| | |
|---|---|
| rRNA | 16S rRNA |
| | 23S rRNA |
| | 5S rRNA |
| Fe oxidases | cyc2 |
| | MtoAB |
| periplasmic electron shuttle | cyc1 |
| cytochrome bc1 complex | ubiquinol-cytochrome c reductase cytochrome b sub |
| | ubiquinol cytochrome c oxidoreductase cytochrome |
| | ubiquinol-cytochrome c reductase iron-sulfur subuni |
| cytochrome c oxidases | cbb3-type cyt c oxidase subunits |
| | aa3-type cyt c oxidase subunits |
| | cyt c oxidase |
| cytochrome c biogenesis System I | heme exporter protein A |
| | heme exporter protein B |
| | heme exporter protein C |
| | heme exporter protein D |
| | cytochrome c-type biogenesis protein ccmE (heme ch |
| | cytochrome c-type biogenesis protein ccmF |
| | cytochrome c-type biogenesis protein ccmG (thiored |
| | cytochrome c-type biogenesis protein ccmH (ccmL) |
| | cytochrome c-type biogenesis protein ccmH (ccmI) |
| cytochrome c biogenesis System II | cytochrome c-type biogenesis protein CcsA/ResC (Ccs |
| | cytochrome c-type biogenesis protein Ccs1/ResB |
| heme biosynthesis | glutamyl-tRNA synthetase |
| | glutamyl-tRNA reductase |
| | glutamate-1-semialdehyde 2,1-aminomutase |
| | porphobilinogen synthase (hemB) |
| | hydroxymethylbilane synthase (hemC) |
| | uroporphyrinogen III synthase/methyltransferase (he |
| | uroporphyrinogen decarboxylase (hemE) |
| | coproporphyrinogen III oxidase, aerobic (HemF) |
| | coproporphyrinogen III oxidase, oxygen-independent |
| | protoporphyrinogen IX oxidase, novel form HemJ (pu |
| | ferrochetelase (hemH) |
| | cyoE, protoheme IX farnesyltransferase (coxE, ctaB) |
| | COX15, cytochrome c oxidase assembly protein subu |
| NADH dehydrogenase | NADH dehydrogenase subunit A |
| | NADH dehydrogenase subunit B |
| | NADH dehydrogenase subunit C |
| | NADH dehydrogenase subunit D |
| | NADH dehydrogenase subunit E |
| | NADH dehydrogenase subunit F |

| | |
|---|---|
| | NADH dehydrogenase subunit G |
| | NADH dehydrogenase subunit H |
| | NADH dehydrogenase subunit I |
| | NADH dehydrogenase subunit J |
| | NADH dehydrogenase subunit K |
| | NADH dehydrogenase subunit L |
| | NADH dehydrogenase subunit M |
| | NADH dehydrogenase subunit N |
| Succinate dehydrogenase | succinate dehydrogenase cytochrome b subunit (sdh |
| | succinate dehydrogenase iron-sulfur protein (sdhB) |
| | succinate dehydrogenase flavoprotein subunit (sdhA |
| | succinate dehydrogenase hydrophobic membrane ar |
| ATP synthase | ATP synthase F0 subcomplex A subunit |
| | ATP synthase F0 subcomplex B subunit |
| | ATP synthase F0 subcomplex C subunit |
| | ATP synthase F1 subcomplex alpha subunit |
| | ATP synthase F1 subcomplex beta subunit |
| | ATP synthase F1 subcomplex gamma subunit |
| | ATP synthase F1 subcomplex delta subunit |
| | ATP synthase F1 subcomplex epsilon subunit |
| Ribonucleotide reductases | RNR class I (oxygen-dependent) |
| | RNR class II (oxygen-independent, requires B12) |
| | RNR class III (anaerobic, oxygen sensitive) |
| carbon catabolite repression pathwa | adenylate cyclase |
| | cAMP receptor protein CRP |
| Type VI secretion system | [ClpV ATPase] ClpA |
| | [ClpV ATPase] ClpB |
| | ATP-dependent Lon protease |
| | [sigma-54 transcriptional regulator] VasH (Thiomona |
| | RNA polymerase, sigma 54 subunit, RpoN/SigL |
| | [Membrane complex: VasK] type VI secretion system |
| | [Membrane complex VasF] type VI secretion system |
| | [Baseplate complex TssK=VasE] ImpJ |
| | [Membrane complex VasD] type VI secretion system |
| | [Tip: VgrG1-3 trimer] type VI secretion system secret |
| | [Tip: PAAR-domain containing proteins] |
| | type VI secretion system protein ImpA |
| | [Baseplate complex TssG=VasB] ImpH |
| | [Baseplate complex TssF=VasA] ImpG |
| | [Tail complex: Hcp] type VI secretion system secreted |
| | [Tail complex: VipB=ImpC] |
| | [Tail complex: VipA=ImpB] |
| | [Baseplate complex TssE=HsiF] ImpF |

| | |
|---|---|
| Competence | twitching motility potein PilT (pilus retraction ATPase |
| | pilA fimbrial protein |
| | pilB type IV pilus assembly protein |
| | pilC type IV pilin biogenesis protein |
| | pilD leader peptidase |
| | pilQ fimbrial assembly protein |
| | pilP fimbrial assembly protein |
| | pilO fimbrial assembly protein |
| | pilN fimbrial assembly protein |
| | pilM fimbrial assembly protein |
| | competence protein ComEC/Rec2 |
| | competence protein ComEA |
| | ComF family protein |
| | DNA protecting protein DprA |
| | recA protein |
| | competence factor comP (type VI pilus assembly prot |
| | Competence protein comM (ATP-binding magnesium |
| Nitrogen metabolism | NirB: Nitrate reductase [NAD(P)H] large subunit (NiR |
| | NirD: Nitrate reductase [NAD(P)H] small subunit (NiR |
| | nitric oxide reductase subunit B (NorB) |
| | nitric oxide reductase subunit C (NorC) |
| | NarGHIJ: Nar respiratory nitrate reductase |
| Sulfur metabolism | Sox |
| | sulfur quinone oxidoreductase Sqr |
| | tetrathionate reductase |
| Calvin-Benson-Bassham cycle | phosphoribulokinase (PRK) |
| | RuBisCo |
| | glyceraldehyde-3-phosphate dehydrogenase |
| | fructose-1,6-biphosphatase |
| | transketolase |
| | ribulose-phosphate-3-epimerase |
| | fructose-bisphosphate aldolase |
| | phosphoglycerate kinase (PGK) |
| Entner-Doudoroff pathway | glucokinase (glK) |
| | glucose-6-phosphate 1-dehydrogenase (GPDH) |
| | 6-phosphogluconolactonase (PGL) |
| | phosphogluconate dehydratase (PglD) |
| | **2-dehydro-3-deoxyphosphogluconate and 4-hydrox** |
| | NAD-dependent glyceraldehyde-3-phosphate dehydr |
| | phosphoglycerate kinase (PgK) |
| | phosphoglycerate mutase (pgm) |
| | enolase (EnO) |
| | pyruvate kinase (PyK) |

