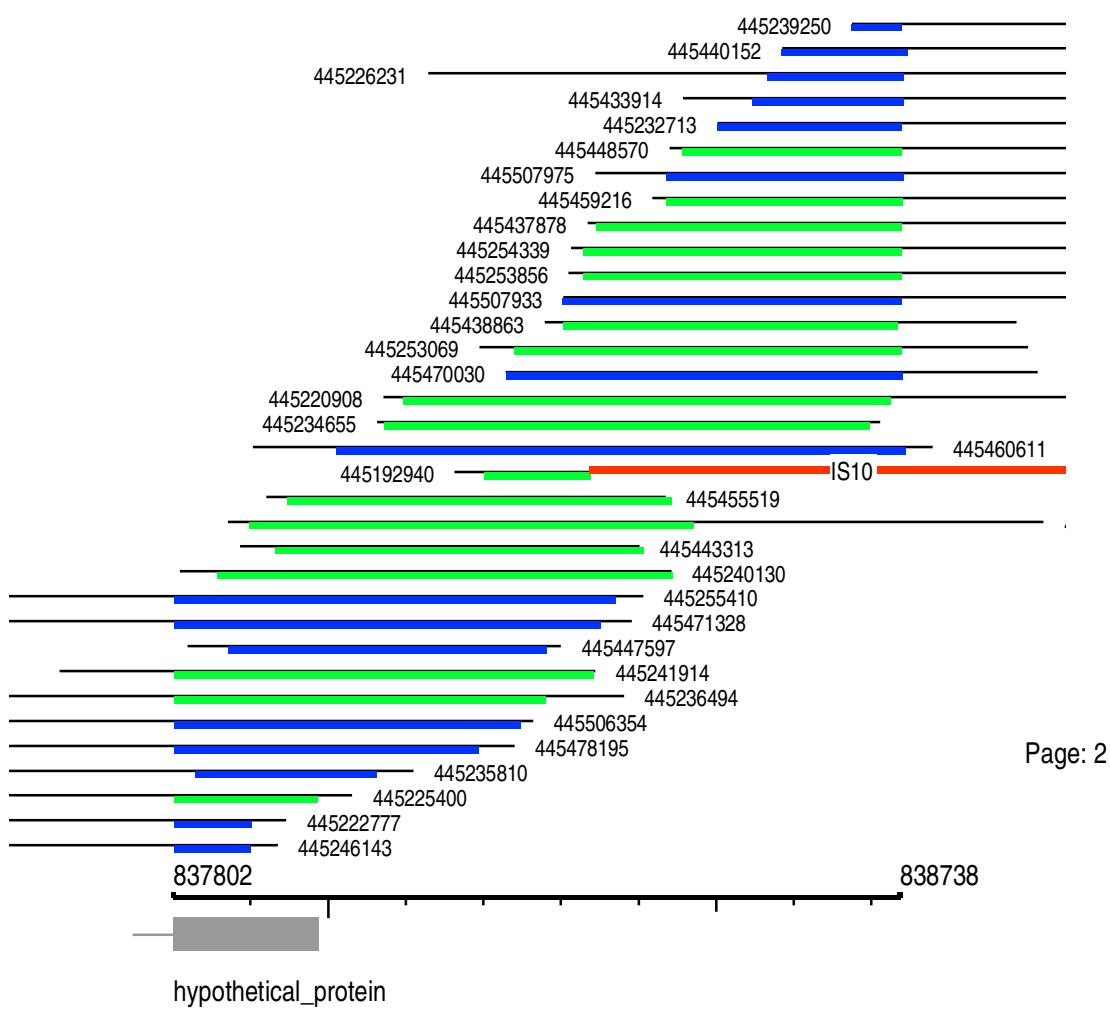
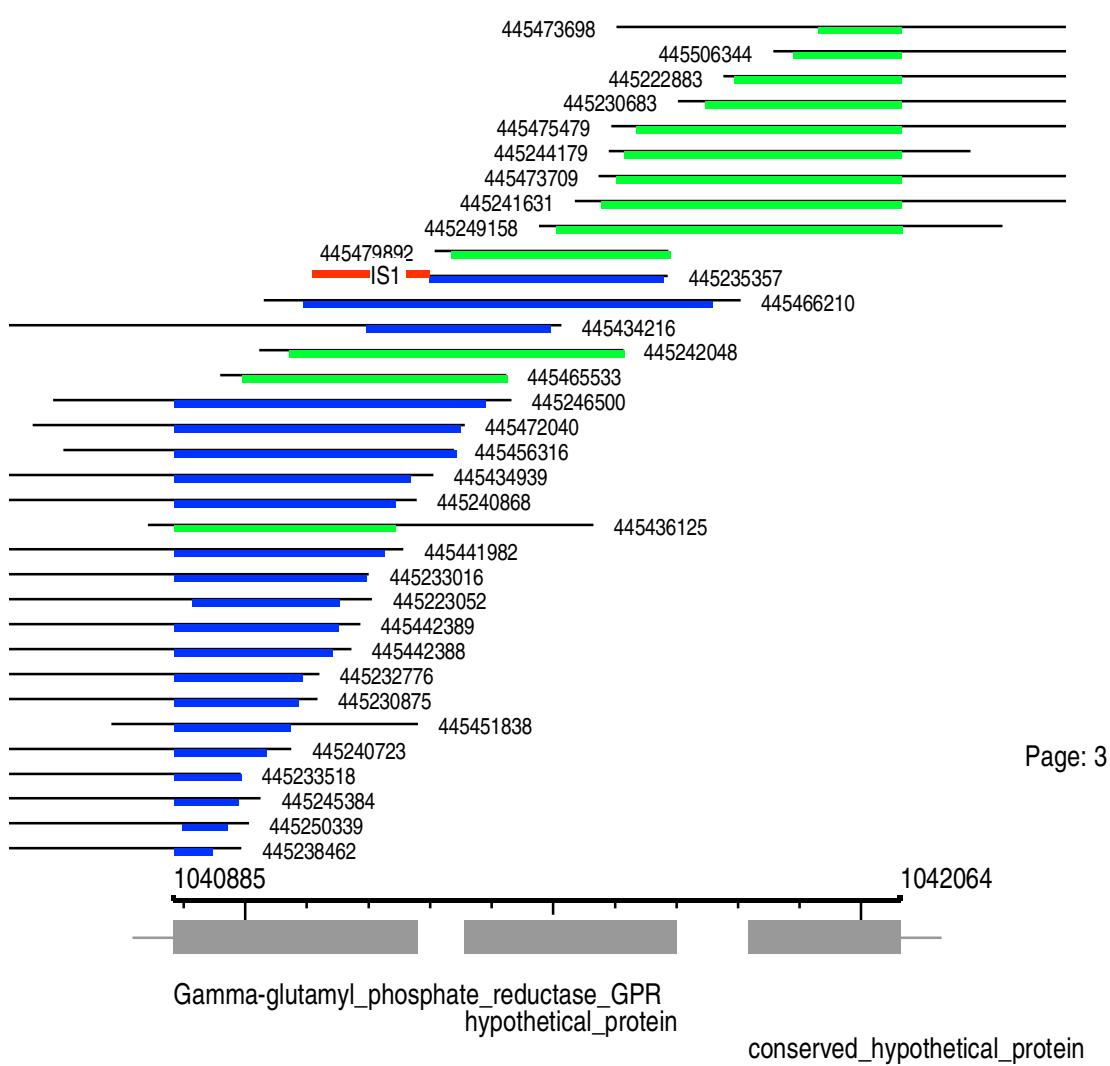


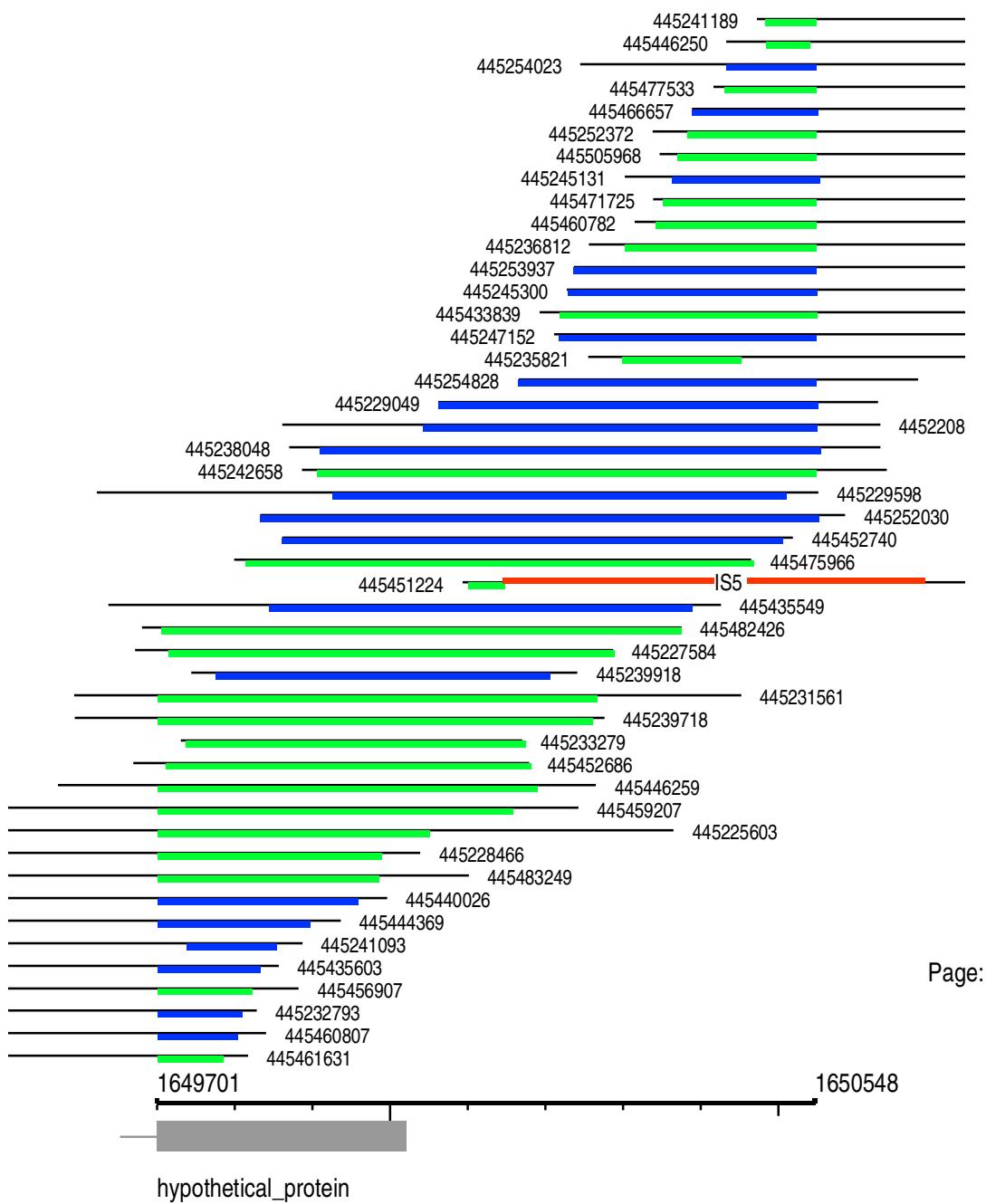
TX1352 Enterococcus faecium



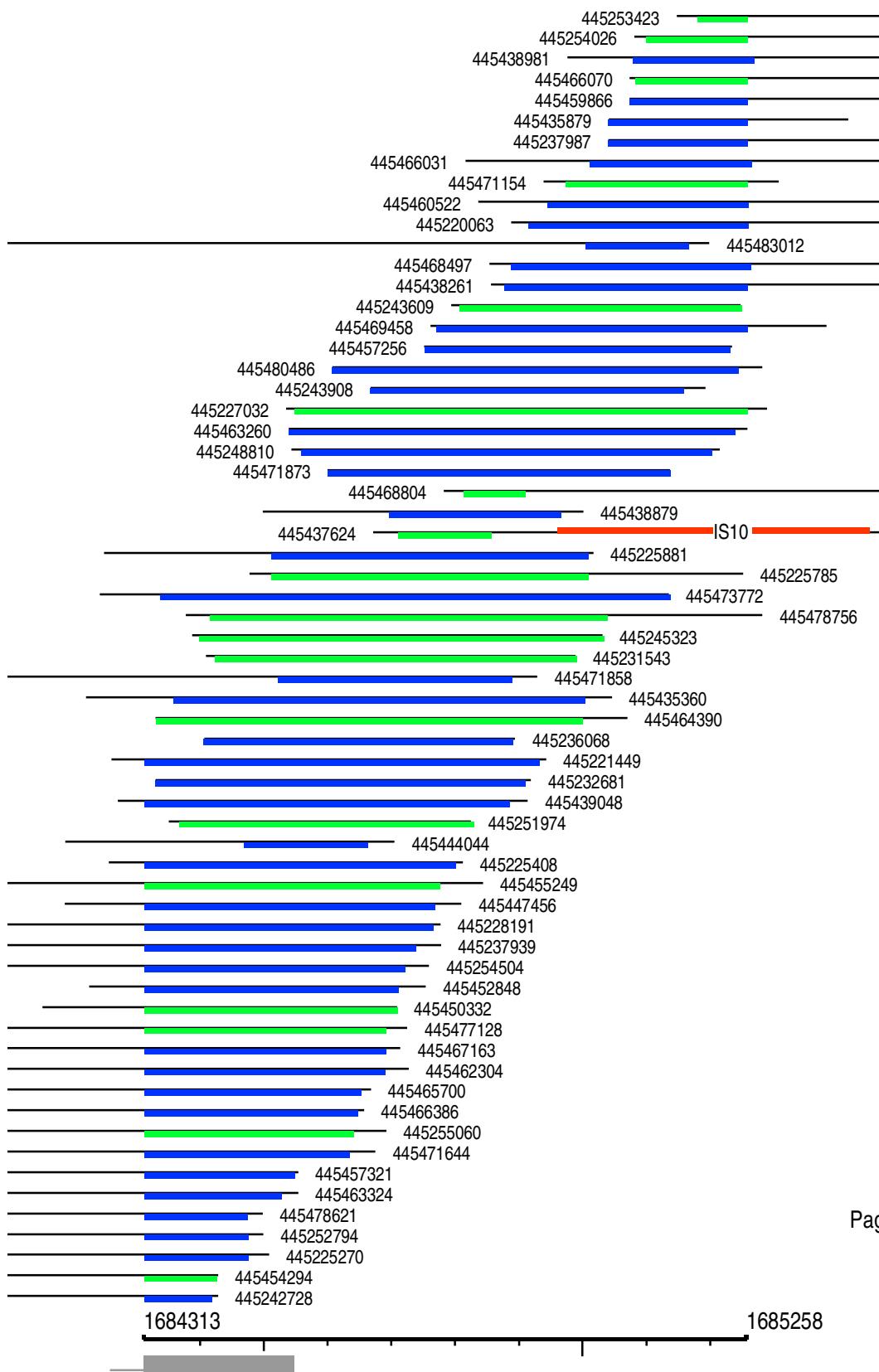
TX1352 Enterococcus faecium



TX1352 Enterococcus faecium



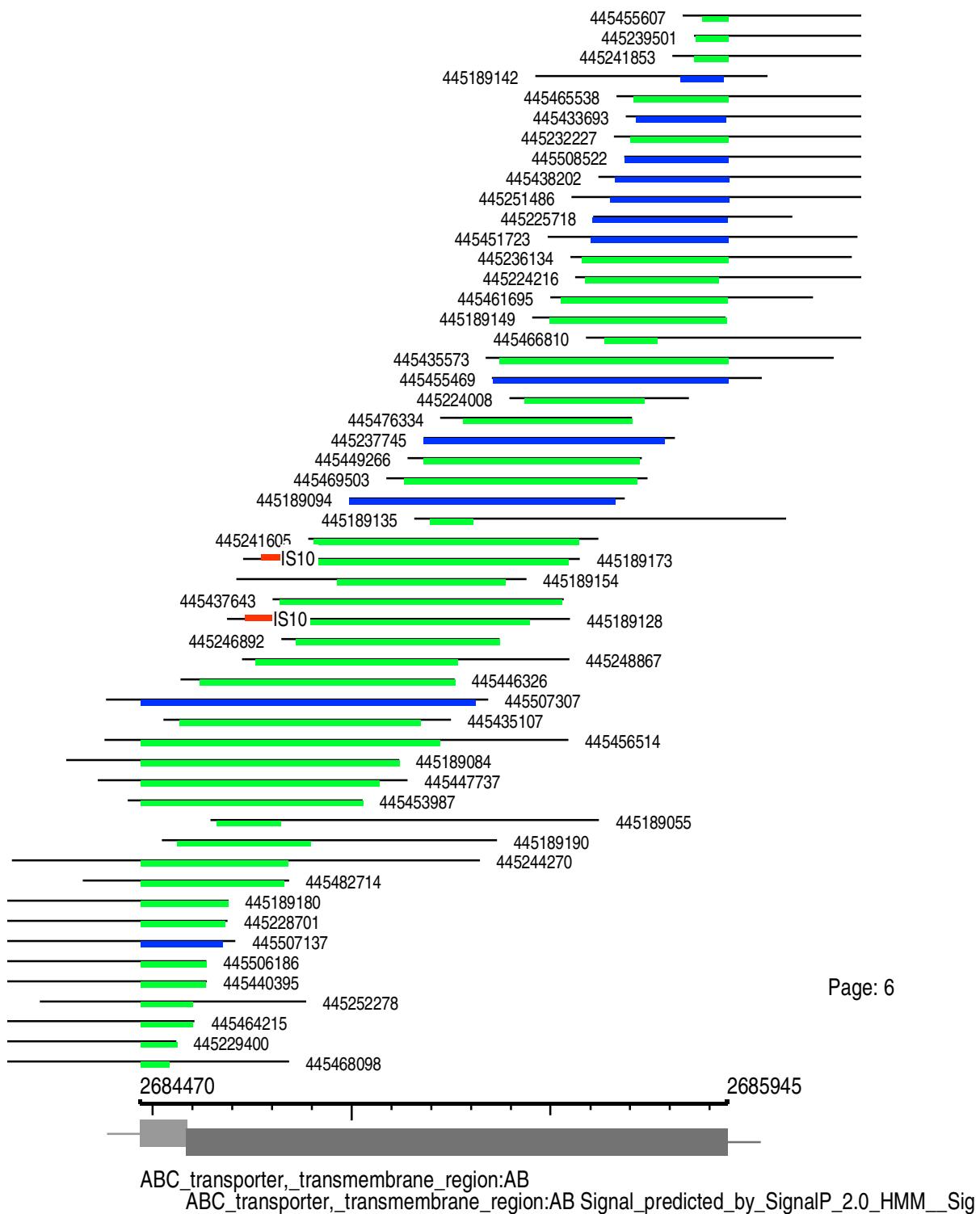
TX1352 Enterococcus faecium



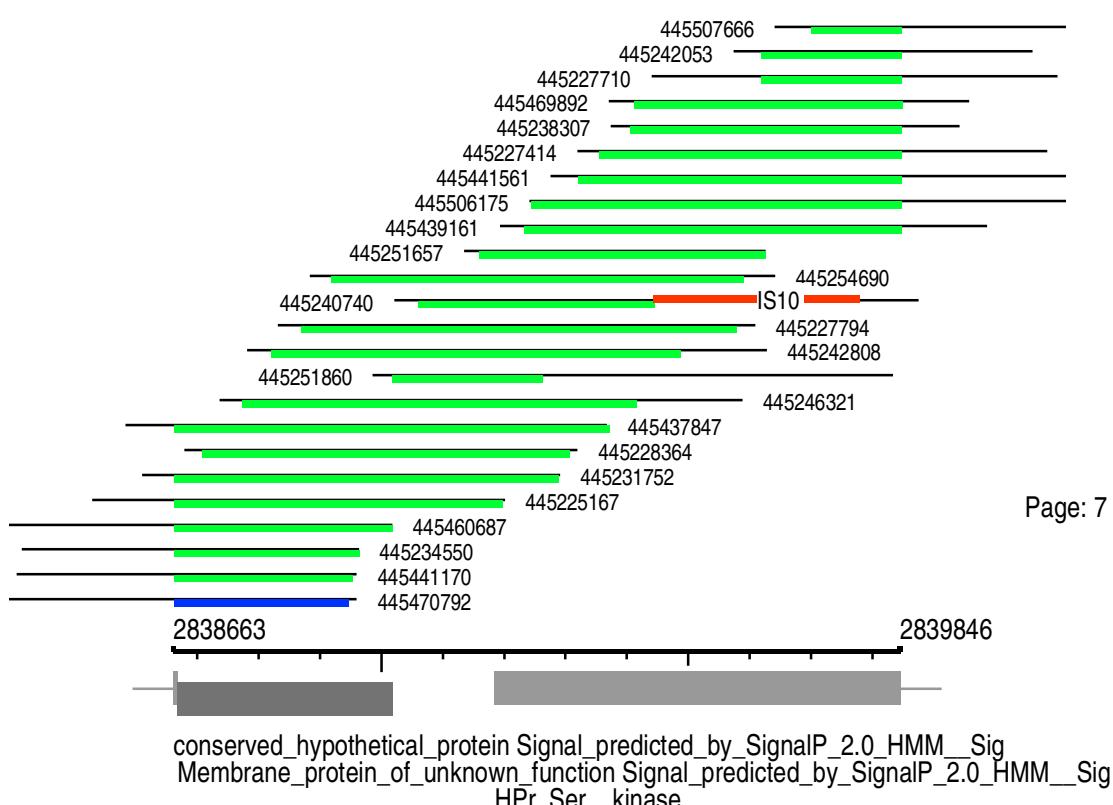
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Helix-turn-helix,_AraC_type:Arac_protein

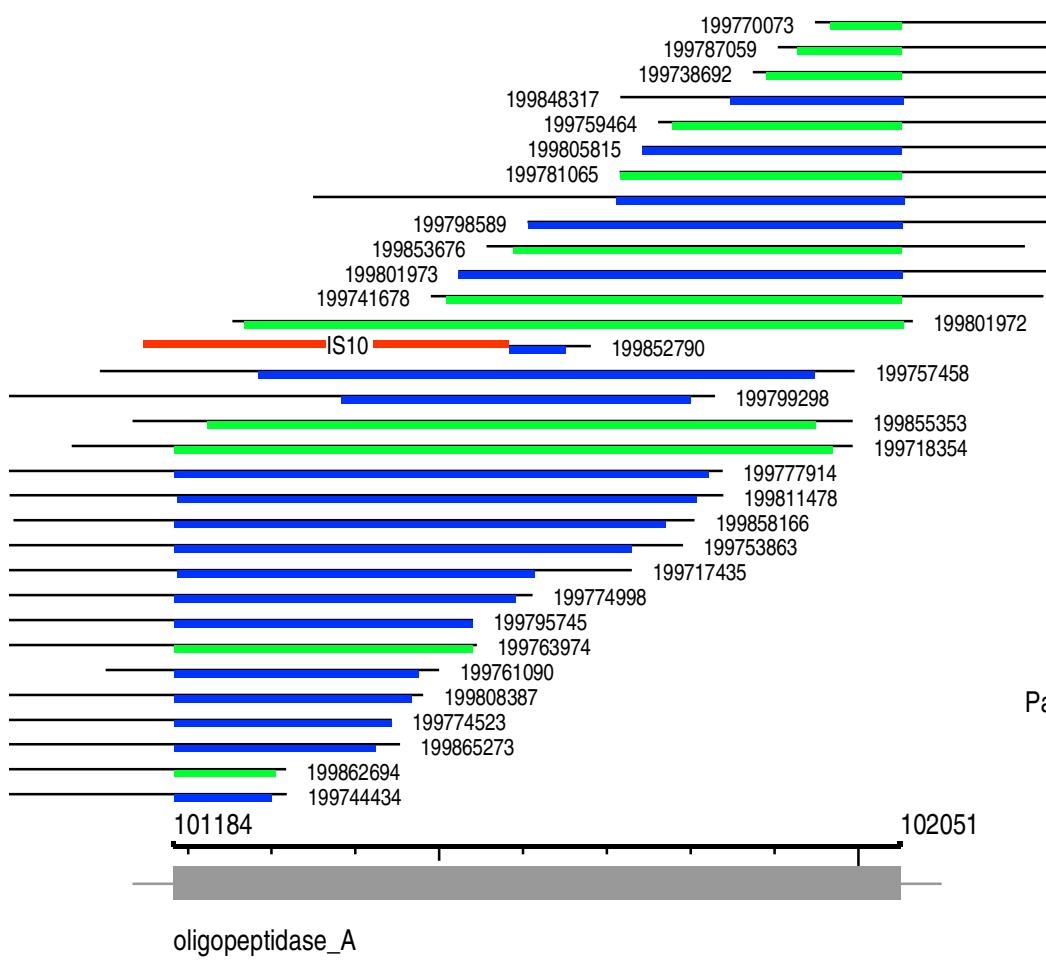
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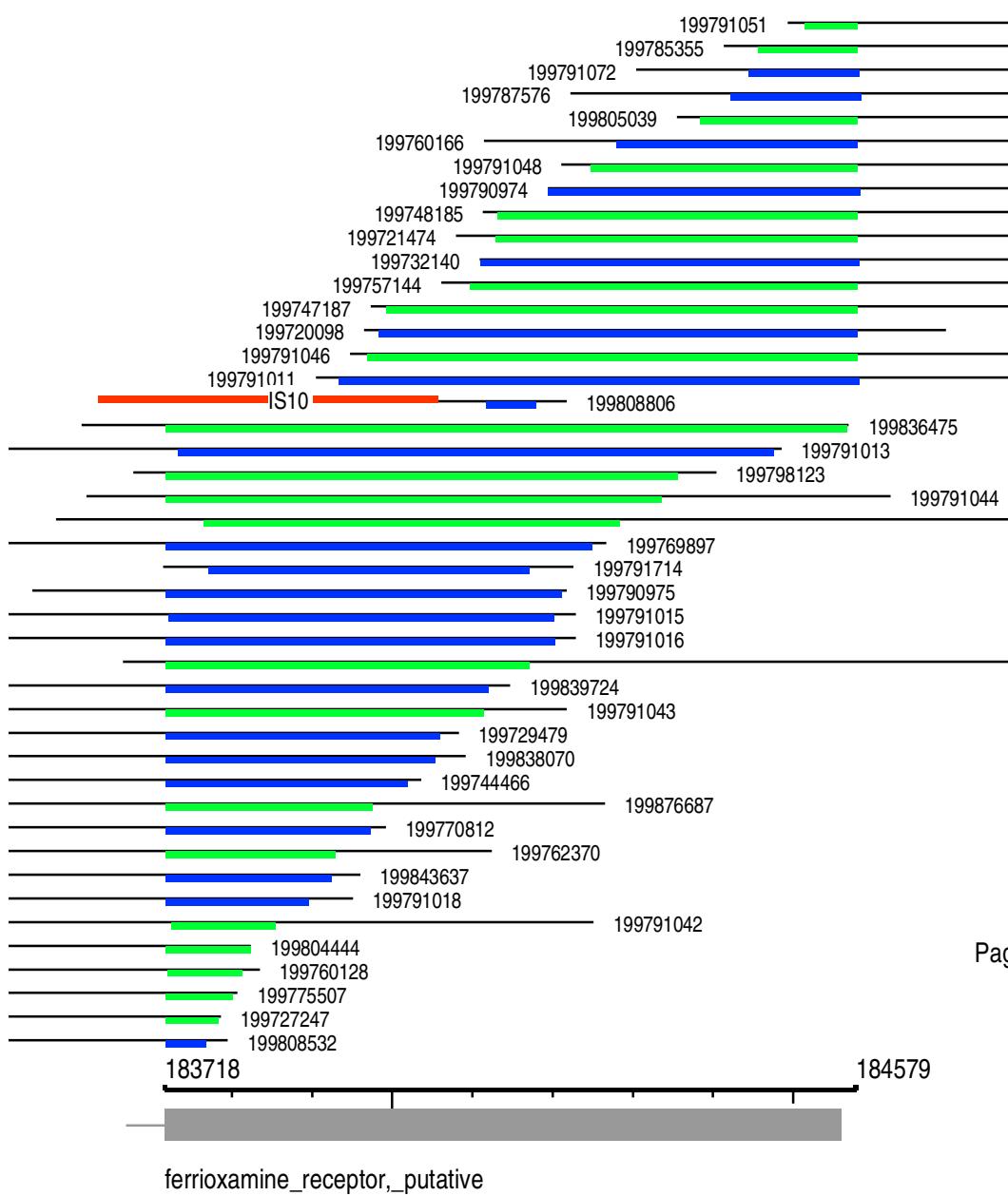
TX1352 Enterococcus faecium



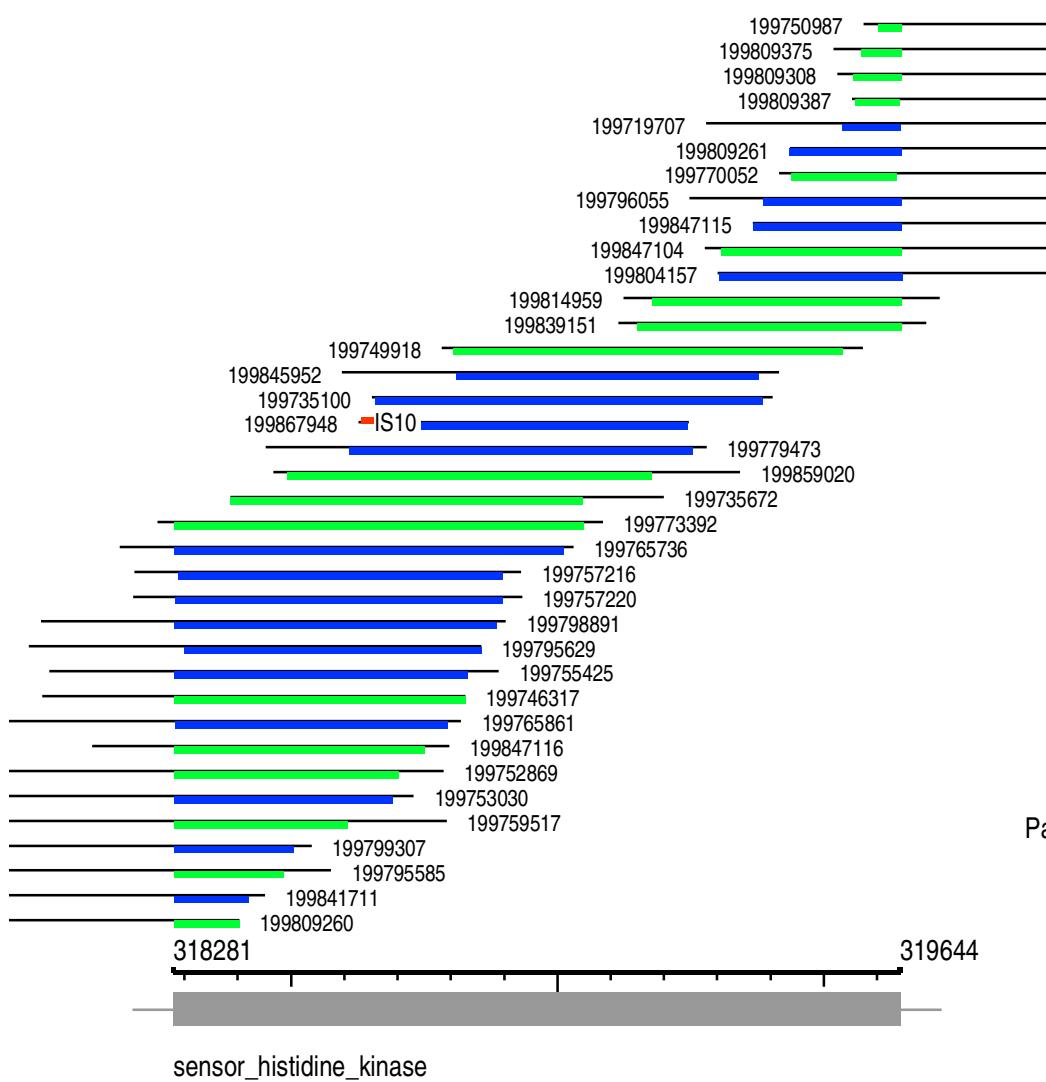
TX160488 *Pseudomonas putida* kt2440



TX160488 *Pseudomonas putida* kt2440

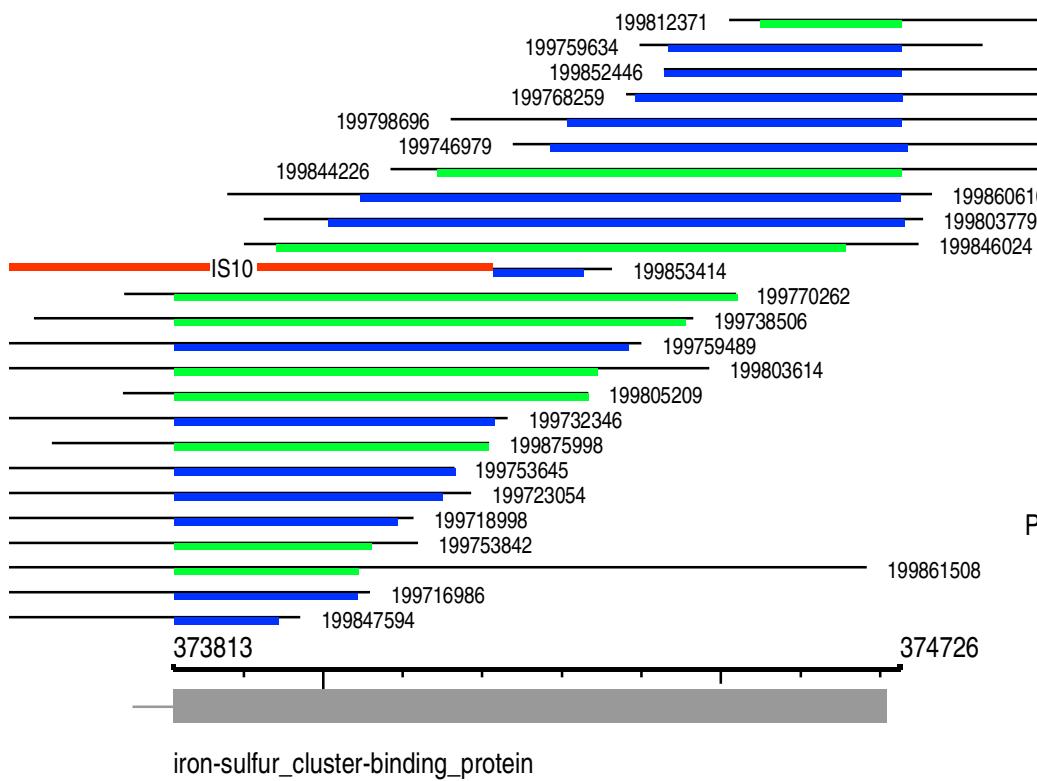


TX160488 *Pseudomonas putida* kt2440

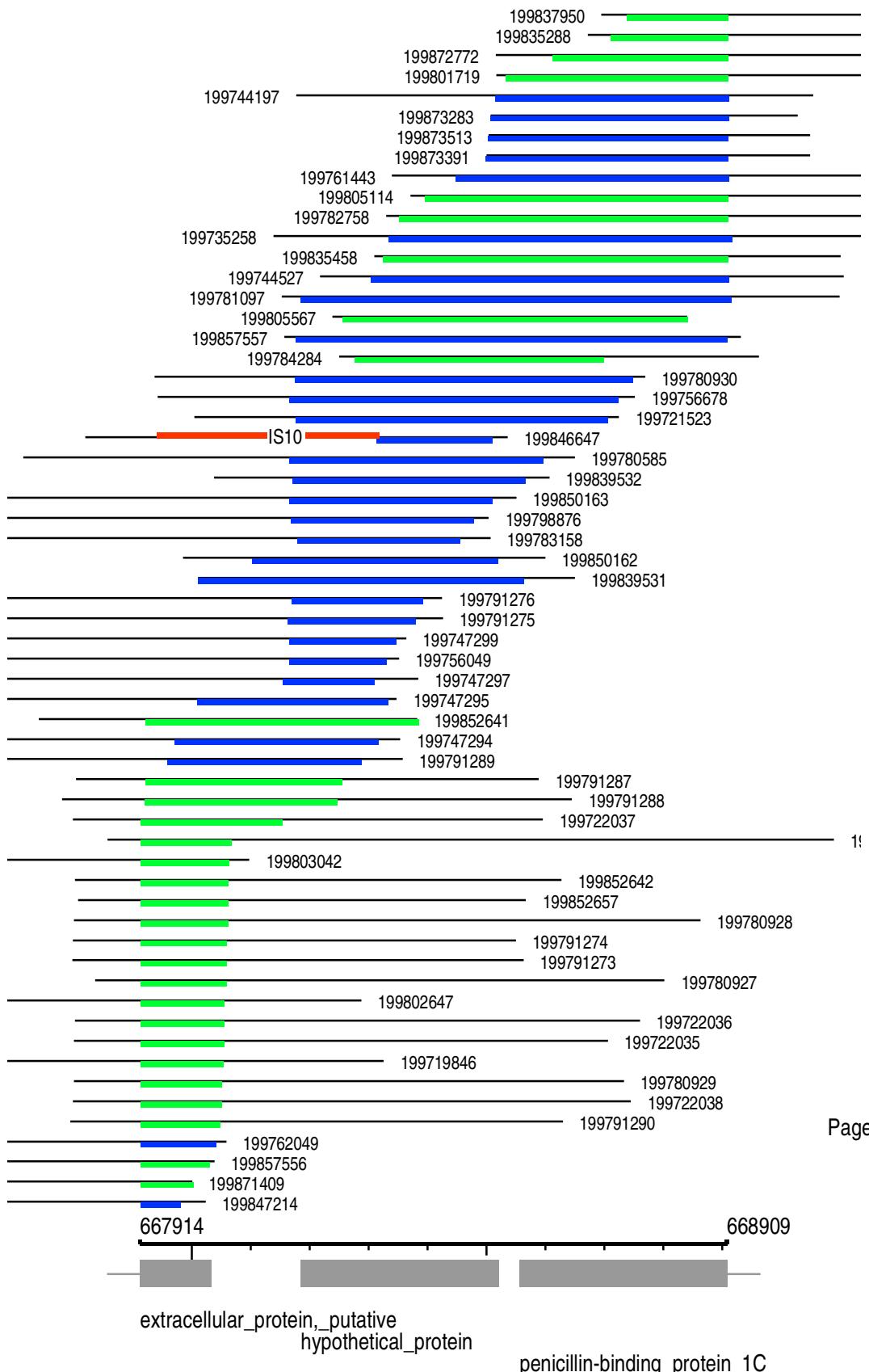


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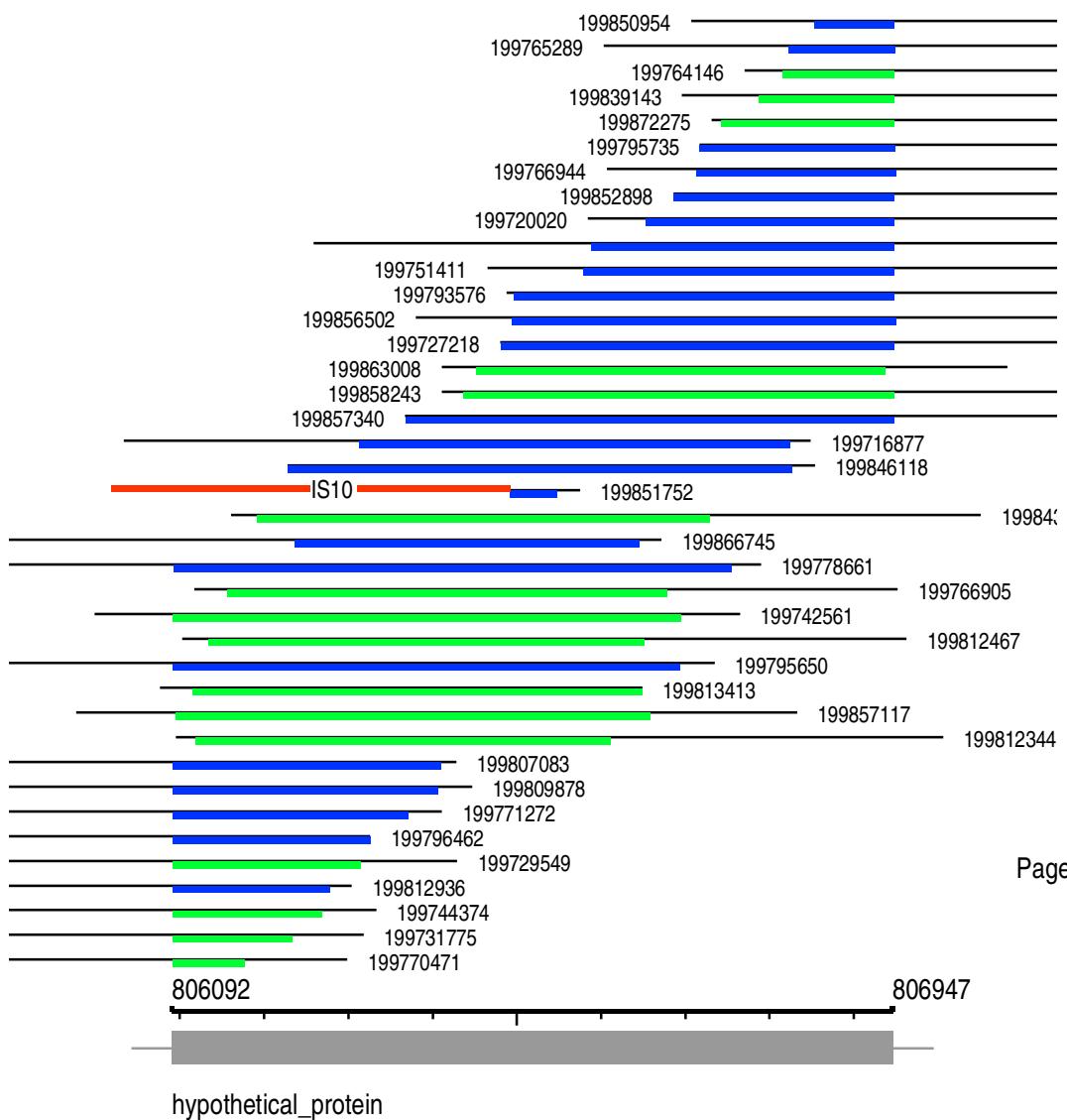
TX160488 *Pseudomonas putida* kt2440



