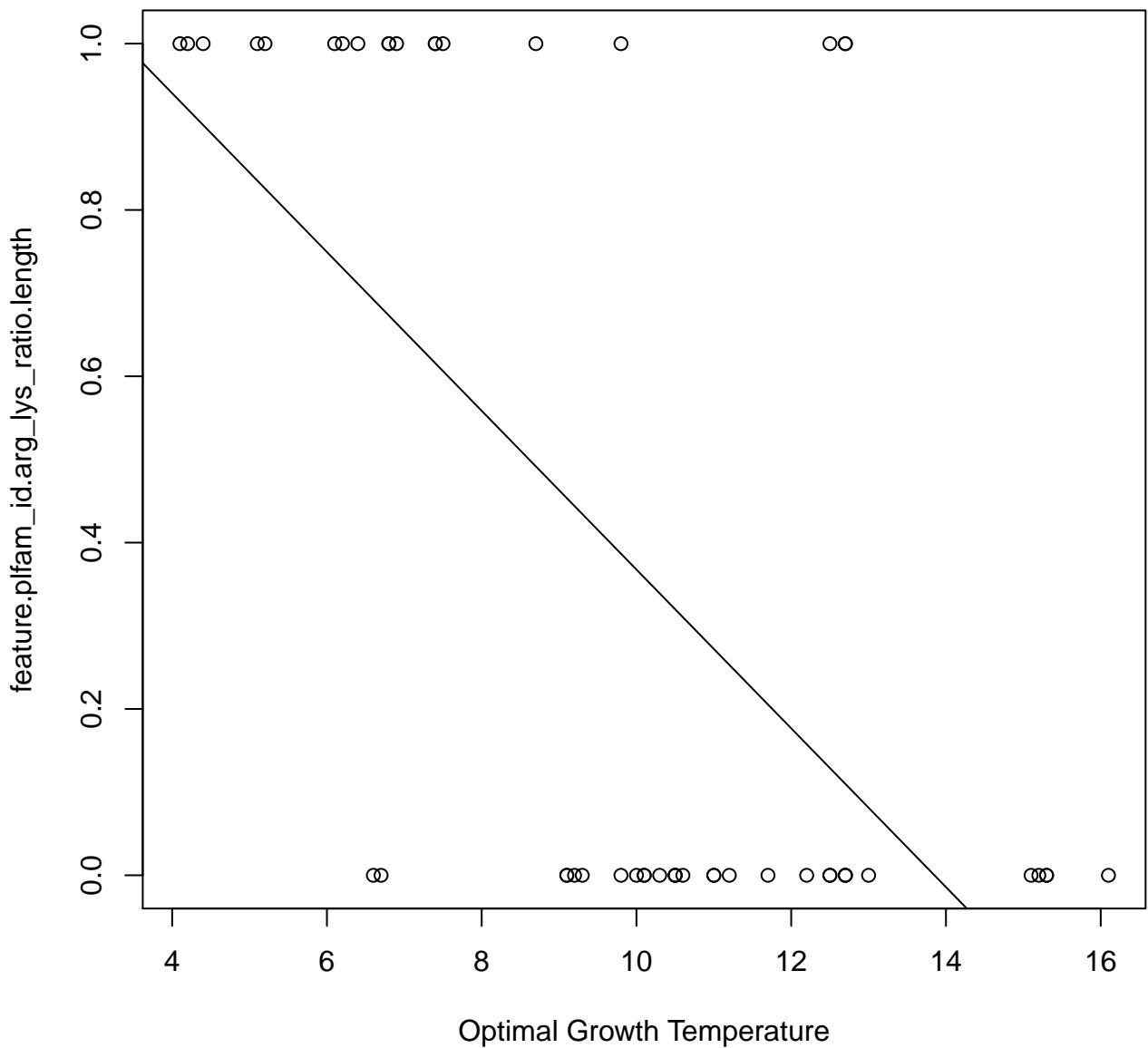
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hypothetical protein



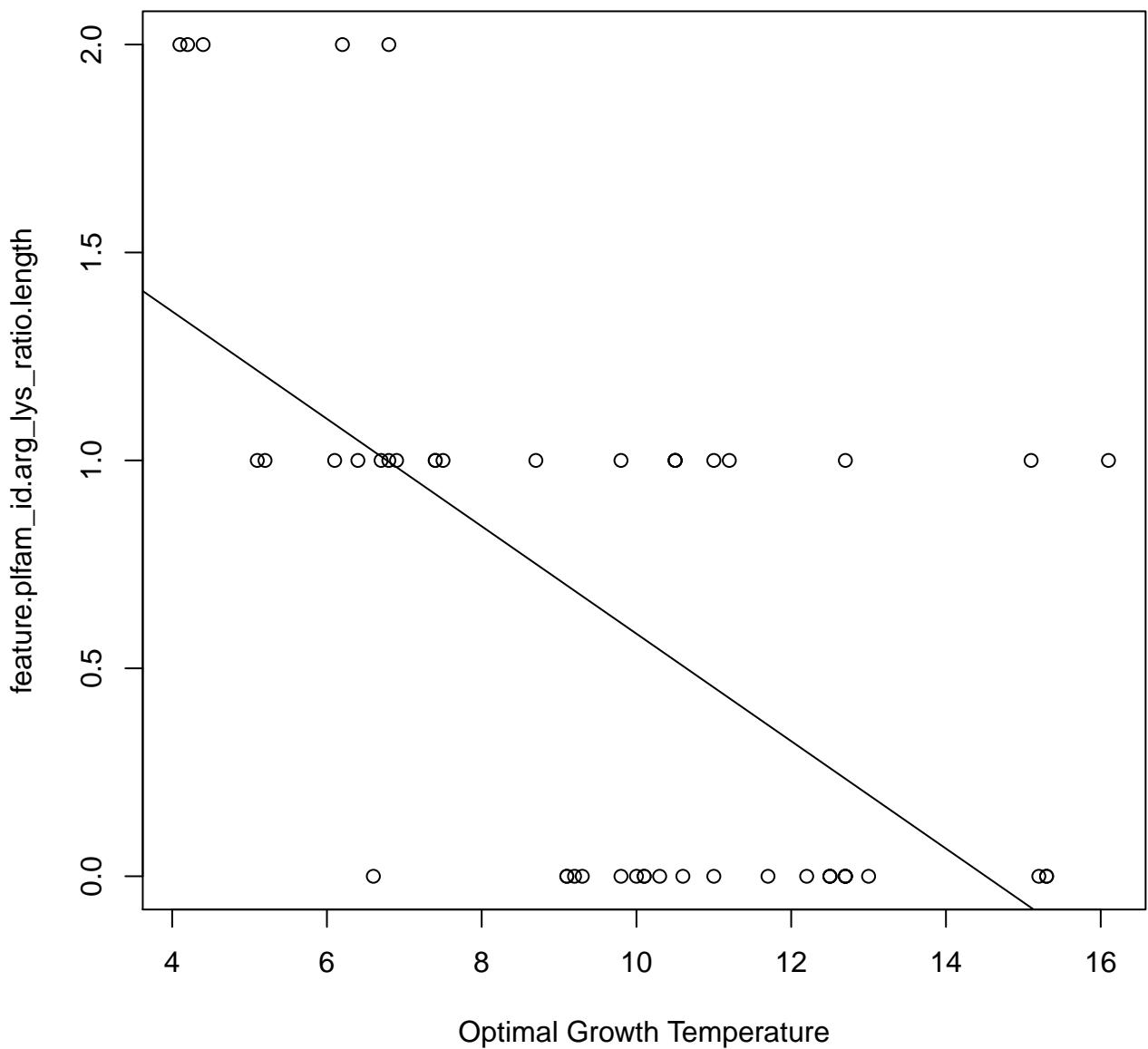
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hypothetical protein



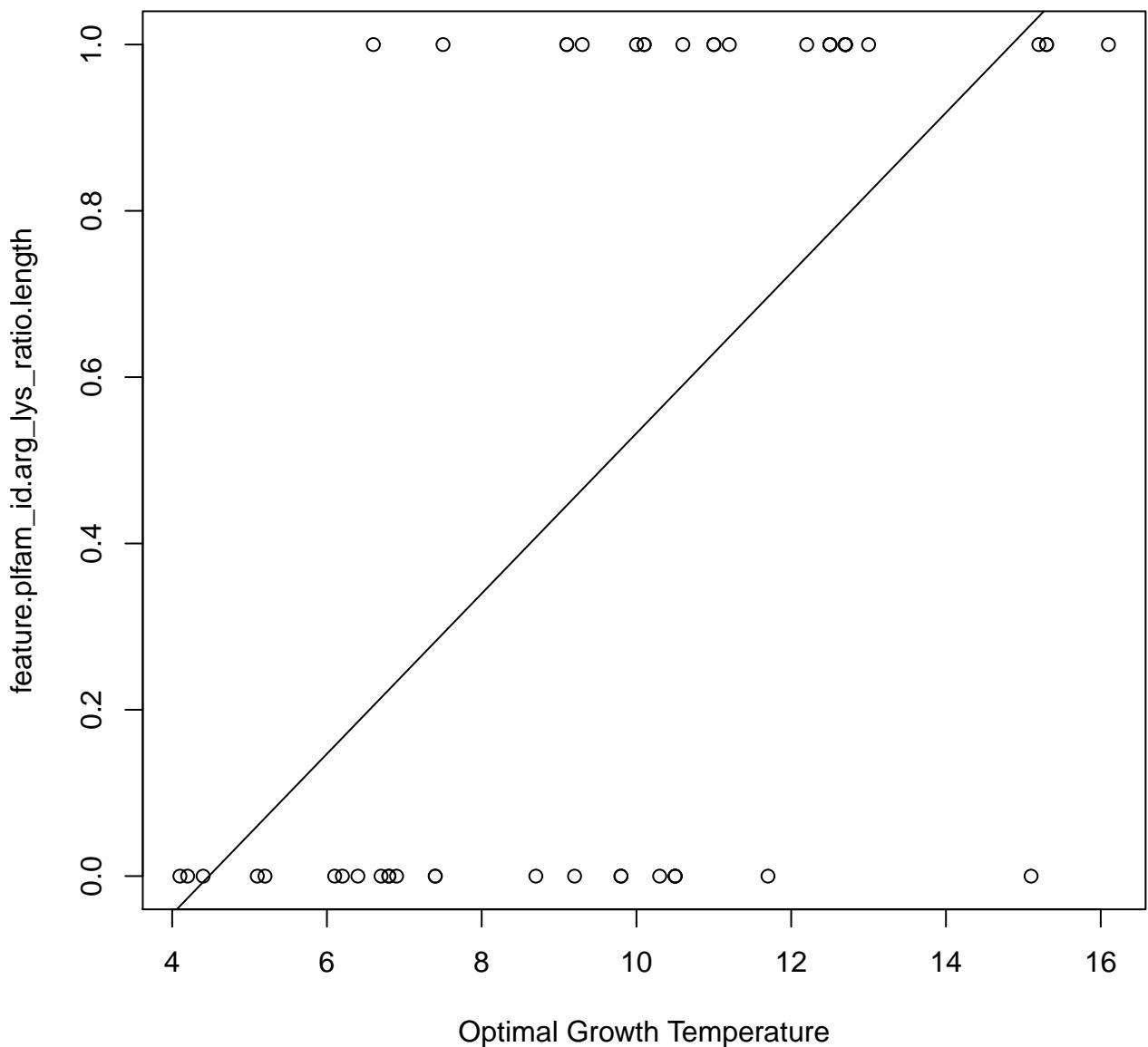
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PLF_28228_00028262
Iron siderophore sensor protein



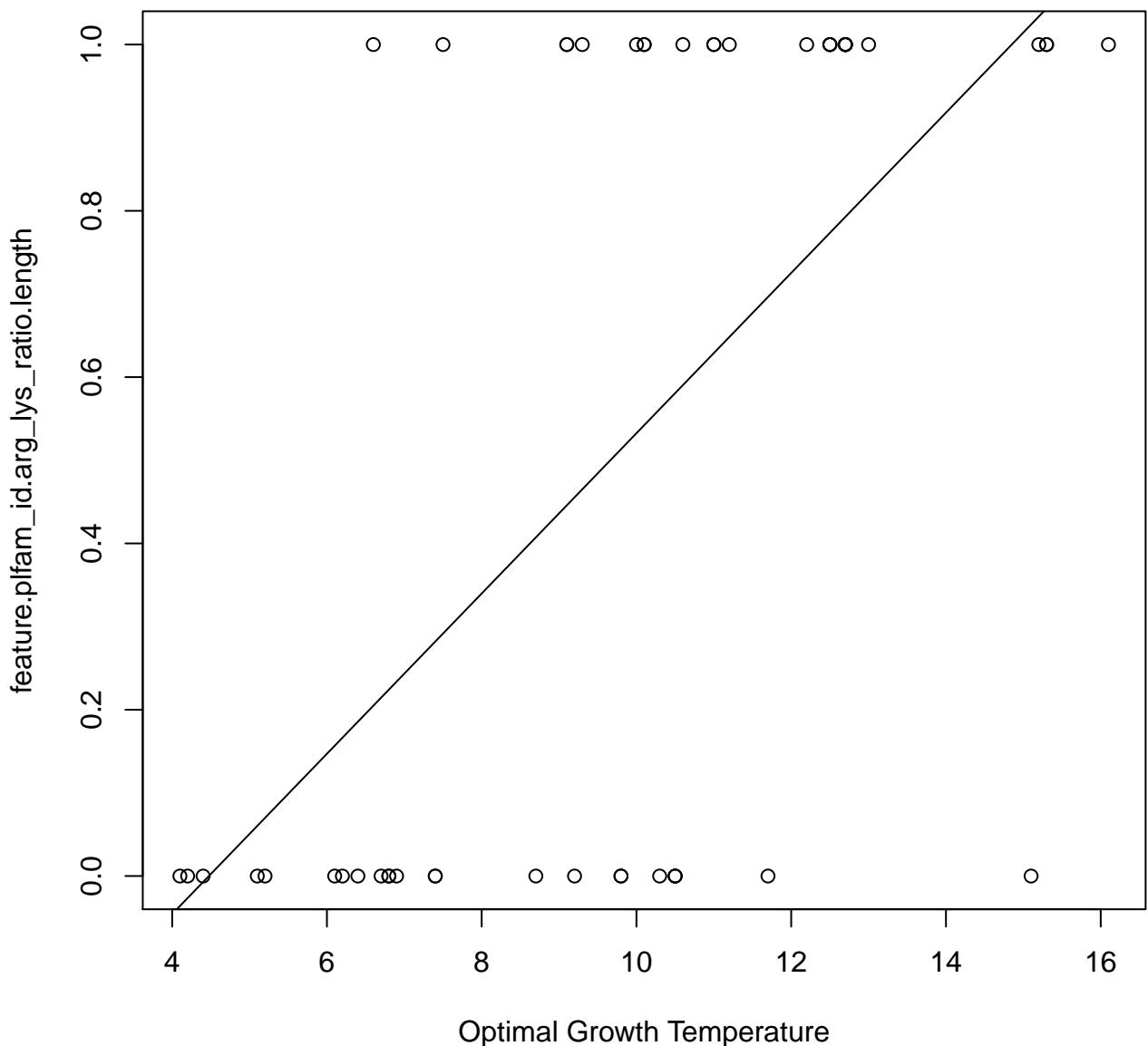
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hypothetical protein



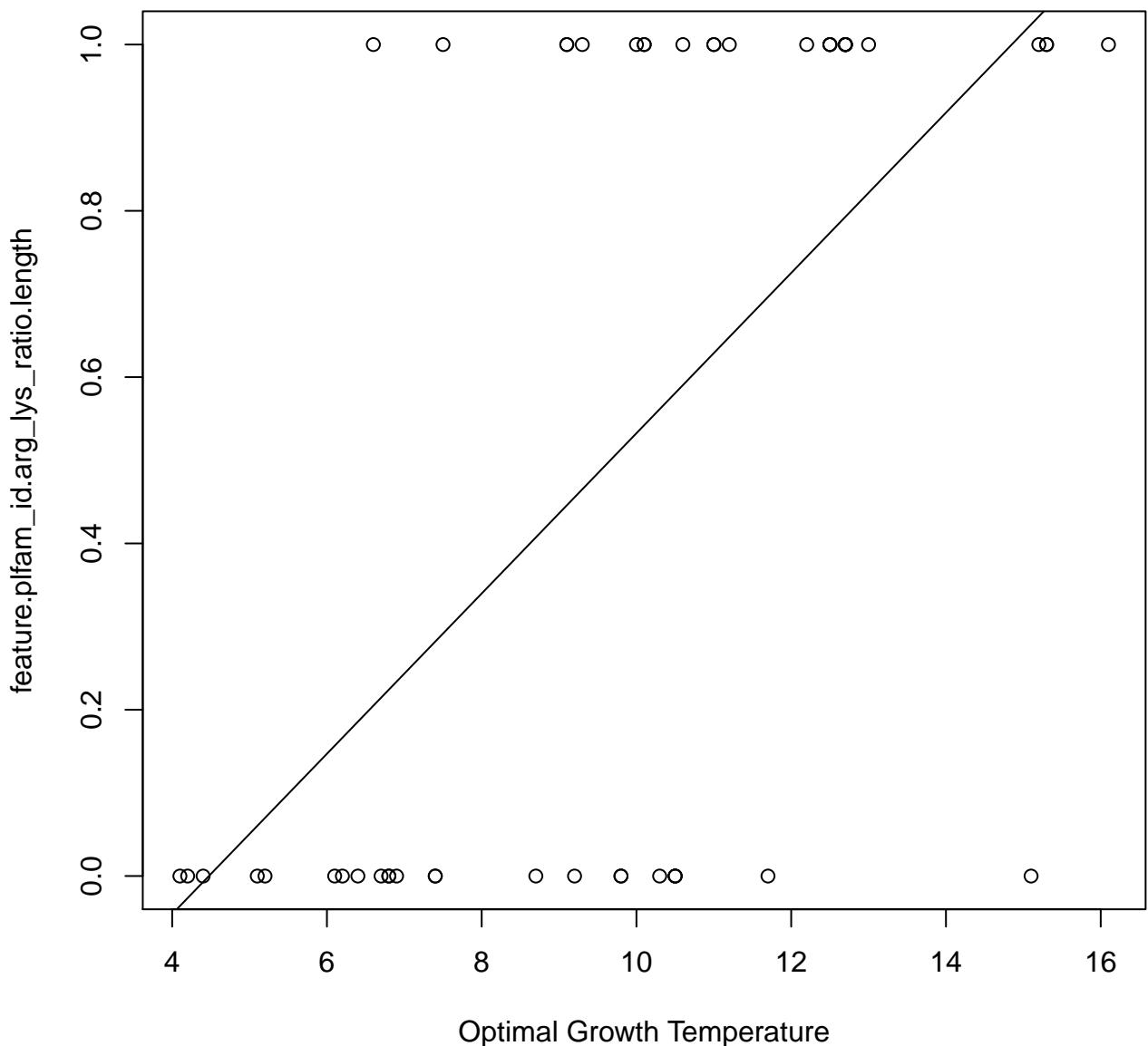
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Capsule biosynthesis protein capA



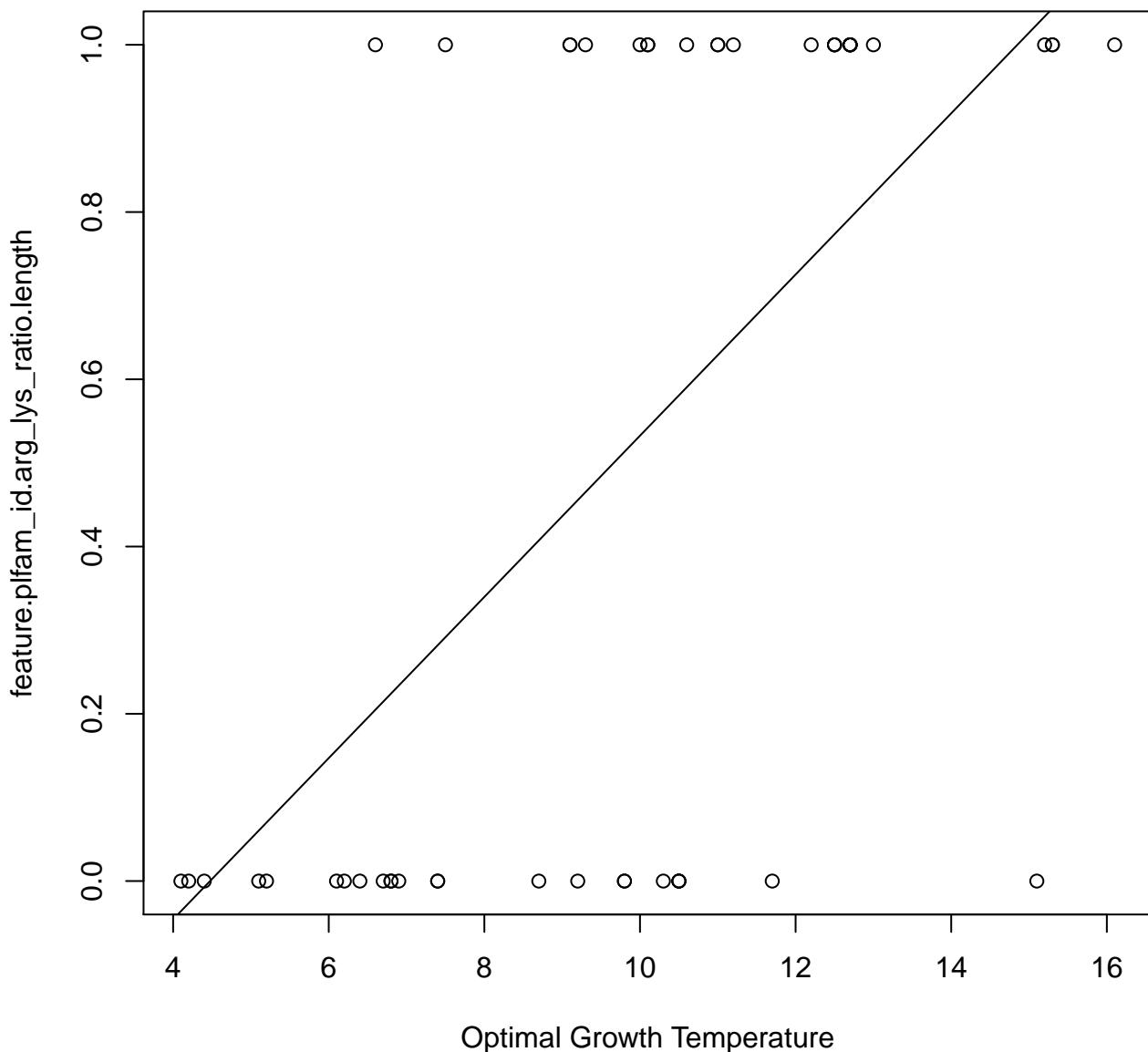
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N-acyl-D-amino-acid deacylase (EC 3.5.1.81)



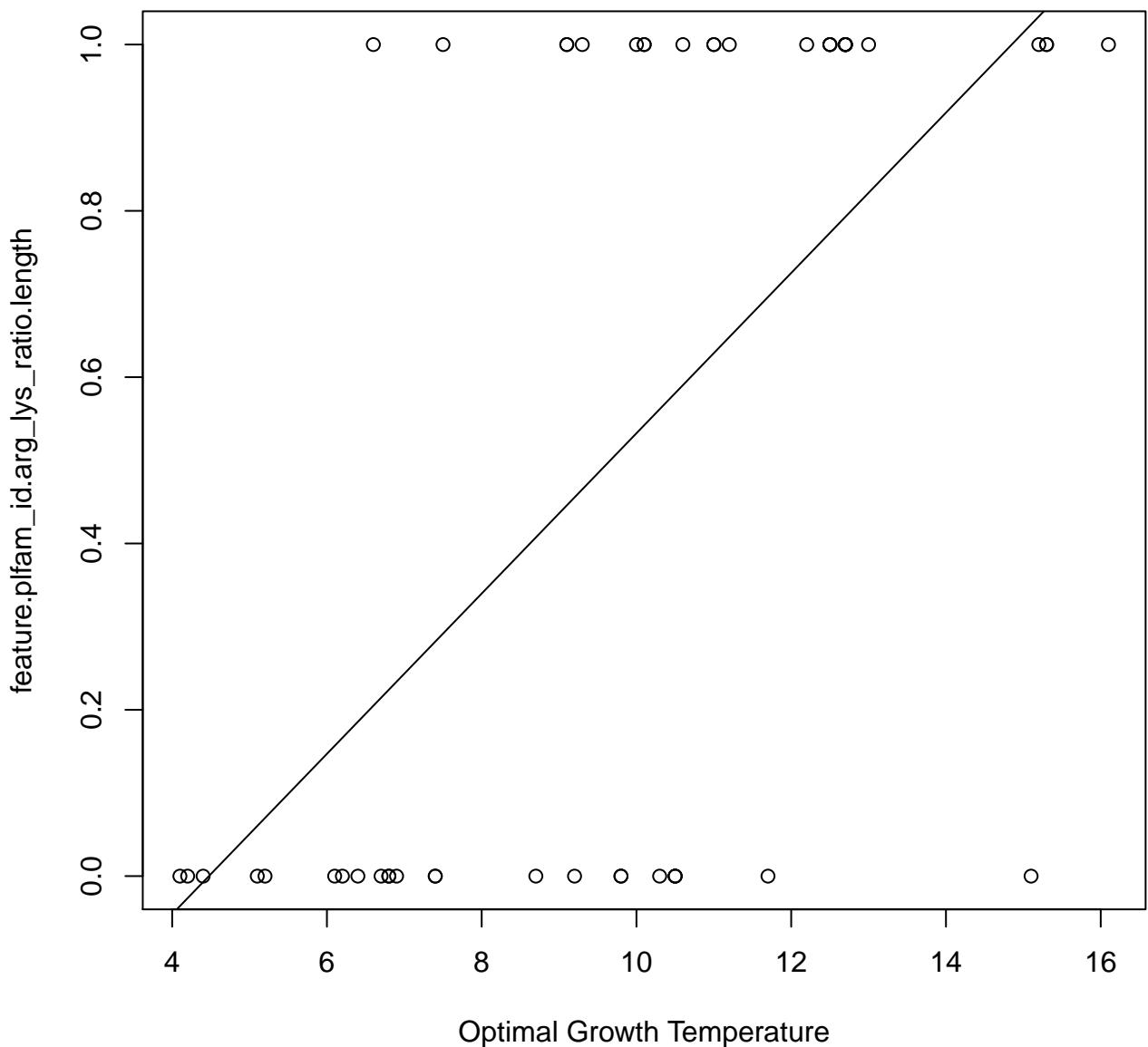
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Sodium/glutamate symporter



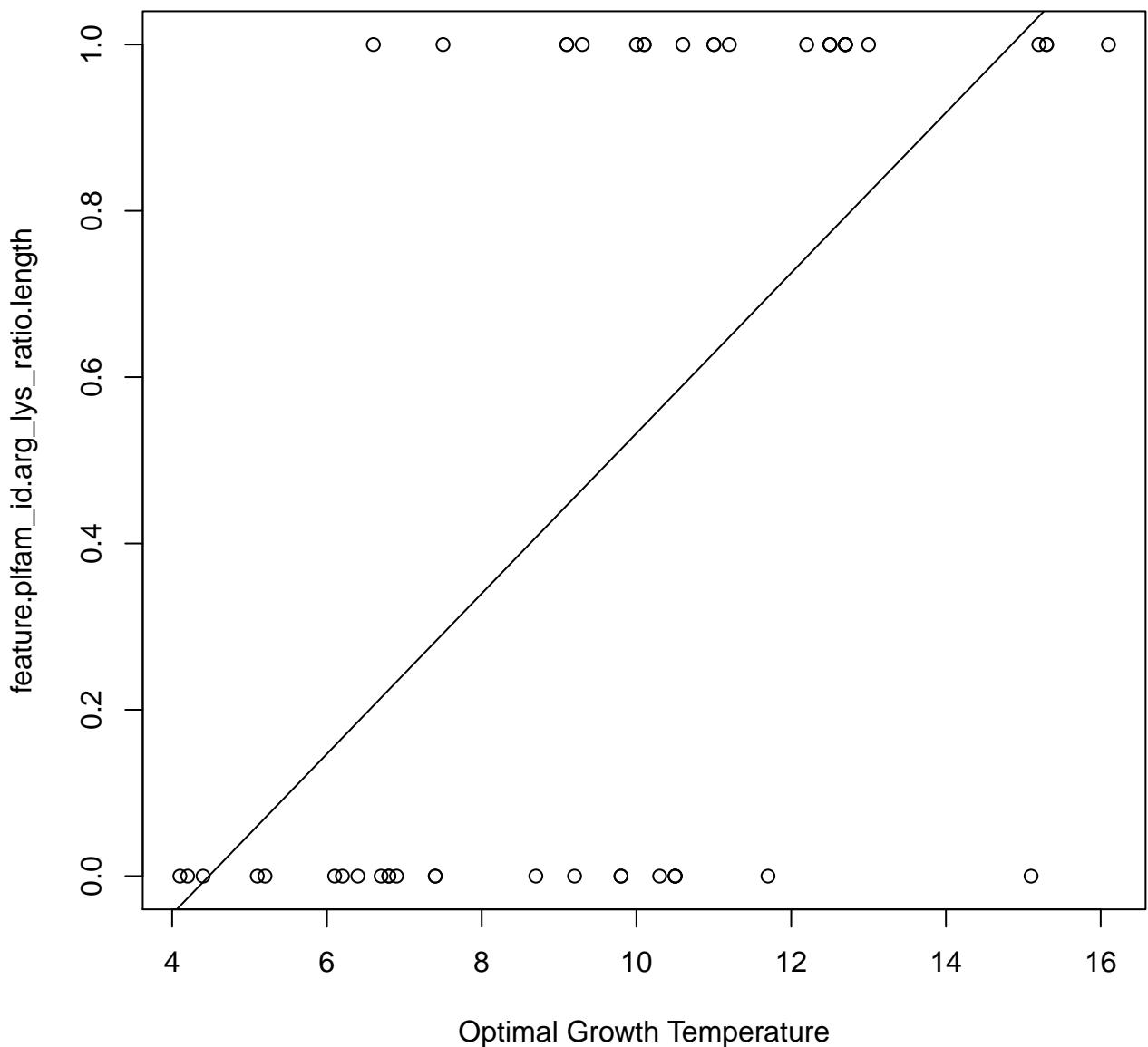
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Transcriptional regulator, LysR family



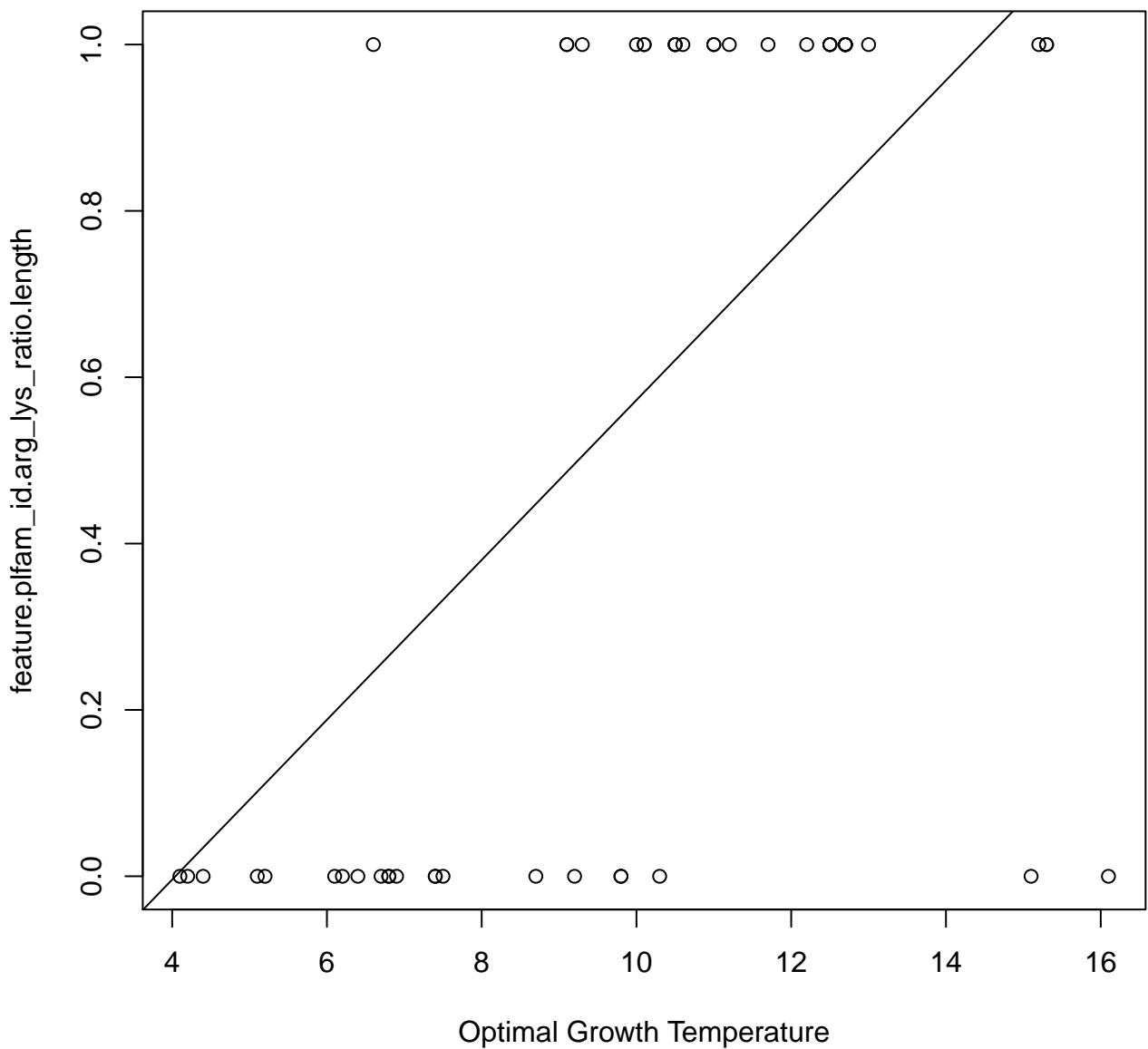
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hypothetical protein



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TonB-dependent receptor



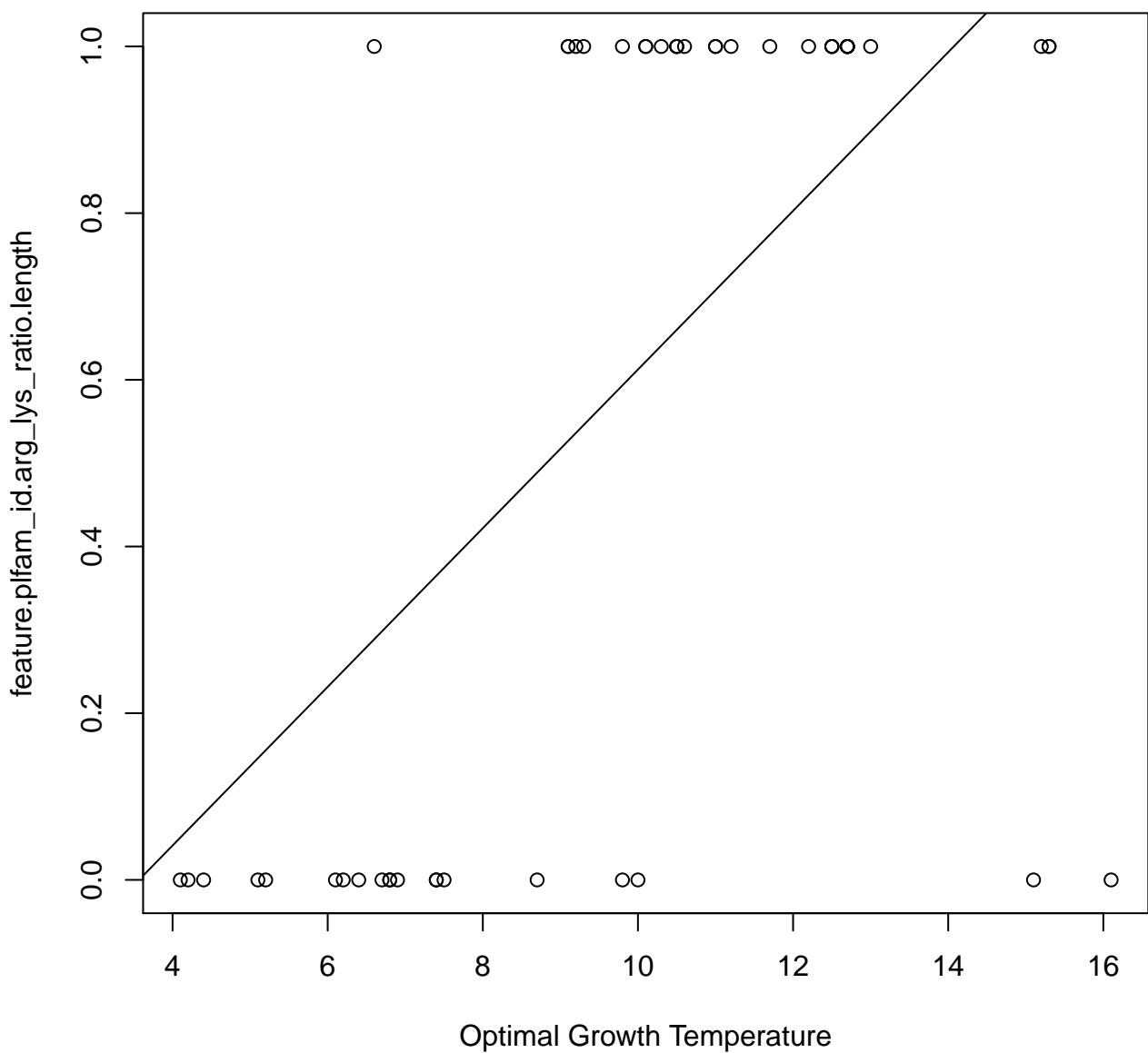
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hypothetical protein



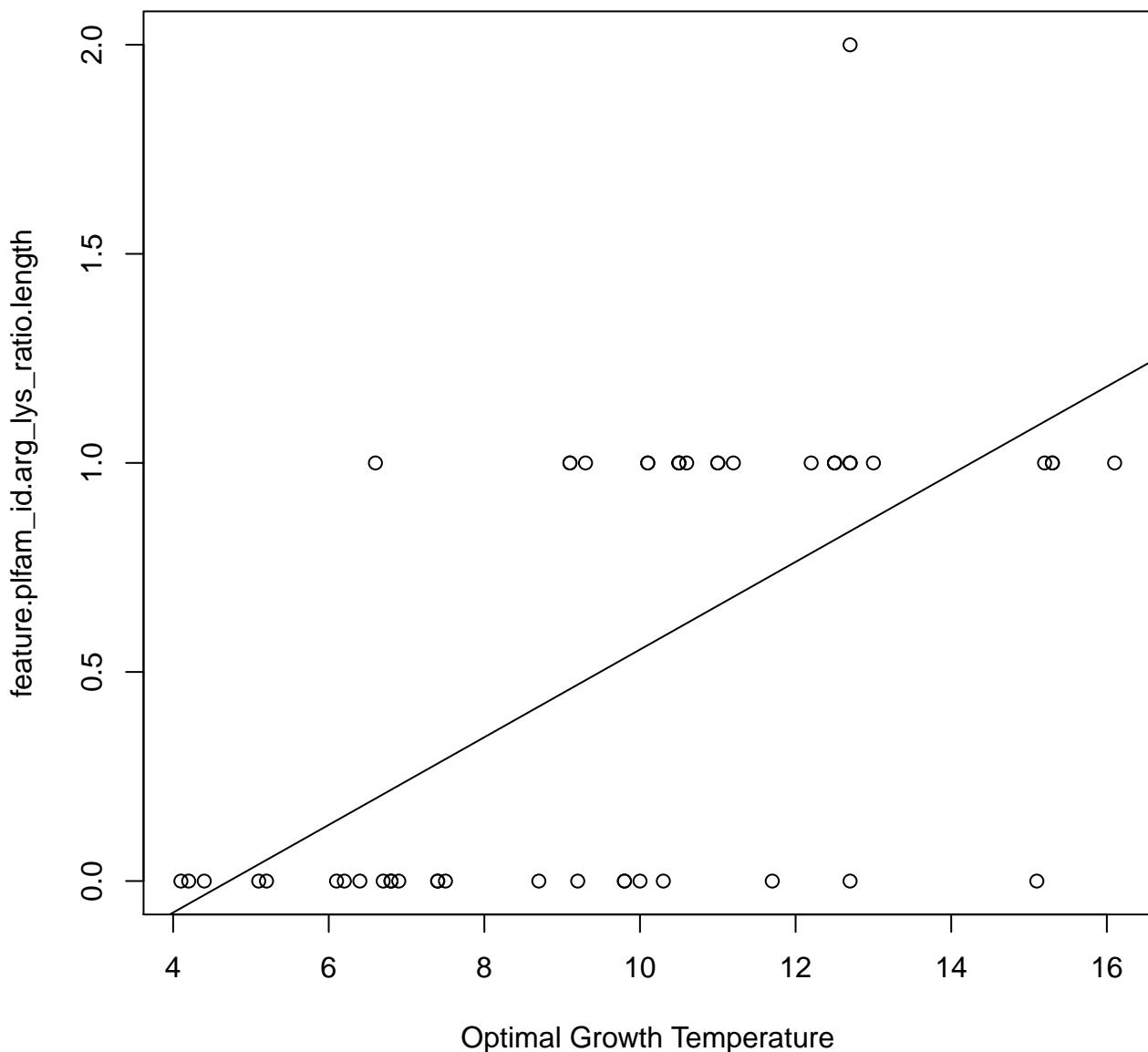
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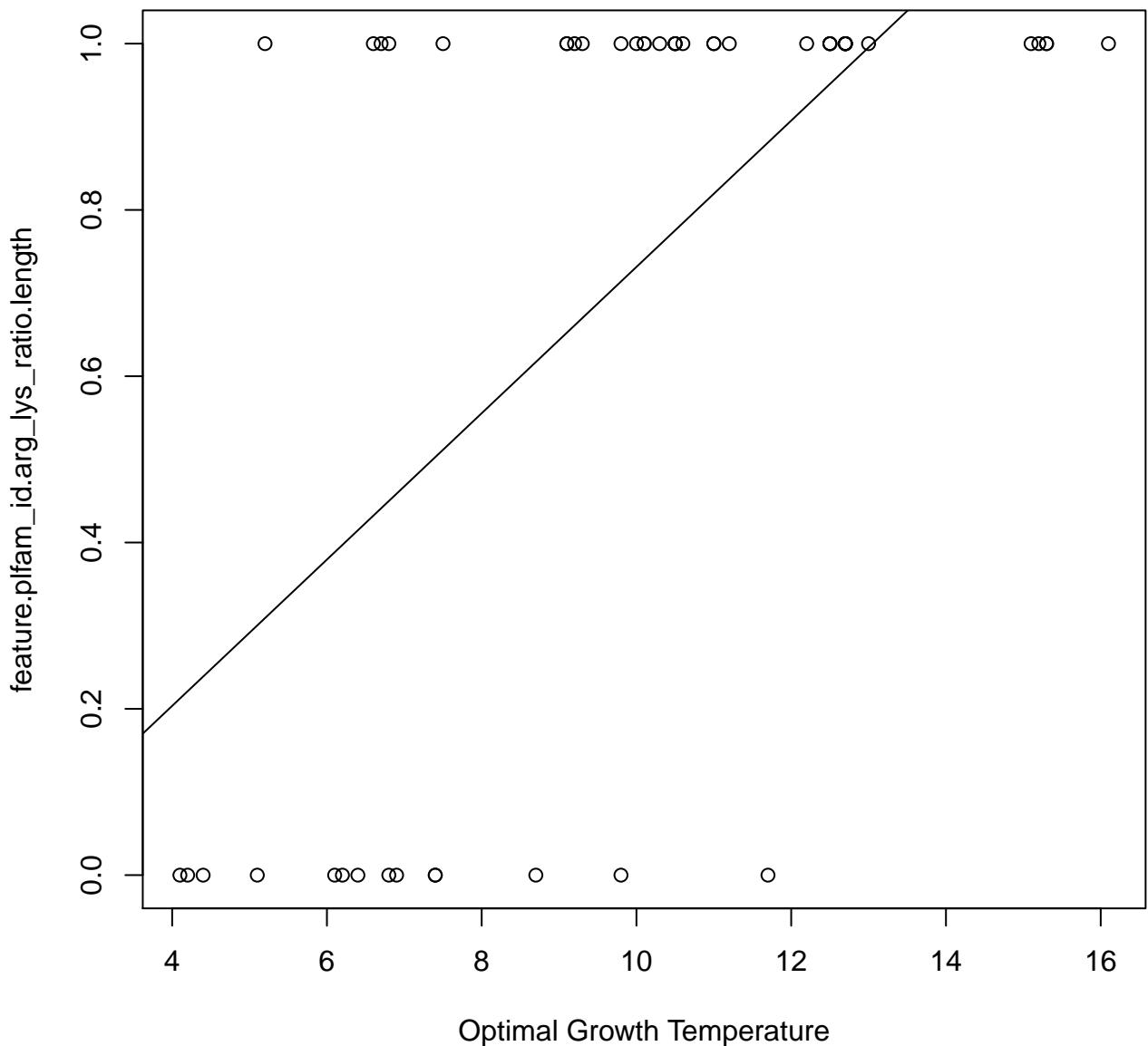
hypothetical protein



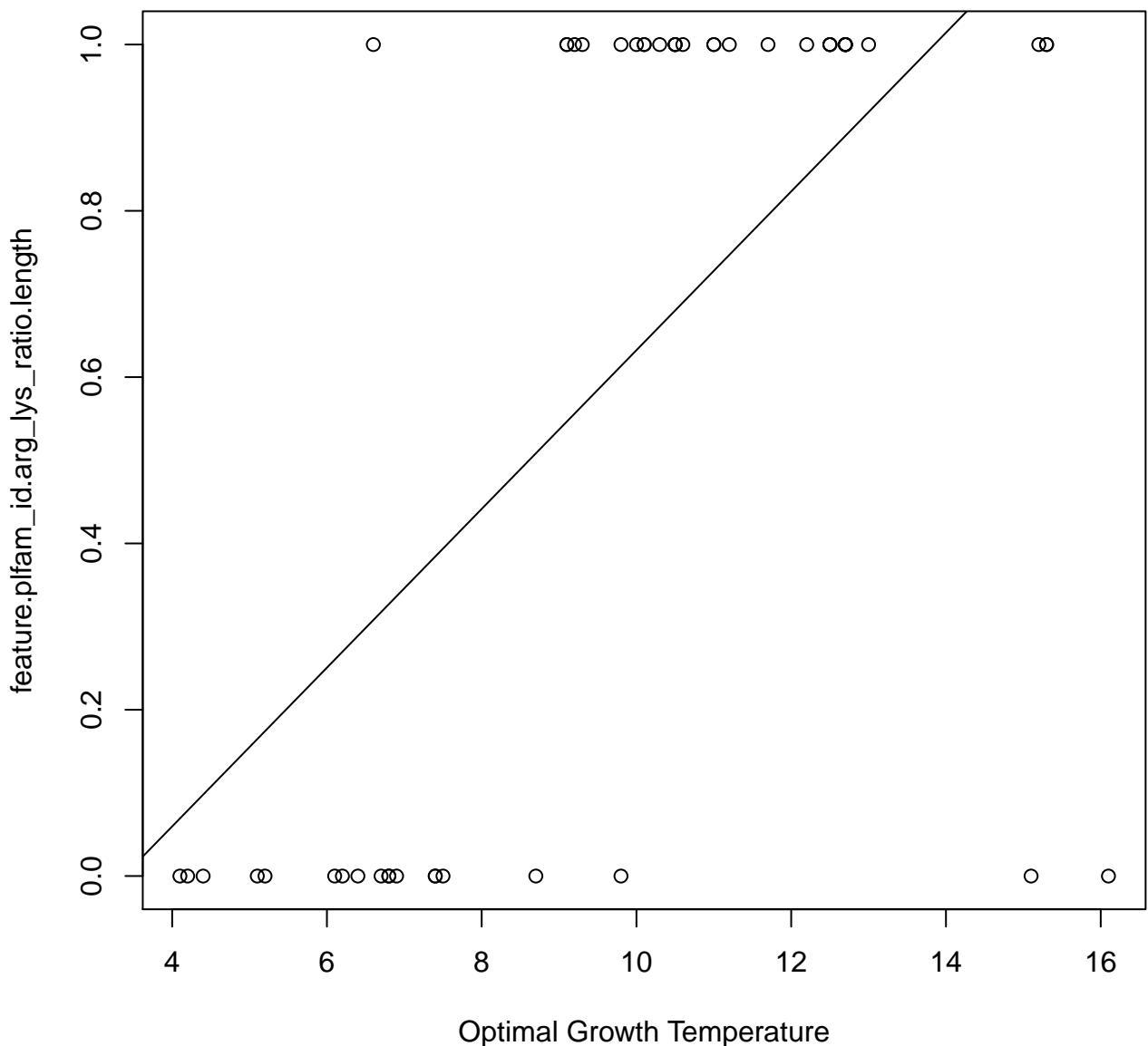
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Nitric oxide reductase activation protein NorQ



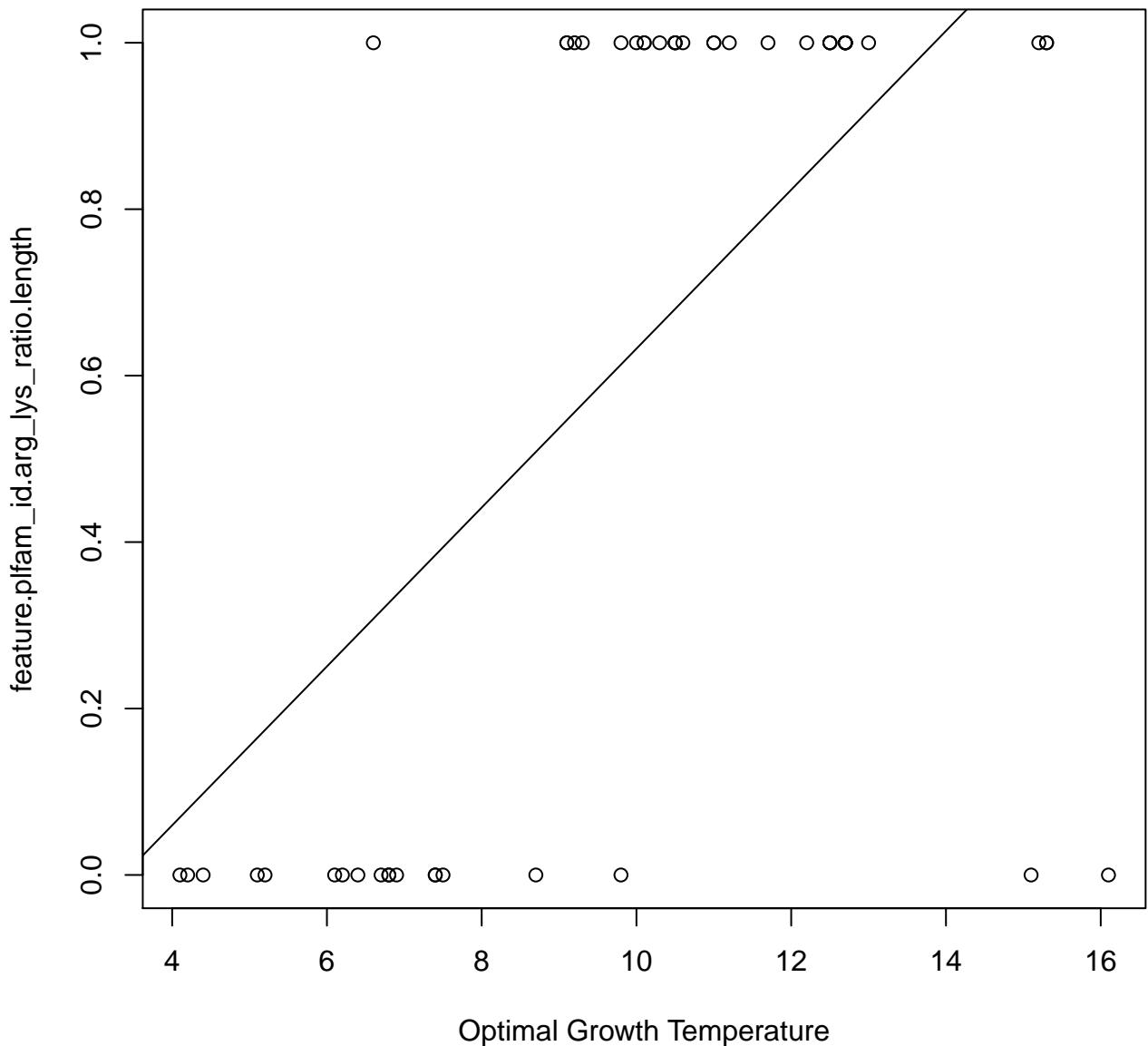
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Molybdenum ABC transporter, substrate-binding protein ModA



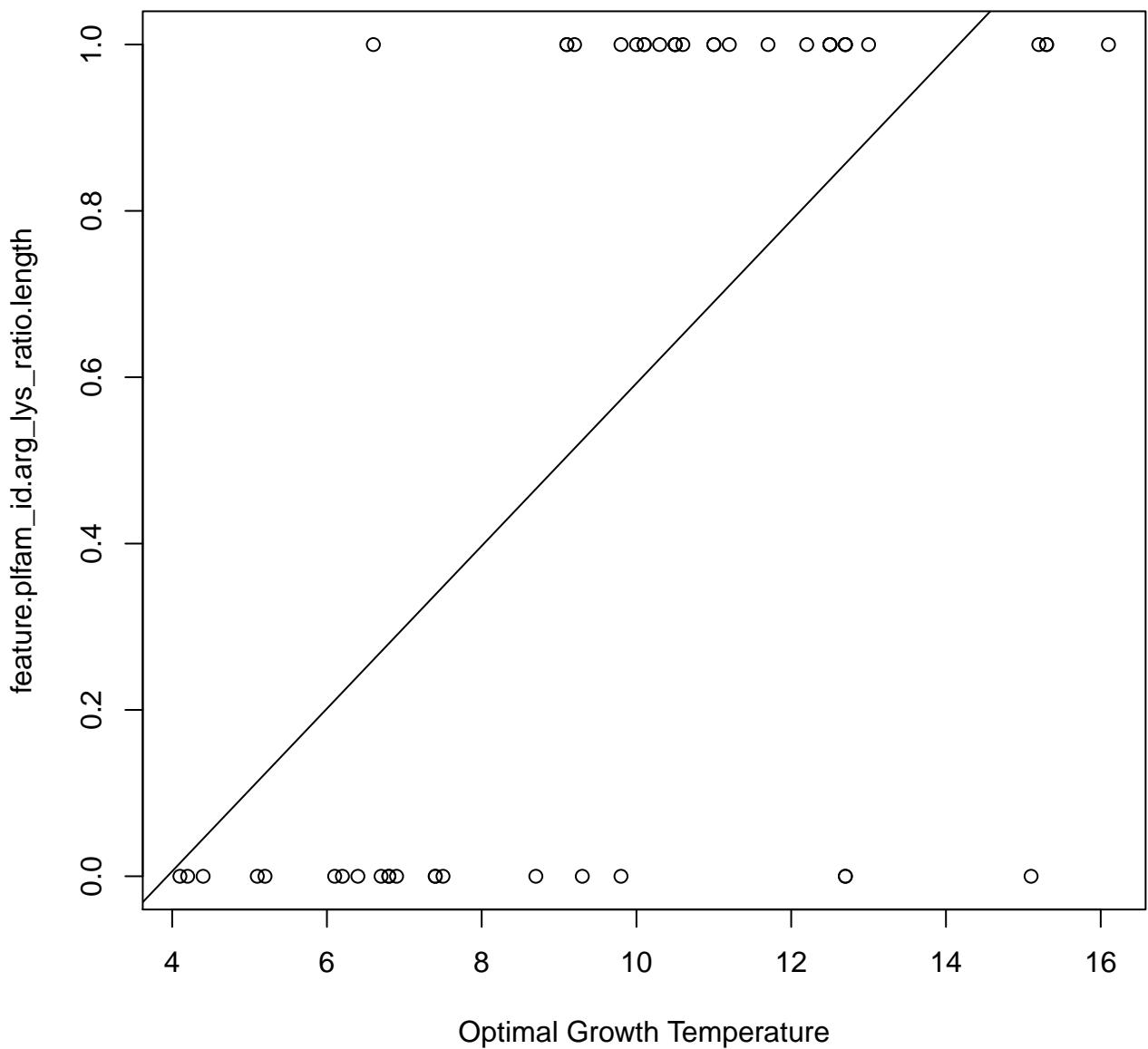
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Paraquat-inducible protein A



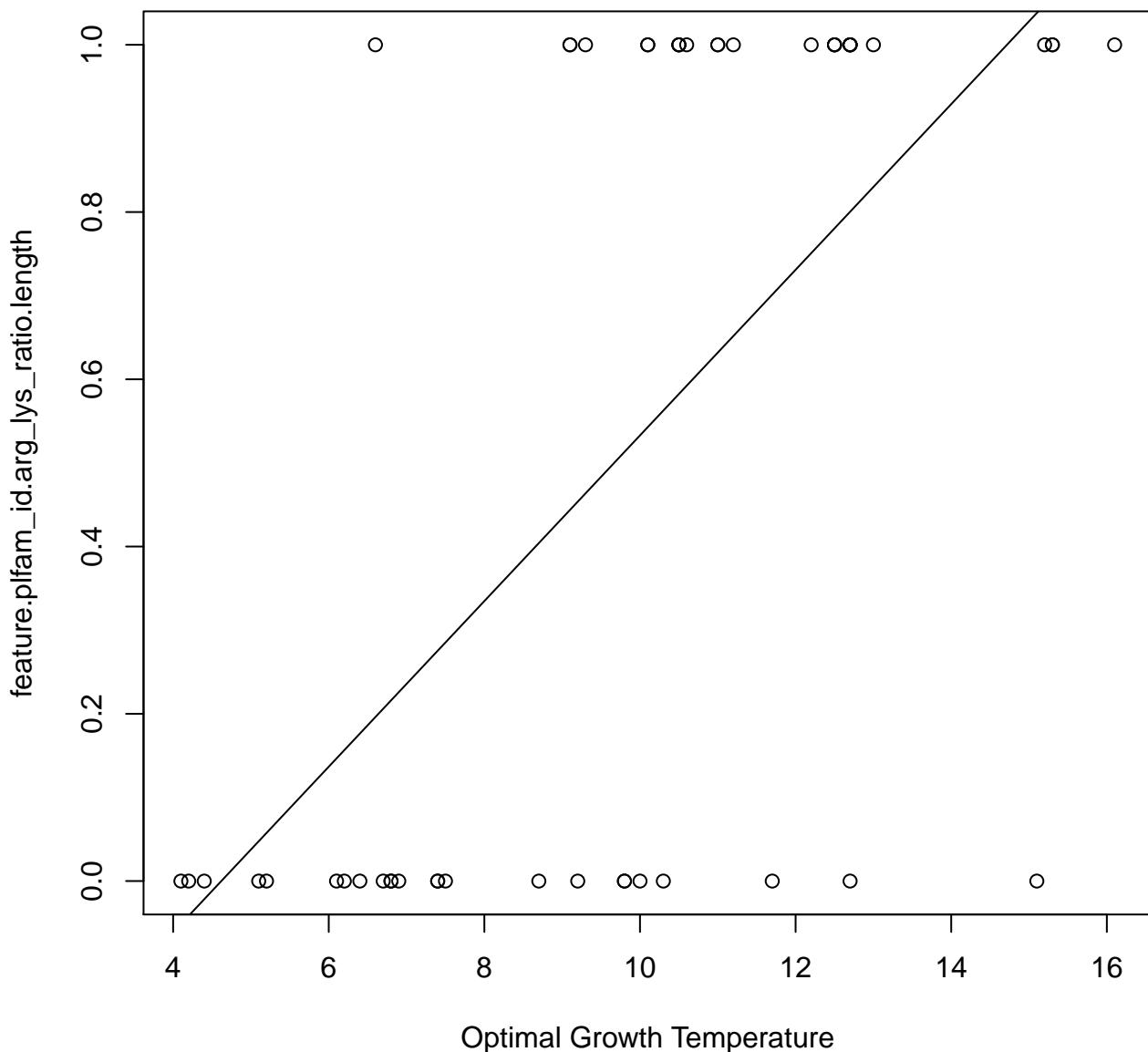
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PLF_28228_00000956
Phosphocarrier protein, nitrogen regulation associated



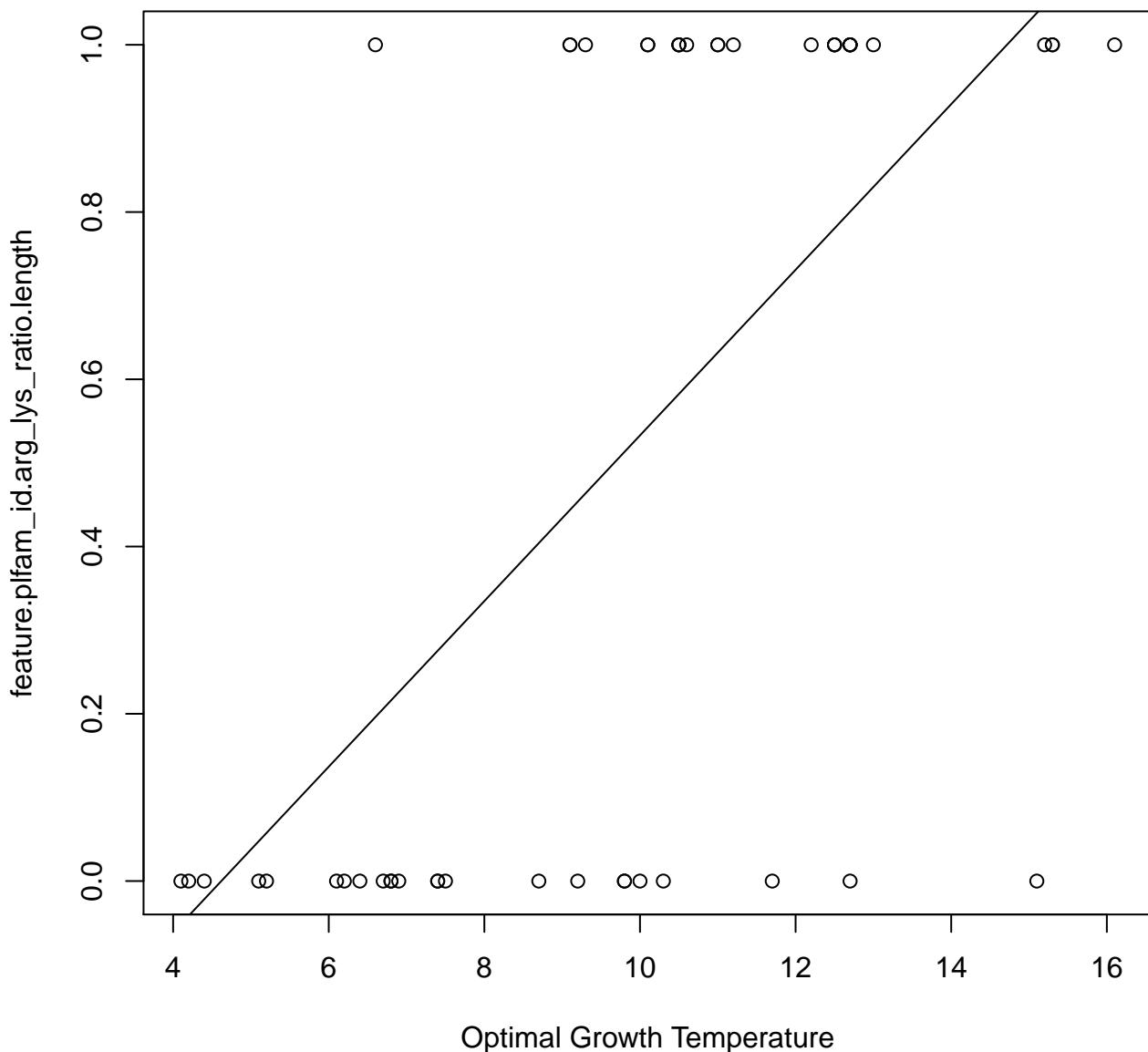
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hypothetical protein



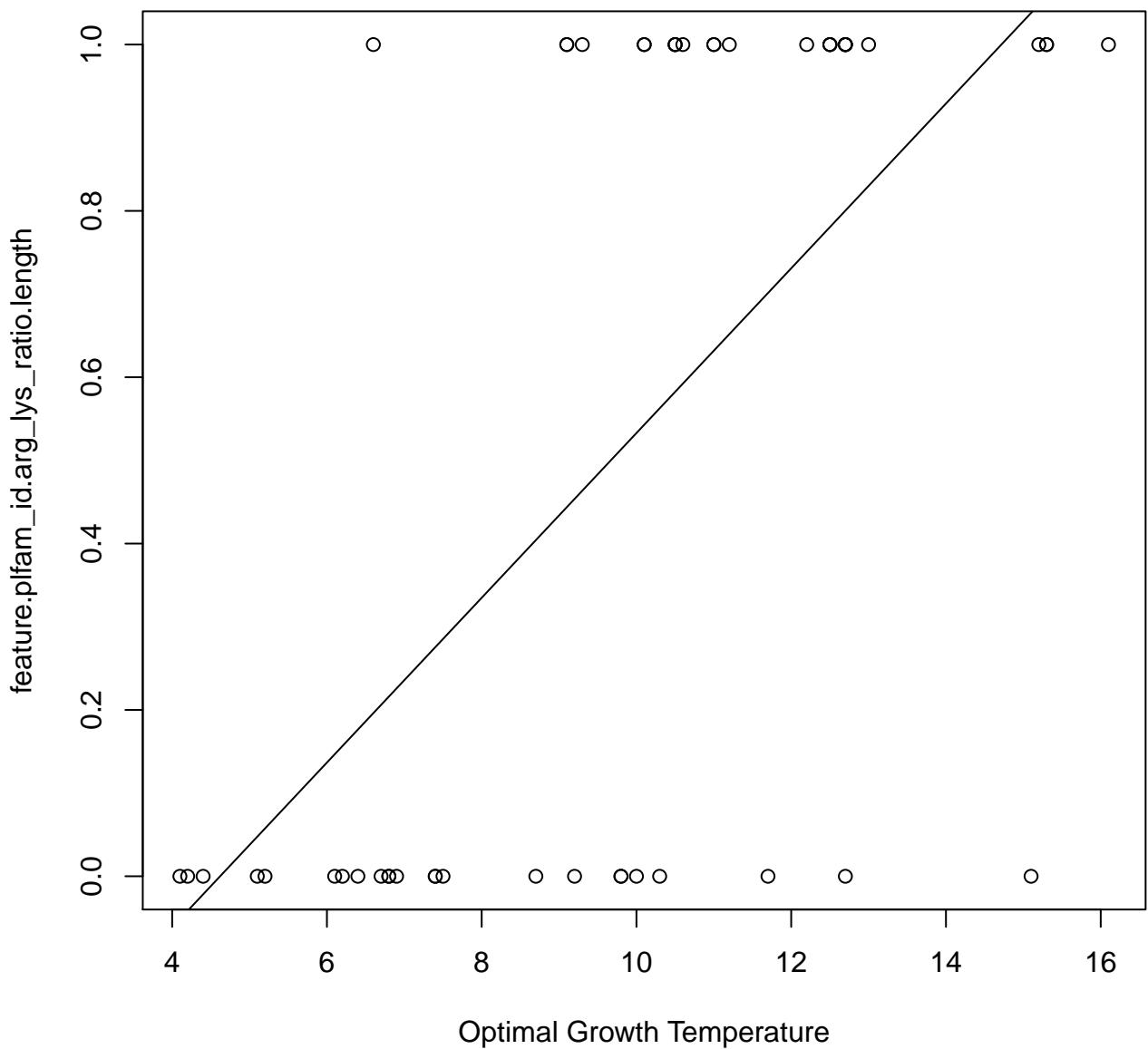
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Nitric oxide reductase activation protein NorE



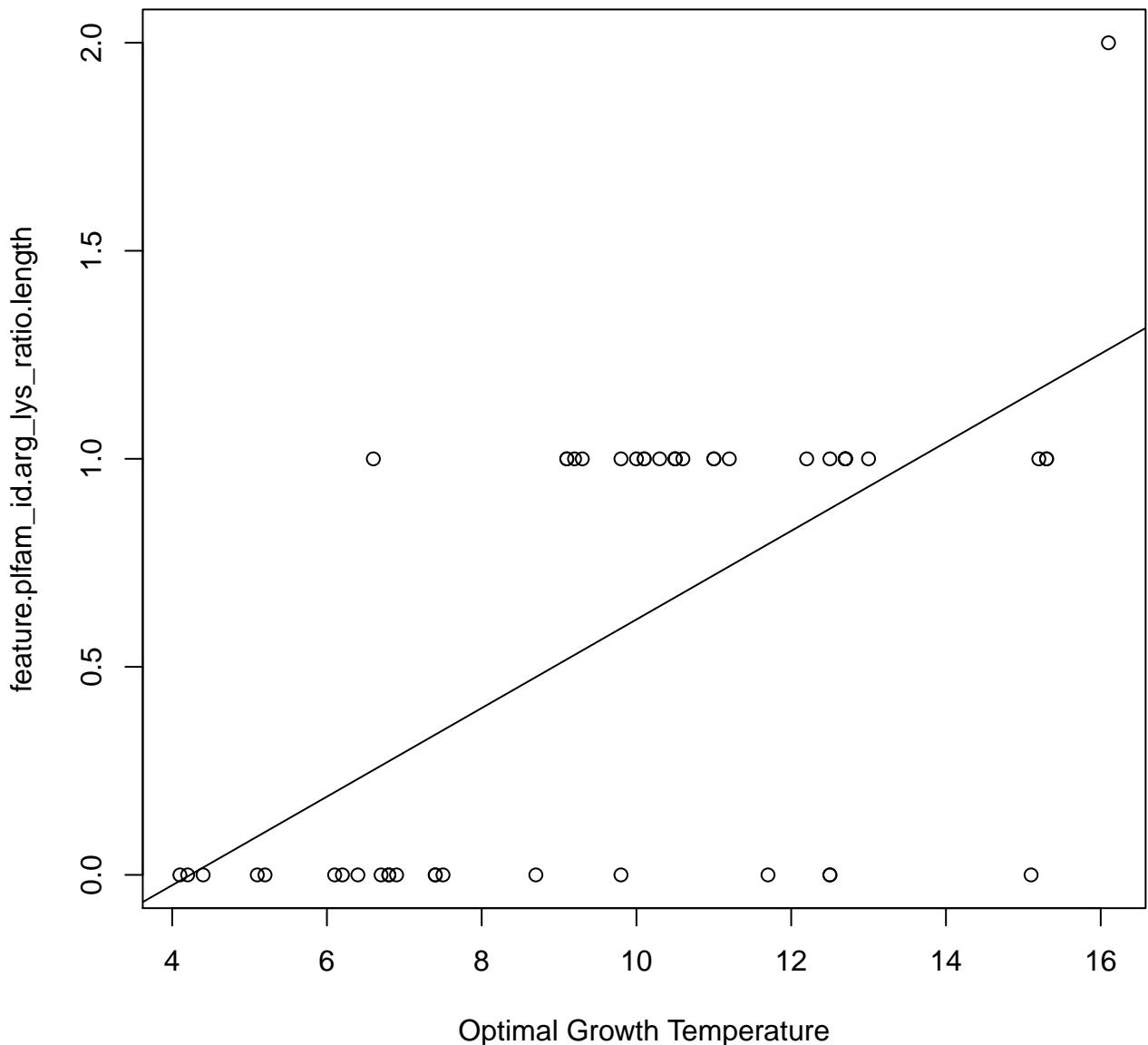
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Nitric oxide reductase activation protein NorF



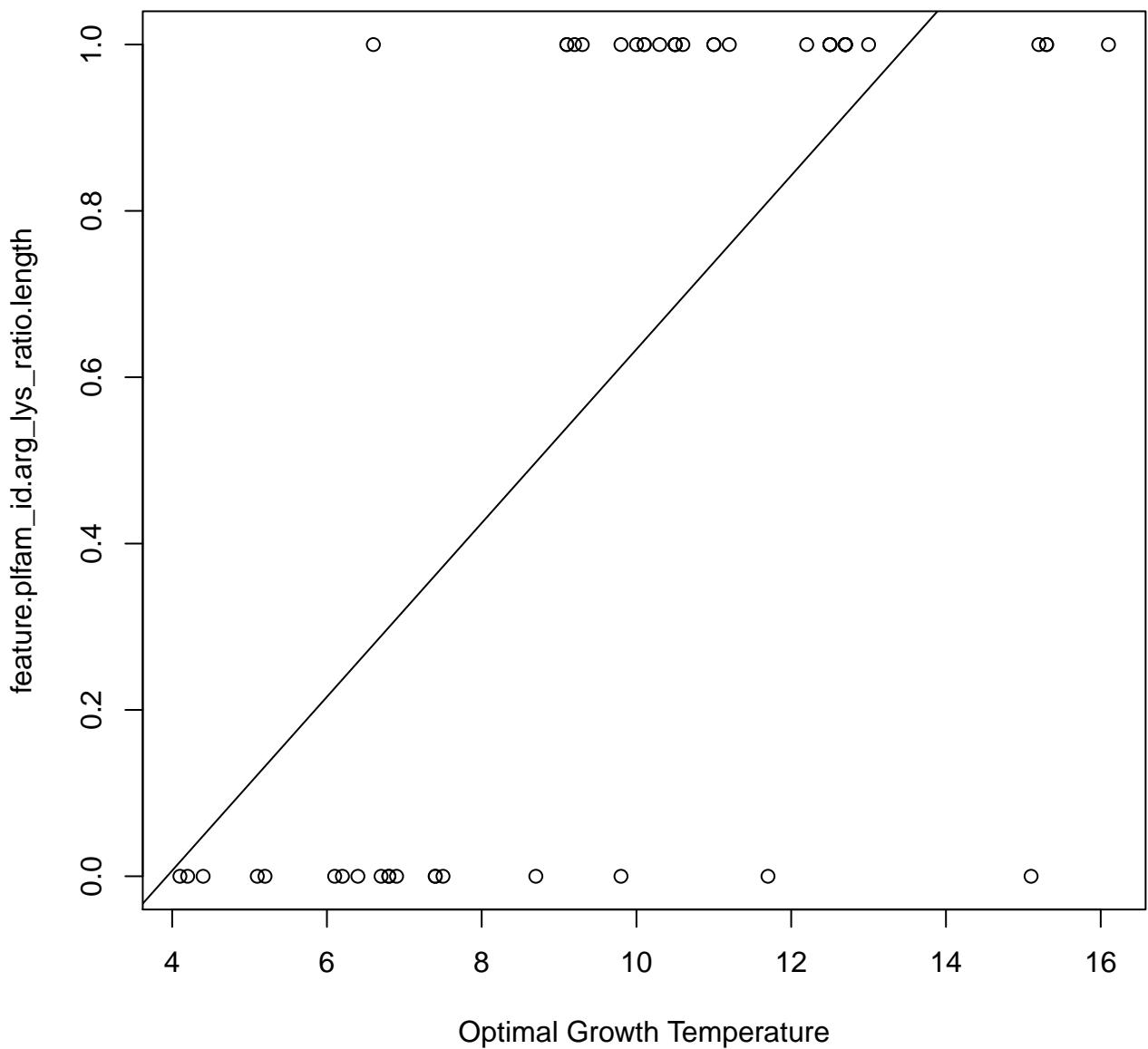
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Nitric-oxide reductase subunit C (EC 1.7.99.7)



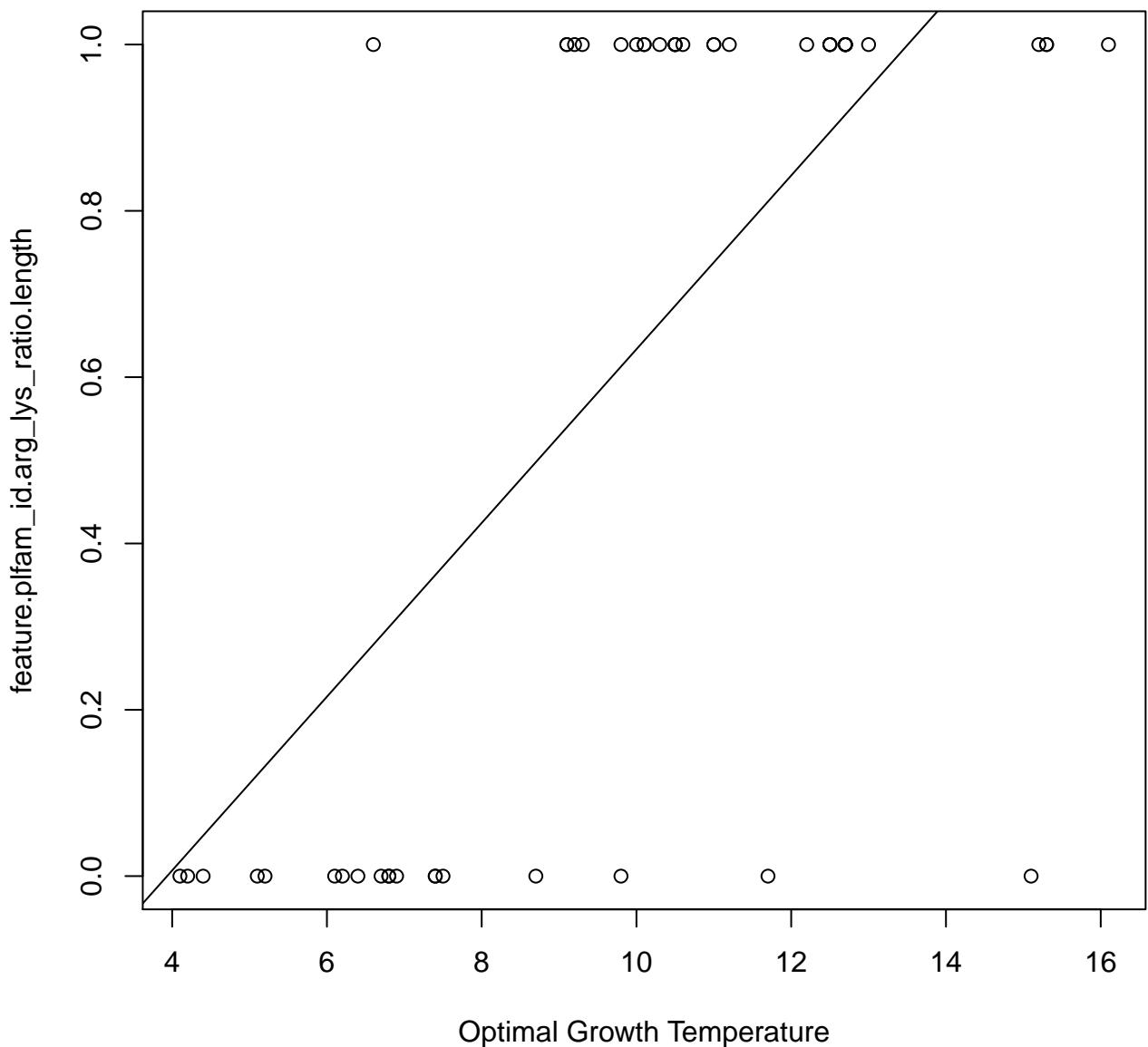
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PLF_28228_00014502
Uncharacterized MFS-type transporter



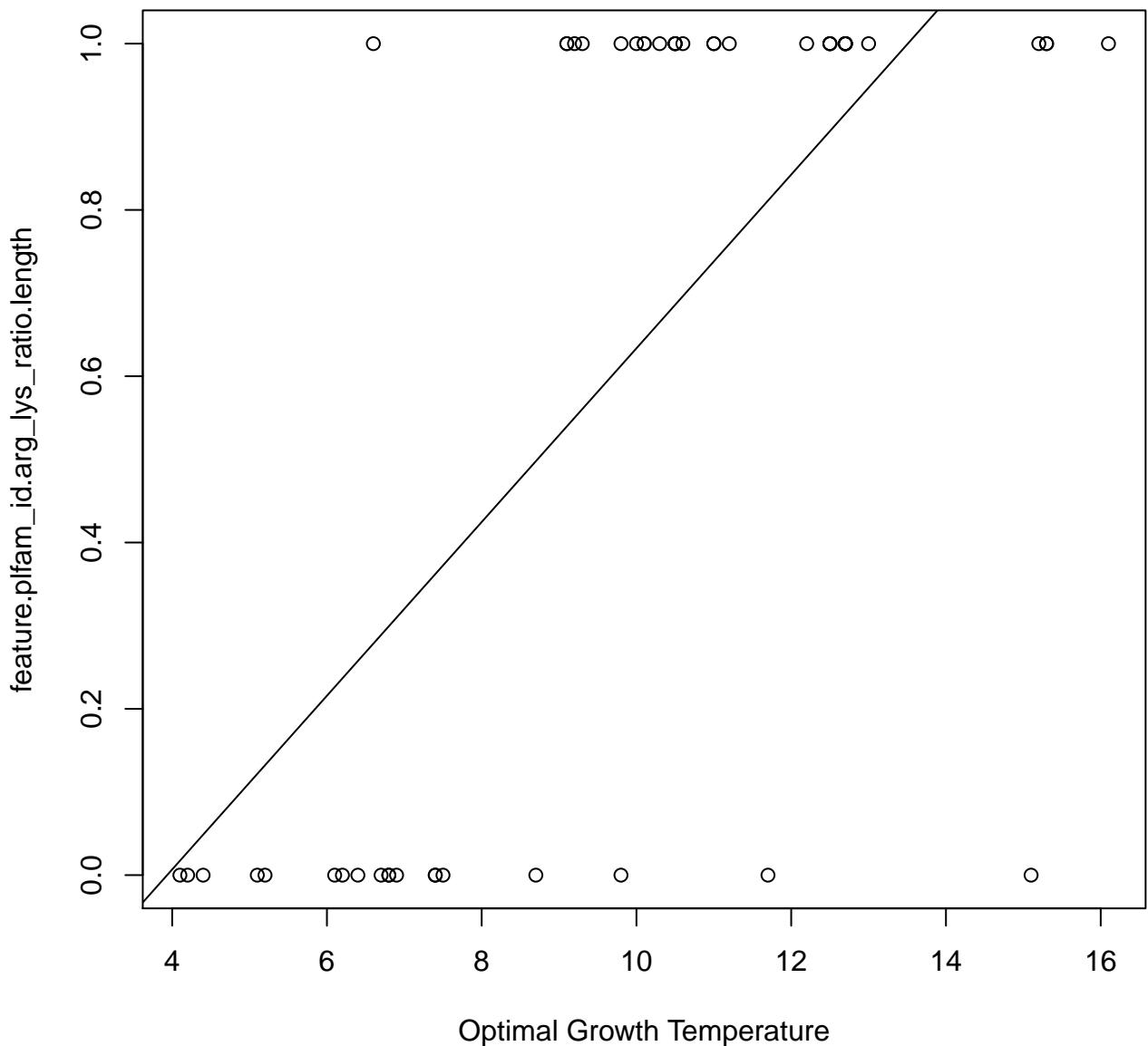
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Acyltransferase



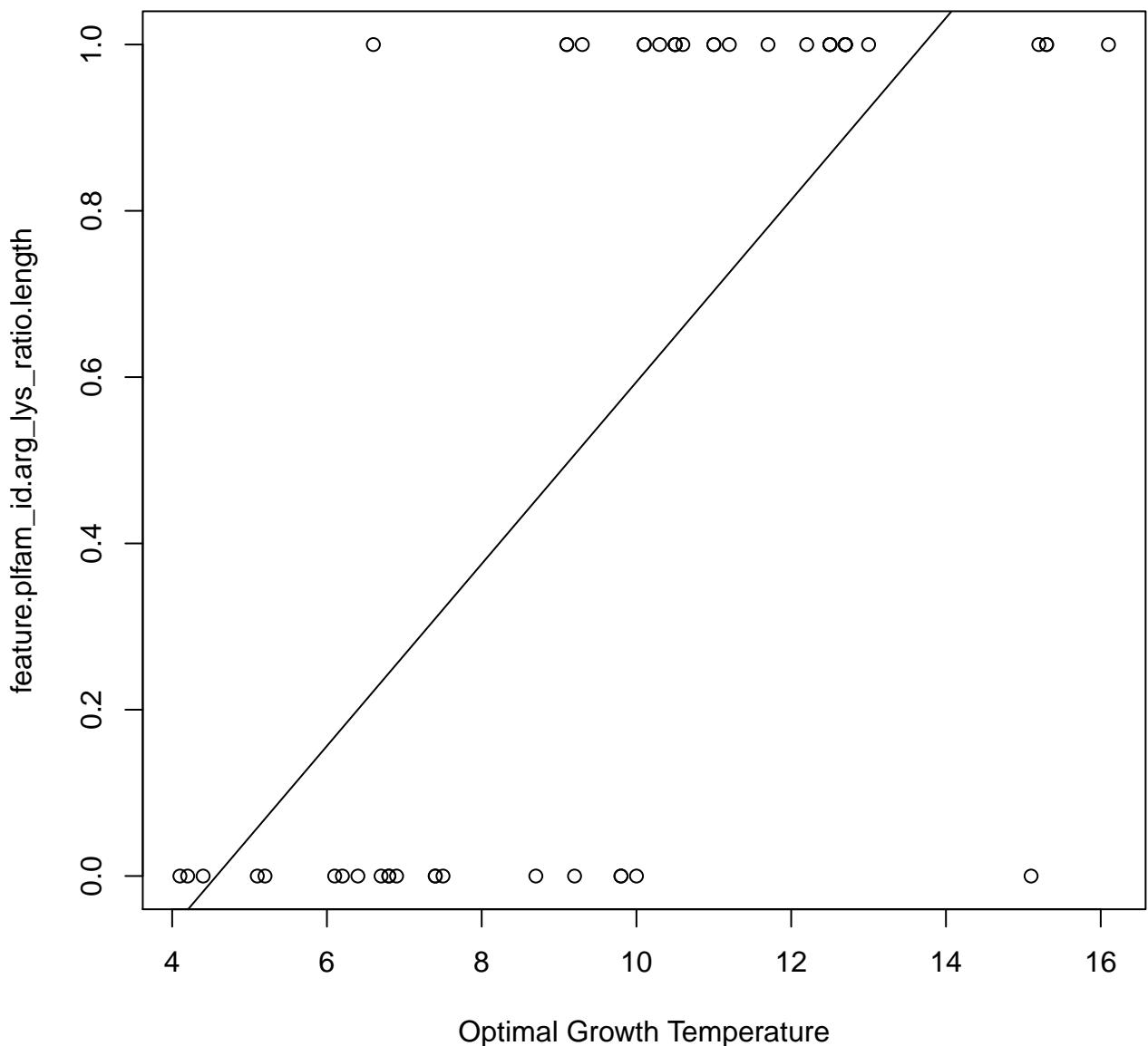
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Enoyl-CoA hydratase (EC 4.2.1.17)



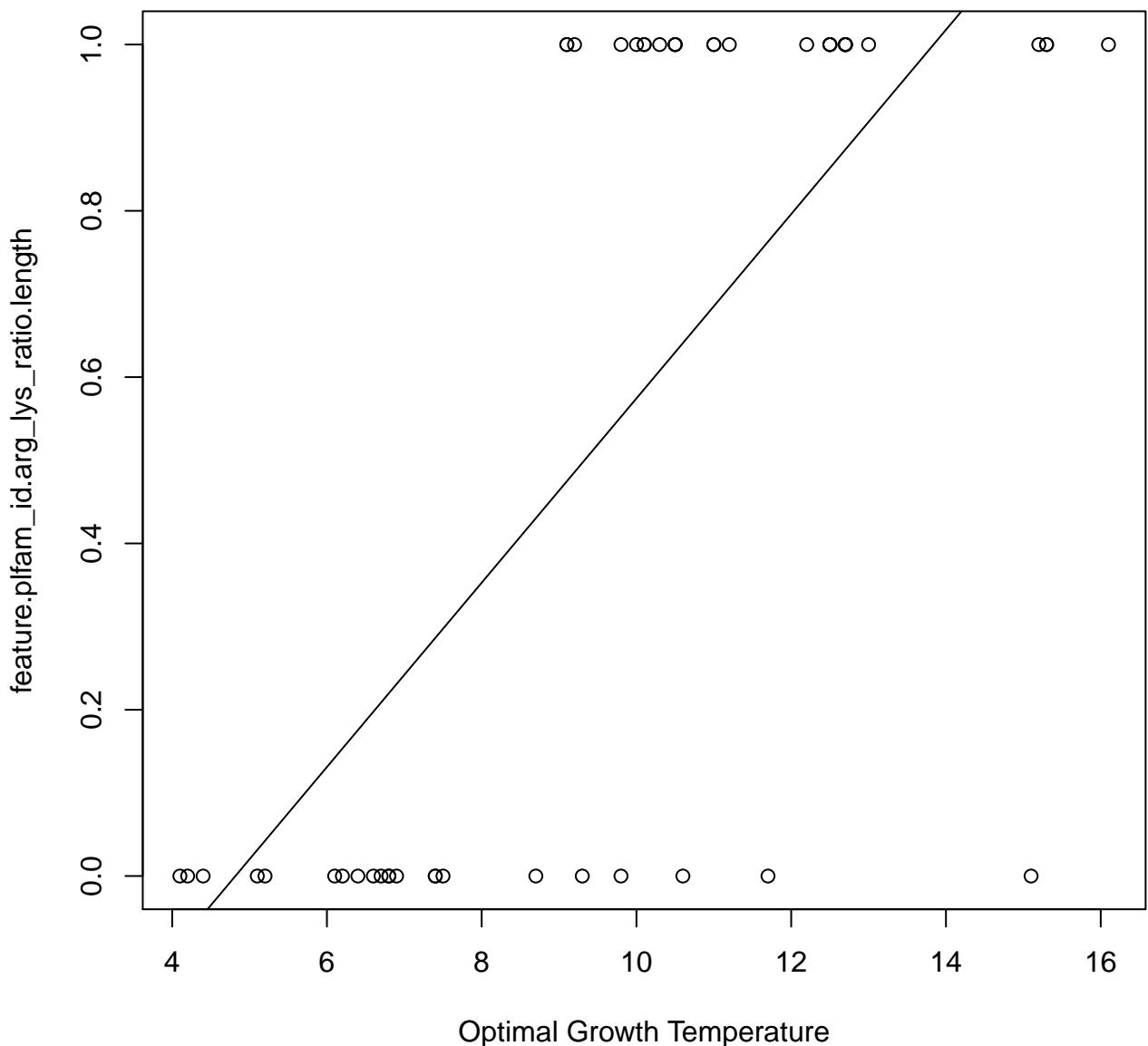
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Chorismate--pyruvate lyase (EC 4.1.3.40)



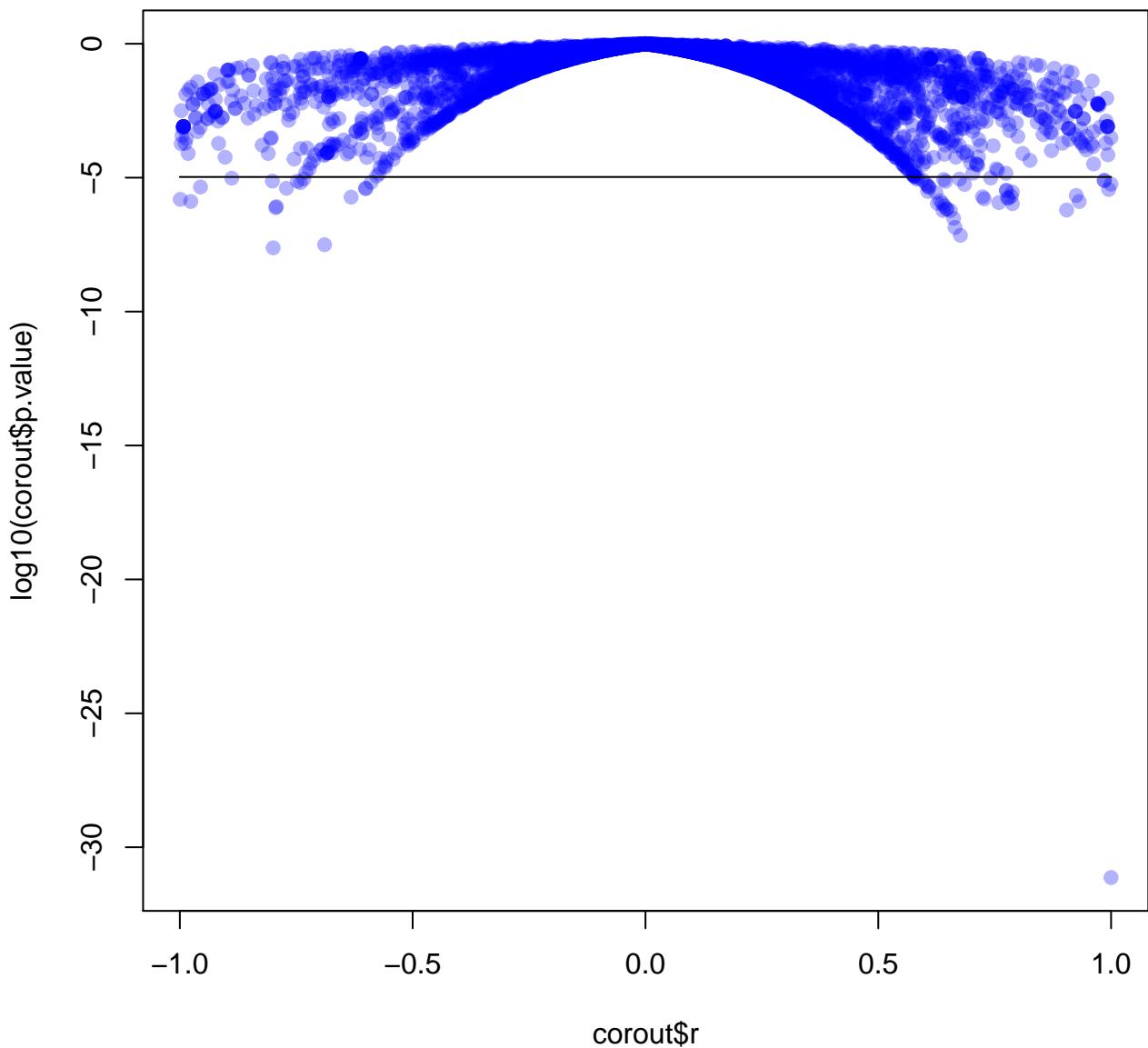
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3-hydroxybutyrate dehydrogenase (EC 1.1.1.30)



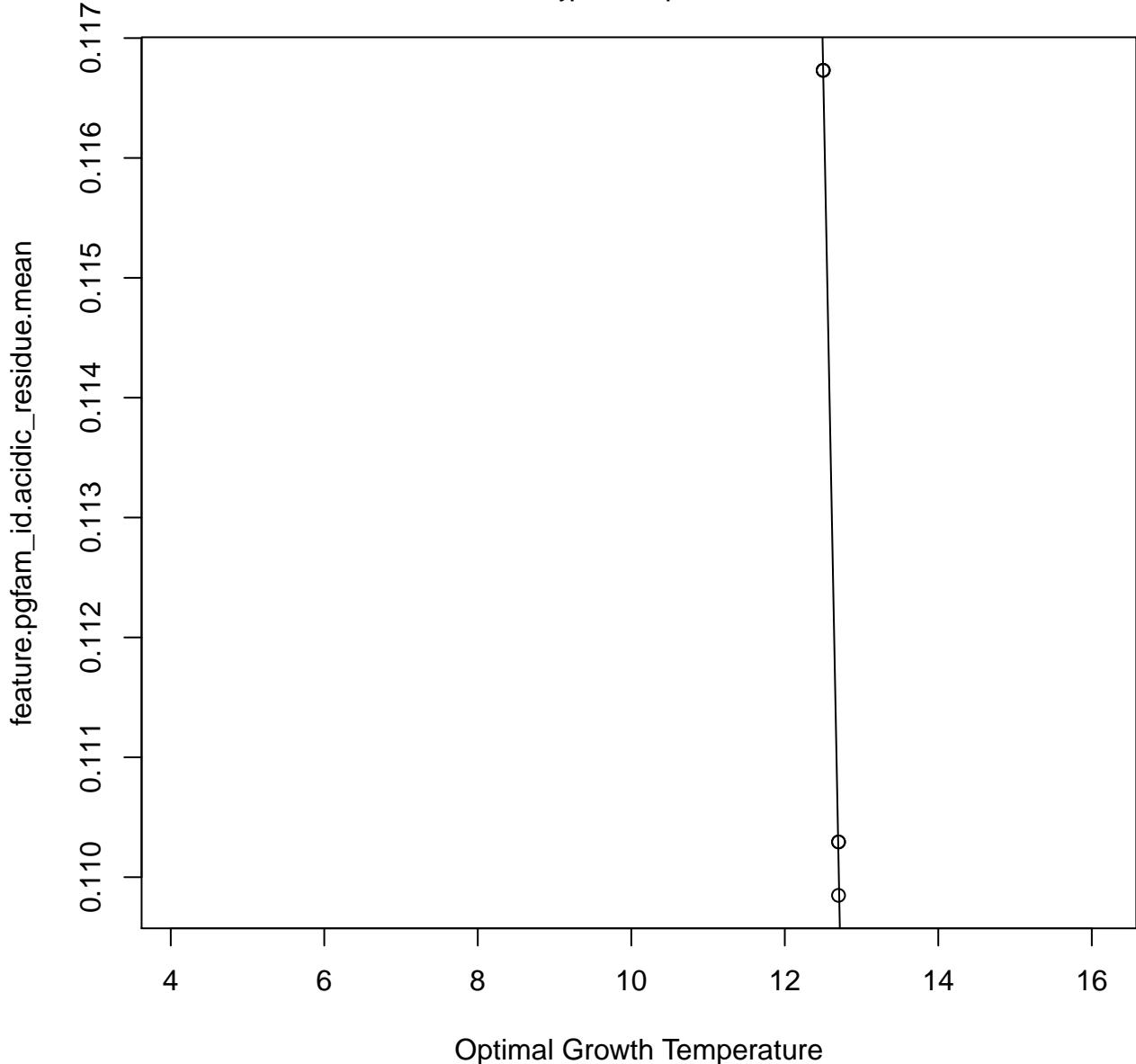
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General secretion pathway protein L



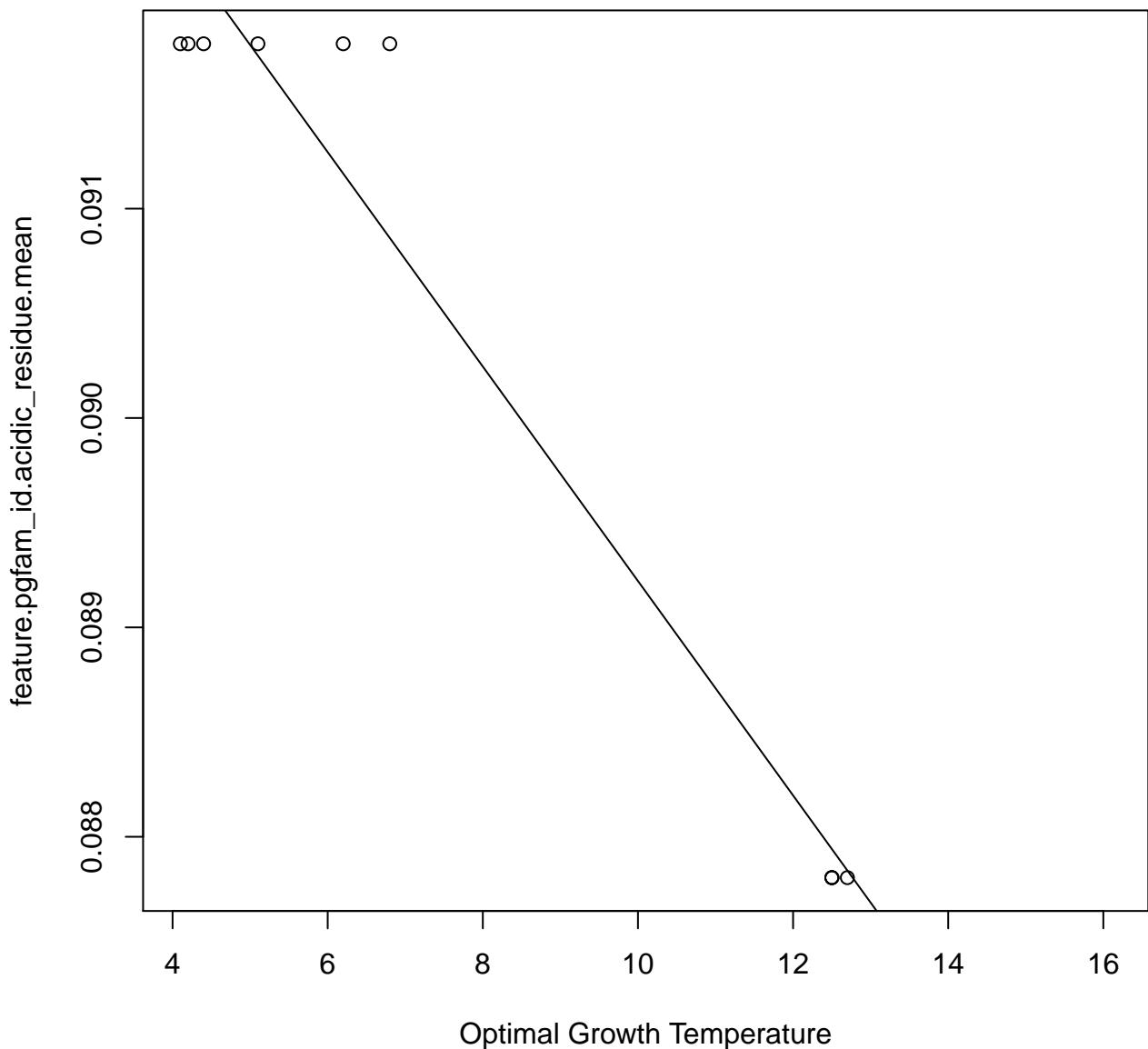
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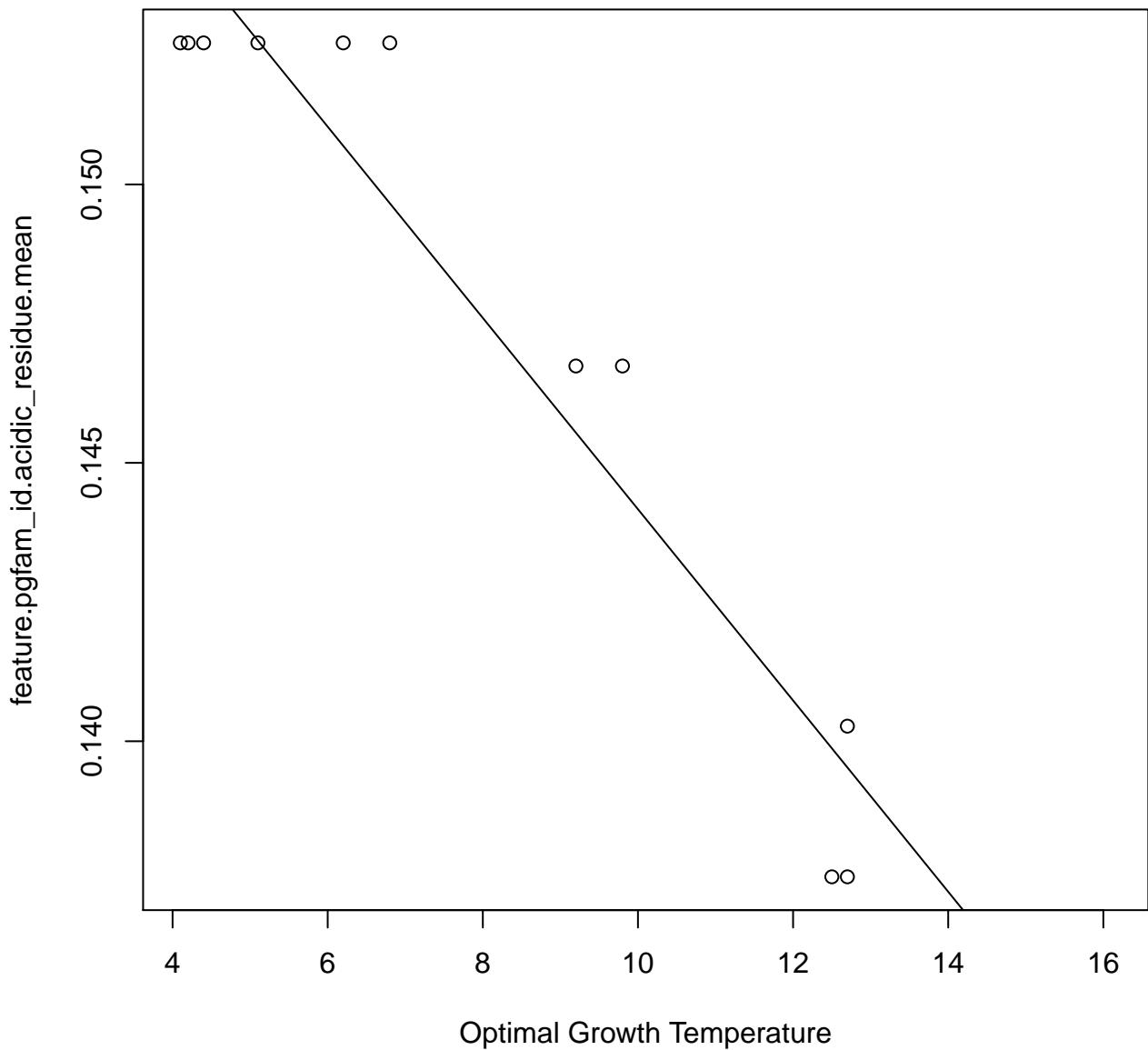
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PGF_01336907
hypothetical protein



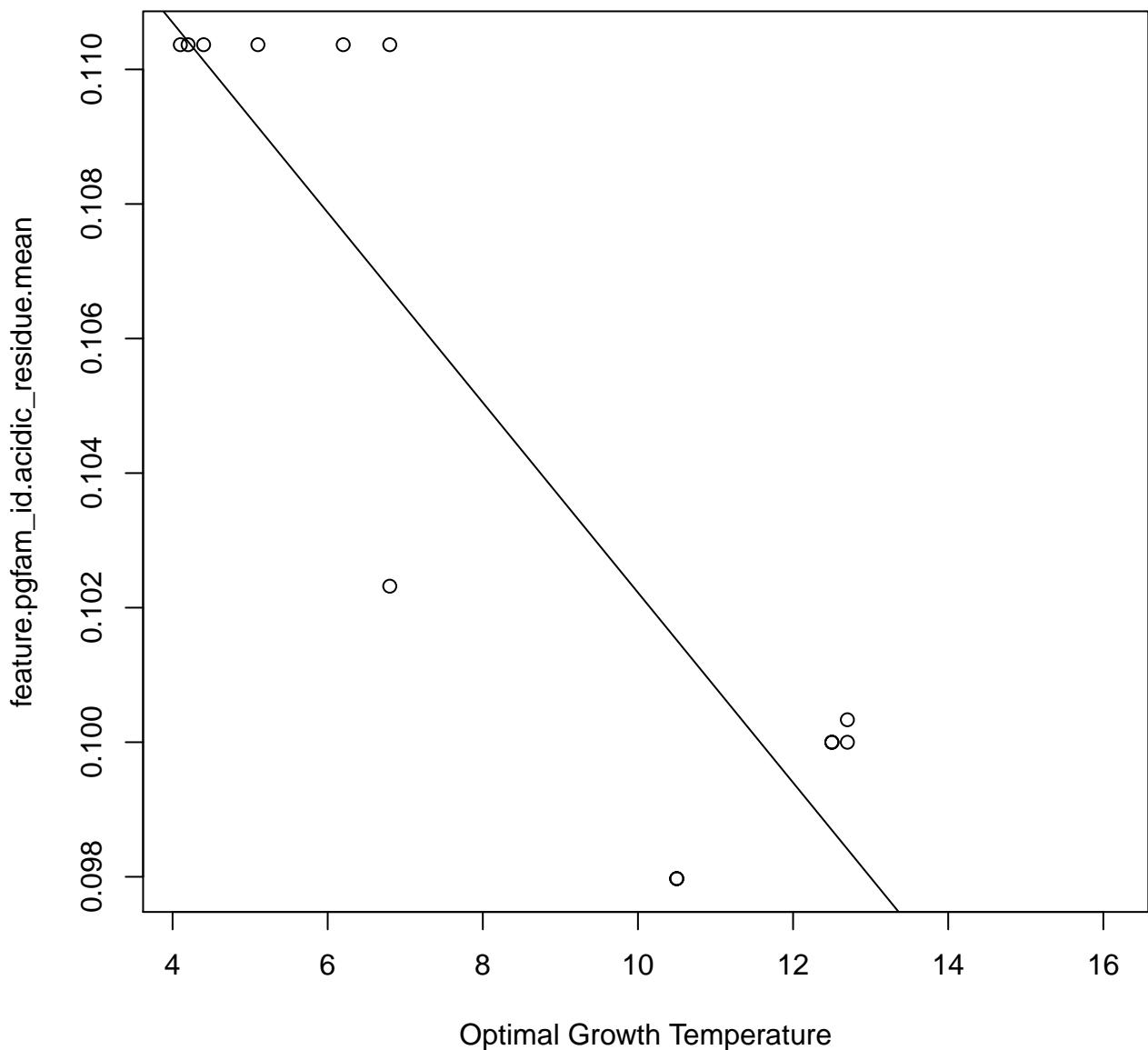
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hypothetical protein



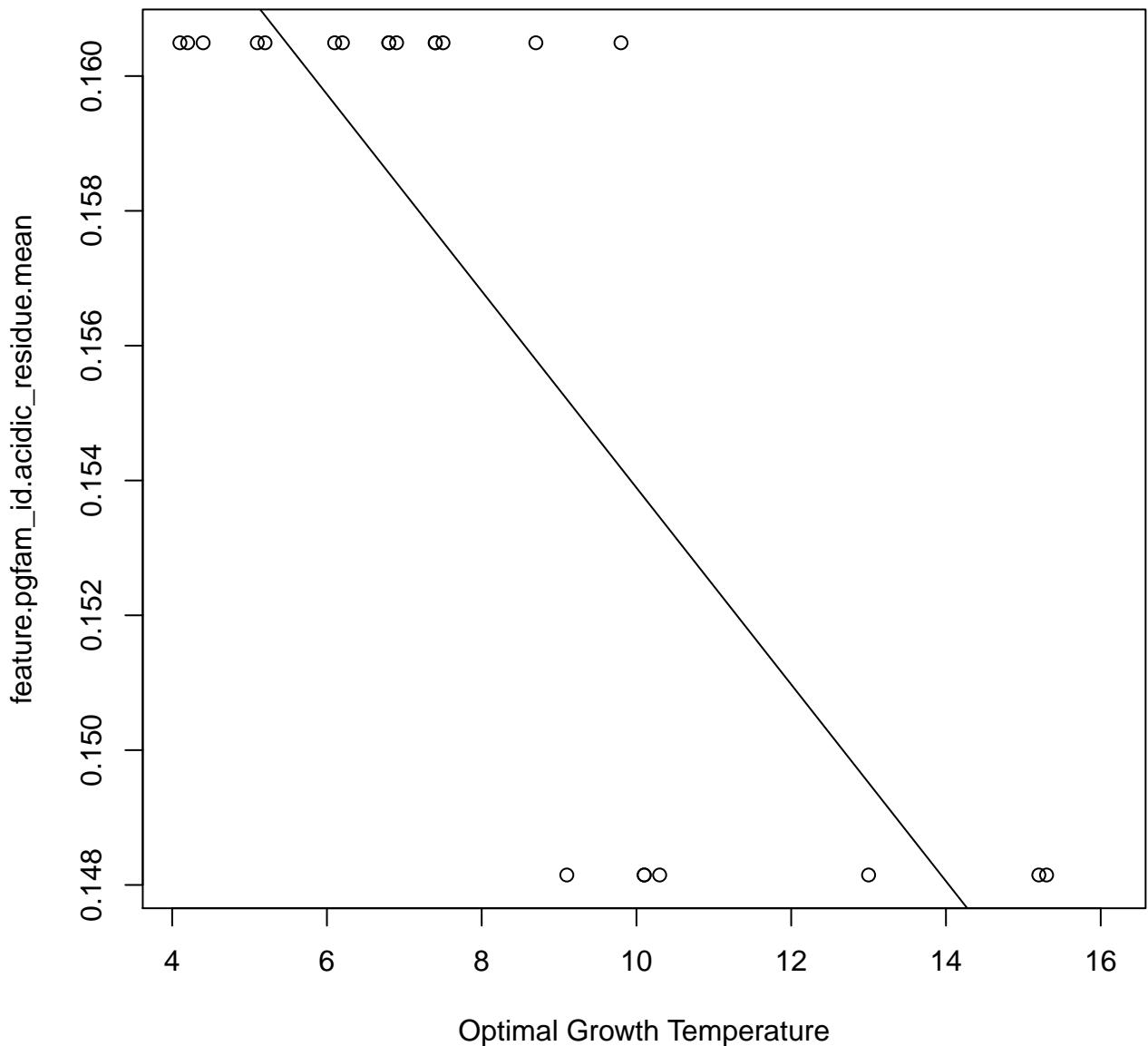
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putative lipoprotein



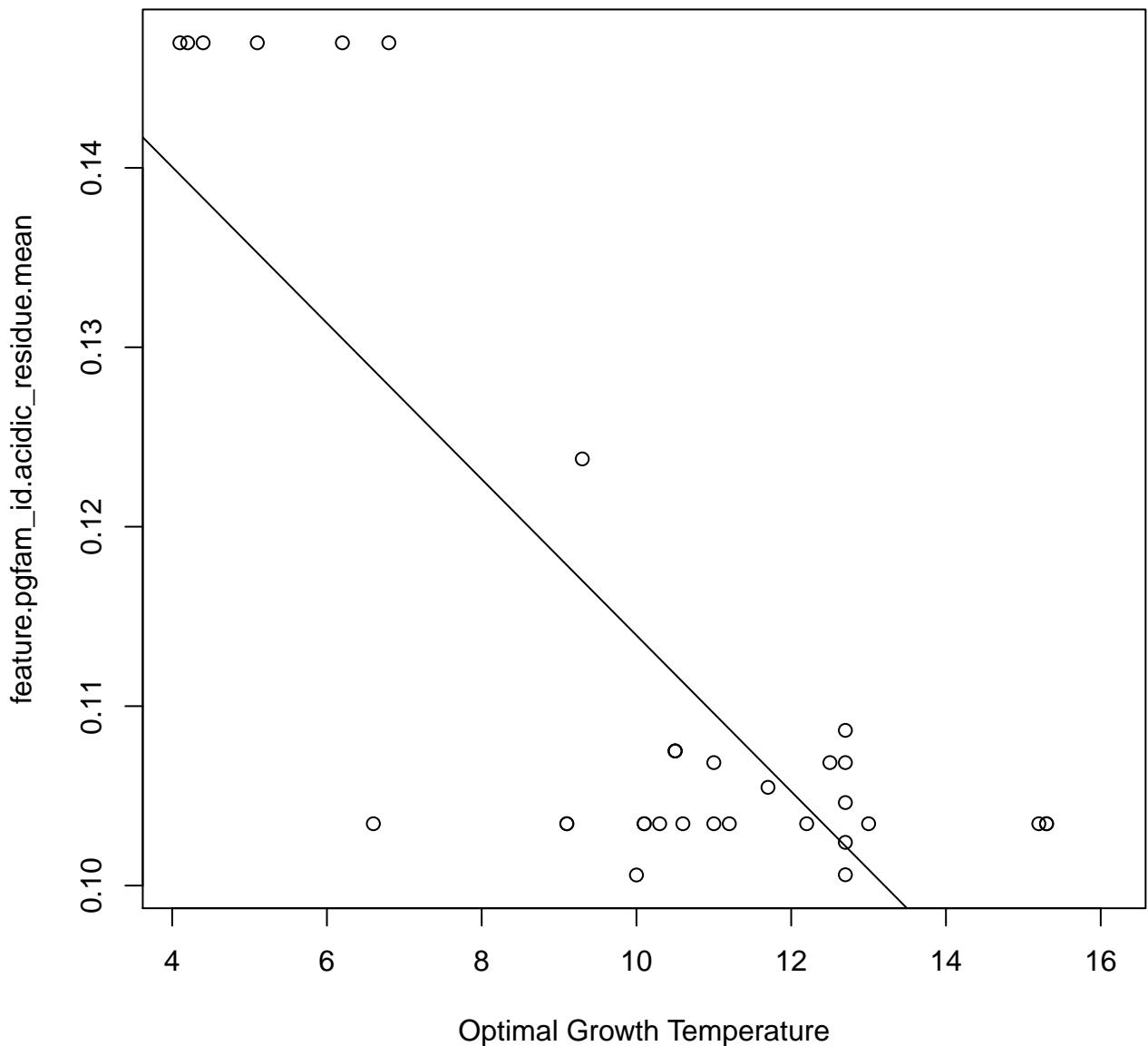
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PGF_01338001
hypothetical protein



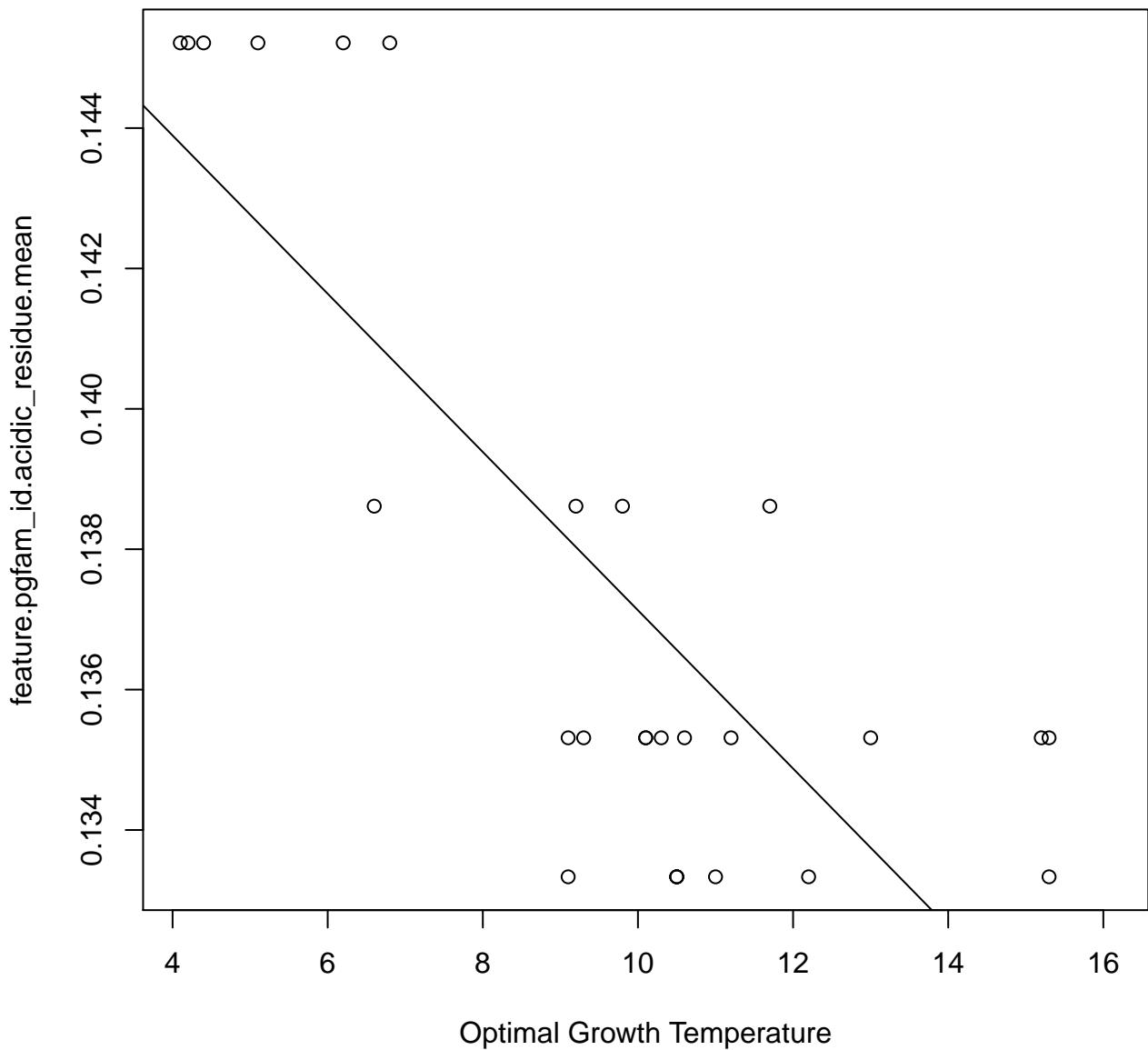
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PGF_00393434
hypothetical protein



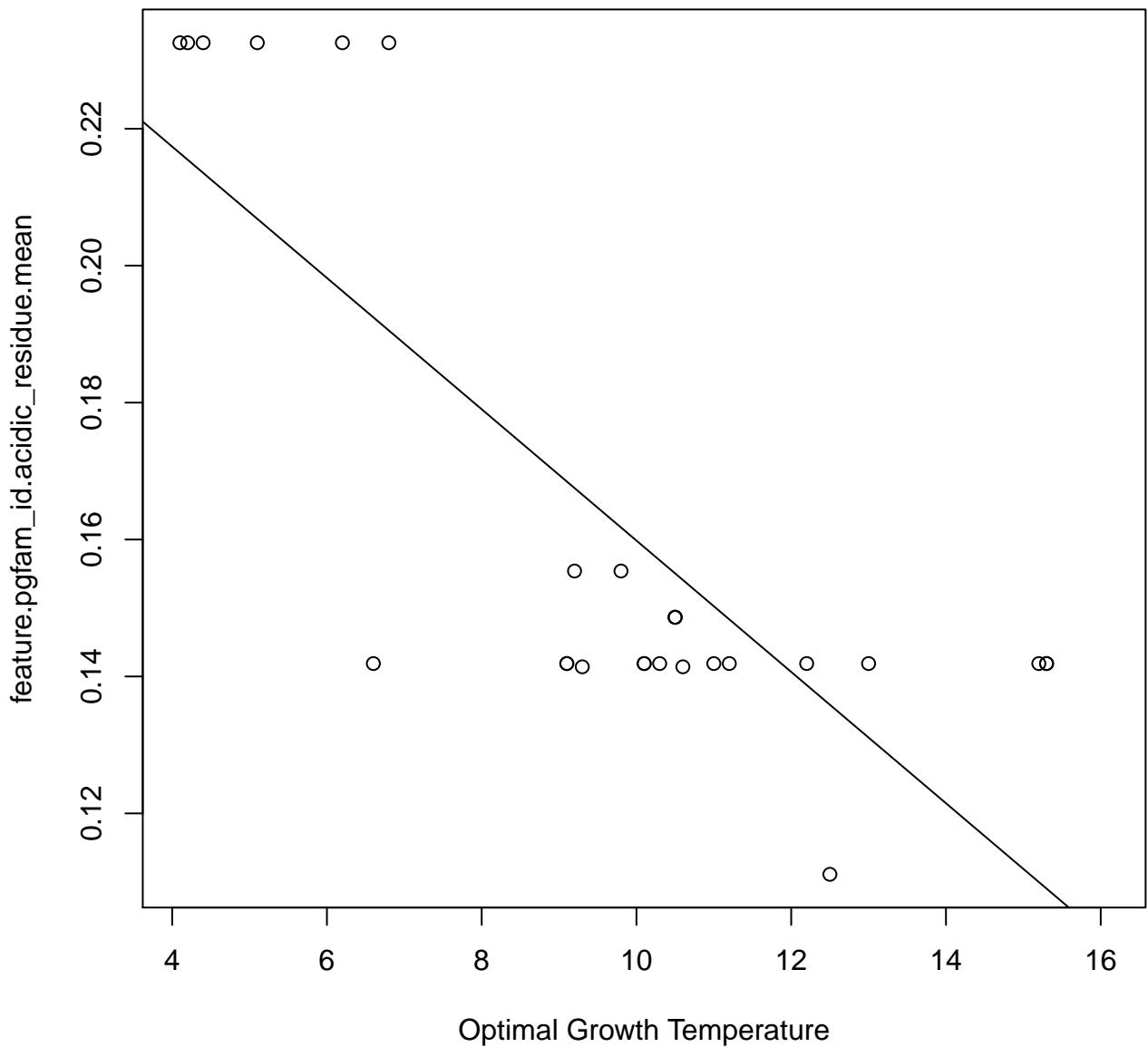
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Two-component system sensor histidine kinase



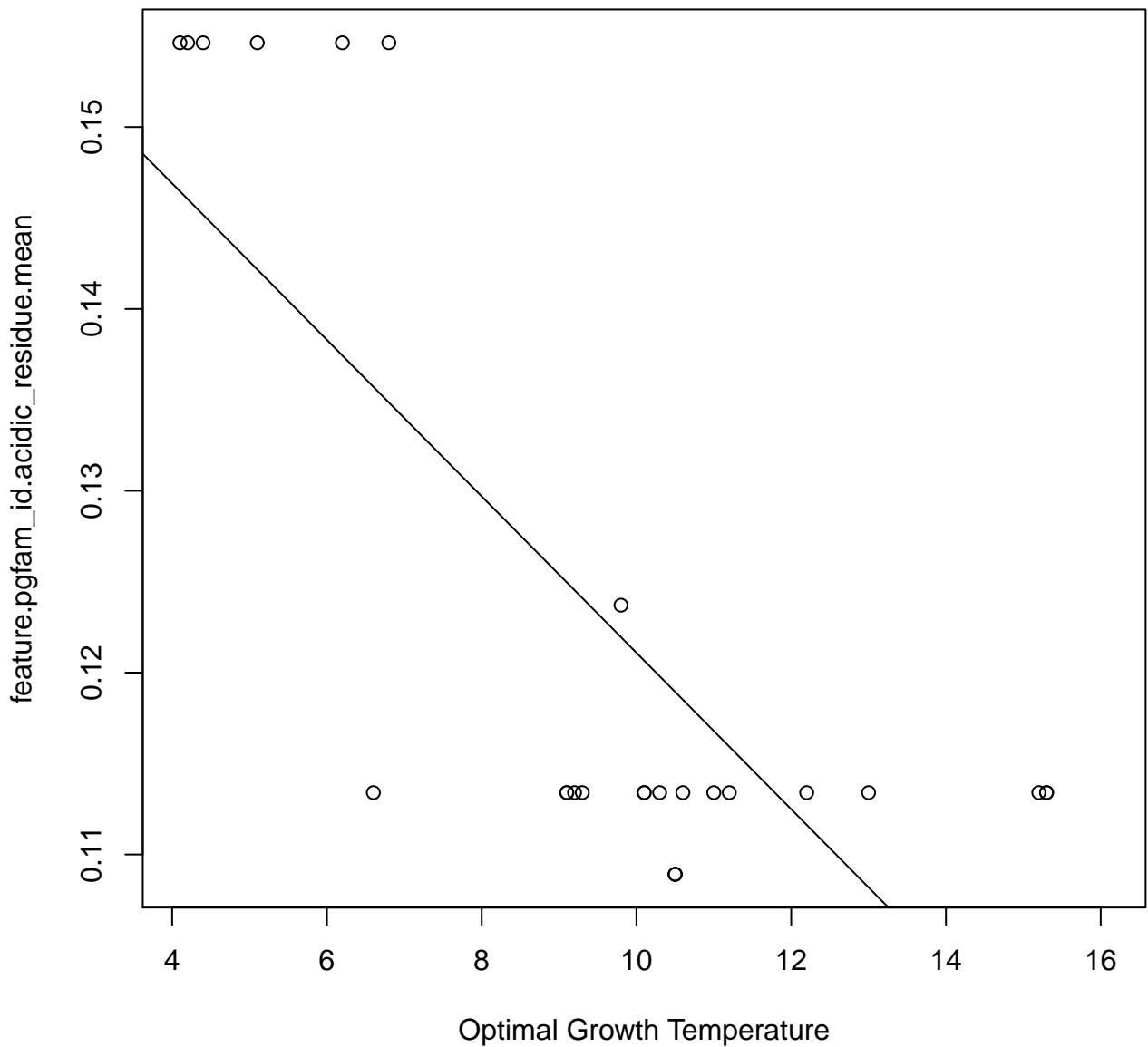
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PGF_12817314
hypothetical protein



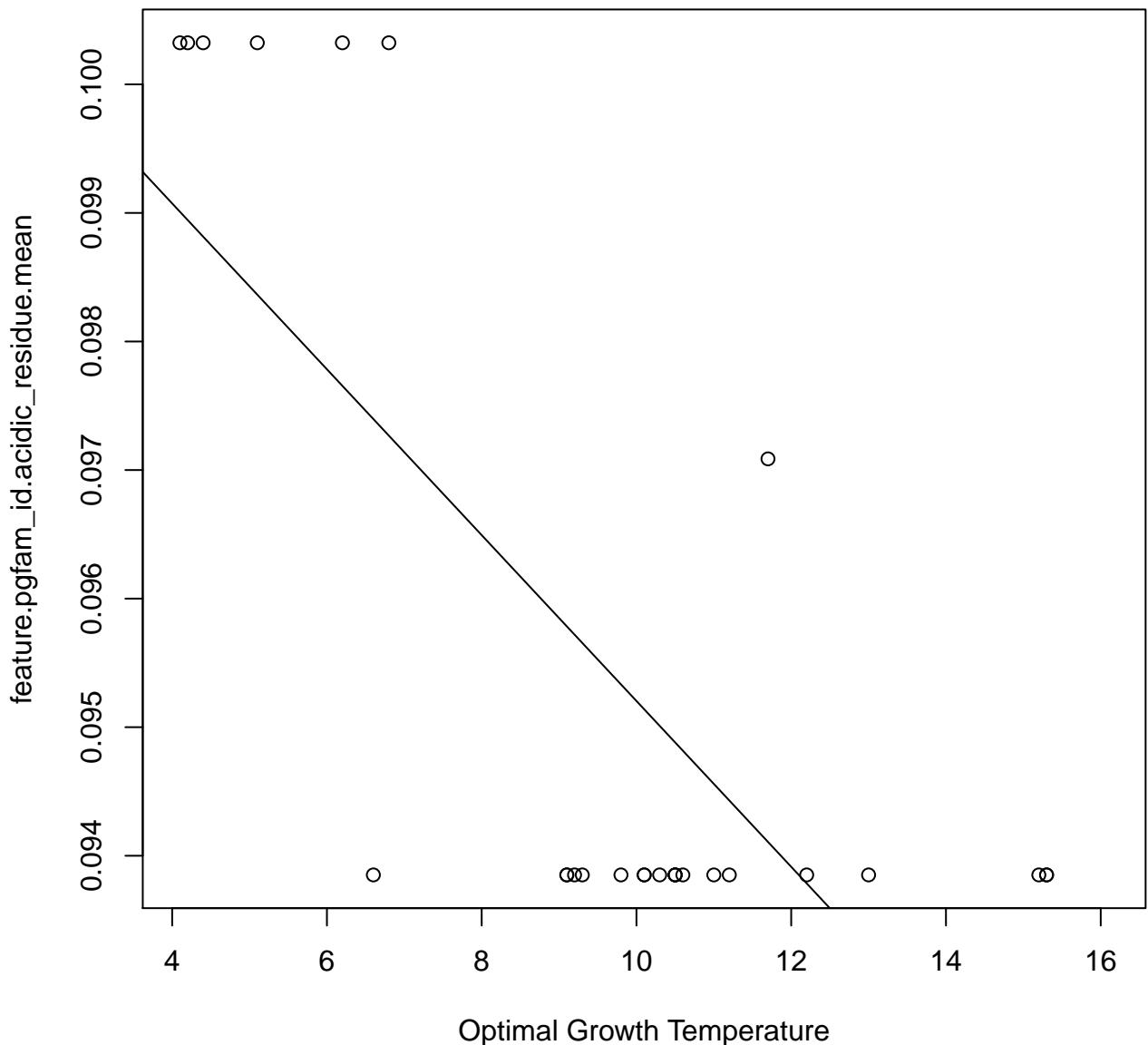
feature.pgfam_id.acidic_residue.mean
PGF_06792096
hypothetical protein



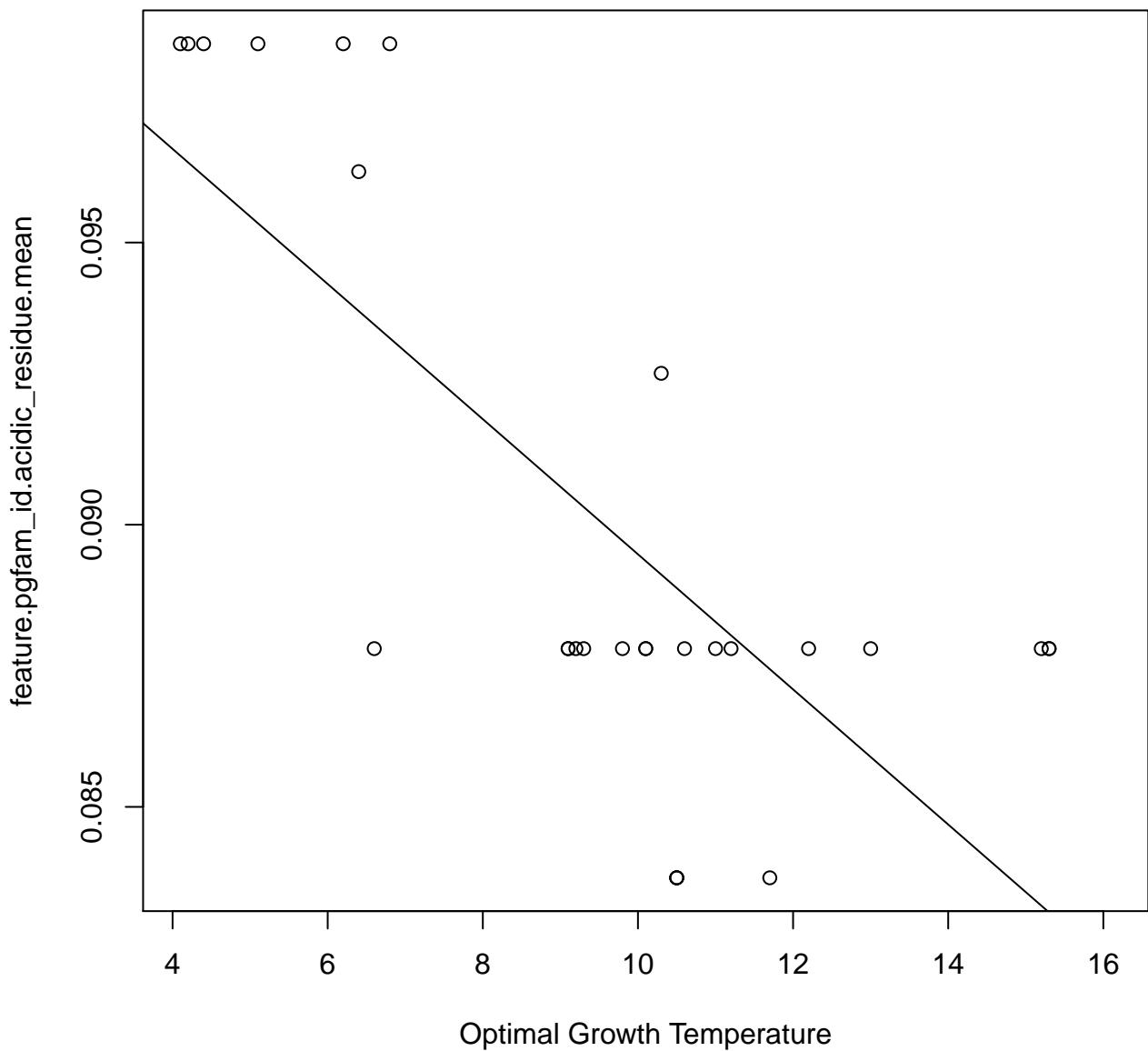
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PGF_11915740
hypothetical protein



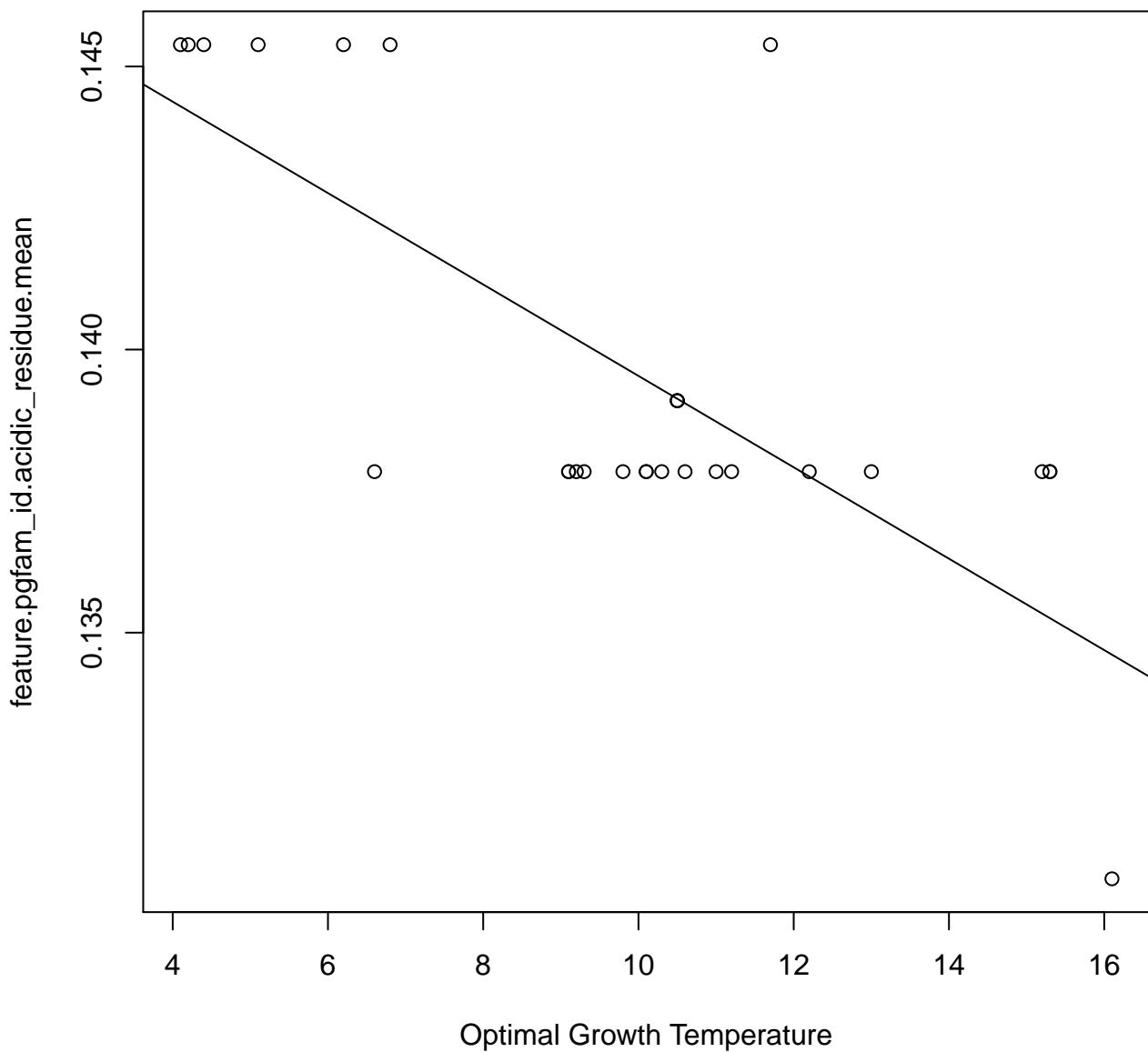
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PGF_00024218
N-linked glycosylation glycosyltransferase PgIG



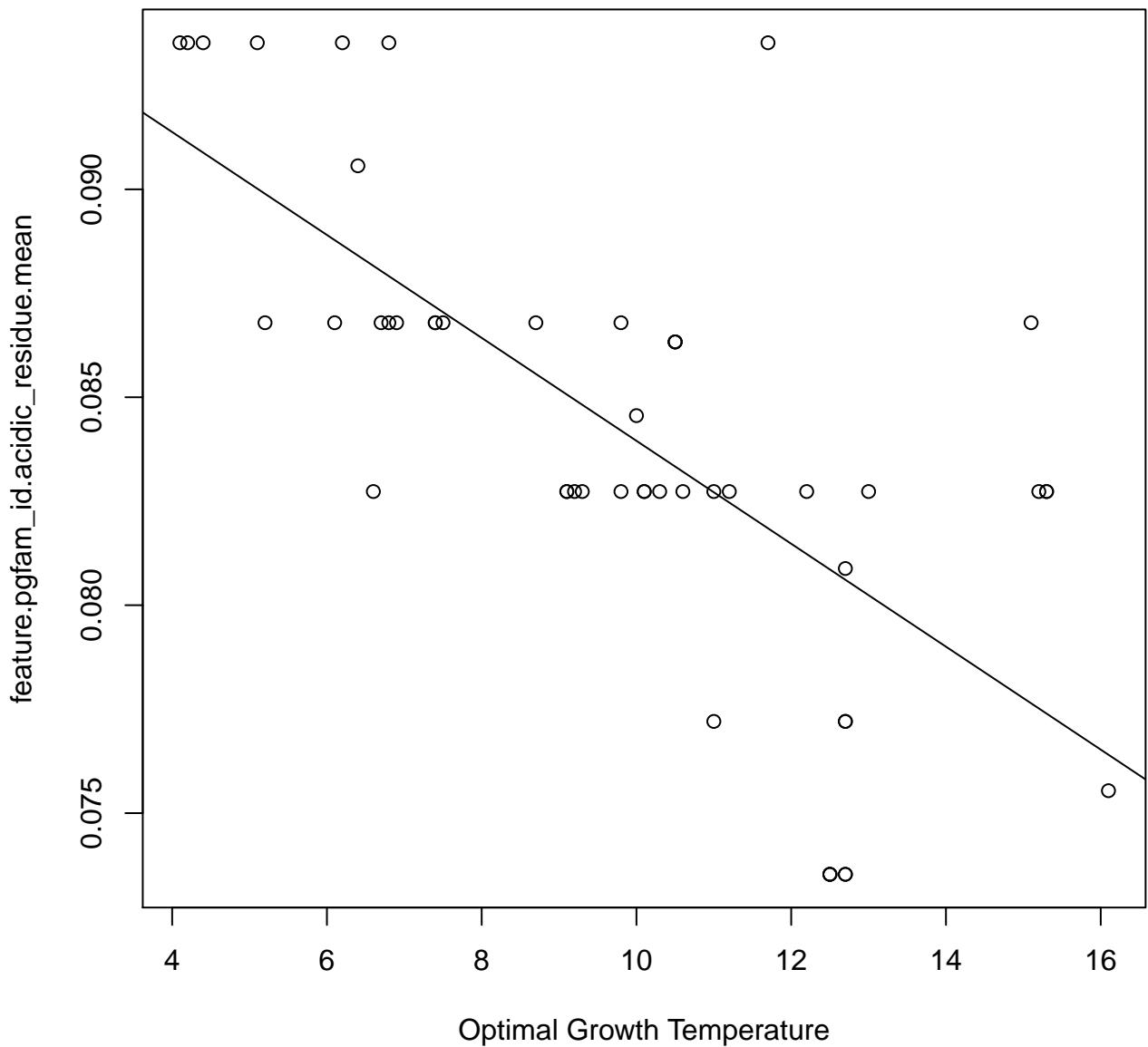
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PGF_12826297
hypothetical protein



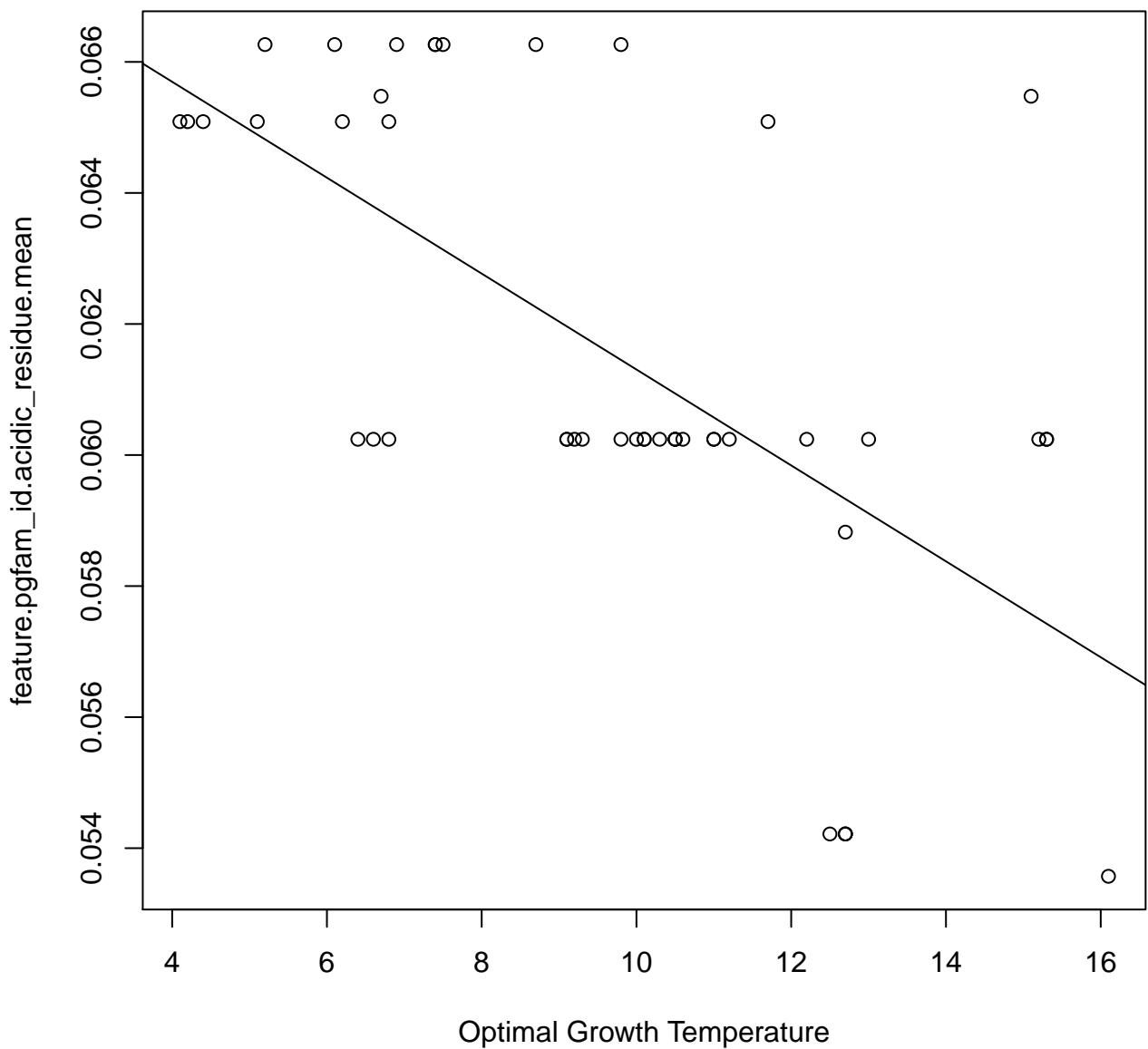
feature.pgfam_id.acidic_residue.mean
PGF_00001616
FIG01056734: hypothetical protein



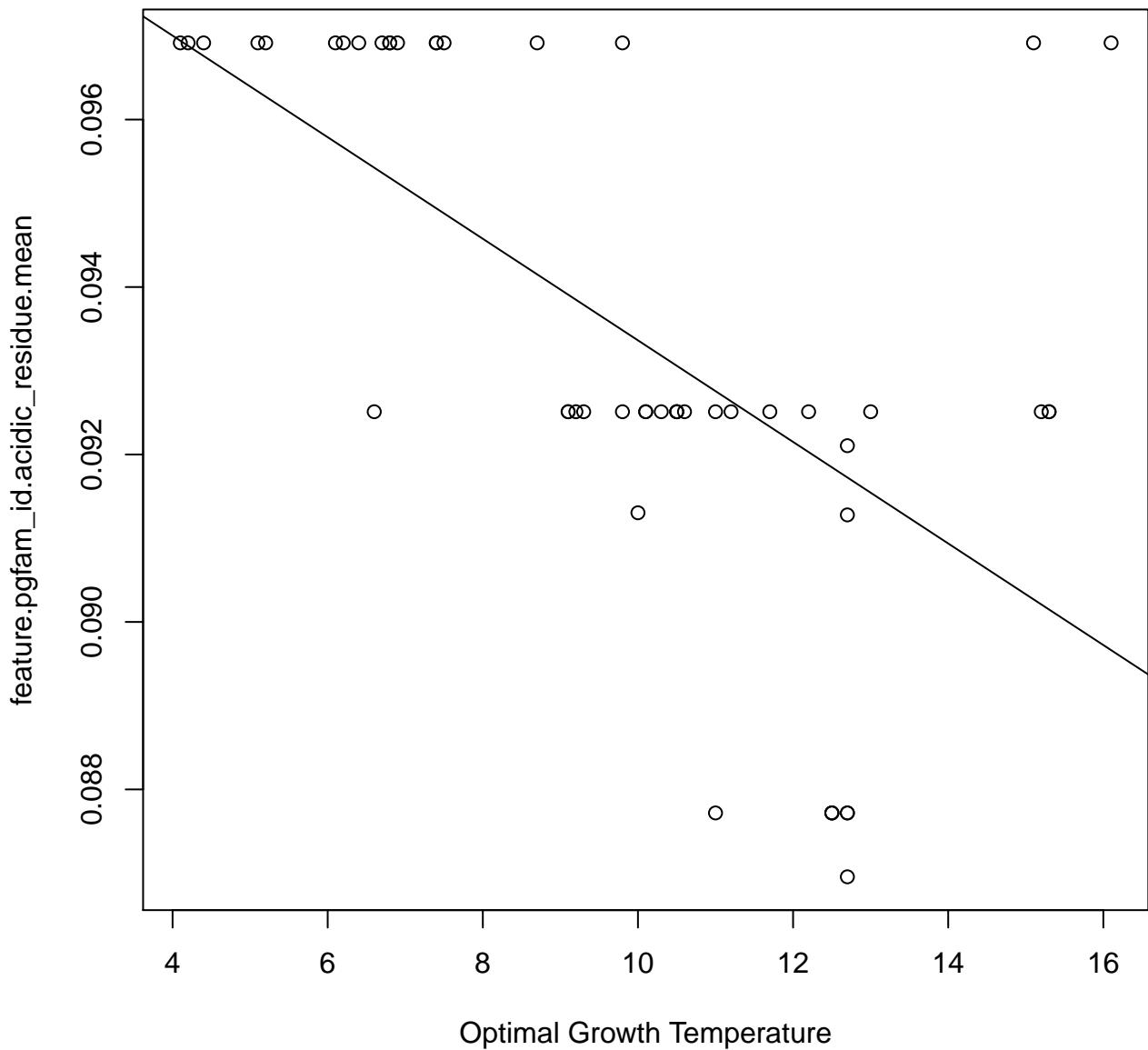
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PGF_00048554
Caulimovirus viroplasmin / Ribonuclease HI (EC 3.1.26.4)



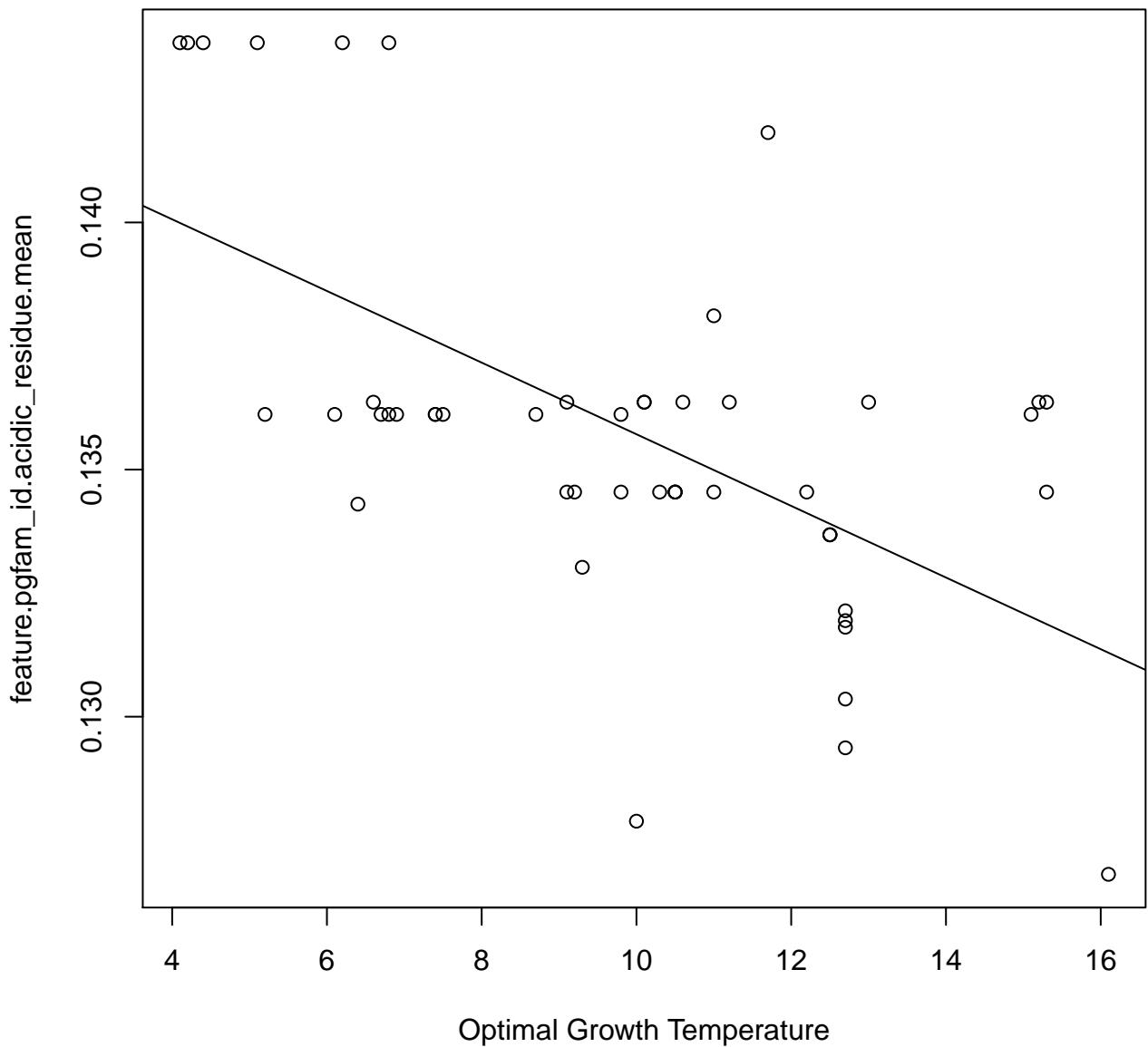
feature.pgfam_id.acidic_residue.mean
PGF_03073036
hypothetical protein



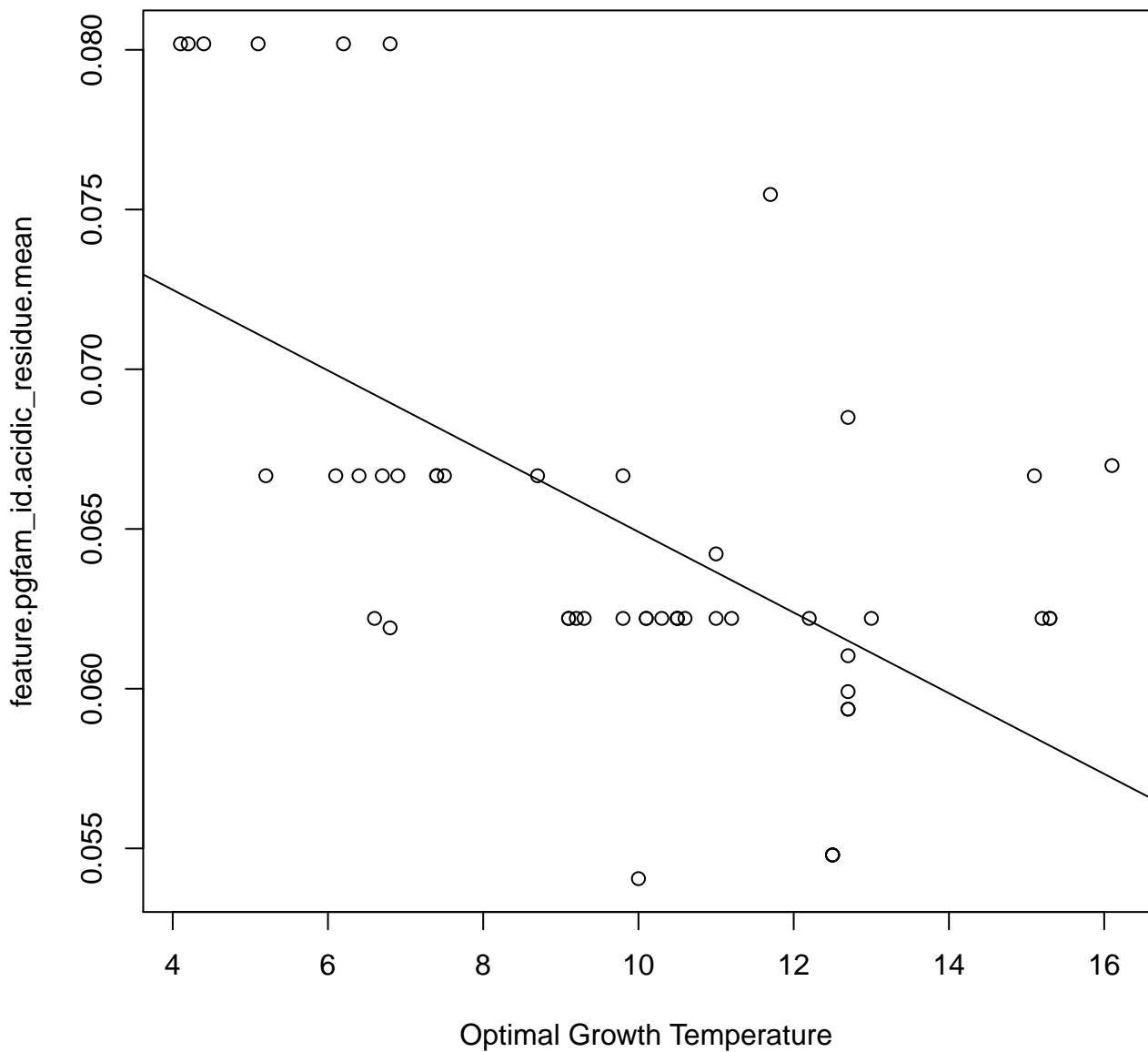
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PGF_00648054
Tol-Pal system protein TolQ



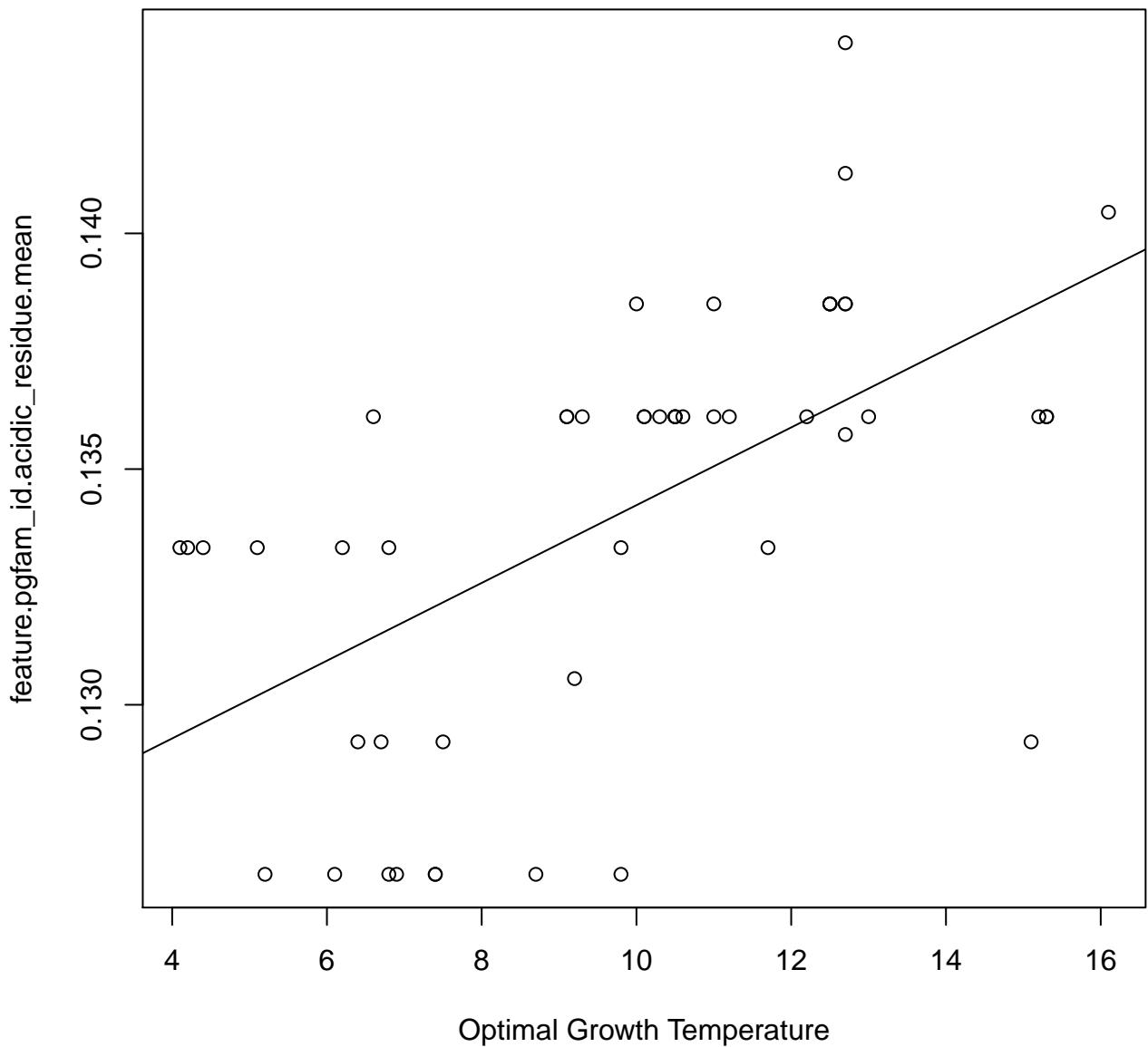
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PGF_00026525
Nudix hydrolase 3 (EC 3.6.1.-)



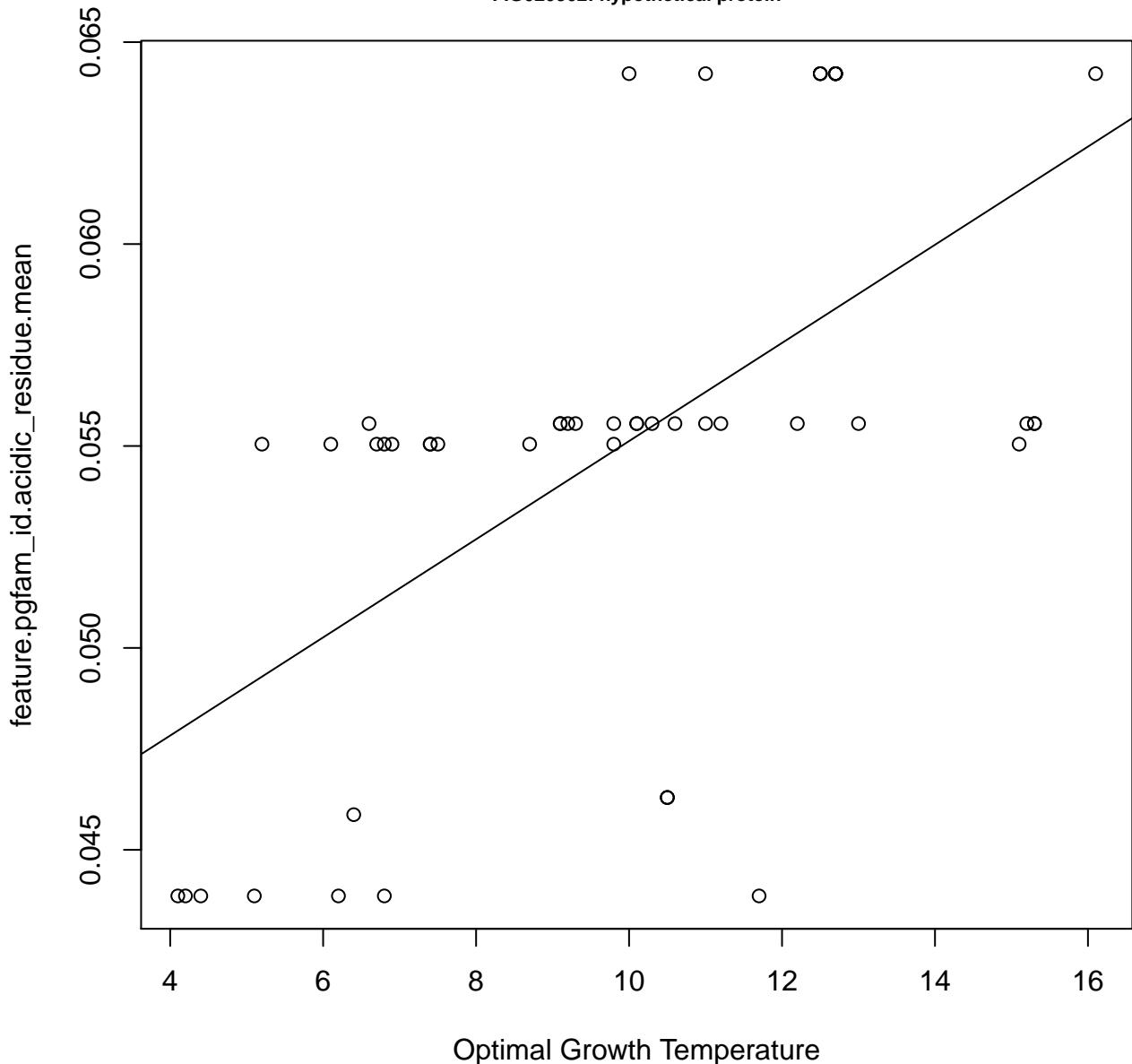
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PGF_00612013
UPF0126 inner membrane protein YadS



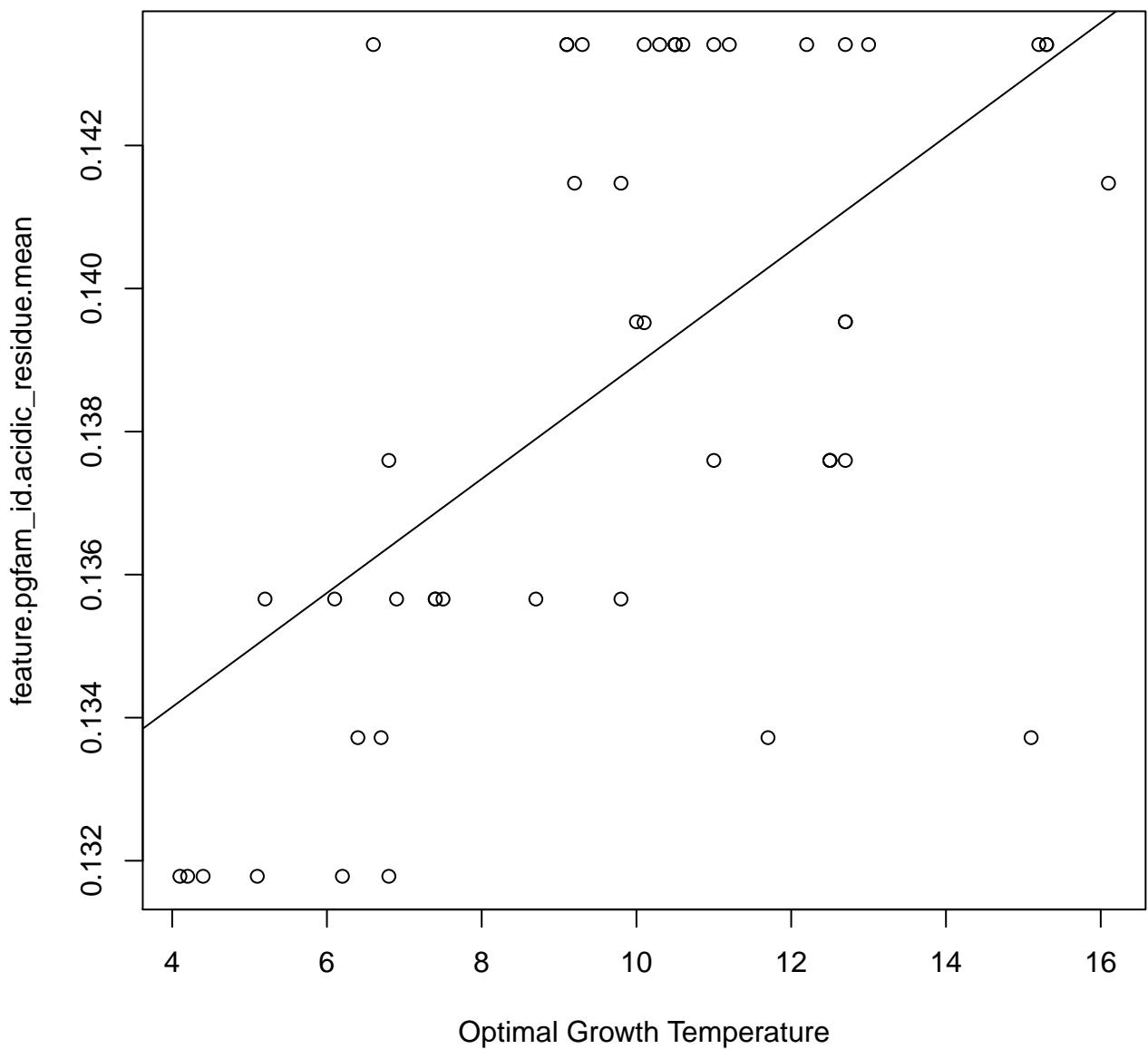
feature.pgfam_id.acidic_residue.mean
PGF_00011990
Histidinol-phosphatase (EC 3.1.3.15) / Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)



feature.pgfam_id.acidic_residue.mean
PGF_03074033
FIG020302: hypothetical protein



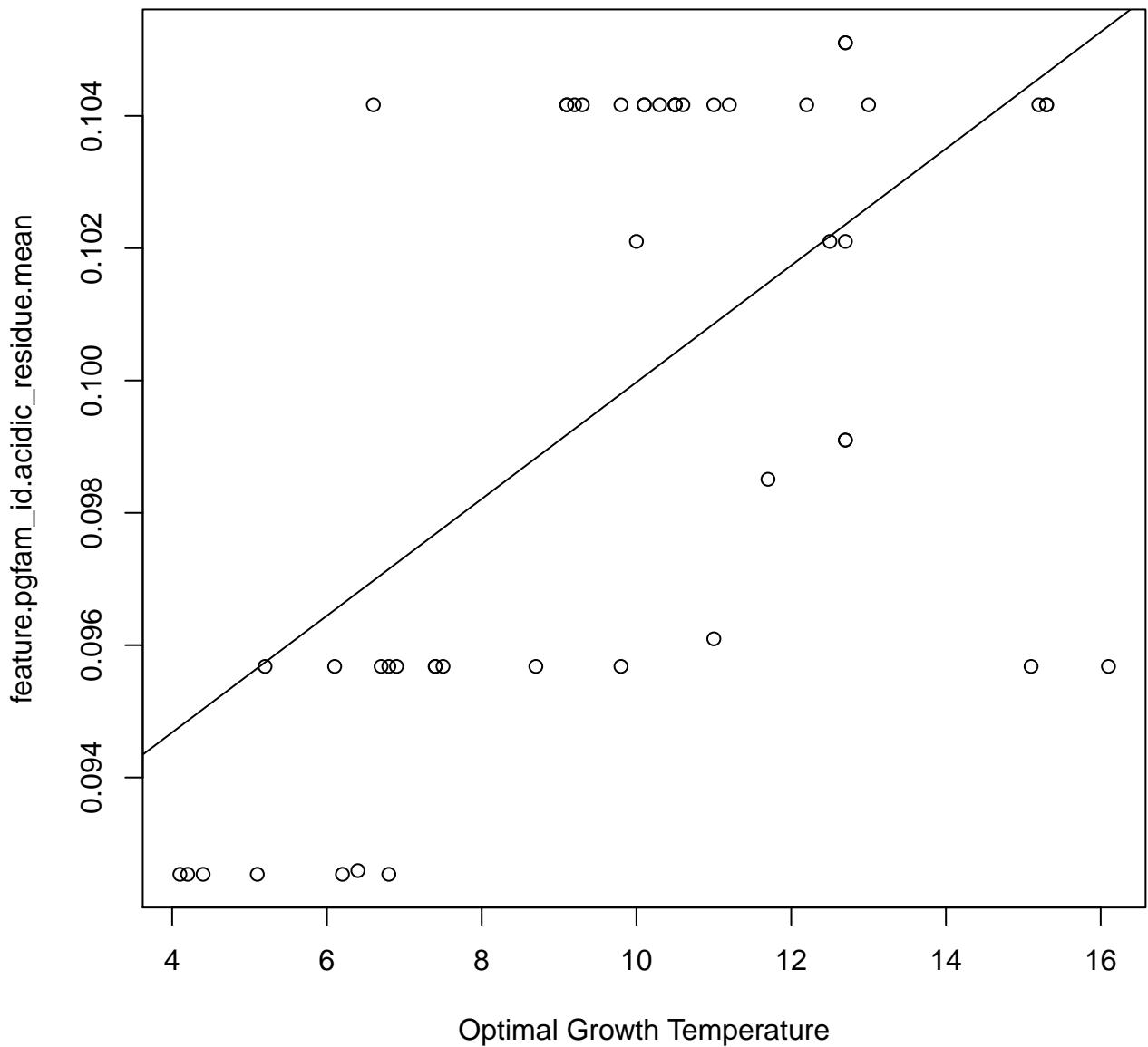
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PGF_00060289
Transcriptional repressor protein TyrR



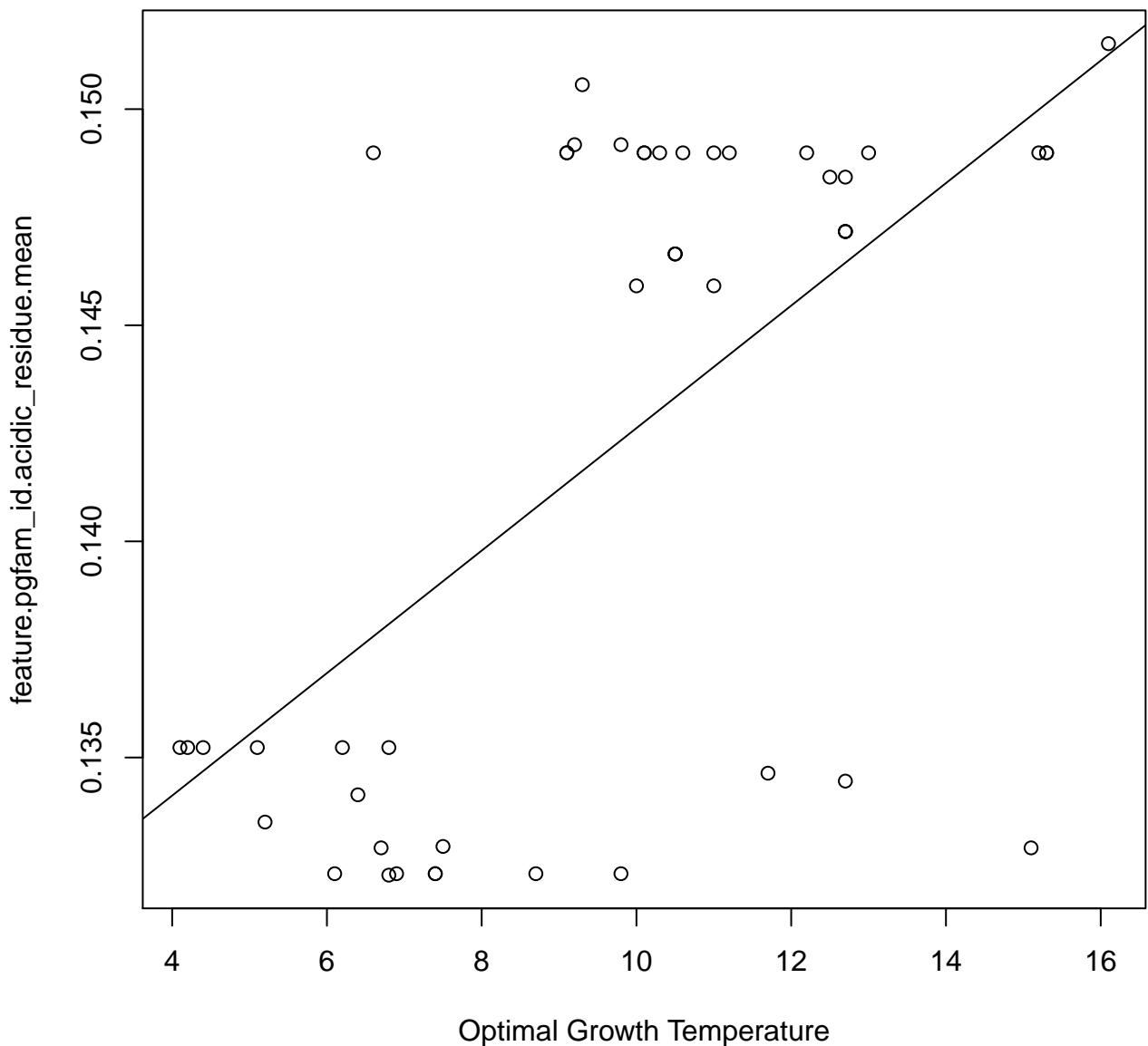
feature.pgfam_id.acidic_residue.mean

PGF_04486278

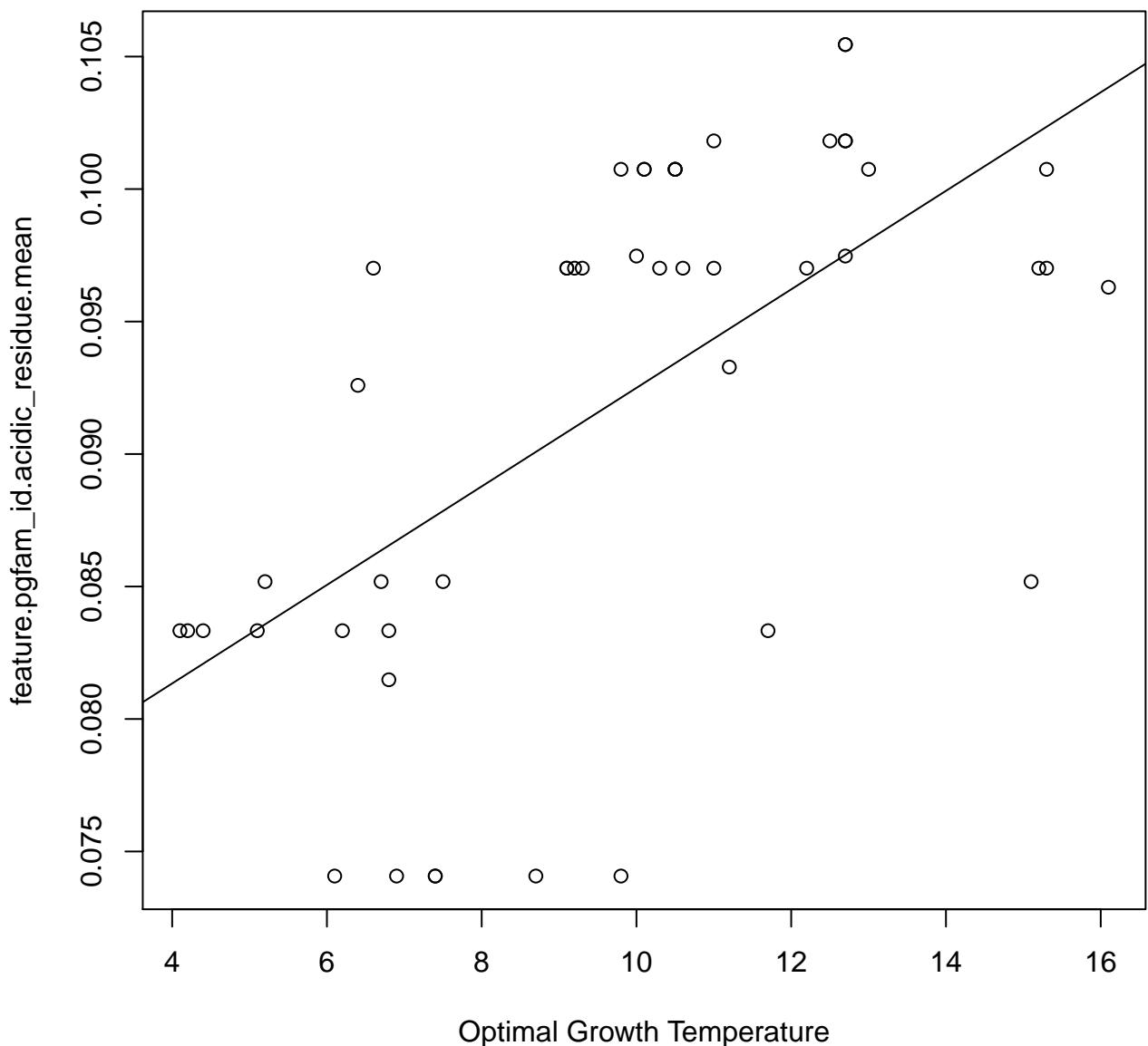
Biotin operon repressor / Biotin--protein ligase (EC 6.3.4.9)(EC 6.3.4.10)(EC 6.3.4.11)(EC 6.3.4.15)



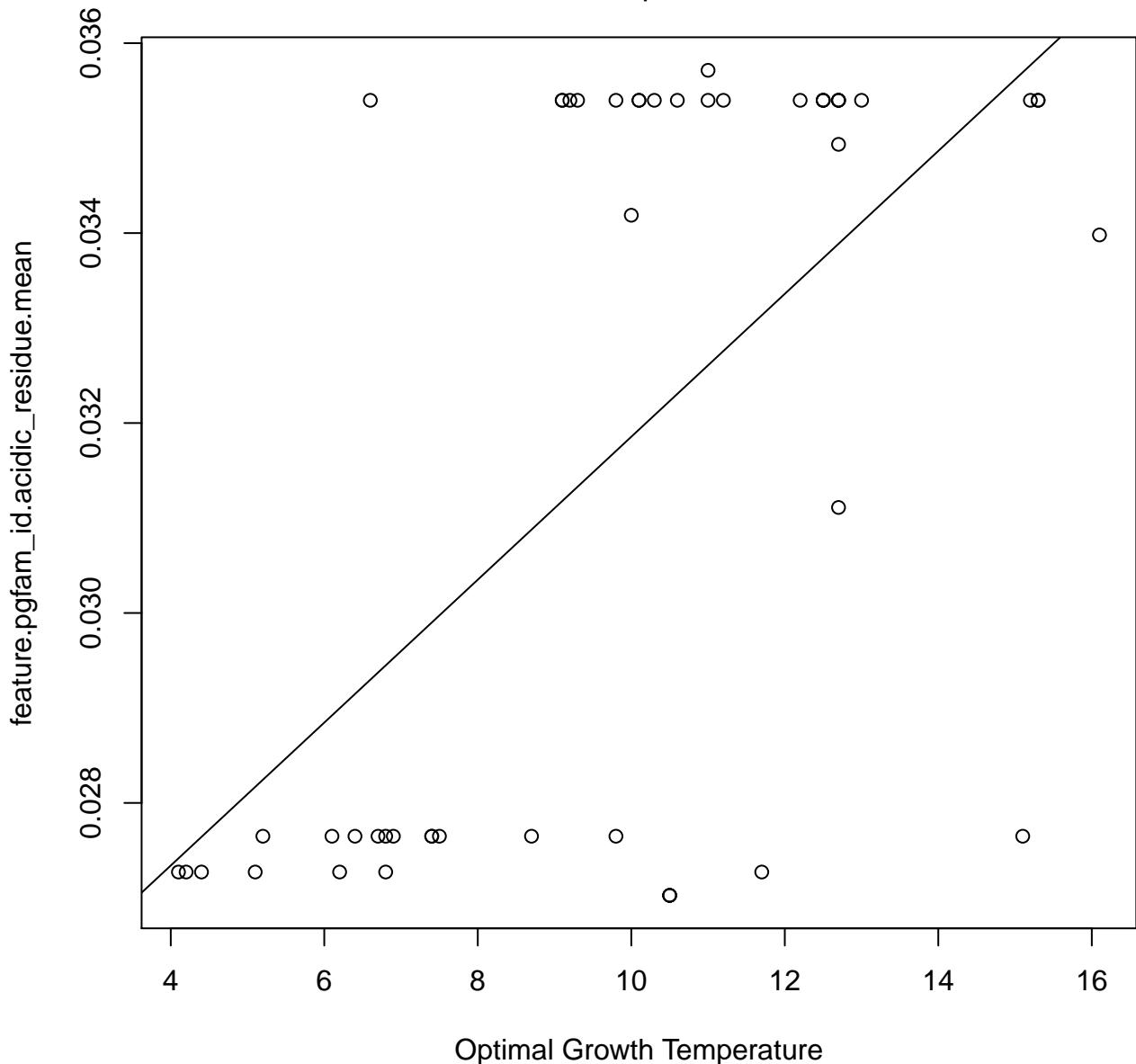
feature.pgfam_id.acidic_residue.mean
PGF_05438553
Phosphoenolpyruvate synthase (EC 2.7.9.2)



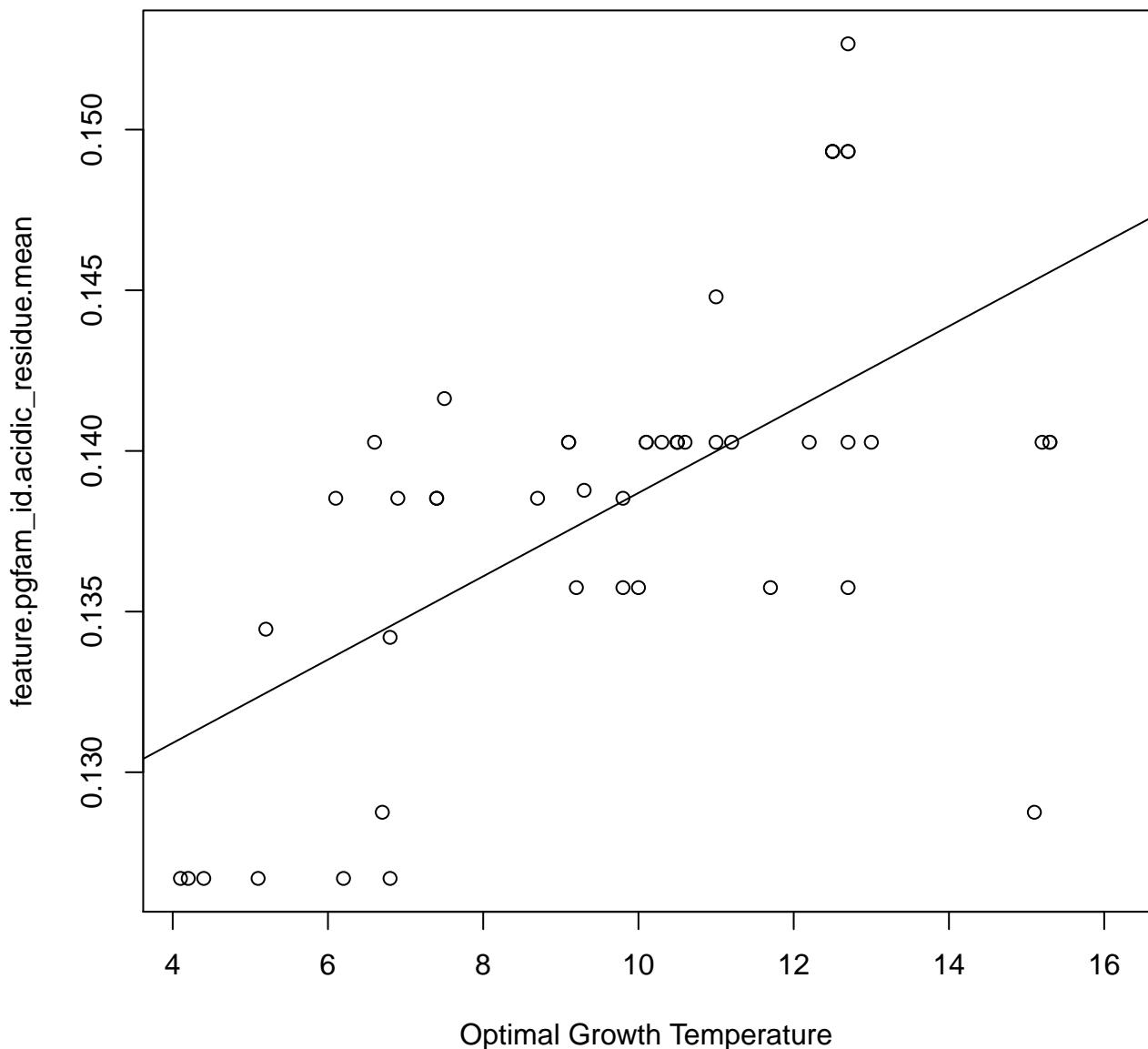
feature.pgfam_id.acidic_residue.mean
PGF_08181546
Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)



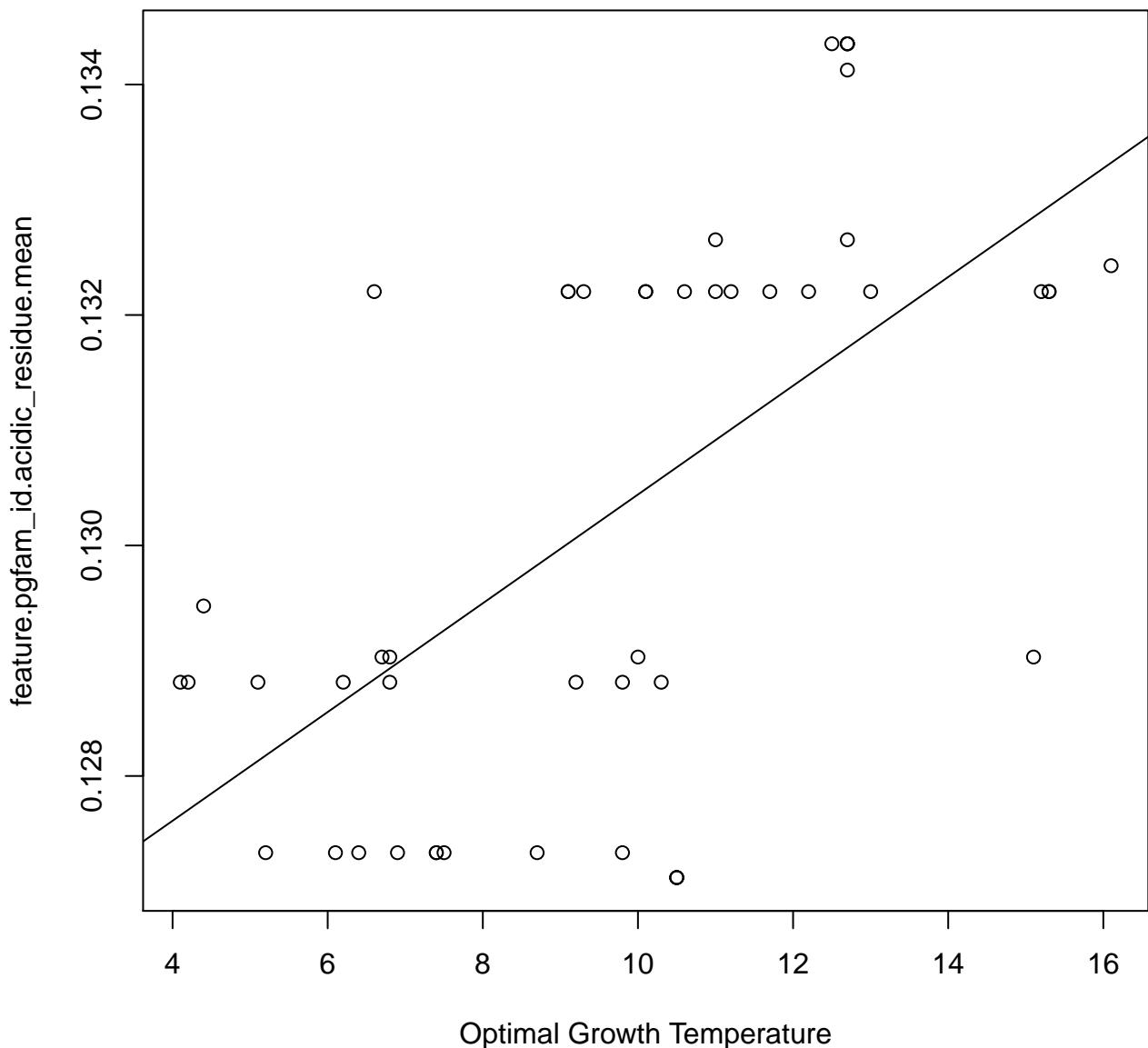
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PGF_00056952
Tlr1621 protein



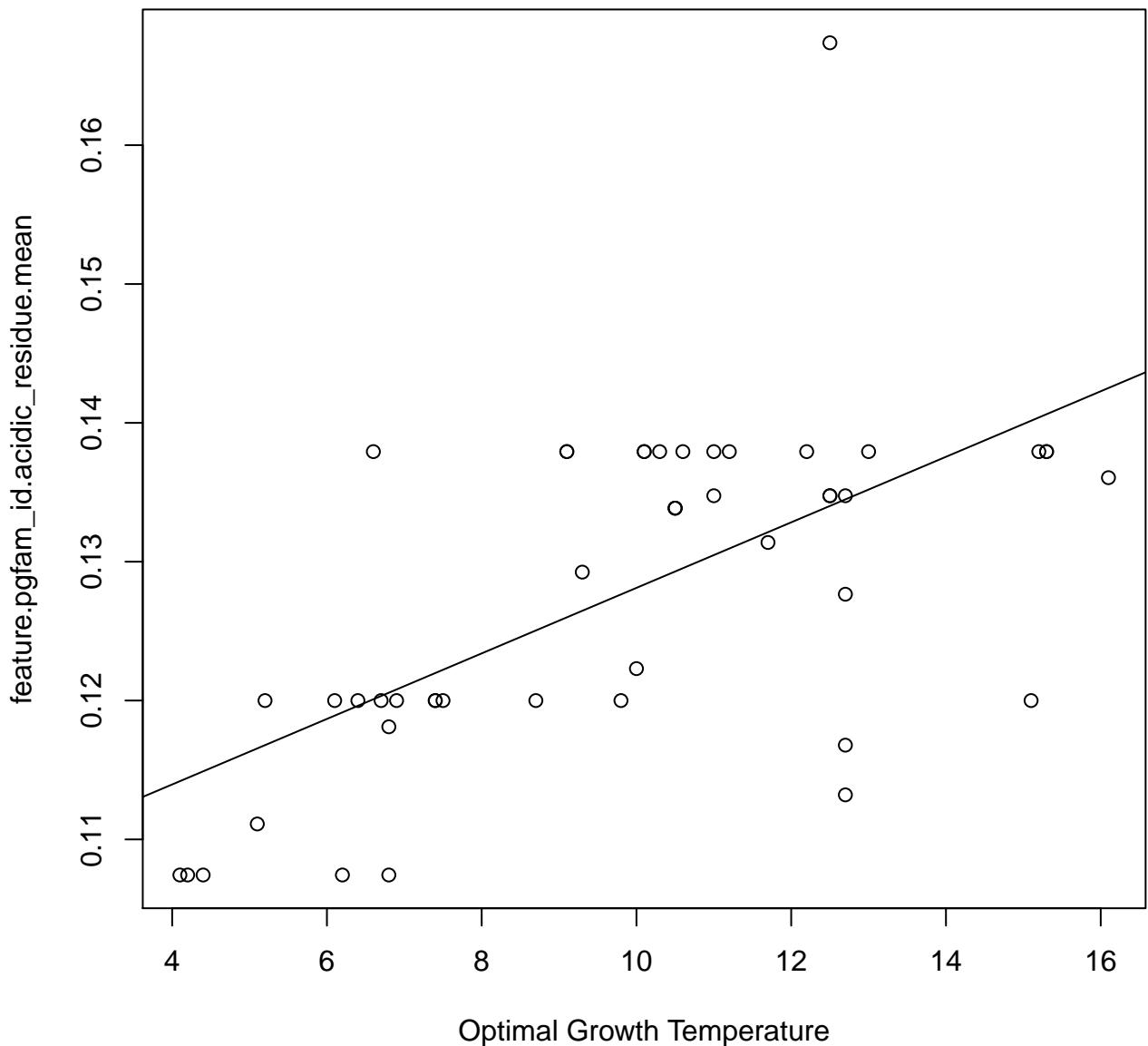
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PGF_00038573
Protein of unknown function YceH



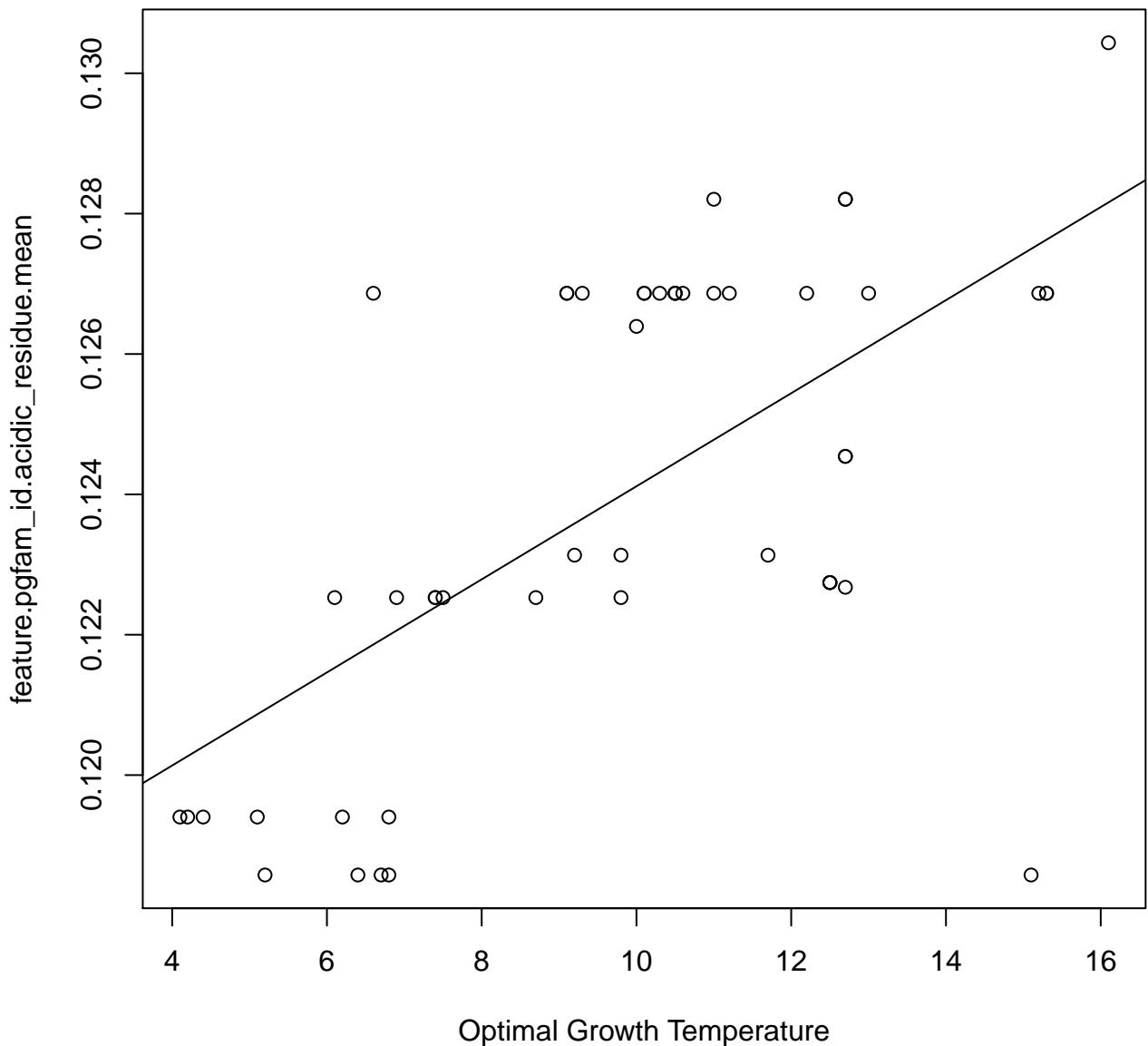
feature.pgfam_id.acidic_residue.mean
PGF_08998238
Succinate dehydrogenase flavoprotein subunit (EC 1.3.5.1)



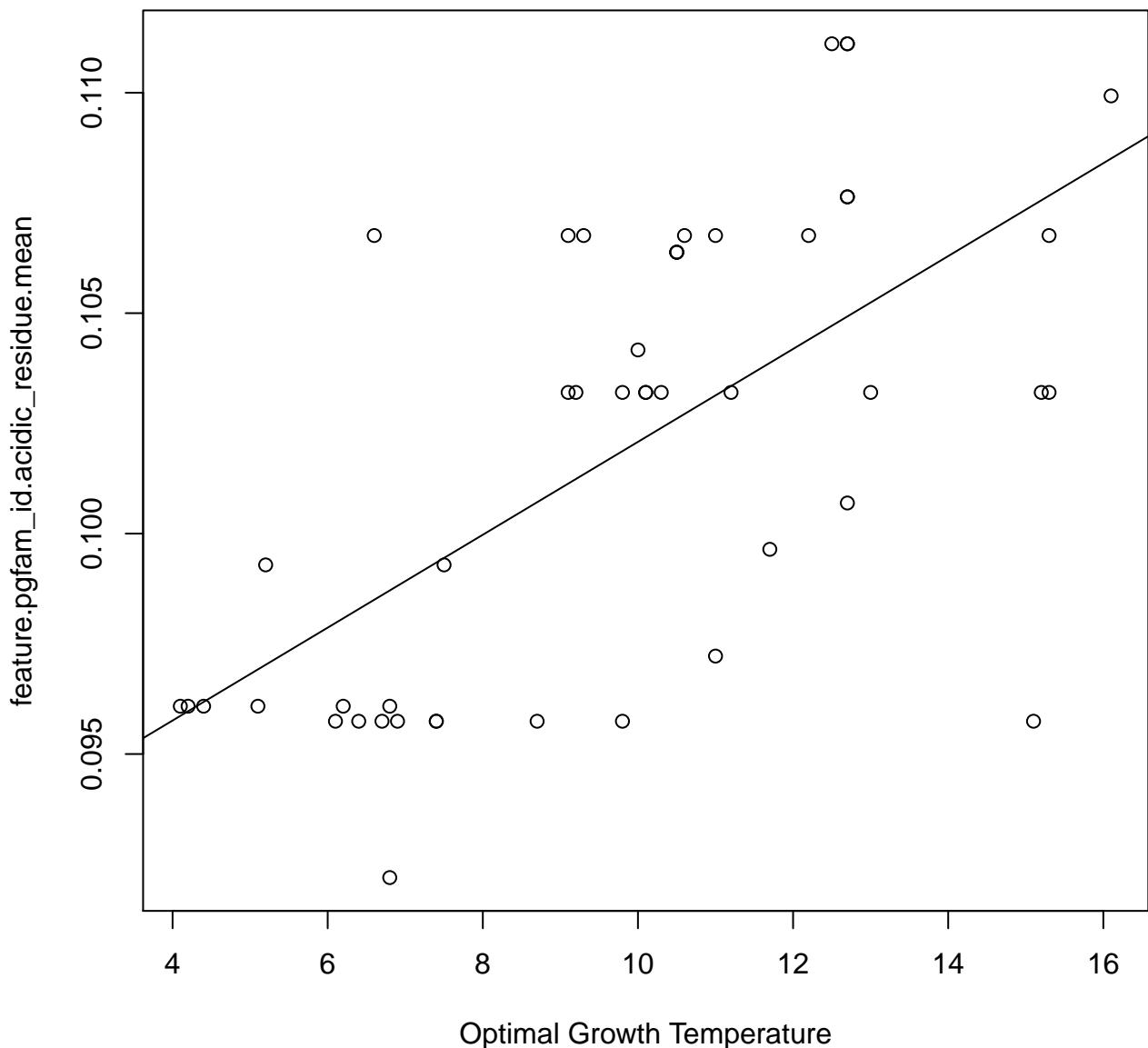
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PGF_00002863
FIG024746: hypothetical protein



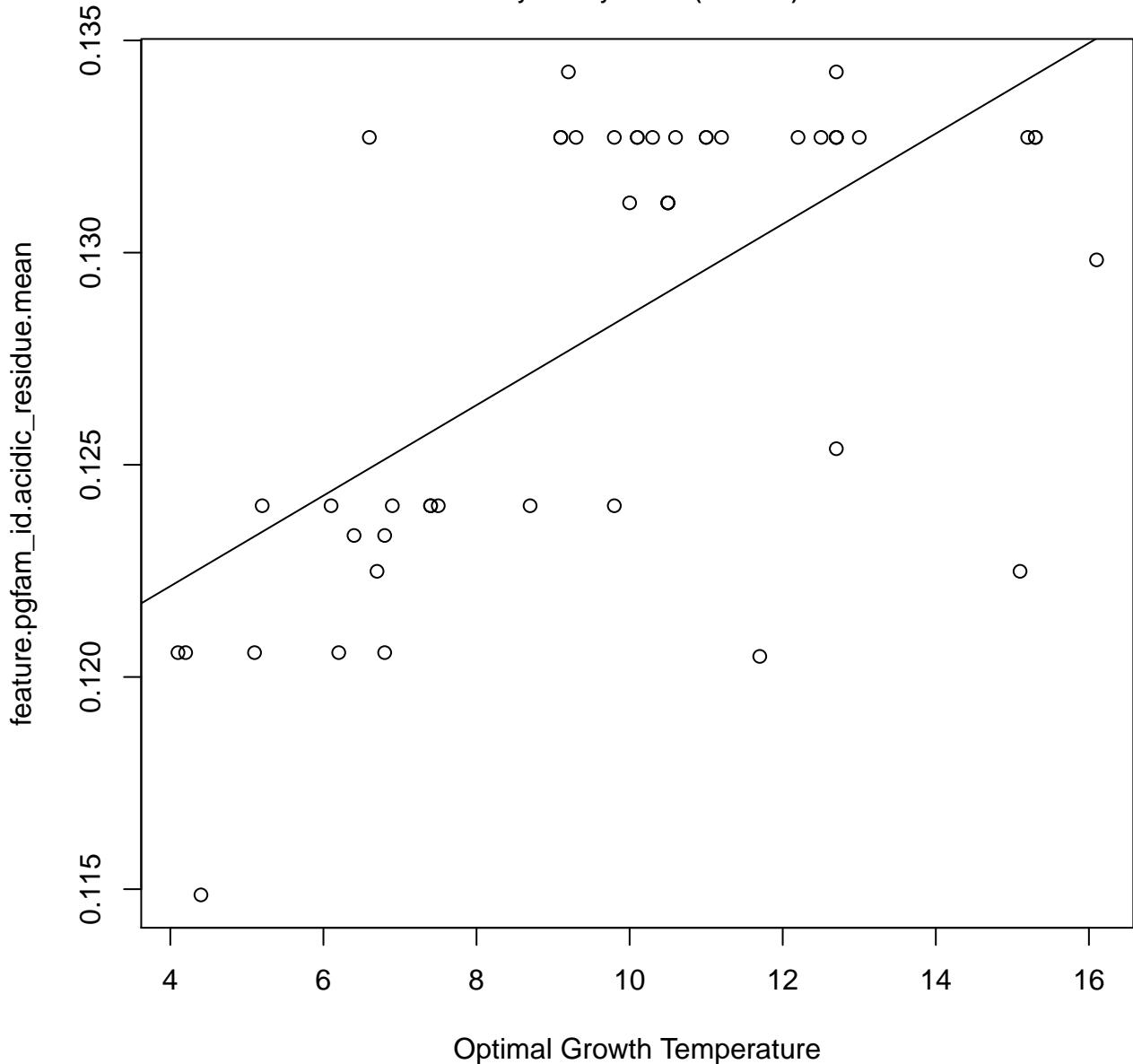
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PGF_02473279
tRNA (cytidine(32)/uridine(32)-2'-O)-methyltransferase (EC 2.1.1.200)



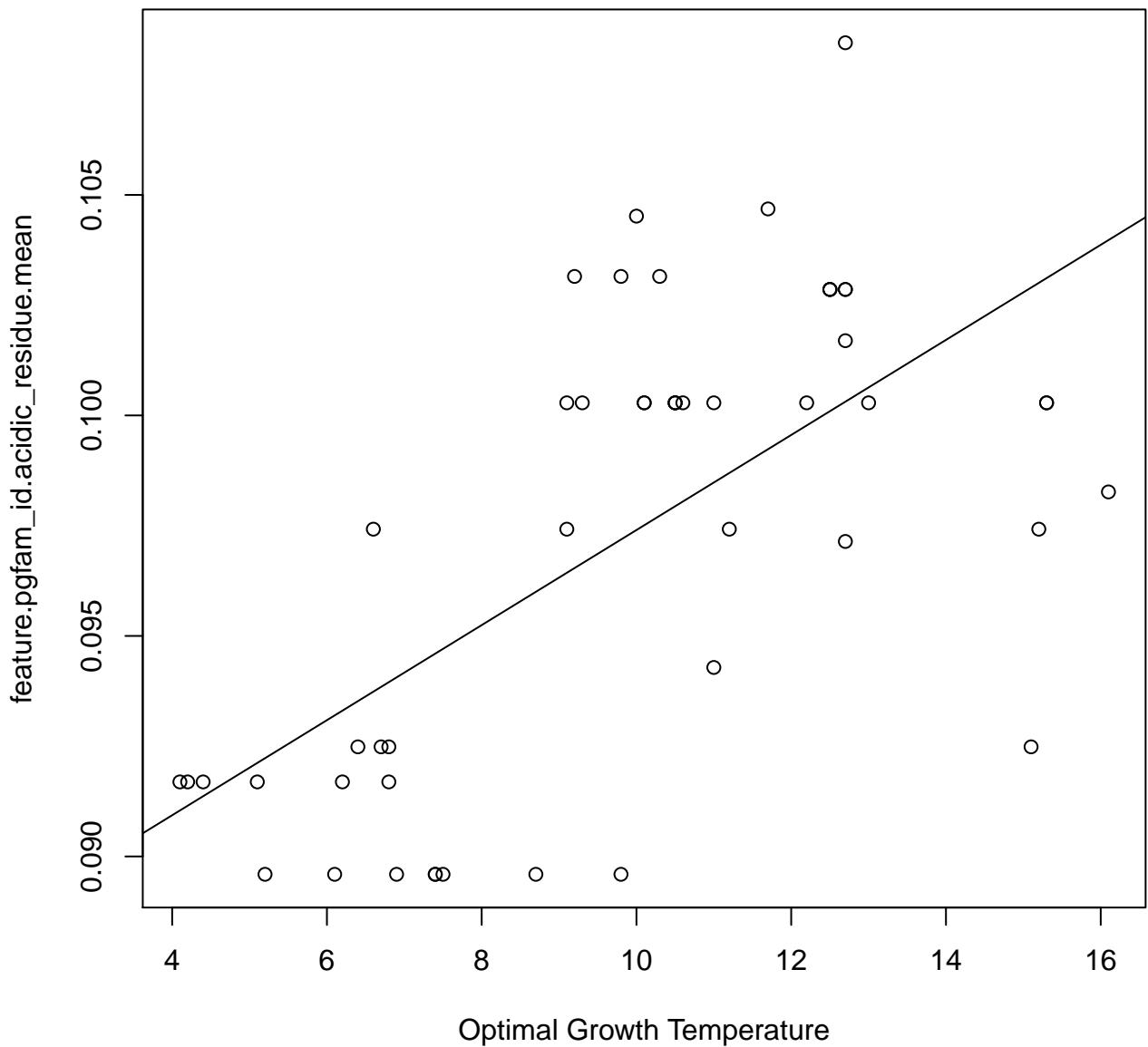
feature.pgfam_id.acidic_residue.mean
PGF_00523822
Pantoate--beta-alanine ligase (EC 6.3.2.1)



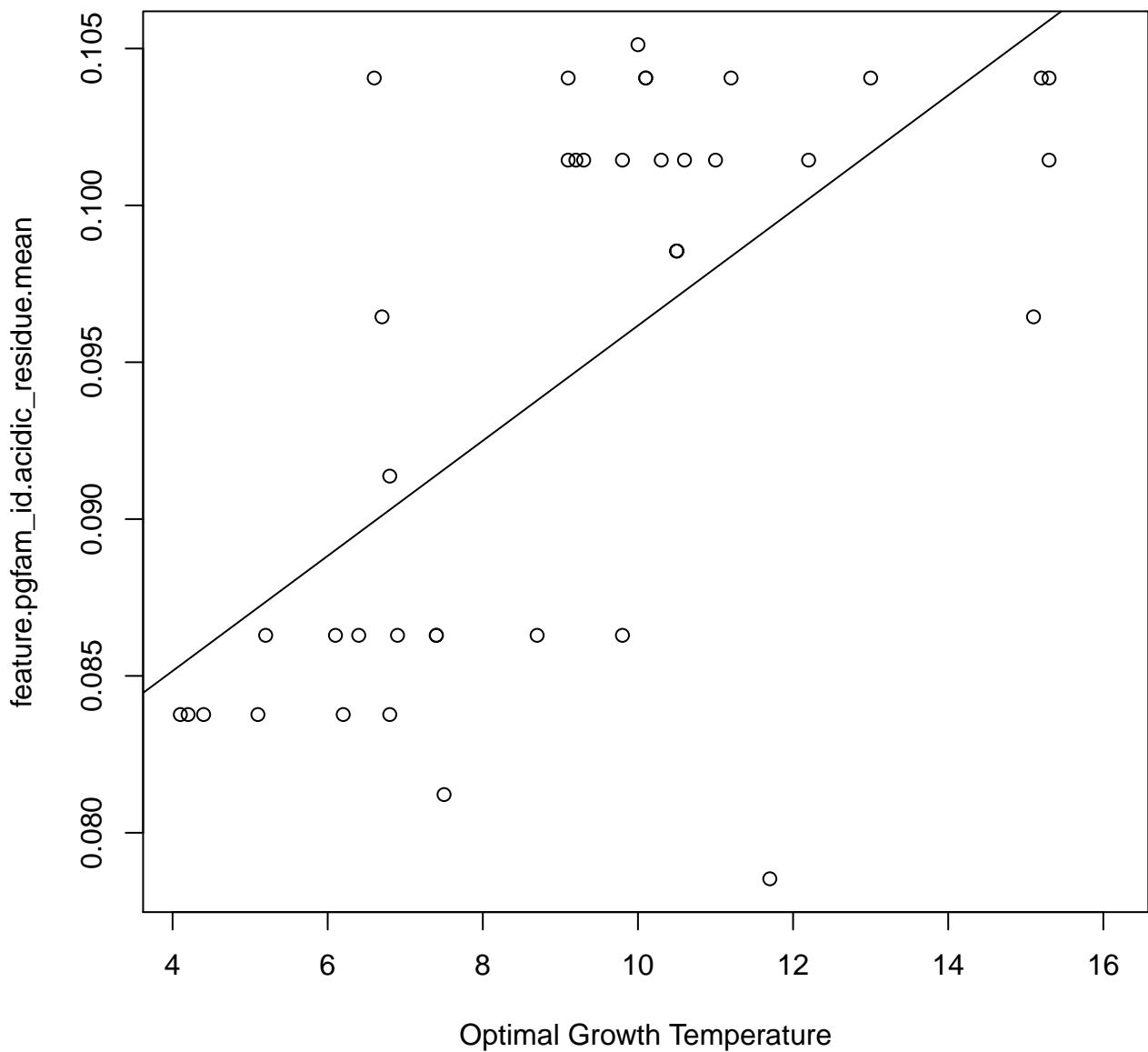
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PGF_10523783
Acetyl-CoA synthetase (EC 6.2.1.1)



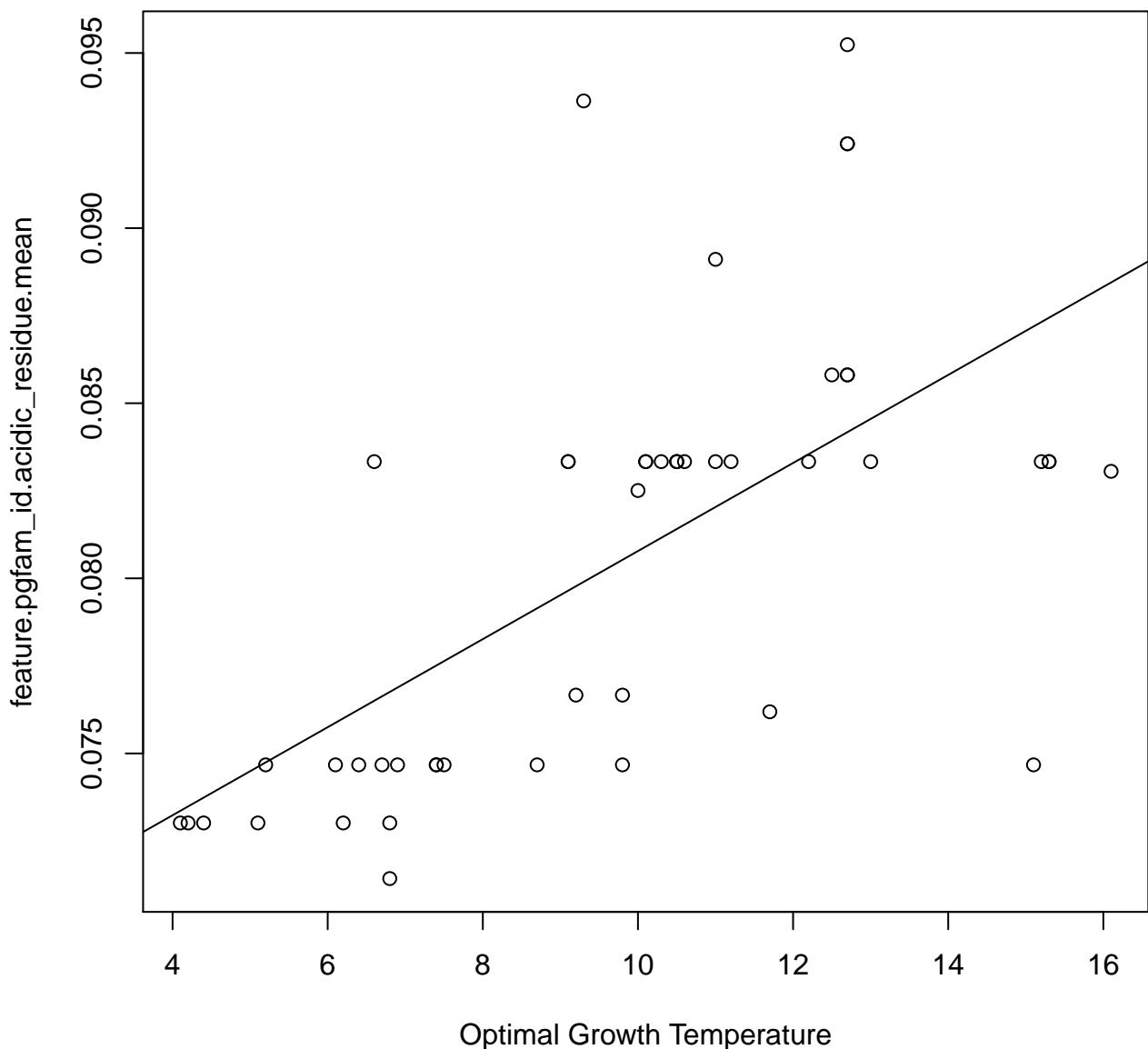
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PGF_03048579
hypothetical protein



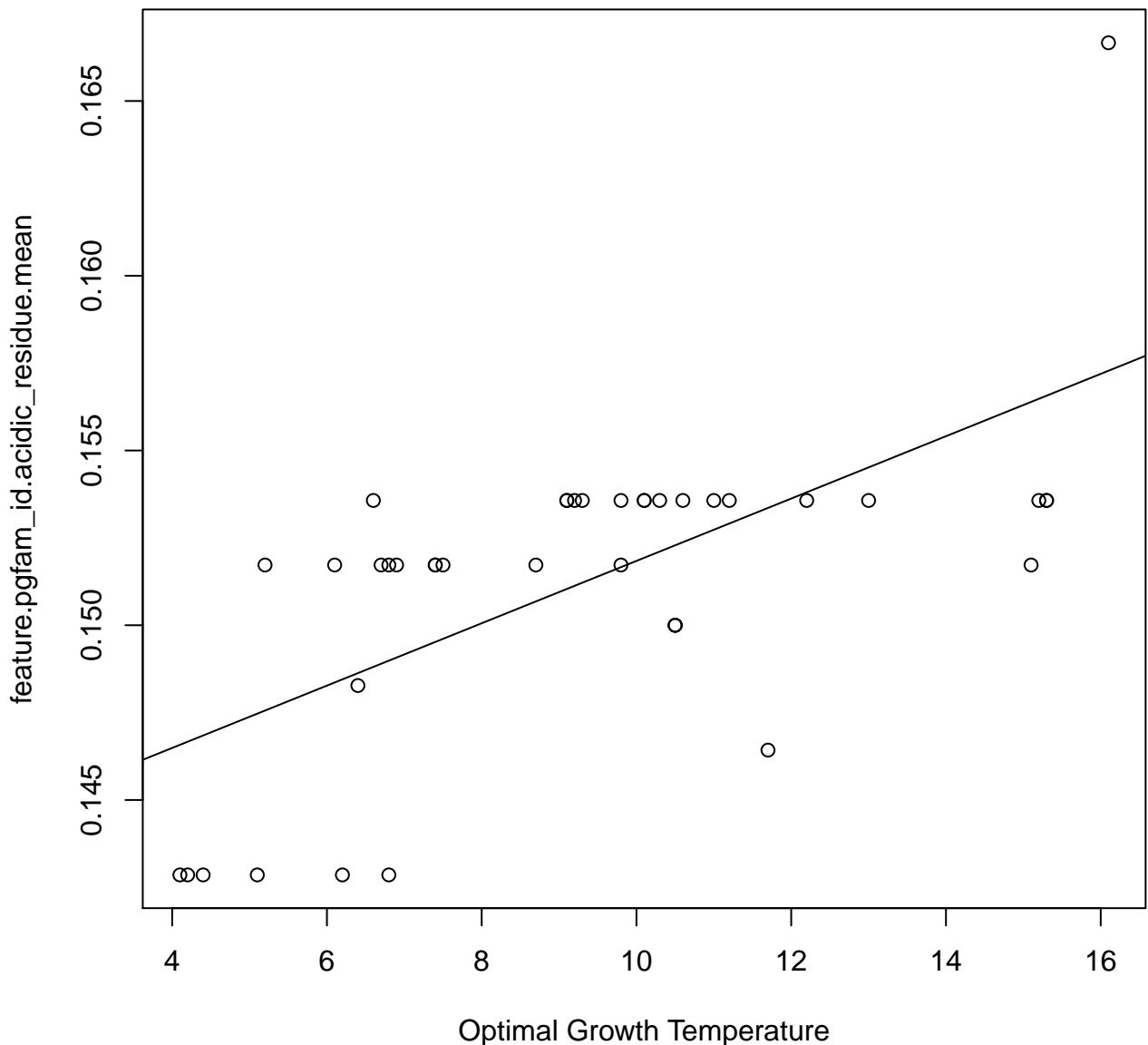
feature.pgfam_id.acidic_residue.mean
PGF_01338555
hypothetical protein



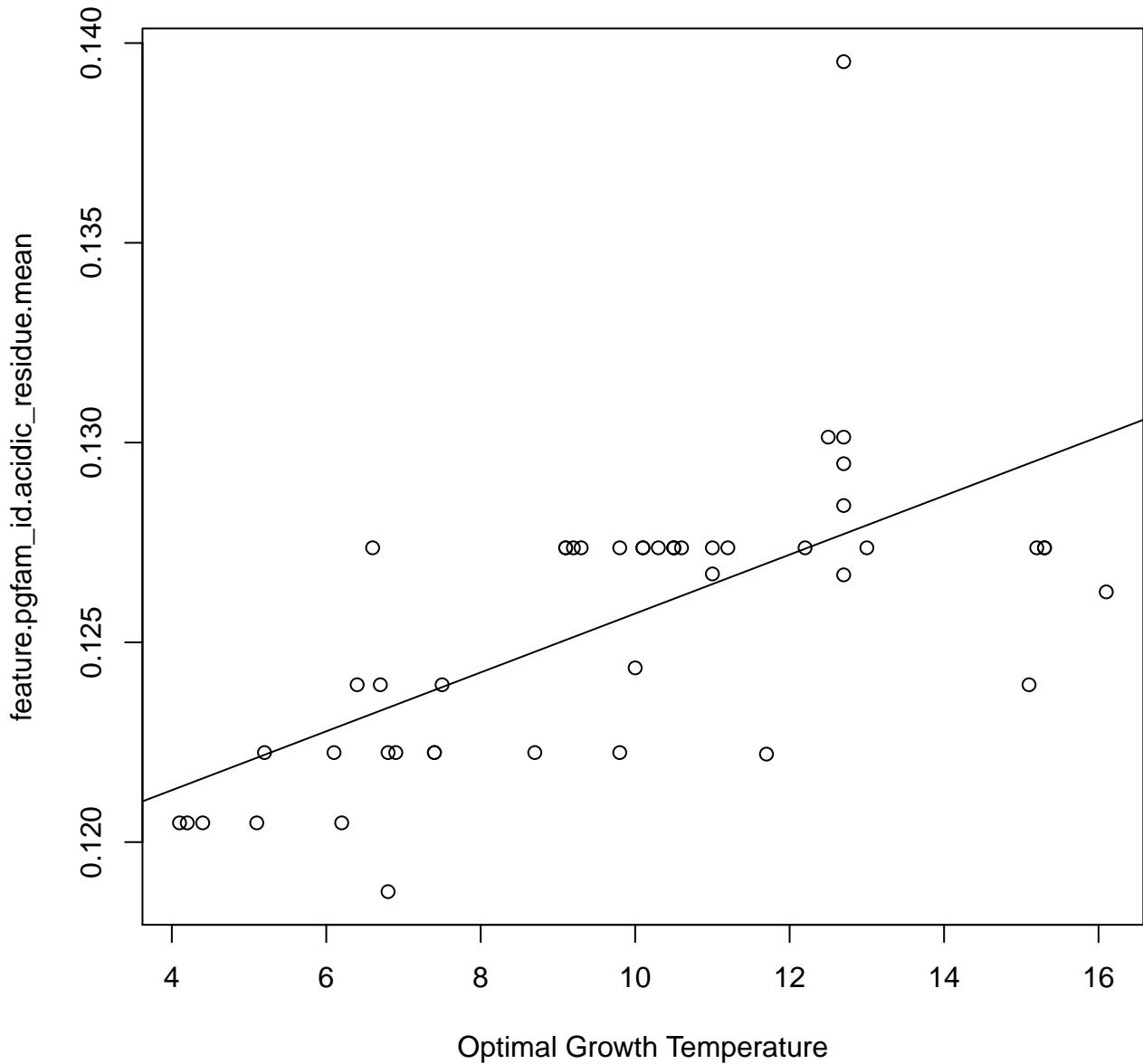
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PGF_05546469
Probable acyltransferase PA0834



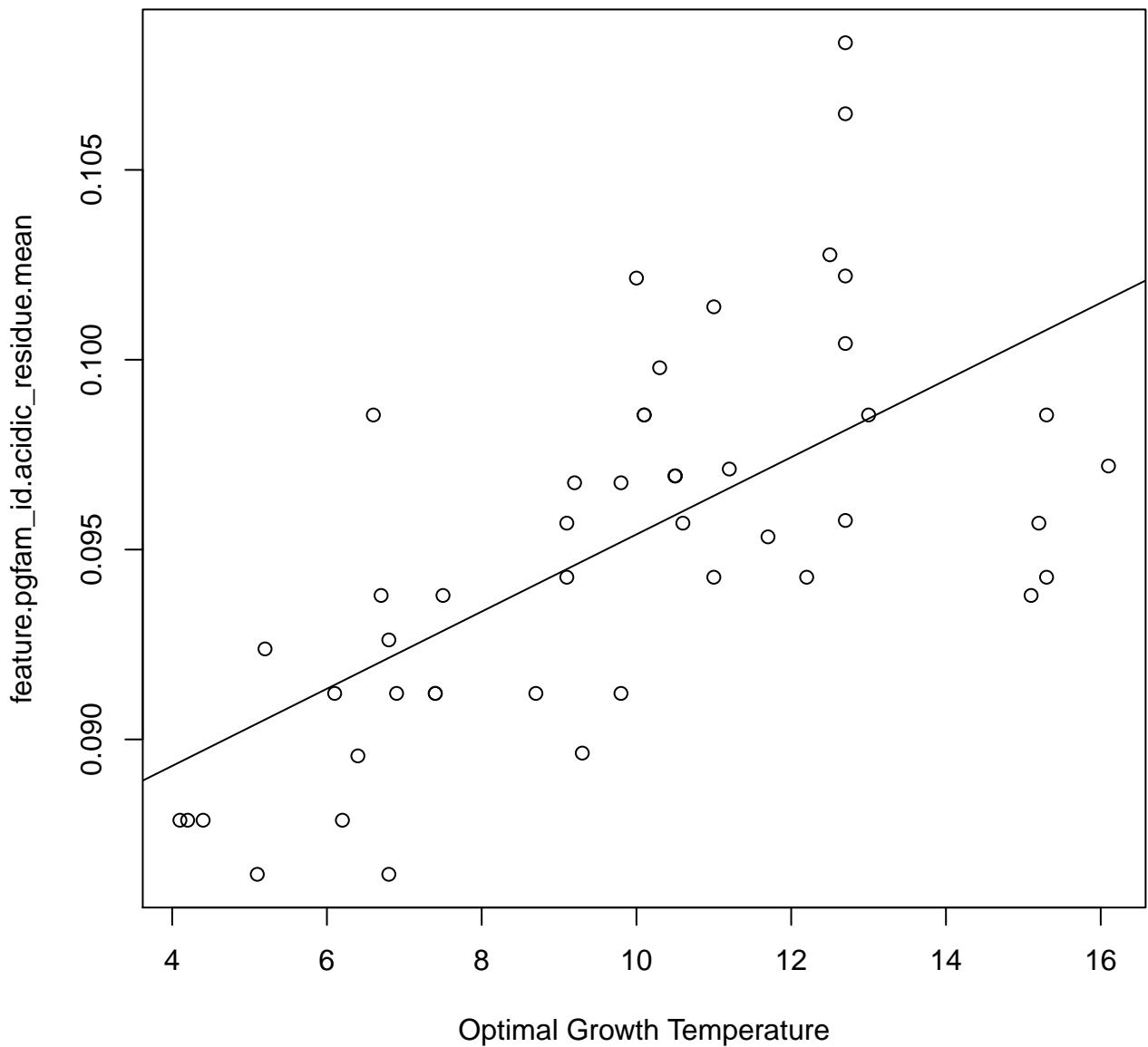
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PGF_02517283
Segregation and condensation protein A



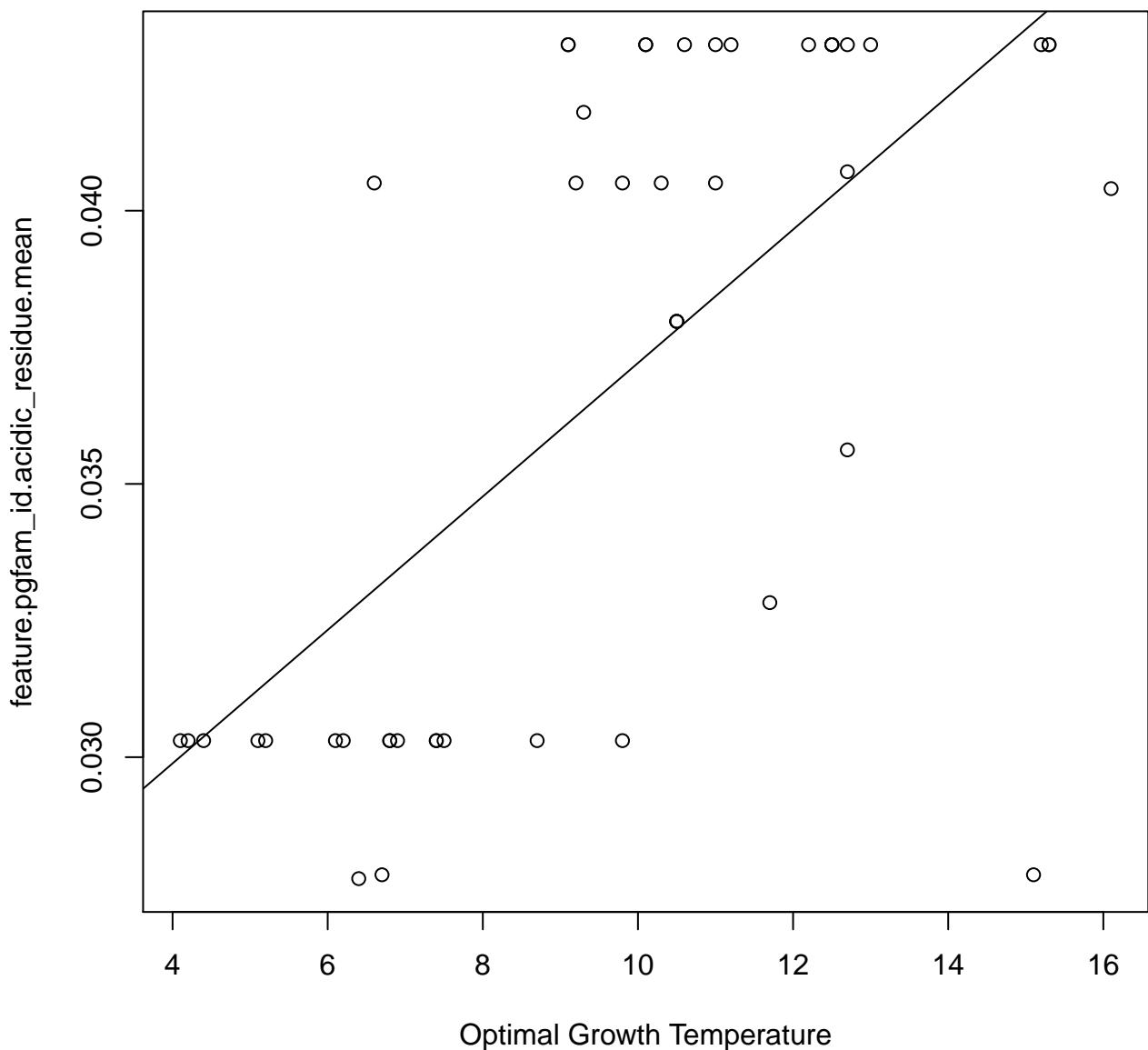
feature.pgfam_id.acidic_residue.mean
PGF_07058357
Single-stranded-DNA-specific exonuclease RecJ



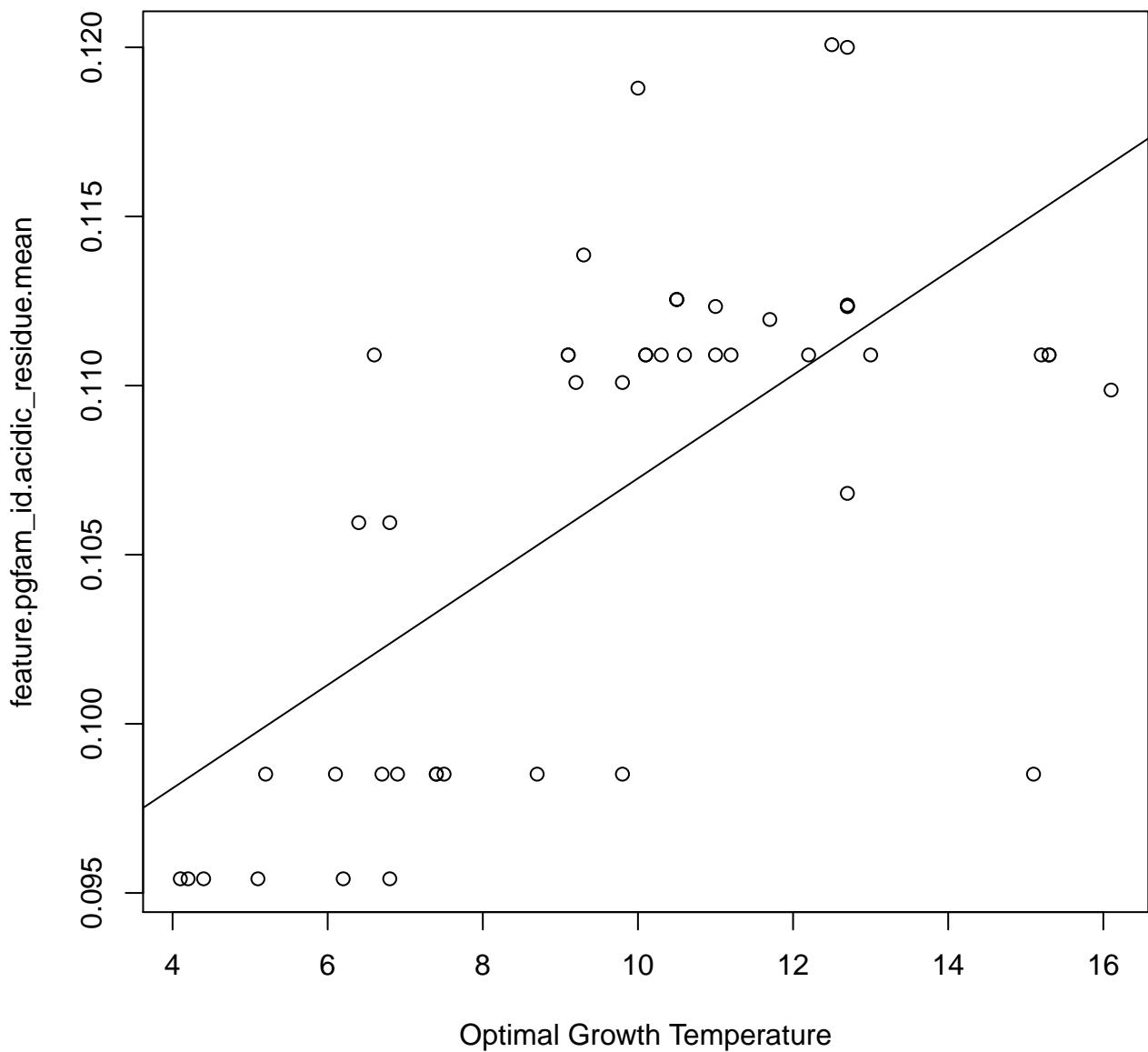
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PGF_03116630
Membrane-bound lytic murein transglycosylase B



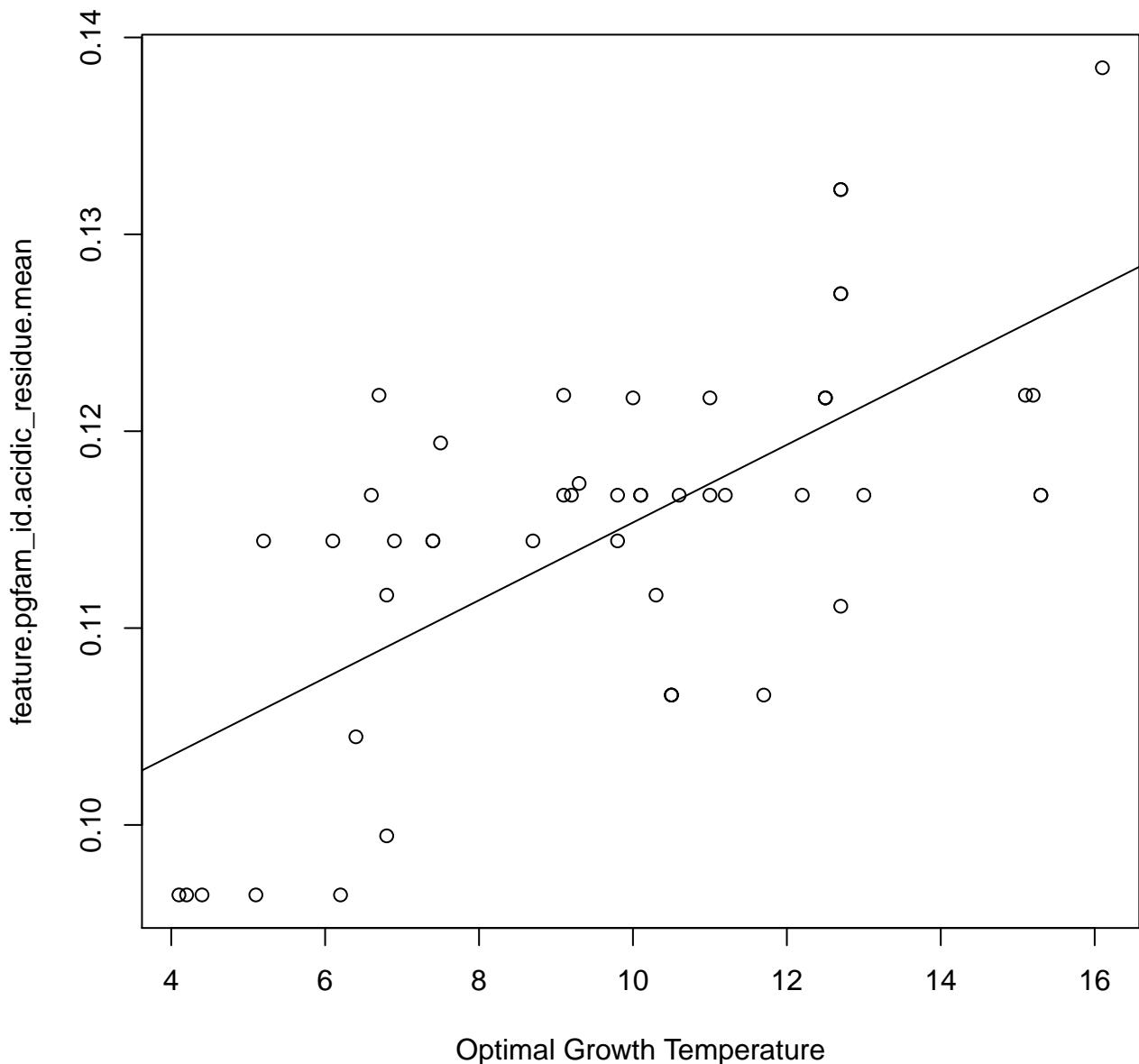
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PGF_00755593
Uncharacterized MFS-type transporter



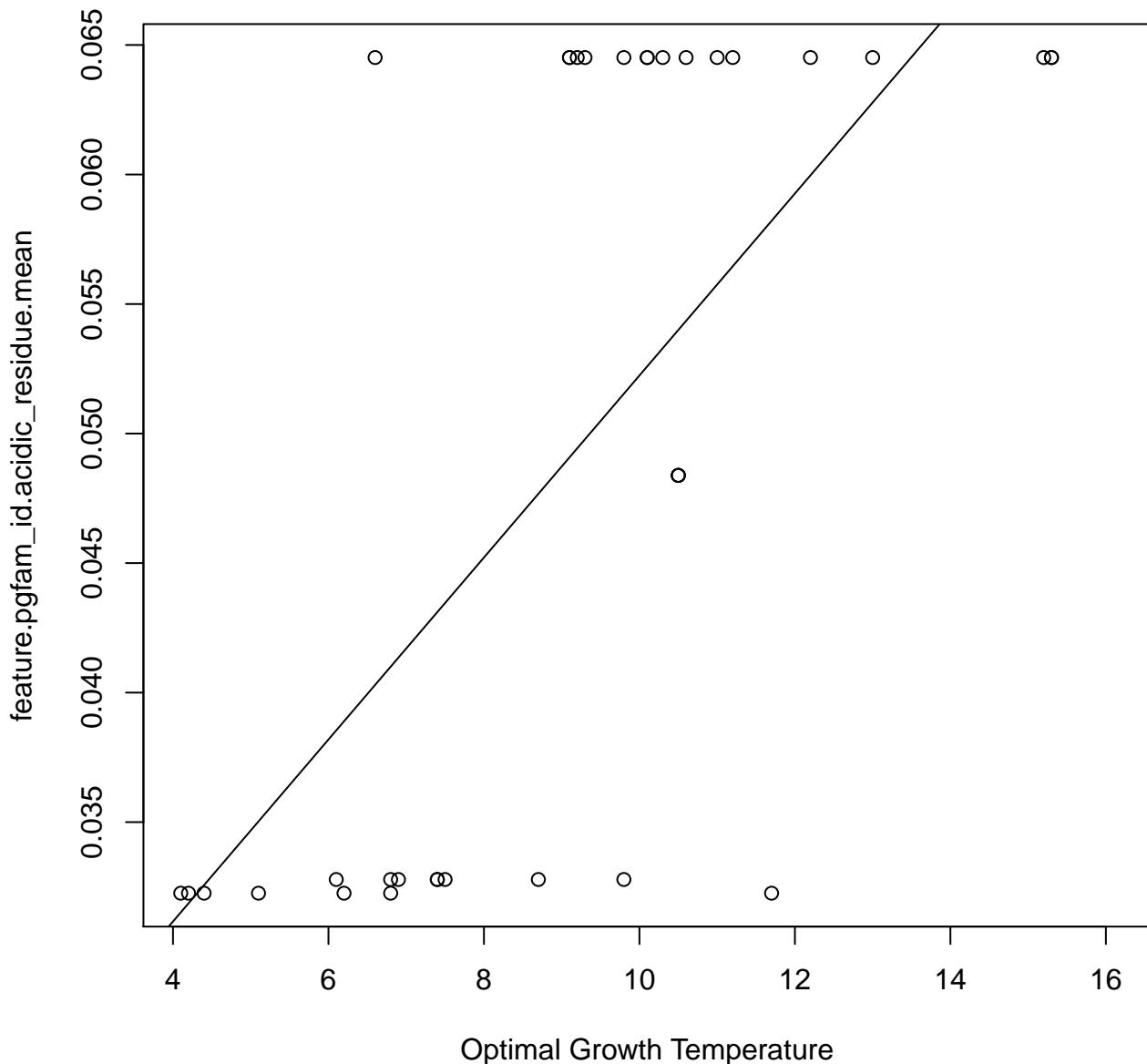
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PGF_01763633
Sensory box histidine kinase



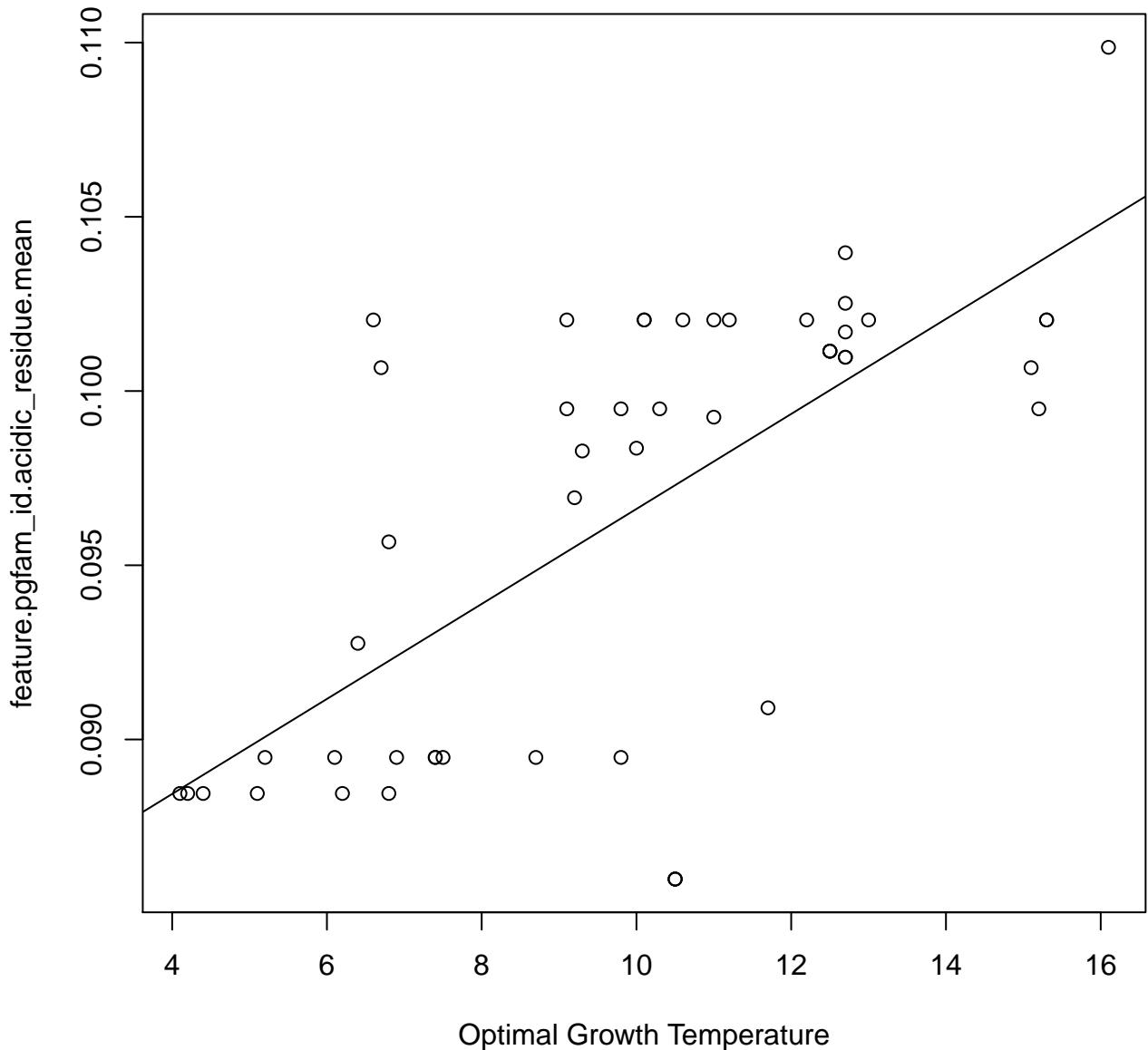
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PGF_00423914
1,6-anhydro-N-acetylMuramyl-L-alanine amidase



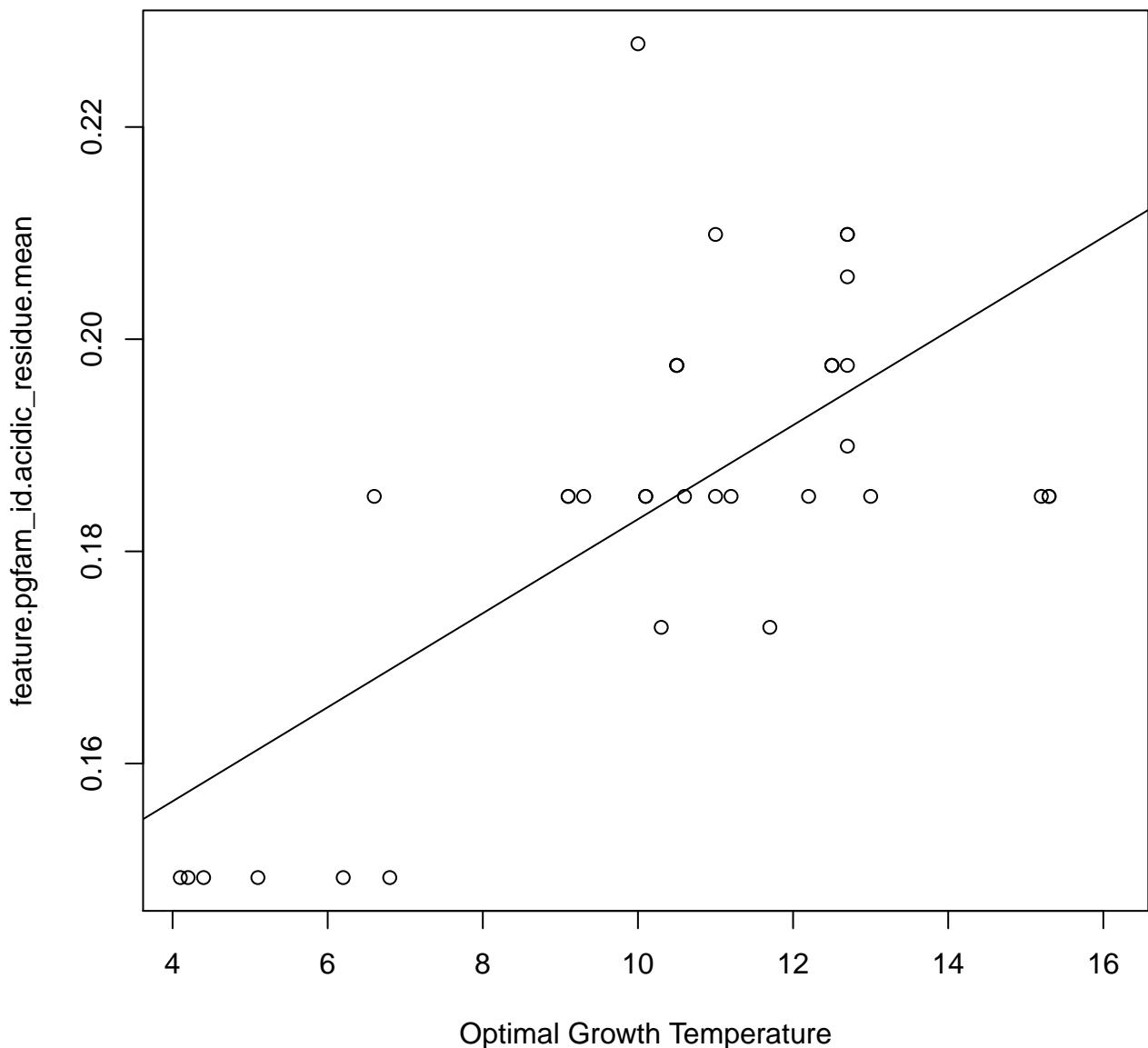
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PGF_07991944
hypothetical protein



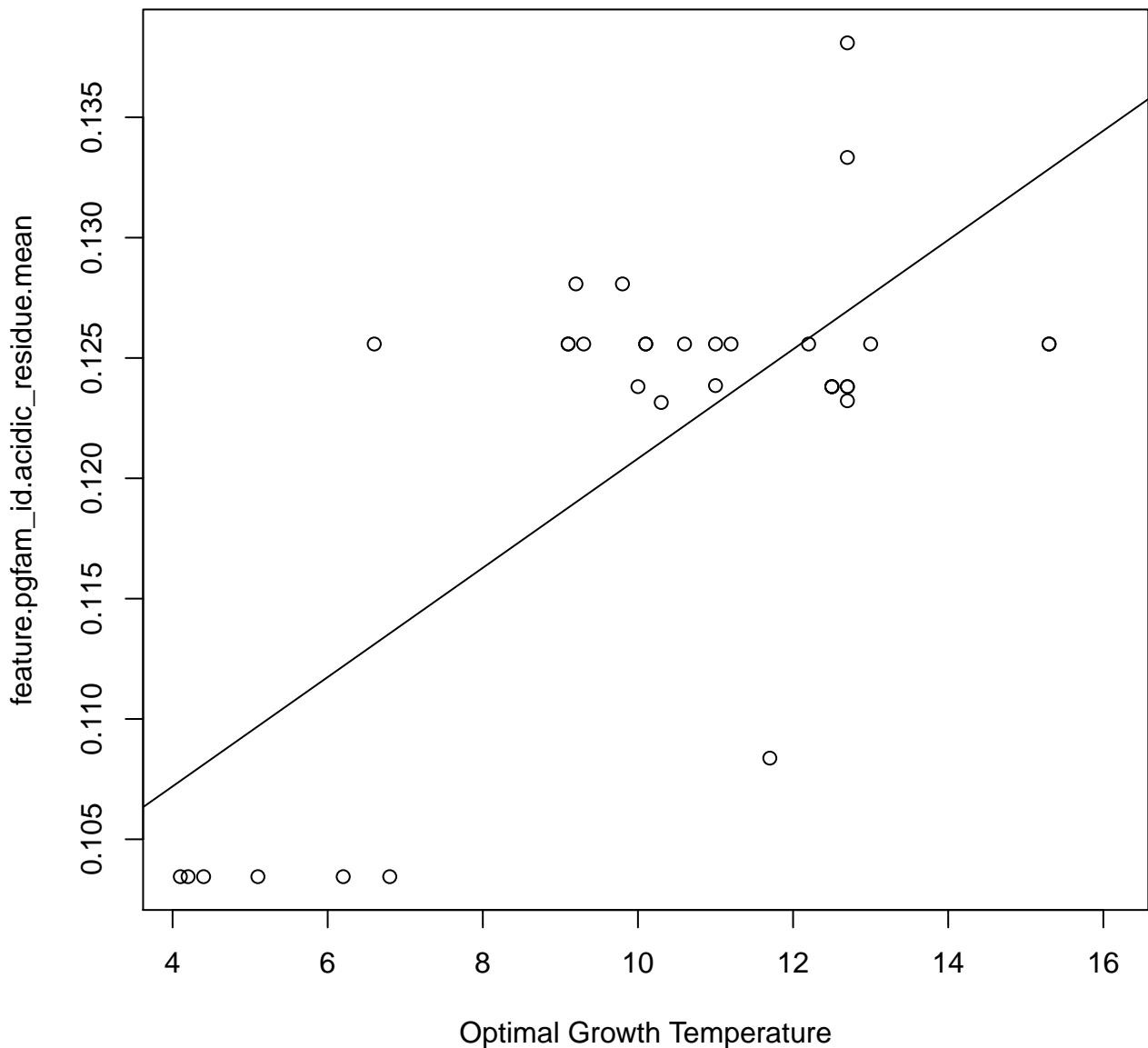
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PGF_02328856
Type IV pilus biogenesis protein PilF



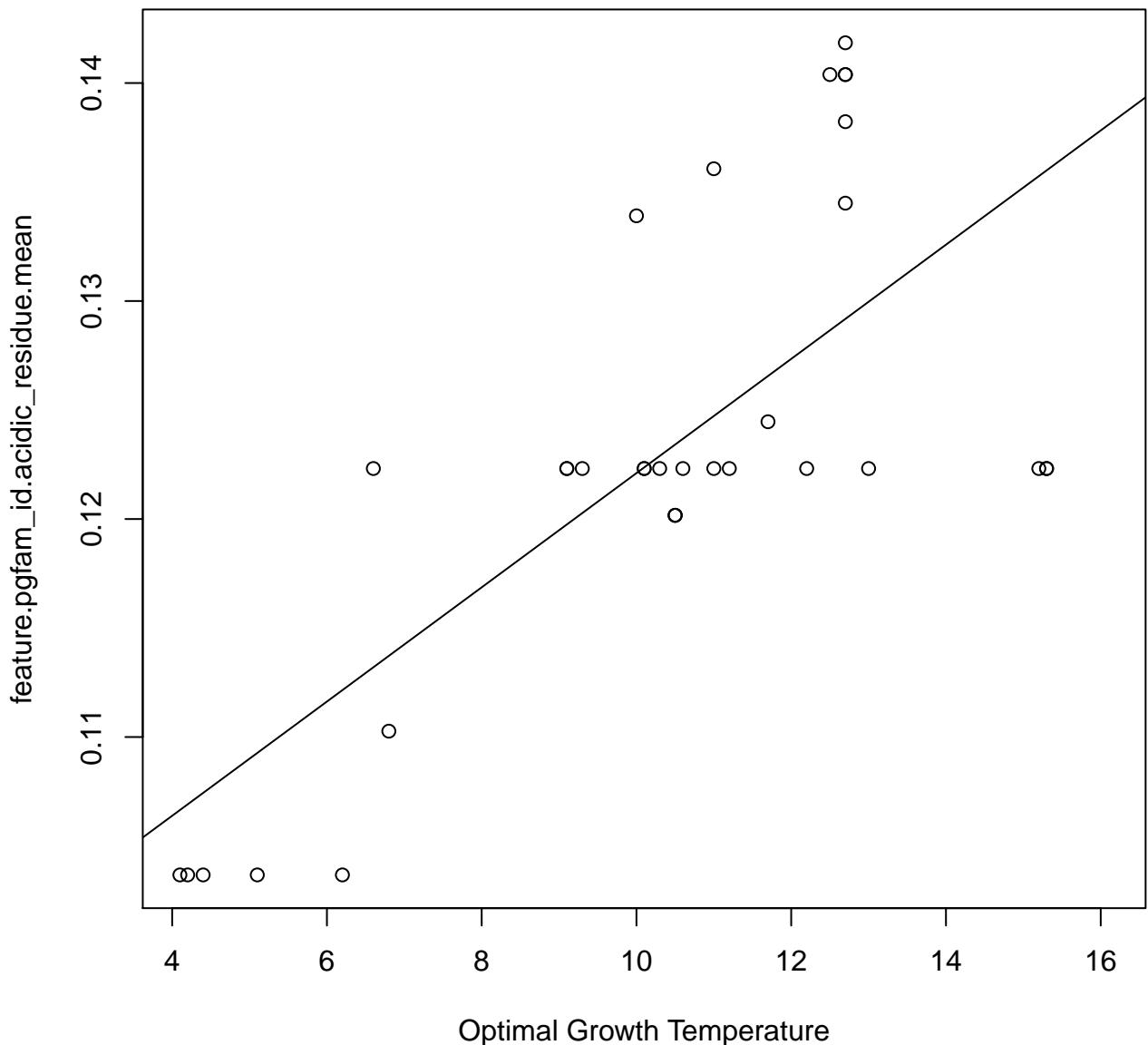
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PGF_00064685
Uncharacterized ferredoxin-like protein YfhL



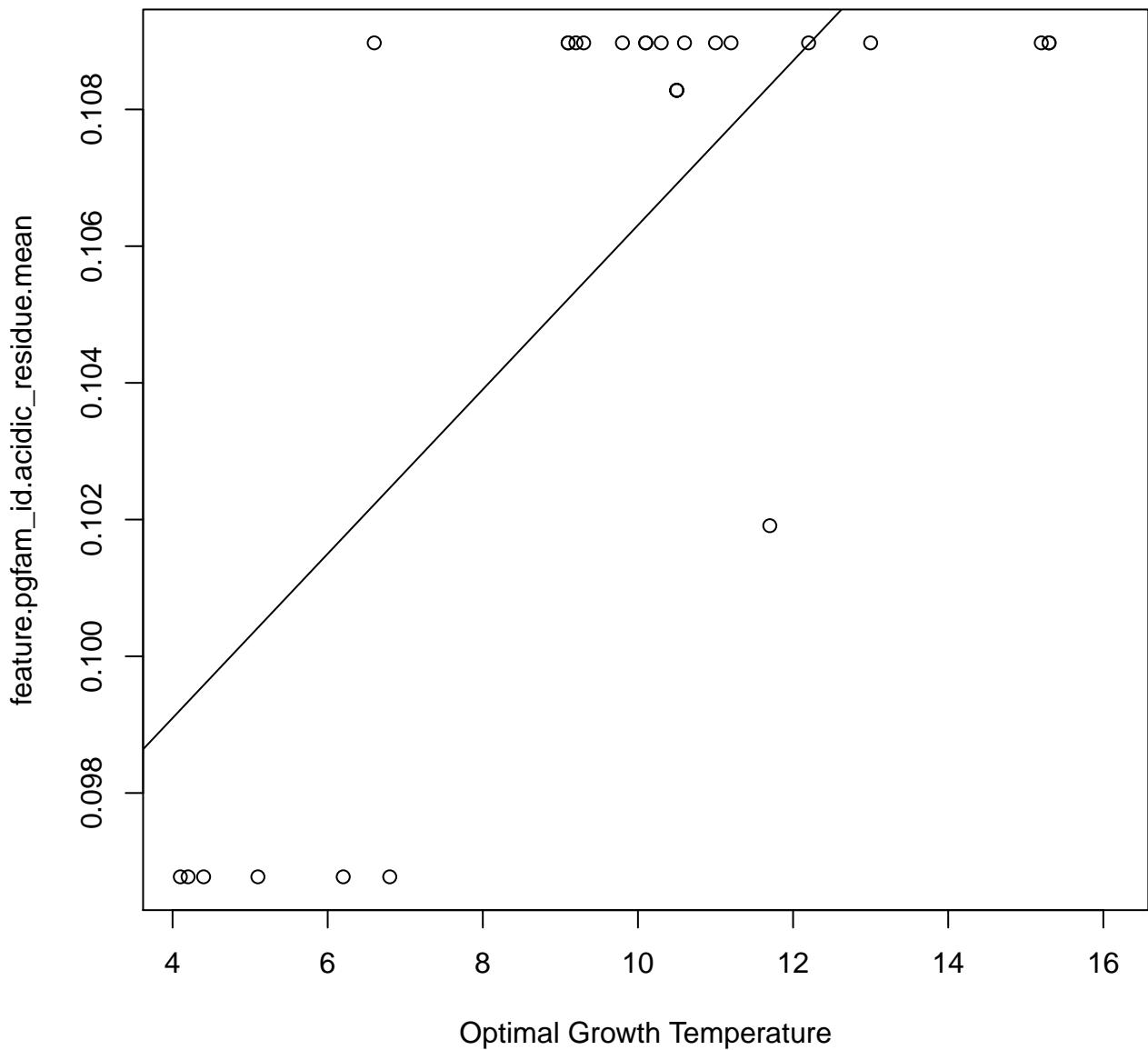
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PGF_03940803
Alkylated DNA repair protein



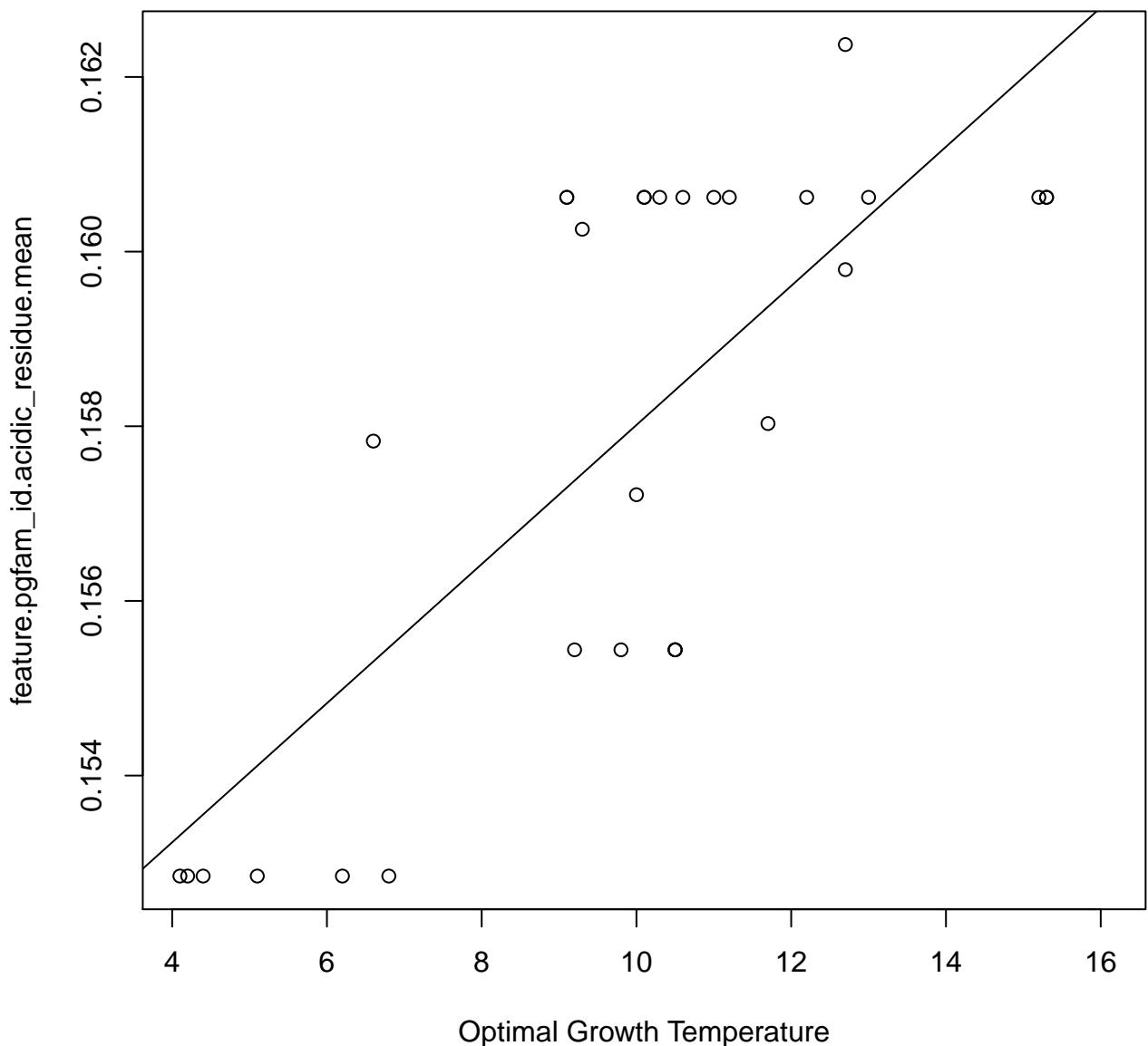
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PGF_02105064
Uncharacterized protease YegQ



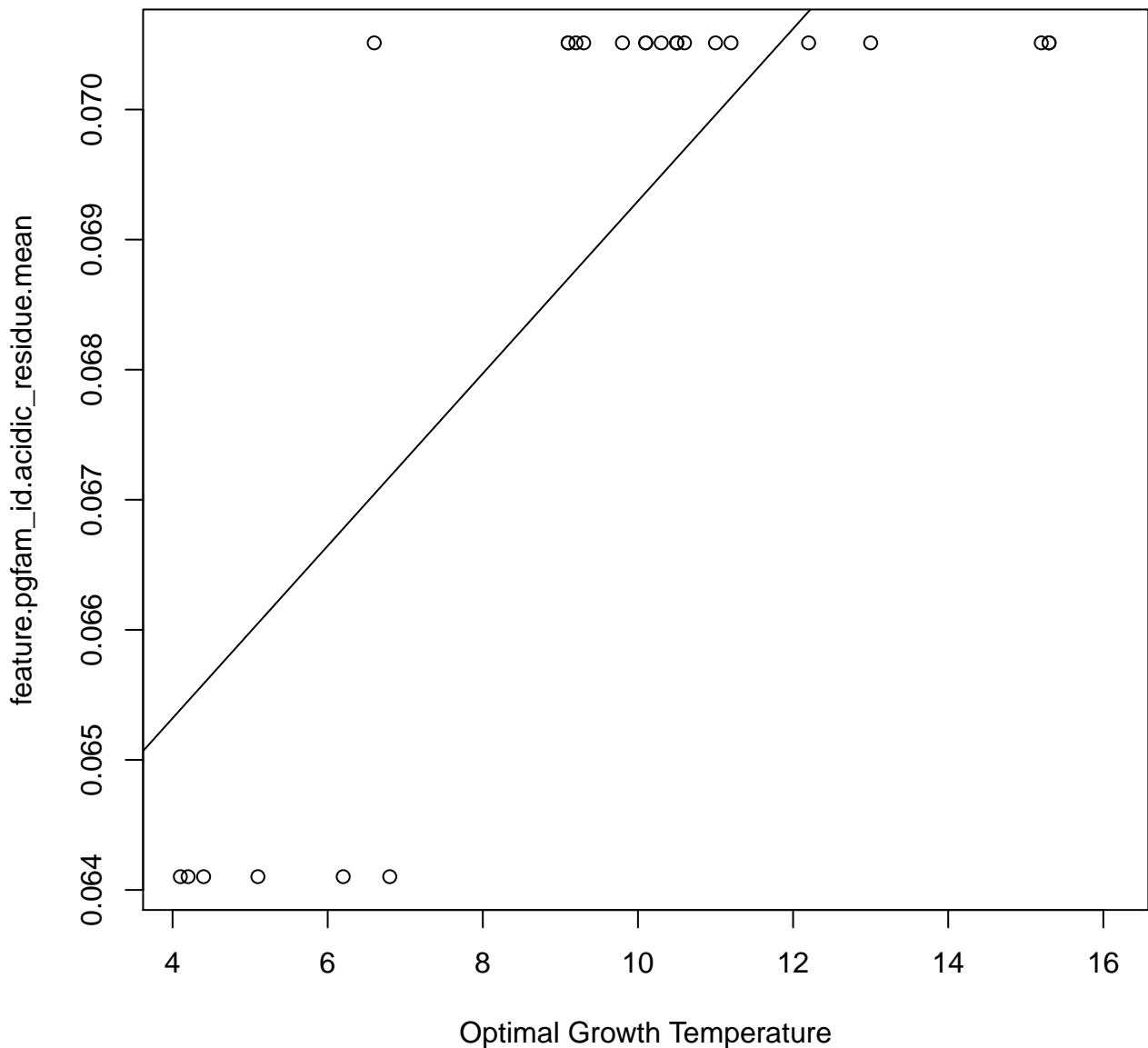
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PGF_07813500
hypothetical protein