| | |
|---|---|
| Oxidative pentose phosphate pathwa | glucose-6-phosphate 1-dehydrogenase (GPDH) |
| | 6-phosphogluconate dehydrogenase |
| | ribose 5-phosphate isomerase |
| | ribulose-5-phosphate 3-epimerase |
| | transketolase |
| | transaldolase |
| | NAD-dependent glyceraldehyde-3-phosphate dehydr |
| | phosphoglycerate kinase (PgK) |
| | phosphoglycerate mutase (pgm) |
| | enolase (EnO) |
| | pyruvate kinase (PyK) |
| Glycolysis | glucokinase (glK) |
| | phosphoglucose isomerase (Pgi) |
| | **1-phosphofructokinase (FruK)** |
| | fructose bisphosphate aldolase (Fba) |
| | NAD-dependent glyceraldehyde-3-phosphate dehydr |
| | phosphoglycerate kinase (PgK) |
| | phosphoglycerate mutase (pgm) |
| | enolase (EnO) |
| | pyruvate kinase (PyK) |
| TCA cycle | citrate synthase (gltA) |
| | aconitate hydratase (AcoH) |
| | 2-oxoglutarate dehydrogenase E1 component (sucA) |
| | dihydrolipoamide succinyltransferase component (E2 |
| | dihydrolipoamide dehydrogenase (lpdA) |
| | succinyl-CoA ligase [ADP-forming] alpha chain (sucD) |
| | succinyl-CoA ligase [ADP-forming] beta chain (sucS) |
| | succinate dehydrogenase iron-sulfur protein (sdhB) |
| | succinate dehydrogenase flavoprotein subunit (sdhA |
| | fumarate hydratase (Fum) |
| | malate dehydrogenase (MD) |
| | isocitrate dehydrogenase [NAD] (icd) |
| Organic carbon transporters | fructose ABC transporter ATP-binding component Fr |
| | fructose ABC transporter substrate-binding compone |
| | fructose ABC transporter permease component FrcC |
| | PTS system, fructose-specific IIA component (FruIIA) |
| | fructose-specific phosphocarrier protein HPr (Fpr) |
| | PTS system, fructose-specific IIB component (FruIIB) |
| | PTS system, fructose-specific IIC component (FruIIC) |
| | GtsA- glucose/mannose transport |
| | GtsB- glucose/mannose transport |
| | GtsC- glucose/mannose transport |
| | MalK- glucose/mannose transport |

| | |
|---|---|
| | FliY- cystine transport<br>YeS- cystine transport<br>YeC- cystine transport |
| | Ribose/xylose/arabinose/galactoside ABC-type transp<br>monosaccharide ABC transporter ATP-binding protei<br>monosaccharide ABC transporter substrate-binding p |
| | polar amino acid (glutamate/aspartate) transport sys<br>polar amino acid transport system permease protein<br>polar amino acid transport system ATP-binding prote |
| | NitT/TauT family transport system substrate-binding<br>NitT/TauT family transport system ATP-binding prote<br>NitT/TauT family transport system permease protein |
| | putrescine transport system substrate-binding protei<br>putrescine transport system permease protein PotI<br>putrescine transport system permease protein PotH<br>putrescine transport system ATP-binding protein Pot |
| | branched-chain amino acid transport ATP-binding pr<br>branched-chain amino acid transport ATP-binding pr<br>branched-chain amino acid transport system permea<br>high-affinity branched-chain amino acid transport sys<br>high-affinity leucine-specific transport system, peripl |
| | various polyols ABC transporter, periplasmic substrat<br>various polyols ABC transporter, permease compone<br>various polyols ABC transporter, permease compone<br>various polyols ABC transporter, ATP-binding compor |
| | alpha-galactosidase<br>beta-galactosidase |
| Heavy metal resistance | cobalt-zinc-cadmium efflux system protein<br>cobalt-zinc-cadmium resistance protein CzcA<br>cobalt-zinc-cadmium resistance protein CzcD<br>heavy metal RND efflux outer membrane protein, Cz<br>probable Co/Zn/Cd efflux system membrane fusion p<br>cation efflux system protein CusA<br>DNA-binding heavy metal response regulator (CzrR/C<br>heavy metal sensor histidine kinase (HMHK) |
| | magnesium and cobalt transport protein CorA<br>magnesium transport ATPase protein C (mgtC)<br>magnesium transport ATPase P-type (mgtA)<br>Mg/Co/Ni transporter (mgtE)<br>magnesium and cobalt efflux protein (corC) |
| | mercuric resistance operon regulatory protein MerR<br>mercuric transport protein MerT<br>periplasmic mercury(+2) binding protein MerP |

| | |
|---|---|
| | mercuric transport protein MerC |
| | mercuric ion reductase MerA |
| | mercuric ion reductase MIR |
| | arsenical resistance operon repressor arsR |
| | arsenical resistance operon trans-acting repressor ar |
| | arsenical pump-driving ATPase arsA |
| | arsenic efflux pump protein arsB |
| | arsenate reductase arsC |
| | arsenical-resistance protein ACR3 (arsenite transport |
| | arsenic resistance protein arsH |
| | arsenite oxidase subunit AioA |
| | arsenite oxidase subunit AioB |
| | PstA- phosphate/arsenate transport |
| | PstB- phosphate/arsenate transport |
| | PstC- phosphate/arsenate transport |
| | PstS- phosphate/arsenate transport |
| | membrane fusion component of tripartite multidrug |
| | inner membrane component of tripartite multidrug r |
| | outer membrane component of tripartite multidrug r |
| | chromate resistance protein ChrB |
| | chromate transport protein ChrA |
| | urea transport subunit UrtA |
| | urea transport subunit UrtB |
| | urea transport subunit UrtC |
| | urea transport subunit UrtD |
| | urea transport subunit UrtE |
| | urease UreC |
| | urease subunit UreA |
| | urease subunit UreB |
| | urease accessory protein UreE |
| | urease accessory protein UreF |
| | urease accessory protein UreG |