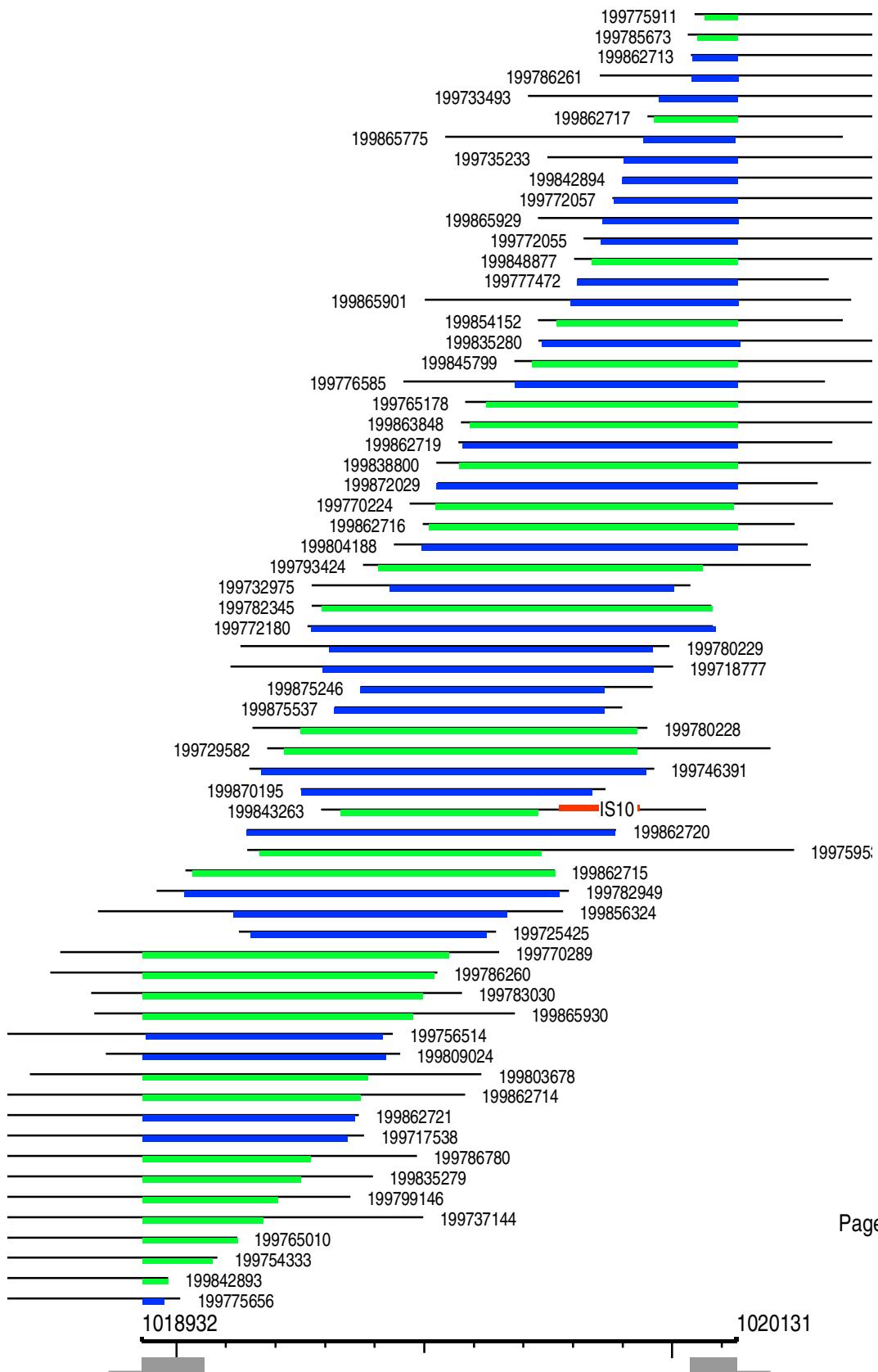
TX160488 *Pseudomonas putida* kt2440



TX160488 *Pseudomonas putida* kt2440



TX160488 Pseudomonas putida kt2440

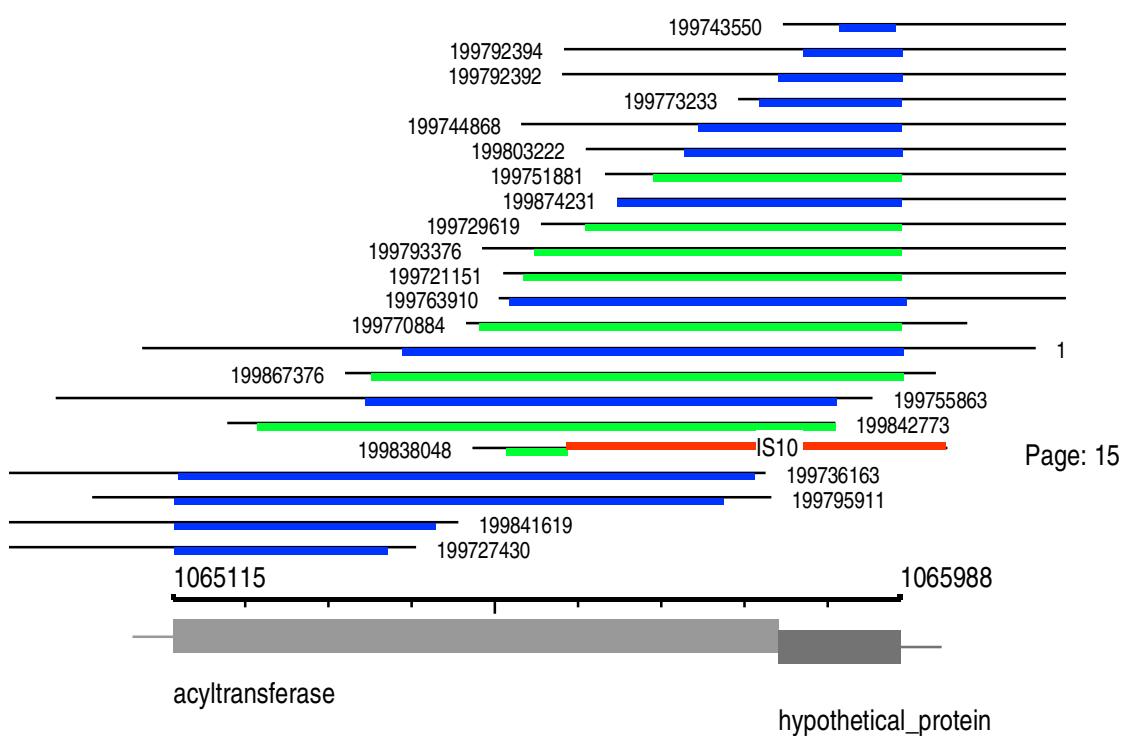


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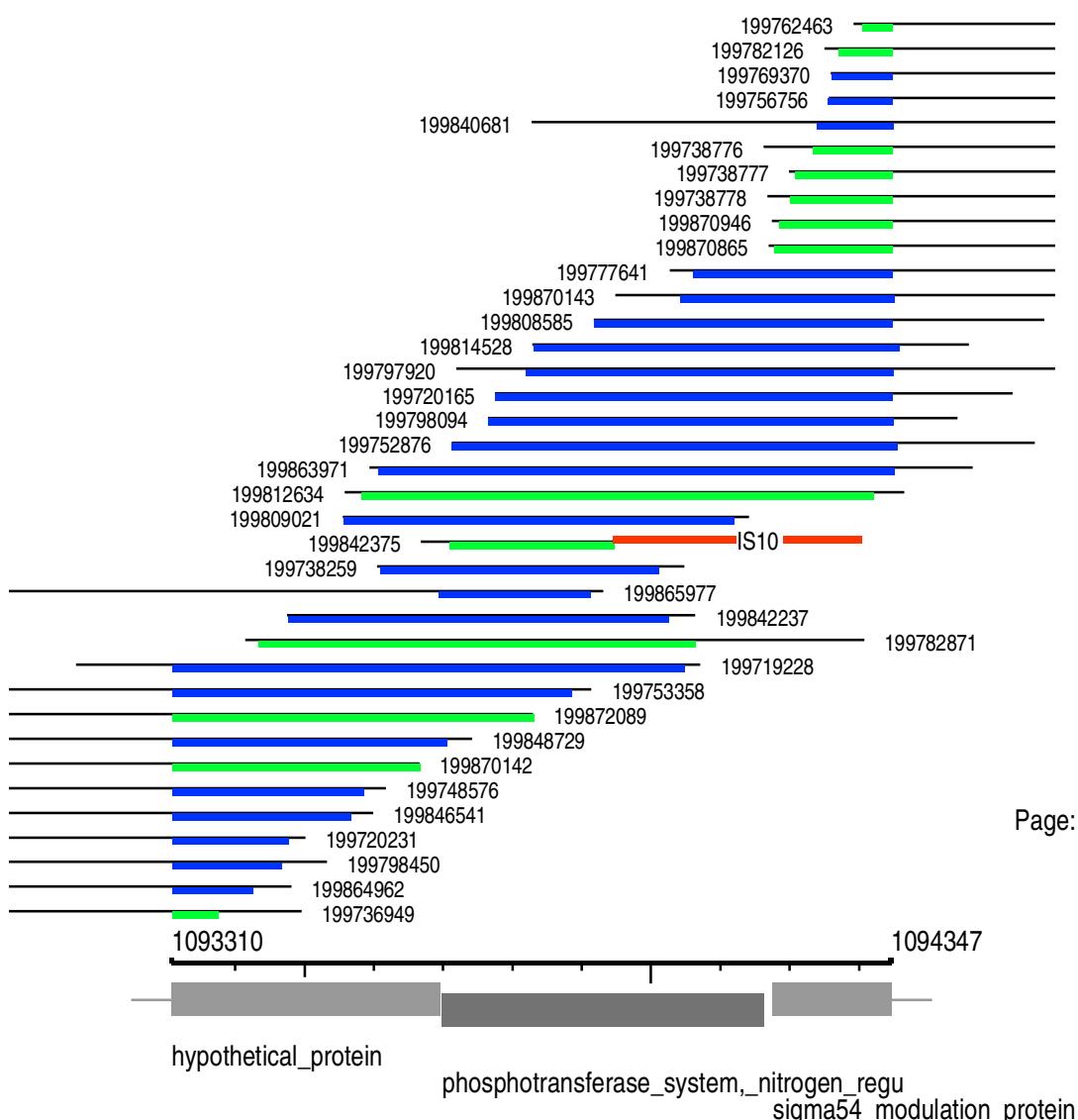
dipeptide_ABC_transporter,_permease_prot

dipeptide_ABC_transporter,_ATP-binding_p

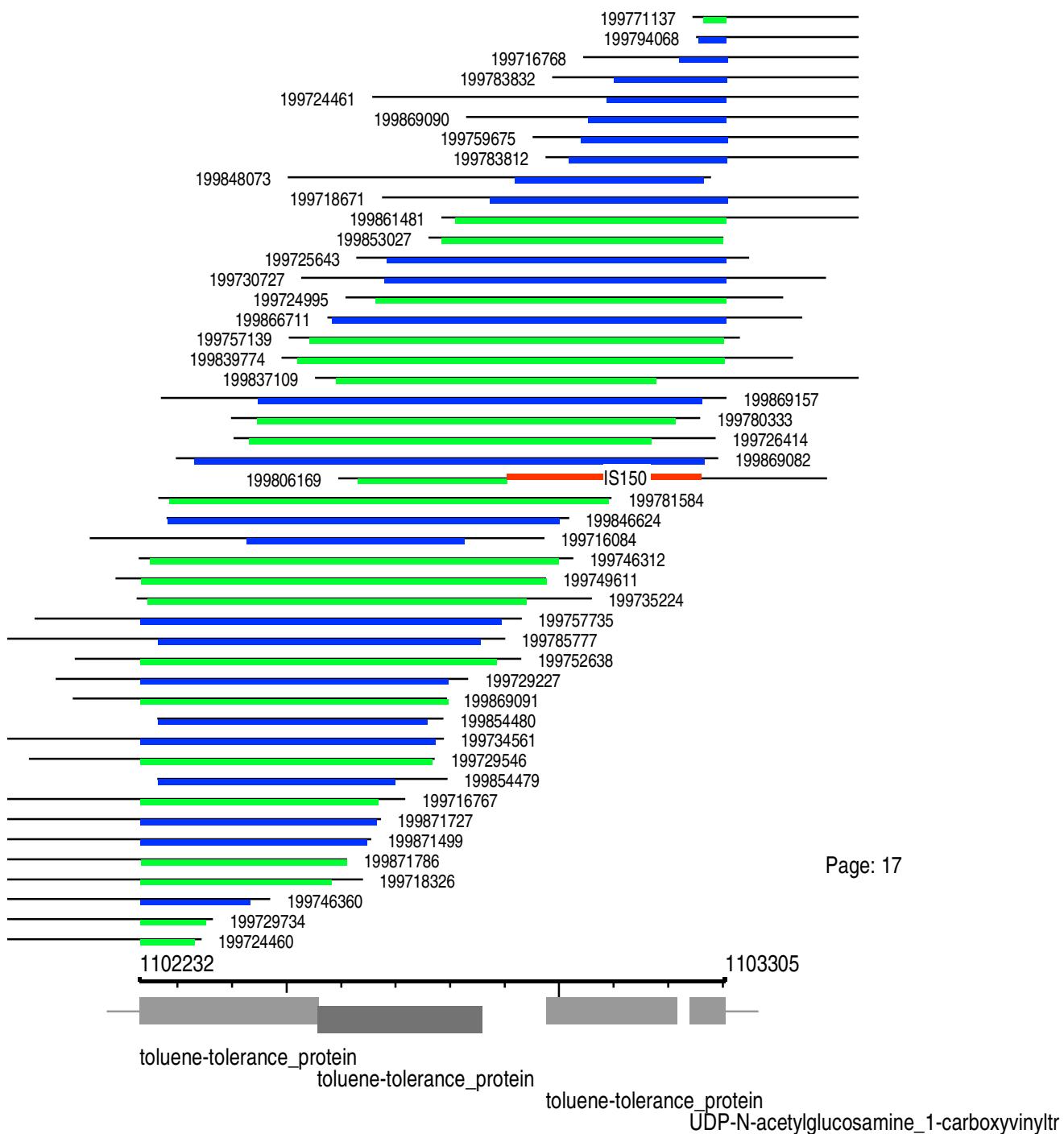
TX160488 *Pseudomonas putida* kt2440



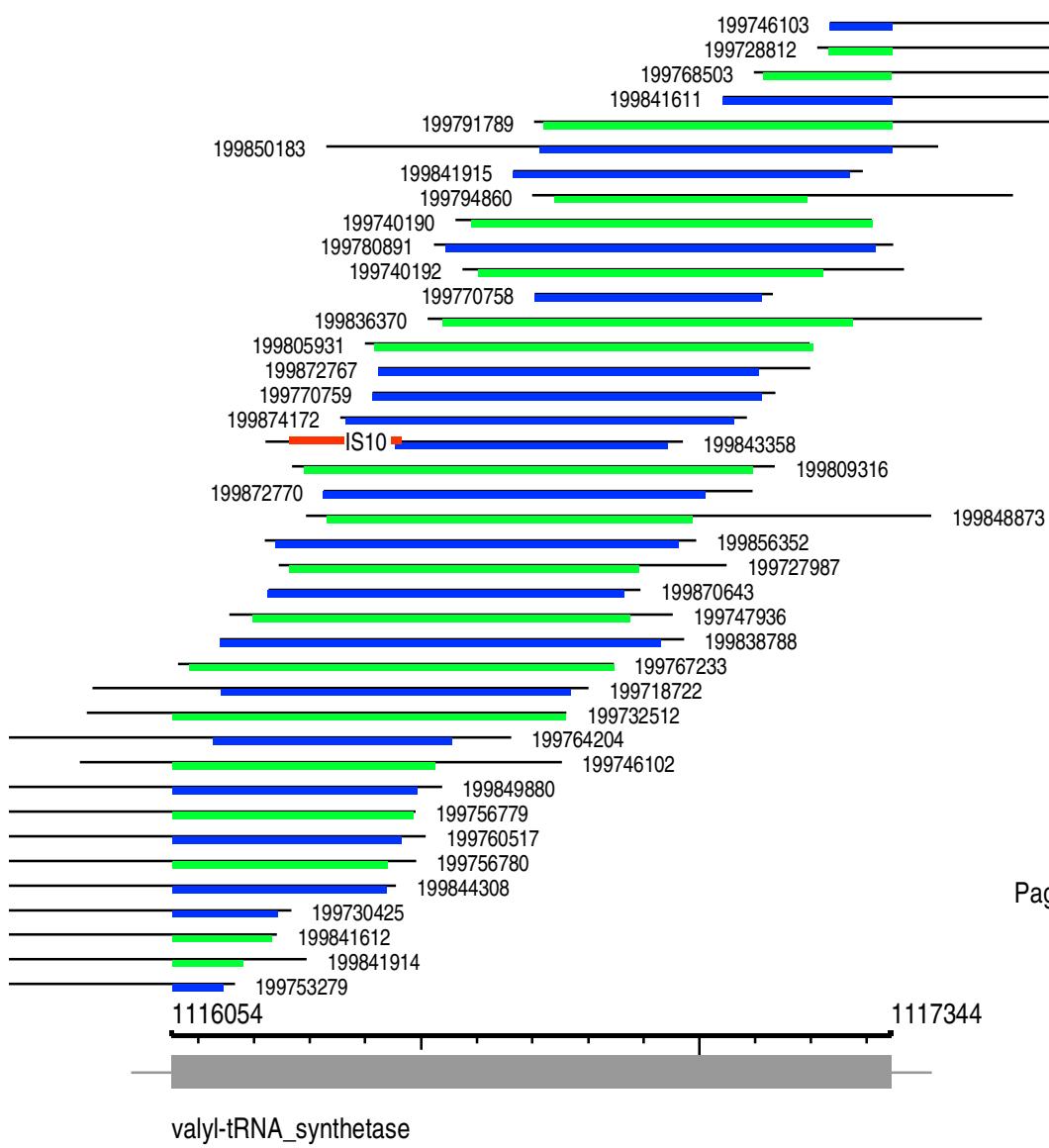
TX160488 Pseudomonas putida kt2440



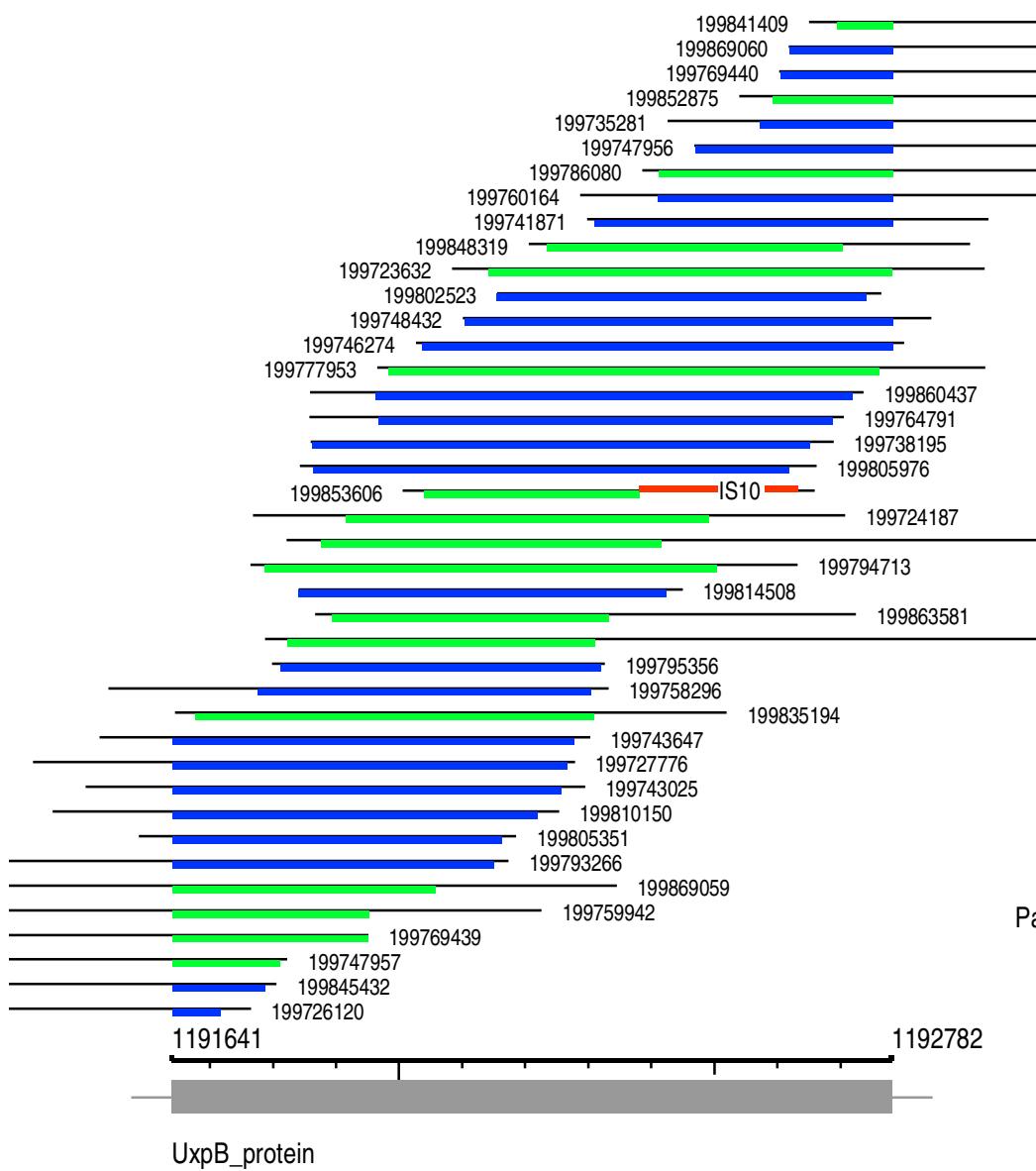
TX160488 *Pseudomonas putida* kt2440



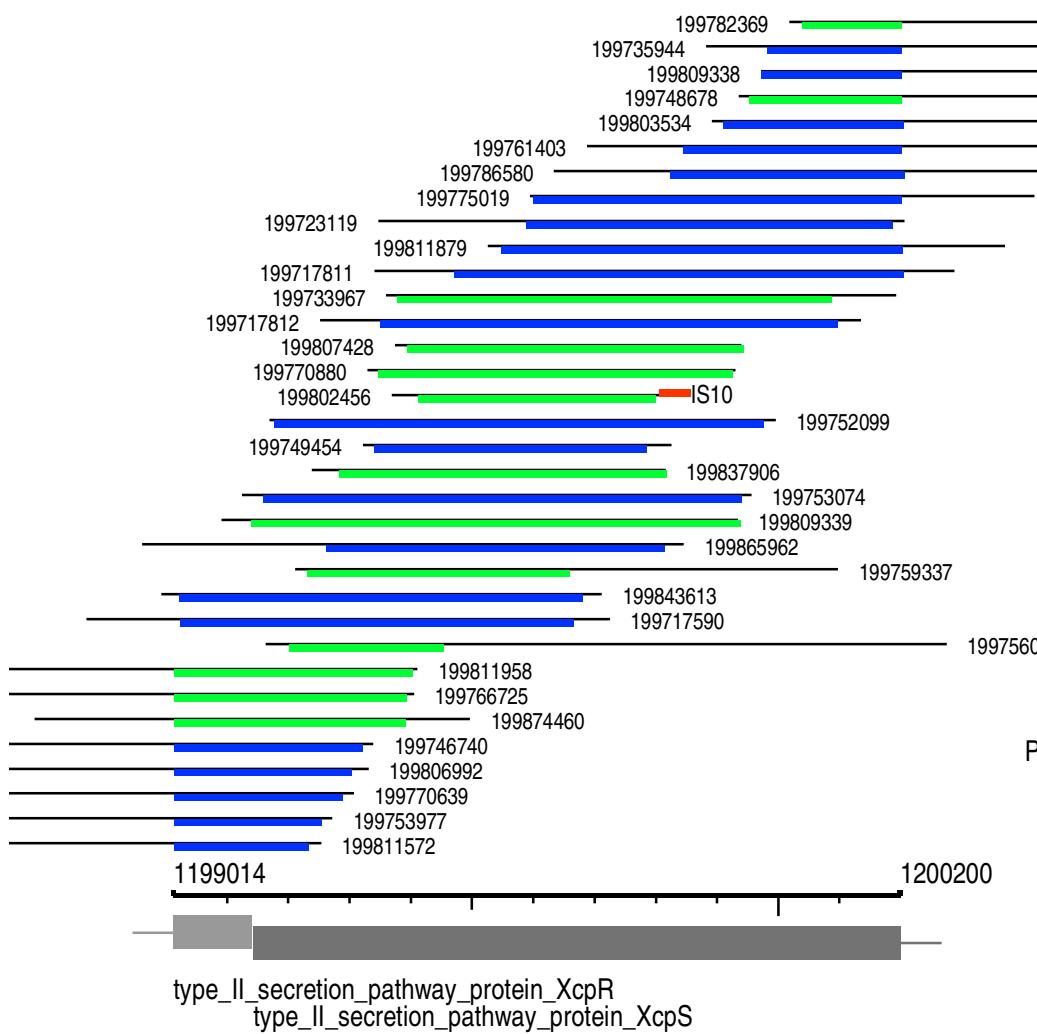
TX160488 *Pseudomonas putida* kt2440



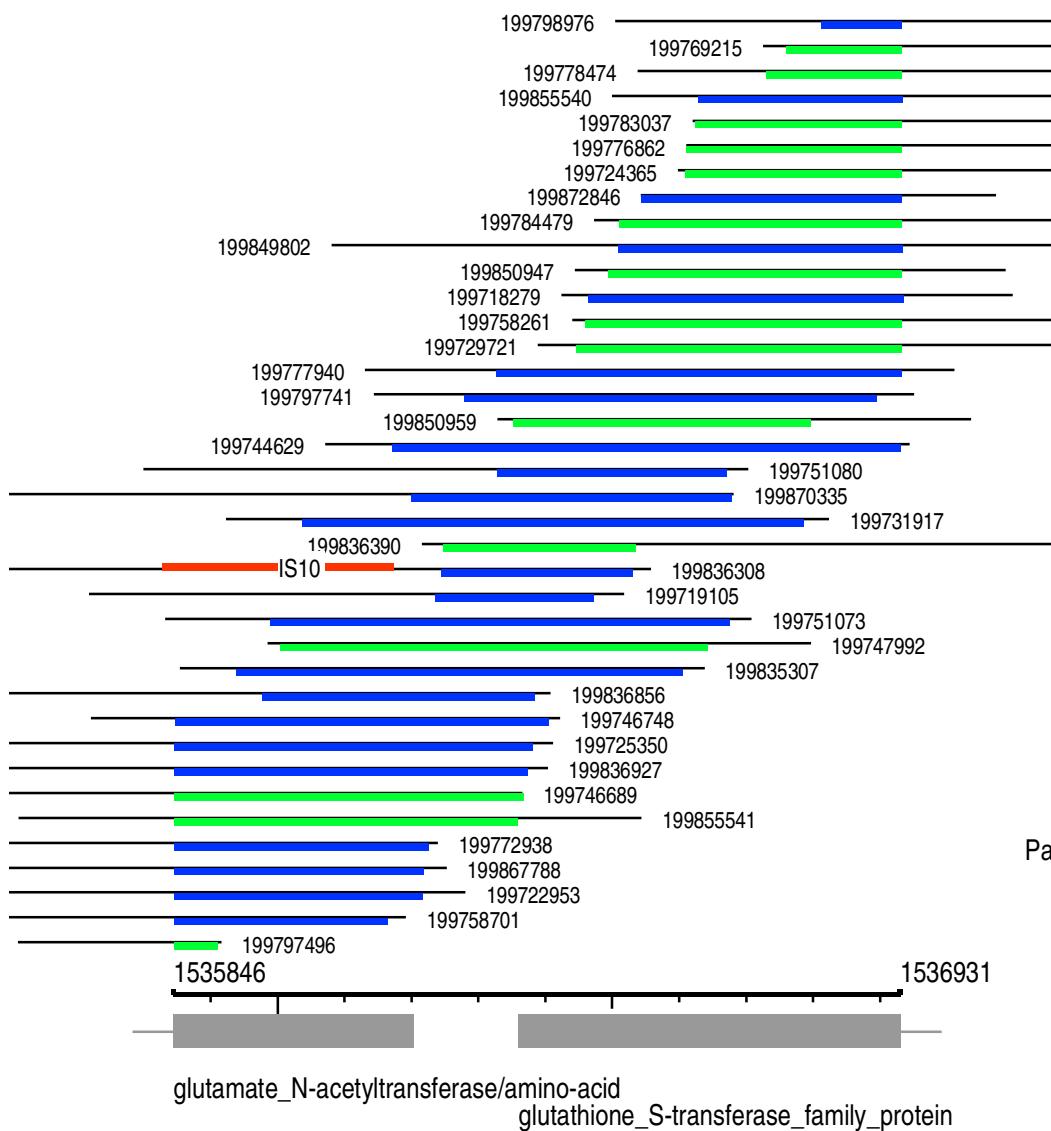
TX160488 *Pseudomonas putida* kt2440



TX160488 *Pseudomonas putida* kt2440

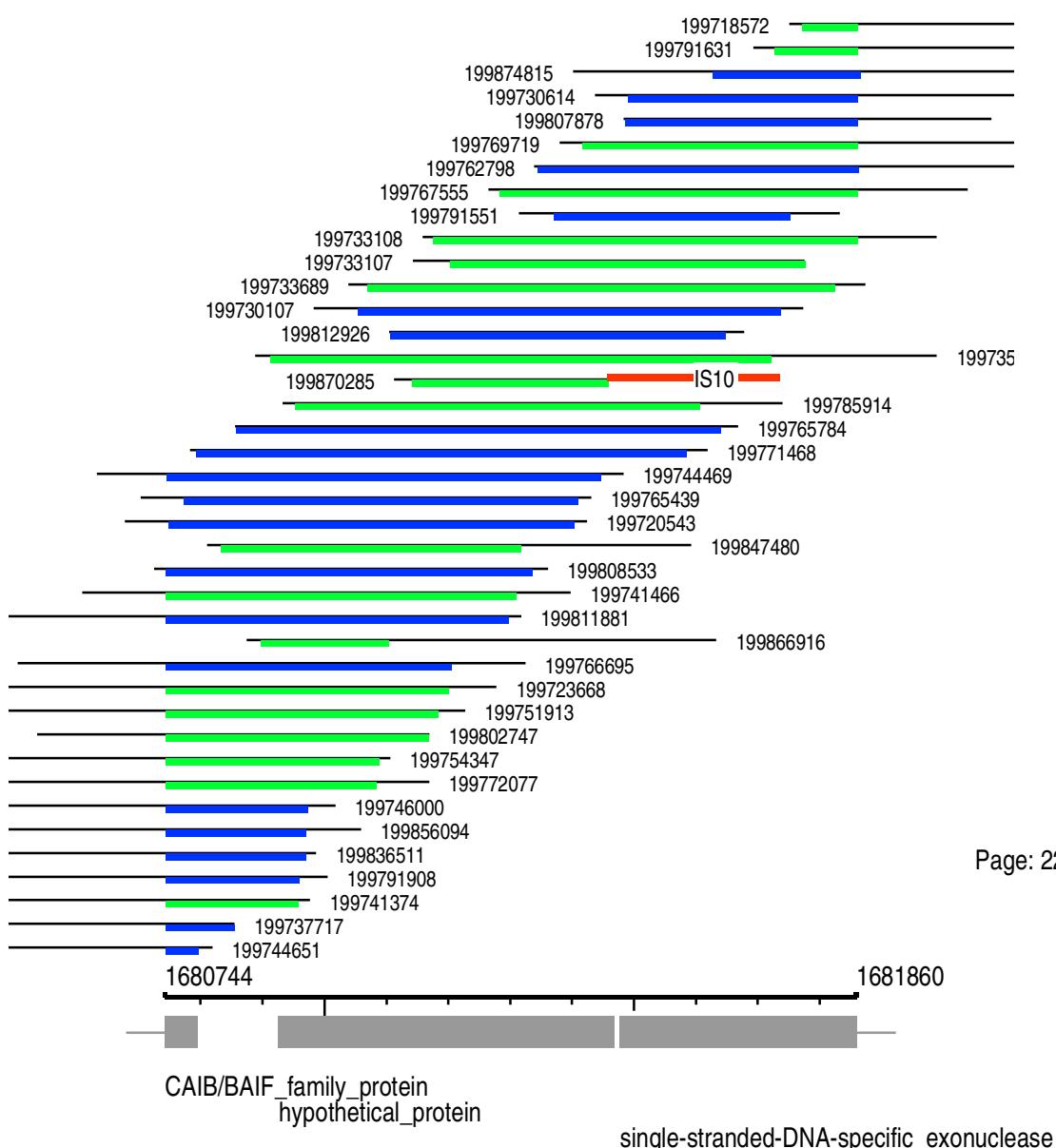


TX160488 *Pseudomonas putida* kt2440

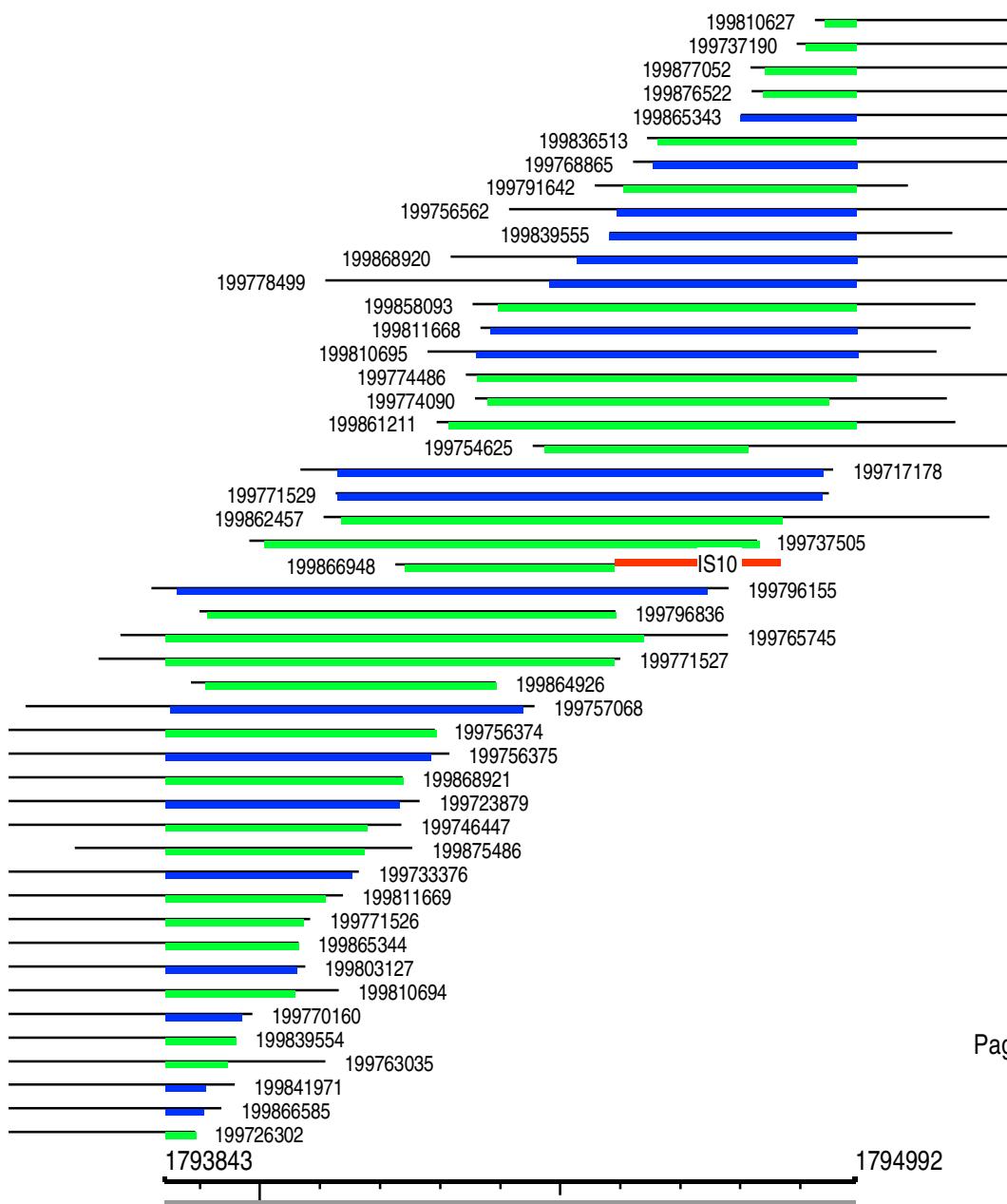


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TX160488 *Pseudomonas putida* kt2440