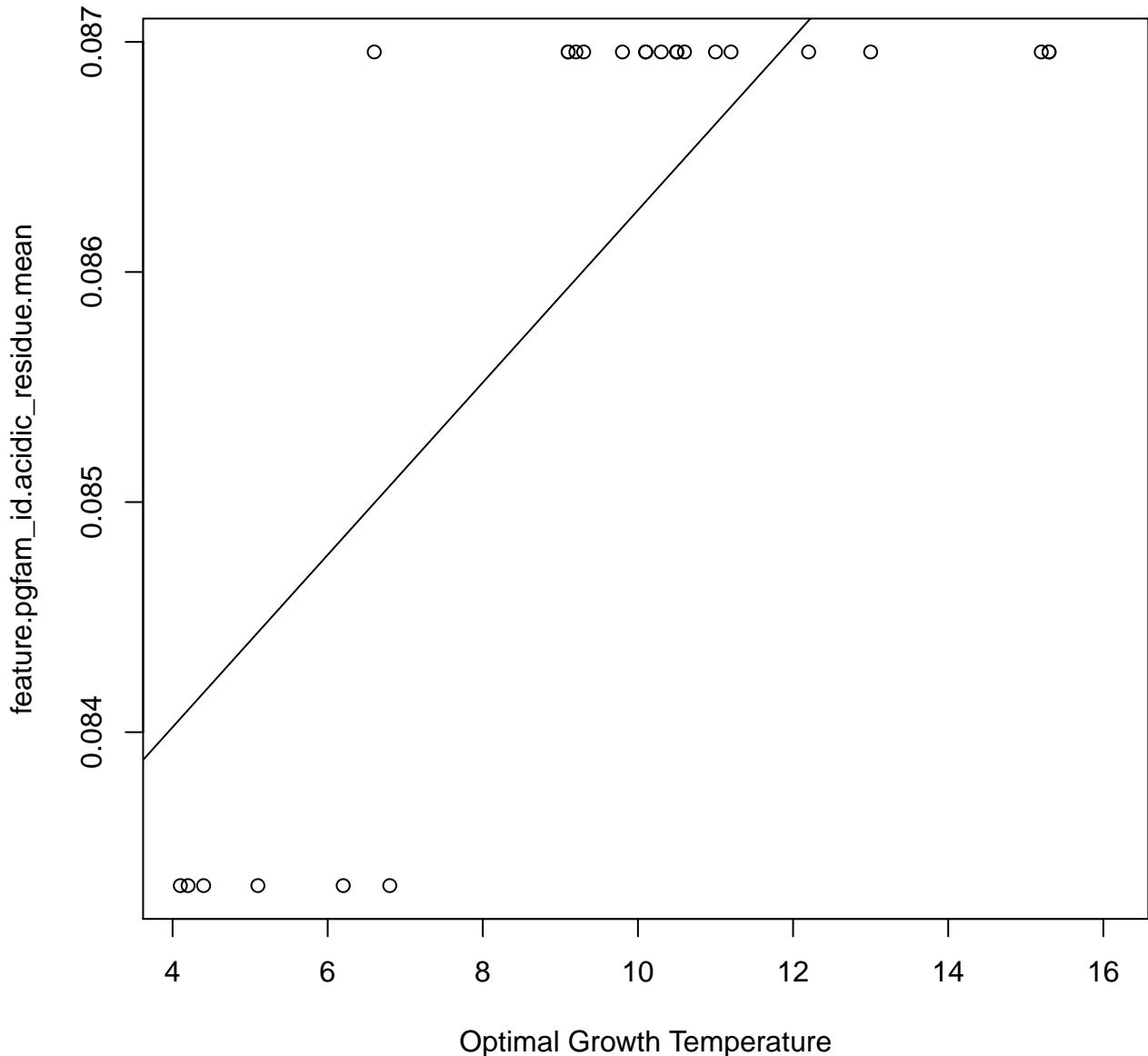
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PGF_01336977
hypothetical protein



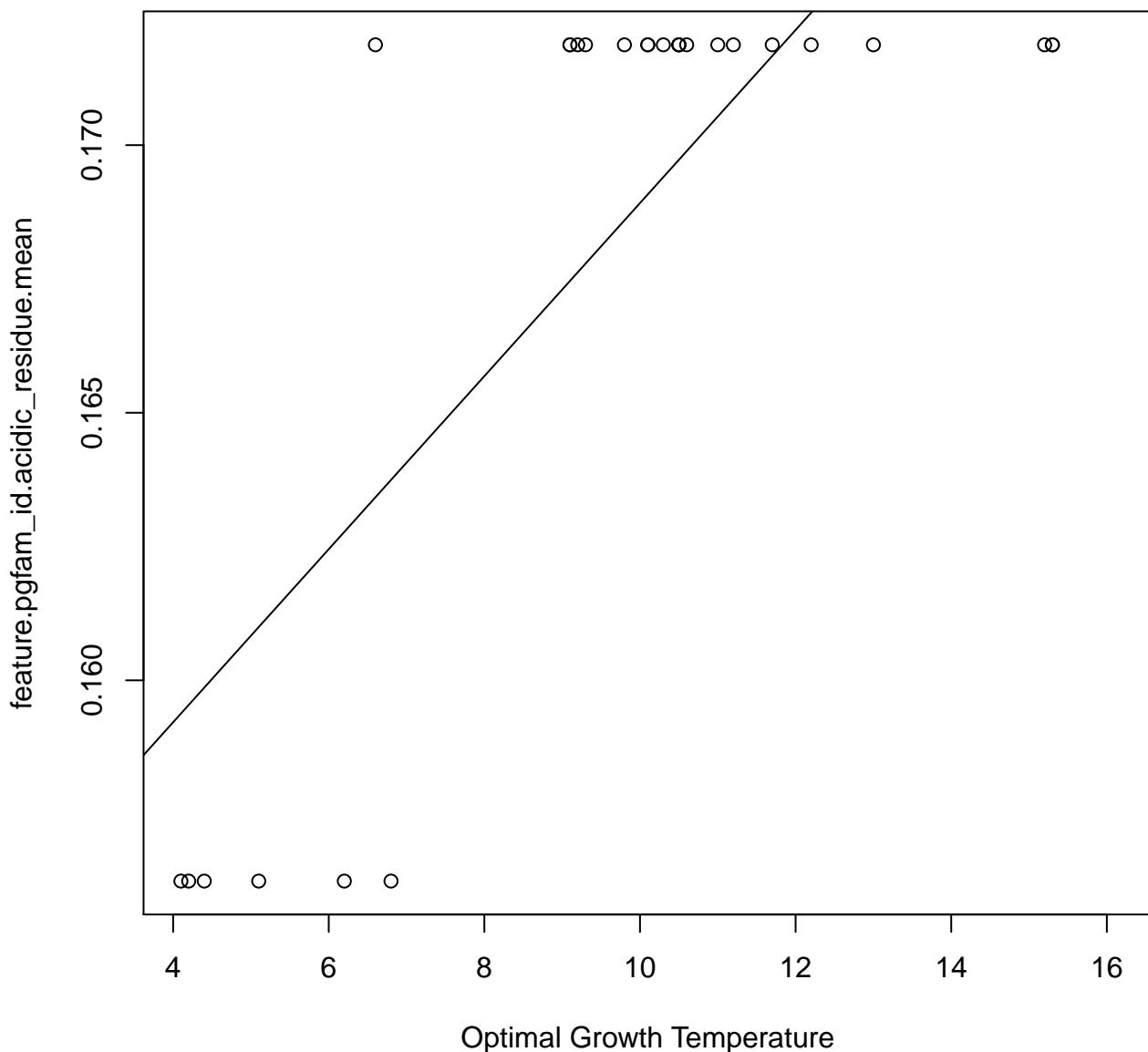
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hypothetical protein



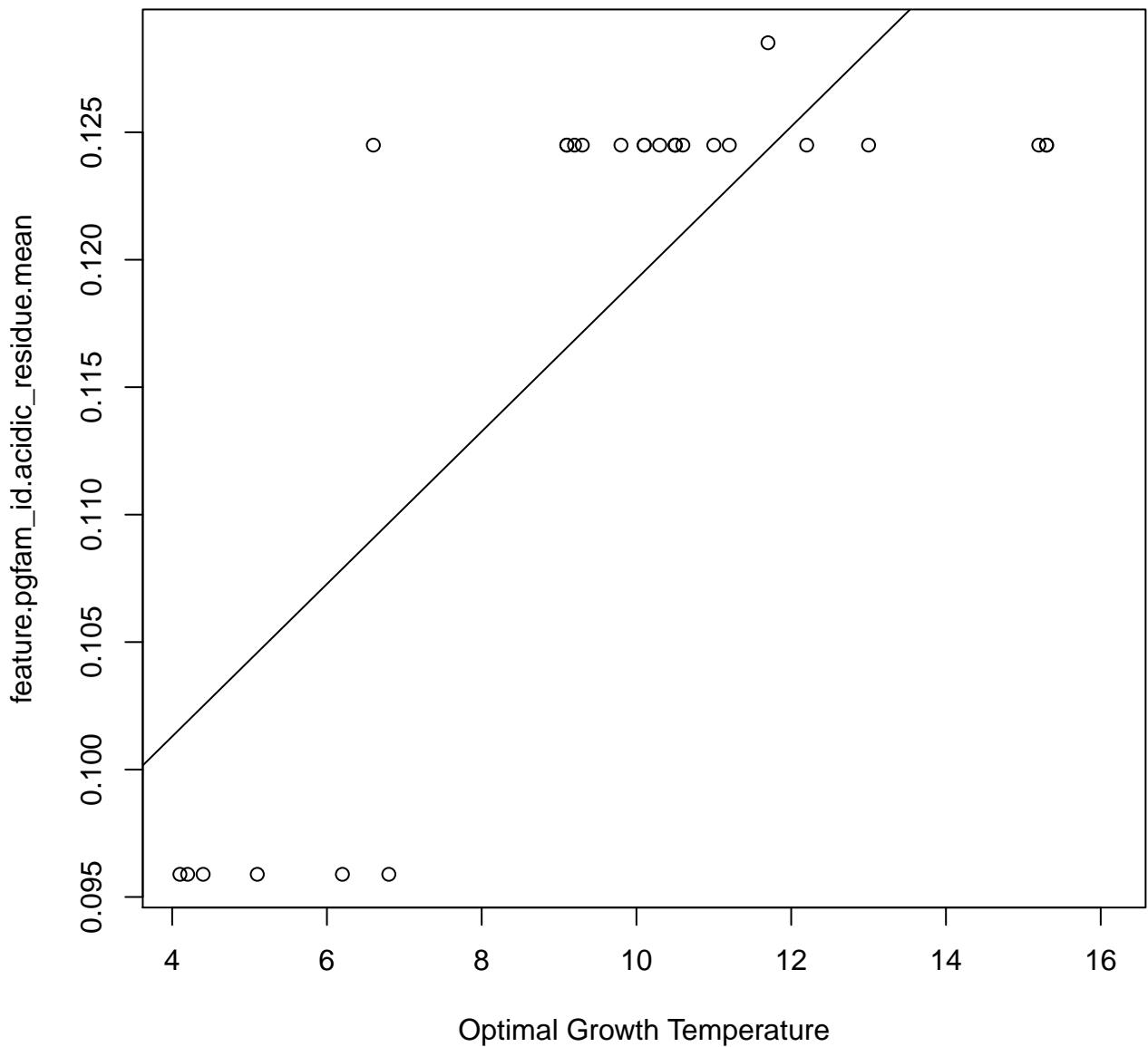
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PGF_12071964
hypothetical protein



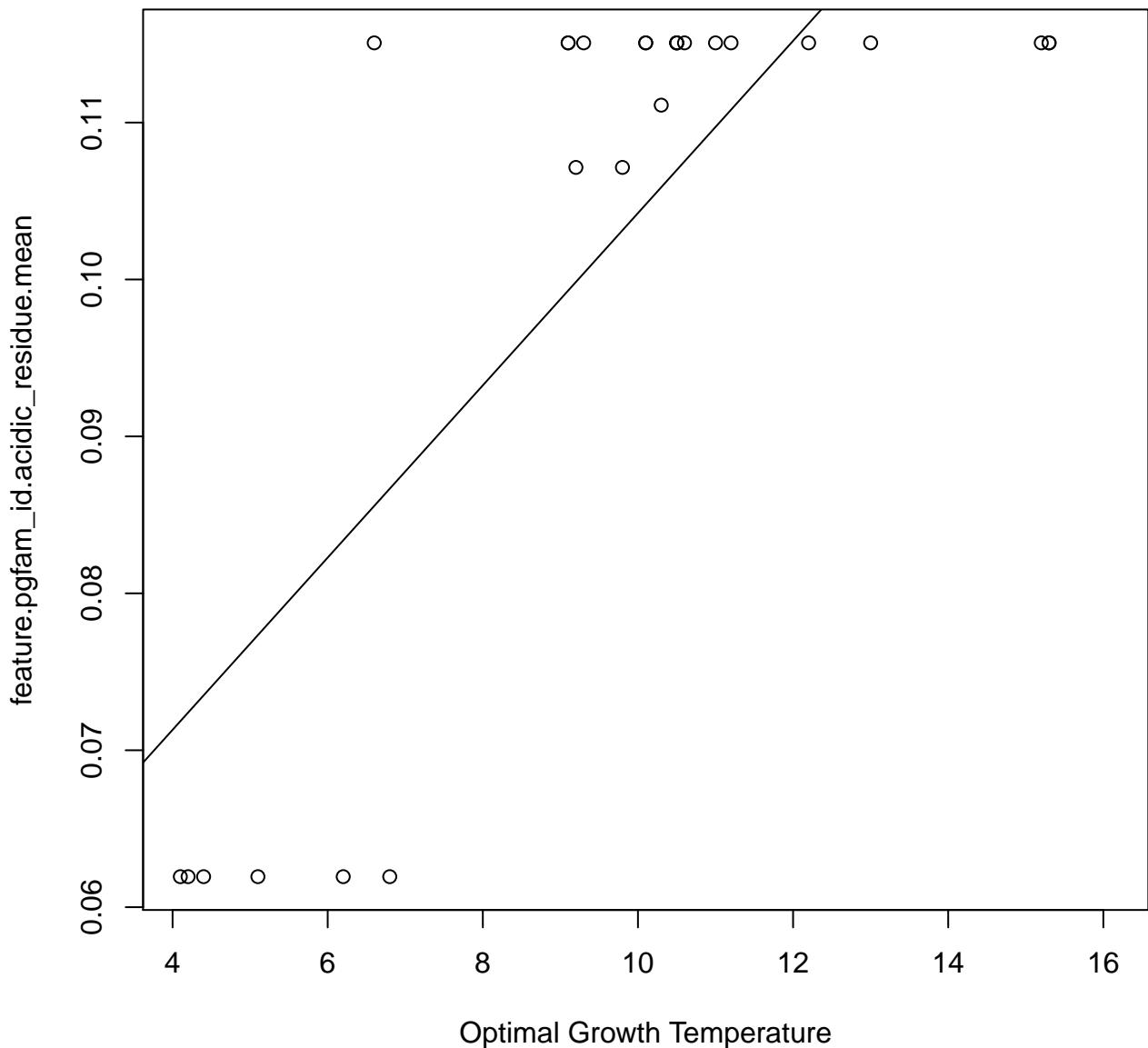
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PGF_07004481
hypothetical protein



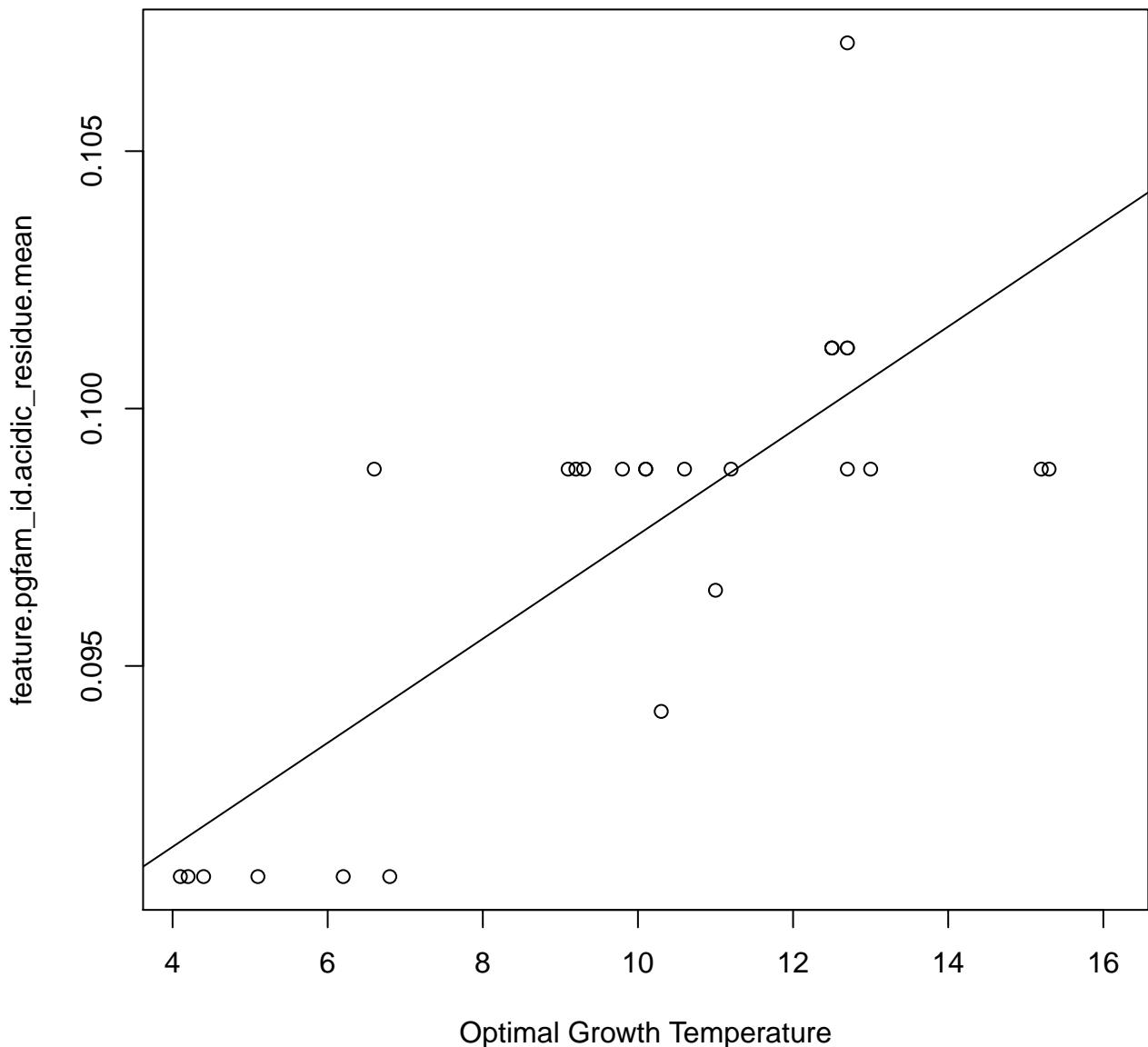
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PGF_11018774
hypothetical protein



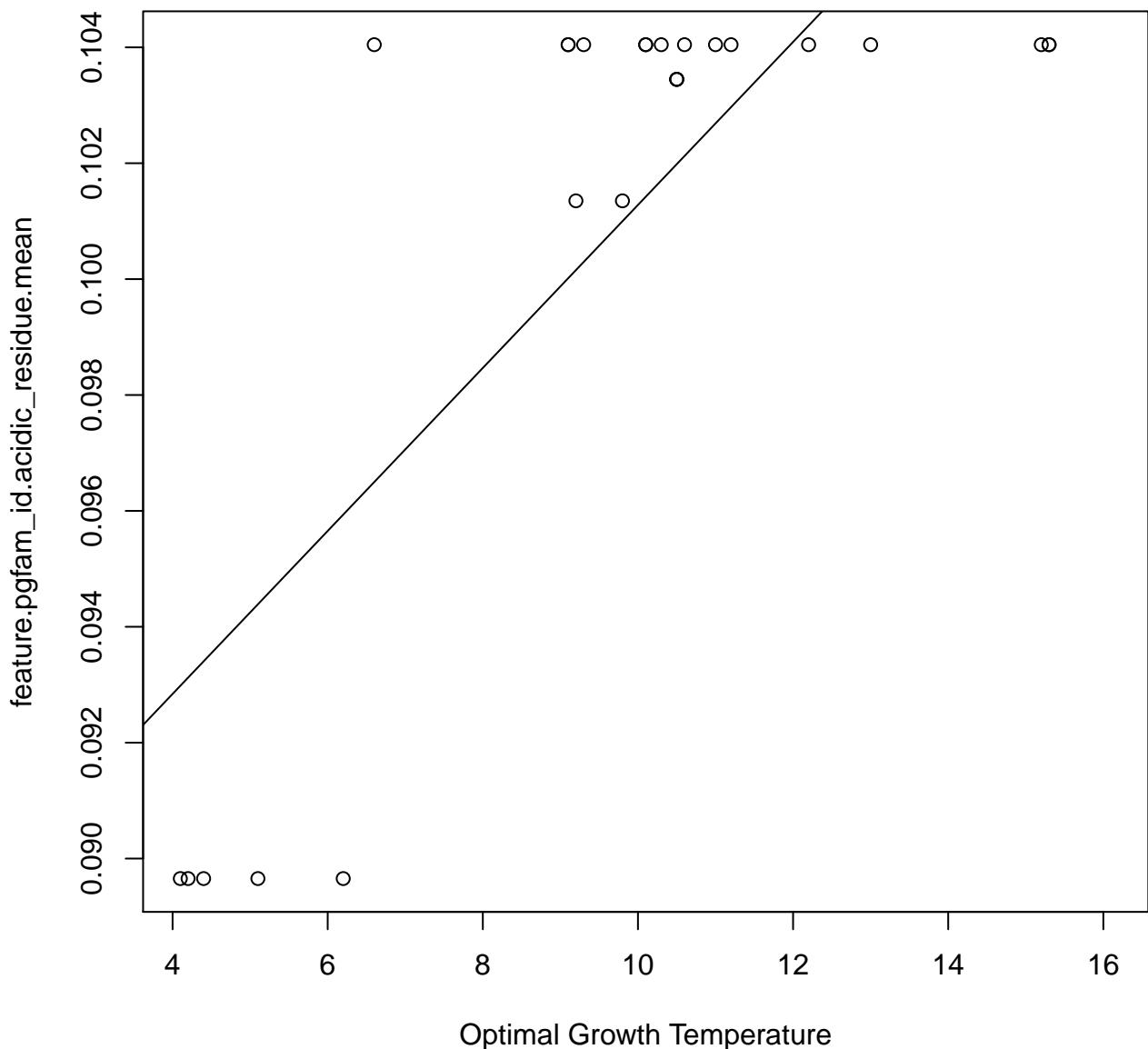
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PGF_12049070
hypothetical protein



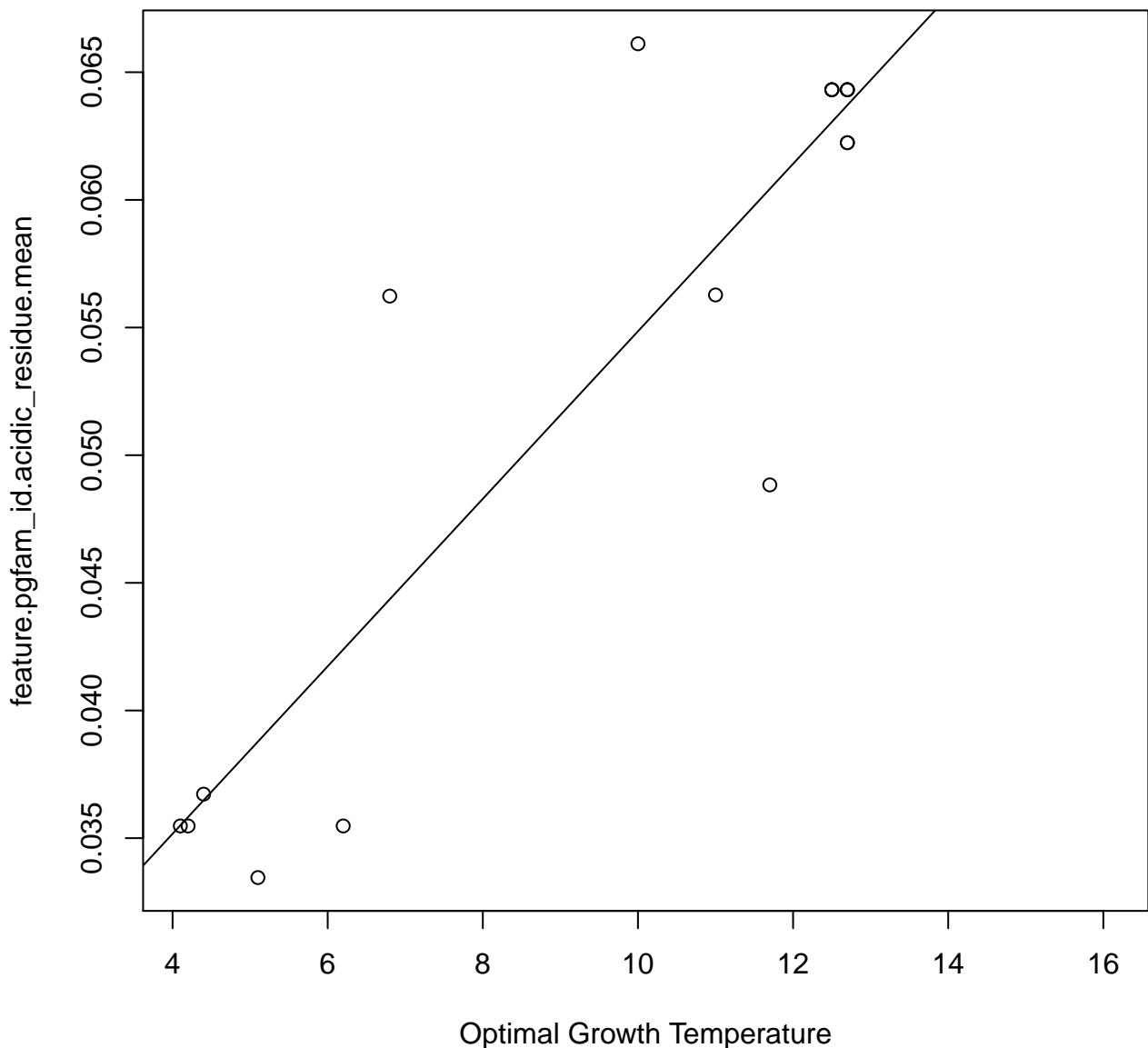
feature.pgfam_id.acidic_residue.mean
PGF_00424021
EPS I polysaccharide export outer membrane protein EPSA precursor



feature.pgfam_id.acidic_residue.mean
PGF_07418929
hypothetical protein



feature.pgfam_id.acidic_residue.mean
PGF_00066964
Xanthine/uracil/thiamine/ascorbate permease family protein

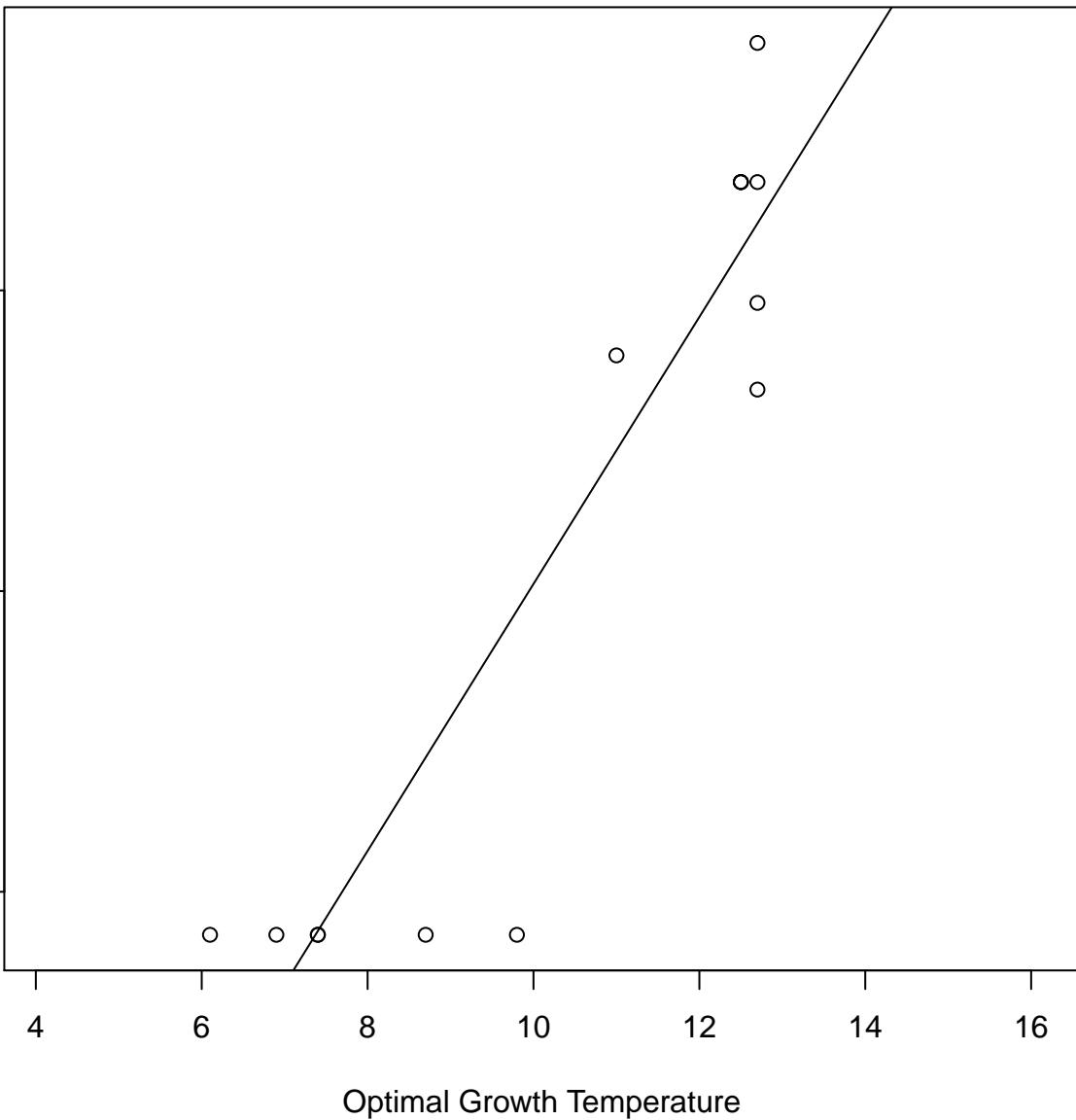


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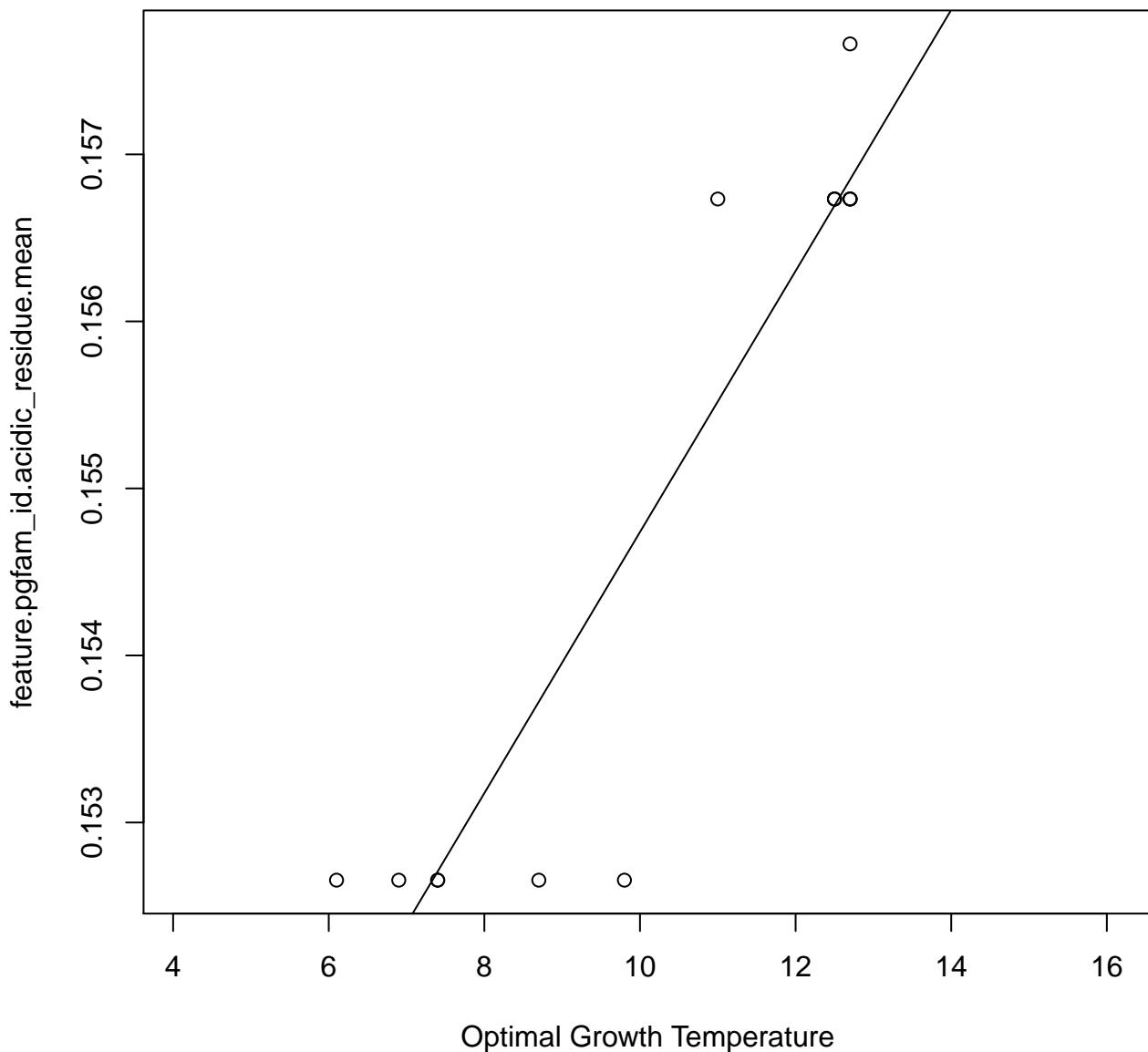
PGF_01336575

Porin

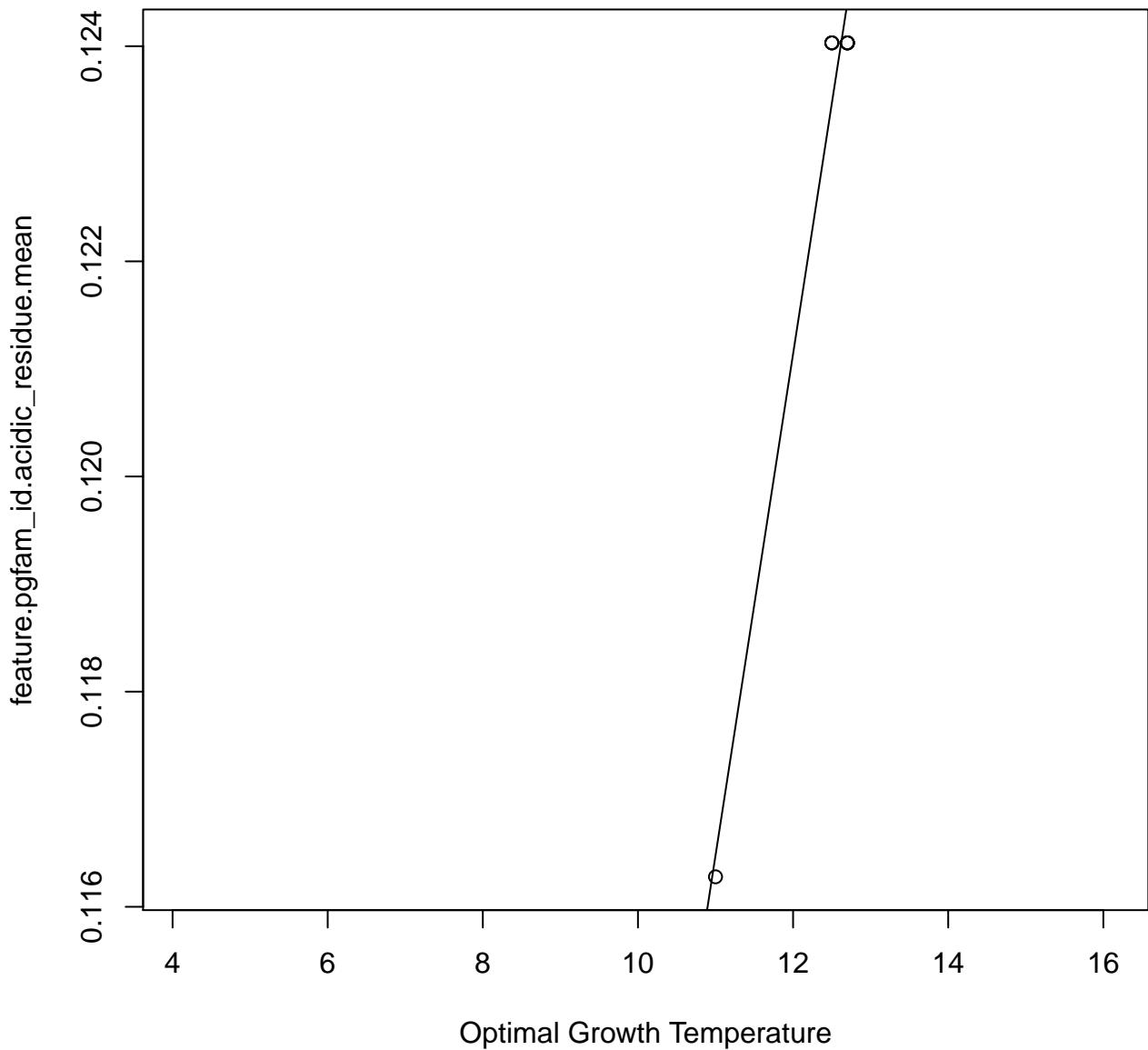
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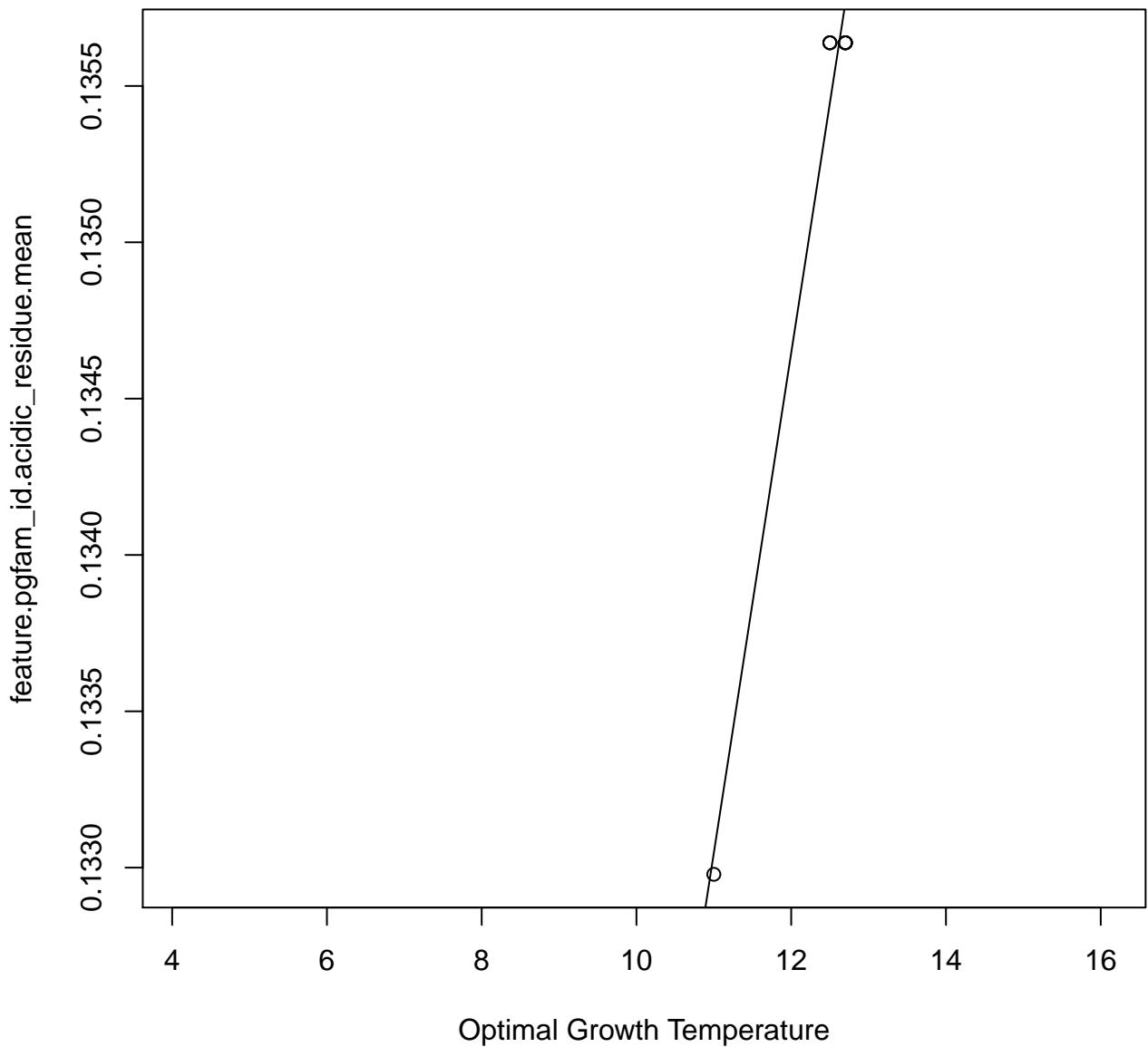
feature.pgfam_id.acidic_residue.mean
PGF_04463652
C4-dicarboxylate transport transcriptional regulatory protein



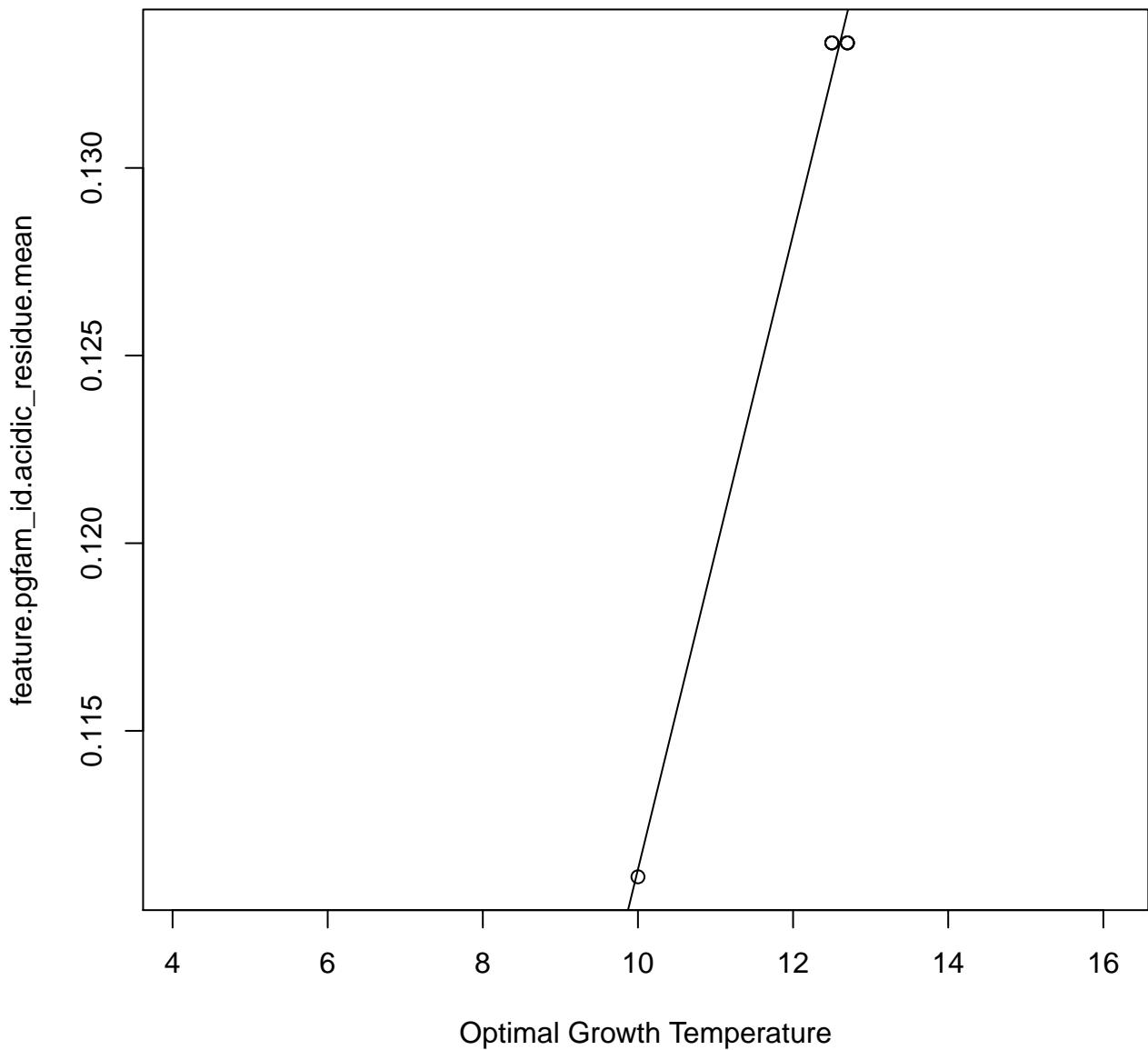
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PGF_01336845
hypothetical protein



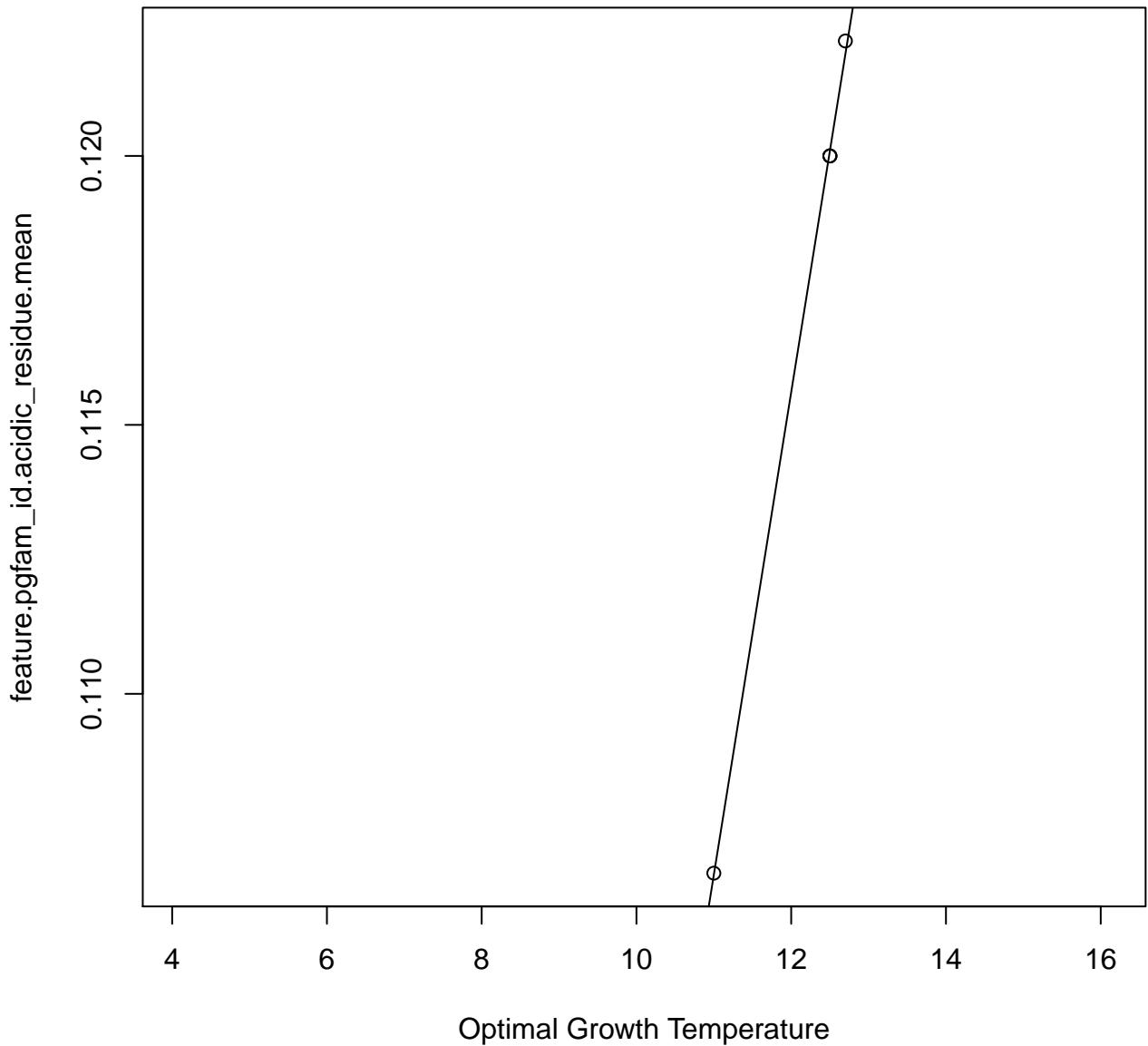
feature.pgfam_id.acidic_residue.mean
PGF_04965976
Putrescine transport ATP-binding protein PotG (TC 3.A.1.11.2)



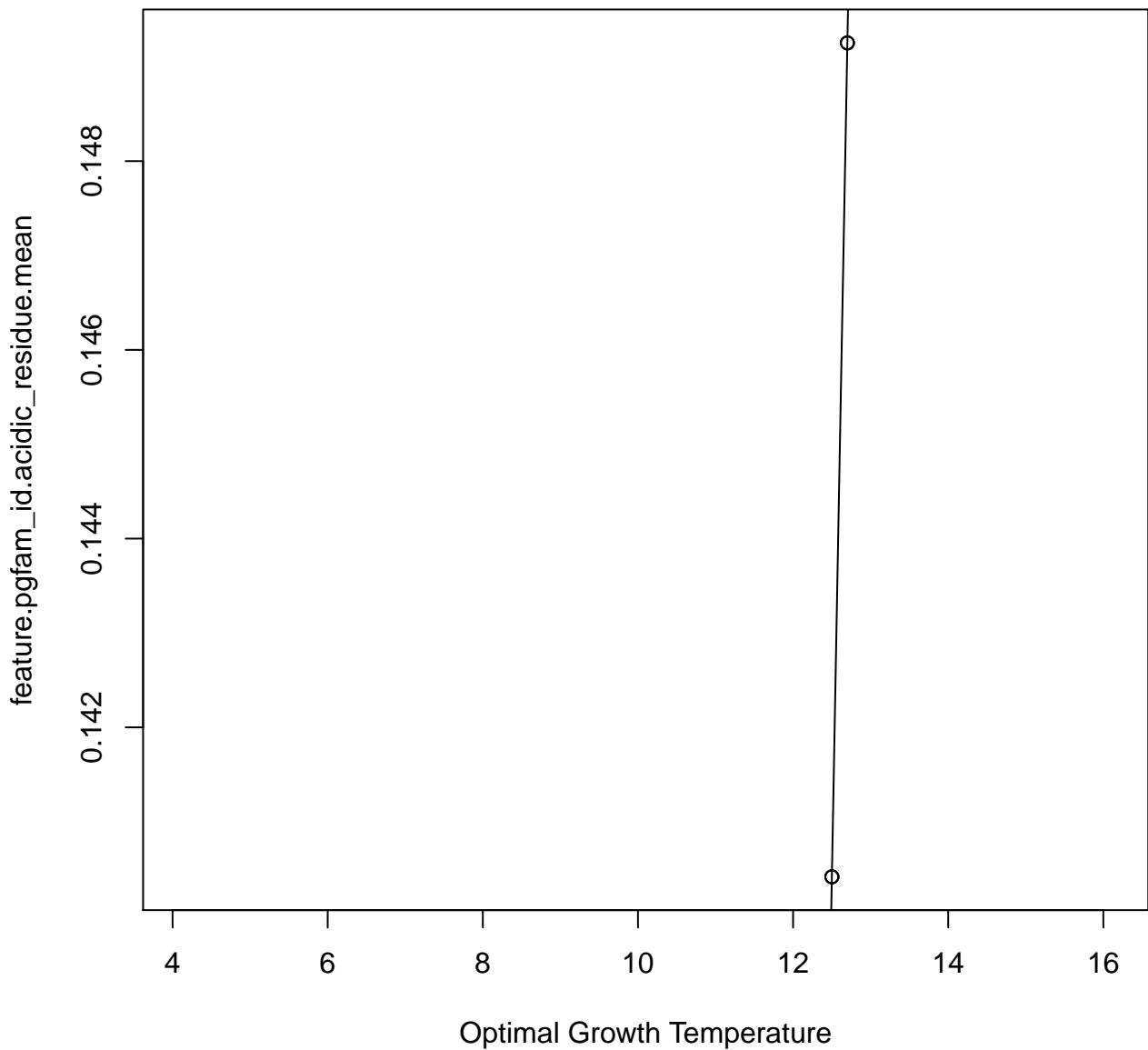
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PGF_01337096
hypothetical protein



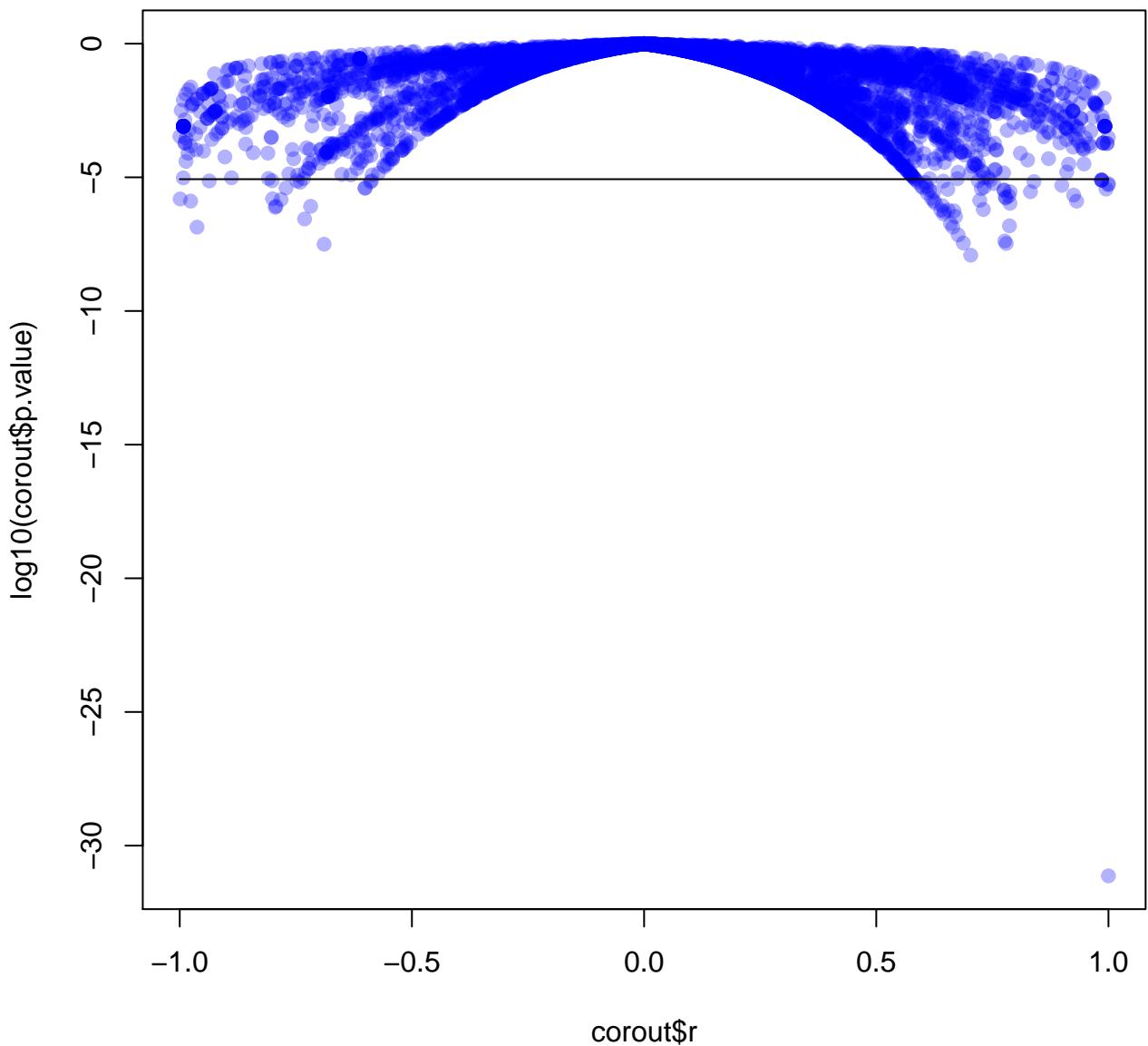
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PGF_00038084
Fluoride ion transporter CrcB



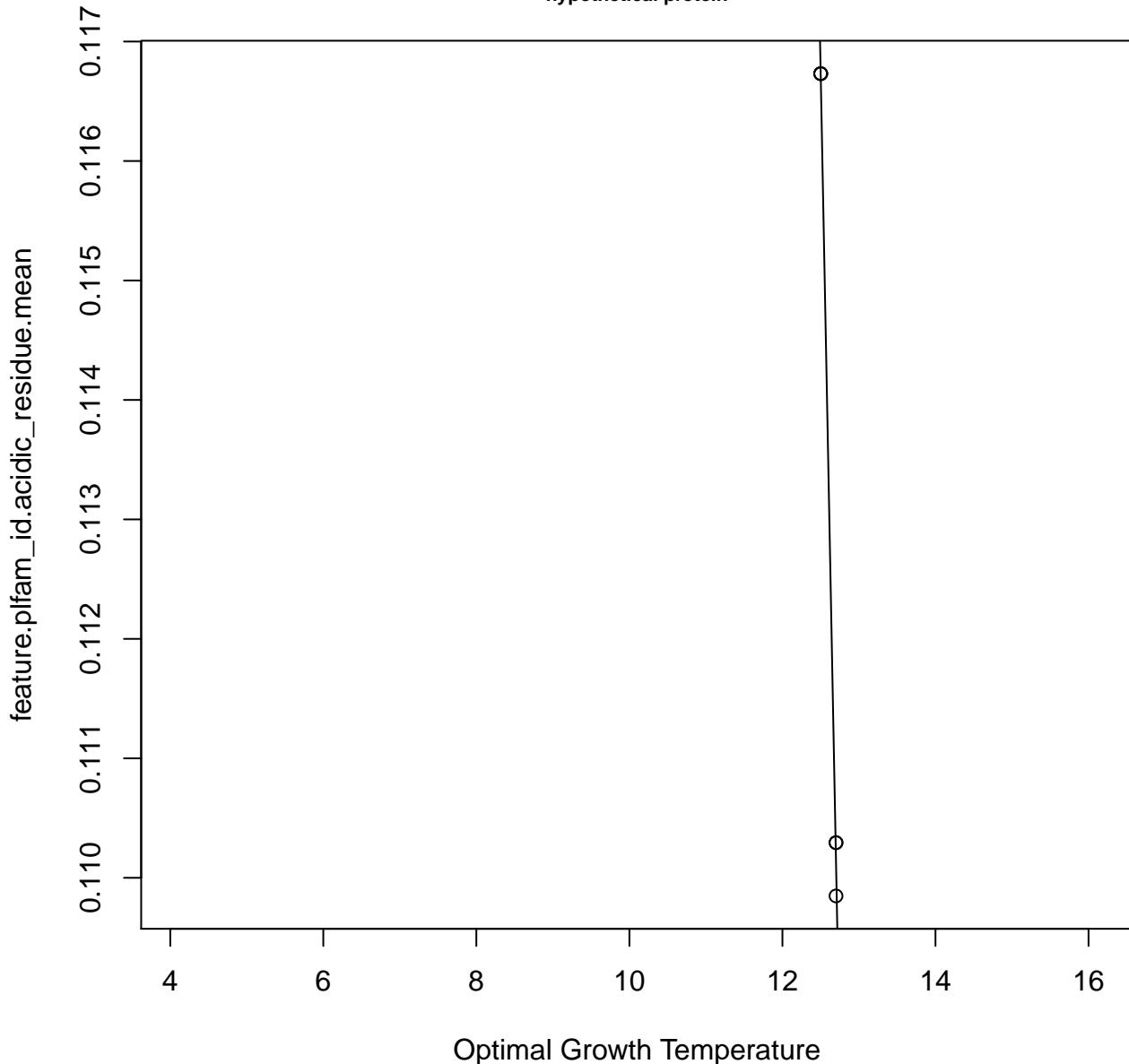
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PGF_01336638
hypothetical protein



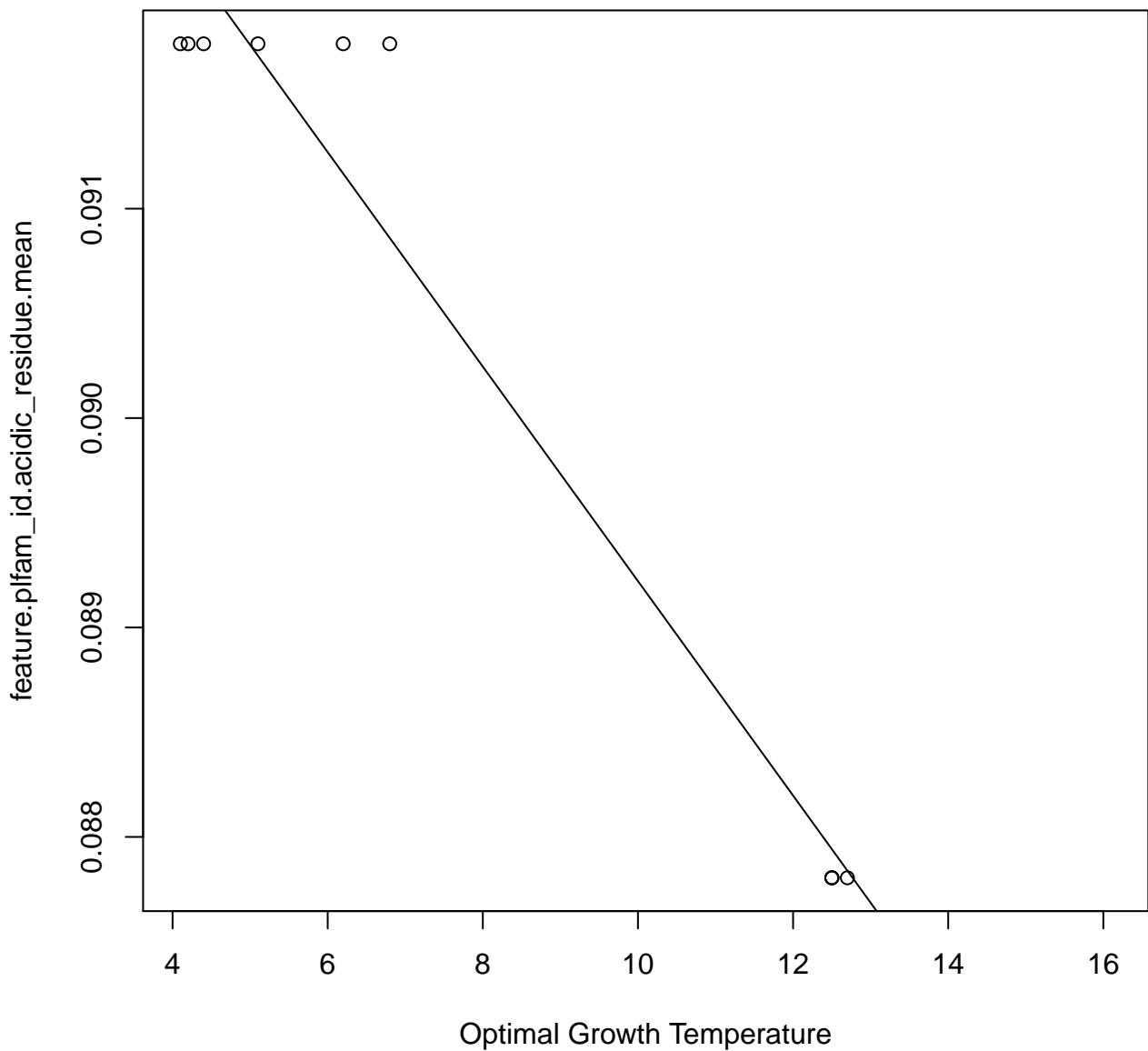
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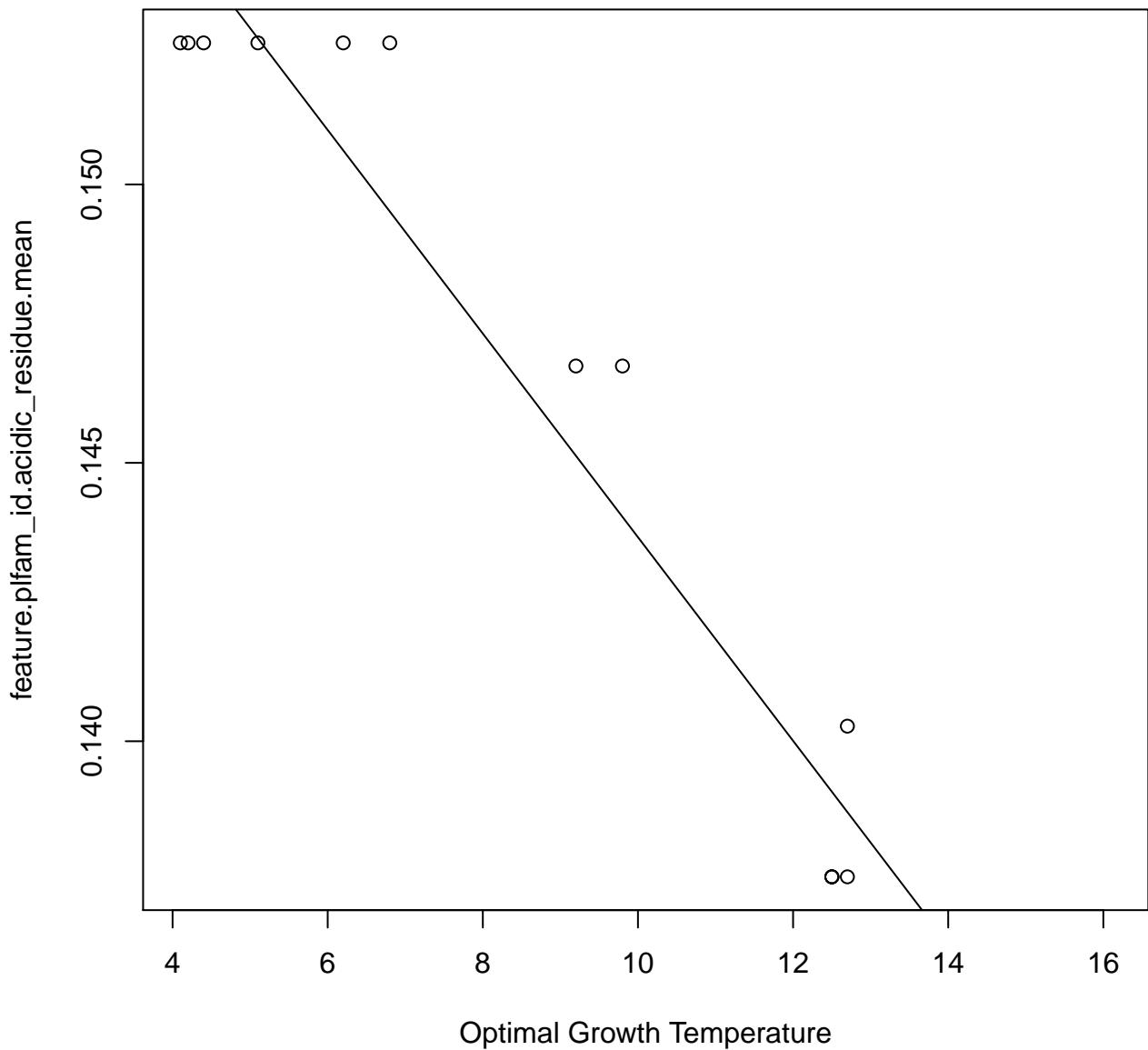
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hypothetical protein



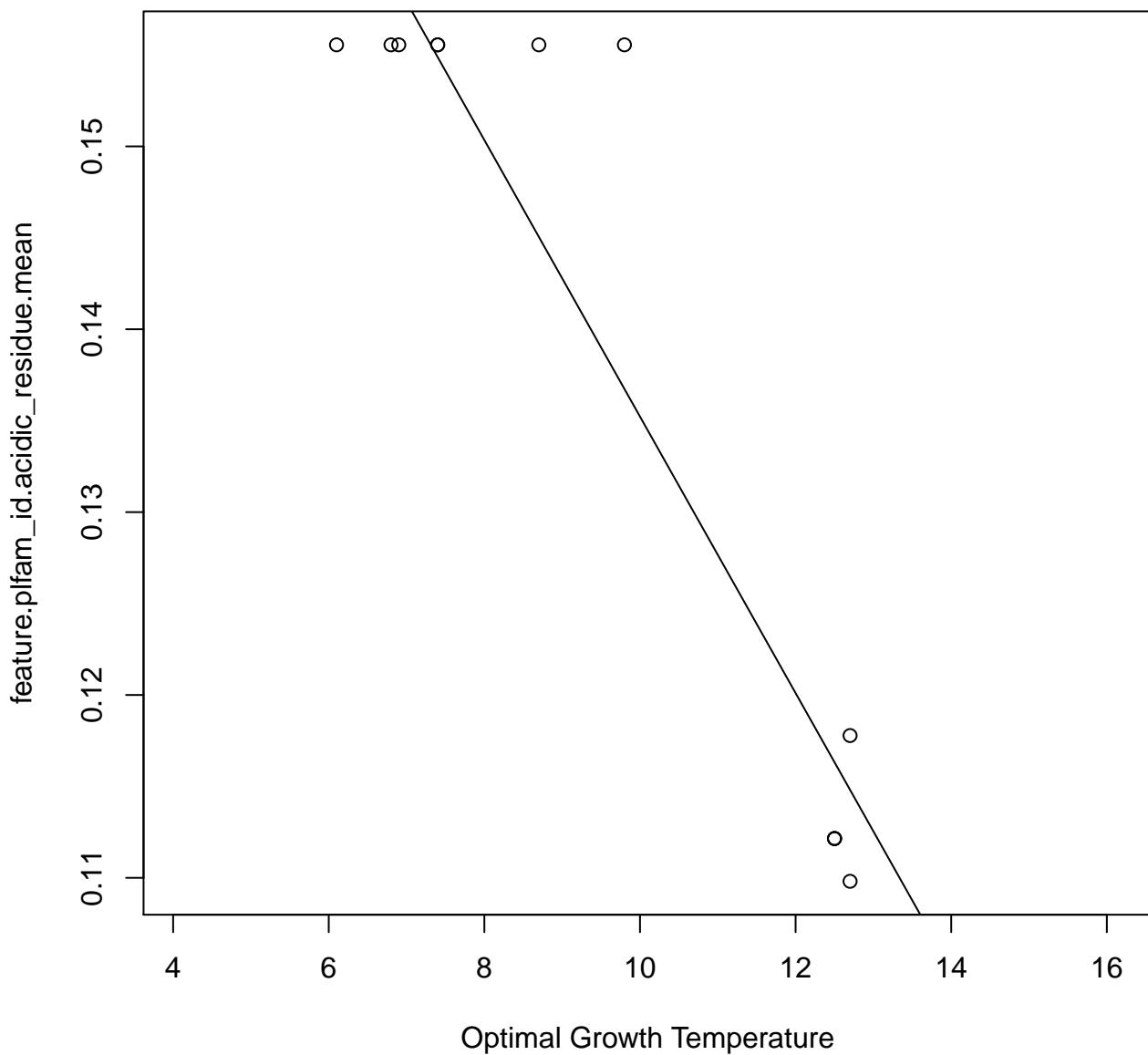
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hypothetical protein



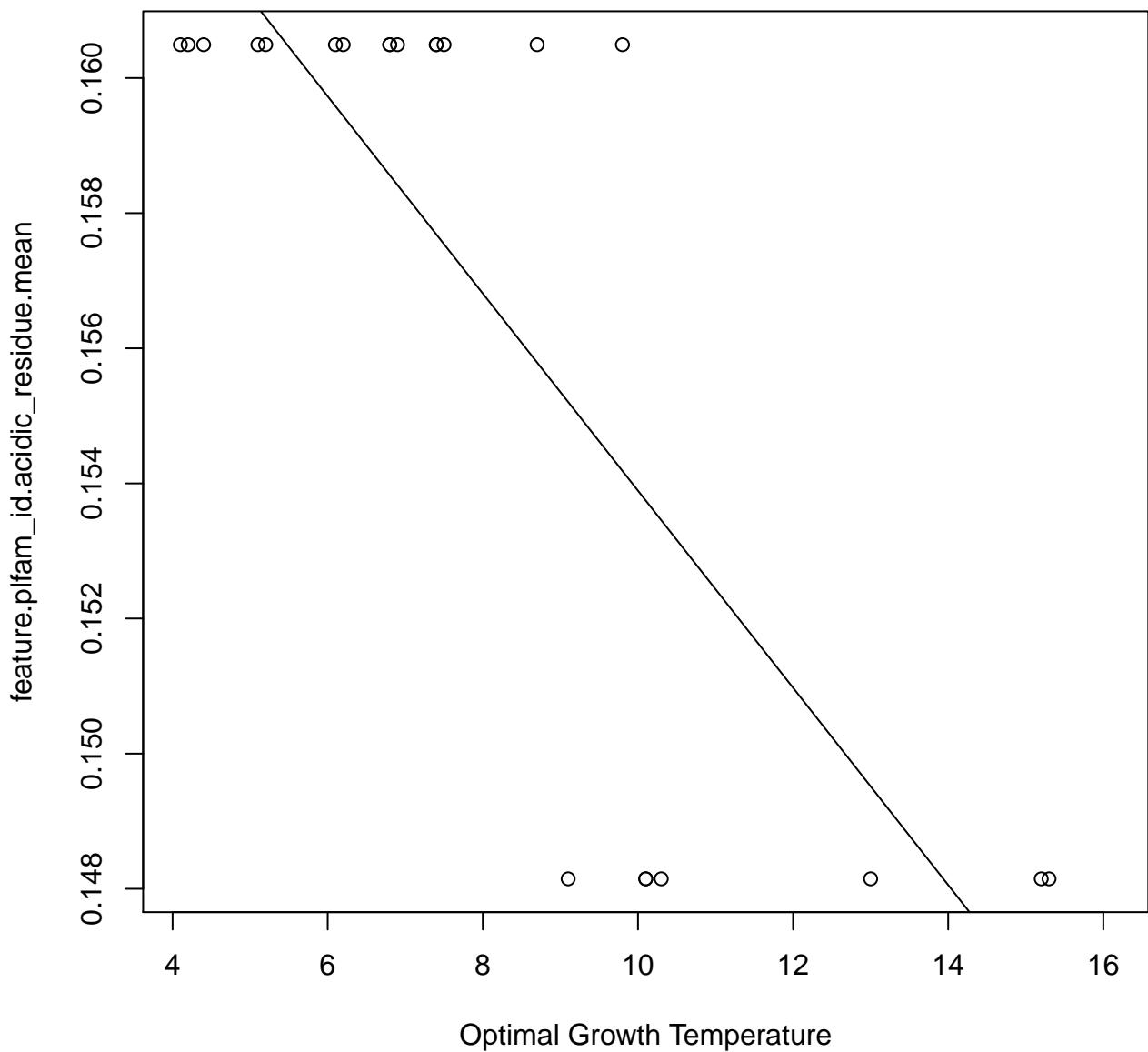
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PLF_28228_00018284
putative lipoprotein



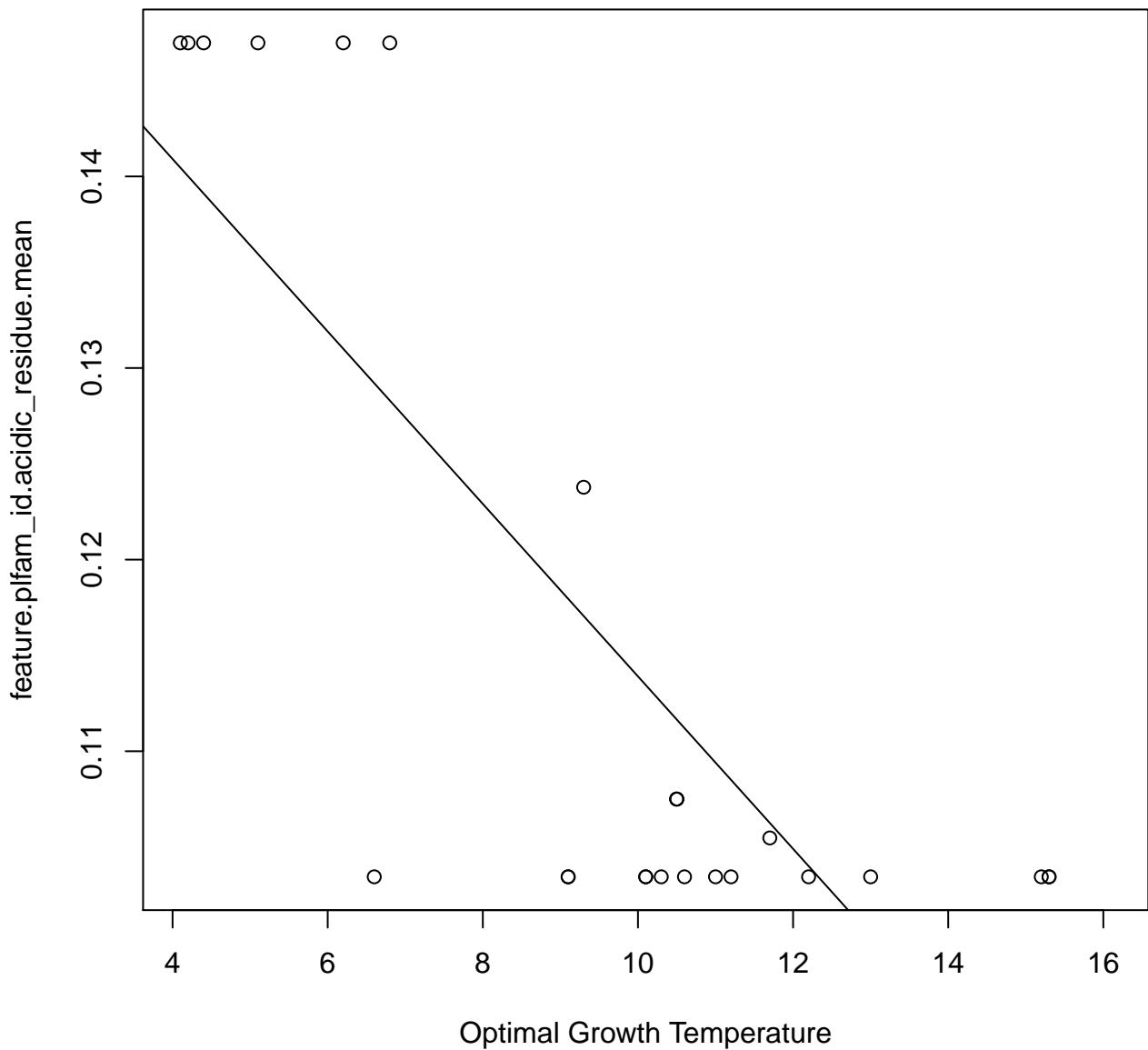
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PLF_28228_00007748
EAL domain protein



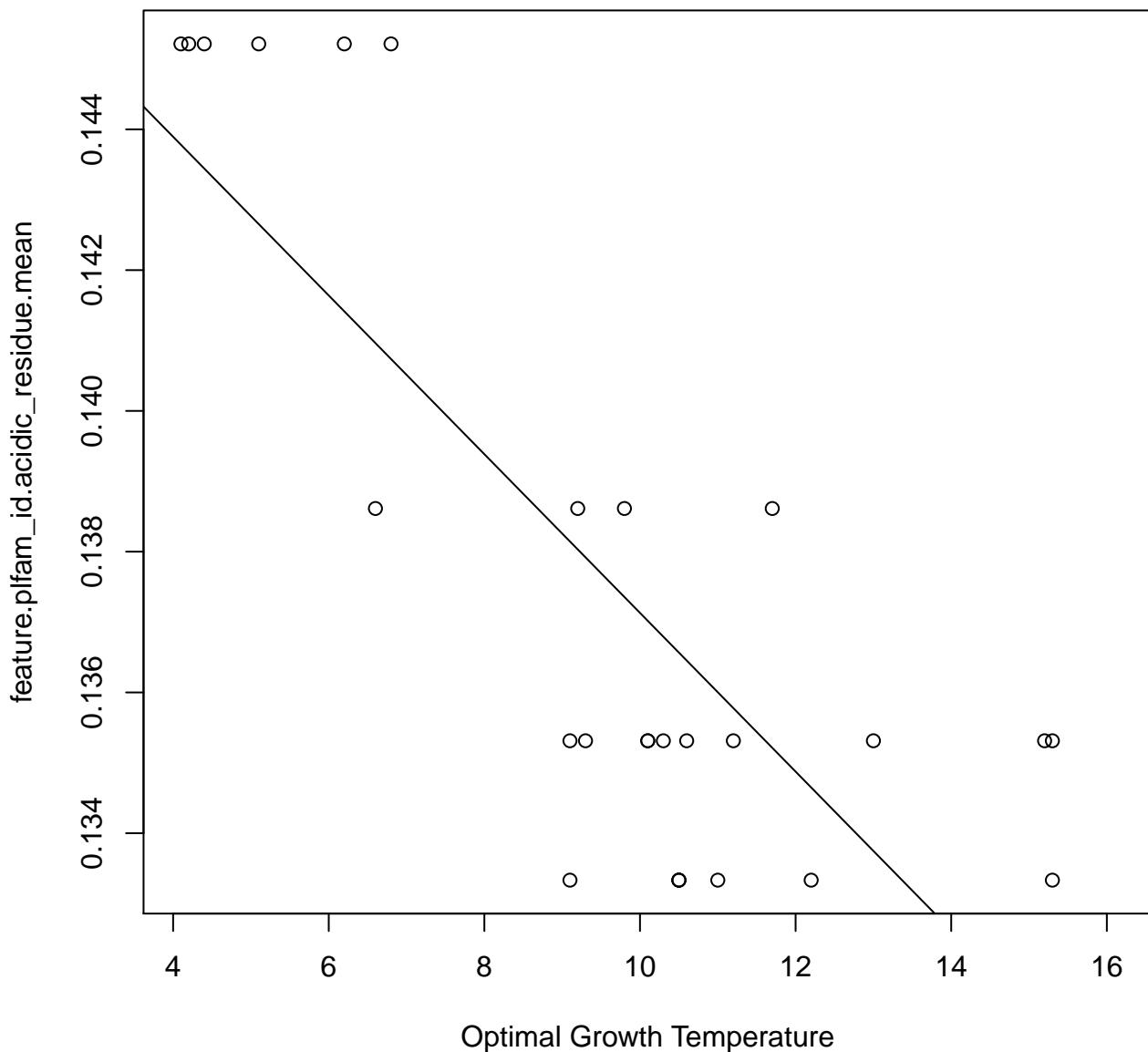
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hypothetical protein



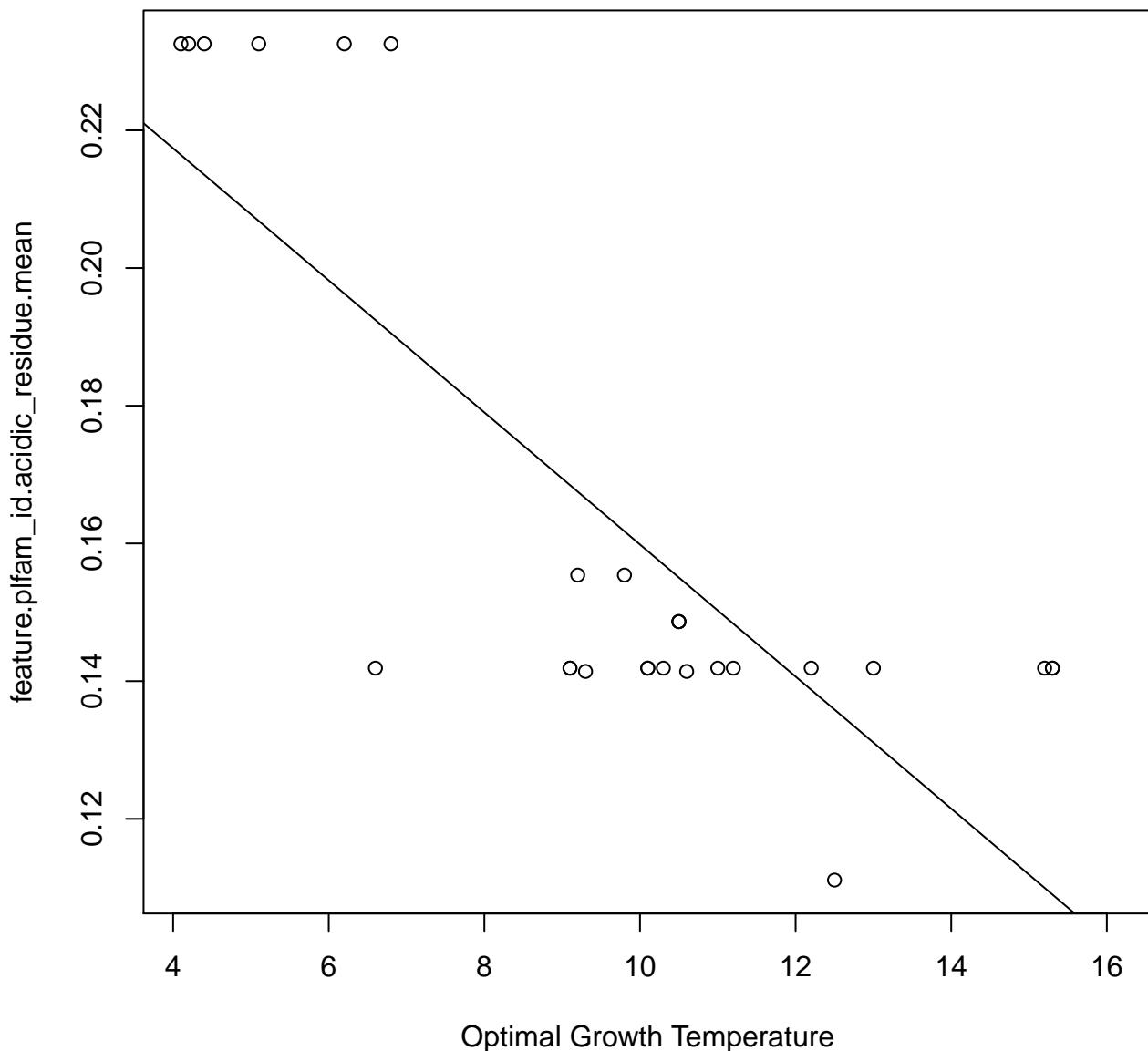
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PLF_28228_00022096
Two-component system sensor histidine kinase



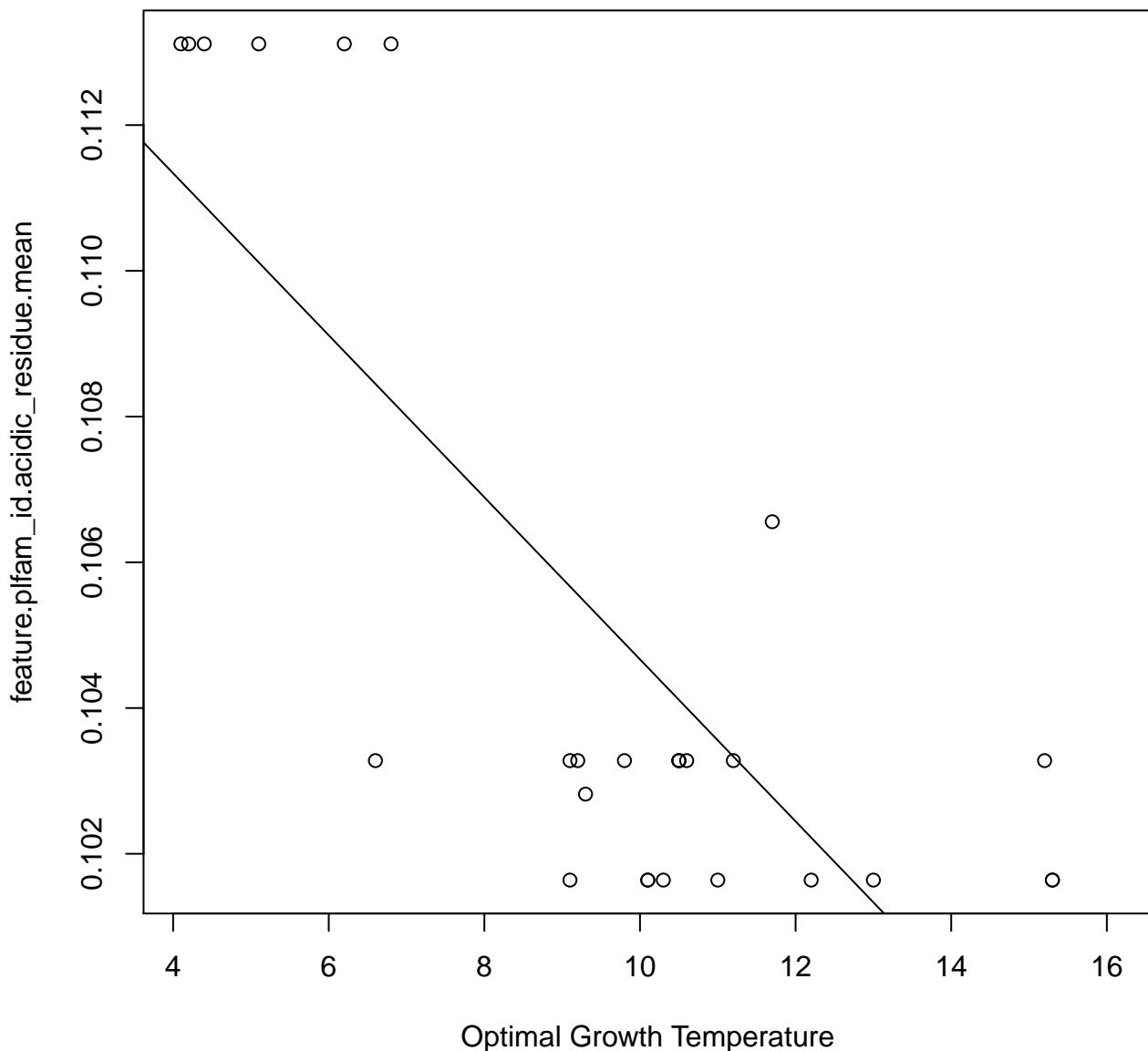
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hypothetical protein



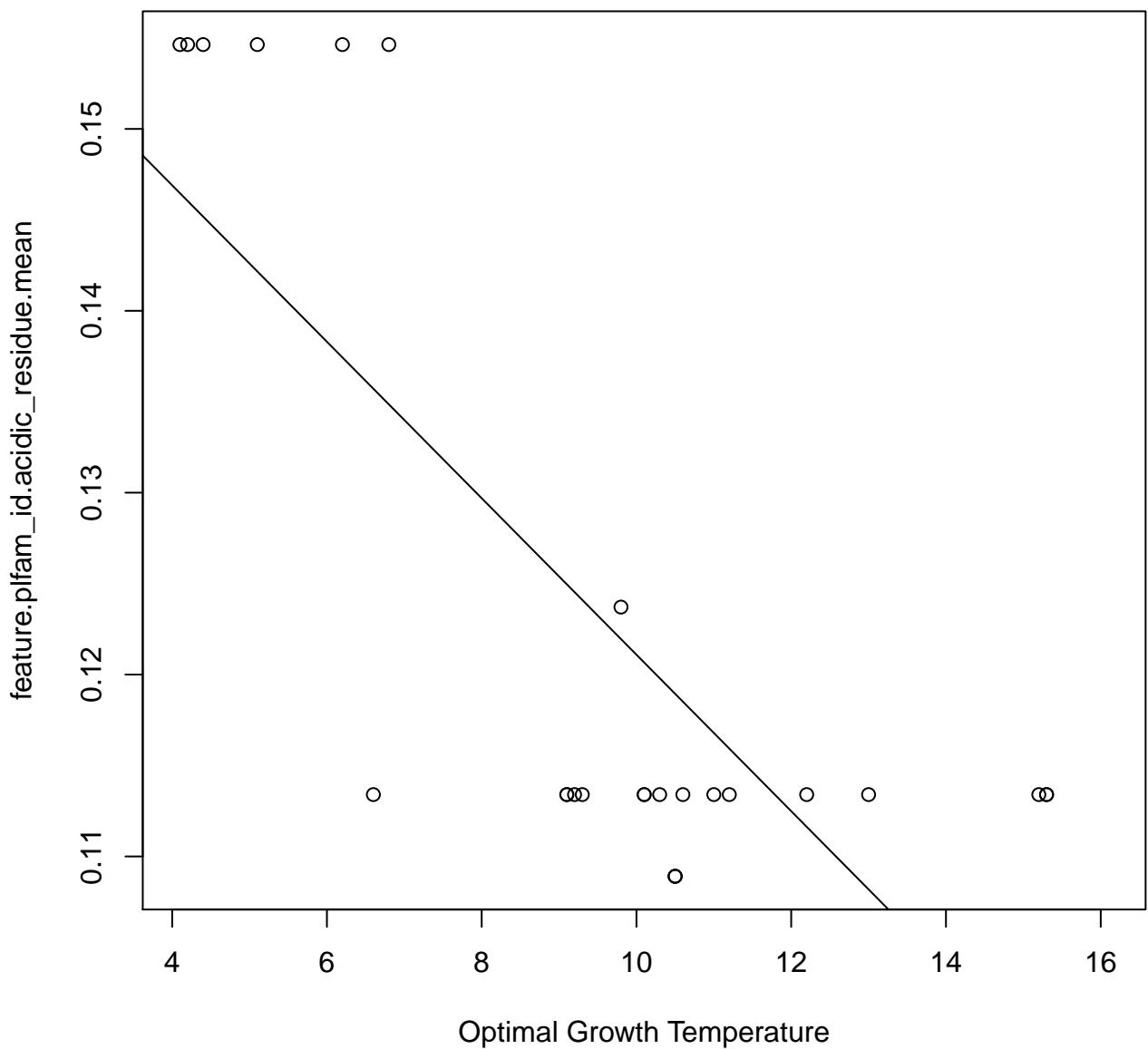
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hypothetical protein



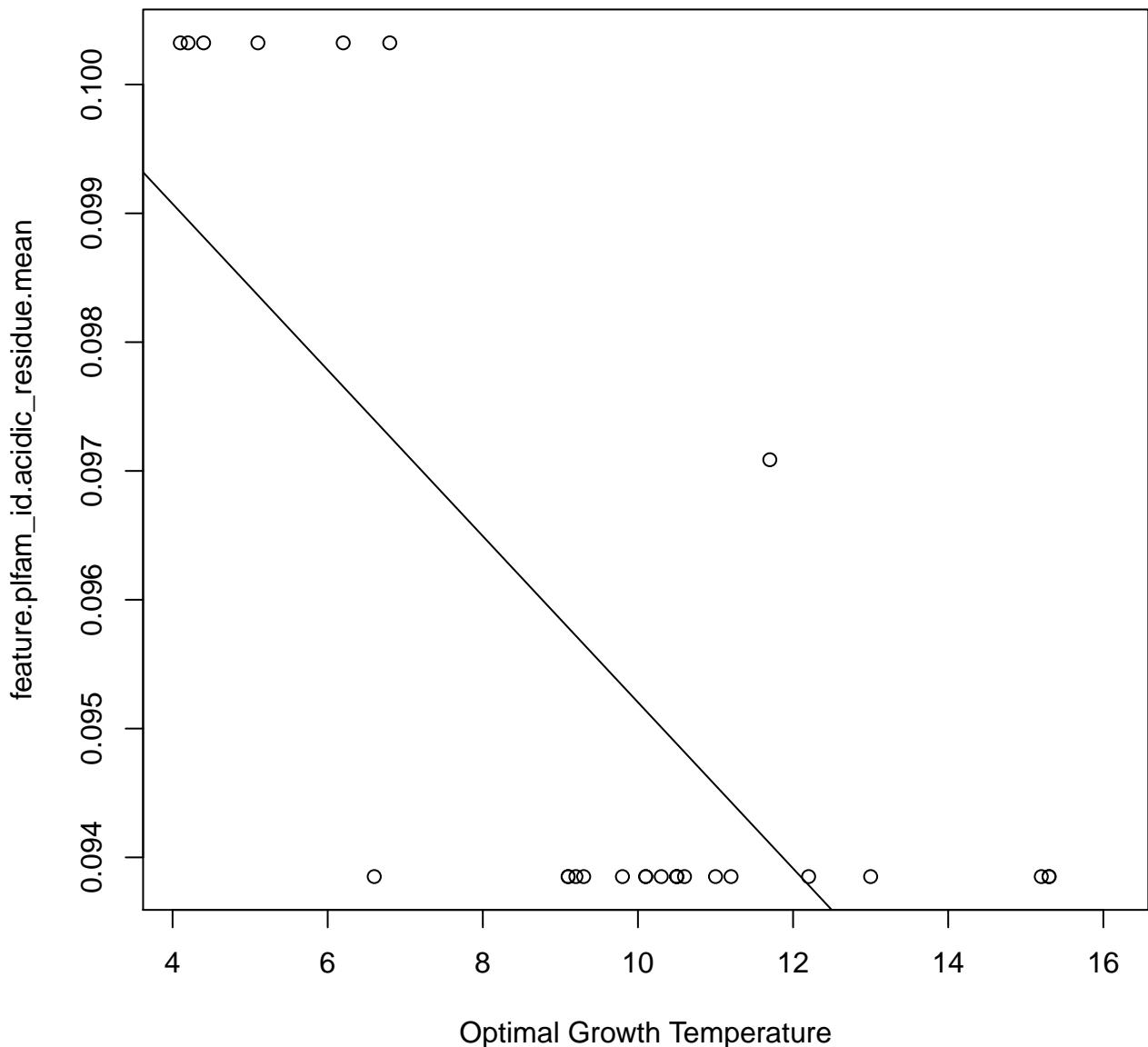
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PLF_28228_00028646
hypothetical protein



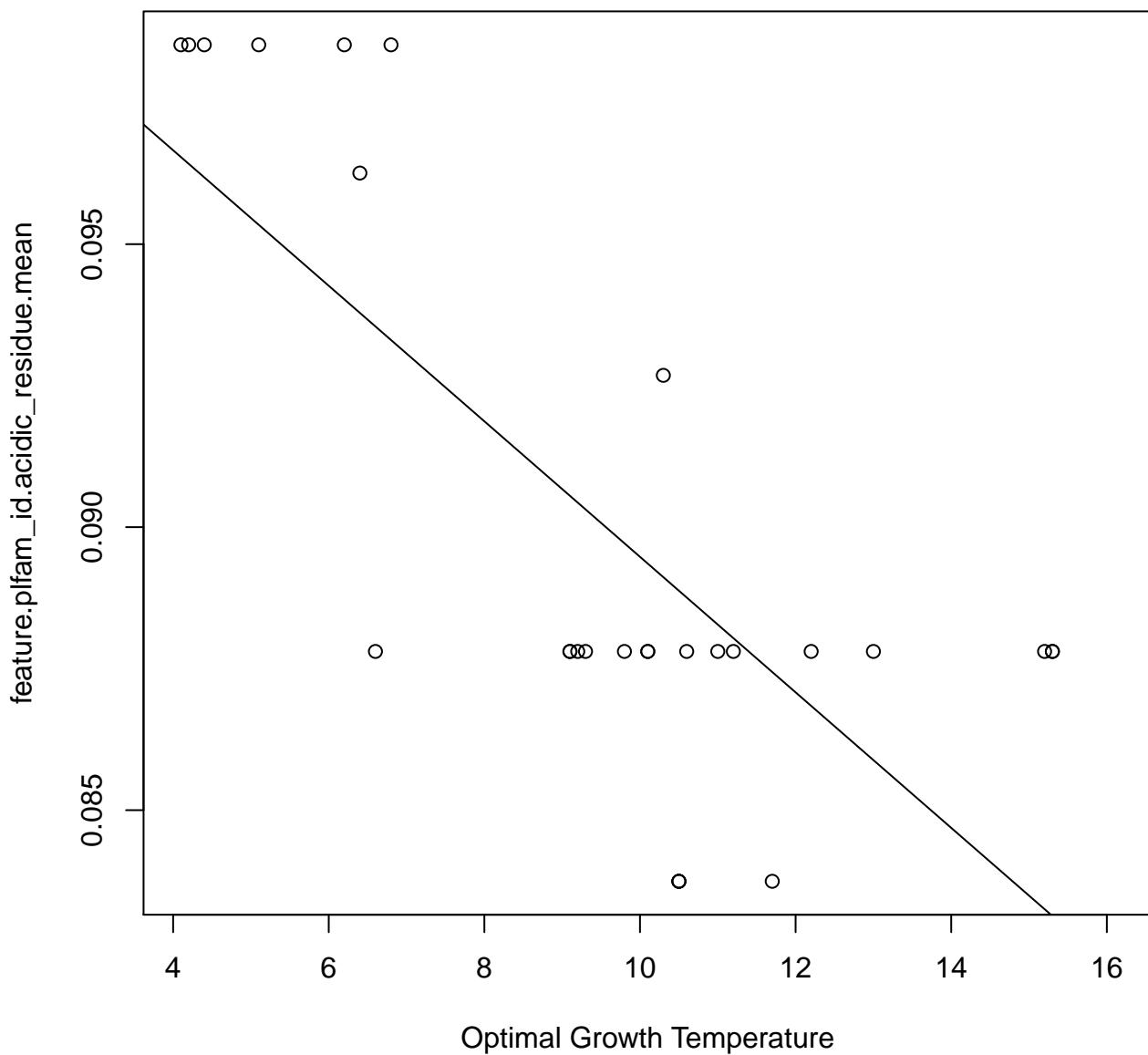
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PLF_28228_00030961
hypothetical protein



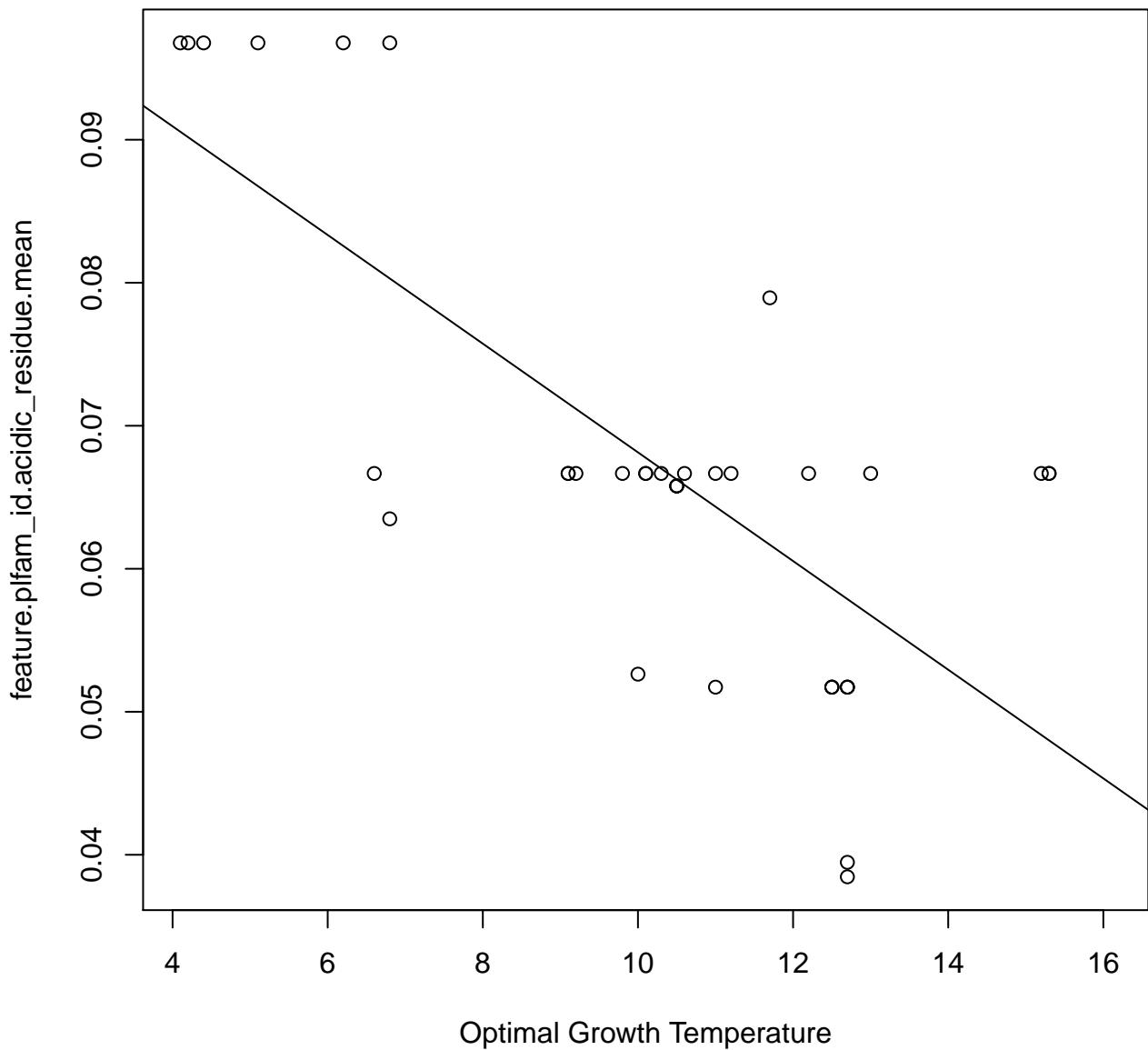
feature.plfam_id.acidic_residue.mean
PLF_28228_00006015
N-linked glycosylation glycosyltransferase PgIG



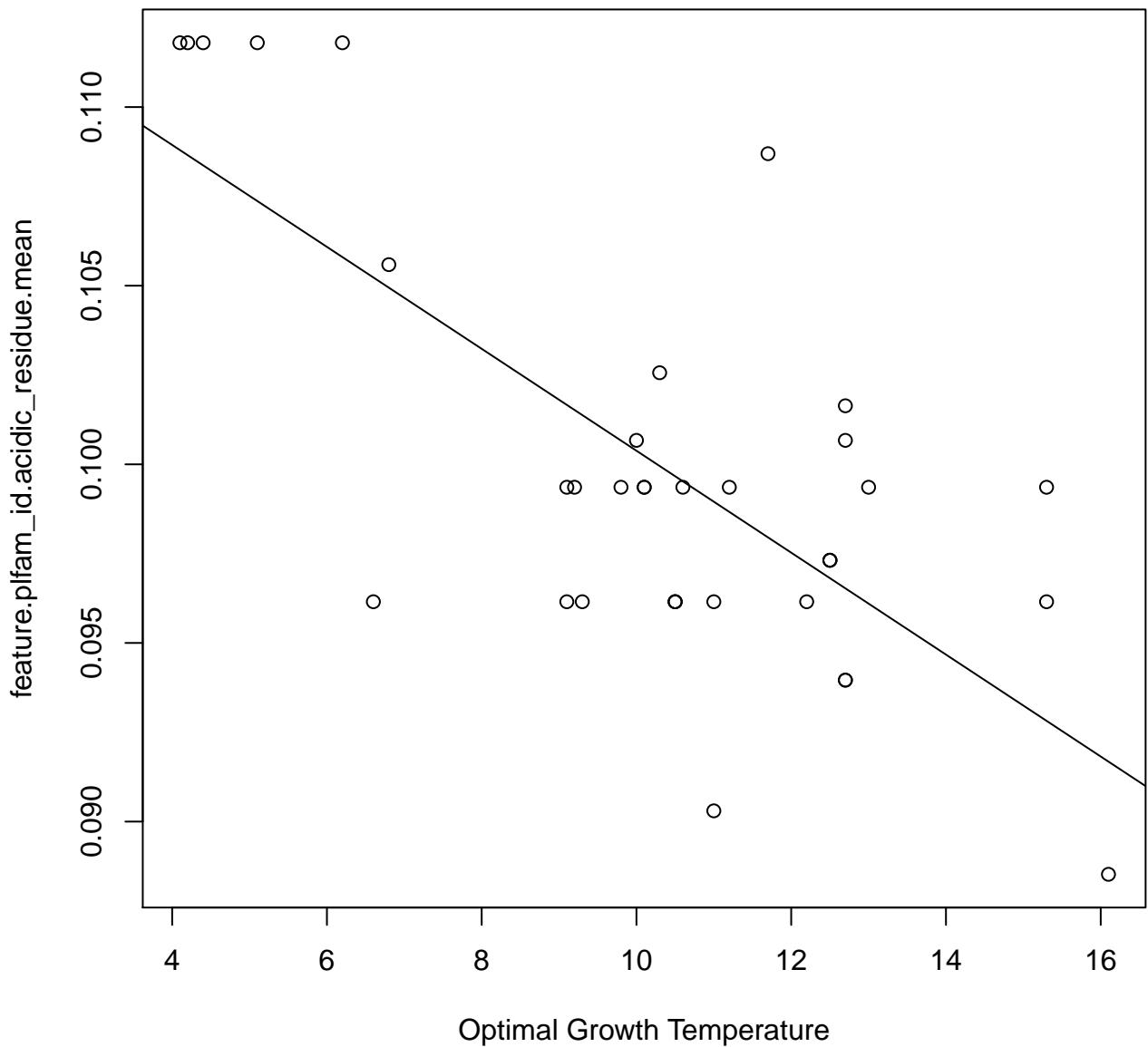
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PLF_28228_00015281
hypothetical protein



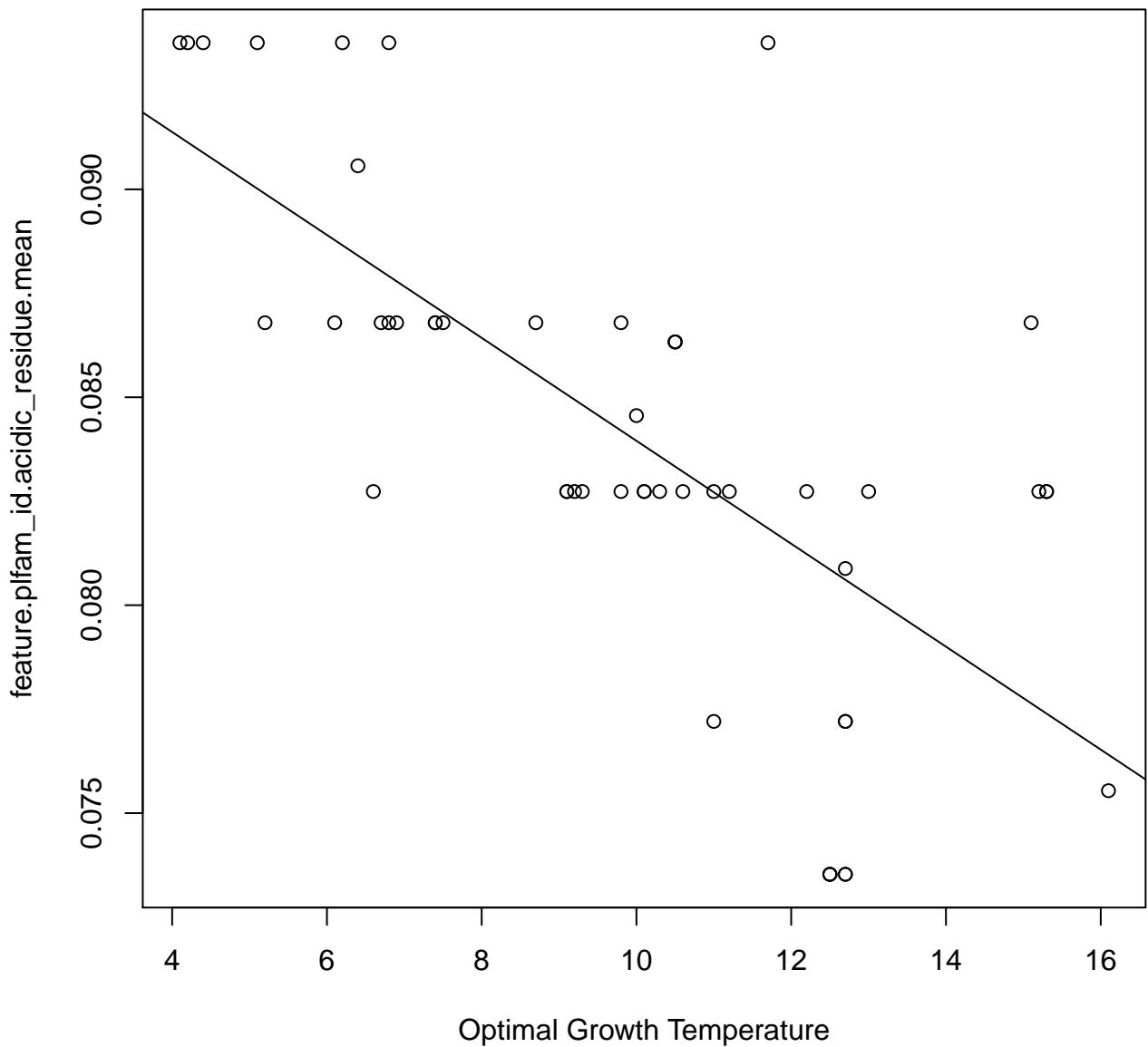
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PLF_28228_00001333
Uncharacterized membrane protein SO_0290



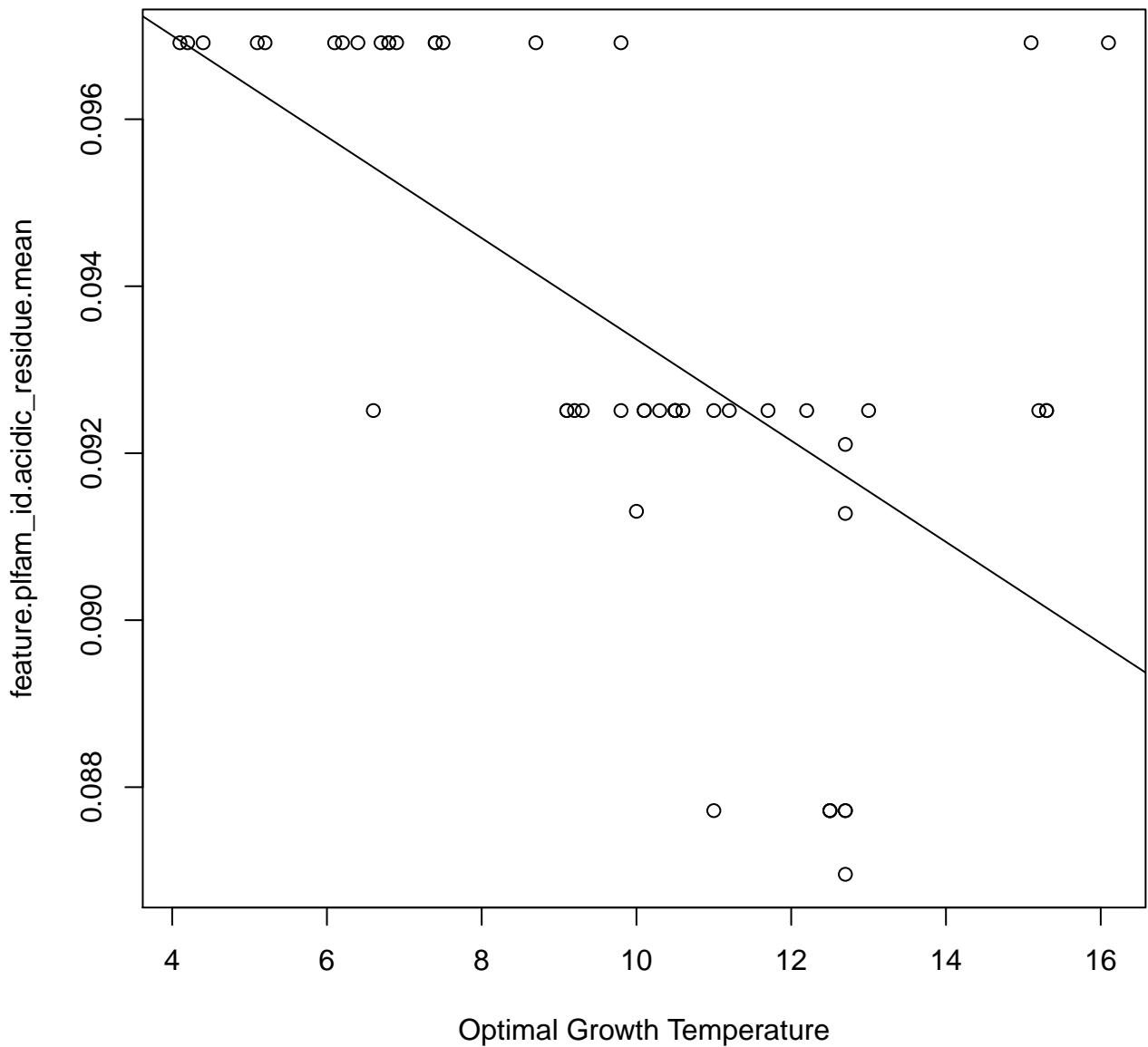
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PLF_28228_00002202
Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family



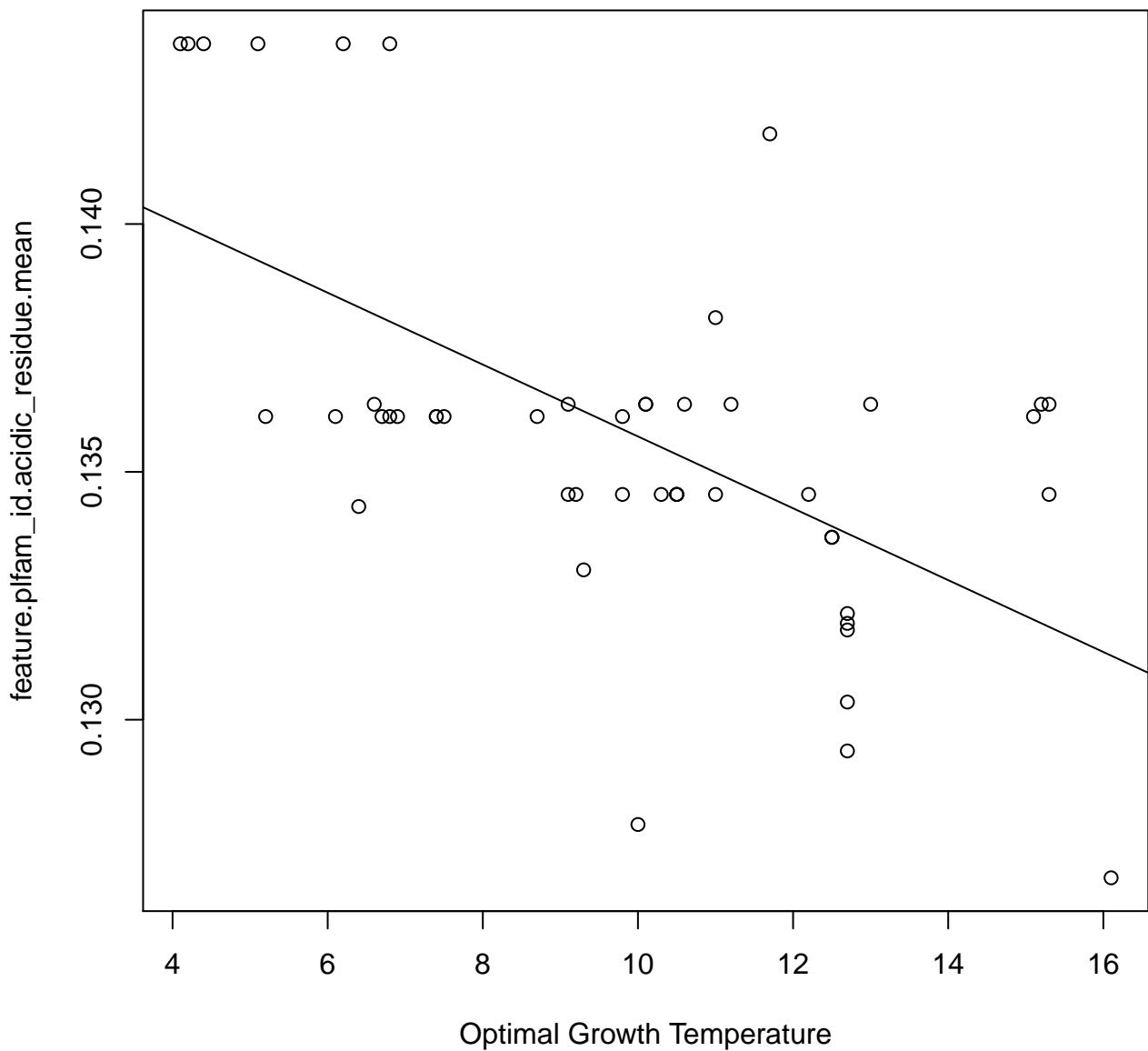
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Caulimovirus viroplasmin / Ribonuclease HI (EC 3.1.26.4)



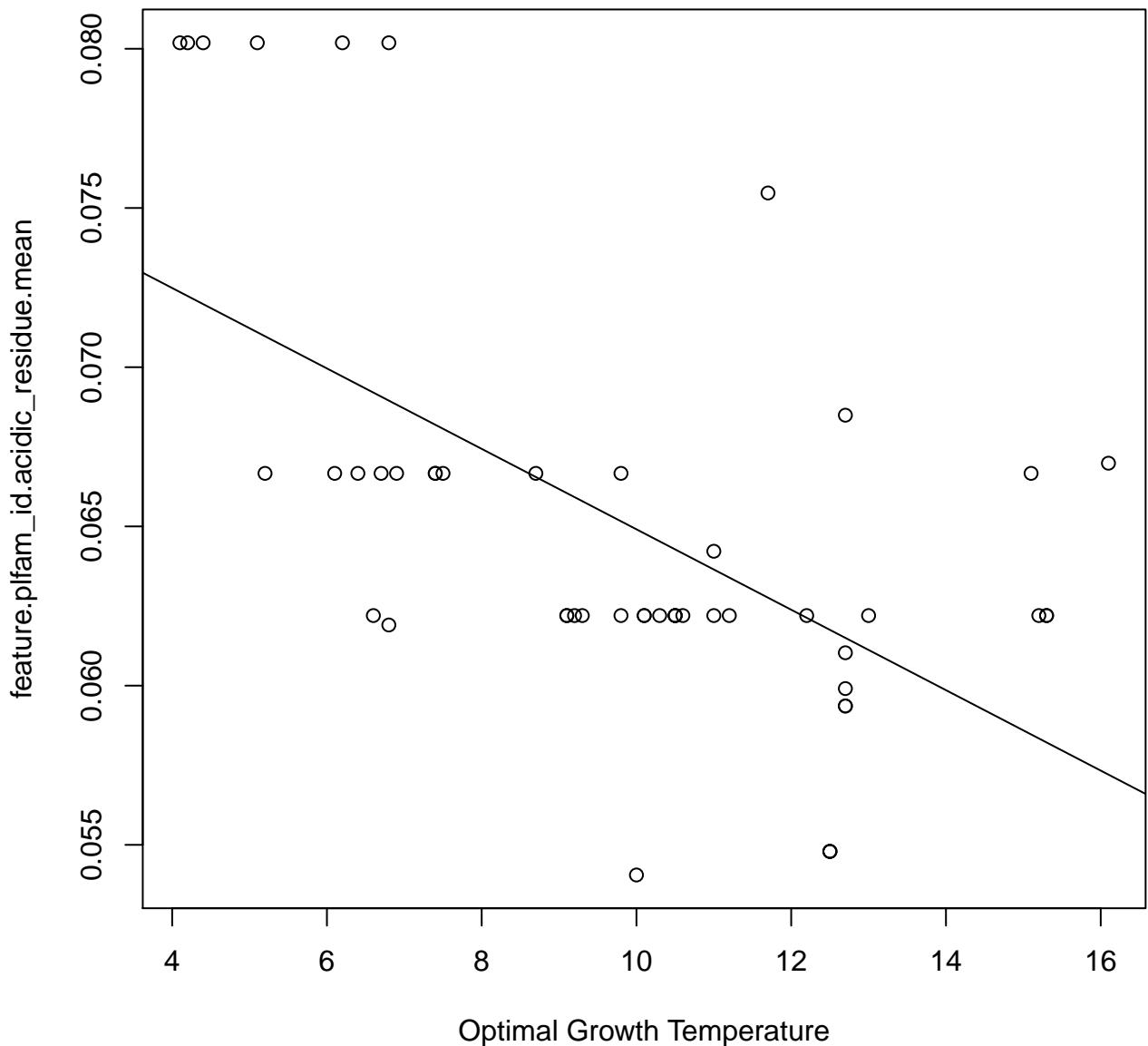
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PLF_28228_00001206
Tol-Pal system protein TolQ



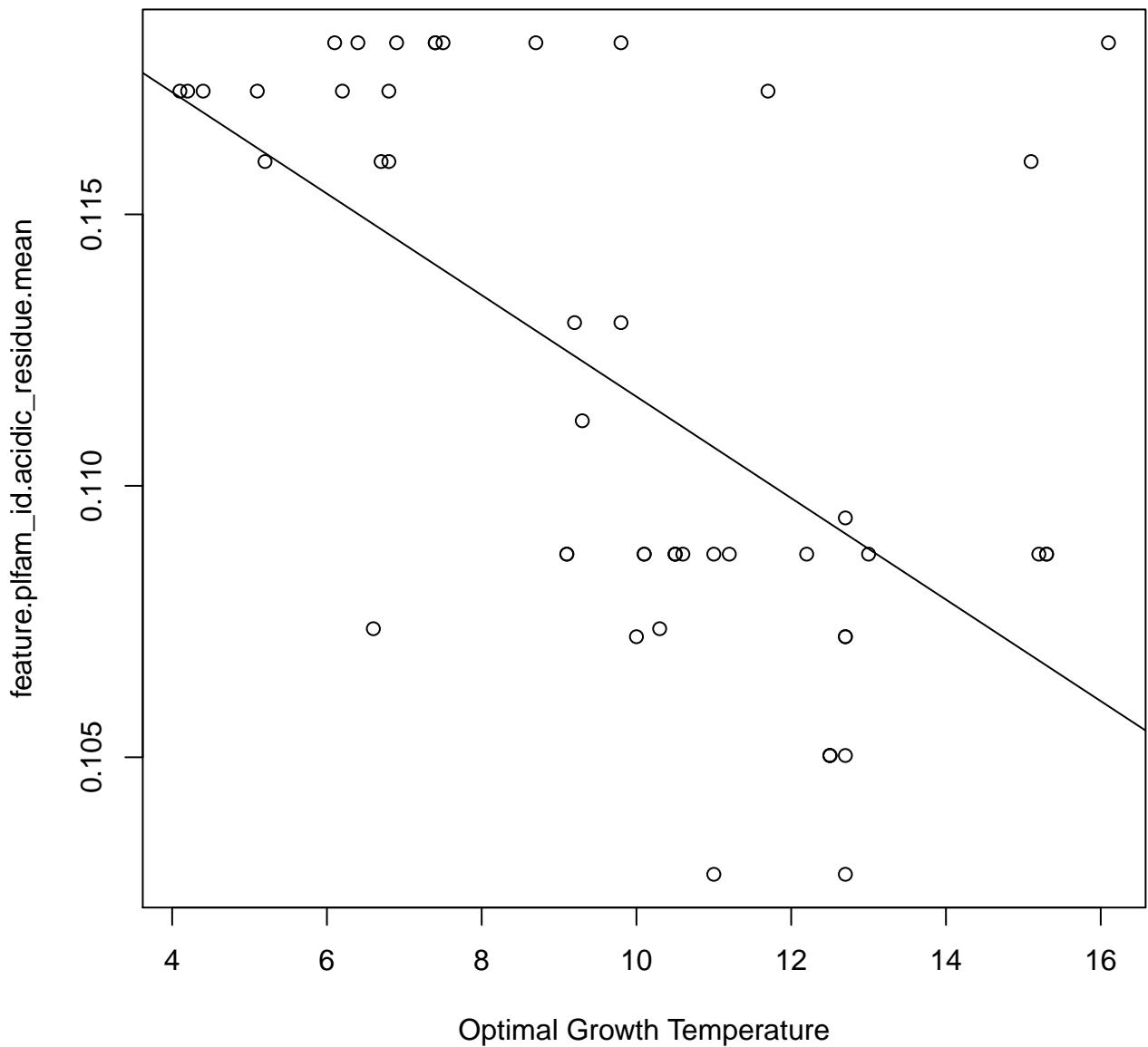
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Nudix hydrolase 3 (EC 3.6.1.-)



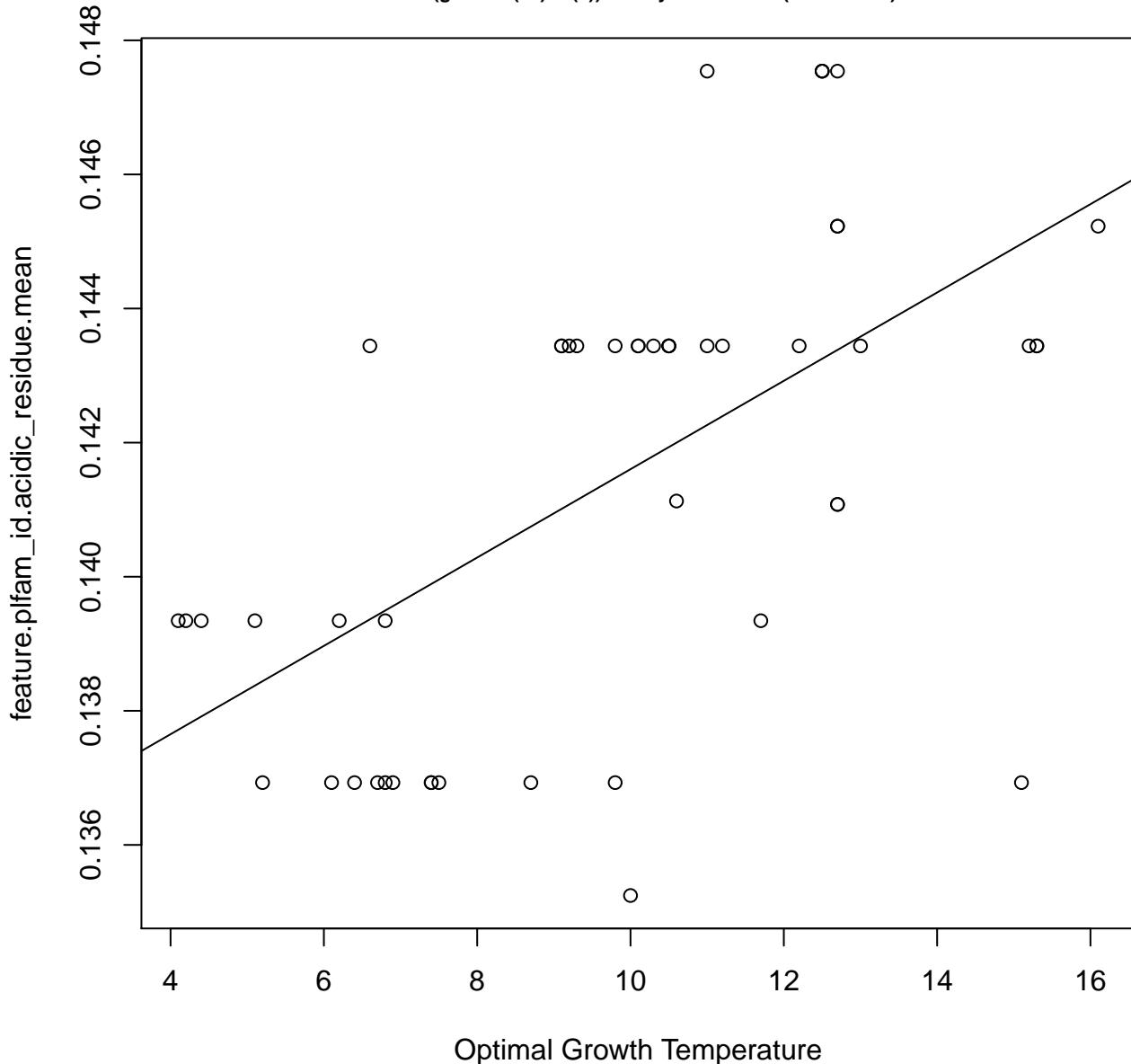
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PLF_28228_00001986
UPF0126 inner membrane protein Yads



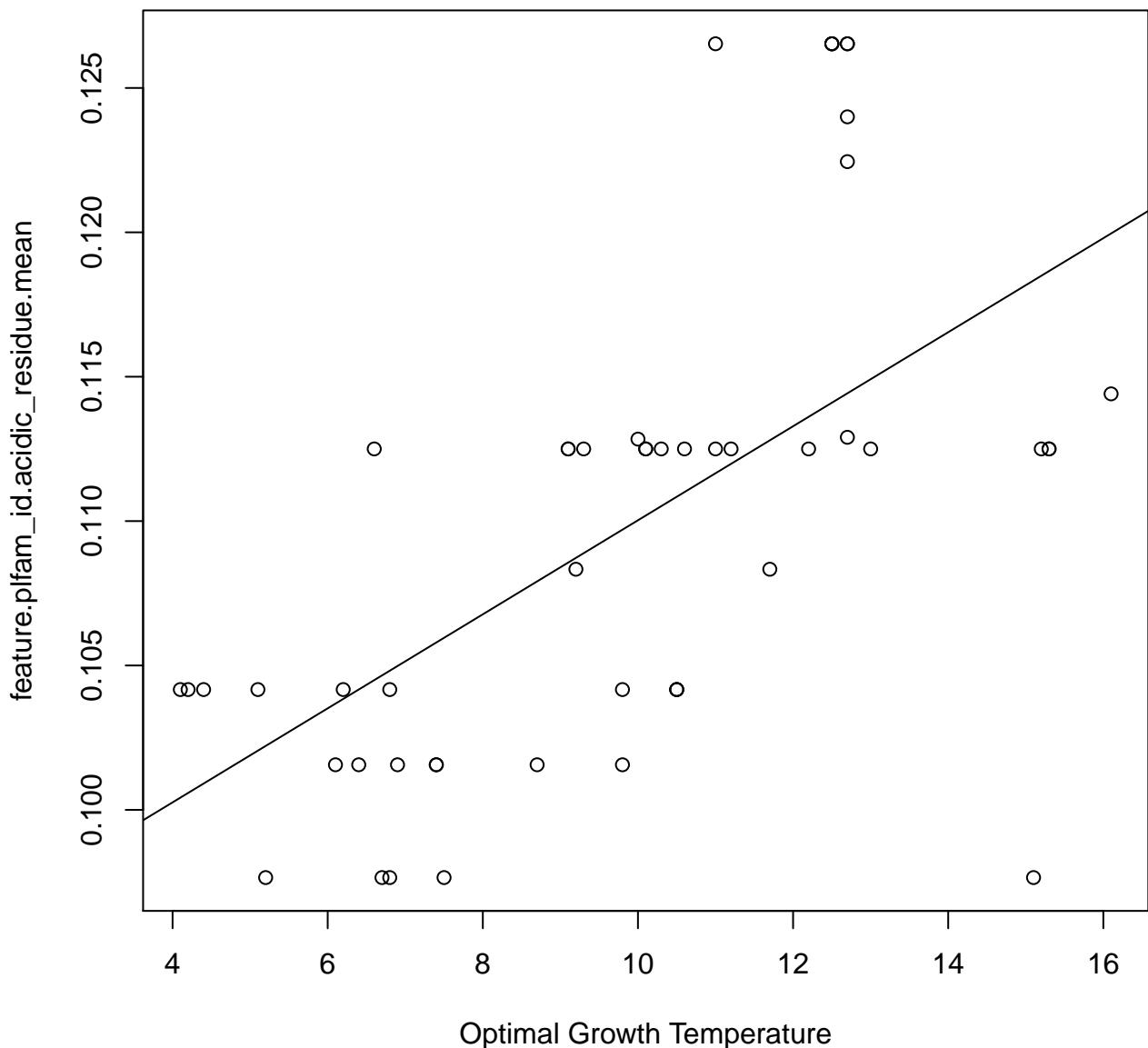
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PLF_28228_00001230
Transcriptional response regulatory protein GlrR



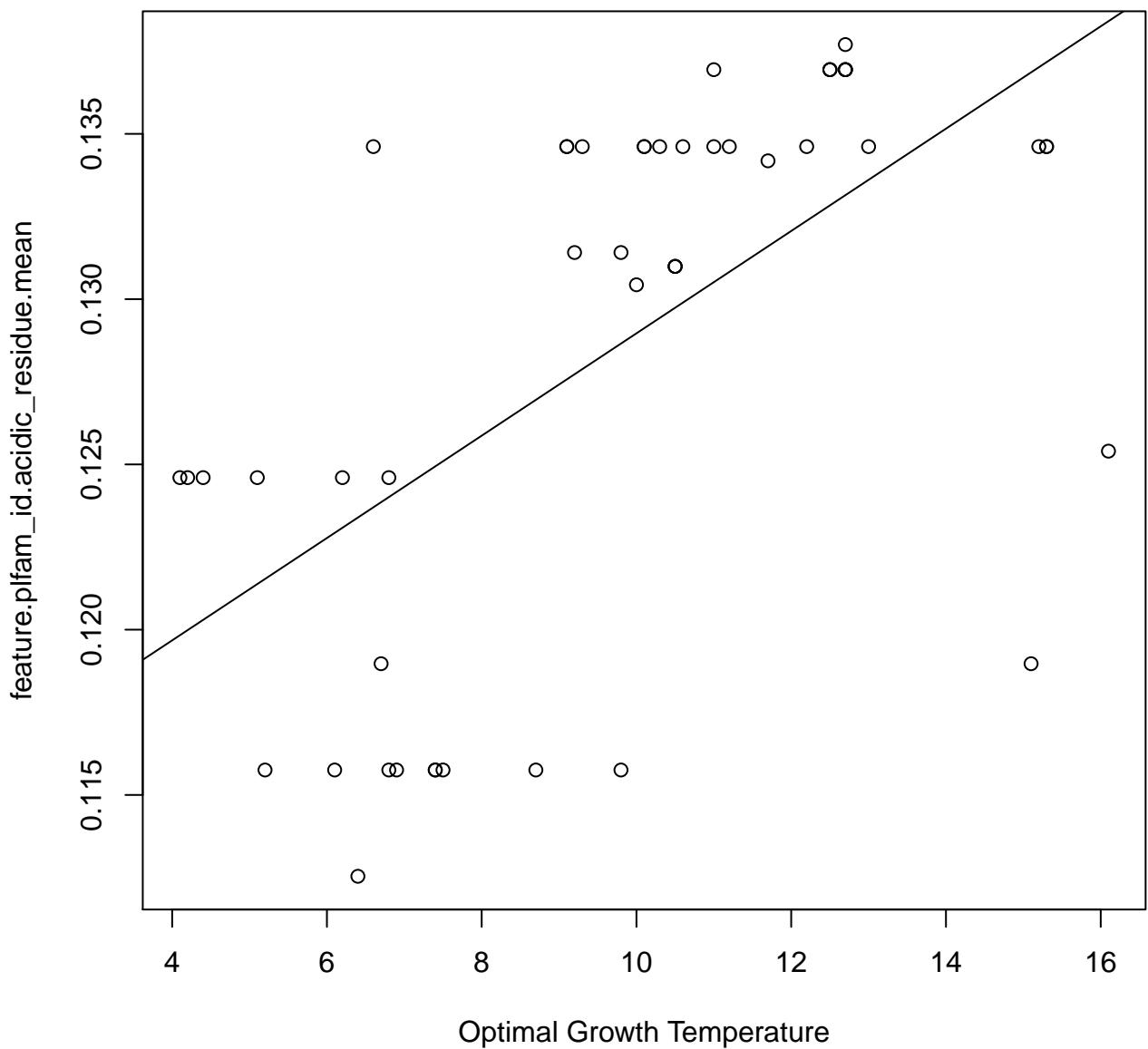
feature.plfam_id.acidic_residue.mean
PLF_28228_00001398
tRNA (guanine(46)-N(7))-methyltransferase (EC 2.1.1.33)



feature.plfam_id.acidic_residue.mean
PLF_28228_00000498
Histidine utilization repressor



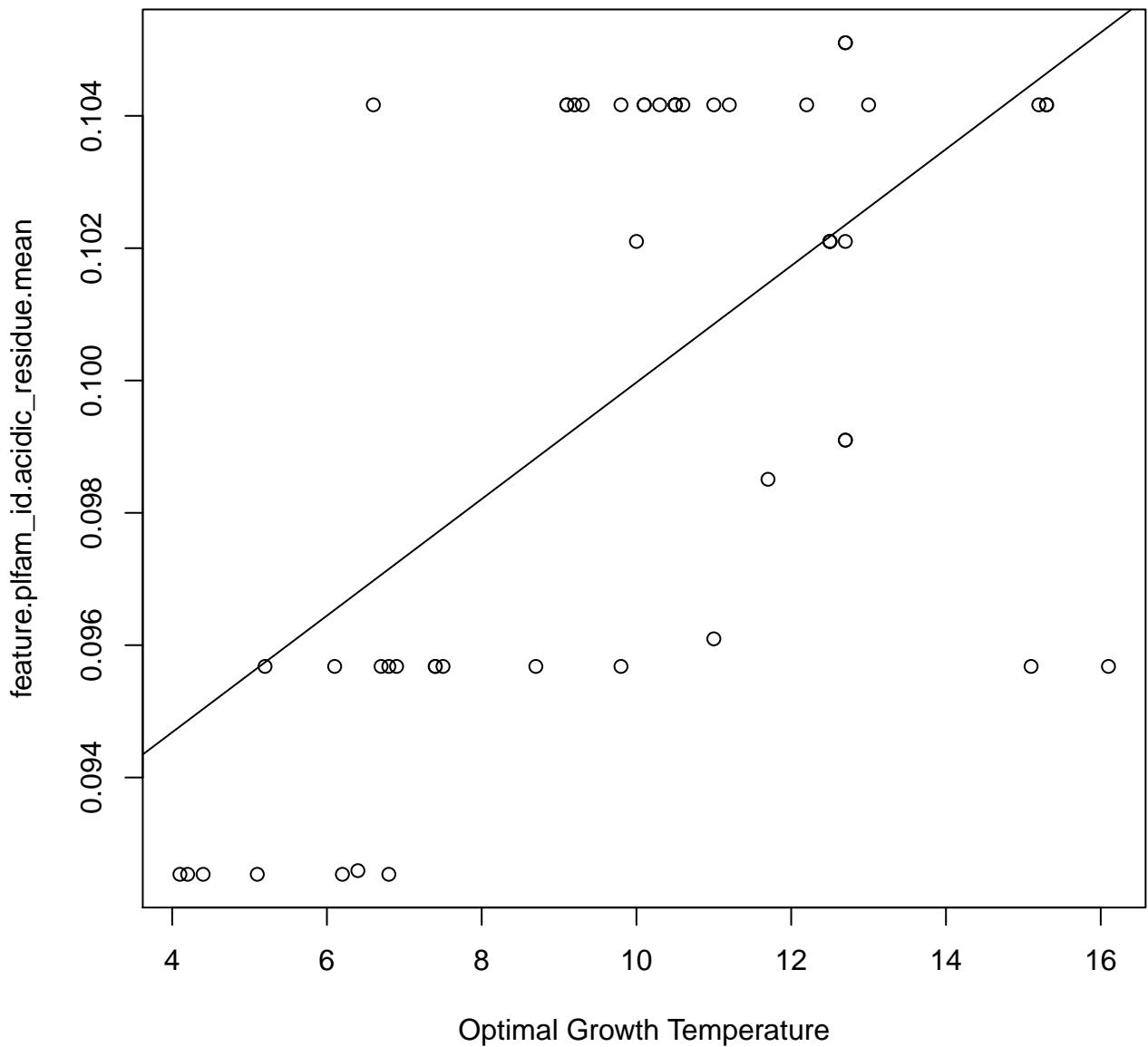
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PLF_28228_00000841
Flagellar motor rotation protein MotB



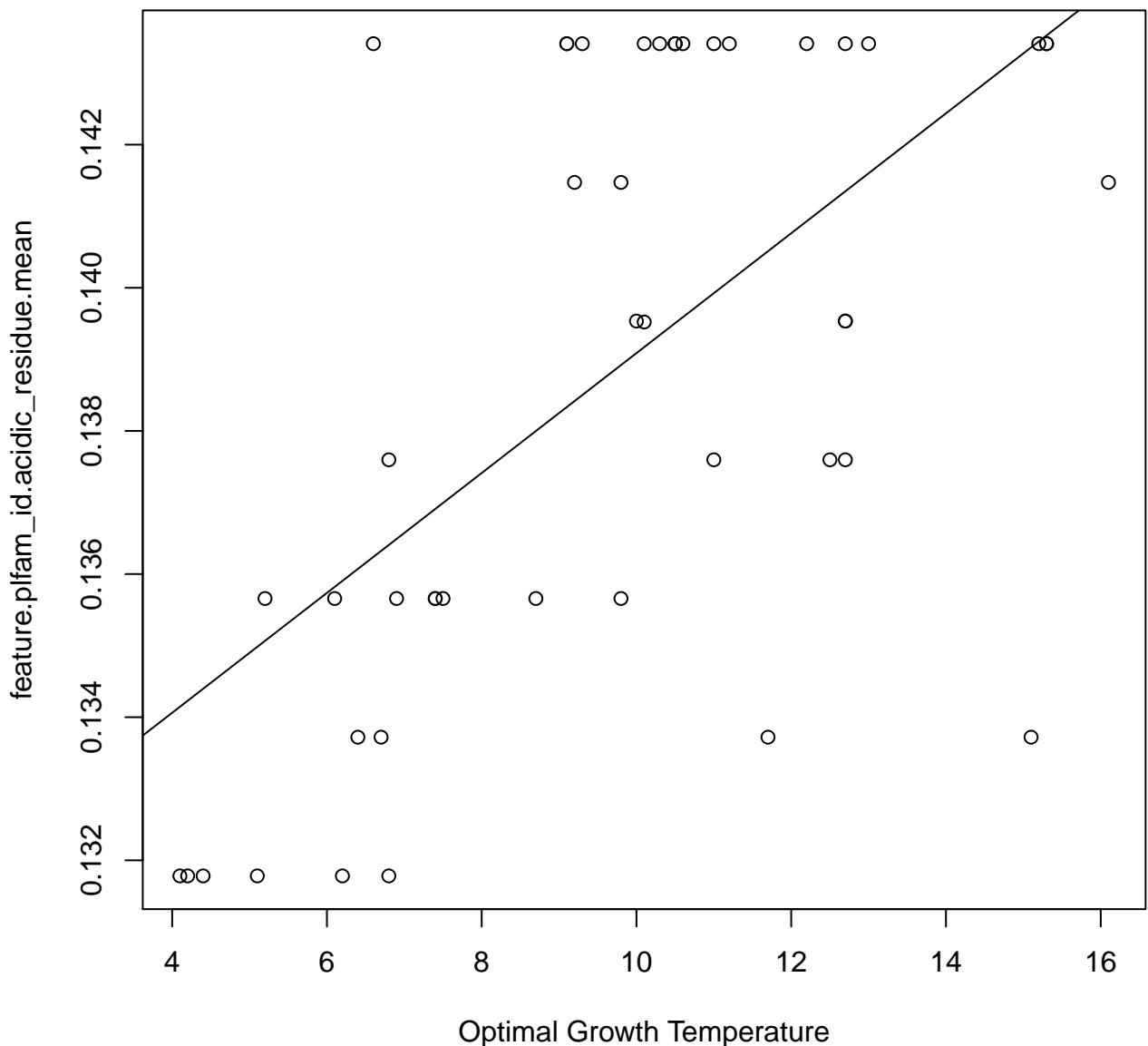
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PLF_28228_00000392

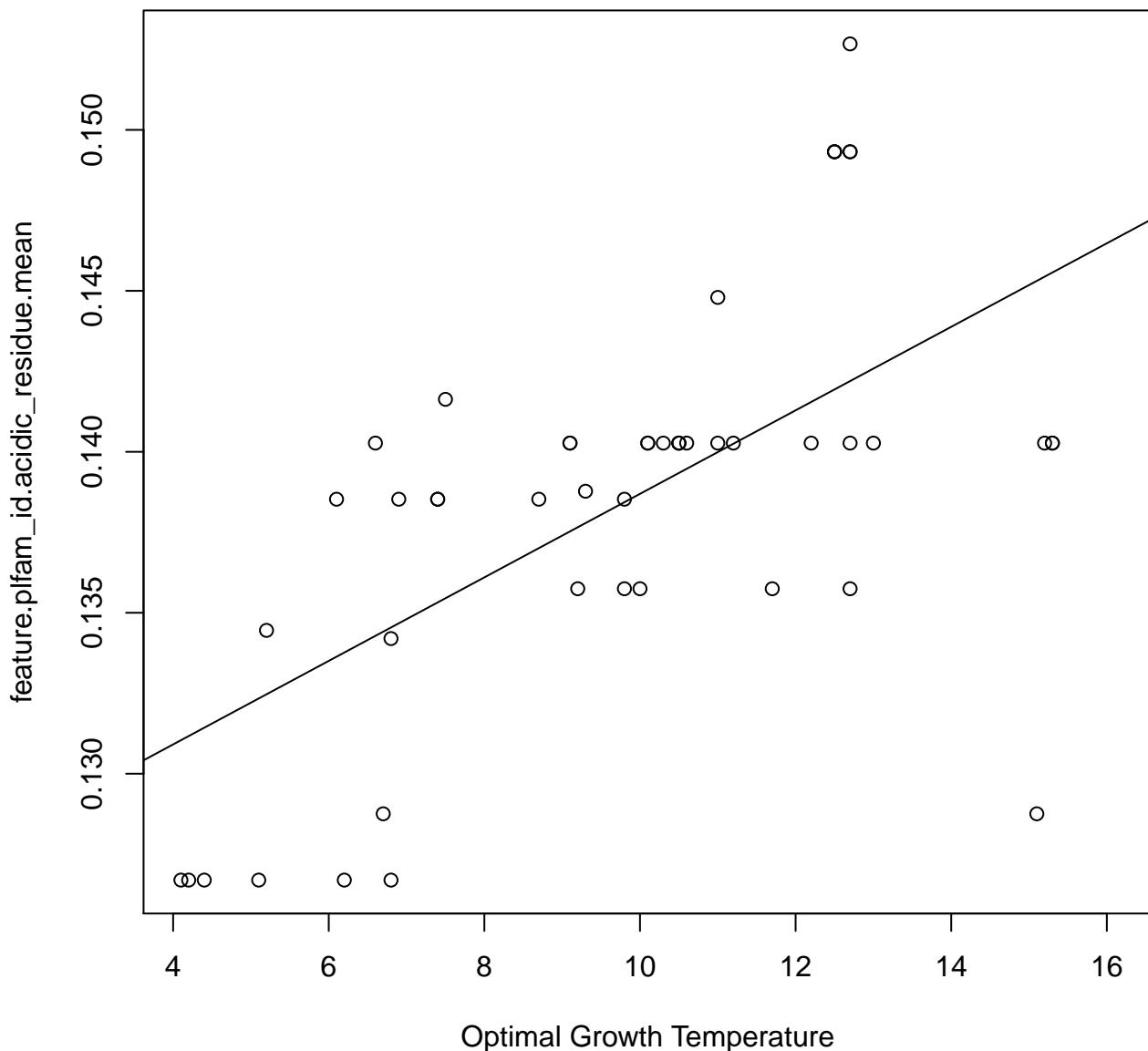
Biotin operon repressor / Biotin--protein ligase (EC 6.3.4.9)(EC 6.3.4.10)(EC 6.3.4.11)(EC 6.3.4.15)



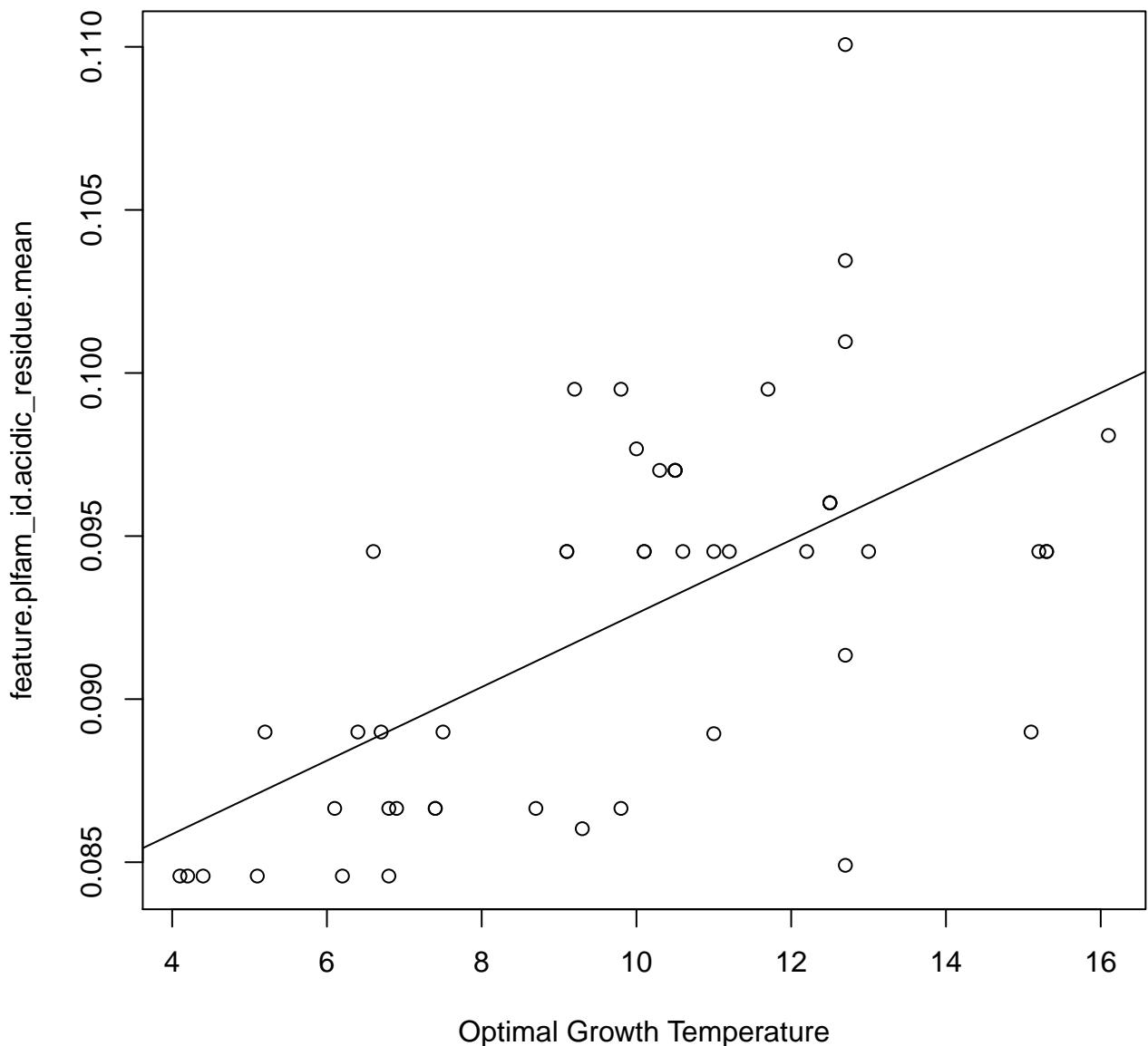
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Transcriptional repressor protein TyrR



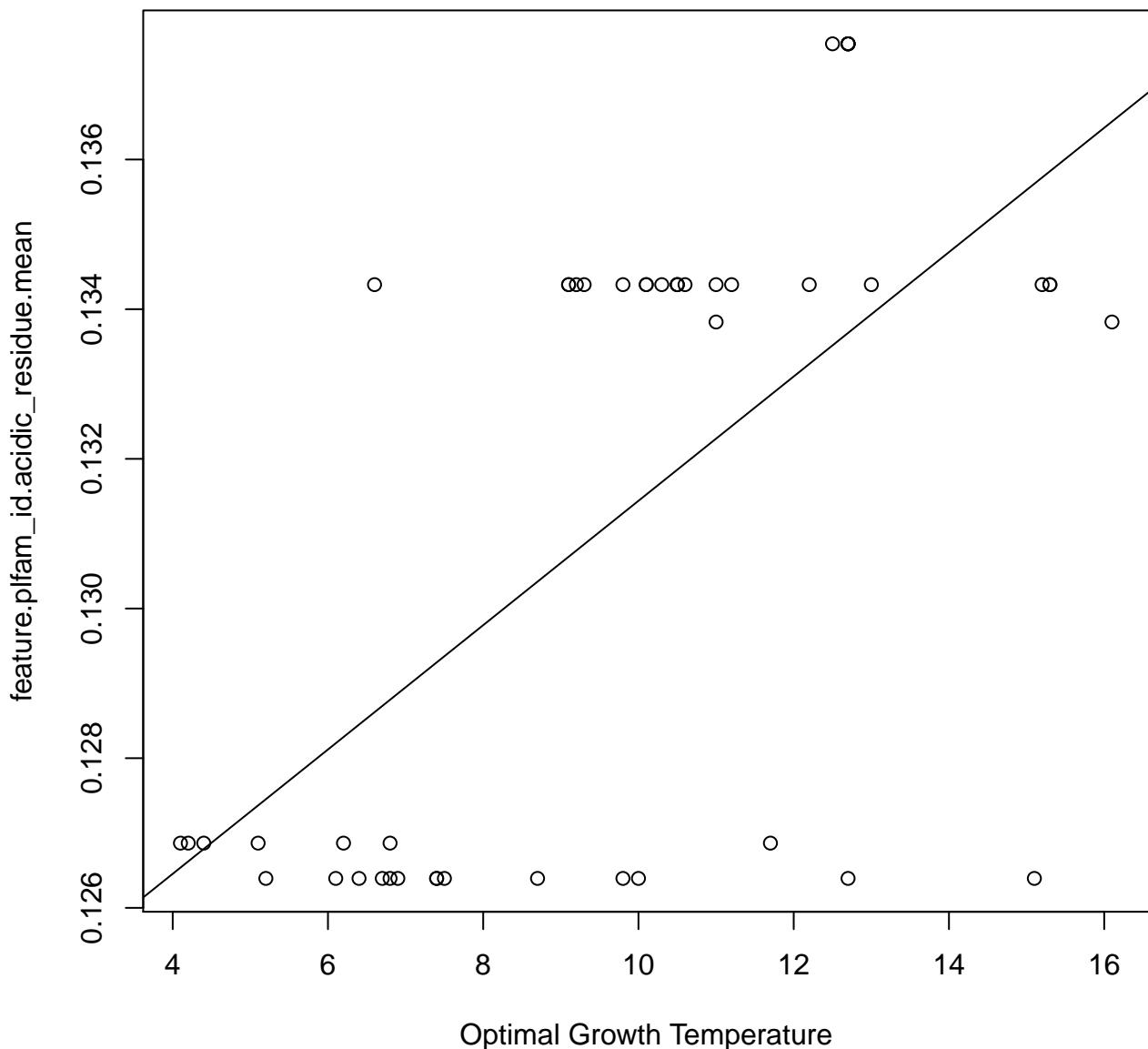
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Protein of unknown function YceH



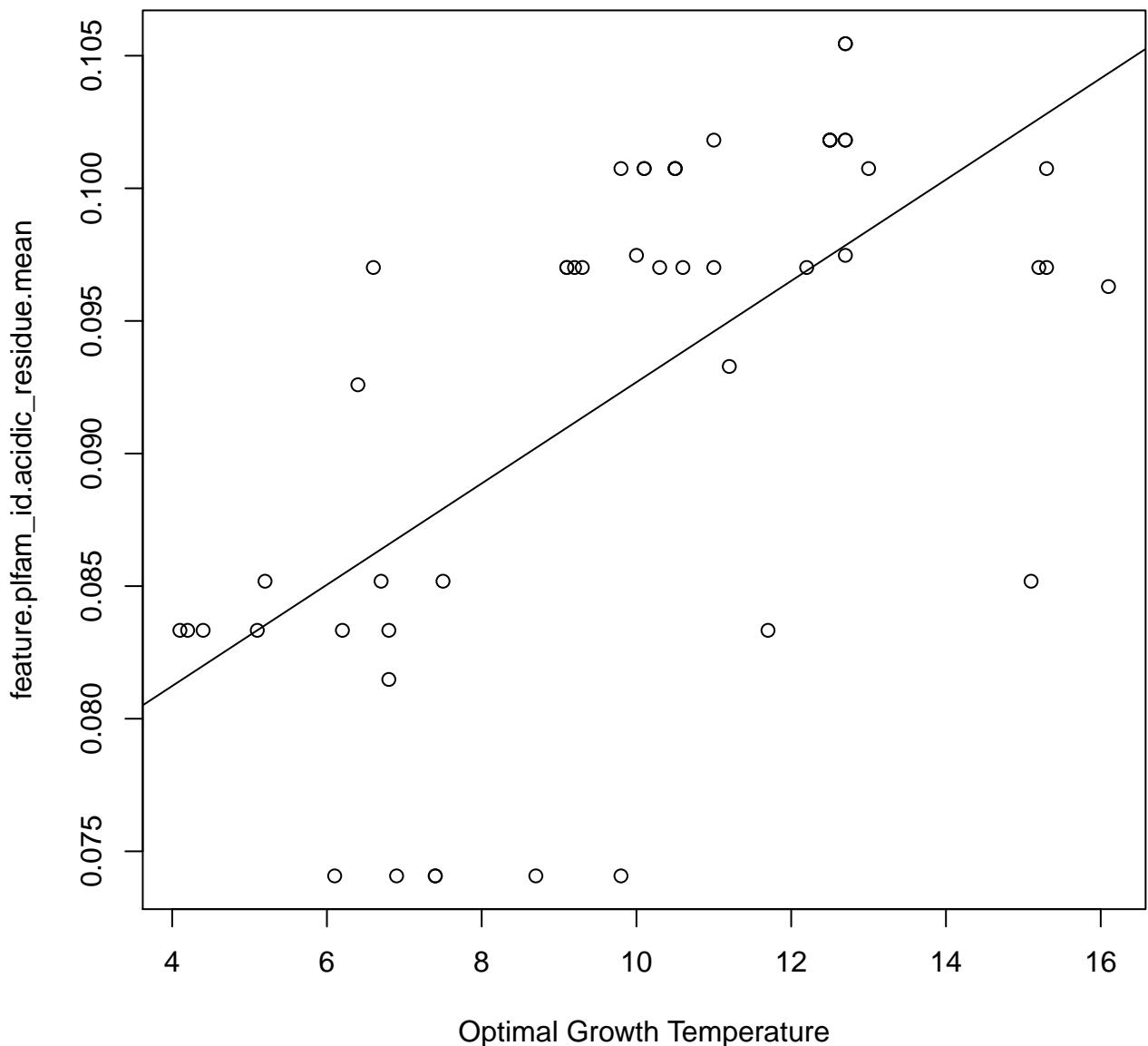
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PLF_28228_00001726
Membrane-bound lytic murein transglycosylase B



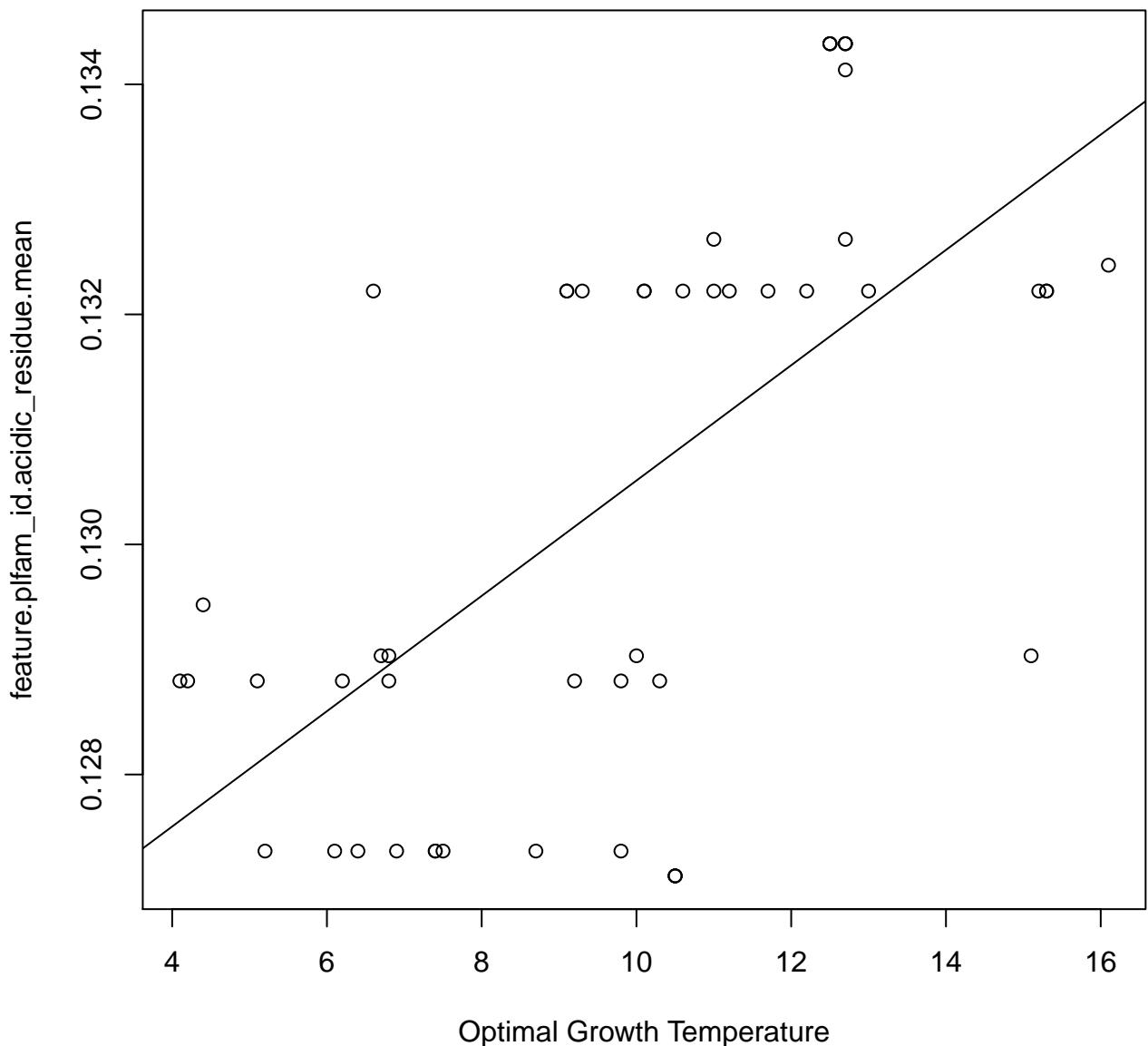
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Serine acetyltransferase (EC 2.3.1.30)



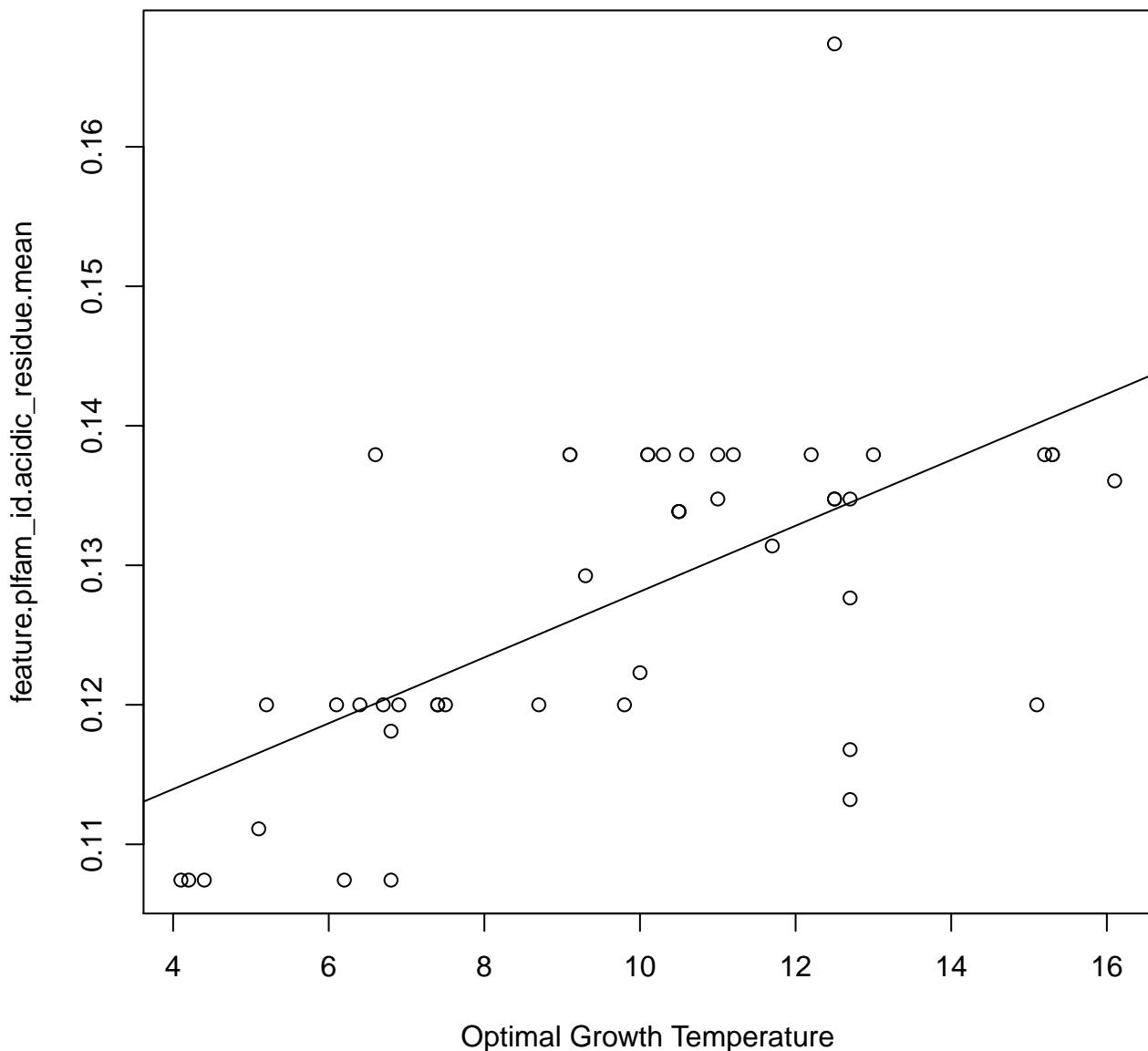
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PLF_28228_00001140
Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)



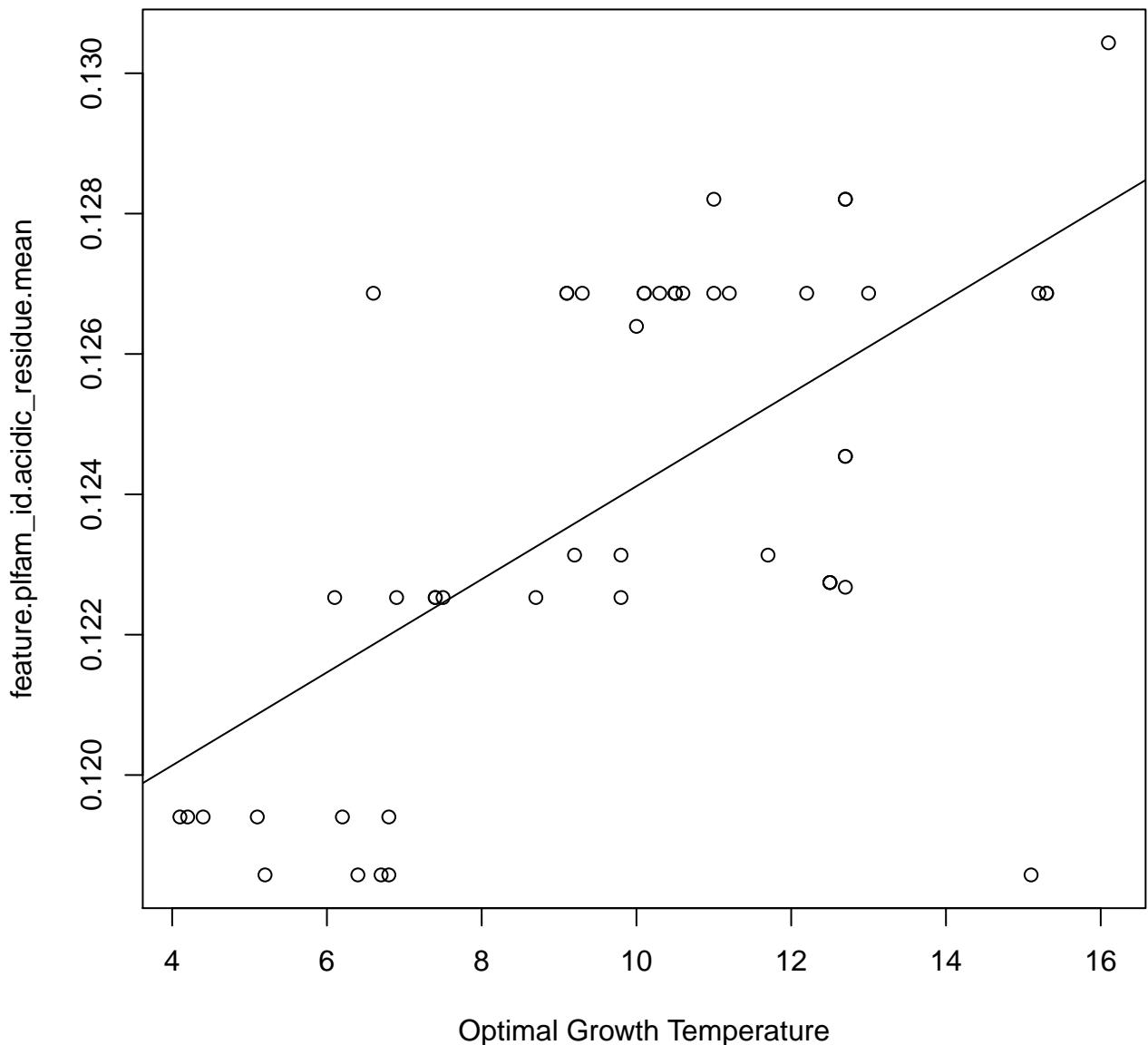
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PLF_28228_00001165
Succinate dehydrogenase flavoprotein subunit (EC 1.3.5.1)



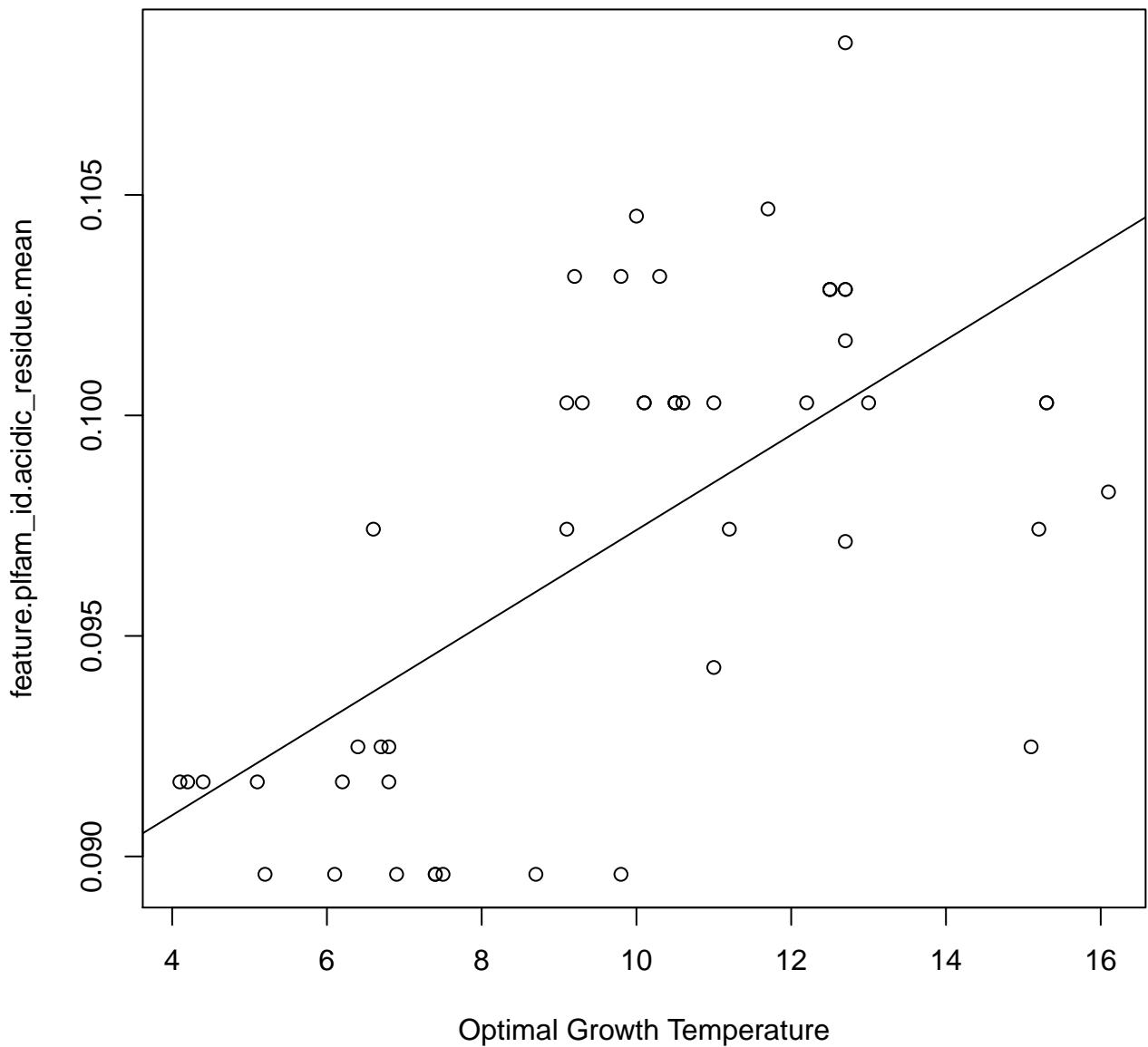
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PLF_28228_00000407
FIG024746: hypothetical protein



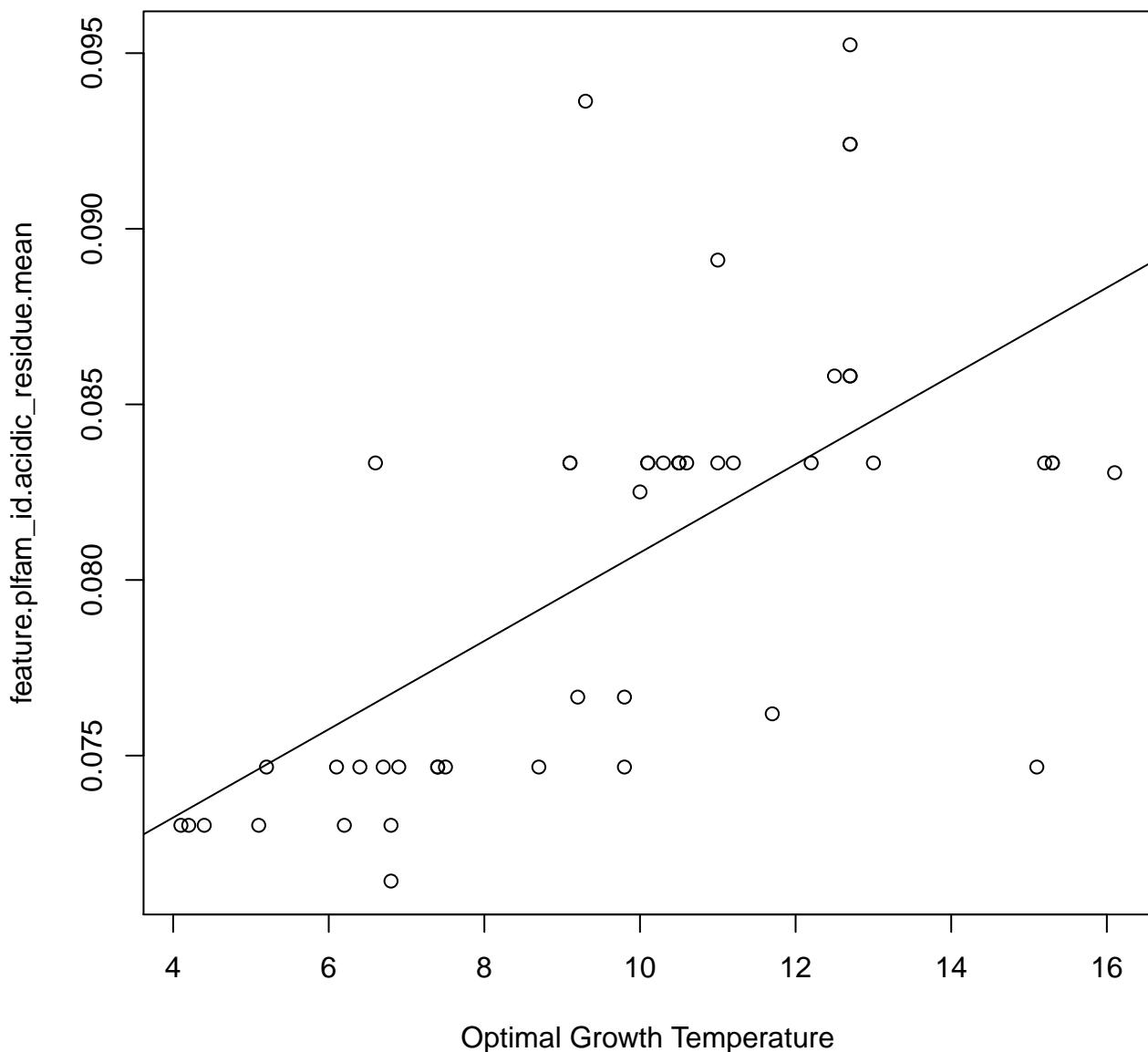
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PLF_28228_00001395
tRNA (cytidine(32)/uridine(32)-2'-O)-methyltransferase (EC 2.1.1.200)



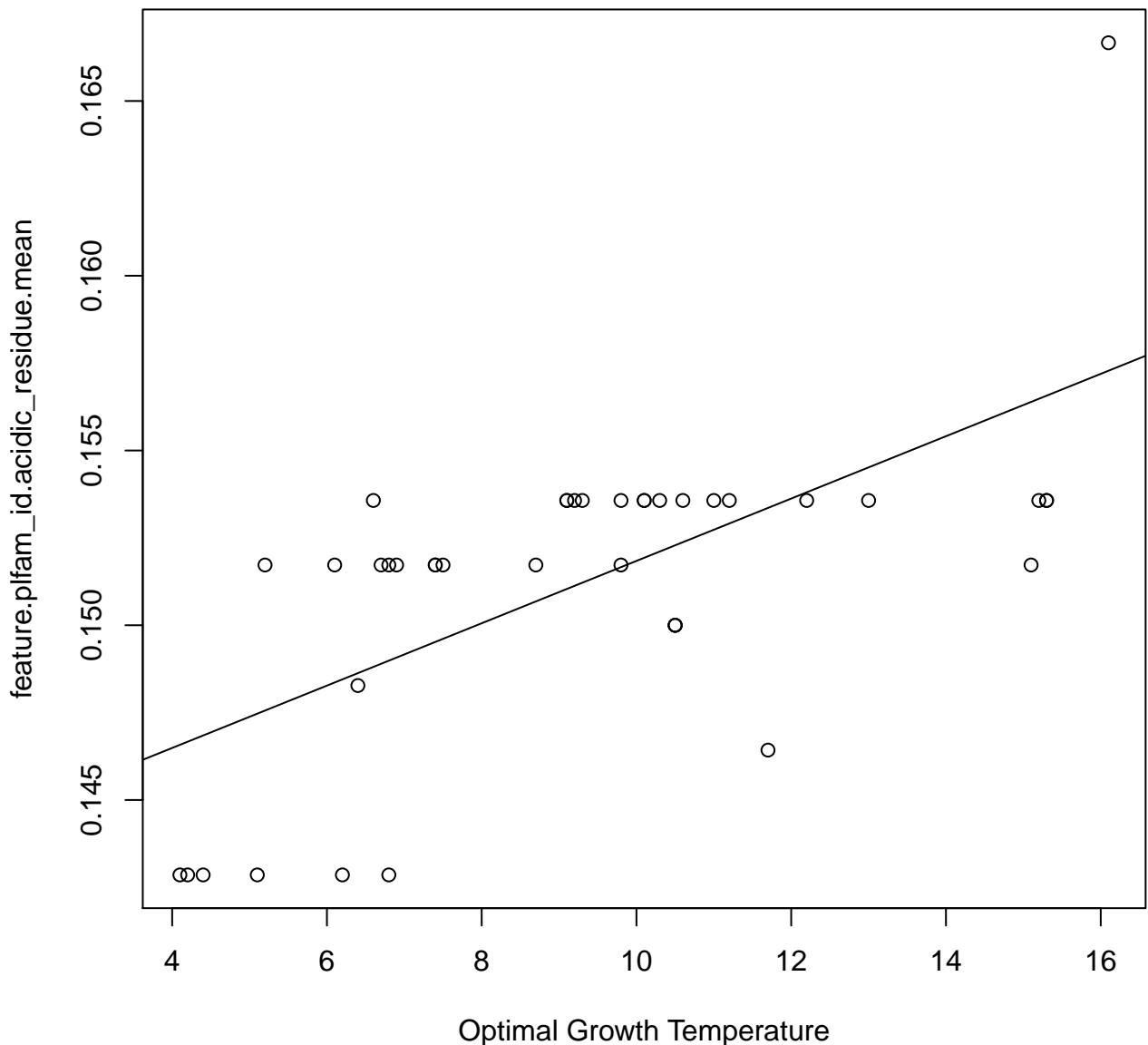
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PLF_28228_00002415
hypothetical protein



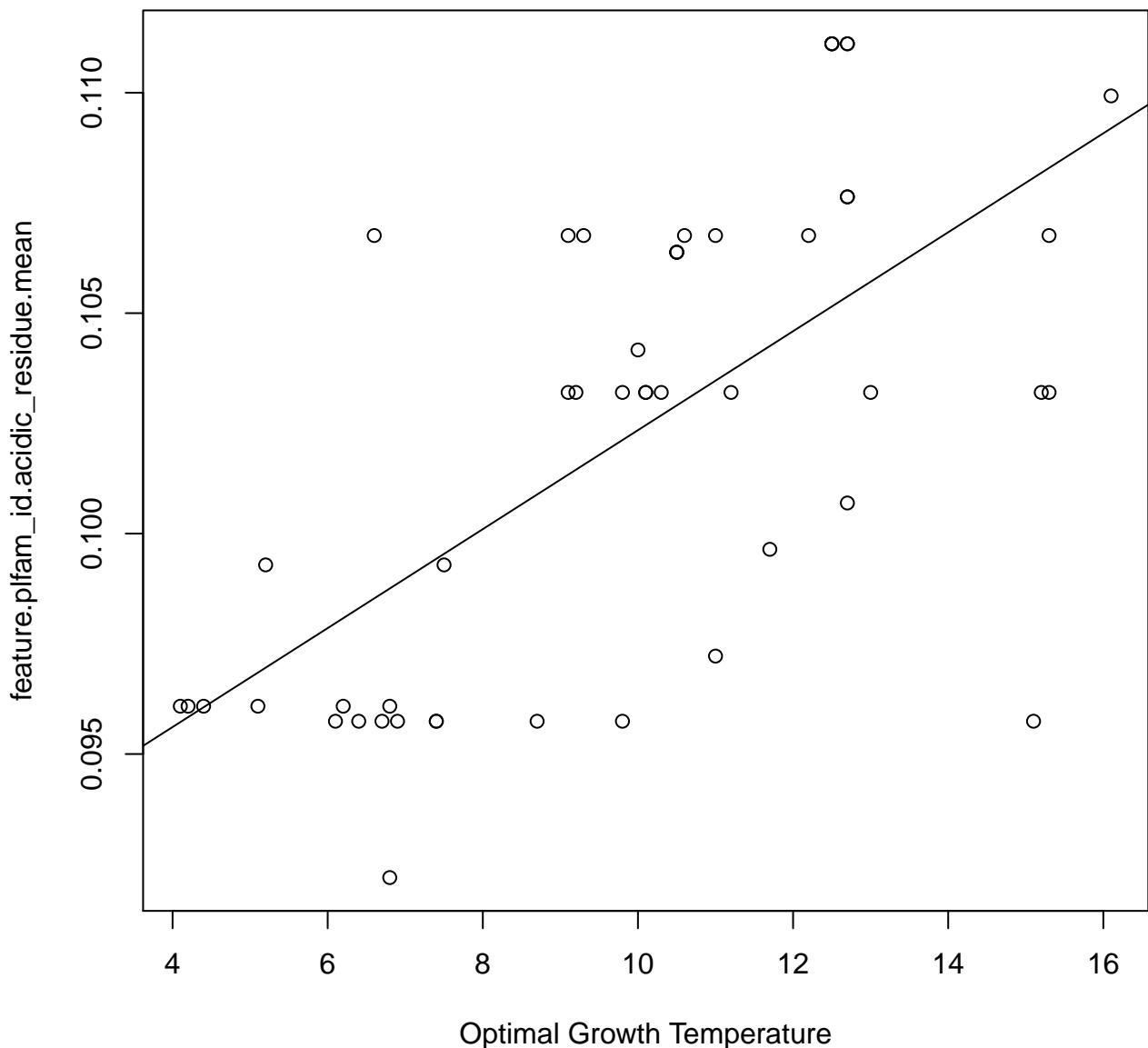
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Probable acyltransferase PA0834



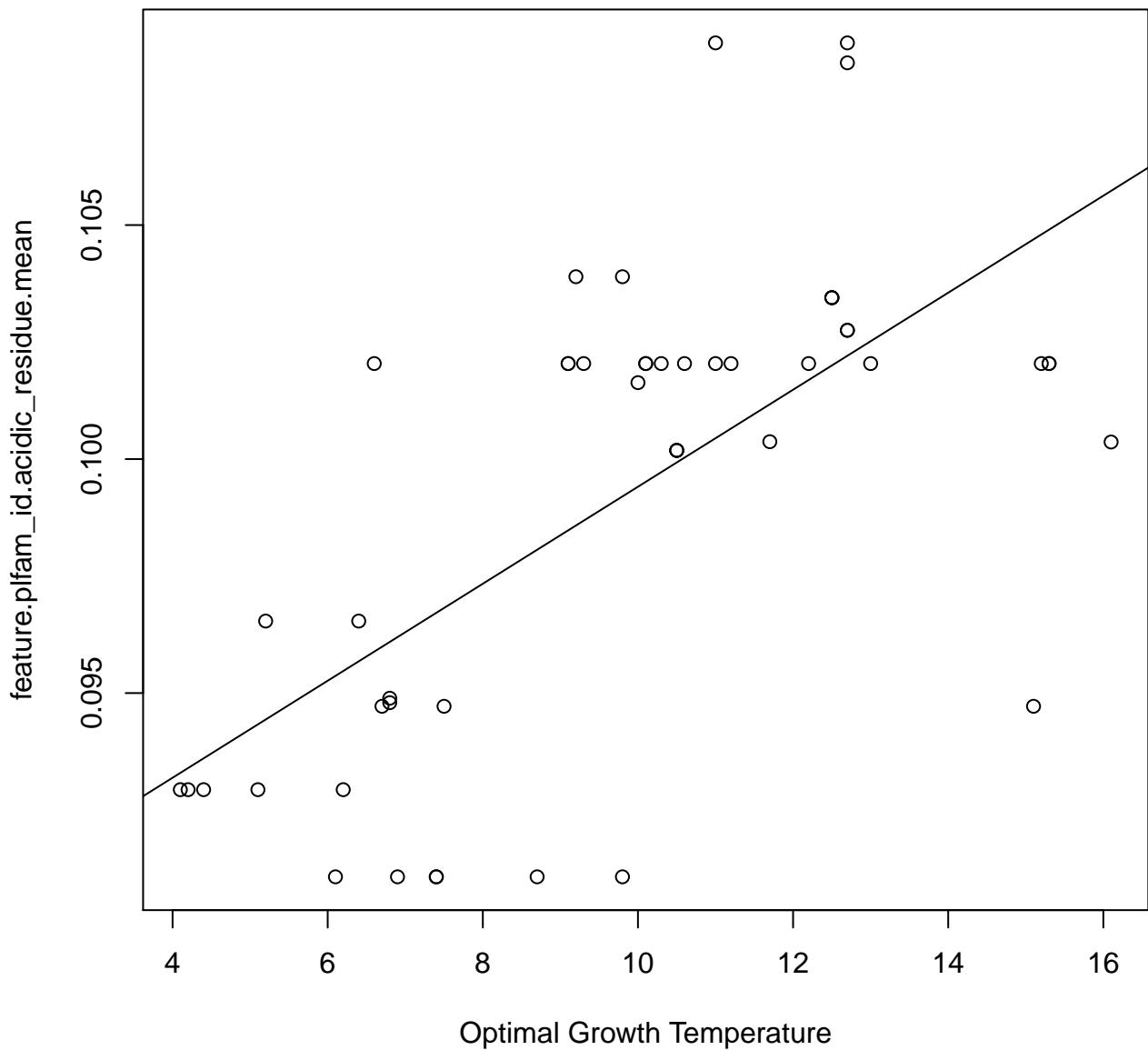
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Segregation and condensation protein A



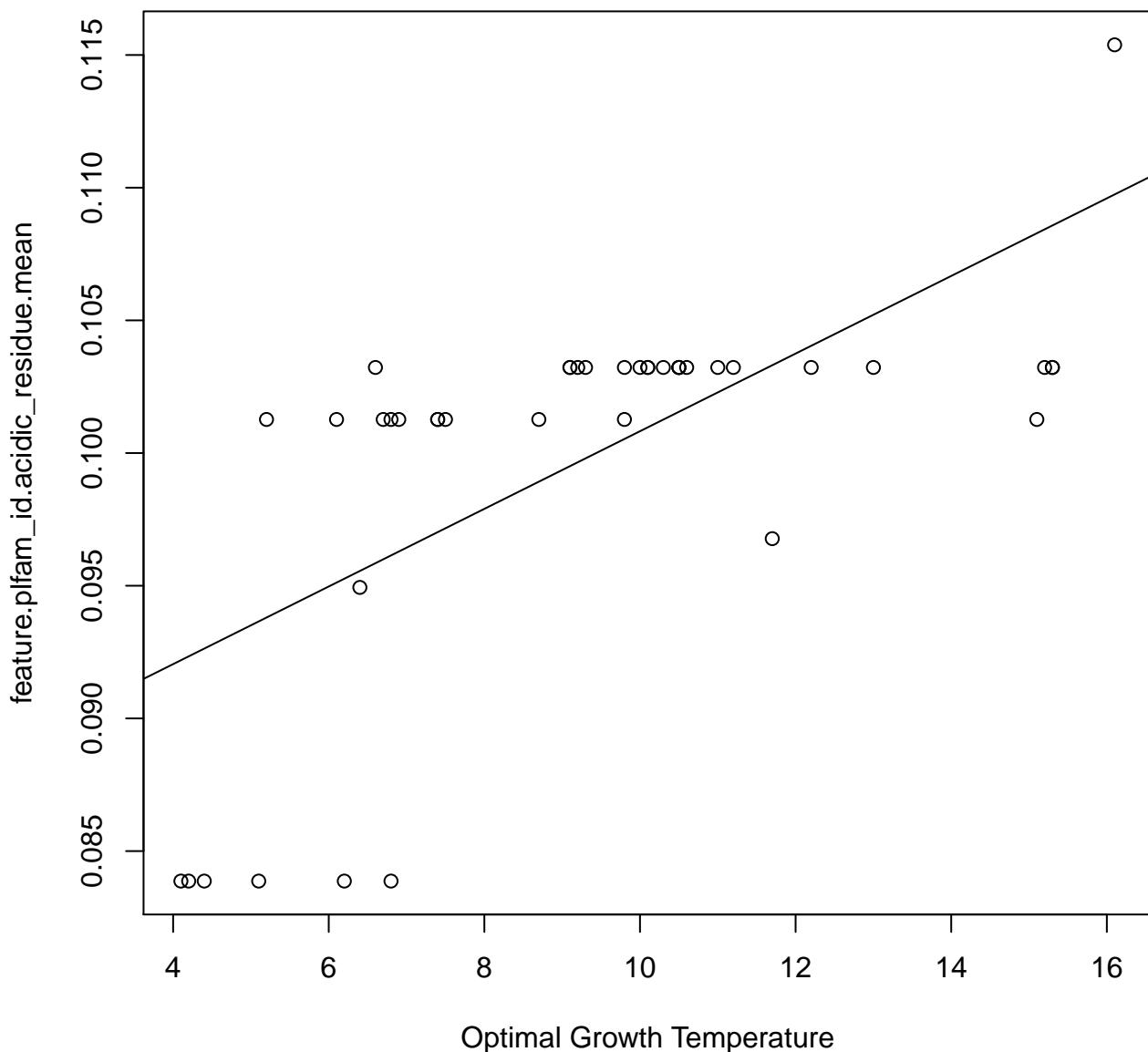
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Pantoate--beta-alanine ligase (EC 6.3.2.1)



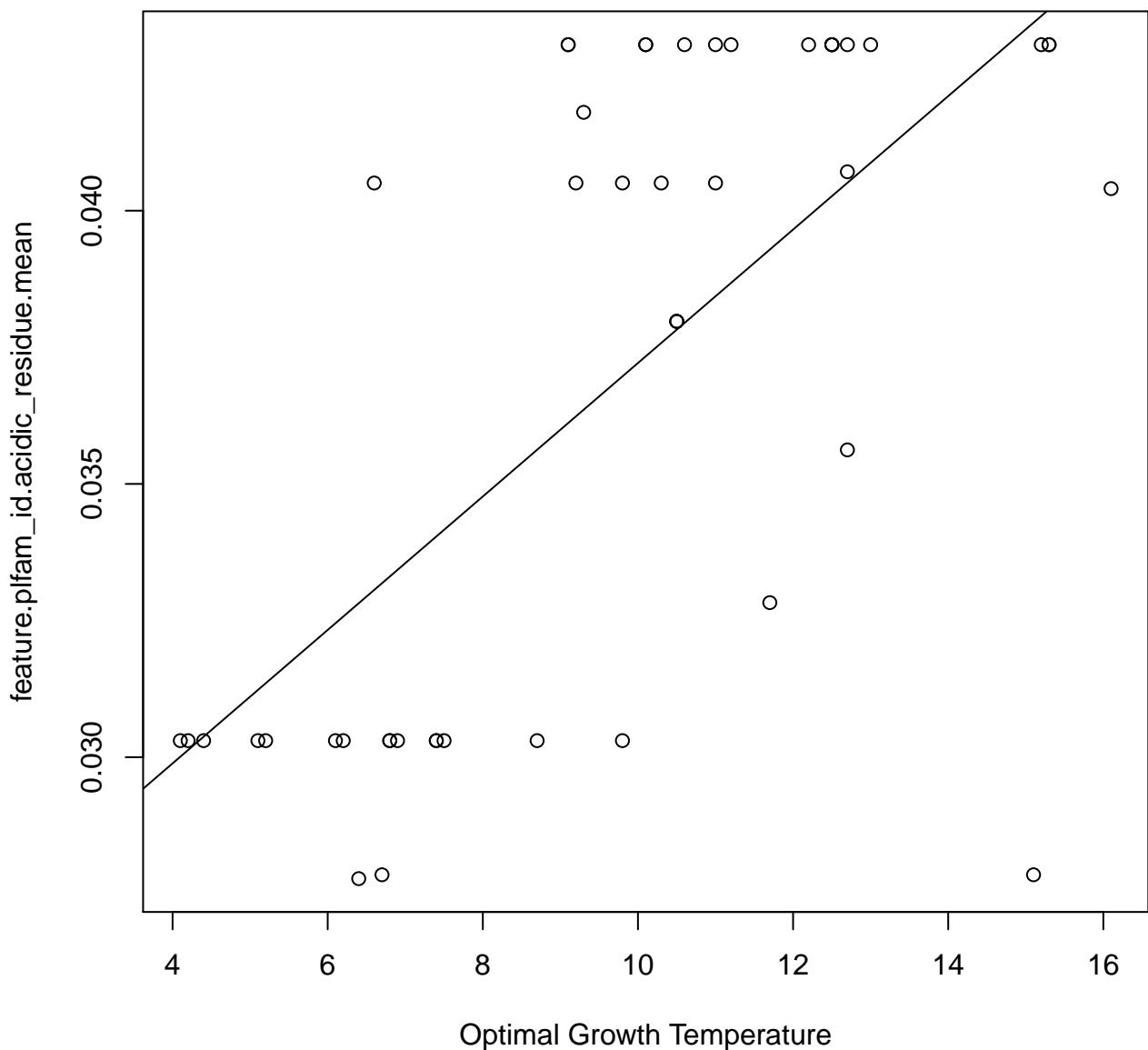
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PLF_28228_00002742
Glucose-6-phosphate isomerase (EC 5.3.1.9)



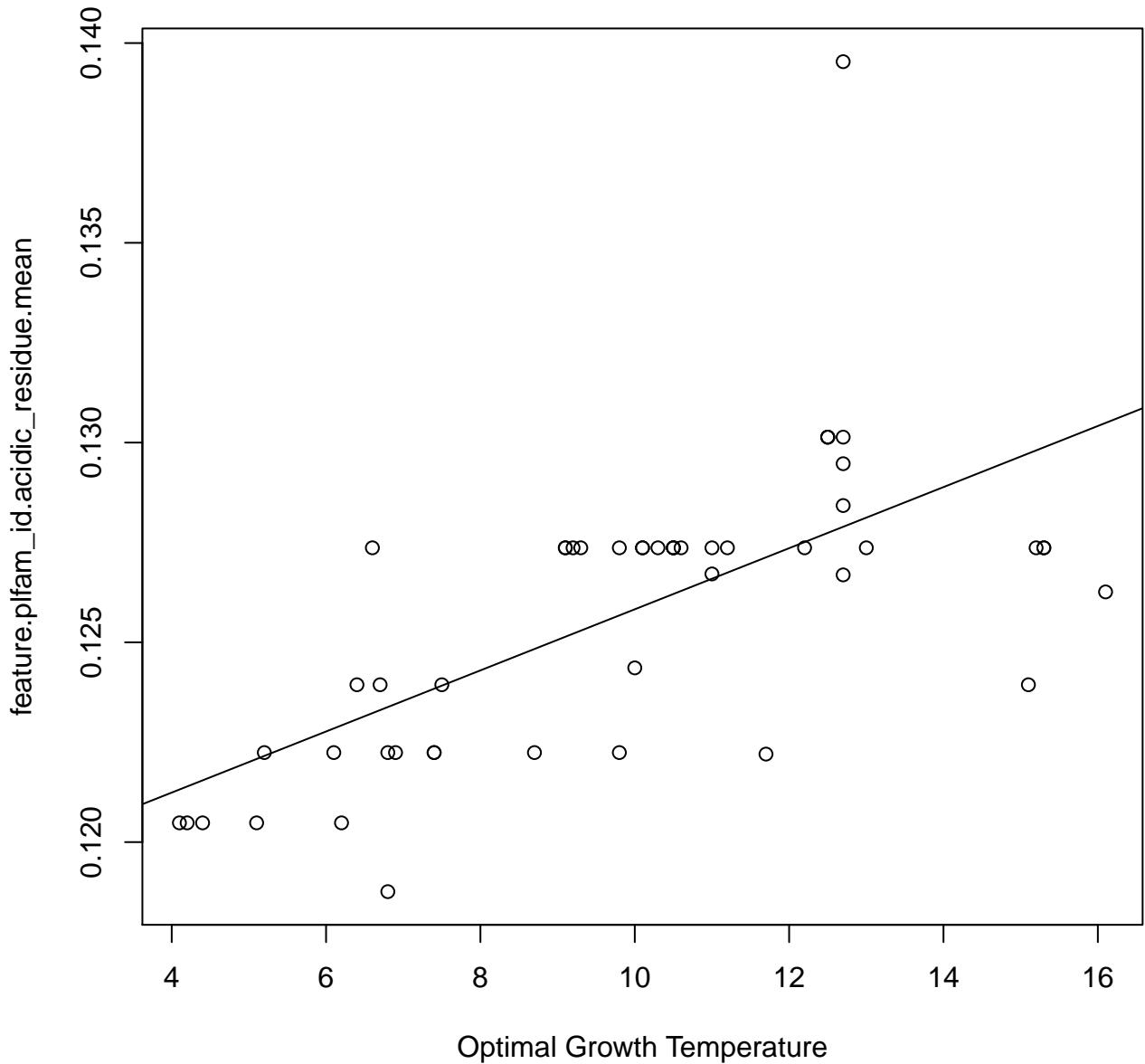
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PLF_28228_00015721
Uncharacterized aldehyde oxidase, 2Fe–2S subunit



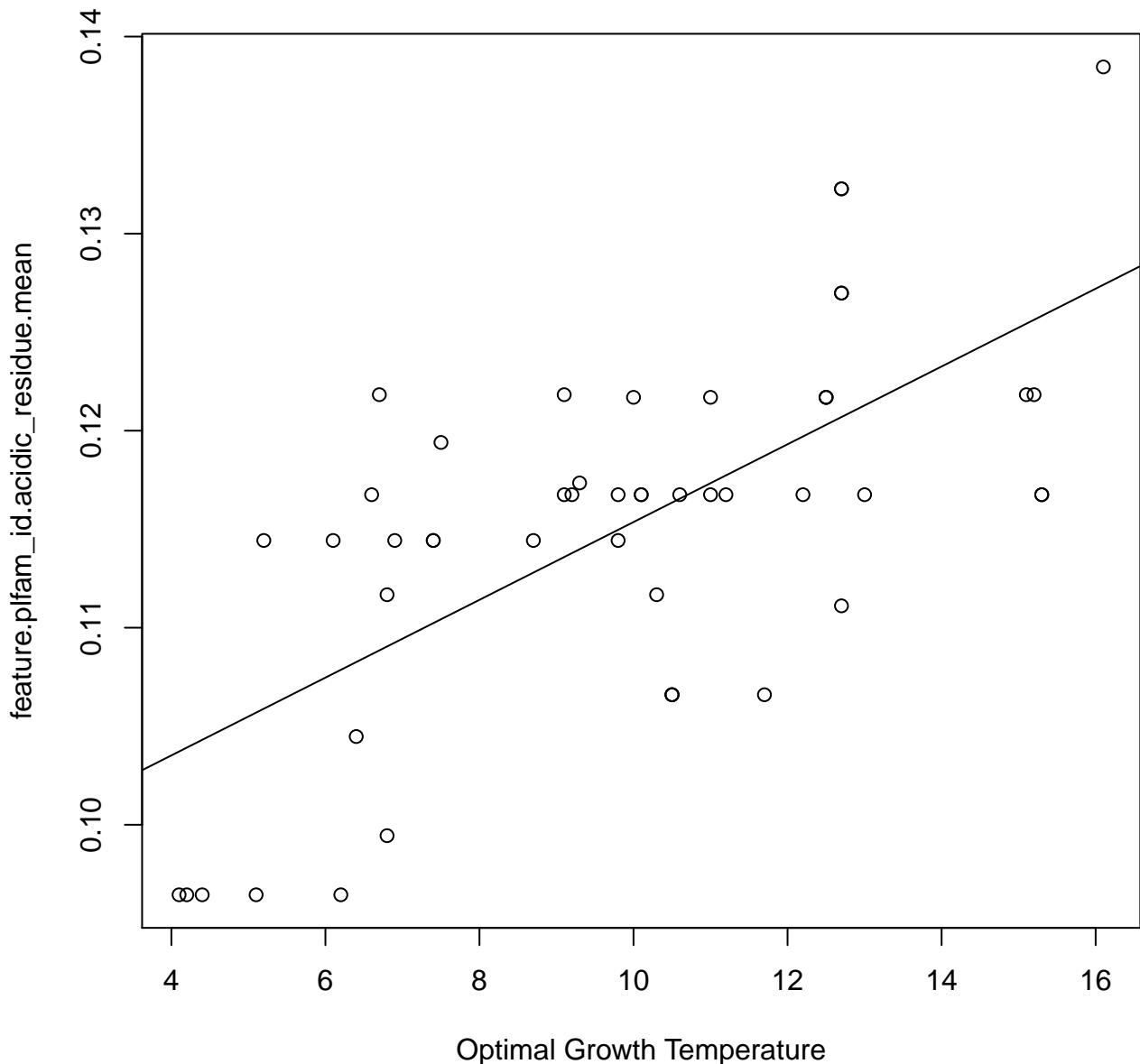
feature.plfam_id.acidic_residue.mean
PLF_28228_00003765
Uncharacterized MFS-type transporter



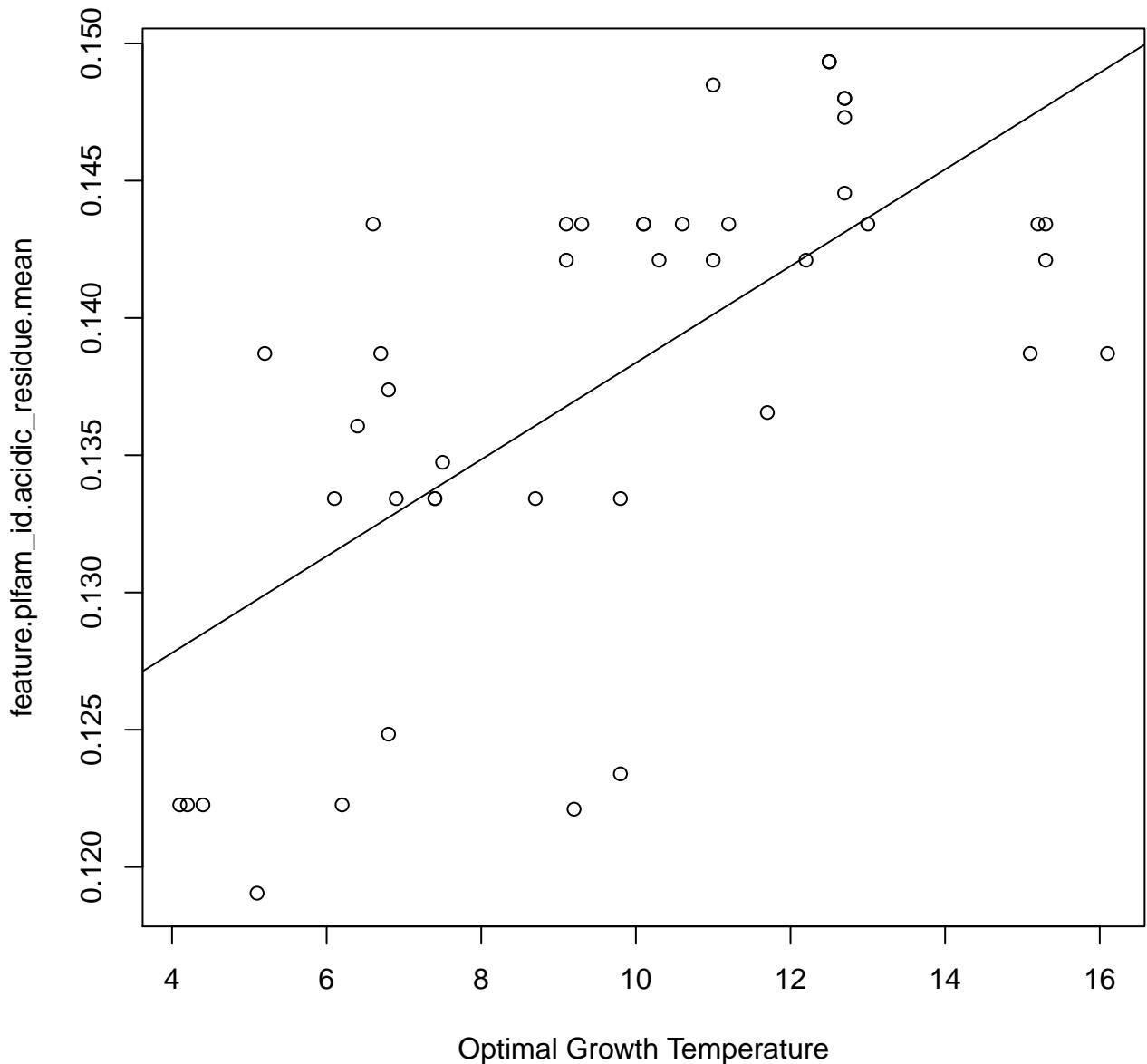
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PLF_28228_00001155
Single-stranded-DNA-specific exonuclease RecJ



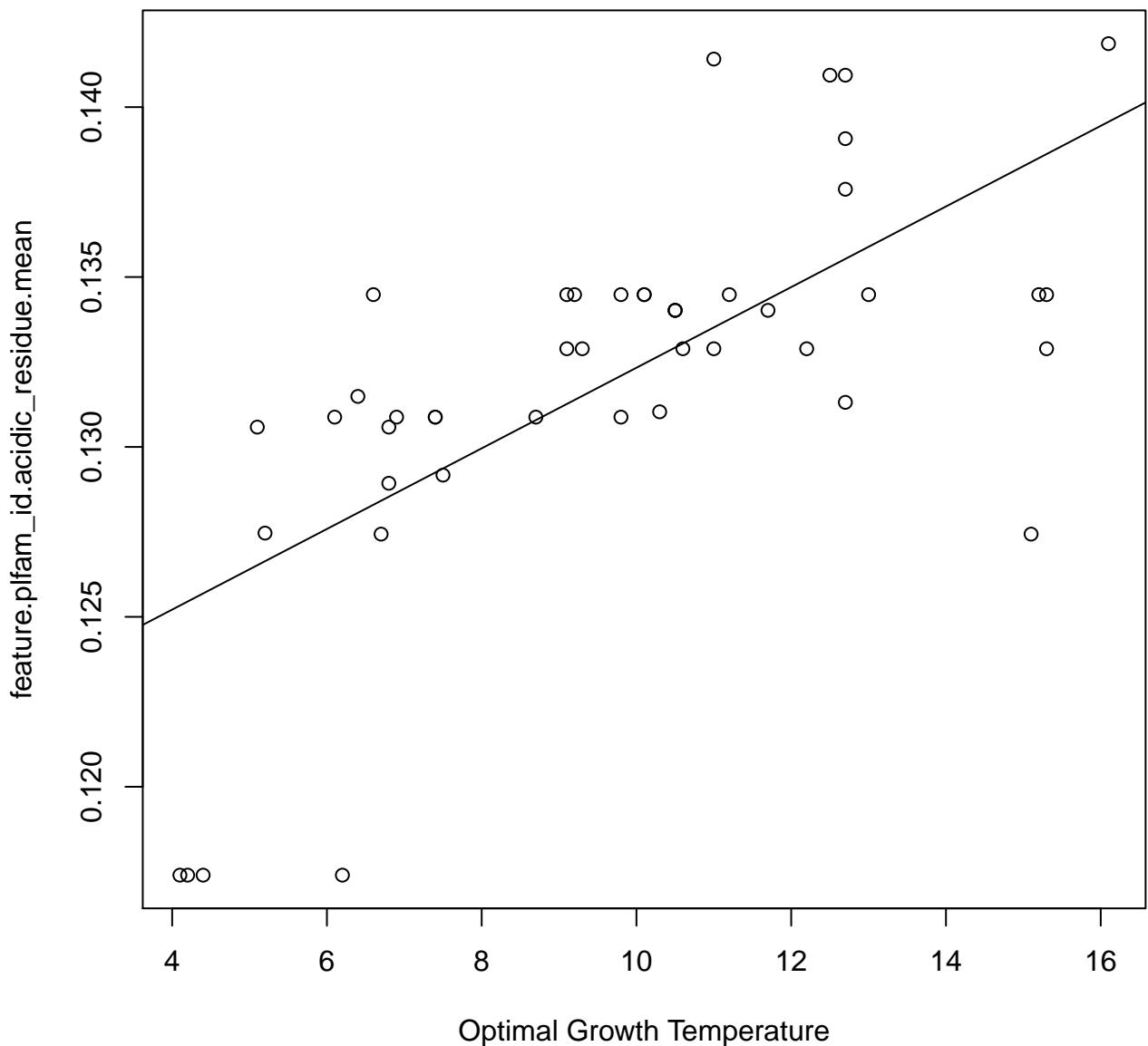
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1,6-anhydro-N-acetylMuramyl-L-alanine amidase



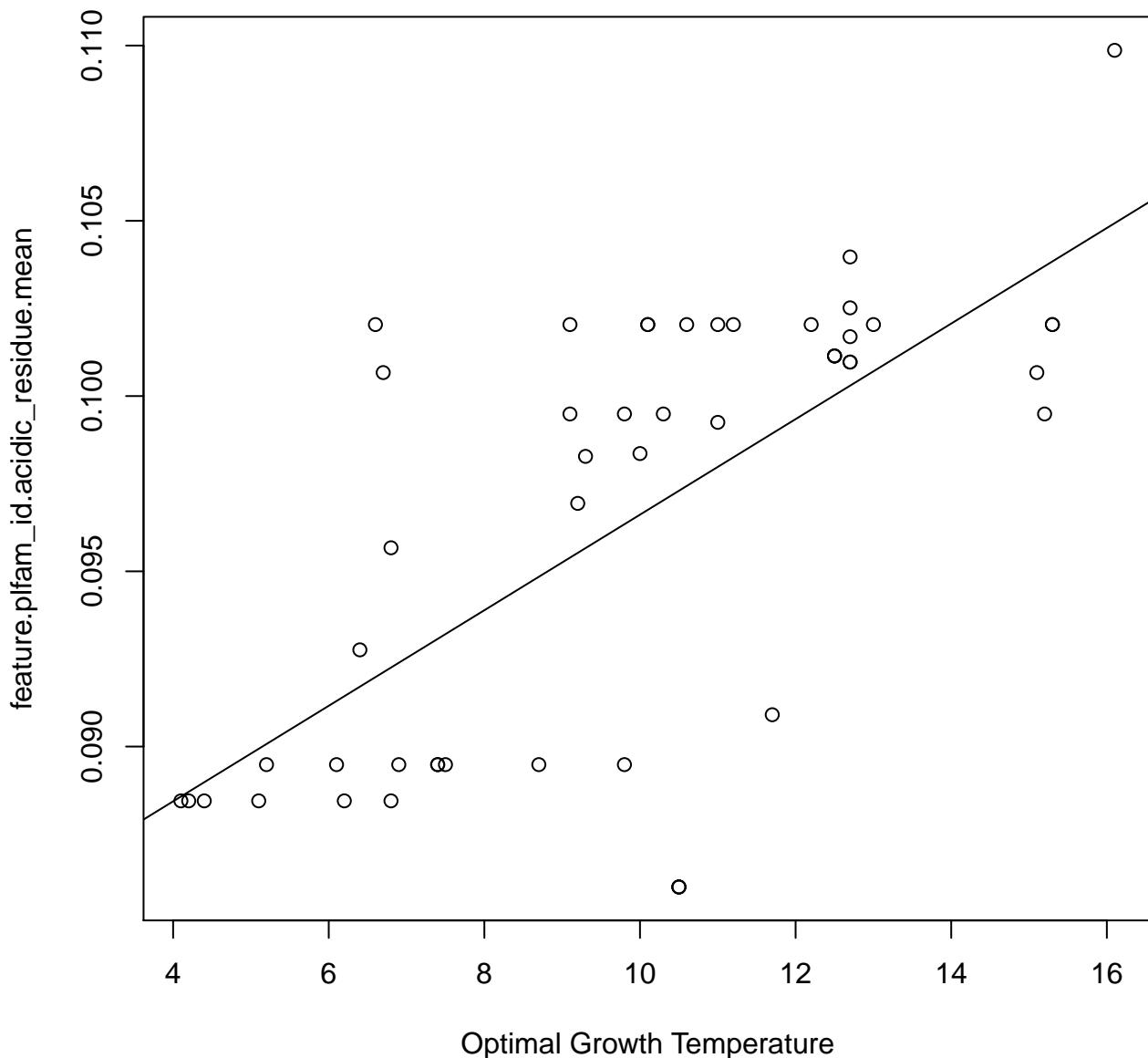
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TonB-dependent receptor



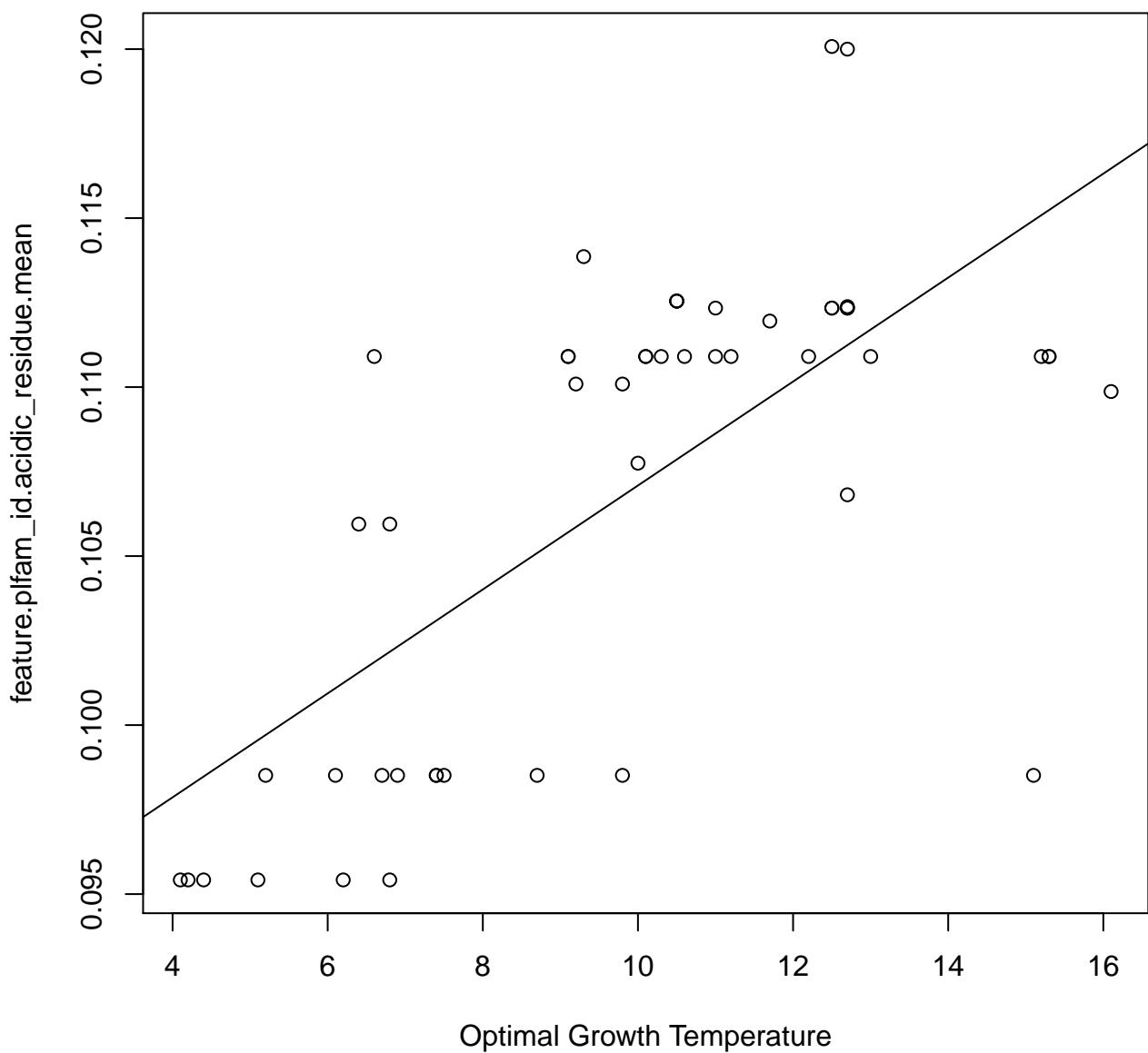
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Glutathione S-transferase (EC 2.5.1.18)



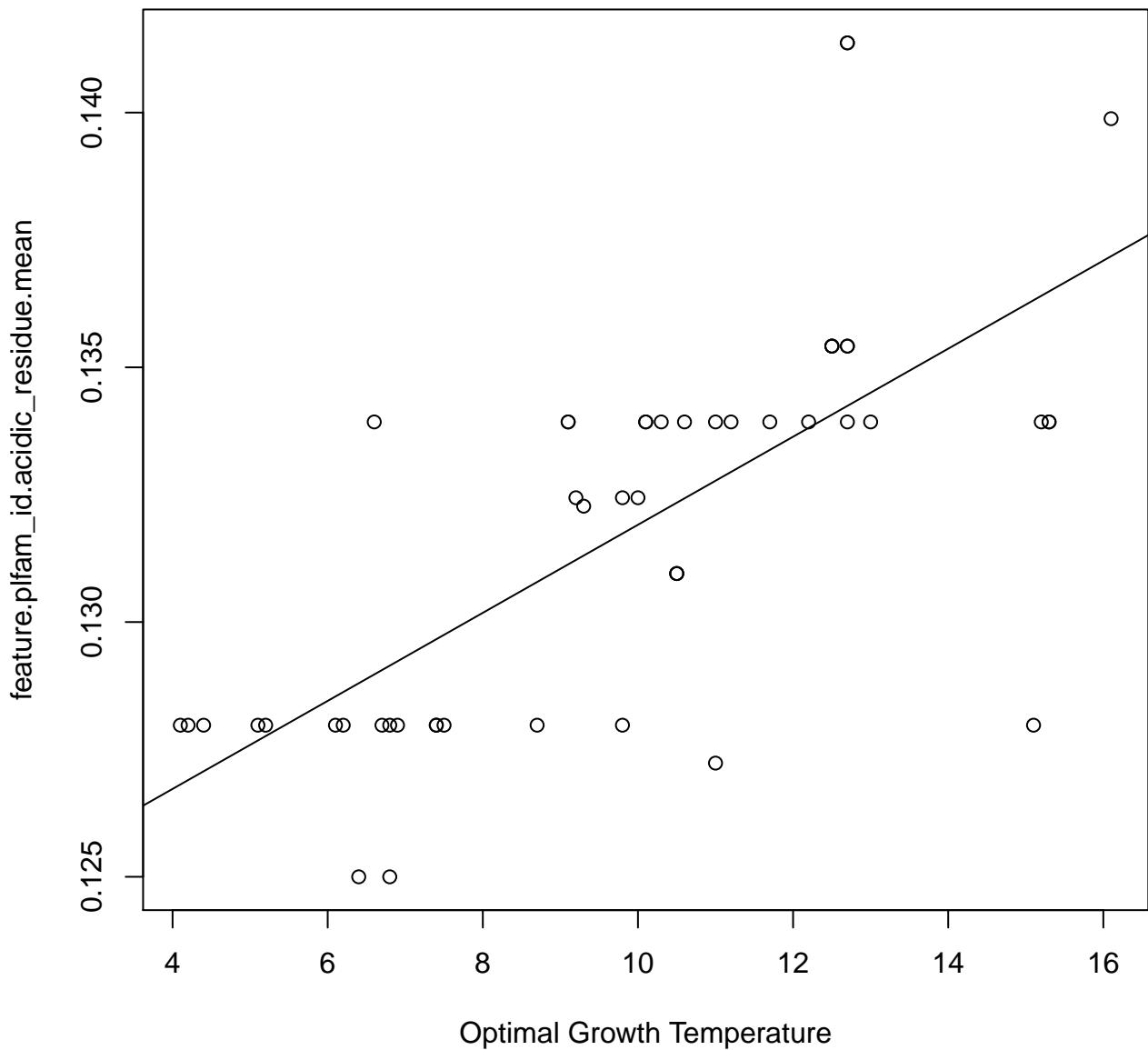
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Type IV pilus biogenesis protein PilF



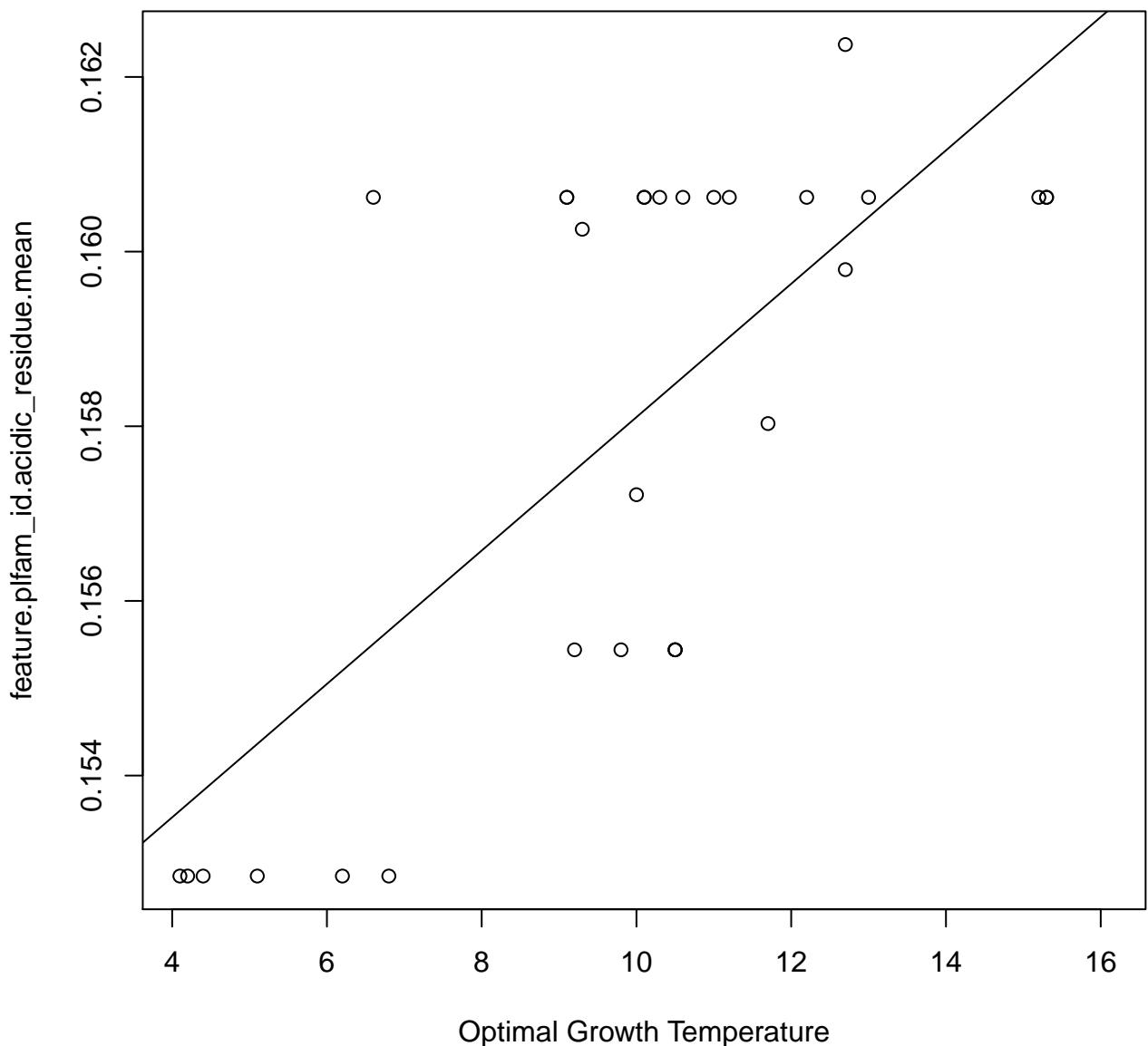
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Sensory box histidine kinase



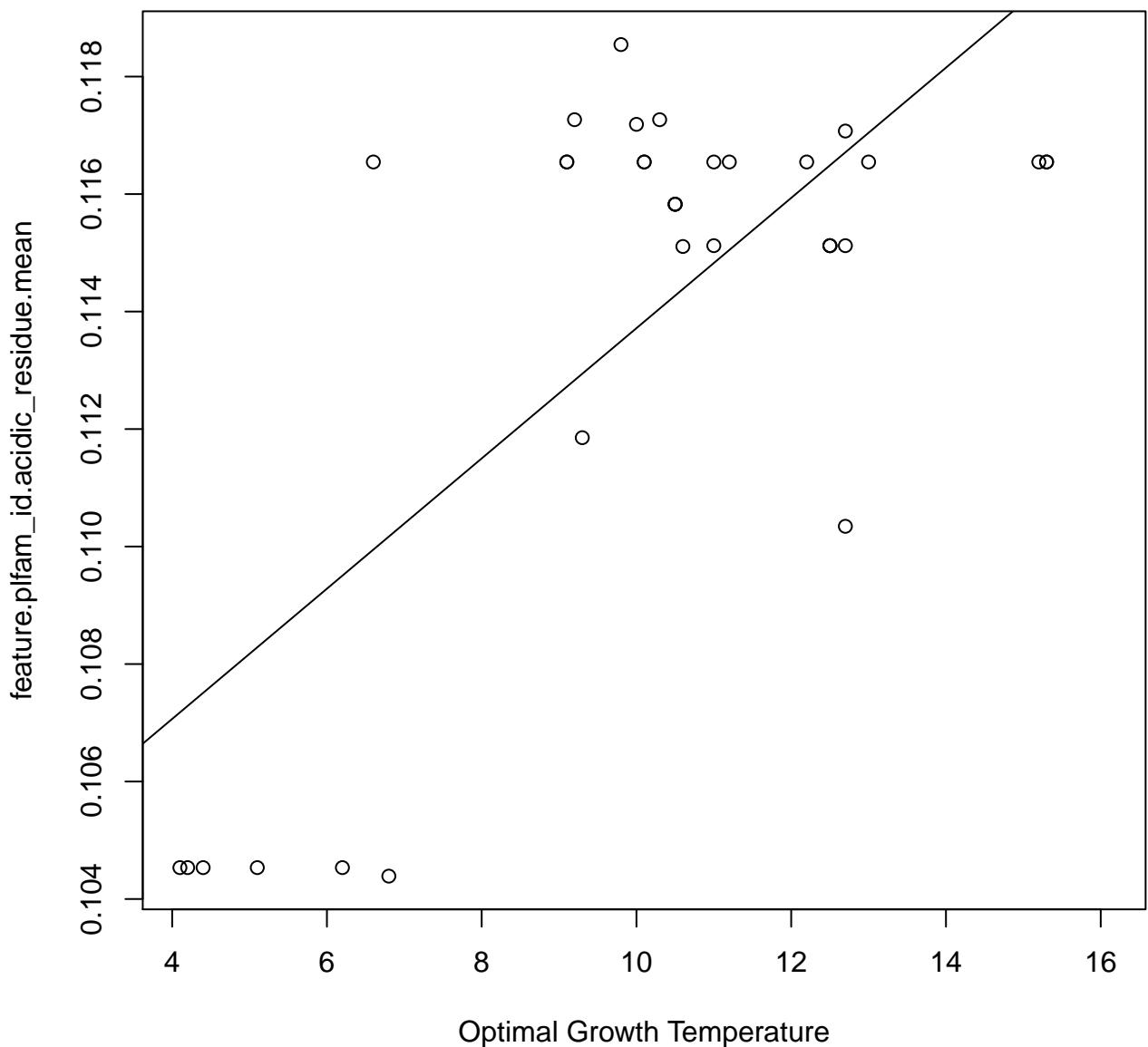
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PLF_28228_00001734
Methyl-accepting chemotaxis sensor/transducer protein



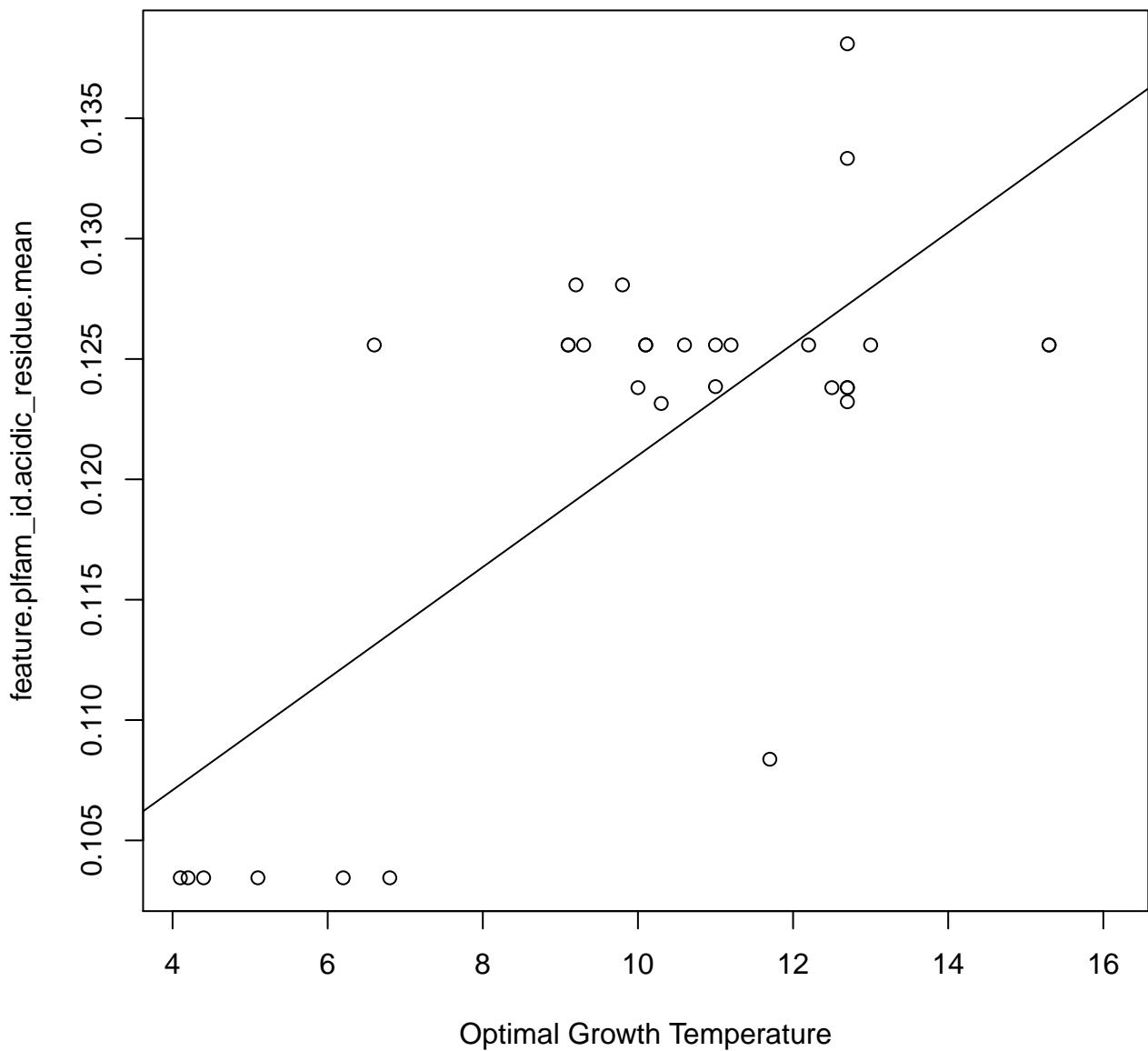
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PLF_28228_00004222
hypothetical protein



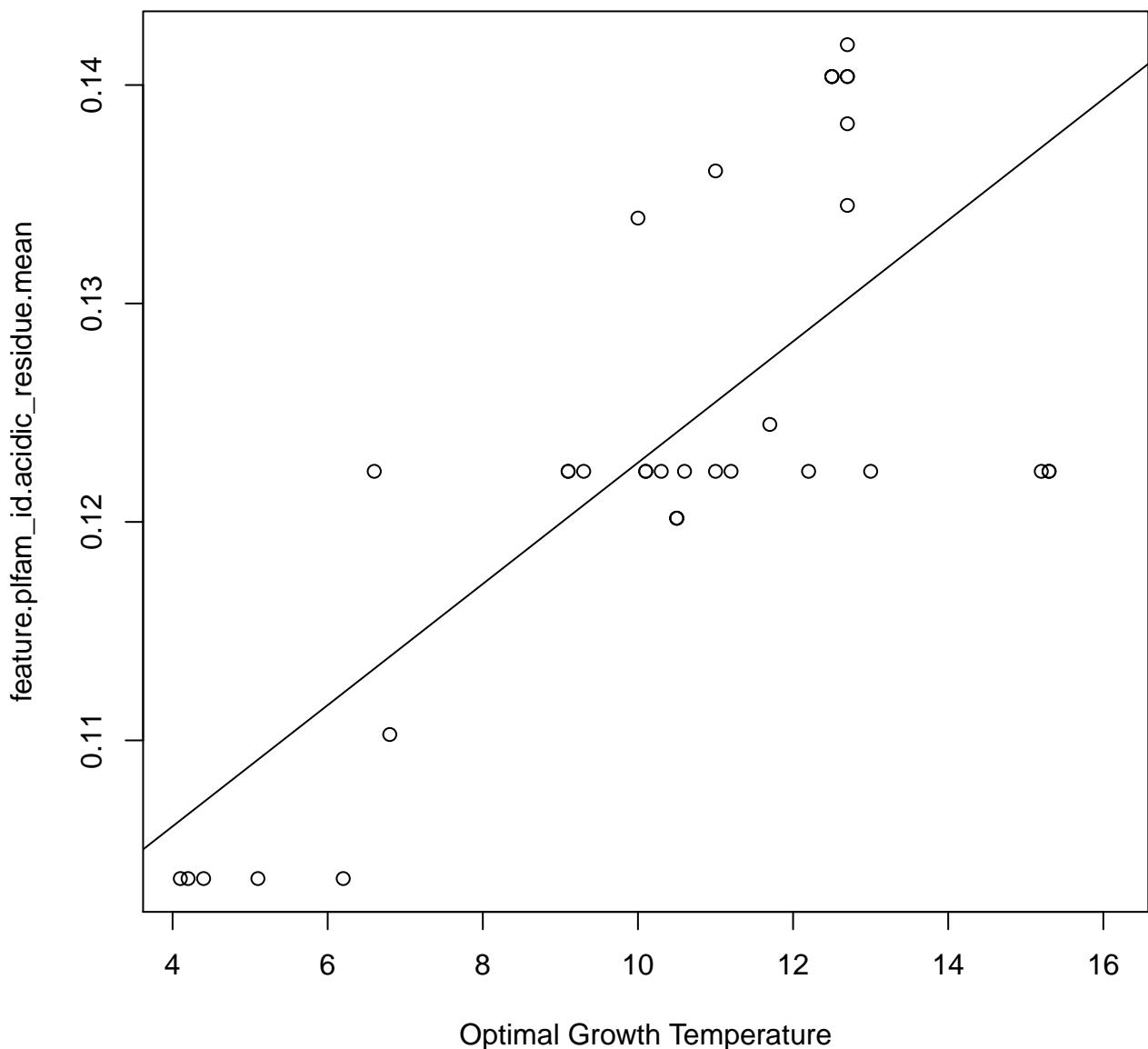
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GGDEF domain protein



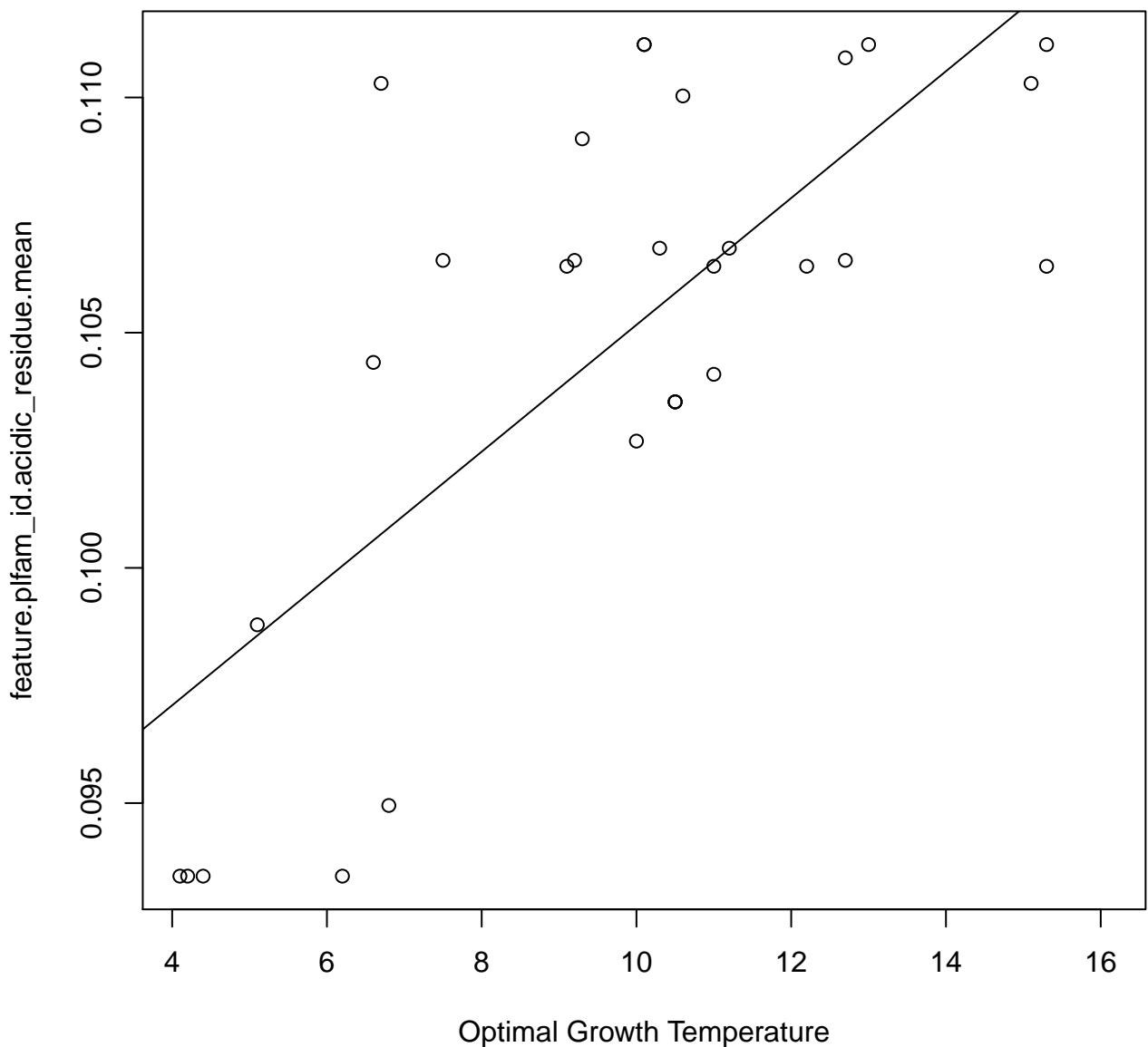
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Alkylated DNA repair protein



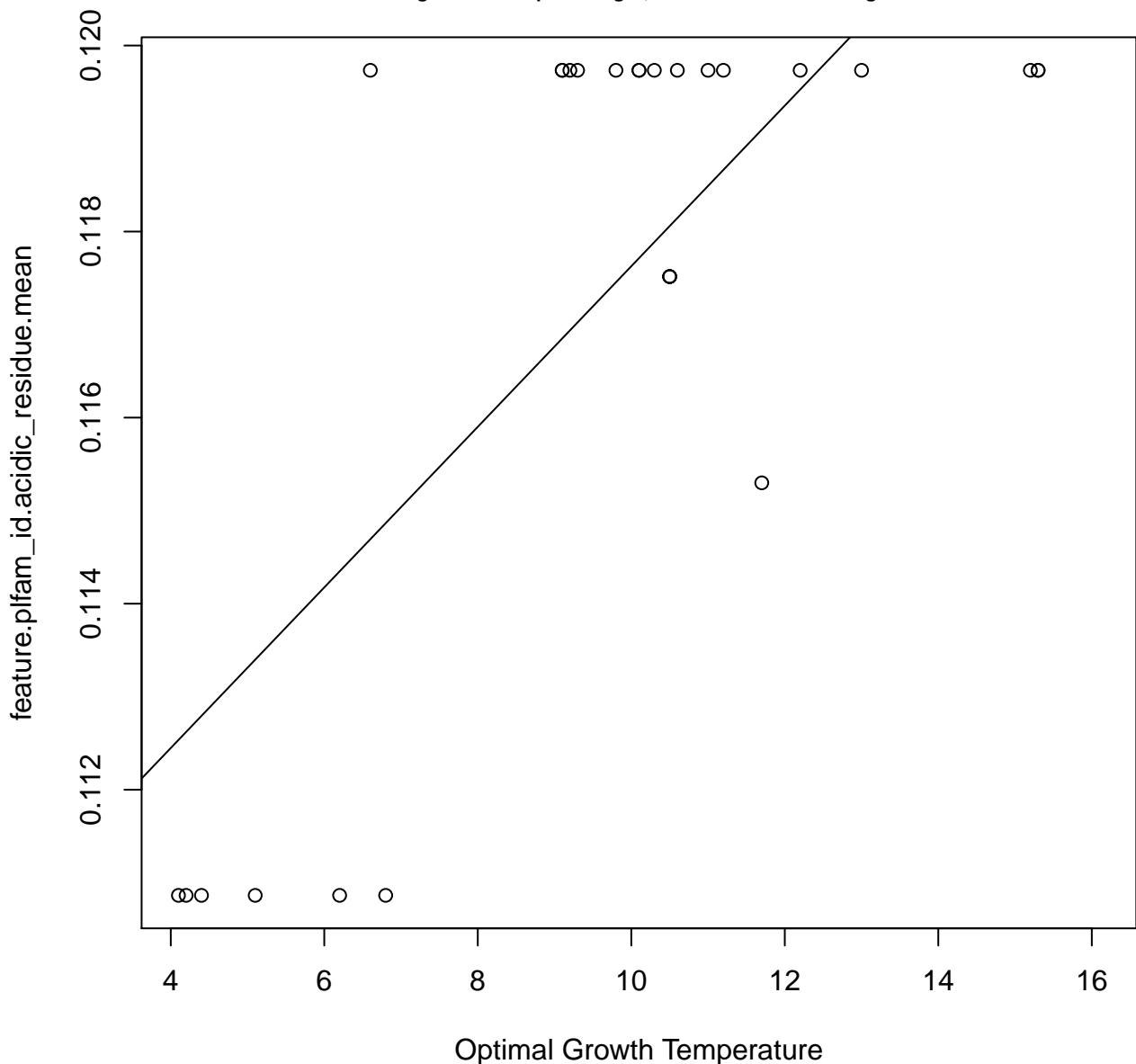
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Uncharacterized protease YegQ



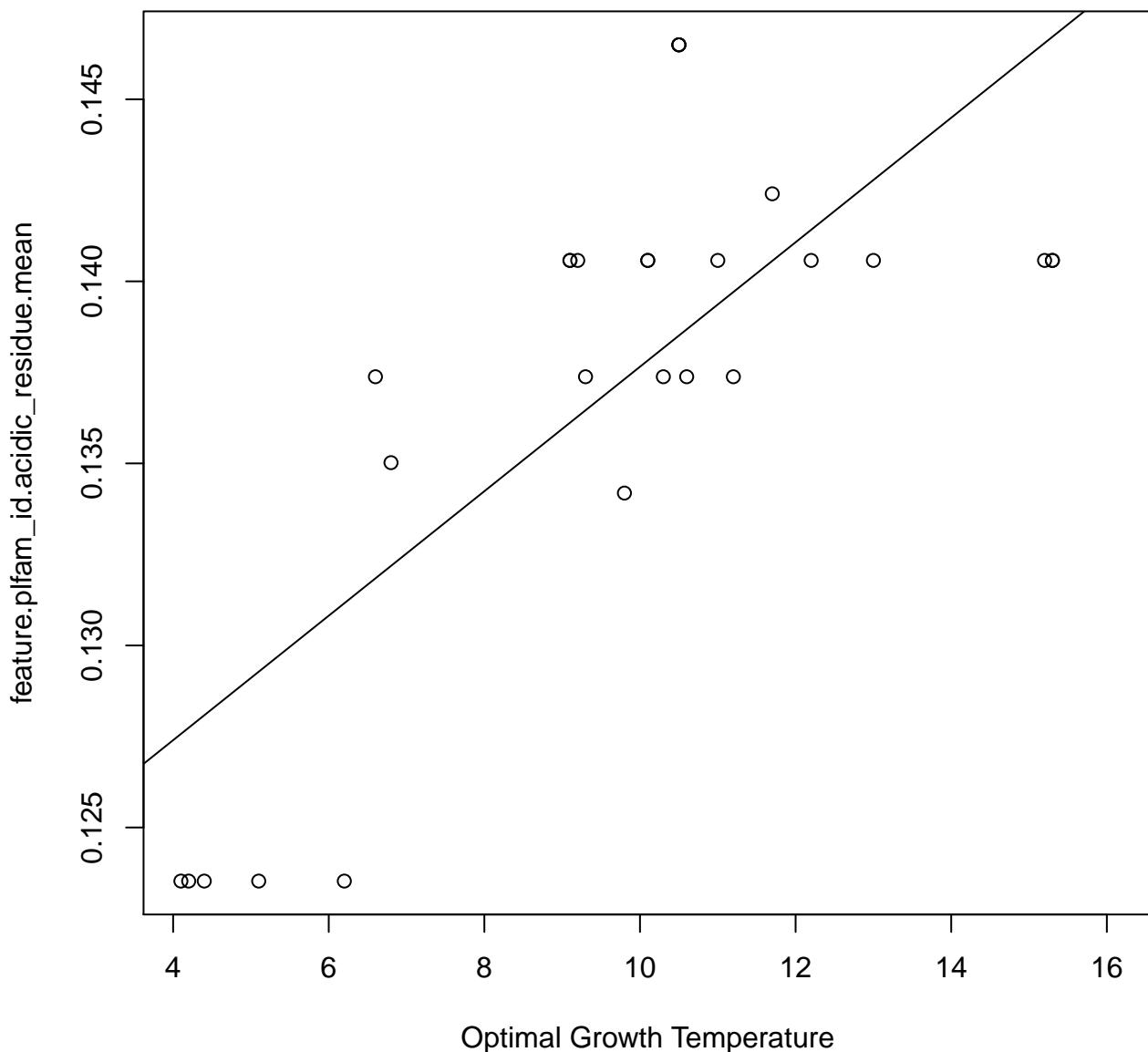
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Phage integrase



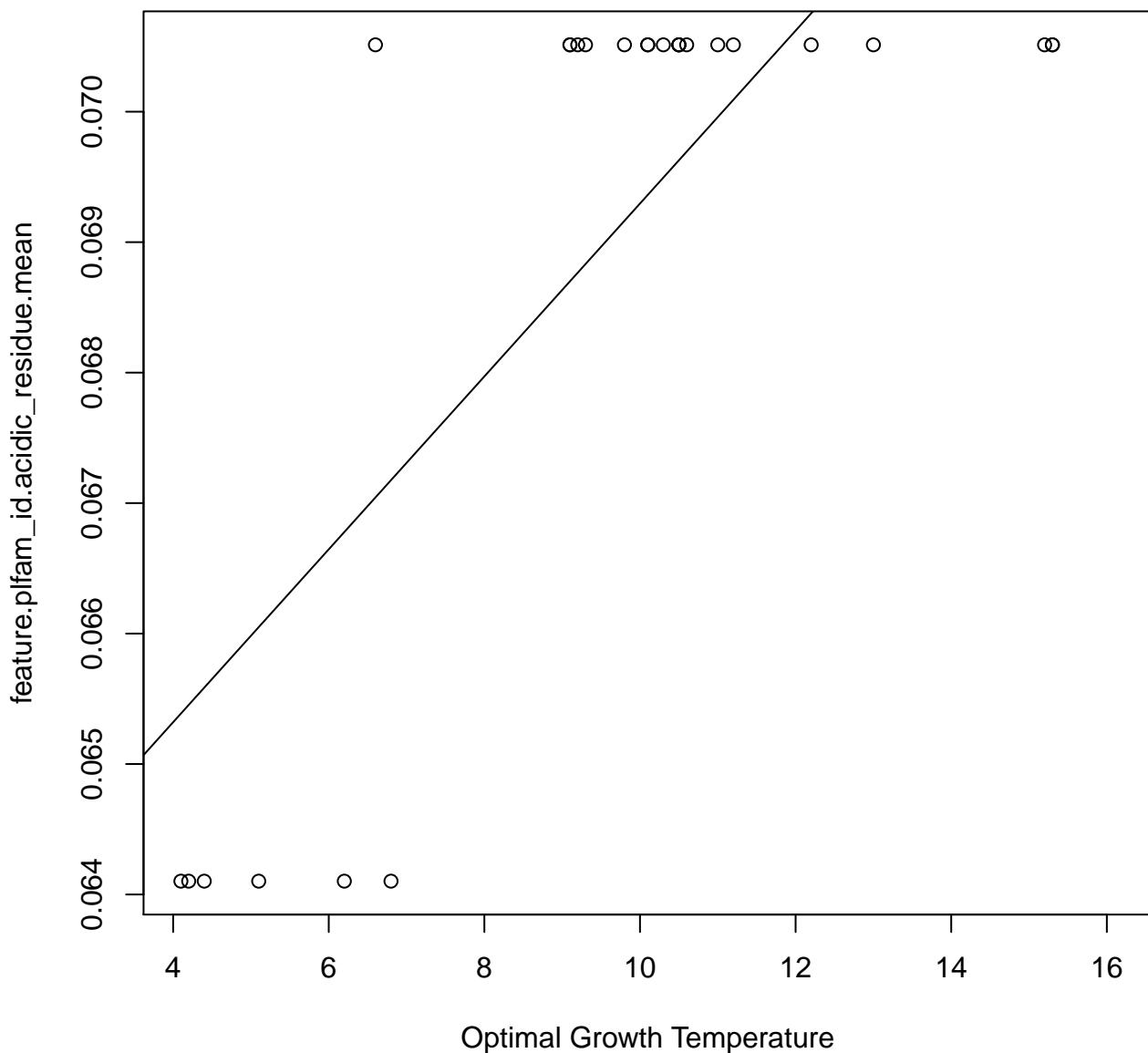
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Mg/Co/Ni transporter MgtE, CBS domain-containing



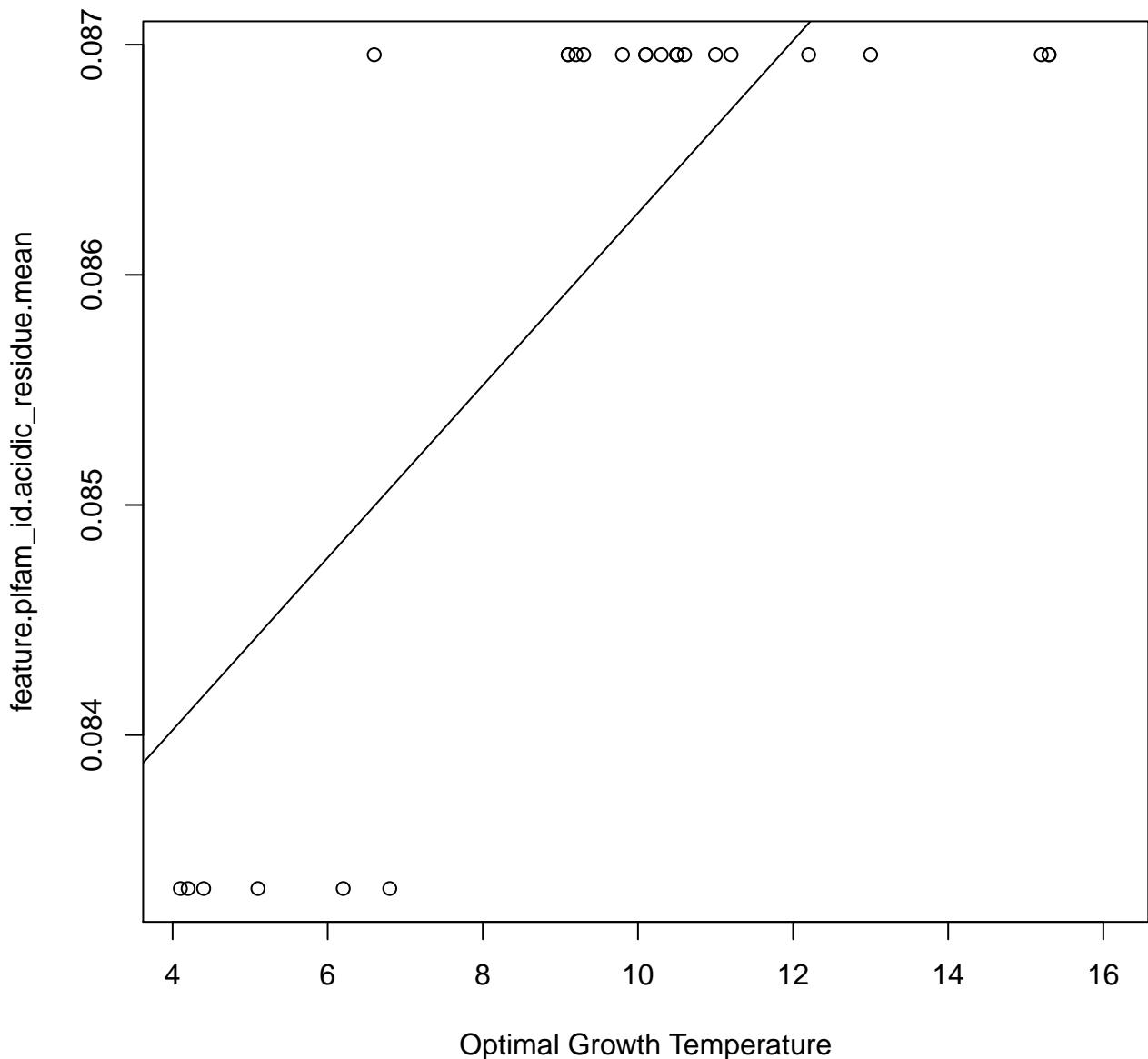
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Agmatinase (EC 3.5.3.11)



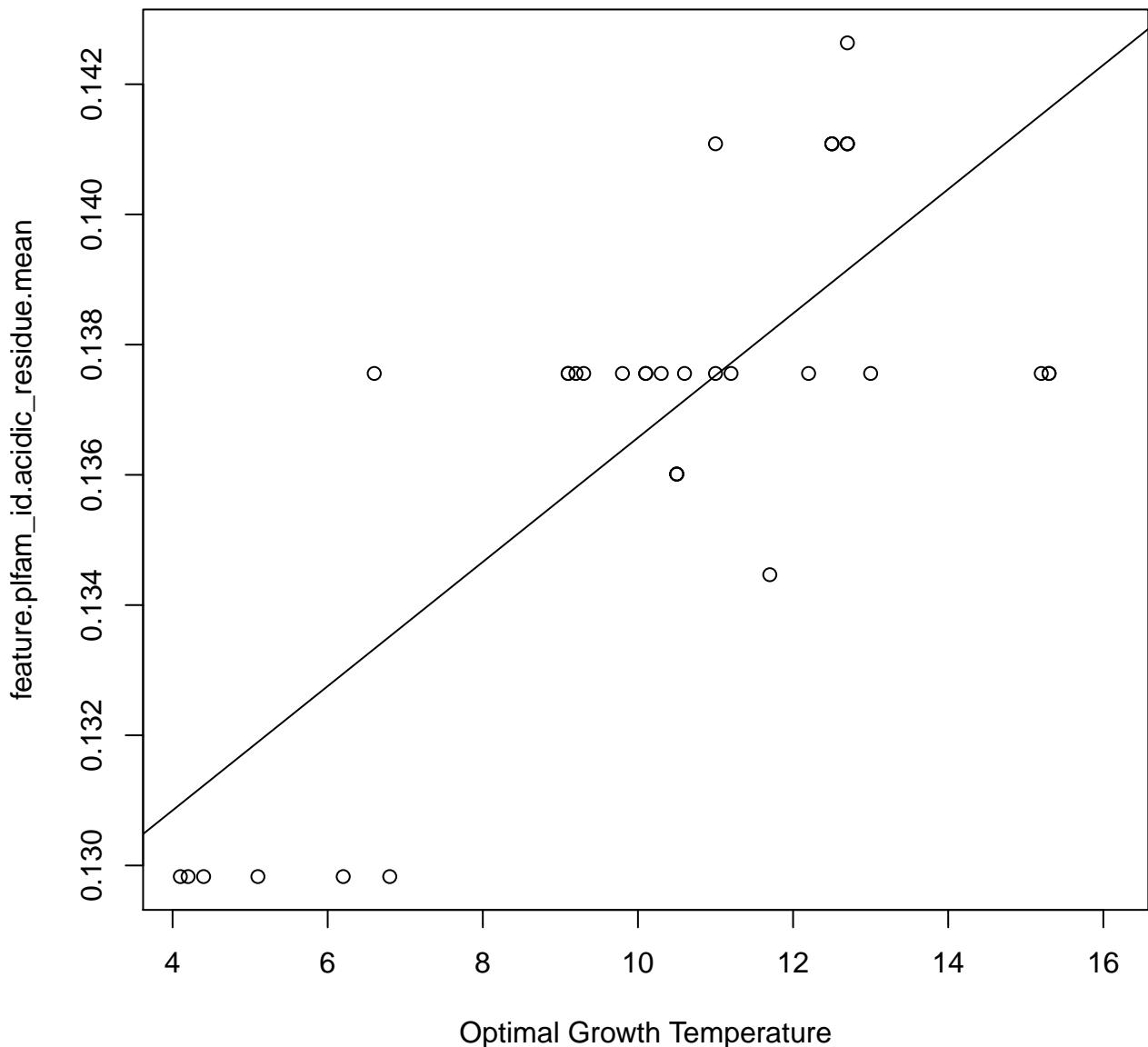
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hypothetical protein



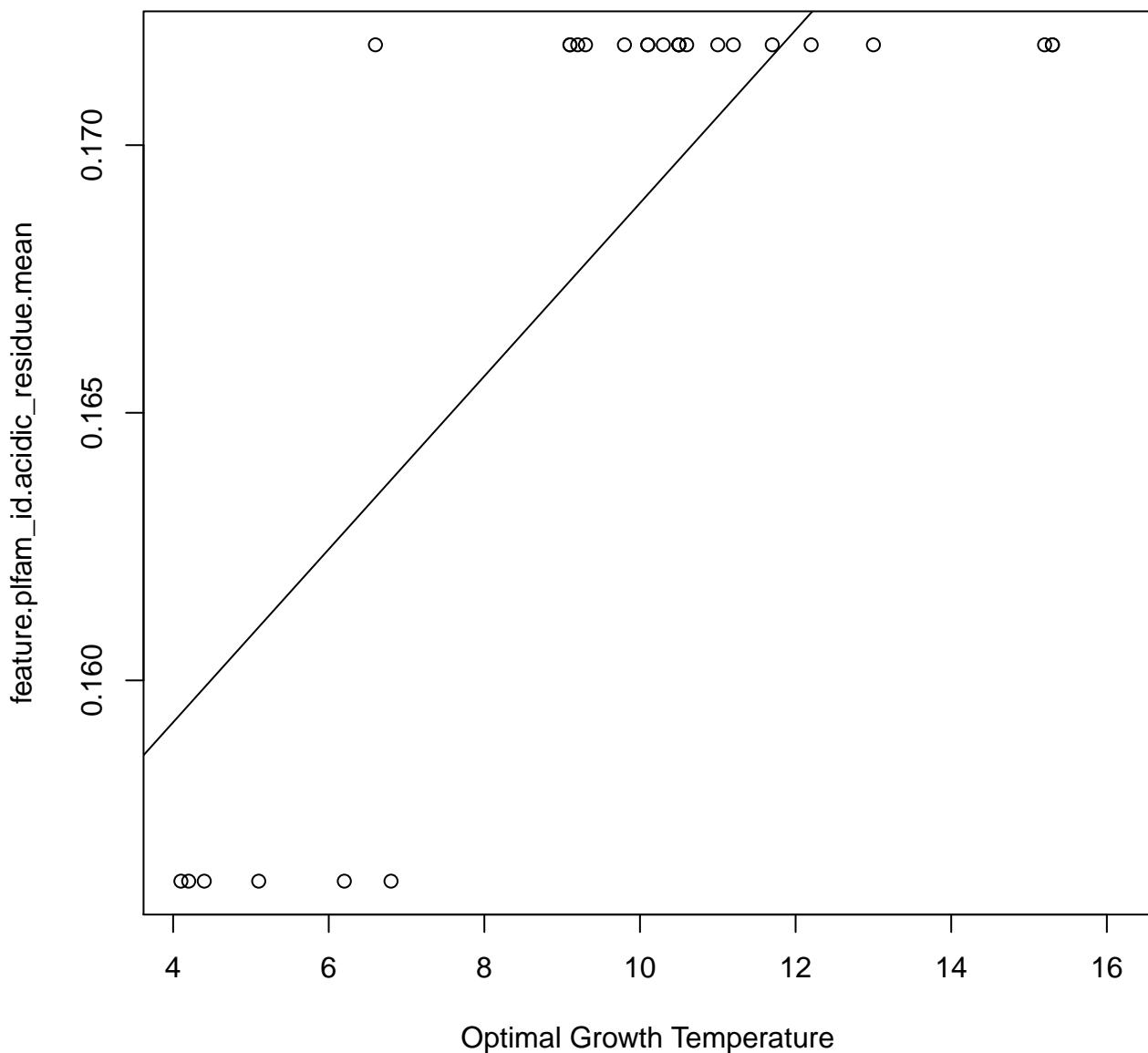
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hypothetical protein