| 3As | K12 | FB-6 | FB-Cd | S10 | b6 | intermedia T |
|---|---|---|---|---|---|---|
| THI_16S_1/N | Tint_R0045 | D466DRAFT_0316, | CD04DRAFT_ | Ga0061069_1 | NR_115341.1 | Ga0198653_1 |
| THI_23S_1 | Tint_R0042 | D466DRAFT_0319, | CD04DRAFT_ | Ga0061069_1 | 1186 | Ga0198653_1 |
| THI_5S_1 | Tint_R0041 | D466DRAFT_0320, | CD04DRAFT_ | Ga0061069_1 | 1185 | Ga0198653_1 |
| THI_0766/CA | Tint_0591/AL | D466DRAFT_0260/ | CD04DRAFT_ | Ga0061069_1 | SBP86925.1 | x |
| x | x | D466DRAFT_2462 ( | CD04DRAFT_ | x | x | x |
| THI_3455, TH | Tint_2893, Ti | D466DRAFT_2957, | CD04DRAFT_ | Ga0061069_1 | SBP86710.1 | Ga0198653_1 |
| THI_2530 | Tint_2193 | D466DRAFT_0456 | CD04DRAFT_ | Ga0061069_1 | SBP86392.1 | WP_0794161 |
| THI_2531 | Tint_2194 | D466DRAFT_0457 | CD04DRAFT_ | Ga0061069_1 | SBP86391.1 | WP_0794203 |
| THI_2529 | Tint_2192 | D466DRAFT_0455 | CD04DRAFT_ | Ga0061069_1 | SBP86393.1 | WP_0794161 |
| THI_1354, TH | Tint_1070, Ti | D466DRAFT_1987, | CD04DRAFT_ | Ga0061069_1 | SBP89836.1, | Ga0198653_1 |
| THI_2995, TH | Tint_2593, Ti | D466DRAFT_1420, | CD04DRAFT_ | Ga0061069_1 | SBP87694.1, | Ga0198653_1 |
| THI_2995 (su | Tint_2593 (su | D466DRAFT_1420 ( | CD04DRAFT_ | Ga0061069_1 | SBP87694.1 ( | WP_0794184 |
| x | x | D466DRAFT_2466 | CD04DRAFT_ | x | x | x |
| x | x | D466DRAFT_2467 | CD04DRAFT_ | x | x | x |
| x | x | D466DRAFT_2468 | CD04DRAFT_ | x | x | x |
| x | x | D466DRAFT_2469 | CD04DRAFT_ | x | x | x |
| x | x | D466DRAFT_2470 | CD04DRAFT_ | x | x | x |
| x | x | D466DRAFT_2471 | CD04DRAFT_ | x | x | x |
| x | x | D466DRAFT_2472 | CD04DRAFT_ | x | x | x |
| x | x | D466DRAFT_2473 | CD04DRAFT_ | x | x | x |
| x | x | D466DRAFT_2474 | CD04DRAFT_ | x | x | x |
| THI_0842 | Tint_0655 | D466DRAFT_2955 | CD04DRAFT_ | Ga0061069_1 | SBP87370.1 | Ga0198653_1 |
| THI_0841 | Tint_0654 | D466DRAFT_2956 | CD04DRAFT_ | Ga0061069_1 | SBP87369.1 | Ga0198653_1 |
| THI_2691 | Tint_2316 | D466DRAFT_0580 | CD04DRAFT_ | Ga0061069_1 | SBP88178.1 | Ga0198653_1 |
| THI_3030 | Tint_2628 | D466DRAFT_3257 | CD04DRAFT_ | Ga0061069_1 | SBP87152.1 | Ga0198653_1 |
| THI_2935, TH | Tint_2536, Ti | D466DRAFT_0816 | CD04DRAFT_ | Ga0061069_1 | SBP88694.1, | Ga0198653_1 |
| THI_0330 | Tint_0292 | D466DRAFT_3180 | CD04DRAFT_ | Ga0061069_1 | SBP87192.1 | Ga0198653_1 |
| THI_2268 | Tint_1836 | D466DRAFT_2332 | CD04DRAFT_ | Ga0061069_1 | SBP89975.1 | Ga0198653_1 |
| THI_2266, TH | Tint_1835 | D466DRAFT_2330, | CD04DRAFT_ | Ga0061069_1 | SBP89974.1, | Ga0198653_1 |
| THI_3745 | Tint_3131 | D466DRAFT_0277 | CD04DRAFT_ | Ga0061069_1 | SBP86899.1 | Ga0198653_1 |
| THI_2743 | Tint_2355 | D466DRAFT_1247 | CD04DRAFT_ | Ga0061069_1 | SBP88775.1 | Ga0198653_1 |
| THI_3202, TH | Tint_2671, Ti | D466DRAFT_1394, | CD04DRAFT_ | Ga0061069_1 | SBP87068.1, | Ga0198653_1 |
| THI_0331 | Tint_0293 | D466DRAFT_3179 | CD04DRAFT_ | Ga0061069_1 | SBP87191.1 | Ga0198653_1 |
| THI_2090 | Tint_1670 | D466DRAFT_1141 | CD04DRAFT_ | Ga0061069_1 | SBP89204.1 | Ga0198653_1 |
| THI_2988 | Tint_2586 | D466DRAFT_3774 | CD04DRAFT_ | Ga0061069_1 | SBP87701.1 | Ga0198653_1 |
| THI_2989 | Tint_2587 | D466DRAFT_3775 | CD04DRAFT_ | Ga0061069_1 | SBP87700.1 | Ga0198653_1 |
| THI_2639 | Tint_2268 | D466DRAFT_2296 | CD04DRAFT_ | Ga0061069_1 | SBP89934.1 | Ga0198653_1 |
| THI_2638 | Tint_2267 | D466DRAFT_2295 | CD04DRAFT_ | Ga0061069_1 | SBP89933.1 | Ga0198653_1 |
| THI_2637 | Tint_2266 | D466DRAFT_2294 | CD04DRAFT_ | Ga0061069_1 | SBP89932.1 | Ga0198653_1 |
| THI_2636 | Tint_2265 | D466DRAFT_2293 | CD04DRAFT_ | Ga0061069_1 | SBP89931.1 | Ga0198653_1 |
| THI_2635 | Tint_2264 | D466DRAFT_2292 | CD04DRAFT_ | Ga0061069_1 | SBP89930.1 | Ga0198653_1 |
| THI_2634 | Tint_2263 | D466DRAFT_2291 | CD04DRAFT_ | Ga0061069_1 | SBP89929.1 | Ga0198653_1 |

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|---|---|---|---|---|---|---|
| THI_2633 | Tint_2262 | D466DRAFT_2290 | CD04DRAFT_ | Ga0061069_1 | SBP89928.1 | Ga0198653_1 |
| THI_2632 | Tint_2261 | D466DRAFT_2289 | CD04DRAFT_ | Ga0061069_1 | SBP89927.1 | Ga0198653_1 |
| THI_2631 | Tint_2260 | D466DRAFT_2288 | CD04DRAFT_ | Ga0061069_1 | SBP89926.1 | Ga0198653_1 |
| THI_2630 | Tint_2259 | D466DRAFT_2287 | CD04DRAFT_ | Ga0061069_1 | SBP89925.1 | Ga0198653_1 |
| THI_2629 | Tint_2258 | D466DRAFT_2286 | CD04DRAFT_ | Ga0061069_1 | SBP89924.1 | Ga0198653_1 |
| THI_2628 | Tint_2257 | D466DRAFT_ 2285 | CDO4DRAFT_ | Ga0061069_1 | SBP89923.1 | Ga0198653_1 |
| THI_2627 | Tint_2256 | D466DRAFT_2284 | CD04DRAFT_ | Ga0061069_1 | SBP89922.1 | Ga0198653_1 |
| THI_2626 | Tint_2255 | D466DRAFT_2283 | CD04DRAFT_ | Ga0061069_1 | SBP89921.1 | Ga0198653_1 |
| THI_2715 | Tint_2340 | D466DRAFT_0559 | CD04DRAFT_ | Ga0061069_1 | SBP88157.1 | Ga0198653_1 |
| THI_2712 | Tint_2337 | D466DRAFT_0562, | CD04DRAFT_ | Ga0061069_1 | SBP88160.1 | Ga0198653_1 |
| THI_2713 | Tint_2338 | D466DRAFT_0561 | CD04DRAFT_ | Ga0061069_1 | SBP88159.1 | Ga0198653_1 |
| THI_2714 | Tint_2339 | D466DRAFT_0560 | CD04DRAFT_ | Ga0061069_1 | SBP88158.1 | Ga0198653_1 |
| THI_3306 | Tint_2760 | D466DRAFT_2115 | CD04DRAFT_ | Ga0061069_1 | SBP87196.1 | Ga0198653_1 |
| THI_3308 | Tint_2758 | D466DRAFT_2113, | CD04DRAFT_ | Ga0061069_1 | SBP87198.1 | Ga0198653_1 |
| THI_3307 | Tint_2759 | D466DRAFT_2114, | CD04DRAFT_ | Ga0061069_1 | SBP87197.1 | Ga0198653_1 |
| THI_3304 | Tint_2756 | D466DRAFT_2112, | CD04DRAFT_ | Ga0061069_1 | SBP87200.1 | Ga0198653_1 |
| THI_3302 | Tint_2754 | D466DRAFT_2119, | CD04DRAFT_ | Ga0061069_1 | SBP87202.1 | Ga0198653_1 |
| THI_3303 | Tint_2755 | D466DRAFT_2111, | CD04DRAFT_ | Ga0061069_1 | SBP87201.1 | Ga0198653_1 |
| THI_3305 | Tint_2757 | D466DRAFT_3187 | CD04DRAFT_ | Ga0061069_1 | SBP87199.1 | Ga0198653_1 |
| THI_3301 | Tint_2753 | D466DRAFT_2118, | CD04DRAFT_ | Ga0061069_1 | SBP87203.1 | Ga0198653_1 |
| THI_0648, TH | Tint_0525, Ti | D466DRAFT_3625, | WP_0314064 | WP_0554500 | SBP87842.1 | WP_0794203 |
| THI_0572 | Tint_0486 | D466DRAFT_0830 | CD04DRAFT_ | Ga0061069_1 | SBP88716.1 | Ga0198653_1 |
| x | x | D466DRAFT_1762, | CD04DRAFT_ | x | SBP87645.1 | x |
| THI_2091 | Tint_1671 | D466DRAFT_1142 | CD04DRAFT_ | Ga0061069_1 | SBP89205.1 | Ga0198653_1 |
| THI_2807 | Tint_2416 | D466DRAFT_0739 | CD04DRAFT_ | Ga0061069_1 | SBP88619.1 | Ga0198653_1 |
| THI_1760 | Tint_1395 | D466DRAFT_1157 | CD04DRAFT_ | Ga0061069_1 | SBP89224.1 | Ga0198653_1 |
| THI_1330 | Tint_1047 | D466DRAFT_1698 | CD04DRAFT_ | Ga0061069_1 | SBP89609.1 | Ga0198653_1 |
| CAZ88732.1 | ADG31027.1 | D466DRAFT_1749, | CD04DRAFT_ | Ga0061069_11436, Ga006 | | Ga0198653_1 |
| THI_0055, TH | Tint_0051, Ti | D466DRAFT_0527 | CD04DRAFT_ | Ga0061069_1 | SBP88417.1, | Ga0198653_1 |
| THI_3293 | Tint_2745 | D466DRAFT_3201 | CD04DRAFT_ | Ga0061069_1 | SBP87211.1 | Ga0198653_1 |
| x | x | D466DRAFT_1292, | x | x | x | x |
| x | x | D466DRAFT_1293, | x | x | x | x |
| x | x | D466DRAFT_1294, | x | x | x | x |
| x | x | D466DRAFT_1295, | x | x | x | x |
| x | x | D466DRAFT_1300, | x | x | x | x |
| x | x | D466DRAFT_0388, | x | x | x | x |
| x | x | D466DRAFT_3231 | x | x | x | x |
| x | x | D466DRAFT_1302, | x | x | x | x |
| x | x | D466DRAFT_1303, | x | x | x | x |
| x | x | D466DRAFT_1305, | x | x | x | x |
| x | x | D466DRAFT_1306, | x | x | x | x |
| x | x | D466DRAFT_1307, | x | x | x | x |
| x | x | D466DRAFT_3234 | x | x | x | x |