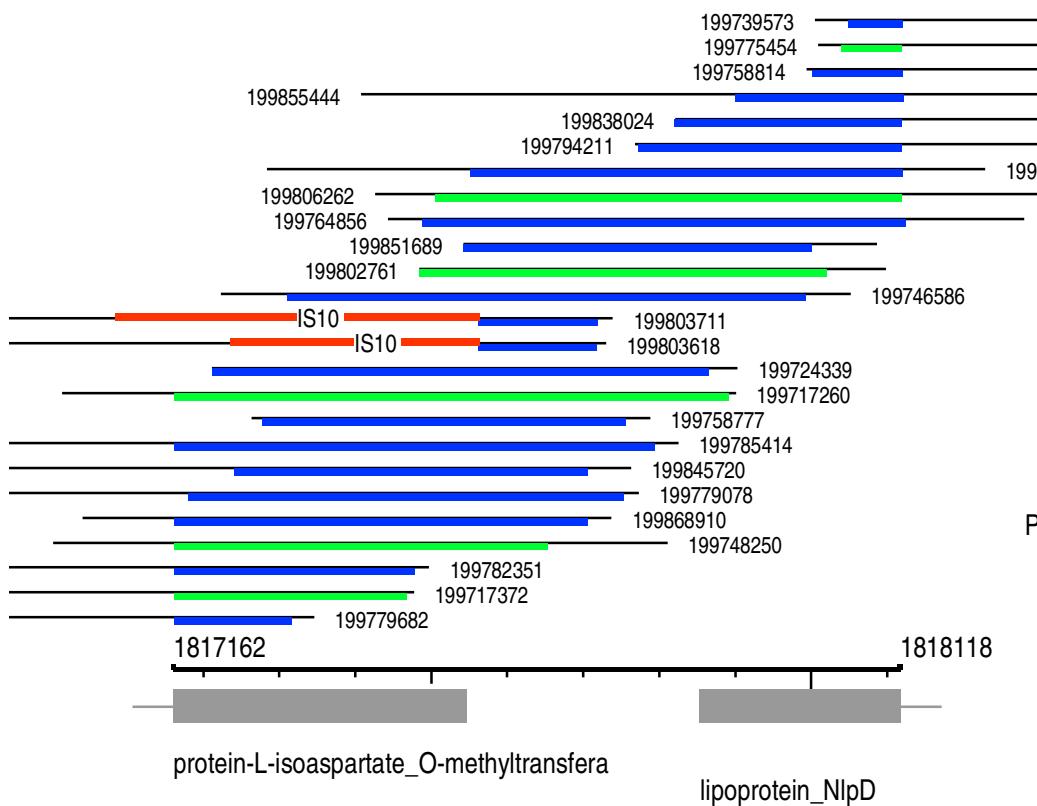
TX160488 *Pseudomonas putida* kt2440



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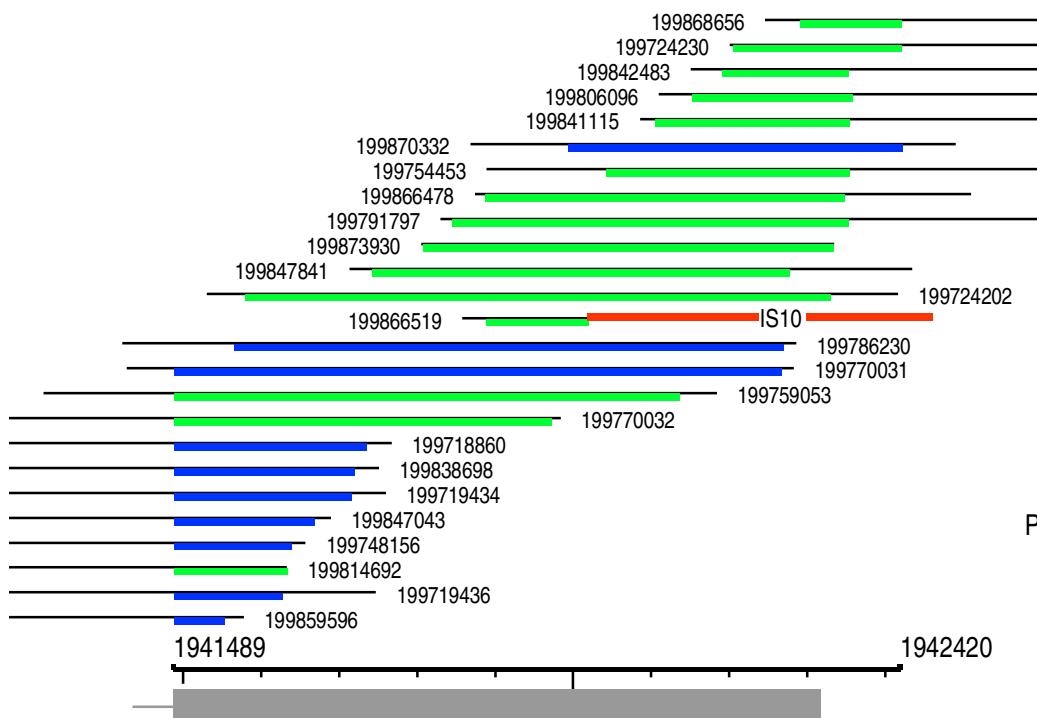
outer_membrane_protein,_bacterial_surfac

TX160488 *Pseudomonas putida* kt2440



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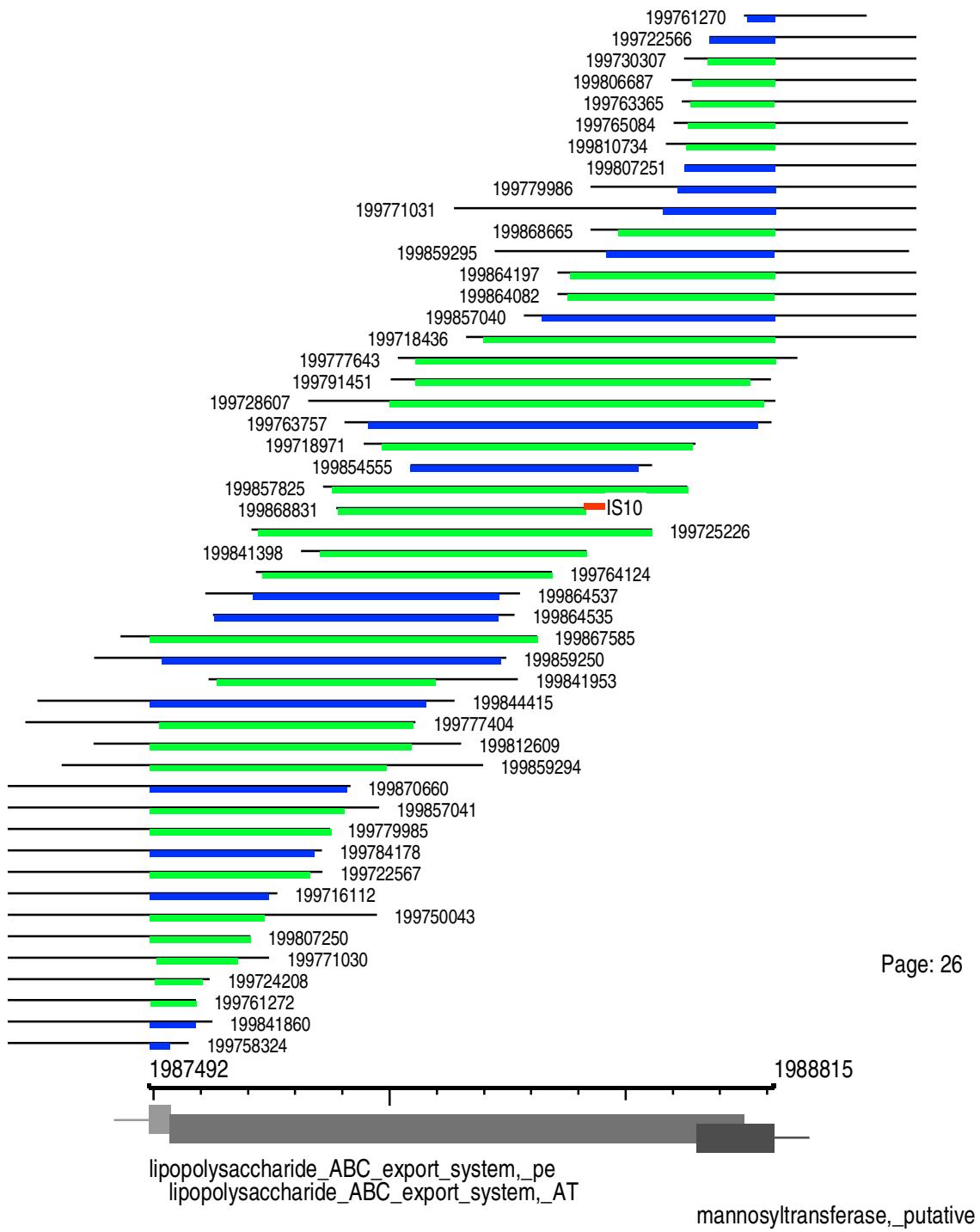
TX160488 *Pseudomonas putida* kt2440



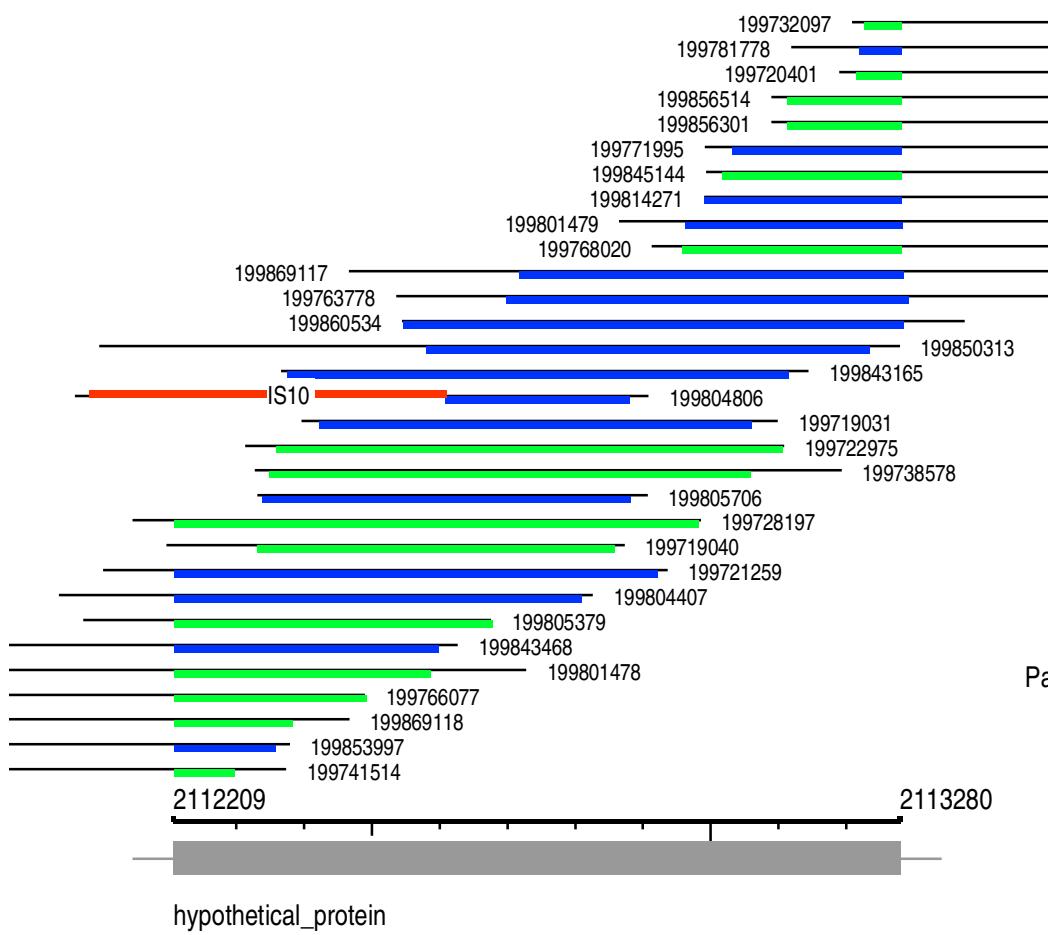
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glycine_betaine-binding_protein,_putativ

TX160488 *Pseudomonas putida* kt2440



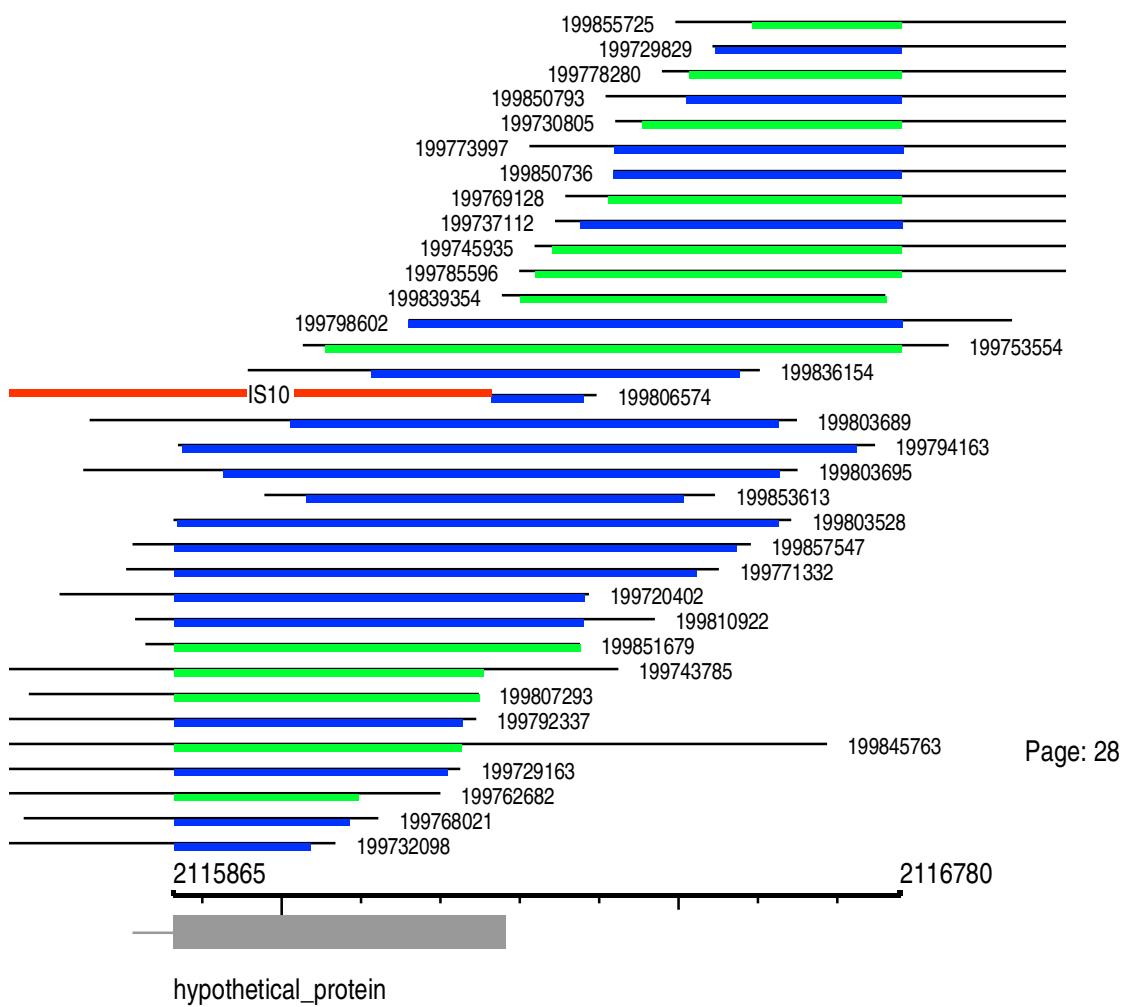
TX160488 *Pseudomonas putida* kt2440



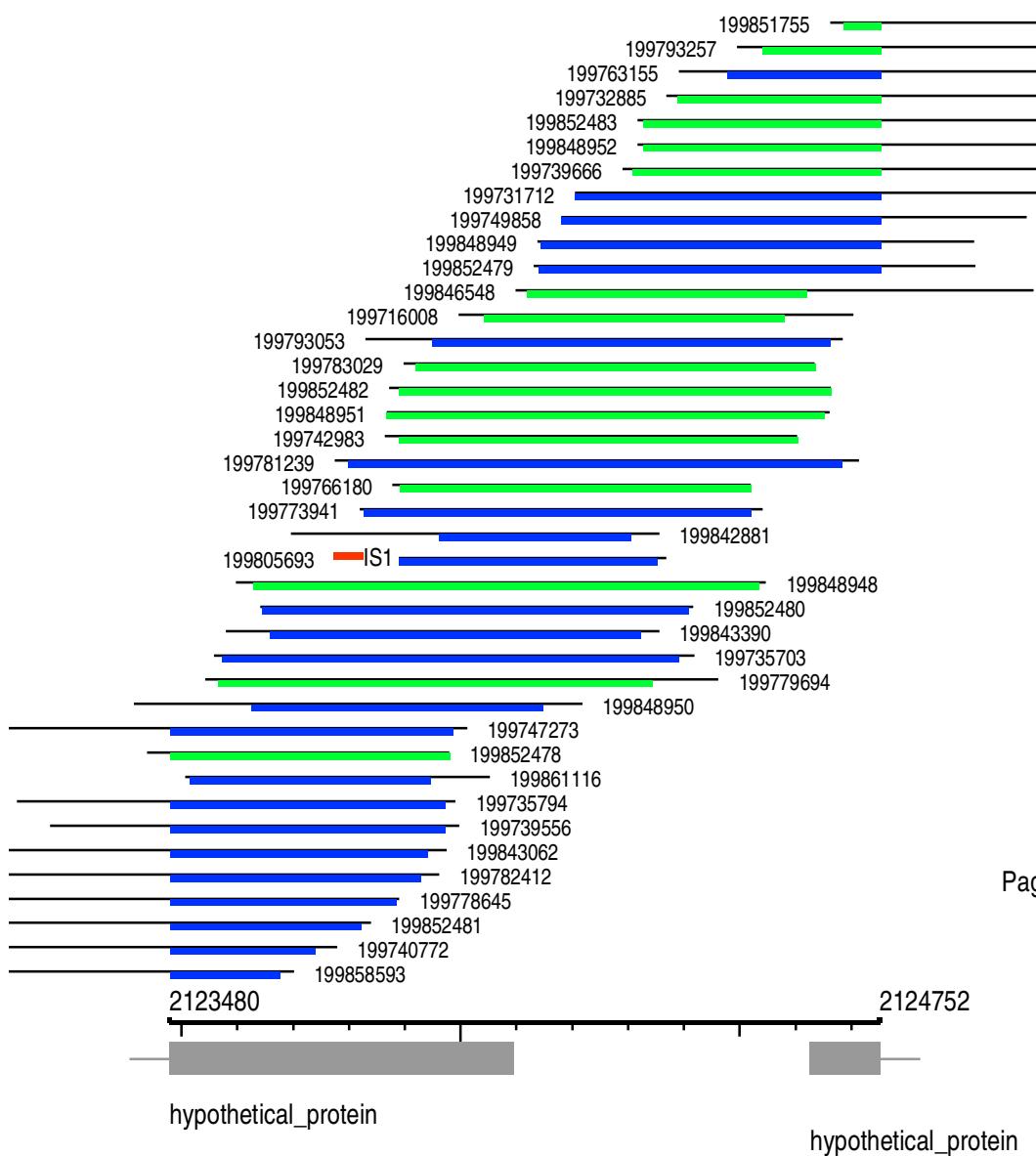
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hypothetical_protein

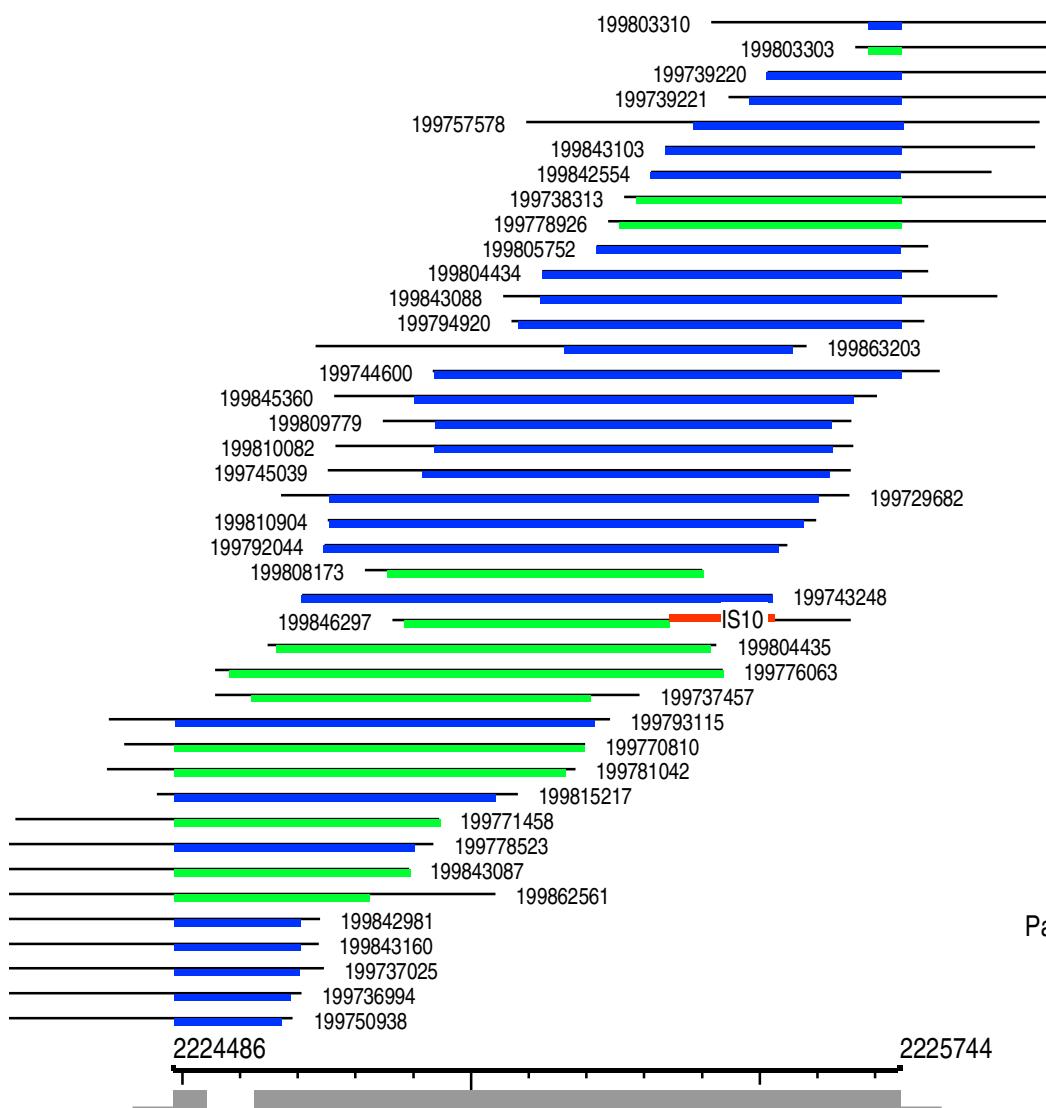
TX160488 *Pseudomonas putida* kt2440



TX160488 *Pseudomonas putida* kt2440



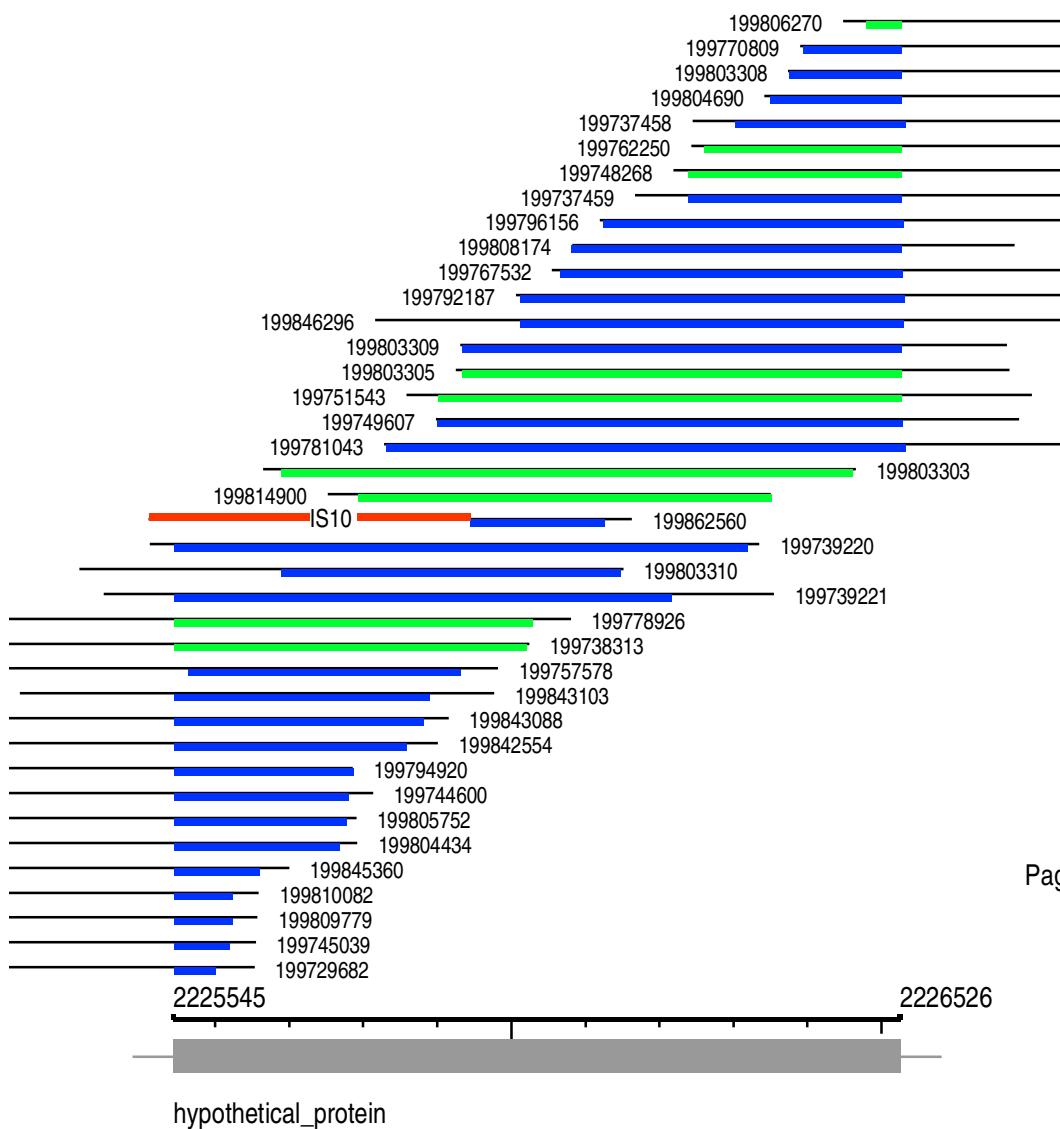
TX160488 *Pseudomonas putida* kt2440



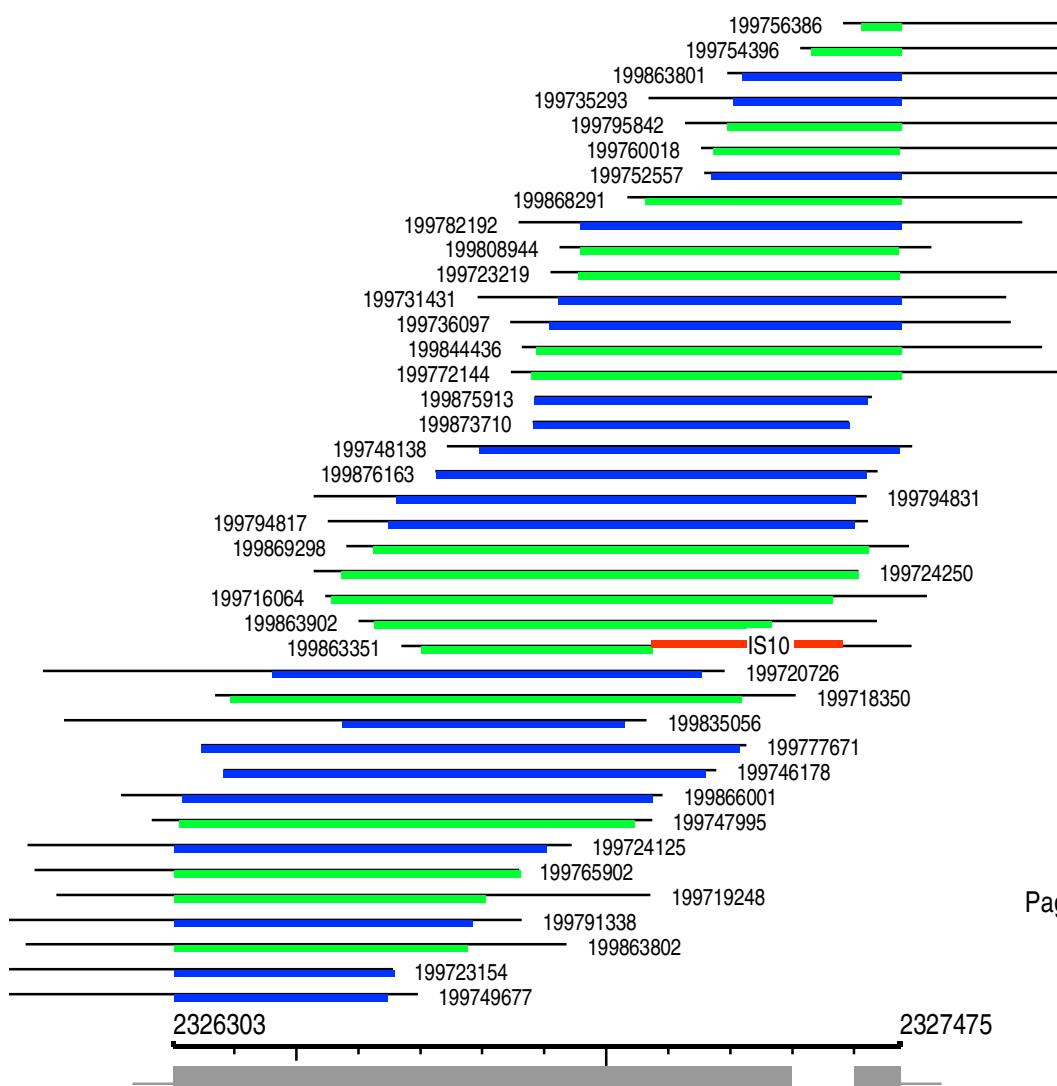
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site-specific_recombinase,_phage_integra
hypothetical_protein

TX160488 *Pseudomonas putida* kt2440



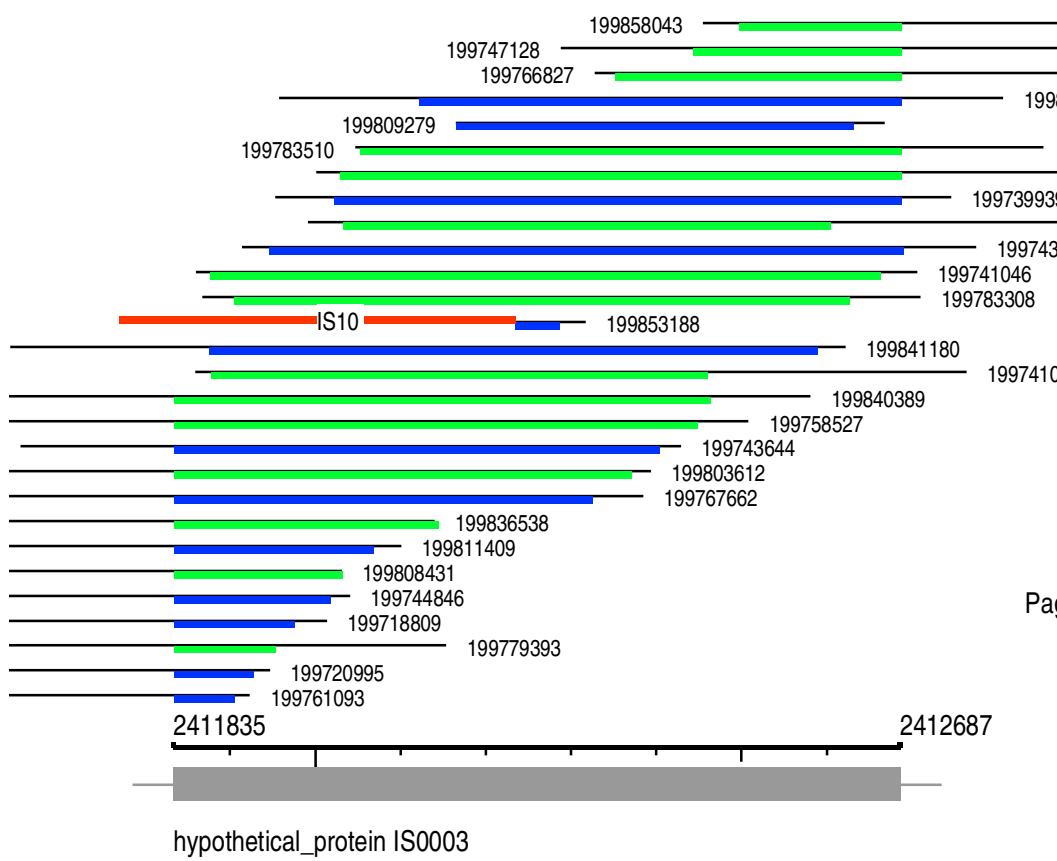
TX160488 *Pseudomonas putida* kt2440



metallo-beta-lactamase_family_protein

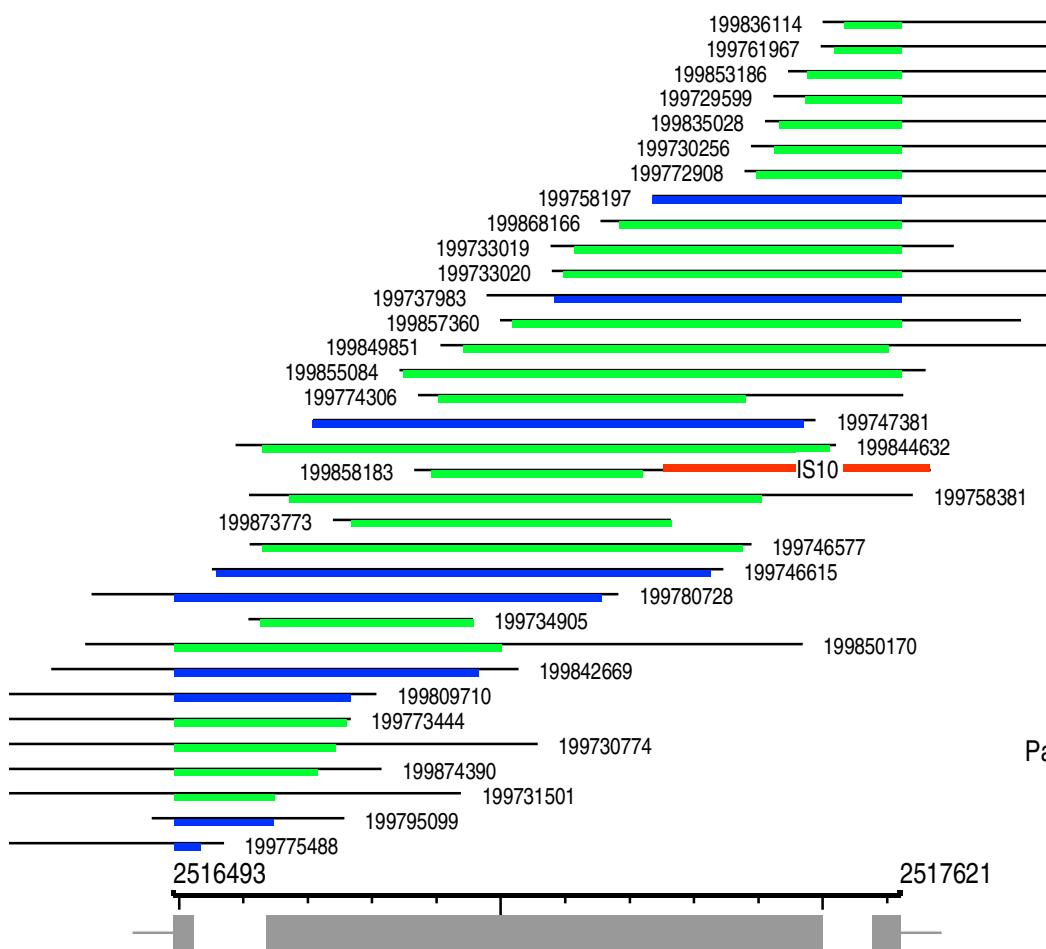
transcriptional_regulator,_LysR_family

TX160488 *Pseudomonas putida* kt2440



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TX160488 *Pseudomonas putida* kt2440