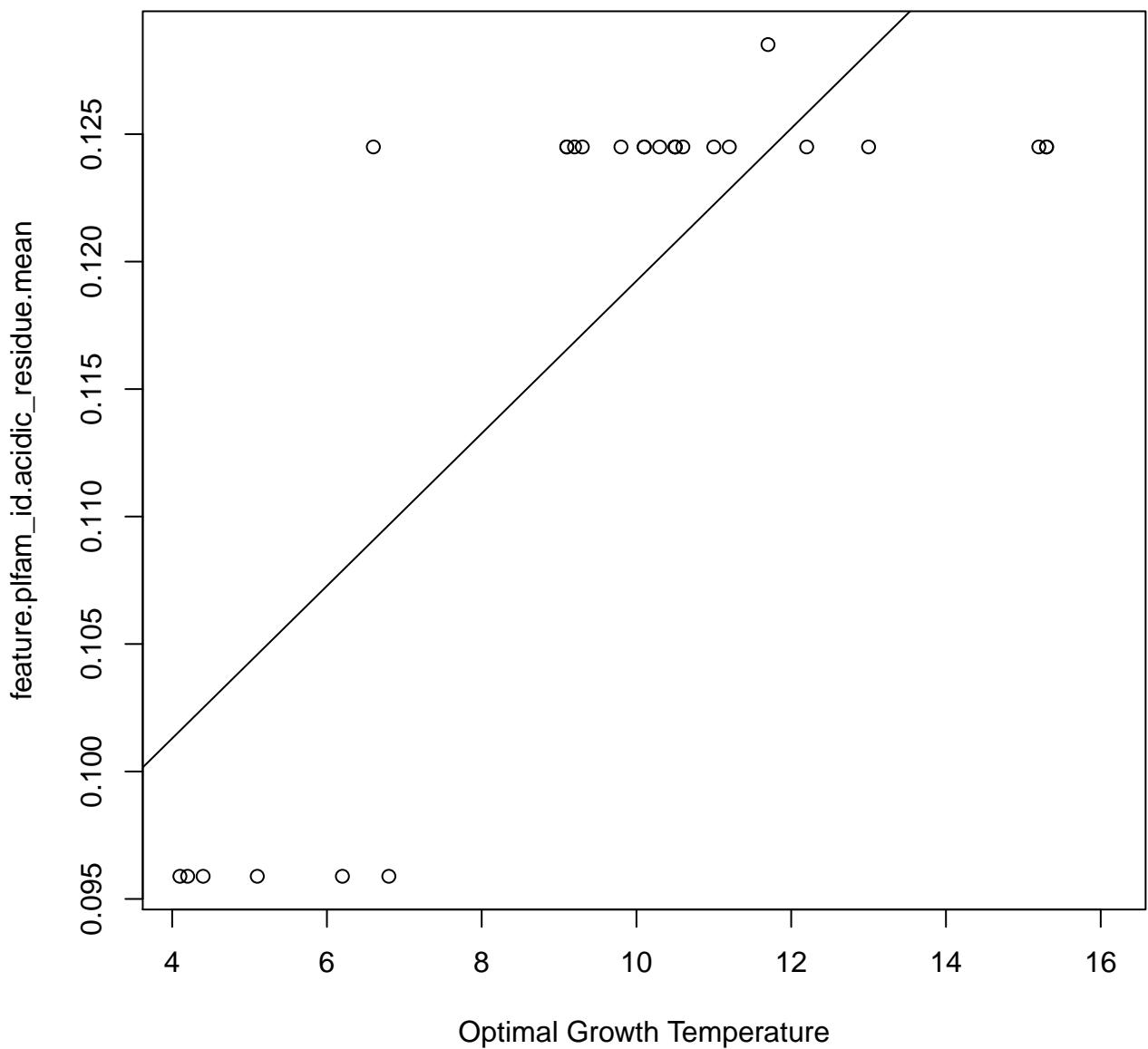
feature.plfam_id.acidic_residue.mean
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Argininosuccinate lyase (EC 4.3.2.1) / N-acetylglutamate synthase (EC 2.3.1.1)



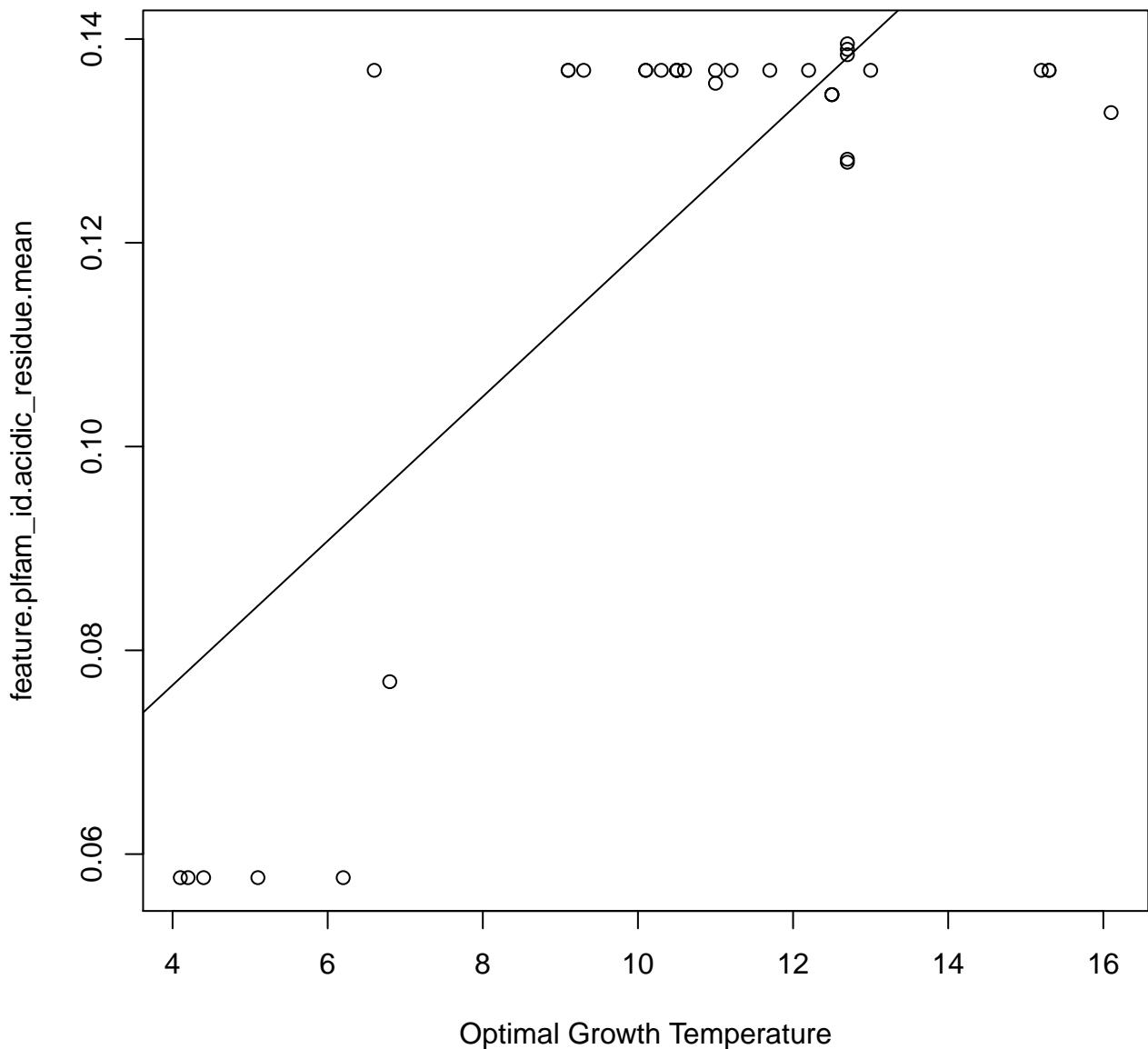
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hypothetical protein



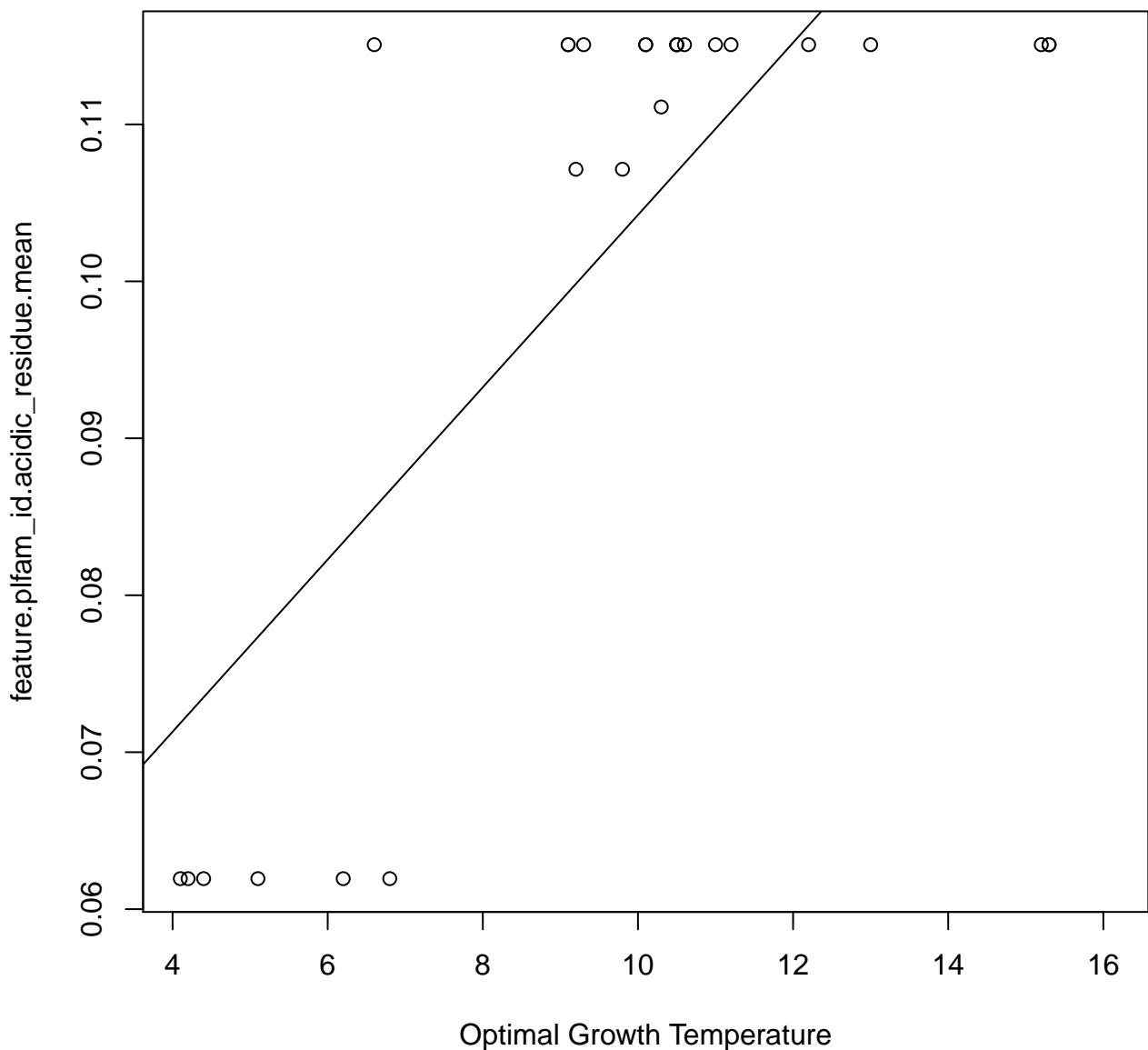
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hypothetical protein



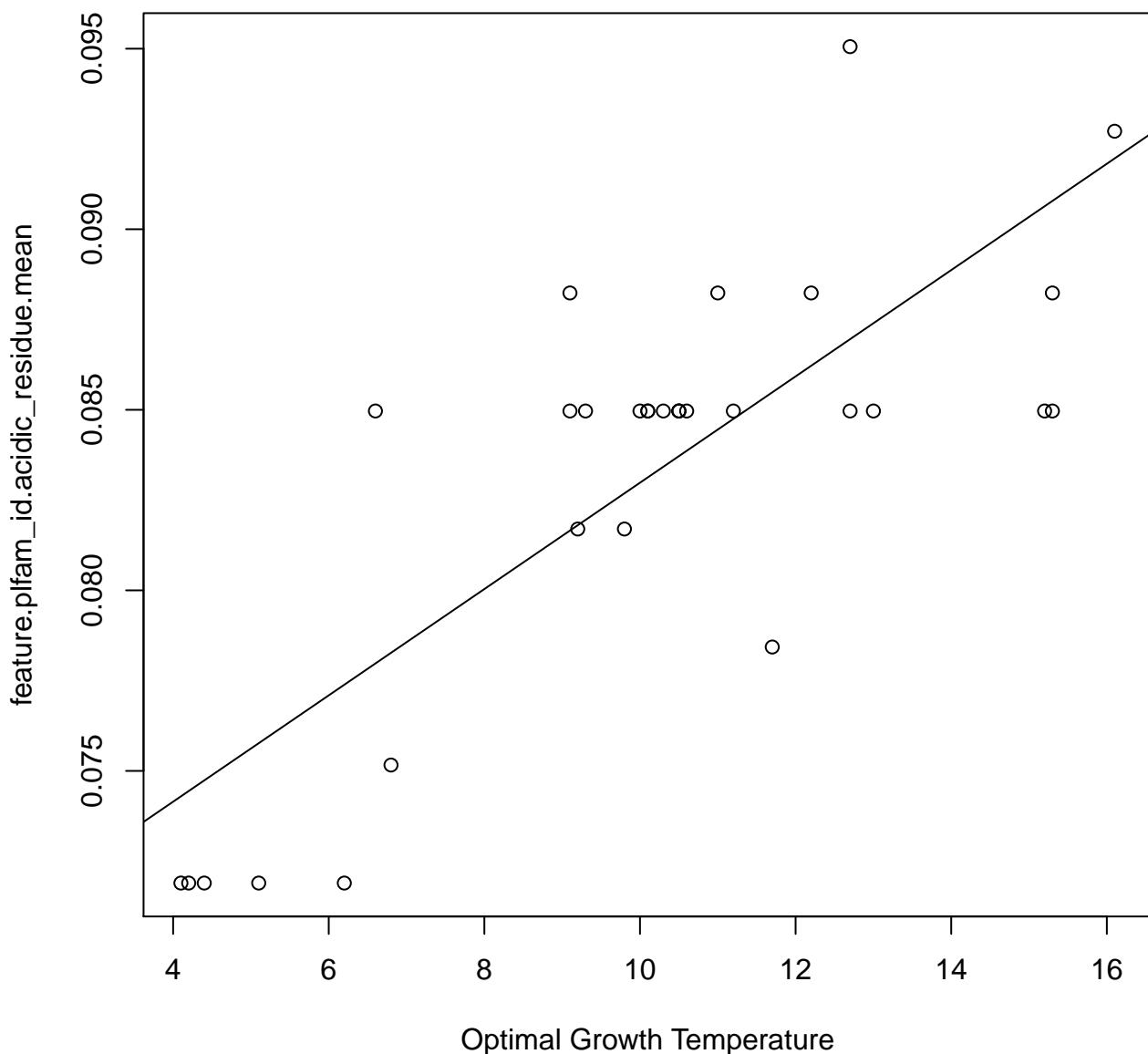
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PLF_28228_00002798
Two-component transcriptional response regulator, OmpR family



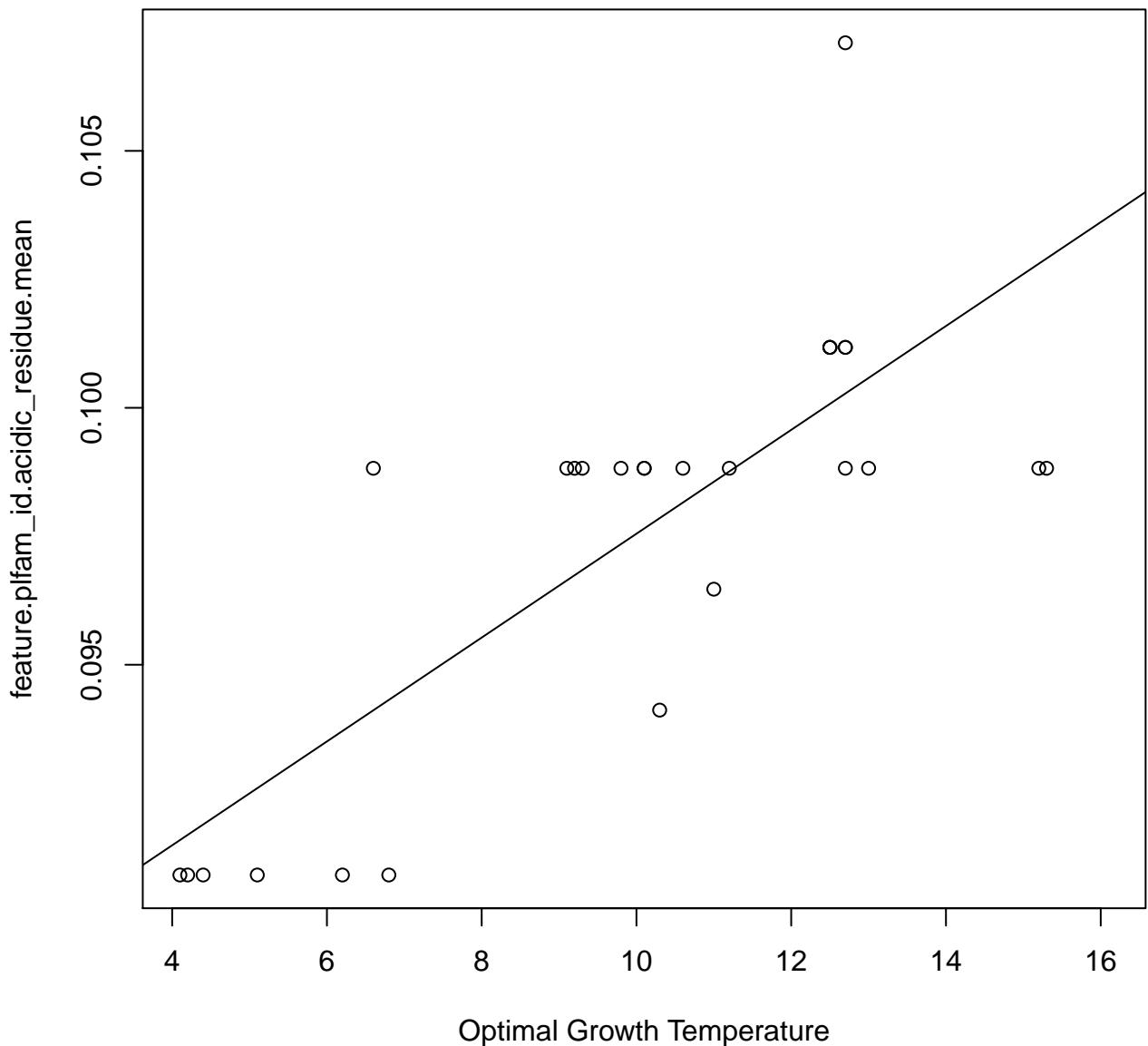
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hypothetical protein



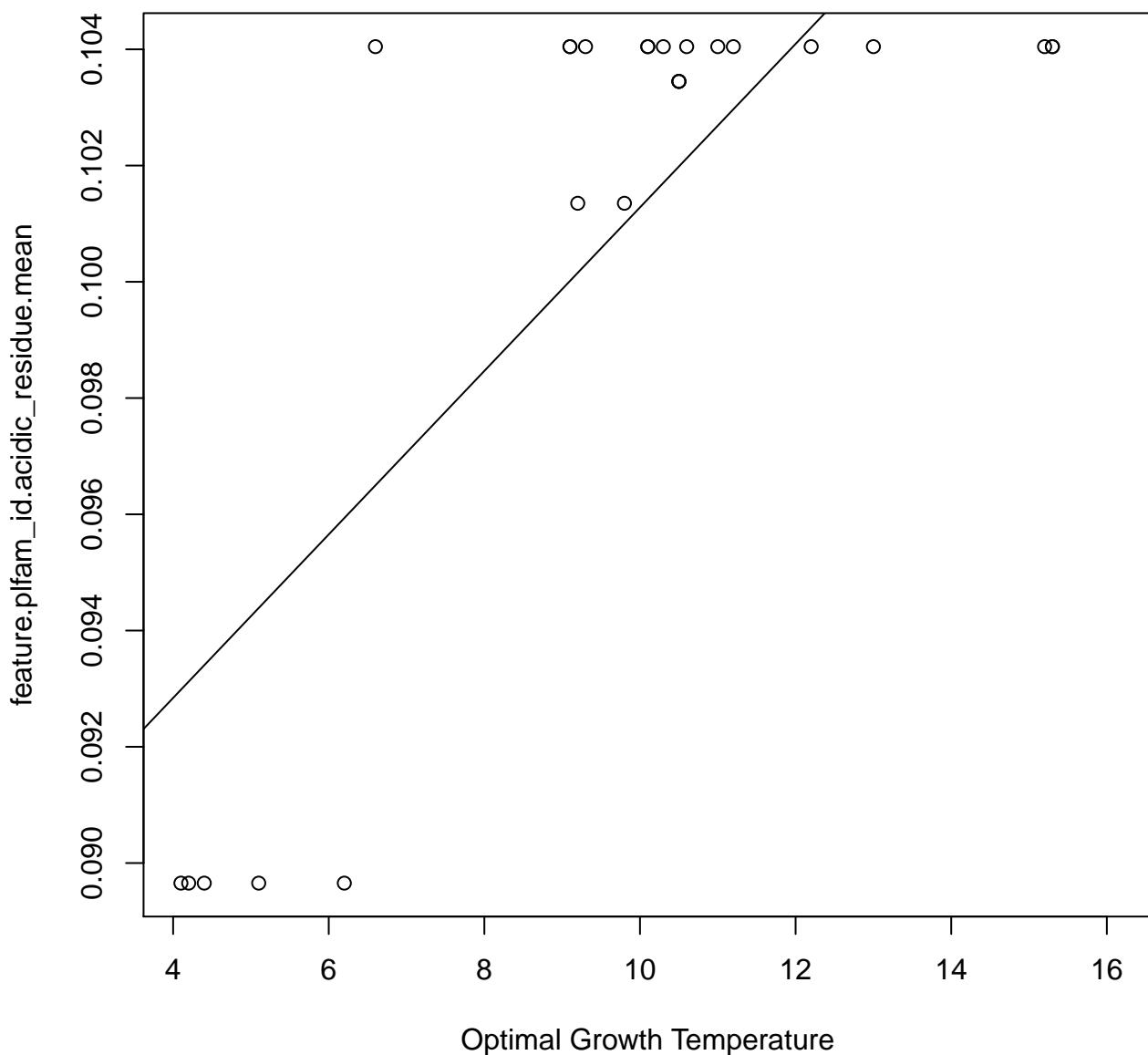
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Protein translocase subunit SecF



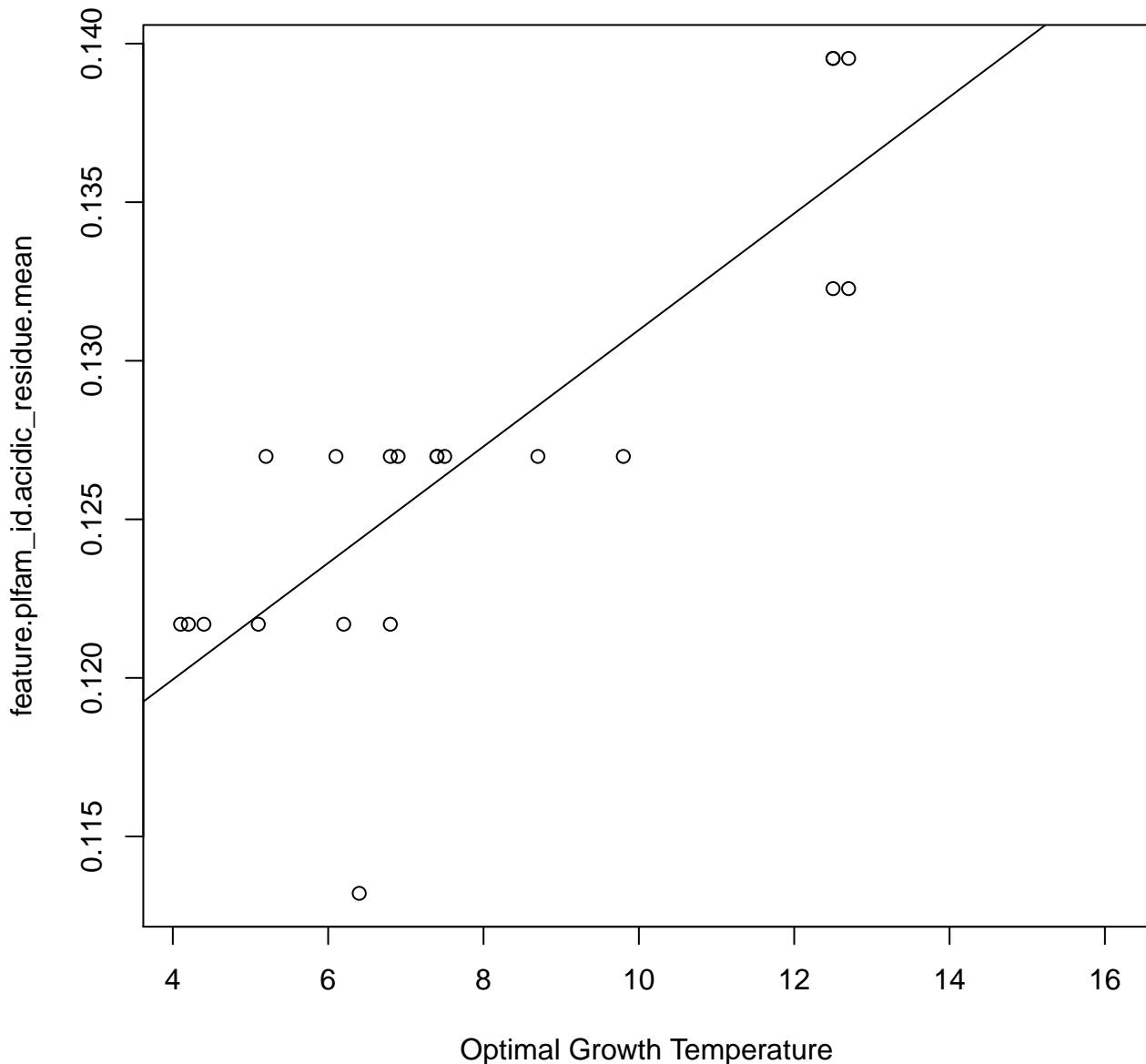
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EPS I polysaccharide export outer membrane protein EPSA precursor



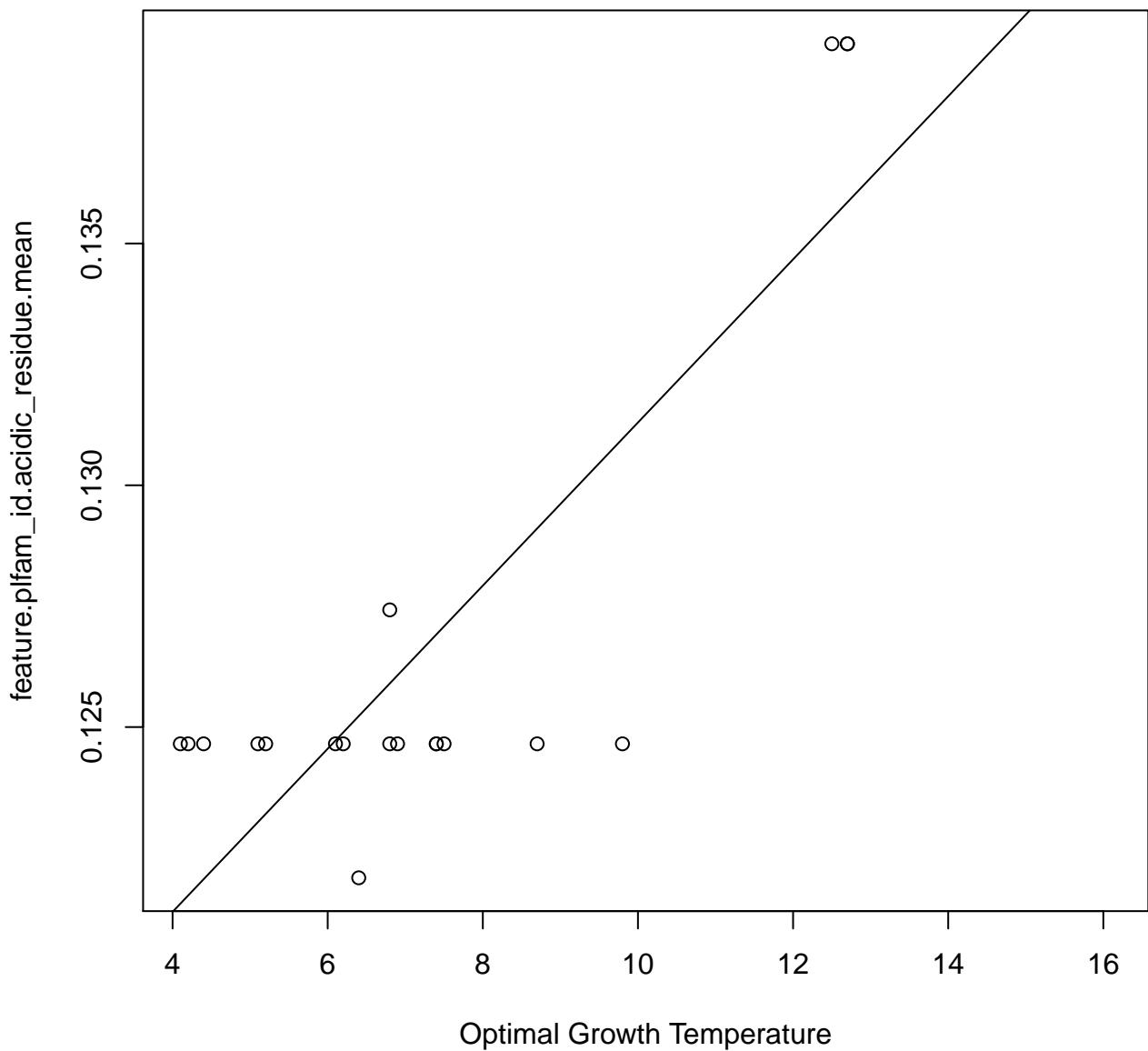
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hypothetical protein



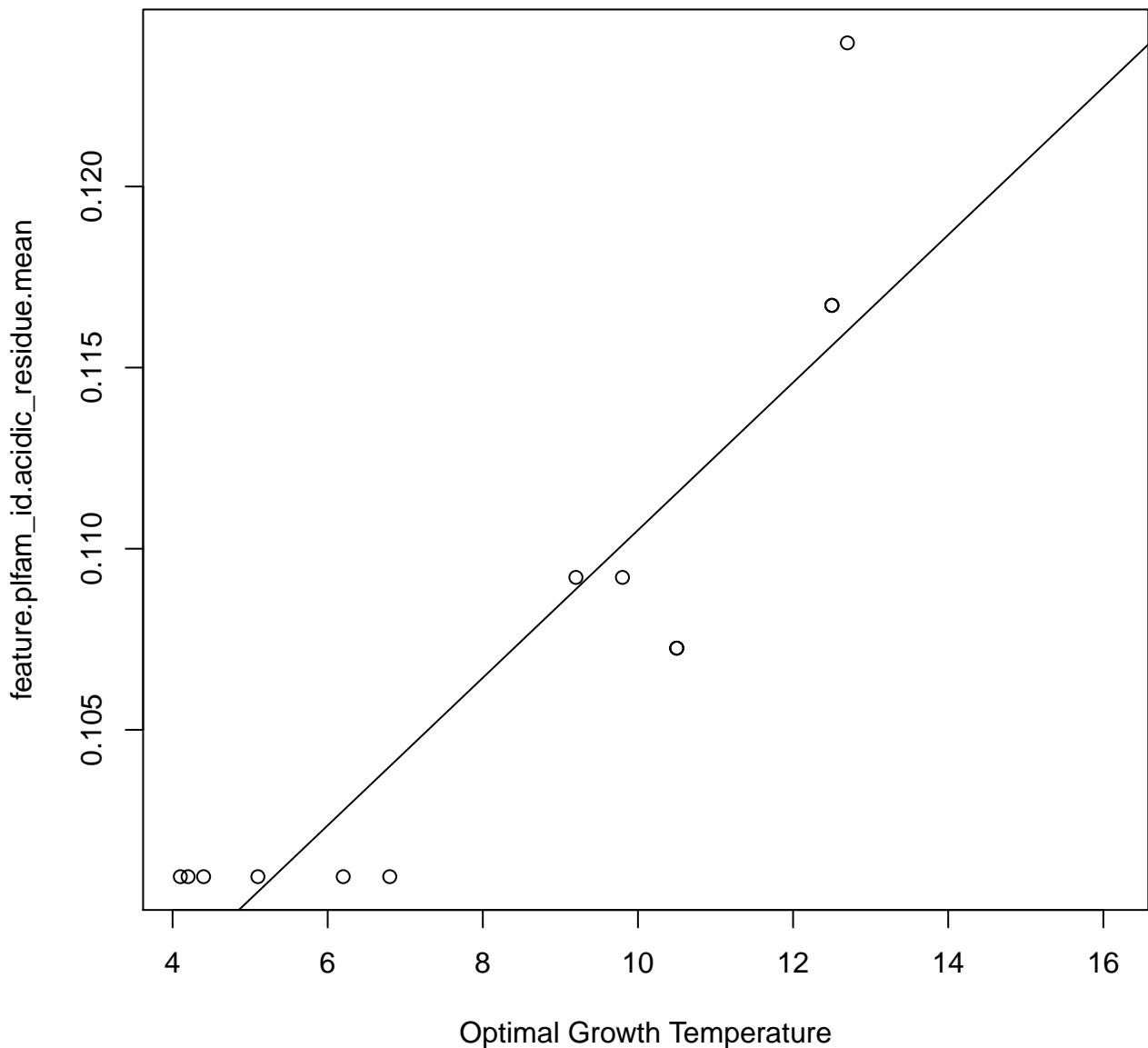
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PLF_28228_00014224
FIG006045: Sigma factor, ECF subfamily



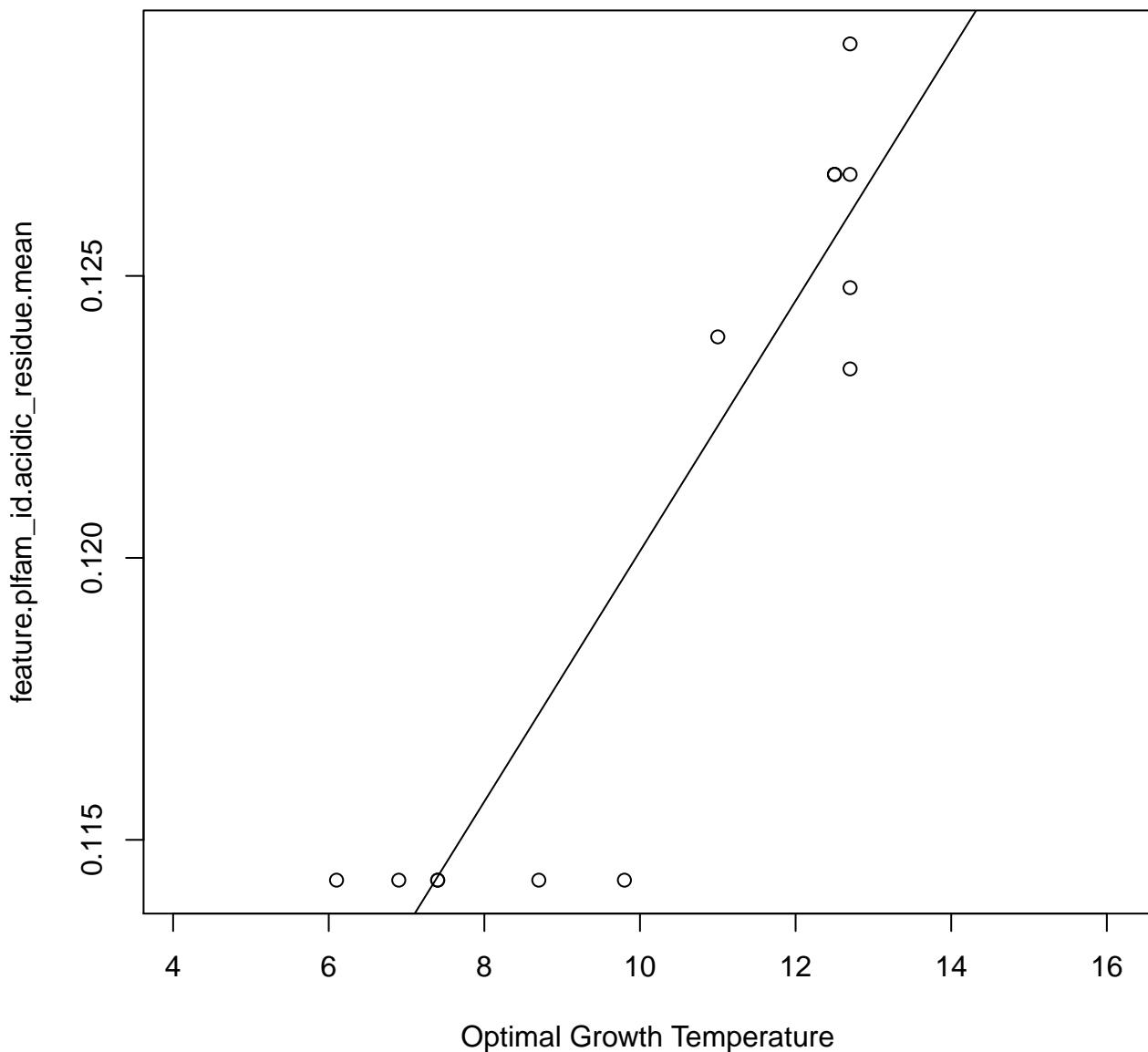
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PLF_28228_00028262
Iron siderophore sensor protein



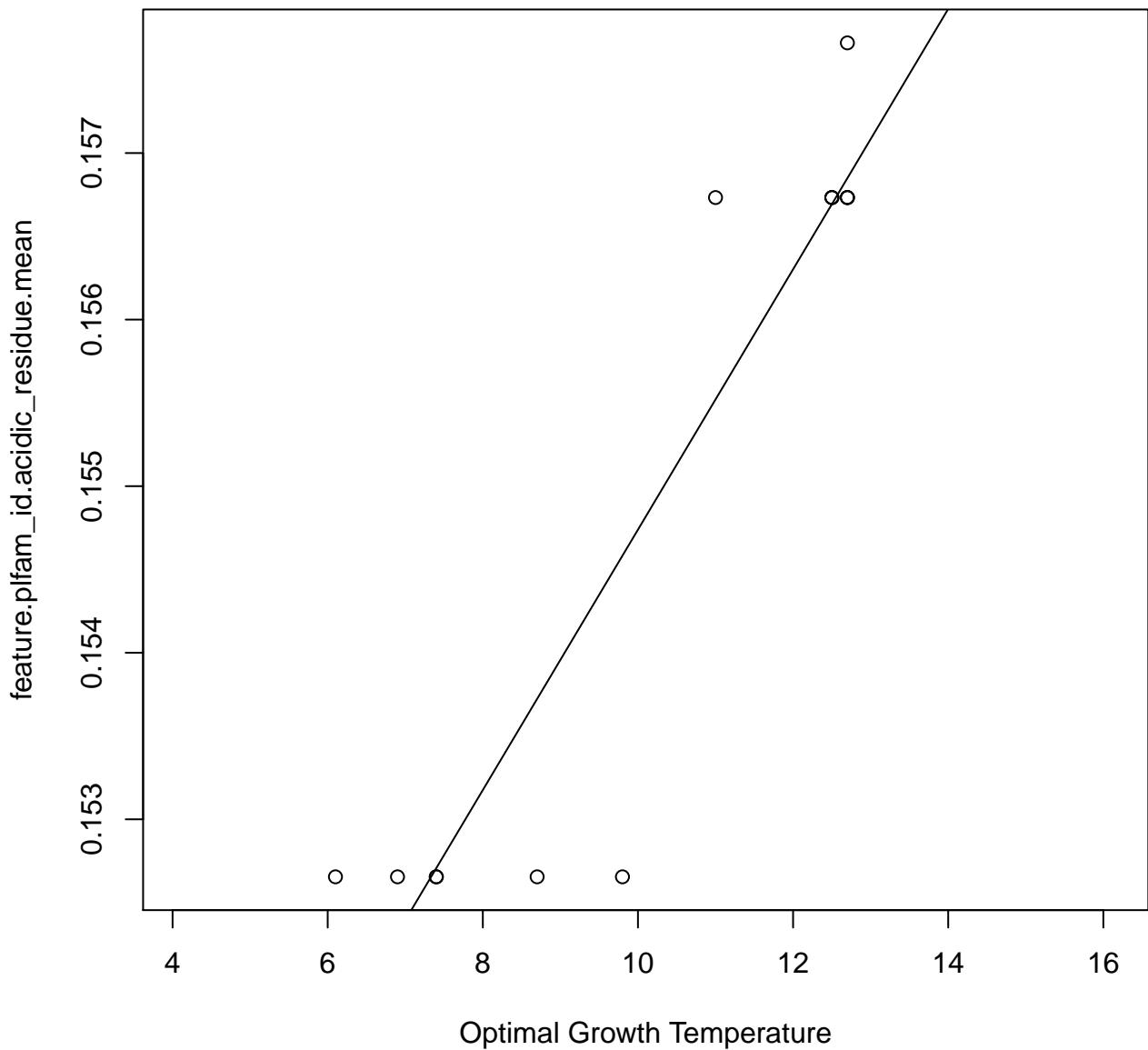
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PLF_28228_00007837
Transcriptional regulator, AraC family



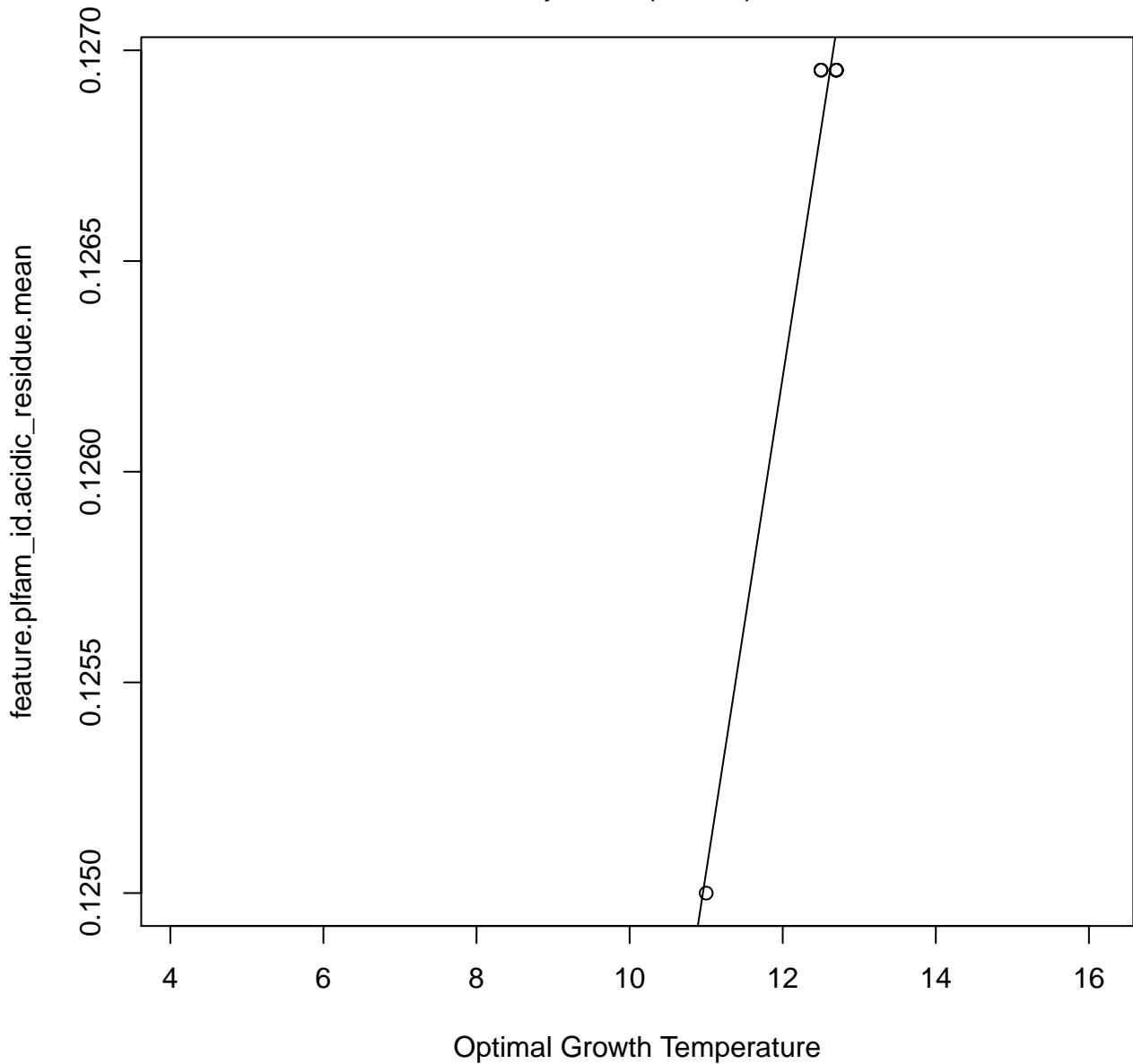
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PLF_28228_00002766
Porin



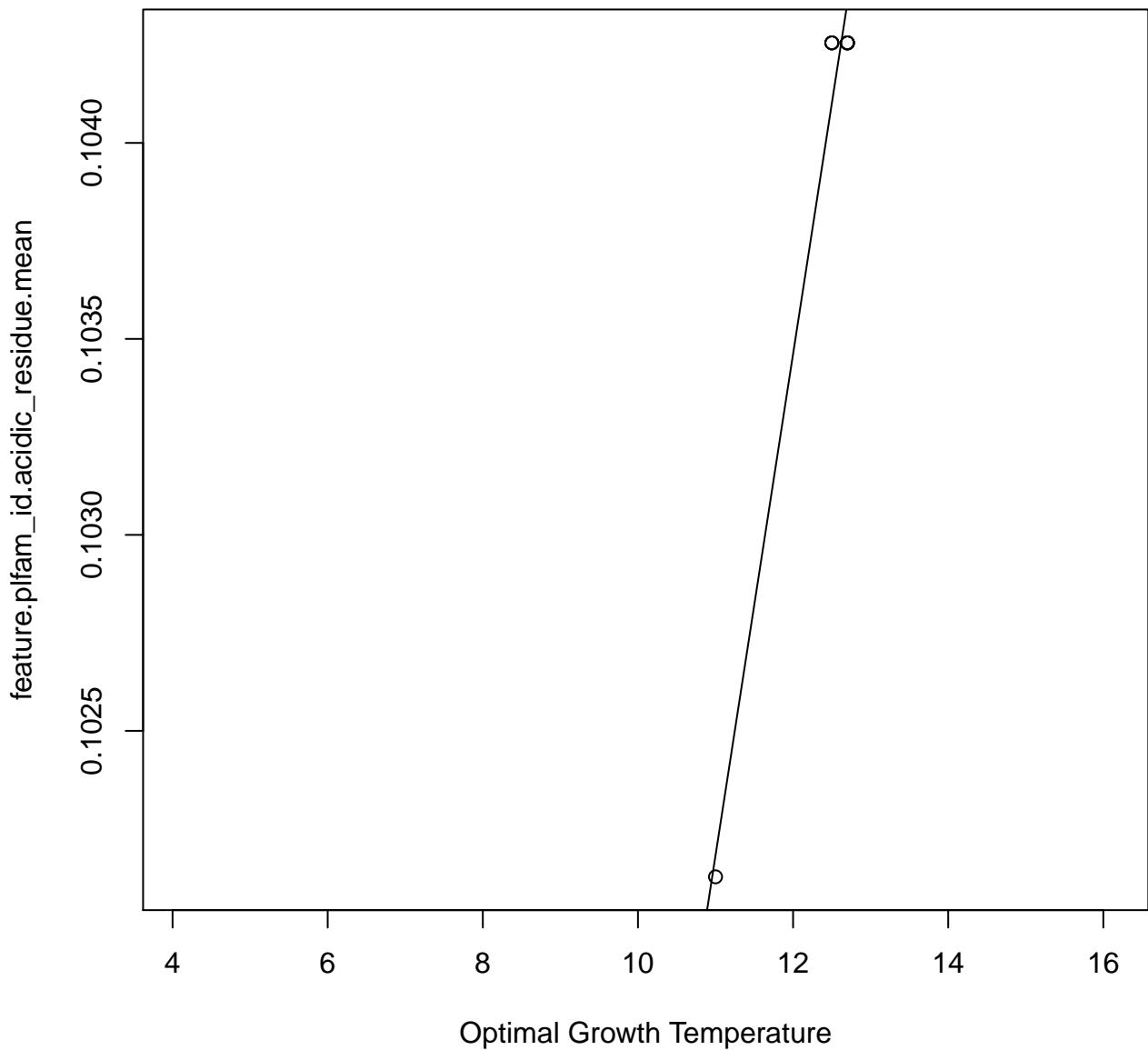
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C4-dicarboxylate transport transcriptional regulatory protein



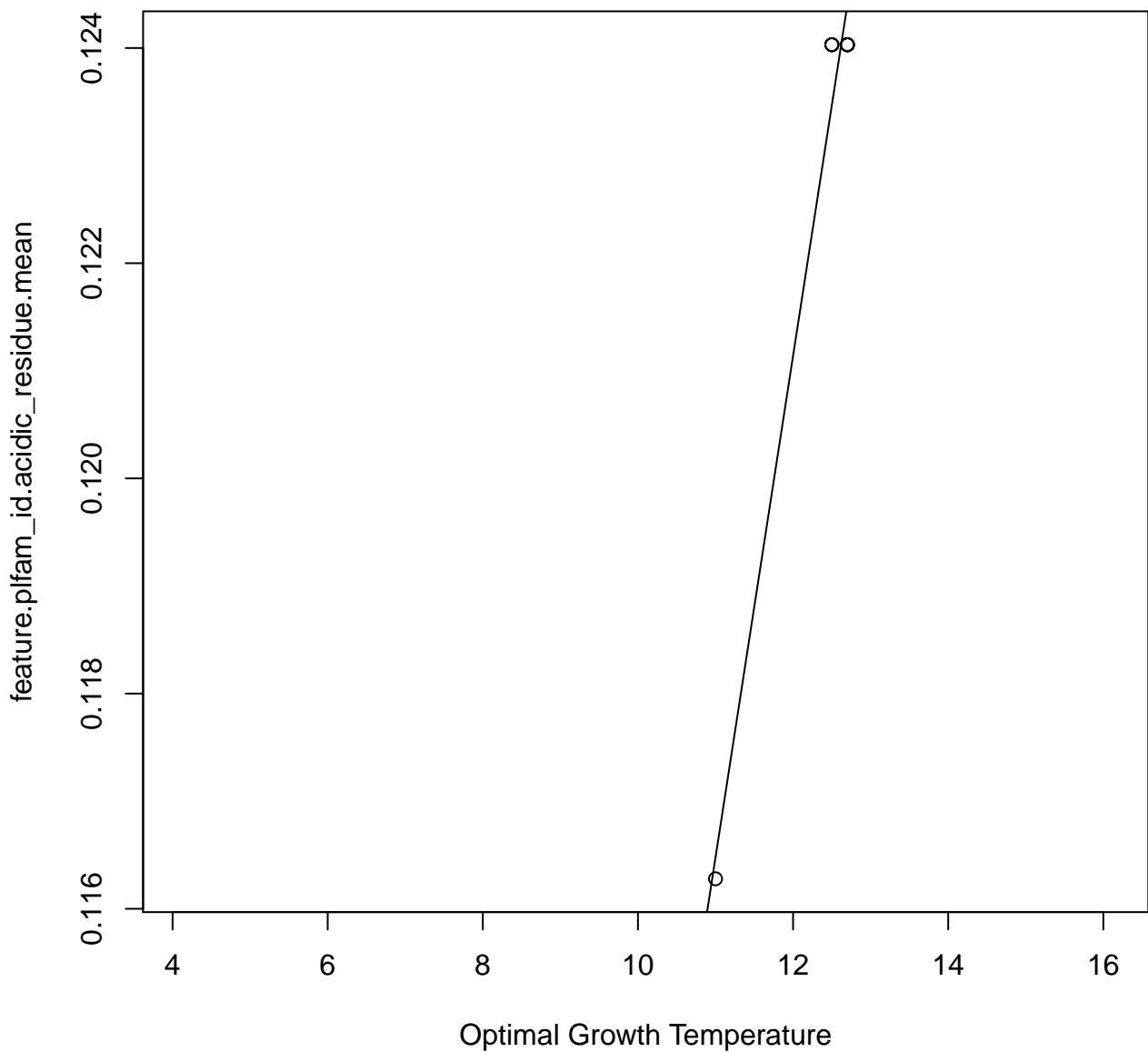
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Arylsulfatase (EC 3.1.6.1)



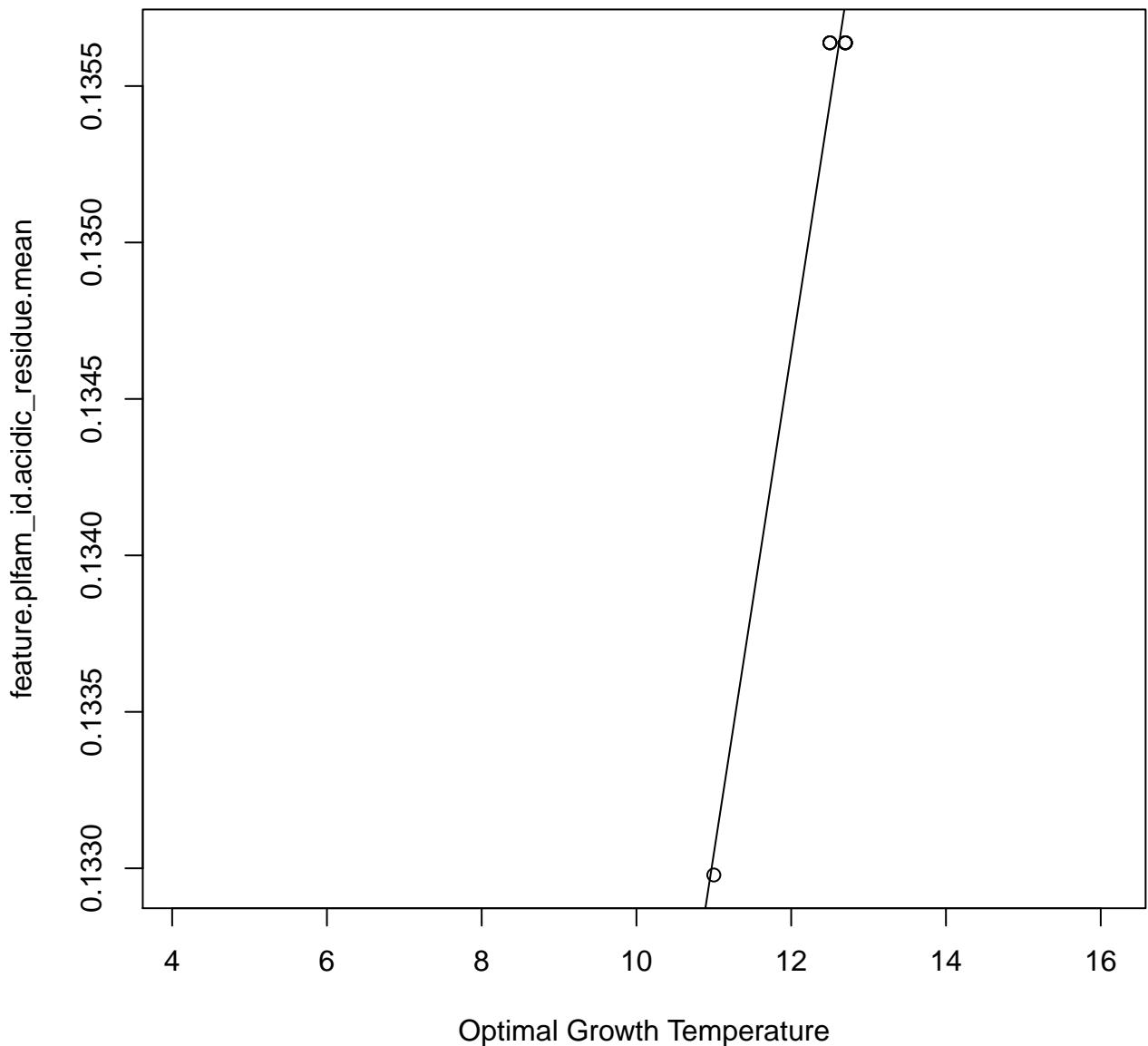
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Alpha-amylase precursor (EC 3.2.1.1)



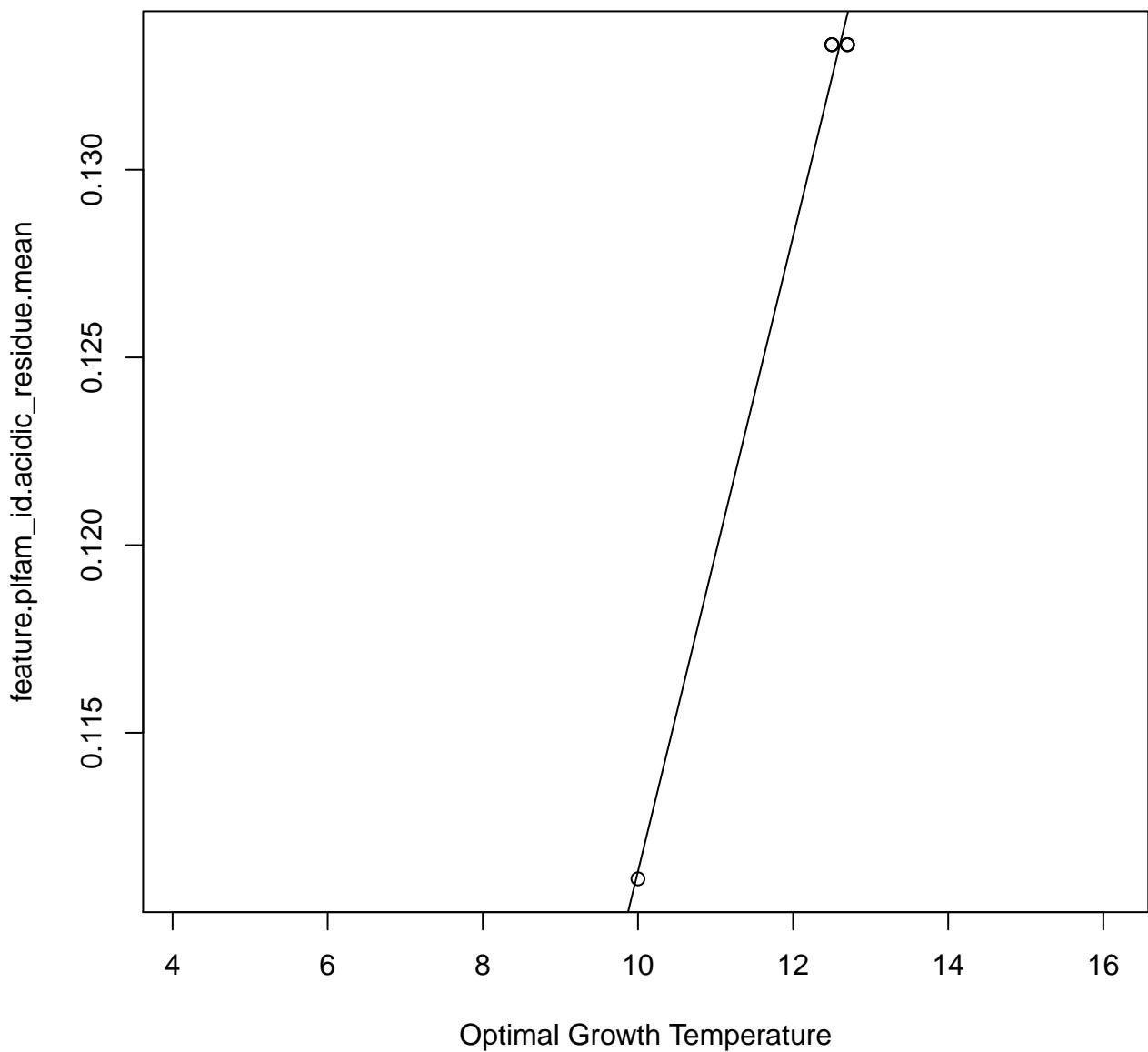
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PLF_28228_00004001
hypothetical protein



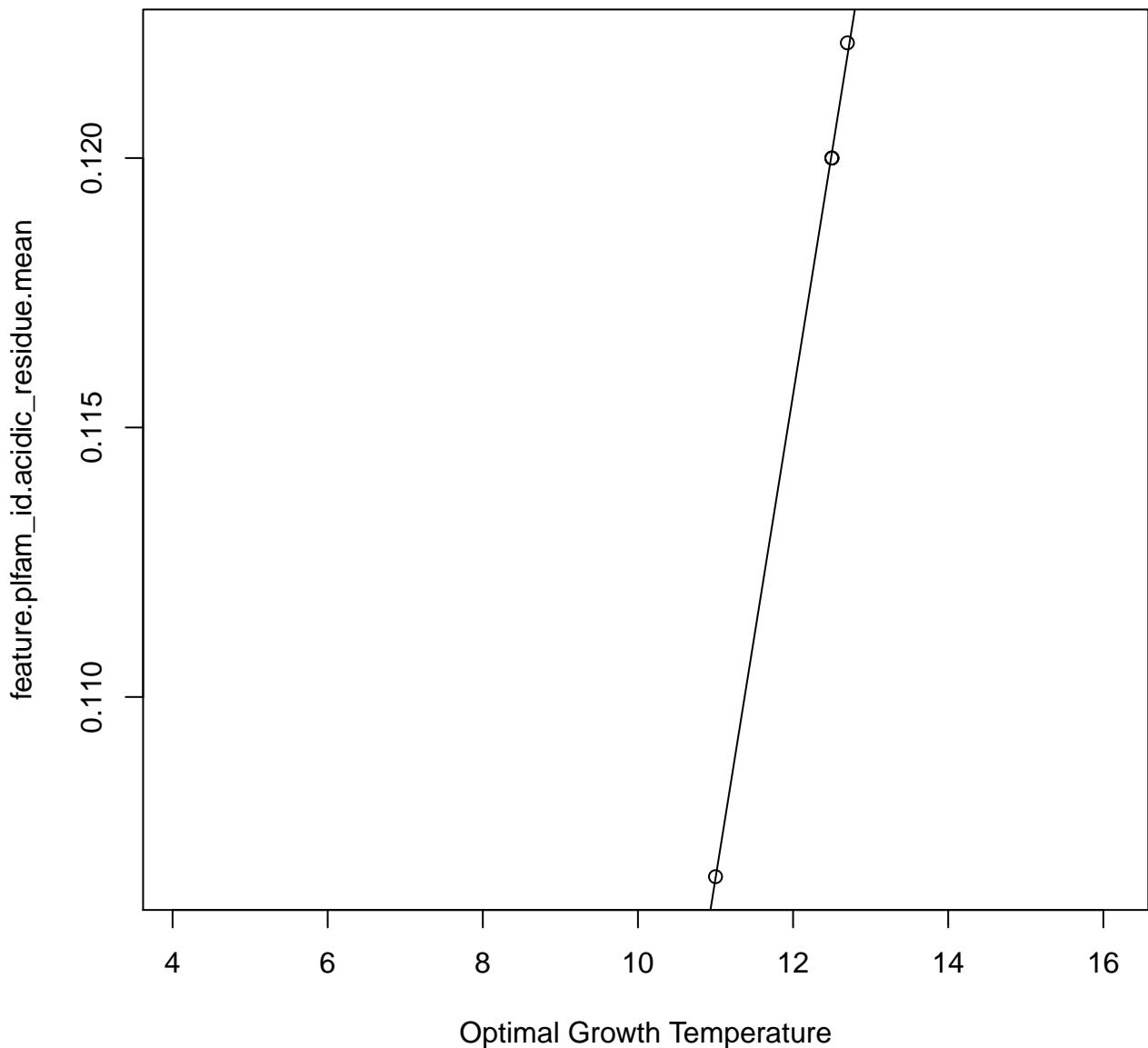
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Putrescine transport ATP-binding protein PotG (TC 3.A.1.11.2)



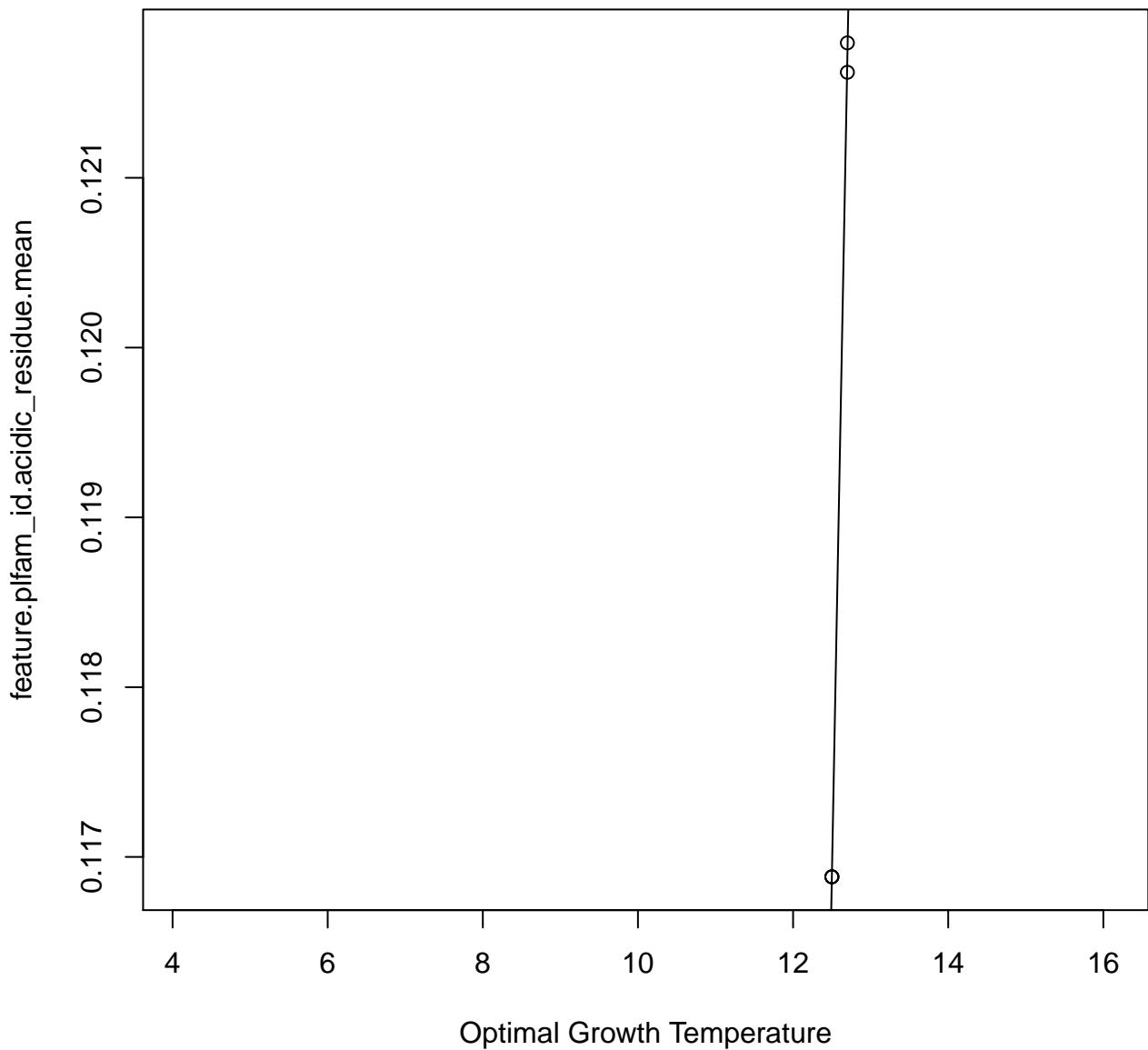
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PLF_28228_00004382
hypothetical protein



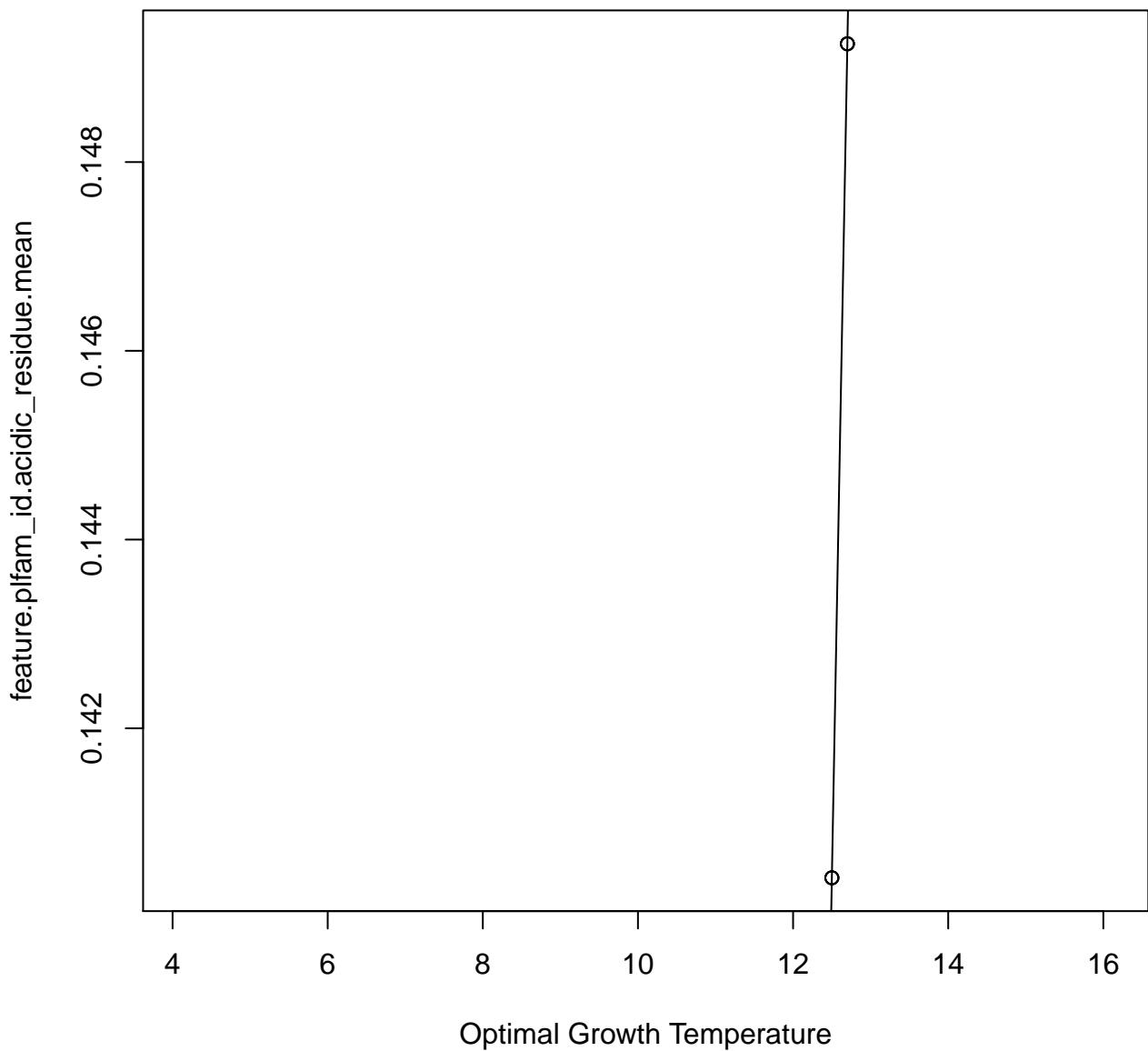
feature.plfam_id.acidic_residue.mean
PLF_28228_00007757
Fluoride ion transporter CrcB



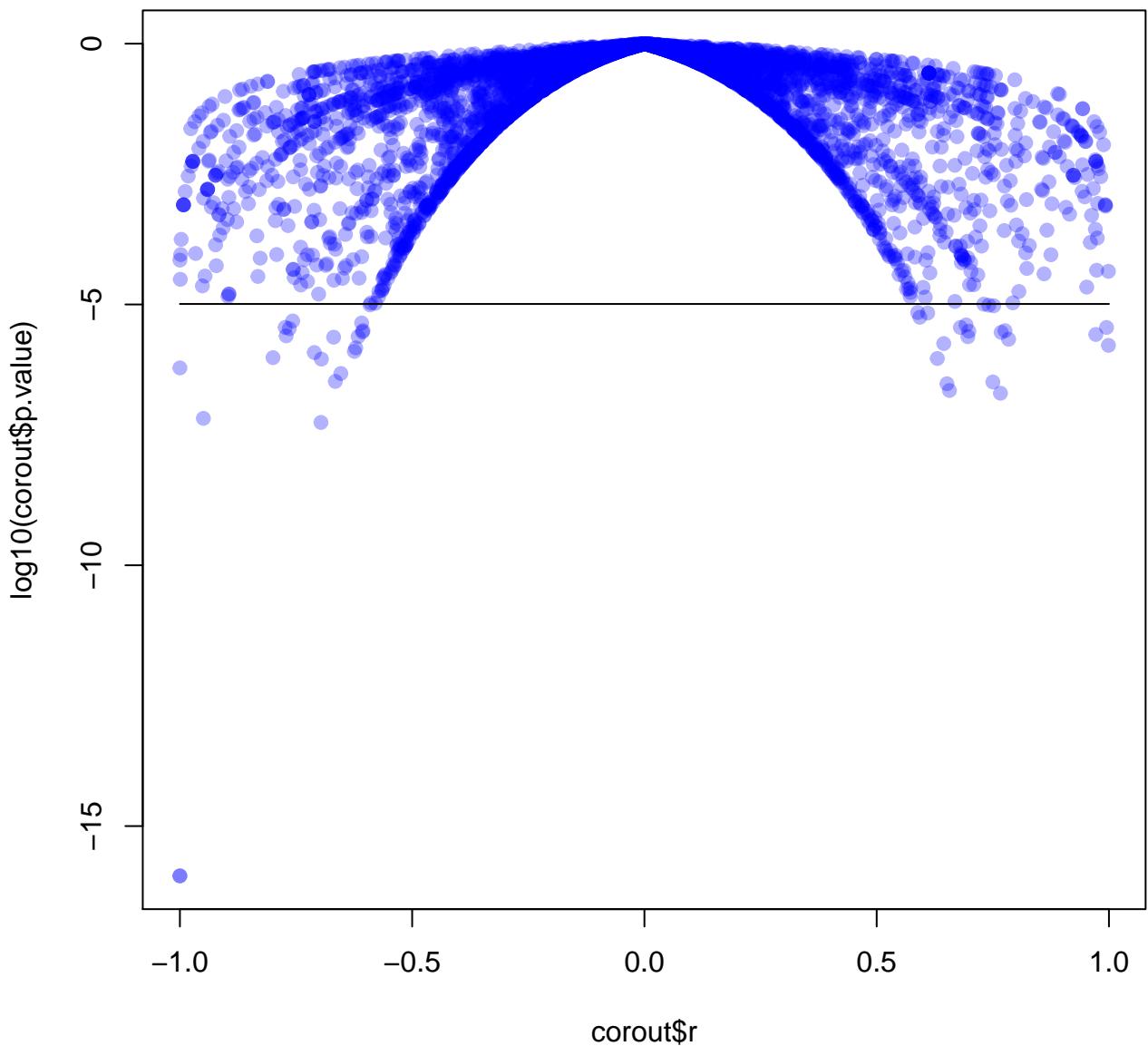
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Regulatory protein LuxR



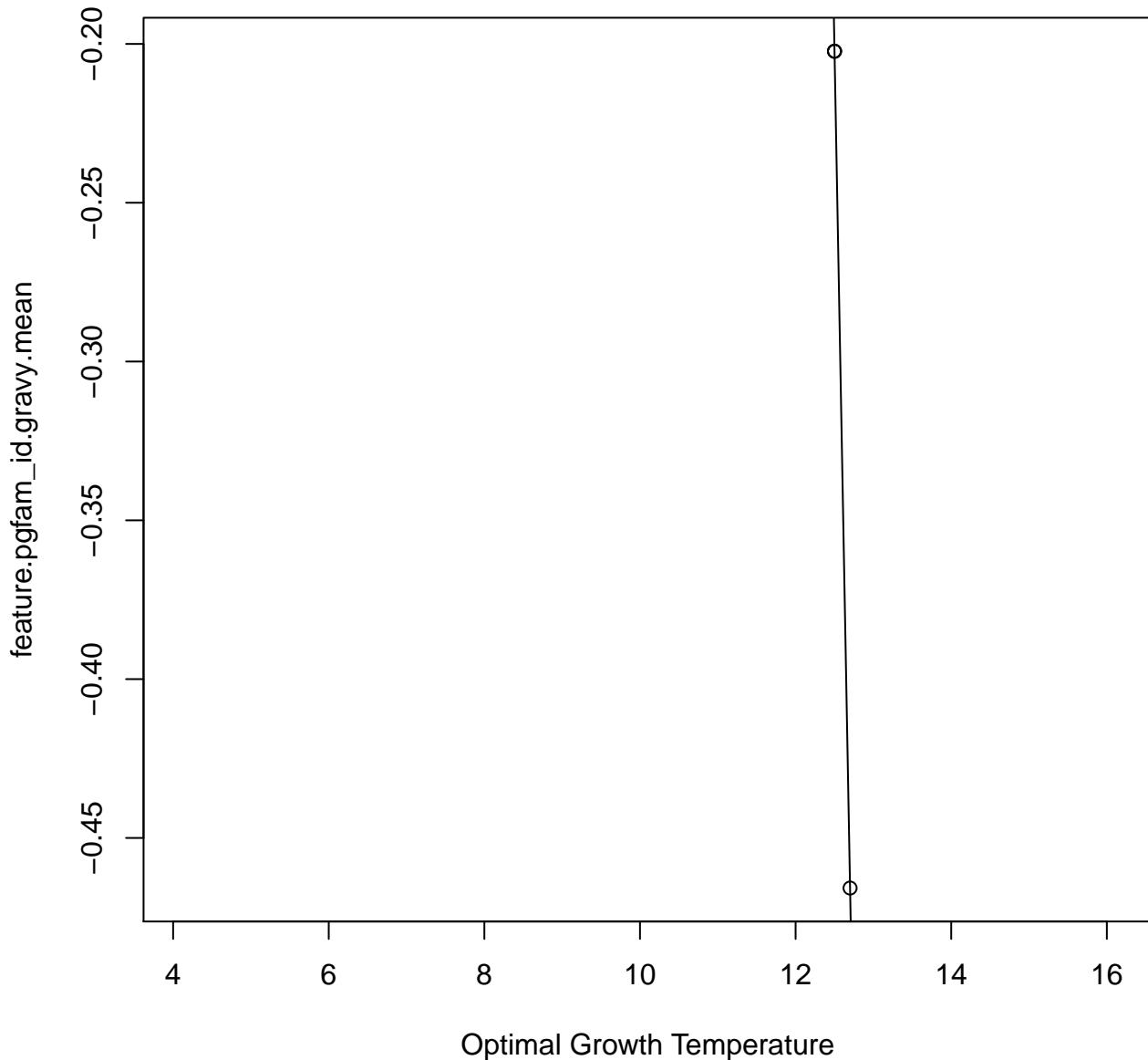
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PLF_28228_00003006
hypothetical protein



feature.pgfam_id.gravy.mean



feature.pgfam_id.gravy.mean
PGF_00211286
hypothetical protein



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PGF_00336673
hypothetical protein

feature.pgfam_id.gravy.mean

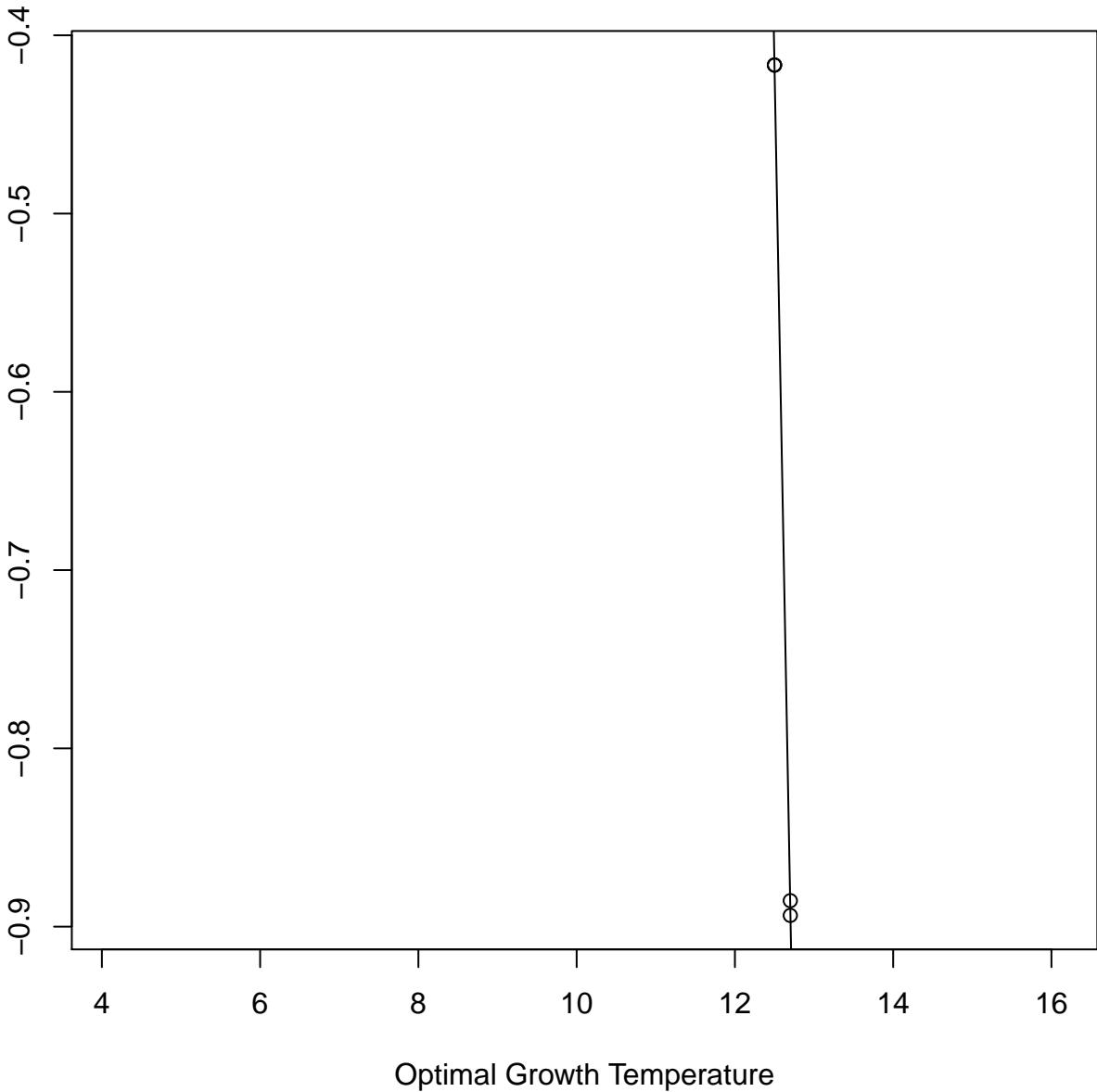
4 6 8 10 12 14 16

Optimal Growth Temperature

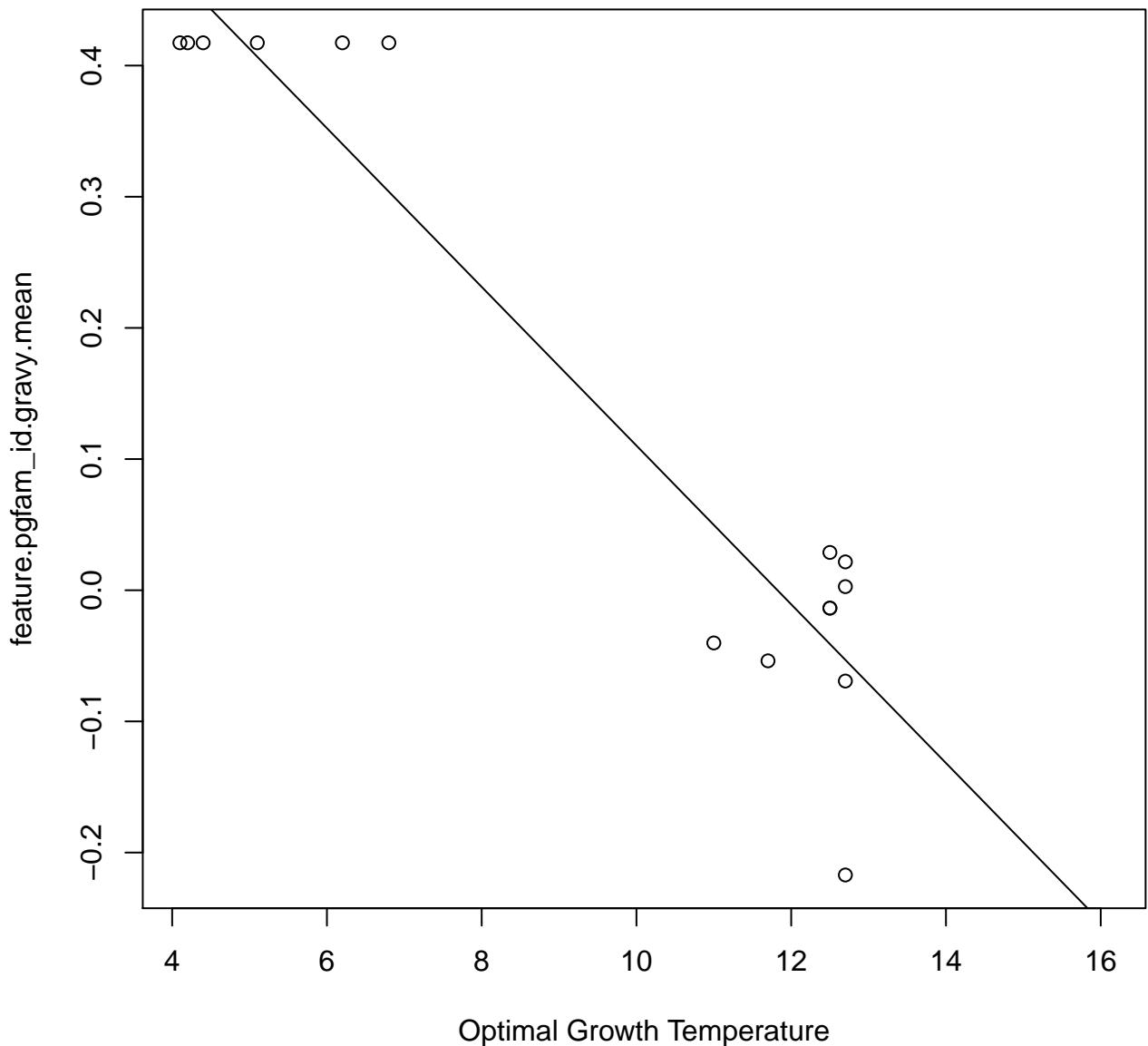


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hypothetical protein

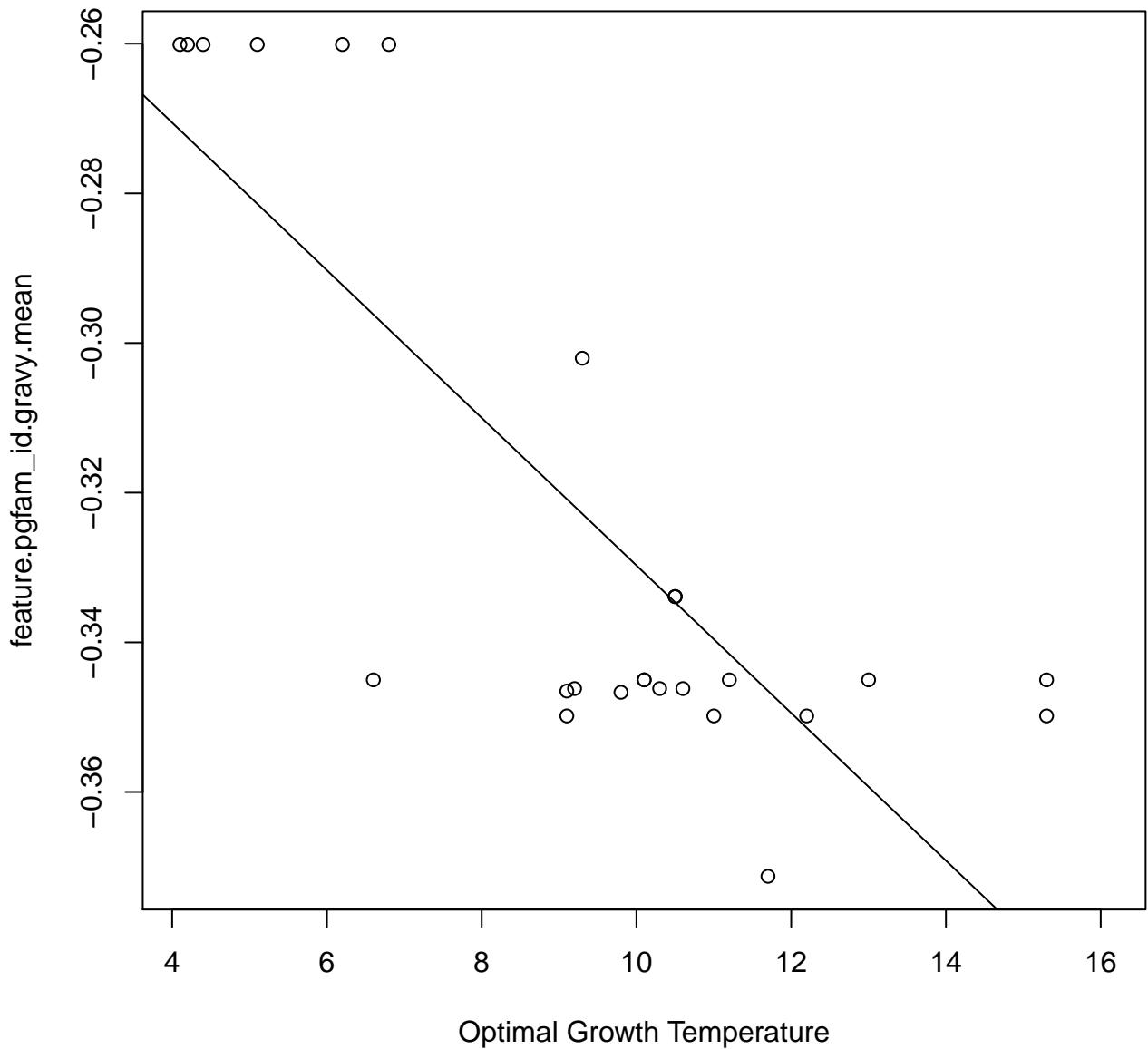
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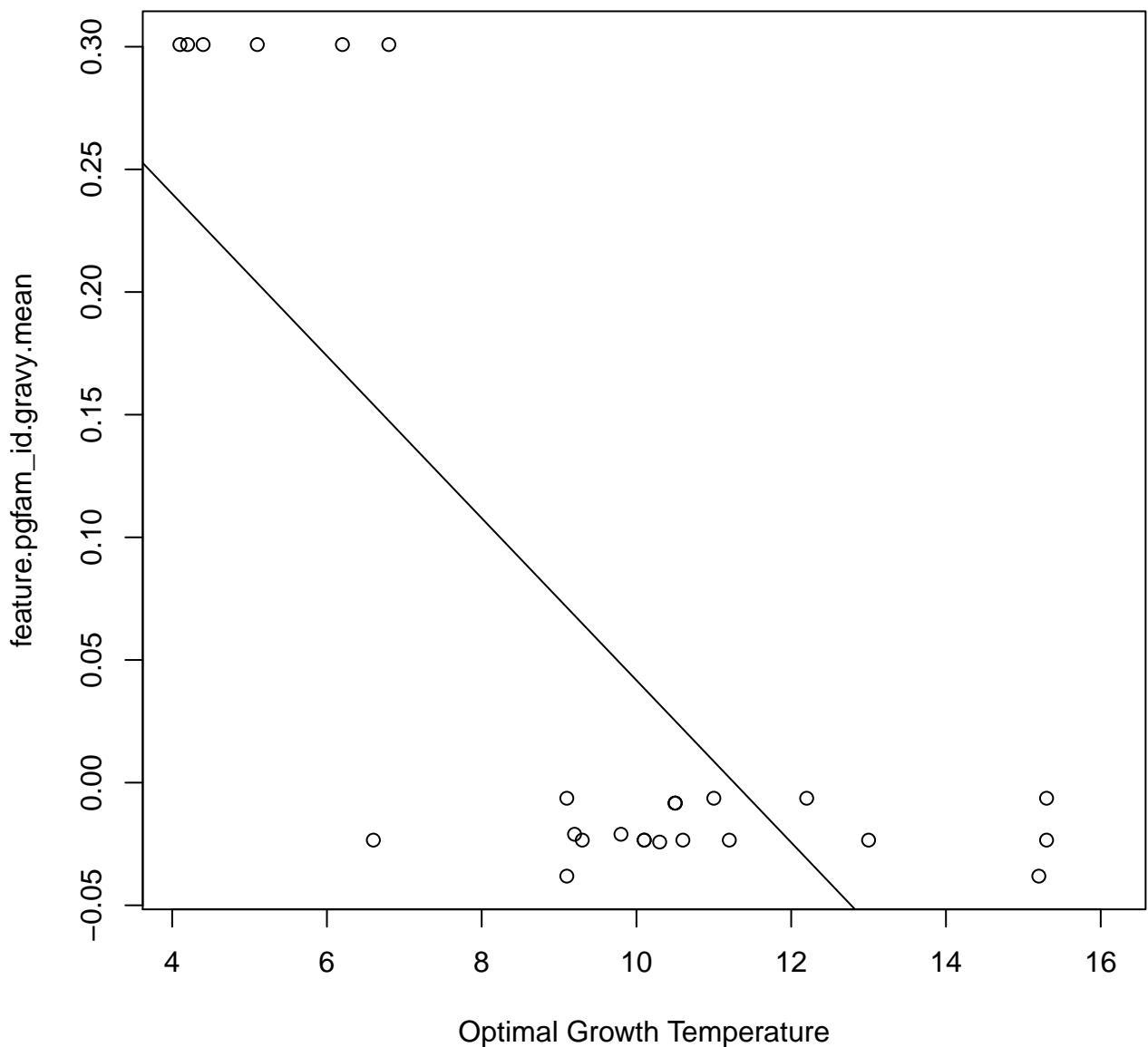
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Cobyricic acid a,c-diamide synthetase (EC 6.3.5.11)



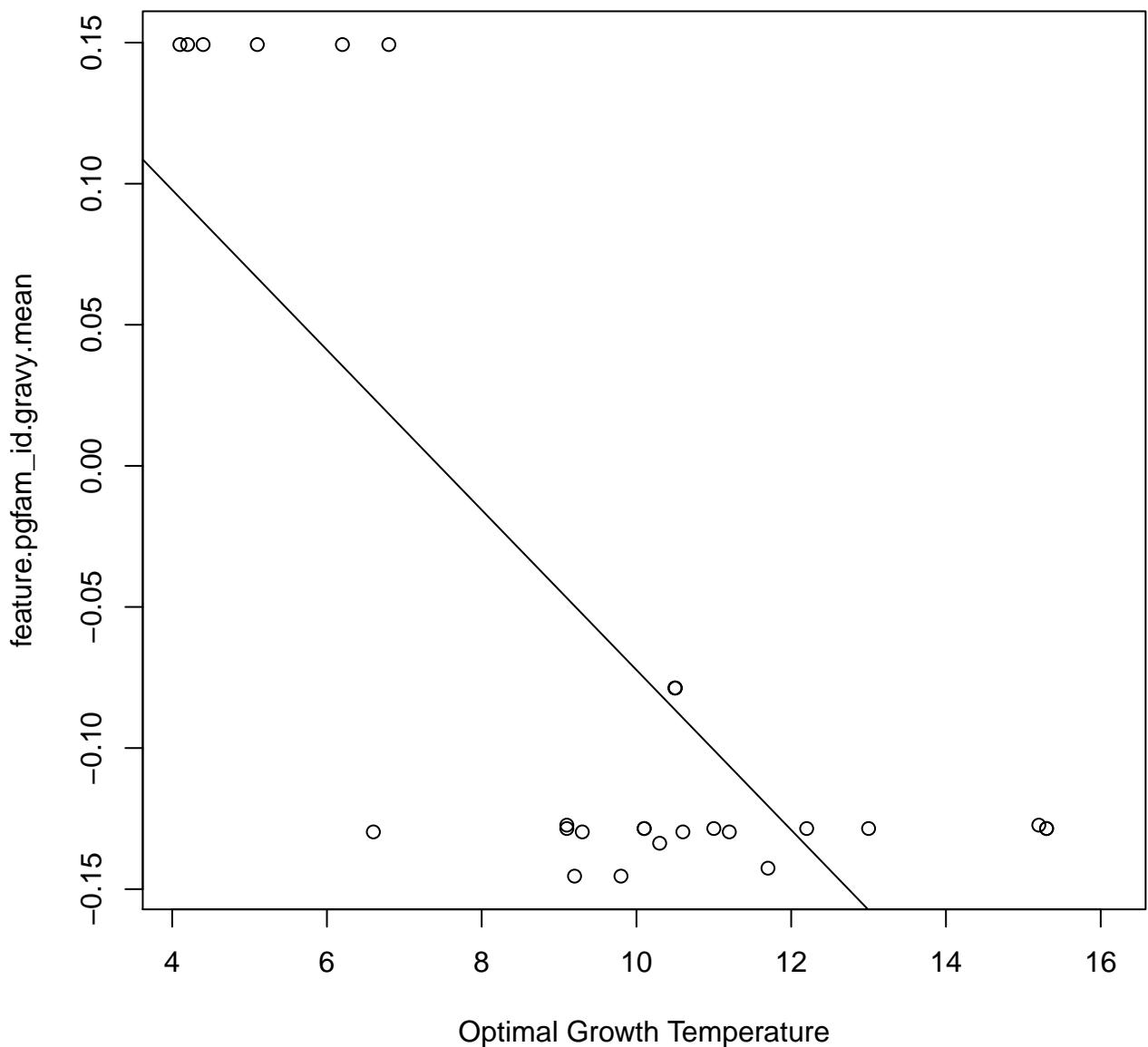
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Maltodextrin glucosidase (EC 3.2.1.20)



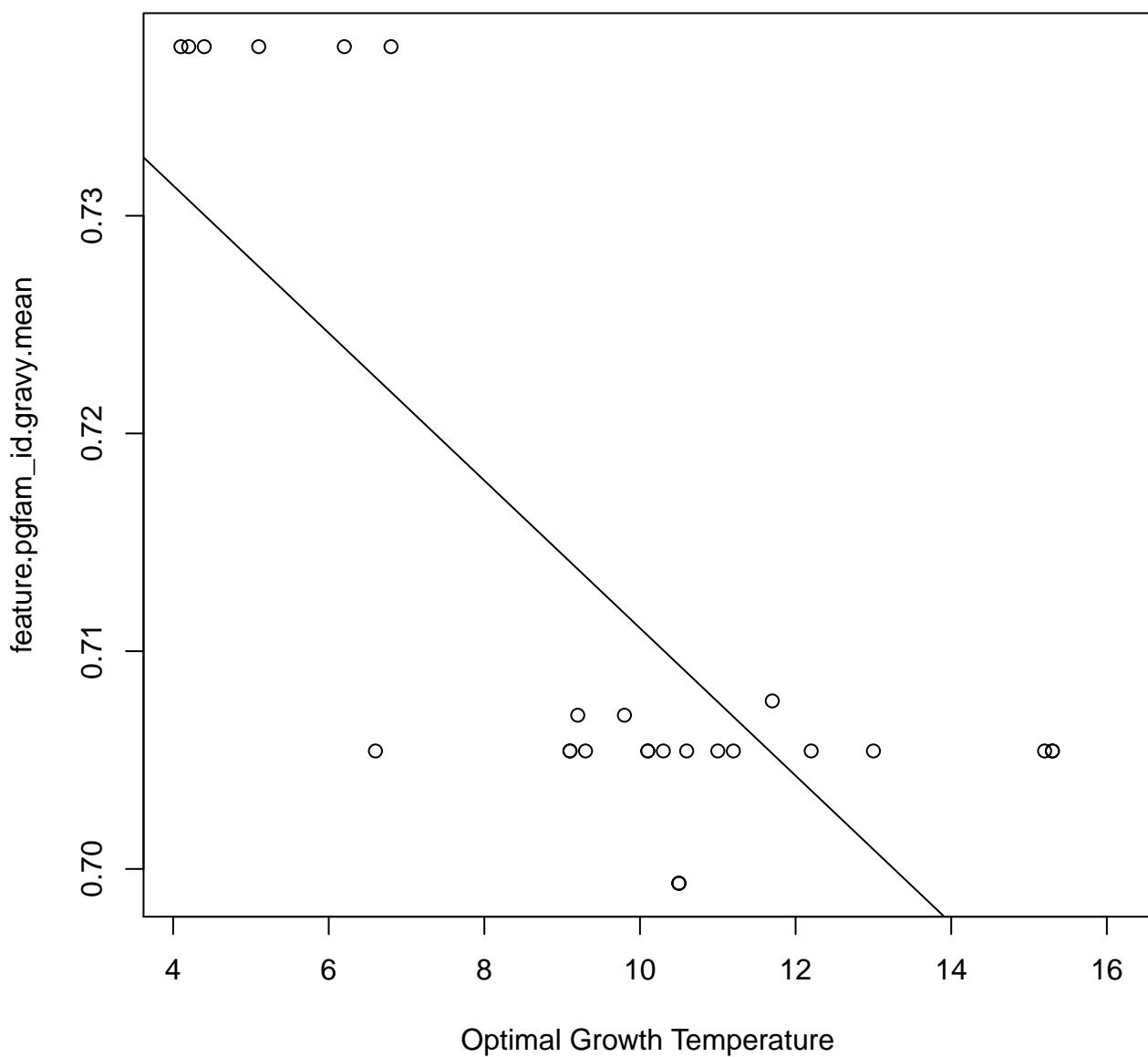
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hypothetical protein



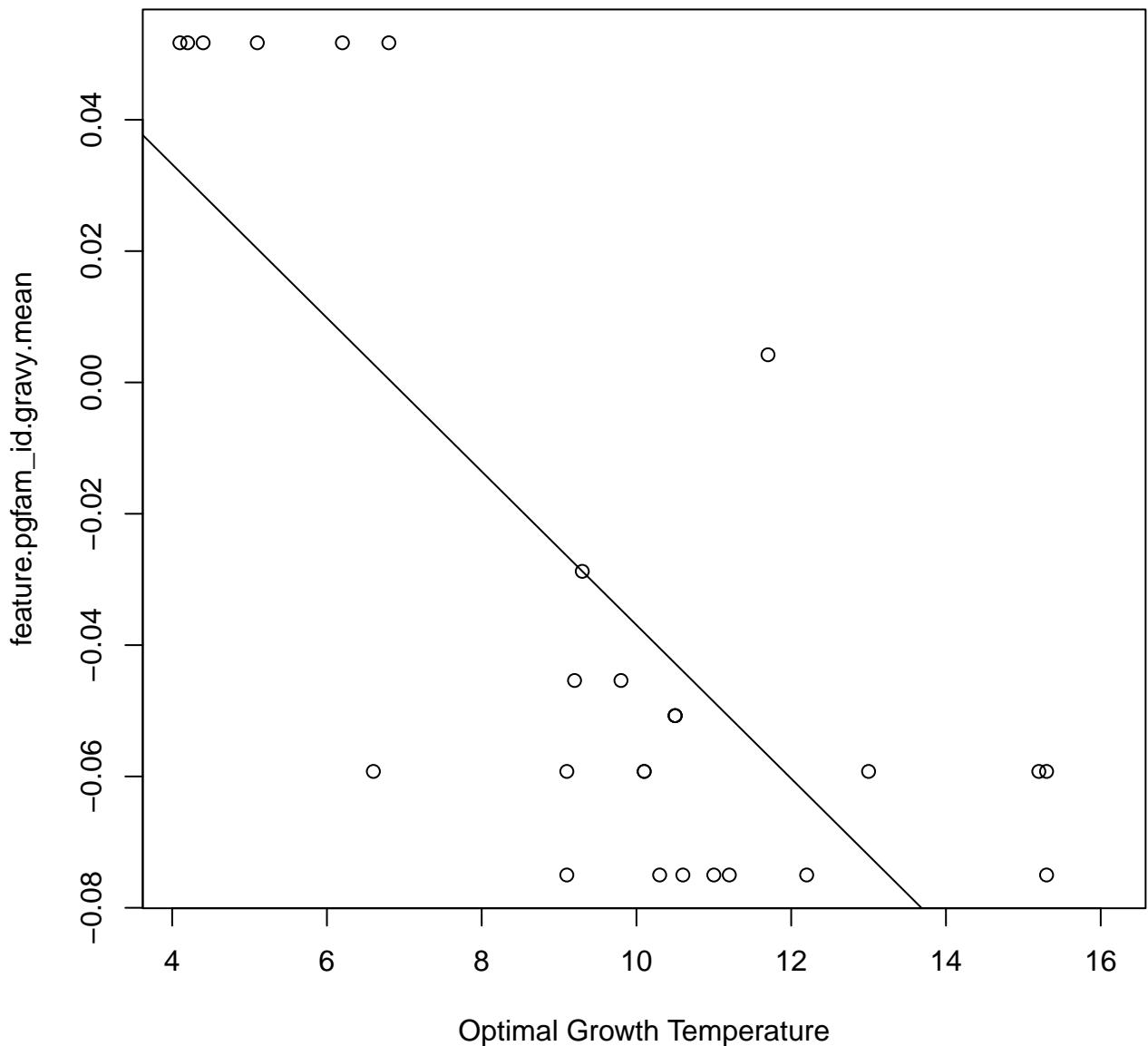
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hypothetical protein



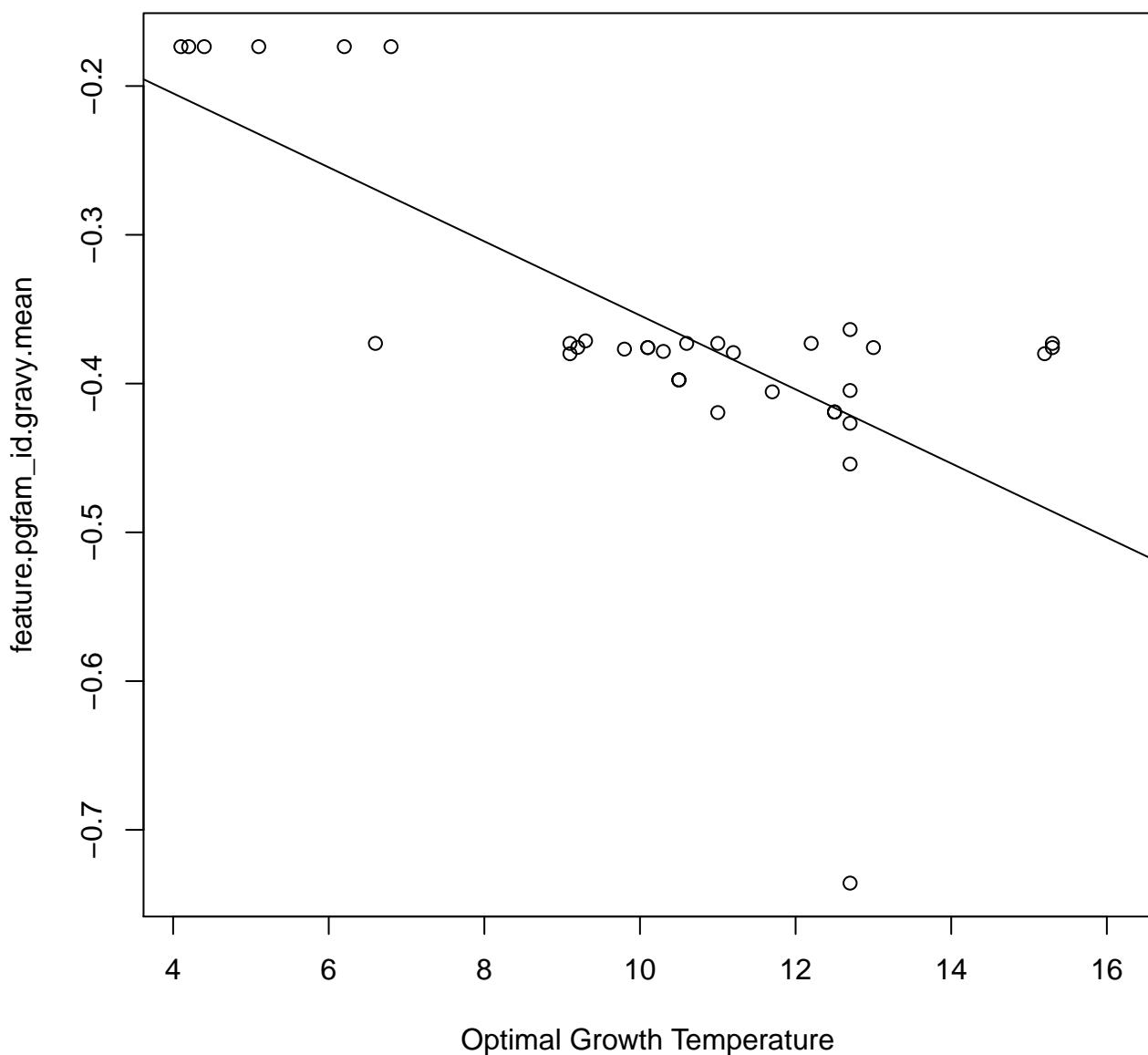
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TrkA-C domain protein



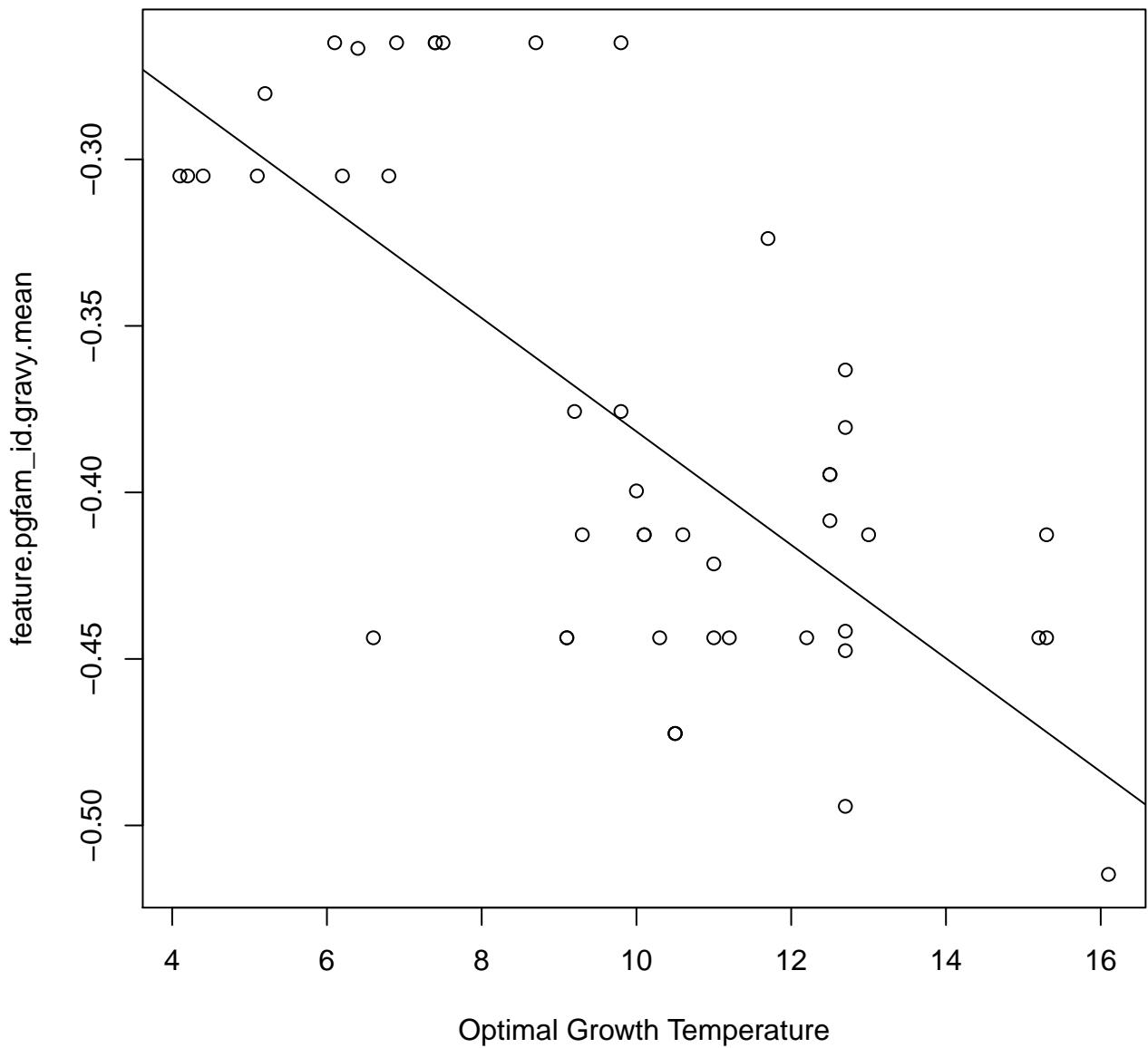
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hypothetical protein



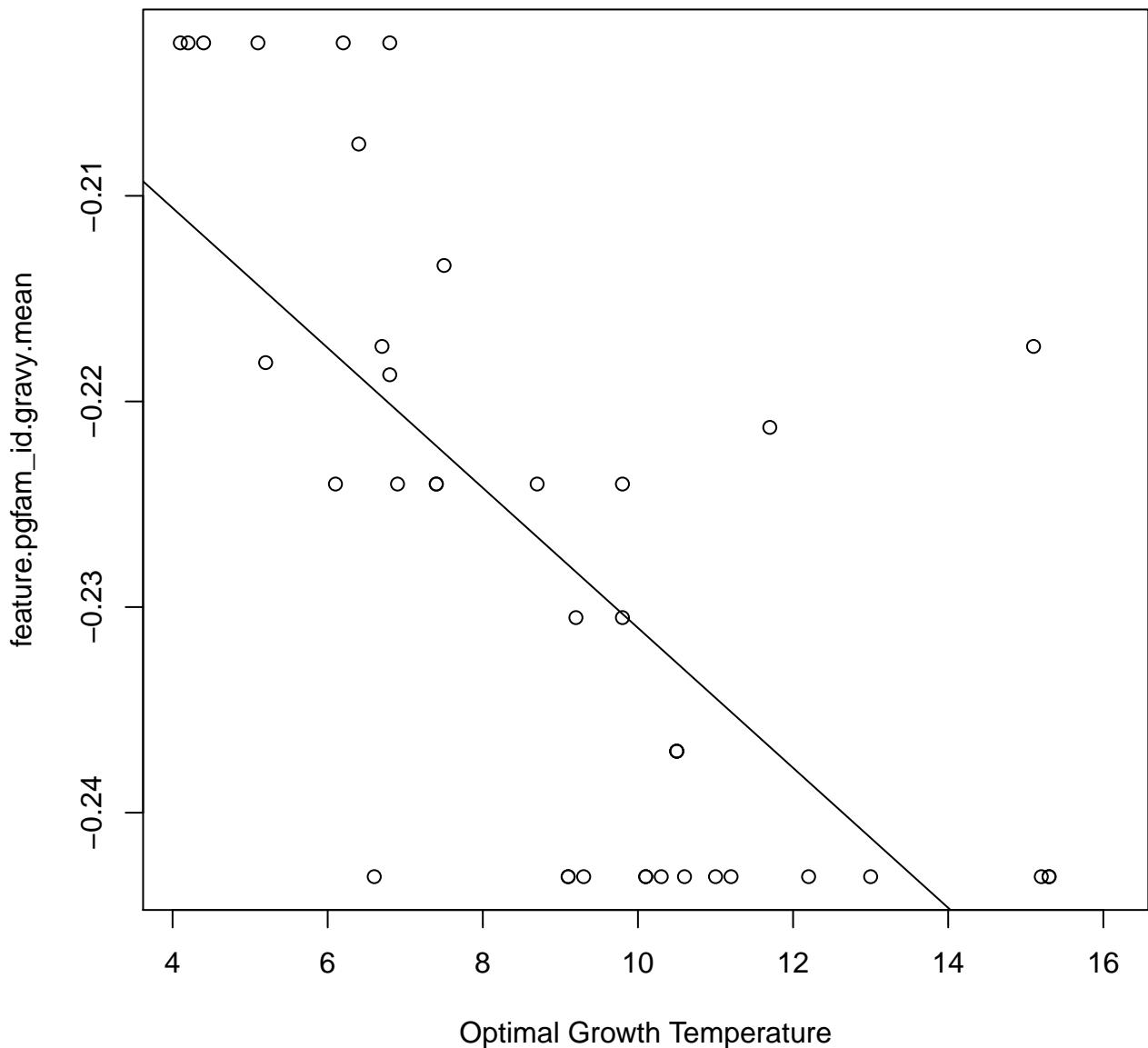
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Fatty acid cis/trans isomerase



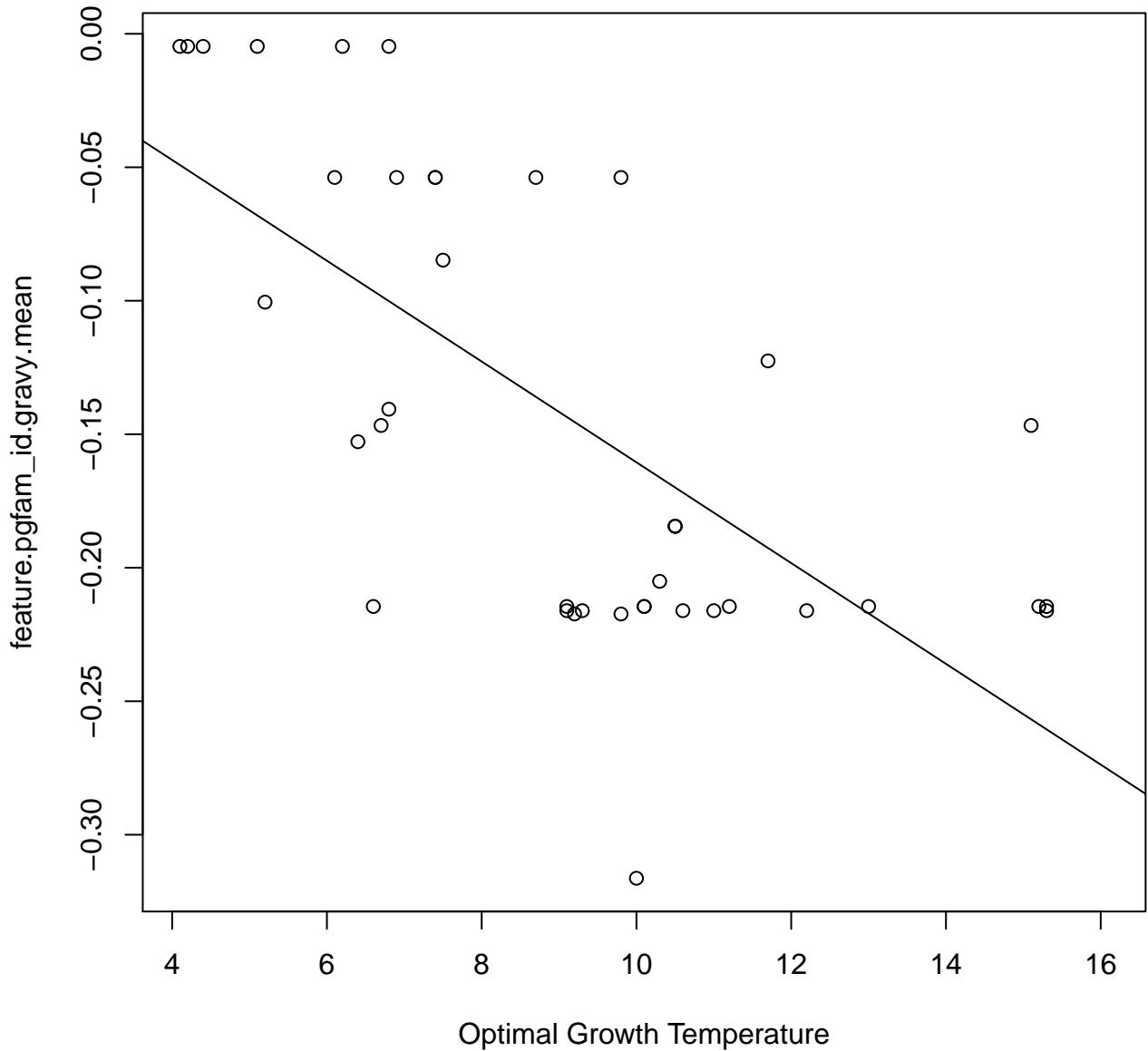
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Potential queD like 2



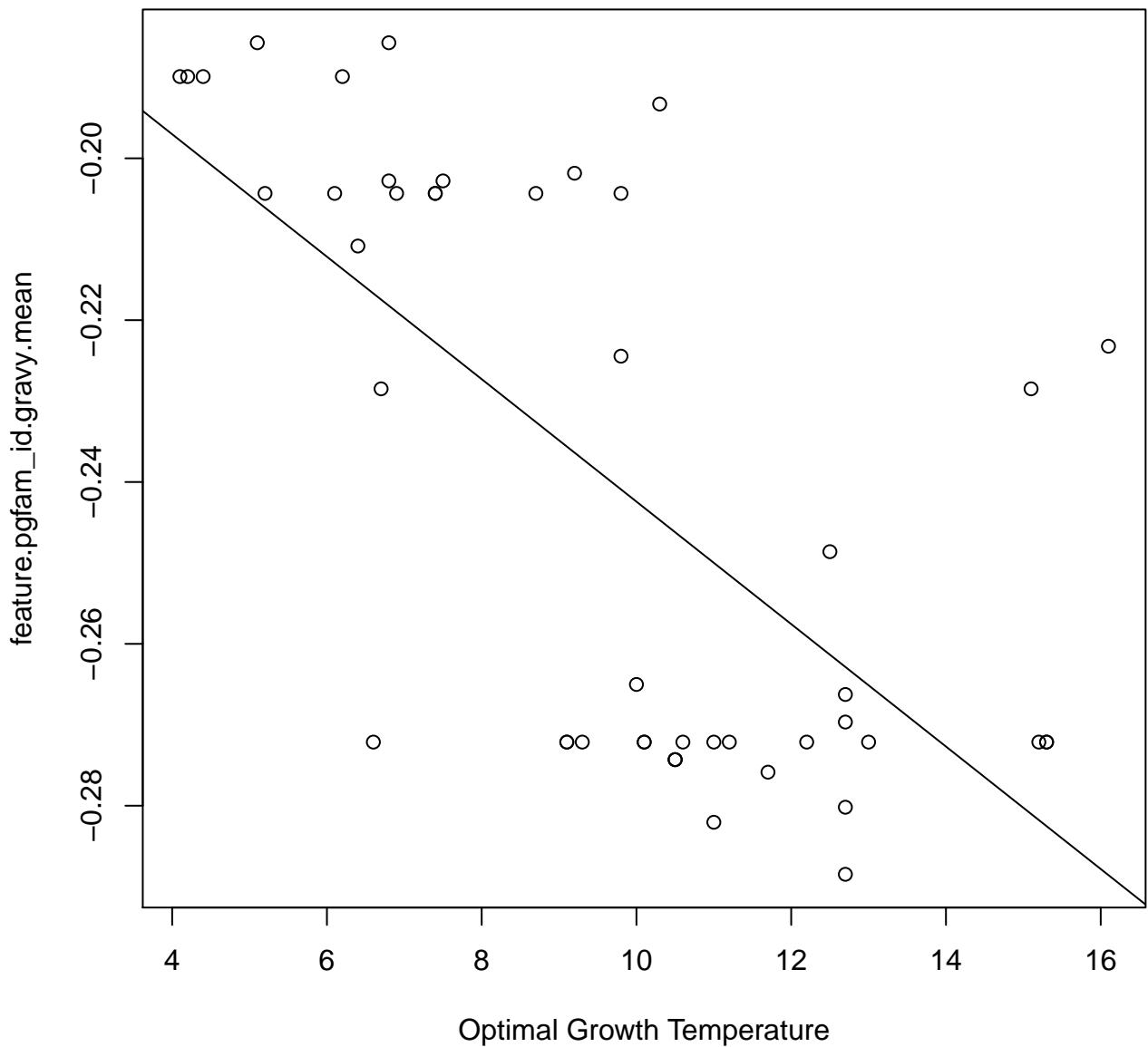
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Carbon–nitrogen hydrolase



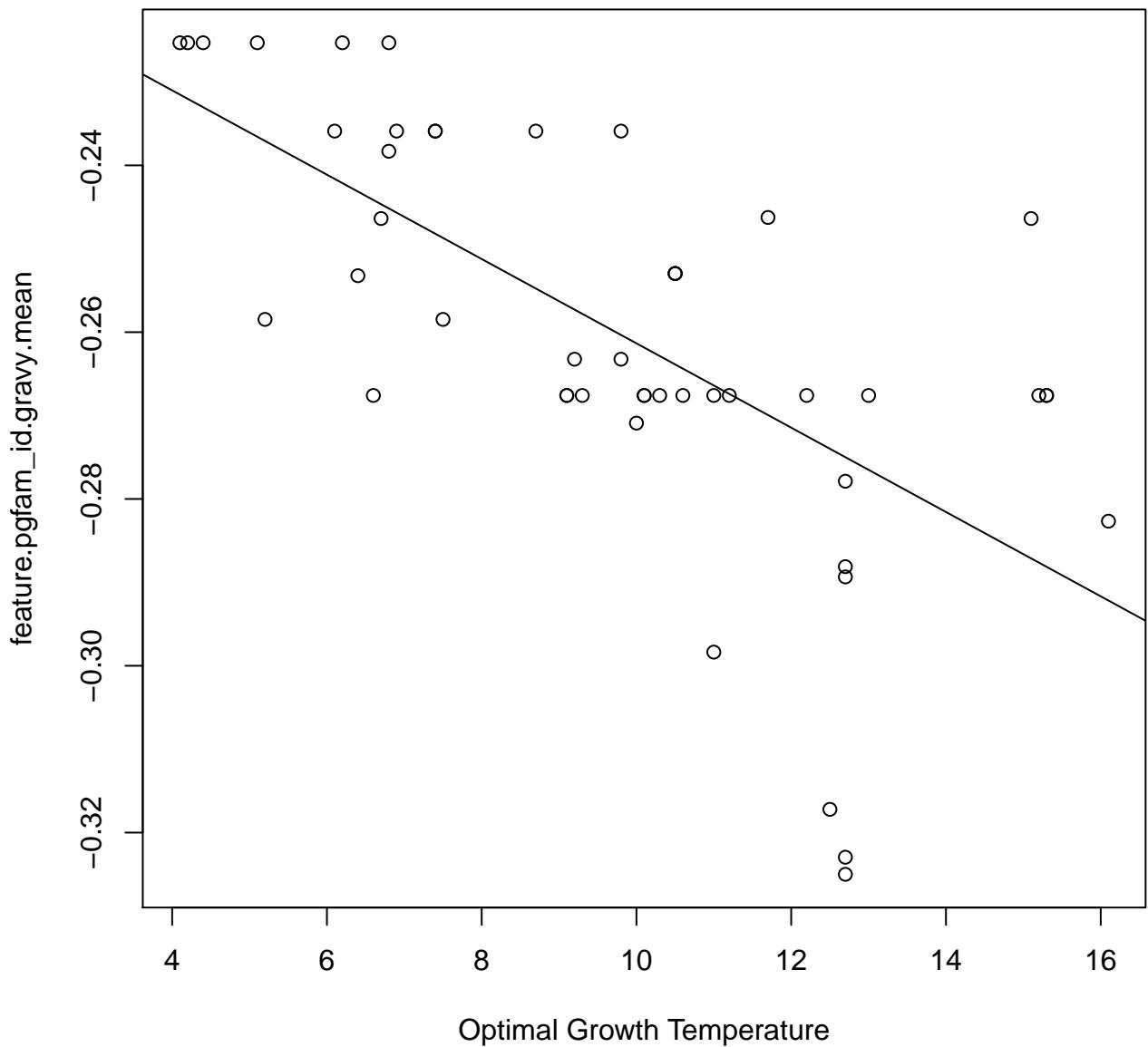
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hypothetical protein



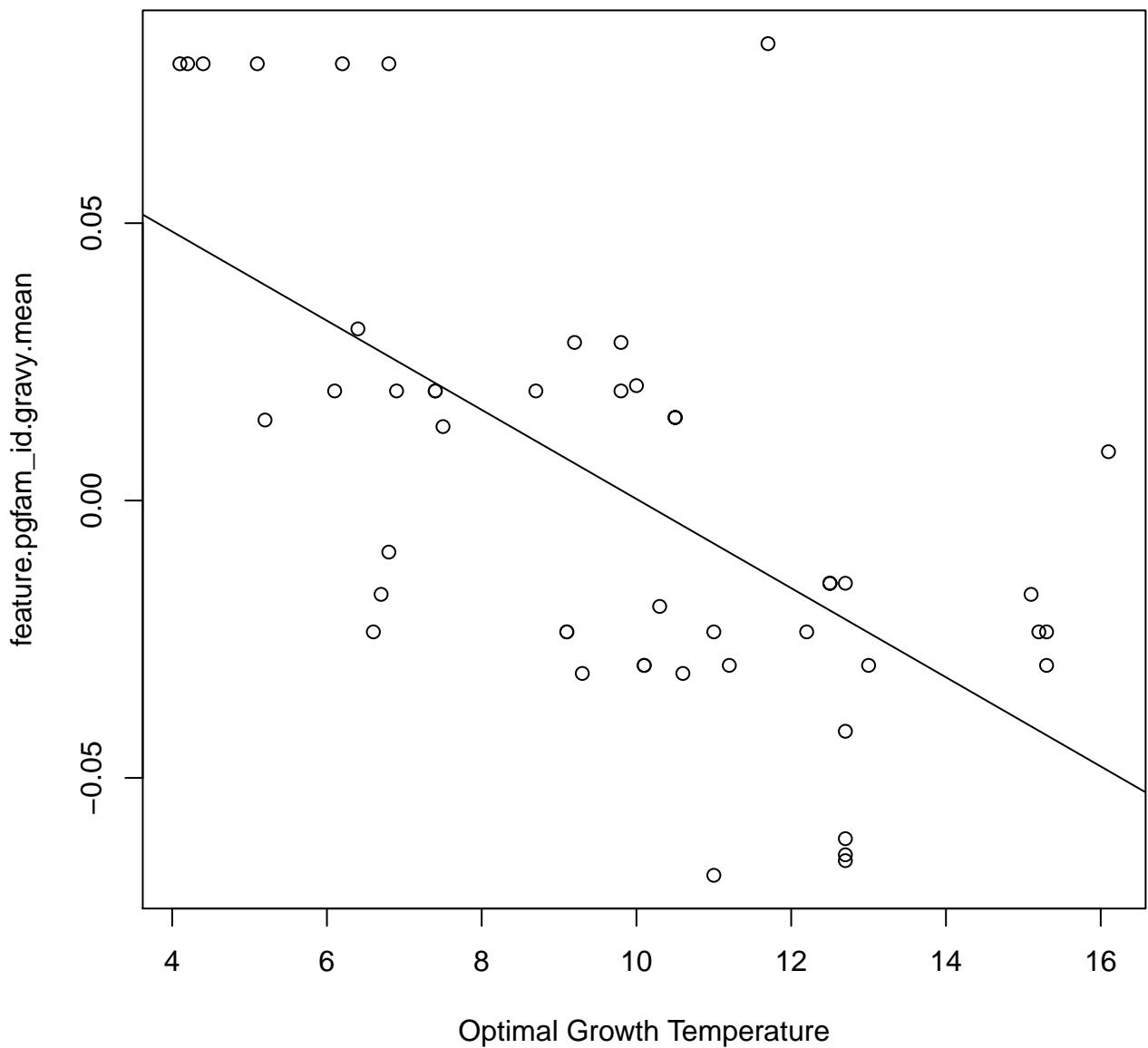
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GTP 3',8-cyclase (EC 4.1.99.22)



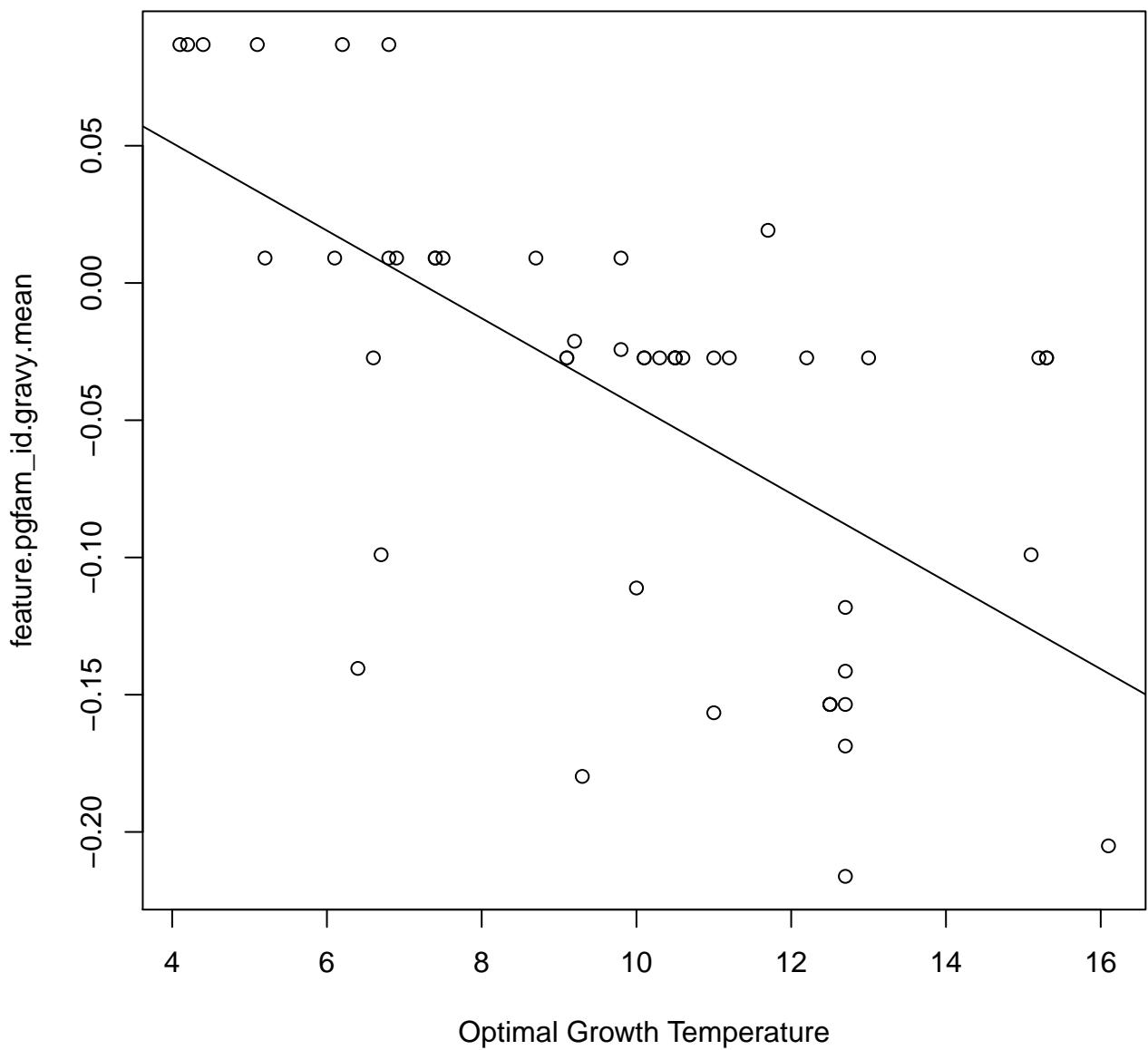
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16S rRNA (uracil(1498)-N(3))-methyltransferase (EC 2.1.1.193)



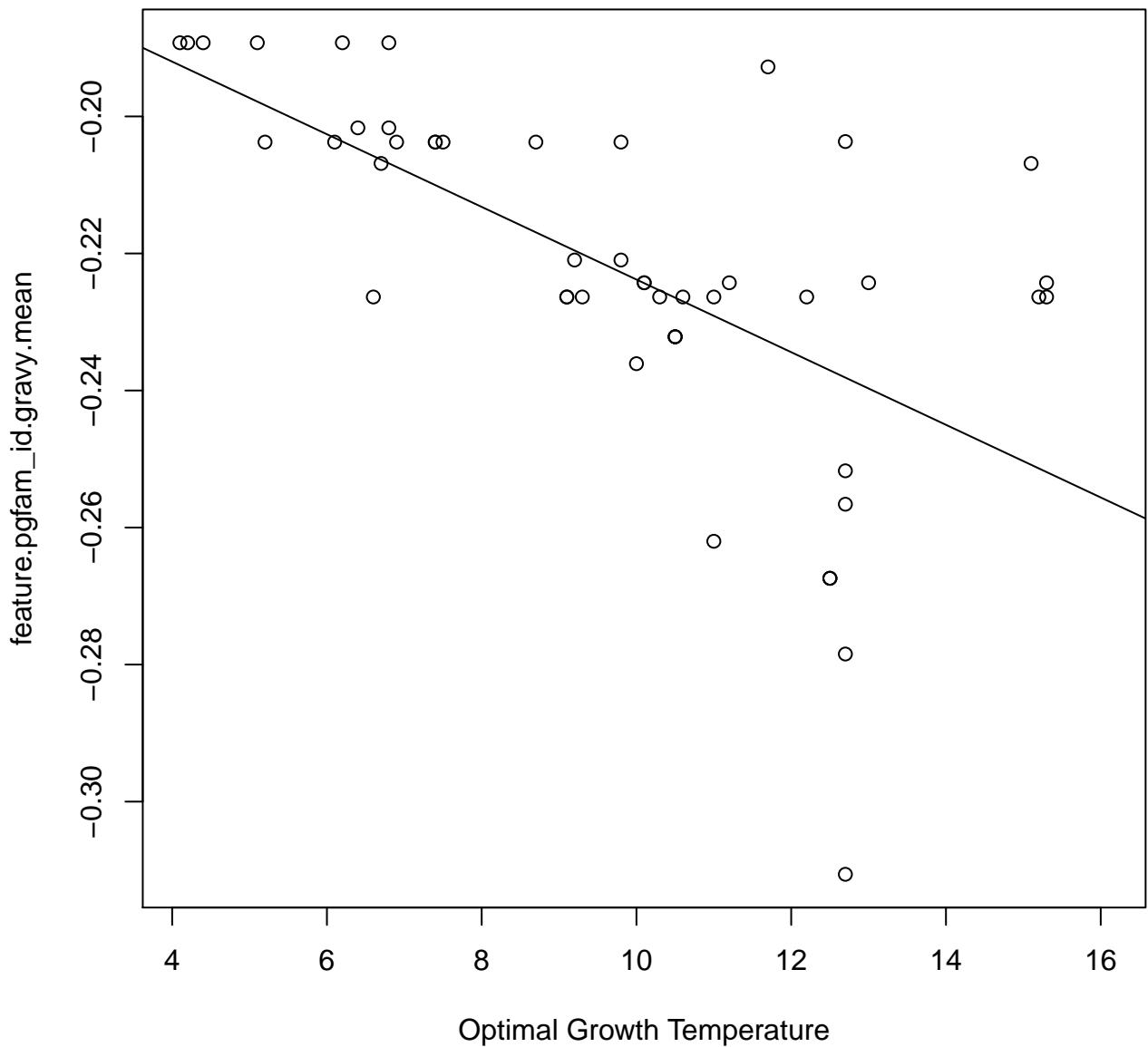
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Orn/DAP/Arg family decarboxylase



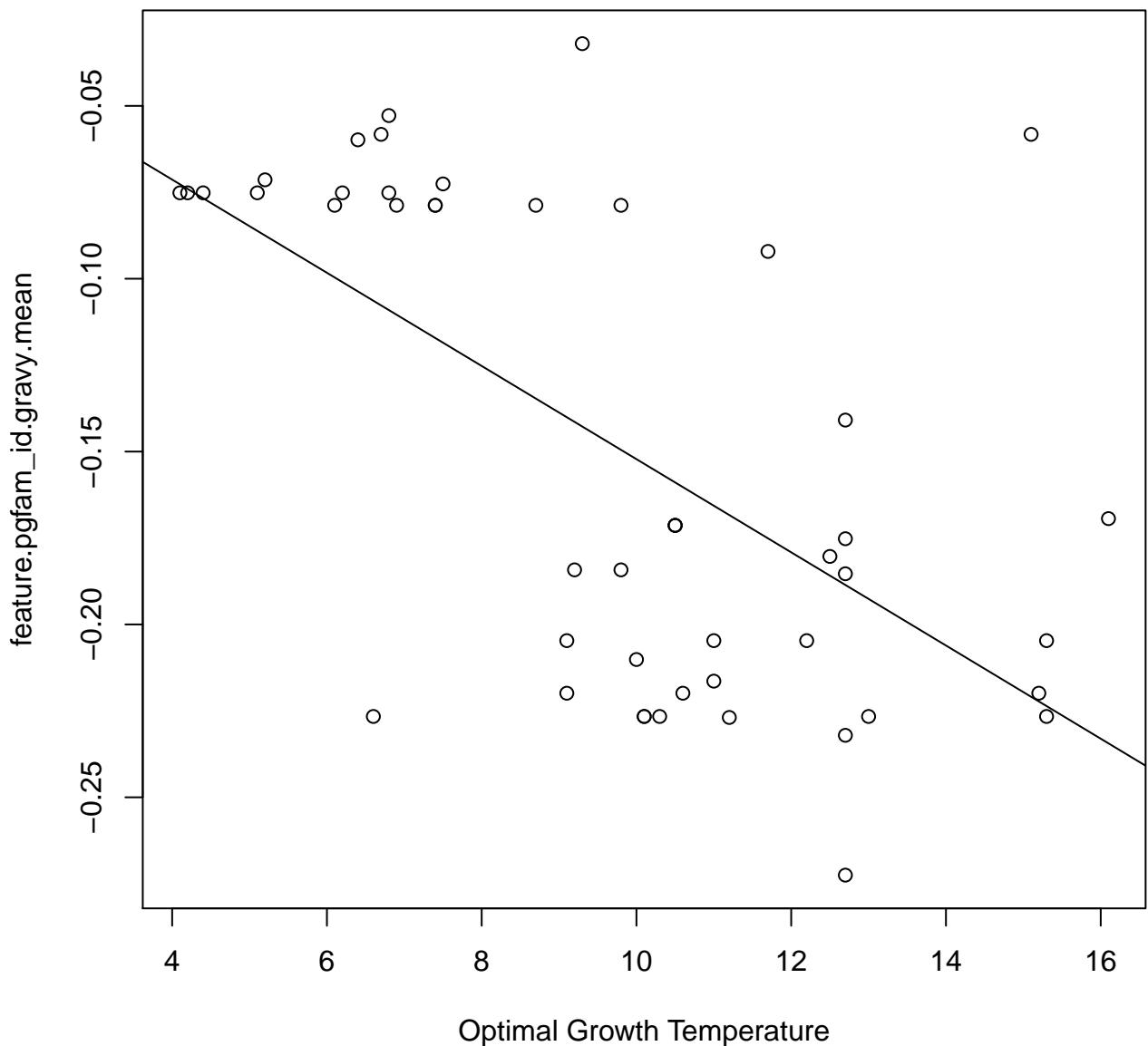
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PGF_01336539
hypothetical protein



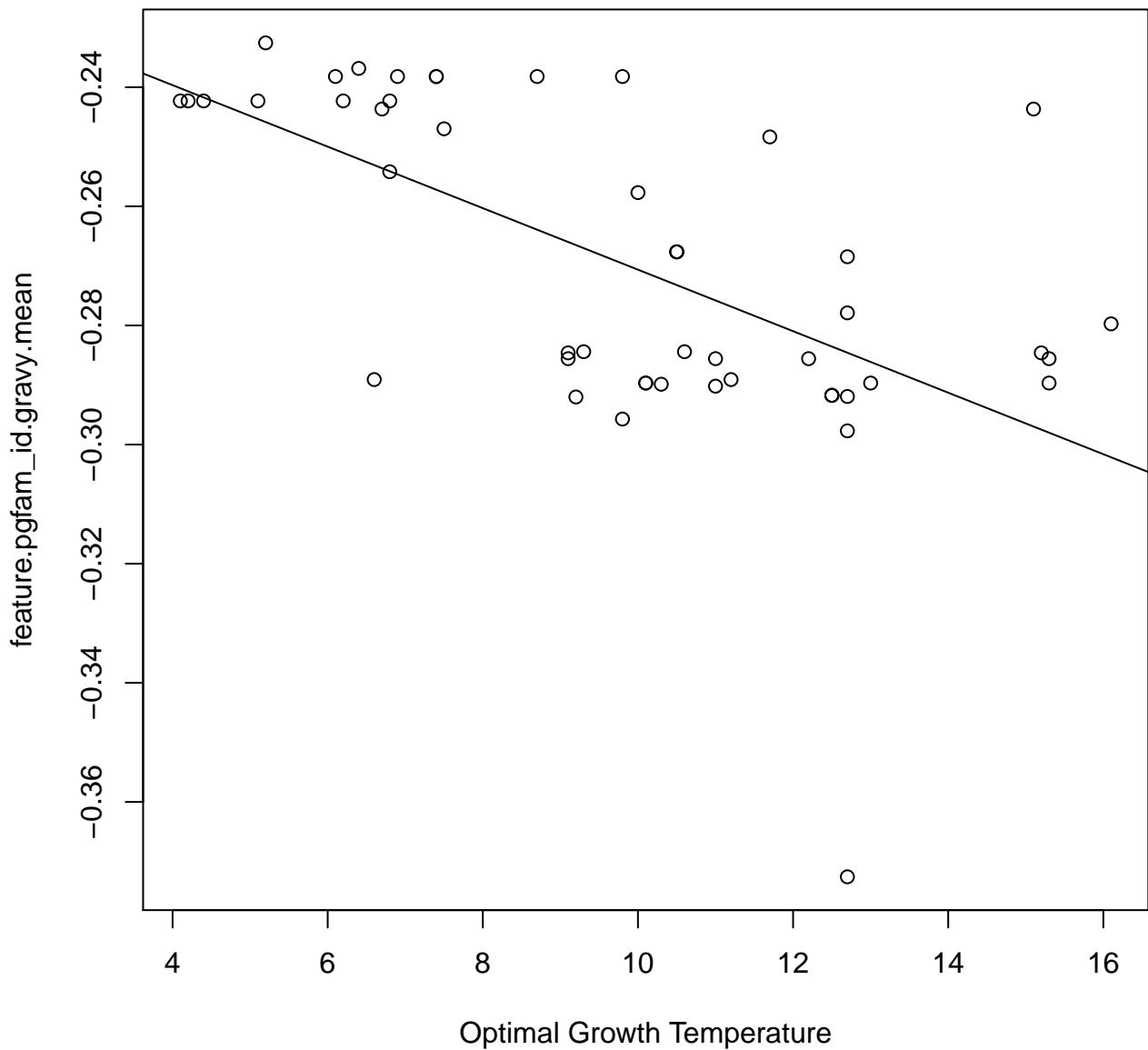
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PGF_06775354
DNA-binding transcriptional regulator, MocR family / aminotransferase domain



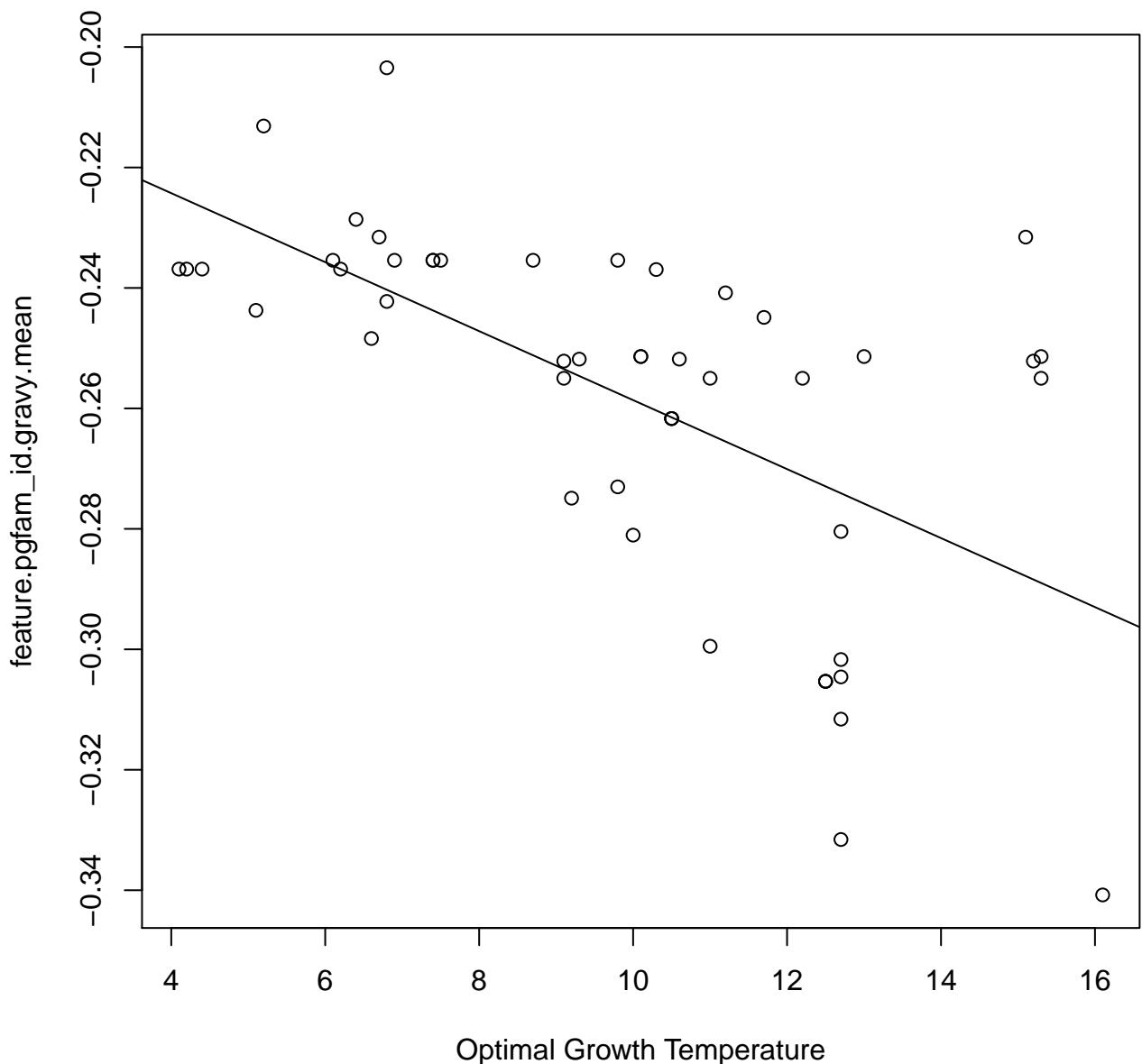
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General secretion pathway protein K



feature.pgfam_id.gravy.mean
PGF_00021217
2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.12)



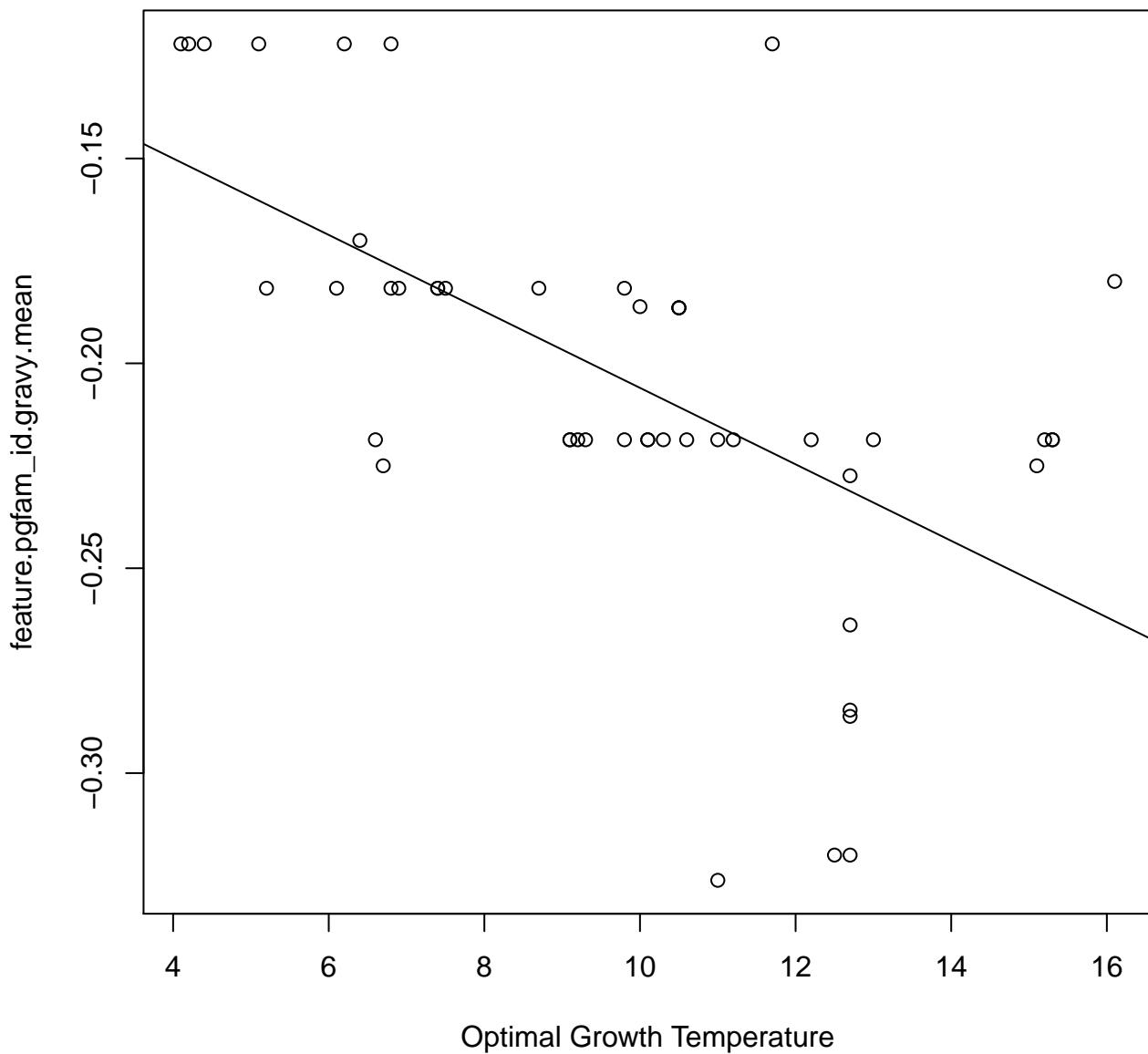
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PGF_02315316
Peptidase, M23/M37 family



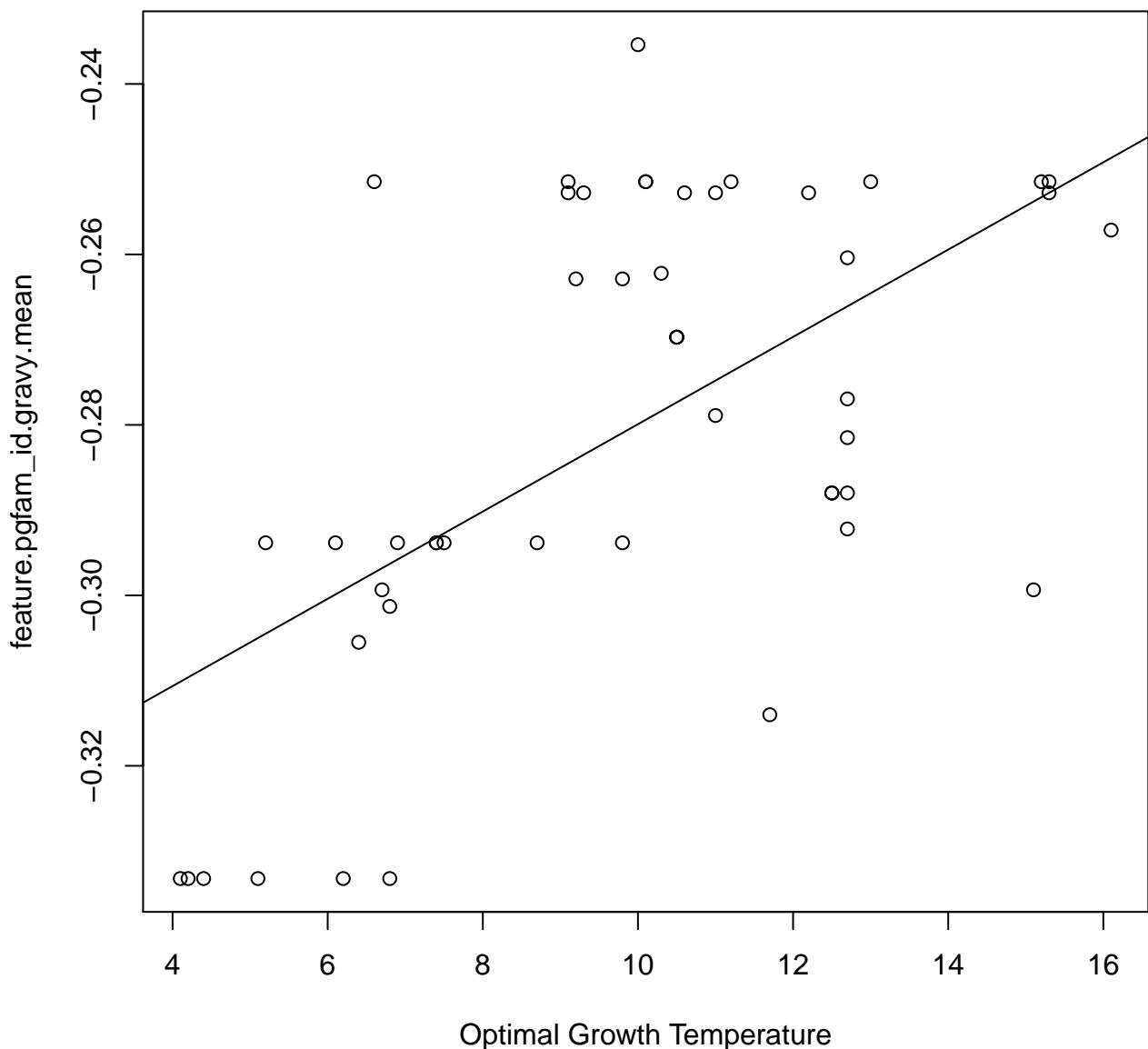
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PGF_07550057

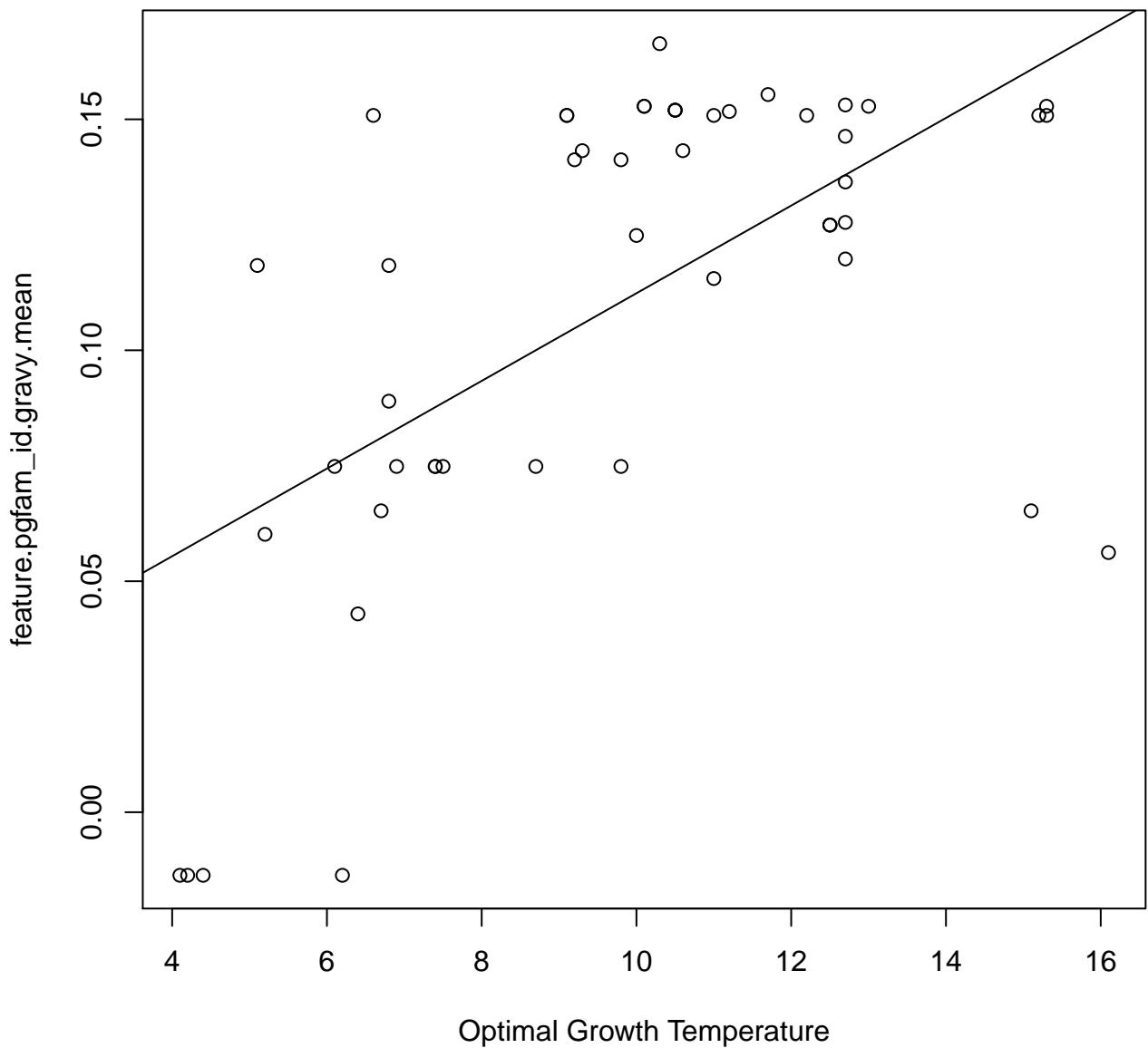
FIG002473: Protein YcaR in KDO2-Lipid A biosynthesis cluster



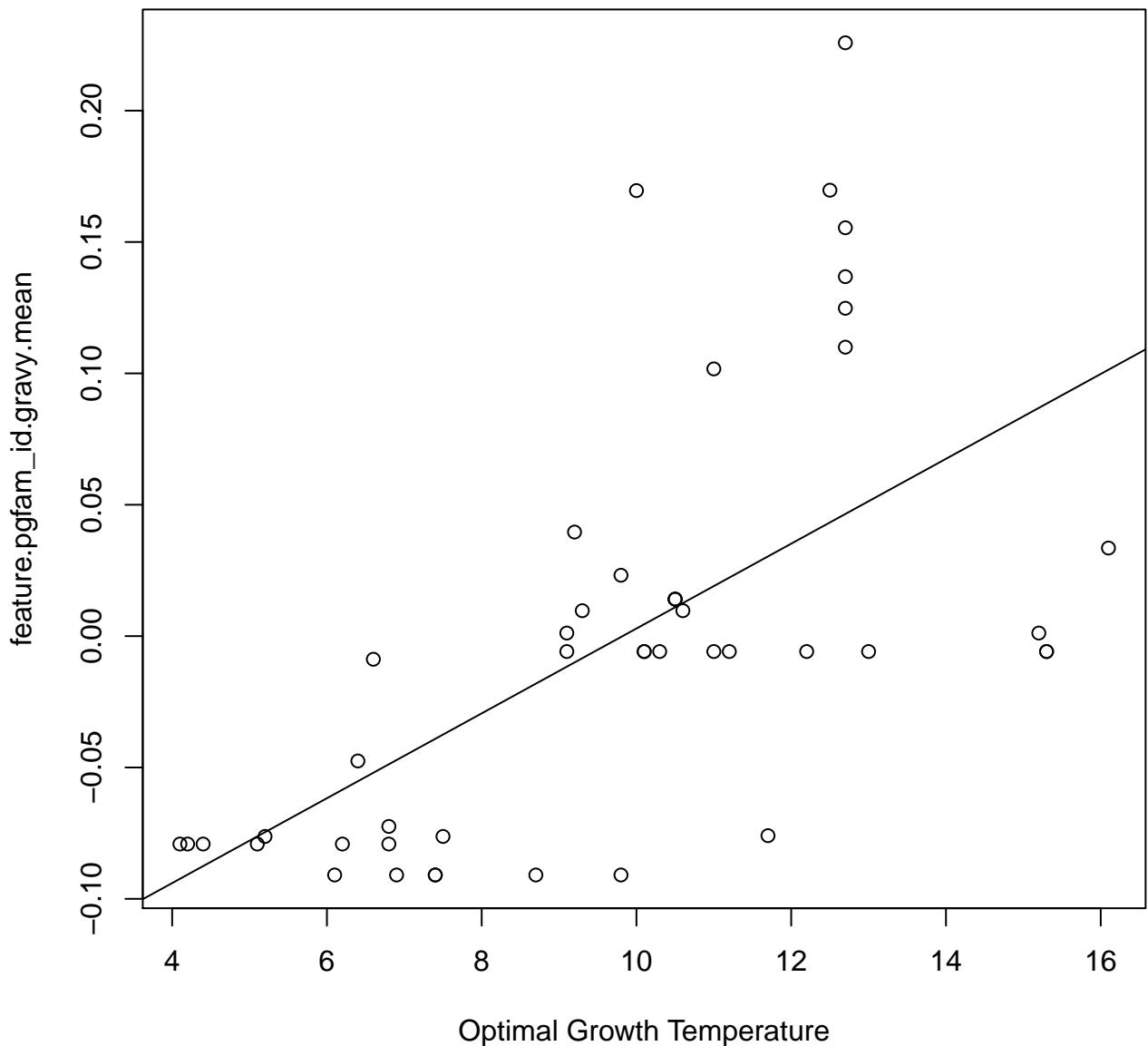
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GTP cyclohydrolase I (EC 3.5.4.16) type 2



feature.pgfam_id.gravy.mean
PGF_00417658
3-dehydroquinate synthase (EC 4.2.3.4)



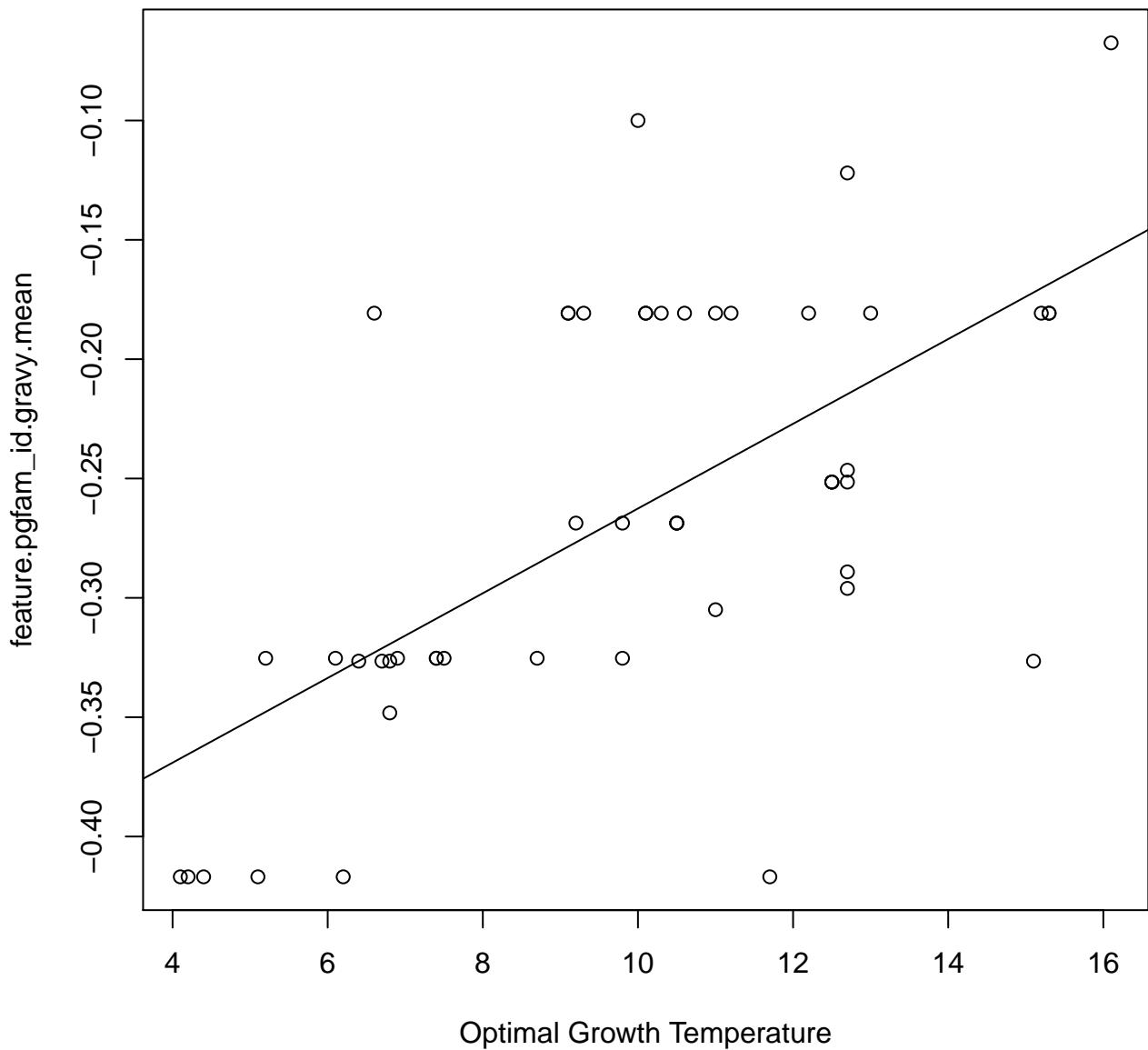
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PGF_02007855
Zinc-type alcohol dehydrogenase-like protein



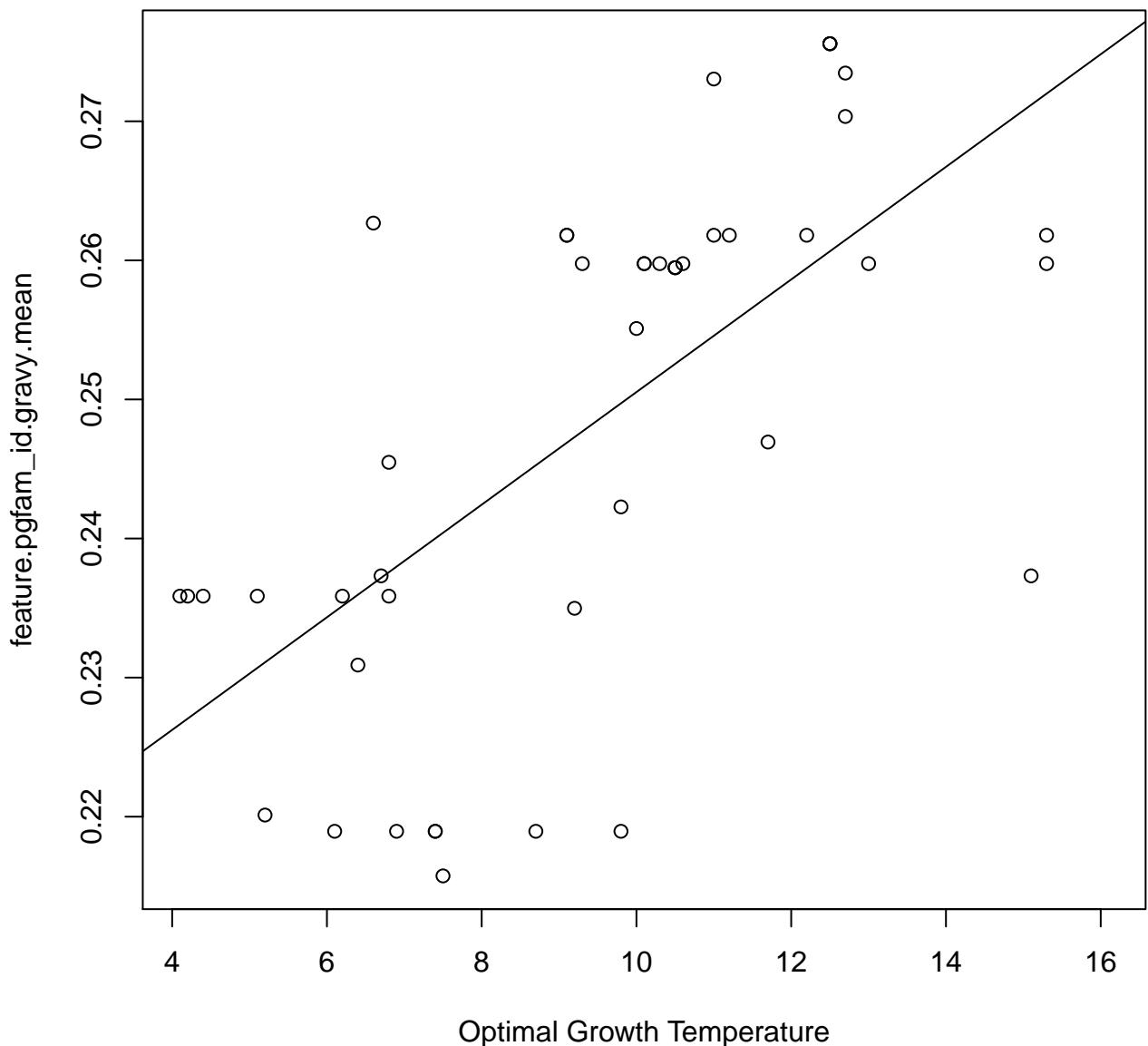
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PGF_02069837

Succinate dehydrogenase flavin-adding protein, antitoxin of CptAB toxin-antitoxin

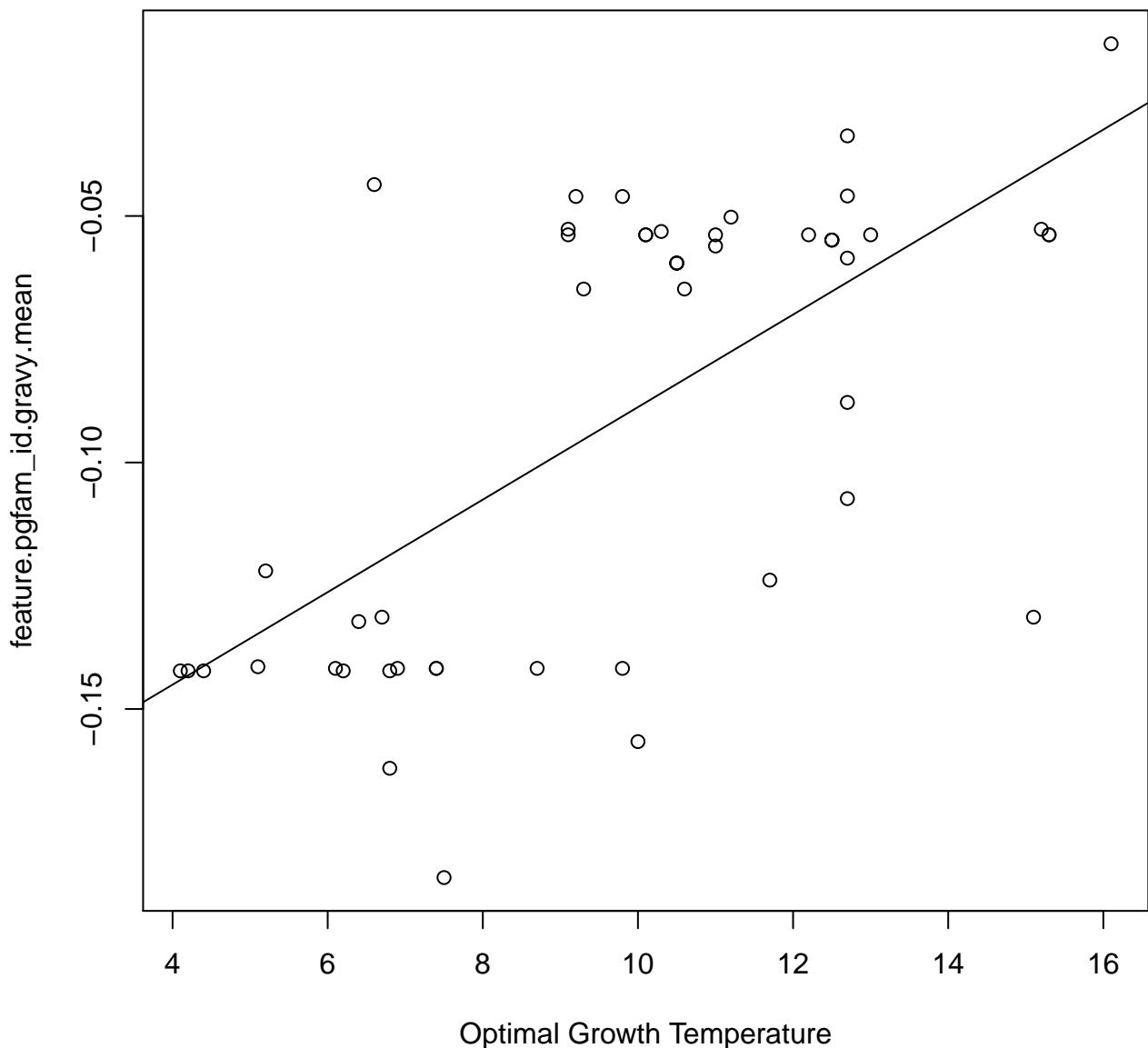


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Selenide,water dikinase (EC 2.7.9.3)

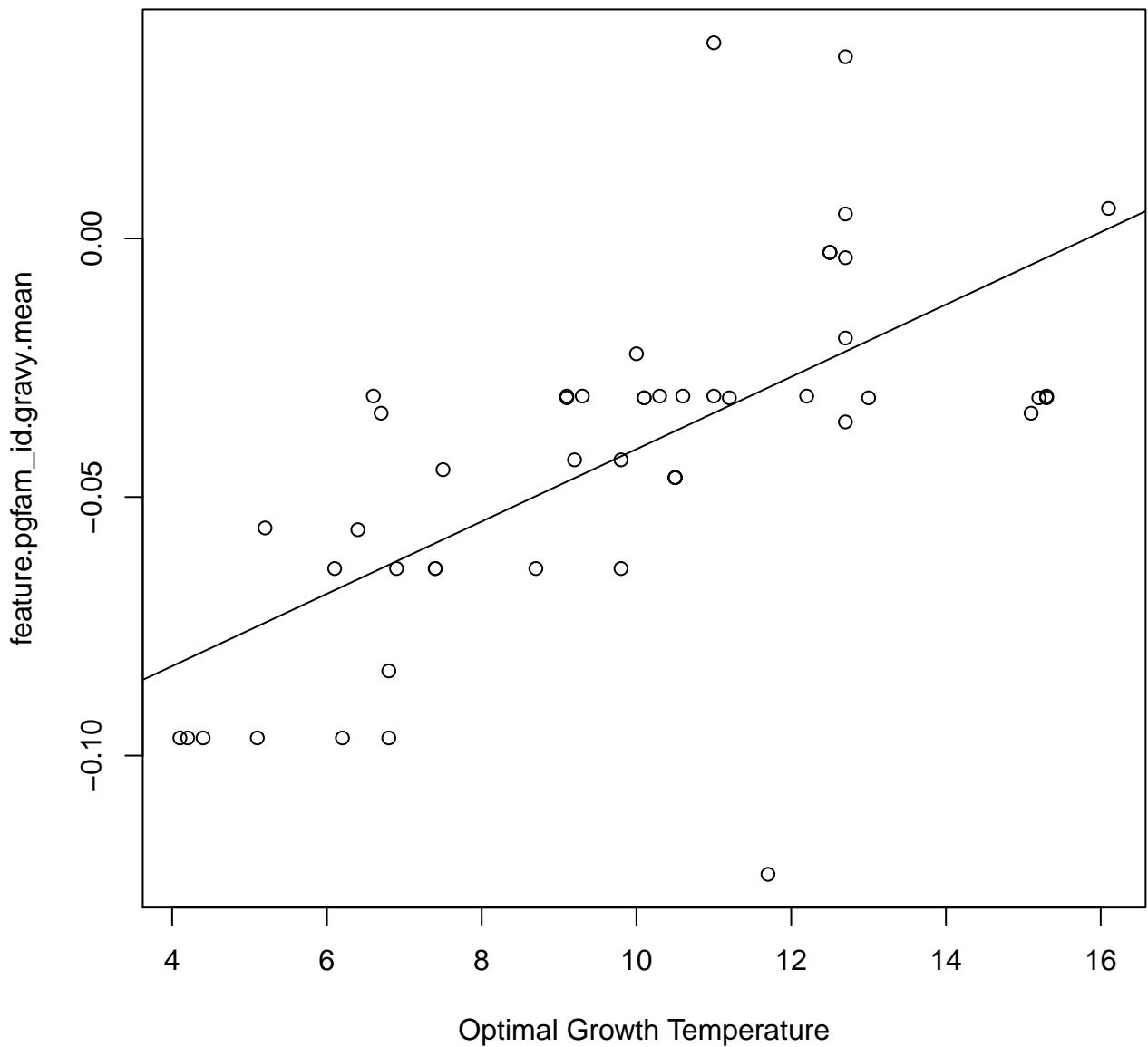


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PGF_00417755

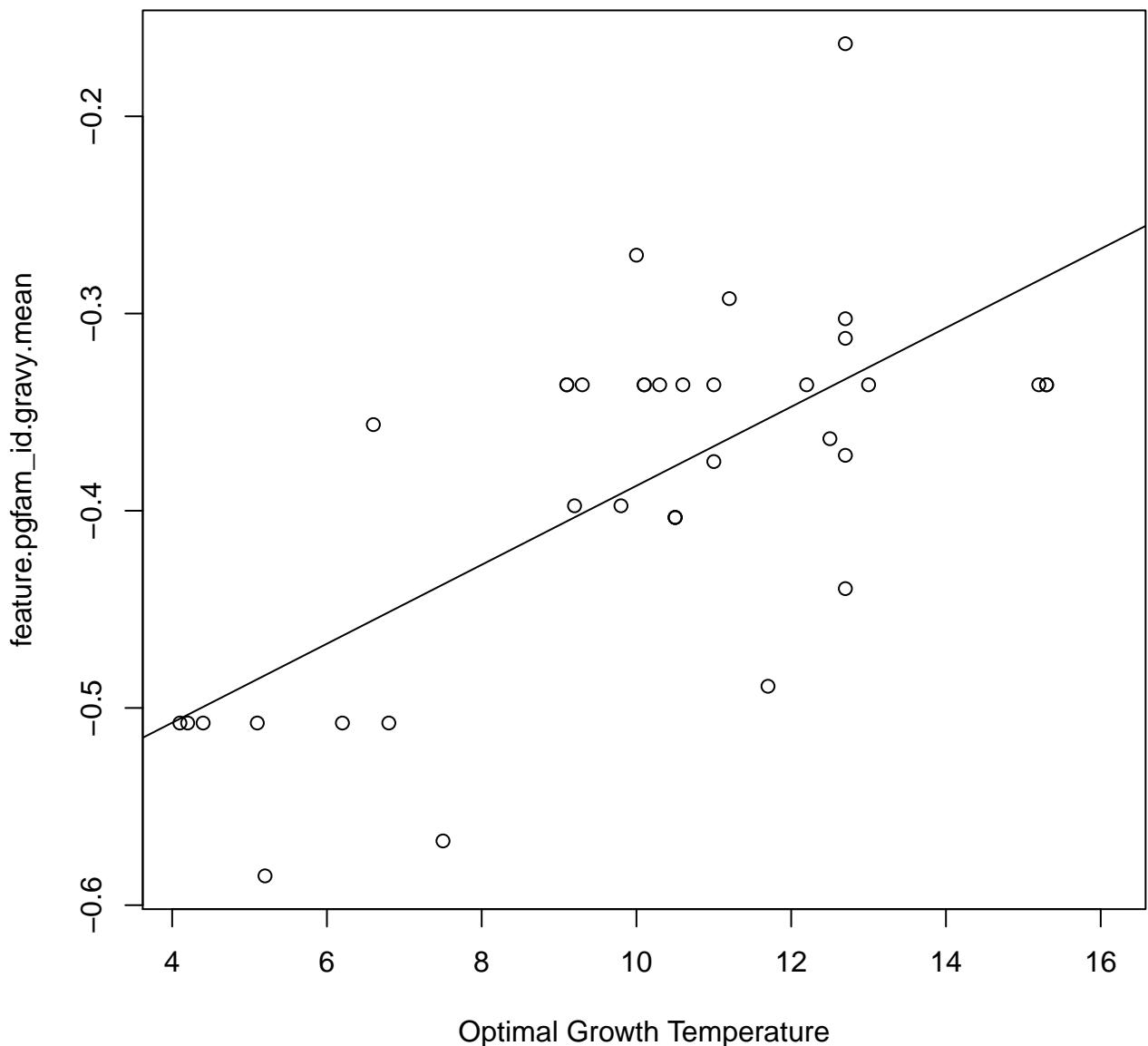
3-demethylubiquinol 3-O-methyltransferase (EC 2.1.1.64) @ 2-polyprenyl-6-hydroxyphenyl methylase (EC 2.1.1.222)



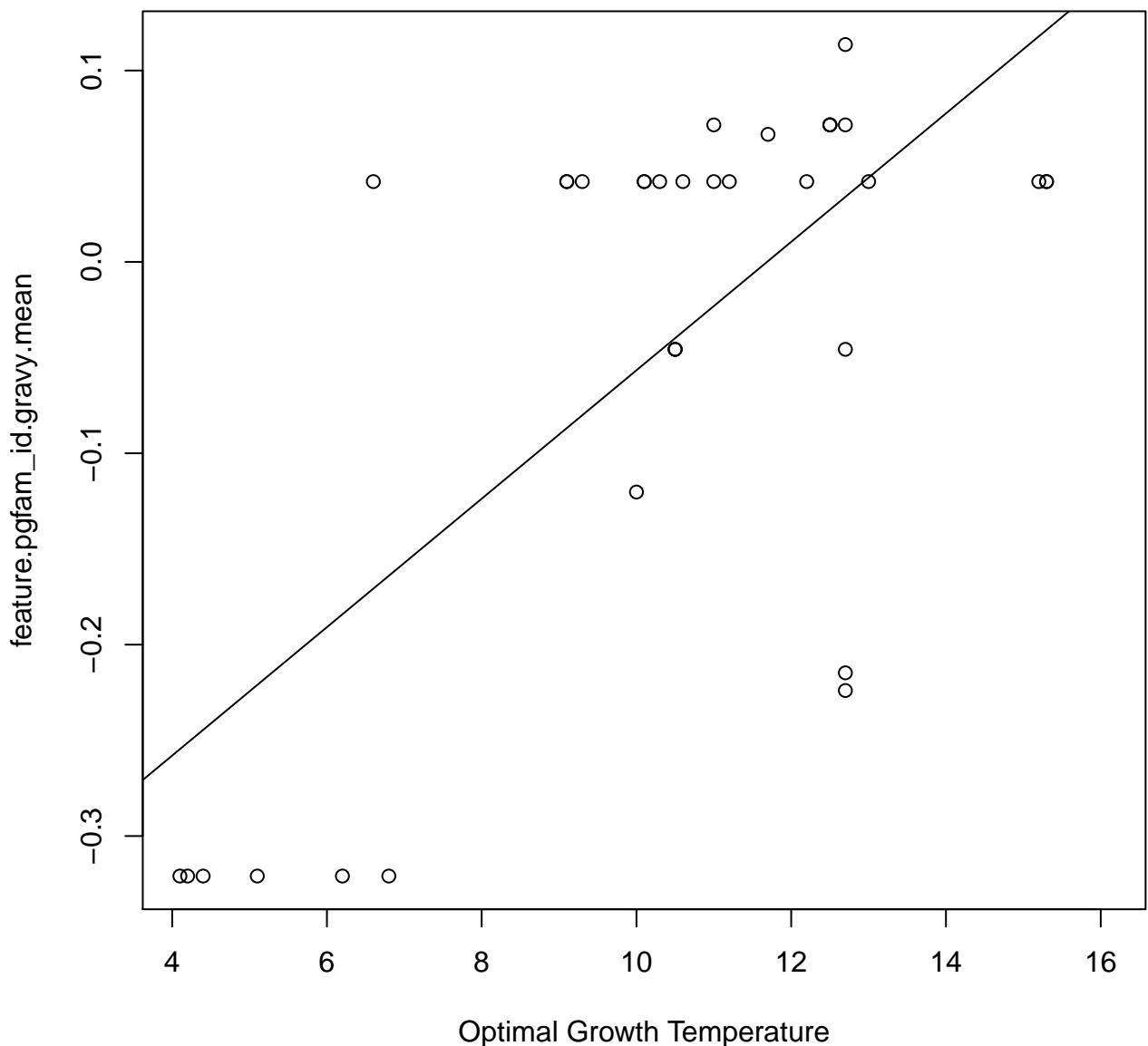
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PGF_03051420
6-carboxy-5,6,7,8-tetrahydropterin synthase (EC 4.1.2.50)



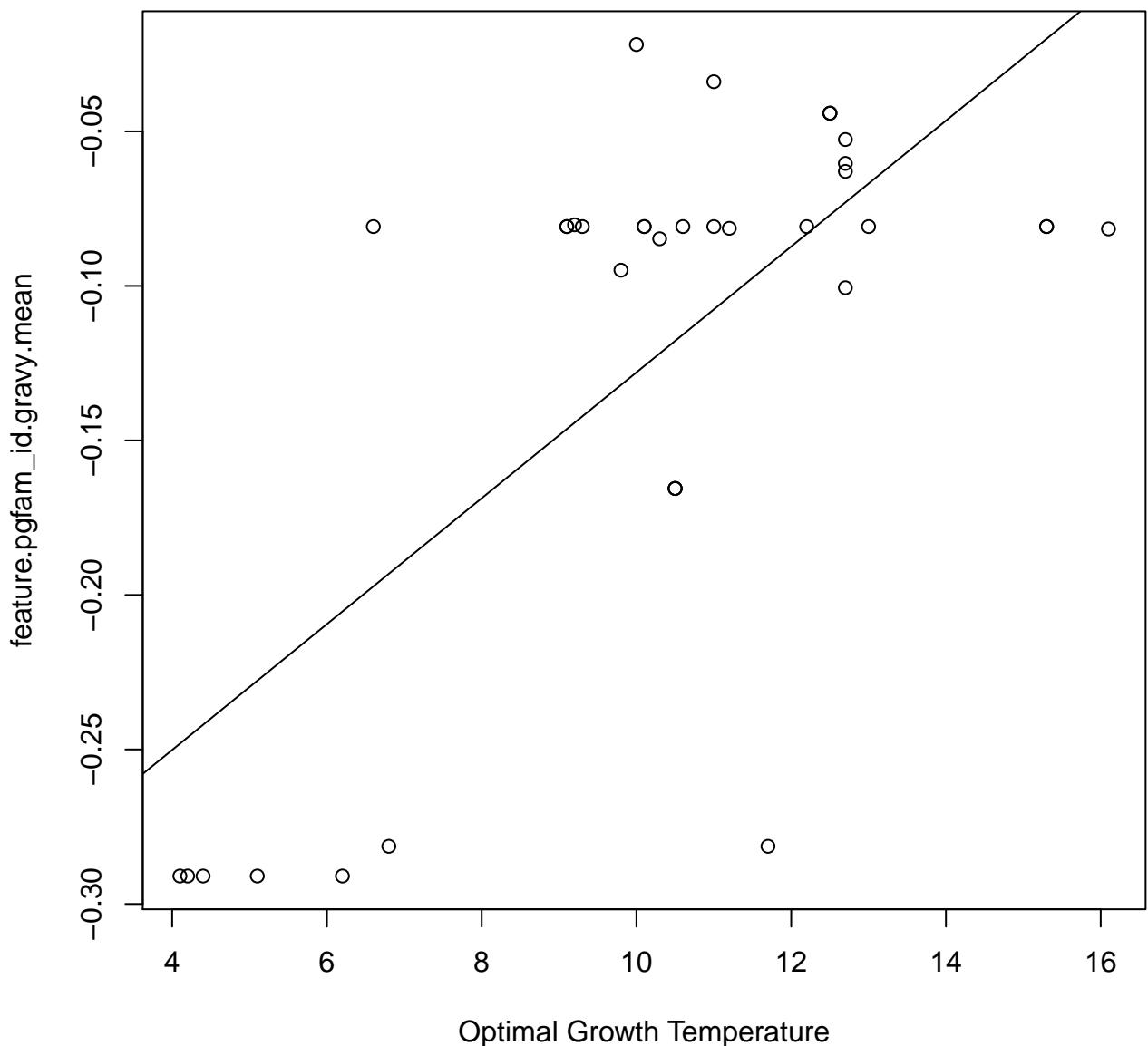
feature.pgfam_id.gravy.mean
PGF_03320197
Transcriptional regulator, HxIR family



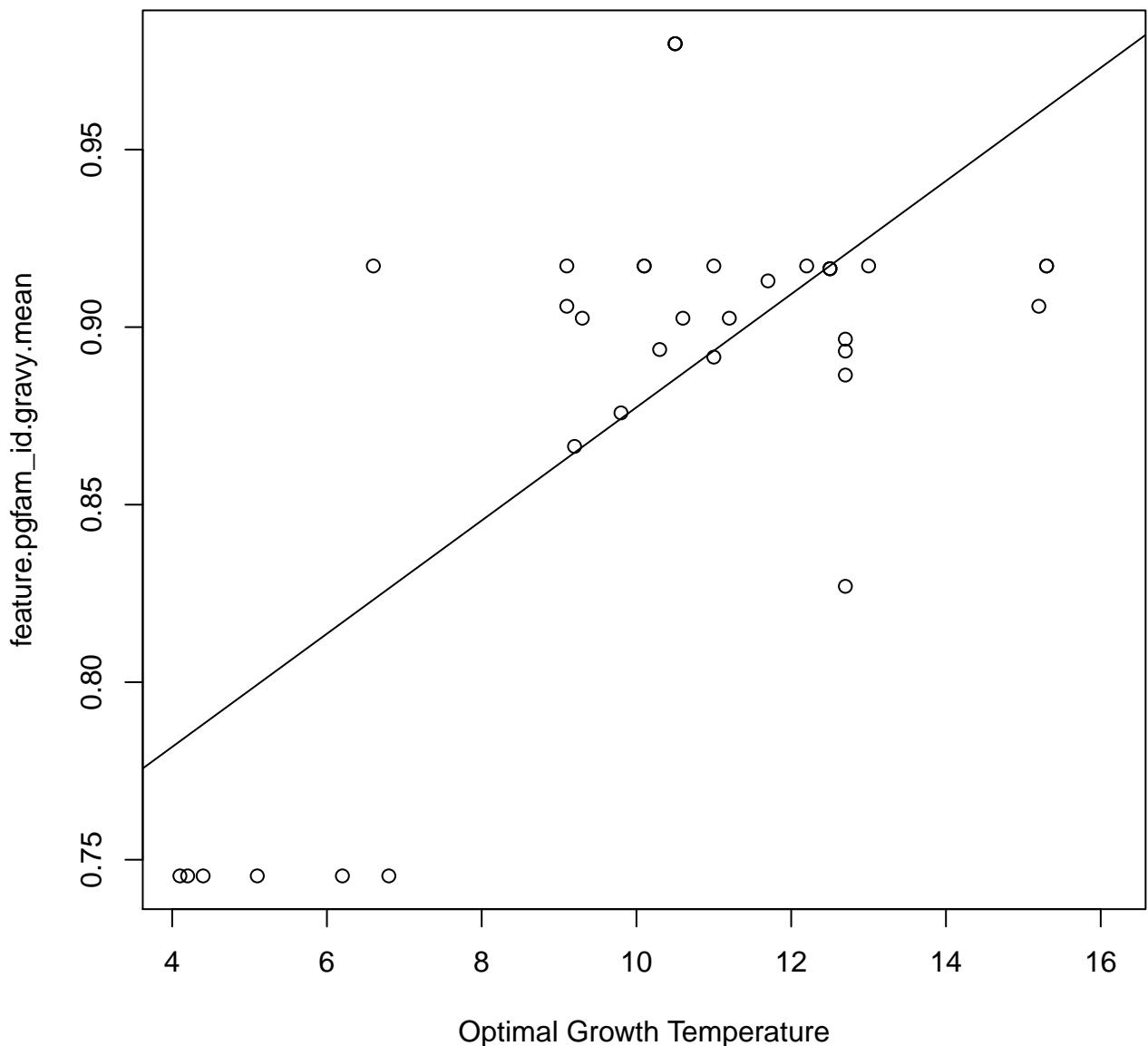
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Uncharacterized ferredoxin-like protein YfhL



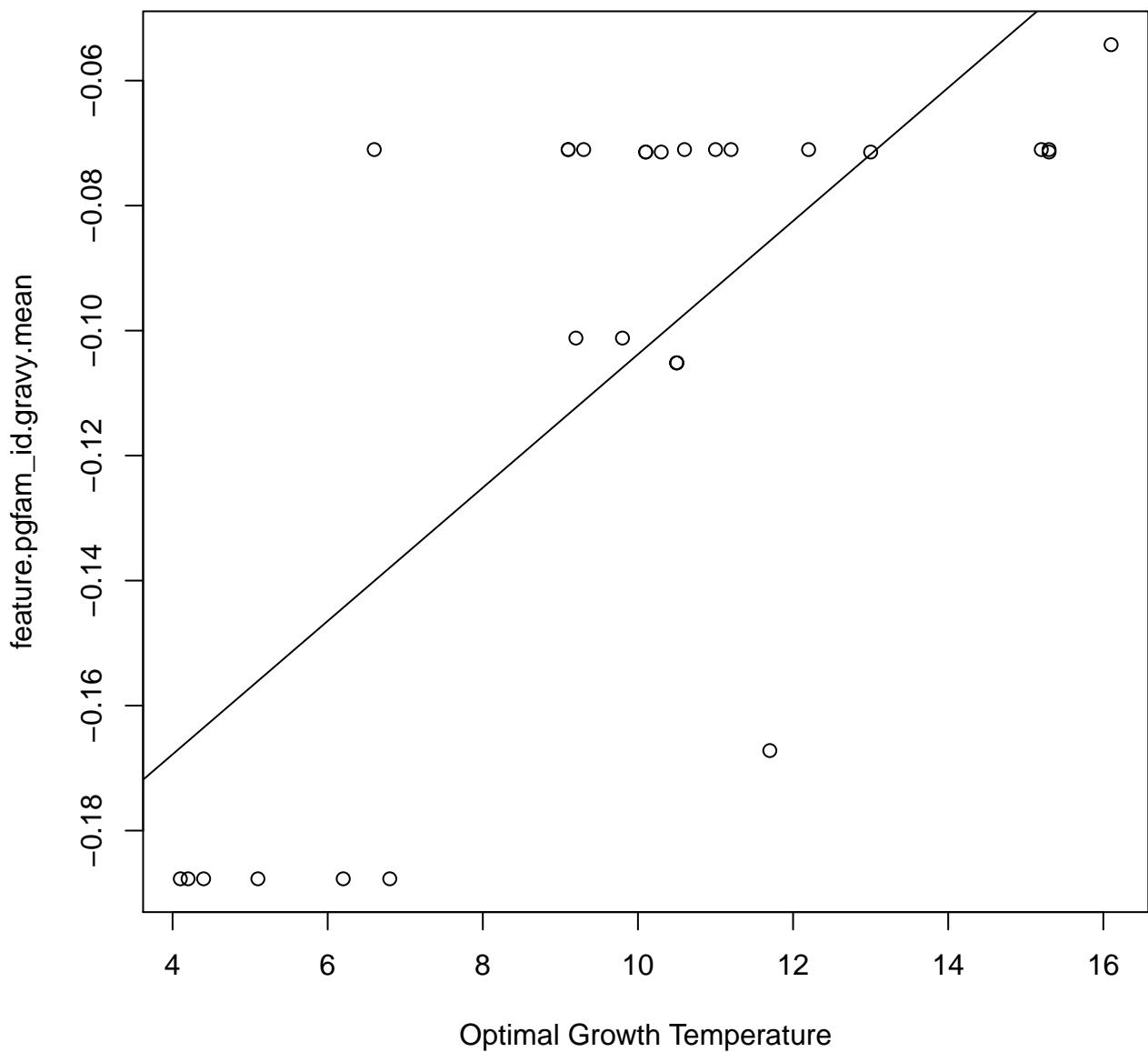
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Ureidoglycolate lyase (EC 4.3.2.3)



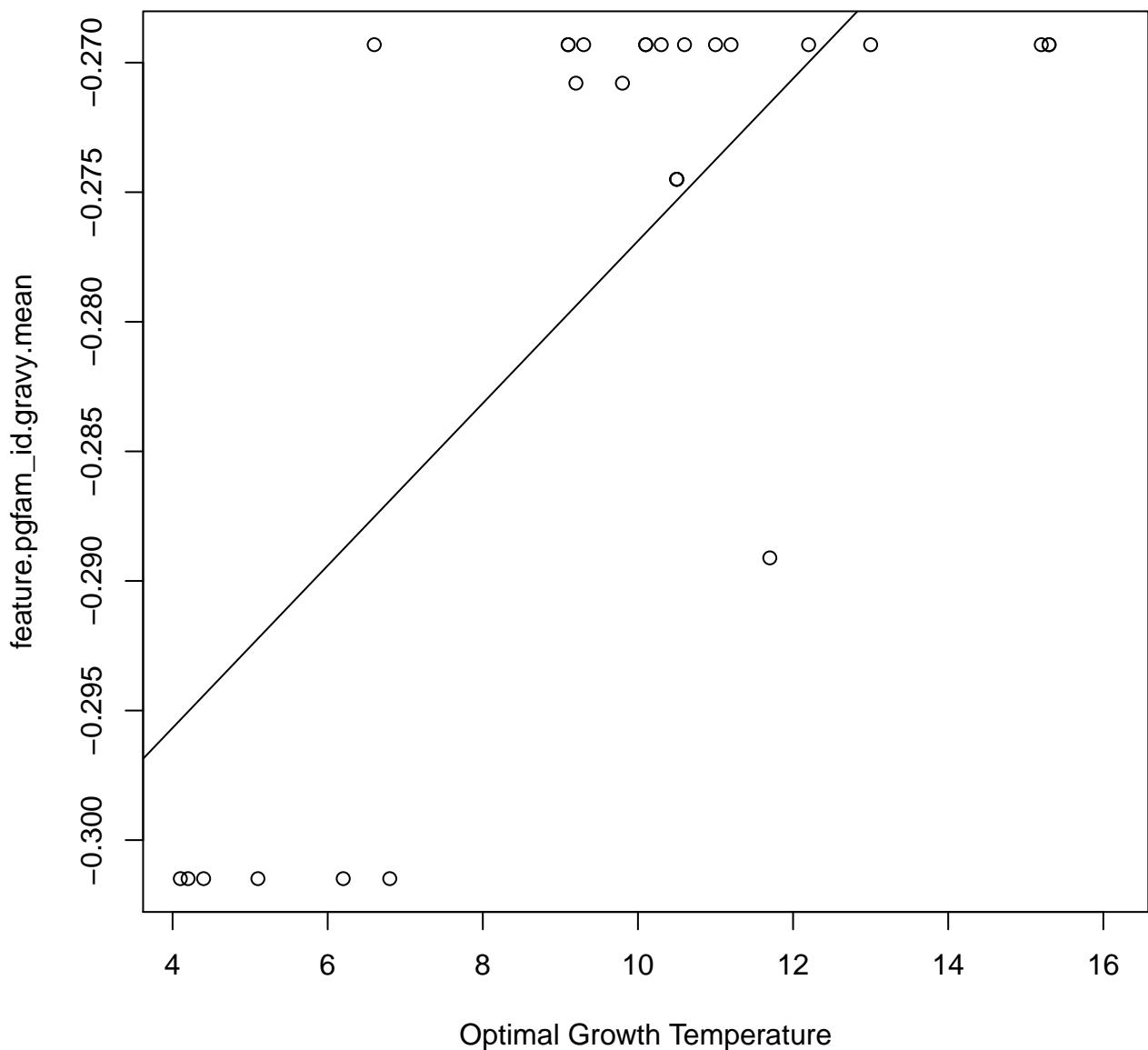
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PGF_00067426
ZIP zinc transporter family protein



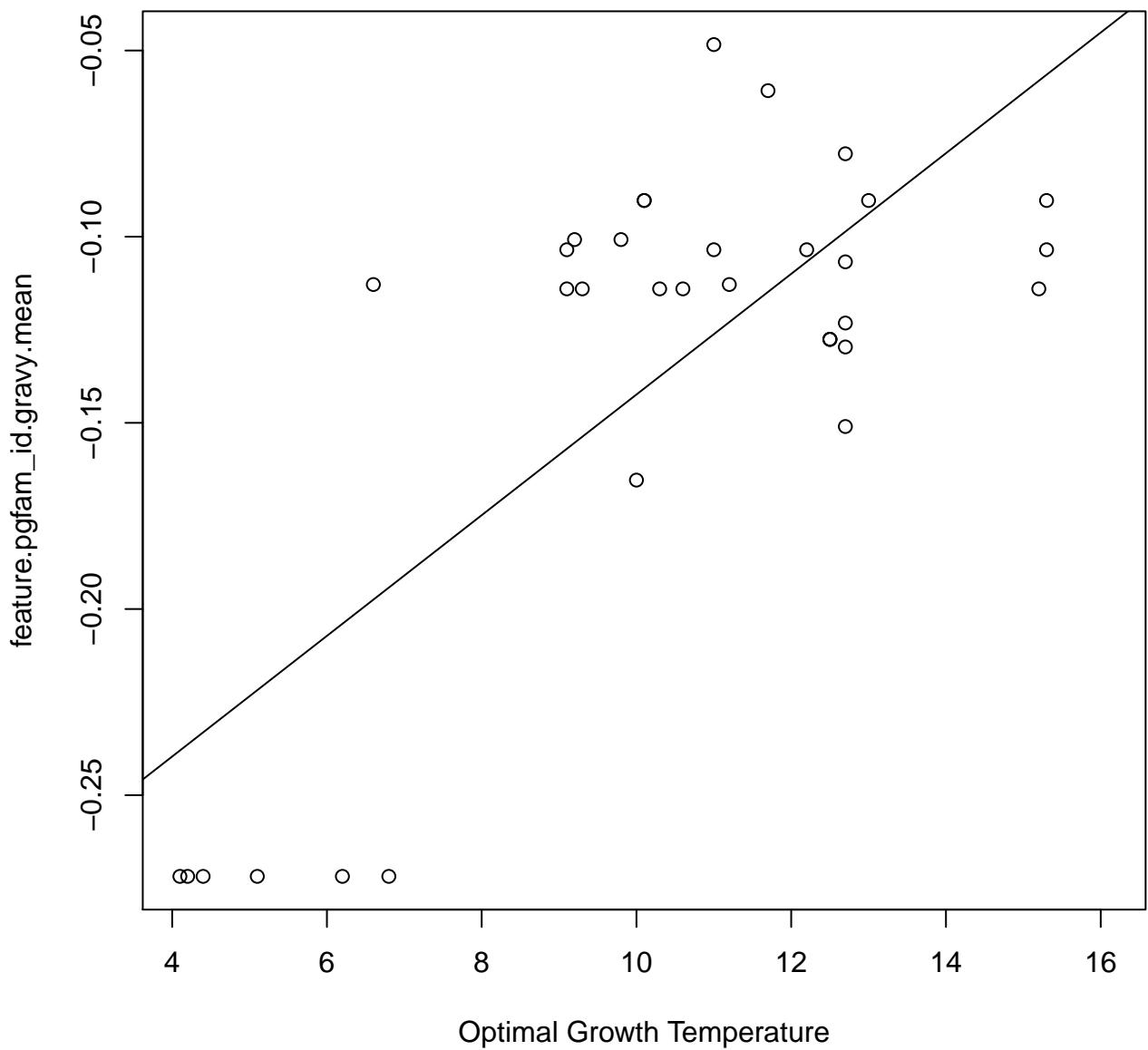
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PGF_07824917
hypothetical protein



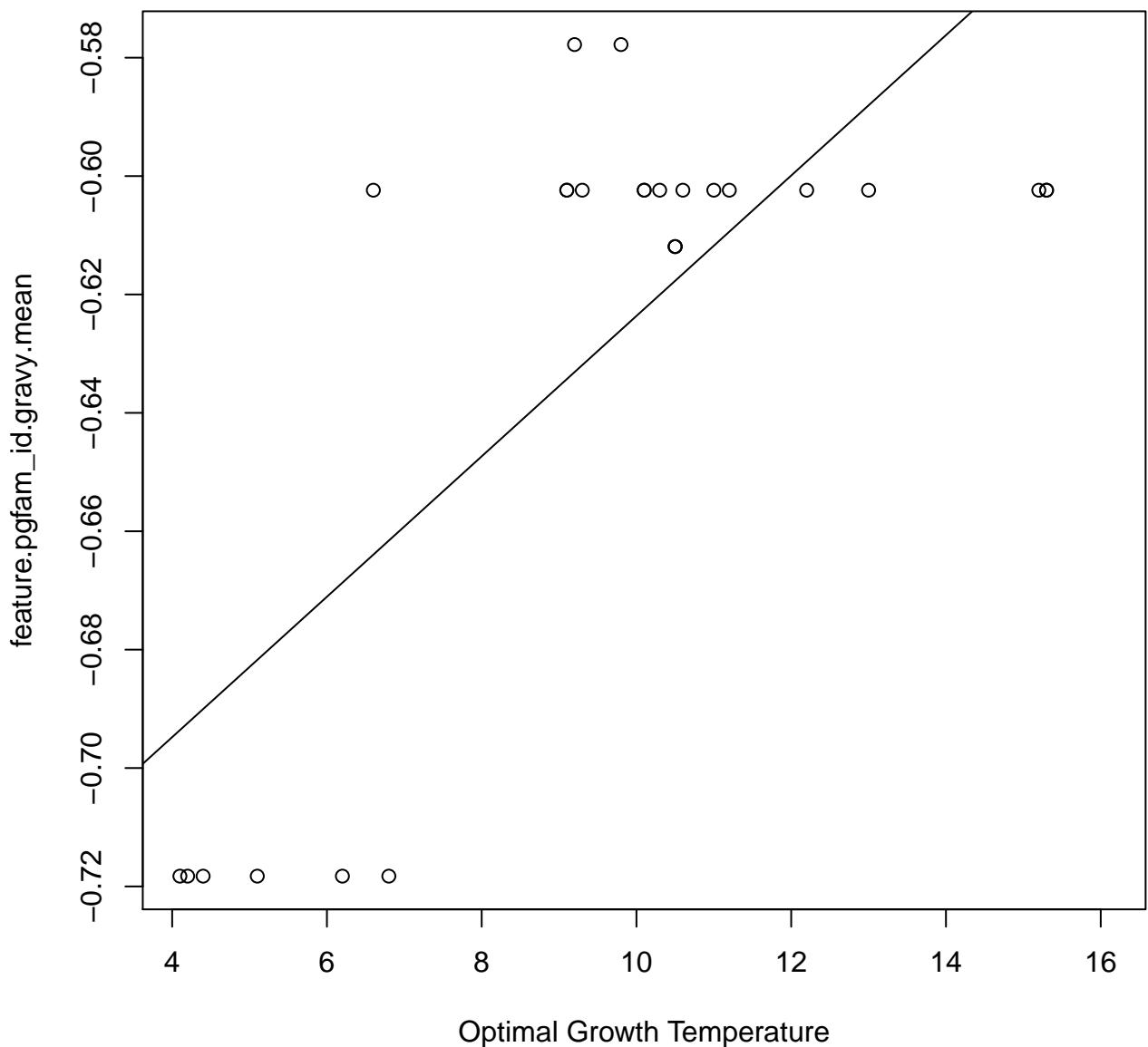
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hypothetical protein



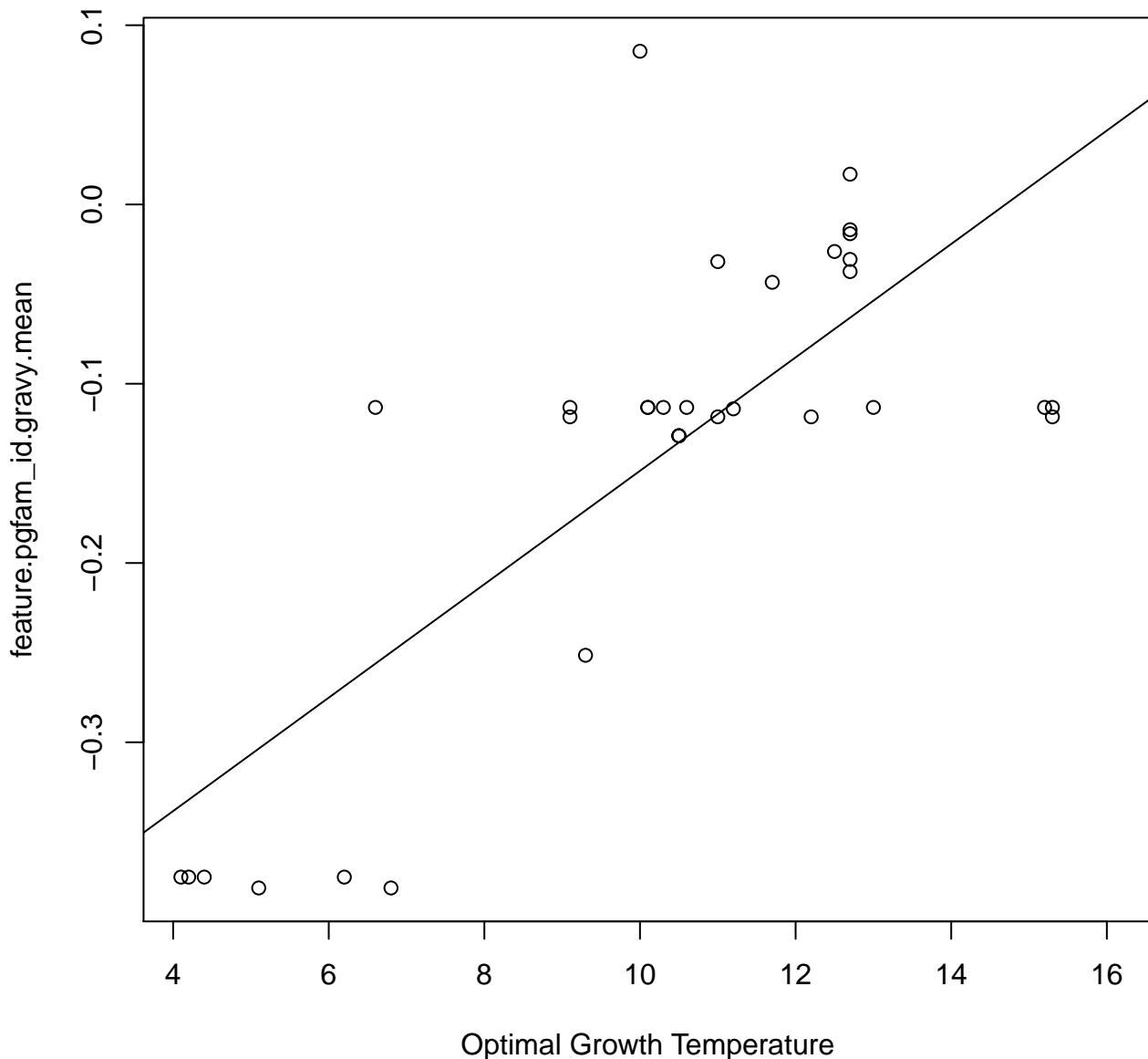
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hypothetical protein



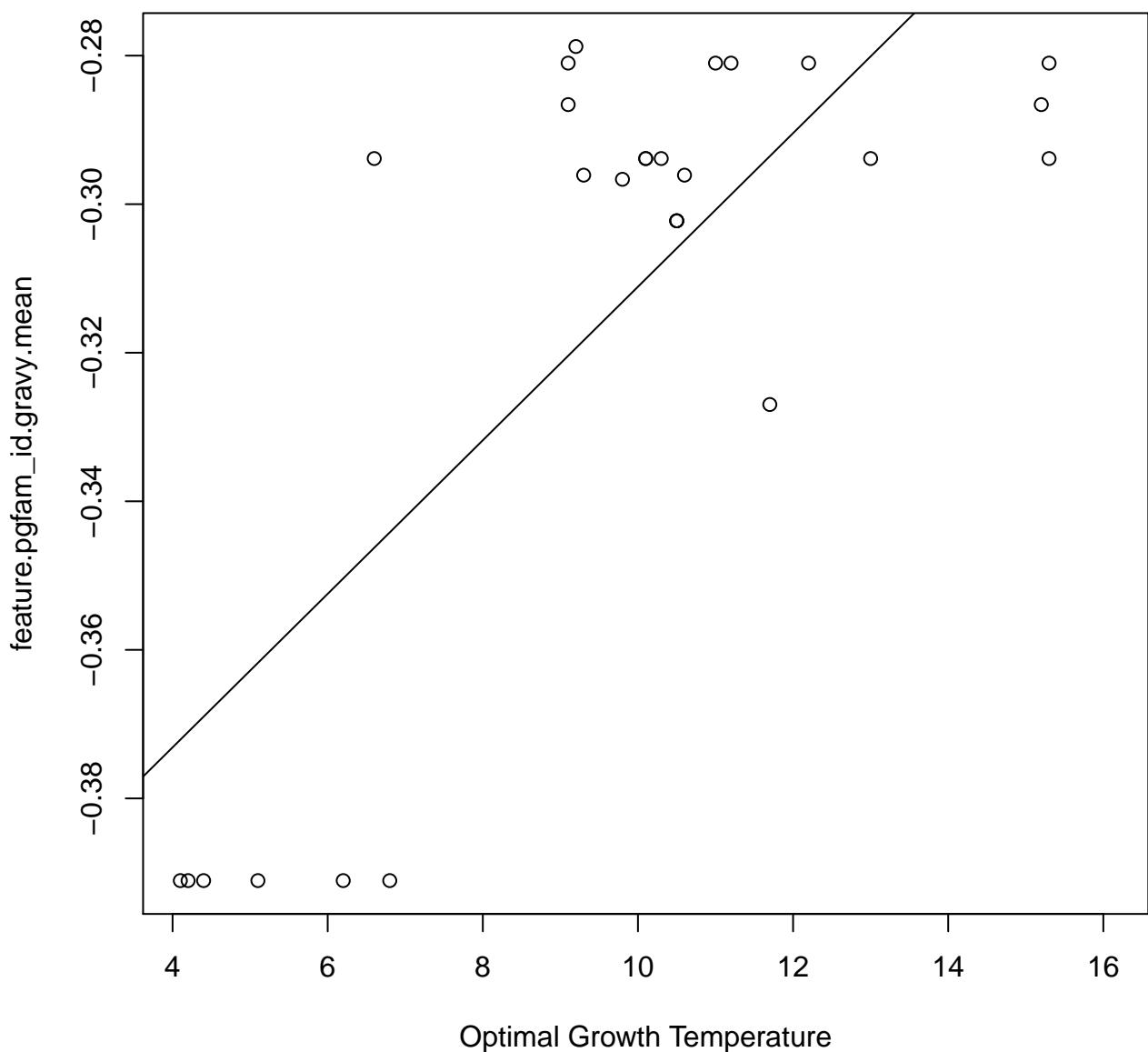
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hypothetical protein



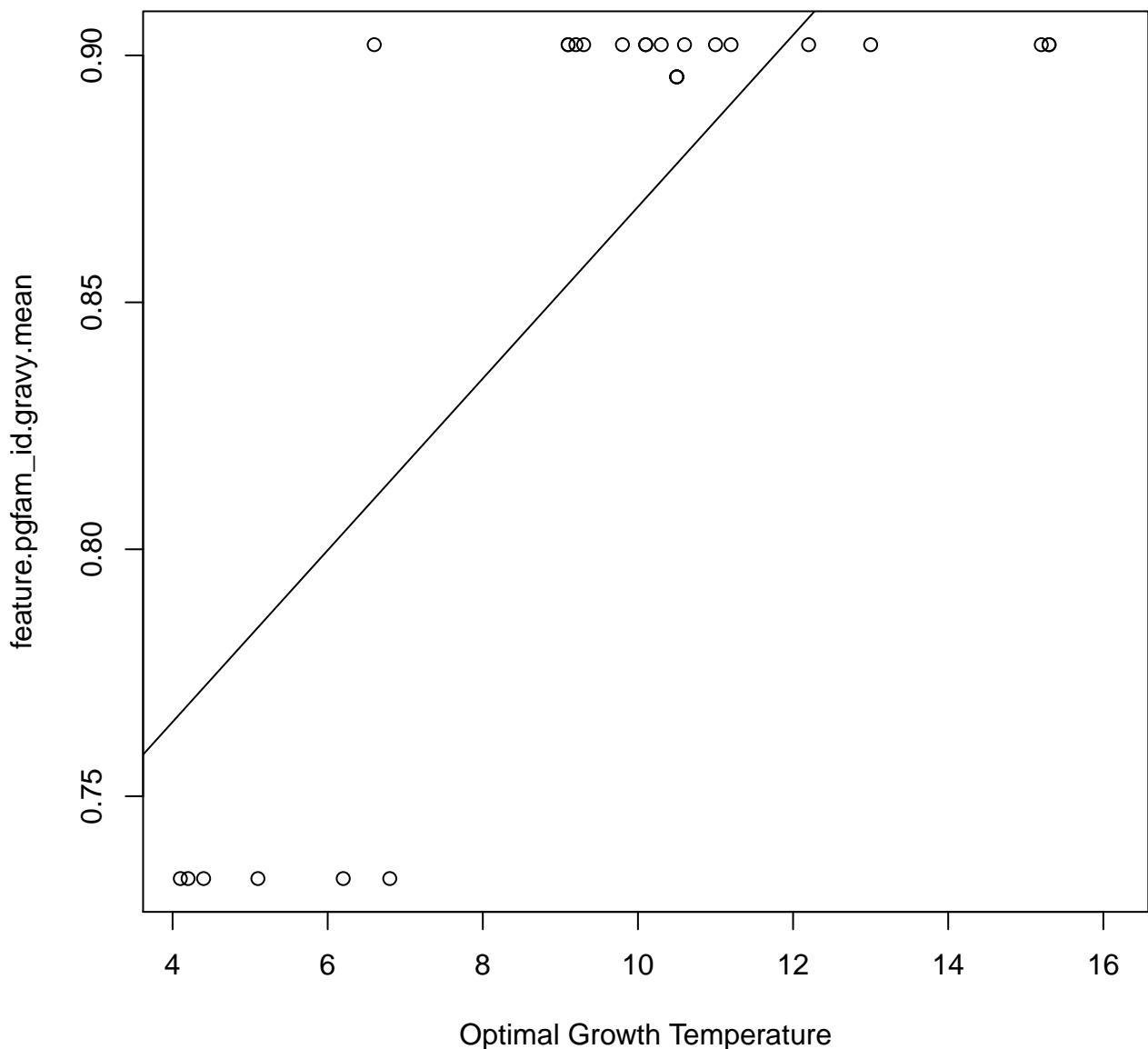
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PGF_12765299
Two-component system sensor histidine kinase



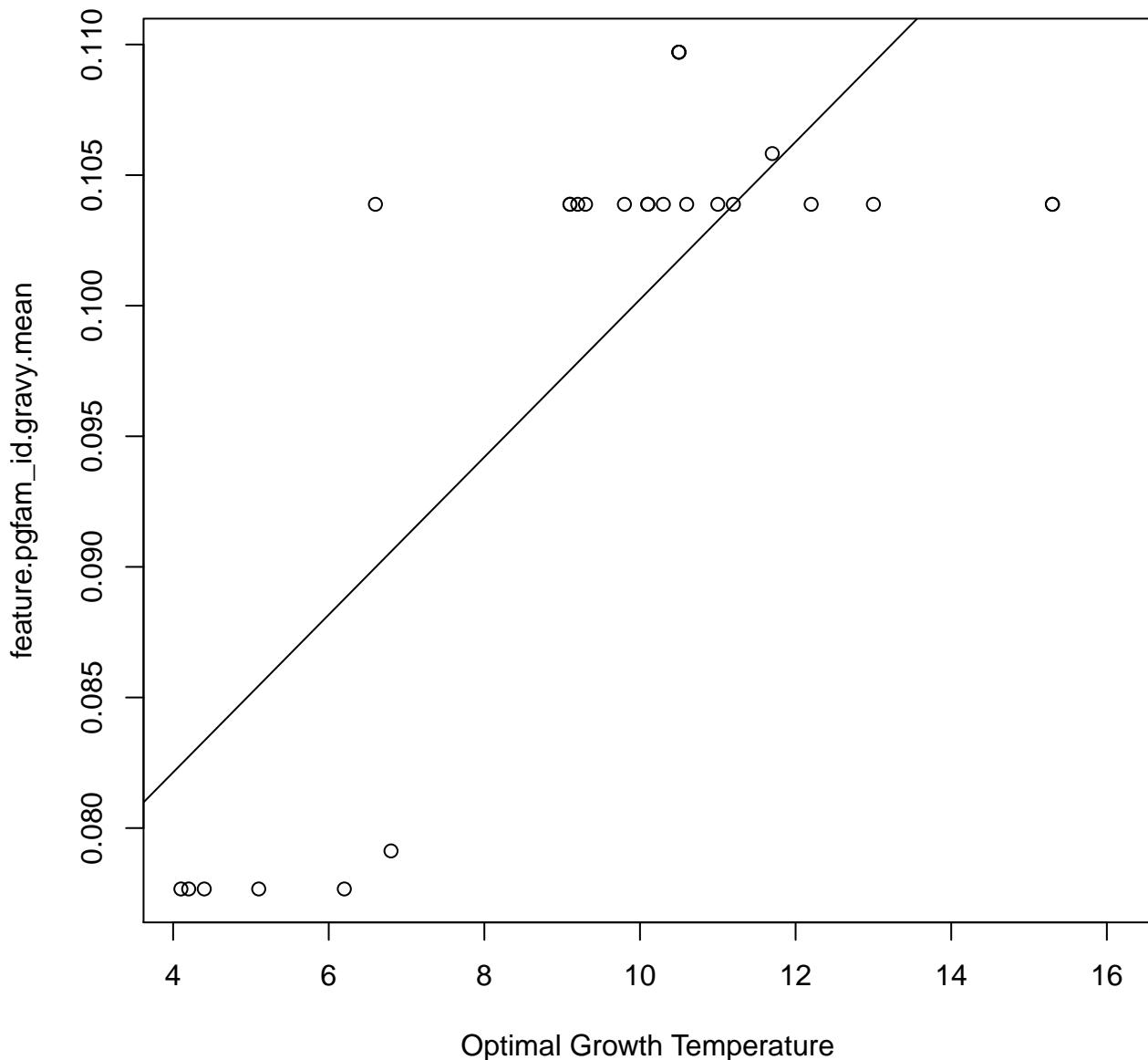
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PGF_07250446
hypothetical protein



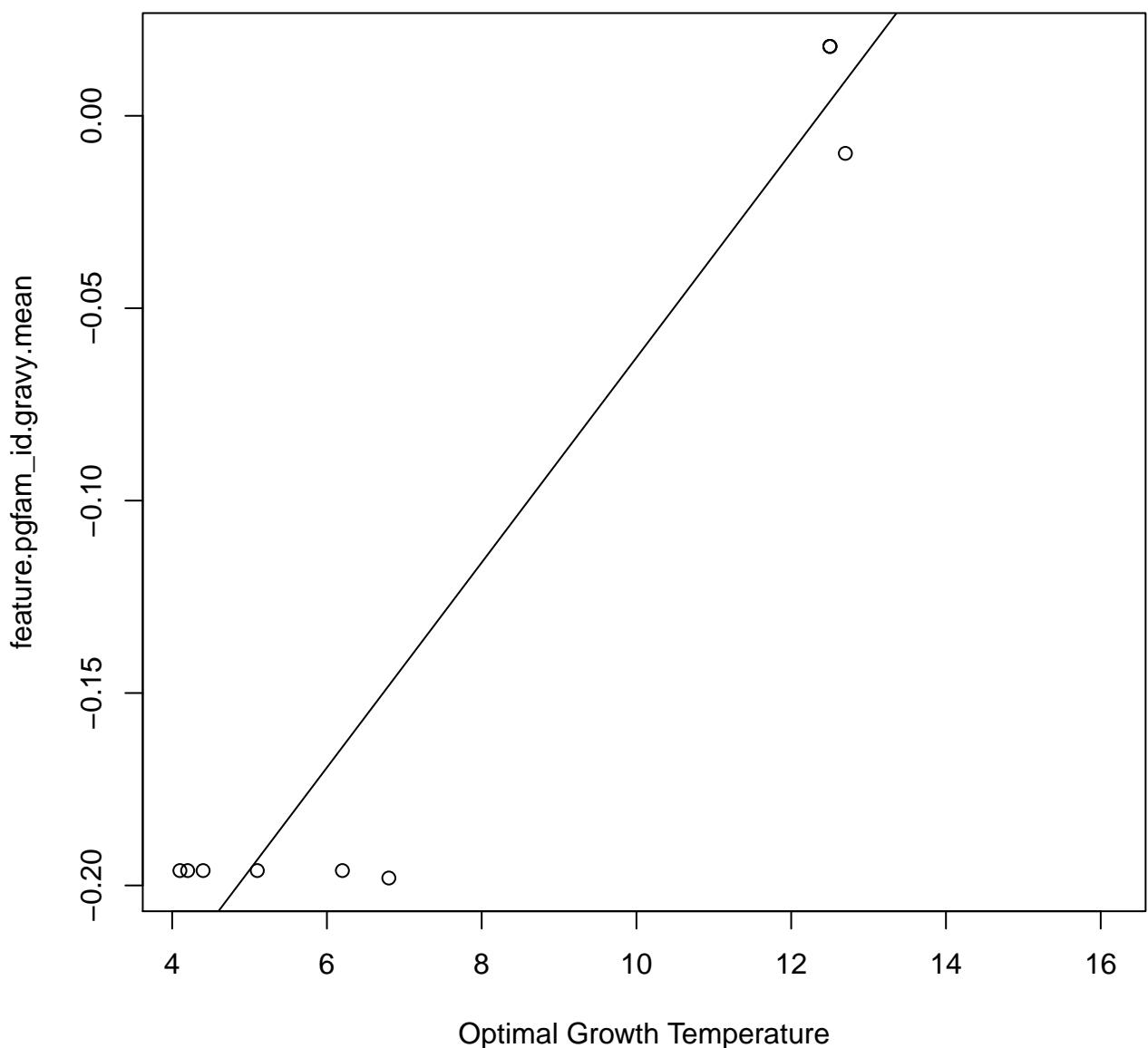
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hypothetical protein



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PGF_07210740
hypothetical protein

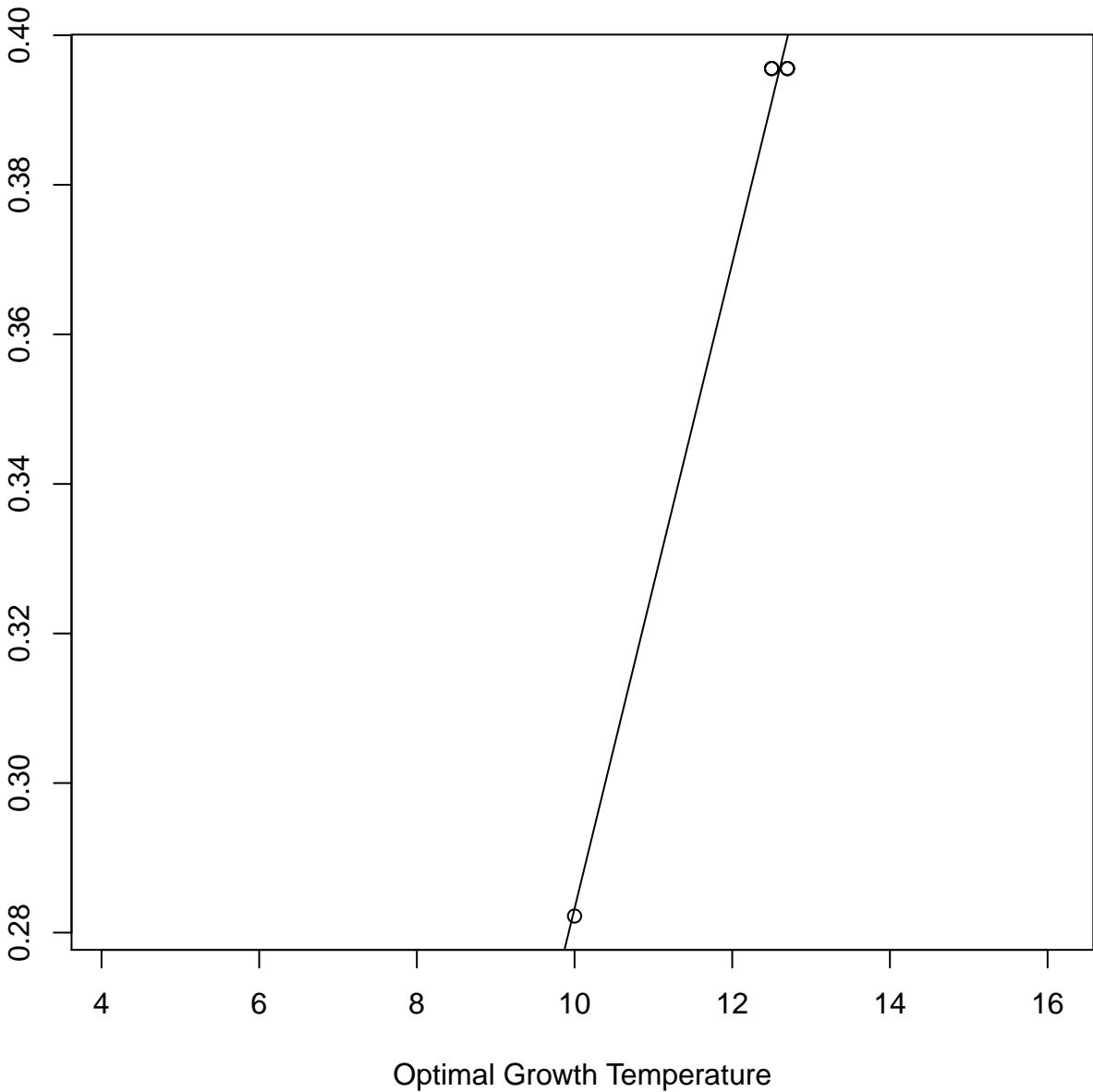


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hypothetical protein

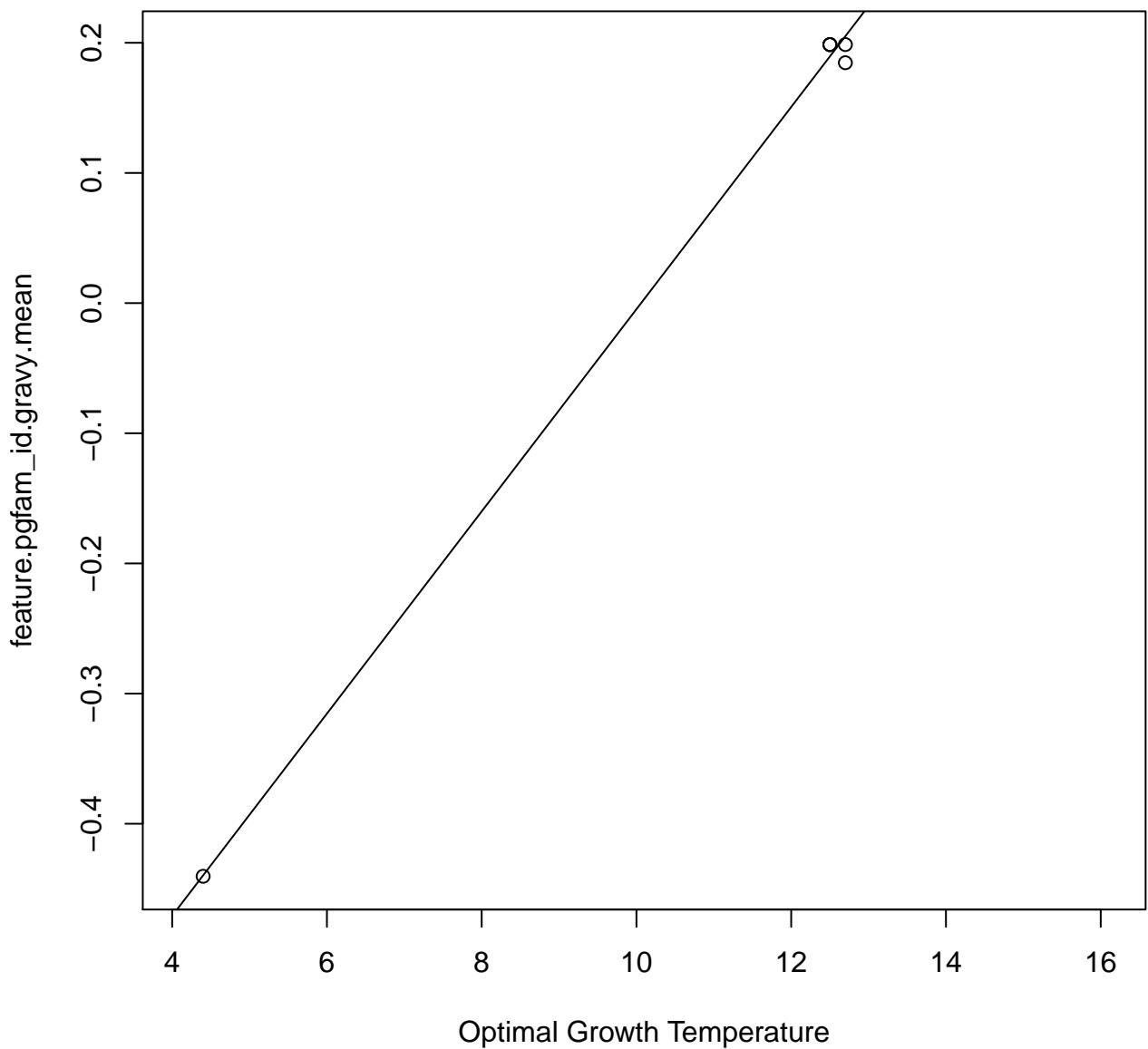


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PGF_01337096
hypothetical protein

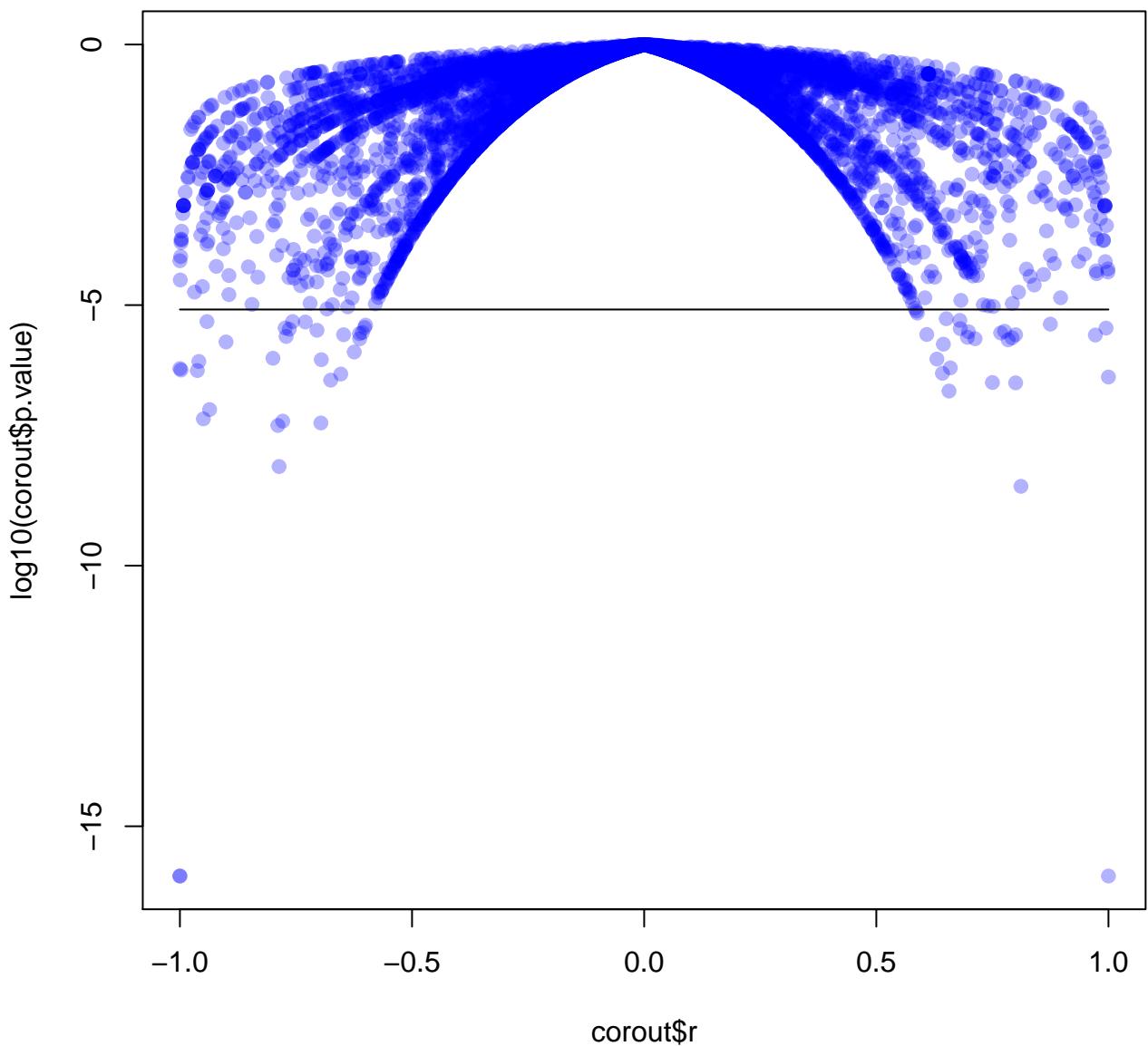
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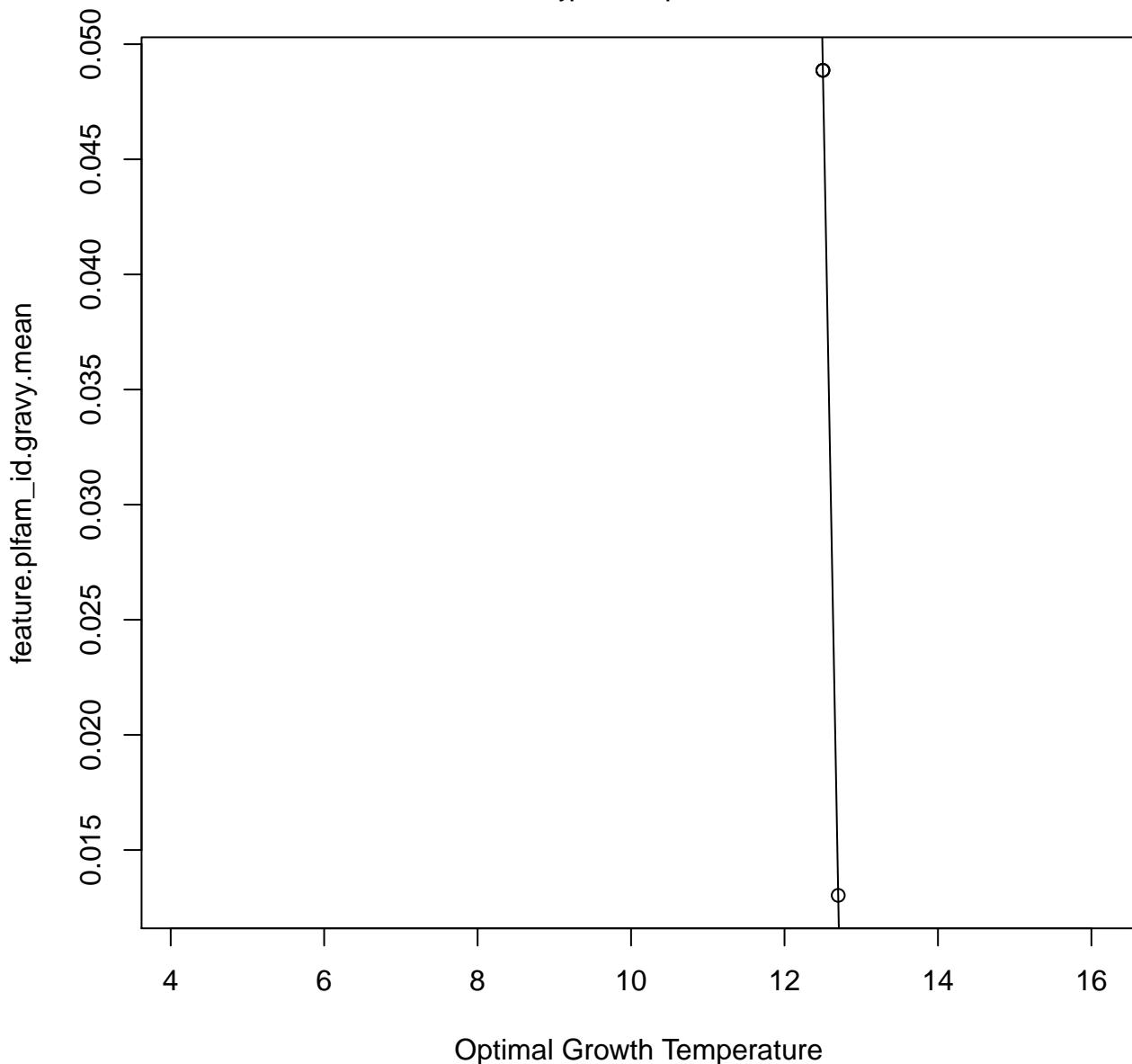
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Beta-phosphoglucomutase (EC 5.4.2.6)



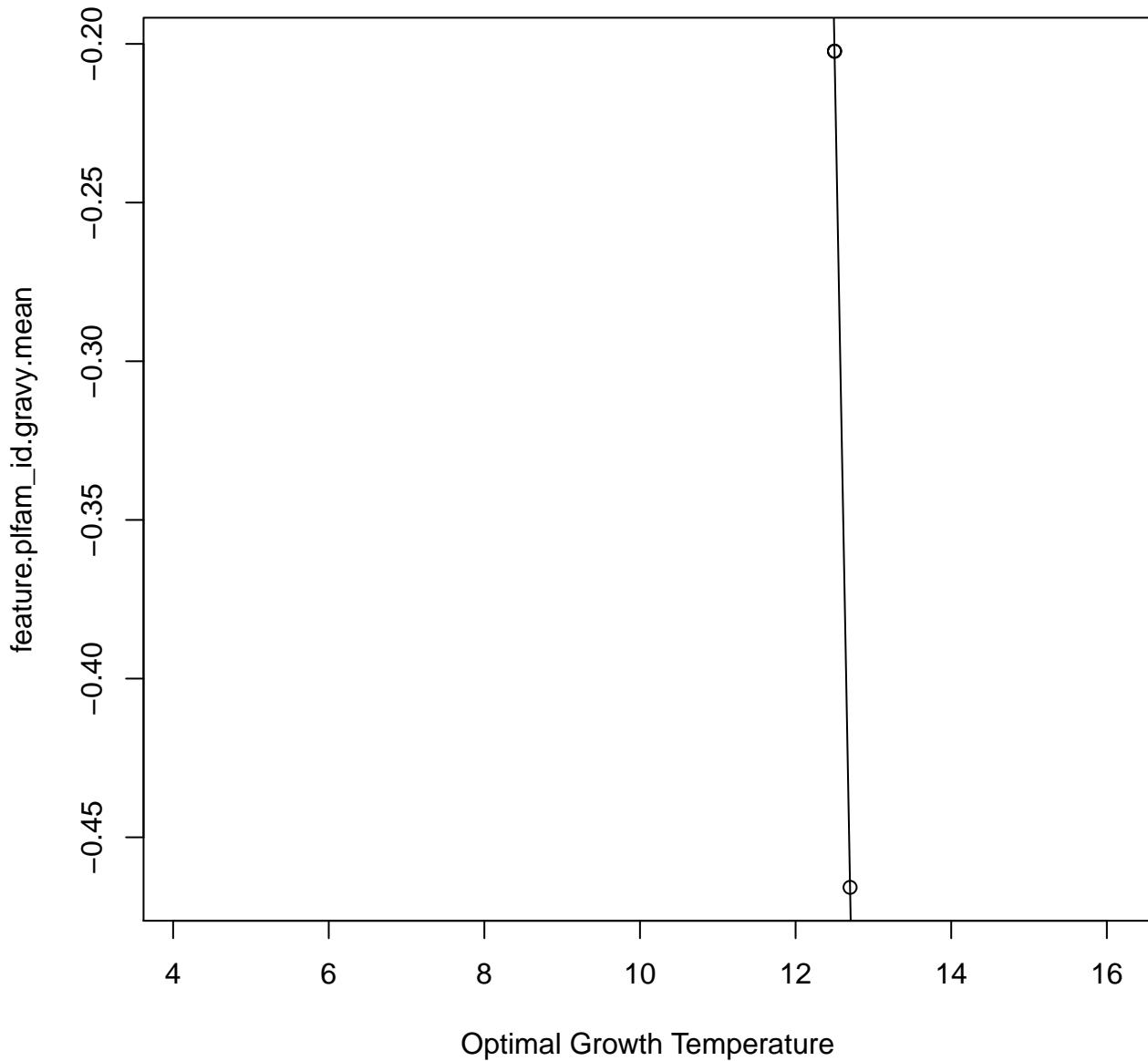
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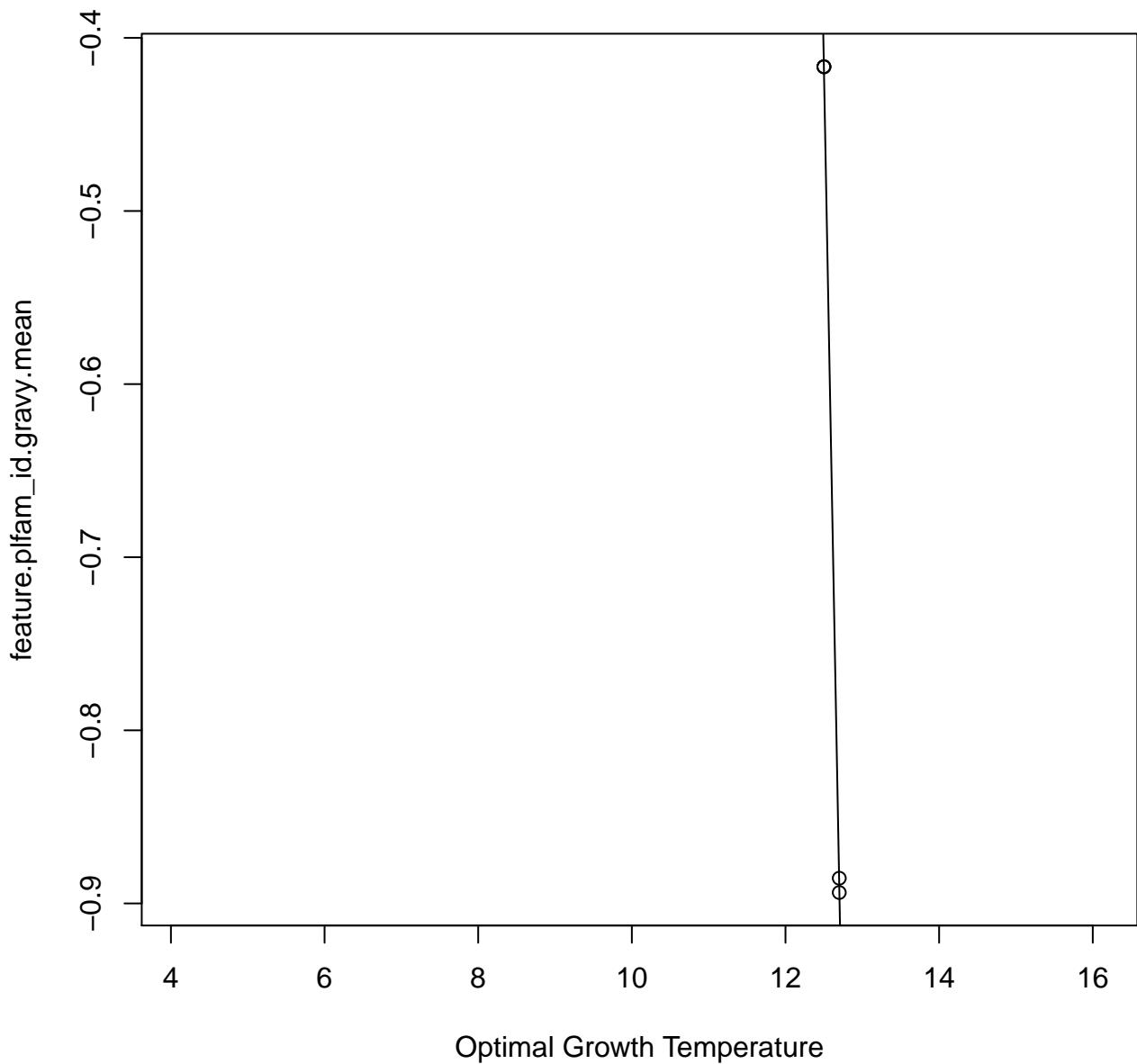
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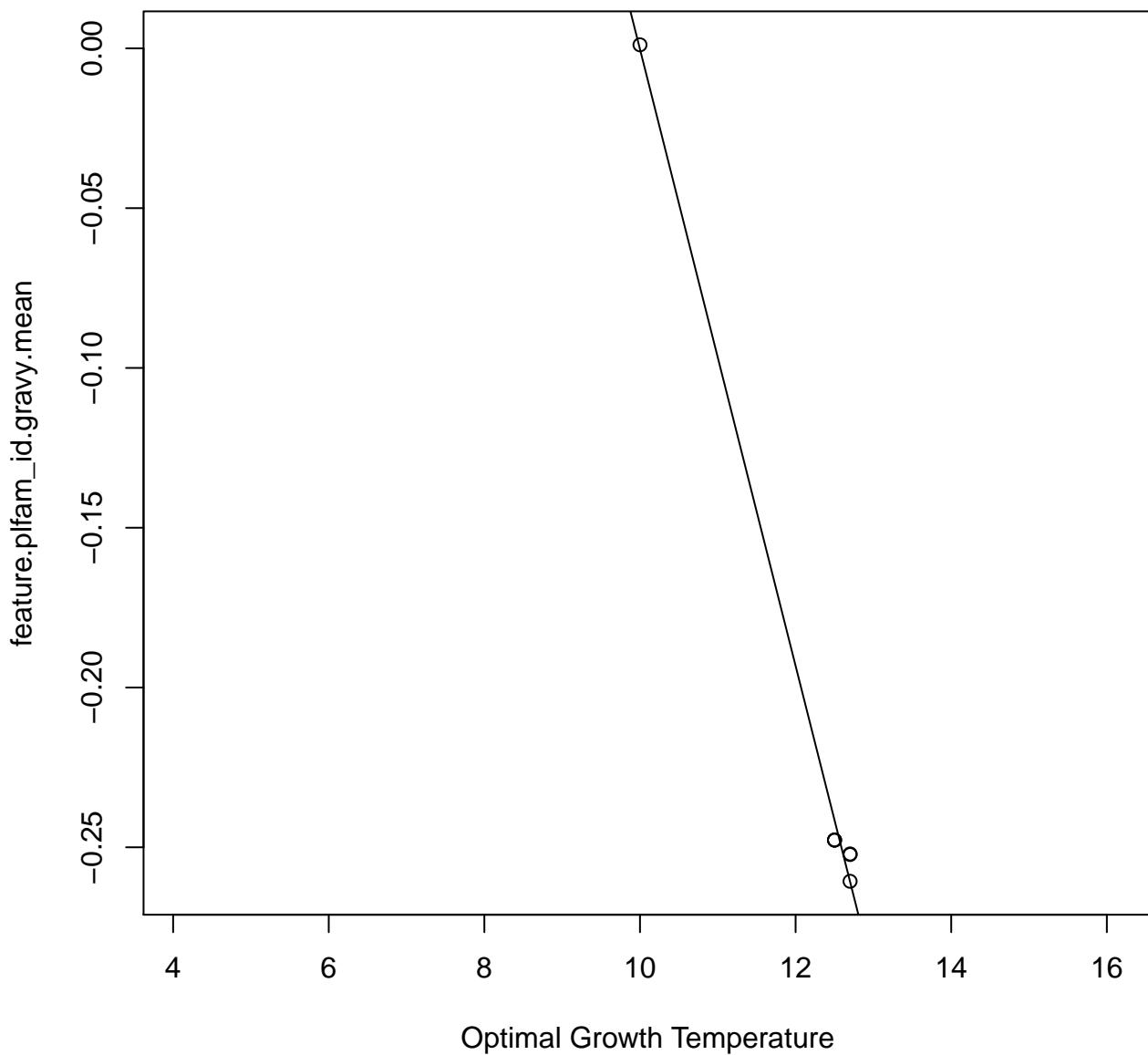
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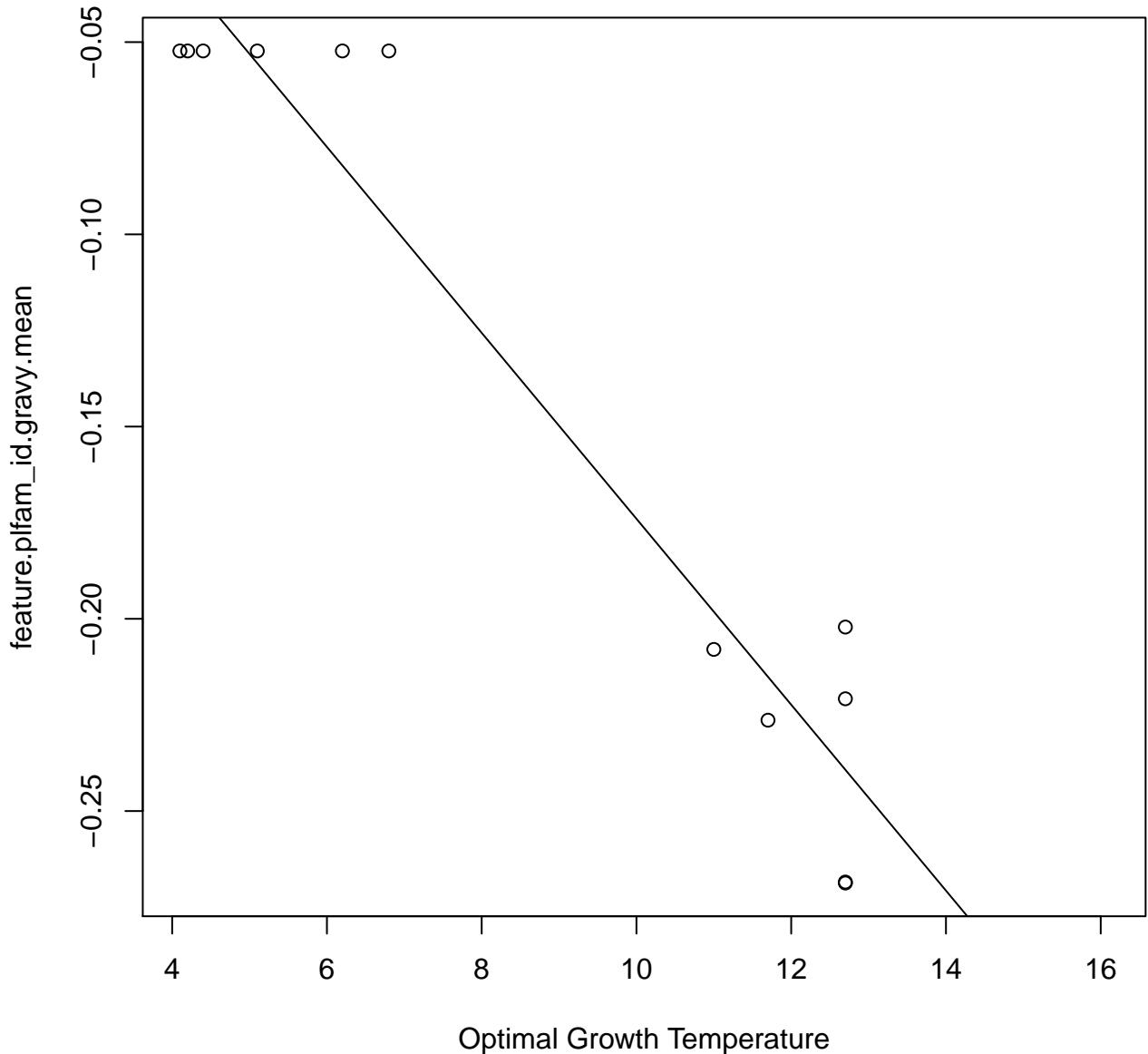
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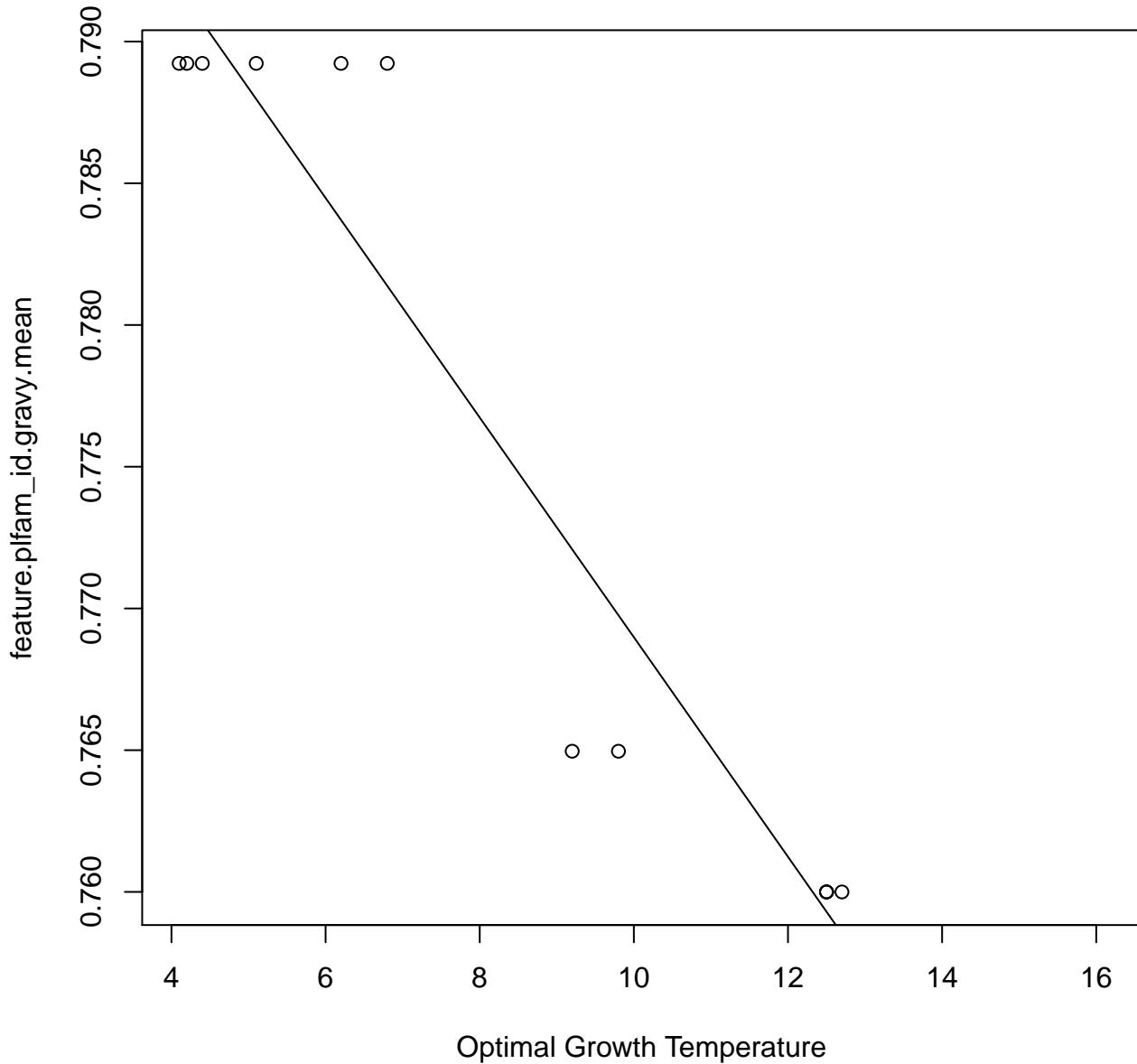
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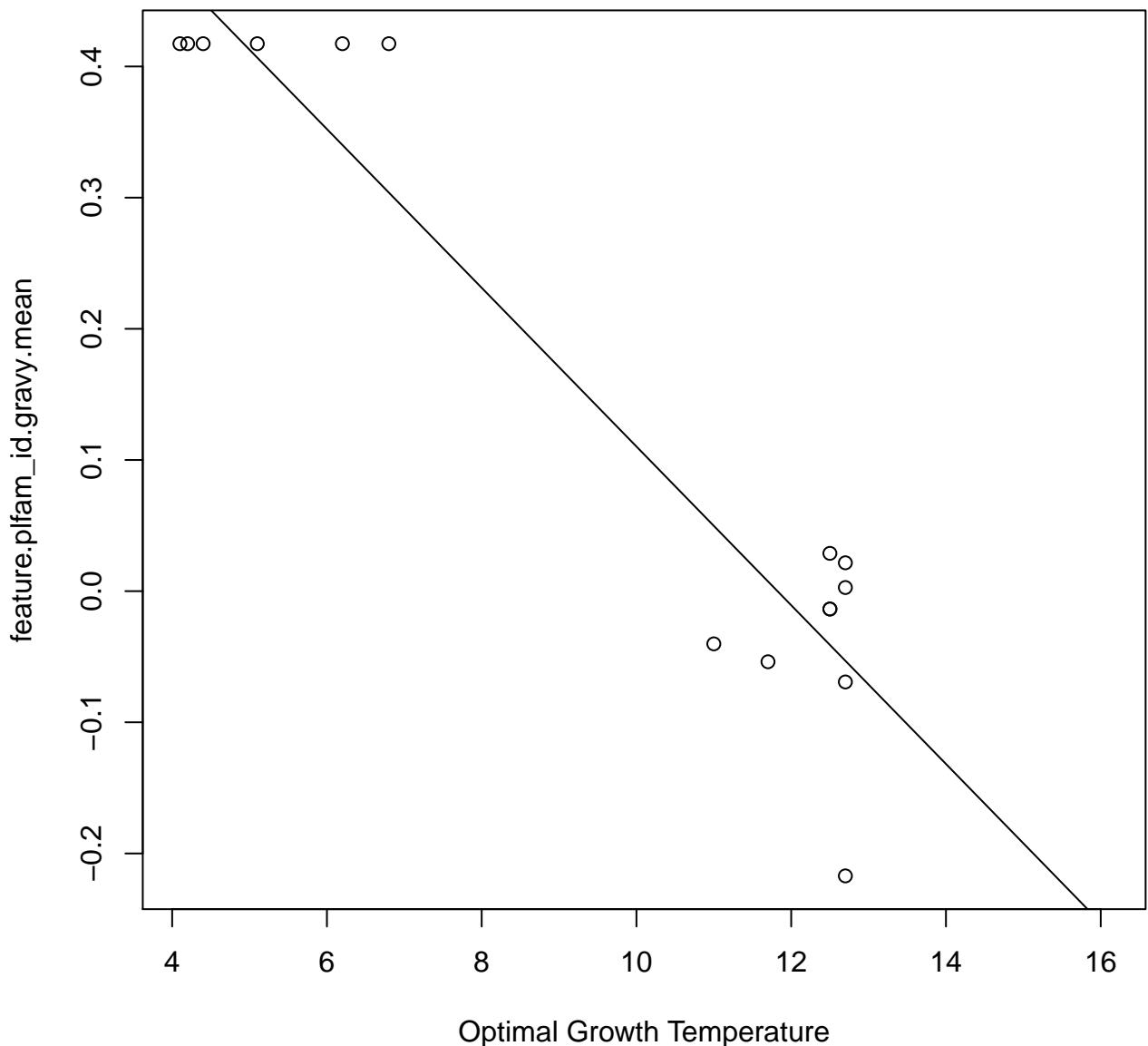
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Glutathione S-transferase, omega (EC 2.5.1.18)



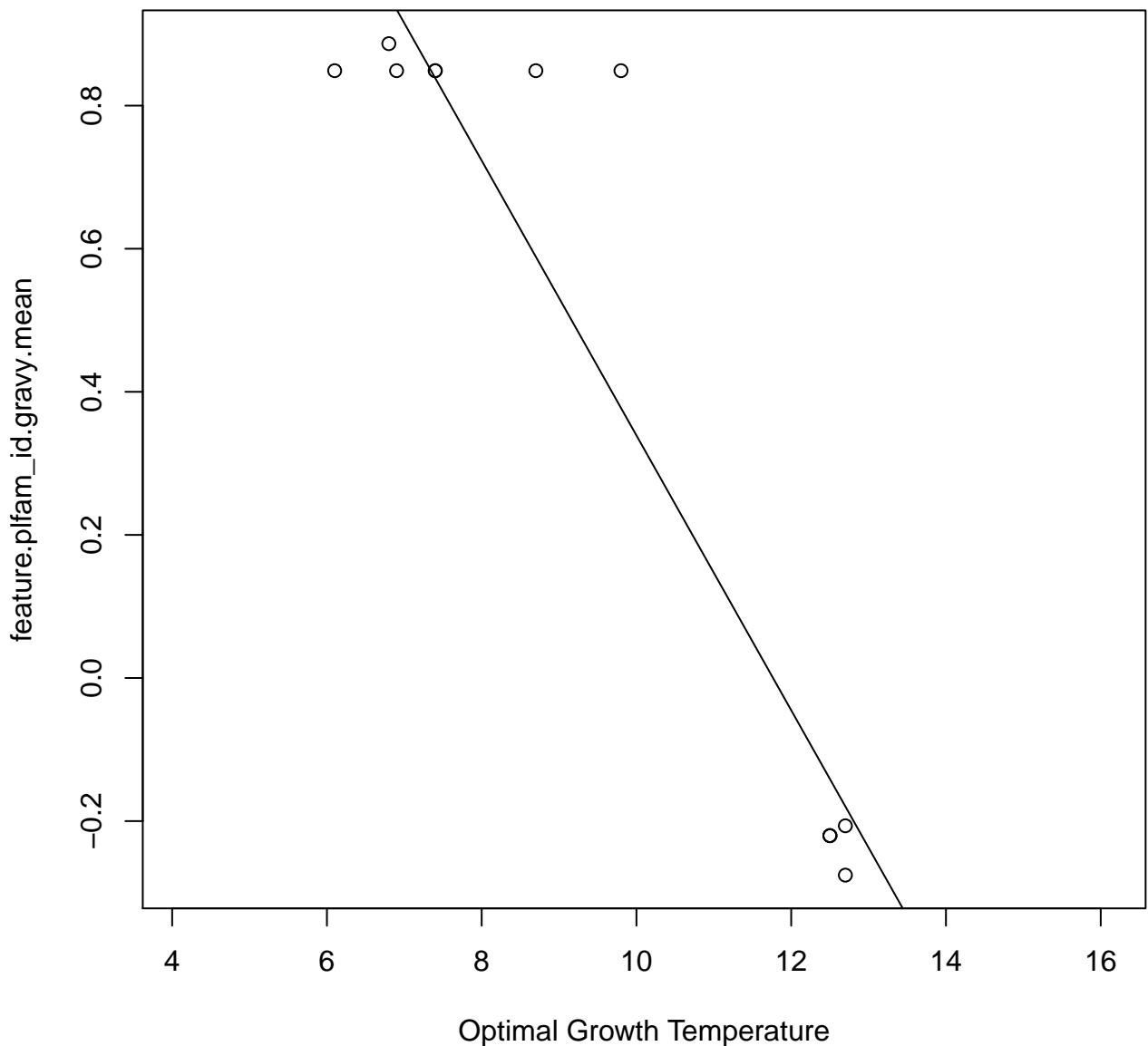
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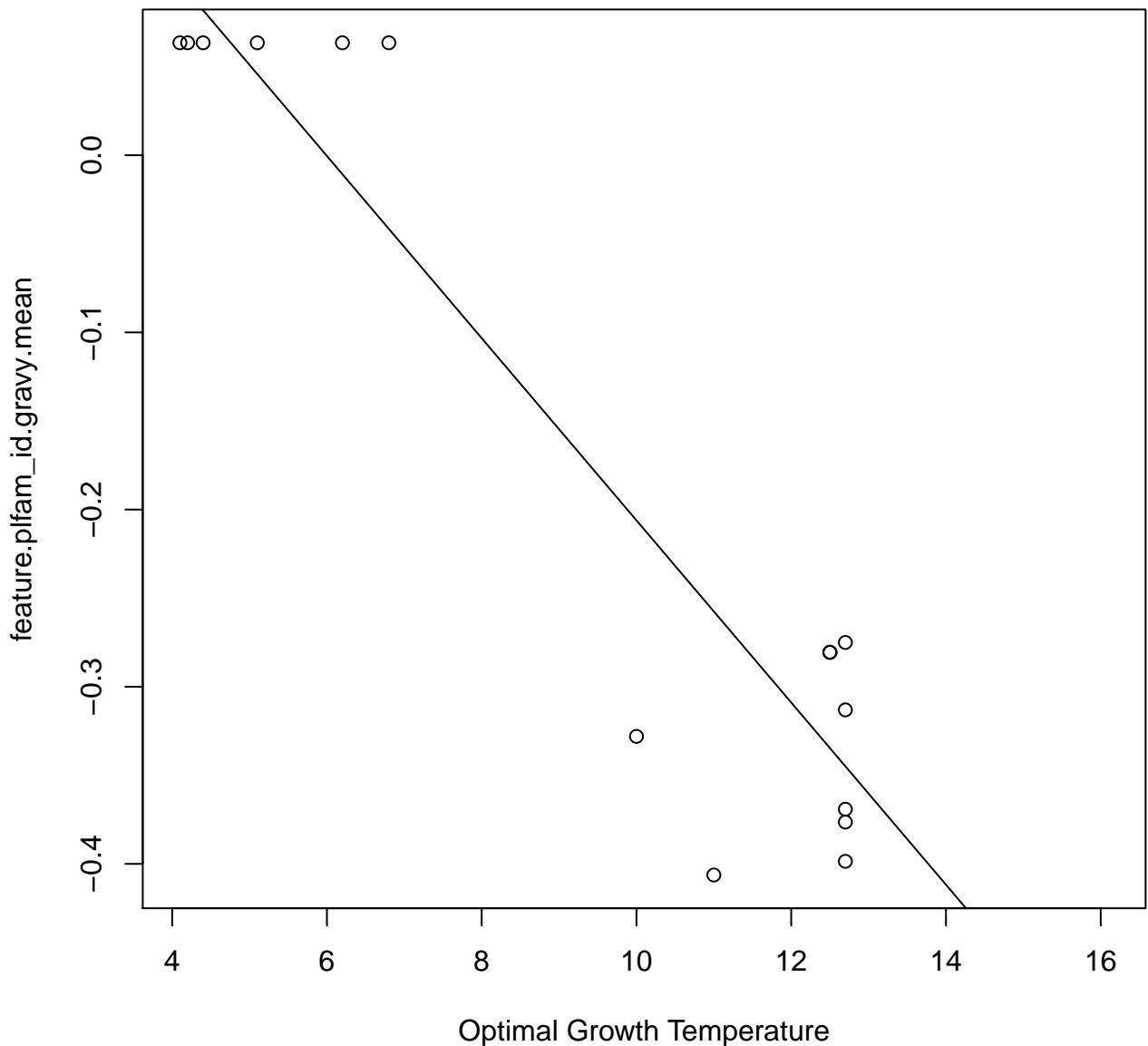
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Cobyricic acid a,c-diamide synthetase (EC 6.3.5.11)