| | | | | | | |
|---|---|---|---|---|---|---|
| THI_0372 | Tint_0337 | D466DRAFT_0533 | CD04DRAFT_ | Ga0061069_1 | WP_0941607 | Ga0198653_1 |
| THI_2376 | Tint_0644 | D466DRAFT_0701 | CD04DRAFT_ | Ga0061069_1 | SBP87442.1 | Ga0198653_1 |
| THI_0419 | Tint_0382 | D466DRAFT_3638 | CD04DRAFT_ | Ga0061069_1 | SBP87330.1 | Ga0198653_1 |
| THI_0418 | Tint_0381 | D466DRAFT_3639 | CD04DRAFT_ | Ga0061069_1 | SBP87758.1 | Ga0198653_1 |
| THI_0417 | Tint_0380 | D466DRAFT_3640 | CD04DRAFT_ | Ga0061069_1 | SBP87757.1 | Ga0198653_1 |
| THI_0854 | Tint_0665 | D466DRAFT_2946 | CD04DRAFT_ | Ga0061069_1 | SBP87380.1 | Ga0198653_1 |
| THI_0853 | Tint_0664 | D466DRAFT_2947 | CD04DRAFT_ | Ga0061069_1 | SBP87379.1 | Ga0198653_1 |
| THI_0852 | Tint_0663 | D466DRAFT_2948 | CD04DRAFT_ | Ga0061069_1 | x | Ga0198653_1 |
| THI_0851 | Tint_0662 | D466DRAFT_2949 | CD04DRAFT_ | Ga0061069_1 | x | Ga0198653_1 |
| THI_0850 | Tint_0661 | D466DRAFT_2950 | CD04DRAFT_ | Ga0061069_1 | SBP87376.1 | Ga0198653_1 |
| THI_3755 | Tint_3141 | D466DRAFT_2274 | x | Ga0061069_1 | SBP89917.1 | Ga0198653_1 |
| THI_1329 | Tint_1046 (ne | D466DRAFT_1990 | CD04DRAFT_ | Ga0061069_1 | x | Ga0198653_1 |
| THI_2999 | Tint_2597 | D466DRAFT_3785 | x | Ga0061069_1 | SBP87690.1 | Ga0198653_1 |
| THI_0104 | Tint_0086 | D466DRAFT_3281 | x | Ga0061069_1 | SBP87240.1 | Ga0198653_1 |
| THI_1042 | Tint_0799 | D466DRAFT_0398 | CD04DRAFT_ | Ga0061069_1 | SBP86457.1 | Ga0198653_1 |
| THI_2376, TH | Tint_0572 | D466DRAFT_0700 | CD04DRAFT_ | Ga0061069_1 | SBP86635.1 | WP_0793203 |
| THI_3363 | ADG32154.1 | D466DRAFT_3496 | x | CUA95376.1 | SBP87095.1 | WP_0794172 |
| THI_3598/CA | x | D466DRAFT_3946/ | x | Ga0061069_1 | SBP87937.1, | Ga0198653_1 |
| THI_3597/CA | x | D466DRAFT_3945/ | x | Ga0061069_1 | SBP87936.1 | Ga0198653_1 |
| x | x | x | CD04DRAFT_ | x | SBP87880.1 | x |
| x | x | x | CD04DRAFT_ | x | SBP87881.1 | x |
| THI_2871 (alp | Tint_2477 (al | D466DRAFT_0904 ( | CD04DRAFT_ | Ga0061069_1 | SBP88671.1 ( | x |
| THI_2673 (So | Tint_2294 (Sc | D466DRAFT_0596 ( | CD04DRAFT_ | Ga0061069_1 | SBP88194.1 ( | WP_0794189 |
| THI_2411, TH | Tint_0632, Ti | D466DRAFT_1335 | CD04DRAFT_ | Ga0061069_1 | SBP88321.1 | WP_0794156 |
| Otr (CAZ8964 | Otr (ADG319 | x | TtrA (WP_03 | Otr (CUA932 | TtrA (SBP887 | Otr (WP_0794 |
| CAZ86913.1 | ADG29550.1 | WP_018912646.1 | WP_0314099 | CUA93887.1 | SBP87272.1 | WP_0794180 |
| RbcL (CAZ868 | RbcL (ADG29 | RbcL (WP_0189128 | RbcL (WP_03 | RbcL (CUA93 | RbcL (SBP893 | RbcL (WP_079 |
| CAZ86916.1 | ADG29553.1 | WP_018912643.1 | WP_0314099 | CUA93881.1 | SBP87275.1 | WP_0794180 |
| CAZ86912.1, | ADG29549.1, | WP_018912647.1, | WP_0314099 | CUA93889.1, | SBP87271.1, | WP_0794180 |
| CAZ86914.1 | ADG29551.1 | WP_018912645.1 | WP_0518494 | CUA93885.1 | SBP87273.1, | WP_0794180 |
| CAZ90311.1 | ADG32449.1 | WP_018914242.1 | WP_0314096 | CUA99995.1 | SBP86881.1 | WP_0794175 |
| CAZ86918.1 | ADG29555.1 | WP_018912641.1 | WP_0314099 | CUA93877.1 | SBP87277.1 | WP_0794180 |
| CAZ86917.1 | ADG29554.1 | WP_018912642.1 | WP_0314099 | CUA93879.1 | SBP87276.1 | WP_0794180 |
| CAZ86773.1 | ADG29423.1 | WP_018914746.1 | WP_0314056 | CUA94066.1 | x | WP_0794178 |
| CAZ88079.1 | ADG30490.1 | WP_026285371.1 | WP_0381675 | CUA99834.1 | x | WP_0794178 |
| CAZ88078.1 | ADG30489.1 | WP_018914745.1 | WP_0314056 | CUA99831.1 | x | WP_0794153 |
| CAZ86774.1 | ADG29424.1 | WP_018914743.1 | WP_0314056 | CUA94063.1 | x | WP_0794178 |
| CAZ86775.1 | ADG29425.1 | WP_018914742.1 | WP_0314056 | CUA94060.1 | x | WP_0794178 |
| CAZ86916.1 | ADG29553.1 | WP_018912643.1 | WP_0314099 | CUA93881.1 | SBP87275.1 | WP_0794180 |
| CAZ86917.1 | ADG29554.1 | WP_018912642.1 | WP_0314099 | CUA93879.1 | SBP87276.1 | WP_0794180 |
| CAZ87019.1, | ADG29636.1, | WP_018915075.1, | WP_0314070 | CUA93645.1, | SBP87388.1 ( | WP_0794205 |
| CAZ89273.1 | ADG31634.1 | WP_018911730.1 | WP_0314060 | CUA97974.1 | SBP88795.1 ( | WP_0794189 |
| CAZ87748.1 | ADG30202.1 | WP_018914548.1 | WP_0314087 | CUA94760.1 | SBP86449.1 | WP_0794162 |