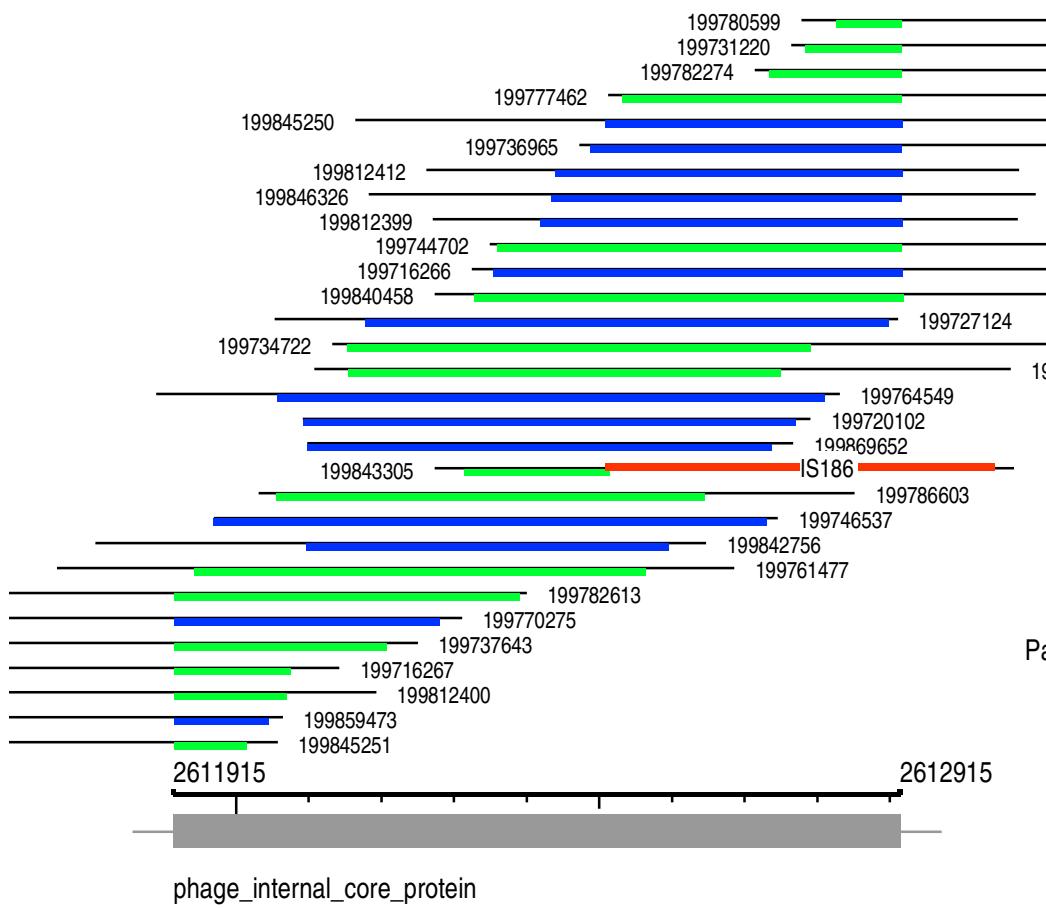


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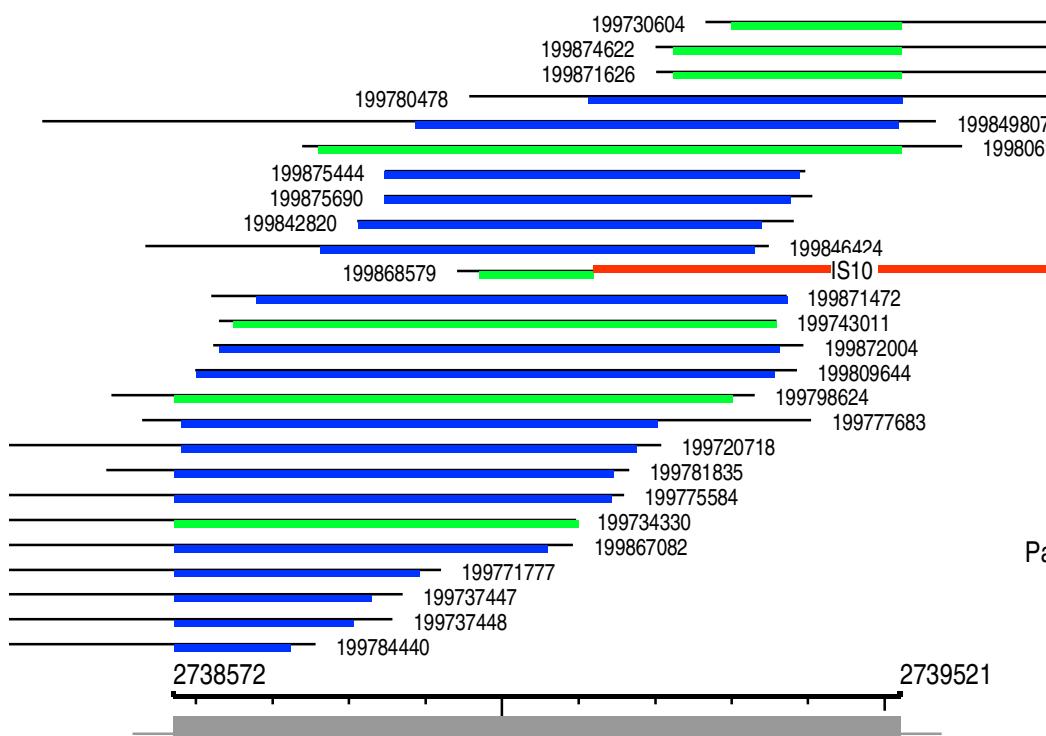
2-aminoethylphosphonate:pyruvate aminotranscriptional regulator, LysR_family

transcriptional regulator, AraC_family

TX160488 *Pseudomonas putida* kt2440



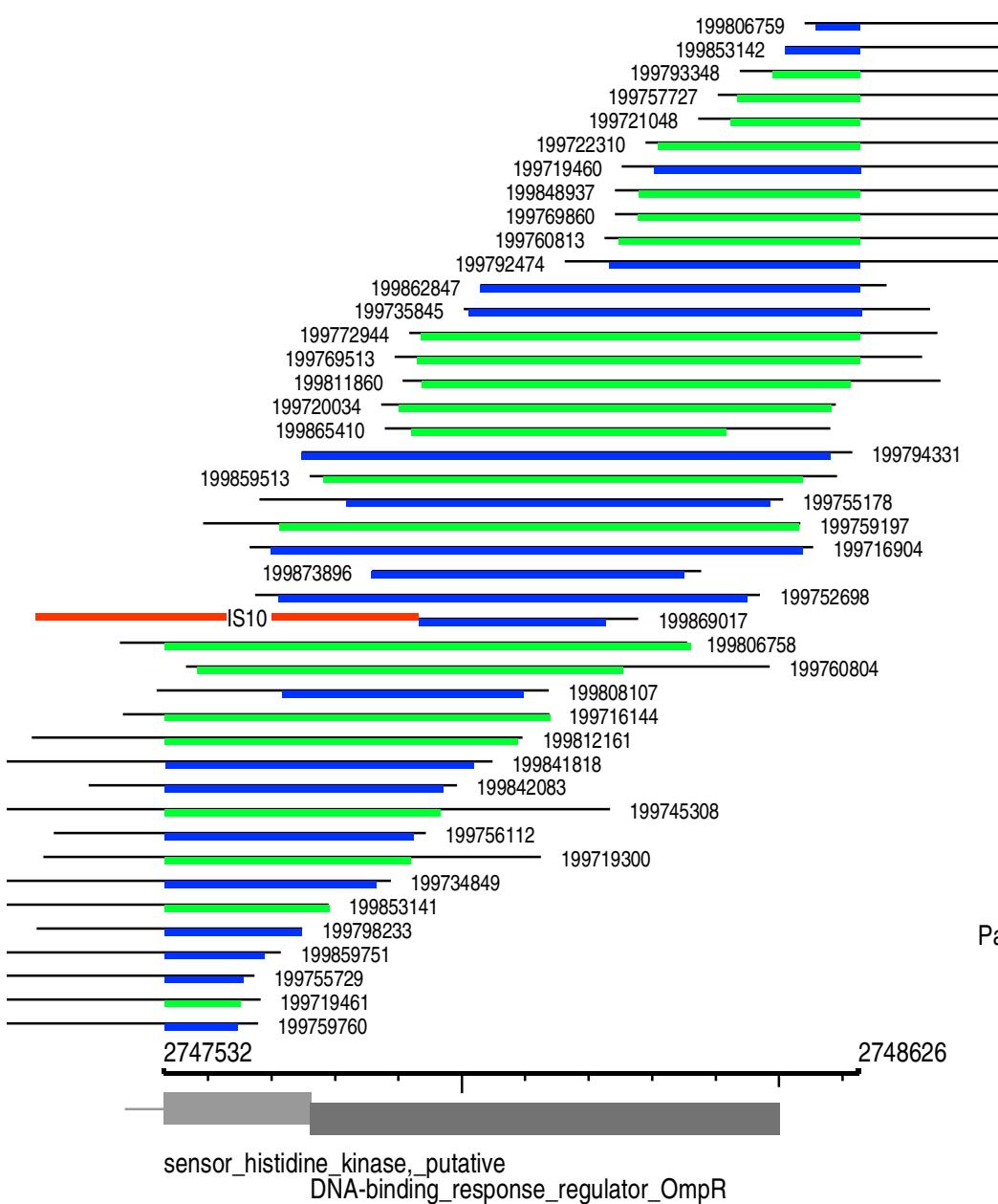
TX160488 *Pseudomonas putida* kt2440



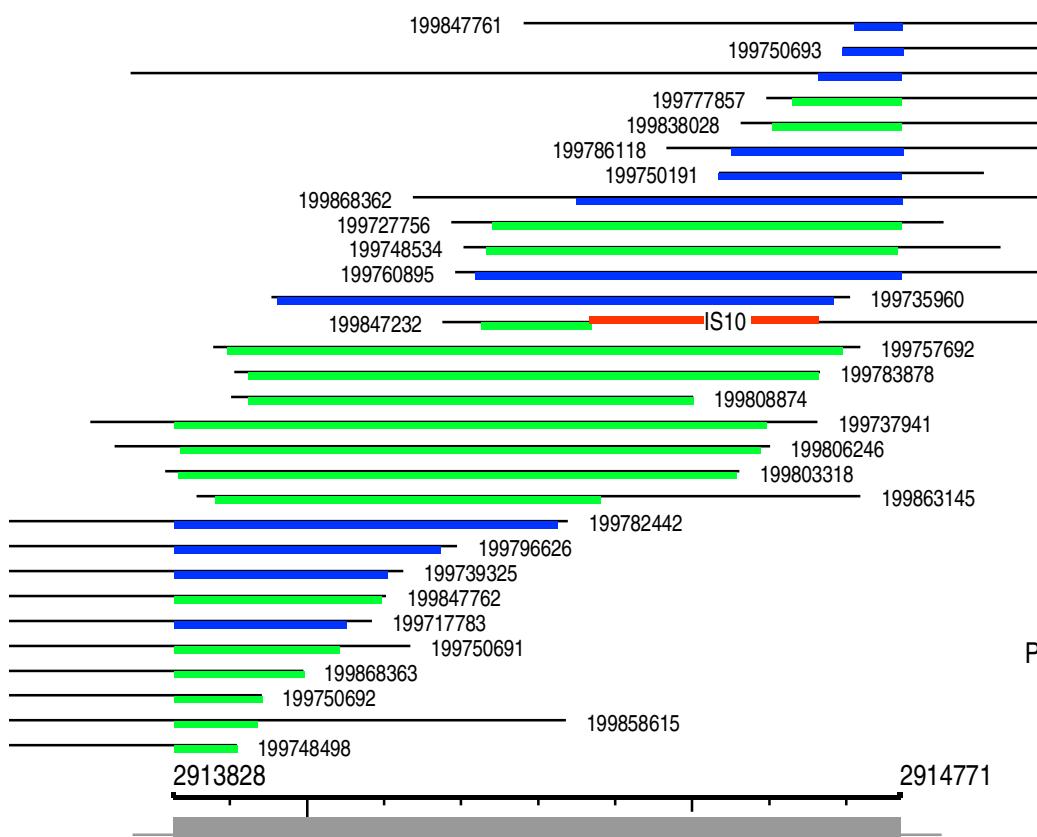
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leucine-rich_repeat_domain_protein

TX160488 *Pseudomonas putida* kt2440



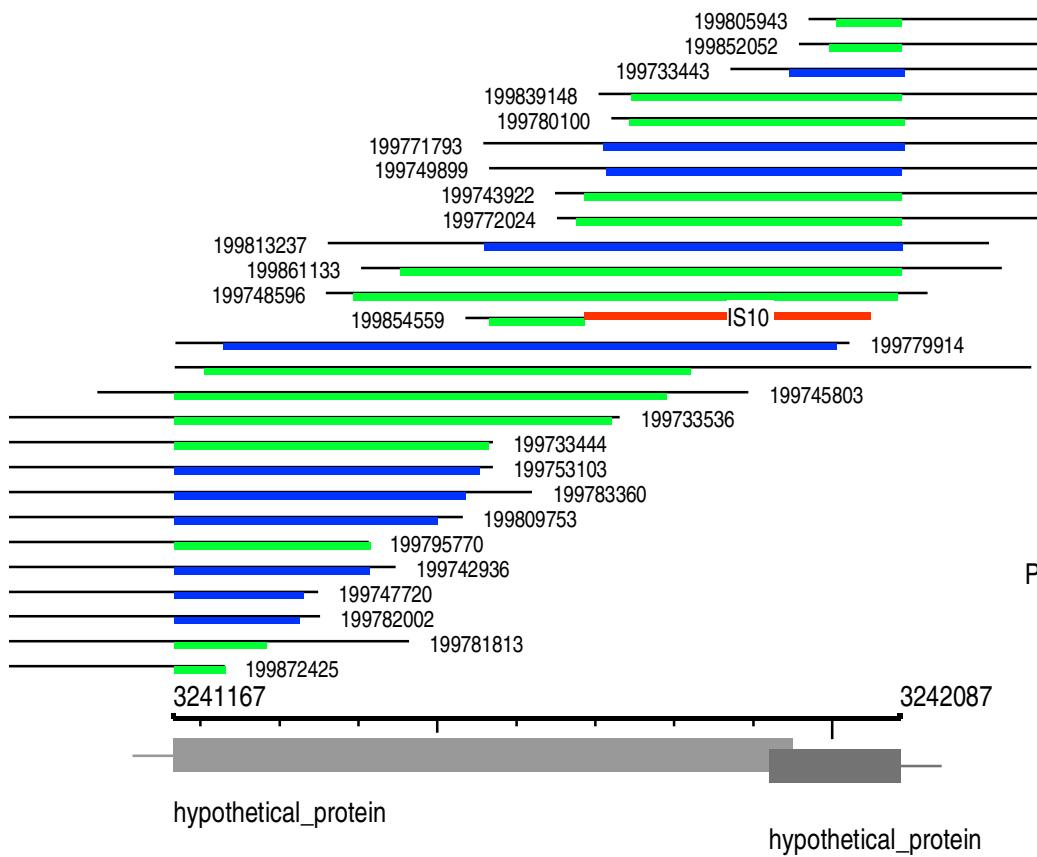
TX160488 *Pseudomonas putida* kt2440



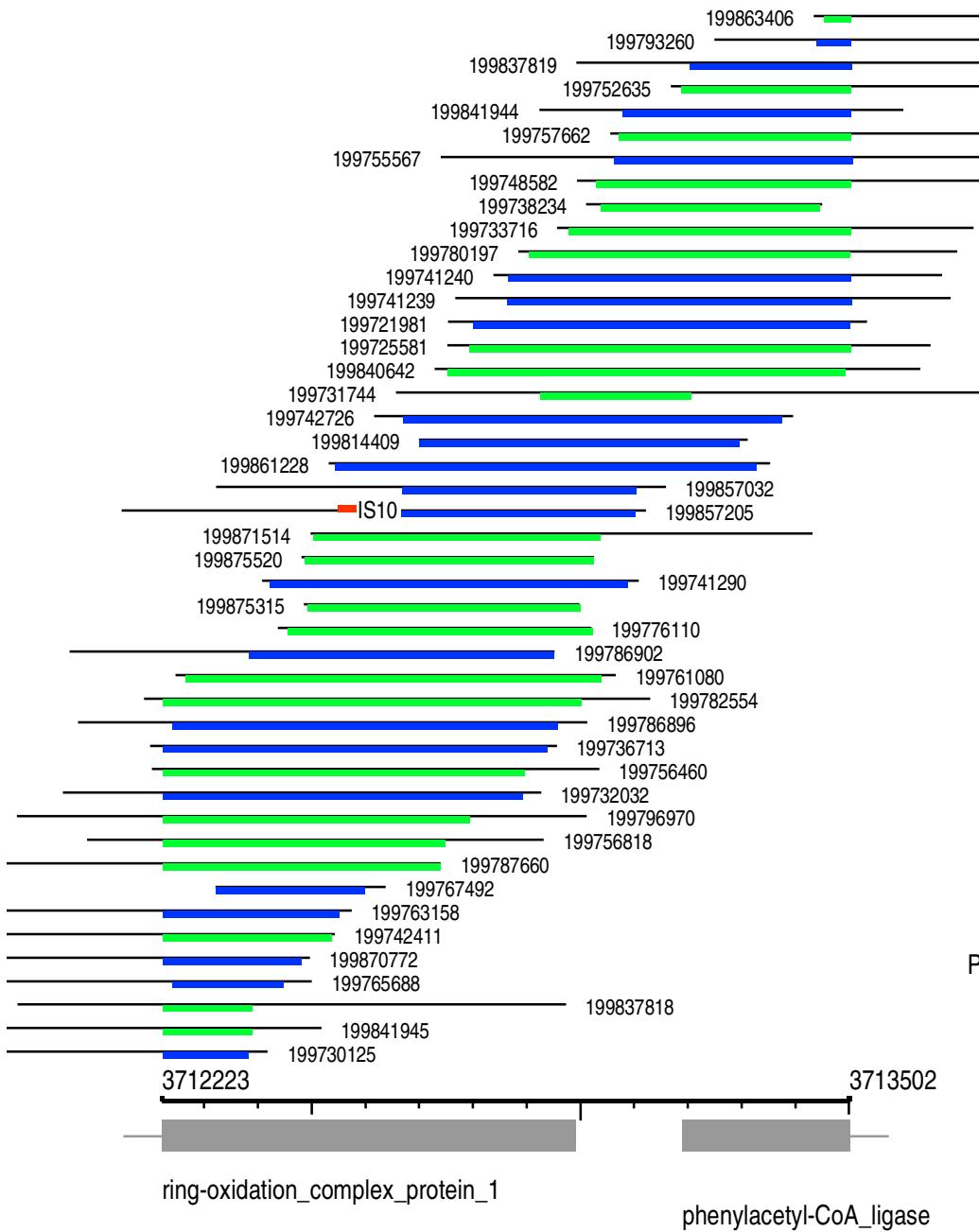
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secreted_hemolysin-type_calcium-binding_

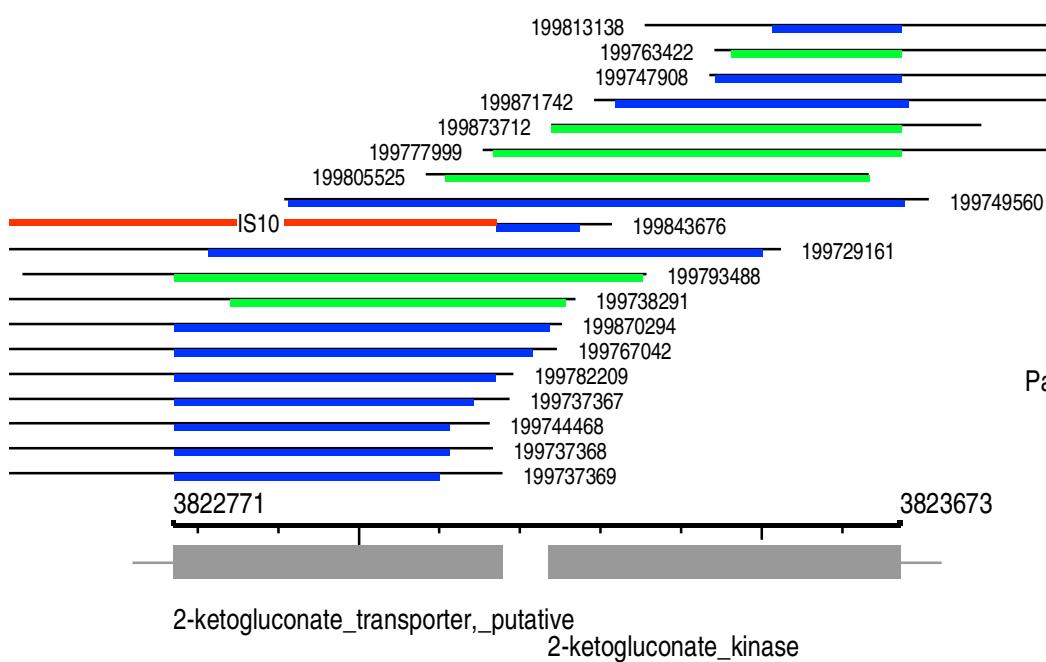
TX160488 *Pseudomonas putida* kt2440



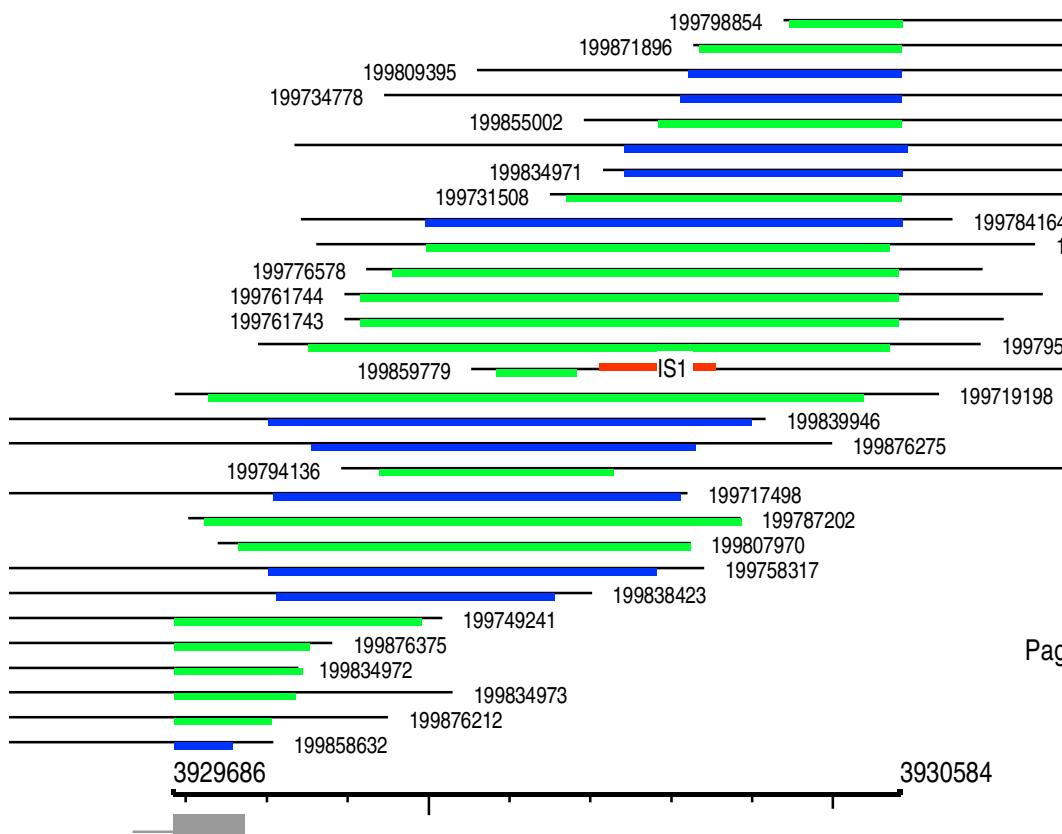
TX160488 *Pseudomonas putida* kt2440



TX160488 *Pseudomonas putida* kt2440



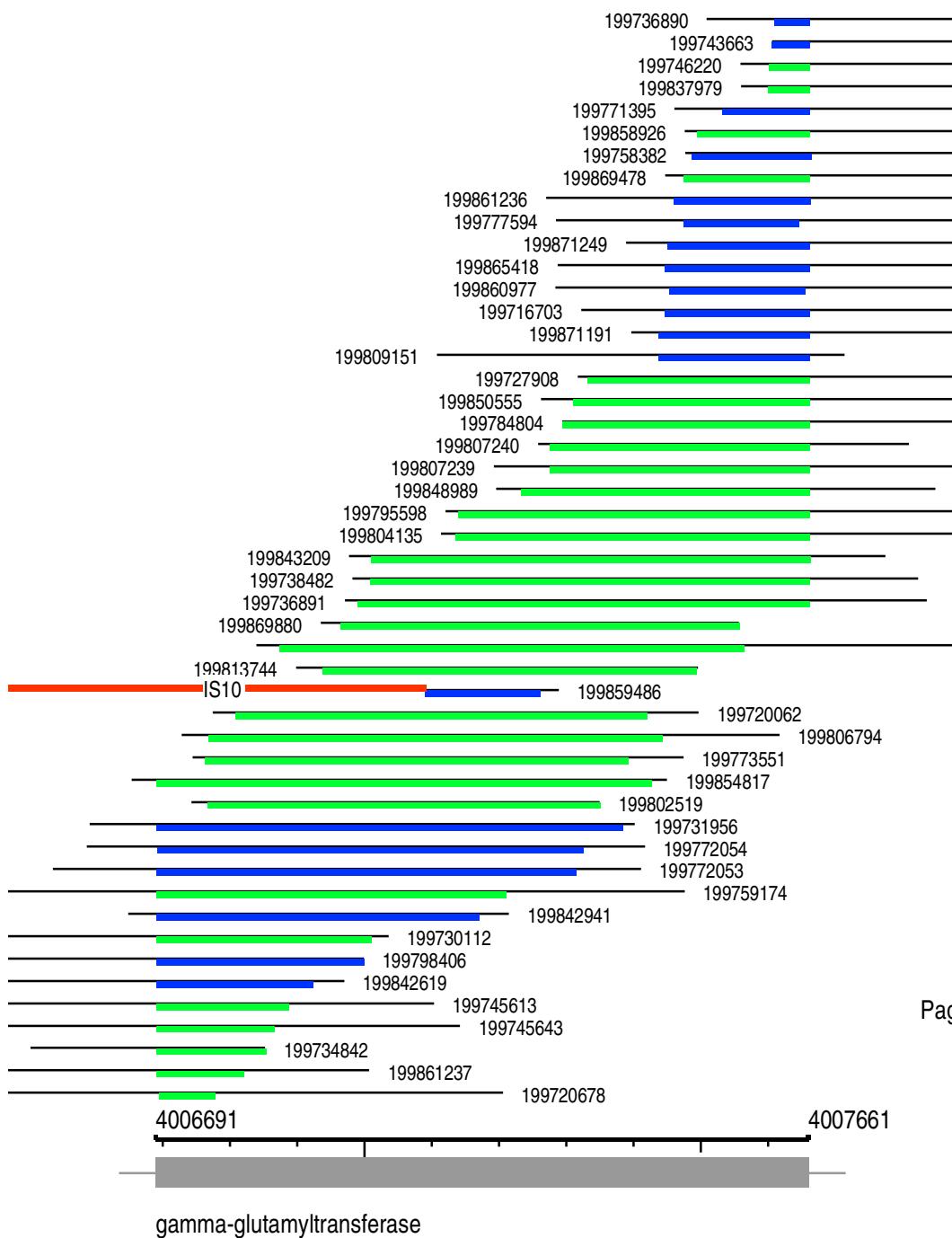
TX160488 *Pseudomonas putida* kt2440



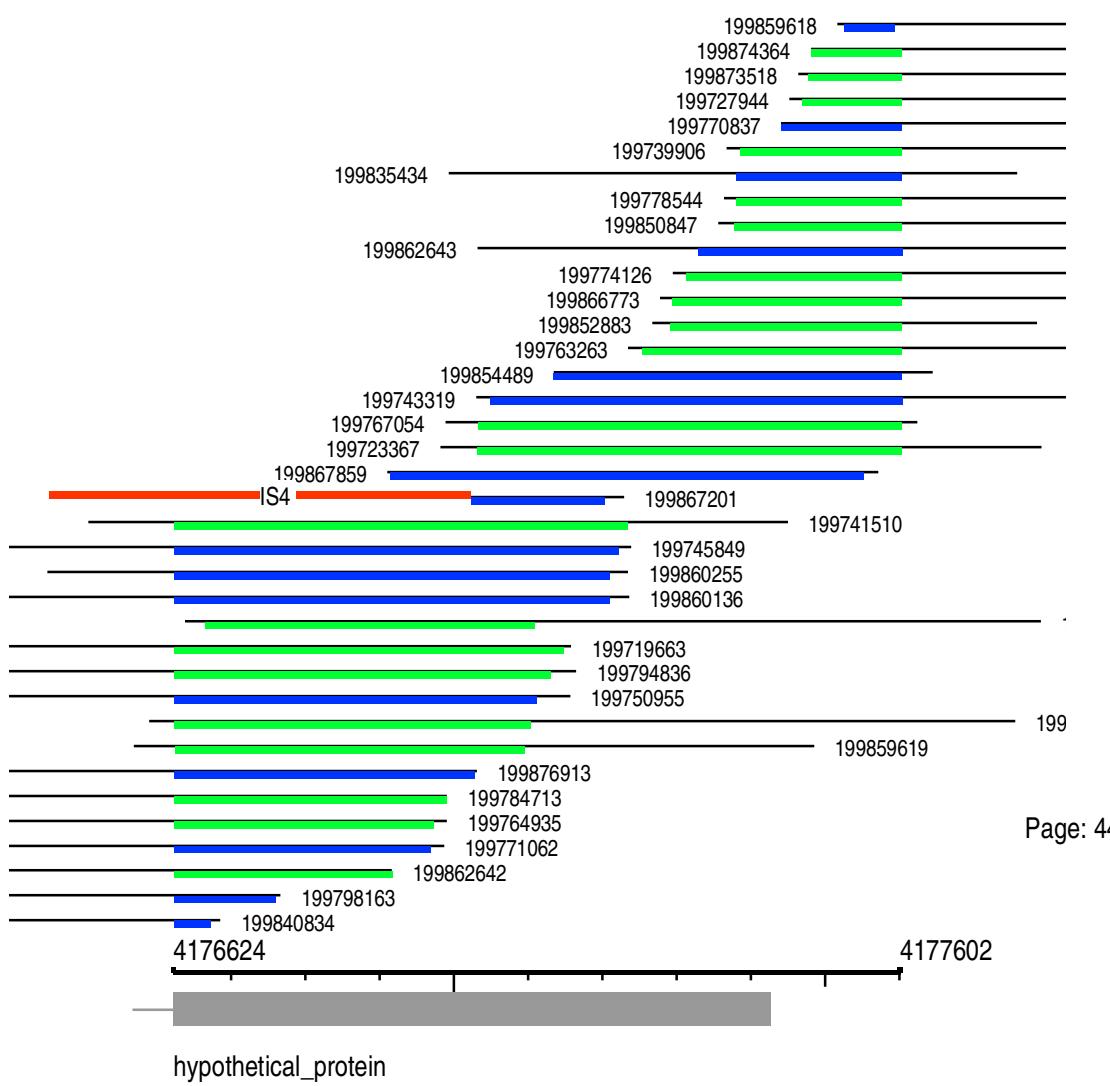
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hypothetical_protein