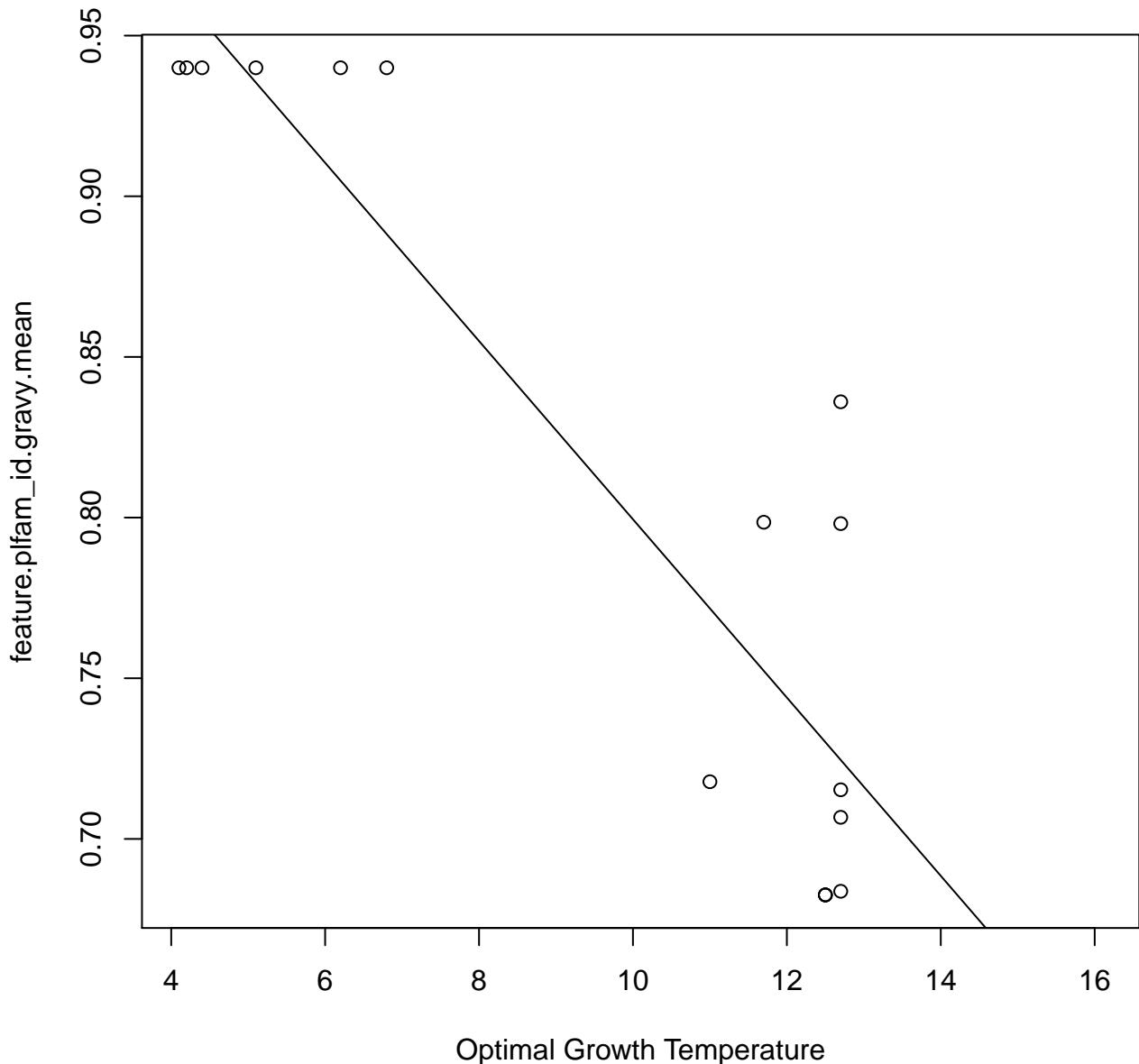
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EAL domain protein



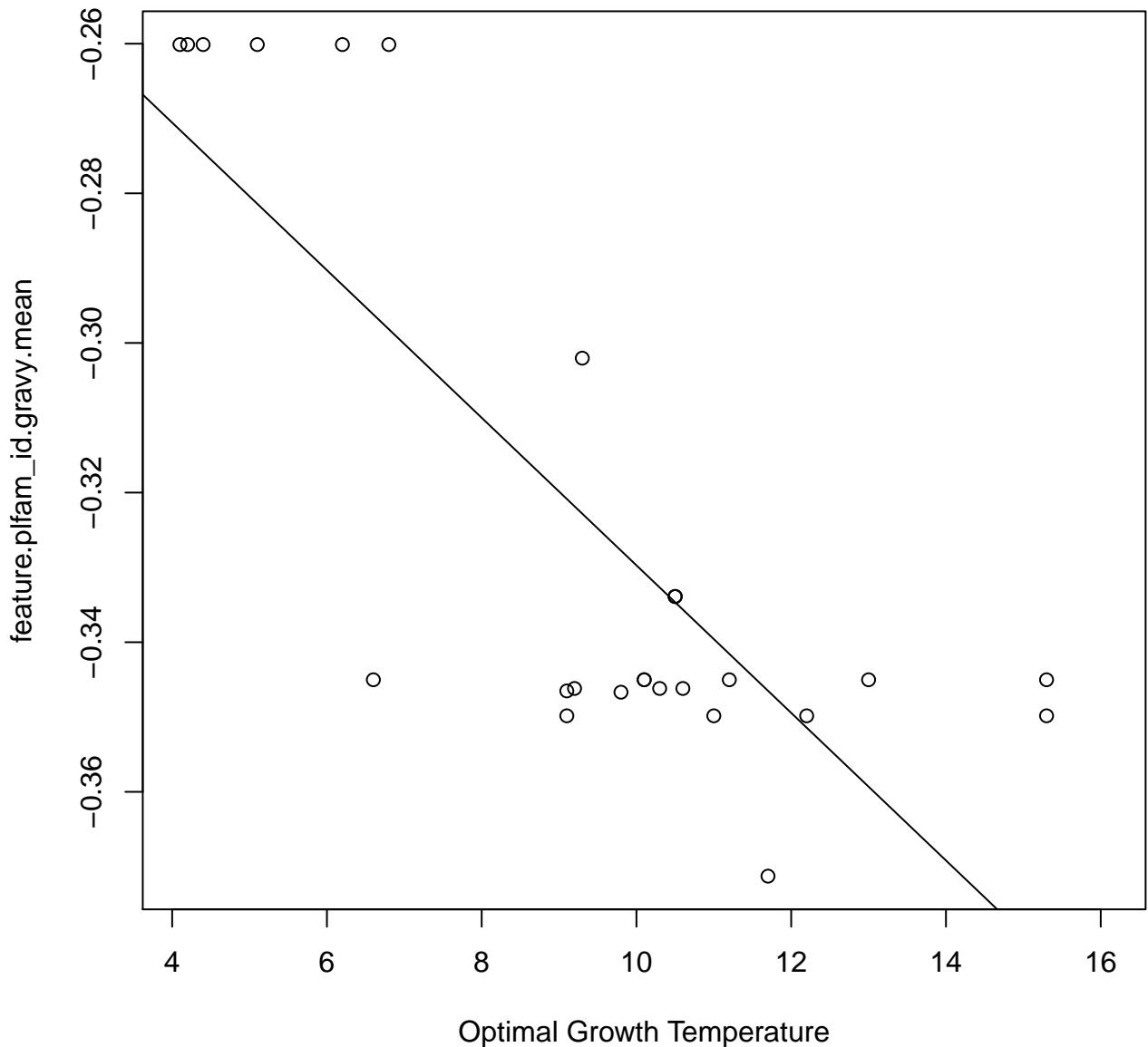
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Outer membrane beta-barrel assembly protein BamE



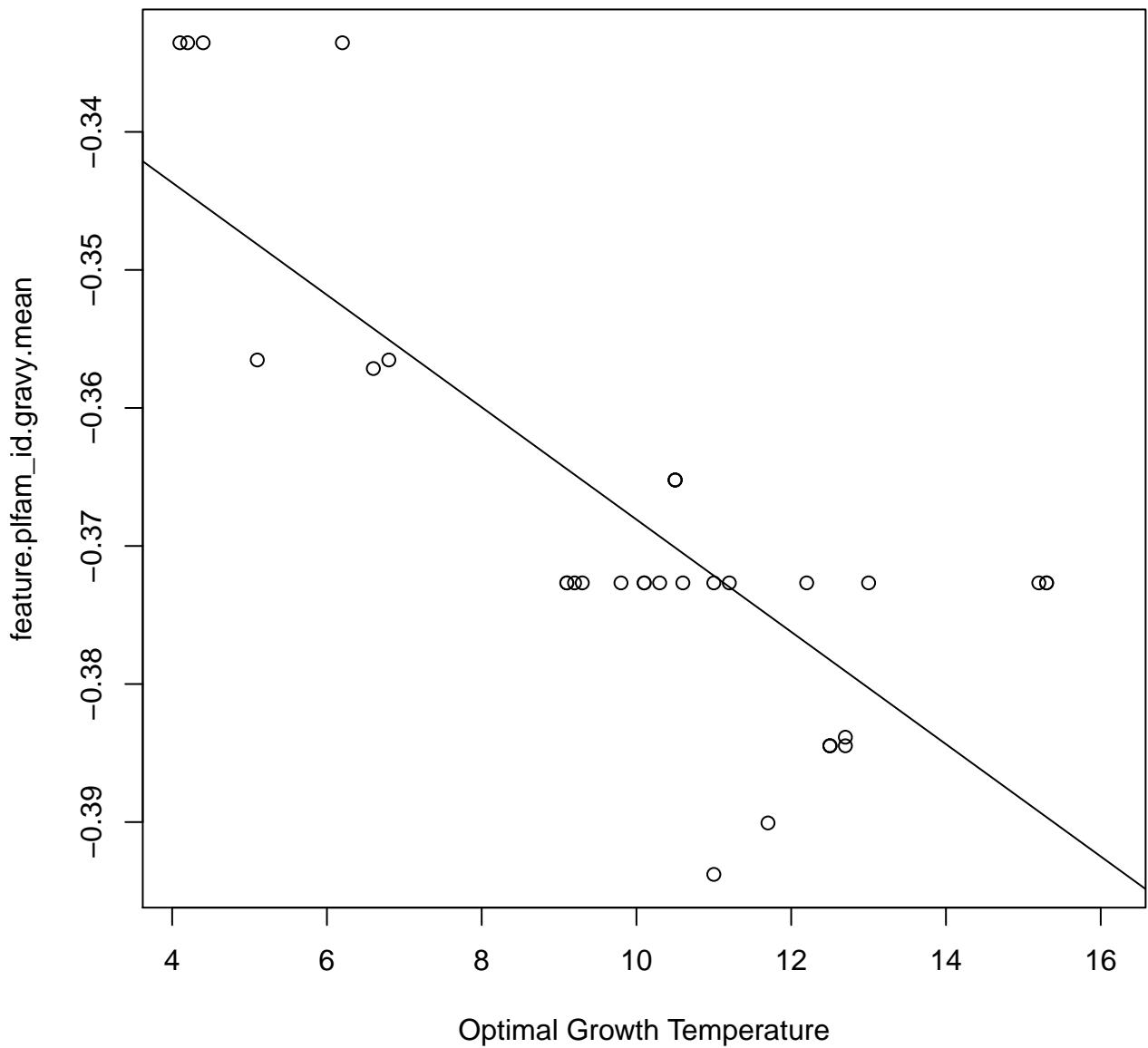
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Uncharacterized MFS-type transporter



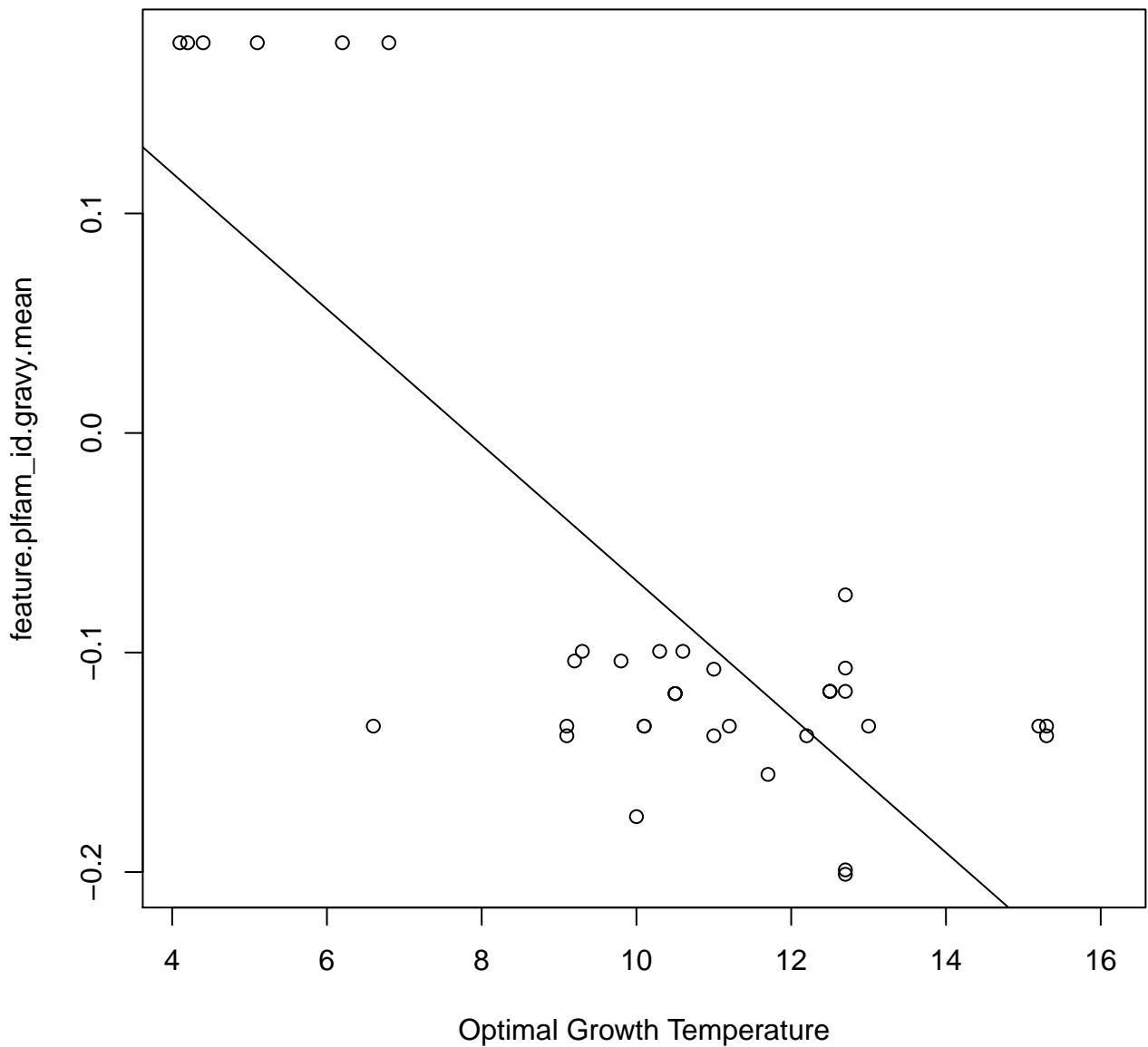
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Maltodextrin glucosidase (EC 3.2.1.20)



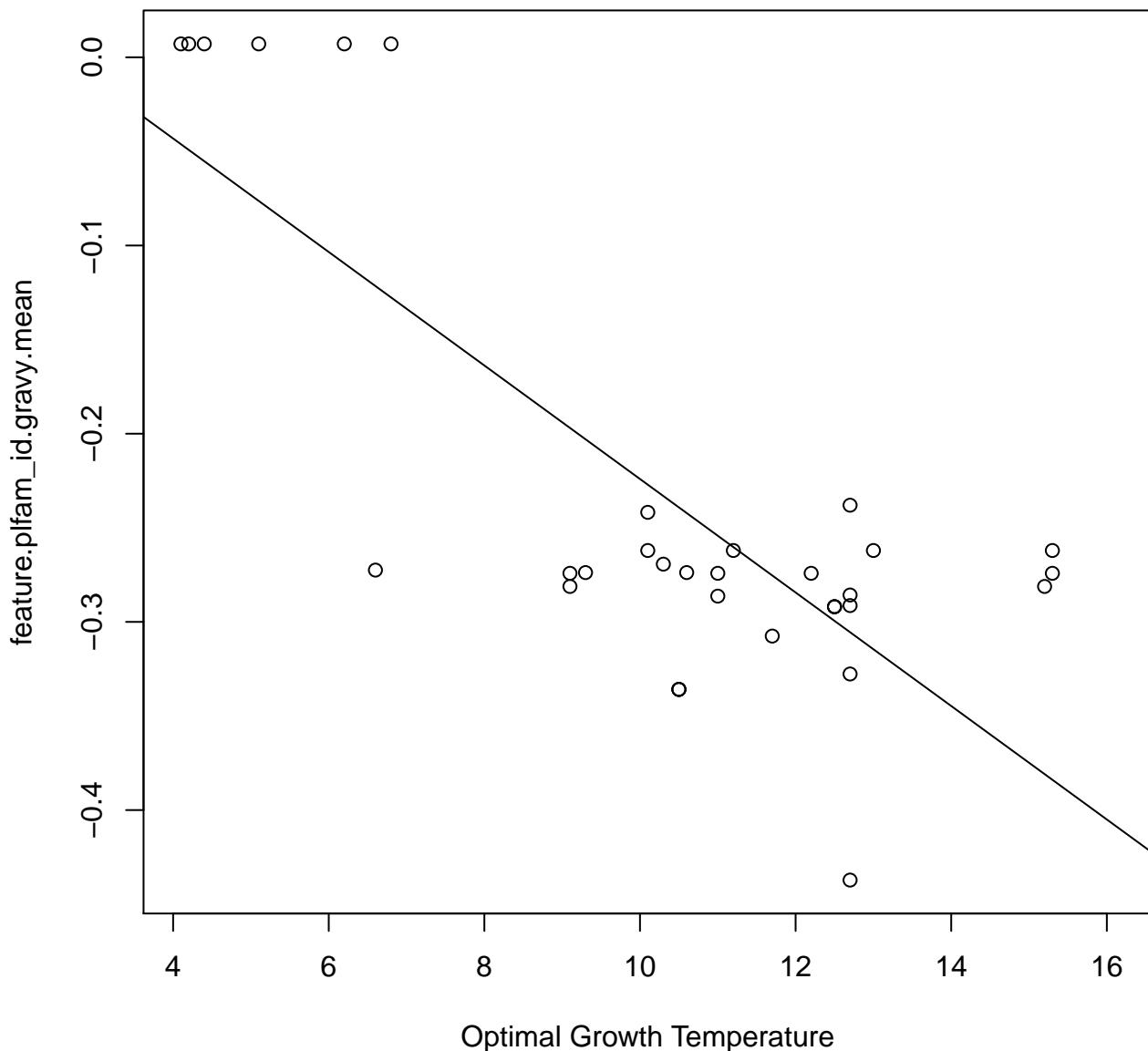
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hypothetical protein



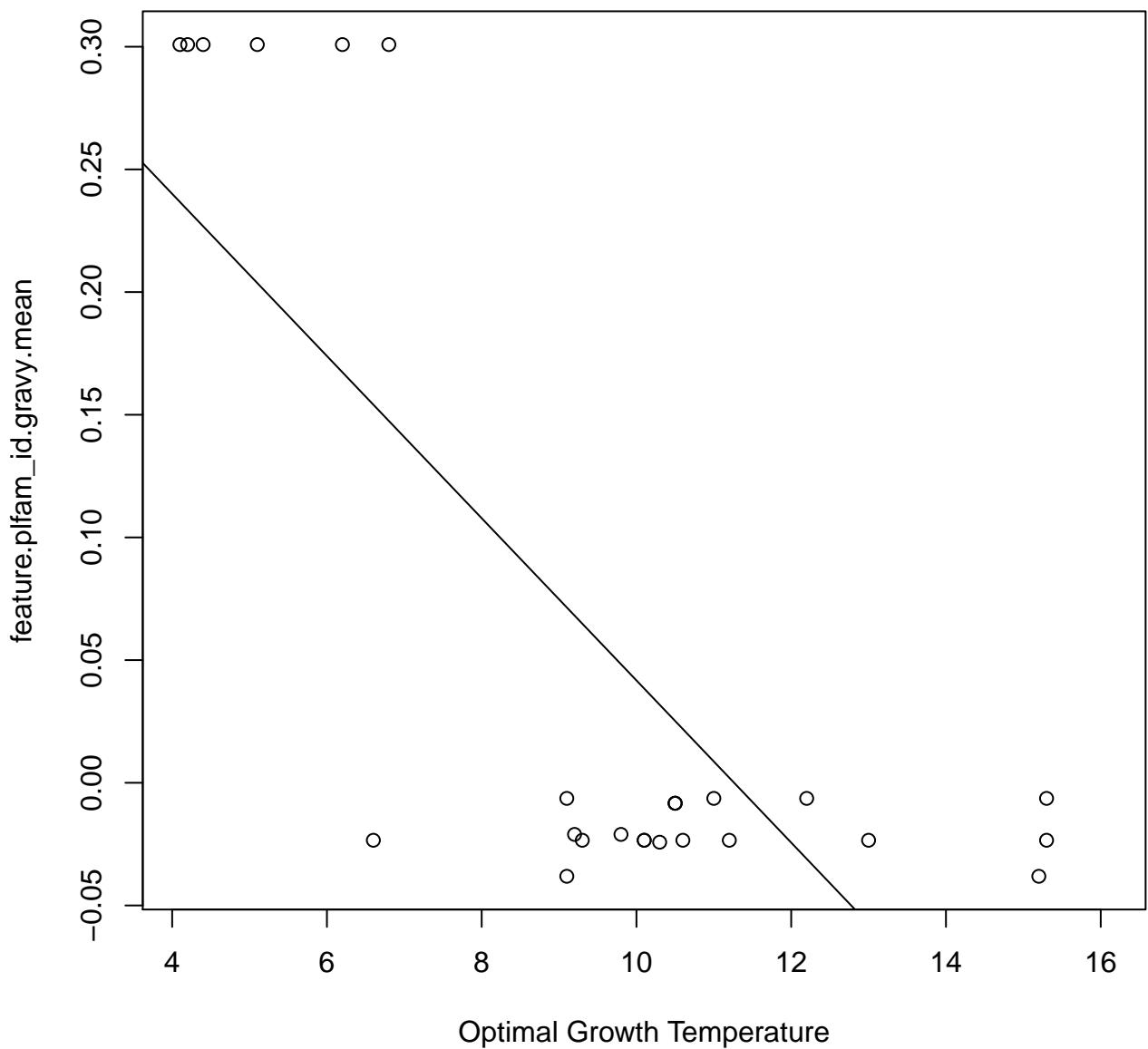
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Putative NAD(P)H nitroreductase YdjA



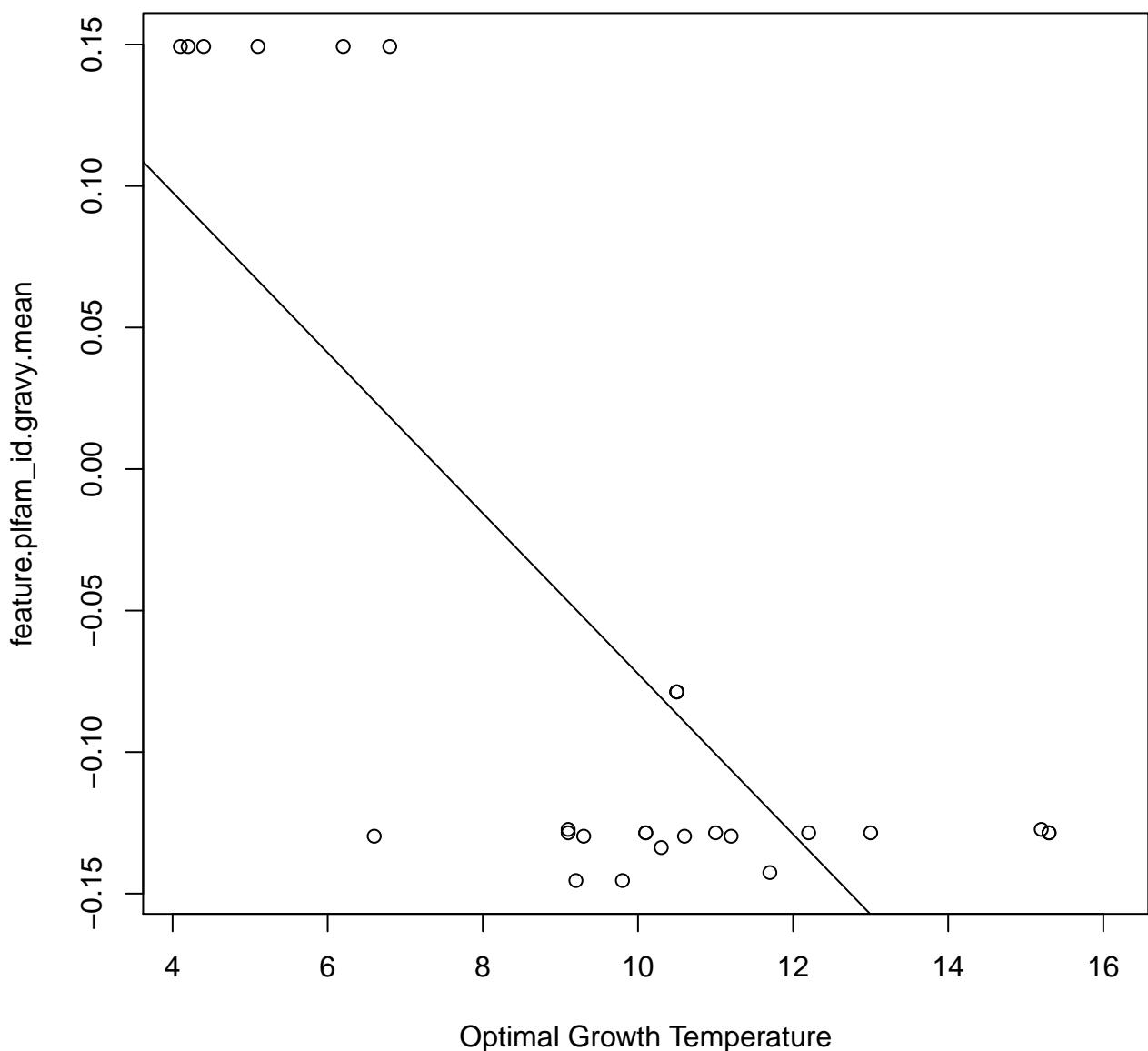
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TonB-dependent receptor



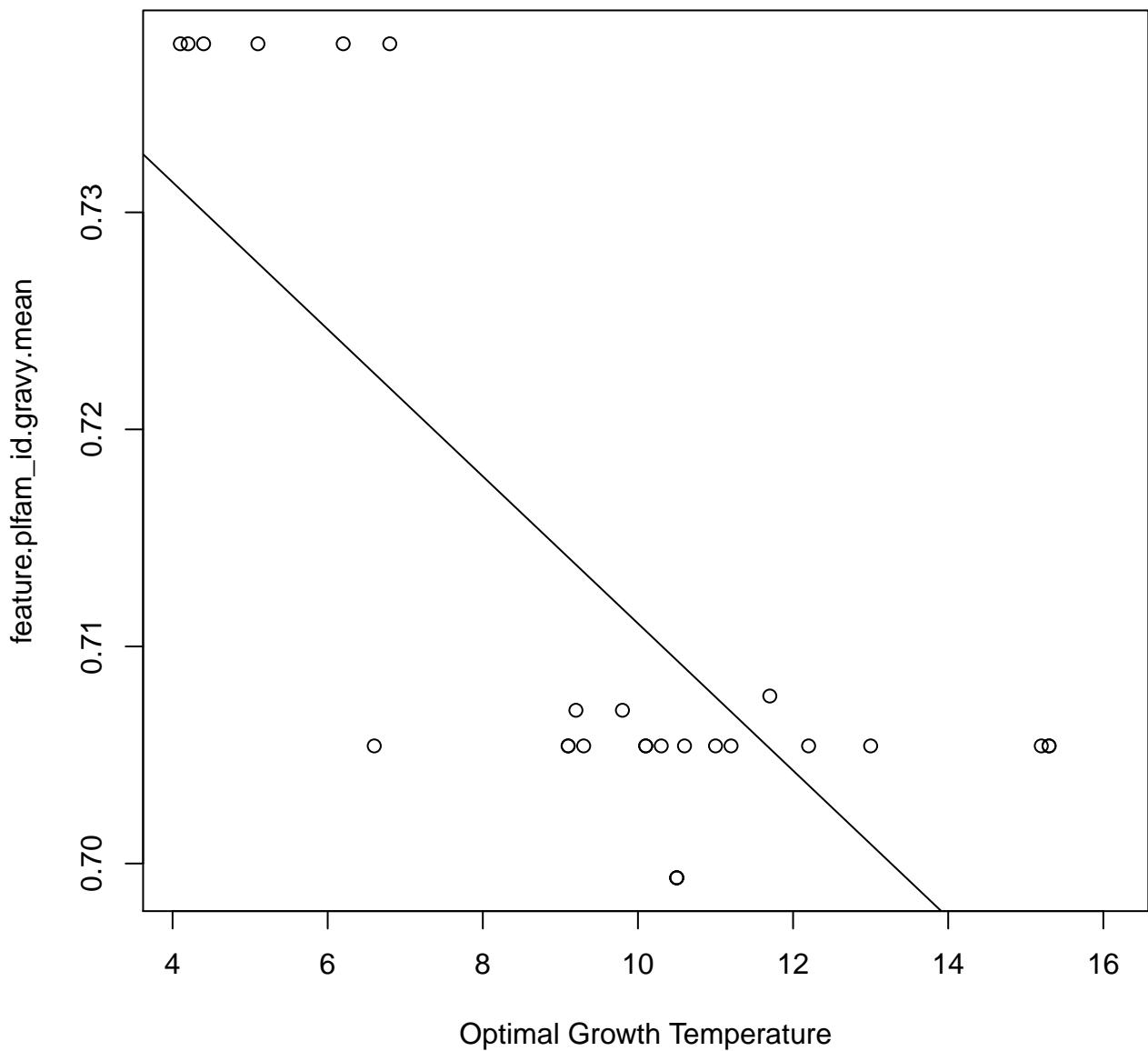
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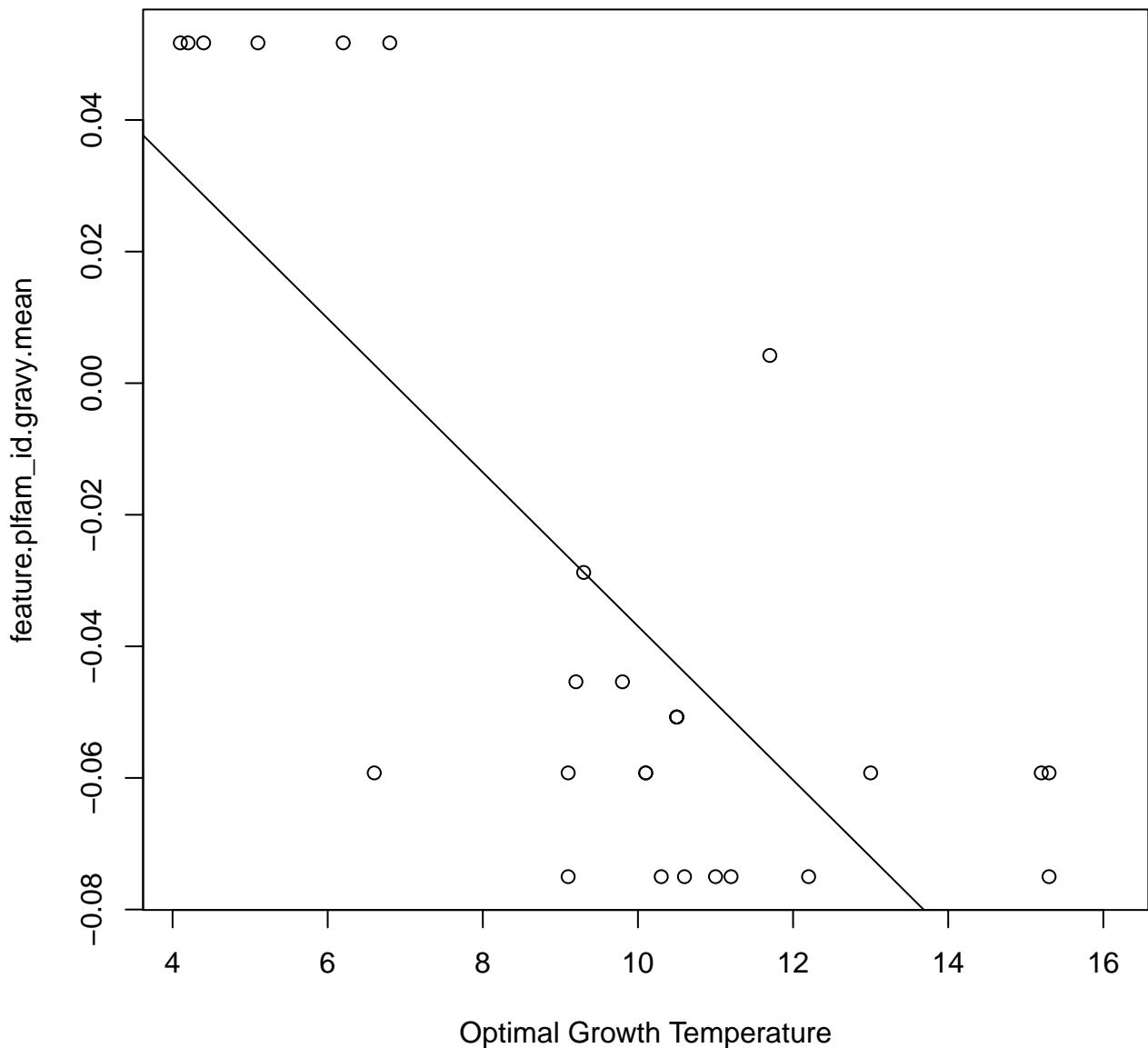
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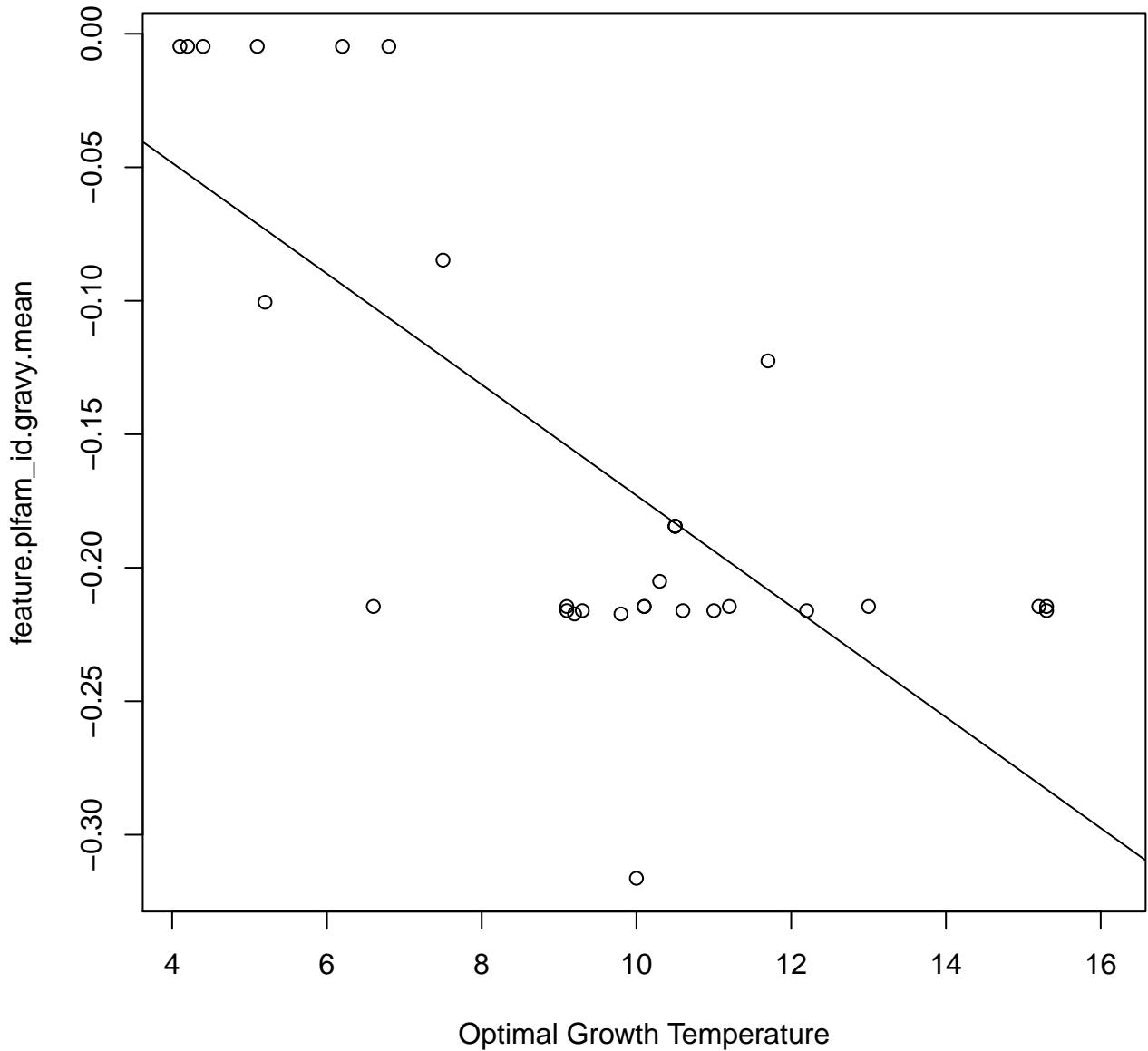
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TrkA-C domain protein



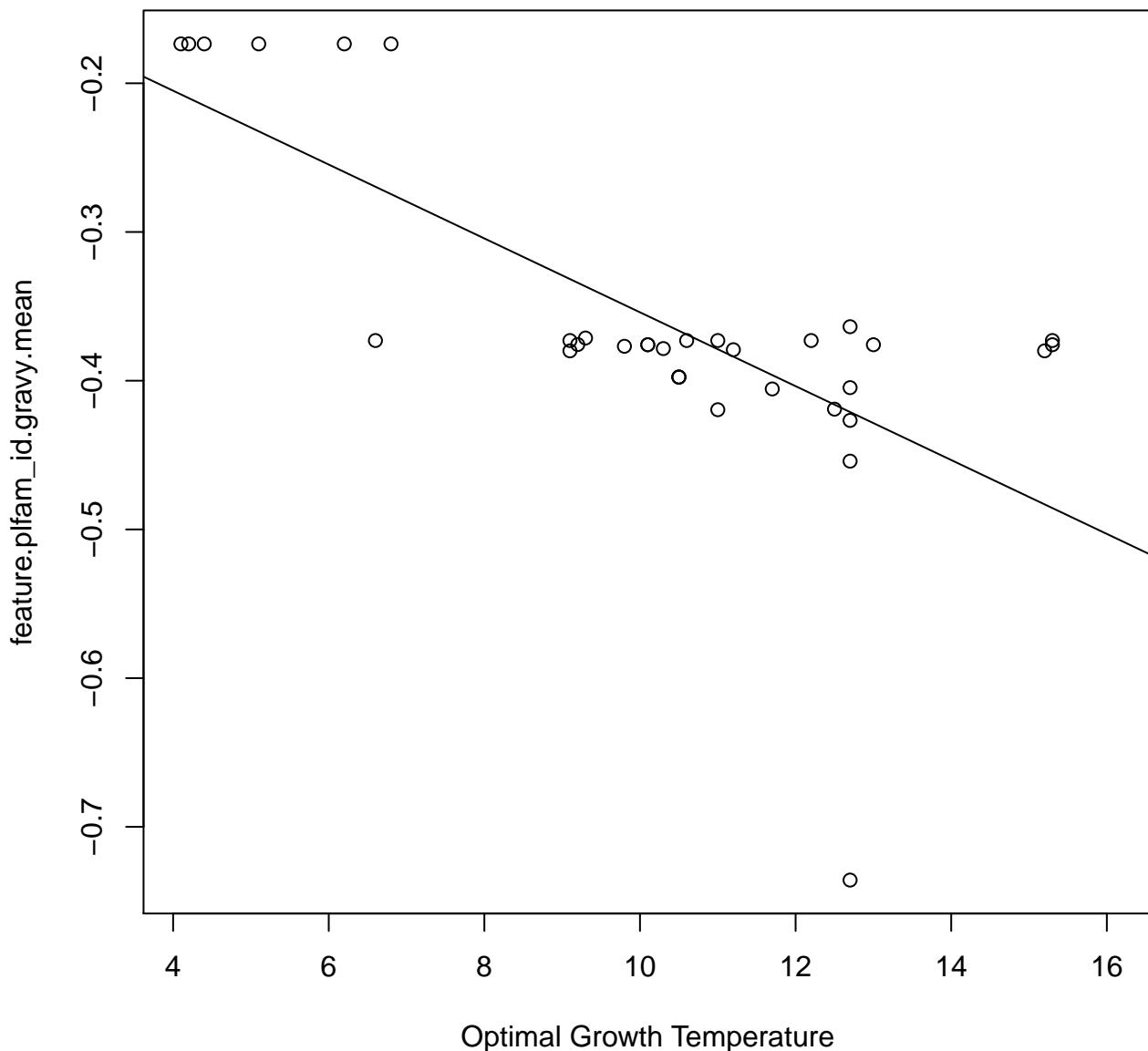
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hypothetical protein



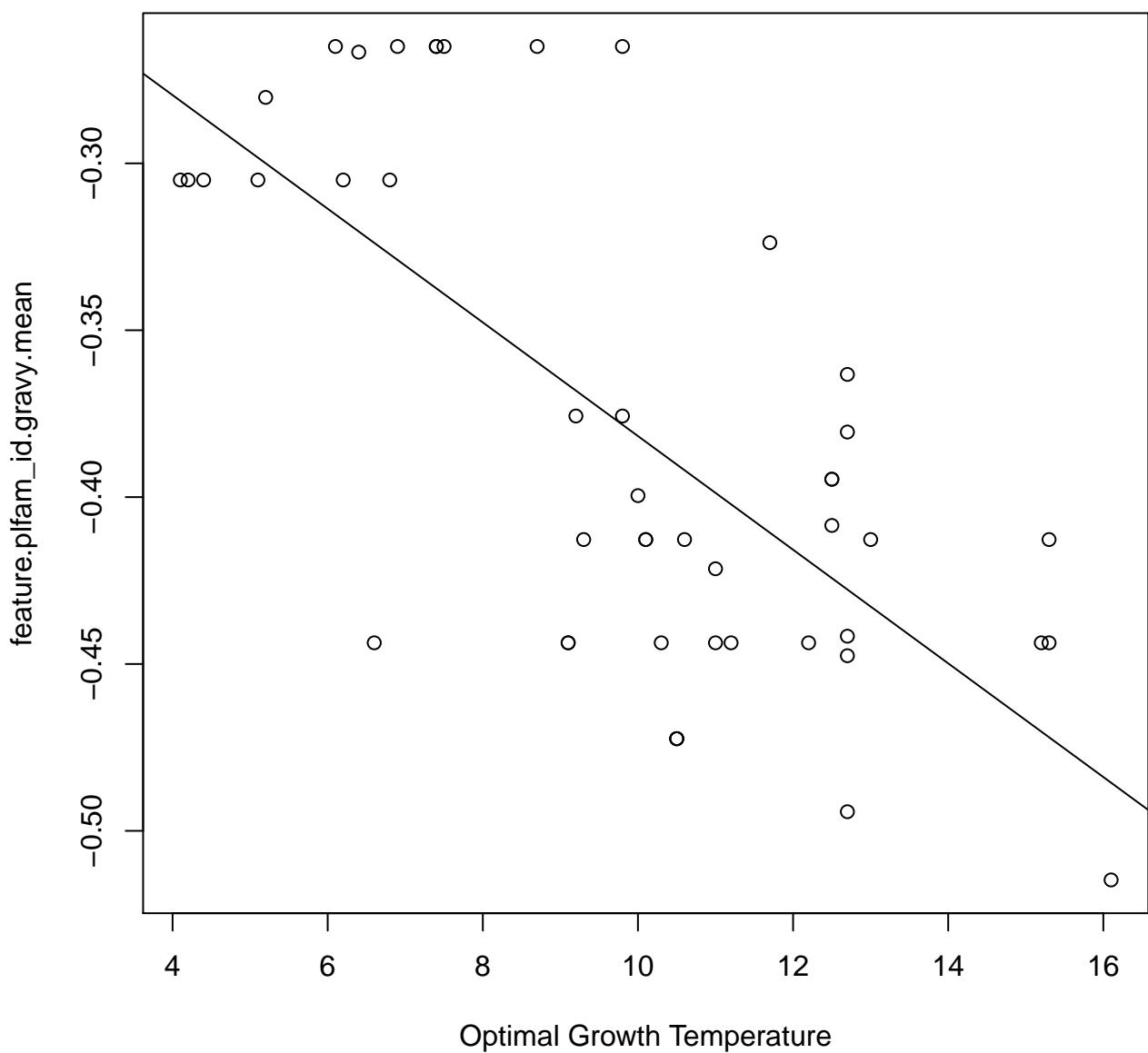
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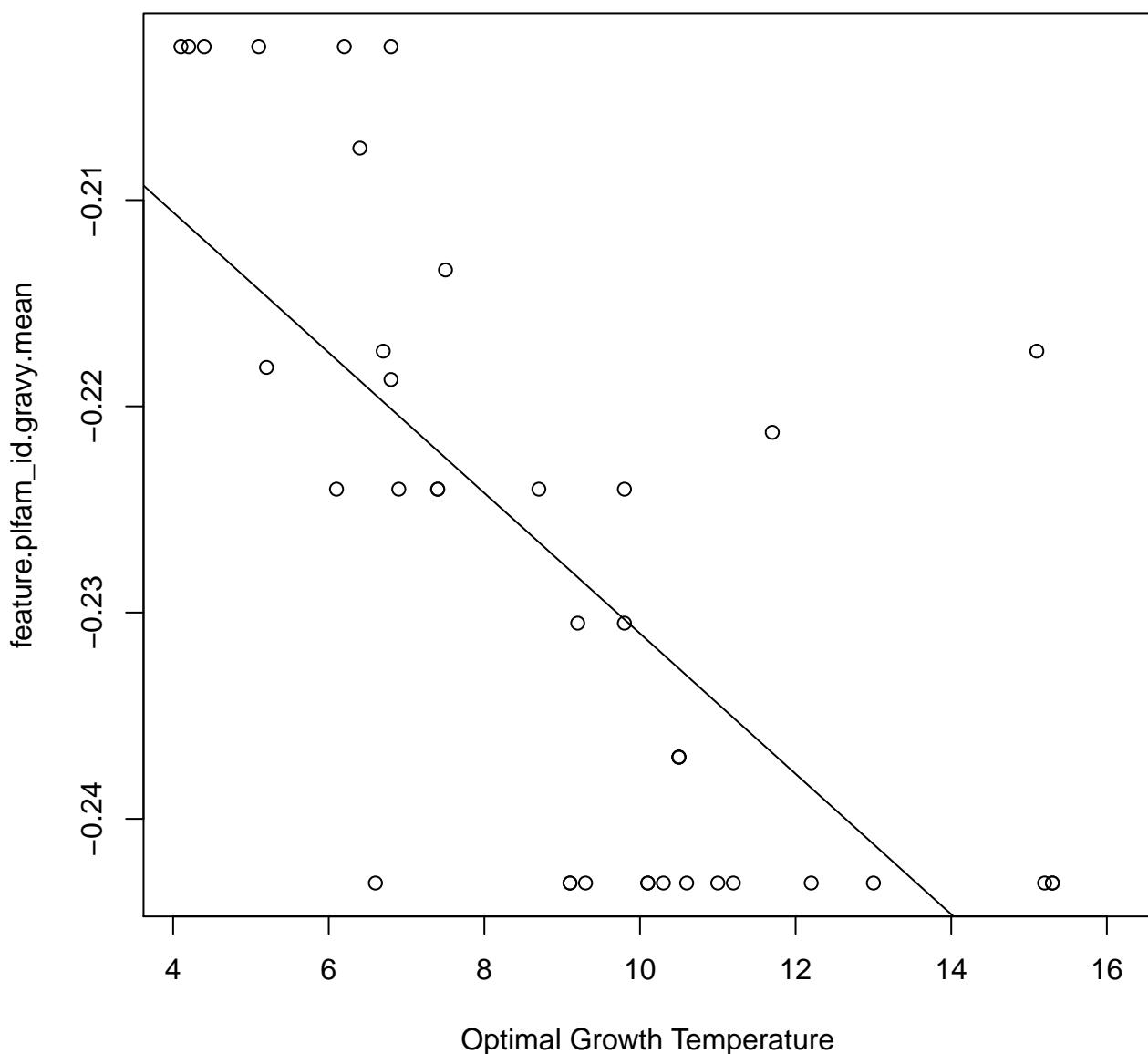
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Fatty acid cis/trans isomerase



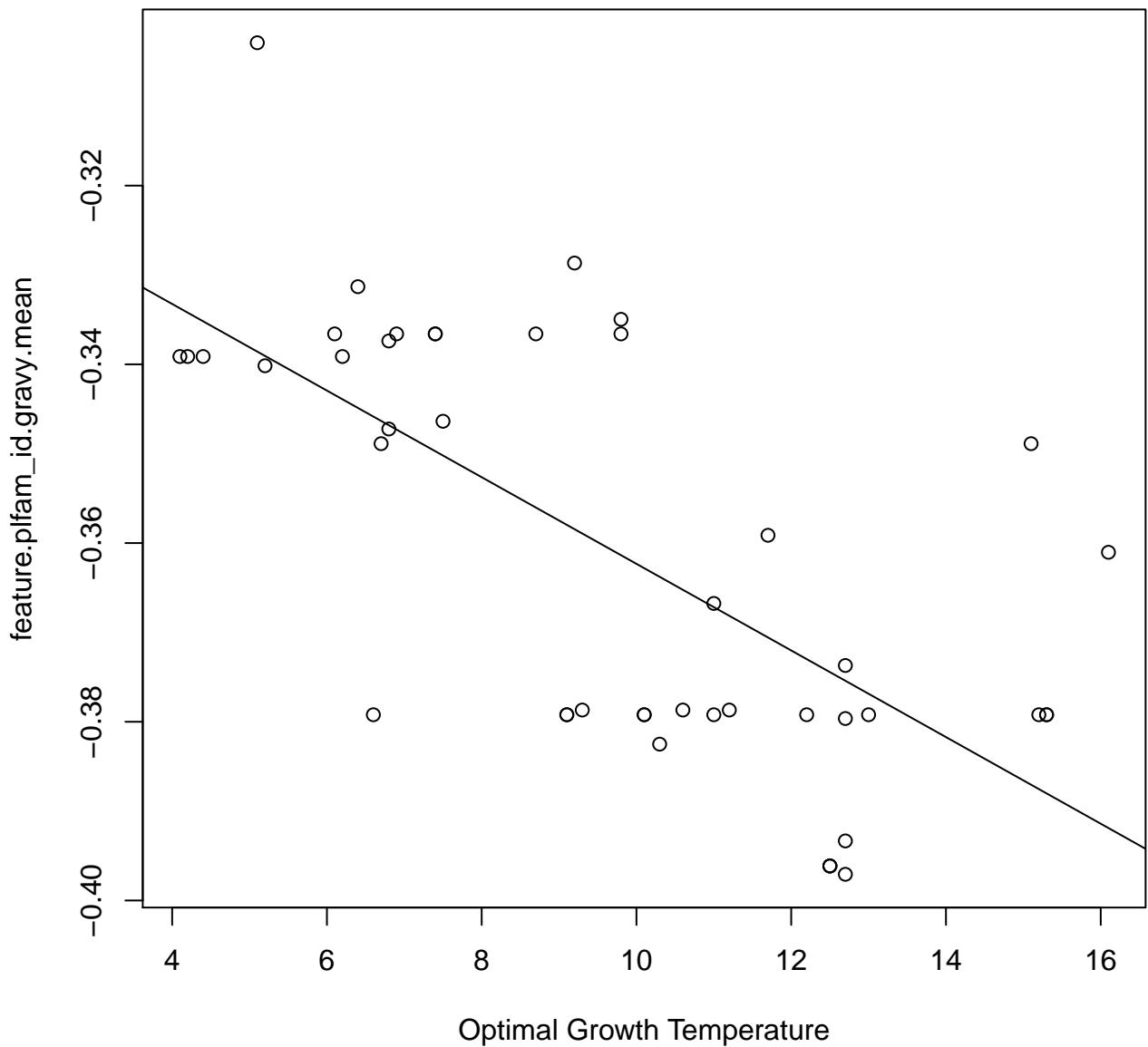
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Potential queD like 2



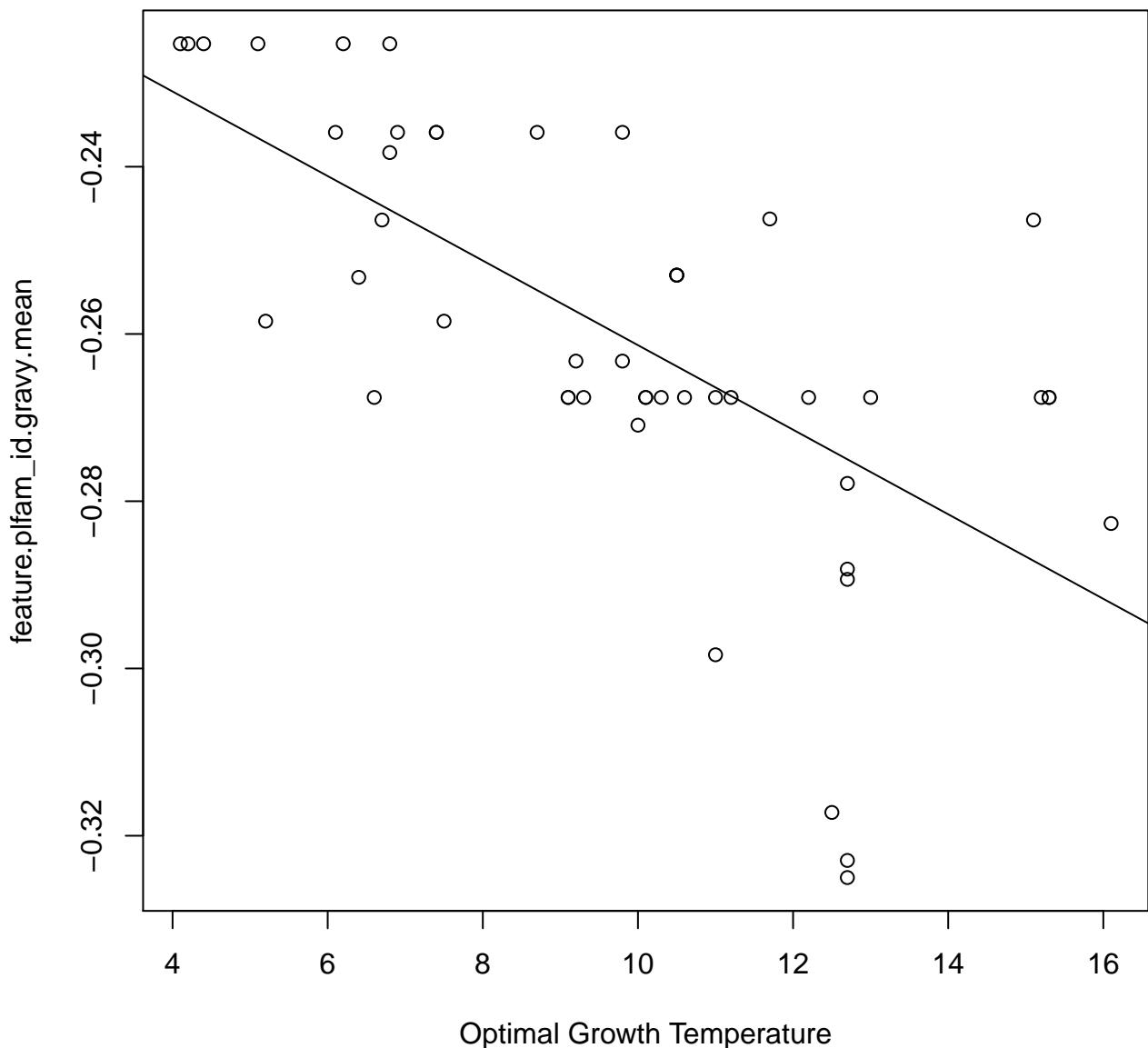
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Carbon–nitrogen hydrolase



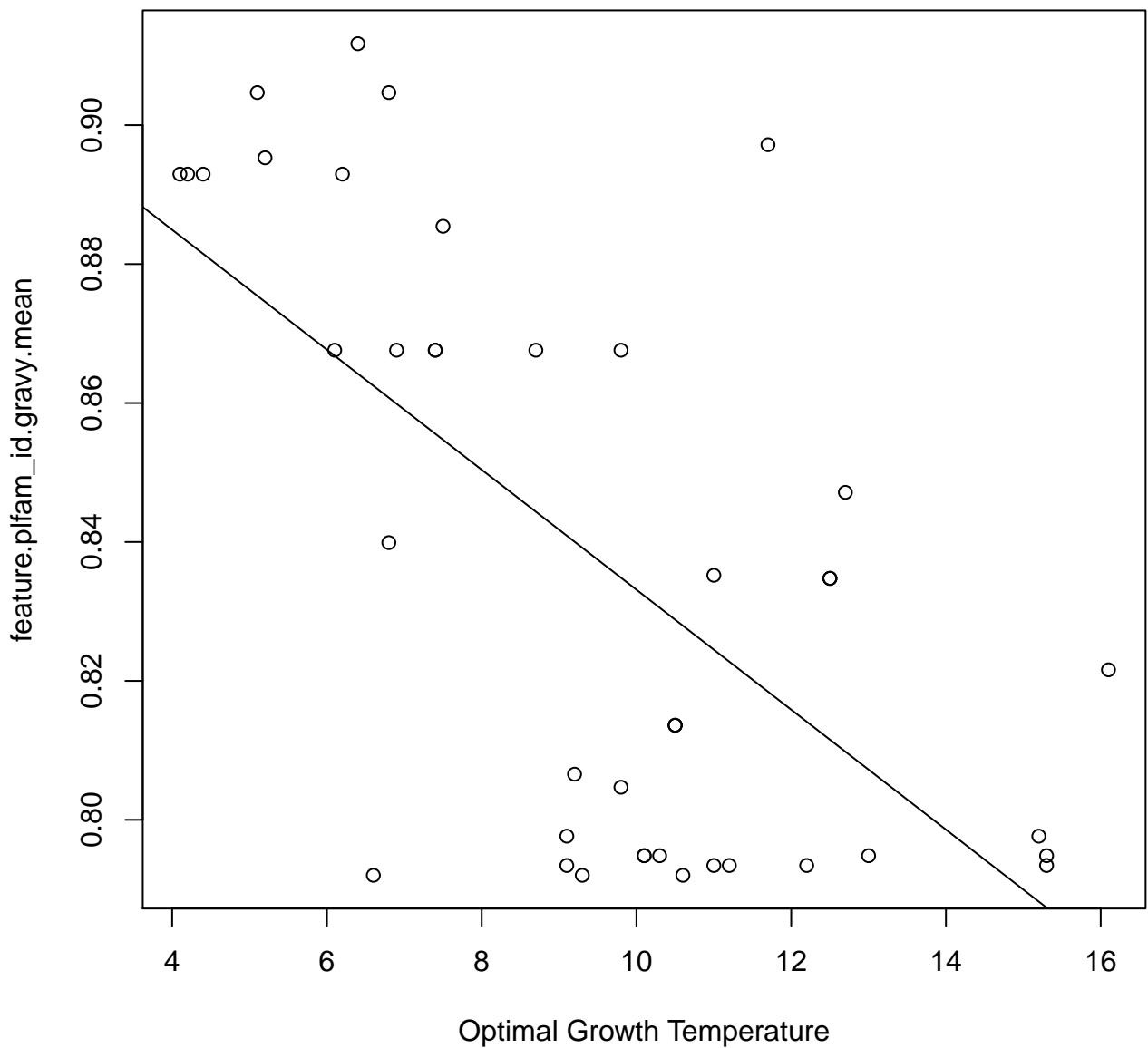
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TonB-dependent receptor



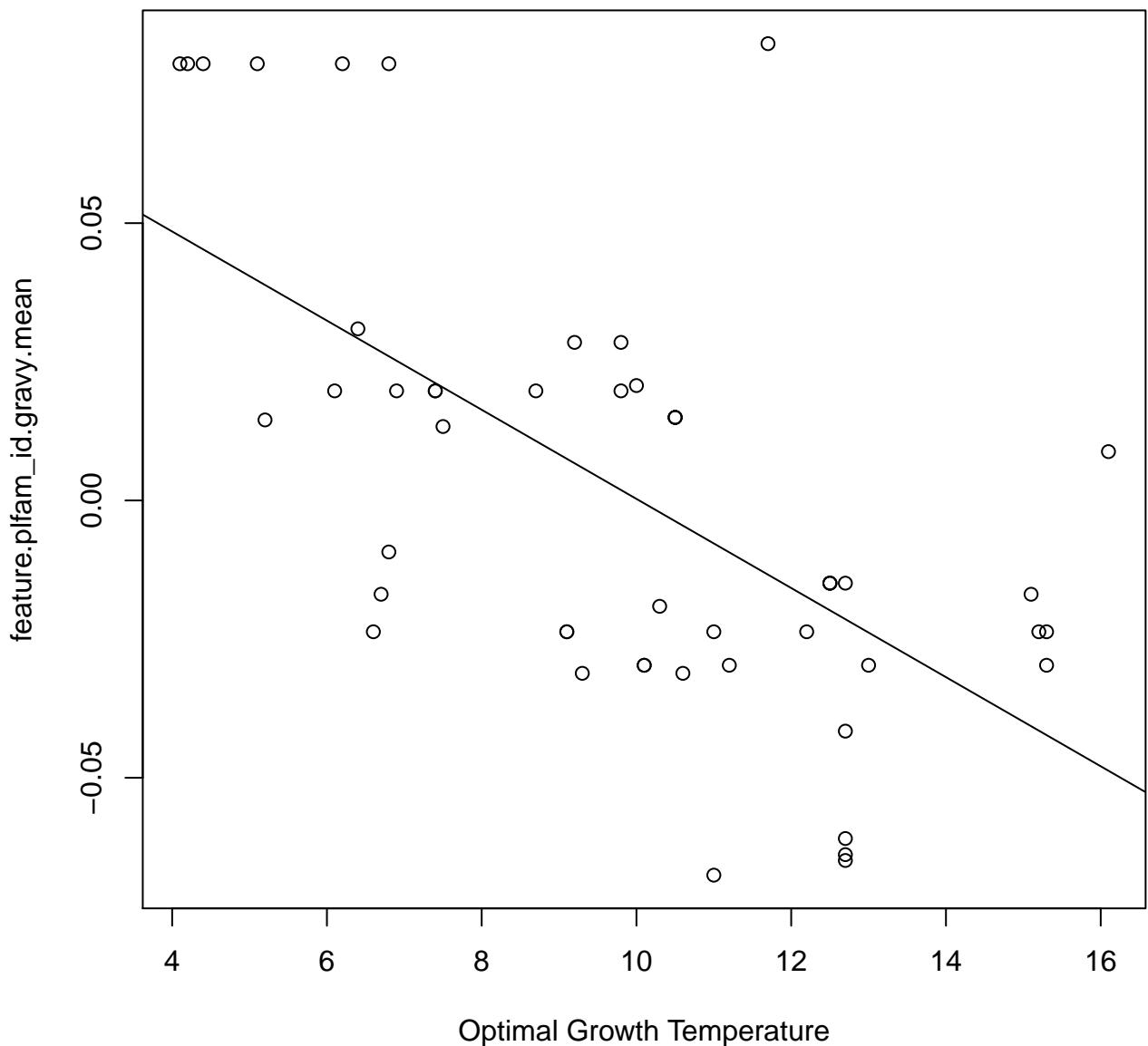
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PLF_28228_00027836
16S rRNA (uracil(1498)-N(3))-methyltransferase (EC 2.1.1.193)



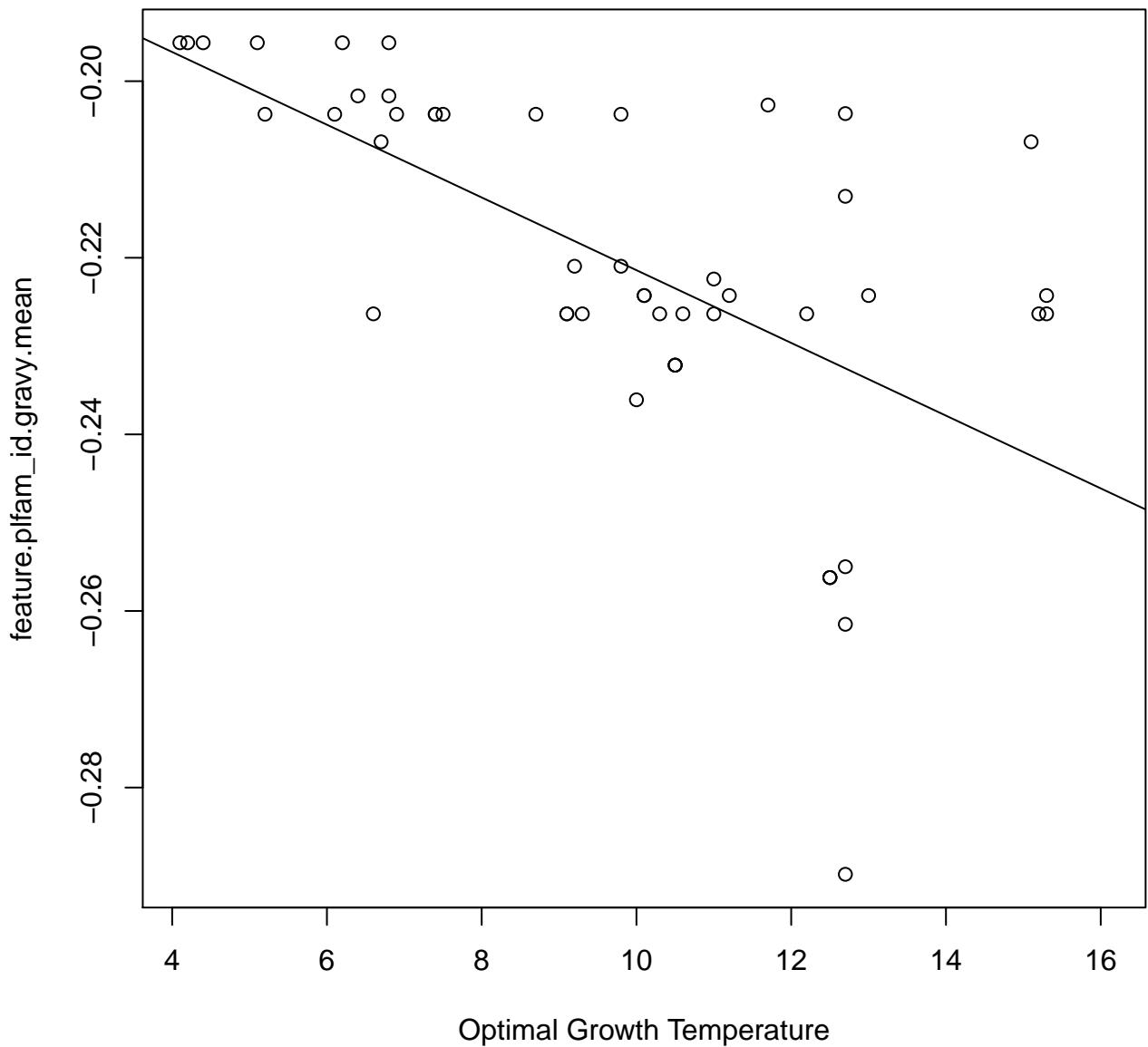
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Threonine efflux protein



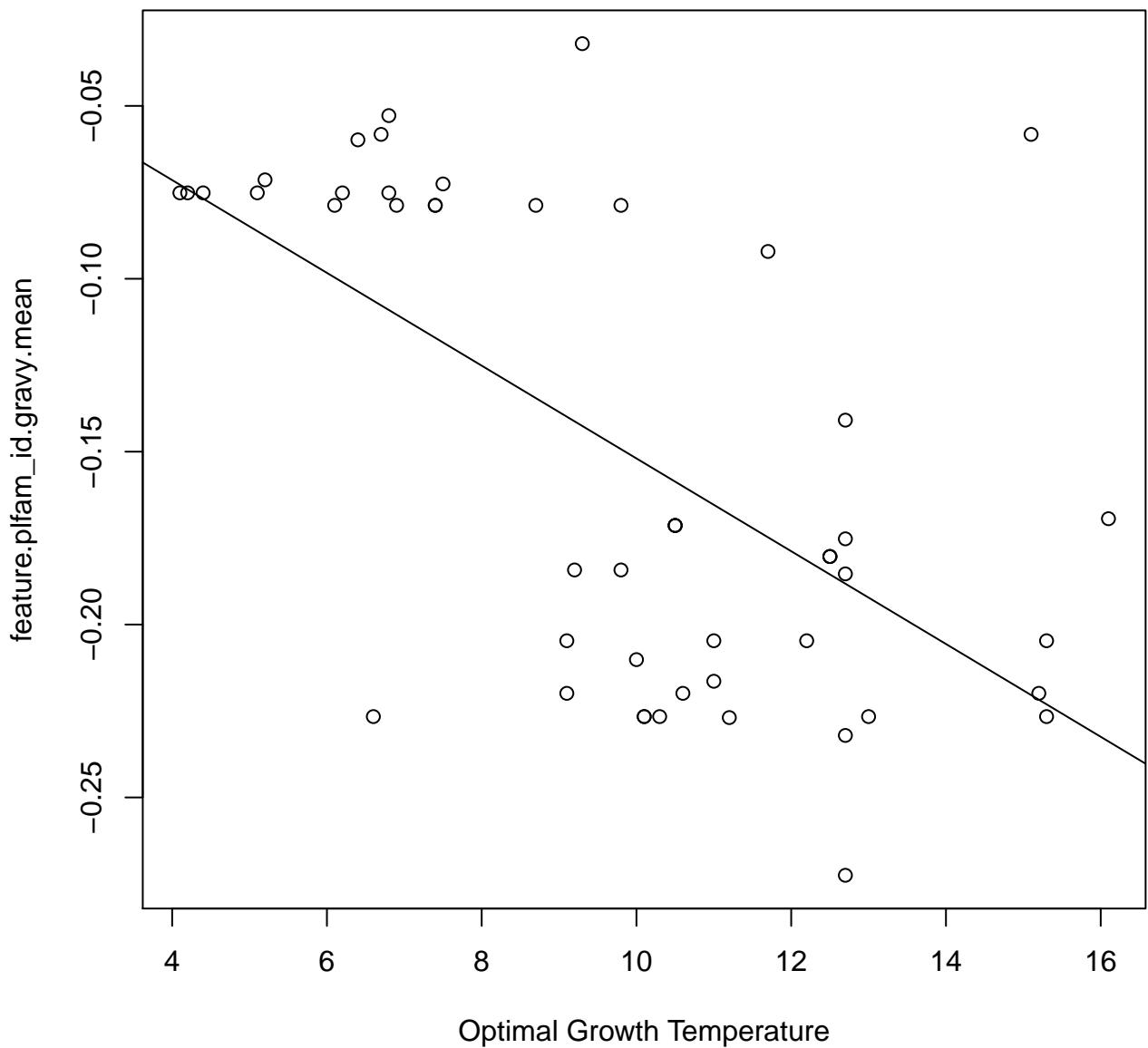
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Orn/DAP/Arg family decarboxylase



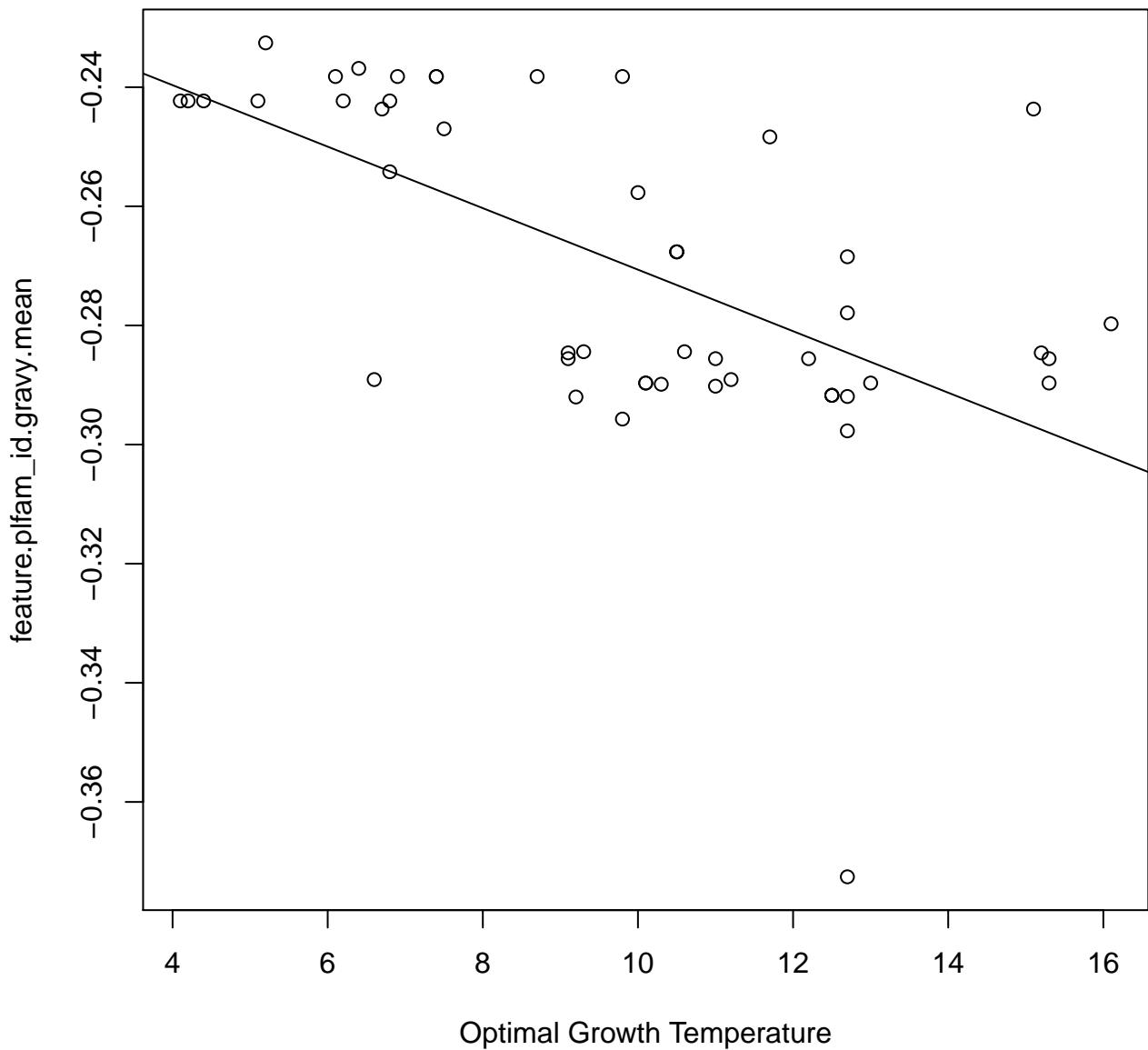
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DNA-binding transcriptional regulator, MocR family / aminotransferase domain



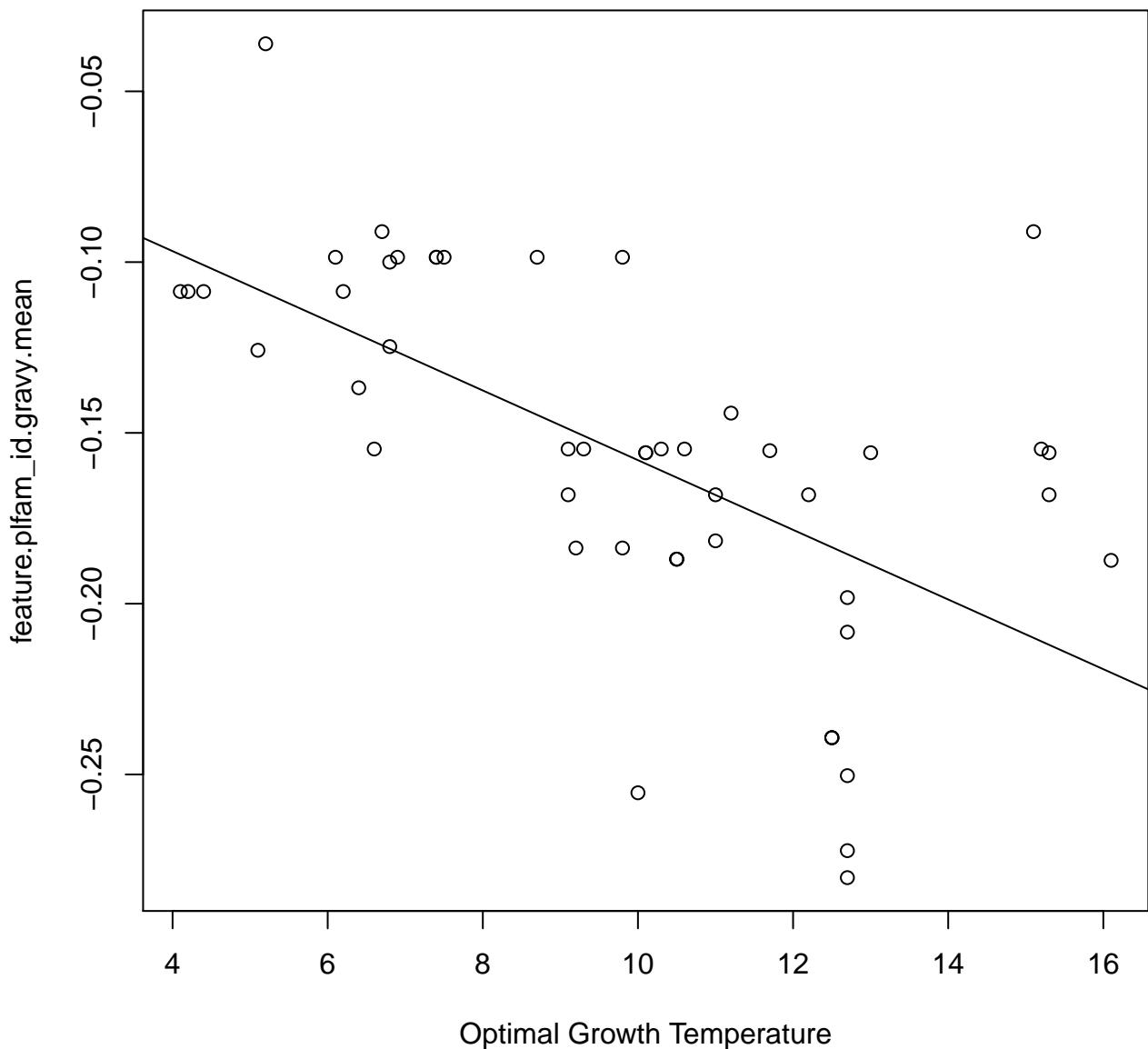
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General secretion pathway protein K



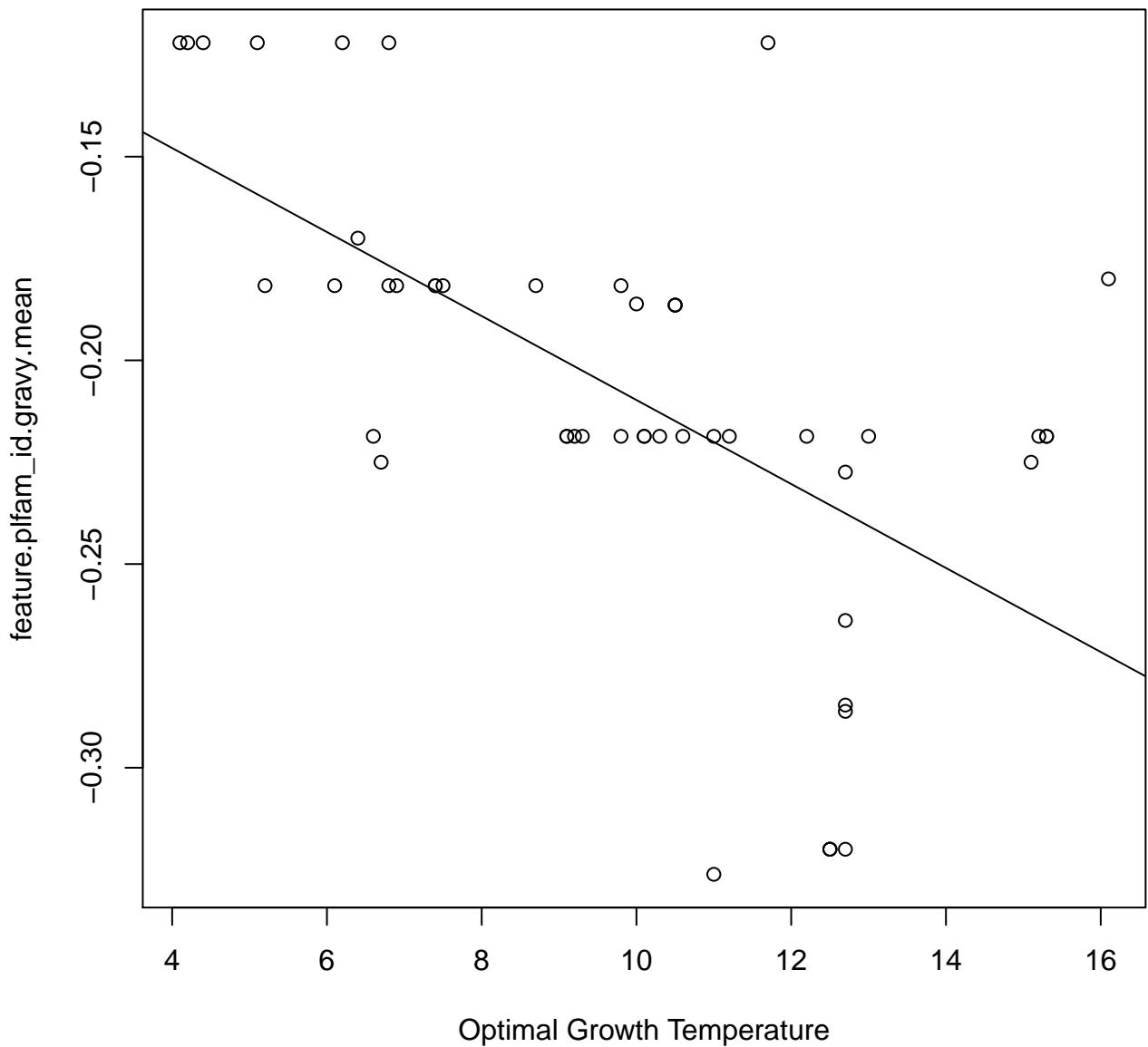
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2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.12)



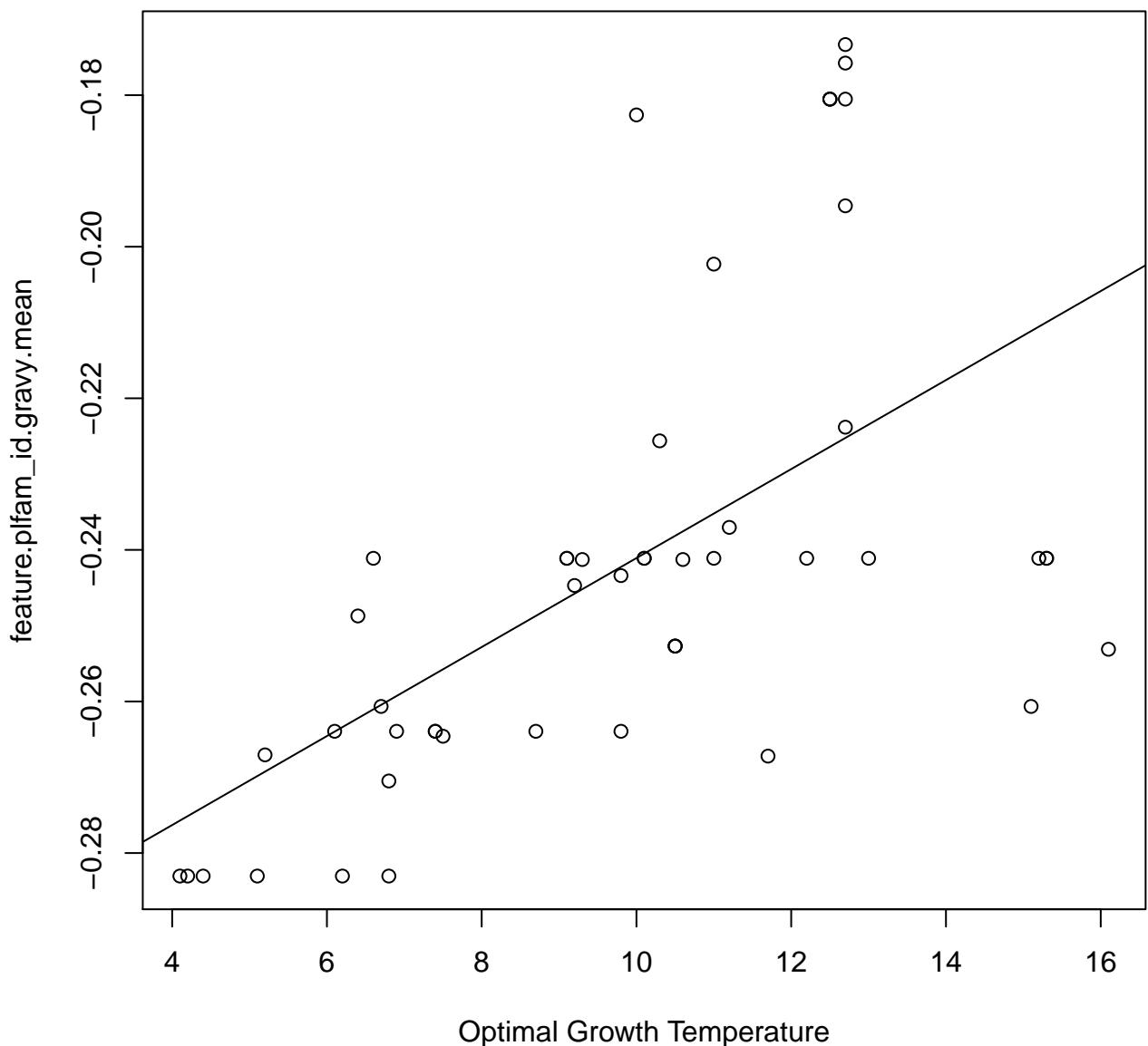
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Peptidase, M23/M37 family



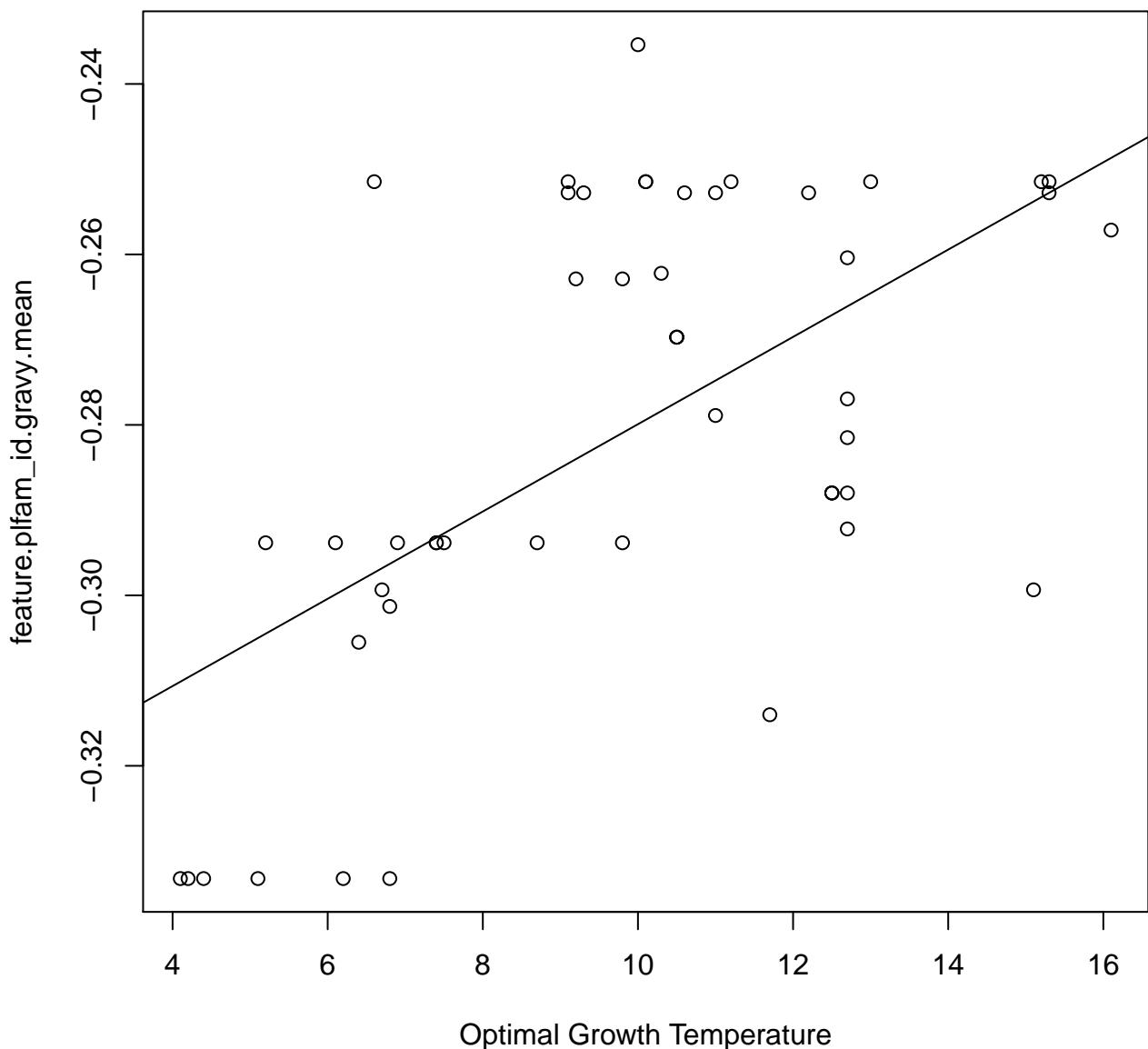
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FIG002473: Protein YcaR in KDO2-Lipid A biosynthesis cluster



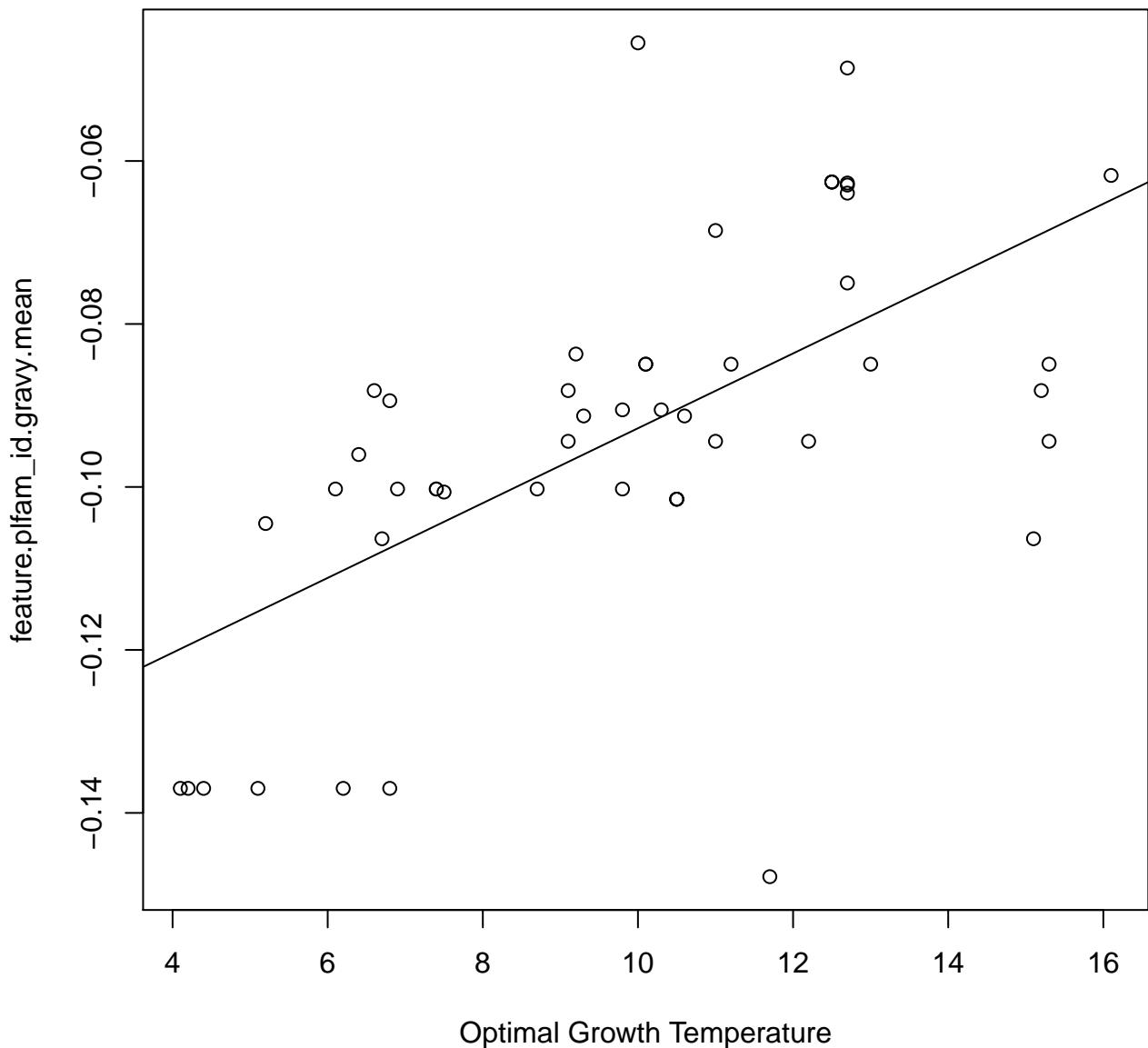
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Protein kinase



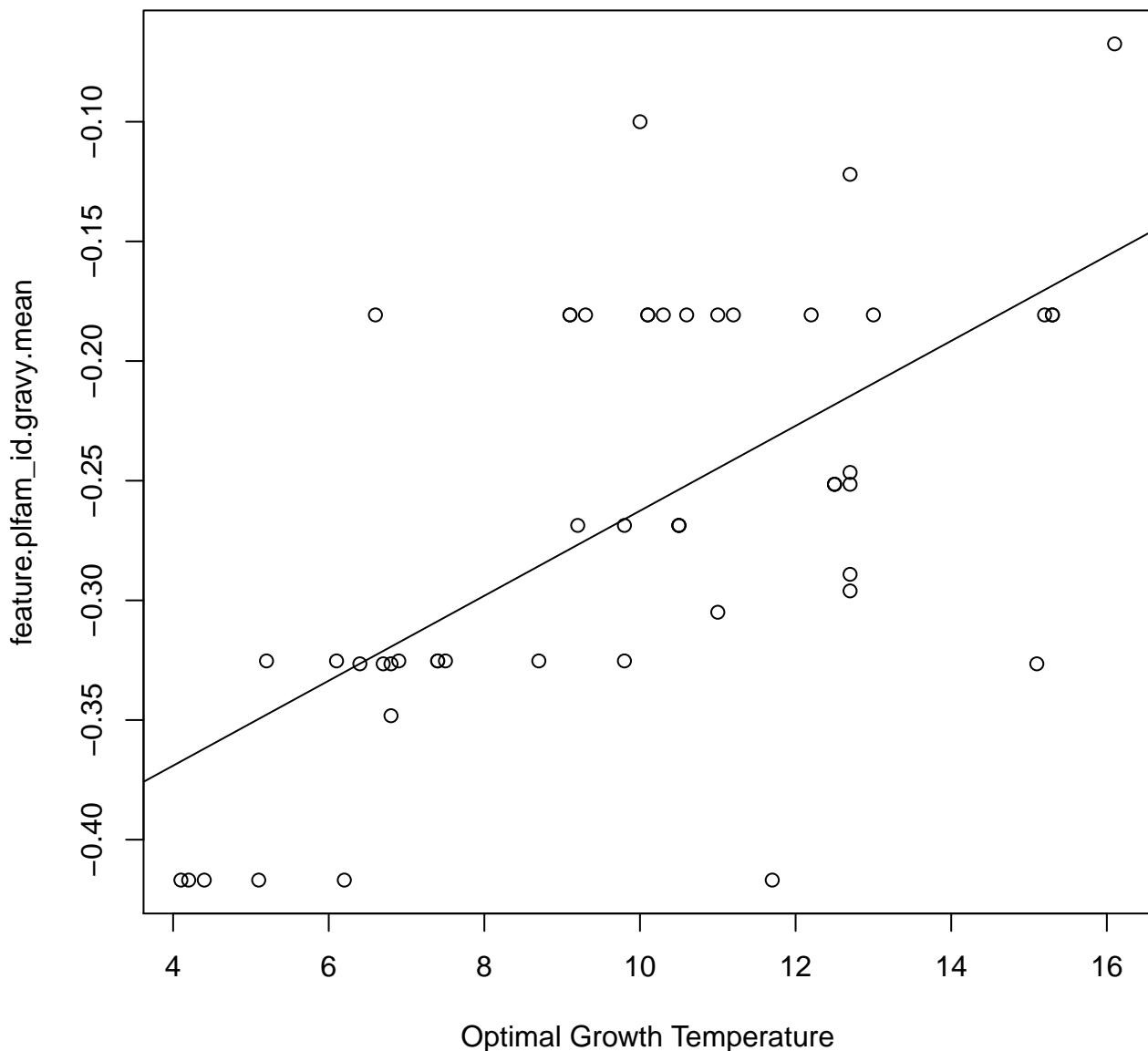
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GTP cyclohydrolase I (EC 3.5.4.16) type 2



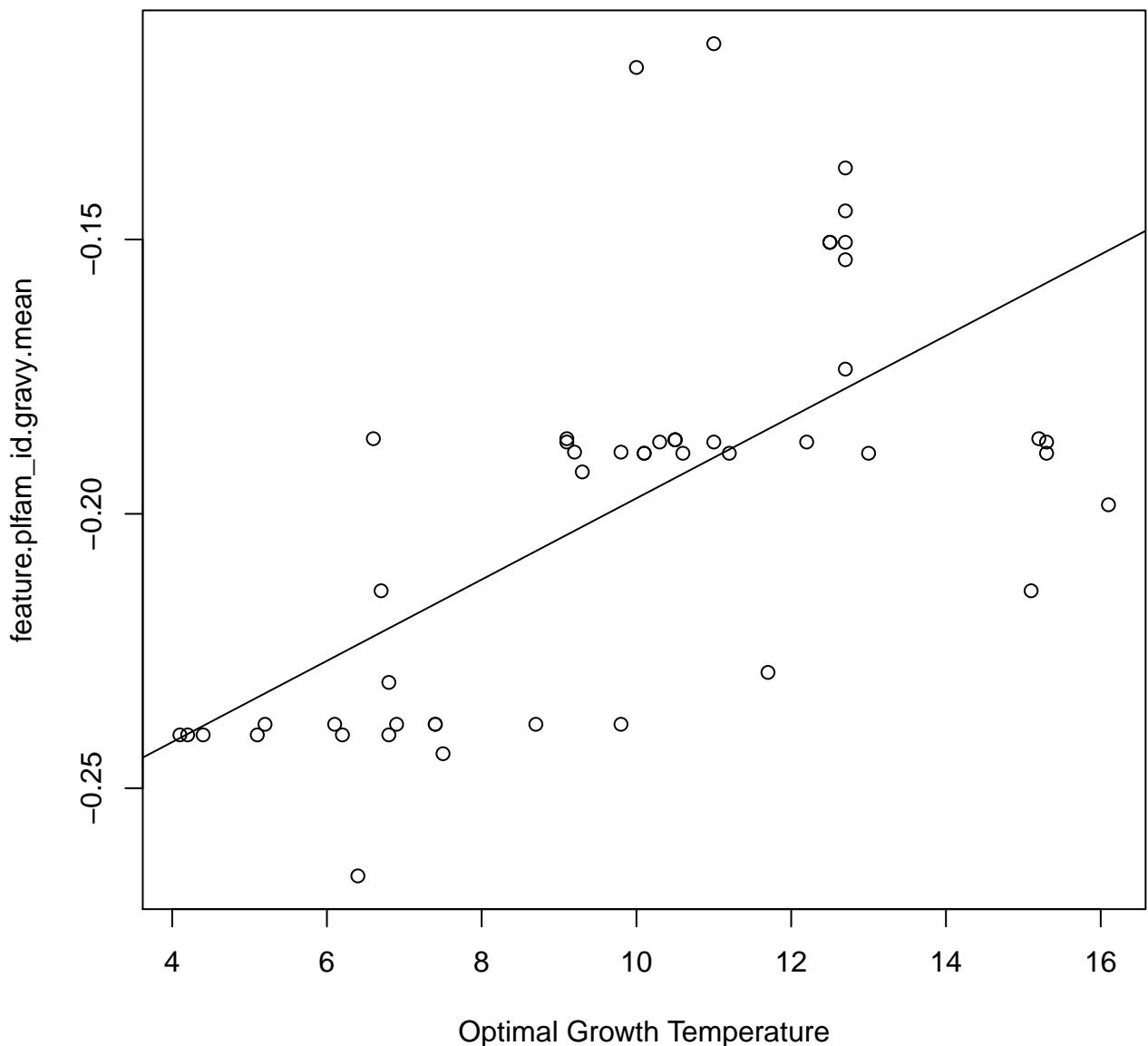
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Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)



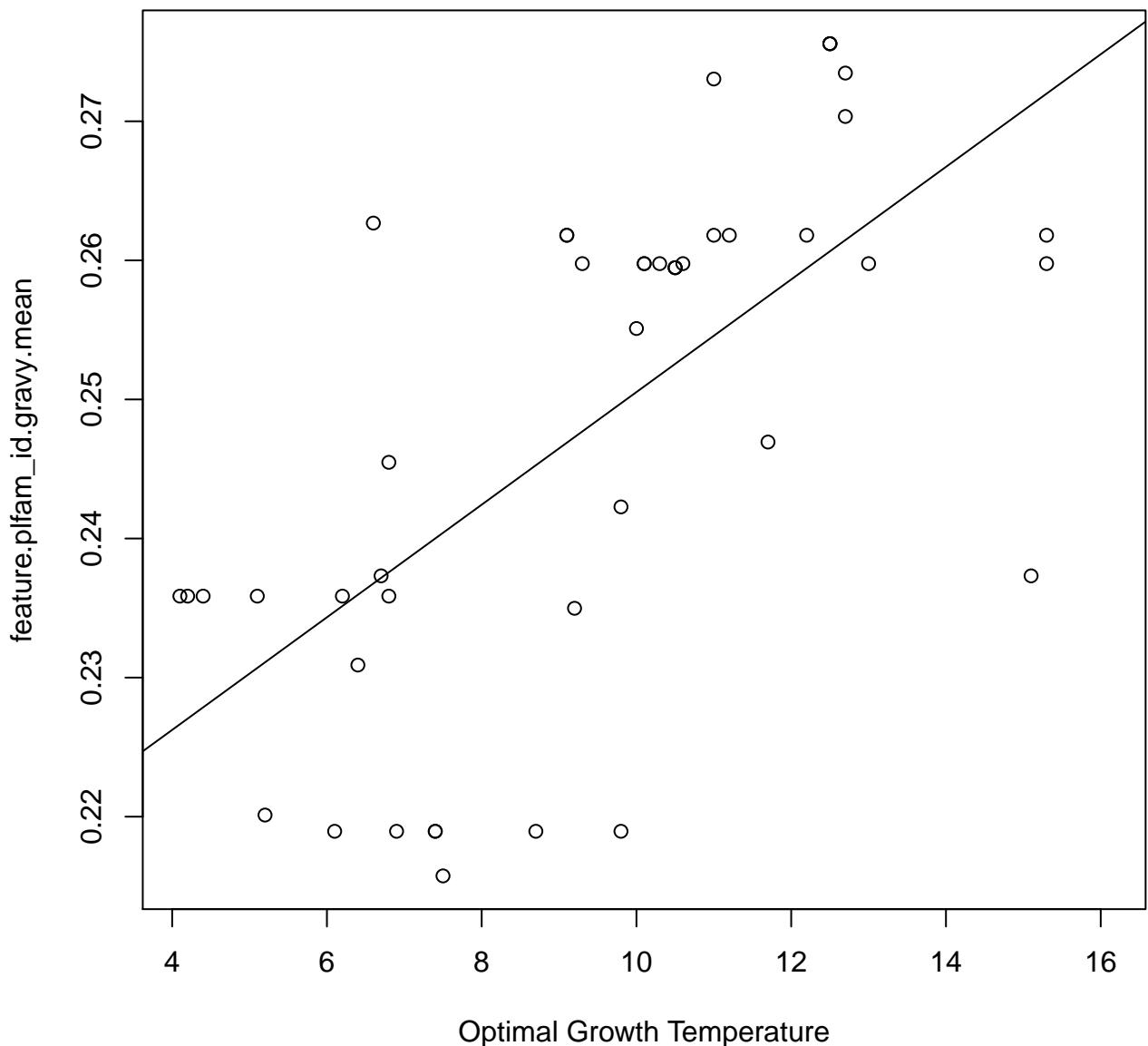
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Succinate dehydrogenase flavin-adding protein, antitoxin of CptAB toxin–antitoxin



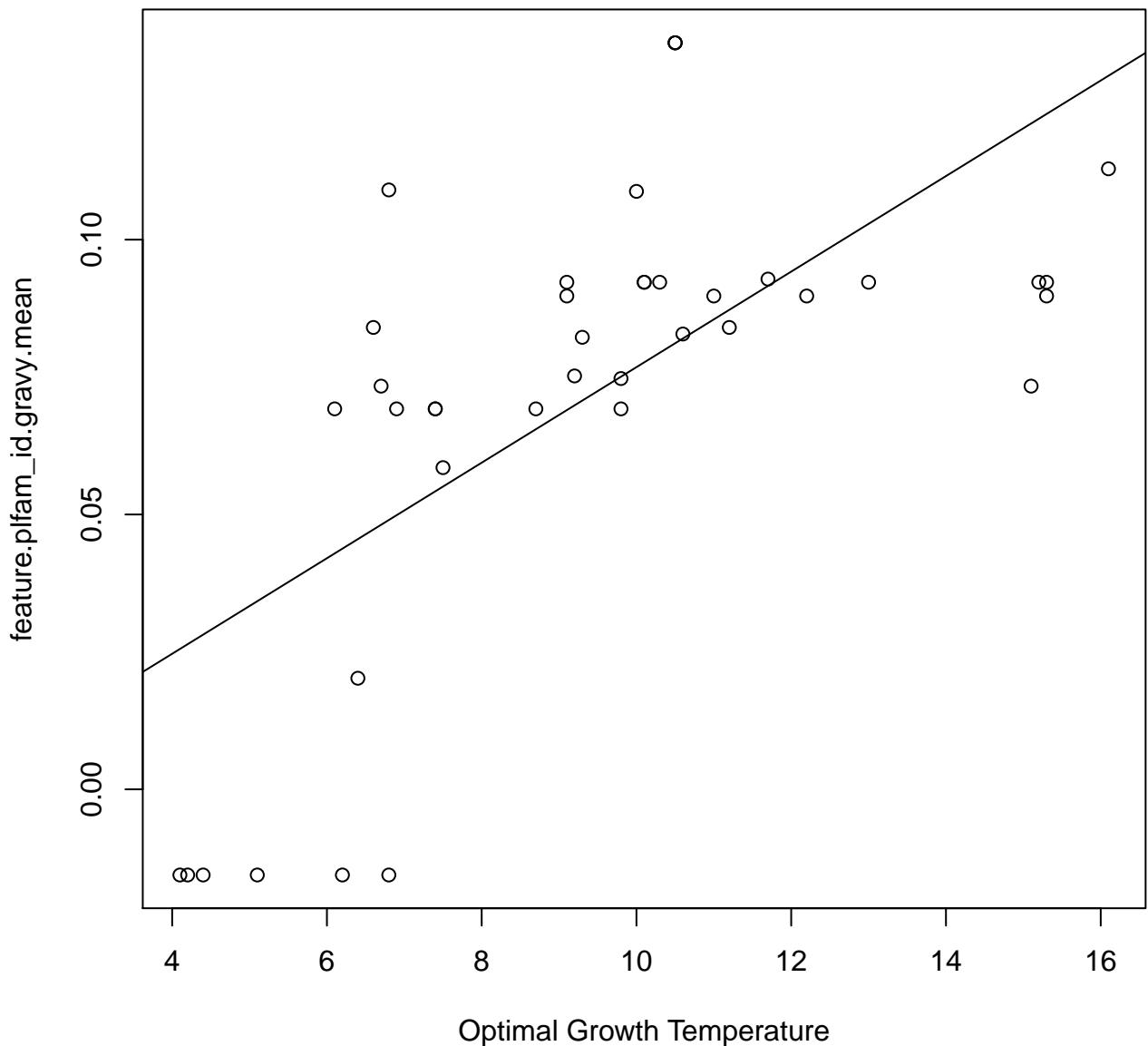
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Exported zinc metalloprotease YfgC precursor



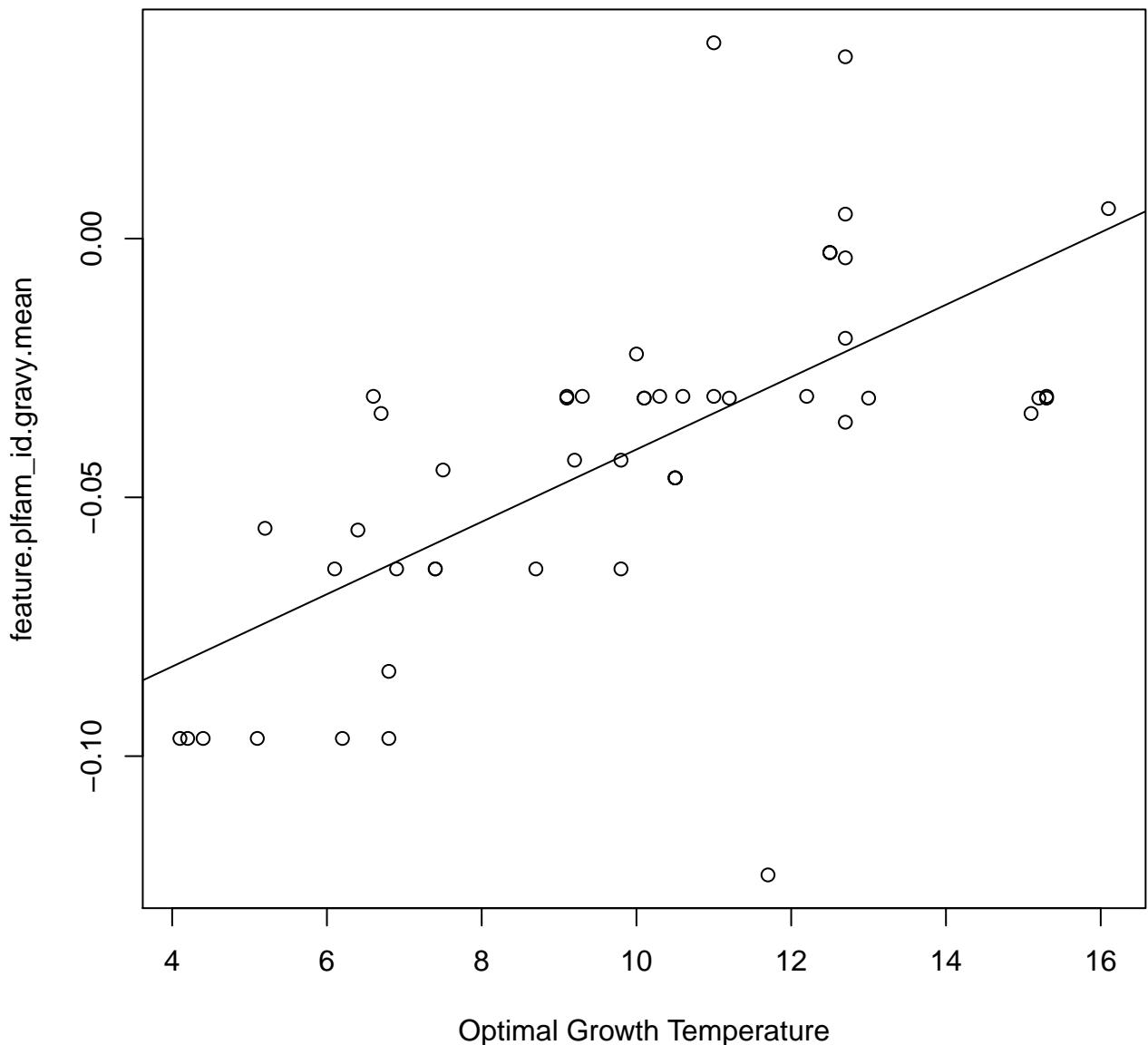
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Selenide,water dikinase (EC 2.7.9.3)



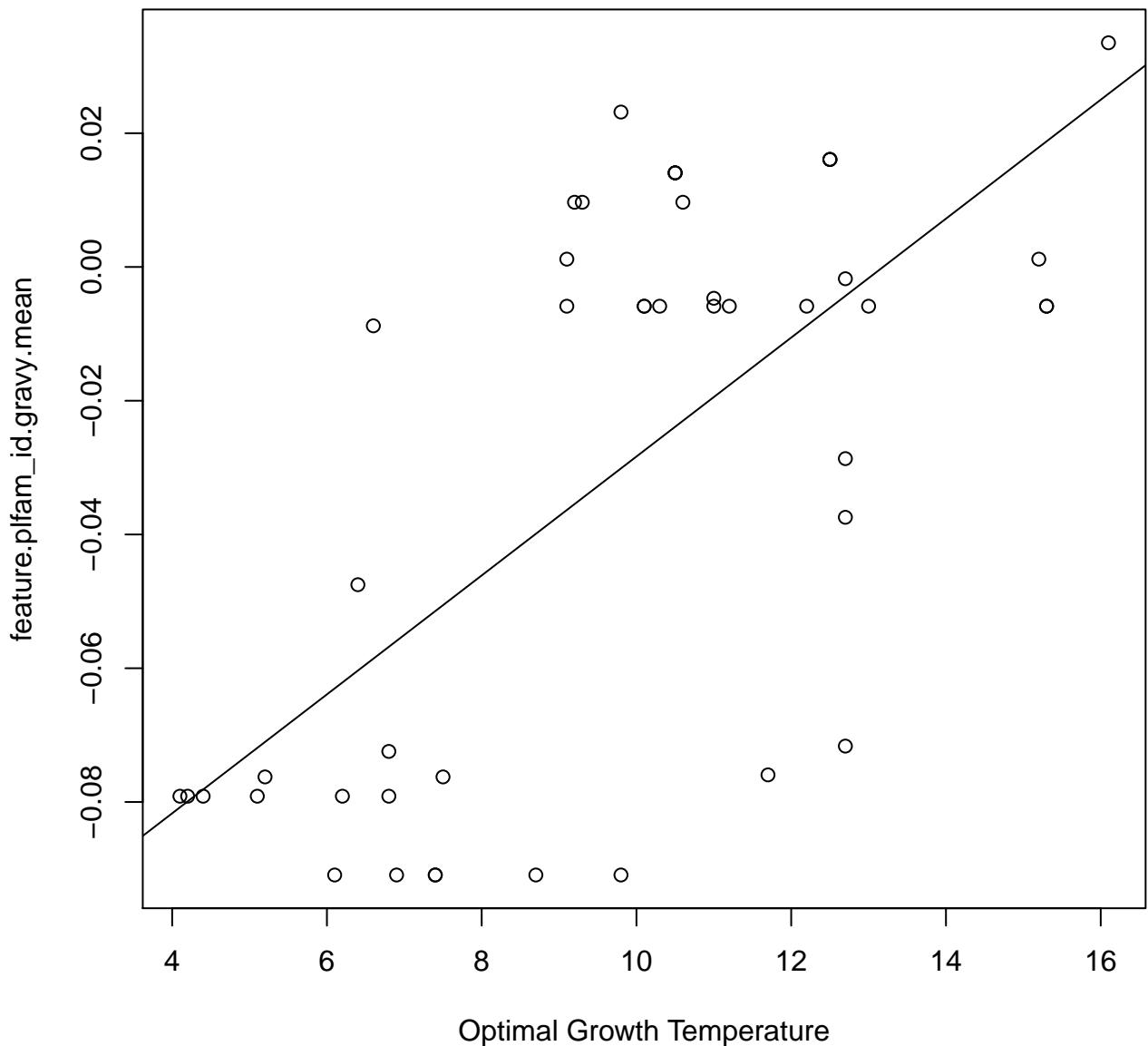
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Invasin domain protein



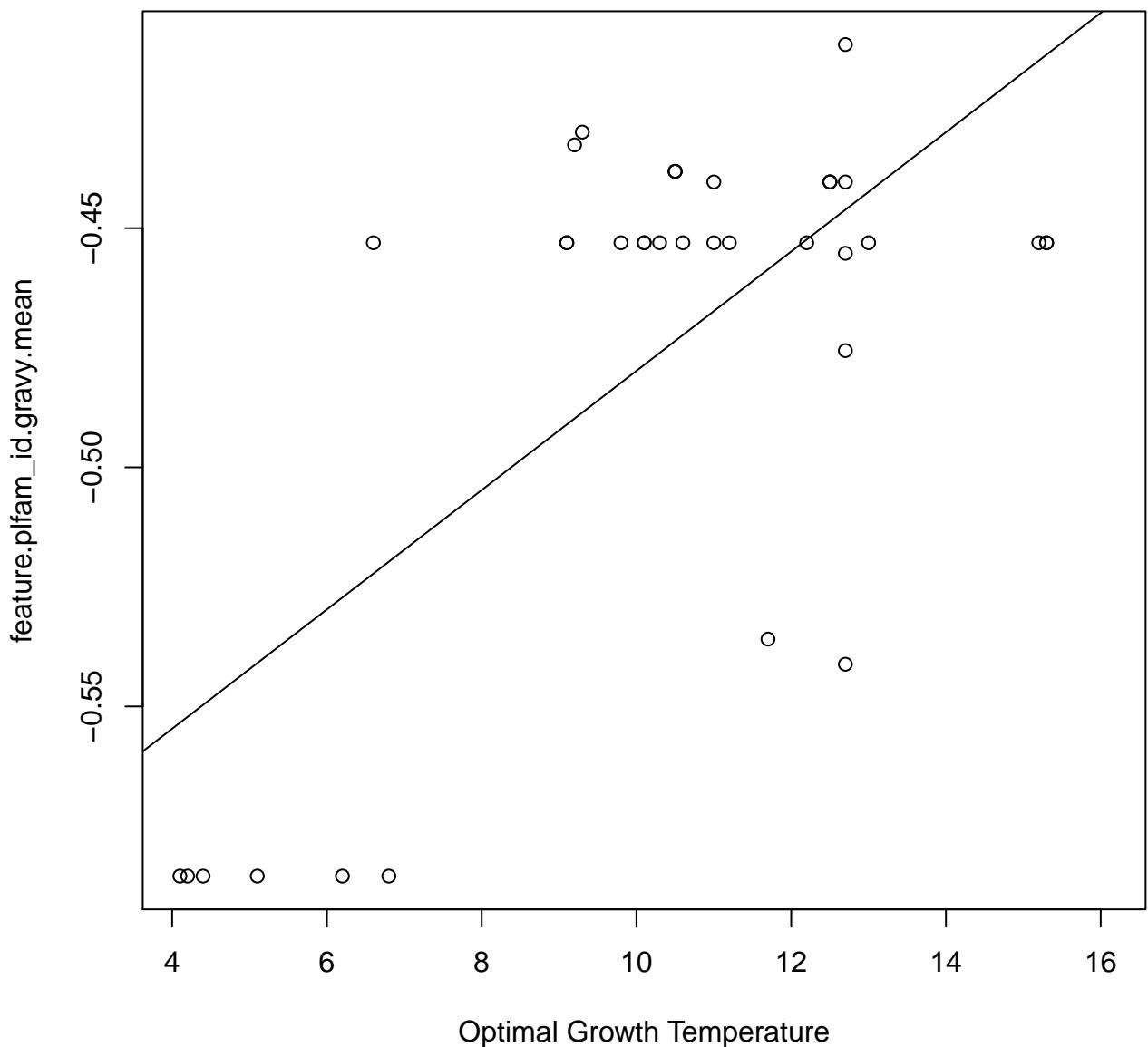
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6-carboxy-5,6,7,8-tetrahydropterin synthase (EC 4.1.2.50)



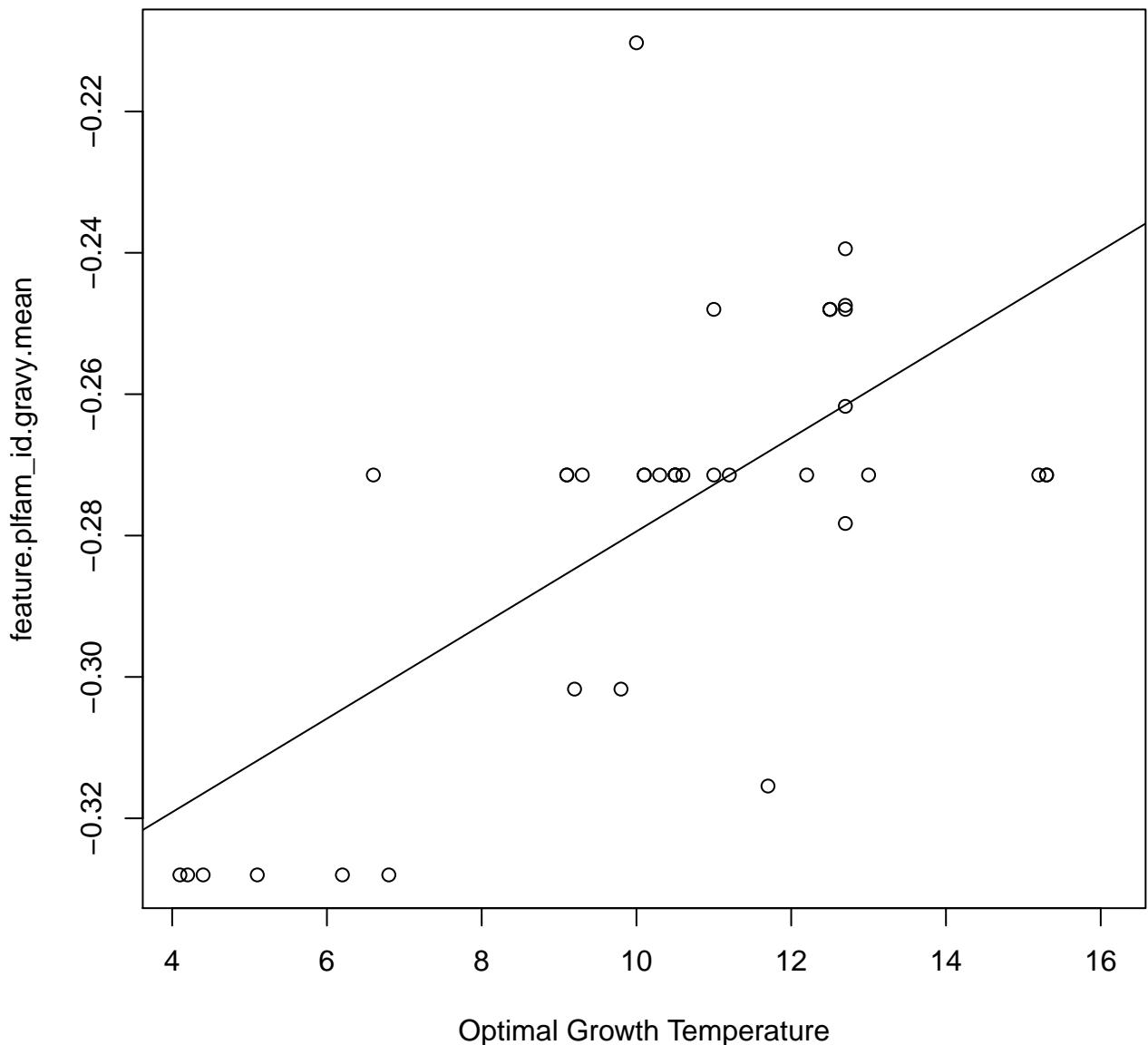
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Zinc-type alcohol dehydrogenase-like protein



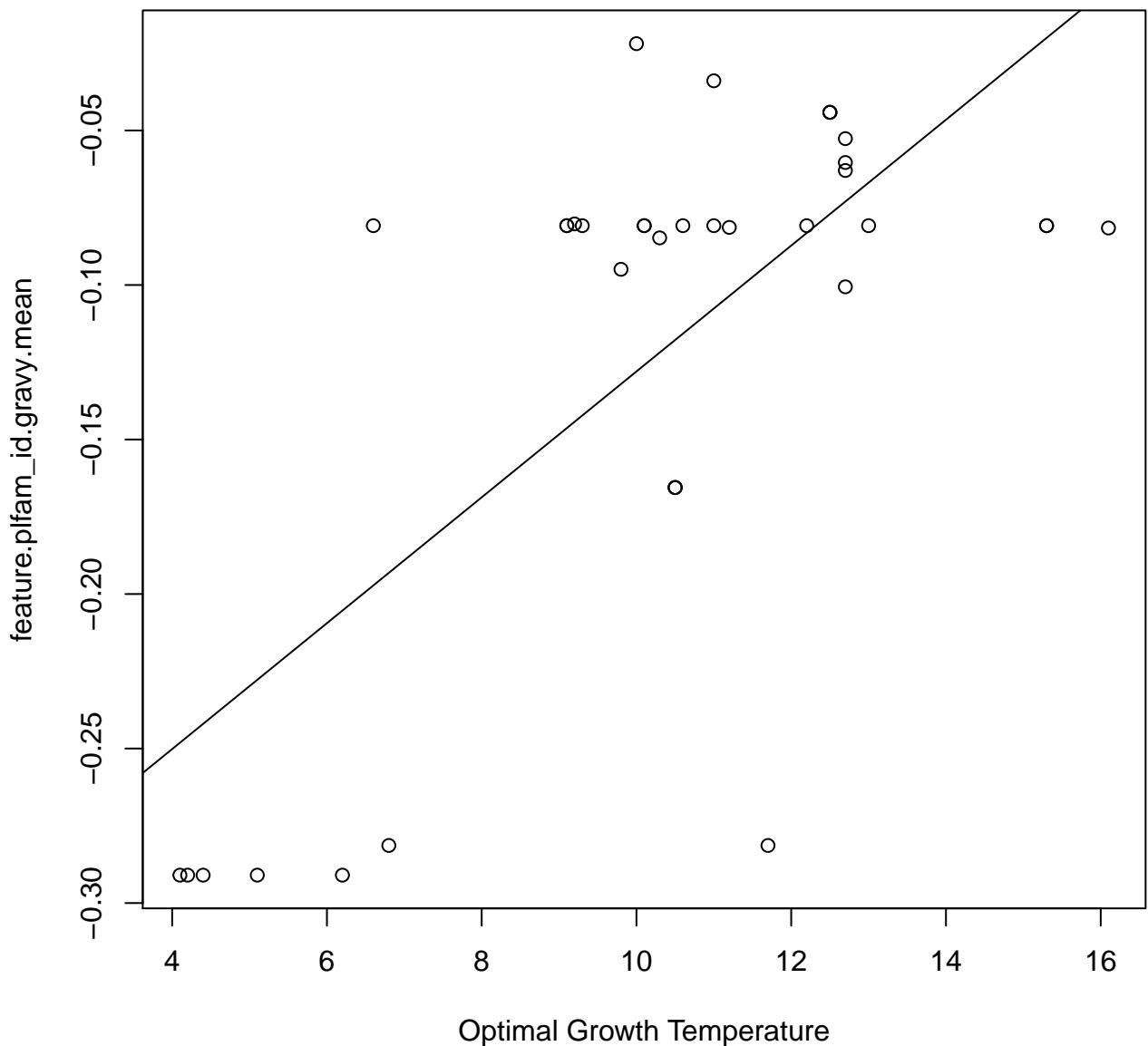
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hypothetical protein



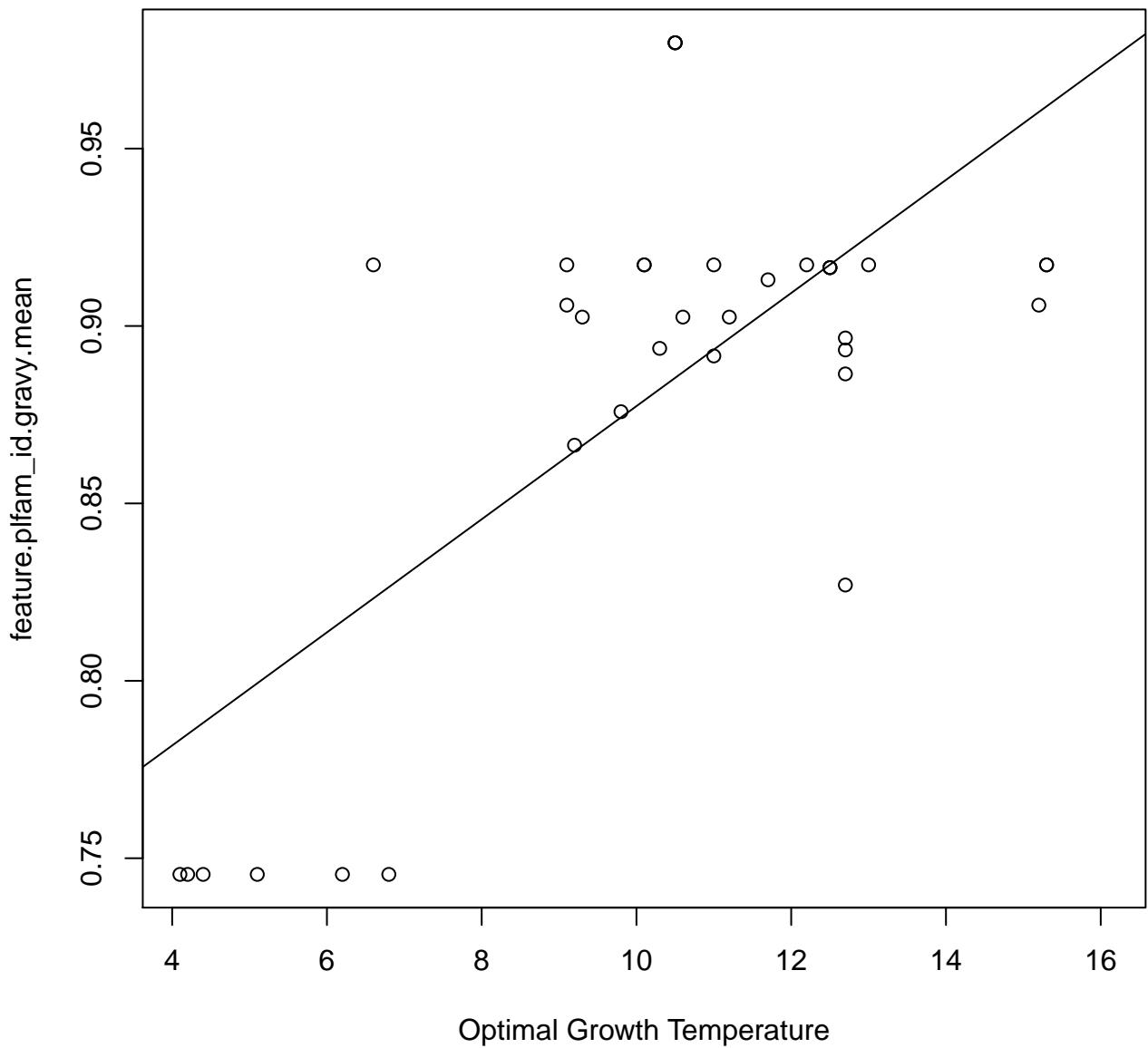
feature.plfam_id.gravy.mean
PLF_28228_00001835
Bacterial non-heme ferritin (EC 1.16.3.2)



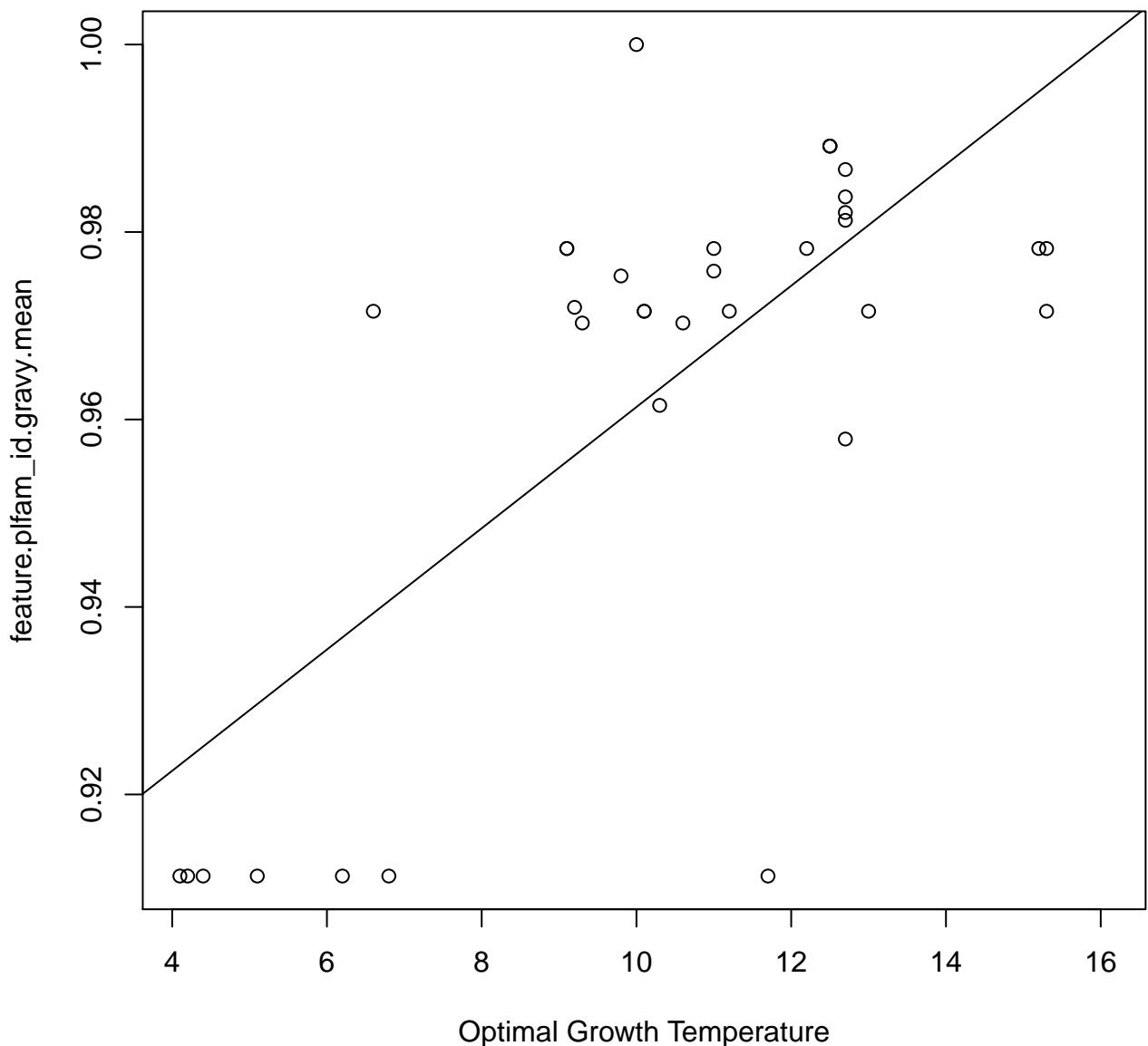
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Ureidoglycolate lyase (EC 4.3.2.3)



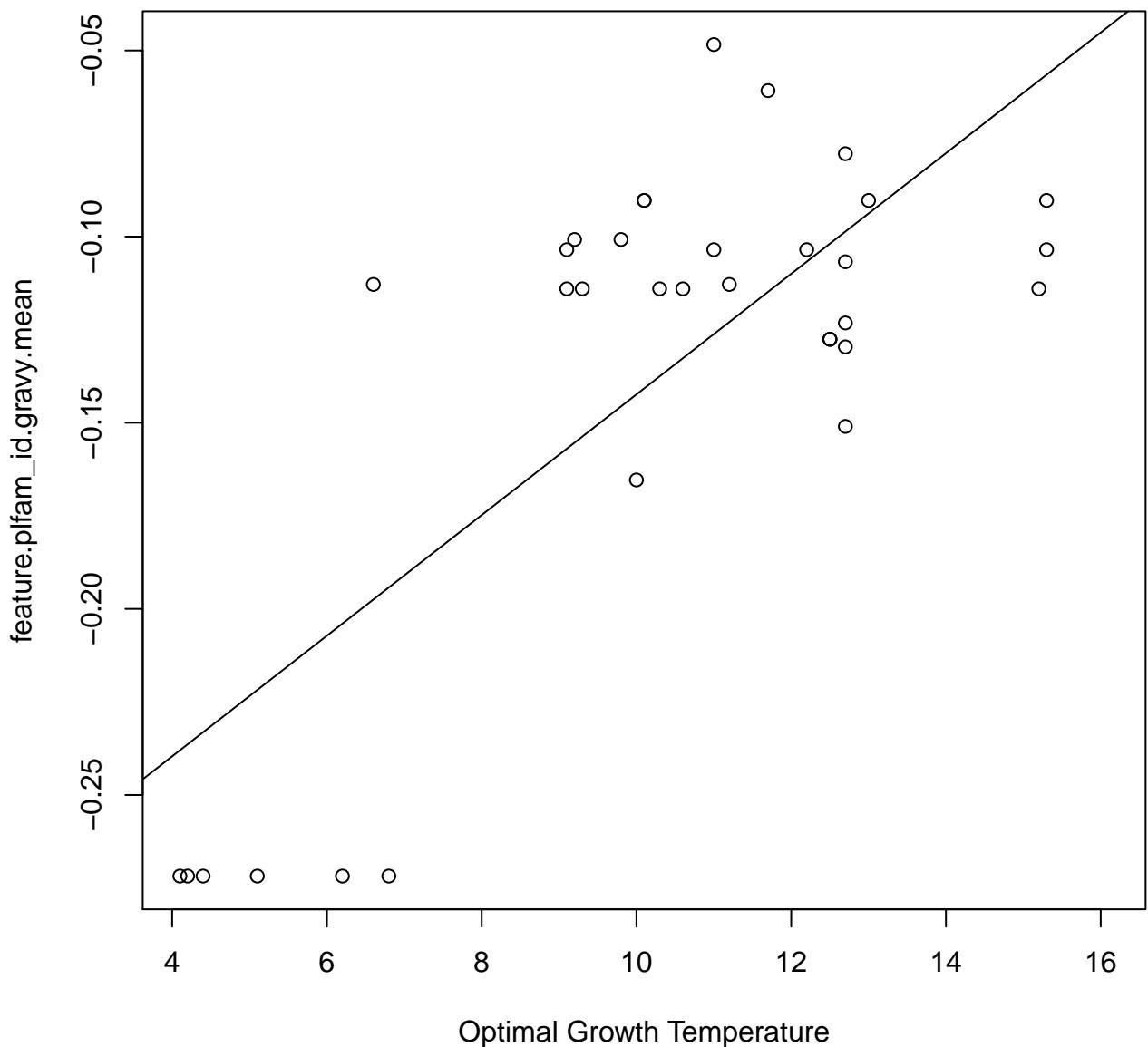
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ZIP zinc transporter family protein



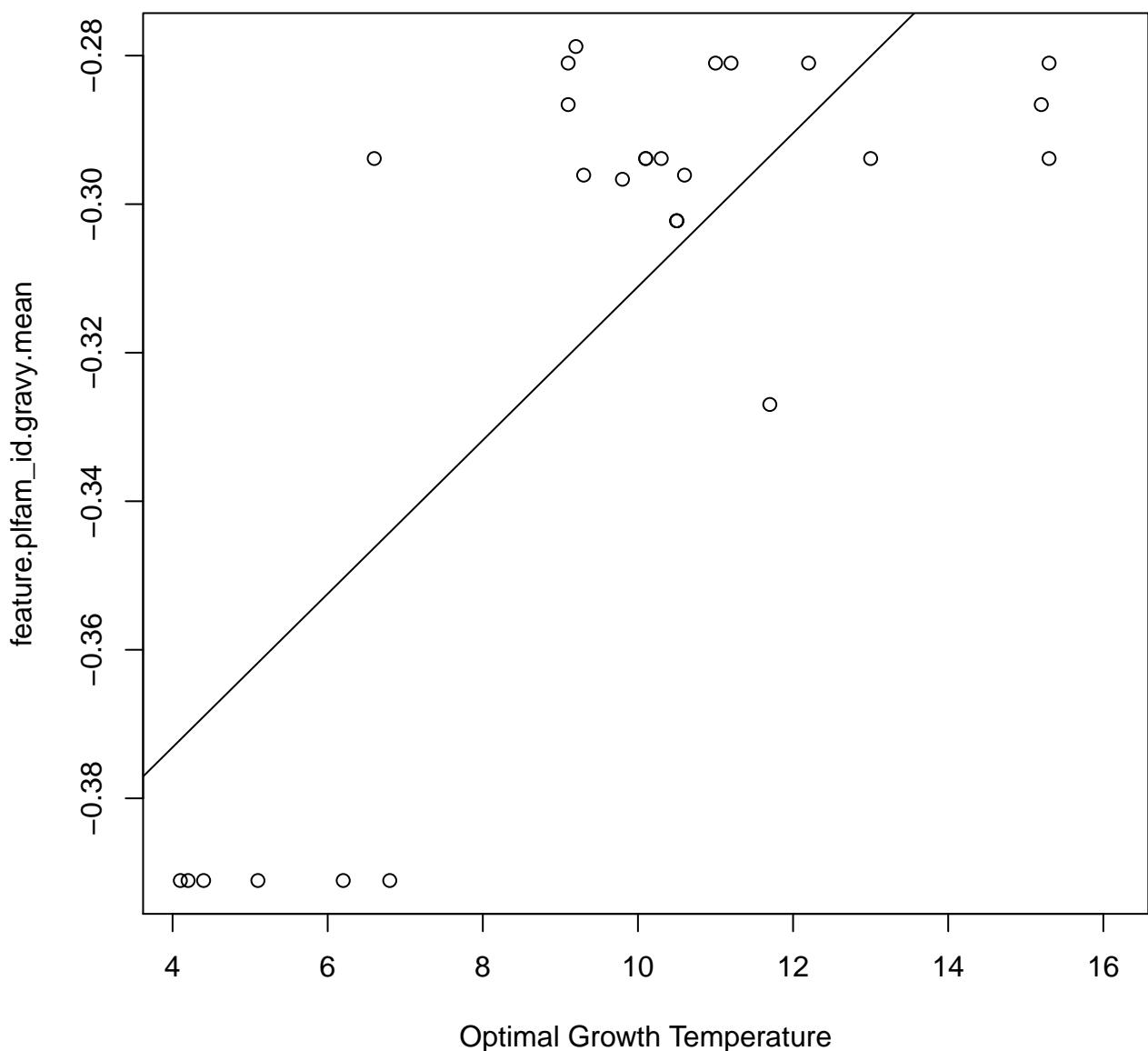
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LrgA-associated membrane protein LrgB



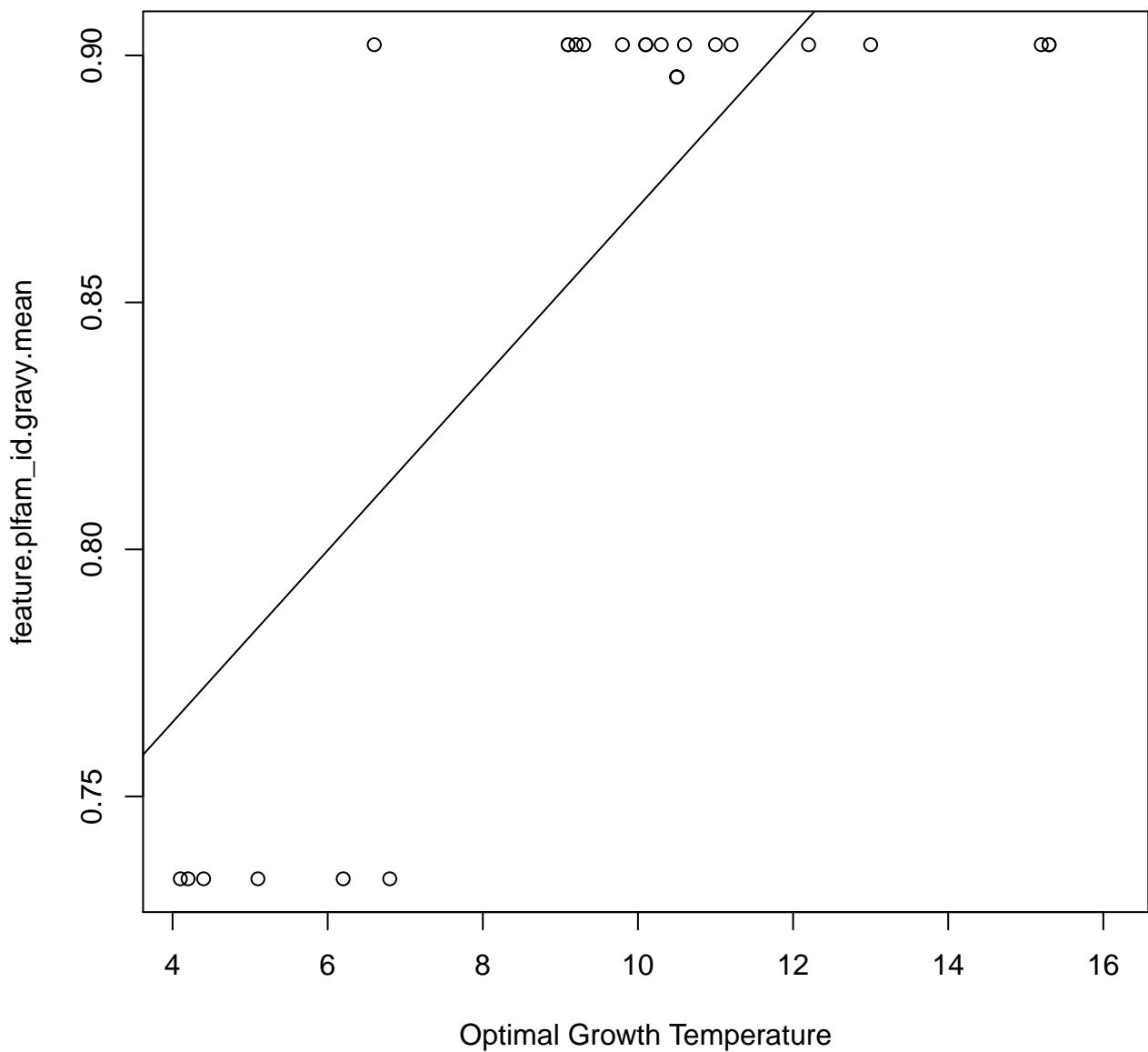
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hypothetical protein



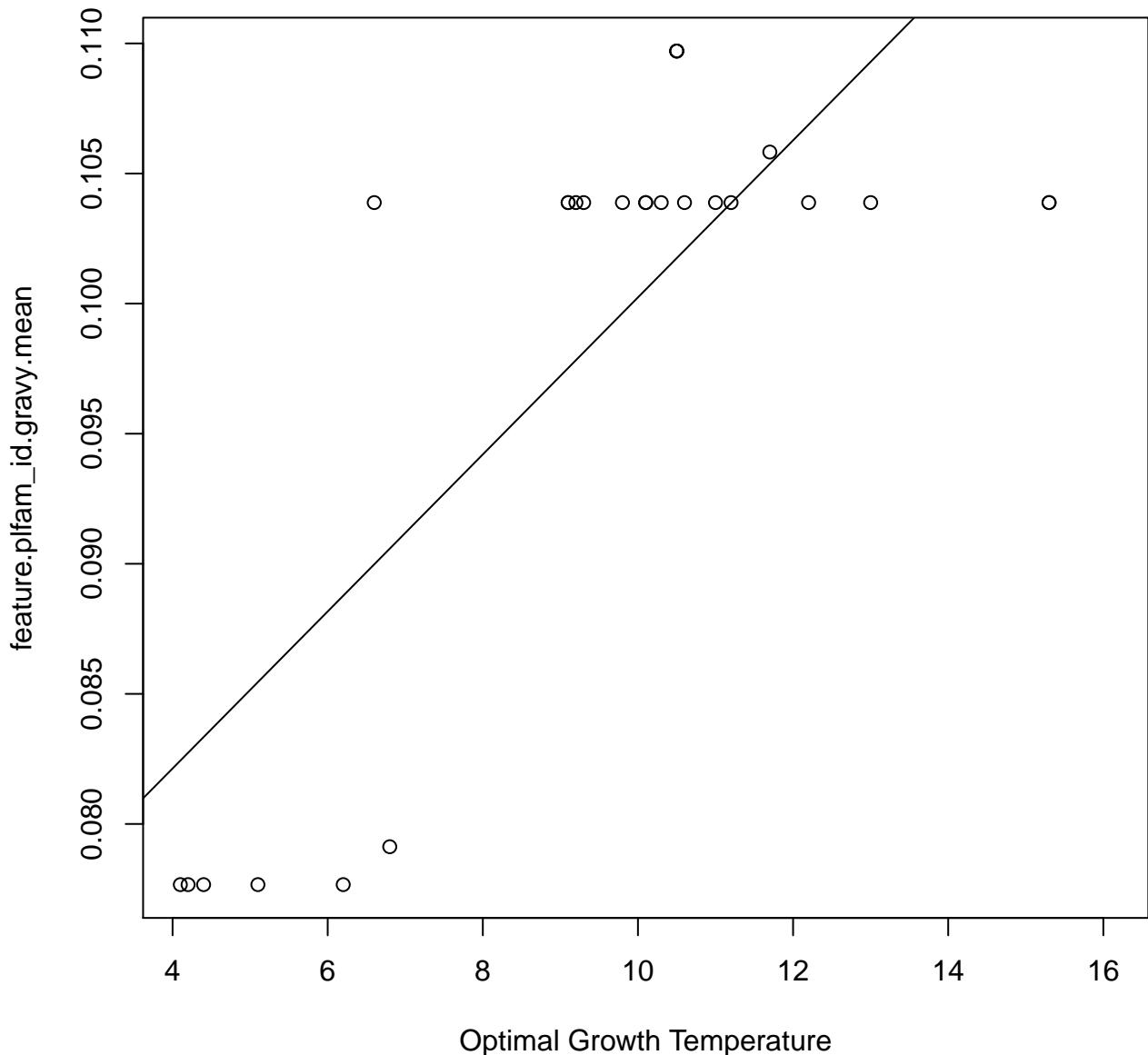
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hypothetical protein



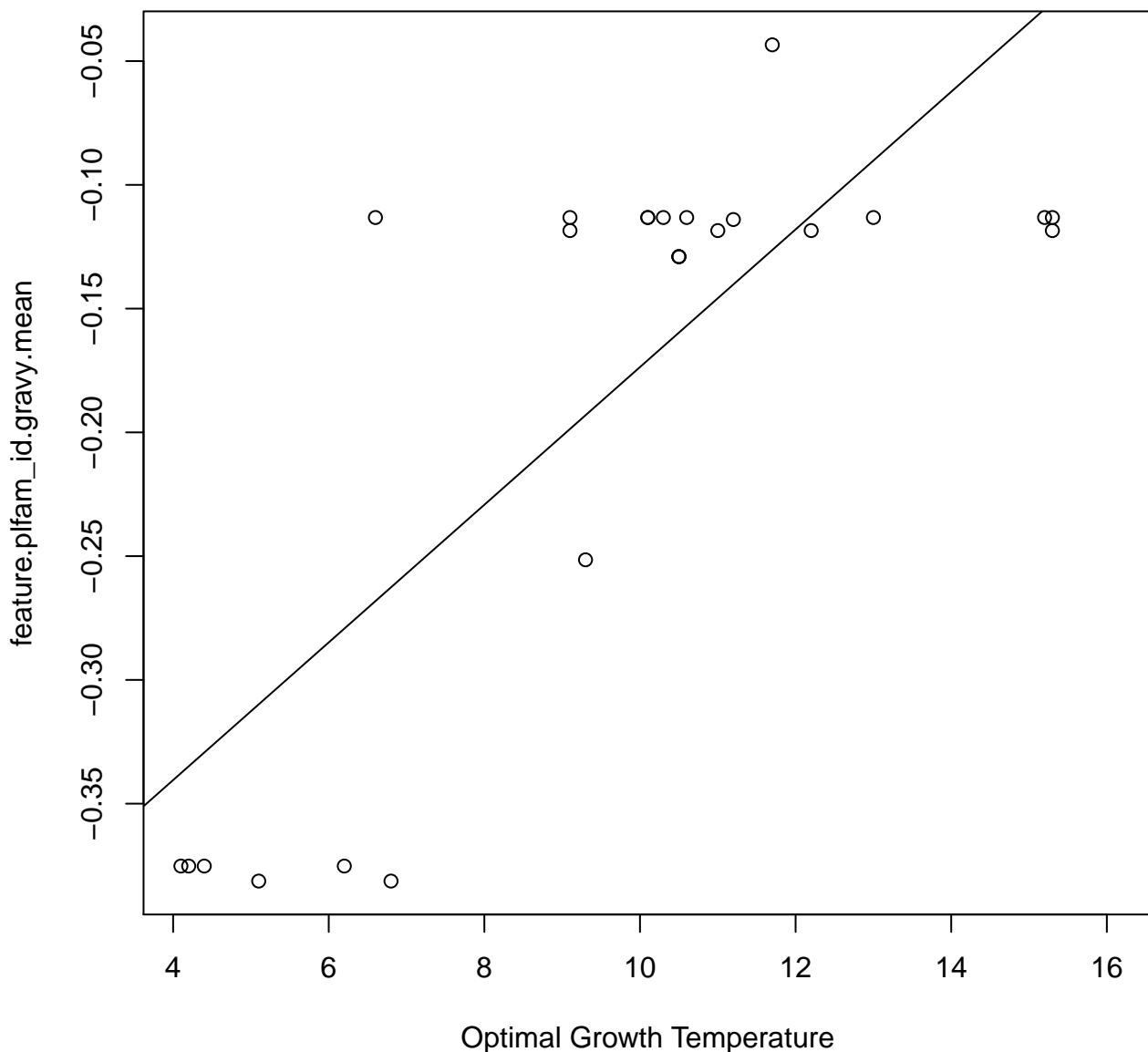
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hypothetical protein



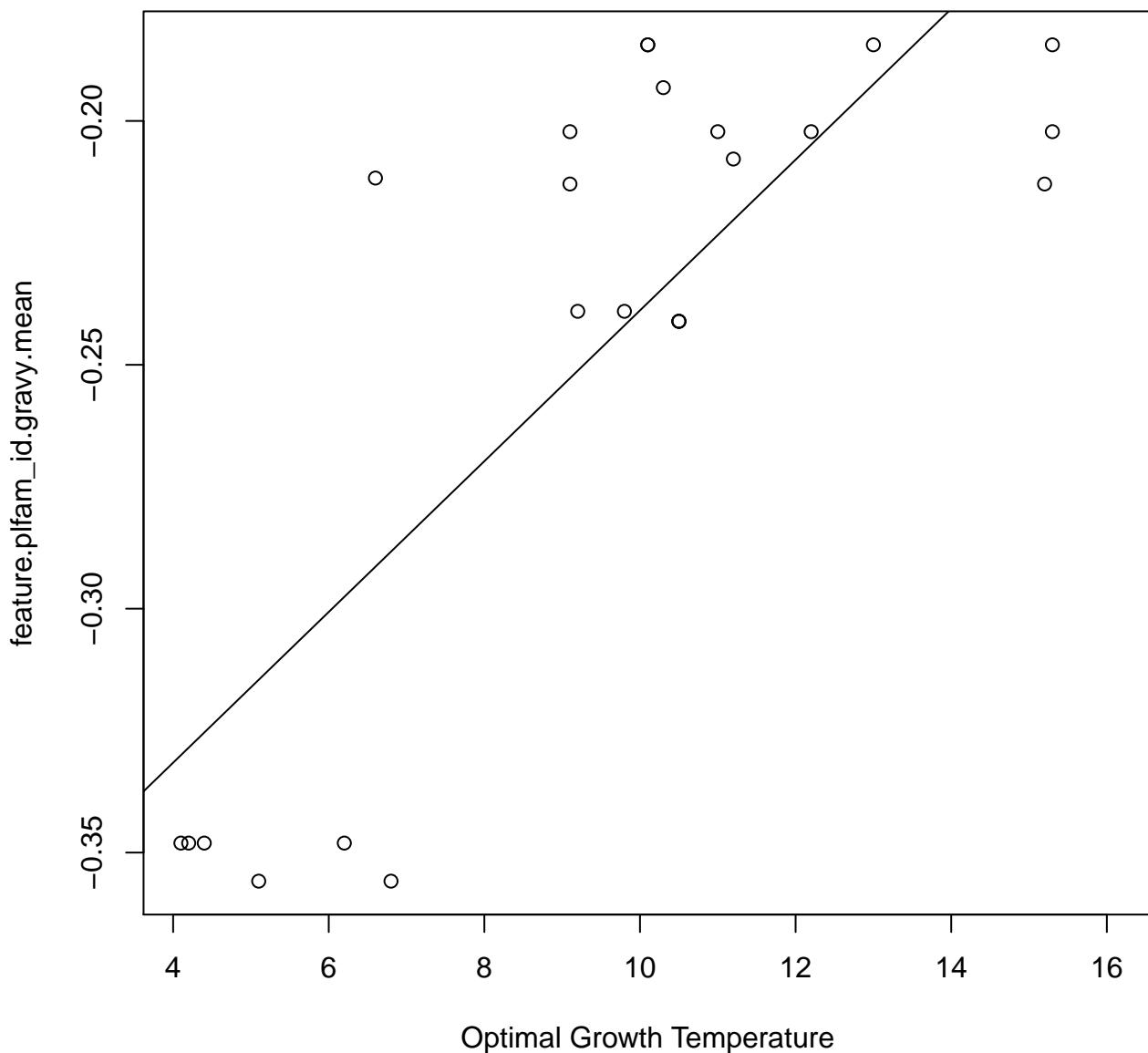
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hypothetical protein



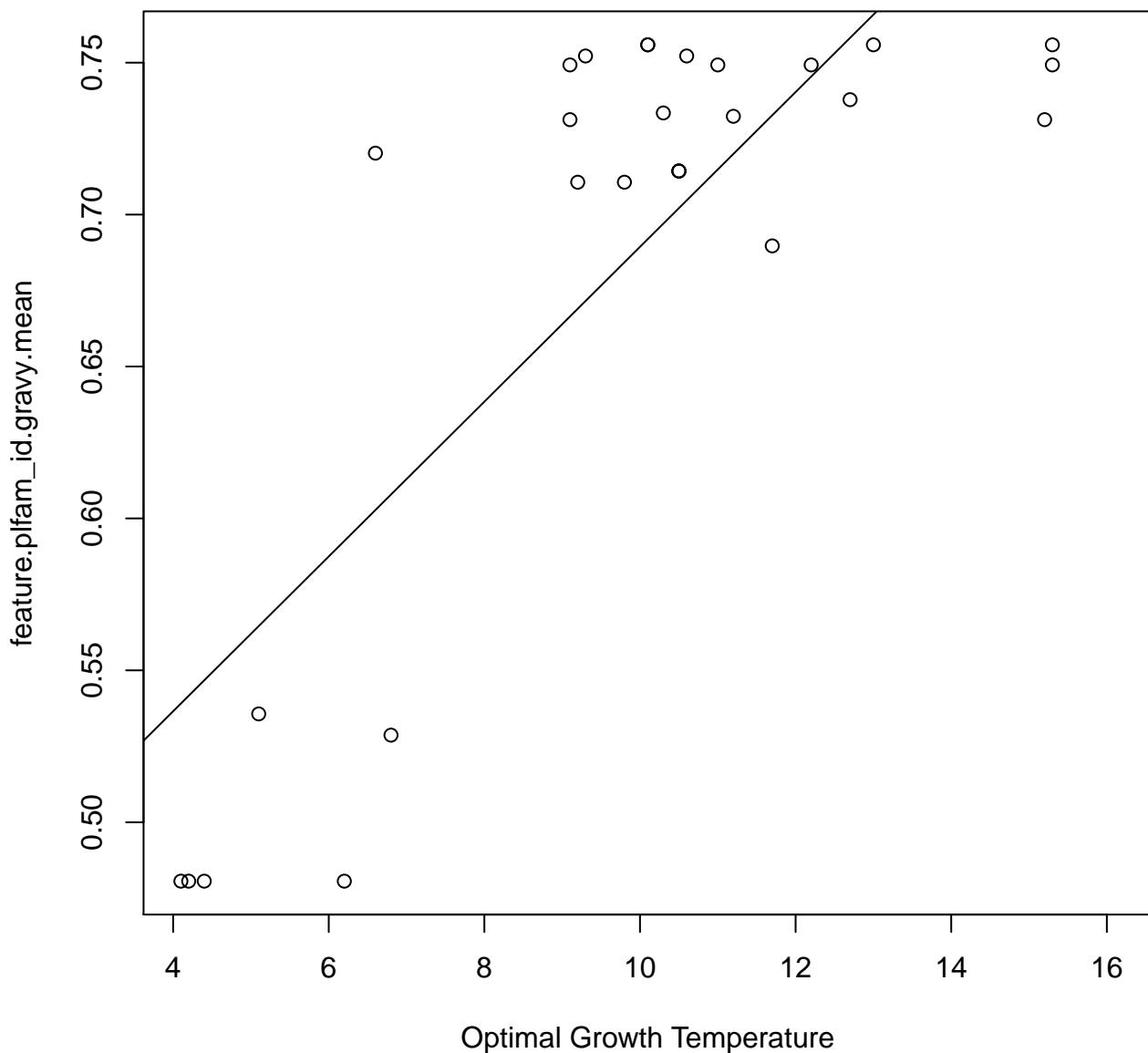
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Two-component system sensor histidine kinase



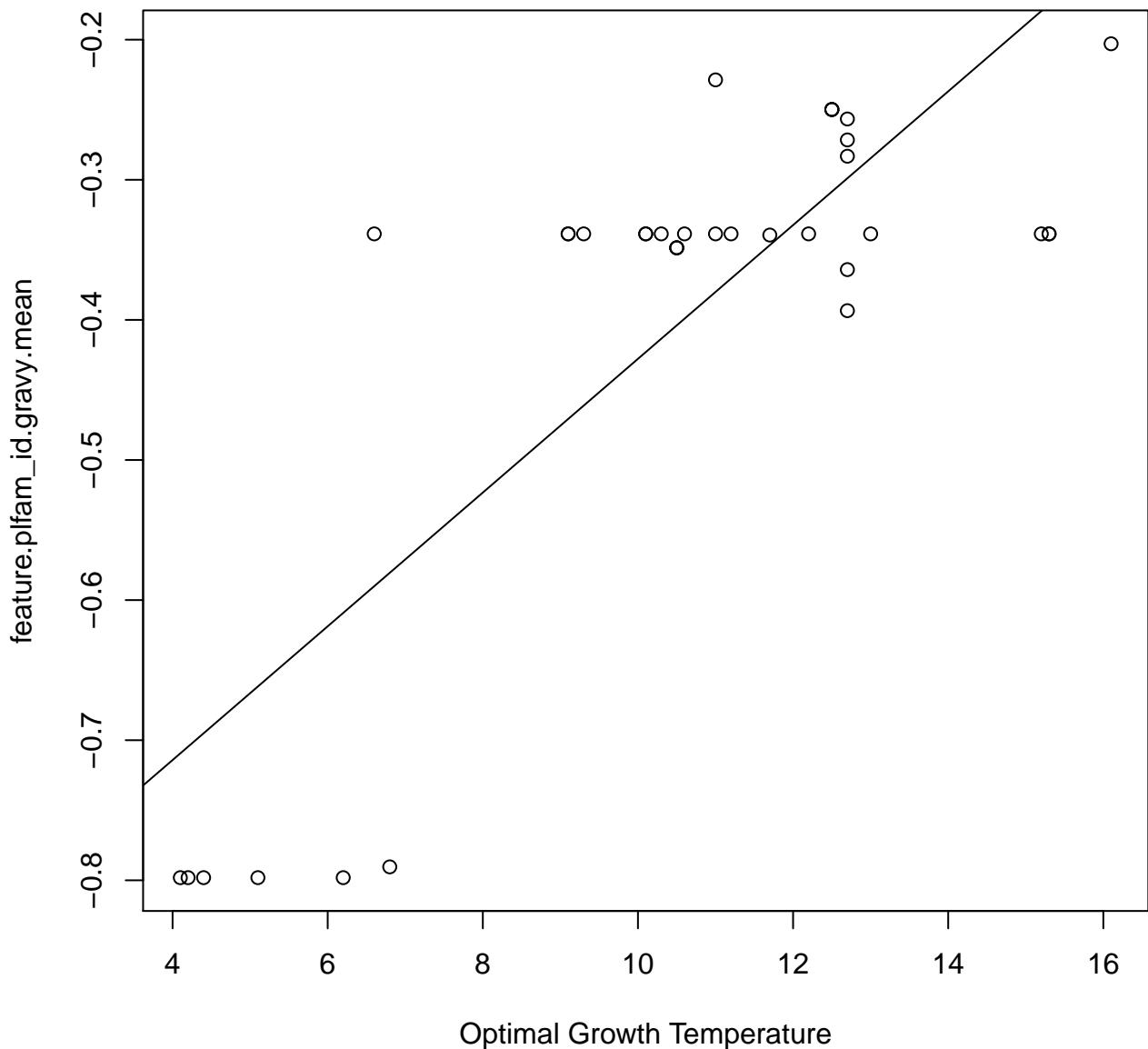
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HD domain protein



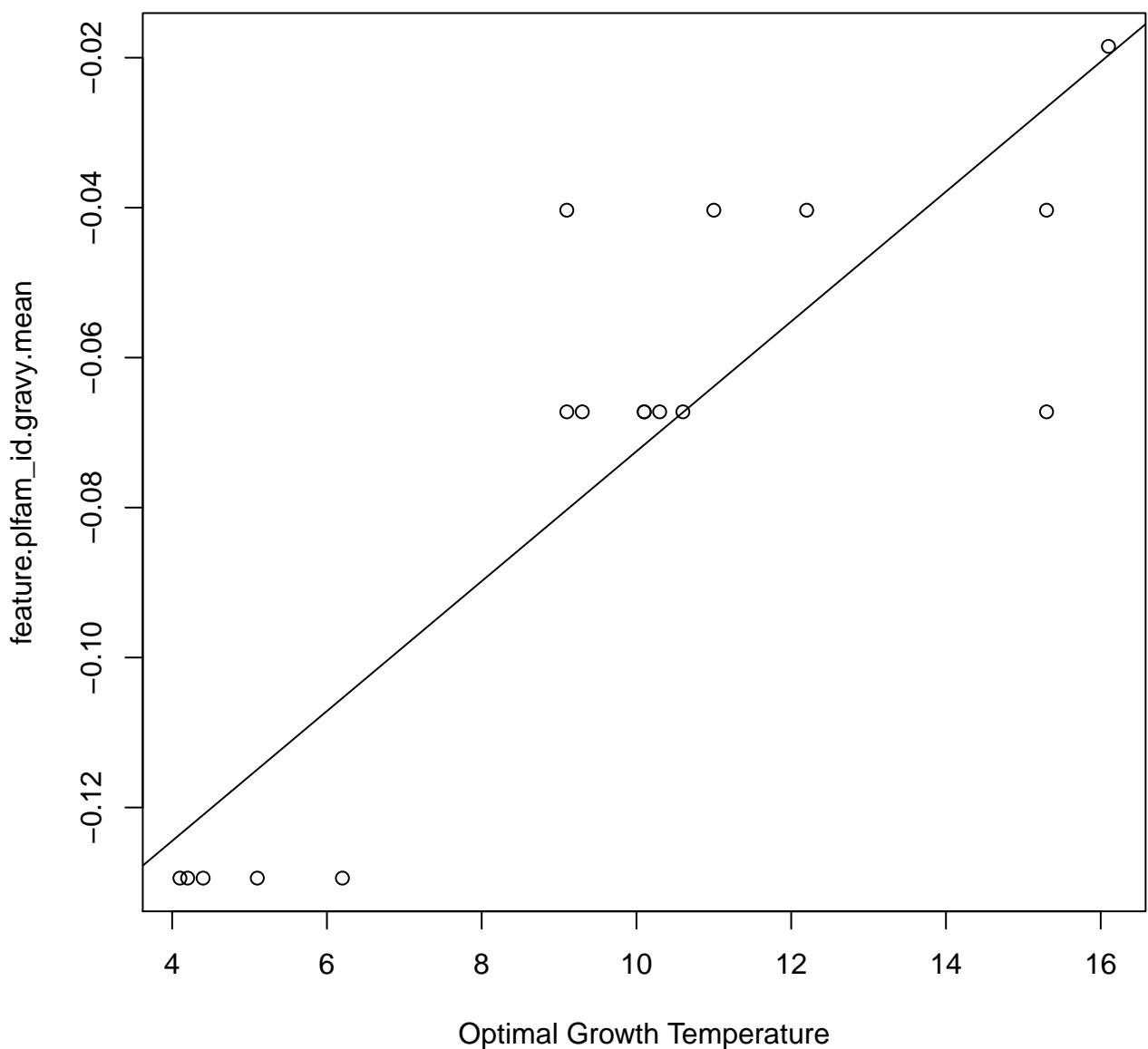
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hypothetical protein



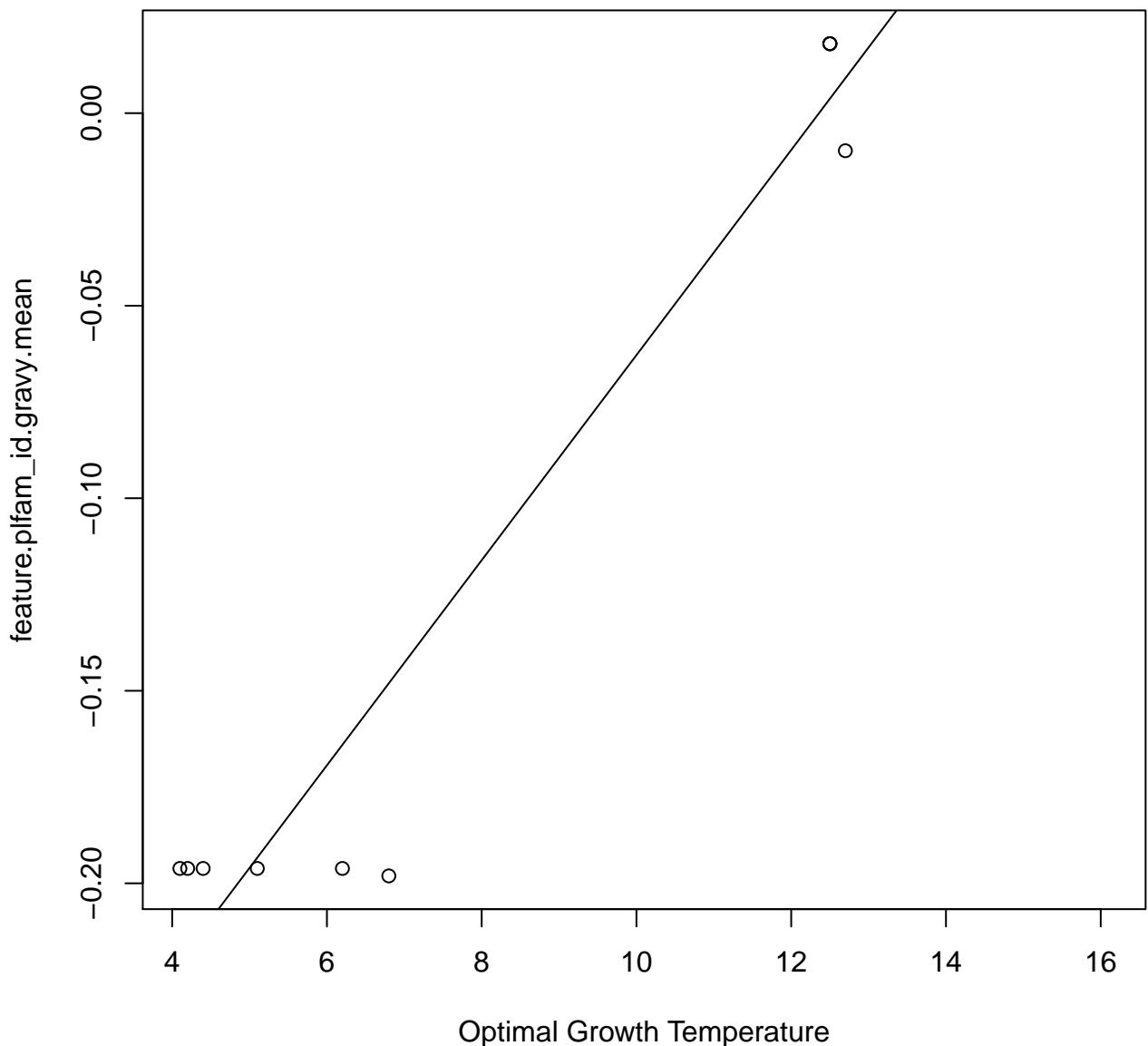
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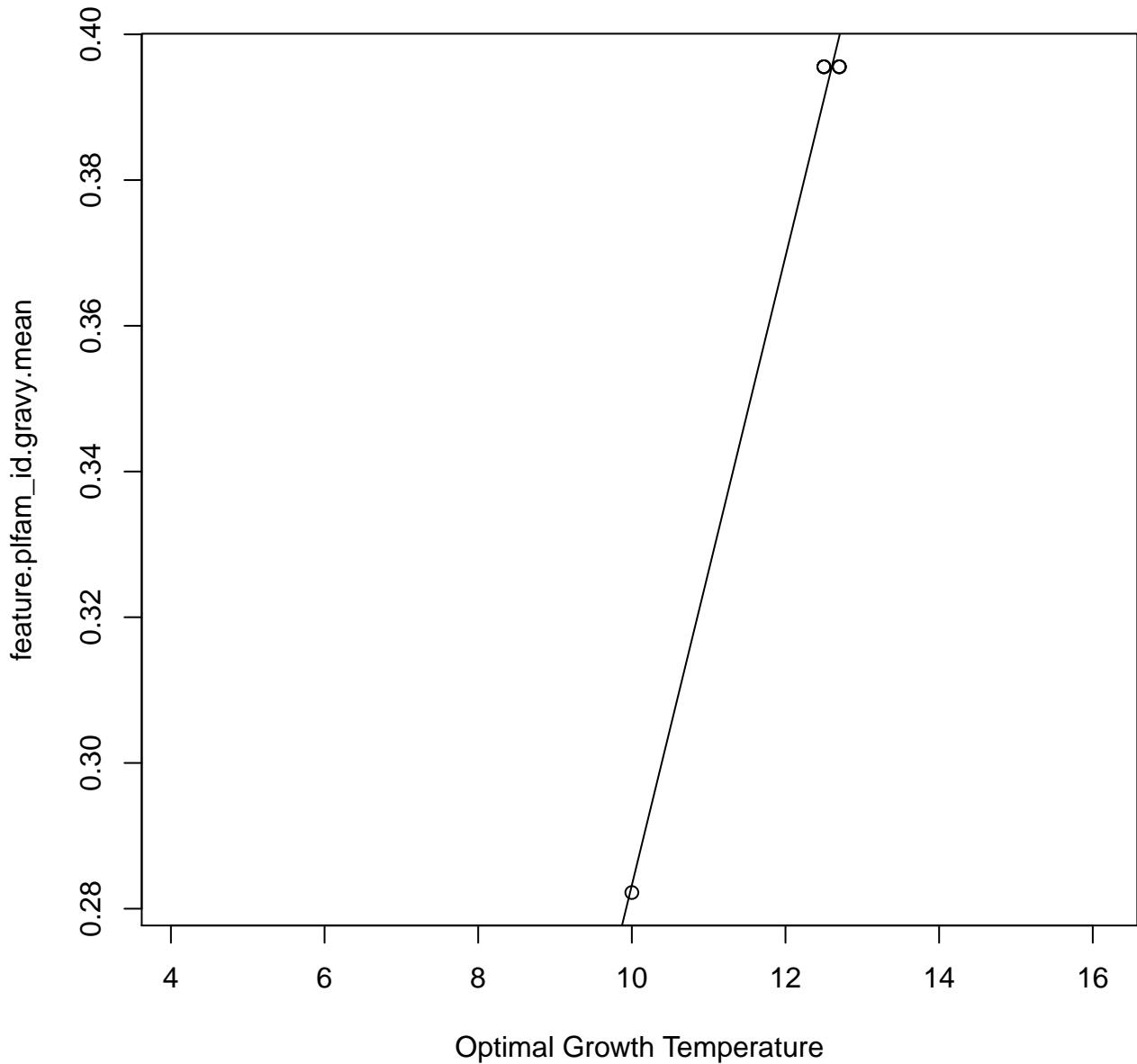
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Glyoxalase family protein



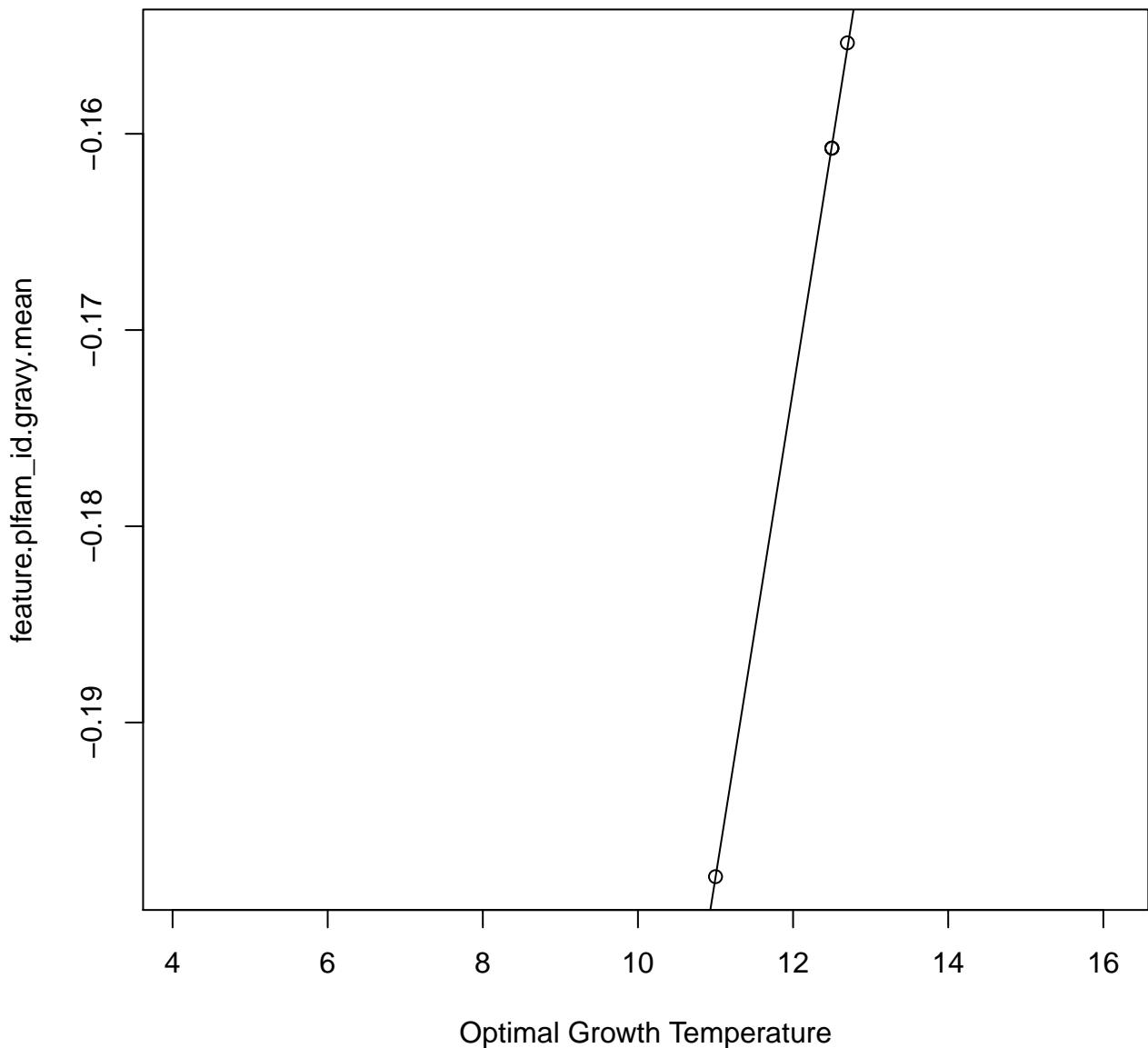
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hypothetical protein



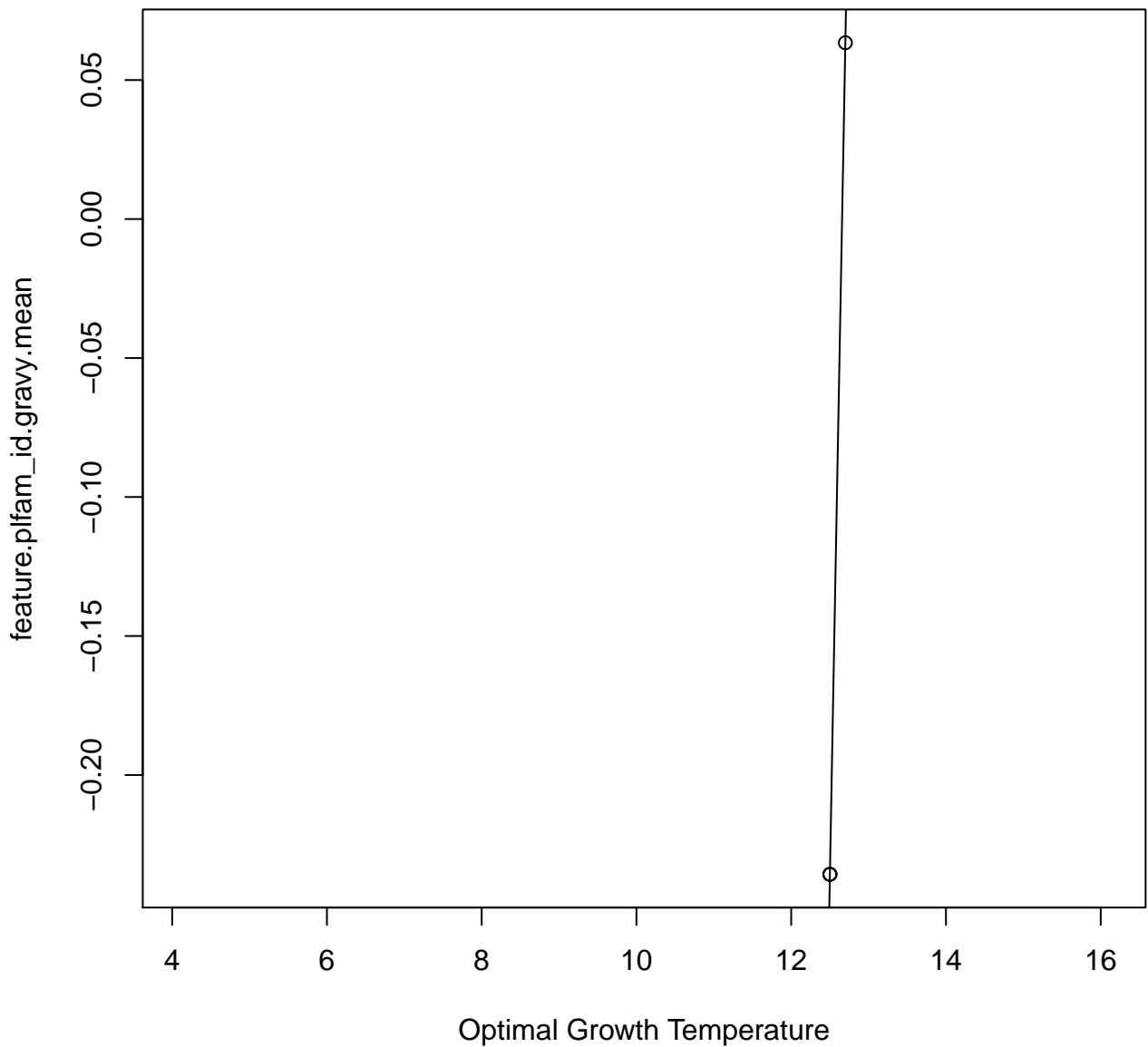
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hypothetical protein



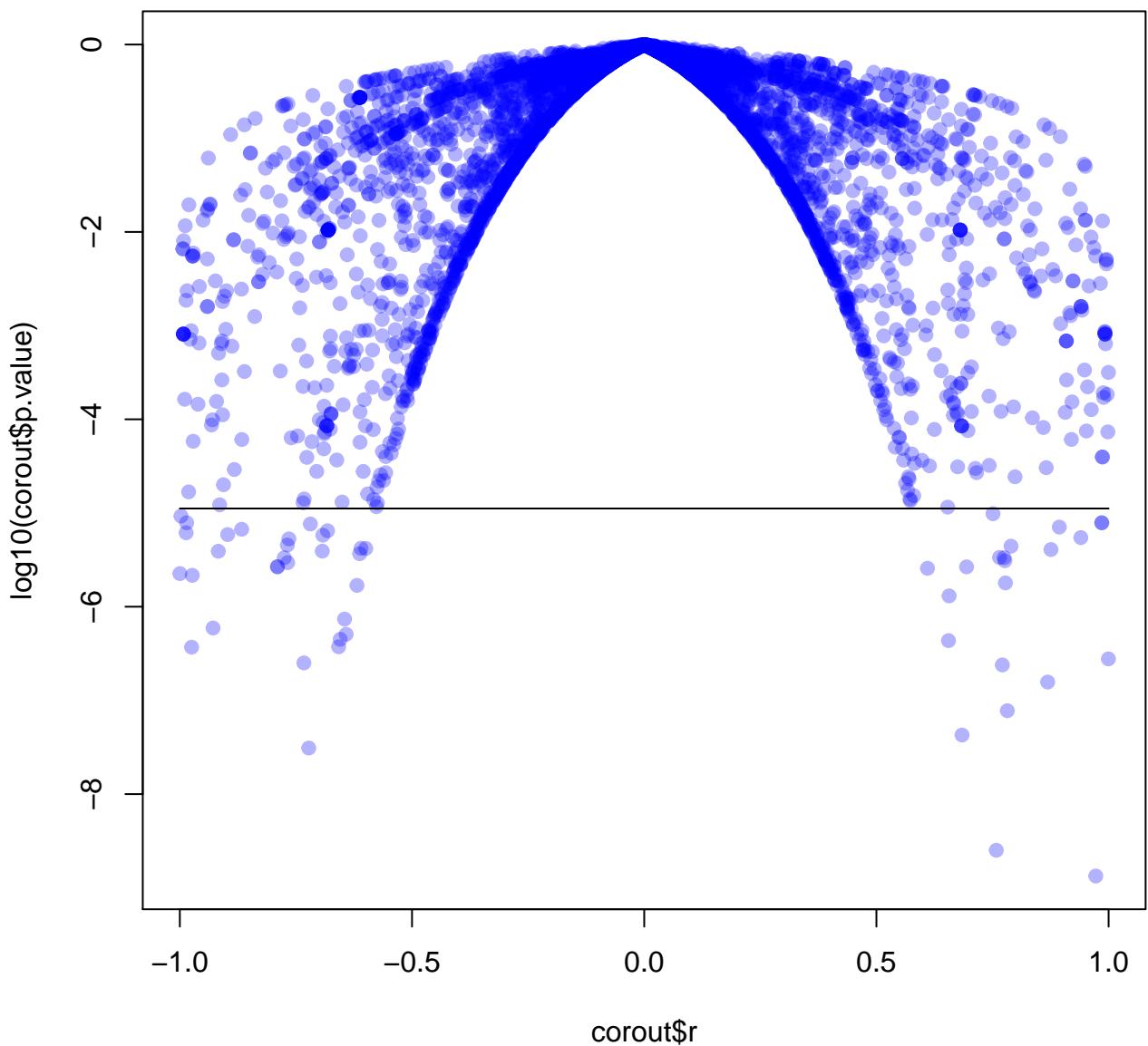
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Efflux transport system, outer membrane factor (OMF) lipoprotein



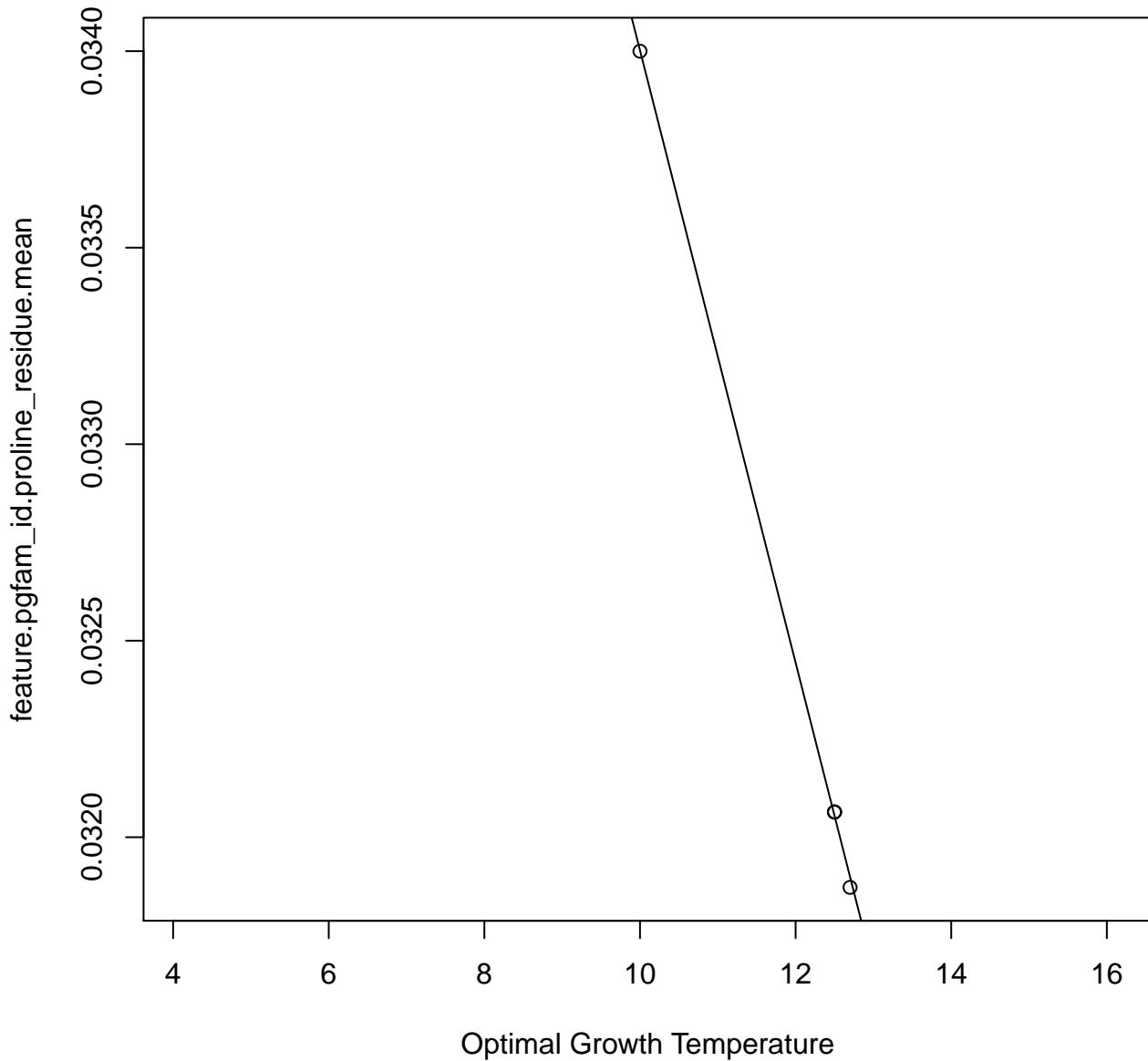
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Lipid A phosphoethanolamine transferase, putative



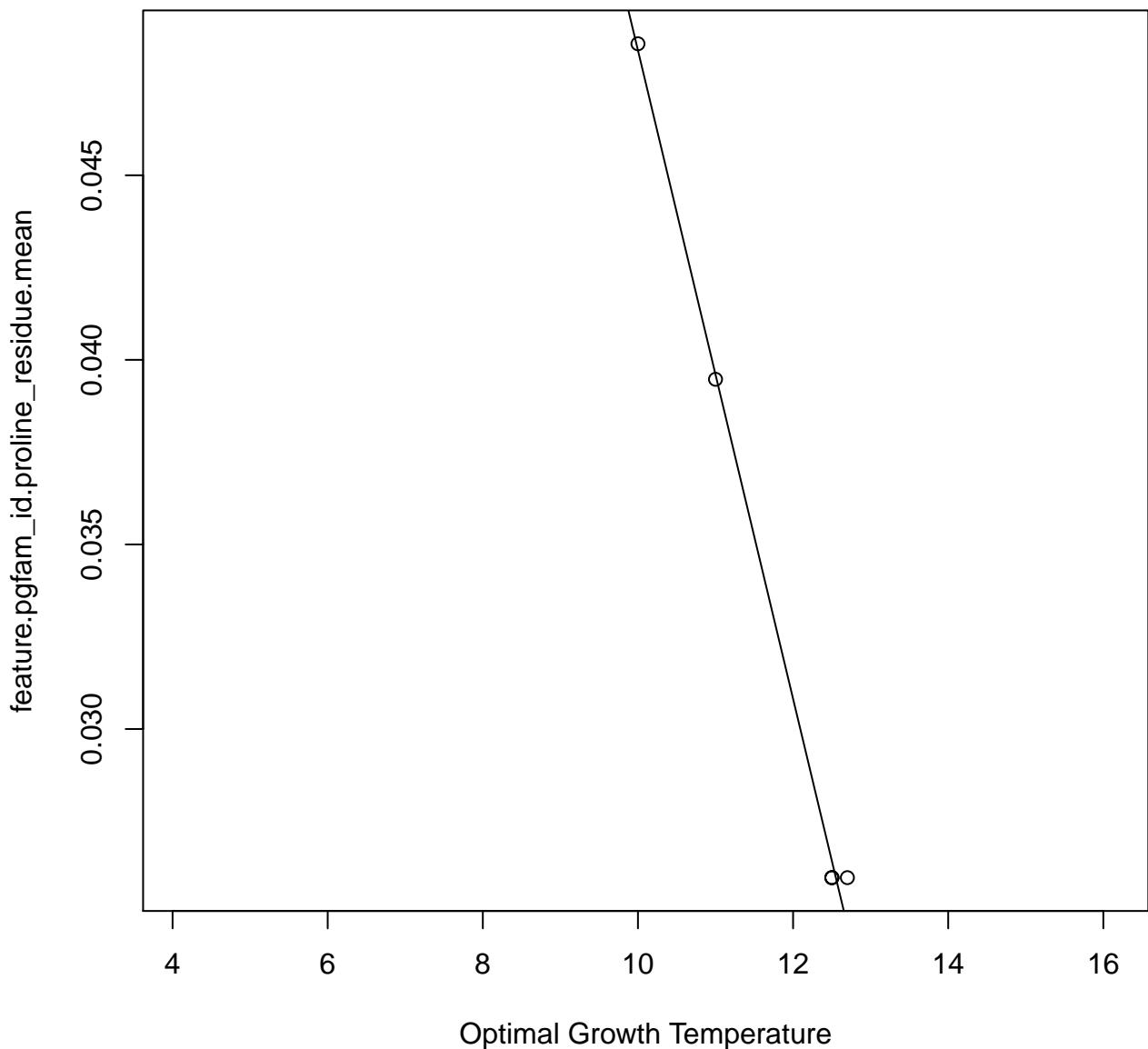
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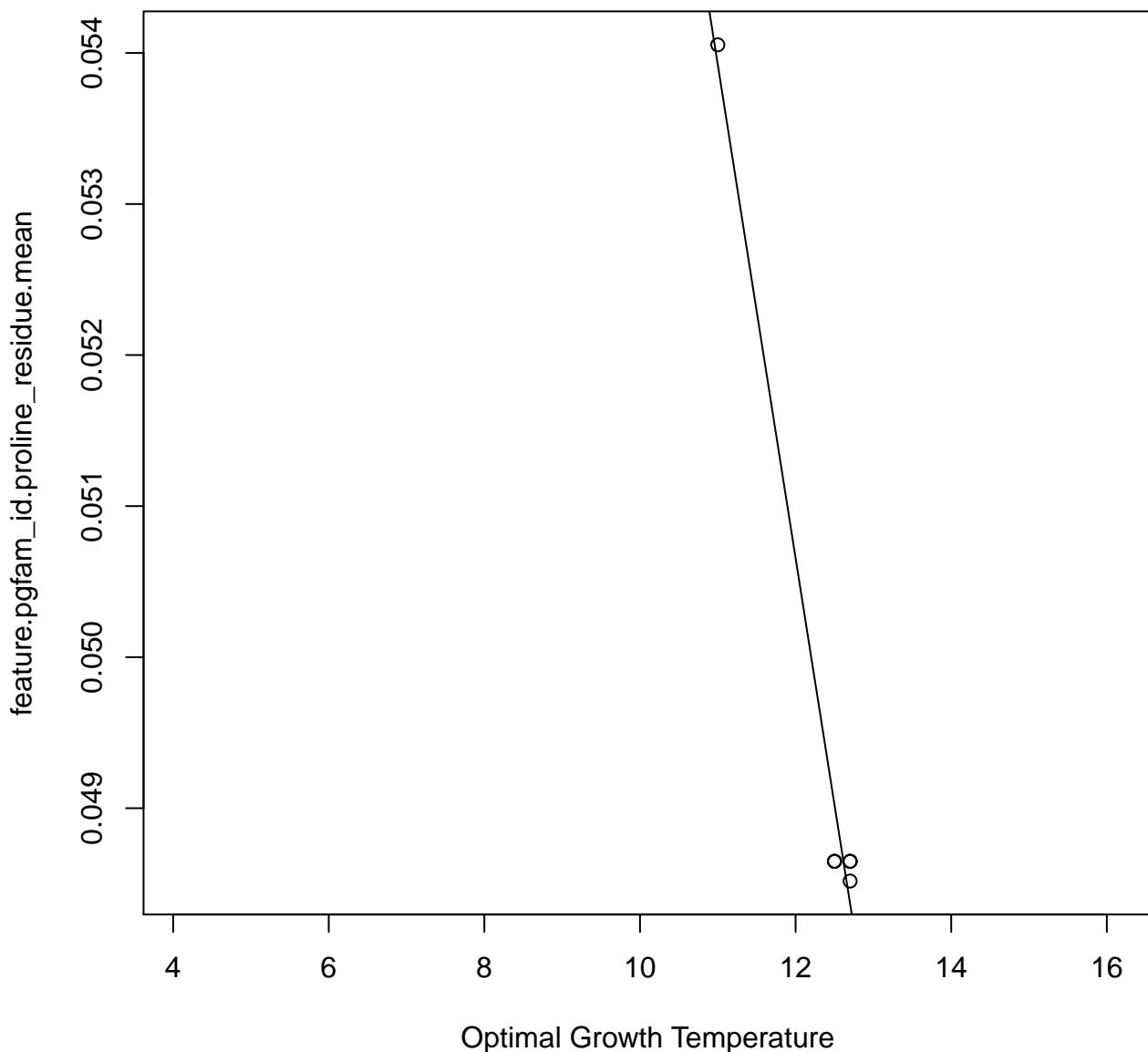
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PGF_01336815
hypothetical protein



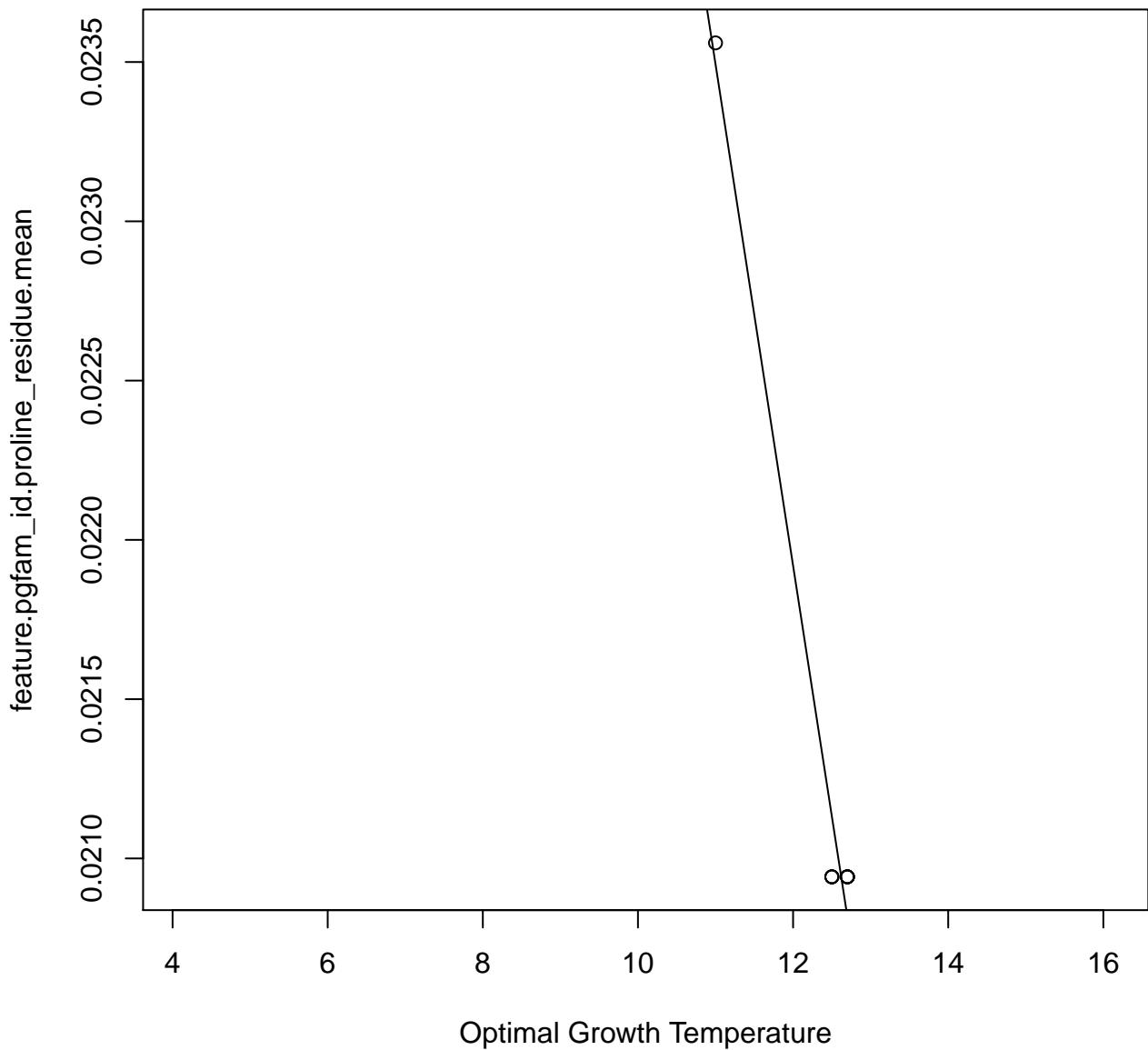
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PGF_08076270
hypothetical protein



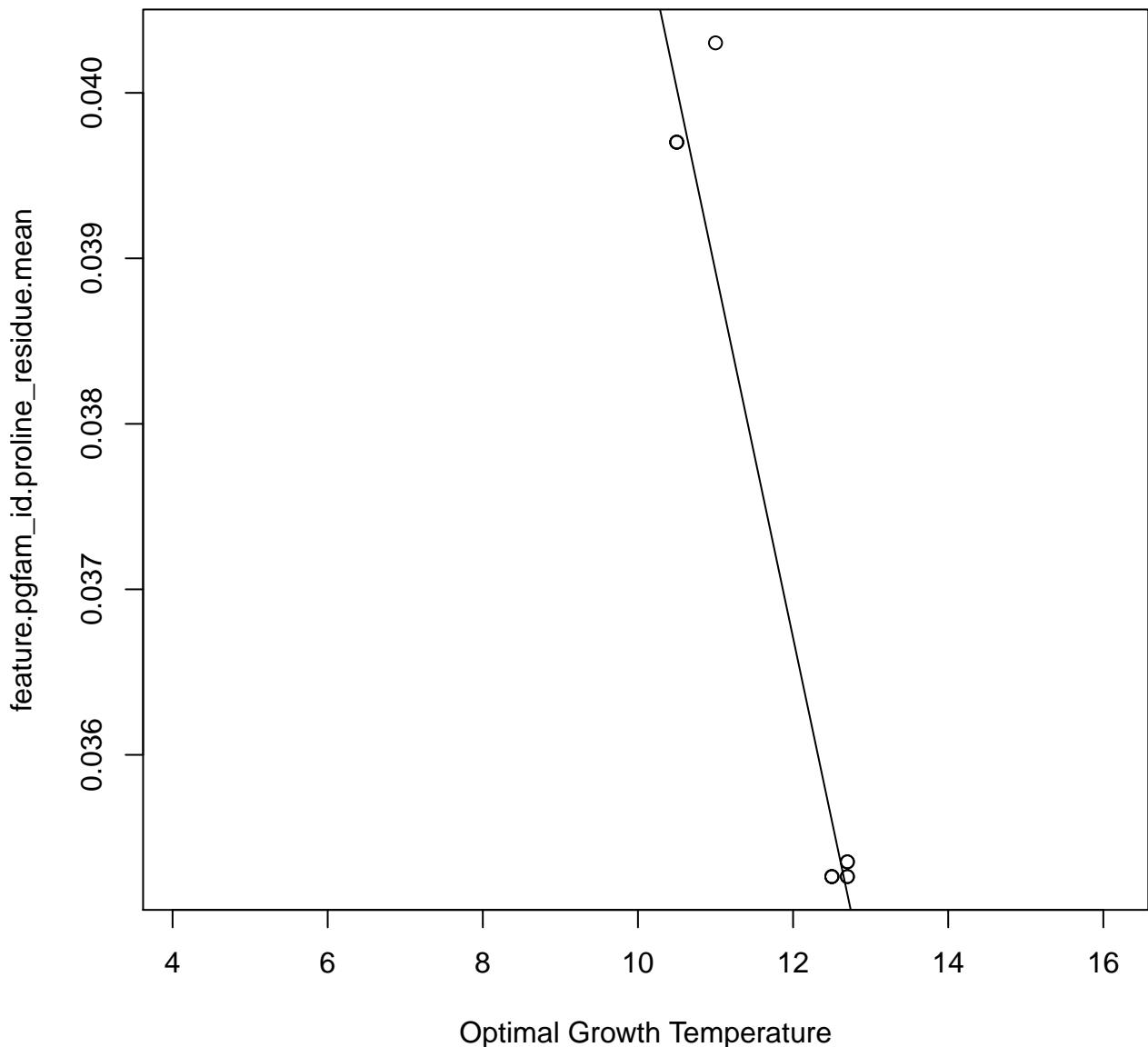
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UPF0098 protein ybcL precursor



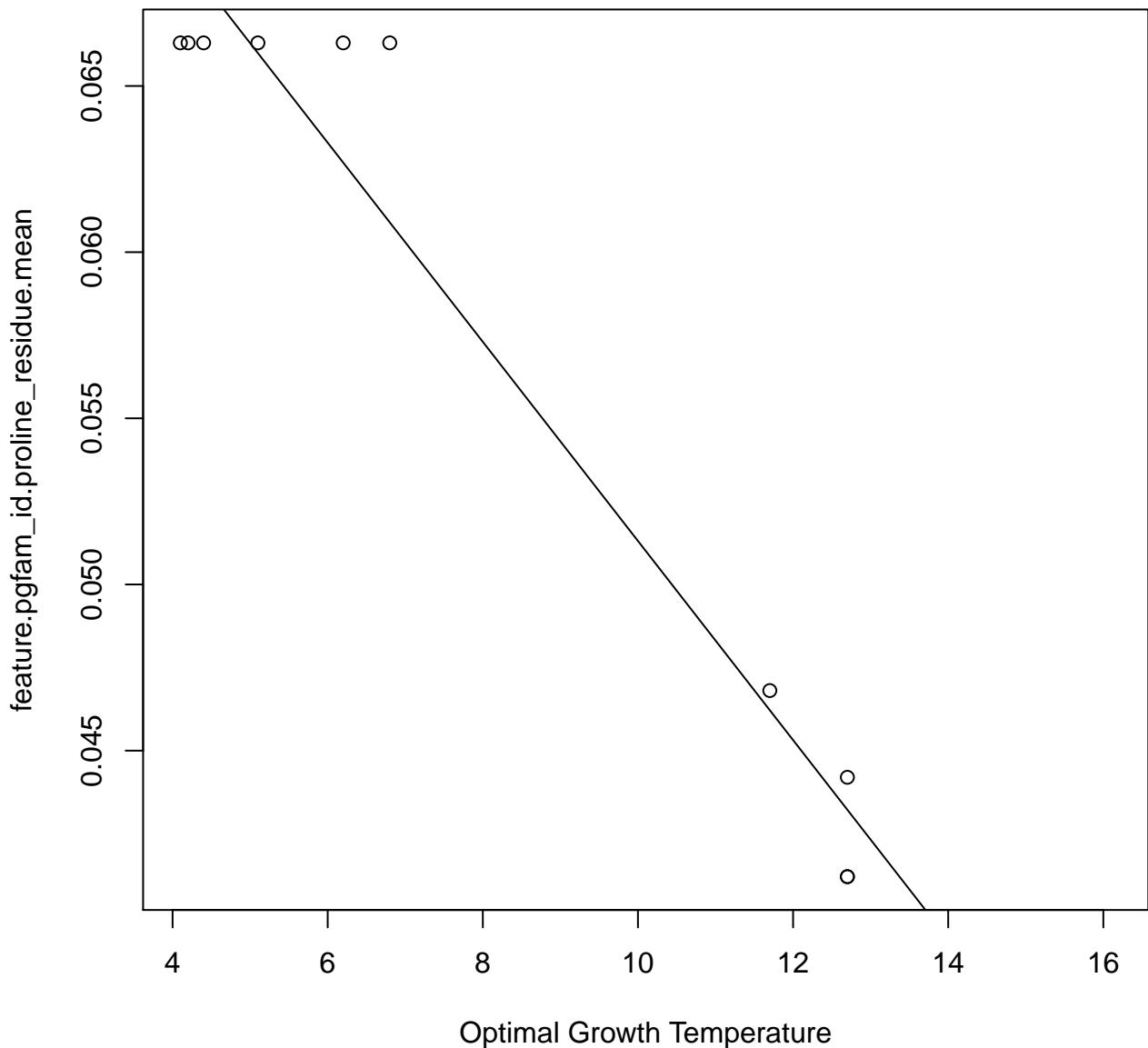
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PGF_00007576
GfdT



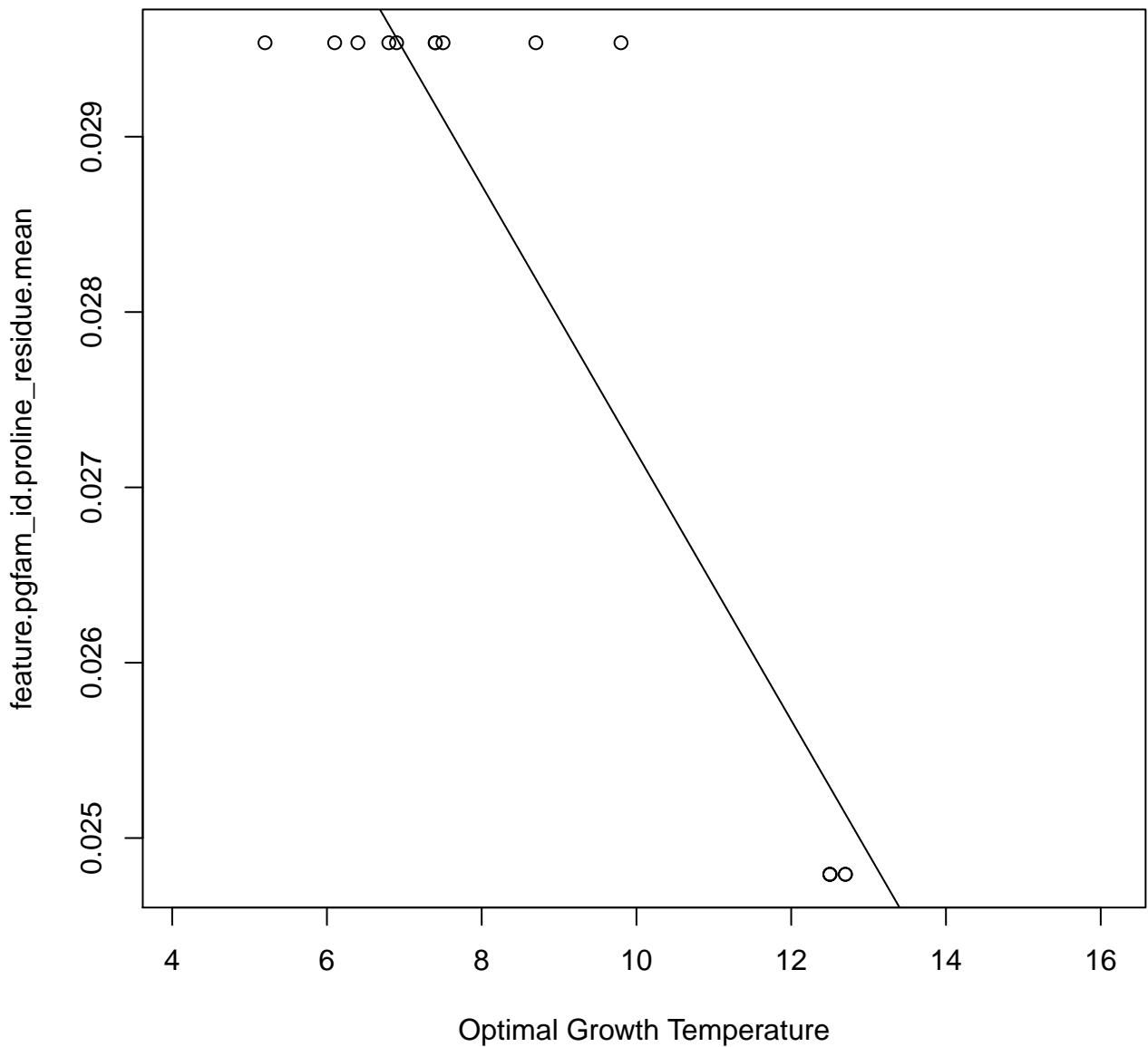
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Putative response regulator



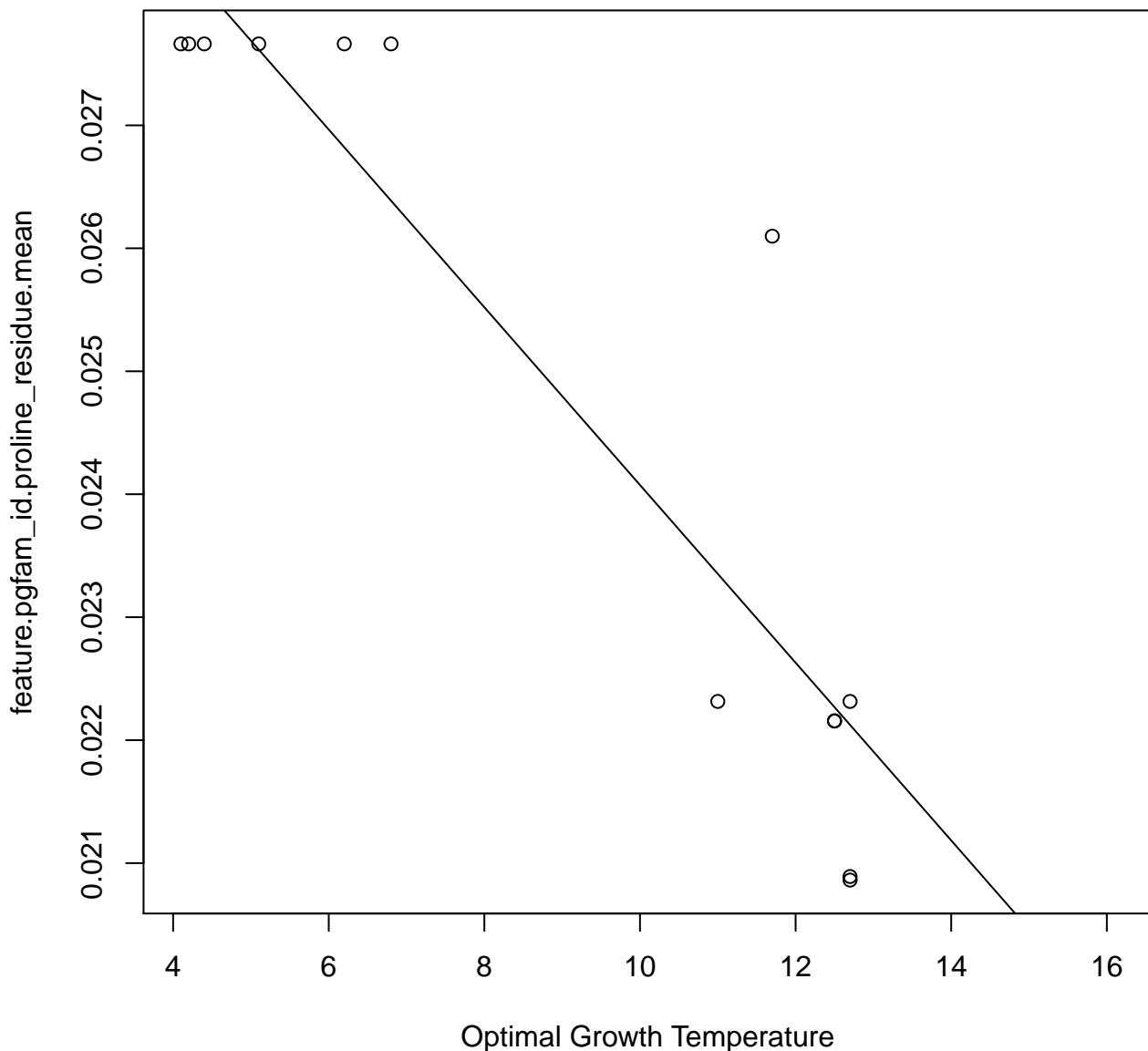
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Phage tail collar domain



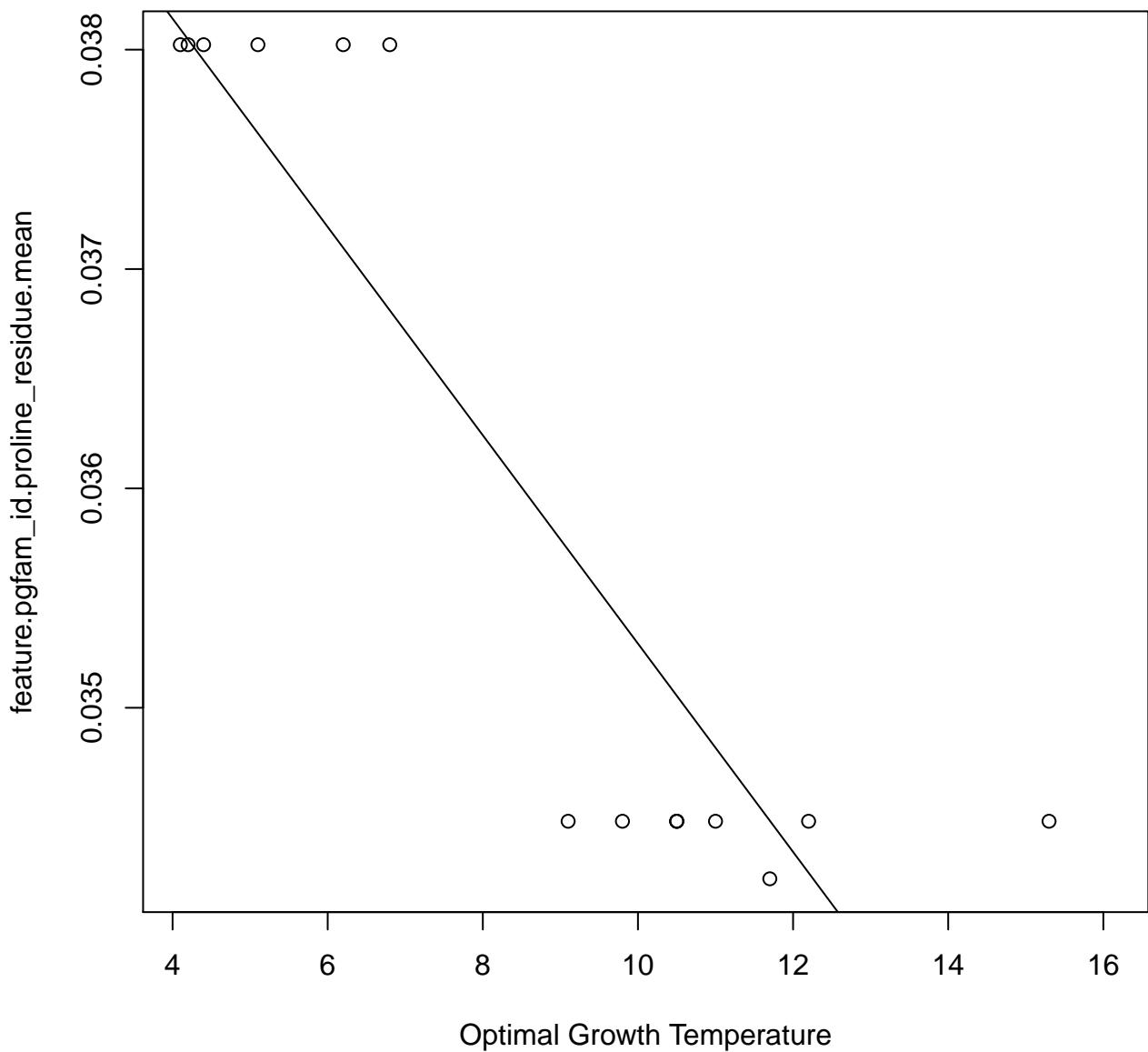
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PGF_06830555
SapC-like S-layer protein



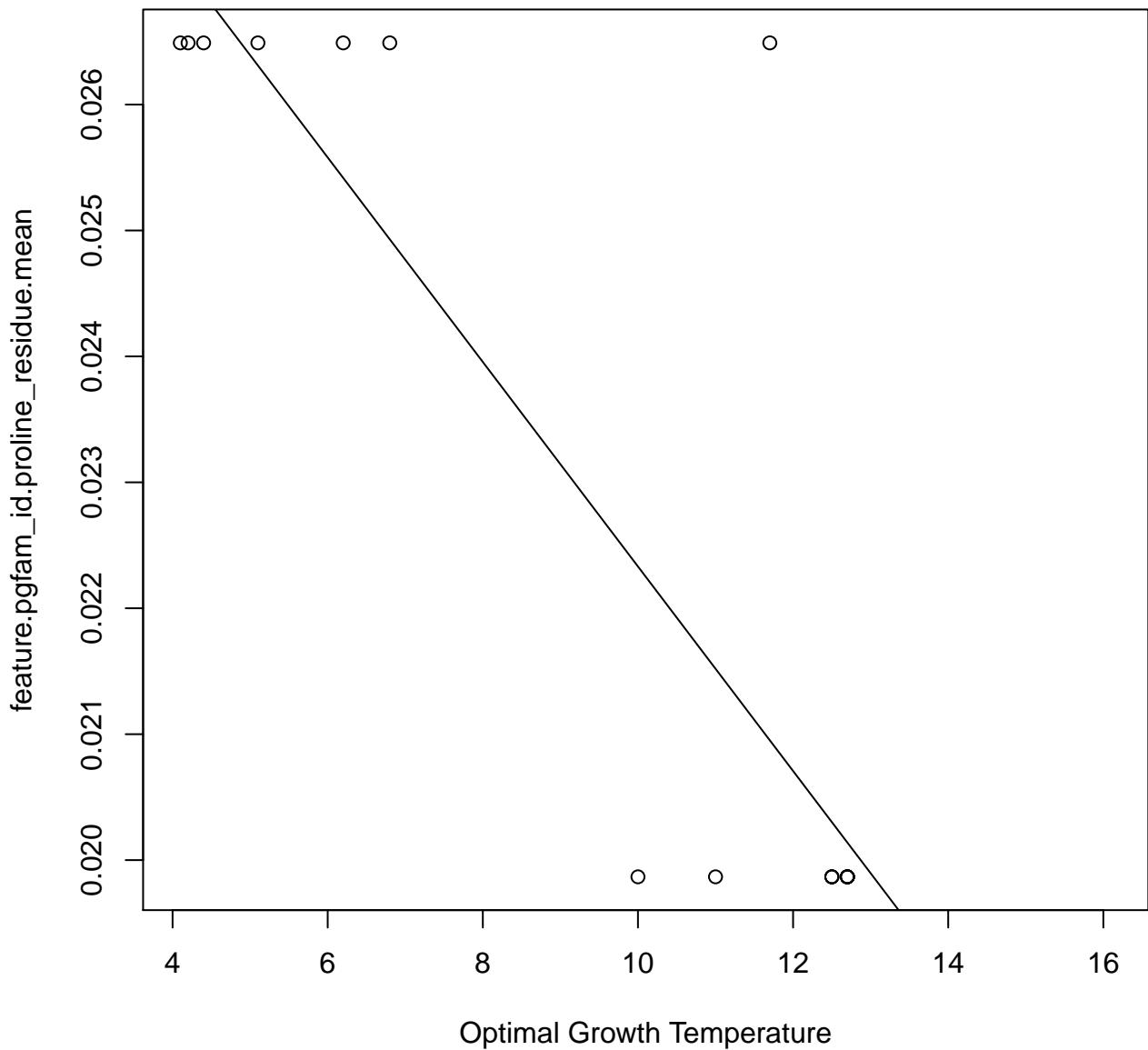
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PGF_01336740
Sensory box sensor/GGDEF/EAL domain protein



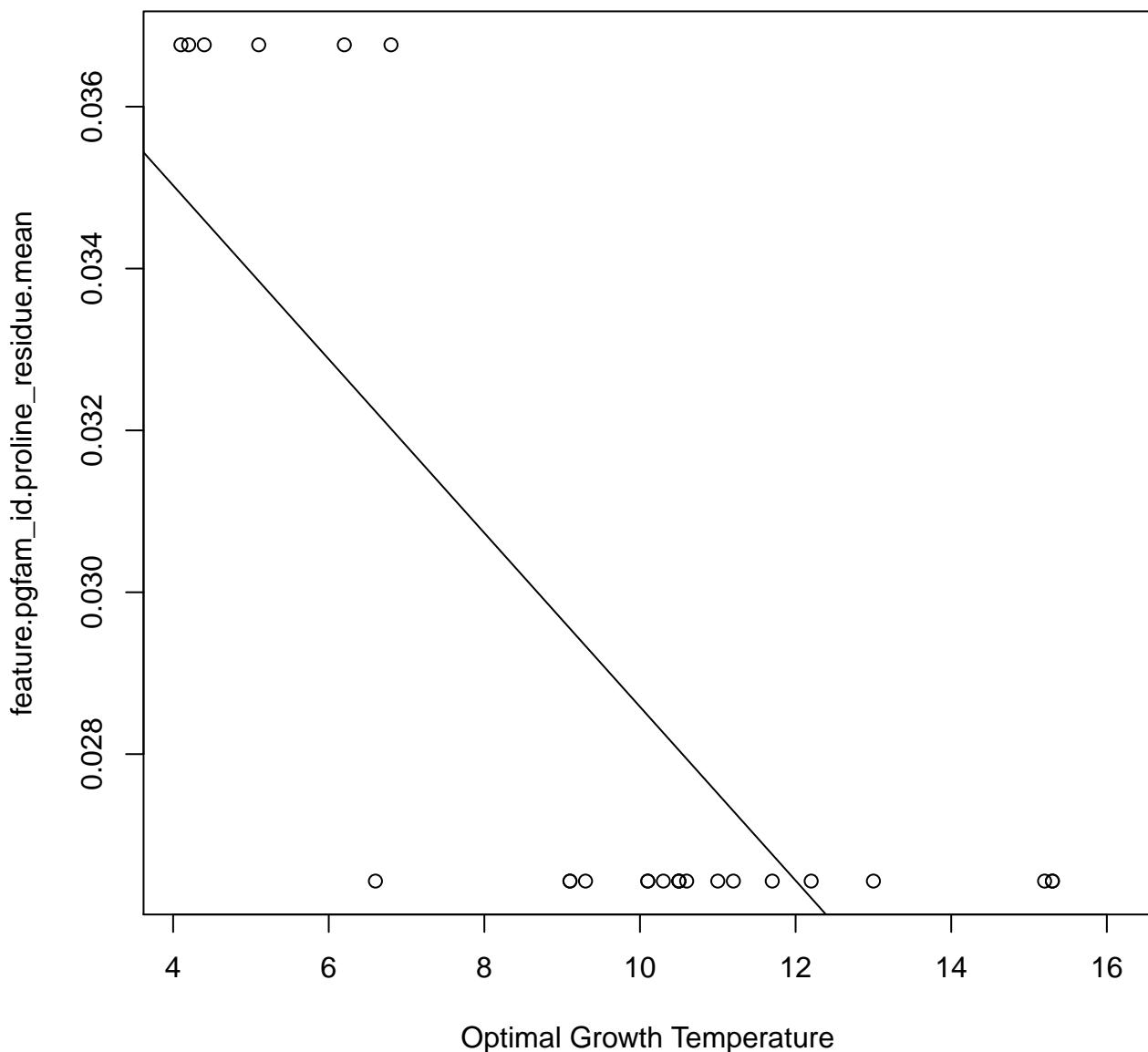
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PGF_10029046
hypothetical protein



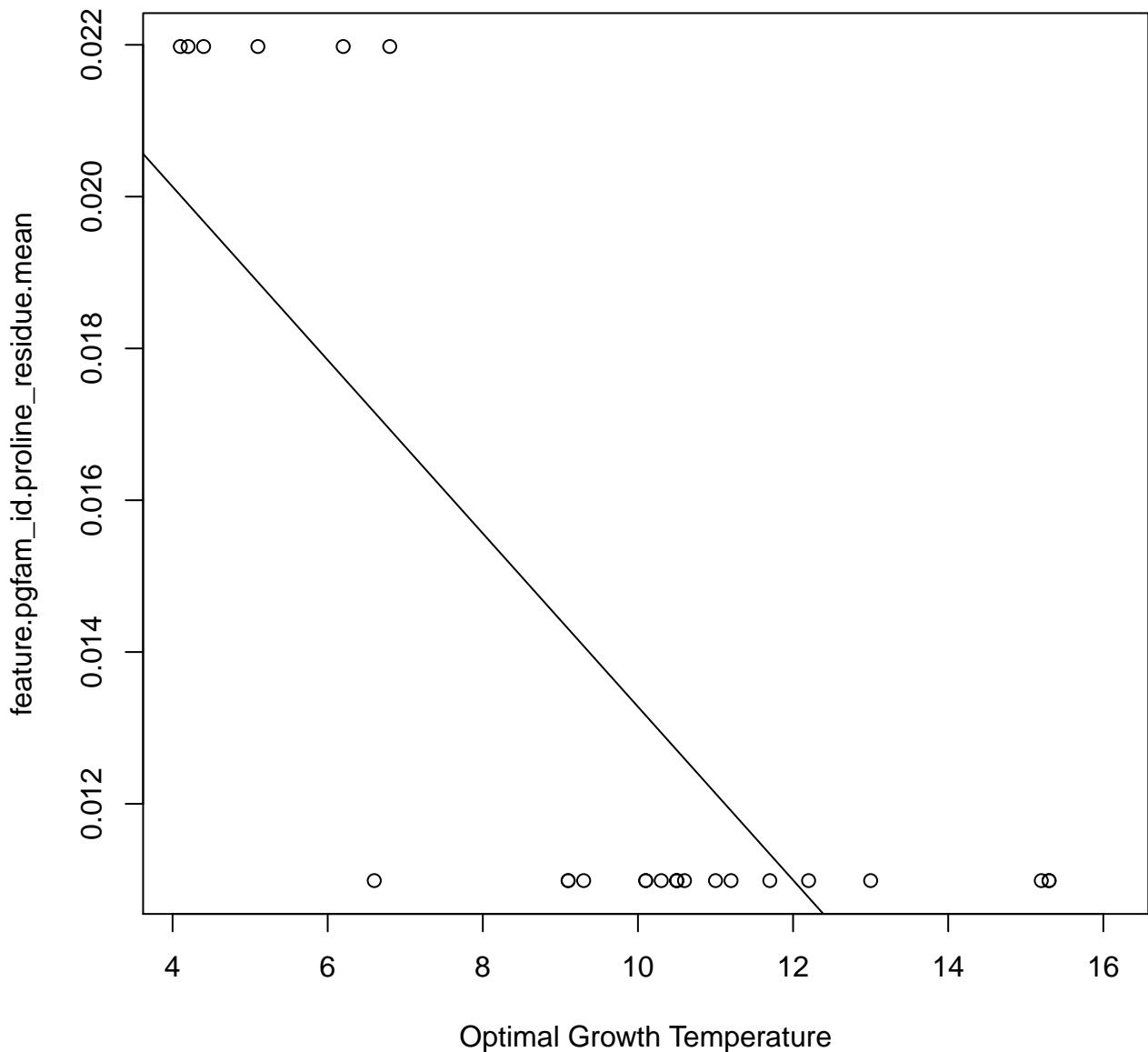
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PGF_01336551
uncharacterized conserved secreted protein



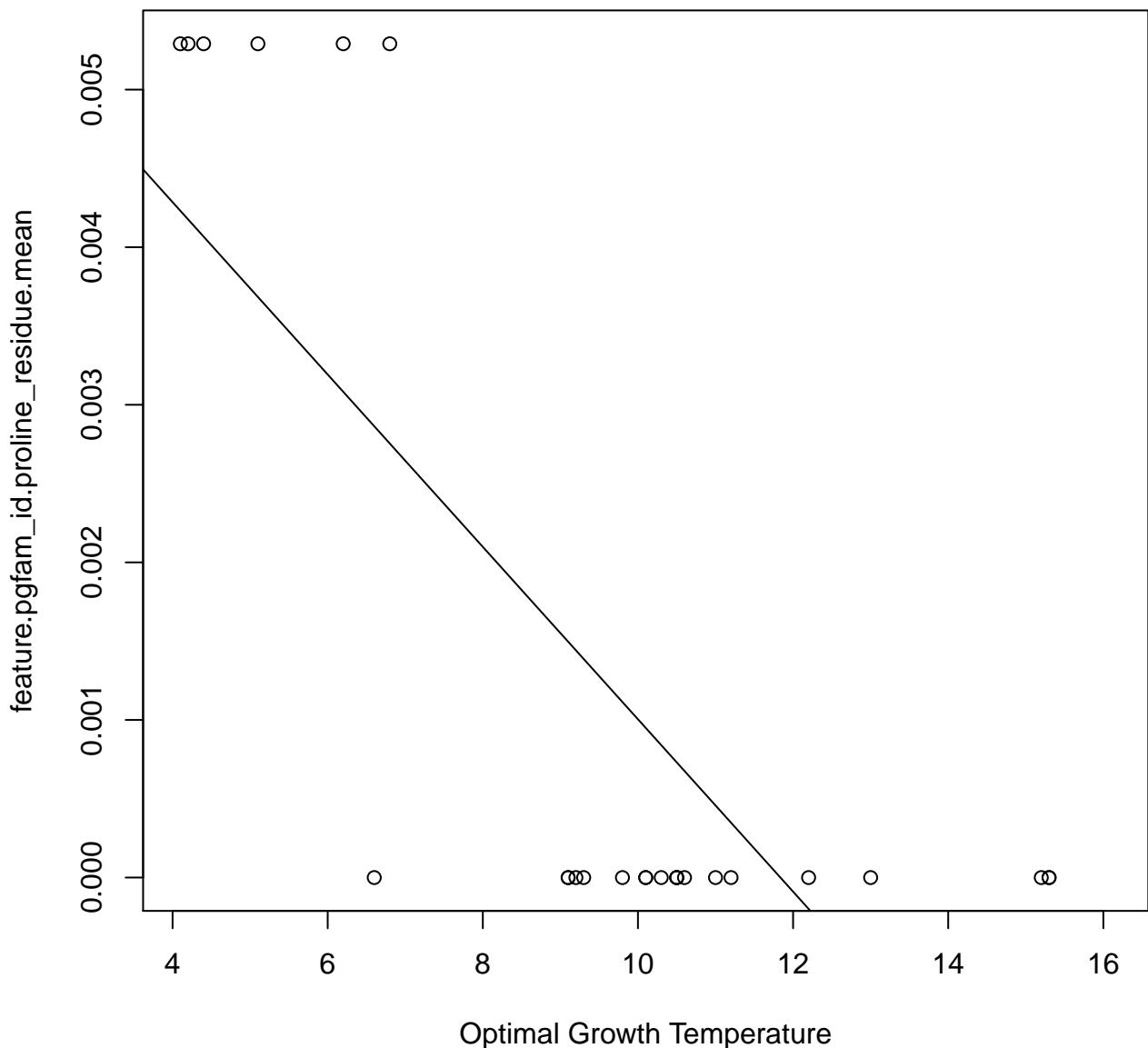
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PGF_11620197
hypothetical protein



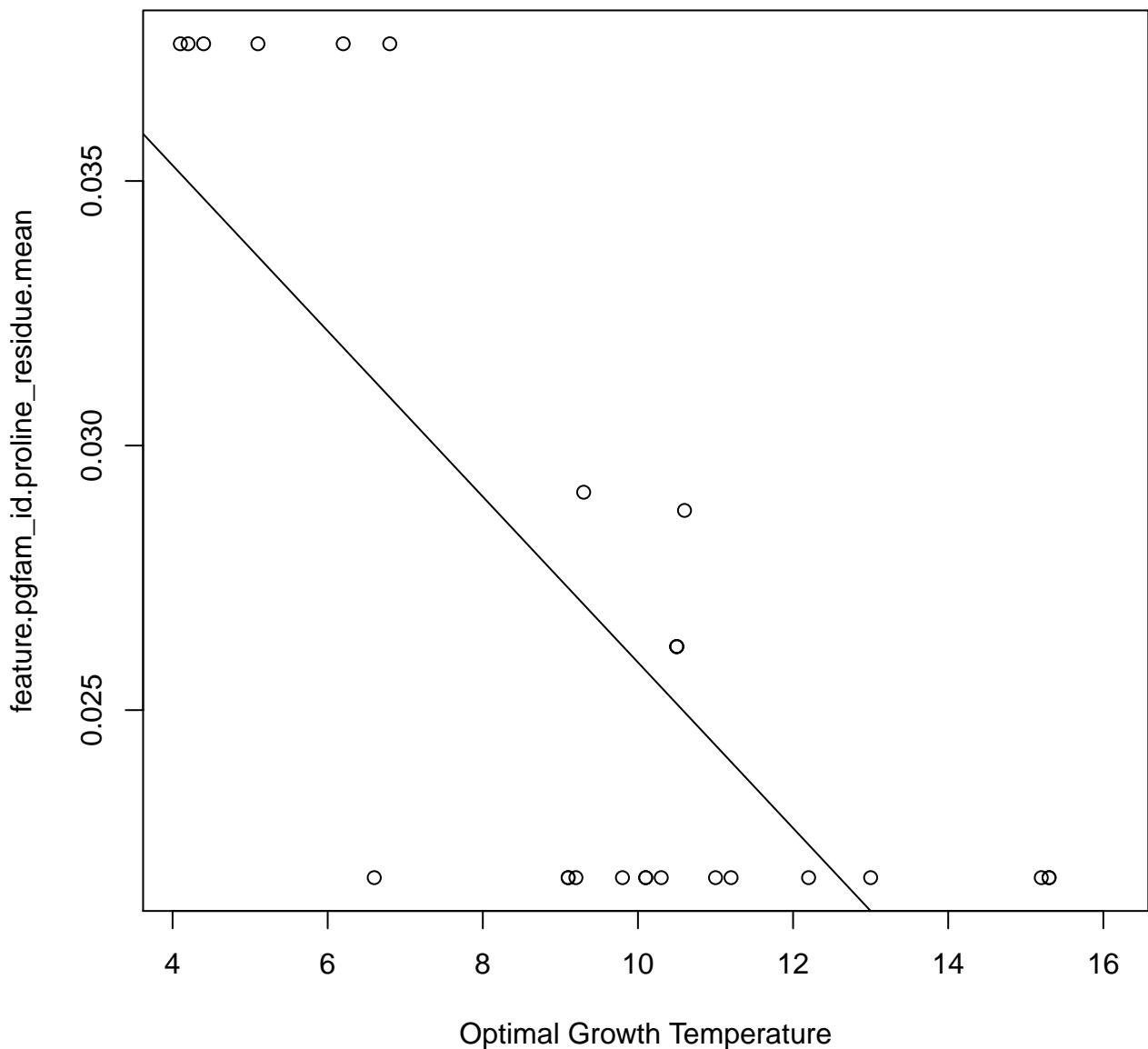
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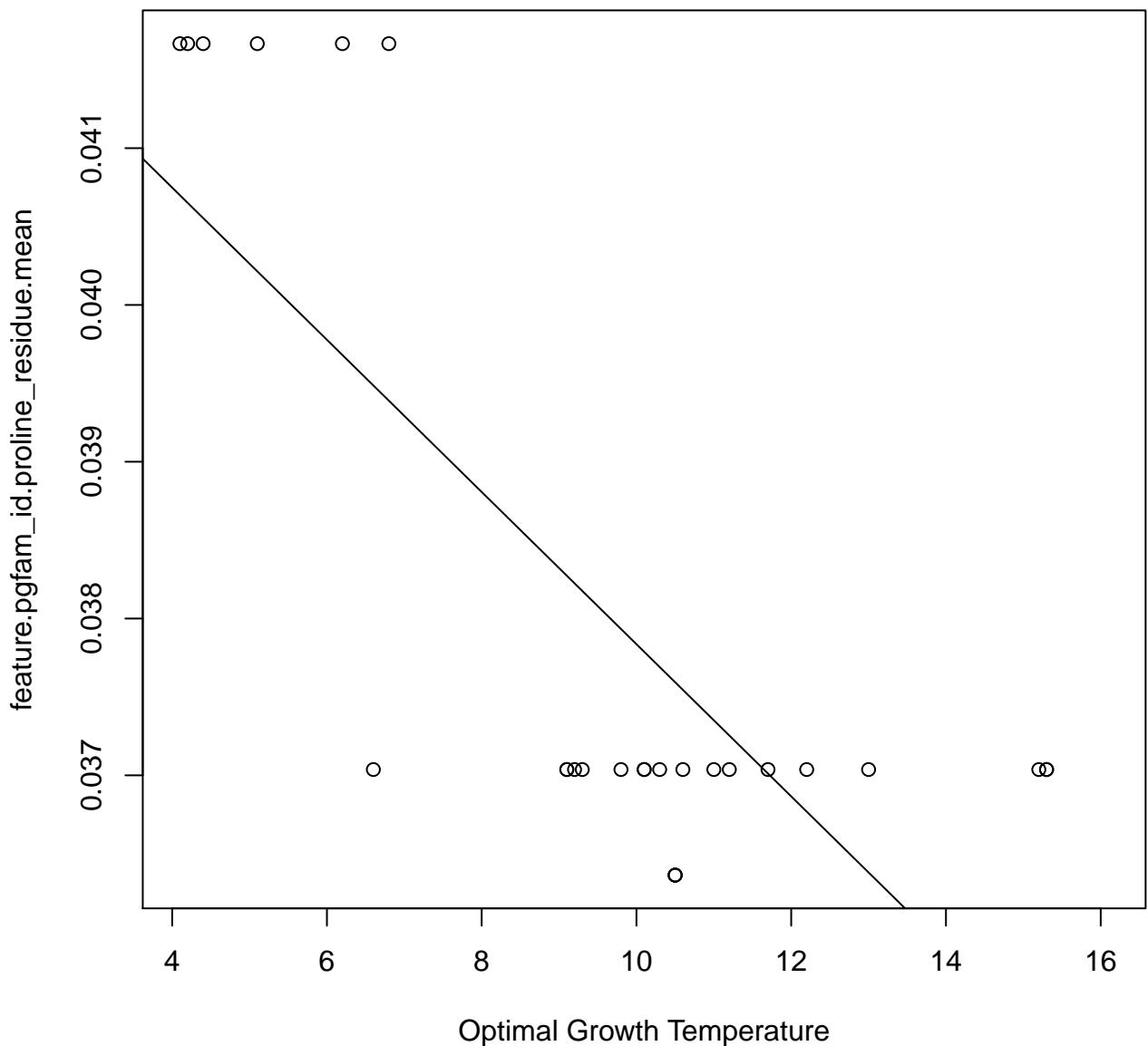
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PGF_12159935
hypothetical protein



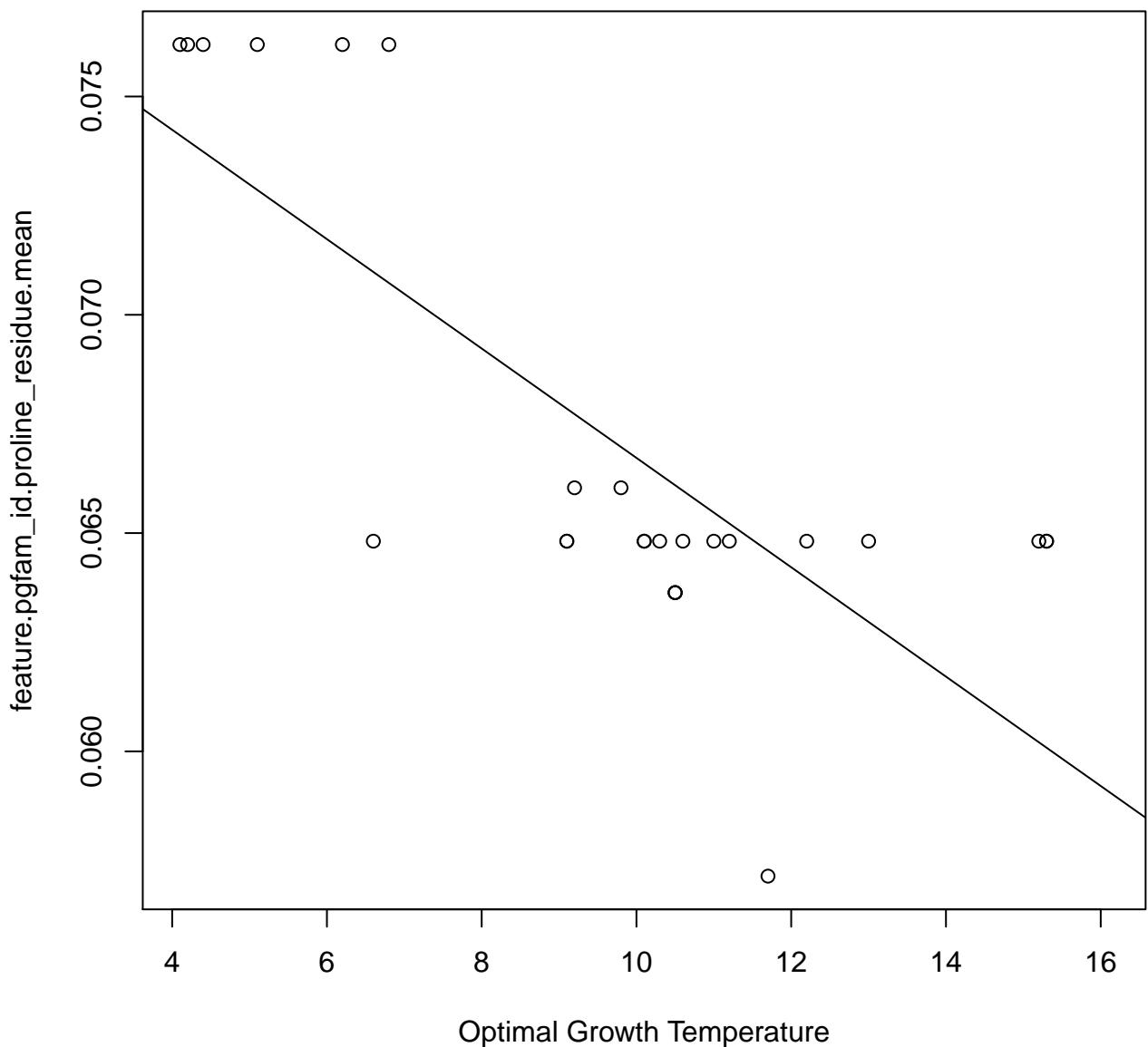
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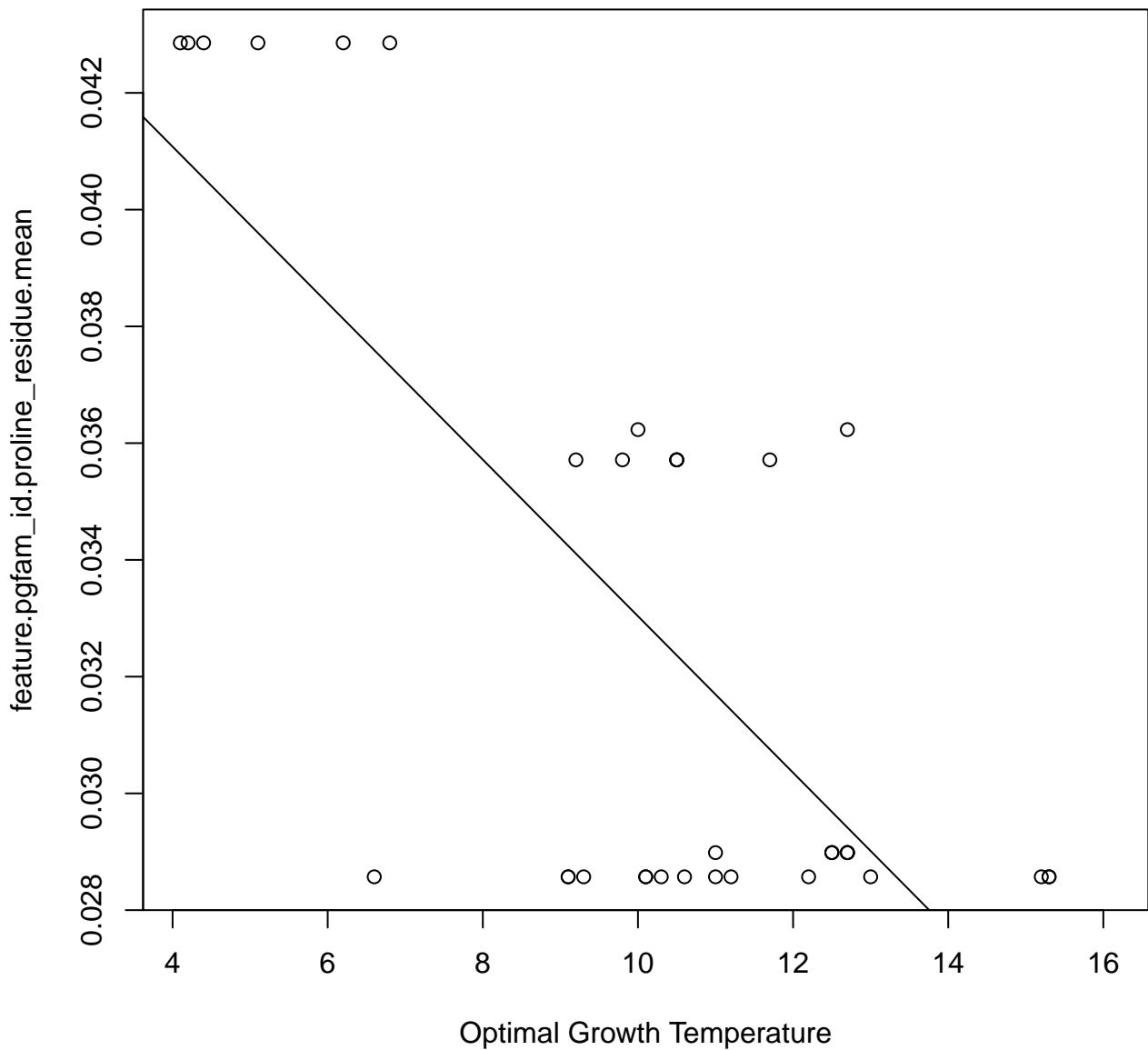
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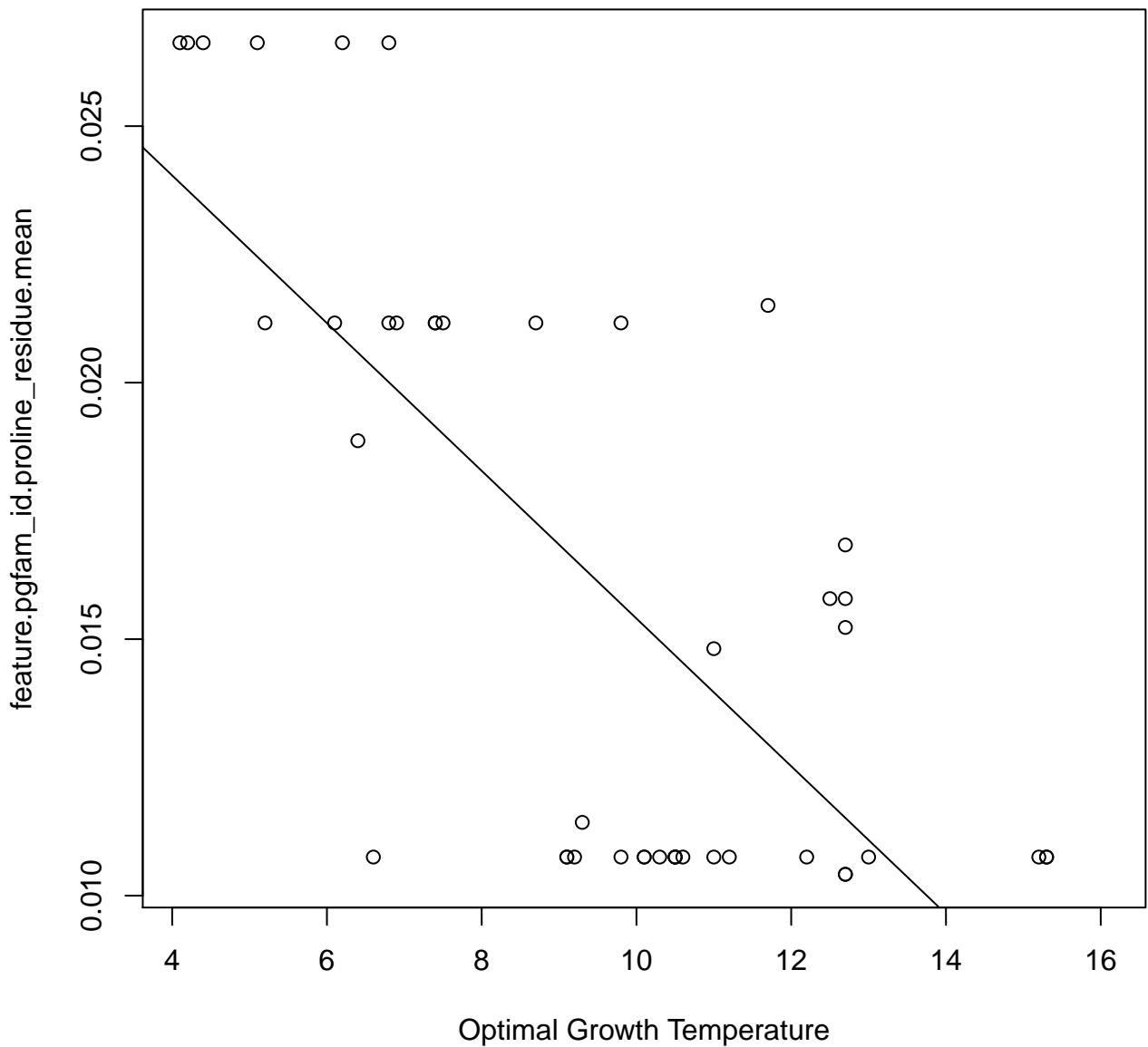
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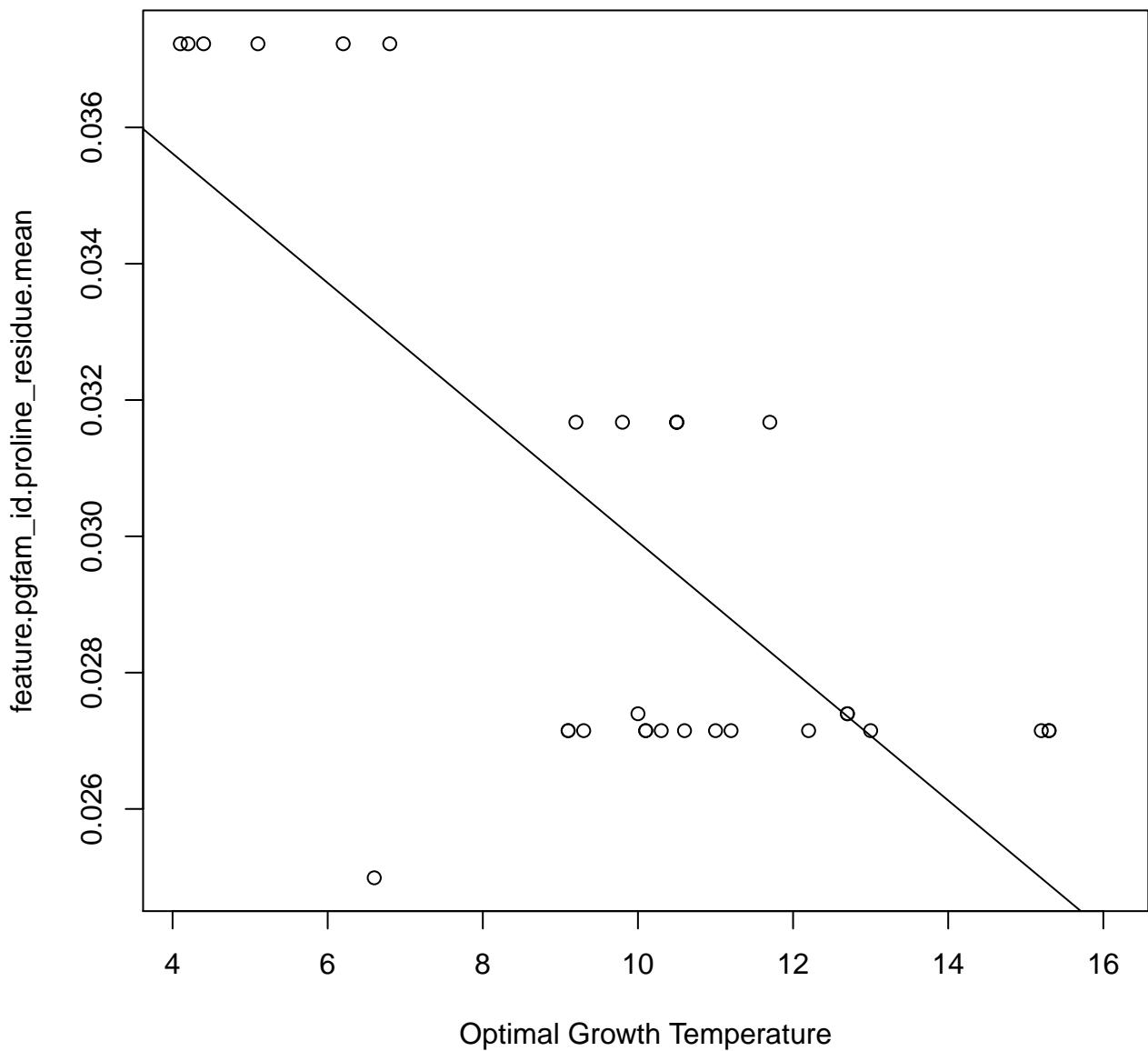
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PGF_01009507
Glyoxalase family protein



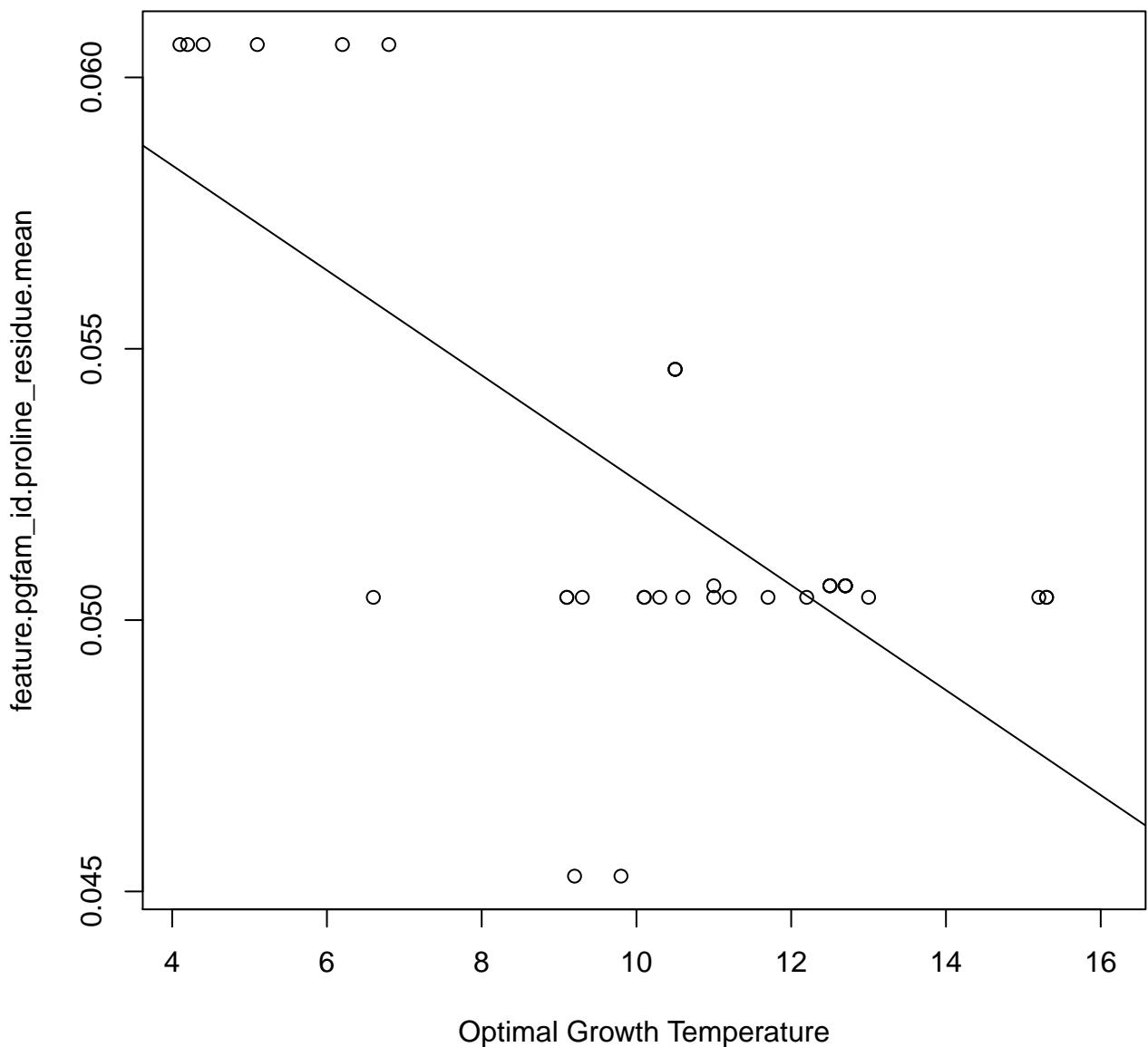
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PGF_12669666
FIG006045: Sigma factor, ECF subfamily



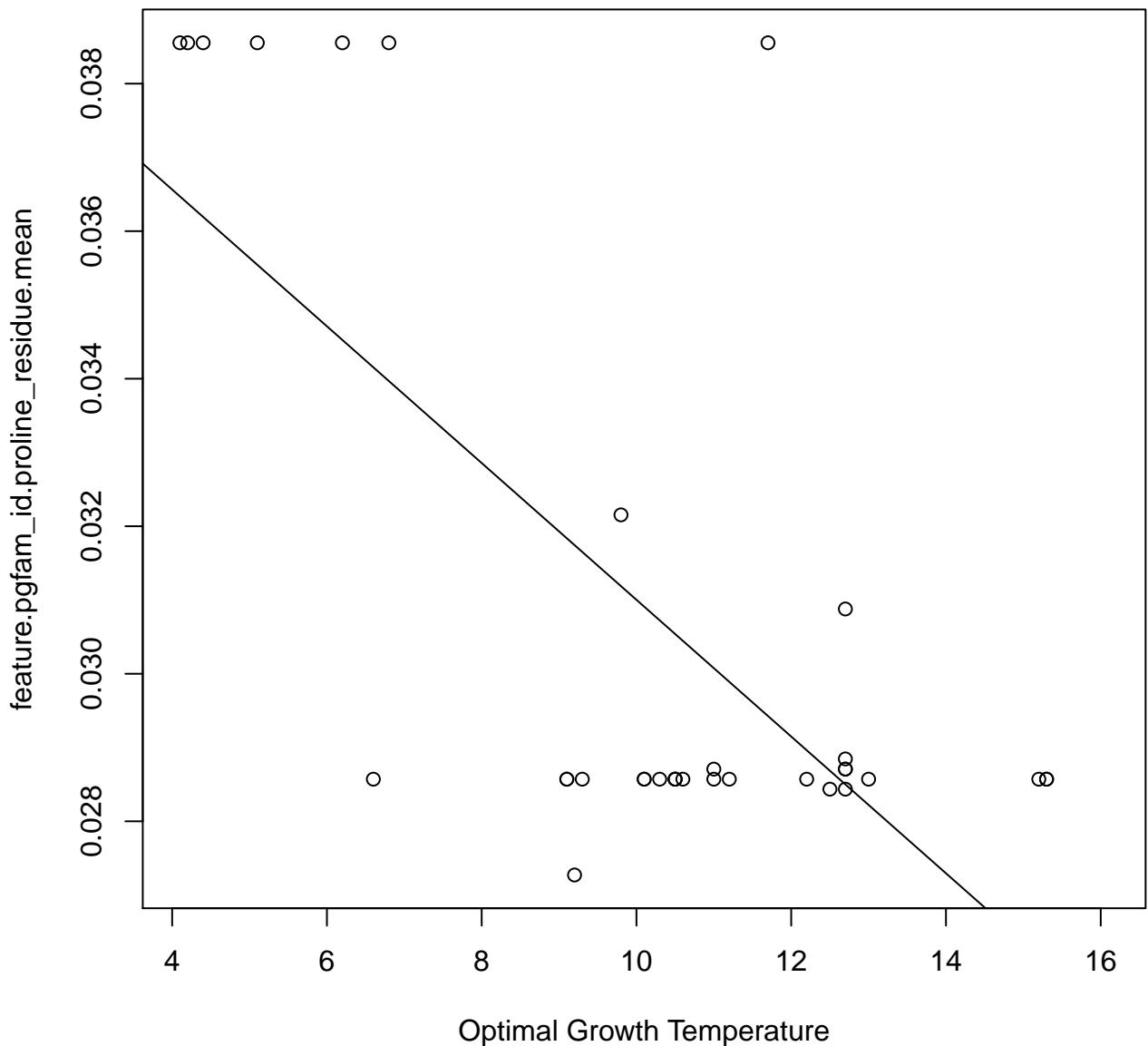
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Chemotaxis protein CheD