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|---|---|---|---|---|---|---|
| CAZ88079.1 | ADG30490.1 | WP_026285371.1 | WP_0381675 | CUA99834.1 | SBP90135.1 | WP_0794178 |
| x | x | x | WP_0314097 | x | SBP87771.1, | x |
| CAZ89302.1 | ADG31662.1 | WP_018914443.1 | WP_0314083 | CUA97896.1 | SBP88181.1 | WP_0794188 |
| CAZ90311.1 | ADG32449.1 | WP_018914242.1 | WP_0314096 | CUA99995.1 | SBP86881.1 | WP_0794175 |
| CAZ86914.1 | ADG29551.1 | WP_018912645.1 | WP_0518494 | CUA93885.1 | SBP87273.1, | WP_0794180 |
| CAZ86909.1 | ADG29546.1 | WP_018912650.1 | WP_0314097 | CUA93895.1 | SBP90133.1, | WP_0794180 |
| CAZ86916.1 | ADG29553.1 | WP_018912643.1 | WP_0314099 | CUA93881.1 | SBP87275.1 | WP_0794180 |
| CAZ86917.1 | ADG29554.1 | WP_018912642.1 | WP_0314099 | CUA93879.1 | SBP87276.1 | WP_0794180 |
| CAZ87019.1, | ADG29636.1, | WP_018915075.1, | WP_0314070 | CUA93645.1, | SBP87388.1 ( | WP_0794205 |
| CAZ89273.1 | ADG31634.1 | WP_018911730.1 | WP_0314060 | CUA97974.1 | SBP88795.1 ( | WP_0794189 |
| CAZ87748.1 | ADG30202.1 | WP_018914548.1 | WP_0314087 | CUA94760.1 | SBP86449.1 | WP_0794162 |
| CAZ86773.1 | ADG29423.1 | WP_018914746.1 | WP_0314056 | CUA94066.1 | x | WP_0794178 |
| THI_1383 | Tint_1091 | D466DRAFT_2107 | CD04DRAFT_ | Ga0061069_1 | SBP88876.1 | Ga0198653_1 |
| CAZ87825.1, | ADG30272.1, | WP_018912991.1 | WP_0314039 | CUA98128.1 ( | x | WP_0794160 |
| CAZ86918.1 | ADG29555.1 | WP_018912641.1 | WP_0314099 | CUA93877.1 | SBP87277.1 | WP_0794180 |
| CAZ86916.1 | ADG29553.1 | WP_018912643.1 | WP_0314099 | CUA93881.1 | SBP87275.1 | WP_0794180 |
| CAZ86917.1 | ADG29554.1 | WP_018912642.1 | WP_0314099 | CUA93879.1 | SBP87276.1 | WP_0794180 |
| CAZ87019.1, | ADG29636.1, | WP_018915075.1, | WP_0314070 | CUA93645.1, | SBP87388.1 ( | WP_0794205 |
| CAZ89273.1 | ADG31634.1 | WP_018911730.1 | WP_0314060 | CUA97974.1 | SBP88795.1 ( | WP_0794189 |
| CAZ87748.1 | ADG30202.1 | WP_018914548.1 | WP_0314087 | CUA94760.1 | SBP86449.1 | WP_0794162 |
| CAZ89323.1 | ADG31684.1 | WP_018914462.1 | WP_0314083 | CUA97838.1 | SBP88162.1 | WP_0794188 |
| CAZ89335.1 | ADG31696.1 | WP_018914471.1 | WP_0314083 | CUA97806.1 | SBP88150.1 | WP_0794188 |
| CAZ88347.1 | ADG30731.1 | WP_018914580.1 | WP_0314082 | CUA96232.1 | SBP88201.1 | WP_0794199 |
| CAZ88348.1 | ADG30732.1 | WP_018914581.1 | WP_0314082 | CUA96235.1 | SBP88202.1 | WP_0794199 |
| CAZ88349.1 | ADG30733.1 | WP_018914582.1 | WP_0314082 | CUA96238.1 | SBP88203.1 | WP_0794199 |
| CAZ87744.1 | ADG30198.1 | WP_018914544.1 | WP_0314087 | CUA94749.1 | SBP87905.1, | WP_0794162 |
| CAZ87743.1 | ADG30197.1 | WP_018914543.1 | WP_0314087 | CUA94747.1 | SBP87906.1, | WP_0794162 |
| THI_2712 | Tint_2337 | D466DRAFT_0562, | CD04DRAFT_ | Ga0061069_1 | SBP88160.1 | Ga0198653_1 |
| THI_2713 | Tint_2338 | D466DRAFT_0561 | CD04DRAFT_ | Ga0061069_1 | SBP88159.1 | Ga0198653_1 |
| THI_2117, TH | Tint_1698, Ti | D466DRAFT_0649, | CD04DRAFT_ | Ga0061069_1 | SBP87349.1, | Ga0198653_1 |
| THI_2717 | Tint_2342 | D466DRAFT_0557 | CD04DRAFT_ | Ga0061069_1 | SBP88155.1, | Ga0198653_1 |
| CAZ88430.1, | ADG30780.1, | WP_018913532.1, | WP_0314054 | CUA96322.1, | SBP88121.1, | WP_0794200 |
| x | x | D466DRAFT_2140 | x | x | x | x |
| x | x | D466DRAFT_2142 | x | x | x | x |
| x | x | D466DRAFT_2141 | x | x | x | x |
| THI_2510 | Tint_2174 | D466DRAFT_0408 | CD04DRAFT_ | CUA94777.1 | SBP86443.1 | Ga0198653_1 |
| THI_2510 | Tint_2174 | D466DRAFT_0408 | CD04DRAFT_ | CUA94777.1 | SBP86443.1 | Ga0198653_1 |
| CAZ89137.1 | ADG31527.1 | x | CD04DRAFT_ | x | x | WP_0794160 |
| CAZ89137.1 | ADG31527.1 | x | CD04DRAFT_ | x | x | WP_0794160 |
| x | x | D466DRAFT_2100 | x | x | x | Ga0198653_1 |
| x | x | D466DRAFT_2099 | x | x | x | Ga0198653_1 |
| x | x | D466DRAFT_2098 | x | x | x | Ga0198653_1 |
| x | x | D466DRAFT_2097 | x | x | x | Ga0198653_1 |