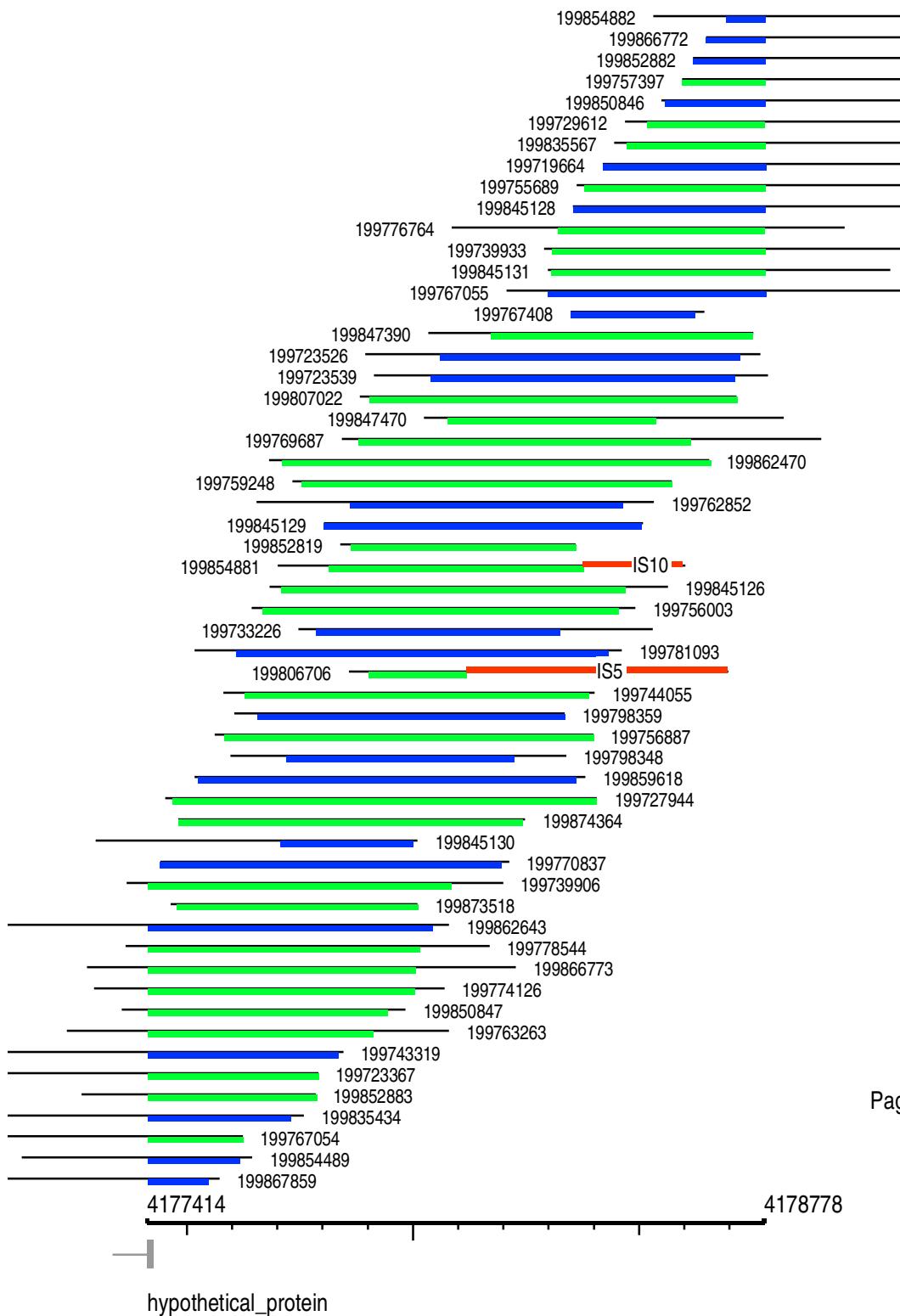
TX160488 *Pseudomonas putida* kt2440



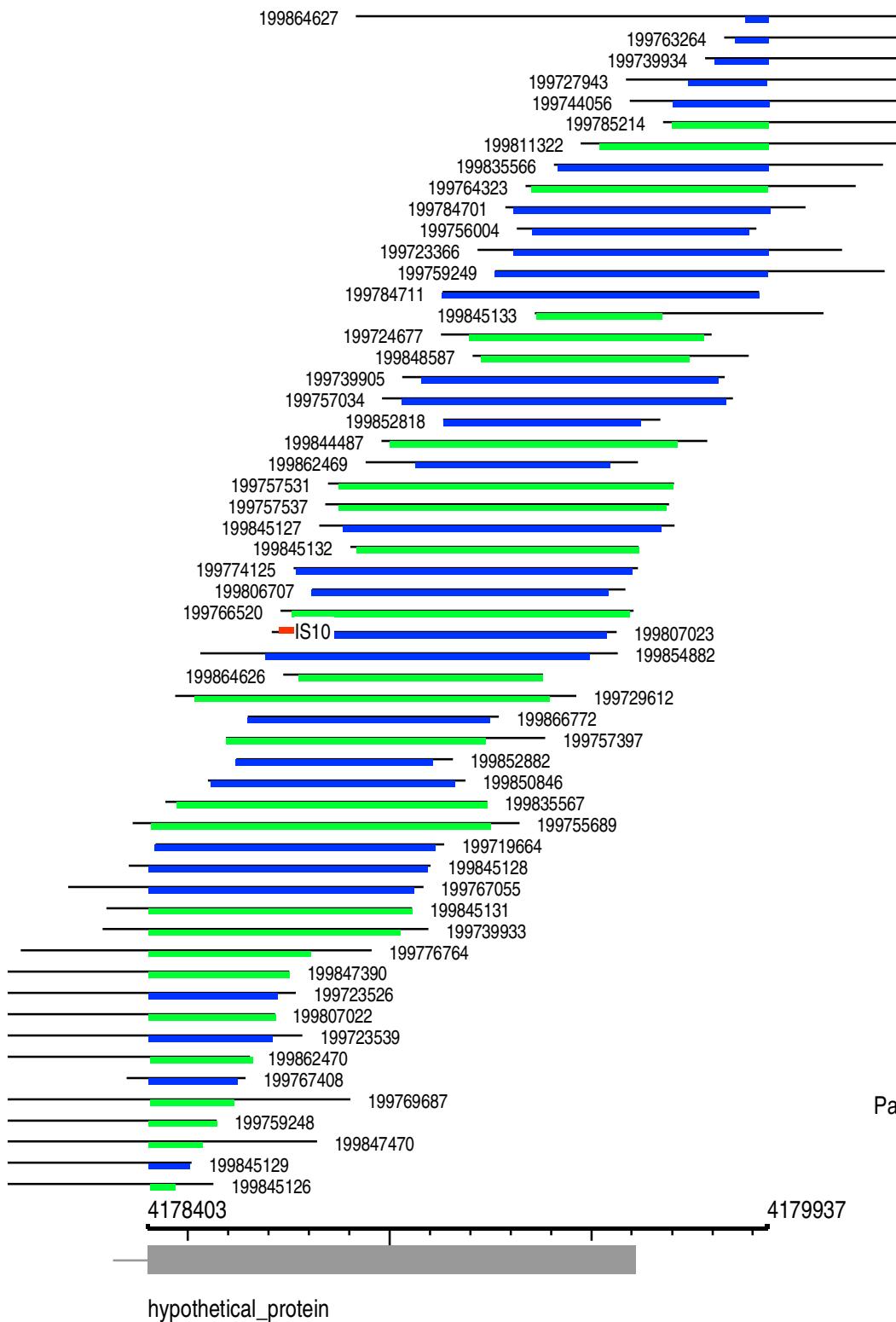
TX160488 *Pseudomonas putida* kt2440



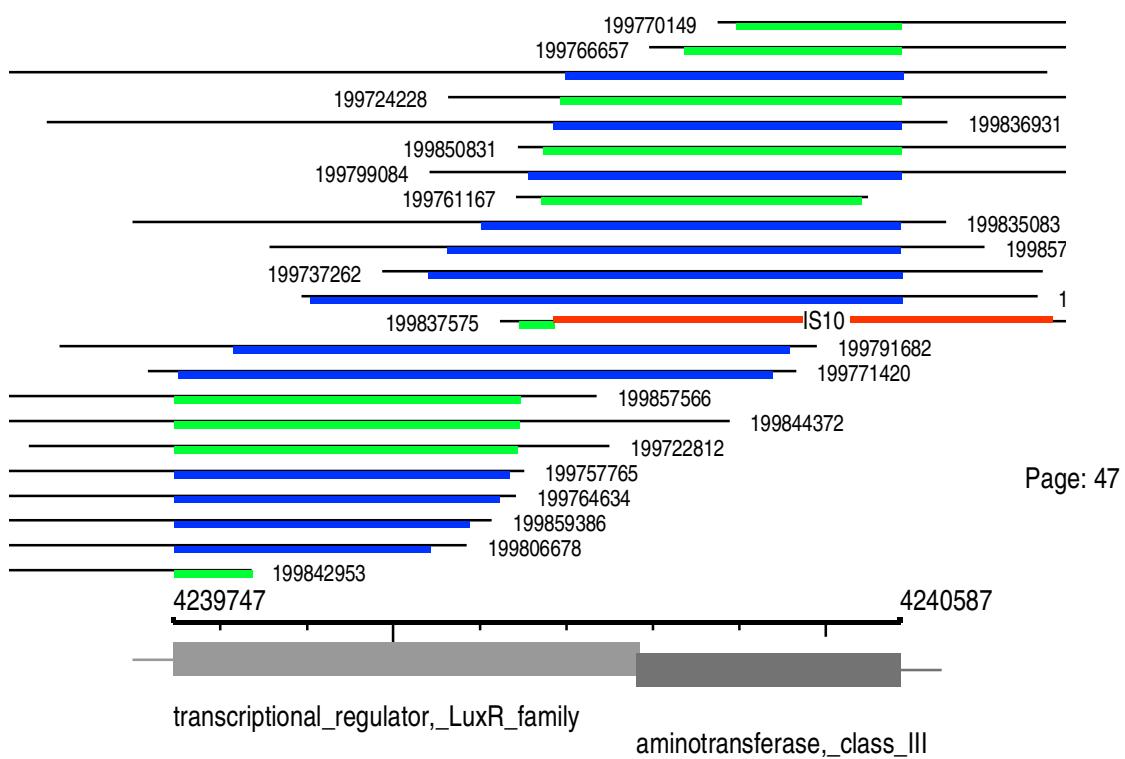
TX160488 *Pseudomonas putida* kt2440



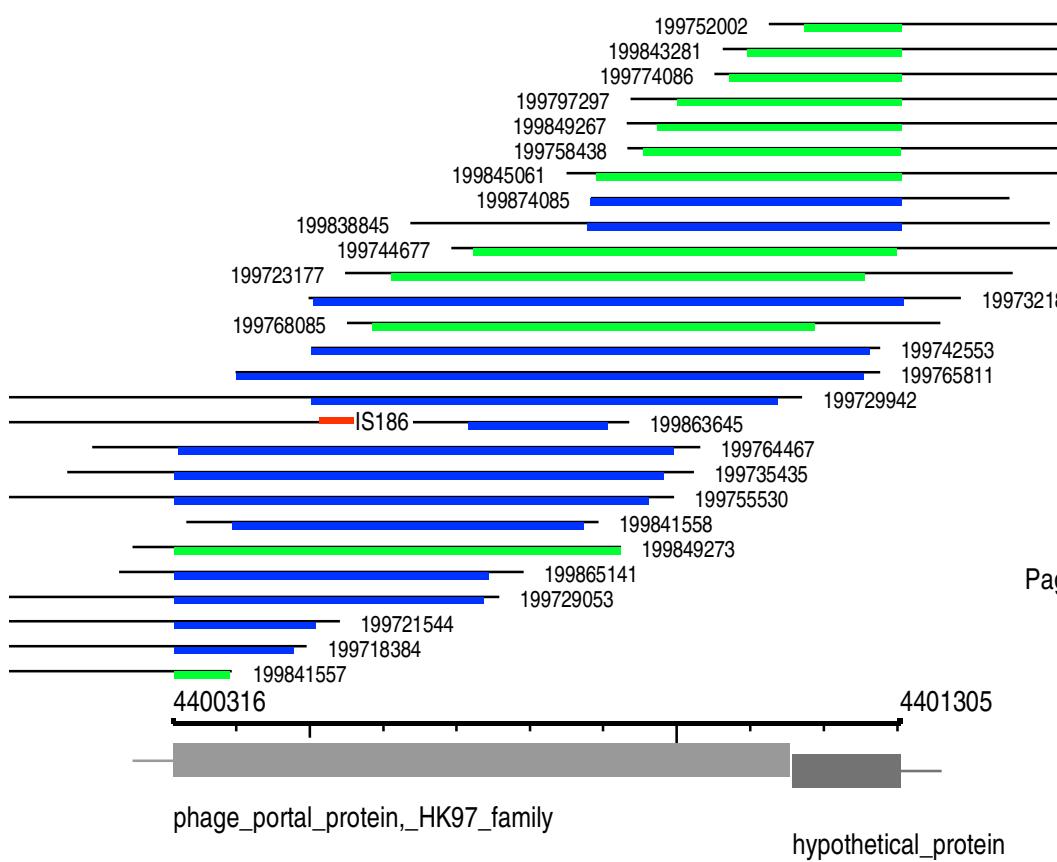
TX160488 *Pseudomonas putida* kt2440



TX160488 *Pseudomonas putida* kt2440

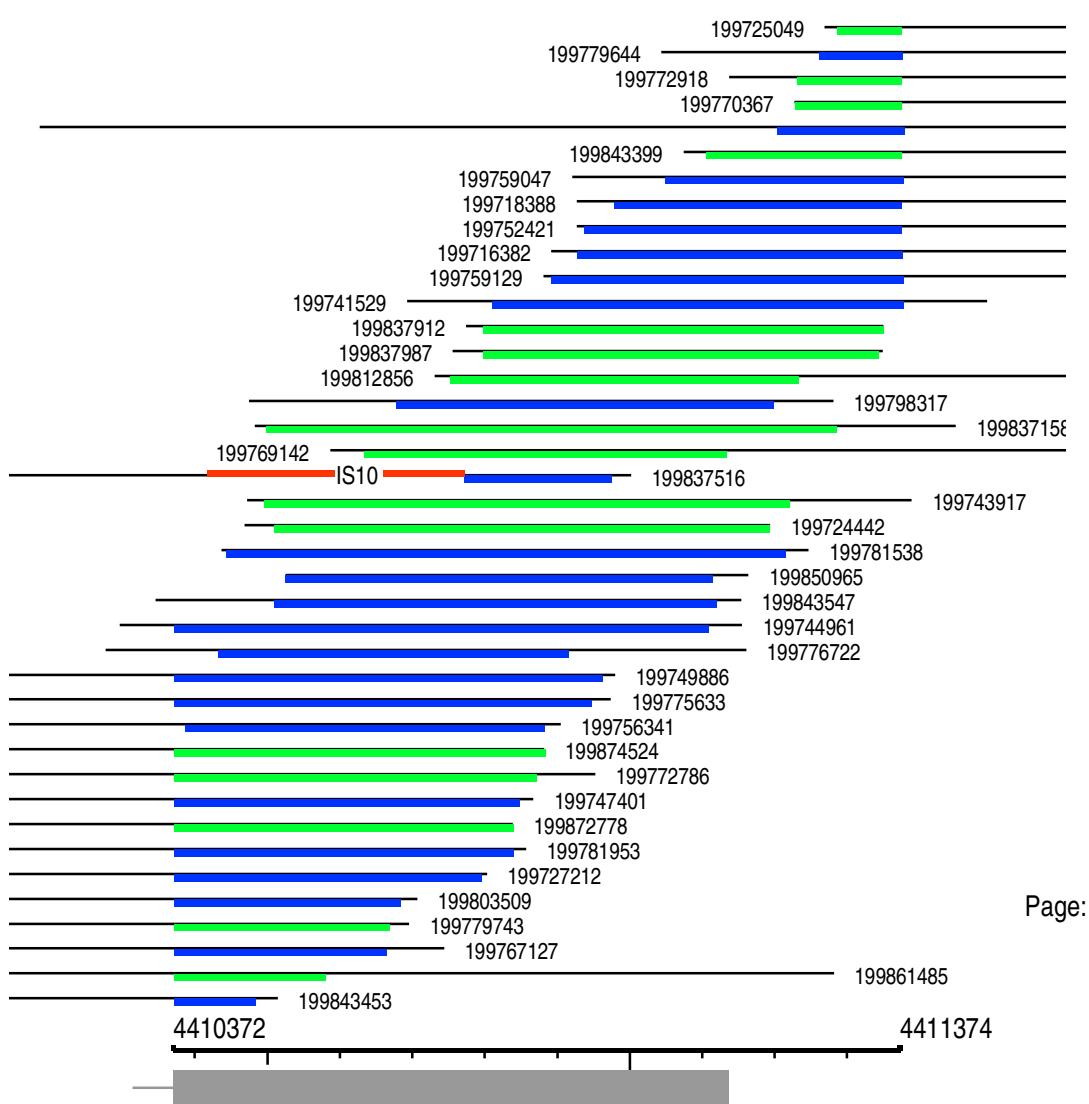


TX160488 *Pseudomonas putida* kt2440



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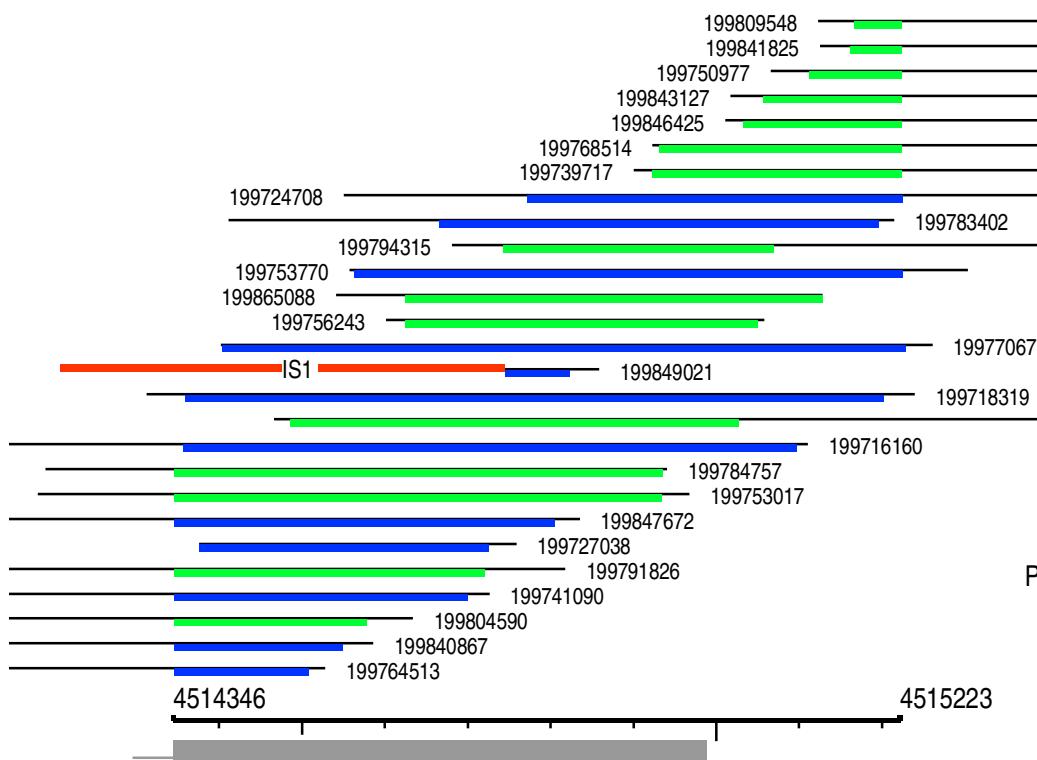
TX160488 *Pseudomonas putida* kt2440



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phage_replication_protein_O,_putative

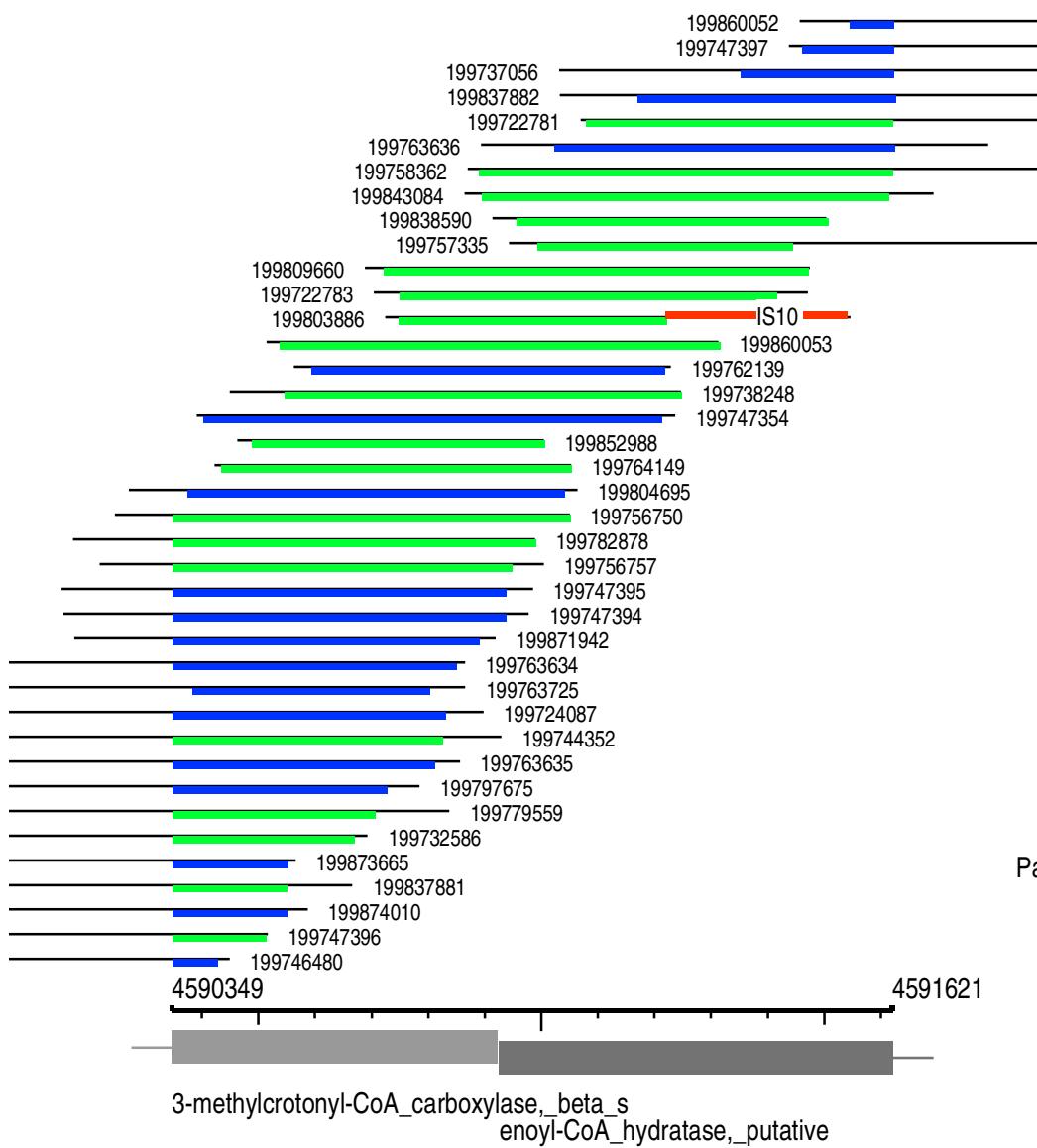
TX160488 *Pseudomonas putida* kt2440



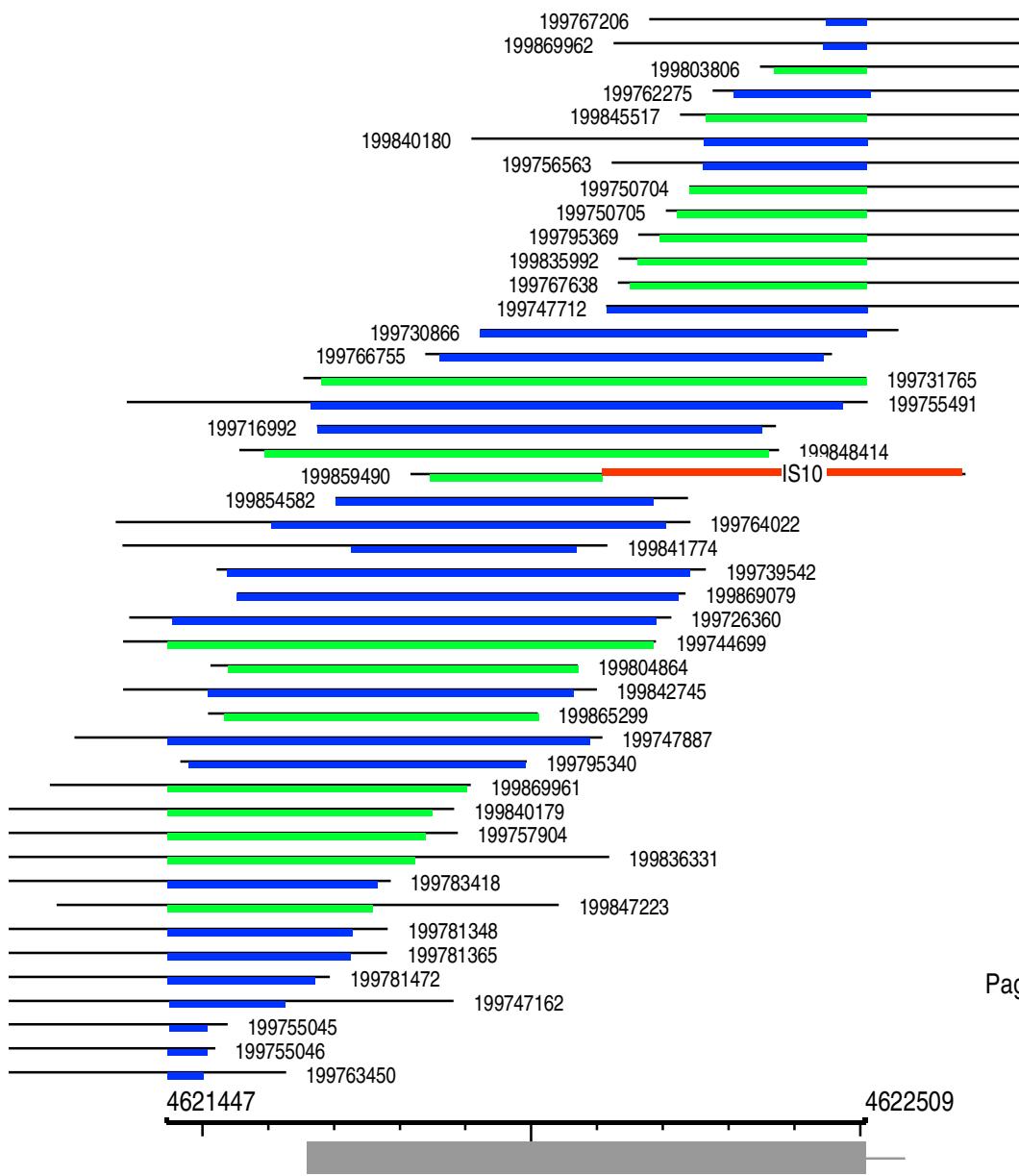
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cell_division_protein_FtsK

TX160488 *Pseudomonas putida* kt2440



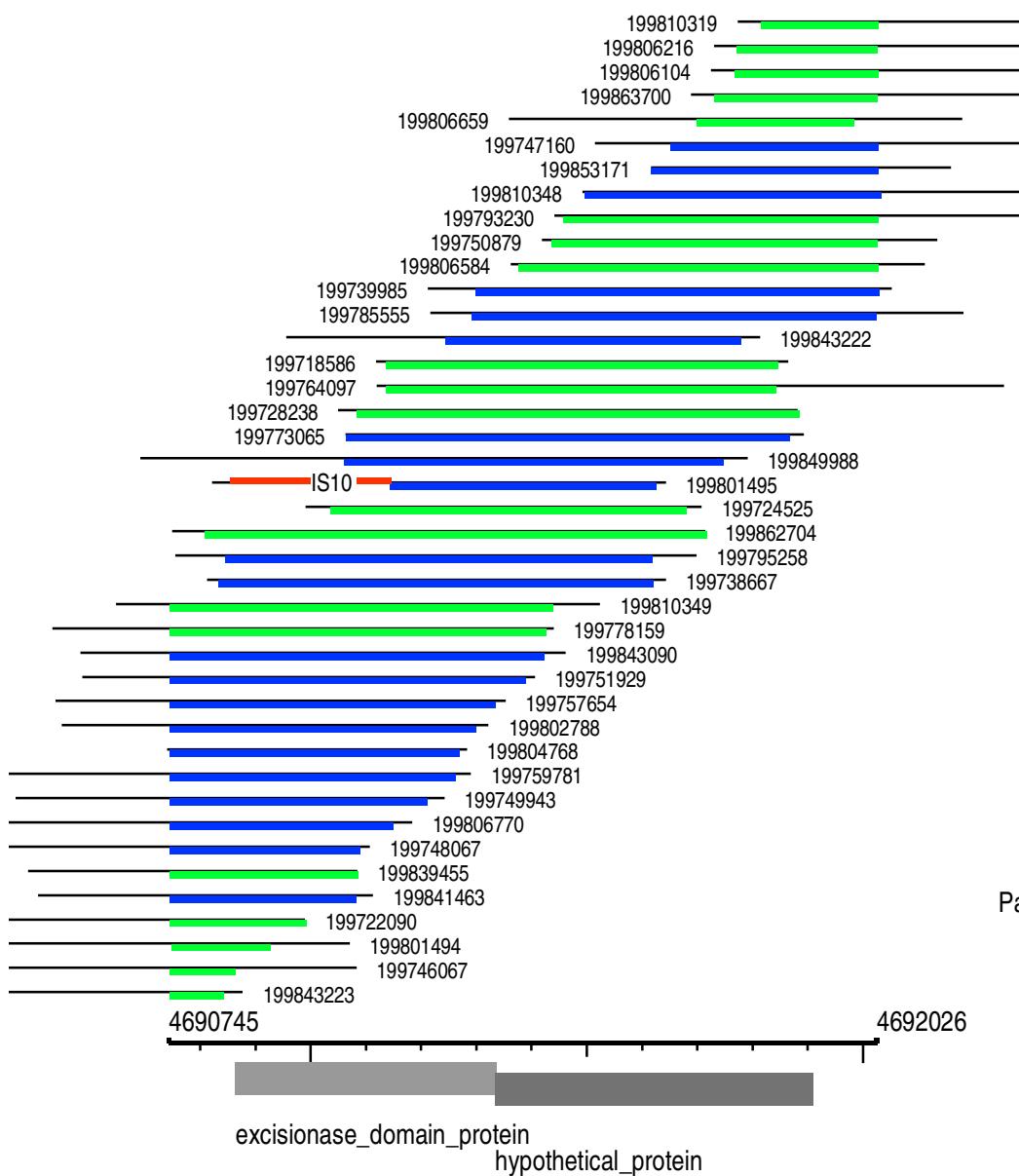
TX160488 *Pseudomonas putida* kt2440



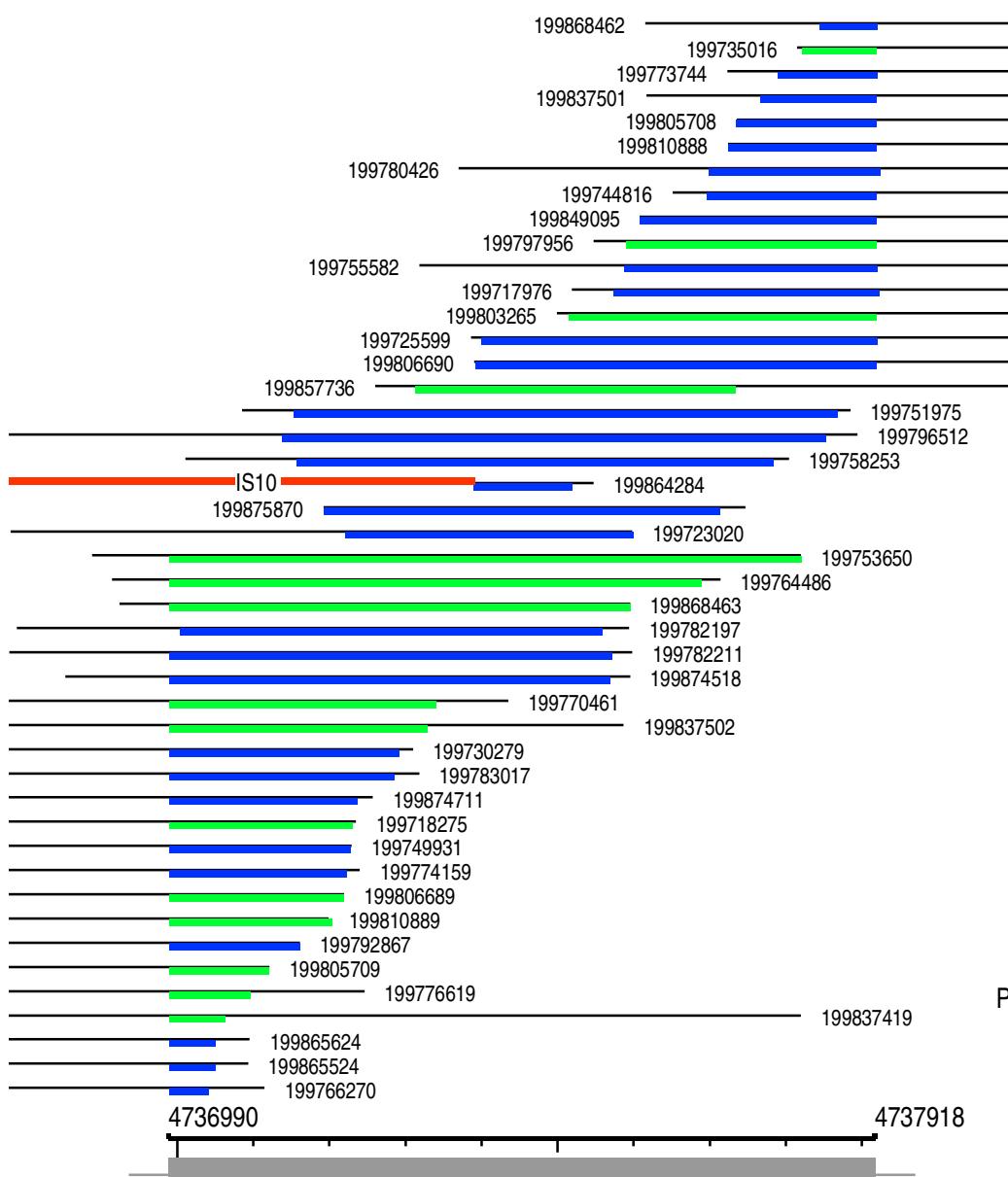
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This_region_contains_a_gene_with_one_or_

TX160488 *Pseudomonas putida* kt2440



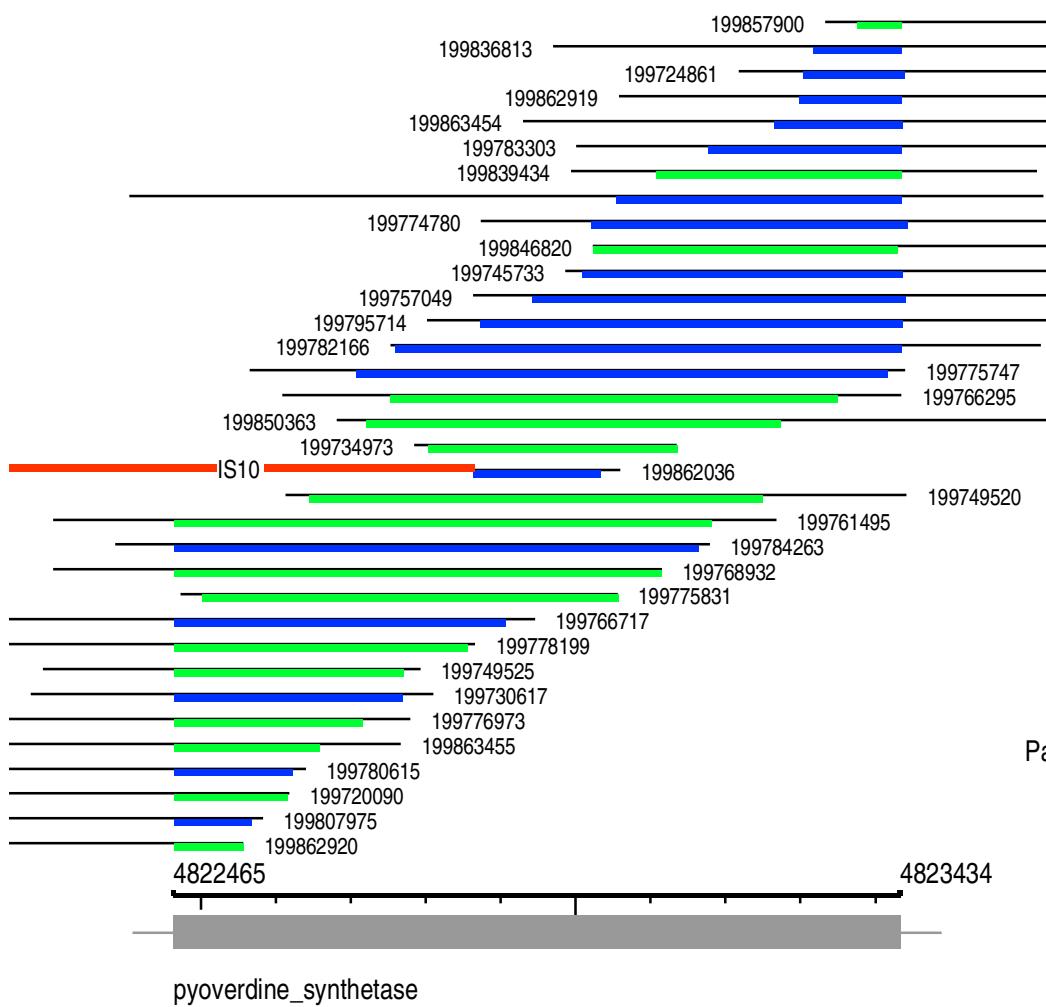
TX160488 *Pseudomonas putida* kt2440



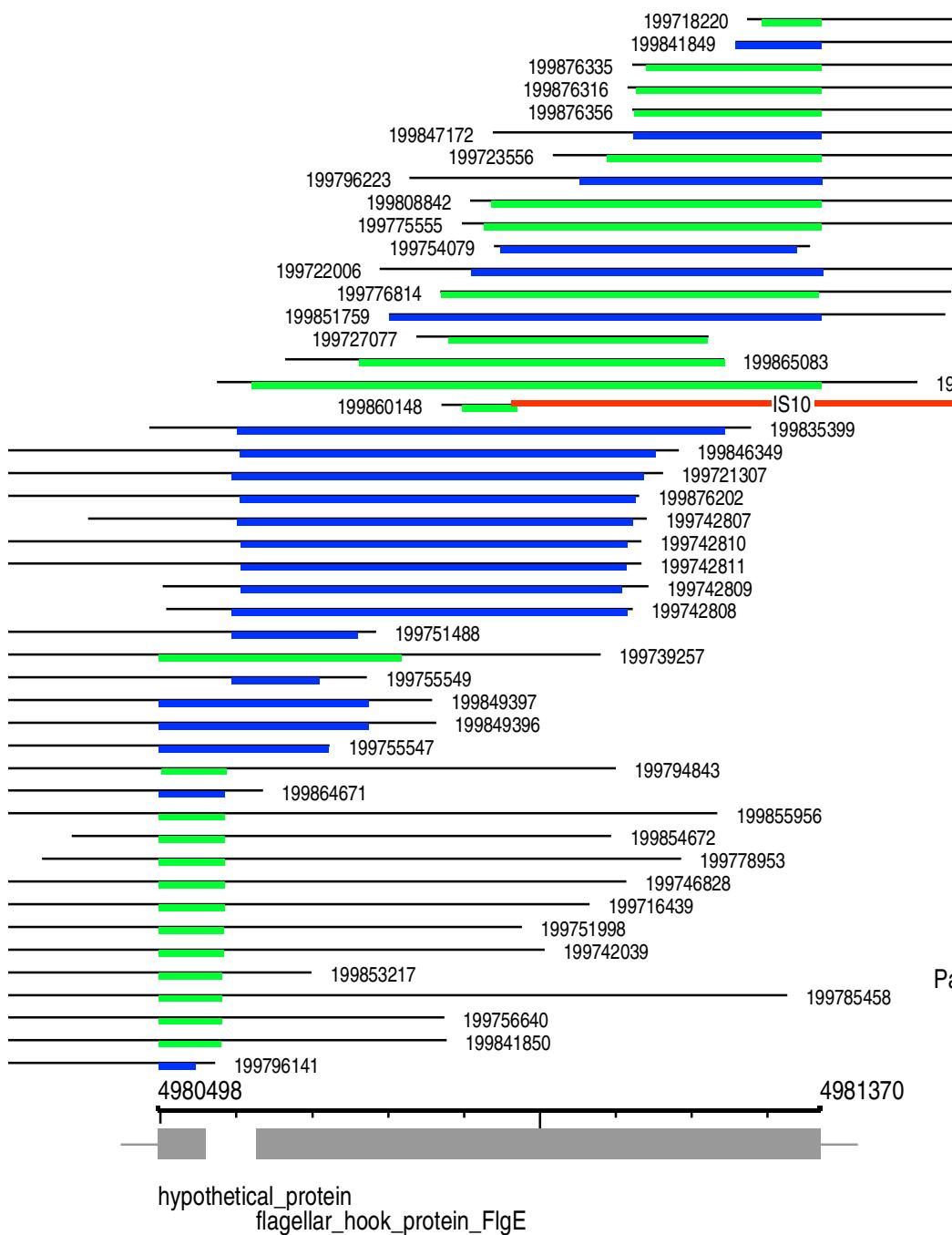
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succinate_dehydrogenase,_flavoprotein_su

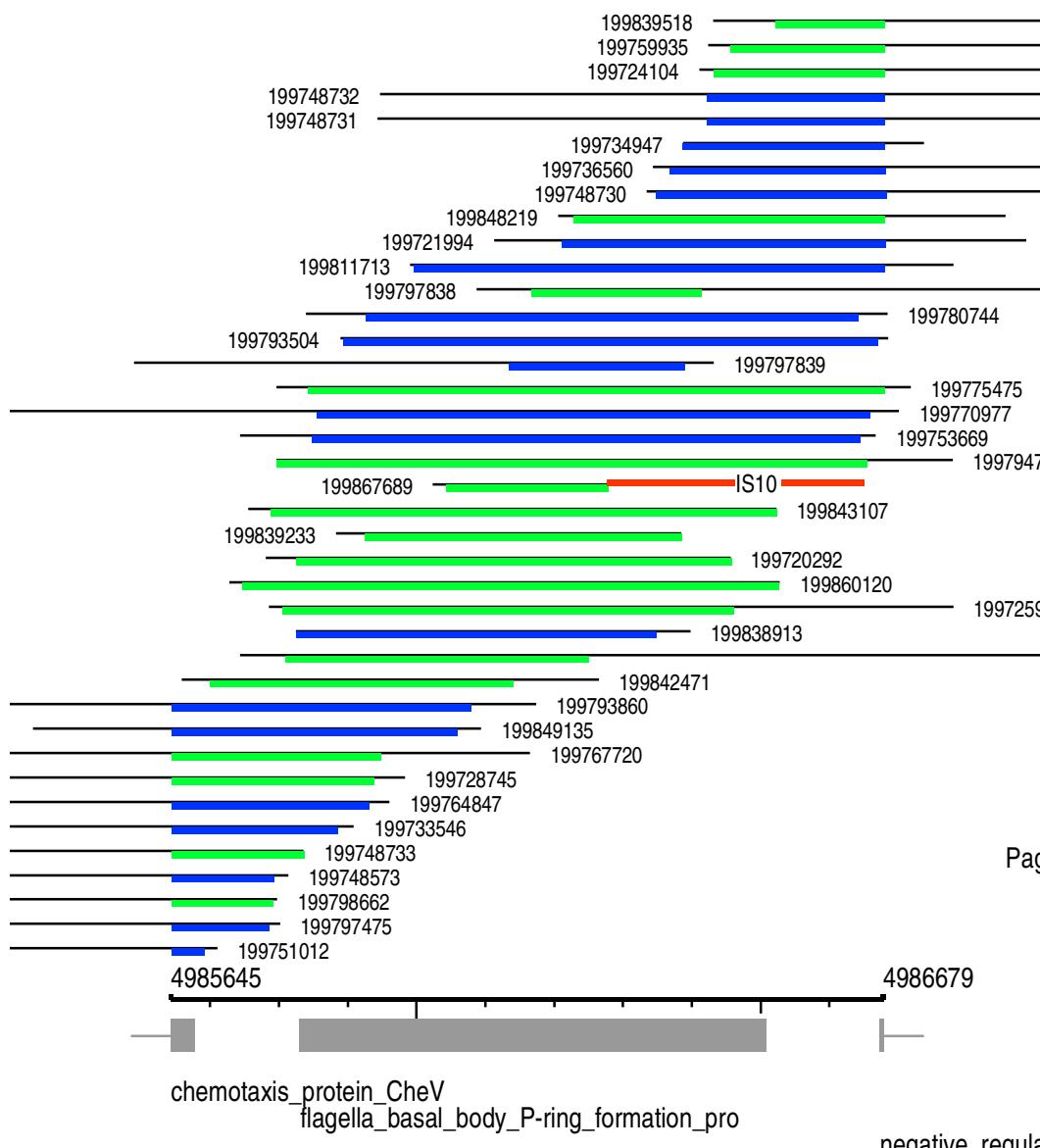
TX160488 *Pseudomonas putida* kt2440



TX160488 *Pseudomonas putida* kt2440



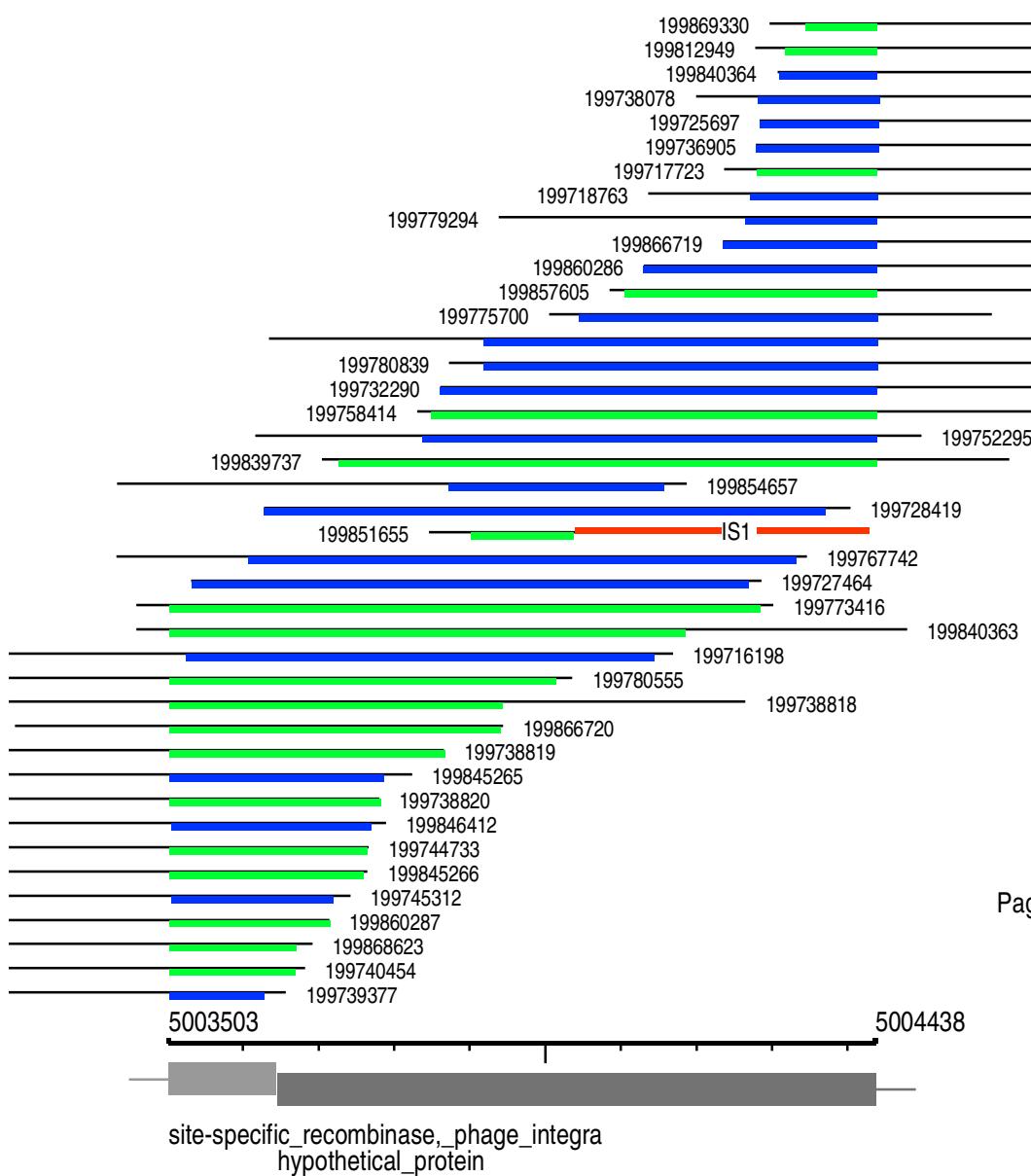
TX160488 *Pseudomonas putida* kt2440



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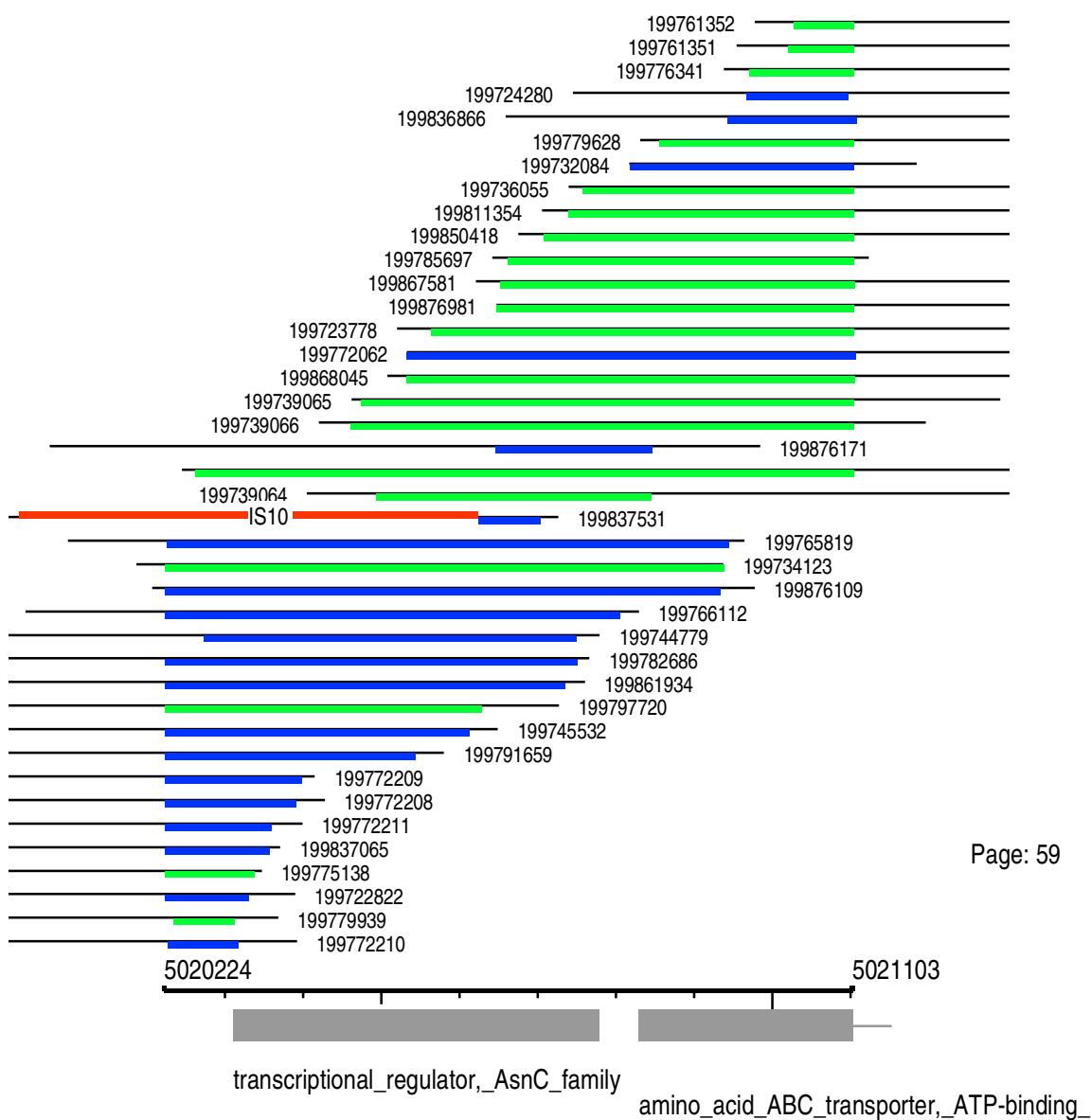
negative_regulator_of_flagellin_synthesis