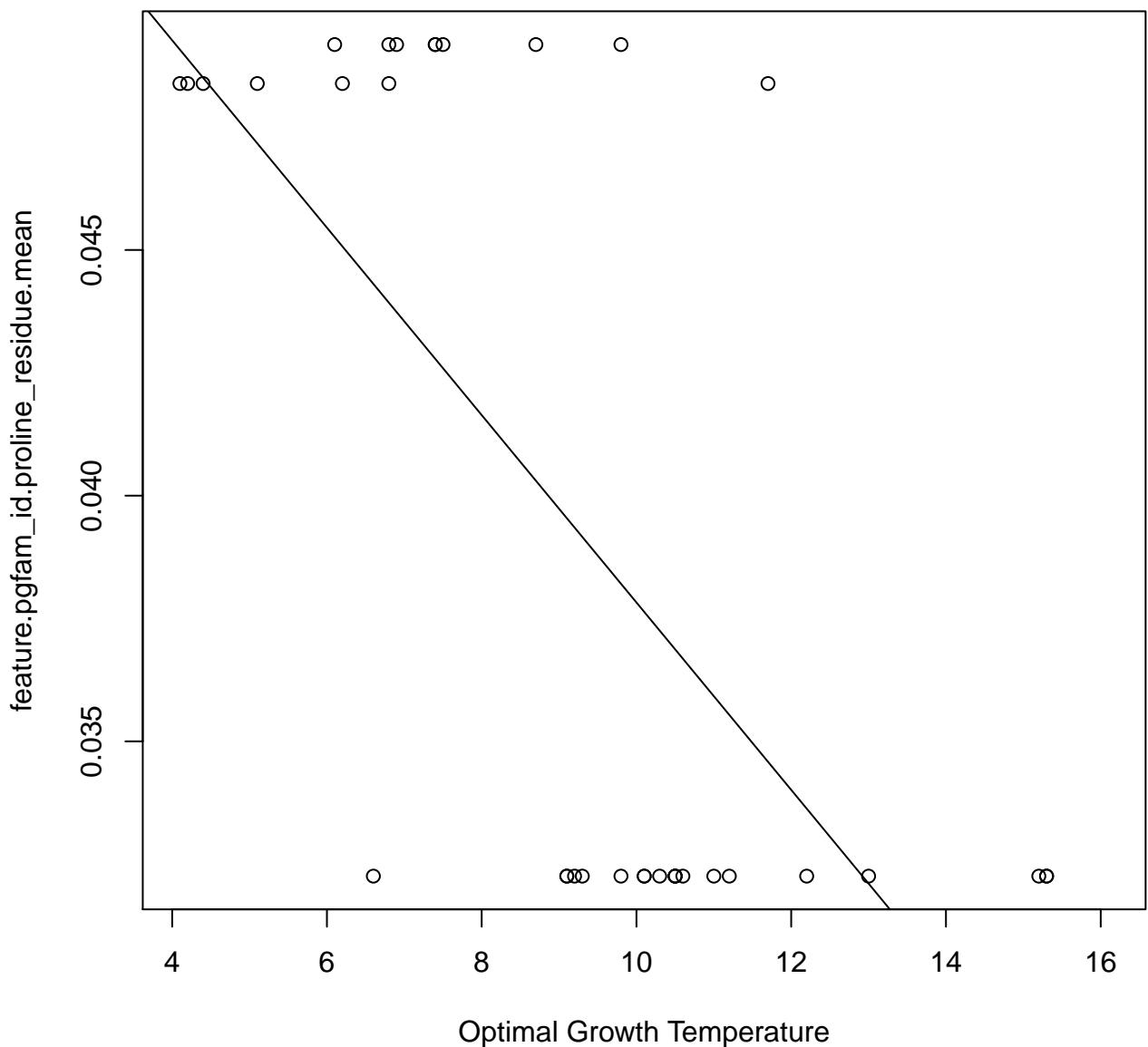
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ZIP zinc transporter family protein



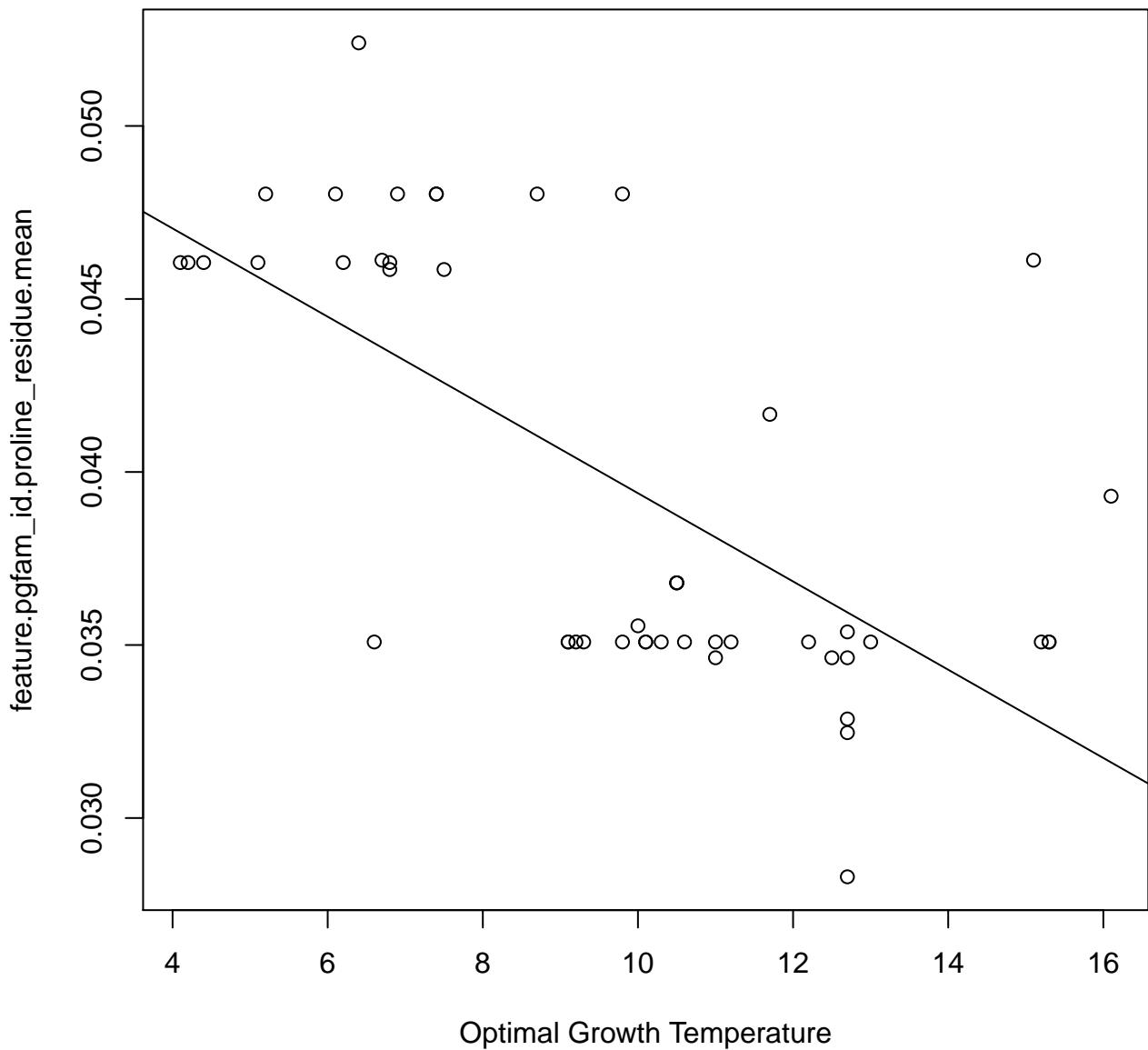
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Sensor histidine kinase PrrB (RegB) (EC 2.7.3.-)



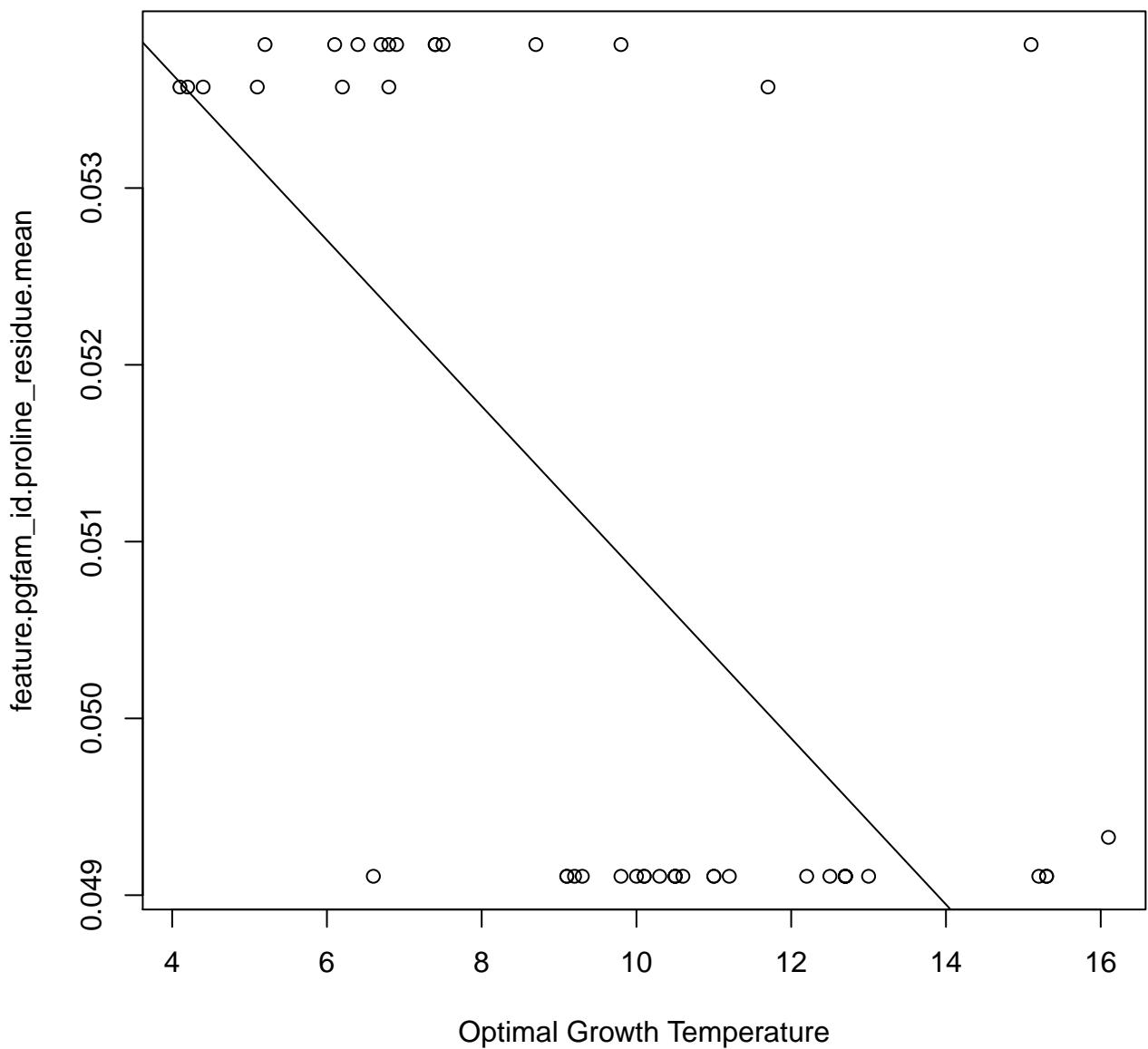
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hypothetical protein



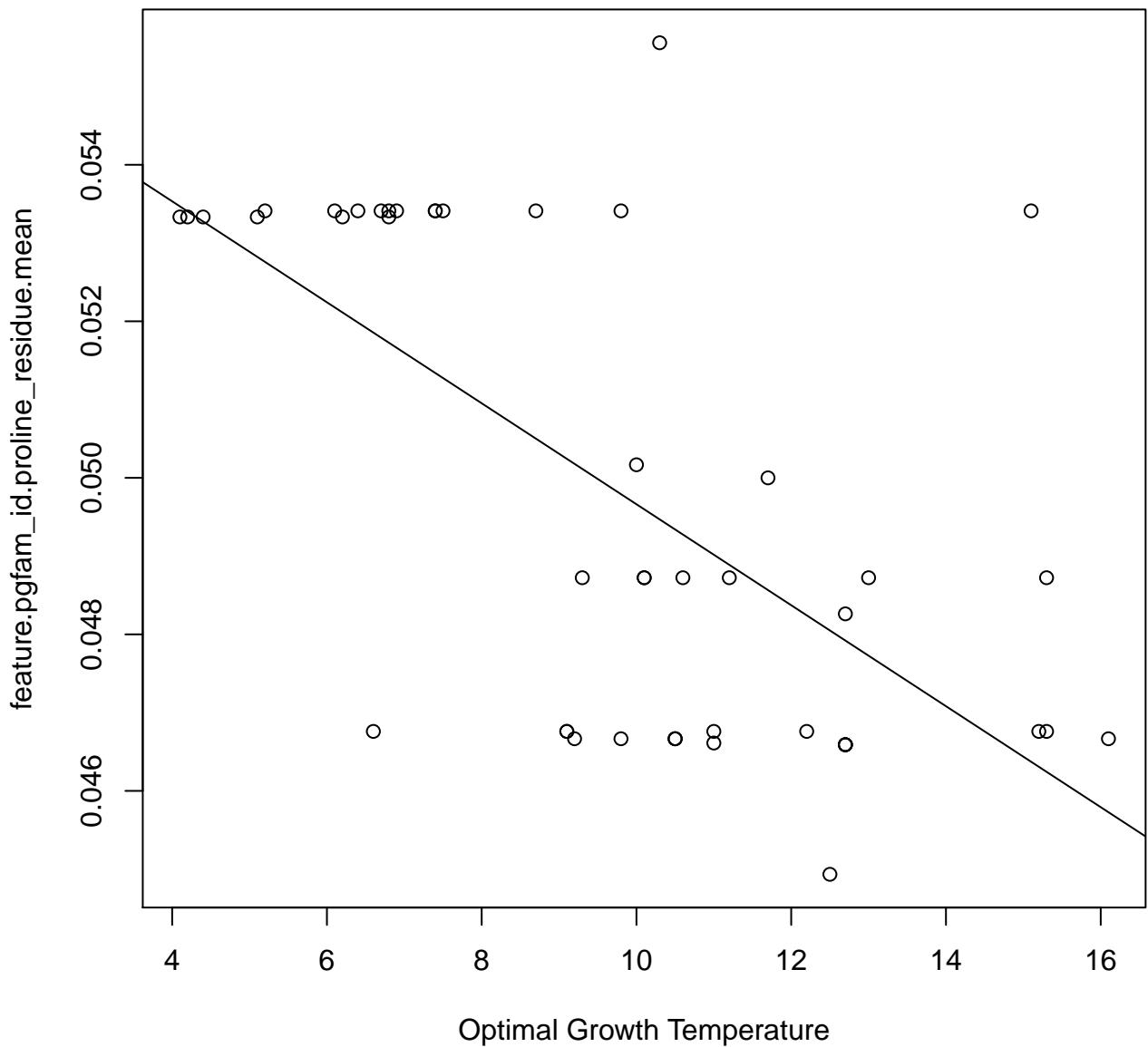
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tRNA(Ile)-lysidine synthetase (EC 6.3.4.19)



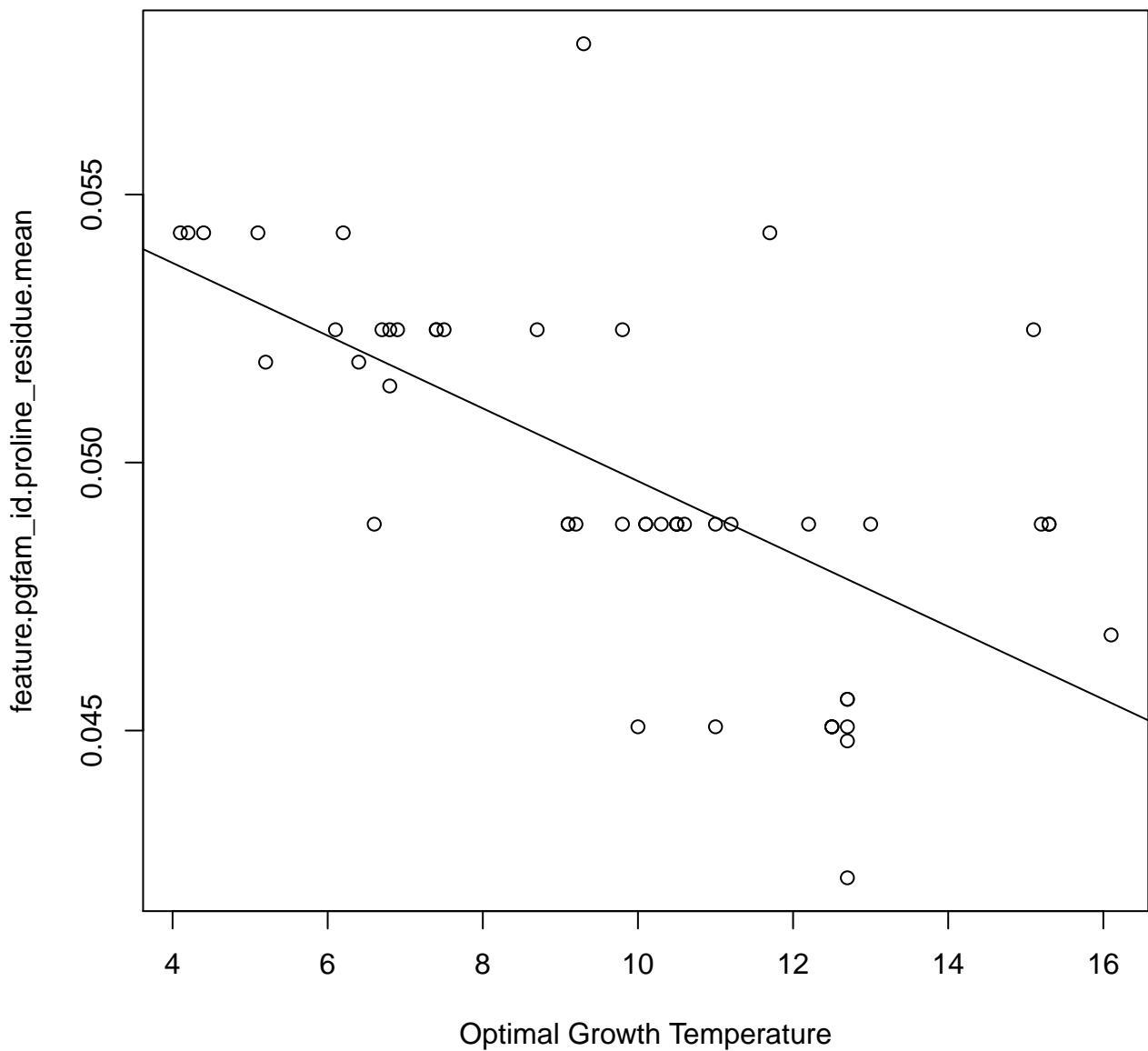
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Ribulose-phosphate 3-epimerase (EC 5.1.3.1)



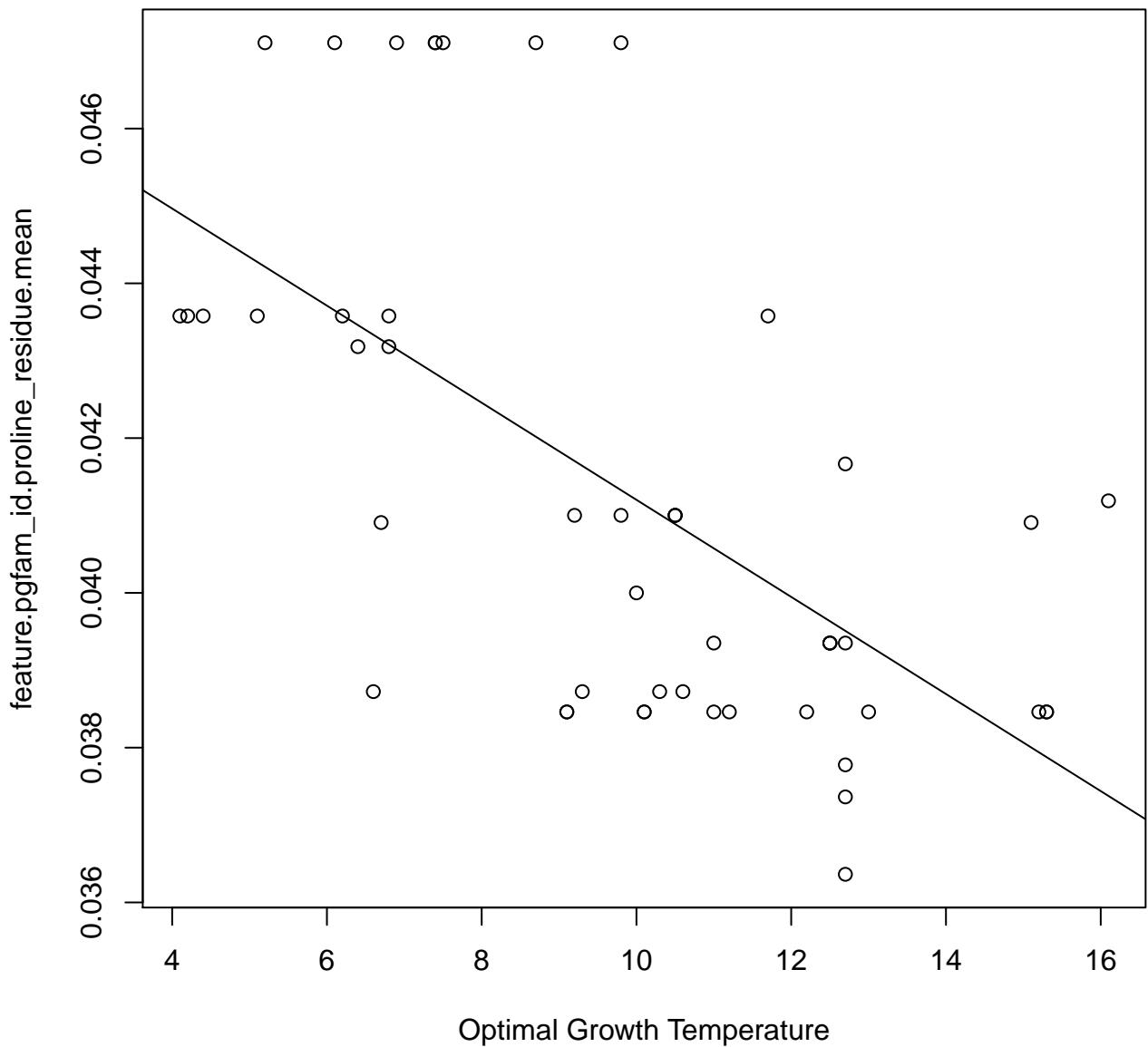
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PGF_05873936
Hydrogen peroxide-inducible genes activator => OxyR



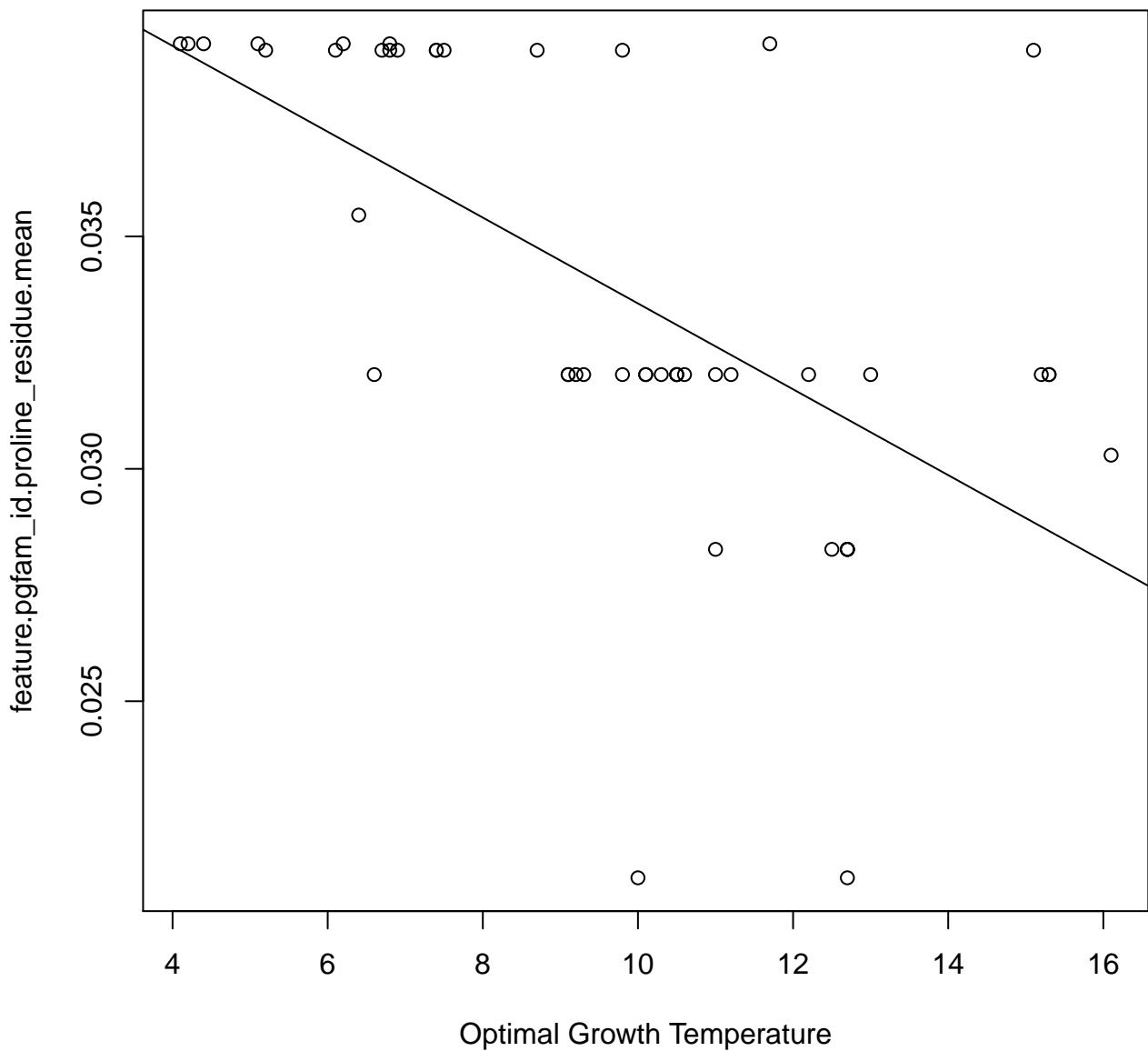
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Dihydroorotate (EC 3.5.2.3)



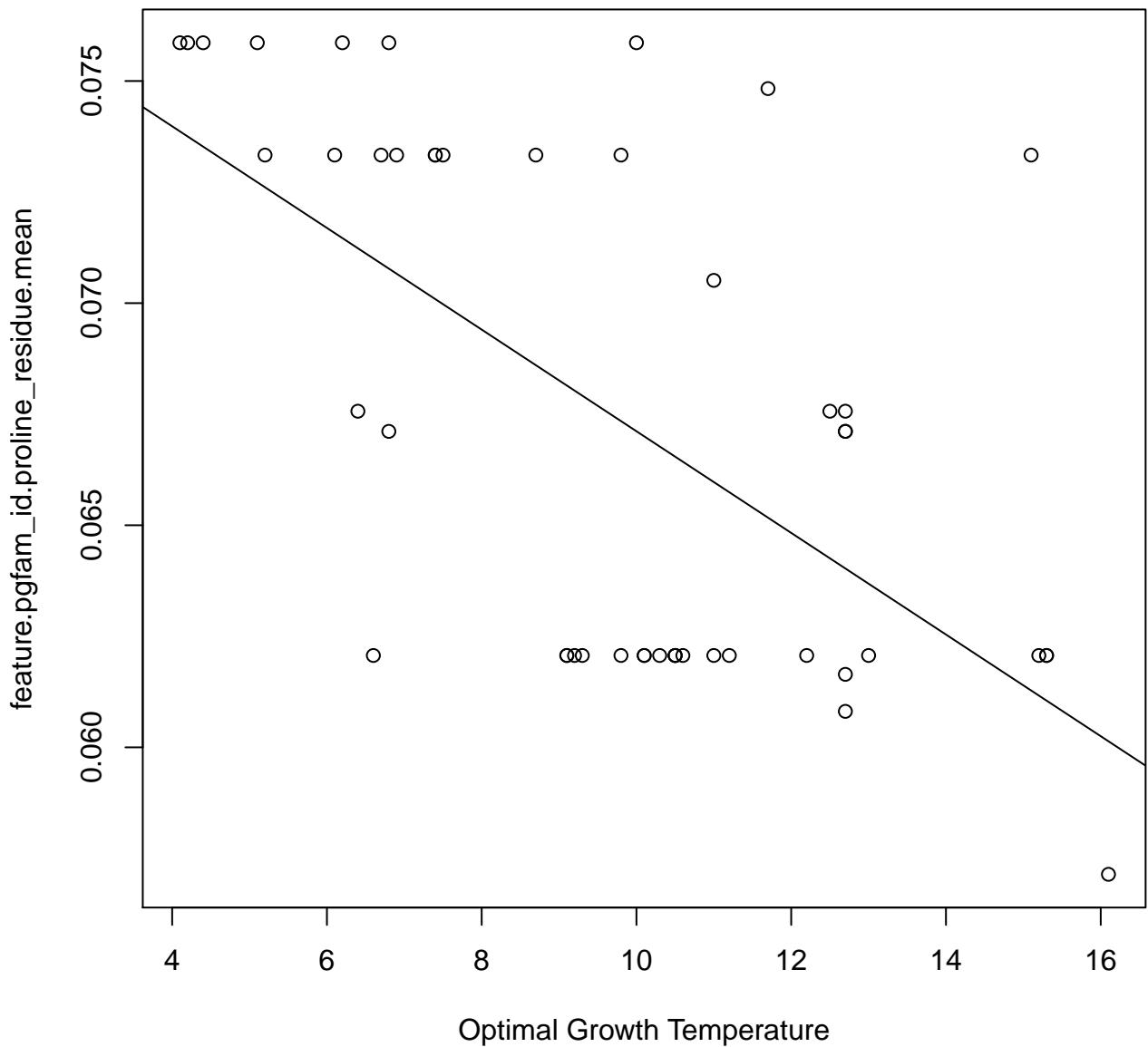
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ATP-dependent RNA helicase VF1437



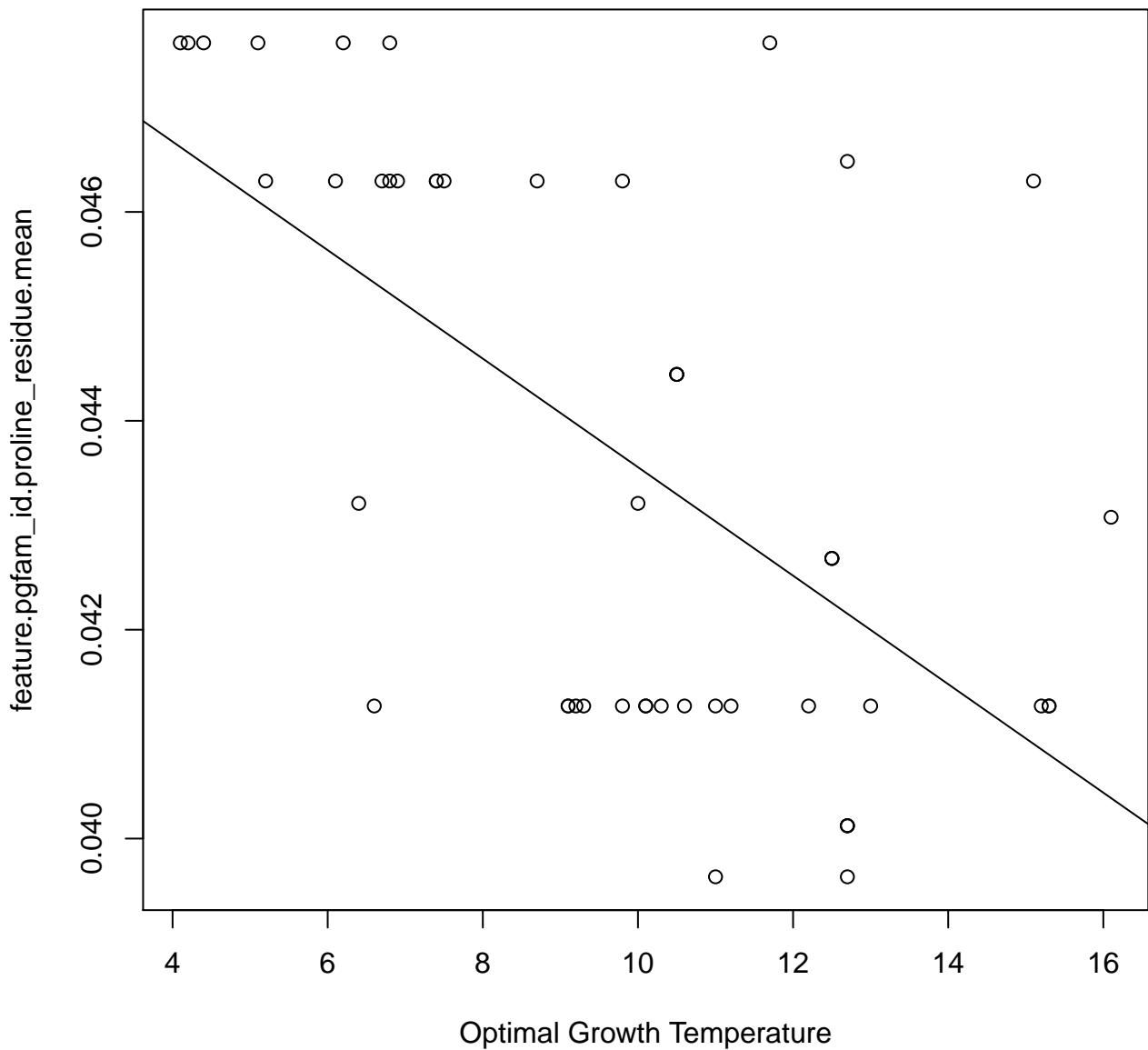
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PGF_00010518
HD domain protein



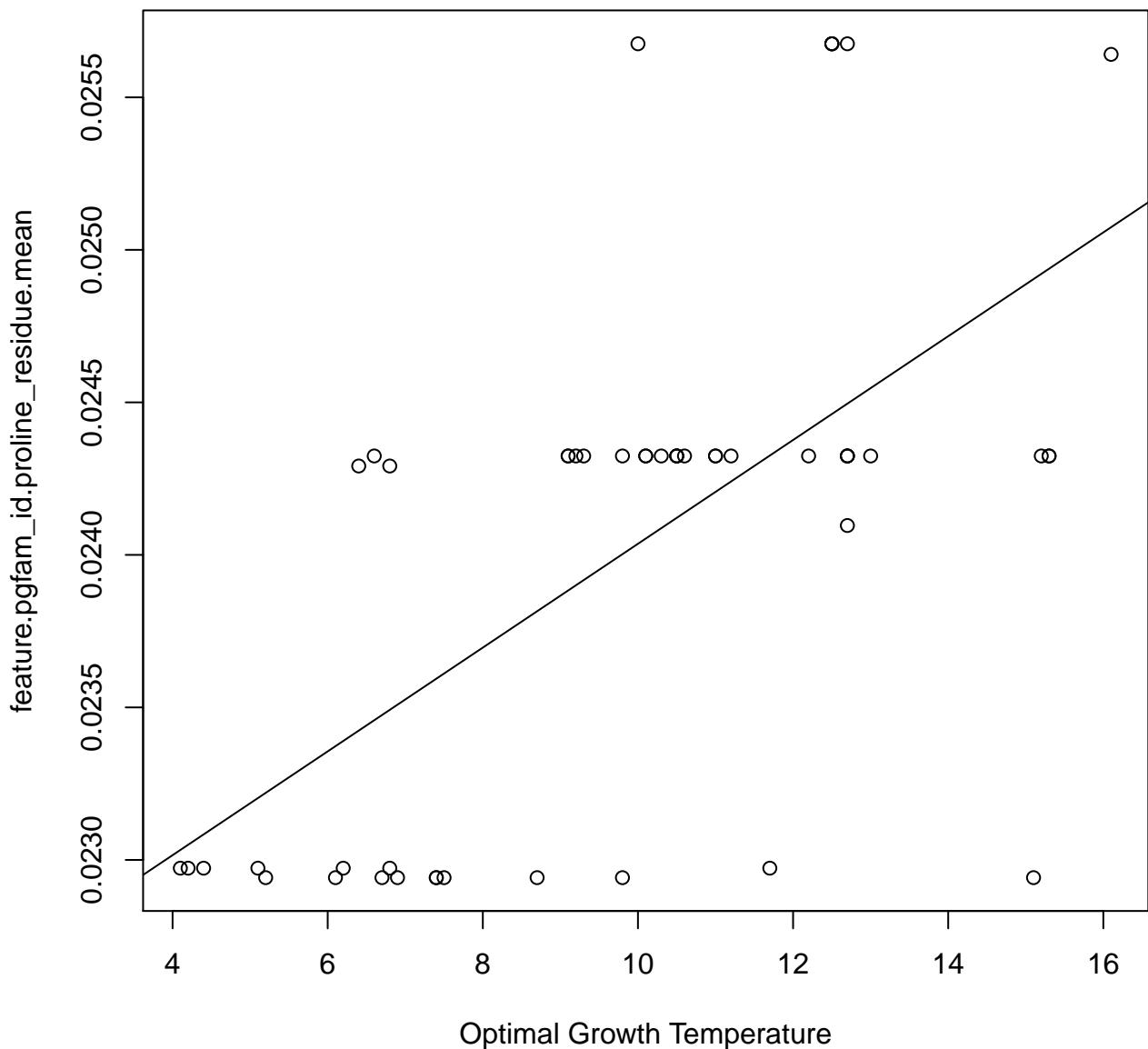
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Biotin carboxyl carrier protein of acetyl-CoA carboxylase



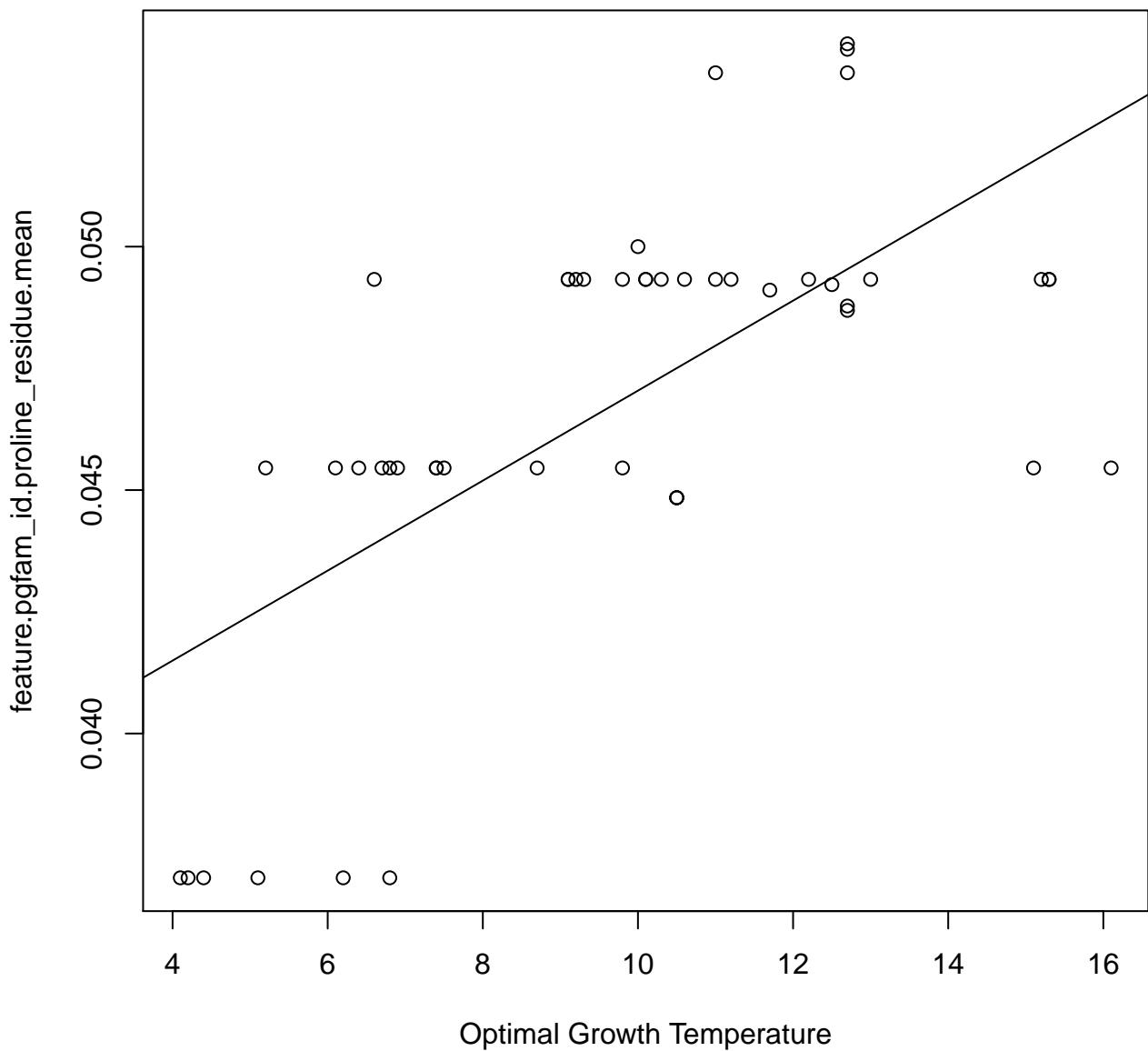
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Homoserine kinase (EC 2.7.1.39)



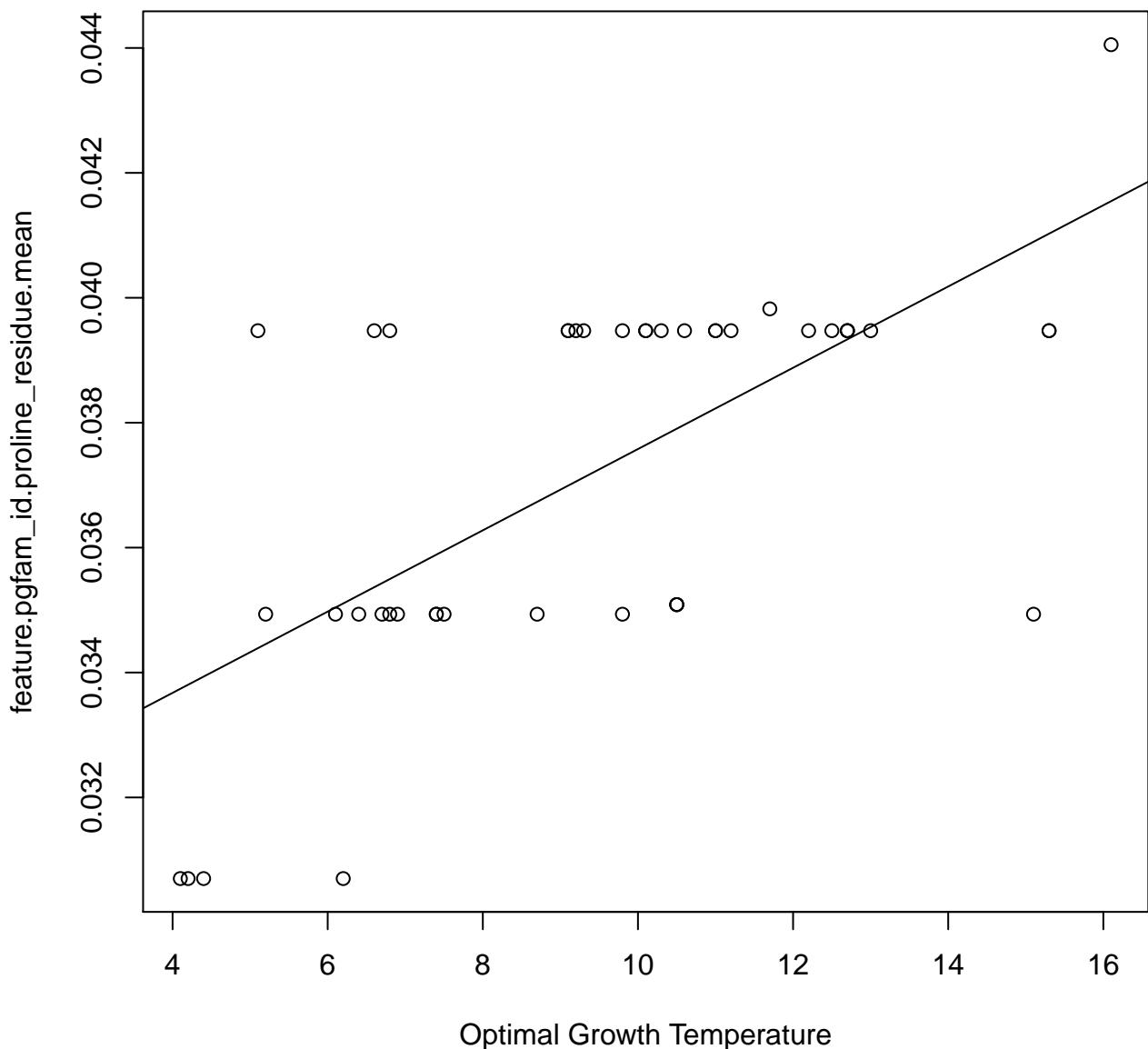
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PGF_01336307
Predicted signal transduction protein



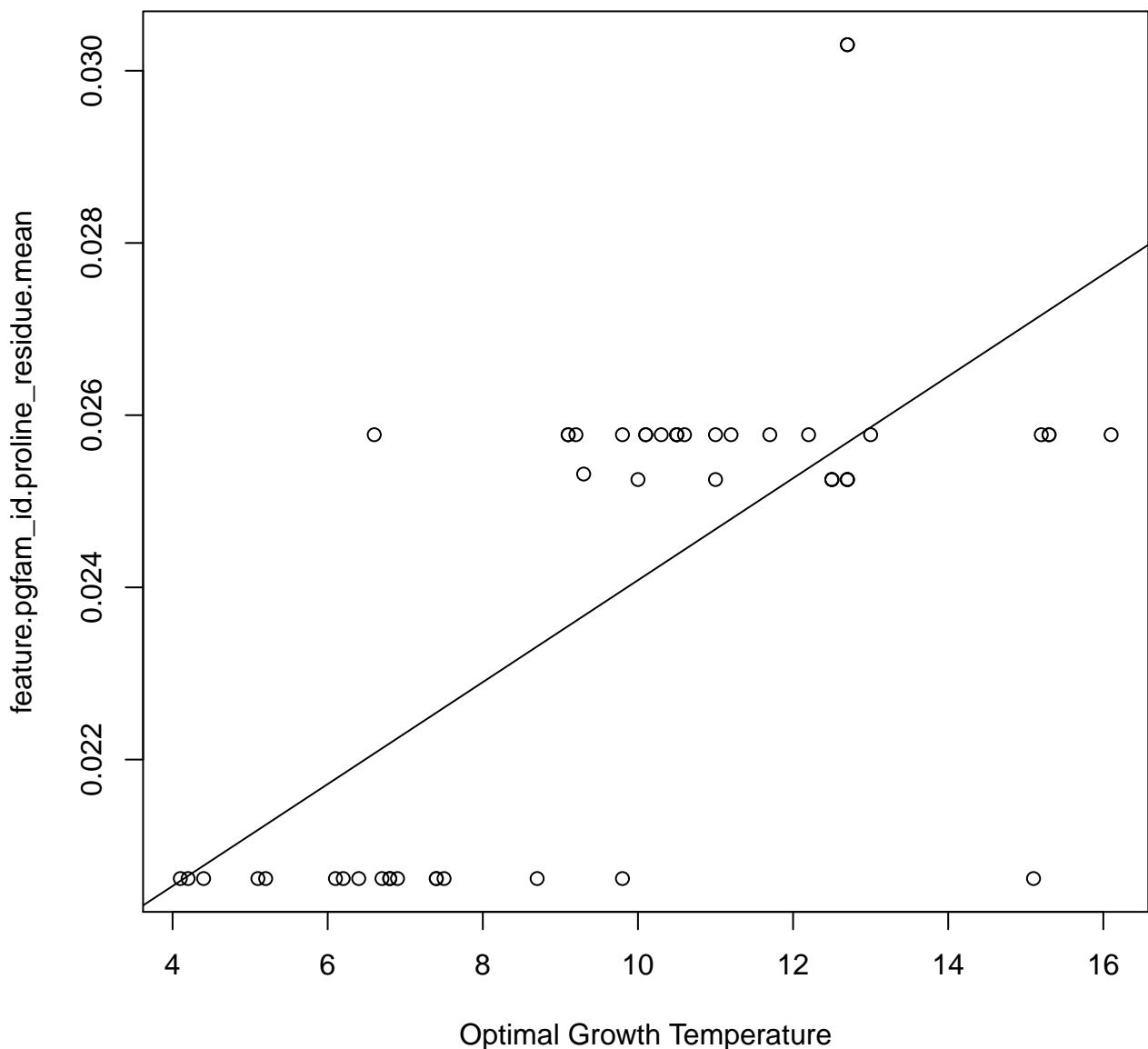
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PGF_04602939
Paraquat-inducible protein A



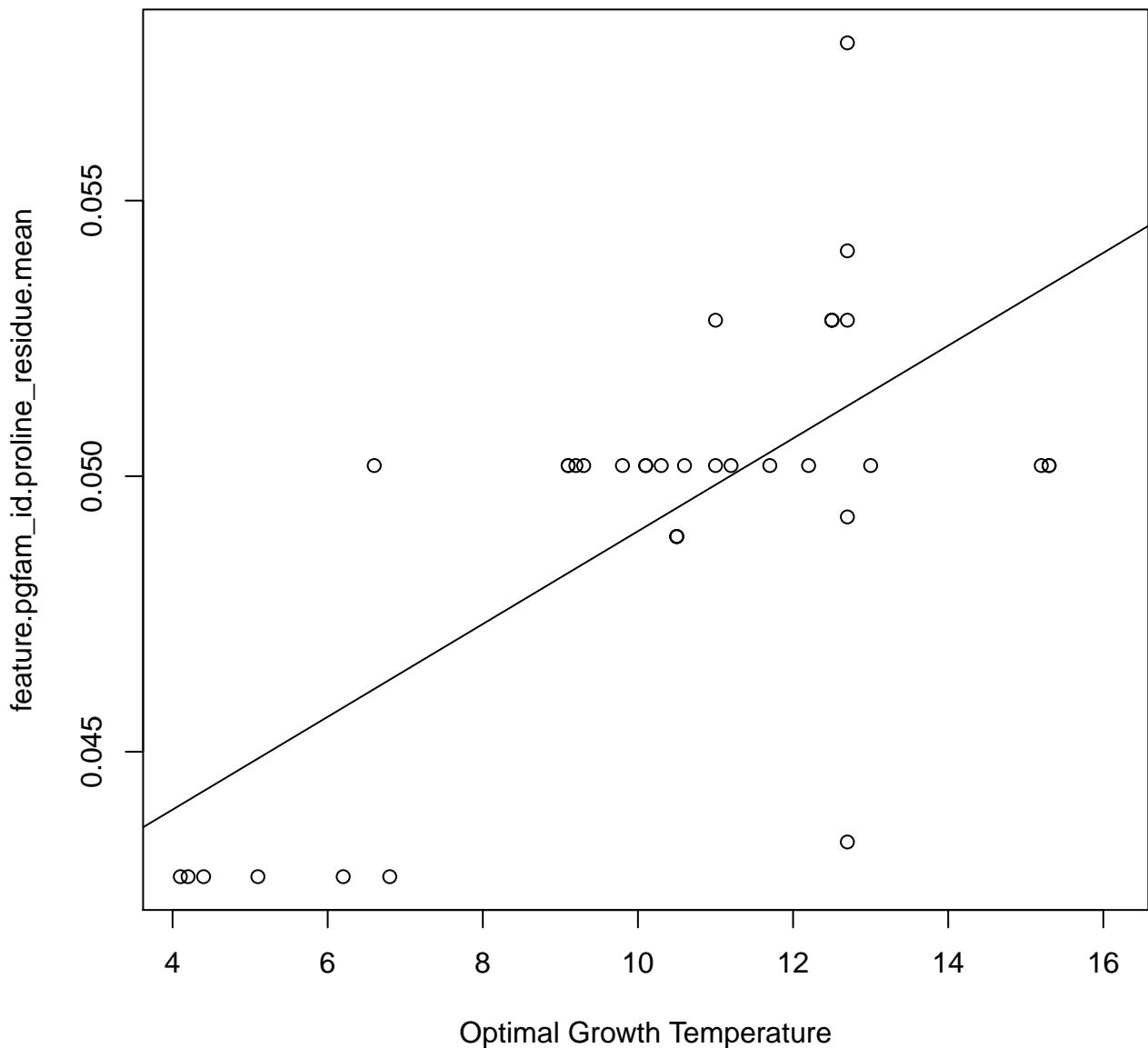
feature.pgfam_id.proline_residue.mean
PGF_03832998
FIG111991: hypothetical protein



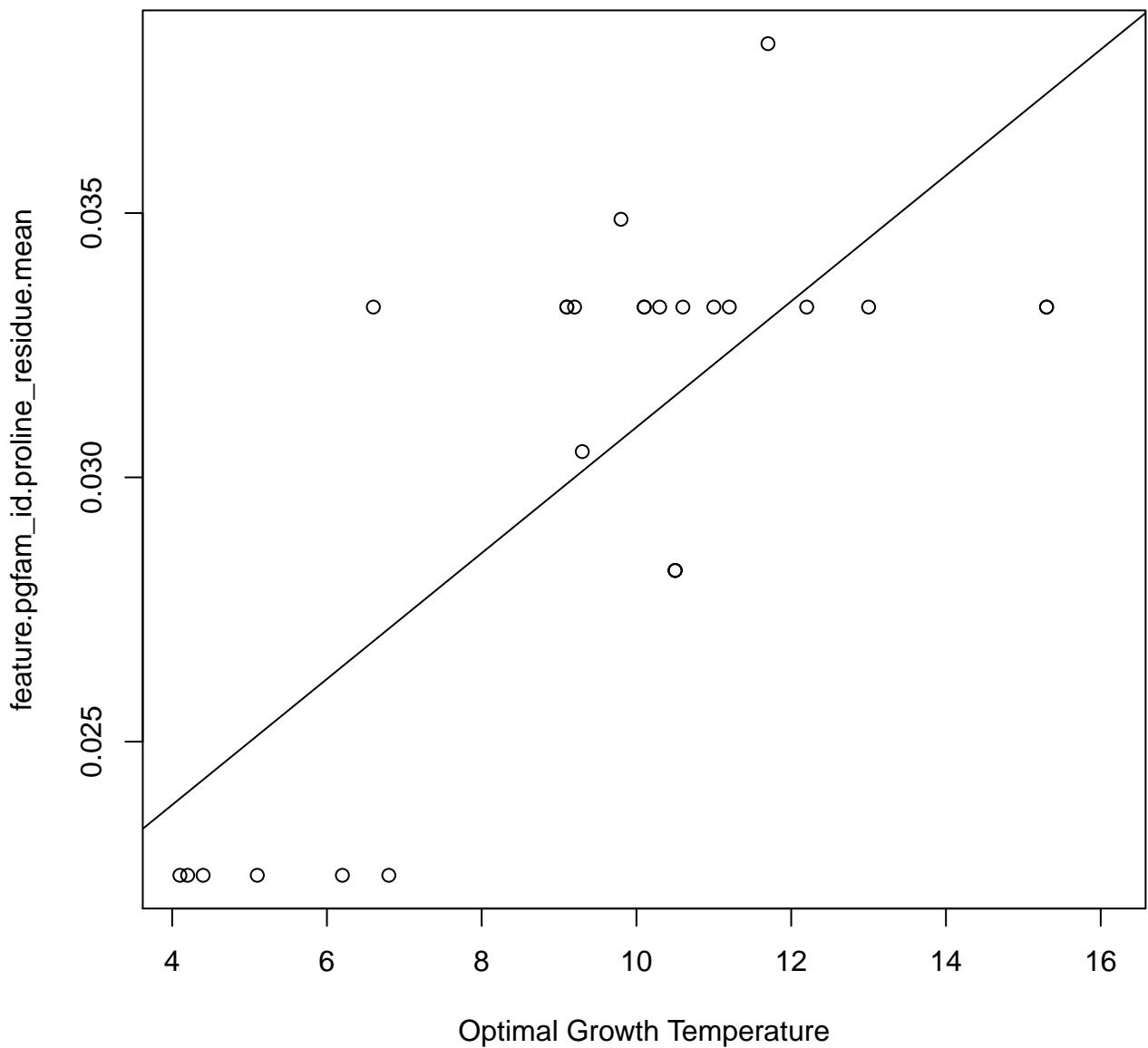
feature.pgfam_id.proline_residue.mean
PGF_00058666
Transcriptional regulator SImA, TetR family



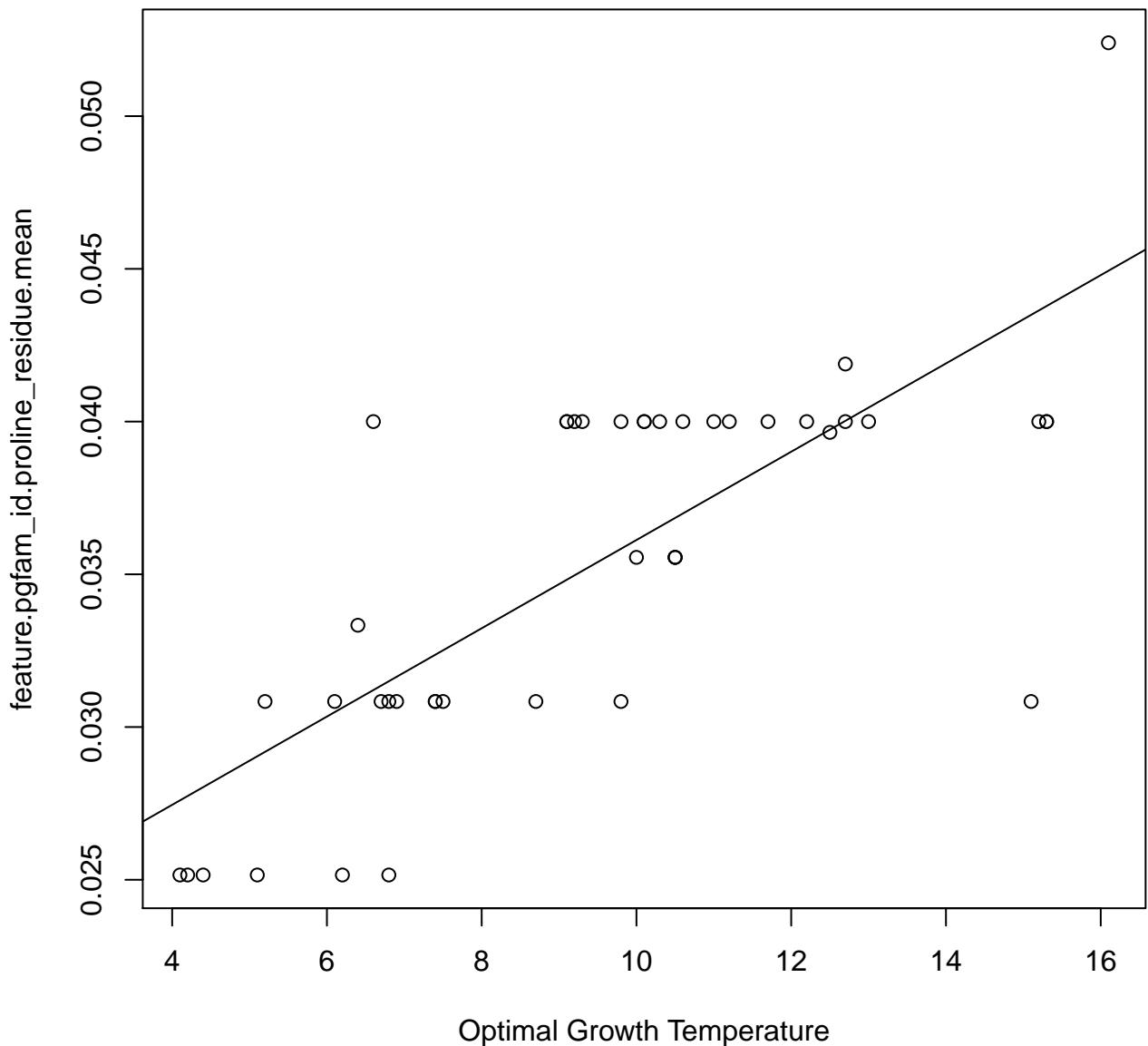
feature.pgfam_id.proline_residue.mean
PGF_00004056
Fatty acid cis/trans isomerase



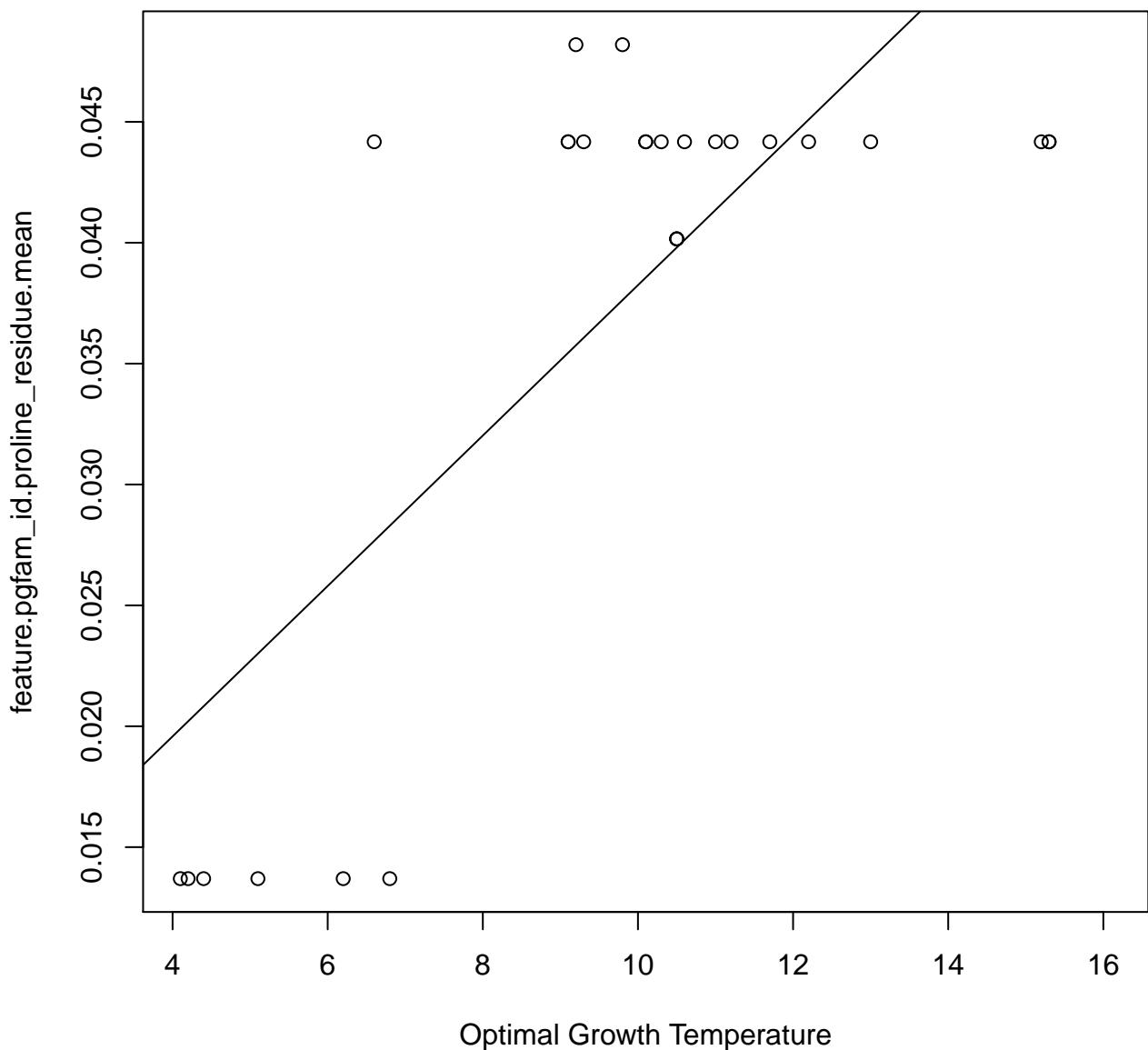
feature.pgfam_id.proline_residue.mean
PGF_03083319
Maltodextrin glucosidase (EC 3.2.1.20)



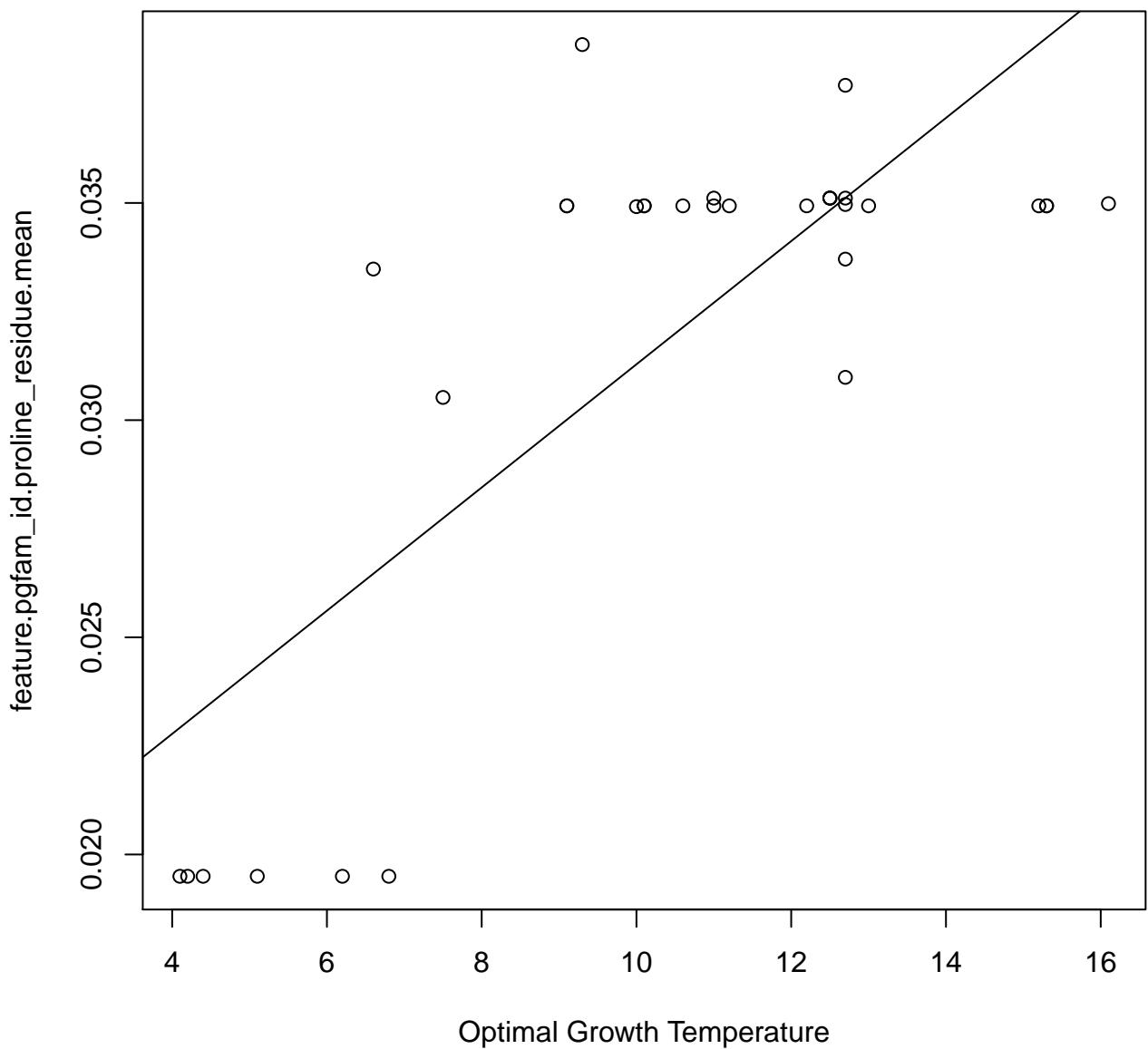
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PGF_02911177
SM-20-related protein



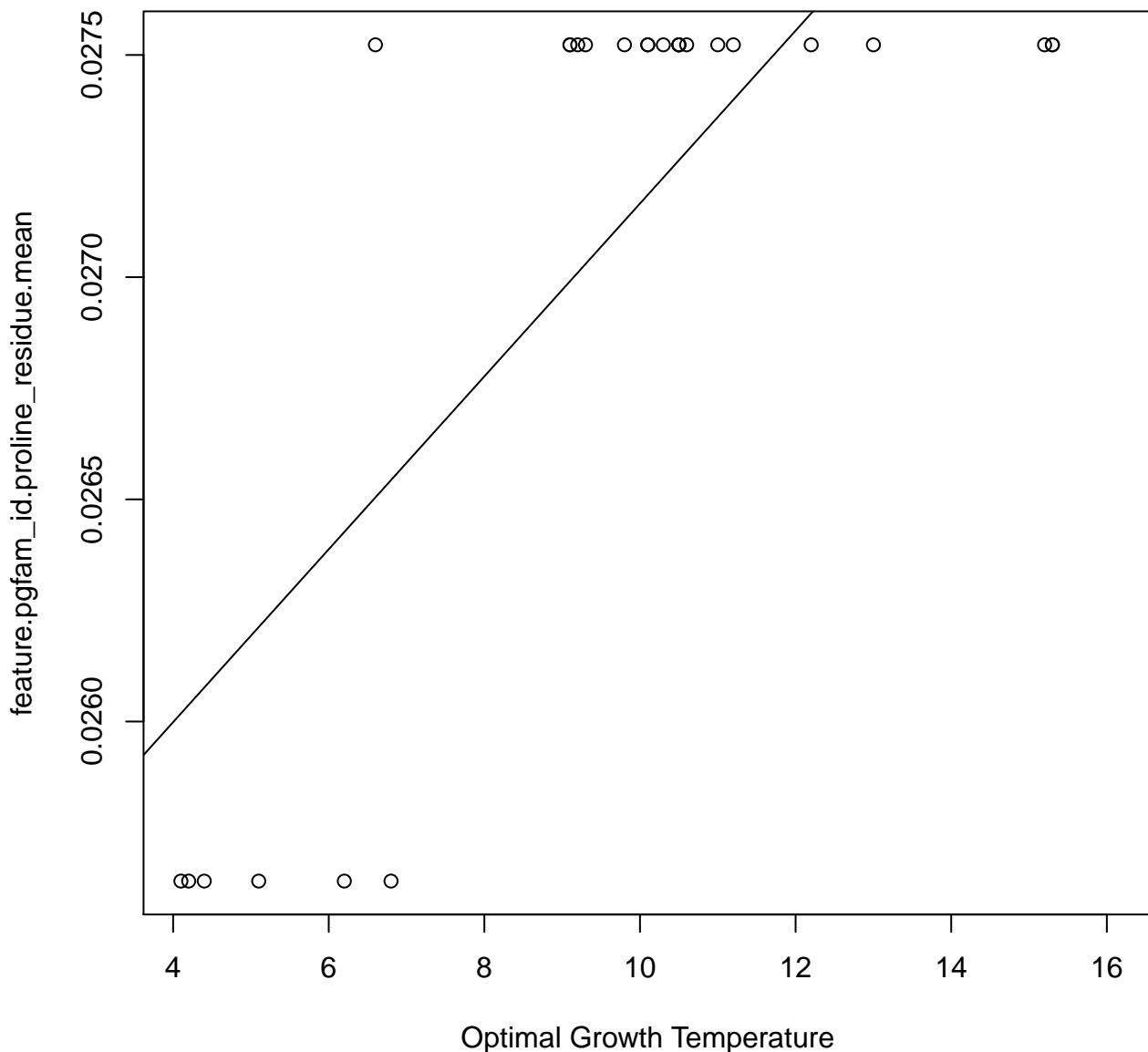
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PGF_11018774
hypothetical protein



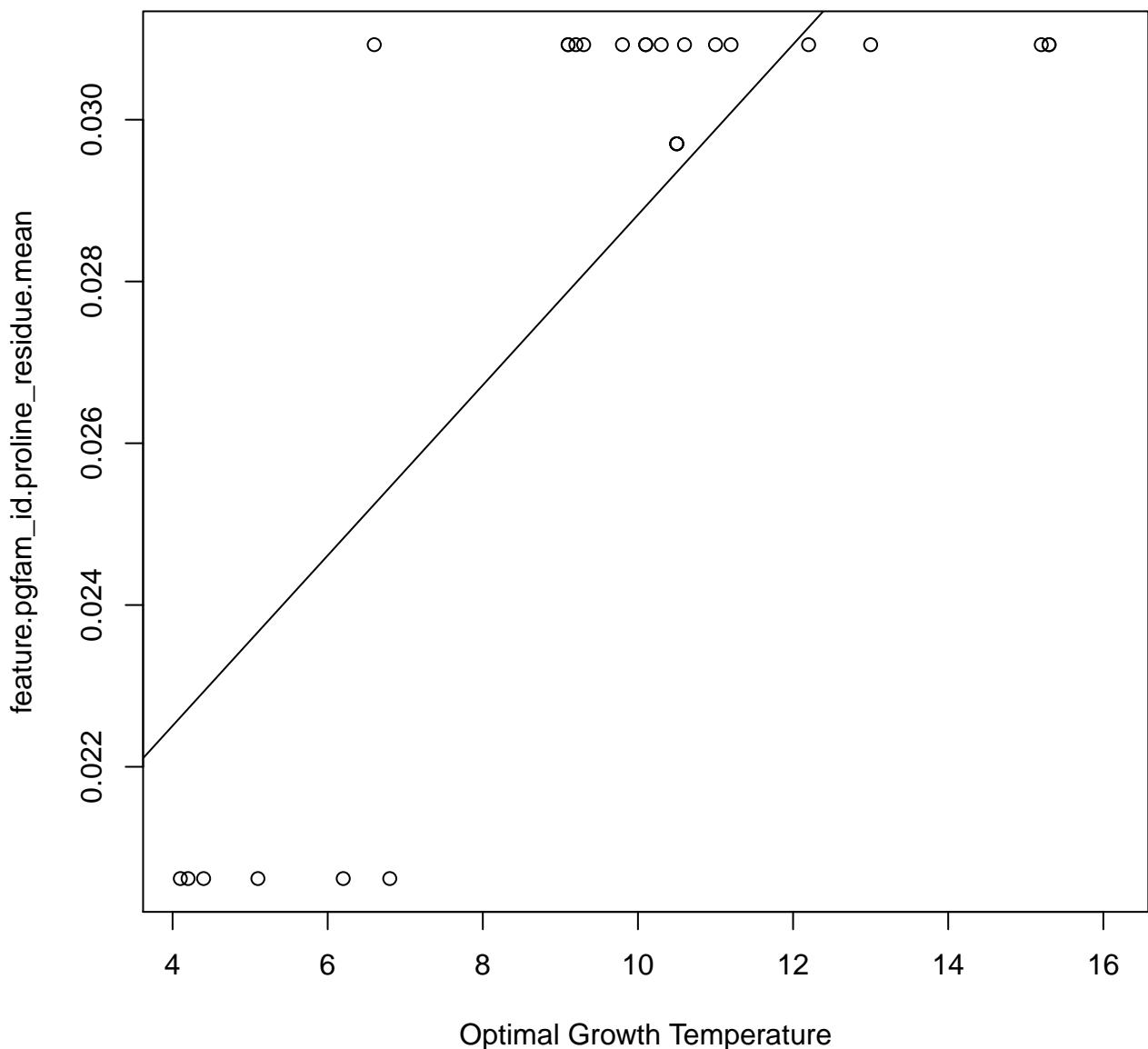
feature.pgfam_id.proline_residue.mean
PGF_06641194
Capsule biosynthesis protein capA



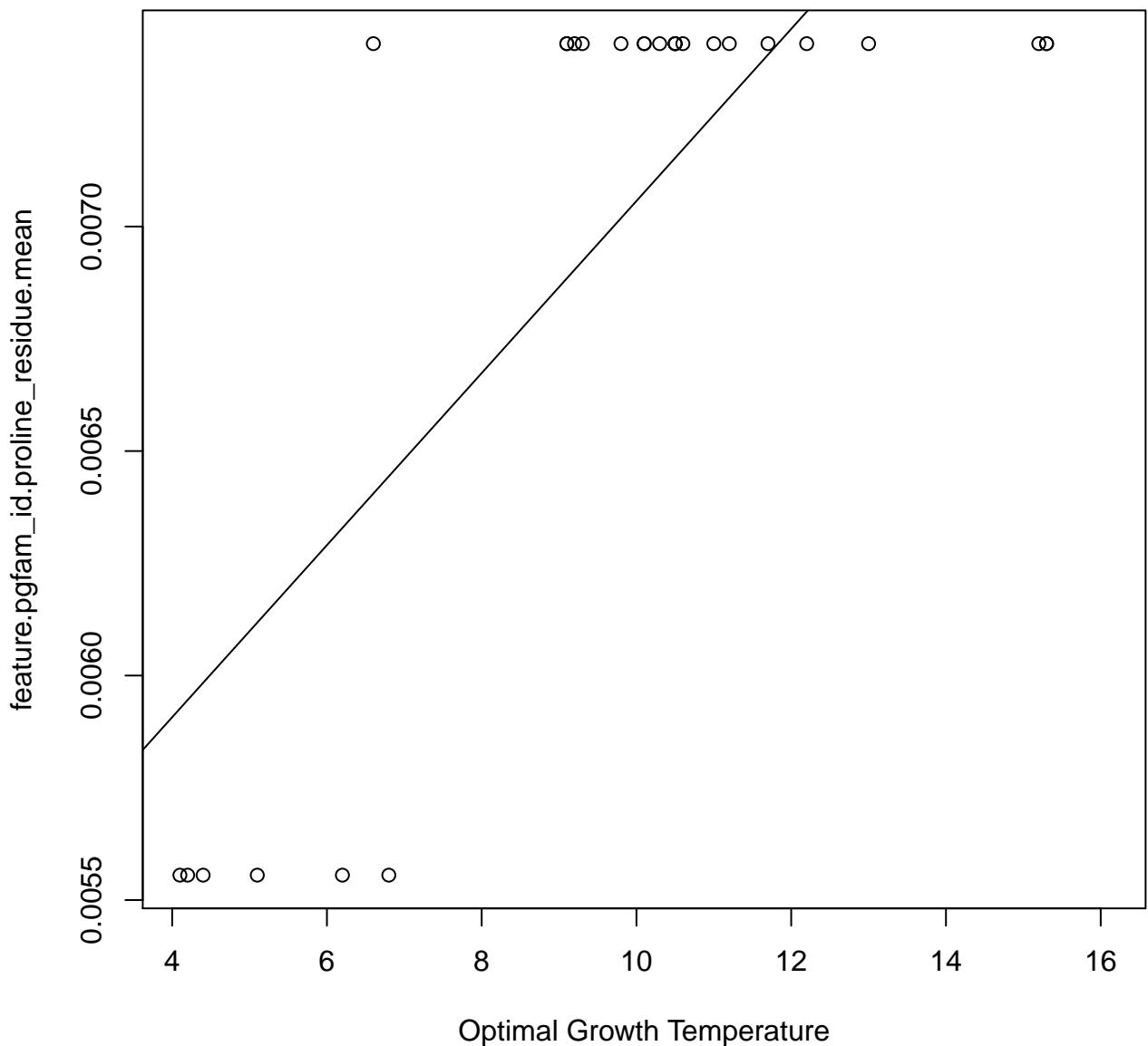
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PGF_11025496
hypothetical protein



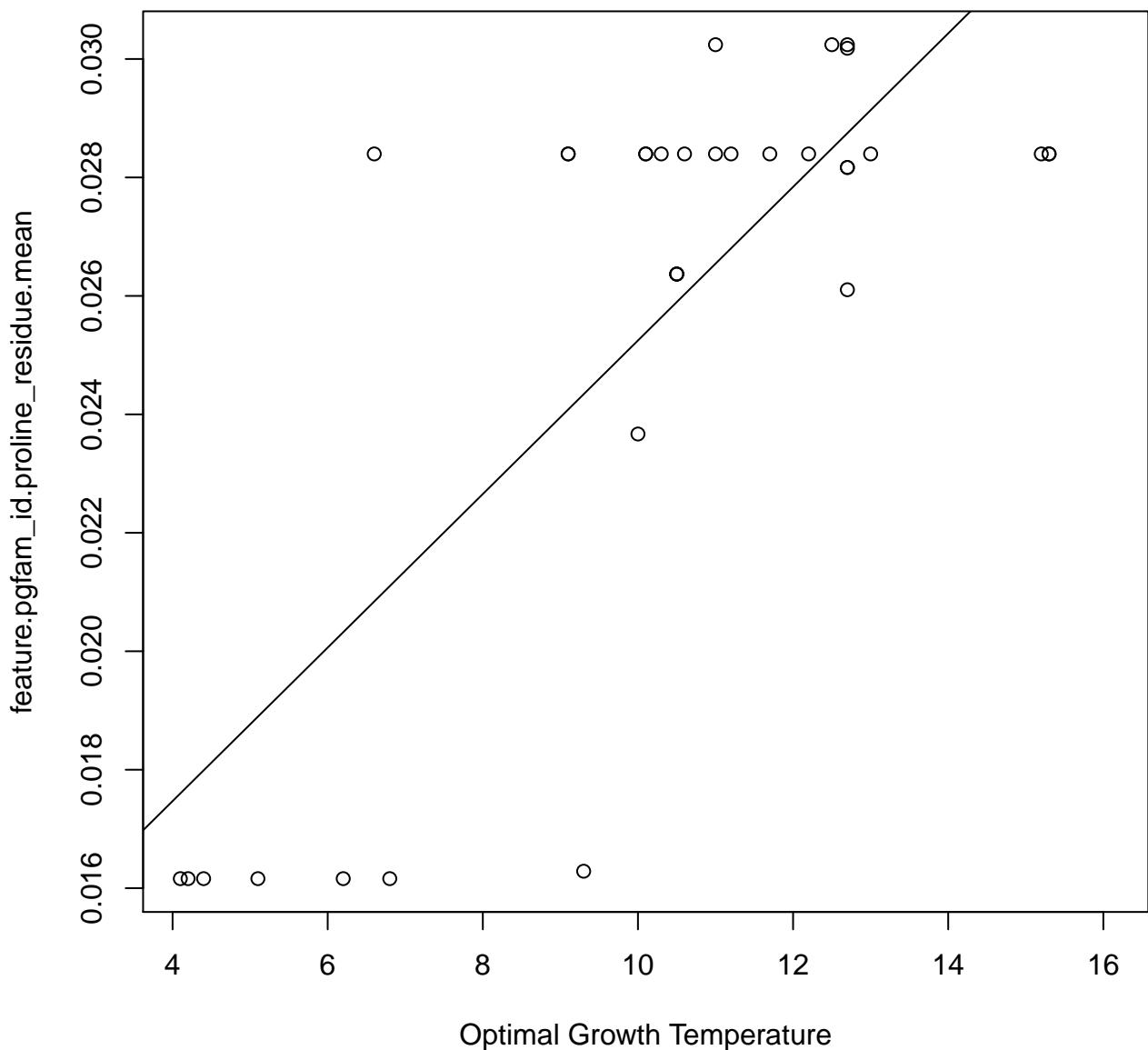
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PGF_11915740
hypothetical protein



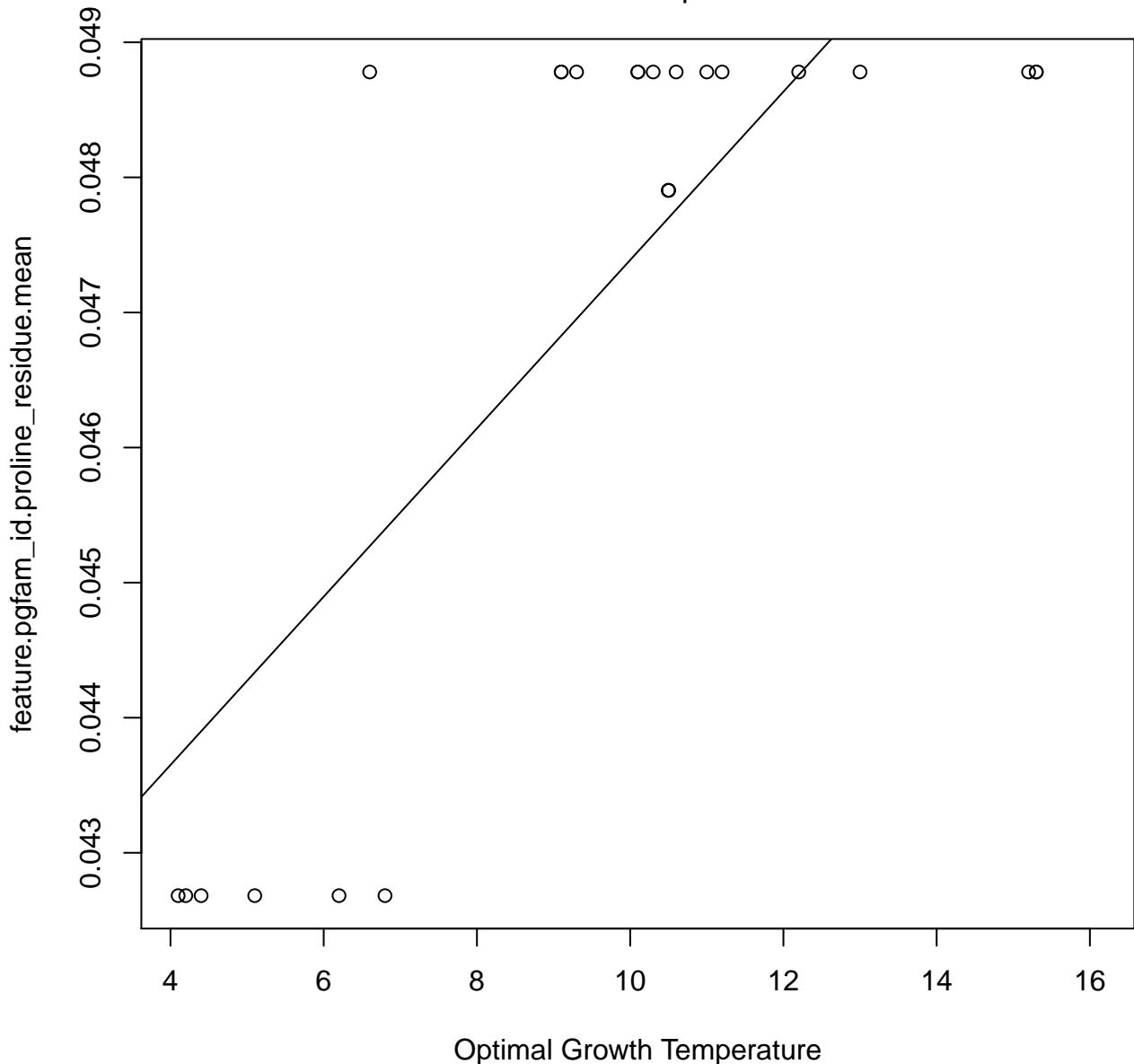
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PGF_10494566
hypothetical protein



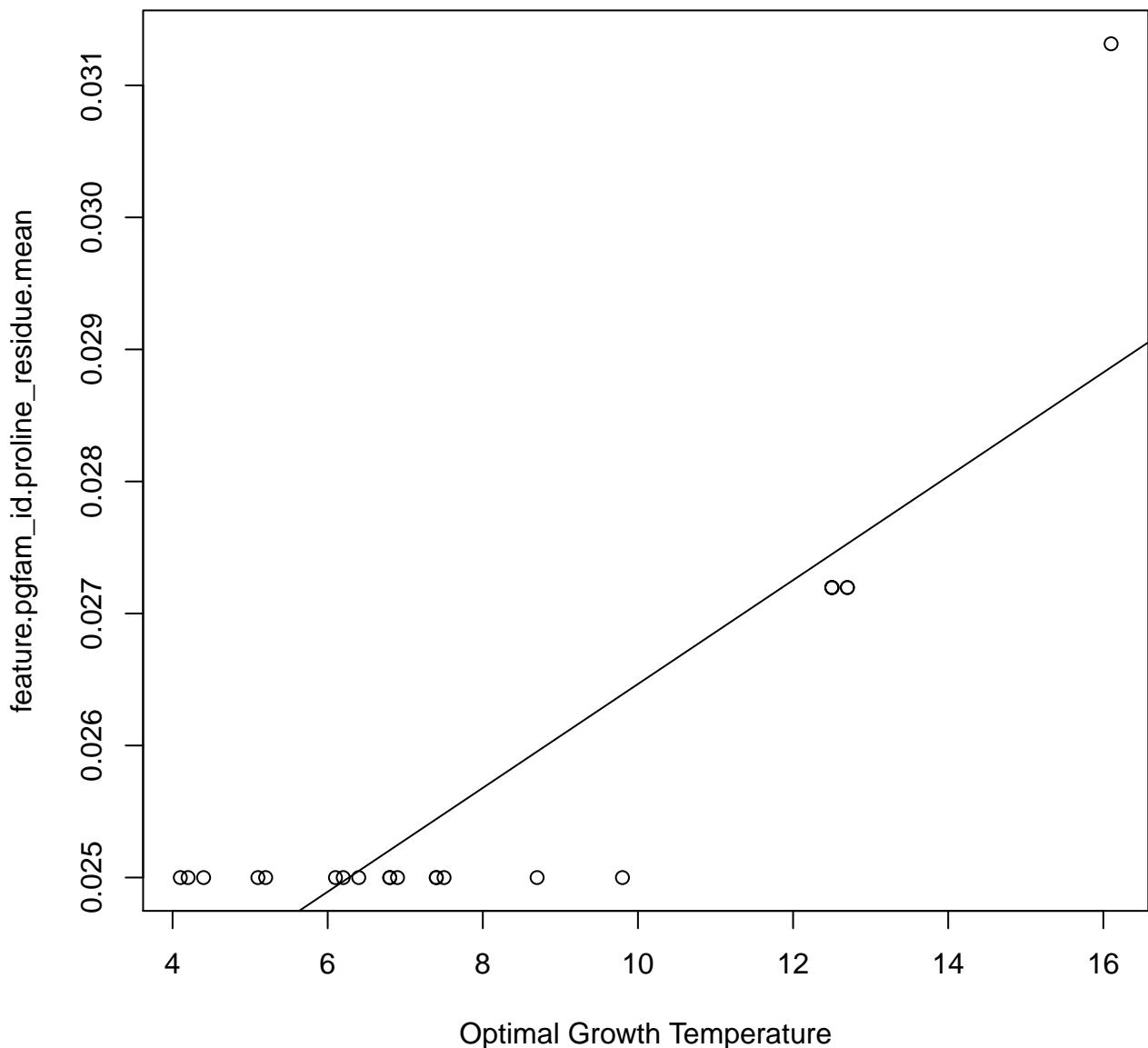
feature.pgfam_id.proline_residue.mean
PGF_12765299
Two-component system sensor histidine kinase



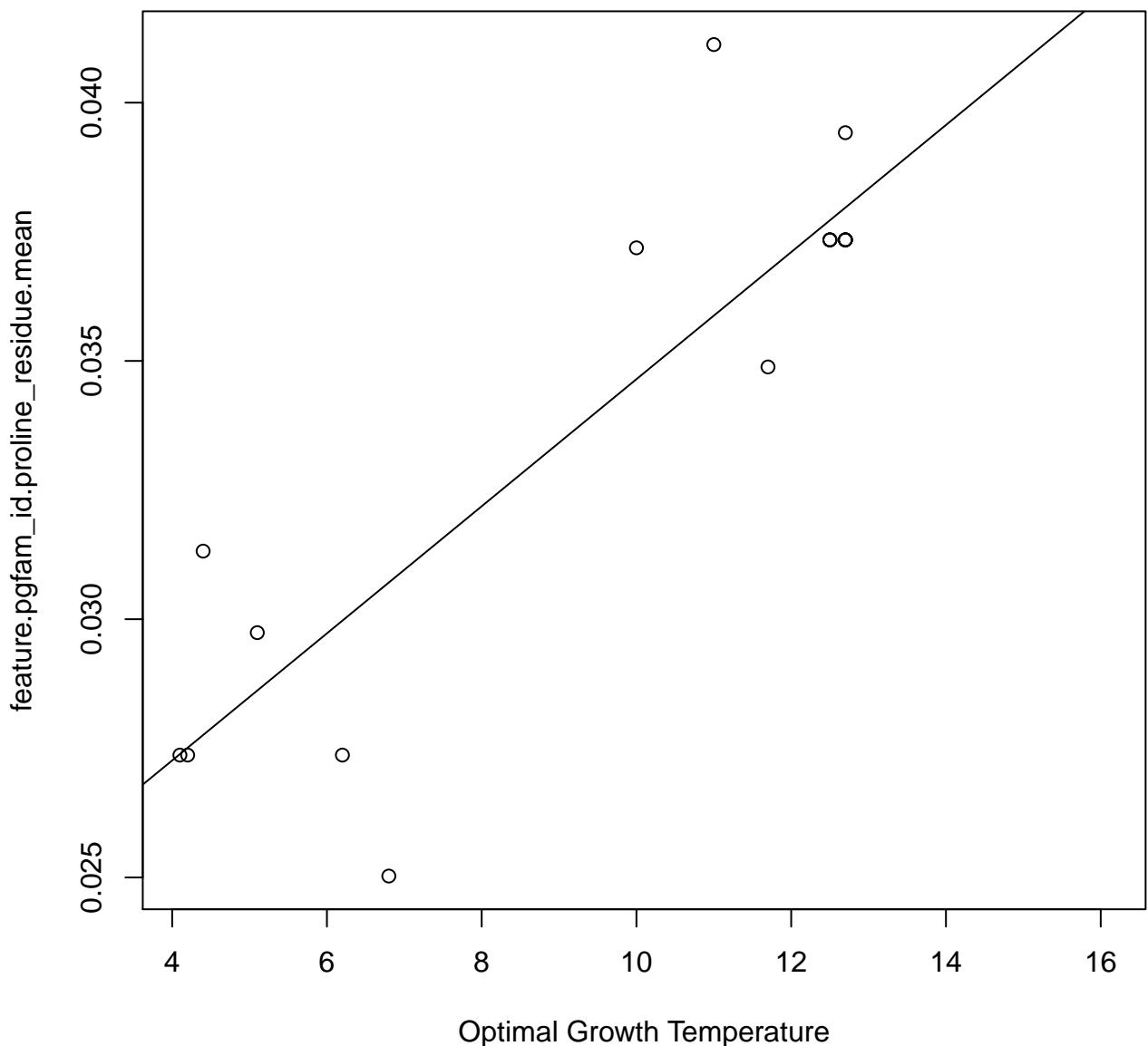
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PGF_10751741
Redoxin domain protein



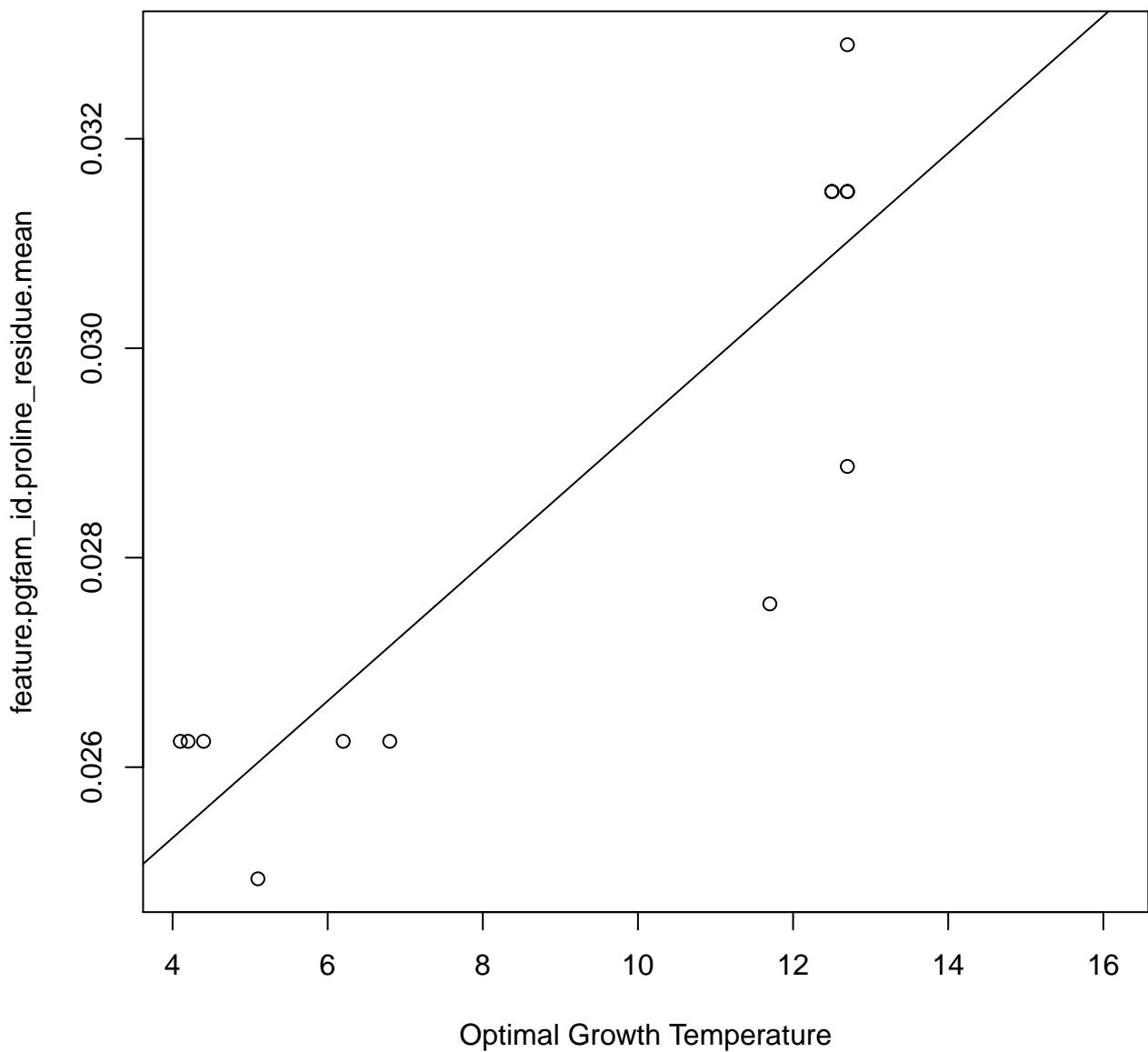
feature.pgfam_id.proline_residue.mean
PGF_02732386
Glucose/mannose:H⁺ symporter GlcP



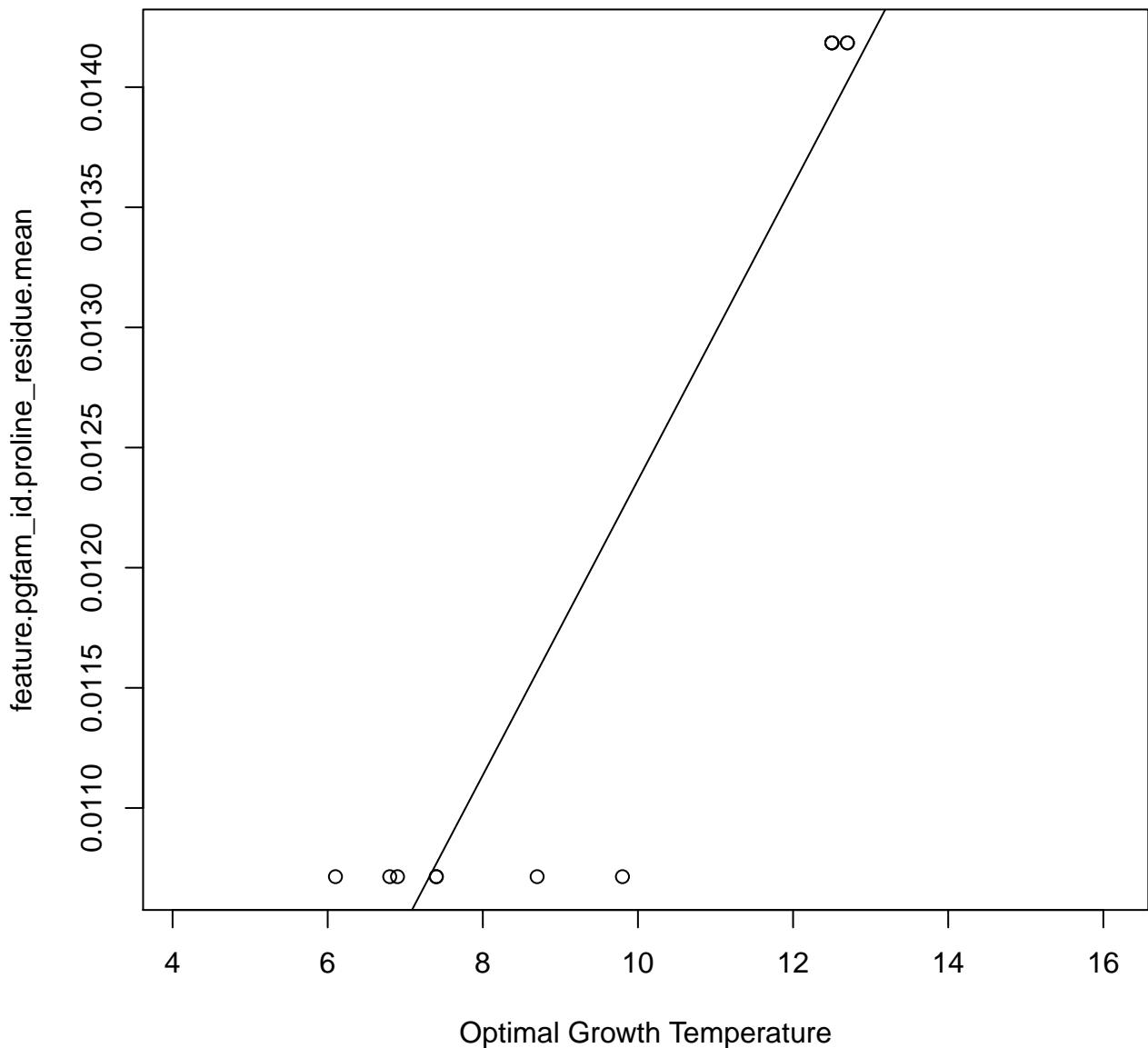
feature.pgfam_id.proline_residue.mean
PGF_00066964
Xanthine/uracil/thiamine/ascorbate permease family protein



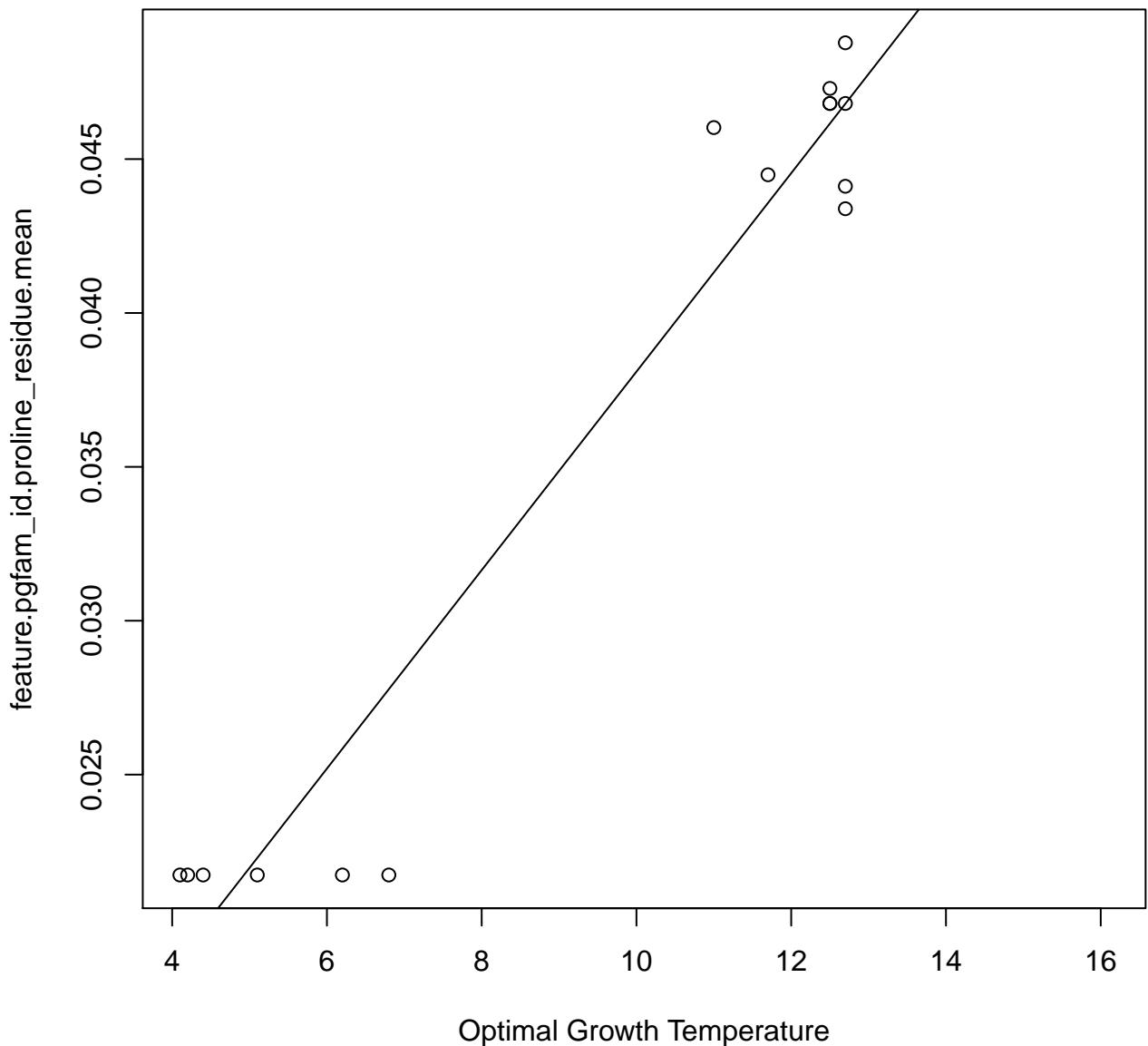
feature.pgfam_id.proline_residue.mean
PGF_00658019
TonB-dependent receptor



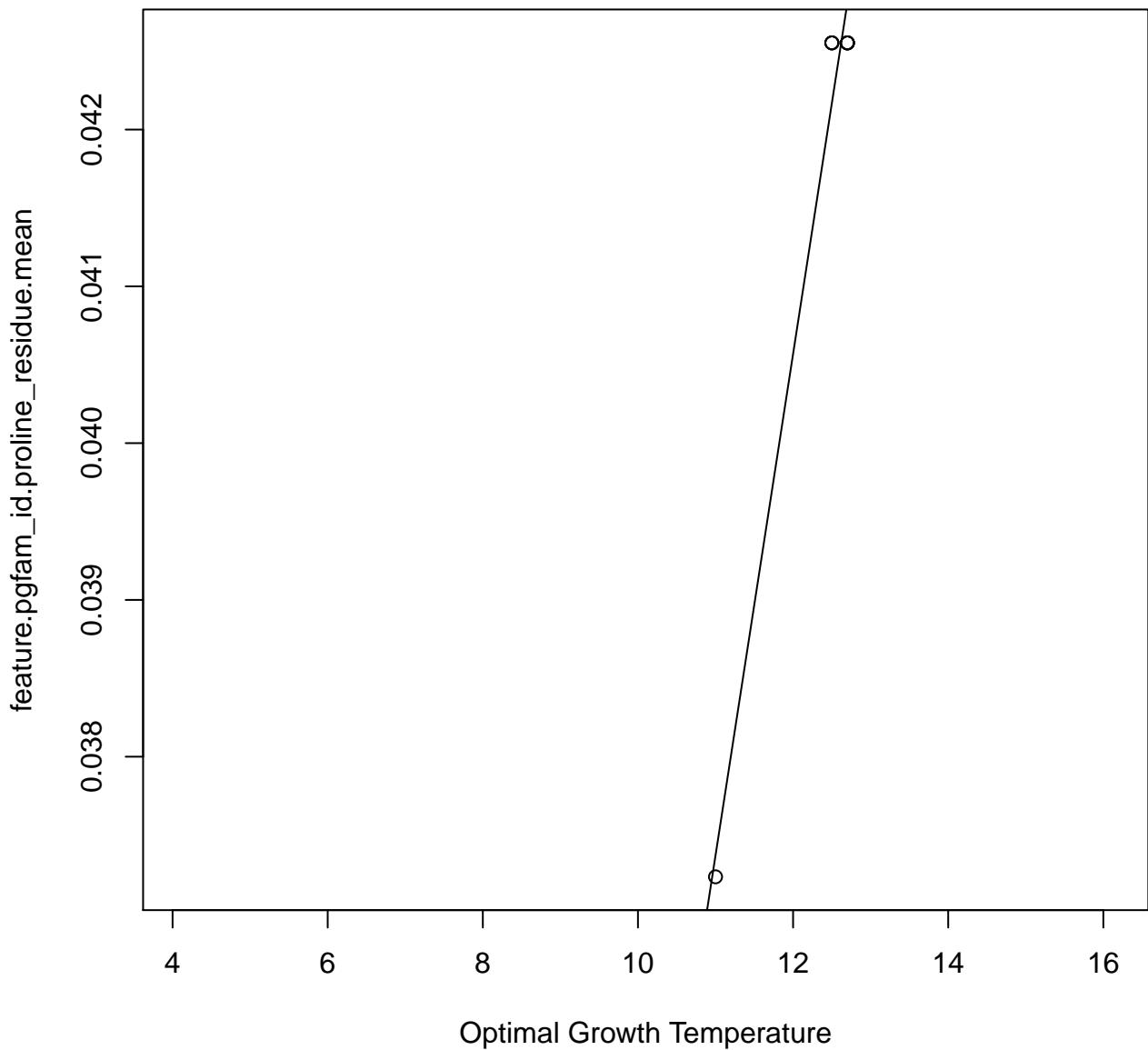
feature.pgfam_id.proline_residue.mean
PGF_01338003
Membrane-associated methyl-accepting chemotaxis protein with HAMP domain



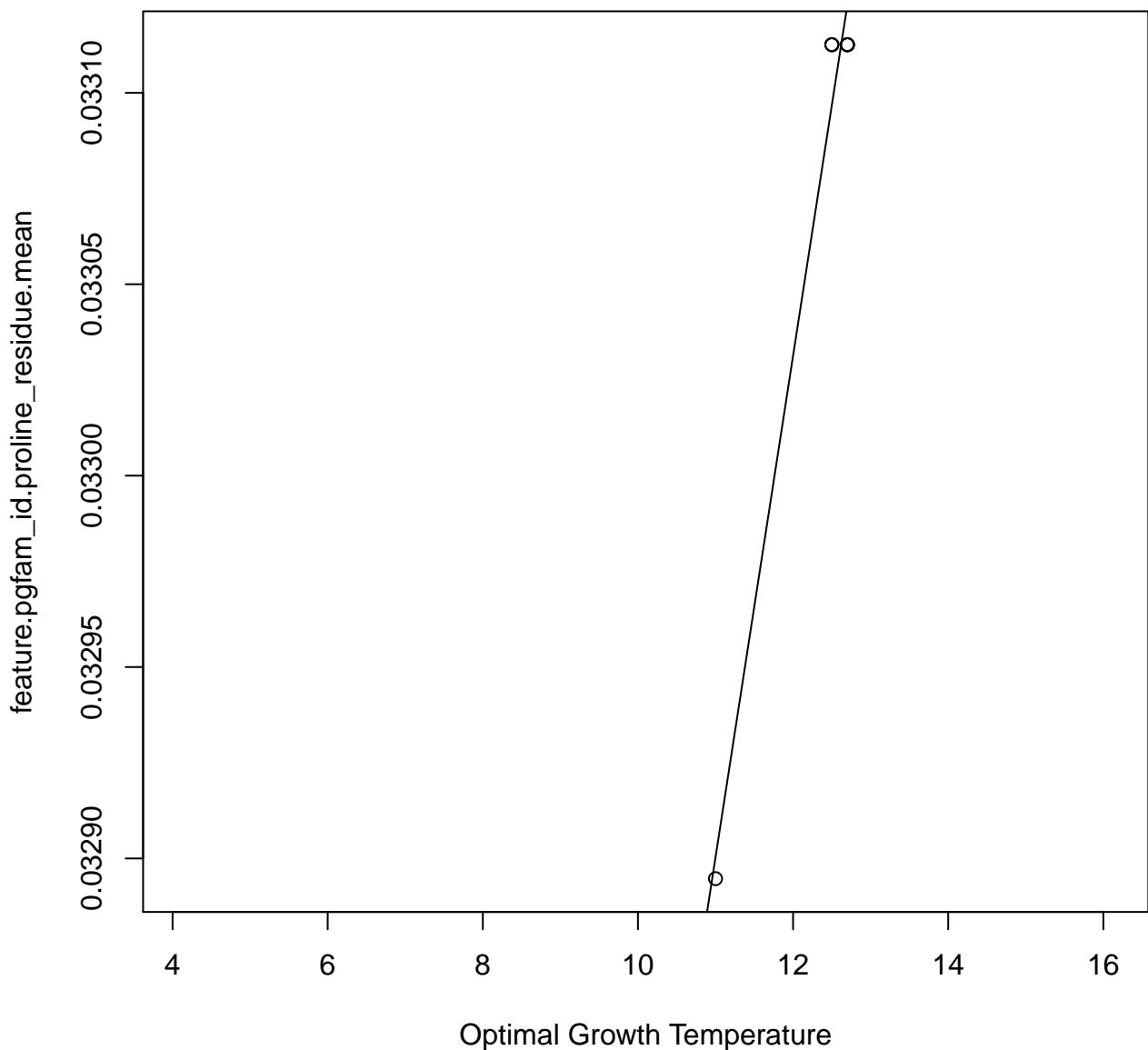
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PGF_00418379
Cobyricin acid a,c-diamide synthetase (EC 6.3.5.11)



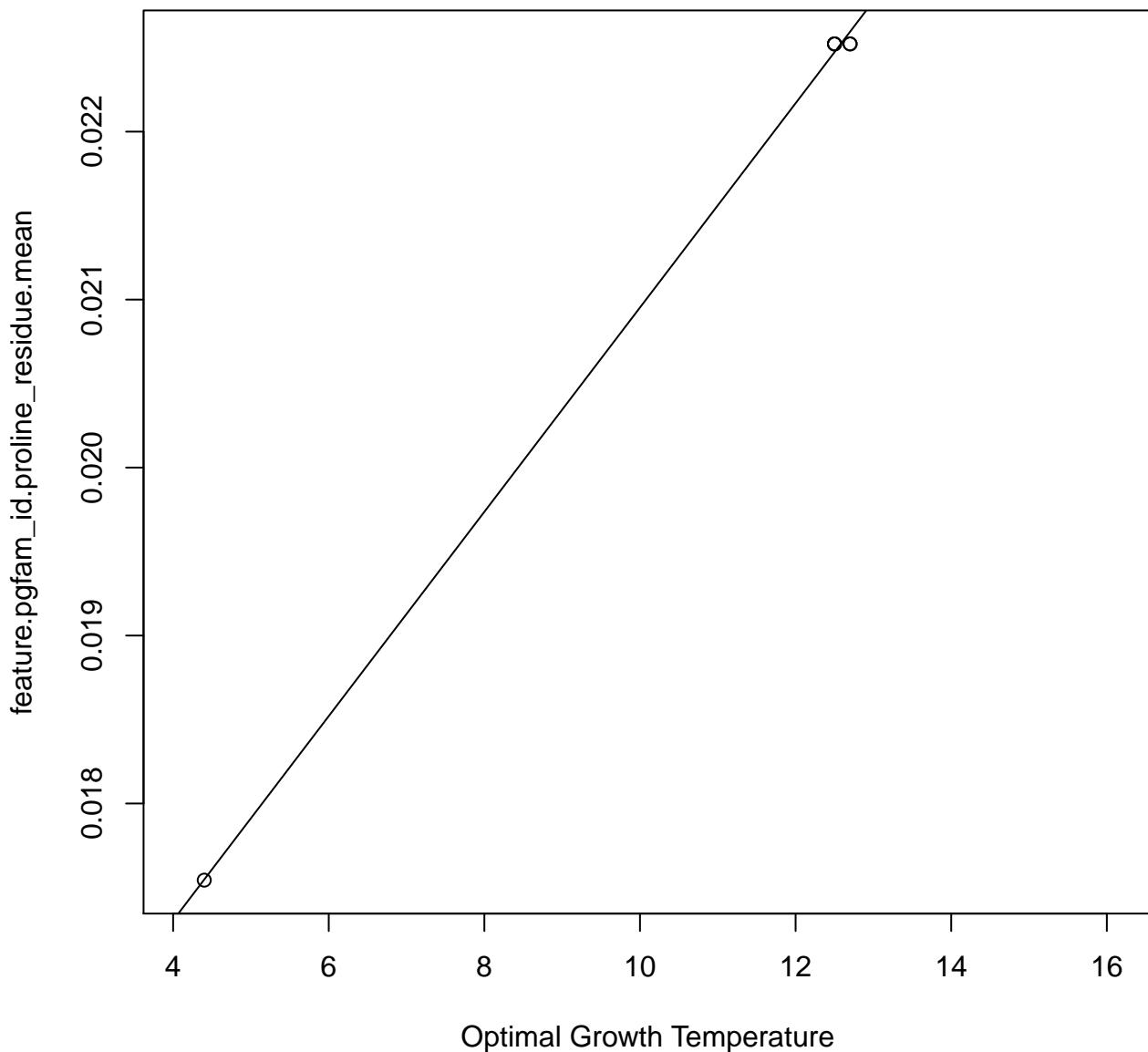
feature.pgfam_id.proline_residue.mean
PGF_00056170
Tellurite methyltransferase (EC 2.1.1.265)



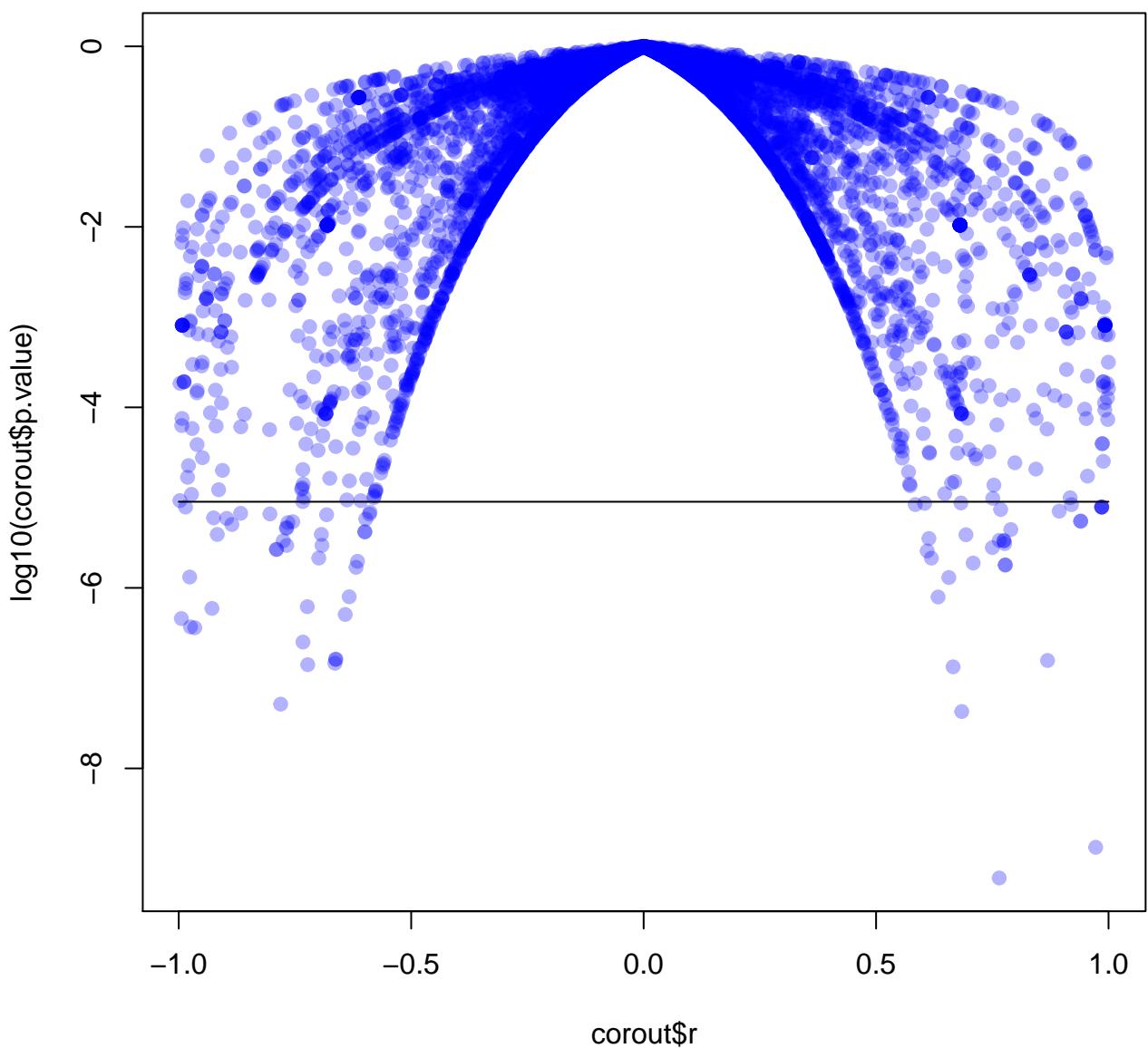
feature.pgfam_id.proline_residue.mean
PGF_01336833
hypothetical protein



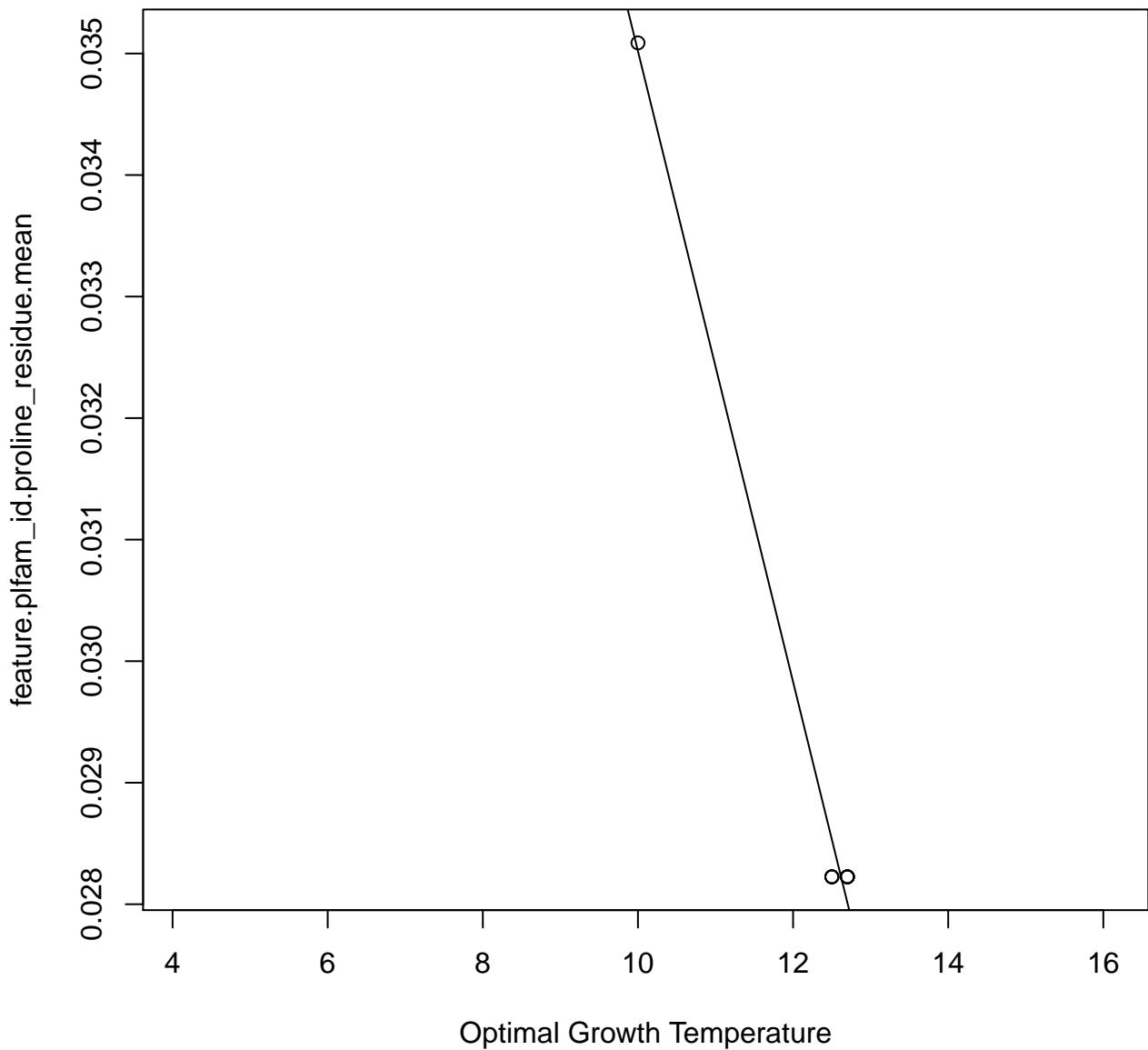
feature.pgfam_id.proline_residue.mean
PGF_06863675
Beta-phosphoglucomutase (EC 5.4.2.6)



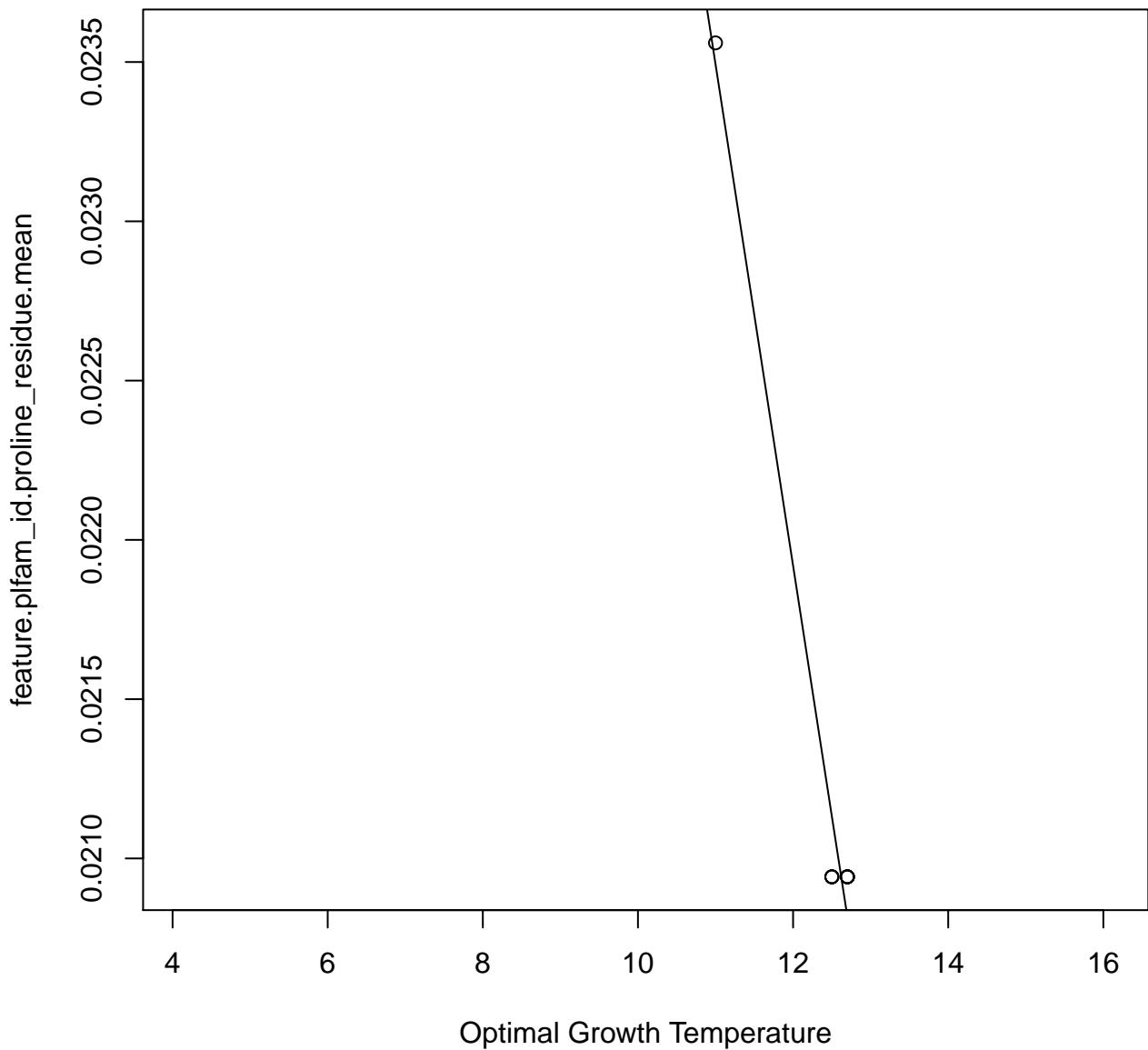
feature.plfam_id.proline_residue.mean



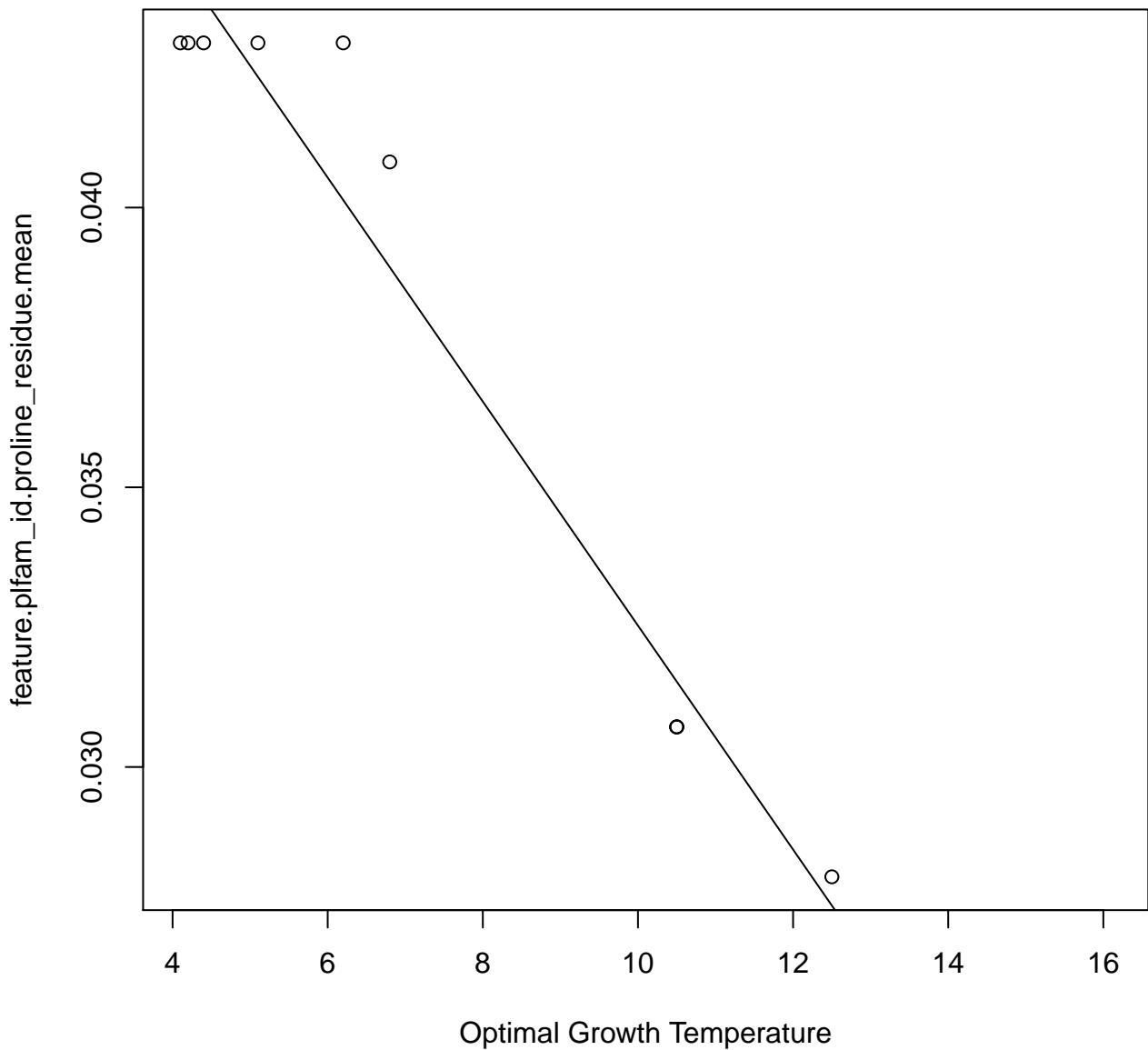
feature.plfam_id.proline_residue.mean
PLF_28228_00002578
Acetoacetyl-CoA reductase (EC 1.1.1.36)



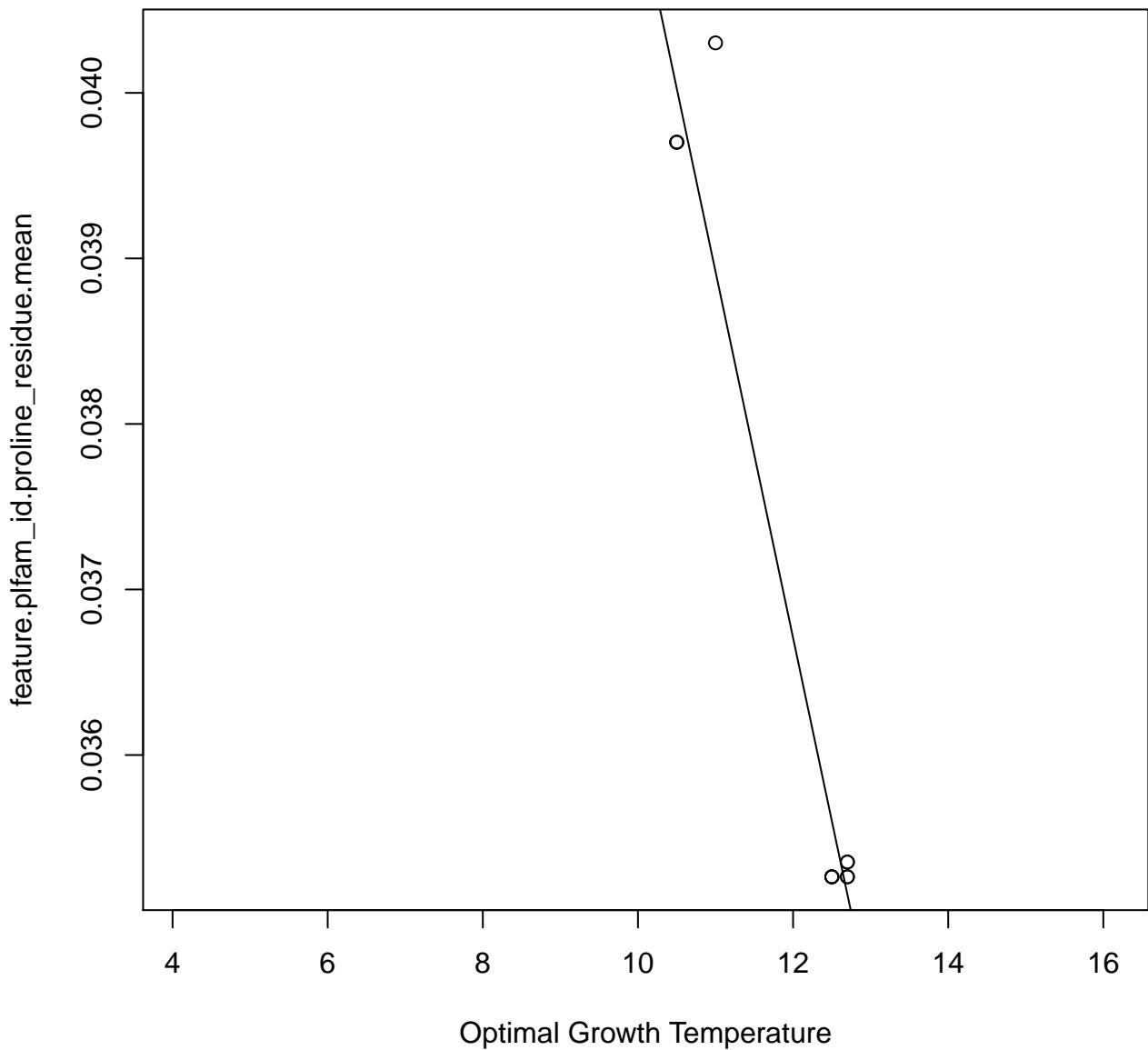
feature.plfam_id.proline_residue.mean
PLF_28228_00003466
GfdT



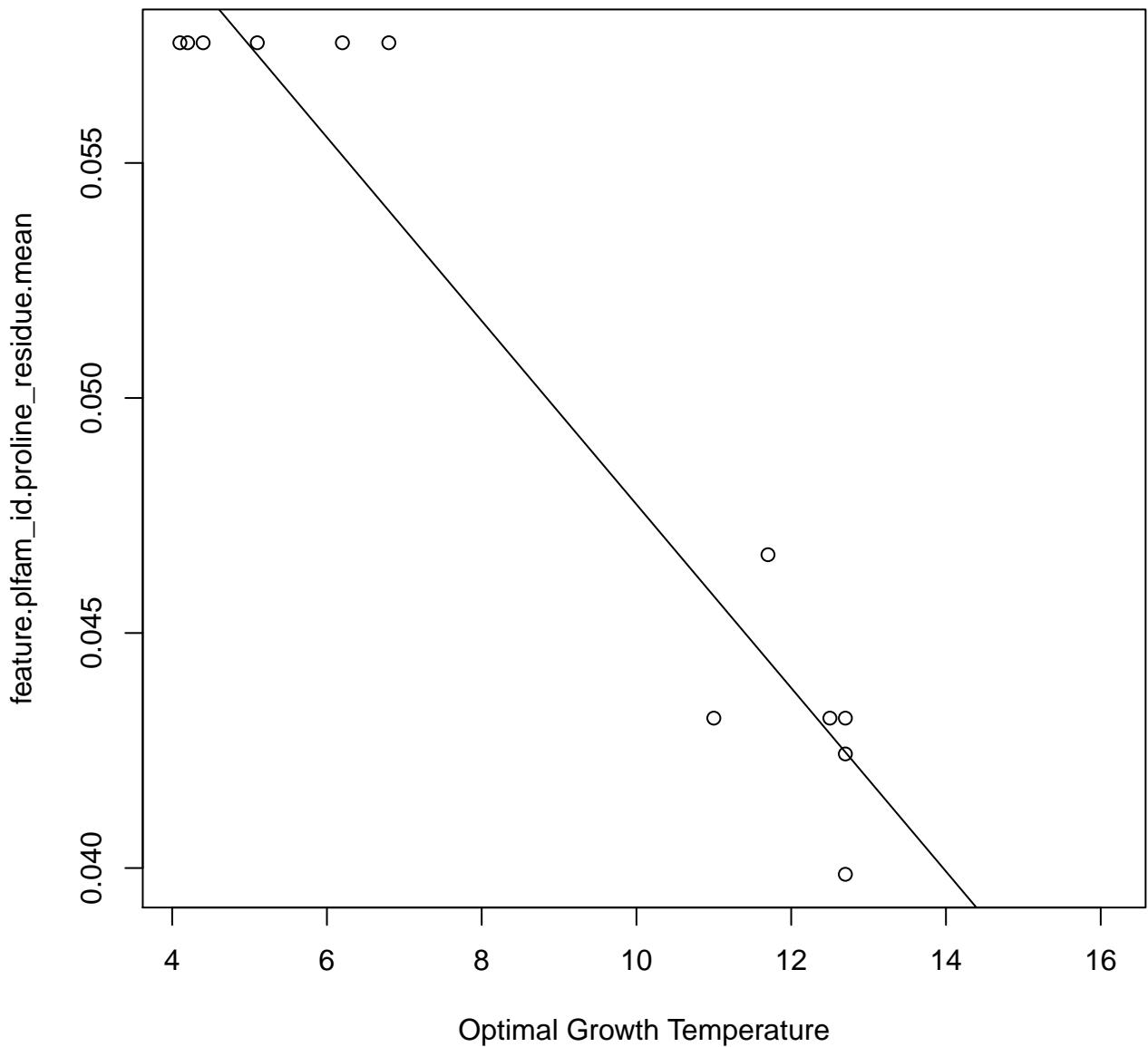
feature.plfam_id.proline_residue.mean
PLF_28228_00023076
Mobile element protein



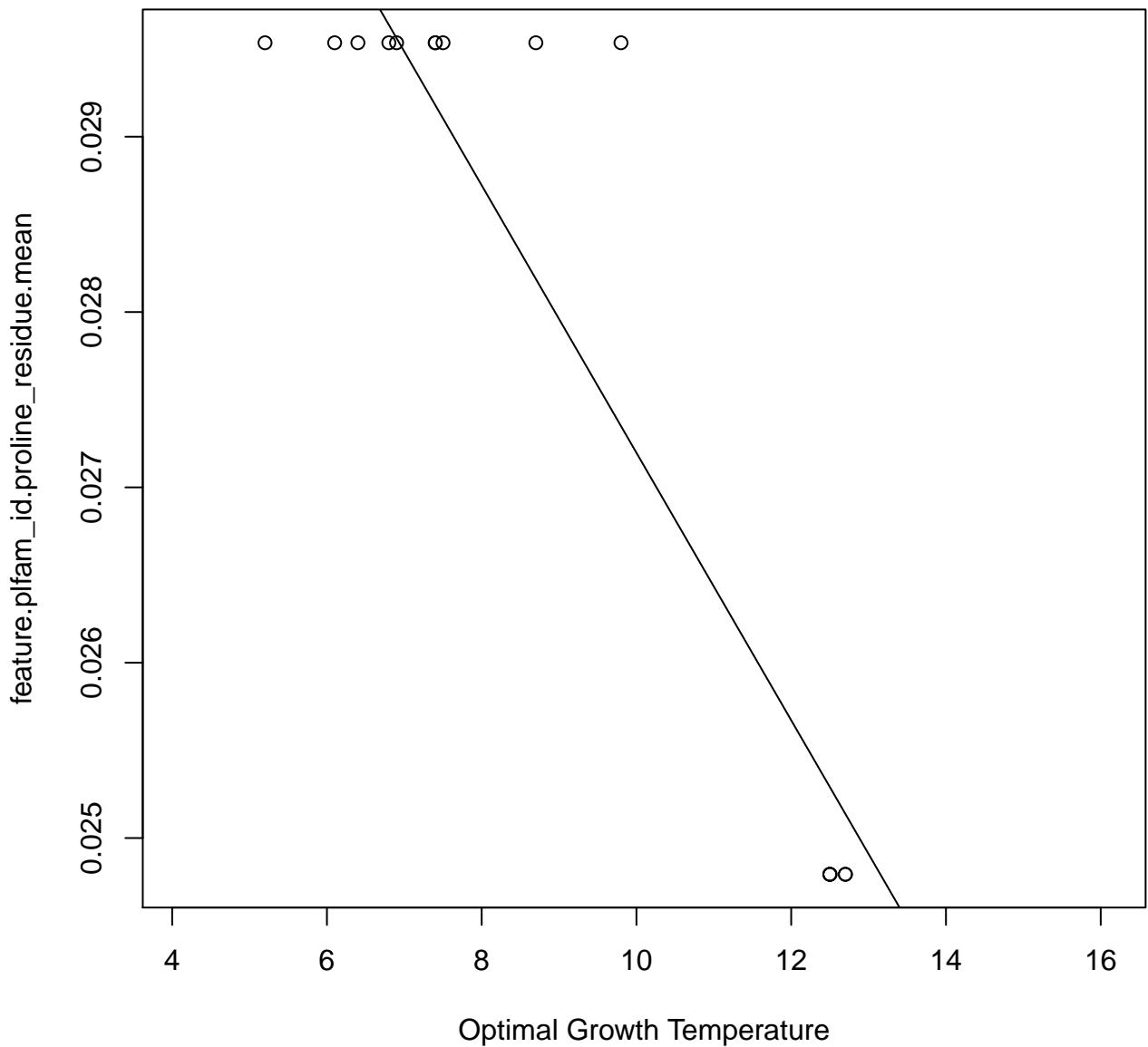
feature.plfam_id.proline_residue.mean
PLF_28228_00003591
Putative response regulator



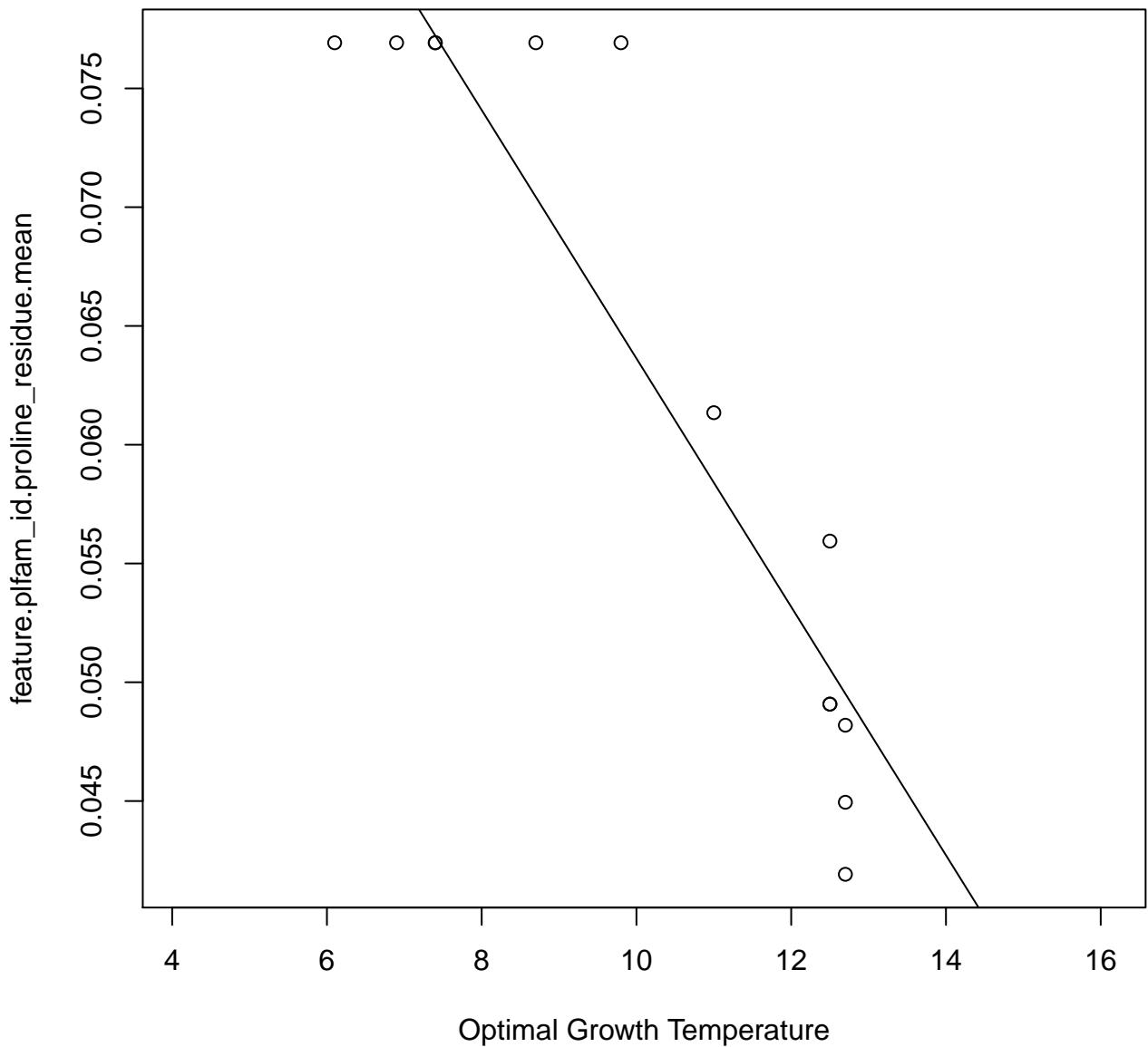
feature.plfam_id.proline_residue.mean
PLF_28228_00028314
Transcriptional regulator, LysR family



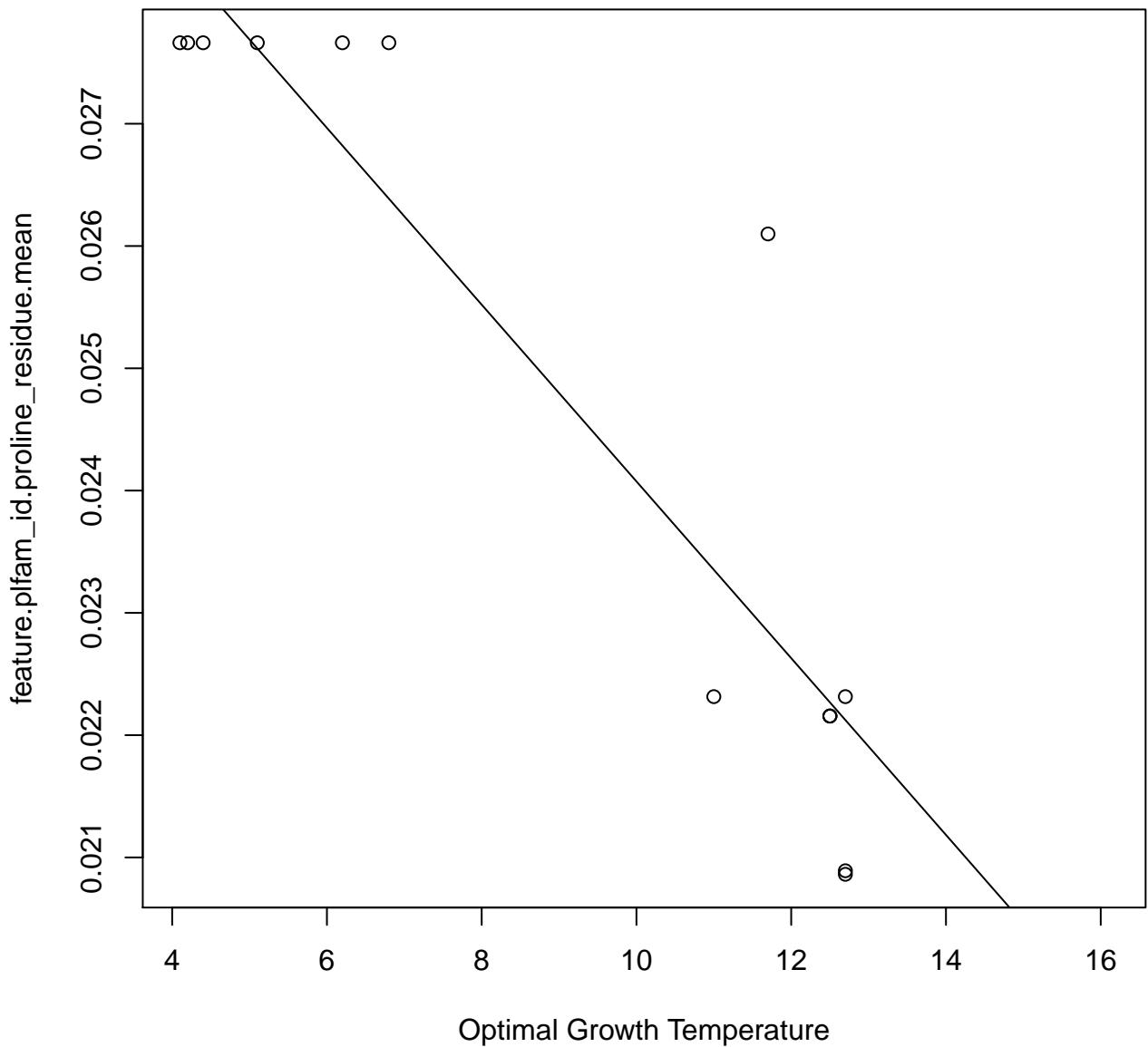
feature.plfam_id.proline_residue.mean
PLF_28228_00007378
SapC-like S-layer protein



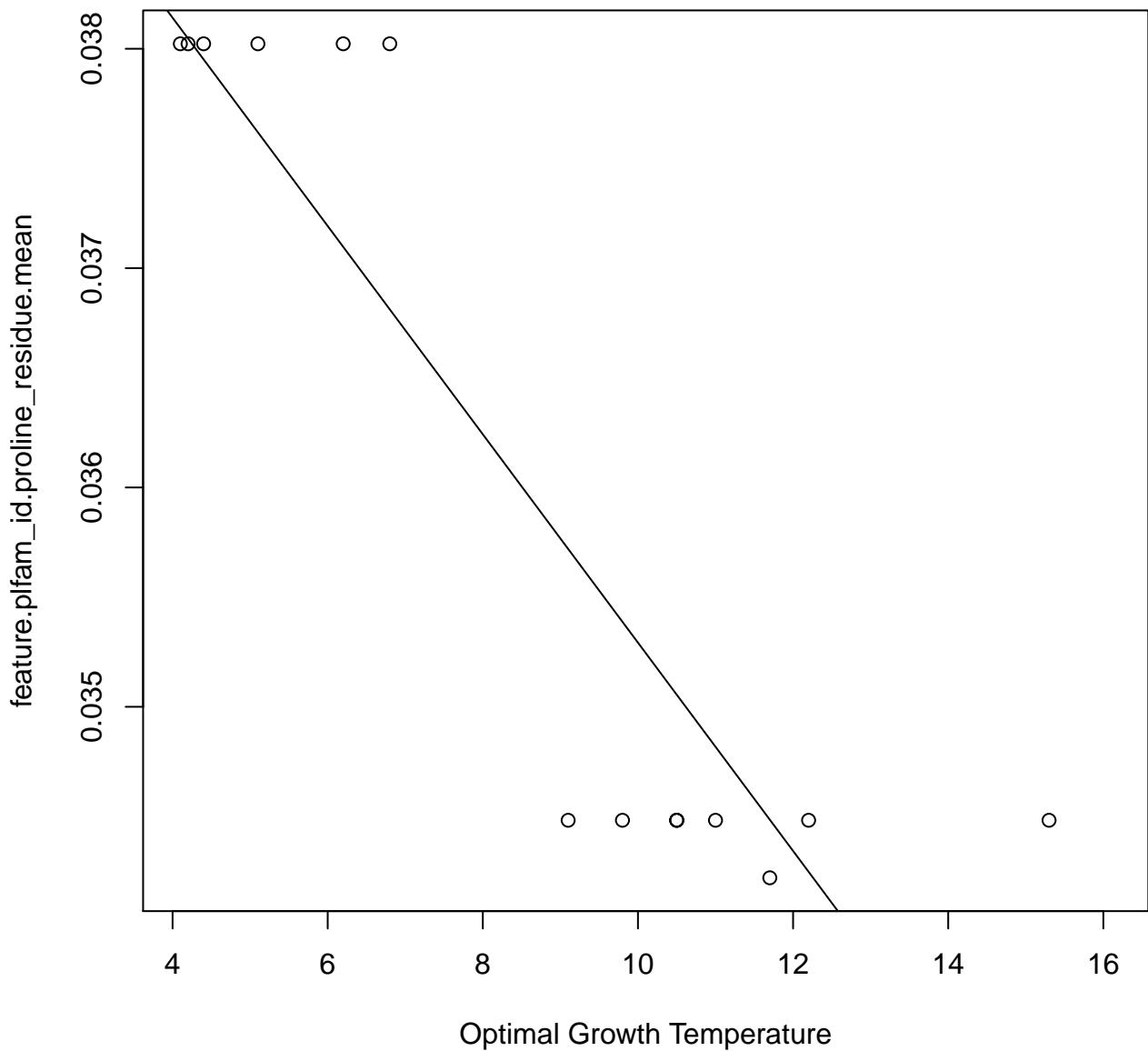
feature.plfam_id.proline_residue.mean
PLF_28228_00002635
Glyoxalase family protein



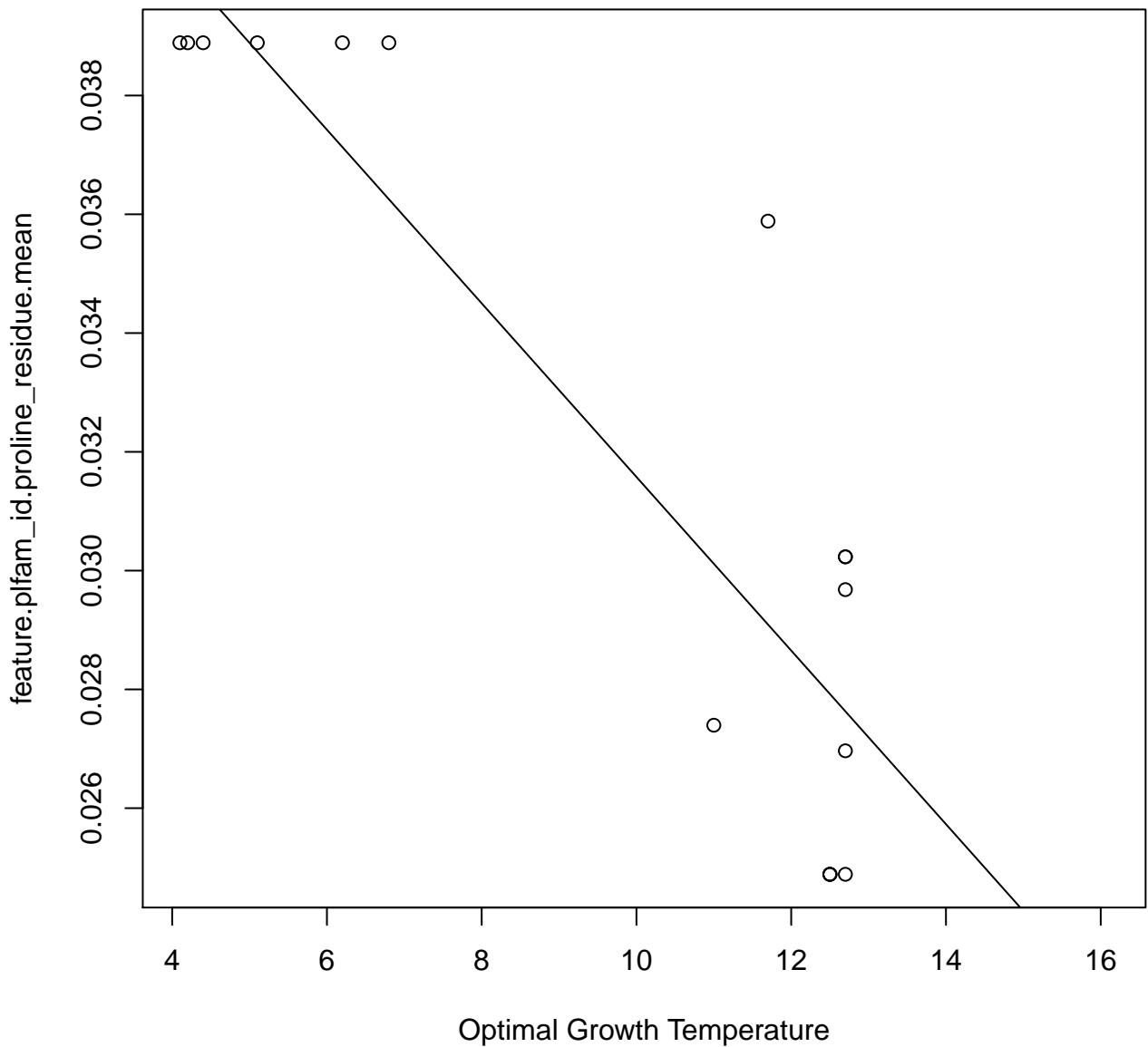
feature.plfam_id.proline_residue.mean
PLF_28228_00003654
Sensory box sensor/GGDEF/EAL domain protein



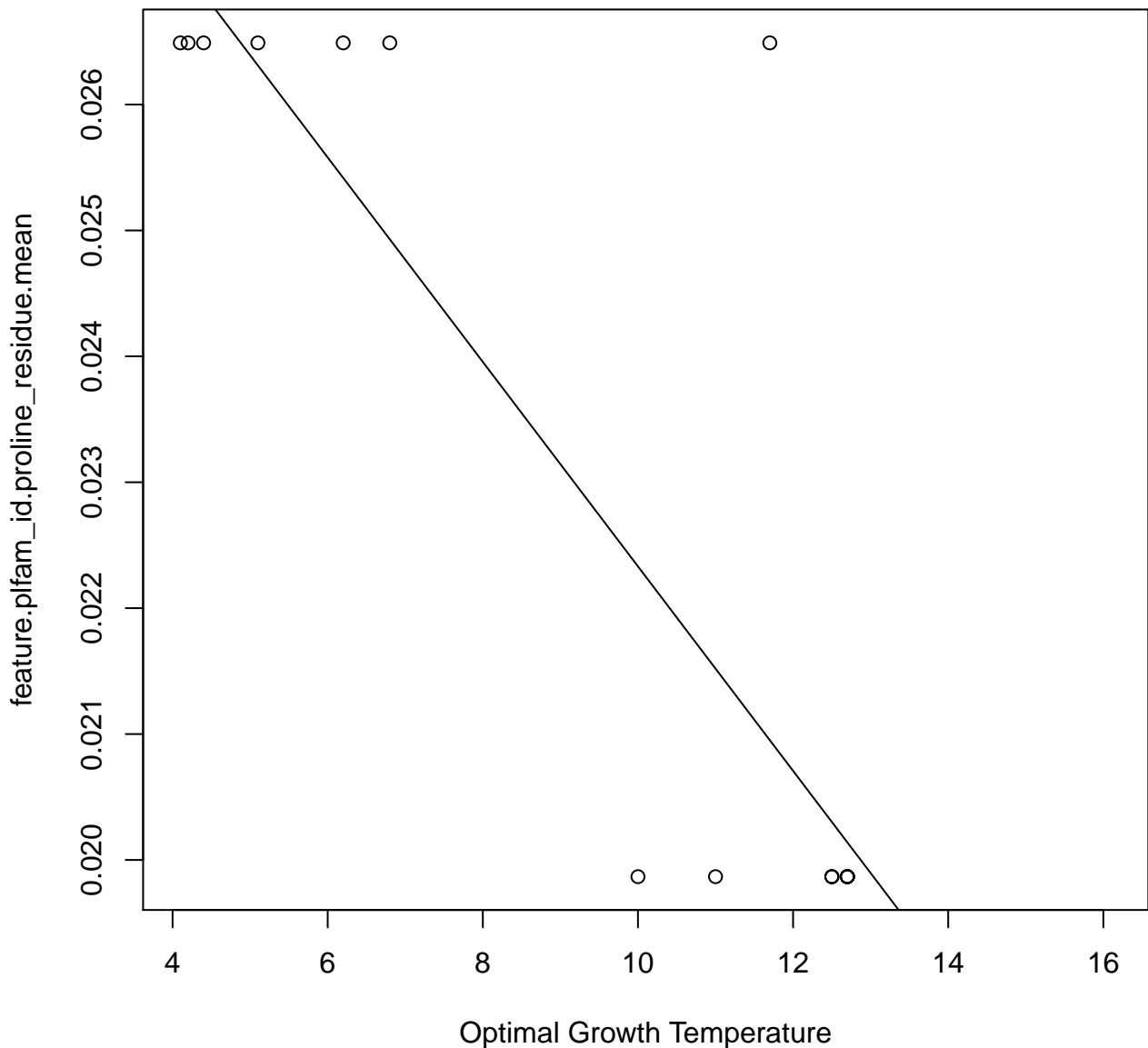
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PLF_28228_00024614
hypothetical protein



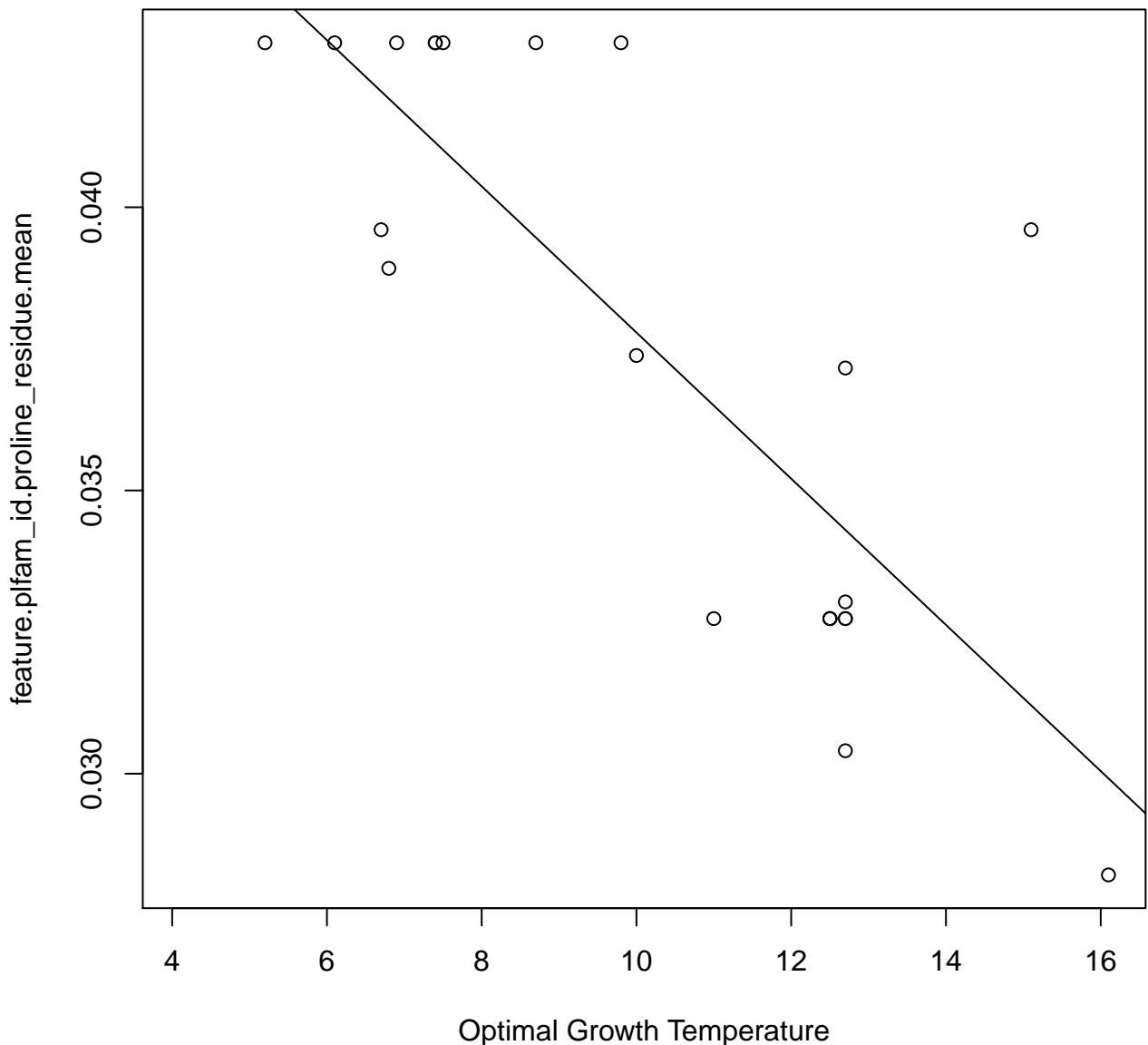
feature.plfam_id.proline_residue.mean
PLF_28228_00002761
Uncharacterized MFS-type transporter



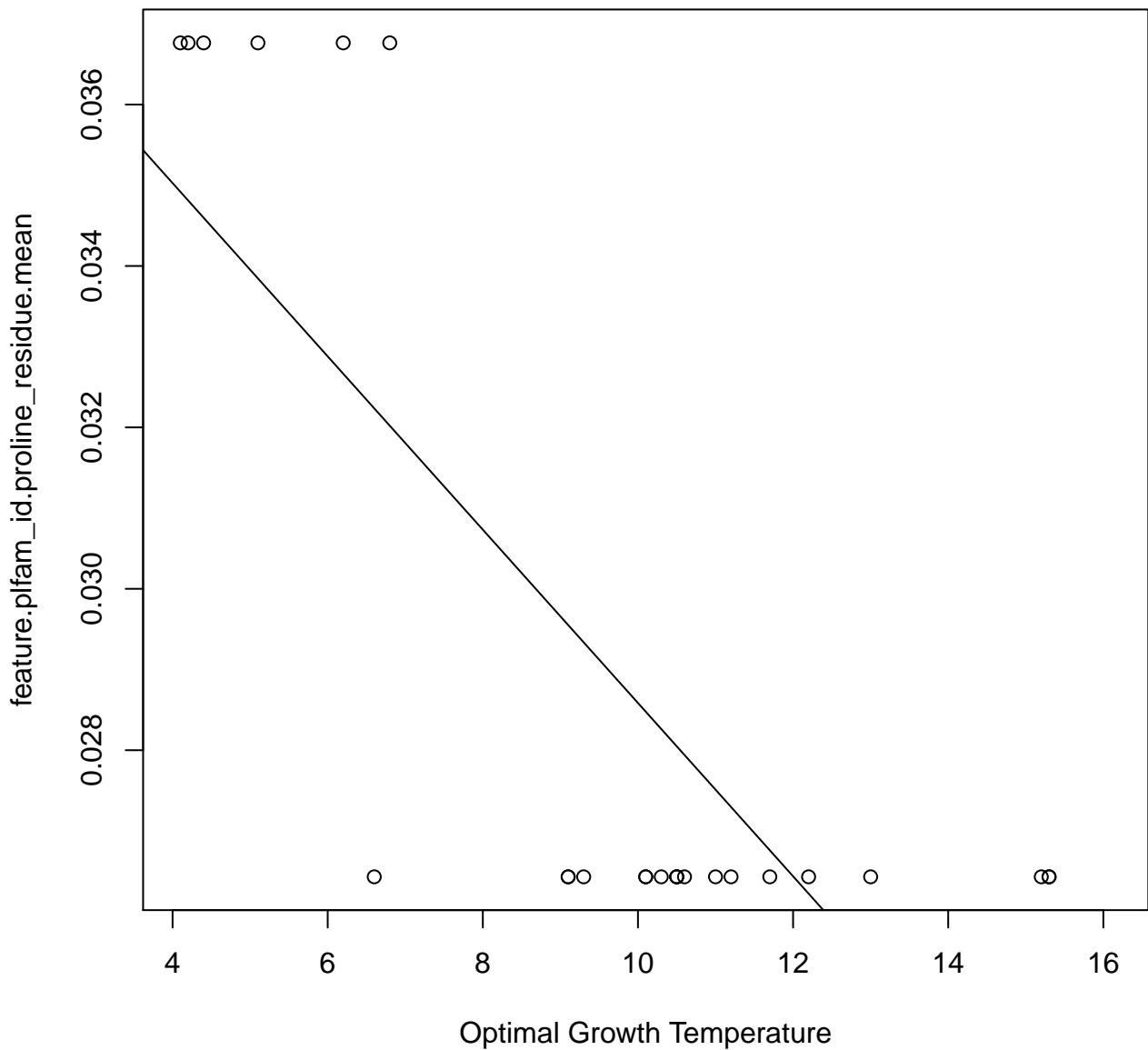
feature.plfam_id.proline_residue.mean
PLF_28228_00002546
uncharacterized conserved secreted protein



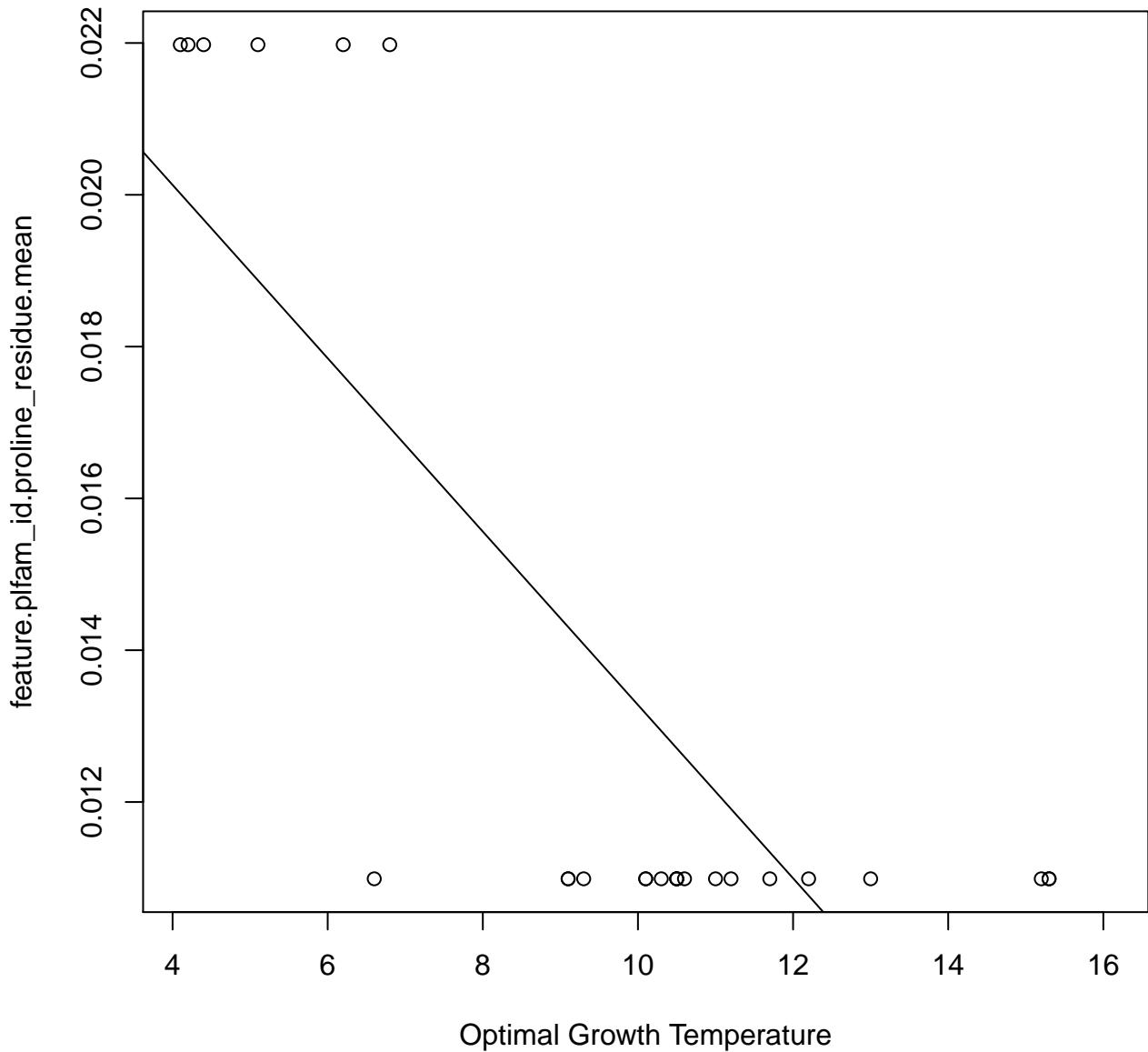
feature.plfam_id.proline_residue.mean
PLF_28228_00002402
ABC transporter, substrate–binding protein (cluster 10, nitrate/sulfonate/bicarbonate)



feature.plfam_id.proline_residue.mean
PLF_28228_00031467
hypothetical protein



feature.plfam_id.proline_residue.mean
PLF_28228_00029549
hypothetical protein



feature.plfam_id.proline_residue.mean
PLF_28228_00002829
TonB-dependent receptor

feature.plfam_id.proline_residue.mean

4 6 8 10 12 14 16

Optimal Growth Temperature

0.066

0.066

0.066

0.028

0.028

0.028

0.028

0.028

0.028

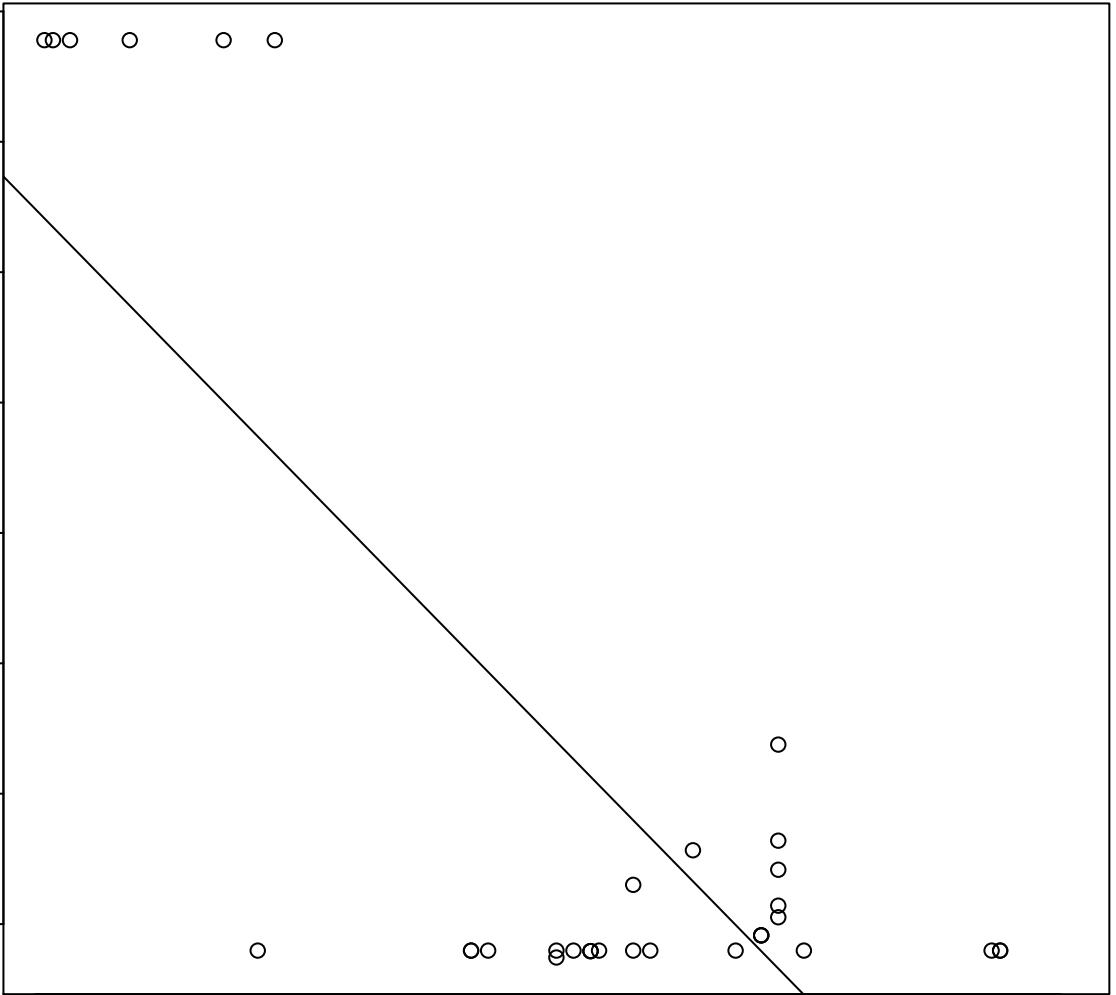
0.028

0.028

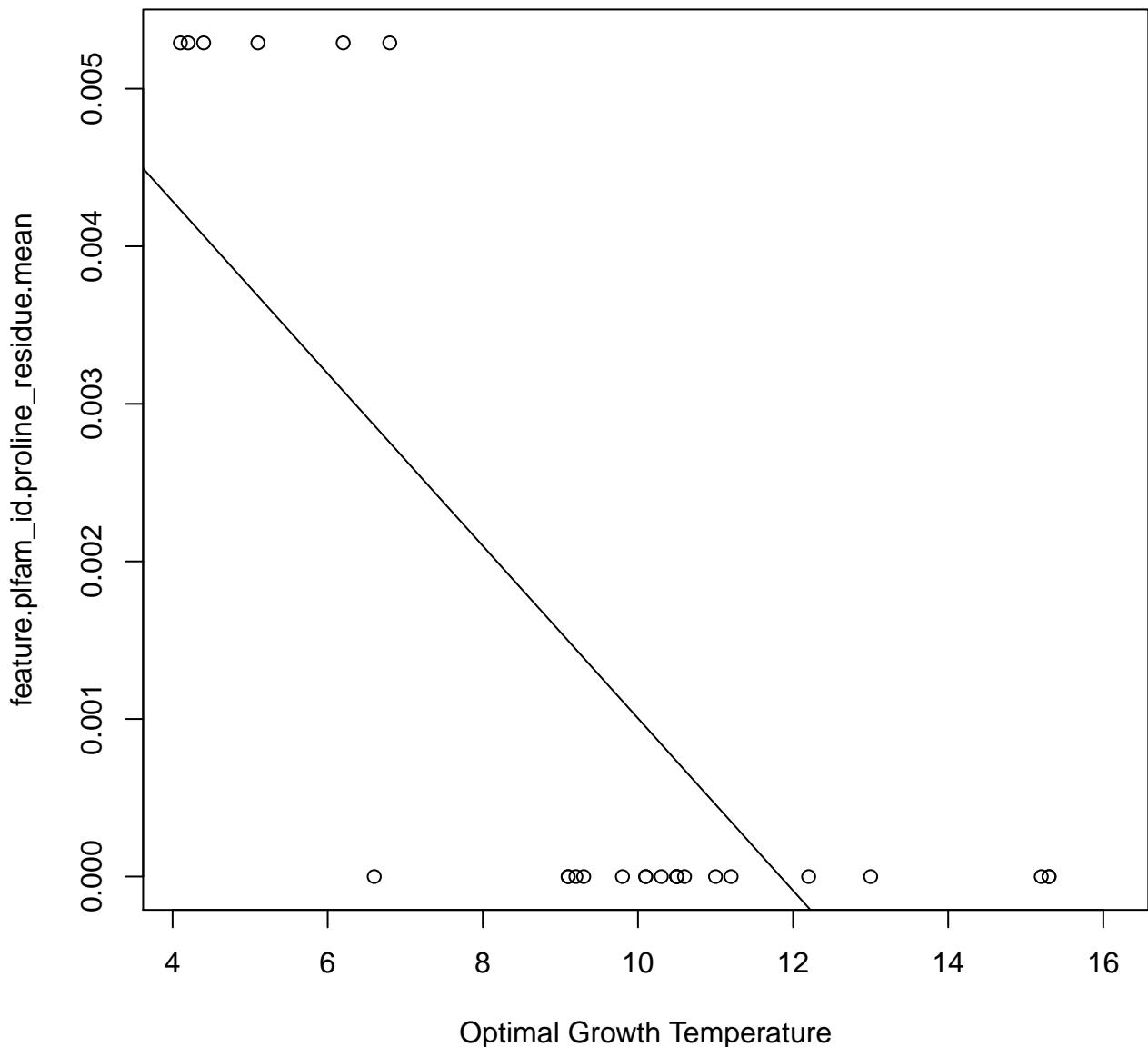
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0.028

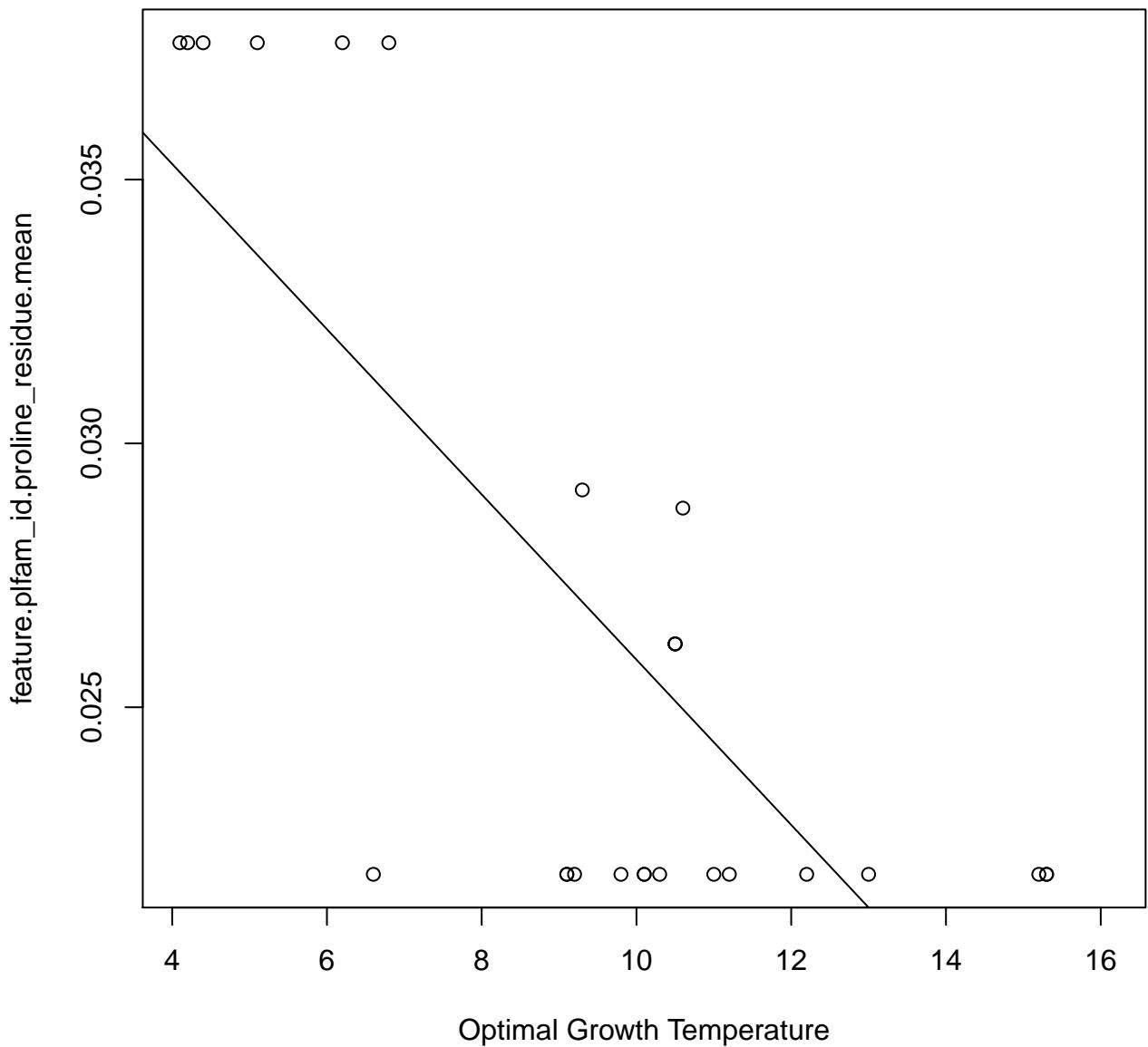
0.065
0.060
0.055
0.050
0.045
0.040
0.035
0.030



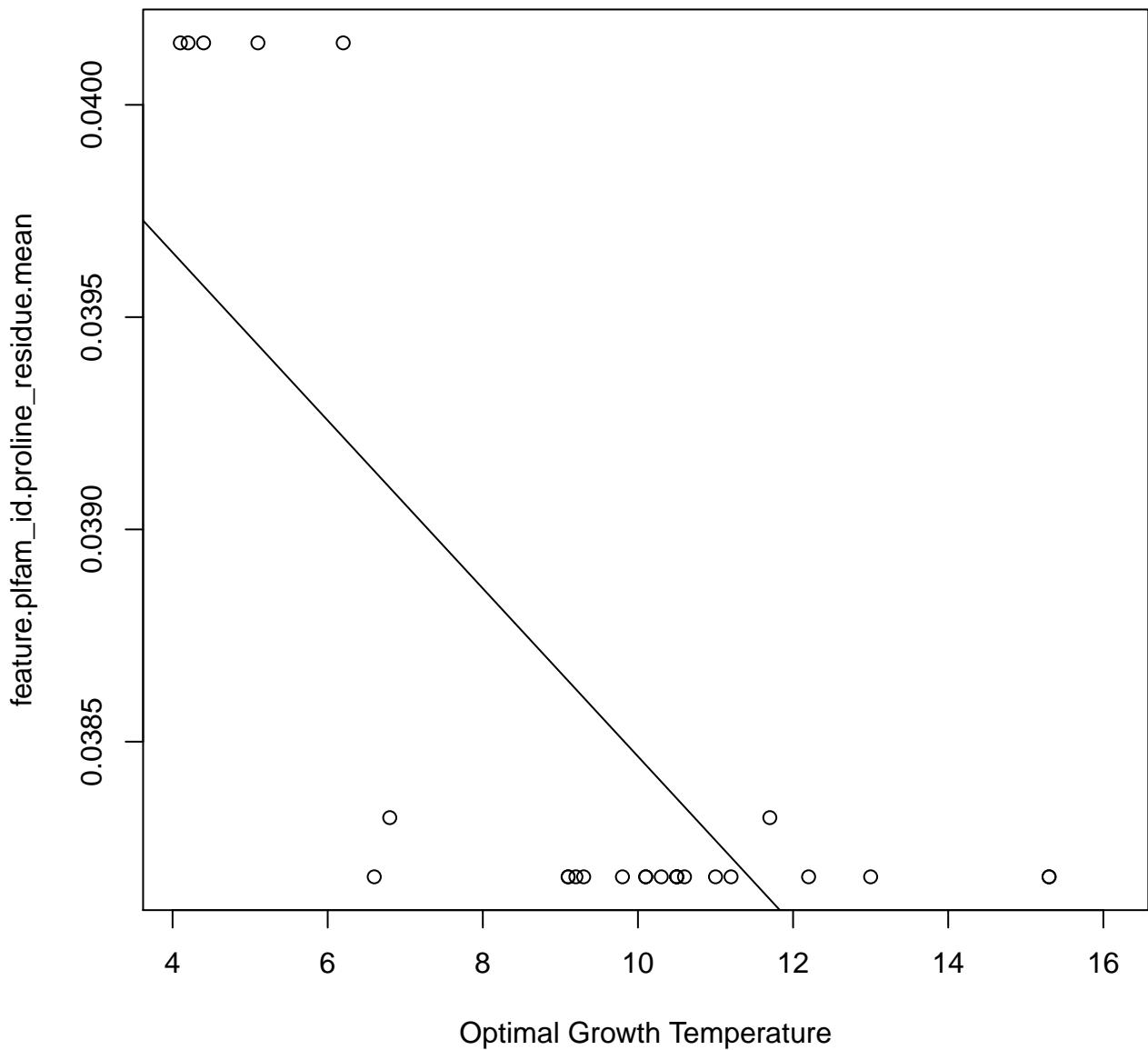
feature.plfam_id.proline_residue.mean
PLF_28228_00031666
hypothetical protein



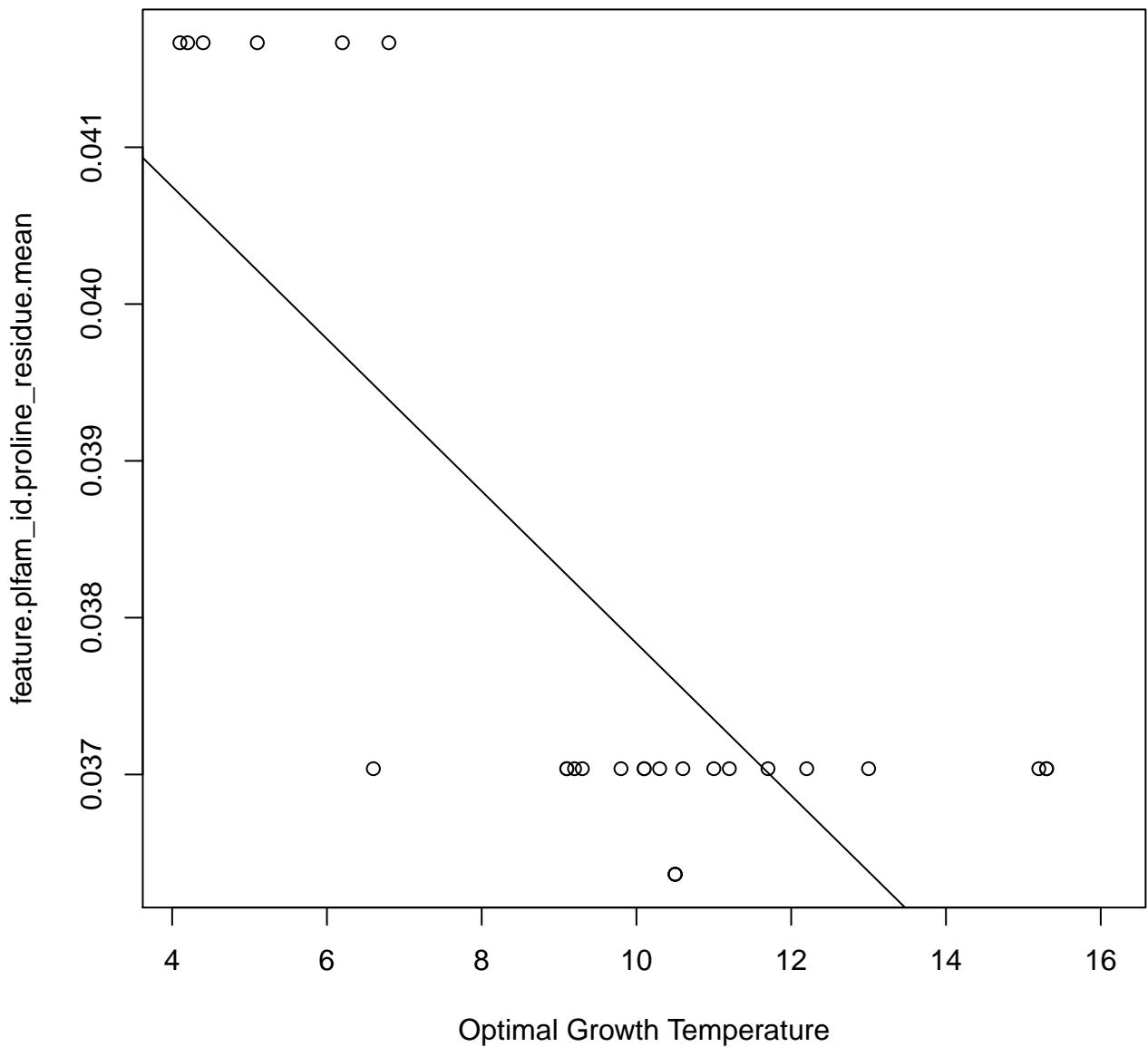
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PLF_28228_00015307
hypothetical protein



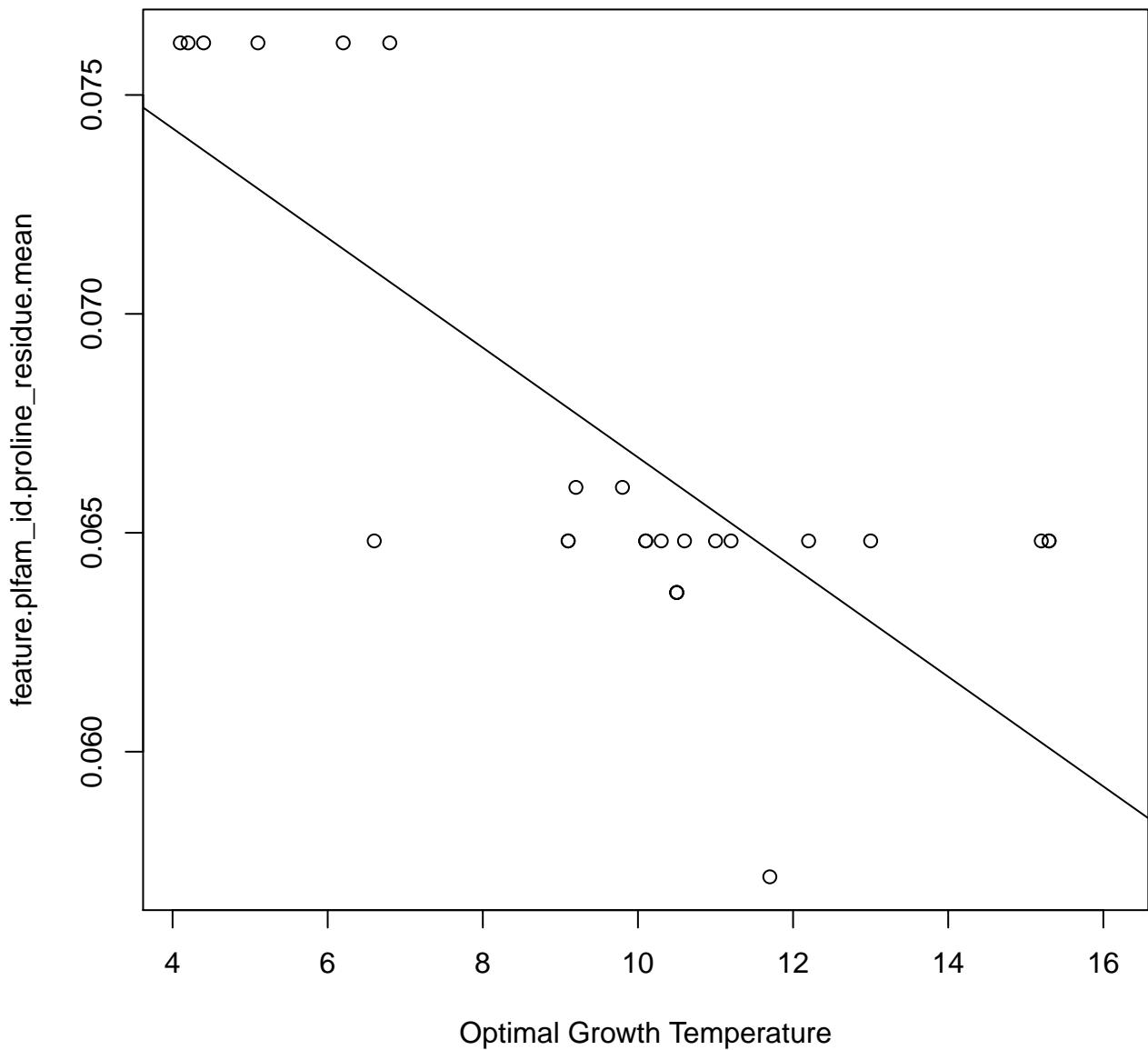
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PLF_28228_00028712
Glucose-6-phosphate isomerase (EC 5.3.1.9)



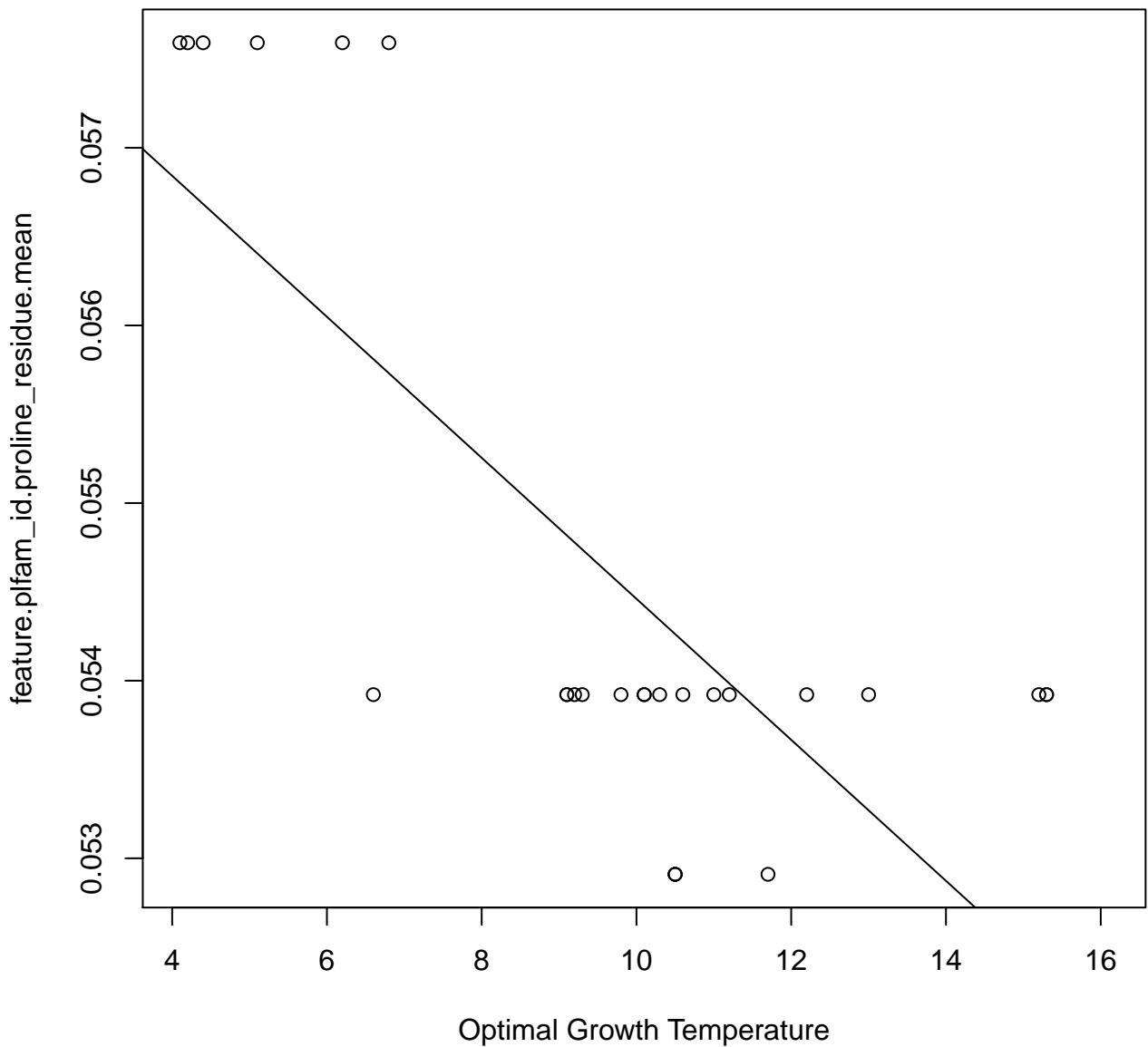
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PLF_28228_00031893
hypothetical protein



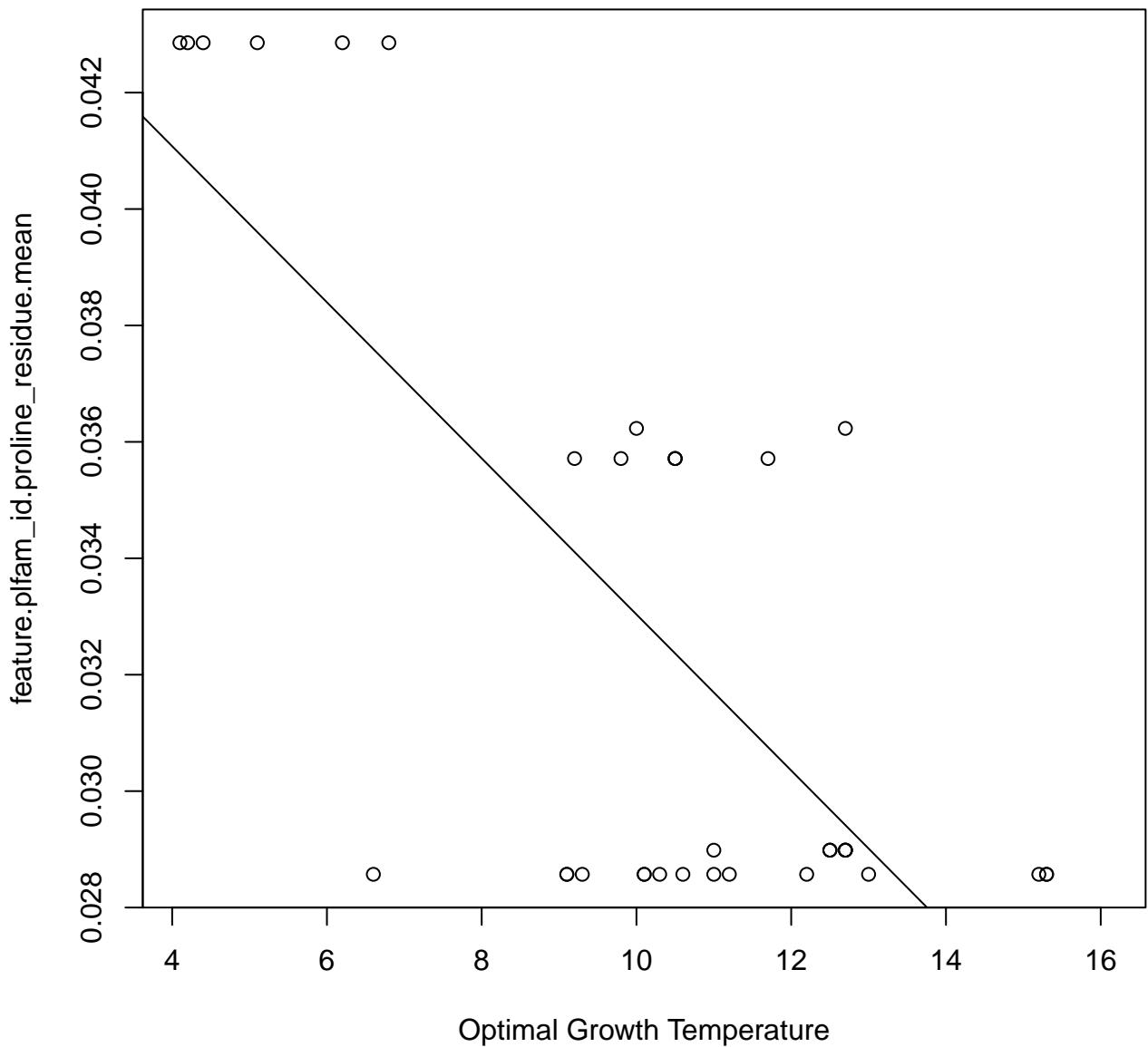
feature.plfam_id.proline_residue.mean
PLF_28228_00016690
hypothetical protein



feature.plfam_id.proline_residue.mean
PLF_28228_00007320
Arylesterase precursor (EC 3.1.1.2)



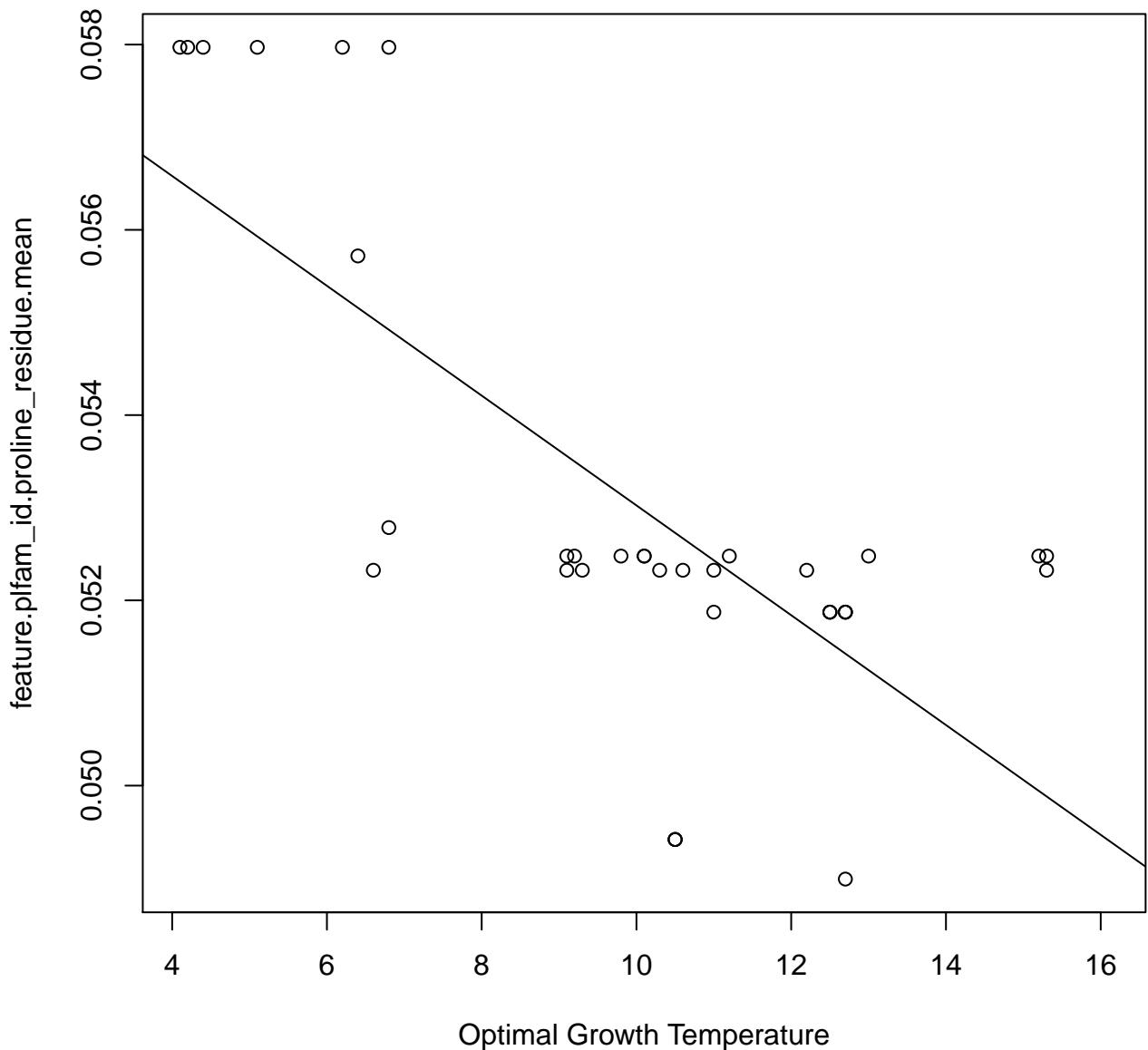
feature.plfam_id.proline_residue.mean
PLF_28228_00000478
Glyoxalase family protein



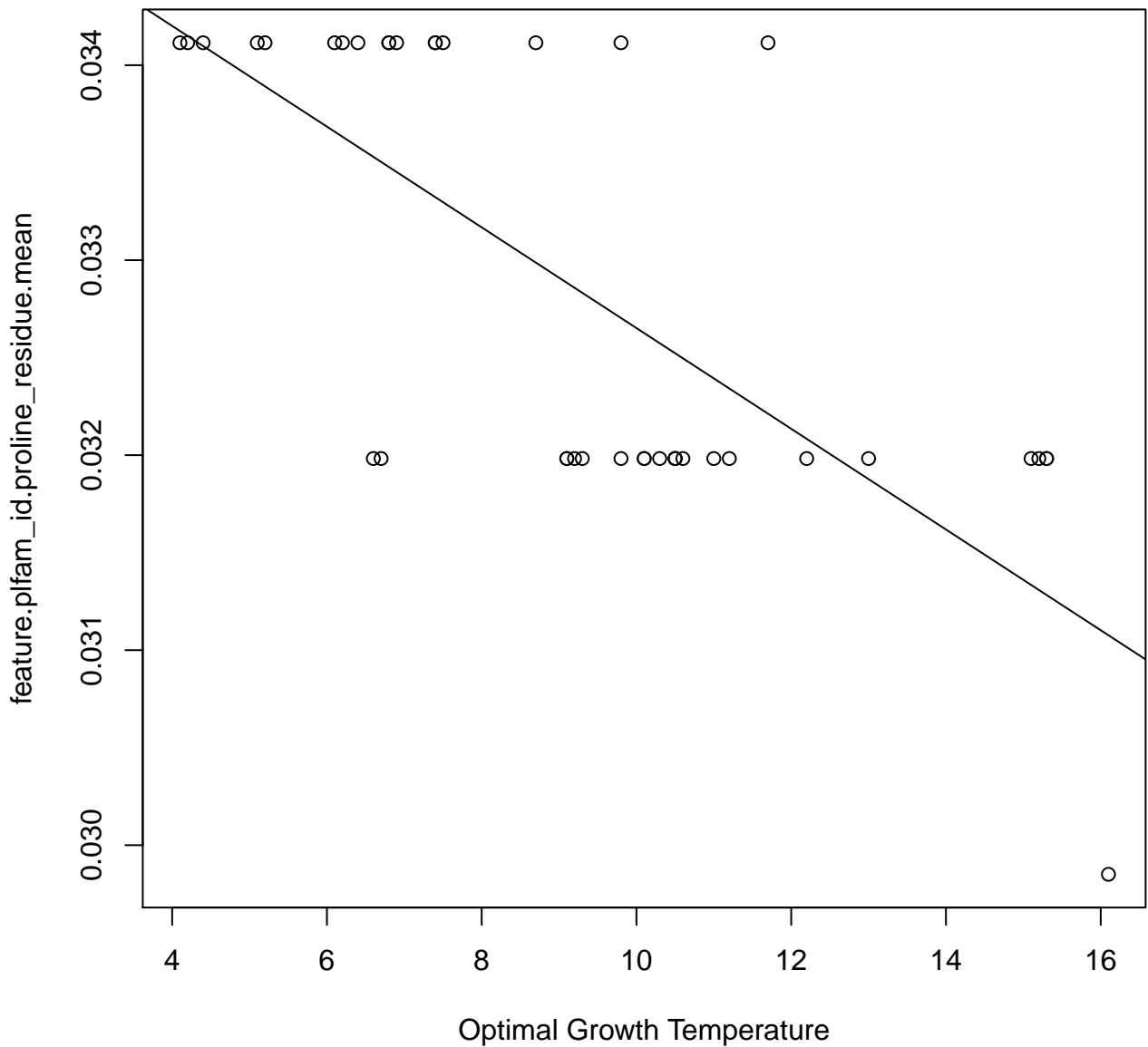
feature.plfam_id.proline_residue.mean

PLF_28228_00003411

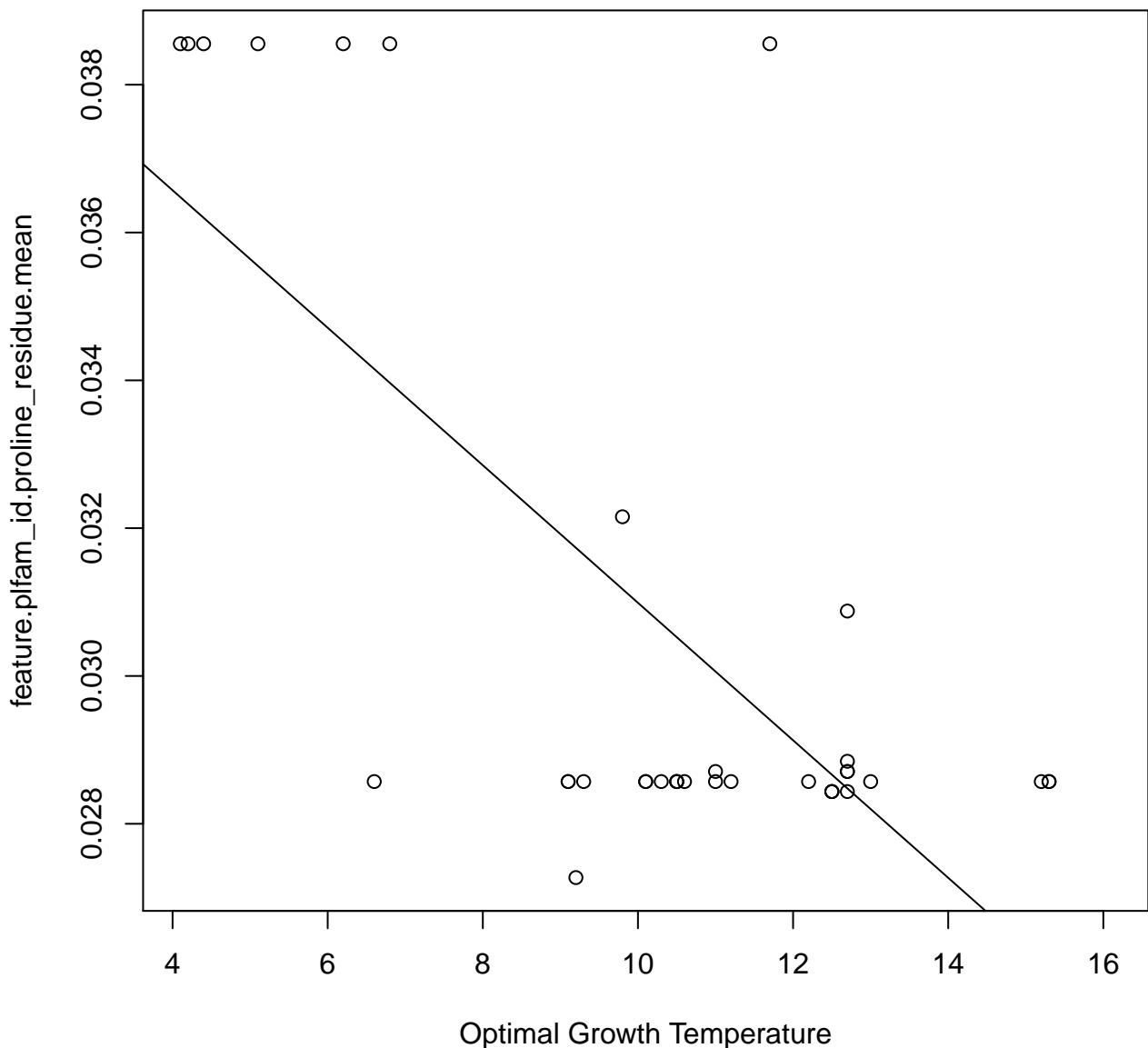
CDP-glycerol: N-acetyl-beta-D-mannosaminyl-1,4-N-acetyl-D-glucosaminylidiphosphoundecaprenyl glycerophosphotransfer



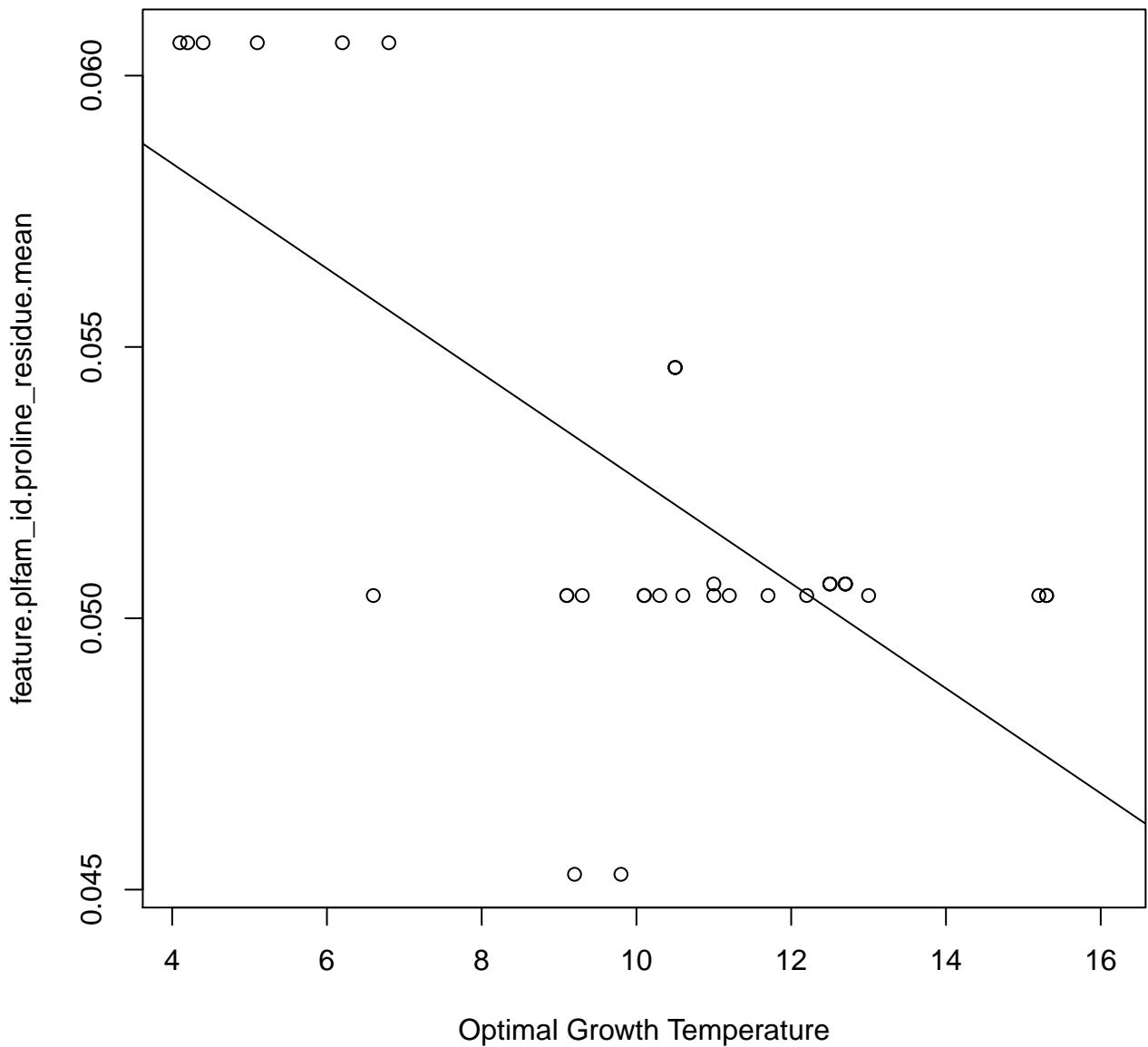
feature.plfam_id.proline_residue.mean
PLF_28228_00014301
Aminopeptidase CC_2544



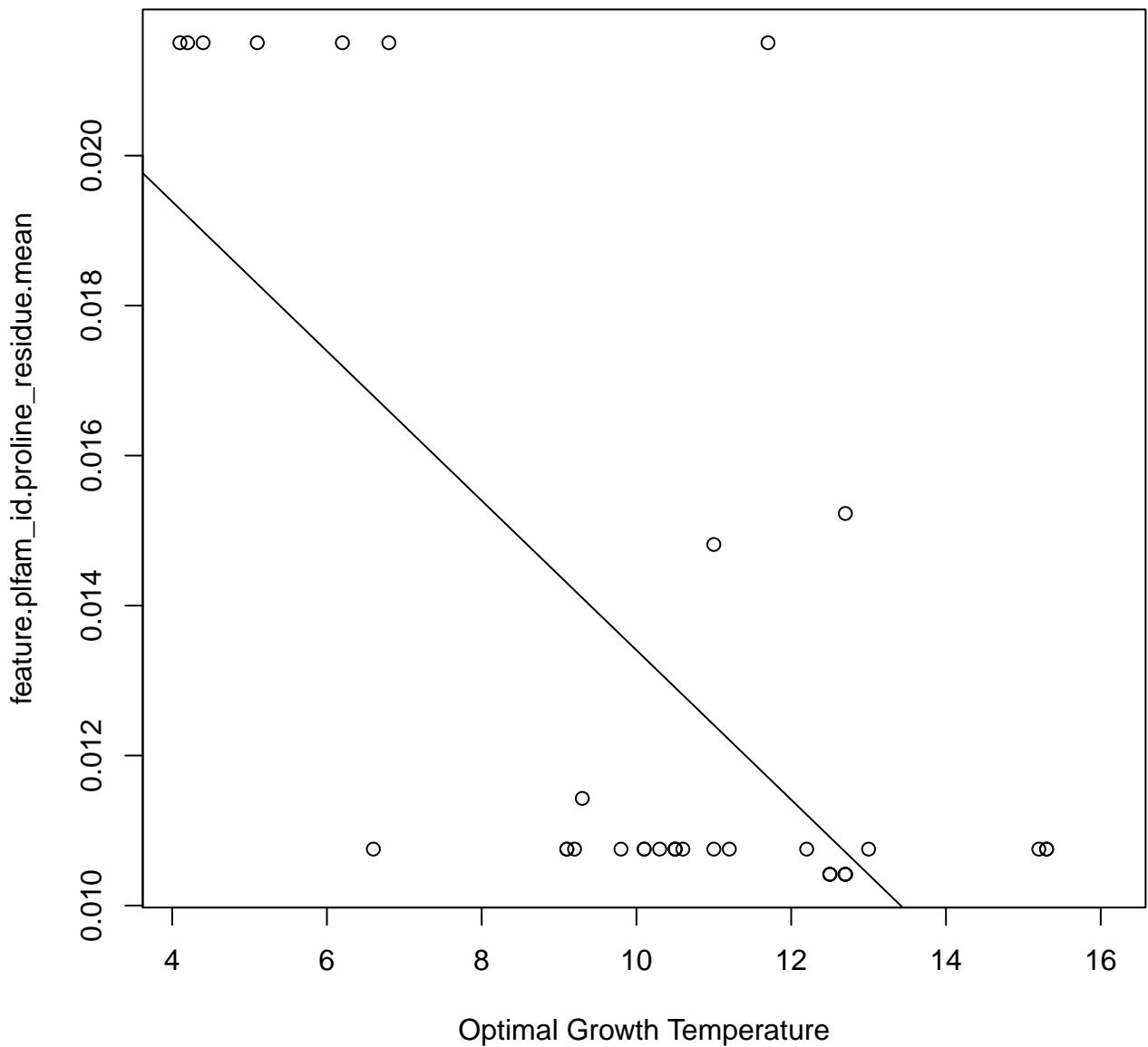
feature.plfam_id.proline_residue.mean
PLF_28228_00002037
Sensor histidine kinase PrrB (RegB) (EC 2.7.3.-)



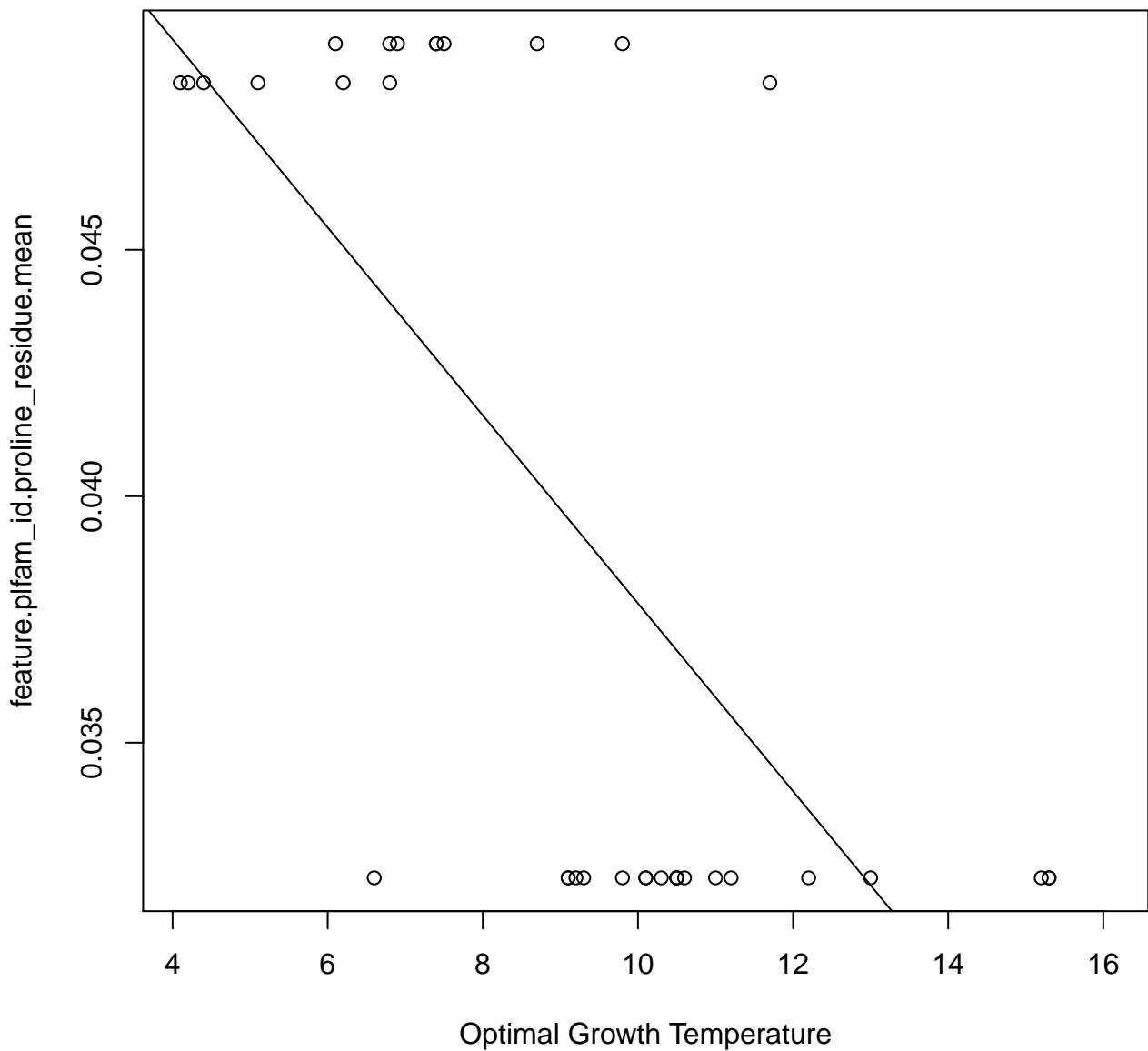
feature.plfam_id.proline_residue.mean
PLF_28228_00003803
ZIP zinc transporter family protein



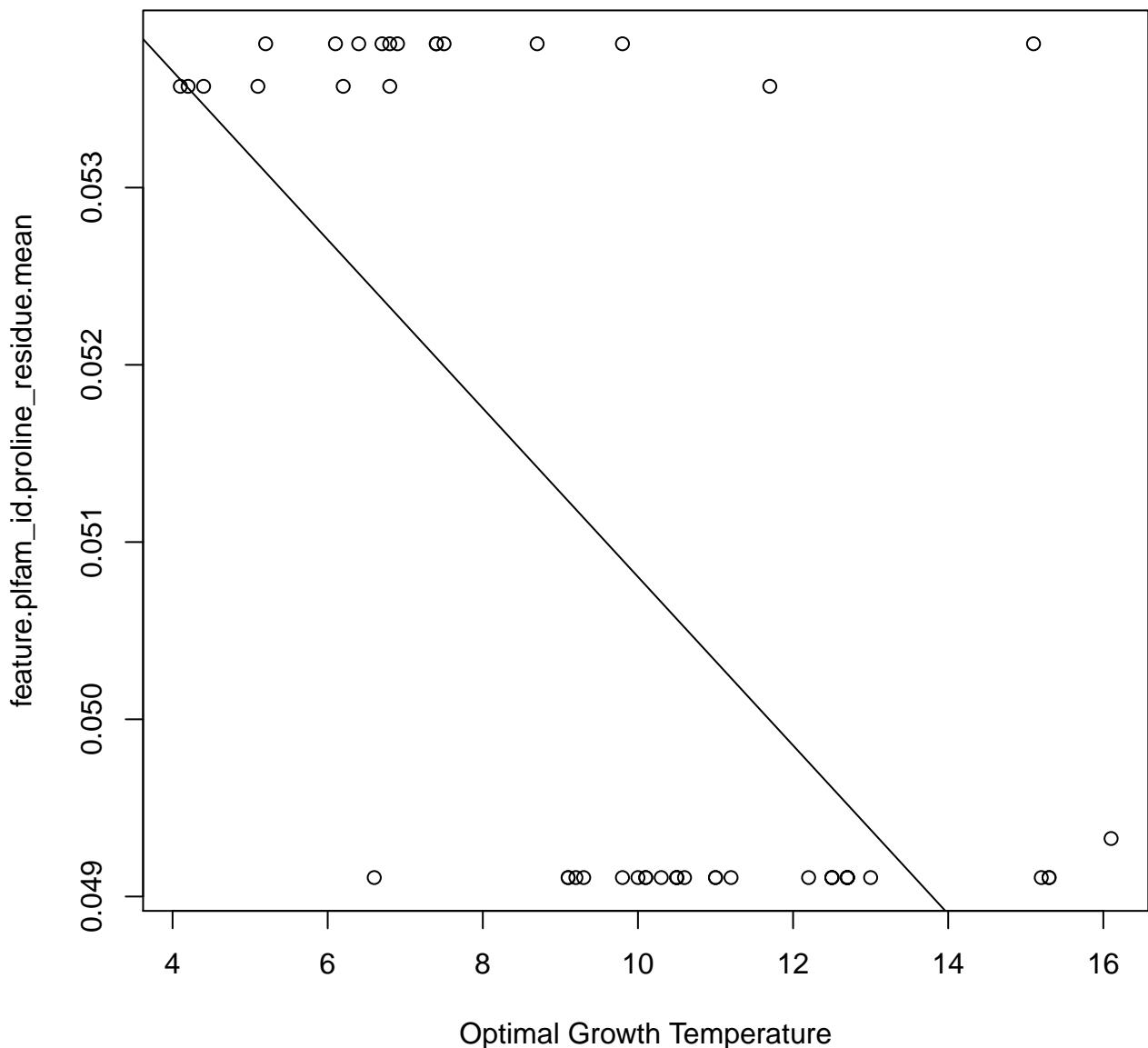
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PLF_28228_00000396
FIG006045: Sigma factor, ECF subfamily



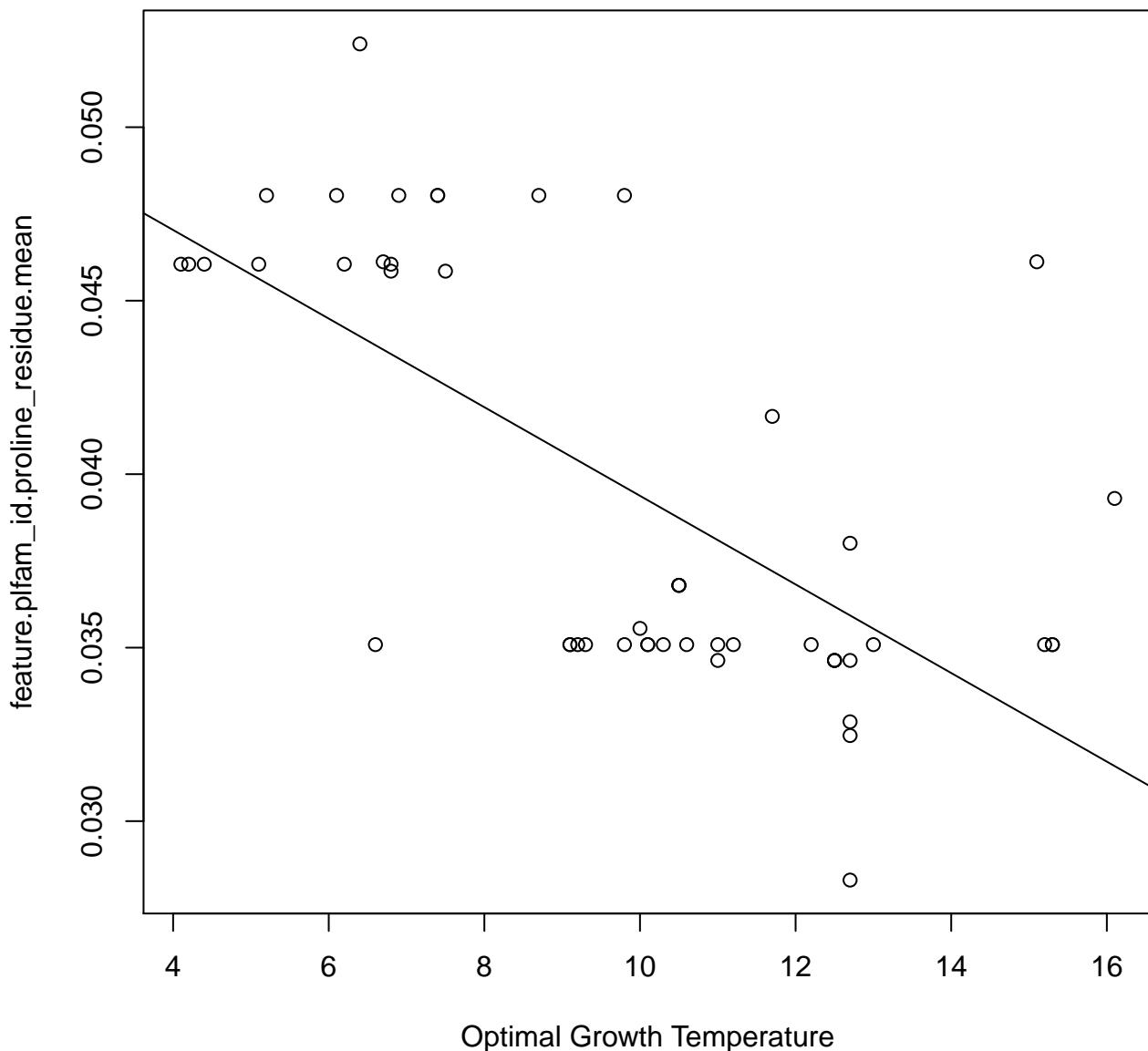
feature.plfam_id.proline_residue.mean
PLF_28228_00019712
hypothetical protein



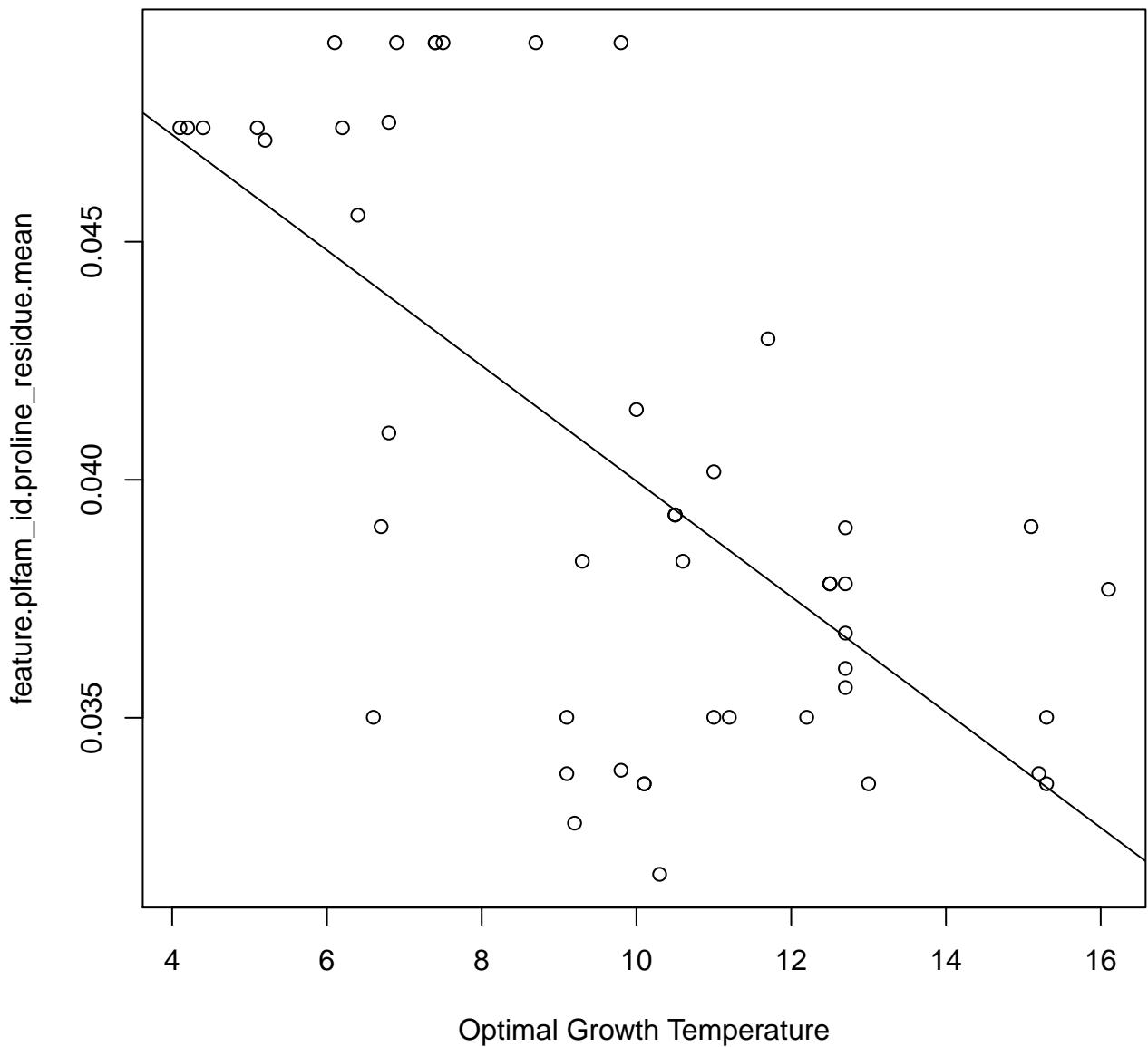
feature.plfam_id.proline_residue.mean
PLF_28228_00001094
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)



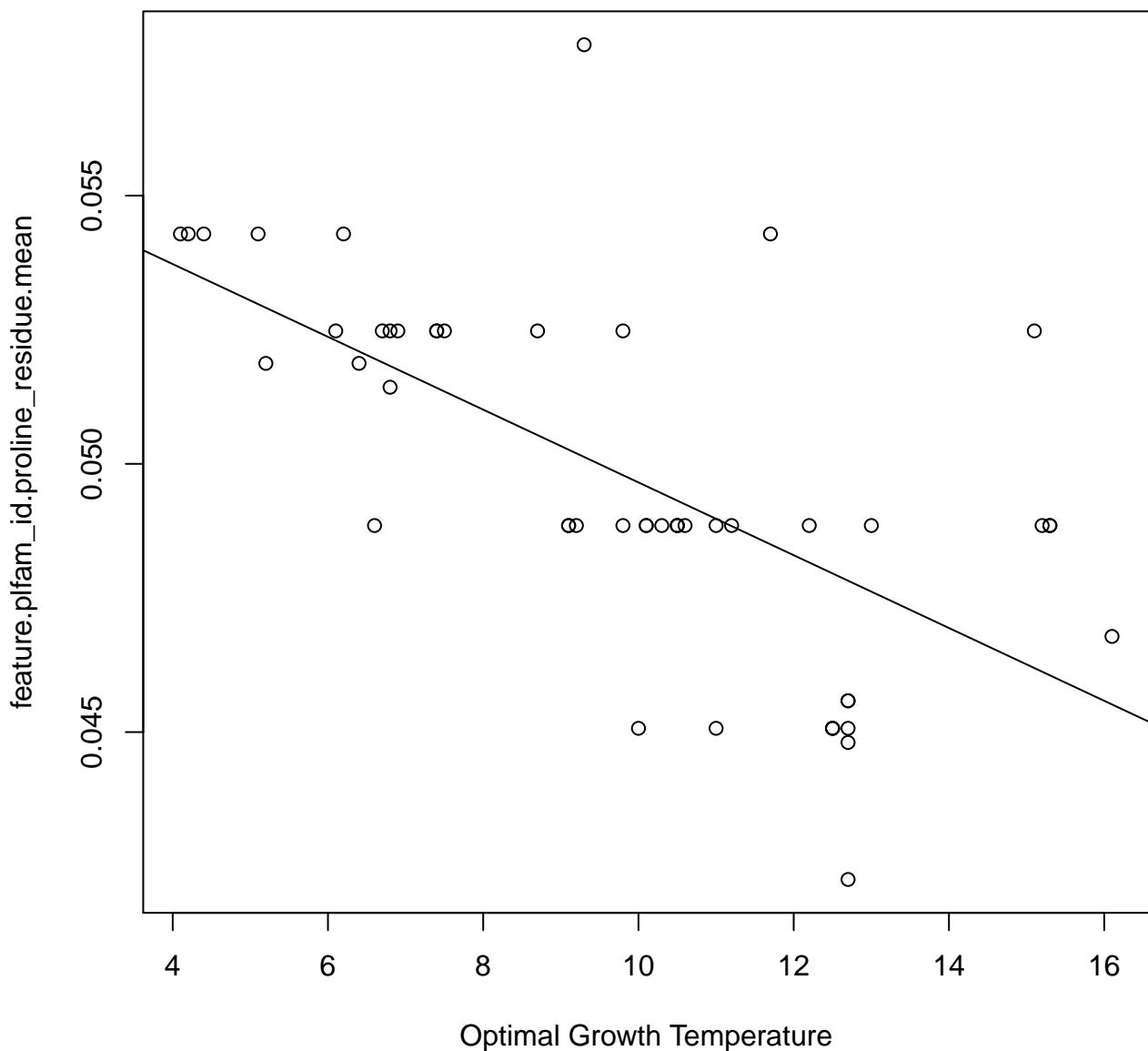
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PLF_28228_00001414
tRNA(Ile)-lysidine synthetase (EC 6.3.4.19)



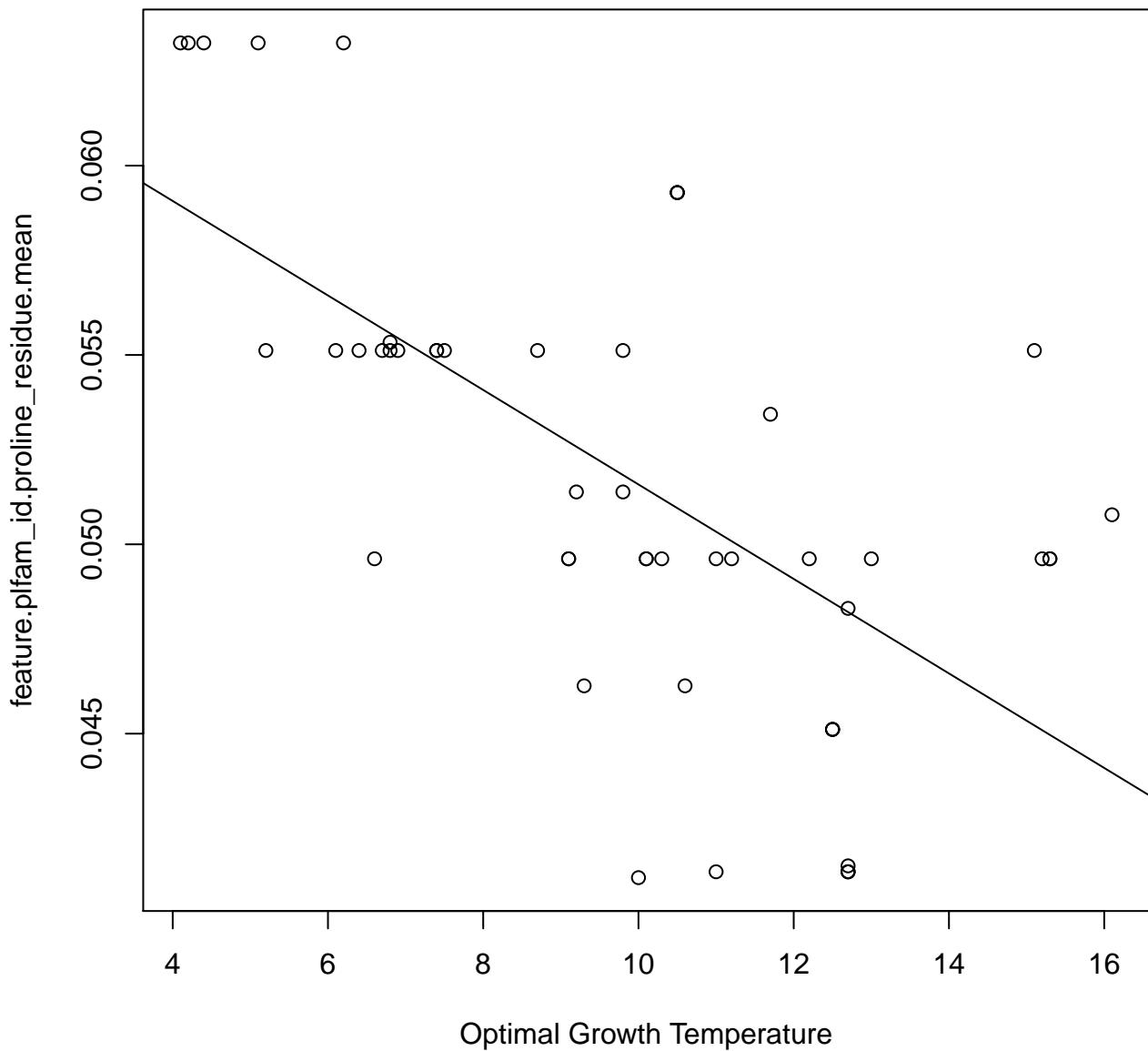
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PLF_28228_00002525
hypothetical protein



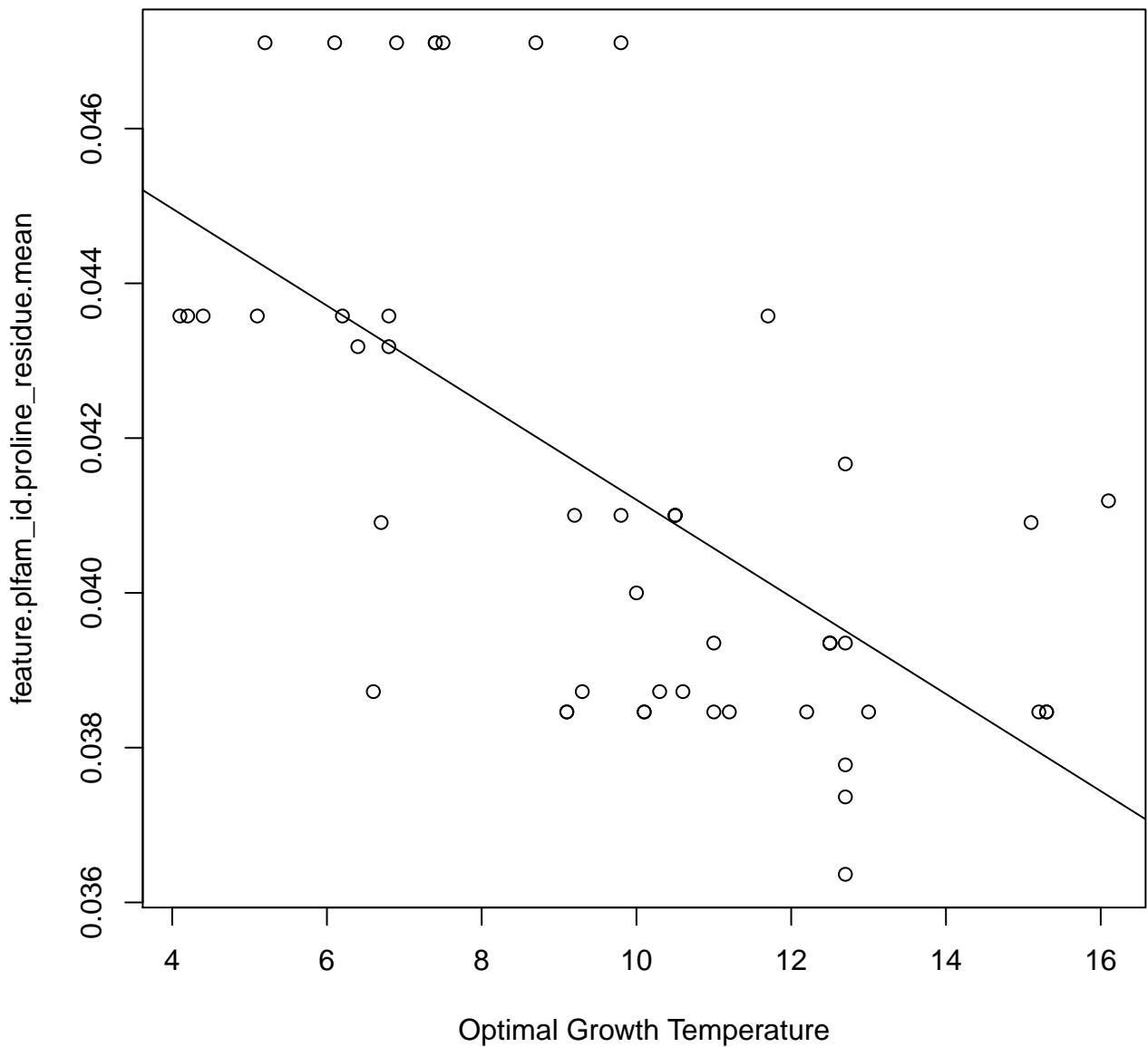
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PLF_28228_00000216
Dihydroorotate (EC 3.5.2.3)



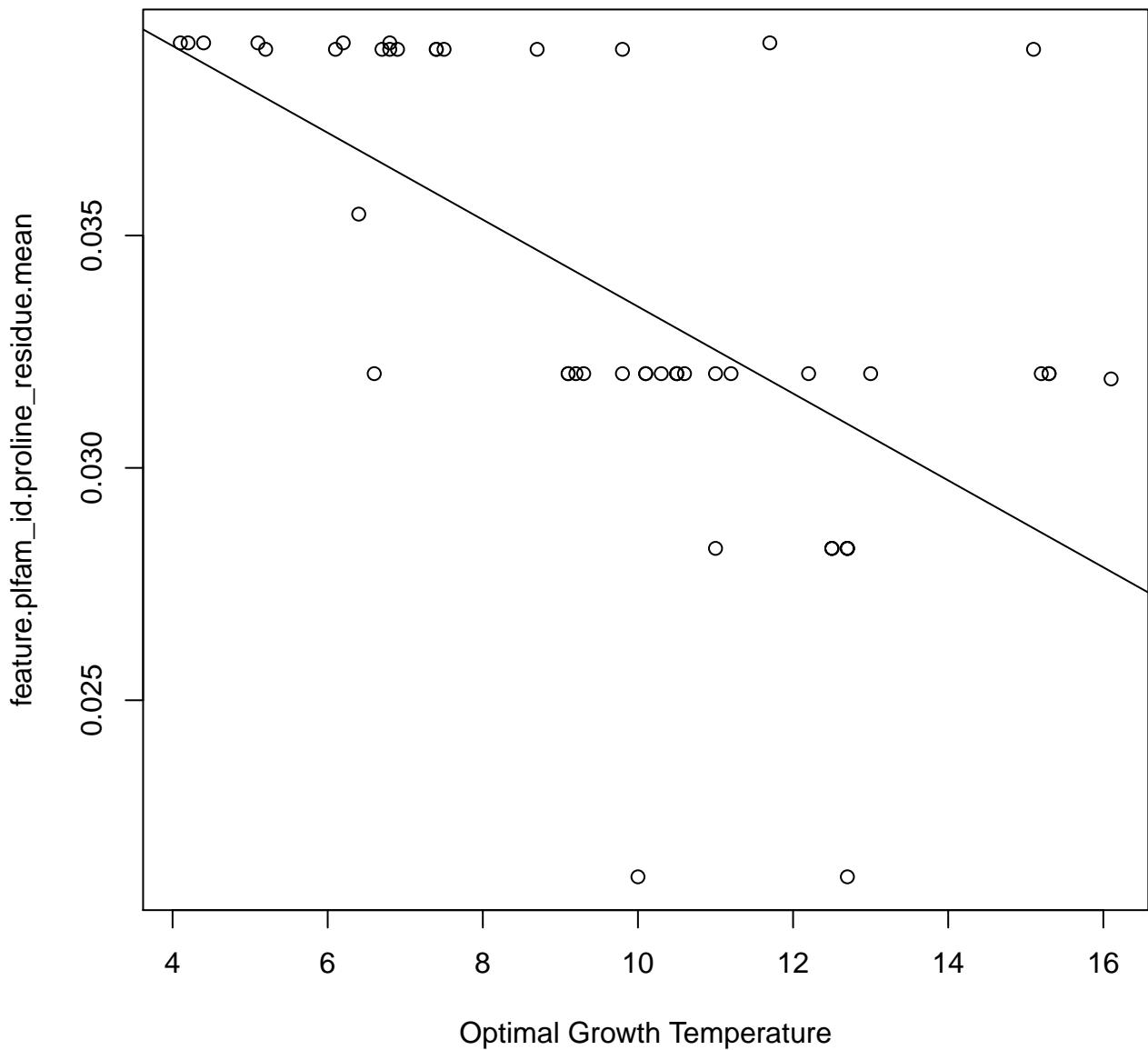
feature.plfam_id.proline_residue.mean
PLF_28228_00001825
Uncharacterized conserved protein YfiP, contains DTW domain



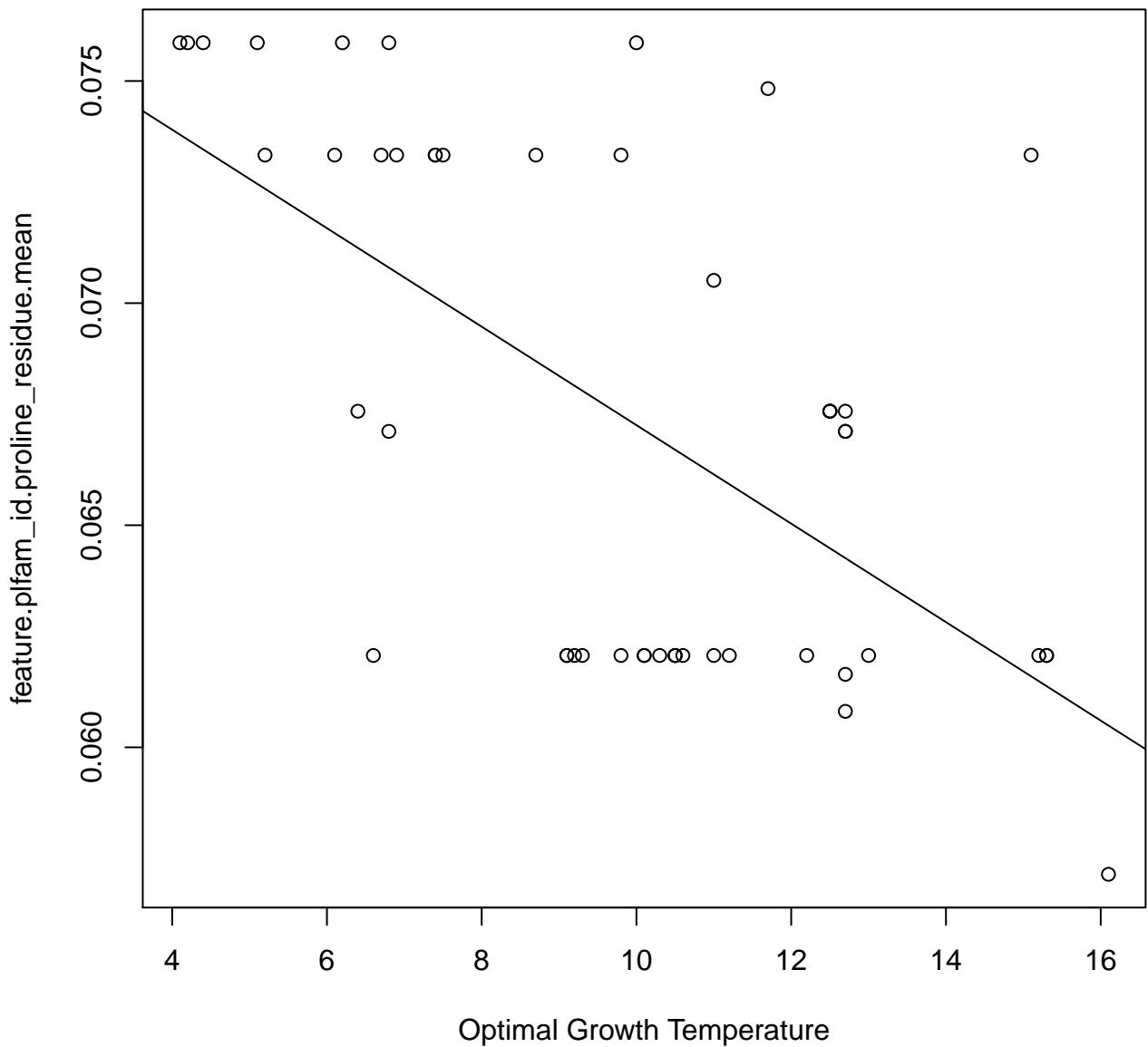
feature.pfam_id.proline_residue.mean
PLF_28228_00000283
ATP-dependent RNA helicase VF1437



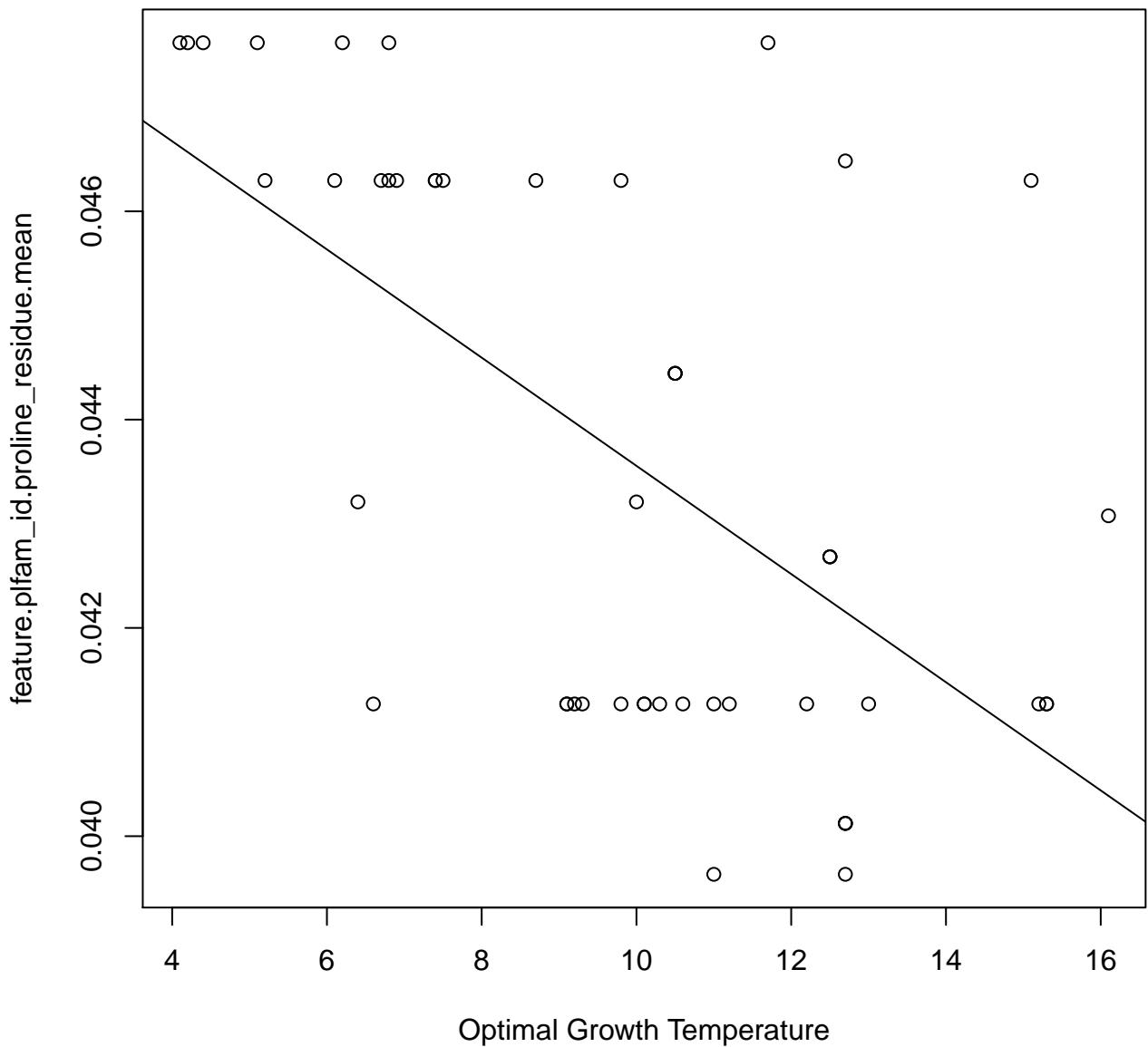
feature.plfam_id.proline_residue.mean
PLF_28228_00001638
HD domain protein



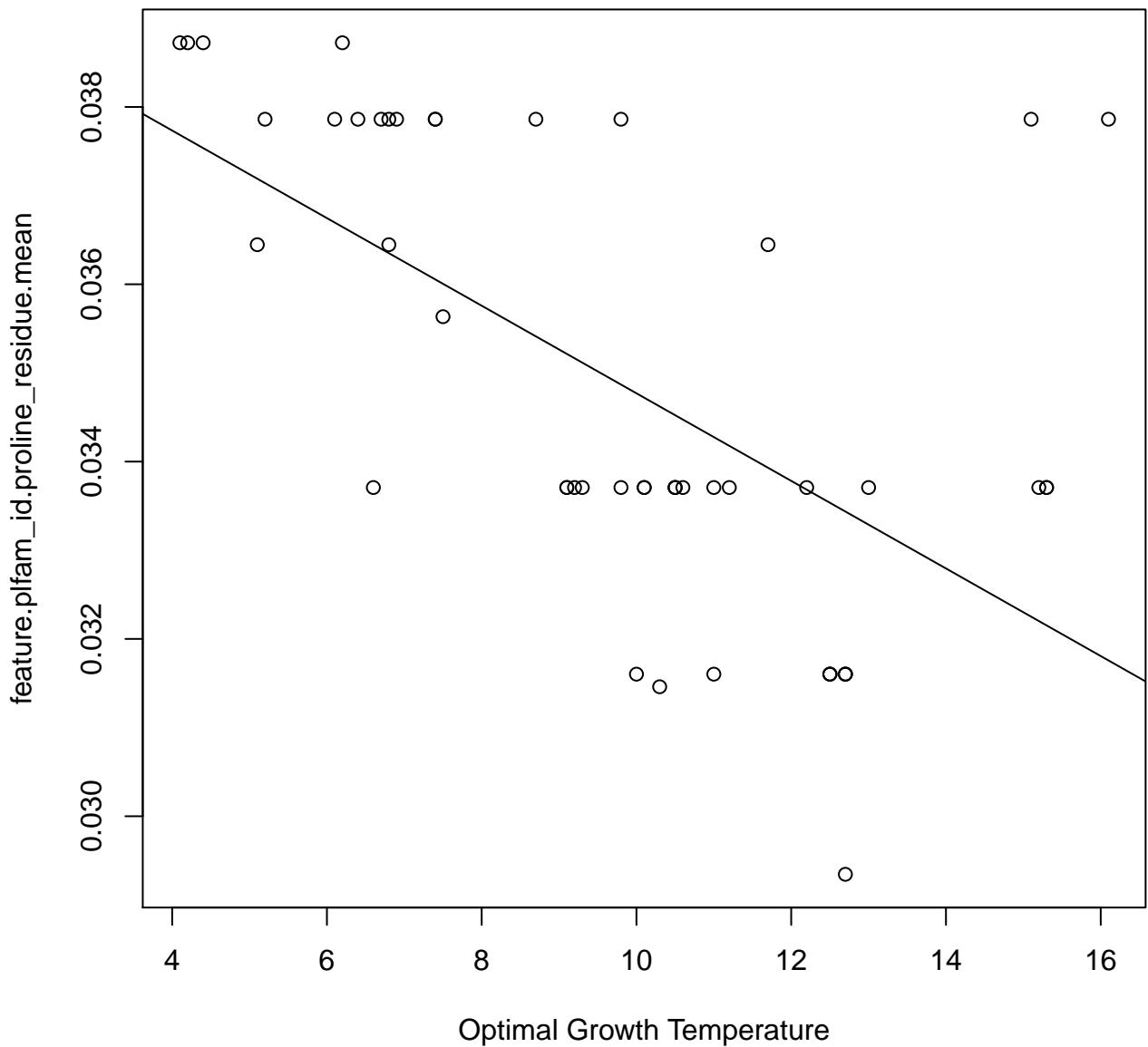
feature.plfam_id.proline_residue.mean
PLF_28228_00000390
Biotin carboxyl carrier protein of acetyl-CoA carboxylase



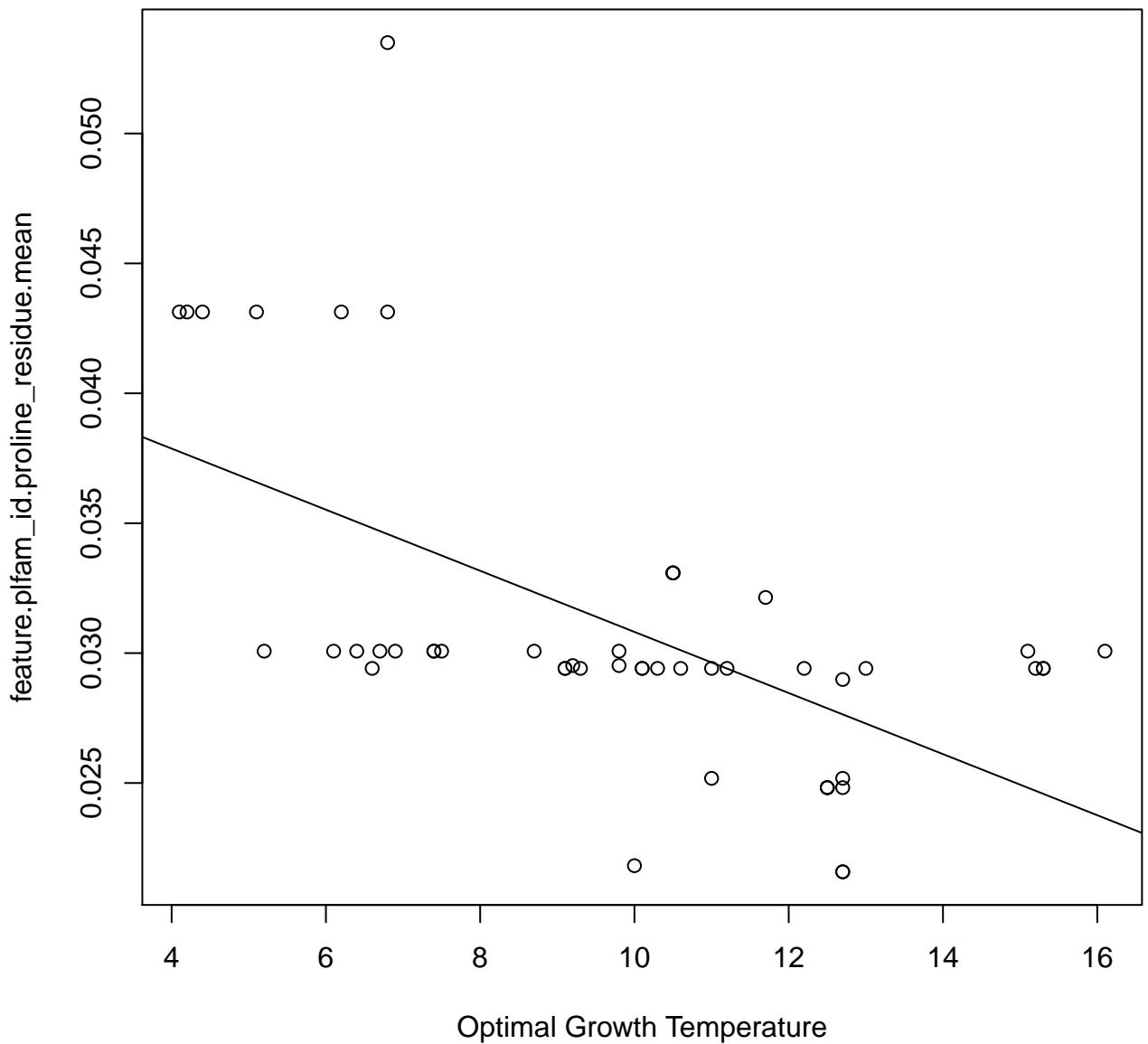
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PLF_28228_00000506
Homoserine kinase (EC 2.7.1.39)



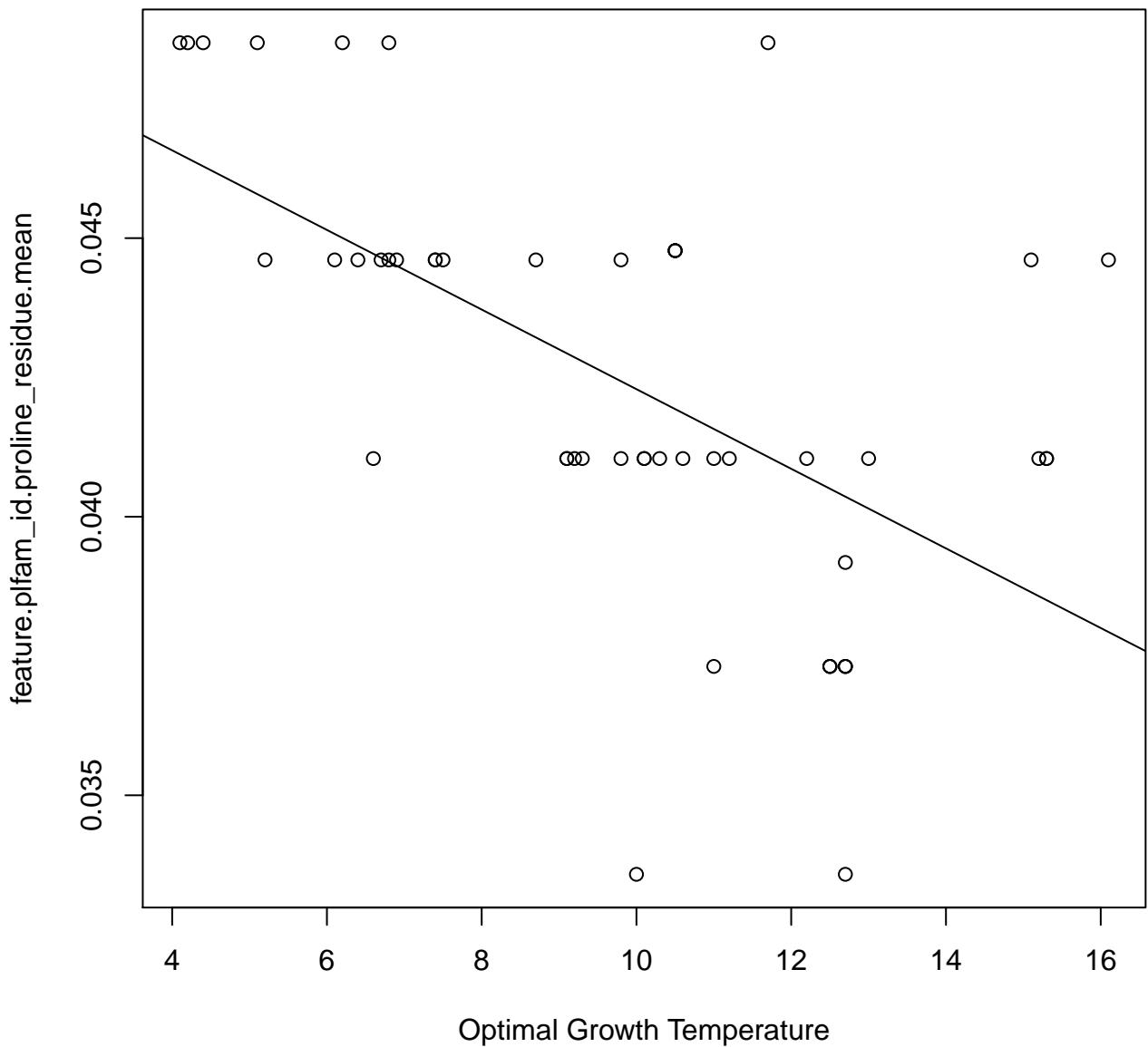
feature.plfam_id.proline_residue.mean
PLF_28228_00000608
Methionine transporter MetT