| | | | | | | |
|---|---|---|---|---|---|---|
| x | x | D466DRAFT_2636 | x | x | x | x |
| x | x | D466DRAFT_2637 | x | x | x | x |
| x | x | D466DRAFT_2638 | x | x | x | x |
| x | x | D466DRAFT_3903 | x | x | x | x |
| CAZ86950.1 | ADG30242.1 | D466DRAFT_3904 | CD04DRAFT_ | CUA93798.1 | SBP86838.1 | WP_0794181 |
| x | x | D466DRAFT_3905 | x | x | x | x |
| x | x | x | CD04DRAFT_ | x | x | x |
| x | x | x | CD04DRAFT_ | x | x | x |
| THI_1061 | Tint_0818 | D466DRAFT_0915 | CD04DRAFT_ | Ga0061069_1 | SBP87728.1 | Ga0198653_1 |
| x | x | D466DRAFT_1034 | x | x | x | x |
| CAZ90276.1 | x | D466DRAFT_1035 | CD04DRAFT_ | CUA99514.1 | SBP88266.1 | WP_0794177 |
| CAZ90277.1 | x | D466DRAFT_1033 | CD04DRAFT_ | CUA99517.1 | SBP88265.1 | WP_0794177 |
| THI_0202 | Tint_0180 | D466DRAFT_0010 | CD04DRAFT_ | Ga0061069_1 | SBP86831.1 | Ga0198653_1 |
| THI_0205 | Tint_0183 | D466DRAFT_0007 | CD04DRAFT_ | Ga0061069_1 | SBP86828.1 | Ga0198653_1 |
| THI_0204 | Tint_0182 | D466DRAFT_0008 | CD04DRAFT_ | Ga0061069_1 | SBP86829.1 | Ga0198653_1 |
| THI_0203 | Tint_0181 | D466DRAFT_0009 | CD04DRAFT_ | Ga0061069_1 | SBP86830.1 | Ga0198653_1 |
| THI_0197 | Tint_0175 | D466DRAFT_0014 | CD04DRAFT_ | Ga0061069_1 | SBP86837.1 | Ga0198653_1 |
| THI_0196 | Tint_0174 | D466DRAFT_0015 | CD04DRAFT_ | Ga0061069_1 | SBP86838.1 | Ga0198653_1 |
| THI_0195 | Tint_0173 | D466DRAFT_0016 | CD04DRAFT_ | Ga0061069_1 | SBP86840.1 | Ga0198653_1 |
| THI_0194 | Tint_0172 | D466DRAFT_0017 | CD04DRAFT_ | Ga0061069_1 | SBP86841.1 | Ga0198653_1 |
| THI_0193 | Tint_0171 | D466DRAFT_0018 | CD04DRAFT_ | Ga0061069_1 | SBP86842.1 | Ga0198653_1 |
| x | x | D466DRAFT_2124/ | x | x | x | x |
| x | x | D466DRAFT_2125/ | x | x | x | x |
| x | x | D466DRAFT_2126/ | x | x | x | x |
| x | x | D466DRAFT_2127/ | CD04DRAFT_ | x | x | x |
| x | x | D466DRAFT_2151/ | x | x | x | x |
| x | x | D466DRAFT_2147/ | x | x | x | x |
| THI_0016, TH | Tint_3042, Ti | D466DRAFT_2976, | CD04DRAFT_ | Ga0061069_101518, Ga00 | | x |
| THI_0859, TH | Tint_0671, Ti | D466DRAFT_1744, | CD04DRAFT_ | Ga0061069_1 | SBP87427.1 | present in RAS |
| CAZ89815.1, | ADG32017.1, | WP_018913004.1, | WP_0314060 | CUA93344.1, | SBP87112.1, | WP_0794183 |
| CAZ87563.1, | ADG30069.1, | WP_018913048.1, | WP_0818579 | CUA94389.1, | SBP87426.1, | WP_0794175 |
| CAZ88668.1, | ADG30023.1, | WP_026284738.1, | WP_0818578 | CUA94273.1, | SBP88233.1, | WP_0794165 |
| CAZ87510.1, | ADG30022.1, | WP_018911781.1, | WP_0818578 | CUA94271.1, | SBP88234.1, | WP_0794165 |
| CAZ88278.1, | ADG30665.1 | WP_018912567.1, | WP_0314043 | CUB00801.1 | SBP86735.1, | present in RAS |
| CAZ89695.1, | ADG30666.1 | WP_038165248.1, | WP_0518488 | WP_0554518 | SBP89143.1, | WP_0794175 |
| THI_2566, TH | Tint_2221, Ti | D466DRAFT_2654 | WP_0314099 | Ga0061069_1 | SBP88546.1 | WP_0794190 |
| x | x | WP_018914335.1 | WP_0314038 | x | x | x |
| CAZ87271.1 ( | ADG29859.1 | x | WP_0518488 | x | SBP89339.1 | x |
| x | x | x | x | x | x | x |
| CAZ88767.1 | ADG31064.1 | WP_018915238.1 | WP_0314042 | CUB00223.1 | SBP89675.1 | WP_0794196 |
| CAZ89678.1, | ADG30978.1 | WP_026284883.1 | WP_0314043 | x | SBP89172.1, | x |
| CAZ88470.1, | ADG30979.1 | x | x | x | SBP86688.1, | x |
| CAZ88469.1, | ADG30980.1 | x | x | x | SBP86687.1, | x |