TX160488 *Pseudomonas putida* kt2440

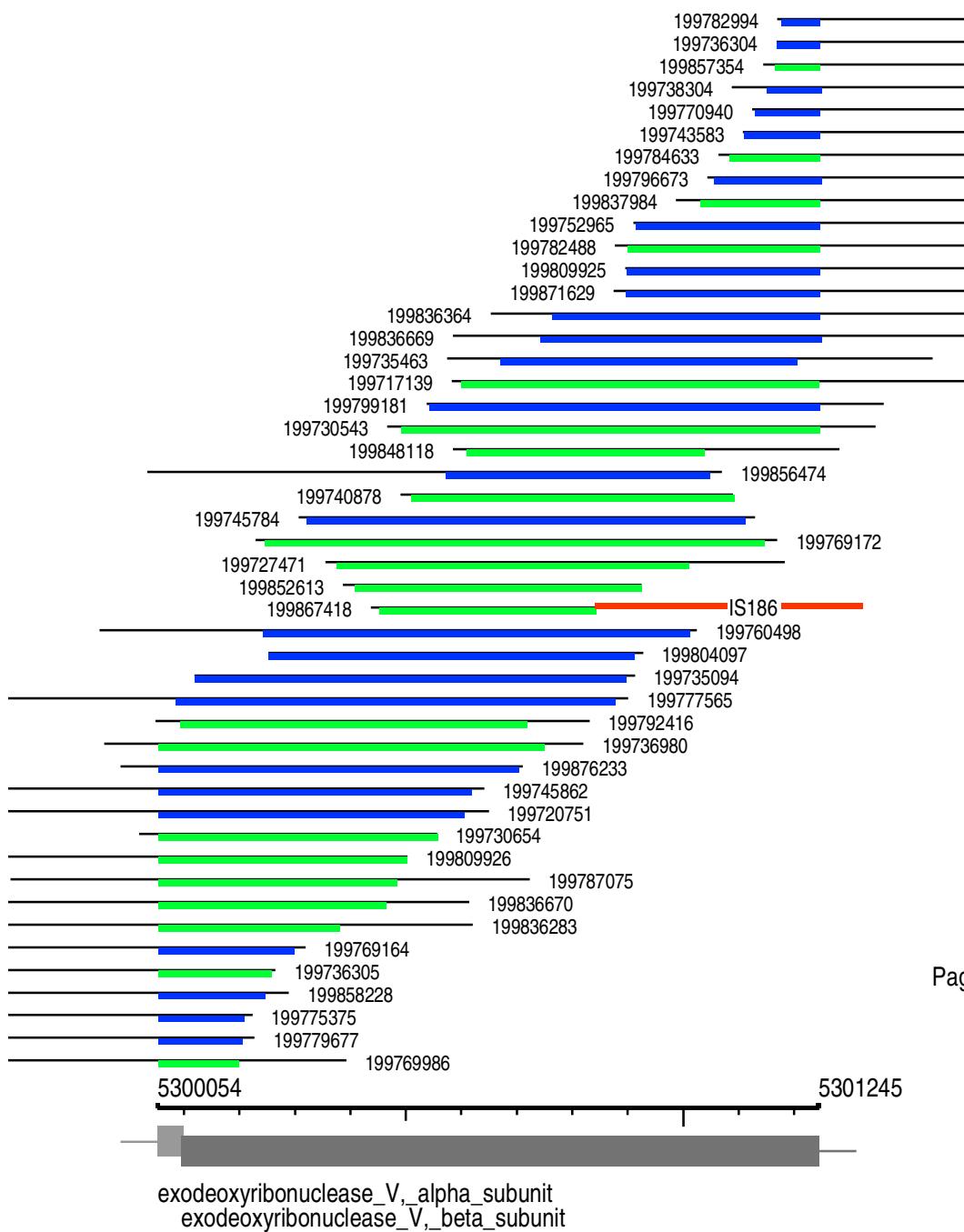


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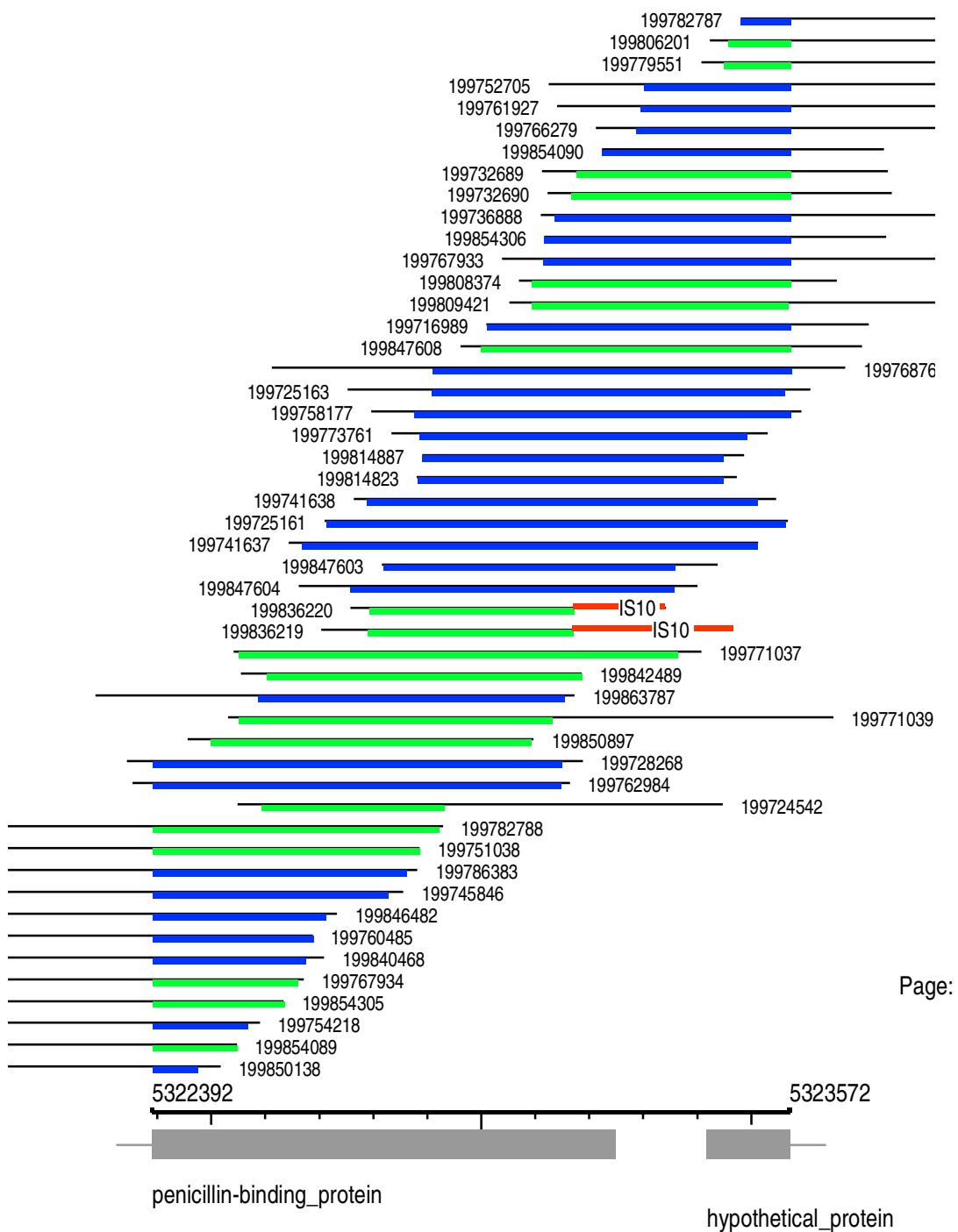
TX160488 *Pseudomonas putida* kt2440



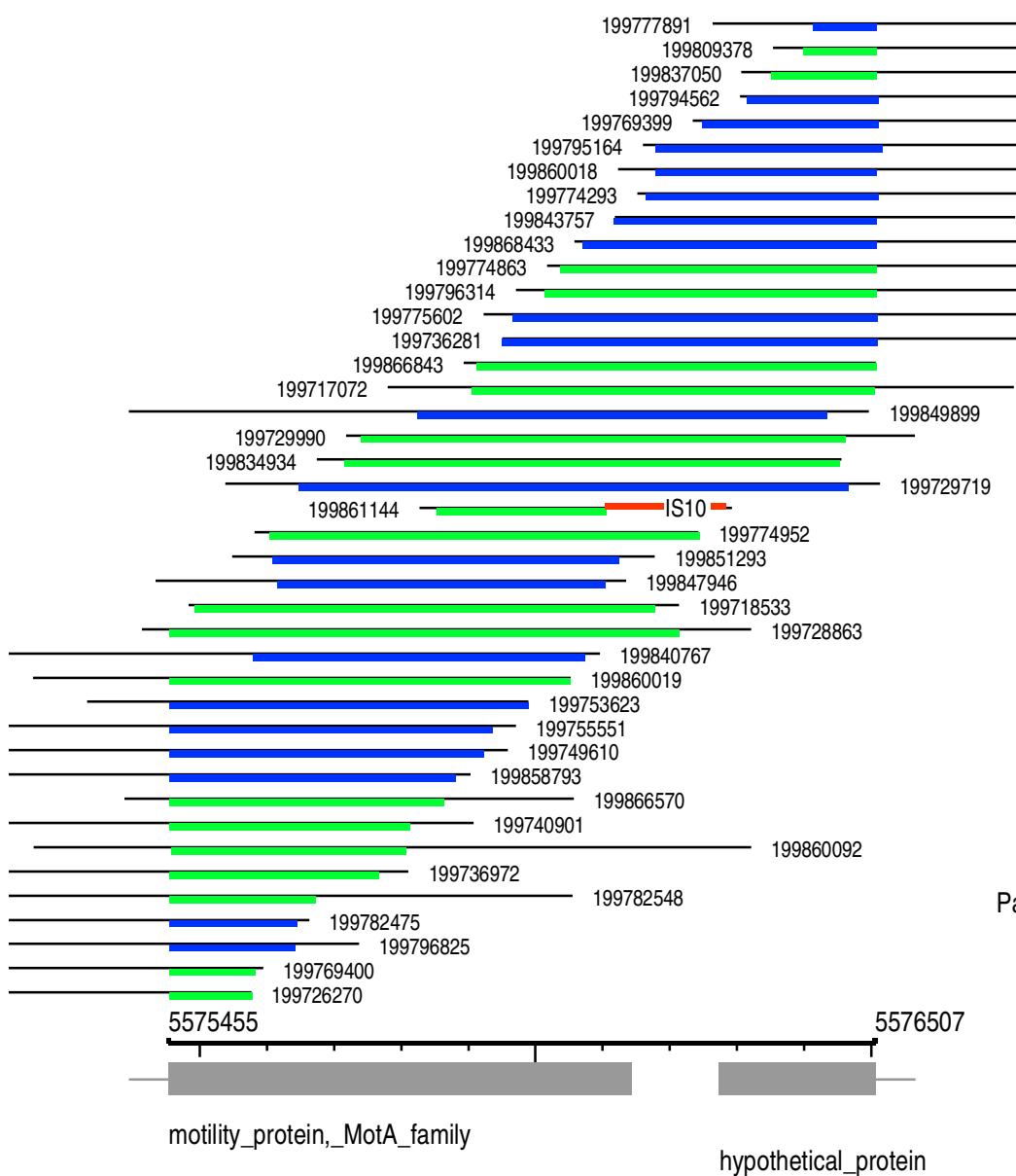
TX160488 *Pseudomonas putida* kt2440



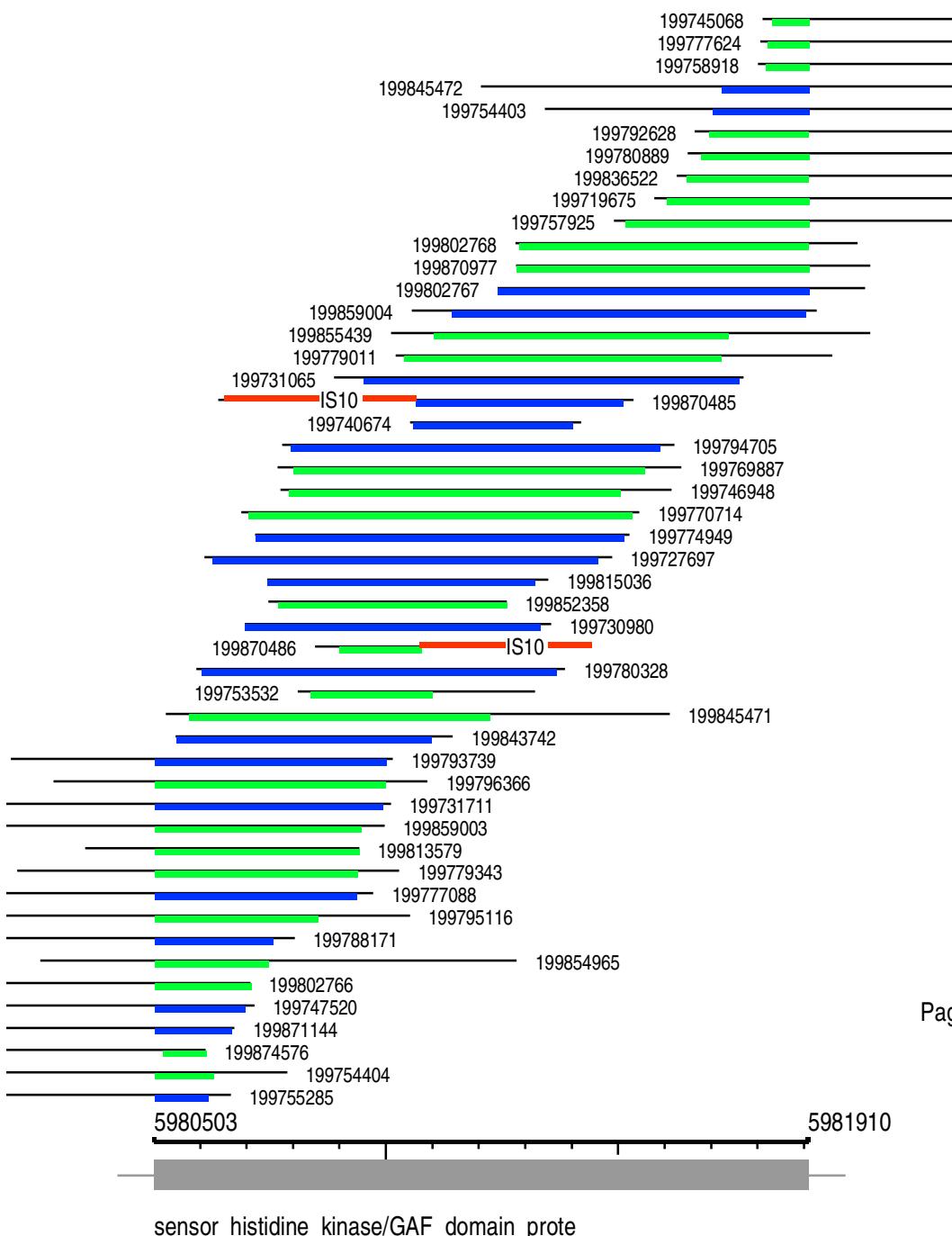
TX160488 *Pseudomonas putida* kt2440



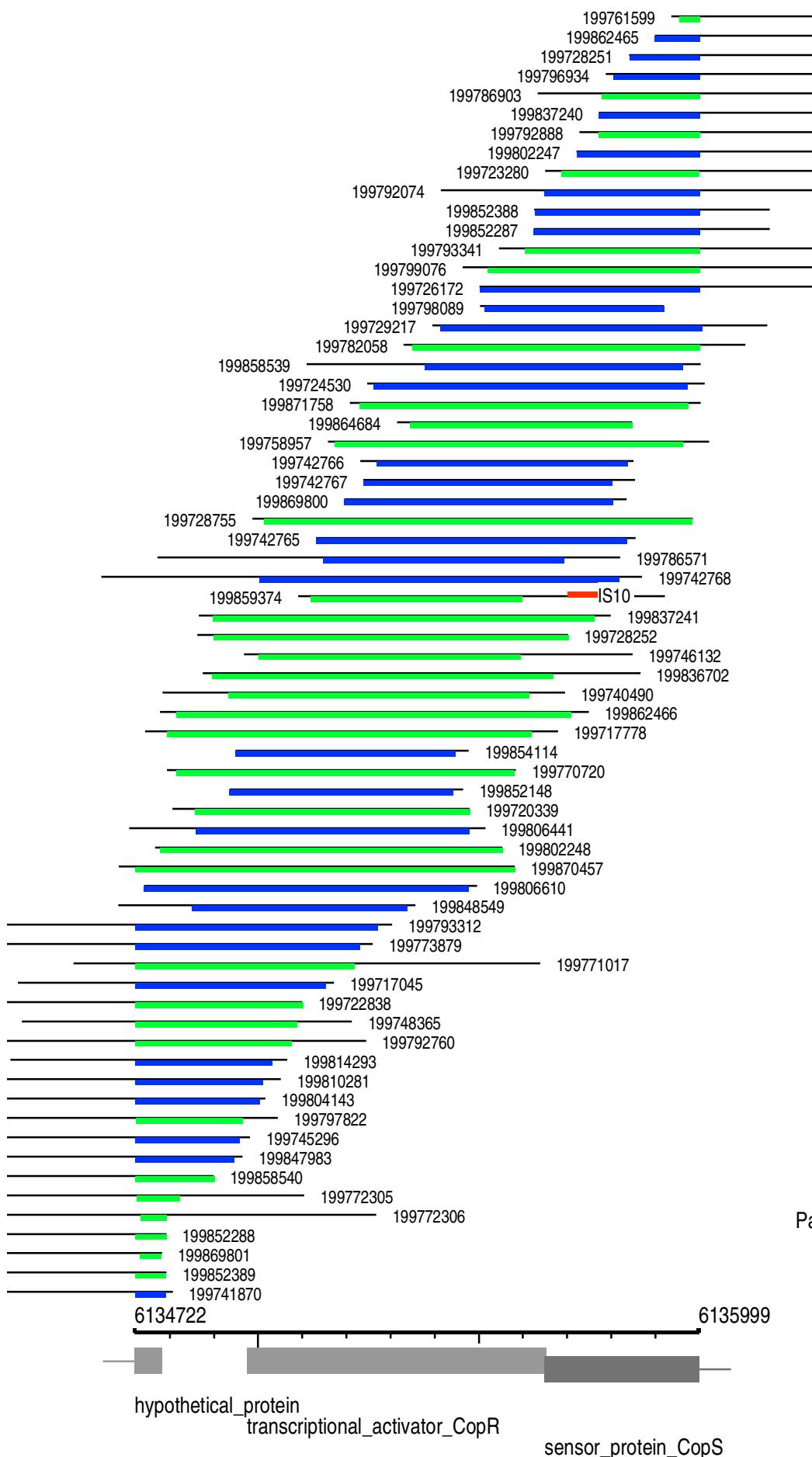
TX160488 *Pseudomonas putida* kt2440



TX160488 *Pseudomonas putida* kt2440

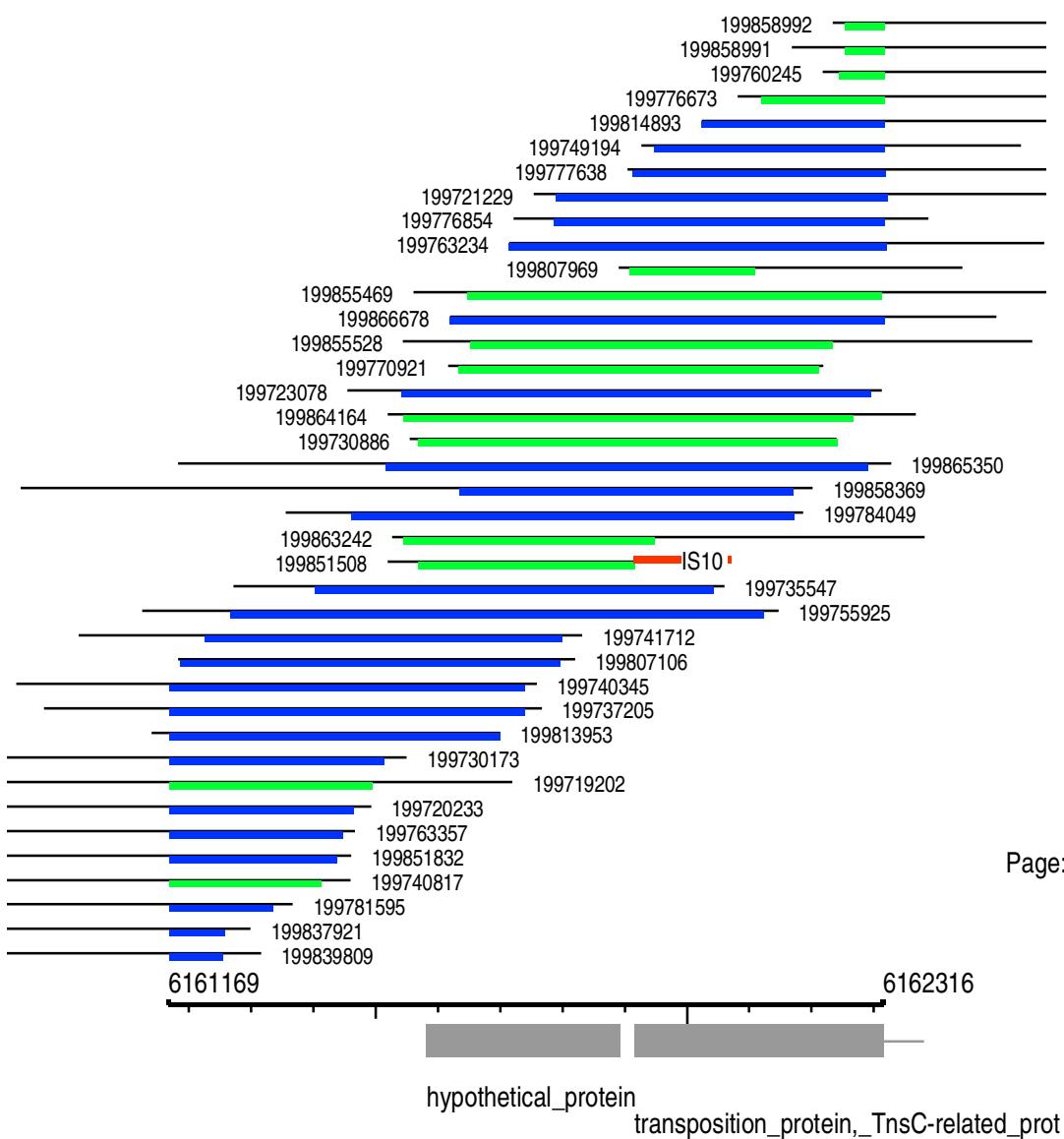


TX160488 *Pseudomonas putida* Kt2440

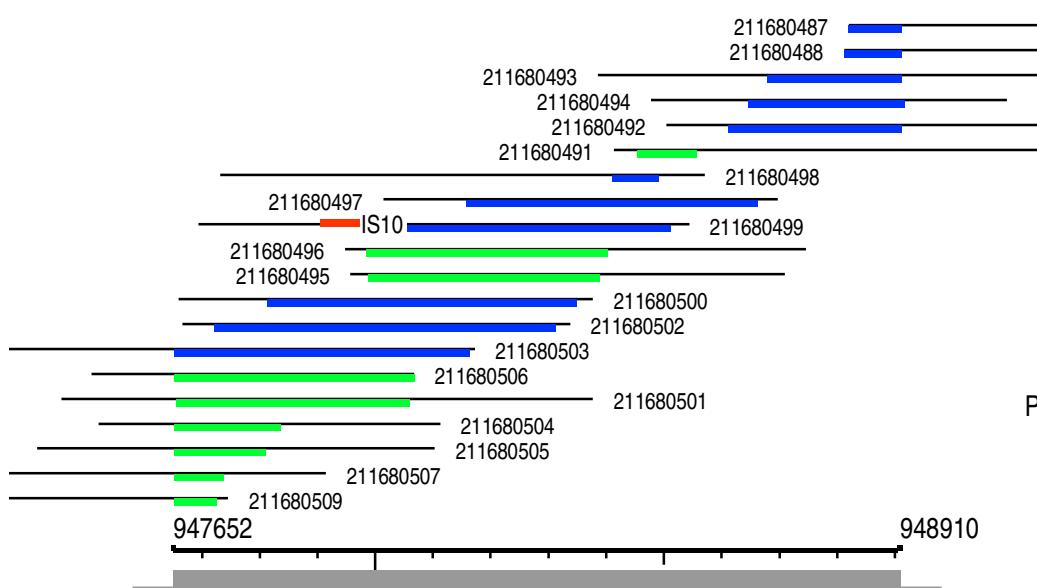


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TX160488 *Pseudomonas putida* kt2440



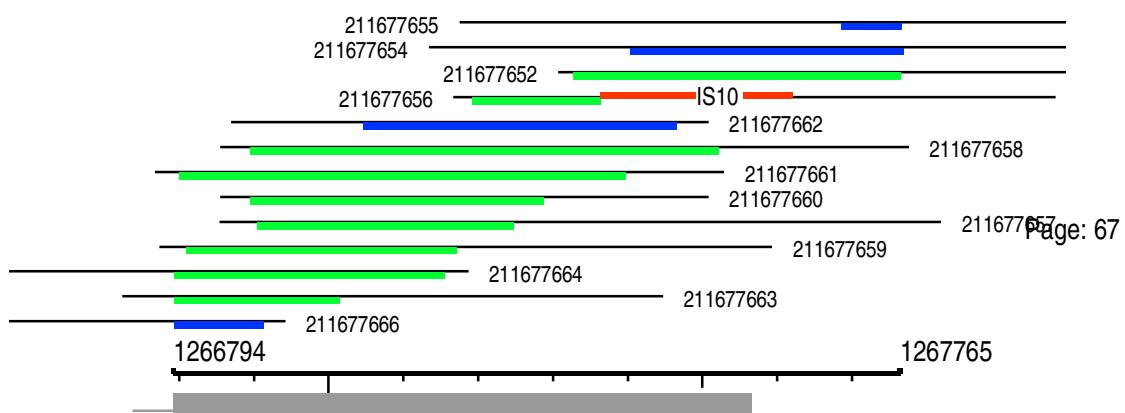
TX160490 Streptococcus pyogenes m1 gas



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DNA_gyrase_A_subunit Best_Blastp_hit=_gb|AAF63266.1|_AF2209

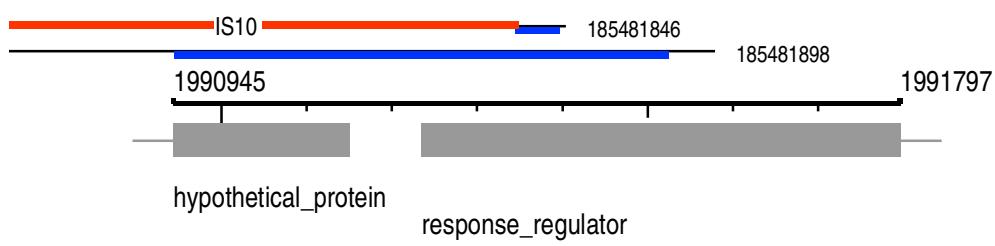
TX160490 Streptococcus pyogenes m1 gas



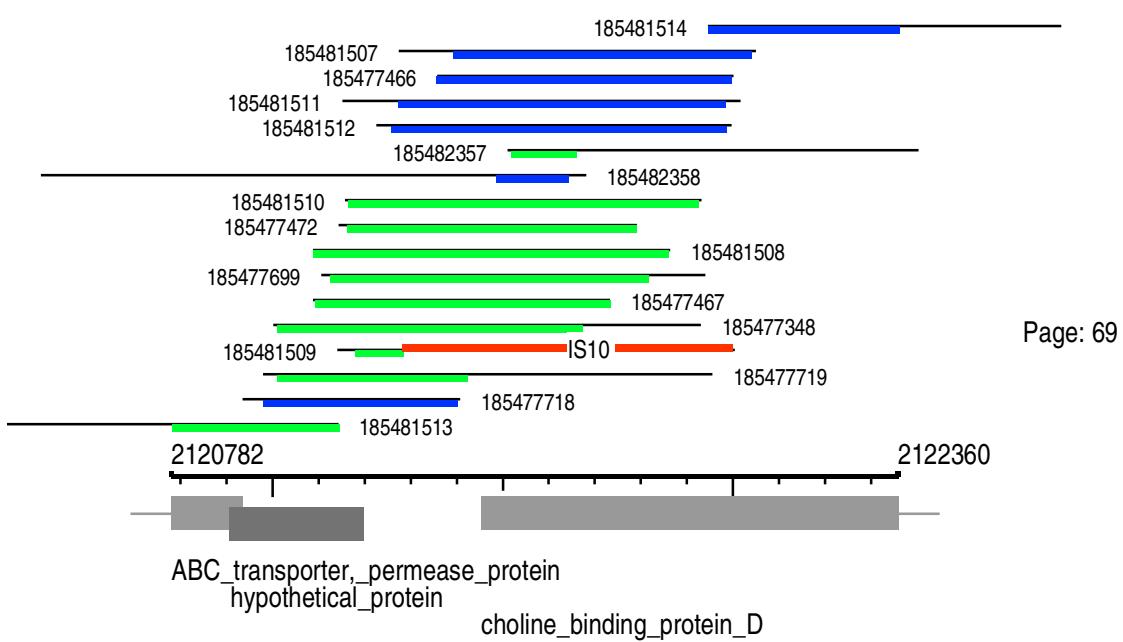
putative_asparagine_synthetase_A Best_Blastp_hit_=_pirlH71309_probable_a

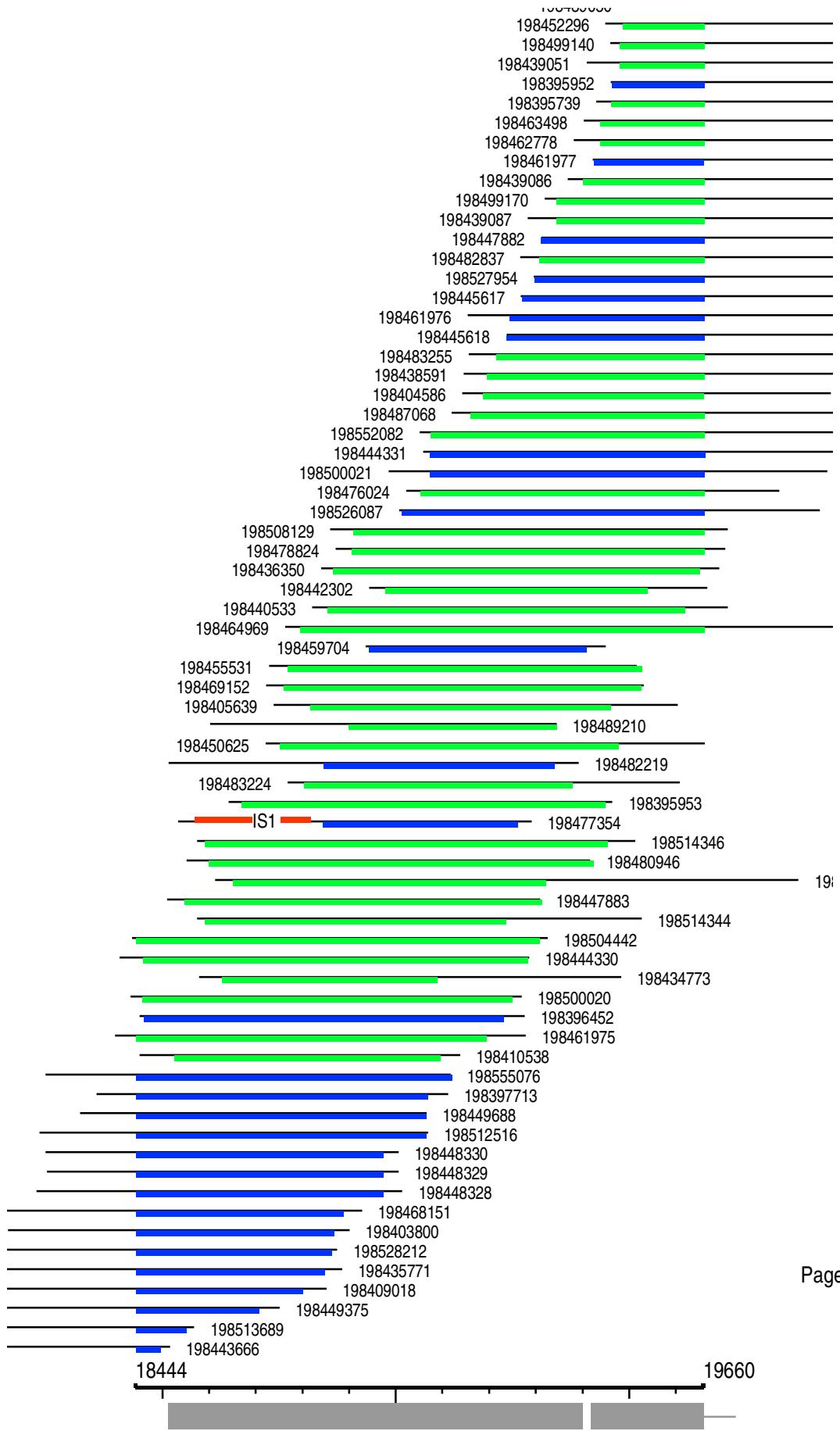
TX170187 Streptococcus pneumoniae tigr4

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TX170187 *Streptococcus pneumoniae* tigr4