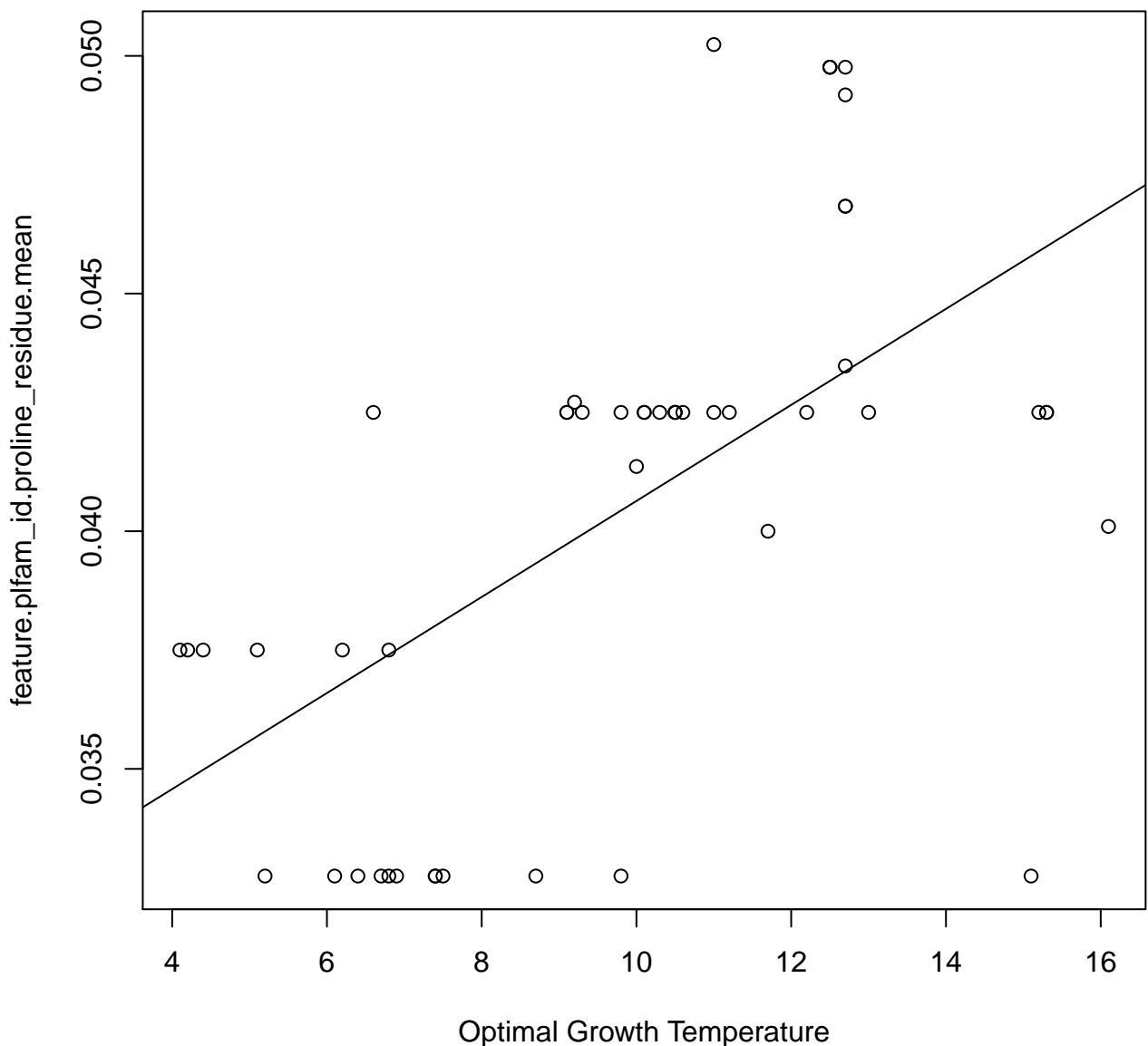
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PLF_28228_00000670
Nucleoside triphosphate pyrophosphohydrolase MazG (EC 3.6.1.8)



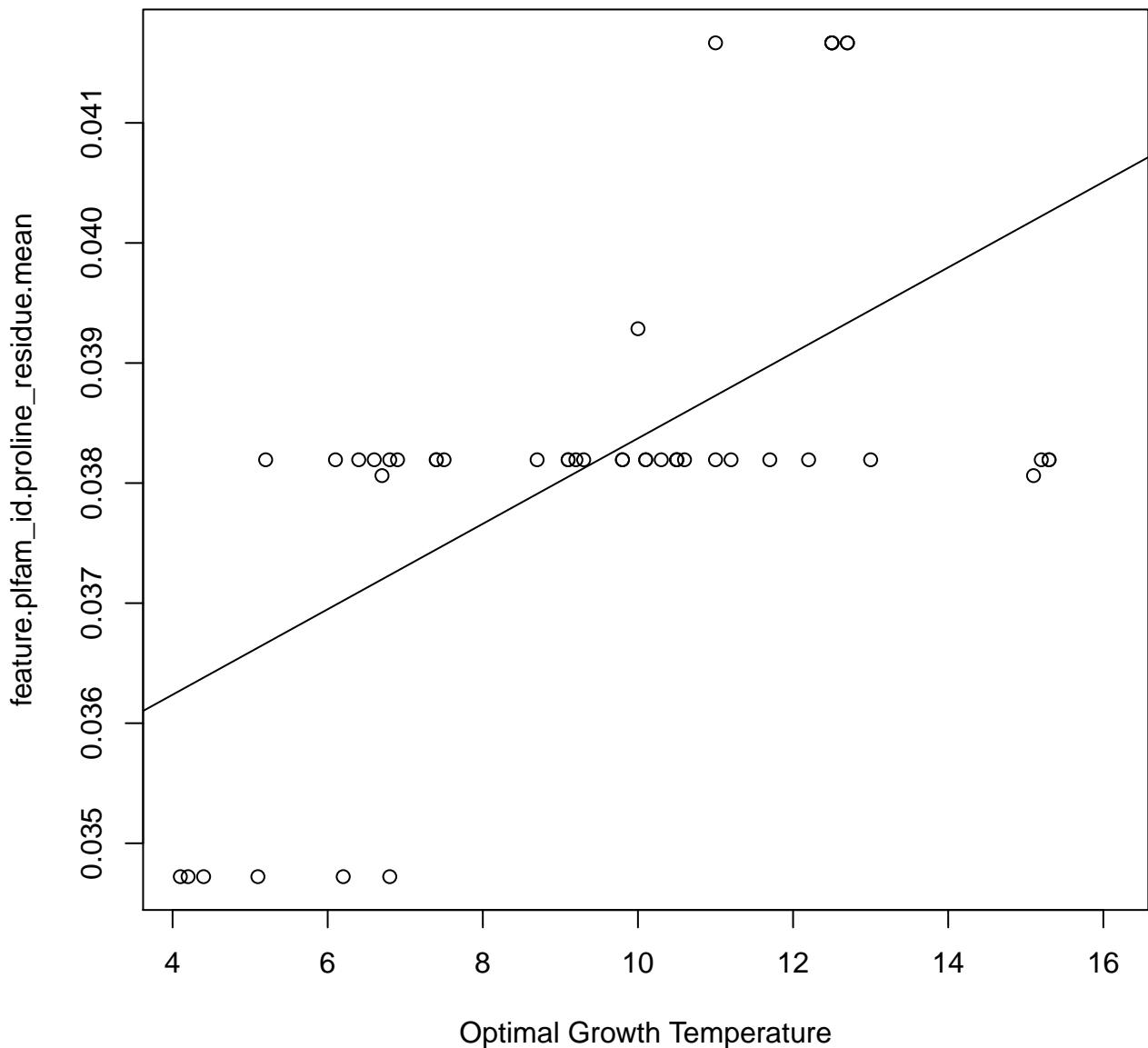
feature.plfam_id.proline_residue.mean
PLF_28228_00000381
Exodeoxyribonuclease III (EC 3.1.11.2)



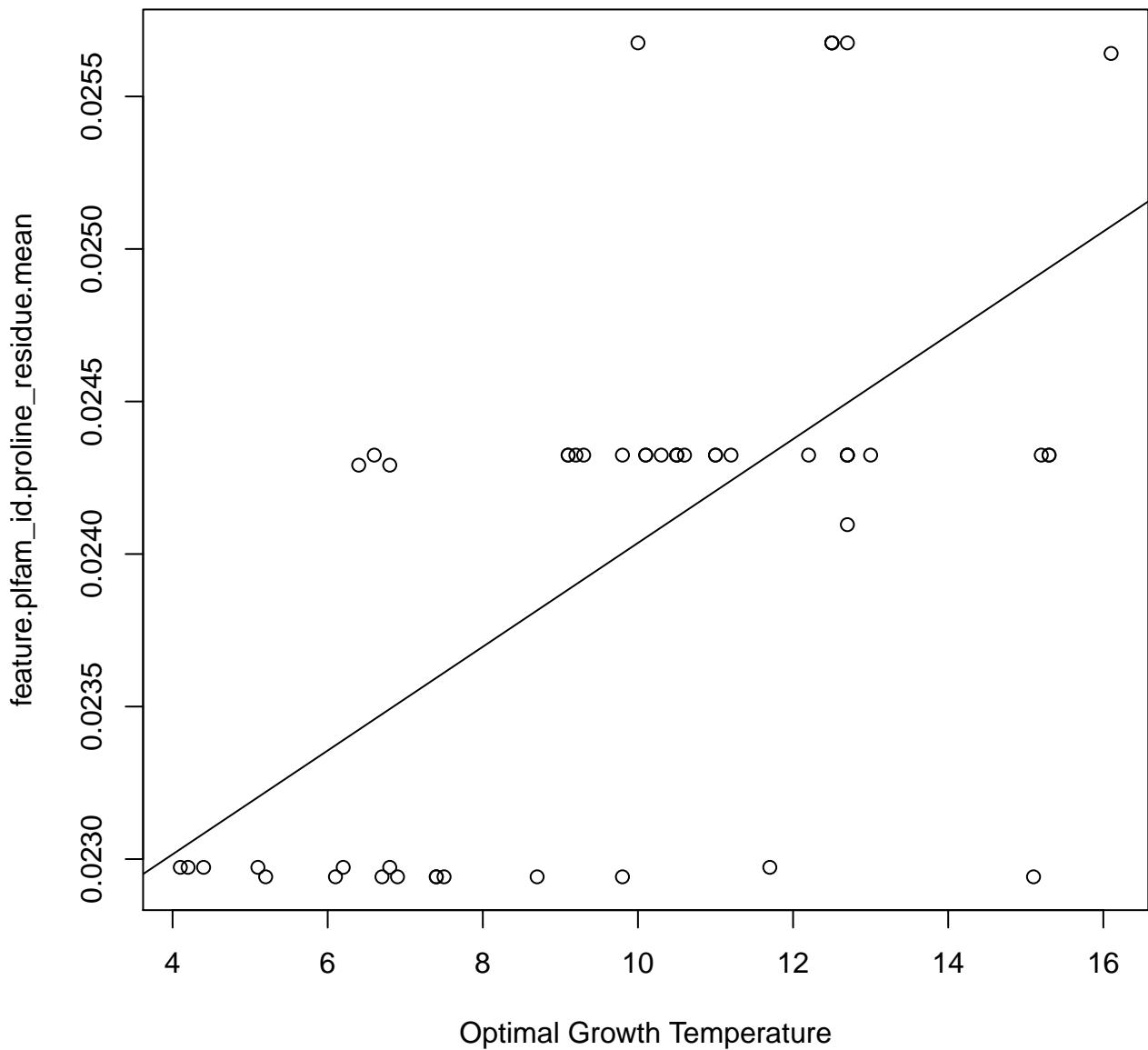
feature.plfam_id.proline_residue.mean
PLF_28228_00001909
Multidrug resistance transporter, Bcr/CflA family



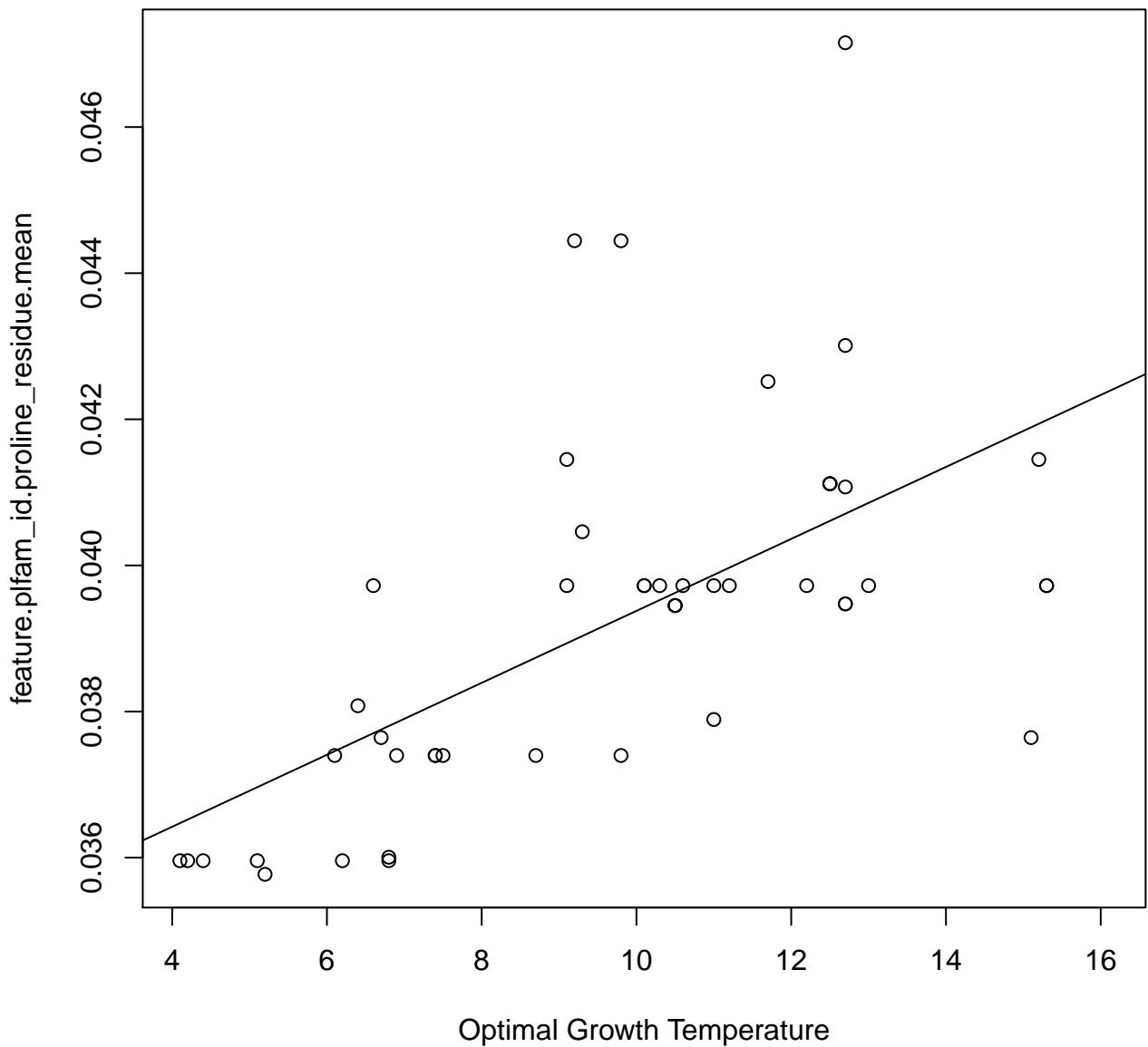
feature.plfam_id.proline_residue.mean
PLF_28228_00003394
ABC transporter, substrate-binding protein (cluster 12, methionine/phosphonates)



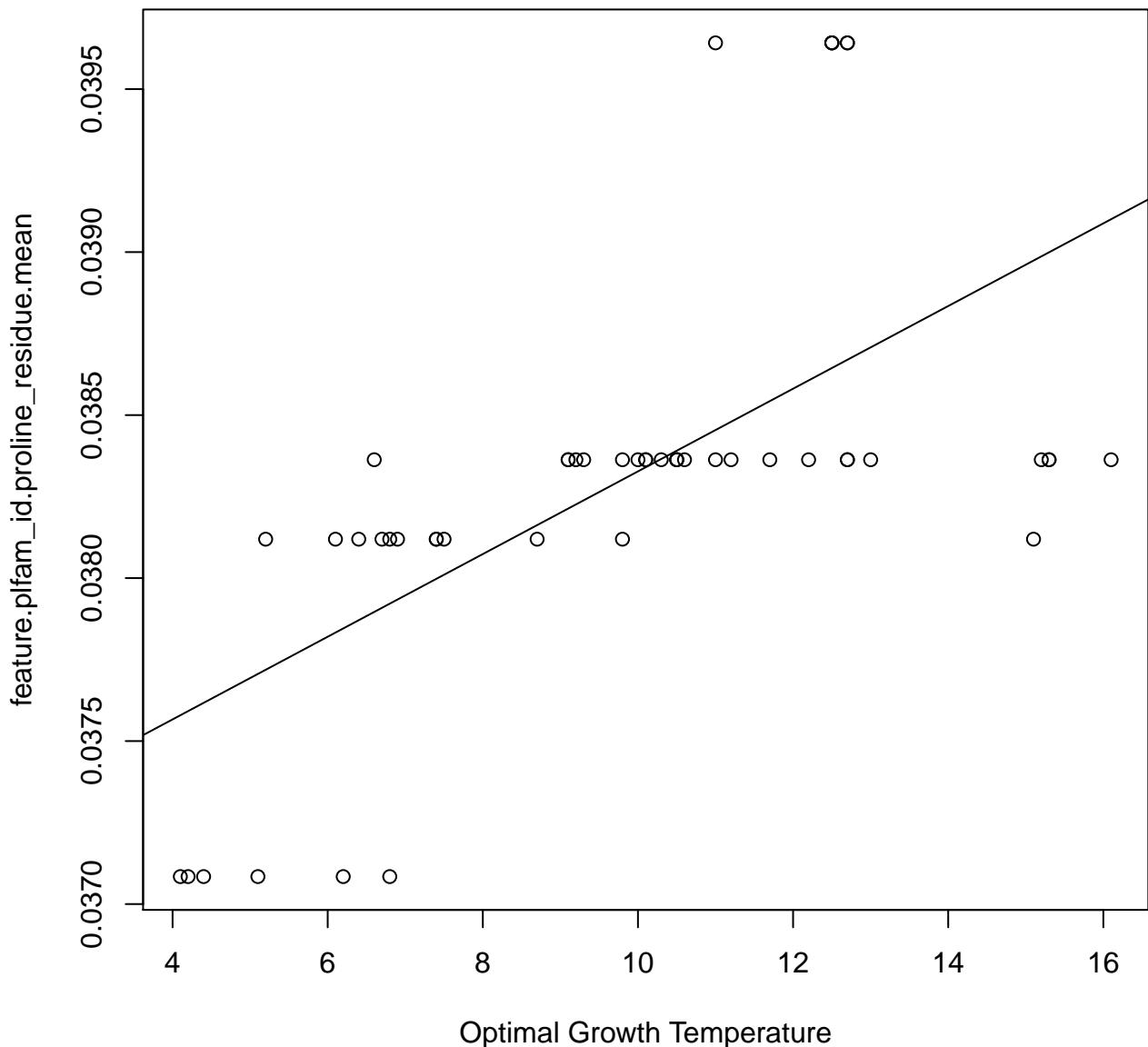
feature.plfam_id.proline_residue.mean
PLF_28228_00001936
Predicted signal transduction protein



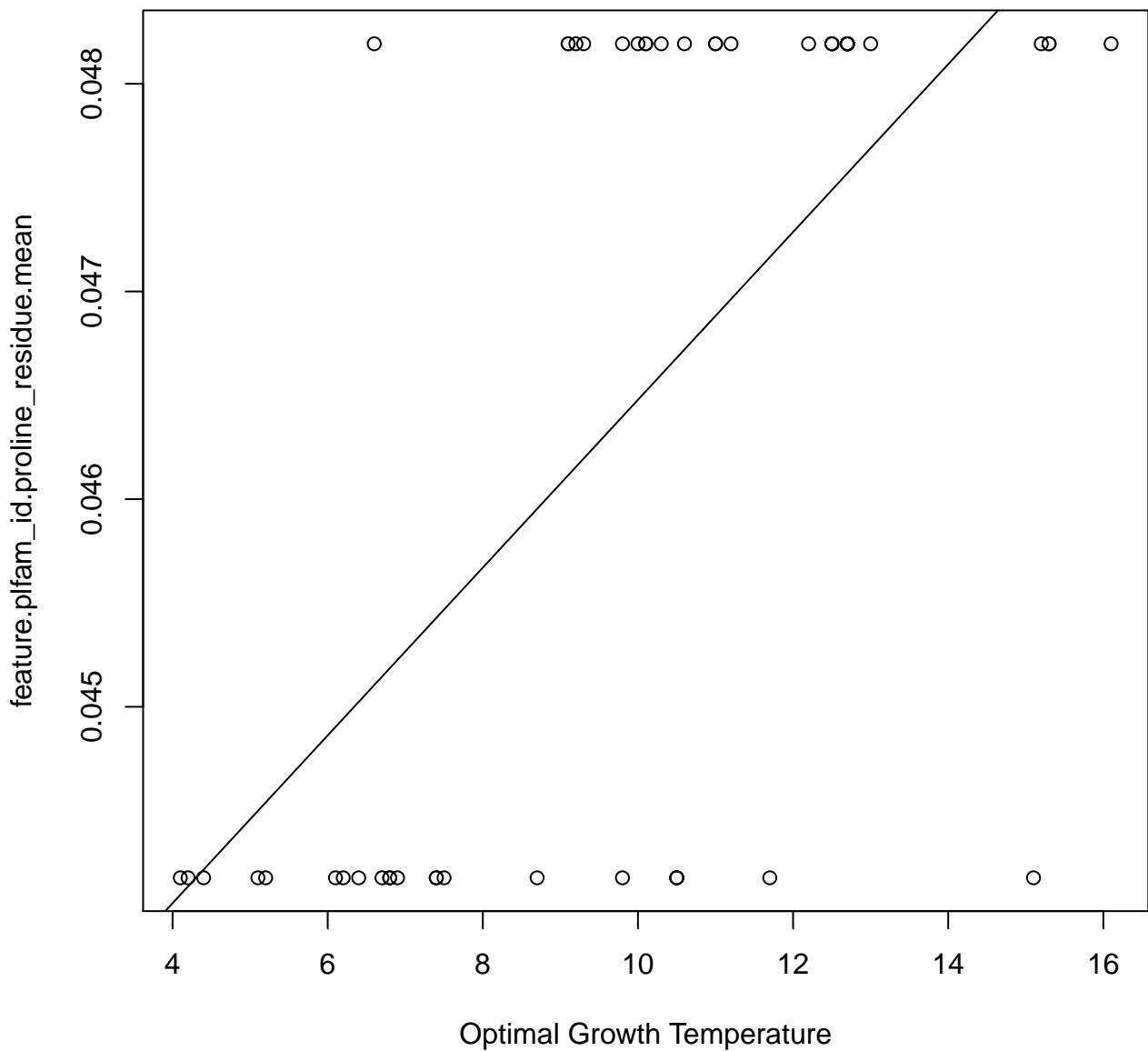
feature.plfam_id.proline_residue.mean
PLF_28228_00002320
hypothetical protein



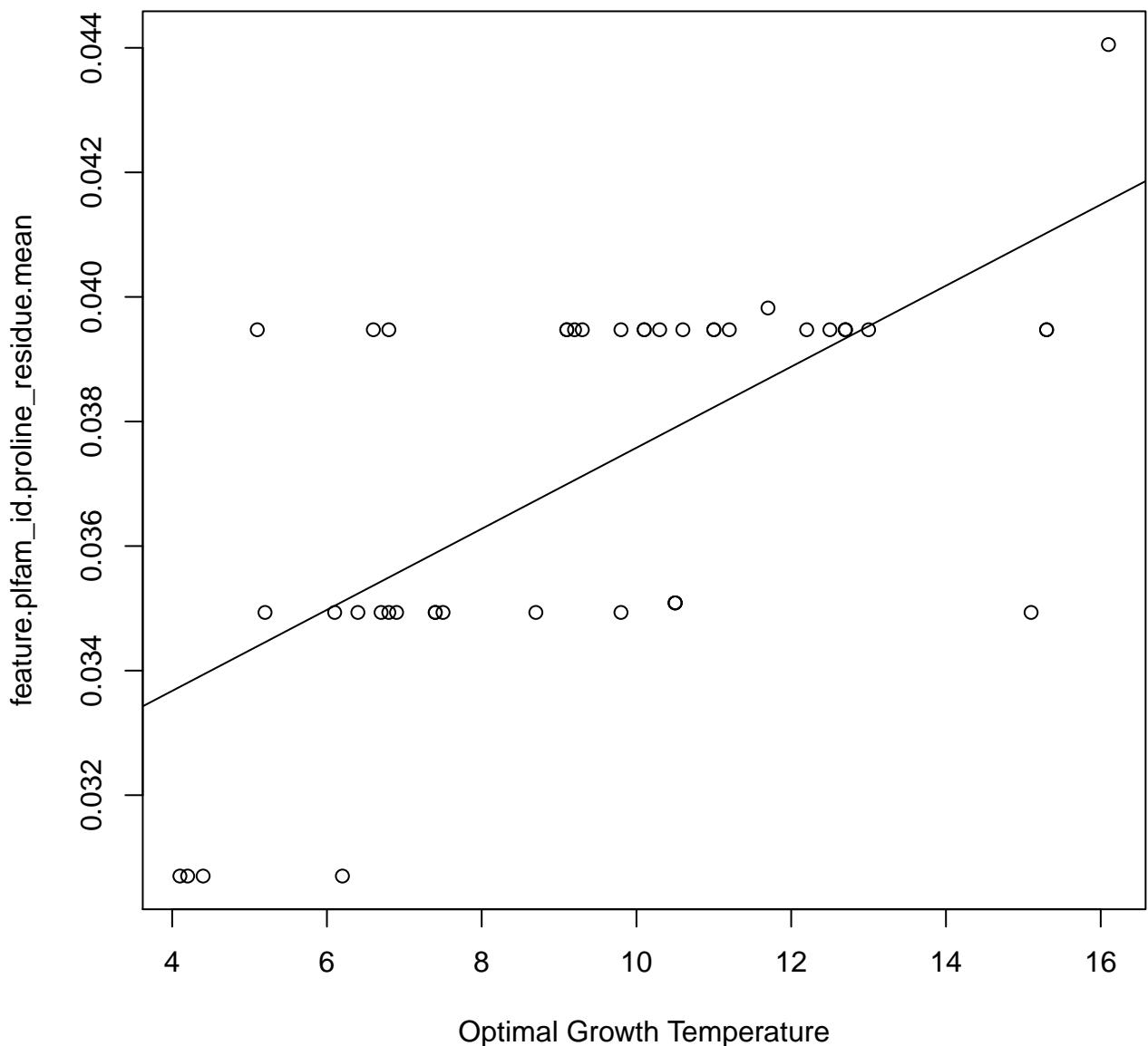
feature.plfam_id.proline_residue.mean
PLF_28228_00000288
ATP-dependent protease La (EC 3.4.21.53) Type I



feature.plfam_id.proline_residue.mean
PLF_28228_00000234
2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117)



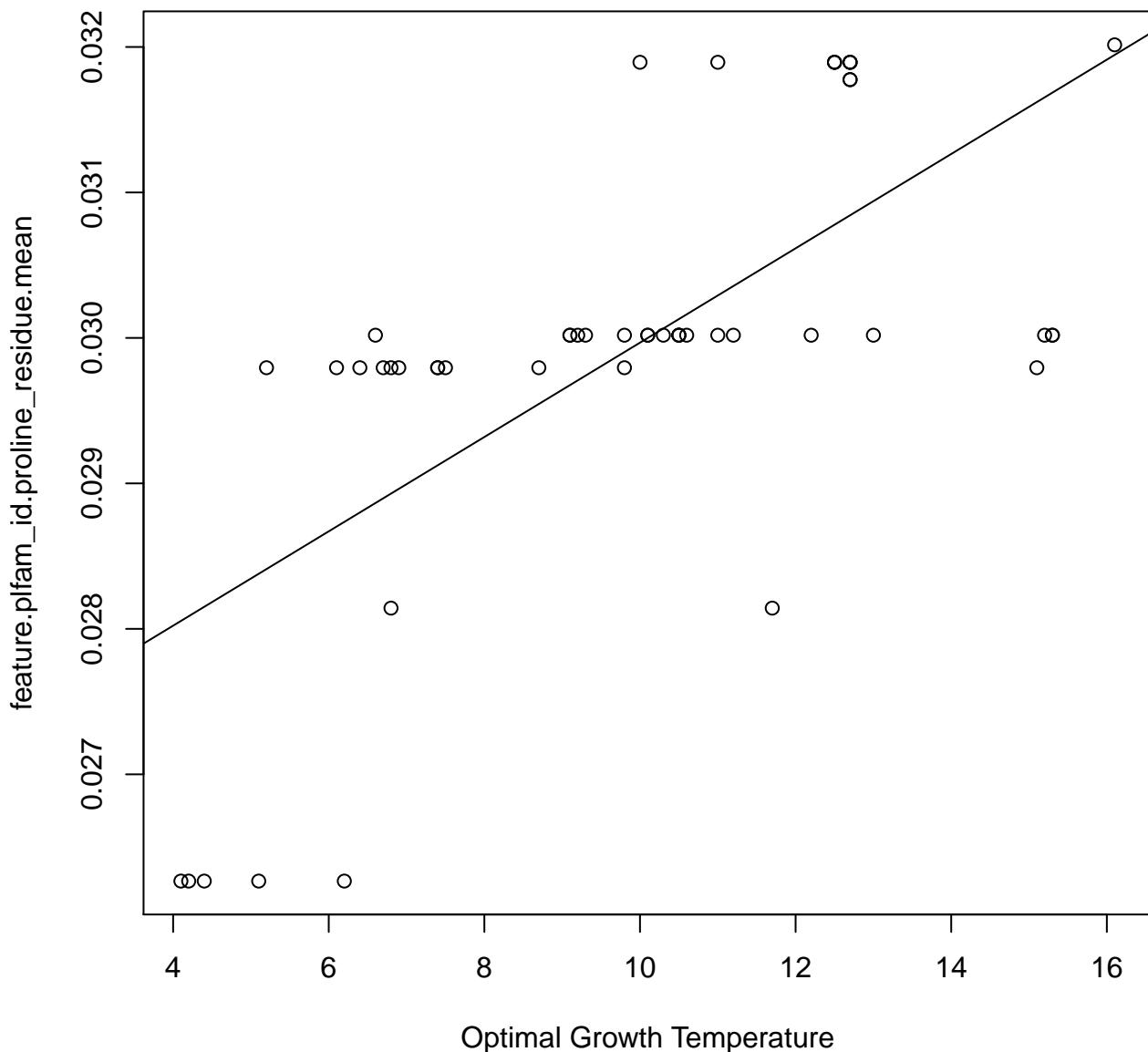
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PLF_28228_00028198
FIG111991: hypothetical protein



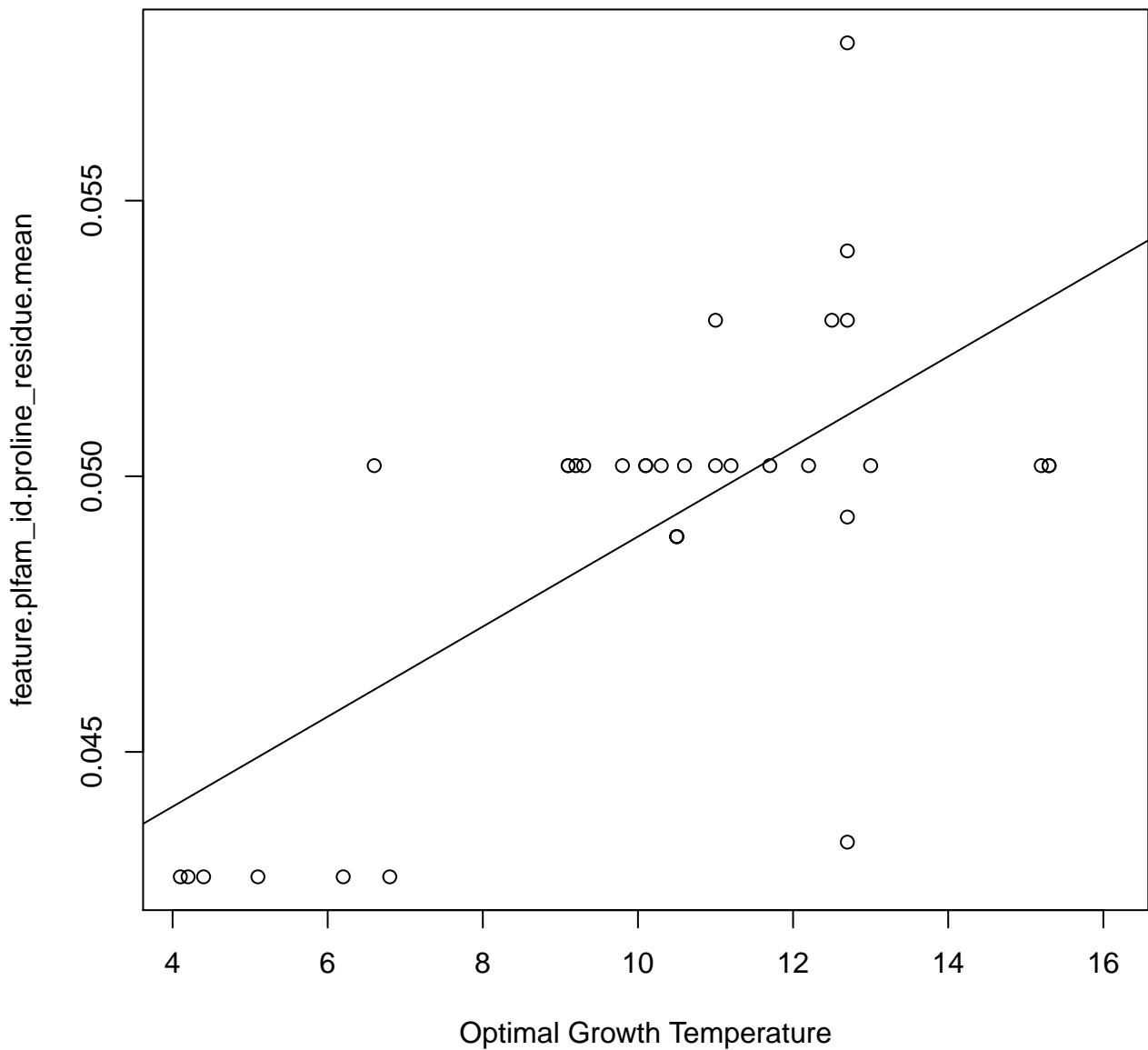
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PLF_28228_00000516

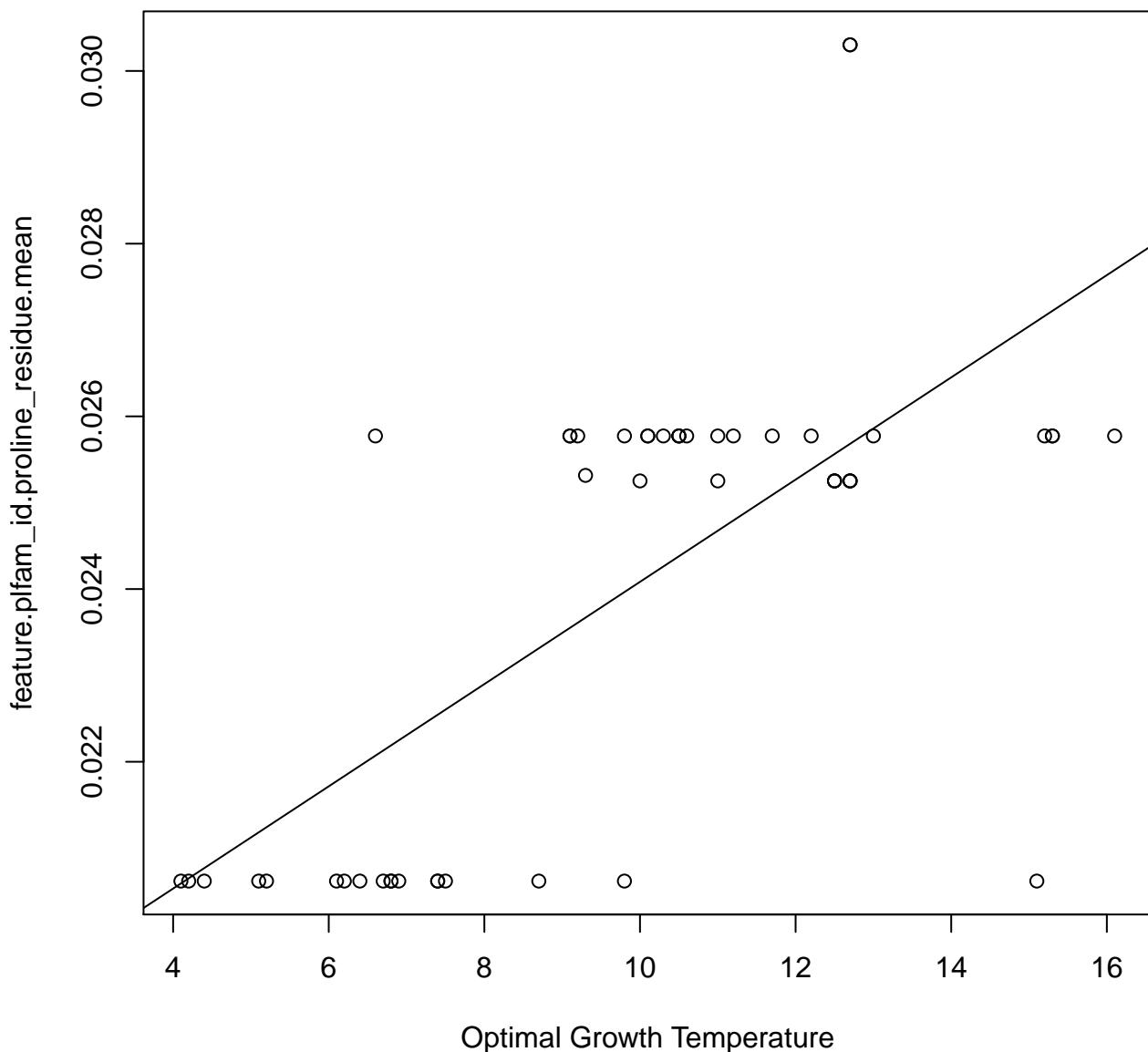
IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)



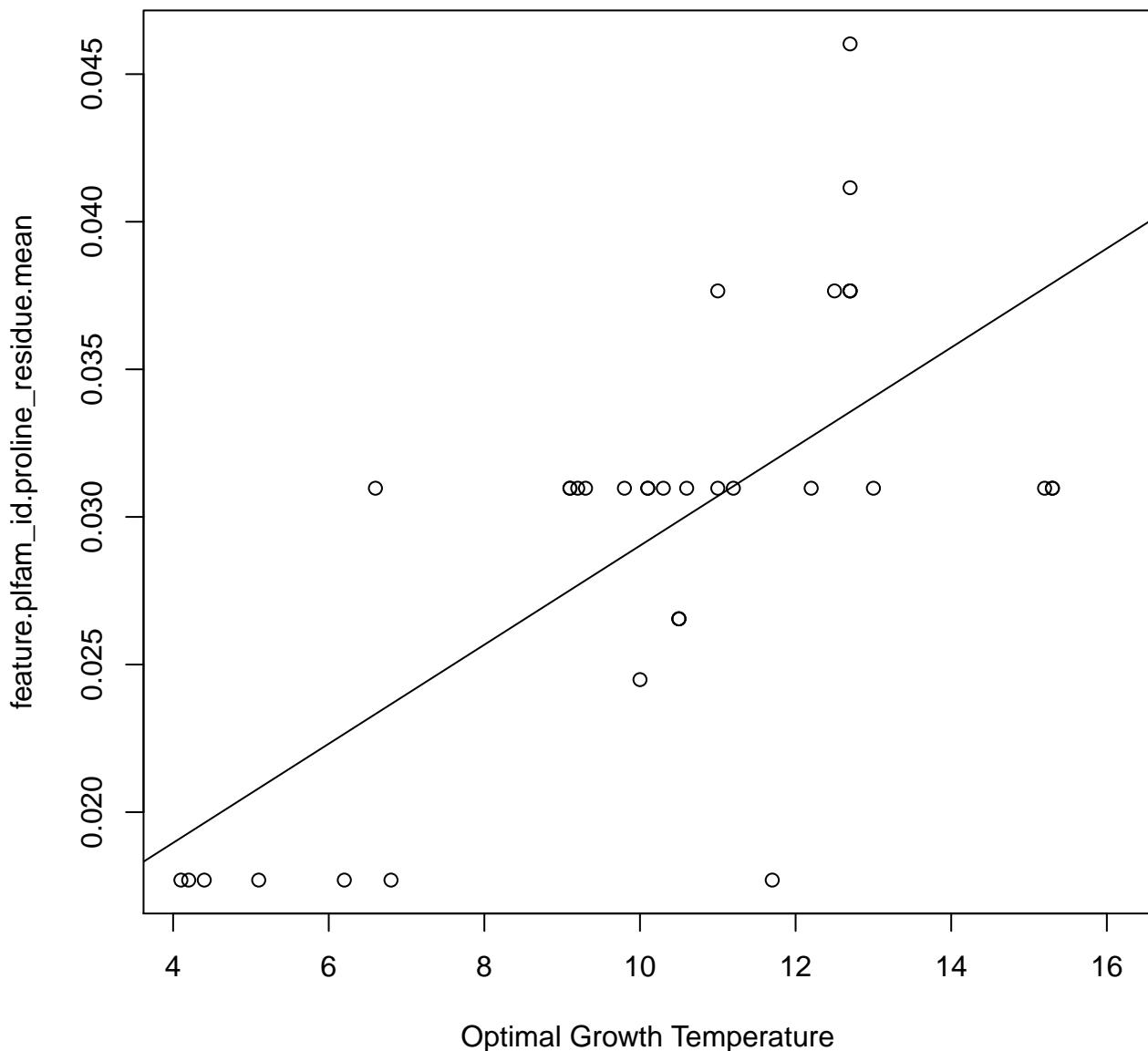
feature.plfam_id.proline_residue.mean
PLF_28228_00028047
Fatty acid cis/trans isomerase



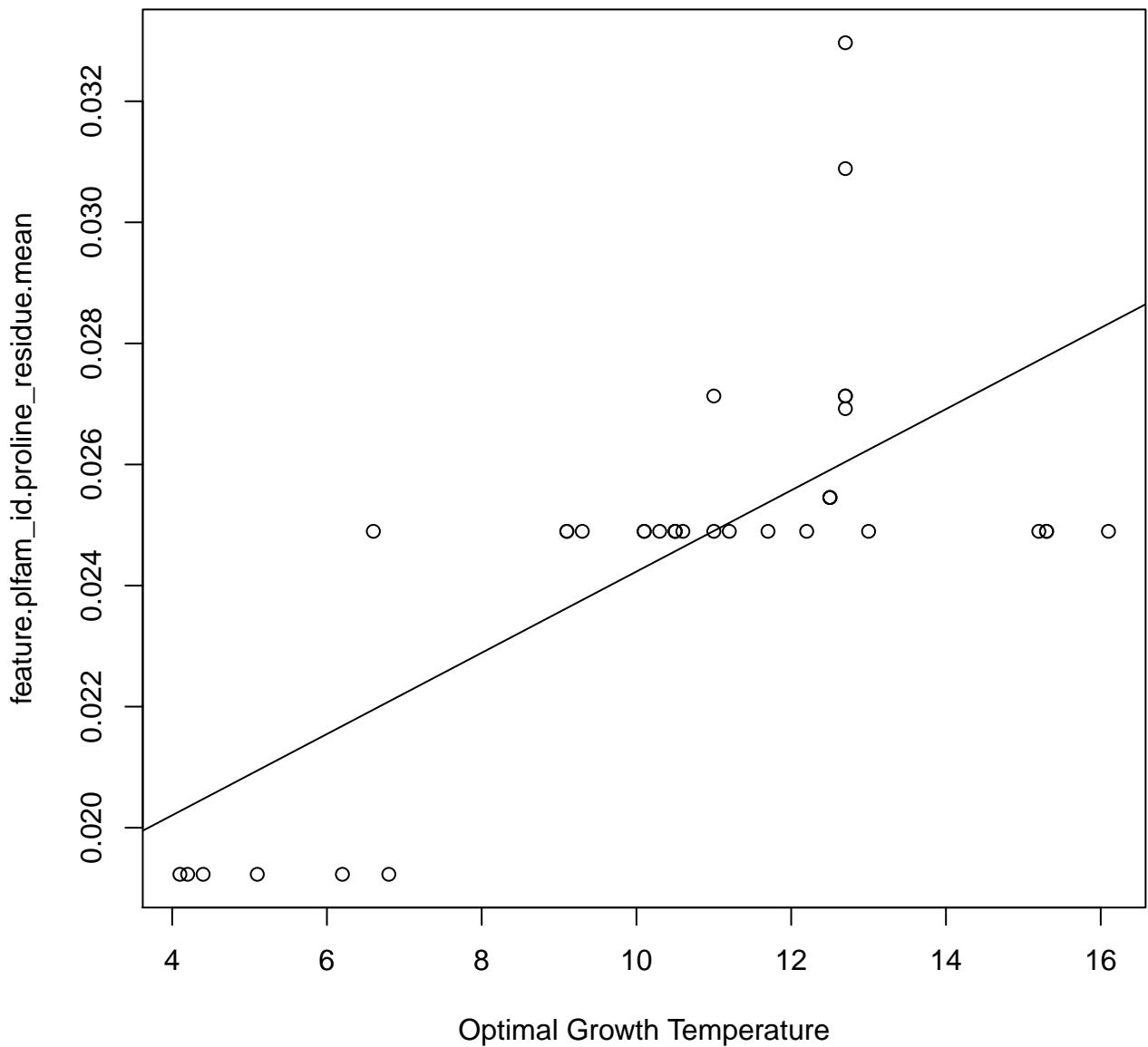
feature.plfam_id.proline_residue.mean
PLF_28228_00001218
Transcriptional regulator SlmA, TetR family



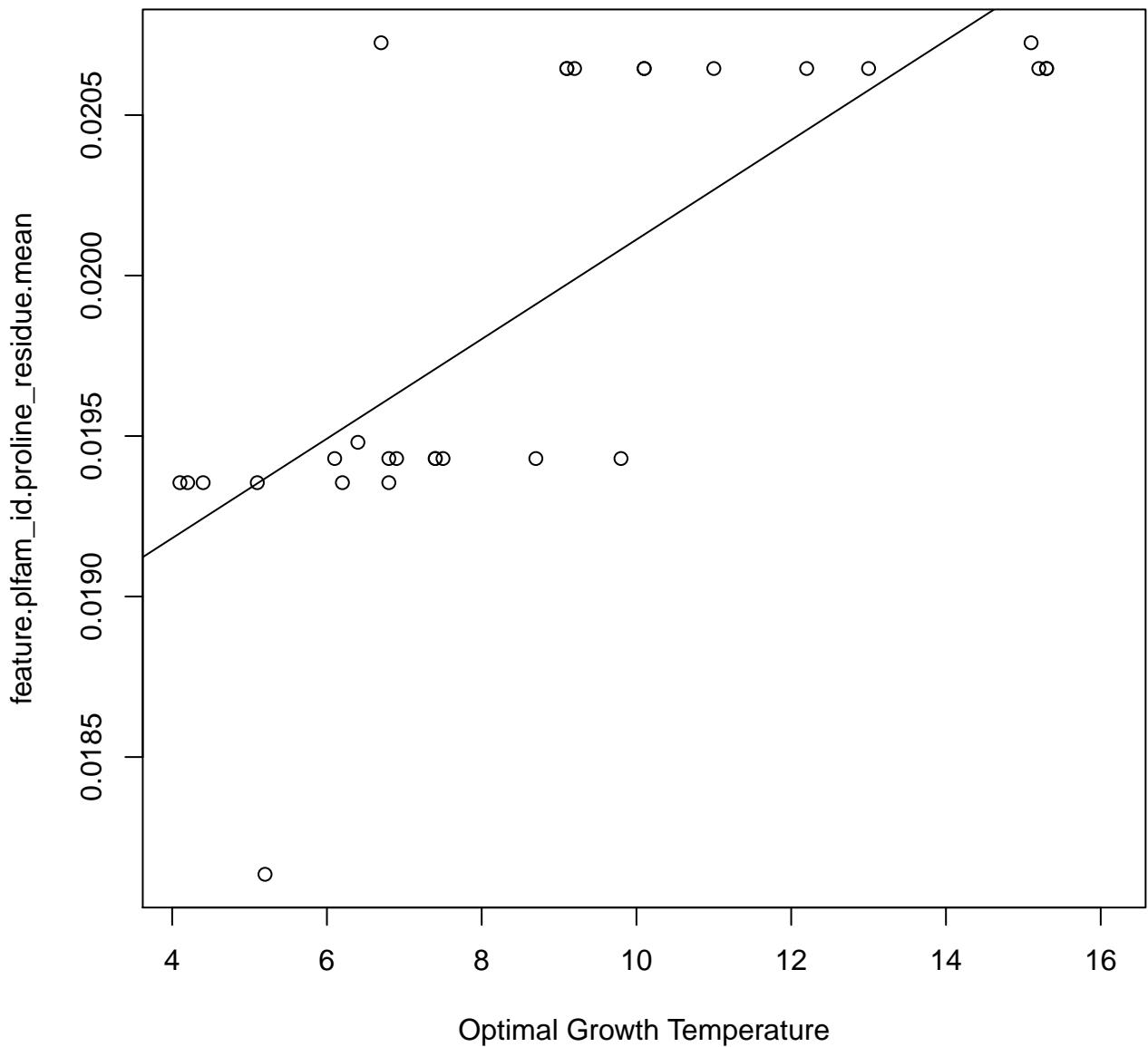
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PLF_28228_00014865
Pyridoxal phosphate-containing protein YggS



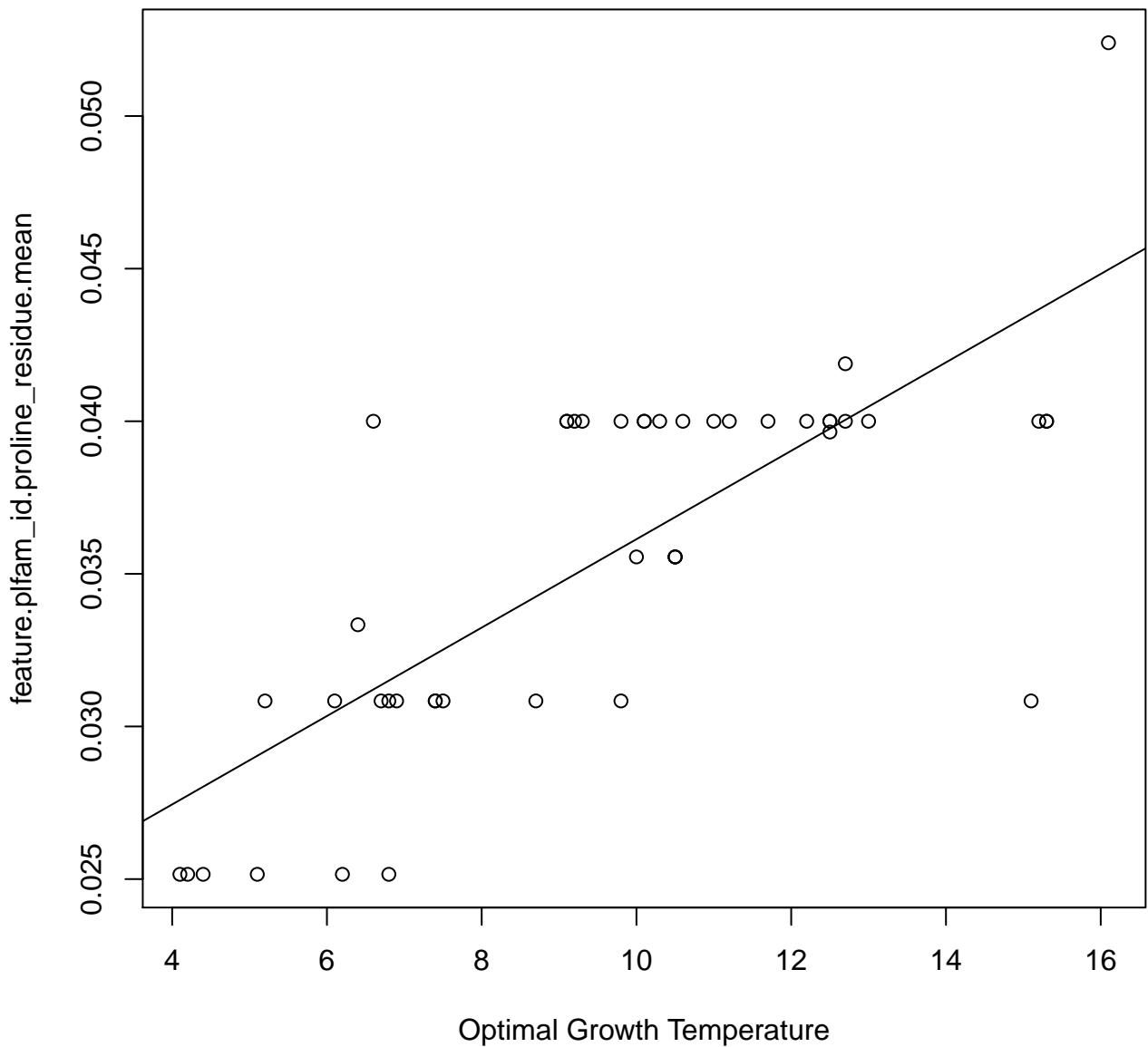
feature.plfam_id.proline_residue.mean
PLF_28228_00002798
Two-component transcriptional response regulator, OmpR family



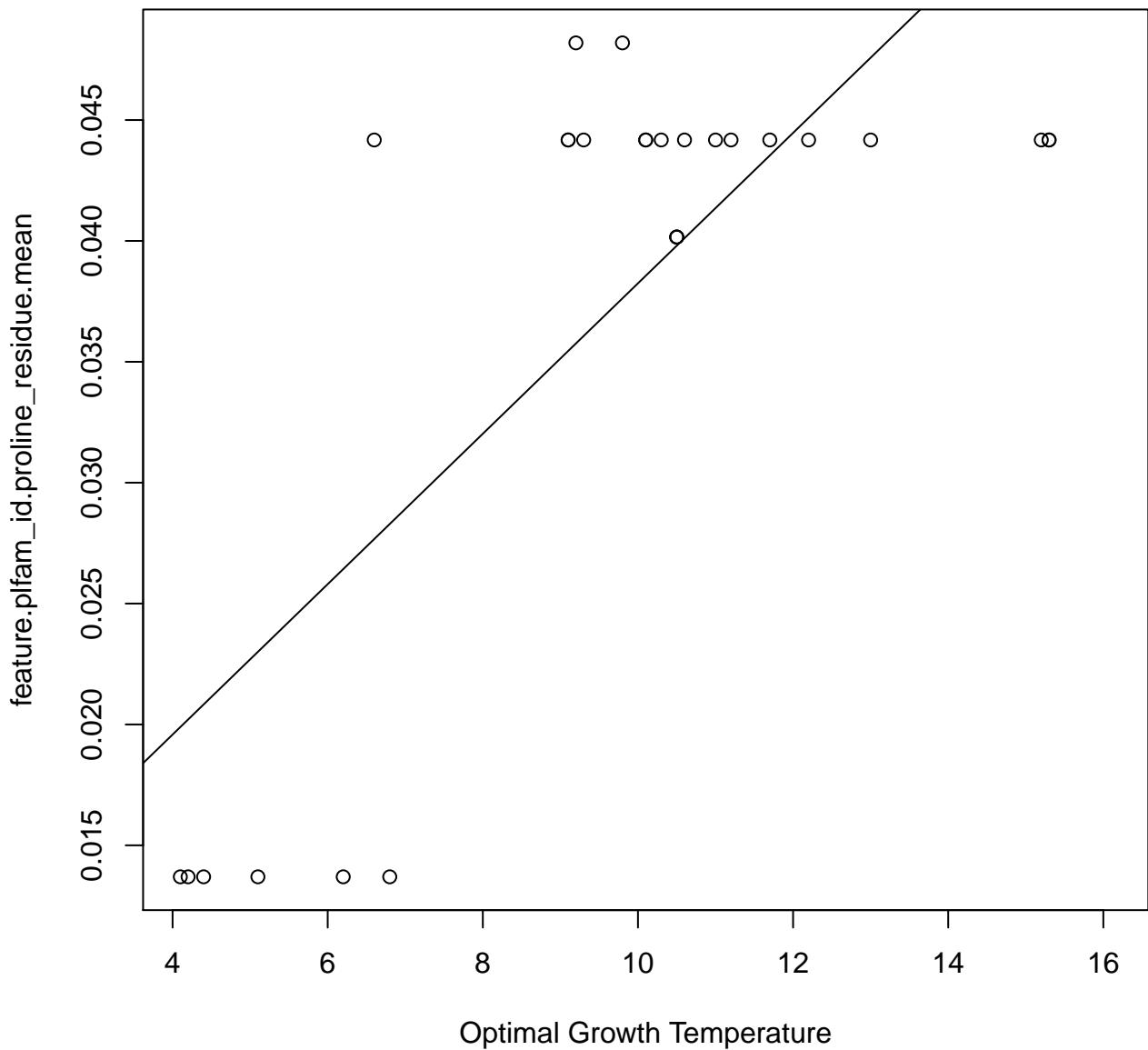
feature.plfam_id.proline_residue.mean
PLF_28228_00021199
diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)



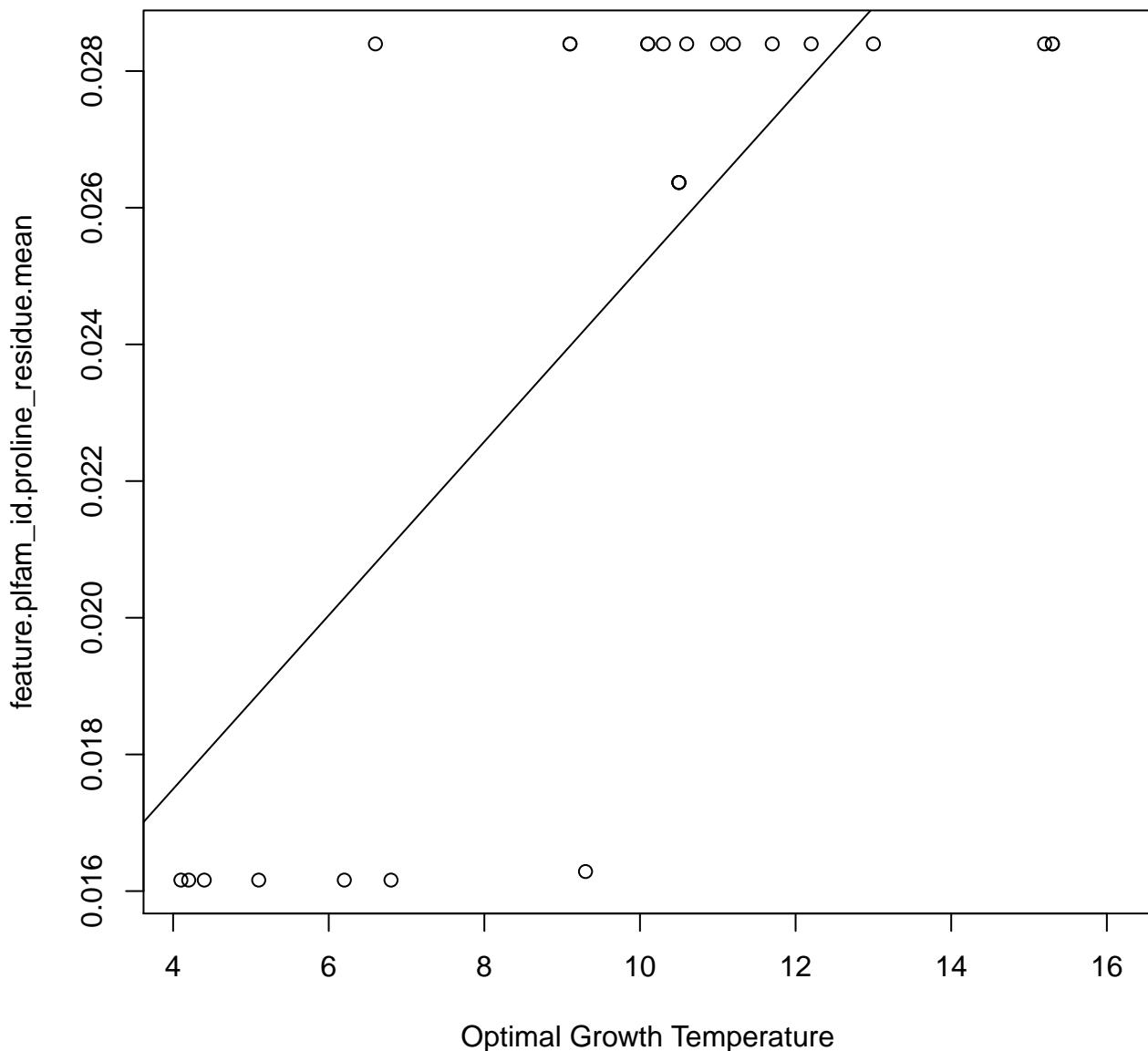
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PLF_28228_00002803
SM-20-related protein



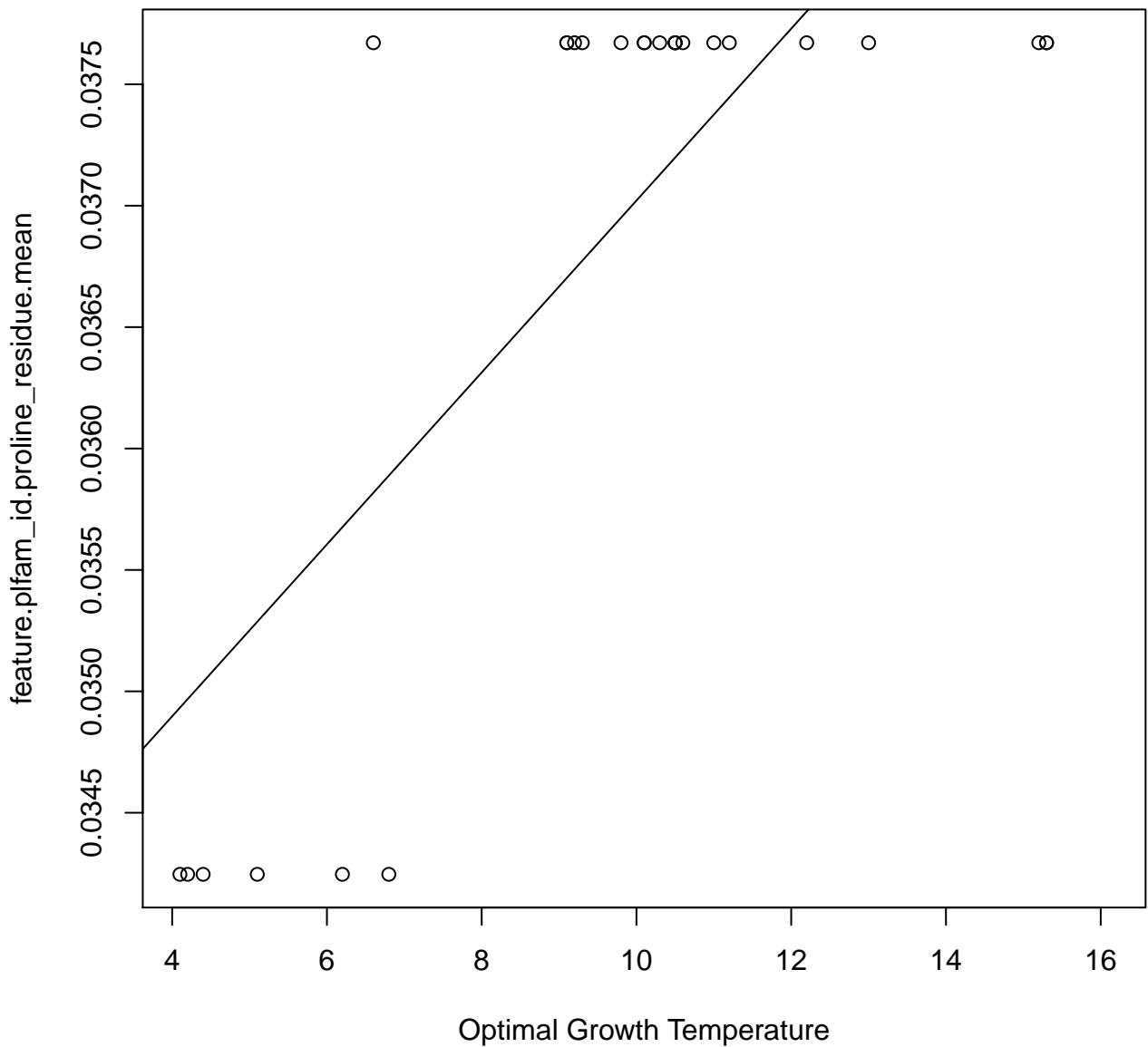
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PLF_28228_00031426
hypothetical protein



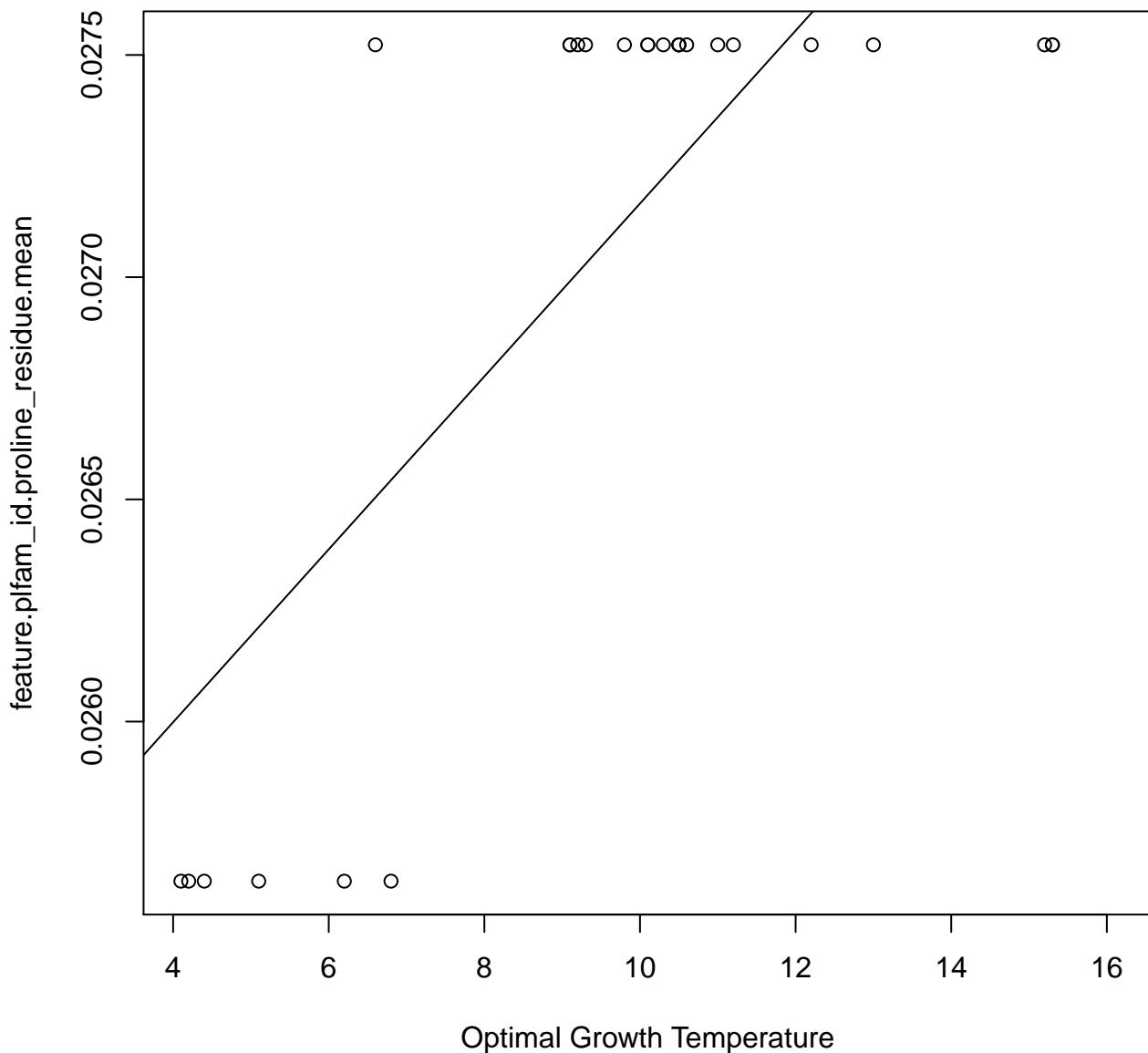
feature.plfam_id.proline_residue.mean
PLF_28228_00022096
Two-component system sensor histidine kinase



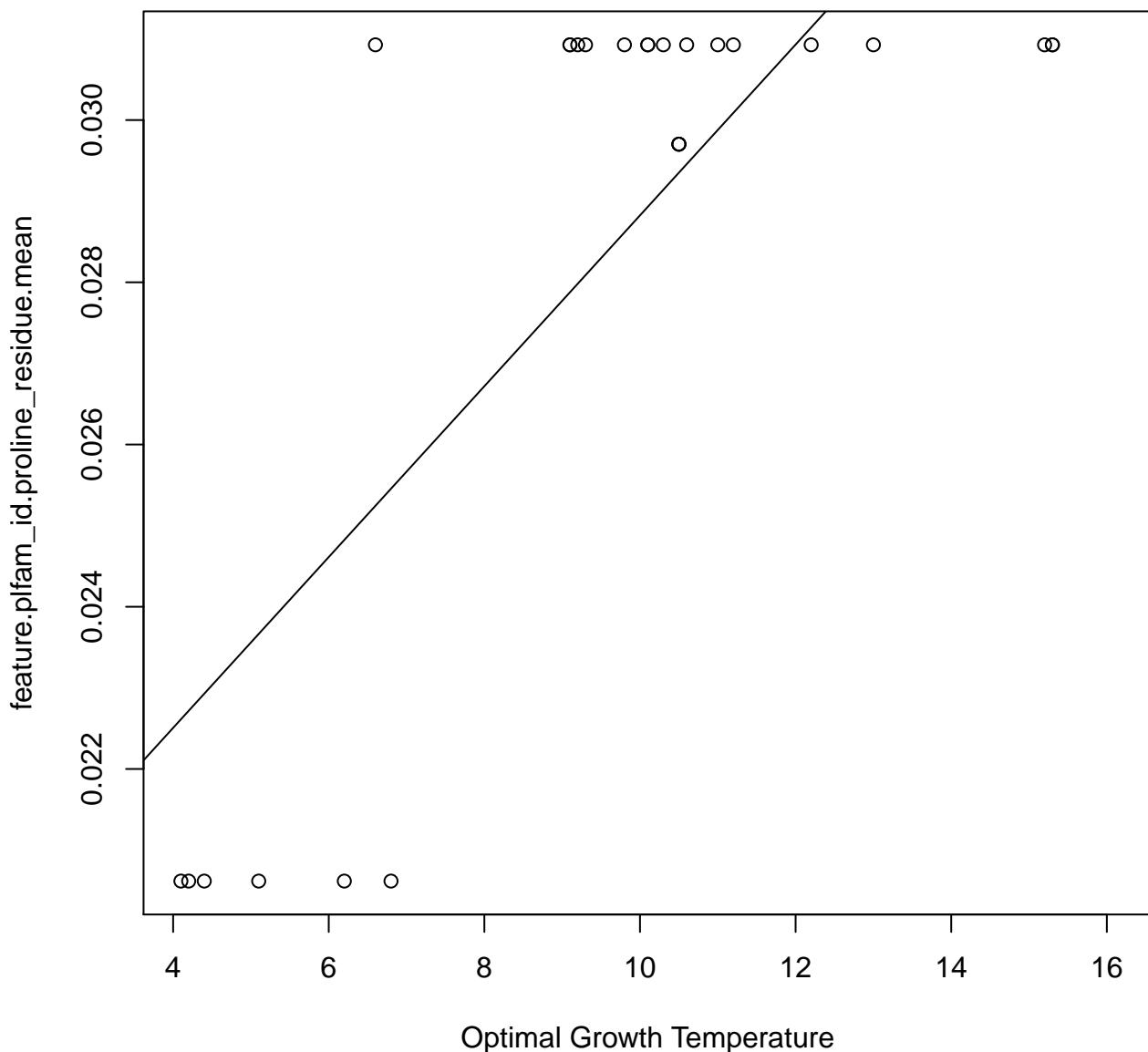
feature.plfam_id.proline_residue.mean
PLF_28228_00023267
Uncharacterized protein conserved in bacteria, NMA0228-like



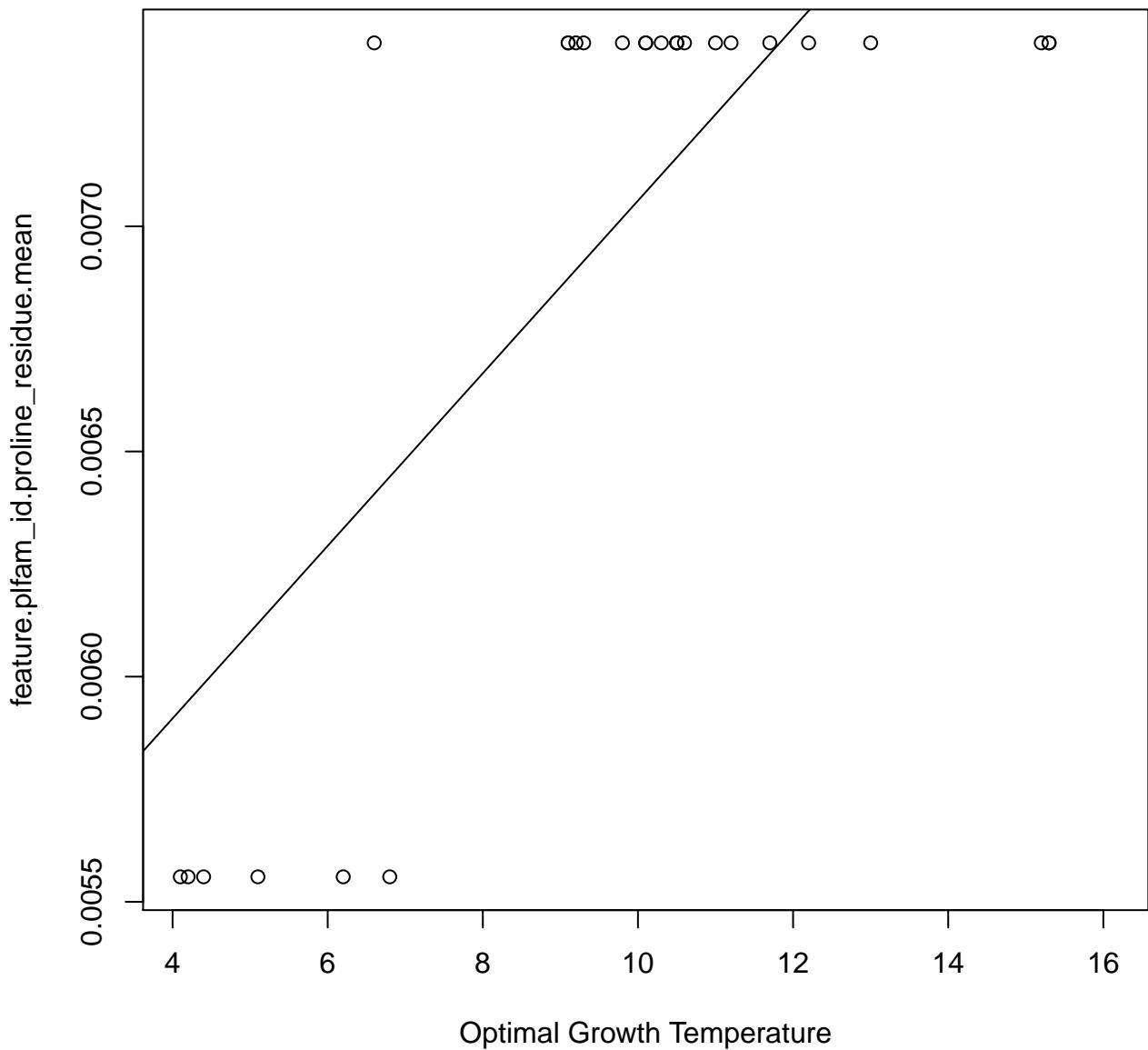
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PLF_28228_00031492
hypothetical protein



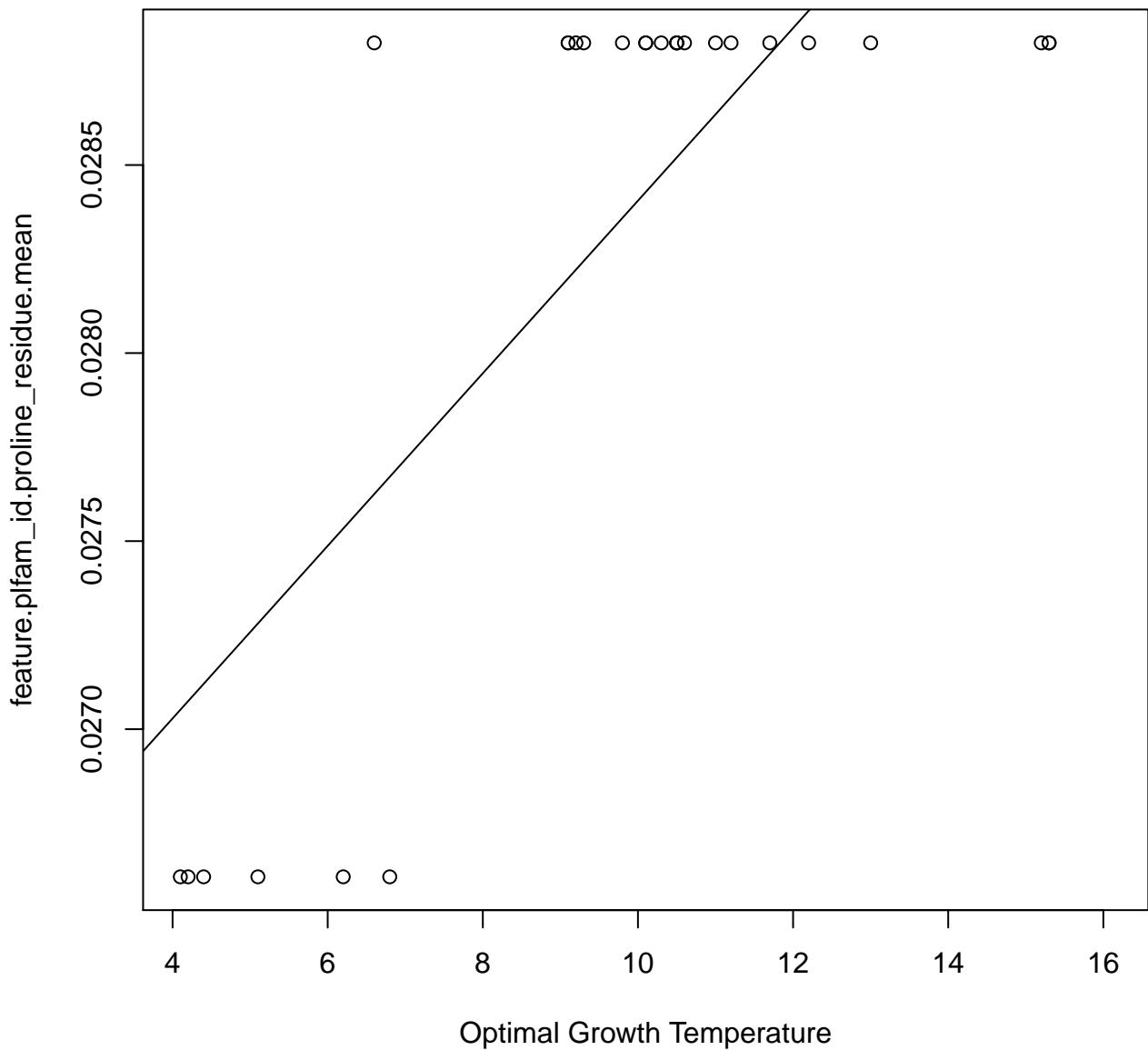
feature.plfam_id.proline_residue.mean
PLF_28228_00030961
hypothetical protein



feature.plfam_id.proline_residue.mean
PLF_28228_00028208
hypothetical protein



feature.plfam_id.proline_residue.mean
PLF_28228_00028633
Mg/Co/Ni transporter MgtE, CBS domain-containing

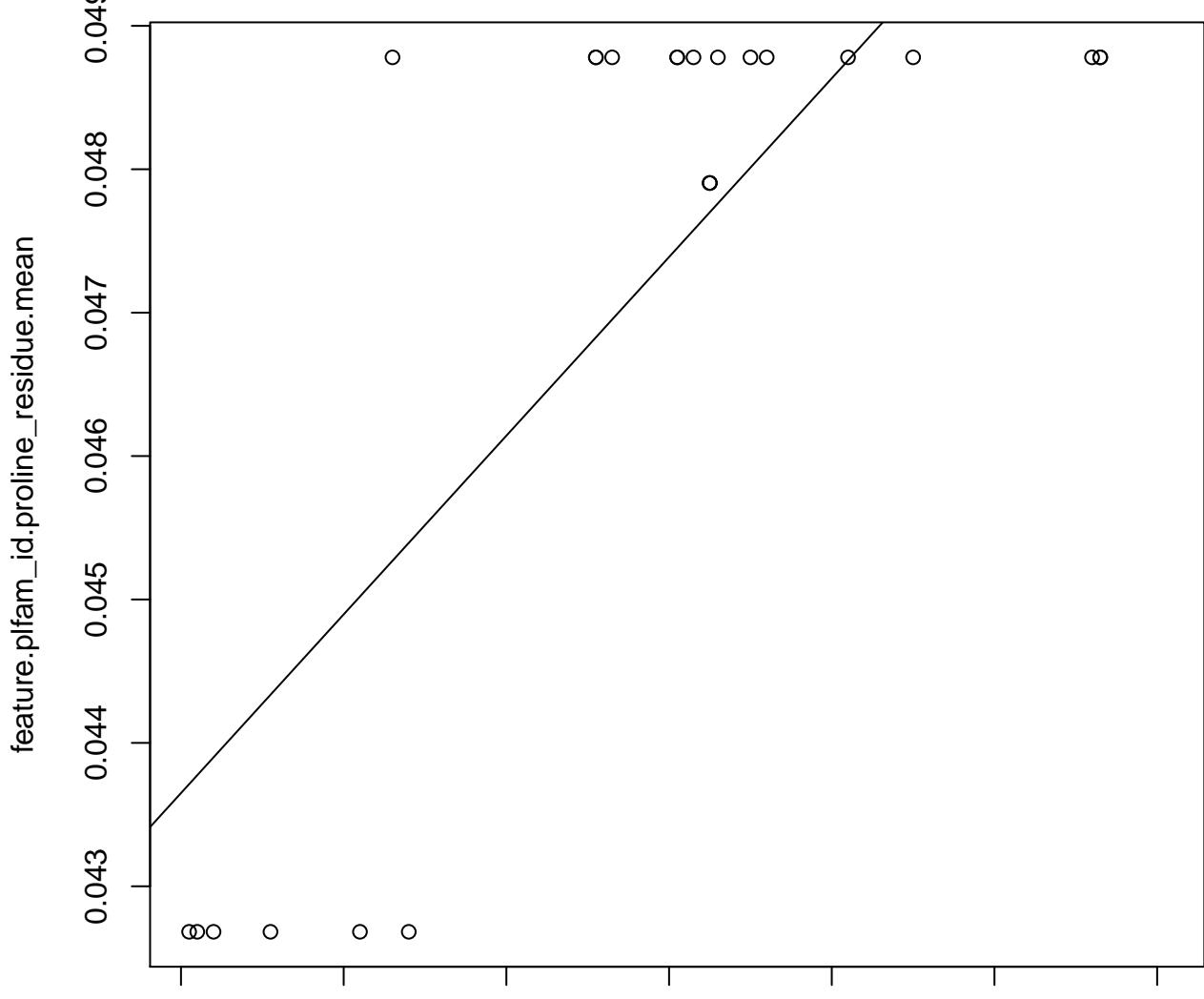


feature.plfam_id.proline_residue.mean
PLF_28228_00030467
Redoxin domain protein

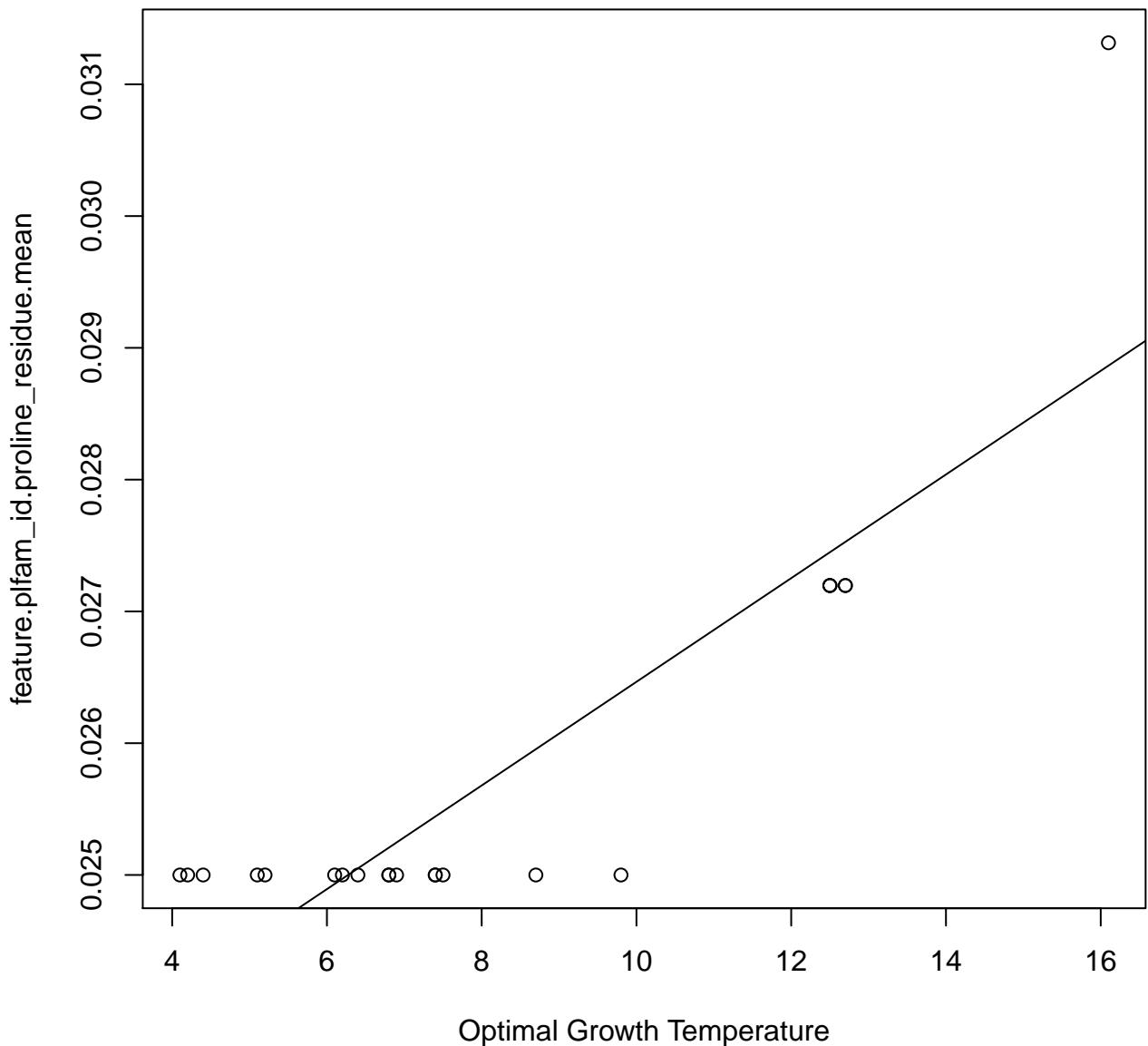
feature.plfam_id.proline_residue.mean

4 6 8 10 12 14 16

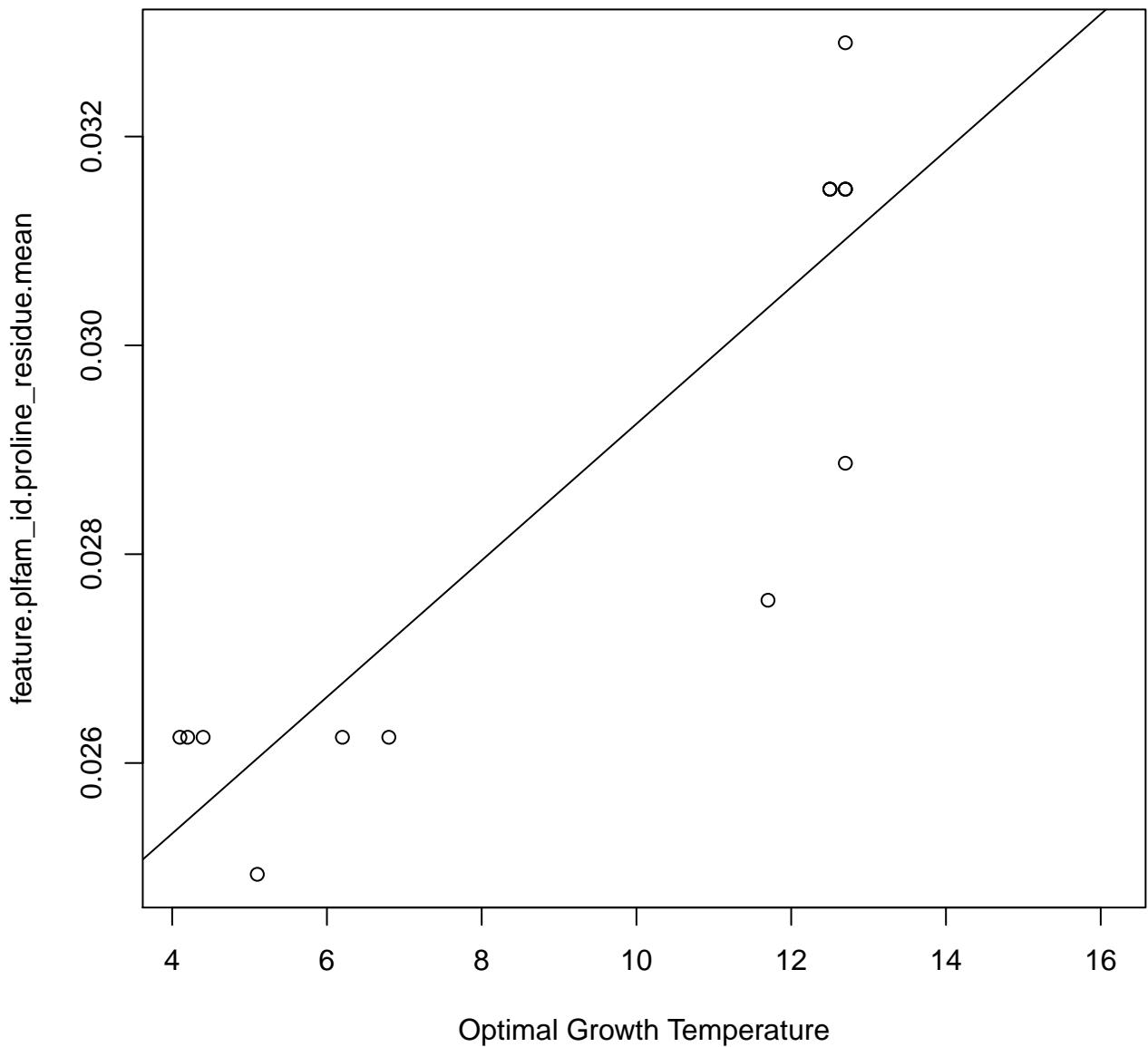
Optimal Growth Temperature



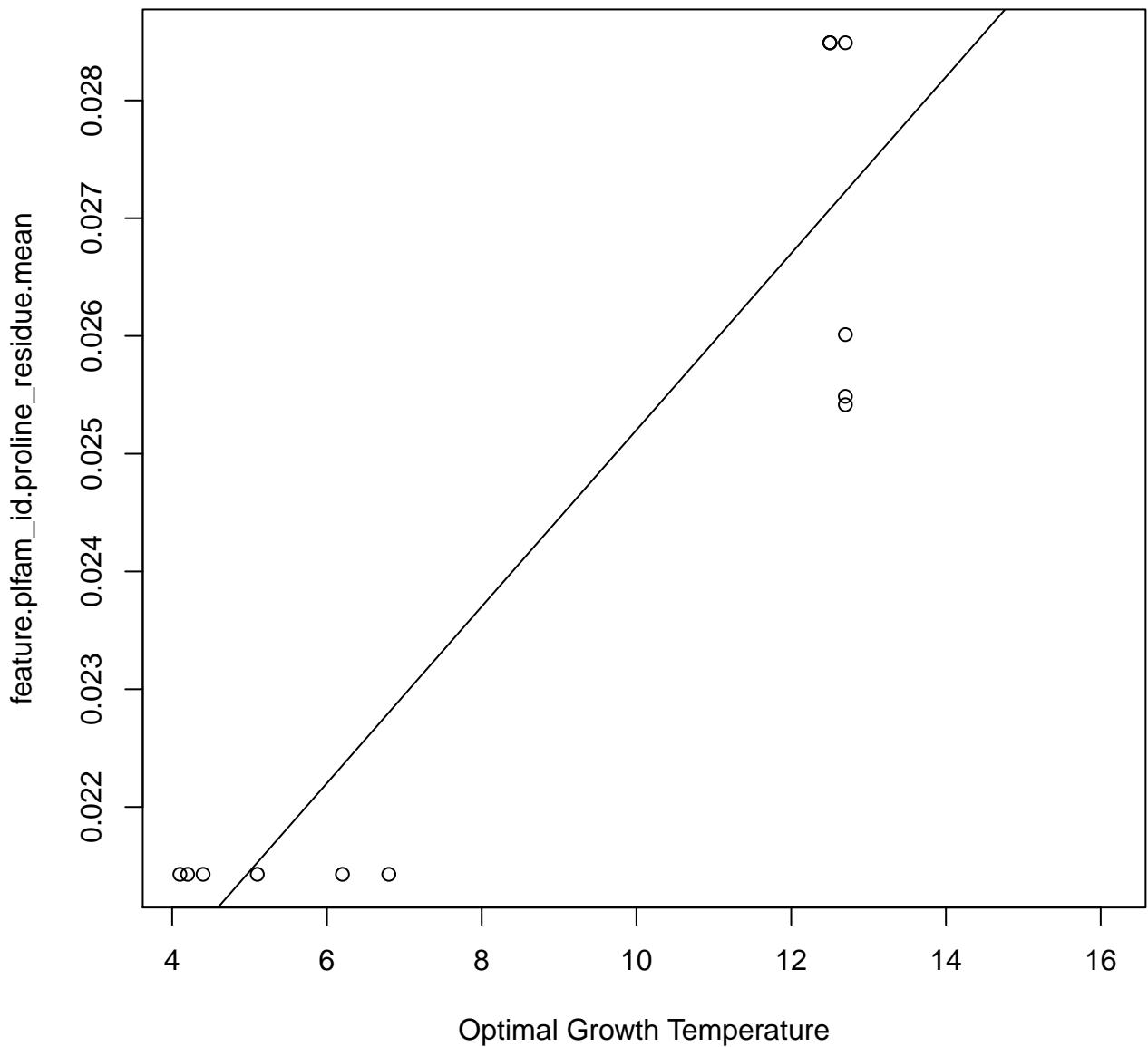
feature.plfam_id.proline_residue.mean
PLF_28228_00003471
Glucose/mannose:H⁺ symporter GlcP



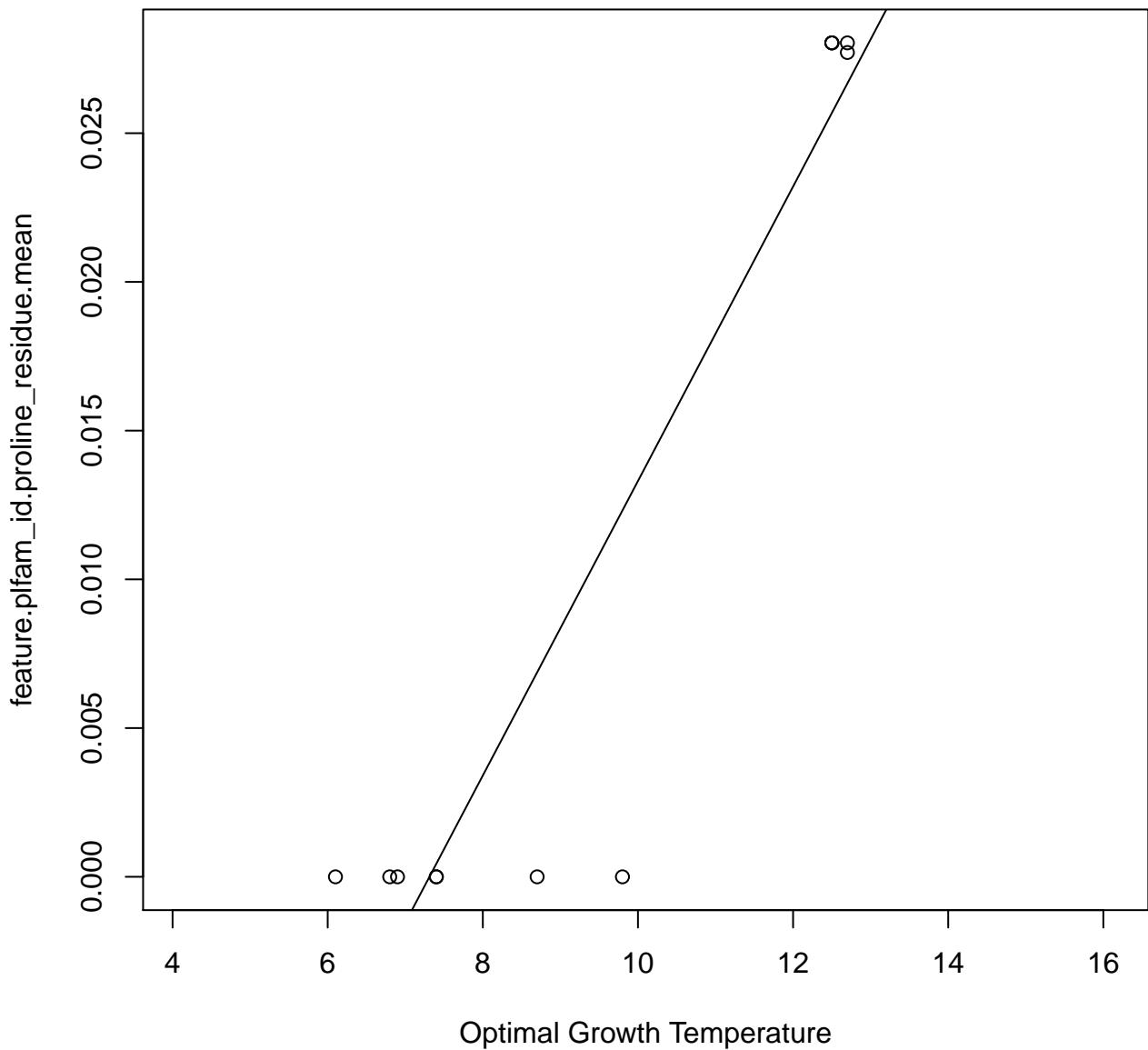
feature.plfam_id.proline_residue.mean
PLF_28228_00002110
TonB-dependent receptor



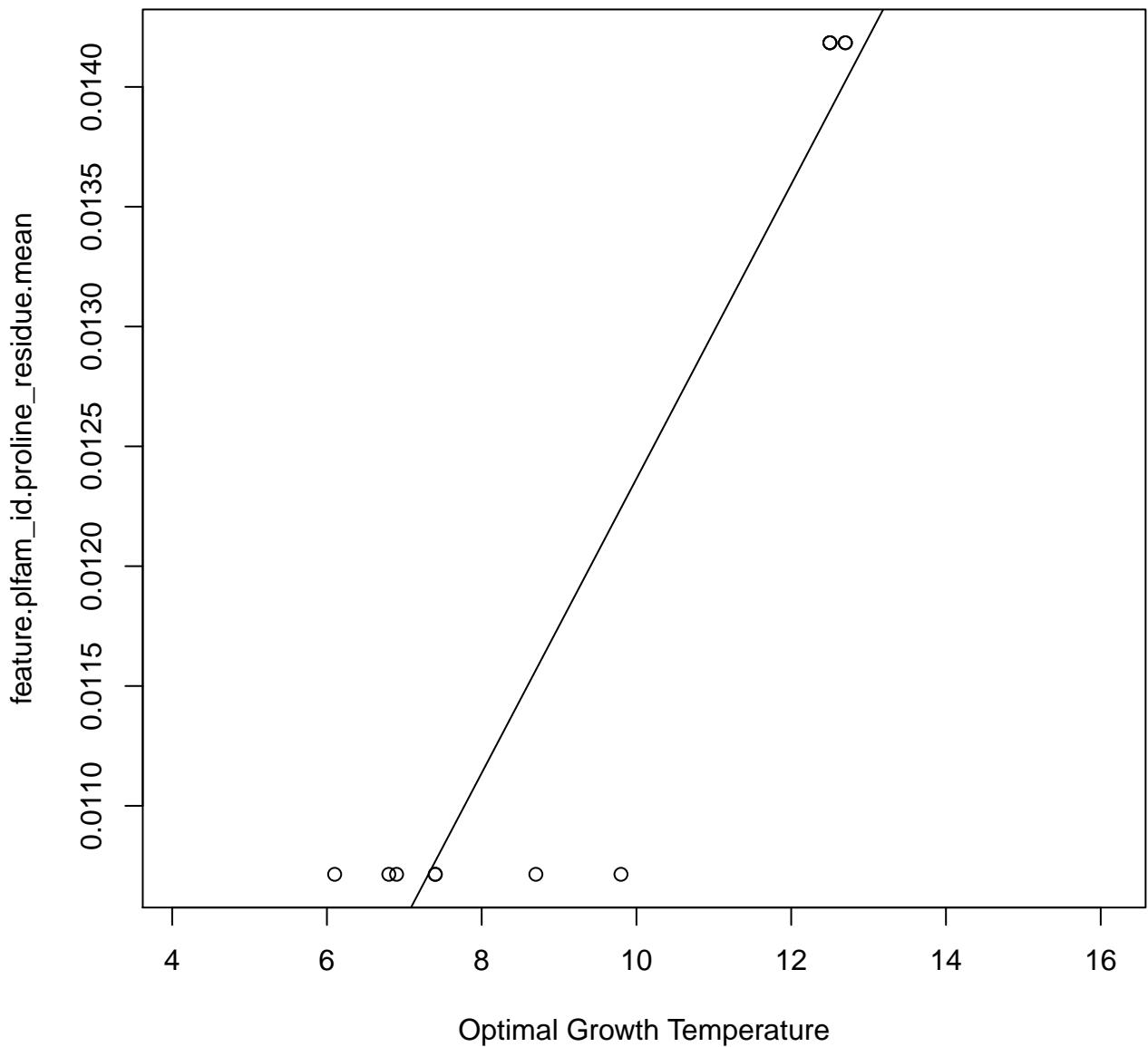
feature.plfam_id.proline_residue.mean
PLF_28228_00003700
TonB-dependent receptor



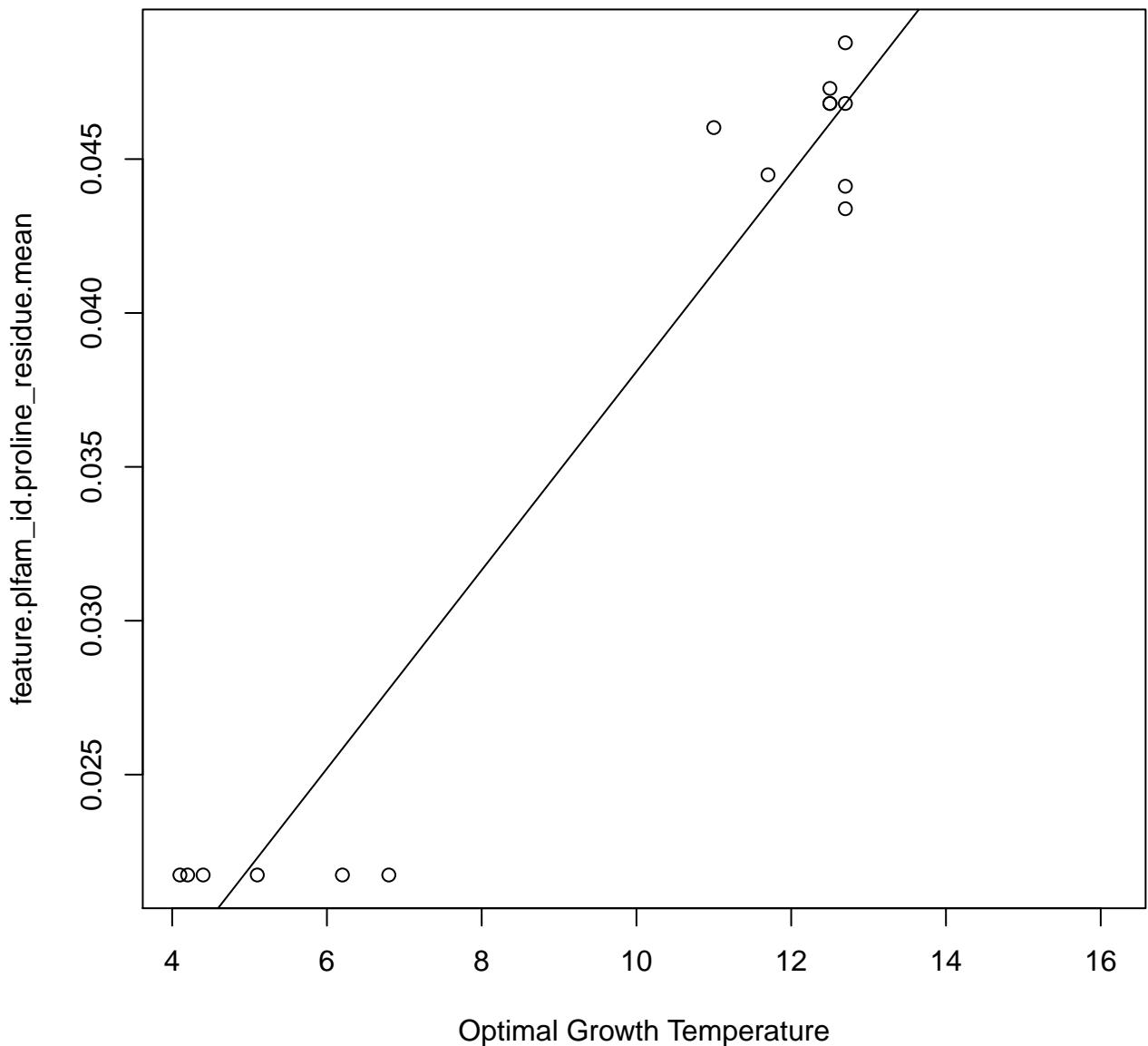
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PLF_28228_00007748
EAL domain protein



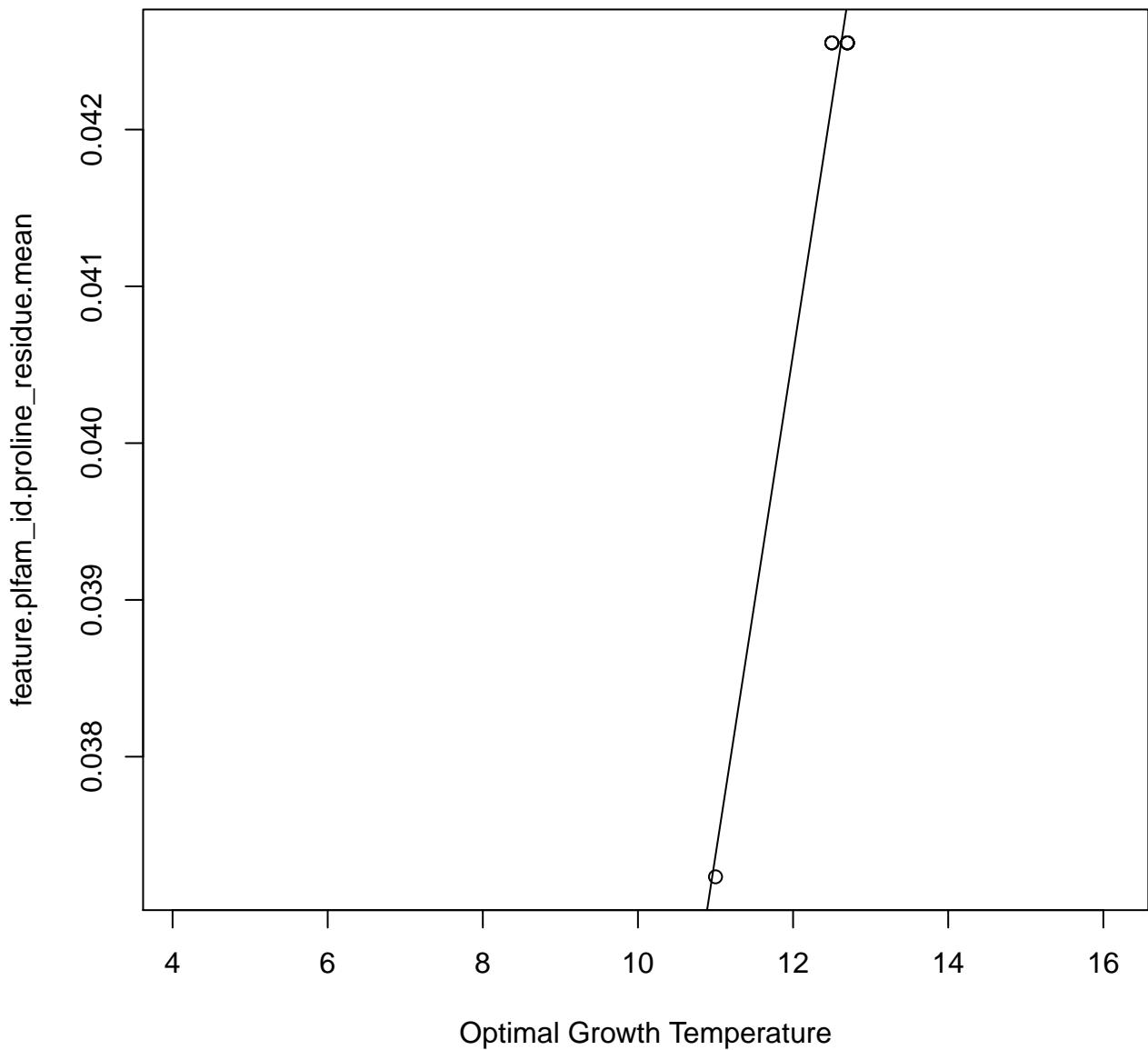
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PLF_28228_00007747
Membrane-associated methyl-accepting chemotaxis protein with HAMP domain



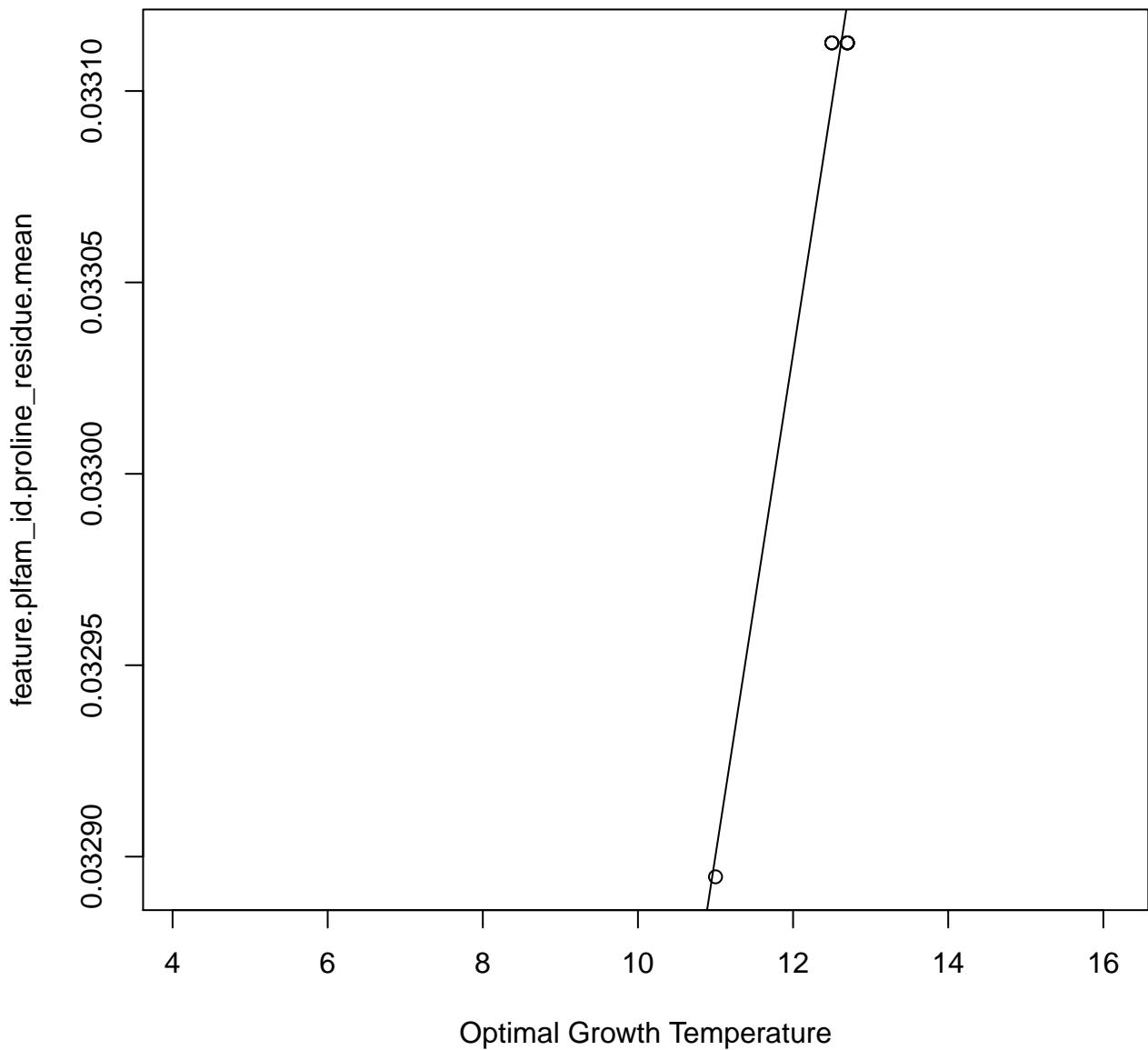
feature.plfam_id.proline_residue.mean
PLF_28228_00003180
Cobyricin acid a,c-diamide synthetase (EC 6.3.5.11)



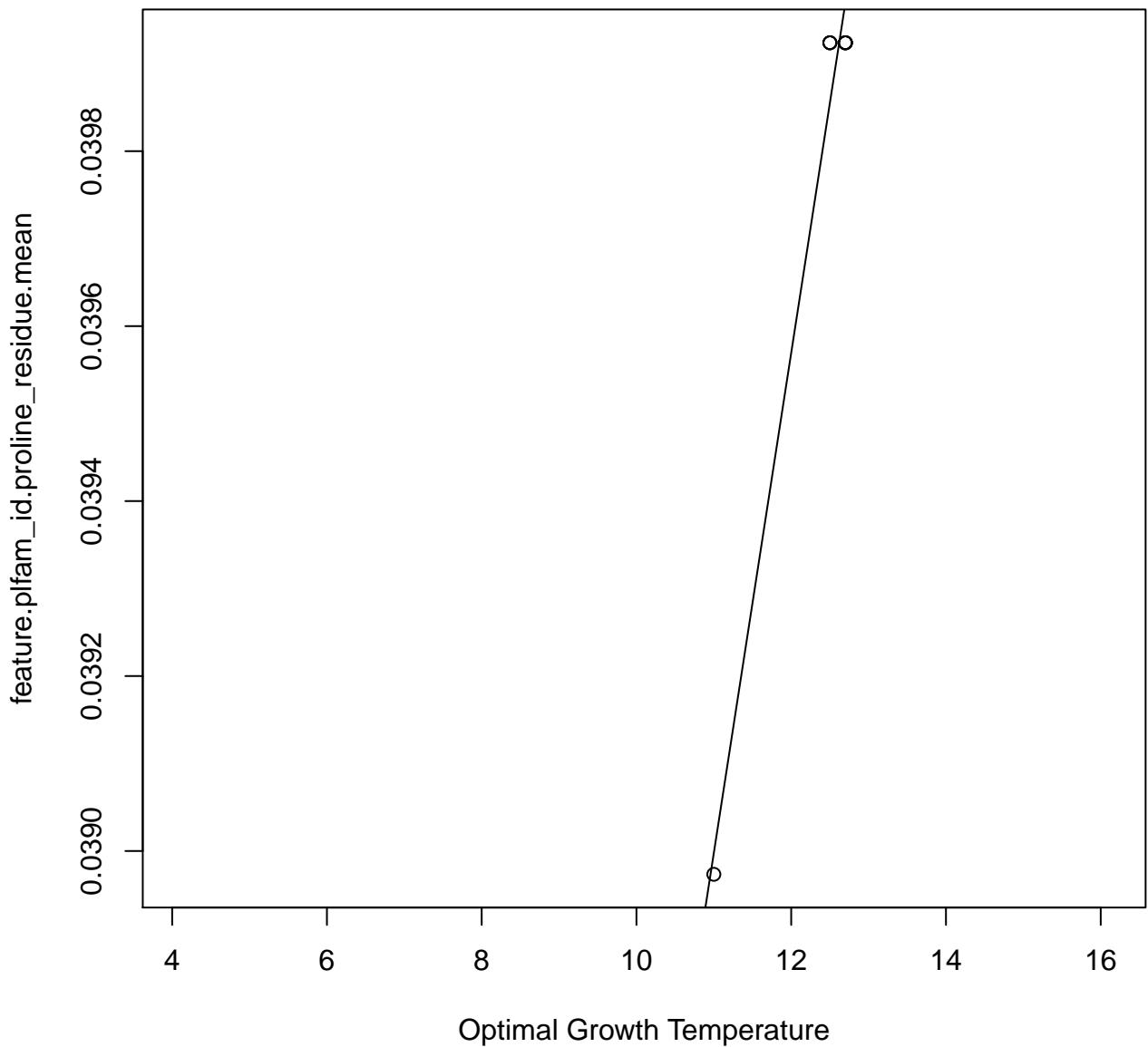
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PLF_28228_00003688
Tellurite methyltransferase (EC 2.1.1.265)



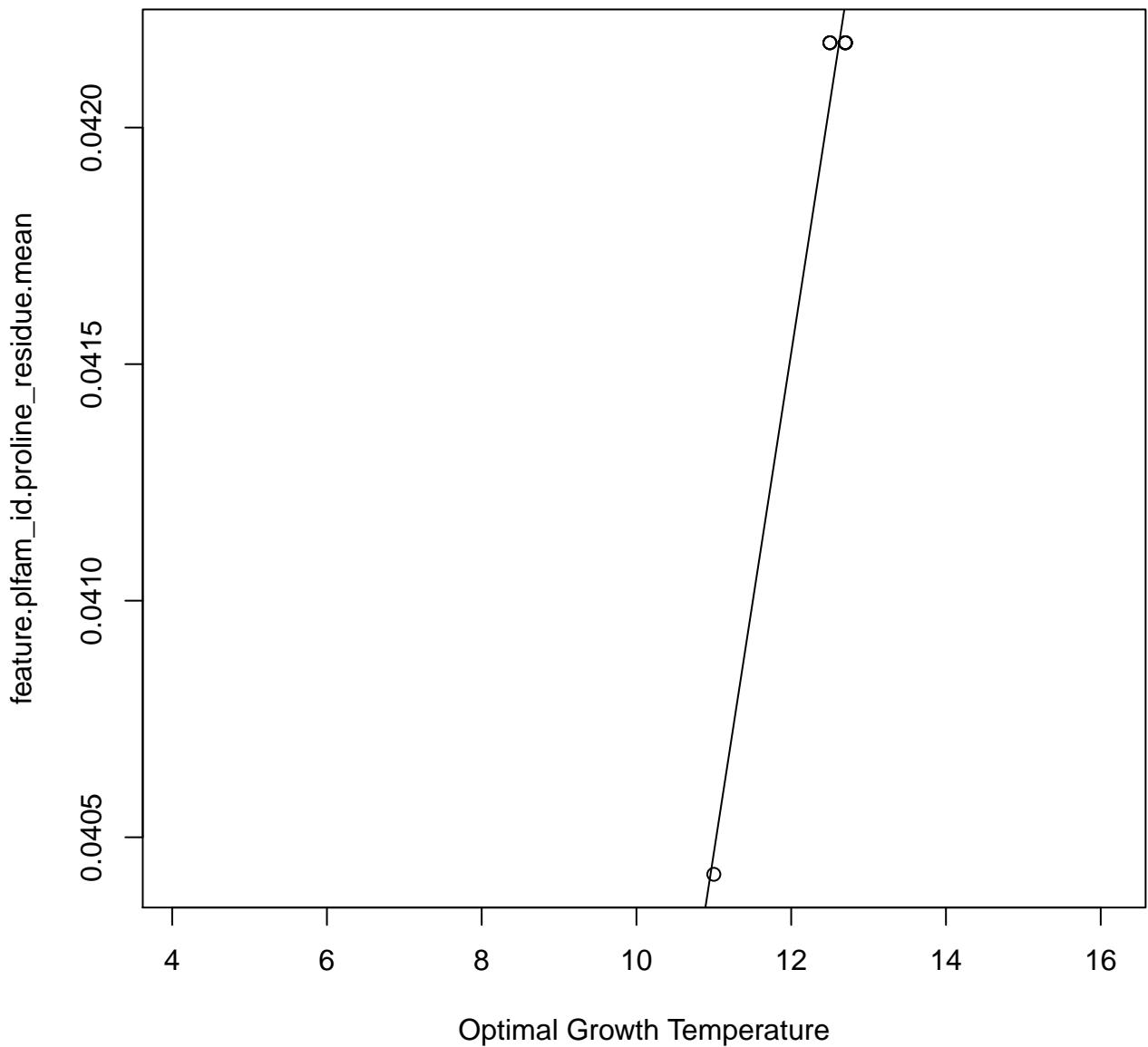
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PLF_28228_00003980
hypothetical protein



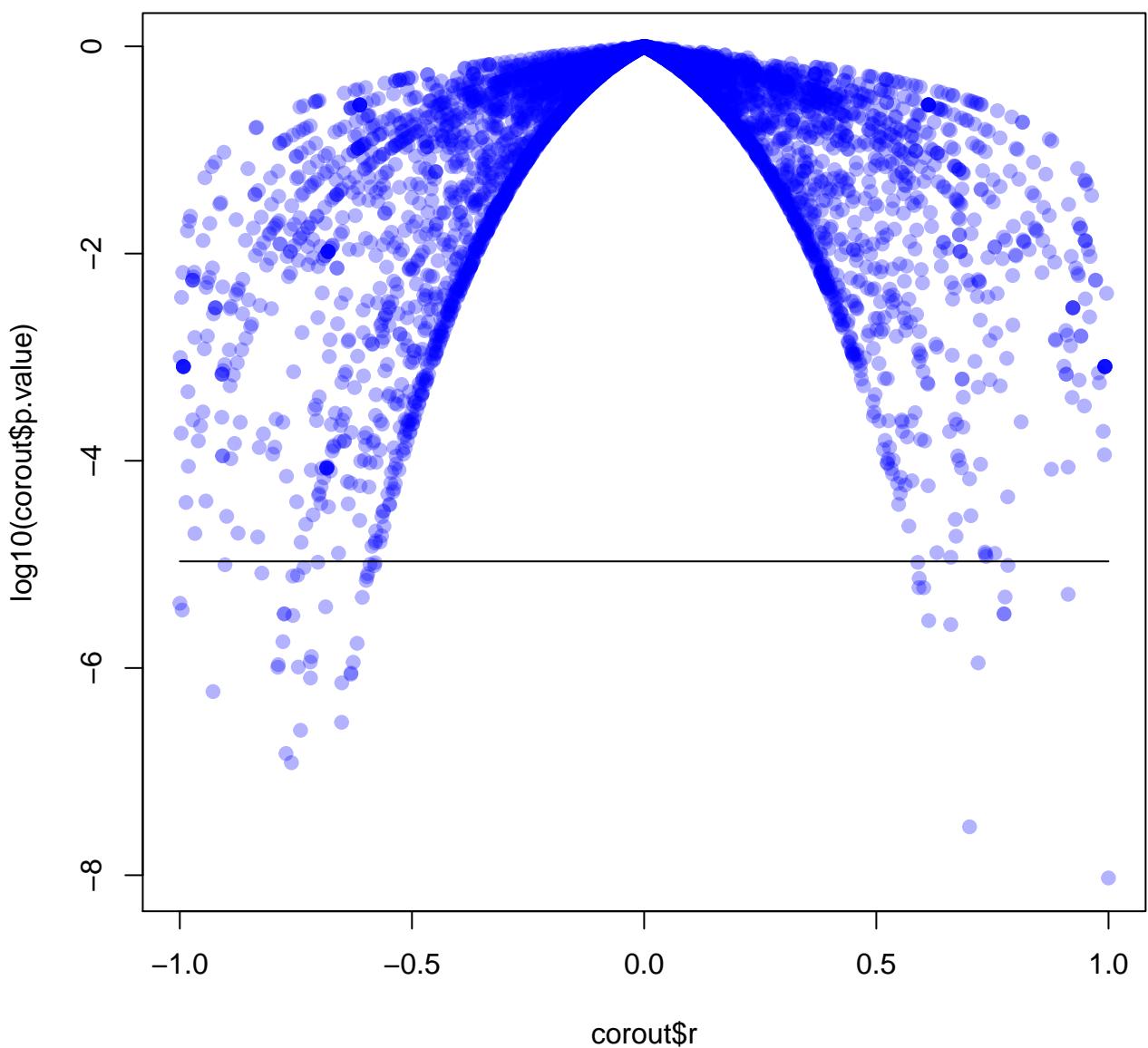
feature.plfam_id.proline_residue.mean
PLF_28228_00014485
RND efflux system, inner membrane transporter



feature.plfam_id.proline_residue.mean
PLF_28228_00018479
hypothetical protein



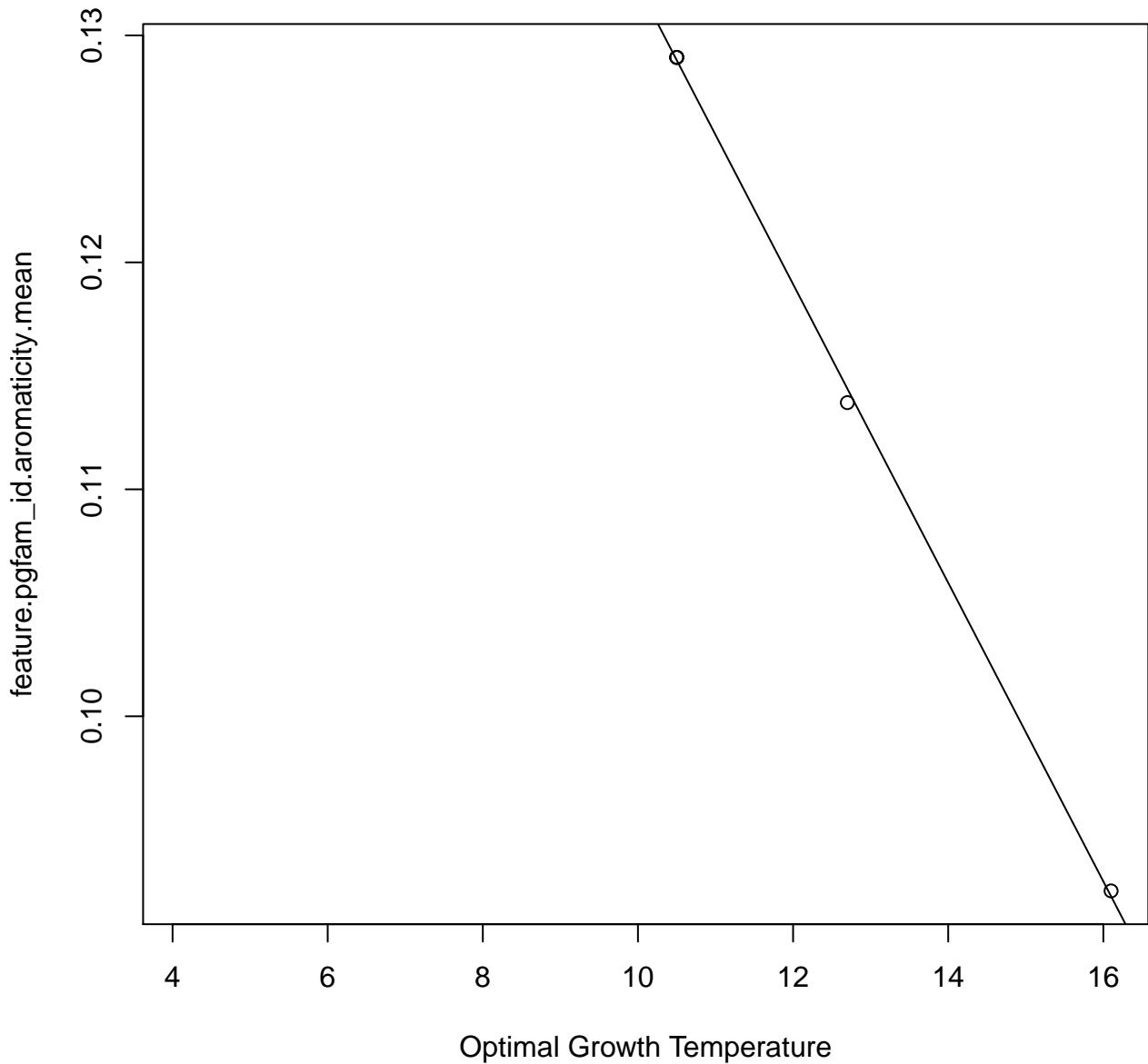
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feature.pgfam_id.aromaticity.mean

PGF_04001813

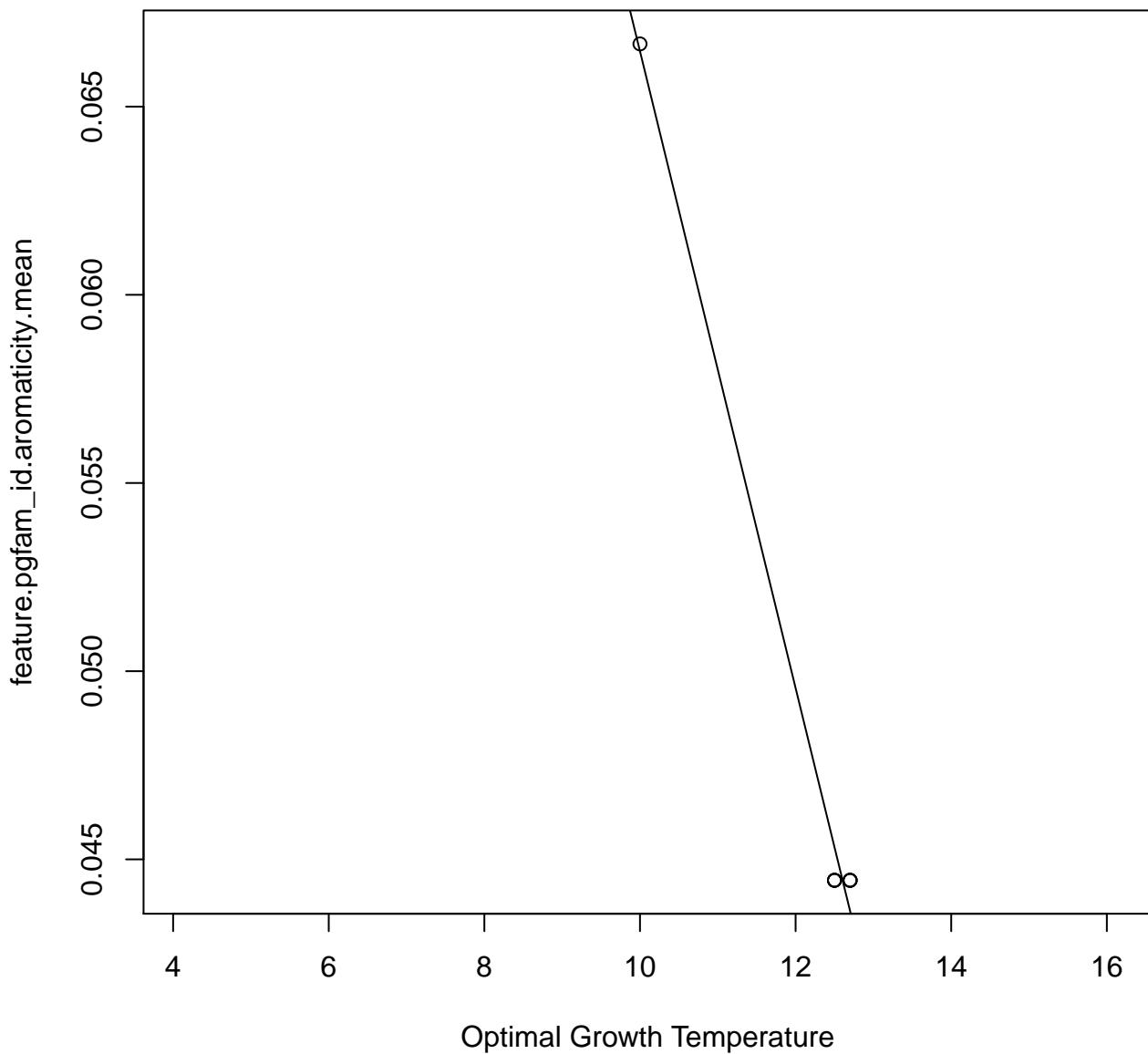
hypothetical protein



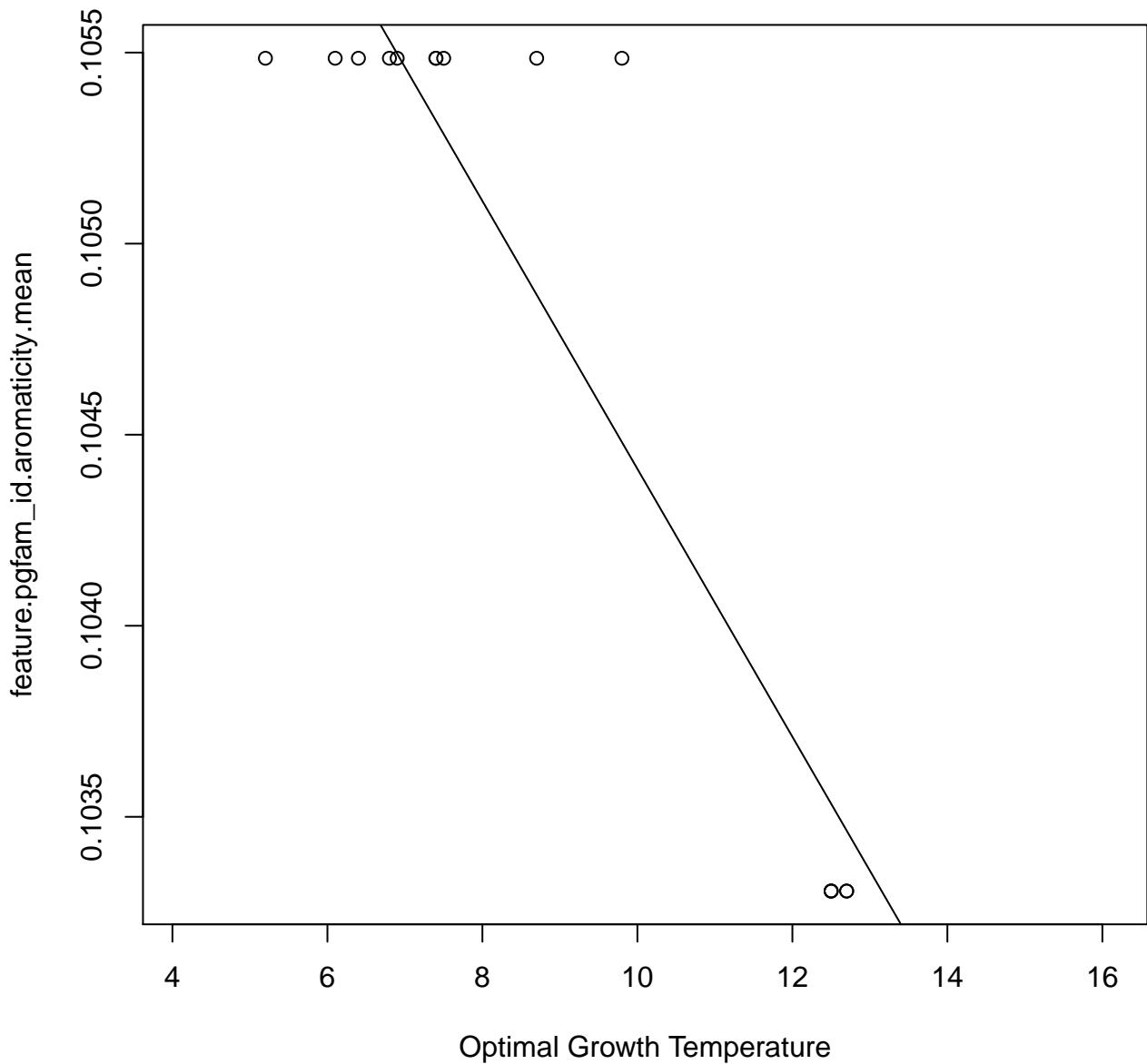
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PGF_01337096

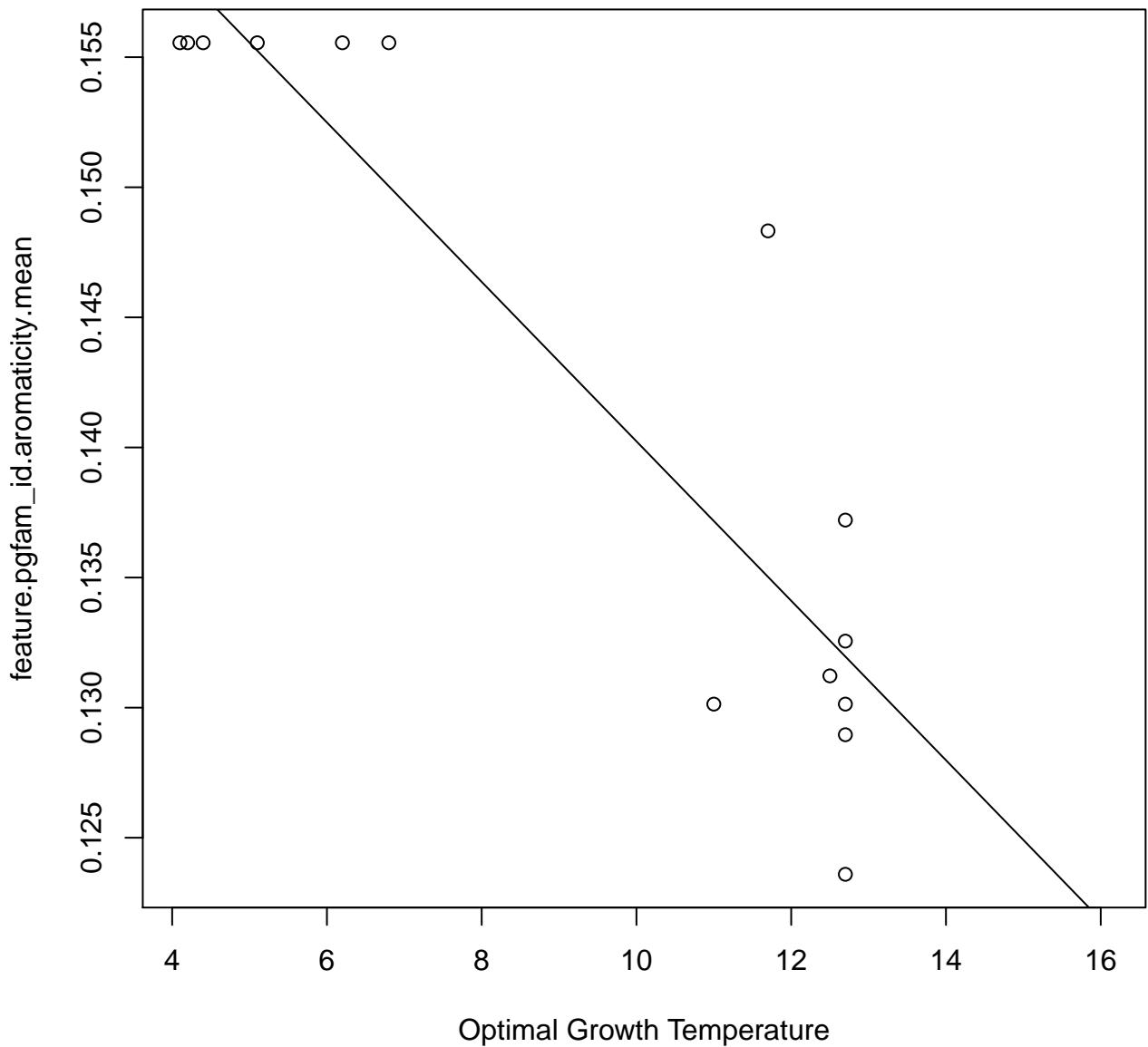
hypothetical protein



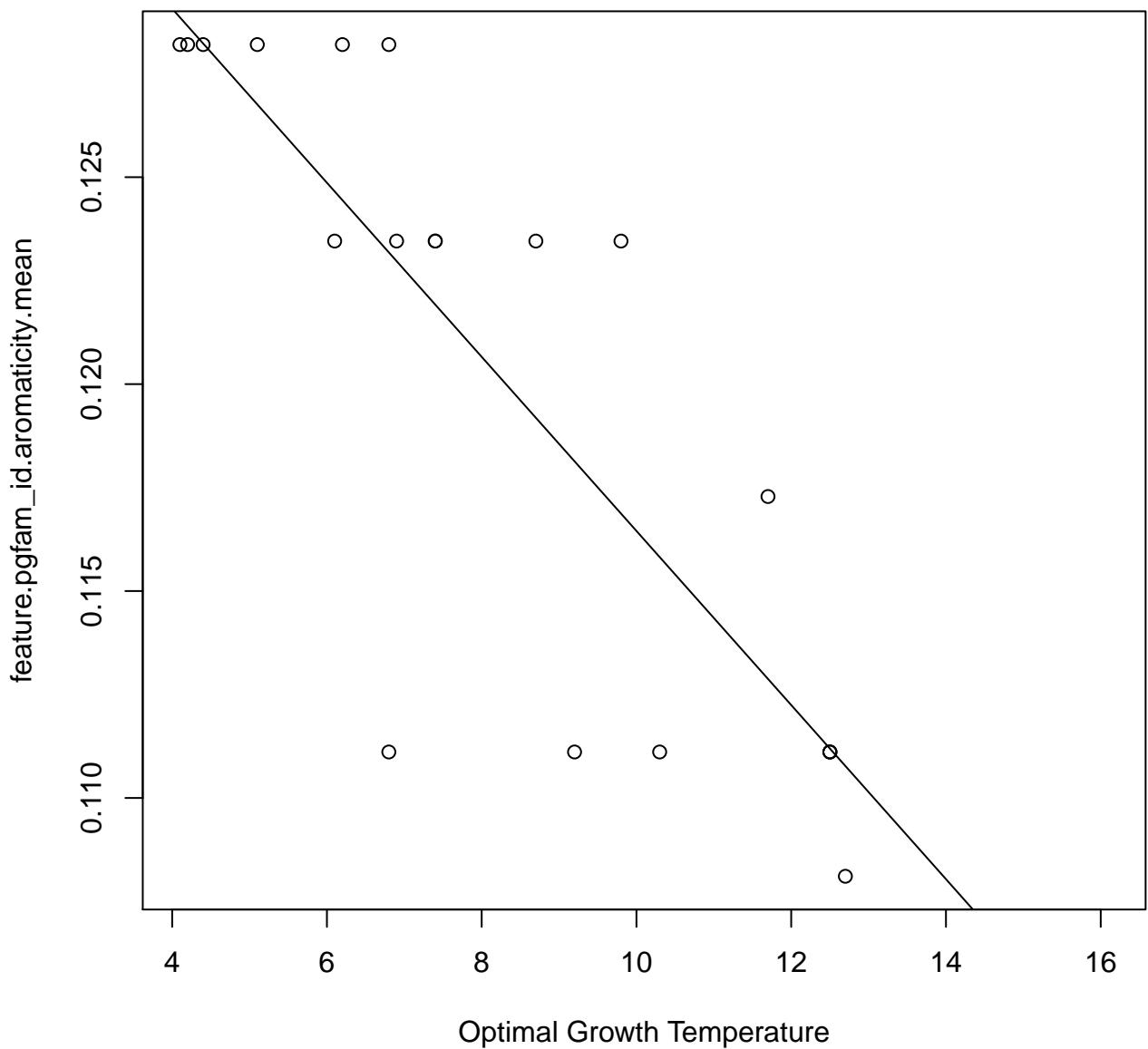
feature.pgfam_id.aromaticity.mean
PGF_06830555
SapC-like S-layer protein



feature.pgfam_id.aromaticity.mean
PGF_12884992
Uncharacterized MFS-type transporter



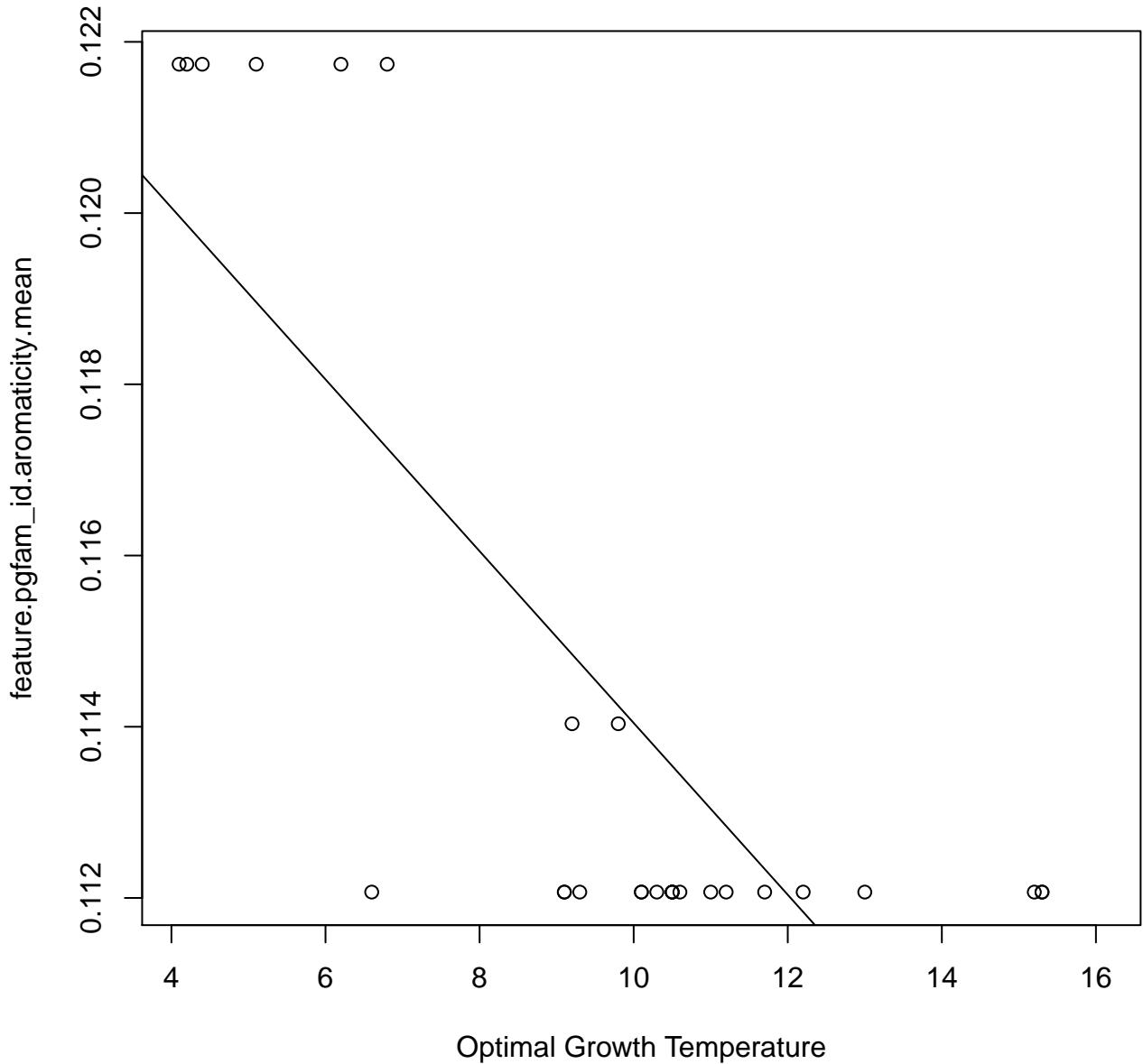
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PGF_00257343
hypothetical protein



feature.pgfam_id.aromaticity.mean

PGF_07361149

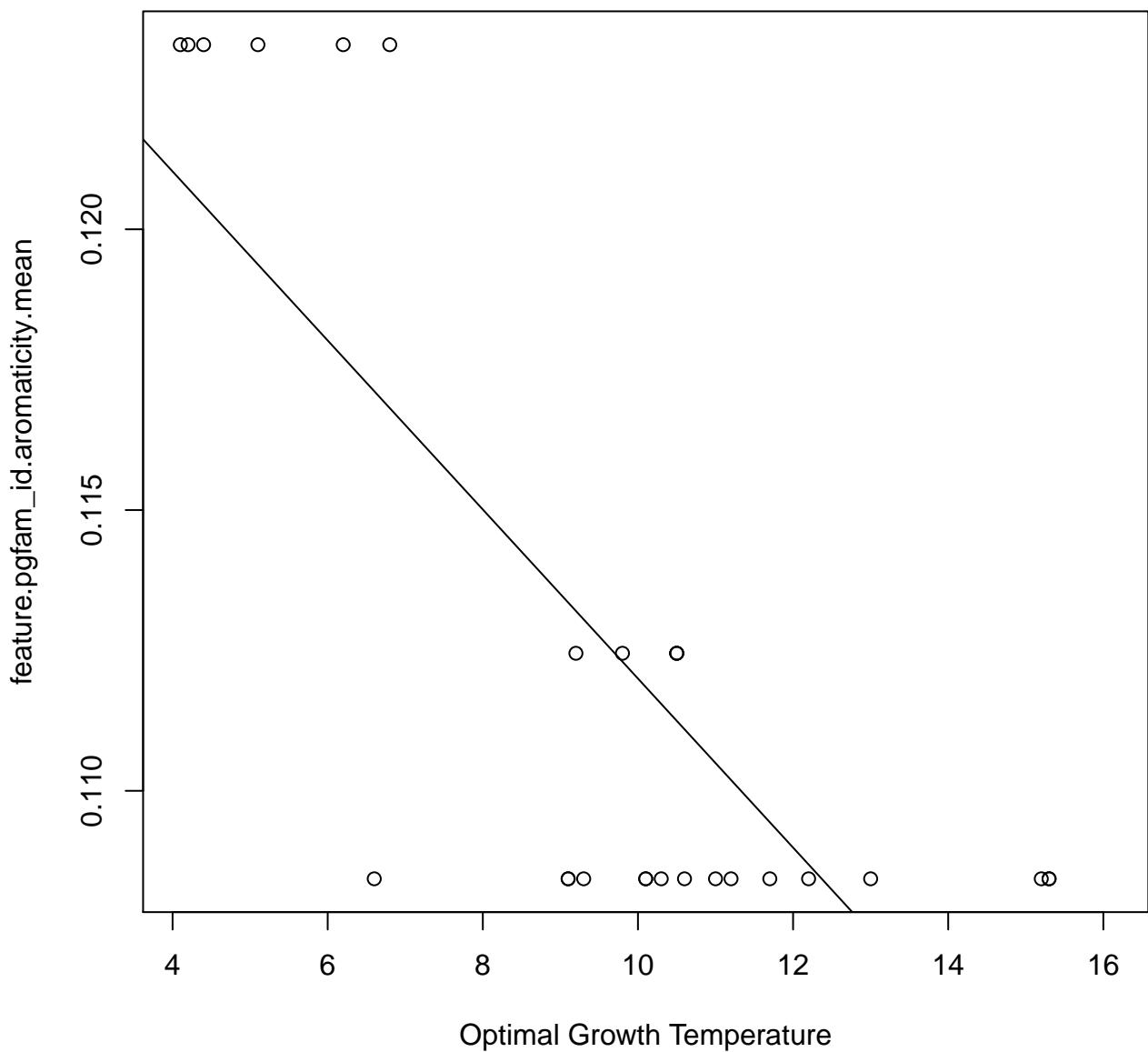
hypothetical protein



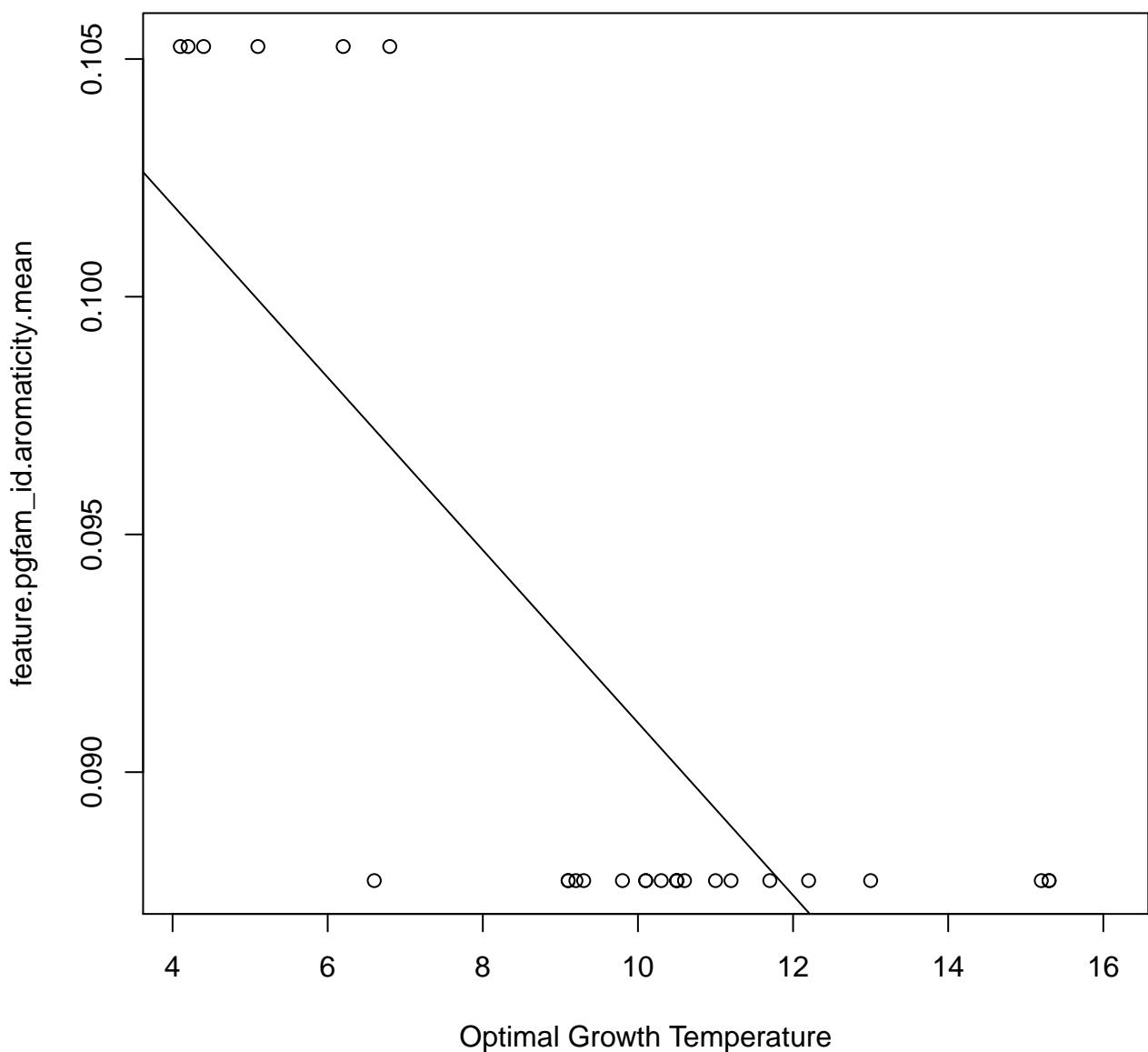
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PGF_11018774

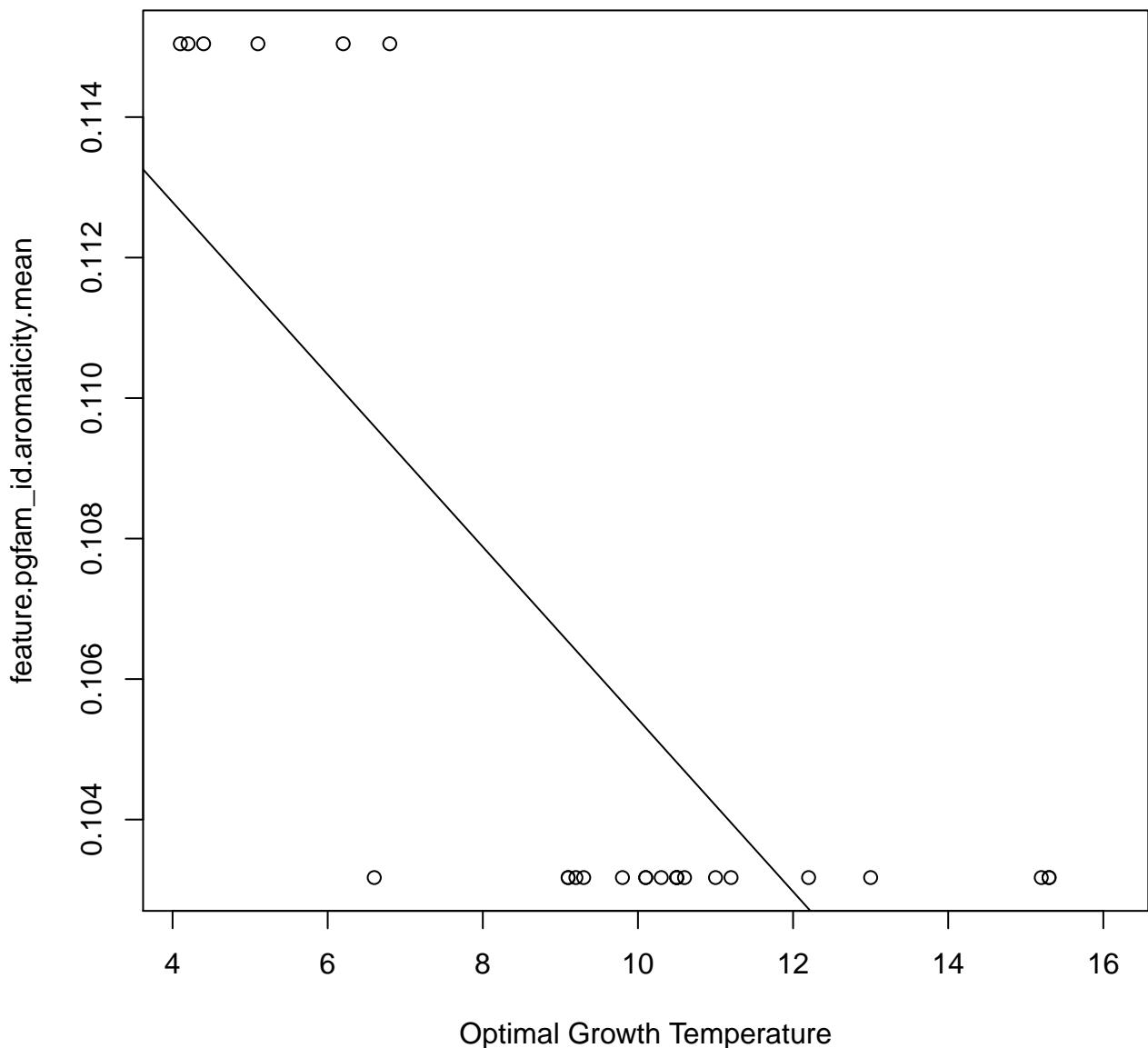
hypothetical protein



feature.pgfam_id.aromaticity.mean
PGF_08289417
hypothetical protein



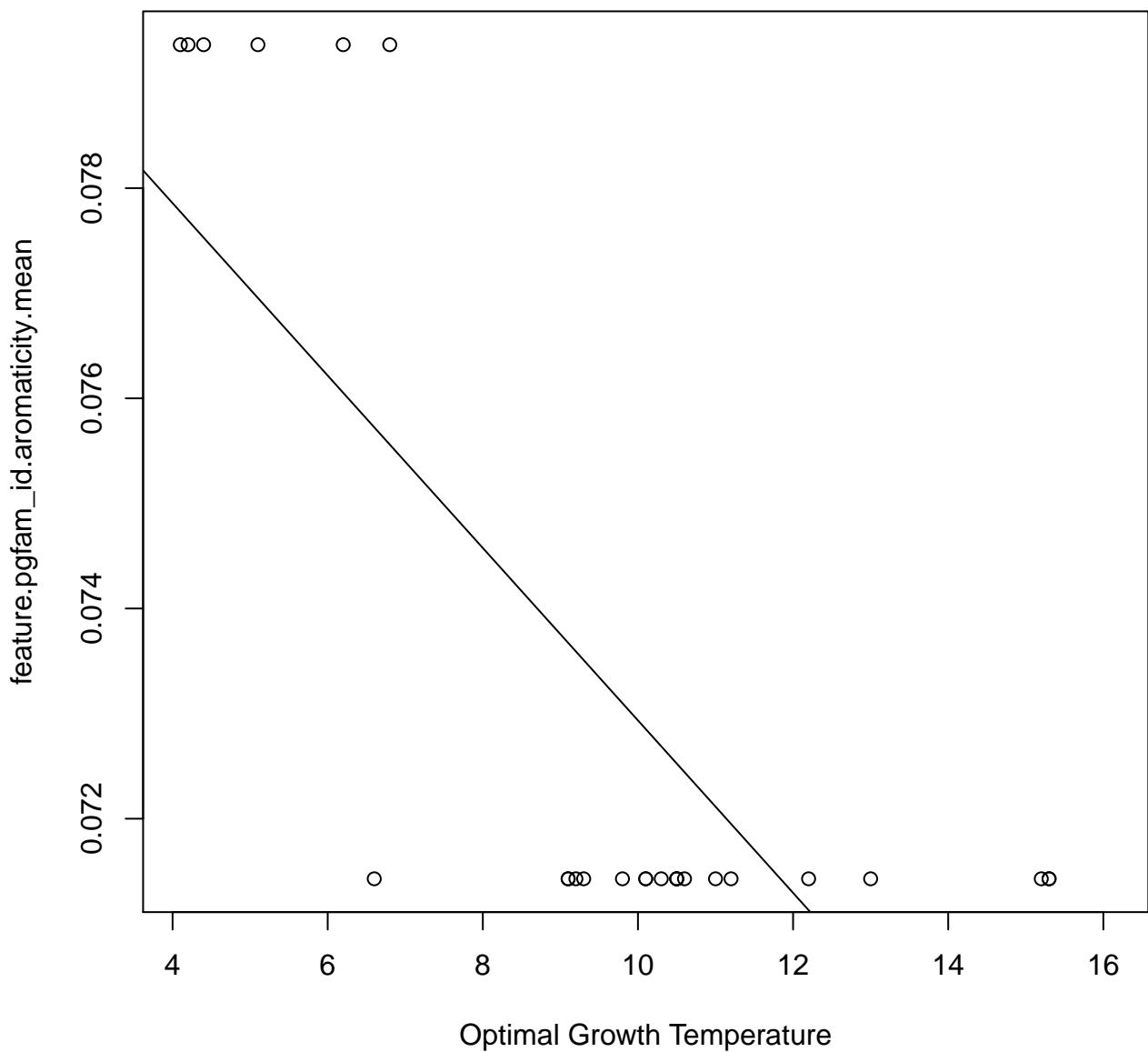
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PGF_12049070
hypothetical protein



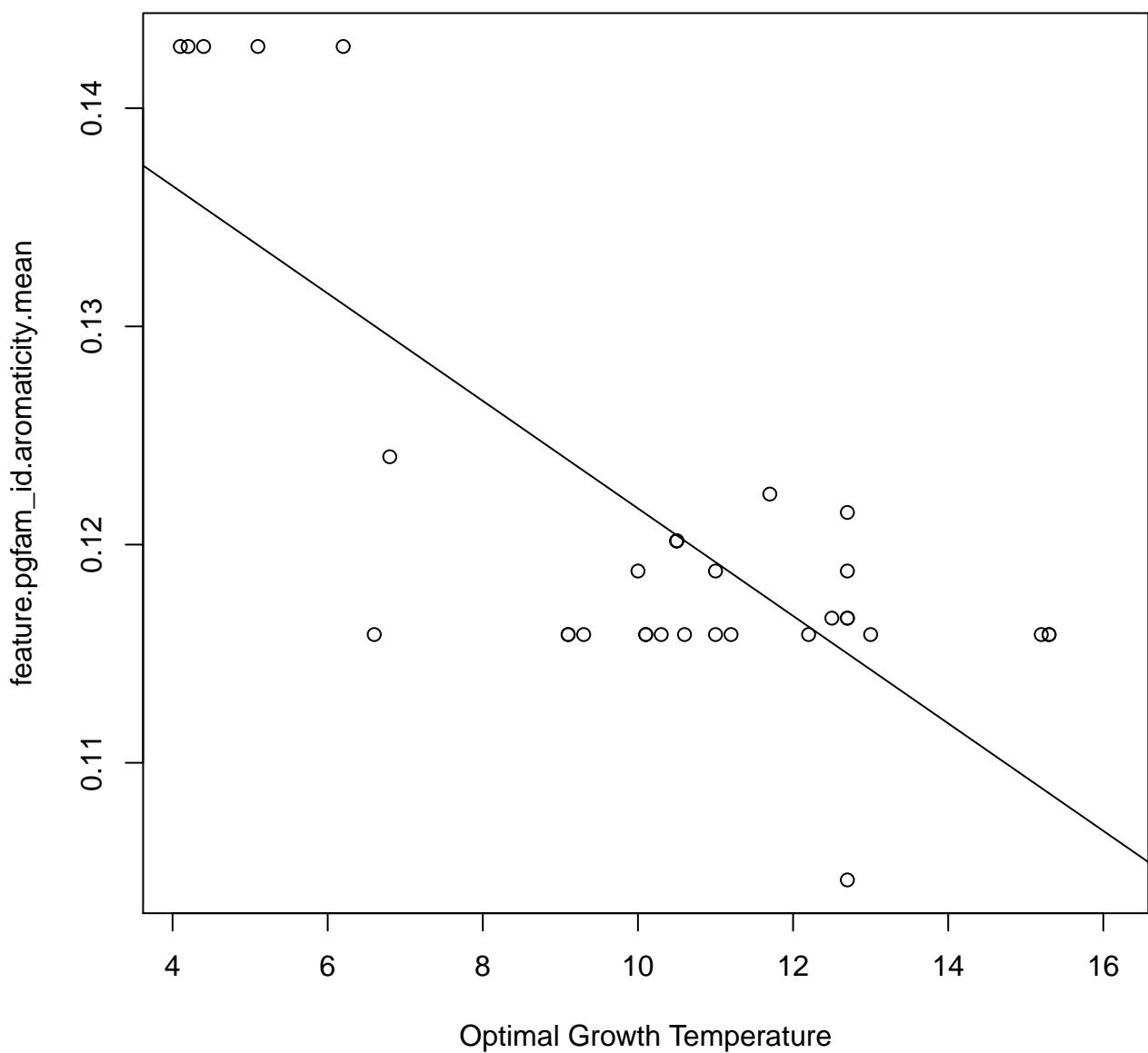
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PGF_12288710

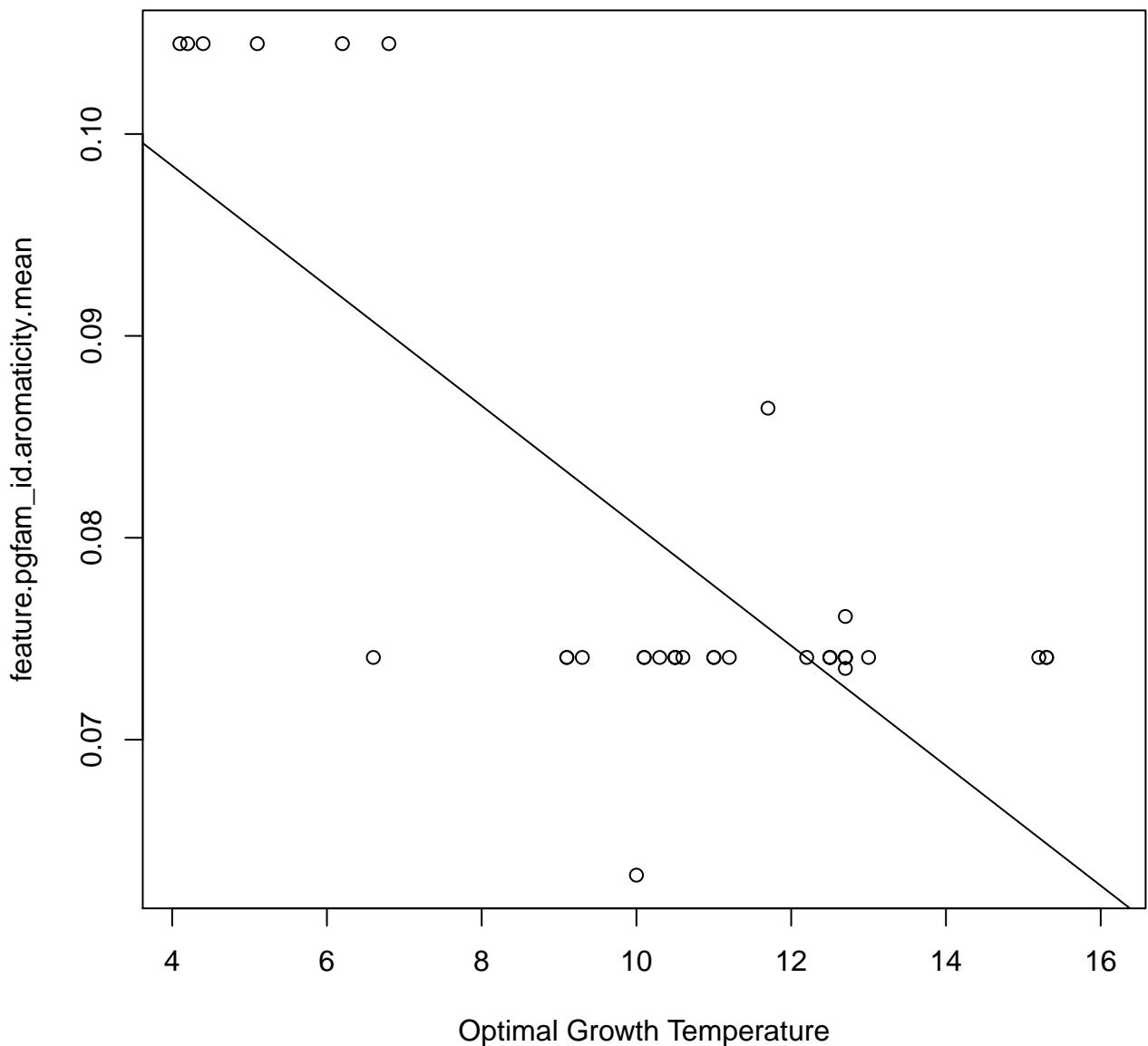
hypothetical protein



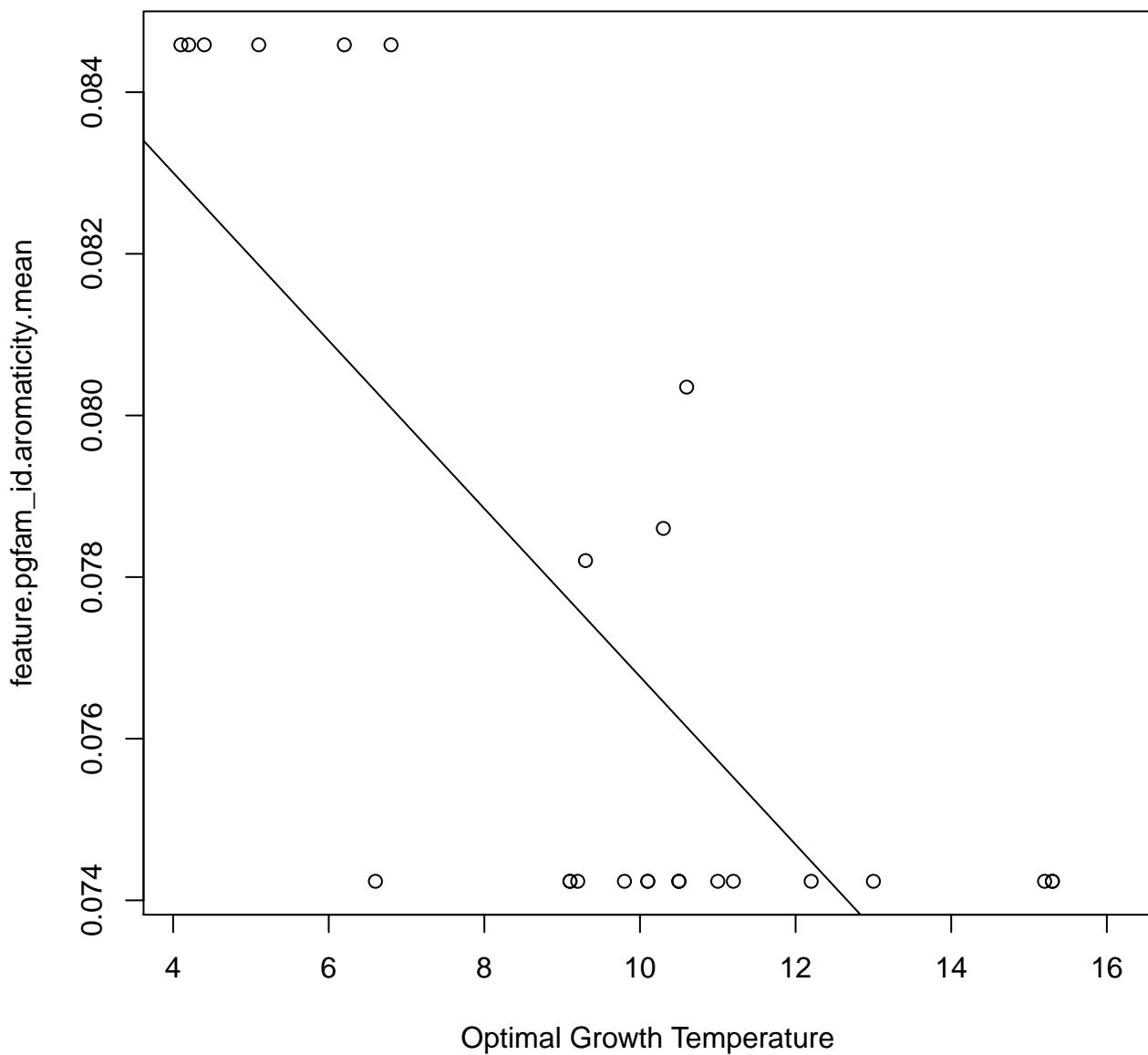
feature.pgfam_id.aromaticity.mean
PGF_02105064
Uncharacterized protease YegQ



feature.pgfam_id.aromaticity.mean
PGF_00064685
Uncharacterized ferredoxin-like protein YfhL



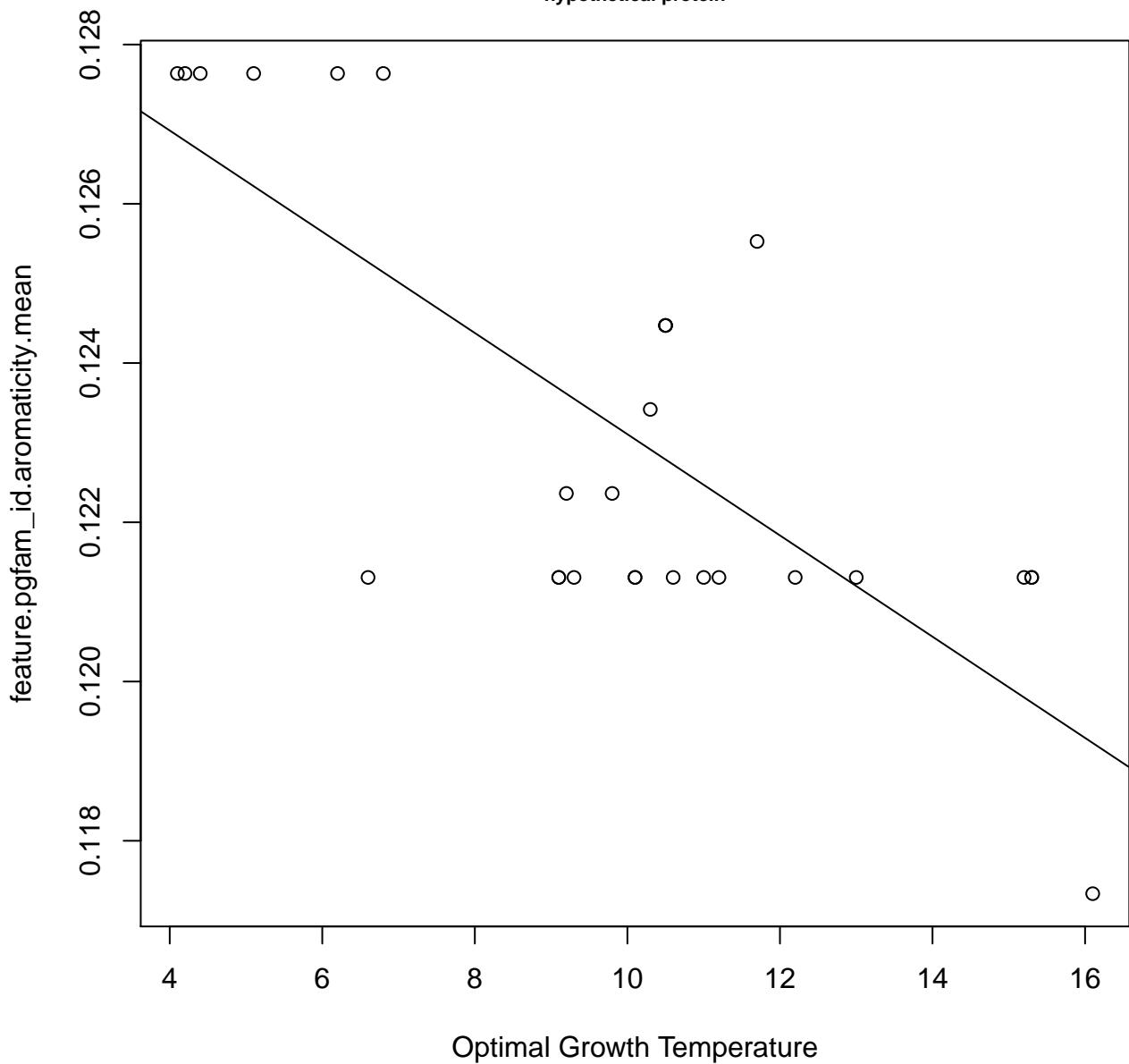
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PGF_07132870
hypothetical protein



feature.pgfam_id.aromaticity.mean

PGF_04802662

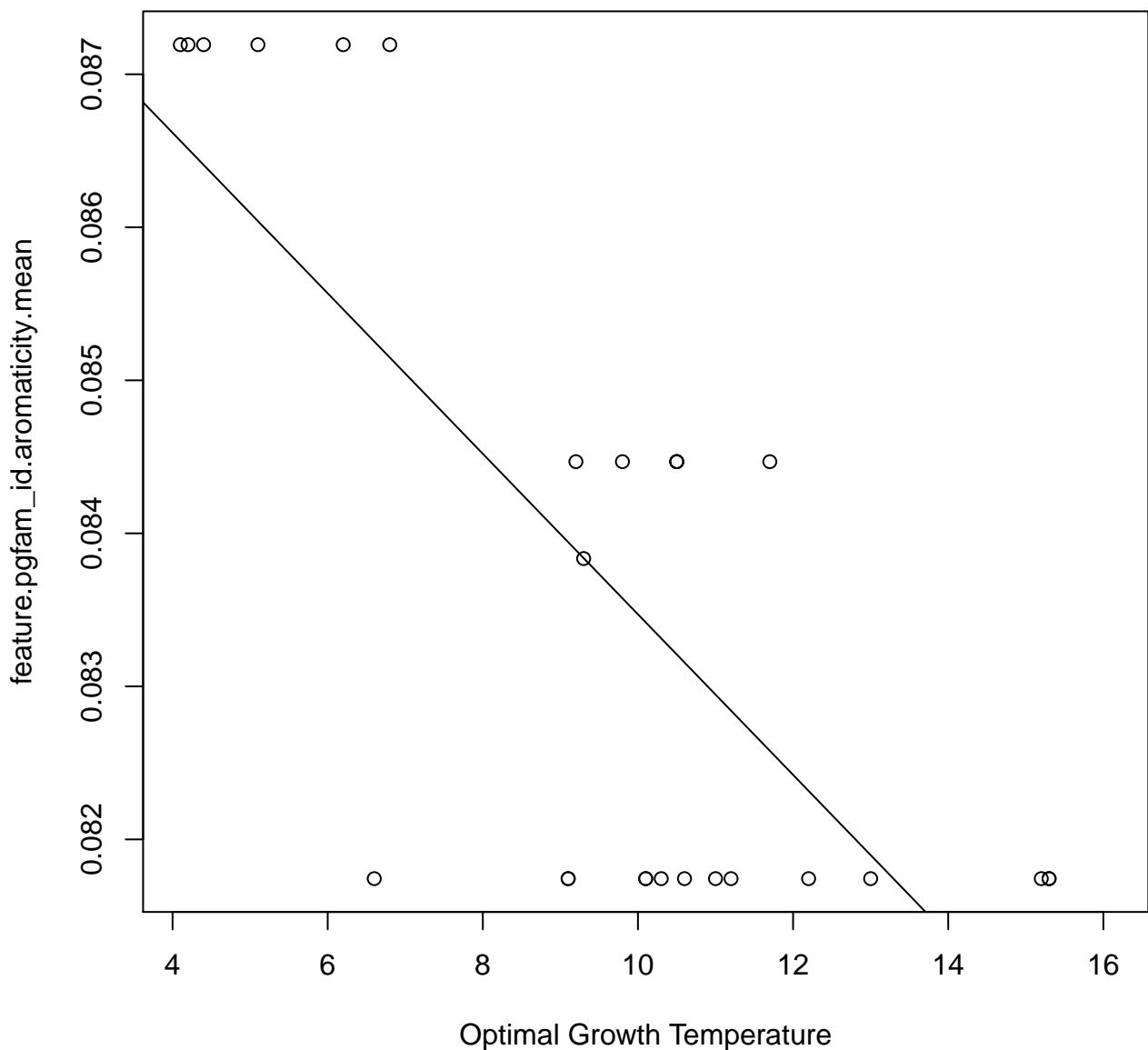
hypothetical protein



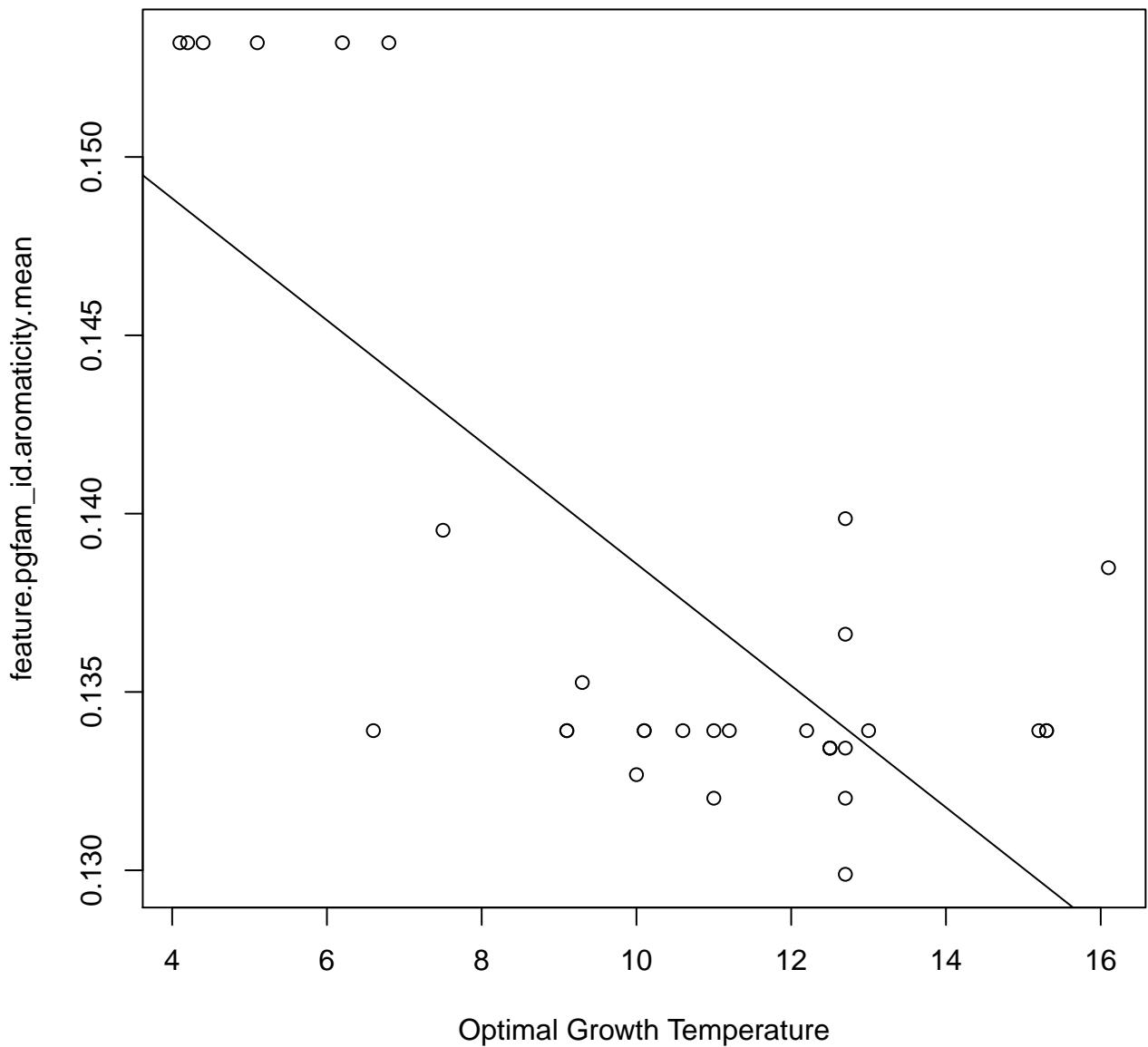
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PGF_09674332

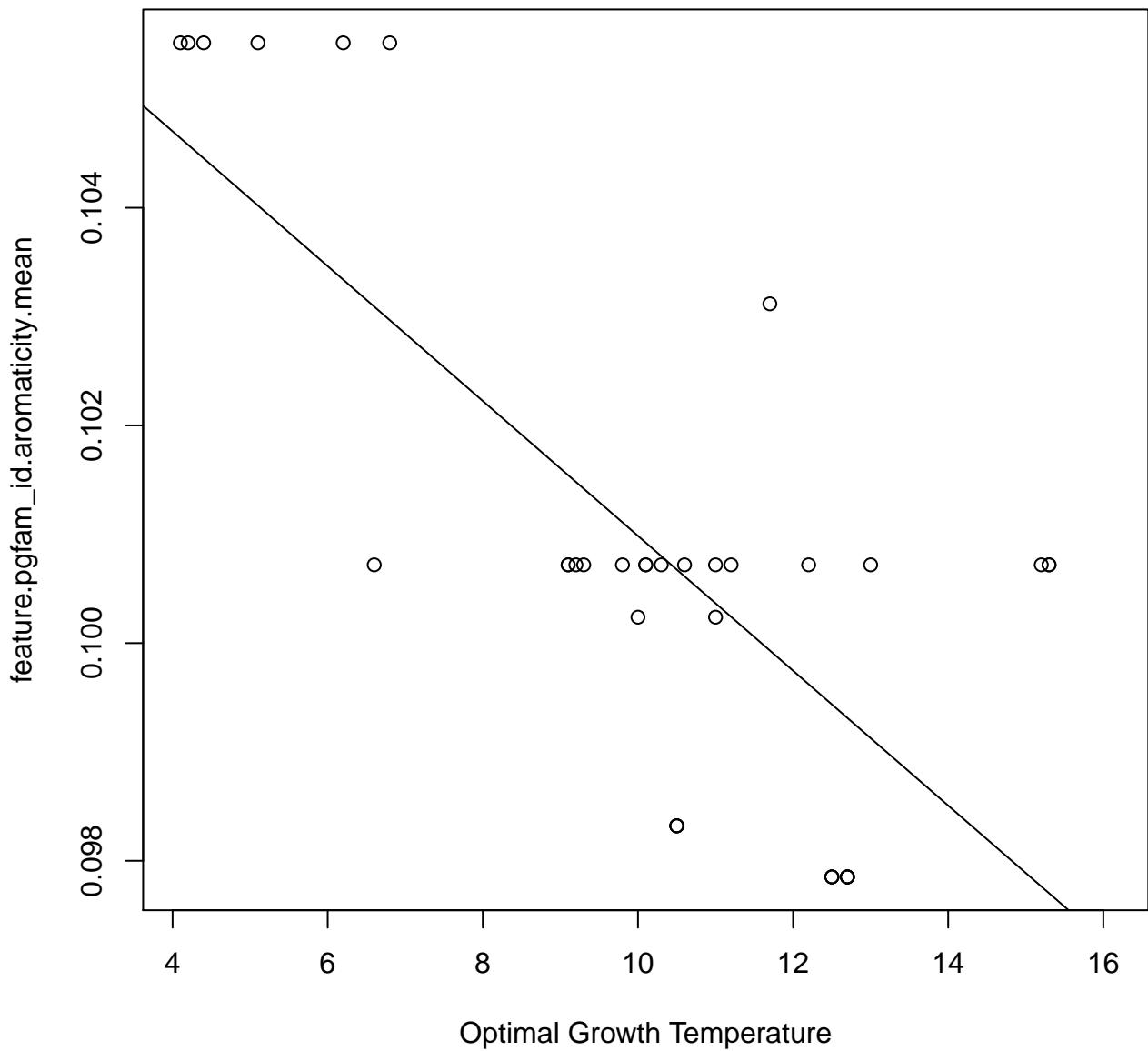
hypothetical protein



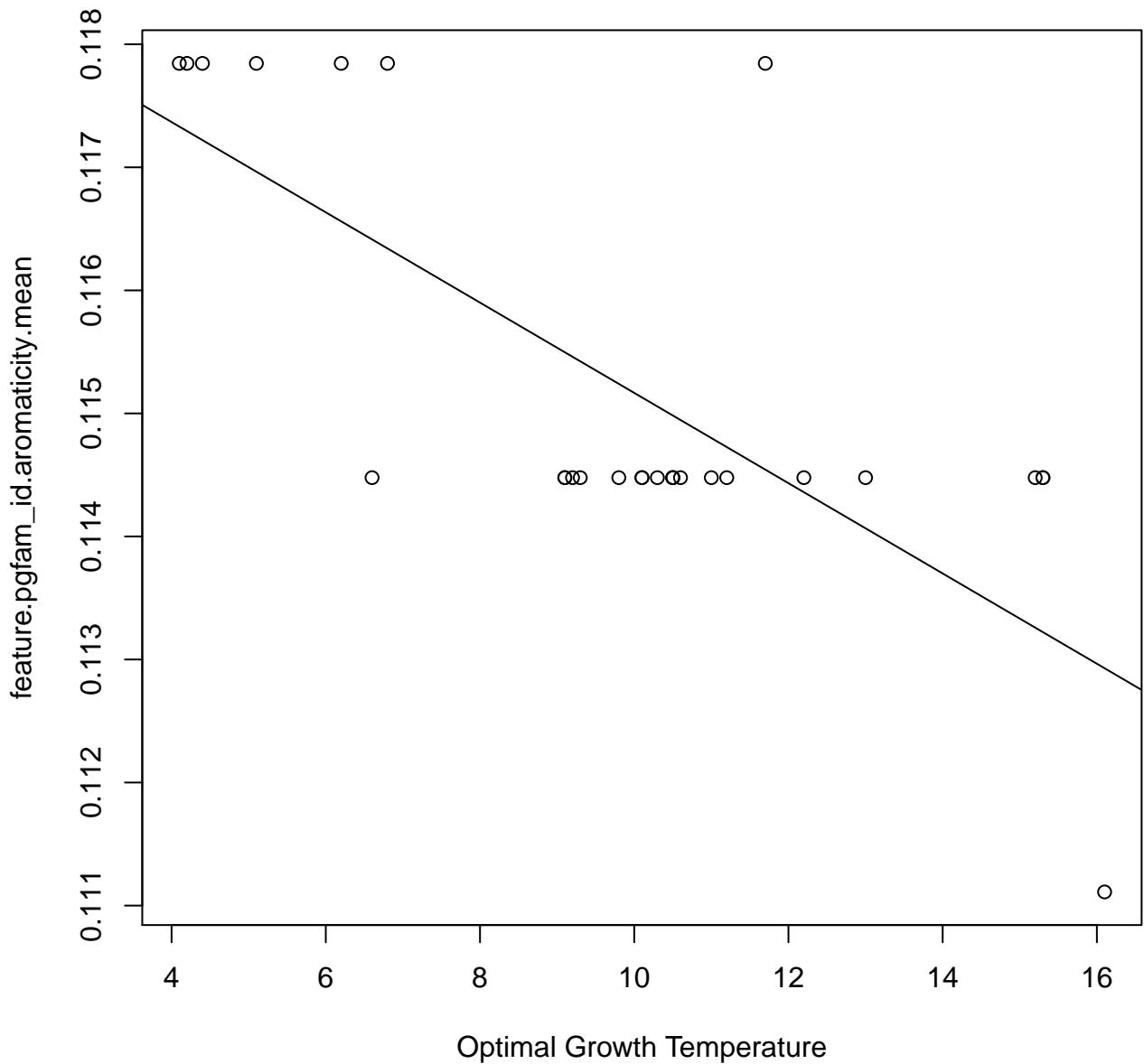
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PGF_06641194
Capsule biosynthesis protein capA



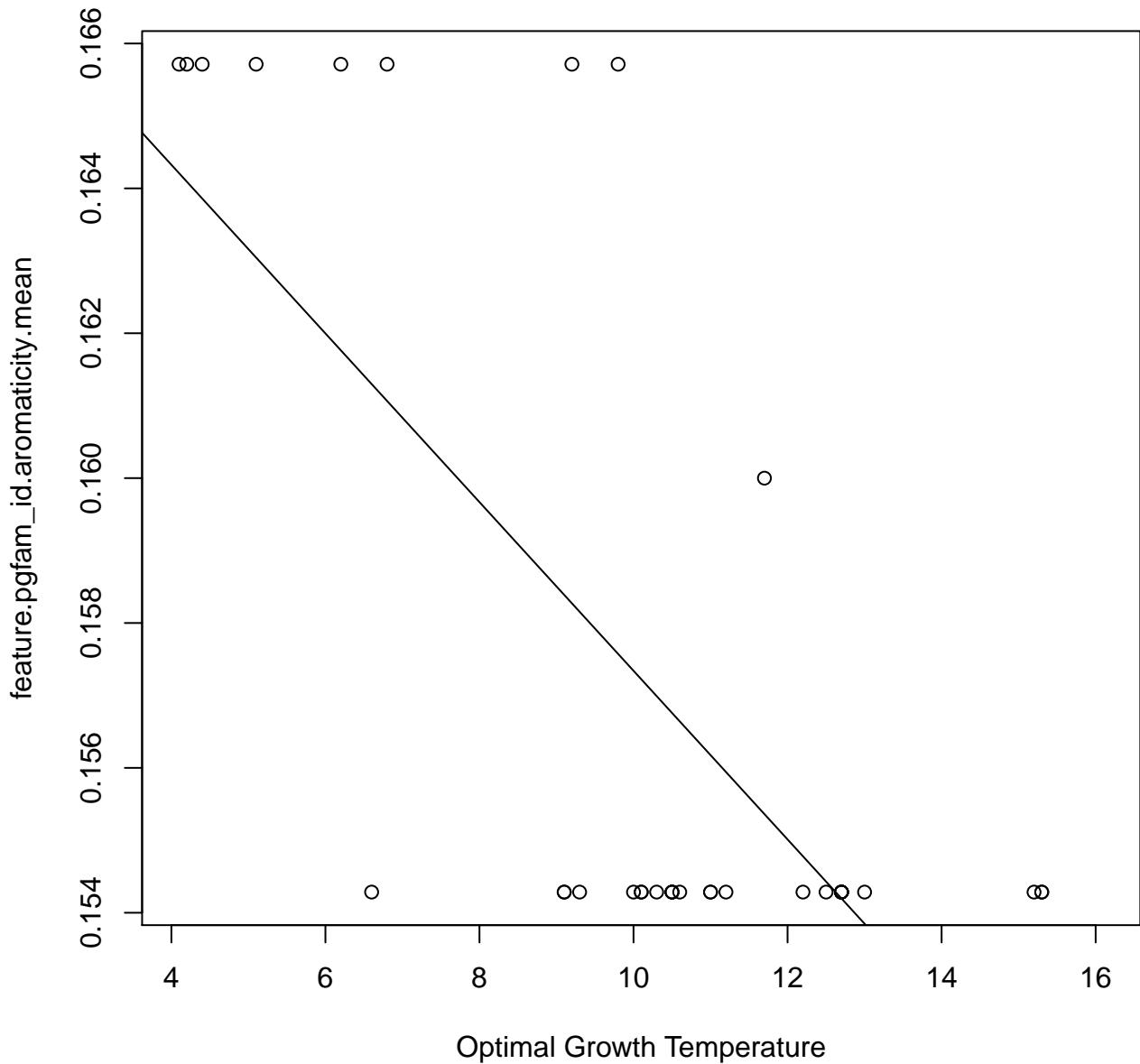
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PGF_01336341
Transcriptional regulator



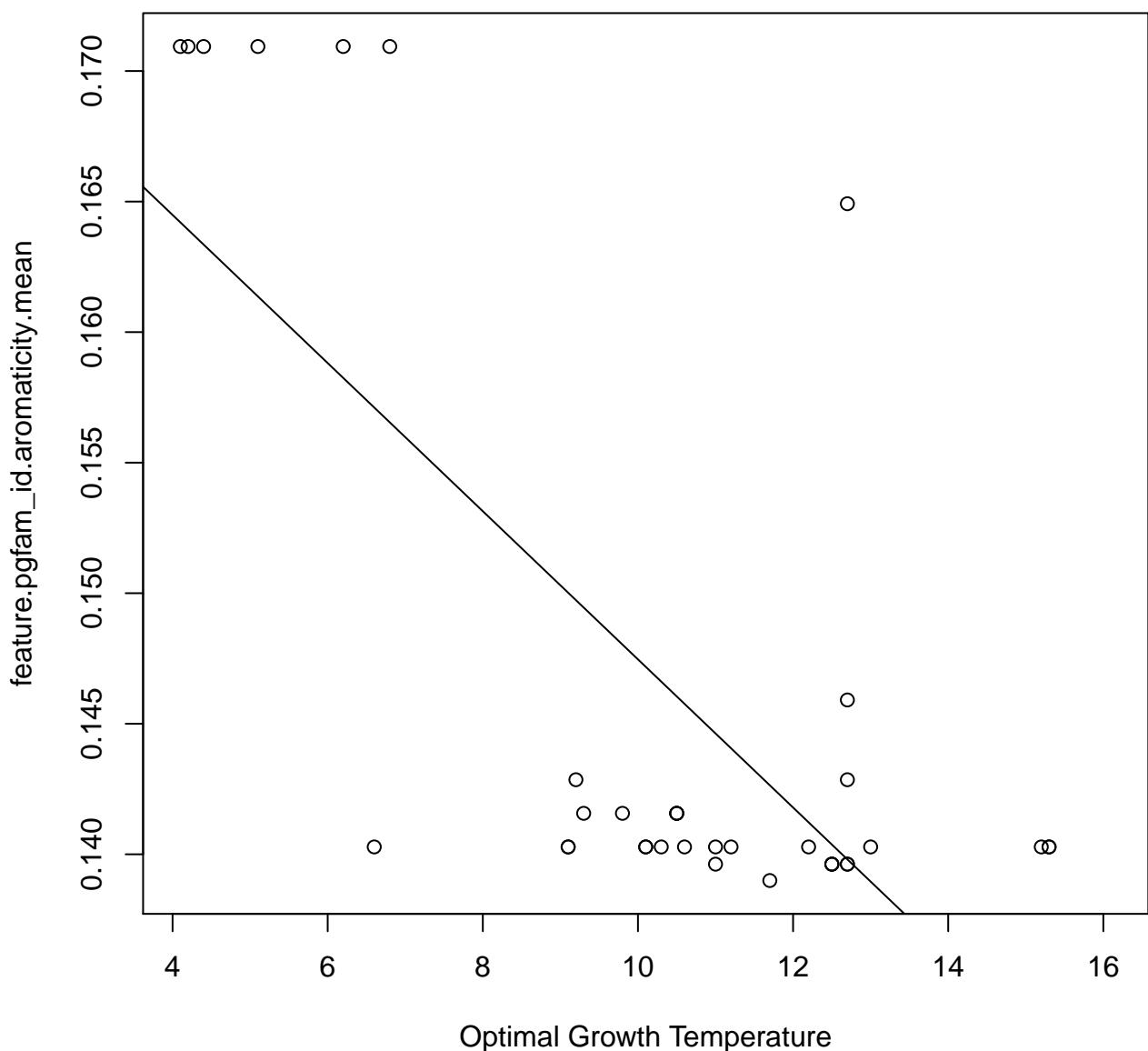
feature.pgfam_id.aromaticity.mean
PGF_00058677
Transcriptional regulator VC0732, LysR family



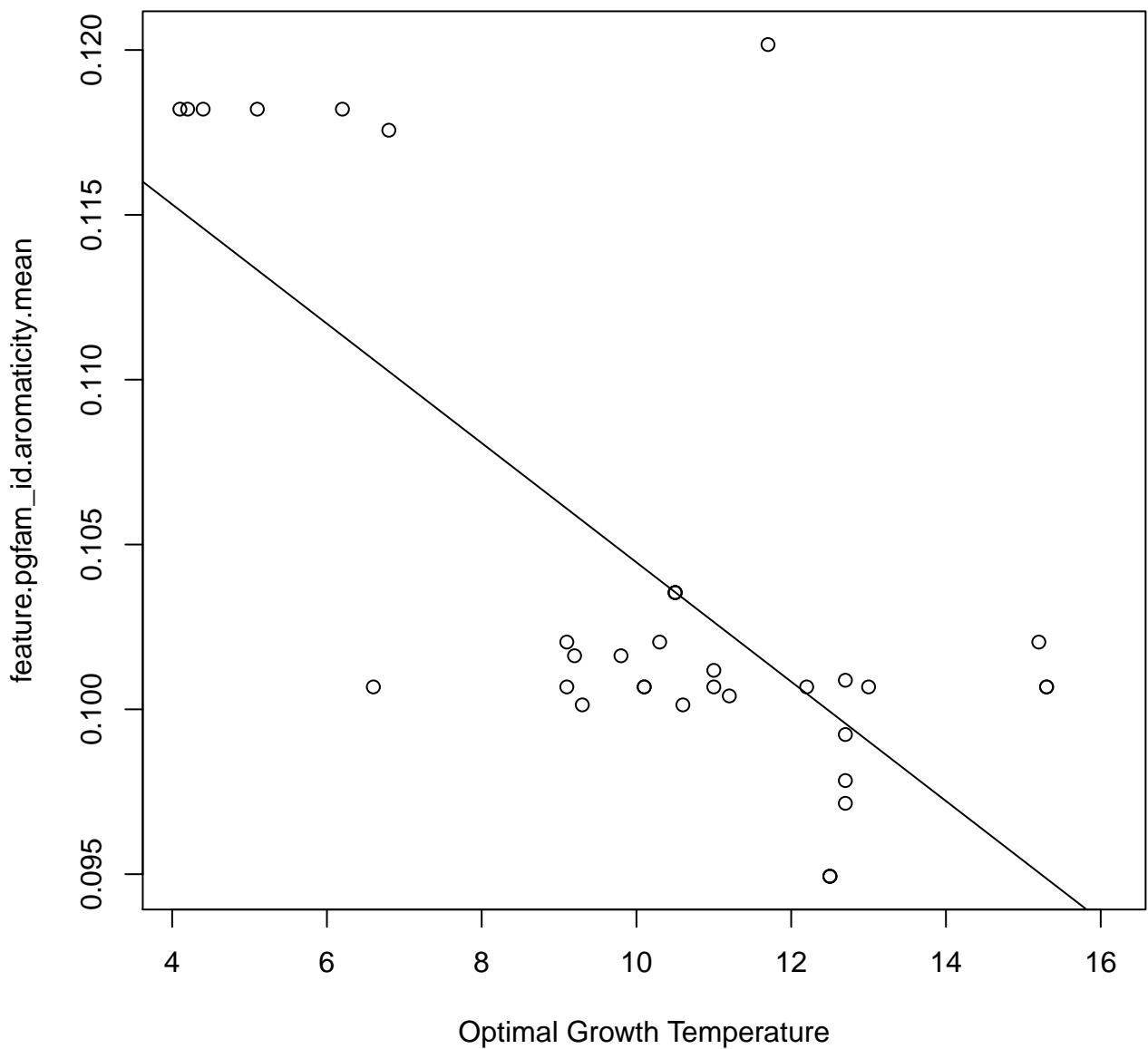
feature.pgfam_id.aromaticity.mean
PGF_06077968
Bacterial non-heme ferritin (EC 1.16.3.2)



feature.pgfam_id.aromaticity.mean
PGF_00004056
Fatty acid cis/trans isomerase



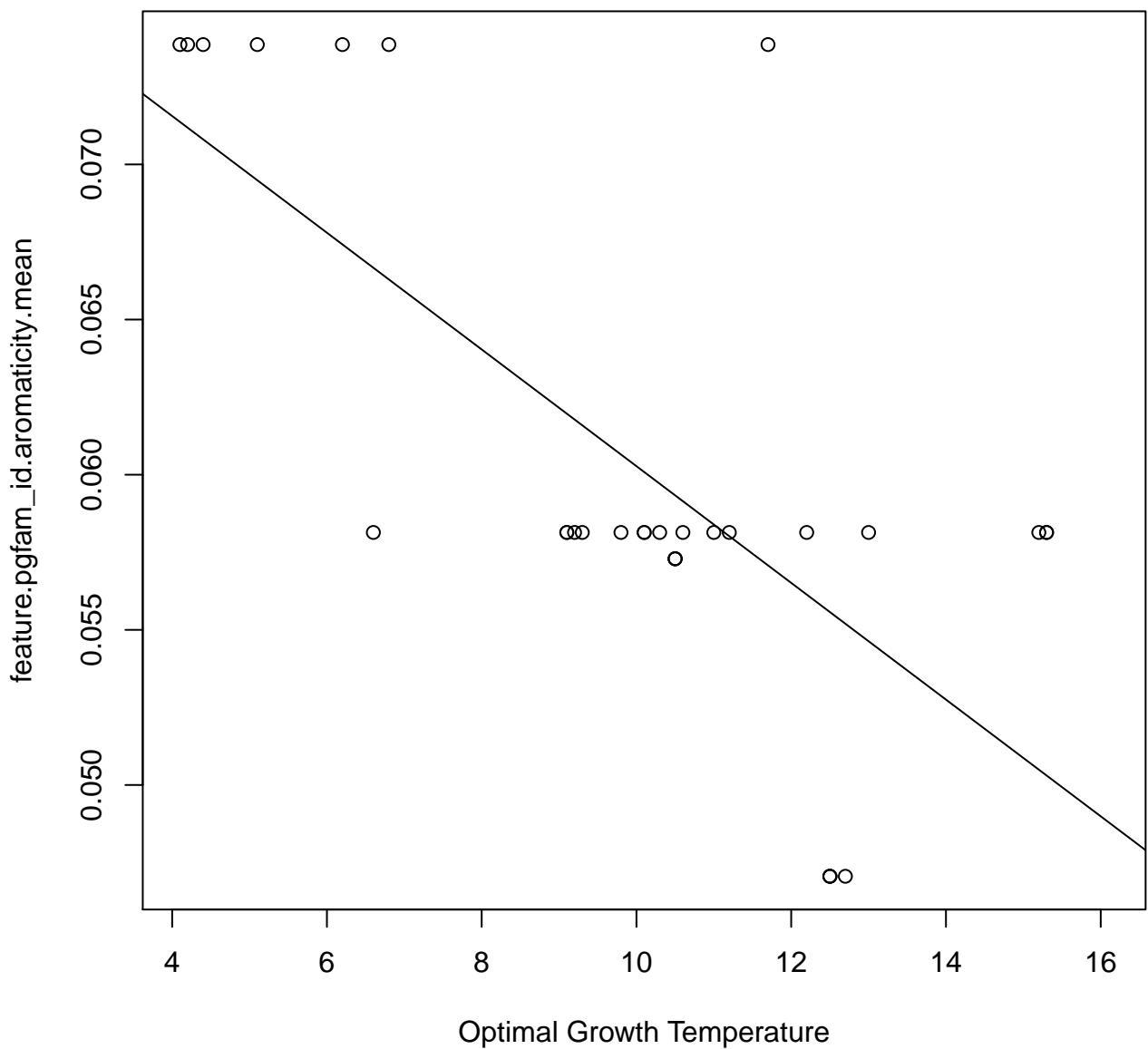
feature.pgfam_id.aromaticity.mean
PGF_00014974
Inter-alpha-trypsin inhibitor domain protein



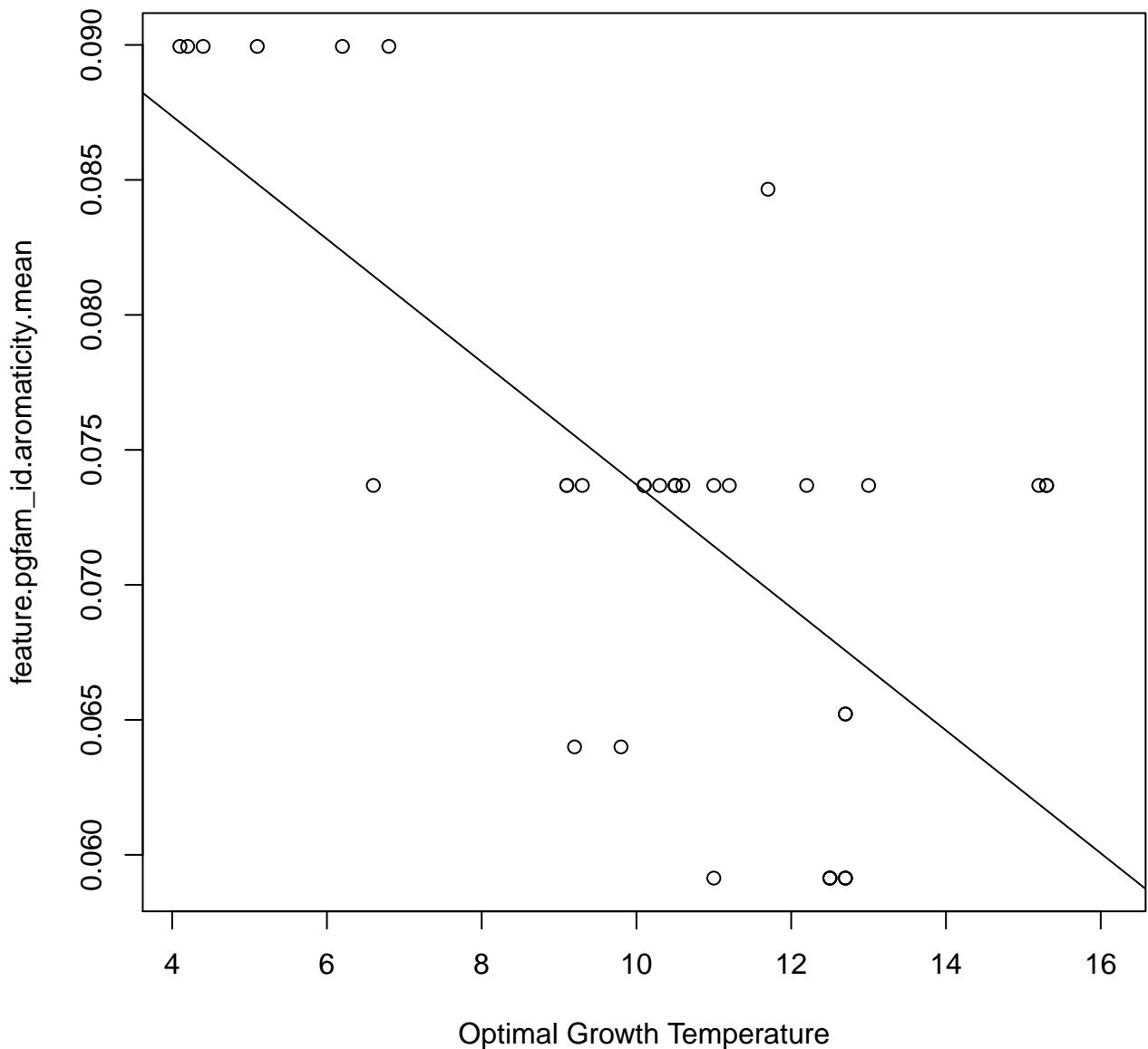
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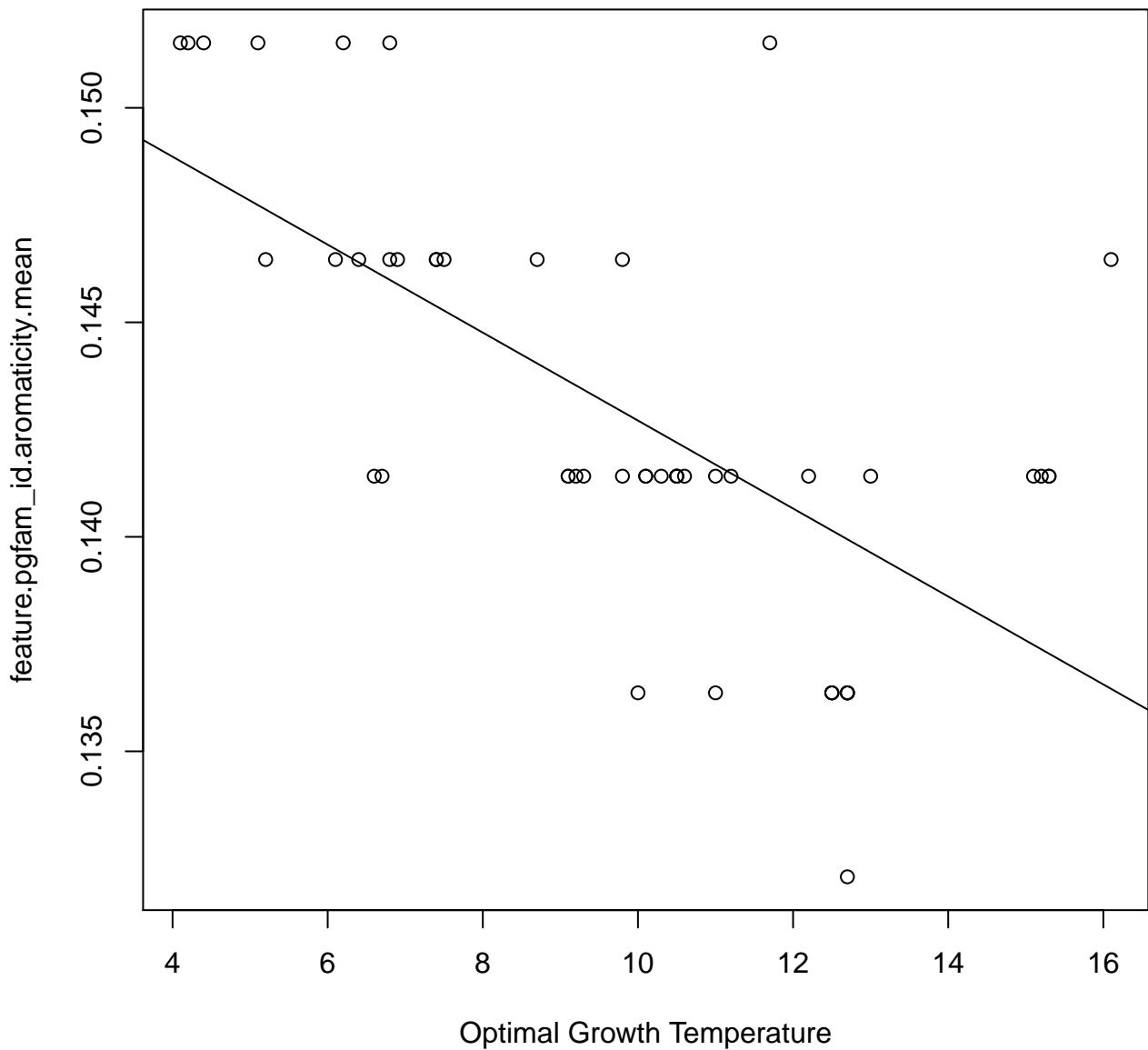
hypothetical protein



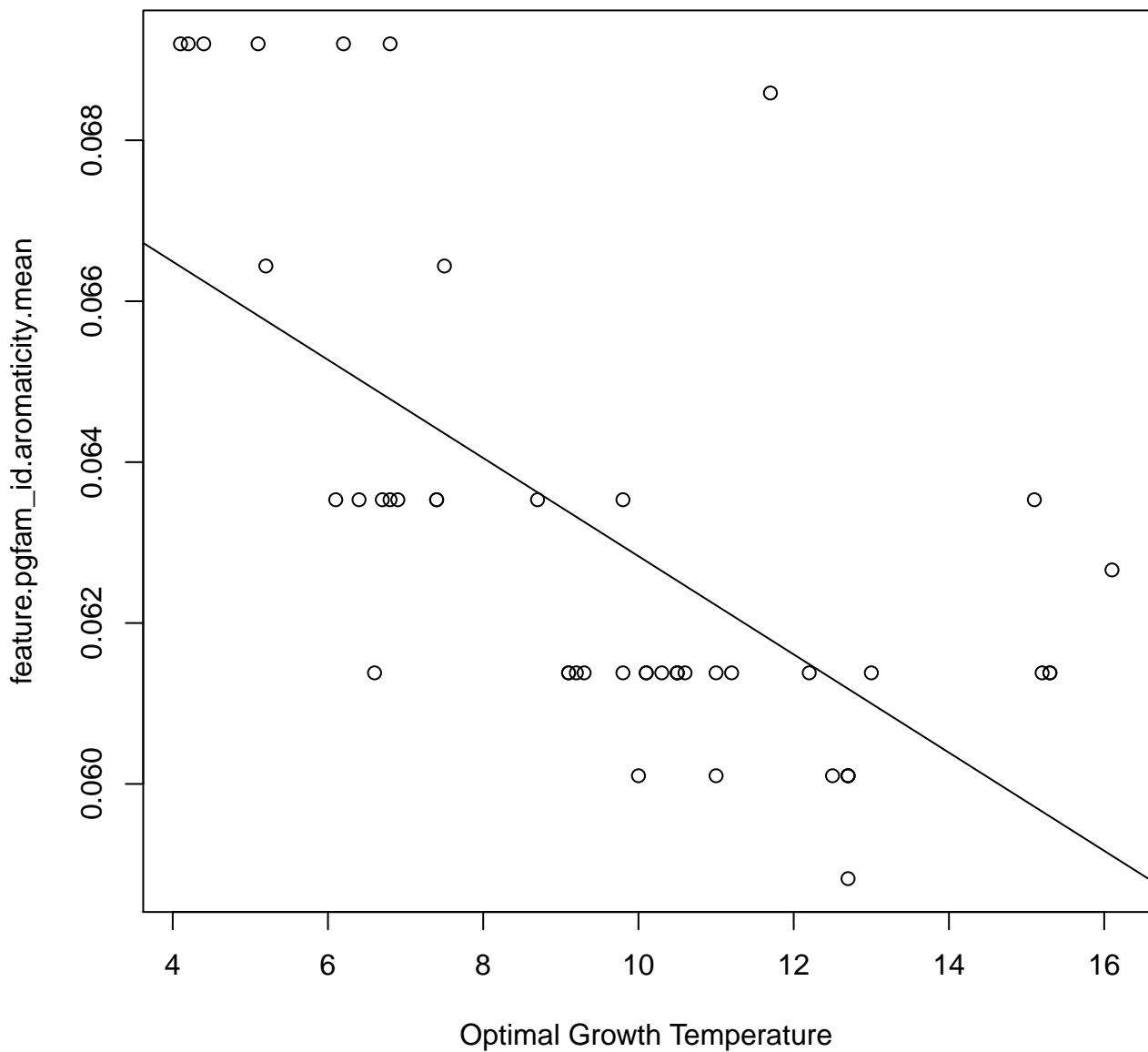
feature.pgfam_id.aromaticity.mean
PGF_00423668
Dna binding response regulator PrrA (RegA)



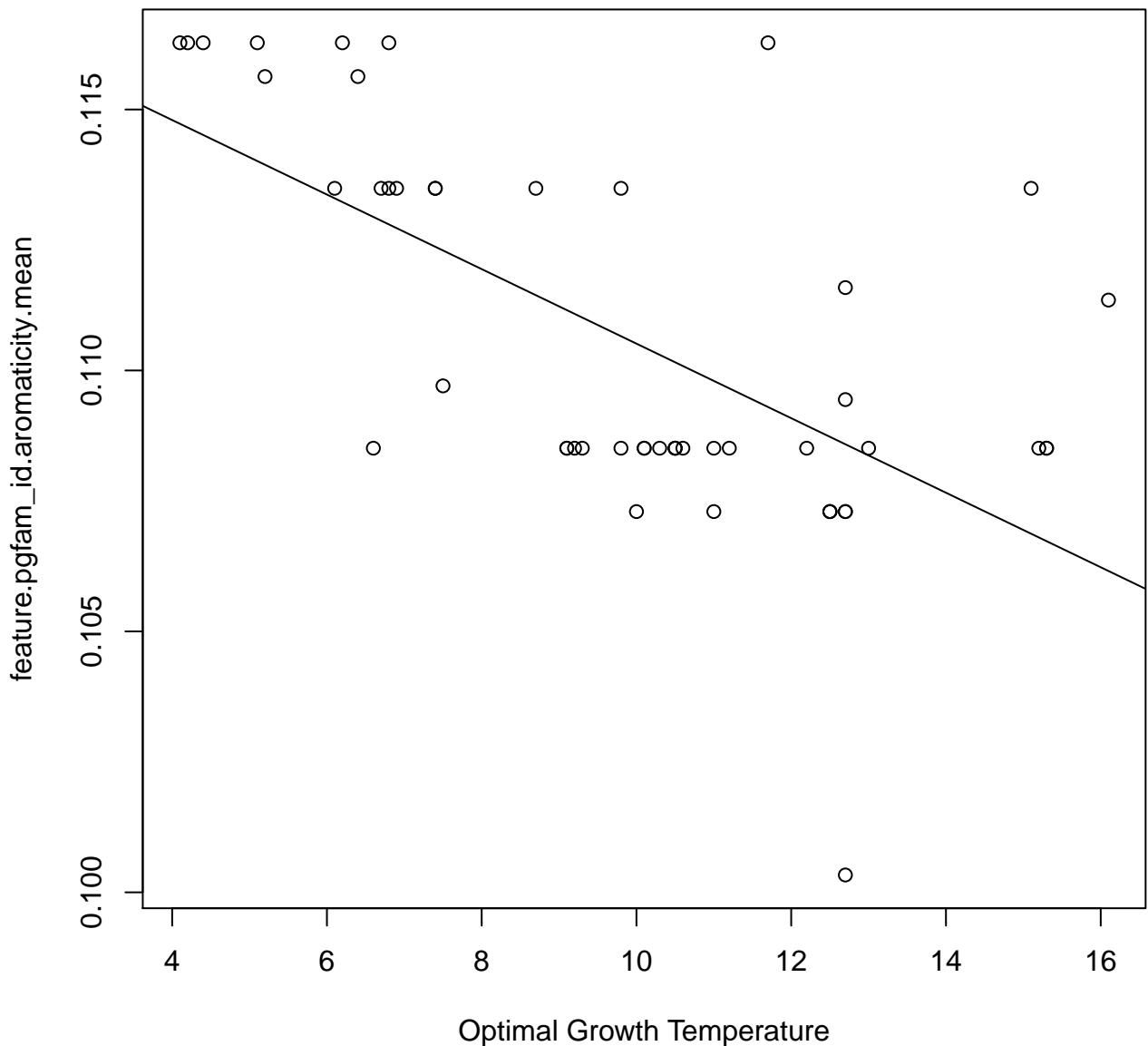
feature.pgfam_id.aromaticity.mean
PGF_06660812
3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)



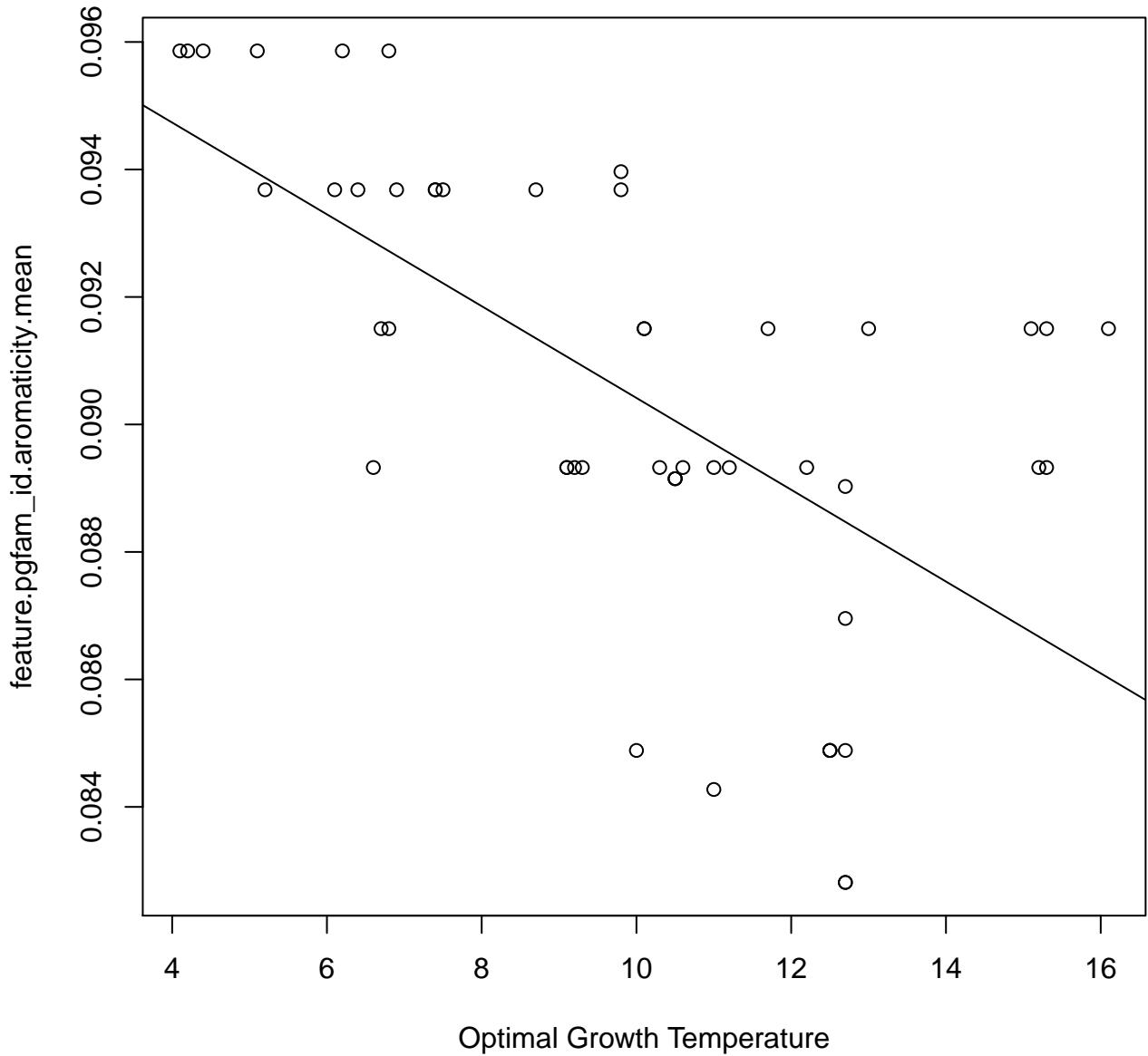
feature.pgfam_id.aromaticity.mean
PGF_04438983
ATP-dependent protease La (EC 3.4.21.53) Type I



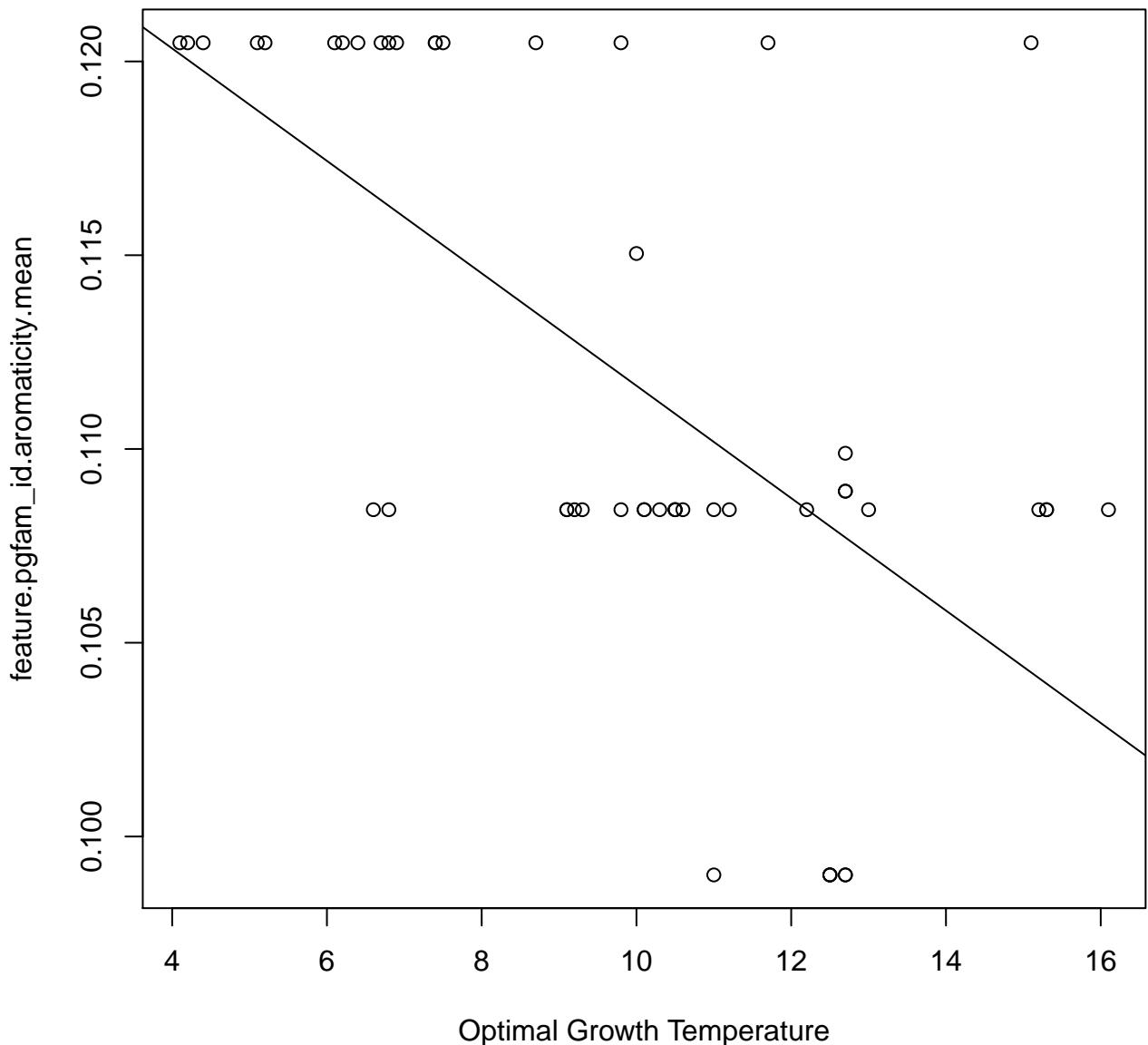
feature.pgfam_id.aromaticity.mean
PGF_00054959
Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4)



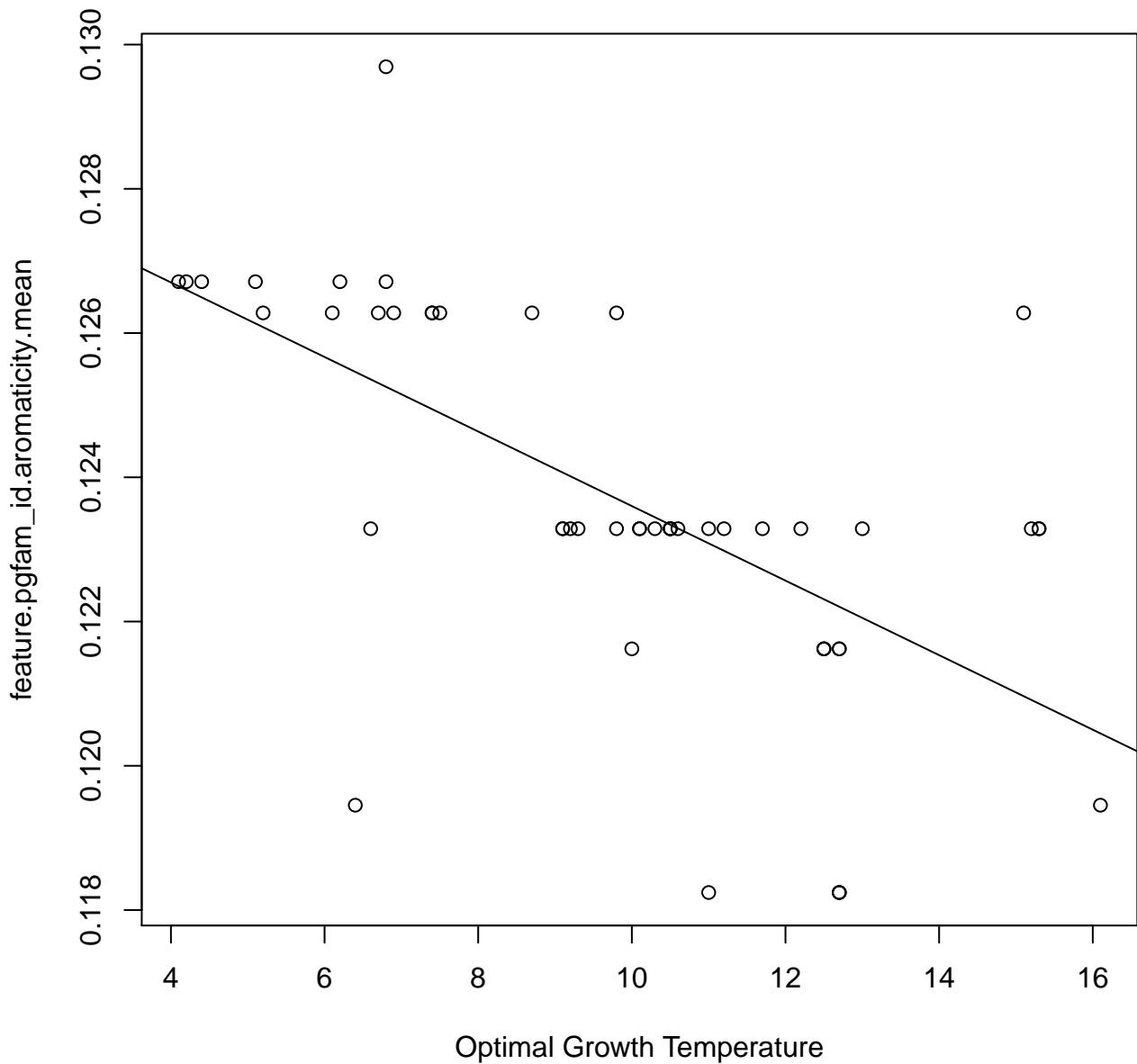
feature.pgfam_id.aromaticity.mean
PGF_06051594
Predicted ATPase related to phosphate starvation-inducible protein PhoH



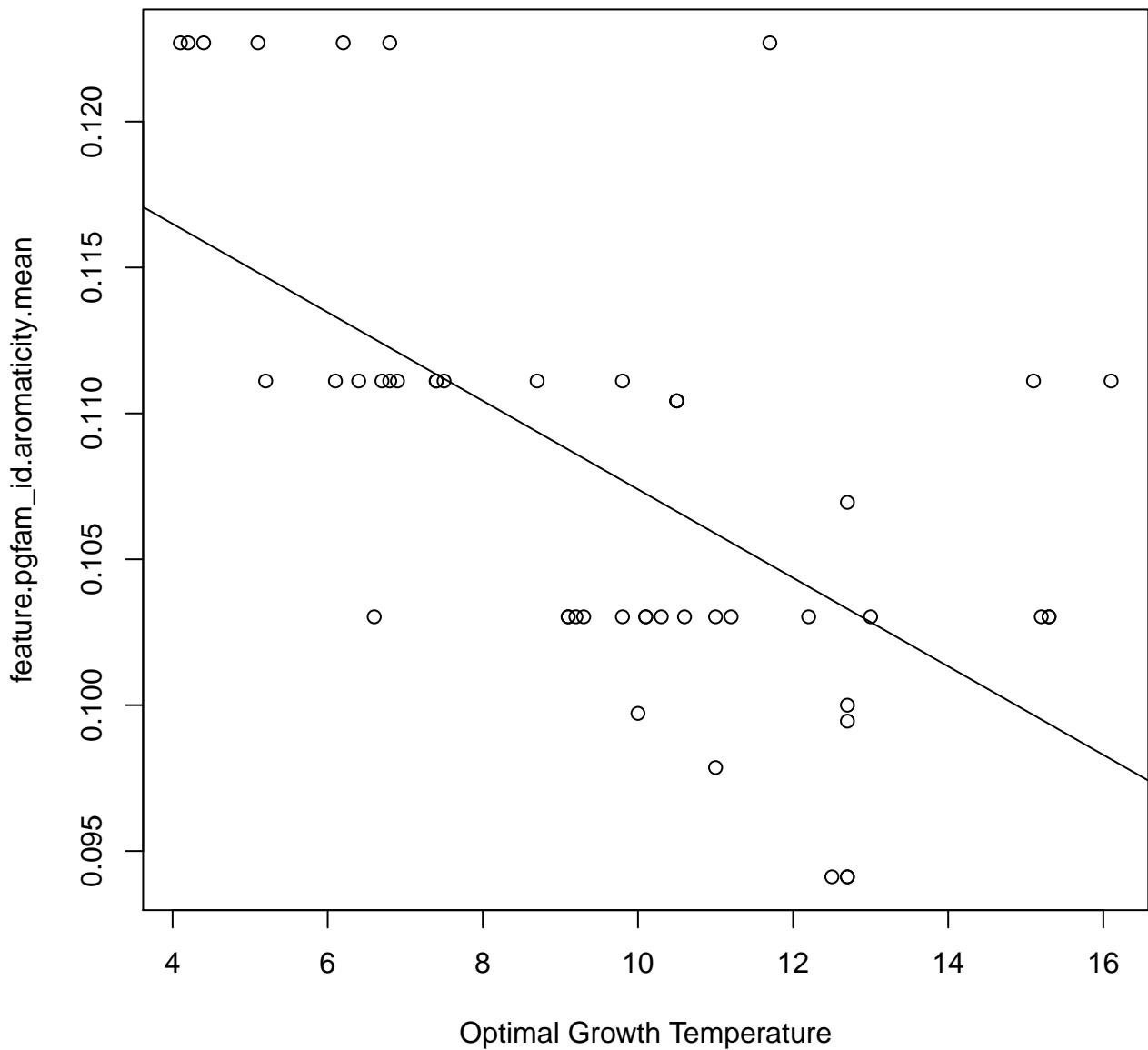
feature.pgfam_id.aromaticity.mean
PGF_02069837
Succinate dehydrogenase flavin-adding protein, antitoxin of CptAB toxin-antitoxin



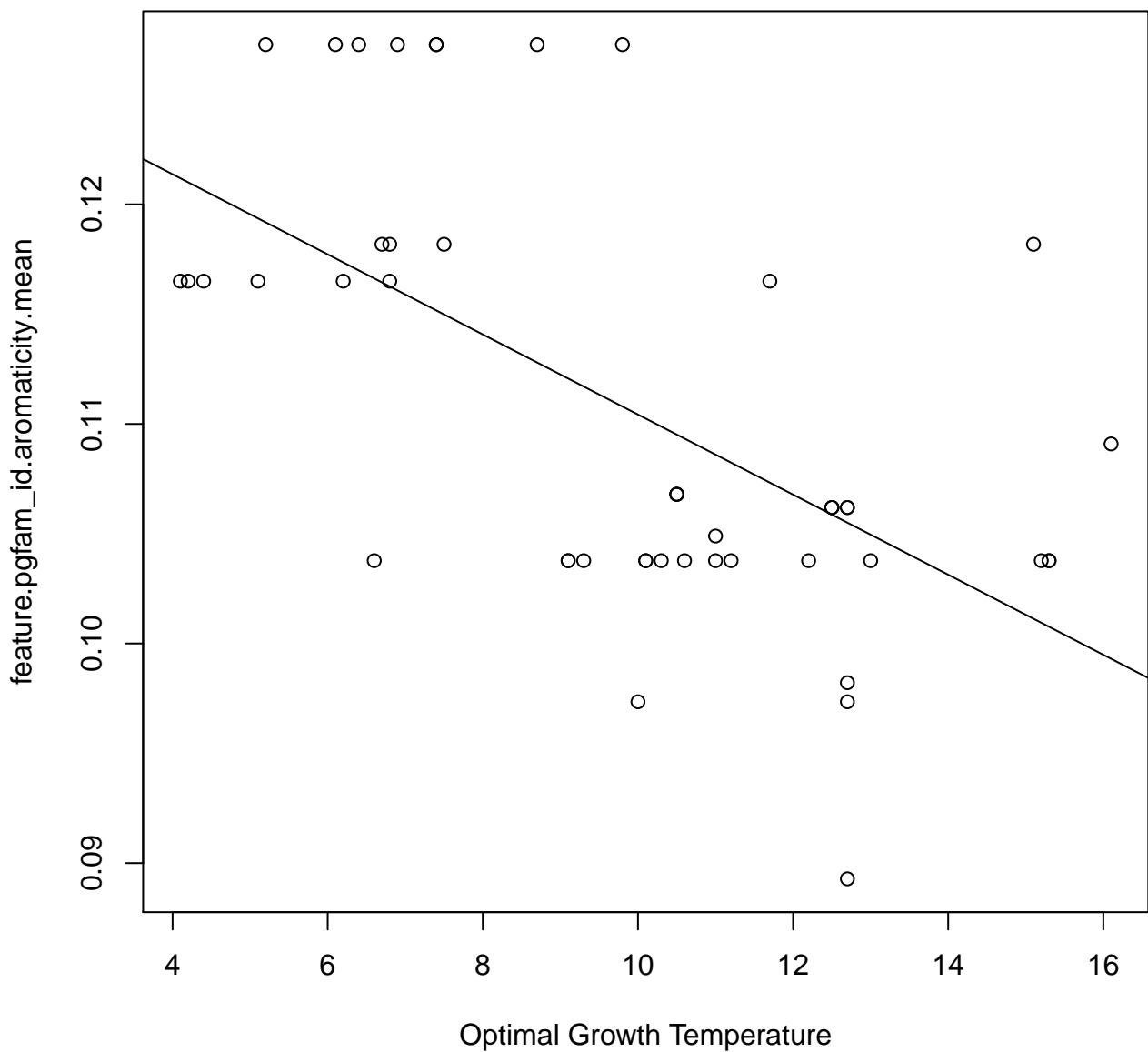
feature.pgfam_id.aromaticity.mean
PGF_03051420
6-carboxy-5,6,7,8-tetrahydropterin synthase (EC 4.1.2.50)



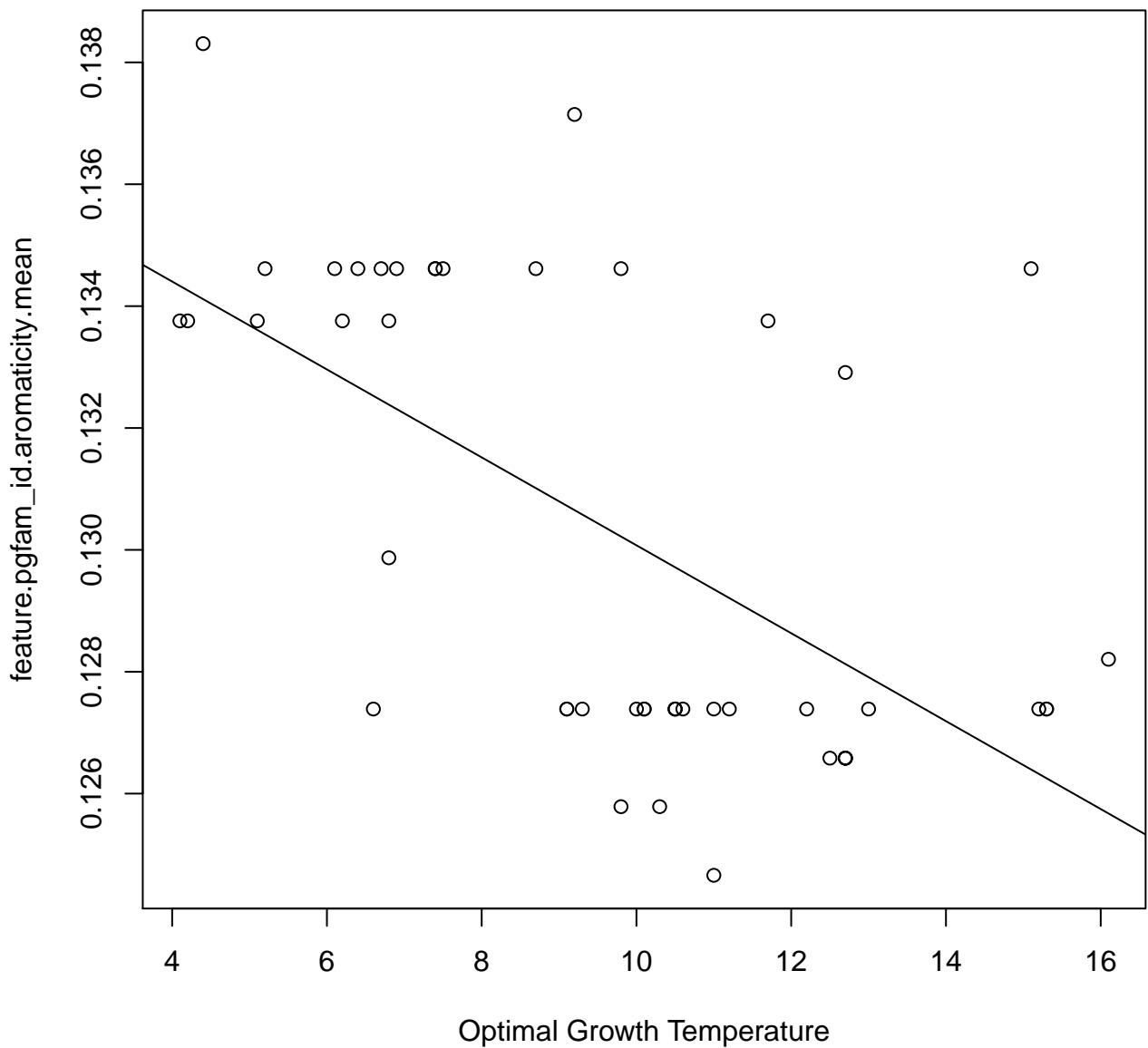
feature.pgfam_id.aromaticity.mean
PGF_09348764
Dihydrofolate reductase (EC 1.5.1.3)



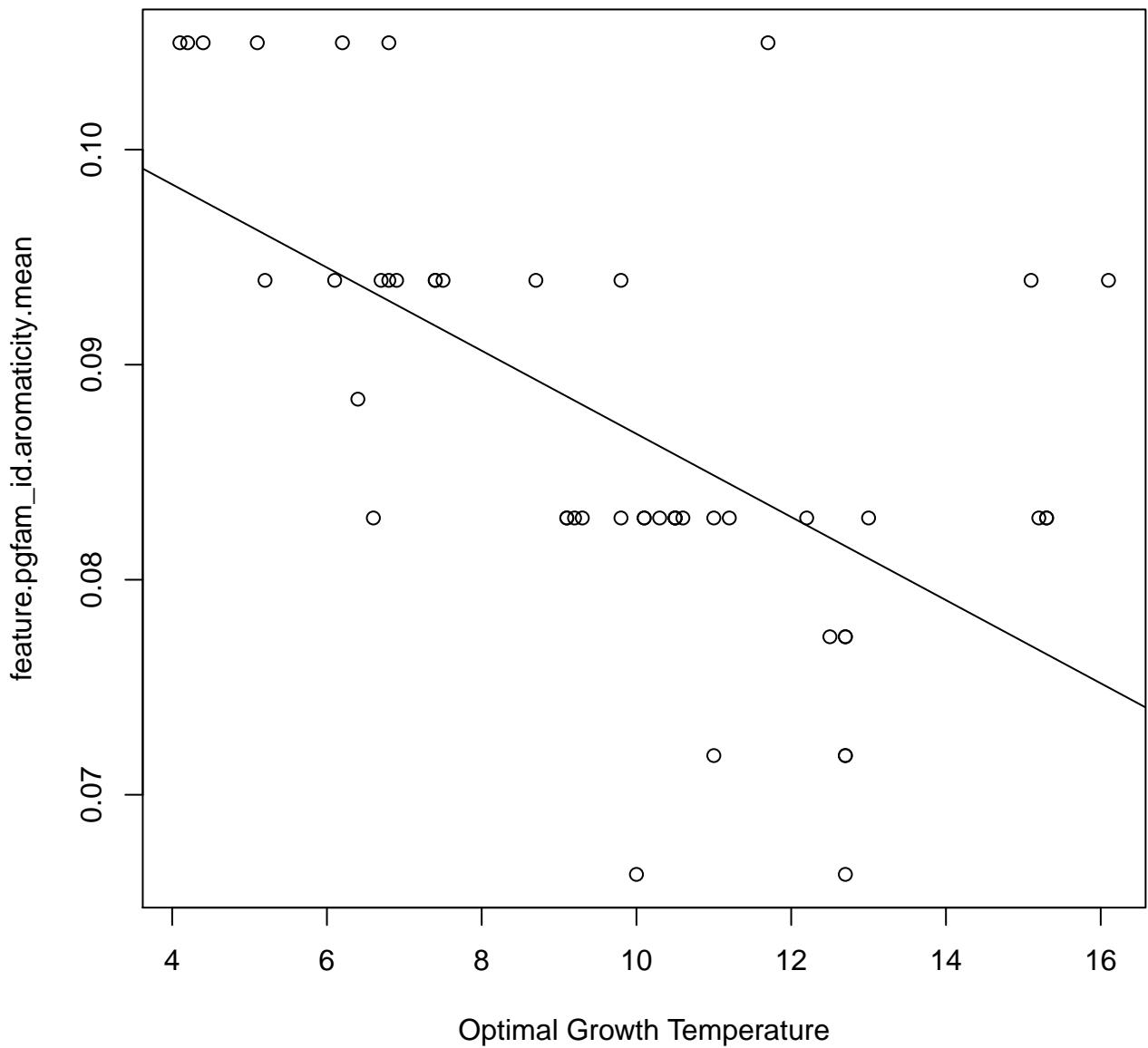
feature.pgfam_id.aromaticity.mean
PGF_01336507
hypothetical protein



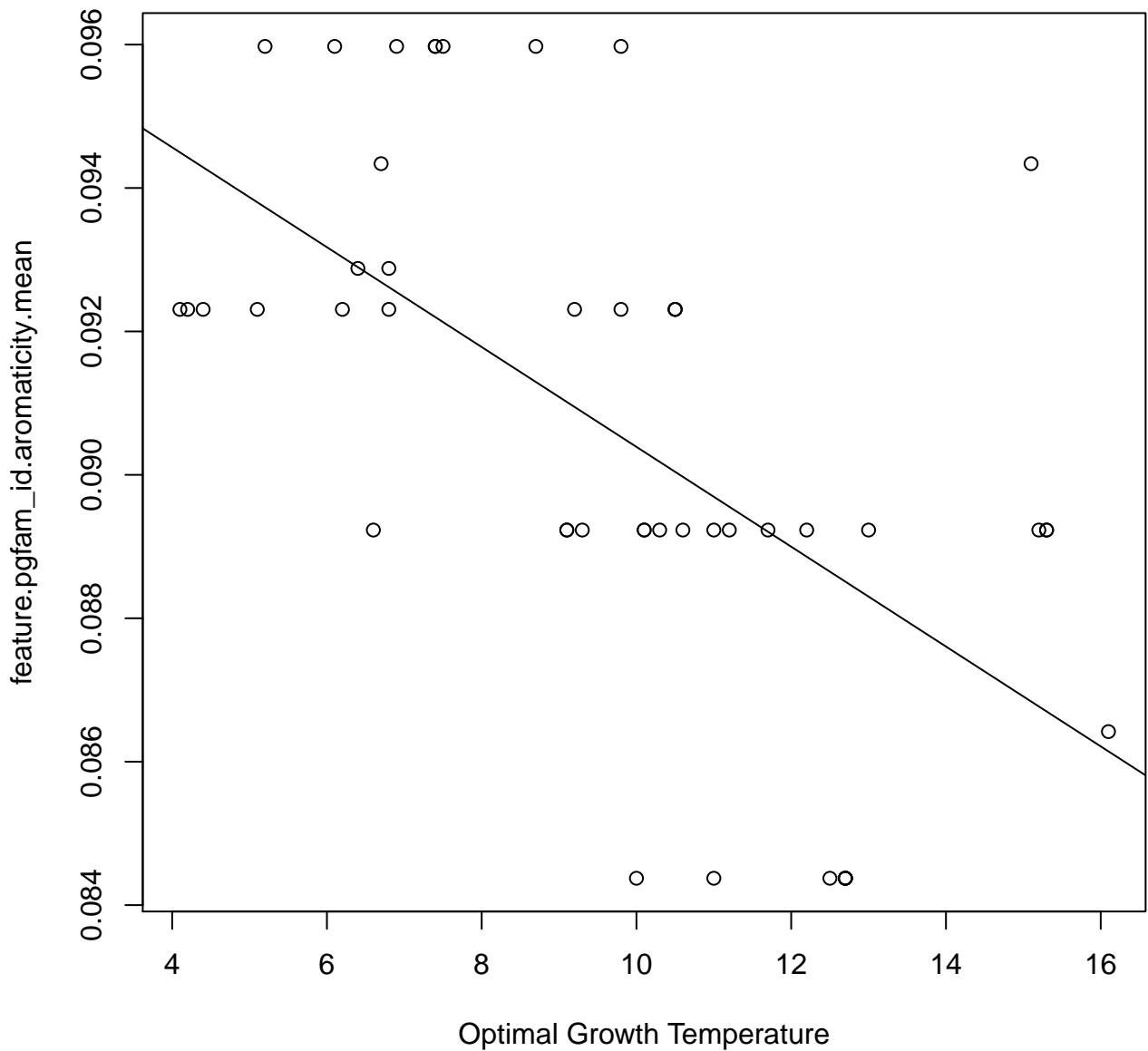
feature.pgfam_id.aromaticity.mean
PGF_00220548
Thiol peroxidase, Bcp-type (EC 1.11.1.15)



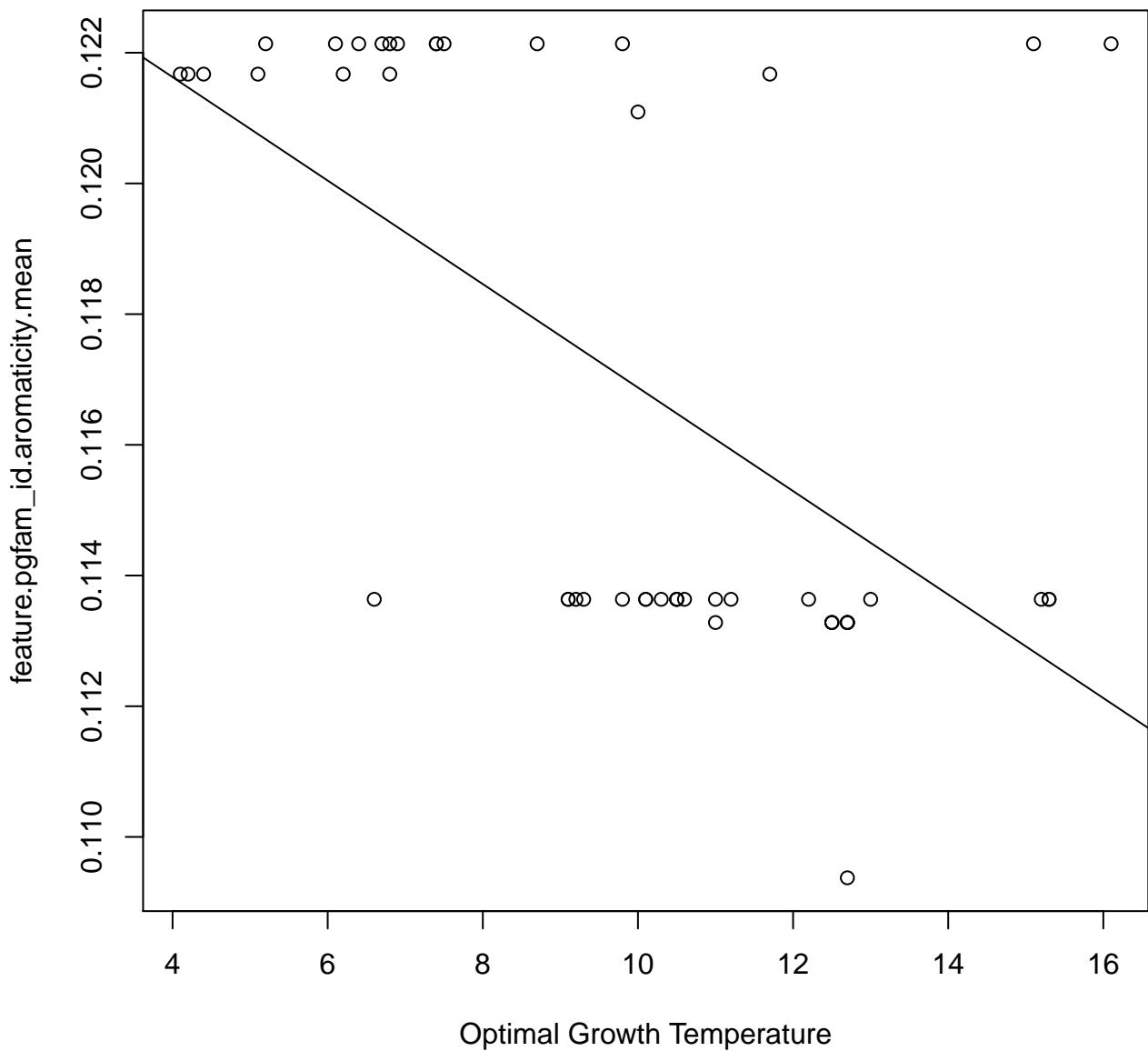
feature.pgfam_id.aromaticity.mean
PGF_06894101
3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)



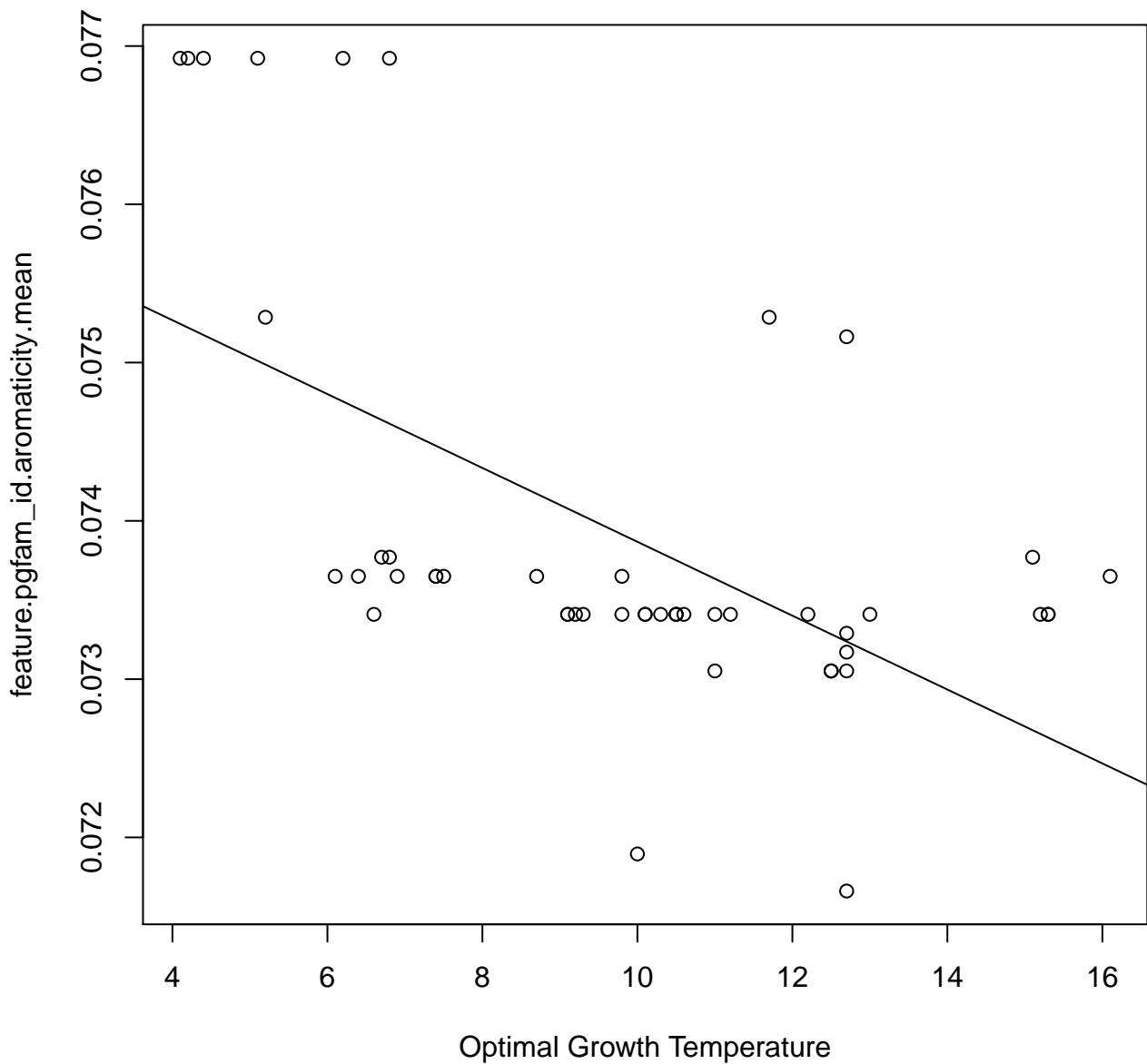
feature.pgfam_id.aromaticity.mean
PGF_02191019
Thiamine-monophosphate kinase (EC 2.7.4.16)



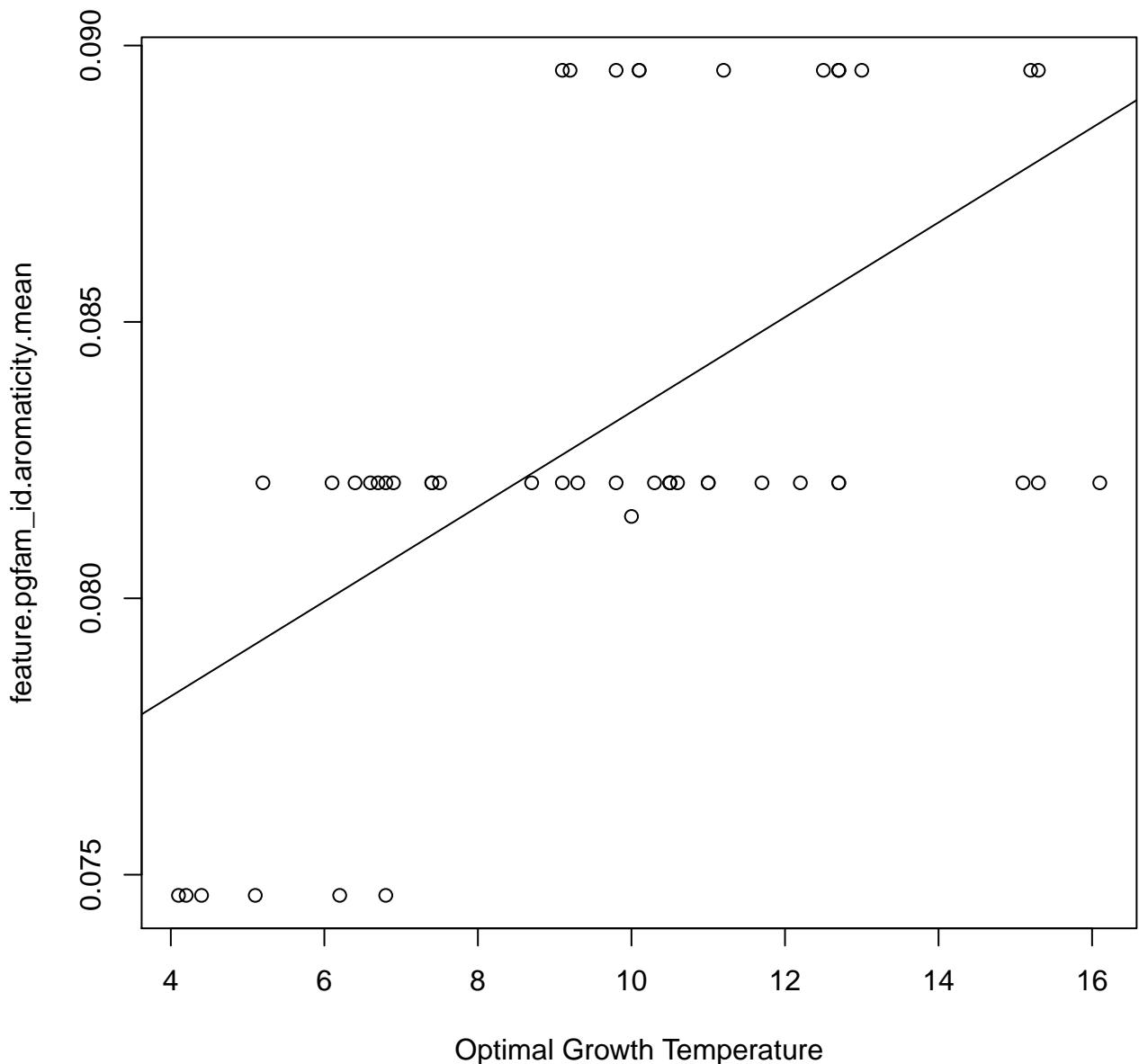
feature.pgfam_id.aromaticity.mean
PGF_00033729
Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase (EC 2.3.1.129)



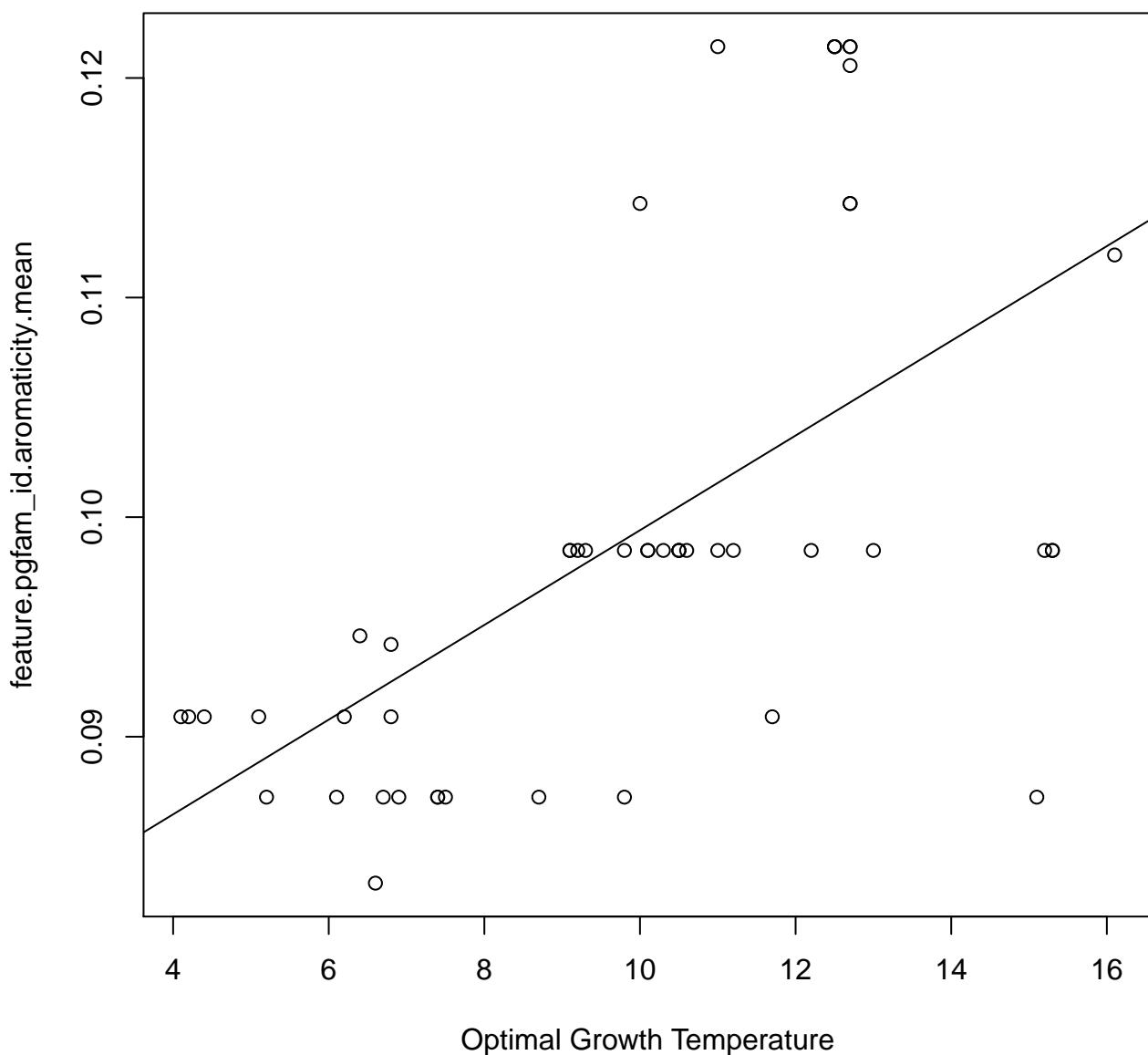
feature.pgfam_id.aromaticity.mean
PGF_07072582
RNA polymerase sigma factor RpoD