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|---|---|---|---|---|---|---|
| CAZ89675.1 | x | x | x | x | SBP89175.1 | x |
| CAZ88468.1, | ADG30981.1 | WP_081629810.1 | WP_0818577 | x | SBP86686.1, | x |
| CAZ88468.1, | ADG30981.1 | WP_081629810.1 | WP_0818577 | x | SBP89176.1, | x |
| THI_3143/CA | Tint_1824/AL | D466DRAFT_0146/ | CD04DRAFT_ | Ga0061069_1 | SBP89103.1, | Ga0198653_1 |
| THI_3145/CA | x | x | CD04DRAFT_ | x | SBP89101.1, | x |
| CAZ89745.1 | x | x | WP_0314069 | x | SBP89100.1, | x |
| CAZ88902.1, | ADG31196.1 | x | WP_0314080 | CUA99709.1 | SBP86609.1, | WP_0794153 |
| CAZ88901.1 | ADG31195.1 | WP_018915341.1 | WP_0314080 | CUA99711.1 | SBP88885.1 | WP_0794153 |
| x | x | D466DRAFT_0144/ | x | x | SBP88886.1 | x |
| x | Tint_3036/AL | x | x | x | x | x |
| THI_3162/CA | Tint_1304/Ti | x | CD04DRAFT_ | x | APY18929.1/ | Ga0198653_1 |
| THI_3163/CA | Tint_3062/AL | x | CD04DRAFT_ | x | SBP89081.1/ | Ga0198653_1 |
| THI_2141 | Tint_1720 | D466DRAFT_1009 | CD04DRAFT_ | Ga0061069_1 | SBP88864.1 | Ga0198653_1 |
| THI_2139 | Tint_1719 | D466DRAFT_1010 | CD04DRAFT_ | Ga0061069_1 | SBP88865.1 | Ga0198653_1 |
| THI_2142 | Tint_1721 | D466DRAFT_1008 | CD04DRAFT_ | Ga0061069_1 | SBP88863.1 | Ga0198653_1 |
| THI_2144 | Tint_1722 | D466DRAFT_1007 | CD04DRAFT_ | Ga0061069_1 | SBP88862.1 | Ga0198653_1 |
| CAZ87022.1 | ADG29643.1 | WP_018915077.1 | WP_0518491 | CUA93637.1 | SBP87386.1 | WP_0794181 |
| CAZ87021.1 | ADG29641.1 | WP_018915076.1, | WP_0314070 | CUA93640.1 | SBP87387.1 | WP_0794181 |
| CAZ87023.1 | ADG29644.1 | WP_018915078.1 | WP_0818580 | CUA93635.1 | SBP87385.1 | WP_0794181 |
| x | x | WP_018912576.1 | x | x | SBP86539.1 | x |
| CAZ87685.1 | ADG30768.1, | WP_018912575.1 | WP_0314041 | CUA96289.1, | SBP89695.1 | WP_0794199 |
| THI_3582 | x | D466DRAFT_0668/I | CD04DRAFT_ | Ga0061069_1 | SBP87953.1 | Ga0198653_1 |
| THI_3583 | x | D466DRAFT_0226/I | CD04DRAFT_ | Ga0061069_1 | SBP87954.1 | Ga0198653_1 |
| THI_3584 | x | D466DRAFT_0670/I | CD04DRAFT_ | Ga0061069_1 | SBP87955.1 | Ga0198653_1 |
| THI_3585 | x | D466DRAFT_0671/I | CD04DRAFT_ | Ga0061069_1 | SBP87956.1 | Ga0198653_1 |
| THI_3586 | x | D466DRAFT_0672/I | CD04DRAFT_ | Ga0061069_1 | SBP87957.1 | Ga0198653_1 |
| THI_3578/CA | x | D466DRAFT_0665/ | CD04DRAFT_ | Ga0061069_1 | SBP87950.1 | Ga0198653_1 |
| THI_3580/CA | x | D466DRAFT_0667/ | CD04DRAFT_ | Ga0061069_1 | SBP87952.1 | Ga0198653_1 |
| THI_3579/CA | x | D466DRAFT_0666 | CD04DRAFT_ | Ga0061069_1 | SBP87951.1 | Ga0198653_1 |
| THI_3573 | Tint_3018 | D466DRAFT_0664 | CD04DRAFT_ | Ga0061069_1 | SBP87946.1 | Ga0198653_1 |
| THI_3572 | x | D466DRAFT_0663 | CD04DRAFT_ | Ga0061069_1 | SBP87945.1 | Ga0198653_1 |
| THI_3571 | x | D466DRAFT_0662/I | CD04DRAFT_ | Ga0061069_1 | SBP87944.1 | Ga0198653_1 |

| CB1 | CB2 | CB3 | X19 | CB6 | ACO3 | ACO7 |
|---|---|---|---|---|---|---|
| AJ549218.1 | AJ549219.1 | AJ549220.1 | FR874242 | CTRJ0100004 | CTRK010000[illegible] | CTRL0100006 |
| 12814 | | | | | | |
| 12813 | | | | | | |
| CQR27229.1 | CDW96384.1 | CQR44024.1 | SCC91592.1 | CQR32897.1 | CQR29625.1 | CQR29639.1 |
| x | x | x | x | x | x | x |
| CQR37197.1 | CDW93804.1 | CQR43182.1 | SCC95868.1 | CQR38301.1 | CQR40314.1 | CQR40377.1 |
| CQR38606.1 | CDW93010.1 | CQR45339.1 | SCC95557.1 | CQR37091.1 | CQR36753.1 | CQR36754.1 |
| CQR38604.1 | CDW93011.1 | CQR45340.1 | SCC95556.1 | CQR37089.1 | CQR36756.1 | CQR36757.1 |
| CQR38609.1 | CDW93009.1 | CQR45338.1 | SCC95558.1 | CQR37094.1 | CQR36750.1 | CQR36749.1 |
| CQR34667.1, | CDW94964.1 | CQR41746.1, | x | CQR40860.1, | CQR32459.1, | CQR31809.1, |
| CQR36420.1, | CDW94174.1 | CQR43518.1, | SCC92177.1, | CQR26855.1, | CQR38771.1, | CQR38888.1, |
| CQR34665.1 ( | CDW94173.1 | CQR41746.1 ( | SCC94766.1 ( | CQR40858.1 ( | CQR32463.1 ( | CQR31813.1 ( |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| CQR27096.1 | CDW94402.1 | CQR44094.1 | SCC91428.1 | CQR32621.1 | CQR29907.1 | CQR29923.1 |
| CQR27097.1 | CDW94403.1 | CQR44093.1 | SCC91427.1 | CQR32625.1 | CQR29904.1 | CQR29919.1 |
| CQR35371.1 | CDW93128.1 | CQR45482.1 | SCC92539.1 | CQR34075.1 | CQR37602.1 | CQR37756.1 |
| CQR36552.1 | CDW94134.1 | CQR43484.1 | SCC92014.1 | CQR26786.1 | CQR38905.1 | CQR39010.1 |
| CQR36208.1, | CDW94246.1 | CQR43575.1, | SCC92742.1, | CQR26982.1, | CQR38536.1, | CQR38632.1, |
| CQR27624.1 | CDW92785.1 | CQR44336.1 | SCC92063.1 | CQR29773.1 | CQR36995.1 | CQR37111.1 |
| CQR29328.1 | CDW95121.1 | CQR42360.1 | SCC94576.1 | CQR35082.1 | CQR35849.1 | CQR35771.1 |
| CQR29326.1, | CDW95124.1 | CQR42361.1, | SCC94575.1, | CQR35086.1, | CQR35831.1, | CQR35745.1, |
| CQR28787.1 | CDW93491.1 | CQR42879.1 | SCC91621.1 | CQR31293.1 | CQR28057.1 | CQR28060.1 |
| CQR35556.1 | CDW93169.1 | CQR45531.1 | SCC92946.1 | CQR33864.1 | CQR37790.1 | CQR37932.1 |
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| CQR35141.1 | CDW93066.1 | CQR45414.1 | SCC93315.1 | CQR34329.1 | CQR37358.1 | CQR37534.1 |
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| CQR26380.1 | CDW95929.1 | CQR44269.1 | SCC94899.1 | CQR28149.1 | CQR35145.1 | CQR35073.1 |
| CQR35767.1 | CDW93232.1 | CQR45592.1 | SCC92674.1 | CQR33593.1 | x | x |
| CQR33248.1 | CDW95620.1 | CQR42073.1 | SCC94880.1 | CQR39718.1 | CQR33873.1 | CQR33599.1 |
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| CQR26394.1 | CDW95914.1 | CQR44255.1 | SCC93237.1 | CQR28085.1 | CQR35093.1 | CQR35022.1 |
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| x | x | x | x | x | x | x |

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| CQR27542.1 | CDW92724.1 | CQR43801.1 | WP_1124854 | CQR29599.1 | CQR40126.1 | CQR39618.1 |
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| CQR27464.1 | CDW92675.1 | CQR43851.1 | SCC92253.1 | CQR29387.1 | CQR41055.1 | CQR41145.1 |
| CQR27465.1 | CDW92676.1 | CQR43850.1 | SCC92252.1 | CQR29390.1 | CQR41053.1 | CQR41142.1 |
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| CQR27086.1 | CDW94392.1 | CQR44104.1 | WP_1124880 | CQR32580.1 | CQR29951.1 | CQR29960.1 |
| x | x | x | x | x | x | x |
| CQR27088.1 | CDW94394.1 | CQR44102.1 | x | CQR32588.1 | CQR29944.1 | CQR29953.1 |
| CQR27089.1 | CDW94395.1 | CQR44101.1 | WP_1124846 | CQR32591.1 | CQR29940.1 | CQR29949.1 |
| CQR28751.1 | CDW93480.1 | CQR42867.1 | SCC93318.1 | CQR31251.1 | CQR28094.1 | CQR28093.1 |
| x | x | x | x | x | x | x |
| CQR36436.1 | CDW94170.1 | CQR43514.1 | SCC92172.1 | CQR26848.1 | CQR38786.1 | CQR38904.1 |
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| CQR30904.1 | CDW93591.1 | CQR42970.1 | SCC95487.1 | CQR36479.1 | CQR40717.1 | CQR40744.1 |
| x | x | CQR42949.1 | SCC94503.1 | x | x | x |
| x | x | CQR42950.1 | SCC94504.1 | x | x | x |
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| RbcL (CQR27( | RbcL (CDW93 | RbcL (CQR42( | RbcL (SCC936 | RbcL (CQR304 | RbcL (CQR318 | RbcL (CQR321 |
| CQR27932.1 | CDW93284.1 | CQR42710.1 | SCC91506.1 | CQR30383.1 | CQR31988.1 | CQR34035.1 |
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| CQR26726.1 | CDW94628.1 | CQR41440.1 | SCC95622.1 | CQR31852.1 | CQR30730.1 | CQR30752.1 |