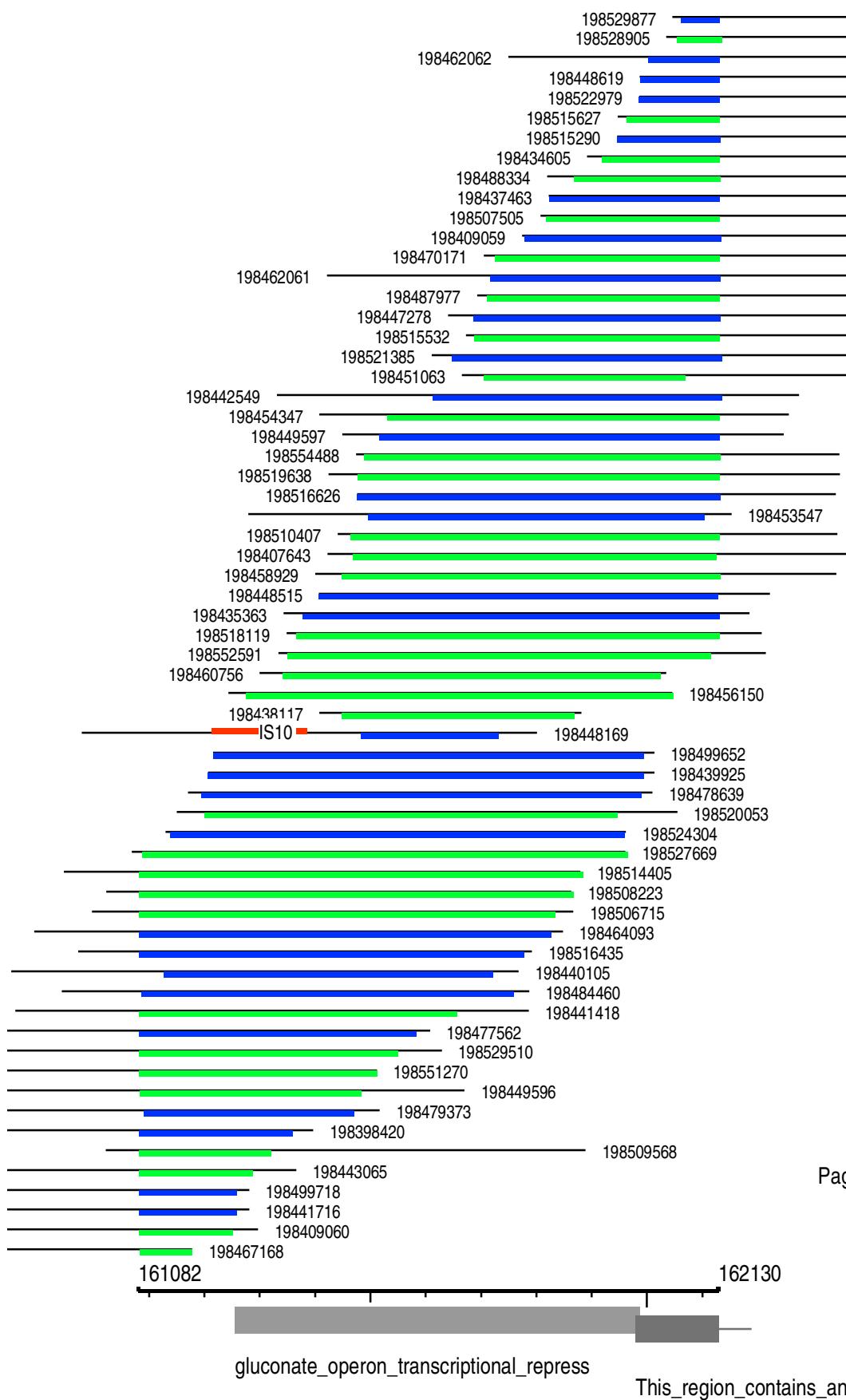


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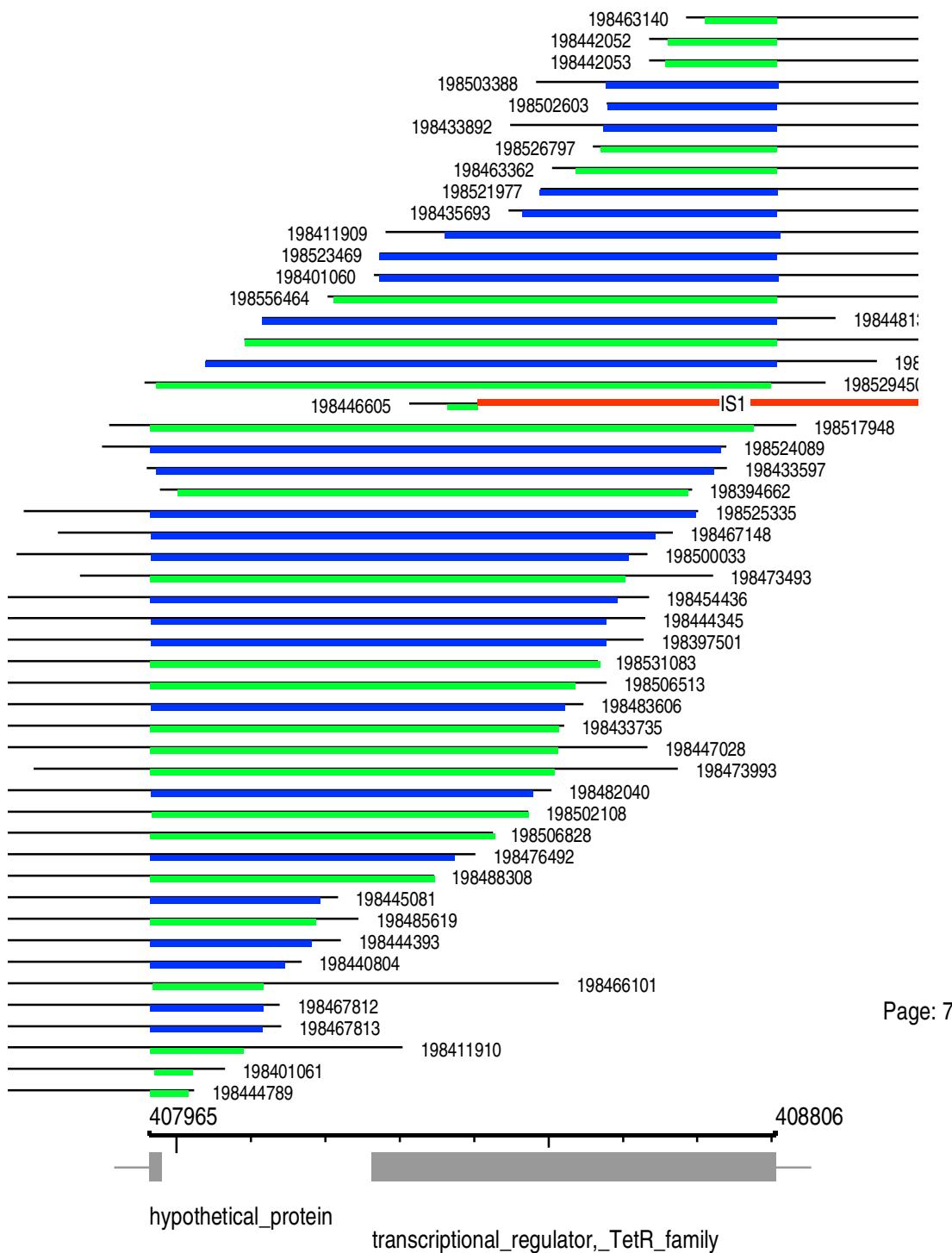
pyridoxine_biosynthesis_protein

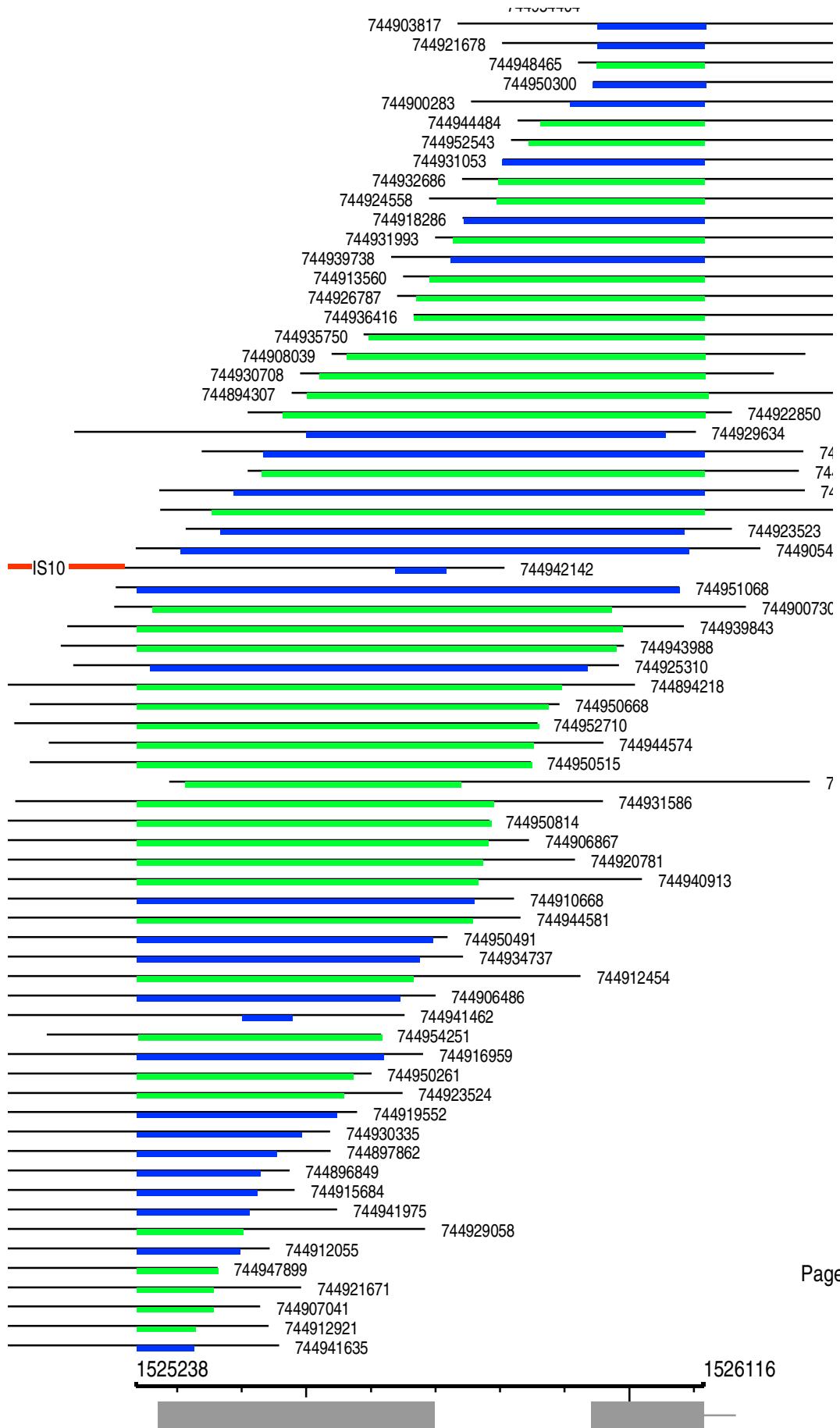
glutamine_amidotransferase,_SNO_family

TX198094 Bacillus anthracis str ames



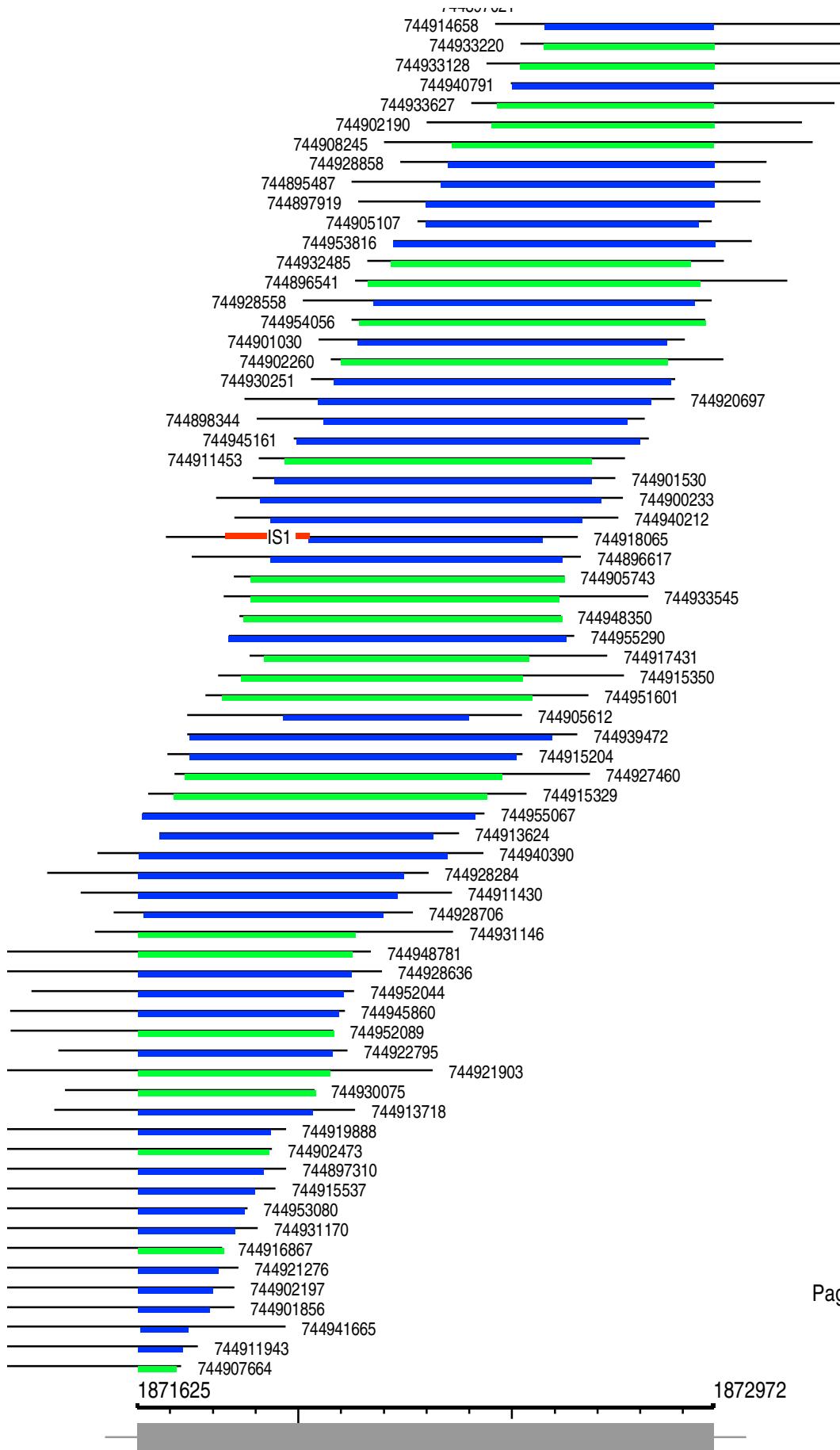
TX198094 *Bacillus anthracis* str ames

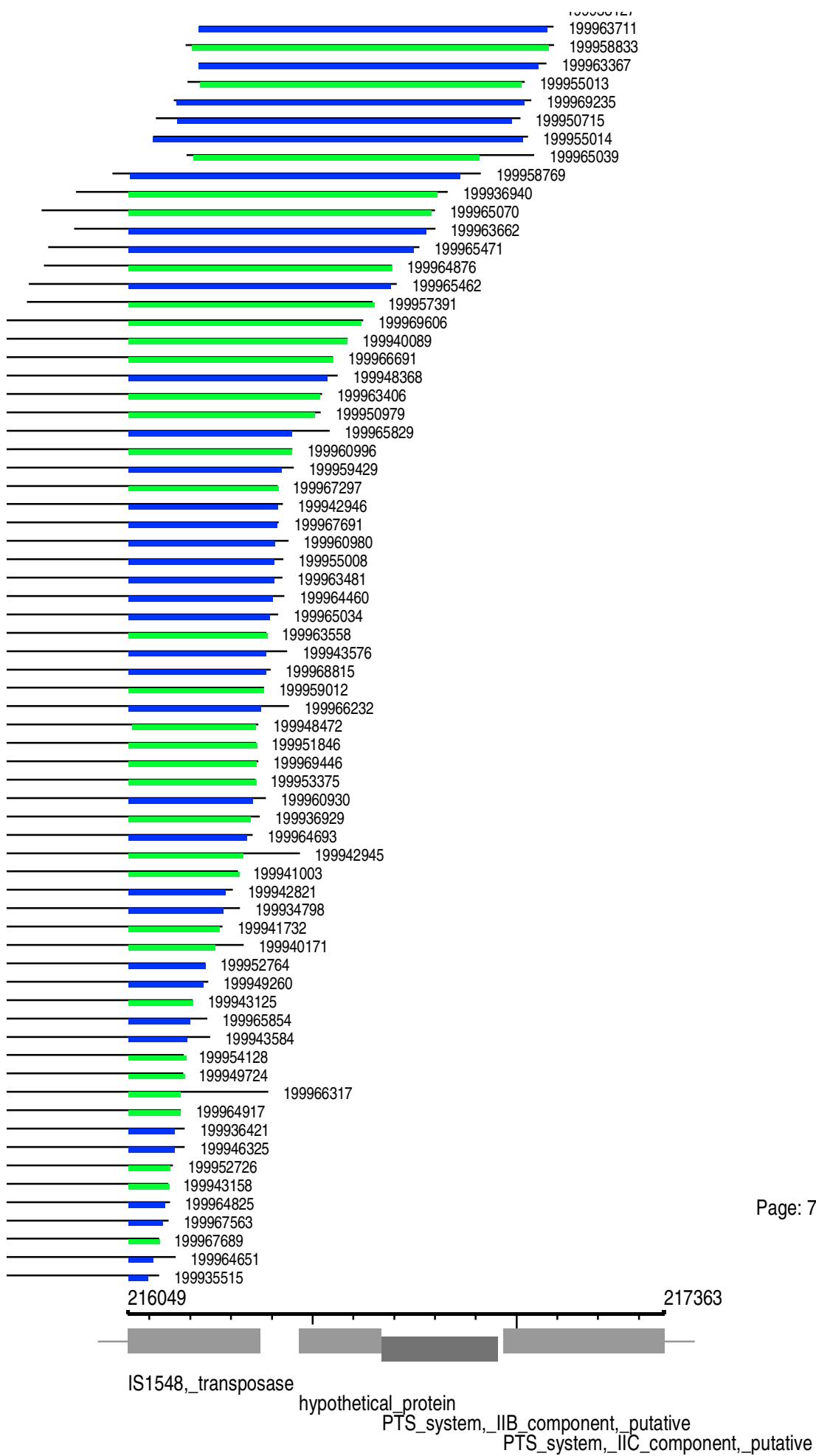




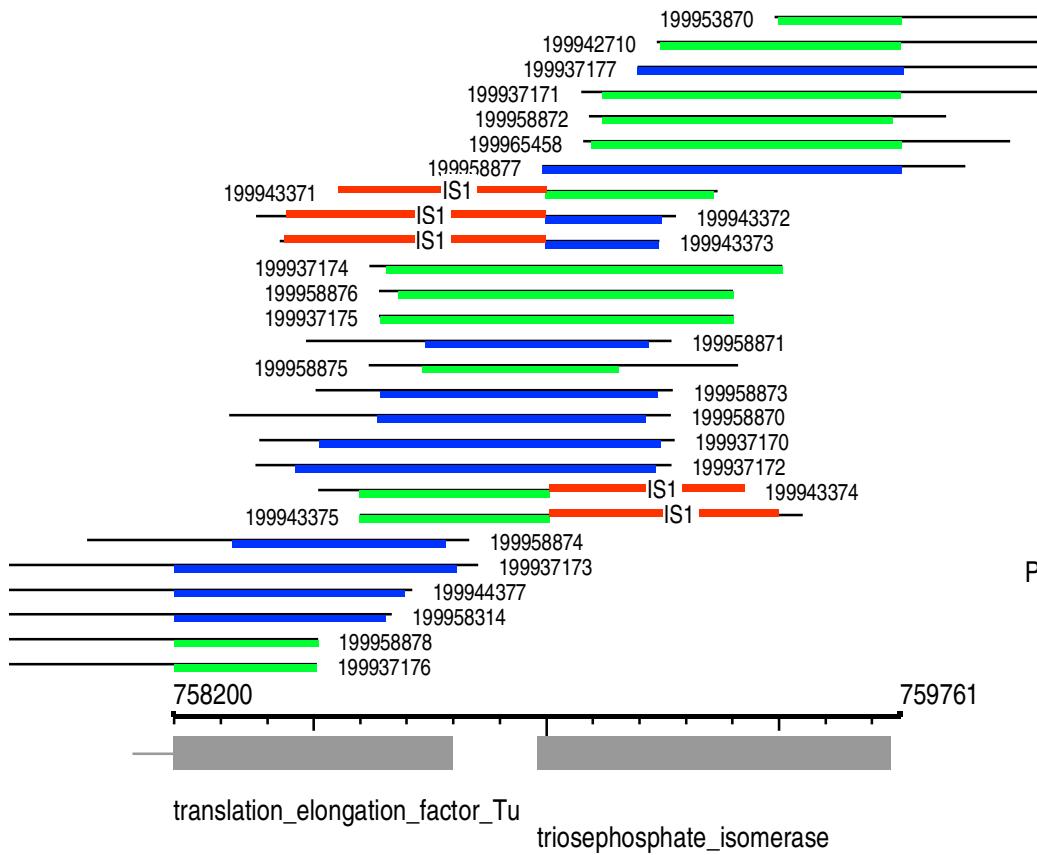
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Haemophilus-specific_protein,_uncharacte



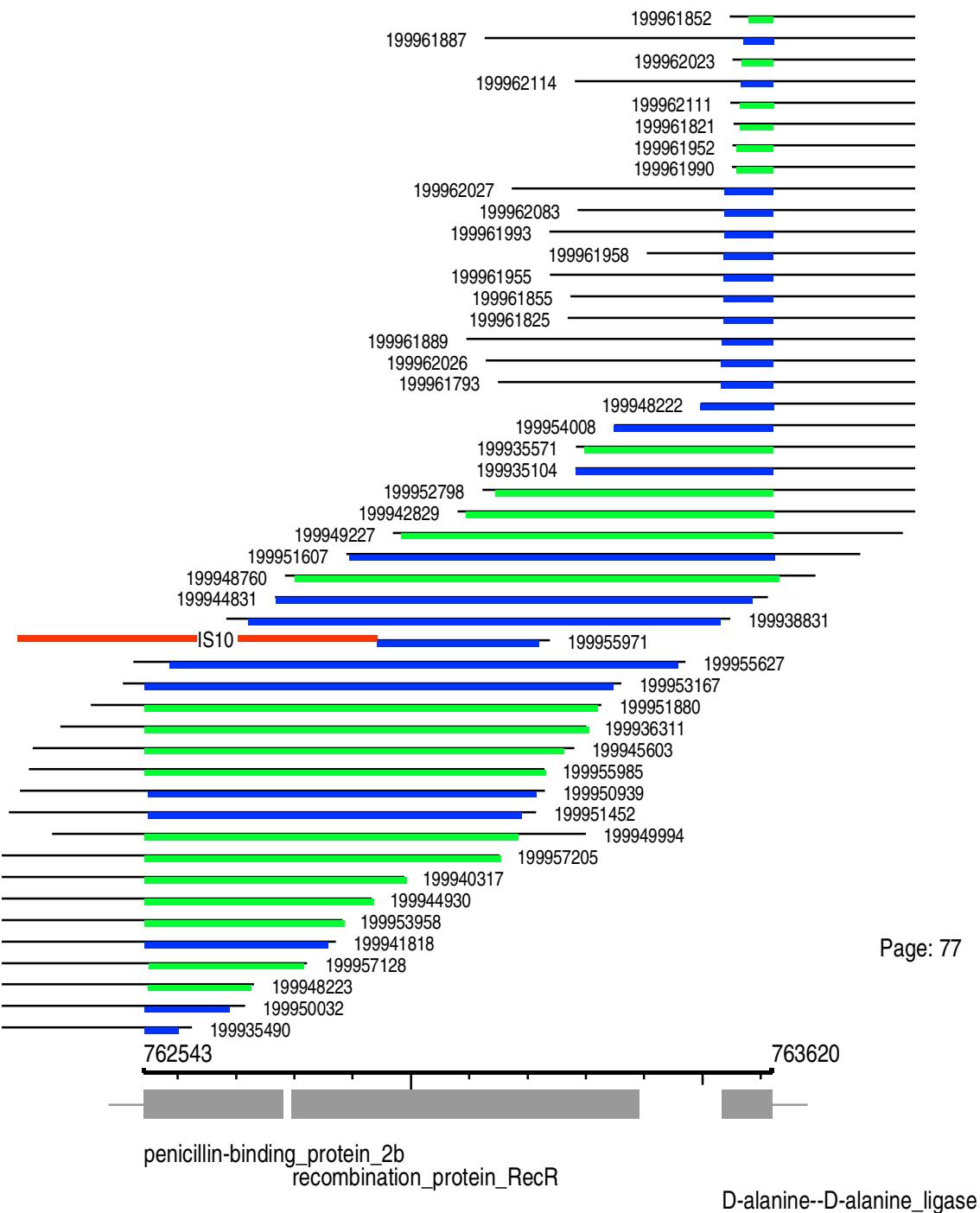


TX208435 Streptococcus agalactiae 2603v r

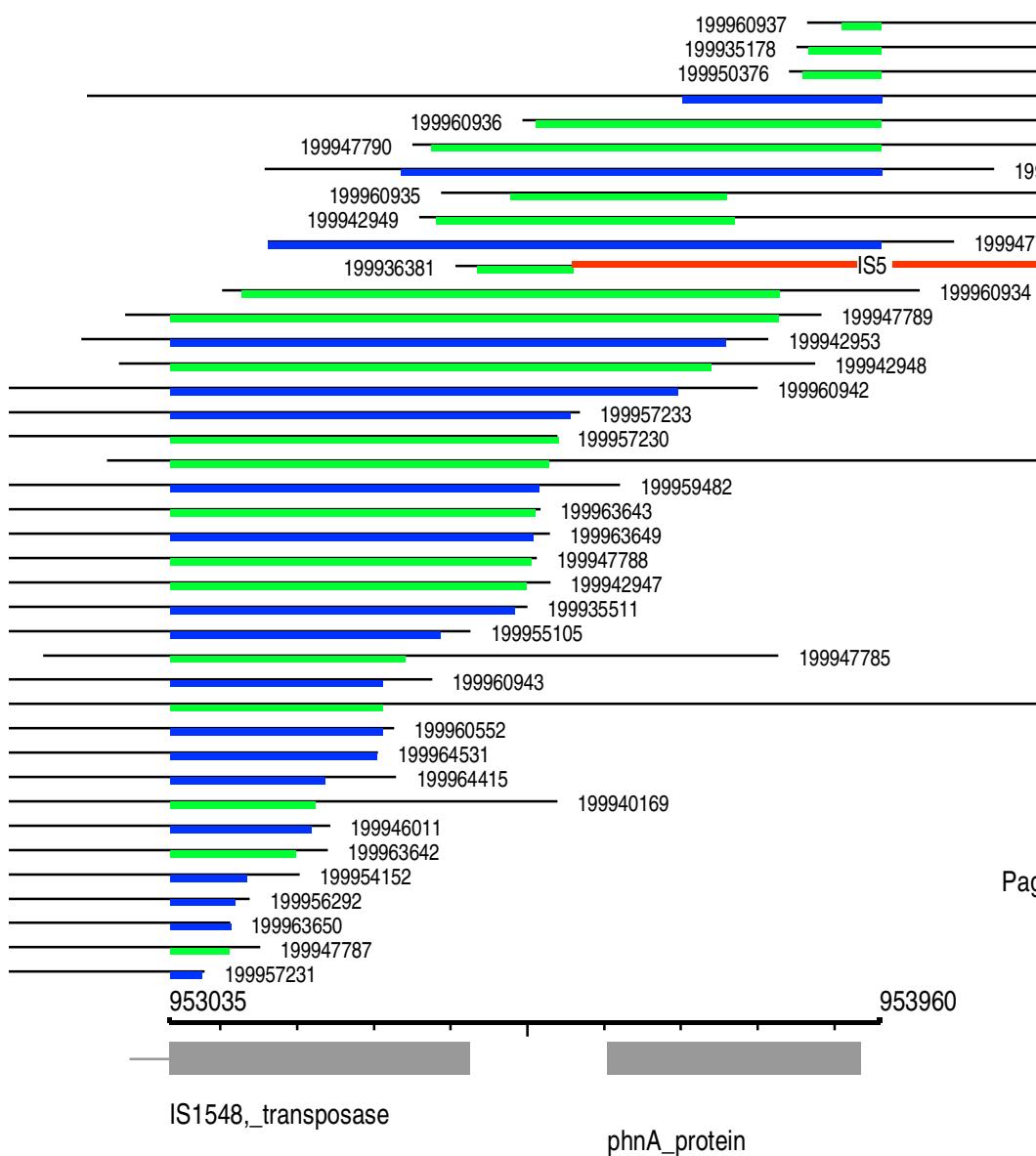


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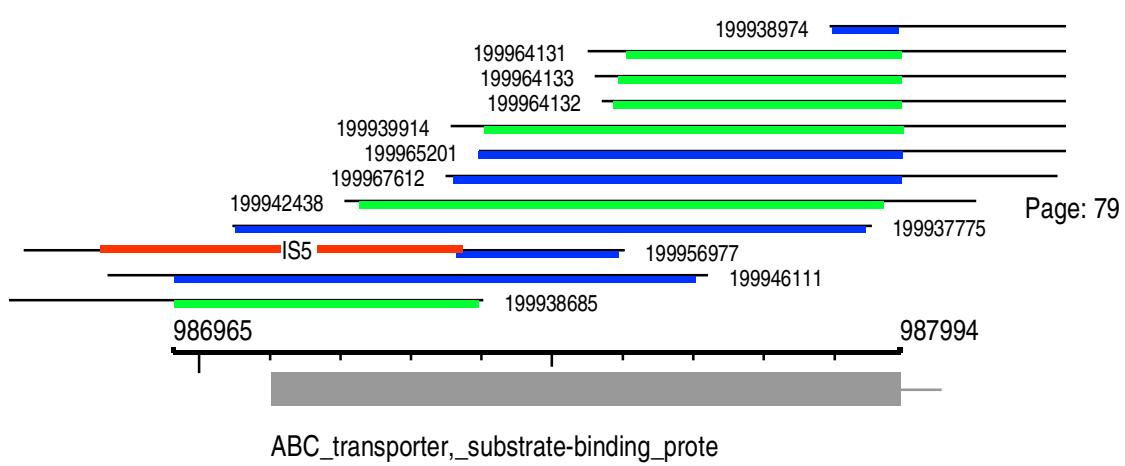
TX208435 Streptococcus agalactiae 2603v r



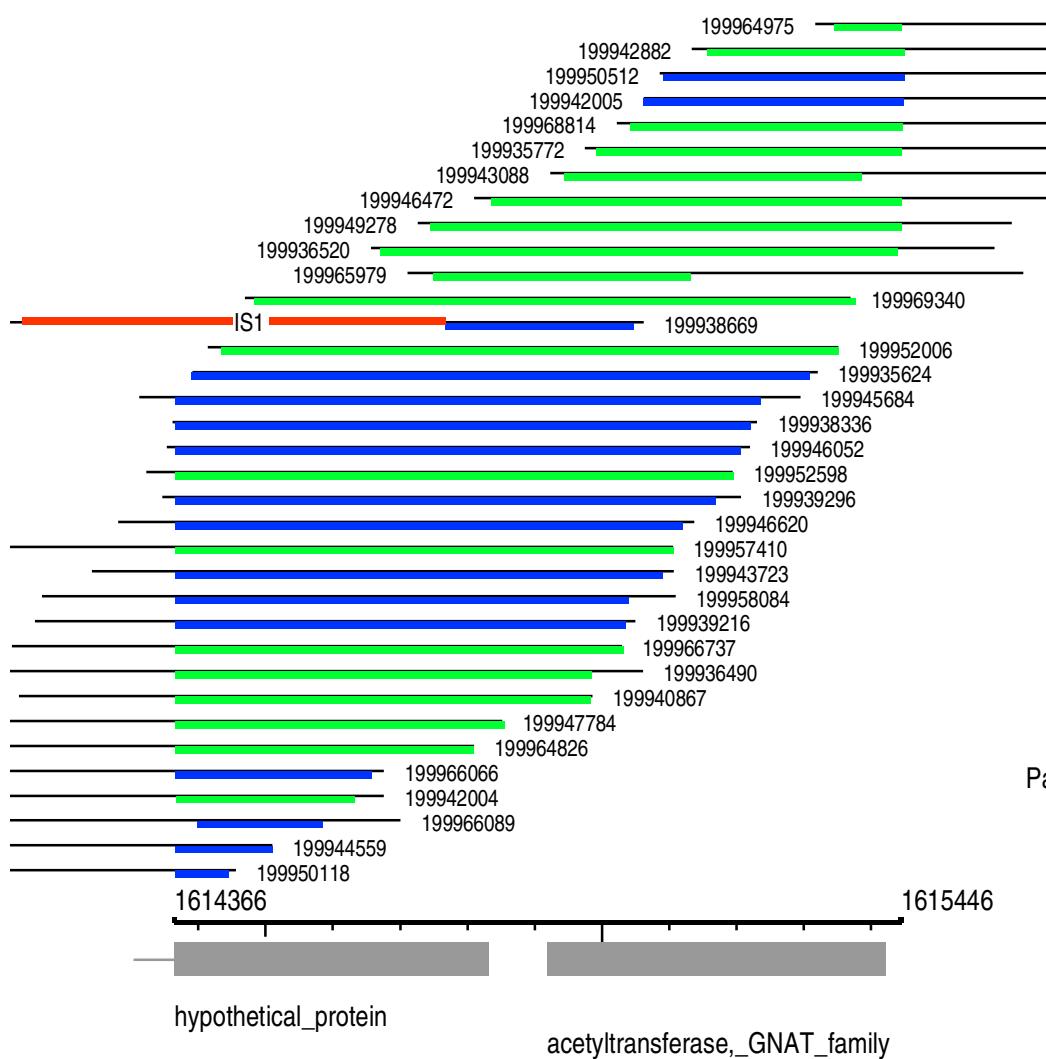
TX208435 *Streptococcus agalactiae* 2603v r



TX208435 Streptococcus agalactiae 2603v r

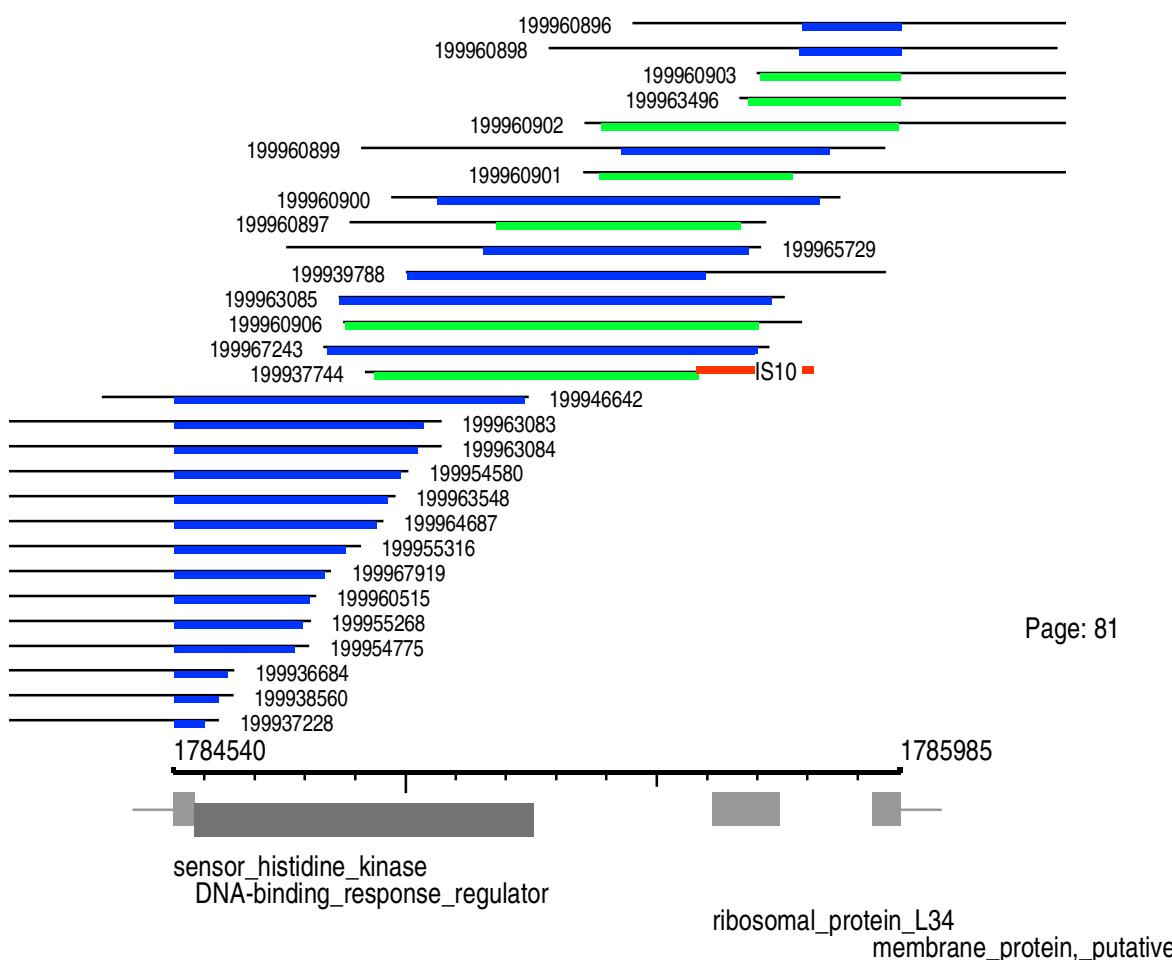


TX208435 Streptococcus agalactiae 2603v r

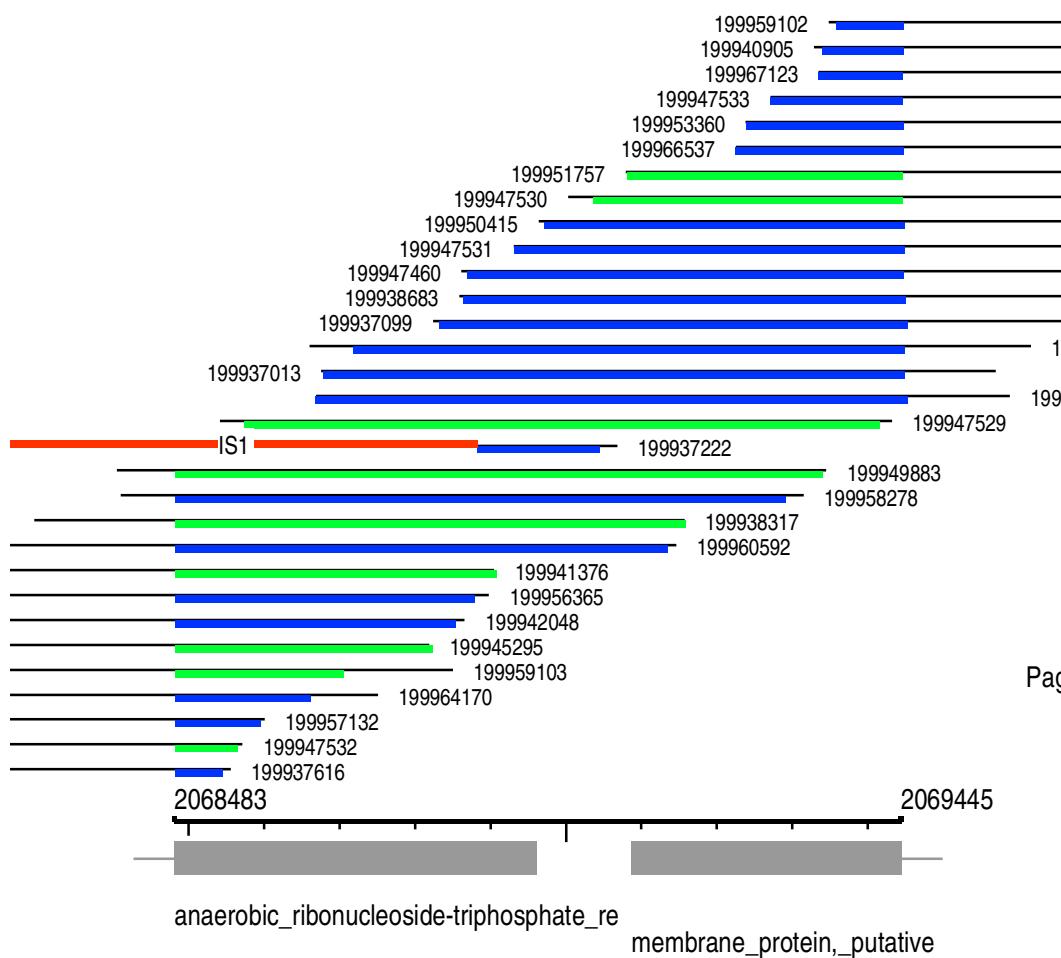


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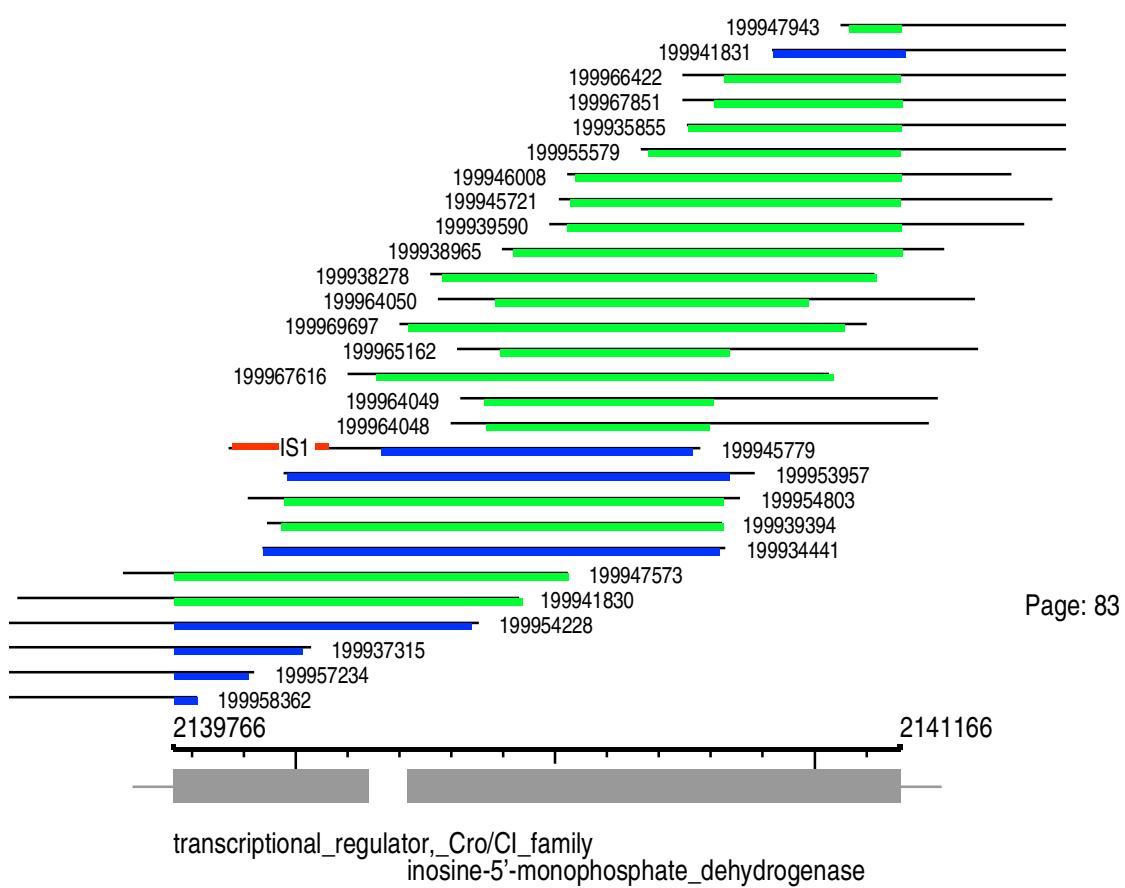
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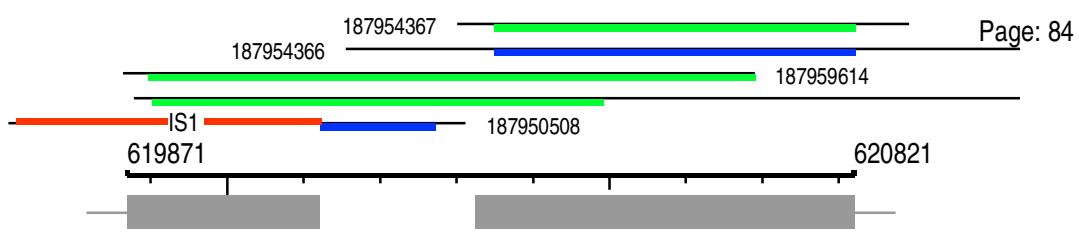
TX208435 Streptococcus agalactiae 2603v r