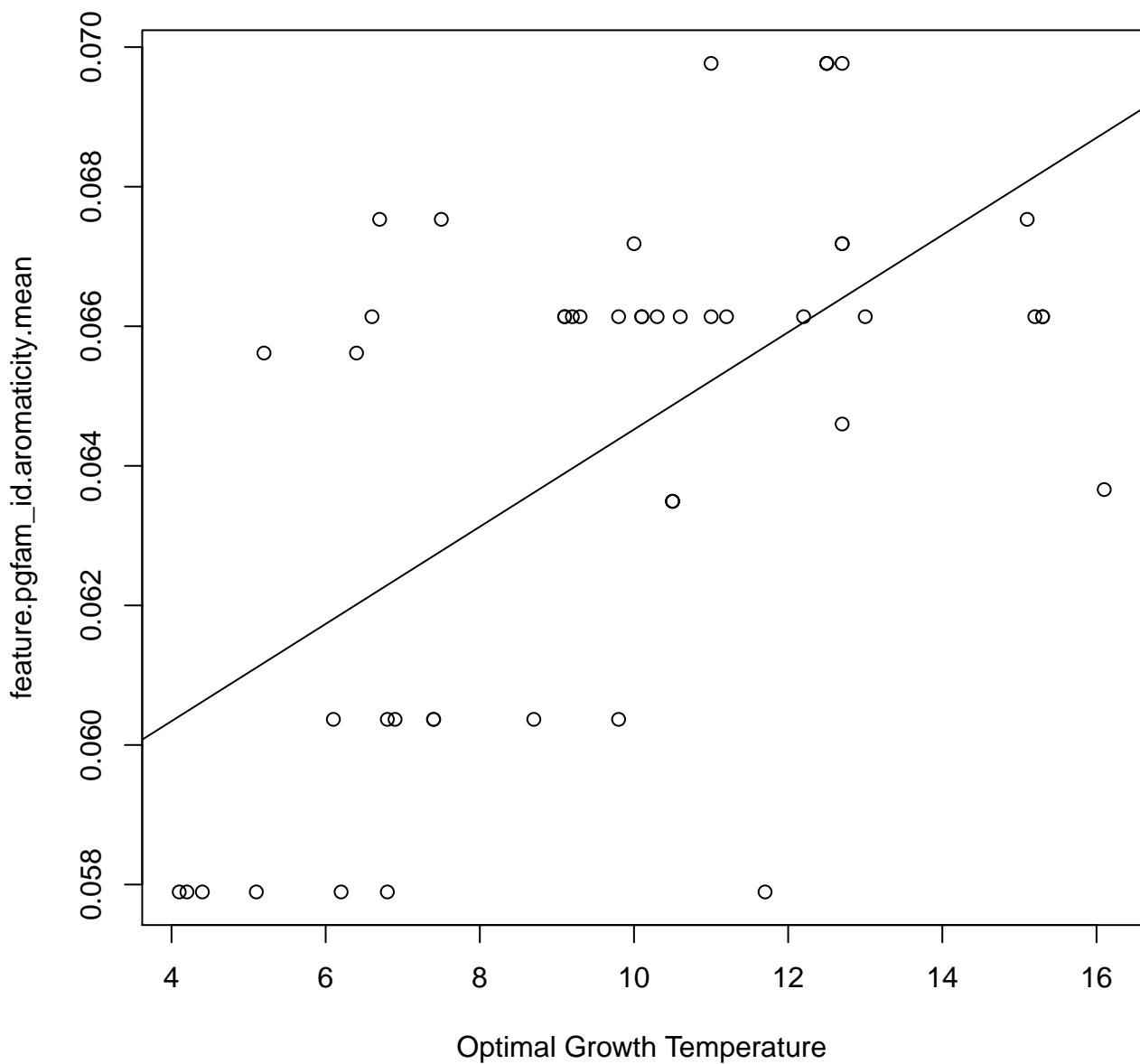
feature.pgfam_id.aromaticity.mean
PGF_03837024
Protein YhfA



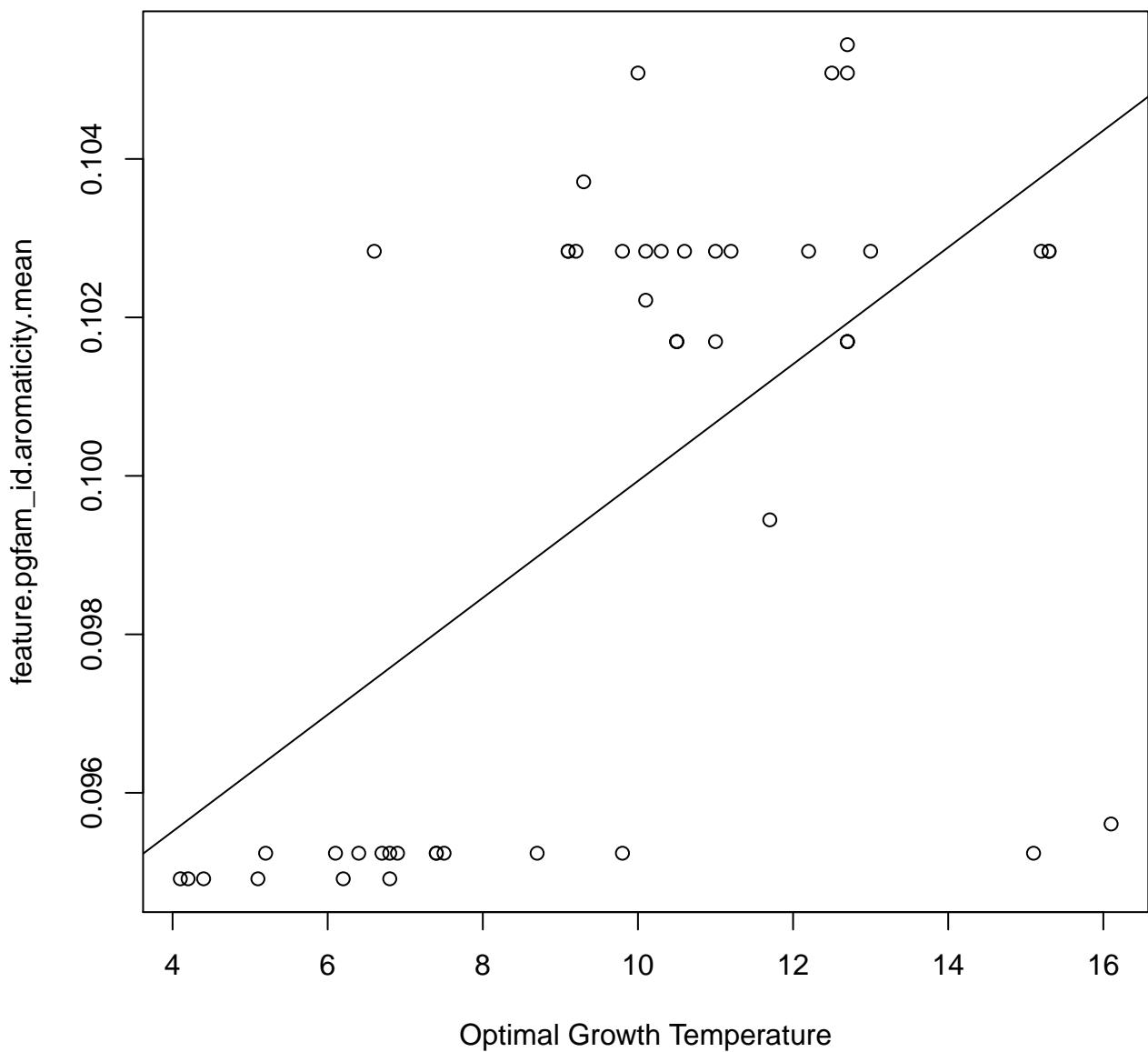
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PGF_00422096
DNA-binding protein, CopG family



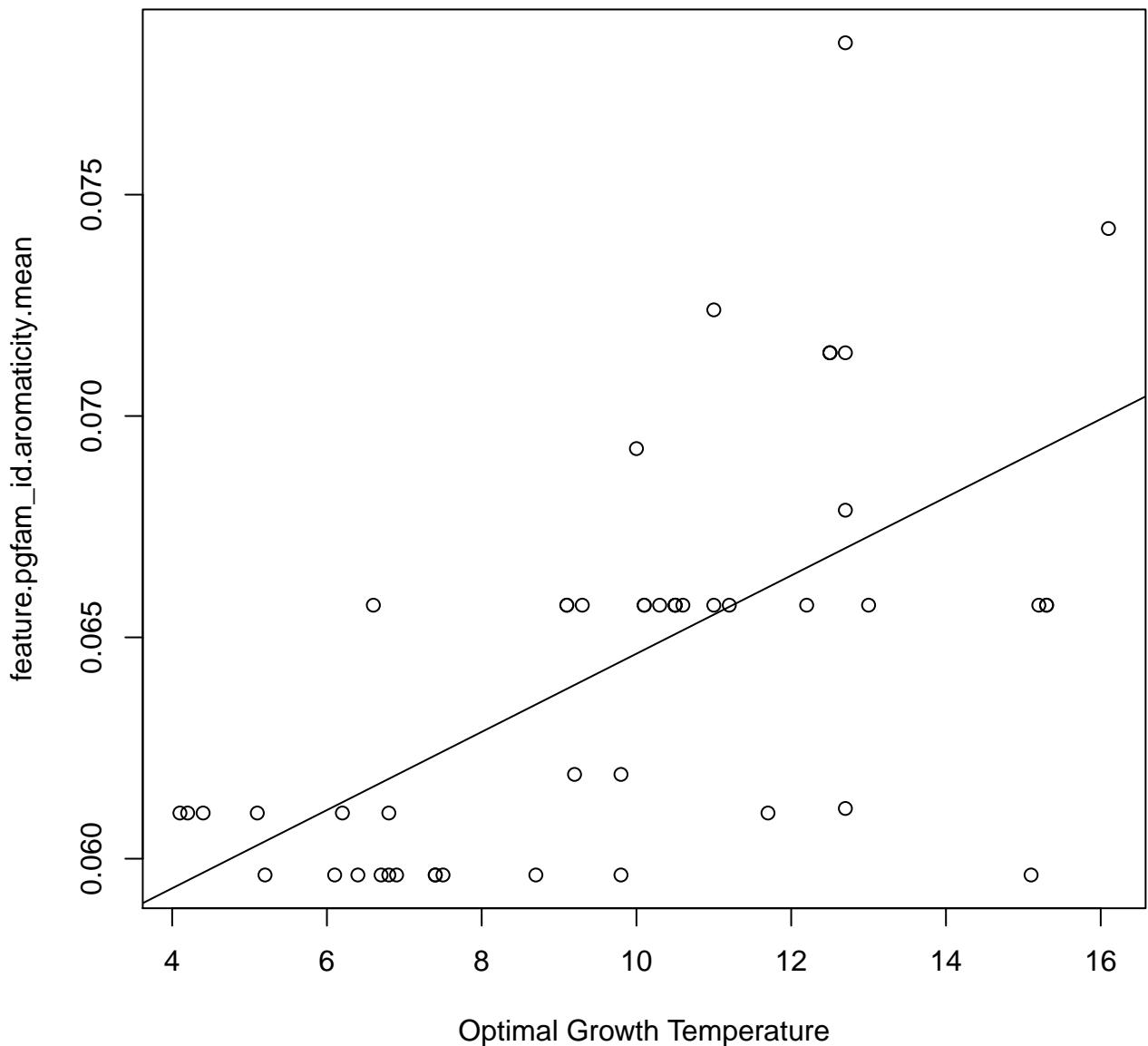
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PGF_00065334
Uncharacterized protein SO_3077



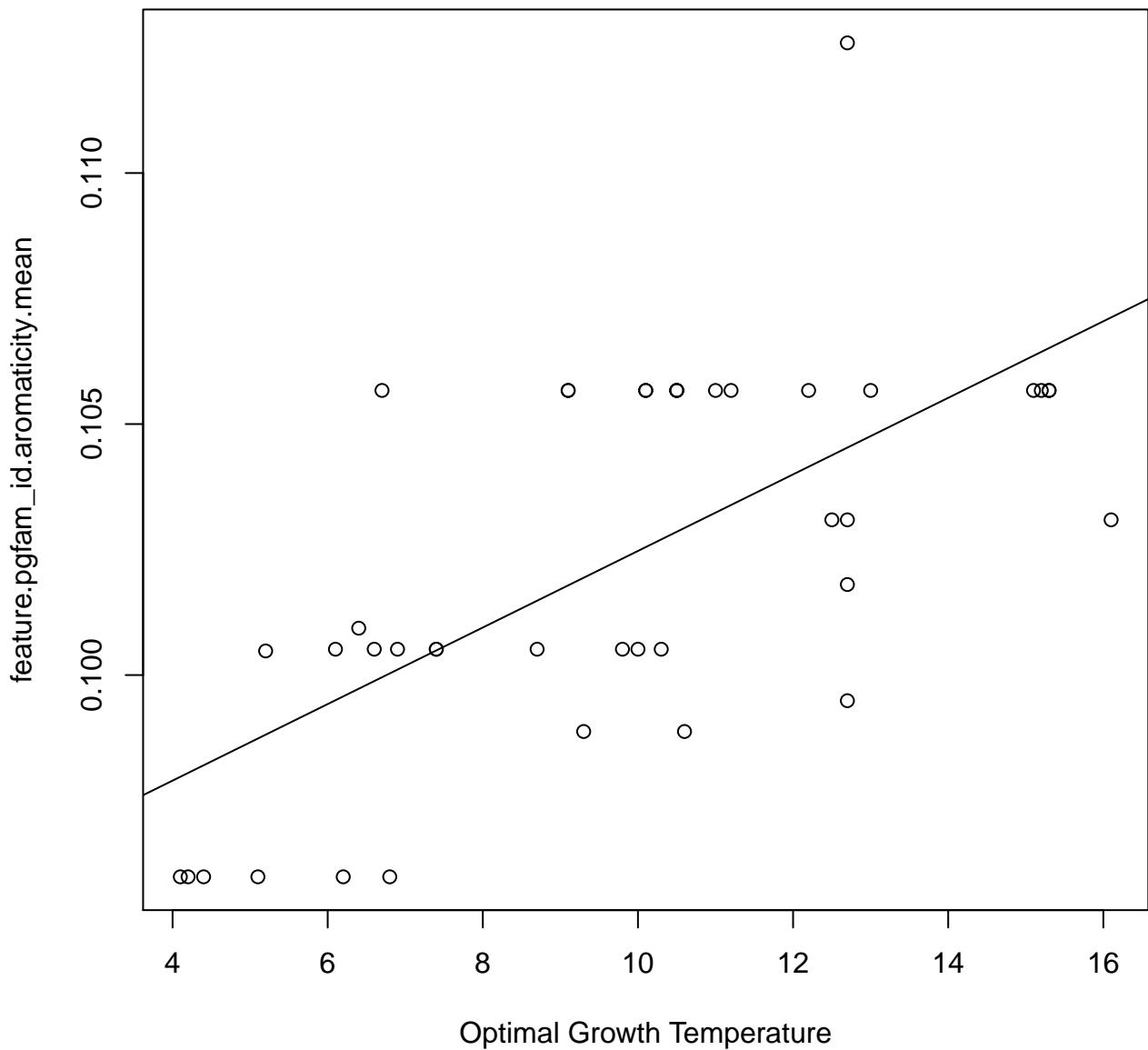
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PGF_00902417
HfIC protein



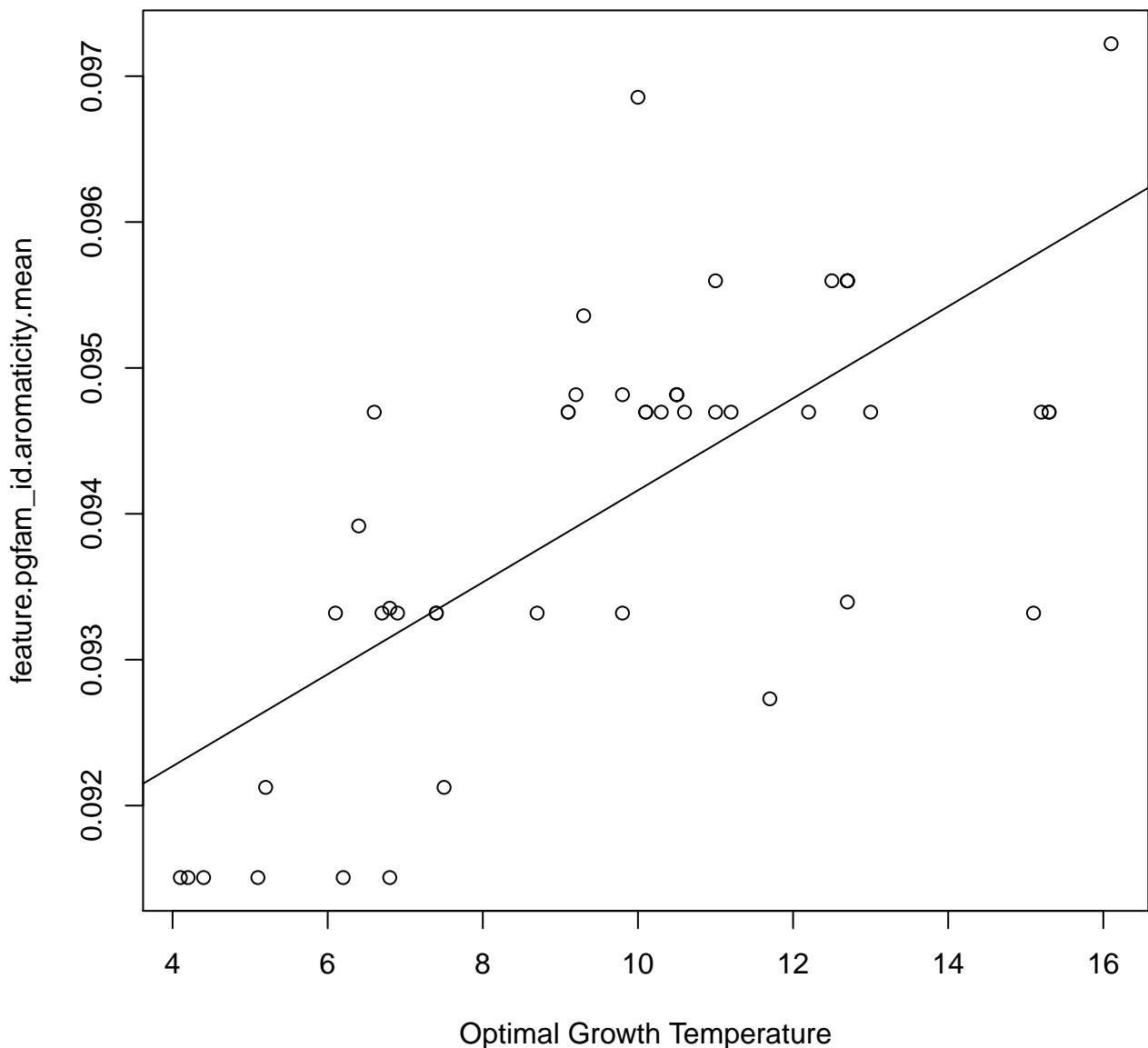
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PGF_00007026
GTP-binding protein EngB



feature.pgfam_id.aromaticity.mean
PGF_10410292
UDP-glucose 6-dehydrogenase (EC 1.1.1.22)



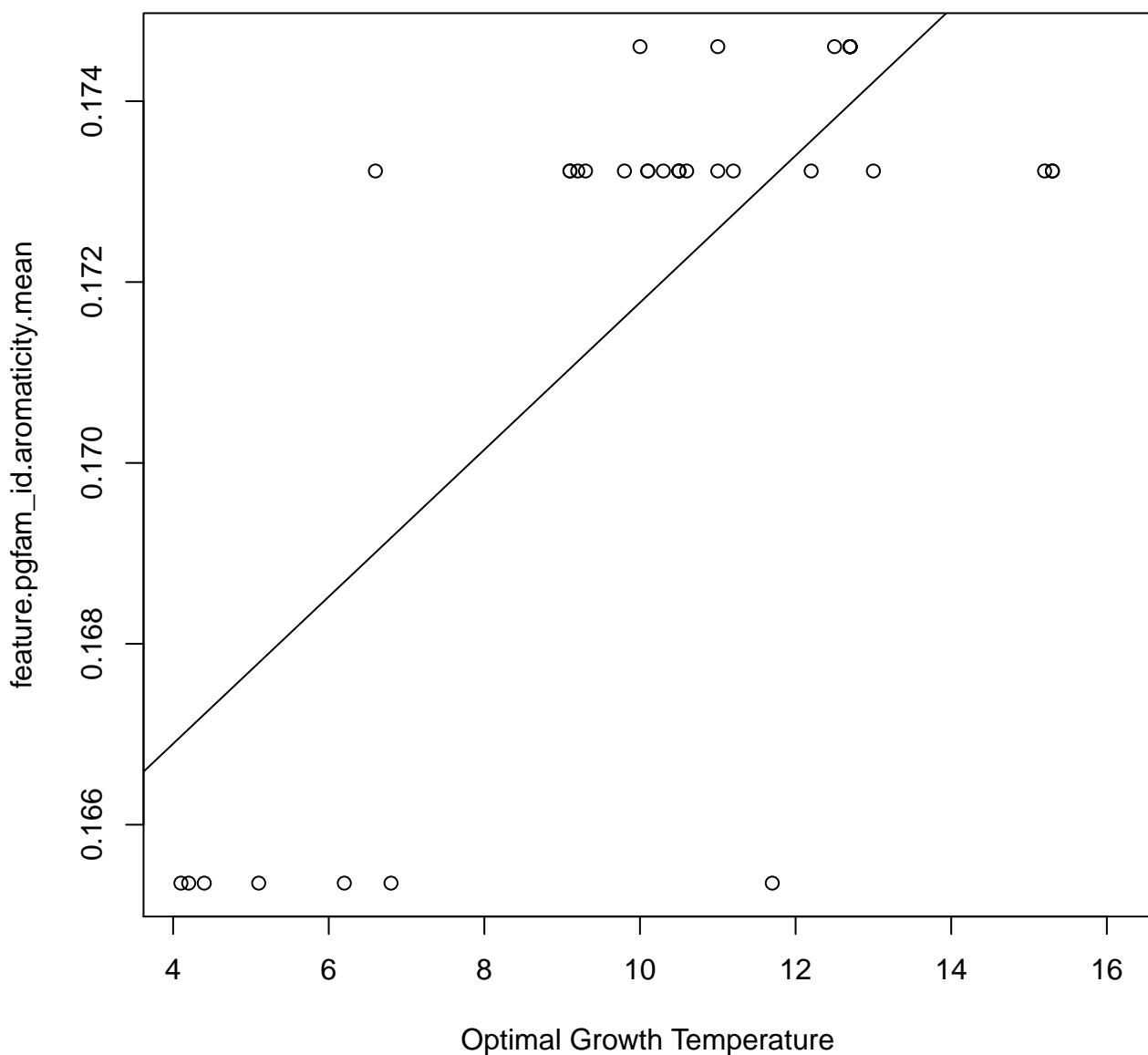
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Phosphoenolpyruvate synthase (EC 2.7.9.2)



feature.pgfam_id.aromaticity.mean

PGF 03072985

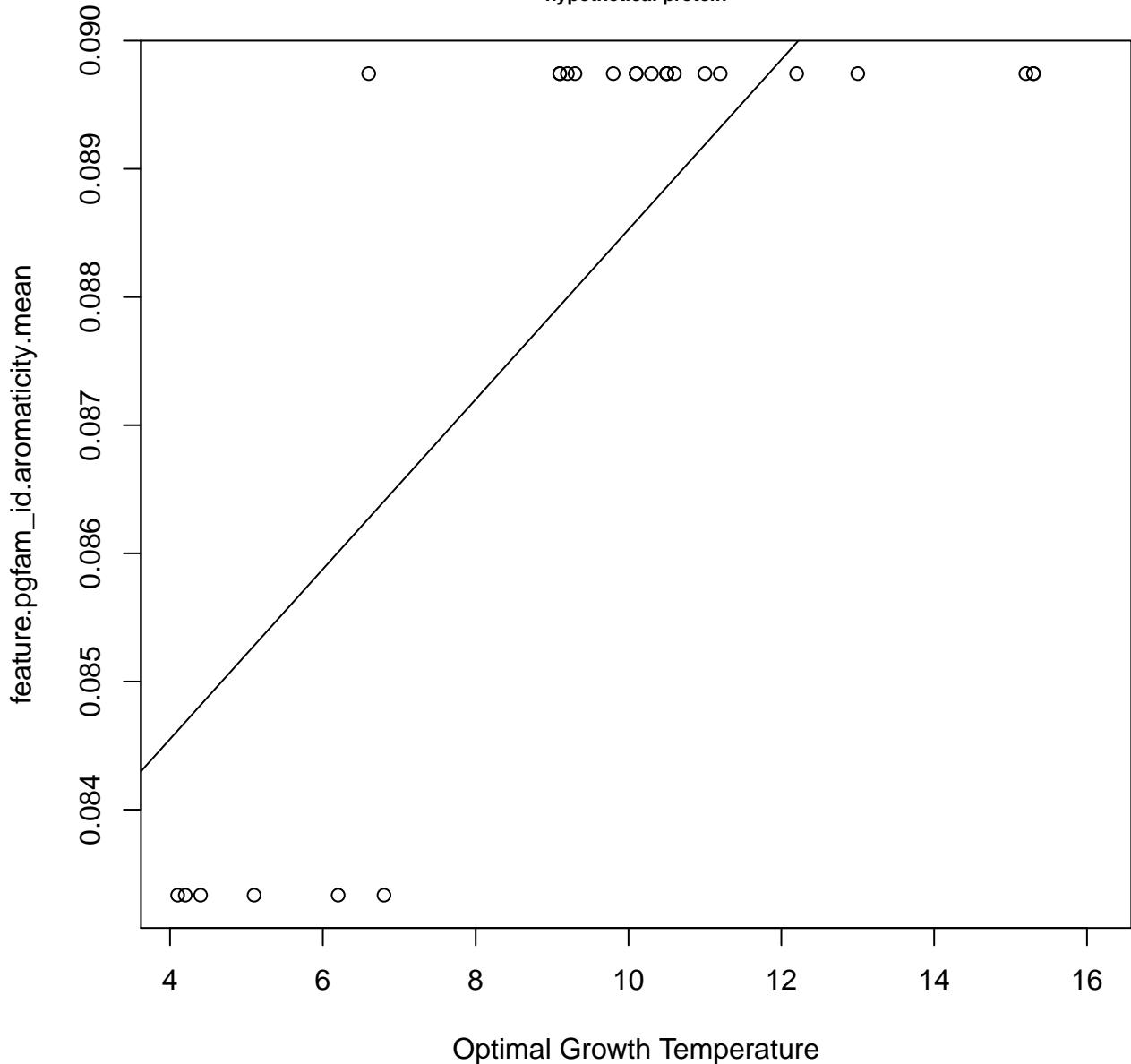
hypothetical protein



feature.pgfam_id.aromaticity.mean

PGF_04213500

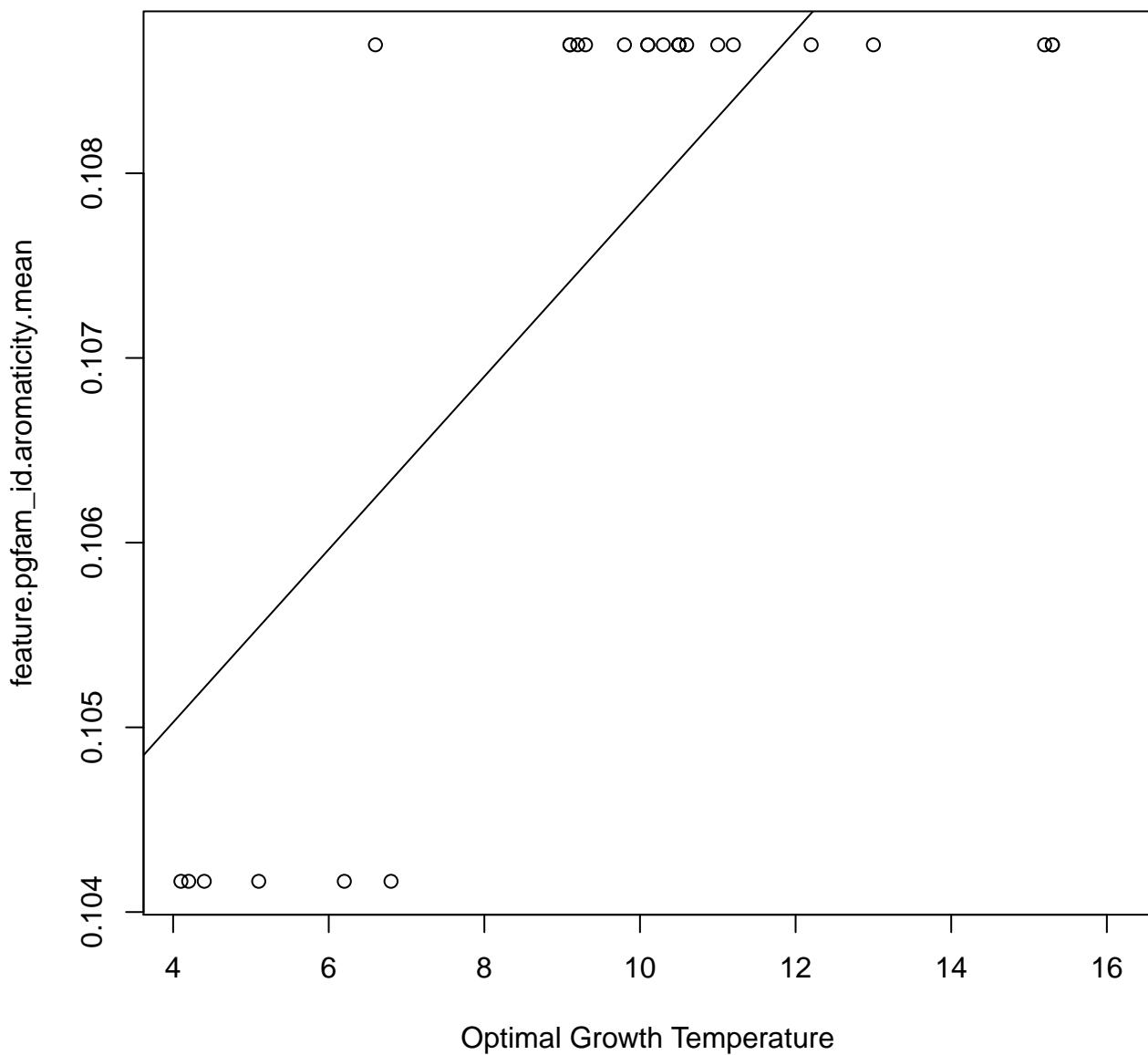
hypothetical protein



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PGF_12071964

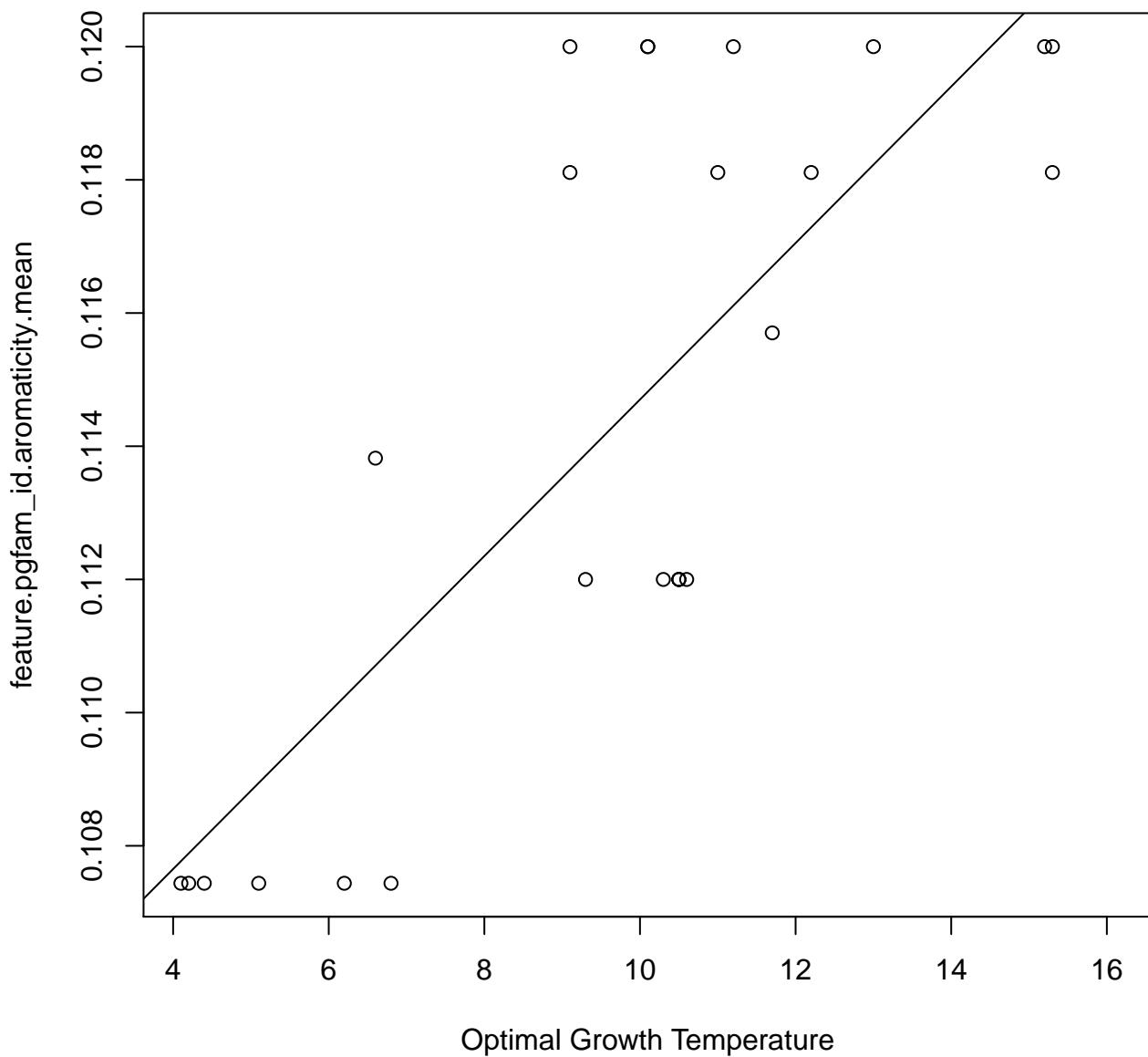
hypothetical protein



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PGF_08025863

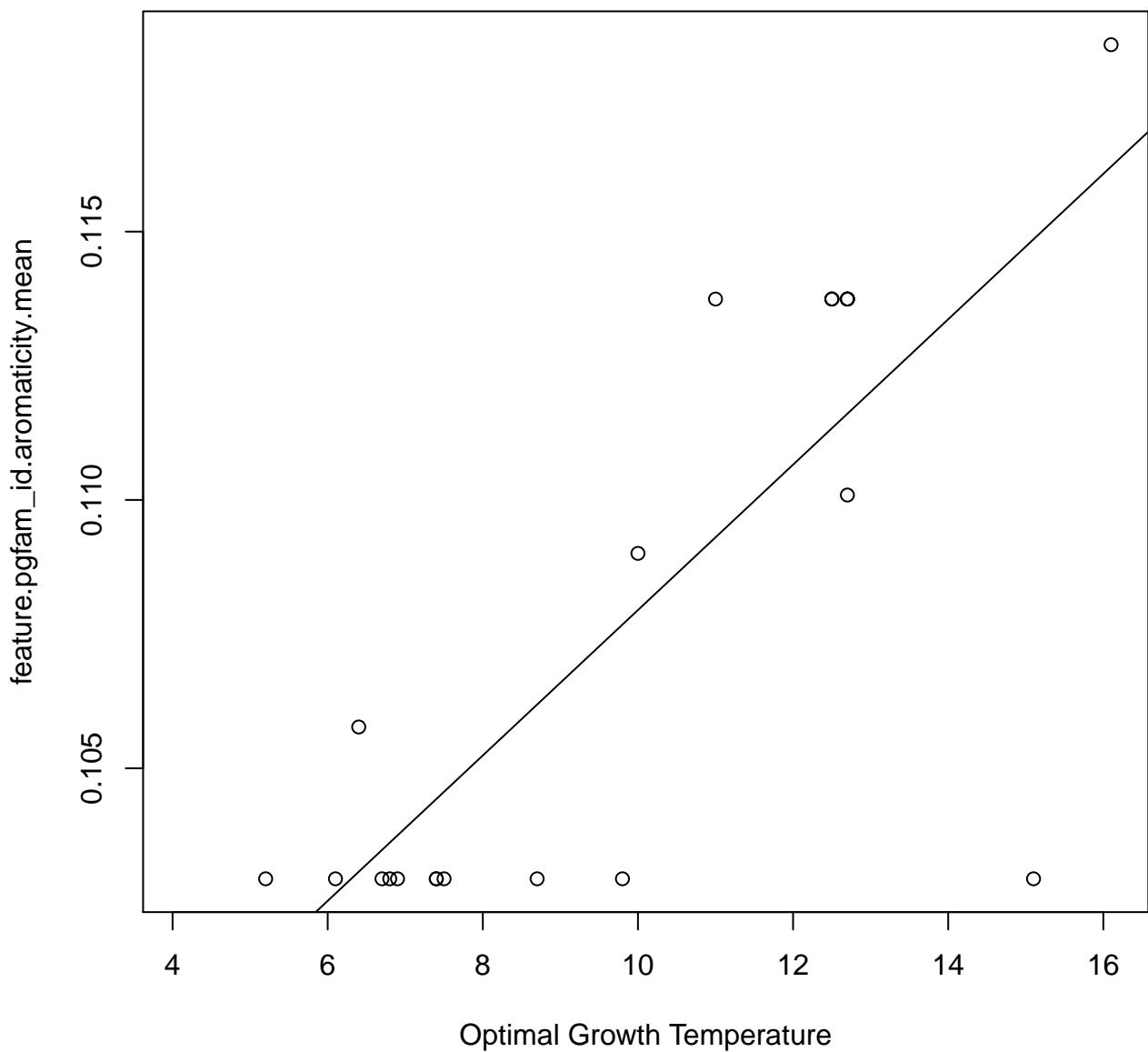
hypothetical protein



feature.pgfam_id.aromaticity.mean

PGF_02880814

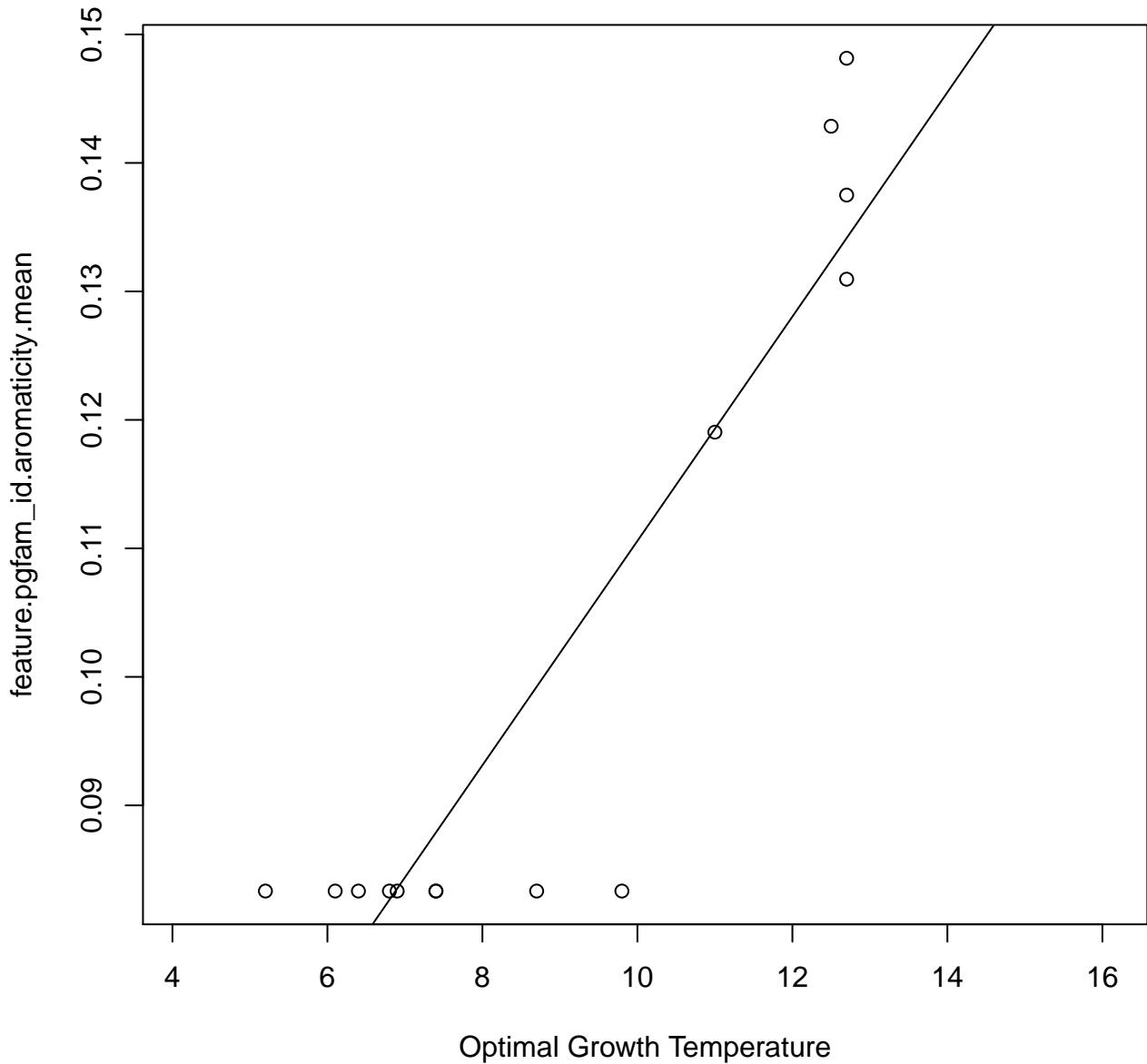
hypothetical protein



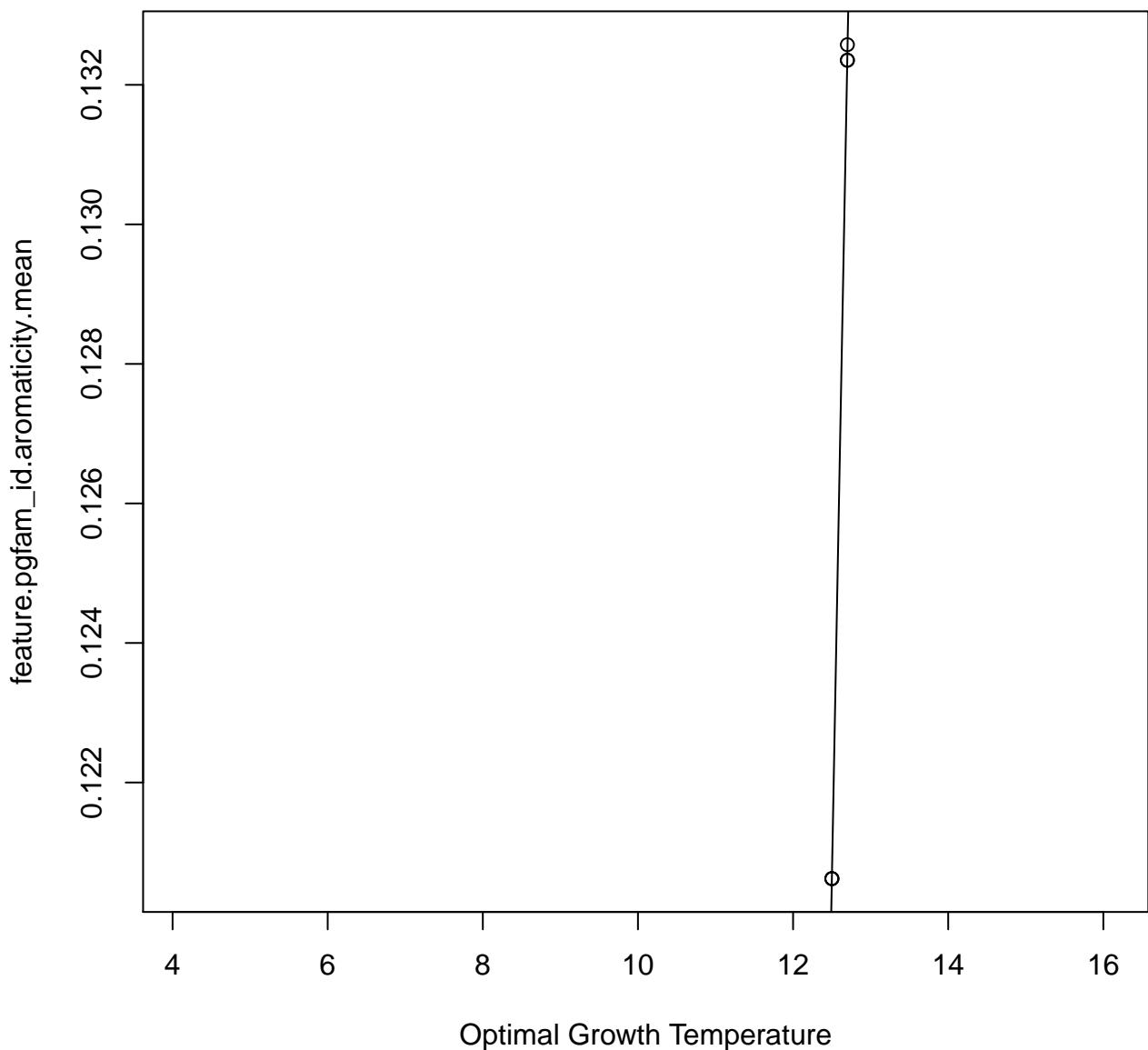
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PGF_01668026

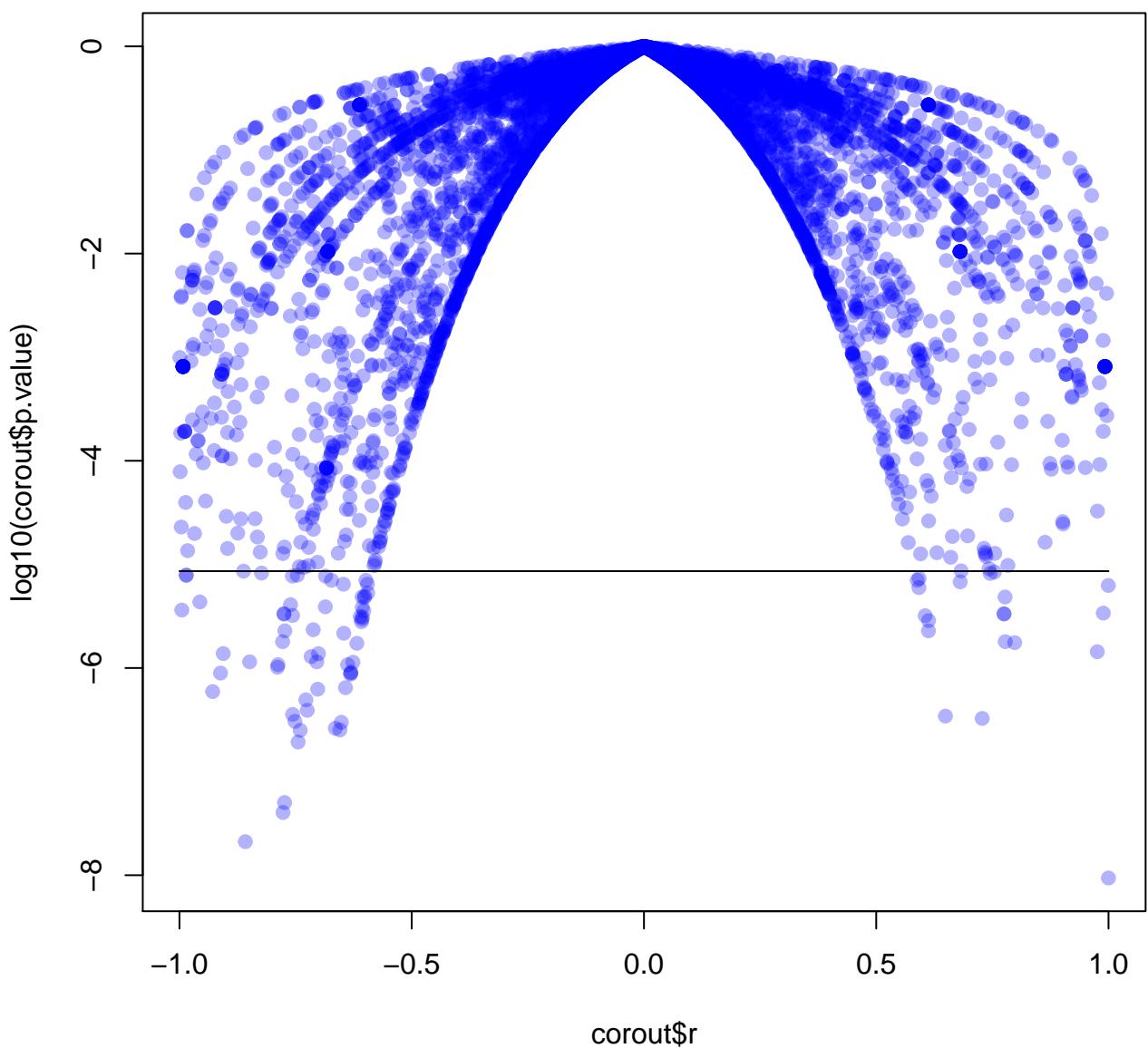
Glutaredoxin 3



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PGF_01336907
hypothetical protein



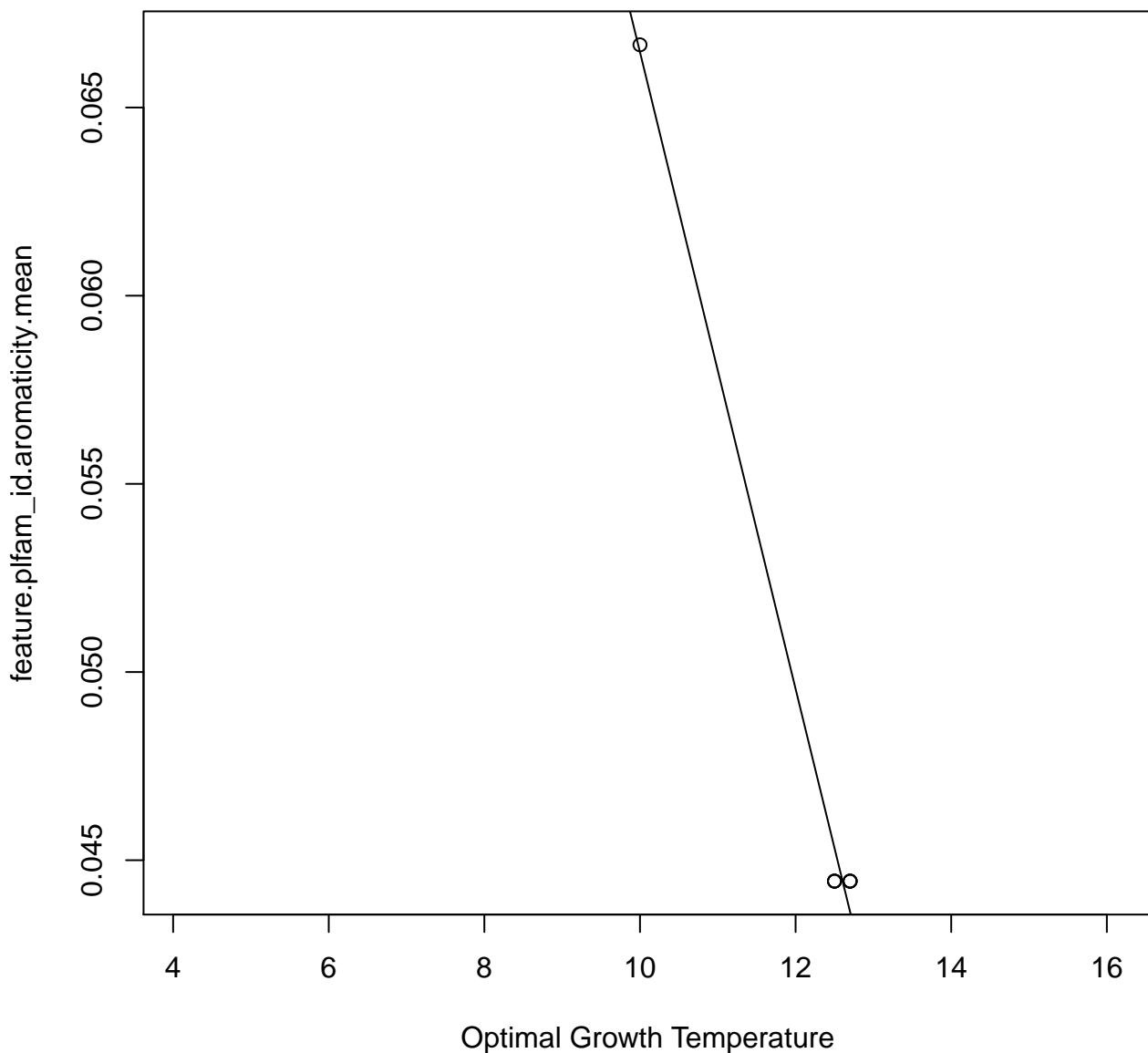
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feature.pfam_id.aromaticity.mean

PLF_28228_00004382

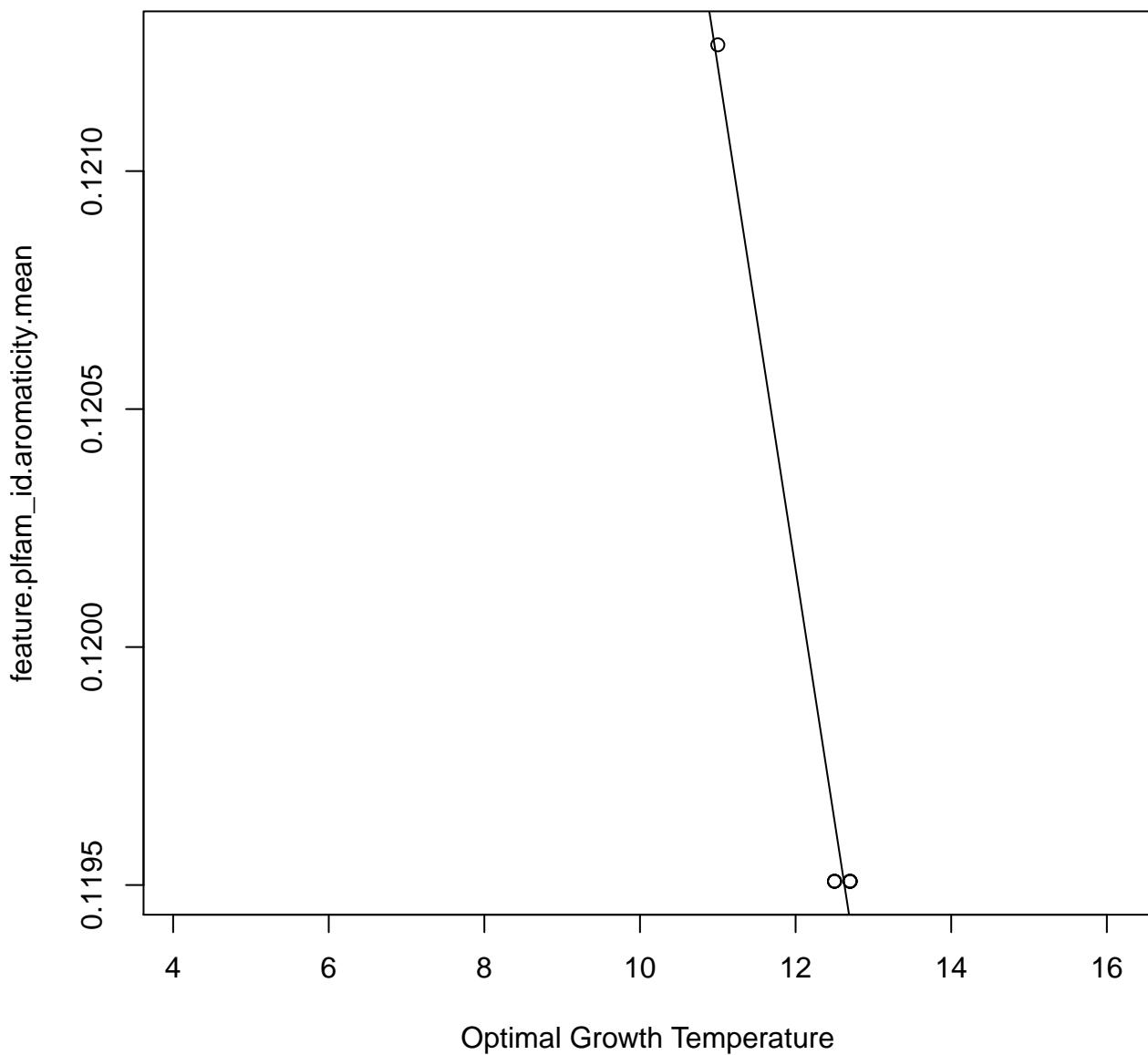
hypothetical protein



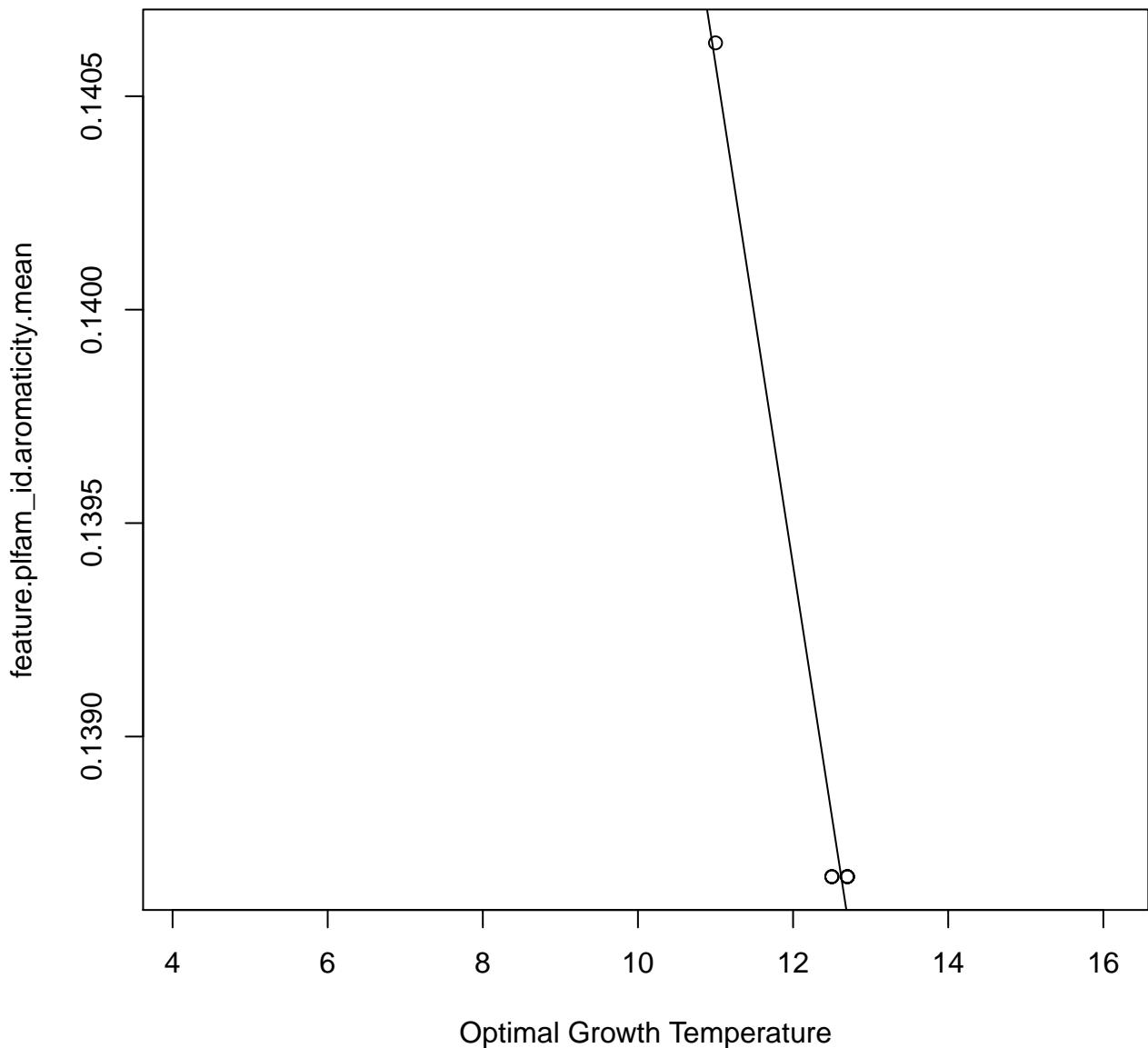
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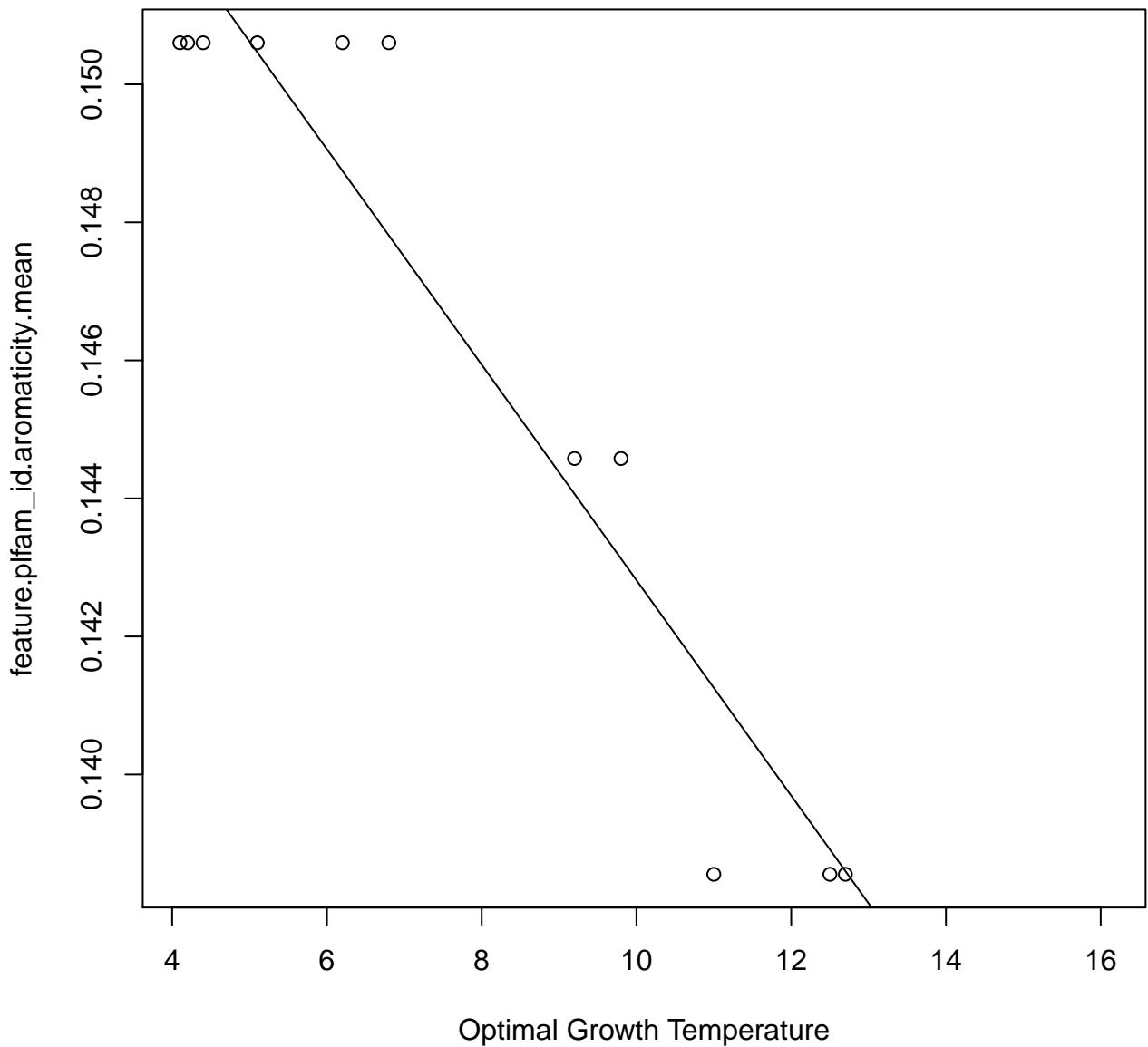
hypothetical protein



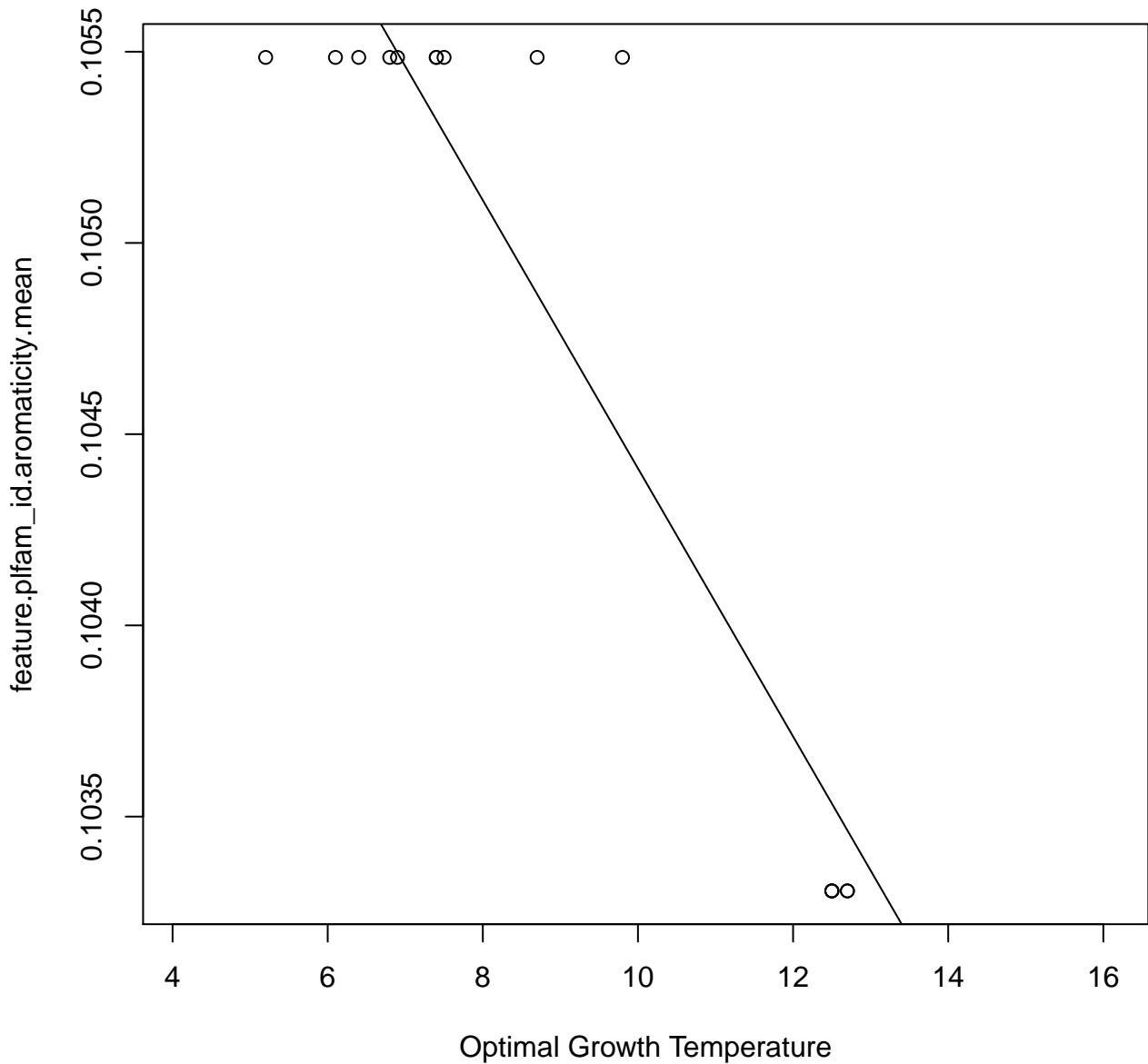
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PLF_28228_00003079
Arylsulfatase (EC 3.1.6.1)



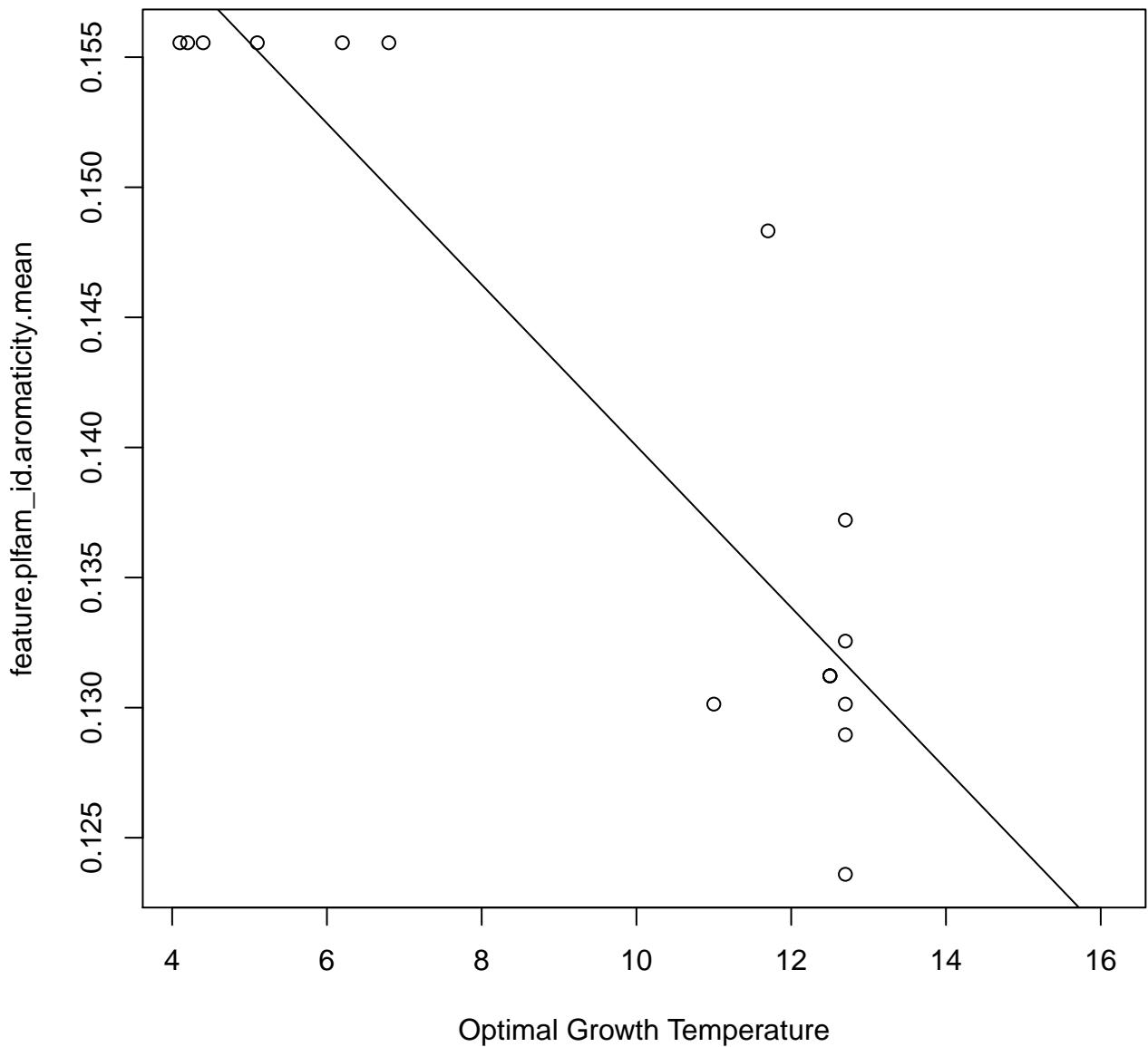
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PLF_28228_00028582
Peptide-methionine (S)-S-oxide reductase MsrA (EC 1.8.4.11)



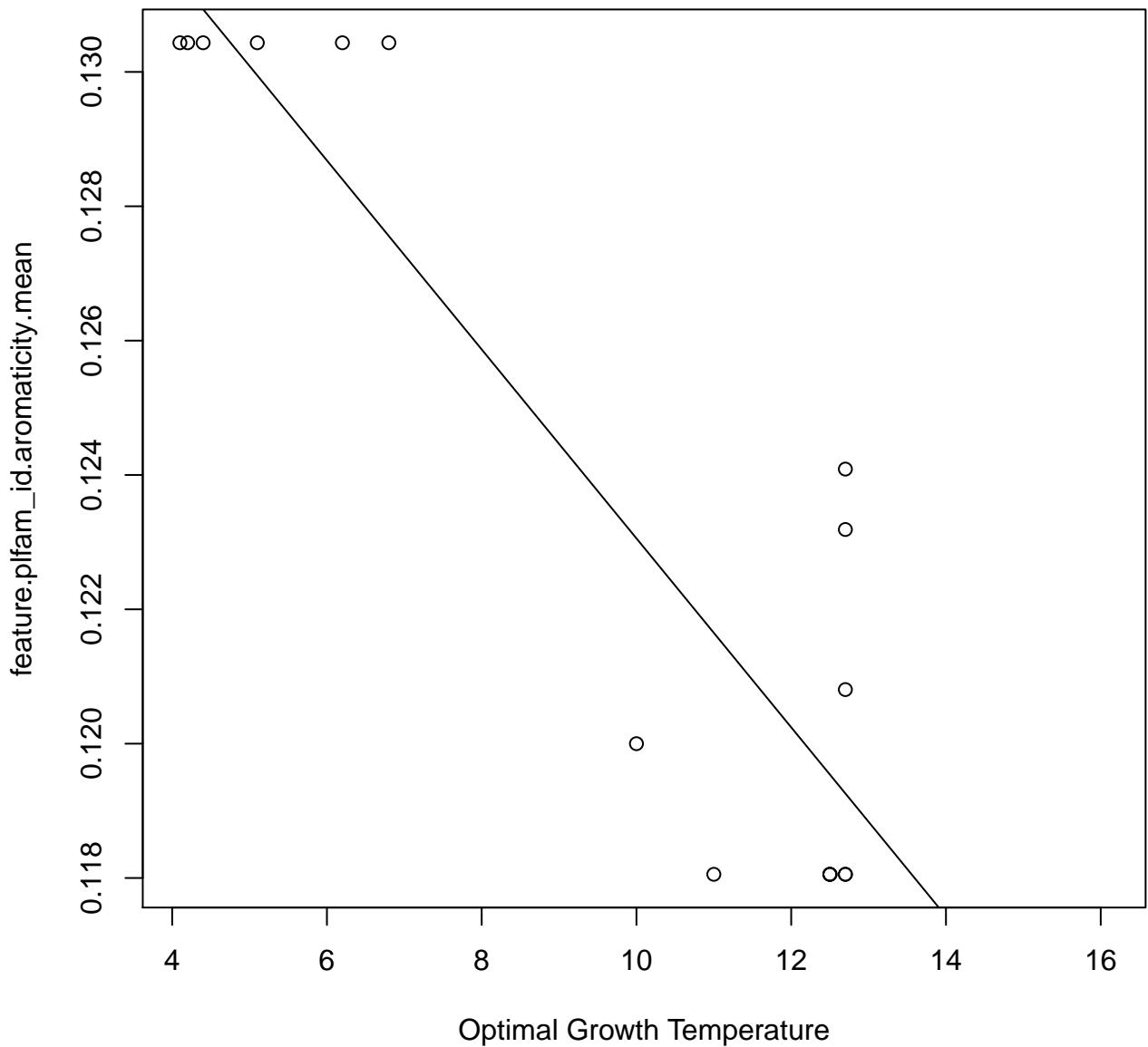
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PLF_28228_00007378
SapC-like S-layer protein



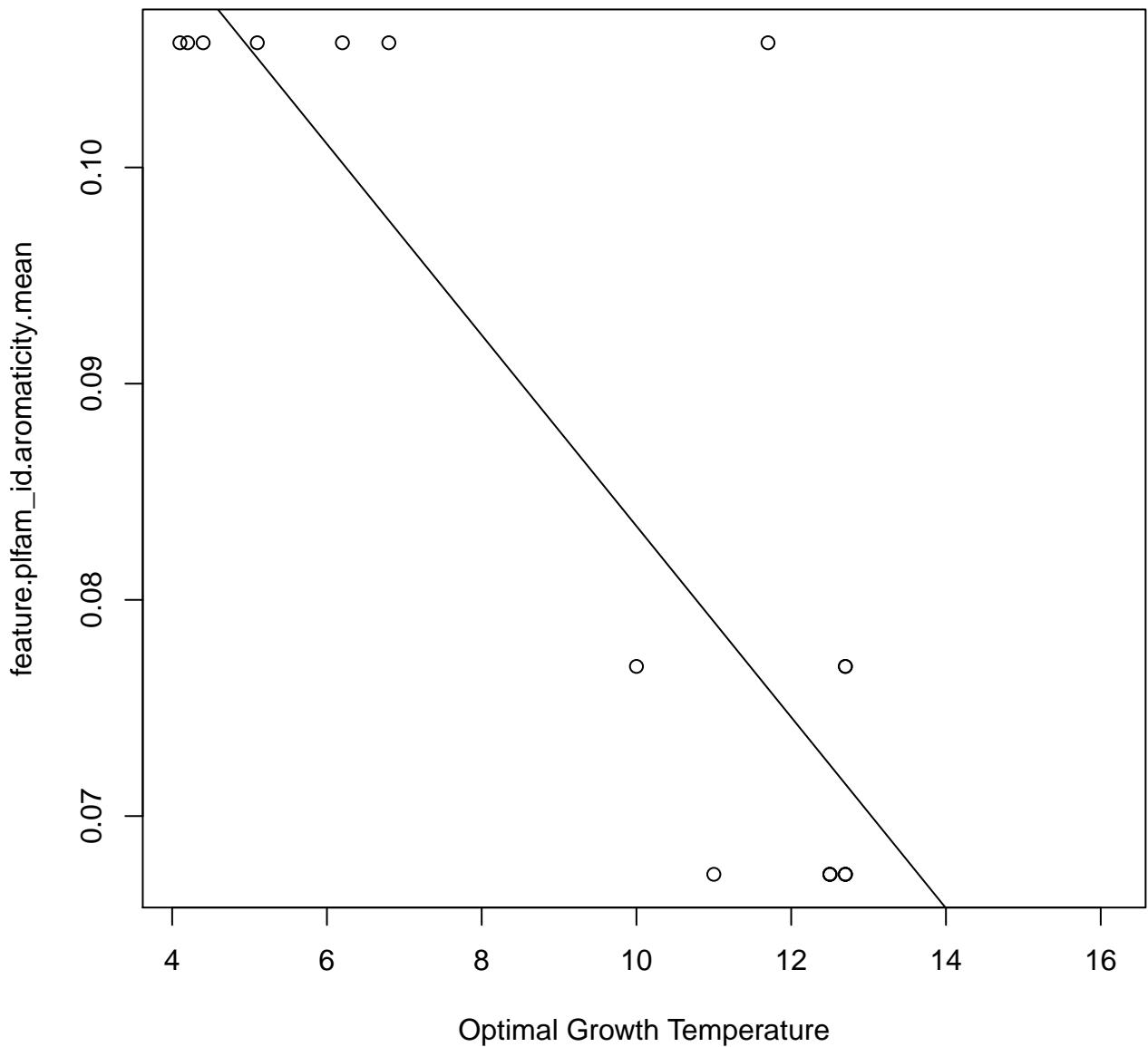
feature.plfam_id.aromaticity.mean
PLF_28228_00002761
Uncharacterized MFS-type transporter



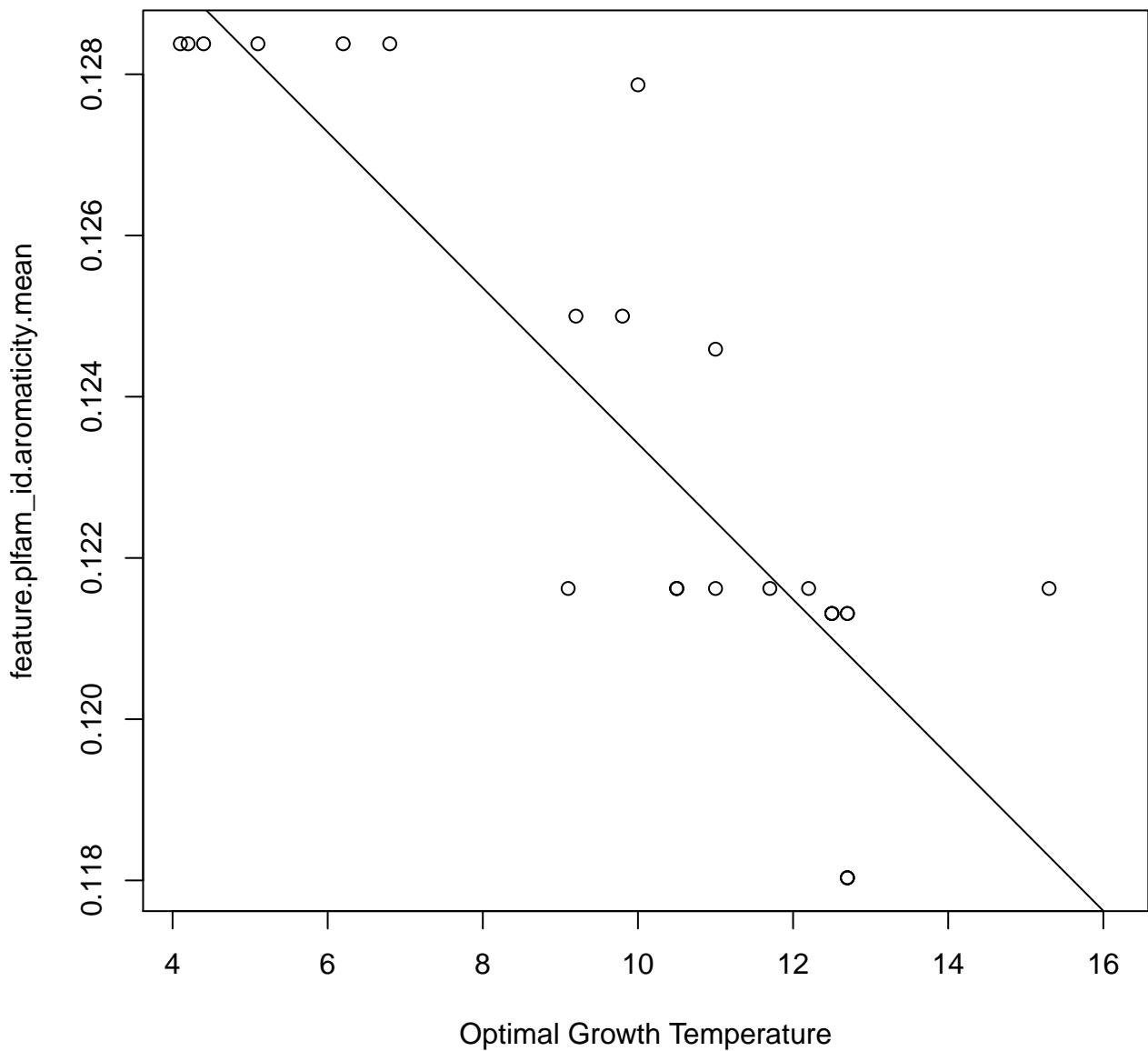
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Outer membrane beta-barrel assembly protein BamE



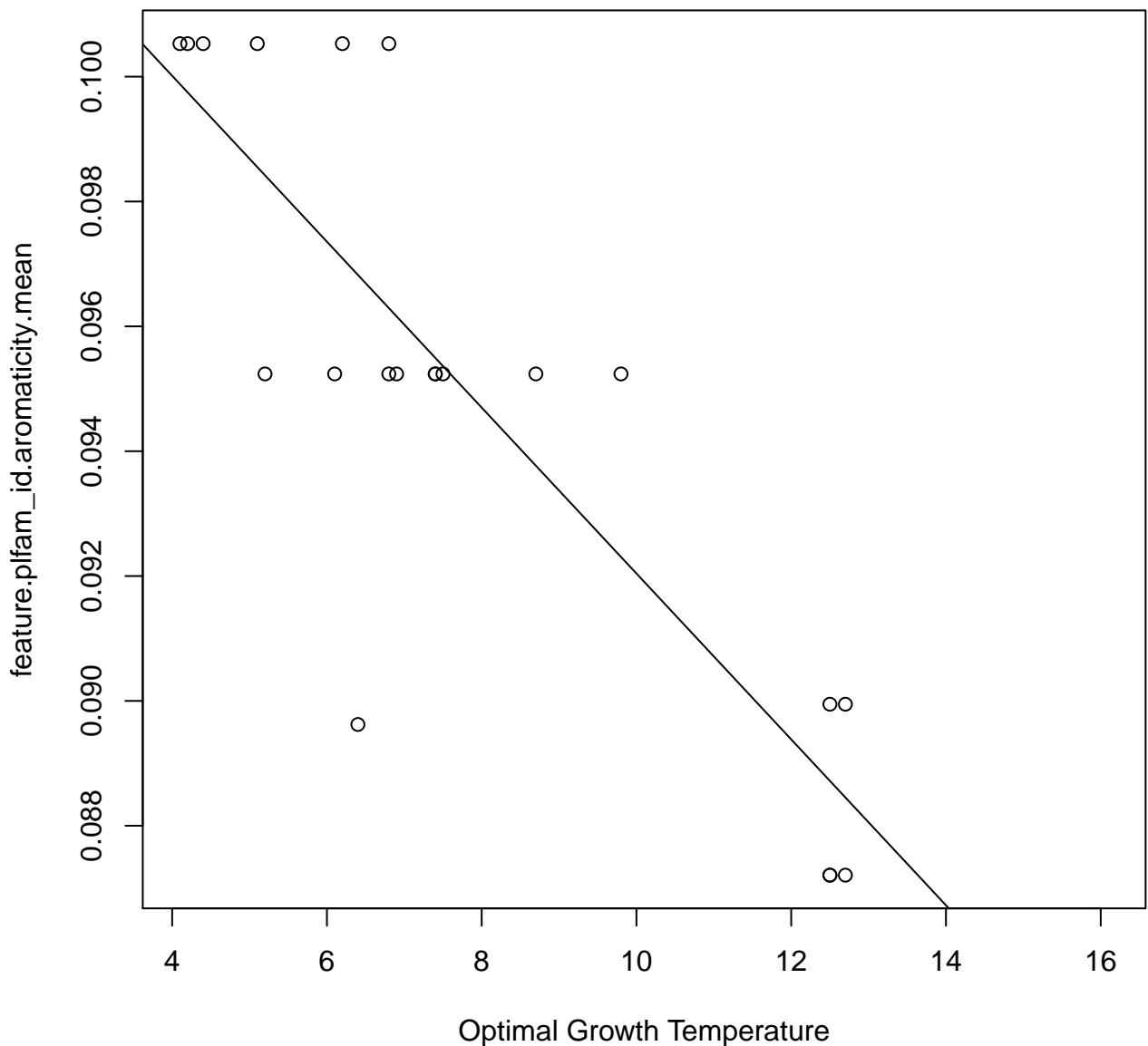
feature.pifam_id.aromaticity.mean
PLF_28228_00001489
RNA polymerase-binding transcription factor DksA



feature.plfam_id.aromaticity.mean
PLF_28228_00001856
GGDEF domain protein



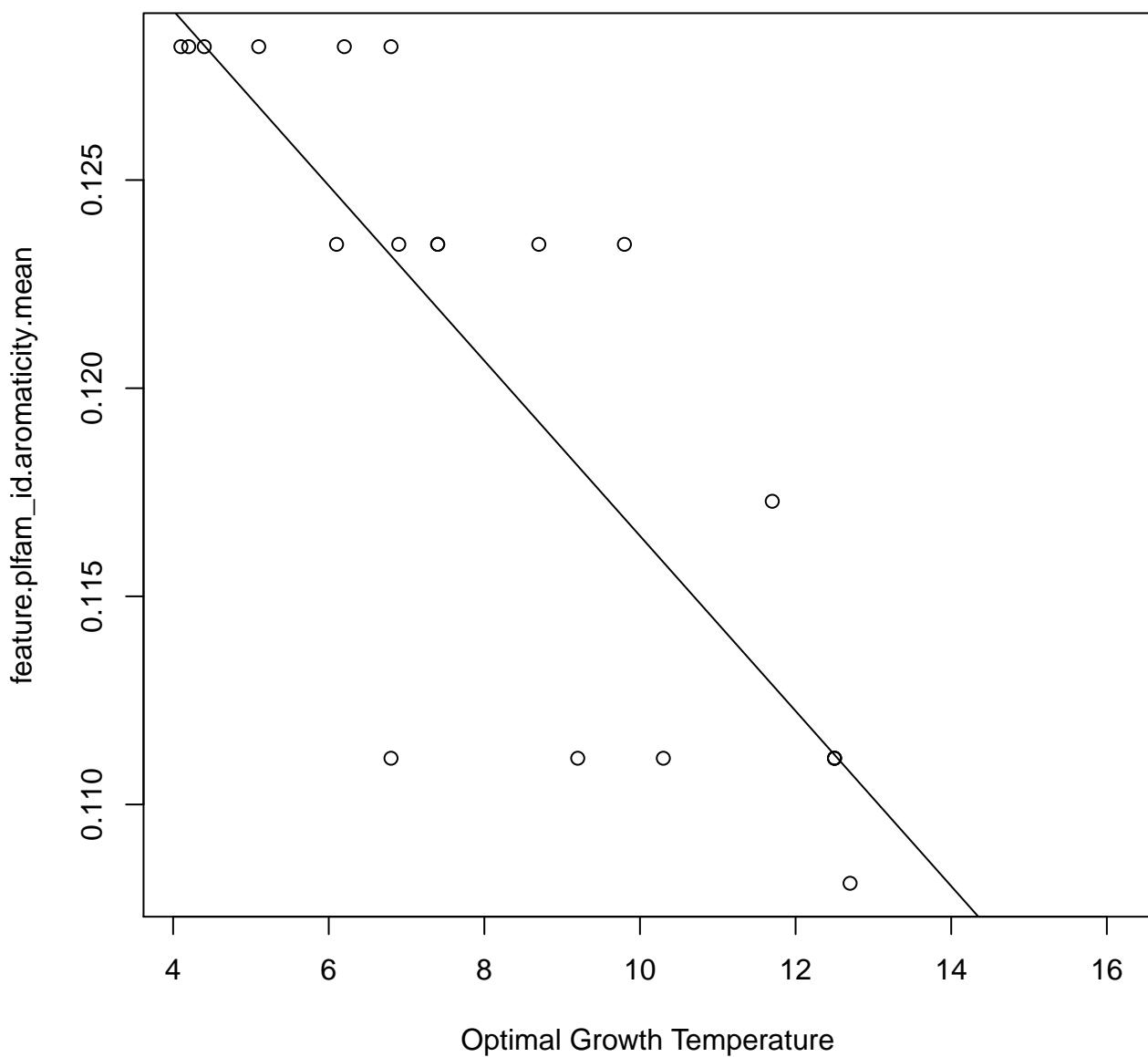
feature.plfam_id.aromaticity.mean
PLF_28228_00014224
FIG006045: Sigma factor, ECF subfamily



feature.plfam_id.aromaticity.mean

PLF_28228_00005149

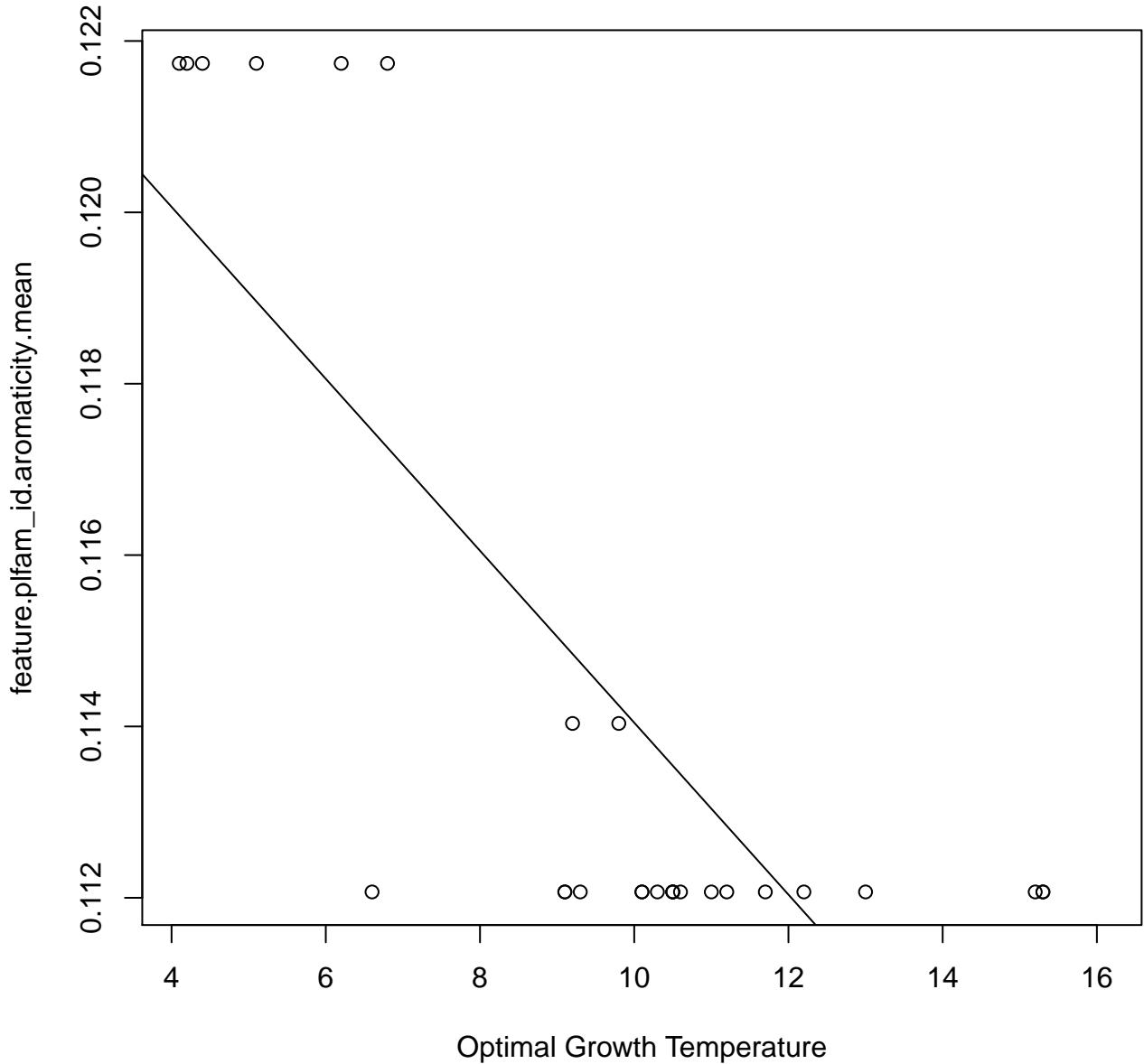
hypothetical protein



feature.pfam_id.aromaticity.mean

PLF_28228_00016319

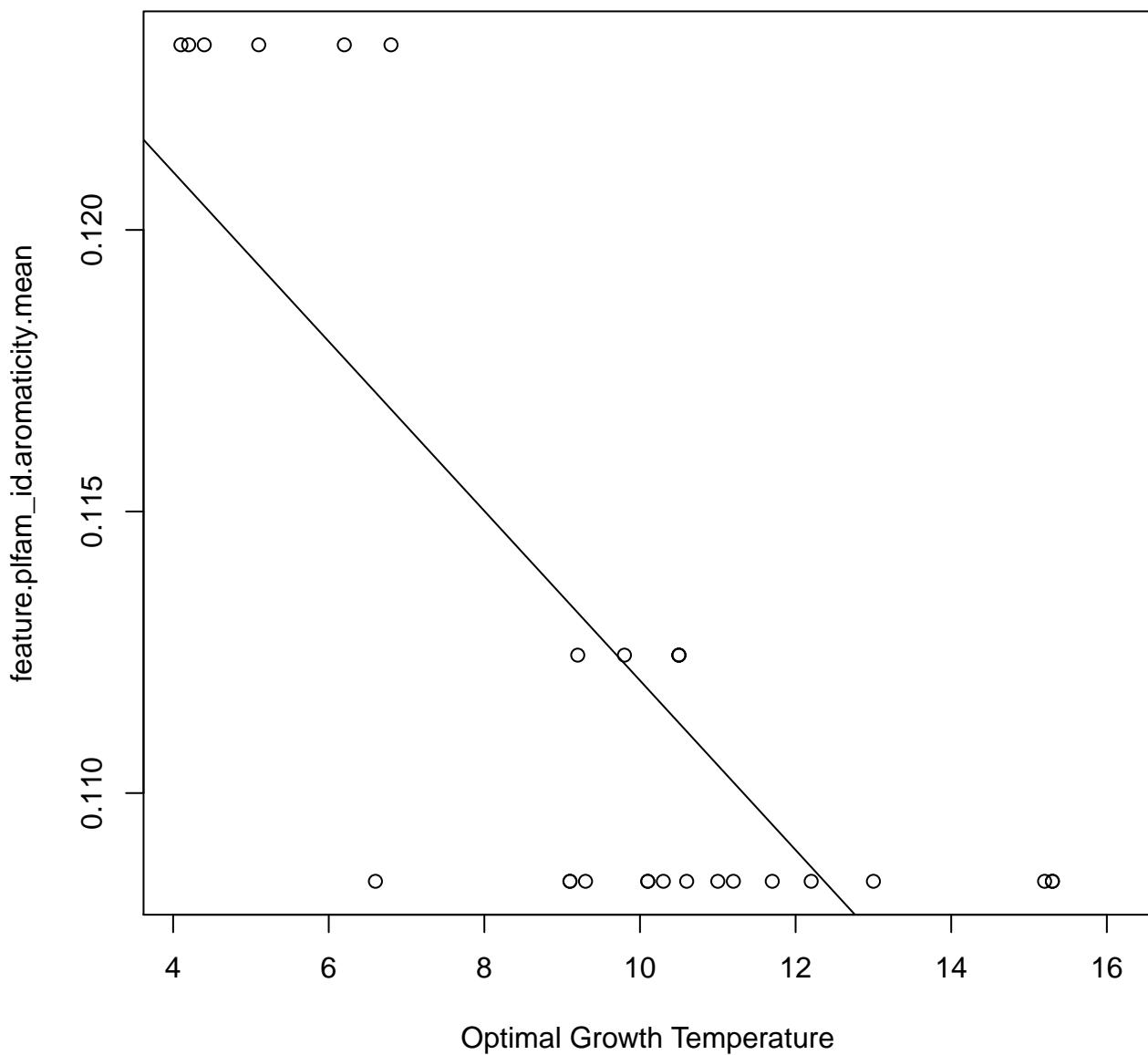
hypothetical protein



feature.pifam_id.aromaticity.mean

PLF_28228_00031426

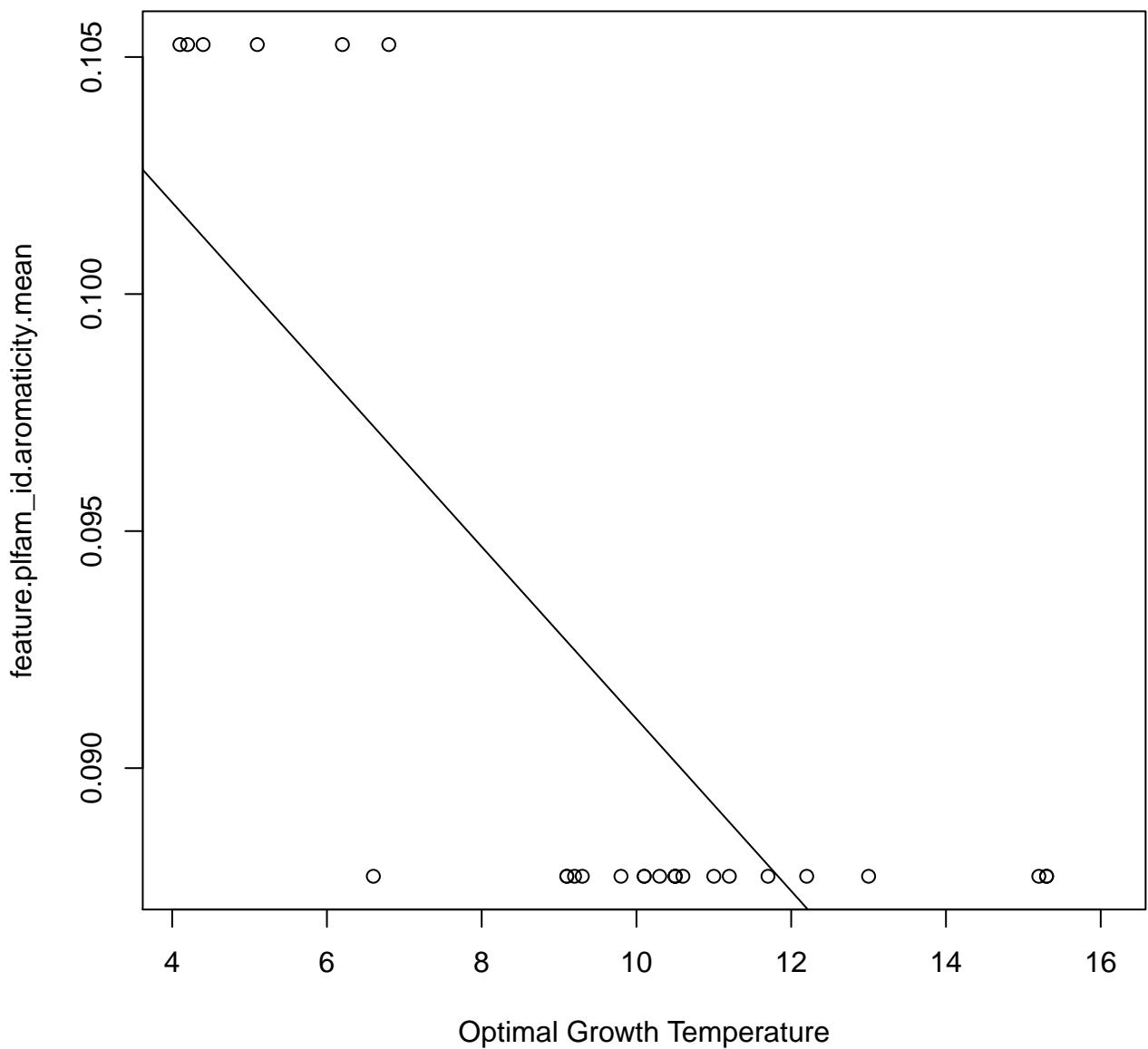
hypothetical protein



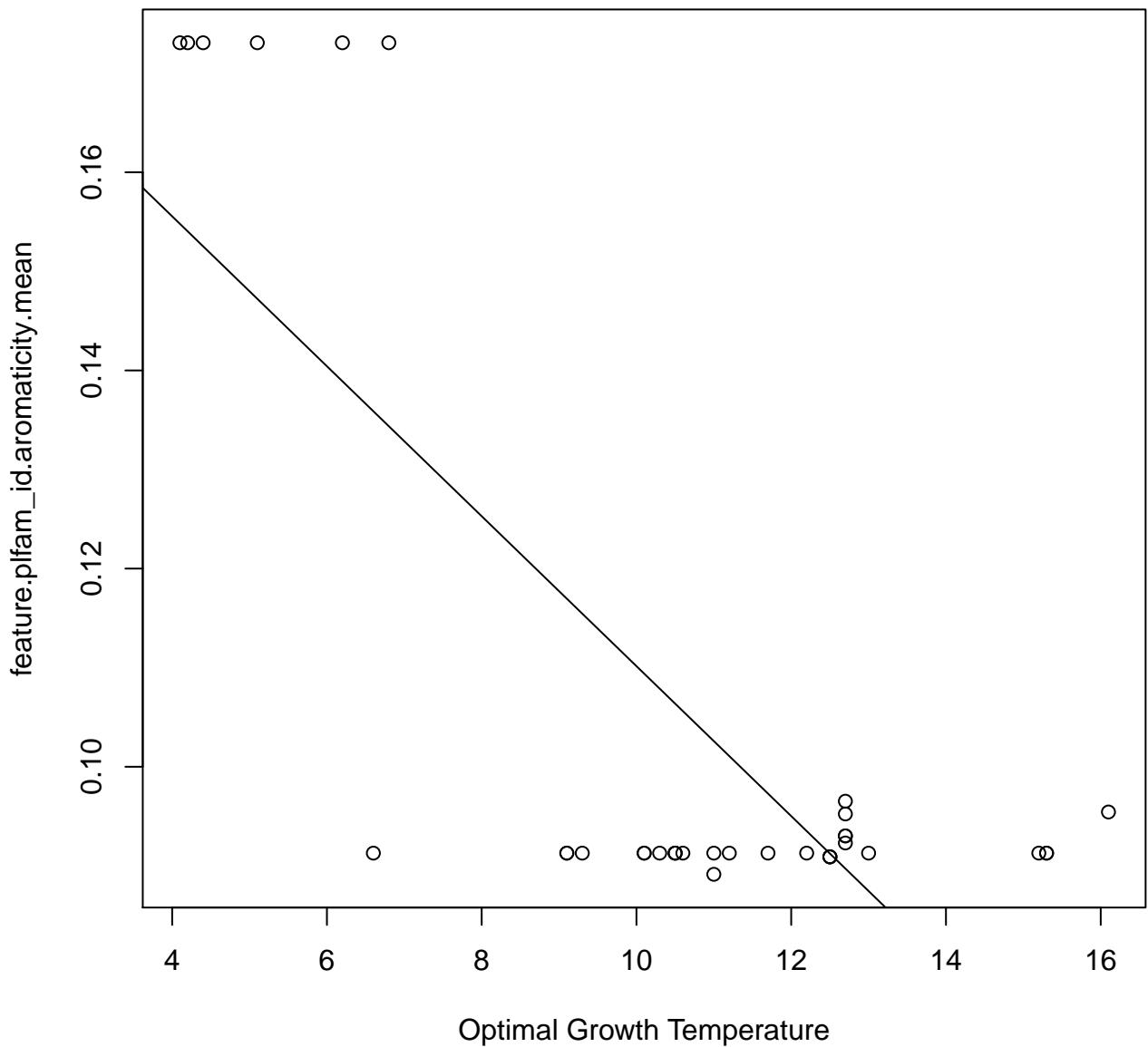
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PLF_28228_00022617

hypothetical protein



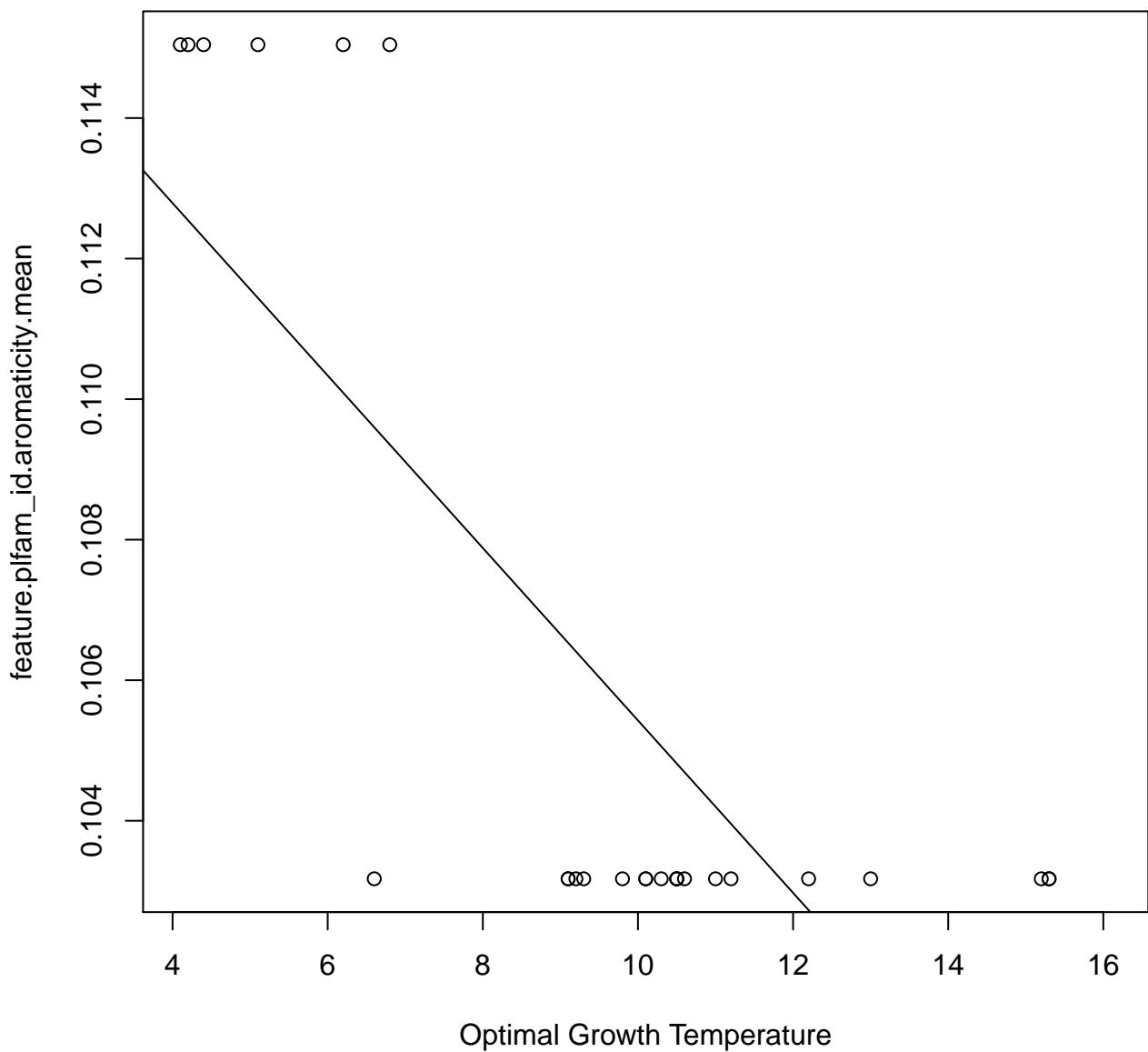
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PLF_28228_00002798
Two-component transcriptional response regulator, OmpR family



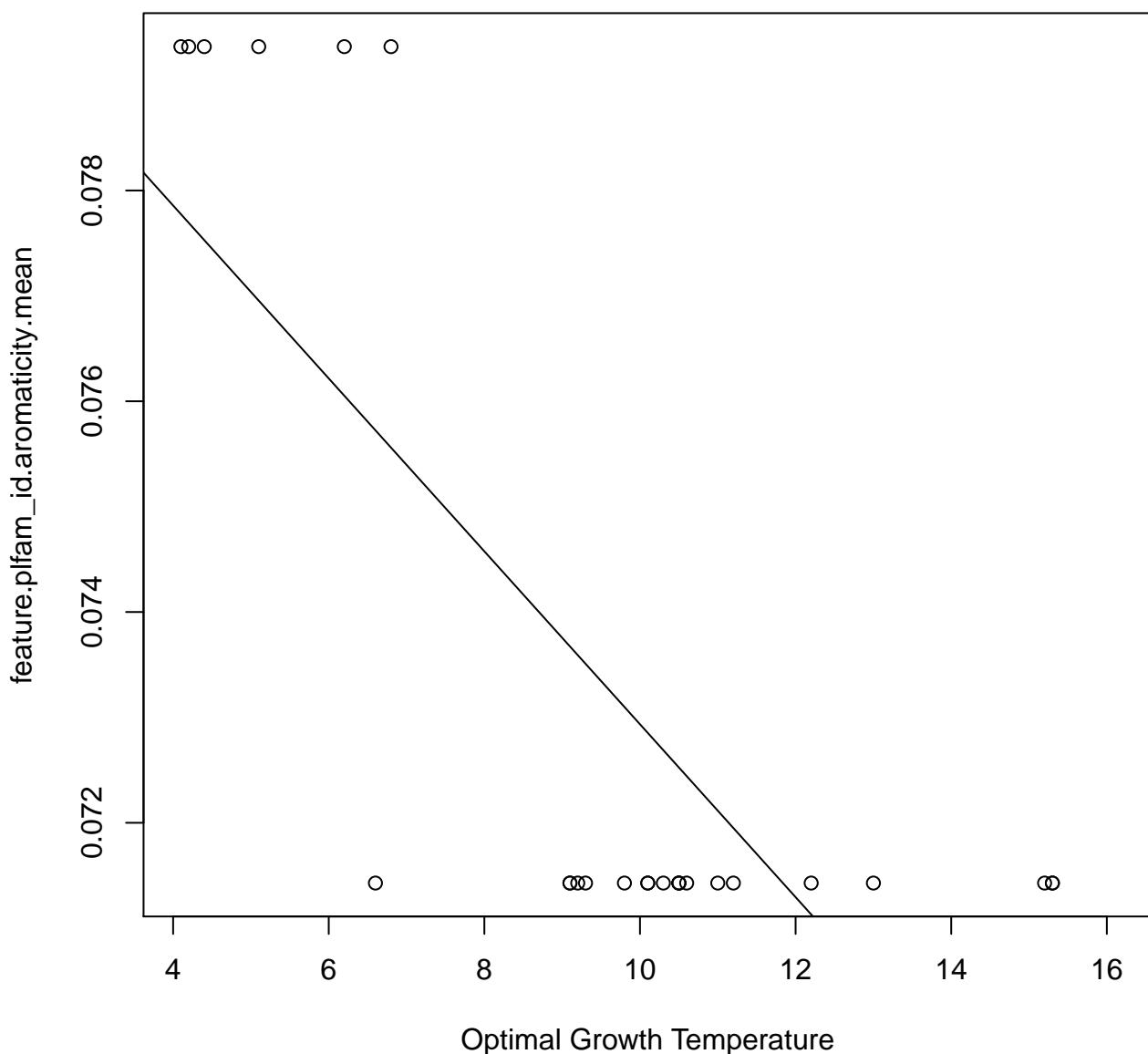
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PLF_28228_00030076

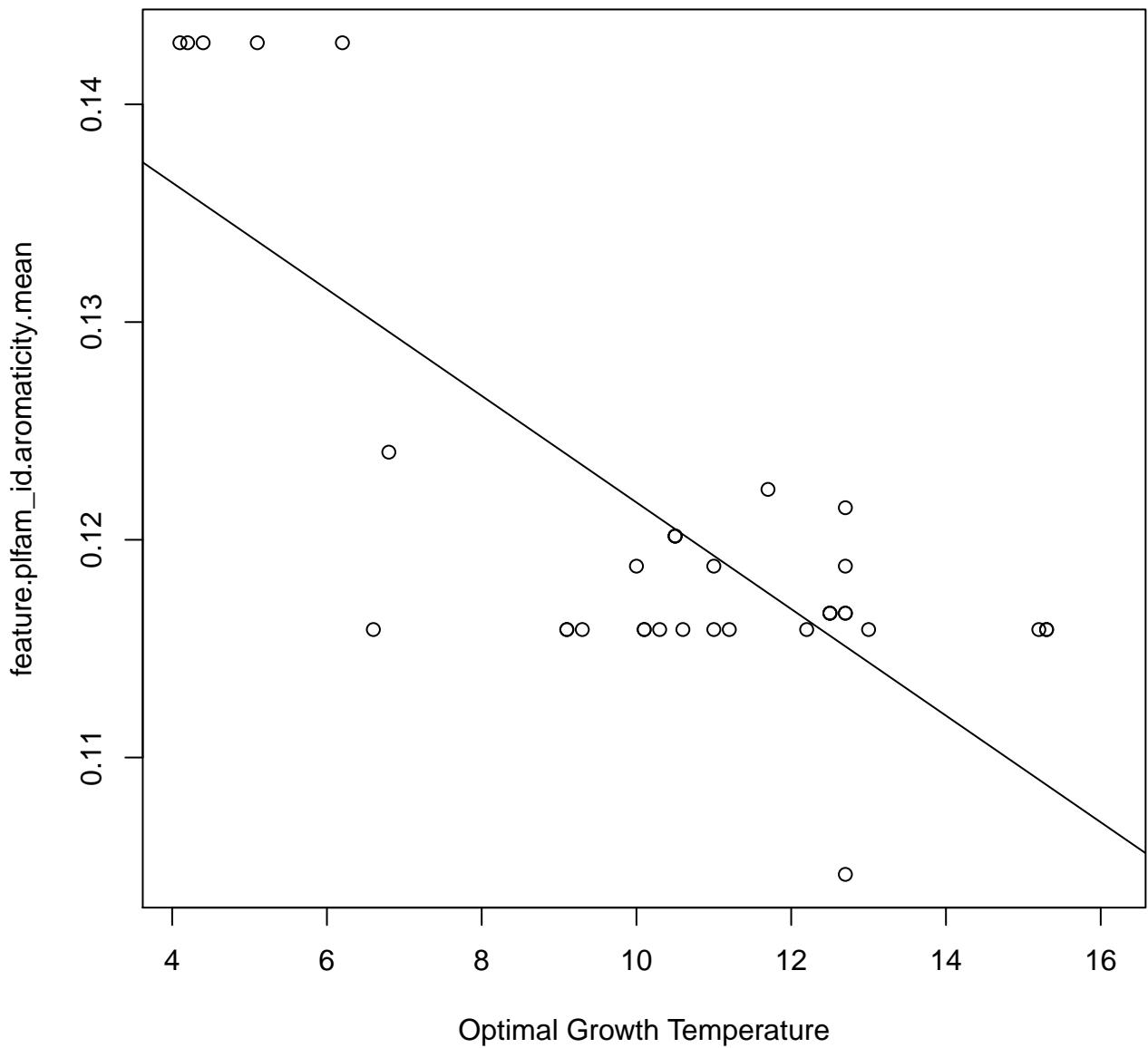
hypothetical protein



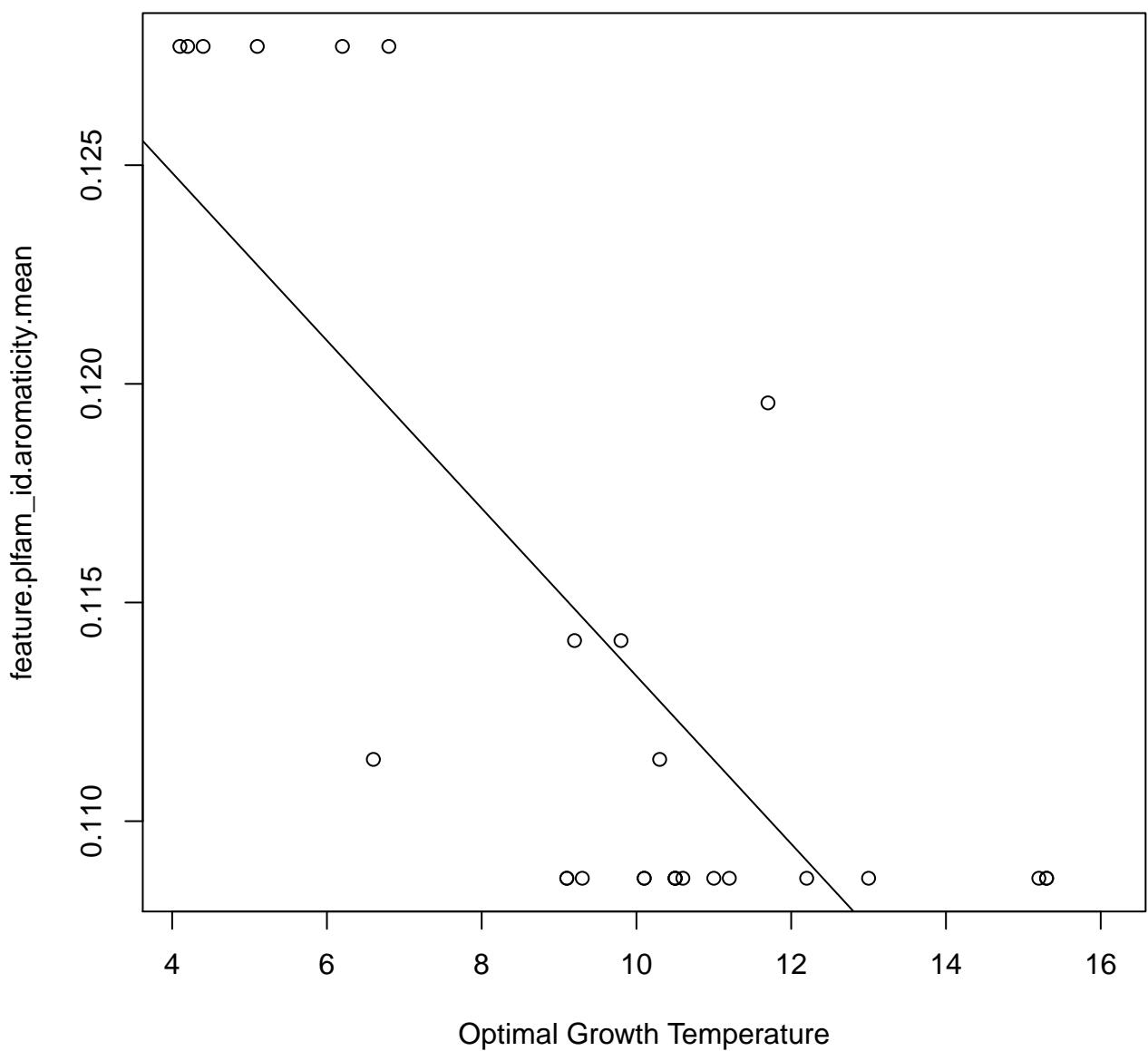
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PLF_28228_00030463
hypothetical protein



feature.plfam_id.aromaticity.mean
PLF_28228_00001289
Uncharacterized protease YegQ



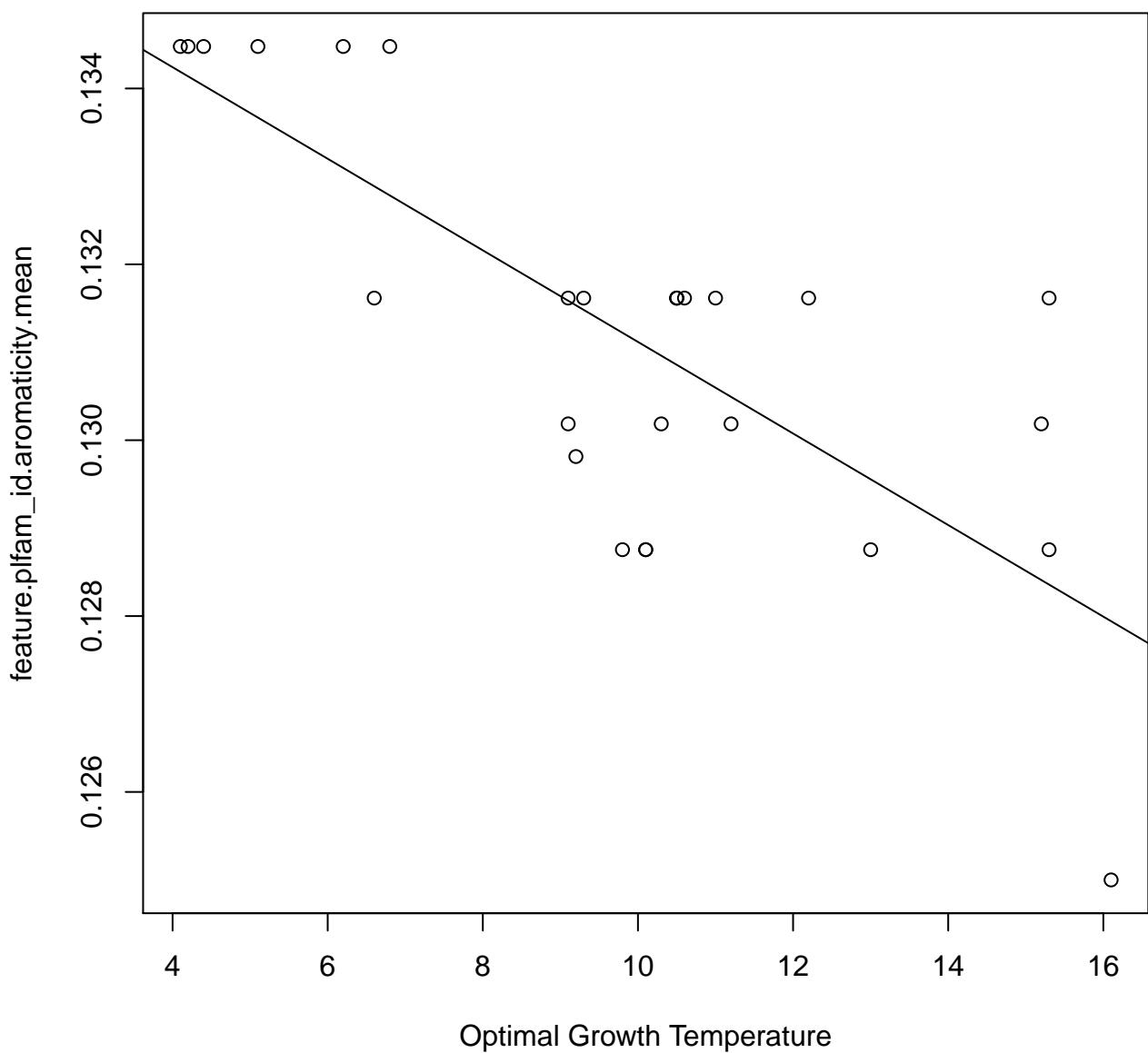
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PLF_28228_00032200
hypothetical protein



feature.plfam_id.aromaticity.mean

PLF_28228_00016855

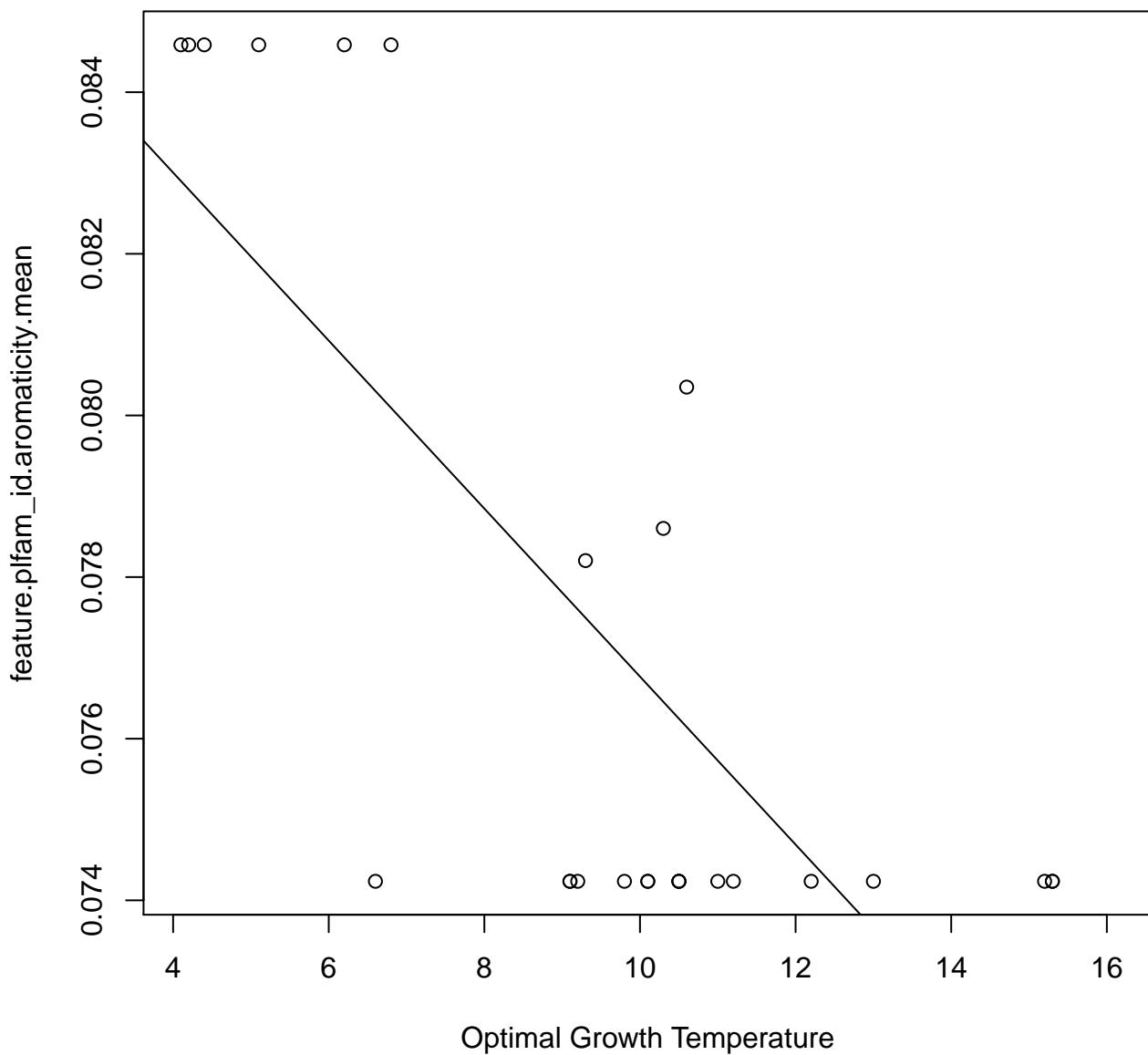
hypothetical protein



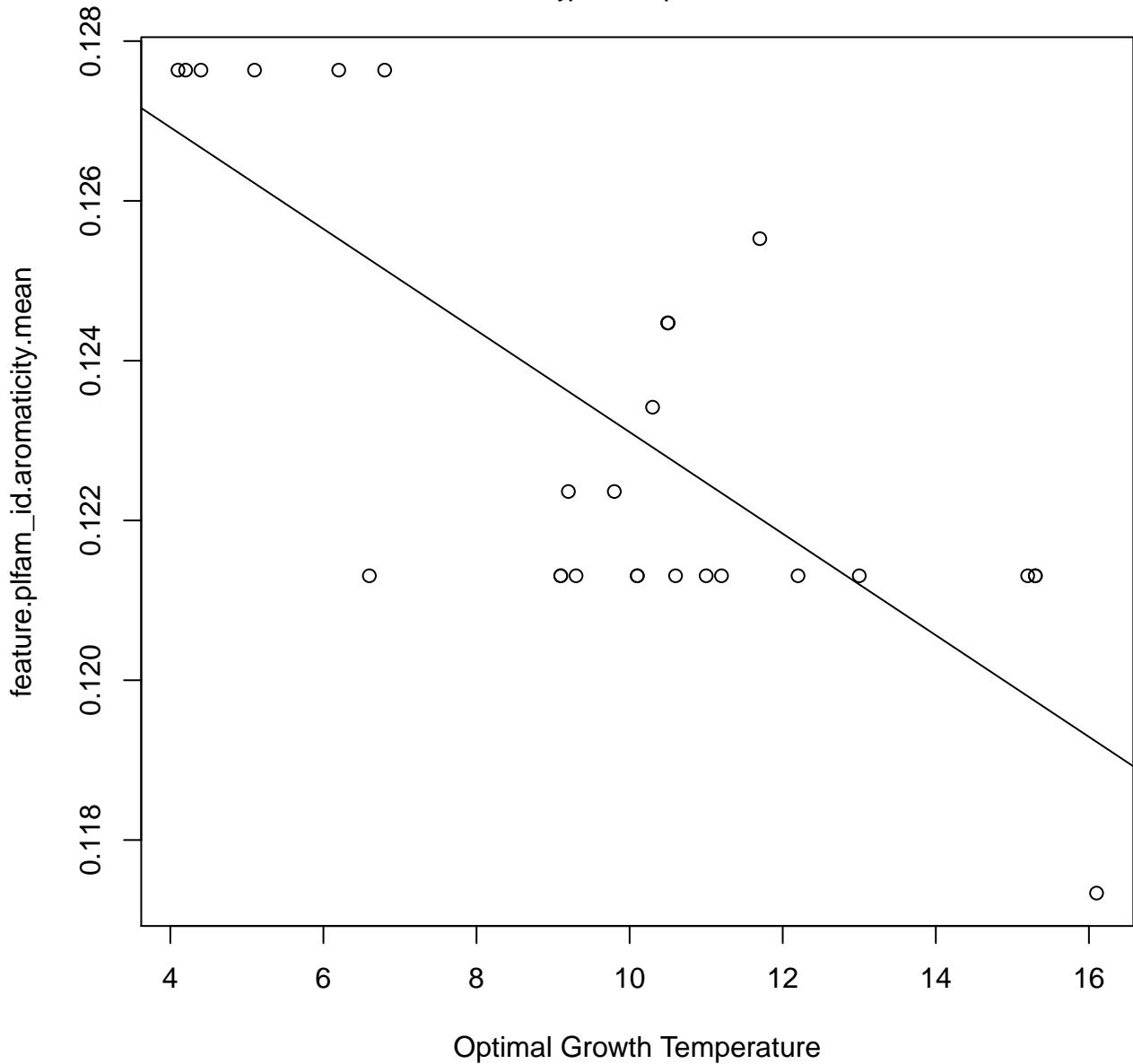
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PLF_28228_00015307

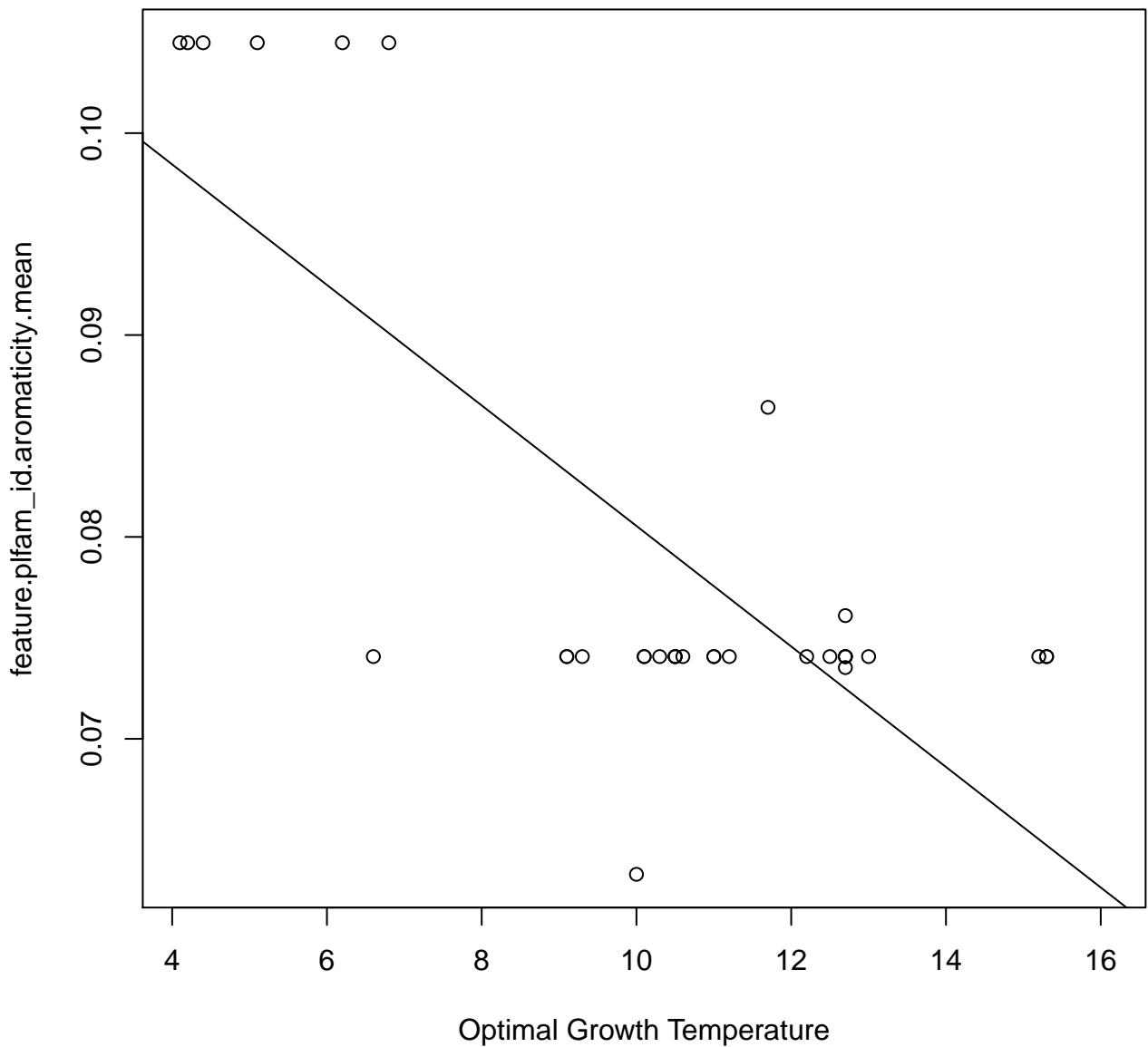
hypothetical protein



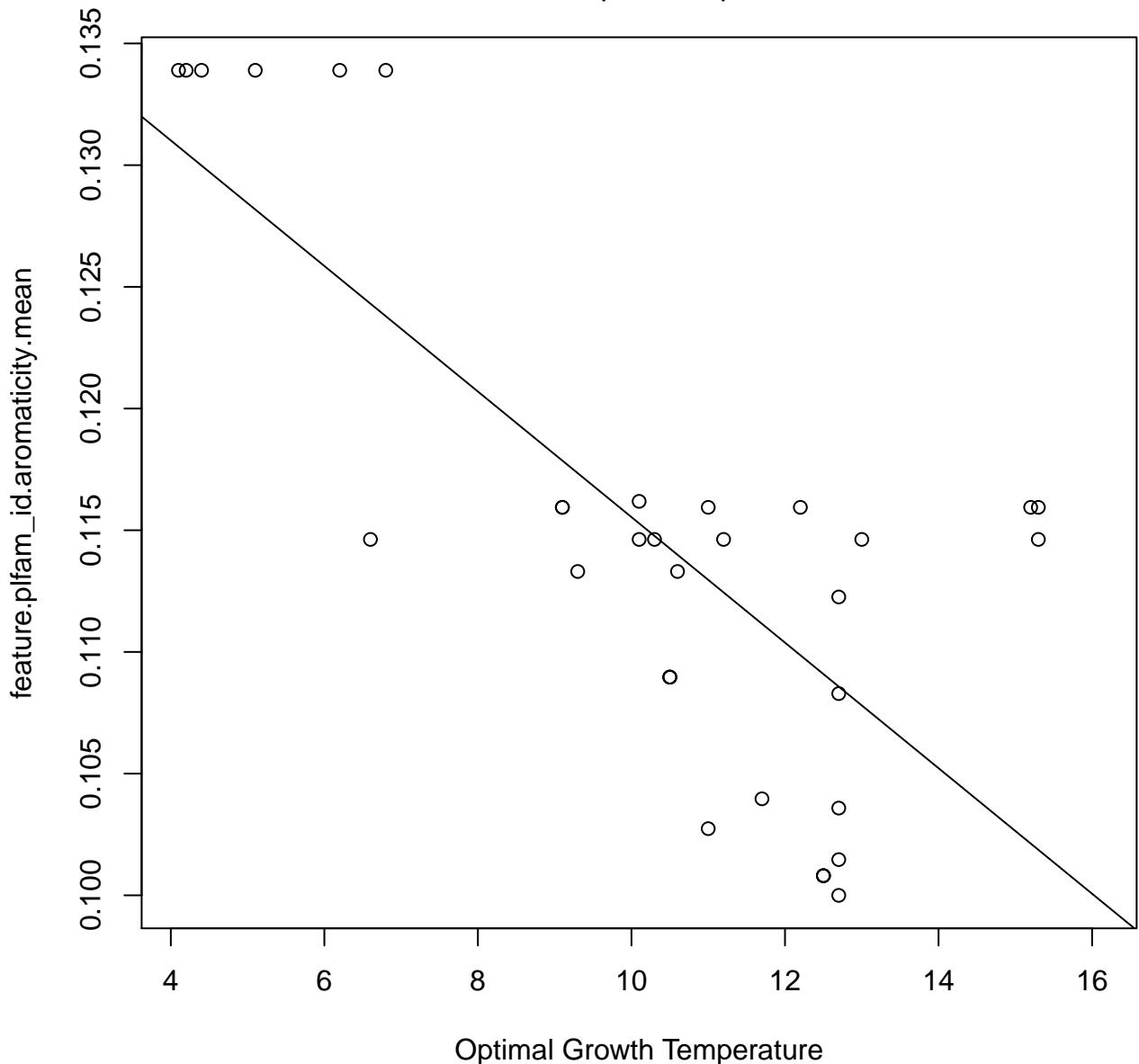
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PLF_28228_00013222
hypothetical protein



feature.plfam_id.aromaticity.mean
PLF_28228_00014184
Uncharacterized ferredoxin-like protein YfhL



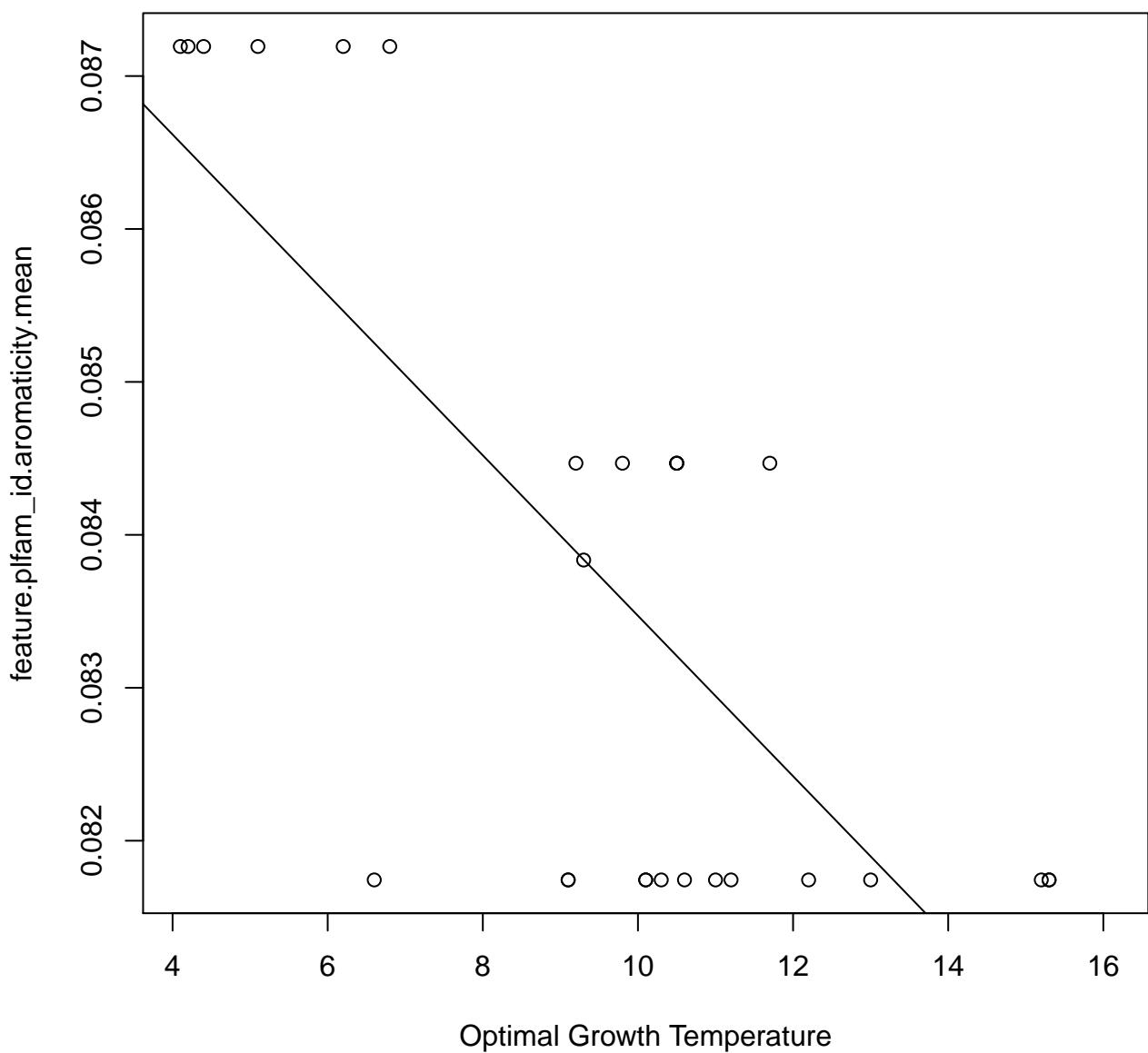
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PLF_28228_00002829
TonB-dependent receptor



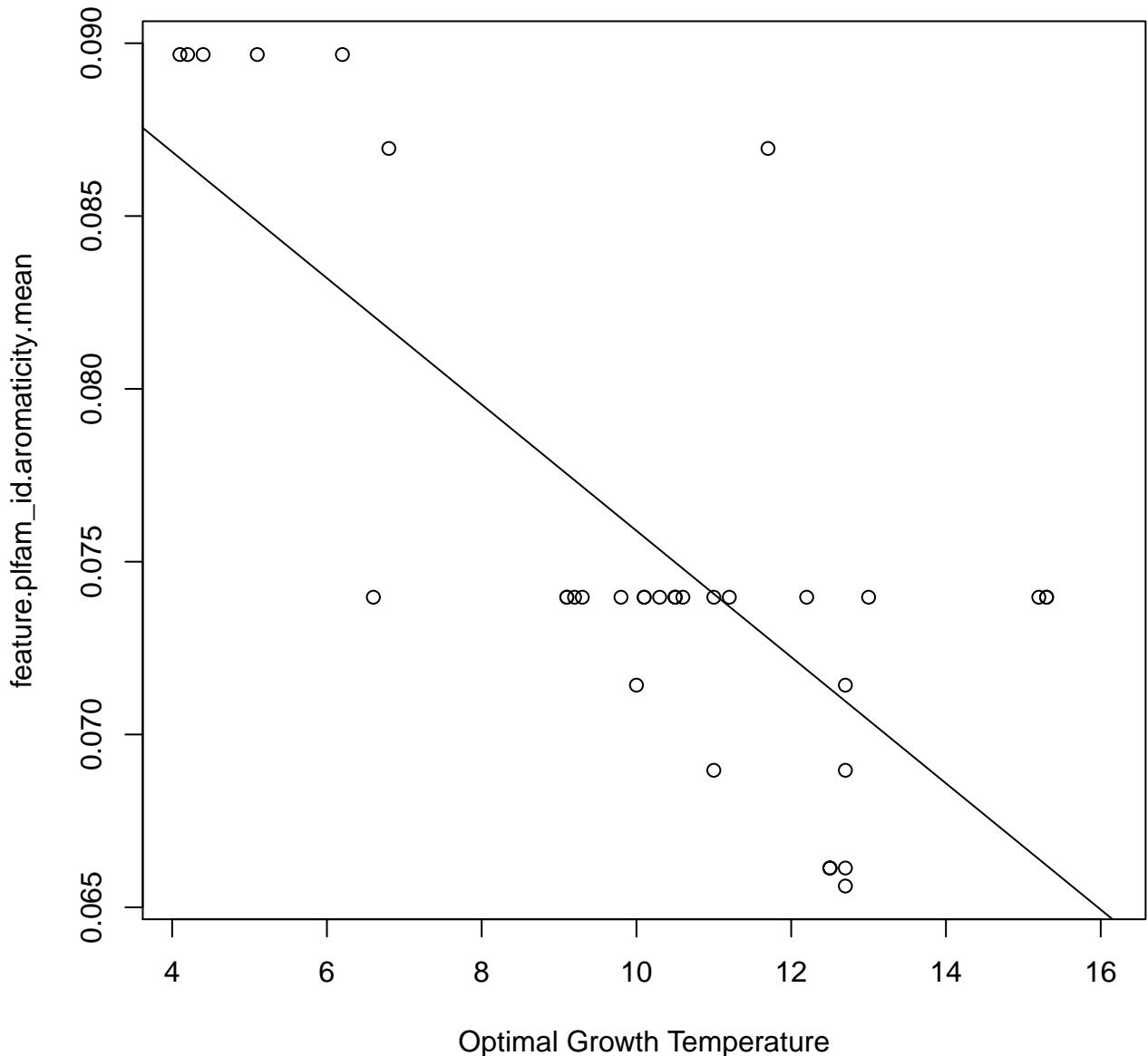
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PLF_28228_00024580

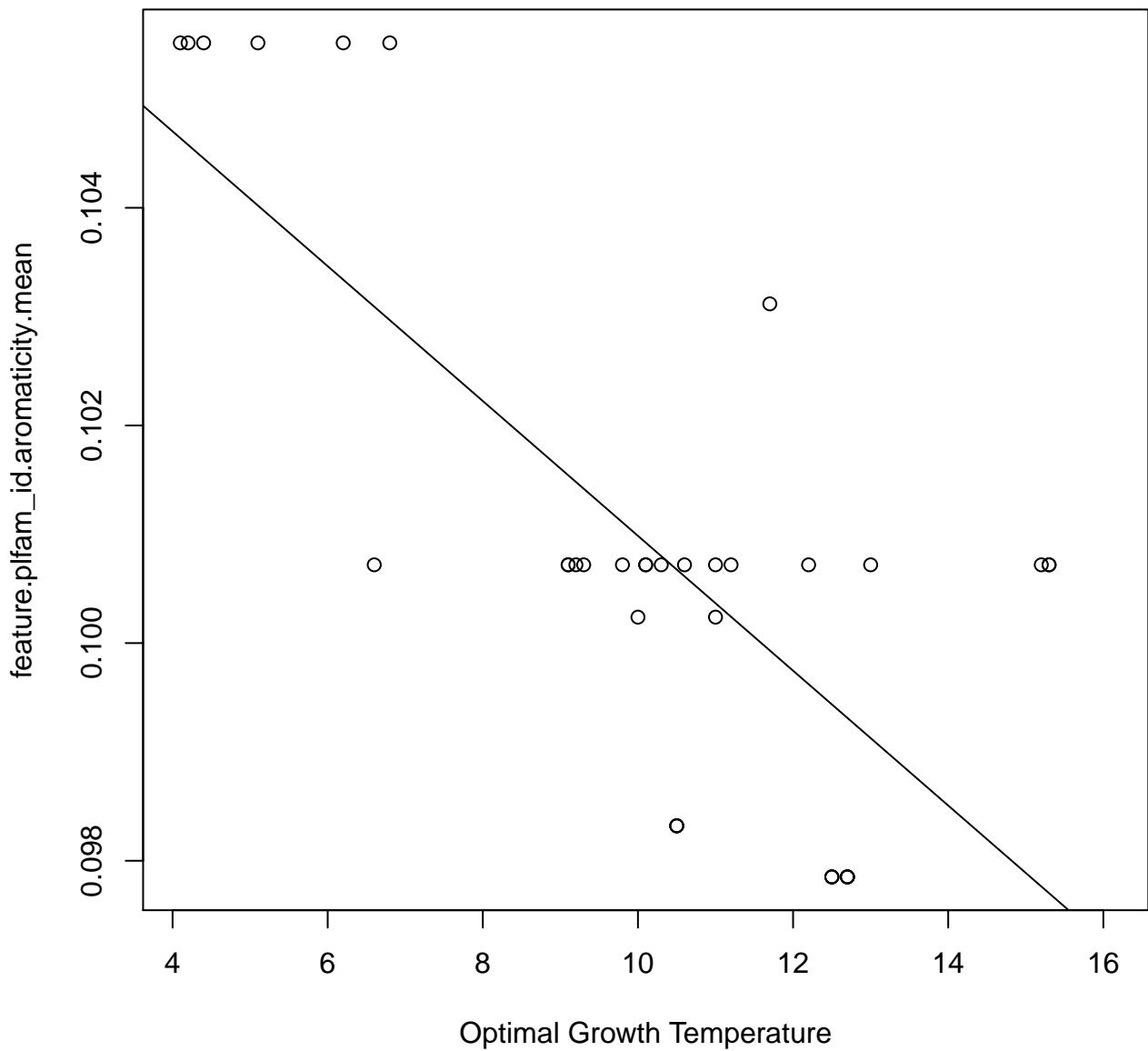
hypothetical protein



feature.plfam_id.aromaticity.mean
PLF_28228_00001942
CzcABC family efflux RND transporter, membrane fusion protein



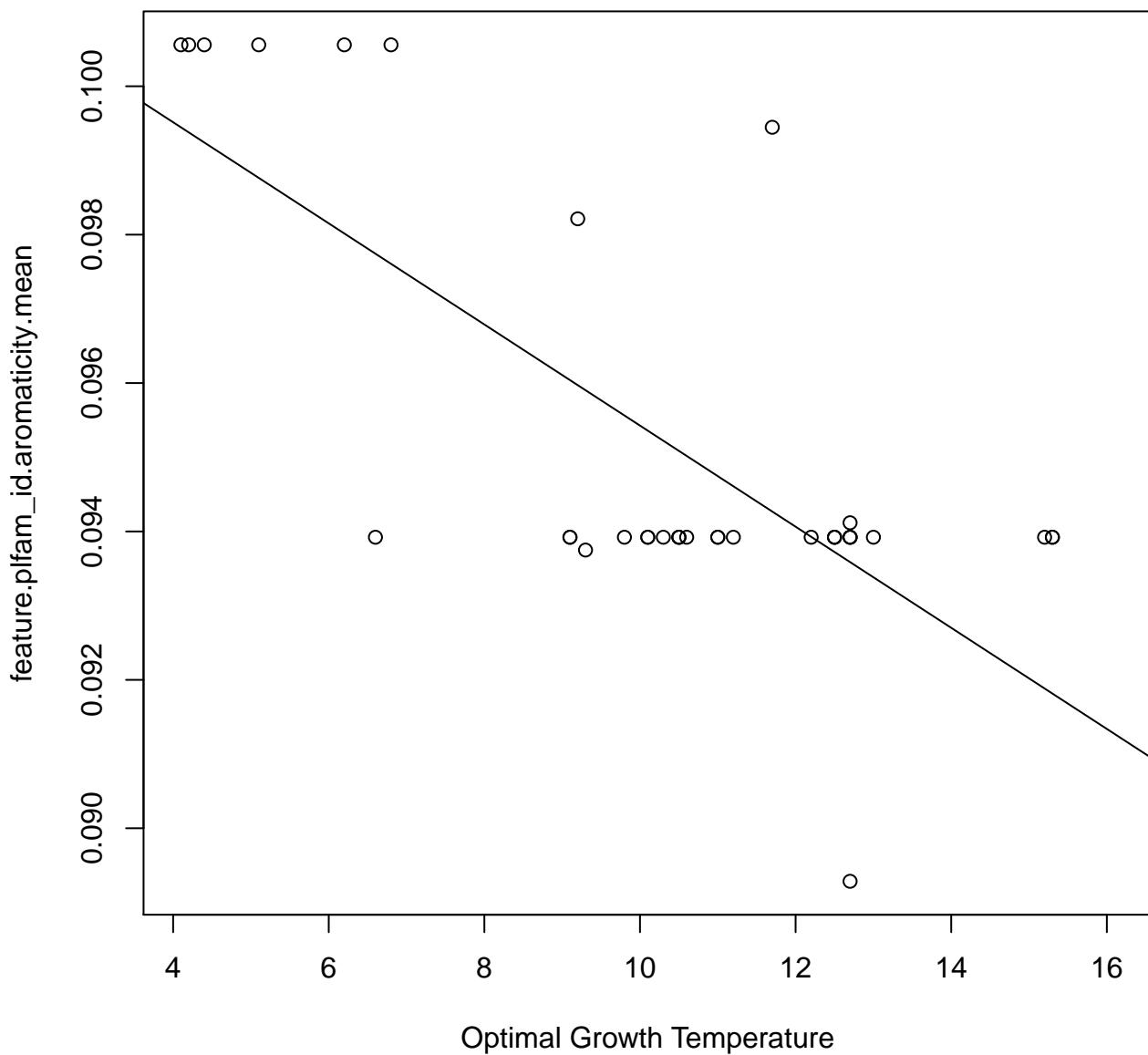
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PLF_28228_00002118
Transcriptional regulator



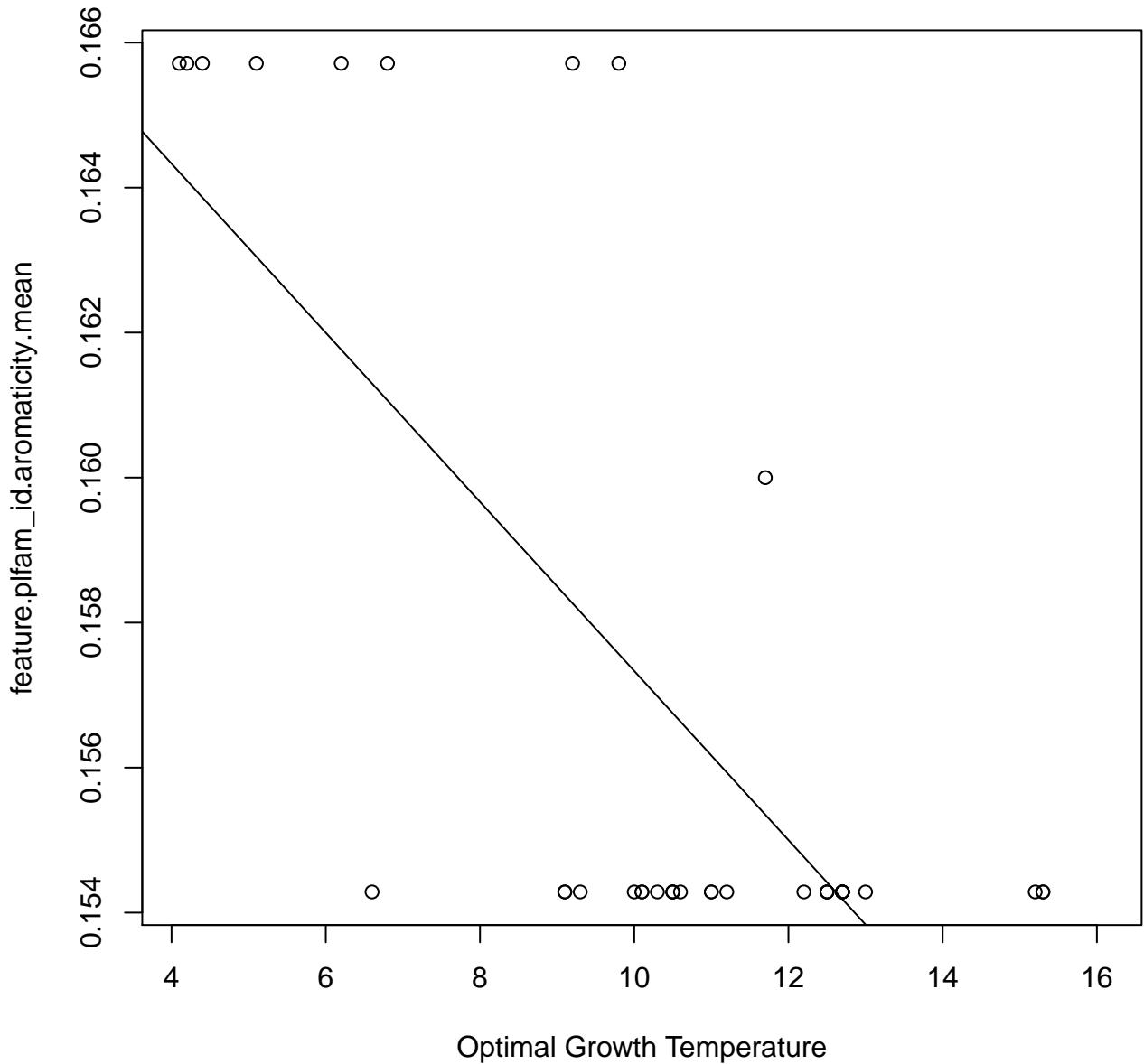
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PLF_28228_00002946

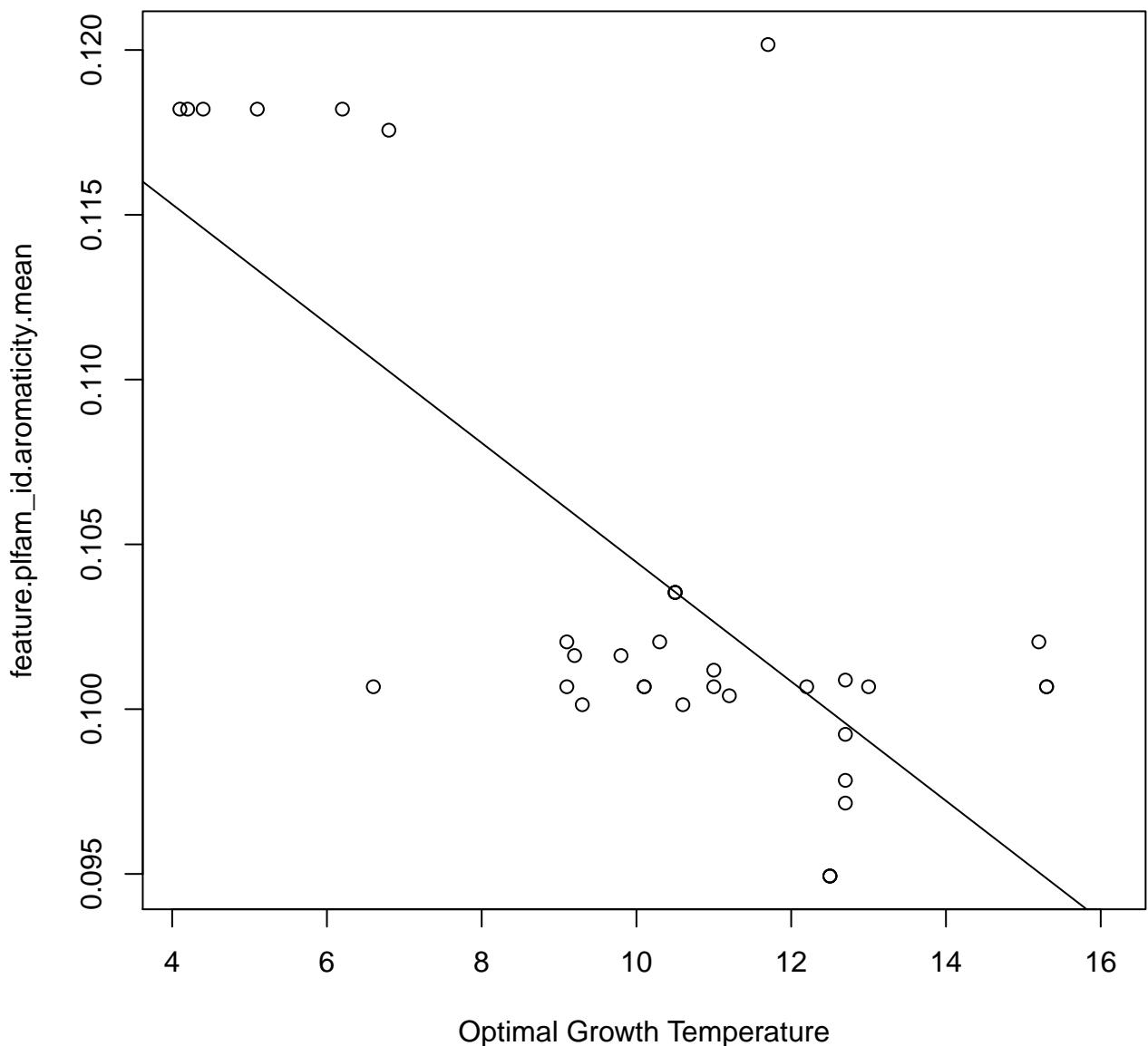
hypothetical protein



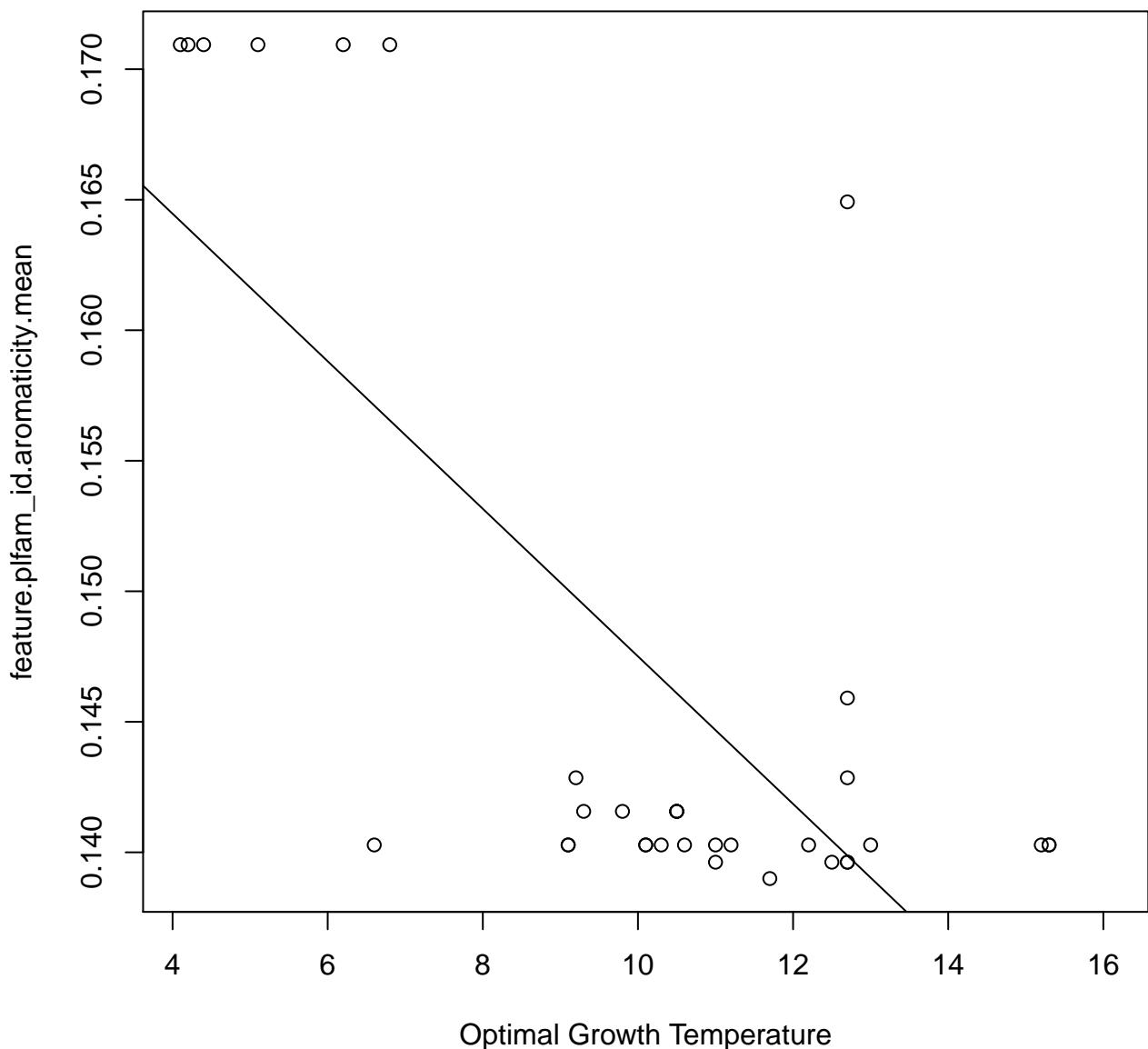
feature.plfam_id.aromaticity.mean
PLF_28228_00001835
Bacterial non-heme ferritin (EC 1.16.3.2)



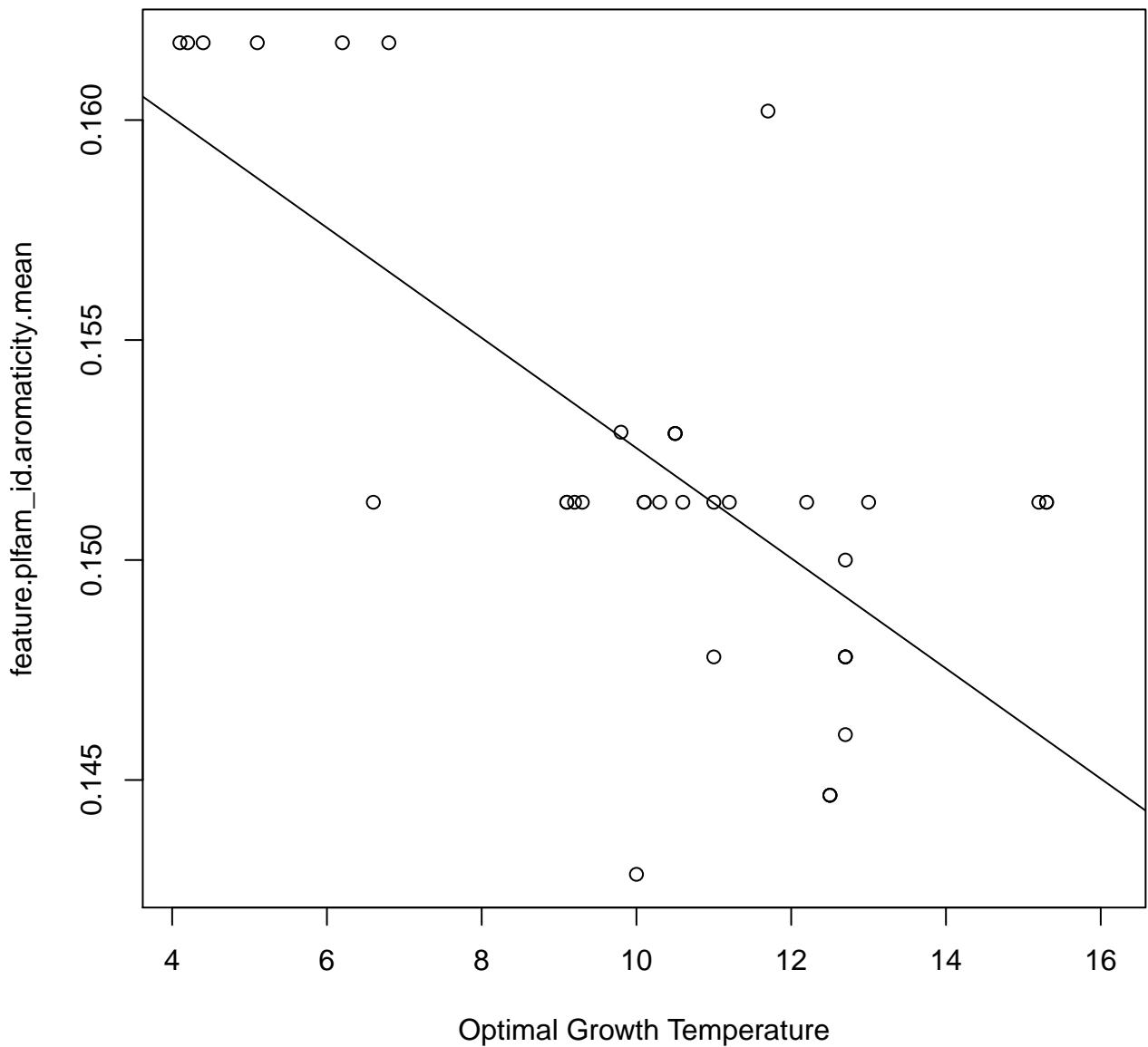
feature.plfam_id.aromaticity.mean
PLF_28228_00003253
Inter-alpha-trypsin inhibitor domain protein



feature.plfam_id.aromaticity.mean
PLF_28228_00028047
Fatty acid cis/trans isomerase



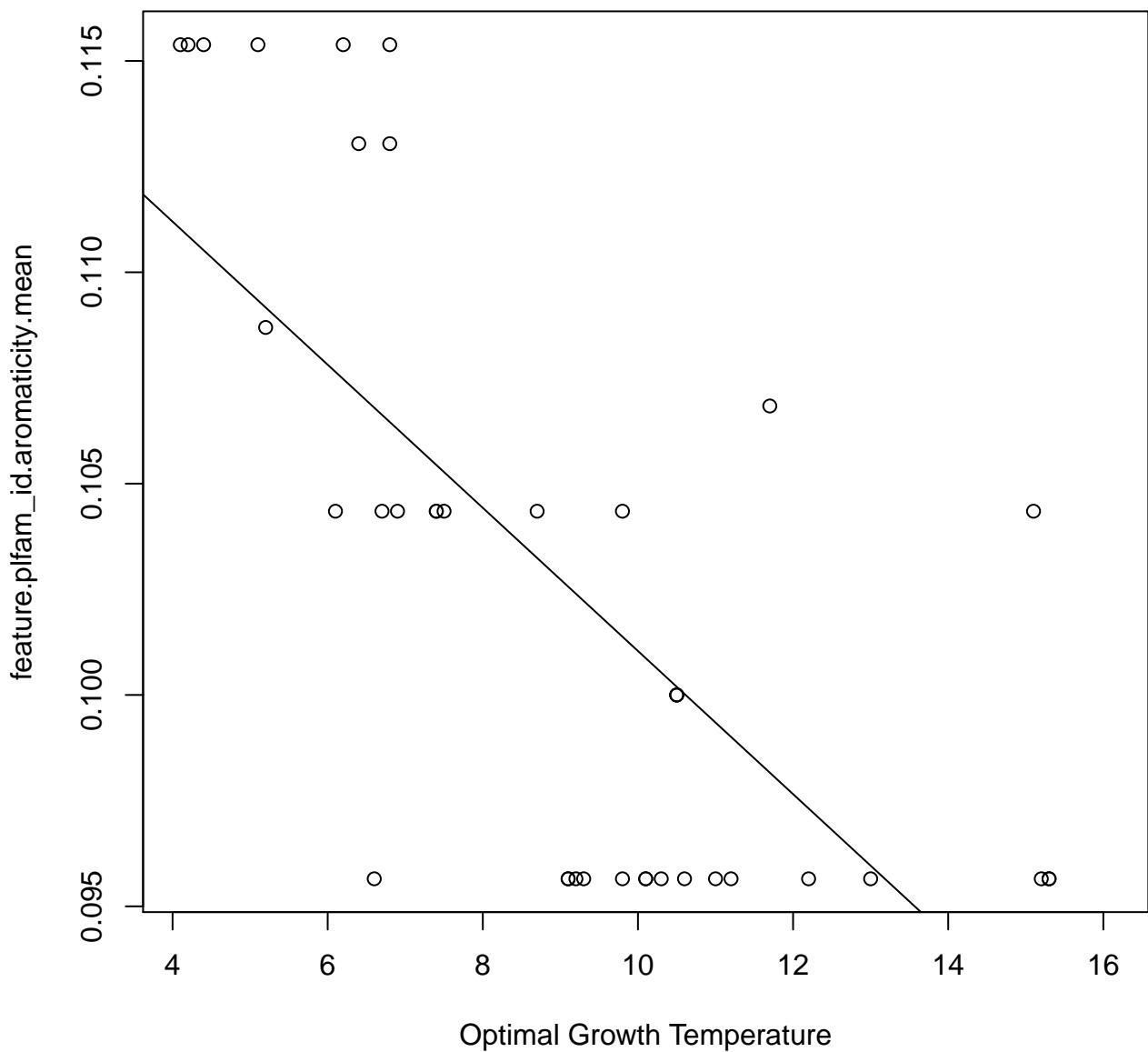
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Proline iminopeptidase (EC 3.4.11.5)



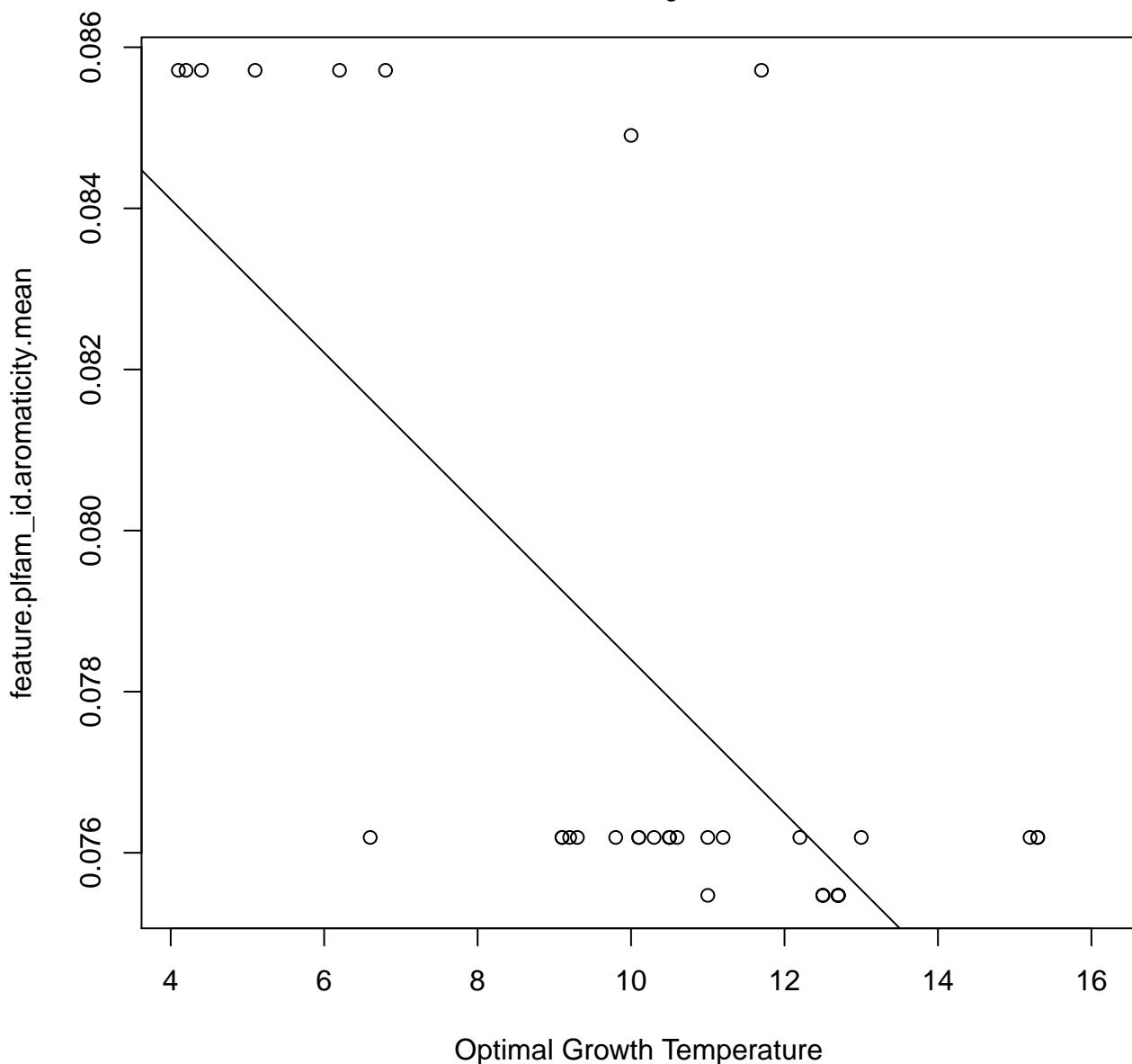
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PLF_28228_00006398

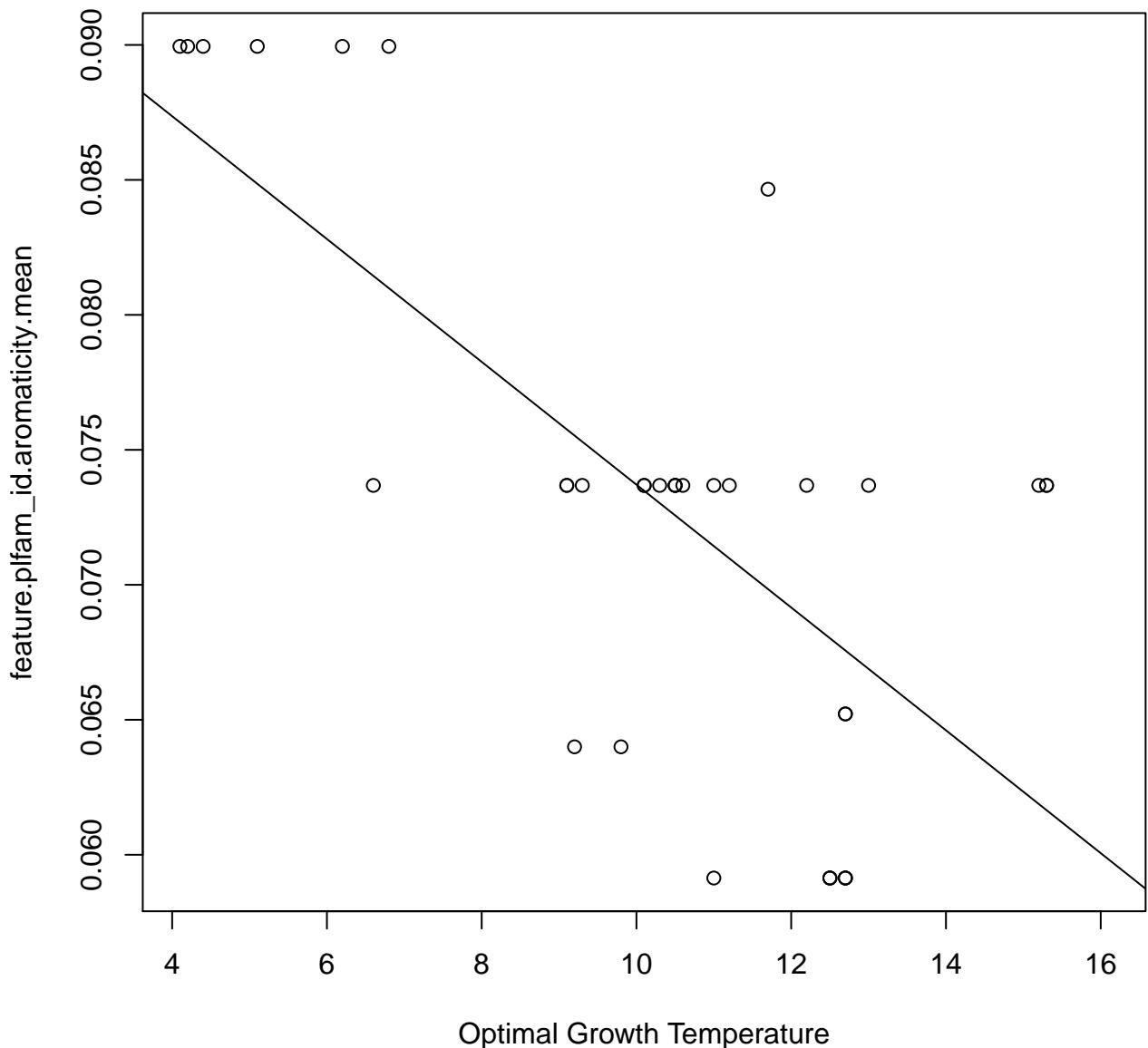
hypothetical protein



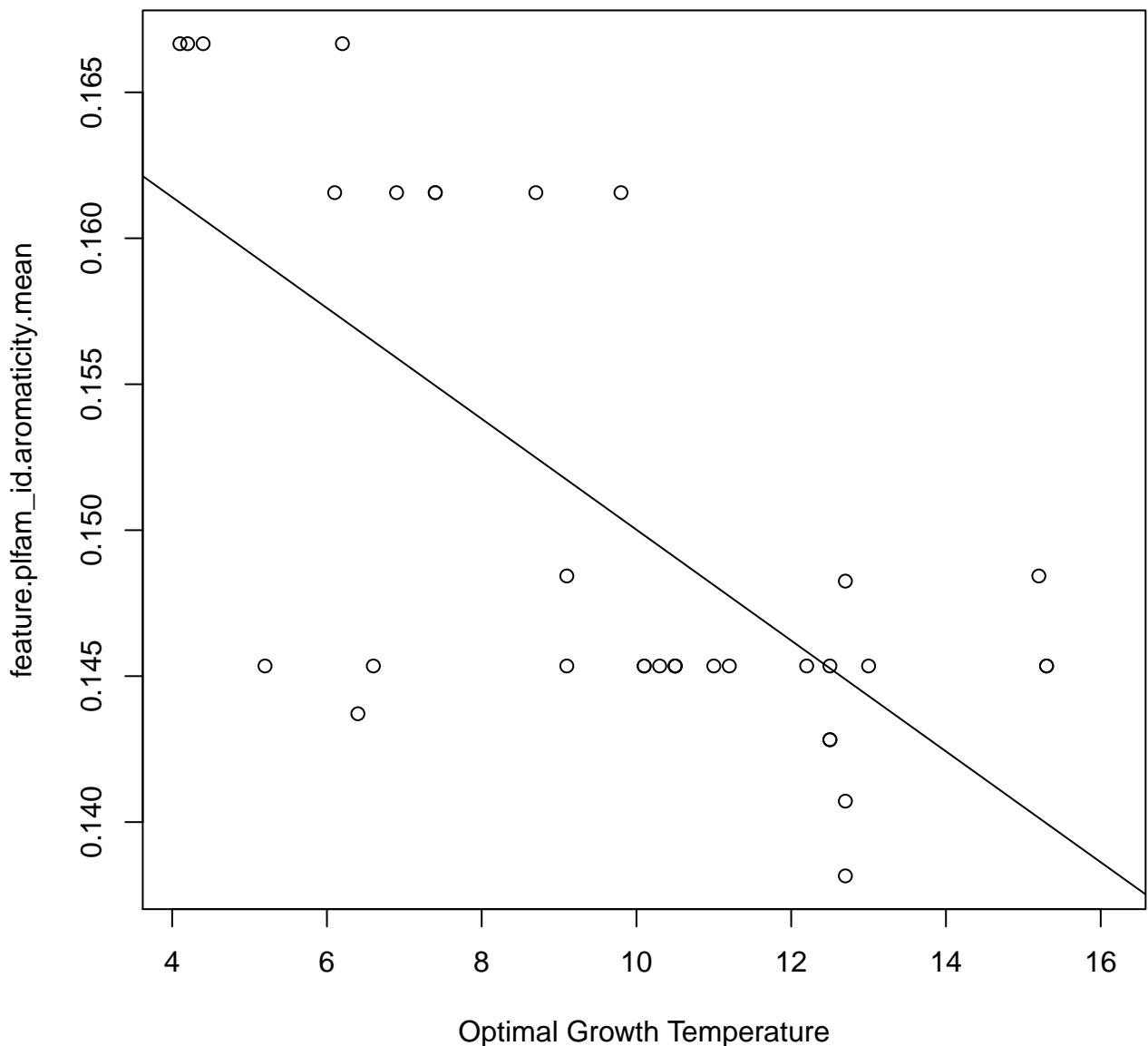
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Ribosomal silencing factor RsfA



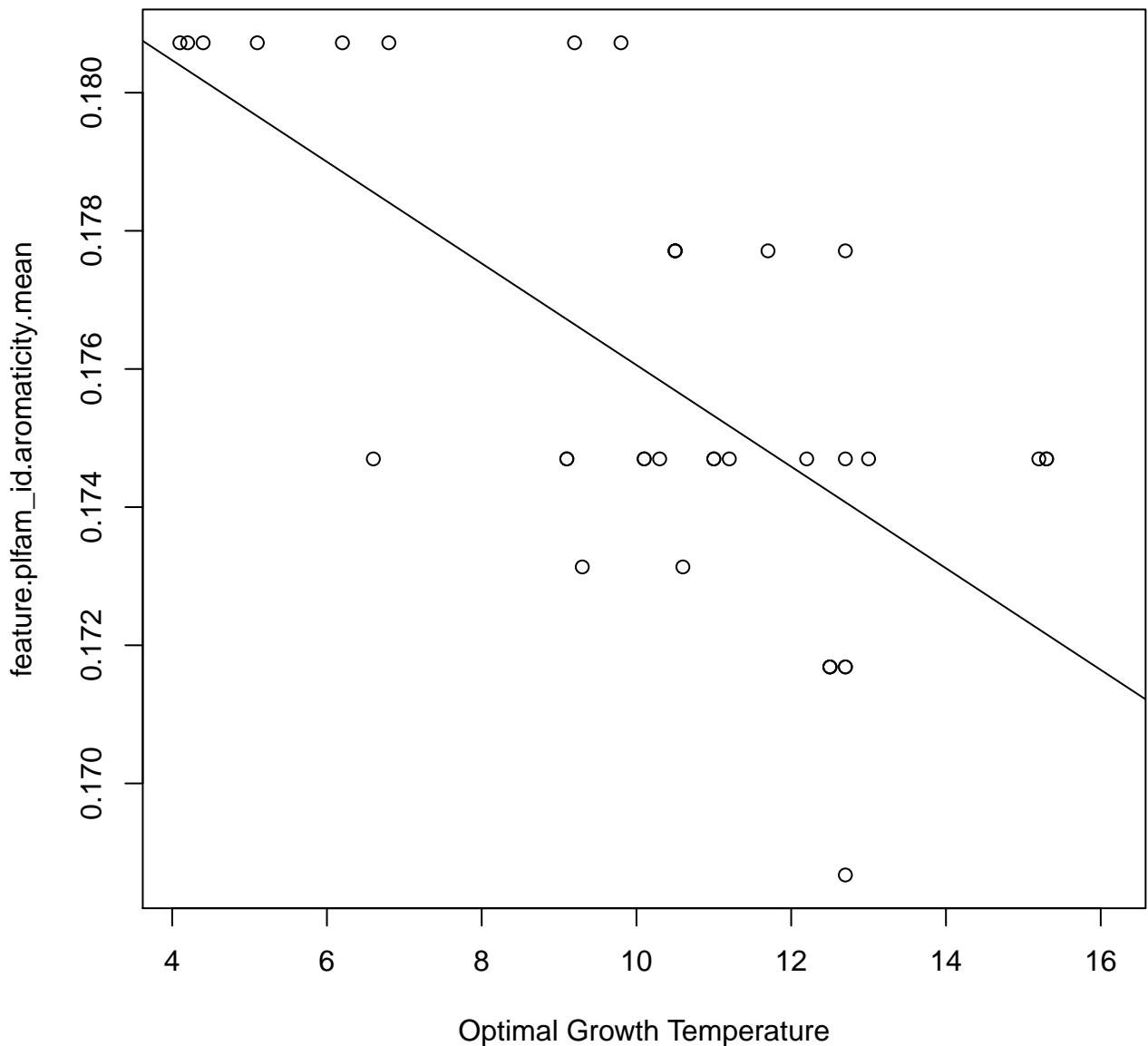
feature.pfam_id.aromaticity.mean
PLF_28228_00001484
Dna binding response regulator PrrA (RegA)



feature.plfam_id.aromaticity.mean
PLF_28228_00003783
UDP-glucuronate 5'-epimerase (EC 5.1.3.12)



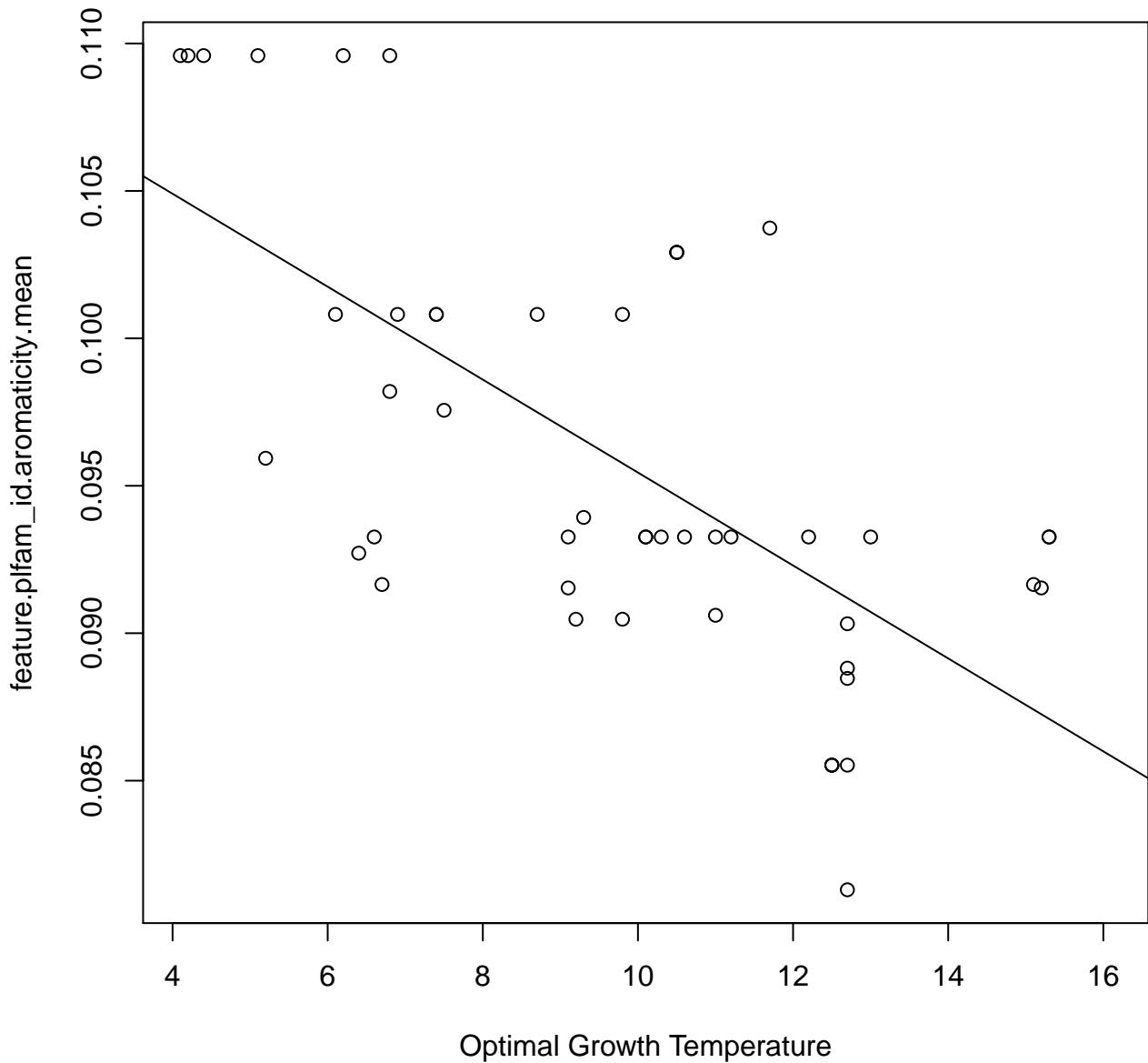
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Cytochrome d ubiquinol oxidase subunit II (EC 1.10.3.-)



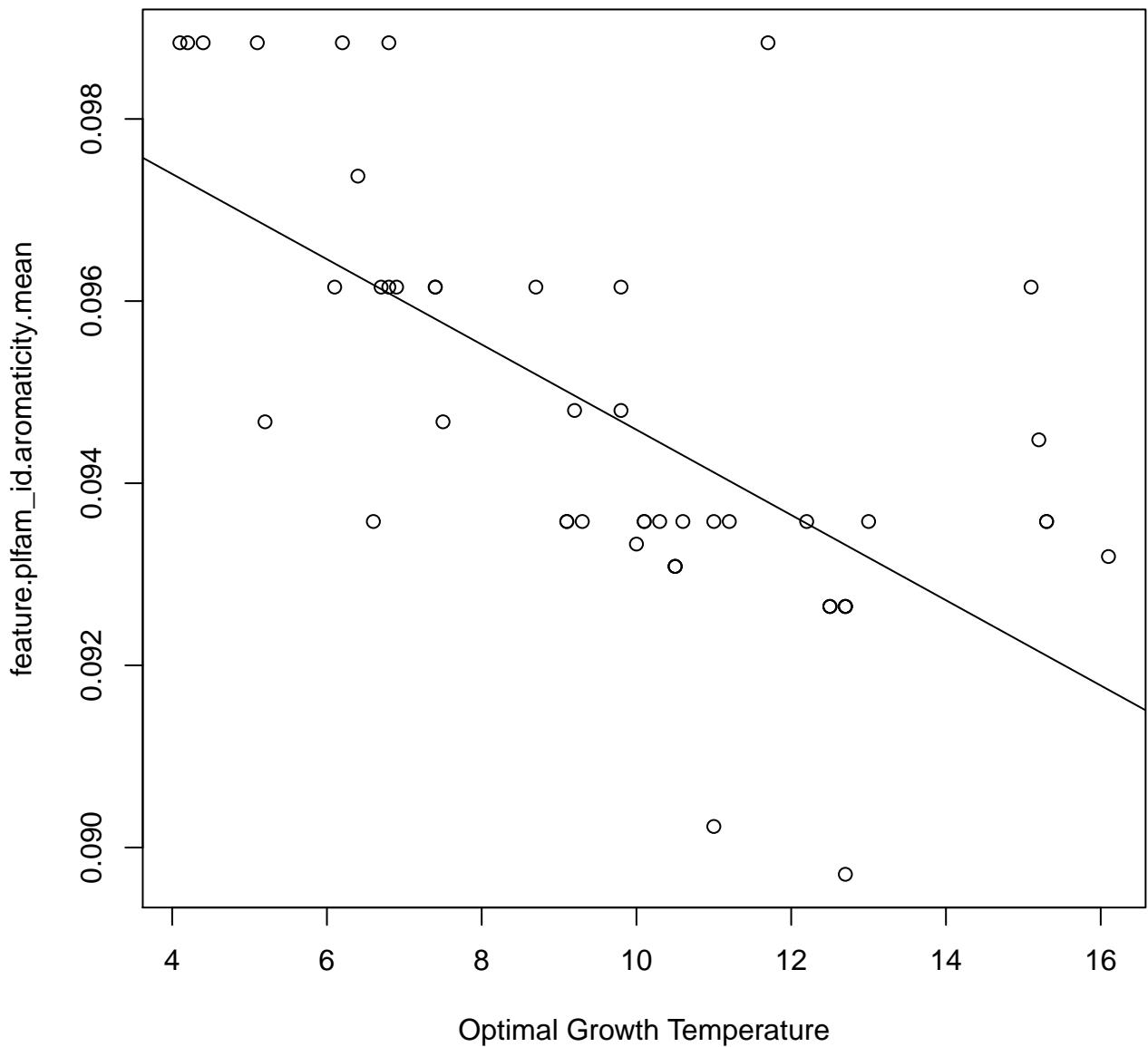
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PLF_28228_00002320

hypothetical protein



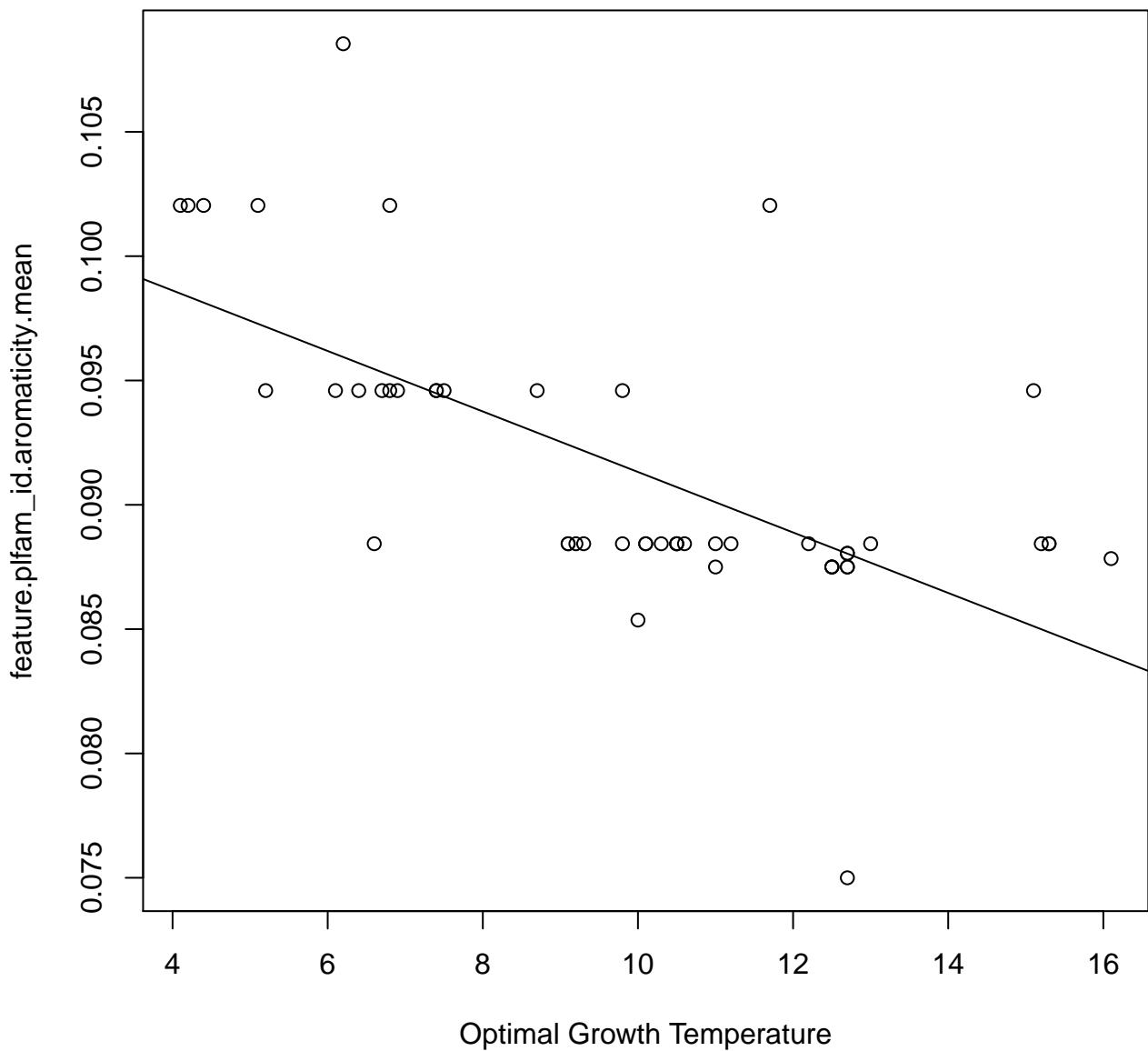
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PLF_28228_00000071
2,4-dienoyl-CoA reductase [NADPH] (EC 1.3.1.34)



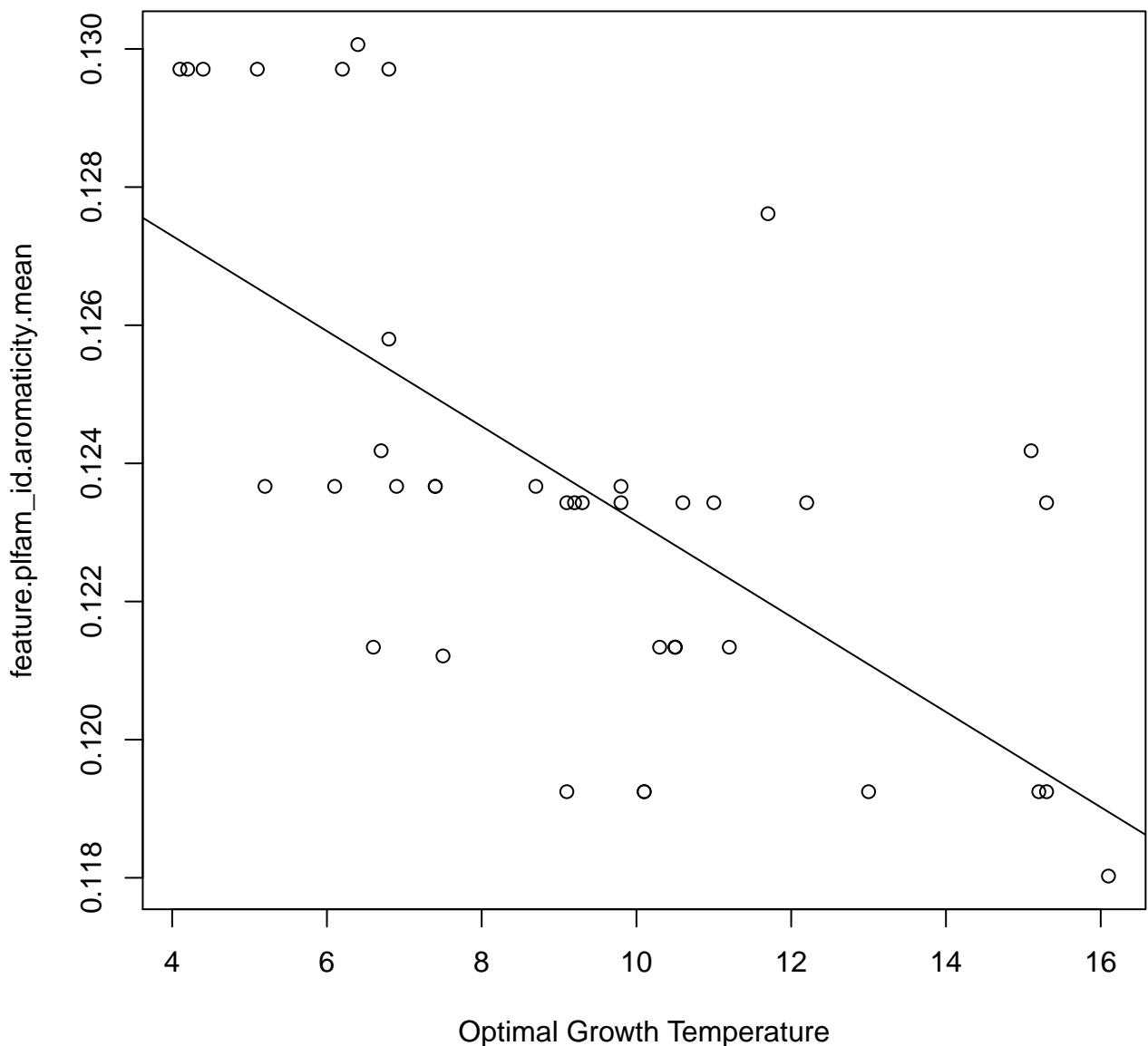
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PLF_28228_00001047

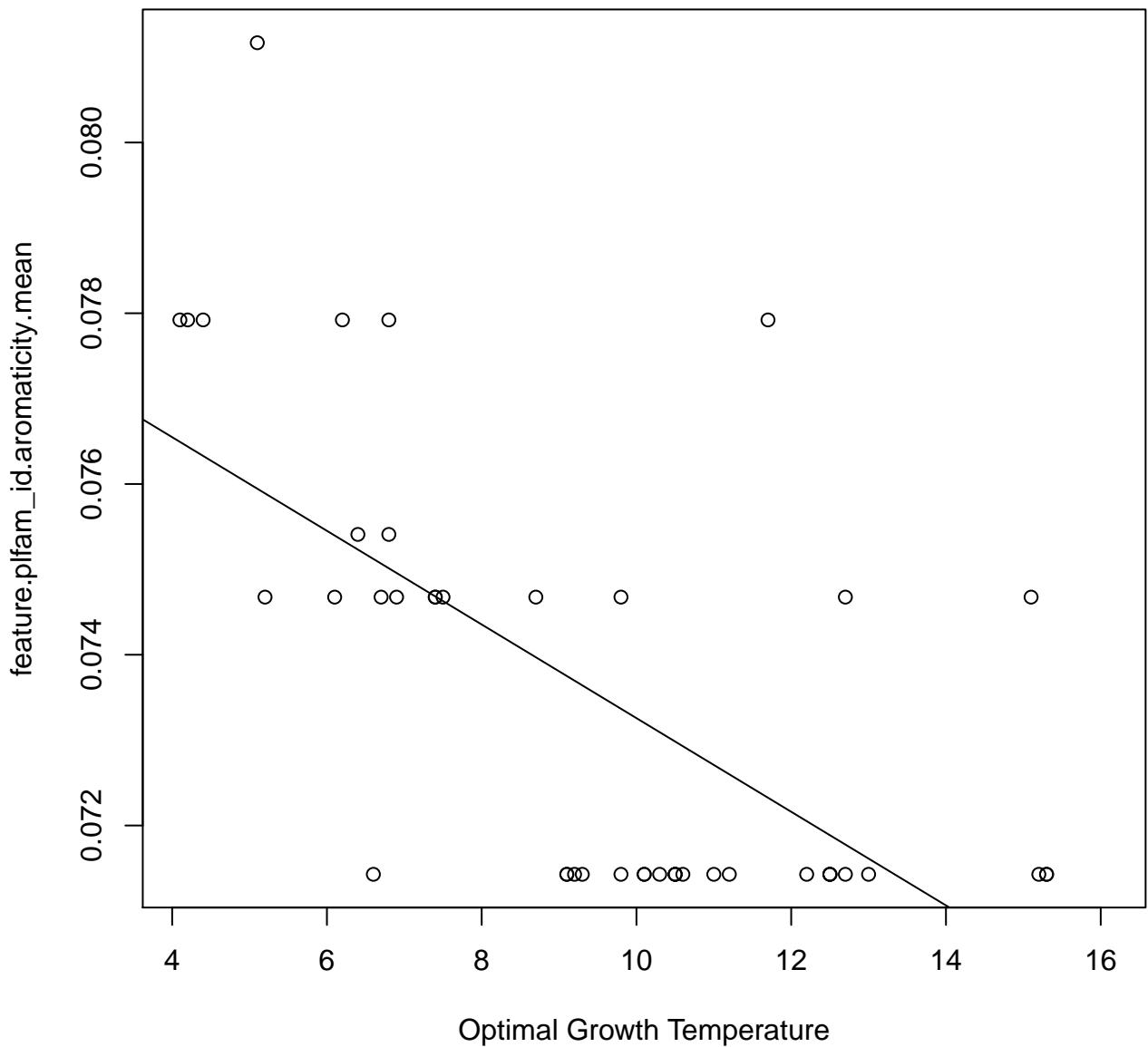
RNA-binding protein



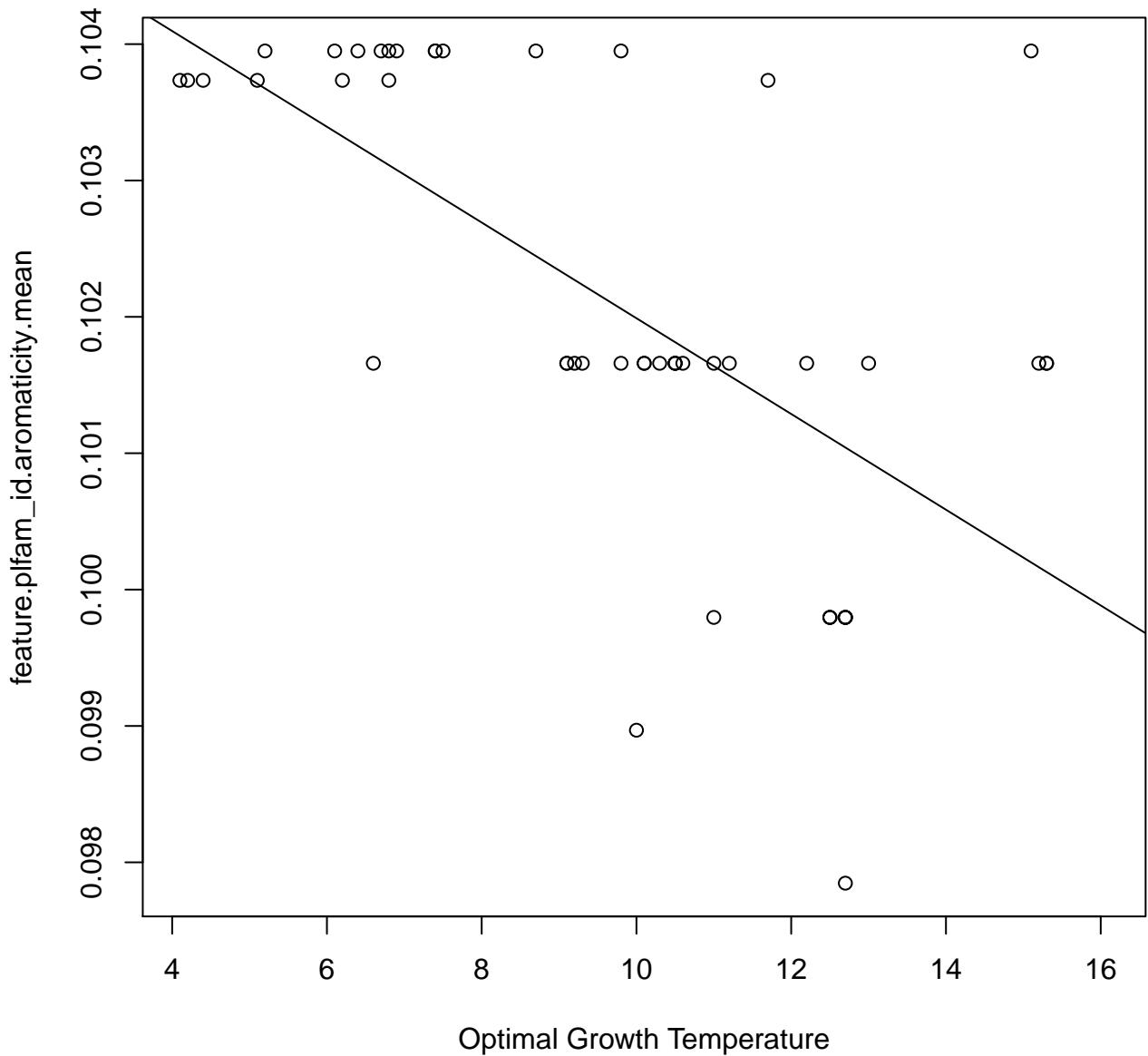
feature.plfam_id.aromaticity.mean
PLF_28228_00016167
Kynurenone 3-monoxygenase (EC 1.14.13.9)



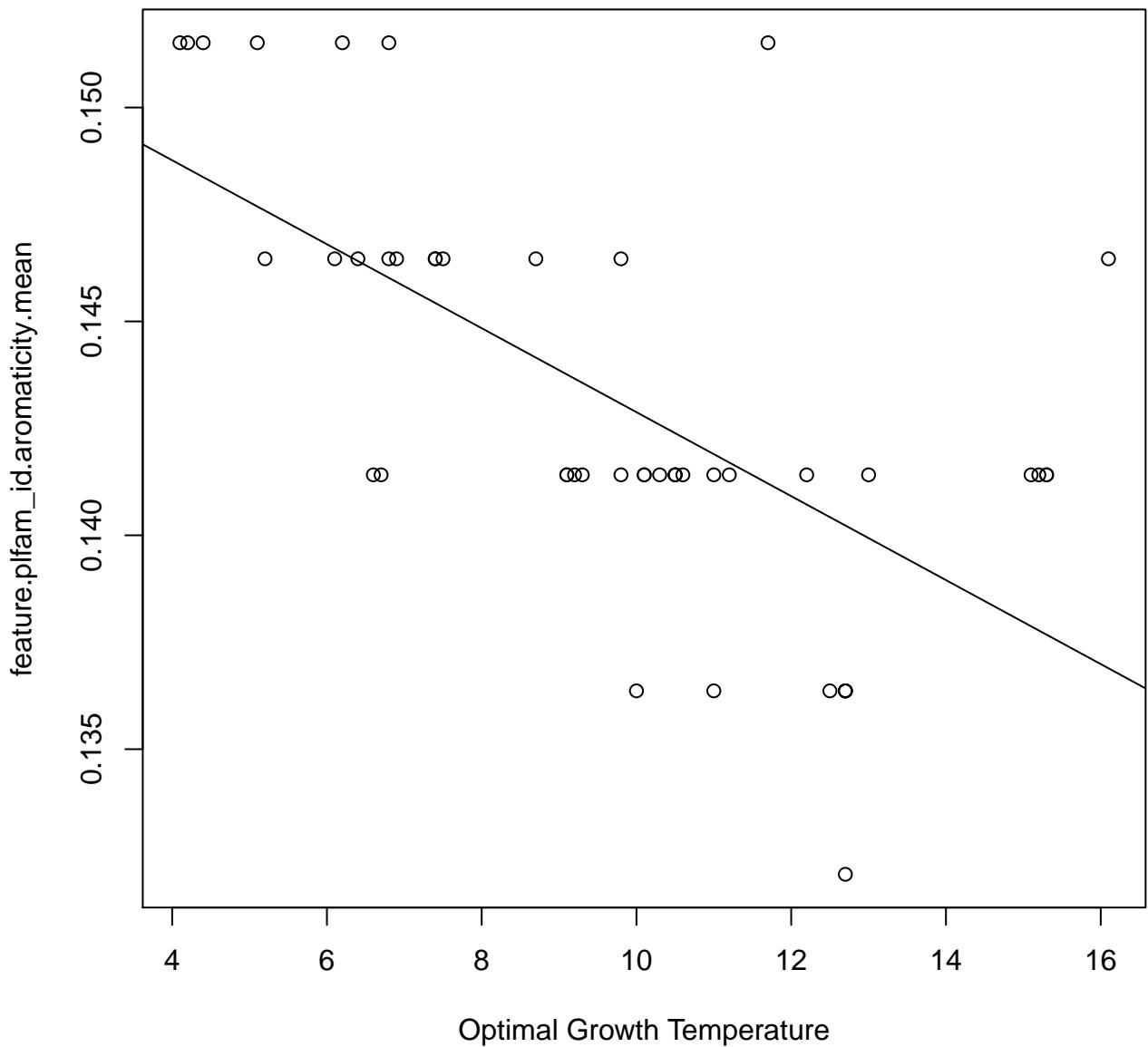
feature.plfam_id.aromaticity.mean
PLF_28228_00007842
Efflux ABC transporter, ATP-binding protein



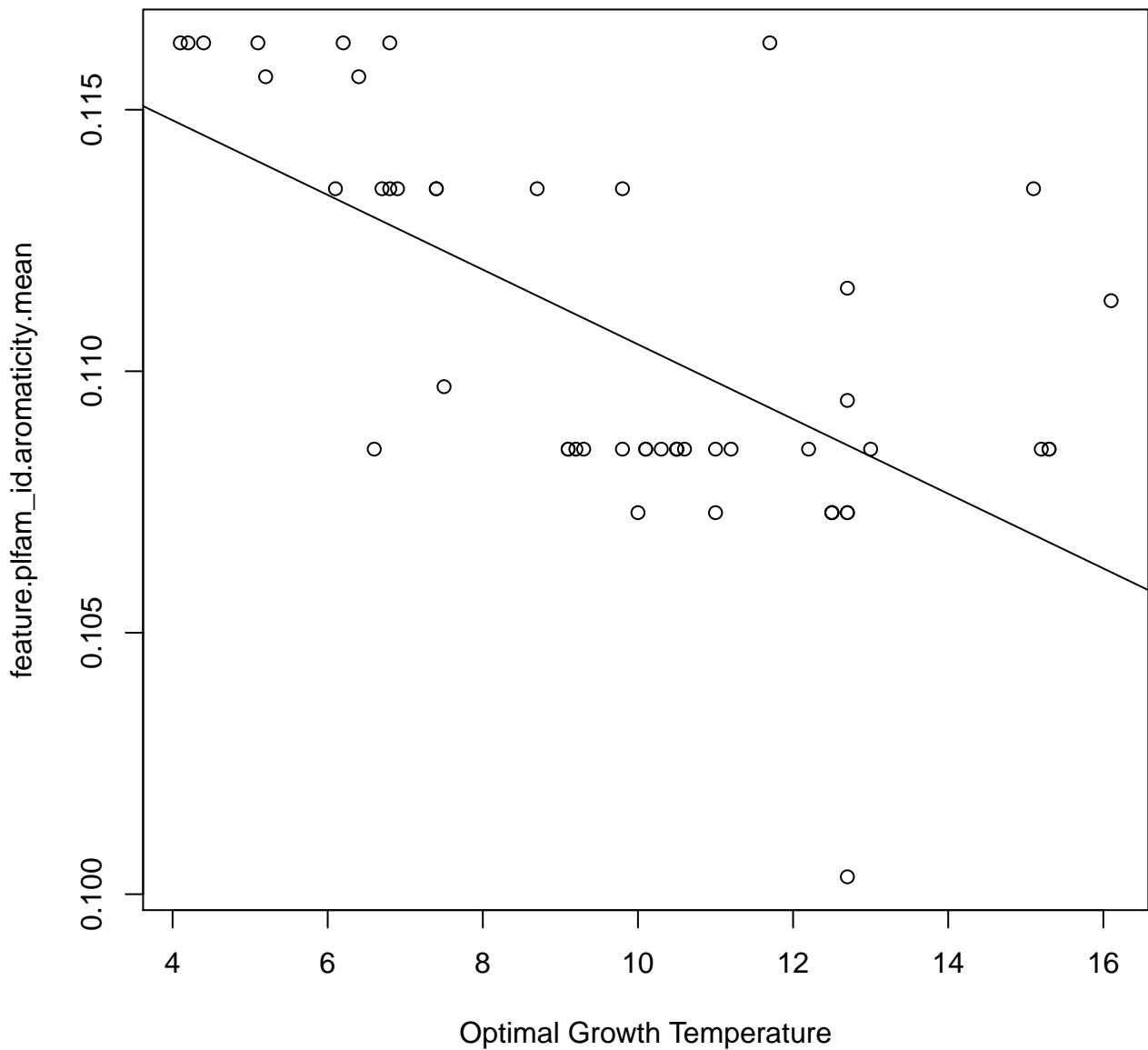
feature.plfam_id.aromaticity.mean
PLF_28228_00001635
DNA-binding transcriptional regulator, MocR family / aminotransferase domain



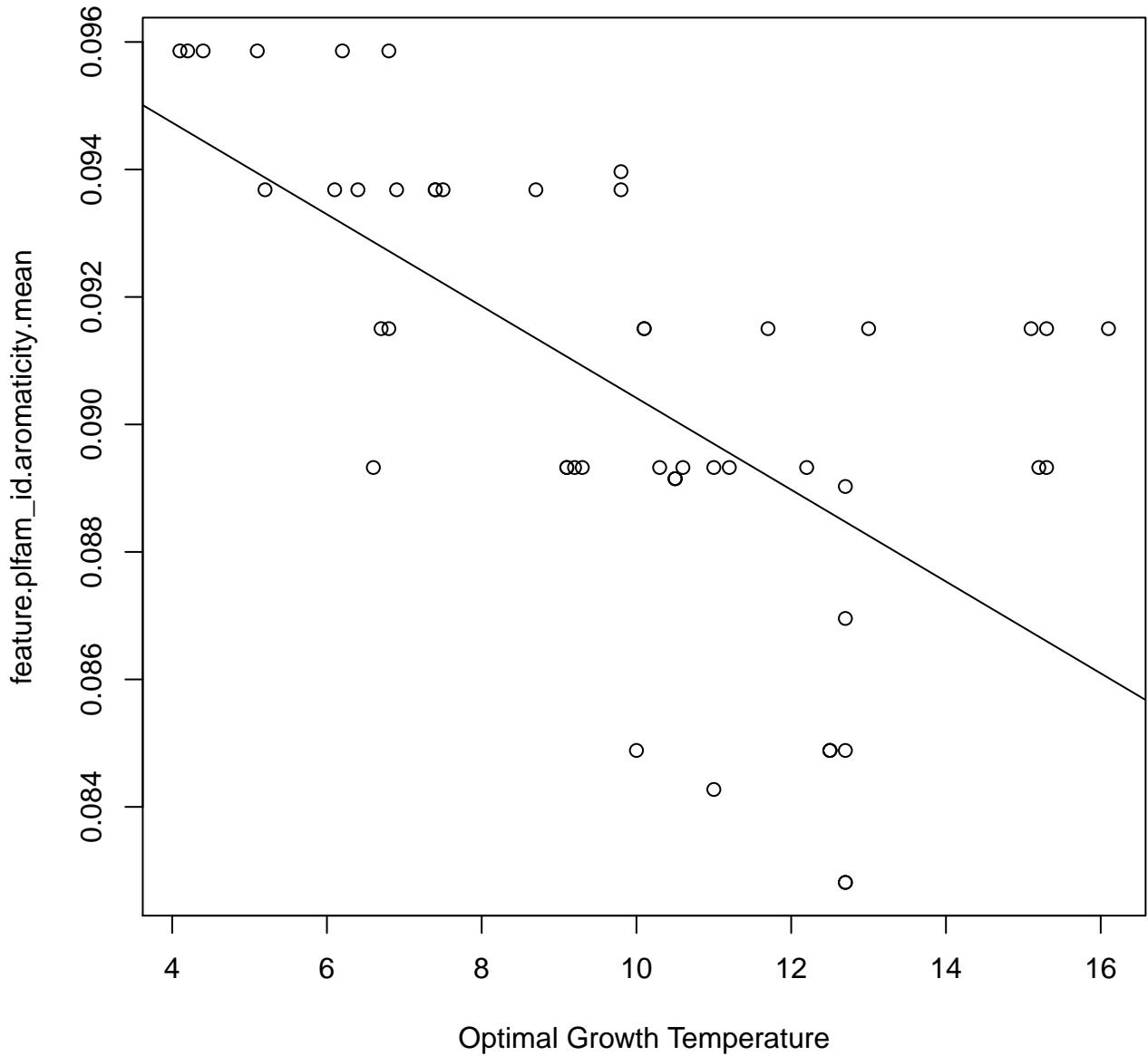
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PLF_28228_00028151
3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)



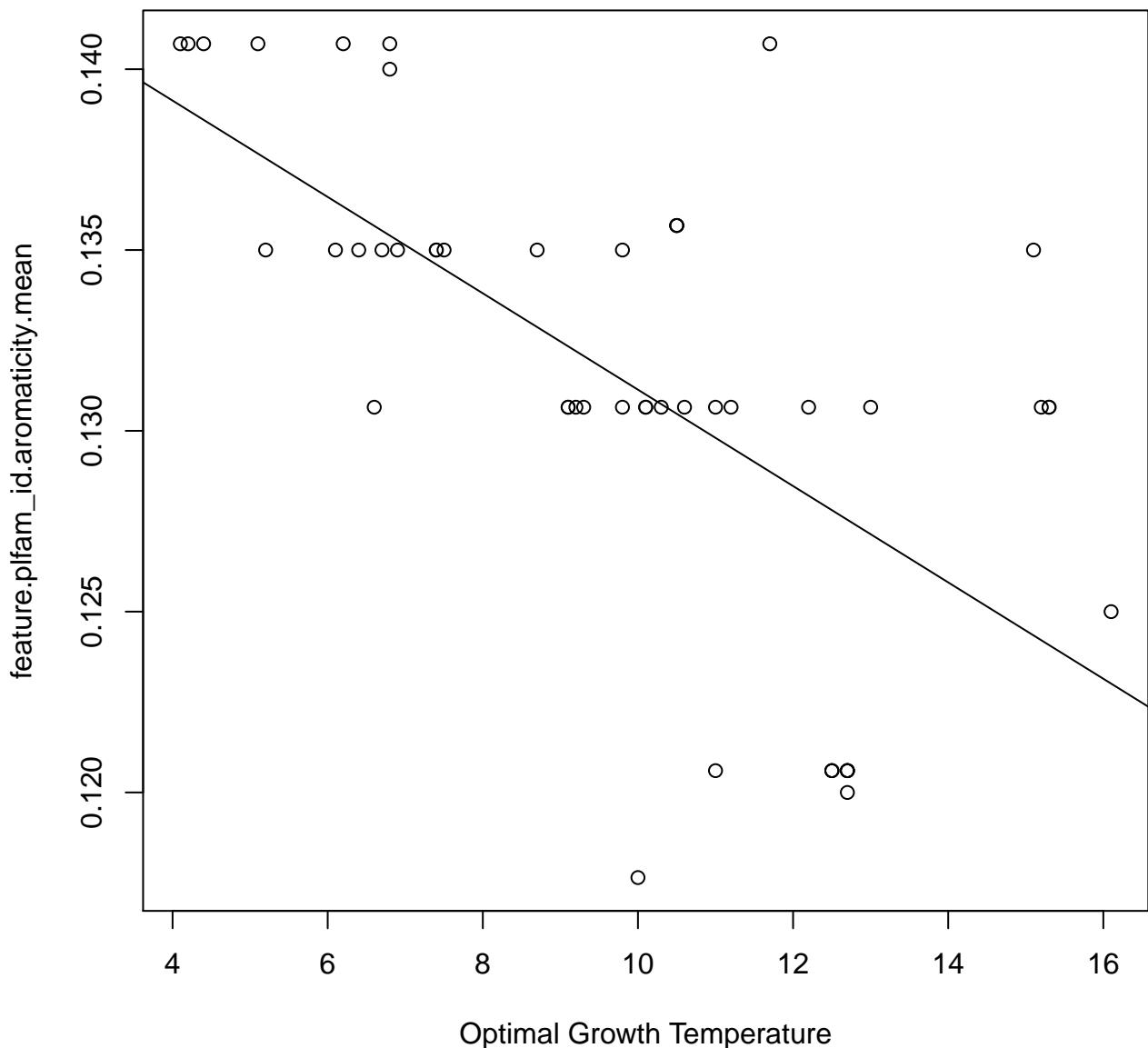
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PLF_28228_00001172
Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4)



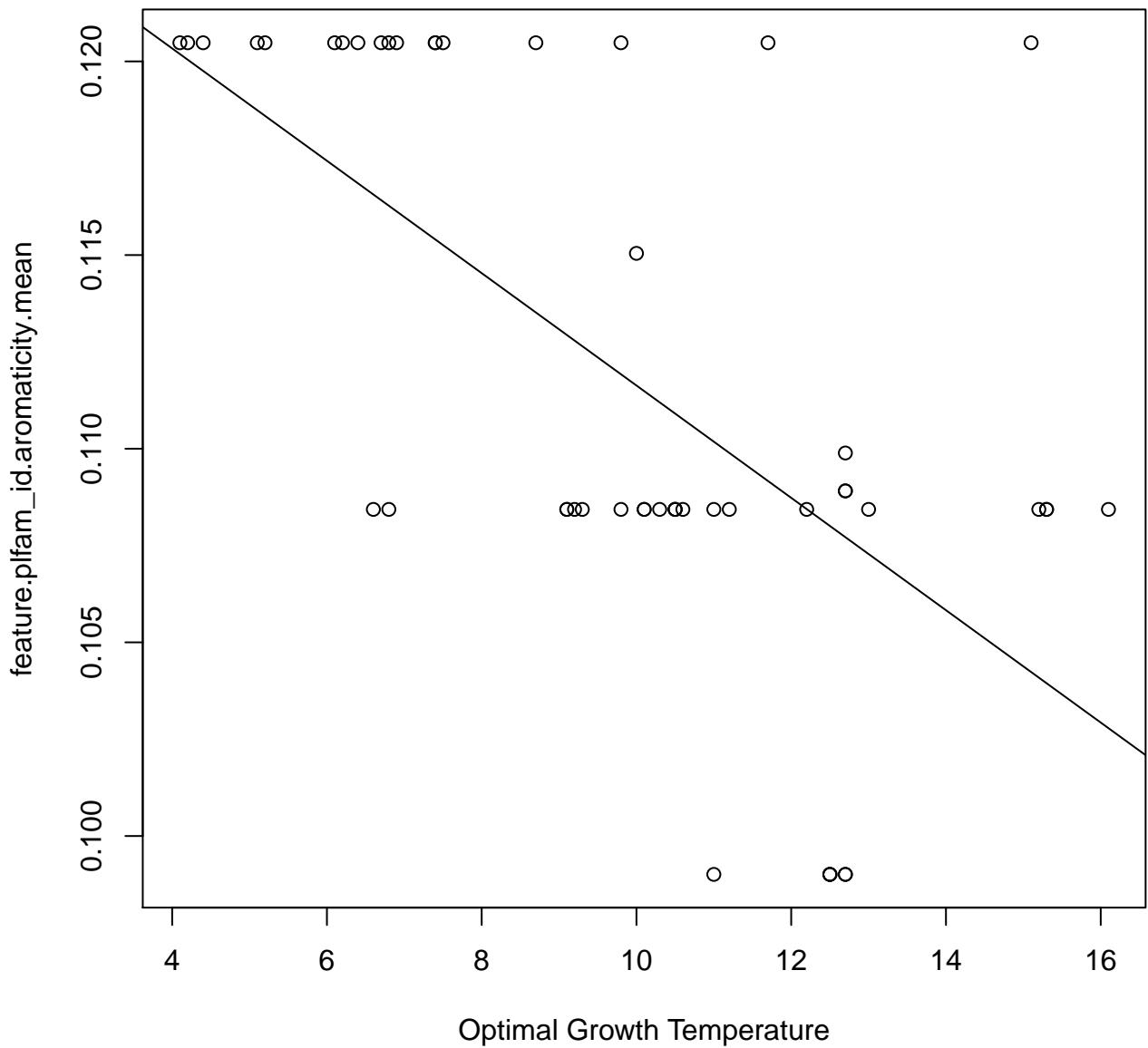
feature.plfam_id.aromaticity.mean
PLF_28228_00000981
Predicted ATPase related to phosphate starvation-inducible protein PhoH



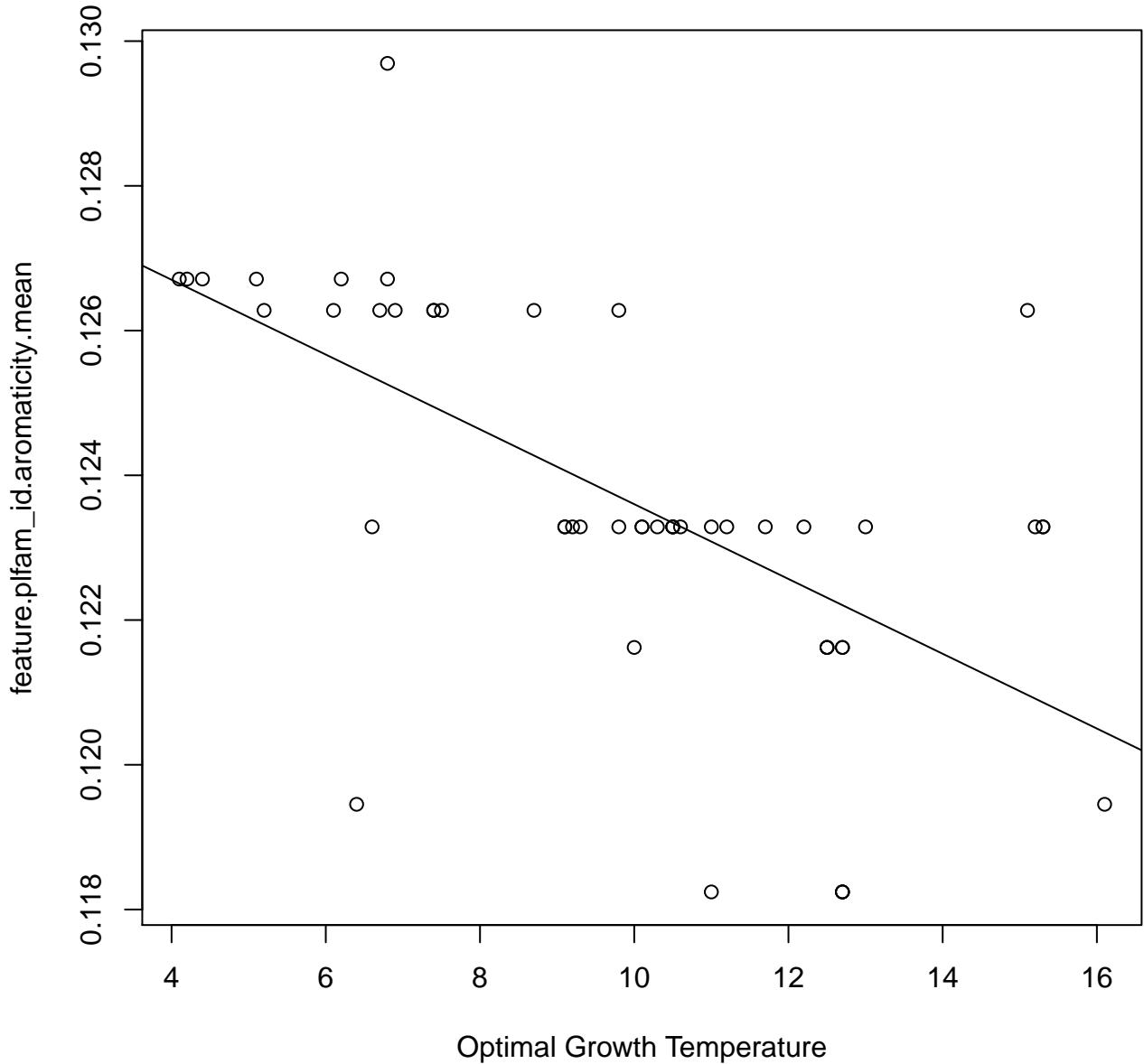
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Carbonic anhydrase, beta class (EC 4.2.1.1)



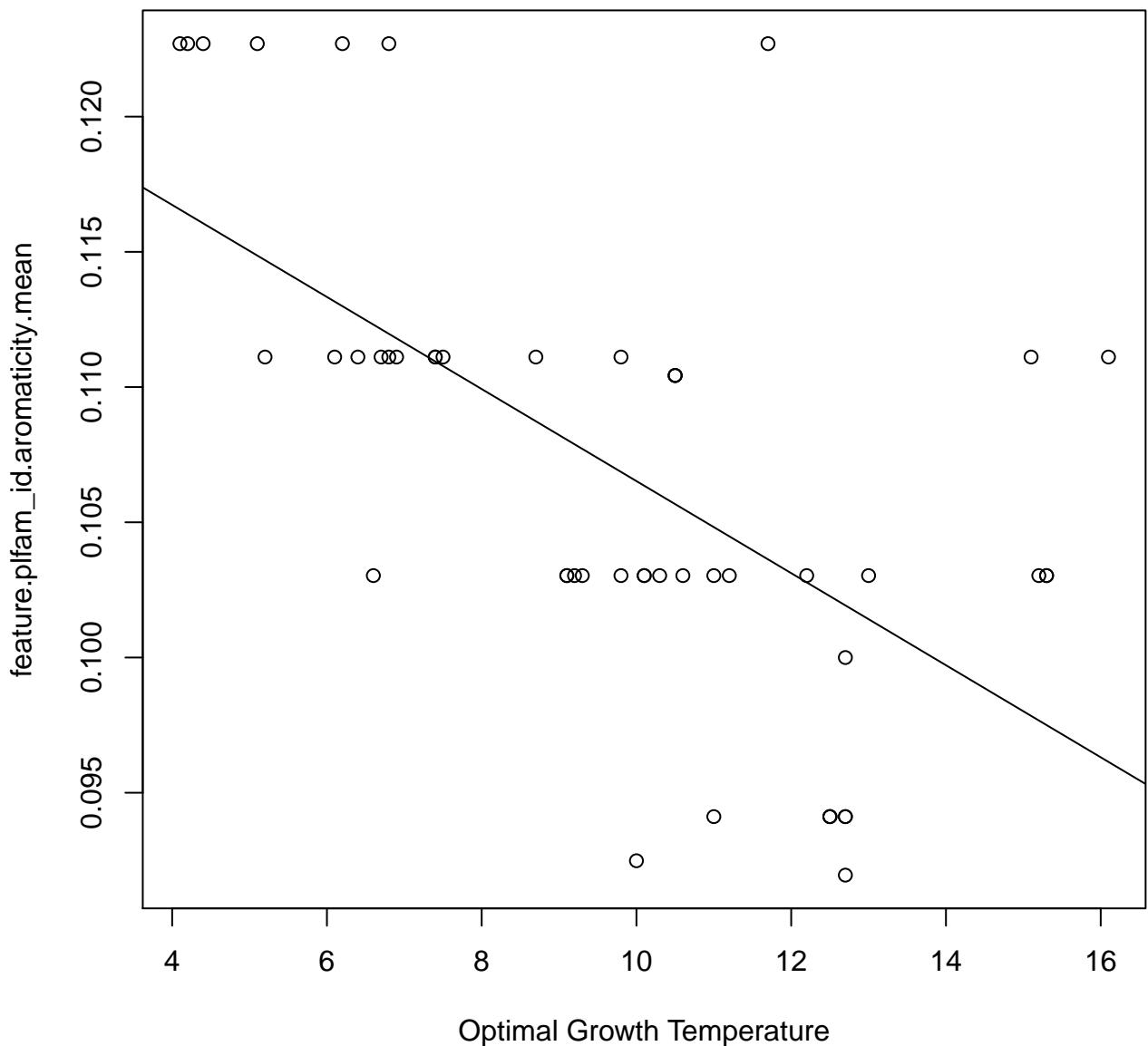
feature.plfam_id.aromaticity.mean
PLF_28228_0000130
Succinate dehydrogenase flavin-adding protein, antitoxin of CptAB toxin-antitoxin



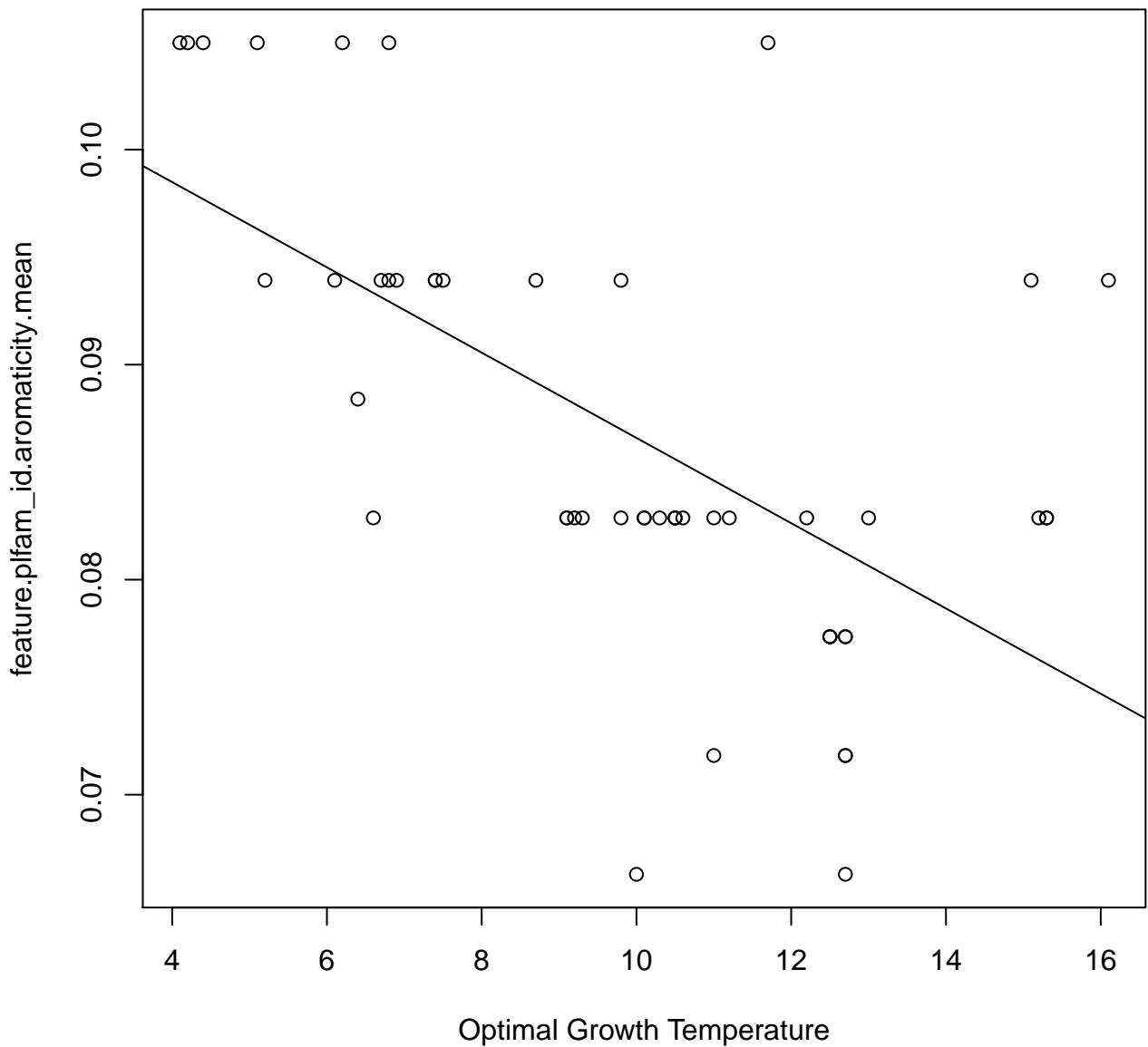
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PLF_28228_00002316
6-carboxy-5,6,7,8-tetrahydropterin synthase (EC 4.1.2.50)



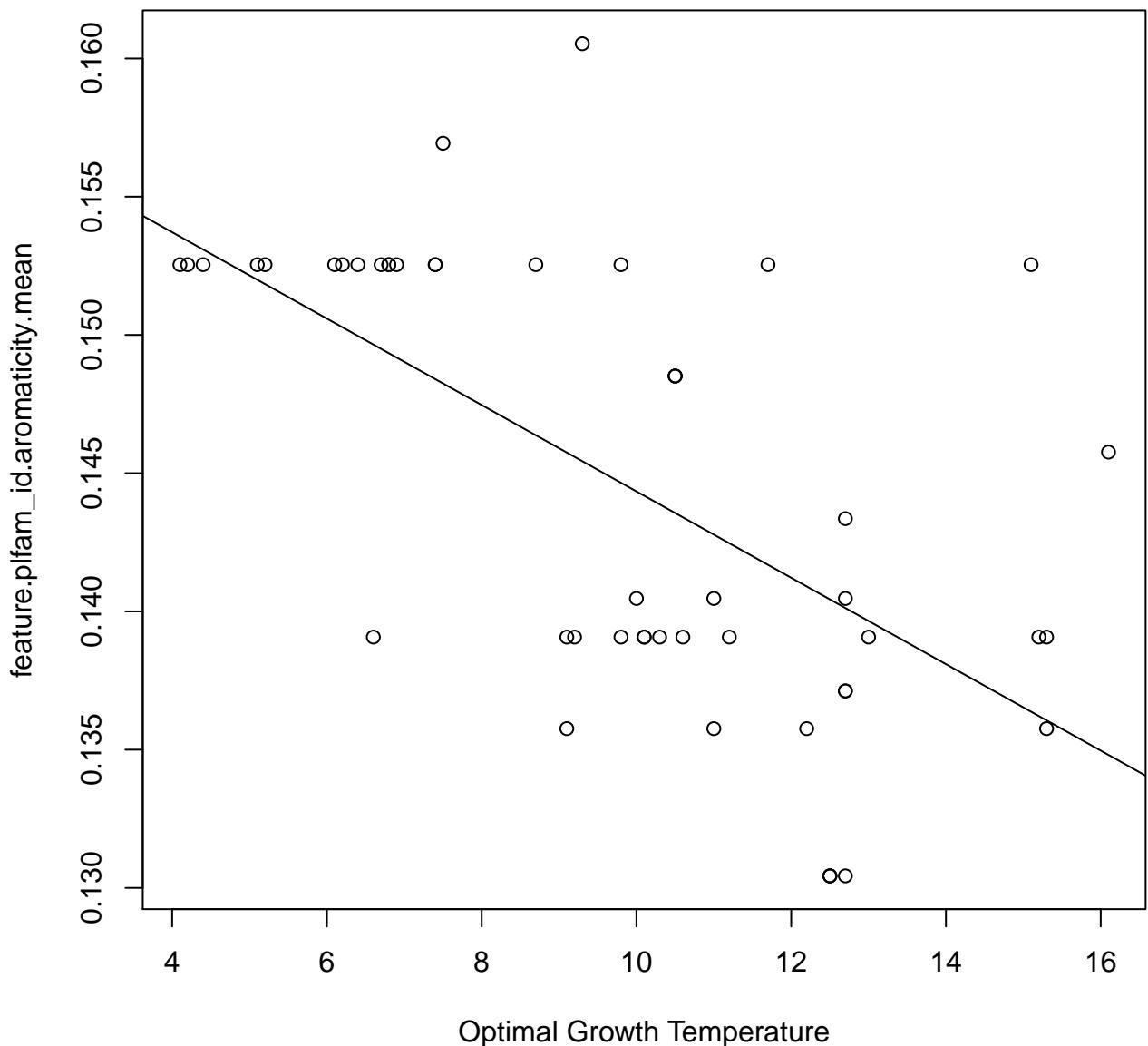
feature.plfam_id.aromaticity.mean
PLF_28228_00000781
Dihydrofolate reductase (EC 1.5.1.3)



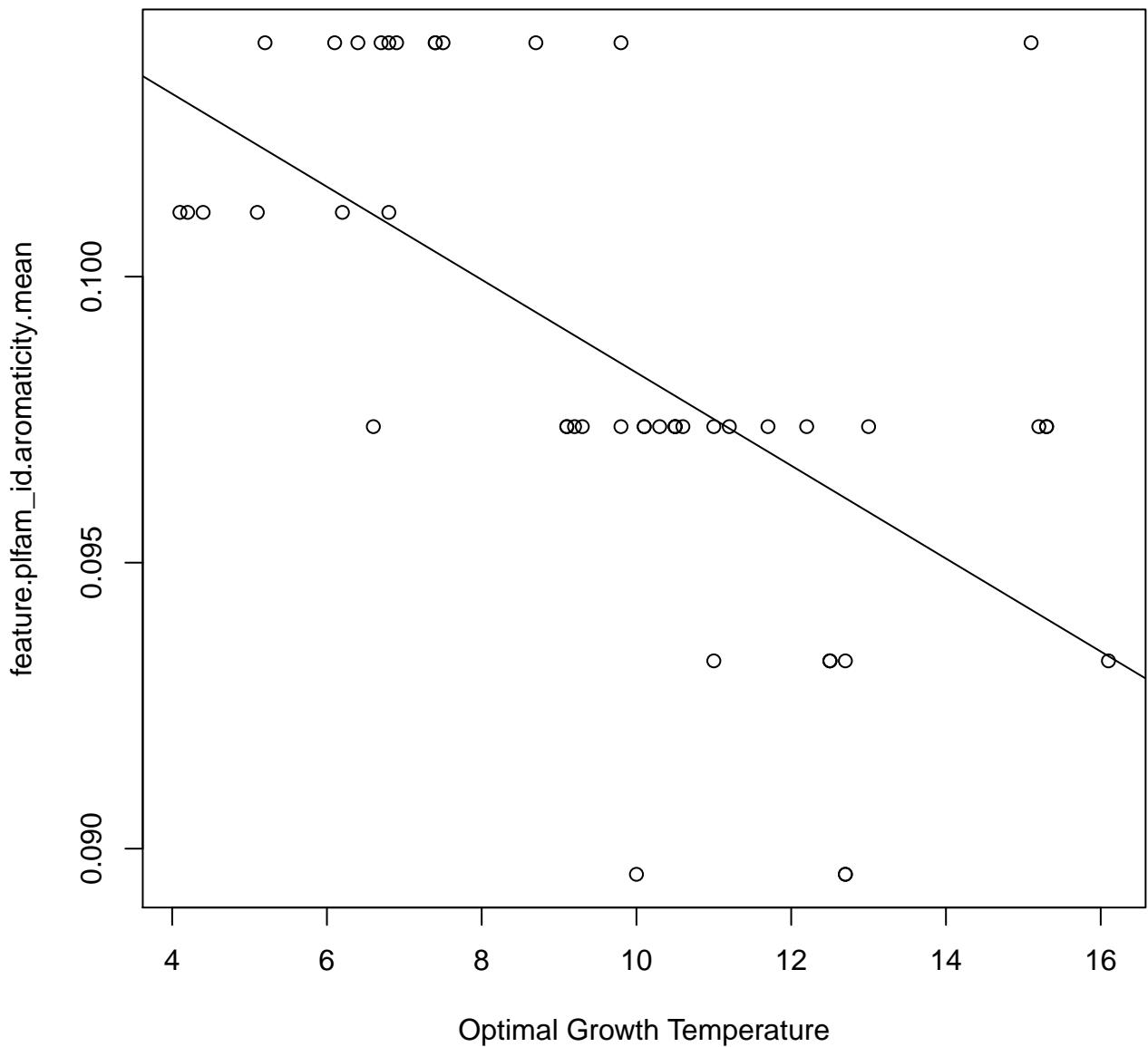
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PLF_28228_00000267
3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)



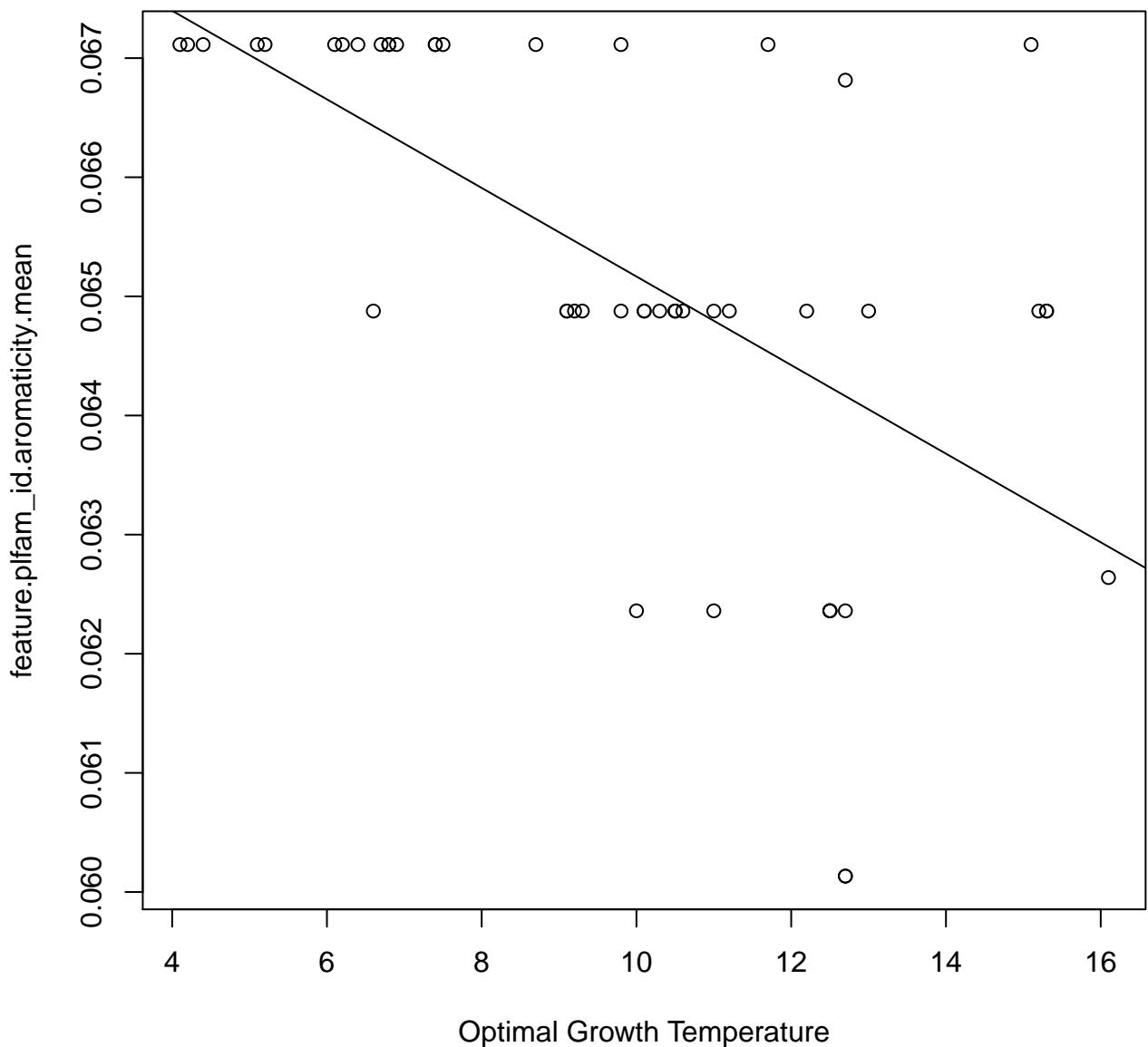
feature.plfam_id.aromaticity.mean
PLF_28228_00001911
Permease of the drug/metabolite transporter (DMT) superfamily



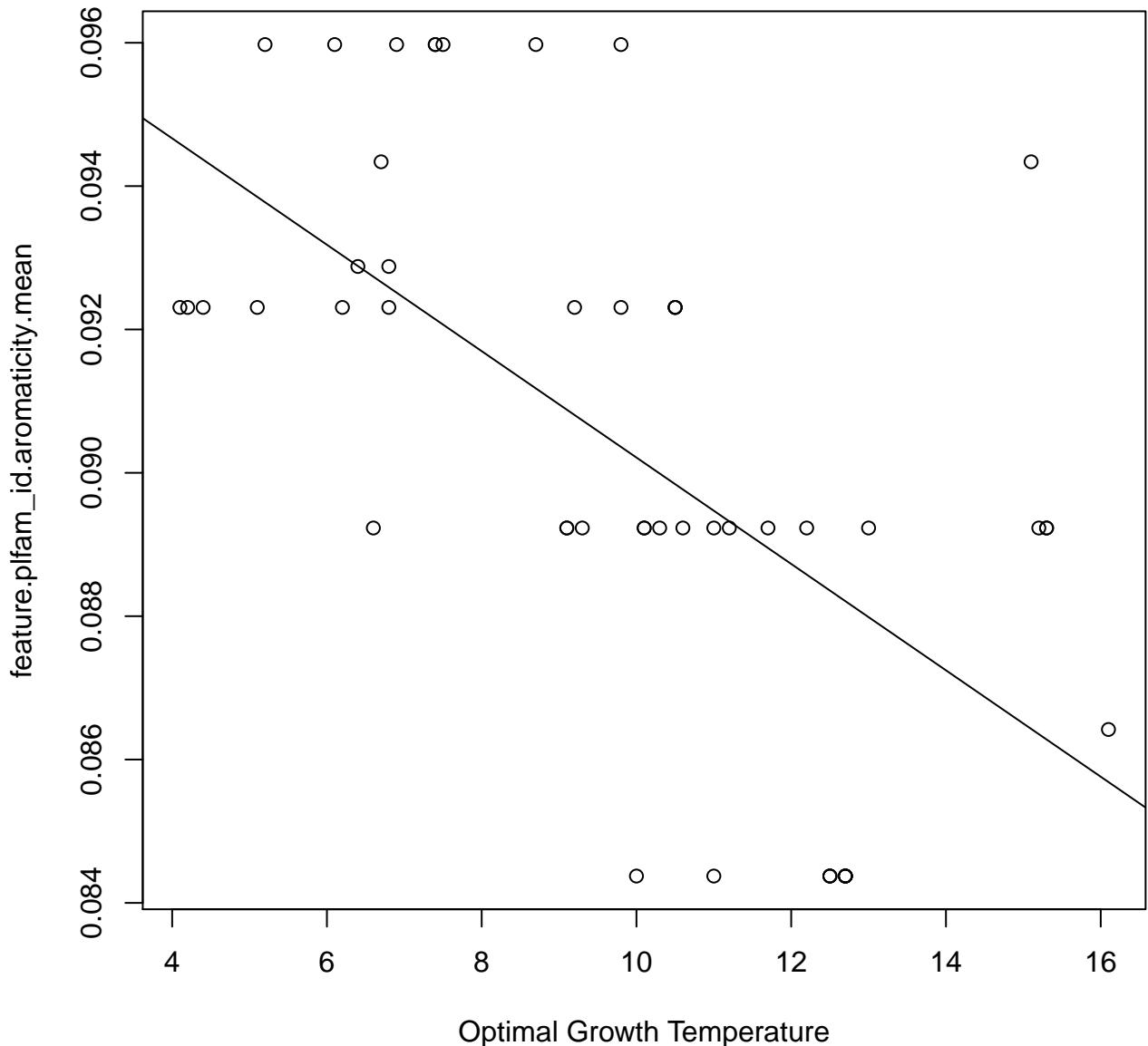
feature.plfam_id.aromaticity.mean
PLF_28228_00000719
4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8)



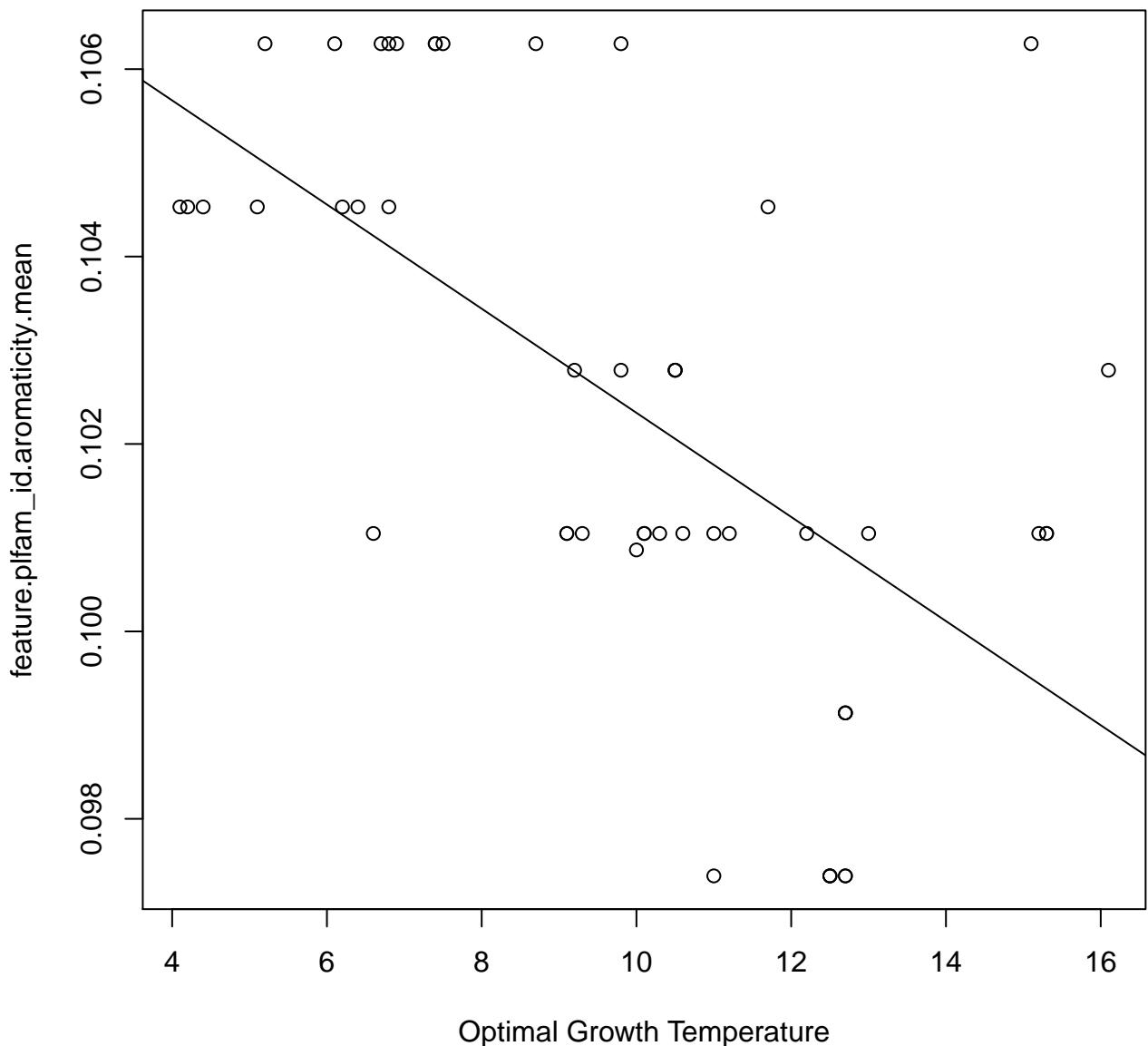
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MotA/ToIQ/ExbB proton channel family protein



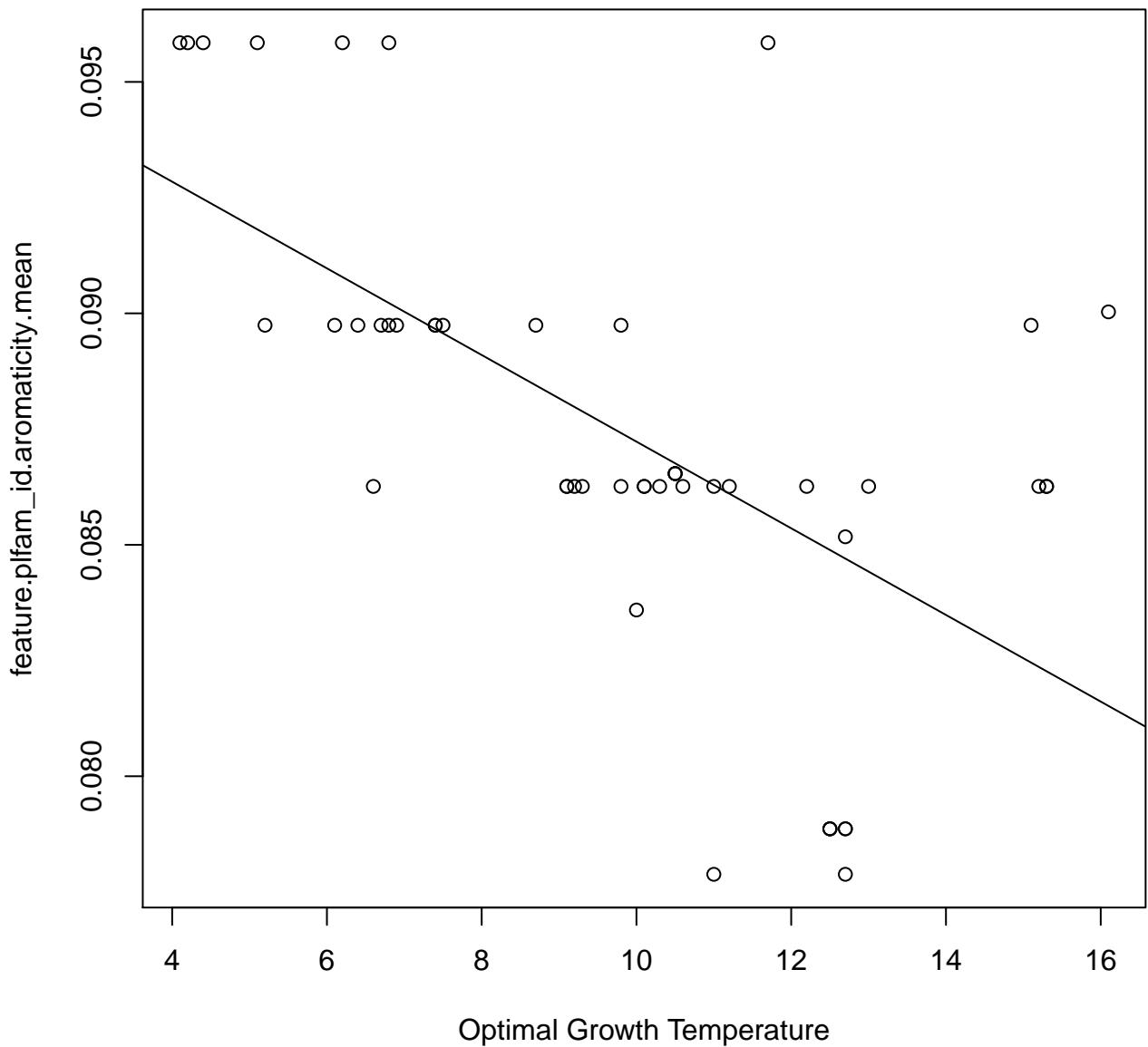
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Thiamine-monophosphate kinase (EC 2.7.4.16)



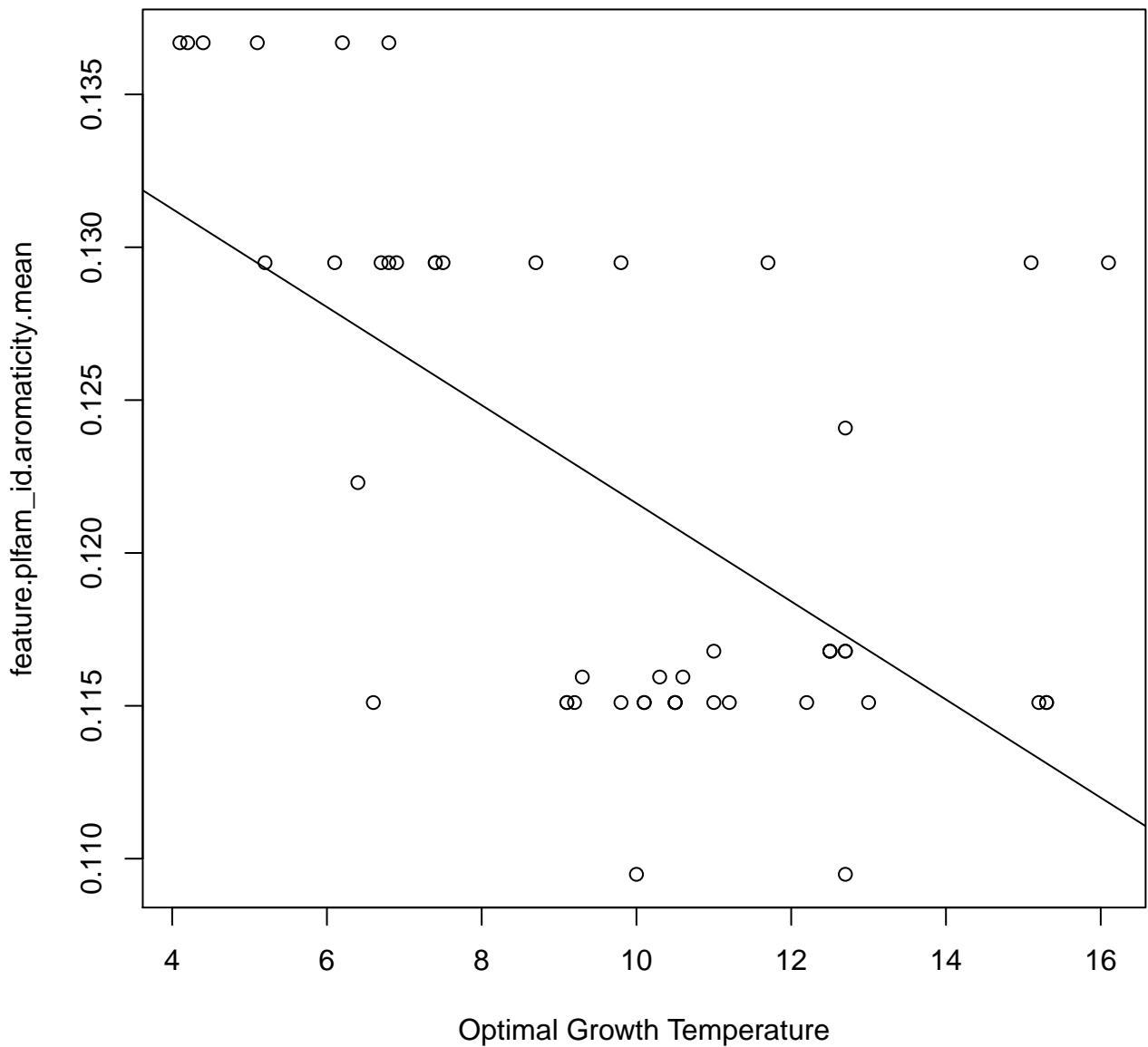
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Acetolactate synthase large subunit (EC 2.2.1.6)



feature.plfam_id.aromaticity.mean
PLF_28228_00000770
D-alanine--D-alanine ligase (EC 6.3.2.4)