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| x | x | x | SCC94601.1 | x | x | x |
| CQR35362.1 | CDW93125.1 | CQR45479.1 | SCC92542.1 | CQR34090.1 | CQR37590.1 | CQR37746.1 |
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| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
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| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |

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|---|---|---|---|---|---|---|
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| CQR27869.1 | CDW92939.1 | CQR42640.1 | SCC95589.1, | CQR30259.1 | CQR32129.1 | CQR34159.1 |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
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| x | x | x | x | x | x | x |
| CQR28948.1 | CDW93527.1 | CQR42973.1 | SCC91151.1 | CQR31489.1 | CQR40894.1 | CQR41016.1 |
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| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
| x | x | x | x | x | x | x |
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| x | x | CQR44568.1 | x | x | x | x |
| CQR29995.1 | x | x | x | CQR28944.1 | CQR28705.1 | CQR28694.1 |
| x | x | x | x | x | x | x |
| CQR26358.1 | CDW95961.1 | CQR41259.1 | SCC94155.1 | CQR28239.1 | CQR35221.1 | CQR35149.1 |
| CQR31278.1, | CDW96159.1 | CQR42485.1, | SCC93884.1, | CQR39601.1 | CQR39105.1, | CQR39203.1, |
| CQR33126.1, | CDW95666.1 | CQR44794.1, | SCC93886.1 | CQR39604.1 | CQR34020.1, | CQR33727.1, |
| CQR33129.1, | CDW95664.1 | CQR42109.1, | SCC93887.1 | CQR39606.1, | CQR34016.1, | CQR33724.1, |

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|---|---|---|---|---|---|---|
| CQR31262.1 | CDW96155.1 | CQR42385.1, | SCC93888.1 | CQR35956.1 | CQR39093.1 | CQR39191.1 |
| CQR33132.1, | CDW95663.1 | CQR42108.1, | SCC93889.1, | CQR39610.1, | CQR34011.1, | CQR33721.1, |
| CQR33132.1, | CDW96154.1 | CQR42479.1, | SCC93152.1, | CQR39610.1, | CQR34011.1, | CQR33721.1, |
| CQR31533.1 | CDW96254.1 | CQR45632.1, | SCC93414.1, | CQR36247.1 | CQR39337.1 | CQR39389.1 |
| CQR31535.1 | CDW96258.1 | CQR45695.1, | SCC93412.1, | CQR36255.1 | CQR39341.1 | CQR39393.1 |
| CQR31536.1 | CDW96259.1 | CQR44610.1, | SCC94813.1, | CQR36258.1 | CQR39343.1 | CQR39395.1 |
| CQR31657.1, | CDW95134.1 | CQR45188.1, | SCC94822.1, | CQR35177.1, | CQR35795.1, | CQR35710.1, |
| CQR31656.1, | CDW95135.1 | CQR45187.1 | SCC94823.1, | CQR35181.1 | CQR35792.1 | CQR35706.1 |
| x | CDW96502.1 | x | SCC95917.1 ( | x | x | x |
| CQR31661.1 | CDW93655.1 | CQR45684.1, | x | CQR36748.1 | x | x |
| CQR31569.1 | CDW96280.1 | CQR44627.1/ | SCC94792.1/ | CQR36328.1 | CQR39380.1 | CQR39418.1 |
| CQR31744.1 | CDW96281.1 | CQR44628.1/ | SCC94791.1/ | CQR36332.1/ | CQR39382.1 | CQR39420.1 |
| CQR26331.1 | CDW95988.1 | CQR41286.1 | SCC93253.1 | CQR28362.1 | CQR35326.1 | CQR35245.1 |
| CQR26332.1 | CDW95987.1 | CQR41285.1 | SCC93254.1 | CQR28357.1 | CQR35322.1 | CQR35240.1 |
| CQR26330.1 | CDW95989.1 | CQR41287.1 | SCC93252.1 | CQR28366.1 | CQR35330.1 | CQR35249.1 |
| CQR26329.1 | CDW95990.1 | CQR41288.1 | SCC93251.1 | CQR28376.1 | CQR35334.1 | CQR35254.1 |
| CQR27740.1 | CDW92866.1 | CQR42562.1 | SCC91444.1 | CQR29975.1 | CQR36813.1 | CQR36927.1 |
| CQR27742.1 | CDW92867.1 | CQR42563.1 | SCC91445.1 | CQR29980.1 | WP_0641350 | CQR36923.1 |
| CQR27738.1 | CDW92865.1 | CQR42561.1 | SCC91443.1 | CQR29971.1 | CQR36816.1 | CQR36932.1 |
| x | x | x | SCC94000.1 | x | x | x |
| CQR33283.1, | CDW95605.1 | CQR42059.1, | SCC94479.1 | CQR39764.1, | CQR33821.1, | CQR33549.1, |
| CQR30870.1 | CDW93606.1 | x | SCC95470.1 | CQR36418.1 | CQR40691.1 | CQR40715.1 |
| CQR30874.1 | CDW93605.1 | x | SCC95469.1 | CQR36423.1 | CQR40693.1 | CQR40716.1 |
| CQR30877.1 | CDW93604.1 | x | SCC95468.1 | CQR36428.1 | CQR40695.1 | CQR40718.1 |
| CQR30880.1 | CDW93603.1 | x | SCC95467.1 | CQR36432.1 | CQR40697.1 | CQR40720.1 |
| CQR30882.1 | CDW93602.1 | x | SCC95466.1 | CQR36435.1 | CQR40699.1 | CQR40722.1 |
| CQR30858.1 | CDW93610.1 | x | SCC95473.1 | CQR36405.1 | CQR40686.1 | CQR40708.1 |
| CQR30867.1 | CDW93608.1 | x | SCC95471.1 | CQR36415.1 | CQR40688.1 | CQR40713.1 |
| CQR30862.1 | CDW93609.1 | x | SCC95472.1 | CQR36411.1 | CQR40687.1 | CQR40710.1 |
| CQR36801.1/ | CDW93614.1 | CQR43117.1 | SCC95477.1 | CQR37865.1/ | CQR40671.1 | CQR40696.1 |
| CQR36803.1/ | CDW93615.1 | CQR43118.1 | SCC95478.1 | CQR37870.1 | CQR40668.1 | CQR40694.1 |
| CQR36805.1/ | CDW93616.1 | CQR43119.1 | SCC95479.1 | CQR37873.1/ | CQR40665.1 | CQR40692.1 |

(cbb3-type monoheme subunit), CQR31821.1 (cbb3-type subunit CcoP), CQR34362.1 (subunit 1),

CQR34359.1 (subunit 2), CQR38892.1 (subunit 2), CQR38888.1 (subunit 1), CQR31809.1 (subunit

t 1), CQR38884.1 (subunit 3)