TX208435 Streptococcus agalactiae 2603v r

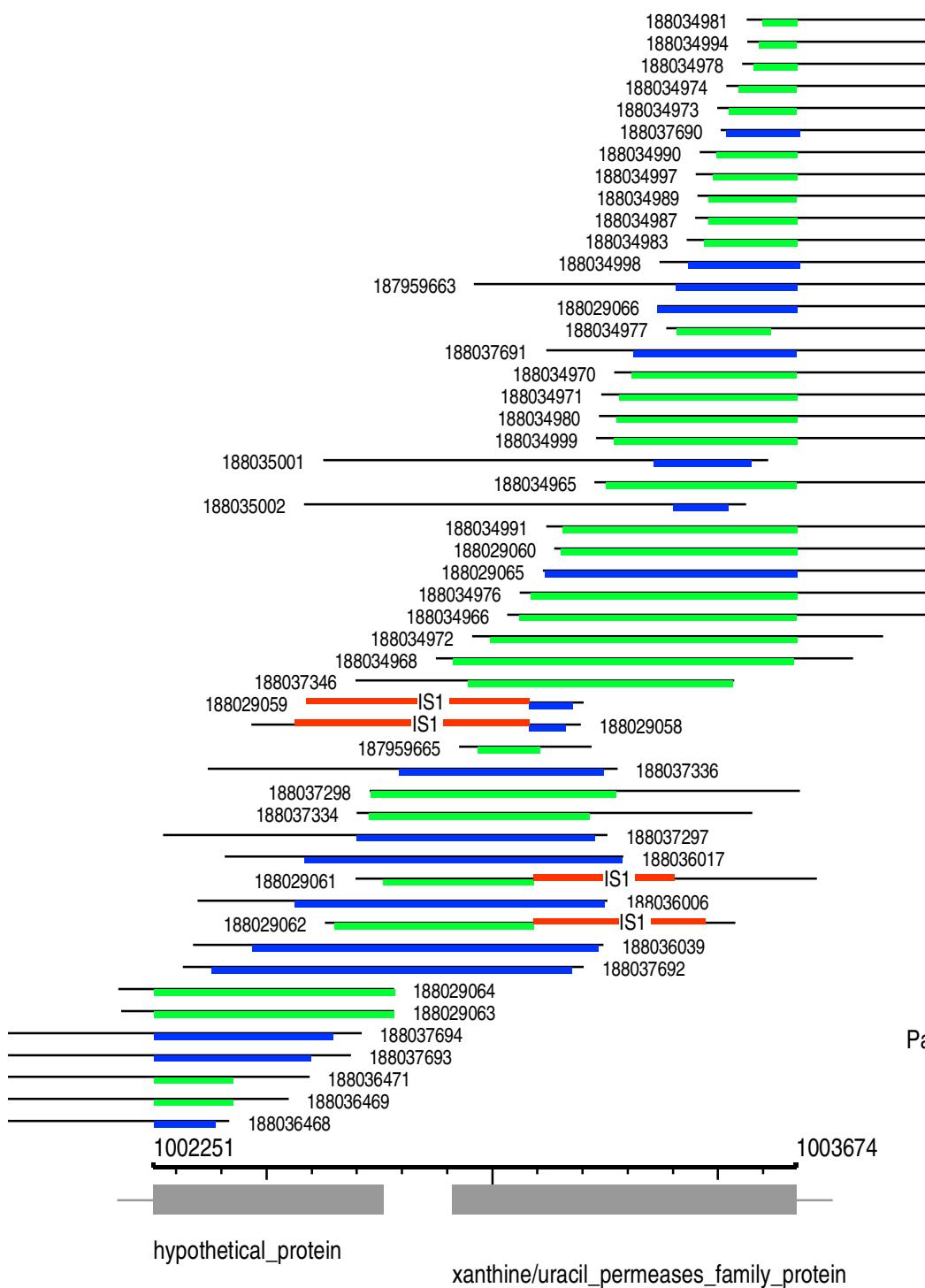


TX226185 Enterococcus faecalis v583



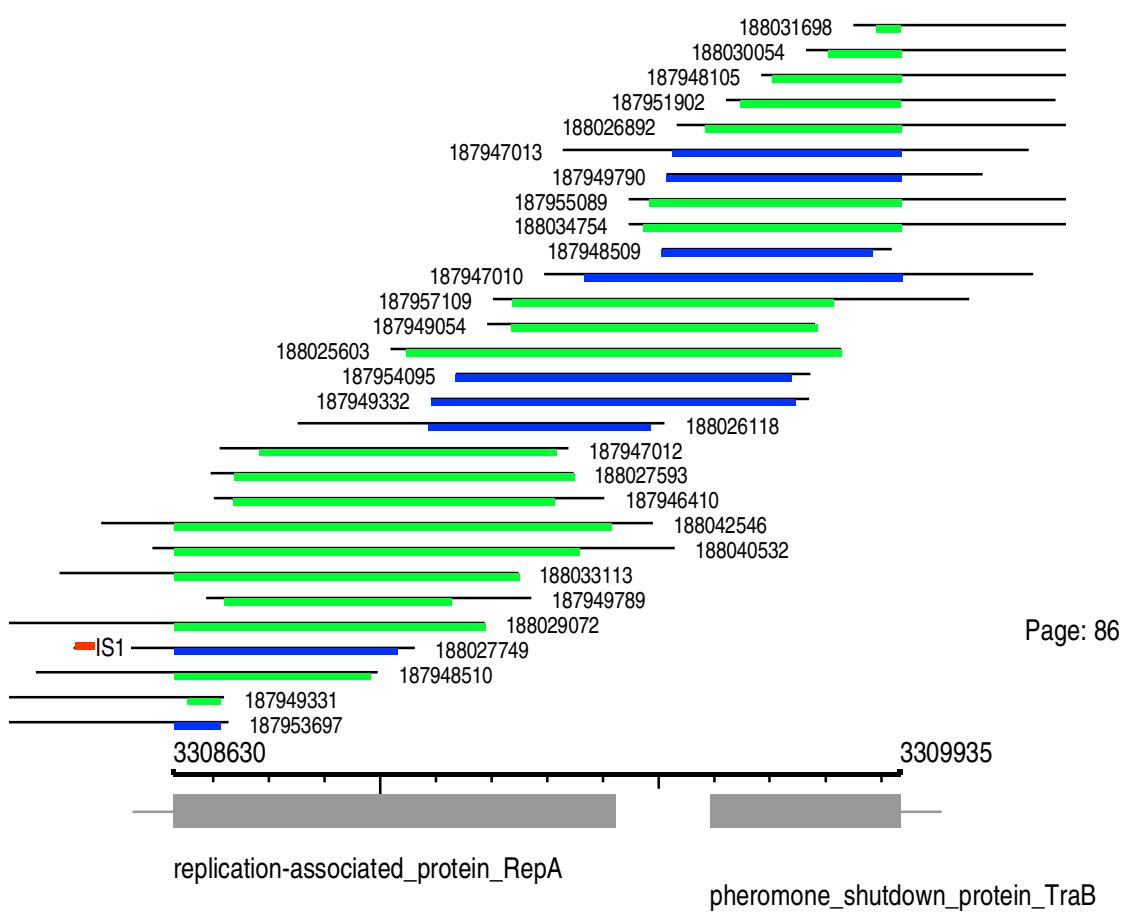
UDP-N-acetylmuramoylalanyl-D-glutamate-- involved_in_cell_wallFormation;_peptido polysaccharide_biosynthesis_family_prote

TX226185 Enterococcus faecalis v583

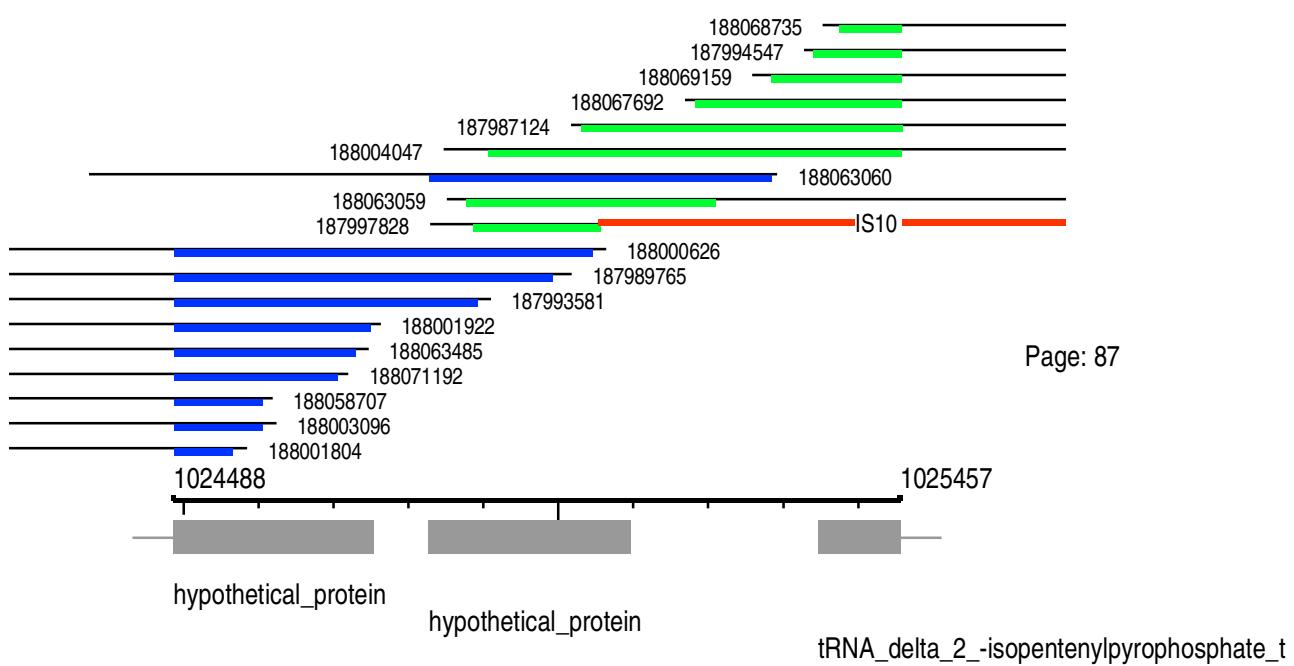


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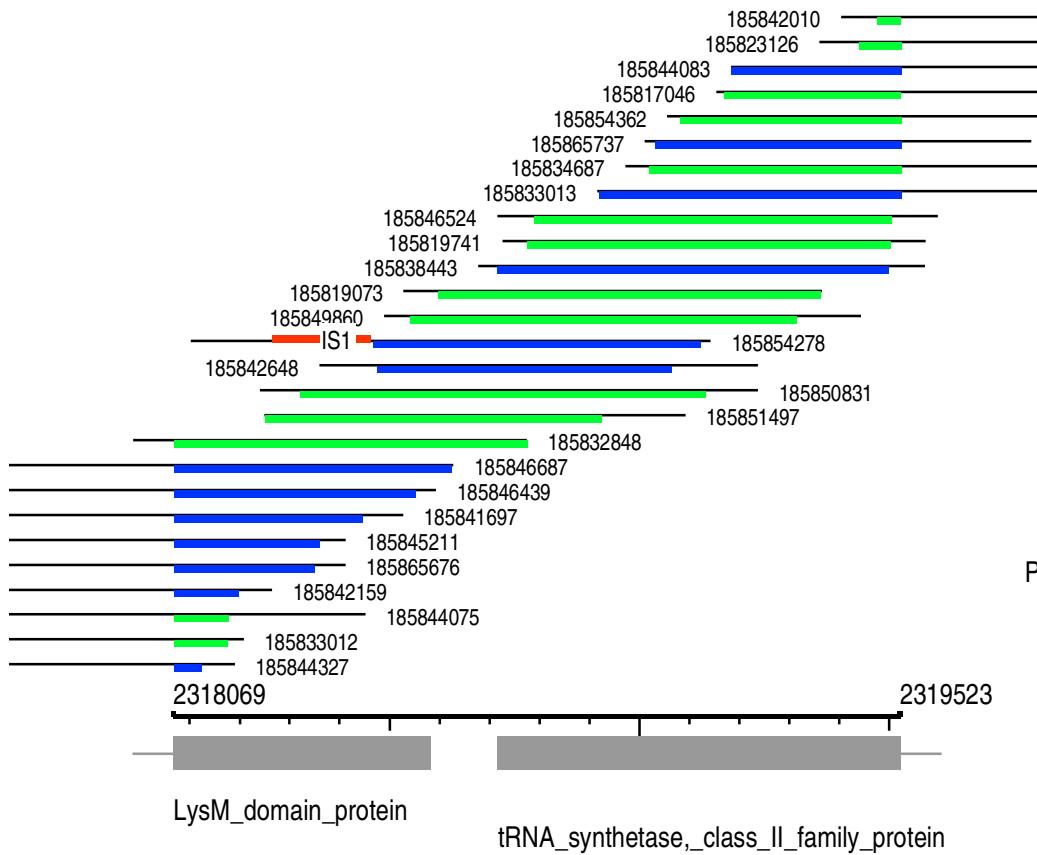
TX226185 Enterococcus faecalis v583



TX227377 *Coxiella burnetii* rsa 493

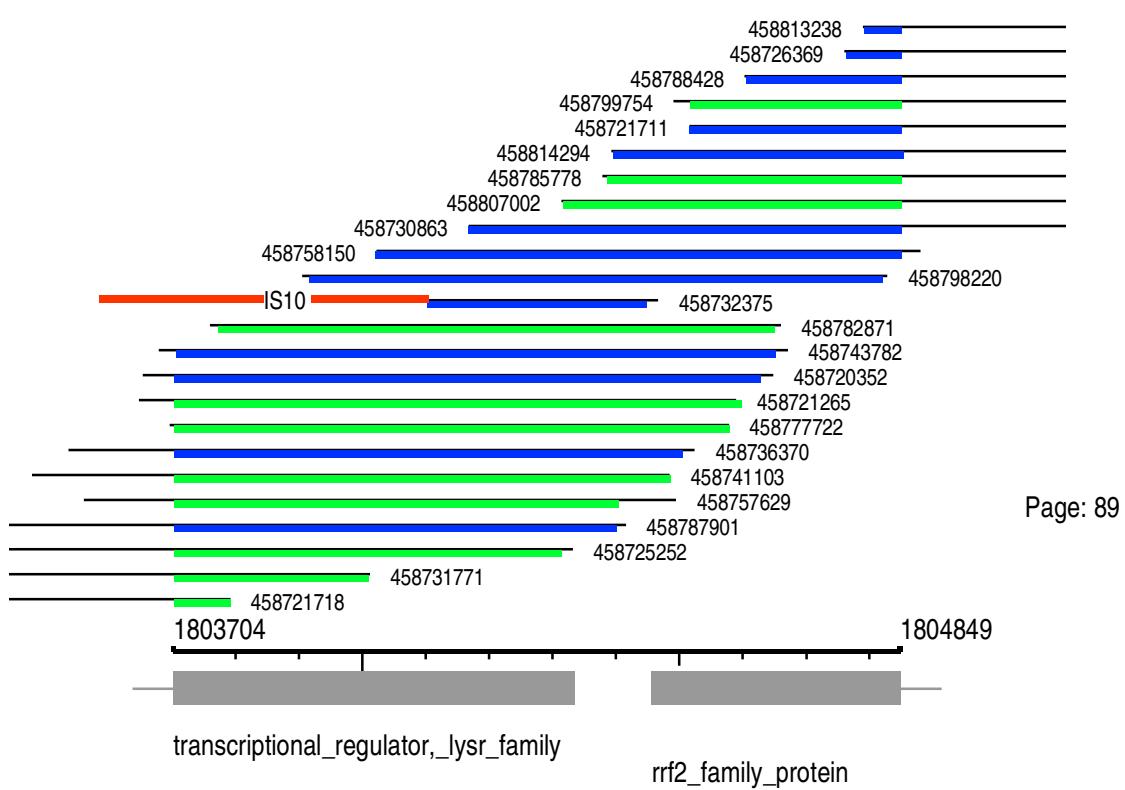


TX243275 *Treponema denticola* atcc 35405

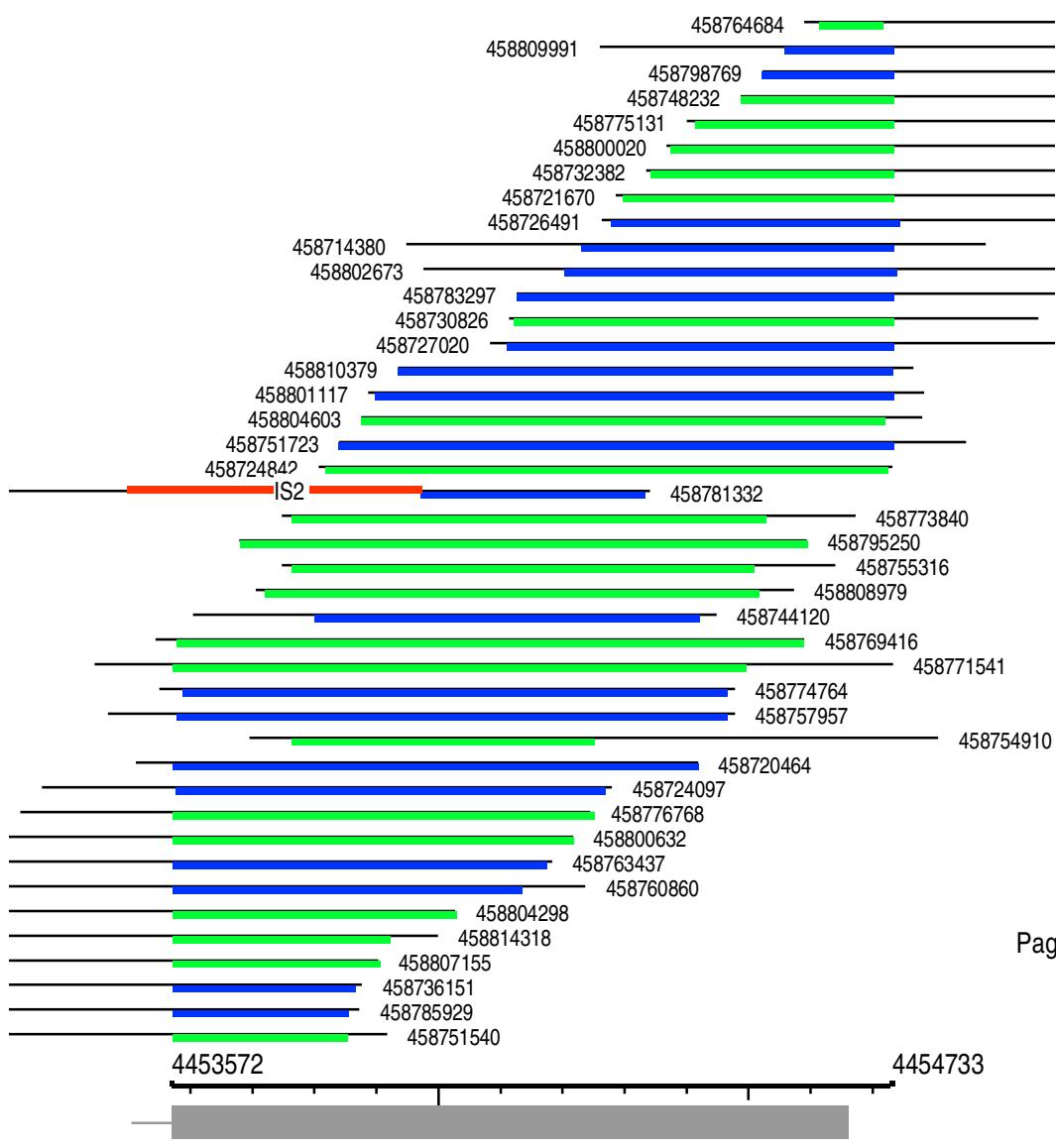


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TX261594 *Bacillus anthracis* str ames 0581



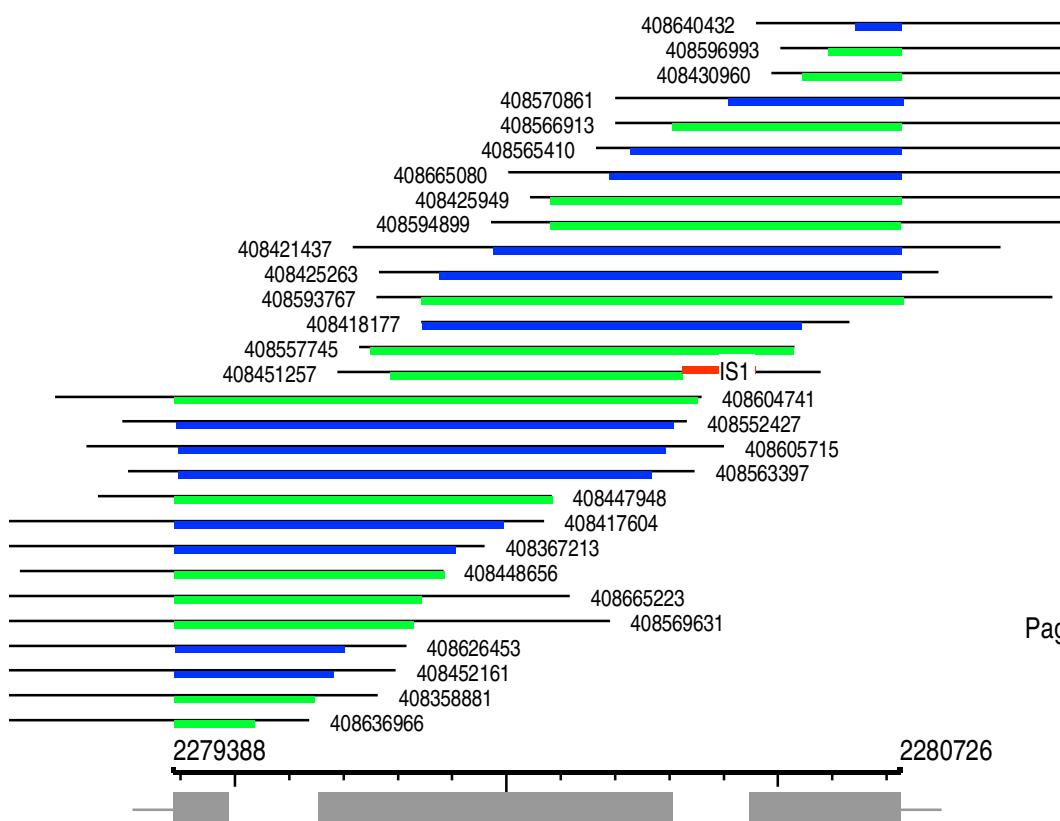
TX261594 *Bacillus anthracis* str ames 0581



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septation_ringFormation_regulator

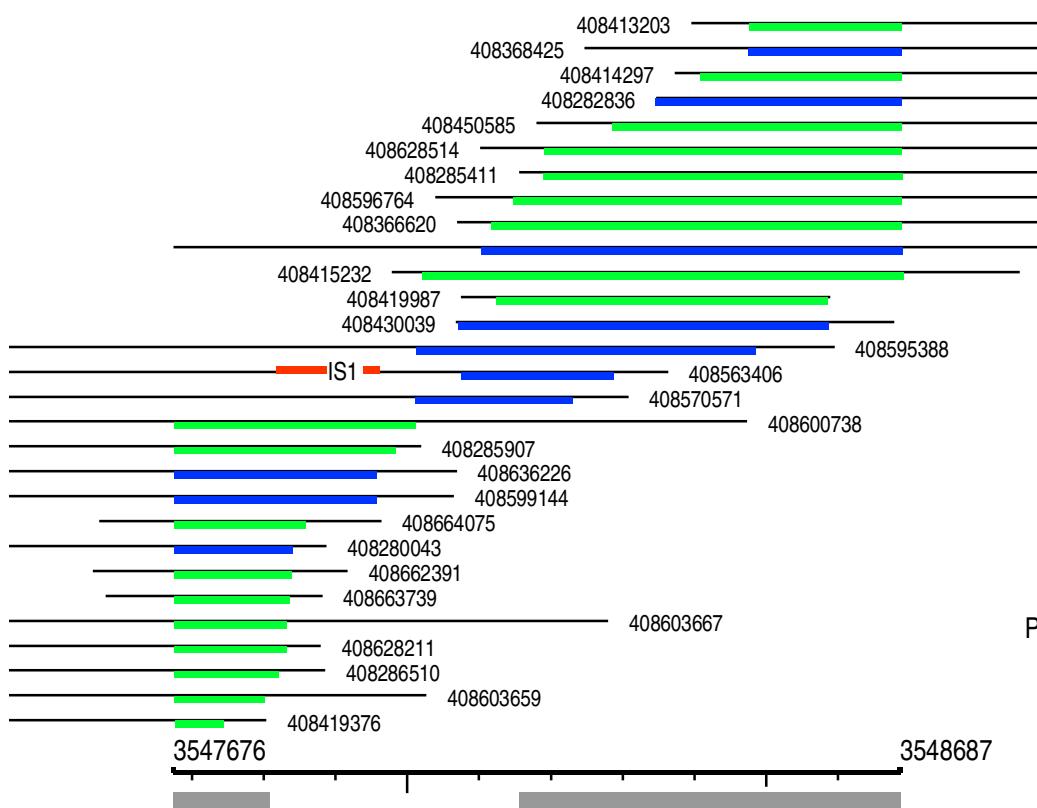
TX269483 Burkholderia cepacia r18194



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ATP-dependent_protease_ATP-binding_subunit_binds_and_unfolds_substrates_as_part_of_ATP-dependent_Clp_protease_proteolytic_s hydrolyzes_proteins_to_small_peptides;_w_trigger_factor_Tig;_RopA;_peptidyl-prolyl_cis/trans_isomerase

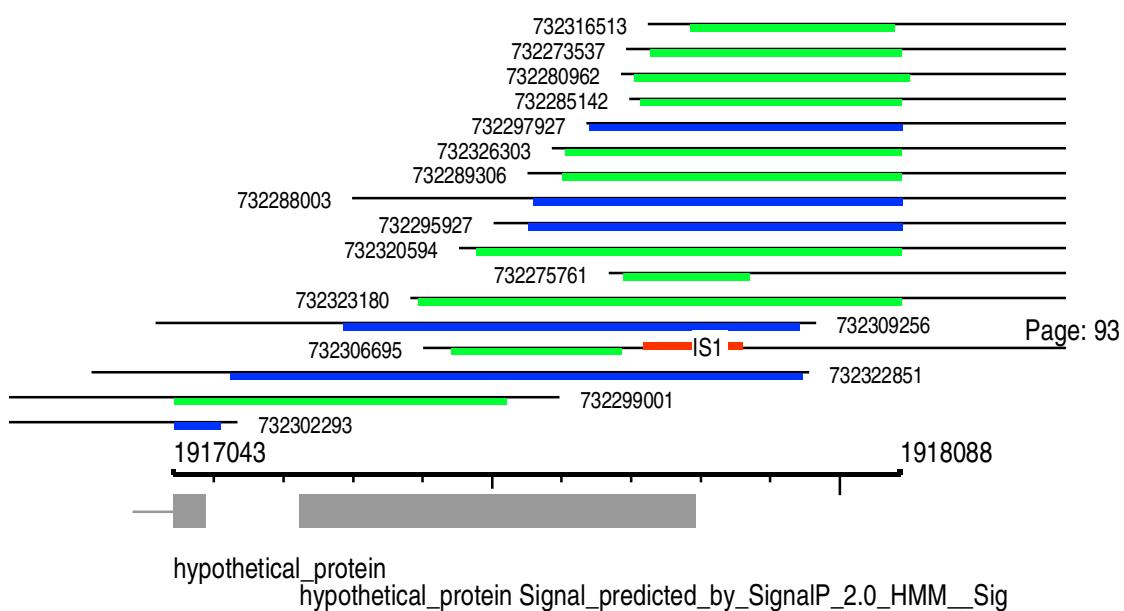
TX269483 Burkholderia cepacia r18194



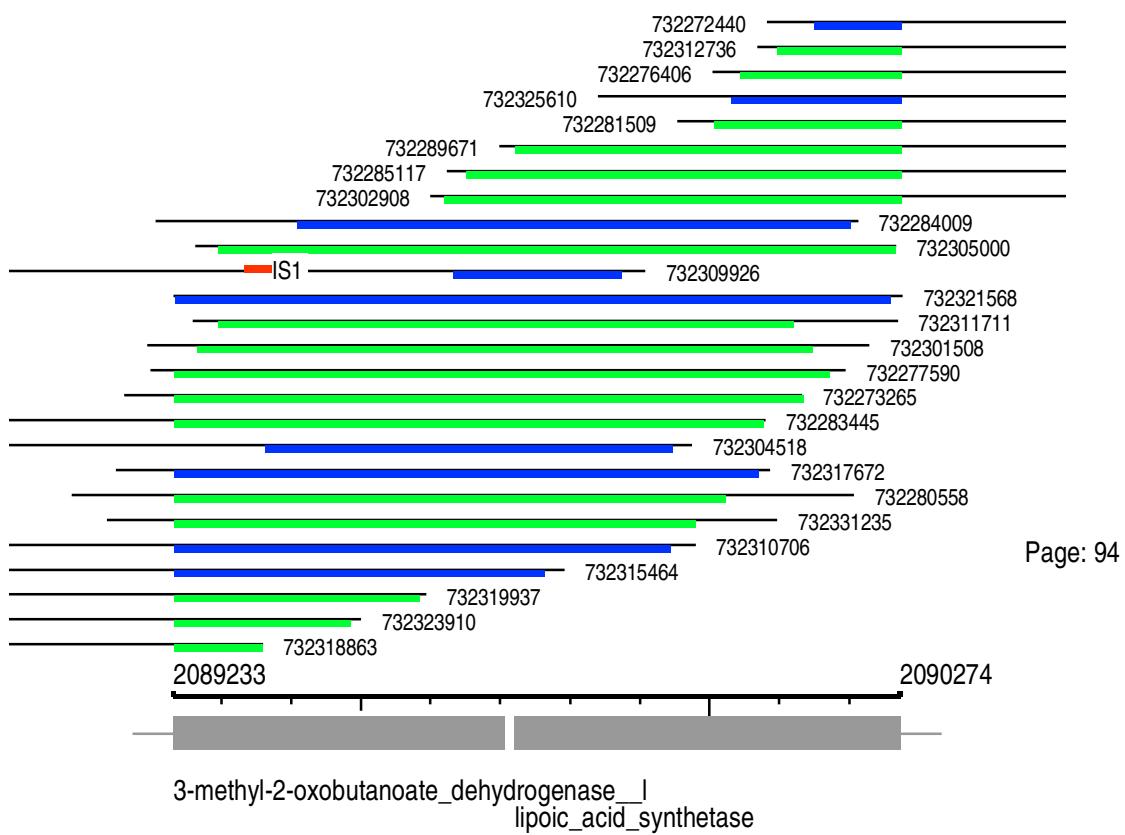
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NAD-dependent_epimerase/dehydratase
Lytic_transglycosylase,_catalytic

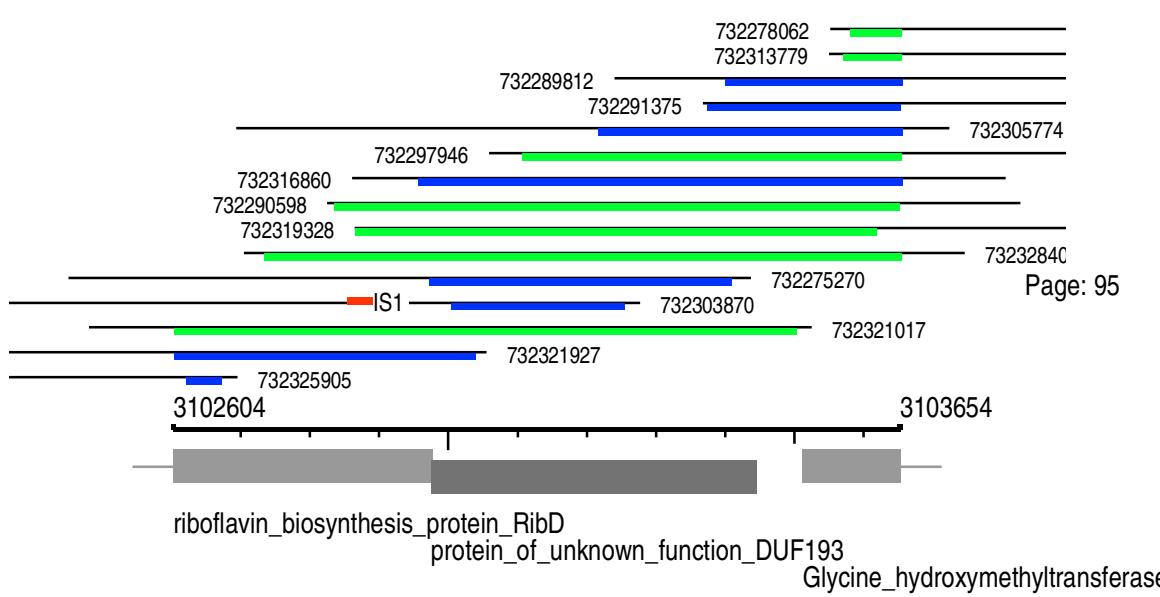
TX290397 *Anaeromyxobacter dehalogenans* 2cp-c



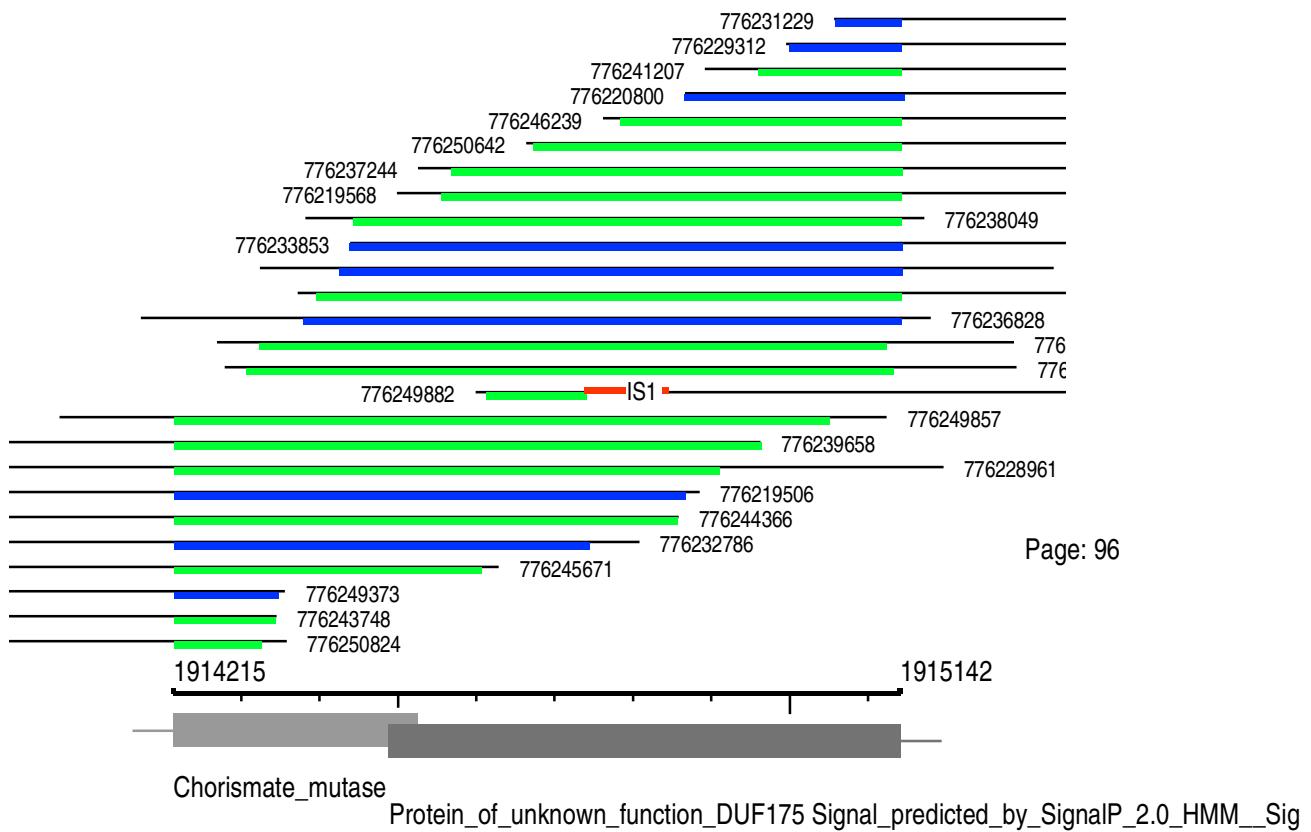
TX290397 Anaeromyxobacter dehalogenans 2cp-c



TX290397 *Anaeromyxobacter dehalogenans* 2cp-c



TX324925 Pelodictyon phaeoclathratiforme bu-1



TX324925 Pelodictyon phaeoclathratiforme bu-1