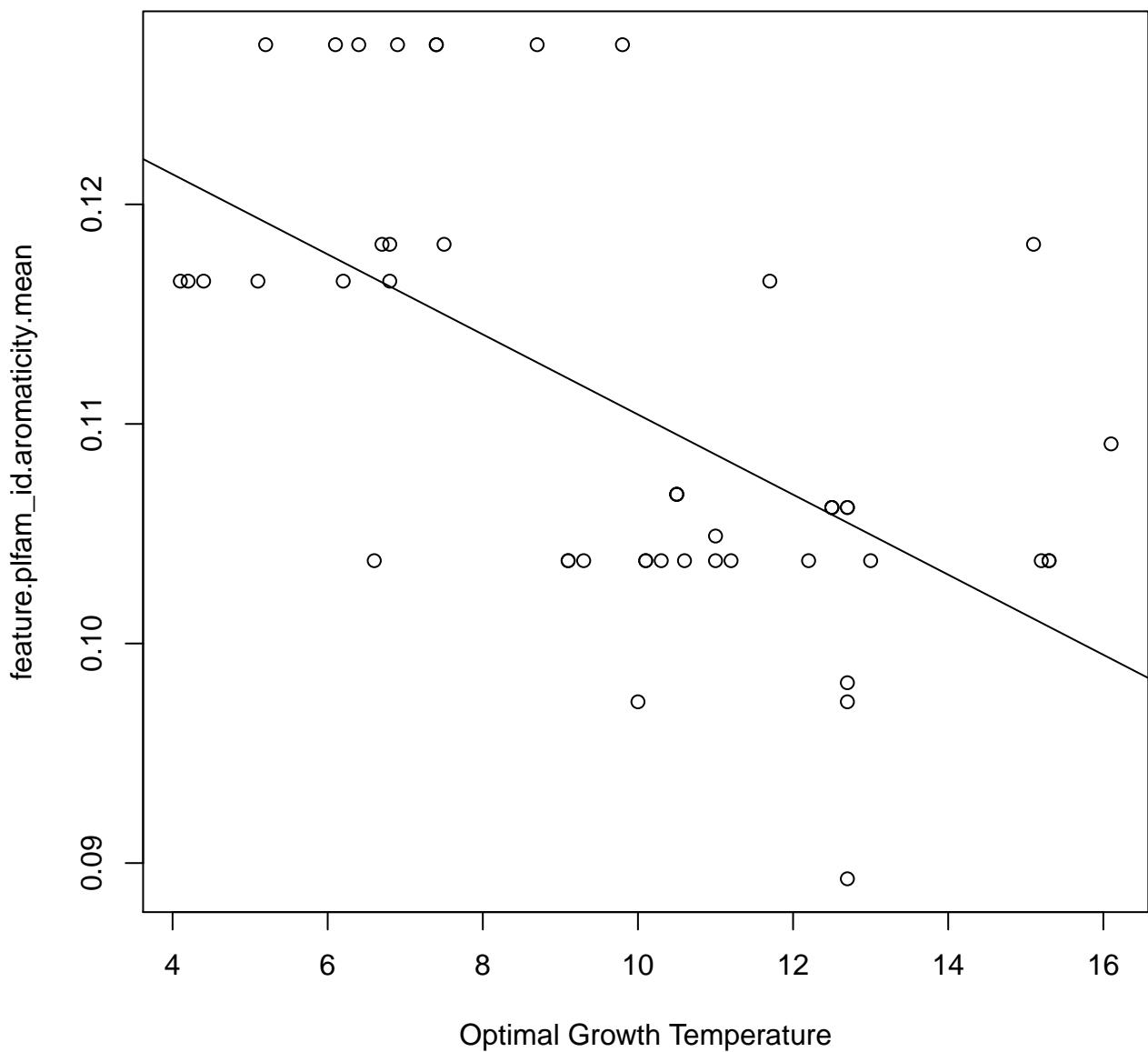
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Acetyltransferase, GNAT family



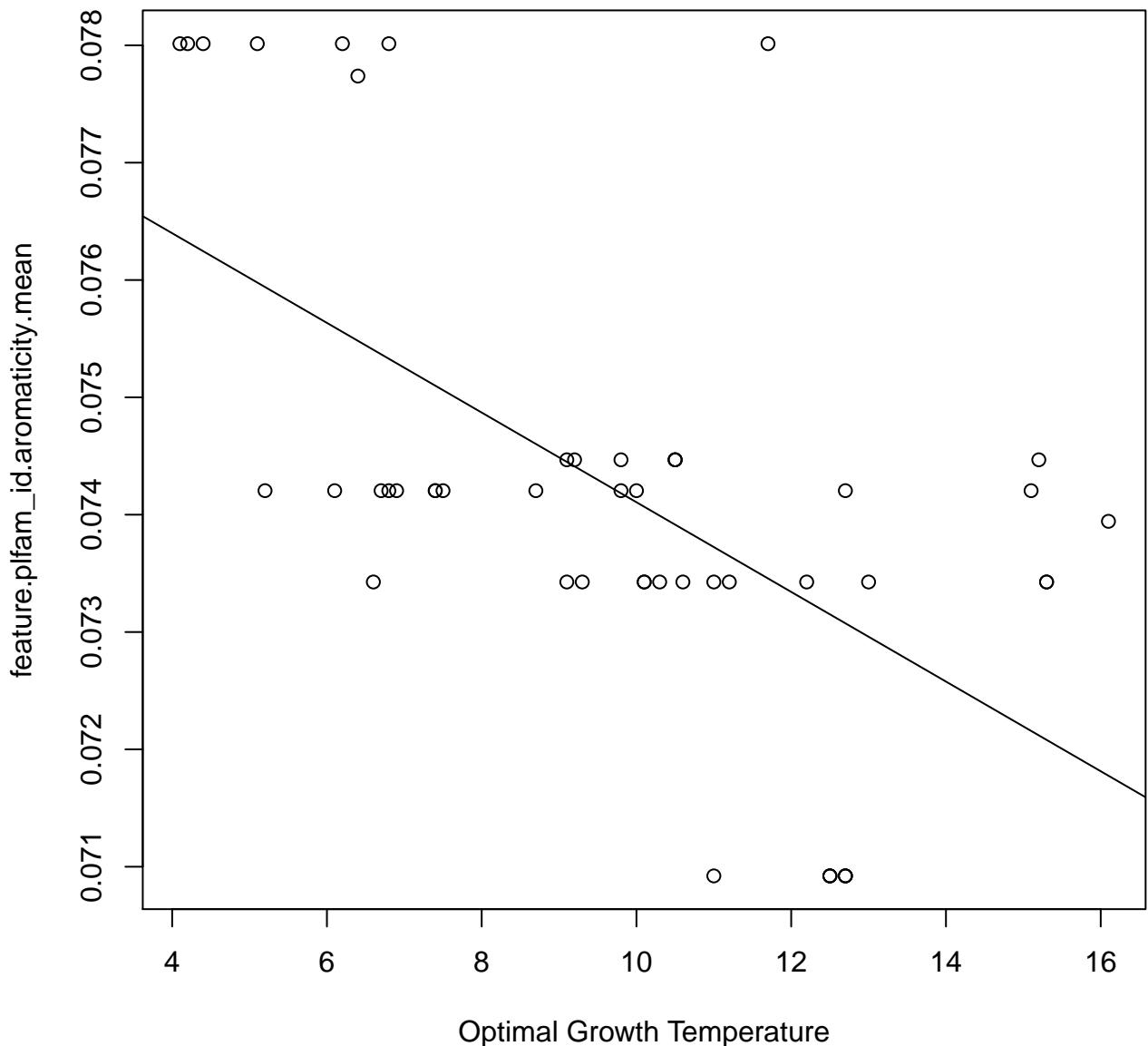
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PLF_28228_00002444

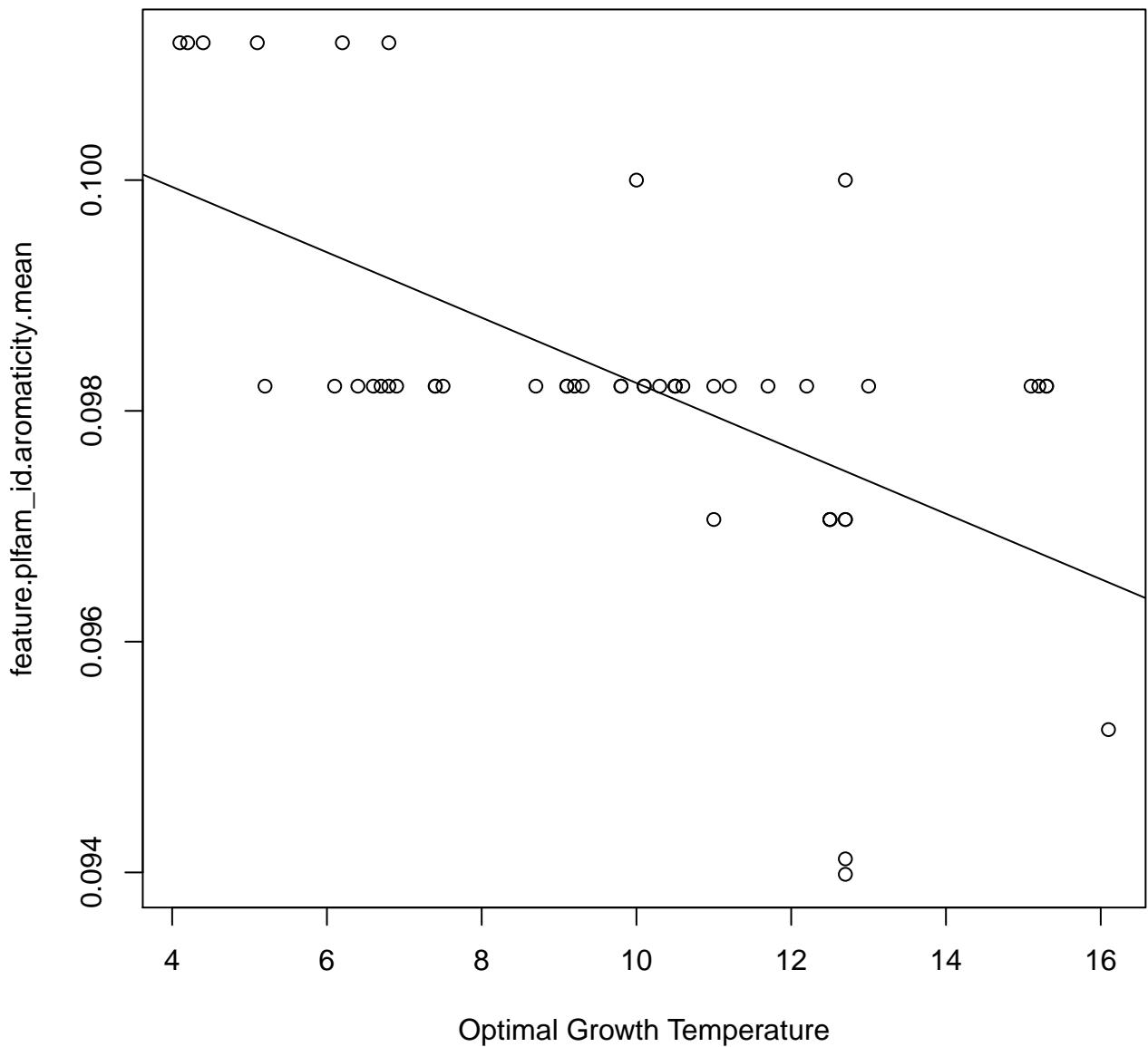
hypothetical protein



feature.plfam_id.aromaticity.mean
PLF_28228_00000702
16S rRNA (cytidine(1402)-2'-O)-methyltransferase (EC 2.1.1.198)



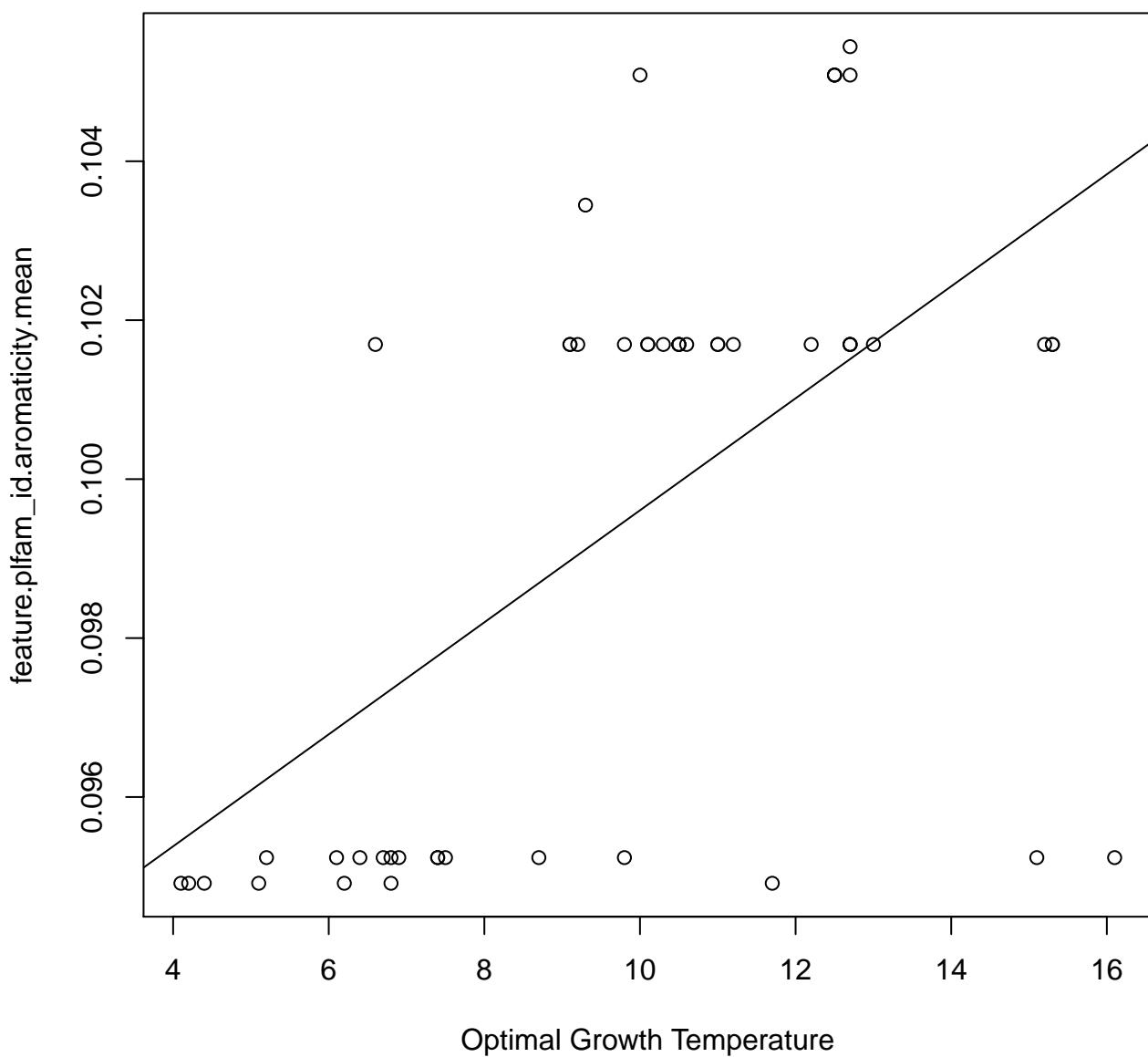
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UDP-glucose 4-epimerase (EC 5.1.3.2)



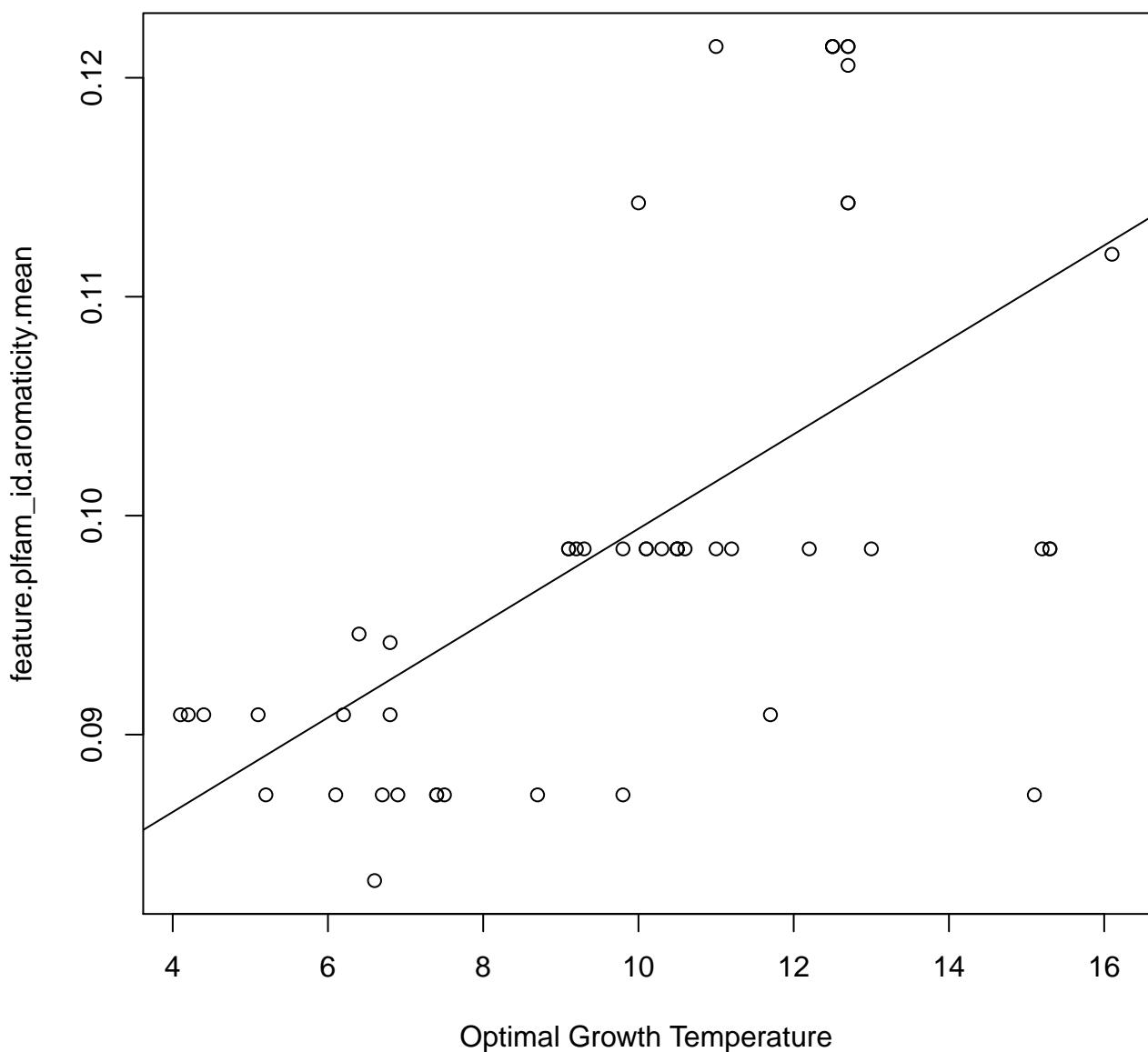
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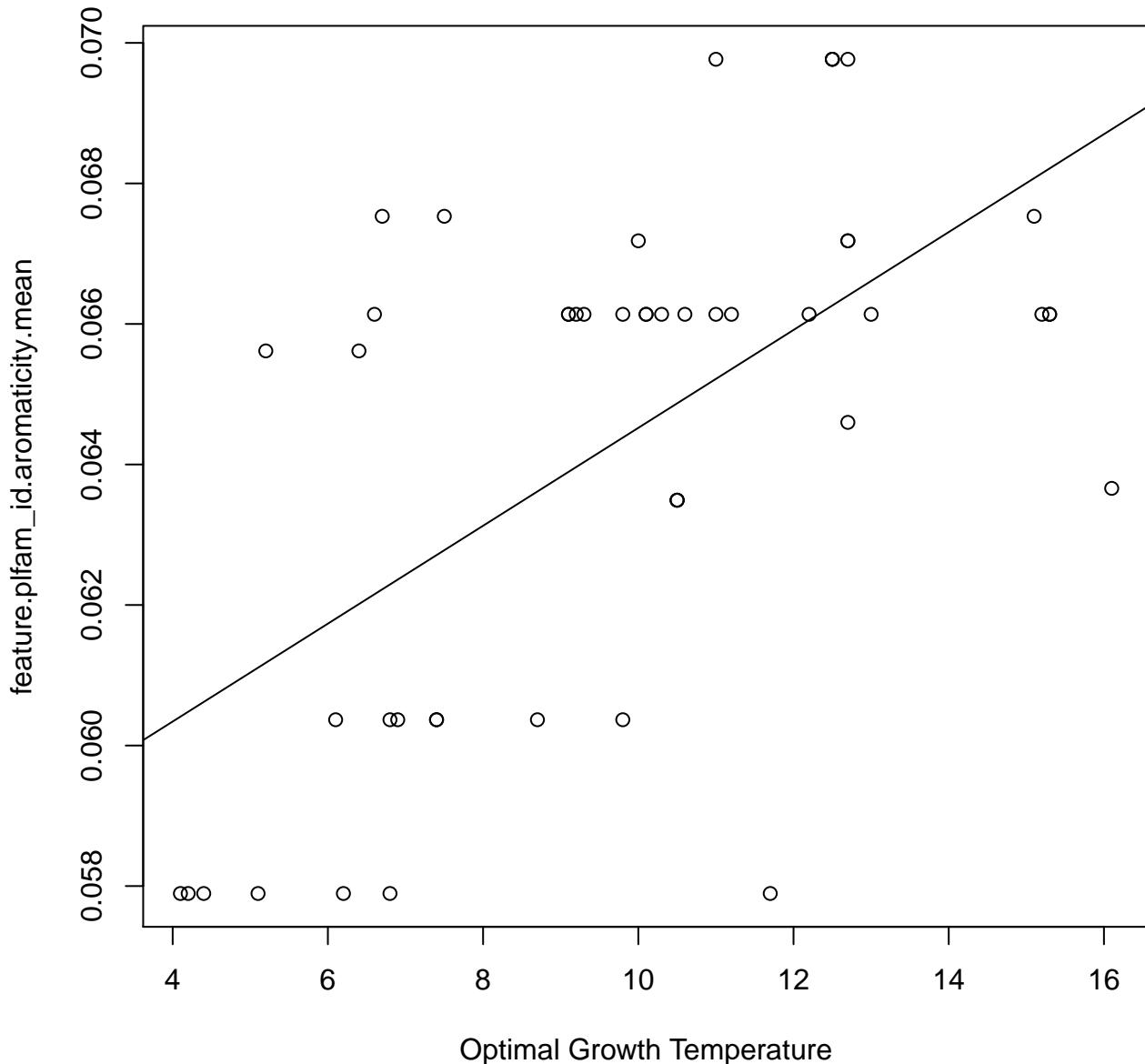
HfIC protein



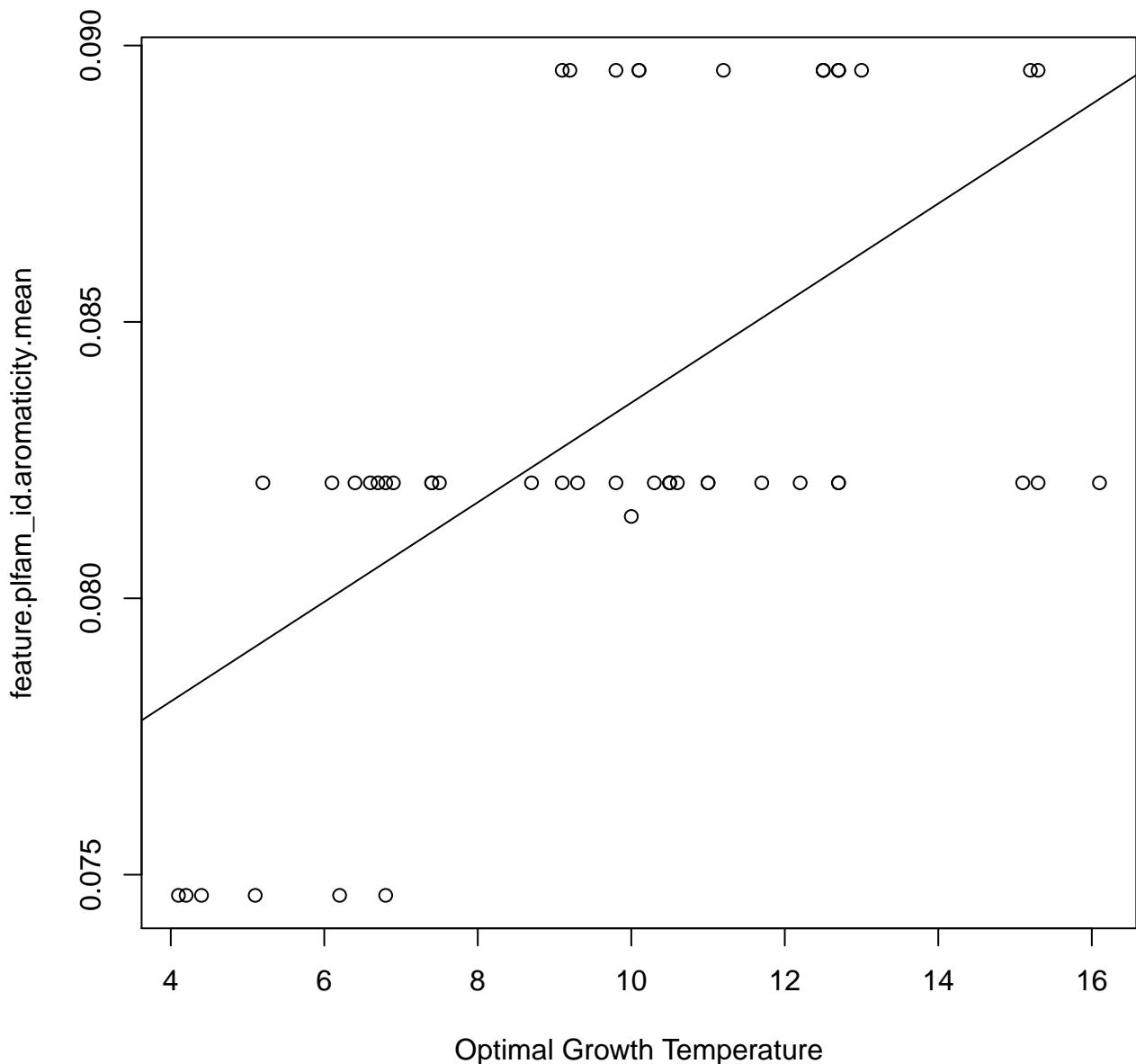
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DNA-binding protein, CopG family



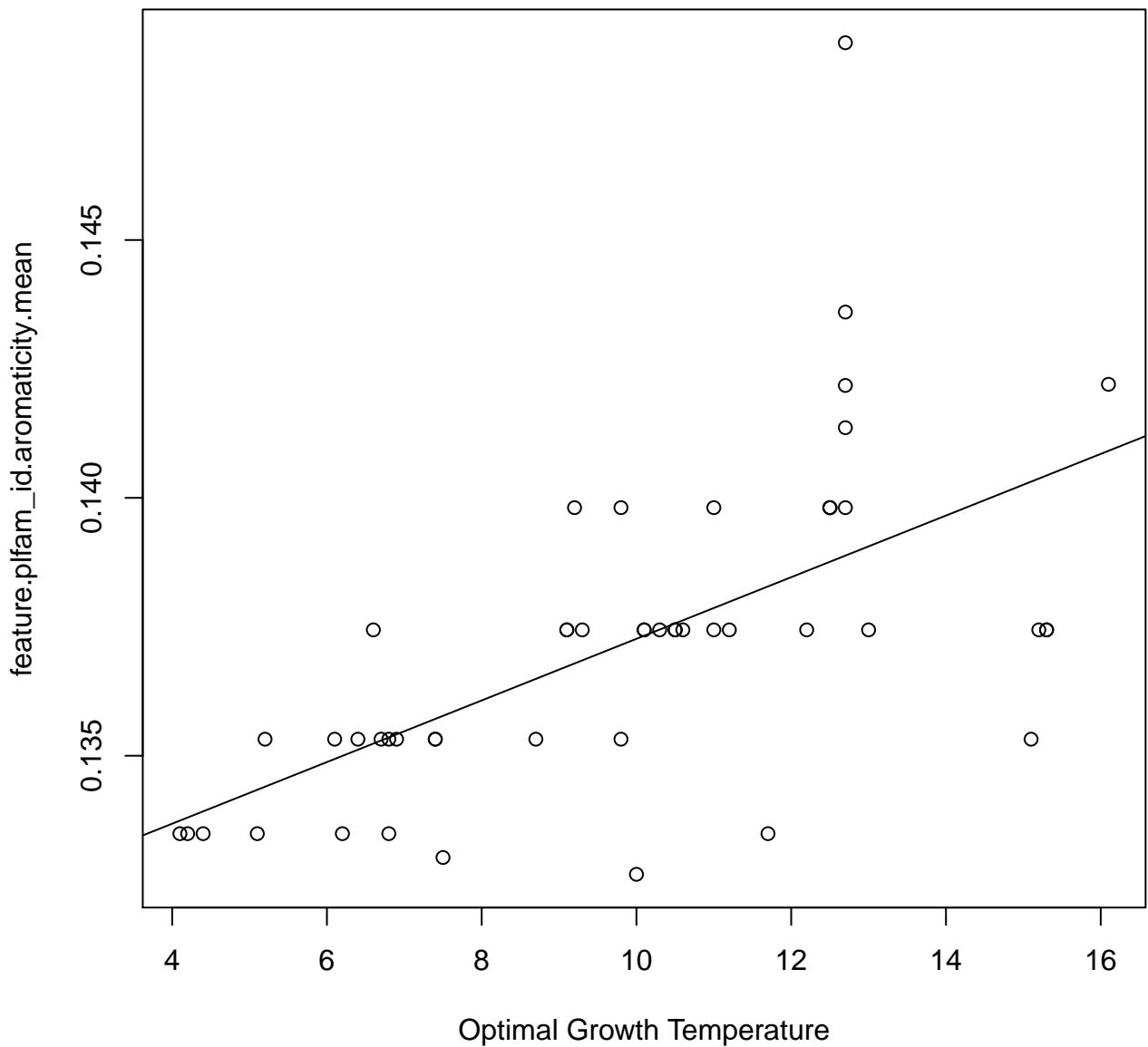
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Uncharacterized protein SO_3077



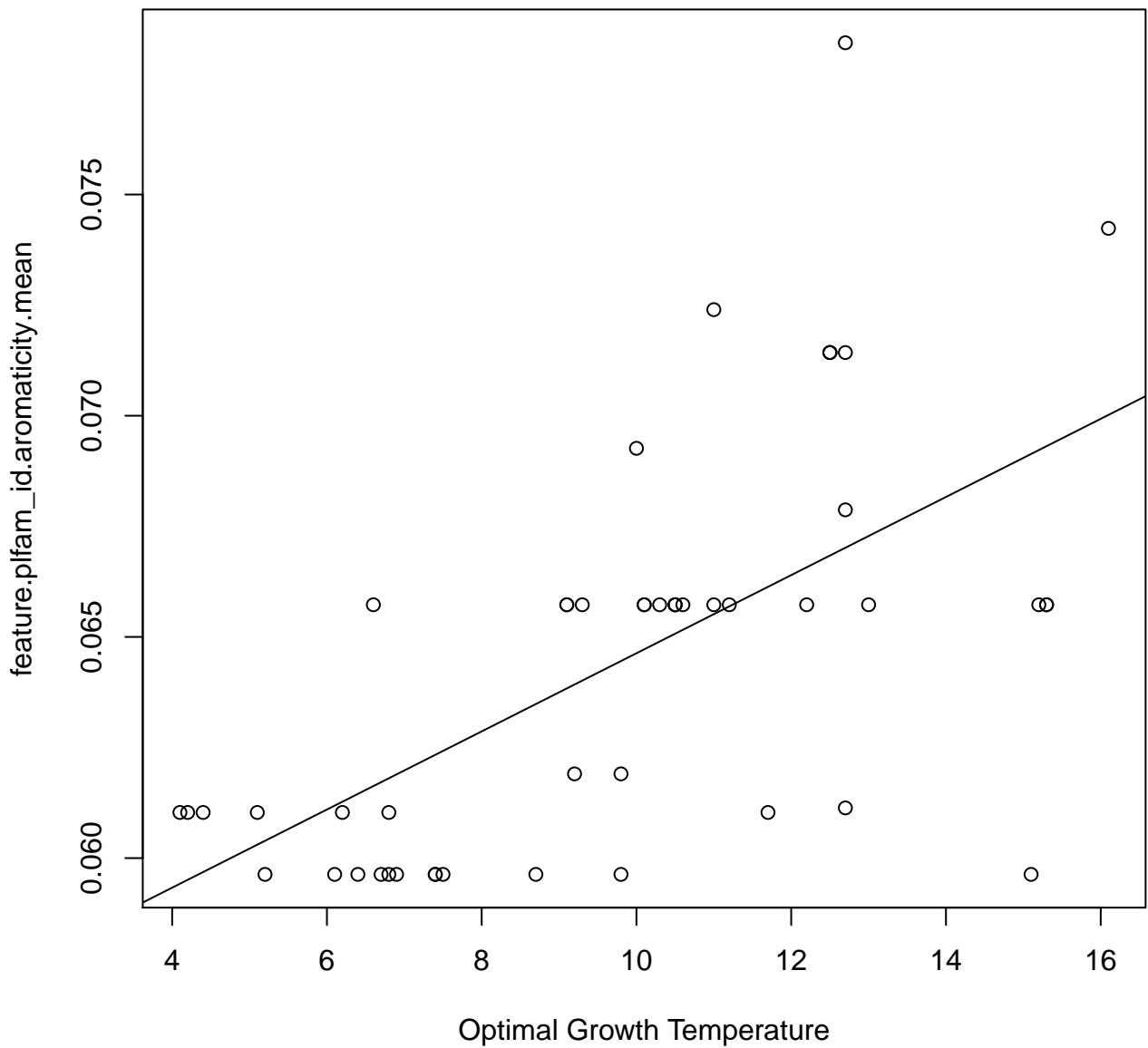
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Protein YhfA



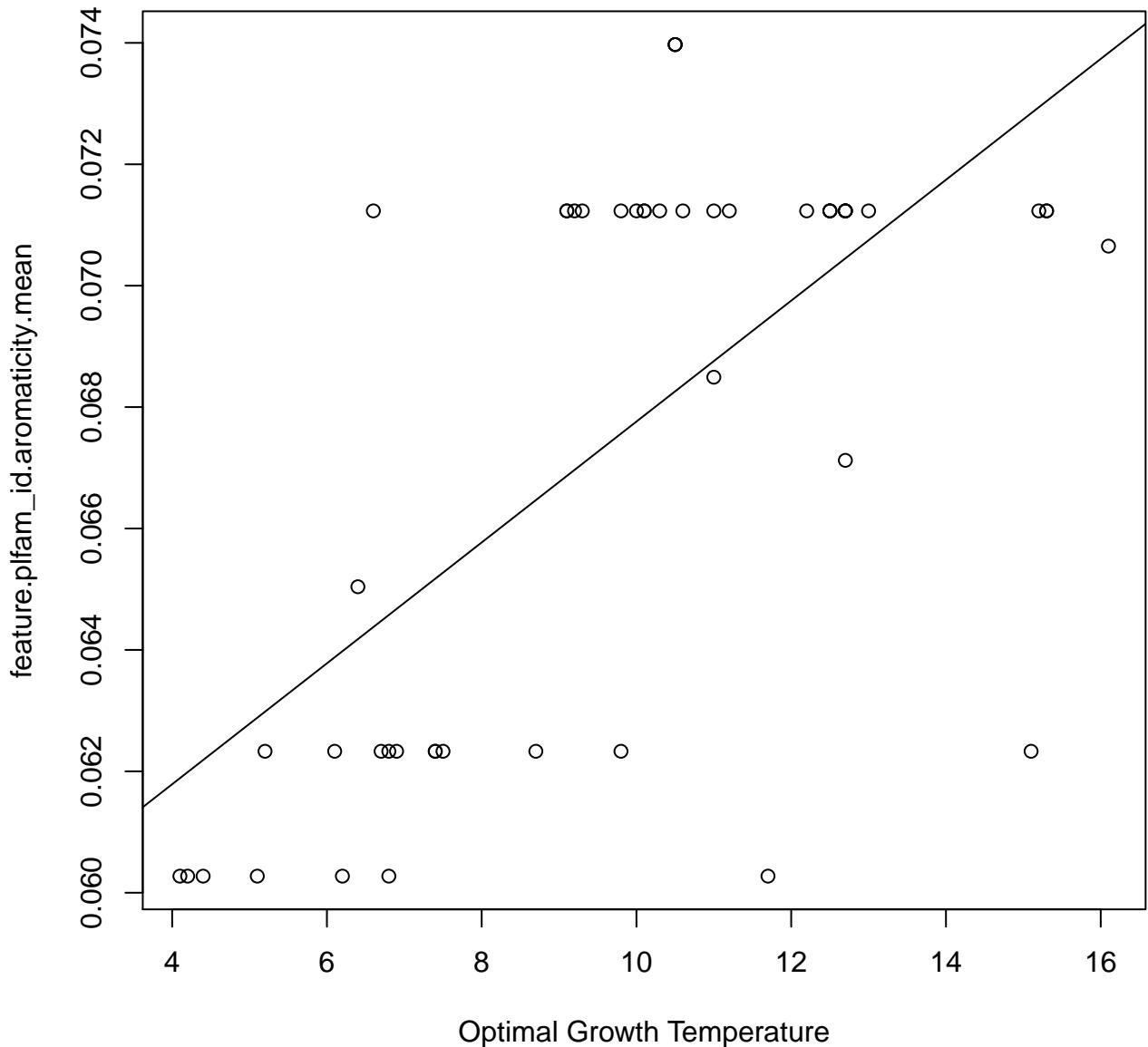
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Uncharacterized MFS-type transporter



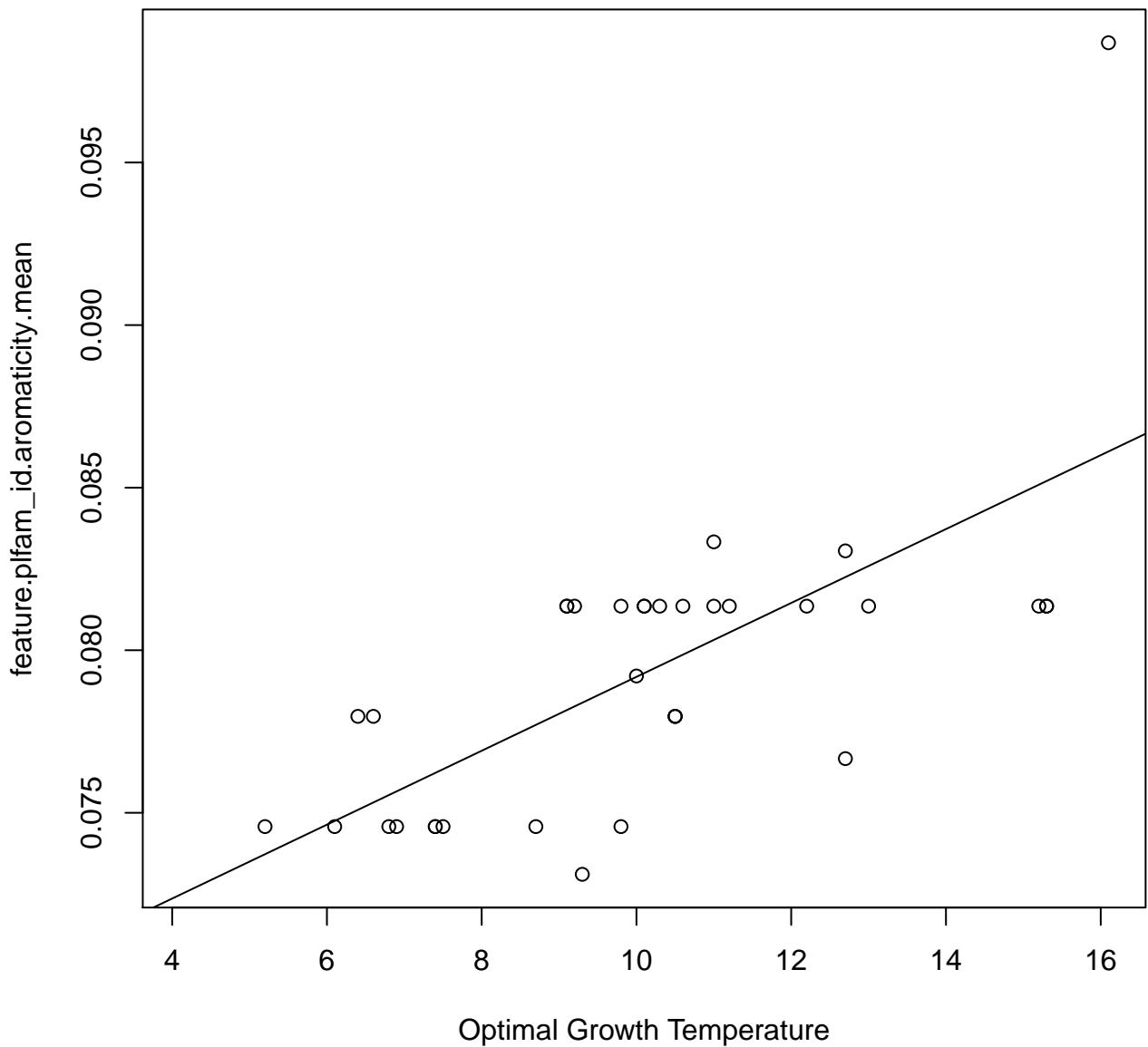
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PLF_28228_00000869
GTP-binding protein EngB



feature.plfam_id.aromaticity.mean
PLF_28228_00001874
Glutamate 5-kinase (EC 2.7.2.11) / RNA-binding C-terminal domain PUA



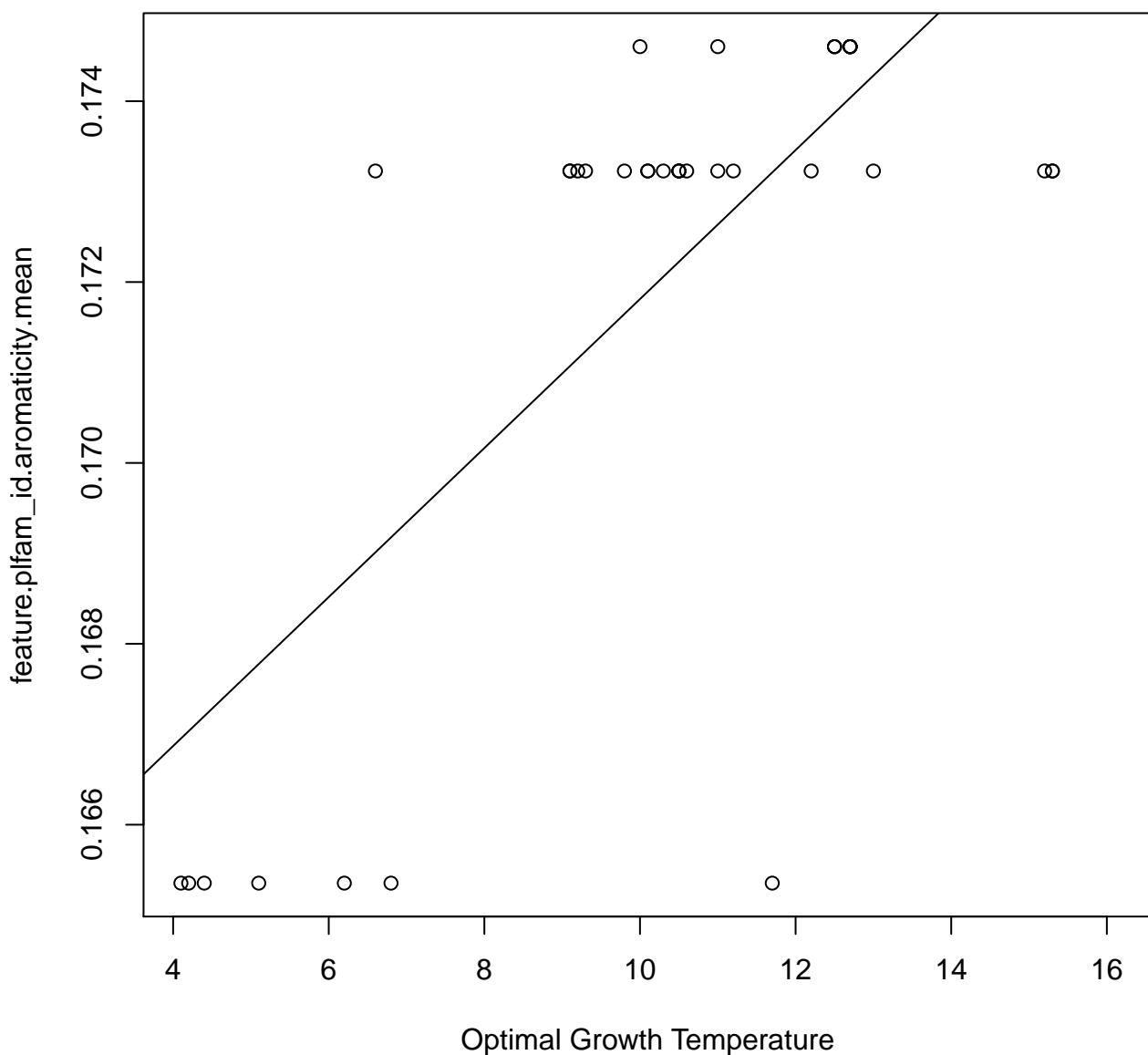
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Transcriptional regulator, LysR family



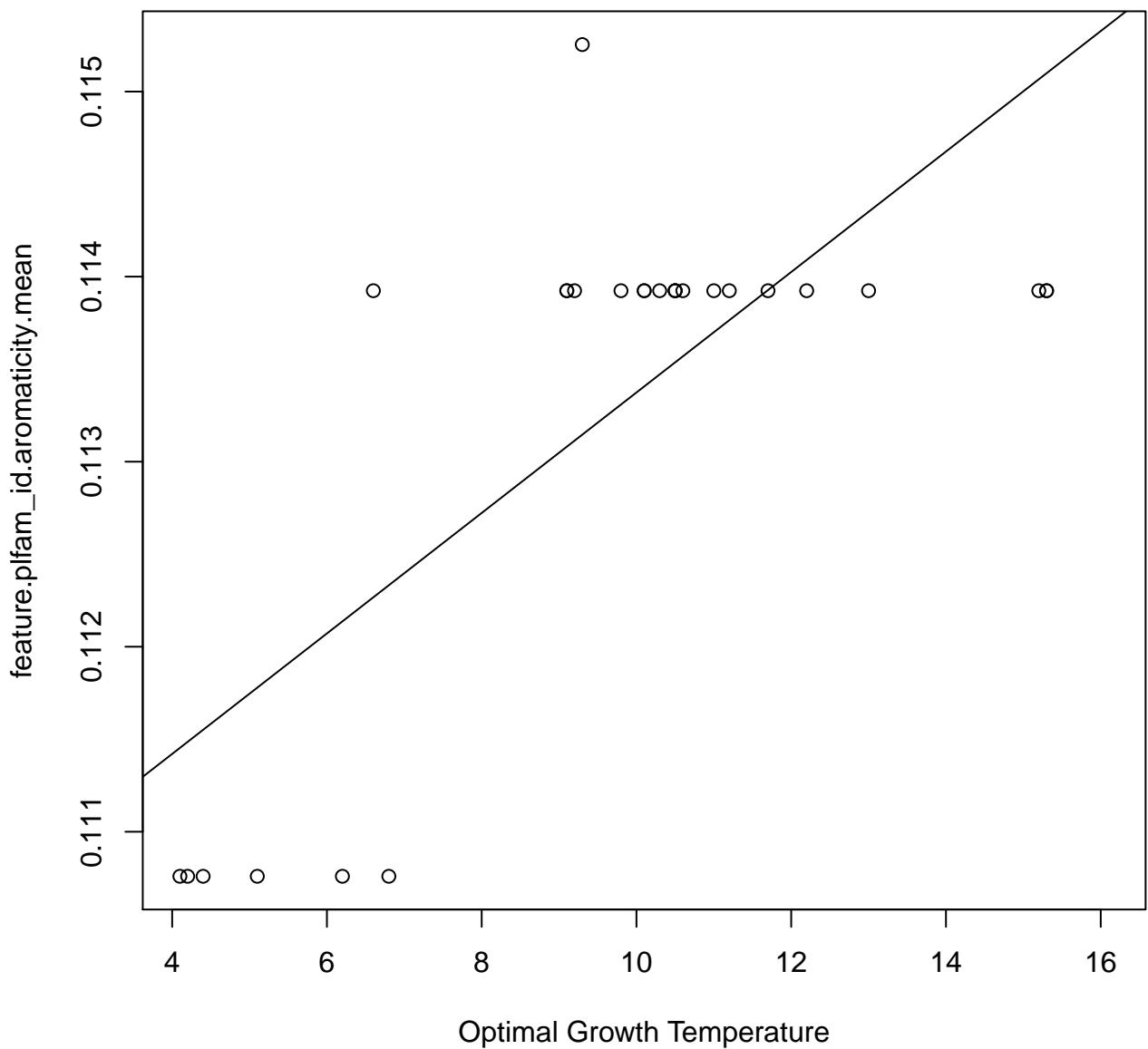
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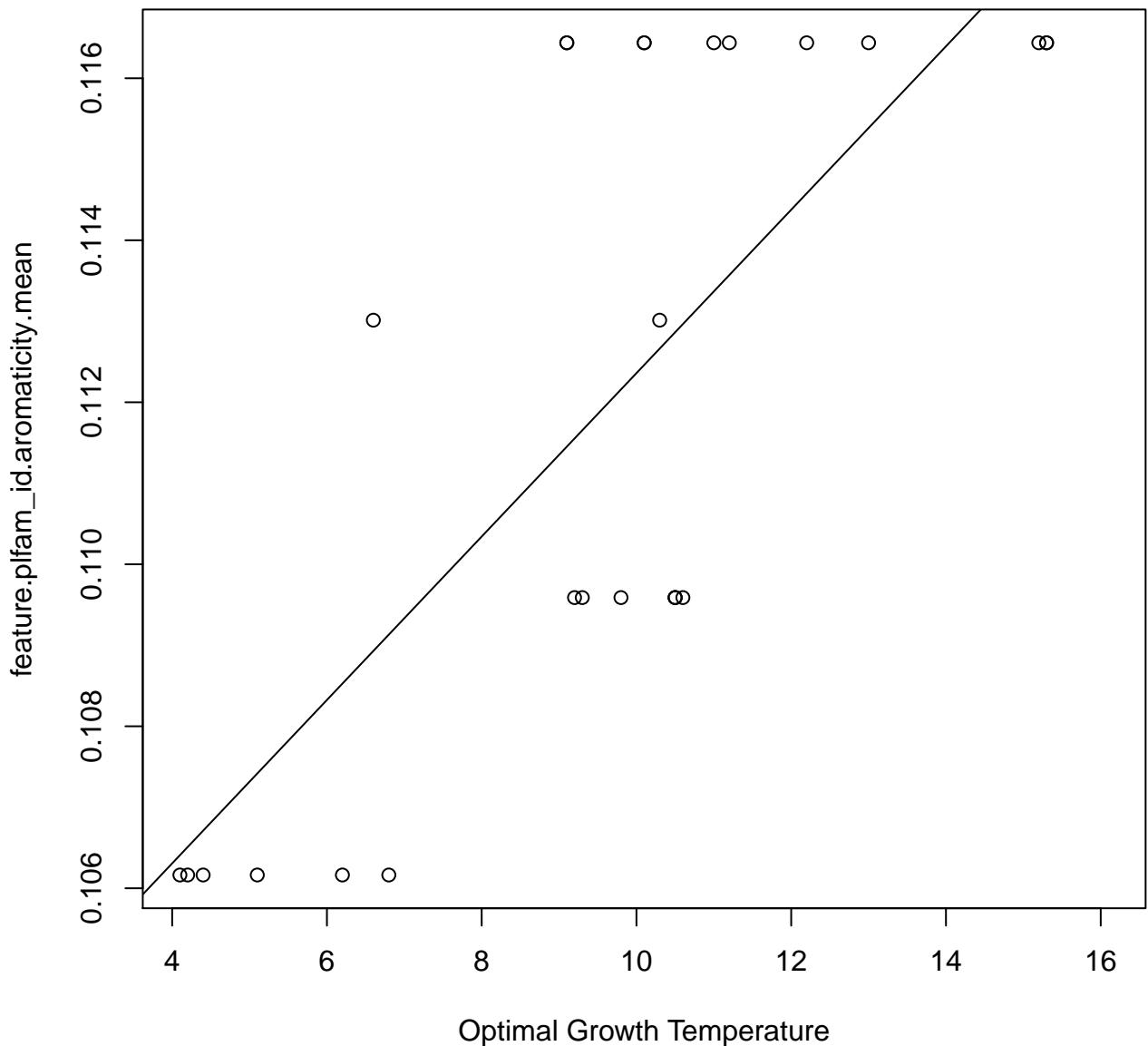
hypothetical protein



feature.plfam_id.aromaticity.mean
PLF_28228_00014559
Transcriptional regulator, LysR family



feature.plfam_id.aromaticity.mean
PLF_28228_00023267
Uncharacterized protein conserved in bacteria, NMA0228-like



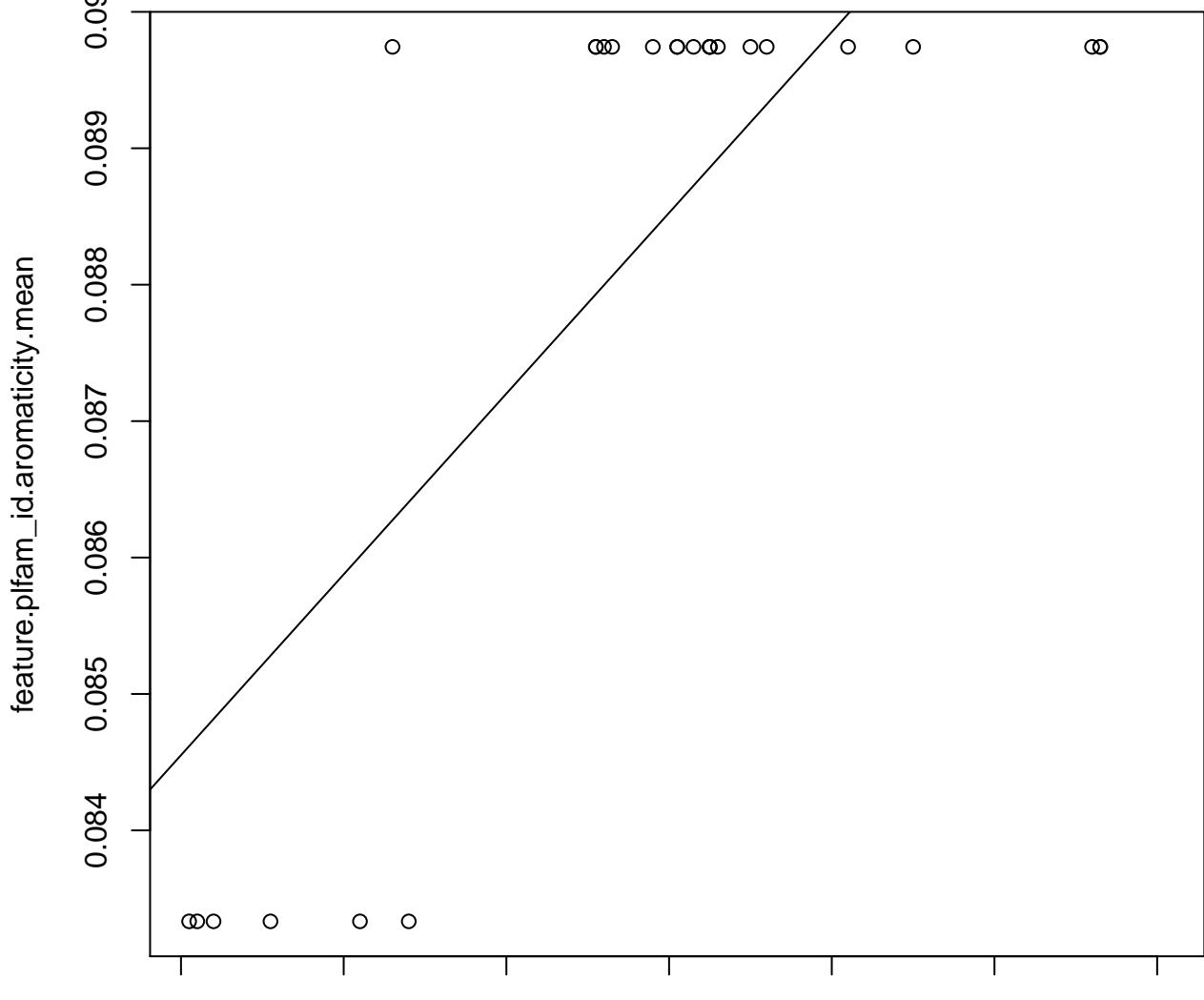
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PLF_28228_00015077

hypothetical protein

feature.pfam_id.aromaticity.mean

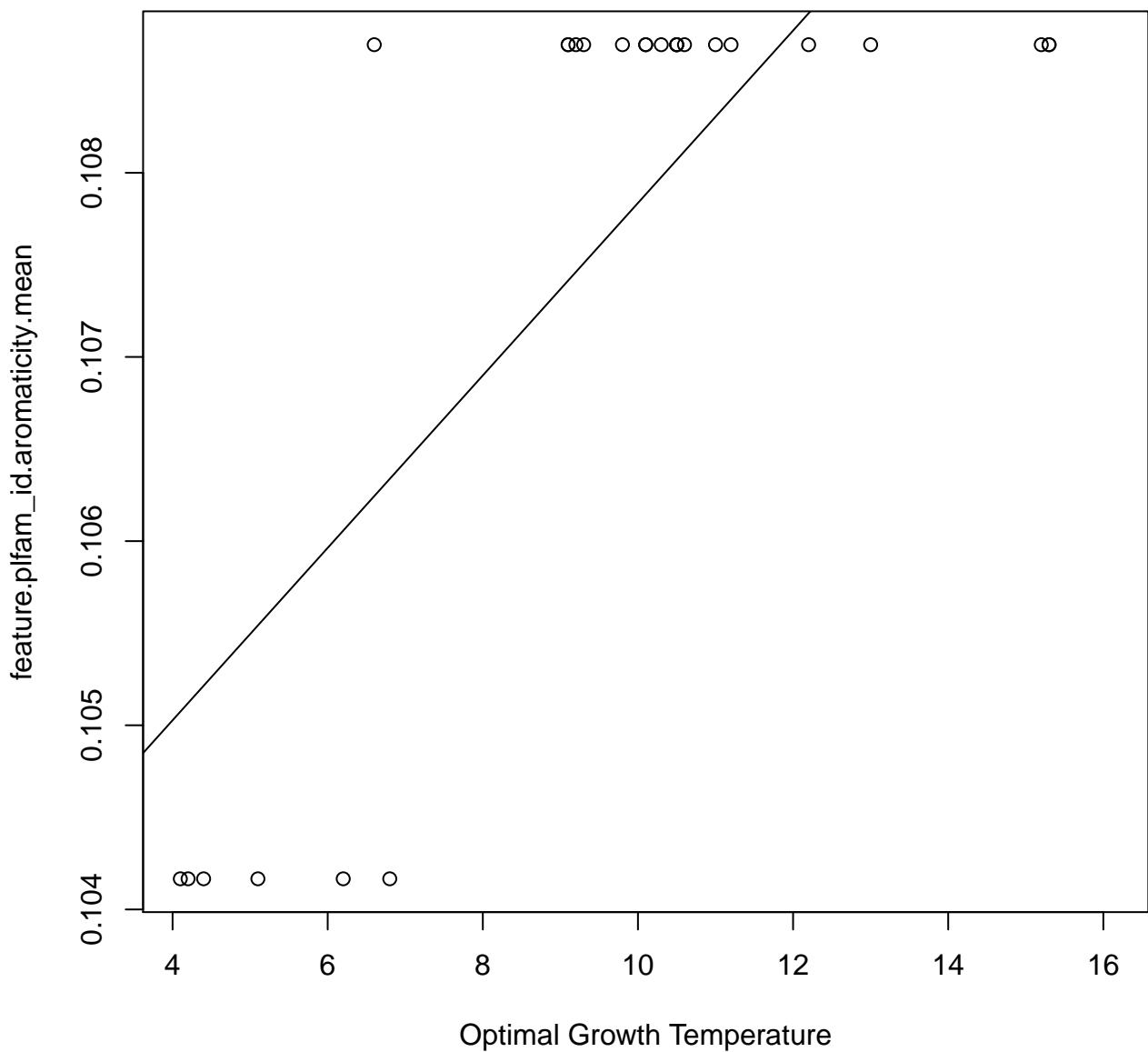
Optimal Growth Temperature



feature.plfam_id.aromaticity.mean

PLF_28228_00029369

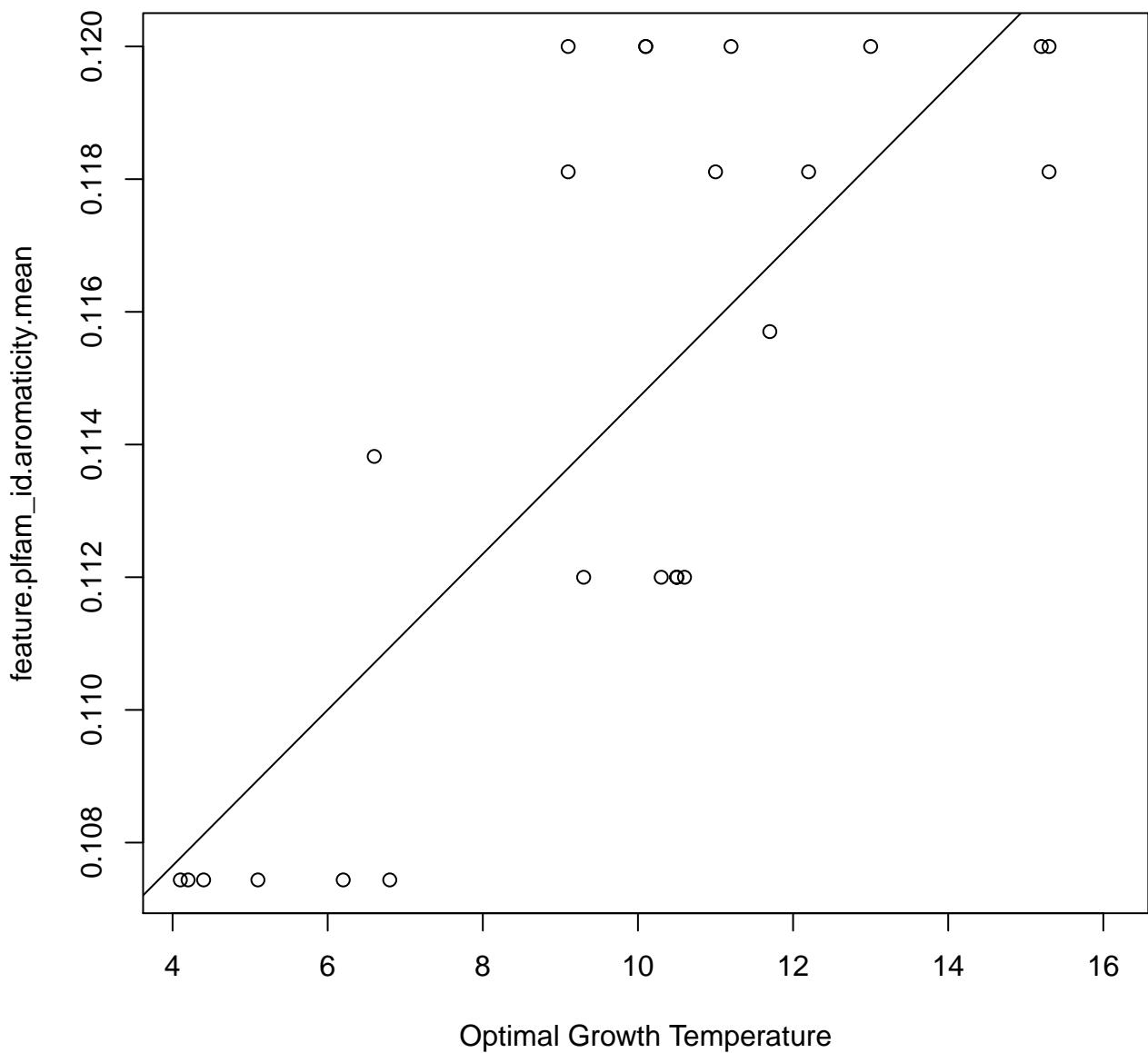
hypothetical protein



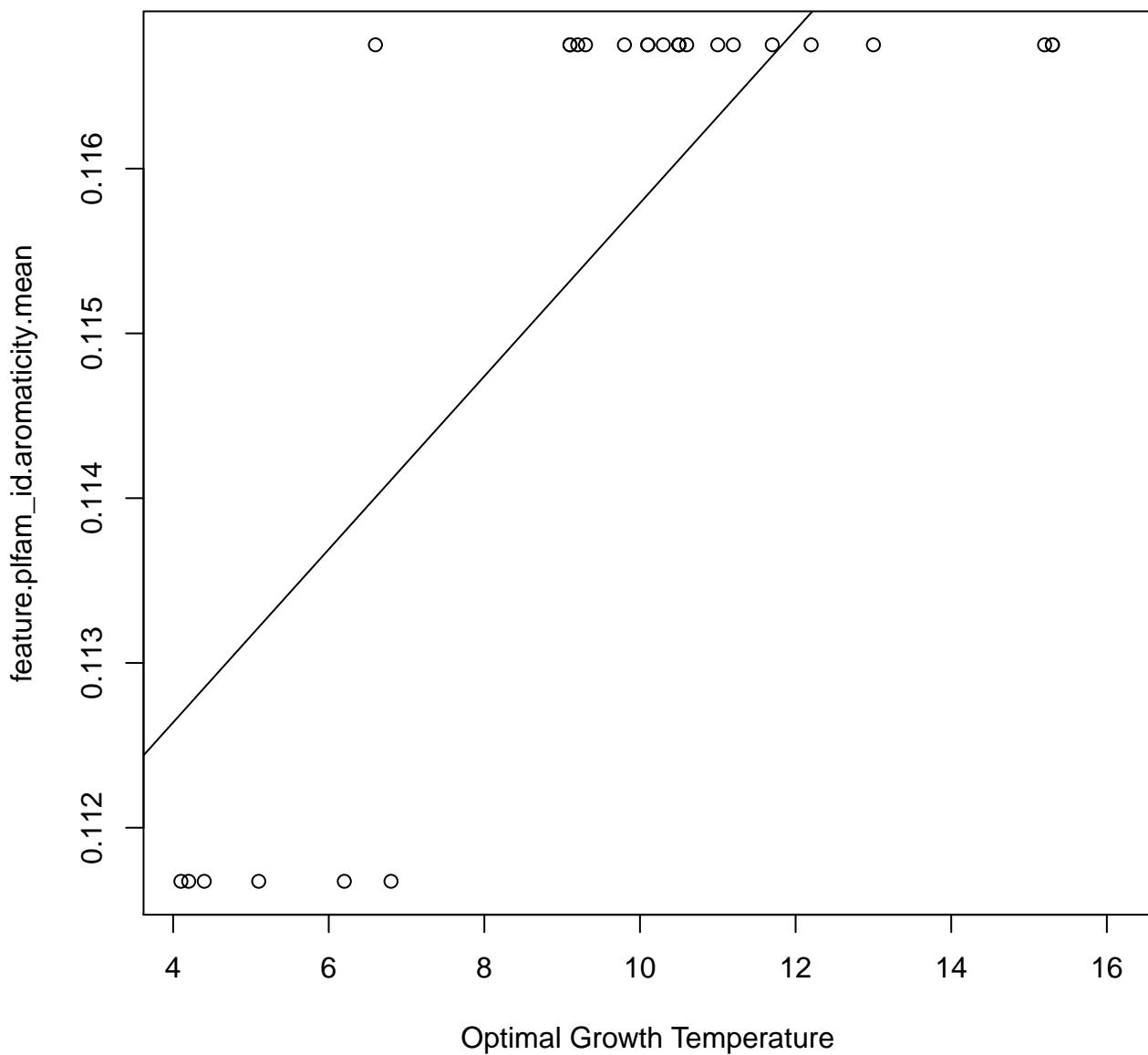
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PLF_28228_00020926

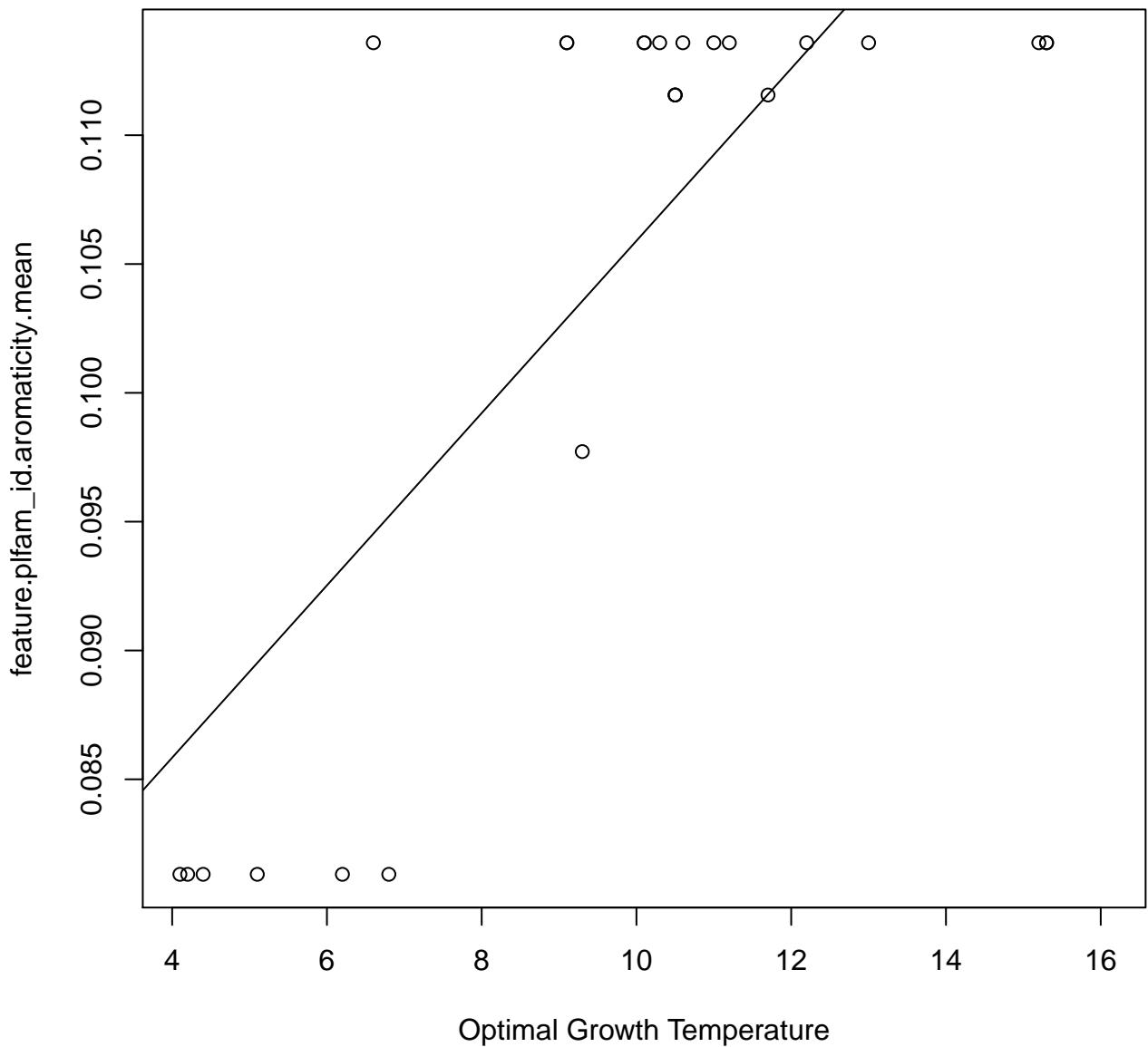
hypothetical protein



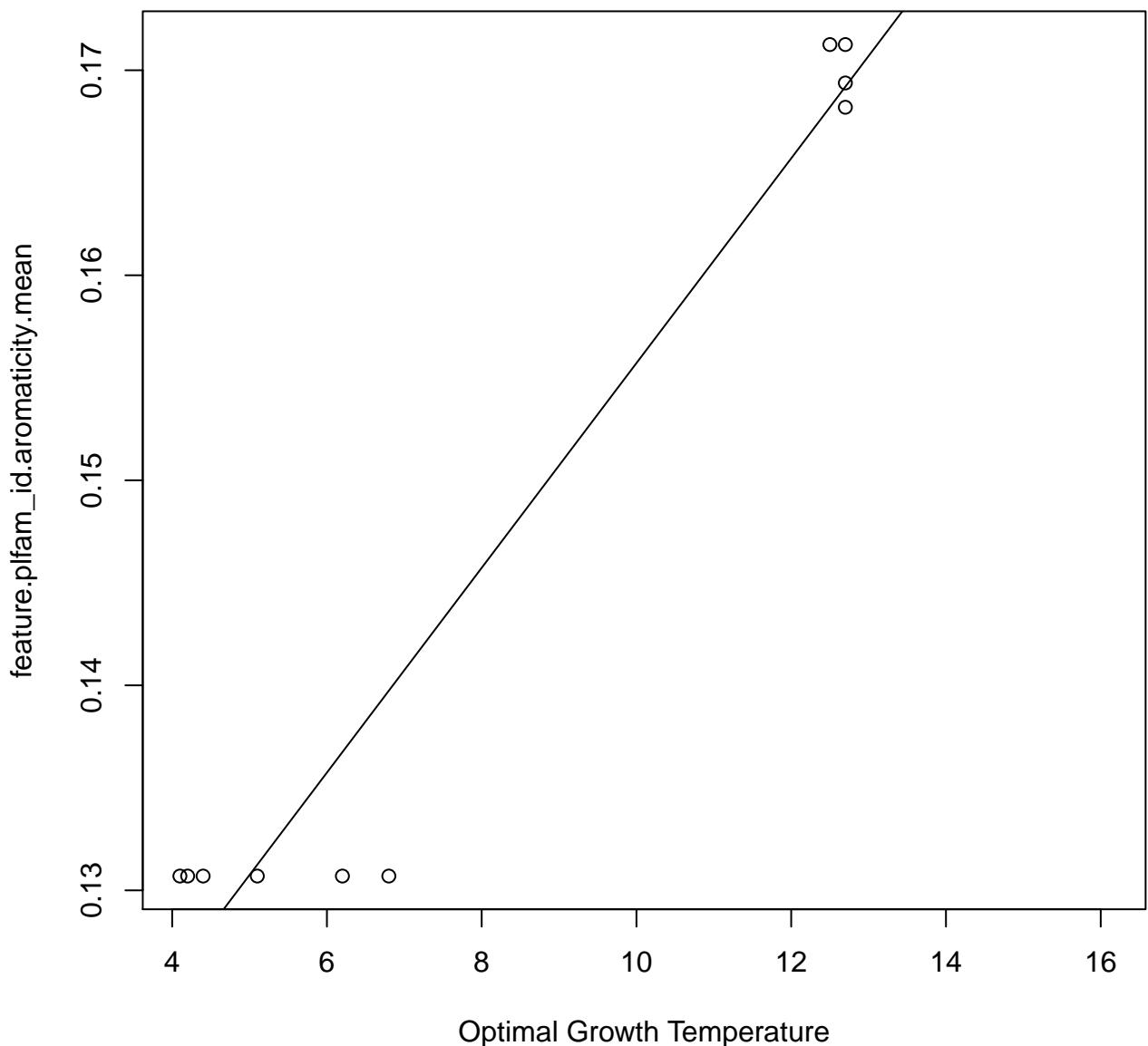
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Uncharacterized hydrolase DSY2054



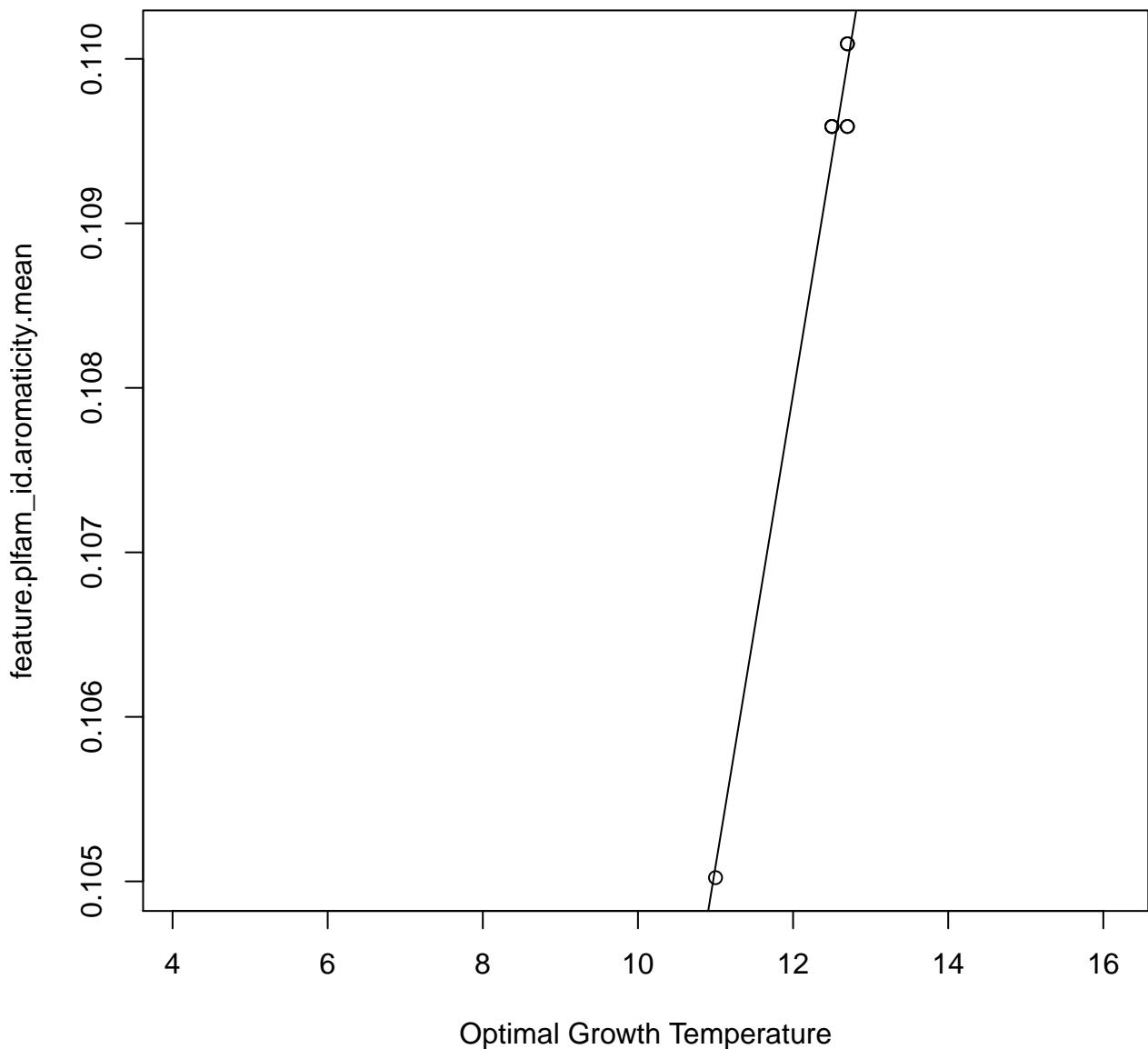
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PLF_28228_00022096
Two-component system sensor histidine kinase



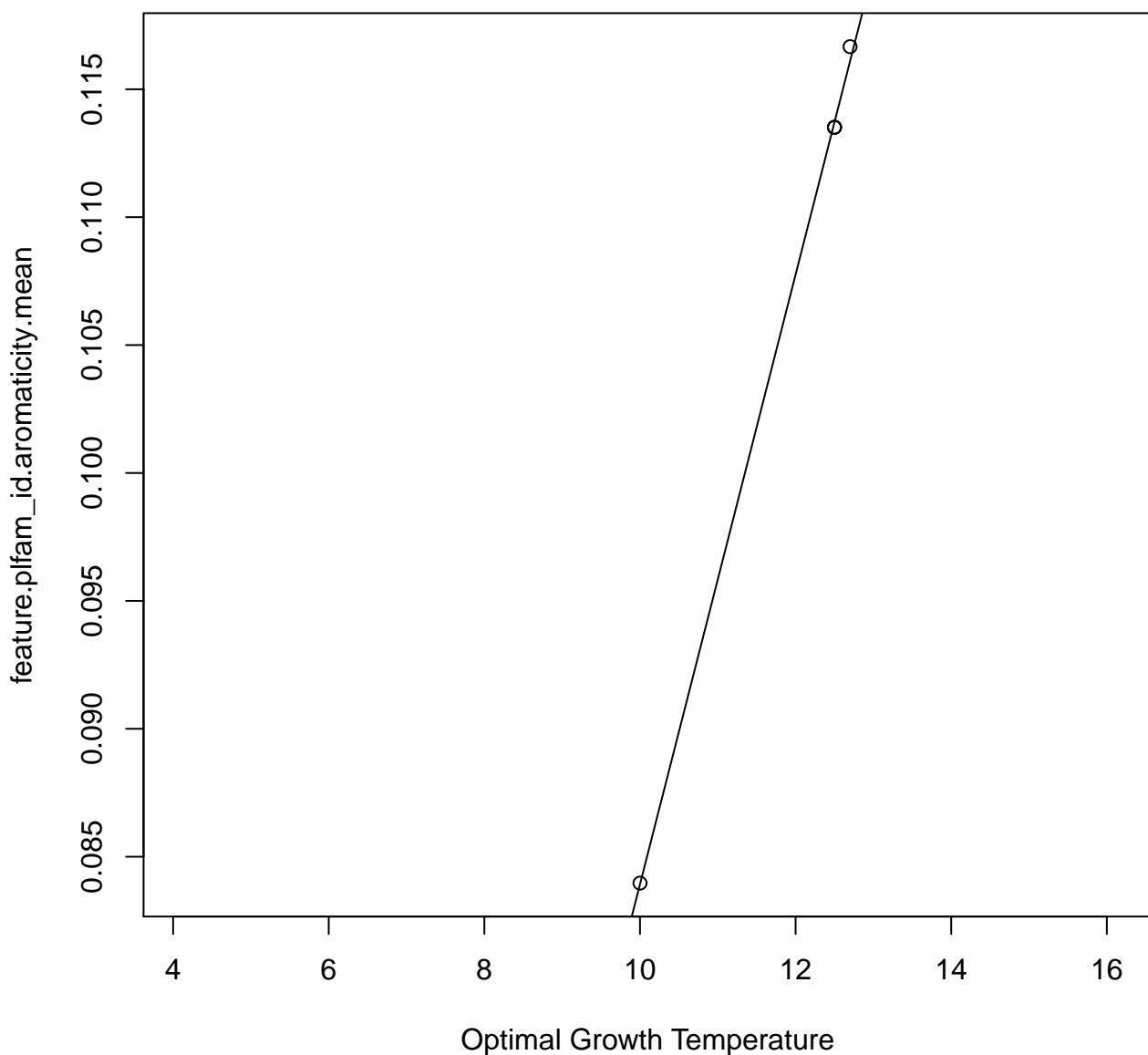
feature.plfam_id.aromaticity.mean
PLF_28228_00028345
Glutathione S-transferase, omega (EC 2.5.1.18)



feature.plfam_id.aromaticity.mean
PLF_28228_00003494
Peptidyl-prolyl cis-trans isomerase



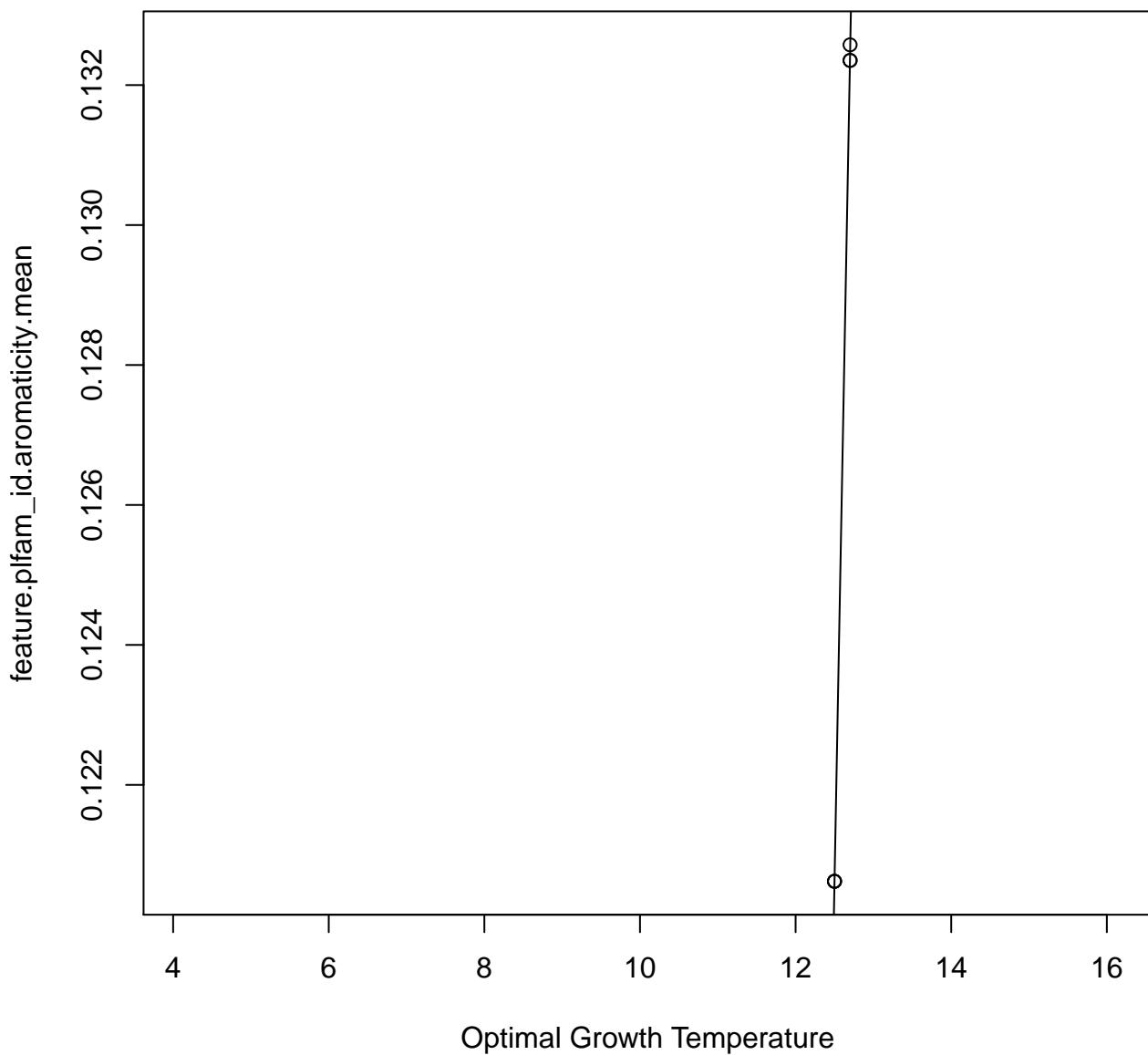
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hypothetical protein



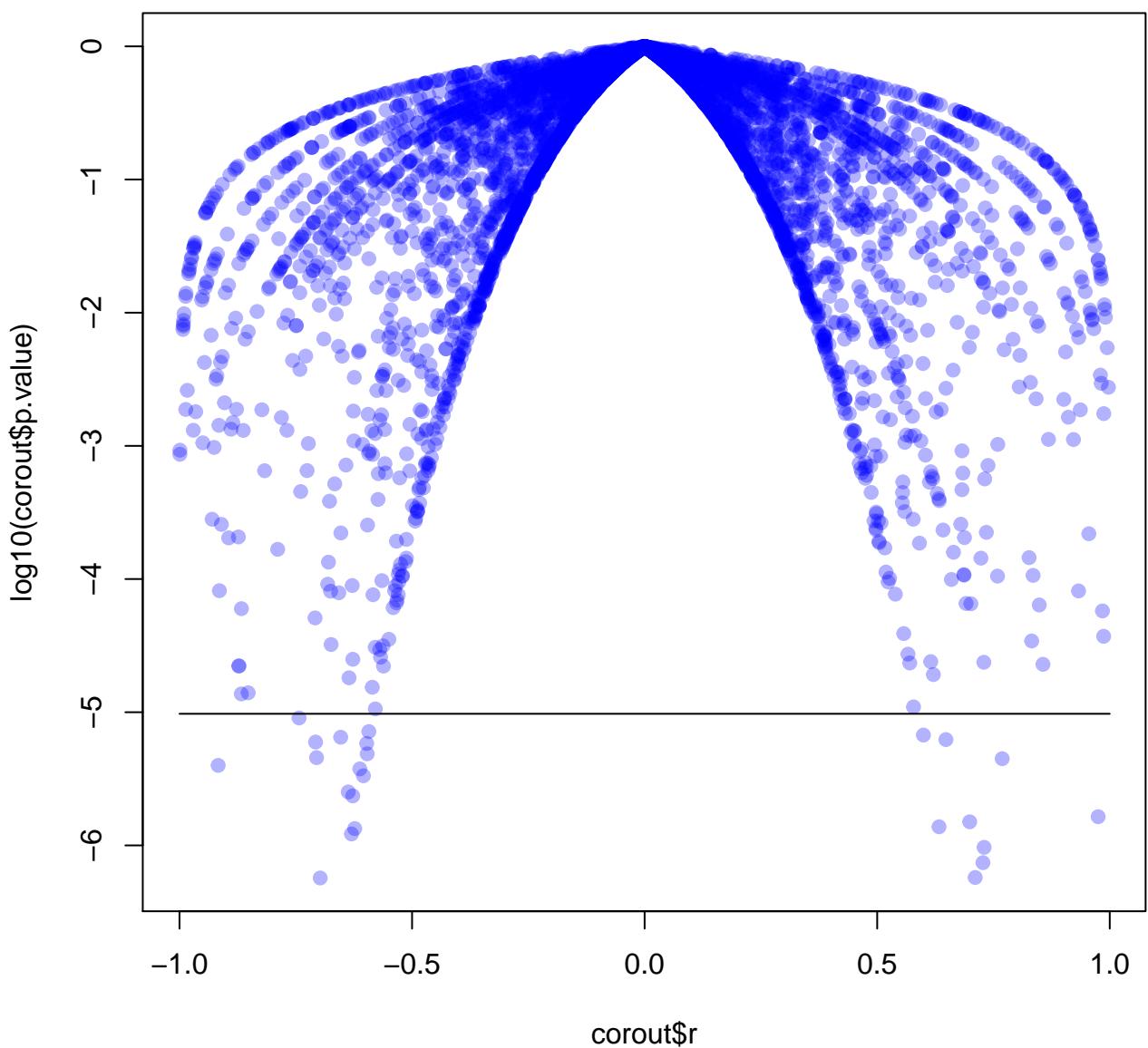
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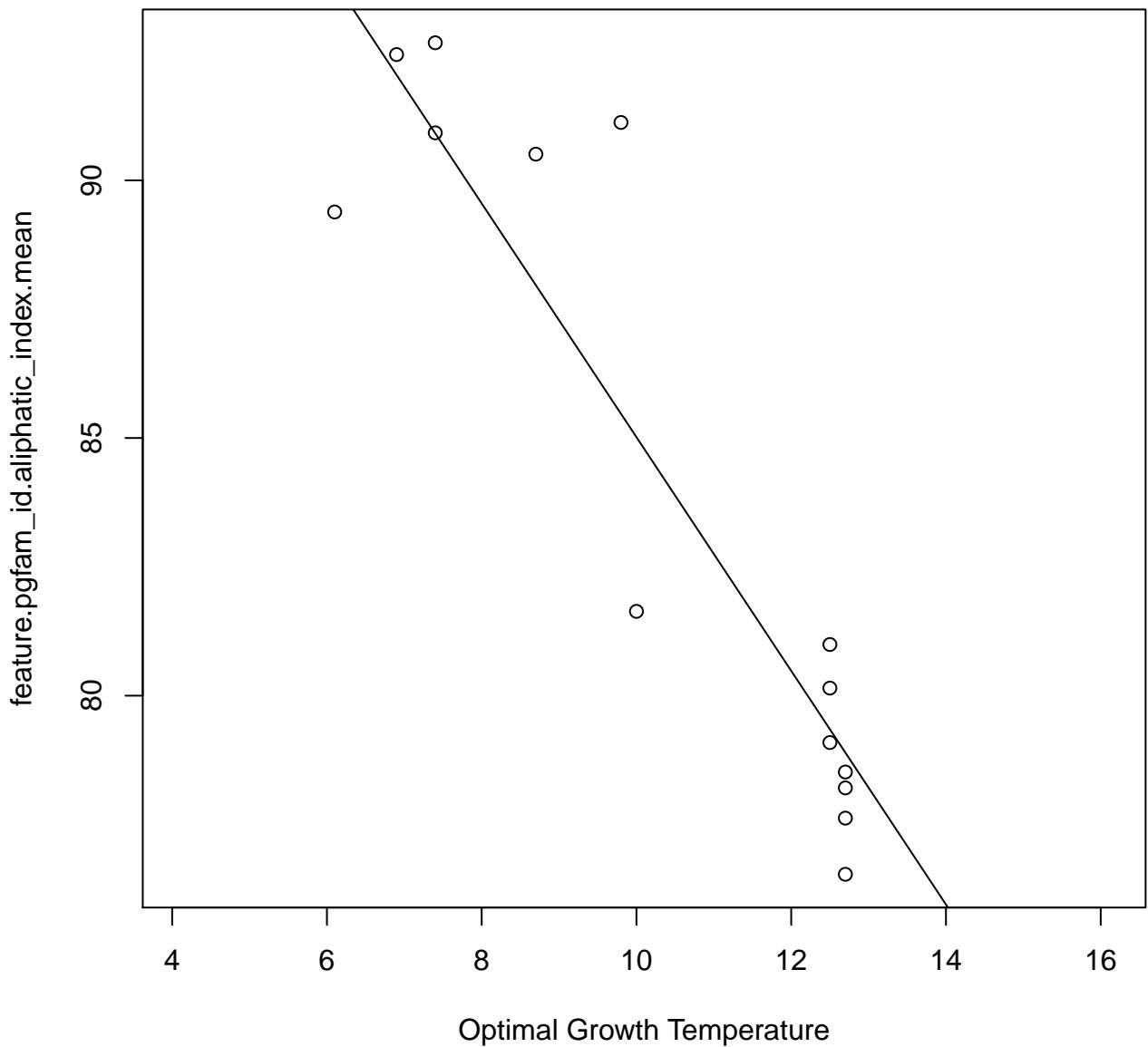
hypothetical protein



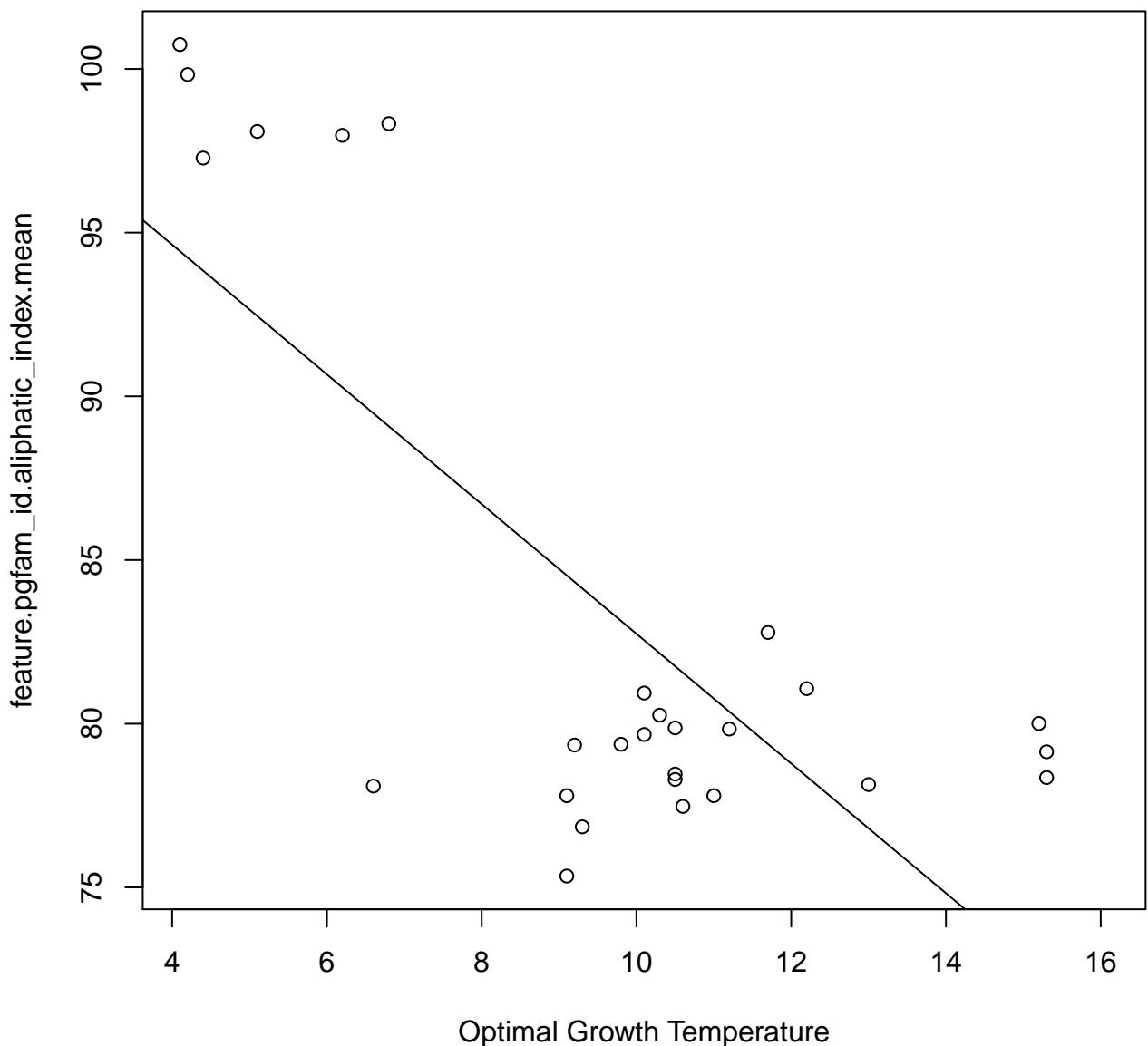
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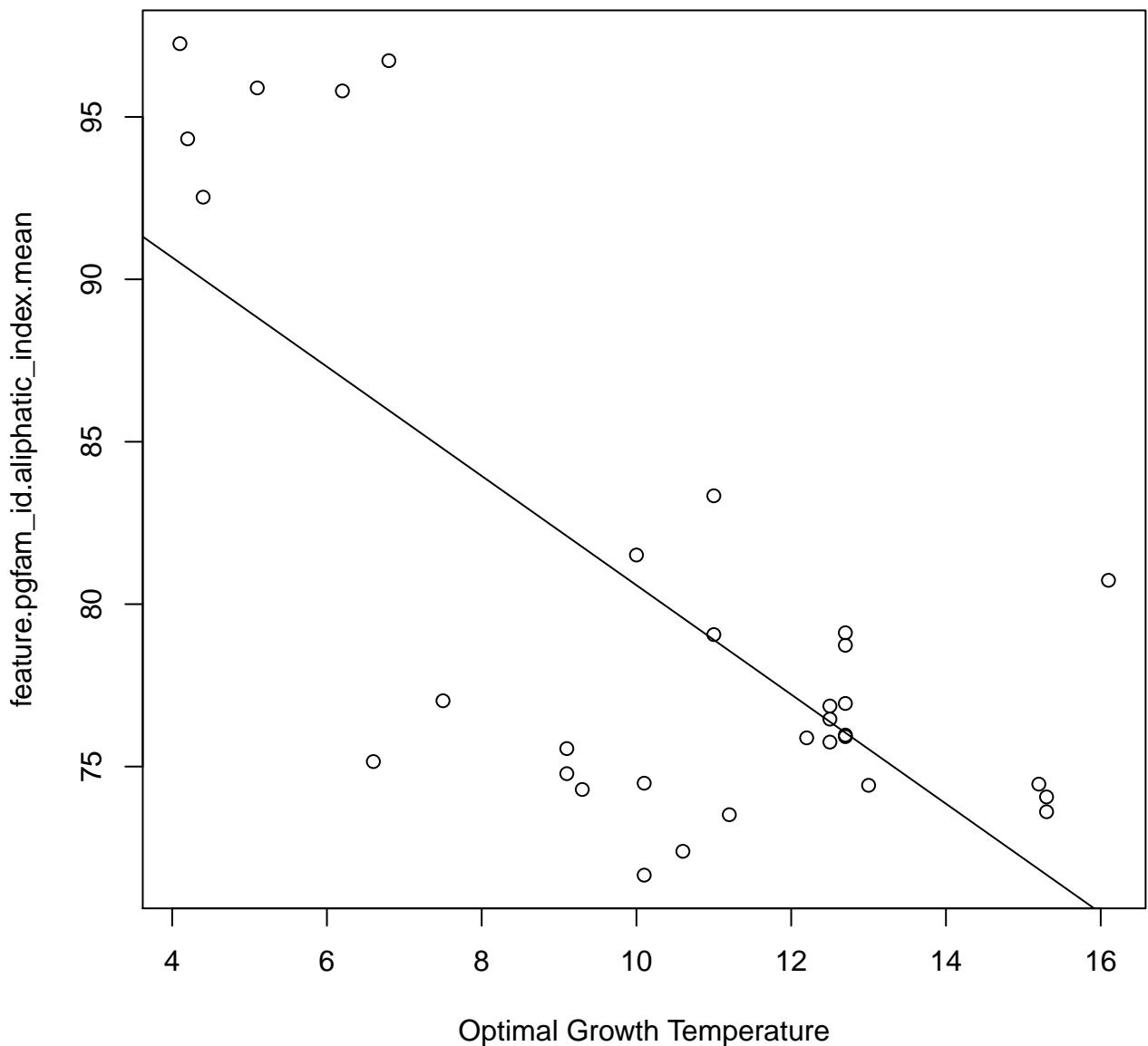
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Alpha-1,2-fucosyltransferase



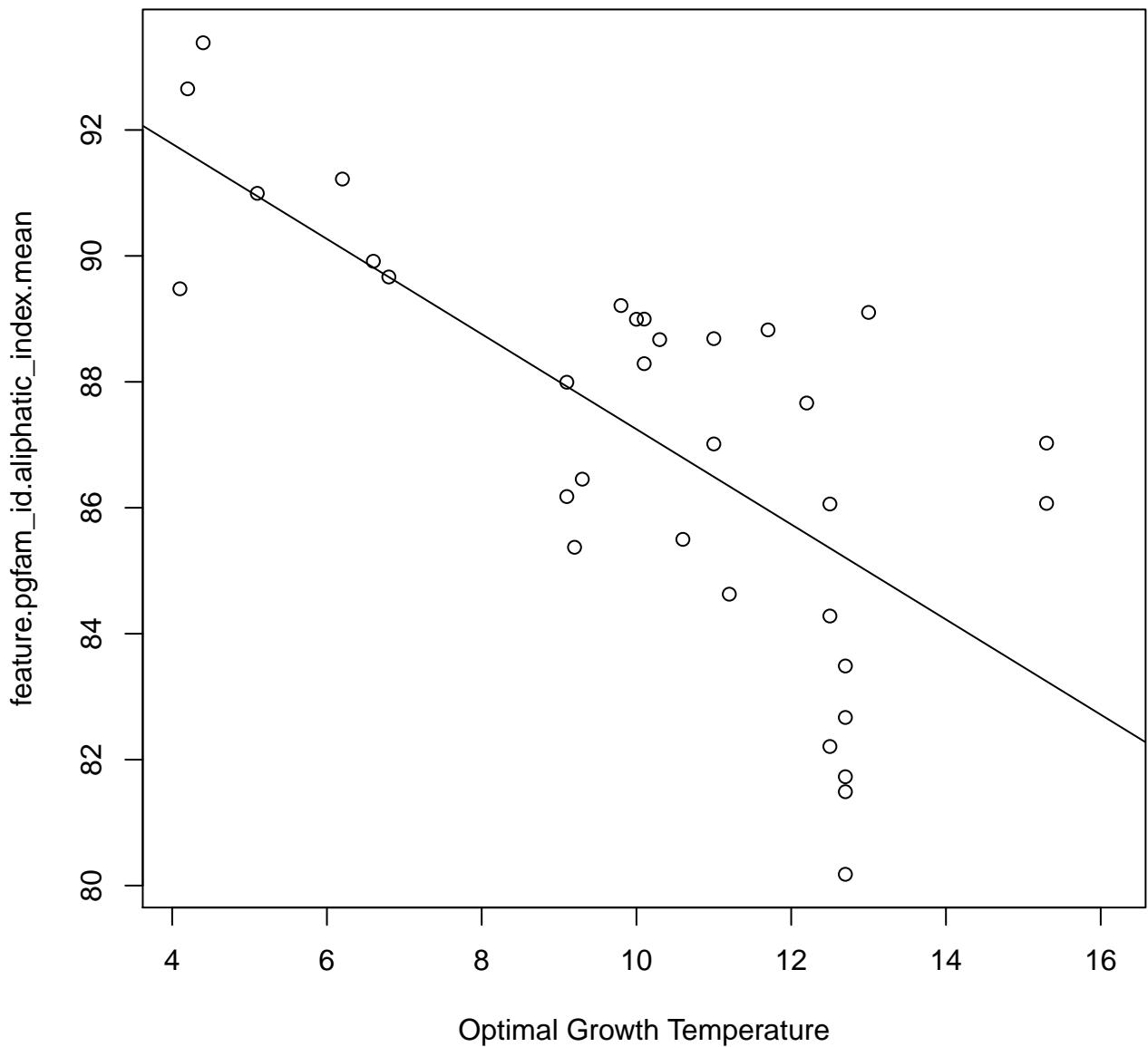
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PGF_11018774
hypothetical protein



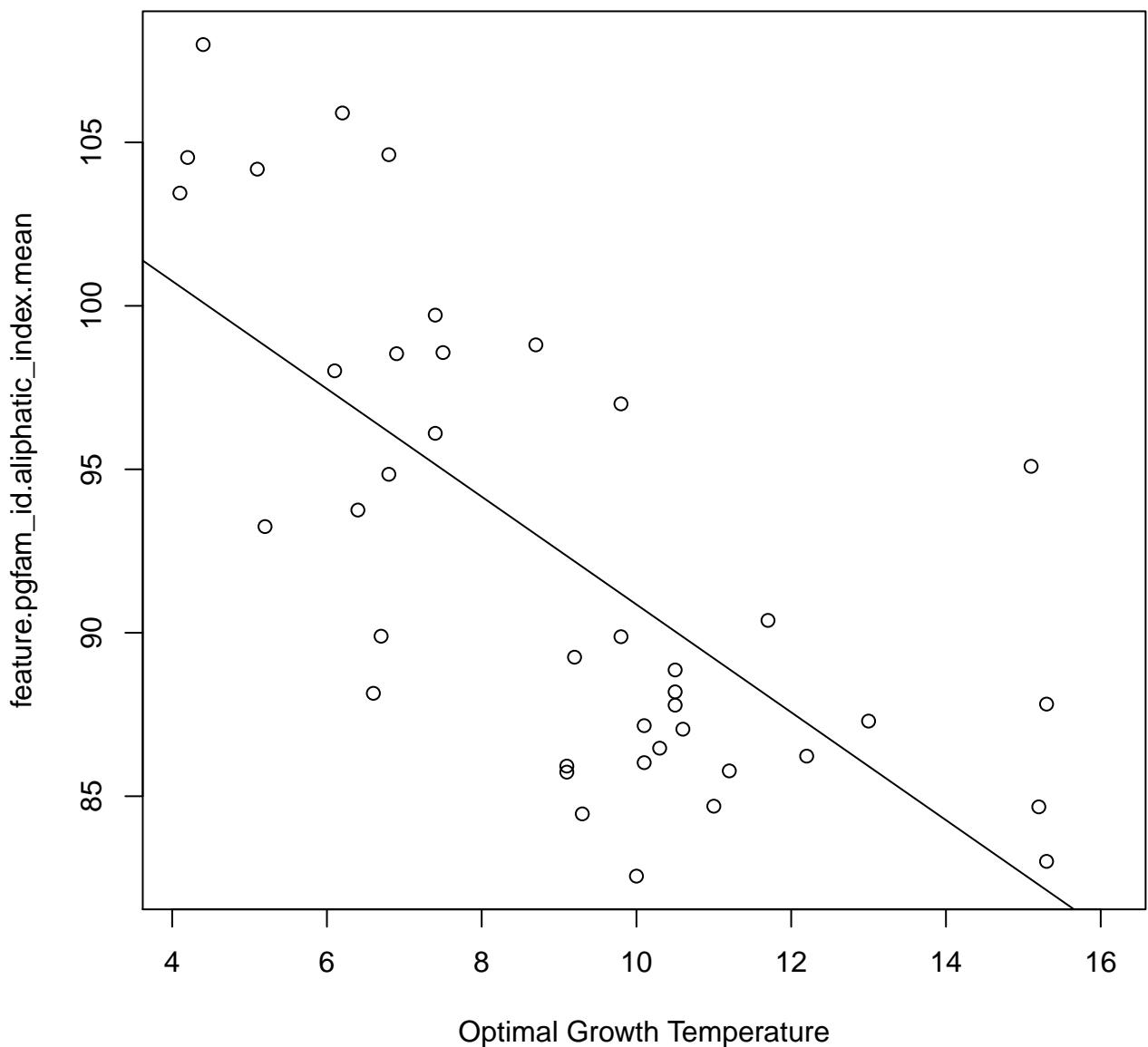
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Capsule biosynthesis protein capA



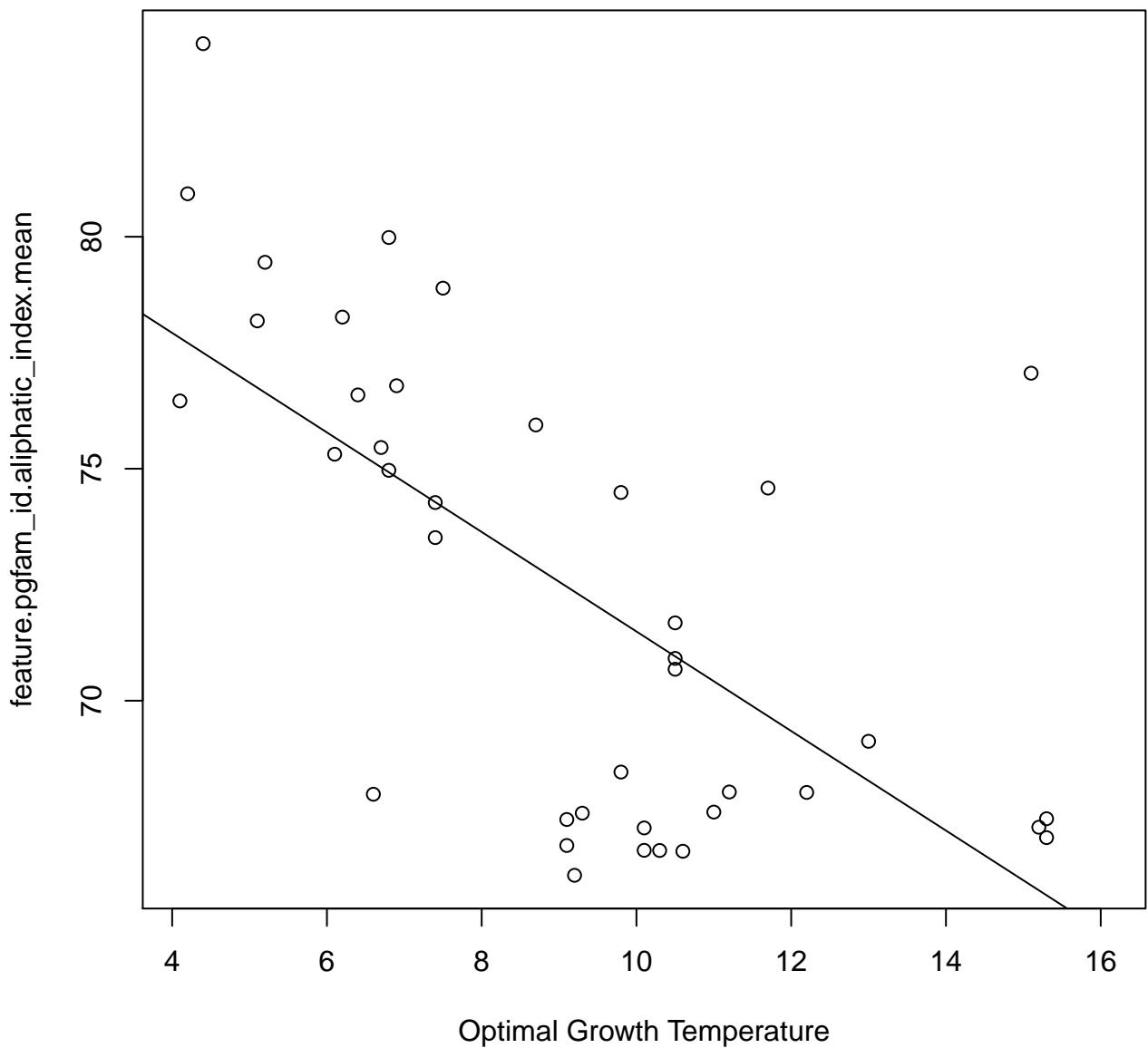
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PGF_03940803
Alkylated DNA repair protein



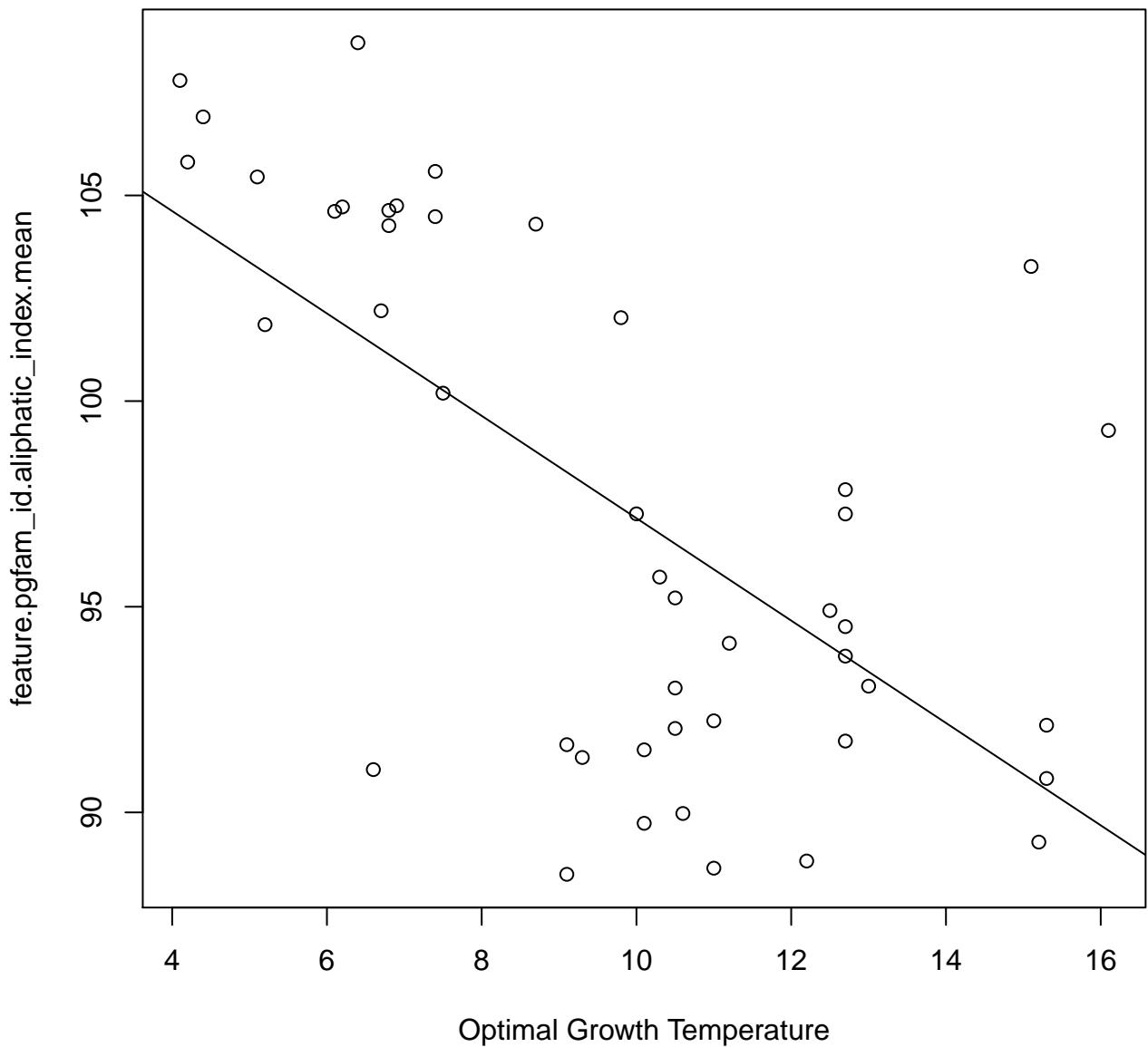
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hypothetical protein



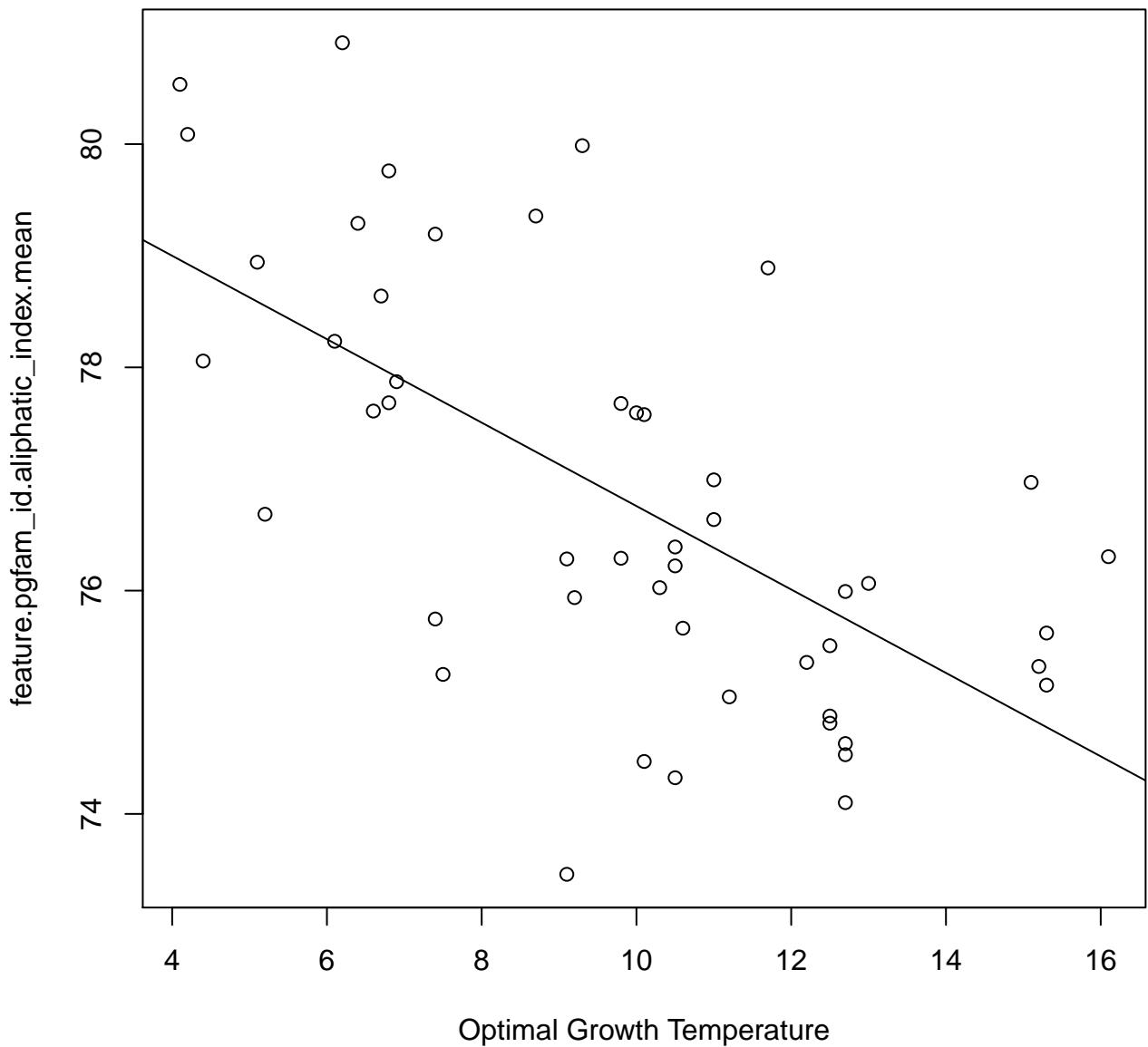
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PGF_00305244
hypothetical protein



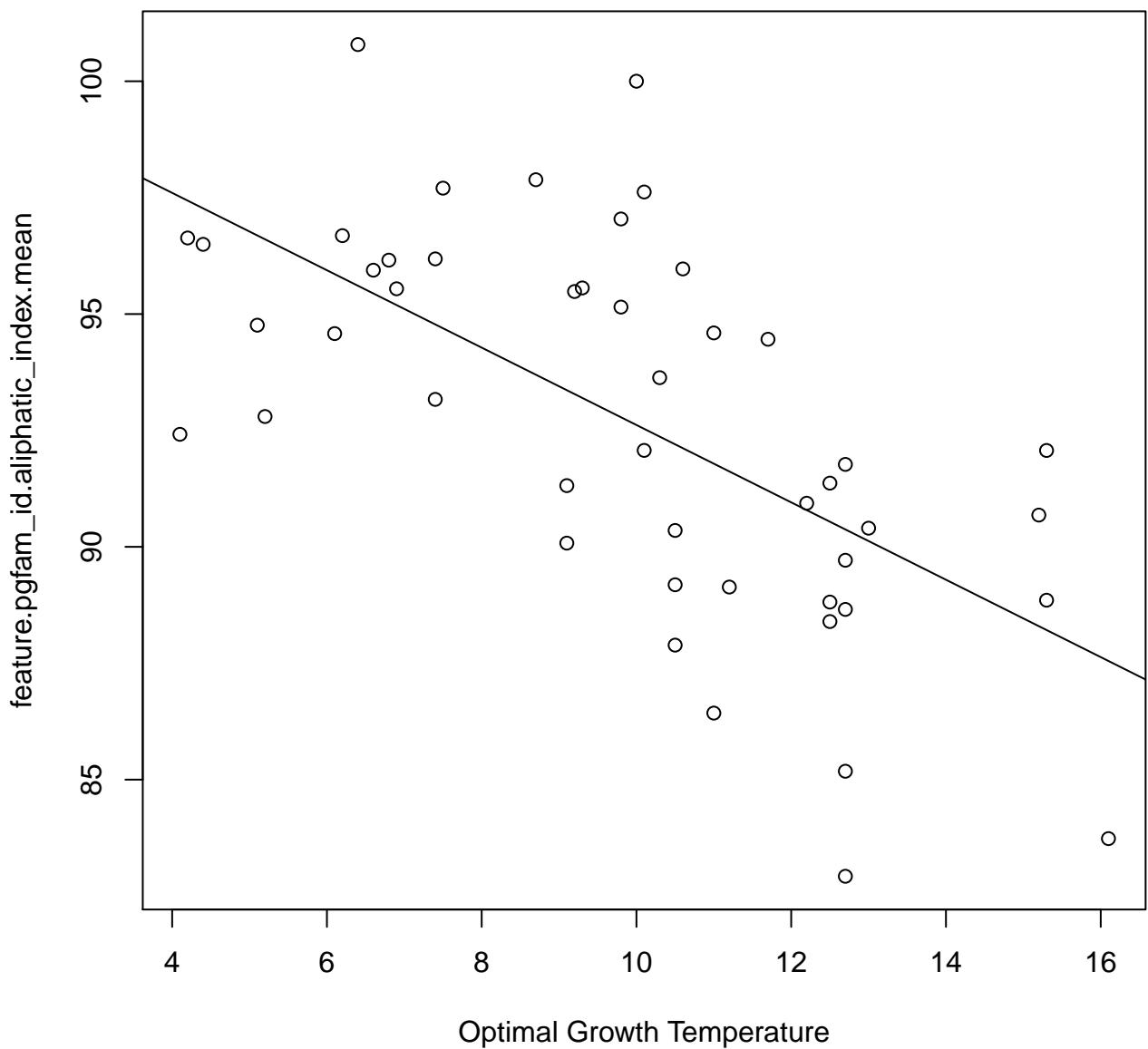
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Flagellar biosynthesis protein FliS



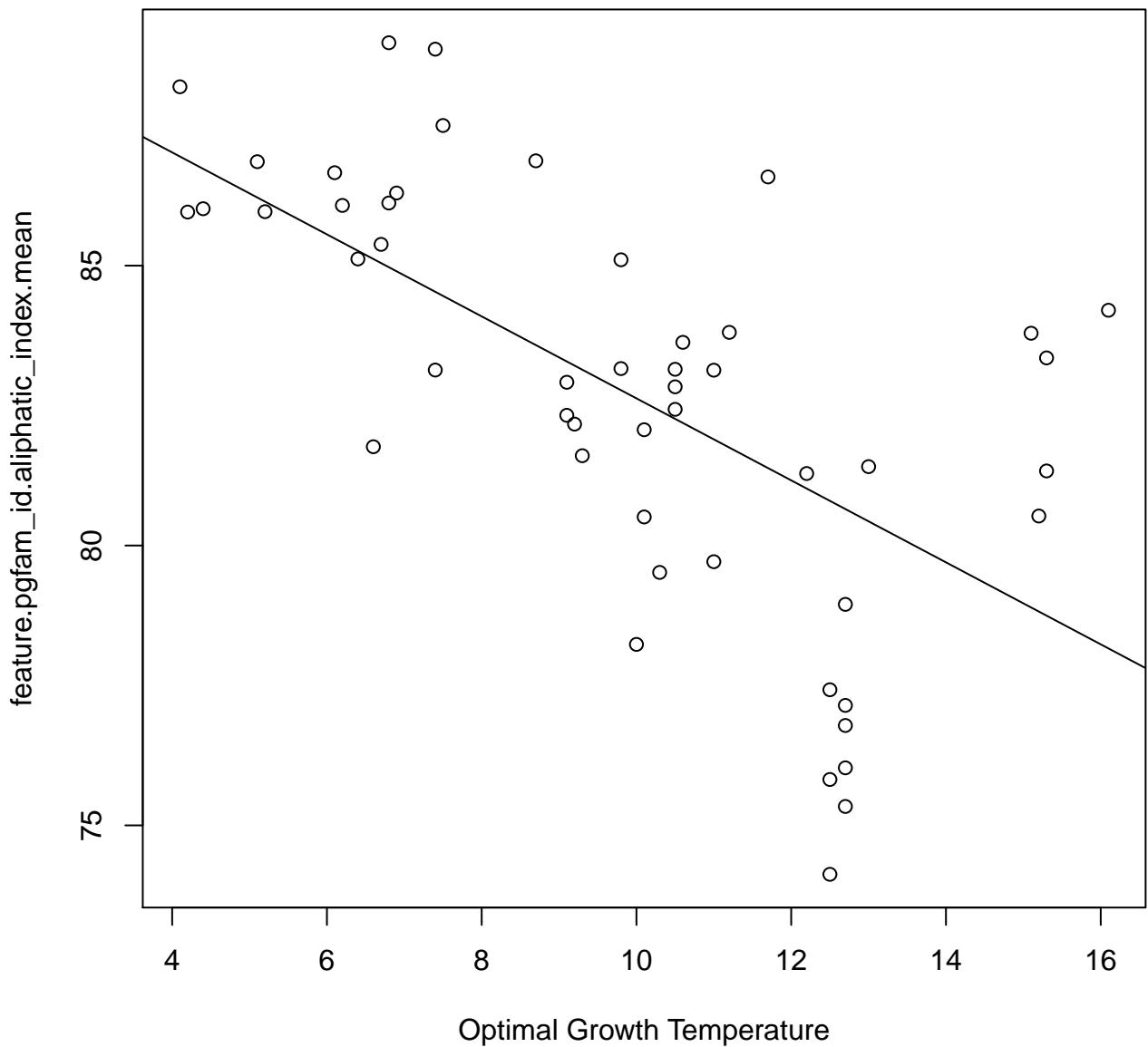
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PGF_00016431
LSU ribosomal protein L3p (L3e)



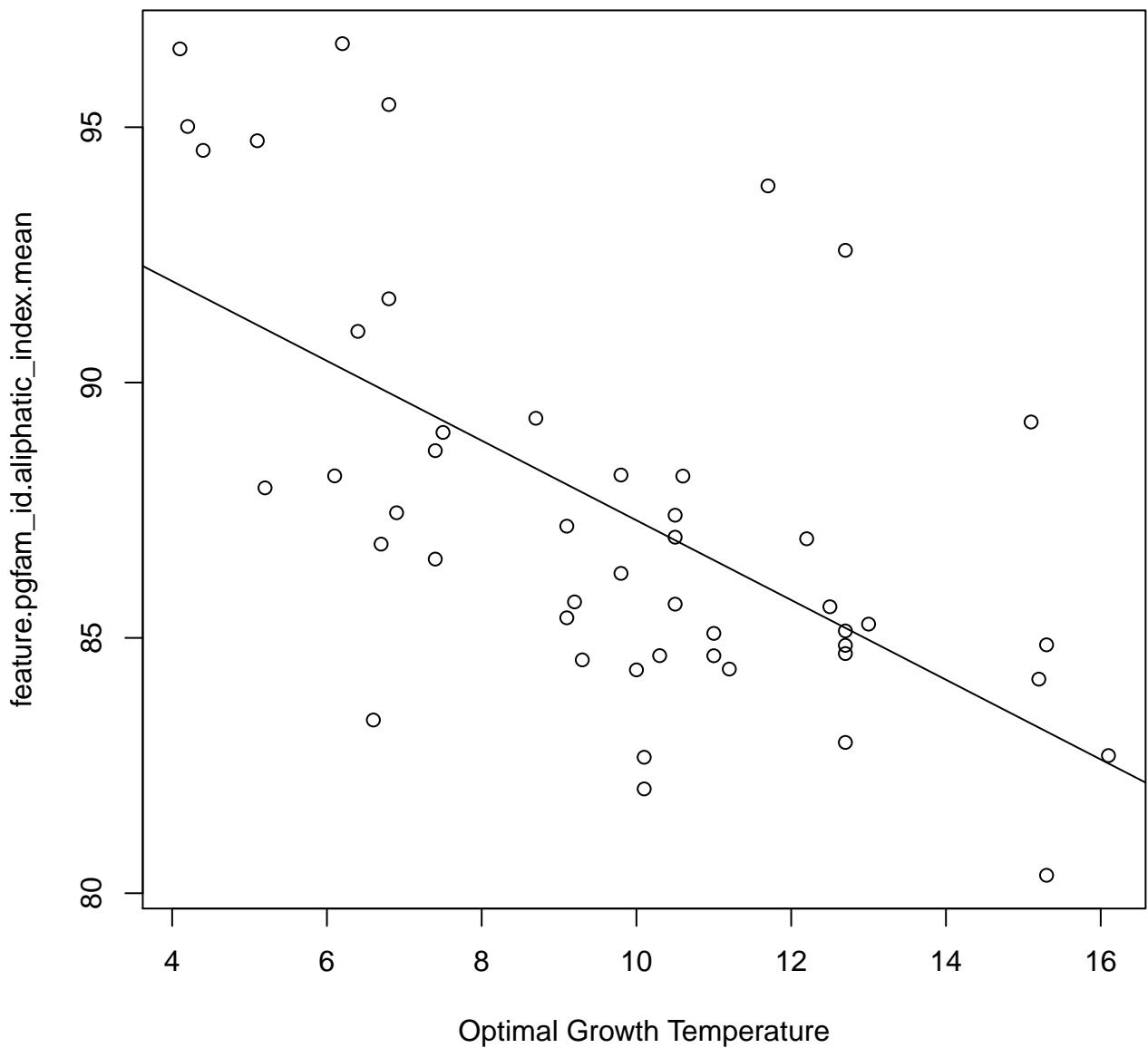
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Potential queD like 2



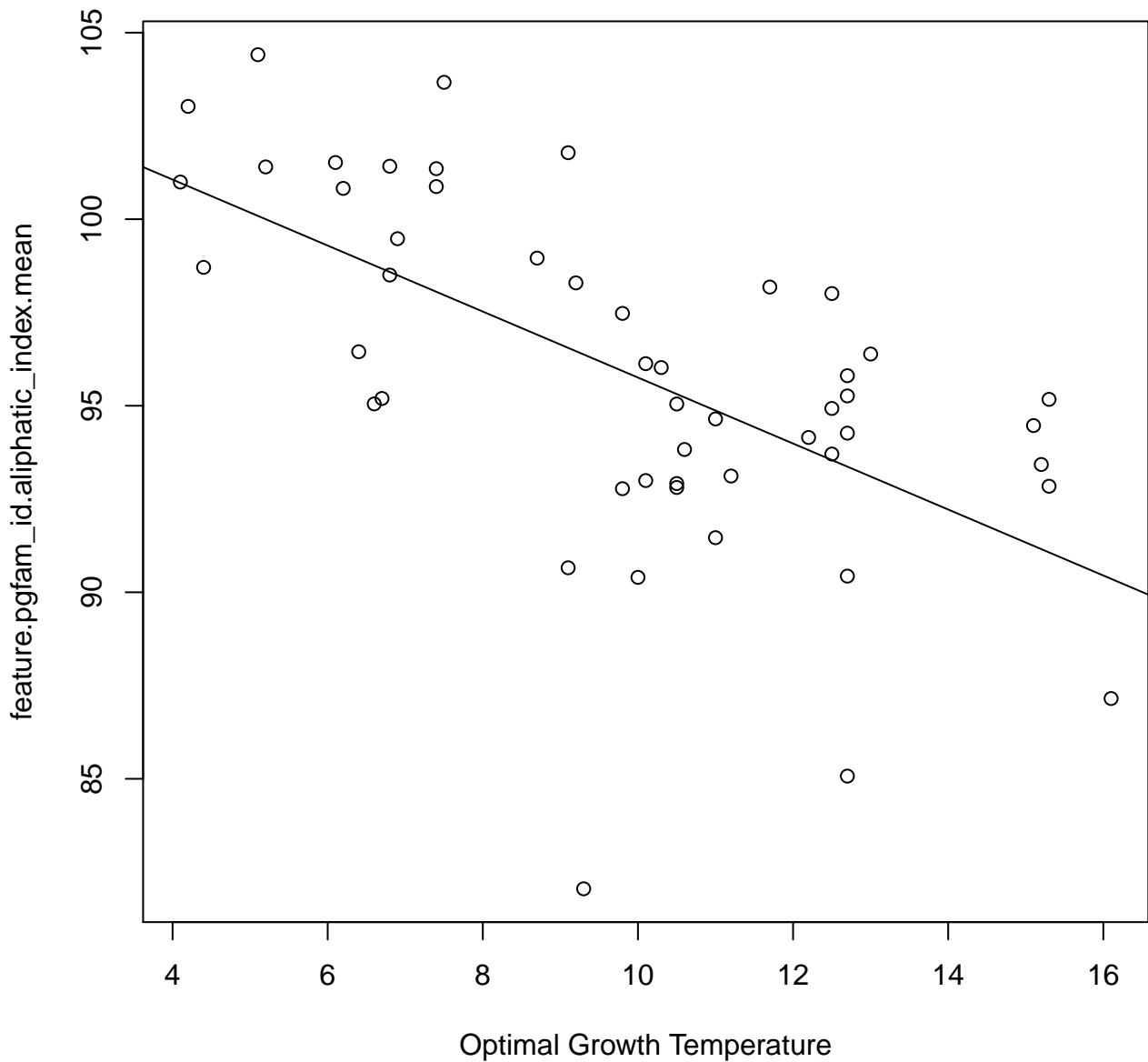
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PGF_02473279
tRNA (cytidine(32)/uridine(32)-2'-O)-methyltransferase (EC 2.1.1.200)



feature.pgfam_id.aliphatic_index.mean
PGF_07058319
General secretion pathway protein K



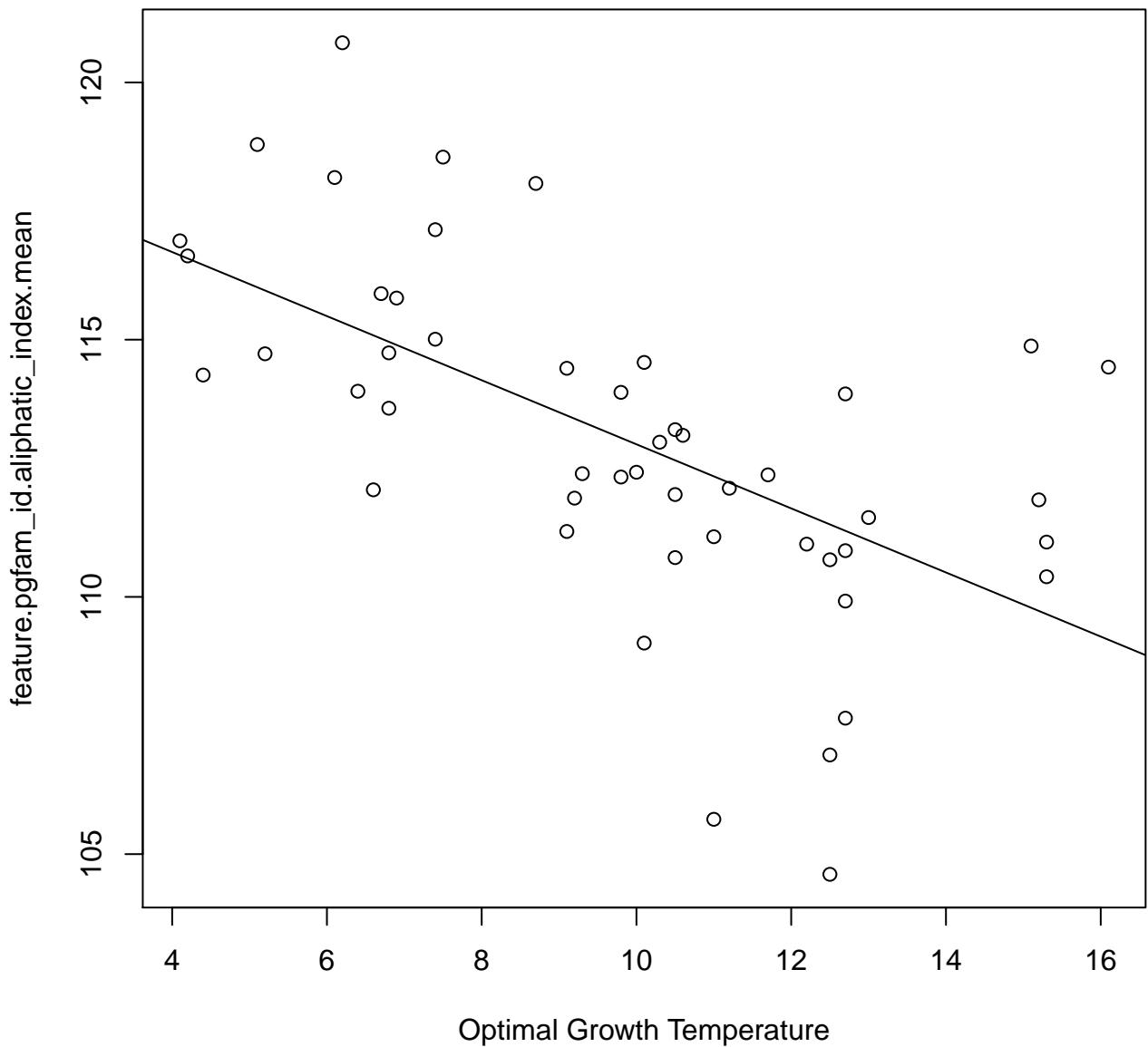
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PGF_01336539
hypothetical protein



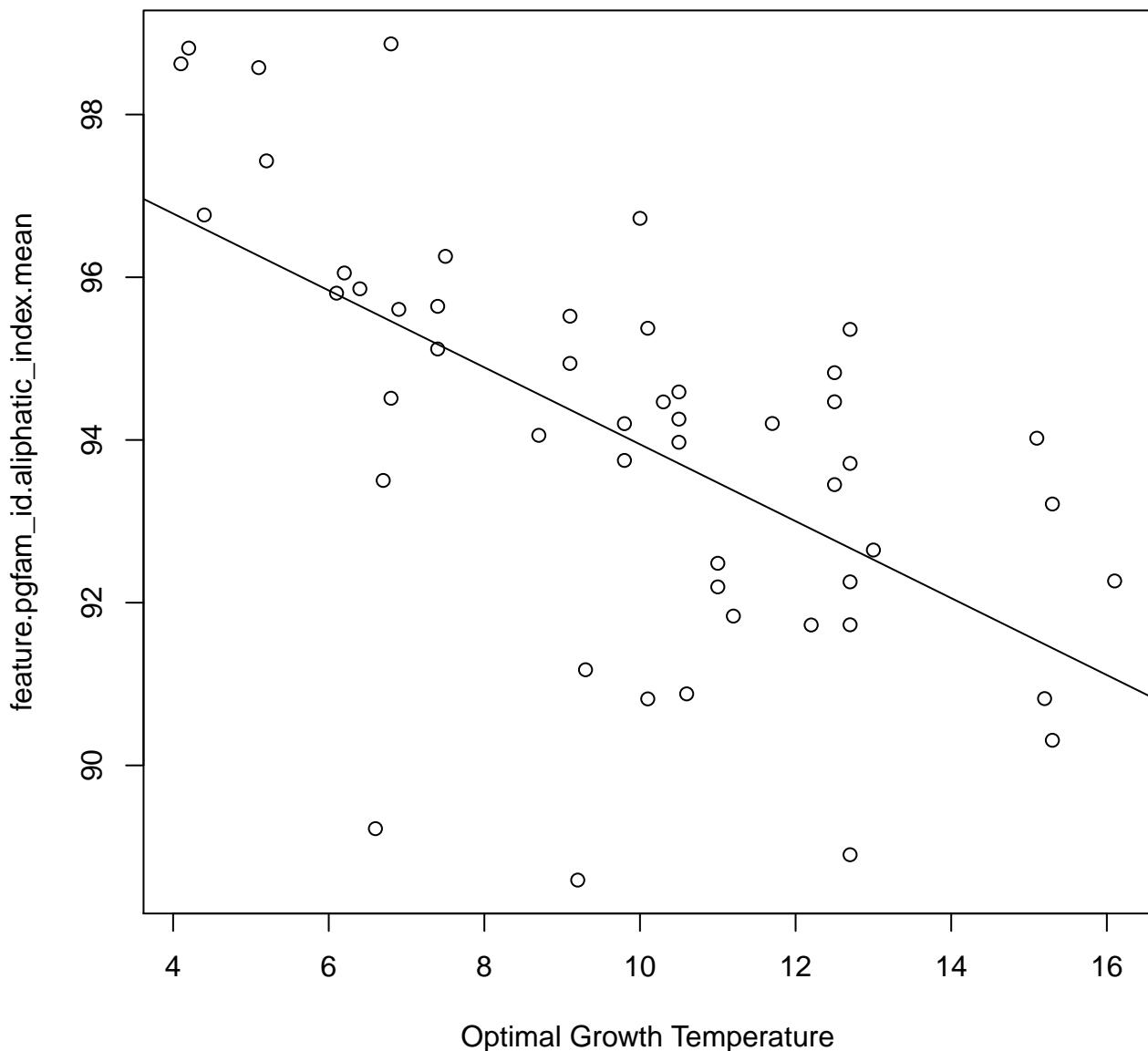
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PGF_00035873

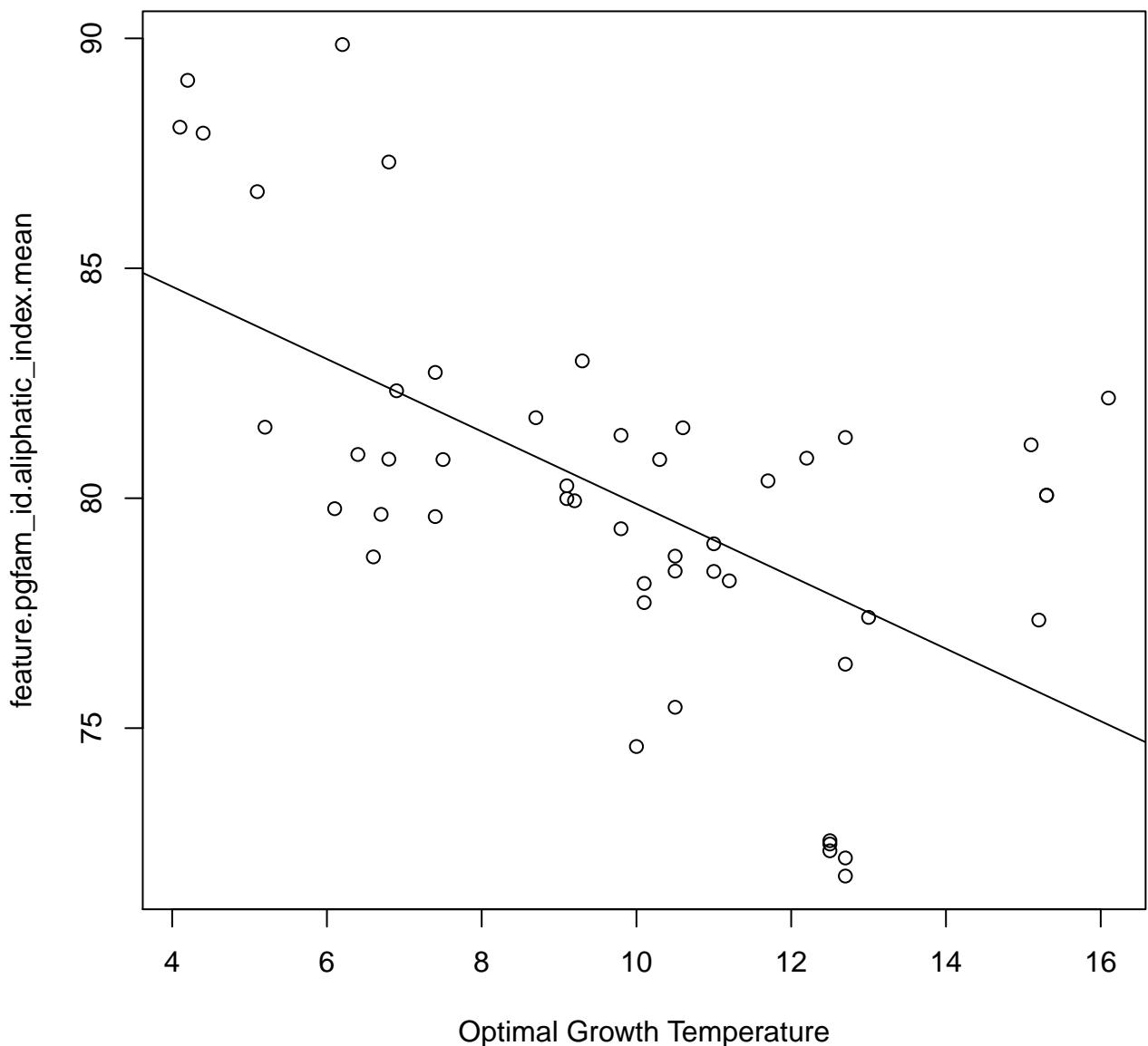
Predicted glucose transporter in beta-glucoside utilization gene cluster



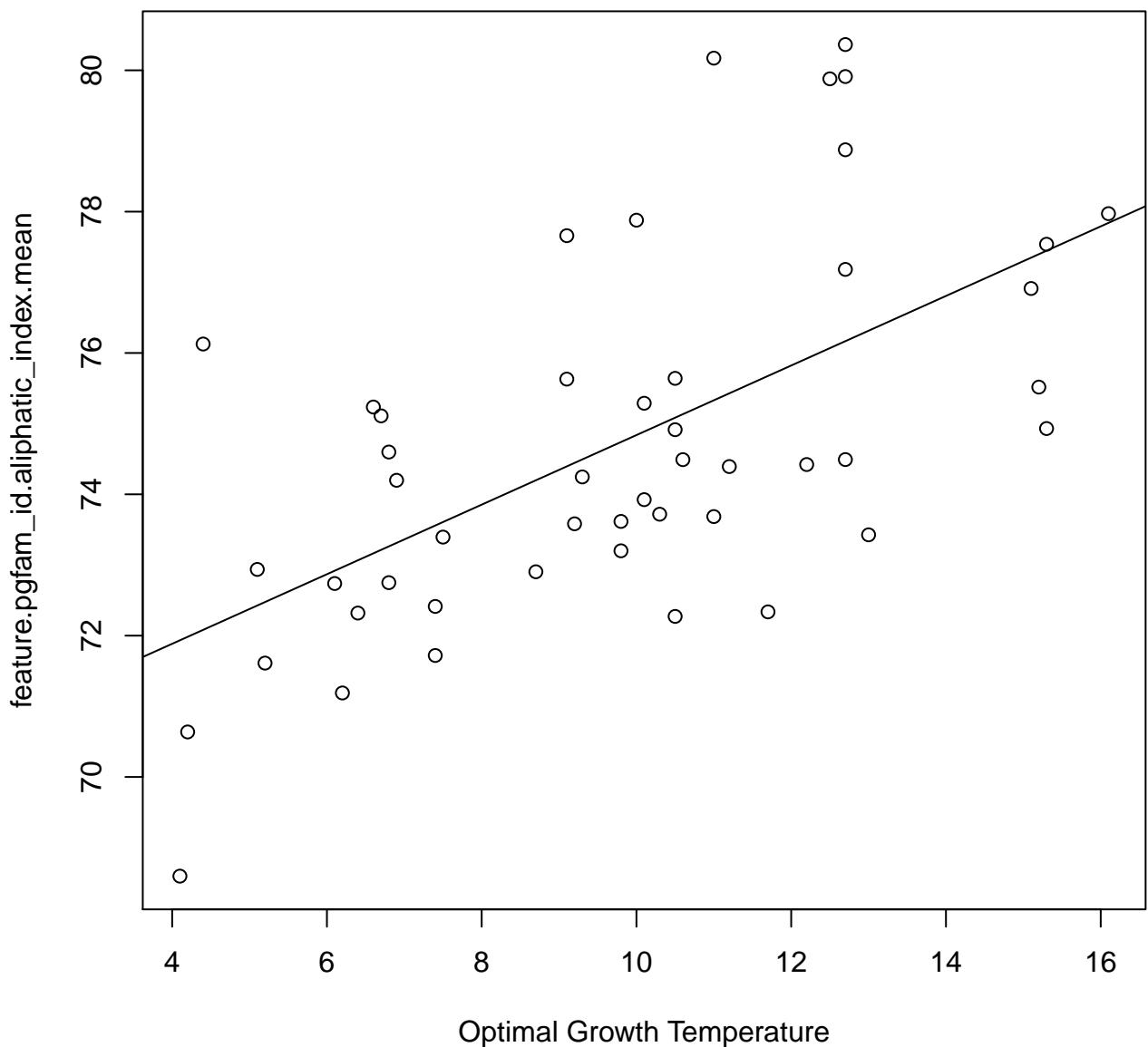
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tRNA dimethylallyltransferase (EC 2.5.1.75)



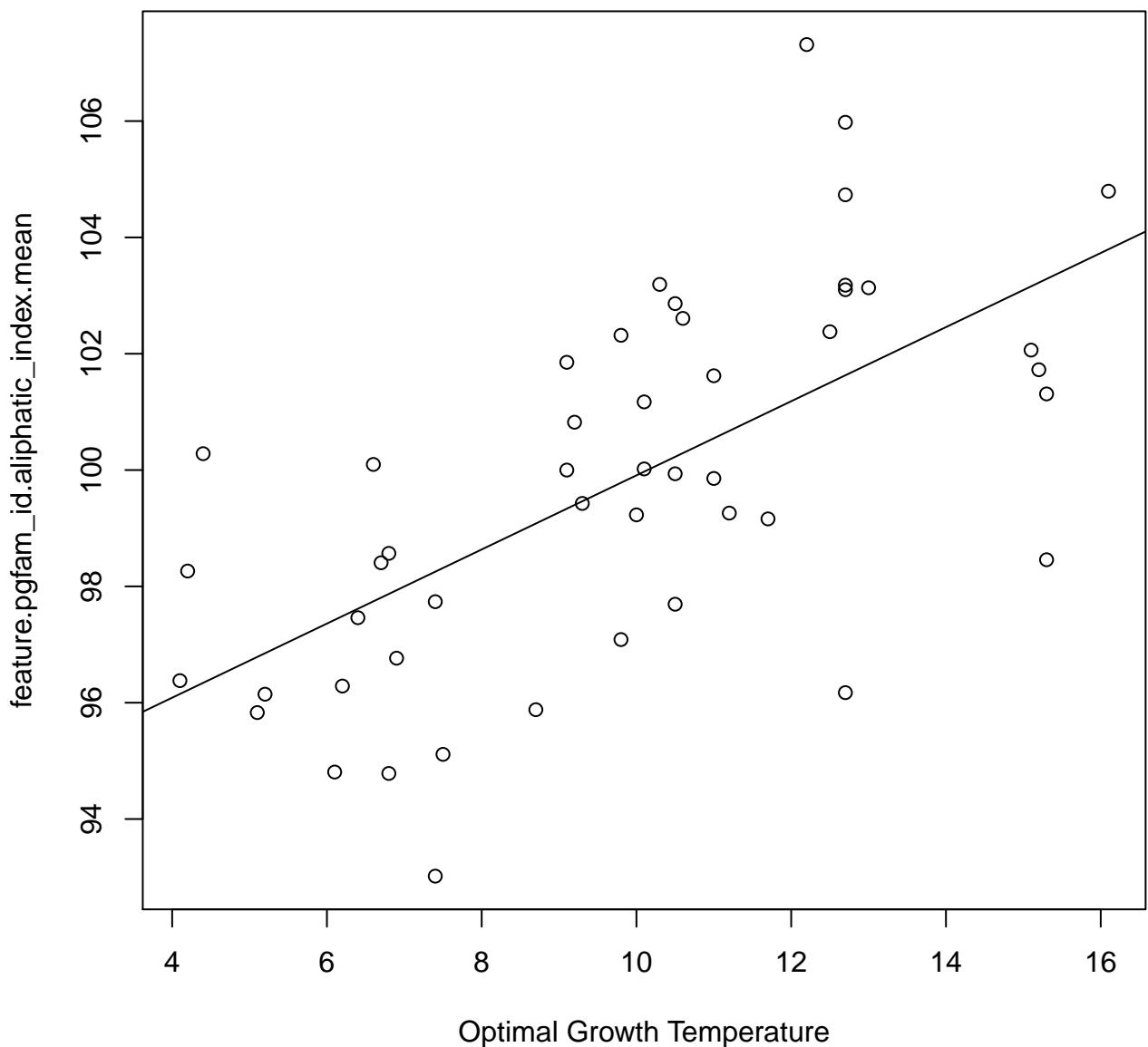
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3-deoxy-D-manno-octulose-2'-acid kinase (EC 2.7.1.166)



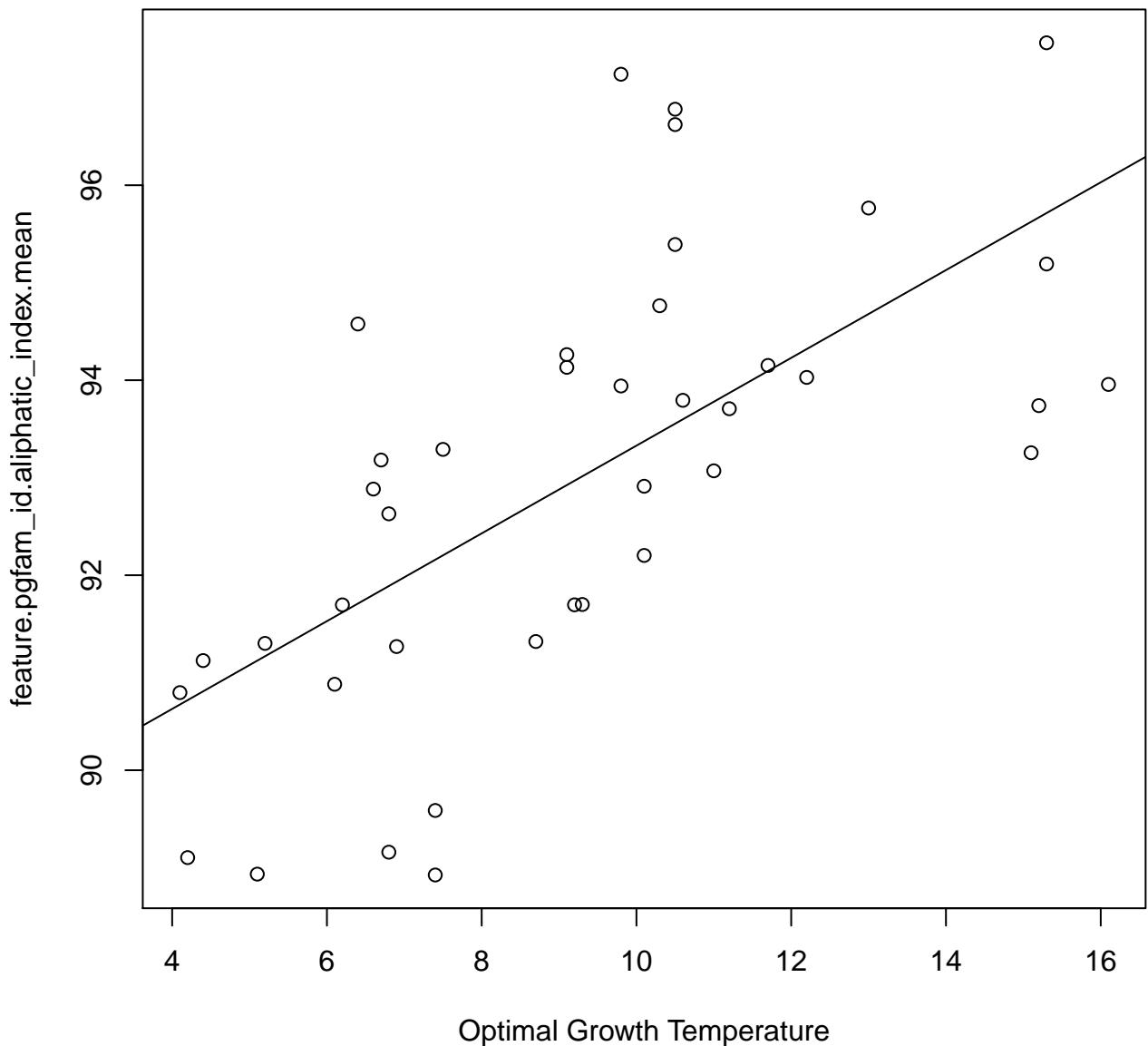
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Flagellar basal-body rod protein FlgF



feature.pgfam_id.aliphatic_index.mean
PGF_10454652
UPF0758 family protein



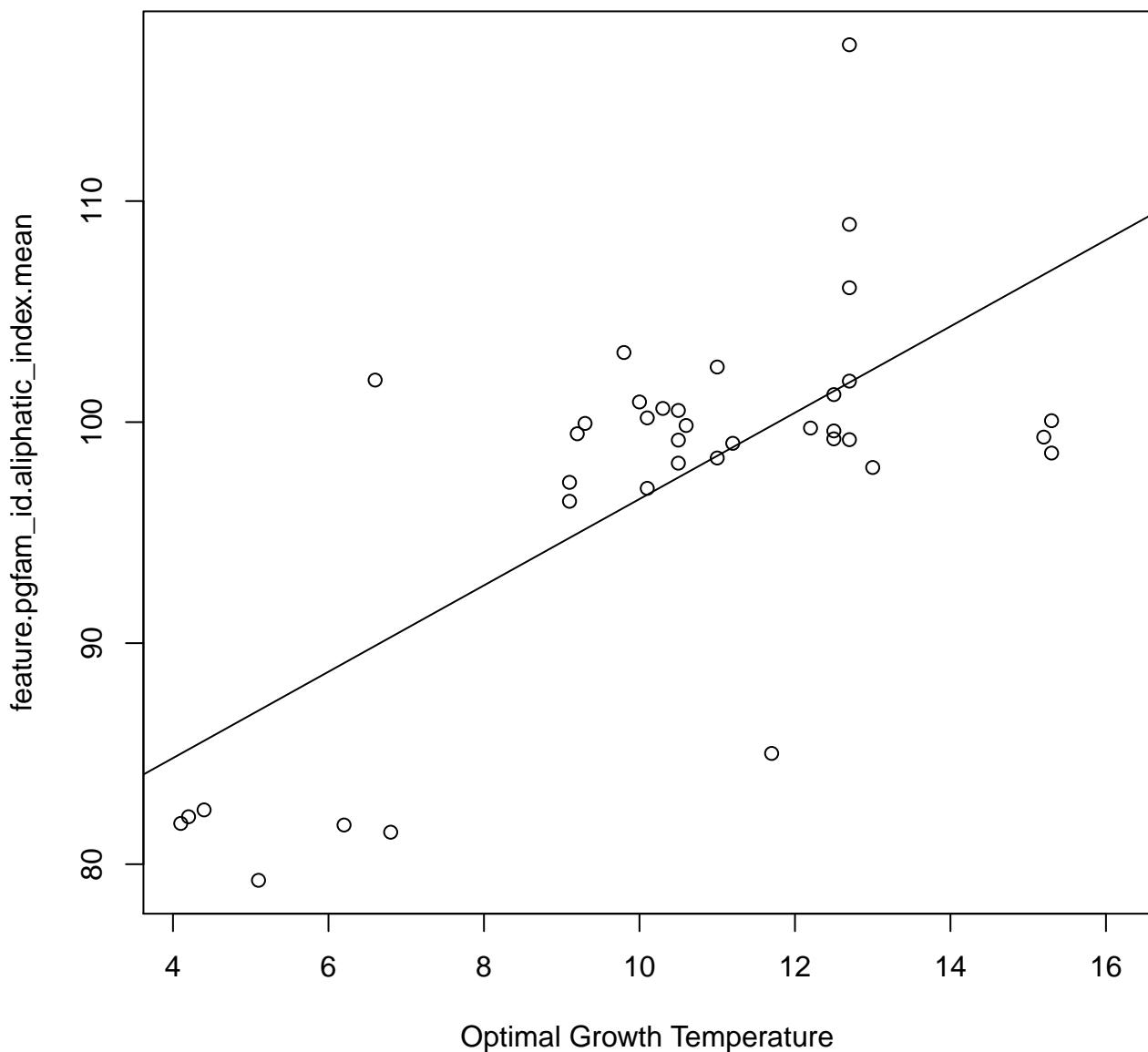
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CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8)



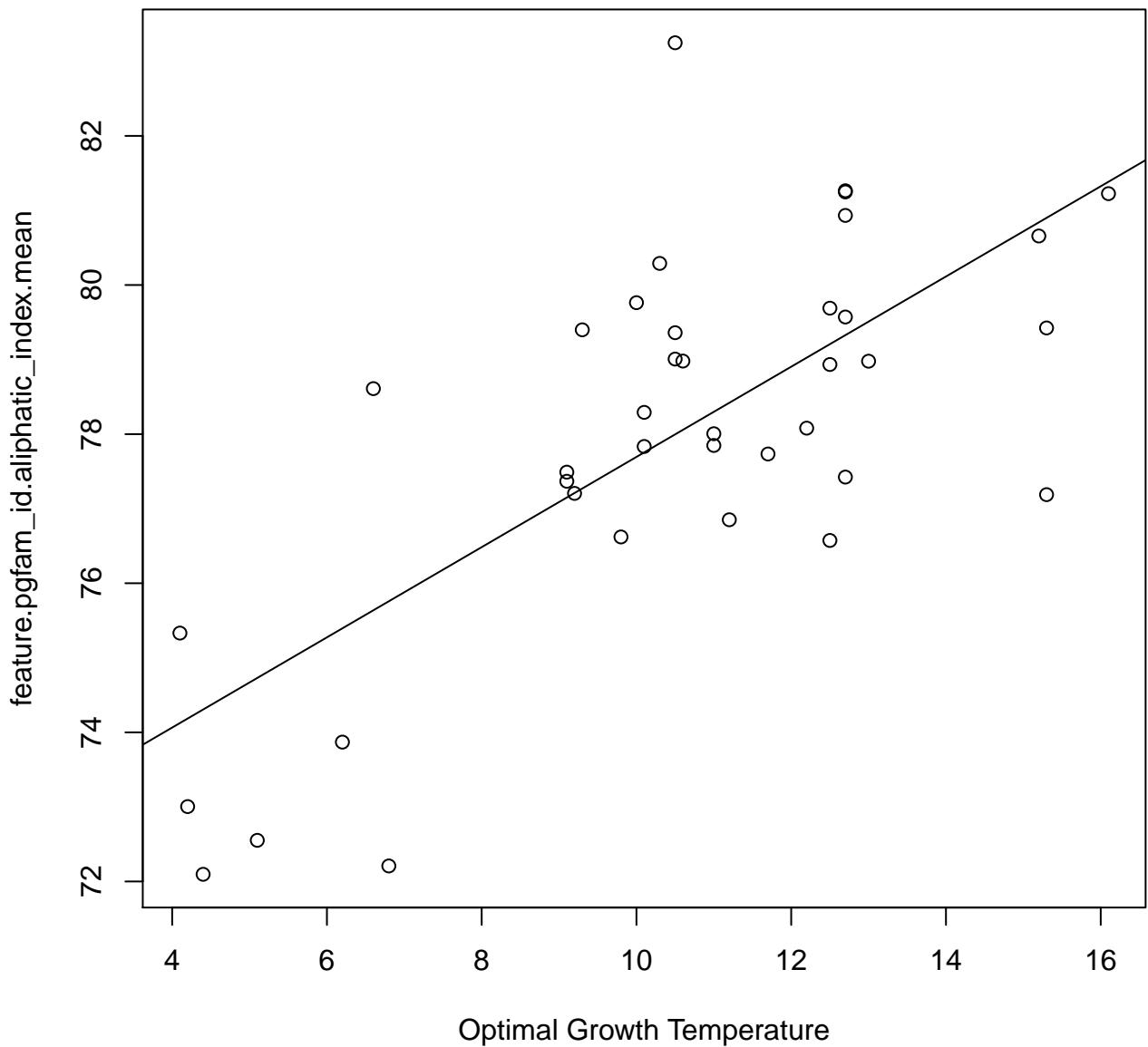
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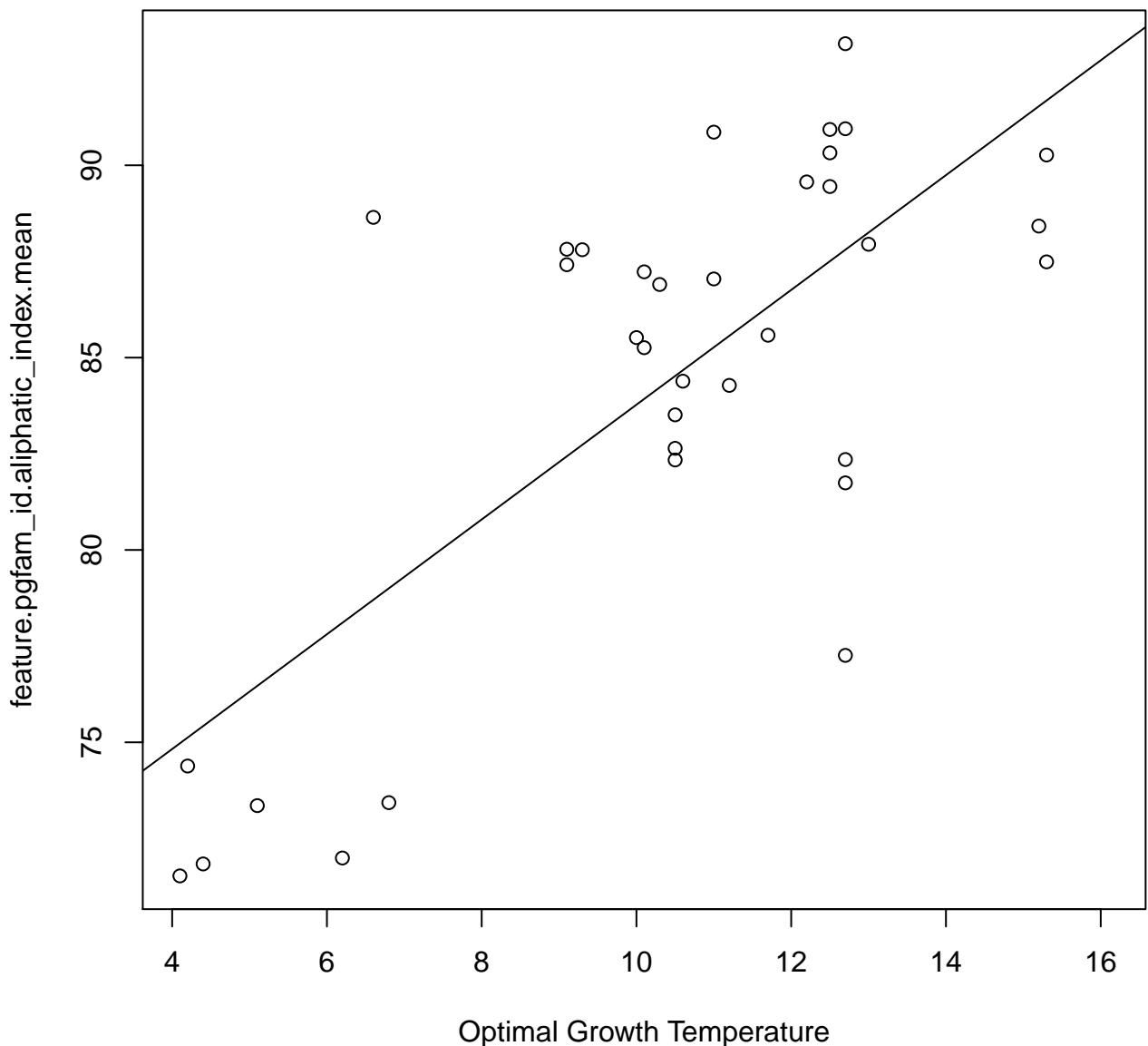
Adenosylcobinamide kinase (EC 2.7.1.156) / Adenosylcobinamide-phosphate guanylyltransferase (EC 2.7.7.62)



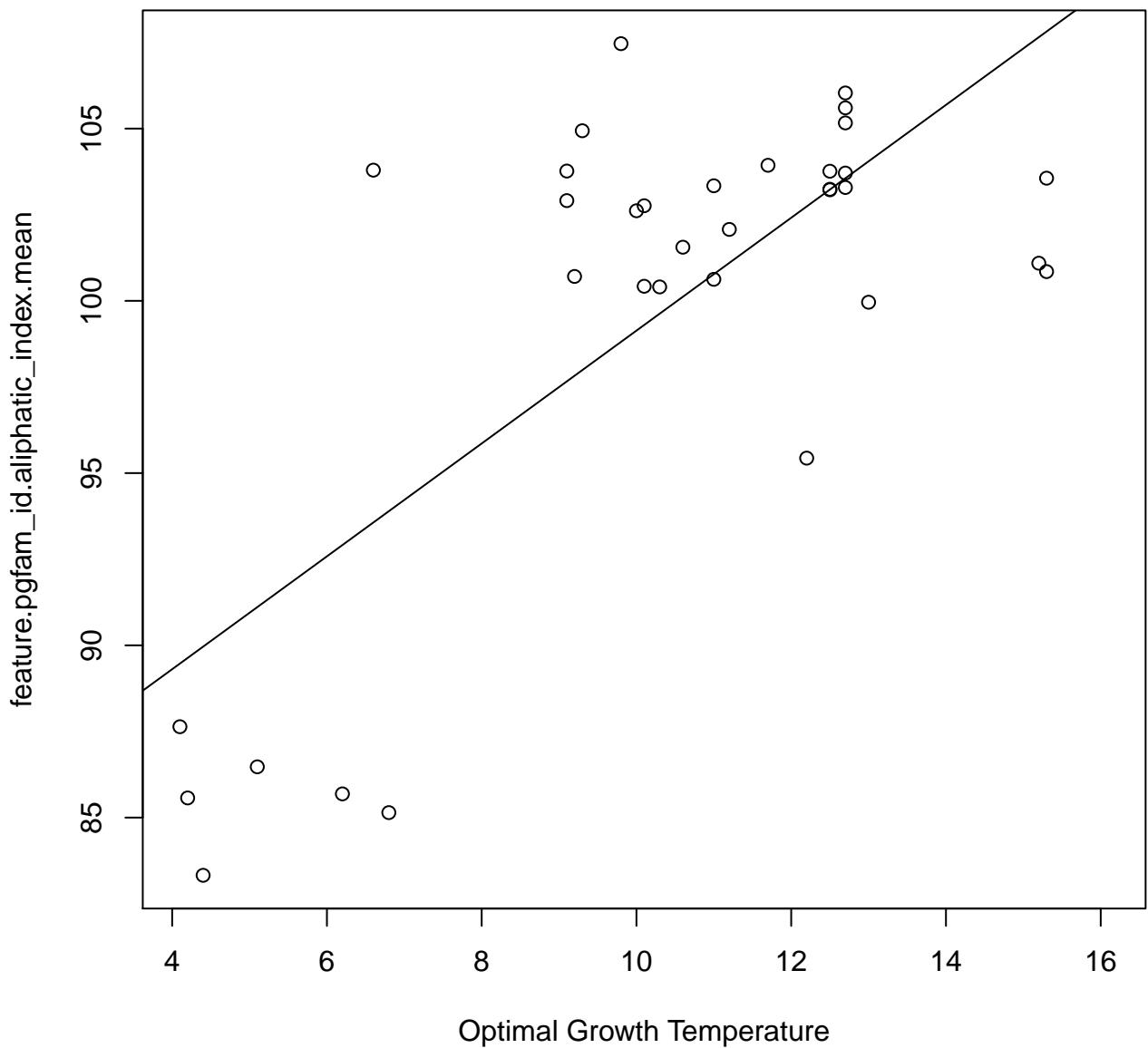
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Flagellar protein FliJ



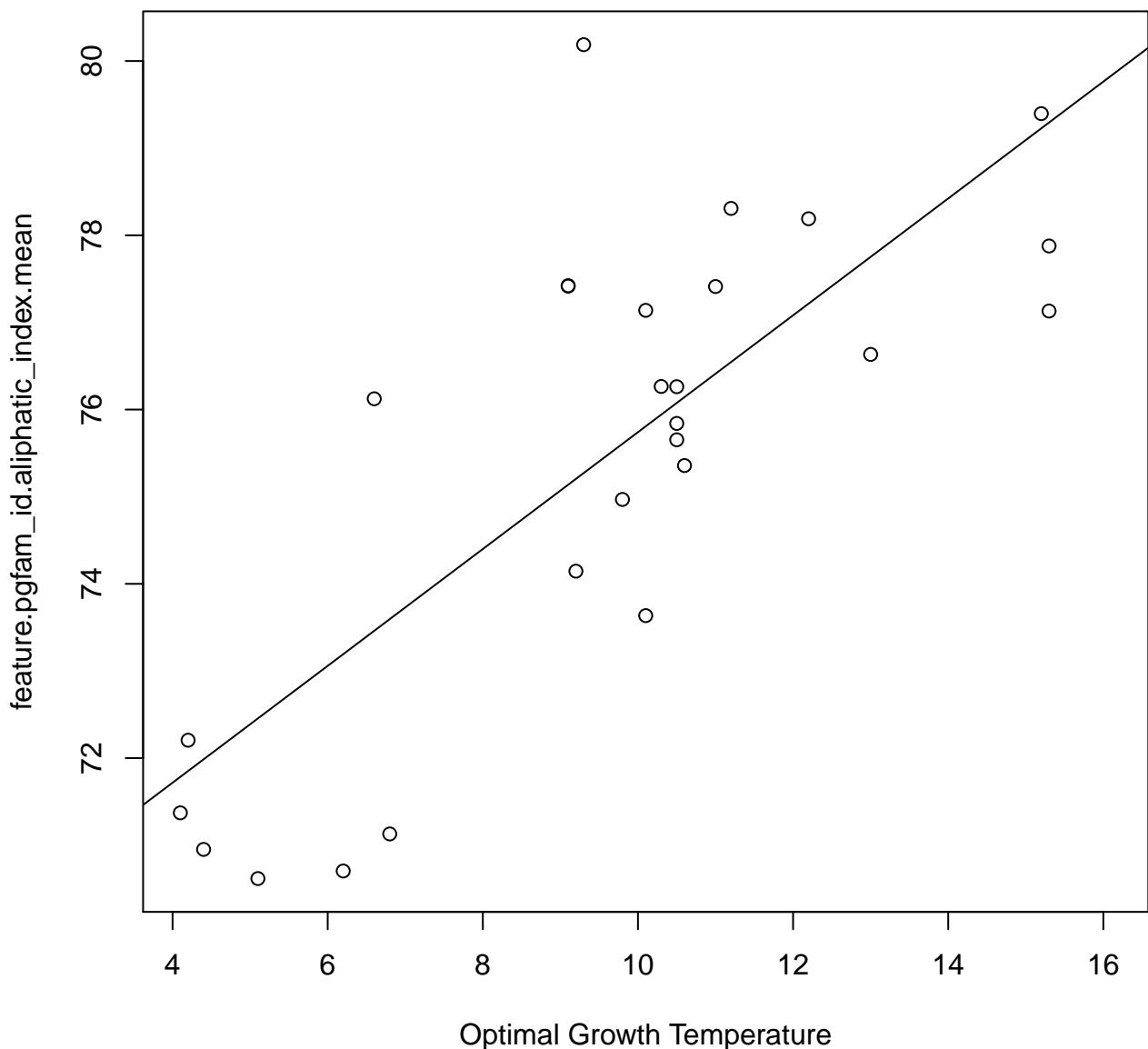
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Uncharacterized ferredoxin-like protein YfhL



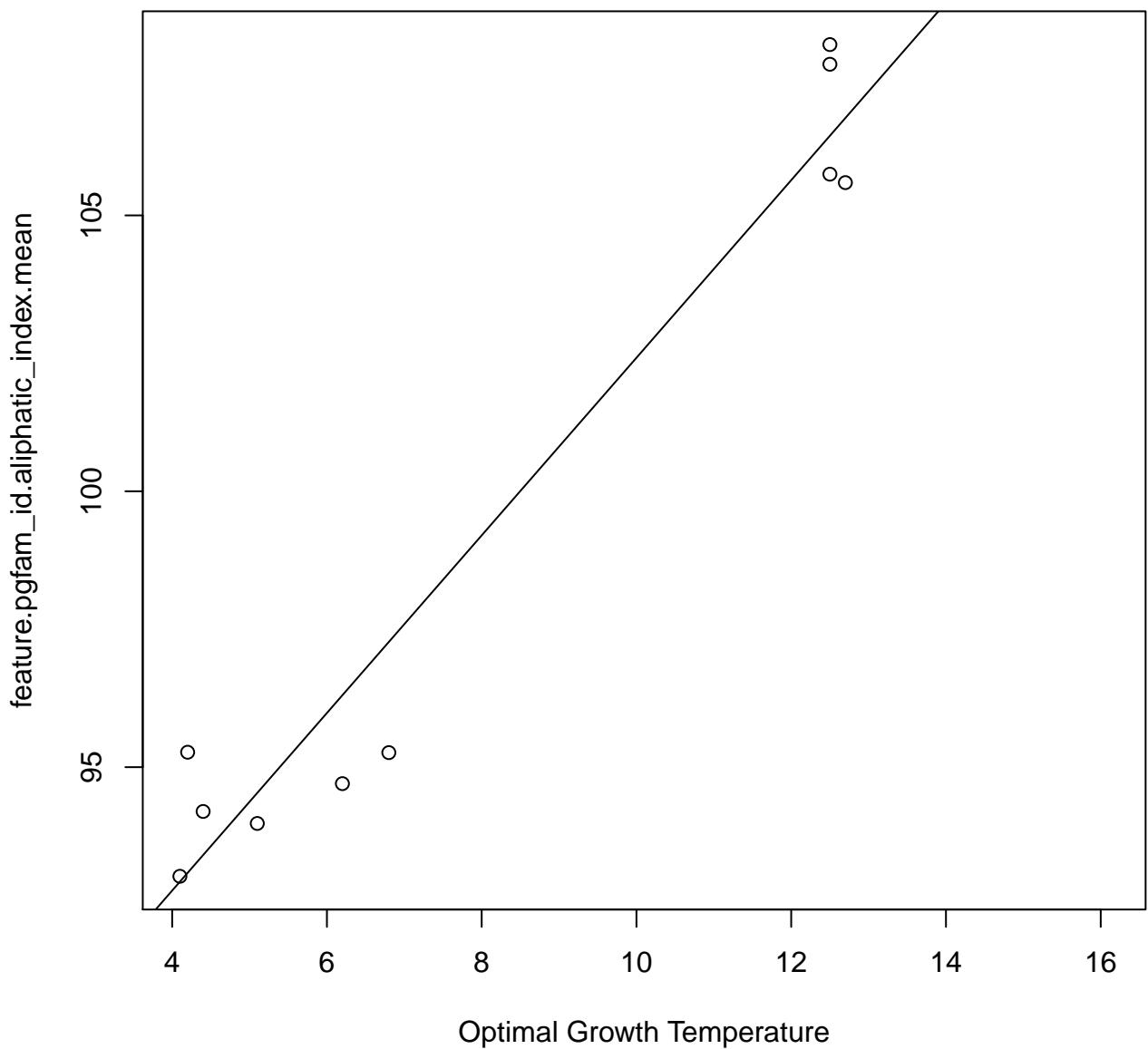
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PGF_01336501
hypothetical protein



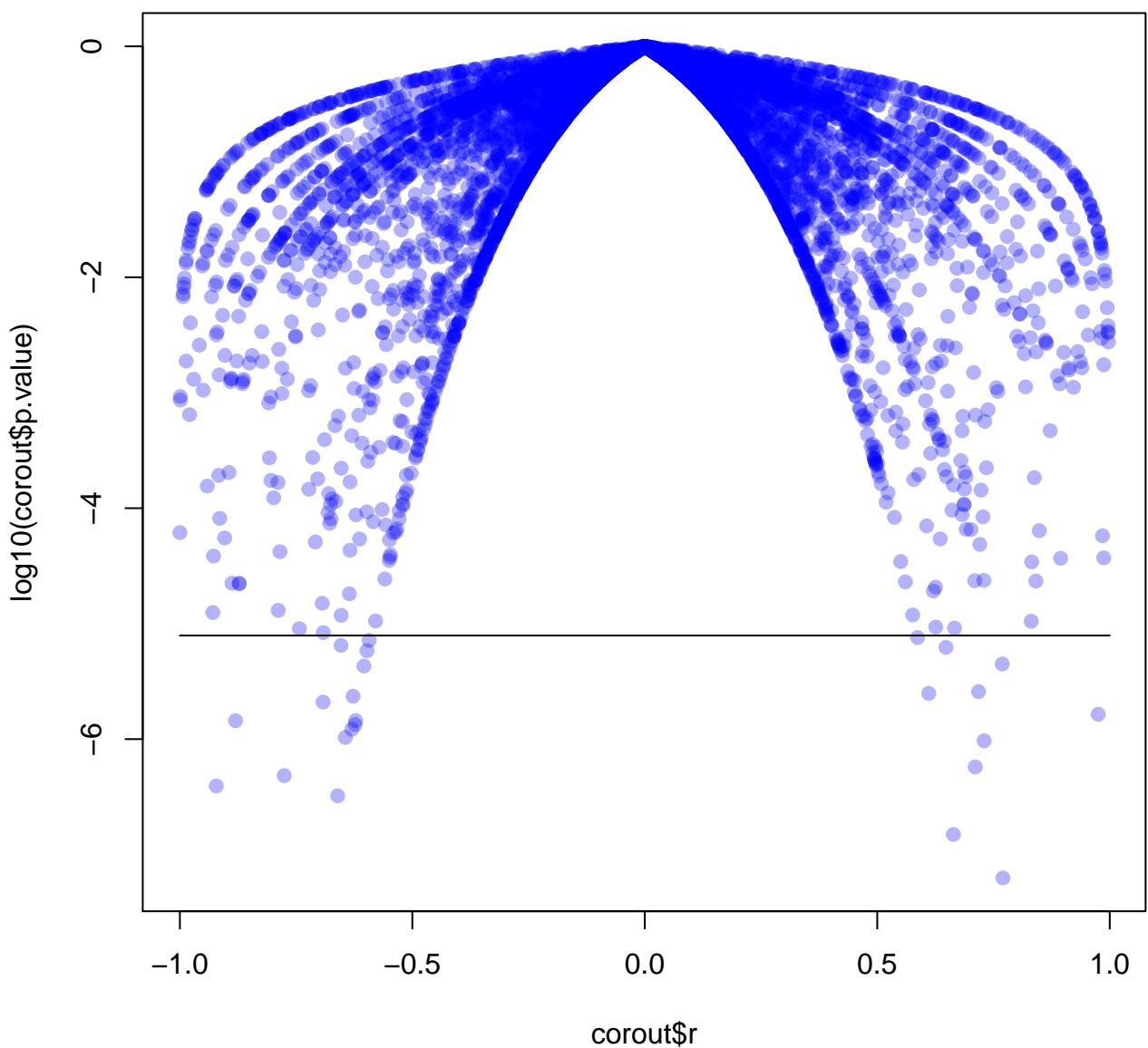
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hypothetical protein



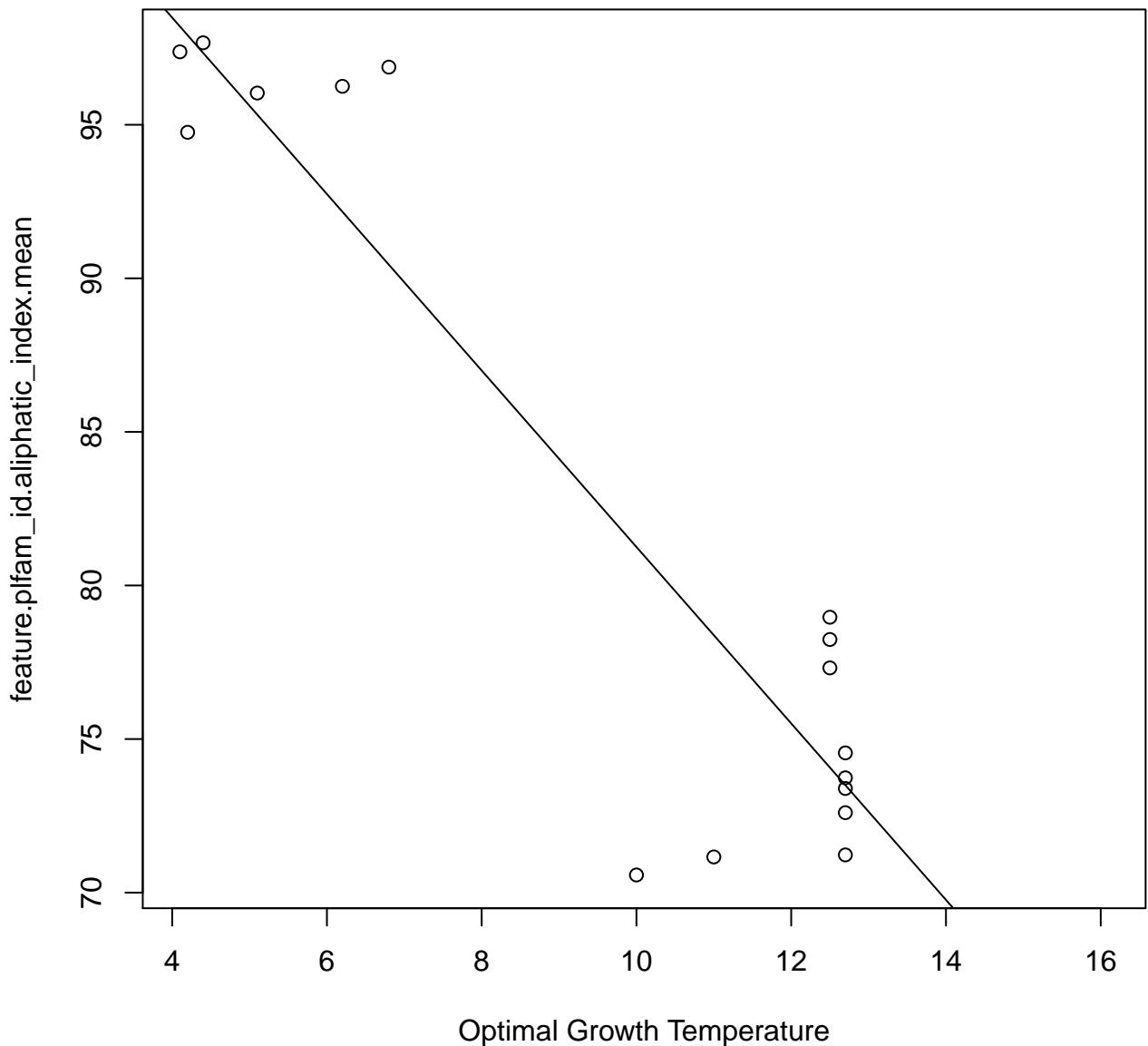
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hypothetical protein



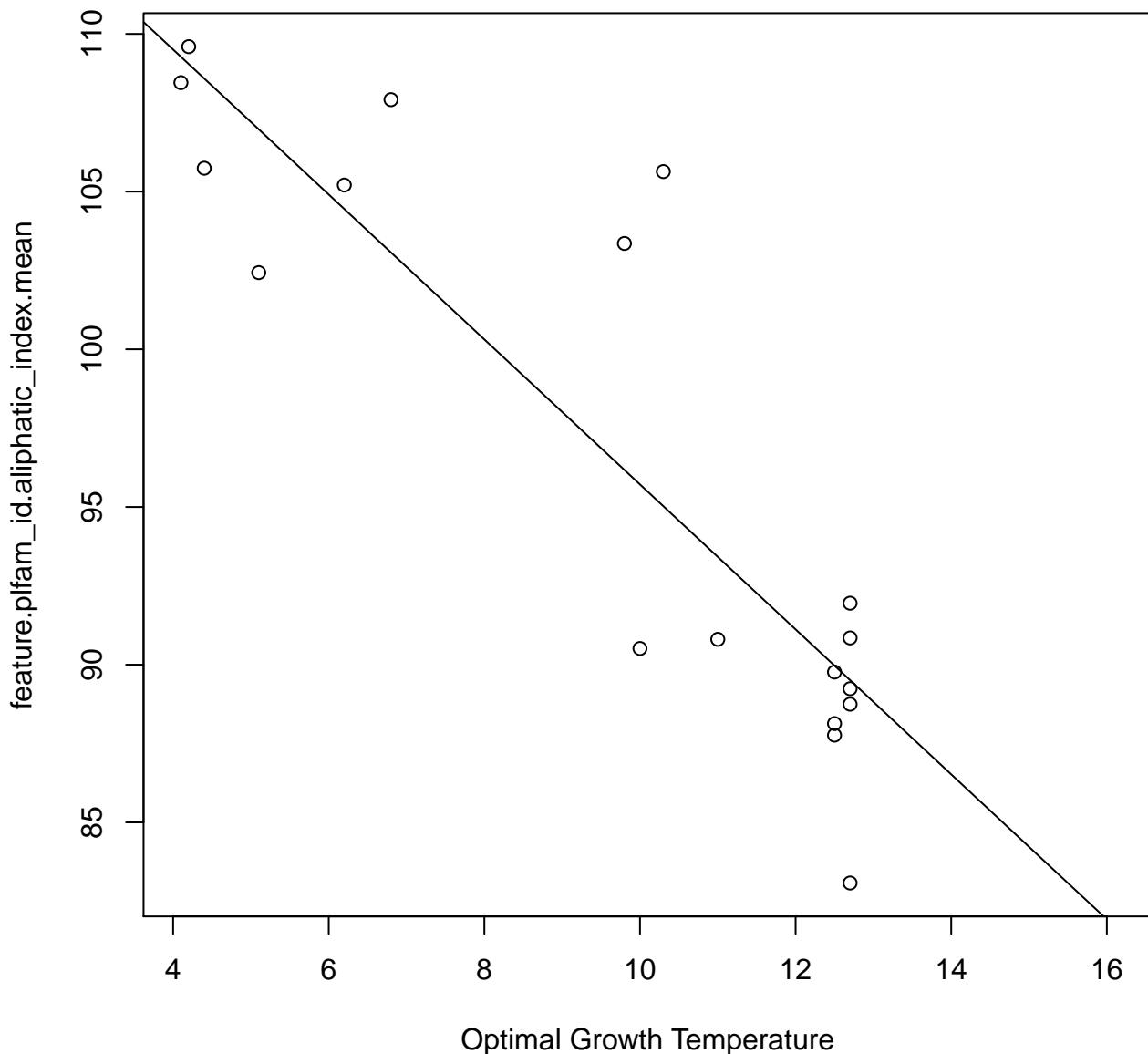
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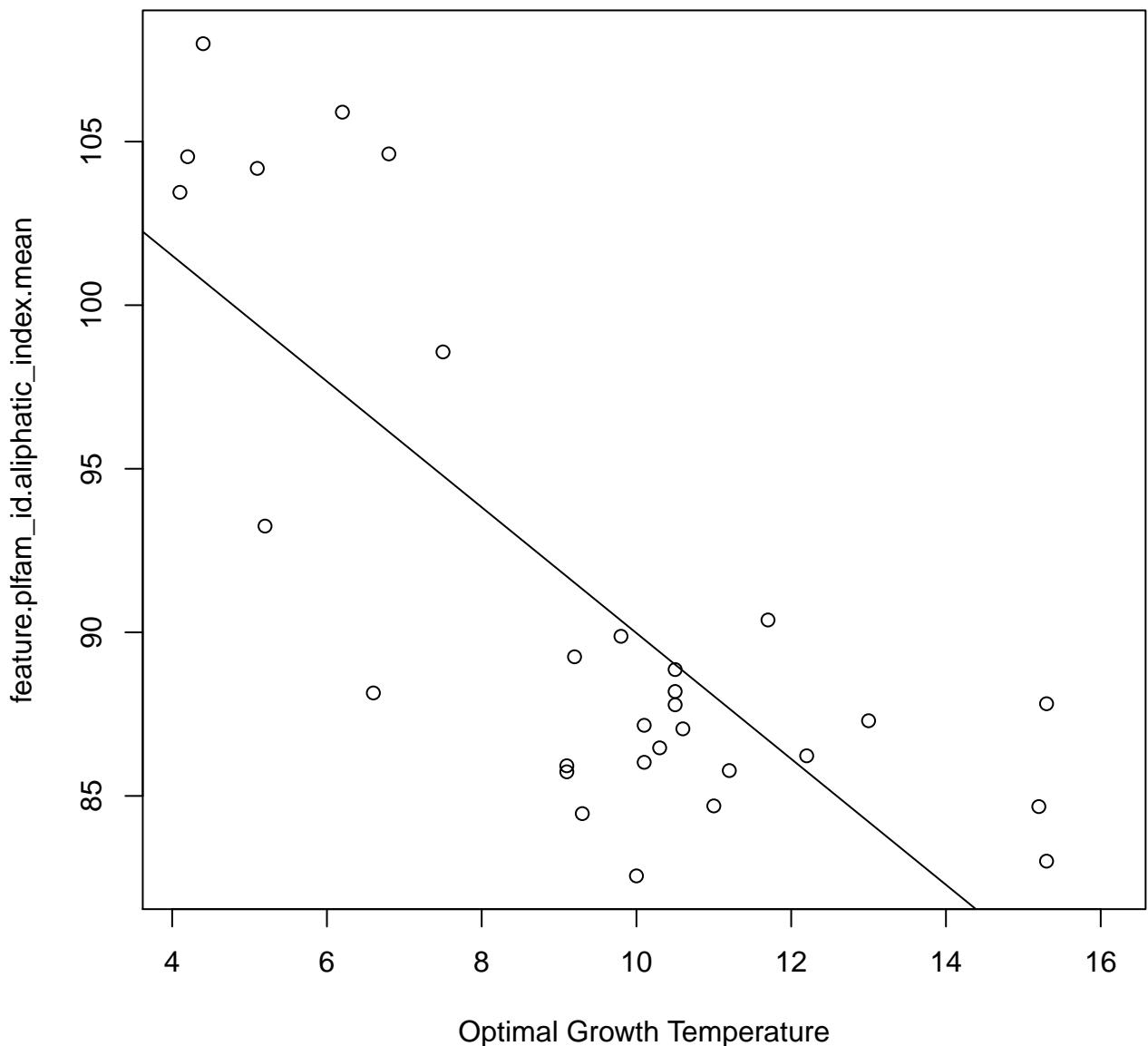
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Outer membrane beta-barrel assembly protein BamE



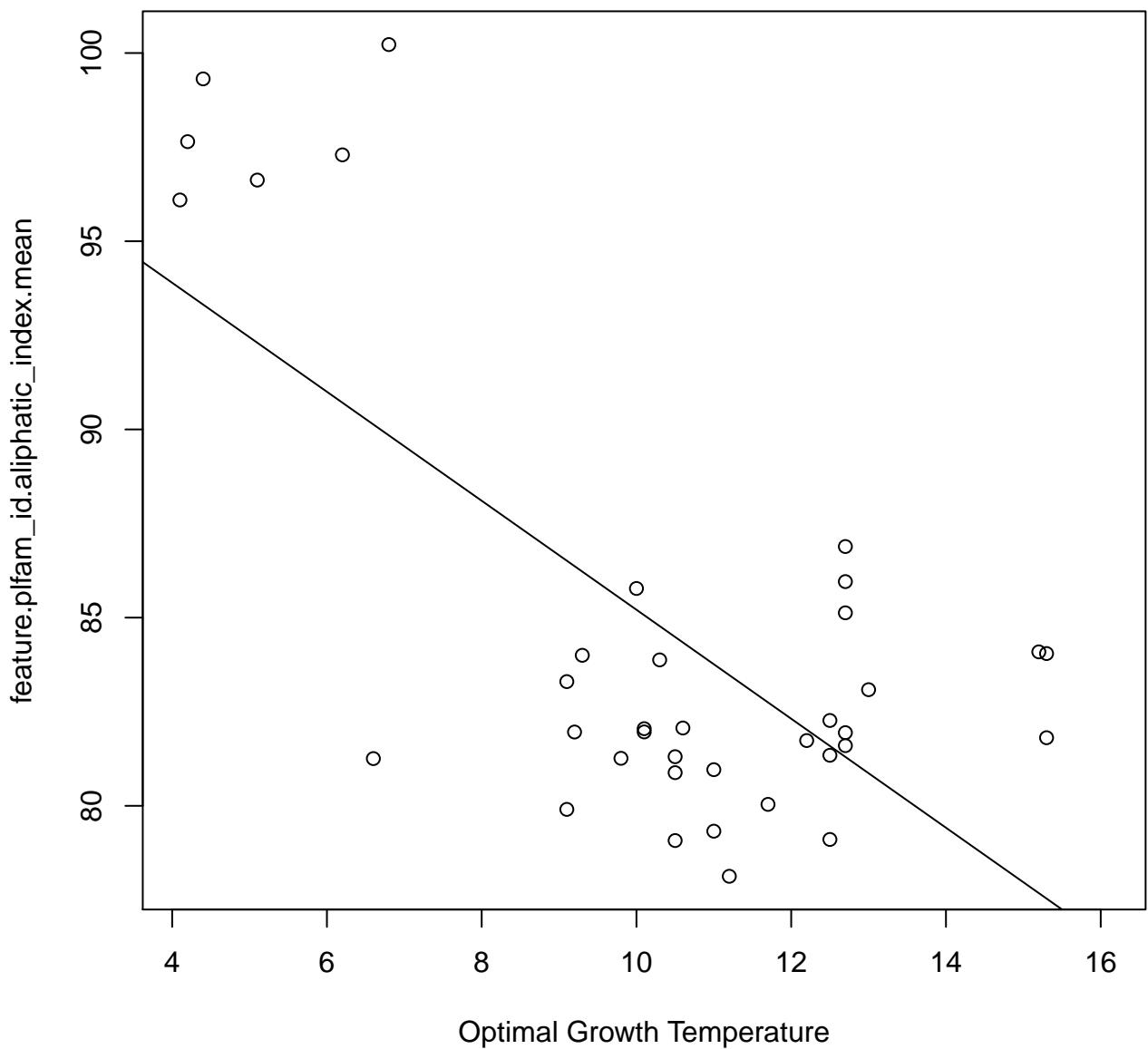
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Two-component system sensor histidine kinase



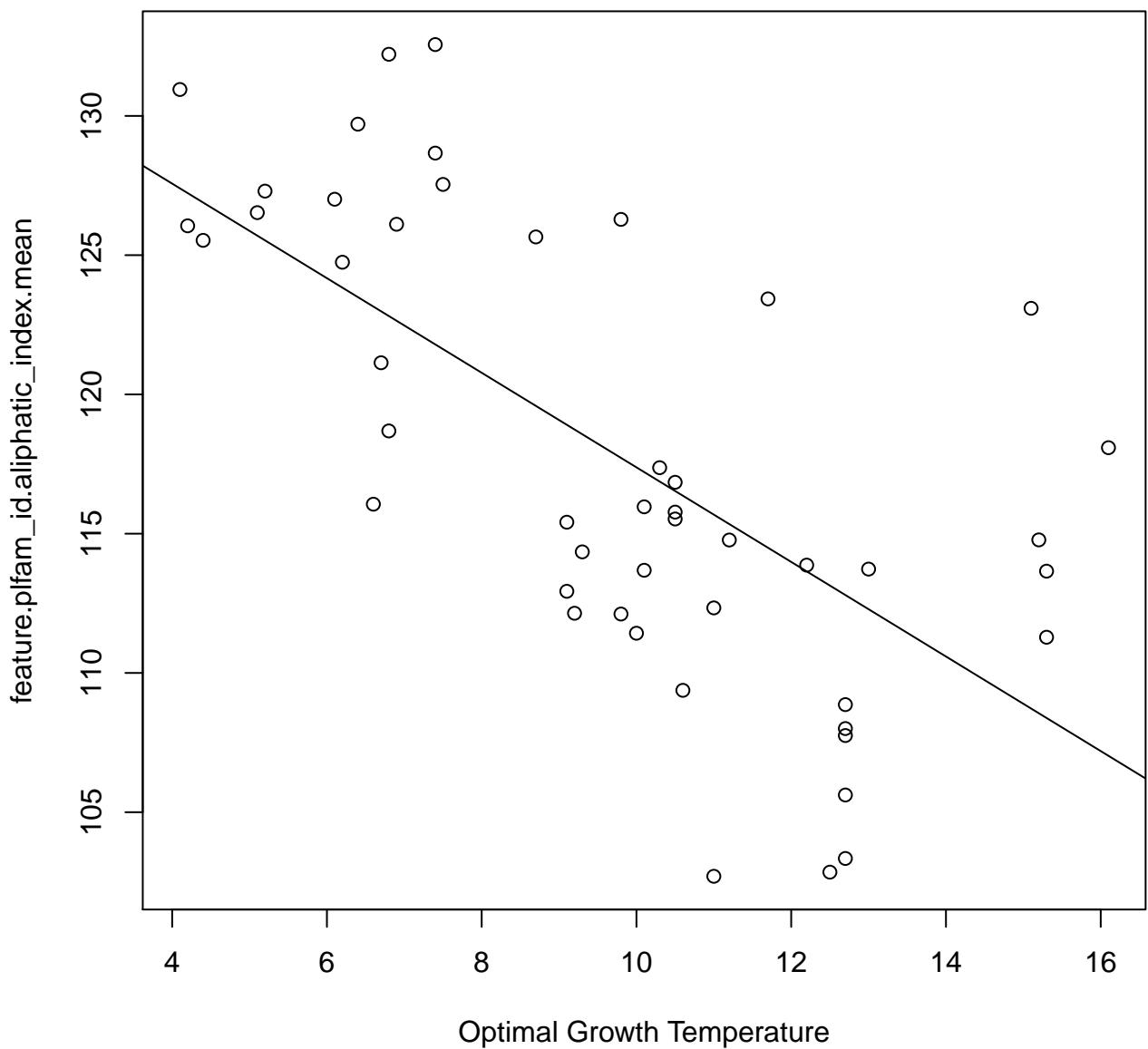
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hypothetical protein



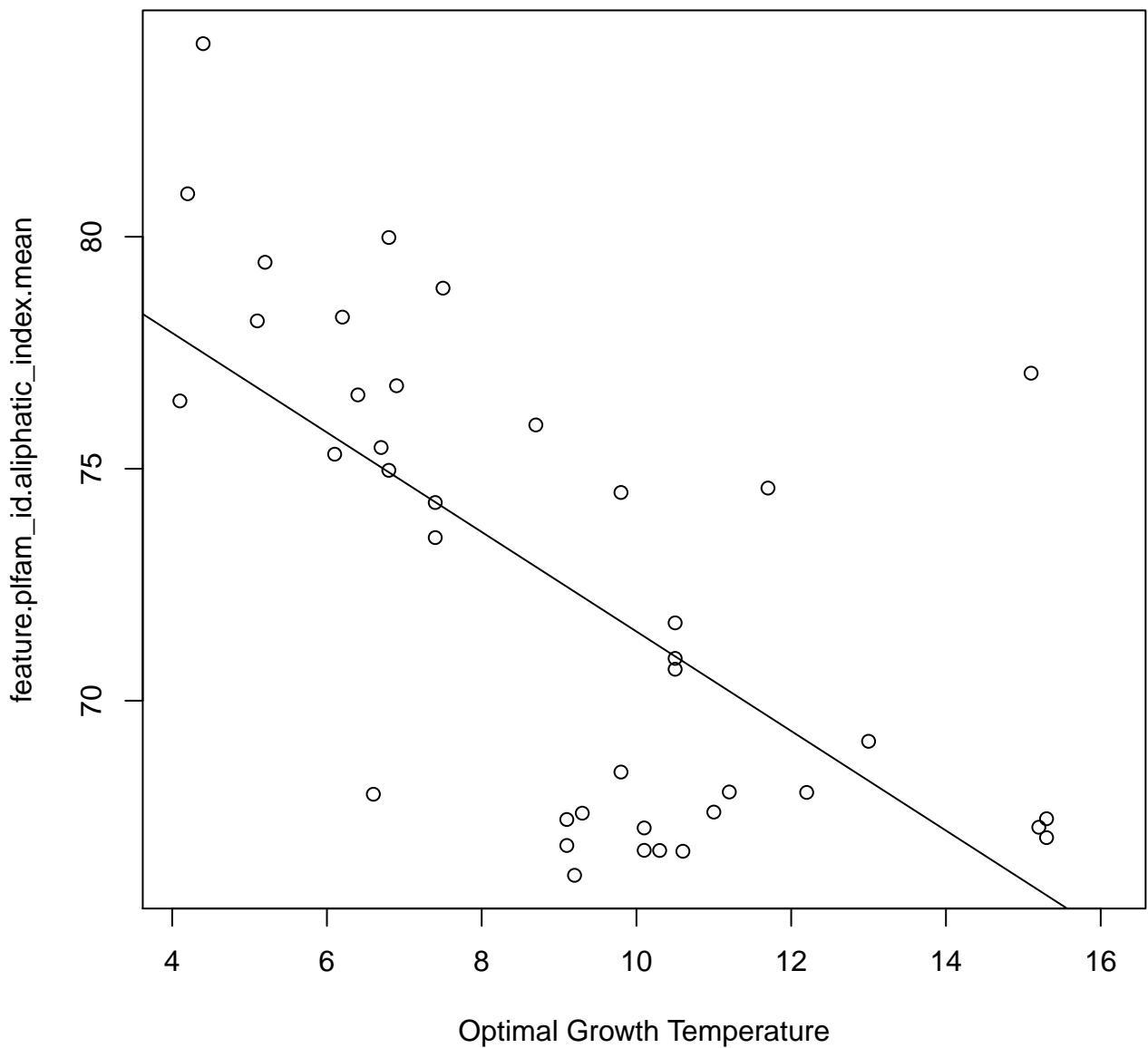
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PLF_28228_00001024
Putative NAD(P)H nitroreductase YdjA



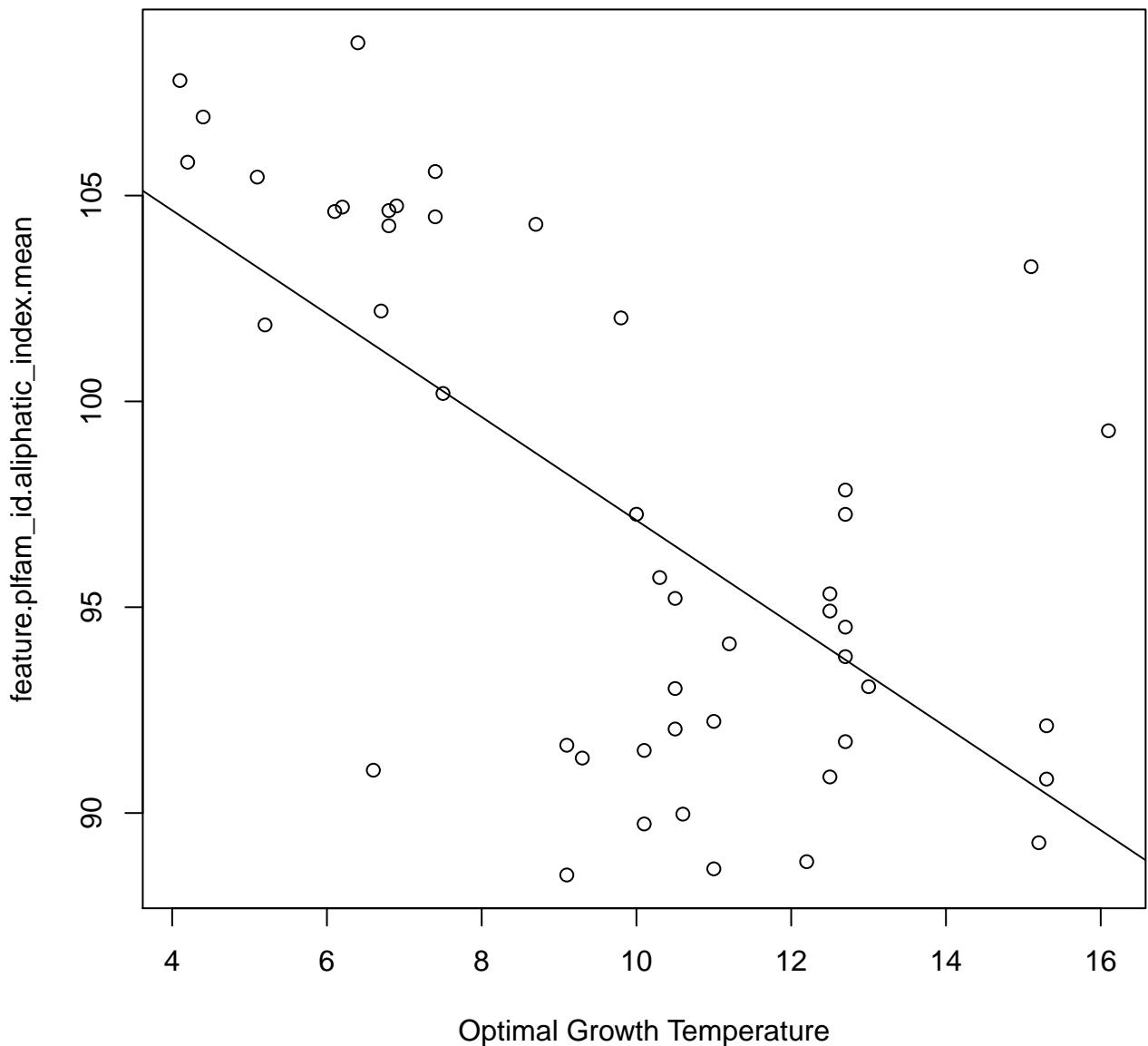
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PLF_28228_00015880
Transporter, LysE family



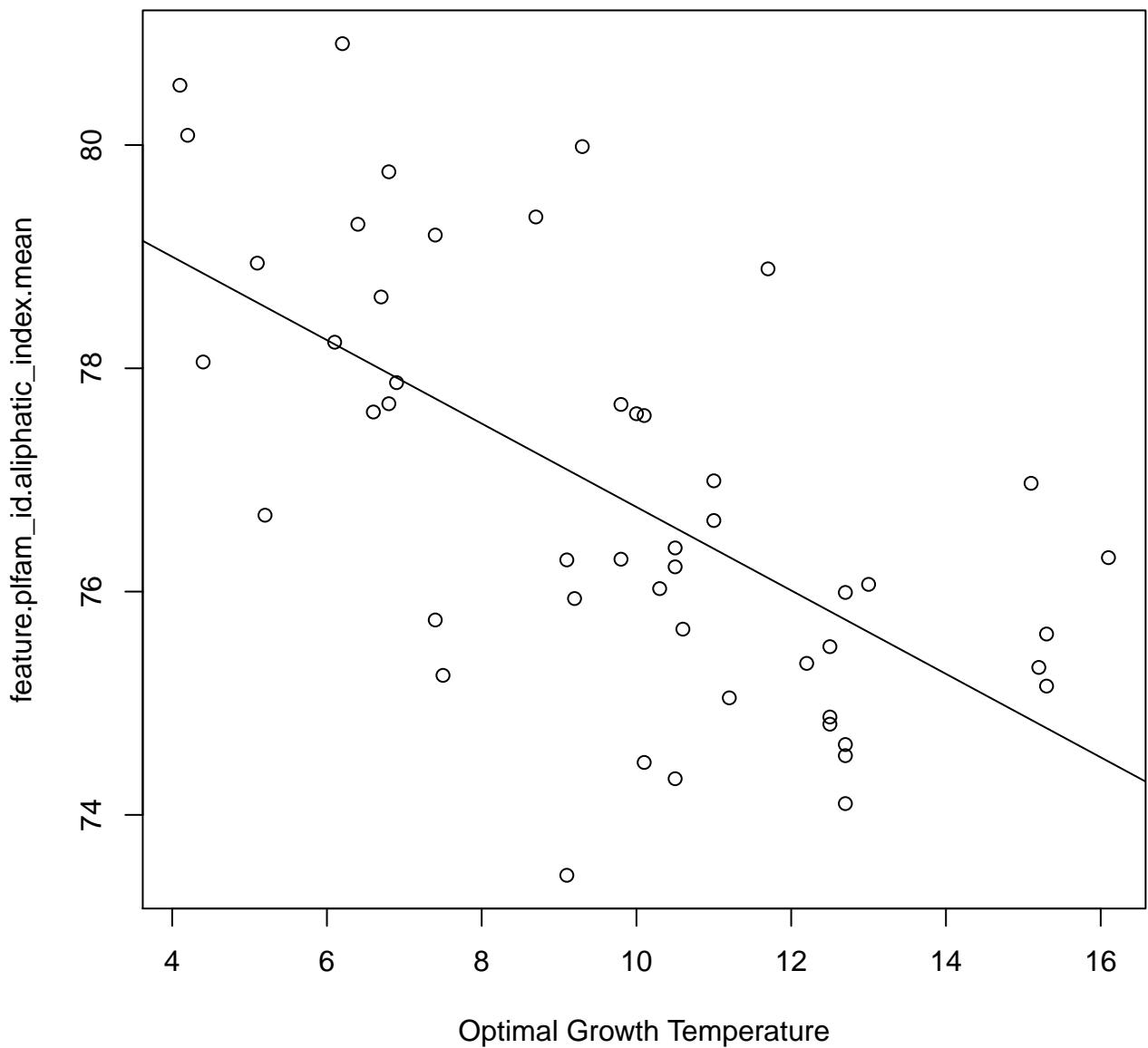
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hypothetical protein



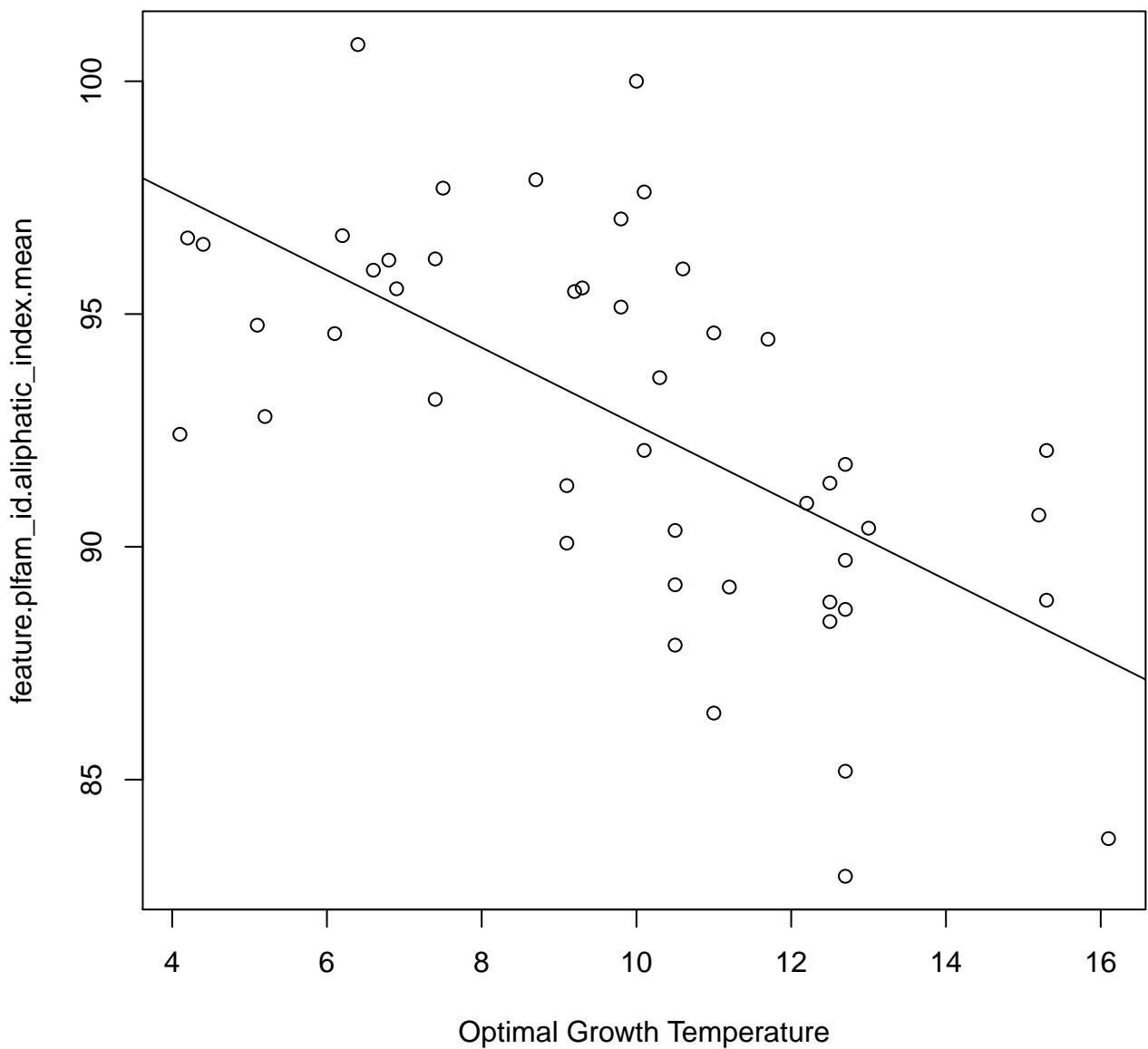
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Flagellar biosynthesis protein FliS



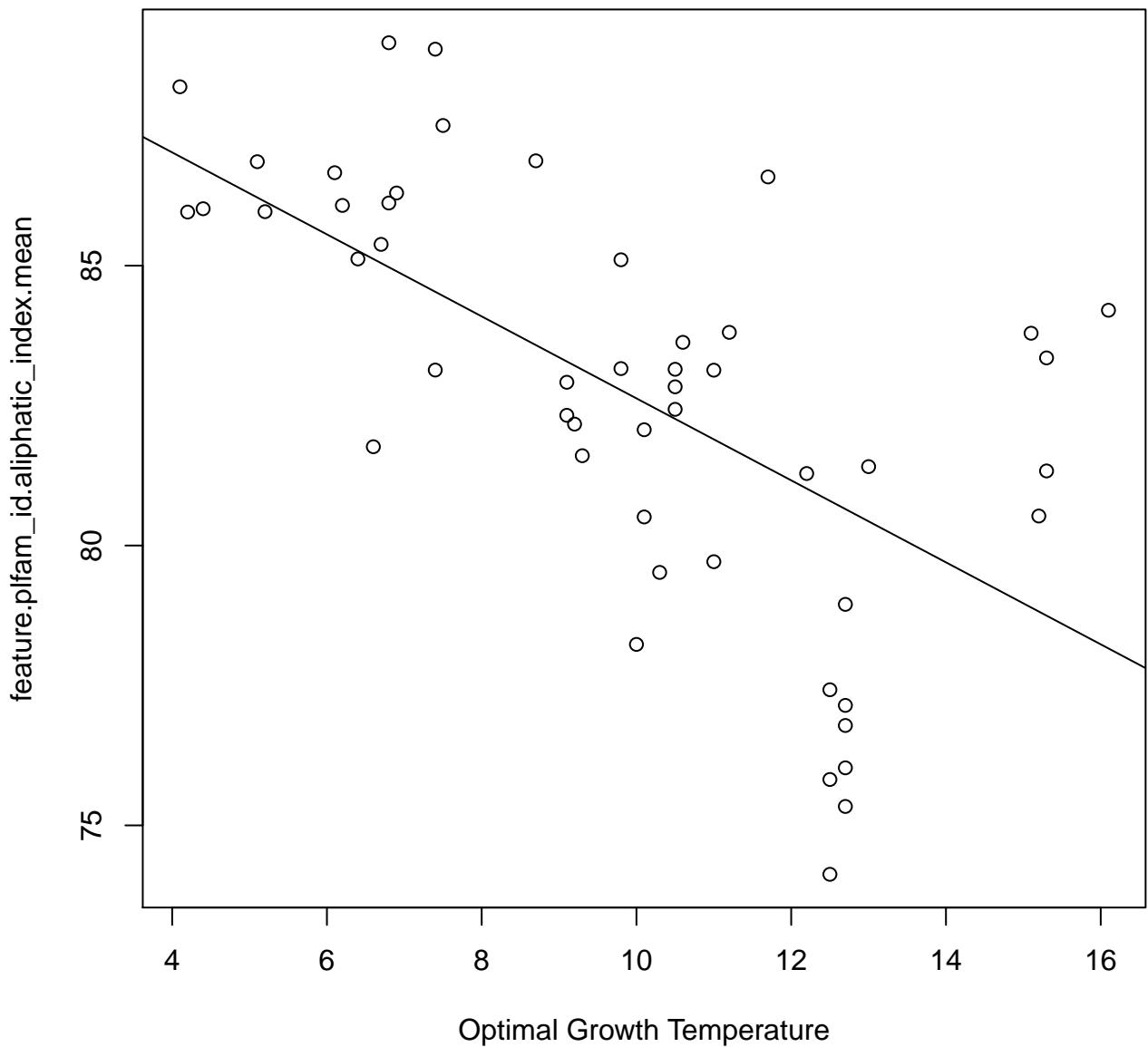
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LSU ribosomal protein L3p (L3e)



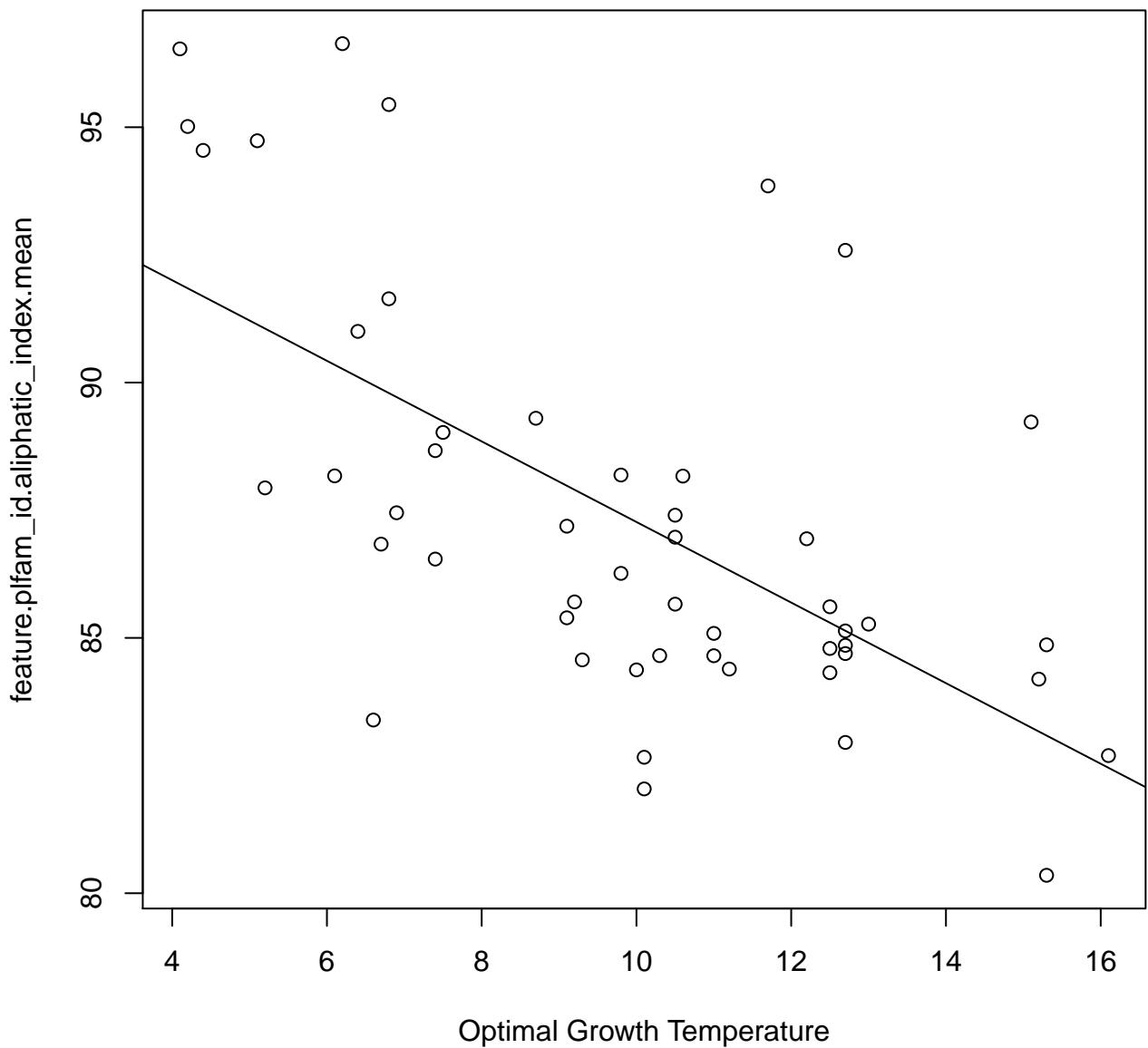
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PLF_28228_00001927
Potential queD like 2



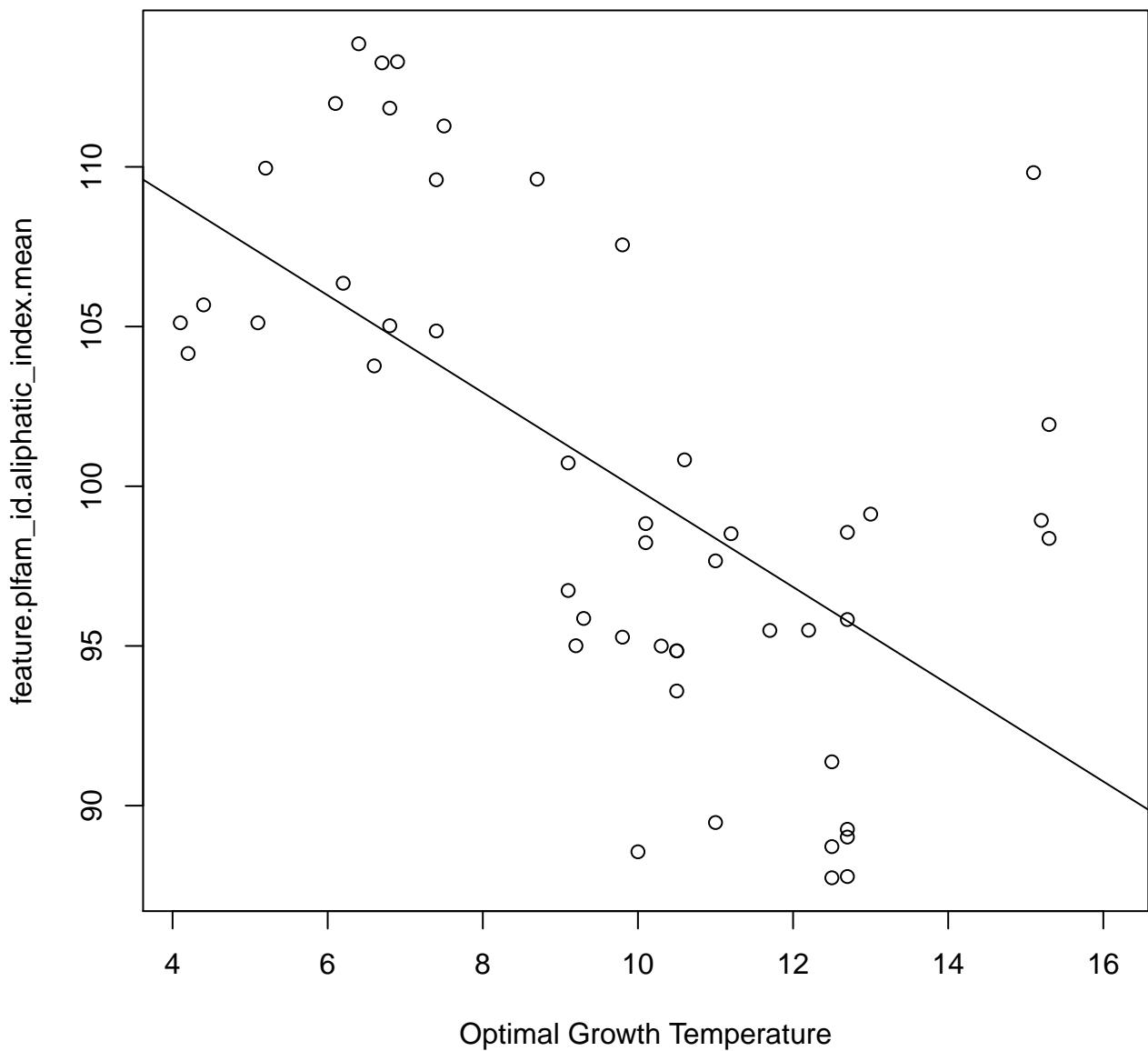
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tRNA (cytidine(32)/uridine(32)-2'-O)-methyltransferase (EC 2.1.1.200)



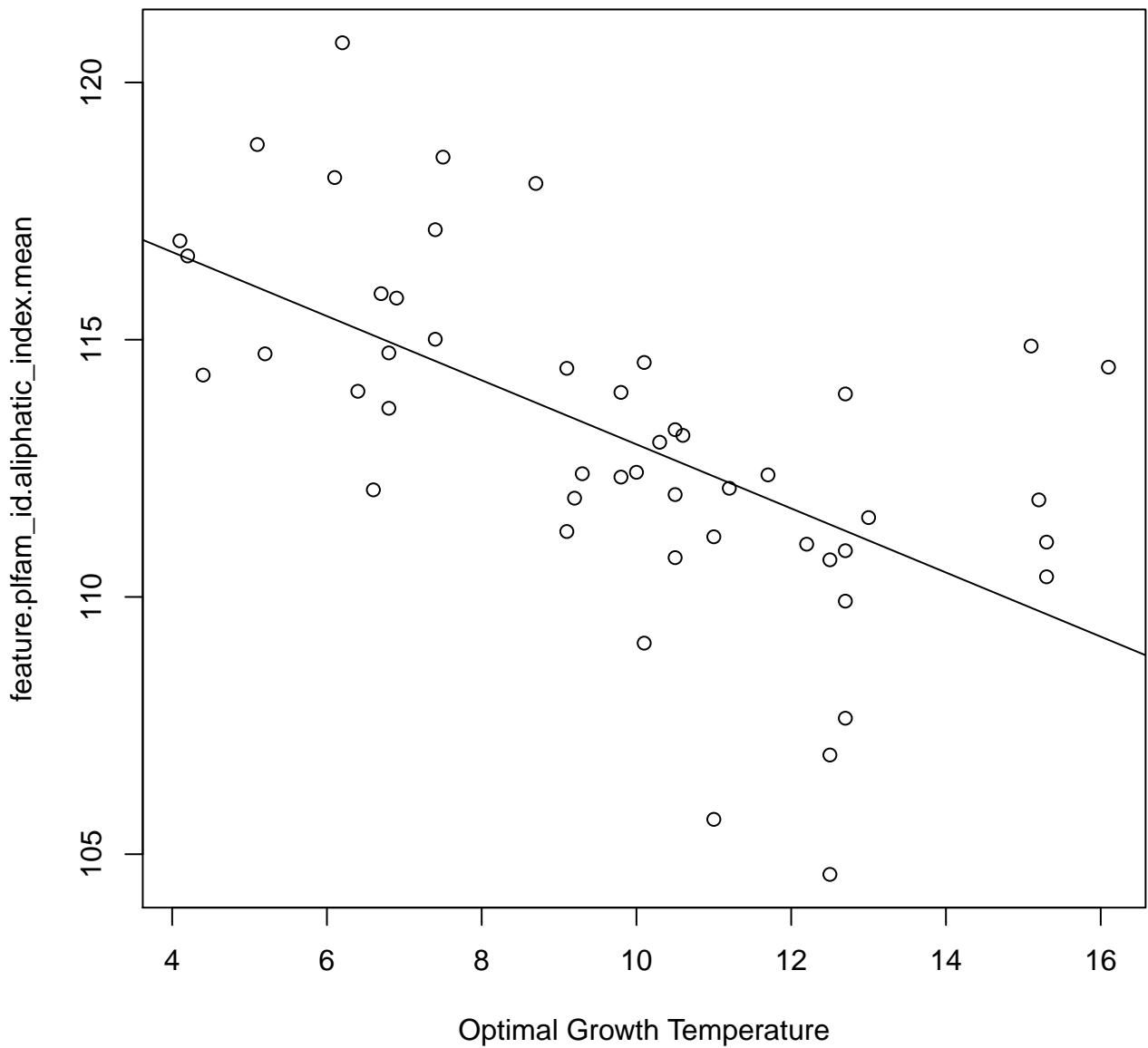
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General secretion pathway protein K



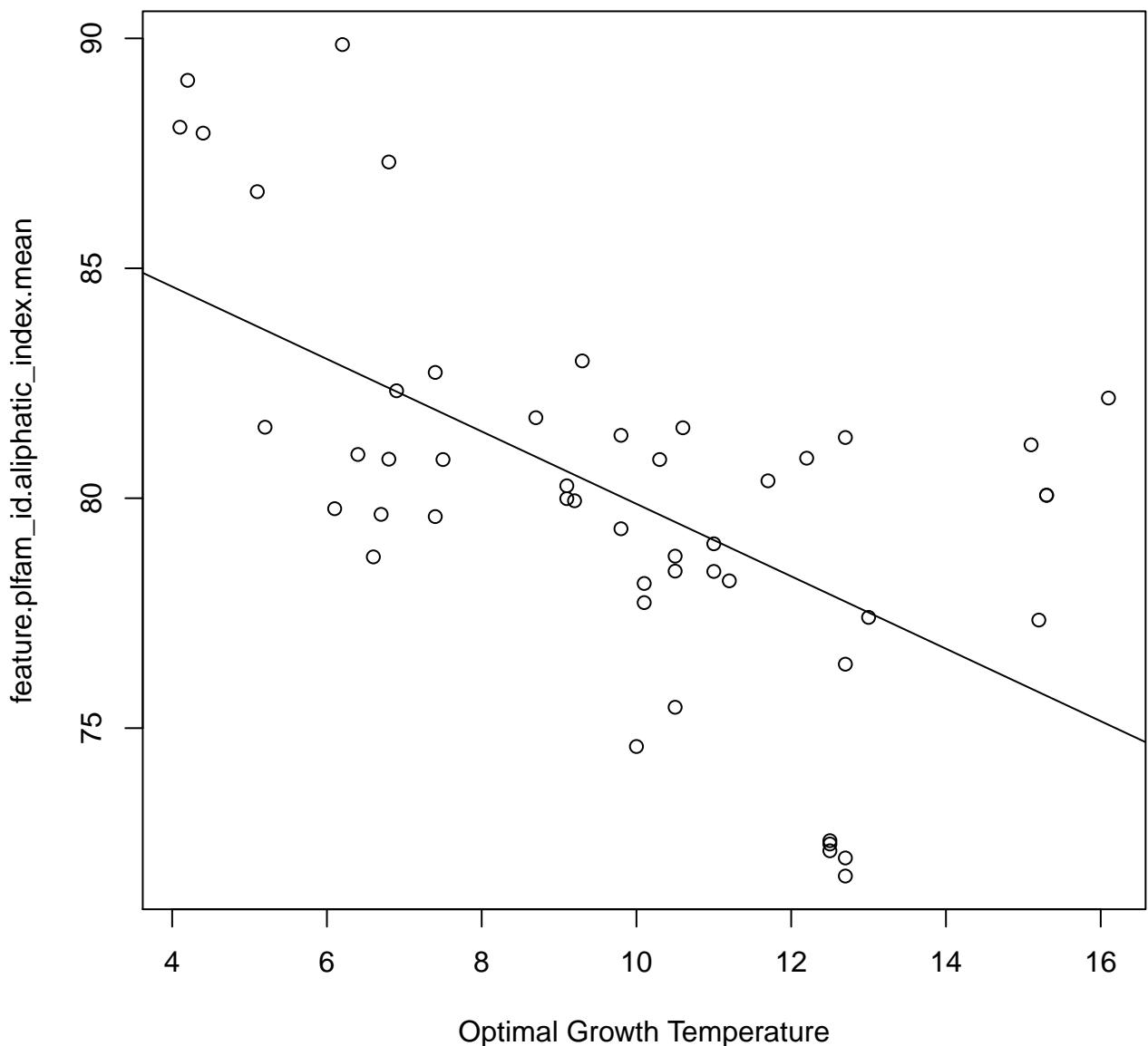
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Cys-tRNA(Pro) deacylase YbaK



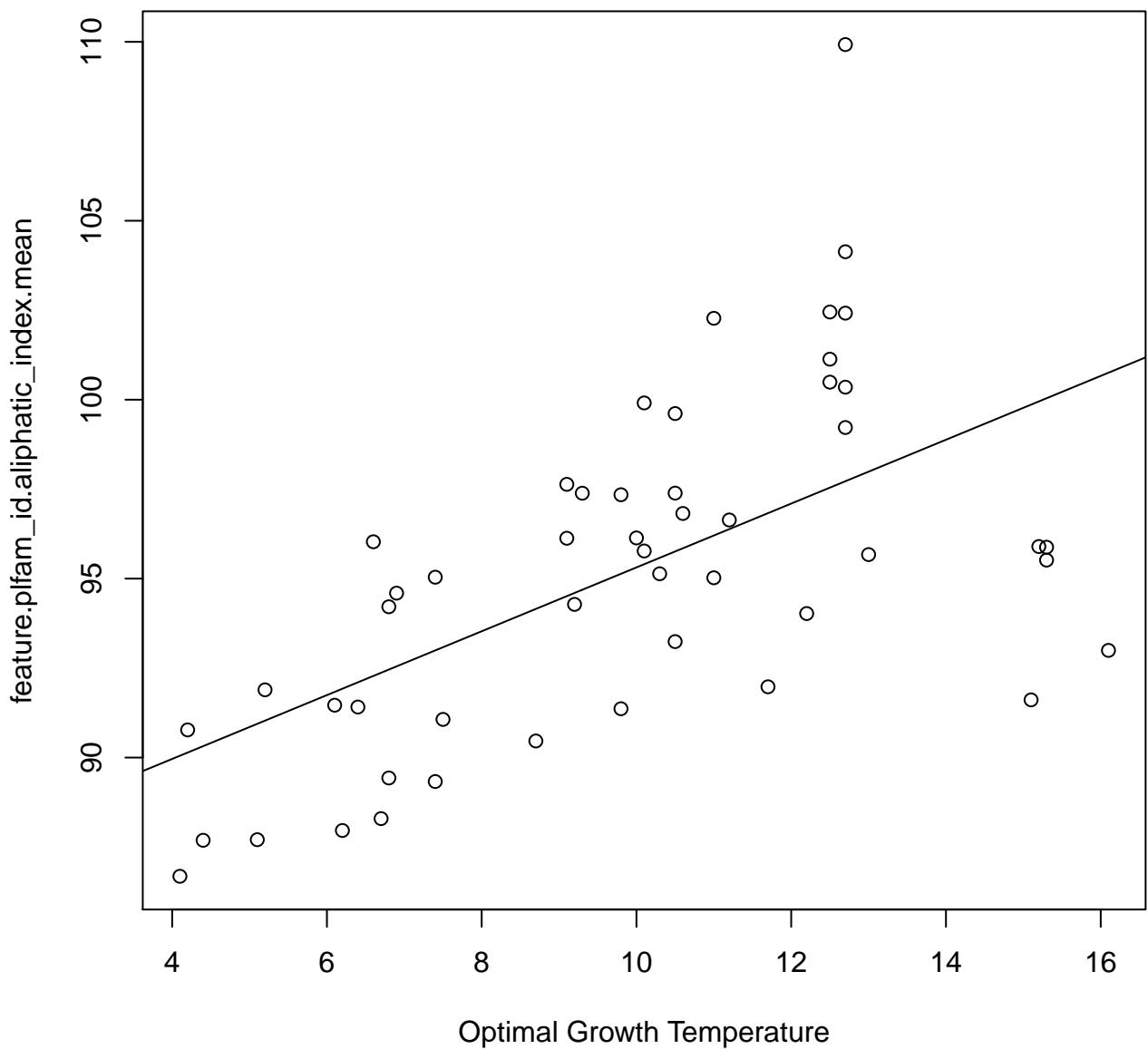
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Predicted glucose transporter in beta-glucoside utilization gene cluster



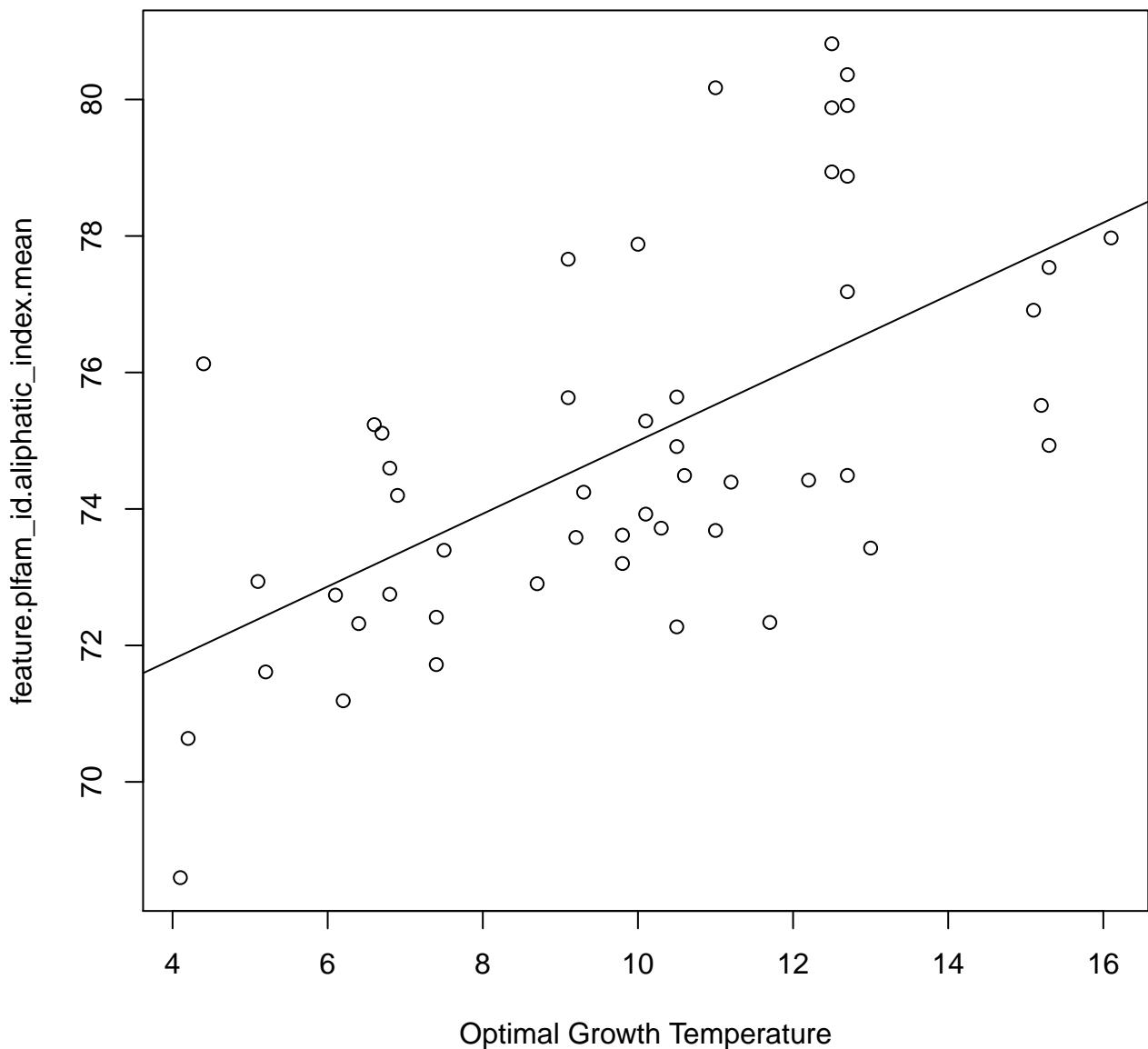
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3-deoxy-D-manno-octulose-2'-acid kinase (EC 2.7.1.166)



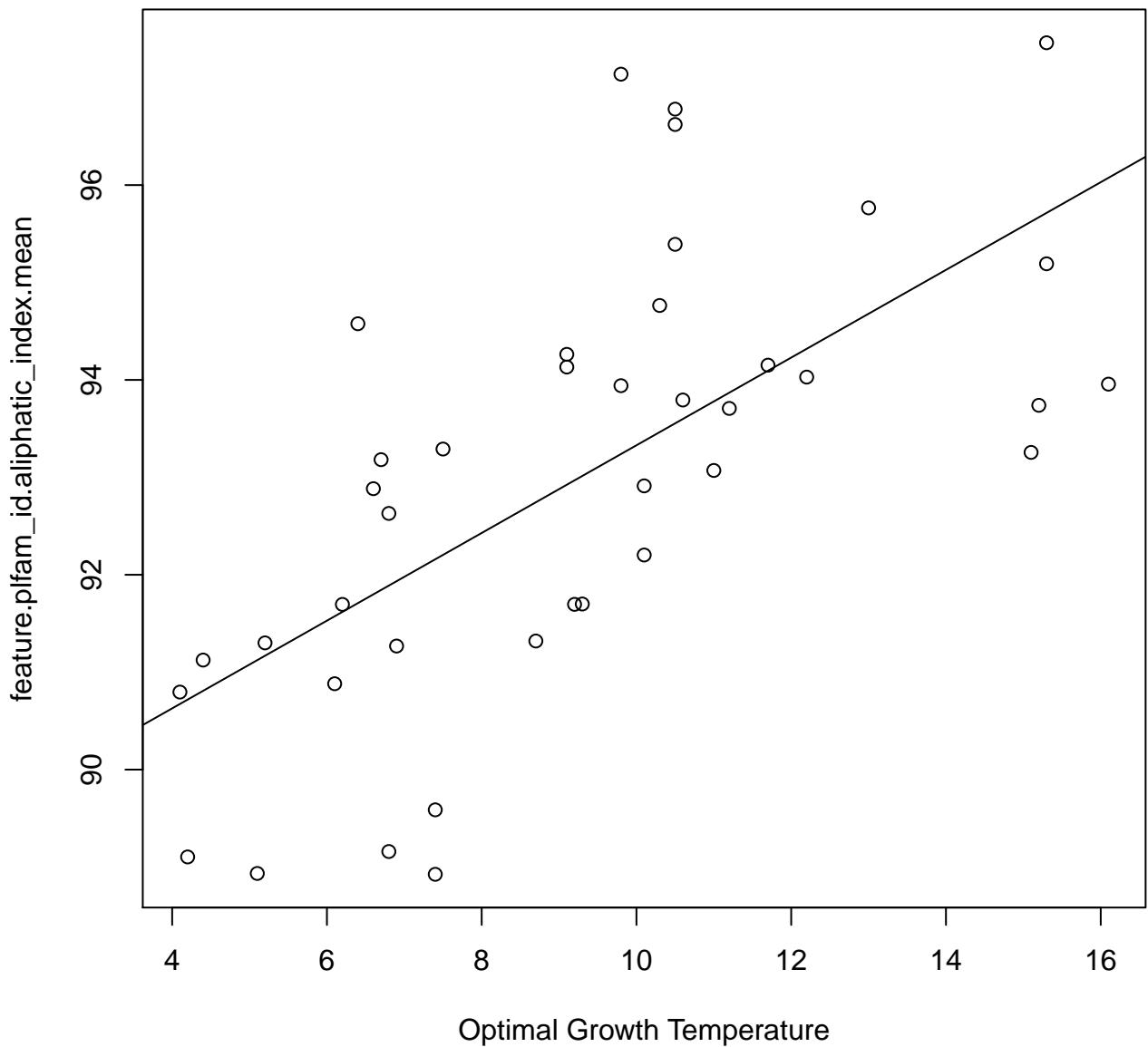
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Esterase ybfF (EC 3.1.-.-)



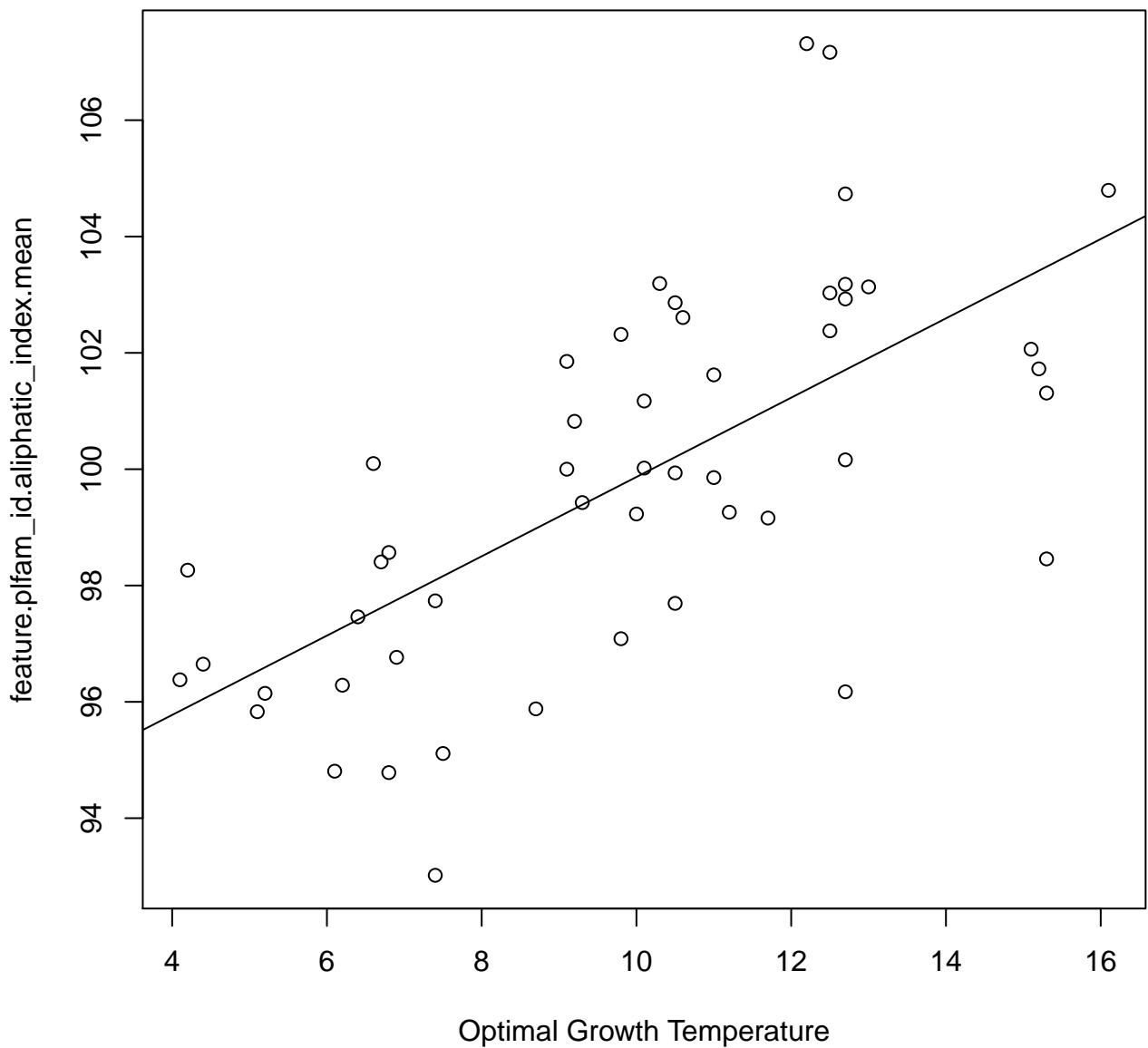
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Flagellar basal-body rod protein FlgF



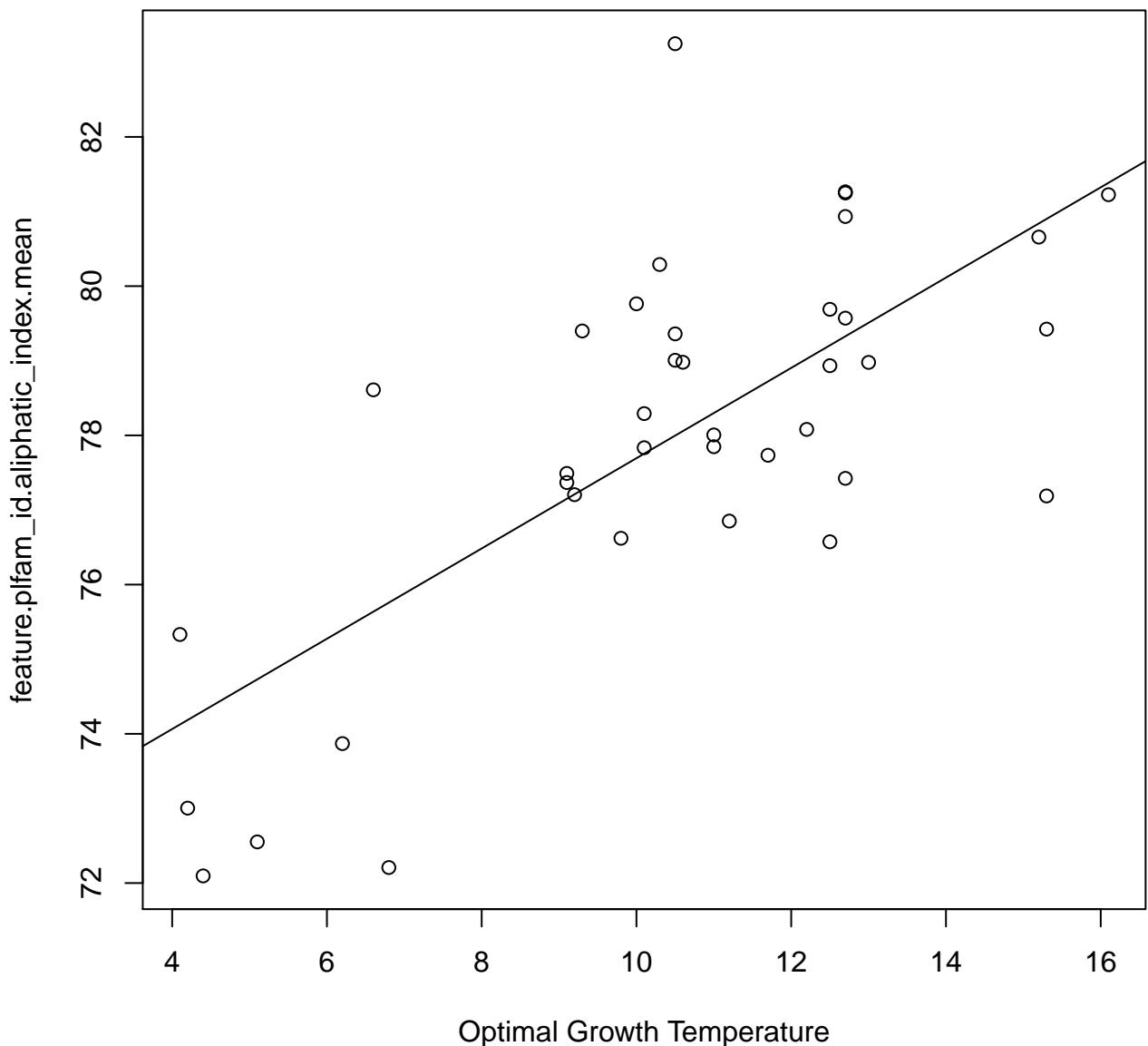
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CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8)



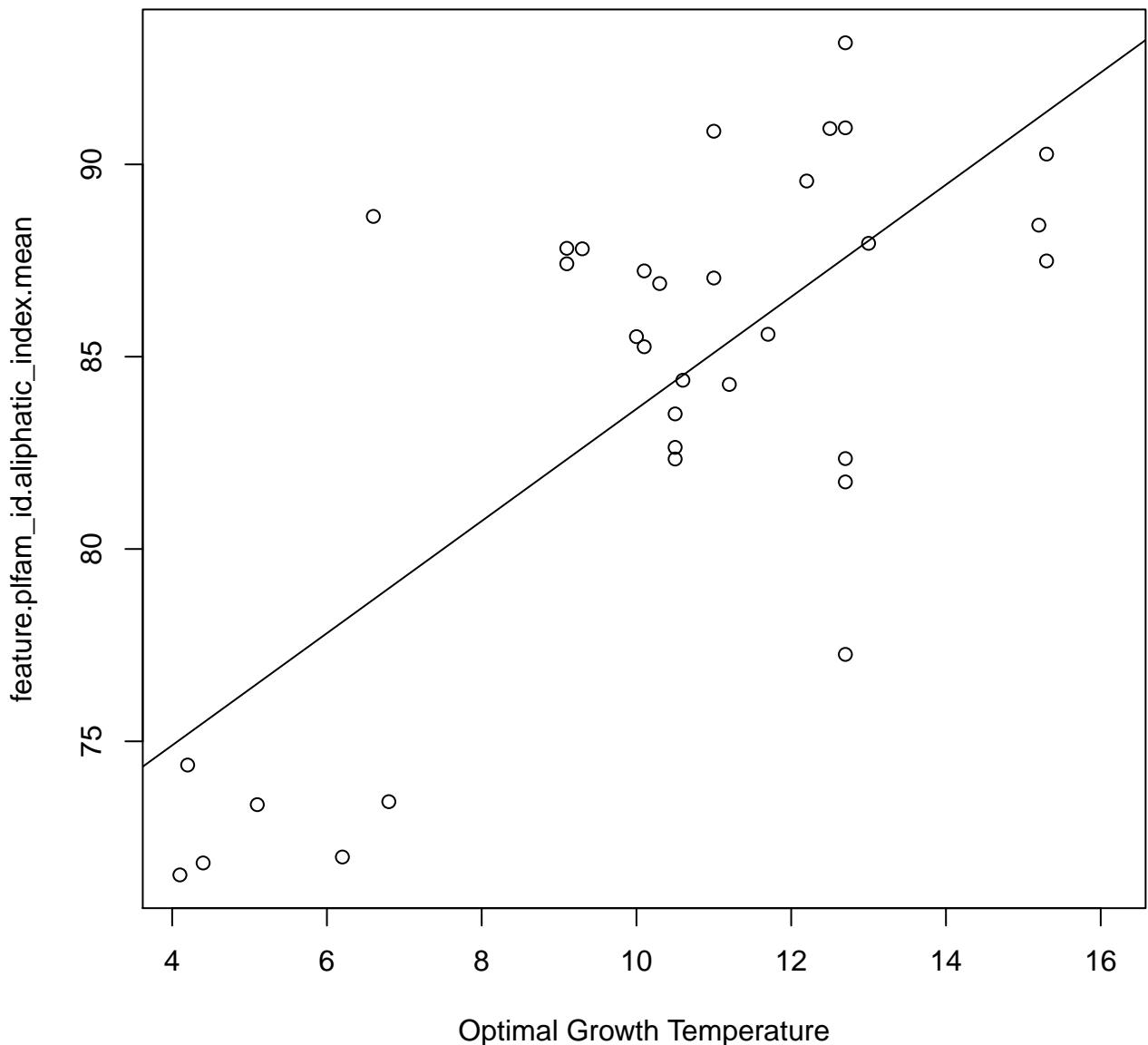
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UPF0758 family protein



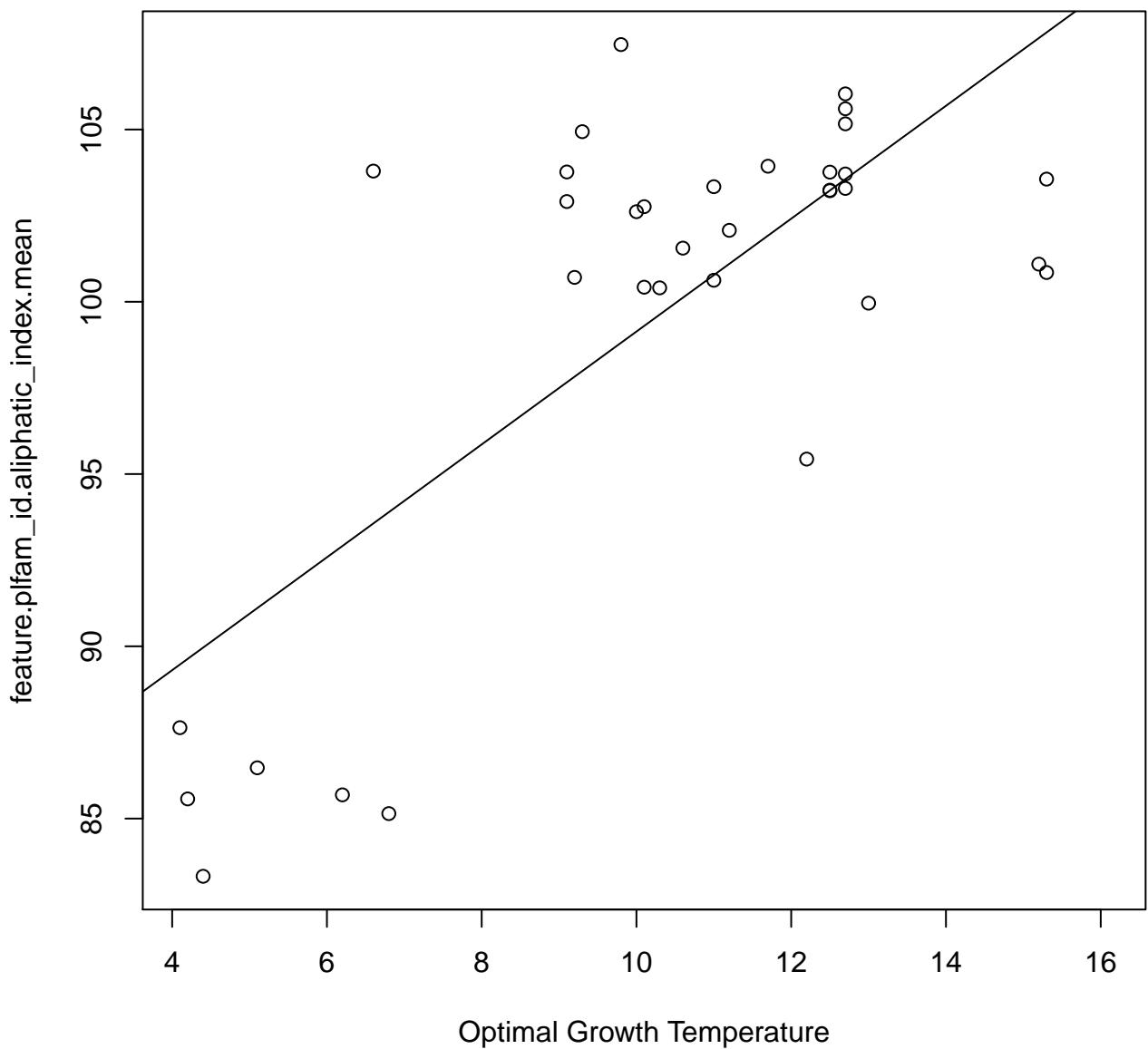
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Flagellar protein FliJ



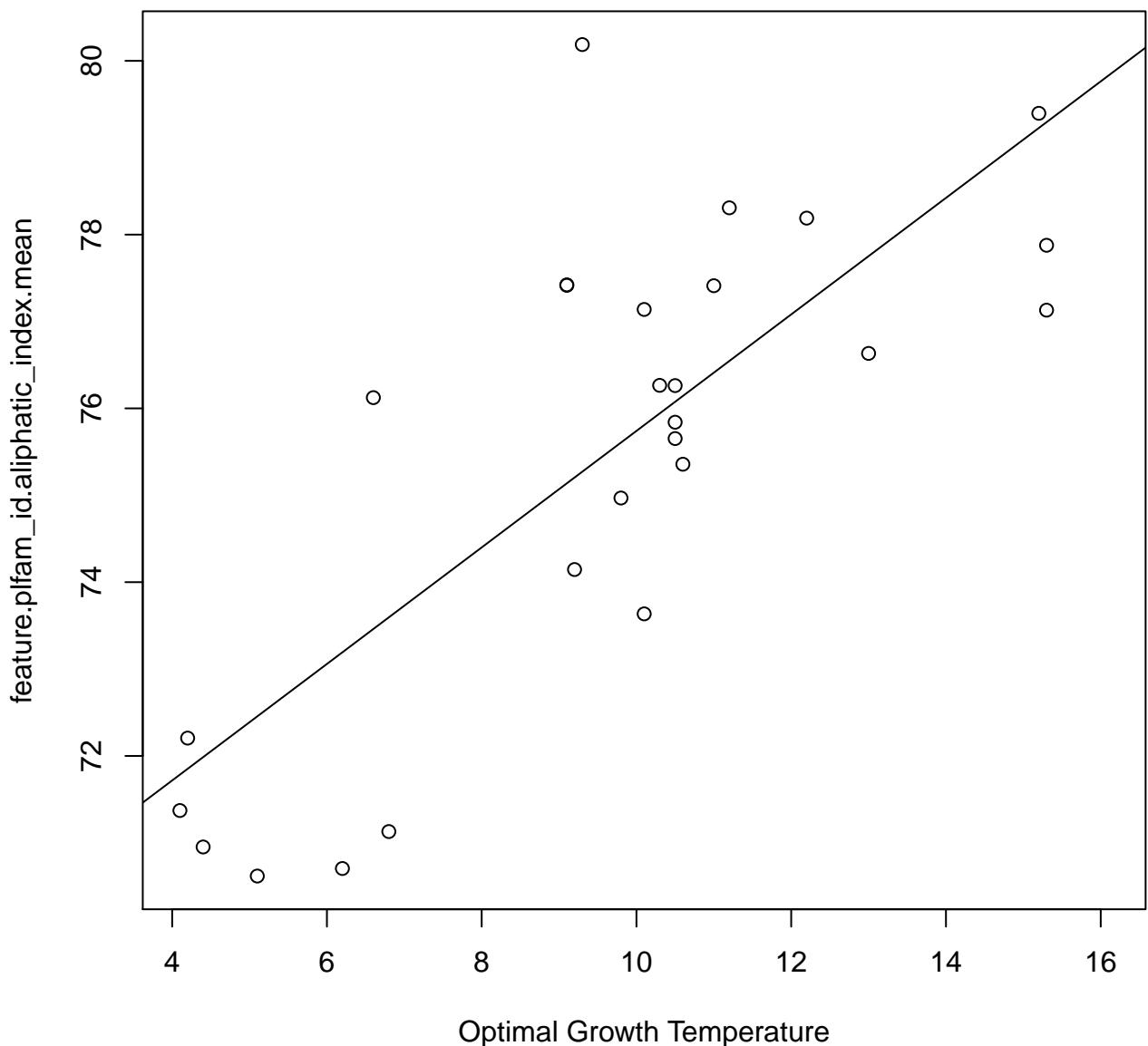
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Uncharacterized ferredoxin-like protein YfhL



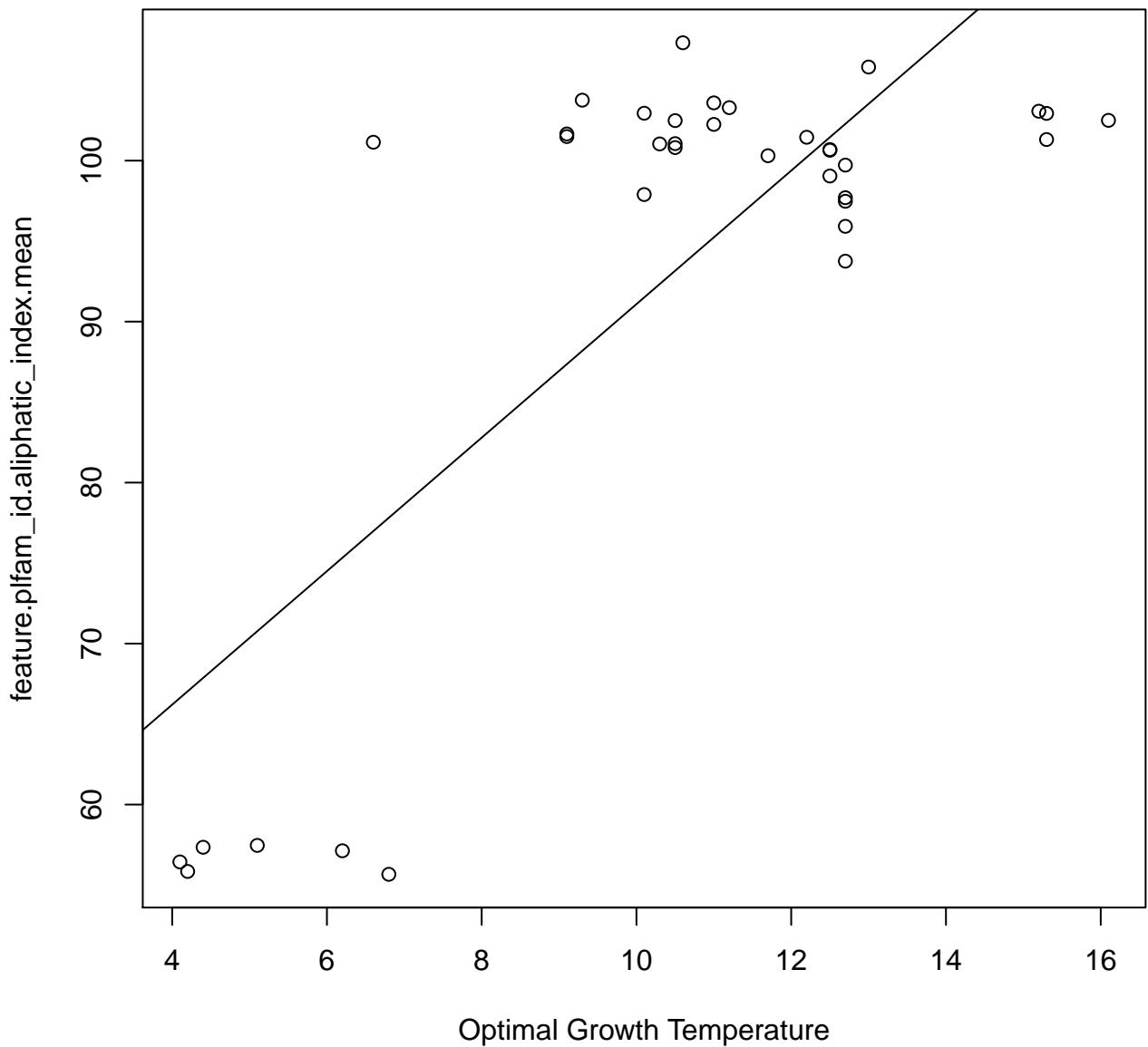
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hypothetical protein



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hypothetical protein



feature.plfam_id.aliphatic_index.mean
PLF_28228_00002798
Two-component transcriptional response regulator, OmpR family



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hypothetical protein

